Full wwPDB X-ray Structure Validation Report (i)

Mar 6, 2026 – 04:25 AM UTC

PDB ID	:	4V4K / pdb_00004v4k
Title	:	Bacteriophage P22 Portal Protein bound to middle Tail Factor GP4. This file contain the second biological assembly
Authors	:	Olia, A.S.; Cingolani, G.
Deposited on	:	2010-04-19
Resolution	:	3.25 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

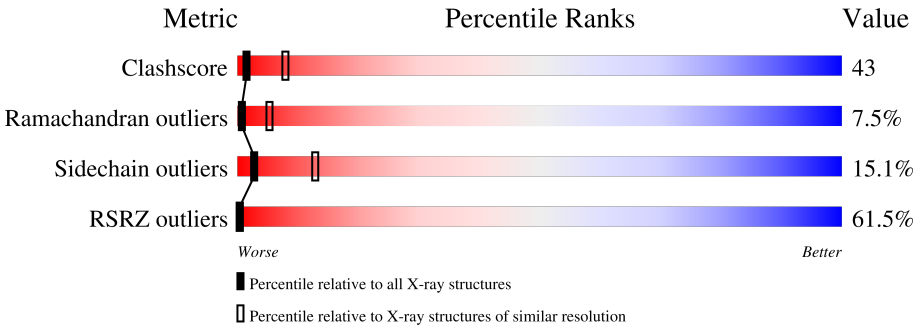
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.25 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	1660 (3.30-3.22)
Ramachandran outliers	187476	1630 (3.30-3.22)
Sidechain outliers	187428	1629 (3.30-3.22)
RSRZ outliers	180081	1605 (3.30-3.22)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	602	62% 37% 44% 12% • 5%
1	B	602	61% 37% 43% 12% • 5%
1	C	602	62% 37% 44% 12% • 5%
1	D	602	58% 37% 43% 13% • 5%
1	E	602	59% 37% 44% 12% • 5%
1	F	602	59% 37% 43% 13% • 5%
1	G	602	60% 37% 44% 13% • 5%

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Mol	Chain	Length	Quality of chain
1	H	602	57% 37% 44% 12% • 5%
1	I	602	63% 38% 43% 12% • 5%
1	J	602	66% 37% 43% 13% • 5%
1	K	602	65% 37% 44% 12% • 5%
1	L	602	65% 37% 44% 12% • 5%
1	M	602	50% 41% 41% 11% • 5%
1	N	602	50% 42% 39% 11% • 5%
1	O	602	52% 41% 41% 11% • 5%
1	P	602	51% 41% 40% 12% • 5%
1	Q	602	53% 41% 41% 11% • 5%
1	R	602	53% 41% 41% 11% • 5%
1	S	602	47% 41% 41% 11% • 5%
1	T	602	50% 42% 40% 11% • 5%
1	U	602	56% 40% 41% 12% • 5%
1	V	602	52% 42% 40% 11% • 5%
1	W	602	52% 41% 40% 12% • 5%
1	X	602	53% 41% 41% 11% • 5%
2	Y	166	60% 37% 37% 12% • 12%
2	Z	166	61% 37% 37% 12% • 12%
2	a	166	52% 36% 37% 12% • 12%
2	b	166	57% 37% 37% 11% • 12%
2	c	166	66% 37% 37% 11% • 12%
2	d	166	64% 38% 34% 13% • 12%
2	e	166	55% 39% 35% 12% • 12%
2	f	166	66% 36% 37% 12% • 12%

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Mol	Chain	Length	Quality of chain
2	g	166	61% 37% 37% 12% 12%
2	h	166	61% 36% 36% 13% 12%
2	i	166	64% 37% 37% 11% 12%
2	j	166	62% 35% 37% 13% 12%
2	k	166	45% 40% 39% 7% 13%
2	l	166	51% 39% 40% 7% 13%
2	m	166	45% 42% 37% 7% 13%
2	n	166	53% 39% 41% 6% 13%
2	o	166	51% 39% 40% 7% 13%
2	p	166	46% 42% 37% 7% 13%
2	q	166	47% 39% 40% 7% 13%
2	r	166	43% 40% 39% 7% 13%
2	s	166	38% 38% 42% 7% 13%
2	t	166	40% 40% 40% 7% 13%
2	u	166	38% 38% 40% 8% 13%
2	v	166	45% 40% 39% 7% 13%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 135120 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called PORTAL PROTEIN.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	M	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	N	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	O	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	P	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	Q	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	R	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	S	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	T	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	U	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	V	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	W	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	X	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	A	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	B	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	C	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	D	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	E	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	F	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	G	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	H	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	I	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	J	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	K	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	L	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			

- Molecule 2 is a protein called PACKAGED DNA STABILIZATION PROTEIN GP4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	k	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	l	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	m	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	n	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	o	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	p	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	q	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	r	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	s	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	t	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	u	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	v	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	Y	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	Z	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	a	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	b	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	c	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	d	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	e	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	f	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	g	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	h	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	i	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	j	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	141	PRO	ALA	engineered mutation	UNP P26746
l	141	PRO	ALA	engineered mutation	UNP P26746
m	141	PRO	ALA	engineered mutation	UNP P26746
n	141	PRO	ALA	engineered mutation	UNP P26746
o	141	PRO	ALA	engineered mutation	UNP P26746
p	141	PRO	ALA	engineered mutation	UNP P26746
q	141	PRO	ALA	engineered mutation	UNP P26746
r	141	PRO	ALA	engineered mutation	UNP P26746
s	141	PRO	ALA	engineered mutation	UNP P26746
t	141	PRO	ALA	engineered mutation	UNP P26746
u	141	PRO	ALA	engineered mutation	UNP P26746
v	141	PRO	ALA	engineered mutation	UNP P26746
Y	150	PRO	ALA	engineered mutation	UNP P26746

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Chain	Residue	Modelled	Actual	Comment	Reference
Z	150	PRO	ALA	engineered mutation	UNP P26746
a	150	PRO	ALA	engineered mutation	UNP P26746
b	150	PRO	ALA	engineered mutation	UNP P26746
c	150	PRO	ALA	engineered mutation	UNP P26746
d	150	PRO	ALA	engineered mutation	UNP P26746
e	150	PRO	ALA	engineered mutation	UNP P26746
f	150	PRO	ALA	engineered mutation	UNP P26746
g	150	PRO	ALA	engineered mutation	UNP P26746
h	150	PRO	ALA	engineered mutation	UNP P26746
i	150	PRO	ALA	engineered mutation	UNP P26746
j	150	PRO	ALA	engineered mutation	UNP P26746

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	M	21	Total O 21 21	0	0
3	N	21	Total O 21 21	0	0
3	O	21	Total O 21 21	0	0
3	P	21	Total O 21 21	0	0
3	Q	21	Total O 21 21	0	0
3	R	21	Total O 21 21	0	0
3	S	21	Total O 21 21	0	0
3	T	21	Total O 21 21	0	0
3	U	21	Total O 21 21	0	0
3	V	21	Total O 21 21	0	0
3	W	21	Total O 21 21	0	0
3	X	21	Total O 21 21	0	0
3	A	22	Total O 22 22	0	0
3	B	22	Total O 22 22	0	0

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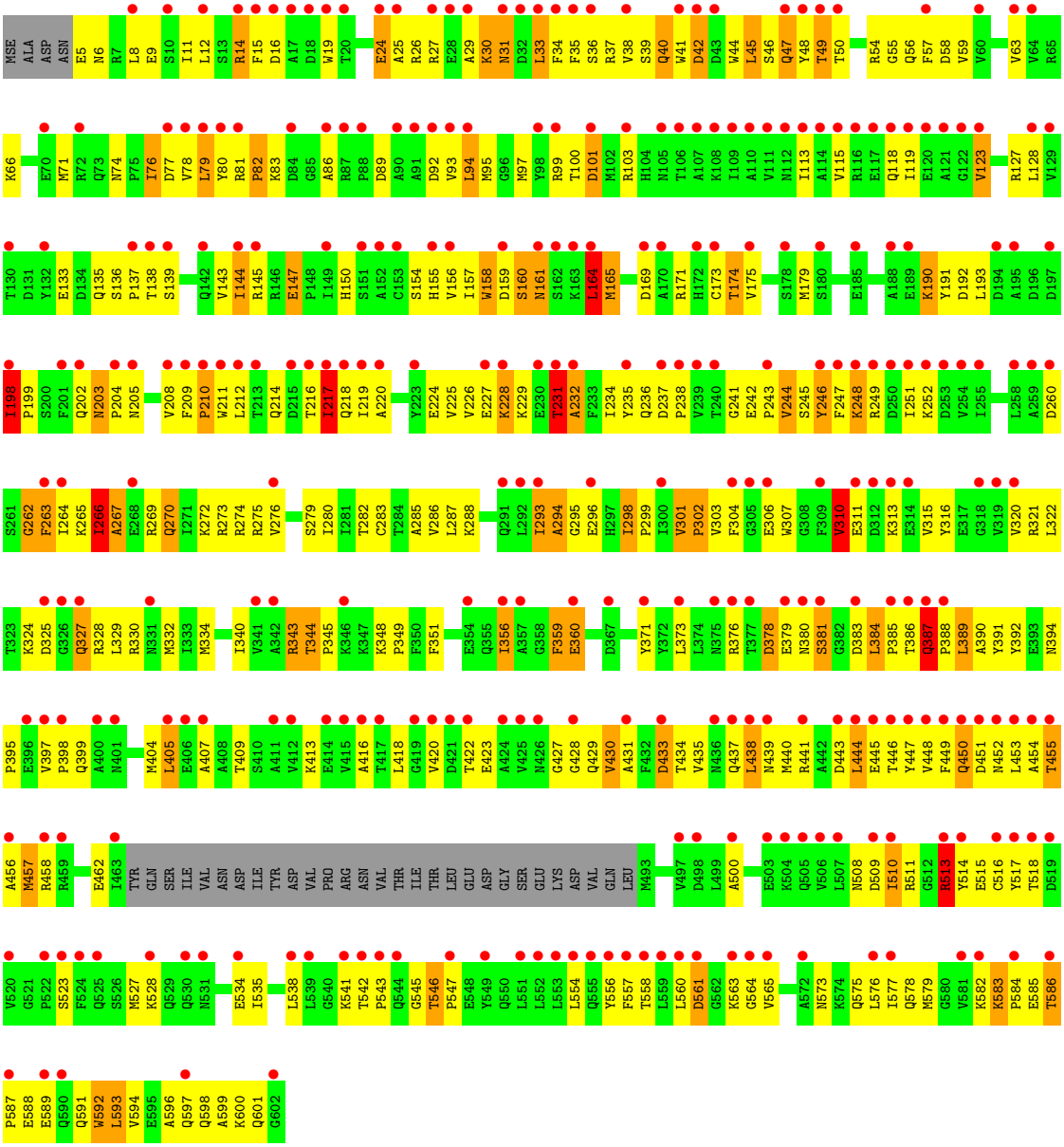
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	22	Total O 22 22	0	0
3	D	22	Total O 22 22	0	0
3	E	22	Total O 22 22	0	0
3	F	22	Total O 22 22	0	0
3	G	22	Total O 22 22	0	0
3	H	22	Total O 22 22	0	0
3	I	22	Total O 22 22	0	0
3	J	22	Total O 22 22	0	0
3	K	22	Total O 22 22	0	0
3	L	22	Total O 22 22	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

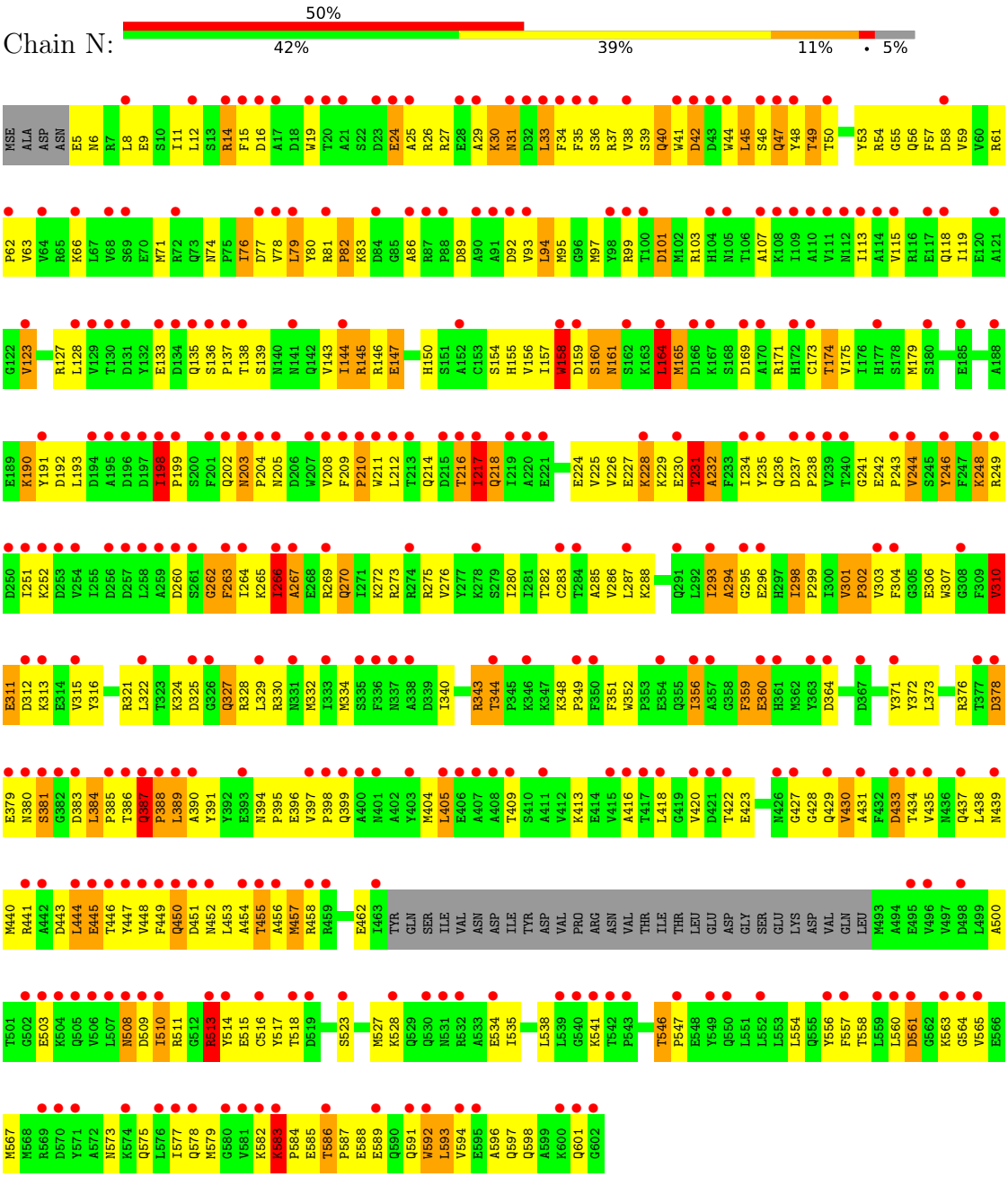
- Molecule 1: PORTAL PROTEIN

Chain M:



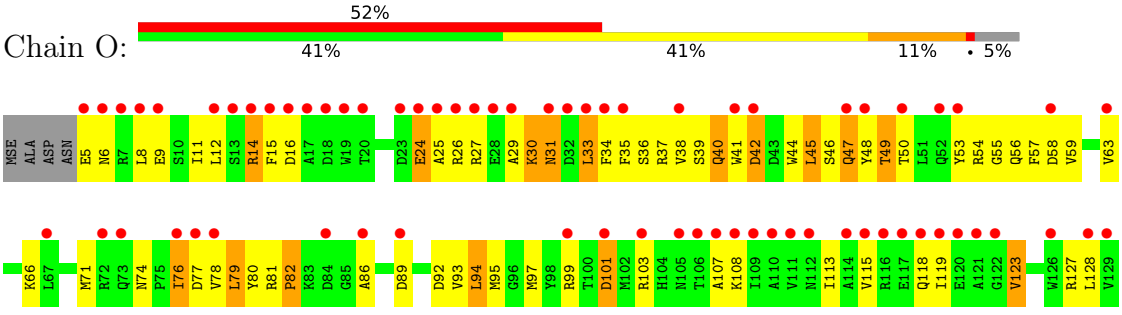
• Molecule 1: PORTAL PROTEIN

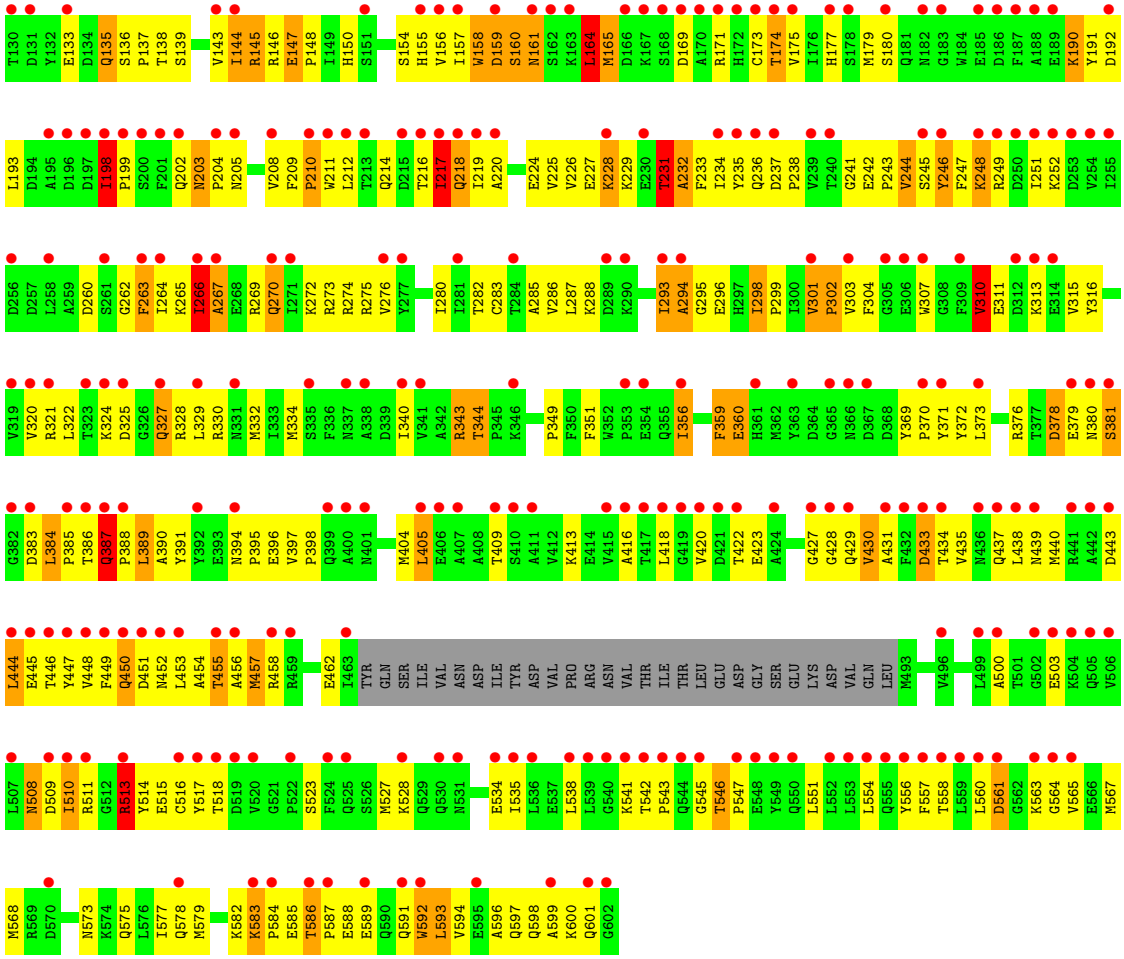
Chain N:



• Molecule 1: PORTAL PROTEIN

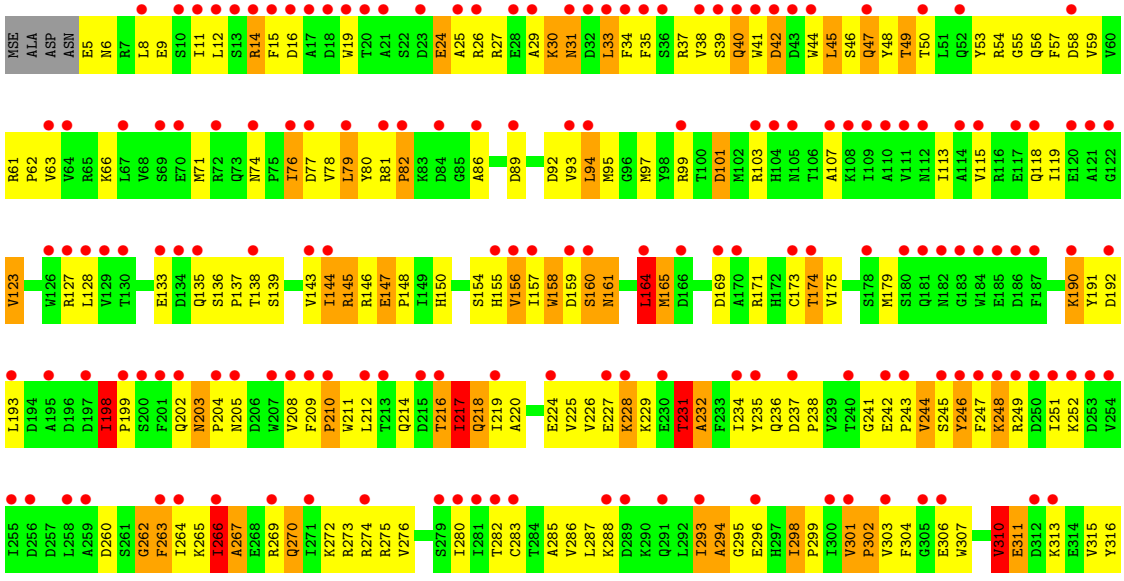
Chain O:

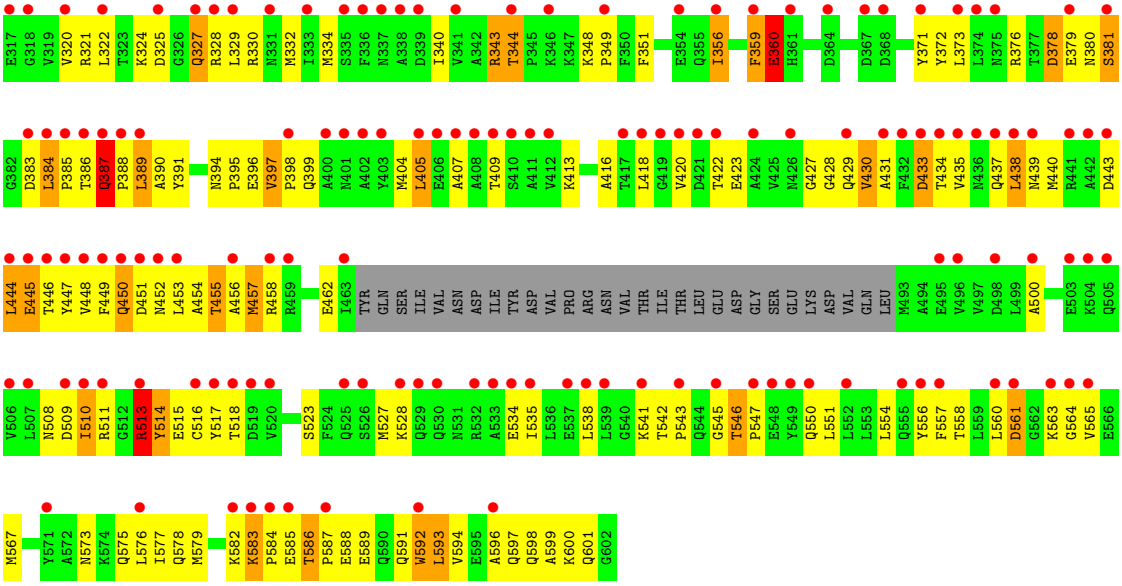




• Molecule 1: PORTAL PROTEIN

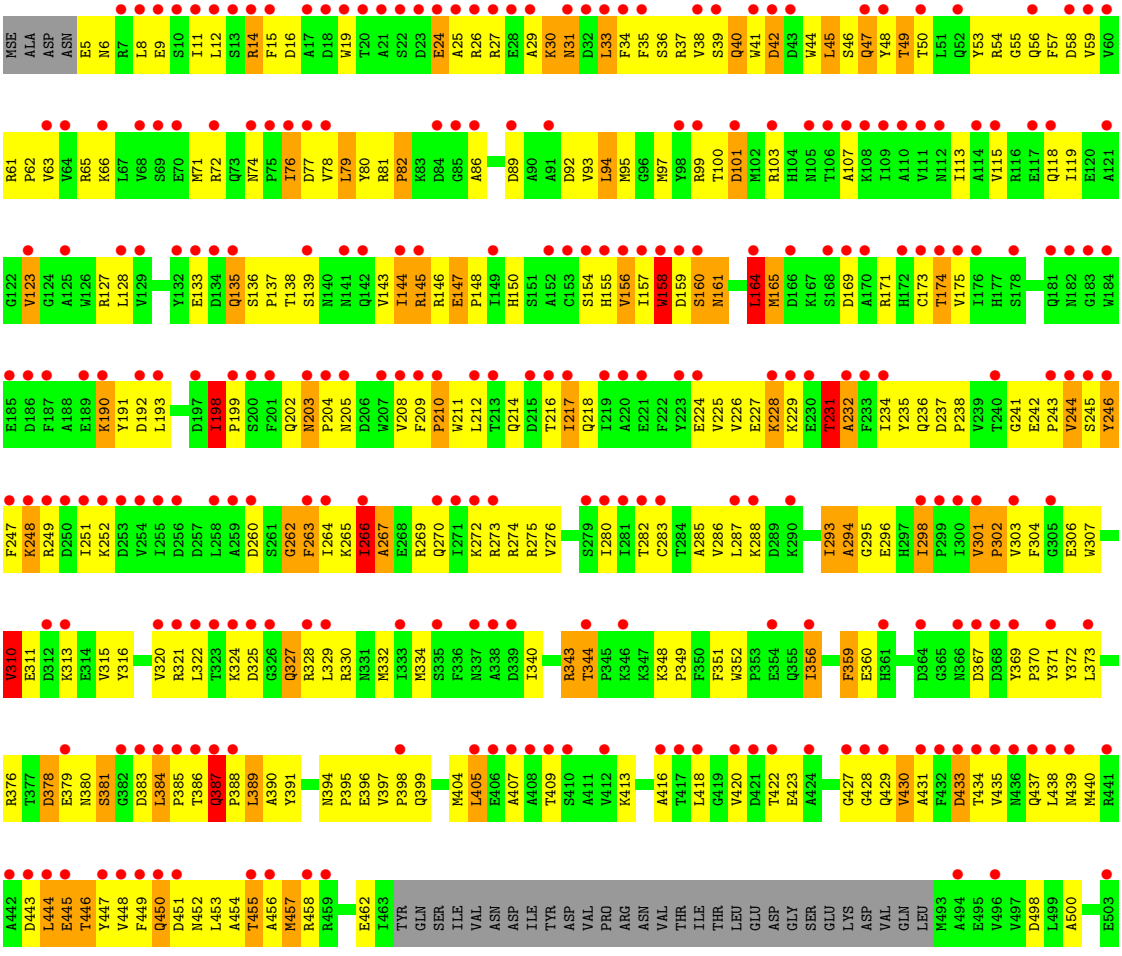
Chain P:

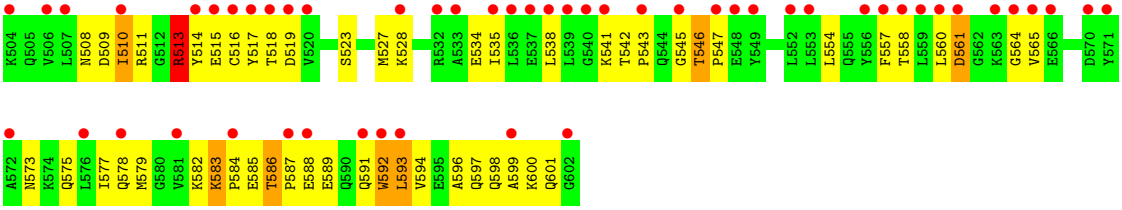




• Molecule 1: PORTAL PROTEIN

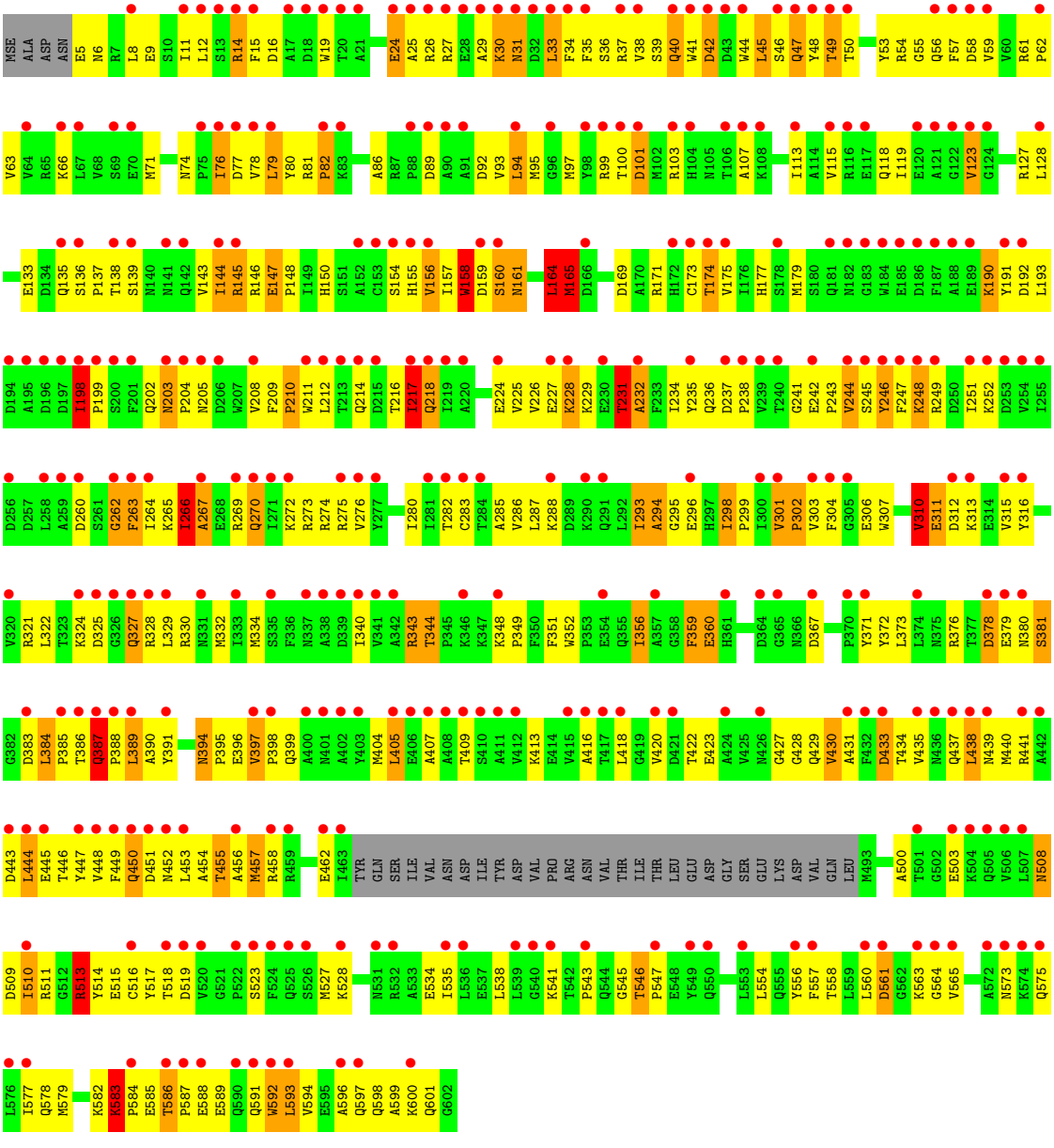
Chain Q:





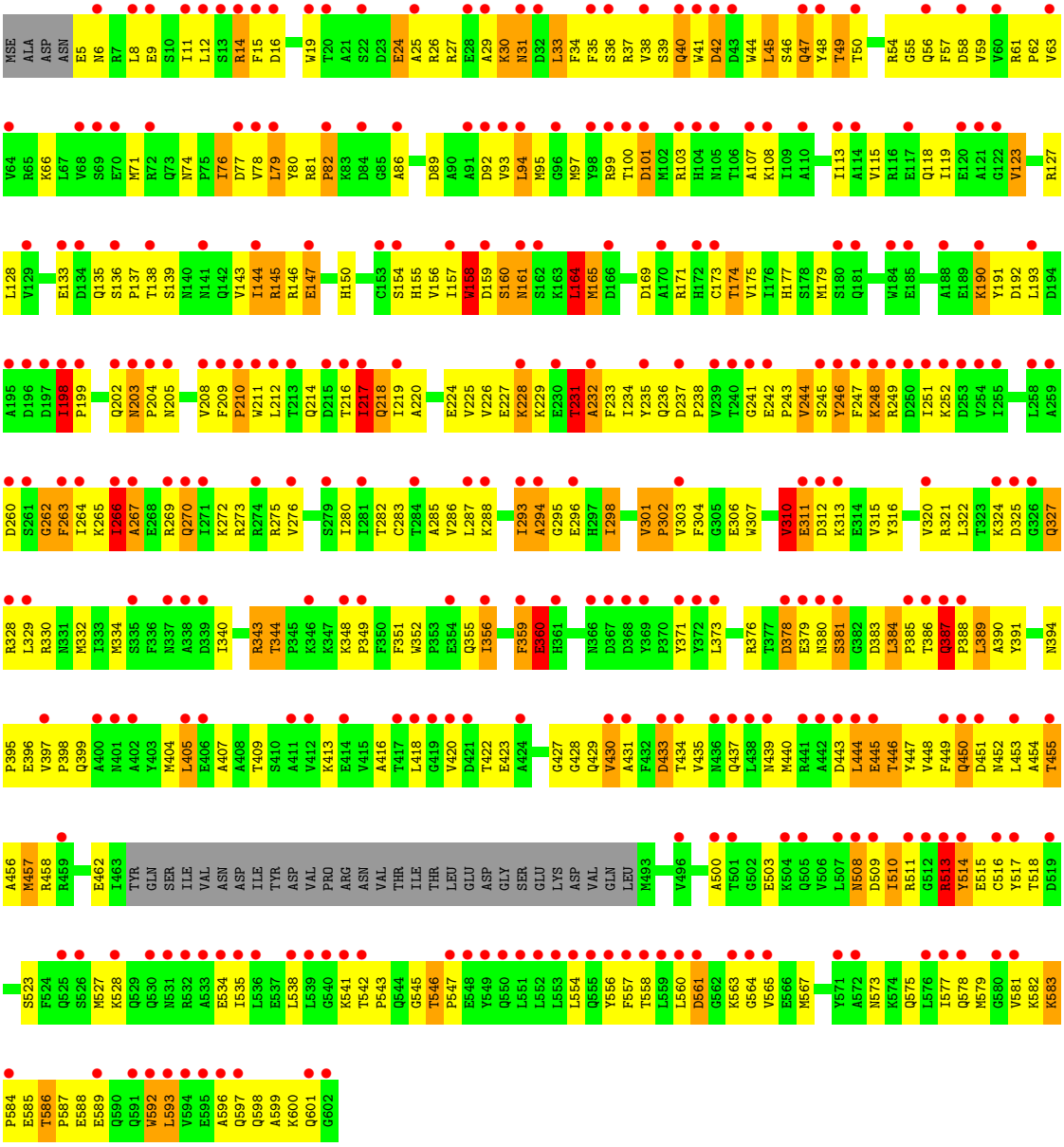
• Molecule 1: PORTAL PROTEIN

Chain R:



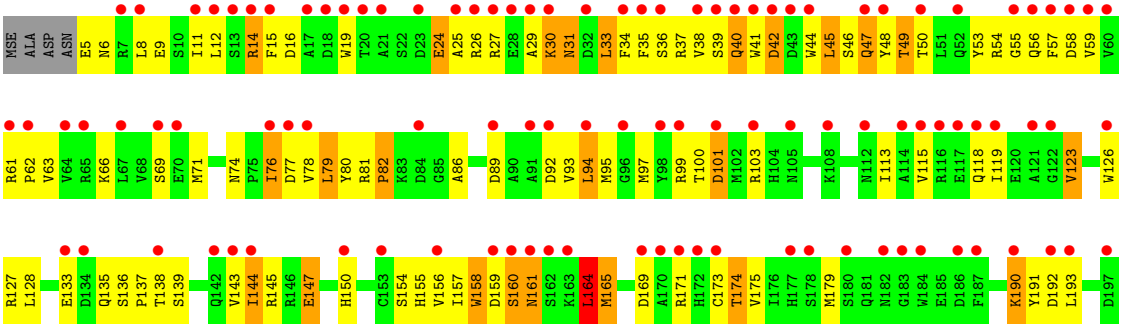
• Molecule 1: PORTAL PROTEIN

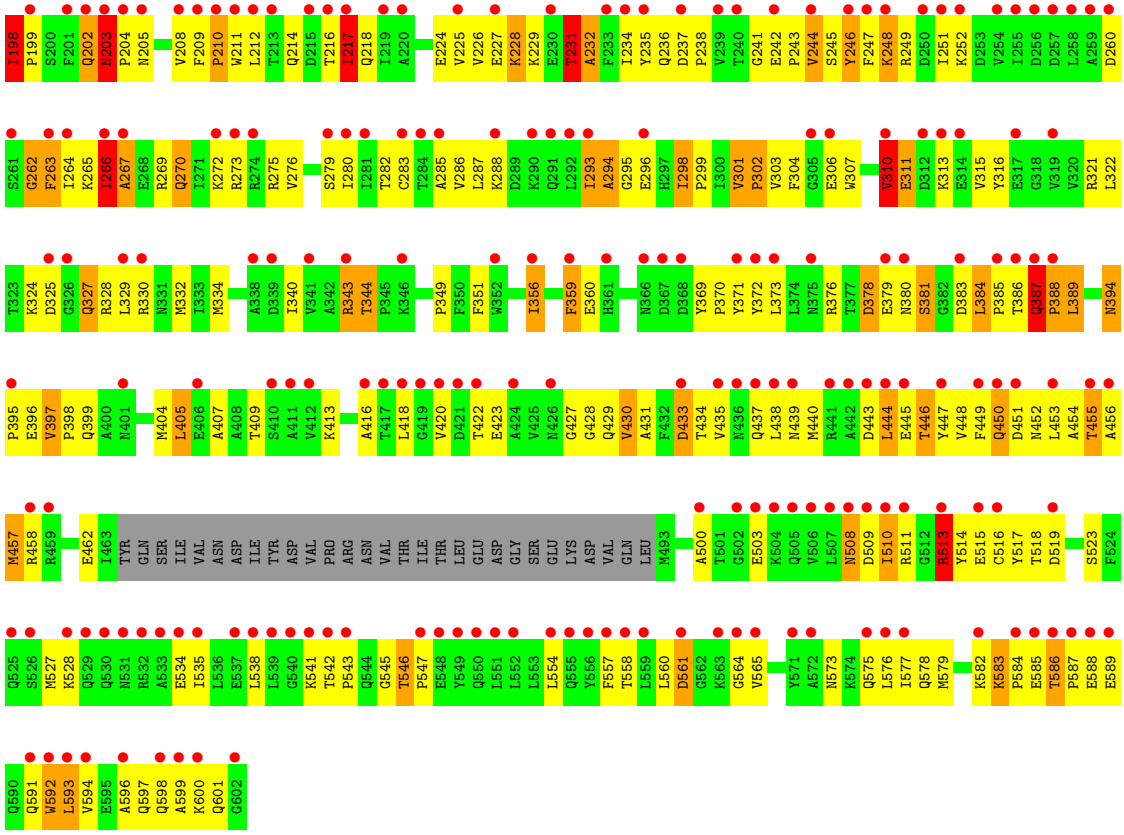
Chain S:



• Molecule 1: PORTAL PROTEIN

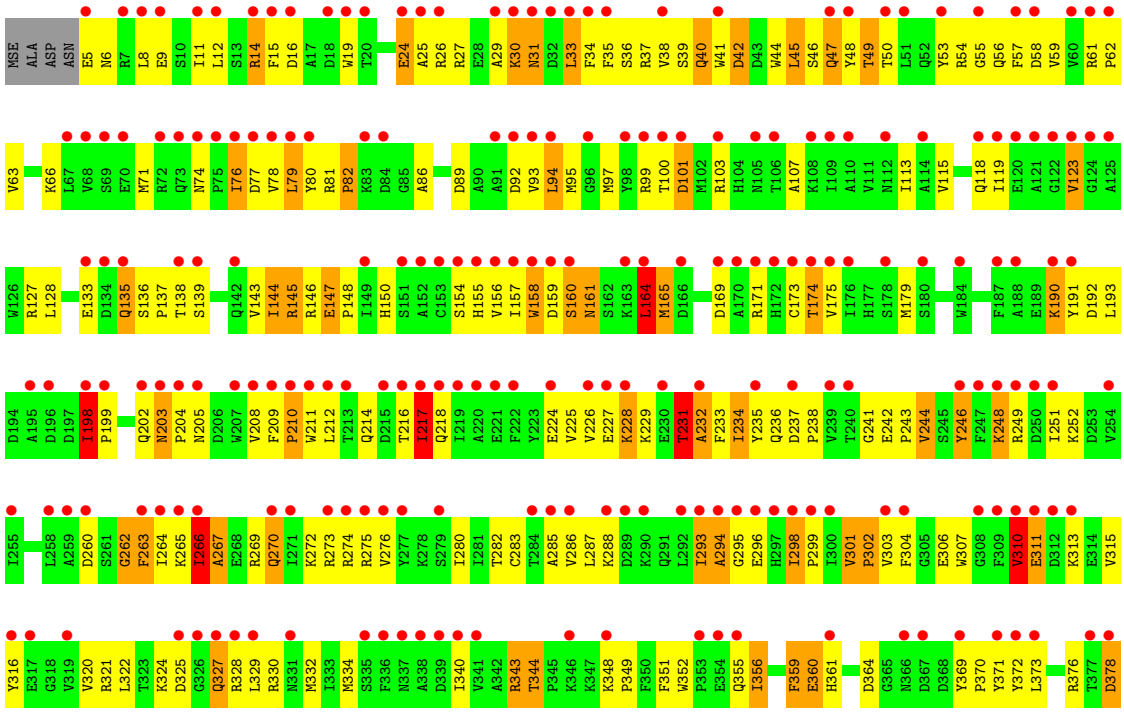
Chain T:

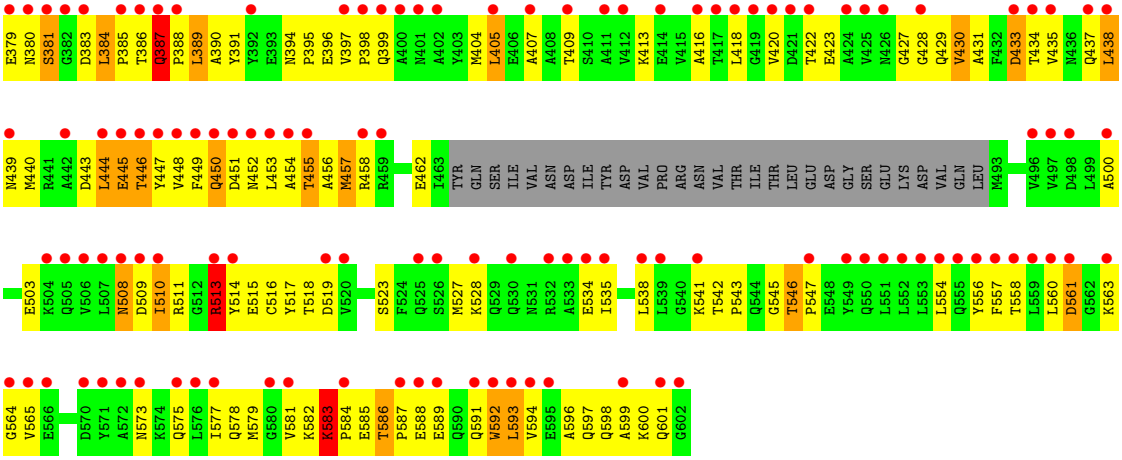


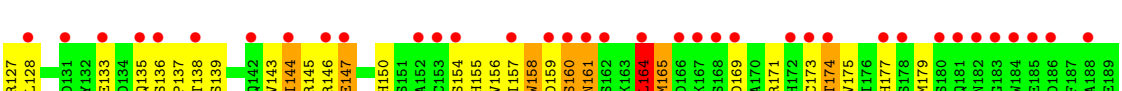


• Molecule 1: PORTAL PROTEIN

Chain U:

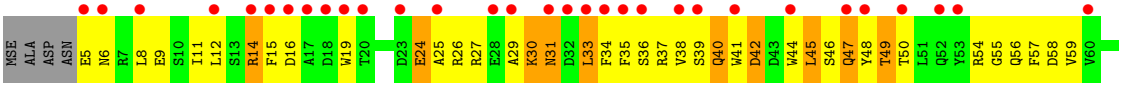


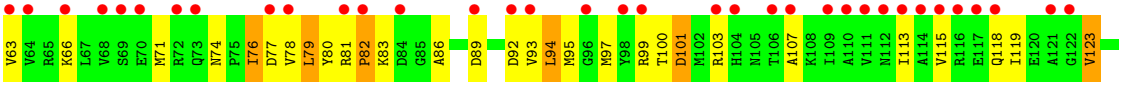


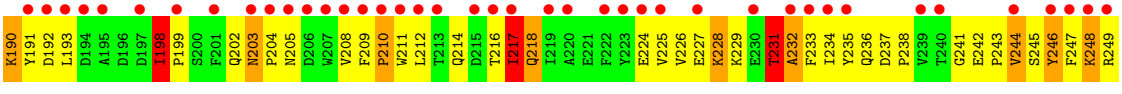


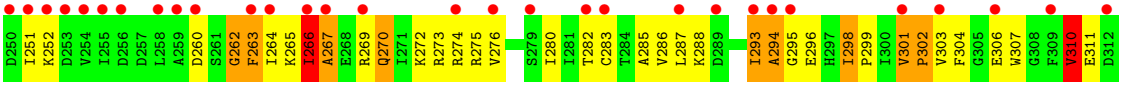
• Molecule 1: PORTAL PROTEIN

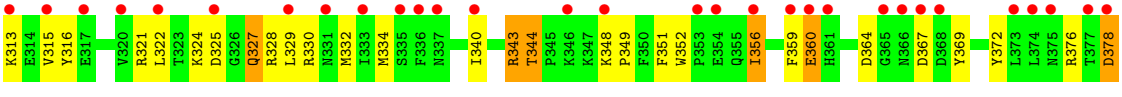
Chain V:

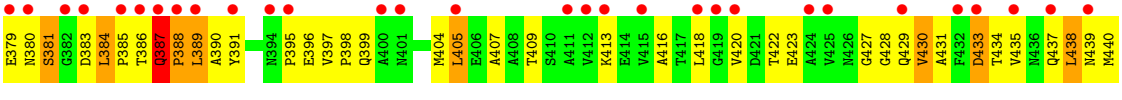


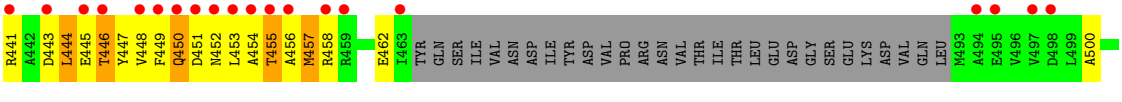


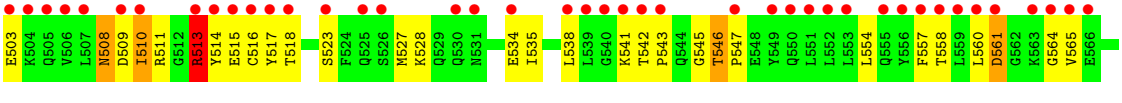


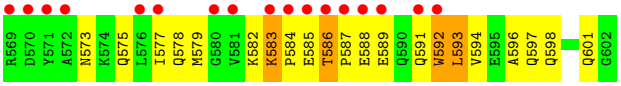






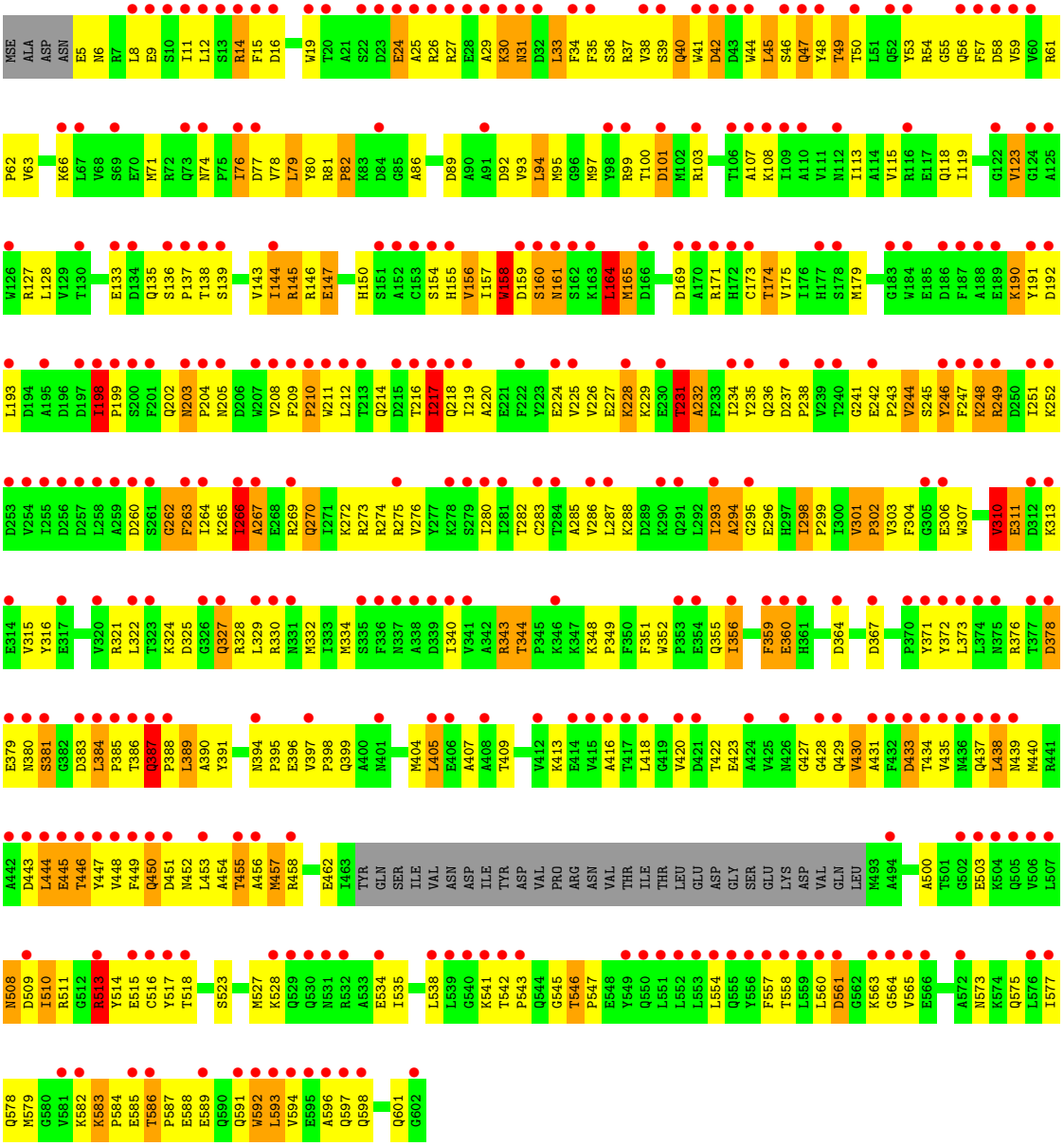






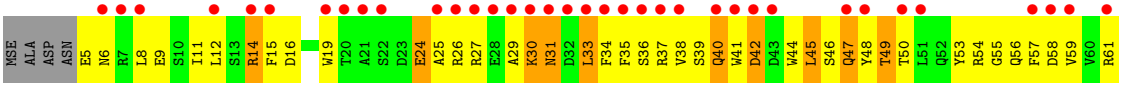
• Molecule 1: PORTAL PROTEIN

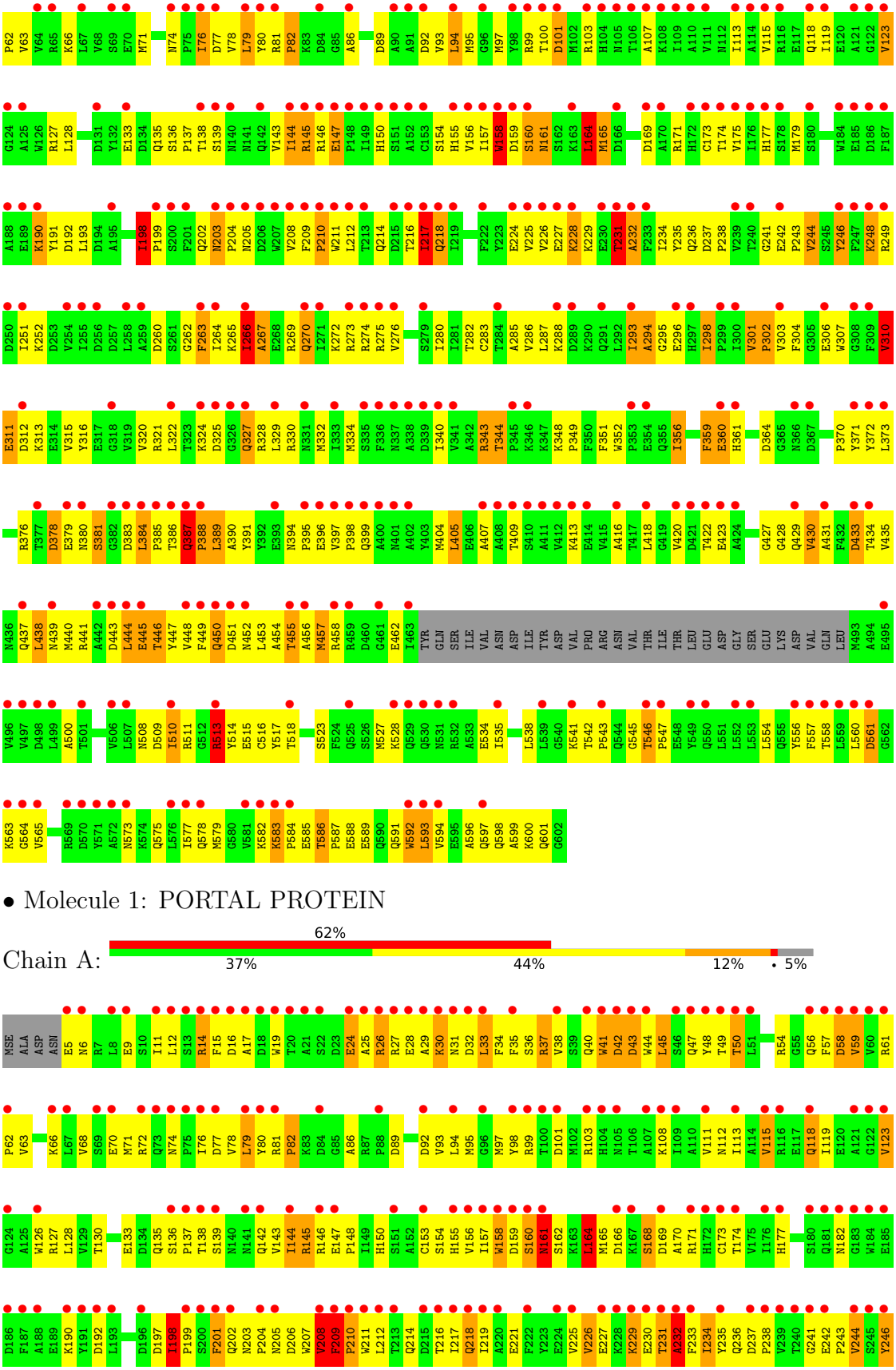
Chain W:



• Molecule 1: PORTAL PROTEIN

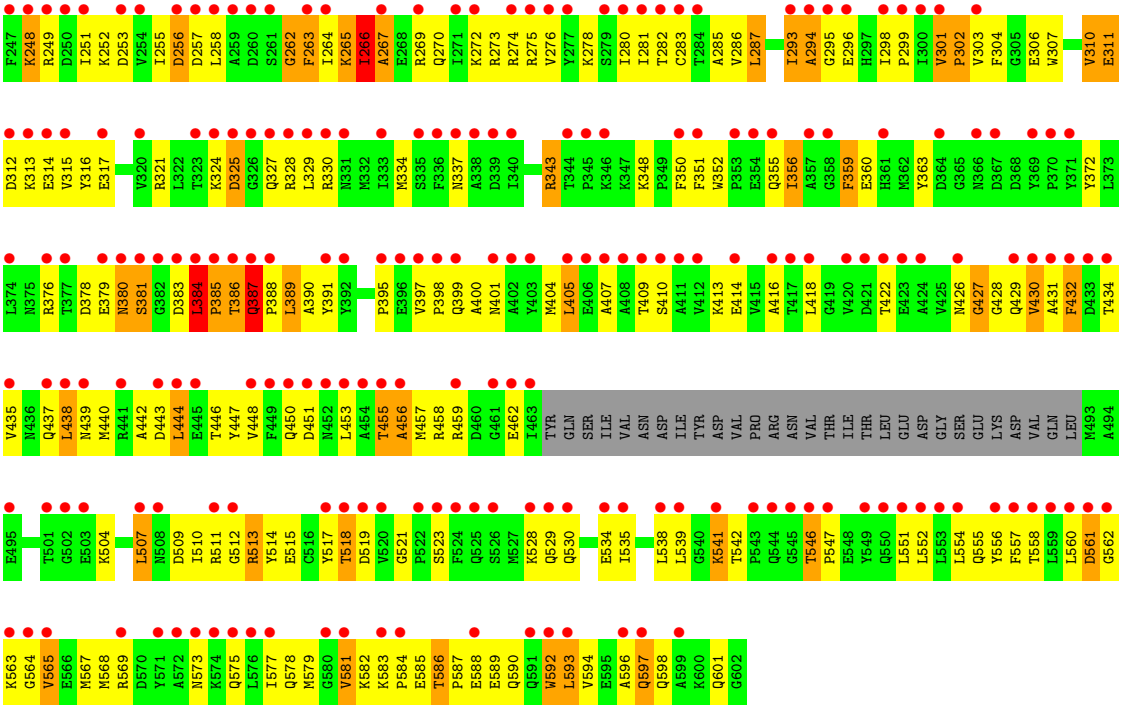
Chain X:





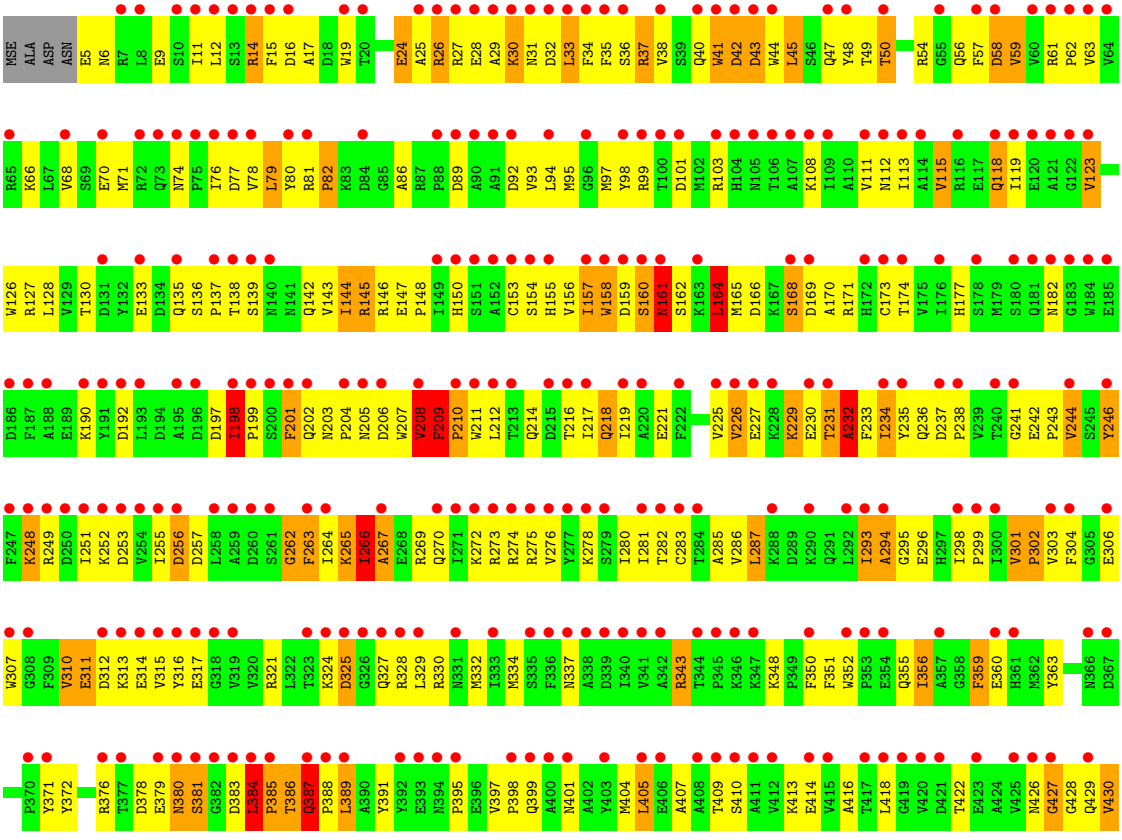
• Molecule 1: PORTAL PROTEIN

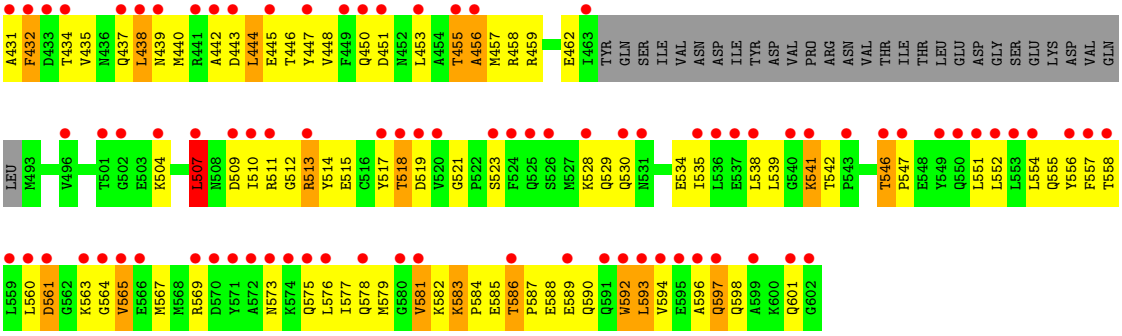
Chain A:



• Molecule 1: PORTAL PROTEIN

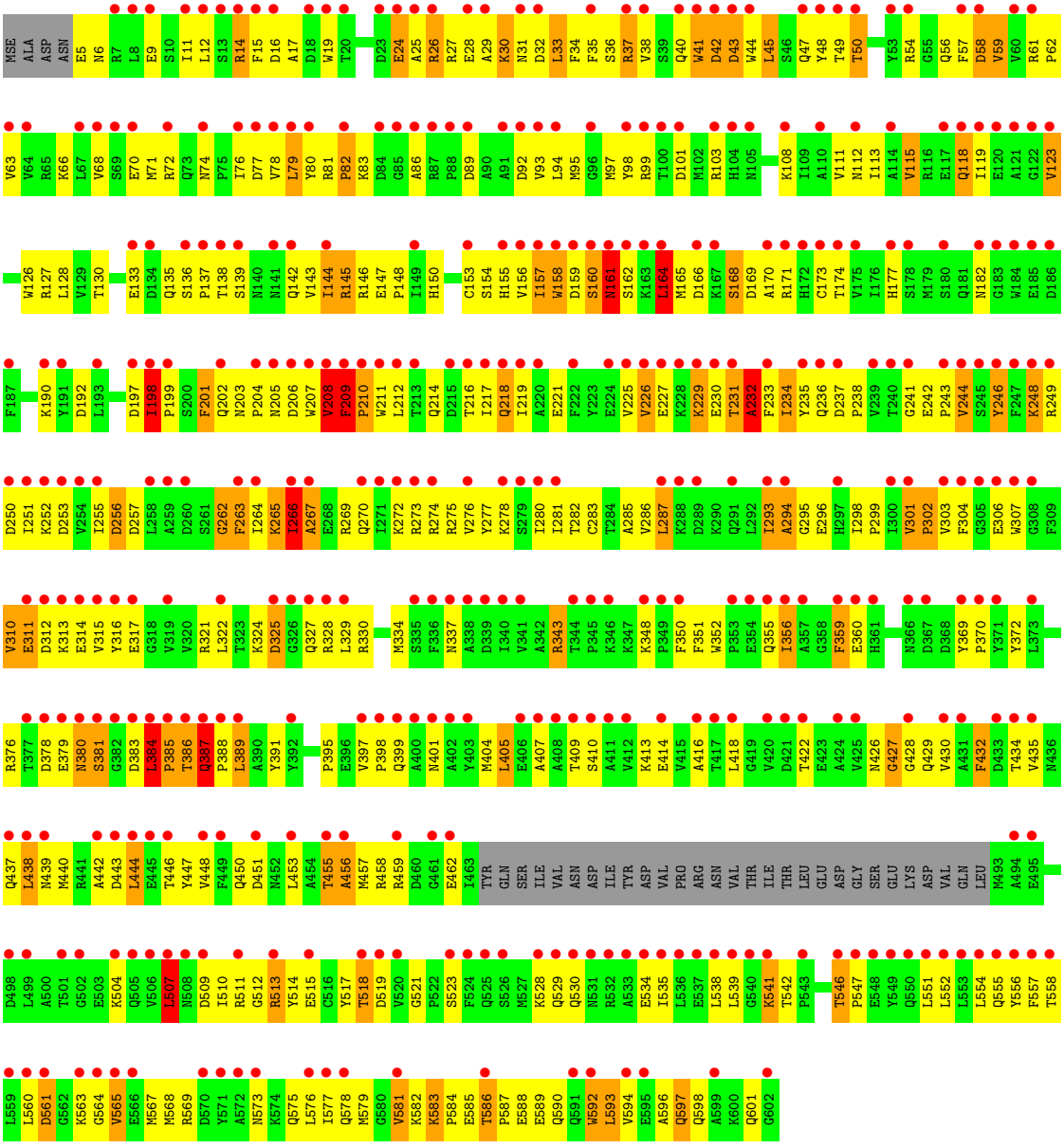
Chain B:



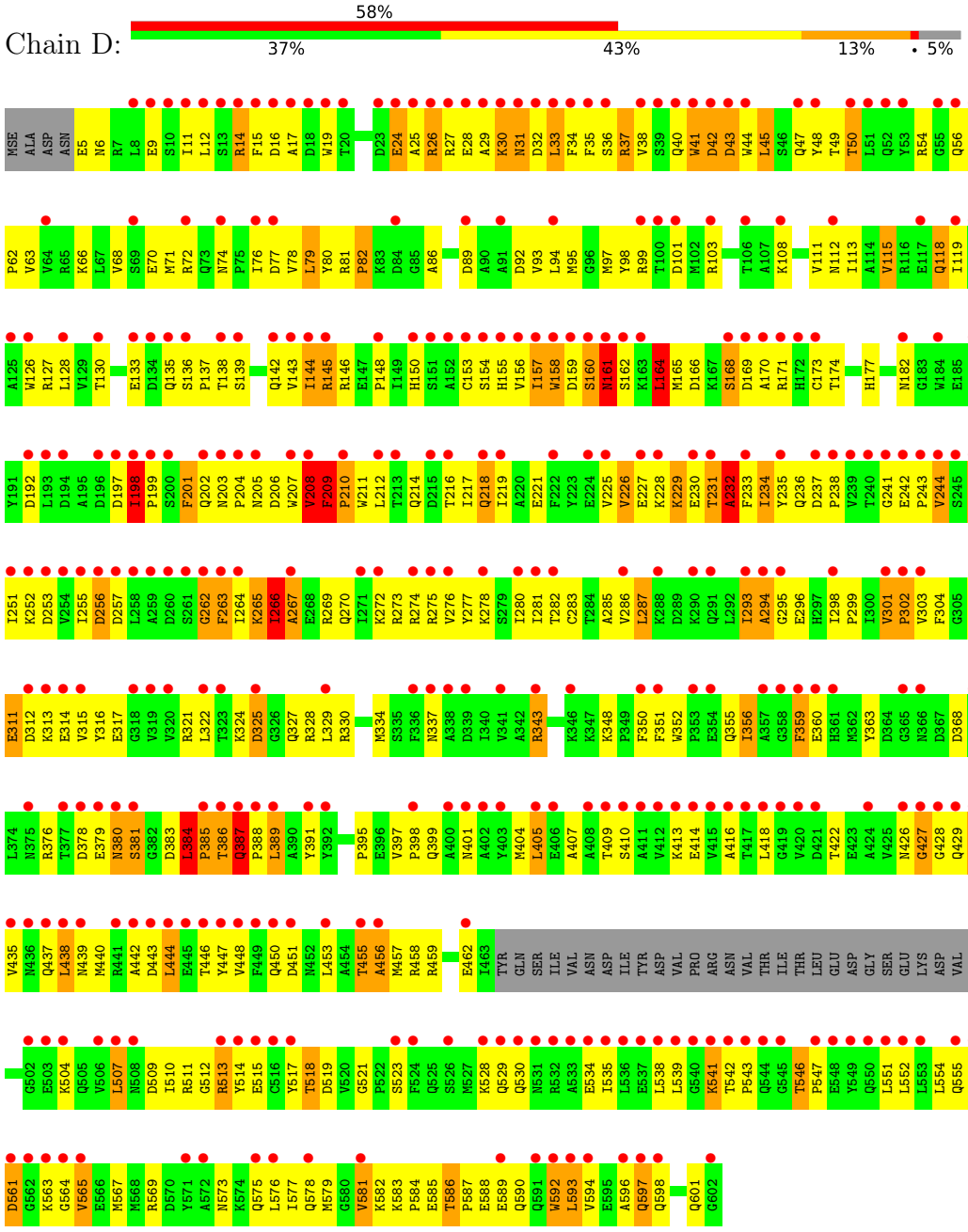


• Molecule 1: PORTAL PROTEIN

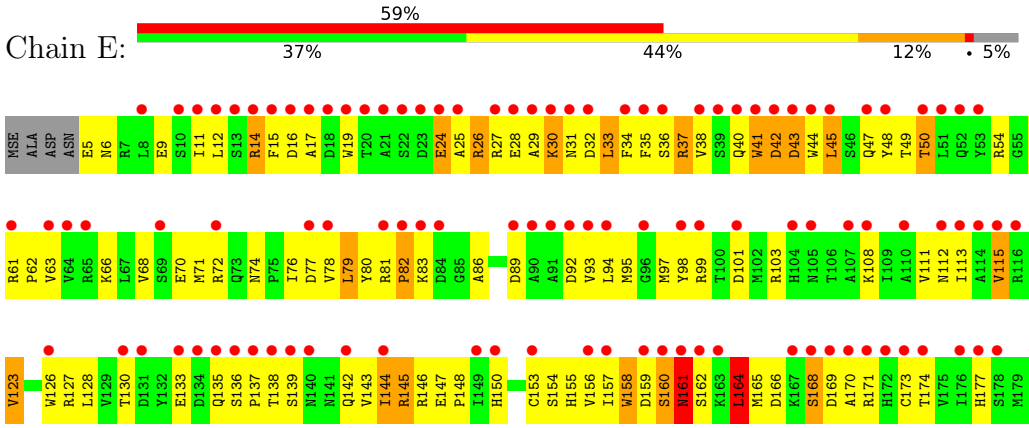
Chain C:

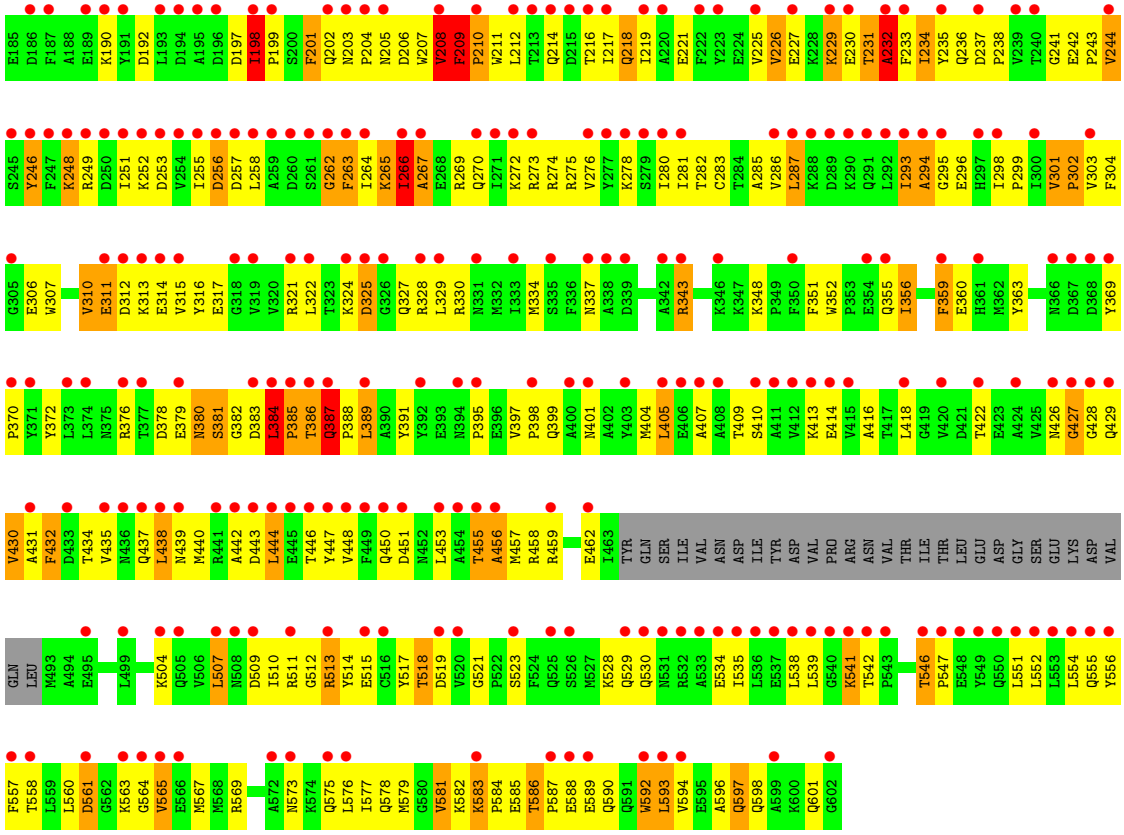


• Molecule 1: PORTAL PROTEIN



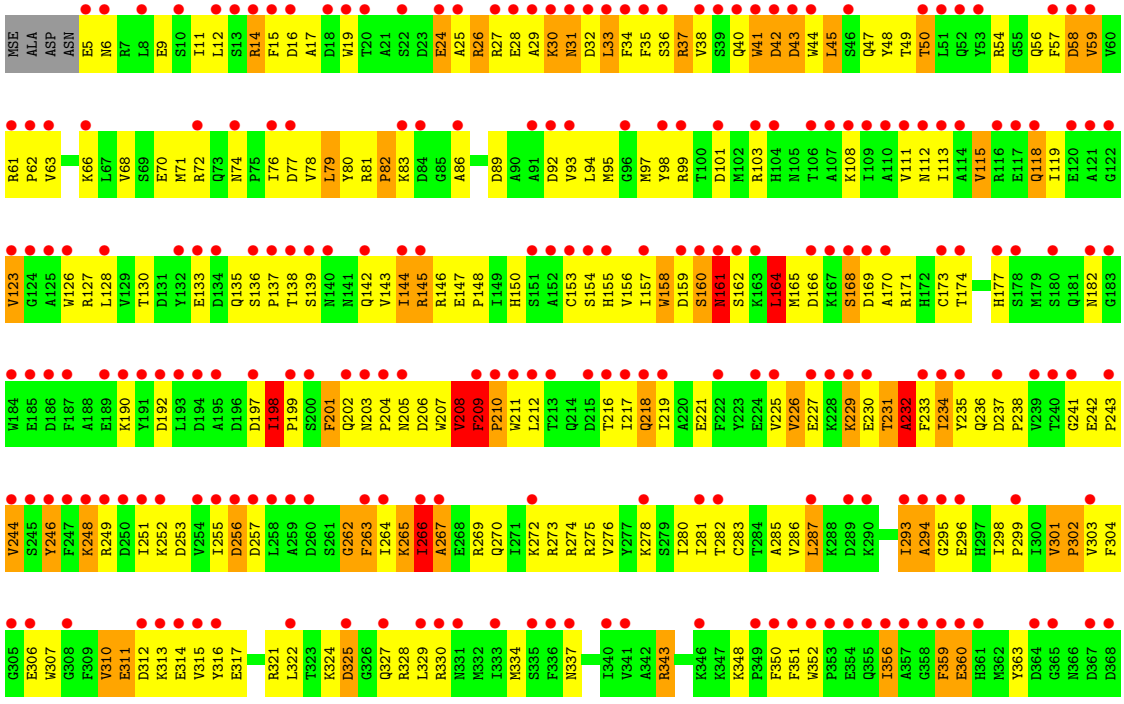
• Molecule 1: PORTAL PROTEIN

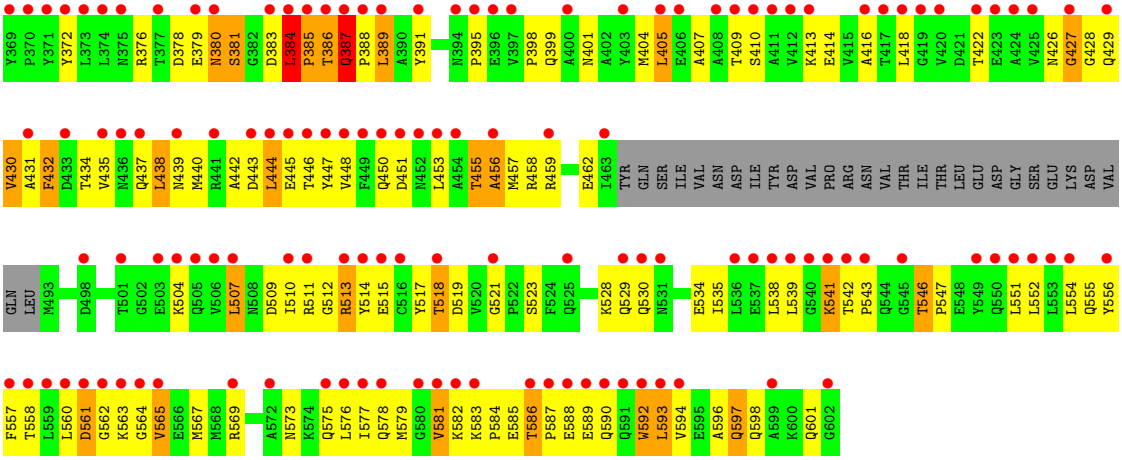




• Molecule 1: PORTAL PROTEIN

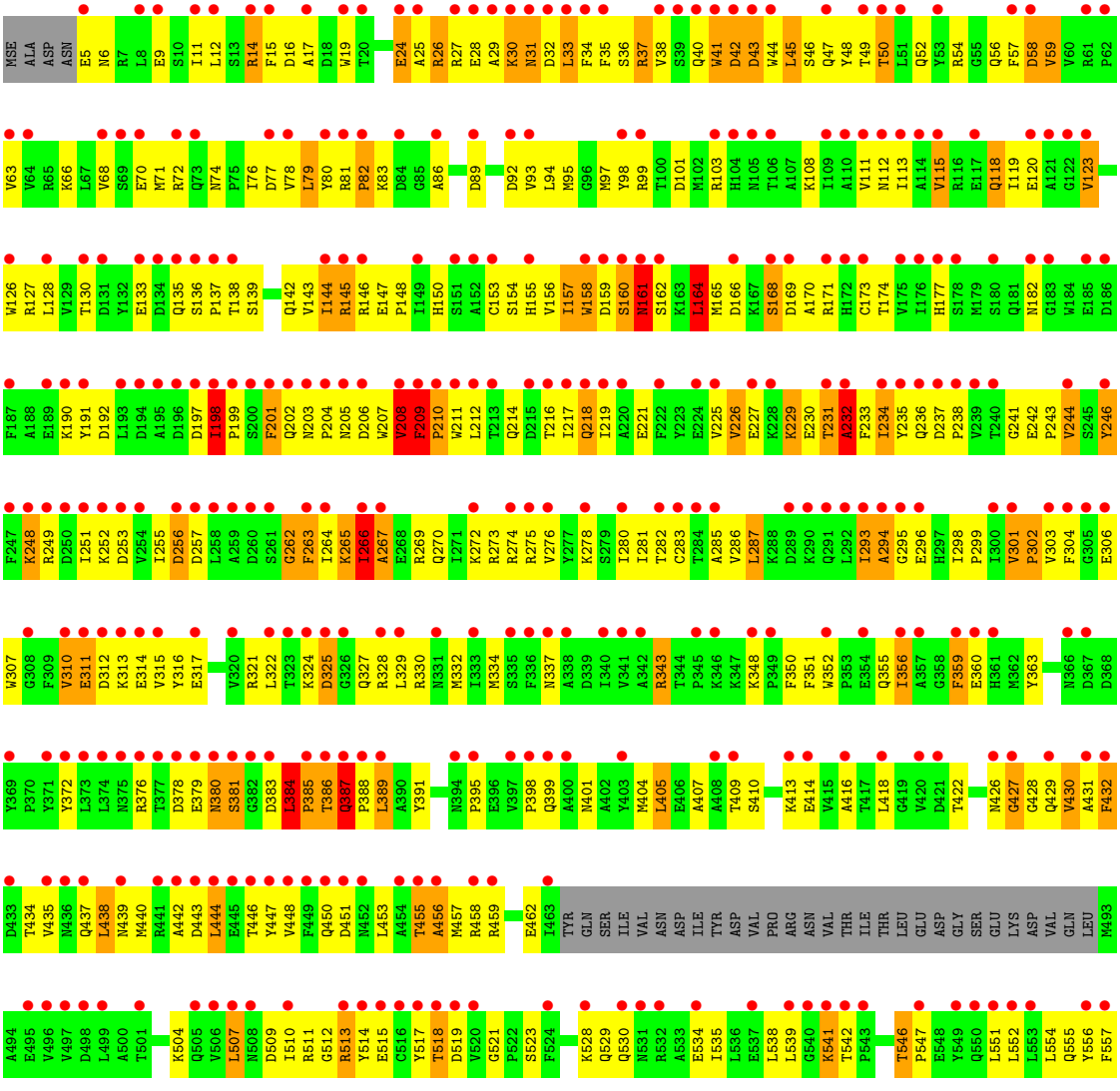
Chain F:

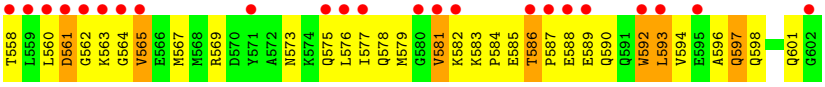




• Molecule 1: PORTAL PROTEIN

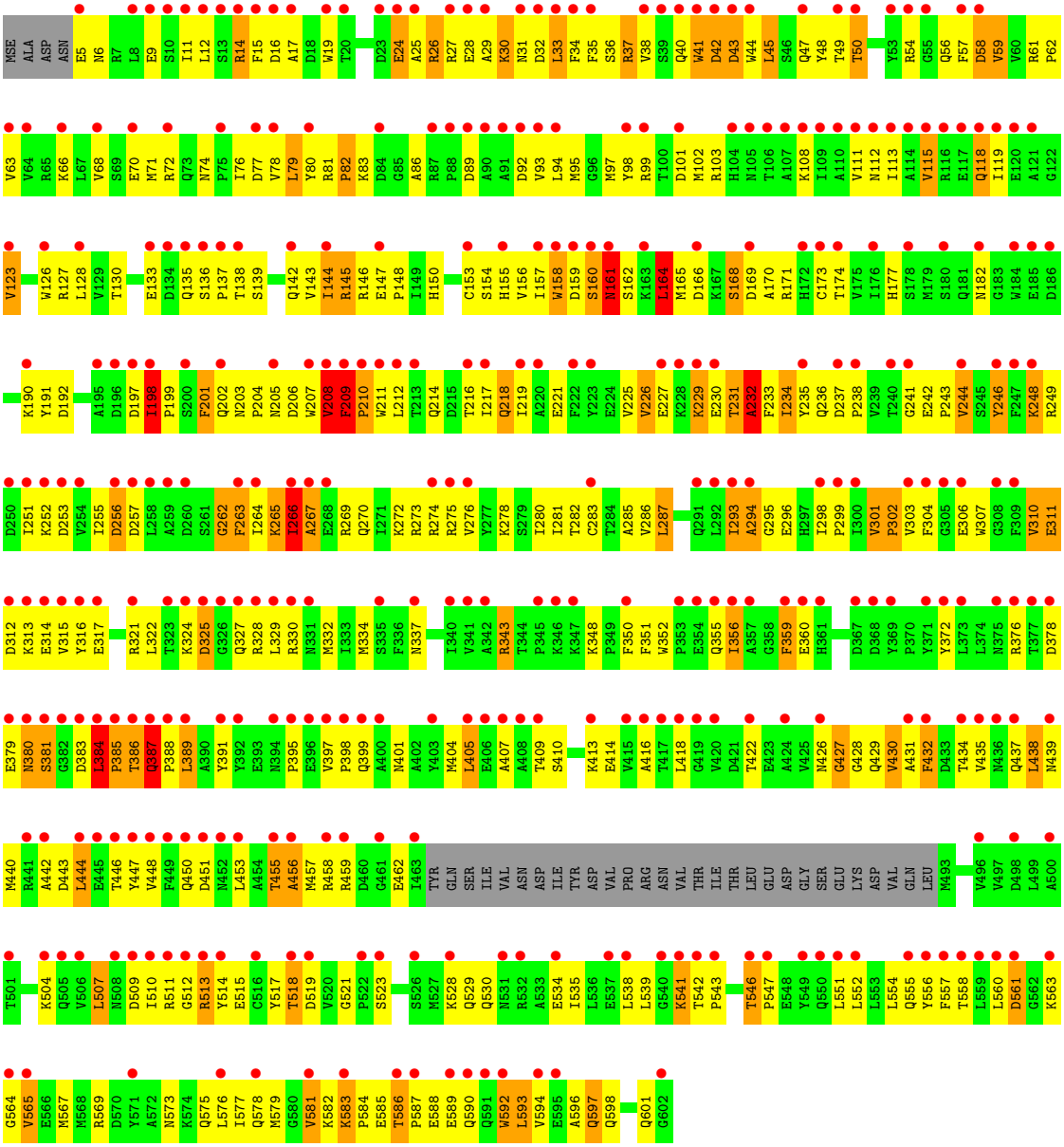
Chain G:





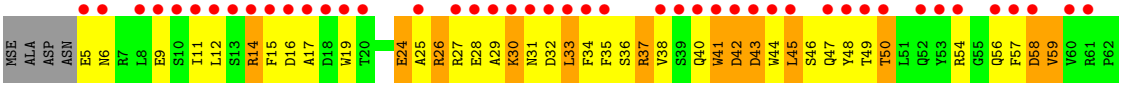
• Molecule 1: PORTAL PROTEIN

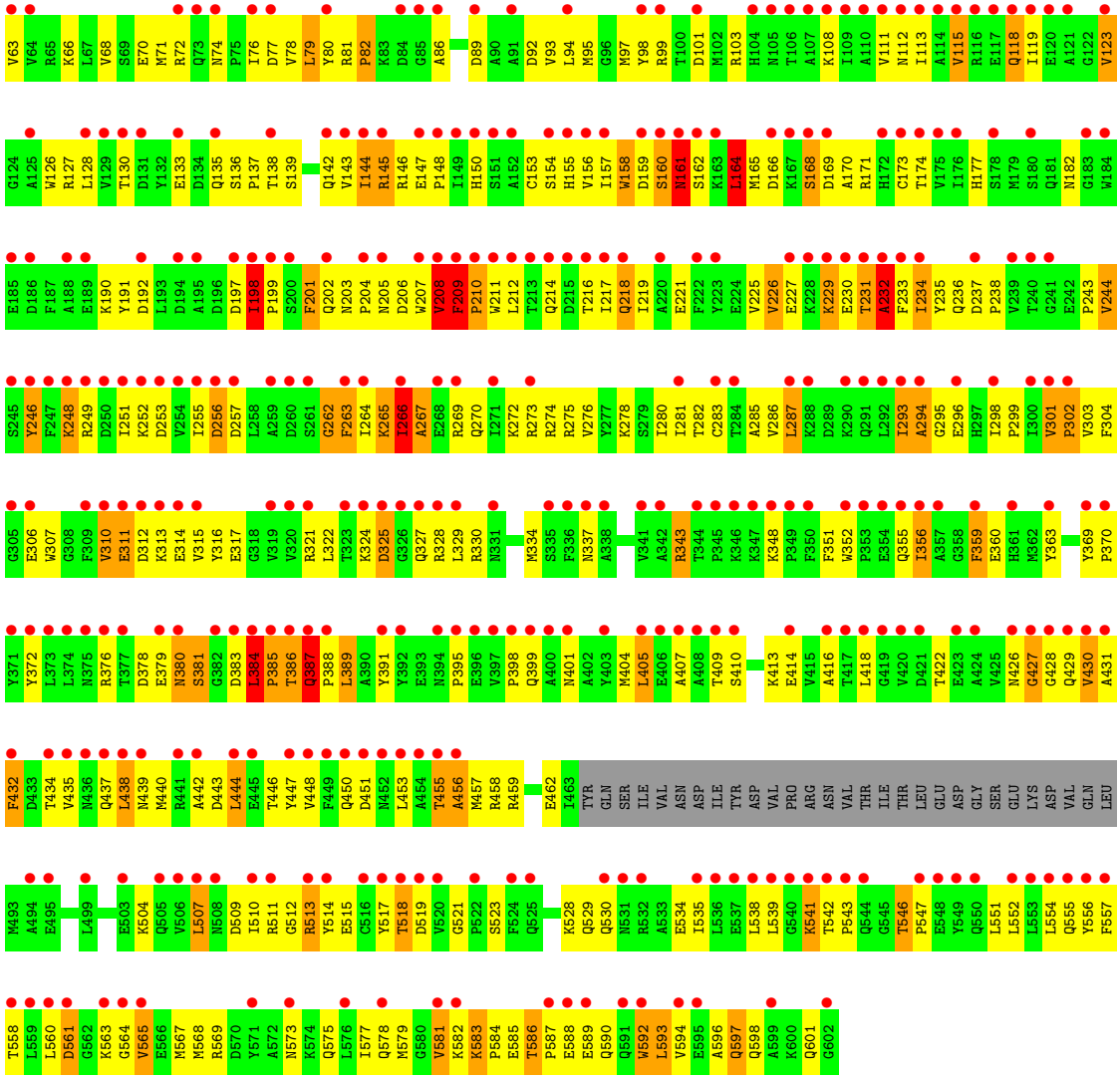
Chain H:



• Molecule 1: PORTAL PROTEIN

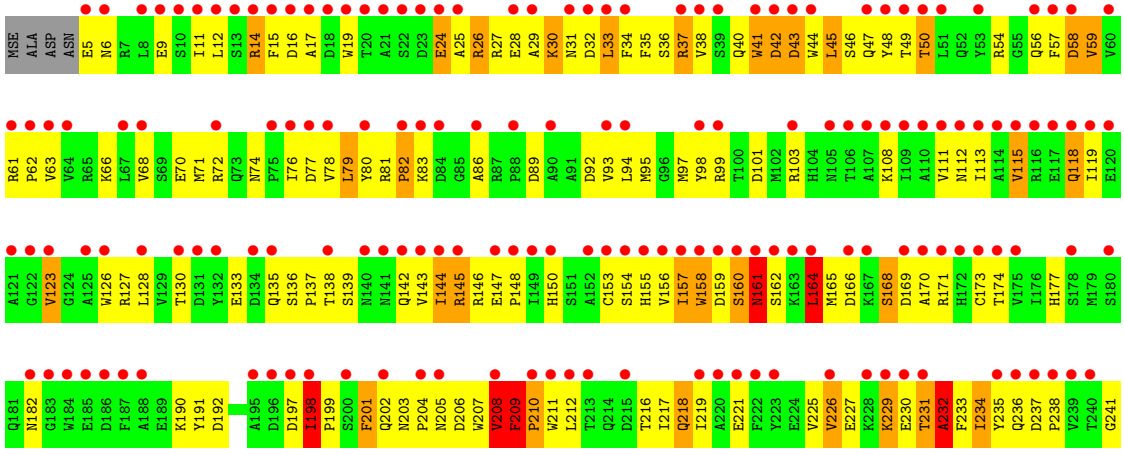
Chain I:

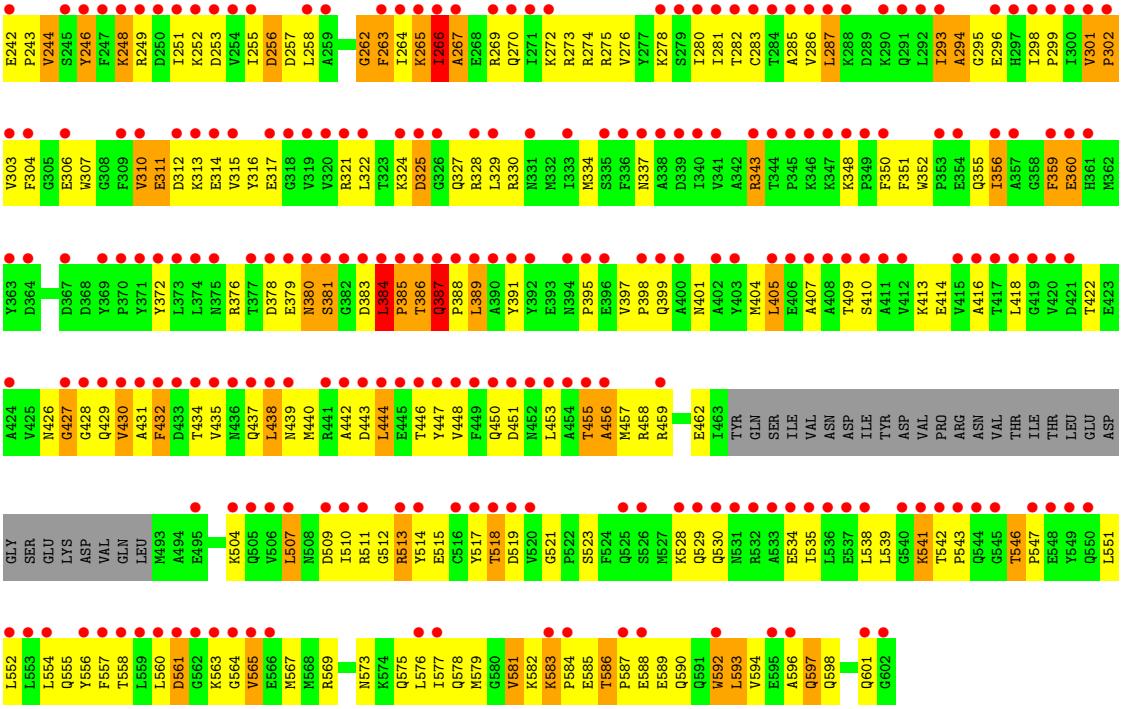




• Molecule 1: PORTAL PROTEIN

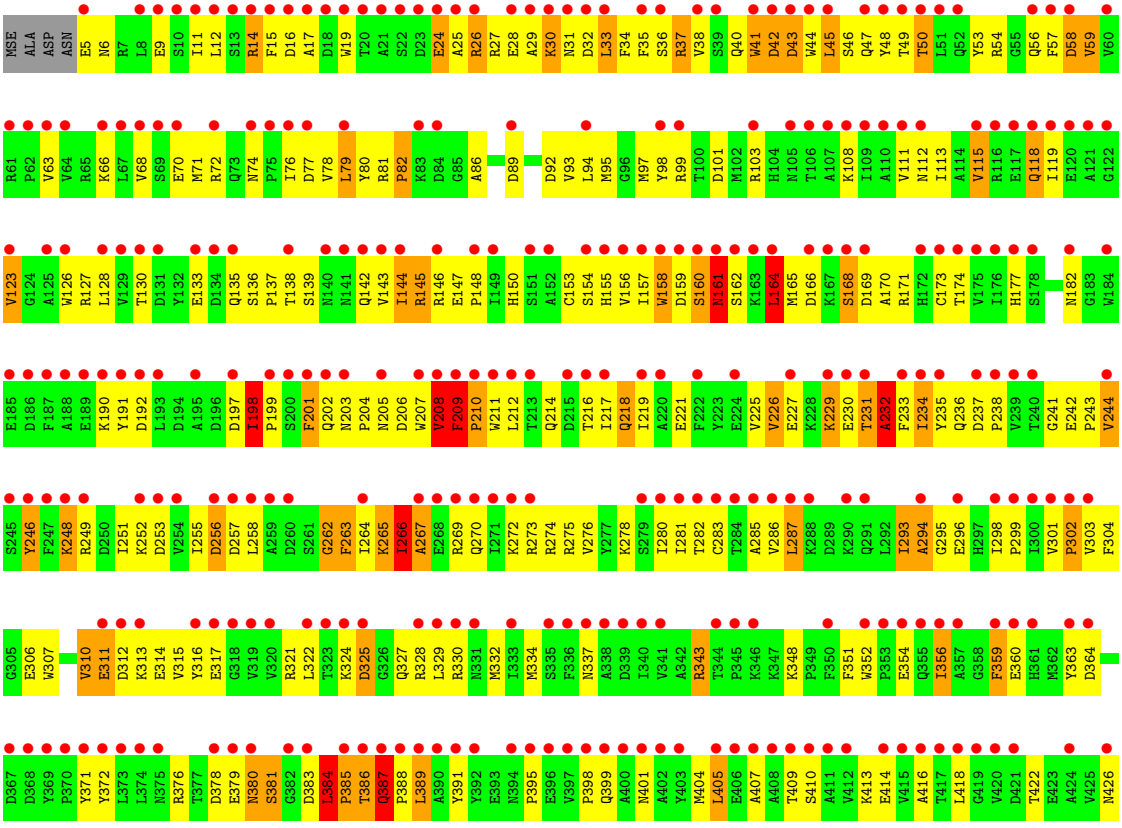
Chain J:

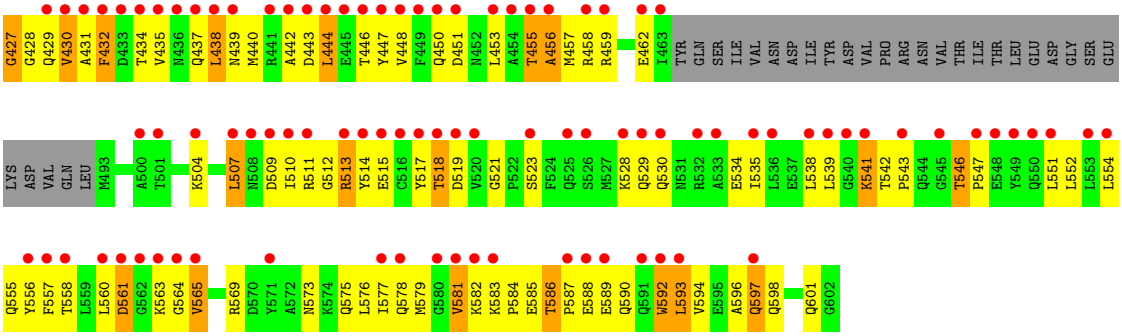




• Molecule 1: PORTAL PROTEIN

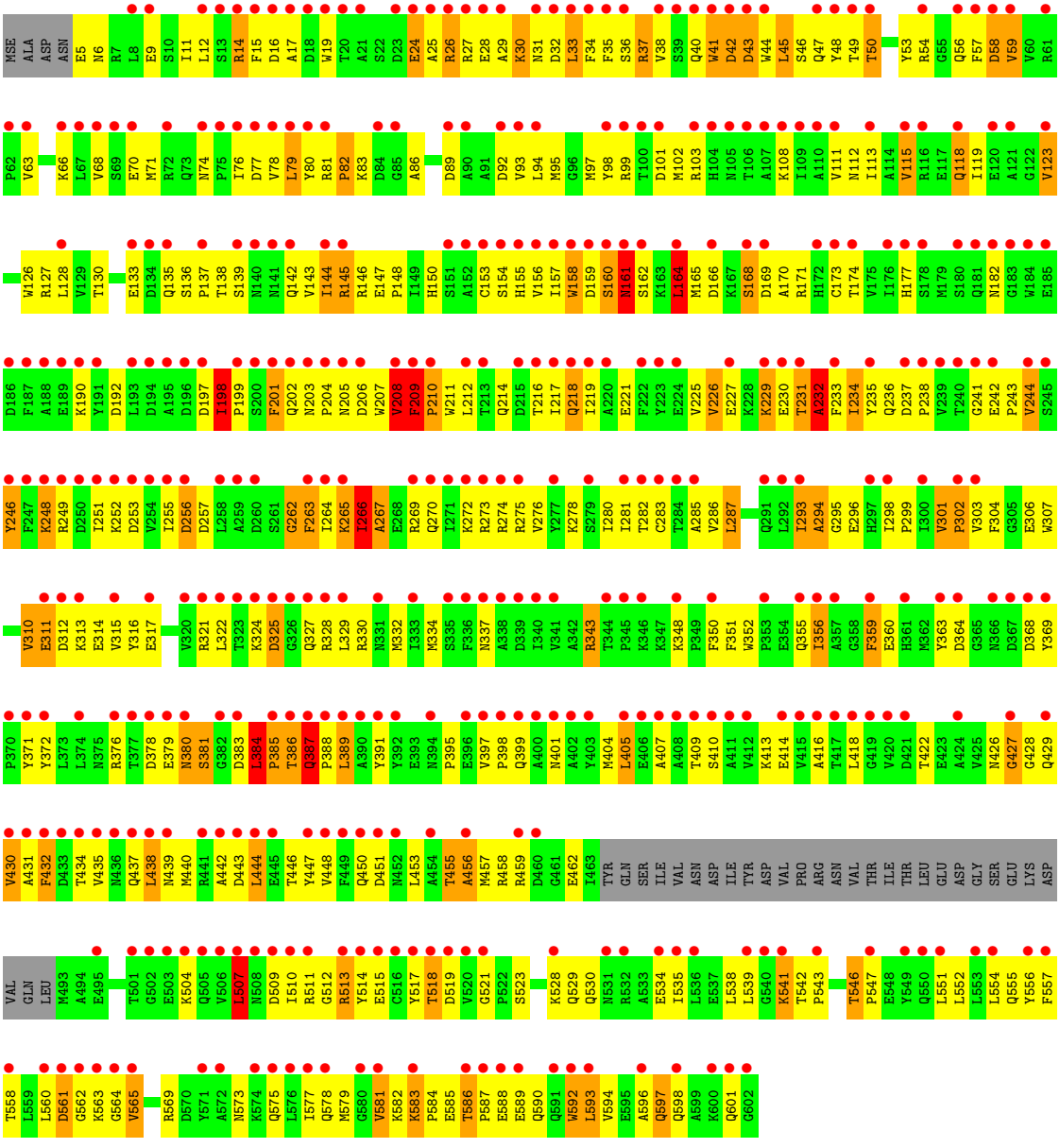
Chain K:





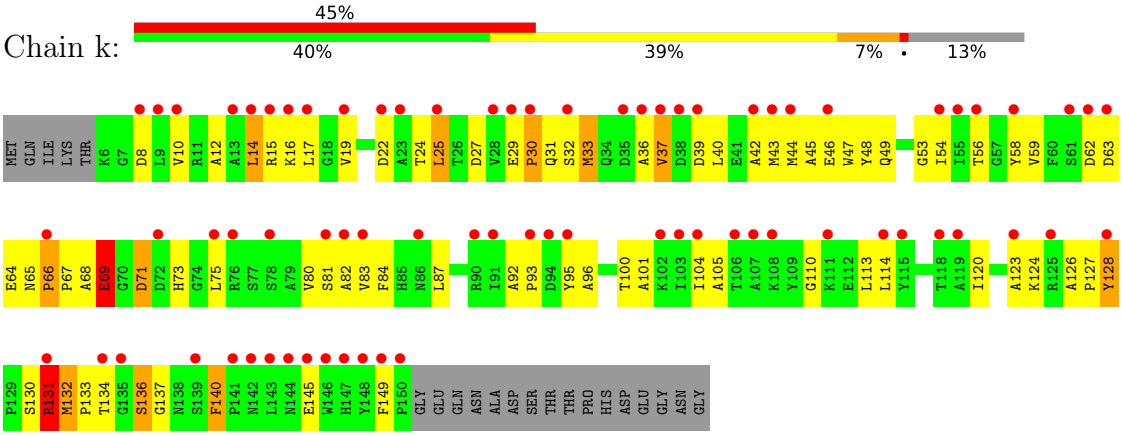
• Molecule 1: PORTAL PROTEIN

Chain L:



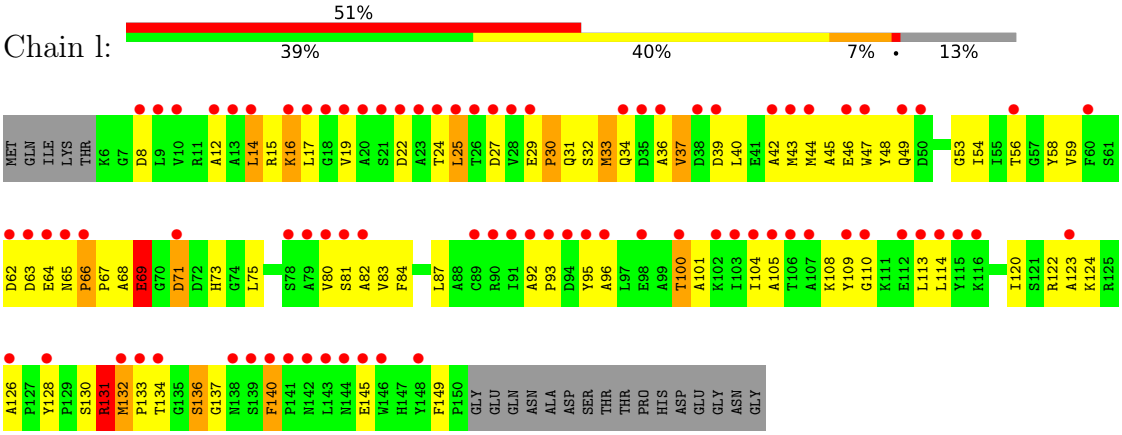
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

Chain k:



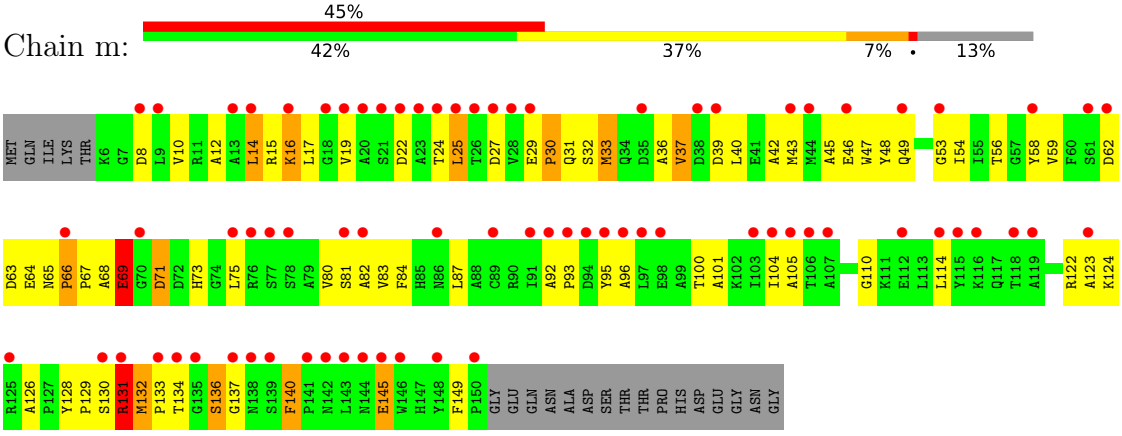
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

Chain l:



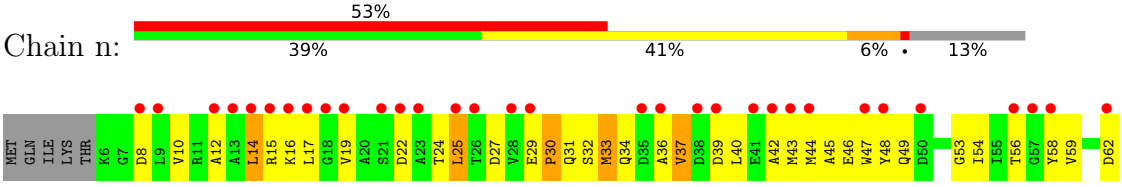
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

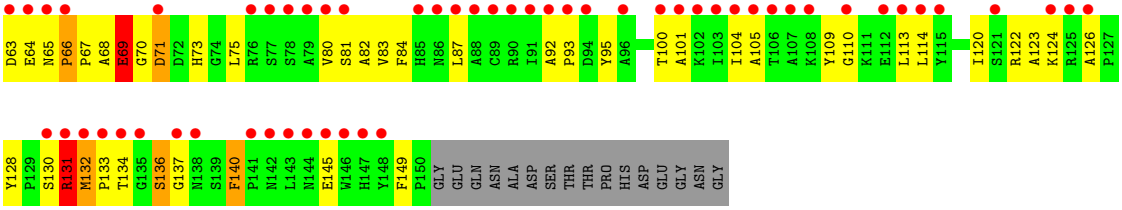
Chain m:



• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

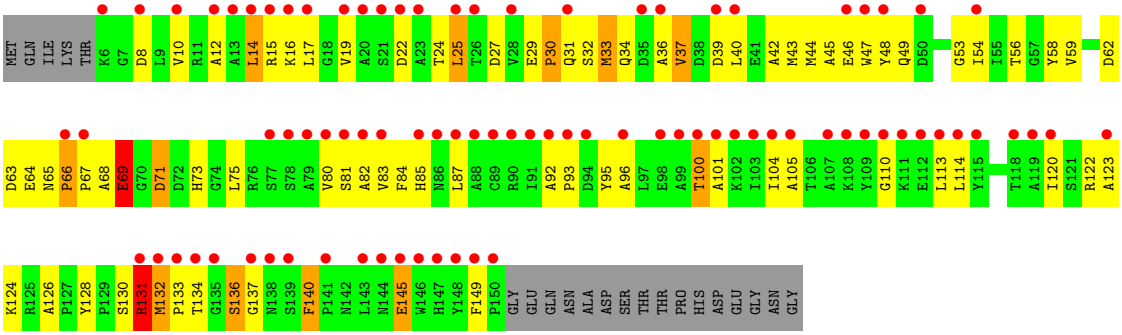
Chain n:





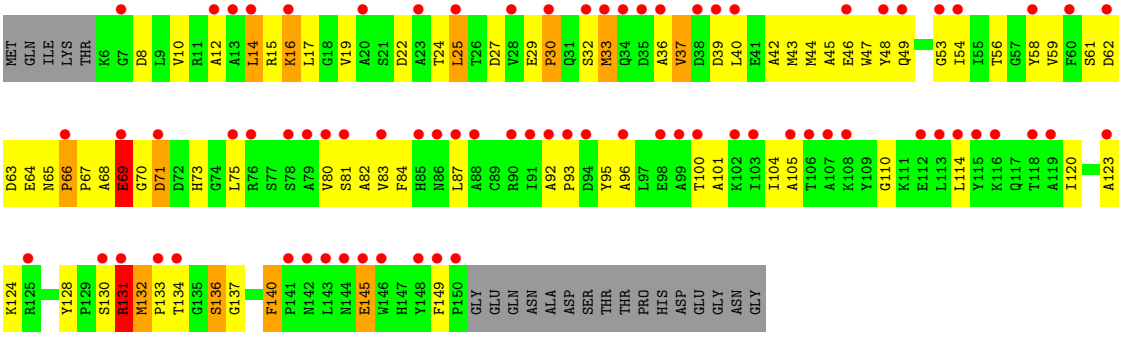
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

Chain o:



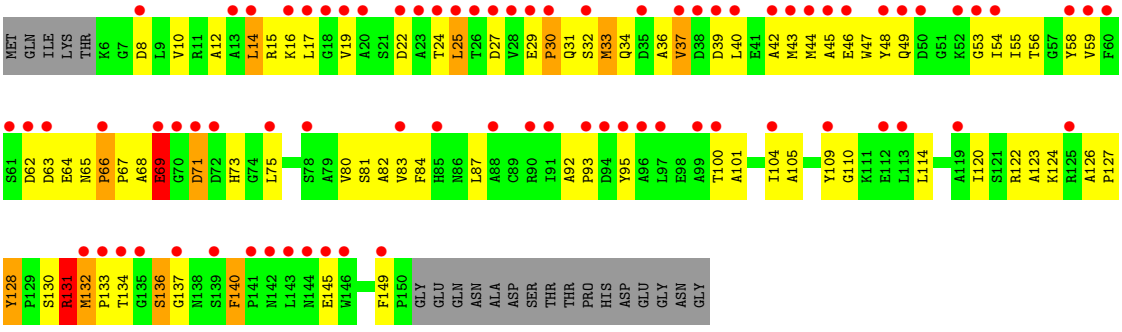
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

Chain p:



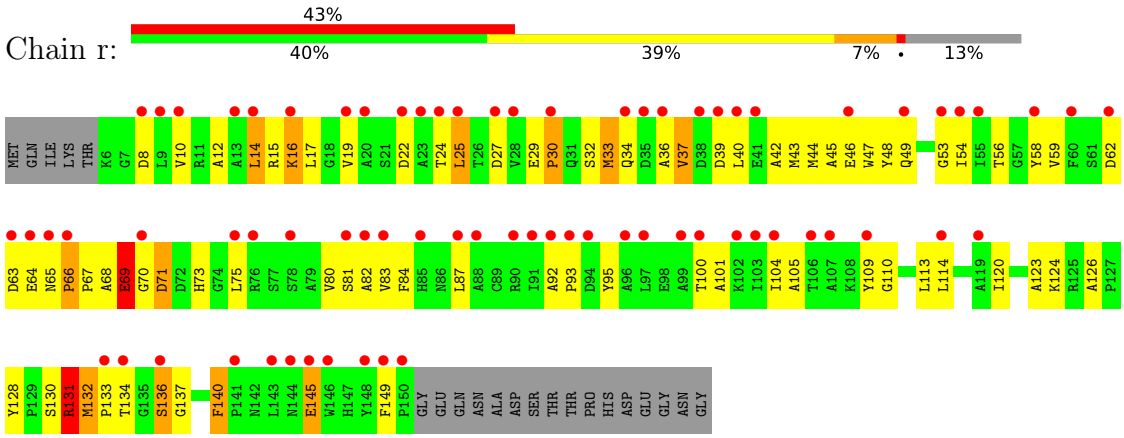
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

Chain q:



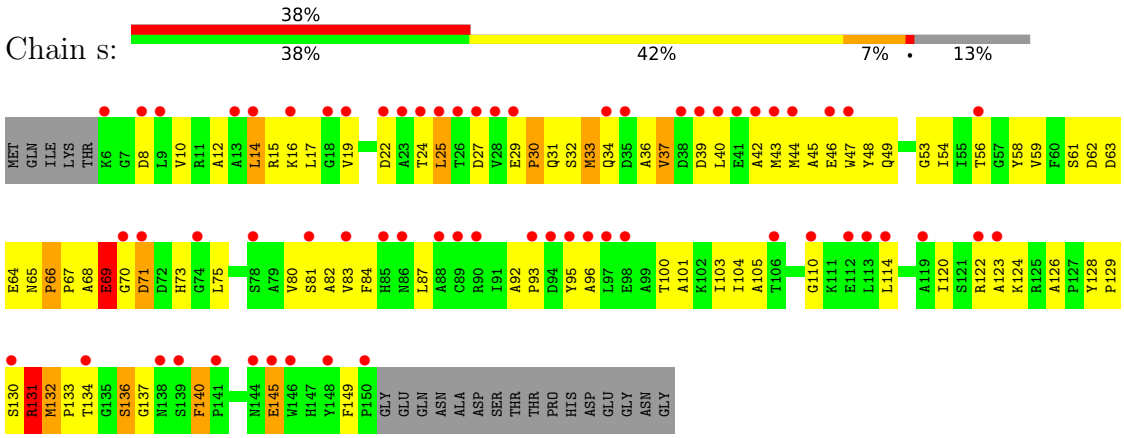
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

Chain r:



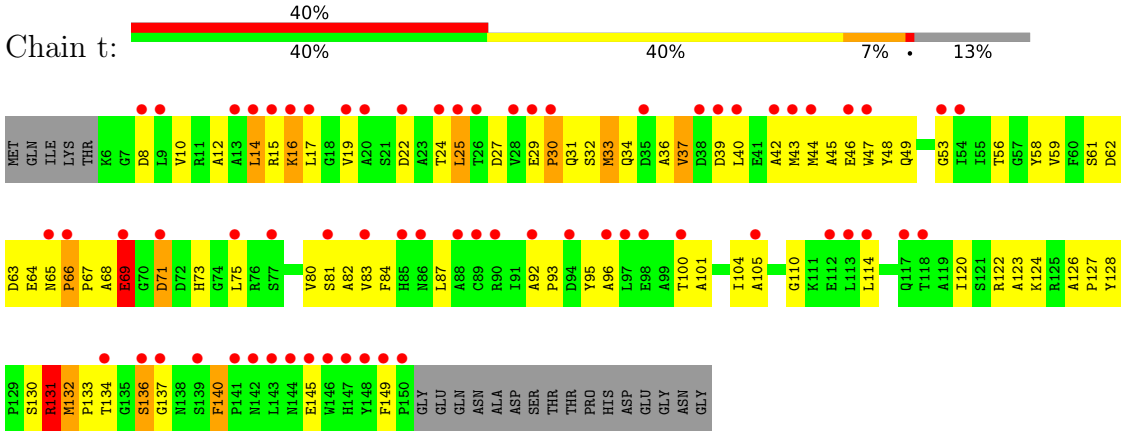
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

Chain s:



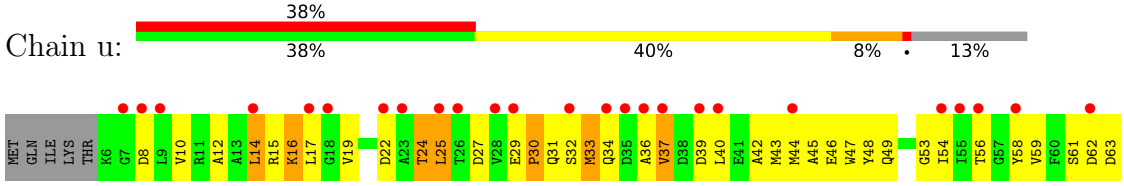
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

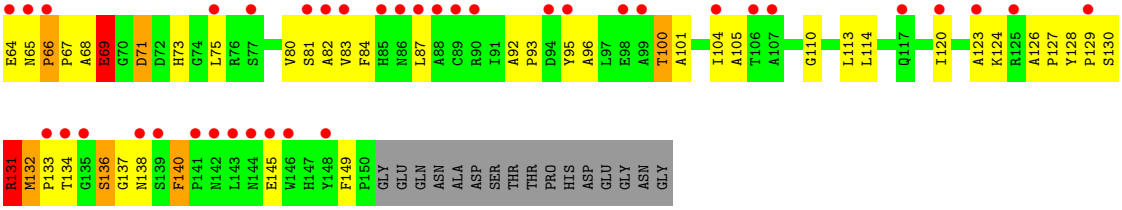
Chain t:



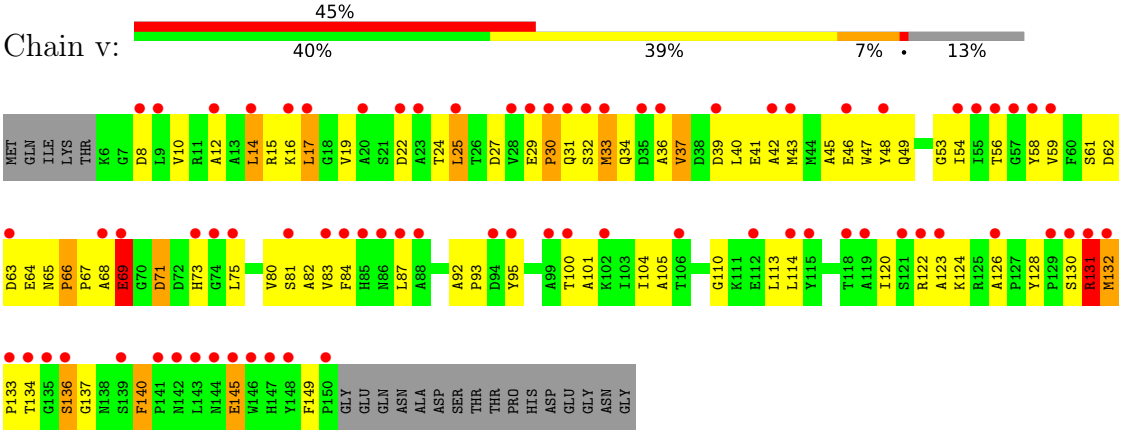
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

Chain u:

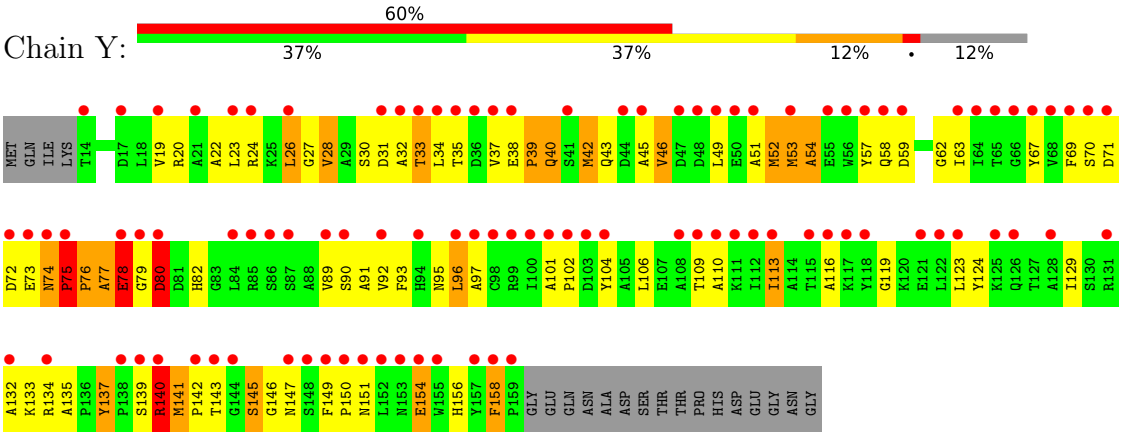




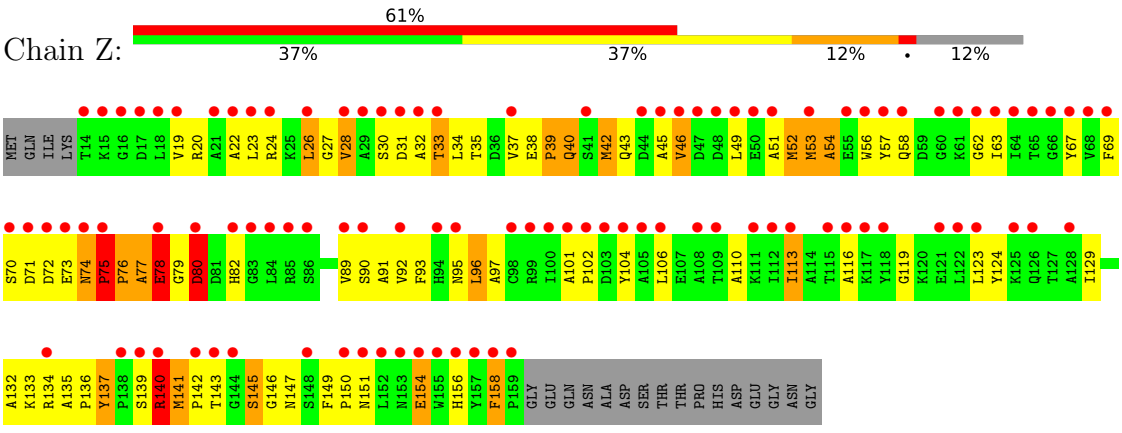
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



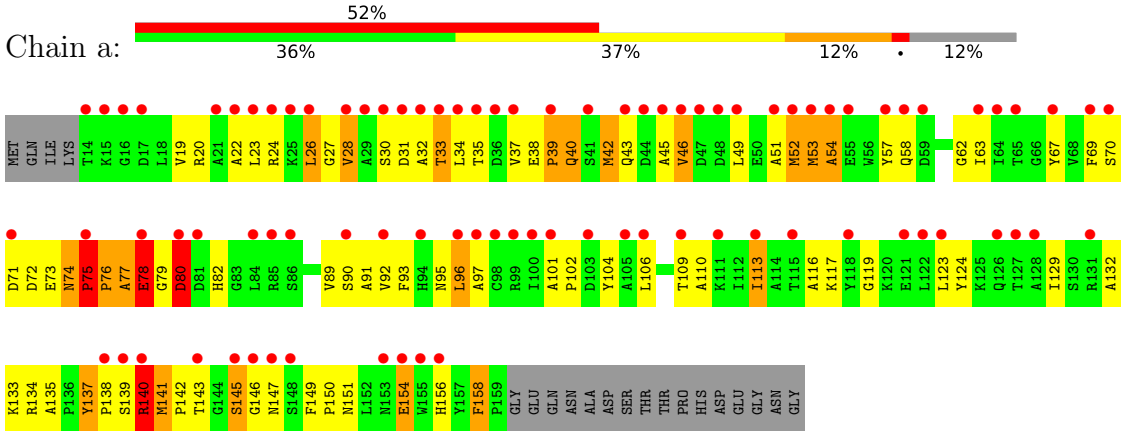
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



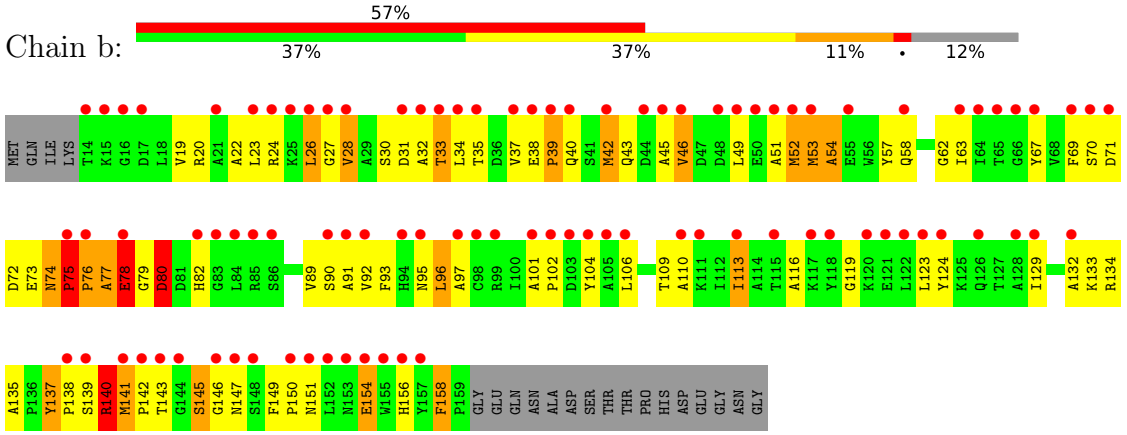
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



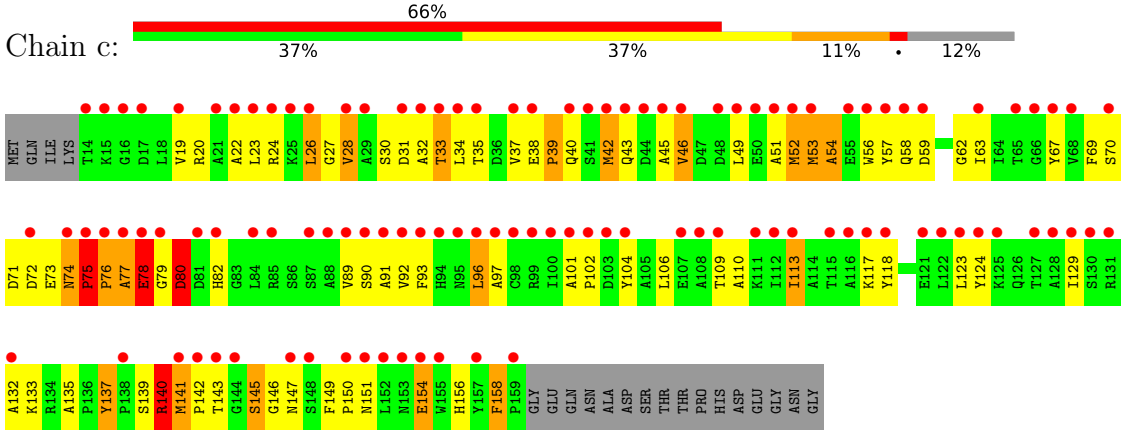
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



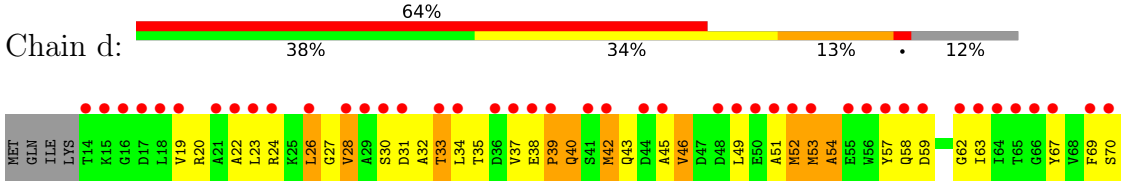
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

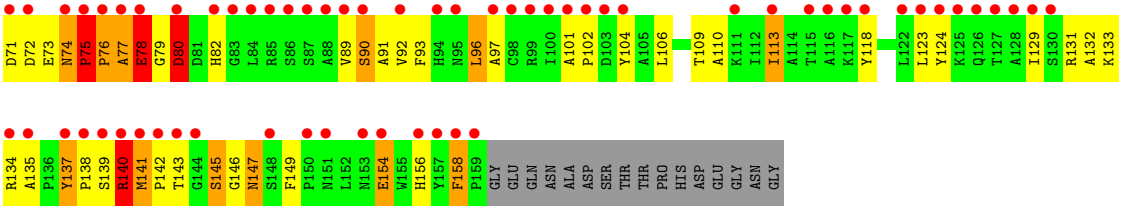


• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



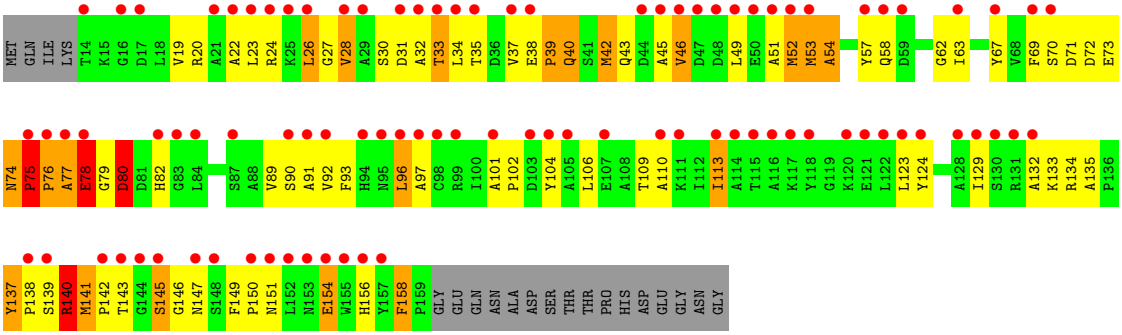
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4





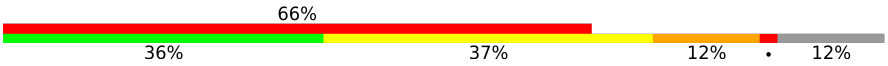
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

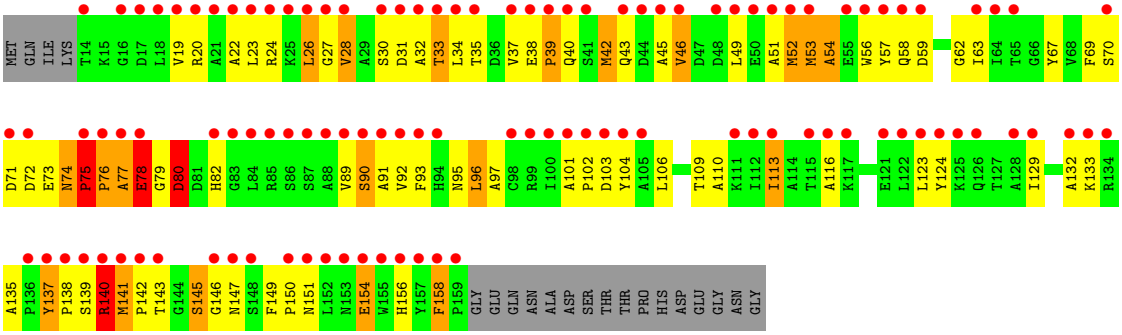
Chain e:



• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

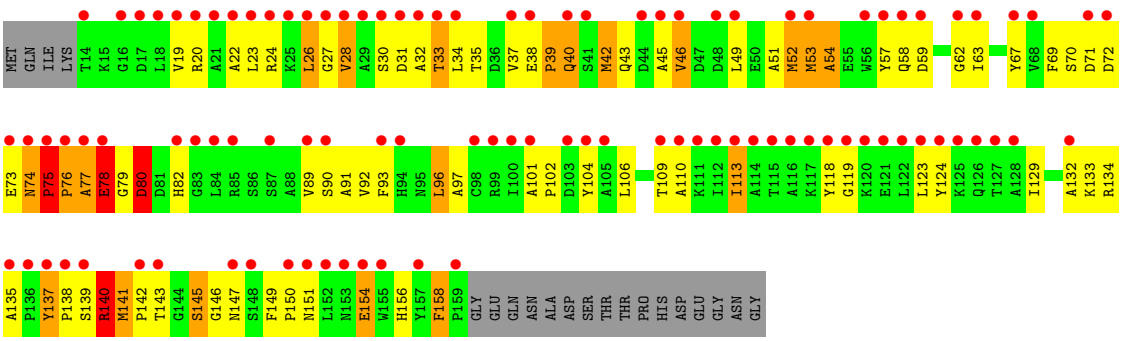
Chain f:





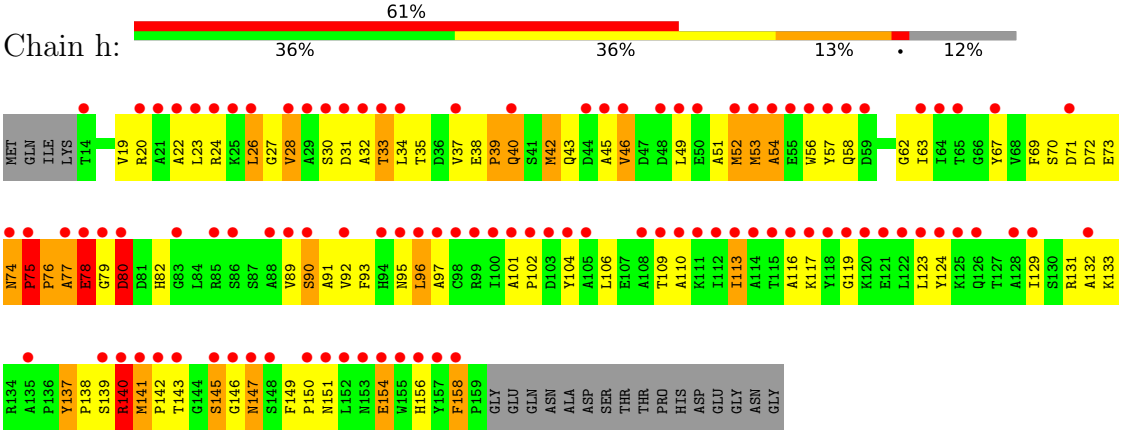
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

Chain g:



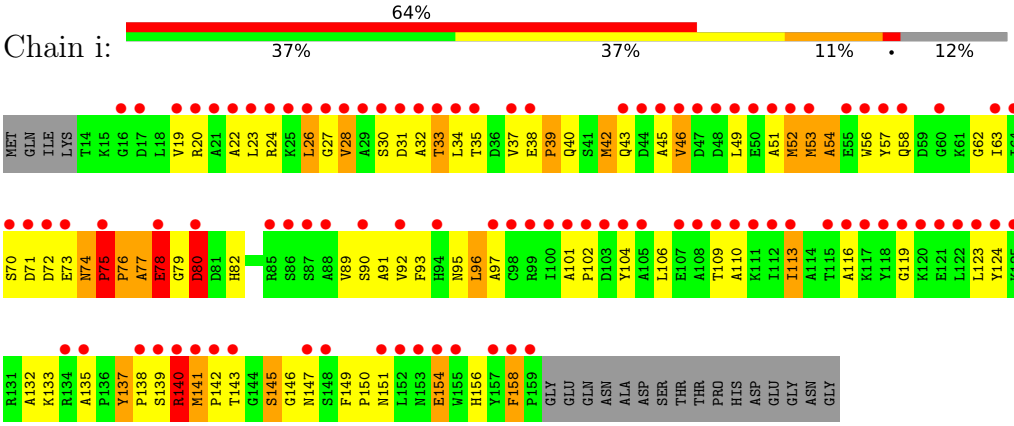
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

Chain h:



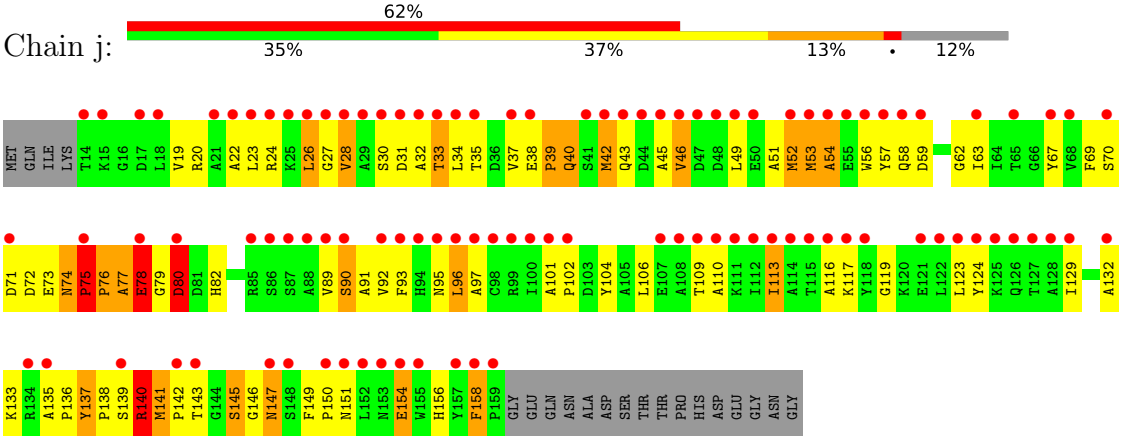
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

Chain i:



• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

Chain j:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	170.17Å 253.28Å 282.73Å 90.00° 90.68° 90.00°	Depositor
Resolution (Å)	19.99 – 3.25 19.99 – 3.25	Depositor EDS
% Data completeness (in resolution range)	59.7 (19.99-3.25) 91.9 (19.99-3.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.15	Depositor
$< I/\sigma(I) >$ [1]	1.88 (at 3.26Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.5_2)	Depositor
R, R_{free}	0.222 , 0.236 0.341 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	65.0	Xtriage
Anisotropy	1.241	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 115.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	0.025 for h,-k,-l	Xtriage
F_o,F_c correlation	0.80	EDS
Total number of atoms	135120	wwPDB-VP
Average B, all atoms (Å^2)	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.69% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.44	0/4635	0.91	14/6265 (0.2%)
1	B	0.44	0/4635	0.92	14/6265 (0.2%)
1	C	0.44	0/4635	0.91	14/6265 (0.2%)
1	D	0.44	0/4635	0.92	14/6265 (0.2%)
1	E	0.44	0/4635	0.92	14/6265 (0.2%)
1	F	0.44	0/4635	0.92	14/6265 (0.2%)
1	G	0.44	0/4635	0.92	14/6265 (0.2%)
1	H	0.44	0/4635	0.92	14/6265 (0.2%)
1	I	0.44	0/4635	0.91	14/6265 (0.2%)
1	J	0.44	0/4635	0.91	14/6265 (0.2%)
1	K	0.44	0/4635	0.92	14/6265 (0.2%)
1	L	0.44	0/4635	0.92	14/6265 (0.2%)
1	M	0.40	0/4646	0.87	20/6278 (0.3%)
1	N	0.41	0/4646	0.87	20/6278 (0.3%)
1	O	0.41	0/4646	0.87	20/6278 (0.3%)
1	P	0.41	0/4646	0.87	23/6278 (0.4%)
1	Q	0.40	0/4646	0.88	21/6278 (0.3%)
1	R	0.41	0/4646	0.87	24/6278 (0.4%)
1	S	0.40	0/4646	0.87	22/6278 (0.4%)
1	T	0.40	0/4646	0.87	21/6278 (0.3%)
1	U	0.40	0/4646	0.87	18/6278 (0.3%)
1	V	0.40	0/4646	0.88	19/6278 (0.3%)
1	W	0.40	0/4646	0.88	22/6278 (0.4%)
1	X	0.40	0/4646	0.87	21/6278 (0.3%)
2	Y	0.53	0/1067	1.17	10/1452 (0.7%)
2	Z	0.53	0/1067	1.18	10/1452 (0.7%)
2	a	0.53	0/1067	1.18	10/1452 (0.7%)
2	b	0.53	0/1067	1.17	10/1452 (0.7%)
2	c	0.53	0/1067	1.17	10/1452 (0.7%)
2	d	0.53	0/1067	1.18	10/1452 (0.7%)
2	e	0.53	0/1067	1.17	10/1452 (0.7%)
2	f	0.53	0/1067	1.17	10/1452 (0.7%)
2	g	0.53	0/1067	1.17	10/1452 (0.7%)
2	h	0.53	0/1067	1.17	10/1452 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
2	i	0.53	0/1067	1.18	10/1452 (0.7%)
2	j	0.53	0/1067	1.18	10/1452 (0.7%)
2	k	0.45	0/1071	0.92	5/1455 (0.3%)
2	l	0.45	0/1071	0.92	3/1455 (0.2%)
2	m	0.45	0/1071	0.91	4/1455 (0.3%)
2	n	0.47	0/1071	0.91	3/1455 (0.2%)
2	o	0.47	0/1071	0.91	4/1455 (0.3%)
2	p	0.45	0/1071	0.91	4/1455 (0.3%)
2	q	0.43	0/1071	0.92	5/1455 (0.3%)
2	r	0.46	0/1071	0.91	4/1455 (0.3%)
2	s	0.43	0/1071	0.91	4/1455 (0.3%)
2	t	0.43	0/1071	0.91	3/1455 (0.2%)
2	u	0.44	0/1071	0.93	3/1455 (0.2%)
2	v	0.45	0/1071	0.91	4/1455 (0.3%)
All	All	0.44	0/137028	0.93	585/185400 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
1	I	0	1
1	J	0	1
1	K	0	1
1	L	0	1
1	M	0	1
1	N	0	1
1	O	0	1
1	P	0	1
1	Q	0	1
1	R	0	1
1	S	0	1
1	T	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	U	0	1
1	V	0	1
1	W	0	1
1	X	0	1
All	All	0	24

There are no bond length outliers.

All (585) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	i	80	ASP	N-CA-CB	18.38	141.54	110.49
2	d	80	ASP	N-CA-CB	18.36	141.52	110.49
2	Z	80	ASP	N-CA-CB	18.36	141.51	110.49
2	Y	80	ASP	N-CA-CB	18.35	141.50	110.49
2	e	80	ASP	N-CA-CB	18.35	141.50	110.49
2	a	80	ASP	N-CA-CB	18.35	141.50	110.49
2	j	80	ASP	N-CA-CB	18.35	141.50	110.49
2	b	80	ASP	N-CA-CB	18.34	141.48	110.49
2	f	80	ASP	N-CA-CB	18.34	141.48	110.49
2	g	80	ASP	N-CA-CB	18.34	141.48	110.49
2	c	80	ASP	N-CA-CB	18.34	141.48	110.49
2	h	80	ASP	N-CA-CB	18.32	141.45	110.49
2	f	80	ASP	N-CA-C	-11.21	86.93	110.80
2	g	80	ASP	N-CA-C	-11.21	86.93	110.80
2	i	80	ASP	N-CA-C	-11.20	86.94	110.80
2	Z	80	ASP	N-CA-C	-11.20	86.95	110.80
2	Y	80	ASP	N-CA-C	-11.19	86.96	110.80
2	e	80	ASP	N-CA-C	-11.19	86.97	110.80
2	c	80	ASP	N-CA-C	-11.19	86.97	110.80
2	d	80	ASP	N-CA-C	-11.18	86.98	110.80
2	b	80	ASP	N-CA-C	-11.18	86.98	110.80
2	j	80	ASP	N-CA-C	-11.18	86.99	110.80
2	h	80	ASP	N-CA-C	-11.18	87.00	110.80
2	a	80	ASP	N-CA-C	-11.17	87.00	110.80
1	W	74	ASN	CA-C-N	9.00	128.60	119.24
1	W	74	ASN	C-N-CA	9.00	128.60	119.24
1	D	266	ILE	N-CA-C	8.95	118.62	107.70
1	A	266	ILE	N-CA-C	8.93	118.59	107.70
1	H	266	ILE	N-CA-C	8.92	118.58	107.70
1	I	266	ILE	N-CA-C	8.92	118.58	107.70
1	B	266	ILE	N-CA-C	8.91	118.58	107.70
1	C	266	ILE	N-CA-C	8.91	118.58	107.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L	266	ILE	N-CA-C	8.91	118.57	107.70
1	K	266	ILE	N-CA-C	8.91	118.57	107.70
1	F	266	ILE	N-CA-C	8.90	118.56	107.70
1	G	266	ILE	N-CA-C	8.90	118.56	107.70
1	E	266	ILE	N-CA-C	8.90	118.56	107.70
1	J	266	ILE	N-CA-C	8.89	118.55	107.70
1	V	74	ASN	CA-C-N	8.64	128.22	119.24
1	V	74	ASN	C-N-CA	8.64	128.22	119.24
1	S	74	ASN	CA-C-N	8.58	128.16	119.24
1	S	74	ASN	C-N-CA	8.58	128.16	119.24
1	X	74	ASN	CA-C-N	8.41	127.99	119.24
1	X	74	ASN	C-N-CA	8.41	127.99	119.24
2	u	140	PHE	CA-C-N	8.19	127.75	119.24
2	u	140	PHE	C-N-CA	8.19	127.75	119.24
1	H	160	SER	N-CA-C	-8.11	103.11	113.16
1	G	160	SER	N-CA-C	-8.08	103.14	113.16
1	I	160	SER	N-CA-C	-8.08	103.14	113.16
1	J	160	SER	N-CA-C	-8.08	103.14	113.16
1	L	160	SER	N-CA-C	-8.07	103.15	113.16
1	F	160	SER	N-CA-C	-8.07	103.15	113.16
1	A	160	SER	N-CA-C	-8.07	103.16	113.16
1	E	160	SER	N-CA-C	-8.07	103.16	113.16
1	C	160	SER	N-CA-C	-8.06	103.16	113.16
1	B	160	SER	N-CA-C	-8.05	103.17	113.16
1	K	160	SER	N-CA-C	-8.05	103.17	113.16
1	D	160	SER	N-CA-C	-8.04	103.20	113.16
1	S	266	ILE	N-CA-C	7.92	118.81	107.88
1	T	266	ILE	N-CA-C	7.82	118.67	107.88
2	j	74	ASN	N-CA-C	7.80	124.24	113.16
1	W	160	SER	N-CA-C	-7.79	103.83	112.72
2	d	74	ASN	N-CA-C	7.79	124.22	113.16
2	b	74	ASN	N-CA-C	7.79	124.22	113.16
2	c	74	ASN	N-CA-C	7.78	124.20	113.16
2	Y	74	ASN	N-CA-C	7.78	124.20	113.16
2	Z	74	ASN	N-CA-C	7.77	124.20	113.16
2	a	74	ASN	N-CA-C	7.77	124.20	113.16
2	i	74	ASN	N-CA-C	7.77	124.19	113.16
1	O	160	SER	N-CA-C	-7.77	103.87	112.72
2	h	74	ASN	N-CA-C	7.76	124.18	113.16
2	g	74	ASN	N-CA-C	7.76	124.17	113.16
2	e	74	ASN	N-CA-C	7.75	124.17	113.16
1	R	160	SER	N-CA-C	-7.75	103.88	112.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	f	74	ASN	N-CA-C	7.74	124.15	113.16
1	V	266	ILE	N-CA-C	7.74	118.56	107.88
1	Q	160	SER	N-CA-C	-7.73	103.91	112.72
1	N	160	SER	N-CA-C	-7.72	103.92	112.72
1	T	160	SER	N-CA-C	-7.70	103.94	112.72
1	U	160	SER	N-CA-C	-7.70	103.94	112.72
1	P	160	SER	N-CA-C	-7.69	103.95	112.72
1	W	266	ILE	N-CA-C	7.69	118.50	107.88
1	L	455	THR	N-CA-C	7.69	119.30	111.07
1	E	455	THR	N-CA-C	7.69	119.30	111.07
1	C	455	THR	N-CA-C	7.68	119.29	111.07
1	F	455	THR	N-CA-C	7.68	119.29	111.07
1	P	266	ILE	N-CA-C	7.67	118.46	107.88
1	H	455	THR	N-CA-C	7.67	119.28	111.07
1	V	160	SER	N-CA-C	-7.67	103.98	112.72
1	B	455	THR	N-CA-C	7.66	119.27	111.07
1	A	455	THR	N-CA-C	7.65	119.26	111.07
1	D	455	THR	N-CA-C	7.65	119.25	111.07
1	I	455	THR	N-CA-C	7.65	119.25	111.07
1	G	455	THR	N-CA-C	7.64	119.25	111.07
1	K	455	THR	N-CA-C	7.64	119.25	111.07
1	J	455	THR	N-CA-C	7.64	119.24	111.07
1	X	160	SER	N-CA-C	-7.63	104.02	112.72
1	O	266	ILE	N-CA-C	7.63	118.40	107.88
1	M	231	THR	N-CA-C	7.61	120.90	108.26
1	O	231	THR	N-CA-C	7.60	120.88	108.26
1	U	266	ILE	N-CA-C	7.60	118.36	107.88
1	M	160	SER	N-CA-C	-7.59	104.07	112.72
1	U	231	THR	N-CA-C	7.55	120.80	108.26
1	X	266	ILE	N-CA-C	7.53	118.27	107.88
1	T	231	THR	N-CA-C	7.51	120.73	108.26
1	X	231	THR	N-CA-C	7.50	120.72	108.26
1	R	266	ILE	N-CA-C	7.50	118.23	107.88
1	Q	231	THR	N-CA-C	7.49	120.70	108.26
1	M	266	ILE	N-CA-C	7.49	118.22	107.88
1	S	160	SER	N-CA-C	-7.47	104.20	112.72
1	R	231	THR	N-CA-C	7.42	120.58	108.26
1	W	231	THR	N-CA-C	7.39	120.52	108.26
2	r	140	PHE	CA-C-N	7.39	127.74	119.32
2	r	140	PHE	C-N-CA	7.39	127.74	119.32
1	V	231	THR	N-CA-C	7.38	120.51	108.26
2	l	140	PHE	CA-C-N	7.29	127.62	119.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	l	140	PHE	C-N-CA	7.29	127.62	119.32
1	P	231	THR	N-CA-C	7.27	120.32	108.26
1	Q	266	ILE	N-CA-C	7.26	117.90	107.88
1	S	231	THR	N-CA-C	7.26	120.32	108.26
1	N	266	ILE	N-CA-C	7.22	117.85	107.88
1	N	74	ASN	CA-C-N	7.21	128.85	119.84
1	N	74	ASN	C-N-CA	7.21	128.85	119.84
2	m	140	PHE	CA-C-N	7.20	127.53	119.32
2	m	140	PHE	C-N-CA	7.20	127.53	119.32
2	s	140	PHE	CA-C-N	7.19	127.52	119.32
2	s	140	PHE	C-N-CA	7.19	127.52	119.32
2	t	140	PHE	CA-C-N	7.18	127.51	119.32
2	t	140	PHE	C-N-CA	7.18	127.51	119.32
2	v	140	PHE	CA-C-N	7.17	127.50	119.32
2	v	140	PHE	C-N-CA	7.17	127.50	119.32
1	W	249	ARG	NE-CZ-NH2	-7.16	112.75	119.20
2	p	140	PHE	CA-C-N	7.16	127.48	119.32
2	p	140	PHE	C-N-CA	7.16	127.48	119.32
2	n	140	PHE	CA-C-N	7.15	127.47	119.32
2	n	140	PHE	C-N-CA	7.15	127.47	119.32
1	T	74	ASN	CA-C-N	7.14	128.76	119.84
1	T	74	ASN	C-N-CA	7.14	128.76	119.84
2	j	77	ALA	N-CA-C	7.10	117.90	107.88
2	i	77	ALA	N-CA-C	7.10	117.89	107.88
2	Z	77	ALA	N-CA-C	7.09	117.88	107.88
2	h	77	ALA	N-CA-C	7.08	117.87	107.88
2	o	140	PHE	CA-C-N	7.08	127.39	119.32
2	o	140	PHE	C-N-CA	7.08	127.39	119.32
2	d	77	ALA	N-CA-C	7.08	117.86	107.88
2	e	77	ALA	N-CA-C	7.07	117.85	107.88
2	Y	77	ALA	N-CA-C	7.07	117.84	107.88
2	g	77	ALA	N-CA-C	7.06	117.83	107.88
2	b	77	ALA	N-CA-C	7.06	117.83	107.88
2	f	77	ALA	N-CA-C	7.06	117.83	107.88
2	a	77	ALA	N-CA-C	7.05	117.83	107.88
2	q	140	PHE	CA-C-N	7.05	127.35	119.32
2	q	140	PHE	C-N-CA	7.05	127.35	119.32
2	c	77	ALA	N-CA-C	7.04	117.81	107.88
2	k	140	PHE	CA-C-N	7.00	127.30	119.32
2	k	140	PHE	C-N-CA	7.00	127.30	119.32
1	P	74	ASN	CA-C-N	6.97	128.56	119.84
1	P	74	ASN	C-N-CA	6.97	128.56	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	O	74	ASN	CA-C-N	6.93	128.50	119.84
1	O	74	ASN	C-N-CA	6.93	128.50	119.84
1	L	231	THR	N-CA-C	6.92	120.94	108.69
1	N	231	THR	N-CA-C	6.92	119.75	108.26
1	Q	74	ASN	CA-C-N	6.92	128.49	119.84
1	Q	74	ASN	C-N-CA	6.92	128.49	119.84
1	C	231	THR	N-CA-C	6.91	120.91	108.69
1	D	231	THR	N-CA-C	6.90	120.91	108.69
1	G	231	THR	N-CA-C	6.90	120.90	108.69
1	H	231	THR	N-CA-C	6.89	120.89	108.69
1	E	231	THR	N-CA-C	6.89	120.89	108.69
1	I	231	THR	N-CA-C	6.89	120.88	108.69
1	A	231	THR	N-CA-C	6.89	120.88	108.69
1	J	231	THR	N-CA-C	6.89	120.88	108.69
1	B	231	THR	N-CA-C	6.88	120.86	108.69
1	F	231	THR	N-CA-C	6.87	120.86	108.69
1	R	74	ASN	CA-C-N	6.87	128.43	119.84
1	R	74	ASN	C-N-CA	6.87	128.43	119.84
1	K	231	THR	N-CA-C	6.87	120.85	108.69
1	M	74	ASN	CA-C-N	6.86	128.42	119.84
1	M	74	ASN	C-N-CA	6.86	128.42	119.84
1	T	387	GLN	CA-C-N	6.82	128.36	119.84
1	T	387	GLN	C-N-CA	6.82	128.36	119.84
1	E	198	ILE	CA-C-N	6.78	128.23	120.98
1	E	198	ILE	C-N-CA	6.78	128.23	120.98
1	B	198	ILE	CA-C-N	6.76	128.22	120.98
1	B	198	ILE	C-N-CA	6.76	128.22	120.98
1	S	198	ILE	CA-C-N	6.75	128.20	120.98
1	S	198	ILE	C-N-CA	6.75	128.20	120.98
1	K	198	ILE	CA-C-N	6.75	128.21	120.98
1	K	198	ILE	C-N-CA	6.75	128.21	120.98
1	D	198	ILE	CA-C-N	6.75	128.20	120.98
1	D	198	ILE	C-N-CA	6.75	128.20	120.98
1	A	198	ILE	CA-C-N	6.74	128.19	120.98
1	A	198	ILE	C-N-CA	6.74	128.19	120.98
1	H	198	ILE	CA-C-N	6.73	128.19	120.98
1	H	198	ILE	C-N-CA	6.73	128.19	120.98
1	L	198	ILE	CA-C-N	6.73	128.18	120.98
1	L	198	ILE	C-N-CA	6.73	128.18	120.98
1	S	387	GLN	CA-C-N	6.73	128.25	119.84
1	S	387	GLN	C-N-CA	6.73	128.25	119.84
1	W	387	GLN	CA-C-N	6.72	128.25	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	W	387	GLN	C-N-CA	6.72	128.25	119.84
1	N	198	ILE	CA-C-N	6.72	128.17	120.98
1	N	198	ILE	C-N-CA	6.72	128.17	120.98
1	I	198	ILE	CA-C-N	6.72	128.17	120.98
1	I	198	ILE	C-N-CA	6.72	128.17	120.98
1	K	74	ASN	CA-C-N	6.72	128.24	119.84
1	K	74	ASN	C-N-CA	6.72	128.24	119.84
1	L	74	ASN	CA-C-N	6.72	128.24	119.84
1	L	74	ASN	C-N-CA	6.72	128.24	119.84
1	G	198	ILE	CA-C-N	6.72	128.17	120.98
1	G	198	ILE	C-N-CA	6.72	128.17	120.98
1	B	74	ASN	CA-C-N	6.72	128.24	119.84
1	B	74	ASN	C-N-CA	6.72	128.24	119.84
1	C	198	ILE	CA-C-N	6.71	128.16	120.98
1	C	198	ILE	C-N-CA	6.71	128.16	120.98
1	V	387	GLN	CA-C-N	6.71	128.22	119.84
1	V	387	GLN	C-N-CA	6.71	128.22	119.84
1	J	198	ILE	CA-C-N	6.70	128.15	120.98
1	J	198	ILE	C-N-CA	6.70	128.15	120.98
1	F	198	ILE	CA-C-N	6.69	128.14	120.98
1	F	198	ILE	C-N-CA	6.69	128.14	120.98
1	D	74	ASN	CA-C-N	6.69	128.20	119.84
1	D	74	ASN	C-N-CA	6.69	128.20	119.84
1	F	74	ASN	CA-C-N	6.69	128.20	119.84
1	F	74	ASN	C-N-CA	6.69	128.20	119.84
1	H	74	ASN	CA-C-N	6.69	128.20	119.84
1	H	74	ASN	C-N-CA	6.69	128.20	119.84
1	A	74	ASN	CA-C-N	6.68	128.19	119.84
1	A	74	ASN	C-N-CA	6.68	128.19	119.84
1	E	74	ASN	CA-C-N	6.67	128.18	119.84
1	E	74	ASN	C-N-CA	6.67	128.18	119.84
1	G	74	ASN	CA-C-N	6.67	128.18	119.84
1	G	74	ASN	C-N-CA	6.67	128.18	119.84
1	U	74	ASN	CA-C-N	6.67	128.18	119.84
1	U	74	ASN	C-N-CA	6.67	128.18	119.84
1	I	74	ASN	CA-C-N	6.66	128.16	119.84
1	I	74	ASN	C-N-CA	6.66	128.16	119.84
1	J	74	ASN	CA-C-N	6.66	128.16	119.84
1	J	74	ASN	C-N-CA	6.66	128.16	119.84
1	C	74	ASN	CA-C-N	6.65	128.16	119.84
1	C	74	ASN	C-N-CA	6.65	128.16	119.84
1	R	198	ILE	CA-C-N	6.65	128.09	120.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	R	198	ILE	C-N-CA	6.65	128.09	120.98
1	P	387	GLN	CA-C-N	6.60	128.09	119.84
1	P	387	GLN	C-N-CA	6.60	128.09	119.84
1	M	387	GLN	CA-C-N	6.56	128.04	119.84
1	M	387	GLN	C-N-CA	6.56	128.04	119.84
1	O	387	GLN	CA-C-N	6.54	128.01	119.84
1	O	387	GLN	C-N-CA	6.54	128.01	119.84
1	P	198	ILE	CA-C-N	6.53	127.96	120.98
1	P	198	ILE	C-N-CA	6.53	127.96	120.98
1	V	198	ILE	CA-C-N	6.52	127.96	120.98
1	V	198	ILE	C-N-CA	6.52	127.96	120.98
1	U	387	GLN	CA-C-N	6.52	127.99	119.84
1	U	387	GLN	C-N-CA	6.52	127.99	119.84
1	W	198	ILE	CA-C-N	6.50	127.93	120.98
1	W	198	ILE	C-N-CA	6.50	127.93	120.98
1	M	198	ILE	CA-C-N	6.50	127.93	120.98
1	M	198	ILE	C-N-CA	6.50	127.93	120.98
1	Q	387	GLN	CA-C-N	6.48	127.94	119.84
1	Q	387	GLN	C-N-CA	6.48	127.94	119.84
1	Q	198	ILE	CA-C-N	6.47	127.91	120.98
1	Q	198	ILE	C-N-CA	6.47	127.91	120.98
1	U	198	ILE	CA-C-N	6.43	127.86	120.98
1	U	198	ILE	C-N-CA	6.43	127.86	120.98
1	R	387	GLN	CA-C-N	6.42	127.86	119.84
1	R	387	GLN	C-N-CA	6.42	127.86	119.84
1	N	387	GLN	CA-C-N	6.41	127.85	119.84
1	N	387	GLN	C-N-CA	6.41	127.85	119.84
1	X	387	GLN	CA-C-N	6.39	127.83	119.84
1	X	387	GLN	C-N-CA	6.39	127.83	119.84
1	T	198	ILE	CA-C-N	6.38	127.81	120.98
1	T	198	ILE	C-N-CA	6.38	127.81	120.98
1	O	198	ILE	CA-C-N	6.37	127.79	120.98
1	O	198	ILE	C-N-CA	6.37	127.79	120.98
1	X	198	ILE	CA-C-N	6.34	127.77	120.98
1	X	198	ILE	C-N-CA	6.34	127.77	120.98
2	q	46	GLU	N-CA-C	-6.30	104.04	111.03
2	u	46	GLU	N-CA-C	-6.21	104.14	111.03
2	k	46	GLU	N-CA-C	-6.07	104.29	111.03
2	v	46	GLU	N-CA-C	-6.05	104.31	111.03
2	l	46	GLU	N-CA-C	-6.00	104.37	111.03
1	R	147	GLU	CA-C-N	5.97	125.94	120.03
1	R	147	GLU	C-N-CA	5.97	125.94	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	a	75	PRO	C-N-CD	-5.96	100.57	125.00
2	c	75	PRO	C-N-CD	-5.95	100.60	125.00
2	Z	75	PRO	C-N-CD	-5.95	100.61	125.00
2	f	75	PRO	C-N-CD	-5.95	100.62	125.00
2	i	75	PRO	C-N-CD	-5.95	100.62	125.00
2	Y	75	PRO	C-N-CD	-5.95	100.62	125.00
2	e	75	PRO	C-N-CD	-5.95	100.62	125.00
2	g	75	PRO	C-N-CD	-5.95	100.62	125.00
2	j	75	PRO	C-N-CD	-5.94	100.63	125.00
2	b	75	PRO	C-N-CD	-5.94	100.64	125.00
2	d	75	PRO	C-N-CD	-5.94	100.64	125.00
2	h	75	PRO	C-N-CD	-5.94	100.65	125.00
1	X	164	LEU	N-CA-C	5.92	117.78	108.96
1	R	164	LEU	N-CA-C	5.88	117.72	108.96
2	n	46	GLU	N-CA-C	-5.85	104.53	111.03
1	N	583	LYS	CA-C-N	5.85	125.87	119.90
1	N	583	LYS	C-N-CA	5.85	125.87	119.90
2	t	46	GLU	N-CA-C	-5.85	104.54	111.03
2	j	137	TYR	CA-C-N	5.83	125.81	120.21
2	j	137	TYR	C-N-CA	5.83	125.81	120.21
1	M	147	GLU	CA-C-N	5.83	125.80	120.03
1	M	147	GLU	C-N-CA	5.83	125.80	120.03
1	M	164	LEU	N-CA-C	5.83	117.64	108.96
2	c	137	TYR	CA-C-N	5.82	125.79	120.21
2	c	137	TYR	C-N-CA	5.82	125.79	120.21
1	T	164	LEU	N-CA-C	5.81	117.62	108.96
2	i	137	TYR	CA-C-N	5.81	125.79	120.21
2	i	137	TYR	C-N-CA	5.81	125.79	120.21
2	a	137	TYR	CA-C-N	5.78	125.76	120.21
2	a	137	TYR	C-N-CA	5.78	125.76	120.21
2	d	137	TYR	CA-C-N	5.78	125.76	120.21
2	d	137	TYR	C-N-CA	5.78	125.76	120.21
2	s	46	GLU	N-CA-C	-5.77	104.62	111.03
2	Y	137	TYR	CA-C-N	5.77	125.75	120.21
2	Y	137	TYR	C-N-CA	5.77	125.75	120.21
2	Z	137	TYR	CA-C-N	5.77	125.75	120.21
2	Z	137	TYR	C-N-CA	5.77	125.75	120.21
1	O	164	LEU	N-CA-C	5.76	117.54	108.96
1	U	164	LEU	N-CA-C	5.76	117.55	108.96
2	o	46	GLU	N-CA-C	-5.76	104.63	111.03
2	f	137	TYR	CA-C-N	5.76	125.74	120.21
2	f	137	TYR	C-N-CA	5.76	125.74	120.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	V	583	LYS	CA-C-N	5.76	126.09	119.93
1	V	583	LYS	C-N-CA	5.76	126.09	119.93
1	N	164	LEU	N-CA-C	5.75	117.53	108.96
1	Q	147	GLU	CA-C-N	5.74	125.71	120.03
1	Q	147	GLU	C-N-CA	5.74	125.71	120.03
1	S	164	LEU	N-CA-C	5.73	117.50	108.96
2	p	46	GLU	N-CA-C	-5.73	104.67	111.03
1	P	583	LYS	CA-C-N	5.72	126.05	119.93
1	P	583	LYS	C-N-CA	5.72	126.05	119.93
2	h	137	TYR	CA-C-N	5.71	125.69	120.21
2	h	137	TYR	C-N-CA	5.71	125.69	120.21
1	R	203	ASN	CA-C-N	5.71	125.38	119.56
1	R	203	ASN	C-N-CA	5.71	125.38	119.56
1	G	232	ALA	N-CA-C	5.67	122.88	110.80
1	L	232	ALA	N-CA-C	5.67	122.88	110.80
1	E	232	ALA	N-CA-C	5.67	122.87	110.80
2	m	46	GLU	N-CA-C	-5.66	104.75	111.03
1	C	232	ALA	N-CA-C	5.66	122.85	110.80
1	H	232	ALA	N-CA-C	5.66	122.85	110.80
1	K	232	ALA	N-CA-C	5.66	122.85	110.80
1	A	232	ALA	N-CA-C	5.65	122.83	110.80
1	F	232	ALA	N-CA-C	5.65	122.83	110.80
1	B	232	ALA	N-CA-C	5.64	122.82	110.80
1	I	232	ALA	N-CA-C	5.64	122.81	110.80
1	D	232	ALA	N-CA-C	5.64	122.81	110.80
1	J	232	ALA	N-CA-C	5.63	122.79	110.80
1	P	232	ALA	N-CA-C	5.62	122.78	110.80
1	T	147	GLU	CA-C-N	5.60	125.58	120.03
1	T	147	GLU	C-N-CA	5.60	125.58	120.03
1	R	583	LYS	CA-C-N	5.60	125.92	119.93
1	R	583	LYS	C-N-CA	5.60	125.92	119.93
1	Q	583	LYS	CA-C-N	5.60	125.92	119.93
1	Q	583	LYS	C-N-CA	5.60	125.92	119.93
1	P	164	LEU	N-CA-C	5.59	117.29	108.96
1	O	583	LYS	CA-C-N	5.59	125.91	119.93
1	O	583	LYS	C-N-CA	5.59	125.91	119.93
1	V	203	ASN	CA-C-N	5.58	125.25	119.56
1	V	203	ASN	C-N-CA	5.58	125.25	119.56
1	Q	232	ALA	N-CA-C	5.58	122.67	110.80
1	V	147	GLU	CA-C-N	5.57	125.54	120.03
1	V	147	GLU	C-N-CA	5.57	125.54	120.03
1	U	583	LYS	CA-C-N	5.57	125.89	119.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	U	583	LYS	C-N-CA	5.57	125.89	119.93
1	N	232	ALA	N-CA-C	5.56	122.65	110.80
1	T	583	LYS	CA-C-N	5.56	125.88	119.93
1	T	583	LYS	C-N-CA	5.56	125.88	119.93
2	r	46	GLU	N-CA-C	-5.56	104.86	111.03
1	U	232	ALA	N-CA-C	5.56	122.64	110.80
1	O	203	ASN	CA-C-N	5.55	125.22	119.56
1	O	203	ASN	C-N-CA	5.55	125.22	119.56
1	O	147	GLU	CA-C-N	5.55	125.45	119.85
1	O	147	GLU	C-N-CA	5.55	125.45	119.85
1	V	164	LEU	N-CA-C	5.54	117.22	108.96
1	X	203	ASN	CA-C-N	5.54	125.21	119.56
1	X	203	ASN	C-N-CA	5.54	125.21	119.56
1	N	394	ASN	CA-C-N	5.53	125.46	119.76
1	N	394	ASN	C-N-CA	5.53	125.46	119.76
1	V	232	ALA	N-CA-C	5.53	122.58	110.80
1	P	394	ASN	CA-C-N	5.53	125.46	119.76
1	P	394	ASN	C-N-CA	5.53	125.46	119.76
1	X	583	LYS	CA-C-N	5.52	125.84	119.93
1	X	583	LYS	C-N-CA	5.52	125.84	119.93
1	R	232	ALA	N-CA-C	5.52	122.55	110.80
1	W	147	GLU	CA-C-N	5.52	125.49	120.03
1	W	147	GLU	C-N-CA	5.52	125.49	120.03
1	T	232	ALA	N-CA-C	5.50	122.51	110.80
2	i	28	VAL	N-CA-C	-5.50	105.49	110.82
1	W	583	LYS	CA-C-N	5.48	125.79	119.93
1	W	583	LYS	C-N-CA	5.48	125.79	119.93
2	j	28	VAL	N-CA-C	-5.48	105.51	110.82
1	M	232	ALA	N-CA-C	5.47	122.46	110.80
1	O	232	ALA	N-CA-C	5.46	122.44	110.80
2	e	28	VAL	N-CA-C	-5.46	105.52	110.82
1	D	58	ASP	CB-CA-C	-5.46	110.30	116.63
1	B	58	ASP	CB-CA-C	-5.45	110.31	116.63
2	Y	28	VAL	N-CA-C	-5.45	105.53	110.82
2	Z	28	VAL	N-CA-C	-5.45	105.54	110.82
2	g	28	VAL	N-CA-C	-5.44	105.54	110.82
1	J	58	ASP	CB-CA-C	-5.44	110.32	116.63
2	f	28	VAL	N-CA-C	-5.44	105.54	110.82
1	M	583	LYS	CA-C-N	5.44	125.75	119.93
1	M	583	LYS	C-N-CA	5.44	125.75	119.93
1	X	232	ALA	N-CA-C	5.44	122.39	110.80
1	L	58	ASP	CB-CA-C	-5.44	110.32	116.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	W	232	ALA	N-CA-C	5.44	122.38	110.80
1	W	367	ASP	N-CA-C	-5.43	106.43	112.57
2	f	40	GLN	N-CA-C	-5.43	106.02	113.30
1	F	58	ASP	CB-CA-C	-5.43	110.33	116.63
2	h	28	VAL	N-CA-C	-5.43	105.55	110.82
1	N	147	GLU	CA-C-N	5.43	125.41	120.03
1	N	147	GLU	C-N-CA	5.43	125.41	120.03
1	S	147	GLU	CA-C-N	5.43	125.41	120.03
1	S	147	GLU	C-N-CA	5.43	125.41	120.03
2	a	40	GLN	N-CA-C	-5.43	106.03	113.30
1	R	367	ASP	N-CA-C	-5.43	106.44	112.57
1	X	320	VAL	N-CA-C	5.43	116.16	110.62
1	A	58	ASP	CB-CA-C	-5.43	110.33	116.63
2	c	40	GLN	N-CA-C	-5.42	106.03	113.30
2	e	40	GLN	N-CA-C	-5.42	106.03	113.30
1	G	58	ASP	CB-CA-C	-5.42	110.34	116.63
2	h	40	GLN	N-CA-C	-5.42	106.03	113.30
2	c	28	VAL	N-CA-C	-5.42	105.56	110.82
1	Q	203	ASN	CA-C-N	5.42	125.09	119.56
1	Q	203	ASN	C-N-CA	5.42	125.09	119.56
1	U	320	VAL	N-CA-C	5.42	116.15	110.62
1	P	203	ASN	CA-C-N	5.42	125.08	119.56
1	P	203	ASN	C-N-CA	5.42	125.08	119.56
2	j	40	GLN	N-CA-C	-5.42	106.04	113.30
1	C	58	ASP	CB-CA-C	-5.42	110.35	116.63
2	b	28	VAL	N-CA-C	-5.42	105.57	110.82
1	K	58	ASP	CB-CA-C	-5.41	110.35	116.63
2	Y	40	GLN	N-CA-C	-5.41	106.05	113.30
1	C	164	LEU	N-CA-C	5.41	117.29	109.07
1	I	58	ASP	CB-CA-C	-5.41	110.36	116.63
2	d	40	GLN	N-CA-C	-5.41	106.05	113.30
1	H	58	ASP	CB-CA-C	-5.41	110.36	116.63
1	E	58	ASP	CB-CA-C	-5.40	110.36	116.63
2	d	28	VAL	N-CA-C	-5.40	105.58	110.82
1	K	164	LEU	N-CA-C	5.40	117.28	109.07
2	a	28	VAL	N-CA-C	-5.40	105.58	110.82
2	b	40	GLN	N-CA-C	-5.40	106.06	113.30
1	D	164	LEU	N-CA-C	5.40	117.27	109.07
1	I	164	LEU	N-CA-C	5.40	117.27	109.07
1	Q	164	LEU	N-CA-C	5.40	117.00	108.96
1	A	164	LEU	N-CA-C	5.39	117.27	109.07
2	Z	40	GLN	N-CA-C	-5.39	106.07	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	g	40	GLN	N-CA-C	-5.39	106.08	113.30
1	X	147	GLU	CA-C-N	5.39	125.36	120.03
1	X	147	GLU	C-N-CA	5.39	125.36	120.03
1	H	164	LEU	N-CA-C	5.39	117.26	109.07
1	L	164	LEU	N-CA-C	5.39	117.26	109.07
1	M	203	ASN	CA-C-N	5.38	125.05	119.56
1	M	203	ASN	C-N-CA	5.38	125.05	119.56
1	S	583	LYS	CA-C-N	5.38	125.69	119.93
1	S	583	LYS	C-N-CA	5.38	125.69	119.93
2	i	40	GLN	N-CA-C	-5.38	106.08	113.30
2	k	128	TYR	CA-C-N	5.38	126.14	120.11
2	k	128	TYR	C-N-CA	5.38	126.14	120.11
1	E	164	LEU	N-CA-C	5.38	117.25	109.07
1	F	164	LEU	N-CA-C	5.38	117.25	109.07
1	S	203	ASN	CA-C-N	5.38	125.04	119.56
1	S	203	ASN	C-N-CA	5.38	125.04	119.56
1	G	164	LEU	N-CA-C	5.38	117.24	109.07
1	W	164	LEU	N-CA-C	5.37	116.96	108.96
1	J	164	LEU	N-CA-C	5.37	117.23	109.07
1	B	164	LEU	N-CA-C	5.36	117.22	109.07
1	T	203	ASN	CA-C-N	5.36	125.03	119.56
1	T	203	ASN	C-N-CA	5.36	125.03	119.56
1	U	147	GLU	CA-C-N	5.36	125.56	120.31
1	U	147	GLU	C-N-CA	5.36	125.56	120.31
1	N	203	ASN	CA-C-N	5.34	125.01	119.56
1	N	203	ASN	C-N-CA	5.34	125.01	119.56
1	H	387	GLN	CA-C-N	5.34	126.52	119.84
1	H	387	GLN	C-N-CA	5.34	126.52	119.84
1	B	387	GLN	CA-C-N	5.34	126.52	119.84
1	B	387	GLN	C-N-CA	5.34	126.52	119.84
1	F	387	GLN	CA-C-N	5.32	126.49	119.84
1	F	387	GLN	C-N-CA	5.32	126.49	119.84
1	E	387	GLN	CA-C-N	5.32	126.49	119.84
1	E	387	GLN	C-N-CA	5.32	126.49	119.84
1	E	456	ALA	CB-CA-C	-5.32	110.42	116.54
1	G	387	GLN	CA-C-N	5.32	126.49	119.84
1	G	387	GLN	C-N-CA	5.32	126.49	119.84
1	U	203	ASN	CA-C-N	5.32	124.98	119.56
1	U	203	ASN	C-N-CA	5.32	124.98	119.56
1	K	387	GLN	CA-C-N	5.32	126.49	119.84
1	K	387	GLN	C-N-CA	5.32	126.49	119.84
1	T	394	ASN	CA-C-N	5.32	125.23	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	T	394	ASN	C-N-CA	5.32	125.23	119.76
1	D	387	GLN	CA-C-N	5.32	126.48	119.84
1	D	387	GLN	C-N-CA	5.32	126.48	119.84
1	H	456	ALA	CB-CA-C	-5.31	110.43	116.54
1	J	456	ALA	CB-CA-C	-5.31	110.43	116.54
1	L	456	ALA	CB-CA-C	-5.31	110.44	116.54
1	A	387	GLN	CA-C-N	5.31	126.47	119.84
1	A	387	GLN	C-N-CA	5.31	126.47	119.84
1	C	387	GLN	CA-C-N	5.31	126.47	119.84
1	C	387	GLN	C-N-CA	5.31	126.47	119.84
1	B	456	ALA	CB-CA-C	-5.30	110.44	116.54
1	D	456	ALA	CB-CA-C	-5.30	110.44	116.54
1	K	456	ALA	CB-CA-C	-5.30	110.44	116.54
1	L	387	GLN	CA-C-N	5.30	126.47	119.84
1	L	387	GLN	C-N-CA	5.30	126.47	119.84
1	G	456	ALA	CB-CA-C	-5.29	110.45	116.54
1	I	387	GLN	CA-C-N	5.29	126.46	119.84
1	I	387	GLN	C-N-CA	5.29	126.46	119.84
1	M	394	ASN	CA-C-N	5.29	125.21	119.76
1	M	394	ASN	C-N-CA	5.29	125.21	119.76
1	P	360	GLU	N-CA-C	-5.29	106.66	113.01
1	A	456	ALA	CB-CA-C	-5.29	110.46	116.54
1	F	456	ALA	CB-CA-C	-5.29	110.46	116.54
1	W	203	ASN	CA-C-N	5.28	124.95	119.56
1	W	203	ASN	C-N-CA	5.28	124.95	119.56
1	I	456	ALA	CB-CA-C	-5.28	110.47	116.54
1	S	360	GLU	N-CA-C	-5.27	106.69	113.01
1	J	387	GLN	CA-C-N	5.27	126.43	119.84
1	J	387	GLN	C-N-CA	5.27	126.43	119.84
1	C	456	ALA	CB-CA-C	-5.26	110.49	116.54
1	P	147	GLU	CA-C-N	5.26	125.23	120.03
1	P	147	GLU	C-N-CA	5.26	125.23	120.03
1	X	158	TRP	N-CA-C	5.25	118.92	112.03
1	S	232	ALA	N-CA-C	5.25	121.97	110.80
1	Q	320	VAL	N-CA-C	5.21	115.94	110.62
2	q	128	TYR	CA-C-N	5.21	125.94	120.11
2	q	128	TYR	C-N-CA	5.21	125.94	120.11
1	R	158	TRP	N-CA-C	5.21	118.85	112.03
1	S	320	VAL	N-CA-C	5.21	115.93	110.62
1	V	367	ASP	N-CA-C	-5.20	106.69	112.57
1	R	397	VAL	CA-C-N	5.20	125.19	119.89
1	R	397	VAL	C-N-CA	5.20	125.19	119.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	R	165	MSE	N-CA-C	5.14	117.78	111.82
1	X	394	ASN	CA-C-N	5.12	125.03	119.76
1	X	394	ASN	C-N-CA	5.12	125.03	119.76
1	O	320	VAL	N-CA-C	5.11	115.84	110.62
1	W	158	TRP	N-CA-C	5.11	118.73	112.03
1	N	158	TRP	N-CA-C	5.11	118.72	112.03
1	P	397	VAL	CA-C-N	5.11	125.10	119.89
1	P	397	VAL	C-N-CA	5.11	125.10	119.89
1	O	394	ASN	CA-C-N	5.10	125.01	119.76
1	O	394	ASN	C-N-CA	5.10	125.01	119.76
1	Q	367	ASP	N-CA-C	-5.08	106.83	112.57
1	P	320	VAL	N-CA-C	5.08	115.80	110.62
2	m	145	GLU	CB-CA-C	-5.08	110.74	116.63
1	Q	158	TRP	N-CA-C	5.07	118.67	112.03
1	V	360	GLU	N-CA-C	-5.06	106.94	113.01
1	Q	445	GLU	N-CA-C	-5.06	105.76	112.34
2	b	137	TYR	CA-C-N	5.06	125.78	120.11
2	b	137	TYR	C-N-CA	5.06	125.78	120.11
2	d	154	GLU	CB-CA-C	-5.06	110.76	116.63
2	e	154	GLU	CB-CA-C	-5.05	110.77	116.63
2	j	154	GLU	CB-CA-C	-5.05	110.77	116.63
2	b	154	GLU	CB-CA-C	-5.05	110.78	116.63
2	f	154	GLU	CB-CA-C	-5.05	110.78	116.63
2	h	154	GLU	CB-CA-C	-5.05	110.78	116.63
2	i	154	GLU	CB-CA-C	-5.04	110.78	116.63
2	g	154	GLU	CB-CA-C	-5.04	110.78	116.63
2	a	154	GLU	CB-CA-C	-5.04	110.78	116.63
1	R	394	ASN	CA-C-N	5.04	124.95	119.76
1	R	394	ASN	C-N-CA	5.04	124.95	119.76
1	S	394	ASN	CA-C-N	5.04	124.95	119.76
1	S	394	ASN	C-N-CA	5.04	124.95	119.76
2	r	145	GLU	CB-CA-C	-5.04	110.79	116.63
2	Z	154	GLU	CB-CA-C	-5.03	110.79	116.63
2	Y	154	GLU	CB-CA-C	-5.03	110.79	116.63
1	T	397	VAL	CA-C-N	5.03	125.02	119.89
1	T	397	VAL	C-N-CA	5.03	125.02	119.89
2	e	137	TYR	CA-C-N	5.03	125.74	120.11
2	e	137	TYR	C-N-CA	5.03	125.74	120.11
2	c	154	GLU	CB-CA-C	-5.03	110.80	116.63
1	S	158	TRP	N-CA-C	5.02	118.61	112.03
1	W	394	ASN	CA-C-N	5.02	124.93	119.76
1	W	394	ASN	C-N-CA	5.02	124.93	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	o	145	GLU	CB-CA-C	-5.02	110.80	116.63
2	s	145	GLU	CB-CA-C	-5.02	110.81	116.63
2	v	145	GLU	CB-CA-C	-5.01	110.82	116.63
1	M	320	VAL	N-CA-C	5.00	115.72	110.62
2	p	145	GLU	CB-CA-C	-5.00	110.83	116.63
2	g	137	TYR	CA-C-N	5.00	125.71	120.11
2	g	137	TYR	C-N-CA	5.00	125.71	120.11

There are no chirality outliers.

All (24) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	231	THR	Peptide
1	B	231	THR	Peptide
1	C	231	THR	Peptide
1	D	231	THR	Peptide
1	E	231	THR	Peptide
1	F	231	THR	Peptide
1	G	231	THR	Peptide
1	H	231	THR	Peptide
1	I	231	THR	Peptide
1	J	231	THR	Peptide
1	K	231	THR	Peptide
1	L	231	THR	Peptide
1	M	231	THR	Peptide
1	N	231	THR	Peptide
1	O	231	THR	Peptide
1	P	231	THR	Peptide
1	Q	231	THR	Peptide
1	R	231	THR	Peptide
1	S	231	THR	Peptide
1	T	231	THR	Peptide
1	U	231	THR	Peptide
1	V	231	THR	Peptide
1	W	231	THR	Peptide
1	X	231	THR	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4553	0	4351	447	0
1	B	4553	0	4351	450	2
1	C	4553	0	4351	449	4
1	D	4553	0	4351	450	0
1	E	4553	0	4351	452	0
1	F	4553	0	4351	449	0
1	G	4553	0	4351	453	0
1	H	4553	0	4351	449	0
1	I	4553	0	4351	452	0
1	J	4553	0	4351	451	0
1	K	4553	0	4351	450	0
1	L	4553	0	4351	457	0
1	M	4564	0	4368	372	0
1	N	4564	0	4368	387	5
1	O	4564	0	4368	376	0
1	P	4564	0	4368	381	0
1	Q	4564	0	4368	384	0
1	R	4564	0	4368	392	0
1	S	4564	0	4368	376	3
1	T	4564	0	4368	373	0
1	U	4564	0	4368	386	0
1	V	4564	0	4368	377	0
1	W	4564	0	4368	381	1
1	X	4564	0	4368	378	0
2	Y	1048	0	957	117	0
2	Z	1048	0	957	115	0
2	a	1048	0	957	118	0
2	b	1048	0	957	116	0
2	c	1048	0	957	117	4
2	d	1048	0	957	120	0
2	e	1048	0	957	114	0
2	f	1048	0	957	117	0
2	g	1048	0	957	120	1
2	h	1048	0	957	122	0
2	i	1048	0	957	116	0
2	j	1048	0	957	126	0
2	k	1052	0	975	65	0
2	l	1052	0	975	67	0
2	m	1052	0	975	69	0
2	n	1052	0	975	74	0
2	o	1052	0	975	74	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	p	1052	0	975	65	0
2	q	1052	0	975	69	0
2	r	1052	0	975	70	3
2	s	1052	0	975	69	0
2	t	1052	0	975	71	0
2	u	1052	0	975	72	0
2	v	1052	0	975	73	3
3	A	22	0	0	1	0
3	B	22	0	0	1	0
3	C	22	0	0	1	0
3	D	22	0	0	1	0
3	E	22	0	0	2	0
3	F	22	0	0	2	0
3	G	22	0	0	1	0
3	H	22	0	0	2	0
3	I	22	0	0	1	0
3	J	22	0	0	2	0
3	K	22	0	0	2	0
3	L	22	0	0	2	0
3	M	21	0	0	4	0
3	N	21	0	0	4	0
3	O	21	0	0	3	0
3	P	21	0	0	5	0
3	Q	21	0	0	5	0
3	R	21	0	0	4	0
3	S	21	0	0	4	0
3	T	21	0	0	5	0
3	U	21	0	0	3	0
3	V	21	0	0	4	0
3	W	21	0	0	4	0
3	X	21	0	0	4	0
All	All	135120	0	127812	11405	13

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 43.

All (11405) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:53:MET:HE1	2:Z:92:VAL:CG1	1.60	1.32
2:e:53:MET:HE1	2:e:92:VAL:CG1	1.60	1.32

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:53:MET:HE1	2:c:92:VAL:CG1	1.60	1.32
2:Y:53:MET:HE1	2:Y:92:VAL:CG1	1.60	1.31
2:d:53:MET:HE1	2:d:92:VAL:CG1	1.60	1.31
2:f:53:MET:HE1	2:f:92:VAL:CG1	1.60	1.31
2:a:53:MET:HE1	2:a:92:VAL:CG1	1.60	1.31
2:h:53:MET:HE1	2:h:92:VAL:CG1	1.60	1.30
2:b:53:MET:HE1	2:b:92:VAL:CG1	1.60	1.30
2:g:53:MET:HE1	2:g:92:VAL:CG1	1.60	1.30
2:i:53:MET:HE1	2:i:92:VAL:CG1	1.60	1.29
2:j:53:MET:HE1	2:j:92:VAL:CG1	1.60	1.29
2:f:32:ALA:O	2:f:33:THR:CG2	1.82	1.27
2:i:32:ALA:O	2:i:33:THR:CG2	1.82	1.27
2:Z:32:ALA:O	2:Z:33:THR:CG2	1.82	1.27
2:d:32:ALA:O	2:d:33:THR:CG2	1.82	1.27
2:f:32:ALA:O	2:f:33:THR:HG23	1.12	1.27
2:a:32:ALA:O	2:a:33:THR:CG2	1.82	1.27
2:b:32:ALA:O	2:b:33:THR:HG23	1.12	1.27
2:b:32:ALA:O	2:b:33:THR:CG2	1.82	1.26
2:d:32:ALA:O	2:d:33:THR:HG23	1.12	1.26
2:g:32:ALA:O	2:g:33:THR:CG2	1.82	1.26
2:j:32:ALA:O	2:j:33:THR:CG2	1.82	1.26
2:c:32:ALA:O	2:c:33:THR:CG2	1.82	1.26
2:e:32:ALA:O	2:e:33:THR:CG2	1.82	1.26
2:Y:32:ALA:O	2:Y:33:THR:CG2	1.82	1.26
2:Z:32:ALA:O	2:Z:33:THR:HG23	1.12	1.26
2:h:32:ALA:O	2:h:33:THR:HG23	1.12	1.26
2:h:32:ALA:O	2:h:33:THR:CG2	1.82	1.25
2:i:32:ALA:O	2:i:33:THR:HG23	1.12	1.25
2:j:32:ALA:O	2:j:33:THR:HG23	1.12	1.25
2:Y:32:ALA:O	2:Y:33:THR:HG23	1.12	1.24
2:e:32:ALA:O	2:e:33:THR:HG23	1.12	1.24
2:a:32:ALA:O	2:a:33:THR:HG23	1.12	1.24
2:c:28:VAL:HG21	2:c:96:LEU:CD1	1.68	1.24
2:b:28:VAL:HG21	2:b:96:LEU:CD1	1.68	1.24
2:e:28:VAL:HG21	2:e:96:LEU:CD1	1.68	1.24
2:i:28:VAL:HG21	2:i:96:LEU:CD1	1.68	1.24
2:f:28:VAL:HG21	2:f:96:LEU:CD1	1.68	1.23
2:Z:28:VAL:HG21	2:Z:96:LEU:CD1	1.68	1.23
2:g:32:ALA:O	2:g:33:THR:HG23	1.12	1.23
2:j:28:VAL:HG21	2:j:96:LEU:CD1	1.68	1.23
2:g:28:VAL:HG21	2:g:96:LEU:CD1	1.68	1.23

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:32:ALA:O	2:c:33:THR:HG23	1.12	1.22
2:d:28:VAL:HG21	2:d:96:LEU:CD1	1.68	1.22
2:h:28:VAL:HG21	2:h:96:LEU:CD1	1.68	1.21
2:Y:28:VAL:HG21	2:Y:96:LEU:CD1	1.68	1.21
2:a:28:VAL:HG21	2:a:96:LEU:CD1	1.68	1.21
2:d:53:MET:CE	2:d:92:VAL:HG12	1.72	1.20
2:e:53:MET:CE	2:e:92:VAL:HG12	1.72	1.20
2:Z:53:MET:CE	2:Z:92:VAL:HG12	1.72	1.20
2:c:53:MET:CE	2:c:92:VAL:HG12	1.72	1.20
2:g:53:MET:CE	2:g:92:VAL:HG12	1.72	1.20
2:b:53:MET:CE	2:b:92:VAL:HG12	1.72	1.19
2:j:53:MET:CE	2:j:92:VAL:HG12	1.72	1.18
2:a:53:MET:CE	2:a:92:VAL:HG12	1.72	1.18
2:Y:53:MET:CE	2:Y:92:VAL:HG12	1.72	1.18
2:h:42:MET:HG3	2:h:42:MET:O	1.42	1.18
2:i:53:MET:CE	2:i:92:VAL:HG12	1.72	1.18
2:f:53:MET:CE	2:f:92:VAL:HG12	1.72	1.17
2:h:53:MET:CE	2:h:92:VAL:HG12	1.72	1.17
2:c:42:MET:HG3	2:c:42:MET:O	1.42	1.17
1:D:78:VAL:HG21	1:D:444:LEU:HD11	1.28	1.16
1:J:78:VAL:HG21	1:J:444:LEU:HD11	1.28	1.16
2:e:53:MET:CE	2:e:92:VAL:CG1	2.24	1.16
1:L:78:VAL:HG21	1:L:444:LEU:HD11	1.29	1.15
2:Y:53:MET:CE	2:Y:92:VAL:CG1	2.24	1.15
2:c:53:MET:CE	2:c:92:VAL:CG1	2.24	1.15
1:E:78:VAL:HG21	1:E:444:LEU:HD11	1.29	1.15
2:Z:53:MET:CE	2:Z:92:VAL:CG1	2.24	1.15
1:B:78:VAL:HG21	1:B:444:LEU:HD11	1.28	1.15
1:I:78:VAL:HG21	1:I:444:LEU:HD11	1.29	1.15
2:b:28:VAL:CG1	2:b:97:ALA:HA	1.77	1.15
2:c:28:VAL:CG1	2:c:97:ALA:HA	1.77	1.15
2:d:53:MET:CE	2:d:92:VAL:CG1	2.24	1.15
2:f:28:VAL:CG1	2:f:97:ALA:HA	1.77	1.15
1:H:78:VAL:HG21	1:H:444:LEU:HD11	1.29	1.15
2:a:28:VAL:CG1	2:a:97:ALA:HA	1.77	1.15
2:h:28:VAL:CG1	2:h:97:ALA:HA	1.77	1.14
2:d:28:VAL:CG1	2:d:97:ALA:HA	1.77	1.14
2:Y:28:VAL:CG1	2:Y:97:ALA:HA	1.77	1.14
2:Z:28:VAL:CG1	2:Z:97:ALA:HA	1.77	1.14
2:b:53:MET:CE	2:b:92:VAL:CG1	2.24	1.14
2:f:53:MET:CE	2:f:92:VAL:CG1	2.24	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:i:28:VAL:CG1	2:i:97:ALA:HA	1.77	1.14
2:i:42:MET:O	2:i:42:MET:HG3	1.42	1.14
2:g:28:VAL:CG1	2:g:97:ALA:HA	1.77	1.14
2:Z:42:MET:HG3	2:Z:42:MET:O	1.42	1.13
2:e:28:VAL:CG1	2:e:97:ALA:HA	1.77	1.13
2:j:42:MET:HG3	2:j:42:MET:O	1.42	1.13
2:i:53:MET:CE	2:i:92:VAL:CG1	2.24	1.13
1:G:78:VAL:HG21	1:G:444:LEU:HD11	1.28	1.13
1:Q:560:LEU:HD13	1:R:82:PRO:HD2	1.31	1.12
1:C:78:VAL:HG21	1:C:444:LEU:HD11	1.28	1.12
2:a:53:MET:CE	2:a:92:VAL:CG1	2.24	1.12
2:g:53:MET:CE	2:g:92:VAL:CG1	2.24	1.13
2:j:28:VAL:CG1	2:j:97:ALA:HA	1.77	1.13
2:j:53:MET:CE	2:j:92:VAL:CG1	2.24	1.12
2:h:53:MET:CE	2:h:92:VAL:CG1	2.24	1.12
2:a:42:MET:O	2:a:42:MET:HG3	1.42	1.11
2:Y:42:MET:O	2:Y:42:MET:HG3	1.42	1.11
2:e:42:MET:HG3	2:e:42:MET:O	1.42	1.11
2:f:42:MET:O	2:f:42:MET:HG3	1.42	1.11
1:K:78:VAL:HG21	1:K:444:LEU:HD11	1.28	1.11
1:K:560:LEU:HD13	1:L:82:PRO:HD2	1.29	1.11
2:g:42:MET:HG3	2:g:42:MET:O	1.42	1.10
1:A:139:SER:HB3	1:A:455:THR:HG23	1.34	1.10
1:F:139:SER:HB3	1:F:455:THR:HG23	1.34	1.10
1:A:78:VAL:HG21	1:A:444:LEU:HD11	1.29	1.09
1:H:139:SER:HB3	1:H:455:THR:HG23	1.34	1.09
2:d:42:MET:HG3	2:d:42:MET:O	1.42	1.09
2:f:31:ASP:OD2	2:f:93:PHE:HE2	1.36	1.09
2:Z:28:VAL:HG13	2:Z:97:ALA:CA	1.83	1.09
2:j:31:ASP:OD2	2:j:93:PHE:HE2	1.36	1.09
2:b:42:MET:HG3	2:b:42:MET:O	1.42	1.08
2:c:28:VAL:HG13	2:c:97:ALA:CA	1.83	1.08
2:f:28:VAL:HG13	2:f:97:ALA:CA	1.83	1.08
1:L:14:ARG:HA	1:L:14:ARG:HE	1.19	1.08
2:i:28:VAL:HG13	2:i:97:ALA:CA	1.83	1.08
2:i:31:ASP:OD2	2:i:93:PHE:HE2	1.36	1.08
2:Z:28:VAL:HG21	2:Z:96:LEU:HD13	1.36	1.08
2:Z:31:ASP:OD2	2:Z:93:PHE:HE2	1.36	1.08
2:c:31:ASP:OD2	2:c:93:PHE:HE2	1.36	1.08
1:F:78:VAL:HG21	1:F:444:LEU:HD11	1.29	1.08
1:G:139:SER:HB3	1:G:455:THR:HG23	1.34	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:139:SER:HB3	1:K:455:THR:HG23	1.34	1.08
1:E:14:ARG:HA	1:E:14:ARG:HE	1.19	1.07
2:b:28:VAL:HG13	2:b:97:ALA:CA	1.83	1.07
2:e:28:VAL:HG13	2:e:97:ALA:CA	1.83	1.07
2:b:31:ASP:OD2	2:b:93:PHE:HE2	1.36	1.07
2:e:28:VAL:HG21	2:e:96:LEU:HD13	1.36	1.07
2:h:28:VAL:HG13	2:h:97:ALA:CA	1.83	1.07
1:F:14:ARG:HA	1:F:14:ARG:HE	1.19	1.07
2:Y:28:VAL:HG13	2:Y:97:ALA:CA	1.83	1.07
2:d:28:VAL:HG13	2:d:97:ALA:CA	1.83	1.07
1:G:14:ARG:HA	1:G:14:ARG:HE	1.19	1.07
1:L:139:SER:HB3	1:L:455:THR:HG23	1.34	1.07
2:Y:28:VAL:HG21	2:Y:96:LEU:HD13	1.35	1.07
2:a:28:VAL:HG13	2:a:97:ALA:CA	1.83	1.07
2:a:31:ASP:OD2	2:a:93:PHE:HE2	1.36	1.07
2:c:28:VAL:HG21	2:c:96:LEU:HD13	1.35	1.07
2:g:28:VAL:HG13	2:g:97:ALA:CA	1.83	1.07
2:j:28:VAL:HG13	2:j:97:ALA:CA	1.83	1.07
2:d:31:ASP:OD2	2:d:93:PHE:HE2	1.36	1.06
2:h:28:VAL:HG21	2:h:96:LEU:HD13	1.35	1.06
1:N:78:VAL:HG21	1:N:444:LEU:HD11	1.37	1.06
1:V:78:VAL:HG21	1:V:444:LEU:HD11	1.35	1.06
1:X:78:VAL:HG21	1:X:444:LEU:HD11	1.38	1.06
1:J:139:SER:HB3	1:J:455:THR:HG23	1.34	1.06
1:C:139:SER:HB3	1:C:455:THR:HG23	1.34	1.06
1:D:41:TRP:CZ3	1:D:42:ASP:HB2	1.91	1.06
1:I:41:TRP:CZ3	1:I:42:ASP:HB2	1.90	1.06
1:U:78:VAL:HG21	1:U:444:LEU:HD11	1.37	1.06
2:i:28:VAL:HG21	2:i:96:LEU:HD13	1.35	1.06
1:J:560:LEU:HD13	1:K:82:PRO:HD2	1.34	1.06
1:K:41:TRP:CZ3	1:K:42:ASP:HB2	1.91	1.06
2:d:28:VAL:HG21	2:d:96:LEU:HD13	1.36	1.06
2:g:28:VAL:CG1	2:g:97:ALA:CA	2.34	1.06
2:j:28:VAL:HG21	2:j:96:LEU:HD13	1.35	1.06
1:F:41:TRP:CZ3	1:F:42:ASP:HB2	1.91	1.05
1:J:41:TRP:CZ3	1:J:42:ASP:HB2	1.91	1.05
2:Y:28:VAL:CG1	2:Y:97:ALA:CA	2.34	1.05
2:e:31:ASP:OD2	2:e:93:PHE:HE2	1.36	1.05
2:g:31:ASP:OD2	2:g:93:PHE:HE2	1.36	1.05
1:H:41:TRP:CZ3	1:H:42:ASP:HB2	1.90	1.05
2:a:28:VAL:HG21	2:a:96:LEU:HD13	1.35	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:28:VAL:CG1	2:c:97:ALA:CA	2.34	1.05
2:i:28:VAL:CG1	2:i:97:ALA:CA	2.34	1.05
2:j:28:VAL:CG1	2:j:97:ALA:CA	2.34	1.05
1:C:41:TRP:CZ3	1:C:42:ASP:HB2	1.90	1.05
1:K:14:ARG:HA	1:K:14:ARG:HE	1.18	1.05
2:e:28:VAL:CG1	2:e:97:ALA:CA	2.34	1.05
1:S:14:ARG:HA	1:S:14:ARG:HE	1.21	1.05
1:T:78:VAL:HG21	1:T:444:LEU:HD11	1.37	1.05
1:L:41:TRP:CZ3	1:L:42:ASP:HB2	1.91	1.05
1:A:41:TRP:CZ3	1:A:42:ASP:HB2	1.90	1.05
1:G:41:TRP:CZ3	1:G:42:ASP:HB2	1.91	1.05
2:b:28:VAL:CG1	2:b:97:ALA:CA	2.34	1.05
1:B:41:TRP:CZ3	1:B:42:ASP:HB2	1.91	1.04
1:B:139:SER:HB3	1:B:455:THR:HG23	1.34	1.04
2:f:28:VAL:CG1	2:f:97:ALA:CA	2.34	1.04
2:h:28:VAL:CG1	2:h:97:ALA:CA	2.34	1.04
1:C:14:ARG:HA	1:C:14:ARG:HE	1.19	1.04
1:E:139:SER:HB3	1:E:455:THR:HG23	1.34	1.04
2:a:28:VAL:CG1	2:a:97:ALA:CA	2.34	1.04
1:M:14:ARG:HA	1:M:14:ARG:HE	1.21	1.04
2:Y:31:ASP:OD2	2:Y:93:PHE:HE2	1.36	1.04
2:Z:28:VAL:CG1	2:Z:97:ALA:CA	2.34	1.04
2:d:28:VAL:CG1	2:d:97:ALA:CA	2.34	1.04
2:h:31:ASP:OD2	2:h:93:PHE:HE2	1.36	1.04
1:O:78:VAL:HG21	1:O:444:LEU:HD11	1.38	1.04
1:X:14:ARG:HA	1:X:14:ARG:HE	1.22	1.04
1:E:41:TRP:CZ3	1:E:42:ASP:HB2	1.90	1.04
1:O:14:ARG:HA	1:O:14:ARG:HE	1.23	1.03
1:A:41:TRP:CE3	1:A:42:ASP:N	2.26	1.03
1:D:41:TRP:CE3	1:D:42:ASP:N	2.26	1.03
2:b:28:VAL:HG21	2:b:96:LEU:HD13	1.36	1.03
1:N:14:ARG:HA	1:N:14:ARG:HE	1.21	1.03
1:R:78:VAL:HG21	1:R:444:LEU:HD11	1.36	1.03
1:D:82:PRO:HD2	1:E:560:LEU:HD13	1.37	1.03
1:I:139:SER:HB3	1:I:455:THR:HG23	1.34	1.03
1:F:41:TRP:CE3	1:F:42:ASP:N	2.26	1.03
1:H:560:LEU:HD13	1:I:82:PRO:HD2	1.40	1.03
1:Q:78:VAL:HG21	1:Q:444:LEU:HD11	1.38	1.03
1:W:78:VAL:HG21	1:W:444:LEU:HD11	1.36	1.03
1:M:78:VAL:HG21	1:M:444:LEU:HD11	1.37	1.03
1:D:14:ARG:HA	1:D:14:ARG:HE	1.19	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:41:TRP:CE3	1:E:42:ASP:N	2.26	1.03
1:P:78:VAL:HG21	1:P:444:LEU:HD11	1.39	1.02
1:W:14:ARG:HA	1:W:14:ARG:HE	1.23	1.02
2:f:28:VAL:HG21	2:f:96:LEU:HD13	1.35	1.02
1:A:14:ARG:HA	1:A:14:ARG:HE	1.19	1.02
1:A:82:PRO:HD2	1:L:560:LEU:HD13	1.38	1.02
1:G:41:TRP:CE3	1:G:42:ASP:N	2.26	1.02
1:H:41:TRP:CE3	1:H:42:ASP:N	2.26	1.02
1:L:41:TRP:CE3	1:L:42:ASP:N	2.26	1.02
2:g:28:VAL:HG21	2:g:96:LEU:HD13	1.36	1.02
1:B:14:ARG:HA	1:B:14:ARG:HE	1.19	1.02
1:K:41:TRP:CE3	1:K:42:ASP:N	2.26	1.02
1:I:41:TRP:CE3	1:I:42:ASP:N	2.26	1.02
1:N:82:PRO:HD2	1:V:560:LEU:HD13	1.38	1.02
1:B:41:TRP:CE3	1:B:42:ASP:N	2.26	1.02
1:D:139:SER:HB3	1:D:455:THR:HG23	1.34	1.01
1:F:560:LEU:HD13	1:G:82:PRO:HD2	1.42	1.01
1:H:14:ARG:HE	1:H:14:ARG:HA	1.19	1.01
1:J:41:TRP:CE3	1:J:42:ASP:N	2.26	1.01
1:V:82:PRO:HD2	1:W:560:LEU:HD13	1.42	1.01
1:C:41:TRP:CE3	1:C:42:ASP:N	2.26	1.01
2:c:24:ARG:O	2:c:28:VAL:HG23	1.61	1.01
1:U:14:ARG:HA	1:U:14:ARG:HE	1.21	1.01
1:V:14:ARG:HA	1:V:14:ARG:HE	1.21	1.01
2:b:24:ARG:O	2:b:28:VAL:HG23	1.61	1.01
1:Q:14:ARG:HA	1:Q:14:ARG:HE	1.23	1.01
1:R:14:ARG:HA	1:R:14:ARG:HE	1.21	1.01
1:I:14:ARG:HA	1:I:14:ARG:HE	1.19	1.01
1:T:546:THR:HG23	1:T:547:PRO:HD3	1.43	1.01
1:J:14:ARG:HA	1:J:14:ARG:HE	1.19	1.01
1:S:78:VAL:HG21	1:S:444:LEU:HD11	1.38	1.00
2:h:24:ARG:O	2:h:28:VAL:HG23	1.61	1.00
2:i:24:ARG:O	2:i:28:VAL:HG23	1.61	1.00
2:f:24:ARG:O	2:f:28:VAL:HG23	1.61	1.00
1:C:58:ASP:O	1:C:59:VAL:HG12	1.62	1.00
1:P:14:ARG:HA	1:P:14:ARG:HE	1.23	1.00
1:T:14:ARG:HA	1:T:14:ARG:HE	1.22	1.00
1:B:58:ASP:O	1:B:59:VAL:HG12	1.62	1.00
1:D:560:LEU:HD13	1:F:82:PRO:HD2	1.44	1.00
1:J:58:ASP:O	1:J:59:VAL:HG12	1.62	1.00
2:e:24:ARG:O	2:e:28:VAL:HG23	1.61	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:546:THR:HG23	1:Q:547:PRO:HD3	1.43	1.00
2:Z:24:ARG:O	2:Z:28:VAL:HG23	1.60	1.00
2:g:24:ARG:O	2:g:28:VAL:HG23	1.61	1.00
1:W:546:THR:HG23	1:W:547:PRO:HD3	1.44	0.99
1:A:58:ASP:O	1:A:59:VAL:HG12	1.62	0.99
1:G:158:TRP:HE3	1:G:173:CYS:HG	1.03	0.99
1:K:58:ASP:O	1:K:59:VAL:HG12	1.62	0.99
1:G:58:ASP:O	1:G:59:VAL:HG12	1.62	0.99
1:H:58:ASP:O	1:H:59:VAL:HG12	1.62	0.99
2:j:24:ARG:O	2:j:28:VAL:HG23	1.61	0.99
1:F:58:ASP:O	1:F:59:VAL:HG12	1.62	0.99
1:K:158:TRP:HE3	1:K:173:CYS:HG	1.03	0.99
2:Y:24:ARG:O	2:Y:28:VAL:HG23	1.61	0.99
1:O:546:THR:HG23	1:O:547:PRO:HD3	1.44	0.99
1:V:546:THR:HG23	1:V:547:PRO:HD3	1.44	0.99
1:L:158:TRP:HE3	1:L:173:CYS:HG	1.05	0.99
1:T:560:LEU:HD13	1:W:82:PRO:HD2	1.41	0.99
1:E:58:ASP:O	1:E:59:VAL:HG12	1.62	0.99
1:X:248:LYS:HB3	1:X:511:ARG:HH11	1.25	0.98
1:U:82:PRO:HD2	1:X:560:LEU:HD13	1.45	0.98
1:P:560:LEU:HD13	1:Q:82:PRO:HD2	1.43	0.98
1:R:248:LYS:HB3	1:R:511:ARG:HH11	1.27	0.98
1:S:248:LYS:HB3	1:S:511:ARG:HH11	1.29	0.98
2:d:24:ARG:O	2:d:28:VAL:HG23	1.61	0.98
1:W:248:LYS:HB3	1:W:511:ARG:HH11	1.28	0.98
1:C:158:TRP:HE3	1:C:173:CYS:HG	1.00	0.98
1:I:58:ASP:O	1:I:59:VAL:HG12	1.62	0.98
1:L:58:ASP:O	1:L:59:VAL:HG12	1.62	0.98
1:M:248:LYS:HB3	1:M:511:ARG:HH11	1.28	0.98
1:O:158:TRP:HB3	1:O:173:CYS:HA	1.46	0.98
2:a:24:ARG:O	2:a:28:VAL:HG23	1.61	0.98
2:b:46:VAL:HG11	2:b:77:ALA:HB1	1.45	0.98
2:j:46:VAL:HG11	2:j:77:ALA:HB1	1.45	0.98
1:V:15:PHE:HZ	1:V:283:CYS:HG	1.12	0.98
1:D:58:ASP:O	1:D:59:VAL:HG12	1.62	0.97
1:P:158:TRP:HE3	1:P:173:CYS:HG	0.98	0.97
2:Y:46:VAL:HG11	2:Y:77:ALA:HB1	1.45	0.97
1:U:248:LYS:HB3	1:U:511:ARG:HH11	1.28	0.97
2:d:46:VAL:HG11	2:d:77:ALA:HB1	1.45	0.97
2:i:46:VAL:HG11	2:i:77:ALA:HB1	1.45	0.97
1:R:546:THR:HG23	1:R:547:PRO:HD3	1.44	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:330:ARG:HH21	1:M:409:THR:HG21	1.29	0.97
1:A:158:TRP:HE3	1:A:173:CYS:HG	1.00	0.97
2:h:46:VAL:HG11	2:h:77:ALA:HB1	1.45	0.97
1:T:248:LYS:HB3	1:T:511:ARG:HH11	1.27	0.97
2:Z:46:VAL:HG11	2:Z:77:ALA:HB1	1.45	0.97
1:V:158:TRP:HB3	1:V:173:CYS:HA	1.44	0.97
1:N:546:THR:HG23	1:N:547:PRO:HD3	1.45	0.96
1:B:158:TRP:HE3	1:B:173:CYS:HG	1.10	0.96
1:F:34:PHE:HZ	1:F:328:ARG:NH2	1.63	0.96
1:A:41:TRP:CZ3	1:A:42:ASP:CB	2.49	0.96
1:H:41:TRP:CZ3	1:H:42:ASP:CB	2.48	0.96
2:e:46:VAL:HG11	2:e:77:ALA:HB1	1.45	0.96
1:M:546:THR:HG23	1:M:547:PRO:HD3	1.47	0.96
1:E:41:TRP:CZ3	1:E:42:ASP:CB	2.48	0.96
1:H:34:PHE:HZ	1:H:328:ARG:NH2	1.63	0.96
2:d:32:ALA:C	2:d:33:THR:HG23	1.91	0.96
2:g:32:ALA:C	2:g:33:THR:HG23	1.91	0.96
1:S:546:THR:HG23	1:S:547:PRO:HD3	1.45	0.96
1:J:34:PHE:HZ	1:J:328:ARG:NH2	1.63	0.96
2:c:32:ALA:C	2:c:33:THR:HG23	1.91	0.96
2:c:34:LEU:O	2:c:35:THR:HG23	1.65	0.96
2:g:46:VAL:HG11	2:g:77:ALA:HB1	1.45	0.96
2:f:32:ALA:C	2:f:33:THR:HG23	1.91	0.96
2:j:34:LEU:O	2:j:35:THR:HG23	1.66	0.96
1:W:158:TRP:HB3	1:W:173:CYS:HA	1.45	0.96
1:C:41:TRP:CZ3	1:C:42:ASP:CB	2.49	0.96
1:L:41:TRP:CZ3	1:L:42:ASP:CB	2.49	0.96
1:O:248:LYS:HB3	1:O:511:ARG:HH11	1.29	0.96
1:J:41:TRP:CZ3	1:J:42:ASP:CB	2.49	0.96
1:P:158:TRP:HB3	1:P:173:CYS:HA	1.45	0.96
1:S:158:TRP:HB3	1:S:173:CYS:HA	1.47	0.96
1:T:330:ARG:HH21	1:T:409:THR:HG21	1.31	0.96
1:B:41:TRP:CZ3	1:B:42:ASP:CB	2.49	0.96
1:I:34:PHE:HZ	1:I:328:ARG:NH2	1.63	0.96
2:Z:34:LEU:O	2:Z:35:THR:HG23	1.66	0.96
2:e:34:LEU:O	2:e:35:THR:HG23	1.65	0.96
1:E:158:TRP:HE3	1:E:173:CYS:HG	1.00	0.96
2:a:32:ALA:C	2:a:33:THR:HG23	1.90	0.96
2:a:34:LEU:O	2:a:35:THR:HG23	1.66	0.96
1:B:34:PHE:HZ	1:B:328:ARG:NH2	1.63	0.95
1:K:41:TRP:CZ3	1:K:42:ASP:CB	2.49	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:i:34:LEU:O	2:i:35:THR:HG23	1.66	0.95
1:E:34:PHE:HZ	1:E:328:ARG:NH2	1.63	0.95
1:F:41:TRP:CZ3	1:F:42:ASP:CB	2.49	0.95
2:a:46:VAL:HG11	2:a:77:ALA:HB1	1.45	0.95
2:c:46:VAL:HG11	2:c:77:ALA:HB1	1.45	0.95
1:V:248:LYS:HB3	1:V:511:ARG:HH11	1.29	0.95
1:X:330:ARG:HH21	1:X:409:THR:HG21	1.30	0.95
2:Z:32:ALA:C	2:Z:33:THR:HG23	1.91	0.95
2:h:34:LEU:O	2:h:35:THR:HG23	1.66	0.95
1:O:330:ARG:HH21	1:O:409:THR:HG21	1.31	0.95
1:F:158:TRP:HE3	1:F:173:CYS:HG	1.00	0.95
1:G:34:PHE:HZ	1:G:328:ARG:NH2	1.63	0.95
2:f:46:VAL:HG11	2:f:77:ALA:HB1	1.45	0.95
2:j:32:ALA:C	2:j:33:THR:HG23	1.90	0.95
1:I:41:TRP:CZ3	1:I:42:ASP:CB	2.49	0.95
2:b:34:LEU:O	2:b:35:THR:HG23	1.65	0.95
1:D:158:TRP:HE3	1:D:173:CYS:HG	1.09	0.95
2:Y:32:ALA:C	2:Y:33:THR:HG23	1.91	0.95
1:X:546:THR:HG23	1:X:547:PRO:HD3	1.46	0.95
1:C:34:PHE:HZ	1:C:328:ARG:NH2	1.63	0.95
2:e:32:ALA:C	2:e:33:THR:HG23	1.90	0.95
2:g:34:LEU:O	2:g:35:THR:HG23	1.65	0.95
1:U:158:TRP:HB3	1:U:173:CYS:HA	1.49	0.95
1:X:158:TRP:HB3	1:X:173:CYS:HA	1.48	0.95
1:D:41:TRP:CZ3	1:D:42:ASP:CB	2.49	0.95
1:G:41:TRP:CZ3	1:G:42:ASP:CB	2.49	0.95
2:d:28:VAL:HG21	2:d:96:LEU:HB3	1.49	0.95
1:Q:158:TRP:HB3	1:Q:173:CYS:HA	1.49	0.94
1:Q:248:LYS:HB3	1:Q:511:ARG:HH11	1.29	0.94
1:R:560:LEU:HD13	1:X:82:PRO:HD2	1.49	0.94
1:D:34:PHE:HZ	1:D:328:ARG:NH2	1.63	0.94
1:I:158:TRP:HE3	1:I:173:CYS:HG	1.00	0.94
1:K:561:ASP:HB2	1:L:89:ASP:HA	1.46	0.94
1:K:560:LEU:HD22	1:L:82:PRO:HG2	1.49	0.94
1:L:34:PHE:HZ	1:L:328:ARG:NH2	1.63	0.94
2:Y:34:LEU:O	2:Y:35:THR:HG23	1.65	0.94
2:b:32:ALA:C	2:b:33:THR:HG23	1.91	0.94
1:P:248:LYS:HB3	1:P:511:ARG:HH11	1.27	0.94
1:S:330:ARG:HH21	1:S:409:THR:HG21	1.30	0.94
1:A:89:ASP:HA	1:L:561:ASP:HB2	1.49	0.94
2:d:34:LEU:O	2:d:35:THR:HG23	1.65	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:i:32:ALA:C	2:i:33:THR:HG23	1.91	0.94
1:T:158:TRP:HB3	1:T:173:CYS:HA	1.44	0.94
1:A:34:PHE:HZ	1:A:328:ARG:NH2	1.63	0.94
2:Z:71:ASP:HB2	2:Z:75:PRO:HD2	1.50	0.94
1:V:330:ARG:HH21	1:V:409:THR:HG21	1.28	0.94
1:E:546:THR:HG23	1:E:547:PRO:HD3	1.50	0.94
1:G:560:LEU:HD13	1:H:82:PRO:HD2	1.50	0.94
2:e:71:ASP:HB2	2:e:75:PRO:HD2	1.50	0.94
2:f:34:LEU:O	2:f:35:THR:HG23	1.66	0.94
1:R:330:ARG:HH21	1:R:409:THR:HG21	1.32	0.94
1:S:158:TRP:HE3	1:S:173:CYS:HG	0.96	0.94
1:D:546:THR:HG23	1:D:547:PRO:HD3	1.50	0.94
2:g:28:VAL:HG21	2:g:96:LEU:HB3	1.49	0.94
1:U:546:THR:HG23	1:U:547:PRO:HD3	1.46	0.94
1:K:34:PHE:HZ	1:K:328:ARG:NH2	1.63	0.94
2:g:78:GLU:OE1	2:g:78:GLU:HA	1.69	0.94
1:M:158:TRP:HB3	1:M:173:CYS:HA	1.50	0.93
1:P:330:ARG:HH21	1:P:409:THR:HG21	1.32	0.93
1:P:546:THR:HG23	1:P:547:PRO:HD3	1.46	0.93
1:Q:561:ASP:HB2	1:R:89:ASP:HA	1.50	0.93
1:R:158:TRP:HB3	1:R:173:CYS:HA	1.48	0.93
1:G:139:SER:HB3	1:G:455:THR:CG2	1.98	0.93
1:I:139:SER:HB3	1:I:455:THR:CG2	1.98	0.93
2:b:28:VAL:HG21	2:b:96:LEU:HB3	1.49	0.93
2:b:71:ASP:HB2	2:b:75:PRO:HD2	1.50	0.93
2:h:32:ALA:C	2:h:33:THR:HG23	1.90	0.93
1:N:158:TRP:HB3	1:N:173:CYS:HA	1.48	0.93
1:C:546:THR:HG23	1:C:547:PRO:HD3	1.50	0.93
2:d:71:ASP:HB2	2:d:75:PRO:HD2	1.50	0.93
2:h:78:GLU:OE1	2:h:78:GLU:HA	1.69	0.93
2:i:28:VAL:HG21	2:i:96:LEU:HB3	1.49	0.93
2:j:71:ASP:HB2	2:j:75:PRO:HD2	1.50	0.93
1:M:560:LEU:HD13	1:O:82:PRO:HD2	1.50	0.93
1:C:139:SER:HB3	1:C:455:THR:CG2	1.98	0.93
1:F:546:THR:HG23	1:F:547:PRO:HD3	1.50	0.93
2:Z:28:VAL:HG21	2:Z:96:LEU:HB3	1.49	0.93
2:e:78:GLU:HA	2:e:78:GLU:OE1	1.68	0.93
1:J:158:TRP:HE3	1:J:173:CYS:HG	1.01	0.93
1:L:139:SER:HB3	1:L:455:THR:CG2	1.98	0.93
2:a:71:ASP:HB2	2:a:75:PRO:HD2	1.50	0.93
1:N:248:LYS:HB3	1:N:511:ARG:HH11	1.30	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:14:ARG:HA	1:F:14:ARG:NE	1.83	0.93
1:F:139:SER:HB3	1:F:455:THR:CG2	1.98	0.93
2:d:34:LEU:O	2:d:35:THR:CG2	2.17	0.93
2:f:28:VAL:HG21	2:f:96:LEU:HB3	1.49	0.93
2:i:71:ASP:HB2	2:i:75:PRO:HD2	1.50	0.93
1:N:15:PHE:HZ	1:N:283:CYS:HG	1.07	0.93
1:U:330:ARG:HH21	1:U:409:THR:HG21	1.29	0.93
1:H:158:TRP:HE3	1:H:173:CYS:HG	1.00	0.93
2:g:71:ASP:HB2	2:g:75:PRO:HD2	1.50	0.93
1:W:330:ARG:HH21	1:W:409:THR:HG21	1.32	0.93
2:Y:71:ASP:HB2	2:Y:75:PRO:HD2	1.50	0.93
2:Y:78:GLU:OE1	2:Y:78:GLU:HA	1.69	0.93
2:a:28:VAL:HG21	2:a:96:LEU:HB3	1.49	0.93
2:h:31:ASP:OD2	2:h:93:PHE:CE2	2.22	0.93
2:j:78:GLU:HA	2:j:78:GLU:OE1	1.68	0.93
1:B:546:THR:HG23	1:B:547:PRO:HD3	1.50	0.93
2:e:34:LEU:O	2:e:35:THR:CG2	2.17	0.93
2:b:34:LEU:O	2:b:35:THR:CG2	2.17	0.92
2:e:28:VAL:HG21	2:e:96:LEU:HB3	1.49	0.92
1:N:158:TRP:HE3	1:N:173:CYS:HG	0.92	0.92
1:E:139:SER:HB3	1:E:455:THR:CG2	1.98	0.92
2:a:31:ASP:OD2	2:a:93:PHE:CE2	2.22	0.92
2:a:53:MET:CE	2:a:92:VAL:HG11	2.00	0.92
2:h:34:LEU:O	2:h:35:THR:CG2	2.17	0.92
1:A:139:SER:HB3	1:A:455:THR:CG2	1.98	0.92
1:H:139:SER:HB3	1:H:455:THR:CG2	1.98	0.92
2:i:78:GLU:OE1	2:i:78:GLU:HA	1.69	0.92
1:Q:330:ARG:HH21	1:Q:409:THR:HG21	1.31	0.92
2:g:34:LEU:O	2:g:35:THR:CG2	2.17	0.92
2:h:71:ASP:HB2	2:h:75:PRO:HD2	1.50	0.92
1:N:330:ARG:HH21	1:N:409:THR:HG21	1.33	0.92
1:B:139:SER:HB3	1:B:455:THR:CG2	1.98	0.92
1:G:546:THR:HG23	1:G:547:PRO:HD3	1.50	0.92
2:Y:34:LEU:O	2:Y:35:THR:CG2	2.17	0.92
2:Z:78:GLU:HA	2:Z:78:GLU:OE1	1.69	0.92
2:b:78:GLU:HA	2:b:78:GLU:OE1	1.69	0.92
1:W:158:TRP:HE3	1:W:173:CYS:HG	0.94	0.92
1:H:14:ARG:HA	1:H:14:ARG:NE	1.83	0.92
2:e:31:ASP:OD2	2:e:93:PHE:CE2	2.22	0.92
2:i:31:ASP:OD2	2:i:93:PHE:CE2	2.22	0.92
1:J:139:SER:HB3	1:J:455:THR:CG2	1.98	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:f:31:ASP:OD2	2:f:93:PHE:CE2	2.22	0.92
1:D:139:SER:HB3	1:D:455:THR:CG2	1.98	0.92
2:c:34:LEU:O	2:c:35:THR:CG2	2.17	0.92
1:N:89:ASP:HA	1:V:561:ASP:HB2	1.48	0.92
1:A:14:ARG:HA	1:A:14:ARG:NE	1.83	0.92
2:d:31:ASP:OD2	2:d:93:PHE:CE2	2.22	0.92
1:A:546:THR:HG23	1:A:547:PRO:HD3	1.50	0.92
2:Y:31:ASP:OD2	2:Y:93:PHE:CE2	2.22	0.92
2:f:78:GLU:OE1	2:f:78:GLU:HA	1.69	0.92
2:i:34:LEU:O	2:i:35:THR:CG2	2.17	0.92
2:a:78:GLU:OE1	2:a:78:GLU:HA	1.68	0.91
2:d:78:GLU:OE1	2:d:78:GLU:HA	1.69	0.91
2:f:34:LEU:O	2:f:35:THR:CG2	2.17	0.91
2:f:53:MET:CE	2:f:92:VAL:HG11	2.00	0.91
2:j:28:VAL:HG21	2:j:96:LEU:HB3	1.49	0.91
2:j:31:ASP:OD2	2:j:93:PHE:CE2	2.22	0.91
2:a:34:LEU:O	2:a:35:THR:CG2	2.17	0.91
2:j:34:LEU:O	2:j:35:THR:CG2	2.17	0.91
1:T:158:TRP:HE3	1:T:173:CYS:HG	0.96	0.91
1:W:144:ILE:HG12	1:W:447:TYR:HE1	1.35	0.91
1:G:14:ARG:HA	1:G:14:ARG:NE	1.83	0.91
1:K:139:SER:HB3	1:K:455:THR:CG2	1.98	0.91
2:Y:28:VAL:HG21	2:Y:96:LEU:HB3	1.49	0.91
1:R:158:TRP:HE3	1:R:173:CYS:HG	0.95	0.91
1:U:158:TRP:HE3	1:U:173:CYS:HG	0.93	0.91
2:Z:31:ASP:OD2	2:Z:93:PHE:CE2	2.22	0.91
2:Z:34:LEU:O	2:Z:35:THR:CG2	2.17	0.91
2:e:53:MET:CE	2:e:92:VAL:HG11	2.00	0.91
2:g:31:ASP:OD2	2:g:93:PHE:CE2	2.22	0.91
1:X:158:TRP:HE3	1:X:173:CYS:HG	0.93	0.91
1:D:14:ARG:HA	1:D:14:ARG:NE	1.83	0.91
1:H:546:THR:HG23	1:H:547:PRO:HD3	1.50	0.91
2:g:53:MET:CE	2:g:92:VAL:HG11	2.00	0.91
2:i:53:MET:CE	2:i:92:VAL:HG11	2.00	0.91
1:N:46:SER:H	1:N:48:TYR:HE2	1.19	0.91
1:O:46:SER:H	1:O:48:TYR:HE2	1.19	0.91
1:P:144:ILE:HG12	1:P:447:TYR:HE1	1.35	0.91
2:c:71:ASP:HB2	2:c:75:PRO:HD2	1.50	0.91
2:j:53:MET:CE	2:j:92:VAL:HG11	2.00	0.91
1:X:46:SER:H	1:X:48:TYR:HE2	1.19	0.91
1:L:546:THR:HG23	1:L:547:PRO:HD3	1.50	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:53:MET:CE	2:Z:92:VAL:HG11	2.00	0.91
2:c:31:ASP:OD2	2:c:93:PHE:CE2	2.22	0.91
2:b:31:ASP:OD2	2:b:93:PHE:CE2	2.22	0.91
2:c:78:GLU:OE1	2:c:78:GLU:HA	1.69	0.91
2:h:28:VAL:HG21	2:h:96:LEU:HB3	1.49	0.91
1:O:158:TRP:HE3	1:O:173:CYS:HG	0.94	0.90
1:W:173:CYS:SG	1:W:298:ILE:HD12	2.12	0.90
1:S:46:SER:H	1:S:48:TYR:HE2	1.19	0.90
1:X:15:PHE:HZ	1:X:283:CYS:HG	1.14	0.90
2:c:53:MET:CE	2:c:92:VAL:HG11	2.00	0.90
1:V:144:ILE:HG12	1:V:447:TYR:HE1	1.34	0.90
1:I:546:THR:HG23	1:I:547:PRO:HD3	1.50	0.90
1:M:144:ILE:HG12	1:M:447:TYR:HE1	1.34	0.90
1:K:546:THR:HG23	1:K:547:PRO:HD3	1.50	0.90
2:Y:53:MET:CE	2:Y:92:VAL:HG11	2.00	0.90
2:f:71:ASP:HB2	2:f:75:PRO:HD2	1.50	0.90
2:h:53:MET:CE	2:h:92:VAL:HG11	2.00	0.90
1:N:144:ILE:HG12	1:N:447:TYR:HE1	1.34	0.90
1:V:46:SER:H	1:V:48:TYR:HE2	1.16	0.90
1:J:546:THR:HG23	1:J:547:PRO:HD3	1.50	0.90
1:N:229:LYS:HA	1:N:272:LYS:HA	1.52	0.89
2:b:53:MET:CE	2:b:92:VAL:HG11	2.00	0.89
1:Q:144:ILE:HG12	1:Q:447:TYR:HE1	1.35	0.89
1:U:144:ILE:HG12	1:U:447:TYR:HE1	1.38	0.89
1:C:560:LEU:HD13	1:E:82:PRO:HD2	1.53	0.89
1:K:14:ARG:HA	1:K:14:ARG:NE	1.83	0.89
1:C:14:ARG:HA	1:C:14:ARG:NE	1.83	0.89
1:E:94:LEU:HA	1:E:97:MSE:HE2	1.55	0.89
1:I:14:ARG:HA	1:I:14:ARG:NE	1.83	0.89
1:J:560:LEU:HD22	1:K:82:PRO:HG2	1.52	0.89
2:e:28:VAL:HG21	2:e:96:LEU:HD12	1.55	0.89
2:c:28:VAL:HG21	2:c:96:LEU:HB3	1.49	0.89
1:T:46:SER:H	1:T:48:TYR:HE2	1.18	0.89
1:B:94:LEU:HA	1:B:97:MSE:HE2	1.55	0.89
1:D:94:LEU:HA	1:D:97:MSE:HE2	1.55	0.89
1:K:94:LEU:HA	1:K:97:MSE:HE2	1.55	0.89
2:d:53:MET:CE	2:d:92:VAL:HG11	2.00	0.89
1:O:144:ILE:HG12	1:O:447:TYR:HE1	1.36	0.89
1:R:165:MSE:HG3	1:R:307:TRP:CE3	2.08	0.89
1:C:94:LEU:HA	1:C:97:MSE:HE2	1.55	0.89
1:F:41:TRP:HE3	1:F:42:ASP:N	1.70	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:g:23:LEU:HA	2:g:26:LEU:HG	1.55	0.89
1:R:144:ILE:HG12	1:R:447:TYR:HE1	1.36	0.89
1:T:165:MSE:HG3	1:T:307:TRP:CE3	2.07	0.89
1:B:564:GLY:HA2	1:C:554:LEU:HD21	1.53	0.89
1:C:41:TRP:CE3	1:C:42:ASP:HB2	2.09	0.89
1:G:94:LEU:HA	1:G:97:MSE:HE2	1.55	0.89
1:W:273:ARG:HH22	1:W:453:LEU:HD11	1.38	0.88
1:I:560:LEU:HD13	1:J:82:PRO:HD2	1.53	0.88
1:K:325:ASP:OD2	2:i:145:SER:HB3	1.73	0.88
1:M:46:SER:H	1:M:48:TYR:HE2	1.19	0.88
1:A:94:LEU:HA	1:A:97:MSE:HE2	1.55	0.88
1:J:561:ASP:HB2	1:K:89:ASP:HA	1.52	0.88
2:d:28:VAL:HG21	2:d:96:LEU:HD12	1.55	0.88
1:K:25:ALA:O	1:K:29:ALA:HB3	1.74	0.88
1:Q:229:LYS:HA	1:Q:272:LYS:HA	1.55	0.88
1:V:158:TRP:HE3	1:V:173:CYS:HG	0.93	0.88
1:B:41:TRP:CE3	1:B:42:ASP:HB2	2.09	0.88
1:I:94:LEU:HA	1:I:97:MSE:HE2	1.55	0.88
2:e:23:LEU:HA	2:e:26:LEU:HG	1.55	0.88
1:Q:158:TRP:HE3	1:Q:173:CYS:HG	0.92	0.88
1:R:14:ARG:HA	1:R:14:ARG:NE	1.87	0.88
1:R:46:SER:H	1:R:48:TYR:HE2	1.20	0.88
1:S:144:ILE:HG12	1:S:447:TYR:HE1	1.36	0.88
1:C:25:ALA:O	1:C:29:ALA:HB3	1.74	0.88
1:E:41:TRP:CE3	1:E:42:ASP:HB2	2.09	0.88
1:I:41:TRP:HE3	1:I:42:ASP:N	1.70	0.88
2:Z:28:VAL:HG21	2:Z:96:LEU:HD12	1.54	0.88
2:b:23:LEU:HA	2:b:26:LEU:HG	1.55	0.88
2:d:23:LEU:HA	2:d:26:LEU:HG	1.55	0.88
1:M:158:TRP:HE3	1:M:173:CYS:HG	0.93	0.88
1:P:229:LYS:HA	1:P:272:LYS:HA	1.55	0.88
1:D:41:TRP:CE3	1:D:42:ASP:HB2	2.09	0.88
1:H:94:LEU:HA	1:H:97:MSE:HE2	1.55	0.88
1:J:14:ARG:HA	1:J:14:ARG:NE	1.83	0.88
1:L:25:ALA:O	1:L:29:ALA:HB3	1.74	0.88
2:i:28:VAL:HG21	2:i:96:LEU:HD12	1.55	0.88
1:Q:46:SER:H	1:Q:48:TYR:HE2	1.18	0.88
1:W:165:MSE:HG3	1:W:307:TRP:CE3	2.08	0.88
1:B:14:ARG:HA	1:B:14:ARG:NE	1.83	0.88
2:g:28:VAL:HG21	2:g:96:LEU:HD12	1.55	0.88
1:V:173:CYS:SG	1:V:298:ILE:HD12	2.13	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:c:28:VAL:HG21	2:c:96:LEU:HD12	1.55	0.88
1:L:41:TRP:HE3	1:L:42:ASP:N	1.70	0.88
2:Z:23:LEU:HA	2:Z:26:LEU:HG	1.55	0.88
2:j:28:VAL:HG21	2:j:96:LEU:HD12	1.55	0.88
1:S:165:MSE:HG3	1:S:307:TRP:CE3	2.09	0.87
1:G:41:TRP:CE3	1:G:42:ASP:HB2	2.09	0.87
1:I:37:ARG:HB3	1:I:37:ARG:HH21	1.39	0.87
1:J:25:ALA:O	1:J:29:ALA:HB3	1.74	0.87
2:h:23:LEU:HA	2:h:26:LEU:HG	1.55	0.87
1:A:37:ARG:HB3	1:A:37:ARG:HH21	1.40	0.87
1:D:41:TRP:HE3	1:D:42:ASP:N	1.70	0.87
1:E:25:ALA:O	1:E:29:ALA:HB3	1.74	0.87
1:F:25:ALA:O	1:F:29:ALA:HB3	1.74	0.87
1:L:41:TRP:CE3	1:L:42:ASP:HB2	2.09	0.87
2:a:28:VAL:HG21	2:a:96:LEU:HD12	1.55	0.87
2:c:23:LEU:HA	2:c:26:LEU:HG	1.55	0.87
1:T:144:ILE:HG12	1:T:447:TYR:HE1	1.37	0.87
1:T:229:LYS:HA	1:T:272:LYS:HA	1.56	0.87
1:F:94:LEU:HA	1:F:97:MSE:HE2	1.55	0.87
1:J:94:LEU:HA	1:J:97:MSE:HE2	1.55	0.87
1:L:94:LEU:HA	1:L:97:MSE:HE2	1.55	0.87
1:V:229:LYS:HA	1:V:272:LYS:HA	1.55	0.87
1:W:229:LYS:HA	1:W:272:LYS:HA	1.56	0.87
1:A:41:TRP:CE3	1:A:42:ASP:HB2	2.09	0.87
1:D:82:PRO:HG2	1:E:560:LEU:HD22	1.57	0.87
1:H:25:ALA:O	1:H:29:ALA:HB3	1.74	0.87
1:J:41:TRP:HE3	1:J:42:ASP:N	1.70	0.87
1:L:325:ASP:OD2	2:h:145:SER:HB3	1.75	0.87
2:Y:28:VAL:HG21	2:Y:96:LEU:HD12	1.55	0.87
2:a:28:VAL:CG2	2:a:96:LEU:CD1	2.53	0.87
1:A:560:LEU:HD13	1:B:82:PRO:HD2	1.54	0.87
1:B:25:ALA:O	1:B:29:ALA:HB3	1.74	0.87
1:G:25:ALA:O	1:G:29:ALA:HB3	1.74	0.87
1:L:14:ARG:HA	1:L:14:ARG:NE	1.83	0.87
2:a:23:LEU:HA	2:a:26:LEU:HG	1.55	0.87
1:V:165:MSE:HG3	1:V:307:TRP:CE3	2.10	0.87
1:B:40:GLN:O	1:B:41:TRP:HB2	1.75	0.87
1:E:41:TRP:HE3	1:E:42:ASP:N	1.70	0.87
1:G:37:ARG:HB3	1:G:37:ARG:HH21	1.39	0.87
1:H:41:TRP:CE3	1:H:42:ASP:HB2	2.09	0.87
1:I:40:GLN:O	1:I:41:TRP:HB2	1.75	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:41:TRP:CE3	1:K:42:ASP:HB2	2.09	0.87
2:f:28:VAL:HG21	2:f:96:LEU:HD12	1.55	0.87
1:F:37:ARG:HB3	1:F:37:ARG:HH21	1.40	0.87
2:j:23:LEU:HA	2:j:26:LEU:HG	1.55	0.87
1:A:25:ALA:O	1:A:29:ALA:HB3	1.74	0.87
1:E:14:ARG:HA	1:E:14:ARG:NE	1.83	0.87
1:F:41:TRP:CE3	1:F:42:ASP:HB2	2.09	0.87
2:b:28:VAL:CG2	2:b:96:LEU:CD1	2.53	0.87
2:h:28:VAL:CG2	2:h:96:LEU:CD1	2.53	0.87
1:O:165:MSE:HG3	1:O:307:TRP:CE3	2.10	0.87
1:P:46:SER:H	1:P:48:TYR:HE2	1.18	0.87
1:Q:173:CYS:SG	1:Q:298:ILE:HD12	2.14	0.87
1:S:173:CYS:SG	1:S:298:ILE:HD12	2.15	0.87
1:B:37:ARG:HH21	1:B:37:ARG:HB3	1.40	0.87
2:i:23:LEU:HA	2:i:26:LEU:HG	1.55	0.87
1:M:165:MSE:HG3	1:M:307:TRP:CE3	2.10	0.86
1:N:14:ARG:HA	1:N:14:ARG:NE	1.87	0.86
1:N:173:CYS:SG	1:N:298:ILE:HD12	2.14	0.86
1:Q:273:ARG:HH22	1:Q:453:LEU:HD11	1.39	0.86
1:V:14:ARG:HA	1:V:14:ARG:NE	1.87	0.86
1:F:40:GLN:O	1:F:41:TRP:HB2	1.75	0.86
2:f:23:LEU:HA	2:f:26:LEU:HG	1.55	0.86
1:R:229:LYS:HA	1:R:272:LYS:HA	1.55	0.86
1:W:46:SER:H	1:W:48:TYR:HE2	1.18	0.86
1:D:25:ALA:O	1:D:29:ALA:HB3	1.74	0.86
1:D:89:ASP:HA	1:E:561:ASP:HB2	1.56	0.86
1:E:37:ARG:HH21	1:E:37:ARG:HB3	1.39	0.86
2:h:28:VAL:HG21	2:h:96:LEU:HD12	1.55	0.86
1:S:15:PHE:HZ	1:S:283:CYS:HG	1.16	0.86
1:I:25:ALA:O	1:I:29:ALA:HB3	1.74	0.86
1:S:273:ARG:HH22	1:S:453:LEU:HD11	1.39	0.86
1:I:41:TRP:CE3	1:I:42:ASP:HB2	2.09	0.86
1:O:273:ARG:HH22	1:O:453:LEU:HD11	1.40	0.86
1:U:165:MSE:HG3	1:U:307:TRP:CE3	2.10	0.86
1:C:37:ARG:HB3	1:C:37:ARG:HH21	1.39	0.86
1:J:236:GLN:HB2	1:J:265:LYS:HZ3	1.40	0.86
2:e:28:VAL:CG2	2:e:96:LEU:CD1	2.53	0.86
1:U:46:SER:H	1:U:48:TYR:HE2	1.20	0.86
1:V:273:ARG:HH22	1:V:453:LEU:HD11	1.40	0.86
2:h:34:LEU:HD12	2:h:104:TYR:CD2	2.11	0.86
1:M:14:ARG:HA	1:M:14:ARG:NE	1.87	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:273:ARG:HH22	1:M:453:LEU:HD11	1.40	0.86
1:O:173:CYS:SG	1:O:298:ILE:HD12	2.15	0.86
1:U:14:ARG:HA	1:U:14:ARG:NE	1.87	0.86
1:X:273:ARG:HH22	1:X:453:LEU:HD11	1.40	0.86
1:A:41:TRP:HE3	1:A:42:ASP:N	1.70	0.86
1:J:41:TRP:CE3	1:J:42:ASP:HB2	2.09	0.86
2:Y:23:LEU:HA	2:Y:26:LEU:HG	1.55	0.86
2:b:28:VAL:HG21	2:b:96:LEU:HD12	1.55	0.86
1:X:248:LYS:CB	1:X:511:ARG:HH11	1.89	0.86
1:G:41:TRP:HE3	1:G:42:ASP:N	1.70	0.86
1:H:41:TRP:HE3	1:H:42:ASP:N	1.70	0.86
2:Y:28:VAL:CG2	2:Y:96:LEU:CD1	2.53	0.86
2:i:34:LEU:HD12	2:i:104:TYR:CD2	2.11	0.86
1:G:40:GLN:O	1:G:41:TRP:HB2	1.75	0.86
1:K:236:GLN:HB2	1:K:265:LYS:HZ3	1.40	0.86
1:A:564:GLY:HA2	1:B:554:LEU:HD21	1.56	0.86
1:H:40:GLN:O	1:H:41:TRP:HB2	1.75	0.86
2:b:34:LEU:HD12	2:b:104:TYR:CD2	2.11	0.86
2:d:34:LEU:HD12	2:d:104:TYR:CD2	2.11	0.86
2:e:34:LEU:HD12	2:e:104:TYR:CD2	2.11	0.86
1:U:229:LYS:HA	1:U:272:LYS:HA	1.56	0.85
1:L:40:GLN:O	1:L:41:TRP:HB2	1.75	0.85
2:g:28:VAL:CG2	2:g:96:LEU:CD1	2.53	0.85
1:M:229:LYS:HA	1:M:272:LYS:HA	1.56	0.85
1:O:229:LYS:HA	1:O:272:LYS:HA	1.56	0.85
1:R:173:CYS:SG	1:R:298:ILE:HD12	2.16	0.85
2:Z:28:VAL:CG2	2:Z:96:LEU:CD1	2.53	0.85
2:c:34:LEU:HD12	2:c:104:TYR:CD2	2.11	0.85
2:f:28:VAL:HG13	2:f:97:ALA:N	1.92	0.85
2:g:28:VAL:HG13	2:g:97:ALA:CB	2.07	0.85
1:S:14:ARG:HA	1:S:14:ARG:NE	1.86	0.85
1:S:229:LYS:HA	1:S:272:LYS:HA	1.57	0.85
1:T:15:PHE:HZ	1:T:283:CYS:HG	1.23	0.85
1:V:89:ASP:HA	1:W:561:ASP:HB2	1.57	0.85
2:b:28:VAL:HG13	2:b:97:ALA:CB	2.06	0.85
2:c:28:VAL:CG2	2:c:96:LEU:CD1	2.53	0.85
2:f:34:LEU:HD12	2:f:104:TYR:CD2	2.11	0.85
1:P:173:CYS:SG	1:P:298:ILE:HD12	2.15	0.85
2:Z:28:VAL:HG13	2:Z:97:ALA:CB	2.06	0.85
2:a:34:LEU:HD12	2:a:104:TYR:CD2	2.11	0.85
1:O:14:ARG:HA	1:O:14:ARG:NE	1.88	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:273:ARG:HH22	1:P:453:LEU:HD11	1.41	0.85
1:R:158:TRP:HE3	1:R:173:CYS:SG	2.00	0.85
1:T:273:ARG:HH22	1:T:453:LEU:HD11	1.40	0.85
1:X:165:MSE:HG3	1:X:307:TRP:CE3	2.11	0.85
2:d:28:VAL:HG13	2:d:97:ALA:CB	2.07	0.85
2:i:28:VAL:CG2	2:i:96:LEU:CD1	2.53	0.85
2:j:28:VAL:HG13	2:j:97:ALA:CB	2.06	0.85
1:P:165:MSE:HG3	1:P:307:TRP:CE3	2.12	0.85
1:R:248:LYS:CB	1:R:511:ARG:HH11	1.89	0.85
1:S:82:PRO:HD2	1:U:560:LEU:HD13	1.58	0.85
1:U:273:ARG:HH22	1:U:453:LEU:HD11	1.37	0.85
1:E:40:GLN:O	1:E:41:TRP:HB2	1.75	0.85
1:G:158:TRP:HE3	1:G:173:CYS:SG	2.00	0.85
2:g:34:LEU:HD12	2:g:104:TYR:CD2	2.11	0.85
1:C:158:TRP:HE3	1:C:173:CYS:SG	2.00	0.85
1:D:236:GLN:HB2	1:D:265:LYS:HZ3	1.41	0.85
1:H:158:TRP:HE3	1:H:173:CYS:SG	2.00	0.85
2:f:28:VAL:HG13	2:f:97:ALA:CB	2.07	0.85
2:h:28:VAL:CG2	2:h:96:LEU:HD13	2.07	0.85
2:i:28:VAL:HG13	2:i:97:ALA:N	1.92	0.85
2:i:28:VAL:CG2	2:i:96:LEU:HD13	2.07	0.85
2:j:28:VAL:CG2	2:j:96:LEU:HD13	2.07	0.85
2:j:34:LEU:HD12	2:j:104:TYR:CD2	2.11	0.85
1:U:173:CYS:SG	1:U:298:ILE:HD12	2.17	0.85
1:A:158:TRP:HE3	1:A:173:CYS:SG	2.00	0.85
1:K:40:GLN:O	1:K:41:TRP:HB2	1.75	0.85
1:K:41:TRP:HE3	1:K:42:ASP:N	1.70	0.85
1:N:165:MSE:HG3	1:N:307:TRP:CE3	2.11	0.85
1:X:229:LYS:HA	1:X:272:LYS:HA	1.56	0.85
1:B:560:LEU:HD13	1:C:82:PRO:HD2	1.59	0.85
2:Y:28:VAL:HG13	2:Y:97:ALA:CB	2.07	0.85
2:Z:34:LEU:HD12	2:Z:104:TYR:CD2	2.11	0.85
2:h:28:VAL:HG13	2:h:97:ALA:N	1.92	0.85
2:j:28:VAL:CG2	2:j:96:LEU:CD1	2.53	0.85
1:R:273:ARG:HH22	1:R:453:LEU:HD11	1.40	0.85
1:S:560:LEU:HD13	1:T:82:PRO:HD2	1.59	0.85
1:B:158:TRP:HE3	1:B:173:CYS:SG	2.00	0.85
1:D:37:ARG:HB3	1:D:37:ARG:HH21	1.40	0.85
2:a:28:VAL:HG13	2:a:97:ALA:N	1.92	0.85
2:c:28:VAL:HG13	2:c:97:ALA:CB	2.07	0.85
1:I:564:GLY:HA2	1:J:554:LEU:HD21	1.59	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:37:ARG:HH21	1:J:37:ARG:HB3	1.40	0.84
1:J:158:TRP:HE3	1:J:173:CYS:SG	2.00	0.84
2:g:28:VAL:HG13	2:g:97:ALA:N	1.92	0.84
2:g:28:VAL:CG2	2:g:96:LEU:HD13	2.07	0.84
1:Q:158:TRP:HE3	1:Q:173:CYS:SG	1.99	0.84
1:Q:165:MSE:HG3	1:Q:307:TRP:CE3	2.11	0.84
1:S:248:LYS:CB	1:S:511:ARG:HH11	1.90	0.84
1:W:158:TRP:HE3	1:W:173:CYS:SG	1.99	0.84
1:A:40:GLN:O	1:A:41:TRP:HB2	1.75	0.84
1:L:37:ARG:HB3	1:L:37:ARG:HH21	1.40	0.84
2:d:28:VAL:CG2	2:d:96:LEU:HD13	2.07	0.84
2:g:28:VAL:HG12	2:g:97:ALA:HA	1.59	0.84
1:M:24:GLU:C	1:M:26:ARG:H	1.85	0.84
1:H:37:ARG:HH21	1:H:37:ARG:HB3	1.40	0.84
2:Z:28:VAL:CG2	2:Z:96:LEU:HD13	2.07	0.84
2:b:28:VAL:HG13	2:b:97:ALA:N	1.92	0.84
2:c:28:VAL:HG13	2:c:97:ALA:N	1.91	0.84
2:i:28:VAL:HG13	2:i:97:ALA:CB	2.07	0.84
1:X:173:CYS:SG	1:X:298:ILE:HD12	2.16	0.84
1:B:41:TRP:HE3	1:B:42:ASP:N	1.70	0.84
1:K:158:TRP:HE3	1:K:173:CYS:SG	2.00	0.84
1:L:158:TRP:HE3	1:L:173:CYS:SG	2.00	0.84
1:S:158:TRP:HE3	1:S:173:CYS:SG	2.00	0.84
1:V:330:ARG:HD2	1:V:409:THR:HG22	1.58	0.84
1:A:212:LEU:HD22	1:B:26:ARG:HG2	1.60	0.84
1:F:158:TRP:HE3	1:F:173:CYS:SG	2.00	0.84
2:Y:34:LEU:HD12	2:Y:104:TYR:CD2	2.11	0.84
2:e:28:VAL:HG13	2:e:97:ALA:CB	2.07	0.84
1:X:144:ILE:HG12	1:X:447:TYR:HE1	1.39	0.84
1:D:158:TRP:HE3	1:D:173:CYS:SG	2.00	0.84
2:a:28:VAL:HG13	2:a:97:ALA:CB	2.07	0.84
2:d:28:VAL:HG12	2:d:97:ALA:HA	1.59	0.84
2:h:28:VAL:HG13	2:h:97:ALA:CB	2.07	0.84
1:N:273:ARG:HH22	1:N:453:LEU:HD11	1.41	0.84
1:A:41:TRP:CE3	1:A:42:ASP:CB	2.61	0.84
1:C:40:GLN:O	1:C:41:TRP:HB2	1.75	0.84
1:F:41:TRP:CE3	1:F:42:ASP:CB	2.61	0.84
1:E:41:TRP:CE3	1:E:42:ASP:CB	2.61	0.84
2:Y:28:VAL:HG13	2:Y:97:ALA:N	1.92	0.84
2:d:28:VAL:CG2	2:d:96:LEU:CD1	2.53	0.84
2:f:28:VAL:CG2	2:f:96:LEU:CD1	2.53	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:i:28:VAL:HG12	2:i:97:ALA:HA	1.59	0.84
1:T:14:ARG:HA	1:T:14:ARG:NE	1.87	0.84
1:V:158:TRP:HE3	1:V:173:CYS:SG	2.00	0.84
1:B:41:TRP:CE3	1:B:42:ASP:CB	2.61	0.84
1:I:41:TRP:CE3	1:I:42:ASP:CB	2.61	0.84
1:I:158:TRP:HE3	1:I:173:CYS:SG	2.00	0.84
1:J:40:GLN:O	1:J:41:TRP:HB2	1.75	0.84
1:L:41:TRP:CE3	1:L:42:ASP:CB	2.61	0.84
1:T:330:ARG:HD2	1:T:409:THR:HG22	1.60	0.84
1:W:14:ARG:HA	1:W:14:ARG:NE	1.88	0.84
2:Z:28:VAL:HG13	2:Z:97:ALA:N	1.91	0.84
2:h:28:VAL:HG12	2:h:97:ALA:HA	1.59	0.84
2:j:28:VAL:HG13	2:j:97:ALA:N	1.91	0.84
1:T:561:ASP:HB2	1:W:89:ASP:HA	1.59	0.83
1:J:41:TRP:CE3	1:J:42:ASP:CB	2.61	0.83
1:K:37:ARG:HB3	1:K:37:ARG:HH21	1.40	0.83
1:K:41:TRP:CE3	1:K:42:ASP:CB	2.61	0.83
2:e:28:VAL:HG13	2:e:97:ALA:N	1.92	0.83
1:N:158:TRP:HE3	1:N:173:CYS:SG	2.00	0.83
1:R:24:GLU:C	1:R:26:ARG:H	1.85	0.83
1:T:173:CYS:SG	1:T:298:ILE:HD12	2.18	0.83
1:D:40:GLN:O	1:D:41:TRP:HB2	1.75	0.83
1:E:158:TRP:HE3	1:E:173:CYS:SG	2.00	0.83
1:H:41:TRP:CE3	1:H:42:ASP:CB	2.61	0.83
1:I:236:GLN:HB2	1:I:265:LYS:HZ3	1.41	0.83
1:L:35:PHE:HE2	1:L:324:LYS:HZ3	1.27	0.83
2:a:28:VAL:CG2	2:a:96:LEU:HD13	2.07	0.83
1:M:82:PRO:HD2	1:N:560:LEU:HD13	1.60	0.83
1:U:15:PHE:HZ	1:U:283:CYS:HG	1.23	0.83
1:X:14:ARG:HA	1:X:14:ARG:NE	1.87	0.83
1:X:158:TRP:HE3	1:X:173:CYS:SG	2.00	0.83
1:D:41:TRP:CE3	1:D:42:ASP:CB	2.61	0.83
2:c:28:VAL:HG12	2:c:97:ALA:HA	1.59	0.83
1:X:330:ARG:HD2	1:X:409:THR:HG22	1.61	0.83
2:f:28:VAL:HG12	2:f:97:ALA:HA	1.59	0.83
1:O:248:LYS:CB	1:O:511:ARG:HH11	1.92	0.83
1:Q:14:ARG:HA	1:Q:14:ARG:NE	1.88	0.83
2:e:28:VAL:CG2	2:e:96:LEU:HD13	2.07	0.83
2:j:28:VAL:HG12	2:j:97:ALA:HA	1.59	0.83
1:M:330:ARG:HD2	1:M:409:THR:HG22	1.61	0.83
1:O:330:ARG:HD2	1:O:409:THR:HG22	1.60	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:330:ARG:HD2	1:W:409:THR:HG22	1.61	0.83
1:G:41:TRP:CE3	1:G:42:ASP:CB	2.61	0.83
2:b:28:VAL:HG12	2:b:97:ALA:HA	1.59	0.83
1:P:158:TRP:HE3	1:P:173:CYS:SG	2.00	0.83
1:A:139:SER:CB	1:A:455:THR:HG23	2.09	0.83
2:Y:28:VAL:HG12	2:Y:97:ALA:HA	1.59	0.83
2:f:28:VAL:CG2	2:f:96:LEU:HD13	2.07	0.83
1:T:158:TRP:HE3	1:T:173:CYS:SG	2.01	0.83
1:A:236:GLN:HB2	1:A:265:LYS:HZ3	1.42	0.83
2:c:28:VAL:CG2	2:c:96:LEU:HD13	2.07	0.83
1:O:24:GLU:C	1:O:26:ARG:H	1.86	0.83
1:O:158:TRP:HE3	1:O:173:CYS:SG	2.01	0.83
1:U:158:TRP:HE3	1:U:173:CYS:SG	2.00	0.83
1:X:24:GLU:C	1:X:26:ARG:H	1.85	0.83
1:B:139:SER:CB	1:B:455:THR:HG23	2.09	0.83
1:C:236:GLN:HB2	1:C:265:LYS:HZ3	1.42	0.83
1:H:139:SER:CB	1:H:455:THR:HG23	2.09	0.83
1:K:139:SER:CB	1:K:455:THR:HG23	2.09	0.83
1:M:158:TRP:HE3	1:M:173:CYS:SG	2.02	0.82
1:N:228:LYS:HA	1:N:228:LYS:HE2	1.61	0.82
1:G:236:GLN:HB2	1:G:265:LYS:HZ3	1.44	0.82
2:a:53:MET:HE2	2:a:92:VAL:HG11	1.61	0.82
1:N:24:GLU:C	1:N:26:ARG:H	1.85	0.82
1:Q:560:LEU:HD22	1:R:82:PRO:HG2	1.60	0.82
1:C:41:TRP:HE3	1:C:42:ASP:N	1.70	0.82
1:J:139:SER:CB	1:J:455:THR:HG23	2.09	0.82
1:M:248:LYS:CB	1:M:511:ARG:HH11	1.92	0.82
1:P:14:ARG:HA	1:P:14:ARG:NE	1.88	0.82
1:R:330:ARG:HD2	1:R:409:THR:HG22	1.62	0.82
1:T:35:PHE:HE2	1:T:324:LYS:HZ3	1.26	0.82
1:U:248:LYS:CB	1:U:511:ARG:HH11	1.91	0.82
2:Y:28:VAL:CG2	2:Y:96:LEU:HD13	2.07	0.82
2:d:28:VAL:HG13	2:d:97:ALA:N	1.91	0.82
1:P:248:LYS:CB	1:P:511:ARG:HH11	1.91	0.82
1:B:325:ASP:OD2	2:Y:145:SER:HB3	1.79	0.82
2:b:28:VAL:CG2	2:b:96:LEU:HD13	2.07	0.82
1:C:139:SER:CB	1:C:455:THR:HG23	2.09	0.82
1:E:236:GLN:HB2	1:E:265:LYS:HZ3	1.44	0.82
1:F:236:GLN:HB2	1:F:265:LYS:HZ3	1.45	0.82
1:T:248:LYS:CB	1:T:511:ARG:HH11	1.91	0.82
1:W:24:GLU:C	1:W:26:ARG:H	1.85	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:325:ASP:OD2	2:a:145:SER:HB3	1.79	0.82
2:Y:53:MET:HE2	2:Y:92:VAL:HG11	1.61	0.82
1:M:173:CYS:SG	1:M:298:ILE:HD12	2.18	0.82
1:S:554:LEU:HD21	1:U:564:GLY:HA2	1.61	0.82
1:C:41:TRP:CE3	1:C:42:ASP:CB	2.61	0.82
1:F:139:SER:CB	1:F:455:THR:HG23	2.09	0.82
1:H:236:GLN:HB2	1:H:265:LYS:HZ3	1.45	0.82
1:L:139:SER:CB	1:L:455:THR:HG23	2.09	0.82
2:g:53:MET:HE2	2:g:92:VAL:HG11	1.61	0.82
1:H:560:LEU:HD22	1:I:82:PRO:HG2	1.60	0.82
2:c:53:MET:HE2	2:c:92:VAL:HG11	1.61	0.82
1:R:11:ILE:HD12	1:R:285:ALA:HA	1.62	0.81
1:G:139:SER:CB	1:G:455:THR:HG23	2.09	0.81
1:I:139:SER:CB	1:I:455:THR:HG23	2.09	0.81
1:L:236:GLN:HB2	1:L:265:LYS:HZ3	1.44	0.81
2:Z:28:VAL:HG12	2:Z:97:ALA:HA	1.59	0.81
2:Z:53:MET:HE2	2:Z:92:VAL:HG11	1.61	0.81
2:e:28:VAL:HG12	2:e:97:ALA:HA	1.59	0.81
1:N:248:LYS:CB	1:N:511:ARG:HH11	1.94	0.81
1:Q:248:LYS:CB	1:Q:511:ARG:HH11	1.93	0.81
1:S:24:GLU:C	1:S:26:ARG:H	1.86	0.81
1:S:330:ARG:HD2	1:S:409:THR:HG22	1.60	0.81
1:T:24:GLU:C	1:T:26:ARG:H	1.86	0.81
1:E:139:SER:CB	1:E:455:THR:HG23	2.09	0.81
1:I:212:LEU:HD22	1:J:26:ARG:HG2	1.62	0.81
2:b:28:VAL:HG13	2:b:97:ALA:HB2	1.63	0.81
2:d:53:MET:HE2	2:d:92:VAL:HG11	1.61	0.81
2:b:53:MET:HE2	2:b:92:VAL:HG11	1.61	0.81
1:N:208:VAL:HG12	1:N:210:PRO:HD3	1.63	0.81
1:R:208:VAL:HG12	1:R:210:PRO:HD3	1.63	0.81
1:F:35:PHE:HE2	1:F:324:LYS:HZ3	1.27	0.81
2:g:28:VAL:HG13	2:g:97:ALA:HB2	1.63	0.81
1:Q:24:GLU:C	1:Q:26:ARG:H	1.87	0.81
1:Q:228:LYS:HE2	1:Q:228:LYS:HA	1.62	0.81
1:D:139:SER:CB	1:D:455:THR:HG23	2.09	0.81
2:Z:28:VAL:HG13	2:Z:97:ALA:HB2	1.63	0.81
2:h:53:MET:HE2	2:h:92:VAL:HG11	1.61	0.81
2:j:53:MET:HE2	2:j:92:VAL:HG11	1.61	0.81
1:Q:15:PHE:HZ	1:Q:283:CYS:HG	1.27	0.81
1:Q:208:VAL:HG12	1:Q:210:PRO:HD3	1.63	0.81
1:R:228:LYS:HE2	1:R:228:LYS:HA	1.63	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:560:LEU:HD22	1:F:82:PRO:HG2	1.62	0.81
1:F:560:LEU:HD22	1:G:82:PRO:HG2	1.60	0.81
1:O:560:LEU:HD13	1:P:82:PRO:HD2	1.61	0.81
1:P:24:GLU:C	1:P:26:ARG:H	1.87	0.81
1:V:63:VAL:HG21	1:V:416:ALA:HB1	1.63	0.81
1:W:208:VAL:HG12	1:W:210:PRO:HD3	1.62	0.81
2:c:28:VAL:HG13	2:c:97:ALA:HB2	1.63	0.81
1:P:376:ARG:O	1:P:383:ASP:HB3	1.81	0.81
1:U:228:LYS:HE2	1:U:228:LYS:HA	1.63	0.81
1:U:330:ARG:HD2	1:U:409:THR:HG22	1.63	0.81
1:V:208:VAL:HG12	1:V:210:PRO:HD3	1.63	0.81
1:X:208:VAL:HG12	1:X:210:PRO:HD3	1.63	0.81
1:X:228:LYS:HE2	1:X:228:LYS:HA	1.63	0.81
2:b:28:VAL:CG1	2:b:97:ALA:N	2.44	0.81
2:e:28:VAL:HG13	2:e:97:ALA:HB2	1.63	0.81
1:V:228:LYS:HA	1:V:228:LYS:HE2	1.62	0.81
2:e:28:VAL:CG1	2:e:97:ALA:N	2.44	0.81
2:e:53:MET:HE2	2:e:92:VAL:HG11	1.61	0.81
1:S:63:VAL:HG21	1:S:416:ALA:HB1	1.63	0.80
1:V:24:GLU:C	1:V:26:ARG:H	1.87	0.80
2:o:37:VAL:HG11	2:o:68:ALA:HB1	1.63	0.80
1:C:564:GLY:HA2	1:E:554:LEU:HD21	1.62	0.80
1:K:35:PHE:HE2	1:K:324:LYS:HZ3	1.28	0.80
2:Y:28:VAL:CG1	2:Y:97:ALA:N	2.44	0.80
2:i:53:MET:HE2	2:i:92:VAL:HG11	1.61	0.80
1:M:228:LYS:HE2	1:M:228:LYS:HA	1.62	0.80
1:W:228:LYS:HE2	1:W:228:LYS:HA	1.63	0.80
1:W:248:LYS:CB	1:W:511:ARG:HH11	1.92	0.80
1:B:236:GLN:HB2	1:B:265:LYS:HZ3	1.44	0.80
1:S:564:GLY:HA2	1:T:554:LEU:HD21	1.64	0.80
1:H:35:PHE:HE2	1:H:324:LYS:HZ3	1.29	0.80
2:g:28:VAL:CG1	2:g:97:ALA:N	2.44	0.80
1:Q:63:VAL:HG21	1:Q:416:ALA:HB1	1.61	0.80
1:Q:11:ILE:HD12	1:Q:285:ALA:HA	1.64	0.80
1:S:228:LYS:HA	1:S:228:LYS:HE2	1.64	0.80
1:C:58:ASP:O	1:C:59:VAL:CG1	2.30	0.80
2:c:28:VAL:CG1	2:c:97:ALA:N	2.44	0.80
2:h:28:VAL:CG1	2:h:97:ALA:N	2.44	0.80
1:Q:330:ARG:HD2	1:Q:409:THR:HG22	1.64	0.80
1:W:303:VAL:HA	1:W:439:ASN:OD1	1.82	0.80
2:a:28:VAL:HG12	2:a:97:ALA:HA	1.59	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:d:28:VAL:HG13	2:d:97:ALA:HB2	1.63	0.80
1:U:35:PHE:HE2	1:U:324:LYS:HZ3	1.28	0.80
1:C:15:PHE:HZ	1:C:283:CYS:HG	1.27	0.80
1:H:325:ASP:OD2	2:d:145:SER:HB3	1.82	0.80
1:M:208:VAL:HG12	1:M:210:PRO:HD3	1.63	0.80
1:E:282:THR:HG23	1:E:287:LEU:HD11	1.64	0.80
1:F:561:ASP:HB2	1:G:89:ASP:HA	1.63	0.80
1:G:282:THR:HG23	1:G:287:LEU:HD11	1.64	0.80
2:i:28:VAL:CG1	2:i:97:ALA:N	2.44	0.80
1:T:208:VAL:HG12	1:T:210:PRO:HD3	1.63	0.80
1:T:228:LYS:HE2	1:T:228:LYS:HA	1.63	0.80
1:U:24:GLU:C	1:U:26:ARG:H	1.86	0.80
1:F:282:THR:HG23	1:F:287:LEU:HD11	1.64	0.80
1:I:58:ASP:O	1:I:59:VAL:CG1	2.30	0.80
2:b:53:MET:HE1	2:b:92:VAL:HG12	0.82	0.80
1:A:82:PRO:HG2	1:L:560:LEU:HD22	1.62	0.80
1:J:58:ASP:O	1:J:59:VAL:CG1	2.30	0.80
2:d:28:VAL:CG1	2:d:97:ALA:N	2.44	0.80
2:j:28:VAL:HG13	2:j:97:ALA:HB2	1.63	0.80
1:P:208:VAL:HG12	1:P:210:PRO:HD3	1.63	0.79
1:B:282:THR:HG23	1:B:287:LEU:HD11	1.64	0.79
1:H:561:ASP:HB2	1:I:89:ASP:HA	1.62	0.79
1:I:282:THR:HG23	1:I:287:LEU:HD11	1.64	0.79
2:f:28:VAL:CG1	2:f:97:ALA:N	2.44	0.79
2:f:53:MET:HE2	2:f:92:VAL:HG11	1.61	0.79
1:S:208:VAL:HG12	1:S:210:PRO:HD3	1.63	0.79
1:V:303:VAL:HA	1:V:439:ASN:OD1	1.81	0.79
1:N:303:VAL:HA	1:N:439:ASN:OD1	1.82	0.79
1:U:11:ILE:HD12	1:U:285:ALA:HA	1.64	0.79
1:A:282:THR:HG23	1:A:287:LEU:HD11	1.64	0.79
2:f:28:VAL:HG13	2:f:97:ALA:HB2	1.63	0.79
2:j:53:MET:HE1	2:j:92:VAL:HG12	0.82	0.79
1:N:11:ILE:HD12	1:N:285:ALA:HA	1.63	0.79
1:S:11:ILE:HD12	1:S:285:ALA:HA	1.64	0.79
1:C:282:THR:HG23	1:C:287:LEU:HD11	1.64	0.79
1:D:58:ASP:O	1:D:59:VAL:CG1	2.30	0.79
1:D:282:THR:HG23	1:D:287:LEU:HD11	1.64	0.79
1:F:58:ASP:O	1:F:59:VAL:CG1	2.30	0.79
1:O:63:VAL:HG21	1:O:416:ALA:HB1	1.64	0.79
1:V:11:ILE:HD12	1:V:285:ALA:HA	1.63	0.79
1:E:58:ASP:O	1:E:59:VAL:CG1	2.30	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:58:ASP:O	1:G:59:VAL:CG1	2.30	0.79
1:H:282:THR:HG23	1:H:287:LEU:HD11	1.64	0.79
2:b:143:THR:HB	2:b:154:GLU:H	1.48	0.79
2:j:28:VAL:CG1	2:j:97:ALA:N	2.44	0.79
1:O:208:VAL:HG12	1:O:210:PRO:HD3	1.63	0.79
1:O:228:LYS:HE2	1:O:228:LYS:HA	1.63	0.79
1:V:248:LYS:CB	1:V:511:ARG:HH11	1.94	0.79
2:o:17:LEU:HD11	2:o:36:ALA:HB3	1.64	0.79
1:E:248:LYS:H	1:E:248:LYS:HD2	1.48	0.79
1:J:248:LYS:H	1:J:248:LYS:HD2	1.48	0.79
2:Y:28:VAL:HG13	2:Y:97:ALA:HB2	1.63	0.79
1:N:248:LYS:H	1:N:248:LYS:HD2	1.47	0.79
1:N:330:ARG:HD2	1:N:409:THR:HG22	1.65	0.79
1:P:63:VAL:HG21	1:P:416:ALA:HB1	1.63	0.79
1:Q:35:PHE:HE2	1:Q:324:LYS:HZ3	1.27	0.79
1:W:63:VAL:HG21	1:W:416:ALA:HB1	1.64	0.79
1:X:11:ILE:HD12	1:X:285:ALA:HA	1.65	0.79
1:A:58:ASP:O	1:A:59:VAL:CG1	2.30	0.79
1:D:248:LYS:H	1:D:248:LYS:HD2	1.48	0.79
1:L:248:LYS:H	1:L:248:LYS:HD2	1.48	0.79
2:e:53:MET:HE1	2:e:92:VAL:HG12	0.82	0.79
1:O:334:MSE:SE	1:P:404:MSE:HE1	2.32	0.79
1:P:228:LYS:HE2	1:P:228:LYS:HA	1.64	0.79
1:W:11:ILE:HD12	1:W:285:ALA:HA	1.63	0.79
1:W:376:ARG:O	1:W:383:ASP:HB3	1.83	0.79
1:G:564:GLY:HA2	1:H:554:LEU:HD21	1.64	0.79
1:K:248:LYS:H	1:K:248:LYS:HD2	1.48	0.79
2:a:28:VAL:HG13	2:a:97:ALA:HB2	1.63	0.79
1:P:35:PHE:HE2	1:P:324:LYS:HZ3	1.31	0.79
1:P:303:VAL:HA	1:P:439:ASN:OD1	1.83	0.79
1:D:35:PHE:HE2	1:D:324:LYS:HZ3	1.29	0.79
1:H:58:ASP:O	1:H:59:VAL:CG1	2.30	0.79
1:L:282:THR:HG23	1:L:287:LEU:HD11	1.64	0.79
2:Z:143:THR:HB	2:Z:154:GLU:H	1.48	0.79
1:M:63:VAL:HG21	1:M:416:ALA:HB1	1.64	0.79
1:T:303:VAL:HA	1:T:439:ASN:OD1	1.83	0.79
1:V:35:PHE:HE2	1:V:324:LYS:HZ3	1.30	0.79
1:B:212:LEU:HD22	1:C:26:ARG:HG2	1.65	0.79
1:K:58:ASP:O	1:K:59:VAL:CG1	2.30	0.79
2:i:28:VAL:HG13	2:i:97:ALA:HB2	1.63	0.79
1:P:11:ILE:HD12	1:P:285:ALA:HA	1.64	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:208:VAL:HG12	1:U:210:PRO:HD3	1.62	0.78
1:C:248:LYS:H	1:C:248:LYS:HD2	1.48	0.78
2:h:143:THR:HB	2:h:154:GLU:H	1.48	0.78
1:M:554:LEU:HD21	1:N:564:GLY:HA2	1.63	0.78
1:Q:561:ASP:OD2	1:R:92:ASP:HB3	1.81	0.78
1:D:325:ASP:OD2	2:b:145:SER:HB3	1.82	0.78
1:N:376:ARG:O	1:N:383:ASP:HB3	1.84	0.78
1:P:144:ILE:HG12	1:P:447:TYR:CE1	2.19	0.78
1:Q:236:GLN:HB2	1:Q:265:LYS:HG2	1.65	0.78
1:Q:303:VAL:HA	1:Q:439:ASN:OD1	1.83	0.78
1:B:248:LYS:H	1:B:248:LYS:HD2	1.48	0.78
1:V:144:ILE:HG12	1:V:447:TYR:CE1	2.18	0.78
2:Z:28:VAL:CG1	2:Z:97:ALA:N	2.44	0.78
2:Z:53:MET:HE1	2:Z:92:VAL:HG12	0.82	0.78
2:b:28:VAL:CG2	2:b:96:LEU:HB3	2.14	0.78
2:d:53:MET:HE1	2:d:92:VAL:HG12	0.82	0.78
2:f:53:MET:HE1	2:f:92:VAL:HG12	0.82	0.78
2:i:143:THR:HB	2:i:154:GLU:H	1.48	0.78
1:N:63:VAL:HG21	1:N:416:ALA:HB1	1.65	0.78
1:T:11:ILE:HD12	1:T:285:ALA:HA	1.62	0.78
1:T:63:VAL:HG21	1:T:416:ALA:HB1	1.65	0.78
1:A:248:LYS:H	1:A:248:LYS:HD2	1.48	0.78
1:D:334:MSE:HE1	1:F:407:ALA:HB1	1.63	0.78
1:J:35:PHE:CZ	1:J:321:ARG:NE	2.52	0.78
1:J:282:THR:HG23	1:J:287:LEU:HD11	1.64	0.78
1:S:303:VAL:HA	1:S:439:ASN:OD1	1.84	0.78
1:W:236:GLN:HB2	1:W:265:LYS:HG2	1.66	0.78
2:n:37:VAL:HG11	2:n:68:ALA:HB1	1.65	0.78
2:Y:28:VAL:CG2	2:Y:96:LEU:HB3	2.14	0.78
2:a:28:VAL:CG1	2:a:97:ALA:N	2.44	0.78
2:a:143:THR:HB	2:a:154:GLU:H	1.48	0.78
2:c:34:LEU:C	2:c:35:THR:HG23	2.09	0.78
2:c:53:MET:HE1	2:c:92:VAL:HG12	0.82	0.78
2:e:143:THR:HB	2:e:154:GLU:H	1.48	0.78
2:f:34:LEU:C	2:f:35:THR:HG23	2.09	0.78
1:O:236:GLN:HB2	1:O:265:LYS:HG2	1.66	0.78
2:l:17:LEU:HD11	2:l:36:ALA:HB3	1.66	0.78
2:n:17:LEU:HD11	2:n:36:ALA:HB3	1.66	0.78
1:I:248:LYS:H	1:I:248:LYS:HD2	1.48	0.78
1:L:58:ASP:O	1:L:59:VAL:CG1	2.30	0.78
2:Y:34:LEU:C	2:Y:35:THR:HG23	2.09	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:g:28:VAL:CG2	2:g:96:LEU:HB3	2.14	0.78
2:h:28:VAL:HG13	2:h:97:ALA:HB2	1.63	0.78
1:M:11:ILE:HD12	1:M:285:ALA:HA	1.64	0.78
1:A:35:PHE:CZ	1:A:321:ARG:NE	2.52	0.78
1:B:58:ASP:O	1:B:59:VAL:CG1	2.30	0.78
1:C:35:PHE:CZ	1:C:321:ARG:NE	2.52	0.78
1:D:561:ASP:HB2	1:F:89:ASP:HA	1.64	0.78
1:M:144:ILE:HG12	1:M:447:TYR:CE1	2.19	0.78
1:O:35:PHE:HE2	1:O:324:LYS:HZ3	1.28	0.78
1:R:236:GLN:HB2	1:R:265:LYS:HG2	1.66	0.78
1:R:303:VAL:HA	1:R:439:ASN:OD1	1.83	0.78
1:V:82:PRO:HG2	1:W:560:LEU:HD22	1.66	0.78
1:V:376:ARG:O	1:V:383:ASP:HB3	1.84	0.78
1:A:334:MSE:HE1	1:B:407:ALA:HB1	1.64	0.78
1:B:35:PHE:CZ	1:B:321:ARG:NE	2.52	0.78
1:H:35:PHE:CZ	1:H:321:ARG:NE	2.52	0.78
1:K:35:PHE:CZ	1:K:321:ARG:NE	2.52	0.78
1:M:236:GLN:HB2	1:M:265:LYS:HG2	1.67	0.77
1:O:303:VAL:HA	1:O:439:ASN:OD1	1.83	0.77
1:A:325:ASP:OD2	2:j:145:SER:HB3	1.84	0.77
1:D:35:PHE:CZ	1:D:321:ARG:NE	2.52	0.77
1:K:282:THR:HG23	1:K:287:LEU:HD11	1.64	0.77
2:g:143:THR:HB	2:g:154:GLU:H	1.48	0.77
2:h:28:VAL:CG2	2:h:96:LEU:HB3	2.14	0.77
2:j:143:THR:HB	2:j:154:GLU:H	1.48	0.77
1:O:564:GLY:HA2	1:P:554:LEU:HD21	1.65	0.77
1:X:35:PHE:HE2	1:X:324:LYS:HZ3	1.30	0.77
2:l:37:VAL:HG11	2:l:68:ALA:HB1	1.66	0.77
1:F:11:ILE:HD12	1:F:285:ALA:HA	1.66	0.77
1:I:35:PHE:CZ	1:I:321:ARG:NE	2.52	0.77
2:Z:28:VAL:CG2	2:Z:96:LEU:HB3	2.14	0.77
2:c:28:VAL:CG2	2:c:96:LEU:HB3	2.14	0.77
2:j:28:VAL:CG2	2:j:96:LEU:HB3	2.14	0.77
1:M:303:VAL:HA	1:M:439:ASN:OD1	1.85	0.77
1:N:236:GLN:HB2	1:N:265:LYS:HG2	1.65	0.77
1:P:236:GLN:HB2	1:P:265:LYS:HG2	1.66	0.77
1:W:248:LYS:H	1:W:248:LYS:HD2	1.48	0.77
1:X:303:VAL:HA	1:X:439:ASN:OD1	1.83	0.77
1:G:35:PHE:CZ	1:G:321:ARG:NE	2.52	0.77
2:Y:143:THR:HB	2:Y:154:GLU:H	1.48	0.77
2:Z:34:LEU:C	2:Z:35:THR:HG23	2.09	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:i:28:VAL:CG2	2:i:96:LEU:HB3	2.14	0.77
1:N:144:ILE:HG12	1:N:447:TYR:CE1	2.19	0.77
1:R:376:ARG:O	1:R:383:ASP:HB3	1.84	0.77
1:V:236:GLN:HB2	1:V:265:LYS:HG2	1.67	0.77
1:B:35:PHE:HE2	1:B:324:LYS:HZ3	1.27	0.77
1:E:35:PHE:CZ	1:E:321:ARG:NE	2.52	0.77
1:I:334:MSE:HE1	1:J:407:ALA:HB1	1.66	0.77
2:d:28:VAL:CG2	2:d:96:LEU:HB3	2.14	0.77
1:O:376:ARG:O	1:O:383:ASP:HB3	1.84	0.77
1:Q:376:ARG:O	1:Q:383:ASP:HB3	1.84	0.77
1:X:37:ARG:HB3	1:X:37:ARG:NH2	2.00	0.77
1:A:182:ASN:ND2	1:B:171:ARG:HH21	1.81	0.77
1:G:11:ILE:HD12	1:G:285:ALA:HA	1.66	0.77
1:H:11:ILE:HD12	1:H:285:ALA:HA	1.66	0.77
1:L:35:PHE:CZ	1:L:321:ARG:NE	2.52	0.77
2:Y:78:GLU:CG	2:Y:79:GLY:H	1.98	0.77
2:d:78:GLU:CG	2:d:79:GLY:H	1.98	0.77
2:e:28:VAL:CG2	2:e:96:LEU:HB3	2.14	0.77
2:j:34:LEU:C	2:j:35:THR:HG23	2.09	0.77
1:R:35:PHE:HE2	1:R:324:LYS:HZ3	1.30	0.77
1:R:144:ILE:HG12	1:R:447:TYR:CE1	2.20	0.77
1:D:11:ILE:HD12	1:D:285:ALA:HA	1.66	0.77
1:L:11:ILE:HD12	1:L:285:ALA:HA	1.66	0.77
2:a:78:GLU:CG	2:a:79:GLY:H	1.98	0.77
2:b:78:GLU:CG	2:b:79:GLY:H	1.98	0.77
2:g:53:MET:HE1	2:g:92:VAL:HG12	0.82	0.77
2:g:78:GLU:CG	2:g:79:GLY:H	1.98	0.77
1:Q:144:ILE:HG12	1:Q:447:TYR:CE1	2.20	0.77
1:W:35:PHE:HE2	1:W:324:LYS:HZ3	1.31	0.77
2:t:37:VAL:HG11	2:t:68:ALA:HB1	1.67	0.77
2:v:17:LEU:HD11	2:v:36:ALA:HB3	1.66	0.77
1:H:15:PHE:HZ	1:H:283:CYS:HG	1.27	0.77
2:c:143:THR:HB	2:c:154:GLU:H	1.48	0.77
1:U:63:VAL:HG21	1:U:416:ALA:HB1	1.65	0.77
2:m:37:VAL:HG11	2:m:68:ALA:HB1	1.65	0.77
2:p:17:LEU:HD11	2:p:36:ALA:HB3	1.67	0.77
1:B:11:ILE:HD12	1:B:285:ALA:HA	1.66	0.77
1:E:273:ARG:HH22	1:E:453:LEU:HD21	1.50	0.77
1:F:248:LYS:H	1:F:248:LYS:HD2	1.48	0.77
2:a:28:VAL:CG2	2:a:96:LEU:HB3	2.14	0.77
1:M:35:PHE:HE2	1:M:324:LYS:HZ3	1.30	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:248:LYS:H	1:O:248:LYS:HD2	1.50	0.77
1:Q:334:MSE:SE	1:R:404:MSE:HE1	2.35	0.77
1:C:35:PHE:HE2	1:C:324:LYS:HZ3	1.31	0.77
1:H:248:LYS:H	1:H:248:LYS:HD2	1.48	0.77
2:d:143:THR:HB	2:d:154:GLU:H	1.48	0.77
2:i:34:LEU:C	2:i:35:THR:HG23	2.09	0.77
1:N:82:PRO:HG2	1:V:560:LEU:HD22	1.66	0.77
1:T:376:ARG:O	1:T:383:ASP:HB3	1.82	0.77
2:u:37:VAL:HG11	2:u:68:ALA:HB1	1.67	0.77
1:F:35:PHE:CZ	1:F:321:ARG:NE	2.52	0.77
1:J:325:ASP:OD2	2:g:145:SER:HB3	1.84	0.77
2:Y:53:MET:HE1	2:Y:92:VAL:HG12	0.82	0.77
2:b:34:LEU:C	2:b:35:THR:HG23	2.09	0.77
2:f:28:VAL:CG2	2:f:96:LEU:HB3	2.14	0.77
2:h:78:GLU:CG	2:h:79:GLY:H	1.98	0.77
2:i:78:GLU:CG	2:i:79:GLY:H	1.98	0.77
1:M:248:LYS:HD2	1:M:248:LYS:H	1.50	0.76
1:O:144:ILE:HG12	1:O:447:TYR:CE1	2.20	0.76
1:X:34:PHE:HZ	1:X:328:ARG:NH2	1.83	0.76
1:F:273:ARG:HH22	1:F:453:LEU:HD21	1.50	0.76
1:G:248:LYS:H	1:G:248:LYS:HD2	1.48	0.76
1:H:273:ARG:HH22	1:H:453:LEU:HD21	1.50	0.76
1:I:273:ARG:HH22	1:I:453:LEU:HD21	1.50	0.76
1:U:236:GLN:HB2	1:U:265:LYS:HG2	1.66	0.76
1:K:11:ILE:HD12	1:K:285:ALA:HA	1.66	0.76
1:K:273:ARG:HH22	1:K:453:LEU:HD21	1.50	0.76
2:a:34:LEU:C	2:a:35:THR:HG23	2.09	0.76
2:e:78:GLU:CG	2:e:79:GLY:H	1.98	0.76
1:T:236:GLN:HB2	1:T:265:LYS:HG2	1.66	0.76
2:q:93:PRO:HB3	2:t:100:THR:HG21	1.67	0.76
1:A:35:PHE:HE2	1:A:324:LYS:HZ3	1.33	0.76
1:A:273:ARG:HH22	1:A:453:LEU:HD21	1.50	0.76
1:G:273:ARG:HH22	1:G:453:LEU:HD21	1.50	0.76
2:a:42:MET:O	2:a:42:MET:CG	2.30	0.76
2:u:17:LEU:HD11	2:u:36:ALA:HB3	1.68	0.76
1:A:11:ILE:HD12	1:A:285:ALA:HA	1.66	0.76
1:C:11:ILE:HD12	1:C:285:ALA:HA	1.66	0.76
1:O:34:PHE:HZ	1:O:328:ARG:NH2	1.83	0.76
1:P:560:LEU:HD22	1:Q:82:PRO:HG2	1.66	0.76
1:V:248:LYS:H	1:V:248:LYS:HD2	1.50	0.76
1:X:376:ARG:O	1:X:383:ASP:HB3	1.84	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:k:17:LEU:HD11	2:k:36:ALA:HB3	1.67	0.76
2:k:37:VAL:HG11	2:k:68:ALA:HB1	1.68	0.76
2:c:78:GLU:CG	2:c:79:GLY:H	1.98	0.76
2:e:34:LEU:C	2:e:35:THR:HG23	2.09	0.76
2:h:53:MET:HE1	2:h:92:VAL:HG12	0.82	0.76
1:O:35:PHE:CZ	1:O:321:ARG:NE	2.54	0.76
1:U:303:VAL:HA	1:U:439:ASN:OD1	1.84	0.76
2:h:34:LEU:C	2:h:35:THR:HG23	2.09	0.76
1:P:44:TRP:O	1:P:45:LEU:HD13	1.86	0.76
1:Q:44:TRP:O	1:Q:45:LEU:HD13	1.86	0.76
2:s:37:VAL:HG11	2:s:68:ALA:HB1	1.66	0.76
2:Z:78:GLU:CG	2:Z:79:GLY:H	1.98	0.76
1:O:11:ILE:HD12	1:O:285:ALA:HA	1.67	0.76
1:S:236:GLN:HB2	1:S:265:LYS:HG2	1.66	0.76
1:U:248:LYS:HD2	1:U:248:LYS:H	1.49	0.76
1:X:63:VAL:HG21	1:X:416:ALA:HB1	1.65	0.76
2:s:17:LEU:HD11	2:s:36:ALA:HB3	1.65	0.76
1:M:35:PHE:CZ	1:M:321:ARG:NE	2.54	0.76
1:S:35:PHE:HE2	1:S:324:LYS:HZ3	1.32	0.76
1:U:376:ARG:O	1:U:383:ASP:HB3	1.84	0.76
1:V:139:SER:HB3	1:V:455:THR:HG23	1.67	0.76
1:D:273:ARG:HH22	1:D:453:LEU:HD21	1.50	0.76
1:G:49:THR:O	1:G:49:THR:HG22	1.86	0.76
1:I:11:ILE:HD12	1:I:285:ALA:HA	1.66	0.76
2:f:143:THR:HB	2:f:154:GLU:H	1.48	0.76
1:Q:35:PHE:CZ	1:Q:321:ARG:NE	2.54	0.76
1:T:34:PHE:HZ	1:T:328:ARG:NH2	1.84	0.76
1:T:248:LYS:H	1:T:248:LYS:HD2	1.50	0.76
2:g:34:LEU:C	2:g:35:THR:HG23	2.09	0.76
2:j:78:GLU:CG	2:j:79:GLY:H	1.98	0.76
1:S:35:PHE:CZ	1:S:321:ARG:NE	2.54	0.75
1:S:144:ILE:HG12	1:S:447:TYR:CE1	2.20	0.75
1:S:376:ARG:O	1:S:383:ASP:HB3	1.84	0.75
1:V:92:ASP:HB3	1:W:561:ASP:OD2	1.86	0.75
1:I:35:PHE:HE2	1:I:324:LYS:HZ3	1.32	0.75
2:i:53:MET:HE1	2:i:92:VAL:HG12	0.82	0.75
1:U:93:VAL:HG11	1:U:458:ARG:HG3	1.68	0.75
1:U:282:THR:HG23	1:U:287:LEU:HD11	1.69	0.75
1:W:511:ARG:HA	1:W:513:ARG:HD2	1.68	0.75
1:J:273:ARG:HH22	1:J:453:LEU:HD21	1.50	0.75
2:f:78:GLU:CG	2:f:79:GLY:H	1.98	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:35:PHE:CZ	1:P:321:ARG:NE	2.55	0.75
1:P:282:THR:HG23	1:P:287:LEU:HD11	1.68	0.75
1:Q:248:LYS:H	1:Q:248:LYS:HD2	1.49	0.75
1:R:63:VAL:HG21	1:R:416:ALA:HB1	1.66	0.75
1:X:93:VAL:HG11	1:X:458:ARG:HG3	1.69	0.75
2:Y:78:GLU:HG3	2:Y:79:GLY:H	1.52	0.75
1:P:232:ALA:HB2	1:P:269:ARG:H	1.51	0.75
1:X:34:PHE:CZ	1:X:328:ARG:NH2	2.55	0.75
1:X:282:THR:HG23	1:X:287:LEU:HD11	1.69	0.75
2:v:37:VAL:HG11	2:v:68:ALA:HB1	1.68	0.75
1:E:11:ILE:HD12	1:E:285:ALA:HA	1.66	0.75
1:F:49:THR:O	1:F:49:THR:HG22	1.86	0.75
1:J:11:ILE:HD12	1:J:285:ALA:HA	1.66	0.75
1:J:35:PHE:HE2	1:J:324:LYS:HZ3	1.32	0.75
2:e:42:MET:HE3	2:e:78:GLU:OE1	1.87	0.75
2:i:78:GLU:HG3	2:i:79:GLY:H	1.52	0.75
1:X:236:GLN:HB2	1:X:265:LYS:HG2	1.66	0.75
1:E:5:GLU:HG2	1:E:6:ASN:H	1.52	0.75
1:E:49:THR:HG22	1:E:49:THR:O	1.86	0.75
2:f:42:MET:HE3	2:f:78:GLU:OE1	1.87	0.75
1:N:232:ALA:HB2	1:N:269:ARG:H	1.51	0.75
1:T:44:TRP:O	1:T:45:LEU:HD13	1.87	0.75
1:T:511:ARG:HA	1:T:513:ARG:HD2	1.68	0.75
1:W:144:ILE:HG12	1:W:447:TYR:CE1	2.20	0.75
1:D:49:THR:O	1:D:49:THR:HG22	1.86	0.75
1:L:273:ARG:HH22	1:L:453:LEU:HD21	1.50	0.75
2:d:34:LEU:C	2:d:35:THR:HG23	2.09	0.75
1:M:232:ALA:HB2	1:M:269:ARG:H	1.51	0.75
1:P:561:ASP:HB2	1:Q:89:ASP:HA	1.67	0.75
1:C:273:ARG:HH22	1:C:453:LEU:HD21	1.50	0.75
1:D:5:GLU:HG2	1:D:6:ASN:H	1.52	0.75
2:Z:34:LEU:HD12	2:Z:104:TYR:HD2	1.51	0.75
2:b:78:GLU:HG3	2:b:79:GLY:H	1.52	0.75
2:g:78:GLU:HG3	2:g:79:GLY:H	1.52	0.75
1:M:44:TRP:O	1:M:45:LEU:HD13	1.86	0.75
1:S:44:TRP:O	1:S:45:LEU:HD13	1.86	0.75
1:S:248:LYS:H	1:S:248:LYS:HD2	1.49	0.75
1:F:236:GLN:HB2	1:F:265:LYS:HG2	1.68	0.75
1:P:34:PHE:HZ	1:P:328:ARG:NH2	1.84	0.75
2:r:17:LEU:HD11	2:r:36:ALA:HB3	1.67	0.75
1:A:5:GLU:HG2	1:A:6:ASN:H	1.52	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:273:ARG:HH22	1:G:453:LEU:CD2	2.00	0.75
1:K:236:GLN:HB2	1:K:265:LYS:HG2	1.68	0.75
2:d:42:MET:HE3	2:d:78:GLU:OE1	1.87	0.75
2:h:42:MET:HE3	2:h:78:GLU:OE1	1.87	0.75
1:N:93:VAL:HG11	1:N:458:ARG:HG3	1.68	0.74
1:N:282:THR:HG23	1:N:287:LEU:HD11	1.67	0.74
1:P:330:ARG:HD2	1:P:409:THR:HG22	1.68	0.74
1:Q:511:ARG:HA	1:Q:513:ARG:HD2	1.69	0.74
1:X:330:ARG:HH21	1:X:409:THR:CG2	2.00	0.74
1:F:273:ARG:HH22	1:F:453:LEU:CD2	2.00	0.74
2:a:34:LEU:HD12	2:a:104:TYR:HD2	1.51	0.74
1:M:34:PHE:HZ	1:M:328:ARG:NH2	1.84	0.74
1:R:93:VAL:HG11	1:R:458:ARG:HG3	1.69	0.74
1:S:93:VAL:HG11	1:S:458:ARG:HG3	1.68	0.74
1:T:34:PHE:CZ	1:T:328:ARG:NH2	2.56	0.74
1:A:78:VAL:CG2	1:A:444:LEU:HD11	2.15	0.74
1:D:236:GLN:HB2	1:D:265:LYS:HG2	1.68	0.74
1:F:325:ASP:OD2	2:e:145:SER:HB3	1.86	0.74
1:G:5:GLU:HG2	1:G:6:ASN:H	1.52	0.74
1:I:35:PHE:C	1:I:37:ARG:H	1.95	0.74
1:M:37:ARG:NH2	1:M:37:ARG:HB3	2.03	0.74
1:A:35:PHE:C	1:A:37:ARG:H	1.95	0.74
1:B:273:ARG:HH22	1:B:453:LEU:CD2	2.00	0.74
1:C:49:THR:O	1:C:49:THR:HG22	1.86	0.74
1:E:273:ARG:HH22	1:E:453:LEU:CD2	2.00	0.74
1:F:34:PHE:CZ	1:F:328:ARG:NH2	2.47	0.74
1:J:49:THR:HG22	1:J:49:THR:O	1.86	0.74
2:i:42:MET:HE3	2:i:78:GLU:OE1	1.87	0.74
1:O:34:PHE:CZ	1:O:328:ARG:NH2	2.56	0.74
1:R:248:LYS:H	1:R:248:LYS:HD2	1.51	0.74
1:X:248:LYS:H	1:X:248:LYS:HD2	1.51	0.74
2:r:62:ASP:C	2:r:64:GLU:H	1.96	0.74
1:F:564:GLY:HA2	1:G:554:LEU:HD21	1.70	0.74
1:H:5:GLU:HG2	1:H:6:ASN:H	1.52	0.74
2:a:78:GLU:OE1	2:a:78:GLU:CA	2.36	0.74
1:N:35:PHE:HE2	1:N:324:LYS:HZ3	1.33	0.74
1:R:282:THR:HG23	1:R:287:LEU:HD11	1.69	0.74
1:W:282:THR:HG23	1:W:287:LEU:HD11	1.69	0.74
2:t:17:LEU:HD11	2:t:36:ALA:HB3	1.67	0.74
1:A:273:ARG:HH22	1:A:453:LEU:CD2	2.00	0.74
1:A:560:LEU:HD22	1:B:82:PRO:HG2	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:212:LEU:HD22	1:E:26:ARG:HG2	1.70	0.74
1:E:577:ILE:HG12	1:E:582:LYS:HG2	1.69	0.74
1:G:35:PHE:C	1:G:37:ARG:H	1.95	0.74
1:K:49:THR:O	1:K:49:THR:HG22	1.86	0.74
1:K:273:ARG:HH22	1:K:453:LEU:CD2	2.00	0.74
1:L:577:ILE:HG12	1:L:582:LYS:HG2	1.69	0.74
2:a:53:MET:HE1	2:a:92:VAL:HG12	0.82	0.74
2:b:42:MET:HE3	2:b:78:GLU:OE1	1.87	0.74
2:c:42:MET:HE3	2:c:78:GLU:OE1	1.87	0.74
1:M:282:THR:HG23	1:M:287:LEU:HD11	1.69	0.74
1:O:93:VAL:HG11	1:O:458:ARG:HG3	1.68	0.74
1:R:34:PHE:HZ	1:R:328:ARG:NH2	1.85	0.74
1:R:139:SER:HB3	1:R:455:THR:HG23	1.69	0.74
1:T:144:ILE:HG12	1:T:447:TYR:CE1	2.21	0.74
1:U:34:PHE:HZ	1:U:328:ARG:NH2	1.85	0.74
1:U:144:ILE:HG12	1:U:447:TYR:CE1	2.21	0.74
1:U:330:ARG:HH21	1:U:409:THR:CG2	2.01	0.74
1:V:44:TRP:O	1:V:45:LEU:HD13	1.88	0.74
2:r:37:VAL:HG11	2:r:68:ALA:HB1	1.69	0.74
2:s:62:ASP:C	2:s:64:GLU:H	1.96	0.74
1:A:236:GLN:HB2	1:A:265:LYS:HG2	1.68	0.74
1:H:273:ARG:HH22	1:H:453:LEU:CD2	2.00	0.74
1:K:577:ILE:HG12	1:K:582:LYS:HG2	1.69	0.74
2:Z:78:GLU:OE1	2:Z:78:GLU:CA	2.36	0.74
2:c:34:LEU:HD12	2:c:104:TYR:HD2	1.51	0.74
1:N:35:PHE:HE1	1:N:321:ARG:HH11	1.36	0.74
1:P:93:VAL:HG11	1:P:458:ARG:HG3	1.69	0.74
1:Q:93:VAL:HG11	1:Q:458:ARG:HG3	1.69	0.74
1:S:35:PHE:HE1	1:S:321:ARG:HH11	1.36	0.74
1:W:232:ALA:HB2	1:W:269:ARG:H	1.53	0.74
1:X:35:PHE:CZ	1:X:321:ARG:NE	2.55	0.74
1:A:577:ILE:HG12	1:A:582:LYS:HG2	1.69	0.74
1:B:236:GLN:HB2	1:B:265:LYS:HG2	1.68	0.74
1:G:236:GLN:HB2	1:G:265:LYS:HG2	1.68	0.74
1:H:564:GLY:HA2	1:I:554:LEU:HD21	1.69	0.74
1:J:577:ILE:HG12	1:J:582:LYS:HG2	1.69	0.74
1:K:35:PHE:C	1:K:37:ARG:H	1.95	0.74
1:L:49:THR:O	1:L:49:THR:HG22	1.86	0.74
1:M:35:PHE:HE1	1:M:321:ARG:HH11	1.35	0.74
1:N:34:PHE:HZ	1:N:328:ARG:NH2	1.86	0.74
1:O:44:TRP:O	1:O:45:LEU:HD13	1.88	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:34:PHE:HZ	1:Q:328:ARG:NH2	1.86	0.74
1:R:34:PHE:CZ	1:R:328:ARG:NH2	2.56	0.74
2:m:17:LEU:HD11	2:m:36:ALA:HB3	1.70	0.74
1:B:273:ARG:HH22	1:B:453:LEU:HD21	1.50	0.74
1:B:577:ILE:HG12	1:B:582:LYS:HG2	1.69	0.74
1:H:236:GLN:HB2	1:H:265:LYS:HG2	1.68	0.74
1:L:5:GLU:HG2	1:L:6:ASN:H	1.52	0.74
1:L:78:VAL:CG2	1:L:444:LEU:HD11	2.15	0.74
1:L:236:GLN:HB2	1:L:265:LYS:HG2	1.69	0.74
1:L:273:ARG:HH22	1:L:453:LEU:CD2	2.00	0.74
2:Z:42:MET:HE3	2:Z:78:GLU:OE1	1.87	0.74
2:b:78:GLU:OE1	2:b:78:GLU:CA	2.36	0.74
2:d:78:GLU:HG3	2:d:79:GLY:H	1.52	0.74
2:e:78:GLU:OE1	2:e:78:GLU:CA	2.36	0.74
2:h:78:GLU:HG3	2:h:79:GLY:H	1.52	0.74
1:P:248:LYS:H	1:P:248:LYS:HD2	1.51	0.74
1:T:34:PHE:HZ	1:T:328:ARG:HH22	1.35	0.74
1:U:35:PHE:CZ	1:U:321:ARG:NE	2.55	0.74
1:V:330:ARG:HH21	1:V:409:THR:CG2	2.00	0.74
1:W:44:TRP:O	1:W:45:LEU:HD13	1.87	0.74
1:C:236:GLN:HB2	1:C:265:LYS:HG2	1.68	0.74
1:E:236:GLN:HB2	1:E:265:LYS:HG2	1.68	0.74
1:G:560:LEU:HD22	1:H:82:PRO:HG2	1.69	0.74
1:I:273:ARG:HH22	1:I:453:LEU:CD2	2.00	0.74
2:a:42:MET:HE3	2:a:78:GLU:OE1	1.87	0.74
2:h:34:LEU:HD12	2:h:104:TYR:HD2	1.52	0.74
1:M:93:VAL:HG11	1:M:458:ARG:HG3	1.68	0.74
1:O:35:PHE:HE1	1:O:321:ARG:HH11	1.36	0.74
1:P:34:PHE:CZ	1:P:328:ARG:NH2	2.56	0.74
1:S:37:ARG:NH2	1:S:37:ARG:HB3	2.03	0.74
2:l:62:ASP:C	2:l:64:GLU:H	1.96	0.74
1:A:554:LEU:HD21	1:L:564:GLY:HA2	1.70	0.74
2:f:78:GLU:HG3	2:f:79:GLY:H	1.52	0.74
1:M:139:SER:HB3	1:M:455:THR:HG23	1.70	0.73
1:S:282:THR:HG23	1:S:287:LEU:HD11	1.70	0.73
1:T:35:PHE:CZ	1:T:321:ARG:NE	2.56	0.73
1:E:35:PHE:C	1:E:37:ARG:H	1.95	0.73
1:H:49:THR:HG22	1:H:49:THR:O	1.86	0.73
1:M:34:PHE:HZ	1:M:328:ARG:HH22	1.36	0.73
1:Q:325:ASP:OD2	2:n:136:SER:HB3	1.87	0.73
1:R:35:PHE:CZ	1:R:321:ARG:NE	2.56	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:34:PHE:CZ	1:V:328:ARG:NH2	2.57	0.73
1:V:93:VAL:HG11	1:V:458:ARG:HG3	1.69	0.73
1:V:325:ASP:OD2	2:u:136:SER:HB3	1.88	0.73
2:u:62:ASP:C	2:u:64:GLU:H	1.96	0.73
1:B:35:PHE:C	1:B:37:ARG:H	1.95	0.73
1:C:5:GLU:HG2	1:C:6:ASN:H	1.52	0.73
1:F:78:VAL:CG2	1:F:444:LEU:HD11	2.15	0.73
1:G:34:PHE:CZ	1:G:328:ARG:NH2	2.48	0.73
1:I:560:LEU:HD22	1:J:82:PRO:HG2	1.70	0.73
1:K:5:GLU:HG2	1:K:6:ASN:H	1.52	0.73
2:f:34:LEU:HD12	2:f:104:TYR:HD2	1.52	0.73
1:W:93:VAL:HG11	1:W:458:ARG:HG3	1.68	0.73
2:p:37:VAL:HG11	2:p:68:ALA:HB1	1.68	0.73
2:q:17:LEU:HD11	2:q:36:ALA:HB3	1.68	0.73
1:C:577:ILE:HG12	1:C:582:LYS:HG2	1.69	0.73
1:J:273:ARG:HH22	1:J:453:LEU:CD2	2.00	0.73
2:a:74:ASN:CB	2:a:75:PRO:HD3	2.18	0.73
2:c:78:GLU:OE1	2:c:78:GLU:CA	2.36	0.73
1:M:15:PHE:HZ	1:M:283:CYS:HG	1.34	0.73
1:M:376:ARG:O	1:M:383:ASP:HB3	1.87	0.73
1:N:92:ASP:HB3	1:V:561:ASP:OD2	1.88	0.73
1:O:282:THR:HG23	1:O:287:LEU:HD11	1.69	0.73
1:S:34:PHE:HZ	1:S:328:ARG:NH2	1.85	0.73
1:T:560:LEU:HD22	1:W:82:PRO:HG2	1.68	0.73
1:X:144:ILE:HG12	1:X:447:TYR:CE1	2.22	0.73
2:p:62:ASP:C	2:p:64:GLU:H	1.96	0.73
1:B:49:THR:HG22	1:B:49:THR:O	1.86	0.73
2:Y:42:MET:HE3	2:Y:78:GLU:OE1	1.87	0.73
2:b:34:LEU:HD12	2:b:104:TYR:HD2	1.51	0.73
2:g:42:MET:HE3	2:g:78:GLU:OE1	1.87	0.73
2:i:78:GLU:OE1	2:i:78:GLU:CA	2.36	0.73
1:X:34:PHE:HZ	1:X:328:ARG:HH22	1.35	0.73
2:q:62:ASP:C	2:q:64:GLU:H	1.96	0.73
1:A:49:THR:O	1:A:49:THR:HG22	1.86	0.73
1:F:577:ILE:HG12	1:F:582:LYS:HG2	1.69	0.73
1:G:35:PHE:HE2	1:G:324:LYS:HZ3	1.34	0.73
1:J:236:GLN:HB2	1:J:265:LYS:HG2	1.69	0.73
2:Y:34:LEU:HD12	2:Y:104:TYR:HD2	1.52	0.73
2:d:78:GLU:OE1	2:d:78:GLU:CA	2.36	0.73
2:g:74:ASN:CB	2:g:75:PRO:HD3	2.18	0.73
2:i:74:ASN:CB	2:i:75:PRO:HD3	2.18	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:j:42:MET:HE3	2:j:78:GLU:OE1	1.87	0.73
1:S:231:THR:HG21	1:S:249:ARG:HH11	1.53	0.73
1:U:89:ASP:HA	1:X:561:ASP:HB2	1.69	0.73
1:U:232:ALA:HB2	1:U:269:ARG:H	1.54	0.73
1:C:560:LEU:HD22	1:E:82:PRO:HG2	1.69	0.73
1:D:44:TRP:O	1:D:45:LEU:HD13	1.89	0.73
1:I:577:ILE:HG12	1:I:582:LYS:HG2	1.69	0.73
1:L:44:TRP:O	1:L:45:LEU:HD13	1.89	0.73
2:e:34:LEU:HD12	2:e:104:TYR:HD2	1.51	0.73
2:g:34:LEU:HD12	2:g:104:TYR:HD2	1.51	0.73
2:h:74:ASN:CB	2:h:75:PRO:HD3	2.18	0.73
2:j:74:ASN:CB	2:j:75:PRO:HD3	2.18	0.73
1:Q:282:THR:HG23	1:Q:287:LEU:HD11	1.71	0.73
1:D:273:ARG:HH22	1:D:453:LEU:CD2	2.00	0.73
1:G:577:ILE:HG12	1:G:582:LYS:HG2	1.69	0.73
1:I:49:THR:O	1:I:49:THR:HG22	1.86	0.73
1:I:236:GLN:HB2	1:I:265:LYS:HG2	1.69	0.73
2:Y:78:GLU:OE1	2:Y:78:GLU:CA	2.36	0.73
2:c:74:ASN:CB	2:c:75:PRO:HD3	2.18	0.73
2:c:78:GLU:HG3	2:c:79:GLY:H	1.52	0.73
2:e:78:GLU:HG3	2:e:79:GLY:H	1.52	0.73
2:j:78:GLU:OE1	2:j:78:GLU:CA	2.36	0.73
1:R:511:ARG:HA	1:R:513:ARG:HD2	1.70	0.73
1:R:561:ASP:HB2	1:X:89:ASP:HA	1.70	0.73
1:T:232:ALA:HB2	1:T:269:ARG:H	1.54	0.73
1:T:561:ASP:OD2	1:W:92:ASP:HB3	1.89	0.73
1:V:34:PHE:HZ	1:V:328:ARG:NH2	1.86	0.73
2:m:62:ASP:C	2:m:64:GLU:H	1.95	0.73
2:t:62:ASP:C	2:t:64:GLU:H	1.96	0.73
2:a:78:GLU:HG3	2:a:79:GLY:H	1.52	0.73
1:O:139:SER:HB3	1:O:455:THR:HG23	1.71	0.73
1:C:35:PHE:C	1:C:37:ARG:H	1.95	0.73
1:J:5:GLU:HG2	1:J:6:ASN:H	1.52	0.73
1:J:334:MSE:HE1	1:K:407:ALA:HB1	1.69	0.73
2:Z:74:ASN:CB	2:Z:75:PRO:HD3	2.18	0.73
2:e:74:ASN:CB	2:e:75:PRO:HD3	2.18	0.73
1:X:44:TRP:O	1:X:45:LEU:HD13	1.88	0.73
2:o:62:ASP:C	2:o:64:GLU:H	1.96	0.73
2:g:46:VAL:CG1	2:g:77:ALA:HB1	2.19	0.73
2:h:102:PRO:HB3	2:j:109:THR:HG21	1.71	0.73
1:M:511:ARG:HA	1:M:513:ARG:HD2	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:139:SER:HB3	1:Q:455:THR:HG23	1.69	0.72
1:R:232:ALA:HB2	1:R:269:ARG:H	1.54	0.72
1:S:232:ALA:HB2	1:S:269:ARG:H	1.53	0.72
2:k:62:ASP:C	2:k:64:GLU:H	1.95	0.72
2:n:62:ASP:C	2:n:64:GLU:H	1.96	0.72
1:C:44:TRP:O	1:C:45:LEU:HD13	1.89	0.72
1:D:35:PHE:C	1:D:37:ARG:H	1.95	0.72
1:D:577:ILE:HG12	1:D:582:LYS:HG2	1.69	0.72
1:G:44:TRP:O	1:G:45:LEU:HD13	1.89	0.72
1:H:577:ILE:HG12	1:H:582:LYS:HG2	1.69	0.72
1:J:191:TYR:HE1	1:J:278:LYS:HZ1	1.37	0.72
1:K:44:TRP:O	1:K:45:LEU:HD13	1.89	0.72
2:Z:78:GLU:HG3	2:Z:79:GLY:H	1.52	0.72
1:Q:37:ARG:NH2	1:Q:37:ARG:HB3	2.04	0.72
1:U:511:ARG:HA	1:U:513:ARG:HD2	1.71	0.72
1:C:405:LEU:O	1:C:409:THR:HG23	1.90	0.72
1:E:158:TRP:HB3	1:E:173:CYS:HA	1.71	0.72
1:G:158:TRP:HB3	1:G:173:CYS:HA	1.72	0.72
1:I:44:TRP:O	1:I:45:LEU:HD13	1.89	0.72
2:a:46:VAL:CG1	2:a:77:ALA:HB1	2.19	0.72
1:M:34:PHE:CZ	1:M:328:ARG:NH2	2.56	0.72
1:V:35:PHE:CZ	1:V:321:ARG:NE	2.58	0.72
1:B:5:GLU:HG2	1:B:6:ASN:H	1.52	0.72
1:D:158:TRP:HB3	1:D:173:CYS:HA	1.72	0.72
1:E:405:LEU:O	1:E:409:THR:HG23	1.90	0.72
1:F:405:LEU:O	1:F:409:THR:HG23	1.90	0.72
2:b:74:ASN:CB	2:b:75:PRO:HD3	2.18	0.72
2:d:102:PRO:HB3	2:f:109:THR:HG21	1.69	0.72
2:j:34:LEU:HD12	2:j:104:TYR:HD2	1.51	0.72
1:R:44:TRP:O	1:R:45:LEU:HD13	1.89	0.72
1:T:93:VAL:HG11	1:T:458:ARG:HG3	1.70	0.72
1:U:34:PHE:CZ	1:U:328:ARG:NH2	2.56	0.72
1:U:554:LEU:HD21	1:X:564:GLY:HA2	1.72	0.72
1:B:34:PHE:CZ	1:B:328:ARG:NH2	2.47	0.72
1:F:334:MSE:HE1	1:G:407:ALA:HB1	1.71	0.72
1:H:44:TRP:O	1:H:45:LEU:HD13	1.89	0.72
2:d:74:ASN:CB	2:d:75:PRO:HD3	2.18	0.72
1:N:511:ARG:HA	1:N:513:ARG:HD2	1.70	0.72
1:R:37:ARG:NH2	1:R:37:ARG:HB3	2.04	0.72
1:U:44:TRP:O	1:U:45:LEU:HD13	1.89	0.72
1:V:232:ALA:HB2	1:V:269:ARG:H	1.54	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:511:ARG:HA	1:V:513:ARG:HD2	1.70	0.72
1:W:34:PHE:HZ	1:W:328:ARG:NH2	1.85	0.72
2:o:19:VAL:HA	2:o:22:ASP:HB3	1.71	0.72
1:B:44:TRP:O	1:B:45:LEU:HD13	1.89	0.72
1:F:5:GLU:HG2	1:F:6:ASN:H	1.52	0.72
1:F:158:TRP:HB3	1:F:173:CYS:HA	1.71	0.72
1:F:585:GLU:C	1:F:587:PRO:HD3	2.15	0.72
1:J:44:TRP:O	1:J:45:LEU:HD13	1.89	0.72
1:K:158:TRP:HB3	1:K:173:CYS:HA	1.71	0.72
1:L:34:PHE:CZ	1:L:328:ARG:NH2	2.48	0.72
2:d:34:LEU:HD12	2:d:104:TYR:HD2	1.52	0.72
1:M:325:ASP:OD2	2:k:136:SER:HB3	1.90	0.72
1:U:37:ARG:NH2	1:U:37:ARG:HB3	2.04	0.72
1:A:405:LEU:O	1:A:409:THR:HG23	1.90	0.72
1:A:585:GLU:C	1:A:587:PRO:HD3	2.15	0.72
1:B:158:TRP:HB3	1:B:173:CYS:HA	1.71	0.72
1:C:325:ASP:OD2	2:Z:145:SER:HB3	1.89	0.72
1:G:325:ASP:OD2	2:c:145:SER:HB3	1.90	0.72
1:G:585:GLU:C	1:G:587:PRO:HD3	2.15	0.72
1:H:585:GLU:C	1:H:587:PRO:HD3	2.15	0.72
1:I:158:TRP:HB3	1:I:173:CYS:HA	1.71	0.72
1:I:585:GLU:C	1:I:587:PRO:HD3	2.15	0.72
1:K:405:LEU:O	1:K:409:THR:HG23	1.90	0.72
2:Y:74:ASN:CB	2:Y:75:PRO:HD3	2.18	0.72
2:c:46:VAL:CG1	2:c:77:ALA:HB1	2.19	0.72
1:O:232:ALA:HB2	1:O:269:ARG:H	1.52	0.72
1:V:577:ILE:HG12	1:V:582:LYS:HG2	1.72	0.72
1:A:26:ARG:HG2	1:L:212:LEU:HD22	1.71	0.72
1:A:44:TRP:O	1:A:45:LEU:HD13	1.89	0.72
1:A:457:MSE:HG3	1:A:457:MSE:O	1.90	0.72
1:E:585:GLU:C	1:E:587:PRO:HD3	2.15	0.72
1:F:44:TRP:O	1:F:45:LEU:HD13	1.89	0.72
2:f:46:VAL:CG1	2:f:77:ALA:HB1	2.19	0.72
2:g:78:GLU:OE1	2:g:78:GLU:CA	2.36	0.72
1:N:34:PHE:HZ	1:N:328:ARG:HH22	1.38	0.72
1:O:330:ARG:HH21	1:O:409:THR:CG2	2.02	0.72
1:V:282:THR:HG23	1:V:287:LEU:HD11	1.70	0.72
2:q:37:VAL:HG11	2:q:68:ALA:HB1	1.72	0.72
1:C:273:ARG:HH22	1:C:453:LEU:CD2	2.00	0.72
1:I:5:GLU:HG2	1:I:6:ASN:H	1.52	0.72
1:L:585:GLU:C	1:L:587:PRO:HD3	2.15	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:34:PHE:CZ	1:N:328:ARG:NH2	2.58	0.72
1:O:37:ARG:NH2	1:O:37:ARG:HB3	2.04	0.72
1:S:330:ARG:NH2	1:S:409:THR:HG21	2.05	0.72
1:X:232:ALA:HB2	1:X:269:ARG:H	1.53	0.72
1:B:585:GLU:C	1:B:587:PRO:HD3	2.15	0.72
1:G:212:LEU:HD22	1:H:26:ARG:HG2	1.71	0.72
1:J:34:PHE:CZ	1:J:328:ARG:NH2	2.47	0.72
2:i:34:LEU:HD12	2:i:104:TYR:HD2	1.52	0.72
1:N:44:TRP:O	1:N:45:LEU:HD13	1.89	0.72
1:N:139:SER:HB3	1:N:455:THR:HG23	1.70	0.72
1:Q:232:ALA:HB2	1:Q:269:ARG:H	1.54	0.72
1:R:564:GLY:HA2	1:X:554:LEU:HD21	1.70	0.72
1:W:34:PHE:HZ	1:W:328:ARG:HH22	1.38	0.72
1:W:450:GLN:HG2	1:W:450:GLN:O	1.90	0.72
1:C:182:ASN:ND2	1:E:171:ARG:HH21	1.88	0.72
1:D:405:LEU:O	1:D:409:THR:HG23	1.90	0.72
1:L:158:TRP:HB3	1:L:173:CYS:HA	1.71	0.72
1:N:35:PHE:CZ	1:N:321:ARG:NE	2.57	0.71
1:X:35:PHE:HE1	1:X:321:ARG:HH11	1.37	0.71
1:A:303:VAL:HA	1:A:439:ASN:ND2	2.05	0.71
1:C:246:TYR:HD2	1:C:511:ARG:HB3	1.55	0.71
1:E:246:TYR:HD2	1:E:511:ARG:HB3	1.55	0.71
2:d:46:VAL:CG1	2:d:77:ALA:HB1	2.19	0.71
1:P:78:VAL:HG12	1:P:79:LEU:N	2.05	0.71
1:V:246:TYR:HD2	1:V:511:ARG:HB2	1.54	0.71
1:W:35:PHE:HE1	1:W:321:ARG:HH11	1.37	0.71
1:C:334:MSE:HE1	1:E:407:ALA:HB1	1.70	0.71
1:H:35:PHE:C	1:H:37:ARG:H	1.95	0.71
1:I:78:VAL:CG2	1:I:444:LEU:HD11	2.15	0.71
1:L:35:PHE:C	1:L:37:ARG:H	1.95	0.71
1:S:139:SER:HB3	1:S:455:THR:HG23	1.73	0.71
2:n:93:PRO:HB3	2:o:100:THR:HG21	1.73	0.71
1:D:585:GLU:C	1:D:587:PRO:HD3	2.15	0.71
1:E:44:TRP:O	1:E:45:LEU:HD13	1.89	0.71
1:F:35:PHE:C	1:F:37:ARG:H	1.95	0.71
1:G:303:VAL:HA	1:G:439:ASN:ND2	2.05	0.71
1:J:303:VAL:HA	1:J:439:ASN:ND2	2.05	0.71
1:J:405:LEU:O	1:J:409:THR:HG23	1.89	0.71
2:i:46:VAL:CG1	2:i:77:ALA:HB1	2.19	0.71
1:P:35:PHE:HE1	1:P:321:ARG:HH11	1.38	0.71
1:P:330:ARG:HH21	1:P:409:THR:CG2	2.01	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:561:ASP:OD2	1:Q:92:ASP:HB3	1.90	0.71
1:Q:34:PHE:CZ	1:Q:328:ARG:NH2	2.57	0.71
1:W:325:ASP:OD2	2:s:136:SER:HB3	1.91	0.71
1:X:248:LYS:HB3	1:X:511:ARG:NH1	2.02	0.71
2:v:62:ASP:C	2:v:64:GLU:H	1.96	0.71
1:B:246:TYR:HD2	1:B:511:ARG:HB3	1.55	0.71
1:B:457:MSE:HG3	1:B:457:MSE:O	1.90	0.71
1:C:158:TRP:HB3	1:C:173:CYS:HA	1.71	0.71
1:F:212:LEU:HD22	1:G:26:ARG:HG2	1.72	0.71
1:H:405:LEU:O	1:H:409:THR:HG23	1.90	0.71
1:I:405:LEU:O	1:I:409:THR:HG23	1.90	0.71
1:J:35:PHE:C	1:J:37:ARG:H	1.95	0.71
1:K:457:MSE:HG3	1:K:457:MSE:O	1.90	0.71
2:h:78:GLU:OE1	2:h:78:GLU:CA	2.36	0.71
1:M:450:GLN:HG2	1:M:450:GLN:O	1.90	0.71
1:M:564:GLY:HA2	1:O:554:LEU:HD21	1.72	0.71
1:W:34:PHE:CZ	1:W:328:ARG:NH2	2.57	0.71
1:B:405:LEU:O	1:B:409:THR:HG23	1.90	0.71
1:L:303:VAL:HA	1:L:439:ASN:ND2	2.05	0.71
1:P:246:TYR:HD2	1:P:511:ARG:HB2	1.55	0.71
1:S:511:ARG:HA	1:S:513:ARG:HD2	1.73	0.71
1:T:577:ILE:HG12	1:T:582:LYS:HG2	1.73	0.71
1:U:82:PRO:HG2	1:X:560:LEU:HD22	1.71	0.71
1:V:37:ARG:NH2	1:V:37:ARG:HB3	2.05	0.71
1:K:303:VAL:HA	1:K:439:ASN:ND2	2.05	0.71
1:O:511:ARG:HA	1:O:513:ARG:HD2	1.71	0.71
1:Q:330:ARG:HH21	1:Q:409:THR:CG2	2.02	0.71
1:R:330:ARG:HH21	1:R:409:THR:CG2	2.02	0.71
1:W:35:PHE:CZ	1:W:321:ARG:NE	2.59	0.71
1:W:78:VAL:HG12	1:W:79:LEU:N	2.05	0.71
1:B:78:VAL:CG2	1:B:444:LEU:HD11	2.15	0.71
1:C:303:VAL:HA	1:C:439:ASN:ND2	2.05	0.71
1:D:34:PHE:CZ	1:D:328:ARG:NH2	2.47	0.71
1:D:78:VAL:CG2	1:D:444:LEU:HD11	2.15	0.71
1:K:78:VAL:CG2	1:K:444:LEU:HD11	2.15	0.71
2:b:46:VAL:CG1	2:b:77:ALA:HB1	2.19	0.71
2:j:78:GLU:HG3	2:j:79:GLY:H	1.52	0.71
1:O:34:PHE:HZ	1:O:328:ARG:HH22	1.34	0.71
1:R:15:PHE:HZ	1:R:283:CYS:HG	1.39	0.71
2:r:19:VAL:HA	2:r:22:ASP:HB3	1.72	0.71
1:A:108:LYS:HD2	1:B:438:LEU:HD11	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:585:GLU:C	1:C:587:PRO:HD3	2.15	0.71
1:D:246:TYR:HD2	1:D:511:ARG:HB3	1.55	0.71
1:D:564:GLY:HA2	1:F:554:LEU:HD21	1.72	0.71
1:H:158:TRP:HB3	1:H:173:CYS:HA	1.71	0.71
1:H:303:VAL:HA	1:H:439:ASN:ND2	2.05	0.71
1:J:158:TRP:HB3	1:J:173:CYS:HA	1.72	0.71
1:K:99:ARG:HH12	1:K:530:GLN:HE21	1.39	0.71
2:Z:46:VAL:CG1	2:Z:77:ALA:HB1	2.19	0.71
2:d:42:MET:O	2:d:42:MET:CG	2.30	0.71
1:M:330:ARG:NH2	1:M:409:THR:HG21	2.06	0.71
1:S:330:ARG:HH21	1:S:409:THR:CG2	2.01	0.71
1:S:450:GLN:O	1:S:450:GLN:HG2	1.91	0.71
1:U:450:GLN:HG2	1:U:450:GLN:O	1.90	0.71
2:n:19:VAL:HA	2:n:22:ASP:HB3	1.73	0.71
1:G:405:LEU:O	1:G:409:THR:HG23	1.90	0.71
1:M:330:ARG:HH21	1:M:409:THR:CG2	2.03	0.71
1:O:113:ILE:HD13	1:O:150:HIS:CE1	2.26	0.71
1:S:34:PHE:CZ	1:S:328:ARG:NH2	2.56	0.71
1:T:325:ASP:OD2	2:t:136:SER:HB3	1.91	0.71
1:X:37:ARG:HB3	1:X:37:ARG:HH21	1.56	0.71
1:X:246:TYR:HD2	1:X:511:ARG:HB2	1.56	0.71
1:F:246:TYR:HD2	1:F:511:ARG:HB3	1.55	0.71
1:G:561:ASP:HB2	1:H:89:ASP:HA	1.70	0.71
1:H:78:VAL:CG2	1:H:444:LEU:HD11	2.15	0.71
1:J:246:TYR:HD2	1:J:511:ARG:HB3	1.56	0.71
1:K:246:TYR:HD2	1:K:511:ARG:HB3	1.55	0.71
1:K:585:GLU:C	1:K:587:PRO:HD3	2.15	0.71
2:f:78:GLU:OE1	2:f:78:GLU:CA	2.36	0.71
1:A:246:TYR:HD2	1:A:511:ARG:HB3	1.55	0.70
1:C:99:ARG:HH12	1:C:530:GLN:HE21	1.39	0.70
1:F:303:VAL:HA	1:F:439:ASN:ND2	2.05	0.70
1:G:246:TYR:HD2	1:G:511:ARG:HB3	1.55	0.70
1:I:34:PHE:CZ	1:I:328:ARG:NH2	2.48	0.70
1:J:78:VAL:CG2	1:J:444:LEU:HD11	2.15	0.70
1:J:457:MSE:HG3	1:J:457:MSE:O	1.90	0.70
2:f:74:ASN:CB	2:f:75:PRO:HD3	2.18	0.70
1:M:238:PRO:HG3	1:M:263:PHE:HB3	1.73	0.70
1:N:113:ILE:HD13	1:N:150:HIS:CE1	2.26	0.70
1:P:334:MSE:SE	1:Q:404:MSE:HE1	2.41	0.70
1:T:575:GLN:O	1:T:579:MSE:HG2	1.92	0.70
1:E:41:TRP:CZ3	1:E:42:ASP:HB3	2.26	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:303:VAL:HA	1:E:439:ASN:ND2	2.05	0.70
1:I:99:ARG:HH12	1:I:530:GLN:HE21	1.39	0.70
1:I:303:VAL:HA	1:I:439:ASN:ND2	2.05	0.70
1:I:457:MSE:HG3	1:I:457:MSE:O	1.90	0.70
1:J:585:GLU:C	1:J:587:PRO:HD3	2.15	0.70
1:K:34:PHE:CZ	1:K:328:ARG:NH2	2.48	0.70
1:L:405:LEU:O	1:L:409:THR:HG23	1.90	0.70
1:O:246:TYR:HD2	1:O:511:ARG:HB2	1.55	0.70
1:Q:35:PHE:HE1	1:Q:321:ARG:HH11	1.39	0.70
1:R:577:ILE:HG12	1:R:582:LYS:HG2	1.73	0.70
1:S:577:ILE:HG12	1:S:582:LYS:HG2	1.71	0.70
1:T:37:ARG:NH2	1:T:37:ARG:HB3	2.07	0.70
1:T:238:PRO:HG3	1:T:263:PHE:HB3	1.73	0.70
1:U:35:PHE:HE1	1:U:321:ARG:HH11	1.37	0.70
1:V:330:ARG:NH2	1:V:409:THR:HG21	2.04	0.70
1:X:450:GLN:O	1:X:450:GLN:HG2	1.91	0.70
1:N:577:ILE:HG12	1:N:582:LYS:HG2	1.73	0.70
1:Q:246:TYR:HD2	1:Q:511:ARG:HB2	1.56	0.70
1:Q:450:GLN:O	1:Q:450:GLN:HG2	1.92	0.70
1:R:94:LEU:HA	1:R:97:MSE:HE2	1.74	0.70
1:U:330:ARG:NH2	1:U:409:THR:HG21	2.05	0.70
1:B:41:TRP:CZ3	1:B:42:ASP:HB3	2.26	0.70
1:C:78:VAL:CG2	1:C:444:LEU:HD11	2.15	0.70
1:E:457:MSE:HG3	1:E:457:MSE:O	1.90	0.70
1:N:246:TYR:HD2	1:N:511:ARG:HB2	1.56	0.70
2:l:19:VAL:HA	2:l:22:ASP:HB3	1.74	0.70
2:v:40:LEU:C	2:v:40:LEU:HD23	2.17	0.70
1:A:158:TRP:HB3	1:A:173:CYS:HA	1.72	0.70
1:D:457:MSE:HG3	1:D:457:MSE:O	1.90	0.70
1:E:99:ARG:HH12	1:E:530:GLN:HE21	1.39	0.70
1:F:457:MSE:O	1:F:457:MSE:HG3	1.90	0.70
1:T:282:THR:HG23	1:T:287:LEU:HD11	1.73	0.70
1:U:577:ILE:HG12	1:U:582:LYS:HG2	1.73	0.70
1:W:37:ARG:NH2	1:W:37:ARG:HB3	2.07	0.70
2:q:19:VAL:HA	2:q:22:ASP:HB3	1.73	0.70
1:A:26:ARG:HH21	1:A:30:LYS:HB2	1.57	0.70
1:F:41:TRP:CZ3	1:F:42:ASP:HB3	2.26	0.70
1:I:26:ARG:HH21	1:I:30:LYS:HB2	1.57	0.70
1:J:26:ARG:HH21	1:J:30:LYS:HB2	1.57	0.70
1:K:26:ARG:HH21	1:K:30:LYS:HB2	1.57	0.70
1:X:577:ILE:HG12	1:X:582:LYS:HG2	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:p:19:VAL:HA	2:p:22:ASP:HB3	1.73	0.70
2:p:96:ALA:HB2	2:r:25:LEU:HD13	1.74	0.70
2:s:19:VAL:HA	2:s:22:ASP:HB3	1.73	0.70
1:B:99:ARG:HH12	1:B:530:GLN:HE21	1.39	0.70
1:C:41:TRP:CZ3	1:C:42:ASP:HB3	2.26	0.70
1:D:303:VAL:HA	1:D:439:ASN:ND2	2.05	0.70
1:G:26:ARG:HH21	1:G:30:LYS:HB2	1.57	0.70
1:G:334:MSE:HE1	1:H:407:ALA:HB1	1.72	0.70
1:H:26:ARG:HH21	1:H:30:LYS:HB2	1.57	0.70
1:L:99:ARG:HH12	1:L:530:GLN:HE21	1.39	0.70
1:M:246:TYR:HD2	1:M:511:ARG:HB2	1.56	0.70
1:M:404:MSE:HE1	1:N:334:MSE:SE	2.41	0.70
1:P:511:ARG:HA	1:P:513:ARG:HD2	1.72	0.70
1:S:246:TYR:HD2	1:S:511:ARG:HB2	1.56	0.70
1:T:330:ARG:HH21	1:T:409:THR:CG2	2.03	0.70
1:U:248:LYS:HD3	1:U:251:ILE:HB	1.74	0.70
1:B:303:VAL:HA	1:B:439:ASN:ND2	2.05	0.70
1:G:78:VAL:CG2	1:G:444:LEU:HD11	2.15	0.70
1:H:212:LEU:HD22	1:I:26:ARG:HG2	1.72	0.70
1:H:246:TYR:HD2	1:H:511:ARG:HB3	1.55	0.70
2:Y:46:VAL:CG1	2:Y:77:ALA:HB1	2.19	0.70
1:O:15:PHE:HZ	1:O:283:CYS:HG	1.39	0.70
1:O:556:TYR:OH	1:P:542:THR:HG21	1.92	0.70
1:P:37:ARG:HB3	1:P:37:ARG:NH2	2.06	0.70
1:P:238:PRO:HG3	1:P:263:PHE:HB3	1.73	0.70
1:S:384:LEU:H	1:S:384:LEU:HD22	1.57	0.70
1:T:35:PHE:HE1	1:T:321:ARG:HH11	1.37	0.70
1:A:567:MSE:SE	1:B:576:LEU:HD13	2.42	0.70
1:F:26:ARG:HH21	1:F:30:LYS:HB2	1.57	0.70
1:L:246:TYR:HD2	1:L:511:ARG:HB3	1.55	0.70
1:L:457:MSE:HG3	1:L:457:MSE:O	1.90	0.70
1:N:330:ARG:HH21	1:N:409:THR:CG2	2.03	0.70
1:P:384:LEU:H	1:P:384:LEU:HD22	1.57	0.70
1:W:330:ARG:HH21	1:W:409:THR:CG2	2.05	0.70
1:X:511:ARG:HA	1:X:513:ARG:HD2	1.73	0.70
1:D:99:ARG:HH12	1:D:530:GLN:HE21	1.39	0.70
1:L:26:ARG:HH21	1:L:30:LYS:HB2	1.57	0.70
1:Q:238:PRO:HG3	1:Q:263:PHE:HB3	1.73	0.69
1:U:139:SER:HB3	1:U:455:THR:HG23	1.73	0.69
1:X:139:SER:HB3	1:X:455:THR:HG23	1.73	0.69
1:B:182:ASN:ND2	1:C:171:ARG:HH21	1.90	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:j:46:VAL:CG1	2:j:77:ALA:HB1	2.19	0.69
1:O:248:LYS:HD3	1:O:251:ILE:HB	1.74	0.69
1:U:246:TYR:HD2	1:U:511:ARG:HB2	1.56	0.69
1:F:99:ARG:HH12	1:F:530:GLN:HE21	1.39	0.69
1:I:376:ARG:O	1:I:383:ASP:HB3	1.92	0.69
1:J:99:ARG:HH12	1:J:530:GLN:HE21	1.39	0.69
2:c:102:PRO:HB3	2:d:109:THR:HG21	1.73	0.69
2:h:46:VAL:CG1	2:h:77:ALA:HB1	2.19	0.69
1:N:158:TRP:N	1:N:158:TRP:CD1	2.60	0.69
1:O:238:PRO:HG3	1:O:263:PHE:HB3	1.74	0.69
1:P:113:ILE:HD13	1:P:150:HIS:CE1	2.28	0.69
1:P:248:LYS:HB3	1:P:511:ARG:NH1	2.04	0.69
1:T:113:ILE:HD13	1:T:150:HIS:CE1	2.27	0.69
1:V:78:VAL:HG12	1:V:79:LEU:N	2.07	0.69
1:G:41:TRP:CZ3	1:G:42:ASP:HB3	2.26	0.69
1:H:457:MSE:HG3	1:H:457:MSE:O	1.90	0.69
1:I:182:ASN:ND2	1:J:171:ARG:HH21	1.90	0.69
1:L:41:TRP:CZ3	1:L:42:ASP:HB3	2.26	0.69
2:e:34:LEU:CD1	2:e:104:TYR:CD2	2.76	0.69
1:P:450:GLN:O	1:P:450:GLN:HG2	1.92	0.69
1:S:334:MSE:SE	1:T:404:MSE:HE1	2.42	0.69
1:A:376:ARG:O	1:A:383:ASP:HB3	1.93	0.69
1:G:376:ARG:O	1:G:383:ASP:HB3	1.92	0.69
1:J:376:ARG:O	1:J:383:ASP:HB3	1.92	0.69
2:Z:28:VAL:HG21	2:Z:96:LEU:CB	2.22	0.69
2:j:42:MET:O	2:j:42:MET:CG	2.30	0.69
1:Q:577:ILE:HG12	1:Q:582:LYS:HG2	1.74	0.69
1:R:248:LYS:HB3	1:R:511:ARG:NH1	2.03	0.69
2:v:17:LEU:HD12	2:v:37:VAL:HG23	1.74	0.69
1:G:457:MSE:HG3	1:G:457:MSE:O	1.90	0.69
1:I:246:TYR:HD2	1:I:511:ARG:HB3	1.55	0.69
1:K:376:ARG:O	1:K:383:ASP:HB3	1.93	0.69
2:c:32:ALA:O	2:c:33:THR:HG22	1.92	0.69
1:M:248:LYS:HB3	1:M:511:ARG:NH1	2.05	0.69
1:O:577:ILE:HG12	1:O:582:LYS:HG2	1.74	0.69
1:S:248:LYS:HB3	1:S:511:ARG:NH1	2.04	0.69
2:t:19:VAL:HA	2:t:22:ASP:HB3	1.74	0.69
2:u:19:VAL:HA	2:u:22:ASP:HB3	1.73	0.69
1:A:99:ARG:HH12	1:A:530:GLN:HE21	1.39	0.69
1:B:26:ARG:HH21	1:B:30:LYS:HB2	1.57	0.69
1:C:26:ARG:HH21	1:C:30:LYS:HB2	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:457:MSE:HG3	1:C:457:MSE:O	1.90	0.69
1:D:554:LEU:HD21	1:E:564:GLY:HA2	1.75	0.69
1:F:376:ARG:O	1:F:383:ASP:HB3	1.92	0.69
1:H:99:ARG:HH12	1:H:530:GLN:HE21	1.39	0.69
2:Y:34:LEU:CD1	2:Y:104:TYR:CD2	2.76	0.69
2:a:34:LEU:CD1	2:a:104:TYR:CD2	2.76	0.69
2:d:34:LEU:CD1	2:d:104:TYR:CD2	2.76	0.69
2:e:28:VAL:HG21	2:e:96:LEU:CB	2.22	0.69
2:i:34:LEU:CD1	2:i:104:TYR:CD2	2.76	0.69
1:V:35:PHE:HE1	1:V:321:ARG:HH11	1.38	0.69
1:C:554:LEU:HD12	1:C:557:PHE:HD2	1.58	0.69
1:H:41:TRP:CZ3	1:H:42:ASP:HB3	2.26	0.69
1:L:158:TRP:N	1:L:158:TRP:CD1	2.60	0.69
1:N:450:GLN:O	1:N:450:GLN:HG2	1.92	0.69
1:N:585:GLU:C	1:N:587:PRO:HD3	2.17	0.69
1:P:577:ILE:HG12	1:P:582:LYS:HG2	1.73	0.69
1:S:534:GLU:O	1:S:538:LEU:HD23	1.92	0.69
1:U:238:PRO:HG3	1:U:263:PHE:HB3	1.74	0.69
1:U:585:GLU:C	1:U:587:PRO:HD3	2.18	0.69
1:V:384:LEU:HD22	1:V:384:LEU:H	1.57	0.69
1:W:246:TYR:HD2	1:W:511:ARG:HB2	1.57	0.69
1:W:577:ILE:HG12	1:W:582:LYS:HG2	1.74	0.69
2:m:17:LEU:HD12	2:m:37:VAL:HG23	1.74	0.69
1:B:376:ARG:O	1:B:383:ASP:HB3	1.92	0.69
1:C:561:ASP:HB2	1:E:89:ASP:HA	1.75	0.69
1:D:26:ARG:HH21	1:D:30:LYS:HB2	1.57	0.69
1:D:554:LEU:HD12	1:D:557:PHE:HD2	1.58	0.69
1:J:554:LEU:HD12	1:J:557:PHE:HD2	1.58	0.69
1:K:212:LEU:HD22	1:L:26:ARG:HG2	1.75	0.69
1:L:209:PHE:N	1:L:210:PRO:HD3	2.08	0.69
2:Y:28:VAL:HG21	2:Y:96:LEU:CB	2.22	0.69
2:Y:28:VAL:CG2	2:Y:96:LEU:HD12	2.22	0.69
2:a:28:VAL:HG21	2:a:96:LEU:CB	2.22	0.69
2:d:28:VAL:HG21	2:d:96:LEU:CB	2.22	0.69
2:g:34:LEU:CD1	2:g:104:TYR:CD2	2.76	0.69
2:h:34:LEU:CD1	2:h:104:TYR:CD2	2.76	0.69
2:i:42:MET:O	2:i:42:MET:CG	2.30	0.69
1:M:577:ILE:HG12	1:M:582:LYS:HG2	1.74	0.69
1:M:585:GLU:C	1:M:587:PRO:HD3	2.18	0.69
1:N:37:ARG:NH2	1:N:37:ARG:HB3	2.07	0.69
1:O:585:GLU:C	1:O:587:PRO:HD3	2.18	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:246:TYR:HD2	1:R:511:ARG:HB2	1.57	0.69
1:D:209:PHE:N	1:D:210:PRO:HD3	2.08	0.69
1:I:209:PHE:N	1:I:210:PRO:HD3	2.08	0.69
1:K:593:LEU:O	1:K:597:GLN:HG2	1.93	0.69
2:b:28:VAL:HG21	2:b:96:LEU:CB	2.22	0.69
1:R:238:PRO:HG3	1:R:263:PHE:HB3	1.73	0.69
1:R:585:GLU:C	1:R:587:PRO:HD3	2.18	0.69
1:S:78:VAL:HG12	1:S:79:LEU:N	2.08	0.69
1:S:238:PRO:HG3	1:S:263:PHE:HB3	1.75	0.69
1:T:384:LEU:HD22	1:T:384:LEU:H	1.58	0.69
2:v:19:VAL:HA	2:v:22:ASP:HB3	1.73	0.69
1:E:78:VAL:CG2	1:E:444:LEU:HD11	2.15	0.69
1:G:209:PHE:N	1:G:210:PRO:HD3	2.08	0.69
1:J:209:PHE:N	1:J:210:PRO:HD3	2.08	0.69
1:K:41:TRP:CZ3	1:K:42:ASP:HB3	2.26	0.69
1:S:404:MSE:HE1	1:U:334:MSE:SE	2.43	0.68
1:T:139:SER:HB3	1:T:455:THR:HG23	1.75	0.68
1:W:238:PRO:HG3	1:W:263:PHE:HB3	1.74	0.68
1:D:376:ARG:O	1:D:383:ASP:HB3	1.92	0.68
1:G:593:LEU:O	1:G:597:GLN:HG2	1.93	0.68
1:H:158:TRP:N	1:H:158:TRP:CD1	2.60	0.68
1:H:209:PHE:N	1:H:210:PRO:HD3	2.08	0.68
1:J:41:TRP:CZ3	1:J:42:ASP:HB3	2.26	0.68
1:L:593:LEU:O	1:L:597:GLN:HG2	1.93	0.68
1:T:450:GLN:O	1:T:450:GLN:HG2	1.93	0.68
1:X:585:GLU:C	1:X:587:PRO:HD3	2.18	0.68
1:A:593:LEU:O	1:A:597:GLN:HG2	1.93	0.68
1:B:158:TRP:CD1	1:B:158:TRP:N	2.60	0.68
1:B:593:LEU:O	1:B:597:GLN:HG2	1.93	0.68
1:F:554:LEU:HD12	1:F:557:PHE:HD2	1.58	0.68
1:K:54:ARG:HB2	2:h:146:GLY:HA3	1.75	0.68
1:K:209:PHE:N	1:K:210:PRO:HD3	2.08	0.68
2:f:34:LEU:CD1	2:f:104:TYR:CD2	2.76	0.68
1:M:561:ASP:HB2	1:O:89:ASP:HA	1.75	0.68
1:N:238:PRO:HG3	1:N:263:PHE:HB3	1.75	0.68
1:O:330:ARG:NH2	1:O:409:THR:HG21	2.07	0.68
1:V:78:VAL:CG2	1:V:444:LEU:HD11	2.20	0.68
2:n:40:LEU:C	2:n:40:LEU:HD23	2.18	0.68
2:u:40:LEU:HD23	2:u:40:LEU:C	2.19	0.68
1:B:37:ARG:HB3	1:B:37:ARG:NH2	2.09	0.68
1:C:376:ARG:O	1:C:383:ASP:HB3	1.92	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:41:TRP:CZ3	1:D:42:ASP:HB3	2.26	0.68
1:F:158:TRP:N	1:F:158:TRP:CD1	2.60	0.68
1:G:99:ARG:HH12	1:G:530:GLN:HE21	1.39	0.68
1:H:376:ARG:O	1:H:383:ASP:HB3	1.92	0.68
1:J:593:LEU:O	1:J:597:GLN:HG2	1.93	0.68
2:g:53:MET:HE2	2:g:92:VAL:CG1	2.20	0.68
1:M:113:ILE:HD13	1:M:150:HIS:CE1	2.28	0.68
1:M:248:LYS:HD3	1:M:251:ILE:HB	1.74	0.68
1:N:248:LYS:HD3	1:N:251:ILE:HB	1.75	0.68
1:R:35:PHE:HE1	1:R:321:ARG:HH11	1.38	0.68
1:T:534:GLU:O	1:T:538:LEU:HD23	1.94	0.68
1:V:585:GLU:C	1:V:587:PRO:HD3	2.19	0.68
1:G:554:LEU:HD12	1:G:557:PHE:HD2	1.58	0.68
1:I:158:TRP:N	1:I:158:TRP:CD1	2.60	0.68
1:J:37:ARG:HB3	1:J:37:ARG:NH2	2.09	0.68
1:O:384:LEU:HD22	1:O:384:LEU:H	1.57	0.68
1:Q:585:GLU:C	1:Q:587:PRO:HD3	2.18	0.68
2:m:19:VAL:HA	2:m:22:ASP:HB3	1.75	0.68
2:q:40:LEU:C	2:q:40:LEU:HD23	2.19	0.68
2:s:17:LEU:HD12	2:s:37:VAL:HG23	1.76	0.68
1:A:209:PHE:N	1:A:210:PRO:HD3	2.08	0.68
1:B:334:MSE:HE1	1:C:407:ALA:HB1	1.75	0.68
1:D:593:LEU:O	1:D:597:GLN:HG2	1.93	0.68
1:L:37:ARG:HB3	1:L:37:ARG:NH2	2.09	0.68
2:b:34:LEU:CD1	2:b:104:TYR:CD2	2.76	0.68
2:h:28:VAL:CG2	2:h:96:LEU:HD12	2.22	0.68
2:j:34:LEU:CD1	2:j:104:TYR:CD2	2.76	0.68
1:P:139:SER:HB3	1:P:455:THR:HG23	1.74	0.68
1:P:585:GLU:C	1:P:587:PRO:HD3	2.18	0.68
1:Q:78:VAL:HG12	1:Q:79:LEU:N	2.08	0.68
1:Q:575:GLN:O	1:Q:579:MSE:HG2	1.94	0.68
2:k:19:VAL:HA	2:k:22:ASP:HB3	1.74	0.68
2:r:40:LEU:HD23	2:r:40:LEU:C	2.19	0.68
1:C:108:LYS:HD2	1:E:438:LEU:HD11	1.76	0.68
1:D:212:LEU:HD22	1:F:26:ARG:HG2	1.75	0.68
1:E:34:PHE:CZ	1:E:328:ARG:NH2	2.47	0.68
1:I:325:ASP:OD2	2:f:145:SER:HB3	1.93	0.68
1:I:593:LEU:O	1:I:597:GLN:HG2	1.93	0.68
1:J:108:LYS:HD2	1:K:438:LEU:HD11	1.75	0.68
1:K:334:MSE:HE1	1:L:407:ALA:HB1	1.73	0.68
2:a:28:VAL:CG2	2:a:96:LEU:HD12	2.22	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:h:53:MET:HE2	2:h:92:VAL:CG1	2.20	0.68
1:R:78:VAL:HG12	1:R:79:LEU:N	2.07	0.68
1:T:585:GLU:C	1:T:587:PRO:HD3	2.18	0.68
1:V:329:LEU:HD22	2:u:133:PRO:HG2	1.75	0.68
1:V:332:MSE:SE	2:u:132:MET:HA	2.44	0.68
2:k:100:THR:HG21	2:v:93:PRO:HB3	1.76	0.68
1:B:158:TRP:CH2	1:B:302:PRO:HG3	2.29	0.68
1:B:351:PHE:CD2	1:B:356:ILE:HD11	2.29	0.68
1:H:225:VAL:HG22	1:H:276:VAL:HG12	1.76	0.68
1:J:158:TRP:CH2	1:J:302:PRO:HG3	2.29	0.68
1:K:37:ARG:HB3	1:K:37:ARG:NH2	2.09	0.68
1:K:108:LYS:HD2	1:L:438:LEU:HD11	1.75	0.68
2:h:28:VAL:HG21	2:h:96:LEU:CB	2.22	0.68
1:O:564:GLY:HA3	1:P:535:ILE:HD11	1.76	0.68
1:T:78:VAL:HG12	1:T:79:LEU:N	2.08	0.68
1:W:139:SER:HB3	1:W:455:THR:HG23	1.73	0.68
1:W:248:LYS:HB3	1:W:511:ARG:NH1	2.05	0.68
1:W:585:GLU:C	1:W:587:PRO:HD3	2.18	0.68
1:C:34:PHE:CZ	1:C:328:ARG:NH2	2.47	0.68
1:E:376:ARG:O	1:E:383:ASP:HB3	1.93	0.68
1:H:158:TRP:CH2	1:H:302:PRO:HG3	2.29	0.68
1:I:41:TRP:CZ3	1:I:42:ASP:HB3	2.26	0.68
1:I:108:LYS:HD3	1:I:112:ASN:HD21	1.59	0.68
1:L:54:ARG:HB2	2:j:146:GLY:HA3	1.76	0.68
1:L:158:TRP:CH2	1:L:302:PRO:HG3	2.29	0.68
2:c:34:LEU:CD1	2:c:104:TYR:CD2	2.76	0.68
2:g:32:ALA:O	2:g:33:THR:HG22	1.92	0.68
2:h:32:ALA:O	2:h:33:THR:HG22	1.92	0.68
1:V:450:GLN:O	1:V:450:GLN:HG2	1.92	0.68
2:t:40:LEU:HD23	2:t:40:LEU:C	2.18	0.68
1:F:225:VAL:HG22	1:F:276:VAL:HG12	1.76	0.68
1:I:225:VAL:HG22	1:I:276:VAL:HG12	1.76	0.68
1:K:158:TRP:N	1:K:158:TRP:CD1	2.60	0.68
2:Z:34:LEU:CD1	2:Z:104:TYR:CD2	2.76	0.68
2:c:42:MET:O	2:c:42:MET:CG	2.30	0.68
2:e:46:VAL:CG1	2:e:77:ALA:HB1	2.19	0.68
1:M:78:VAL:HG12	1:M:79:LEU:N	2.09	0.68
1:P:158:TRP:HB3	1:P:173:CYS:CA	2.24	0.68
1:P:575:GLN:O	1:P:579:MSE:HG2	1.94	0.68
1:Q:384:LEU:HD22	1:Q:384:LEU:H	1.59	0.68
1:R:325:ASP:OD2	2:o:136:SER:HB3	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:238:PRO:HG3	1:V:263:PHE:HB3	1.75	0.68
2:r:64:GLU:OE1	2:r:64:GLU:HA	1.94	0.68
1:D:158:TRP:CH2	1:D:302:PRO:HG3	2.29	0.68
1:E:26:ARG:HH21	1:E:30:LYS:HB2	1.57	0.68
1:E:158:TRP:CD1	1:E:158:TRP:N	2.60	0.68
1:H:108:LYS:HD3	1:H:112:ASN:HD21	1.59	0.68
1:I:108:LYS:HD2	1:J:438:LEU:HD11	1.76	0.68
1:J:351:PHE:CD2	1:J:356:ILE:HD11	2.29	0.68
1:K:225:VAL:HG22	1:K:276:VAL:HG12	1.76	0.68
1:S:209:PHE:CZ	1:S:214:GLN:HG2	2.29	0.67
1:U:575:GLN:O	1:U:579:MSE:HG2	1.95	0.67
1:W:534:GLU:O	1:W:538:LEU:HD23	1.94	0.67
1:X:238:PRO:HG3	1:X:263:PHE:HB3	1.74	0.67
2:q:101:ALA:O	2:q:104:ILE:HG13	1.94	0.67
1:E:209:PHE:N	1:E:210:PRO:HD3	2.08	0.67
1:F:158:TRP:CH2	1:F:302:PRO:HG3	2.29	0.67
1:F:209:PHE:N	1:F:210:PRO:HD3	2.08	0.67
1:F:351:PHE:CD2	1:F:356:ILE:HD11	2.29	0.67
1:I:237:ASP:H	1:I:243:PRO:HA	1.60	0.67
1:K:351:PHE:CD2	1:K:356:ILE:HD11	2.29	0.67
2:g:28:VAL:HG21	2:g:96:LEU:CB	2.22	0.67
2:g:42:MET:O	2:g:42:MET:CG	2.30	0.67
1:O:158:TRP:N	1:O:158:TRP:CD1	2.62	0.67
1:T:246:TYR:HD2	1:T:511:ARG:HB2	1.59	0.67
1:V:248:LYS:HD3	1:V:251:ILE:HB	1.75	0.67
2:m:101:ALA:O	2:m:104:ILE:HG13	1.94	0.67
2:q:67:PRO:HG2	2:t:8:ASP:CB	2.24	0.67
1:A:351:PHE:CD2	1:A:356:ILE:HD11	2.29	0.67
1:B:442:ALA:HB1	3:B:702:HOH:O	1.95	0.67
1:B:554:LEU:HD12	1:B:557:PHE:HD2	1.58	0.67
1:C:593:LEU:O	1:C:597:GLN:HG2	1.93	0.67
1:D:37:ARG:HB3	1:D:37:ARG:NH2	2.09	0.67
1:I:442:ALA:HB1	3:I:702:HOH:O	1.95	0.67
1:I:554:LEU:HD12	1:I:557:PHE:HD2	1.58	0.67
1:L:351:PHE:CD2	1:L:356:ILE:HD11	2.29	0.67
2:b:28:VAL:CG2	2:b:96:LEU:HD12	2.22	0.67
1:R:248:LYS:HD3	1:R:251:ILE:HB	1.76	0.67
1:X:158:TRP:N	1:X:158:TRP:CD1	2.62	0.67
1:X:330:ARG:NH2	1:X:409:THR:HG21	2.05	0.67
1:X:384:LEU:H	1:X:384:LEU:HD22	1.59	0.67
2:q:15:ARG:H	2:q:15:ARG:HD2	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:r:17:LEU:HD12	2:r:37:VAL:HG23	1.77	0.67
1:A:108:LYS:HD3	1:A:112:ASN:HD21	1.59	0.67
1:A:442:ALA:HB1	3:A:702:HOH:O	1.95	0.67
1:C:158:TRP:CH2	1:C:302:PRO:HG3	2.29	0.67
1:I:158:TRP:CH2	1:I:302:PRO:HG3	2.29	0.67
1:K:237:ASP:H	1:K:243:PRO:HA	1.59	0.67
2:e:32:ALA:O	2:e:33:THR:HG22	1.92	0.67
2:i:28:VAL:CG2	2:i:96:LEU:HD12	2.22	0.67
1:N:78:VAL:HG12	1:N:79:LEU:N	2.09	0.67
1:O:209:PHE:CZ	1:O:214:GLN:HG2	2.30	0.67
1:O:450:GLN:HG2	1:O:450:GLN:O	1.94	0.67
1:R:66:LYS:HZ1	1:R:420:VAL:HG11	1.59	0.67
2:t:17:LEU:HD12	2:t:37:VAL:HG23	1.76	0.67
1:D:158:TRP:N	1:D:158:TRP:CD1	2.60	0.67
1:E:351:PHE:CD2	1:E:356:ILE:HD11	2.29	0.67
1:G:225:VAL:HG22	1:G:276:VAL:HG12	1.76	0.67
1:H:554:LEU:HD12	1:H:557:PHE:HD2	1.58	0.67
1:H:593:LEU:O	1:H:597:GLN:HG2	1.93	0.67
1:J:158:TRP:N	1:J:158:TRP:CD1	2.60	0.67
1:L:376:ARG:O	1:L:383:ASP:HB3	1.92	0.67
2:b:42:MET:O	2:b:42:MET:CG	2.30	0.67
1:O:158:TRP:HB3	1:O:173:CYS:CA	2.24	0.67
1:U:273:ARG:HH22	1:U:453:LEU:CD1	2.08	0.67
1:A:41:TRP:CZ3	1:A:42:ASP:HB3	2.26	0.67
1:A:158:TRP:CH2	1:A:302:PRO:HG3	2.29	0.67
1:C:237:ASP:H	1:C:243:PRO:HA	1.59	0.67
1:G:37:ARG:HB3	1:G:37:ARG:NH2	2.09	0.67
1:I:37:ARG:HB3	1:I:37:ARG:NH2	2.09	0.67
1:I:161:ASN:HD22	1:I:161:ASN:C	2.03	0.67
1:J:108:LYS:HD3	1:J:112:ASN:HD21	1.59	0.67
1:J:225:VAL:HG22	1:J:276:VAL:HG12	1.76	0.67
1:K:108:LYS:HD3	1:K:112:ASN:HD21	1.59	0.67
1:K:554:LEU:HD12	1:K:557:PHE:HD2	1.58	0.67
1:M:158:TRP:CD1	1:M:158:TRP:N	2.60	0.67
1:O:78:VAL:HG12	1:O:79:LEU:N	2.09	0.67
1:P:209:PHE:CZ	1:P:214:GLN:HG2	2.30	0.67
1:Q:248:LYS:HD3	1:Q:251:ILE:HB	1.77	0.67
1:S:585:GLU:C	1:S:587:PRO:HD3	2.18	0.67
1:U:113:ILE:HD13	1:U:150:HIS:CE1	2.29	0.67
1:U:534:GLU:O	1:U:538:LEU:HD23	1.95	0.67
2:q:17:LEU:HD12	2:q:37:VAL:HG23	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:407:ALA:HB1	1:E:334:MSE:HE1	1.77	0.67
1:F:593:LEU:O	1:F:597:GLN:HG2	1.93	0.67
1:G:351:PHE:CD2	1:G:356:ILE:HD11	2.29	0.67
1:K:158:TRP:CH2	1:K:302:PRO:HG3	2.29	0.67
1:Q:248:LYS:HB3	1:Q:511:ARG:NH1	2.06	0.67
1:R:450:GLN:HG2	1:R:450:GLN:O	1.94	0.67
1:S:248:LYS:HD3	1:S:251:ILE:HB	1.75	0.67
1:U:37:ARG:HB3	1:U:37:ARG:HH21	1.60	0.67
1:U:78:VAL:HG12	1:U:79:LEU:N	2.09	0.67
1:W:158:TRP:N	1:W:158:TRP:CD1	2.62	0.67
1:W:248:LYS:HD3	1:W:251:ILE:HB	1.76	0.67
2:n:42:ALA:HB1	2:o:81:SER:HB3	1.75	0.67
1:A:561:ASP:HB2	1:B:89:ASP:HA	1.77	0.67
1:C:158:TRP:N	1:C:158:TRP:CD1	2.60	0.67
1:E:593:LEU:O	1:E:597:GLN:HG2	1.93	0.67
1:G:108:LYS:HD3	1:G:112:ASN:HD21	1.59	0.67
1:J:237:ASP:H	1:J:243:PRO:HA	1.60	0.67
1:J:442:ALA:HB1	3:J:702:HOH:O	1.95	0.67
1:K:379:GLU:O	1:K:380:ASN:HB2	1.95	0.67
1:M:37:ARG:HB3	1:M:37:ARG:HH21	1.60	0.67
1:N:209:PHE:CZ	1:N:214:GLN:HG2	2.29	0.67
1:N:232:ALA:CB	1:N:269:ARG:H	2.08	0.67
1:Q:209:PHE:CZ	1:Q:214:GLN:HG2	2.30	0.67
1:R:158:TRP:N	1:R:158:TRP:CD1	2.63	0.67
2:o:40:LEU:HD23	2:o:40:LEU:C	2.19	0.67
1:A:237:ASP:H	1:A:243:PRO:HA	1.59	0.67
1:C:161:ASN:C	1:C:161:ASN:HD22	2.03	0.67
1:C:209:PHE:N	1:C:210:PRO:HD3	2.08	0.67
1:C:442:ALA:HB1	3:C:702:HOH:O	1.95	0.67
1:D:237:ASP:H	1:D:243:PRO:HA	1.59	0.67
1:F:161:ASN:HD22	1:F:161:ASN:C	2.03	0.67
1:G:158:TRP:CH2	1:G:302:PRO:HG3	2.29	0.67
1:H:442:ALA:HB1	3:H:702:HOH:O	1.95	0.67
1:I:351:PHE:CD2	1:I:356:ILE:HD11	2.29	0.67
1:L:237:ASP:H	1:L:243:PRO:HA	1.59	0.67
1:T:248:LYS:HD3	1:T:251:ILE:HB	1.76	0.67
1:U:384:LEU:H	1:U:384:LEU:HD22	1.59	0.67
1:X:209:PHE:CZ	1:X:214:GLN:HG2	2.30	0.67
1:B:237:ASP:H	1:B:243:PRO:HA	1.59	0.67
1:D:108:LYS:HD3	1:D:112:ASN:HD21	1.59	0.67
1:E:554:LEU:HD12	1:E:557:PHE:HD2	1.58	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:561:ASP:OD2	1:K:92:ASP:HB3	1.95	0.67
1:K:561:ASP:OD2	1:L:92:ASP:HB3	1.93	0.67
1:L:379:GLU:O	1:L:380:ASN:HB2	1.95	0.67
2:f:28:VAL:HG21	2:f:96:LEU:CB	2.22	0.67
2:j:28:VAL:HG21	2:j:96:LEU:CB	2.22	0.67
1:M:534:GLU:O	1:M:538:LEU:HD23	1.95	0.67
1:R:560:LEU:HD22	1:X:82:PRO:HG2	1.75	0.67
1:X:113:ILE:HD13	1:X:150:HIS:CE1	2.31	0.67
2:p:17:LEU:HD12	2:p:37:VAL:HG23	1.77	0.67
1:C:351:PHE:CD2	1:C:356:ILE:HD11	2.29	0.67
1:D:351:PHE:CD2	1:D:356:ILE:HD11	2.29	0.67
1:E:161:ASN:C	1:E:161:ASN:HD22	2.03	0.67
1:H:165:MSE:HG3	1:H:307:TRP:CE3	2.30	0.67
1:L:165:MSE:HG3	1:L:307:TRP:CE3	2.30	0.67
1:M:209:PHE:CZ	1:M:214:GLN:HG2	2.29	0.66
1:M:560:LEU:HD22	1:O:82:PRO:HG2	1.78	0.66
1:R:534:GLU:O	1:R:538:LEU:HD23	1.95	0.66
1:W:384:LEU:HD22	1:W:384:LEU:H	1.59	0.66
2:t:15:ARG:H	2:t:15:ARG:HD2	1.61	0.66
1:A:554:LEU:HD12	1:A:557:PHE:HD2	1.58	0.66
1:B:379:GLU:O	1:B:380:ASN:HB2	1.95	0.66
1:D:379:GLU:O	1:D:380:ASN:HB2	1.95	0.66
1:E:165:MSE:HG3	1:E:307:TRP:CE3	2.30	0.66
1:H:351:PHE:CD2	1:H:356:ILE:HD11	2.29	0.66
2:e:28:VAL:CG2	2:e:96:LEU:HD12	2.22	0.66
2:h:42:MET:O	2:h:42:MET:CG	2.30	0.66
1:N:330:ARG:NH2	1:N:409:THR:HG21	2.08	0.66
1:O:248:LYS:HB3	1:O:511:ARG:NH1	2.06	0.66
2:n:64:GLU:HG3	2:n:66:PRO:HD2	1.78	0.66
2:u:17:LEU:HD12	2:u:37:VAL:HG23	1.75	0.66
1:A:34:PHE:CZ	1:A:328:ARG:NH2	2.47	0.66
1:A:78:VAL:HG22	1:A:444:LEU:HD21	1.78	0.66
1:C:108:LYS:HD3	1:C:112:ASN:HD21	1.59	0.66
1:C:225:VAL:HG22	1:C:276:VAL:HG12	1.76	0.66
1:D:78:VAL:HG22	1:D:444:LEU:HD21	1.78	0.66
1:E:78:VAL:HG22	1:E:444:LEU:HD21	1.78	0.66
1:E:379:GLU:O	1:E:380:ASN:HB2	1.95	0.66
1:H:37:ARG:HB3	1:H:37:ARG:NH2	2.09	0.66
1:J:379:GLU:O	1:J:380:ASN:HB2	1.95	0.66
1:N:384:LEU:HD22	1:N:384:LEU:H	1.58	0.66
1:N:575:GLN:O	1:N:579:MSE:HG2	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:94:LEU:HA	1:Q:97:MSE:HE2	1.77	0.66
1:R:78:VAL:CG2	1:R:444:LEU:HD11	2.22	0.66
1:R:231:THR:HG21	1:R:249:ARG:HH11	1.60	0.66
1:W:209:PHE:CZ	1:W:214:GLN:HG2	2.30	0.66
2:r:15:ARG:H	2:r:15:ARG:HD2	1.60	0.66
1:A:182:ASN:HD22	1:B:171:ARG:HH21	1.42	0.66
1:B:225:VAL:HG22	1:B:276:VAL:HG12	1.76	0.66
1:G:165:MSE:HG3	1:G:307:TRP:CE3	2.30	0.66
1:G:379:GLU:O	1:G:380:ASN:HB2	1.95	0.66
1:H:78:VAL:HG22	1:H:444:LEU:HD21	1.78	0.66
1:H:379:GLU:O	1:H:380:ASN:HB2	1.95	0.66
1:K:227:GLU:HA	1:K:274:ARG:HA	1.78	0.66
1:L:225:VAL:HG22	1:L:276:VAL:HG12	1.76	0.66
1:L:554:LEU:HD12	1:L:557:PHE:HD2	1.58	0.66
1:M:94:LEU:HA	1:M:97:MSE:HE2	1.77	0.66
1:N:248:LYS:HB3	1:N:511:ARG:NH1	2.07	0.66
1:Q:113:ILE:HD13	1:Q:150:HIS:CE1	2.30	0.66
1:Q:158:TRP:N	1:Q:158:TRP:CD1	2.62	0.66
1:Q:534:GLU:O	1:Q:538:LEU:HD23	1.95	0.66
1:S:158:TRP:N	1:S:158:TRP:CD1	2.62	0.66
1:W:113:ILE:HD13	1:W:150:HIS:CE1	2.31	0.66
1:W:231:THR:HG21	1:W:249:ARG:HH11	1.60	0.66
2:l:64:GLU:HG3	2:l:66:PRO:HD2	1.78	0.66
1:A:227:GLU:HA	1:A:274:ARG:HA	1.78	0.66
1:C:37:ARG:HB3	1:C:37:ARG:NH2	2.09	0.66
1:D:161:ASN:HD22	1:D:161:ASN:C	2.03	0.66
1:D:182:ASN:ND2	1:F:171:ARG:HH21	1.94	0.66
1:F:78:VAL:HG22	1:F:444:LEU:HD21	1.78	0.66
1:G:237:ASP:H	1:G:243:PRO:HA	1.60	0.66
1:I:165:MSE:HG3	1:I:307:TRP:CE3	2.30	0.66
1:J:165:MSE:HG3	1:J:307:TRP:CE3	2.30	0.66
2:f:42:MET:O	2:f:42:MET:CG	2.30	0.66
2:i:28:VAL:HG21	2:i:96:LEU:CB	2.22	0.66
1:N:94:LEU:HA	1:N:97:MSE:HE2	1.76	0.66
1:Q:330:ARG:NH2	1:Q:409:THR:HG21	2.06	0.66
2:r:64:GLU:HG3	2:r:66:PRO:HD2	1.77	0.66
1:C:78:VAL:HG22	1:C:444:LEU:HD21	1.78	0.66
1:E:158:TRP:CH2	1:E:302:PRO:HG3	2.29	0.66
1:F:37:ARG:HB3	1:F:37:ARG:NH2	2.09	0.66
1:F:108:LYS:HD3	1:F:112:ASN:HD21	1.59	0.66
1:G:158:TRP:N	1:G:158:TRP:CD1	2.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:41:TRP:HZ3	1:I:42:ASP:HB3	1.61	0.66
1:L:41:TRP:HZ3	1:L:42:ASP:HB3	1.61	0.66
1:L:227:GLU:HA	1:L:274:ARG:HA	1.78	0.66
1:O:534:GLU:O	1:O:538:LEU:HD23	1.96	0.66
1:O:560:LEU:O	1:O:565:VAL:HG21	1.96	0.66
1:P:248:LYS:HD3	1:P:251:ILE:HB	1.77	0.66
1:S:575:GLN:O	1:S:579:MSE:HG2	1.94	0.66
1:T:158:TRP:N	1:T:158:TRP:CD1	2.62	0.66
1:T:209:PHE:CZ	1:T:214:GLN:HG2	2.30	0.66
1:W:94:LEU:HA	1:W:97:MSE:HE2	1.78	0.66
2:p:40:LEU:HD23	2:p:40:LEU:C	2.21	0.66
2:t:101:ALA:O	2:t:104:ILE:HG13	1.96	0.66
1:B:165:MSE:HG3	1:B:307:TRP:CE3	2.30	0.66
1:B:227:GLU:HA	1:B:274:ARG:HA	1.78	0.66
1:E:225:VAL:HG22	1:E:276:VAL:HG12	1.76	0.66
1:G:442:ALA:HB1	3:G:702:HOH:O	1.95	0.66
1:H:227:GLU:HA	1:H:274:ARG:HA	1.78	0.66
1:K:41:TRP:HZ3	1:K:42:ASP:HB3	1.61	0.66
1:K:161:ASN:C	1:K:161:ASN:HD22	2.03	0.66
1:M:575:GLN:O	1:M:579:MSE:HG2	1.96	0.66
1:O:231:THR:HG21	1:O:249:ARG:HH11	1.61	0.66
1:R:209:PHE:CZ	1:R:214:GLN:HG2	2.29	0.66
1:T:158:TRP:HB3	1:T:173:CYS:CA	2.24	0.66
1:U:248:LYS:HB3	1:U:511:ARG:NH1	2.05	0.66
1:W:330:ARG:NH2	1:W:409:THR:HG21	2.09	0.66
1:F:379:GLU:O	1:F:380:ASN:HB2	1.95	0.66
1:H:237:ASP:H	1:H:243:PRO:HA	1.60	0.66
1:J:227:GLU:HA	1:J:274:ARG:HA	1.78	0.66
1:K:442:ALA:HB1	3:K:702:HOH:O	1.95	0.66
2:Z:110:ALA:O	2:Z:113:ILE:HG13	1.96	0.66
2:g:110:ALA:O	2:g:113:ILE:HG13	1.96	0.66
1:P:232:ALA:CB	1:P:269:ARG:H	2.08	0.66
1:R:330:ARG:NH2	1:R:409:THR:HG21	2.06	0.66
1:S:273:ARG:HH22	1:S:453:LEU:CD1	2.09	0.66
1:B:108:LYS:HD3	1:B:112:ASN:HD21	1.59	0.66
1:B:161:ASN:C	1:B:161:ASN:HD22	2.03	0.66
1:E:37:ARG:HB3	1:E:37:ARG:NH2	2.09	0.66
1:E:108:LYS:HD3	1:E:112:ASN:HD21	1.59	0.66
1:G:161:ASN:C	1:G:161:ASN:HD22	2.03	0.66
1:J:41:TRP:HZ3	1:J:42:ASP:HB3	1.61	0.66
1:L:108:LYS:HD3	1:L:112:ASN:HD21	1.59	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:i:110:ALA:O	2:i:113:ILE:HG13	1.96	0.66
2:j:110:ALA:O	2:j:113:ILE:HG13	1.96	0.66
1:O:232:ALA:CB	1:O:269:ARG:H	2.09	0.66
1:P:325:ASP:OD2	2:l:136:SER:HB3	1.96	0.66
1:V:66:LYS:HZ1	1:V:420:VAL:HG11	1.61	0.66
1:V:248:LYS:HB3	1:V:511:ARG:NH1	2.07	0.66
1:X:248:LYS:HD3	1:X:251:ILE:HB	1.77	0.66
1:A:165:MSE:HG3	1:A:307:TRP:CE3	2.30	0.66
1:A:225:VAL:HG22	1:A:276:VAL:HG12	1.76	0.66
1:B:209:PHE:N	1:B:210:PRO:HD3	2.08	0.66
1:B:561:ASP:HB2	1:C:89:ASP:HA	1.78	0.66
1:F:237:ASP:H	1:F:243:PRO:HA	1.60	0.66
1:K:41:TRP:CE3	1:K:42:ASP:CA	2.79	0.66
1:K:78:VAL:HG22	1:K:444:LEU:HD21	1.78	0.66
1:K:165:MSE:HG3	1:K:307:TRP:CE3	2.30	0.66
1:M:334:MSE:SE	1:O:404:MSE:HE1	2.46	0.66
1:O:94:LEU:HA	1:O:97:MSE:HE2	1.77	0.66
1:P:534:GLU:O	1:P:538:LEU:HD23	1.96	0.66
1:S:94:LEU:HA	1:S:97:MSE:HE2	1.76	0.66
1:V:94:LEU:HA	1:V:97:MSE:HE2	1.77	0.66
1:V:575:GLN:O	1:V:579:MSE:HG2	1.96	0.66
1:W:26:ARG:NH2	1:W:30:LYS:HD3	2.11	0.66
2:o:101:ALA:O	2:o:104:ILE:HG13	1.96	0.66
2:s:64:GLU:HG3	2:s:66:PRO:HD2	1.78	0.66
2:t:64:GLU:HG3	2:t:66:PRO:HD2	1.78	0.66
1:B:41:TRP:HZ3	1:B:42:ASP:HB3	1.61	0.66
1:C:379:GLU:O	1:C:380:ASN:HB2	1.95	0.66
1:C:556:TYR:OH	1:E:542:THR:HG21	1.96	0.66
1:D:442:ALA:HB1	3:D:702:HOH:O	1.95	0.66
1:E:227:GLU:HA	1:E:274:ARG:HA	1.78	0.66
1:E:442:ALA:HB1	3:E:702:HOH:O	1.95	0.66
1:J:212:LEU:HD22	1:K:26:ARG:HG2	1.78	0.66
2:d:28:VAL:CG2	2:d:96:LEU:HD12	2.22	0.66
1:P:330:ARG:NH2	1:P:409:THR:HG21	2.07	0.65
1:R:575:GLN:O	1:R:579:MSE:HG2	1.96	0.65
1:W:158:TRP:HB3	1:W:173:CYS:CA	2.23	0.65
1:W:575:GLN:O	1:W:579:MSE:HG2	1.96	0.65
1:C:165:MSE:HG3	1:C:307:TRP:CE3	2.30	0.65
1:D:58:ASP:O	1:D:59:VAL:CB	2.45	0.65
1:E:58:ASP:O	1:E:59:VAL:CB	2.45	0.65
1:E:237:ASP:H	1:E:243:PRO:HA	1.59	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:227:GLU:HA	1:F:274:ARG:HA	1.78	0.65
1:H:41:TRP:CE3	1:H:42:ASP:CA	2.79	0.65
1:J:161:ASN:C	1:J:161:ASN:HD22	2.03	0.65
2:b:32:ALA:O	2:b:33:THR:HG22	1.92	0.65
1:M:232:ALA:CB	1:M:269:ARG:H	2.08	0.65
1:N:26:ARG:NH2	1:N:30:LYS:HD3	2.11	0.65
1:P:78:VAL:CG2	1:P:444:LEU:HD11	2.23	0.65
1:W:15:PHE:HZ	1:W:283:CYS:HG	1.42	0.65
2:l:15:ARG:H	2:l:15:ARG:HD2	1.61	0.65
1:A:37:ARG:HB3	1:A:37:ARG:NH2	2.09	0.65
1:A:352:TRP:CG	1:L:376:ARG:HB2	2.31	0.65
1:F:442:ALA:HB1	3:F:702:HOH:O	1.95	0.65
1:G:58:ASP:O	1:G:59:VAL:CB	2.45	0.65
1:I:227:GLU:HA	1:I:274:ARG:HA	1.78	0.65
1:I:561:ASP:HB2	1:J:89:ASP:HA	1.78	0.65
2:Y:32:ALA:O	2:Y:33:THR:HG22	1.92	0.65
2:f:110:ALA:O	2:f:113:ILE:HG13	1.96	0.65
1:R:37:ARG:HB3	1:R:37:ARG:HH21	1.60	0.65
1:S:158:TRP:HB3	1:S:173:CYS:CA	2.25	0.65
1:U:158:TRP:CD1	1:U:158:TRP:N	2.64	0.65
1:U:404:MSE:HE1	1:X:334:MSE:SE	2.47	0.65
2:k:8:ASP:CB	2:v:67:PRO:HG2	2.27	0.65
2:n:67:PRO:HG2	2:o:8:ASP:CB	2.27	0.65
1:D:26:ARG:HG2	1:E:212:LEU:HD22	1.77	0.65
1:G:78:VAL:HG22	1:G:444:LEU:HD21	1.78	0.65
1:I:379:GLU:O	1:I:380:ASN:HB2	1.95	0.65
1:J:78:VAL:HG22	1:J:444:LEU:HD21	1.78	0.65
2:Z:32:ALA:O	2:Z:33:THR:HG22	1.92	0.65
2:a:32:ALA:O	2:a:33:THR:HG22	1.92	0.65
2:e:42:MET:O	2:e:42:MET:CG	2.30	0.65
1:S:232:ALA:CB	1:S:269:ARG:H	2.10	0.65
2:u:101:ALA:O	2:u:104:ILE:HG13	1.96	0.65
1:H:58:ASP:O	1:H:59:VAL:CB	2.45	0.65
1:I:556:TYR:OH	1:J:542:THR:HG21	1.95	0.65
2:Y:110:ALA:O	2:Y:113:ILE:HG13	1.96	0.65
1:O:575:GLN:O	1:O:579:MSE:HG2	1.97	0.65
1:P:158:TRP:N	1:P:158:TRP:CD1	2.63	0.65
1:T:248:LYS:HB3	1:T:511:ARG:NH1	2.04	0.65
1:U:209:PHE:CZ	1:U:214:GLN:HG2	2.30	0.65
1:X:78:VAL:CG2	1:X:444:LEU:HD11	2.23	0.65
1:X:231:THR:HG21	1:X:249:ARG:HH11	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:560:LEU:O	1:X:565:VAL:HG21	1.97	0.65
2:k:40:LEU:HD23	2:k:40:LEU:C	2.22	0.65
2:p:15:ARG:H	2:p:15:ARG:HD2	1.61	0.65
2:q:42:ALA:HB1	2:t:81:SER:HB3	1.78	0.65
2:s:40:LEU:HD23	2:s:40:LEU:C	2.22	0.65
2:v:101:ALA:O	2:v:104:ILE:HG13	1.97	0.65
1:A:379:GLU:O	1:A:380:ASN:HB2	1.95	0.65
1:B:41:TRP:CE3	1:B:42:ASP:CA	2.79	0.65
1:B:560:LEU:HD22	1:C:82:PRO:HG2	1.78	0.65
1:D:227:GLU:HA	1:D:274:ARG:HA	1.78	0.65
1:F:165:MSE:HG3	1:F:307:TRP:CE3	2.30	0.65
1:L:161:ASN:HD22	1:L:161:ASN:C	2.03	0.65
2:c:28:VAL:CG2	2:c:96:LEU:HD12	2.22	0.65
2:f:32:ALA:O	2:f:33:THR:HG22	1.92	0.65
2:g:28:VAL:CG2	2:g:96:LEU:HD12	2.22	0.65
1:S:34:PHE:HZ	1:S:328:ARG:HH22	1.38	0.65
1:S:37:ARG:HB3	1:S:37:ARG:HH21	1.61	0.65
1:V:209:PHE:CZ	1:V:214:GLN:HG2	2.30	0.65
2:l:40:LEU:HD23	2:l:40:LEU:C	2.22	0.65
2:r:101:ALA:O	2:r:104:ILE:HG13	1.96	0.65
2:u:64:GLU:HG3	2:u:66:PRO:HD2	1.78	0.65
1:D:225:VAL:HG22	1:D:276:VAL:HG12	1.76	0.65
1:E:41:TRP:CE3	1:E:42:ASP:CA	2.79	0.65
1:H:41:TRP:HZ3	1:H:42:ASP:HB3	1.61	0.65
1:I:78:VAL:HG22	1:I:444:LEU:HD21	1.78	0.65
1:L:442:ALA:HB1	3:L:702:HOH:O	1.95	0.65
1:R:561:ASP:OD2	1:X:92:ASP:HB3	1.97	0.65
1:S:158:TRP:CH2	1:S:302:PRO:HG3	2.31	0.65
1:T:273:ARG:HH22	1:T:453:LEU:CD1	2.09	0.65
2:p:101:ALA:O	2:p:104:ILE:HG13	1.97	0.65
1:C:227:GLU:HA	1:C:274:ARG:HA	1.78	0.65
1:F:41:TRP:CE3	1:F:42:ASP:CA	2.79	0.65
2:d:32:ALA:O	2:d:33:THR:HG22	1.92	0.65
1:P:94:LEU:HA	1:P:97:MSE:HE2	1.79	0.65
1:Q:158:TRP:CH2	1:Q:302:PRO:HG3	2.31	0.65
1:Q:231:THR:HG21	1:Q:249:ARG:HH11	1.62	0.65
1:S:431:ALA:O	1:S:435:VAL:HG22	1.96	0.65
2:l:25:LEU:HD13	2:m:96:ALA:HB2	1.79	0.65
2:m:40:LEU:HD23	2:m:40:LEU:C	2.21	0.65
1:C:58:ASP:O	1:C:59:VAL:CB	2.45	0.65
1:D:438:LEU:HD11	1:E:108:LYS:HD2	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:108:LYS:HD2	1:G:438:LEU:HD11	1.79	0.65
1:L:58:ASP:O	1:L:59:VAL:CB	2.45	0.65
2:Z:28:VAL:CG2	2:Z:96:LEU:HD12	2.22	0.65
1:N:12:LEU:O	1:N:16:ASP:HB2	1.97	0.65
1:R:273:ARG:HH22	1:R:453:LEU:CD1	2.10	0.65
1:S:26:ARG:NH2	1:S:30:LYS:HD3	2.11	0.65
1:T:287:LEU:HD12	1:T:287:LEU:N	2.12	0.65
2:k:17:LEU:HD12	2:k:37:VAL:HG23	1.78	0.65
1:A:58:ASP:O	1:A:59:VAL:CB	2.45	0.65
1:A:158:TRP:N	1:A:158:TRP:CD1	2.60	0.65
1:C:41:TRP:HZ3	1:C:42:ASP:HB3	1.61	0.65
1:D:41:TRP:CE3	1:D:42:ASP:CA	2.79	0.65
1:F:58:ASP:O	1:F:59:VAL:CB	2.45	0.65
1:G:5:GLU:HG2	1:G:6:ASN:N	2.12	0.65
1:G:41:TRP:HZ3	1:G:42:ASP:HB3	1.61	0.65
1:G:227:GLU:HA	1:G:274:ARG:HA	1.78	0.65
1:H:47:GLN:OE1	1:H:47:GLN:N	2.30	0.65
1:I:47:GLN:OE1	1:I:47:GLN:N	2.30	0.65
1:J:47:GLN:OE1	1:J:47:GLN:N	2.30	0.65
1:K:158:TRP:CE3	1:K:173:CYS:SG	2.88	0.65
2:b:110:ALA:O	2:b:113:ILE:HG13	1.96	0.65
1:W:273:ARG:HH22	1:W:453:LEU:CD1	2.09	0.65
1:A:41:TRP:HZ3	1:A:42:ASP:HB3	1.61	0.65
1:D:5:GLU:HG2	1:D:6:ASN:N	2.12	0.65
1:G:41:TRP:CE3	1:G:42:ASP:CA	2.79	0.65
1:G:182:ASN:ND2	1:H:171:ARG:HH21	1.95	0.65
2:e:74:ASN:HB2	2:e:75:PRO:HD3	1.79	0.65
1:M:384:LEU:H	1:M:384:LEU:HD22	1.61	0.64
1:N:560:LEU:O	1:N:565:VAL:HG21	1.97	0.64
1:O:212:LEU:HD22	1:P:26:ARG:HG2	1.79	0.64
1:Q:444:LEU:C	1:Q:446:THR:N	2.53	0.64
1:T:330:ARG:NH2	1:T:409:THR:HG21	2.07	0.64
1:X:444:LEU:C	1:X:446:THR:N	2.53	0.64
2:n:101:ALA:O	2:n:104:ILE:HG13	1.97	0.64
2:s:101:ALA:O	2:s:104:ILE:HG13	1.97	0.64
2:v:15:ARG:H	2:v:15:ARG:HD2	1.62	0.64
1:A:144:ILE:HG12	1:A:447:TYR:HE1	1.62	0.64
1:B:5:GLU:HG2	1:B:6:ASN:N	2.12	0.64
1:D:165:MSE:HG3	1:D:307:TRP:CE3	2.30	0.64
2:c:28:VAL:HG21	2:c:96:LEU:CB	2.22	0.64
1:R:158:TRP:CE3	1:R:173:CYS:SG	2.86	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:26:ARG:NH2	1:U:30:LYS:HD3	2.13	0.64
2:v:64:GLU:HG3	2:v:66:PRO:HD2	1.79	0.64
1:A:41:TRP:CE3	1:A:42:ASP:CA	2.79	0.64
1:B:95:MSE:HE1	1:B:99:ARG:CZ	2.27	0.64
1:H:57:PHE:HD2	1:H:330:ARG:CB	2.10	0.64
1:I:41:TRP:CE3	1:I:42:ASP:CA	2.79	0.64
1:I:57:PHE:HD2	1:I:330:ARG:CB	2.10	0.64
1:J:71:MSE:HE2	1:J:119:ILE:HD11	1.80	0.64
1:J:95:MSE:HE1	1:J:99:ARG:CZ	2.28	0.64
1:K:58:ASP:O	1:K:59:VAL:CB	2.45	0.64
1:K:95:MSE:HE1	1:K:99:ARG:CZ	2.27	0.64
1:L:5:GLU:HG2	1:L:6:ASN:N	2.13	0.64
1:L:41:TRP:CE3	1:L:42:ASP:CA	2.79	0.64
2:c:74:ASN:HB2	2:c:75:PRO:HD3	1.79	0.64
2:d:110:ALA:O	2:d:113:ILE:HG13	1.96	0.64
1:N:78:VAL:CG2	1:N:444:LEU:HD11	2.22	0.64
1:N:128:LEU:HD12	1:N:446:THR:HG23	1.79	0.64
1:O:567:MSE:SE	1:P:576:LEU:HD13	2.47	0.64
1:R:384:LEU:H	1:R:384:LEU:HD22	1.63	0.64
1:V:37:ARG:HB3	1:V:37:ARG:HH21	1.62	0.64
1:V:158:TRP:HB3	1:V:173:CYS:CA	2.23	0.64
1:W:329:LEU:HD22	2:s:133:PRO:HG2	1.80	0.64
1:B:57:PHE:HD2	1:B:330:ARG:CB	2.11	0.64
1:C:41:TRP:CE3	1:C:42:ASP:CA	2.79	0.64
1:E:57:PHE:HD2	1:E:330:ARG:CB	2.10	0.64
1:F:15:PHE:CE1	1:F:283:CYS:HA	2.33	0.64
1:F:57:PHE:HD2	1:F:330:ARG:CB	2.10	0.64
1:I:5:GLU:HG2	1:I:6:ASN:N	2.12	0.64
1:I:58:ASP:O	1:I:59:VAL:CB	2.45	0.64
1:J:41:TRP:CE3	1:J:42:ASP:CA	2.79	0.64
2:d:74:ASN:HB2	2:d:75:PRO:HD3	1.79	0.64
2:h:110:ALA:O	2:h:113:ILE:HG13	1.96	0.64
1:P:15:PHE:CE1	1:P:283:CYS:HA	2.32	0.64
1:S:325:ASP:OD2	2:q:136:SER:HB3	1.97	0.64
1:T:158:TRP:CH2	1:T:302:PRO:HG3	2.33	0.64
1:U:92:ASP:HB3	1:X:561:ASP:OD2	1.97	0.64
1:V:113:ILE:HD13	1:V:150:HIS:CE1	2.33	0.64
1:V:231:THR:HG21	1:V:249:ARG:HH11	1.62	0.64
2:k:64:GLU:HG3	2:k:66:PRO:HD2	1.78	0.64
2:m:64:GLU:HG3	2:m:66:PRO:HD2	1.78	0.64
1:D:144:ILE:HG12	1:D:447:TYR:HE1	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:15:PHE:CE1	1:H:283:CYS:HA	2.33	0.64
1:H:35:PHE:HE1	1:H:321:ARG:HH11	1.46	0.64
1:K:71:MSE:HE2	1:K:119:ILE:HD11	1.80	0.64
1:L:78:VAL:HG22	1:L:444:LEU:HD21	1.78	0.64
1:L:528:LYS:NZ	1:L:560:LEU:HD21	2.13	0.64
1:S:113:ILE:HD13	1:S:150:HIS:CE1	2.32	0.64
1:X:158:TRP:CH2	1:X:302:PRO:HG3	2.33	0.64
1:X:273:ARG:HH22	1:X:453:LEU:CD1	2.09	0.64
1:A:95:MSE:HE1	1:A:99:ARG:CZ	2.28	0.64
1:E:35:PHE:HE1	1:E:321:ARG:HH11	1.46	0.64
1:E:95:MSE:HE1	1:E:99:ARG:CZ	2.28	0.64
1:G:15:PHE:CE1	1:G:283:CYS:HA	2.33	0.64
1:G:95:MSE:HE1	1:G:99:ARG:CZ	2.28	0.64
1:I:15:PHE:CE1	1:I:283:CYS:HA	2.33	0.64
1:I:35:PHE:HE1	1:I:321:ARG:HH11	1.46	0.64
1:I:528:LYS:NZ	1:I:560:LEU:HD21	2.13	0.64
1:N:158:TRP:CH2	1:N:302:PRO:HG3	2.33	0.64
1:N:534:GLU:O	1:N:538:LEU:HD23	1.98	0.64
1:S:561:ASP:HB2	1:T:89:ASP:HA	1.80	0.64
1:A:57:PHE:HD2	1:A:330:ARG:CB	2.10	0.64
1:B:78:VAL:HG22	1:B:444:LEU:HD21	1.78	0.64
1:B:528:LYS:NZ	1:B:560:LEU:HD21	2.13	0.64
1:D:15:PHE:CE1	1:D:283:CYS:HA	2.33	0.64
1:E:47:GLN:OE1	1:E:47:GLN:N	2.30	0.64
1:H:95:MSE:HE1	1:H:99:ARG:CZ	2.27	0.64
1:H:236:GLN:HA	1:H:244:VAL:H	1.63	0.64
1:J:5:GLU:HG2	1:J:6:ASN:N	2.12	0.64
1:L:95:MSE:HE1	1:L:99:ARG:CZ	2.28	0.64
1:N:37:ARG:NH2	1:N:41:TRP:HB3	2.13	0.64
1:O:26:ARG:NH2	1:O:30:LYS:HD3	2.13	0.64
1:O:37:ARG:HB3	1:O:37:ARG:HH21	1.61	0.64
1:Q:273:ARG:HH22	1:Q:453:LEU:CD1	2.09	0.64
1:U:94:LEU:HA	1:U:97:MSE:HE2	1.80	0.64
1:W:232:ALA:CB	1:W:269:ARG:H	2.10	0.64
1:X:78:VAL:HG12	1:X:79:LEU:N	2.12	0.64
1:X:534:GLU:O	1:X:538:LEU:HD23	1.97	0.64
1:A:71:MSE:HE2	1:A:119:ILE:HD11	1.80	0.64
1:A:236:GLN:HA	1:A:244:VAL:H	1.63	0.64
1:A:528:LYS:NZ	1:A:560:LEU:HD21	2.13	0.64
1:B:236:GLN:HA	1:B:244:VAL:H	1.63	0.64
1:E:15:PHE:CE1	1:E:283:CYS:HA	2.33	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:34:PHE:HE1	1:E:324:LYS:HZ2	1.43	0.64
1:E:144:ILE:HG12	1:E:447:TYR:HE1	1.63	0.64
1:G:546:THR:CG2	1:G:547:PRO:HD3	2.28	0.64
1:H:71:MSE:HE2	1:H:119:ILE:HD11	1.80	0.64
1:J:58:ASP:O	1:J:59:VAL:CB	2.45	0.64
2:h:74:ASN:HB2	2:h:75:PRO:HD3	1.79	0.64
1:Q:560:LEU:O	1:Q:565:VAL:HG21	1.98	0.64
1:V:273:ARG:HH22	1:V:453:LEU:CD1	2.10	0.64
2:o:64:GLU:HG3	2:o:66:PRO:HD2	1.78	0.64
1:A:47:GLN:OE1	1:A:47:GLN:N	2.30	0.64
1:B:15:PHE:CE1	1:B:283:CYS:HA	2.33	0.64
1:B:144:ILE:HG12	1:B:447:TYR:HE1	1.62	0.64
1:F:47:GLN:OE1	1:F:47:GLN:N	2.30	0.64
1:G:47:GLN:N	1:G:47:GLN:OE1	2.30	0.64
1:G:528:LYS:NZ	1:G:560:LEU:HD21	2.13	0.64
1:I:144:ILE:HG12	1:I:447:TYR:HE1	1.62	0.64
1:K:78:VAL:HG12	1:K:79:LEU:N	2.13	0.64
2:Y:42:MET:O	2:Y:42:MET:CG	2.30	0.64
1:Q:37:ARG:HB3	1:Q:37:ARG:HH21	1.61	0.64
1:R:113:ILE:HD13	1:R:150:HIS:CE1	2.32	0.64
1:R:273:ARG:NH2	1:R:453:LEU:HD21	2.13	0.64
1:R:560:LEU:O	1:R:565:VAL:HG21	1.98	0.64
1:V:534:GLU:O	1:V:538:LEU:HD23	1.98	0.64
1:V:560:LEU:O	1:V:565:VAL:HG21	1.97	0.64
1:X:325:ASP:OD2	2:p:136:SER:HB3	1.97	0.64
1:A:15:PHE:CE1	1:A:283:CYS:HA	2.33	0.64
1:B:15:PHE:HZ	1:B:283:CYS:HG	1.45	0.64
1:C:236:GLN:HA	1:C:244:VAL:H	1.63	0.64
1:C:528:LYS:NZ	1:C:560:LEU:HD21	2.13	0.64
1:D:528:LYS:NZ	1:D:560:LEU:HD21	2.13	0.64
1:E:528:LYS:NZ	1:E:560:LEU:HD21	2.13	0.64
1:G:236:GLN:HA	1:G:244:VAL:H	1.63	0.64
1:I:71:MSE:HE2	1:I:119:ILE:HD11	1.80	0.64
1:I:236:GLN:HA	1:I:244:VAL:H	1.63	0.64
2:a:110:ALA:O	2:a:113:ILE:HG13	1.96	0.64
2:e:110:ALA:O	2:e:113:ILE:HG13	1.96	0.64
1:M:231:THR:HG21	1:M:249:ARG:HH11	1.63	0.64
1:O:24:GLU:C	1:O:26:ARG:N	2.56	0.64
1:Q:26:ARG:NH2	1:Q:30:LYS:HD3	2.13	0.64
1:U:560:LEU:O	1:U:565:VAL:HG21	1.98	0.64
1:C:71:MSE:HE2	1:C:119:ILE:HD11	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:78:VAL:HG12	1:E:79:LEU:N	2.13	0.64
1:F:71:MSE:HE2	1:F:119:ILE:HD11	1.80	0.64
1:F:78:VAL:HG12	1:F:79:LEU:N	2.13	0.64
1:G:48:TYR:O	1:G:49:THR:HB	1.98	0.64
1:H:144:ILE:HG12	1:H:447:TYR:HE1	1.62	0.64
1:J:15:PHE:CE1	1:J:283:CYS:HA	2.33	0.64
1:J:564:GLY:HA2	1:K:554:LEU:HD21	1.80	0.64
1:K:15:PHE:CE1	1:K:283:CYS:HA	2.33	0.64
1:P:231:THR:HG21	1:P:249:ARG:HH11	1.63	0.63
1:P:329:LEU:HD22	2:l:133:PRO:HG2	1.80	0.63
1:P:560:LEU:O	1:P:565:VAL:HG21	1.97	0.63
1:Q:273:ARG:NH2	1:Q:453:LEU:HD11	2.12	0.63
1:U:232:ALA:CB	1:U:269:ARG:H	2.12	0.63
1:W:128:LEU:HD12	1:W:446:THR:HG23	1.80	0.63
2:n:15:ARG:H	2:n:15:ARG:HD2	1.62	0.63
2:o:93:PRO:HB3	2:p:100:THR:HG21	1.80	0.63
1:A:546:THR:CG2	1:A:547:PRO:HD3	2.27	0.63
1:B:58:ASP:O	1:B:59:VAL:CB	2.45	0.63
1:B:71:MSE:HE2	1:B:119:ILE:HD11	1.80	0.63
1:E:41:TRP:HZ3	1:E:42:ASP:HB3	1.61	0.63
1:F:48:TYR:O	1:F:49:THR:HB	1.99	0.63
1:G:158:TRP:CE3	1:G:173:CYS:SG	2.88	0.63
1:H:34:PHE:CZ	1:H:328:ARG:NH2	2.48	0.63
1:H:108:LYS:HD2	1:I:438:LEU:HD11	1.80	0.63
1:J:35:PHE:HE1	1:J:321:ARG:HH11	1.46	0.63
1:J:546:THR:CG2	1:J:547:PRO:HD3	2.28	0.63
1:K:57:PHE:HD2	1:K:330:ARG:CB	2.10	0.63
2:Z:42:MET:O	2:Z:42:MET:CG	2.30	0.63
2:f:28:VAL:CG2	2:f:96:LEU:HD12	2.22	0.63
2:g:74:ASN:HB2	2:g:75:PRO:HD3	1.79	0.63
2:j:74:ASN:HB2	2:j:75:PRO:HD3	1.79	0.63
1:N:15:PHE:CE1	1:N:283:CYS:HA	2.33	0.63
1:O:444:LEU:C	1:O:446:THR:N	2.55	0.63
1:P:158:TRP:CE3	1:P:173:CYS:SG	2.86	0.63
1:R:273:ARG:NH2	1:R:453:LEU:HD11	2.12	0.63
1:U:24:GLU:C	1:U:26:ARG:N	2.56	0.63
1:X:158:TRP:HB3	1:X:173:CYS:CA	2.26	0.63
2:q:64:GLU:HG3	2:q:66:PRO:HD2	1.79	0.63
2:s:15:ARG:H	2:s:15:ARG:HD2	1.63	0.63
1:B:556:TYR:OH	1:C:542:THR:HG21	1.99	0.63
1:F:246:TYR:CD2	1:F:511:ARG:HB3	2.34	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:161:ASN:C	1:H:161:ASN:HD22	2.03	0.63
1:I:48:TYR:O	1:I:49:THR:HB	1.98	0.63
1:J:78:VAL:HG12	1:J:79:LEU:N	2.13	0.63
1:J:236:GLN:HA	1:J:244:VAL:H	1.63	0.63
1:L:57:PHE:HD2	1:L:330:ARG:CB	2.10	0.63
2:Y:74:ASN:HB2	2:Y:75:PRO:HD3	1.79	0.63
2:c:110:ALA:O	2:c:113:ILE:HG13	1.96	0.63
1:M:12:LEU:O	1:M:16:ASP:HB2	1.99	0.63
1:X:12:LEU:O	1:X:16:ASP:HB2	1.98	0.63
1:D:35:PHE:HE1	1:D:321:ARG:HH11	1.46	0.63
1:D:71:MSE:HE2	1:D:119:ILE:HD11	1.80	0.63
1:D:95:MSE:HE1	1:D:99:ARG:CZ	2.28	0.63
1:F:95:MSE:HE1	1:F:99:ARG:CZ	2.28	0.63
1:G:78:VAL:HG12	1:G:79:LEU:N	2.13	0.63
1:H:5:GLU:HG2	1:H:6:ASN:N	2.12	0.63
1:I:78:VAL:HG12	1:I:79:LEU:N	2.13	0.63
1:K:144:ILE:HG12	1:K:447:TYR:CE1	2.34	0.63
1:N:325:ASP:OD2	2:v:136:SER:HB3	1.99	0.63
1:O:12:LEU:O	1:O:16:ASP:HB2	1.98	0.63
1:P:12:LEU:O	1:P:16:ASP:HB2	1.98	0.63
1:T:12:LEU:O	1:T:16:ASP:HB2	1.98	0.63
1:T:444:LEU:C	1:T:446:THR:N	2.55	0.63
1:V:232:ALA:CB	1:V:269:ARG:H	2.11	0.63
2:l:101:ALA:O	2:l:104:ILE:HG13	1.99	0.63
1:C:15:PHE:CE1	1:C:283:CYS:HA	2.33	0.63
1:C:95:MSE:HE1	1:C:99:ARG:CZ	2.28	0.63
1:C:144:ILE:HG12	1:C:447:TYR:CE1	2.34	0.63
1:D:57:PHE:HD2	1:D:330:ARG:CB	2.11	0.63
1:E:5:GLU:HG2	1:E:6:ASN:N	2.12	0.63
1:E:236:GLN:HA	1:E:244:VAL:H	1.63	0.63
1:F:144:ILE:HG12	1:F:447:TYR:CE1	2.34	0.63
1:G:12:LEU:O	1:G:16:ASP:HB2	1.99	0.63
1:G:144:ILE:HG12	1:G:447:TYR:HE1	1.63	0.63
1:H:12:LEU:O	1:H:16:ASP:HB2	1.99	0.63
1:J:528:LYS:NZ	1:J:560:LEU:HD21	2.13	0.63
1:K:5:GLU:HG2	1:K:6:ASN:N	2.12	0.63
1:K:12:LEU:O	1:K:16:ASP:HB2	1.99	0.63
1:L:236:GLN:HA	1:L:244:VAL:H	1.63	0.63
2:d:53:MET:HG2	2:d:67:TYR:CD1	2.34	0.63
1:P:34:PHE:HZ	1:P:328:ARG:HH22	1.36	0.63
1:Q:232:ALA:CB	1:Q:269:ARG:H	2.11	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:444:LEU:C	1:U:446:THR:N	2.52	0.63
2:u:15:ARG:H	2:u:15:ARG:HD2	1.64	0.63
1:A:144:ILE:HG12	1:A:447:TYR:CE1	2.34	0.63
1:A:161:ASN:HD22	1:A:161:ASN:C	2.03	0.63
1:C:246:TYR:CD2	1:C:511:ARG:HB3	2.34	0.63
1:D:41:TRP:HZ3	1:D:42:ASP:HB3	1.61	0.63
1:E:71:MSE:HE2	1:E:119:ILE:HD11	1.80	0.63
1:E:144:ILE:HG12	1:E:447:TYR:CE1	2.34	0.63
1:E:246:TYR:CD2	1:E:511:ARG:HB3	2.34	0.63
1:F:5:GLU:HG2	1:F:6:ASN:N	2.13	0.63
1:G:57:PHE:HD2	1:G:330:ARG:CB	2.10	0.63
1:I:95:MSE:HE1	1:I:99:ARG:CZ	2.28	0.63
1:J:48:TYR:O	1:J:49:THR:HB	1.98	0.63
1:K:144:ILE:HG12	1:K:447:TYR:HE1	1.63	0.63
2:f:74:ASN:HB2	2:f:75:PRO:HD3	1.79	0.63
1:N:273:ARG:HH22	1:N:453:LEU:CD1	2.11	0.63
1:R:15:PHE:CE1	1:R:283:CYS:HA	2.34	0.63
1:R:273:ARG:HH22	1:R:453:LEU:HD21	1.64	0.63
1:S:12:LEU:O	1:S:16:ASP:HB2	1.98	0.63
1:T:26:ARG:NH2	1:T:30:LYS:HD3	2.14	0.63
1:T:232:ALA:CB	1:T:269:ARG:H	2.11	0.63
1:V:158:TRP:N	1:V:158:TRP:CD1	2.63	0.63
1:V:158:TRP:CH2	1:V:302:PRO:HG3	2.34	0.63
1:V:398:PRO:HB3	1:W:395:PRO:HD2	1.81	0.63
1:X:575:GLN:O	1:X:579:MSE:HG2	1.99	0.63
2:n:17:LEU:HD12	2:n:37:VAL:HG23	1.81	0.63
1:C:48:TYR:O	1:C:49:THR:HB	1.98	0.63
1:C:57:PHE:HD2	1:C:330:ARG:CB	2.10	0.63
1:E:35:PHE:HE2	1:E:324:LYS:HZ3	1.42	0.63
1:F:144:ILE:HG12	1:F:447:TYR:HE1	1.62	0.63
1:F:236:GLN:HA	1:F:244:VAL:H	1.63	0.63
1:G:71:MSE:HE2	1:G:119:ILE:HD11	1.80	0.63
1:H:528:LYS:NZ	1:H:560:LEU:HD21	2.13	0.63
1:J:144:ILE:HG12	1:J:447:TYR:HE1	1.63	0.63
1:K:236:GLN:HA	1:K:244:VAL:H	1.63	0.63
1:L:15:PHE:CE1	1:L:283:CYS:HA	2.33	0.63
1:L:47:GLN:N	1:L:47:GLN:OE1	2.30	0.63
2:i:53:MET:HG2	2:i:67:TYR:CD1	2.34	0.63
1:M:15:PHE:HZ	1:M:283:CYS:SG	2.21	0.63
1:O:158:TRP:CH2	1:O:302:PRO:HG3	2.34	0.63
1:P:26:ARG:NH2	1:P:30:LYS:HD3	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:k:81:SER:HB3	2:v:42:ALA:HB1	1.80	0.63
1:A:35:PHE:HE1	1:A:321:ARG:HH11	1.46	0.63
1:A:48:TYR:O	1:A:49:THR:HB	1.98	0.63
1:C:99:ARG:O	1:C:103:ARG:HG3	1.99	0.63
1:D:47:GLN:N	1:D:47:GLN:OE1	2.30	0.63
1:D:48:TYR:O	1:D:49:THR:HB	1.98	0.63
1:D:99:ARG:O	1:D:103:ARG:HG3	1.99	0.63
1:D:546:THR:CG2	1:D:547:PRO:HD3	2.28	0.63
1:F:12:LEU:O	1:F:16:ASP:HB2	1.99	0.63
1:F:47:GLN:O	1:F:47:GLN:CD	2.42	0.63
1:L:158:TRP:CE3	1:L:173:CYS:SG	2.88	0.63
2:Z:74:ASN:HB2	2:Z:75:PRO:HD3	1.79	0.63
2:e:53:MET:HG2	2:e:67:TYR:CD1	2.34	0.63
2:g:53:MET:HG2	2:g:67:TYR:CD1	2.34	0.63
2:j:28:VAL:CG2	2:j:96:LEU:HD12	2.22	0.63
1:S:560:LEU:O	1:S:565:VAL:HG21	1.99	0.63
1:T:128:LEU:HD12	1:T:446:THR:HG23	1.81	0.63
1:V:12:LEU:O	1:V:16:ASP:HB2	1.98	0.63
1:V:15:PHE:CE1	1:V:283:CYS:HA	2.34	0.63
1:W:37:ARG:NH2	1:W:41:TRP:HB3	2.13	0.63
2:l:17:LEU:HD12	2:l:37:VAL:HG23	1.80	0.63
2:n:64:GLU:OE1	1:D:228:LYS:HG2	1.99	0.63
1:A:5:GLU:HG2	1:A:6:ASN:N	2.12	0.63
1:B:78:VAL:HG12	1:B:79:LEU:N	2.13	0.63
1:C:47:GLN:O	1:C:47:GLN:CD	2.42	0.63
1:D:236:GLN:HA	1:D:244:VAL:H	1.63	0.63
1:E:47:GLN:O	1:E:47:GLN:CD	2.42	0.63
1:G:99:ARG:O	1:G:103:ARG:HG3	1.99	0.63
1:H:334:MSE:HE3	1:I:404:MSE:CE	2.29	0.63
1:J:57:PHE:HD2	1:J:330:ARG:CB	2.10	0.63
1:L:337:ASN:HD21	1:L:401:ASN:HD22	1.47	0.63
2:h:43:GLN:C	2:h:45:ALA:H	2.07	0.63
2:i:74:ASN:HB2	2:i:75:PRO:HD3	1.79	0.63
1:Q:40:GLN:HG2	1:R:310:VAL:HG22	1.81	0.63
1:U:12:LEU:O	1:U:16:ASP:HB2	1.99	0.63
1:W:12:LEU:O	1:W:16:ASP:HB2	1.98	0.63
1:W:34:PHE:HE2	1:W:45:LEU:HG	1.64	0.63
2:p:64:GLU:HG3	2:p:66:PRO:HD2	1.79	0.63
1:E:99:ARG:O	1:E:103:ARG:HG3	1.99	0.63
1:F:528:LYS:NZ	1:F:560:LEU:HD21	2.13	0.63
1:G:144:ILE:HG12	1:G:447:TYR:CE1	2.34	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:528:LYS:NZ	1:K:560:LEU:HD21	2.13	0.63
1:K:564:GLY:HA2	1:L:554:LEU:HD21	1.80	0.63
1:L:99:ARG:O	1:L:103:ARG:HG3	1.99	0.63
2:b:74:ASN:HB2	2:b:75:PRO:HD3	1.79	0.63
2:i:43:GLN:C	2:i:45:ALA:H	2.07	0.63
1:M:26:ARG:NH2	1:M:30:LYS:HD3	2.13	0.62
1:N:34:PHE:HE2	1:N:45:LEU:HG	1.64	0.62
1:O:560:LEU:HD22	1:P:82:PRO:HG2	1.81	0.62
1:T:15:PHE:CE1	1:T:283:CYS:HA	2.34	0.62
1:T:24:GLU:C	1:T:26:ARG:N	2.57	0.62
1:T:440:MSE:O	1:T:444:LEU:HD22	1.99	0.62
1:W:15:PHE:CE1	1:W:283:CYS:HA	2.34	0.62
1:W:287:LEU:HD12	1:W:287:LEU:N	2.14	0.62
1:W:431:ALA:O	1:W:435:VAL:HG22	1.98	0.62
1:W:444:LEU:C	1:W:446:THR:N	2.54	0.62
2:k:101:ALA:O	2:k:104:ILE:HG13	1.98	0.62
1:B:246:TYR:CD2	1:B:511:ARG:HB3	2.34	0.62
1:F:35:PHE:HE1	1:F:321:ARG:HH11	1.46	0.62
1:H:144:ILE:HG12	1:H:447:TYR:CE1	2.34	0.62
1:I:246:TYR:CD2	1:I:511:ARG:HB3	2.34	0.62
1:L:12:LEU:O	1:L:16:ASP:HB2	1.99	0.62
1:N:37:ARG:HB3	1:N:37:ARG:HH21	1.64	0.62
1:O:34:PHE:HE2	1:O:45:LEU:HG	1.64	0.62
1:P:37:ARG:HB3	1:P:37:ARG:HH21	1.62	0.62
1:U:34:PHE:HE2	1:U:45:LEU:HG	1.64	0.62
1:W:24:GLU:C	1:W:26:ARG:N	2.56	0.62
1:X:24:GLU:C	1:X:26:ARG:N	2.55	0.62
1:A:47:GLN:O	1:A:47:GLN:CD	2.42	0.62
1:A:158:TRP:CE3	1:A:173:CYS:SG	2.88	0.62
1:B:35:PHE:HE1	1:B:321:ARG:HH11	1.46	0.62
1:B:47:GLN:OE1	1:B:47:GLN:N	2.30	0.62
1:B:144:ILE:HG12	1:B:447:TYR:CE1	2.34	0.62
1:B:546:THR:CG2	1:B:547:PRO:HD3	2.28	0.62
1:C:12:LEU:O	1:C:16:ASP:HB2	1.99	0.62
1:D:78:VAL:HG12	1:D:79:LEU:N	2.13	0.62
1:D:144:ILE:HG12	1:D:447:TYR:CE1	2.34	0.62
1:E:337:ASN:HD21	1:E:401:ASN:HD22	1.47	0.62
1:F:99:ARG:O	1:F:103:ARG:HG3	1.99	0.62
1:G:47:GLN:O	1:G:47:GLN:CD	2.42	0.62
1:J:99:ARG:O	1:J:103:ARG:HG3	1.99	0.62
1:K:47:GLN:O	1:K:47:GLN:CD	2.42	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:329:LEU:HD22	2:i:142:PRO:HG2	1.80	0.62
1:K:337:ASN:HD21	1:K:401:ASN:HD22	1.47	0.62
2:e:43:GLN:C	2:e:45:ALA:H	2.07	0.62
1:M:444:LEU:C	1:M:446:THR:N	2.54	0.62
1:O:273:ARG:HH22	1:O:453:LEU:CD1	2.10	0.62
1:Q:15:PHE:HZ	1:Q:283:CYS:SG	2.22	0.62
1:U:158:TRP:HB3	1:U:173:CYS:CA	2.27	0.62
1:W:15:PHE:HZ	1:W:283:CYS:SG	2.22	0.62
1:X:94:LEU:HA	1:X:97:MSE:HE2	1.81	0.62
1:A:78:VAL:HG12	1:A:79:LEU:N	2.13	0.62
1:E:48:TYR:O	1:E:49:THR:HB	1.98	0.62
1:H:99:ARG:O	1:H:103:ARG:HG3	1.99	0.62
1:I:144:ILE:HG12	1:I:447:TYR:CE1	2.34	0.62
1:L:144:ILE:HG12	1:L:447:TYR:CE1	2.34	0.62
1:L:546:THR:CG2	1:L:547:PRO:HD3	2.27	0.62
2:a:53:MET:HG2	2:a:67:TYR:CD1	2.34	0.62
1:N:89:ASP:HA	1:V:561:ASP:CB	2.26	0.62
1:O:37:ARG:NH2	1:O:41:TRP:HB3	2.14	0.62
1:Q:15:PHE:CE1	1:Q:283:CYS:HA	2.34	0.62
2:s:100:THR:HG21	2:t:93:PRO:HB3	1.82	0.62
1:B:47:GLN:O	1:B:47:GLN:CD	2.42	0.62
1:C:5:GLU:HG2	1:C:6:ASN:N	2.12	0.62
1:G:246:TYR:CD2	1:G:511:ARG:HB3	2.34	0.62
1:J:47:GLN:O	1:J:47:GLN:CD	2.42	0.62
1:K:99:ARG:O	1:K:103:ARG:HG3	1.99	0.62
1:L:35:PHE:HE1	1:L:321:ARG:HH11	1.46	0.62
1:L:48:TYR:O	1:L:49:THR:HB	1.98	0.62
2:i:78:GLU:CG	2:i:79:GLY:N	2.63	0.62
2:j:53:MET:HG2	2:j:67:TYR:CD1	2.34	0.62
1:P:15:PHE:CZ	1:P:283:CYS:HA	2.35	0.62
1:Q:34:PHE:HE2	1:Q:45:LEU:HG	1.65	0.62
1:T:37:ARG:HB3	1:T:37:ARG:HH21	1.63	0.62
1:U:431:ALA:O	1:U:435:VAL:HG22	2.00	0.62
1:V:24:GLU:C	1:V:26:ARG:N	2.57	0.62
1:W:560:LEU:O	1:W:565:VAL:HG21	1.97	0.62
1:X:232:ALA:CB	1:X:269:ARG:H	2.12	0.62
2:o:17:LEU:HD12	2:o:37:VAL:HG23	1.80	0.62
1:B:12:LEU:O	1:B:16:ASP:HB2	1.99	0.62
1:C:35:PHE:HE1	1:C:321:ARG:HH11	1.46	0.62
1:C:158:TRP:CE3	1:C:173:CYS:SG	2.88	0.62
1:D:12:LEU:O	1:D:16:ASP:HB2	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:372:TYR:CE2	1:F:348:LYS:HB2	2.34	0.62
1:H:546:THR:CG2	1:H:547:PRO:HD3	2.27	0.62
1:I:99:ARG:O	1:I:103:ARG:HG3	1.99	0.62
1:L:144:ILE:HG12	1:L:447:TYR:HE1	1.63	0.62
2:a:43:GLN:C	2:a:45:ALA:H	2.07	0.62
2:a:74:ASN:HB2	2:a:75:PRO:HD3	1.79	0.62
2:f:43:GLN:C	2:f:45:ALA:H	2.07	0.62
1:P:47:GLN:HG2	1:P:48:TYR:H	1.64	0.62
1:P:444:LEU:C	1:P:446:THR:N	2.53	0.62
1:Q:12:LEU:O	1:Q:16:ASP:HB2	1.99	0.62
1:R:232:ALA:CB	1:R:269:ARG:H	2.12	0.62
1:V:78:VAL:HG22	1:V:444:LEU:HD21	1.81	0.62
1:A:12:LEU:O	1:A:16:ASP:HB2	1.99	0.62
1:C:337:ASN:HD21	1:C:401:ASN:HD22	1.47	0.62
1:C:546:THR:CG2	1:C:547:PRO:HD3	2.27	0.62
1:J:144:ILE:HG12	1:J:447:TYR:CE1	2.34	0.62
1:J:246:TYR:CD2	1:J:511:ARG:HB3	2.34	0.62
1:K:48:TYR:O	1:K:49:THR:HB	1.98	0.62
2:Z:43:GLN:C	2:Z:45:ALA:H	2.07	0.62
2:b:53:MET:HG2	2:b:67:TYR:CD1	2.34	0.62
2:f:53:MET:HG2	2:f:67:TYR:CD1	2.34	0.62
1:R:440:MSE:O	1:R:444:LEU:HD22	2.00	0.62
1:V:26:ARG:NH2	1:V:30:LYS:HD3	2.13	0.62
1:W:273:ARG:NH2	1:W:453:LEU:HD11	2.11	0.62
1:A:246:TYR:CD2	1:A:511:ARG:HB3	2.34	0.62
1:A:556:TYR:OH	1:B:542:THR:HG21	2.00	0.62
1:E:12:LEU:O	1:E:16:ASP:HB2	1.99	0.62
1:J:337:ASN:HD21	1:J:401:ASN:HD22	1.47	0.62
1:M:34:PHE:HE2	1:M:45:LEU:HG	1.65	0.62
1:R:158:TRP:HB3	1:R:173:CYS:CA	2.27	0.62
1:S:444:LEU:C	1:S:446:THR:N	2.53	0.62
1:U:231:THR:HG21	1:U:249:ARG:HH11	1.64	0.62
1:A:407:ALA:HB1	1:L:334:MSE:HE1	1.81	0.62
1:D:47:GLN:O	1:D:47:GLN:CD	2.42	0.62
1:D:108:LYS:HD2	1:F:438:LEU:HD11	1.82	0.62
1:D:158:TRP:CE3	1:D:173:CYS:SG	2.88	0.62
1:D:246:TYR:CD2	1:D:511:ARG:HB3	2.34	0.62
1:F:182:ASN:ND2	1:G:171:ARG:HH21	1.98	0.62
1:G:287:LEU:HD12	1:G:287:LEU:N	2.15	0.62
1:H:246:TYR:CD2	1:H:511:ARG:HB3	2.34	0.62
1:K:246:TYR:CD2	1:K:511:ARG:HB3	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:287:LEU:HD12	1:L:287:LEU:N	2.15	0.62
2:a:78:GLU:CG	2:a:79:GLY:N	2.63	0.62
1:M:431:ALA:O	1:M:435:VAL:HG22	1.99	0.62
1:P:15:PHE:HZ	1:P:283:CYS:SG	2.22	0.62
1:T:231:THR:HG21	1:T:249:ARG:HH11	1.62	0.62
1:C:144:ILE:HG12	1:C:447:TYR:HE1	1.63	0.62
1:J:575:GLN:O	1:J:579:MSE:HG2	2.00	0.62
1:L:71:MSE:HE2	1:L:119:ILE:HD11	1.80	0.62
2:Y:34:LEU:O	2:Y:35:THR:HG22	2.00	0.62
2:Y:43:GLN:C	2:Y:45:ALA:H	2.07	0.62
2:Z:53:MET:HG2	2:Z:67:TYR:CD1	2.34	0.62
2:c:53:MET:HG2	2:c:67:TYR:CD1	2.34	0.62
2:h:53:MET:HG2	2:h:67:TYR:CD1	2.34	0.62
1:N:276:VAL:HG23	1:N:293:ILE:HG23	1.81	0.62
1:V:34:PHE:HE2	1:V:45:LEU:HG	1.64	0.62
1:V:210:PRO:HD2	1:V:211:TRP:CE3	2.35	0.62
1:W:37:ARG:HB3	1:W:37:ARG:HH21	1.65	0.62
1:A:287:LEU:N	1:A:287:LEU:HD12	2.15	0.62
1:C:287:LEU:N	1:C:287:LEU:HD12	2.15	0.62
1:F:330:ARG:O	1:F:334:MSE:HB2	2.00	0.62
1:I:12:LEU:O	1:I:16:ASP:HB2	1.99	0.62
1:J:12:LEU:O	1:J:16:ASP:HB2	1.99	0.62
2:j:53:MET:O	2:j:69:PHE:HE1	1.83	0.62
1:O:440:MSE:O	1:O:444:LEU:HD22	2.00	0.61
1:Q:138:THR:H	1:Q:143:VAL:HG22	1.63	0.61
1:R:334:MSE:SE	1:X:404:MSE:HE1	2.50	0.61
1:W:5:GLU:HG2	1:W:6:ASN:H	1.65	0.61
1:W:276:VAL:HG23	1:W:293:ILE:HG23	1.82	0.61
1:W:440:MSE:O	1:W:444:LEU:HD22	2.00	0.61
1:X:210:PRO:HD2	1:X:211:TRP:CE3	2.35	0.61
1:A:575:GLN:O	1:A:579:MSE:HG2	2.00	0.61
1:H:47:GLN:O	1:H:47:GLN:CD	2.42	0.61
1:H:287:LEU:HD12	1:H:287:LEU:N	2.15	0.61
1:I:287:LEU:N	1:I:287:LEU:HD12	2.15	0.61
1:L:47:GLN:O	1:L:47:GLN:CD	2.42	0.61
1:L:78:VAL:HG12	1:L:79:LEU:N	2.13	0.61
1:L:330:ARG:O	1:L:334:MSE:HB2	2.00	0.61
1:L:575:GLN:O	1:L:579:MSE:HG2	2.00	0.61
2:Y:53:MET:HG2	2:Y:67:TYR:CD1	2.34	0.61
2:Y:53:MET:O	2:Y:69:PHE:HE1	1.83	0.61
2:Z:34:LEU:O	2:Z:35:THR:HG22	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:d:43:GLN:C	2:d:45:ALA:H	2.07	0.61
1:M:560:LEU:O	1:M:565:VAL:HG21	1.98	0.61
1:N:5:GLU:HG2	1:N:6:ASN:H	1.65	0.61
1:P:24:GLU:C	1:P:26:ARG:N	2.57	0.61
3:P:719:HOH:O	1:Q:430:VAL:CG1	2.47	0.61
1:Q:34:PHE:HZ	1:Q:328:ARG:HH22	1.40	0.61
1:Q:287:LEU:N	1:Q:287:LEU:HD12	2.16	0.61
1:S:15:PHE:CE1	1:S:283:CYS:HA	2.35	0.61
1:T:5:GLU:HG2	1:T:6:ASN:H	1.66	0.61
1:T:15:PHE:HZ	1:T:283:CYS:SG	2.23	0.61
1:T:94:LEU:HA	1:T:97:MSE:HE2	1.81	0.61
1:T:273:ARG:NH2	1:T:453:LEU:HD11	2.13	0.61
1:A:398:PRO:HB3	1:L:395:PRO:HD2	1.81	0.61
1:B:287:LEU:HD12	1:B:287:LEU:N	2.15	0.61
1:C:41:TRP:HE3	1:C:42:ASP:CA	2.14	0.61
1:C:47:GLN:OE1	1:C:47:GLN:N	2.30	0.61
1:E:287:LEU:HD12	1:E:287:LEU:N	2.15	0.61
1:H:48:TYR:O	1:H:49:THR:HB	1.98	0.61
1:H:337:ASN:HD21	1:H:401:ASN:HD22	1.47	0.61
1:I:47:GLN:O	1:I:47:GLN:CD	2.42	0.61
1:J:158:TRP:CE3	1:J:173:CYS:SG	2.88	0.61
2:g:43:GLN:C	2:g:45:ALA:H	2.07	0.61
2:i:53:MET:O	2:i:69:PHE:HE1	1.83	0.61
1:M:78:VAL:HG22	1:M:444:LEU:HD21	1.82	0.61
1:M:89:ASP:HA	1:N:561:ASP:HB2	1.82	0.61
1:M:273:ARG:HH22	1:M:453:LEU:CD1	2.10	0.61
1:N:440:MSE:O	1:N:444:LEU:HD22	1.99	0.61
1:R:5:GLU:HG2	1:R:6:ASN:H	1.65	0.61
1:T:158:TRP:CE3	1:T:173:CYS:SG	2.87	0.61
1:U:210:PRO:HD2	1:U:211:TRP:CE3	2.36	0.61
1:V:128:LEU:HD12	1:V:446:THR:HG23	1.82	0.61
2:q:8:ASP:CB	2:r:67:PRO:HG2	2.30	0.61
2:q:100:THR:HG21	2:r:93:PRO:HB3	1.82	0.61
1:B:99:ARG:O	1:B:103:ARG:HG3	1.99	0.61
1:B:575:GLN:O	1:B:579:MSE:HG2	2.00	0.61
1:C:78:VAL:HG12	1:C:79:LEU:N	2.13	0.61
1:C:330:ARG:O	1:C:334:MSE:HB2	2.00	0.61
1:E:330:ARG:O	1:E:334:MSE:HB2	2.00	0.61
1:E:546:THR:CG2	1:E:547:PRO:HD3	2.27	0.61
2:d:34:LEU:O	2:d:35:THR:HG22	2.00	0.61
2:e:53:MET:O	2:e:69:PHE:HE1	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:273:ARG:NH2	1:N:453:LEU:HD11	2.14	0.61
1:O:15:PHE:CE1	1:O:283:CYS:HA	2.35	0.61
1:R:24:GLU:C	1:R:26:ARG:N	2.55	0.61
1:T:34:PHE:HE2	1:T:45:LEU:HG	1.64	0.61
1:F:41:TRP:HZ3	1:F:42:ASP:HB3	1.61	0.61
1:H:78:VAL:HG12	1:H:79:LEU:N	2.13	0.61
1:I:337:ASN:HD21	1:I:401:ASN:HD22	1.47	0.61
1:I:575:GLN:O	1:I:579:MSE:HG2	2.00	0.61
1:L:246:TYR:CD2	1:L:511:ARG:HB3	2.34	0.61
1:O:78:VAL:HG22	1:O:444:LEU:HD21	1.83	0.61
1:O:138:THR:H	1:O:143:VAL:HG22	1.66	0.61
1:Q:329:LEU:HD22	2:n:133:PRO:HG2	1.82	0.61
1:R:34:PHE:HE2	1:R:45:LEU:HG	1.64	0.61
1:R:37:ARG:NH2	1:R:41:TRP:HB3	2.15	0.61
1:S:78:VAL:CG2	1:S:444:LEU:HD11	2.22	0.61
1:T:273:ARG:NH2	1:T:453:LEU:HD21	2.15	0.61
1:U:158:TRP:CH2	1:U:302:PRO:HG3	2.35	0.61
1:U:440:MSE:O	1:U:444:LEU:HD22	2.01	0.61
1:X:26:ARG:NH2	1:X:30:LYS:HD3	2.15	0.61
1:A:99:ARG:O	1:A:103:ARG:HG3	1.99	0.61
1:A:337:ASN:HD21	1:A:401:ASN:HD22	1.47	0.61
1:B:48:TYR:O	1:B:49:THR:HB	1.98	0.61
1:B:586:THR:N	1:B:587:PRO:HD3	2.16	0.61
1:E:586:THR:N	1:E:587:PRO:HD3	2.16	0.61
1:F:337:ASN:HD21	1:F:401:ASN:HD22	1.47	0.61
1:F:586:THR:N	1:F:587:PRO:HD3	2.16	0.61
1:G:35:PHE:HE1	1:G:321:ARG:HH11	1.46	0.61
1:H:158:TRP:CE3	1:H:173:CYS:SG	2.88	0.61
1:K:35:PHE:HE1	1:K:321:ARG:HH11	1.46	0.61
2:g:34:LEU:O	2:g:35:THR:HG22	2.00	0.61
2:h:34:LEU:O	2:h:35:THR:HG22	2.00	0.61
1:M:273:ARG:NH2	1:M:453:LEU:HD11	2.14	0.61
1:N:15:PHE:CZ	1:N:283:CYS:HA	2.36	0.61
1:P:440:MSE:O	1:P:444:LEU:HD22	2.00	0.61
1:Q:47:GLN:HG2	1:Q:48:TYR:H	1.66	0.61
1:Q:78:VAL:CG2	1:Q:444:LEU:HD11	2.23	0.61
1:R:12:LEU:O	1:R:16:ASP:HB2	2.00	0.61
1:S:5:GLU:HG2	1:S:6:ASN:H	1.65	0.61
1:V:273:ARG:NH2	1:V:453:LEU:HD11	2.14	0.61
1:W:78:VAL:CG2	1:W:444:LEU:HD11	2.21	0.61
2:m:15:ARG:H	2:m:15:ARG:HD2	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:337:ASN:HD21	1:B:401:ASN:HD22	1.47	0.61
1:C:586:THR:N	1:C:587:PRO:HD3	2.16	0.61
1:D:330:ARG:O	1:D:334:MSE:HB2	2.00	0.61
1:D:586:THR:N	1:D:587:PRO:HD3	2.16	0.61
1:E:575:GLN:O	1:E:579:MSE:HG2	2.00	0.61
1:H:330:ARG:O	1:H:334:MSE:HB2	2.00	0.61
1:I:586:THR:N	1:I:587:PRO:HD3	2.16	0.61
1:K:395:PRO:HD2	1:L:398:PRO:HB3	1.83	0.61
1:K:575:GLN:O	1:K:579:MSE:HG2	2.00	0.61
1:L:586:THR:N	1:L:587:PRO:HD3	2.16	0.61
1:M:5:GLU:HG2	1:M:6:ASN:H	1.66	0.61
1:Q:210:PRO:HD2	1:Q:211:TRP:CE3	2.36	0.61
1:R:287:LEU:HD12	1:R:287:LEU:N	2.15	0.61
1:S:210:PRO:HD2	1:S:211:TRP:CE3	2.35	0.61
1:S:287:LEU:N	1:S:287:LEU:HD12	2.15	0.61
1:T:15:PHE:CZ	1:T:283:CYS:HA	2.35	0.61
1:T:560:LEU:O	1:T:565:VAL:HG21	1.99	0.61
1:U:5:GLU:HG2	1:U:6:ASN:H	1.65	0.61
1:U:128:LEU:HD12	1:U:446:THR:HG23	1.82	0.61
1:V:158:TRP:CE3	1:V:173:CYS:SG	2.86	0.61
1:W:210:PRO:HD2	1:W:211:TRP:CE3	2.36	0.61
2:n:64:GLU:HG2	1:D:277:TYR:OH	2.00	0.61
1:F:287:LEU:N	1:F:287:LEU:HD12	2.15	0.61
1:G:54:ARG:HB2	2:d:146:GLY:HA3	1.83	0.61
1:G:586:THR:N	1:G:587:PRO:HD3	2.16	0.61
1:I:330:ARG:O	1:I:334:MSE:HB2	2.00	0.61
1:J:41:TRP:HE3	1:J:42:ASP:CA	2.14	0.61
1:J:182:ASN:ND2	1:K:171:ARG:HH21	1.98	0.61
1:K:47:GLN:OE1	1:K:47:GLN:N	2.30	0.61
1:K:287:LEU:N	1:K:287:LEU:HD12	2.15	0.61
2:a:34:LEU:O	2:a:35:THR:HG22	2.00	0.61
1:N:15:PHE:HZ	1:N:283:CYS:SG	2.18	0.61
1:N:41:TRP:CE3	1:N:42:ASP:HB3	2.36	0.61
1:O:5:GLU:HG2	1:O:6:ASN:H	1.65	0.61
1:P:564:GLY:HA2	1:Q:554:LEU:HD21	1.81	0.61
1:R:158:TRP:CH2	1:R:302:PRO:HG3	2.36	0.61
1:V:273:ARG:NH2	1:V:453:LEU:HD21	2.16	0.61
1:X:273:ARG:NH2	1:X:453:LEU:HD11	2.13	0.61
2:o:67:PRO:HG2	2:p:8:ASP:CB	2.31	0.61
1:D:337:ASN:HD21	1:D:401:ASN:HD22	1.47	0.61
1:H:41:TRP:HE3	1:H:42:ASP:CA	2.14	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:g:53:MET:O	2:g:69:PHE:HE1	1.83	0.61
1:M:15:PHE:CE1	1:M:283:CYS:HA	2.35	0.61
1:M:246:TYR:CD2	1:M:511:ARG:HB2	2.36	0.61
1:N:78:VAL:HG22	1:N:444:LEU:HD21	1.83	0.61
1:O:128:LEU:HD12	1:O:446:THR:HG23	1.83	0.61
1:P:5:GLU:HG2	1:P:6:ASN:H	1.65	0.61
1:T:47:GLN:HG2	1:T:48:TYR:H	1.65	0.61
1:V:440:MSE:O	1:V:444:LEU:HD22	2.00	0.61
1:X:5:GLU:HG2	1:X:6:ASN:H	1.65	0.61
2:n:15:ARG:HD2	2:n:15:ARG:N	2.16	0.61
2:o:17:LEU:HD11	2:o:36:ALA:CB	2.31	0.61
1:D:287:LEU:HD12	1:D:287:LEU:N	2.15	0.61
1:E:233:PHE:CE2	1:E:249:ARG:HD3	2.36	0.61
1:H:233:PHE:CE2	1:H:249:ARG:HD3	2.36	0.61
1:J:233:PHE:CE2	1:J:249:ARG:HD3	2.36	0.61
1:J:287:LEU:HD12	1:J:287:LEU:N	2.15	0.61
2:b:43:GLN:C	2:b:45:ALA:H	2.07	0.61
2:h:53:MET:O	2:h:69:PHE:HE1	1.83	0.61
1:N:47:GLN:HG2	1:N:48:TYR:H	1.66	0.61
1:P:41:TRP:CE3	1:P:42:ASP:HB3	2.36	0.61
1:R:15:PHE:CZ	1:R:283:CYS:HA	2.36	0.61
1:S:379:GLU:O	1:S:380:ASN:HB2	2.01	0.61
1:U:15:PHE:CE1	1:U:283:CYS:HA	2.36	0.61
1:V:15:PHE:CZ	1:V:283:CYS:HA	2.36	0.61
1:X:34:PHE:HE2	1:X:45:LEU:HG	1.64	0.61
1:A:330:ARG:O	1:A:334:MSE:HB2	2.00	0.61
1:G:330:ARG:O	1:G:334:MSE:HB2	2.00	0.61
2:Z:102:PRO:HB3	2:a:109:THR:HG21	1.82	0.61
2:e:34:LEU:O	2:e:35:THR:HG22	2.00	0.61
2:f:53:MET:O	2:f:69:PHE:HE1	1.83	0.61
1:M:47:GLN:HG2	1:M:48:TYR:H	1.65	0.60
1:M:128:LEU:HD12	1:M:446:THR:HG23	1.82	0.60
1:M:210:PRO:HD2	1:M:211:TRP:CE3	2.36	0.60
1:N:390:ALA:CB	1:V:387:GLN:HB3	2.30	0.60
1:R:78:VAL:HG22	1:R:444:LEU:HD21	1.82	0.60
1:T:334:MSE:SE	1:W:404:MSE:HE1	2.51	0.60
1:U:41:TRP:CE3	1:U:42:ASP:HB3	2.36	0.60
1:X:287:LEU:HD12	1:X:287:LEU:N	2.16	0.60
1:H:42:ASP:OD2	2:f:145:SER:O	2.19	0.60
1:H:575:GLN:O	1:H:579:MSE:HG2	2.00	0.60
1:M:542:THR:HG21	1:N:556:TYR:OH	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:237:ASP:H	1:O:243:PRO:HA	1.65	0.60
1:O:276:VAL:HG23	1:O:293:ILE:HG23	1.83	0.60
1:P:34:PHE:HE2	1:P:45:LEU:HG	1.65	0.60
1:P:210:PRO:HD2	1:P:211:TRP:CE3	2.36	0.60
1:P:287:LEU:HD12	1:P:287:LEU:N	2.15	0.60
1:Q:332:MSE:SE	2:n:132:MET:HA	2.50	0.60
1:R:210:PRO:HD2	1:R:211:TRP:CE3	2.36	0.60
1:S:542:THR:HG21	1:U:556:TYR:OH	2.01	0.60
1:T:37:ARG:NH2	1:T:41:TRP:HB3	2.15	0.60
1:T:41:TRP:CE3	1:T:42:ASP:HB3	2.37	0.60
1:T:564:GLY:HA2	1:W:554:LEU:HD21	1.82	0.60
1:V:165:MSE:HE3	1:V:304:PHE:HB2	1.82	0.60
1:V:287:LEU:N	1:V:287:LEU:HD12	2.16	0.60
1:A:234:ILE:CG1	1:A:267:ALA:HB3	2.32	0.60
1:B:234:ILE:CG1	1:B:267:ALA:HB3	2.31	0.60
1:C:233:PHE:CE2	1:C:249:ARG:HD3	2.36	0.60
1:H:586:THR:N	1:H:587:PRO:HD3	2.16	0.60
1:I:233:PHE:CE2	1:I:249:ARG:HD3	2.36	0.60
1:I:372:TYR:CE2	1:J:348:LYS:HB2	2.35	0.60
1:K:586:THR:N	1:K:587:PRO:HD3	2.16	0.60
1:L:233:PHE:CE2	1:L:249:ARG:HD3	2.36	0.60
1:L:234:ILE:CG1	1:L:267:ALA:HB3	2.32	0.60
2:d:78:GLU:CG	2:d:79:GLY:N	2.63	0.60
1:M:37:ARG:NH2	1:M:41:TRP:HB3	2.16	0.60
1:O:246:TYR:CD2	1:O:511:ARG:HB2	2.36	0.60
1:O:287:LEU:HD12	1:O:287:LEU:N	2.16	0.60
1:P:246:TYR:CD2	1:P:511:ARG:HB2	2.36	0.60
1:Q:37:ARG:NH2	1:Q:41:TRP:HB3	2.17	0.60
1:S:276:VAL:HG23	1:S:293:ILE:HG23	1.83	0.60
1:V:276:VAL:HG23	1:V:293:ILE:HG23	1.83	0.60
1:W:273:ARG:NH2	1:W:453:LEU:HD21	2.16	0.60
2:l:15:ARG:HD2	2:l:15:ARG:N	2.16	0.60
1:B:330:ARG:O	1:B:334:MSE:HB2	2.00	0.60
1:J:234:ILE:CG1	1:J:267:ALA:HB3	2.31	0.60
1:J:586:THR:N	1:J:587:PRO:HD3	2.16	0.60
1:K:561:ASP:CB	1:L:89:ASP:HA	2.28	0.60
2:c:53:MET:O	2:c:69:PHE:HE1	1.83	0.60
2:i:28:VAL:HG22	2:i:93:PHE:O	2.02	0.60
1:O:15:PHE:CZ	1:O:283:CYS:HA	2.36	0.60
1:P:273:ARG:NH2	1:P:453:LEU:HD11	2.14	0.60
1:Q:15:PHE:CZ	1:Q:283:CYS:HA	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:158:TRP:O	1:R:160:SER:N	2.34	0.60
1:T:78:VAL:CG2	1:T:444:LEU:HD11	2.22	0.60
1:T:577:ILE:HA	1:T:582:LYS:HB3	1.83	0.60
1:V:246:TYR:CD2	1:V:511:ARG:HB2	2.35	0.60
2:o:15:ARG:H	2:o:15:ARG:HD2	1.66	0.60
1:C:154:SER:O	1:C:204:PRO:HB3	2.02	0.60
1:E:161:ASN:C	1:E:161:ASN:ND2	2.59	0.60
2:b:28:VAL:HG22	2:b:93:PHE:O	2.02	0.60
2:c:43:GLN:C	2:c:45:ALA:H	2.07	0.60
2:e:137:TYR:CD1	2:e:141:MET:HG2	2.37	0.60
2:g:28:VAL:HG22	2:g:93:PHE:O	2.02	0.60
1:M:276:VAL:HG23	1:M:293:ILE:HG23	1.82	0.60
1:M:440:MSE:O	1:M:444:LEU:HD22	2.01	0.60
1:P:273:ARG:HH22	1:P:453:LEU:CD1	2.11	0.60
1:R:78:VAL:HG11	1:R:444:LEU:HG	1.83	0.60
1:V:37:ARG:NH2	1:V:41:TRP:HB3	2.15	0.60
1:W:41:TRP:CE3	1:W:42:ASP:HB3	2.37	0.60
1:A:586:THR:N	1:A:587:PRO:HD3	2.16	0.60
1:B:233:PHE:CE2	1:B:249:ARG:HD3	2.36	0.60
1:D:575:GLN:O	1:D:579:MSE:HG2	2.00	0.60
1:E:199:PRO:HB3	1:E:282:THR:HG22	1.84	0.60
1:F:154:SER:O	1:F:204:PRO:HB3	2.02	0.60
1:F:575:GLN:O	1:F:579:MSE:HG2	2.00	0.60
1:G:154:SER:O	1:G:204:PRO:HB3	2.02	0.60
1:I:41:TRP:HE3	1:I:42:ASP:CA	2.14	0.60
1:K:330:ARG:O	1:K:334:MSE:HB2	2.00	0.60
1:L:154:SER:O	1:L:204:PRO:HB3	2.02	0.60
2:a:137:TYR:CD1	2:a:141:MET:HG2	2.37	0.60
2:d:137:TYR:CD1	2:d:141:MET:HG2	2.37	0.60
2:h:28:VAL:HG22	2:h:93:PHE:O	2.02	0.60
2:i:32:ALA:O	2:i:33:THR:HG22	1.92	0.60
2:i:34:LEU:O	2:i:35:THR:HG22	2.00	0.60
1:N:379:GLU:O	1:N:380:ASN:HB2	2.02	0.60
1:O:5:GLU:HG2	1:O:6:ASN:N	2.16	0.60
1:Q:128:LEU:HD12	1:Q:446:THR:HG23	1.83	0.60
1:Q:236:GLN:CB	1:Q:265:LYS:HG2	2.32	0.60
1:R:15:PHE:HZ	1:R:283:CYS:SG	2.24	0.60
1:S:47:GLN:HG2	1:S:48:TYR:H	1.66	0.60
1:S:246:TYR:CD2	1:S:511:ARG:HB2	2.36	0.60
1:T:78:VAL:HG22	1:T:444:LEU:HD21	1.84	0.60
1:T:210:PRO:HD2	1:T:211:TRP:CE3	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:236:GLN:CB	1:T:265:LYS:HG2	2.32	0.60
1:U:577:ILE:HA	1:U:582:LYS:HB3	1.84	0.60
1:W:47:GLN:HG2	1:W:48:TYR:H	1.67	0.60
1:X:37:ARG:NH2	1:X:41:TRP:HB3	2.17	0.60
1:X:440:MSE:O	1:X:444:LEU:HD22	2.02	0.60
1:A:395:PRO:HD2	1:B:398:PRO:HB3	1.84	0.60
1:B:154:SER:O	1:B:204:PRO:HB3	2.02	0.60
1:C:567:MSE:SE	1:E:576:LEU:HD13	2.52	0.60
1:C:575:GLN:O	1:C:579:MSE:HG2	2.00	0.60
1:D:233:PHE:CE2	1:D:249:ARG:HD3	2.36	0.60
1:E:158:TRP:CE3	1:E:173:CYS:SG	2.88	0.60
1:F:47:GLN:CD	1:F:47:GLN:H	2.10	0.60
1:F:161:ASN:C	1:F:161:ASN:ND2	2.59	0.60
1:H:154:SER:O	1:H:204:PRO:HB3	2.02	0.60
1:J:598:GLN:HB2	1:J:601:GLN:HB2	1.84	0.60
2:Z:53:MET:O	2:Z:69:PHE:HE1	1.83	0.60
2:b:53:MET:O	2:b:69:PHE:HE1	1.83	0.60
2:b:137:TYR:CD1	2:b:141:MET:HG2	2.37	0.60
2:j:32:ALA:O	2:j:33:THR:HG22	1.92	0.60
1:N:210:PRO:HD2	1:N:211:TRP:CE3	2.35	0.60
1:N:398:PRO:HB3	1:V:395:PRO:HD2	1.84	0.60
1:S:34:PHE:HE2	1:S:45:LEU:HG	1.65	0.60
1:S:236:GLN:CB	1:S:265:LYS:HG2	2.32	0.60
1:X:15:PHE:CE1	1:X:283:CYS:HA	2.36	0.60
1:X:431:ALA:O	1:X:435:VAL:HG22	2.02	0.60
2:k:15:ARG:HD2	2:k:15:ARG:H	1.65	0.60
1:A:41:TRP:HE3	1:A:42:ASP:CA	2.14	0.60
1:A:154:SER:O	1:A:204:PRO:HB3	2.02	0.60
1:A:233:PHE:CE2	1:A:249:ARG:HD3	2.36	0.60
1:C:598:GLN:HB2	1:C:601:GLN:HB2	1.84	0.60
1:D:47:GLN:CD	1:D:47:GLN:H	2.10	0.60
1:E:54:ARG:HB2	2:b:146:GLY:HA3	1.84	0.60
1:F:199:PRO:HB3	1:F:282:THR:HG22	1.84	0.60
1:F:234:ILE:CG1	1:F:267:ALA:HB3	2.32	0.60
1:G:41:TRP:HE3	1:G:42:ASP:CA	2.14	0.60
1:G:108:LYS:HD2	1:H:438:LEU:HD11	1.82	0.60
1:G:598:GLN:HB2	1:G:601:GLN:HB2	1.84	0.60
1:I:154:SER:O	1:I:204:PRO:HB3	2.02	0.60
2:f:34:LEU:O	2:f:35:THR:HG22	2.00	0.60
1:N:236:GLN:CB	1:N:265:LYS:HG2	2.32	0.60
1:O:210:PRO:HD2	1:O:211:TRP:CE3	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:577:ILE:HA	1:S:582:LYS:HB3	1.84	0.60
1:U:5:GLU:HG2	1:U:6:ASN:N	2.17	0.60
1:X:237:ASP:H	1:X:243:PRO:HA	1.67	0.60
2:q:15:ARG:HD2	2:q:15:ARG:N	2.17	0.60
1:C:577:ILE:HA	1:C:582:LYS:HB3	1.84	0.60
1:D:154:SER:O	1:D:204:PRO:HB3	2.02	0.60
2:a:53:MET:O	2:a:69:PHE:HE1	1.83	0.60
2:i:137:TYR:CD1	2:i:141:MET:HG2	2.37	0.60
1:N:246:TYR:CD2	1:N:511:ARG:HB2	2.37	0.60
1:N:390:ALA:HB2	1:V:387:GLN:HB2	1.84	0.60
1:P:37:ARG:NH2	1:P:41:TRP:HB3	2.17	0.60
1:P:165:MSE:HE3	1:P:304:PHE:HB2	1.84	0.60
1:P:273:ARG:NH2	1:P:453:LEU:HD21	2.16	0.60
1:Q:44:TRP:C	1:Q:45:LEU:HD22	2.26	0.60
1:R:26:ARG:NH2	1:R:30:LYS:HD3	2.16	0.60
1:R:444:LEU:C	1:R:446:THR:N	2.54	0.60
1:S:158:TRP:CE3	1:S:173:CYS:SG	2.87	0.60
1:U:236:GLN:CB	1:U:265:LYS:HG2	2.32	0.60
1:U:276:VAL:HG23	1:U:293:ILE:HG23	1.83	0.60
1:V:47:GLN:HG2	1:V:48:TYR:H	1.67	0.60
1:W:5:GLU:HG2	1:W:6:ASN:N	2.17	0.60
1:X:66:LYS:HZ3	1:X:420:VAL:HG11	1.67	0.60
1:X:154:SER:O	1:X:204:PRO:HB3	2.02	0.60
2:v:134:THR:HB	2:v:145:GLU:H	1.67	0.60
1:A:89:ASP:HA	1:L:561:ASP:CB	2.25	0.60
1:G:47:GLN:CD	1:G:47:GLN:H	2.10	0.60
1:G:337:ASN:HD21	1:G:401:ASN:HD22	1.47	0.60
1:G:575:GLN:O	1:G:579:MSE:HG2	2.00	0.60
1:J:199:PRO:HB3	1:J:282:THR:HG22	1.84	0.60
1:K:154:SER:O	1:K:204:PRO:HB3	2.02	0.60
2:g:78:GLU:CG	2:g:79:GLY:N	2.63	0.60
2:j:28:VAL:HG22	2:j:93:PHE:O	2.02	0.60
2:j:137:TYR:CD1	2:j:141:MET:HG2	2.37	0.60
1:M:287:LEU:HD12	1:M:287:LEU:N	2.16	0.60
1:O:41:TRP:CE3	1:O:42:ASP:HB3	2.37	0.60
1:O:47:GLN:HG2	1:O:48:TYR:H	1.67	0.60
1:O:158:TRP:CE3	1:O:173:CYS:SG	2.87	0.60
1:Q:41:TRP:CE3	1:Q:42:ASP:HB3	2.37	0.60
1:S:41:TRP:CE3	1:S:42:ASP:HB3	2.36	0.60
1:U:246:TYR:CD2	1:U:511:ARG:HB2	2.36	0.60
1:V:5:GLU:HG2	1:V:6:ASN:N	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:m:65:ASN:N	2:m:66:PRO:HD2	2.17	0.60
2:r:15:ARG:HD2	2:r:15:ARG:N	2.15	0.60
1:B:54:ARG:HB2	2:Z:146:GLY:HA3	1.83	0.60
1:F:233:PHE:CE2	1:F:249:ARG:HD3	2.36	0.60
1:I:199:PRO:HB3	1:I:282:THR:HG22	1.84	0.60
1:K:598:GLN:HB2	1:K:601:GLN:HB2	1.84	0.60
2:Y:137:TYR:CD1	2:Y:141:MET:HG2	2.37	0.60
2:c:34:LEU:O	2:c:35:THR:HG22	2.00	0.60
2:c:78:GLU:CG	2:c:79:GLY:N	2.63	0.60
2:f:137:TYR:CD1	2:f:141:MET:HG2	2.37	0.60
2:g:137:TYR:CD1	2:g:141:MET:HG2	2.37	0.60
2:j:34:LEU:O	2:j:35:THR:HG22	2.00	0.60
1:M:15:PHE:CZ	1:M:283:CYS:HA	2.37	0.59
1:N:158:TRP:CE3	1:N:173:CYS:SG	2.86	0.59
1:N:444:LEU:C	1:N:446:THR:N	2.53	0.59
1:P:5:GLU:HG2	1:P:6:ASN:N	2.17	0.59
1:P:15:PHE:HZ	1:P:283:CYS:HG	1.49	0.59
1:P:237:ASP:H	1:P:243:PRO:HA	1.65	0.59
1:P:554:LEU:HD12	1:P:557:PHE:HD2	1.66	0.59
1:S:37:ARG:NH2	1:S:41:TRP:HB3	2.16	0.59
1:S:560:LEU:HD22	1:T:82:PRO:HG2	1.84	0.59
1:V:138:THR:H	1:V:143:VAL:HG22	1.67	0.59
1:V:273:ARG:HH22	1:V:453:LEU:HD21	1.67	0.59
2:t:15:ARG:HD2	2:t:15:ARG:N	2.16	0.59
2:u:93:PRO:HB3	2:v:100:THR:HG21	1.83	0.59
1:B:444:LEU:O	1:B:448:VAL:HG23	2.02	0.59
1:B:598:GLN:HB2	1:B:601:GLN:HB2	1.84	0.59
1:C:199:PRO:HB3	1:C:282:THR:HG22	1.84	0.59
1:D:234:ILE:CG1	1:D:267:ALA:HB3	2.32	0.59
1:E:598:GLN:HB2	1:E:601:GLN:HB2	1.84	0.59
1:G:233:PHE:CE2	1:G:249:ARG:HD3	2.36	0.59
1:J:47:GLN:CD	1:J:47:GLN:H	2.10	0.59
1:J:161:ASN:C	1:J:161:ASN:ND2	2.59	0.59
1:J:330:ARG:O	1:J:334:MSE:HB2	2.00	0.59
1:K:199:PRO:HB3	1:K:282:THR:HG22	1.84	0.59
1:L:41:TRP:HE3	1:L:42:ASP:CA	2.14	0.59
1:L:598:GLN:HB2	1:L:601:GLN:HB2	1.84	0.59
2:b:34:LEU:C	2:b:35:THR:CG2	2.73	0.59
2:d:53:MET:O	2:d:69:PHE:HE1	1.83	0.59
2:h:137:TYR:CD1	2:h:141:MET:HG2	2.37	0.59
1:O:15:PHE:HZ	1:O:283:CYS:SG	2.25	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:5:GLU:HG2	1:Q:6:ASN:H	1.65	0.59
1:S:78:VAL:HG22	1:S:444:LEU:HD21	1.84	0.59
1:T:5:GLU:HG2	1:T:6:ASN:N	2.17	0.59
1:U:237:ASP:H	1:U:243:PRO:HA	1.66	0.59
1:W:15:PHE:CZ	1:W:283:CYS:HA	2.36	0.59
1:W:66:LYS:HZ3	1:W:420:VAL:HG11	1.67	0.59
1:X:5:GLU:HG2	1:X:6:ASN:N	2.17	0.59
1:X:78:VAL:HG11	1:X:444:LEU:HG	1.83	0.59
2:l:17:LEU:HD11	2:l:36:ALA:CB	2.32	0.59
1:B:26:ARG:NH2	1:B:30:LYS:HD3	2.17	0.59
1:E:154:SER:O	1:E:204:PRO:HB3	2.02	0.59
1:H:47:GLN:CD	1:H:47:GLN:H	2.10	0.59
1:I:234:ILE:CG1	1:I:267:ALA:HB3	2.32	0.59
1:K:233:PHE:CE2	1:K:249:ARG:HD3	2.36	0.59
1:L:199:PRO:HB3	1:L:282:THR:HG22	1.84	0.59
2:d:28:VAL:HG22	2:d:93:PHE:O	2.02	0.59
2:e:78:GLU:CG	2:e:79:GLY:N	2.63	0.59
2:f:28:VAL:HG22	2:f:93:PHE:O	2.02	0.59
2:j:43:GLN:C	2:j:45:ALA:H	2.07	0.59
1:M:165:MSE:HE3	1:M:304:PHE:HB2	1.84	0.59
1:O:236:GLN:CB	1:O:265:LYS:HG2	2.32	0.59
1:Q:5:GLU:HG2	1:Q:6:ASN:N	2.17	0.59
1:S:5:GLU:HG2	1:S:6:ASN:N	2.17	0.59
1:U:287:LEU:HD12	1:U:287:LEU:N	2.16	0.59
1:X:128:LEU:HD12	1:X:446:THR:HG23	1.83	0.59
2:r:65:ASN:N	2:r:66:PRO:HD2	2.17	0.59
1:H:234:ILE:CG1	1:H:267:ALA:HB3	2.32	0.59
1:J:154:SER:O	1:J:204:PRO:HB3	2.02	0.59
2:Y:28:VAL:HG22	2:Y:93:PHE:O	2.02	0.59
2:Y:34:LEU:C	2:Y:35:THR:CG2	2.73	0.59
1:N:5:GLU:HG2	1:N:6:ASN:N	2.17	0.59
1:N:390:ALA:HB2	1:V:387:GLN:CB	2.32	0.59
1:P:78:VAL:HG22	1:P:444:LEU:HD21	1.85	0.59
1:S:15:PHE:CZ	1:S:283:CYS:HA	2.38	0.59
1:U:273:ARG:NH2	1:U:453:LEU:HD11	2.11	0.59
1:W:78:VAL:HG22	1:W:444:LEU:HD21	1.84	0.59
1:W:158:TRP:CH2	1:W:302:PRO:HG3	2.36	0.59
1:C:234:ILE:CG1	1:C:267:ALA:HB3	2.32	0.59
1:E:234:ILE:CG1	1:E:267:ALA:HB3	2.32	0.59
1:E:577:ILE:HA	1:E:582:LYS:HB3	1.84	0.59
1:F:41:TRP:HE3	1:F:42:ASP:CA	2.14	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:234:ILE:CG1	1:G:267:ALA:HB3	2.32	0.59
1:H:161:ASN:C	1:H:161:ASN:ND2	2.59	0.59
1:I:444:LEU:O	1:I:448:VAL:HG23	2.03	0.59
2:Z:28:VAL:HG22	2:Z:93:PHE:O	2.02	0.59
2:a:32:ALA:C	2:a:33:THR:CG2	2.60	0.59
1:M:138:THR:H	1:M:143:VAL:HG22	1.67	0.59
1:M:158:TRP:CE3	1:M:173:CYS:SG	2.87	0.59
1:O:273:ARG:NH2	1:O:453:LEU:HD11	2.14	0.59
1:O:431:ALA:O	1:O:435:VAL:HG22	2.01	0.59
1:O:564:GLY:O	1:P:554:LEU:HD21	2.02	0.59
1:R:5:GLU:HG2	1:R:6:ASN:N	2.17	0.59
1:S:273:ARG:NH2	1:S:453:LEU:HD11	2.13	0.59
1:S:440:MSE:O	1:S:444:LEU:HD22	2.02	0.59
1:T:379:GLU:O	1:T:380:ASN:HB2	2.03	0.59
1:V:554:LEU:HD21	1:W:564:GLY:HA2	1.84	0.59
1:W:78:VAL:HG12	1:W:79:LEU:H	1.67	0.59
1:W:237:ASP:H	1:W:243:PRO:HA	1.67	0.59
1:W:273:ARG:HH22	1:W:453:LEU:HD21	1.68	0.59
2:v:65:ASN:N	2:v:66:PRO:HD2	2.17	0.59
1:A:26:ARG:NH2	1:A:30:LYS:HD3	2.17	0.59
1:D:26:ARG:NH2	1:D:30:LYS:HD3	2.17	0.59
1:H:264:ILE:O	1:H:265:LYS:HD3	2.03	0.59
1:J:26:ARG:NH2	1:J:30:LYS:HD3	2.18	0.59
1:J:444:LEU:O	1:J:448:VAL:HG23	2.02	0.59
1:K:26:ARG:NH2	1:K:30:LYS:HD3	2.17	0.59
2:b:78:GLU:CD	2:b:79:GLY:H	2.11	0.59
1:M:158:TRP:CH2	1:M:302:PRO:HG3	2.38	0.59
1:N:287:LEU:N	1:N:287:LEU:HD12	2.16	0.59
1:P:44:TRP:C	1:P:45:LEU:HD22	2.27	0.59
1:Q:99:ARG:O	1:Q:103:ARG:HG3	2.02	0.59
1:Q:273:ARG:NH2	1:Q:453:LEU:HD21	2.18	0.59
1:U:15:PHE:CZ	1:U:283:CYS:HA	2.38	0.59
1:U:138:THR:H	1:U:143:VAL:HG22	1.68	0.59
2:p:15:ARG:HD2	2:p:15:ARG:N	2.17	0.59
1:C:26:ARG:NH2	1:C:30:LYS:HD3	2.17	0.59
1:C:444:LEU:O	1:C:448:VAL:HG23	2.03	0.59
1:E:236:GLN:CB	1:E:265:LYS:HZ3	2.15	0.59
1:E:444:LEU:O	1:E:448:VAL:HG23	2.03	0.59
1:F:577:ILE:HA	1:F:582:LYS:HB3	1.84	0.59
1:H:577:ILE:HA	1:H:582:LYS:HB3	1.84	0.59
1:H:598:GLN:HB2	1:H:601:GLN:HB2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:384:LEU:O	1:L:386:THR:N	2.36	0.59
2:Z:137:TYR:CD1	2:Z:141:MET:HG2	2.37	0.59
1:M:5:GLU:HG2	1:M:6:ASN:N	2.17	0.59
1:N:273:ARG:NH2	1:N:453:LEU:HD21	2.18	0.59
1:N:390:ALA:CB	1:V:387:GLN:CB	2.80	0.59
1:P:86:ALA:HB2	1:P:515:GLU:HG3	1.85	0.59
1:P:236:GLN:CB	1:P:265:LYS:HG2	2.32	0.59
1:S:237:ASP:H	1:S:243:PRO:HA	1.66	0.59
1:T:138:THR:H	1:T:143:VAL:HG22	1.67	0.59
1:U:158:TRP:CE3	1:U:173:CYS:SG	2.86	0.59
1:V:444:LEU:C	1:V:446:THR:N	2.55	0.59
2:m:15:ARG:HD2	2:m:15:ARG:N	2.18	0.59
2:r:62:ASP:C	2:r:64:GLU:N	2.61	0.59
2:s:71:ASP:OD2	2:s:71:ASP:N	2.36	0.59
1:A:577:ILE:HA	1:A:582:LYS:HB3	1.84	0.59
1:B:158:TRP:CE3	1:B:173:CYS:SG	2.88	0.59
1:B:264:ILE:O	1:B:265:LYS:HD3	2.03	0.59
1:D:199:PRO:HB3	1:D:282:THR:HG22	1.84	0.59
1:D:444:LEU:O	1:D:448:VAL:HG23	2.03	0.59
1:E:384:LEU:H	1:E:384:LEU:HD22	1.68	0.59
1:F:384:LEU:HD22	1:F:384:LEU:H	1.68	0.59
1:G:161:ASN:C	1:G:161:ASN:ND2	2.59	0.59
1:I:26:ARG:NH2	1:I:30:LYS:HD3	2.17	0.59
1:K:161:ASN:C	1:K:161:ASN:ND2	2.59	0.59
1:K:234:ILE:CG1	1:K:267:ALA:HB3	2.32	0.59
2:e:28:VAL:HG22	2:e:93:PHE:O	2.02	0.59
1:M:158:TRP:HB3	1:M:173:CYS:CA	2.28	0.59
1:N:431:ALA:O	1:N:435:VAL:HG22	2.03	0.59
1:O:273:ARG:NH2	1:O:453:LEU:HD21	2.17	0.59
1:R:41:TRP:CE3	1:R:42:ASP:HB3	2.37	0.59
1:R:554:LEU:HD12	1:R:557:PHE:HD2	1.68	0.59
1:S:44:TRP:C	1:S:45:LEU:HD22	2.27	0.59
1:S:89:ASP:HA	1:U:561:ASP:HB2	1.85	0.59
1:U:15:PHE:HZ	1:U:283:CYS:SG	2.25	0.59
1:U:78:VAL:HG22	1:U:444:LEU:HD21	1.84	0.59
1:V:5:GLU:HG2	1:V:6:ASN:H	1.65	0.59
1:X:41:TRP:CE3	1:X:42:ASP:HB3	2.36	0.59
1:X:236:GLN:CB	1:X:265:LYS:HG2	2.32	0.59
2:s:93:PRO:HB3	2:u:100:THR:HG21	1.83	0.59
1:D:158:TRP:O	1:D:160:SER:N	2.36	0.59
1:D:236:GLN:CB	1:D:265:LYS:HZ3	2.15	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:34:PHE:HZ	1:E:328:ARG:HH22	0.80	0.59
1:G:556:TYR:OH	1:H:542:THR:HG21	2.03	0.59
1:H:26:ARG:NH2	1:H:30:LYS:HD3	2.17	0.59
1:H:54:ARG:HB2	2:f:146:GLY:HA3	1.85	0.59
1:H:158:TRP:O	1:H:160:SER:N	2.36	0.59
1:H:334:MSE:SE	1:I:404:MSE:HE1	2.53	0.59
1:I:47:GLN:CD	1:I:47:GLN:H	2.10	0.59
1:J:384:LEU:O	1:J:386:THR:N	2.36	0.59
1:K:264:ILE:O	1:K:265:LYS:HD3	2.03	0.59
1:K:384:LEU:O	1:K:386:THR:N	2.36	0.59
1:M:82:PRO:HG2	1:N:560:LEU:HD22	1.84	0.59
1:M:561:ASP:OD2	1:O:92:ASP:HB3	2.02	0.59
1:N:165:MSE:HE3	1:N:304:PHE:HB2	1.85	0.59
1:P:35:PHE:C	1:P:37:ARG:H	2.11	0.59
1:P:379:GLU:O	1:P:380:ASN:HB2	2.03	0.59
1:Q:237:ASP:H	1:Q:243:PRO:HA	1.67	0.59
1:V:236:GLN:CB	1:V:265:LYS:HG2	2.32	0.59
1:W:246:TYR:CD2	1:W:511:ARG:HB2	2.38	0.59
2:m:62:ASP:C	2:m:64:GLU:N	2.61	0.59
1:D:384:LEU:O	1:D:386:THR:N	2.36	0.59
1:K:49:THR:O	1:K:49:THR:CG2	2.51	0.59
1:L:47:GLN:CD	1:L:47:GLN:H	2.10	0.59
1:L:384:LEU:HD22	1:L:384:LEU:H	1.68	0.59
2:a:28:VAL:HG22	2:a:93:PHE:O	2.02	0.59
2:a:78:GLU:CD	2:a:79:GLY:H	2.11	0.59
1:M:236:GLN:CB	1:M:265:LYS:HG2	2.32	0.59
3:O:719:HOH:O	1:P:430:VAL:CG1	2.51	0.59
1:Q:246:TYR:CD2	1:Q:511:ARG:HB2	2.36	0.59
1:R:128:LEU:HD12	1:R:446:THR:HG23	1.85	0.59
1:U:379:GLU:O	1:U:380:ASN:HB2	2.03	0.59
1:V:41:TRP:CE3	1:V:42:ASP:HB3	2.38	0.59
1:V:390:ALA:HB2	1:W:387:GLN:HB2	1.83	0.59
2:o:65:ASN:N	2:o:66:PRO:HD2	2.18	0.59
1:A:49:THR:O	1:A:49:THR:CG2	2.51	0.59
1:A:161:ASN:C	1:A:161:ASN:ND2	2.59	0.59
1:A:384:LEU:O	1:A:386:THR:N	2.36	0.59
1:C:158:TRP:O	1:C:160:SER:N	2.36	0.59
1:D:92:ASP:HB3	1:E:561:ASP:OD2	2.03	0.59
1:D:598:GLN:HB2	1:D:601:GLN:HB2	1.84	0.59
1:E:44:TRP:C	1:E:45:LEU:HD22	2.28	0.59
1:E:173:CYS:SG	1:E:298:ILE:HD13	2.43	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:115:VAL:HA	1:F:118:GLN:HB3	1.85	0.59
1:G:26:ARG:NH2	1:G:30:LYS:HD3	2.17	0.59
1:G:384:LEU:O	1:G:386:THR:N	2.36	0.59
1:H:44:TRP:C	1:H:45:LEU:HD22	2.28	0.59
1:H:384:LEU:O	1:H:386:THR:N	2.36	0.59
1:I:158:TRP:O	1:I:160:SER:N	2.36	0.59
1:J:49:THR:O	1:J:49:THR:CG2	2.51	0.59
1:K:50:THR:HG21	1:K:54:ARG:NH2	2.18	0.59
2:c:137:TYR:CD1	2:c:141:MET:HG2	2.37	0.59
2:h:78:GLU:CD	2:h:79:GLY:H	2.11	0.59
1:M:199:PRO:HB3	1:M:282:THR:HG22	1.85	0.58
1:O:78:VAL:CG2	1:O:444:LEU:HD11	2.23	0.58
1:S:554:LEU:HD12	1:S:557:PHE:HD2	1.68	0.58
1:X:246:TYR:CD2	1:X:511:ARG:HB2	2.36	0.58
2:k:15:ARG:HD2	2:k:15:ARG:N	2.18	0.58
2:u:15:ARG:HD2	2:u:15:ARG:N	2.18	0.58
1:A:47:GLN:CD	1:A:47:GLN:H	2.10	0.58
1:D:577:ILE:HA	1:D:582:LYS:HB3	1.84	0.58
1:E:26:ARG:NH2	1:E:30:LYS:HD3	2.17	0.58
1:F:264:ILE:O	1:F:265:LYS:HD3	2.03	0.58
1:F:343:ARG:NH1	2:c:135:ALA:O	2.31	0.58
1:G:173:CYS:SG	1:G:298:ILE:HD13	2.43	0.58
1:H:236:GLN:CB	1:H:265:LYS:HZ3	2.16	0.58
1:H:444:LEU:O	1:H:448:VAL:HG23	2.03	0.58
1:J:50:THR:HG21	1:J:54:ARG:NH2	2.18	0.58
1:K:384:LEU:H	1:K:384:LEU:HD22	1.68	0.58
1:L:264:ILE:O	1:L:265:LYS:HD3	2.03	0.58
1:O:379:GLU:O	1:O:380:ASN:HB2	2.03	0.58
1:P:273:ARG:HH22	1:P:453:LEU:HD21	1.66	0.58
1:P:276:VAL:HG23	1:P:293:ILE:HG23	1.85	0.58
1:Q:440:MSE:O	1:Q:444:LEU:HD22	2.03	0.58
1:T:273:ARG:HH22	1:T:453:LEU:HD21	1.66	0.58
1:U:444:LEU:C	1:U:446:THR:H	2.11	0.58
2:l:65:ASN:N	2:l:66:PRO:HD2	2.18	0.58
2:t:62:ASP:C	2:t:64:GLU:N	2.61	0.58
2:v:62:ASP:C	2:v:64:GLU:N	2.61	0.58
1:A:438:LEU:HD11	1:L:108:LYS:HD2	1.85	0.58
1:A:563:LYS:HD3	1:B:557:PHE:CE2	2.38	0.58
1:A:598:GLN:HB2	1:A:601:GLN:HB2	1.84	0.58
1:B:158:TRP:O	1:B:160:SER:N	2.36	0.58
1:B:577:ILE:HA	1:B:582:LYS:HB3	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:44:TRP:C	1:C:45:LEU:HD22	2.28	0.58
1:D:44:TRP:C	1:D:45:LEU:HD22	2.28	0.58
1:F:158:TRP:O	1:F:160:SER:N	2.36	0.58
1:F:444:LEU:O	1:F:448:VAL:HG23	2.03	0.58
1:G:35:PHE:C	1:G:37:ARG:N	2.62	0.58
1:G:158:TRP:O	1:G:160:SER:N	2.36	0.58
1:I:161:ASN:C	1:I:161:ASN:ND2	2.59	0.58
1:I:384:LEU:HD22	1:I:384:LEU:H	1.68	0.58
1:I:384:LEU:O	1:I:386:THR:N	2.36	0.58
1:I:598:GLN:HB2	1:I:601:GLN:HB2	1.84	0.58
1:J:115:VAL:HA	1:J:118:GLN:HB3	1.85	0.58
1:J:158:TRP:O	1:J:160:SER:N	2.36	0.58
1:L:26:ARG:NH2	1:L:30:LYS:HD3	2.17	0.58
2:c:28:VAL:HG22	2:c:93:PHE:O	2.02	0.58
2:g:78:GLU:CD	2:g:79:GLY:H	2.11	0.58
1:P:99:ARG:O	1:P:103:ARG:HG3	2.04	0.58
1:Q:24:GLU:C	1:Q:26:ARG:N	2.57	0.58
1:T:554:LEU:HD12	1:T:557:PHE:HD2	1.69	0.58
1:U:325:ASP:OD2	2:r:136:SER:HB3	2.03	0.58
1:U:430:VAL:CG1	3:X:719:HOH:O	2.51	0.58
1:V:158:TRP:O	1:V:160:SER:N	2.36	0.58
1:W:332:MSE:SE	2:s:132:MET:HA	2.53	0.58
1:X:78:VAL:HG22	1:X:444:LEU:HD21	1.85	0.58
2:s:17:LEU:HD11	2:s:36:ALA:CB	2.33	0.58
1:A:158:TRP:O	1:A:160:SER:N	2.36	0.58
1:B:199:PRO:HB3	1:B:282:THR:HG22	1.84	0.58
1:D:161:ASN:C	1:D:161:ASN:ND2	2.59	0.58
1:D:264:ILE:O	1:D:265:LYS:HD3	2.03	0.58
1:E:384:LEU:O	1:E:386:THR:N	2.36	0.58
1:F:26:ARG:NH2	1:F:30:LYS:HD3	2.17	0.58
1:F:598:GLN:HB2	1:F:601:GLN:HB2	1.84	0.58
1:G:389:LEU:H	1:G:389:LEU:HD12	1.68	0.58
1:I:49:THR:O	1:I:49:THR:CG2	2.51	0.58
1:J:384:LEU:H	1:J:384:LEU:HD22	1.68	0.58
1:K:41:TRP:HE3	1:K:42:ASP:CA	2.14	0.58
1:K:158:TRP:O	1:K:160:SER:N	2.36	0.58
2:Y:78:GLU:CD	2:Y:79:GLY:H	2.11	0.58
2:Z:78:GLU:CD	2:Z:79:GLY:H	2.11	0.58
2:j:78:GLU:CD	2:j:79:GLY:H	2.11	0.58
1:M:41:TRP:CE3	1:M:42:ASP:HB3	2.38	0.58
1:M:86:ALA:HB2	1:M:515:GLU:HG3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:237:ASP:H	1:M:243:PRO:HA	1.68	0.58
1:N:586:THR:N	1:N:587:PRO:HD3	2.18	0.58
1:O:577:ILE:HA	1:O:582:LYS:HB3	1.85	0.58
1:Q:78:VAL:HG11	1:Q:444:LEU:HG	1.84	0.58
1:Q:554:LEU:HD12	1:Q:557:PHE:HD2	1.69	0.58
1:R:237:ASP:H	1:R:243:PRO:HA	1.68	0.58
1:T:276:VAL:HG23	1:T:293:ILE:HG23	1.85	0.58
1:T:431:ALA:O	1:T:435:VAL:HG22	2.03	0.58
1:X:47:GLN:HG2	1:X:48:TYR:H	1.67	0.58
2:r:71:ASP:OD2	2:r:71:ASP:N	2.36	0.58
1:A:35:PHE:C	1:A:37:ARG:N	2.62	0.58
1:C:276:VAL:HG23	1:C:293:ILE:CG2	2.34	0.58
1:D:173:CYS:SG	1:D:298:ILE:HD13	2.43	0.58
1:E:47:GLN:CD	1:E:47:GLN:H	2.10	0.58
1:E:50:THR:HG21	1:E:54:ARG:NH2	2.18	0.58
1:G:577:ILE:HA	1:G:582:LYS:HB3	1.84	0.58
1:H:384:LEU:H	1:H:384:LEU:HD22	1.68	0.58
1:I:389:LEU:H	1:I:389:LEU:HD12	1.68	0.58
1:J:276:VAL:HG23	1:J:293:ILE:CG2	2.34	0.58
1:K:47:GLN:CD	1:K:47:GLN:H	2.10	0.58
1:K:276:VAL:HG23	1:K:293:ILE:CG2	2.34	0.58
1:L:158:TRP:O	1:L:160:SER:N	2.36	0.58
1:L:389:LEU:H	1:L:389:LEU:HD12	1.68	0.58
1:L:444:LEU:O	1:L:448:VAL:HG23	2.03	0.58
2:a:34:LEU:C	2:a:35:THR:CG2	2.73	0.58
2:i:78:GLU:CD	2:i:79:GLY:H	2.11	0.58
1:P:138:THR:H	1:P:143:VAL:HG22	1.67	0.58
1:R:94:LEU:HA	1:R:97:MSE:CE	2.34	0.58
1:S:128:LEU:HD12	1:S:446:THR:HG23	1.84	0.58
1:S:586:THR:N	1:S:587:PRO:HD3	2.19	0.58
1:U:35:PHE:C	1:U:37:ARG:H	2.11	0.58
2:k:62:ASP:C	2:k:64:GLU:N	2.61	0.58
2:q:65:ASN:N	2:q:66:PRO:HD2	2.18	0.58
2:s:15:ARG:HD2	2:s:15:ARG:N	2.18	0.58
1:A:276:VAL:HG23	1:A:293:ILE:CG2	2.34	0.58
1:D:50:THR:HG21	1:D:54:ARG:NH2	2.18	0.58
1:E:276:VAL:HG23	1:E:293:ILE:CG2	2.34	0.58
1:F:384:LEU:O	1:F:386:THR:N	2.36	0.58
1:G:384:LEU:HD22	1:G:384:LEU:H	1.68	0.58
1:H:199:PRO:HB3	1:H:282:THR:HG22	1.84	0.58
1:J:44:TRP:C	1:J:45:LEU:HD22	2.28	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:577:ILE:HA	1:J:582:LYS:HB3	1.84	0.58
1:L:49:THR:O	1:L:49:THR:CG2	2.51	0.58
1:L:115:VAL:HA	1:L:118:GLN:HB3	1.86	0.58
1:L:276:VAL:HG23	1:L:293:ILE:CG2	2.34	0.58
1:M:577:ILE:HA	1:M:582:LYS:HB3	1.85	0.58
1:N:273:ARG:HH22	1:N:453:LEU:HD21	1.68	0.58
1:P:444:LEU:C	1:P:446:THR:H	2.11	0.58
1:R:99:ARG:O	1:R:103:ARG:HG3	2.03	0.58
1:R:246:TYR:CD2	1:R:511:ARG:HB2	2.38	0.58
1:S:273:ARG:NH2	1:S:453:LEU:HD21	2.19	0.58
1:S:556:TYR:OH	1:T:542:THR:HG21	2.03	0.58
1:T:237:ASP:H	1:T:243:PRO:HA	1.68	0.58
1:V:199:PRO:HB3	1:V:282:THR:HG22	1.85	0.58
1:W:577:ILE:HA	1:W:582:LYS:HB3	1.84	0.58
2:o:134:THR:HB	2:o:145:GLU:H	1.68	0.58
1:A:444:LEU:O	1:A:448:VAL:HG23	2.02	0.58
1:B:50:THR:HG21	1:B:54:ARG:NH2	2.18	0.58
1:B:173:CYS:SG	1:B:298:ILE:HD13	2.43	0.58
1:B:384:LEU:H	1:B:384:LEU:HD22	1.68	0.58
1:C:35:PHE:C	1:C:37:ARG:N	2.62	0.58
1:C:47:GLN:CD	1:C:47:GLN:H	2.10	0.58
1:C:334:MSE:SE	1:E:404:MSE:HE1	2.53	0.58
1:E:115:VAL:HA	1:E:118:GLN:HB3	1.86	0.58
1:F:158:TRP:CE3	1:F:173:CYS:SG	2.88	0.58
1:F:389:LEU:H	1:F:389:LEU:HD12	1.68	0.58
1:G:14:ARG:HH11	1:G:17:ALA:CB	2.17	0.58
1:G:49:THR:O	1:G:49:THR:CG2	2.51	0.58
1:G:444:LEU:O	1:G:448:VAL:HG23	2.02	0.58
1:H:276:VAL:HG23	1:H:293:ILE:CG2	2.34	0.58
1:H:444:LEU:C	1:H:446:THR:N	2.61	0.58
1:I:158:TRP:CE3	1:I:173:CYS:SG	2.88	0.58
1:J:35:PHE:C	1:J:37:ARG:N	2.61	0.58
1:J:173:CYS:SG	1:J:298:ILE:HD13	2.43	0.58
1:K:44:TRP:C	1:K:45:LEU:HD22	2.28	0.58
2:Y:28:VAL:HG11	2:Y:97:ALA:N	2.19	0.58
2:f:78:GLU:CG	2:f:79:GLY:N	2.63	0.58
2:j:78:GLU:CG	2:j:79:GLY:N	2.63	0.58
1:N:237:ASP:H	1:N:243:PRO:HA	1.67	0.58
1:P:66:LYS:HZ3	1:P:420:VAL:HG11	1.67	0.58
3:Q:719:HOH:O	1:R:430:VAL:CG1	2.50	0.58
1:S:35:PHE:C	1:S:37:ARG:H	2.12	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:404:MSE:HE1	1:W:334:MSE:SE	2.52	0.58
1:V:577:ILE:HA	1:V:582:LYS:HB3	1.85	0.58
1:W:138:THR:H	1:W:143:VAL:HG22	1.69	0.58
1:X:554:LEU:HD12	1:X:557:PHE:HD2	1.68	0.58
2:v:15:ARG:HD2	2:v:15:ARG:N	2.17	0.58
1:A:264:ILE:O	1:A:265:LYS:HD3	2.03	0.58
1:B:47:GLN:CD	1:B:47:GLN:H	2.10	0.58
1:C:115:VAL:HA	1:C:118:GLN:HB3	1.86	0.58
1:E:118:GLN:NE2	1:E:303:VAL:HB	2.19	0.58
1:F:173:CYS:SG	1:F:298:ILE:HD13	2.43	0.58
1:G:264:ILE:O	1:G:265:LYS:HD3	2.03	0.58
1:I:14:ARG:HH11	1:I:17:ALA:CB	2.17	0.58
1:I:173:CYS:SG	1:I:298:ILE:HD13	2.43	0.58
1:I:264:ILE:O	1:I:265:LYS:HD3	2.03	0.58
1:J:248:LYS:NZ	1:J:513:ARG:HH12	2.02	0.58
1:J:264:ILE:O	1:J:265:LYS:HD3	2.03	0.58
1:K:173:CYS:SG	1:K:298:ILE:HD13	2.43	0.58
1:L:161:ASN:C	1:L:161:ASN:ND2	2.59	0.58
2:c:78:GLU:CD	2:c:79:GLY:H	2.11	0.58
2:d:78:GLU:CD	2:d:79:GLY:H	2.11	0.58
1:N:231:THR:HG21	1:N:249:ARG:HH11	1.69	0.58
1:O:199:PRO:HB3	1:O:282:THR:HG22	1.86	0.58
1:Q:199:PRO:HB3	1:Q:282:THR:HG22	1.86	0.58
1:Q:586:THR:N	1:Q:587:PRO:HD3	2.19	0.58
1:U:554:LEU:HD12	1:U:557:PHE:HD2	1.69	0.58
1:V:237:ASP:H	1:V:243:PRO:HA	1.68	0.58
1:X:586:THR:N	1:X:587:PRO:HD3	2.19	0.58
2:o:15:ARG:HD2	2:o:15:ARG:N	2.19	0.58
2:p:62:ASP:C	2:p:64:GLU:N	2.61	0.58
1:B:182:ASN:HD22	1:C:171:ARG:HH21	1.50	0.58
1:B:276:VAL:HG23	1:B:293:ILE:CG2	2.34	0.58
1:C:118:GLN:NE2	1:C:303:VAL:HB	2.19	0.58
1:C:161:ASN:C	1:C:161:ASN:ND2	2.59	0.58
1:C:384:LEU:H	1:C:384:LEU:HD22	1.68	0.58
1:C:384:LEU:O	1:C:386:THR:N	2.36	0.58
1:D:248:LYS:NZ	1:D:513:ARG:HH12	2.02	0.58
1:F:276:VAL:HG23	1:F:293:ILE:CG2	2.34	0.58
1:G:276:VAL:HG23	1:G:293:ILE:CG2	2.34	0.58
1:I:44:TRP:C	1:I:45:LEU:HD22	2.28	0.58
1:I:577:ILE:HA	1:I:582:LYS:HB3	1.84	0.58
1:K:372:TYR:CE2	1:L:348:LYS:HB2	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:389:LEU:HD12	1:K:389:LEU:H	1.68	0.58
1:K:444:LEU:O	1:K:448:VAL:HG23	2.02	0.58
1:K:577:ILE:HA	1:K:582:LYS:HB3	1.84	0.58
1:L:577:ILE:HA	1:L:582:LYS:HB3	1.84	0.58
2:c:92:VAL:O	2:c:96:LEU:HB2	2.04	0.58
2:h:109:THR:HG21	2:i:102:PRO:HB3	1.86	0.58
1:M:95:MSE:HB3	1:M:527:MSE:HE1	1.85	0.58
1:M:379:GLU:O	1:M:380:ASN:HB2	2.04	0.58
1:M:586:THR:N	1:M:587:PRO:HD3	2.19	0.58
1:N:554:LEU:HD12	1:N:557:PHE:HD2	1.69	0.58
1:Q:273:ARG:HH22	1:Q:453:LEU:HD21	1.69	0.58
1:Q:379:GLU:O	1:Q:380:ASN:HB2	2.03	0.58
1:Q:444:LEU:C	1:Q:446:THR:H	2.12	0.58
1:T:586:THR:N	1:T:587:PRO:HD3	2.19	0.58
1:V:154:SER:O	1:V:204:PRO:HB3	2.03	0.58
1:W:44:TRP:C	1:W:45:LEU:HD22	2.28	0.58
1:X:158:TRP:O	1:X:160:SER:N	2.37	0.58
2:n:65:ASN:N	2:n:66:PRO:HD2	2.18	0.58
2:u:65:ASN:N	2:u:66:PRO:HD2	2.18	0.58
1:A:50:THR:HG21	1:A:54:ARG:NH2	2.18	0.58
1:A:54:ARG:HB2	2:Y:146:GLY:HA3	1.84	0.58
1:A:89:ASP:CA	1:L:561:ASP:HB2	2.30	0.58
1:A:118:GLN:NE2	1:A:303:VAL:HB	2.19	0.58
1:A:348:LYS:HB2	1:L:372:TYR:CE2	2.39	0.58
1:C:182:ASN:HD22	1:E:171:ARG:HH21	1.51	0.58
1:C:248:LYS:NZ	1:C:513:ARG:HH12	2.02	0.58
1:D:41:TRP:HE3	1:D:42:ASP:CA	2.14	0.58
1:D:118:GLN:NE2	1:D:303:VAL:HB	2.19	0.58
1:D:389:LEU:H	1:D:389:LEU:HD12	1.68	0.58
1:E:248:LYS:NZ	1:E:513:ARG:HH12	2.02	0.58
1:F:50:THR:HG21	1:F:54:ARG:NH2	2.18	0.58
1:G:44:TRP:C	1:G:45:LEU:HD22	2.28	0.58
1:G:334:MSE:HE3	1:H:404:MSE:CE	2.34	0.58
1:H:173:CYS:SG	1:H:298:ILE:HD13	2.43	0.58
1:J:158:TRP:H	1:J:158:TRP:HD1	1.52	0.58
2:g:28:VAL:HG11	2:g:97:ALA:N	2.19	0.58
2:h:92:VAL:O	2:h:96:LEU:HB2	2.04	0.58
1:N:86:ALA:HB2	1:N:515:GLU:HG3	1.85	0.58
1:O:86:ALA:HB2	1:O:515:GLU:HG3	1.84	0.58
1:O:325:ASP:OD2	2:m:136:SER:HB3	2.04	0.58
1:S:15:PHE:HZ	1:S:283:CYS:SG	2.26	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:44:TRP:C	1:T:45:LEU:HD22	2.29	0.58
1:V:598:GLN:HB2	1:V:601:GLN:CB	2.34	0.58
1:W:379:GLU:O	1:W:380:ASN:HB2	2.04	0.58
2:p:71:ASP:OD2	2:p:71:ASP:N	2.37	0.58
1:A:14:ARG:HH11	1:A:17:ALA:CB	2.17	0.58
1:A:34:PHE:HZ	1:A:328:ARG:HH22	0.80	0.58
1:A:173:CYS:SG	1:A:298:ILE:HD13	2.43	0.58
1:A:199:PRO:HB3	1:A:282:THR:HG22	1.84	0.58
1:A:363:TYR:HE1	1:B:350:PHE:HE1	1.52	0.58
1:B:158:TRP:H	1:B:158:TRP:HD1	1.52	0.58
1:B:384:LEU:O	1:B:386:THR:N	2.36	0.58
1:C:49:THR:O	1:C:49:THR:CG2	2.51	0.58
1:D:238:PRO:HG3	1:D:263:PHE:HB3	1.86	0.58
1:D:598:GLN:HB2	1:D:601:GLN:CB	2.34	0.58
1:E:158:TRP:O	1:E:160:SER:N	2.36	0.58
1:F:14:ARG:HH11	1:F:17:ALA:CB	2.17	0.58
1:F:49:THR:O	1:F:49:THR:CG2	2.51	0.58
1:F:158:TRP:HD1	1:F:158:TRP:H	1.52	0.58
1:G:329:LEU:HD22	2:c:142:PRO:HG2	1.85	0.58
1:H:14:ARG:HH11	1:H:17:ALA:CB	2.17	0.58
1:H:334:MSE:HE1	1:I:407:ALA:HB1	1.86	0.58
1:H:598:GLN:HB2	1:H:601:GLN:CB	2.34	0.58
1:I:50:THR:HG21	1:I:54:ARG:NH2	2.18	0.58
1:K:598:GLN:HB2	1:K:601:GLN:CB	2.34	0.58
1:L:50:THR:HG21	1:L:54:ARG:NH2	2.18	0.58
1:L:173:CYS:SG	1:L:298:ILE:HD13	2.43	0.58
2:a:92:VAL:O	2:a:96:LEU:HB2	2.04	0.58
2:i:92:VAL:O	2:i:96:LEU:HB2	2.04	0.58
1:N:352:TRP:CG	1:V:376:ARG:HB2	2.40	0.57
1:O:427:GLY:C	1:O:429:GLN:H	2.12	0.57
1:Q:35:PHE:C	1:Q:37:ARG:H	2.12	0.57
1:Q:158:TRP:CE3	1:Q:173:CYS:SG	2.85	0.57
1:R:236:GLN:CB	1:R:265:LYS:HG2	2.33	0.57
1:R:276:VAL:HG23	1:R:293:ILE:HG23	1.85	0.57
1:T:395:PRO:HD2	1:W:398:PRO:HB3	1.86	0.57
1:U:586:THR:N	1:U:587:PRO:HD3	2.19	0.57
1:V:15:PHE:HZ	1:V:283:CYS:SG	2.22	0.57
1:V:99:ARG:O	1:V:103:ARG:HG3	2.03	0.57
1:W:35:PHE:C	1:W:37:ARG:H	2.10	0.57
1:X:15:PHE:CZ	1:X:283:CYS:HA	2.38	0.57
1:X:44:TRP:C	1:X:45:LEU:HD22	2.29	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:o:62:ASP:C	2:o:64:GLU:N	2.61	0.57
2:t:17:LEU:HD11	2:t:36:ALA:CB	2.34	0.57
1:A:238:PRO:HG3	1:A:263:PHE:HB3	1.86	0.57
1:A:384:LEU:HD22	1:A:384:LEU:H	1.68	0.57
1:B:118:GLN:NE2	1:B:303:VAL:HB	2.19	0.57
1:B:598:GLN:HB2	1:B:601:GLN:CB	2.34	0.57
1:C:173:CYS:SG	1:C:298:ILE:HD13	2.43	0.57
1:C:238:PRO:HG3	1:C:263:PHE:HB3	1.86	0.57
1:C:343:ARG:NH1	2:a:135:ALA:O	2.34	0.57
1:E:41:TRP:HE3	1:E:42:ASP:CA	2.14	0.57
1:H:35:PHE:C	1:H:37:ARG:N	2.62	0.57
1:J:54:ARG:HB2	2:i:146:GLY:HA3	1.84	0.57
1:J:389:LEU:H	1:J:389:LEU:HD12	1.68	0.57
1:J:444:LEU:C	1:J:446:THR:N	2.61	0.57
1:K:560:LEU:HD13	1:L:82:PRO:CD	2.20	0.57
2:c:28:VAL:HG11	2:c:97:ALA:N	2.19	0.57
2:d:92:VAL:O	2:d:96:LEU:HB2	2.04	0.57
2:e:51:ALA:O	2:e:54:ALA:HB3	2.04	0.57
2:f:78:GLU:CD	2:f:79:GLY:H	2.11	0.57
1:M:26:ARG:HG2	1:N:212:LEU:HD22	1.86	0.57
1:M:554:LEU:HD12	1:M:557:PHE:HD2	1.69	0.57
1:N:78:VAL:HG11	1:N:444:LEU:HG	1.86	0.57
1:O:586:THR:N	1:O:587:PRO:HD3	2.18	0.57
1:P:128:LEU:HD12	1:P:446:THR:HG23	1.84	0.57
1:R:35:PHE:C	1:R:37:ARG:H	2.11	0.57
1:R:427:GLY:C	1:R:429:GLN:H	2.12	0.57
1:S:86:ALA:HB2	1:S:515:GLU:HG3	1.86	0.57
1:S:563:LYS:HD3	1:T:557:PHE:CE2	2.38	0.57
1:T:46:SER:N	1:T:48:TYR:HE2	1.97	0.57
1:T:86:ALA:HB2	1:T:515:GLU:HG3	1.86	0.57
1:U:47:GLN:HG2	1:U:48:TYR:H	1.69	0.57
1:U:510:ILE:HG12	1:U:511:ARG:N	2.19	0.57
1:V:431:ALA:O	1:V:435:VAL:HG22	2.04	0.57
2:s:62:ASP:C	2:s:64:GLU:N	2.61	0.57
2:t:65:ASN:N	2:t:66:PRO:HD2	2.18	0.57
1:A:158:TRP:HD1	1:A:158:TRP:H	1.52	0.57
1:A:444:LEU:C	1:A:446:THR:N	2.61	0.57
1:B:44:TRP:C	1:B:45:LEU:HD22	2.28	0.57
1:C:42:ASP:OD2	2:a:145:SER:O	2.22	0.57
1:C:144:ILE:HD12	1:C:145:ARG:N	2.20	0.57
1:C:264:ILE:O	1:C:265:LYS:HD3	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:264:ILE:O	1:E:265:LYS:HD3	2.03	0.57
1:F:238:PRO:HG3	1:F:263:PHE:HB3	1.86	0.57
1:G:248:LYS:NZ	1:G:513:ARG:HH12	2.02	0.57
1:H:50:THR:HG21	1:H:54:ARG:NH2	2.18	0.57
1:H:118:GLN:NE2	1:H:303:VAL:HB	2.19	0.57
1:I:546:THR:CG2	1:I:547:PRO:HD3	2.27	0.57
1:K:35:PHE:C	1:K:37:ARG:N	2.61	0.57
3:M:719:HOH:O	1:O:430:VAL:CG1	2.52	0.57
1:N:138:THR:H	1:N:143:VAL:HG22	1.67	0.57
1:Q:78:VAL:HG22	1:Q:444:LEU:HD21	1.87	0.57
1:Q:427:GLY:C	1:Q:429:GLN:H	2.12	0.57
1:R:47:GLN:HG2	1:R:48:TYR:H	1.67	0.57
1:R:510:ILE:HG12	1:R:511:ARG:N	2.20	0.57
1:R:577:ILE:HA	1:R:582:LYS:HB3	1.86	0.57
1:S:82:PRO:HG2	1:U:560:LEU:HD22	1.86	0.57
1:S:444:LEU:C	1:S:446:THR:H	2.11	0.57
1:V:71:MSE:HE2	1:V:119:ILE:HD11	1.85	0.57
1:V:510:ILE:HG12	1:V:511:ARG:N	2.19	0.57
1:W:86:ALA:HB2	1:W:515:GLU:HG3	1.86	0.57
1:X:138:THR:H	1:X:143:VAL:HG22	1.69	0.57
1:X:276:VAL:HG23	1:X:293:ILE:HG23	1.86	0.57
2:k:65:ASN:N	2:k:66:PRO:HD2	2.19	0.57
2:u:12:ALA:H	2:u:15:ARG:HD3	1.70	0.57
1:B:49:THR:O	1:B:49:THR:CG2	2.51	0.57
1:C:236:GLN:CB	1:C:265:LYS:HZ3	2.15	0.57
1:C:389:LEU:HD12	1:C:389:LEU:H	1.68	0.57
1:D:384:LEU:HD22	1:D:384:LEU:H	1.68	0.57
1:D:541:LYS:HD3	1:D:542:THR:HG23	1.87	0.57
1:E:598:GLN:HB2	1:E:601:GLN:CB	2.34	0.57
1:F:248:LYS:NZ	1:F:513:ARG:HH12	2.02	0.57
1:G:144:ILE:HD12	1:G:145:ARG:N	2.20	0.57
1:G:199:PRO:HB3	1:G:282:THR:HG22	1.84	0.57
1:G:598:GLN:HB2	1:G:601:GLN:CB	2.34	0.57
1:H:144:ILE:HD12	1:H:145:ARG:N	2.20	0.57
1:H:389:LEU:HD12	1:H:389:LEU:H	1.68	0.57
1:I:182:ASN:HD22	1:J:171:ARG:HH21	1.51	0.57
1:I:210:PRO:HD2	1:I:211:TRP:CZ3	2.39	0.57
1:J:210:PRO:HD2	1:J:211:TRP:CZ3	2.39	0.57
1:K:210:PRO:HD2	1:K:211:TRP:CZ3	2.39	0.57
1:K:238:PRO:HG3	1:K:263:PHE:HB3	1.86	0.57
1:L:44:TRP:C	1:L:45:LEU:HD22	2.28	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:528:LYS:HZ3	1:L:560:LEU:HD21	1.68	0.57
2:Y:51:ALA:O	2:Y:54:ALA:HB3	2.04	0.57
2:Y:92:VAL:O	2:Y:96:LEU:HB2	2.04	0.57
2:a:53:MET:HE2	2:a:92:VAL:CG1	2.20	0.57
2:d:28:VAL:HG11	2:d:97:ALA:N	2.19	0.57
1:N:510:ILE:HG12	1:N:511:ARG:N	2.19	0.57
1:O:273:ARG:HH22	1:O:453:LEU:HD21	1.68	0.57
1:P:577:ILE:HA	1:P:582:LYS:HB3	1.85	0.57
1:Q:577:ILE:HA	1:Q:582:LYS:HB3	1.86	0.57
1:R:164:LEU:HD22	1:R:169:ASP:CG	2.29	0.57
1:R:431:ALA:O	1:R:435:VAL:HG22	2.04	0.57
1:T:598:GLN:HB2	1:T:601:GLN:CB	2.34	0.57
1:V:35:PHE:C	1:V:37:ARG:H	2.11	0.57
1:V:78:VAL:HG11	1:V:444:LEU:HG	1.86	0.57
1:V:379:GLU:O	1:V:380:ASN:HB2	2.04	0.57
1:W:586:THR:N	1:W:587:PRO:HD3	2.19	0.57
1:X:86:ALA:HB2	1:X:515:GLU:HG3	1.85	0.57
2:l:67:PRO:HG2	2:n:8:ASP:CB	2.34	0.57
2:n:17:LEU:HD11	2:n:36:ALA:CB	2.34	0.57
2:p:134:THR:HB	2:p:145:GLU:H	1.69	0.57
1:A:44:TRP:C	1:A:45:LEU:HD22	2.28	0.57
1:A:144:ILE:HD12	1:A:145:ARG:N	2.20	0.57
1:A:210:PRO:HD2	1:A:211:TRP:CZ3	2.39	0.57
1:A:598:GLN:HB2	1:A:601:GLN:CB	2.34	0.57
1:B:14:ARG:HH11	1:B:17:ALA:CB	2.17	0.57
1:B:166:ASP:OD2	1:B:168:SER:HB3	2.05	0.57
1:B:248:LYS:NZ	1:B:513:ARG:HH12	2.02	0.57
1:B:541:LYS:HD3	1:B:542:THR:HG23	1.87	0.57
1:C:14:ARG:HH11	1:C:17:ALA:CB	2.17	0.57
1:D:14:ARG:HH11	1:D:17:ALA:CB	2.17	0.57
1:D:395:PRO:HD2	1:F:398:PRO:HB3	1.86	0.57
1:E:210:PRO:HD2	1:E:211:TRP:CZ3	2.39	0.57
1:E:389:LEU:H	1:E:389:LEU:HD12	1.68	0.57
1:G:50:THR:HG21	1:G:54:ARG:NH2	2.18	0.57
1:G:210:PRO:HD2	1:G:211:TRP:CZ3	2.39	0.57
1:H:210:PRO:HD2	1:H:211:TRP:CZ3	2.39	0.57
1:I:166:ASP:OD2	1:I:168:SER:HB3	2.05	0.57
2:b:34:LEU:O	2:b:35:THR:HG22	2.00	0.57
2:e:92:VAL:O	2:e:96:LEU:HB2	2.04	0.57
2:f:92:VAL:O	2:f:96:LEU:HB2	2.04	0.57
2:h:51:ALA:O	2:h:54:ALA:HB3	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:j:92:VAL:O	2:j:96:LEU:HB2	2.04	0.57
1:N:444:LEU:C	1:N:446:THR:H	2.13	0.57
1:S:138:THR:H	1:S:143:VAL:HG22	1.68	0.57
1:X:99:ARG:O	1:X:103:ARG:HG3	2.04	0.57
1:X:199:PRO:HB3	1:X:282:THR:HG22	1.86	0.57
2:l:71:ASP:OD2	2:l:71:ASP:N	2.37	0.57
2:s:65:ASN:N	2:s:66:PRO:HD2	2.18	0.57
1:A:166:ASP:OD2	1:A:168:SER:HB3	2.05	0.57
1:B:41:TRP:HE3	1:B:42:ASP:CA	2.14	0.57
1:B:108:LYS:HD2	1:C:438:LEU:HD11	1.86	0.57
1:B:144:ILE:HD12	1:B:145:ARG:N	2.19	0.57
1:B:161:ASN:C	1:B:161:ASN:ND2	2.59	0.57
1:B:238:PRO:HG3	1:B:263:PHE:HB3	1.86	0.57
1:D:363:TYR:HE1	1:F:350:PHE:HE1	1.50	0.57
1:F:118:GLN:NE2	1:F:303:VAL:HB	2.19	0.57
1:F:210:PRO:HD2	1:F:211:TRP:CZ3	2.39	0.57
1:G:238:PRO:HG3	1:G:263:PHE:HB3	1.86	0.57
1:H:49:THR:O	1:H:49:THR:CG2	2.51	0.57
1:J:14:ARG:HH11	1:J:17:ALA:CB	2.17	0.57
1:J:144:ILE:HD12	1:J:145:ARG:N	2.20	0.57
1:K:546:THR:CG2	1:K:547:PRO:HD3	2.27	0.57
1:L:118:GLN:NE2	1:L:303:VAL:HB	2.19	0.57
1:L:210:PRO:HD2	1:L:211:TRP:CZ3	2.39	0.57
2:Z:28:VAL:HG11	2:Z:97:ALA:N	2.19	0.57
2:b:92:VAL:O	2:b:96:LEU:HB2	2.04	0.57
2:e:78:GLU:CD	2:e:79:GLY:H	2.11	0.57
1:N:99:ARG:O	1:N:103:ARG:HG3	2.05	0.57
1:O:554:LEU:HD12	1:O:557:PHE:HD2	1.69	0.57
1:P:199:PRO:HB3	1:P:282:THR:HG22	1.87	0.57
1:R:586:THR:N	1:R:587:PRO:HD3	2.19	0.57
1:V:86:ALA:HB2	1:V:515:GLU:HG3	1.86	0.57
1:W:554:LEU:HD12	1:W:557:PHE:HD2	1.68	0.57
1:X:379:GLU:O	1:X:380:ASN:HB2	2.04	0.57
1:X:444:LEU:C	1:X:446:THR:H	2.13	0.57
1:X:577:ILE:HA	1:X:582:LYS:HB3	1.85	0.57
2:k:17:LEU:HD11	2:k:36:ALA:CB	2.34	0.57
2:l:62:ASP:C	2:l:64:GLU:N	2.62	0.57
2:p:17:LEU:HD11	2:p:36:ALA:CB	2.33	0.57
2:r:17:LEU:HD11	2:r:36:ALA:CB	2.34	0.57
1:B:236:GLN:CB	1:B:265:LYS:HZ3	2.15	0.57
1:C:34:PHE:HZ	1:C:328:ARG:HH22	0.80	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:166:ASP:OD2	1:C:168:SER:HB3	2.05	0.57
1:D:158:TRP:HD1	1:D:158:TRP:H	1.52	0.57
1:D:166:ASP:OD2	1:D:168:SER:HB3	2.05	0.57
1:D:276:VAL:HG23	1:D:293:ILE:CG2	2.34	0.57
1:E:14:ARG:HH11	1:E:17:ALA:CB	2.17	0.57
1:F:144:ILE:HD12	1:F:145:ARG:N	2.19	0.57
1:G:118:GLN:NE2	1:G:303:VAL:HB	2.19	0.57
1:I:158:TRP:HD1	1:I:158:TRP:H	1.52	0.57
1:I:238:PRO:HG3	1:I:263:PHE:HB3	1.86	0.57
1:I:248:LYS:NZ	1:I:513:ARG:HH12	2.02	0.57
1:I:334:MSE:SE	1:J:404:MSE:HE1	2.55	0.57
1:J:118:GLN:NE2	1:J:303:VAL:HB	2.19	0.57
1:J:334:MSE:SE	1:K:404:MSE:HE1	2.55	0.57
1:K:14:ARG:HH11	1:K:17:ALA:CB	2.17	0.57
1:K:115:VAL:HA	1:K:118:GLN:HB3	1.86	0.57
1:K:541:LYS:HD3	1:K:542:THR:HG23	1.87	0.57
1:L:236:GLN:CB	1:L:265:LYS:HZ3	2.15	0.57
1:L:598:GLN:HB2	1:L:601:GLN:CB	2.34	0.57
2:Z:78:GLU:CG	2:Z:79:GLY:N	2.63	0.57
2:i:51:ALA:O	2:i:54:ALA:HB3	2.04	0.57
1:M:444:LEU:C	1:M:446:THR:H	2.13	0.57
1:N:158:TRP:HB3	1:N:173:CYS:CA	2.27	0.57
1:N:310:VAL:HG22	1:V:40:GLN:HG2	1.86	0.57
1:O:564:GLY:CA	1:P:554:LEU:HD21	2.34	0.57
1:P:154:SER:O	1:P:204:PRO:HB3	2.03	0.57
1:Q:276:VAL:HG23	1:Q:293:ILE:HG23	1.85	0.57
1:Q:598:GLN:HB2	1:Q:601:GLN:CB	2.35	0.57
1:R:165:MSE:HE3	1:R:304:PHE:HB2	1.87	0.57
1:V:390:ALA:CB	1:W:387:GLN:CB	2.83	0.57
2:k:104:ILE:HD12	2:k:105:ALA:N	2.19	0.57
2:o:42:ALA:HB1	2:p:81:SER:HB3	1.86	0.57
2:q:17:LEU:HD11	2:q:36:ALA:CB	2.35	0.57
2:v:134:THR:HB	2:v:145:GLU:N	2.20	0.57
1:A:115:VAL:HA	1:A:118:GLN:HB3	1.86	0.57
1:B:563:LYS:HD3	1:C:557:PHE:CE2	2.40	0.57
1:C:50:THR:HG21	1:C:54:ARG:NH2	2.18	0.57
1:C:54:ARG:HB2	2:a:146:GLY:HA3	1.87	0.57
1:D:210:PRO:HD2	1:D:211:TRP:CZ3	2.39	0.57
1:E:49:THR:O	1:E:49:THR:CG2	2.51	0.57
1:F:166:ASP:OD2	1:F:168:SER:HB3	2.05	0.57
1:H:37:ARG:HH21	1:H:37:ARG:CB	2.16	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:144:ILE:HD12	1:I:145:ARG:N	2.20	0.57
1:I:598:GLN:HB2	1:I:601:GLN:CB	2.34	0.57
1:J:343:ARG:NH1	2:i:135:ALA:O	2.34	0.57
1:K:440:MSE:O	1:K:444:LEU:HD22	2.05	0.57
1:L:14:ARG:HH11	1:L:17:ALA:CB	2.17	0.57
1:L:238:PRO:HG3	1:L:263:PHE:HB3	1.86	0.57
2:a:51:ALA:O	2:a:54:ALA:HB3	2.05	0.57
1:M:154:SER:O	1:M:204:PRO:HB3	2.04	0.57
1:M:273:ARG:NH2	1:M:453:LEU:HD21	2.19	0.57
1:O:165:MSE:HE3	1:O:304:PHE:HB2	1.85	0.57
1:R:379:GLU:O	1:R:380:ASN:HB2	2.04	0.57
1:S:199:PRO:HB3	1:S:282:THR:HG22	1.85	0.57
1:U:95:MSE:HB3	1:U:527:MSE:HE1	1.87	0.57
1:U:273:ARG:NH2	1:U:453:LEU:HD21	2.19	0.57
1:V:586:THR:N	1:V:587:PRO:HD3	2.19	0.57
1:W:598:GLN:HB2	1:W:601:GLN:CB	2.35	0.57
1:X:427:GLY:C	1:X:429:GLN:H	2.12	0.57
2:q:62:ASP:C	2:q:64:GLU:N	2.61	0.57
2:t:12:ALA:H	2:t:15:ARG:HD3	1.70	0.57
2:v:17:LEU:HD11	2:v:36:ALA:CB	2.34	0.57
1:B:389:LEU:H	1:B:389:LEU:HD12	1.68	0.57
1:B:597:GLN:HA	1:B:597:GLN:HE21	1.70	0.57
1:C:37:ARG:HH21	1:C:37:ARG:CB	2.16	0.57
1:C:597:GLN:HA	1:C:597:GLN:HE21	1.70	0.57
1:D:49:THR:O	1:D:49:THR:CG2	2.51	0.57
1:D:171:ARG:HH21	1:E:182:ASN:ND2	2.02	0.57
1:E:144:ILE:HD12	1:E:145:ARG:N	2.20	0.57
1:F:372:TYR:CE2	1:G:348:LYS:HB2	2.40	0.57
1:F:598:GLN:HB2	1:F:601:GLN:CB	2.34	0.57
1:G:115:VAL:HA	1:G:118:GLN:HB3	1.86	0.57
1:H:166:ASP:OD2	1:H:168:SER:HB3	2.05	0.57
1:I:276:VAL:HG23	1:I:293:ILE:CG2	2.34	0.57
1:I:310:VAL:C	1:I:312:ASP:H	2.13	0.57
1:J:310:VAL:C	1:J:312:ASP:H	2.13	0.57
1:K:376:ARG:HB2	1:L:352:TRP:CG	2.40	0.57
2:Z:51:ALA:O	2:Z:54:ALA:HB3	2.04	0.57
2:Z:92:VAL:O	2:Z:96:LEU:HB2	2.04	0.57
2:b:51:ALA:O	2:b:54:ALA:HB3	2.04	0.57
2:f:51:ALA:O	2:f:54:ALA:HB3	2.05	0.57
2:g:51:ALA:O	2:g:54:ALA:HB3	2.04	0.57
2:g:78:GLU:HG3	2:g:79:GLY:N	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:332:MSE:SE	2:k:132:MET:HA	2.55	0.57
1:O:99:ARG:O	1:O:103:ARG:HG3	2.05	0.57
1:O:561:ASP:OD2	1:P:92:ASP:HB3	2.04	0.57
1:P:586:THR:N	1:P:587:PRO:HD3	2.19	0.57
1:R:138:THR:H	1:R:143:VAL:HG22	1.69	0.57
1:T:35:PHE:C	1:T:37:ARG:H	2.11	0.57
1:T:78:VAL:HG11	1:T:444:LEU:HG	1.86	0.57
1:V:210:PRO:HD2	1:V:211:TRP:CD2	2.40	0.57
1:V:390:ALA:CB	1:W:387:GLN:HB3	2.35	0.57
1:W:78:VAL:HG11	1:W:444:LEU:HG	1.87	0.57
1:W:236:GLN:CB	1:W:265:LYS:HG2	2.32	0.57
2:p:65:ASN:N	2:p:66:PRO:HD2	2.18	0.57
1:A:248:LYS:NZ	1:A:513:ARG:HH12	2.02	0.57
1:A:389:LEU:H	1:A:389:LEU:HD12	1.68	0.57
1:B:210:PRO:HD2	1:B:211:TRP:CZ3	2.39	0.57
1:B:440:MSE:O	1:B:444:LEU:HD22	2.05	0.57
1:B:444:LEU:C	1:B:446:THR:N	2.61	0.57
1:C:541:LYS:HD3	1:C:542:THR:HG23	1.87	0.57
1:C:598:GLN:HB2	1:C:601:GLN:CB	2.34	0.57
1:E:440:MSE:O	1:E:444:LEU:HD22	2.05	0.57
1:E:444:LEU:C	1:E:446:THR:N	2.61	0.57
1:E:541:LYS:HD3	1:E:542:THR:HG23	1.87	0.57
1:F:44:TRP:C	1:F:45:LEU:HD22	2.28	0.57
1:G:310:VAL:C	1:G:312:ASP:H	2.13	0.57
1:H:440:MSE:O	1:H:444:LEU:HD22	2.05	0.57
1:L:597:GLN:HE21	1:L:597:GLN:HA	1.70	0.57
2:b:28:VAL:HG11	2:b:97:ALA:N	2.19	0.57
1:N:44:TRP:C	1:N:45:LEU:HD22	2.30	0.57
1:O:598:GLN:HB2	1:O:601:GLN:CB	2.35	0.57
1:P:431:ALA:O	1:P:435:VAL:HG22	2.05	0.57
1:R:598:GLN:HB2	1:R:601:GLN:CB	2.35	0.57
3:S:719:HOH:O	1:T:430:VAL:CG1	2.53	0.57
1:T:165:MSE:HE3	1:T:304:PHE:HB2	1.87	0.57
1:X:598:GLN:HB2	1:X:601:GLN:CB	2.35	0.57
2:k:93:PRO:HB3	2:m:100:THR:HG21	1.85	0.57
1:B:248:LYS:HG3	1:B:511:ARG:HH11	1.70	0.57
1:C:334:MSE:HE3	1:E:404:MSE:CE	2.34	0.57
1:D:248:LYS:HG3	1:D:511:ARG:HH11	1.70	0.57
1:E:238:PRO:HG3	1:E:263:PHE:HB3	1.86	0.57
1:E:597:GLN:HA	1:E:597:GLN:HE21	1.70	0.57
1:H:115:VAL:HA	1:H:118:GLN:HB3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:597:GLN:HA	1:H:597:GLN:HE21	1.70	0.57
1:I:115:VAL:HA	1:I:118:GLN:HB3	1.86	0.57
1:J:597:GLN:HE21	1:J:597:GLN:HA	1.70	0.57
1:J:598:GLN:HB2	1:J:601:GLN:CB	2.34	0.57
1:K:248:LYS:NZ	1:K:513:ARG:HH12	2.02	0.57
2:Z:78:GLU:HG3	2:Z:79:GLY:N	2.20	0.57
2:j:28:VAL:HG11	2:j:97:ALA:N	2.19	0.57
1:M:158:TRP:O	1:M:160:SER:N	2.38	0.56
1:P:46:SER:N	1:P:48:TYR:HE2	1.97	0.56
1:S:561:ASP:OD2	1:T:92:ASP:HB3	2.03	0.56
1:T:209:PHE:HZ	1:T:214:GLN:HG2	1.70	0.56
1:T:427:GLY:C	1:T:429:GLN:H	2.13	0.56
1:U:37:ARG:NH2	1:U:41:TRP:HB3	2.20	0.56
1:U:54:ARG:HB2	2:q:137:GLY:HA3	1.87	0.56
1:U:78:VAL:HG11	1:U:444:LEU:HG	1.86	0.56
1:U:94:LEU:HA	1:U:97:MSE:CE	2.34	0.56
2:p:12:ALA:H	2:p:15:ARG:HD3	1.70	0.56
1:D:115:VAL:HA	1:D:118:GLN:HB3	1.86	0.56
1:D:144:ILE:HD12	1:D:145:ARG:N	2.19	0.56
1:D:597:GLN:HE21	1:D:597:GLN:HA	1.70	0.56
1:E:166:ASP:OD2	1:E:168:SER:HB3	2.05	0.56
1:F:34:PHE:HZ	1:F:328:ARG:HH22	0.80	0.56
1:H:334:MSE:HE3	1:I:404:MSE:HE3	1.86	0.56
1:J:42:ASP:OD2	2:i:145:SER:O	2.23	0.56
1:L:248:LYS:NZ	1:L:513:ARG:HH12	2.02	0.56
2:Y:78:GLU:CG	2:Y:79:GLY:N	2.63	0.56
1:M:598:GLN:HB2	1:M:601:GLN:CB	2.35	0.56
1:O:158:TRP:O	1:O:160:SER:N	2.37	0.56
1:P:158:TRP:O	1:P:160:SER:N	2.38	0.56
1:P:158:TRP:CH2	1:P:302:PRO:HG3	2.39	0.56
1:Q:94:LEU:HA	1:Q:97:MSE:CE	2.35	0.56
1:U:86:ALA:HB2	1:U:515:GLU:HG3	1.86	0.56
1:V:273:ARG:NH1	1:V:275:ARG:HE	2.03	0.56
2:s:12:ALA:H	2:s:15:ARG:HD3	1.69	0.56
2:u:71:ASP:OD2	2:u:71:ASP:N	2.37	0.56
2:u:134:THR:HB	2:u:145:GLU:N	2.20	0.56
1:A:372:TYR:CE2	1:B:348:LYS:HB2	2.39	0.56
1:B:115:VAL:HA	1:B:118:GLN:HB3	1.86	0.56
1:B:310:VAL:C	1:B:312:ASP:H	2.13	0.56
1:G:440:MSE:O	1:G:444:LEU:HD22	2.05	0.56
1:I:440:MSE:O	1:I:444:LEU:HD22	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:118:GLN:NE2	1:K:303:VAL:HB	2.19	0.56
1:K:248:LYS:CG	1:K:511:ARG:HH11	2.19	0.56
1:L:440:MSE:O	1:L:444:LEU:HD22	2.05	0.56
1:L:541:LYS:HD3	1:L:542:THR:HG23	1.87	0.56
1:M:71:MSE:HE2	1:M:119:ILE:HD11	1.86	0.56
1:M:78:VAL:CG2	1:M:444:LEU:HD11	2.23	0.56
1:M:430:VAL:CG1	3:N:719:HOH:O	2.53	0.56
1:M:578:GLN:HG2	1:M:596:ALA:HB2	1.87	0.56
1:N:24:GLU:C	1:N:26:ARG:N	2.56	0.56
1:N:577:ILE:HA	1:N:582:LYS:HB3	1.85	0.56
1:P:427:GLY:C	1:P:429:GLN:H	2.13	0.56
1:R:44:TRP:C	1:R:45:LEU:HD22	2.30	0.56
1:S:24:GLU:C	1:S:26:ARG:N	2.56	0.56
1:S:165:MSE:HE3	1:S:304:PHE:HB2	1.86	0.56
1:S:598:GLN:HB2	1:S:601:GLN:CB	2.35	0.56
1:U:273:ARG:HH22	1:U:453:LEU:HD21	1.70	0.56
1:V:78:VAL:HG12	1:V:79:LEU:H	1.70	0.56
1:V:578:GLN:HG2	1:V:596:ALA:HB2	1.87	0.56
1:W:158:TRP:O	1:W:160:SER:N	2.38	0.56
1:X:210:PRO:HD2	1:X:211:TRP:CD2	2.40	0.56
1:X:456:ALA:HB1	1:X:509:ASP:OD1	2.05	0.56
2:k:134:THR:HB	2:k:145:GLU:H	1.68	0.56
1:A:310:VAL:C	1:A:312:ASP:H	2.13	0.56
1:C:310:VAL:C	1:C:312:ASP:H	2.13	0.56
1:D:310:VAL:C	1:D:312:ASP:H	2.13	0.56
1:F:248:LYS:HG3	1:F:511:ARG:HH11	1.70	0.56
1:F:310:VAL:C	1:F:312:ASP:H	2.13	0.56
1:F:444:LEU:C	1:F:446:THR:N	2.61	0.56
1:G:34:PHE:HE1	1:G:324:LYS:HZ2	1.50	0.56
1:G:42:ASP:OD2	2:d:145:SER:O	2.23	0.56
1:G:166:ASP:OD2	1:G:168:SER:HB3	2.05	0.56
1:G:444:LEU:C	1:G:446:THR:N	2.61	0.56
1:I:118:GLN:NE2	1:I:303:VAL:HB	2.19	0.56
1:I:334:MSE:HE3	1:J:404:MSE:CE	2.35	0.56
1:I:567:MSE:SE	1:J:576:LEU:HD13	2.55	0.56
1:I:597:GLN:HA	1:I:597:GLN:HE21	1.70	0.56
1:J:166:ASP:OD2	1:J:168:SER:HB3	2.05	0.56
1:J:248:LYS:HG3	1:J:511:ARG:HH11	1.70	0.56
1:J:440:MSE:O	1:J:444:LEU:HD22	2.05	0.56
1:K:248:LYS:HG3	1:K:511:ARG:HH11	1.70	0.56
1:K:310:VAL:C	1:K:312:ASP:H	2.13	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:248:LYS:HG3	1:L:511:ARG:HH11	1.70	0.56
2:a:28:VAL:HG11	2:a:97:ALA:N	2.19	0.56
2:c:51:ALA:O	2:c:54:ALA:HB3	2.05	0.56
2:d:51:ALA:O	2:d:54:ALA:HB3	2.05	0.56
2:d:78:GLU:HG3	2:d:79:GLY:N	2.20	0.56
2:e:28:VAL:HG11	2:e:97:ALA:N	2.19	0.56
2:e:53:MET:HE2	2:e:92:VAL:CG1	2.20	0.56
2:h:34:LEU:C	2:h:35:THR:CG2	2.73	0.56
1:M:210:PRO:HD2	1:M:211:TRP:CD2	2.41	0.56
1:N:71:MSE:HE2	1:N:119:ILE:HD11	1.85	0.56
1:N:598:GLN:HB2	1:N:601:GLN:CB	2.35	0.56
1:O:144:ILE:HD12	1:O:145:ARG:N	2.20	0.56
1:O:164:LEU:HD22	1:O:169:ASP:CG	2.31	0.56
1:P:510:ILE:HG12	1:P:511:ARG:N	2.20	0.56
1:P:598:GLN:HB2	1:P:601:GLN:CB	2.35	0.56
1:Q:46:SER:N	1:Q:48:TYR:HE2	1.98	0.56
1:Q:158:TRP:O	1:Q:160:SER:N	2.39	0.56
1:Q:210:PRO:HD2	1:Q:211:TRP:CD2	2.40	0.56
1:Q:564:GLY:HA2	1:R:554:LEU:HD21	1.87	0.56
1:R:165:MSE:HE1	1:R:435:VAL:HB	1.87	0.56
1:S:209:PHE:N	1:S:210:PRO:HD3	2.21	0.56
1:U:99:ARG:O	1:U:103:ARG:HG3	2.05	0.56
1:U:199:PRO:HB3	1:U:282:THR:HG22	1.87	0.56
1:U:210:PRO:HD2	1:U:211:TRP:CD2	2.40	0.56
1:V:164:LEU:HD22	1:V:169:ASP:CG	2.30	0.56
1:V:209:PHE:HZ	1:V:214:GLN:HG2	1.70	0.56
1:X:35:PHE:C	1:X:37:ARG:H	2.12	0.56
2:u:17:LEU:HD11	2:u:36:ALA:CB	2.35	0.56
2:u:134:THR:HB	2:u:145:GLU:H	1.68	0.56
2:v:12:ALA:H	2:v:15:ARG:HD3	1.70	0.56
1:A:72:ARG:HD2	1:B:434:THR:HG21	1.87	0.56
1:A:236:GLN:CB	1:A:265:LYS:HZ3	2.15	0.56
1:C:210:PRO:HD2	1:C:211:TRP:CZ3	2.39	0.56
1:D:35:PHE:C	1:D:37:ARG:N	2.62	0.56
1:D:444:LEU:C	1:D:446:THR:N	2.61	0.56
1:F:35:PHE:C	1:F:37:ARG:N	2.62	0.56
1:G:37:ARG:HH21	1:G:37:ARG:CB	2.16	0.56
1:H:158:TRP:HD1	1:H:158:TRP:H	1.52	0.56
1:H:248:LYS:CG	1:H:511:ARG:HH11	2.19	0.56
1:I:210:PRO:HD2	1:I:211:TRP:CE3	2.41	0.56
1:J:210:PRO:HD2	1:J:211:TRP:CE3	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:166:ASP:OD2	1:K:168:SER:HB3	2.05	0.56
1:K:273:ARG:NH2	1:K:453:LEU:HD21	2.21	0.56
1:L:144:ILE:HD12	1:L:145:ARG:N	2.20	0.56
2:g:92:VAL:O	2:g:96:LEU:HB2	2.04	0.56
2:i:28:VAL:HG11	2:i:97:ALA:N	2.19	0.56
1:N:54:ARG:HB2	2:k:137:GLY:HA3	1.88	0.56
1:N:210:PRO:HD2	1:N:211:TRP:CD2	2.41	0.56
1:N:554:LEU:HD21	1:V:564:GLY:HA2	1.86	0.56
1:O:210:PRO:HD2	1:O:211:TRP:CD2	2.41	0.56
1:R:199:PRO:HB3	1:R:282:THR:HG22	1.86	0.56
1:S:510:ILE:HG12	1:S:511:ARG:N	2.20	0.56
1:U:598:GLN:HB2	1:U:601:GLN:CB	2.35	0.56
1:X:158:TRP:CE3	1:X:173:CYS:SG	2.85	0.56
2:m:134:THR:HB	2:m:145:GLU:H	1.70	0.56
2:q:134:THR:HB	2:q:145:GLU:H	1.70	0.56
1:A:440:MSE:O	1:A:444:LEU:HD22	2.05	0.56
1:A:597:GLN:HA	1:A:597:GLN:HE21	1.70	0.56
1:D:248:LYS:CG	1:D:511:ARG:HH11	2.19	0.56
1:E:158:TRP:H	1:E:158:TRP:HD1	1.52	0.56
1:E:210:PRO:HD2	1:E:211:TRP:CE3	2.41	0.56
1:E:248:LYS:CG	1:E:511:ARG:HH11	2.19	0.56
1:E:443:ASP:C	1:E:444:LEU:HD13	2.31	0.56
1:G:248:LYS:HG3	1:G:511:ARG:HH11	1.70	0.56
1:I:443:ASP:C	1:I:444:LEU:HD13	2.31	0.56
1:J:236:GLN:CB	1:J:265:LYS:HZ3	2.16	0.56
1:J:443:ASP:C	1:J:444:LEU:HD13	2.31	0.56
1:K:144:ILE:HD12	1:K:145:ARG:N	2.20	0.56
1:K:443:ASP:C	1:K:444:LEU:HD13	2.31	0.56
1:K:444:LEU:C	1:K:446:THR:N	2.61	0.56
1:L:35:PHE:C	1:L:37:ARG:N	2.61	0.56
2:j:51:ALA:O	2:j:54:ALA:HB3	2.05	0.56
1:N:66:LYS:HZ3	1:N:420:VAL:HG11	1.70	0.56
1:Q:164:LEU:HD22	1:Q:169:ASP:CG	2.31	0.56
1:R:578:GLN:HG2	1:R:596:ALA:HB2	1.88	0.56
1:S:78:VAL:HG11	1:S:444:LEU:HG	1.86	0.56
1:S:273:ARG:HH22	1:S:453:LEU:HD21	1.70	0.56
1:S:427:GLY:C	1:S:429:GLN:H	2.14	0.56
1:T:158:TRP:O	1:T:160:SER:N	2.39	0.56
1:U:44:TRP:C	1:U:45:LEU:HD22	2.30	0.56
1:U:158:TRP:O	1:U:160:SER:N	2.39	0.56
1:U:165:MSE:HE3	1:U:304:PHE:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:209:PHE:N	1:V:210:PRO:HD3	2.21	0.56
1:W:158:TRP:CE3	1:W:173:CYS:SG	2.85	0.56
1:X:510:ILE:HG12	1:X:511:ARG:N	2.19	0.56
2:p:58:TYR:HB2	2:p:75:LEU:HD21	1.86	0.56
2:s:134:THR:HB	2:s:145:GLU:H	1.69	0.56
2:v:58:TYR:HB2	2:v:75:LEU:HD21	1.88	0.56
1:A:302:PRO:O	1:A:439:ASN:CG	2.49	0.56
1:A:443:ASP:C	1:A:444:LEU:HD13	2.31	0.56
1:A:541:LYS:HD3	1:A:542:THR:HG23	1.87	0.56
1:C:302:PRO:O	1:C:439:ASN:CG	2.49	0.56
1:D:337:ASN:ND2	1:D:401:ASN:HD22	2.04	0.56
1:F:210:PRO:HD2	1:F:211:TRP:CE3	2.41	0.56
1:F:363:TYR:HE1	1:G:350:PHE:HE1	1.53	0.56
1:H:210:PRO:HD2	1:H:211:TRP:CE3	2.41	0.56
1:I:248:LYS:CG	1:I:511:ARG:HH11	2.19	0.56
1:I:248:LYS:HG3	1:I:511:ARG:HH11	1.70	0.56
1:J:238:PRO:HG3	1:J:263:PHE:HB3	1.86	0.56
1:J:248:LYS:CG	1:J:511:ARG:HH11	2.19	0.56
2:Z:78:GLU:O	2:Z:80:ASP:OD2	2.24	0.56
1:N:35:PHE:C	1:N:37:ARG:H	2.14	0.56
1:O:273:ARG:NH1	1:O:275:ARG:HE	2.04	0.56
1:S:158:TRP:O	1:S:160:SER:N	2.39	0.56
1:T:66:LYS:HZ3	1:T:420:VAL:HG11	1.71	0.56
1:T:456:ALA:HB1	1:T:509:ASP:OD1	2.05	0.56
1:V:44:TRP:C	1:V:45:LEU:HD22	2.31	0.56
1:V:95:MSE:HB3	1:V:527:MSE:HE1	1.88	0.56
1:W:165:MSE:HE3	1:W:304:PHE:HB2	1.86	0.56
1:X:273:ARG:NH2	1:X:453:LEU:HD21	2.21	0.56
1:X:273:ARG:NH1	1:X:275:ARG:HE	2.04	0.56
1:A:210:PRO:HD2	1:A:211:TRP:CE3	2.41	0.56
1:A:352:TRP:CD2	1:L:376:ARG:HB2	2.41	0.56
1:C:158:TRP:HD1	1:C:158:TRP:H	1.52	0.56
1:D:302:PRO:O	1:D:439:ASN:CG	2.49	0.56
1:E:337:ASN:ND2	1:E:401:ASN:HD22	2.04	0.56
1:F:597:GLN:HA	1:F:597:GLN:HE21	1.70	0.56
1:G:158:TRP:HD1	1:G:158:TRP:H	1.52	0.56
1:G:334:MSE:SE	1:H:404:MSE:HE1	2.55	0.56
1:G:597:GLN:HE21	1:G:597:GLN:HA	1.70	0.56
1:H:248:LYS:NZ	1:H:513:ARG:HH12	2.02	0.56
1:K:597:GLN:HA	1:K:597:GLN:HE21	1.70	0.56
1:L:310:VAL:C	1:L:312:ASP:H	2.13	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:443:ASP:C	1:L:444:LEU:HD13	2.31	0.56
2:e:78:GLU:O	2:e:80:ASP:OD2	2.24	0.56
2:i:78:GLU:O	2:i:80:ASP:OD2	2.24	0.56
1:N:158:TRP:O	1:N:160:SER:N	2.38	0.56
1:O:35:PHE:C	1:O:37:ARG:H	2.12	0.56
1:O:35:PHE:CE1	1:O:321:ARG:NE	2.73	0.56
1:O:209:PHE:N	1:O:210:PRO:HD3	2.21	0.56
1:S:210:PRO:HD2	1:S:211:TRP:CD2	2.40	0.56
1:S:430:VAL:CG1	3:U:719:HOH:O	2.52	0.56
1:T:578:GLN:HG2	1:T:596:ALA:HB2	1.86	0.56
1:A:248:LYS:CG	1:A:511:ARG:HH11	2.19	0.56
1:C:248:LYS:CG	1:C:511:ARG:HH11	2.19	0.56
1:E:302:PRO:O	1:E:439:ASN:CG	2.49	0.56
1:F:546:THR:CG2	1:F:547:PRO:HD3	2.27	0.56
1:G:443:ASP:C	1:G:444:LEU:HD13	2.31	0.56
1:H:443:ASP:C	1:H:444:LEU:HD13	2.31	0.56
1:I:541:LYS:HD3	1:I:542:THR:HG23	1.87	0.56
1:K:182:ASN:ND2	1:L:171:ARG:HH21	2.03	0.56
2:Y:78:GLU:O	2:Y:80:ASP:OD2	2.24	0.56
2:j:78:GLU:O	2:j:80:ASP:OD2	2.24	0.56
1:N:94:LEU:HA	1:N:97:MSE:CE	2.36	0.56
1:N:164:LEU:HD22	1:N:169:ASP:CG	2.30	0.56
1:N:199:PRO:HB3	1:N:282:THR:HG22	1.87	0.56
1:N:209:PHE:HZ	1:N:214:GLN:HG2	1.70	0.56
1:Q:86:ALA:HB2	1:Q:515:GLU:HG3	1.87	0.56
1:Q:158:TRP:HB3	1:Q:173:CYS:CA	2.27	0.56
1:Q:431:ALA:O	1:Q:435:VAL:HG22	2.05	0.56
1:Q:510:ILE:HG12	1:Q:511:ARG:N	2.20	0.56
1:Q:578:GLN:HG2	1:Q:596:ALA:HB2	1.86	0.56
1:R:443:ASP:C	1:R:446:THR:HG22	2.31	0.56
1:S:212:LEU:HD22	1:T:26:ARG:HG2	1.86	0.56
1:S:578:GLN:HG2	1:S:596:ALA:HB2	1.87	0.56
1:T:209:PHE:N	1:T:210:PRO:HD3	2.21	0.56
3:T:719:HOH:O	1:W:430:VAL:CG1	2.53	0.56
1:U:434:THR:O	1:U:437:GLN:HG2	2.06	0.56
1:W:444:LEU:C	1:W:446:THR:H	2.13	0.56
2:m:71:ASP:OD2	2:m:71:ASP:N	2.37	0.56
1:B:302:PRO:O	1:B:439:ASN:CG	2.49	0.56
1:B:443:ASP:C	1:B:444:LEU:HD13	2.31	0.56
1:C:210:PRO:HD2	1:C:211:TRP:CE3	2.41	0.56
1:C:440:MSE:O	1:C:444:LEU:HD22	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:248:LYS:CG	1:G:511:ARG:HH11	2.19	0.56
1:H:329:LEU:HD22	2:d:142:PRO:HG2	1.87	0.56
1:H:337:ASN:ND2	1:H:401:ASN:HD22	2.04	0.56
1:I:337:ASN:ND2	1:I:401:ASN:HD22	2.04	0.56
1:J:273:ARG:NH2	1:J:453:LEU:HD21	2.21	0.56
1:J:302:PRO:O	1:J:439:ASN:CG	2.49	0.56
1:K:158:TRP:HB3	1:K:173:CYS:CA	2.36	0.56
1:K:158:TRP:HD1	1:K:158:TRP:H	1.52	0.56
1:O:578:GLN:HG2	1:O:596:ALA:HB2	1.88	0.56
1:P:54:ARG:HB2	2:n:137:GLY:HA3	1.87	0.56
1:P:144:ILE:HD12	1:P:145:ARG:N	2.21	0.56
1:P:296:GLU:HG2	1:P:449:PHE:HB3	1.88	0.56
1:Q:41:TRP:HE1	1:R:27:ARG:HH21	1.54	0.56
1:Q:101:ASP:HB2	1:Q:144:ILE:O	2.06	0.56
1:Q:209:PHE:N	1:Q:210:PRO:HD3	2.21	0.56
1:R:210:PRO:HD2	1:R:211:TRP:CD2	2.41	0.56
1:S:564:GLY:CA	1:T:554:LEU:HD21	2.36	0.56
1:V:430:VAL:CG1	3:W:719:HOH:O	2.54	0.56
1:W:199:PRO:HB3	1:W:282:THR:HG22	1.87	0.56
1:W:209:PHE:HZ	1:W:214:GLN:HG2	1.70	0.56
1:W:209:PHE:N	1:W:210:PRO:HD3	2.21	0.56
2:k:71:ASP:OD2	2:k:71:ASP:N	2.36	0.56
2:l:104:ILE:HD12	2:l:105:ALA:N	2.21	0.56
2:m:58:TYR:HB2	2:m:75:LEU:HD21	1.88	0.56
2:q:81:SER:HB3	2:r:42:ALA:HB1	1.86	0.56
2:s:58:TYR:HB2	2:s:75:LEU:HD21	1.88	0.56
1:B:27:ARG:HB2	1:B:313:LYS:HE3	1.88	0.56
1:E:380:ASN:O	1:E:381:SER:HB3	2.06	0.56
1:F:248:LYS:CG	1:F:511:ARG:HH11	2.19	0.56
1:G:34:PHE:HZ	1:G:328:ARG:HH22	0.80	0.56
1:I:248:LYS:HZ1	1:I:513:ARG:HH12	1.52	0.56
2:f:27:GLY:HA2	2:f:30:SER:HB3	1.88	0.56
1:M:78:VAL:HG11	1:M:444:LEU:HG	1.87	0.55
1:N:332:MSE:SE	2:v:132:MET:HA	2.56	0.55
1:P:94:LEU:HA	1:P:97:MSE:CE	2.36	0.55
1:Q:273:ARG:NH1	1:Q:275:ARG:HE	2.04	0.55
1:R:71:MSE:HE2	1:R:119:ILE:HD11	1.86	0.55
1:R:209:PHE:N	1:R:210:PRO:HD3	2.21	0.55
1:R:420:VAL:HG22	1:R:428:GLY:HA3	1.88	0.55
1:U:390:ALA:CB	1:X:387:GLN:HB3	2.36	0.55
1:V:94:LEU:HA	1:V:97:MSE:CE	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:593:LEU:O	1:W:597:GLN:HG2	2.06	0.55
1:X:101:ASP:HB2	1:X:144:ILE:O	2.07	0.55
2:u:42:ALA:HB1	2:v:81:SER:HB3	1.88	0.55
1:A:158:TRP:HB3	1:A:173:CYS:CA	2.36	0.55
1:A:427:GLY:C	1:A:429:GLN:H	2.15	0.55
1:B:158:TRP:HB3	1:B:173:CYS:CA	2.36	0.55
1:B:210:PRO:HD2	1:B:211:TRP:CE3	2.41	0.55
1:D:404:MSE:CE	1:E:334:MSE:HE3	2.36	0.55
1:D:440:MSE:O	1:D:444:LEU:HD22	2.05	0.55
1:E:248:LYS:HG3	1:E:511:ARG:HH11	1.70	0.55
1:F:541:LYS:HD3	1:F:542:THR:HG23	1.87	0.55
1:G:302:PRO:O	1:G:439:ASN:CG	2.49	0.55
1:G:541:LYS:HD3	1:G:542:THR:HG23	1.87	0.55
1:H:248:LYS:HG3	1:H:511:ARG:HH11	1.70	0.55
1:H:302:PRO:O	1:H:439:ASN:CG	2.49	0.55
1:I:302:PRO:O	1:I:439:ASN:CG	2.49	0.55
1:I:380:ASN:O	1:I:381:SER:HB3	2.07	0.55
1:K:302:PRO:O	1:K:439:ASN:CG	2.49	0.55
1:L:158:TRP:HD1	1:L:158:TRP:H	1.52	0.55
1:L:248:LYS:CG	1:L:511:ARG:HH11	2.19	0.55
2:a:19:VAL:O	2:a:82:HIS:CD2	2.60	0.55
1:N:546:THR:CG2	1:N:547:PRO:HD3	2.29	0.55
1:O:44:TRP:CE2	1:O:54:ARG:HB3	2.41	0.55
1:Q:296:GLU:HG2	1:Q:449:PHE:HB3	1.87	0.55
1:R:296:GLU:HG2	1:R:449:PHE:HB3	1.88	0.55
1:S:99:ARG:O	1:S:103:ARG:HG3	2.05	0.55
1:T:99:ARG:O	1:T:103:ARG:HG3	2.04	0.55
1:T:210:PRO:HD2	1:T:211:TRP:CD2	2.41	0.55
1:U:35:PHE:CE1	1:U:321:ARG:NE	2.74	0.55
1:U:71:MSE:HE2	1:U:119:ILE:HD11	1.88	0.55
1:X:81:ARG:HB2	1:X:517:TYR:CZ	2.41	0.55
1:X:273:ARG:HH22	1:X:453:LEU:HD21	1.71	0.55
1:X:578:GLN:HG2	1:X:596:ALA:HB2	1.87	0.55
2:l:12:ALA:H	2:l:15:ARG:HD3	1.70	0.55
2:l:134:THR:HB	2:l:145:GLU:H	1.70	0.55
2:q:12:ALA:H	2:q:15:ARG:HD3	1.69	0.55
1:G:27:ARG:HB2	1:G:313:LYS:HE3	1.89	0.55
1:G:210:PRO:HD2	1:G:211:TRP:CE3	2.41	0.55
1:G:380:ASN:O	1:G:381:SER:HB3	2.07	0.55
1:H:238:PRO:HG3	1:H:263:PHE:HB3	1.87	0.55
1:I:444:LEU:C	1:I:446:THR:N	2.61	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:395:PRO:HD2	1:K:398:PRO:HB3	1.87	0.55
1:K:34:PHE:CE1	1:K:324:LYS:NZ	2.72	0.55
1:L:337:ASN:ND2	1:L:401:ASN:HD22	2.04	0.55
1:L:589:GLU:HA	1:L:592:TRP:HB2	1.88	0.55
2:b:78:GLU:O	2:b:80:ASP:OD2	2.24	0.55
2:h:78:GLU:O	2:h:80:ASP:OD2	2.24	0.55
1:M:92:ASP:HB3	1:N:561:ASP:OD2	2.06	0.55
1:O:94:LEU:HA	1:O:97:MSE:CE	2.36	0.55
1:Q:165:MSE:HE3	1:Q:304:PHE:HB2	1.87	0.55
1:Q:456:ALA:HB1	1:Q:509:ASP:OD1	2.06	0.55
1:R:273:ARG:NH1	1:R:275:ARG:HE	2.05	0.55
1:S:71:MSE:HE2	1:S:119:ILE:HD11	1.87	0.55
1:S:296:GLU:HG2	1:S:449:PHE:HB3	1.87	0.55
1:T:246:TYR:CD2	1:T:511:ARG:HB2	2.39	0.55
1:T:444:LEU:C	1:T:446:THR:H	2.14	0.55
1:V:427:GLY:C	1:V:429:GLN:H	2.13	0.55
1:W:99:ARG:O	1:W:103:ARG:HG3	2.05	0.55
1:X:15:PHE:HZ	1:X:283:CYS:SG	2.26	0.55
1:X:296:GLU:HG2	1:X:449:PHE:HB3	1.88	0.55
2:o:134:THR:HB	2:o:145:GLU:N	2.21	0.55
2:r:104:ILE:HD12	2:r:105:ALA:N	2.21	0.55
1:C:444:LEU:C	1:C:446:THR:N	2.61	0.55
1:D:589:GLU:HA	1:D:592:TRP:HB2	1.89	0.55
1:E:310:VAL:C	1:E:312:ASP:H	2.13	0.55
1:F:440:MSE:O	1:F:444:LEU:HD22	2.05	0.55
1:G:236:GLN:CB	1:G:265:LYS:HZ3	2.15	0.55
1:H:310:VAL:C	1:H:312:ASP:H	2.13	0.55
1:I:427:GLY:C	1:I:429:GLN:H	2.14	0.55
1:K:210:PRO:HD2	1:K:211:TRP:CE3	2.41	0.55
1:L:380:ASN:O	1:L:381:SER:HB3	2.06	0.55
1:L:444:LEU:C	1:L:446:THR:N	2.61	0.55
2:d:27:GLY:HA2	2:d:30:SER:HB3	1.88	0.55
2:e:19:VAL:O	2:e:82:HIS:CD2	2.60	0.55
2:g:78:GLU:O	2:g:80:ASP:OD2	2.24	0.55
2:j:32:ALA:C	2:j:33:THR:CG2	2.60	0.55
1:N:404:MSE:HE1	1:V:334:MSE:SE	2.56	0.55
1:N:413:LYS:HA	1:N:416:ALA:HB3	1.88	0.55
1:P:578:GLN:HG2	1:P:596:ALA:HB2	1.87	0.55
1:R:209:PHE:HZ	1:R:214:GLN:HG2	1.70	0.55
1:T:71:MSE:HE2	1:T:119:ILE:HD11	1.87	0.55
1:W:546:THR:CG2	1:W:547:PRO:HD3	2.29	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:k:58:TYR:HB2	2:k:75:LEU:HD21	1.89	0.55
2:n:134:THR:HB	2:n:145:GLU:H	1.70	0.55
2:t:58:TYR:HB2	2:t:75:LEU:HD21	1.87	0.55
2:t:134:THR:HB	2:t:145:GLU:H	1.70	0.55
1:A:158:TRP:CD1	1:A:158:TRP:H	2.25	0.55
1:A:557:PHE:CE2	1:L:563:LYS:HD3	2.41	0.55
1:B:34:PHE:CE1	1:B:324:LYS:NZ	2.72	0.55
1:B:589:GLU:HA	1:B:592:TRP:HB2	1.88	0.55
1:D:404:MSE:HE1	1:E:334:MSE:SE	2.57	0.55
1:E:329:LEU:HD22	2:a:142:PRO:HG2	1.87	0.55
1:F:302:PRO:O	1:F:439:ASN:CG	2.49	0.55
1:H:589:GLU:HA	1:H:592:TRP:HB2	1.89	0.55
1:I:42:ASP:OD2	2:g:145:SER:O	2.24	0.55
1:J:380:ASN:O	1:J:381:SER:HB3	2.07	0.55
1:J:589:GLU:HA	1:J:592:TRP:HB2	1.89	0.55
1:K:427:GLY:C	1:K:429:GLN:H	2.15	0.55
1:L:27:ARG:HB2	1:L:313:LYS:HE3	1.89	0.55
1:L:158:TRP:HB3	1:L:173:CYS:CA	2.36	0.55
1:L:166:ASP:OD2	1:L:168:SER:HB3	2.05	0.55
1:L:210:PRO:HD2	1:L:211:TRP:CE3	2.41	0.55
2:f:28:VAL:HG11	2:f:97:ALA:N	2.19	0.55
2:h:19:VAL:O	2:h:82:HIS:CD2	2.60	0.55
2:h:27:GLY:HA2	2:h:30:SER:HB3	1.88	0.55
1:N:209:PHE:N	1:N:210:PRO:HD3	2.21	0.55
1:N:296:GLU:HG2	1:N:449:PHE:HB3	1.89	0.55
1:N:427:GLY:C	1:N:429:GLN:H	2.13	0.55
1:R:546:THR:CG2	1:R:547:PRO:HD3	2.29	0.55
1:S:557:PHE:CE2	1:U:563:LYS:HD3	2.42	0.55
1:V:456:ALA:HB1	1:V:509:ASP:OD1	2.06	0.55
1:X:94:LEU:HA	1:X:97:MSE:CE	2.36	0.55
2:k:42:ALA:HB1	2:m:81:SER:HB3	1.88	0.55
2:v:104:ILE:HD12	2:v:105:ALA:N	2.21	0.55
1:A:248:LYS:HG3	1:A:511:ARG:HH11	1.70	0.55
1:C:380:ASN:O	1:C:381:SER:HB3	2.07	0.55
1:C:443:ASP:C	1:C:444:LEU:HD13	2.31	0.55
1:D:210:PRO:HD2	1:D:211:TRP:CE3	2.41	0.55
1:D:443:ASP:C	1:D:444:LEU:HD13	2.31	0.55
1:G:337:ASN:ND2	1:G:401:ASN:HD22	2.04	0.55
1:G:427:GLY:C	1:G:429:GLN:H	2.15	0.55
1:K:108:LYS:HD3	1:K:112:ASN:ND2	2.21	0.55
1:K:236:GLN:CB	1:K:265:LYS:HZ3	2.17	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:f:34:LEU:C	2:f:35:THR:CG2	2.73	0.55
2:j:19:VAL:O	2:j:82:HIS:CD2	2.60	0.55
2:j:53:MET:HE2	2:j:92:VAL:CG1	2.20	0.55
1:M:273:ARG:HH22	1:M:453:LEU:HD21	1.71	0.55
1:O:444:LEU:C	1:O:446:THR:H	2.13	0.55
1:S:78:VAL:HG12	1:S:79:LEU:H	1.71	0.55
1:U:35:PHE:HE1	1:U:321:ARG:NH1	2.05	0.55
1:U:359:PHE:HD1	2:s:120:ILE:HD11	1.72	0.55
1:V:546:THR:CG2	1:V:547:PRO:HD3	2.29	0.55
1:W:95:MSE:HB3	1:W:527:MSE:HE1	1.87	0.55
1:W:210:PRO:HD2	1:W:211:TRP:CD2	2.41	0.55
1:X:46:SER:N	1:X:48:TYR:HE2	1.98	0.55
1:A:27:ARG:HB2	1:A:313:LYS:HE3	1.89	0.55
1:B:35:PHE:C	1:B:37:ARG:N	2.61	0.55
1:B:380:ASN:O	1:B:381:SER:HB3	2.06	0.55
1:C:158:TRP:CD1	1:C:158:TRP:H	2.25	0.55
1:F:80:TYR:CE2	1:F:94:LEU:HD22	2.42	0.55
1:G:235:TYR:HA	1:G:265:LYS:HB3	1.89	0.55
1:H:541:LYS:HD3	1:H:542:THR:HG23	1.87	0.55
1:J:541:LYS:HD3	1:J:542:THR:HG23	1.87	0.55
1:L:273:ARG:NH2	1:L:453:LEU:HD21	2.21	0.55
2:Y:19:VAL:O	2:Y:82:HIS:CD2	2.60	0.55
2:Z:19:VAL:O	2:Z:82:HIS:CD2	2.60	0.55
2:c:27:GLY:HA2	2:c:30:SER:HB3	1.88	0.55
2:d:19:VAL:O	2:d:82:HIS:CD2	2.60	0.55
1:M:99:ARG:O	1:M:103:ARG:HG3	2.07	0.55
1:O:71:MSE:HE2	1:O:119:ILE:HD11	1.87	0.55
1:O:510:ILE:HG12	1:O:511:ARG:N	2.21	0.55
1:R:351:PHE:CD2	1:R:356:ILE:HD12	2.41	0.55
1:X:93:VAL:CG1	1:X:458:ARG:HG3	2.37	0.55
1:X:164:LEU:HD22	1:X:169:ASP:CG	2.32	0.55
2:k:134:THR:HB	2:k:145:GLU:N	2.22	0.55
2:m:12:ALA:H	2:m:15:ARG:HD3	1.72	0.55
2:m:17:LEU:HD11	2:m:36:ALA:CB	2.36	0.55
2:n:12:ALA:H	2:n:15:ARG:HD3	1.71	0.55
1:B:108:LYS:HD3	1:B:112:ASN:ND2	2.21	0.55
1:D:27:ARG:HB2	1:D:313:LYS:HE3	1.89	0.55
1:E:235:TYR:HA	1:E:265:LYS:HB3	1.89	0.55
1:F:235:TYR:HA	1:F:265:LYS:HB3	1.89	0.55
1:F:273:ARG:NH2	1:F:453:LEU:HD21	2.21	0.55
1:G:311:GLU:O	1:G:312:ASP:HB2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:372:TYR:CE2	1:K:348:LYS:HB2	2.41	0.55
1:K:276:VAL:HG23	1:K:293:ILE:HG23	1.89	0.55
1:L:158:TRP:CD1	1:L:158:TRP:H	2.25	0.55
2:a:78:GLU:O	2:a:80:ASP:OD2	2.24	0.55
2:b:19:VAL:O	2:b:82:HIS:CD2	2.60	0.55
2:b:78:GLU:HG3	2:b:79:GLY:N	2.20	0.55
2:c:78:GLU:O	2:c:80:ASP:OD2	2.24	0.55
2:f:78:GLU:O	2:f:80:ASP:OD2	2.24	0.55
2:j:78:GLU:HG3	2:j:79:GLY:N	2.20	0.55
1:S:273:ARG:NH1	1:S:275:ARG:HE	2.05	0.55
1:S:420:VAL:HG22	1:S:428:GLY:HA3	1.88	0.55
1:U:164:LEU:HD22	1:U:169:ASP:CG	2.32	0.55
1:U:165:MSE:HE1	1:U:435:VAL:HB	1.89	0.55
1:W:296:GLU:HG2	1:W:449:PHE:HB3	1.89	0.55
2:l:134:THR:HB	2:l:145:GLU:N	2.22	0.55
2:m:104:ILE:HD12	2:m:105:ALA:N	2.21	0.55
1:A:171:ARG:HH21	1:L:182:ASN:ND2	2.05	0.55
1:B:235:TYR:HA	1:B:265:LYS:HB3	1.89	0.55
1:C:235:TYR:HA	1:C:265:LYS:HB3	1.89	0.55
1:C:248:LYS:HG3	1:C:511:ARG:HH11	1.70	0.55
1:C:276:VAL:HG23	1:C:293:ILE:HG23	1.89	0.55
1:C:589:GLU:HA	1:C:592:TRP:HB2	1.89	0.55
1:D:158:TRP:HB3	1:D:173:CYS:CA	2.36	0.55
1:D:306:GLU:O	1:D:316:TYR:HA	2.07	0.55
1:E:27:ARG:HB2	1:E:313:LYS:HE3	1.88	0.55
1:E:80:TYR:CE2	1:E:94:LEU:HD22	2.42	0.55
1:F:108:LYS:HD3	1:F:112:ASN:ND2	2.21	0.55
1:F:443:ASP:C	1:F:444:LEU:HD13	2.31	0.55
1:H:108:LYS:HD3	1:H:112:ASN:ND2	2.21	0.55
1:I:108:LYS:HD3	1:I:112:ASN:ND2	2.21	0.55
1:K:236:GLN:CB	1:K:265:LYS:HG2	2.37	0.55
1:L:302:PRO:O	1:L:439:ASN:CG	2.49	0.55
2:Y:89:VAL:C	2:Y:91:ALA:H	2.15	0.55
1:M:209:PHE:N	1:M:210:PRO:HD3	2.21	0.55
1:M:296:GLU:HG2	1:M:449:PHE:HB3	1.89	0.55
1:P:164:LEU:HD22	1:P:169:ASP:CG	2.31	0.55
1:Q:47:GLN:HG2	1:Q:48:TYR:N	2.22	0.55
1:U:578:GLN:HG2	1:U:596:ALA:HB2	1.88	0.55
1:V:554:LEU:HD12	1:V:557:PHE:HD2	1.70	0.55
2:n:58:TYR:HB2	2:n:75:LEU:HD21	1.89	0.55
2:r:65:ASN:O	2:r:67:PRO:CD	2.55	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:t:134:THR:HB	2:t:145:GLU:N	2.22	0.55
1:A:108:LYS:HD3	1:A:112:ASN:ND2	2.21	0.55
1:A:306:GLU:O	1:A:316:TYR:HA	2.07	0.55
1:A:589:GLU:HA	1:A:592:TRP:HB2	1.89	0.55
1:C:108:LYS:HD3	1:C:112:ASN:ND2	2.21	0.55
1:D:108:LYS:HD3	1:D:112:ASN:ND2	2.21	0.55
1:D:276:VAL:HG23	1:D:293:ILE:HG23	1.89	0.55
1:E:589:GLU:HA	1:E:592:TRP:HB2	1.89	0.55
1:F:158:TRP:HB3	1:F:173:CYS:CA	2.36	0.55
1:F:158:TRP:CD1	1:F:158:TRP:H	2.25	0.55
1:F:306:GLU:O	1:F:316:TYR:HA	2.07	0.55
1:H:427:GLY:C	1:H:429:GLN:H	2.15	0.55
1:I:235:TYR:HA	1:I:265:LYS:HB3	1.89	0.55
1:K:80:TYR:CE2	1:K:94:LEU:HD22	2.42	0.55
1:K:337:ASN:ND2	1:K:401:ASN:HD22	2.04	0.55
1:L:108:LYS:HD3	1:L:112:ASN:ND2	2.21	0.55
2:c:19:VAL:O	2:c:82:HIS:CD2	2.60	0.55
2:d:78:GLU:O	2:d:80:ASP:OD2	2.24	0.55
2:i:19:VAL:O	2:i:82:HIS:CD2	2.60	0.55
2:i:27:GLY:HA2	2:i:30:SER:HB3	1.88	0.55
1:P:47:GLN:HG2	1:P:48:TYR:N	2.20	0.55
1:P:584:PRO:HG2	1:P:593:LEU:HD12	1.89	0.55
1:P:593:LEU:O	1:P:597:GLN:HG2	2.07	0.55
1:R:86:ALA:HB2	1:R:515:GLU:HG3	1.87	0.55
3:R:719:HOH:O	1:X:430:VAL:CG1	2.55	0.55
1:V:302:PRO:O	1:V:439:ASN:ND2	2.40	0.55
1:W:510:ILE:HG12	1:W:511:ARG:N	2.20	0.55
2:r:134:THR:HB	2:r:145:GLU:H	1.71	0.55
2:s:134:THR:HB	2:s:145:GLU:N	2.21	0.55
1:C:158:TRP:HB3	1:C:173:CYS:CA	2.36	0.55
1:C:337:ASN:ND2	1:C:401:ASN:HD22	2.04	0.55
1:D:311:GLU:O	1:D:312:ASP:HB2	2.07	0.55
1:D:380:ASN:O	1:D:381:SER:HB3	2.07	0.55
1:E:276:VAL:HG23	1:E:293:ILE:HG23	1.89	0.55
1:F:334:MSE:HE3	1:G:404:MSE:CE	2.37	0.55
1:F:380:ASN:O	1:F:381:SER:HB3	2.06	0.55
1:I:589:GLU:HA	1:I:592:TRP:HB2	1.89	0.55
1:L:34:PHE:HZ	1:L:328:ARG:HH22	0.80	0.55
2:Y:27:GLY:HA2	2:Y:30:SER:HB3	1.88	0.55
2:e:27:GLY:HA2	2:e:30:SER:HB3	1.88	0.55
2:g:27:GLY:HA2	2:g:30:SER:HB3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:35:PHE:HE1	1:M:321:ARG:NH1	2.04	0.54
1:N:78:VAL:HG12	1:N:79:LEU:H	1.72	0.54
1:N:93:VAL:CG1	1:N:458:ARG:HG3	2.38	0.54
1:P:210:PRO:HD2	1:P:211:TRP:CD2	2.41	0.54
1:P:343:ARG:HD3	2:n:128:TYR:CE1	2.42	0.54
1:P:389:LEU:HD12	1:P:389:LEU:H	1.73	0.54
1:Q:35:PHE:CE1	1:Q:321:ARG:NE	2.75	0.54
1:Q:154:SER:O	1:Q:204:PRO:HB3	2.07	0.54
1:S:593:LEU:O	1:S:597:GLN:HG2	2.06	0.54
1:T:199:PRO:HB3	1:T:282:THR:HG22	1.87	0.54
1:W:443:ASP:C	1:W:446:THR:HG22	2.32	0.54
1:X:44:TRP:CE2	1:X:54:ARG:HB3	2.42	0.54
2:s:96:ALA:HB2	2:u:25:LEU:HD13	1.89	0.54
1:A:380:ASN:O	1:A:381:SER:HB3	2.07	0.54
1:B:337:ASN:ND2	1:B:401:ASN:HD22	2.04	0.54
1:E:236:GLN:CB	1:E:265:LYS:HG2	2.37	0.54
1:E:427:GLY:C	1:E:429:GLN:H	2.15	0.54
1:H:158:TRP:HB3	1:H:173:CYS:CA	2.36	0.54
1:I:276:VAL:HG23	1:I:293:ILE:HG23	1.89	0.54
1:J:108:LYS:HD3	1:J:112:ASN:ND2	2.21	0.54
1:K:380:ASN:O	1:K:381:SER:HB3	2.06	0.54
1:L:37:ARG:HH21	1:L:37:ARG:CB	2.16	0.54
1:L:306:GLU:O	1:L:316:TYR:HA	2.07	0.54
1:M:359:PHE:HD1	2:n:120:ILE:HD11	1.72	0.54
1:M:456:ALA:HB1	1:M:509:ASP:OD1	2.07	0.54
1:M:557:PHE:CE2	1:N:563:LYS:HD3	2.42	0.54
1:M:593:LEU:O	1:M:597:GLN:HG2	2.07	0.54
1:N:158:TRP:N	1:N:158:TRP:HD1	2.06	0.54
1:N:578:GLN:HG2	1:N:596:ALA:HB2	1.89	0.54
1:O:35:PHE:HE1	1:O:321:ARG:NH1	2.05	0.54
1:S:35:PHE:CE1	1:S:321:ARG:NE	2.75	0.54
1:S:546:THR:CG2	1:S:547:PRO:HD3	2.30	0.54
1:T:47:GLN:HG2	1:T:48:TYR:N	2.22	0.54
1:U:209:PHE:N	1:U:210:PRO:HD3	2.21	0.54
1:W:164:LEU:HD22	1:W:169:ASP:CG	2.33	0.54
1:X:165:MSE:HE3	1:X:304:PHE:HB2	1.88	0.54
2:n:134:THR:HB	2:n:145:GLU:N	2.23	0.54
2:q:58:TYR:HB2	2:q:75:LEU:HD21	1.89	0.54
2:q:134:THR:HB	2:q:145:GLU:N	2.22	0.54
1:A:235:TYR:HA	1:A:265:LYS:HB3	1.89	0.54
1:B:248:LYS:CG	1:B:511:ARG:HH11	2.19	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:80:TYR:CE2	1:C:94:LEU:HD22	2.42	0.54
1:C:236:GLN:HE21	1:C:265:LYS:NZ	2.06	0.54
1:E:108:LYS:HD3	1:E:112:ASN:ND2	2.21	0.54
1:F:27:ARG:HB2	1:F:313:LYS:HE3	1.88	0.54
1:G:80:TYR:CE2	1:G:94:LEU:HD22	2.42	0.54
1:H:80:TYR:CE2	1:H:94:LEU:HD22	2.42	0.54
1:J:72:ARG:HD2	1:K:434:THR:HG21	1.89	0.54
1:J:276:VAL:HG23	1:J:293:ILE:HG23	1.89	0.54
1:J:306:GLU:O	1:J:316:TYR:HA	2.07	0.54
1:J:337:ASN:ND2	1:J:401:ASN:HD22	2.04	0.54
1:K:34:PHE:HZ	1:K:328:ARG:HH22	0.80	0.54
1:K:158:TRP:CD1	1:K:158:TRP:H	2.25	0.54
1:L:427:GLY:C	1:L:429:GLN:H	2.15	0.54
2:h:28:VAL:HG11	2:h:97:ALA:N	2.19	0.54
1:M:101:ASP:HB2	1:M:144:ILE:O	2.07	0.54
1:P:35:PHE:CE1	1:P:321:ARG:NE	2.76	0.54
1:P:78:VAL:CG1	1:P:79:LEU:N	2.70	0.54
1:P:209:PHE:N	1:P:210:PRO:HD3	2.21	0.54
1:T:94:LEU:HA	1:T:97:MSE:CE	2.36	0.54
1:T:510:ILE:HG12	1:T:511:ARG:N	2.22	0.54
1:U:93:VAL:CG1	1:U:458:ARG:HG3	2.36	0.54
1:U:209:PHE:HZ	1:U:214:GLN:HG2	1.71	0.54
2:r:12:ALA:H	2:r:15:ARG:HD3	1.71	0.54
1:A:80:TYR:CE2	1:A:94:LEU:HD22	2.42	0.54
1:B:80:TYR:CE2	1:B:94:LEU:HD22	2.42	0.54
1:C:311:GLU:O	1:C:312:ASP:HB2	2.07	0.54
1:D:427:GLY:C	1:D:429:GLN:H	2.14	0.54
1:E:236:GLN:HE21	1:E:265:LYS:NZ	2.06	0.54
1:E:306:GLU:O	1:E:316:TYR:HA	2.07	0.54
1:F:123:VAL:HG22	1:F:316:TYR:CE2	2.43	0.54
1:F:337:ASN:ND2	1:F:401:ASN:HD22	2.04	0.54
1:F:427:GLY:C	1:F:429:GLN:H	2.15	0.54
1:G:138:THR:H	1:G:143:VAL:HG22	1.73	0.54
1:I:158:TRP:HB3	1:I:173:CYS:CA	2.36	0.54
1:K:589:GLU:HA	1:K:592:TRP:HB2	1.89	0.54
2:Y:28:VAL:HG11	2:Y:96:LEU:C	2.33	0.54
2:a:27:GLY:HA2	2:a:30:SER:HB3	1.88	0.54
2:b:89:VAL:C	2:b:91:ALA:H	2.15	0.54
2:c:89:VAL:C	2:c:91:ALA:H	2.15	0.54
2:e:89:VAL:C	2:e:91:ALA:H	2.15	0.54
2:f:19:VAL:O	2:f:82:HIS:CD2	2.60	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:158:TRP:N	1:M:158:TRP:HD1	2.04	0.54
1:M:273:ARG:NH1	1:M:275:ARG:HE	2.05	0.54
1:M:302:PRO:O	1:M:439:ASN:ND2	2.41	0.54
1:S:94:LEU:HA	1:S:97:MSE:CE	2.37	0.54
1:S:154:SER:O	1:S:204:PRO:HB3	2.07	0.54
1:S:209:PHE:HZ	1:S:214:GLN:HG2	1.70	0.54
1:T:584:PRO:HG2	1:T:593:LEU:HD12	1.90	0.54
1:U:26:ARG:HG2	1:X:212:LEU:HD22	1.88	0.54
1:V:390:ALA:HB2	1:W:387:GLN:CB	2.38	0.54
1:W:578:GLN:HG2	1:W:596:ALA:HB2	1.87	0.54
1:X:35:PHE:CE1	1:X:321:ARG:NE	2.75	0.54
1:X:209:PHE:HZ	1:X:214:GLN:HG2	1.70	0.54
1:A:123:VAL:HG22	1:A:316:TYR:CE2	2.43	0.54
1:A:337:ASN:ND2	1:A:401:ASN:HD22	2.04	0.54
1:B:37:ARG:HH21	1:B:37:ARG:CB	2.16	0.54
1:B:123:VAL:HG22	1:B:316:TYR:CE2	2.43	0.54
1:C:72:ARG:HD2	1:E:434:THR:HG21	1.90	0.54
1:C:236:GLN:CB	1:C:265:LYS:HG2	2.37	0.54
1:C:306:GLU:O	1:C:316:TYR:HA	2.07	0.54
1:F:236:GLN:HE21	1:F:265:LYS:NZ	2.06	0.54
1:F:561:ASP:OD2	1:G:92:ASP:HB3	2.07	0.54
1:G:15:PHE:HZ	1:G:283:CYS:SG	2.31	0.54
1:I:158:TRP:CD1	1:I:158:TRP:H	2.25	0.54
1:J:80:TYR:CE2	1:J:94:LEU:HD22	2.42	0.54
1:J:123:VAL:HG22	1:J:316:TYR:CE2	2.43	0.54
2:g:19:VAL:O	2:g:82:HIS:CD2	2.60	0.54
1:M:47:GLN:HG2	1:M:48:TYR:N	2.22	0.54
1:M:584:PRO:HG2	1:M:593:LEU:HD12	1.90	0.54
1:N:443:ASP:C	1:N:446:THR:HG22	2.33	0.54
1:O:101:ASP:HB2	1:O:144:ILE:O	2.07	0.54
1:Q:561:ASP:CB	1:R:89:ASP:HA	2.31	0.54
1:T:66:LYS:NZ	1:T:420:VAL:HG11	2.23	0.54
1:T:387:GLN:HB2	1:W:390:ALA:HB2	1.90	0.54
1:U:144:ILE:HD12	1:U:145:ARG:N	2.22	0.54
1:V:93:VAL:CG1	1:V:458:ARG:HG3	2.37	0.54
1:X:209:PHE:N	1:X:210:PRO:HD3	2.21	0.54
2:q:65:ASN:O	2:q:67:PRO:CD	2.55	0.54
1:A:15:PHE:HZ	1:A:283:CYS:SG	2.31	0.54
1:C:273:ARG:NH2	1:C:453:LEU:HD21	2.21	0.54
1:D:15:PHE:HZ	1:D:283:CYS:SG	2.31	0.54
1:D:235:TYR:HA	1:D:265:LYS:HB3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:236:GLN:CB	1:F:265:LYS:HZ3	2.16	0.54
1:F:311:GLU:O	1:F:312:ASP:HB2	2.07	0.54
1:F:589:GLU:HA	1:F:592:TRP:HB2	1.89	0.54
1:H:138:THR:H	1:H:143:VAL:HG22	1.73	0.54
1:H:235:TYR:HA	1:H:265:LYS:HB3	1.89	0.54
1:I:236:GLN:CB	1:I:265:LYS:HG2	2.37	0.54
1:K:236:GLN:HE21	1:K:265:LYS:NZ	2.06	0.54
1:L:15:PHE:HZ	1:L:283:CYS:SG	2.31	0.54
2:h:28:VAL:HG11	2:h:96:LEU:C	2.33	0.54
2:i:89:VAL:C	2:i:91:ALA:H	2.15	0.54
1:M:510:ILE:HG12	1:M:511:ARG:N	2.22	0.54
1:N:95:MSE:HB3	1:N:527:MSE:HE1	1.88	0.54
1:P:273:ARG:NH1	1:P:275:ARG:HE	2.06	0.54
1:P:302:PRO:O	1:P:439:ASN:ND2	2.41	0.54
1:Q:78:VAL:HG12	1:Q:79:LEU:H	1.70	0.54
1:Q:593:LEU:O	1:Q:597:GLN:HG2	2.08	0.54
1:R:573:ASN:O	1:R:577:ILE:HG13	2.08	0.54
1:S:46:SER:N	1:S:48:TYR:HE2	1.99	0.54
1:T:420:VAL:HG22	1:T:428:GLY:HA3	1.90	0.54
1:V:144:ILE:HD12	1:V:145:ARG:N	2.22	0.54
1:W:456:ALA:HB1	1:W:509:ASP:OD1	2.08	0.54
1:X:420:VAL:HG22	1:X:428:GLY:HA3	1.90	0.54
2:t:104:ILE:HD12	2:t:105:ALA:N	2.23	0.54
1:A:273:ARG:NH2	1:A:453:LEU:HD21	2.21	0.54
1:G:306:GLU:O	1:G:316:TYR:HA	2.07	0.54
1:G:372:TYR:CE2	1:H:348:LYS:HB2	2.42	0.54
1:H:311:GLU:O	1:H:312:ASP:HB2	2.07	0.54
1:I:306:GLU:O	1:I:316:TYR:HA	2.07	0.54
1:J:34:PHE:HZ	1:J:328:ARG:HH22	0.80	0.54
1:J:138:THR:H	1:J:143:VAL:HG22	1.73	0.54
1:K:27:ARG:HB2	1:K:313:LYS:HE3	1.89	0.54
1:K:37:ARG:HH21	1:K:37:ARG:CB	2.16	0.54
1:K:306:GLU:O	1:K:316:TYR:HA	2.07	0.54
1:K:311:GLU:O	1:K:312:ASP:HB2	2.07	0.54
2:Z:27:GLY:HA2	2:Z:30:SER:HB3	1.88	0.54
2:d:28:VAL:HG11	2:d:96:LEU:C	2.33	0.54
2:d:53:MET:HE2	2:d:92:VAL:CG1	2.20	0.54
2:d:89:VAL:C	2:d:91:ALA:H	2.15	0.54
2:f:28:VAL:HG11	2:f:96:LEU:C	2.33	0.54
2:g:89:VAL:C	2:g:91:ALA:H	2.15	0.54
2:h:89:VAL:C	2:h:91:ALA:H	2.15	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:i:28:VAL:HG11	2:i:96:LEU:C	2.33	0.54
2:j:34:LEU:C	2:j:35:THR:CG2	2.73	0.54
1:M:443:ASP:C	1:M:446:THR:HG22	2.32	0.54
1:O:66:LYS:NZ	1:O:420:VAL:HG11	2.23	0.54
1:O:81:ARG:HB2	1:O:517:TYR:CZ	2.42	0.54
1:O:443:ASP:C	1:O:444:LEU:HD13	2.32	0.54
1:R:154:SER:O	1:R:204:PRO:HB3	2.08	0.54
1:S:40:GLN:HG2	1:T:310:VAL:HG22	1.90	0.54
1:S:456:ALA:HB1	1:S:509:ASP:OD1	2.07	0.54
1:T:296:GLU:HG2	1:T:449:PHE:HB3	1.89	0.54
1:U:332:MSE:SE	2:r:132:MET:HA	2.57	0.54
1:V:386:THR:O	1:V:387:GLN:C	2.51	0.54
1:W:46:SER:N	1:W:48:TYR:HE2	1.97	0.54
1:X:71:MSE:HE2	1:X:119:ILE:HD11	1.88	0.54
2:o:104:ILE:HD12	2:o:105:ALA:N	2.23	0.54
2:r:58:TYR:HB2	2:r:75:LEU:HD21	1.90	0.54
2:r:62:ASP:HB2	2:r:64:GLU:HB3	1.89	0.54
1:C:138:THR:H	1:C:143:VAL:HG22	1.73	0.54
1:D:236:GLN:HE21	1:D:265:LYS:NZ	2.06	0.54
1:D:384:LEU:HD22	1:D:384:LEU:N	2.23	0.54
1:D:561:ASP:OD2	1:F:92:ASP:HB3	2.07	0.54
1:G:236:GLN:CB	1:G:265:LYS:HG2	2.37	0.54
1:H:27:ARG:HB2	1:H:313:LYS:HE3	1.89	0.54
1:H:236:GLN:HE21	1:H:265:LYS:NZ	2.06	0.54
1:L:235:TYR:HA	1:L:265:LYS:HB3	1.89	0.54
2:Z:71:ASP:O	2:Z:72:ASP:HB3	2.08	0.54
2:b:71:ASP:O	2:b:72:ASP:HB3	2.08	0.54
2:d:71:ASP:O	2:d:72:ASP:HB3	2.08	0.54
2:f:89:VAL:C	2:f:91:ALA:H	2.15	0.54
2:j:71:ASP:O	2:j:72:ASP:HB3	2.08	0.54
1:M:78:VAL:HG12	1:M:79:LEU:H	1.73	0.54
1:M:164:LEU:HD22	1:M:169:ASP:CG	2.33	0.54
1:O:593:LEU:O	1:O:597:GLN:HG2	2.07	0.54
1:S:47:GLN:HG2	1:S:48:TYR:N	2.22	0.54
1:S:66:LYS:HZ1	1:S:420:VAL:HG11	1.73	0.54
1:V:80:TYR:CE1	1:V:448:VAL:HG22	2.43	0.54
1:V:101:ASP:HB2	1:V:144:ILE:O	2.08	0.54
2:k:12:ALA:H	2:k:15:ARG:HD3	1.73	0.54
2:q:62:ASP:HB2	2:q:64:GLU:HB3	1.90	0.54
1:B:306:GLU:O	1:B:316:TYR:HA	2.07	0.54
1:E:15:PHE:HZ	1:E:283:CYS:SG	2.31	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:42:ASP:OD2	2:b:145:SER:O	2.26	0.54
1:E:123:VAL:HG22	1:E:316:TYR:CE2	2.43	0.54
1:G:236:GLN:HE21	1:G:265:LYS:NZ	2.06	0.54
1:I:14:ARG:NE	1:I:14:ARG:CA	2.67	0.54
1:J:47:GLN:O	1:J:47:GLN:NE2	2.41	0.54
1:K:15:PHE:HZ	1:K:283:CYS:SG	2.31	0.54
1:K:47:GLN:O	1:K:47:GLN:NE2	2.41	0.54
2:Y:58:GLN:H	2:Y:62:GLY:HA3	1.73	0.54
2:a:71:ASP:O	2:a:72:ASP:HB3	2.08	0.54
2:a:89:VAL:C	2:a:91:ALA:H	2.15	0.54
2:b:28:VAL:HG11	2:b:96:LEU:C	2.33	0.54
2:d:32:ALA:C	2:d:33:THR:CG2	2.61	0.54
2:e:28:VAL:HG11	2:e:96:LEU:C	2.33	0.54
2:g:28:VAL:HG11	2:g:96:LEU:C	2.33	0.54
2:j:89:VAL:C	2:j:91:ALA:H	2.15	0.54
1:M:93:VAL:CG1	1:M:458:ARG:HG3	2.37	0.54
1:M:209:PHE:HZ	1:M:214:GLN:HG2	1.70	0.54
1:O:236:GLN:HA	1:O:244:VAL:H	1.73	0.54
1:O:360:GLU:HG3	2:n:122:ARG:HB3	1.88	0.54
1:O:584:PRO:HG2	1:O:593:LEU:HD12	1.90	0.54
1:Q:209:PHE:HZ	1:Q:214:GLN:HG2	1.70	0.54
1:Q:405:LEU:O	1:Q:409:THR:HG23	2.08	0.54
1:U:420:VAL:HG22	1:U:428:GLY:HA3	1.89	0.54
1:W:81:ARG:HB2	1:W:517:TYR:CZ	2.43	0.54
1:W:584:PRO:HG2	1:W:593:LEU:HD12	1.89	0.54
2:m:65:ASN:O	2:m:67:PRO:CD	2.56	0.54
1:B:234:ILE:HG13	1:B:267:ALA:HB3	1.90	0.54
1:B:236:GLN:HE21	1:B:265:LYS:NZ	2.06	0.54
1:B:311:GLU:O	1:B:312:ASP:HB2	2.07	0.54
1:C:27:ARG:HB2	1:C:313:LYS:HE3	1.89	0.54
1:D:47:GLN:O	1:D:47:GLN:NE2	2.41	0.54
1:D:80:TYR:CE2	1:D:94:LEU:HD22	2.42	0.54
1:E:37:ARG:HH21	1:E:37:ARG:CB	2.16	0.54
1:E:384:LEU:HD22	1:E:384:LEU:N	2.23	0.54
1:F:234:ILE:HG13	1:F:267:ALA:HB3	1.90	0.54
1:G:80:TYR:CE1	1:G:448:VAL:HG22	2.43	0.54
1:G:108:LYS:HD3	1:G:112:ASN:ND2	2.21	0.54
1:H:123:VAL:HG22	1:H:316:TYR:CE2	2.43	0.54
1:I:15:PHE:HZ	1:I:283:CYS:SG	2.31	0.54
1:I:47:GLN:O	1:I:47:GLN:NE2	2.41	0.54
1:I:311:GLU:O	1:I:312:ASP:HB2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:235:TYR:HA	1:J:265:LYS:HB3	1.89	0.54
1:J:236:GLN:CB	1:J:265:LYS:HG2	2.37	0.54
1:K:80:TYR:CE1	1:K:448:VAL:HG22	2.43	0.54
1:L:80:TYR:CE2	1:L:94:LEU:HD22	2.42	0.54
2:a:28:VAL:HG11	2:a:96:LEU:C	2.33	0.54
1:M:54:ARG:HB2	2:m:137:GLY:HA3	1.89	0.54
1:N:47:GLN:HG2	1:N:48:TYR:N	2.22	0.54
1:N:101:ASP:HB2	1:N:144:ILE:O	2.08	0.54
1:O:563:LYS:HD3	1:P:557:PHE:CE2	2.42	0.54
1:Q:344:THR:HG23	1:Q:344:THR:O	2.07	0.54
1:Q:584:PRO:HG2	1:Q:593:LEU:HD12	1.90	0.54
1:S:66:LYS:NZ	1:S:420:VAL:HG11	2.22	0.54
1:T:123:VAL:HG22	1:T:316:TYR:CE2	2.42	0.54
1:T:451:ASP:C	1:T:453:LEU:H	2.15	0.54
1:U:66:LYS:HZ3	1:U:420:VAL:HG11	1.72	0.54
1:U:390:ALA:HB2	1:X:387:GLN:HB2	1.89	0.54
1:U:443:ASP:C	1:U:446:THR:HG22	2.32	0.54
1:X:66:LYS:NZ	1:X:420:VAL:HG11	2.23	0.54
2:r:134:THR:HB	2:r:145:GLU:N	2.23	0.54
2:u:58:TYR:HB2	2:u:75:LEU:HD21	1.90	0.54
2:v:65:ASN:O	2:v:67:PRO:CD	2.56	0.54
1:A:528:LYS:HZ2	1:A:560:LEU:HD21	1.72	0.54
1:D:123:VAL:HG22	1:D:316:TYR:CE2	2.43	0.54
1:E:138:THR:H	1:E:143:VAL:HG22	1.73	0.54
1:F:80:TYR:CE1	1:F:448:VAL:HG22	2.43	0.54
1:F:560:LEU:O	1:F:561:ASP:O	2.26	0.54
1:G:158:TRP:HB3	1:G:173:CYS:CA	2.36	0.54
1:G:266:ILE:HG23	1:G:267:ALA:N	2.23	0.54
1:G:589:GLU:HA	1:G:592:TRP:HB2	1.89	0.54
1:J:15:PHE:HZ	1:J:283:CYS:SG	2.31	0.54
1:J:427:GLY:C	1:J:429:GLN:H	2.15	0.54
1:J:560:LEU:O	1:J:561:ASP:O	2.26	0.54
1:J:579:MSE:HB2	1:J:581:VAL:HG12	1.90	0.54
1:K:14:ARG:NE	1:K:14:ARG:CA	2.67	0.54
1:L:123:VAL:HG22	1:L:316:TYR:CE2	2.43	0.54
2:g:58:GLN:H	2:g:62:GLY:HA3	1.73	0.54
1:M:44:TRP:C	1:M:45:LEU:HD22	2.33	0.53
1:M:81:ARG:HB2	1:M:517:TYR:CZ	2.43	0.53
1:M:389:LEU:H	1:M:389:LEU:HD12	1.72	0.53
1:M:444:LEU:O	1:M:448:VAL:HG23	2.08	0.53
1:N:273:ARG:NH1	1:N:275:ARG:HE	2.05	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:389:LEU:H	1:N:389:LEU:HD12	1.72	0.53
1:N:535:ILE:HD13	1:N:554:LEU:HG	1.89	0.53
1:O:296:GLU:HG2	1:O:449:PHE:HB3	1.89	0.53
1:P:101:ASP:HB2	1:P:144:ILE:O	2.08	0.53
1:P:209:PHE:HZ	1:P:214:GLN:HG2	1.70	0.53
1:P:443:ASP:C	1:P:446:THR:HG22	2.33	0.53
1:T:443:ASP:C	1:T:446:THR:HG22	2.34	0.53
1:U:58:ASP:HA	1:U:327:GLN:NE2	2.23	0.53
1:U:78:VAL:CG2	1:U:444:LEU:HD11	2.22	0.53
1:U:390:ALA:HB2	1:X:387:GLN:CB	2.38	0.53
1:V:389:LEU:HD12	1:V:389:LEU:H	1.72	0.53
1:W:94:LEU:HA	1:W:97:MSE:CE	2.37	0.53
2:o:12:ALA:H	2:o:15:ARG:HD3	1.73	0.53
2:p:65:ASN:O	2:p:67:PRO:CD	2.56	0.53
2:q:104:ILE:HD12	2:q:105:ALA:N	2.22	0.53
1:C:80:TYR:CE1	1:C:448:VAL:HG22	2.43	0.53
1:E:234:ILE:HG13	1:E:267:ALA:HB3	1.91	0.53
1:F:266:ILE:HG23	1:F:267:ALA:N	2.23	0.53
1:F:384:LEU:HD22	1:F:384:LEU:N	2.23	0.53
1:G:384:LEU:HD22	1:G:384:LEU:N	2.23	0.53
1:H:47:GLN:O	1:H:47:GLN:NE2	2.41	0.53
1:H:78:VAL:HG11	1:H:444:LEU:HG	1.90	0.53
1:H:266:ILE:HG23	1:H:267:ALA:N	2.23	0.53
1:K:123:VAL:HG22	1:K:316:TYR:CE2	2.43	0.53
1:K:234:ILE:HG13	1:K:267:ALA:HB3	1.90	0.53
1:K:560:LEU:O	1:K:561:ASP:O	2.26	0.53
2:Y:78:GLU:HG3	2:Y:79:GLY:N	2.20	0.53
2:Z:89:VAL:C	2:Z:91:ALA:H	2.15	0.53
2:b:27:GLY:HA2	2:b:30:SER:HB3	1.89	0.53
2:j:28:VAL:HG11	2:j:96:LEU:C	2.33	0.53
1:M:35:PHE:C	1:M:37:ARG:H	2.16	0.53
1:M:398:PRO:HB3	1:N:395:PRO:HD2	1.90	0.53
1:N:46:SER:N	1:N:48:TYR:HE2	1.98	0.53
1:N:456:ALA:HB1	1:N:509:ASP:OD1	2.08	0.53
1:O:344:THR:O	1:O:344:THR:HG23	2.08	0.53
1:O:434:THR:HA	1:O:437:GLN:HG2	1.90	0.53
1:P:405:LEU:O	1:P:409:THR:HG23	2.08	0.53
1:P:443:ASP:C	1:P:444:LEU:HD13	2.34	0.53
1:Q:66:LYS:NZ	1:Q:420:VAL:HG11	2.23	0.53
1:Q:443:ASP:C	1:Q:446:THR:HG22	2.34	0.53
1:S:584:PRO:HG2	1:S:593:LEU:HD12	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:386:THR:O	1:T:387:GLN:C	2.51	0.53
1:W:154:SER:O	1:W:204:PRO:HB3	2.08	0.53
1:W:434:THR:O	1:W:437:GLN:HG2	2.08	0.53
1:X:37:ARG:HH21	1:X:37:ARG:CB	2.20	0.53
2:t:62:ASP:HB2	2:t:64:GLU:HB3	1.91	0.53
2:t:65:ASN:O	2:t:67:PRO:CD	2.56	0.53
1:A:37:ARG:HH21	1:A:37:ARG:CB	2.16	0.53
1:A:236:GLN:CB	1:A:265:LYS:HG2	2.37	0.53
1:A:236:GLN:HE21	1:A:265:LYS:NZ	2.06	0.53
1:B:47:GLN:O	1:B:47:GLN:NE2	2.41	0.53
1:B:273:ARG:NH2	1:B:453:LEU:HD21	2.21	0.53
1:B:328:ARG:HB3	2:Y:142:PRO:HG3	1.90	0.53
1:C:47:GLN:O	1:C:47:GLN:NE2	2.41	0.53
1:D:158:TRP:CD1	1:D:158:TRP:H	2.25	0.53
1:E:80:TYR:CE1	1:E:448:VAL:HG22	2.43	0.53
1:E:311:GLU:O	1:E:312:ASP:HB2	2.07	0.53
1:G:78:VAL:HG11	1:G:444:LEU:HG	1.90	0.53
1:G:177:HIS:O	1:G:218:GLN:HA	2.08	0.53
1:G:560:LEU:O	1:G:561:ASP:O	2.26	0.53
1:H:306:GLU:O	1:H:316:TYR:HA	2.07	0.53
1:I:78:VAL:HG11	1:I:444:LEU:HG	1.90	0.53
1:I:80:TYR:CE1	1:I:448:VAL:HG22	2.43	0.53
1:I:236:GLN:HE21	1:I:265:LYS:NZ	2.06	0.53
1:I:560:LEU:O	1:I:561:ASP:O	2.26	0.53
1:J:78:VAL:HG11	1:J:444:LEU:HG	1.90	0.53
1:L:177:HIS:O	1:L:218:GLN:HA	2.09	0.53
1:L:234:ILE:HG13	1:L:267:ALA:HB3	1.90	0.53
2:a:58:GLN:H	2:a:62:GLY:HA3	1.73	0.53
2:j:27:GLY:HA2	2:j:30:SER:HB3	1.89	0.53
1:N:81:ARG:HB2	1:N:517:TYR:CZ	2.44	0.53
1:N:236:GLN:HA	1:N:244:VAL:H	1.74	0.53
1:O:154:SER:O	1:O:204:PRO:HB3	2.07	0.53
1:P:66:LYS:NZ	1:P:420:VAL:HG11	2.24	0.53
1:R:47:GLN:HG2	1:R:48:TYR:N	2.23	0.53
1:S:26:ARG:HG2	1:U:212:LEU:HD22	1.90	0.53
1:S:80:TYR:CE1	1:S:448:VAL:HG22	2.43	0.53
1:T:593:LEU:O	1:T:597:GLN:HG2	2.08	0.53
1:U:427:GLY:C	1:U:429:GLN:H	2.15	0.53
1:W:66:LYS:NZ	1:W:420:VAL:HG11	2.23	0.53
1:W:273:ARG:NH1	1:W:275:ARG:HE	2.06	0.53
1:W:344:THR:O	1:W:344:THR:HG23	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:593:LEU:O	1:X:597:GLN:HG2	2.08	0.53
2:l:65:ASN:O	2:l:67:PRO:CD	2.57	0.53
2:t:71:ASP:OD2	2:t:71:ASP:N	2.37	0.53
1:A:266:ILE:HG23	1:A:267:ALA:N	2.23	0.53
1:B:384:LEU:HD22	1:B:384:LEU:N	2.23	0.53
1:C:123:VAL:HG22	1:C:316:TYR:CE2	2.43	0.53
1:C:384:LEU:HD22	1:C:384:LEU:N	2.23	0.53
1:D:42:ASP:OD2	2:e:145:SER:O	2.26	0.53
1:D:266:ILE:HG23	1:D:267:ALA:N	2.23	0.53
1:E:158:TRP:CD1	1:E:158:TRP:H	2.25	0.53
1:F:78:VAL:HG11	1:F:444:LEU:HG	1.90	0.53
1:F:138:THR:H	1:F:143:VAL:HG22	1.73	0.53
1:G:123:VAL:HG22	1:G:316:TYR:CE2	2.43	0.53
1:H:276:VAL:HG23	1:H:293:ILE:HG23	1.89	0.53
1:I:80:TYR:CE2	1:I:94:LEU:HD22	2.42	0.53
1:K:78:VAL:HG11	1:K:444:LEU:HG	1.91	0.53
1:L:276:VAL:HG23	1:L:293:ILE:HG23	1.89	0.53
2:c:71:ASP:O	2:c:72:ASP:HB3	2.08	0.53
2:e:58:GLN:H	2:e:62:GLY:HA3	1.73	0.53
1:M:44:TRP:CE2	1:M:54:ARG:HB3	2.43	0.53
1:N:44:TRP:CE2	1:N:54:ARG:HB3	2.43	0.53
1:N:584:PRO:HG2	1:N:593:LEU:HD12	1.91	0.53
1:O:444:LEU:O	1:O:448:VAL:HG23	2.08	0.53
1:O:451:ASP:C	1:O:453:LEU:H	2.17	0.53
1:P:58:ASP:HA	1:P:327:GLN:NE2	2.24	0.53
1:P:236:GLN:HA	1:P:244:VAL:H	1.72	0.53
1:Q:236:GLN:HA	1:Q:244:VAL:H	1.74	0.53
3:Q:718:HOH:O	1:R:438:LEU:HD22	2.08	0.53
1:R:395:PRO:HD2	1:X:398:PRO:HB3	1.90	0.53
1:T:158:TRP:N	1:T:158:TRP:HD1	2.07	0.53
1:V:420:VAL:HG22	1:V:428:GLY:HA3	1.90	0.53
1:V:584:PRO:HG2	1:V:593:LEU:HD12	1.90	0.53
1:W:35:PHE:HE1	1:W:321:ARG:NH1	2.05	0.53
1:W:78:VAL:CG1	1:W:79:LEU:N	2.71	0.53
2:k:67:PRO:HG2	2:m:8:ASP:CB	2.38	0.53
2:l:42:ALA:HB1	2:n:81:SER:HB3	1.89	0.53
2:m:12:ALA:C	2:m:14:LEU:N	2.65	0.53
1:A:384:LEU:HD22	1:A:384:LEU:N	2.23	0.53
1:A:560:LEU:O	1:A:561:ASP:O	2.26	0.53
1:B:15:PHE:HZ	1:B:283:CYS:SG	2.31	0.53
1:B:138:THR:H	1:B:143:VAL:HG22	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:177:HIS:O	1:B:218:GLN:HA	2.09	0.53
1:C:334:MSE:HE3	1:E:404:MSE:HE3	1.90	0.53
1:D:78:VAL:HG11	1:D:444:LEU:HG	1.90	0.53
1:E:47:GLN:O	1:E:47:GLN:NE2	2.41	0.53
1:E:266:ILE:HG23	1:E:267:ALA:N	2.23	0.53
1:F:42:ASP:OD2	2:c:145:SER:O	2.27	0.53
1:F:177:HIS:O	1:F:218:GLN:HA	2.09	0.53
1:F:276:VAL:HG23	1:F:293:ILE:HG23	1.89	0.53
1:G:273:ARG:NH2	1:G:453:LEU:HD21	2.21	0.53
1:G:276:VAL:HG23	1:G:293:ILE:HG23	1.89	0.53
1:H:236:GLN:CB	1:H:265:LYS:HG2	2.37	0.53
1:H:380:ASN:O	1:H:381:SER:HB3	2.06	0.53
1:H:560:LEU:O	1:H:561:ASP:O	2.26	0.53
1:I:27:ARG:HB2	1:I:313:LYS:HE3	1.89	0.53
1:K:138:THR:H	1:K:143:VAL:HG22	1.73	0.53
1:K:235:TYR:HA	1:K:265:LYS:HB3	1.89	0.53
1:K:266:ILE:HG23	1:K:267:ALA:N	2.23	0.53
1:K:579:MSE:HB2	1:K:581:VAL:HG12	1.91	0.53
1:L:78:VAL:HG11	1:L:444:LEU:HG	1.90	0.53
1:L:80:TYR:CE1	1:L:448:VAL:HG22	2.43	0.53
2:f:58:GLN:H	2:f:62:GLY:HA3	1.73	0.53
2:g:71:ASP:O	2:g:72:ASP:HB3	2.08	0.53
2:h:78:GLU:CG	2:h:79:GLY:N	2.63	0.53
2:i:78:GLU:HG3	2:i:79:GLY:N	2.20	0.53
1:M:427:GLY:C	1:M:429:GLN:H	2.15	0.53
1:N:593:LEU:O	1:N:597:GLN:HG2	2.08	0.53
1:O:443:ASP:C	1:O:446:THR:HG22	2.34	0.53
1:P:78:VAL:HG12	1:P:79:LEU:H	1.69	0.53
1:R:451:ASP:C	1:R:453:LEU:H	2.17	0.53
1:S:44:TRP:CE2	1:S:54:ARG:HB3	2.44	0.53
1:S:443:ASP:C	1:S:444:LEU:HD13	2.34	0.53
1:S:443:ASP:C	1:S:446:THR:HG22	2.34	0.53
1:T:78:VAL:HG12	1:T:79:LEU:H	1.72	0.53
1:T:164:LEU:HD22	1:T:169:ASP:CG	2.33	0.53
1:T:344:THR:O	1:T:344:THR:HG23	2.06	0.53
1:T:444:LEU:O	1:T:448:VAL:HG23	2.09	0.53
1:U:380:ASN:O	1:U:381:SER:HB3	2.08	0.53
1:V:66:LYS:NZ	1:V:420:VAL:HG11	2.22	0.53
1:W:123:VAL:HG22	1:W:316:TYR:CE2	2.43	0.53
2:m:62:ASP:HB2	2:m:64:GLU:HB3	1.91	0.53
2:m:134:THR:HB	2:m:145:GLU:N	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:n:62:ASP:HB2	2:n:64:GLU:HB3	1.89	0.53
2:p:134:THR:HB	2:p:145:GLU:N	2.22	0.53
1:A:80:TYR:CE1	1:A:448:VAL:HG22	2.43	0.53
1:C:78:VAL:HG11	1:C:444:LEU:HG	1.90	0.53
1:F:15:PHE:HZ	1:F:283:CYS:SG	2.31	0.53
1:F:78:VAL:CG1	1:F:79:LEU:N	2.72	0.53
1:G:229:LYS:HA	1:G:272:LYS:HA	1.90	0.53
1:G:343:ARG:NH1	2:d:135:ALA:O	2.33	0.53
1:H:177:HIS:O	1:H:218:GLN:HA	2.09	0.53
1:L:266:ILE:HG23	1:L:267:ALA:N	2.23	0.53
2:c:28:VAL:HG11	2:c:96:LEU:C	2.33	0.53
2:h:71:ASP:O	2:h:72:ASP:HB3	2.08	0.53
1:M:94:LEU:HA	1:M:97:MSE:CE	2.38	0.53
1:M:236:GLN:HA	1:M:244:VAL:H	1.74	0.53
1:O:47:GLN:HG2	1:O:48:TYR:N	2.23	0.53
1:Q:44:TRP:CE2	1:Q:54:ARG:HB3	2.44	0.53
1:R:101:ASP:HB2	1:R:144:ILE:O	2.08	0.53
1:R:380:ASN:O	1:R:381:SER:HB3	2.09	0.53
1:R:444:LEU:C	1:R:446:THR:H	2.15	0.53
1:S:236:GLN:HA	1:S:244:VAL:H	1.74	0.53
1:T:380:ASN:O	1:T:381:SER:HB3	2.09	0.53
1:U:81:ARG:HB2	1:U:517:TYR:CZ	2.44	0.53
1:U:101:ASP:HB2	1:U:144:ILE:O	2.09	0.53
1:V:593:LEU:O	1:V:597:GLN:HG2	2.08	0.53
1:W:144:ILE:HD12	1:W:145:ARG:N	2.24	0.53
1:X:47:GLN:HG2	1:X:48:TYR:N	2.24	0.53
1:X:584:PRO:HG2	1:X:593:LEU:HD12	1.90	0.53
2:k:65:ASN:O	2:k:67:PRO:CD	2.56	0.53
2:l:58:TYR:HB2	2:l:75:LEU:HD21	1.89	0.53
2:n:131:ARG:O	2:n:132:MET:HB3	2.09	0.53
1:A:78:VAL:CG1	1:A:79:LEU:N	2.72	0.53
1:B:276:VAL:HG23	1:B:293:ILE:HG23	1.89	0.53
1:B:329:LEU:HD22	2:Y:142:PRO:HG2	1.89	0.53
1:C:511:ARG:HA	1:C:513:ARG:HD2	1.91	0.53
1:D:138:THR:H	1:D:143:VAL:HG22	1.73	0.53
1:E:158:TRP:HB3	1:E:173:CYS:CA	2.36	0.53
1:F:54:ARG:HB2	2:c:146:GLY:HA3	1.90	0.53
1:F:236:GLN:CB	1:F:265:LYS:HG2	2.37	0.53
1:F:579:MSE:HB2	1:F:581:VAL:HG12	1.90	0.53
1:H:78:VAL:CG1	1:H:79:LEU:N	2.72	0.53
1:I:384:LEU:HD22	1:I:384:LEU:N	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:511:ARG:HA	1:I:513:ARG:HD2	1.91	0.53
1:I:579:MSE:HB2	1:I:581:VAL:HG12	1.90	0.53
1:J:27:ARG:HB2	1:J:313:LYS:HE3	1.89	0.53
1:J:177:HIS:O	1:J:218:GLN:HA	2.09	0.53
1:J:229:LYS:HA	1:J:272:LYS:HA	1.90	0.53
1:J:236:GLN:HE21	1:J:265:LYS:NZ	2.06	0.53
2:Z:28:VAL:HG11	2:Z:96:LEU:C	2.33	0.53
2:a:57:TYR:CD2	2:a:57:TYR:O	2.62	0.53
2:c:58:GLN:H	2:c:62:GLY:HA3	1.73	0.53
1:N:66:LYS:NZ	1:N:420:VAL:HG11	2.23	0.53
1:Q:37:ARG:C	1:Q:39:SER:H	2.16	0.53
1:Q:165:MSE:HE1	1:Q:435:VAL:HB	1.91	0.53
1:Q:386:THR:O	1:Q:387:GLN:C	2.52	0.53
1:R:78:VAL:HG12	1:R:79:LEU:H	1.72	0.53
1:S:123:VAL:HG22	1:S:316:TYR:CE2	2.44	0.53
1:T:58:ASP:HA	1:T:327:GLN:NE2	2.24	0.53
1:T:80:TYR:CE1	1:T:448:VAL:HG22	2.44	0.53
1:U:236:GLN:HA	1:U:244:VAL:H	1.73	0.53
1:U:348:LYS:HB2	1:X:372:TYR:CE2	2.43	0.53
1:U:389:LEU:H	1:U:389:LEU:HD12	1.73	0.53
1:V:81:ARG:HB2	1:V:517:TYR:CZ	2.44	0.53
1:V:598:GLN:HB2	1:V:601:GLN:HB2	1.91	0.53
1:W:44:TRP:CE2	1:W:54:ARG:HB3	2.44	0.53
1:W:47:GLN:HG2	1:W:48:TYR:N	2.23	0.53
1:W:427:GLY:C	1:W:429:GLN:H	2.14	0.53
1:X:380:ASN:O	1:X:381:SER:HB3	2.07	0.53
1:A:311:GLU:O	1:A:312:ASP:HB2	2.07	0.53
1:B:80:TYR:CE1	1:B:448:VAL:HG22	2.43	0.53
1:B:158:TRP:CD1	1:B:158:TRP:H	2.25	0.53
1:C:177:HIS:O	1:C:218:GLN:HA	2.09	0.53
1:C:234:ILE:HG13	1:C:267:ALA:HB3	1.91	0.53
1:C:528:LYS:HZ3	1:C:560:LEU:HD21	1.73	0.53
1:E:32:ASP:HA	1:E:35:PHE:CE1	2.44	0.53
1:E:78:VAL:HG11	1:E:444:LEU:HG	1.91	0.53
1:G:78:VAL:CG1	1:G:79:LEU:N	2.72	0.53
1:H:34:PHE:CE1	1:H:324:LYS:NZ	2.72	0.53
1:I:123:VAL:HG22	1:I:316:TYR:CE2	2.43	0.53
1:I:177:HIS:O	1:I:218:GLN:HA	2.09	0.53
1:J:80:TYR:CE1	1:J:448:VAL:HG22	2.43	0.53
1:J:386:THR:O	1:J:387:GLN:C	2.52	0.53
1:J:511:ARG:HA	1:J:513:ARG:HD2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:511:ARG:HA	1:K:513:ARG:HD2	1.91	0.53
1:L:236:GLN:HE21	1:L:265:LYS:NZ	2.06	0.53
2:a:102:PRO:HB3	2:b:109:THR:HG21	1.89	0.53
2:b:57:TYR:CD2	2:b:57:TYR:O	2.62	0.53
2:c:57:TYR:CD2	2:c:57:TYR:O	2.62	0.53
2:e:57:TYR:CD2	2:e:57:TYR:O	2.62	0.53
1:M:35:PHE:CE1	1:M:321:ARG:NE	2.75	0.53
1:M:344:THR:HG23	1:M:344:THR:O	2.07	0.53
1:M:386:THR:O	1:M:387:GLN:C	2.51	0.53
1:P:456:ALA:HB1	1:P:509:ASP:OD1	2.09	0.53
1:Q:41:TRP:HE1	1:R:27:ARG:NH2	2.07	0.53
1:R:456:ALA:HB1	1:R:509:ASP:OD1	2.08	0.53
1:R:593:LEU:O	1:R:597:GLN:HG2	2.08	0.53
1:U:66:LYS:NZ	1:U:420:VAL:HG11	2.23	0.53
1:U:352:TRP:CG	1:X:376:ARG:HB2	2.44	0.53
1:U:593:LEU:O	1:U:597:GLN:HG2	2.08	0.53
1:V:35:PHE:HE1	1:V:321:ARG:NH1	2.06	0.53
1:V:351:PHE:CD2	1:V:356:ILE:HD12	2.44	0.53
2:l:62:ASP:HB2	2:l:64:GLU:HB3	1.91	0.53
2:u:65:ASN:O	2:u:67:PRO:CD	2.57	0.53
1:A:177:HIS:O	1:A:218:GLN:HA	2.09	0.53
1:A:234:ILE:HG13	1:A:267:ALA:HB3	1.90	0.53
1:A:276:VAL:HG23	1:A:293:ILE:HG23	1.89	0.53
1:A:511:ARG:HA	1:A:513:ARG:HD2	1.91	0.53
1:B:32:ASP:HA	1:B:35:PHE:CE1	2.44	0.53
1:B:386:THR:O	1:B:387:GLN:C	2.52	0.53
1:D:177:HIS:O	1:D:218:GLN:HA	2.09	0.53
1:E:177:HIS:O	1:E:218:GLN:HA	2.09	0.53
1:F:32:ASP:HA	1:F:35:PHE:CE1	2.44	0.53
1:F:395:PRO:HD2	1:G:398:PRO:HB3	1.91	0.53
1:F:511:ARG:HA	1:F:513:ARG:HD2	1.91	0.53
1:H:32:ASP:HA	1:H:35:PHE:CE1	2.44	0.53
1:H:229:LYS:HA	1:H:272:LYS:HA	1.90	0.53
1:H:384:LEU:HD22	1:H:384:LEU:N	2.23	0.53
1:I:229:LYS:HA	1:I:272:LYS:HA	1.90	0.53
1:K:386:THR:O	1:K:387:GLN:C	2.52	0.53
1:L:47:GLN:O	1:L:47:GLN:NE2	2.41	0.53
2:Z:58:GLN:H	2:Z:62:GLY:HA3	1.73	0.53
2:i:57:TYR:CD2	2:i:57:TYR:O	2.62	0.53
2:i:58:GLN:H	2:i:62:GLY:HA3	1.73	0.53
1:M:351:PHE:CD2	1:M:356:ILE:HD12	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:35:PHE:HE1	1:N:321:ARG:NH1	2.05	0.53
1:N:302:PRO:O	1:N:439:ASN:ND2	2.41	0.53
1:N:434:THR:HA	1:N:437:GLN:HG2	1.90	0.53
1:N:434:THR:O	1:N:437:GLN:HG2	2.09	0.53
1:N:443:ASP:C	1:N:444:LEU:HD13	2.34	0.53
1:O:359:PHE:HD1	2:o:120:ILE:HD11	1.73	0.53
1:P:55:GLY:HA3	1:P:57:PHE:CE1	2.44	0.53
1:P:386:THR:O	1:P:387:GLN:C	2.51	0.53
1:Q:81:ARG:HB2	1:Q:517:TYR:CZ	2.44	0.53
1:Q:420:VAL:HG22	1:Q:428:GLY:HA3	1.91	0.53
1:V:158:TRP:N	1:V:158:TRP:HD1	2.07	0.53
1:V:444:LEU:C	1:V:446:THR:H	2.16	0.53
1:W:386:THR:O	1:W:387:GLN:C	2.52	0.53
2:o:58:TYR:HB2	2:o:75:LEU:HD21	1.89	0.53
2:q:110:GLY:O	2:q:114:LEU:HD13	2.09	0.53
2:s:104:ILE:HD12	2:s:105:ALA:N	2.24	0.53
1:A:47:GLN:O	1:A:47:GLN:NE2	2.41	0.53
1:A:138:THR:H	1:A:143:VAL:HG22	1.73	0.53
1:C:560:LEU:O	1:C:561:ASP:O	2.26	0.53
1:D:560:LEU:O	1:D:561:ASP:O	2.26	0.53
1:E:229:LYS:HA	1:E:272:LYS:HA	1.90	0.53
1:E:511:ARG:HA	1:E:513:ARG:HD2	1.91	0.53
1:H:80:TYR:CE1	1:H:448:VAL:HG22	2.43	0.53
1:H:158:TRP:CD1	1:H:158:TRP:H	2.25	0.53
1:H:511:ARG:HA	1:H:513:ARG:HD2	1.91	0.53
1:L:229:LYS:HA	1:L:272:LYS:HA	1.90	0.53
1:L:311:GLU:O	1:L:312:ASP:HB2	2.07	0.53
2:e:71:ASP:O	2:e:72:ASP:HB3	2.08	0.53
1:M:380:ASN:O	1:M:381:SER:HB3	2.09	0.53
1:P:71:MSE:HE2	1:P:119:ILE:HD11	1.90	0.53
1:Q:71:MSE:HE2	1:Q:119:ILE:HD11	1.91	0.53
1:S:101:ASP:HB2	1:S:144:ILE:O	2.09	0.53
1:S:164:LEU:HD22	1:S:169:ASP:CG	2.34	0.53
1:T:35:PHE:CE1	1:T:321:ARG:NE	2.76	0.53
1:U:386:THR:O	1:U:387:GLN:C	2.52	0.53
1:V:236:GLN:HA	1:V:244:VAL:H	1.73	0.53
1:V:325:ASP:O	1:V:329:LEU:HD23	2.09	0.53
1:W:80:TYR:CE1	1:W:448:VAL:HG22	2.44	0.53
1:W:302:PRO:O	1:W:439:ASN:ND2	2.42	0.53
1:X:80:TYR:CE1	1:X:448:VAL:HG22	2.44	0.53
1:X:325:ASP:O	1:X:329:LEU:HD23	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:389:LEU:H	1:X:389:LEU:HD12	1.74	0.53
2:n:71:ASP:OD2	2:n:71:ASP:N	2.37	0.53
2:o:71:ASP:OD2	2:o:71:ASP:N	2.36	0.53
2:p:104:ILE:HD12	2:p:105:ALA:N	2.24	0.53
2:s:128:TYR:CD1	2:s:132:MET:HG2	2.44	0.53
1:B:334:MSE:HE3	1:C:404:MSE:CE	2.39	0.53
1:B:427:GLY:C	1:B:429:GLN:H	2.15	0.53
1:B:560:LEU:O	1:B:561:ASP:O	2.26	0.53
1:C:386:THR:O	1:C:387:GLN:C	2.52	0.53
1:C:427:GLY:C	1:C:429:GLN:H	2.15	0.53
1:D:34:PHE:HZ	1:D:328:ARG:HH22	0.80	0.53
1:D:80:TYR:CE1	1:D:448:VAL:HG22	2.43	0.53
1:D:511:ARG:HA	1:D:513:ARG:HD2	1.91	0.53
1:E:35:PHE:HE2	1:E:324:LYS:NZ	2.07	0.53
1:H:15:PHE:HZ	1:H:283:CYS:SG	2.31	0.53
1:I:266:ILE:HG23	1:I:267:ALA:N	2.23	0.53
1:J:34:PHE:CE1	1:J:324:LYS:NZ	2.72	0.53
1:J:311:GLU:O	1:J:312:ASP:HB2	2.07	0.53
1:L:511:ARG:HA	1:L:513:ARG:HD2	1.91	0.53
2:f:57:TYR:CD2	2:f:57:TYR:O	2.62	0.53
2:h:57:TYR:CD2	2:h:57:TYR:O	2.62	0.53
2:j:57:TYR:CD2	2:j:57:TYR:O	2.62	0.53
1:N:154:SER:O	1:N:204:PRO:HB3	2.09	0.52
1:O:78:VAL:HG11	1:O:444:LEU:HG	1.90	0.52
1:R:46:SER:N	1:R:48:TYR:HE2	1.98	0.52
1:R:302:PRO:O	1:R:439:ASN:ND2	2.42	0.52
1:R:344:THR:HG23	1:R:344:THR:O	2.08	0.52
1:V:34:PHE:HZ	1:V:328:ARG:HH22	1.40	0.52
1:X:434:THR:HA	1:X:437:GLN:HG2	1.91	0.52
1:B:78:VAL:HG11	1:B:444:LEU:HG	1.90	0.52
1:B:511:ARG:HA	1:B:513:ARG:HD2	1.91	0.52
1:D:273:ARG:NH2	1:D:453:LEU:HD21	2.21	0.52
1:F:47:GLN:O	1:F:47:GLN:NE2	2.41	0.52
1:F:329:LEU:HD22	2:e:142:PRO:HG2	1.91	0.52
1:G:32:ASP:HA	1:G:35:PHE:CE1	2.44	0.52
1:I:15:PHE:CZ	1:I:283:CYS:HA	2.45	0.52
1:I:72:ARG:HD2	1:J:434:THR:HG21	1.91	0.52
1:I:138:THR:H	1:I:143:VAL:HG22	1.73	0.52
1:I:563:LYS:HD3	1:J:557:PHE:CE2	2.44	0.52
1:J:158:TRP:CD1	1:J:158:TRP:H	2.25	0.52
1:J:234:ILE:HG13	1:J:267:ALA:HB3	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:32:ASP:HA	1:K:35:PHE:CE1	2.44	0.52
2:Y:53:MET:HE2	2:Y:92:VAL:CG1	2.20	0.52
2:f:57:TYR:O	2:f:57:TYR:HD2	1.92	0.52
2:f:71:ASP:O	2:f:72:ASP:HB3	2.08	0.52
2:g:57:TYR:O	2:g:57:TYR:CD2	2.62	0.52
2:i:71:ASP:O	2:i:72:ASP:HB3	2.08	0.52
1:M:66:LYS:NZ	1:M:420:VAL:HG11	2.24	0.52
1:M:123:VAL:HG22	1:M:316:TYR:CE2	2.45	0.52
1:O:66:LYS:HZ3	1:O:420:VAL:HG11	1.75	0.52
1:O:420:VAL:HG22	1:O:428:GLY:HA3	1.90	0.52
1:Q:37:ARG:C	1:Q:39:SER:N	2.66	0.52
1:Q:443:ASP:C	1:Q:444:LEU:HD13	2.34	0.52
1:R:81:ARG:HB2	1:R:517:TYR:CZ	2.45	0.52
1:R:93:VAL:CG1	1:R:458:ARG:HG3	2.38	0.52
1:R:584:PRO:HG2	1:R:593:LEU:HD12	1.90	0.52
1:S:380:ASN:O	1:S:381:SER:HB3	2.10	0.52
1:S:434:THR:HA	1:S:437:GLN:HG2	1.91	0.52
1:T:81:ARG:HB2	1:T:517:TYR:CZ	2.44	0.52
1:T:546:THR:CG2	1:T:547:PRO:HD3	2.28	0.52
1:T:573:ASN:O	1:T:577:ILE:HG13	2.09	0.52
1:V:47:GLN:HG2	1:V:48:TYR:N	2.23	0.52
1:W:328:ARG:HB3	2:s:133:PRO:HG3	1.90	0.52
1:X:386:THR:O	1:X:387:GLN:C	2.52	0.52
1:B:78:VAL:CG1	1:B:79:LEU:N	2.72	0.52
1:C:15:PHE:CZ	1:C:283:CYS:HA	2.45	0.52
1:C:229:LYS:HA	1:C:272:LYS:HA	1.90	0.52
1:D:229:LYS:HA	1:D:272:LYS:HA	1.90	0.52
1:D:556:TYR:OH	1:F:542:THR:HG21	2.09	0.52
1:F:15:PHE:CZ	1:F:283:CYS:HA	2.45	0.52
1:G:265:LYS:O	1:G:266:ILE:HG12	2.10	0.52
1:G:579:MSE:HB2	1:G:581:VAL:HG12	1.91	0.52
1:J:158:TRP:HB3	1:J:173:CYS:CA	2.36	0.52
1:K:78:VAL:CG1	1:K:79:LEU:N	2.72	0.52
1:K:229:LYS:HA	1:K:272:LYS:HA	1.90	0.52
1:K:384:LEU:HD22	1:K:384:LEU:N	2.23	0.52
1:L:138:THR:H	1:L:143:VAL:HG22	1.73	0.52
1:L:209:PHE:HA	1:L:211:TRP:NE1	2.24	0.52
1:L:236:GLN:CB	1:L:265:LYS:HG2	2.37	0.52
1:L:265:LYS:O	1:L:266:ILE:HG12	2.10	0.52
1:L:384:LEU:HD22	1:L:384:LEU:N	2.23	0.52
1:L:386:THR:O	1:L:387:GLN:C	2.52	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:380:ASN:O	1:N:381:SER:HB3	2.09	0.52
1:Q:380:ASN:O	1:Q:381:SER:HB3	2.10	0.52
1:R:66:LYS:NZ	1:R:420:VAL:HG11	2.22	0.52
1:S:95:MSE:HB3	1:S:527:MSE:HE1	1.90	0.52
1:S:165:MSE:HE1	1:S:435:VAL:HB	1.91	0.52
1:T:35:PHE:HE1	1:T:321:ARG:NH1	2.06	0.52
1:T:144:ILE:HD12	1:T:145:ARG:N	2.25	0.52
1:U:296:GLU:HG2	1:U:449:PHE:HB3	1.90	0.52
1:U:398:PRO:HB3	1:X:395:PRO:HD2	1.90	0.52
2:o:80:VAL:C	2:o:82:ALA:H	2.18	0.52
2:r:128:TYR:CD1	2:r:132:MET:HG2	2.45	0.52
2:t:110:GLY:O	2:t:114:LEU:HD13	2.09	0.52
1:A:78:VAL:HG11	1:A:444:LEU:HG	1.90	0.52
1:A:434:THR:HA	1:A:437:GLN:CD	2.35	0.52
1:A:579:MSE:HB2	1:A:581:VAL:HG12	1.91	0.52
1:B:229:LYS:HA	1:B:272:LYS:HA	1.90	0.52
1:D:376:ARG:HB2	1:F:352:TRP:CG	2.44	0.52
1:E:560:LEU:O	1:E:561:ASP:O	2.26	0.52
1:G:47:GLN:O	1:G:47:GLN:NE2	2.41	0.52
1:I:457:MSE:O	1:I:458:ARG:HD2	2.10	0.52
1:L:32:ASP:HA	1:L:35:PHE:CE1	2.44	0.52
1:L:579:MSE:HB2	1:L:581:VAL:HG12	1.90	0.52
2:b:58:GLN:H	2:b:62:GLY:HA3	1.73	0.52
2:c:57:TYR:O	2:c:57:TYR:HD2	1.92	0.52
2:d:58:GLN:H	2:d:62:GLY:HA3	1.73	0.52
2:g:57:TYR:O	2:g:57:TYR:HD2	1.92	0.52
2:j:58:GLN:H	2:j:62:GLY:HA3	1.73	0.52
1:M:24:GLU:C	1:M:26:ARG:N	2.55	0.52
1:M:37:ARG:C	1:M:39:SER:N	2.67	0.52
1:R:434:THR:HA	1:R:437:GLN:HG2	1.90	0.52
1:S:93:VAL:CG1	1:S:458:ARG:HG3	2.37	0.52
1:T:93:VAL:CG1	1:T:458:ARG:HG3	2.39	0.52
1:T:434:THR:HA	1:T:437:GLN:HG2	1.91	0.52
1:X:443:ASP:C	1:X:444:LEU:HD13	2.35	0.52
2:k:131:ARG:O	2:k:132:MET:HB3	2.10	0.52
2:n:65:ASN:O	2:n:67:PRO:CD	2.57	0.52
2:o:65:ASN:O	2:o:67:PRO:CD	2.58	0.52
2:p:131:ARG:O	2:p:132:MET:HB3	2.09	0.52
2:q:43:MET:C	2:q:45:ALA:H	2.18	0.52
2:u:110:GLY:O	2:u:114:LEU:HD13	2.09	0.52
1:D:209:PHE:HA	1:D:211:TRP:NE1	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:234:ILE:HG13	1:D:267:ALA:HB3	1.90	0.52
1:D:379:GLU:O	1:D:380:ASN:CB	2.58	0.52
1:F:265:LYS:O	1:F:266:ILE:HG12	2.10	0.52
1:J:334:MSE:HE3	1:K:404:MSE:CE	2.40	0.52
1:L:78:VAL:CG1	1:L:79:LEU:N	2.72	0.52
2:Y:57:TYR:CD2	2:Y:57:TYR:O	2.62	0.52
2:b:57:TYR:O	2:b:57:TYR:HD2	1.92	0.52
2:i:57:TYR:O	2:i:57:TYR:HD2	1.92	0.52
1:M:40:GLN:HG2	1:O:310:VAL:HG22	1.90	0.52
1:M:556:TYR:OH	1:O:542:THR:HG21	2.10	0.52
1:P:93:VAL:CG1	1:P:458:ARG:HG3	2.38	0.52
1:Q:66:LYS:HZ3	1:Q:420:VAL:HG11	1.74	0.52
1:R:236:GLN:HA	1:R:244:VAL:H	1.74	0.52
1:R:386:THR:O	1:R:387:GLN:C	2.51	0.52
1:S:81:ARG:HB2	1:S:517:TYR:CZ	2.44	0.52
1:S:144:ILE:HD12	1:S:145:ARG:N	2.24	0.52
1:U:302:PRO:O	1:U:439:ASN:ND2	2.42	0.52
1:U:344:THR:HG23	1:U:344:THR:O	2.10	0.52
1:U:456:ALA:HB1	1:U:509:ASP:OD1	2.09	0.52
1:V:296:GLU:HG2	1:V:449:PHE:HB3	1.91	0.52
1:V:352:TRP:CG	1:W:376:ARG:HB2	2.45	0.52
1:W:93:VAL:CG1	1:W:458:ARG:HG3	2.37	0.52
1:W:598:GLN:HB2	1:W:601:GLN:HB2	1.92	0.52
2:l:48:TYR:O	2:l:48:TYR:HD2	1.93	0.52
2:t:80:VAL:C	2:t:82:ALA:H	2.18	0.52
1:C:457:MSE:O	1:C:458:ARG:HD2	2.10	0.52
1:F:229:LYS:HA	1:F:272:LYS:HA	1.90	0.52
1:F:334:MSE:SE	1:G:404:MSE:HE1	2.60	0.52
1:F:379:GLU:O	1:F:380:ASN:CB	2.58	0.52
1:G:209:PHE:HA	1:G:211:TRP:NE1	2.24	0.52
1:H:273:ARG:NH2	1:H:453:LEU:HD21	2.21	0.52
1:J:457:MSE:O	1:J:458:ARG:HD2	2.10	0.52
1:K:209:PHE:HA	1:K:211:TRP:NE1	2.24	0.52
2:d:57:TYR:HD2	2:d:57:TYR:O	1.92	0.52
2:f:78:GLU:HG3	2:f:79:GLY:N	2.20	0.52
2:h:78:GLU:HG3	2:h:79:GLY:N	2.20	0.52
1:M:165:MSE:HE1	1:M:435:VAL:HB	1.92	0.52
1:P:44:TRP:CE2	1:P:54:ARG:HB3	2.44	0.52
1:P:165:MSE:HE1	1:P:435:VAL:HB	1.91	0.52
1:P:380:ASN:O	1:P:381:SER:HB3	2.09	0.52
1:T:434:THR:O	1:T:437:GLN:HG2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:44:TRP:CE2	1:U:54:ARG:HB3	2.45	0.52
1:U:360:GLU:HG3	2:t:122:ARG:HB3	1.92	0.52
1:U:434:THR:HA	1:U:437:GLN:HG2	1.91	0.52
1:V:329:LEU:HD21	1:W:53:TYR:OH	2.10	0.52
1:V:443:ASP:C	1:V:446:THR:HG22	2.34	0.52
1:V:444:LEU:O	1:V:448:VAL:HG23	2.10	0.52
1:W:165:MSE:HG3	1:W:307:TRP:CD2	2.44	0.52
1:W:165:MSE:HE1	1:W:435:VAL:HB	1.91	0.52
1:W:380:ASN:O	1:W:381:SER:HB3	2.10	0.52
2:o:62:ASP:HB2	2:o:64:GLU:HB3	1.91	0.52
2:s:81:SER:HB3	2:t:42:ALA:HB1	1.92	0.52
2:v:62:ASP:HB2	2:v:64:GLU:HB3	1.91	0.52
1:A:15:PHE:CZ	1:A:283:CYS:HA	2.45	0.52
1:A:209:PHE:HA	1:A:211:TRP:NE1	2.24	0.52
1:A:350:PHE:HE1	1:L:363:TYR:HE1	1.57	0.52
1:A:379:GLU:O	1:A:380:ASN:CB	2.58	0.52
1:B:266:ILE:HG23	1:B:267:ALA:N	2.23	0.52
1:B:363:TYR:HE1	1:C:350:PHE:HE1	1.56	0.52
1:C:32:ASP:HA	1:C:35:PHE:CE1	2.44	0.52
1:C:113:ILE:HD13	1:C:150:HIS:CE1	2.45	0.52
1:C:266:ILE:HG23	1:C:267:ALA:N	2.23	0.52
1:D:32:ASP:HA	1:D:35:PHE:CE1	2.44	0.52
1:D:221:GLU:OE2	1:D:278:LYS:HD2	2.10	0.52
1:E:113:ILE:HD13	1:E:150:HIS:CE1	2.45	0.52
1:E:265:LYS:O	1:E:266:ILE:HG12	2.10	0.52
1:F:434:THR:HA	1:F:437:GLN:CD	2.35	0.52
1:G:234:ILE:HG13	1:G:267:ALA:HB3	1.91	0.52
1:G:386:THR:O	1:G:387:GLN:C	2.52	0.52
1:H:15:PHE:CZ	1:H:283:CYS:HA	2.45	0.52
1:H:234:ILE:HG13	1:H:267:ALA:HB3	1.90	0.52
1:I:78:VAL:CG1	1:I:79:LEU:N	2.72	0.52
1:I:209:PHE:HA	1:I:211:TRP:NE1	2.24	0.52
1:I:221:GLU:OE2	1:I:278:LYS:HD2	2.10	0.52
1:I:343:ARG:NH2	2:g:134:ARG:HD3	2.25	0.52
1:I:386:THR:O	1:I:387:GLN:C	2.52	0.52
1:J:78:VAL:CG1	1:J:79:LEU:N	2.72	0.52
1:J:209:PHE:HA	1:J:211:TRP:NE1	2.24	0.52
1:J:384:LEU:HD22	1:J:384:LEU:N	2.23	0.52
1:K:113:ILE:HD13	1:K:150:HIS:CE1	2.45	0.52
1:K:177:HIS:O	1:K:218:GLN:HA	2.09	0.52
1:L:434:THR:HA	1:L:437:GLN:CD	2.35	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:a:57:TYR:O	2:a:57:TYR:HD2	1.92	0.52
2:i:53:MET:O	2:i:69:PHE:CE1	2.63	0.52
1:M:443:ASP:C	1:M:444:LEU:HD13	2.35	0.52
1:N:165:MSE:HE1	1:N:435:VAL:HB	1.92	0.52
1:N:329:LEU:HD22	2:v:133:PRO:HG2	1.90	0.52
1:N:352:TRP:CD1	1:V:376:ARG:HB2	2.45	0.52
1:N:386:THR:O	1:N:387:GLN:C	2.52	0.52
1:O:53:TYR:OH	1:P:329:LEU:HD21	2.07	0.52
1:Q:55:GLY:HA3	1:Q:57:PHE:CE1	2.45	0.52
1:Q:144:ILE:HD12	1:Q:145:ARG:N	2.25	0.52
1:R:80:TYR:CE1	1:R:448:VAL:HG22	2.43	0.52
1:S:389:LEU:HD12	1:S:389:LEU:H	1.75	0.52
1:S:434:THR:O	1:S:437:GLN:HG2	2.09	0.52
1:T:236:GLN:HA	1:T:244:VAL:H	1.74	0.52
1:U:273:ARG:NH1	1:U:275:ARG:HE	2.07	0.52
1:W:35:PHE:CE1	1:W:321:ARG:NE	2.78	0.52
2:u:104:ILE:HD12	2:u:105:ALA:N	2.25	0.52
1:A:32:ASP:HA	1:A:35:PHE:CE1	2.44	0.52
1:A:438:LEU:HD22	3:L:719:HOH:O	2.09	0.52
1:B:434:THR:HA	1:B:437:GLN:CD	2.35	0.52
1:C:209:PHE:HA	1:C:211:TRP:NE1	2.24	0.52
1:D:265:LYS:O	1:D:266:ILE:HG12	2.10	0.52
1:G:457:MSE:O	1:G:458:ARG:HD2	2.10	0.52
1:I:32:ASP:HA	1:I:35:PHE:CE1	2.44	0.52
1:I:363:TYR:HE1	1:J:350:PHE:HE1	1.56	0.52
1:J:113:ILE:HD13	1:J:150:HIS:CE1	2.45	0.52
1:L:113:ILE:HD13	1:L:150:HIS:CE1	2.45	0.52
1:L:139:SER:CB	1:L:455:THR:CG2	2.80	0.52
1:L:457:MSE:O	1:L:458:ARG:HD2	2.10	0.52
2:Y:71:ASP:O	2:Y:72:ASP:HB3	2.08	0.52
1:M:598:GLN:HB2	1:M:601:GLN:HB2	1.92	0.52
1:N:598:GLN:HB2	1:N:601:GLN:HB2	1.92	0.52
1:O:44:TRP:C	1:O:45:LEU:HD22	2.35	0.52
1:O:209:PHE:HZ	1:O:214:GLN:HG2	1.70	0.52
1:O:546:THR:CG2	1:O:547:PRO:HD3	2.29	0.52
1:P:95:MSE:HB3	1:P:527:MSE:HE1	1.90	0.52
1:P:344:THR:HG23	1:P:344:THR:O	2.08	0.52
1:Q:58:ASP:HA	1:Q:327:GLN:NE2	2.24	0.52
1:R:35:PHE:HE1	1:R:321:ARG:NH1	2.07	0.52
1:T:273:ARG:NH1	1:T:275:ARG:HE	2.08	0.52
1:T:454:ALA:O	1:T:455:THR:C	2.53	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:598:GLN:HB2	1:T:601:GLN:HB2	1.91	0.52
1:U:37:ARG:C	1:U:39:SER:N	2.68	0.52
2:m:48:TYR:HD2	2:m:48:TYR:O	1.93	0.52
2:m:80:VAL:C	2:m:82:ALA:H	2.18	0.52
2:p:62:ASP:HB2	2:p:64:GLU:HB3	1.91	0.52
1:A:386:THR:O	1:A:387:GLN:C	2.52	0.52
1:B:113:ILE:HD13	1:B:150:HIS:CE1	2.45	0.52
1:B:379:GLU:O	1:B:380:ASN:CB	2.58	0.52
1:B:579:MSE:HB2	1:B:581:VAL:HG12	1.91	0.52
1:C:434:THR:HA	1:C:437:GLN:CD	2.35	0.52
1:D:139:SER:CB	1:D:455:THR:CG2	2.80	0.52
1:D:386:THR:O	1:D:387:GLN:C	2.52	0.52
1:E:457:MSE:O	1:E:458:ARG:HD2	2.10	0.52
1:E:579:MSE:HB2	1:E:581:VAL:HG12	1.91	0.52
1:H:386:THR:O	1:H:387:GLN:C	2.52	0.52
1:H:556:TYR:OH	1:I:542:THR:HG21	2.09	0.52
1:J:32:ASP:HA	1:J:35:PHE:CE1	2.44	0.52
1:J:379:GLU:O	1:J:380:ASN:CB	2.58	0.52
1:K:457:MSE:O	1:K:458:ARG:HD2	2.10	0.52
2:a:78:GLU:HG3	2:a:79:GLY:N	2.20	0.52
2:d:57:TYR:O	2:d:57:TYR:CD2	2.62	0.52
2:h:58:GLN:H	2:h:62:GLY:HA3	1.73	0.52
2:j:57:TYR:O	2:j:57:TYR:HD2	1.92	0.52
1:M:66:LYS:HZ1	1:M:420:VAL:HG11	1.75	0.52
1:M:325:ASP:O	1:M:329:LEU:HD23	2.10	0.52
1:M:451:ASP:C	1:M:453:LEU:H	2.17	0.52
1:O:93:VAL:CG1	1:O:458:ARG:HG3	2.38	0.52
1:P:420:VAL:HG22	1:P:428:GLY:HA3	1.91	0.52
1:Q:389:LEU:H	1:Q:389:LEU:HD12	1.74	0.52
1:R:37:ARG:C	1:R:39:SER:N	2.66	0.52
1:R:325:ASP:O	1:R:329:LEU:HD23	2.09	0.52
1:U:343:ARG:HD3	2:q:128:TYR:CE1	2.45	0.52
1:W:236:GLN:HA	1:W:244:VAL:H	1.74	0.52
1:W:359:PHE:HD1	2:k:120:ILE:HD11	1.75	0.52
1:X:37:ARG:C	1:X:39:SER:N	2.66	0.52
2:l:131:ARG:O	2:l:132:MET:HB3	2.10	0.52
1:A:221:GLU:OE2	1:A:278:LYS:HD2	2.10	0.52
1:A:457:MSE:O	1:A:458:ARG:HD2	2.10	0.52
1:A:573:ASN:O	1:A:577:ILE:HG13	2.10	0.52
1:B:209:PHE:HA	1:B:211:TRP:NE1	2.24	0.52
1:D:579:MSE:HB2	1:D:581:VAL:HG12	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:15:PHE:CZ	1:E:283:CYS:HA	2.45	0.52
1:E:273:ARG:NH2	1:E:453:LEU:HD21	2.21	0.52
1:F:113:ILE:HD13	1:F:150:HIS:CE1	2.45	0.52
1:G:113:ILE:HD13	1:G:150:HIS:CE1	2.45	0.52
1:H:579:MSE:HB2	1:H:581:VAL:HG12	1.90	0.52
1:I:113:ILE:HD13	1:I:150:HIS:CE1	2.45	0.52
1:I:395:PRO:HD2	1:J:398:PRO:HB3	1.92	0.52
1:J:15:PHE:CZ	1:J:283:CYS:HA	2.45	0.52
1:L:560:LEU:O	1:L:561:ASP:O	2.26	0.52
2:d:51:ALA:HB1	2:f:90:SER:OG	2.10	0.52
2:e:78:GLU:HG3	2:e:79:GLY:N	2.20	0.52
2:g:77:ALA:O	2:g:78:GLU:HB3	2.10	0.52
2:j:53:MET:O	2:j:69:PHE:CE1	2.63	0.52
2:j:77:ALA:O	2:j:78:GLU:HB3	2.10	0.52
1:O:386:THR:O	1:O:387:GLN:C	2.52	0.52
3:P:719:HOH:O	1:Q:430:VAL:HG11	2.10	0.52
1:Q:451:ASP:C	1:Q:453:LEU:H	2.17	0.52
1:R:387:GLN:HB3	1:X:390:ALA:CB	2.40	0.52
1:U:34:PHE:CE2	1:U:45:LEU:HG	2.45	0.52
1:U:325:ASP:O	1:U:329:LEU:HD23	2.10	0.52
1:U:451:ASP:C	1:U:453:LEU:H	2.18	0.52
1:V:454:ALA:O	1:V:455:THR:C	2.53	0.52
1:W:444:LEU:O	1:W:448:VAL:HG23	2.10	0.52
1:X:37:ARG:C	1:X:39:SER:H	2.18	0.52
1:X:535:ILE:HD13	1:X:554:LEU:HG	1.92	0.52
2:k:62:ASP:HB2	2:k:64:GLU:HB3	1.90	0.52
2:n:64:GLU:CD	1:D:228:LYS:HG2	2.35	0.52
2:q:71:ASP:OD2	2:q:71:ASP:N	2.36	0.52
1:A:229:LYS:HA	1:A:272:LYS:HA	1.90	0.52
1:A:561:ASP:OD2	1:B:92:ASP:HB3	2.10	0.52
1:B:15:PHE:CZ	1:B:283:CYS:HA	2.45	0.52
1:B:35:PHE:CE2	1:B:321:ARG:HG3	2.45	0.52
1:C:221:GLU:OE2	1:C:278:LYS:HD2	2.10	0.52
1:C:379:GLU:O	1:C:380:ASN:CB	2.58	0.52
1:C:573:ASN:O	1:C:577:ILE:HG13	2.10	0.52
1:D:78:VAL:CG1	1:D:79:LEU:N	2.72	0.52
1:E:14:ARG:NE	1:E:14:ARG:CA	2.67	0.52
1:E:78:VAL:CG1	1:E:79:LEU:N	2.72	0.52
1:F:35:PHE:CE2	1:F:321:ARG:HG3	2.45	0.52
1:G:35:PHE:HE2	1:G:324:LYS:NZ	2.07	0.52
1:G:334:MSE:HE3	1:H:404:MSE:HE3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:457:MSE:O	1:H:458:ARG:HD2	2.10	0.52
1:I:265:LYS:O	1:I:266:ILE:HG12	2.10	0.52
1:J:14:ARG:NE	1:J:14:ARG:CA	2.67	0.52
1:J:248:LYS:HZ1	1:J:513:ARG:HH12	1.58	0.52
1:K:573:ASN:O	1:K:577:ILE:HG13	2.11	0.52
3:K:719:HOH:O	1:L:438:LEU:HD22	2.10	0.52
1:L:15:PHE:CZ	1:L:283:CYS:HA	2.45	0.52
2:Y:77:ALA:O	2:Y:78:GLU:HB3	2.10	0.52
2:Z:53:MET:O	2:Z:69:PHE:CE1	2.63	0.52
2:Z:57:TYR:CD2	2:Z:57:TYR:O	2.62	0.52
2:Z:57:TYR:O	2:Z:57:TYR:HD2	1.92	0.52
2:e:57:TYR:O	2:e:57:TYR:HD2	1.92	0.52
1:O:78:VAL:HG12	1:O:79:LEU:H	1.74	0.51
1:O:334:MSE:HE1	1:P:407:ALA:HB1	1.91	0.51
1:O:434:THR:O	1:O:437:GLN:HG2	2.10	0.51
1:O:456:ALA:HB1	1:O:509:ASP:OD1	2.09	0.51
3:O:719:HOH:O	1:P:430:VAL:HG11	2.10	0.51
1:P:78:VAL:HG11	1:P:444:LEU:HG	1.91	0.51
1:P:332:MSE:SE	2:l:132:MET:HA	2.60	0.51
1:P:573:ASN:O	1:P:577:ILE:HG13	2.10	0.51
1:R:434:THR:O	1:R:437:GLN:HG2	2.10	0.51
1:S:386:THR:O	1:S:387:GLN:C	2.52	0.51
1:V:328:ARG:HB3	2:u:133:PRO:HG3	1.92	0.51
1:V:380:ASN:O	1:V:381:SER:HB3	2.10	0.51
1:X:236:GLN:HA	1:X:244:VAL:H	1.74	0.51
2:s:131:ARG:O	2:s:132:MET:HB3	2.09	0.51
1:A:35:PHE:CE2	1:A:321:ARG:HG3	2.45	0.51
1:B:457:MSE:O	1:B:458:ARG:HD2	2.10	0.51
1:C:14:ARG:NE	1:C:14:ARG:CA	2.67	0.51
1:C:35:PHE:CE2	1:C:321:ARG:HG3	2.45	0.51
1:C:207:TRP:O	1:C:208:VAL:C	2.54	0.51
1:C:265:LYS:O	1:C:266:ILE:HG12	2.10	0.51
1:C:429:GLN:O	1:C:429:GLN:HG2	2.10	0.51
1:D:113:ILE:HD13	1:D:150:HIS:CE1	2.45	0.51
1:F:160:SER:O	1:F:161:ASN:ND2	2.43	0.51
1:F:209:PHE:HA	1:F:211:TRP:NE1	2.24	0.51
1:G:160:SER:O	1:G:161:ASN:ND2	2.44	0.51
1:G:511:ARG:HA	1:G:513:ARG:HD2	1.91	0.51
1:J:35:PHE:CE2	1:J:321:ARG:HG3	2.45	0.51
1:J:37:ARG:HH21	1:J:37:ARG:CB	2.16	0.51
1:J:329:LEU:HD22	2:g:142:PRO:HG2	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:434:THR:HA	1:J:437:GLN:CD	2.35	0.51
1:L:35:PHE:CE2	1:L:321:ARG:HG3	2.45	0.51
1:L:207:TRP:O	1:L:208:VAL:C	2.53	0.51
2:Z:77:ALA:O	2:Z:78:GLU:HB3	2.10	0.51
2:a:52:MET:HE1	2:a:92:VAL:O	2.10	0.51
1:M:37:ARG:HH21	1:M:37:ARG:CB	2.23	0.51
1:M:95:MSE:HE1	1:M:99:ARG:CZ	2.41	0.51
1:N:34:PHE:CE2	1:N:45:LEU:HG	2.46	0.51
1:N:80:TYR:CE1	1:N:448:VAL:HG22	2.45	0.51
1:Q:598:GLN:HB2	1:Q:601:GLN:HB2	1.92	0.51
1:R:389:LEU:H	1:R:389:LEU:HD12	1.74	0.51
1:U:154:SER:O	1:U:204:PRO:HB3	2.10	0.51
1:V:123:VAL:HG22	1:V:316:TYR:CE2	2.45	0.51
1:W:389:LEU:H	1:W:389:LEU:HD12	1.75	0.51
1:W:451:ASP:C	1:W:453:LEU:H	2.18	0.51
1:X:123:VAL:HG22	1:X:316:TYR:CE2	2.45	0.51
1:B:221:GLU:OE2	1:B:278:LYS:HD2	2.10	0.51
1:B:372:TYR:CE2	1:C:348:LYS:HB2	2.45	0.51
1:C:563:LYS:HD3	1:E:557:PHE:CE2	2.45	0.51
1:D:15:PHE:CZ	1:D:283:CYS:HA	2.45	0.51
1:D:160:SER:O	1:D:161:ASN:ND2	2.44	0.51
1:D:334:MSE:HE3	1:F:404:MSE:CE	2.40	0.51
1:D:573:ASN:O	1:D:577:ILE:HG13	2.10	0.51
1:E:379:GLU:O	1:E:380:ASN:CB	2.58	0.51
1:F:556:TYR:OH	1:G:542:THR:HG21	2.09	0.51
1:H:182:ASN:ND2	1:I:171:ARG:HH21	2.08	0.51
1:I:434:THR:HA	1:I:437:GLN:CD	2.35	0.51
1:J:207:TRP:O	1:J:208:VAL:C	2.53	0.51
1:K:265:LYS:O	1:K:266:ILE:HG12	2.10	0.51
1:K:434:THR:HA	1:K:437:GLN:CD	2.35	0.51
2:b:52:MET:HE1	2:b:92:VAL:O	2.10	0.51
2:b:77:ALA:O	2:b:78:GLU:HB3	2.10	0.51
2:e:52:MET:HE1	2:e:92:VAL:O	2.11	0.51
2:f:52:MET:HE1	2:f:92:VAL:O	2.10	0.51
2:g:53:MET:O	2:g:69:PHE:CE1	2.63	0.51
1:M:322:LEU:HD22	1:M:322:LEU:N	2.25	0.51
1:N:37:ARG:C	1:N:39:SER:N	2.67	0.51
1:N:351:PHE:CD2	1:N:356:ILE:HD12	2.46	0.51
1:O:58:ASP:HA	1:O:327:GLN:NE2	2.26	0.51
1:O:598:GLN:HB2	1:O:601:GLN:HB2	1.92	0.51
1:Q:158:TRP:N	1:Q:158:TRP:HD1	2.07	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:434:THR:HA	1:Q:437:GLN:HG2	1.92	0.51
1:S:35:PHE:HE1	1:S:321:ARG:NH1	2.06	0.51
1:S:379:GLU:O	1:S:380:ASN:CB	2.58	0.51
1:U:390:ALA:CB	1:X:387:GLN:CB	2.88	0.51
1:V:451:ASP:C	1:V:453:LEU:H	2.19	0.51
1:X:158:TRP:N	1:X:158:TRP:HD1	2.07	0.51
2:u:62:ASP:C	2:u:64:GLU:N	2.61	0.51
1:B:395:PRO:HD2	1:C:398:PRO:HB3	1.92	0.51
1:C:63:VAL:HG21	1:C:416:ALA:HB1	1.93	0.51
1:C:579:MSE:HB2	1:C:581:VAL:HG12	1.91	0.51
1:D:37:ARG:HH21	1:D:37:ARG:CB	2.16	0.51
1:D:63:VAL:HG21	1:D:416:ALA:HB1	1.93	0.51
1:E:207:TRP:O	1:E:208:VAL:C	2.53	0.51
1:E:221:GLU:OE2	1:E:278:LYS:HD2	2.10	0.51
1:E:386:THR:O	1:E:387:GLN:C	2.52	0.51
1:E:434:THR:HA	1:E:437:GLN:CD	2.35	0.51
1:F:63:VAL:HG21	1:F:416:ALA:HB1	1.93	0.51
1:F:207:TRP:O	1:F:208:VAL:C	2.54	0.51
1:F:386:THR:O	1:F:387:GLN:C	2.52	0.51
1:G:221:GLU:OE2	1:G:278:LYS:HD2	2.10	0.51
1:H:113:ILE:HD13	1:H:150:HIS:CE1	2.45	0.51
1:H:139:SER:CB	1:H:455:THR:CG2	2.80	0.51
1:H:265:LYS:O	1:H:266:ILE:HG12	2.10	0.51
1:H:434:THR:HA	1:H:437:GLN:CD	2.35	0.51
1:I:160:SER:O	1:I:161:ASN:ND2	2.44	0.51
1:I:236:GLN:CB	1:I:265:LYS:HZ3	2.16	0.51
1:I:573:ASN:O	1:I:577:ILE:HG13	2.10	0.51
1:J:265:LYS:O	1:J:266:ILE:HG12	2.10	0.51
1:J:266:ILE:HG23	1:J:267:ALA:N	2.23	0.51
2:Y:57:TYR:O	2:Y:57:TYR:HD2	1.92	0.51
2:e:77:ALA:O	2:e:78:GLU:HB3	2.10	0.51
2:f:77:ALA:O	2:f:78:GLU:HB3	2.10	0.51
2:g:52:MET:HE1	2:g:92:VAL:O	2.11	0.51
2:h:57:TYR:O	2:h:57:TYR:HD2	1.92	0.51
2:i:77:ALA:O	2:i:78:GLU:HB3	2.10	0.51
1:M:434:THR:O	1:M:437:GLN:HG2	2.09	0.51
1:O:46:SER:N	1:O:48:TYR:HE2	1.98	0.51
1:O:302:PRO:O	1:O:439:ASN:ND2	2.43	0.51
1:P:81:ARG:HB2	1:P:517:TYR:CZ	2.45	0.51
1:P:395:PRO:HD2	1:Q:398:PRO:HB3	1.91	0.51
1:P:434:THR:HA	1:P:437:GLN:HG2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:302:PRO:O	1:Q:439:ASN:ND2	2.44	0.51
1:Q:546:THR:CG2	1:Q:547:PRO:HD3	2.29	0.51
1:R:34:PHE:CE2	1:R:45:LEU:HG	2.44	0.51
1:S:329:LEU:HD22	2:q:133:PRO:HG2	1.93	0.51
1:T:95:MSE:HB3	1:T:527:MSE:HE1	1.91	0.51
1:T:101:ASP:HB2	1:T:144:ILE:O	2.11	0.51
1:T:154:SER:O	1:T:204:PRO:HB3	2.09	0.51
1:U:351:PHE:CD2	1:U:356:ILE:HD12	2.44	0.51
1:U:598:GLN:HB2	1:U:601:GLN:HB2	1.92	0.51
1:V:44:TRP:CE2	1:V:54:ARG:HB3	2.46	0.51
1:V:348:LYS:HB2	1:W:372:TYR:CE2	2.46	0.51
1:W:535:ILE:HD13	1:W:554:LEU:HG	1.93	0.51
1:X:144:ILE:HD12	1:X:145:ARG:N	2.25	0.51
2:n:104:ILE:HD12	2:n:105:ALA:N	2.25	0.51
2:t:131:ARG:O	2:t:132:MET:HB3	2.10	0.51
1:A:63:VAL:HG21	1:A:416:ALA:HB1	1.93	0.51
1:A:207:TRP:O	1:A:208:VAL:C	2.53	0.51
1:A:348:LYS:HB3	1:L:371:TYR:HA	1.92	0.51
1:C:78:VAL:CG1	1:C:79:LEU:N	2.72	0.51
1:D:111:VAL:O	1:D:115:VAL:HG13	2.11	0.51
1:D:457:MSE:O	1:D:458:ARG:HD2	2.10	0.51
1:E:573:ASN:O	1:E:577:ILE:HG13	2.11	0.51
1:F:111:VAL:O	1:F:115:VAL:HG13	2.11	0.51
1:F:573:ASN:O	1:F:577:ILE:HG13	2.11	0.51
1:G:429:GLN:HG2	1:G:429:GLN:O	2.10	0.51
1:G:434:THR:HA	1:G:437:GLN:CD	2.35	0.51
1:H:35:PHE:CE2	1:H:321:ARG:HG3	2.45	0.51
1:H:429:GLN:O	1:H:429:GLN:HG2	2.10	0.51
1:I:35:PHE:CE2	1:I:321:ARG:HG3	2.45	0.51
1:I:379:GLU:O	1:I:380:ASN:CB	2.58	0.51
1:I:444:LEU:C	1:I:446:THR:H	2.19	0.51
1:J:63:VAL:HG21	1:J:416:ALA:HB1	1.93	0.51
1:K:363:TYR:HE1	1:L:350:PHE:HE1	1.57	0.51
1:K:379:GLU:O	1:K:380:ASN:CB	2.58	0.51
1:L:444:LEU:C	1:L:446:THR:H	2.19	0.51
1:L:573:ASN:O	1:L:577:ILE:HG13	2.10	0.51
2:Y:52:MET:HE1	2:Y:92:VAL:O	2.11	0.51
2:d:52:MET:HE1	2:d:92:VAL:O	2.11	0.51
2:f:102:PRO:HB3	2:g:109:THR:HG21	1.92	0.51
2:h:52:MET:HE1	2:h:92:VAL:O	2.11	0.51
2:h:77:ALA:O	2:h:78:GLU:HB3	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:420:VAL:HG22	1:M:428:GLY:HA3	1.92	0.51
1:N:344:THR:HG23	1:N:344:THR:O	2.09	0.51
1:N:430:VAL:CG1	3:V:719:HOH:O	2.59	0.51
1:N:438:LEU:HD22	3:V:718:HOH:O	2.09	0.51
1:P:598:GLN:HB2	1:P:601:GLN:HB2	1.92	0.51
1:T:37:ARG:C	1:T:39:SER:N	2.66	0.51
1:U:123:VAL:HG22	1:U:316:TYR:CE2	2.46	0.51
1:U:584:PRO:HG2	1:U:593:LEU:HD12	1.91	0.51
1:X:344:THR:HG23	1:X:344:THR:O	2.09	0.51
1:X:434:THR:O	1:X:437:GLN:HG2	2.10	0.51
2:n:64:GLU:OE1	2:n:64:GLU:HA	2.10	0.51
2:r:65:ASN:O	2:r:67:PRO:HD3	2.10	0.51
2:s:43:MET:C	2:s:45:ALA:H	2.19	0.51
2:v:80:VAL:C	2:v:82:ALA:H	2.18	0.51
1:A:101:ASP:HB3	1:A:138:THR:HG21	1.93	0.51
1:A:160:SER:O	1:A:161:ASN:ND2	2.44	0.51
1:B:34:PHE:HZ	1:B:328:ARG:HH22	0.80	0.51
1:B:573:ASN:O	1:B:577:ILE:HG13	2.11	0.51
1:C:111:VAL:O	1:C:115:VAL:HG13	2.11	0.51
1:D:207:TRP:O	1:D:208:VAL:C	2.54	0.51
1:E:14:ARG:HH11	1:E:17:ALA:HB2	1.76	0.51
1:F:14:ARG:NE	1:F:14:ARG:CA	2.67	0.51
1:F:34:PHE:CE1	1:F:324:LYS:NZ	2.72	0.51
1:F:429:GLN:O	1:F:429:GLN:HG2	2.10	0.51
1:G:14:ARG:HH11	1:G:17:ALA:HB2	1.76	0.51
1:H:561:ASP:OD2	1:I:92:ASP:HB3	2.10	0.51
1:I:234:ILE:HG13	1:I:267:ALA:HB3	1.90	0.51
1:I:359:PHE:HD1	2:h:129:ILE:HD11	1.76	0.51
1:J:101:ASP:HB3	1:J:138:THR:HG21	1.93	0.51
1:K:63:VAL:HG21	1:K:416:ALA:HB1	1.93	0.51
2:b:53:MET:HE2	2:b:92:VAL:CG1	2.20	0.51
2:b:53:MET:O	2:b:69:PHE:CE1	2.63	0.51
2:c:77:ALA:O	2:c:78:GLU:HB3	2.10	0.51
2:e:53:MET:O	2:e:69:PHE:CE1	2.63	0.51
1:O:456:ALA:O	1:O:457:MSE:HB2	2.11	0.51
1:Q:37:ARG:HH21	1:Q:37:ARG:CB	2.24	0.51
1:Q:54:ARG:HB2	2:o:137:GLY:HA3	1.92	0.51
1:Q:454:ALA:O	1:Q:455:THR:C	2.53	0.51
1:R:598:GLN:HB2	1:R:601:GLN:HB2	1.92	0.51
1:S:37:ARG:C	1:S:39:SER:N	2.68	0.51
1:S:351:PHE:CD2	1:S:356:ILE:HD12	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:58:ASP:HA	1:V:327:GLN:NE2	2.25	0.51
1:V:344:THR:HG23	1:V:344:THR:O	2.09	0.51
1:W:434:THR:HA	1:W:437:GLN:HG2	1.92	0.51
1:X:302:PRO:O	1:X:439:ASN:ND2	2.43	0.51
2:m:48:TYR:O	2:m:48:TYR:CD2	2.63	0.51
2:q:131:ARG:O	2:q:132:MET:HB3	2.08	0.51
2:s:48:TYR:CD2	2:s:48:TYR:O	2.64	0.51
2:s:48:TYR:O	2:s:48:TYR:HD2	1.94	0.51
2:u:131:ARG:O	2:u:132:MET:HB3	2.10	0.51
1:E:63:VAL:HG21	1:E:416:ALA:HB1	1.93	0.51
1:E:209:PHE:HA	1:E:211:TRP:NE1	2.24	0.51
1:E:328:ARG:HB3	2:a:142:PRO:HG3	1.93	0.51
1:F:14:ARG:HH11	1:F:17:ALA:HB2	1.76	0.51
1:G:15:PHE:CZ	1:G:283:CYS:HA	2.45	0.51
1:H:101:ASP:HB3	1:H:138:THR:HG21	1.93	0.51
1:H:160:SER:O	1:H:161:ASN:ND2	2.44	0.51
1:H:209:PHE:HA	1:H:211:TRP:NE1	2.24	0.51
1:H:221:GLU:OE2	1:H:278:LYS:HD2	2.10	0.51
1:H:573:ASN:O	1:H:577:ILE:HG13	2.10	0.51
1:J:111:VAL:O	1:J:115:VAL:HG13	2.11	0.51
1:J:160:SER:O	1:J:161:ASN:ND2	2.44	0.51
1:K:15:PHE:CZ	1:K:283:CYS:HA	2.45	0.51
1:K:221:GLU:OE2	1:K:278:LYS:HD2	2.10	0.51
2:Y:53:MET:O	2:Y:69:PHE:CE1	2.63	0.51
2:a:53:MET:O	2:a:69:PHE:CE1	2.63	0.51
1:O:380:ASN:O	1:O:381:SER:HB3	2.11	0.51
1:O:389:LEU:H	1:O:389:LEU:HD12	1.75	0.51
1:P:80:TYR:CE1	1:P:448:VAL:HG22	2.45	0.51
1:P:546:THR:CG2	1:P:547:PRO:HD3	2.31	0.51
1:R:44:TRP:CE2	1:R:54:ARG:HB3	2.46	0.51
1:R:78:VAL:CG1	1:R:79:LEU:N	2.73	0.51
1:S:58:ASP:HA	1:S:327:GLN:NE2	2.25	0.51
1:T:34:PHE:CE2	1:T:45:LEU:HG	2.45	0.51
1:V:35:PHE:CE1	1:V:321:ARG:NE	2.76	0.51
1:W:443:ASP:C	1:W:444:LEU:HD13	2.36	0.51
1:X:351:PHE:CD2	1:X:356:ILE:HD12	2.45	0.51
1:X:573:ASN:O	1:X:577:ILE:HG13	2.10	0.51
2:s:12:ALA:C	2:s:14:LEU:N	2.66	0.51
1:A:111:VAL:O	1:A:115:VAL:HG13	2.11	0.51
1:A:113:ILE:HD13	1:A:150:HIS:CE1	2.45	0.51
1:A:564:GLY:CA	1:B:554:LEU:HD21	2.35	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:207:TRP:O	1:B:208:VAL:C	2.53	0.51
1:D:14:ARG:NE	1:D:14:ARG:CA	2.67	0.51
1:D:434:THR:HA	1:D:437:GLN:CD	2.35	0.51
1:F:37:ARG:HH21	1:F:37:ARG:CB	2.16	0.51
1:F:457:MSE:O	1:F:458:ARG:HD2	2.10	0.51
1:G:35:PHE:CE2	1:G:321:ARG:HG3	2.45	0.51
1:G:379:GLU:O	1:G:380:ASN:CB	2.58	0.51
1:H:251:ILE:O	1:H:507:LEU:HD13	2.11	0.51
1:I:207:TRP:O	1:I:208:VAL:C	2.53	0.51
1:L:34:PHE:CE1	1:L:324:LYS:NZ	2.72	0.51
1:L:160:SER:O	1:L:161:ASN:ND2	2.44	0.51
2:a:77:ALA:O	2:a:78:GLU:HB3	2.10	0.51
2:j:52:MET:HE1	2:j:92:VAL:O	2.10	0.51
1:M:144:ILE:HD12	1:M:145:ARG:N	2.26	0.51
1:M:430:VAL:HG11	3:N:719:HOH:O	2.11	0.51
1:N:325:ASP:O	1:N:329:LEU:HD23	2.10	0.51
1:N:456:ALA:O	1:N:457:MSE:HB2	2.11	0.51
1:O:78:VAL:CG1	1:O:79:LEU:N	2.74	0.51
1:O:165:MSE:HE1	1:O:435:VAL:HB	1.93	0.51
1:Q:80:TYR:CE1	1:Q:448:VAL:HG22	2.46	0.51
1:R:58:ASP:HA	1:R:327:GLN:NE2	2.26	0.51
1:R:95:MSE:HB3	1:R:527:MSE:HE1	1.93	0.51
1:R:123:VAL:HG22	1:R:316:TYR:CE2	2.45	0.51
1:R:456:ALA:O	1:R:457:MSE:HB2	2.11	0.51
1:S:37:ARG:HH21	1:S:37:ARG:CB	2.24	0.51
1:T:37:ARG:C	1:T:39:SER:H	2.18	0.51
1:U:78:VAL:HG12	1:U:79:LEU:H	1.75	0.51
1:U:535:ILE:HD13	1:U:554:LEU:HG	1.93	0.51
1:V:399:GLN:OE1	1:W:396:GLU:O	2.29	0.51
1:V:443:ASP:C	1:V:444:LEU:HD13	2.35	0.51
1:W:34:PHE:CE2	1:W:45:LEU:HG	2.45	0.51
1:X:34:PHE:CE2	1:X:45:LEU:HG	2.45	0.51
1:X:95:MSE:HB3	1:X:527:MSE:HE1	1.92	0.51
1:X:405:LEU:O	1:X:409:THR:HG23	2.10	0.51
2:l:100:THR:HG21	2:m:93:PRO:HB3	1.92	0.51
2:m:131:ARG:O	2:m:132:MET:HB3	2.10	0.51
2:n:110:GLY:O	2:n:114:LEU:HD13	2.10	0.51
2:r:12:ALA:C	2:r:14:LEU:N	2.68	0.51
2:s:8:ASP:CB	2:t:67:PRO:HG2	2.41	0.51
2:u:62:ASP:HB2	2:u:64:GLU:HB3	1.91	0.51
1:B:37:ARG:HH22	1:B:45:LEU:CD1	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:111:VAL:O	1:B:115:VAL:HG13	2.11	0.51
1:C:248:LYS:HD3	1:C:251:ILE:HB	1.93	0.51
1:D:376:ARG:HB2	1:F:352:TRP:CD2	2.46	0.51
1:F:101:ASP:HB3	1:F:138:THR:HG21	1.93	0.51
1:F:251:ILE:O	1:F:507:LEU:HD13	2.11	0.51
1:F:444:LEU:C	1:F:446:THR:H	2.19	0.51
1:H:379:GLU:O	1:H:380:ASN:CB	2.58	0.51
1:I:37:ARG:HH22	1:I:45:LEU:CD1	2.24	0.51
1:I:273:ARG:NH2	1:I:453:LEU:HD21	2.21	0.51
1:J:221:GLU:OE2	1:J:278:LYS:HD2	2.10	0.51
1:J:573:ASN:O	1:J:577:ILE:HG13	2.10	0.51
1:L:37:ARG:HH22	1:L:45:LEU:CD1	2.24	0.51
1:L:111:VAL:O	1:L:115:VAL:HG13	2.11	0.51
1:L:379:GLU:O	1:L:380:ASN:CB	2.58	0.51
2:i:52:MET:HE1	2:i:92:VAL:O	2.10	0.51
1:N:144:ILE:HD12	1:N:145:ARG:N	2.26	0.51
1:N:420:VAL:HG22	1:N:428:GLY:HA3	1.92	0.51
1:O:37:ARG:C	1:O:39:SER:H	2.19	0.51
1:R:535:ILE:HD13	1:R:554:LEU:HG	1.92	0.51
1:S:55:GLY:HA3	1:S:57:PHE:CE1	2.46	0.51
1:T:44:TRP:CE2	1:T:54:ARG:HB3	2.46	0.51
1:T:302:PRO:O	1:T:439:ASN:ND2	2.44	0.51
1:T:332:MSE:SE	2:t:132:MET:HA	2.60	0.51
1:W:454:ALA:O	1:W:455:THR:C	2.52	0.51
1:W:456:ALA:O	1:W:457:MSE:HB2	2.11	0.51
2:l:43:MET:C	2:l:45:ALA:H	2.18	0.51
2:l:48:TYR:O	2:l:48:TYR:CD2	2.64	0.51
2:s:62:ASP:HB2	2:s:64:GLU:HB3	1.91	0.51
2:s:65:ASN:O	2:s:67:PRO:CD	2.58	0.51
1:A:265:LYS:O	1:A:266:ILE:HG12	2.10	0.51
1:C:160:SER:O	1:C:161:ASN:ND2	2.44	0.51
1:D:14:ARG:HH11	1:D:17:ALA:HB2	1.76	0.51
1:E:429:GLN:HG2	1:E:429:GLN:O	2.10	0.51
1:F:221:GLU:OE2	1:F:278:LYS:HD2	2.10	0.51
1:J:14:ARG:HH11	1:J:17:ALA:HB2	1.76	0.51
1:L:14:ARG:NE	1:L:14:ARG:CA	2.67	0.51
1:L:101:ASP:HB3	1:L:138:THR:HG21	1.93	0.51
1:L:221:GLU:OE2	1:L:278:LYS:HD2	2.10	0.51
2:d:77:ALA:O	2:d:78:GLU:HB3	2.10	0.51
1:M:429:GLN:HG2	1:M:429:GLN:O	2.11	0.51
1:M:434:THR:HA	1:M:437:GLN:HG2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:719:HOH:O	1:O:430:VAL:HG11	2.11	0.51
1:O:158:TRP:N	1:O:158:TRP:HD1	2.07	0.51
1:R:212:LEU:HD22	1:X:26:ARG:HG2	1.93	0.51
1:S:456:ALA:O	1:S:457:MSE:HB2	2.10	0.51
1:T:78:VAL:CG1	1:T:79:LEU:N	2.74	0.51
1:U:80:TYR:CE1	1:U:448:VAL:HG22	2.45	0.51
1:W:413:LYS:HA	1:W:416:ALA:HB3	1.93	0.51
2:k:12:ALA:C	2:k:14:LEU:N	2.66	0.51
2:l:95:TYR:N	2:l:95:TYR:CD1	2.78	0.51
2:l:128:TYR:CD1	2:l:132:MET:HG2	2.45	0.51
2:o:12:ALA:C	2:o:14:LEU:N	2.67	0.51
1:B:63:VAL:HG21	1:B:416:ALA:HB1	1.93	0.51
1:B:160:SER:O	1:B:161:ASN:ND2	2.44	0.51
1:B:251:ILE:O	1:B:507:LEU:HD13	2.11	0.51
1:B:429:GLN:HG2	1:B:429:GLN:O	2.10	0.51
1:C:101:ASP:HB3	1:C:138:THR:HG21	1.93	0.51
1:D:236:GLN:CB	1:D:265:LYS:HG2	2.37	0.51
1:D:444:LEU:C	1:D:446:THR:H	2.19	0.51
1:E:160:SER:O	1:E:161:ASN:ND2	2.44	0.51
1:F:248:LYS:HD3	1:F:251:ILE:HB	1.93	0.51
1:F:560:LEU:O	1:F:565:VAL:HG21	2.11	0.51
1:G:560:LEU:O	1:G:565:VAL:HG21	2.11	0.51
1:H:560:LEU:O	1:H:565:VAL:HG21	2.11	0.51
1:I:429:GLN:O	1:I:429:GLN:HG2	2.10	0.51
1:K:72:ARG:HD2	1:L:434:THR:HG21	1.93	0.51
2:d:53:MET:O	2:d:69:PHE:CE1	2.63	0.51
2:f:70:SER:HB2	2:f:75:PRO:O	2.11	0.51
1:M:37:ARG:C	1:M:39:SER:H	2.19	0.50
1:N:35:PHE:CE1	1:N:321:ARG:NE	2.78	0.50
1:N:58:ASP:HA	1:N:327:GLN:NE2	2.26	0.50
1:O:80:TYR:CE1	1:O:448:VAL:HG22	2.46	0.50
1:O:171:ARG:O	1:O:224:GLU:HA	2.11	0.50
1:Q:78:VAL:CG1	1:Q:79:LEU:N	2.74	0.50
1:R:35:PHE:CE1	1:R:321:ARG:NE	2.77	0.50
1:S:54:ARG:HB2	2:t:137:GLY:HA3	1.92	0.50
1:T:389:LEU:H	1:T:389:LEU:HD12	1.76	0.50
1:U:37:ARG:C	1:U:39:SER:H	2.19	0.50
1:V:37:ARG:C	1:V:39:SER:N	2.68	0.50
1:V:46:SER:N	1:V:48:TYR:HE2	1.96	0.50
1:X:413:LYS:HA	1:X:416:ALA:HB3	1.92	0.50
1:A:37:ARG:HH22	1:A:45:LEU:CD1	2.24	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:248:LYS:HD3	1:A:251:ILE:HB	1.93	0.50
1:B:265:LYS:O	1:B:266:ILE:HG12	2.10	0.50
1:D:35:PHE:CE2	1:D:321:ARG:HG3	2.45	0.50
1:E:35:PHE:CE2	1:E:321:ARG:HG3	2.45	0.50
1:G:63:VAL:HG21	1:G:416:ALA:HB1	1.93	0.50
1:G:111:VAL:O	1:G:115:VAL:HG13	2.11	0.50
1:H:63:VAL:HG21	1:H:416:ALA:HB1	1.93	0.50
1:I:63:VAL:HG21	1:I:416:ALA:HB1	1.93	0.50
1:I:111:VAL:O	1:I:115:VAL:HG13	2.11	0.50
1:I:513:ARG:HD3	1:I:513:ARG:H	1.77	0.50
1:J:560:LEU:O	1:J:565:VAL:HG21	2.11	0.50
1:K:35:PHE:CE2	1:K:321:ARG:HG3	2.45	0.50
1:K:81:ARG:HB2	1:K:517:TYR:CE2	2.46	0.50
1:K:101:ASP:HB3	1:K:138:THR:HG21	1.93	0.50
1:K:160:SER:O	1:K:161:ASN:ND2	2.44	0.50
1:K:376:ARG:HB2	1:L:352:TRP:CD2	2.46	0.50
1:L:81:ARG:HB2	1:L:517:TYR:CE2	2.46	0.50
1:L:329:LEU:HD22	2:h:142:PRO:HG2	1.93	0.50
2:Z:38:GLU:N	2:Z:39:PRO:HD3	2.26	0.50
2:Z:52:MET:HE1	2:Z:92:VAL:O	2.11	0.50
2:h:53:MET:O	2:h:69:PHE:CE1	2.63	0.50
1:M:405:LEU:O	1:M:409:THR:HG23	2.12	0.50
1:Q:325:ASP:O	1:Q:329:LEU:HD23	2.11	0.50
1:R:405:LEU:O	1:R:409:THR:HG23	2.12	0.50
1:R:451:ASP:C	1:R:453:LEU:N	2.69	0.50
1:T:456:ALA:O	1:T:457:MSE:HB2	2.11	0.50
1:W:35:PHE:C	1:W:37:ARG:N	2.69	0.50
2:k:43:MET:C	2:k:45:ALA:H	2.20	0.50
2:m:95:TYR:N	2:m:95:TYR:CD1	2.77	0.50
1:A:92:ASP:HB3	1:L:561:ASP:OD2	2.10	0.50
1:A:251:ILE:O	1:A:507:LEU:HD13	2.11	0.50
1:A:328:ARG:HB3	2:j:142:PRO:HG3	1.93	0.50
1:A:329:LEU:HD22	2:j:142:PRO:HG2	1.93	0.50
1:A:429:GLN:O	1:A:429:GLN:HG2	2.10	0.50
1:B:248:LYS:HD3	1:B:251:ILE:HB	1.93	0.50
1:B:560:LEU:O	1:B:565:VAL:HG21	2.11	0.50
1:C:513:ARG:H	1:C:513:ARG:HD3	1.77	0.50
1:D:429:GLN:HG2	1:D:429:GLN:O	2.10	0.50
1:E:444:LEU:C	1:E:446:THR:H	2.19	0.50
1:F:418:LEU:HB2	1:F:428:GLY:O	2.12	0.50
1:F:586:THR:N	1:F:587:PRO:CD	2.74	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:207:TRP:O	1:G:208:VAL:C	2.53	0.50
1:H:111:VAL:O	1:H:115:VAL:HG13	2.11	0.50
1:I:343:ARG:NH1	2:g:135:ALA:O	2.37	0.50
1:I:418:LEU:HB2	1:I:428:GLY:O	2.12	0.50
1:J:81:ARG:HB2	1:J:517:TYR:CE2	2.46	0.50
1:J:246:TYR:HE2	1:J:512:GLY:N	2.10	0.50
1:J:586:THR:N	1:J:587:PRO:CD	2.75	0.50
1:K:444:LEU:C	1:K:446:THR:H	2.19	0.50
1:L:429:GLN:O	1:L:429:GLN:HG2	2.10	0.50
2:Z:70:SER:HB2	2:Z:75:PRO:O	2.12	0.50
2:a:70:SER:HB2	2:a:75:PRO:O	2.11	0.50
2:c:51:ALA:HB1	2:d:90:SER:OG	2.11	0.50
2:c:53:MET:O	2:c:69:PHE:CE1	2.63	0.50
2:d:38:GLU:N	2:d:39:PRO:HD3	2.26	0.50
2:e:38:GLU:N	2:e:39:PRO:HD3	2.26	0.50
2:h:38:GLU:N	2:h:39:PRO:HD3	2.26	0.50
1:N:174:THR:N	3:N:705:HOH:O	2.44	0.50
1:O:135:GLN:NE2	1:P:514:TYR:HE2	2.09	0.50
1:P:325:ASP:O	1:P:329:LEU:HD23	2.11	0.50
1:R:37:ARG:C	1:R:39:SER:H	2.18	0.50
1:R:158:TRP:N	1:R:158:TRP:HD1	2.08	0.50
1:R:454:ALA:O	1:R:455:THR:C	2.54	0.50
1:T:396:GLU:O	1:W:399:GLN:OE1	2.29	0.50
1:U:546:THR:CG2	1:U:547:PRO:HD3	2.31	0.50
1:V:9:GLU:HG3	1:V:12:LEU:H	1.77	0.50
1:W:420:VAL:HG22	1:W:428:GLY:HA3	1.91	0.50
2:l:93:PRO:HB3	2:n:100:THR:HG21	1.93	0.50
2:m:43:MET:C	2:m:45:ALA:H	2.18	0.50
2:o:131:ARG:O	2:o:132:MET:HB3	2.11	0.50
2:q:128:TYR:CD1	2:q:132:MET:HG2	2.46	0.50
2:r:131:ARG:O	2:r:132:MET:HB3	2.11	0.50
1:B:101:ASP:HB3	1:B:138:THR:HG21	1.93	0.50
1:B:246:TYR:HE2	1:B:512:GLY:N	2.10	0.50
1:C:81:ARG:HB2	1:C:517:TYR:CE2	2.46	0.50
1:C:418:LEU:HB2	1:C:428:GLY:O	2.12	0.50
1:D:37:ARG:HH22	1:D:45:LEU:CD1	2.24	0.50
1:D:404:MSE:HE3	1:E:334:MSE:HE3	1.93	0.50
1:D:560:LEU:O	1:D:565:VAL:HG21	2.11	0.50
1:E:513:ARG:H	1:E:513:ARG:HD3	1.76	0.50
1:E:586:THR:N	1:E:587:PRO:CD	2.75	0.50
1:G:37:ARG:HH22	1:G:45:LEU:CD1	2.24	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:81:ARG:HB2	1:G:517:TYR:CE2	2.46	0.50
1:G:563:LYS:HD3	1:H:557:PHE:CE2	2.47	0.50
1:G:573:ASN:O	1:G:577:ILE:HG13	2.10	0.50
1:I:101:ASP:HB3	1:I:138:THR:HG21	1.93	0.50
1:I:586:THR:N	1:I:587:PRO:CD	2.75	0.50
1:J:251:ILE:O	1:J:507:LEU:HD13	2.11	0.50
1:K:418:LEU:HB2	1:K:428:GLY:O	2.12	0.50
1:L:113:ILE:HD12	1:L:148:PRO:HB3	1.94	0.50
1:L:251:ILE:O	1:L:507:LEU:HD13	2.11	0.50
2:c:43:GLN:C	2:c:45:ALA:N	2.70	0.50
2:c:70:SER:HB2	2:c:75:PRO:O	2.11	0.50
2:c:78:GLU:HG3	2:c:79:GLY:N	2.20	0.50
1:M:456:ALA:O	1:M:457:MSE:HB2	2.11	0.50
1:M:535:ILE:HD13	1:M:554:LEU:HG	1.93	0.50
1:Q:34:PHE:CE2	1:Q:45:LEU:HG	2.46	0.50
1:Q:266:ILE:HG23	1:Q:267:ALA:N	2.26	0.50
1:R:37:ARG:HH21	1:R:37:ARG:CB	2.24	0.50
1:S:37:ARG:C	1:S:39:SER:H	2.20	0.50
1:S:235:TYR:HA	1:S:265:LYS:HB3	1.94	0.50
1:S:302:PRO:O	1:S:439:ASN:ND2	2.44	0.50
1:S:451:ASP:C	1:S:453:LEU:H	2.19	0.50
1:T:235:TYR:HA	1:T:265:LYS:HB3	1.94	0.50
1:V:26:ARG:HG2	1:W:212:LEU:HD22	1.94	0.50
1:V:266:ILE:HG23	1:V:267:ALA:N	2.26	0.50
1:X:598:GLN:HB2	1:X:601:GLN:HB2	1.92	0.50
2:q:65:ASN:O	2:q:67:PRO:HD3	2.10	0.50
2:s:42:ALA:HB1	2:u:81:SER:HB3	1.93	0.50
2:v:12:ALA:C	2:v:14:LEU:N	2.68	0.50
1:A:14:ARG:NE	1:A:14:ARG:CA	2.67	0.50
1:A:81:ARG:HB2	1:A:517:TYR:CE2	2.46	0.50
1:A:126:TRP:CD1	1:A:146:ARG:HG3	2.46	0.50
1:B:409:THR:O	1:B:413:LYS:HG2	2.12	0.50
1:C:584:PRO:HG2	1:C:593:LEU:HD12	1.94	0.50
1:E:535:ILE:HD11	1:E:554:LEU:HG	1.94	0.50
1:G:15:PHE:HZ	1:G:283:CYS:HG	1.60	0.50
1:G:198:ILE:O	1:G:198:ILE:HG22	2.12	0.50
1:H:14:ARG:HH11	1:H:17:ALA:HB2	1.76	0.50
1:H:126:TRP:CD1	1:H:146:ARG:HG3	2.46	0.50
1:I:14:ARG:HH11	1:I:17:ALA:HB2	1.76	0.50
1:I:126:TRP:CD1	1:I:146:ARG:HG3	2.46	0.50
1:K:246:TYR:HE2	1:K:512:GLY:N	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:251:ILE:O	1:K:507:LEU:HD13	2.11	0.50
1:K:429:GLN:O	1:K:429:GLN:HG2	2.10	0.50
1:K:510:ILE:O	1:K:513:ARG:HD2	2.12	0.50
1:L:246:TYR:HE2	1:L:512:GLY:N	2.10	0.50
1:L:248:LYS:HD3	1:L:251:ILE:HB	1.93	0.50
1:L:409:THR:O	1:L:413:LYS:HG2	2.12	0.50
1:L:535:ILE:HD11	1:L:554:LEU:HG	1.94	0.50
2:Z:104:TYR:HB2	2:Z:106:LEU:HD12	1.93	0.50
2:a:38:GLU:N	2:a:39:PRO:HD3	2.26	0.50
2:a:104:TYR:HB2	2:a:106:LEU:HD12	1.93	0.50
2:b:43:GLN:C	2:b:45:ALA:N	2.70	0.50
2:f:38:GLU:N	2:f:39:PRO:HD3	2.26	0.50
2:j:70:SER:HB2	2:j:75:PRO:O	2.11	0.50
1:N:379:GLU:O	1:N:380:ASN:CB	2.59	0.50
1:O:37:ARG:C	1:O:39:SER:N	2.67	0.50
1:P:158:TRP:N	1:P:158:TRP:HD1	2.07	0.50
1:Q:573:ASN:O	1:Q:577:ILE:HG13	2.12	0.50
1:R:443:ASP:C	1:R:444:LEU:HD13	2.36	0.50
1:S:332:MSE:SE	2:q:132:MET:HA	2.61	0.50
1:S:344:THR:HG23	1:S:344:THR:O	2.11	0.50
1:S:598:GLN:HB2	1:S:601:GLN:HB2	1.92	0.50
1:T:535:ILE:HD13	1:T:554:LEU:HG	1.93	0.50
1:U:37:ARG:HH21	1:U:37:ARG:CB	2.24	0.50
1:U:55:GLY:HA3	1:U:57:PHE:CE1	2.46	0.50
1:V:34:PHE:CE2	1:V:45:LEU:HG	2.46	0.50
1:W:37:ARG:C	1:W:39:SER:N	2.67	0.50
1:W:351:PHE:CD2	1:W:356:ILE:HD12	2.46	0.50
1:W:434:THR:HG23	1:W:435:VAL:N	2.26	0.50
2:p:65:ASN:O	2:p:67:PRO:HD3	2.12	0.50
2:r:48:TYR:O	2:r:48:TYR:CD2	2.64	0.50
2:s:110:GLY:O	2:s:114:LEU:HD13	2.12	0.50
2:v:128:TYR:CD1	2:v:132:MET:HG2	2.46	0.50
1:A:246:TYR:HE2	1:A:512:GLY:N	2.10	0.50
1:C:409:THR:O	1:C:413:LYS:HG2	2.12	0.50
1:C:535:ILE:HD11	1:C:554:LEU:HG	1.94	0.50
1:D:34:PHE:CE1	1:D:324:LYS:NZ	2.72	0.50
1:D:81:ARG:HB2	1:D:517:TYR:CE2	2.46	0.50
1:D:248:LYS:HZ2	1:D:251:ILE:HD12	1.77	0.50
1:D:248:LYS:HD3	1:D:251:ILE:HB	1.93	0.50
1:D:251:ILE:O	1:D:507:LEU:HD13	2.11	0.50
1:D:535:ILE:HD11	1:D:554:LEU:HG	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:37:ARG:HH22	1:E:45:LEU:CD1	2.24	0.50
1:E:81:ARG:HB2	1:E:517:TYR:CE2	2.46	0.50
1:E:94:LEU:HA	1:E:97:MSE:CE	2.37	0.50
1:E:113:ILE:HD12	1:E:148:PRO:HB3	1.94	0.50
1:F:113:ILE:HD12	1:F:148:PRO:HB3	1.94	0.50
1:F:246:TYR:HE2	1:F:512:GLY:N	2.10	0.50
1:G:586:THR:N	1:G:587:PRO:CD	2.75	0.50
1:H:37:ARG:HH22	1:H:45:LEU:CD1	2.24	0.50
1:H:81:ARG:HB2	1:H:517:TYR:CE2	2.46	0.50
1:H:510:ILE:O	1:H:513:ARG:HD2	2.12	0.50
1:K:14:ARG:HH11	1:K:17:ALA:HB2	1.76	0.50
1:K:126:TRP:CD1	1:K:146:ARG:HG3	2.46	0.50
1:K:560:LEU:O	1:K:565:VAL:HG21	2.11	0.50
1:L:57:PHE:CD2	1:L:330:ARG:CB	2.95	0.50
2:e:70:SER:HB2	2:e:75:PRO:O	2.11	0.50
2:f:104:TYR:HB2	2:f:106:LEU:HD12	1.93	0.50
2:g:34:LEU:C	2:g:35:THR:CG2	2.73	0.50
2:g:104:TYR:HB2	2:g:106:LEU:HD12	1.93	0.50
1:M:322:LEU:HD22	1:M:322:LEU:H	1.77	0.50
1:N:586:THR:N	1:N:587:PRO:CD	2.75	0.50
1:P:37:ARG:C	1:P:39:SER:N	2.68	0.50
1:Q:9:GLU:HG3	1:Q:12:LEU:H	1.77	0.50
1:S:573:ASN:O	1:S:577:ILE:HG13	2.12	0.50
1:U:235:TYR:HA	1:U:265:LYS:HB3	1.94	0.50
1:V:165:MSE:HE1	1:V:435:VAL:HB	1.94	0.50
1:W:37:ARG:C	1:W:39:SER:H	2.19	0.50
2:m:128:TYR:CD1	2:m:132:MET:HG2	2.46	0.50
2:u:80:VAL:C	2:u:82:ALA:H	2.19	0.50
1:A:510:ILE:O	1:A:513:ARG:HD2	2.12	0.50
1:A:513:ARG:HD3	1:A:513:ARG:H	1.76	0.50
1:B:14:ARG:HH11	1:B:17:ALA:HB2	1.76	0.50
1:B:81:ARG:HB2	1:B:517:TYR:CE2	2.46	0.50
1:B:113:ILE:HD12	1:B:148:PRO:HB3	1.94	0.50
1:B:513:ARG:H	1:B:513:ARG:HD3	1.77	0.50
1:C:251:ILE:O	1:C:507:LEU:HD13	2.11	0.50
1:D:101:ASP:HB3	1:D:138:THR:HG21	1.93	0.50
1:D:126:TRP:CD1	1:D:146:ARG:HG3	2.46	0.50
1:D:136:SER:N	1:D:137:PRO:HD3	2.27	0.50
1:D:246:TYR:HE2	1:D:512:GLY:N	2.10	0.50
1:D:409:THR:O	1:D:413:LYS:HG2	2.12	0.50
1:D:418:LEU:HB2	1:D:428:GLY:O	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:510:ILE:O	1:D:513:ARG:HD2	2.12	0.50
1:E:251:ILE:O	1:E:507:LEU:HD13	2.11	0.50
1:E:560:LEU:O	1:E:565:VAL:HG21	2.11	0.50
1:F:57:PHE:CD2	1:F:330:ARG:CB	2.95	0.50
1:H:248:LYS:HD3	1:H:251:ILE:HB	1.93	0.50
1:I:535:ILE:HD11	1:I:554:LEU:HG	1.94	0.50
1:J:126:TRP:CD1	1:J:146:ARG:HG3	2.46	0.50
1:K:113:ILE:HD12	1:K:148:PRO:HB3	1.94	0.50
1:K:409:THR:O	1:K:413:LYS:HG2	2.12	0.50
1:K:513:ARG:H	1:K:513:ARG:HD3	1.77	0.50
1:L:560:LEU:O	1:L:565:VAL:HG21	2.11	0.50
2:Y:70:SER:HB2	2:Y:75:PRO:O	2.12	0.50
2:Y:72:ASP:OD1	2:Y:72:ASP:O	2.30	0.50
2:Z:72:ASP:O	2:Z:72:ASP:OD1	2.30	0.50
2:e:43:GLN:C	2:e:45:ALA:N	2.70	0.50
2:g:38:GLU:N	2:g:39:PRO:HD3	2.26	0.50
1:N:27:ARG:NH2	1:V:41:TRP:HE1	2.10	0.50
1:N:359:PHE:HD1	2:l:120:ILE:HD11	1.76	0.50
1:P:34:PHE:CE2	1:P:45:LEU:HG	2.46	0.50
1:R:235:TYR:HA	1:R:265:LYS:HB3	1.94	0.50
1:R:444:LEU:O	1:R:448:VAL:HG23	2.11	0.50
1:S:9:GLU:HG3	1:S:12:LEU:H	1.77	0.50
1:S:14:ARG:NE	1:S:14:ARG:CA	2.69	0.50
1:U:47:GLN:HG2	1:U:48:TYR:N	2.26	0.50
1:U:78:VAL:CG1	1:U:79:LEU:N	2.74	0.50
1:U:379:GLU:O	1:U:380:ASN:CB	2.59	0.50
1:V:322:LEU:N	1:V:322:LEU:HD22	2.27	0.50
2:v:43:MET:C	2:v:45:ALA:H	2.19	0.50
1:A:136:SER:N	1:A:137:PRO:HD3	2.27	0.50
1:A:160:SER:HB3	1:A:171:ARG:NH2	2.27	0.50
1:A:352:TRP:CD1	1:L:376:ARG:HB2	2.47	0.50
1:C:37:ARG:HH22	1:C:45:LEU:CD1	2.24	0.50
1:C:136:SER:N	1:C:137:PRO:HD3	2.27	0.50
1:C:561:ASP:OD2	1:E:92:ASP:HB3	2.12	0.50
1:D:54:ARG:HB2	2:e:146:GLY:HA3	1.92	0.50
1:D:513:ARG:HD3	1:D:513:ARG:H	1.77	0.50
1:D:586:THR:N	1:D:587:PRO:CD	2.75	0.50
1:E:126:TRP:CD1	1:E:146:ARG:HG3	2.46	0.50
1:E:409:THR:O	1:E:413:LYS:HG2	2.12	0.50
1:E:418:LEU:HB2	1:E:428:GLY:O	2.12	0.50
1:E:427:GLY:C	1:E:429:GLN:N	2.70	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:126:TRP:CD1	1:G:146:ARG:HG3	2.46	0.50
1:G:409:THR:O	1:G:413:LYS:HG2	2.12	0.50
1:G:418:LEU:HB2	1:G:428:GLY:O	2.12	0.50
1:H:444:LEU:C	1:H:446:THR:H	2.19	0.50
1:I:334:MSE:HE3	1:J:404:MSE:HE3	1.93	0.50
1:I:560:LEU:O	1:I:565:VAL:HG21	2.11	0.50
1:J:128:LEU:HD12	1:J:446:THR:HG23	1.94	0.50
1:K:207:TRP:O	1:K:208:VAL:C	2.53	0.50
1:L:586:THR:N	1:L:587:PRO:CD	2.75	0.50
2:Z:28:VAL:HG21	2:Z:96:LEU:CG	2.40	0.50
2:d:72:ASP:OD1	2:d:72:ASP:O	2.30	0.50
1:M:413:LYS:HA	1:M:416:ALA:HB3	1.93	0.50
1:Q:434:THR:O	1:Q:437:GLN:HG2	2.11	0.50
1:Q:444:LEU:O	1:Q:448:VAL:HG23	2.11	0.50
1:Q:535:ILE:HD13	1:Q:554:LEU:HG	1.94	0.50
1:R:27:ARG:HB2	1:R:313:LYS:HE3	1.94	0.50
1:T:387:GLN:CB	1:W:390:ALA:CB	2.89	0.50
1:V:248:LYS:HG3	1:V:511:ARG:HE	1.77	0.50
1:V:343:ARG:O	1:V:344:THR:HB	2.12	0.50
1:W:235:TYR:OH	1:W:252:LYS:NZ	2.45	0.50
1:W:343:ARG:NH1	2:u:126:ALA:O	2.42	0.50
1:X:35:PHE:HE1	1:X:321:ARG:NH1	2.06	0.50
1:X:78:VAL:CG1	1:X:444:LEU:HG	2.42	0.50
2:k:128:TYR:CD1	2:k:132:MET:HG2	2.46	0.50
2:l:80:VAL:C	2:l:82:ALA:H	2.19	0.50
2:o:48:TYR:O	2:o:48:TYR:HD2	1.95	0.50
2:q:80:VAL:C	2:q:82:ALA:H	2.19	0.50
2:t:12:ALA:C	2:t:14:LEU:N	2.66	0.50
2:t:95:TYR:N	2:t:95:TYR:CD1	2.79	0.50
1:B:57:PHE:CD2	1:B:330:ARG:CB	2.95	0.50
1:C:586:THR:N	1:C:587:PRO:CD	2.75	0.50
1:E:15:PHE:HZ	1:E:283:CYS:HG	1.58	0.50
1:E:111:VAL:O	1:E:115:VAL:HG13	2.11	0.50
1:E:160:SER:HB3	1:E:171:ARG:NH2	2.27	0.50
1:E:198:ILE:O	1:E:198:ILE:HG22	2.12	0.50
1:F:160:SER:HB3	1:F:171:ARG:NH2	2.27	0.50
1:F:409:THR:O	1:F:413:LYS:HG2	2.12	0.50
1:G:251:ILE:O	1:G:507:LEU:HD13	2.11	0.50
1:H:535:ILE:HD11	1:H:554:LEU:HG	1.94	0.50
1:I:81:ARG:HB2	1:I:517:TYR:CE2	2.46	0.50
1:I:160:SER:HB3	1:I:171:ARG:NH2	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:248:LYS:HD3	1:I:251:ILE:HB	1.93	0.50
1:J:328:ARG:HB3	2:g:142:PRO:HG3	1.94	0.50
1:J:409:THR:O	1:J:413:LYS:HG2	2.12	0.50
1:L:14:ARG:HH11	1:L:17:ALA:HB2	1.76	0.50
1:L:126:TRP:CD1	1:L:146:ARG:HG3	2.46	0.50
1:L:513:ARG:HD3	1:L:513:ARG:H	1.77	0.50
2:c:52:MET:HE1	2:c:92:VAL:O	2.11	0.50
2:f:72:ASP:OD1	2:f:72:ASP:O	2.30	0.50
2:h:43:GLN:C	2:h:45:ALA:N	2.70	0.50
2:j:38:GLU:N	2:j:39:PRO:HD3	2.26	0.50
1:O:95:MSE:HE1	1:O:99:ARG:CZ	2.41	0.50
1:P:35:PHE:C	1:P:37:ARG:N	2.70	0.50
1:P:95:MSE:HE1	1:P:99:ARG:CZ	2.42	0.50
1:S:34:PHE:CE2	1:S:45:LEU:HG	2.46	0.50
1:T:27:ARG:HB2	1:T:313:LYS:HE3	1.94	0.50
1:T:443:ASP:C	1:T:444:LEU:HD13	2.36	0.50
1:U:443:ASP:C	1:U:444:LEU:HD13	2.37	0.50
1:V:89:ASP:HA	1:W:561:ASP:CB	2.37	0.50
1:X:78:VAL:HG12	1:X:79:LEU:H	1.74	0.50
2:k:80:VAL:C	2:k:82:ALA:H	2.19	0.50
2:n:62:ASP:C	2:n:64:GLU:N	2.61	0.50
2:p:67:PRO:HG2	2:r:8:ASP:CB	2.42	0.50
2:u:43:MET:C	2:u:45:ALA:H	2.19	0.50
1:A:14:ARG:HH11	1:A:17:ALA:HB2	1.76	0.50
1:A:128:LEU:HD12	1:A:446:THR:HG23	1.94	0.50
1:A:280:ILE:HG22	1:A:287:LEU:HD13	1.94	0.50
1:A:418:LEU:HB2	1:A:428:GLY:O	2.12	0.50
1:B:160:SER:HB3	1:B:171:ARG:NH2	2.27	0.50
1:B:584:PRO:HG2	1:B:593:LEU:HD12	1.94	0.50
1:B:586:THR:N	1:B:587:PRO:CD	2.75	0.50
1:C:113:ILE:HD12	1:C:148:PRO:HB3	1.94	0.50
1:C:126:TRP:CD1	1:C:146:ARG:HG3	2.46	0.50
1:D:160:SER:HB3	1:D:171:ARG:NH2	2.27	0.50
1:D:280:ILE:HG22	1:D:287:LEU:HD13	1.94	0.50
1:D:584:PRO:CG	1:D:593:LEU:HD12	2.42	0.50
1:E:248:LYS:HD3	1:E:251:ILE:HB	1.93	0.50
1:E:280:ILE:HG22	1:E:287:LEU:HD13	1.94	0.50
1:F:126:TRP:CD1	1:F:146:ARG:HG3	2.46	0.50
1:G:160:SER:HB3	1:G:171:ARG:NH2	2.27	0.50
1:G:510:ILE:O	1:G:513:ARG:HD2	2.12	0.50
1:G:513:ARG:H	1:G:513:ARG:HD3	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:584:PRO:HG2	1:G:593:LEU:HD12	1.94	0.50
1:H:119:ILE:HA	1:H:432:PHE:HE2	1.77	0.50
1:H:207:TRP:O	1:H:208:VAL:C	2.54	0.50
1:H:418:LEU:HB2	1:H:428:GLY:O	2.12	0.50
1:I:57:PHE:CD2	1:I:330:ARG:CB	2.95	0.50
1:I:584:PRO:HG2	1:I:593:LEU:HD12	1.94	0.50
1:J:15:PHE:HZ	1:J:283:CYS:HG	1.60	0.50
1:J:37:ARG:HH22	1:J:45:LEU:CD1	2.24	0.50
1:J:57:PHE:CD2	1:J:330:ARG:CB	2.95	0.50
1:J:451:ASP:O	1:J:456:ALA:N	2.41	0.50
1:K:160:SER:HB3	1:K:171:ARG:NH2	2.27	0.50
1:K:198:ILE:O	1:K:198:ILE:HG22	2.12	0.50
1:K:586:THR:N	1:K:587:PRO:CD	2.75	0.50
1:L:280:ILE:HG22	1:L:287:LEU:HD13	1.94	0.50
2:c:38:GLU:N	2:c:39:PRO:HD3	2.26	0.50
2:c:109:THR:HG21	2:e:102:PRO:HB3	1.93	0.50
2:d:70:SER:HB2	2:d:75:PRO:O	2.11	0.50
2:e:72:ASP:O	2:e:72:ASP:OD1	2.30	0.50
2:f:53:MET:O	2:f:69:PHE:CE1	2.63	0.50
2:i:38:GLU:N	2:i:39:PRO:HD3	2.26	0.50
1:M:379:GLU:O	1:M:380:ASN:CB	2.60	0.49
1:O:248:LYS:H	1:O:248:LYS:CD	2.17	0.49
1:Q:456:ALA:O	1:Q:457:MSE:HB2	2.12	0.49
1:R:329:LEU:HD22	2:o:133:PRO:HG2	1.93	0.49
1:T:9:GLU:HG3	1:T:12:LEU:H	1.76	0.49
1:U:27:ARG:HB2	1:U:313:LYS:HE3	1.94	0.49
1:U:329:LEU:HD22	2:r:133:PRO:HG2	1.92	0.49
1:V:322:LEU:HD22	1:V:322:LEU:H	1.77	0.49
1:W:58:ASP:HA	1:W:327:GLN:NE2	2.27	0.49
1:X:343:ARG:O	1:X:344:THR:HB	2.12	0.49
2:n:12:ALA:C	2:n:14:LEU:N	2.67	0.49
2:n:128:TYR:CD1	2:n:132:MET:HG2	2.47	0.49
2:q:48:TYR:CD2	2:q:48:TYR:O	2.65	0.49
1:A:535:ILE:HD11	1:A:554:LEU:HG	1.94	0.49
1:B:44:TRP:CE2	1:B:54:ARG:HB3	2.48	0.49
1:C:14:ARG:HH11	1:C:17:ALA:HB2	1.76	0.49
1:D:334:MSE:SE	1:F:404:MSE:HE1	2.61	0.49
1:F:81:ARG:HB2	1:F:517:TYR:CE2	2.46	0.49
1:H:160:SER:HB3	1:H:171:ARG:NH2	2.27	0.49
1:H:409:THR:O	1:H:413:LYS:HG2	2.12	0.49
1:H:584:PRO:HG2	1:H:593:LEU:HD12	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:111:VAL:O	1:K:115:VAL:HG13	2.11	0.49
1:L:128:LEU:HD12	1:L:446:THR:HG23	1.94	0.49
1:L:255:ILE:O	1:L:257:ASP:N	2.45	0.49
1:L:584:PRO:HG2	1:L:593:LEU:HD12	1.94	0.49
2:a:72:ASP:OD1	2:a:72:ASP:O	2.30	0.49
2:b:38:GLU:N	2:b:39:PRO:HD3	2.27	0.49
2:b:72:ASP:O	2:b:72:ASP:OD1	2.30	0.49
1:M:164:LEU:HA	1:M:307:TRP:HH2	1.77	0.49
1:M:573:ASN:O	1:M:577:ILE:HG13	2.12	0.49
1:N:82:PRO:CD	1:V:560:LEU:HD13	2.27	0.49
1:N:405:LEU:O	1:N:409:THR:HG23	2.11	0.49
1:P:95:MSE:HE1	1:P:99:ARG:NH2	2.26	0.49
1:P:451:ASP:C	1:P:453:LEU:H	2.18	0.49
1:Q:387:GLN:CB	1:R:390:ALA:CB	2.90	0.49
1:R:35:PHE:C	1:R:37:ARG:N	2.70	0.49
1:T:40:GLN:HG2	1:W:310:VAL:HG22	1.93	0.49
1:T:359:PHE:HD1	2:v:120:ILE:HD11	1.76	0.49
1:U:35:PHE:C	1:U:37:ARG:N	2.69	0.49
1:U:46:SER:N	1:U:48:TYR:HE2	1.99	0.49
1:V:434:THR:HA	1:V:437:GLN:HG2	1.93	0.49
1:W:586:THR:N	1:W:587:PRO:CD	2.75	0.49
1:X:360:GLU:HG3	2:q:122:ARG:HB3	1.93	0.49
1:A:44:TRP:CE2	1:A:54:ARG:HB3	2.48	0.49
1:A:586:THR:N	1:A:587:PRO:CD	2.75	0.49
1:B:444:LEU:C	1:B:446:THR:H	2.19	0.49
1:C:128:LEU:HD12	1:C:446:THR:HG23	1.94	0.49
1:C:246:TYR:HE2	1:C:512:GLY:N	2.10	0.49
1:C:584:PRO:CG	1:C:593:LEU:HD12	2.42	0.49
1:D:584:PRO:HG2	1:D:593:LEU:HD12	1.94	0.49
1:E:80:TYR:CE1	1:E:444:LEU:HB3	2.48	0.49
1:E:584:PRO:HG2	1:E:593:LEU:HD12	1.94	0.49
1:F:119:ILE:HA	1:F:432:PHE:HE2	1.78	0.49
1:G:182:ASN:HD22	1:H:171:ARG:HH21	1.58	0.49
1:H:280:ILE:HG22	1:H:287:LEU:HD13	1.94	0.49
1:H:578:GLN:HG2	1:H:596:ALA:HB2	1.94	0.49
1:I:136:SER:N	1:I:137:PRO:HD3	2.27	0.49
1:I:255:ILE:O	1:I:257:ASP:N	2.45	0.49
1:I:280:ILE:HG22	1:I:287:LEU:HD13	1.94	0.49
1:I:510:ILE:O	1:I:513:ARG:HD2	2.12	0.49
1:J:160:SER:HB3	1:J:171:ARG:NH2	2.27	0.49
1:J:248:LYS:HD3	1:J:251:ILE:HB	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:429:GLN:HG2	1:J:429:GLN:O	2.10	0.49
1:J:510:ILE:O	1:J:513:ARG:HD2	2.12	0.49
1:J:584:PRO:CG	1:J:593:LEU:HD12	2.42	0.49
1:K:128:LEU:HD12	1:K:446:THR:HG23	1.94	0.49
1:L:418:LEU:HB2	1:L:428:GLY:O	2.12	0.49
1:L:584:PRO:CG	1:L:593:LEU:HD12	2.42	0.49
2:Y:28:VAL:HG21	2:Y:96:LEU:CG	2.40	0.49
2:Y:38:GLU:N	2:Y:39:PRO:HD3	2.26	0.49
2:Y:104:TYR:HB2	2:Y:106:LEU:HD12	1.93	0.49
2:i:104:TYR:HB2	2:i:106:LEU:HD12	1.93	0.49
1:O:54:ARG:HB2	2:l:137:GLY:HA3	1.94	0.49
1:P:37:ARG:C	1:P:39:SER:H	2.20	0.49
1:Q:93:VAL:CG1	1:Q:458:ARG:HG3	2.38	0.49
1:Q:451:ASP:C	1:Q:453:LEU:N	2.70	0.49
1:R:332:MSE:SE	2:o:132:MET:HA	2.62	0.49
1:S:78:VAL:CG1	1:S:79:LEU:N	2.74	0.49
1:V:245:SER:HG	1:V:247:PHE:HE1	1.59	0.49
1:X:58:ASP:HA	1:X:327:GLN:NE2	2.27	0.49
1:X:95:MSE:HE1	1:X:99:ARG:CZ	2.42	0.49
1:X:235:TYR:HA	1:X:265:LYS:HB3	1.94	0.49
2:n:43:MET:C	2:n:45:ALA:H	2.20	0.49
1:A:255:ILE:O	1:A:257:ASP:N	2.45	0.49
1:A:409:THR:O	1:A:413:LYS:HG2	2.12	0.49
1:A:456:ALA:HB1	1:A:509:ASP:OD2	2.13	0.49
1:B:126:TRP:CD1	1:B:146:ARG:HG3	2.46	0.49
1:B:584:PRO:CG	1:B:593:LEU:HD12	2.42	0.49
1:C:328:ARG:HB3	2:Z:142:PRO:HG3	1.94	0.49
1:C:456:ALA:HB1	1:C:509:ASP:OD2	2.13	0.49
1:D:119:ILE:HA	1:D:432:PHE:HE2	1.78	0.49
1:G:119:ILE:HA	1:G:432:PHE:HE2	1.77	0.49
1:G:280:ILE:HG22	1:G:287:LEU:HD13	1.94	0.49
1:G:427:GLY:C	1:G:429:GLN:N	2.70	0.49
1:G:584:PRO:CG	1:G:593:LEU:HD12	2.42	0.49
1:H:584:PRO:CG	1:H:593:LEU:HD12	2.42	0.49
1:H:586:THR:N	1:H:587:PRO:CD	2.75	0.49
1:J:535:ILE:HD11	1:J:554:LEU:HG	1.94	0.49
1:K:37:ARG:HH22	1:K:45:LEU:CD1	2.24	0.49
1:K:535:ILE:HD11	1:K:554:LEU:HG	1.94	0.49
1:L:160:SER:HB3	1:L:171:ARG:NH2	2.27	0.49
1:L:328:ARG:HB3	2:h:142:PRO:HG3	1.94	0.49
1:L:359:PHE:HD1	2:Z:129:ILE:HD11	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:386:THR:O	1:L:387:GLN:O	2.31	0.49
2:b:70:SER:HB2	2:b:75:PRO:O	2.12	0.49
2:f:43:GLN:C	2:f:45:ALA:N	2.70	0.49
2:i:23:LEU:HD23	2:i:26:LEU:HD11	1.95	0.49
2:j:72:ASP:O	2:j:72:ASP:OD1	2.30	0.49
1:M:46:SER:N	1:M:48:TYR:HE2	1.98	0.49
1:M:80:TYR:CE1	1:M:448:VAL:HG22	2.48	0.49
1:M:266:ILE:HG23	1:M:267:ALA:N	2.27	0.49
1:M:329:LEU:HD22	2:k:133:PRO:HG2	1.95	0.49
1:O:35:PHE:C	1:O:37:ARG:N	2.70	0.49
1:O:95:MSE:HB3	1:O:527:MSE:HE1	1.93	0.49
1:O:384:LEU:HD22	1:O:384:LEU:N	2.27	0.49
1:O:586:THR:N	1:O:587:PRO:CD	2.75	0.49
1:P:235:TYR:HA	1:P:265:LYS:HB3	1.95	0.49
1:P:266:ILE:HG23	1:P:267:ALA:N	2.27	0.49
1:Q:343:ARG:HD3	2:o:128:TYR:CE1	2.48	0.49
1:Q:379:GLU:O	1:Q:380:ASN:CB	2.60	0.49
1:Q:409:THR:O	1:Q:413:LYS:HG2	2.12	0.49
1:S:434:THR:HG23	1:S:435:VAL:N	2.26	0.49
1:T:451:ASP:C	1:T:453:LEU:N	2.69	0.49
1:U:123:VAL:CG1	1:U:304:PHE:CE1	2.95	0.49
1:V:95:MSE:HE1	1:V:99:ARG:CZ	2.42	0.49
1:V:434:THR:O	1:V:437:GLN:HG2	2.11	0.49
1:V:586:THR:N	1:V:587:PRO:CD	2.76	0.49
1:X:95:MSE:HE1	1:X:99:ARG:NH2	2.28	0.49
2:k:96:ALA:HB2	2:m:25:LEU:HD13	1.94	0.49
2:o:48:TYR:O	2:o:48:TYR:CD2	2.64	0.49
1:A:560:LEU:O	1:A:565:VAL:HG21	2.11	0.49
1:B:119:ILE:HA	1:B:432:PHE:HE2	1.77	0.49
1:B:280:ILE:HG22	1:B:287:LEU:HD13	1.94	0.49
1:C:34:PHE:CE1	1:C:324:LYS:NZ	2.72	0.49
1:C:34:PHE:O	1:C:34:PHE:CG	2.66	0.49
1:D:386:THR:O	1:D:387:GLN:O	2.31	0.49
1:D:456:ALA:HB1	1:D:509:ASP:OD2	2.13	0.49
1:E:101:ASP:HB3	1:E:138:THR:HG21	1.93	0.49
1:E:136:SER:N	1:E:137:PRO:HD3	2.27	0.49
1:E:451:ASP:O	1:E:456:ALA:N	2.41	0.49
1:F:456:ALA:HB1	1:F:509:ASP:OD2	2.13	0.49
1:G:47:GLN:HG3	1:G:54:ARG:NH1	2.28	0.49
1:G:101:ASP:HB3	1:G:138:THR:HG21	1.93	0.49
1:G:456:ALA:HB1	1:G:509:ASP:OD2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:535:ILE:HD11	1:G:554:LEU:HG	1.94	0.49
1:H:128:LEU:HD12	1:H:446:THR:HG23	1.94	0.49
1:H:198:ILE:O	1:H:198:ILE:HG22	2.12	0.49
1:H:246:TYR:HE2	1:H:512:GLY:N	2.10	0.49
1:H:513:ARG:H	1:H:513:ARG:HD3	1.77	0.49
1:I:34:PHE:HZ	1:I:328:ARG:HH22	0.80	0.49
1:I:34:PHE:HE1	1:I:324:LYS:HZ2	1.52	0.49
1:I:191:TYR:HE1	1:I:278:LYS:HZ3	1.58	0.49
1:I:246:TYR:HE2	1:I:512:GLY:N	2.10	0.49
1:J:113:ILE:HD12	1:J:148:PRO:HB3	1.94	0.49
1:J:280:ILE:HG22	1:J:287:LEU:HD13	1.94	0.49
1:J:456:ALA:HB1	1:J:509:ASP:OD2	2.13	0.49
1:J:578:GLN:HG2	1:J:596:ALA:HB2	1.94	0.49
1:J:584:PRO:HG2	1:J:593:LEU:HD12	1.94	0.49
1:K:44:TRP:CE2	1:K:54:ARG:HB3	2.47	0.49
1:K:136:SER:N	1:K:137:PRO:HD3	2.27	0.49
1:K:280:ILE:HG22	1:K:287:LEU:HD13	1.95	0.49
1:K:386:THR:O	1:K:387:GLN:O	2.31	0.49
1:K:456:ALA:HB1	1:K:509:ASP:OD2	2.13	0.49
1:L:44:TRP:CE2	1:L:54:ARG:HB3	2.48	0.49
1:L:63:VAL:HG21	1:L:416:ALA:HB1	1.93	0.49
1:L:119:ILE:HA	1:L:432:PHE:HE2	1.77	0.49
2:b:37:VAL:C	2:b:39:PRO:HD3	2.38	0.49
2:c:72:ASP:OD1	2:c:72:ASP:O	2.30	0.49
2:f:37:VAL:C	2:f:39:PRO:HD3	2.38	0.49
2:g:37:VAL:C	2:g:39:PRO:HD3	2.38	0.49
2:h:104:TYR:HB2	2:h:106:LEU:HD12	1.93	0.49
1:M:390:ALA:HB2	1:N:387:GLN:HB2	1.95	0.49
1:N:328:ARG:HB3	2:v:133:PRO:HG3	1.94	0.49
1:N:451:ASP:C	1:N:453:LEU:H	2.19	0.49
1:O:379:GLU:O	1:O:380:ASN:CB	2.60	0.49
1:P:456:ALA:O	1:P:457:MSE:HB2	2.11	0.49
1:P:586:THR:N	1:P:587:PRO:CD	2.76	0.49
1:Q:235:TYR:HA	1:Q:265:LYS:HB3	1.94	0.49
1:Q:586:THR:N	1:Q:587:PRO:CD	2.76	0.49
1:S:360:GLU:HG3	2:s:122:ARG:HB3	1.93	0.49
1:S:407:ALA:HB1	1:U:334:MSE:HE1	1.94	0.49
1:S:586:THR:N	1:S:587:PRO:CD	2.76	0.49
1:W:101:ASP:HB2	1:W:144:ILE:O	2.11	0.49
2:p:48:TYR:CD2	2:p:48:TYR:O	2.65	0.49
2:q:12:ALA:C	2:q:14:LEU:N	2.69	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:r:48:TYR:O	2:r:48:TYR:HD2	1.95	0.49
2:t:16:LYS:HA	2:t:16:LYS:HZ2	1.78	0.49
2:t:48:TYR:CD2	2:t:48:TYR:O	2.66	0.49
2:u:95:TYR:N	2:u:95:TYR:CD1	2.77	0.49
1:A:113:ILE:HD12	1:A:148:PRO:HB3	1.94	0.49
1:A:198:ILE:HG22	1:A:198:ILE:O	2.12	0.49
1:B:34:PHE:O	1:B:34:PHE:CG	2.66	0.49
1:B:418:LEU:HB2	1:B:428:GLY:O	2.12	0.49
1:C:160:SER:HB3	1:C:171:ARG:NH2	2.27	0.49
1:C:198:ILE:O	1:C:198:ILE:HG22	2.12	0.49
1:D:255:ILE:O	1:D:257:ASP:N	2.45	0.49
1:D:348:LYS:HB2	1:E:372:TYR:CE2	2.47	0.49
1:F:37:ARG:HH22	1:F:45:LEU:CD1	2.24	0.49
1:F:513:ARG:HD3	1:F:513:ARG:H	1.76	0.49
1:F:535:ILE:HD11	1:F:554:LEU:HG	1.94	0.49
1:H:343:ARG:NH1	2:f:135:ALA:O	2.35	0.49
1:I:251:ILE:O	1:I:507:LEU:HD13	2.11	0.49
1:J:44:TRP:CE2	1:J:54:ARG:HB3	2.47	0.49
1:J:255:ILE:O	1:J:257:ASP:N	2.45	0.49
1:J:334:MSE:HE3	1:K:404:MSE:HE3	1.94	0.49
1:J:418:LEU:HB2	1:J:428:GLY:O	2.12	0.49
2:a:37:VAL:C	2:a:39:PRO:HD3	2.38	0.49
2:e:23:LEU:HD23	2:e:26:LEU:HD11	1.94	0.49
2:h:70:SER:HB2	2:h:75:PRO:O	2.11	0.49
2:i:37:VAL:C	2:i:39:PRO:HD3	2.38	0.49
2:i:72:ASP:OD1	2:i:72:ASP:O	2.30	0.49
1:M:95:MSE:HE1	1:M:99:ARG:NH2	2.28	0.49
1:N:37:ARG:C	1:N:39:SER:H	2.19	0.49
1:O:34:PHE:CE2	1:O:45:LEU:HG	2.45	0.49
1:O:372:TYR:CE2	1:P:348:LYS:HB2	2.47	0.49
1:O:405:LEU:O	1:O:409:THR:HG23	2.12	0.49
1:P:418:LEU:HB2	1:P:428:GLY:O	2.13	0.49
1:Q:95:MSE:HB3	1:Q:527:MSE:HE1	1.93	0.49
1:R:165:MSE:HG3	1:R:307:TRP:CD2	2.47	0.49
1:U:454:ALA:O	1:U:455:THR:C	2.54	0.49
1:V:78:VAL:CG1	1:V:79:LEU:N	2.73	0.49
1:X:33:LEU:HD12	1:X:34:PHE:N	2.28	0.49
2:n:48:TYR:HD2	2:n:48:TYR:O	1.96	0.49
2:n:95:TYR:CD1	2:n:95:TYR:N	2.79	0.49
2:p:12:ALA:C	2:p:14:LEU:N	2.67	0.49
2:r:110:GLY:O	2:r:114:LEU:HD13	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:t:43:MET:C	2:t:45:ALA:H	2.21	0.49
1:A:444:LEU:C	1:A:446:THR:H	2.19	0.49
1:A:584:PRO:CG	1:A:593:LEU:HD12	2.42	0.49
1:B:136:SER:N	1:B:137:PRO:HD3	2.27	0.49
1:B:236:GLN:CB	1:B:265:LYS:HG2	2.37	0.49
1:B:255:ILE:O	1:B:257:ASP:N	2.45	0.49
1:B:535:ILE:HD11	1:B:554:LEU:HG	1.94	0.49
1:C:44:TRP:CE2	1:C:54:ARG:HB3	2.47	0.49
1:C:560:LEU:O	1:C:565:VAL:HG21	2.11	0.49
1:D:398:PRO:HB3	1:E:395:PRO:HD2	1.93	0.49
1:D:578:GLN:HG2	1:D:596:ALA:HB2	1.94	0.49
1:E:35:PHE:C	1:E:37:ARG:N	2.62	0.49
1:E:44:TRP:CE2	1:E:54:ARG:HB3	2.47	0.49
1:E:255:ILE:O	1:E:257:ASP:N	2.45	0.49
1:E:386:THR:O	1:E:387:GLN:O	2.31	0.49
1:E:528:LYS:HZ3	1:E:560:LEU:HD21	1.77	0.49
1:F:34:PHE:O	1:F:34:PHE:CG	2.65	0.49
1:G:113:ILE:HD12	1:G:148:PRO:HB3	1.94	0.49
1:I:37:ARG:HH21	1:I:37:ARG:CB	2.16	0.49
1:I:47:GLN:HG3	1:I:54:ARG:NH1	2.28	0.49
1:I:119:ILE:HA	1:I:432:PHE:HE2	1.77	0.49
1:I:226:VAL:O	1:I:274:ARG:HA	2.13	0.49
1:L:47:GLN:HG3	1:L:54:ARG:NH1	2.28	0.49
1:L:80:TYR:CE1	1:L:444:LEU:HB3	2.48	0.49
2:Z:37:VAL:C	2:Z:39:PRO:HD3	2.38	0.49
2:d:104:TYR:HB2	2:d:106:LEU:HD12	1.93	0.49
2:e:37:VAL:C	2:e:39:PRO:HD3	2.38	0.49
2:i:43:GLN:C	2:i:45:ALA:N	2.70	0.49
2:j:104:TYR:HB2	2:j:106:LEU:HD12	1.93	0.49
1:N:95:MSE:HE1	1:N:99:ARG:NH2	2.27	0.49
1:N:454:ALA:O	1:N:455:THR:C	2.54	0.49
1:O:27:ARG:HB2	1:O:313:LYS:HE3	1.94	0.49
1:O:95:MSE:HE1	1:O:99:ARG:NH2	2.28	0.49
1:O:418:LEU:HB2	1:O:428:GLY:O	2.13	0.49
1:P:248:LYS:HG3	1:P:511:ARG:HE	1.77	0.49
1:P:359:PHE:HD1	2:p:120:ILE:HD11	1.78	0.49
1:P:379:GLU:O	1:P:380:ASN:CB	2.60	0.49
1:Q:123:VAL:HG22	1:Q:316:TYR:CE2	2.48	0.49
1:R:379:GLU:O	1:R:380:ASN:CB	2.61	0.49
1:R:586:THR:N	1:R:587:PRO:CD	2.76	0.49
1:S:92:ASP:HB3	1:U:561:ASP:OD2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:430:VAL:HG11	3:U:719:HOH:O	2.10	0.49
1:S:454:ALA:O	1:S:455:THR:C	2.54	0.49
1:T:35:PHE:C	1:T:37:ARG:N	2.70	0.49
1:T:328:ARG:HB3	2:t:133:PRO:HG3	1.93	0.49
1:T:351:PHE:CD2	1:T:356:ILE:HD12	2.47	0.49
1:U:248:LYS:HG3	1:U:511:ARG:HE	1.78	0.49
1:V:235:TYR:HA	1:V:265:LYS:HB3	1.93	0.49
1:X:14:ARG:NE	1:X:14:ARG:CA	2.71	0.49
1:X:35:PHE:C	1:X:37:ARG:N	2.70	0.49
1:X:443:ASP:C	1:X:446:THR:HG22	2.36	0.49
2:r:43:MET:C	2:r:45:ALA:H	2.21	0.49
1:B:510:ILE:O	1:B:513:ARG:HD2	2.12	0.49
1:C:94:LEU:HA	1:C:97:MSE:CE	2.37	0.49
1:E:34:PHE:O	1:E:34:PHE:CG	2.66	0.49
1:E:128:LEU:HD12	1:E:446:THR:HG23	1.94	0.49
1:E:456:ALA:HB1	1:E:509:ASP:OD2	2.13	0.49
1:G:80:TYR:CE1	1:G:444:LEU:HB3	2.48	0.49
1:G:226:VAL:O	1:G:274:ARG:HA	2.13	0.49
1:H:255:ILE:O	1:H:257:ASP:N	2.45	0.49
1:I:44:TRP:CE2	1:I:54:ARG:HB3	2.48	0.49
1:I:578:GLN:HG2	1:I:596:ALA:HB2	1.94	0.49
1:J:198:ILE:O	1:J:198:ILE:HG22	2.12	0.49
1:J:444:LEU:C	1:J:446:THR:H	2.19	0.49
1:K:561:ASP:HB2	1:L:89:ASP:CA	2.32	0.49
1:L:510:ILE:O	1:L:513:ARG:HD2	2.12	0.49
2:Z:23:LEU:HD23	2:Z:26:LEU:HD11	1.94	0.49
2:b:104:TYR:HB2	2:b:106:LEU:HD12	1.93	0.49
2:c:104:TYR:HB2	2:c:106:LEU:HD12	1.94	0.49
2:d:37:VAL:C	2:d:39:PRO:HD3	2.38	0.49
2:j:23:LEU:HD23	2:j:26:LEU:HD11	1.95	0.49
1:M:171:ARG:O	1:M:224:GLU:HA	2.13	0.49
1:O:535:ILE:HD13	1:O:554:LEU:HG	1.95	0.49
1:P:37:ARG:HH21	1:P:37:ARG:CB	2.26	0.49
3:R:719:HOH:O	1:X:430:VAL:HG11	2.13	0.49
1:U:9:GLU:HG3	1:U:12:LEU:H	1.78	0.49
1:V:55:GLY:HA3	1:V:57:PHE:CE1	2.48	0.49
1:V:535:ILE:HD13	1:V:554:LEU:HG	1.94	0.49
1:V:598:GLN:HB2	1:V:601:GLN:HB3	1.94	0.49
1:W:9:GLU:HG3	1:W:12:LEU:H	1.78	0.49
2:k:48:TYR:HD2	2:k:48:TYR:O	1.95	0.49
2:k:110:GLY:O	2:k:114:LEU:HD13	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:427:GLY:C	1:B:429:GLN:N	2.70	0.49
1:C:15:PHE:CE2	1:C:19:TRP:NE1	2.81	0.49
1:C:577:ILE:HG12	1:C:582:LYS:CG	2.41	0.49
1:D:113:ILE:HD12	1:D:148:PRO:HB3	1.94	0.49
1:E:246:TYR:HE2	1:E:512:GLY:N	2.10	0.49
1:F:80:TYR:CE1	1:F:444:LEU:HB3	2.48	0.49
1:F:386:THR:O	1:F:387:GLN:O	2.31	0.49
1:G:136:SER:N	1:G:137:PRO:HD3	2.27	0.49
1:G:444:LEU:C	1:G:446:THR:H	2.19	0.49
1:G:577:ILE:HG12	1:G:582:LYS:CG	2.41	0.49
1:H:47:GLN:HG3	1:H:54:ARG:NH1	2.28	0.49
3:H:719:HOH:O	1:I:438:LEU:HD22	2.12	0.49
1:I:80:TYR:CE1	1:I:444:LEU:HB3	2.48	0.49
1:I:386:THR:O	1:I:387:GLN:O	2.31	0.49
1:I:409:THR:O	1:I:413:LYS:HG2	2.12	0.49
1:J:80:TYR:CE1	1:J:444:LEU:HB3	2.47	0.49
1:K:119:ILE:HA	1:K:432:PHE:HE2	1.78	0.49
1:K:584:PRO:CG	1:K:593:LEU:HD12	2.42	0.49
1:L:226:VAL:O	1:L:274:ARG:HA	2.13	0.49
2:g:23:LEU:HD23	2:g:26:LEU:HD11	1.95	0.49
1:M:554:LEU:HD21	1:N:564:GLY:CA	2.38	0.49
1:N:451:ASP:C	1:N:453:LEU:N	2.71	0.49
1:P:454:ALA:O	1:P:455:THR:C	2.56	0.49
1:Q:27:ARG:HB2	1:Q:313:LYS:HE3	1.94	0.49
1:S:405:LEU:O	1:S:409:THR:HG23	2.12	0.49
1:T:329:LEU:HD22	2:t:133:PRO:HG2	1.94	0.49
1:T:586:THR:N	1:T:587:PRO:CD	2.75	0.49
1:U:451:ASP:C	1:U:453:LEU:N	2.70	0.49
1:W:71:MSE:HE2	1:W:119:ILE:HD11	1.94	0.49
1:X:266:ILE:HG23	1:X:267:ALA:N	2.26	0.49
1:X:383:ASP:C	1:X:385:PRO:HD3	2.38	0.49
1:X:454:ALA:O	1:X:455:THR:C	2.56	0.49
2:k:48:TYR:O	2:k:48:TYR:CD2	2.66	0.49
2:m:65:ASN:O	2:m:67:PRO:HD3	2.13	0.49
2:t:65:ASN:O	2:t:67:PRO:HD3	2.12	0.49
2:u:67:PRO:HG2	2:v:8:ASP:CB	2.42	0.49
1:B:80:TYR:CE1	1:B:444:LEU:HB3	2.48	0.49
1:B:386:THR:O	1:B:387:GLN:O	2.31	0.49
1:B:456:ALA:HB1	1:B:509:ASP:OD2	2.13	0.49
1:C:15:PHE:HZ	1:C:283:CYS:SG	2.31	0.49
1:C:47:GLN:HG3	1:C:54:ARG:NH1	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:510:ILE:O	1:C:513:ARG:HD2	2.12	0.49
1:C:578:GLN:HG2	1:C:596:ALA:HB2	1.94	0.49
1:E:15:PHE:CE2	1:E:19:TRP:NE1	2.81	0.49
1:F:280:ILE:HG22	1:F:287:LEU:HD13	1.94	0.49
1:F:383:ASP:C	1:F:385:PRO:CD	2.86	0.49
1:F:510:ILE:O	1:F:513:ARG:HD2	2.12	0.49
1:F:578:GLN:HG2	1:F:596:ALA:HB2	1.94	0.49
1:G:246:TYR:HE2	1:G:512:GLY:N	2.10	0.49
1:H:80:TYR:CE1	1:H:444:LEU:HB3	2.47	0.49
1:H:113:ILE:HD12	1:H:148:PRO:HB3	1.94	0.49
1:H:386:THR:O	1:H:387:GLN:O	2.31	0.49
1:H:443:ASP:C	1:H:446:THR:HG22	2.38	0.49
1:I:34:PHE:CG	1:I:34:PHE:O	2.66	0.49
1:J:47:GLN:HG3	1:J:54:ARG:NH1	2.28	0.49
1:J:513:ARG:H	1:J:513:ARG:HD3	1.77	0.49
1:K:80:TYR:CE1	1:K:444:LEU:HB3	2.48	0.49
1:K:248:LYS:HD3	1:K:251:ILE:HB	1.93	0.49
1:K:334:MSE:SE	1:L:404:MSE:HE1	2.62	0.49
1:L:198:ILE:O	1:L:198:ILE:HG22	2.12	0.49
1:L:578:GLN:HG2	1:L:596:ALA:HB2	1.94	0.49
2:f:23:LEU:HD23	2:f:26:LEU:HD11	1.95	0.49
2:g:70:SER:HB2	2:g:75:PRO:O	2.11	0.49
2:j:43:GLN:C	2:j:45:ALA:N	2.70	0.49
1:M:78:VAL:CG1	1:M:79:LEU:N	2.75	0.49
1:N:14:ARG:NE	1:N:14:ARG:CA	2.70	0.49
1:N:235:TYR:OH	1:N:252:LYS:NZ	2.45	0.49
1:O:55:GLY:HA3	1:O:57:PHE:CE1	2.48	0.49
1:P:451:ASP:C	1:P:453:LEU:N	2.71	0.49
1:P:535:ILE:HD13	1:P:554:LEU:HG	1.95	0.49
1:Q:35:PHE:C	1:Q:37:ARG:N	2.71	0.49
1:Q:95:MSE:HE1	1:Q:99:ARG:NH2	2.28	0.49
1:Q:383:ASP:C	1:Q:385:PRO:HD3	2.38	0.49
1:R:78:VAL:CG1	1:R:444:LEU:HG	2.43	0.49
1:R:164:LEU:HA	1:R:307:TRP:HH2	1.78	0.49
1:R:387:GLN:HB2	1:X:390:ALA:HB2	1.94	0.49
1:S:413:LYS:HA	1:S:416:ALA:HB3	1.94	0.49
1:S:535:ILE:HD13	1:S:554:LEU:HG	1.95	0.49
1:V:31:ASN:O	1:V:34:PHE:HB3	2.12	0.49
1:V:456:ALA:O	1:V:457:MSE:HB2	2.13	0.49
2:p:64:GLU:OE1	2:p:64:GLU:HA	2.13	0.49
2:v:65:ASN:O	2:v:67:PRO:HD3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:v:131:ARG:O	2:v:132:MET:HB3	2.12	0.49
1:B:14:ARG:NE	1:B:14:ARG:CA	2.67	0.49
1:D:47:GLN:HG3	1:D:54:ARG:NH1	2.28	0.49
1:E:510:ILE:O	1:E:513:ARG:HD2	2.12	0.49
1:F:136:SER:N	1:F:137:PRO:HD3	2.27	0.49
1:G:255:ILE:O	1:G:257:ASP:N	2.45	0.49
1:G:383:ASP:C	1:G:385:PRO:CD	2.86	0.49
1:H:136:SER:N	1:H:137:PRO:HD3	2.27	0.49
1:H:427:GLY:C	1:H:429:GLN:N	2.70	0.49
1:H:456:ALA:HB1	1:H:509:ASP:OD2	2.13	0.49
1:K:255:ILE:O	1:K:257:ASP:N	2.45	0.49
1:K:332:MSE:SE	2:i:141:MET:HA	2.63	0.49
2:e:104:TYR:HB2	2:e:106:LEU:HD12	1.93	0.49
2:g:72:ASP:OD1	2:g:72:ASP:O	2.30	0.49
2:h:72:ASP:O	2:h:72:ASP:OD1	2.30	0.49
2:i:70:SER:HB2	2:i:75:PRO:O	2.11	0.49
1:M:31:ASN:O	1:M:34:PHE:HB3	2.12	0.48
1:M:235:TYR:OH	1:M:252:LYS:NZ	2.45	0.48
1:N:384:LEU:HD22	1:N:384:LEU:N	2.28	0.48
1:P:434:THR:O	1:P:437:GLN:HG2	2.12	0.48
1:Q:235:TYR:OH	1:Q:252:LYS:NZ	2.46	0.48
1:S:35:PHE:C	1:S:37:ARG:N	2.71	0.48
1:S:598:GLN:HB2	1:S:601:GLN:HB3	1.95	0.48
1:T:598:GLN:HB2	1:T:601:GLN:HB3	1.95	0.48
1:V:379:GLU:O	1:V:380:ASN:CB	2.61	0.48
1:V:573:ASN:O	1:V:577:ILE:HG13	2.13	0.48
1:W:95:MSE:HE1	1:W:99:ARG:CZ	2.43	0.48
1:W:598:GLN:HB2	1:W:601:GLN:HB3	1.95	0.48
1:X:293:ILE:HD13	1:X:294:ALA:N	2.28	0.48
1:X:456:ALA:O	1:X:457:MSE:HB2	2.12	0.48
1:X:586:THR:N	1:X:587:PRO:CD	2.76	0.48
2:p:30:PRO:HD2	2:p:32:SER:HB3	1.95	0.48
2:p:80:VAL:C	2:p:82:ALA:H	2.20	0.48
2:t:48:TYR:O	2:t:48:TYR:HD2	1.95	0.48
1:A:34:PHE:O	1:A:34:PHE:CG	2.66	0.48
1:A:578:GLN:HG2	1:A:596:ALA:HB2	1.94	0.48
1:C:80:TYR:CE1	1:C:444:LEU:HB3	2.48	0.48
1:C:226:VAL:O	1:C:274:ARG:HA	2.13	0.48
1:C:329:LEU:HD22	2:Z:142:PRO:HG2	1.94	0.48
1:D:359:PHE:HD1	2:d:129:ILE:HD11	1.78	0.48
1:E:47:GLN:HG3	1:E:54:ARG:NH1	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:443:ASP:C	1:E:446:THR:HG22	2.38	0.48
1:F:44:TRP:CE2	1:F:54:ARG:HB3	2.47	0.48
1:F:236:GLN:HE21	1:F:265:LYS:HZ3	1.61	0.48
1:G:15:PHE:CE2	1:G:19:TRP:NE1	2.81	0.48
1:G:57:PHE:CD2	1:G:330:ARG:CB	2.95	0.48
1:G:142:GLN:O	1:G:143:VAL:HG23	2.13	0.48
1:G:248:LYS:HD3	1:G:251:ILE:HB	1.93	0.48
1:G:443:ASP:C	1:G:446:THR:HG22	2.38	0.48
1:I:15:PHE:CE2	1:I:19:TRP:NE1	2.81	0.48
1:I:443:ASP:C	1:I:446:THR:HG22	2.38	0.48
1:I:456:ALA:HB1	1:I:509:ASP:OD2	2.13	0.48
1:I:584:PRO:CG	1:I:593:LEU:HD12	2.42	0.48
1:J:383:ASP:C	1:J:385:PRO:CD	2.86	0.48
1:K:226:VAL:O	1:K:274:ARG:HA	2.13	0.48
1:L:15:PHE:CE2	1:L:19:TRP:NE1	2.81	0.48
1:M:9:GLU:HG3	1:M:12:LEU:H	1.77	0.48
1:M:212:LEU:HD22	1:O:26:ARG:HG2	1.95	0.48
1:N:95:MSE:HE1	1:N:99:ARG:CZ	2.44	0.48
1:N:429:GLN:O	1:N:429:GLN:HG2	2.13	0.48
1:O:325:ASP:O	1:O:329:LEU:HD23	2.12	0.48
1:R:26:ARG:O	1:R:27:ARG:C	2.56	0.48
1:R:359:PHE:HD1	2:q:120:ILE:HD11	1.77	0.48
1:R:387:GLN:CB	1:X:390:ALA:CB	2.91	0.48
1:S:235:TYR:OH	1:S:252:LYS:NZ	2.47	0.48
1:S:398:PRO:HB3	1:U:395:PRO:HD2	1.95	0.48
1:T:561:ASP:CB	1:W:89:ASP:HA	2.38	0.48
1:U:322:LEU:HD22	1:U:322:LEU:N	2.29	0.48
1:U:378:ASP:O	1:U:381:SER:O	2.31	0.48
1:U:560:LEU:O	1:U:561:ASP:O	2.32	0.48
1:U:586:THR:N	1:U:587:PRO:CD	2.76	0.48
1:V:293:ILE:HD13	1:V:294:ALA:N	2.27	0.48
1:W:405:LEU:O	1:W:409:THR:HG23	2.13	0.48
1:X:164:LEU:HA	1:X:307:TRP:CH2	2.48	0.48
2:l:33:MET:HB3	2:l:33:MET:HE3	1.66	0.48
2:n:80:VAL:C	2:n:82:ALA:H	2.20	0.48
2:o:64:GLU:HA	2:o:64:GLU:OE1	2.14	0.48
2:p:128:TYR:CD1	2:p:132:MET:HG2	2.49	0.48
2:s:67:PRO:HG2	2:u:8:ASP:CB	2.43	0.48
1:A:15:PHE:CE2	1:A:19:TRP:NE1	2.81	0.48
1:B:198:ILE:O	1:B:198:ILE:HG22	2.12	0.48
1:C:11:ILE:O	1:C:15:PHE:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:444:LEU:C	1:C:446:THR:H	2.19	0.48
1:D:198:ILE:O	1:D:198:ILE:HG22	2.12	0.48
1:E:11:ILE:O	1:E:15:PHE:HB2	2.13	0.48
1:E:584:PRO:CG	1:E:593:LEU:HD12	2.42	0.48
1:F:255:ILE:O	1:F:257:ASP:N	2.45	0.48
1:F:376:ARG:HB2	1:G:352:TRP:CG	2.48	0.48
1:F:427:GLY:C	1:F:429:GLN:N	2.70	0.48
1:G:34:PHE:O	1:G:34:PHE:CG	2.66	0.48
1:H:44:TRP:CE2	1:H:54:ARG:HB3	2.47	0.48
1:H:248:LYS:HZ1	1:H:513:ARG:HH12	1.62	0.48
1:H:383:ASP:C	1:H:385:PRO:CD	2.86	0.48
1:I:567:MSE:HE2	1:J:554:LEU:HD22	1.94	0.48
1:J:34:PHE:O	1:J:34:PHE:CG	2.65	0.48
1:J:386:THR:O	1:J:387:GLN:O	2.31	0.48
1:J:443:ASP:C	1:J:446:THR:HG22	2.38	0.48
1:K:47:GLN:HG3	1:K:54:ARG:NH1	2.28	0.48
1:K:142:GLN:O	1:K:143:VAL:HG23	2.13	0.48
1:K:528:LYS:HZ3	1:K:560:LEU:HD21	1.77	0.48
2:g:43:GLN:C	2:g:45:ALA:N	2.70	0.48
2:h:23:LEU:HD23	2:h:26:LEU:HD11	1.94	0.48
2:h:75:PRO:HA	2:h:76:PRO:HD3	1.42	0.48
2:j:37:VAL:C	2:j:39:PRO:HD3	2.38	0.48
1:M:164:LEU:HA	1:M:307:TRP:CH2	2.48	0.48
1:M:563:LYS:HD3	1:O:557:PHE:CE2	2.48	0.48
1:N:27:ARG:HH21	1:V:41:TRP:HE1	1.61	0.48
1:N:123:VAL:CG1	1:N:304:PHE:CE1	2.96	0.48
1:N:266:ILE:HG23	1:N:267:ALA:N	2.29	0.48
1:N:343:ARG:O	1:N:344:THR:HB	2.13	0.48
1:O:451:ASP:C	1:O:453:LEU:N	2.70	0.48
1:P:123:VAL:HG22	1:P:316:TYR:CE2	2.48	0.48
1:P:351:PHE:CD2	1:P:356:ILE:HD12	2.48	0.48
1:P:444:LEU:O	1:P:448:VAL:HG23	2.13	0.48
3:Q:719:HOH:O	1:R:430:VAL:HG13	2.12	0.48
1:S:266:ILE:HG23	1:S:267:ALA:N	2.28	0.48
1:T:293:ILE:HD13	1:T:294:ALA:N	2.29	0.48
1:U:266:ILE:HG23	1:U:267:ALA:N	2.28	0.48
1:V:37:ARG:HH21	1:V:37:ARG:CB	2.25	0.48
1:V:95:MSE:HE1	1:V:99:ARG:NH2	2.29	0.48
1:W:158:TRP:N	1:W:158:TRP:HD1	2.07	0.48
1:W:164:LEU:HA	1:W:307:TRP:HH2	1.79	0.48
1:W:248:LYS:HG3	1:W:511:ARG:HE	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:451:ASP:C	1:X:453:LEU:N	2.71	0.48
2:s:80:VAL:C	2:s:82:ALA:H	2.21	0.48
2:u:48:TYR:O	2:u:48:TYR:CD2	2.66	0.48
2:v:110:GLY:O	2:v:114:LEU:HD13	2.12	0.48
1:A:119:ILE:HA	1:A:432:PHE:HE2	1.77	0.48
1:A:386:THR:O	1:A:387:GLN:O	2.31	0.48
1:A:443:ASP:C	1:A:446:THR:HG22	2.38	0.48
1:A:584:PRO:HG2	1:A:593:LEU:HD12	1.94	0.48
1:B:11:ILE:O	1:B:15:PHE:HB2	2.13	0.48
1:B:128:LEU:HD12	1:B:446:THR:HG23	1.94	0.48
1:B:567:MSE:SE	1:C:576:LEU:HD13	2.63	0.48
1:C:359:PHE:HD1	2:e:129:ILE:HD11	1.78	0.48
1:D:72:ARG:HD2	1:F:434:THR:HG21	1.96	0.48
1:D:89:ASP:HA	1:E:561:ASP:CB	2.36	0.48
1:D:208:VAL:HG12	1:D:210:PRO:HD3	1.96	0.48
1:F:47:GLN:HG3	1:F:54:ARG:NH1	2.28	0.48
1:F:72:ARG:HD2	1:G:434:THR:HG21	1.95	0.48
1:F:584:PRO:CG	1:F:593:LEU:HD12	2.42	0.48
1:G:128:LEU:HD12	1:G:446:THR:HG23	1.94	0.48
1:G:395:PRO:HD2	1:H:398:PRO:HB3	1.94	0.48
1:H:248:LYS:H	1:H:248:LYS:CD	2.16	0.48
1:H:563:LYS:HD3	1:I:557:PHE:CE2	2.48	0.48
1:I:208:VAL:HG12	1:I:210:PRO:HD3	1.95	0.48
1:J:208:VAL:HG12	1:J:210:PRO:HD3	1.96	0.48
1:K:94:LEU:HA	1:K:97:MSE:CE	2.37	0.48
1:L:208:VAL:HG12	1:L:210:PRO:HD3	1.95	0.48
1:L:383:ASP:C	1:L:385:PRO:CD	2.86	0.48
1:L:443:ASP:C	1:L:446:THR:HG22	2.38	0.48
2:c:37:VAL:C	2:c:39:PRO:HD3	2.38	0.48
2:h:51:ALA:HB1	2:j:90:SER:OG	2.14	0.48
1:M:586:THR:N	1:M:587:PRO:CD	2.76	0.48
1:O:293:ILE:HD13	1:O:294:ALA:N	2.28	0.48
1:O:322:LEU:HD22	1:O:322:LEU:N	2.28	0.48
1:P:47:GLN:H	1:P:48:TYR:HD2	1.61	0.48
1:Q:95:MSE:HE1	1:Q:99:ARG:CZ	2.43	0.48
1:R:387:GLN:CB	1:X:390:ALA:HB2	2.44	0.48
1:S:41:TRP:HE1	1:T:27:ARG:HH21	1.62	0.48
1:T:379:GLU:O	1:T:380:ASN:CB	2.60	0.48
1:T:418:LEU:HB2	1:T:428:GLY:O	2.13	0.48
1:U:407:ALA:HB1	1:X:334:MSE:HE1	1.96	0.48
1:U:434:THR:HG23	1:U:435:VAL:N	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:r:80:VAL:C	2:r:82:ALA:H	2.20	0.48
2:v:71:ASP:OD2	2:v:71:ASP:N	2.38	0.48
1:A:80:TYR:CE1	1:A:444:LEU:HB3	2.47	0.48
1:A:427:GLY:C	1:A:429:GLN:N	2.70	0.48
1:B:226:VAL:O	1:B:274:ARG:HA	2.13	0.48
1:C:280:ILE:HG22	1:C:287:LEU:HD13	1.94	0.48
1:D:15:PHE:CE2	1:D:19:TRP:NE1	2.81	0.48
1:D:34:PHE:CG	1:D:34:PHE:O	2.66	0.48
1:D:80:TYR:CE1	1:D:444:LEU:HB3	2.48	0.48
1:D:334:MSE:SE	1:D:405:LEU:HD11	2.64	0.48
1:E:119:ILE:HA	1:E:432:PHE:HE2	1.77	0.48
1:E:343:ARG:NH1	2:b:135:ALA:O	2.40	0.48
1:E:383:ASP:C	1:E:385:PRO:CD	2.86	0.48
1:F:142:GLN:O	1:F:143:VAL:HG23	2.13	0.48
1:F:198:ILE:HG22	1:F:198:ILE:O	2.12	0.48
1:G:24:GLU:N	1:G:24:GLU:CD	2.71	0.48
1:H:15:PHE:CE2	1:H:19:TRP:NE1	2.81	0.48
1:I:54:ARG:HB2	2:g:146:GLY:HA3	1.94	0.48
1:I:198:ILE:HG22	1:I:198:ILE:O	2.12	0.48
1:J:119:ILE:HA	1:J:432:PHE:HE2	1.77	0.48
1:J:136:SER:N	1:J:137:PRO:HD3	2.27	0.48
1:K:584:PRO:HG2	1:K:593:LEU:HD12	1.94	0.48
1:L:142:GLN:O	1:L:143:VAL:HG23	2.13	0.48
2:h:37:VAL:C	2:h:39:PRO:HD3	2.38	0.48
1:M:248:LYS:HG3	1:M:511:ARG:HE	1.79	0.48
1:N:35:PHE:C	1:N:37:ARG:N	2.71	0.48
1:O:37:ARG:HH21	1:O:37:ARG:CB	2.24	0.48
1:O:413:LYS:HA	1:O:416:ALA:HB3	1.95	0.48
1:O:454:ALA:O	1:O:455:THR:C	2.56	0.48
1:O:561:ASP:HB2	1:P:89:ASP:HA	1.95	0.48
1:P:360:GLU:HG3	2:o:122:ARG:HB3	1.94	0.48
1:Q:35:PHE:HE1	1:Q:321:ARG:NH1	2.08	0.48
1:Q:164:LEU:HA	1:Q:307:TRP:HH2	1.79	0.48
1:Q:293:ILE:HD13	1:Q:294:ALA:N	2.29	0.48
1:S:325:ASP:O	1:S:329:LEU:HD23	2.13	0.48
1:S:418:LEU:HB2	1:S:428:GLY:O	2.13	0.48
1:S:444:LEU:O	1:S:446:THR:N	2.46	0.48
1:T:266:ILE:HG23	1:T:267:ALA:N	2.29	0.48
1:U:95:MSE:HE1	1:U:99:ARG:NH2	2.28	0.48
1:U:444:LEU:O	1:U:446:THR:N	2.46	0.48
1:V:164:LEU:HA	1:V:307:TRP:CH2	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:78:VAL:CG1	1:W:79:LEU:H	2.26	0.48
1:X:9:GLU:HG3	1:X:12:LEU:H	1.79	0.48
1:X:379:GLU:O	1:X:380:ASN:CB	2.61	0.48
2:p:48:TYR:O	2:p:48:TYR:HD2	1.95	0.48
2:q:95:TYR:CD1	2:q:95:TYR:N	2.81	0.48
2:u:128:TYR:CD1	2:u:132:MET:HG2	2.47	0.48
1:B:47:GLN:HG3	1:B:54:ARG:NH1	2.28	0.48
1:B:208:VAL:HG12	1:B:210:PRO:HD3	1.95	0.48
1:B:343:ARG:NH1	2:Z:135:ALA:O	2.41	0.48
1:B:578:GLN:HG2	1:B:596:ALA:HB2	1.94	0.48
1:C:386:THR:CG2	1:C:389:LEU:HD21	2.44	0.48
1:D:44:TRP:CE2	1:D:54:ARG:HB3	2.48	0.48
1:D:383:ASP:C	1:D:385:PRO:CD	2.86	0.48
1:D:434:THR:HG21	1:E:72:ARG:HD2	1.96	0.48
1:D:443:ASP:C	1:D:446:THR:HG22	2.38	0.48
1:D:577:ILE:HG12	1:D:582:LYS:CG	2.41	0.48
1:F:208:VAL:HG12	1:F:210:PRO:HD3	1.95	0.48
1:F:383:ASP:C	1:F:385:PRO:HD3	2.39	0.48
1:F:443:ASP:C	1:F:446:THR:HG22	2.38	0.48
1:G:334:MSE:SE	1:G:405:LEU:HD11	2.64	0.48
1:G:386:THR:O	1:G:387:GLN:O	2.31	0.48
1:I:128:LEU:HD12	1:I:446:THR:HG23	1.94	0.48
1:I:383:ASP:C	1:I:385:PRO:CD	2.86	0.48
1:J:226:VAL:O	1:J:274:ARG:HA	2.13	0.48
1:J:376:ARG:HB2	1:K:352:TRP:CG	2.48	0.48
1:K:15:PHE:CE2	1:K:19:TRP:NE1	2.81	0.48
1:K:383:ASP:C	1:K:385:PRO:HD3	2.39	0.48
1:M:58:ASP:HA	1:M:327:GLN:NE2	2.28	0.48
1:N:273:ARG:CZ	1:N:275:ARG:HE	2.27	0.48
1:N:322:LEU:H	1:N:322:LEU:HD22	1.78	0.48
1:N:343:ARG:HD3	2:k:128:TYR:CE1	2.48	0.48
1:O:573:ASN:O	1:O:577:ILE:HG13	2.13	0.48
1:P:71:MSE:CE	1:P:115:VAL:HB	2.44	0.48
1:P:560:LEU:O	1:P:561:ASP:O	2.32	0.48
1:Q:82:PRO:O	1:Q:516:CYS:HA	2.13	0.48
1:Q:164:LEU:HA	1:Q:307:TRP:CH2	2.49	0.48
1:Q:351:PHE:CD2	1:Q:356:ILE:HD12	2.49	0.48
1:R:273:ARG:HH22	1:R:453:LEU:CD2	2.27	0.48
1:S:343:ARG:HD3	2:t:128:TYR:CE1	2.49	0.48
1:U:164:LEU:HA	1:U:307:TRP:HH2	1.79	0.48
1:V:118:GLN:OE1	1:V:303:VAL:HB	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:413:LYS:HA	1:V:416:ALA:HB3	1.95	0.48
1:W:379:GLU:O	1:W:380:ASN:CB	2.61	0.48
1:W:418:LEU:HB2	1:W:428:GLY:O	2.13	0.48
1:X:164:LEU:HA	1:X:307:TRP:HH2	1.78	0.48
1:X:598:GLN:HB2	1:X:601:GLN:HB3	1.95	0.48
2:k:95:TYR:N	2:k:95:TYR:CD1	2.77	0.48
2:l:12:ALA:C	2:l:14:LEU:N	2.68	0.48
2:l:110:GLY:O	2:l:114:LEU:HD13	2.13	0.48
2:o:30:PRO:HD2	2:o:32:SER:HB3	1.95	0.48
2:o:128:TYR:CD1	2:o:132:MET:HG2	2.48	0.48
2:q:64:GLU:OE1	2:q:64:GLU:HA	2.14	0.48
2:u:48:TYR:O	2:u:48:TYR:HD2	1.96	0.48
2:u:65:ASN:O	2:u:67:PRO:HD3	2.14	0.48
1:A:57:PHE:CD2	1:A:330:ARG:CB	2.95	0.48
1:A:94:LEU:HA	1:A:97:MSE:CE	2.37	0.48
1:B:15:PHE:CE2	1:B:19:TRP:NE1	2.81	0.48
1:B:383:ASP:C	1:B:385:PRO:CD	2.86	0.48
1:C:255:ILE:O	1:C:257:ASP:N	2.45	0.48
1:C:383:ASP:C	1:C:385:PRO:HD3	2.39	0.48
1:D:528:LYS:HZ3	1:D:560:LEU:HD21	1.77	0.48
1:E:139:SER:CB	1:E:455:THR:CG2	2.80	0.48
1:E:142:GLN:O	1:E:143:VAL:HG23	2.13	0.48
1:E:578:GLN:HG2	1:E:596:ALA:HB2	1.94	0.48
1:F:24:GLU:N	1:F:24:GLU:CD	2.71	0.48
1:F:226:VAL:O	1:F:274:ARG:HA	2.13	0.48
1:F:227:GLU:HA	1:F:274:ARG:CA	2.44	0.48
1:F:334:MSE:SE	1:F:405:LEU:HD11	2.64	0.48
1:F:584:PRO:HG2	1:F:593:LEU:HD12	1.94	0.48
1:G:383:ASP:C	1:G:385:PRO:HD3	2.39	0.48
1:G:578:GLN:HG2	1:G:596:ALA:HB2	1.94	0.48
1:H:208:VAL:HG12	1:H:210:PRO:HD3	1.96	0.48
1:I:49:THR:O	1:I:50:THR:C	2.56	0.48
1:J:427:GLY:C	1:J:429:GLN:N	2.70	0.48
1:K:34:PHE:O	1:K:34:PHE:CG	2.66	0.48
1:L:34:PHE:CG	1:L:34:PHE:O	2.66	0.48
2:Y:23:LEU:HD23	2:Y:26:LEU:HD11	1.94	0.48
2:a:23:LEU:HD23	2:a:26:LEU:HD11	1.95	0.48
2:b:23:LEU:HD23	2:b:26:LEU:HD11	1.95	0.48
2:c:23:LEU:HD23	2:c:26:LEU:HD11	1.94	0.48
1:N:158:TRP:HD1	1:N:158:TRP:H	1.62	0.48
1:N:322:LEU:HD22	1:N:322:LEU:N	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:248:LYS:HG3	1:O:511:ARG:HE	1.79	0.48
1:O:266:ILE:HG23	1:O:267:ALA:N	2.27	0.48
1:O:343:ARG:NH1	2:l:126:ALA:O	2.46	0.48
1:R:164:LEU:HA	1:R:307:TRP:CH2	2.48	0.48
1:R:235:TYR:OH	1:R:252:LYS:NZ	2.46	0.48
1:R:322:LEU:HD22	1:R:322:LEU:N	2.29	0.48
1:R:371:TYR:HE2	1:R:373:LEU:HD21	1.79	0.48
1:R:383:ASP:C	1:R:385:PRO:HD3	2.39	0.48
1:S:322:LEU:HD22	1:S:322:LEU:N	2.28	0.48
1:S:384:LEU:HD22	1:S:384:LEU:N	2.28	0.48
1:T:387:GLN:HB3	1:W:390:ALA:CB	2.44	0.48
1:T:434:THR:HG23	1:T:435:VAL:N	2.28	0.48
1:U:310:VAL:HG22	1:X:40:GLN:HG2	1.96	0.48
1:U:456:ALA:O	1:U:457:MSE:HB2	2.12	0.48
1:W:235:TYR:HA	1:W:265:LYS:HB3	1.96	0.48
1:W:266:ILE:HG23	1:W:267:ALA:N	2.28	0.48
1:X:165:MSE:HE1	1:X:435:VAL:HB	1.95	0.48
2:m:110:GLY:O	2:m:114:LEU:HD13	2.14	0.48
2:n:48:TYR:O	2:n:48:TYR:CD2	2.67	0.48
2:q:48:TYR:O	2:q:48:TYR:HD2	1.96	0.48
2:t:64:GLU:OE1	2:t:64:GLU:HA	2.14	0.48
2:v:64:GLU:OE1	2:v:64:GLU:HA	2.13	0.48
1:A:11:ILE:O	1:A:15:PHE:HB2	2.13	0.48
1:A:577:ILE:HG12	1:A:582:LYS:CG	2.41	0.48
1:B:42:ASP:OD2	2:Z:145:SER:O	2.31	0.48
1:B:383:ASP:C	1:B:385:PRO:HD3	2.39	0.48
1:C:142:GLN:O	1:C:143:VAL:HG23	2.13	0.48
1:C:208:VAL:HG12	1:C:210:PRO:HD3	1.95	0.48
1:D:11:ILE:O	1:D:15:PHE:HB2	2.13	0.48
1:D:24:GLU:N	1:D:24:GLU:CD	2.71	0.48
1:E:208:VAL:HG12	1:E:210:PRO:HD3	1.96	0.48
1:H:11:ILE:O	1:H:15:PHE:HB2	2.13	0.48
1:H:142:GLN:O	1:H:143:VAL:HG23	2.13	0.48
1:H:334:MSE:SE	1:H:405:LEU:HD11	2.64	0.48
1:H:577:ILE:HG12	1:H:582:LYS:CG	2.41	0.48
1:I:142:GLN:O	1:I:143:VAL:HG23	2.13	0.48
1:J:15:PHE:CE2	1:J:19:TRP:NE1	2.81	0.48
1:J:334:MSE:SE	1:J:405:LEU:HD11	2.64	0.48
1:J:383:ASP:C	1:J:385:PRO:HD3	2.39	0.48
1:K:42:ASP:OD2	2:h:145:SER:O	2.31	0.48
1:K:248:LYS:H	1:K:248:LYS:CD	2.16	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:383:ASP:C	1:K:385:PRO:CD	2.86	0.48
1:K:386:THR:CG2	1:K:389:LEU:HD21	2.44	0.48
1:N:9:GLU:HG3	1:N:12:LEU:H	1.77	0.48
1:N:89:ASP:CA	1:V:561:ASP:HB2	2.31	0.48
1:N:248:LYS:HG3	1:N:511:ARG:HE	1.79	0.48
1:N:598:GLN:HB2	1:N:601:GLN:HB3	1.96	0.48
1:P:35:PHE:HE1	1:P:321:ARG:NH1	2.08	0.48
1:Q:395:PRO:HD2	1:R:398:PRO:HB3	1.95	0.48
1:S:27:ARG:HB2	1:S:313:LYS:HE3	1.95	0.48
1:S:560:LEU:O	1:S:561:ASP:O	2.31	0.48
1:U:26:ARG:O	1:U:27:ARG:C	2.56	0.48
1:U:164:LEU:HA	1:U:307:TRP:CH2	2.49	0.48
1:U:329:LEU:HD21	1:X:53:TYR:OH	2.13	0.48
1:V:27:ARG:HB2	1:V:313:LYS:HE3	1.96	0.48
1:V:248:LYS:H	1:V:248:LYS:CD	2.18	0.48
1:V:384:LEU:HD22	1:V:384:LEU:N	2.27	0.48
1:W:123:VAL:HG22	1:W:316:TYR:HE2	1.79	0.48
2:k:65:ASN:O	2:k:67:PRO:HD3	2.13	0.48
2:v:48:TYR:CD2	2:v:48:TYR:O	2.67	0.48
1:A:47:GLN:HG3	1:A:54:ARG:NH1	2.28	0.48
1:A:165:MSE:HG3	1:A:307:TRP:CD2	2.49	0.48
1:A:376:ARG:HB2	1:B:352:TRP:CG	2.49	0.48
1:A:386:THR:CG2	1:A:389:LEU:HD21	2.44	0.48
1:C:165:MSE:HG3	1:C:307:TRP:CD2	2.49	0.48
1:C:372:TYR:CE2	1:E:348:LYS:HB2	2.49	0.48
1:D:328:ARG:HB3	2:b:142:PRO:HG3	1.95	0.48
1:D:383:ASP:C	1:D:385:PRO:HD3	2.39	0.48
1:D:386:THR:CG2	1:D:389:LEU:HD21	2.44	0.48
1:E:226:VAL:O	1:E:274:ARG:HA	2.13	0.48
1:E:227:GLU:HA	1:E:274:ARG:CA	2.44	0.48
1:F:11:ILE:O	1:F:15:PHE:HB2	2.13	0.48
1:G:11:ILE:O	1:G:15:PHE:HB2	2.13	0.48
1:G:14:ARG:NE	1:G:14:ARG:CA	2.67	0.48
1:G:44:TRP:CE2	1:G:54:ARG:HB3	2.48	0.48
1:G:47:GLN:N	1:G:47:GLN:CD	2.72	0.48
1:H:34:PHE:HZ	1:H:328:ARG:HH22	0.80	0.48
1:H:165:MSE:HG3	1:H:307:TRP:CD2	2.49	0.48
1:I:11:ILE:O	1:I:15:PHE:HB2	2.13	0.48
1:I:34:PHE:CE1	1:I:324:LYS:NZ	2.72	0.48
1:J:386:THR:CG2	1:J:389:LEU:HD21	2.44	0.48
1:K:328:ARG:HB3	2:i:142:PRO:HG3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:334:MSE:HE3	1:L:404:MSE:CE	2.44	0.48
1:K:578:GLN:HG2	1:K:596:ALA:HB2	1.94	0.48
2:d:43:GLN:C	2:d:45:ALA:N	2.70	0.48
1:M:47:GLN:H	1:M:48:TYR:HD2	1.62	0.48
1:M:343:ARG:HD3	2:m:128:TYR:CE1	2.48	0.48
1:N:123:VAL:HG22	1:N:316:TYR:CE2	2.49	0.48
1:O:123:VAL:HG22	1:O:316:TYR:CE2	2.49	0.48
1:O:155:HIS:CE1	1:O:204:PRO:HB2	2.49	0.48
1:P:9:GLU:HG3	1:P:12:LEU:H	1.77	0.48
1:P:78:VAL:CG1	1:P:79:LEU:H	2.27	0.48
1:S:47:GLN:CG	1:S:48:TYR:H	2.27	0.48
1:S:95:MSE:HE1	1:S:99:ARG:NH2	2.29	0.48
1:S:158:TRP:N	1:S:158:TRP:HD1	2.07	0.48
1:S:248:LYS:H	1:S:248:LYS:CD	2.17	0.48
1:S:293:ILE:HD13	1:S:294:ALA:N	2.28	0.48
1:T:14:ARG:NE	1:T:14:ARG:CA	2.70	0.48
1:T:33:LEU:HD12	1:T:34:PHE:N	2.29	0.48
1:T:95:MSE:HE1	1:T:99:ARG:CZ	2.44	0.48
1:T:384:LEU:HD22	1:T:384:LEU:N	2.28	0.48
1:W:31:ASN:O	1:W:34:PHE:HB3	2.14	0.48
1:X:78:VAL:CG1	1:X:79:LEU:N	2.77	0.48
1:X:127:ARG:HG2	1:X:147:GLU:HB2	1.96	0.48
1:X:248:LYS:HG3	1:X:511:ARG:HE	1.77	0.48
2:l:64:GLU:OE1	2:l:64:GLU:HA	2.14	0.48
1:A:24:GLU:CD	1:A:24:GLU:N	2.71	0.48
1:A:49:THR:O	1:A:50:THR:C	2.56	0.48
1:A:383:ASP:C	1:A:385:PRO:HD3	2.39	0.48
1:B:49:THR:O	1:B:50:THR:C	2.56	0.48
1:B:165:MSE:HG3	1:B:307:TRP:CD2	2.49	0.48
1:B:334:MSE:SE	1:C:404:MSE:HE1	2.64	0.48
1:B:386:THR:CG2	1:B:389:LEU:HD21	2.44	0.48
1:C:386:THR:O	1:C:387:GLN:O	2.31	0.48
1:D:182:ASN:HD22	1:F:171:ARG:HH21	1.62	0.48
1:E:334:MSE:SE	1:E:405:LEU:HD11	2.64	0.48
1:F:165:MSE:HG3	1:F:307:TRP:CD2	2.49	0.48
1:F:386:THR:CG2	1:F:389:LEU:HD21	2.44	0.48
1:H:236:GLN:HE21	1:H:265:LYS:HZ3	1.60	0.48
1:I:24:GLU:N	1:I:24:GLU:CD	2.71	0.48
1:J:165:MSE:HG3	1:J:307:TRP:CD2	2.49	0.48
1:K:11:ILE:O	1:K:15:PHE:HB2	2.13	0.48
1:K:24:GLU:CD	1:K:24:GLU:N	2.71	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:165:MSE:HG3	1:K:307:TRP:CD2	2.49	0.48
1:K:577:ILE:HG12	1:K:582:LYS:CG	2.41	0.48
1:L:227:GLU:HA	1:L:274:ARG:CA	2.44	0.48
1:L:386:THR:CG2	1:L:389:LEU:HD21	2.44	0.48
2:Y:37:VAL:C	2:Y:39:PRO:HD3	2.38	0.48
1:M:235:TYR:HA	1:M:265:LYS:HB3	1.94	0.48
1:M:329:LEU:HD21	1:N:53:TYR:OH	2.13	0.48
1:N:47:GLN:CG	1:N:48:TYR:H	2.27	0.48
1:P:82:PRO:O	1:P:516:CYS:HA	2.13	0.48
1:P:238:PRO:HD3	1:P:263:PHE:HB2	1.95	0.48
1:P:444:LEU:O	1:P:446:THR:N	2.46	0.48
1:Q:322:LEU:HD22	1:Q:322:LEU:N	2.29	0.48
1:R:55:GLY:HA3	1:R:57:PHE:CE1	2.48	0.48
1:R:266:ILE:HG23	1:R:267:ALA:N	2.28	0.48
1:T:38:VAL:HG21	1:T:324:LYS:HD2	1.96	0.48
1:T:165:MSE:HE1	1:T:435:VAL:HB	1.95	0.48
1:U:444:LEU:O	1:U:448:VAL:HG23	2.14	0.48
1:V:37:ARG:C	1:V:39:SER:H	2.20	0.48
1:W:164:LEU:HA	1:W:307:TRP:CH2	2.49	0.48
1:X:444:LEU:O	1:X:446:THR:N	2.47	0.48
1:X:451:ASP:C	1:X:453:LEU:H	2.20	0.48
2:o:110:GLY:O	2:o:114:LEU:HD13	2.14	0.48
2:v:30:PRO:HD2	2:v:32:SER:HB3	1.96	0.48
2:v:48:TYR:O	2:v:48:TYR:HD2	1.97	0.48
1:A:234:ILE:HG12	1:A:267:ALA:HB3	1.96	0.48
1:A:334:MSE:SE	1:A:405:LEU:HD11	2.64	0.48
1:A:383:ASP:C	1:A:385:PRO:CD	2.86	0.48
1:C:49:THR:O	1:C:50:THR:C	2.56	0.48
1:C:119:ILE:HA	1:C:432:PHE:HE2	1.77	0.48
1:C:227:GLU:HA	1:C:274:ARG:CA	2.44	0.48
1:C:443:ASP:C	1:C:446:THR:HG22	2.38	0.48
1:D:40:GLN:O	1:D:41:TRP:CB	2.54	0.48
1:D:128:LEU:HD12	1:D:446:THR:HG23	1.94	0.48
1:D:227:GLU:HA	1:D:274:ARG:CA	2.44	0.48
1:D:427:GLY:C	1:D:429:GLN:N	2.70	0.48
1:D:539:LEU:HD21	1:D:551:LEU:HB3	1.96	0.48
1:F:15:PHE:CE2	1:F:19:TRP:NE1	2.81	0.48
1:F:128:LEU:HD12	1:F:446:THR:HG23	1.94	0.48
1:H:24:GLU:CD	1:H:24:GLU:N	2.71	0.48
1:H:386:THR:CG2	1:H:389:LEU:HD21	2.44	0.48
1:J:561:ASP:CB	1:K:89:ASP:HA	2.33	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:227:GLU:HA	1:K:274:ARG:CA	2.44	0.48
1:K:248:LYS:HZ1	1:K:513:ARG:HH12	1.60	0.48
1:K:427:GLY:C	1:K:429:GLN:N	2.70	0.48
1:L:101:ASP:HB2	1:L:144:ILE:O	2.14	0.48
1:L:136:SER:N	1:L:137:PRO:HD3	2.27	0.48
1:L:164:LEU:HA	1:L:307:TRP:HH2	1.79	0.48
1:L:334:MSE:SE	1:L:405:LEU:HD11	2.64	0.48
2:d:23:LEU:HD23	2:d:26:LEU:HD11	1.94	0.48
1:N:26:ARG:O	1:N:27:ARG:C	2.57	0.47
1:O:14:ARG:NE	1:O:14:ARG:CA	2.71	0.47
1:O:434:THR:HG23	1:O:435:VAL:N	2.28	0.47
1:P:71:MSE:HE3	1:P:115:VAL:HB	1.95	0.47
1:Q:165:MSE:HG3	1:Q:307:TRP:CD2	2.48	0.47
1:Q:387:GLN:HB3	1:R:390:ALA:CB	2.44	0.47
1:Q:387:GLN:HB2	1:R:390:ALA:HB2	1.94	0.47
1:R:9:GLU:HG3	1:R:12:LEU:H	1.78	0.47
1:S:123:VAL:CG1	1:S:304:PHE:CE1	2.97	0.47
1:S:127:ARG:HG2	1:S:147:GLU:HB2	1.96	0.47
1:T:248:LYS:HG3	1:T:511:ARG:HE	1.79	0.47
1:V:330:ARG:HD2	1:V:409:THR:CG2	2.38	0.47
1:X:86:ALA:CB	1:X:515:GLU:HG3	2.44	0.47
2:m:33:MET:HE3	2:m:33:MET:HB3	1.66	0.47
2:n:30:PRO:HD2	2:n:32:SER:HB3	1.95	0.47
1:A:226:VAL:O	1:A:274:ARG:HA	2.13	0.47
1:B:234:ILE:HG12	1:B:267:ALA:HB3	1.96	0.47
1:B:577:ILE:HG12	1:B:582:LYS:CG	2.41	0.47
1:D:226:VAL:O	1:D:274:ARG:HA	2.13	0.47
1:F:230:GLU:HG2	1:F:273:ARG:HB2	1.96	0.47
1:G:26:ARG:NH2	1:G:30:LYS:HB2	2.28	0.47
1:G:58:ASP:O	1:G:59:VAL:HB	2.14	0.47
1:G:158:TRP:CD1	1:G:158:TRP:H	2.25	0.47
1:G:165:MSE:HG3	1:G:307:TRP:CD2	2.49	0.47
1:H:226:VAL:O	1:H:274:ARG:HA	2.13	0.47
1:I:165:MSE:HG3	1:I:307:TRP:CD2	2.49	0.47
1:I:334:MSE:SE	1:I:405:LEU:HD11	2.64	0.47
1:J:101:ASP:HB2	1:J:144:ILE:O	2.14	0.47
1:J:142:GLN:O	1:J:143:VAL:HG23	2.13	0.47
1:J:539:LEU:HD21	1:J:551:LEU:CB	2.44	0.47
1:K:58:ASP:O	1:K:59:VAL:HB	2.14	0.47
1:K:208:VAL:HG12	1:K:210:PRO:HD3	1.96	0.47
1:K:334:MSE:SE	1:K:405:LEU:HD11	2.64	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:86:ALA:HB2	1:L:515:GLU:HG3	1.96	0.47
1:L:230:GLU:HG2	1:L:273:ARG:HB2	1.96	0.47
1:L:383:ASP:C	1:L:385:PRO:HD3	2.39	0.47
1:L:456:ALA:HB1	1:L:509:ASP:OD2	2.13	0.47
1:L:539:LEU:HD21	1:L:551:LEU:HB3	1.96	0.47
2:Z:75:PRO:HA	2:Z:76:PRO:HD3	1.42	0.47
2:f:75:PRO:HA	2:f:76:PRO:HD3	1.42	0.47
1:M:434:THR:HG23	1:M:435:VAL:N	2.29	0.47
1:N:573:ASN:O	1:N:577:ILE:HG13	2.14	0.47
1:O:123:VAL:CG1	1:O:304:PHE:CE1	2.97	0.47
1:Q:245:SER:HG	1:Q:247:PHE:HE1	1.60	0.47
1:S:35:PHE:HZ	1:S:321:ARG:NE	2.11	0.47
1:T:193:LEU:HD22	1:T:287:LEU:HB3	1.96	0.47
1:U:31:ASN:O	1:U:34:PHE:HB3	2.14	0.47
1:U:127:ARG:HG2	1:U:147:GLU:HB2	1.96	0.47
1:U:383:ASP:C	1:U:385:PRO:HD3	2.39	0.47
1:U:598:GLN:HB2	1:U:601:GLN:HB3	1.95	0.47
1:W:27:ARG:HB2	1:W:313:LYS:HE3	1.96	0.47
1:W:95:MSE:HE1	1:W:99:ARG:NH2	2.29	0.47
1:X:359:PHE:HD1	2:t:120:ILE:HD11	1.79	0.47
1:X:444:LEU:O	1:X:448:VAL:HG23	2.13	0.47
2:m:64:GLU:OE1	2:m:64:GLU:HA	2.13	0.47
2:n:65:ASN:O	2:n:67:PRO:HD3	2.14	0.47
1:B:86:ALA:HB2	1:B:515:GLU:HG3	1.96	0.47
1:C:81:ARG:HB2	1:C:517:TYR:CZ	2.50	0.47
1:D:230:GLU:HG2	1:D:273:ARG:HB2	1.96	0.47
1:E:535:ILE:CD1	1:E:554:LEU:HG	2.44	0.47
1:H:101:ASP:HB2	1:H:144:ILE:O	2.14	0.47
1:I:86:ALA:HB2	1:I:515:GLU:HG3	1.96	0.47
1:I:113:ILE:HD12	1:I:148:PRO:HB3	1.94	0.47
1:I:227:GLU:HA	1:I:274:ARG:CA	2.44	0.47
1:K:101:ASP:HB2	1:K:144:ILE:O	2.14	0.47
1:K:539:LEU:HD21	1:K:551:LEU:HB3	1.96	0.47
1:L:11:ILE:O	1:L:15:PHE:HB2	2.13	0.47
1:M:27:ARG:HB2	1:M:313:LYS:HE3	1.94	0.47
1:N:78:VAL:CG1	1:N:444:LEU:HG	2.44	0.47
1:N:293:ILE:HD13	1:N:294:ALA:N	2.29	0.47
1:O:227:GLU:O	1:O:227:GLU:CG	2.63	0.47
1:Q:35:PHE:HZ	1:Q:321:ARG:NE	2.10	0.47
1:R:378:ASP:O	1:R:381:SER:O	2.33	0.47
1:S:95:MSE:HE1	1:S:99:ARG:CZ	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:564:GLY:HA3	1:T:535:ILE:HD11	1.96	0.47
1:T:325:ASP:O	1:T:329:LEU:HD23	2.14	0.47
1:T:409:THR:O	1:T:413:LYS:HG2	2.15	0.47
1:U:430:VAL:HG11	3:X:719:HOH:O	2.13	0.47
1:X:27:ARG:HB2	1:X:313:LYS:HE3	1.95	0.47
1:X:47:GLN:H	1:X:48:TYR:HD2	1.61	0.47
1:X:238:PRO:HD3	1:X:263:PHE:HB2	1.96	0.47
2:k:33:MET:HE3	2:k:33:MET:HB3	1.68	0.47
2:o:95:TYR:N	2:o:95:TYR:CD1	2.81	0.47
2:q:30:PRO:HB2	2:q:31:GLN:H	1.58	0.47
1:A:198:ILE:HA	1:A:199:PRO:HD3	1.64	0.47
1:A:334:MSE:SE	1:B:404:MSE:HE1	2.64	0.47
1:A:535:ILE:CD1	1:A:554:LEU:HG	2.44	0.47
1:B:273:ARG:HH22	1:B:453:LEU:CD1	2.28	0.47
1:D:142:GLN:O	1:D:143:VAL:HG23	2.13	0.47
1:E:86:ALA:HB2	1:E:515:GLU:HG3	1.96	0.47
1:E:162:SER:HB2	1:E:170:ALA:HB2	1.97	0.47
1:E:386:THR:CG2	1:E:389:LEU:HD21	2.44	0.47
1:G:567:MSE:HE2	1:H:554:LEU:HD22	1.96	0.47
1:H:40:GLN:O	1:H:41:TRP:CB	2.55	0.47
1:H:383:ASP:C	1:H:385:PRO:HD3	2.39	0.47
1:I:101:ASP:HB2	1:I:144:ILE:O	2.14	0.47
1:I:535:ILE:CD1	1:I:554:LEU:HG	2.44	0.47
1:K:273:ARG:HH22	1:K:453:LEU:CD1	2.28	0.47
1:K:539:LEU:HD21	1:K:551:LEU:CB	2.44	0.47
2:b:78:GLU:CG	2:b:79:GLY:N	2.63	0.47
1:N:38:VAL:HG21	1:N:324:LYS:HD2	1.96	0.47
1:N:118:GLN:OE1	1:N:303:VAL:HB	2.14	0.47
1:O:164:LEU:HA	1:O:307:TRP:CH2	2.50	0.47
1:O:568:MSE:HG3	1:P:551:LEU:CD2	2.44	0.47
1:P:35:PHE:HZ	1:P:321:ARG:NE	2.11	0.47
1:Q:158:TRP:HD1	1:Q:158:TRP:H	1.62	0.47
1:Q:560:LEU:O	1:Q:561:ASP:O	2.33	0.47
1:R:376:ARG:HB2	1:X:352:TRP:CG	2.49	0.47
1:R:418:LEU:HB2	1:R:428:GLY:O	2.14	0.47
1:R:563:LYS:HD3	1:X:557:PHE:CE2	2.49	0.47
1:S:227:GLU:CG	1:S:227:GLU:O	2.62	0.47
1:T:95:MSE:HE1	1:T:99:ARG:NH2	2.29	0.47
1:U:413:LYS:HA	1:U:416:ALA:HB3	1.96	0.47
1:V:33:LEU:HD12	1:V:34:PHE:N	2.30	0.47
1:W:293:ILE:HD13	1:W:294:ALA:N	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:123:VAL:CG1	1:X:304:PHE:CE1	2.97	0.47
2:o:59:VAL:HG22	2:o:73:HIS:O	2.15	0.47
2:p:43:MET:C	2:p:45:ALA:H	2.21	0.47
1:B:35:PHE:HE1	1:B:321:ARG:NH1	2.13	0.47
1:B:443:ASP:C	1:B:446:THR:HG22	2.38	0.47
1:C:567:MSE:HE2	1:E:554:LEU:HD22	1.95	0.47
1:D:164:LEU:HA	1:D:307:TRP:HH2	1.79	0.47
1:E:34:PHE:O	1:E:34:PHE:CD2	2.68	0.47
1:E:539:LEU:HD21	1:E:551:LEU:CB	2.45	0.47
1:G:101:ASP:HB2	1:G:144:ILE:O	2.14	0.47
1:H:34:PHE:O	1:H:34:PHE:CG	2.66	0.47
1:H:57:PHE:CD2	1:H:330:ARG:CB	2.95	0.47
1:H:58:ASP:O	1:H:59:VAL:HB	2.14	0.47
1:H:130:THR:HG22	1:H:144:ILE:HA	1.97	0.47
1:I:58:ASP:O	1:I:59:VAL:HB	2.14	0.47
1:I:115:VAL:O	1:I:119:ILE:HG13	2.15	0.47
1:I:230:GLU:HG2	1:I:273:ARG:HB2	1.96	0.47
1:J:35:PHE:HE2	1:J:324:LYS:NZ	2.08	0.47
1:J:164:LEU:HA	1:J:307:TRP:HH2	1.79	0.47
1:K:86:ALA:HB2	1:K:515:GLU:HG3	1.96	0.47
1:K:535:ILE:CD1	1:K:554:LEU:HG	2.44	0.47
1:L:24:GLU:CD	1:L:24:GLU:N	2.71	0.47
1:L:81:ARG:HB2	1:L:517:TYR:CZ	2.50	0.47
1:L:165:MSE:HG3	1:L:307:TRP:CD2	2.49	0.47
1:L:451:ASP:O	1:L:456:ALA:N	2.41	0.47
1:M:238:PRO:HD3	1:M:263:PHE:HB2	1.97	0.47
1:N:235:TYR:HA	1:N:265:LYS:HB3	1.95	0.47
1:N:444:LEU:O	1:N:446:THR:N	2.48	0.47
1:O:383:ASP:C	1:O:385:PRO:HD3	2.39	0.47
1:P:86:ALA:CB	1:P:515:GLU:HG3	2.44	0.47
1:P:260:ASP:HA	1:P:264:ILE:HB	1.97	0.47
1:P:316:TYR:O	1:P:321:ARG:NH1	2.48	0.47
1:Q:34:PHE:O	1:Q:37:ARG:HB2	2.14	0.47
1:Q:78:VAL:CG1	1:Q:444:LEU:HG	2.44	0.47
1:Q:260:ASP:HA	1:Q:264:ILE:HB	1.97	0.47
1:R:434:THR:HG23	1:R:435:VAL:N	2.28	0.47
1:W:325:ASP:O	1:W:329:LEU:HD23	2.13	0.47
1:X:235:TYR:OH	1:X:252:LYS:NZ	2.48	0.47
2:k:64:GLU:OE1	2:k:64:GLU:HA	2.13	0.47
2:l:30:PRO:HD2	2:l:32:SER:HB3	1.96	0.47
2:o:80:VAL:C	2:o:82:ALA:N	2.72	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s:64:GLU:OE1	2:s:64:GLU:HA	2.14	0.47
2:s:95:TYR:N	2:s:95:TYR:CD1	2.80	0.47
2:t:30:PRO:HD2	2:t:32:SER:HB3	1.95	0.47
2:u:12:ALA:C	2:u:14:LEU:N	2.69	0.47
1:A:86:ALA:HB2	1:A:515:GLU:HG3	1.96	0.47
1:A:130:THR:HG22	1:A:144:ILE:HA	1.97	0.47
1:A:208:VAL:HG12	1:A:210:PRO:HD3	1.96	0.47
1:B:101:ASP:HB2	1:B:144:ILE:O	2.14	0.47
1:B:539:LEU:HD21	1:B:551:LEU:HB3	1.96	0.47
1:C:101:ASP:HB2	1:C:144:ILE:O	2.14	0.47
1:E:24:GLU:N	1:E:24:GLU:CD	2.71	0.47
1:E:383:ASP:C	1:E:385:PRO:HD3	2.39	0.47
1:F:81:ARG:HB2	1:F:517:TYR:CZ	2.50	0.47
1:F:86:ALA:HB2	1:F:515:GLU:HG3	1.96	0.47
1:F:535:ILE:CD1	1:F:554:LEU:HG	2.44	0.47
1:G:29:ALA:O	1:G:33:LEU:HG	2.15	0.47
1:G:81:ARG:HB2	1:G:517:TYR:CZ	2.50	0.47
1:H:34:PHE:O	1:H:34:PHE:CD2	2.68	0.47
1:H:539:LEU:HD21	1:H:551:LEU:CB	2.44	0.47
1:J:81:ARG:HB2	1:J:517:TYR:CZ	2.50	0.47
1:L:535:ILE:CD1	1:L:554:LEU:HG	2.44	0.47
1:L:539:LEU:HD21	1:L:551:LEU:CB	2.45	0.47
2:f:28:VAL:HG21	2:f:96:LEU:CG	2.40	0.47
2:f:156:HIS:C	2:f:158:PHE:H	2.23	0.47
1:M:24:GLU:CD	1:M:24:GLU:N	2.73	0.47
1:M:371:TYR:HE2	1:M:373:LEU:HD21	1.79	0.47
1:N:37:ARG:HH21	1:N:37:ARG:CB	2.28	0.47
1:N:444:LEU:O	1:N:447:TYR:N	2.47	0.47
1:N:444:LEU:O	1:N:448:VAL:HG23	2.14	0.47
1:O:235:TYR:HA	1:O:265:LYS:HB3	1.95	0.47
1:O:260:ASP:HA	1:O:264:ILE:HB	1.97	0.47
1:O:330:ARG:HD2	1:O:409:THR:CG2	2.40	0.47
1:P:40:GLN:HG2	1:Q:310:VAL:HG22	1.95	0.47
1:P:212:LEU:HD22	1:Q:26:ARG:HG2	1.96	0.47
1:P:235:TYR:OH	1:P:252:LYS:NZ	2.48	0.47
1:P:413:LYS:HA	1:P:416:ALA:HB3	1.97	0.47
1:R:164:LEU:HD22	1:R:169:ASP:OD1	2.15	0.47
1:R:556:TYR:OH	1:X:542:THR:HG21	2.13	0.47
1:R:598:GLN:HB2	1:R:601:GLN:HB3	1.95	0.47
1:S:248:LYS:HG3	1:S:511:ARG:HE	1.78	0.47
1:S:420:VAL:HA	1:S:428:GLY:HA2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:405:LEU:O	1:T:409:THR:HG23	2.14	0.47
1:U:14:ARG:NE	1:U:14:ARG:CA	2.70	0.47
1:V:235:TYR:OH	1:V:252:LYS:NZ	2.47	0.47
1:V:260:ASP:HA	1:V:264:ILE:HB	1.96	0.47
1:V:434:THR:HG23	1:V:435:VAL:N	2.29	0.47
1:W:171:ARG:O	1:W:224:GLU:HA	2.15	0.47
1:W:238:PRO:HD3	1:W:263:PHE:HB2	1.96	0.47
1:X:47:GLN:N	1:X:48:TYR:HD2	2.13	0.47
1:X:82:PRO:O	1:X:516:CYS:HA	2.14	0.47
2:o:96:ALA:HB2	2:p:25:LEU:HD13	1.96	0.47
2:r:95:TYR:N	2:r:95:TYR:CD1	2.80	0.47
1:A:34:PHE:O	1:A:34:PHE:CD2	2.68	0.47
1:A:42:ASP:OD2	2:Y:145:SER:O	2.32	0.47
1:B:142:GLN:O	1:B:143:VAL:HG23	2.13	0.47
1:B:164:LEU:HA	1:B:307:TRP:HH2	1.80	0.47
1:B:334:MSE:SE	1:B:405:LEU:HD11	2.64	0.47
1:C:197:ASP:O	1:C:198:ILE:HB	2.15	0.47
1:C:334:MSE:SE	1:C:405:LEU:HD11	2.64	0.47
1:C:383:ASP:C	1:C:385:PRO:CD	2.86	0.47
1:D:58:ASP:O	1:D:59:VAL:HB	2.14	0.47
1:E:165:MSE:HG3	1:E:307:TRP:CD2	2.49	0.47
1:F:29:ALA:O	1:F:33:LEU:HG	2.15	0.47
1:F:101:ASP:HB2	1:F:144:ILE:O	2.14	0.47
1:F:130:THR:HG22	1:F:144:ILE:HA	1.97	0.47
1:F:164:LEU:HA	1:F:307:TRP:HH2	1.80	0.47
1:F:563:LYS:HD3	1:G:557:PHE:CE2	2.49	0.47
1:G:539:LEU:HD21	1:G:551:LEU:CB	2.44	0.47
1:J:26:ARG:NH2	1:J:30:LYS:HB2	2.28	0.47
1:J:34:PHE:O	1:J:34:PHE:CD2	2.68	0.47
1:J:71:MSE:CE	1:J:115:VAL:HB	2.45	0.47
1:J:230:GLU:HG2	1:J:273:ARG:HB2	1.96	0.47
1:K:443:ASP:C	1:K:446:THR:HG22	2.38	0.47
1:L:35:PHE:HE1	1:L:321:ARG:NH1	2.13	0.47
1:L:130:THR:HG22	1:L:144:ILE:HA	1.97	0.47
1:L:197:ASP:O	1:L:198:ILE:HB	2.15	0.47
1:M:35:PHE:C	1:M:37:ARG:N	2.73	0.47
1:M:248:LYS:H	1:M:248:LYS:CD	2.17	0.47
1:M:418:LEU:HB2	1:M:428:GLY:O	2.15	0.47
1:M:451:ASP:C	1:M:453:LEU:N	2.71	0.47
1:N:27:ARG:HB2	1:N:313:LYS:HE3	1.96	0.47
1:N:47:GLN:H	1:N:48:TYR:HD2	1.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:164:LEU:HA	1:N:307:TRP:CH2	2.50	0.47
1:N:348:LYS:HB2	1:V:372:TYR:CE2	2.50	0.47
1:O:31:ASN:O	1:O:34:PHE:HB3	2.14	0.47
1:O:47:GLN:H	1:O:48:TYR:HD2	1.63	0.47
1:O:158:TRP:HH2	1:O:302:PRO:HG3	1.80	0.47
1:O:164:LEU:HA	1:O:307:TRP:HH2	1.80	0.47
1:P:136:SER:N	1:P:137:PRO:HD3	2.30	0.47
1:P:554:LEU:O	1:P:557:PHE:HB3	2.14	0.47
1:Q:14:ARG:NE	1:Q:14:ARG:CA	2.71	0.47
1:Q:238:PRO:HD3	1:Q:263:PHE:HB2	1.95	0.47
1:Q:561:ASP:HB2	1:R:89:ASP:CA	2.35	0.47
1:R:238:PRO:HD3	1:R:263:PHE:HB2	1.97	0.47
1:R:248:LYS:HG3	1:R:511:ARG:HE	1.78	0.47
1:S:322:LEU:HD22	1:S:322:LEU:H	1.79	0.47
1:T:123:VAL:HG22	1:T:316:TYR:HE2	1.79	0.47
1:U:418:LEU:HB2	1:U:428:GLY:O	2.14	0.47
1:U:573:ASN:O	1:U:577:ILE:HG13	2.13	0.47
1:V:29:ALA:O	1:V:33:LEU:HG	2.15	0.47
1:V:438:LEU:HD22	3:W:718:HOH:O	2.13	0.47
1:W:47:GLN:CG	1:W:48:TYR:H	2.28	0.47
1:W:293:ILE:HG12	1:W:294:ALA:H	1.80	0.47
1:W:528:LYS:CD	1:W:560:LEU:HD21	2.45	0.47
1:X:26:ARG:O	1:X:27:ARG:C	2.56	0.47
1:X:31:ASN:O	1:X:34:PHE:HB3	2.15	0.47
1:X:155:HIS:CE1	1:X:204:PRO:HB2	2.50	0.47
1:X:260:ASP:HA	1:X:264:ILE:HB	1.96	0.47
1:X:560:LEU:O	1:X:561:ASP:O	2.33	0.47
2:k:92:ALA:N	2:k:93:PRO:CD	2.78	0.47
2:o:65:ASN:O	2:o:67:PRO:HD3	2.15	0.47
2:t:128:TYR:CD1	2:t:132:MET:HG2	2.49	0.47
2:u:30:PRO:HD2	2:u:32:SER:HB3	1.97	0.47
2:u:64:GLU:OE1	2:u:64:GLU:HA	2.13	0.47
1:A:81:ARG:HB2	1:A:517:TYR:CZ	2.50	0.47
1:A:273:ARG:HH22	1:A:453:LEU:CD1	2.28	0.47
1:B:58:ASP:O	1:B:59:VAL:HB	2.14	0.47
1:B:162:SER:HB2	1:B:170:ALA:HB2	1.97	0.47
1:B:197:ASP:O	1:B:198:ILE:HB	2.15	0.47
1:B:451:ASP:O	1:B:456:ALA:N	2.41	0.47
1:B:535:ILE:CD1	1:B:554:LEU:HG	2.44	0.47
1:C:47:GLN:CD	1:C:47:GLN:N	2.72	0.47
1:C:57:PHE:CD2	1:C:330:ARG:CB	2.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:115:VAL:O	1:C:119:ILE:HG13	2.15	0.47
1:C:427:GLY:C	1:C:429:GLN:N	2.70	0.47
1:D:29:ALA:O	1:D:33:LEU:HG	2.15	0.47
1:D:57:PHE:CD2	1:D:330:ARG:CB	2.95	0.47
1:D:81:ARG:HB2	1:D:517:TYR:CZ	2.50	0.47
1:D:101:ASP:HB2	1:D:144:ILE:O	2.14	0.47
1:D:162:SER:HB2	1:D:170:ALA:HB2	1.97	0.47
1:D:329:LEU:HD22	2:b:142:PRO:HG2	1.96	0.47
1:D:378:ASP:HA	2:d:118:TYR:HD2	1.79	0.47
1:E:71:MSE:CE	1:E:115:VAL:HB	2.45	0.47
1:E:115:VAL:O	1:E:119:ILE:HG13	2.15	0.47
1:E:130:THR:HG22	1:E:144:ILE:HA	1.97	0.47
1:E:230:GLU:HG2	1:E:273:ARG:HB2	1.96	0.47
1:E:539:LEU:HD21	1:E:551:LEU:HB3	1.96	0.47
1:F:34:PHE:O	1:F:34:PHE:CD2	2.68	0.47
1:F:115:VAL:O	1:F:119:ILE:HG13	2.15	0.47
1:F:334:MSE:HE3	1:G:404:MSE:HE3	1.96	0.47
1:F:577:ILE:HG12	1:F:582:LYS:CG	2.41	0.47
1:G:86:ALA:HB2	1:G:515:GLU:HG3	1.96	0.47
1:G:115:VAL:O	1:G:119:ILE:HG13	2.15	0.47
1:G:162:SER:HB2	1:G:170:ALA:HB2	1.97	0.47
1:G:208:VAL:HG12	1:G:210:PRO:HD3	1.95	0.47
1:G:230:GLU:HG2	1:G:273:ARG:HB2	1.96	0.47
1:G:359:PHE:HD1	2:g:129:ILE:HD11	1.79	0.47
1:G:565:VAL:O	1:G:569:ARG:HB3	2.15	0.47
1:I:35:PHE:C	1:I:37:ARG:N	2.62	0.47
1:I:47:GLN:N	1:I:47:GLN:CD	2.72	0.47
1:I:130:THR:HG22	1:I:144:ILE:HA	1.97	0.47
1:I:162:SER:HB2	1:I:170:ALA:HB2	1.96	0.47
1:J:11:ILE:O	1:J:15:PHE:HB2	2.13	0.47
1:J:24:GLU:CD	1:J:24:GLU:N	2.71	0.47
1:J:49:THR:O	1:J:50:THR:C	2.56	0.47
1:J:130:THR:HG22	1:J:144:ILE:HA	1.97	0.47
1:J:535:ILE:CD1	1:J:554:LEU:HG	2.44	0.47
1:K:34:PHE:O	1:K:34:PHE:CD2	2.68	0.47
1:K:49:THR:O	1:K:50:THR:C	2.56	0.47
1:K:130:THR:HG22	1:K:144:ILE:HA	1.97	0.47
1:K:563:LYS:HD3	1:L:557:PHE:CE2	2.50	0.47
1:L:49:THR:O	1:L:50:THR:C	2.56	0.47
2:e:28:VAL:HG21	2:e:96:LEU:CG	2.40	0.47
2:j:39:PRO:HB2	2:j:40:GLN:H	1.51	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:47:GLN:CG	1:M:48:TYR:H	2.27	0.47
1:M:343:ARG:O	1:M:344:THR:HB	2.15	0.47
1:M:383:ASP:C	1:M:385:PRO:HD3	2.40	0.47
1:M:511:ARG:HA	1:M:513:ARG:CD	2.44	0.47
1:M:546:THR:CG2	1:M:547:PRO:HD3	2.31	0.47
1:P:293:ILE:HD13	1:P:294:ALA:N	2.30	0.47
1:Q:47:GLN:H	1:Q:48:TYR:HD2	1.62	0.47
1:Q:434:THR:HG23	1:Q:435:VAL:N	2.29	0.47
1:Q:598:GLN:HB2	1:Q:601:GLN:HB3	1.95	0.47
1:T:413:LYS:HA	1:T:416:ALA:HB3	1.96	0.47
1:T:554:LEU:O	1:T:557:PHE:HB3	2.15	0.47
1:V:47:GLN:N	1:V:48:TYR:HD2	2.13	0.47
1:V:273:ARG:CZ	1:V:275:ARG:HE	2.28	0.47
1:V:451:ASP:C	1:V:453:LEU:N	2.71	0.47
1:X:332:MSE:SE	2:p:132:MET:HA	2.65	0.47
2:m:80:VAL:C	2:m:82:ALA:N	2.73	0.47
1:A:142:GLN:O	1:A:143:VAL:HG23	2.13	0.47
1:B:130:THR:HG22	1:B:144:ILE:HA	1.97	0.47
1:C:92:ASP:OD2	1:C:92:ASP:N	2.48	0.47
1:C:535:ILE:CD1	1:C:554:LEU:HG	2.44	0.47
1:D:26:ARG:NH2	1:D:30:LYS:HB2	2.28	0.47
1:D:197:ASP:O	1:D:198:ILE:HB	2.15	0.47
1:E:81:ARG:HB2	1:E:517:TYR:CZ	2.50	0.47
1:E:197:ASP:O	1:E:198:ILE:HB	2.15	0.47
1:G:234:ILE:HG12	1:G:267:ALA:HB3	1.96	0.47
1:H:29:ALA:O	1:H:33:LEU:HG	2.15	0.47
1:H:81:ARG:HB2	1:H:517:TYR:CZ	2.50	0.47
1:H:273:ARG:HH22	1:H:453:LEU:CD1	2.28	0.47
1:I:29:ALA:O	1:I:33:LEU:HG	2.15	0.47
1:I:34:PHE:O	1:I:34:PHE:CD2	2.68	0.47
1:I:273:ARG:HH22	1:I:453:LEU:CD1	2.28	0.47
1:I:386:THR:CG2	1:I:389:LEU:HD21	2.44	0.47
1:J:47:GLN:N	1:J:47:GLN:CD	2.72	0.47
1:J:234:ILE:HG12	1:J:267:ALA:HB3	1.96	0.47
1:J:565:VAL:O	1:J:569:ARG:HB3	2.15	0.47
1:J:577:ILE:HG12	1:J:582:LYS:CG	2.41	0.47
2:b:28:VAL:HG21	2:b:96:LEU:CG	2.40	0.47
2:d:75:PRO:HA	2:d:76:PRO:HD3	1.42	0.47
2:g:156:HIS:C	2:g:158:PHE:H	2.23	0.47
1:M:38:VAL:HG21	1:M:324:LYS:HD2	1.97	0.47
1:M:232:ALA:HB2	1:M:269:ARG:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:273:ARG:CZ	1:M:275:ARG:HE	2.27	0.47
1:M:598:GLN:HB2	1:M:601:GLN:HB3	1.96	0.47
1:N:71:MSE:HE3	1:N:115:VAL:HB	1.97	0.47
1:O:9:GLU:HG3	1:O:12:LEU:H	1.78	0.47
1:O:160:SER:O	1:O:161:ASN:ND2	2.44	0.47
1:O:568:MSE:SE	1:P:550:GLN:HB3	2.65	0.47
1:P:155:HIS:CE1	1:P:204:PRO:HB2	2.50	0.47
1:P:383:ASP:C	1:P:385:PRO:HD3	2.40	0.47
1:P:434:THR:HG23	1:P:435:VAL:N	2.29	0.47
3:P:719:HOH:O	1:Q:430:VAL:HG13	2.13	0.47
1:Q:444:LEU:O	1:Q:446:THR:N	2.47	0.47
1:R:171:ARG:O	1:R:224:GLU:HA	2.14	0.47
1:R:227:GLU:O	1:R:227:GLU:CG	2.63	0.47
1:R:293:ILE:HG12	1:R:294:ALA:H	1.80	0.47
1:S:444:LEU:O	1:S:448:VAL:HG23	2.15	0.47
1:S:528:LYS:CD	1:S:560:LEU:HD21	2.45	0.47
1:S:554:LEU:O	1:S:557:PHE:HB3	2.14	0.47
1:T:158:TRP:HH2	1:T:302:PRO:HG3	1.80	0.47
1:U:76:ILE:HD12	1:U:433:ASP:OD1	2.15	0.47
1:U:78:VAL:CG1	1:U:444:LEU:HG	2.44	0.47
1:U:123:VAL:HG13	1:U:304:PHE:CE1	2.50	0.47
1:U:273:ARG:CZ	1:U:275:ARG:HE	2.28	0.47
1:W:322:LEU:HD22	1:W:322:LEU:N	2.30	0.47
2:l:8:ASP:CB	2:m:67:PRO:HG2	2.44	0.47
2:n:30:PRO:HB2	2:n:31:GLN:H	1.58	0.47
2:o:43:MET:C	2:o:45:ALA:H	2.22	0.47
2:s:30:PRO:HD2	2:s:32:SER:HB3	1.96	0.47
2:v:33:MET:HE3	2:v:33:MET:HB3	1.65	0.47
1:A:101:ASP:HB2	1:A:144:ILE:O	2.14	0.47
1:A:248:LYS:HZ1	1:A:513:ARG:HH12	1.62	0.47
1:B:115:VAL:O	1:B:119:ILE:HG13	2.15	0.47
1:B:248:LYS:HB3	1:B:511:ARG:NH1	2.30	0.47
1:C:230:GLU:HG2	1:C:273:ARG:HB2	1.96	0.47
1:D:535:ILE:CD1	1:D:554:LEU:HG	2.44	0.47
1:E:49:THR:O	1:E:50:THR:C	2.56	0.47
1:F:539:LEU:HD21	1:F:551:LEU:CB	2.44	0.47
1:G:49:THR:O	1:G:50:THR:C	2.56	0.47
1:G:539:LEU:HD21	1:G:551:LEU:HB3	1.96	0.47
1:H:164:LEU:HA	1:H:307:TRP:HH2	1.80	0.47
1:H:535:ILE:CD1	1:H:554:LEU:HG	2.44	0.47
1:K:162:SER:HB2	1:K:170:ALA:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:201:PHE:HE2	1:K:281:ILE:HG22	1.80	0.47
1:L:34:PHE:O	1:L:34:PHE:CD2	2.68	0.47
1:L:227:GLU:OE2	1:L:227:GLU:N	2.47	0.47
2:e:156:HIS:C	2:e:158:PHE:H	2.23	0.47
1:M:55:GLY:HA3	1:M:57:PHE:CE1	2.49	0.47
1:N:78:VAL:CG1	1:N:79:LEU:N	2.75	0.47
1:Q:444:LEU:HD13	1:Q:444:LEU:N	2.30	0.47
1:R:293:ILE:HD13	1:R:294:ALA:N	2.29	0.47
1:R:560:LEU:O	1:R:561:ASP:O	2.32	0.47
1:S:38:VAL:HG21	1:S:324:LYS:HD2	1.97	0.47
1:S:41:TRP:HE1	1:T:27:ARG:NH2	2.13	0.47
1:S:86:ALA:CB	1:S:515:GLU:HG3	2.45	0.47
1:S:238:PRO:HD3	1:S:263:PHE:HB2	1.97	0.47
1:S:383:ASP:C	1:S:385:PRO:HD3	2.40	0.47
1:S:577:ILE:HG12	1:S:582:LYS:CG	2.43	0.47
1:T:37:ARG:HH21	1:T:37:ARG:CB	2.28	0.47
1:T:235:TYR:OH	1:T:252:LYS:NZ	2.48	0.47
1:T:266:ILE:O	1:T:267:ALA:HB2	2.16	0.47
1:U:235:TYR:OH	1:U:252:LYS:NZ	2.48	0.47
1:U:384:LEU:HD22	1:U:384:LEU:N	2.29	0.47
1:U:557:PHE:CE2	1:X:563:LYS:HD3	2.49	0.47
1:V:364:ASP:CG	2:k:126:ALA:HB2	2.39	0.47
1:V:409:THR:O	1:V:413:LYS:HG2	2.15	0.47
1:W:118:GLN:OE1	1:W:303:VAL:HB	2.14	0.47
1:W:193:LEU:HD22	1:W:287:LEU:HB3	1.97	0.47
1:W:343:ARG:O	1:W:344:THR:HB	2.15	0.47
1:W:451:ASP:C	1:W:453:LEU:N	2.70	0.47
1:X:227:GLU:CG	1:X:227:GLU:O	2.63	0.47
1:A:248:LYS:HB3	1:A:511:ARG:NH1	2.30	0.47
1:B:81:ARG:HB2	1:B:517:TYR:CZ	2.50	0.47
1:B:227:GLU:OE2	1:B:227:GLU:N	2.47	0.47
1:B:565:VAL:O	1:B:569:ARG:HB3	2.15	0.47
1:C:35:PHE:HE1	1:C:321:ARG:NH1	2.13	0.47
1:C:451:ASP:O	1:C:456:ALA:N	2.41	0.47
1:C:539:LEU:HD21	1:C:551:LEU:HB3	1.96	0.47
1:D:130:THR:HG22	1:D:144:ILE:HA	1.97	0.47
1:D:165:MSE:HG3	1:D:307:TRP:CD2	2.49	0.47
1:D:542:THR:HG21	1:E:556:TYR:OH	2.15	0.47
1:E:24:GLU:C	1:E:26:ARG:N	2.73	0.47
1:E:57:PHE:CD2	1:E:330:ARG:CB	2.95	0.47
1:E:58:ASP:O	1:E:59:VAL:HB	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:248:LYS:HB3	1:E:511:ARG:NH1	2.30	0.47
1:F:92:ASP:OD2	1:F:92:ASP:N	2.48	0.47
1:F:273:ARG:HH22	1:F:453:LEU:CD1	2.28	0.47
1:F:539:LEU:HD21	1:F:551:LEU:HB3	1.96	0.47
1:H:201:PHE:HE2	1:H:281:ILE:HG22	1.80	0.47
1:I:164:LEU:HA	1:I:307:TRP:HH2	1.80	0.47
1:I:383:ASP:C	1:I:385:PRO:HD3	2.39	0.47
1:J:28:GLU:HG3	1:J:32:ASP:OD2	2.15	0.47
1:J:29:ALA:O	1:J:33:LEU:HG	2.15	0.47
1:J:86:ALA:HB2	1:J:515:GLU:HG3	1.96	0.47
1:K:115:VAL:O	1:K:119:ILE:HG13	2.15	0.47
1:K:426:ASN:O	1:K:427:GLY:C	2.58	0.47
2:g:28:VAL:HG21	2:g:96:LEU:CG	2.40	0.47
1:M:78:VAL:CG1	1:M:444:LEU:HG	2.45	0.46
1:M:198:ILE:O	1:M:198:ILE:HG22	2.14	0.46
1:M:260:ASP:HA	1:M:264:ILE:HB	1.98	0.46
1:N:165:MSE:HG3	1:N:307:TRP:CD2	2.49	0.46
1:N:198:ILE:O	1:N:198:ILE:HG22	2.15	0.46
1:N:348:LYS:HE2	1:V:369:TYR:O	2.15	0.46
1:O:598:GLN:HB2	1:O:601:GLN:HB3	1.95	0.46
1:P:27:ARG:HB2	1:P:313:LYS:HE3	1.96	0.46
1:P:47:GLN:N	1:P:48:TYR:HD2	2.13	0.46
1:R:47:GLN:N	1:R:48:TYR:HD2	2.13	0.46
1:R:273:ARG:CZ	1:R:275:ARG:HE	2.28	0.46
1:R:343:ARG:O	1:R:344:THR:HB	2.15	0.46
1:S:78:VAL:CG1	1:S:444:LEU:HG	2.45	0.46
1:T:260:ASP:HA	1:T:264:ILE:HB	1.96	0.46
1:U:24:GLU:CD	1:U:24:GLU:N	2.73	0.46
1:U:80:TYR:OH	1:U:444:LEU:HD12	2.15	0.46
1:U:82:PRO:O	1:U:516:CYS:HA	2.15	0.46
1:U:86:ALA:CB	1:U:515:GLU:HG3	2.45	0.46
1:U:95:MSE:HE1	1:U:99:ARG:CZ	2.44	0.46
1:U:405:LEU:O	1:U:409:THR:HG23	2.15	0.46
1:W:123:VAL:CG1	1:W:304:PHE:CE1	2.98	0.46
2:k:30:PRO:HB2	2:k:31:GLN:H	1.58	0.46
2:l:30:PRO:HB2	2:l:31:GLN:H	1.57	0.46
2:p:95:TYR:N	2:p:95:TYR:CD1	2.81	0.46
1:A:29:ALA:O	1:A:33:LEU:HG	2.15	0.46
1:B:94:LEU:HA	1:B:97:MSE:CE	2.37	0.46
1:B:376:ARG:HB2	1:C:352:TRP:CG	2.50	0.46
1:C:395:PRO:HD2	1:E:398:PRO:HB3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:47:GLN:N	1:D:47:GLN:CD	2.72	0.46
1:D:71:MSE:CE	1:D:115:VAL:HB	2.45	0.46
1:D:86:ALA:HB2	1:D:515:GLU:HG3	1.96	0.46
1:D:92:ASP:OD2	1:D:92:ASP:N	2.48	0.46
1:D:115:VAL:O	1:D:119:ILE:HG13	2.15	0.46
1:F:197:ASP:O	1:F:198:ILE:HB	2.15	0.46
1:G:386:THR:CG2	1:G:389:LEU:HD21	2.44	0.46
1:H:86:ALA:HB2	1:H:515:GLU:HG3	1.96	0.46
1:H:92:ASP:OD2	1:H:92:ASP:N	2.48	0.46
1:H:248:LYS:HB3	1:H:511:ARG:NH1	2.30	0.46
1:H:539:LEU:HD21	1:H:551:LEU:HB3	1.96	0.46
1:I:539:LEU:HD21	1:I:551:LEU:HB3	1.96	0.46
1:I:565:VAL:O	1:I:569:ARG:HB3	2.15	0.46
1:J:58:ASP:O	1:J:59:VAL:HB	2.14	0.46
1:J:92:ASP:OD2	1:J:92:ASP:N	2.48	0.46
1:J:359:PHE:HD1	2:j:129:ILE:HD11	1.80	0.46
1:K:230:GLU:HG2	1:K:273:ARG:HB2	1.96	0.46
1:L:201:PHE:HE2	1:L:281:ILE:HG22	1.80	0.46
1:L:577:ILE:HG12	1:L:582:LYS:CG	2.41	0.46
2:Y:43:GLN:C	2:Y:45:ALA:N	2.70	0.46
1:M:26:ARG:O	1:M:27:ARG:C	2.58	0.46
1:M:127:ARG:HG2	1:M:147:GLU:HB2	1.96	0.46
1:M:193:LEU:HD22	1:M:287:LEU:HB3	1.97	0.46
1:M:293:ILE:HD13	1:M:294:ALA:N	2.31	0.46
1:M:560:LEU:O	1:M:561:ASP:O	2.33	0.46
1:N:171:ARG:O	1:N:224:GLU:HA	2.15	0.46
1:O:322:LEU:HD22	1:O:322:LEU:H	1.79	0.46
1:O:343:ARG:HD3	2:l:128:TYR:CE1	2.50	0.46
1:O:395:PRO:HD2	1:P:398:PRO:HB3	1.96	0.46
1:O:560:LEU:O	1:O:561:ASP:O	2.33	0.46
1:P:343:ARG:O	1:P:344:THR:HB	2.14	0.46
1:P:598:GLN:HB2	1:P:601:GLN:HB3	1.95	0.46
1:R:47:GLN:H	1:R:48:TYR:HD2	1.62	0.46
1:R:82:PRO:O	1:R:516:CYS:HA	2.15	0.46
1:R:413:LYS:HA	1:R:416:ALA:HB3	1.96	0.46
1:R:420:VAL:HA	1:R:428:GLY:HA2	1.98	0.46
1:R:564:GLY:CA	1:X:554:LEU:HD21	2.42	0.46
1:T:47:GLN:CG	1:T:48:TYR:H	2.27	0.46
1:T:47:GLN:H	1:T:48:TYR:HD2	1.64	0.46
1:U:71:MSE:HE3	1:U:115:VAL:HB	1.96	0.46
1:U:542:THR:HG21	1:X:556:TYR:OH	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:54:ARG:HB2	2:v:137:GLY:HA3	1.97	0.46
1:X:165:MSE:HG3	1:X:307:TRP:CD2	2.49	0.46
1:X:378:ASP:O	1:X:381:SER:O	2.33	0.46
1:X:434:THR:HG23	1:X:435:VAL:N	2.30	0.46
2:l:65:ASN:O	2:l:67:PRO:HD3	2.14	0.46
2:l:96:ALA:HB2	2:n:25:LEU:HD13	1.97	0.46
2:n:47:TRP:N	2:n:47:TRP:CD1	2.82	0.46
2:p:110:GLY:O	2:p:114:LEU:HD13	2.14	0.46
1:A:201:PHE:HE2	1:A:281:ILE:HG22	1.80	0.46
1:A:539:LEU:HD21	1:A:551:LEU:CB	2.44	0.46
1:B:230:GLU:HG2	1:B:273:ARG:HB2	1.96	0.46
1:C:86:ALA:HB2	1:C:515:GLU:HG3	1.96	0.46
1:C:162:SER:HB2	1:C:170:ALA:HB2	1.97	0.46
1:D:34:PHE:O	1:D:34:PHE:CD2	2.68	0.46
1:D:317:GLU:HB3	1:D:321:ARG:CZ	2.46	0.46
1:D:343:ARG:NH1	2:e:135:ALA:O	2.39	0.46
1:D:438:LEU:HD22	3:E:719:HOH:O	2.15	0.46
1:D:539:LEU:HD21	1:D:551:LEU:CB	2.44	0.46
1:E:565:VAL:O	1:E:569:ARG:HB3	2.15	0.46
1:F:376:ARG:HB2	1:G:352:TRP:CD2	2.50	0.46
1:G:34:PHE:O	1:G:34:PHE:CD2	2.68	0.46
1:G:164:LEU:HA	1:G:307:TRP:HH2	1.80	0.46
1:G:273:ARG:HH22	1:G:453:LEU:CD1	2.28	0.46
1:G:317:GLU:HB3	1:G:321:ARG:CZ	2.46	0.46
1:G:413:LYS:HE2	1:G:413:LYS:HB3	1.74	0.46
1:H:565:VAL:O	1:H:569:ARG:HB3	2.15	0.46
1:H:567:MSE:HE2	1:I:554:LEU:HD22	1.96	0.46
1:I:343:ARG:H	1:I:343:ARG:HG2	1.52	0.46
1:I:539:LEU:HD21	1:I:551:LEU:CB	2.44	0.46
1:J:227:GLU:HA	1:J:274:ARG:CA	2.44	0.46
1:J:317:GLU:HB3	1:J:321:ARG:CZ	2.46	0.46
1:J:343:ARG:H	1:J:343:ARG:HG2	1.52	0.46
1:K:53:TYR:HA	2:h:147:ASN:HD21	1.80	0.46
1:K:434:THR:HA	1:K:437:GLN:HG2	1.97	0.46
1:L:426:ASN:O	1:L:427:GLY:C	2.58	0.46
2:a:43:GLN:C	2:a:45:ALA:N	2.70	0.46
2:b:28:VAL:HG11	2:b:97:ALA:HA	1.88	0.46
2:g:28:VAL:CB	2:g:96:LEU:HD13	2.45	0.46
2:g:140:ARG:O	2:g:141:MET:HB3	2.16	0.46
2:i:28:VAL:CB	2:i:96:LEU:HD13	2.45	0.46
1:M:158:TRP:HD1	1:M:158:TRP:H	1.61	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:510:ILE:O	1:M:513:ARG:HD2	2.15	0.46
1:N:26:ARG:HG2	1:V:212:LEU:HD22	1.98	0.46
1:N:238:PRO:HD3	1:N:263:PHE:HB2	1.97	0.46
1:O:127:ARG:HG2	1:O:147:GLU:HB2	1.96	0.46
1:O:238:PRO:HD3	1:O:263:PHE:HB2	1.96	0.46
1:P:322:LEU:HD22	1:P:322:LEU:N	2.29	0.46
1:Q:127:ARG:HG2	1:Q:147:GLU:HB2	1.96	0.46
1:Q:174:THR:N	3:Q:705:HOH:O	2.47	0.46
1:Q:560:LEU:HD13	1:R:82:PRO:CD	2.22	0.46
1:R:95:MSE:HE1	1:R:99:ARG:NH2	2.31	0.46
1:R:510:ILE:O	1:R:513:ARG:HD2	2.15	0.46
1:T:164:LEU:HA	1:T:307:TRP:CH2	2.51	0.46
1:T:165:MSE:HG3	1:T:307:TRP:CD2	2.49	0.46
1:T:383:ASP:C	1:T:385:PRO:HD3	2.40	0.46
1:T:387:GLN:H	1:T:387:GLN:HG2	1.57	0.46
1:T:429:GLN:O	1:T:429:GLN:HG2	2.15	0.46
1:U:33:LEU:HD12	1:U:34:PHE:N	2.30	0.46
1:U:165:MSE:HG3	1:U:307:TRP:CD2	2.50	0.46
1:U:260:ASP:HA	1:U:264:ILE:HB	1.97	0.46
1:V:78:VAL:CG1	1:V:444:LEU:HG	2.45	0.46
1:V:280:ILE:HG22	1:V:287:LEU:HD13	1.97	0.46
1:V:378:ASP:O	1:V:381:SER:O	2.34	0.46
1:V:418:LEU:HB2	1:V:428:GLY:O	2.15	0.46
1:W:227:GLU:CG	1:W:227:GLU:O	2.63	0.46
1:X:41:TRP:HE3	1:X:42:ASP:HB3	1.81	0.46
1:X:273:ARG:CZ	1:X:275:ARG:HE	2.28	0.46
1:X:546:THR:CG2	1:X:547:PRO:HD3	2.30	0.46
2:q:33:MET:HE3	2:q:33:MET:HB3	1.68	0.46
1:A:162:SER:HB2	1:A:170:ALA:HB2	1.96	0.46
1:A:164:LEU:HA	1:A:307:TRP:HH2	1.80	0.46
1:A:227:GLU:HA	1:A:274:ARG:CA	2.44	0.46
1:B:139:SER:CB	1:B:455:THR:CG2	2.80	0.46
1:B:539:LEU:HD21	1:B:551:LEU:CB	2.44	0.46
1:C:28:GLU:HG3	1:C:32:ASP:OD2	2.15	0.46
1:C:29:ALA:O	1:C:33:LEU:HG	2.15	0.46
1:C:34:PHE:O	1:C:34:PHE:CD2	2.68	0.46
1:C:539:LEU:HD21	1:C:551:LEU:CB	2.44	0.46
1:D:426:ASN:O	1:D:427:GLY:C	2.58	0.46
1:D:444:LEU:HD13	1:D:444:LEU:N	2.31	0.46
1:E:273:ARG:HH22	1:E:453:LEU:CD1	2.28	0.46
1:E:410:SER:O	1:E:414:GLU:HG2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:162:SER:HB2	1:F:170:ALA:HB2	1.96	0.46
1:F:565:VAL:O	1:F:569:ARG:HB3	2.15	0.46
1:H:28:GLU:HG3	1:H:32:ASP:OD2	2.15	0.46
1:H:359:PHE:HD1	2:i:129:ILE:HD11	1.80	0.46
1:H:444:LEU:HD13	1:H:444:LEU:N	2.31	0.46
1:I:71:MSE:CE	1:I:115:VAL:HB	2.45	0.46
1:I:376:ARG:HB2	1:J:352:TRP:CG	2.51	0.46
1:I:410:SER:O	1:I:414:GLU:HG2	2.16	0.46
1:J:197:ASP:O	1:J:198:ILE:HB	2.15	0.46
1:J:273:ARG:HH22	1:J:453:LEU:CD1	2.28	0.46
1:J:410:SER:O	1:J:414:GLU:HG2	2.16	0.46
1:J:539:LEU:HD21	1:J:551:LEU:HB3	1.96	0.46
1:K:28:GLU:HG3	1:K:32:ASP:OD2	2.15	0.46
1:K:29:ALA:O	1:K:33:LEU:HG	2.15	0.46
1:K:81:ARG:HB2	1:K:517:TYR:CZ	2.50	0.46
1:K:92:ASP:OD2	1:K:92:ASP:N	2.48	0.46
1:K:234:ILE:HG12	1:K:267:ALA:HB3	1.96	0.46
2:Z:140:ARG:O	2:Z:141:MET:HB3	2.16	0.46
2:c:140:ARG:O	2:c:141:MET:HB3	2.16	0.46
2:d:156:HIS:C	2:d:158:PHE:H	2.23	0.46
2:e:75:PRO:HA	2:e:76:PRO:HD3	1.42	0.46
1:O:164:LEU:HD22	1:O:169:ASP:OD1	2.15	0.46
1:P:164:LEU:HA	1:P:307:TRP:CH2	2.51	0.46
1:P:409:THR:O	1:P:413:LYS:HG2	2.15	0.46
1:Q:316:TYR:O	1:Q:321:ARG:NH1	2.49	0.46
1:R:444:LEU:O	1:R:445:GLU:C	2.58	0.46
1:S:33:LEU:HD12	1:S:34:PHE:N	2.31	0.46
3:S:719:HOH:O	1:T:430:VAL:HG11	2.15	0.46
1:T:80:TYR:OH	1:T:444:LEU:HD12	2.16	0.46
1:T:86:ALA:CB	1:T:515:GLU:HG3	2.45	0.46
1:T:227:GLU:O	1:T:227:GLU:CG	2.63	0.46
1:T:330:ARG:O	1:T:334:MSE:HB2	2.16	0.46
1:T:577:ILE:HG12	1:T:582:LYS:CG	2.45	0.46
3:T:718:HOH:O	1:W:438:LEU:HD22	2.15	0.46
1:U:238:PRO:HD3	1:U:263:PHE:HB2	1.98	0.46
1:U:322:LEU:HD22	1:U:322:LEU:H	1.80	0.46
1:V:47:GLN:CG	1:V:48:TYR:H	2.28	0.46
1:V:560:LEU:O	1:V:561:ASP:O	2.33	0.46
1:W:47:GLN:N	1:W:48:TYR:HD2	2.14	0.46
1:W:198:ILE:HG22	1:W:198:ILE:O	2.14	0.46
1:W:409:THR:O	1:W:413:LYS:HG2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:193:LEU:HD22	1:X:287:LEU:HB3	1.97	0.46
1:X:427:GLY:C	1:X:429:GLN:N	2.74	0.46
2:s:65:ASN:O	2:s:67:PRO:HD3	2.15	0.46
1:A:230:GLU:HG2	1:A:273:ARG:HB2	1.96	0.46
1:A:238:PRO:HG3	1:A:263:PHE:CB	2.46	0.46
1:A:539:LEU:HD21	1:A:551:LEU:HB3	1.96	0.46
1:A:565:VAL:O	1:A:569:ARG:HB3	2.15	0.46
1:B:48:TYR:O	1:B:49:THR:CB	2.64	0.46
1:B:227:GLU:HA	1:B:274:ARG:CA	2.44	0.46
1:C:26:ARG:NH2	1:C:30:LYS:HB2	2.28	0.46
1:C:273:ARG:HH22	1:C:453:LEU:CD1	2.28	0.46
1:D:49:THR:O	1:D:50:THR:C	2.56	0.46
1:D:248:LYS:HB3	1:D:511:ARG:NH1	2.30	0.46
1:E:28:GLU:HG3	1:E:32:ASP:OD2	2.15	0.46
1:E:101:ASP:HB2	1:E:144:ILE:O	2.14	0.46
1:E:434:THR:HA	1:E:437:GLN:HG2	1.98	0.46
1:E:444:LEU:HD13	1:E:444:LEU:N	2.31	0.46
1:F:219:ILE:HD12	1:F:281:ILE:O	2.16	0.46
1:G:71:MSE:CE	1:G:115:VAL:HB	2.45	0.46
1:G:410:SER:O	1:G:414:GLU:HG2	2.16	0.46
1:H:71:MSE:CE	1:H:115:VAL:HB	2.45	0.46
1:H:115:VAL:O	1:H:119:ILE:HG13	2.15	0.46
1:H:230:GLU:HG2	1:H:273:ARG:HB2	1.96	0.46
1:I:77:ASP:HB2	1:I:523:SER:HB2	1.98	0.46
1:I:317:GLU:HB3	1:I:321:ARG:CZ	2.46	0.46
1:J:78:VAL:CG2	1:J:444:LEU:HD21	2.46	0.46
1:K:191:TYR:HE1	1:K:278:LYS:HZ3	1.63	0.46
1:K:248:LYS:HB3	1:K:511:ARG:NH1	2.30	0.46
1:L:162:SER:HB2	1:L:170:ALA:HB2	1.96	0.46
1:L:248:LYS:HB3	1:L:511:ARG:NH1	2.30	0.46
1:L:273:ARG:HH22	1:L:453:LEU:CD1	2.28	0.46
1:L:565:VAL:O	1:L:569:ARG:HB3	2.15	0.46
2:Y:156:HIS:C	2:Y:158:PHE:H	2.23	0.46
2:Z:156:HIS:C	2:Z:158:PHE:H	2.23	0.46
2:c:156:HIS:C	2:c:158:PHE:H	2.23	0.46
2:d:140:ARG:O	2:d:141:MET:HB3	2.16	0.46
2:h:140:ARG:O	2:h:141:MET:HB3	2.16	0.46
2:h:156:HIS:C	2:h:158:PHE:H	2.23	0.46
1:M:80:TYR:OH	1:M:444:LEU:HD12	2.16	0.46
1:N:29:ALA:O	1:N:33:LEU:HG	2.16	0.46
1:N:47:GLN:N	1:N:48:TYR:HD2	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:86:ALA:CB	1:N:515:GLU:HG3	2.44	0.46
1:N:193:LEU:HD22	1:N:287:LEU:HB3	1.97	0.46
1:N:262:GLY:O	1:N:263:PHE:HB3	2.14	0.46
1:N:560:LEU:O	1:N:561:ASP:O	2.33	0.46
1:O:66:LYS:HZ3	1:O:420:VAL:HG21	1.80	0.46
1:O:108:LYS:HD2	1:P:438:LEU:HD11	1.97	0.46
1:O:198:ILE:O	1:O:198:ILE:HG22	2.14	0.46
1:P:165:MSE:HG3	1:P:307:TRP:CD2	2.50	0.46
1:P:387:GLN:HB2	1:Q:390:ALA:HB2	1.98	0.46
1:P:556:TYR:OH	1:Q:542:THR:HG21	2.15	0.46
1:R:144:ILE:HD12	1:R:145:ARG:N	2.30	0.46
1:R:422:THR:HG22	1:R:423:GLU:N	2.31	0.46
1:S:24:GLU:N	1:S:24:GLU:CD	2.74	0.46
1:S:31:ASN:O	1:S:34:PHE:HB3	2.15	0.46
1:S:348:LYS:HB2	1:U:372:TYR:CE2	2.50	0.46
1:T:78:VAL:CG1	1:T:444:LEU:HG	2.45	0.46
1:T:82:PRO:O	1:T:516:CYS:HA	2.15	0.46
1:T:238:PRO:HD3	1:T:263:PHE:HB2	1.96	0.46
1:T:387:GLN:CB	1:W:390:ALA:HB2	2.46	0.46
1:U:293:ILE:HD13	1:U:294:ALA:N	2.30	0.46
1:U:438:LEU:HD22	3:X:718:HOH:O	2.15	0.46
1:U:554:LEU:O	1:U:557:PHE:HB3	2.15	0.46
1:V:193:LEU:HD22	1:V:287:LEU:HB3	1.98	0.46
1:V:343:ARG:HD3	2:v:128:TYR:CE1	2.50	0.46
1:W:47:GLN:H	1:W:48:TYR:HD2	1.63	0.46
1:W:100:THR:HG22	1:W:138:THR:HG22	1.96	0.46
1:W:232:ALA:HB2	1:W:269:ARG:O	2.15	0.46
1:W:422:THR:HG22	1:W:423:GLU:N	2.31	0.46
1:W:554:LEU:O	1:W:557:PHE:HB3	2.16	0.46
1:W:560:LEU:O	1:W:561:ASP:O	2.32	0.46
1:X:293:ILE:HG12	1:X:294:ALA:H	1.81	0.46
2:m:30:PRO:HD2	2:m:32:SER:HB3	1.96	0.46
1:A:34:PHE:HE1	1:A:324:LYS:HZ2	1.52	0.46
1:A:35:PHE:HE1	1:A:321:ARG:NH1	2.13	0.46
1:A:219:ILE:HD12	1:A:281:ILE:O	2.16	0.46
1:B:28:GLU:HG3	1:B:32:ASP:OD2	2.15	0.46
1:B:71:MSE:CE	1:B:115:VAL:HB	2.45	0.46
1:B:92:ASP:OD2	1:B:92:ASP:N	2.48	0.46
1:B:201:PHE:HE2	1:B:281:ILE:HG22	1.80	0.46
1:C:248:LYS:HB3	1:C:511:ARG:NH1	2.30	0.46
1:D:219:ILE:HD12	1:D:281:ILE:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:343:ARG:NH2	2:e:134:ARG:HD3	2.30	0.46
1:D:557:PHE:CE2	1:E:563:LYS:HD3	2.50	0.46
1:E:92:ASP:OD2	1:E:92:ASP:N	2.48	0.46
1:E:426:ASN:O	1:E:427:GLY:C	2.59	0.46
1:F:71:MSE:CE	1:F:115:VAL:HB	2.45	0.46
1:F:234:ILE:HG12	1:F:267:ALA:HB3	1.96	0.46
1:G:426:ASN:O	1:G:427:GLY:C	2.59	0.46
1:G:535:ILE:CD1	1:G:554:LEU:HG	2.44	0.46
1:H:234:ILE:HG22	1:H:246:TYR:HB3	1.98	0.46
1:I:81:ARG:HB2	1:I:517:TYR:CZ	2.50	0.46
1:I:328:ARG:HB3	2:f:142:PRO:HG3	1.97	0.46
1:J:77:ASP:HB2	1:J:523:SER:HB2	1.98	0.46
1:J:115:VAL:O	1:J:119:ILE:HG13	2.15	0.46
1:J:162:SER:HB2	1:J:170:ALA:HB2	1.97	0.46
1:J:273:ARG:O	1:J:274:ARG:CB	2.64	0.46
1:K:164:LEU:HA	1:K:307:TRP:HH2	1.80	0.46
1:L:28:GLU:HG3	1:L:32:ASP:OD2	2.15	0.46
1:L:47:GLN:N	1:L:47:GLN:CD	2.72	0.46
1:L:427:GLY:C	1:L:429:GLN:N	2.70	0.46
2:Y:28:VAL:CB	2:Y:96:LEU:HD13	2.45	0.46
2:Z:28:VAL:CB	2:Z:96:LEU:HD13	2.45	0.46
2:h:90:SER:OG	2:i:51:ALA:HB1	2.15	0.46
1:M:34:PHE:CE2	1:M:45:LEU:HG	2.46	0.46
1:M:378:ASP:O	1:M:381:SER:O	2.34	0.46
1:M:409:THR:O	1:M:413:LYS:HG2	2.16	0.46
1:M:528:LYS:CD	1:M:560:LEU:HD21	2.46	0.46
1:N:71:MSE:CE	1:N:115:VAL:HB	2.46	0.46
1:O:29:ALA:O	1:O:33:LEU:HG	2.16	0.46
1:O:528:LYS:CD	1:O:560:LEU:HD21	2.46	0.46
1:P:47:GLN:CG	1:P:48:TYR:H	2.26	0.46
1:Q:24:GLU:N	1:Q:24:GLU:CD	2.74	0.46
1:Q:71:MSE:CE	1:Q:115:VAL:HB	2.46	0.46
1:Q:293:ILE:HG12	1:Q:294:ALA:H	1.81	0.46
1:S:41:TRP:HE3	1:S:42:ASP:HB3	1.81	0.46
1:S:390:ALA:HB2	1:U:387:GLN:HB2	1.98	0.46
1:S:429:GLN:O	1:S:429:GLN:HG2	2.16	0.46
1:S:444:LEU:O	1:S:445:GLU:C	2.57	0.46
1:V:82:PRO:O	1:V:516:CYS:HA	2.16	0.46
1:V:164:LEU:HA	1:V:307:TRP:HH2	1.79	0.46
1:W:266:ILE:O	1:W:267:ALA:HB2	2.15	0.46
1:W:429:GLN:HG2	1:W:429:GLN:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:573:ASN:O	1:W:577:ILE:HG13	2.16	0.46
1:W:577:ILE:HG12	1:W:582:LYS:CG	2.44	0.46
1:X:123:VAL:HG22	1:X:316:TYR:HE2	1.81	0.46
1:X:528:LYS:CD	1:X:560:LEU:HD21	2.46	0.46
1:A:227:GLU:OE2	1:A:227:GLU:N	2.47	0.46
1:A:426:ASN:O	1:A:427:GLY:C	2.58	0.46
1:B:24:GLU:CD	1:B:24:GLU:N	2.71	0.46
1:B:359:PHE:HD1	2:b:129:ILE:HD11	1.81	0.46
1:C:34:PHE:HE1	1:C:324:LYS:HZ2	1.54	0.46
1:D:24:GLU:C	1:D:26:ARG:N	2.73	0.46
1:E:164:LEU:HA	1:E:307:TRP:CH2	2.51	0.46
1:E:317:GLU:HB3	1:E:321:ARG:CZ	2.46	0.46
1:E:378:ASP:HA	2:c:118:TYR:HD2	1.80	0.46
1:F:28:GLU:HG3	1:F:32:ASP:OD2	2.15	0.46
1:F:32:ASP:CG	1:F:316:TYR:CE2	2.94	0.46
1:F:201:PHE:HE2	1:F:281:ILE:HG22	1.80	0.46
1:F:273:ARG:O	1:F:274:ARG:CB	2.64	0.46
1:G:248:LYS:HB3	1:G:511:ARG:NH1	2.30	0.46
1:H:162:SER:HB2	1:H:170:ALA:HB2	1.97	0.46
1:H:198:ILE:HA	1:H:199:PRO:HD3	1.64	0.46
1:I:26:ARG:NH2	1:I:30:LYS:HB2	2.28	0.46
1:I:234:ILE:HG12	1:I:267:ALA:HB3	1.96	0.46
1:I:248:LYS:HB3	1:I:511:ARG:NH1	2.30	0.46
1:J:32:ASP:CG	1:J:316:TYR:CE2	2.94	0.46
1:J:434:THR:HA	1:J:437:GLN:HG2	1.98	0.46
1:K:77:ASP:HB2	1:K:523:SER:HB2	1.98	0.46
1:K:219:ILE:HD12	1:K:281:ILE:O	2.16	0.46
1:L:219:ILE:HD12	1:L:281:ILE:O	2.16	0.46
1:L:234:ILE:HG12	1:L:267:ALA:HB3	1.96	0.46
2:f:28:VAL:CB	2:f:96:LEU:HD13	2.45	0.46
1:M:47:GLN:N	1:M:48:TYR:HD2	2.14	0.46
1:M:86:ALA:CB	1:M:515:GLU:HG3	2.45	0.46
1:M:535:ILE:HD11	1:N:564:GLY:HA3	1.98	0.46
1:M:554:LEU:O	1:M:557:PHE:HB3	2.15	0.46
1:N:434:THR:HG23	1:N:435:VAL:N	2.30	0.46
1:O:47:GLN:CG	1:O:48:TYR:H	2.28	0.46
1:P:387:GLN:CB	1:Q:390:ALA:CB	2.94	0.46
1:Q:71:MSE:HE3	1:Q:115:VAL:HB	1.97	0.46
1:Q:444:LEU:O	1:Q:445:GLU:C	2.58	0.46
1:Q:528:LYS:CD	1:Q:560:LEU:HD21	2.46	0.46
1:R:24:GLU:CD	1:R:24:GLU:N	2.74	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:280:ILE:HD12	1:R:280:ILE:N	2.31	0.46
1:S:171:ARG:O	1:S:224:GLU:HA	2.15	0.46
1:S:174:THR:N	3:S:705:HOH:O	2.49	0.46
1:T:123:VAL:CG1	1:T:304:PHE:CE1	2.99	0.46
1:T:155:HIS:CE1	1:T:204:PRO:HB2	2.51	0.46
1:T:322:LEU:HD22	1:T:322:LEU:N	2.31	0.46
1:V:227:GLU:CG	1:V:227:GLU:O	2.64	0.46
1:V:405:LEU:O	1:V:409:THR:HG23	2.16	0.46
1:V:420:VAL:HA	1:V:428:GLY:HA2	1.98	0.46
1:W:378:ASP:O	1:W:381:SER:O	2.34	0.46
1:X:77:ASP:HB2	1:X:523:SER:HB2	1.98	0.46
2:k:30:PRO:HD2	2:k:32:SER:HB3	1.96	0.46
2:l:69:GLU:C	2:l:69:GLU:OE1	2.59	0.46
2:l:80:VAL:C	2:l:82:ALA:N	2.73	0.46
2:l:81:SER:HB3	2:m:42:ALA:HB1	1.98	0.46
2:l:83:VAL:HG23	2:l:84:PHE:N	2.31	0.46
2:o:83:VAL:HG23	2:o:84:PHE:N	2.31	0.46
2:r:59:VAL:HG22	2:r:73:HIS:O	2.16	0.46
2:v:80:VAL:C	2:v:82:ALA:N	2.73	0.46
1:A:48:TYR:O	1:A:49:THR:CB	2.64	0.46
1:B:34:PHE:O	1:B:34:PHE:CD2	2.68	0.46
1:C:164:LEU:HA	1:C:307:TRP:HH2	1.80	0.46
1:D:28:GLU:HG3	1:D:32:ASP:OD2	2.15	0.46
1:D:234:ILE:HG12	1:D:267:ALA:HB3	1.96	0.46
1:D:434:THR:HA	1:D:437:GLN:HG2	1.98	0.46
1:E:29:ALA:O	1:E:33:LEU:HG	2.15	0.46
1:E:164:LEU:HA	1:E:307:TRP:HH2	1.79	0.46
1:E:238:PRO:HG3	1:E:263:PHE:CB	2.46	0.46
1:F:248:LYS:HB3	1:F:511:ARG:NH1	2.30	0.46
1:G:72:ARG:HD2	1:H:434:THR:HG21	1.98	0.46
1:G:130:THR:HG22	1:G:144:ILE:HA	1.97	0.46
1:I:219:ILE:HD12	1:I:281:ILE:O	2.16	0.46
1:I:427:GLY:C	1:I:429:GLN:N	2.70	0.46
1:J:82:PRO:HB2	1:J:83:LYS:H	1.58	0.46
1:J:164:LEU:HA	1:J:307:TRP:CH2	2.51	0.46
1:J:542:THR:HA	1:J:543:PRO:HD3	1.82	0.46
1:K:273:ARG:O	1:K:274:ARG:CB	2.64	0.46
1:L:42:ASP:OD2	2:j:145:SER:O	2.34	0.46
1:L:78:VAL:CG2	1:L:444:LEU:HD21	2.46	0.46
1:L:115:VAL:O	1:L:119:ILE:HG13	2.15	0.46
1:L:317:GLU:HB3	1:L:321:ARG:CZ	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:343:ARG:H	1:L:343:ARG:HG2	1.52	0.46
1:L:413:LYS:HE2	1:L:413:LYS:HB3	1.74	0.46
2:Z:78:GLU:O	2:Z:79:GLY:C	2.59	0.46
2:b:28:VAL:CB	2:b:96:LEU:HD13	2.45	0.46
2:c:75:PRO:HA	2:c:76:PRO:HD3	1.42	0.46
2:d:28:VAL:HG21	2:d:96:LEU:CG	2.40	0.46
2:i:140:ARG:O	2:i:141:MET:HB3	2.16	0.46
2:i:156:HIS:C	2:i:158:PHE:H	2.23	0.46
1:N:82:PRO:O	1:N:516:CYS:HA	2.16	0.46
1:N:155:HIS:CE1	1:N:204:PRO:HB2	2.50	0.46
1:O:76:ILE:HD12	1:O:433:ASP:OD1	2.16	0.46
1:O:273:ARG:CZ	1:O:275:ARG:HE	2.29	0.46
1:P:123:VAL:CG1	1:P:304:PHE:CE1	2.99	0.46
1:P:160:SER:O	1:P:161:ASN:ND2	2.44	0.46
1:Q:31:ASN:O	1:Q:34:PHE:HB3	2.15	0.46
1:Q:376:ARG:HB2	1:R:352:TRP:CG	2.50	0.46
1:R:47:GLN:CG	1:R:48:TYR:H	2.28	0.46
1:R:95:MSE:HE1	1:R:99:ARG:CZ	2.46	0.46
1:R:260:ASP:HA	1:R:264:ILE:HB	1.97	0.46
1:R:274:ARG:O	1:R:275:ARG:HD2	2.15	0.46
1:R:343:ARG:H	1:R:343:ARG:HG2	1.56	0.46
1:S:118:GLN:OE1	1:S:303:VAL:HB	2.15	0.46
1:S:260:ASP:HA	1:S:264:ILE:HB	1.96	0.46
1:S:340:ILE:O	1:S:344:THR:HG21	2.16	0.46
1:S:359:PHE:HD1	2:u:120:ILE:HD11	1.81	0.46
1:S:396:GLU:O	1:T:399:GLN:OE1	2.34	0.46
1:T:24:GLU:CD	1:T:24:GLU:N	2.74	0.46
1:T:164:LEU:HA	1:T:307:TRP:HH2	1.81	0.46
1:T:330:ARG:HD2	1:T:409:THR:CG2	2.39	0.46
1:V:35:PHE:C	1:V:37:ARG:N	2.70	0.46
1:W:55:GLY:HA3	1:W:57:PHE:CE1	2.50	0.46
1:W:260:ASP:HA	1:W:264:ILE:HB	1.97	0.46
1:W:444:LEU:O	1:W:446:THR:N	2.49	0.46
1:X:55:GLY:HA3	1:X:57:PHE:CE1	2.50	0.46
1:X:444:LEU:O	1:X:445:GLU:C	2.58	0.46
1:A:28:GLU:HG3	1:A:32:ASP:OD2	2.15	0.46
1:A:32:ASP:CG	1:A:316:TYR:CE2	2.94	0.46
1:A:115:VAL:O	1:A:119:ILE:HG13	2.15	0.46
1:B:219:ILE:HD12	1:B:281:ILE:O	2.16	0.46
1:B:413:LYS:HE2	1:B:413:LYS:HB3	1.73	0.46
1:D:565:VAL:O	1:D:569:ARG:HB3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:58:ASP:O	1:F:59:VAL:HB	2.14	0.46
1:F:94:LEU:HA	1:F:97:MSE:CE	2.37	0.46
1:F:139:SER:CB	1:F:455:THR:CG2	2.80	0.46
1:F:410:SER:O	1:F:414:GLU:HG2	2.16	0.46
1:F:567:MSE:HE2	1:G:554:LEU:HD22	1.97	0.46
1:G:92:ASP:OD2	1:G:92:ASP:N	2.48	0.46
1:G:201:PHE:HE2	1:G:281:ILE:HG22	1.80	0.46
1:G:219:ILE:HD12	1:G:281:ILE:O	2.16	0.46
1:G:363:TYR:HE1	1:H:350:PHE:HE1	1.64	0.46
1:I:197:ASP:O	1:I:198:ILE:HB	2.15	0.46
1:I:426:ASN:O	1:I:427:GLY:C	2.58	0.46
1:I:561:ASP:OD2	1:J:92:ASP:HB3	2.16	0.46
1:J:219:ILE:HD12	1:J:281:ILE:O	2.16	0.46
1:J:248:LYS:HB3	1:J:511:ARG:NH1	2.30	0.46
1:K:197:ASP:O	1:K:198:ILE:HB	2.15	0.46
2:Y:78:GLU:O	2:Y:79:GLY:C	2.59	0.46
2:c:28:VAL:CB	2:c:96:LEU:HD13	2.45	0.46
2:f:140:ARG:O	2:f:141:MET:HB3	2.16	0.46
2:j:28:VAL:CB	2:j:96:LEU:HD13	2.45	0.46
1:M:227:GLU:CG	1:M:227:GLU:O	2.64	0.46
1:M:444:LEU:HD13	1:M:444:LEU:N	2.30	0.46
1:N:77:ASP:HB2	1:N:523:SER:HB2	1.98	0.46
1:O:24:GLU:O	1:O:26:ARG:N	2.49	0.46
1:O:82:PRO:O	1:O:516:CYS:HA	2.16	0.46
1:O:371:TYR:HE2	1:O:373:LEU:HD21	1.81	0.46
1:P:273:ARG:HH22	1:P:453:LEU:CD2	2.29	0.46
1:Q:198:ILE:HG22	1:Q:198:ILE:O	2.16	0.46
1:Q:378:ASP:O	1:Q:381:SER:O	2.34	0.46
1:S:66:LYS:HZ1	1:S:420:VAL:HG21	1.80	0.46
1:S:158:TRP:HD1	1:S:158:TRP:H	1.63	0.46
1:T:66:LYS:HZ3	1:T:420:VAL:HG21	1.81	0.46
1:T:575:GLN:O	1:T:579:MSE:CG	2.63	0.46
1:U:26:ARG:HG3	1:U:27:ARG:N	2.31	0.46
1:U:66:LYS:HZ3	1:U:420:VAL:HG21	1.81	0.46
1:U:437:GLN:HA	1:U:440:MSE:HB2	1.98	0.46
1:V:238:PRO:HD3	1:V:263:PHE:HB2	1.98	0.46
1:W:86:ALA:CB	1:W:515:GLU:HG3	2.45	0.46
1:W:322:LEU:HD22	1:W:322:LEU:H	1.80	0.46
1:X:329:LEU:HD22	2:p:133:PRO:HG2	1.96	0.46
2:m:92:ALA:N	2:m:93:PRO:CD	2.78	0.46
2:q:30:PRO:HD2	2:q:32:SER:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:171:ARG:HH21	1:L:182:ASN:HD22	1.64	0.46
1:A:410:SER:O	1:A:414:GLU:HG2	2.16	0.46
1:B:77:ASP:HB2	1:B:523:SER:HB2	1.98	0.46
1:B:164:LEU:HA	1:B:307:TRP:CH2	2.51	0.46
1:B:317:GLU:HB3	1:B:321:ARG:CZ	2.46	0.46
1:C:234:ILE:HG22	1:C:246:TYR:HB3	1.98	0.46
1:C:426:ASN:O	1:C:427:GLY:C	2.58	0.46
1:D:32:ASP:CG	1:D:316:TYR:CE2	2.94	0.46
1:D:273:ARG:O	1:D:274:ARG:CB	2.64	0.46
1:D:567:MSE:HE2	1:F:554:LEU:HD22	1.97	0.46
1:E:219:ILE:HD12	1:E:281:ILE:O	2.16	0.46
1:F:234:ILE:HG22	1:F:246:TYR:HB3	1.98	0.46
1:G:35:PHE:HE1	1:G:321:ARG:NH1	2.13	0.46
1:G:273:ARG:O	1:G:274:ARG:CB	2.64	0.46
1:H:49:THR:O	1:H:50:THR:C	2.56	0.46
1:H:197:ASP:O	1:H:198:ILE:HB	2.15	0.46
1:H:234:ILE:HG12	1:H:267:ALA:HB3	1.96	0.46
1:I:35:PHE:CE1	1:I:321:ARG:NH1	2.84	0.46
1:K:293:ILE:HD13	1:K:294:ALA:N	2.31	0.46
1:K:565:VAL:O	1:K:569:ARG:HB3	2.15	0.46
1:L:29:ALA:O	1:L:33:LEU:HG	2.15	0.46
1:L:410:SER:O	1:L:414:GLU:HG2	2.16	0.46
1:M:14:ARG:NE	1:M:14:ARG:CA	2.70	0.46
1:M:35:PHE:CE1	1:M:321:ARG:NH1	2.83	0.46
1:M:165:MSE:HG3	1:M:307:TRP:CD2	2.51	0.46
1:M:270:GLN:OE1	1:M:270:GLN:HA	2.16	0.46
1:M:349:PRO:HG3	1:M:391:TYR:CE1	2.51	0.46
1:M:390:ALA:CB	1:N:387:GLN:CB	2.94	0.46
1:N:35:PHE:CE1	1:N:321:ARG:NH1	2.84	0.46
1:N:227:GLU:CG	1:N:227:GLU:O	2.64	0.46
1:N:383:ASP:C	1:N:385:PRO:HD3	2.40	0.46
1:N:554:LEU:O	1:N:557:PHE:HB3	2.15	0.46
1:O:33:LEU:HD12	1:O:34:PHE:N	2.31	0.46
1:O:232:ALA:HB2	1:O:269:ARG:O	2.16	0.46
1:P:171:ARG:O	1:P:224:GLU:HA	2.15	0.46
1:P:422:THR:HG22	1:P:423:GLU:N	2.31	0.46
1:P:528:LYS:CD	1:P:560:LEU:HD21	2.46	0.46
1:Q:38:VAL:HG21	1:Q:324:LYS:HD2	1.98	0.46
1:Q:78:VAL:CG1	1:Q:79:LEU:H	2.29	0.46
1:Q:80:TYR:OH	1:Q:444:LEU:HD12	2.16	0.46
1:R:316:TYR:O	1:R:321:ARG:NH1	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:429:GLN:HG2	1:R:429:GLN:O	2.16	0.46
1:S:71:MSE:HE3	1:S:115:VAL:HB	1.97	0.46
1:S:236:GLN:HG3	1:S:265:LYS:HG2	1.98	0.46
1:T:55:GLY:HA3	1:T:57:PHE:CE1	2.51	0.46
1:T:171:ARG:O	1:T:224:GLU:HA	2.16	0.46
1:T:560:LEU:O	1:T:561:ASP:O	2.33	0.46
1:V:71:MSE:HE3	1:V:115:VAL:HB	1.98	0.46
1:V:86:ALA:CB	1:V:515:GLU:HG3	2.45	0.46
1:V:310:VAL:HG22	1:W:40:GLN:HG2	1.98	0.46
1:W:37:ARG:HH21	1:W:37:ARG:CB	2.28	0.46
1:W:78:VAL:CG1	1:W:444:LEU:HG	2.45	0.46
1:X:248:LYS:H	1:X:248:LYS:CD	2.17	0.46
1:X:422:THR:HG22	1:X:423:GLU:N	2.31	0.46
1:X:437:GLN:HA	1:X:440:MSE:HB2	1.98	0.46
2:k:80:VAL:C	2:k:82:ALA:N	2.74	0.46
2:k:83:VAL:HG23	2:k:84:PHE:N	2.30	0.46
1:A:197:ASP:O	1:A:198:ILE:HB	2.15	0.46
1:A:273:ARG:O	1:A:274:ARG:CB	2.64	0.46
1:A:317:GLU:HB3	1:A:321:ARG:CZ	2.46	0.46
1:A:334:MSE:HE3	1:B:404:MSE:CE	2.46	0.46
1:A:376:ARG:HB2	1:B:352:TRP:CD2	2.51	0.46
1:C:24:GLU:N	1:C:24:GLU:CD	2.71	0.46
1:C:35:PHE:HE2	1:C:324:LYS:NZ	2.08	0.46
1:C:71:MSE:CE	1:C:115:VAL:HB	2.45	0.46
1:C:219:ILE:HD12	1:C:281:ILE:O	2.16	0.46
1:D:78:VAL:HG21	1:D:444:LEU:CD1	2.21	0.46
1:F:48:TYR:O	1:F:49:THR:CB	2.64	0.46
1:F:426:ASN:O	1:F:427:GLY:C	2.58	0.46
1:G:32:ASP:CG	1:G:316:TYR:CE2	2.94	0.46
1:G:35:PHE:CE1	1:G:321:ARG:NH1	2.84	0.46
1:H:234:ILE:CG2	1:H:246:TYR:HB3	2.46	0.46
1:I:15:PHE:HZ	1:I:283:CYS:HG	1.61	0.46
1:I:28:GLU:HG3	1:I:32:ASP:OD2	2.15	0.46
1:I:234:ILE:HG22	1:I:246:TYR:HB3	1.98	0.46
1:J:293:ILE:HD13	1:J:294:ALA:N	2.31	0.46
1:K:71:MSE:CE	1:K:115:VAL:HB	2.45	0.46
1:K:78:VAL:CG2	1:K:444:LEU:HD21	2.46	0.46
1:K:238:PRO:HG3	1:K:263:PHE:CB	2.46	0.46
2:c:28:VAL:HG21	2:c:96:LEU:CG	2.40	0.46
2:e:28:VAL:CB	2:e:96:LEU:HD13	2.45	0.46
1:N:160:SER:O	1:N:161:ASN:ND2	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:418:LEU:HB2	1:N:428:GLY:O	2.15	0.45
1:O:34:PHE:O	1:O:37:ARG:HB2	2.16	0.45
1:P:429:GLN:O	1:P:429:GLN:HG2	2.17	0.45
1:Q:47:GLN:CG	1:Q:48:TYR:H	2.28	0.45
1:Q:248:LYS:HG3	1:Q:511:ARG:HE	1.81	0.45
1:R:26:ARG:HG3	1:R:27:ARG:N	2.31	0.45
1:R:409:THR:O	1:R:413:LYS:HG2	2.16	0.45
1:S:231:THR:CG2	1:S:249:ARG:HH11	2.23	0.45
1:S:343:ARG:O	1:S:344:THR:HB	2.16	0.45
1:S:378:ASP:O	1:S:381:SER:O	2.34	0.45
1:T:293:ILE:HG12	1:T:294:ALA:H	1.81	0.45
1:U:41:TRP:HE3	1:U:42:ASP:HB3	1.81	0.45
1:V:26:ARG:O	1:V:27:ARG:C	2.58	0.45
1:V:38:VAL:HG21	1:V:324:LYS:HD2	1.98	0.45
1:V:47:GLN:H	1:V:48:TYR:HD2	1.62	0.45
1:V:160:SER:O	1:V:161:ASN:ND2	2.46	0.45
1:V:554:LEU:O	1:V:557:PHE:HB3	2.16	0.45
2:k:59:VAL:HG22	2:k:73:HIS:O	2.16	0.45
2:r:30:PRO:HD2	2:r:32:SER:HB3	1.97	0.45
2:v:40:LEU:C	2:v:40:LEU:CD2	2.88	0.45
2:v:95:TYR:N	2:v:95:TYR:CD1	2.79	0.45
1:A:71:MSE:CE	1:A:115:VAL:HB	2.45	0.45
1:A:92:ASP:OD2	1:A:92:ASP:N	2.48	0.45
1:A:434:THR:HA	1:A:437:GLN:HG2	1.98	0.45
1:A:444:LEU:HD13	1:A:444:LEU:N	2.31	0.45
1:B:238:PRO:HG3	1:B:263:PHE:CB	2.46	0.45
1:B:426:ASN:O	1:B:427:GLY:C	2.59	0.45
1:C:24:GLU:C	1:C:26:ARG:N	2.73	0.45
1:C:130:THR:HG22	1:C:144:ILE:HA	1.97	0.45
1:C:246:TYR:HD2	1:C:511:ARG:CB	2.28	0.45
1:C:565:VAL:O	1:C:569:ARG:HB3	2.15	0.45
1:D:48:TYR:O	1:D:49:THR:CB	2.64	0.45
1:D:234:ILE:CG2	1:D:246:TYR:HB3	2.47	0.45
1:D:273:ARG:HH22	1:D:453:LEU:CD1	2.28	0.45
1:D:528:LYS:HD2	1:D:560:LEU:HD21	1.99	0.45
1:D:563:LYS:HD3	1:F:557:PHE:CE2	2.51	0.45
1:E:201:PHE:HE2	1:E:281:ILE:HG22	1.80	0.45
1:E:234:ILE:HG12	1:E:267:ALA:HB3	1.96	0.45
1:F:238:PRO:HG3	1:F:263:PHE:CB	2.46	0.45
1:F:444:LEU:HD13	1:F:444:LEU:N	2.31	0.45
1:G:164:LEU:HA	1:G:307:TRP:CH2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:164:LEU:HD22	1:H:169:ASP:CG	2.42	0.45
1:H:426:ASN:O	1:H:427:GLY:C	2.58	0.45
1:H:590:GLN:O	1:H:594:VAL:HG23	2.16	0.45
1:I:293:ILE:HD13	1:I:294:ALA:N	2.31	0.45
1:I:590:GLN:O	1:I:594:VAL:HG23	2.16	0.45
1:J:164:LEU:HD22	1:J:169:ASP:CG	2.42	0.45
1:J:234:ILE:CG2	1:J:246:TYR:HB3	2.46	0.45
1:J:426:ASN:O	1:J:427:GLY:C	2.58	0.45
1:K:40:GLN:O	1:K:41:TRP:CB	2.54	0.45
1:K:234:ILE:HG22	1:K:246:TYR:HB3	1.98	0.45
1:K:273:ARG:O	1:K:274:ARG:HB3	2.17	0.45
1:K:590:GLN:O	1:K:594:VAL:HG23	2.16	0.45
1:L:164:LEU:HA	1:L:307:TRP:CH2	2.51	0.45
2:d:78:GLU:O	2:d:79:GLY:C	2.59	0.45
2:i:78:GLU:O	2:i:79:GLY:C	2.59	0.45
1:M:155:HIS:CE1	1:M:204:PRO:HB2	2.52	0.45
1:M:360:GLU:HG3	2:l:122:ARG:HB3	1.98	0.45
1:N:343:ARG:NH1	2:k:126:ALA:O	2.47	0.45
1:N:444:LEU:HD13	1:N:444:LEU:N	2.31	0.45
1:O:101:ASP:HB3	1:O:138:THR:HG21	1.98	0.45
1:O:136:SER:N	1:O:137:PRO:HD3	2.31	0.45
1:O:332:MSE:SE	2:m:132:MET:HA	2.67	0.45
1:O:422:THR:HG22	1:O:423:GLU:N	2.31	0.45
1:P:127:ARG:HG2	1:P:147:GLU:HB2	1.97	0.45
1:Q:47:GLN:N	1:Q:48:TYR:HD2	2.14	0.45
1:Q:86:ALA:CB	1:Q:515:GLU:HG3	2.45	0.45
1:Q:227:GLU:O	1:Q:227:GLU:CG	2.64	0.45
1:R:86:ALA:CB	1:R:515:GLU:HG3	2.46	0.45
1:R:136:SER:N	1:R:137:PRO:HD3	2.31	0.45
1:R:444:LEU:HD13	1:R:444:LEU:N	2.31	0.45
1:S:40:GLN:HE21	1:S:40:GLN:HB2	1.58	0.45
1:S:158:TRP:HH2	1:S:302:PRO:HG3	1.78	0.45
1:S:316:TYR:O	1:S:321:ARG:NH1	2.50	0.45
1:S:395:PRO:HD2	1:T:398:PRO:HB3	1.99	0.45
1:T:26:ARG:HG3	1:T:27:ARG:N	2.30	0.45
1:T:118:GLN:OE1	1:T:303:VAL:HB	2.16	0.45
1:U:193:LEU:HD22	1:U:287:LEU:HB3	1.98	0.45
1:V:171:ARG:O	1:V:224:GLU:HA	2.15	0.45
1:W:24:GLU:CD	1:W:24:GLU:N	2.74	0.45
1:W:38:VAL:HG21	1:W:324:LYS:HD2	1.99	0.45
1:W:136:SER:N	1:W:137:PRO:HD3	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:273:ARG:CZ	1:W:275:ARG:HE	2.29	0.45
1:X:364:ASP:CG	2:q:126:ALA:HB2	2.41	0.45
2:m:10:VAL:HA	2:m:15:ARG:HG2	1.97	0.45
2:p:92:ALA:N	2:p:93:PRO:CD	2.79	0.45
1:A:35:PHE:CE1	1:A:321:ARG:NH1	2.84	0.45
1:B:24:GLU:C	1:B:26:ARG:N	2.73	0.45
1:B:29:ALA:O	1:B:33:LEU:HG	2.15	0.45
1:B:32:ASP:CG	1:B:316:TYR:CE2	2.94	0.45
1:B:234:ILE:CG2	1:B:246:TYR:HB3	2.47	0.45
1:B:234:ILE:HG22	1:B:246:TYR:HB3	1.98	0.45
1:B:434:THR:HA	1:B:437:GLN:HG2	1.97	0.45
1:C:413:LYS:HE2	1:C:413:LYS:HB3	1.74	0.45
1:E:77:ASP:HB2	1:E:523:SER:HB2	1.98	0.45
1:F:24:GLU:C	1:F:26:ARG:N	2.73	0.45
1:G:78:VAL:HG21	1:G:444:LEU:CD1	2.21	0.45
1:G:82:PRO:HB2	1:G:83:LYS:H	1.58	0.45
1:G:164:LEU:HD22	1:G:169:ASP:CG	2.42	0.45
1:G:227:GLU:HA	1:G:274:ARG:CA	2.44	0.45
1:G:234:ILE:HG22	1:G:246:TYR:HB3	1.98	0.45
1:G:451:ASP:O	1:G:456:ALA:N	2.40	0.45
1:H:219:ILE:HD12	1:H:281:ILE:O	2.16	0.45
1:H:273:ARG:O	1:H:274:ARG:HB3	2.17	0.45
1:H:528:LYS:HZ2	1:H:560:LEU:HD21	1.79	0.45
1:I:238:PRO:HG3	1:I:263:PHE:CB	2.46	0.45
1:J:444:LEU:HD13	1:J:444:LEU:N	2.31	0.45
1:K:24:GLU:C	1:K:26:ARG:N	2.73	0.45
1:K:32:ASP:CG	1:K:316:TYR:CE2	2.94	0.45
1:K:35:PHE:CE1	1:K:321:ARG:NH1	2.84	0.45
1:K:164:LEU:HD22	1:K:169:ASP:CG	2.42	0.45
1:L:24:GLU:C	1:L:26:ARG:N	2.73	0.45
1:L:236:GLN:HE21	1:L:265:LYS:HZ3	1.63	0.45
2:Y:140:ARG:O	2:Y:141:MET:HB3	2.16	0.45
2:a:156:HIS:C	2:a:158:PHE:H	2.23	0.45
2:d:28:VAL:CB	2:d:96:LEU:HD13	2.45	0.45
2:j:156:HIS:C	2:j:158:PHE:H	2.23	0.45
1:M:123:VAL:HG22	1:M:316:TYR:HE2	1.82	0.45
1:N:31:ASN:O	1:N:34:PHE:HB3	2.15	0.45
1:N:371:TYR:HE2	1:N:373:LEU:HD21	1.82	0.45
1:O:71:MSE:HE3	1:O:115:VAL:HB	1.98	0.45
1:O:86:ALA:CB	1:O:515:GLU:HG3	2.44	0.45
1:O:118:GLN:OE1	1:O:303:VAL:HB	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:351:PHE:CD2	1:O:356:ILE:HD12	2.51	0.45
1:P:232:ALA:HB2	1:P:269:ARG:O	2.16	0.45
1:P:282:THR:HG23	1:P:287:LEU:CD1	2.44	0.45
1:P:564:GLY:HA3	1:Q:535:ILE:HD11	1.99	0.45
1:Q:273:ARG:CZ	1:Q:275:ARG:HE	2.30	0.45
1:Q:413:LYS:HA	1:Q:416:ALA:HB3	1.99	0.45
1:R:334:MSE:HE1	1:X:407:ALA:HB1	1.99	0.45
1:U:71:MSE:CE	1:U:115:VAL:HB	2.46	0.45
1:U:409:THR:O	1:U:413:LYS:HG2	2.16	0.45
1:U:528:LYS:CD	1:U:560:LEU:HD21	2.46	0.45
1:V:383:ASP:C	1:V:385:PRO:HD3	2.41	0.45
1:W:71:MSE:HE3	1:W:115:VAL:HB	1.98	0.45
2:p:59:VAL:HG22	2:p:73:HIS:O	2.17	0.45
1:A:78:VAL:CG2	1:A:444:LEU:HD21	2.46	0.45
1:A:234:ILE:HG22	1:A:246:TYR:HB3	1.98	0.45
1:A:273:ARG:O	1:A:274:ARG:HB3	2.17	0.45
1:A:293:ILE:HD13	1:A:294:ALA:N	2.31	0.45
1:A:459:ARG:HD2	1:A:459:ARG:C	2.42	0.45
1:C:164:LEU:HD22	1:C:169:ASP:CG	2.42	0.45
1:C:232:ALA:N	1:C:269:ARG:O	2.50	0.45
1:C:317:GLU:HB3	1:C:321:ARG:CZ	2.46	0.45
1:C:444:LEU:HD13	1:C:444:LEU:N	2.31	0.45
1:D:164:LEU:HA	1:D:307:TRP:CH2	2.51	0.45
1:D:251:ILE:HG23	1:D:507:LEU:HD22	1.98	0.45
1:E:45:LEU:HD21	1:E:328:ARG:HH21	1.82	0.45
1:E:164:LEU:HD22	1:E:169:ASP:CG	2.42	0.45
1:F:35:PHE:CE1	1:F:321:ARG:NH1	2.84	0.45
1:F:246:TYR:HD2	1:F:511:ARG:CB	2.28	0.45
1:G:234:ILE:CG2	1:G:246:TYR:HB3	2.47	0.45
1:G:236:GLN:HE21	1:G:265:LYS:HZ3	1.63	0.45
1:G:444:LEU:HD13	1:G:444:LEU:N	2.31	0.45
1:H:232:ALA:N	1:H:269:ARG:O	2.50	0.45
1:H:317:GLU:HB3	1:H:321:ARG:CZ	2.46	0.45
1:H:459:ARG:HD2	1:H:459:ARG:C	2.42	0.45
1:I:24:GLU:C	1:I:26:ARG:N	2.73	0.45
1:I:92:ASP:OD2	1:I:92:ASP:N	2.48	0.45
1:I:273:ARG:O	1:I:274:ARG:CB	2.64	0.45
1:I:577:ILE:HG12	1:I:582:LYS:CG	2.41	0.45
1:J:234:ILE:HG22	1:J:246:TYR:HB3	1.98	0.45
1:K:47:GLN:CD	1:K:47:GLN:N	2.72	0.45
1:K:139:SER:CB	1:K:455:THR:CG2	2.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:317:GLU:HB3	1:K:321:ARG:CZ	2.46	0.45
1:K:444:LEU:HD13	1:K:444:LEU:N	2.31	0.45
2:a:39:PRO:HB2	2:a:40:GLN:H	1.51	0.45
2:a:140:ARG:O	2:a:141:MET:HB3	2.16	0.45
2:b:75:PRO:HA	2:b:76:PRO:HD3	1.42	0.45
2:b:156:HIS:C	2:b:158:PHE:H	2.23	0.45
2:e:78:GLU:O	2:e:79:GLY:C	2.59	0.45
1:M:29:ALA:O	1:M:33:LEU:HG	2.16	0.45
1:M:34:PHE:O	1:M:37:ARG:HB2	2.17	0.45
1:M:454:ALA:O	1:M:455:THR:C	2.58	0.45
1:N:444:LEU:O	1:N:445:GLU:C	2.60	0.45
1:O:343:ARG:O	1:O:344:THR:HB	2.16	0.45
1:P:14:ARG:NE	1:P:14:ARG:CA	2.71	0.45
1:P:76:ILE:HD12	1:P:433:ASP:OD1	2.16	0.45
1:P:396:GLU:O	1:Q:399:GLN:OE1	2.34	0.45
3:Q:719:HOH:O	1:R:430:VAL:HG11	2.15	0.45
1:R:443:ASP:O	1:R:446:THR:HG22	2.17	0.45
1:S:164:LEU:HA	1:S:307:TRP:CH2	2.51	0.45
1:T:26:ARG:O	1:T:27:ARG:C	2.59	0.45
1:T:41:TRP:HE3	1:T:42:ASP:HB3	1.82	0.45
1:U:34:PHE:O	1:U:37:ARG:HB2	2.16	0.45
1:U:174:THR:N	3:U:705:HOH:O	2.50	0.45
1:V:26:ARG:HG3	1:V:27:ARG:N	2.31	0.45
1:V:127:ARG:HG2	1:V:147:GLU:HB2	1.98	0.45
1:V:316:TYR:O	1:V:321:ARG:NH1	2.50	0.45
1:V:528:LYS:CD	1:V:560:LEU:HD21	2.46	0.45
1:W:24:GLU:HG3	1:W:313:LYS:HE2	1.98	0.45
1:W:82:PRO:O	1:W:516:CYS:HA	2.17	0.45
1:W:198:ILE:HA	1:W:199:PRO:HD3	1.71	0.45
1:W:444:LEU:HD13	1:W:444:LEU:N	2.32	0.45
1:X:24:GLU:O	1:X:26:ARG:N	2.48	0.45
1:X:136:SER:N	1:X:137:PRO:HD3	2.32	0.45
1:X:409:THR:O	1:X:413:LYS:HG2	2.16	0.45
1:X:429:GLN:O	1:X:429:GLN:HG2	2.16	0.45
2:s:47:TRP:N	2:s:47:TRP:CD1	2.84	0.45
1:A:9:GLU:HG3	1:A:12:LEU:H	1.81	0.45
1:A:35:PHE:HE2	1:A:324:LYS:NZ	2.08	0.45
1:B:26:ARG:NH2	1:B:30:LYS:HB2	2.28	0.45
1:B:273:ARG:O	1:B:274:ARG:HB3	2.17	0.45
1:C:32:ASP:CG	1:C:316:TYR:CE2	2.94	0.45
1:C:164:LEU:HA	1:C:307:TRP:CH2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:273:ARG:O	1:C:274:ARG:CB	2.64	0.45
1:D:86:ALA:CB	1:D:515:GLU:HG3	2.47	0.45
1:D:410:SER:O	1:D:414:GLU:HG2	2.16	0.45
1:E:32:ASP:CG	1:E:316:TYR:CE2	2.94	0.45
1:E:262:GLY:O	1:E:263:PHE:HB3	2.17	0.45
1:E:590:GLN:O	1:E:594:VAL:HG23	2.16	0.45
1:F:9:GLU:HG3	1:F:12:LEU:H	1.82	0.45
1:F:164:LEU:HA	1:F:307:TRP:CH2	2.51	0.45
1:G:28:GLU:HG3	1:G:32:ASP:OD2	2.15	0.45
1:G:528:LYS:HD2	1:G:560:LEU:HD21	1.99	0.45
1:G:561:ASP:OD2	1:H:92:ASP:HB3	2.16	0.45
1:H:78:VAL:CG2	1:H:444:LEU:HD21	2.46	0.45
1:H:164:LEU:HA	1:H:307:TRP:CH2	2.51	0.45
1:H:262:GLY:O	1:H:263:PHE:HB3	2.17	0.45
1:H:293:ILE:HD13	1:H:294:ALA:N	2.31	0.45
1:J:182:ASN:HD22	1:K:171:ARG:HH21	1.65	0.45
1:J:201:PHE:HE2	1:J:281:ILE:HG22	1.80	0.45
1:L:92:ASP:OD2	1:L:92:ASP:N	2.48	0.45
1:L:273:ARG:O	1:L:274:ARG:HB3	2.17	0.45
1:L:293:ILE:HD13	1:L:294:ALA:N	2.31	0.45
2:a:75:PRO:HA	2:a:76:PRO:HD3	1.42	0.45
2:b:140:ARG:O	2:b:141:MET:HB3	2.16	0.45
2:e:140:ARG:O	2:e:141:MET:HB3	2.16	0.45
1:N:343:ARG:H	1:N:343:ARG:HG2	1.53	0.45
1:N:378:ASP:O	1:N:381:SER:O	2.34	0.45
1:N:528:LYS:CD	1:N:560:LEU:HD21	2.46	0.45
1:O:24:GLU:CD	1:O:24:GLU:N	2.74	0.45
1:O:26:ARG:HG3	1:O:27:ARG:N	2.32	0.45
1:O:165:MSE:HG3	1:O:307:TRP:CD2	2.49	0.45
1:P:53:TYR:OH	1:Q:329:LEU:HD21	2.16	0.45
1:Q:66:LYS:HZ3	1:Q:420:VAL:HG21	1.82	0.45
1:Q:322:LEU:HD22	1:Q:322:LEU:H	1.82	0.45
1:Q:396:GLU:O	1:R:399:GLN:OE1	2.34	0.45
1:R:24:GLU:O	1:R:26:ARG:N	2.50	0.45
1:R:53:TYR:OH	1:X:329:LEU:HD21	2.16	0.45
1:S:193:LEU:HD22	1:S:287:LEU:HB3	1.97	0.45
1:S:273:ARG:CZ	1:S:275:ARG:HE	2.29	0.45
1:T:31:ASN:O	1:T:34:PHE:HB3	2.16	0.45
1:T:528:LYS:CD	1:T:560:LEU:HD21	2.47	0.45
1:U:198:ILE:HA	1:U:199:PRO:HD3	1.71	0.45
1:U:227:GLU:CG	1:U:227:GLU:O	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:444:LEU:O	1:U:445:GLU:C	2.58	0.45
1:V:136:SER:N	1:V:137:PRO:HD3	2.31	0.45
1:W:420:VAL:HA	1:W:428:GLY:HA2	1.98	0.45
1:X:24:GLU:CD	1:X:24:GLU:N	2.75	0.45
1:X:384:LEU:HD22	1:X:384:LEU:N	2.29	0.45
2:l:47:TRP:CD1	2:l:47:TRP:N	2.84	0.45
2:o:10:VAL:HA	2:o:15:ARG:HG2	1.98	0.45
1:A:24:GLU:C	1:A:26:ARG:N	2.73	0.45
1:A:26:ARG:NH2	1:A:30:LYS:HB2	2.28	0.45
1:A:77:ASP:HB2	1:A:523:SER:HB2	1.98	0.45
1:A:86:ALA:CB	1:A:515:GLU:HG3	2.47	0.45
1:A:164:LEU:HD22	1:A:169:ASP:CG	2.42	0.45
1:B:410:SER:O	1:B:414:GLU:HG2	2.16	0.45
1:B:444:LEU:HD13	1:B:444:LEU:N	2.31	0.45
1:C:77:ASP:HB2	1:C:523:SER:HB2	1.98	0.45
1:C:234:ILE:HG12	1:C:267:ALA:HB3	1.96	0.45
1:C:251:ILE:HG23	1:C:507:LEU:HD22	1.98	0.45
1:C:410:SER:O	1:C:414:GLU:HG2	2.16	0.45
1:D:293:ILE:HD13	1:D:294:ALA:N	2.31	0.45
1:E:251:ILE:HG23	1:E:507:LEU:HD22	1.98	0.45
1:E:293:ILE:HD13	1:E:294:ALA:N	2.31	0.45
1:F:182:ASN:HD22	1:G:171:ARG:HH21	1.61	0.45
1:F:232:ALA:N	1:F:269:ARG:O	2.50	0.45
1:F:234:ILE:CG2	1:F:246:TYR:HB3	2.47	0.45
1:F:251:ILE:HG23	1:F:507:LEU:HD22	1.98	0.45
1:F:434:THR:HA	1:F:437:GLN:HG2	1.97	0.45
1:F:528:LYS:HD2	1:F:560:LEU:HD21	1.99	0.45
1:F:567:MSE:SE	1:G:576:LEU:HD13	2.66	0.45
1:G:77:ASP:HB2	1:G:523:SER:HB2	1.98	0.45
1:G:232:ALA:N	1:G:269:ARG:O	2.50	0.45
1:G:590:GLN:O	1:G:594:VAL:HG23	2.16	0.45
1:K:57:PHE:CD2	1:K:330:ARG:CB	2.95	0.45
1:L:32:ASP:CG	1:L:316:TYR:CE2	2.94	0.45
1:L:71:MSE:CE	1:L:115:VAL:HB	2.45	0.45
1:L:164:LEU:HD22	1:L:169:ASP:CG	2.41	0.45
1:L:232:ALA:N	1:L:269:ARG:O	2.50	0.45
1:L:255:ILE:O	1:L:256:ASP:C	2.60	0.45
2:j:140:ARG:O	2:j:141:MET:HB3	2.16	0.45
1:M:66:LYS:HZ1	1:M:420:VAL:HG21	1.80	0.45
1:N:422:THR:HG22	1:N:423:GLU:N	2.32	0.45
1:O:193:LEU:HD22	1:O:287:LEU:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:554:LEU:O	1:O:557:PHE:HB3	2.16	0.45
1:P:343:ARG:NH1	2:n:126:ALA:O	2.47	0.45
1:Q:510:ILE:O	1:Q:513:ARG:HD2	2.17	0.45
1:R:31:ASN:O	1:R:34:PHE:HB3	2.16	0.45
1:R:40:GLN:HG2	1:X:310:VAL:HG22	1.98	0.45
1:R:127:ARG:HG2	1:R:147:GLU:HB2	1.97	0.45
1:T:47:GLN:N	1:T:48:TYR:HD2	2.15	0.45
1:T:160:SER:O	1:T:161:ASN:ND2	2.43	0.45
1:T:270:GLN:OE1	1:T:270:GLN:HA	2.17	0.45
1:T:334:MSE:HE1	1:W:407:ALA:HB1	1.98	0.45
1:T:427:GLY:C	1:T:429:GLN:N	2.75	0.45
1:T:511:ARG:HA	1:T:513:ARG:CD	2.44	0.45
1:U:136:SER:N	1:U:137:PRO:HD3	2.31	0.45
1:V:165:MSE:HG3	1:V:307:TRP:CD2	2.49	0.45
1:V:343:ARG:H	1:V:343:ARG:HG2	1.55	0.45
1:V:422:THR:HG22	1:V:423:GLU:N	2.31	0.45
1:X:158:TRP:HH2	1:X:302:PRO:HG3	1.80	0.45
1:X:171:ARG:O	1:X:224:GLU:HA	2.17	0.45
2:u:48:TYR:H	2:u:54:ILE:H	1.64	0.45
2:v:24:THR:HG22	2:v:25:LEU:N	2.32	0.45
1:A:47:GLN:O	1:A:47:GLN:CG	2.65	0.45
1:A:232:ALA:N	1:A:269:ARG:O	2.50	0.45
1:B:459:ARG:HD2	1:B:459:ARG:C	2.42	0.45
1:B:590:GLN:O	1:B:594:VAL:HG23	2.17	0.45
1:C:58:ASP:O	1:C:59:VAL:HB	2.15	0.45
1:C:273:ARG:O	1:C:274:ARG:HB3	2.17	0.45
1:D:238:PRO:HG3	1:D:263:PHE:CB	2.46	0.45
1:D:262:GLY:O	1:D:263:PHE:HB3	2.17	0.45
1:E:35:PHE:CE1	1:E:321:ARG:NH1	2.84	0.45
1:E:234:ILE:HG22	1:E:246:TYR:HB3	1.98	0.45
1:F:45:LEU:HD21	1:F:328:ARG:HH21	1.82	0.45
1:F:590:GLN:O	1:F:594:VAL:HG23	2.16	0.45
1:G:9:GLU:HG3	1:G:12:LEU:H	1.82	0.45
1:G:48:TYR:O	1:G:49:THR:CB	2.64	0.45
1:I:201:PHE:HE2	1:I:281:ILE:HG22	1.80	0.45
1:I:227:GLU:OE2	1:I:227:GLU:N	2.47	0.45
1:J:86:ALA:CB	1:J:515:GLU:HG3	2.47	0.45
1:K:9:GLU:HG3	1:K:12:LEU:H	1.82	0.45
1:K:47:GLN:O	1:K:47:GLN:CG	2.65	0.45
1:K:410:SER:O	1:K:414:GLU:HG2	2.16	0.45
1:L:364:ASP:CG	2:Y:135:ALA:HB2	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Y:20:ARG:C	2:Y:22:ALA:N	2.74	0.45
2:Y:71:ASP:O	2:Y:72:ASP:CB	2.65	0.45
2:Y:75:PRO:HA	2:Y:76:PRO:HD3	1.42	0.45
2:d:20:ARG:C	2:d:22:ALA:N	2.74	0.45
2:e:143:THR:N	2:e:154:GLU:HA	2.32	0.45
2:h:28:VAL:CB	2:h:96:LEU:HD13	2.45	0.45
1:M:24:GLU:O	1:M:26:ARG:N	2.49	0.45
1:M:41:TRP:HE1	1:O:27:ARG:NH2	2.14	0.45
1:M:276:VAL:CG2	1:M:293:ILE:HG23	2.47	0.45
1:M:298:ILE:HA	1:M:299:PRO:HD3	1.79	0.45
1:M:422:THR:HG22	1:M:423:GLU:N	2.32	0.45
1:N:55:GLY:HA3	1:N:57:PHE:CE1	2.51	0.45
1:O:35:PHE:CE1	1:O:321:ARG:NH1	2.84	0.45
1:O:316:TYR:O	1:O:321:ARG:NH1	2.49	0.45
1:O:510:ILE:O	1:O:513:ARG:HD2	2.17	0.45
1:P:24:GLU:CD	1:P:24:GLU:N	2.74	0.45
1:P:227:GLU:CG	1:P:227:GLU:O	2.64	0.45
1:P:334:MSE:HE1	1:Q:407:ALA:HB1	1.99	0.45
1:P:378:ASP:O	1:P:381:SER:O	2.35	0.45
1:Q:171:ARG:O	1:Q:224:GLU:HA	2.17	0.45
1:Q:343:ARG:O	1:Q:344:THR:HB	2.16	0.45
1:S:310:VAL:HG22	1:U:40:GLN:HG2	1.99	0.45
1:S:451:ASP:C	1:S:453:LEU:N	2.72	0.45
1:T:316:TYR:O	1:T:321:ARG:NH1	2.50	0.45
1:T:451:ASP:O	1:T:453:LEU:N	2.49	0.45
1:U:371:TYR:HE2	1:U:373:LEU:HD21	1.81	0.45
1:U:420:VAL:HA	1:U:428:GLY:HA2	1.98	0.45
1:V:123:VAL:CG1	1:V:304:PHE:CE1	3.00	0.45
1:X:26:ARG:HG3	1:X:27:ARG:N	2.31	0.45
1:X:232:ALA:HB2	1:X:269:ARG:O	2.17	0.45
1:X:444:LEU:HD13	1:X:444:LEU:N	2.30	0.45
2:n:92:ALA:N	2:n:93:PRO:CD	2.80	0.45
2:s:92:ALA:N	2:s:93:PRO:CD	2.79	0.45
1:A:234:ILE:CG2	1:A:246:TYR:HB3	2.46	0.45
1:B:86:ALA:CB	1:B:515:GLU:HG3	2.47	0.45
1:B:164:LEU:HD22	1:B:169:ASP:CG	2.42	0.45
1:B:293:ILE:HD13	1:B:294:ALA:N	2.31	0.45
1:B:456:ALA:CB	1:B:509:ASP:OD2	2.65	0.45
1:C:201:PHE:HE2	1:C:281:ILE:HG22	1.80	0.45
1:C:238:PRO:HG3	1:C:263:PHE:CB	2.46	0.45
1:E:47:GLN:O	1:E:47:GLN:CG	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:177:HIS:HE1	1:E:221:GLU:OE1	2.00	0.45
1:E:234:ILE:CG2	1:E:246:TYR:HB3	2.47	0.45
1:E:248:LYS:HZ1	1:E:513:ARG:HH12	1.64	0.45
1:E:273:ARG:O	1:E:274:ARG:CB	2.64	0.45
1:E:273:ARG:O	1:E:274:ARG:HB3	2.17	0.45
1:E:459:ARG:HD2	1:E:459:ARG:C	2.42	0.45
1:F:255:ILE:O	1:F:256:ASP:C	2.60	0.45
1:F:293:ILE:HD13	1:F:294:ALA:N	2.31	0.45
1:F:459:ARG:HD2	1:F:459:ARG:C	2.42	0.45
1:G:273:ARG:O	1:G:274:ARG:HB3	2.16	0.45
1:G:459:ARG:HD2	1:G:459:ARG:C	2.42	0.45
1:G:534:GLU:O	1:G:538:LEU:HD23	2.17	0.45
1:H:72:ARG:HD2	1:I:434:THR:HG21	1.99	0.45
1:H:410:SER:O	1:H:414:GLU:HG2	2.16	0.45
1:I:32:ASP:CG	1:I:316:TYR:CE2	2.94	0.45
1:I:94:LEU:HA	1:I:97:MSE:CE	2.37	0.45
1:I:232:ALA:N	1:I:269:ARG:O	2.50	0.45
1:I:528:LYS:HZ3	1:I:560:LEU:HD21	1.80	0.45
1:J:48:TYR:O	1:J:49:THR:CB	2.64	0.45
1:J:590:GLN:O	1:J:594:VAL:HG23	2.17	0.45
3:J:719:HOH:O	1:K:438:LEU:HD22	2.16	0.45
1:K:451:ASP:O	1:K:456:ALA:N	2.41	0.45
1:L:273:ARG:O	1:L:274:ARG:CB	2.64	0.45
1:L:444:LEU:HD13	1:L:444:LEU:N	2.31	0.45
1:L:456:ALA:CB	1:L:509:ASP:OD2	2.65	0.45
2:Z:71:ASP:O	2:Z:72:ASP:CB	2.65	0.45
2:g:57:TYR:H	2:g:63:ILE:H	1.65	0.45
2:h:143:THR:N	2:h:154:GLU:HA	2.32	0.45
2:i:20:ARG:C	2:i:22:ALA:N	2.74	0.45
2:j:75:PRO:HA	2:j:76:PRO:HD3	1.42	0.45
1:M:82:PRO:O	1:M:516:CYS:HA	2.17	0.45
1:M:100:THR:HG22	1:M:138:THR:HG22	1.97	0.45
1:M:348:LYS:HB2	1:N:372:TYR:CE2	2.52	0.45
1:N:41:TRP:HE3	1:N:42:ASP:HB3	1.80	0.45
1:N:164:LEU:HA	1:N:307:TRP:HH2	1.81	0.45
1:O:190:LYS:HA	1:O:190:LYS:HE3	1.99	0.45
1:O:409:THR:O	1:O:413:LYS:HG2	2.16	0.45
1:O:420:VAL:HA	1:O:428:GLY:HA2	1.98	0.45
1:O:444:LEU:O	1:O:446:THR:N	2.50	0.45
1:P:31:ASN:O	1:P:34:PHE:HB3	2.15	0.45
1:Q:26:ARG:HG3	1:Q:27:ARG:N	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:41:TRP:HE3	1:Q:42:ASP:HB3	1.82	0.45
1:Q:422:THR:HG22	1:Q:423:GLU:N	2.32	0.45
1:R:77:ASP:HB2	1:R:523:SER:HB2	1.98	0.45
1:R:301:VAL:HA	1:R:302:PRO:HD3	1.79	0.45
1:R:322:LEU:HD22	1:R:322:LEU:H	1.81	0.45
1:S:123:VAL:HG22	1:S:316:TYR:HE2	1.80	0.45
1:S:301:VAL:HA	1:S:302:PRO:HD3	1.80	0.45
1:T:76:ILE:HD12	1:T:433:ASP:OD1	2.16	0.45
1:T:273:ARG:HH22	1:T:453:LEU:CD2	2.28	0.45
1:U:47:GLN:H	1:U:48:TYR:HD2	1.65	0.45
1:W:443:ASP:O	1:W:446:THR:HG22	2.17	0.45
1:W:511:ARG:HA	1:W:513:ARG:CD	2.44	0.45
1:X:118:GLN:OE1	1:X:303:VAL:HB	2.17	0.45
1:X:164:LEU:HD22	1:X:169:ASP:OD1	2.17	0.45
2:o:92:ALA:N	2:o:93:PRO:CD	2.80	0.45
2:v:59:VAL:HG22	2:v:73:HIS:O	2.17	0.45
1:A:45:LEU:HD21	1:A:328:ARG:HH21	1.82	0.45
1:A:404:MSE:CE	1:L:334:MSE:HE3	2.47	0.45
1:B:47:GLN:N	1:B:47:GLN:CD	2.72	0.45
1:B:47:GLN:O	1:B:47:GLN:CG	2.65	0.45
1:B:246:TYR:HD2	1:B:511:ARG:CB	2.28	0.45
1:B:248:LYS:HZ2	1:B:251:ILE:HD12	1.81	0.45
1:B:273:ARG:O	1:B:274:ARG:CB	2.64	0.45
1:C:35:PHE:CE1	1:C:321:ARG:NH1	2.84	0.45
1:C:47:GLN:C	1:C:48:TYR:CD2	2.95	0.45
1:D:177:HIS:HE1	1:D:221:GLU:OE1	2.00	0.45
1:D:590:GLN:O	1:D:594:VAL:HG23	2.17	0.45
1:E:9:GLU:HG3	1:E:12:LEU:H	1.82	0.45
1:E:236:GLN:HE21	1:E:265:LYS:HZ3	1.63	0.45
1:E:577:ILE:HG12	1:E:582:LYS:CG	2.41	0.45
1:F:317:GLU:HB3	1:F:321:ARG:CZ	2.46	0.45
1:G:293:ILE:HD13	1:G:294:ALA:N	2.31	0.45
1:G:434:THR:HA	1:G:437:GLN:HG2	1.98	0.45
1:H:24:GLU:C	1:H:26:ARG:N	2.73	0.45
1:H:77:ASP:HB2	1:H:523:SER:HB2	1.98	0.45
1:H:177:HIS:HE1	1:H:221:GLU:OE1	2.00	0.45
1:H:413:LYS:HE2	1:H:413:LYS:HB3	1.74	0.45
1:I:48:TYR:O	1:I:49:THR:CB	2.64	0.45
1:I:251:ILE:HG23	1:I:507:LEU:HD22	1.98	0.45
1:I:528:LYS:HD2	1:I:560:LEU:HD21	1.99	0.45
1:J:78:VAL:HG21	1:J:444:LEU:CD1	2.21	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:528:LYS:HZ3	1:J:560:LEU:HD21	1.80	0.45
1:K:234:ILE:CG2	1:K:246:TYR:HB3	2.47	0.45
1:K:255:ILE:O	1:K:256:ASP:C	2.60	0.45
1:K:534:GLU:O	1:K:538:LEU:HD23	2.17	0.45
1:L:35:PHE:CE1	1:L:321:ARG:NH1	2.84	0.45
1:L:251:ILE:HG23	1:L:507:LEU:HD22	1.99	0.45
2:f:71:ASP:O	2:f:72:ASP:CB	2.65	0.45
1:N:260:ASP:HA	1:N:264:ILE:HB	1.97	0.45
1:N:378:ASP:HA	2:l:109:TYR:HD2	1.82	0.45
1:O:444:LEU:HD13	1:O:444:LEU:N	2.31	0.45
1:P:26:ARG:HG3	1:P:27:ARG:N	2.31	0.45
1:P:26:ARG:O	1:P:27:ARG:C	2.59	0.45
1:P:193:LEU:HD22	1:P:287:LEU:HB3	1.98	0.45
1:P:444:LEU:O	1:P:445:GLU:C	2.57	0.45
1:R:444:LEU:O	1:R:446:THR:N	2.49	0.45
1:S:26:ARG:O	1:S:27:ARG:C	2.59	0.45
1:S:78:VAL:CG1	1:S:79:LEU:H	2.30	0.45
1:S:123:VAL:HG13	1:S:304:PHE:CE1	2.52	0.45
1:S:266:ILE:O	1:S:267:ALA:HB2	2.17	0.45
1:U:232:ALA:HB1	1:U:233:PHE:H	1.57	0.45
1:U:429:GLN:HG2	1:U:429:GLN:O	2.16	0.45
1:W:77:ASP:HB2	1:W:523:SER:HB2	1.99	0.45
1:W:127:ARG:HG2	1:W:147:GLU:HB2	1.98	0.45
1:W:383:ASP:C	1:W:385:PRO:HD3	2.40	0.45
1:X:76:ILE:HD12	1:X:433:ASP:OD1	2.17	0.45
2:l:92:ALA:N	2:l:93:PRO:CD	2.80	0.45
2:r:69:GLU:C	2:r:69:GLU:OE1	2.60	0.45
2:t:80:VAL:C	2:t:82:ALA:N	2.72	0.45
2:u:92:ALA:N	2:u:93:PRO:CD	2.80	0.45
1:A:47:GLN:N	1:A:47:GLN:CD	2.72	0.45
1:A:177:HIS:HE1	1:A:221:GLU:OE1	2.00	0.45
1:A:534:GLU:O	1:A:538:LEU:HD23	2.17	0.45
1:B:232:ALA:N	1:B:269:ARG:O	2.50	0.45
1:B:255:ILE:O	1:B:256:ASP:C	2.60	0.45
1:C:456:ALA:CB	1:C:509:ASP:OD2	2.65	0.45
1:C:459:ARG:HD2	1:C:459:ARG:C	2.42	0.45
1:D:456:ALA:CB	1:D:509:ASP:OD2	2.65	0.45
1:E:48:TYR:O	1:E:49:THR:CB	2.64	0.45
1:F:49:THR:O	1:F:50:THR:C	2.56	0.45
1:F:164:LEU:HD22	1:F:169:ASP:CG	2.41	0.45
1:F:456:ALA:CB	1:F:509:ASP:OD2	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:86:ALA:CB	1:G:515:GLU:HG3	2.47	0.45
1:G:197:ASP:O	1:G:198:ILE:HB	2.15	0.45
1:G:567:MSE:SE	1:H:576:LEU:HD13	2.67	0.45
1:H:47:GLN:O	1:H:47:GLN:CG	2.65	0.45
1:H:534:GLU:O	1:H:538:LEU:HD23	2.17	0.45
1:I:164:LEU:HA	1:I:307:TRP:CH2	2.51	0.45
1:I:177:HIS:HE1	1:I:221:GLU:OE1	2.00	0.45
1:I:273:ARG:O	1:I:274:ARG:HB3	2.16	0.45
1:I:434:THR:HA	1:I:437:GLN:HG2	1.98	0.45
1:I:451:ASP:O	1:I:456:ALA:N	2.41	0.45
1:J:47:GLN:C	1:J:48:TYR:CD2	2.95	0.45
1:J:563:LYS:HD3	1:K:557:PHE:CE2	2.52	0.45
1:K:47:GLN:C	1:K:48:TYR:CD2	2.95	0.45
1:L:234:ILE:HG22	1:L:246:TYR:HB3	1.98	0.45
1:L:434:THR:HA	1:L:437:GLN:HG2	1.98	0.45
1:L:534:GLU:O	1:L:538:LEU:HD23	2.17	0.45
2:a:28:VAL:CB	2:a:96:LEU:HD13	2.45	0.45
1:M:26:ARG:HG3	1:M:27:ARG:N	2.31	0.45
1:N:24:GLU:N	1:N:24:GLU:CD	2.75	0.45
1:N:198:ILE:HA	1:N:199:PRO:HD3	1.70	0.45
1:O:35:PHE:HZ	1:O:321:ARG:NE	2.11	0.45
1:P:80:TYR:OH	1:P:444:LEU:HD12	2.17	0.45
1:P:273:ARG:CZ	1:P:275:ARG:HE	2.30	0.45
1:P:444:LEU:HD13	1:P:444:LEU:N	2.30	0.45
1:Q:136:SER:N	1:Q:137:PRO:HD3	2.33	0.45
1:S:15:PHE:CE2	1:S:19:TRP:NE1	2.85	0.45
1:T:232:ALA:HB2	1:T:269:ARG:O	2.17	0.45
1:T:378:ASP:O	1:T:381:SER:O	2.35	0.45
1:U:330:ARG:O	1:U:334:MSE:HB2	2.17	0.45
1:U:343:ARG:O	1:U:344:THR:HB	2.16	0.45
1:V:198:ILE:O	1:V:198:ILE:HG22	2.17	0.45
1:W:33:LEU:HD12	1:W:34:PHE:N	2.31	0.45
1:W:280:ILE:N	1:W:280:ILE:HD12	2.32	0.45
1:W:330:ARG:HD2	1:W:409:THR:CG2	2.40	0.45
1:X:158:TRP:HD1	1:X:158:TRP:H	1.65	0.45
1:X:418:LEU:HB2	1:X:428:GLY:O	2.16	0.45
2:k:47:TRP:N	2:k:47:TRP:CD1	2.84	0.45
2:l:12:ALA:HB3	2:l:15:ARG:CD	2.47	0.45
2:p:80:VAL:C	2:p:82:ALA:N	2.74	0.45
2:q:80:VAL:C	2:q:82:ALA:N	2.74	0.45
2:s:83:VAL:HG23	2:s:84:PHE:N	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:t:10:VAL:HA	2:t:15:ARG:HG2	1.98	0.45
2:v:30:PRO:HB2	2:v:31:GLN:H	1.57	0.45
1:A:348:LYS:HB2	1:L:372:TYR:CD2	2.50	0.45
1:B:9:GLU:HG3	1:B:12:LEU:H	1.81	0.45
1:B:47:GLN:C	1:B:48:TYR:CD2	2.95	0.45
1:B:334:MSE:HE3	1:C:404:MSE:HE3	1.99	0.45
1:C:139:SER:CB	1:C:455:THR:CG2	2.80	0.45
1:C:234:ILE:CG2	1:C:246:TYR:HB3	2.47	0.45
1:C:434:THR:HA	1:C:437:GLN:HG2	1.98	0.45
1:D:45:LEU:HD21	1:D:328:ARG:HH21	1.82	0.45
1:D:201:PHE:HE2	1:D:281:ILE:HG22	1.80	0.45
1:D:534:GLU:O	1:D:538:LEU:HD23	2.17	0.45
1:D:554:LEU:HD22	1:E:567:MSE:HE2	1.99	0.45
1:E:86:ALA:CB	1:E:515:GLU:HG3	2.47	0.45
1:F:31:ASN:HD22	1:F:31:ASN:HA	1.62	0.45
1:F:86:ALA:CB	1:F:515:GLU:HG3	2.47	0.45
1:G:238:PRO:HG3	1:G:263:PHE:CB	2.46	0.45
1:G:255:ILE:O	1:G:256:ASP:C	2.60	0.45
1:G:376:ARG:HB2	1:H:352:TRP:CG	2.52	0.45
1:H:32:ASP:CG	1:H:316:TYR:CE2	2.94	0.45
1:H:227:GLU:HA	1:H:274:ARG:CA	2.44	0.45
1:H:372:TYR:CE2	1:I:348:LYS:HB2	2.51	0.45
1:H:434:THR:HA	1:H:437:GLN:HG2	1.97	0.45
1:H:542:THR:HA	1:H:543:PRO:HD3	1.82	0.45
1:I:45:LEU:HD22	1:I:45:LEU:N	2.32	0.45
1:I:329:LEU:HD22	2:f:142:PRO:HG2	1.98	0.45
1:K:26:ARG:NH2	1:K:30:LYS:HB2	2.28	0.45
1:K:164:LEU:HA	1:K:307:TRP:CH2	2.51	0.45
1:L:47:GLN:O	1:L:47:GLN:CG	2.65	0.45
1:L:246:TYR:HD2	1:L:511:ARG:CB	2.28	0.45
2:a:57:TYR:H	2:a:63:ILE:H	1.65	0.45
2:b:143:THR:N	2:b:154:GLU:HA	2.32	0.45
2:c:57:TYR:H	2:c:63:ILE:H	1.65	0.45
2:c:78:GLU:O	2:c:79:GLY:C	2.59	0.45
2:e:71:ASP:O	2:e:72:ASP:CB	2.65	0.45
2:h:71:ASP:O	2:h:72:ASP:CB	2.65	0.45
2:i:57:TYR:H	2:i:63:ILE:H	1.65	0.45
2:j:20:ARG:C	2:j:22:ALA:N	2.74	0.45
1:M:41:TRP:HE1	1:O:27:ARG:HH21	1.63	0.44
1:M:118:GLN:OE1	1:M:303:VAL:HB	2.17	0.44
1:M:274:ARG:O	1:M:275:ARG:HD2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:378:ASP:HA	2:n:109:TYR:HD2	1.82	0.44
1:M:437:GLN:HA	1:M:440:MSE:HB2	1.97	0.44
1:N:136:SER:N	1:N:137:PRO:HD3	2.31	0.44
1:N:236:GLN:H	1:N:265:LYS:HB2	1.82	0.44
1:N:577:ILE:HG12	1:N:582:LYS:CG	2.45	0.44
1:O:161:ASN:O	1:O:161:ASN:CG	2.60	0.44
1:Q:26:ARG:O	1:Q:27:ARG:C	2.60	0.44
1:Q:57:PHE:N	1:Q:57:PHE:CD1	2.84	0.44
1:Q:193:LEU:HD22	1:Q:287:LEU:HB3	1.97	0.44
1:Q:273:ARG:HH22	1:Q:453:LEU:CD2	2.30	0.44
1:Q:280:ILE:N	1:Q:280:ILE:HD12	2.33	0.44
1:Q:359:PHE:HD1	2:r:120:ILE:HD11	1.82	0.44
1:Q:429:GLN:O	1:Q:429:GLN:HG2	2.17	0.44
1:R:71:MSE:HE3	1:R:115:VAL:HB	1.98	0.44
1:R:123:VAL:CG1	1:R:304:PHE:CE1	3.00	0.44
1:R:236:GLN:H	1:R:265:LYS:HB2	1.82	0.44
1:R:511:ARG:HA	1:R:513:ARG:CD	2.45	0.44
1:S:82:PRO:O	1:S:516:CYS:HA	2.17	0.44
1:T:158:TRP:HD1	1:T:158:TRP:H	1.64	0.44
1:T:420:VAL:HA	1:T:428:GLY:HA2	1.98	0.44
1:T:444:LEU:O	1:T:445:GLU:C	2.60	0.44
1:U:100:THR:HG22	1:U:138:THR:HG22	1.98	0.44
1:U:147:GLU:HA	1:U:148:PRO:HD3	1.81	0.44
1:U:316:TYR:O	1:U:321:ARG:NH1	2.50	0.44
1:V:444:LEU:HD13	1:V:444:LEU:N	2.32	0.44
1:X:34:PHE:O	1:X:37:ARG:HB2	2.17	0.44
1:X:343:ARG:NH1	2:r:126:ALA:O	2.48	0.44
2:m:69:GLU:OE1	2:m:69:GLU:C	2.60	0.44
2:n:80:VAL:C	2:n:82:ALA:N	2.75	0.44
2:o:69:GLU:C	2:o:69:GLU:OE1	2.61	0.44
2:o:113:LEU:HD23	2:o:113:LEU:HA	1.78	0.44
1:A:45:LEU:HD22	1:A:45:LEU:N	2.32	0.44
1:B:35:PHE:CE1	1:B:321:ARG:NH1	2.84	0.44
1:B:78:VAL:HG21	1:B:444:LEU:CD1	2.21	0.44
1:C:78:VAL:HG21	1:C:444:LEU:CD1	2.21	0.44
1:D:232:ALA:N	1:D:269:ARG:O	2.50	0.44
1:D:255:ILE:O	1:D:256:ASP:C	2.60	0.44
1:E:434:THR:O	1:E:437:GLN:HG2	2.17	0.44
1:E:528:LYS:HD2	1:E:560:LEU:HD21	1.99	0.44
1:F:47:GLN:O	1:F:47:GLN:CG	2.65	0.44
1:F:177:HIS:HE1	1:F:221:GLU:OE1	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:534:GLU:O	1:F:538:LEU:HD23	2.17	0.44
1:G:262:GLY:O	1:G:263:PHE:HB3	2.17	0.44
1:G:434:THR:O	1:G:437:GLN:HG2	2.17	0.44
1:H:9:GLU:HG3	1:H:12:LEU:H	1.81	0.44
1:I:459:ARG:HD2	1:I:459:ARG:C	2.42	0.44
1:J:9:GLU:HG3	1:J:12:LEU:H	1.81	0.44
1:J:238:PRO:HG3	1:J:263:PHE:CB	2.46	0.44
1:J:255:ILE:O	1:J:256:ASP:C	2.60	0.44
1:J:273:ARG:NH2	1:J:453:LEU:HD11	2.32	0.44
1:J:528:LYS:HD2	1:J:560:LEU:HD21	1.99	0.44
1:K:86:ALA:CB	1:K:515:GLU:HG3	2.47	0.44
1:K:232:ALA:N	1:K:269:ARG:O	2.50	0.44
1:K:262:GLY:O	1:K:263:PHE:HB3	2.17	0.44
1:K:273:ARG:NH2	1:K:453:LEU:HD11	2.33	0.44
1:L:45:LEU:HD21	1:L:328:ARG:HH21	1.82	0.44
1:L:47:GLN:C	1:L:48:TYR:CD2	2.95	0.44
1:L:77:ASP:HB2	1:L:523:SER:HB2	1.98	0.44
2:Z:39:PRO:HB2	2:Z:40:GLN:H	1.51	0.44
2:a:20:ARG:C	2:a:22:ALA:N	2.74	0.44
2:e:57:TYR:H	2:e:63:ILE:H	1.65	0.44
2:f:104:TYR:N	2:f:104:TYR:CD1	2.85	0.44
2:g:71:ASP:CB	2:g:75:PRO:HD2	2.36	0.44
2:g:143:THR:N	2:g:154:GLU:HA	2.32	0.44
2:h:57:TYR:H	2:h:63:ILE:H	1.65	0.44
1:M:136:SER:N	1:M:137:PRO:HD3	2.32	0.44
1:M:236:GLN:H	1:M:265:LYS:HB2	1.83	0.44
1:O:47:GLN:N	1:O:48:TYR:HD2	2.15	0.44
1:O:78:VAL:CG1	1:O:444:LEU:HG	2.47	0.44
1:O:427:GLY:C	1:O:429:GLN:N	2.75	0.44
1:P:57:PHE:CD1	1:P:57:PHE:N	2.86	0.44
1:P:164:LEU:HA	1:P:307:TRP:HH2	1.81	0.44
1:P:198:ILE:O	1:P:198:ILE:HG22	2.16	0.44
1:P:322:LEU:HD22	1:P:322:LEU:H	1.81	0.44
1:Q:418:LEU:HB2	1:Q:428:GLY:O	2.16	0.44
1:R:118:GLN:OE1	1:R:303:VAL:HB	2.16	0.44
1:R:528:LYS:CD	1:R:560:LEU:HD21	2.47	0.44
1:S:155:HIS:CE1	1:S:204:PRO:HB2	2.52	0.44
1:S:236:GLN:H	1:S:265:LYS:HB2	1.82	0.44
1:S:564:GLY:O	1:T:554:LEU:HD21	2.17	0.44
1:T:71:MSE:HE3	1:T:115:VAL:HB	1.98	0.44
1:U:161:ASN:O	1:U:161:ASN:CG	2.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:190:LYS:HA	1:V:190:LYS:HE3	2.00	0.44
1:V:387:GLN:H	1:V:387:GLN:HG2	1.57	0.44
1:W:24:GLU:O	1:W:26:ARG:N	2.49	0.44
1:W:236:GLN:HG3	1:W:265:LYS:HG2	1.99	0.44
1:W:427:GLY:C	1:W:429:GLN:N	2.76	0.44
1:X:38:VAL:HG21	1:X:324:LYS:HD2	1.99	0.44
1:X:71:MSE:HE3	1:X:115:VAL:HB	1.99	0.44
1:X:322:LEU:HD22	1:X:322:LEU:N	2.32	0.44
1:X:340:ILE:O	1:X:344:THR:HG21	2.16	0.44
2:n:67:PRO:O	2:n:68:ALA:HB2	2.16	0.44
1:A:590:GLN:O	1:A:594:VAL:HG23	2.16	0.44
1:B:35:PHE:HE2	1:B:324:LYS:NZ	2.07	0.44
1:B:251:ILE:HG23	1:B:507:LEU:HD22	1.98	0.44
1:B:343:ARG:H	1:B:343:ARG:HG2	1.52	0.44
1:C:590:GLN:O	1:C:594:VAL:HG23	2.16	0.44
1:D:77:ASP:HB2	1:D:523:SER:HB2	1.98	0.44
1:D:383:ASP:CG	1:D:385:PRO:HD3	2.43	0.44
1:D:459:ARG:C	1:D:459:ARG:HD2	2.42	0.44
1:E:78:VAL:CG2	1:E:444:LEU:HD21	2.46	0.44
1:E:246:TYR:HD2	1:E:511:ARG:CB	2.28	0.44
1:E:383:ASP:CG	1:E:385:PRO:HD3	2.43	0.44
1:F:45:LEU:HD22	1:F:45:LEU:N	2.32	0.44
1:F:227:GLU:OE2	1:F:227:GLU:N	2.47	0.44
1:F:273:ARG:O	1:F:274:ARG:HB3	2.17	0.44
1:F:383:ASP:CG	1:F:385:PRO:HD3	2.43	0.44
1:F:451:ASP:O	1:F:456:ALA:N	2.41	0.44
1:G:47:GLN:O	1:G:47:GLN:CG	2.65	0.44
1:G:456:ALA:CB	1:G:509:ASP:OD2	2.65	0.44
1:H:45:LEU:HD21	1:H:328:ARG:HH21	1.82	0.44
1:H:251:ILE:HG23	1:H:507:LEU:HD22	1.99	0.44
1:H:255:ILE:O	1:H:256:ASP:C	2.60	0.44
1:I:234:ILE:CG2	1:I:246:TYR:HB3	2.47	0.44
1:J:45:LEU:HD22	1:J:45:LEU:N	2.32	0.44
1:J:177:HIS:HE1	1:J:221:GLU:OE1	2.00	0.44
1:J:459:ARG:HD2	1:J:459:ARG:C	2.42	0.44
1:K:538:LEU:HB3	1:K:551:LEU:HD13	2.00	0.44
1:L:9:GLU:HG3	1:L:12:LEU:H	1.81	0.44
1:L:26:ARG:NH2	1:L:30:LYS:HB2	2.28	0.44
1:L:177:HIS:HE1	1:L:221:GLU:OE1	2.00	0.44
1:L:234:ILE:CG2	1:L:246:TYR:HB3	2.47	0.44
2:i:75:PRO:HA	2:i:76:PRO:HD3	1.42	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:j:71:ASP:O	2:j:72:ASP:CB	2.65	0.44
2:j:143:THR:N	2:j:154:GLU:HA	2.32	0.44
1:N:232:ALA:HB2	1:N:269:ARG:O	2.18	0.44
1:O:236:GLN:HG3	1:O:265:LYS:HG2	2.00	0.44
1:O:273:ARG:HH22	1:O:453:LEU:CD2	2.30	0.44
1:P:118:GLN:OE1	1:P:303:VAL:HB	2.17	0.44
1:Q:236:GLN:H	1:Q:265:LYS:HB2	1.82	0.44
1:Q:420:VAL:HA	1:Q:428:GLY:HA2	1.99	0.44
1:S:26:ARG:HG3	1:S:27:ARG:N	2.31	0.44
1:S:422:THR:HG22	1:S:423:GLU:N	2.32	0.44
1:S:444:LEU:HD13	1:S:444:LEU:N	2.32	0.44
1:T:136:SER:N	1:T:137:PRO:HD3	2.32	0.44
1:T:422:THR:HG22	1:T:423:GLU:N	2.31	0.44
1:U:164:LEU:HD22	1:U:169:ASP:OD1	2.17	0.44
1:V:77:ASP:HB2	1:V:523:SER:HB2	1.98	0.44
1:W:26:ARG:HG3	1:W:27:ARG:N	2.32	0.44
1:W:34:PHE:O	1:W:37:ARG:HB2	2.18	0.44
1:W:316:TYR:O	1:W:321:ARG:NH1	2.50	0.44
1:X:316:TYR:O	1:X:321:ARG:NH1	2.50	0.44
2:n:48:TYR:H	2:n:54:ILE:H	1.65	0.44
2:q:59:VAL:HG22	2:q:73:HIS:O	2.18	0.44
2:q:83:VAL:HG23	2:q:84:PHE:N	2.33	0.44
2:s:12:ALA:HB3	2:s:15:ARG:CD	2.47	0.44
2:u:30:PRO:HB2	2:u:31:GLN:H	1.58	0.44
1:A:47:GLN:C	1:A:48:TYR:CD2	2.95	0.44
1:A:400:ALA:HB3	1:L:395:PRO:HB2	1.99	0.44
1:C:48:TYR:O	1:C:49:THR:CB	2.64	0.44
1:C:262:GLY:O	1:C:263:PHE:HB3	2.17	0.44
1:C:343:ARG:H	1:C:343:ARG:HG2	1.52	0.44
1:D:45:LEU:HD22	1:D:45:LEU:N	2.32	0.44
1:D:273:ARG:NH2	1:D:453:LEU:HD11	2.32	0.44
1:D:399:GLN:OE1	1:D:399:GLN:C	2.61	0.44
1:D:451:ASP:O	1:D:456:ALA:N	2.41	0.44
1:E:26:ARG:NH2	1:E:30:LYS:HB2	2.28	0.44
1:E:456:ALA:CB	1:E:509:ASP:OD2	2.65	0.44
1:F:15:PHE:HE2	1:F:19:TRP:HE1	1.66	0.44
1:F:528:LYS:HZ2	1:F:560:LEU:HD21	1.79	0.44
1:G:47:GLN:C	1:G:48:TYR:CD2	2.95	0.44
1:G:251:ILE:HG23	1:G:507:LEU:HD22	1.99	0.44
1:H:86:ALA:CB	1:H:515:GLU:HG3	2.47	0.44
1:H:334:MSE:HE3	1:I:404:MSE:HE1	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:25:ALA:O	1:I:29:ALA:CB	2.58	0.44
1:I:86:ALA:CB	1:I:515:GLU:HG3	2.47	0.44
1:I:164:LEU:HD22	1:I:169:ASP:CG	2.42	0.44
1:I:399:GLN:C	1:I:399:GLN:OE1	2.61	0.44
1:I:444:LEU:HD13	1:I:444:LEU:N	2.31	0.44
1:I:456:ALA:CB	1:I:509:ASP:OD2	2.65	0.44
1:J:232:ALA:N	1:J:269:ARG:O	2.50	0.44
1:J:273:ARG:O	1:J:274:ARG:HB3	2.17	0.44
1:K:142:GLN:C	1:K:143:VAL:HG23	2.43	0.44
1:K:177:HIS:HE1	1:K:221:GLU:OE1	2.00	0.44
2:Y:39:PRO:HB2	2:Y:40:GLN:H	1.51	0.44
2:Y:57:TYR:H	2:Y:63:ILE:H	1.65	0.44
2:f:143:THR:N	2:f:154:GLU:HA	2.32	0.44
2:h:71:ASP:C	2:h:73:GLU:H	2.26	0.44
1:M:443:ASP:O	1:M:446:THR:HG22	2.18	0.44
1:N:276:VAL:CG2	1:N:293:ILE:HG23	2.47	0.44
1:N:427:GLY:C	1:N:429:GLN:N	2.75	0.44
1:O:429:GLN:HG2	1:O:429:GLN:O	2.18	0.44
1:P:33:LEU:HD12	1:P:34:PHE:N	2.32	0.44
1:P:38:VAL:HG21	1:P:324:LYS:HD2	1.98	0.44
1:P:78:VAL:CG1	1:P:444:LEU:HG	2.47	0.44
1:P:274:ARG:O	1:P:275:ARG:HD2	2.18	0.44
1:P:437:GLN:HA	1:P:440:MSE:HB2	2.00	0.44
1:P:510:ILE:O	1:P:513:ARG:HD2	2.16	0.44
1:Q:40:GLN:HE21	1:Q:40:GLN:HB2	1.58	0.44
1:Q:118:GLN:OE1	1:Q:303:VAL:HB	2.17	0.44
1:Q:190:LYS:HA	1:Q:190:LYS:HE3	2.00	0.44
1:R:100:THR:HG22	1:R:138:THR:HG22	1.98	0.44
1:R:174:THR:N	3:R:705:HOH:O	2.50	0.44
1:S:80:TYR:OH	1:S:444:LEU:HD12	2.18	0.44
1:S:437:GLN:HA	1:S:440:MSE:HB2	1.99	0.44
1:T:236:GLN:H	1:T:265:LYS:HB2	1.82	0.44
1:U:29:ALA:O	1:U:33:LEU:HG	2.18	0.44
1:U:422:THR:HG22	1:U:423:GLU:N	2.31	0.44
1:V:34:PHE:O	1:V:37:ARG:HB2	2.17	0.44
1:W:35:PHE:CE1	1:W:321:ARG:NH1	2.85	0.44
1:W:71:MSE:CE	1:W:115:VAL:HB	2.47	0.44
1:W:276:VAL:CG2	1:W:293:ILE:HG23	2.47	0.44
1:X:190:LYS:HE3	1:X:190:LYS:HA	2.00	0.44
1:X:236:GLN:H	1:X:265:LYS:HB2	1.83	0.44
2:r:80:VAL:C	2:r:82:ALA:N	2.75	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s:33:MET:HE3	2:s:33:MET:HB3	1.67	0.44
2:s:128:TYR:HA	2:s:129:PRO:HD3	1.83	0.44
1:A:142:GLN:C	1:A:143:VAL:HG23	2.43	0.44
1:B:538:LEU:HB3	1:B:551:LEU:HD13	2.00	0.44
1:C:47:GLN:O	1:C:47:GLN:CG	2.65	0.44
1:C:538:LEU:HB3	1:C:551:LEU:HD13	2.00	0.44
1:D:66:LYS:O	1:D:70:GLU:HG3	2.18	0.44
1:D:219:ILE:HD13	1:D:282:THR:HG22	2.00	0.44
1:E:45:LEU:HD22	1:E:45:LEU:N	2.32	0.44
1:F:77:ASP:HB2	1:F:523:SER:HB2	1.98	0.44
1:F:262:GLY:O	1:F:263:PHE:HB3	2.17	0.44
1:G:45:LEU:HD22	1:G:45:LEU:N	2.32	0.44
1:H:182:ASN:HD22	1:I:171:ARG:HH21	1.65	0.44
1:H:383:ASP:CG	1:H:385:PRO:HD3	2.43	0.44
1:H:456:ALA:CB	1:H:509:ASP:OD2	2.65	0.44
1:I:434:THR:O	1:I:437:GLN:HG2	2.18	0.44
1:I:538:LEU:HB3	1:I:551:LEU:HD13	2.00	0.44
1:J:251:ILE:HG23	1:J:507:LEU:HD22	1.98	0.44
1:K:45:LEU:HD21	1:K:328:ARG:HH21	1.82	0.44
1:L:86:ALA:CB	1:L:515:GLU:HG3	2.47	0.44
1:L:273:ARG:NH2	1:L:453:LEU:HD11	2.33	0.44
1:L:383:ASP:CG	1:L:385:PRO:HD3	2.43	0.44
1:L:434:THR:O	1:L:437:GLN:HG2	2.18	0.44
2:Y:104:TYR:N	2:Y:104:TYR:CD1	2.85	0.44
2:Z:143:THR:N	2:Z:154:GLU:HA	2.32	0.44
2:b:71:ASP:O	2:b:72:ASP:CB	2.65	0.44
2:c:71:ASP:O	2:c:72:ASP:CB	2.65	0.44
2:d:71:ASP:O	2:d:72:ASP:CB	2.65	0.44
2:d:143:THR:N	2:d:154:GLU:HA	2.32	0.44
1:M:310:VAL:HG22	1:N:40:GLN:HG2	1.98	0.44
1:M:387:GLN:H	1:M:387:GLN:HG2	1.58	0.44
1:M:444:LEU:O	1:M:446:THR:N	2.50	0.44
1:O:266:ILE:O	1:O:267:ALA:HB2	2.17	0.44
1:Q:155:HIS:CE1	1:Q:204:PRO:HB2	2.53	0.44
1:Q:161:ASN:O	1:Q:161:ASN:CG	2.61	0.44
1:S:198:ILE:O	1:S:198:ILE:HG22	2.16	0.44
1:S:444:LEU:O	1:S:447:TYR:N	2.50	0.44
1:T:343:ARG:O	1:T:344:THR:HB	2.18	0.44
1:U:35:PHE:CE1	1:U:321:ARG:NH1	2.85	0.44
1:U:77:ASP:HB2	1:U:523:SER:HB2	1.99	0.44
1:U:266:ILE:O	1:U:267:ALA:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:301:VAL:HA	1:U:302:PRO:HD3	1.79	0.44
1:U:301:VAL:HG23	1:U:439:ASN:HB3	2.00	0.44
1:U:399:GLN:OE1	1:X:396:GLU:O	2.35	0.44
1:V:24:GLU:N	1:V:24:GLU:CD	2.74	0.44
1:V:57:PHE:CD1	1:V:57:PHE:N	2.85	0.44
1:V:232:ALA:HB2	1:V:269:ARG:O	2.17	0.44
1:V:444:LEU:O	1:V:445:GLU:C	2.61	0.44
1:W:76:ILE:HD12	1:W:433:ASP:OD1	2.18	0.44
1:W:80:TYR:OH	1:W:444:LEU:HD12	2.18	0.44
1:X:107:ALA:HA	1:X:146:ARG:HB3	2.00	0.44
1:X:160:SER:O	1:X:161:ASN:ND2	2.46	0.44
1:X:577:ILE:HG12	1:X:582:LYS:CG	2.45	0.44
2:p:10:VAL:HA	2:p:15:ARG:HG2	2.00	0.44
1:A:164:LEU:HA	1:A:307:TRP:CH2	2.51	0.44
1:A:251:ILE:HG23	1:A:507:LEU:HD22	1.99	0.44
1:A:456:ALA:CB	1:A:509:ASP:OD2	2.65	0.44
1:B:383:ASP:CG	1:B:385:PRO:HD3	2.43	0.44
1:C:9:GLU:HG3	1:C:12:LEU:H	1.81	0.44
1:C:78:VAL:CG2	1:C:444:LEU:HD21	2.46	0.44
1:C:86:ALA:CB	1:C:515:GLU:HG3	2.47	0.44
1:D:78:VAL:CG2	1:D:444:LEU:HD21	2.46	0.44
1:D:164:LEU:HD22	1:D:169:ASP:CG	2.42	0.44
1:D:234:ILE:HG22	1:D:246:TYR:HB3	1.98	0.44
1:D:434:THR:O	1:D:437:GLN:HG2	2.18	0.44
1:D:538:LEU:HB3	1:D:551:LEU:HD13	2.00	0.44
1:E:444:LEU:HD23	1:E:518:THR:OG1	2.18	0.44
1:F:40:GLN:O	1:F:41:TRP:CB	2.55	0.44
1:F:444:LEU:HD23	1:F:518:THR:OG1	2.18	0.44
1:G:45:LEU:HD21	1:G:328:ARG:HH21	1.82	0.44
1:G:399:GLN:OE1	1:G:399:GLN:C	2.61	0.44
1:G:444:LEU:HD23	1:G:518:THR:OG1	2.18	0.44
1:H:238:PRO:HG3	1:H:263:PHE:CB	2.46	0.44
1:H:328:ARG:HB3	2:d:142:PRO:HG3	2.00	0.44
1:H:434:THR:O	1:H:437:GLN:HG2	2.18	0.44
1:H:528:LYS:HD2	1:H:560:LEU:HD21	1.99	0.44
1:I:444:LEU:HD23	1:I:518:THR:OG1	2.18	0.44
1:J:35:PHE:CE1	1:J:321:ARG:NH1	2.84	0.44
1:J:227:GLU:OE2	1:J:227:GLU:N	2.47	0.44
1:J:434:THR:O	1:J:437:GLN:HG2	2.18	0.44
1:J:534:GLU:O	1:J:538:LEU:HD23	2.17	0.44
1:K:45:LEU:HD22	1:K:45:LEU:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:399:GLN:C	1:K:399:GLN:OE1	2.61	0.44
1:K:456:ALA:CB	1:K:509:ASP:OD2	2.65	0.44
1:L:94:LEU:HA	1:L:97:MSE:CE	2.37	0.44
1:L:262:GLY:O	1:L:263:PHE:HB3	2.17	0.44
1:L:399:GLN:OE1	1:L:399:GLN:C	2.61	0.44
1:L:459:ARG:HD2	1:L:459:ARG:C	2.42	0.44
1:L:590:GLN:O	1:L:594:VAL:HG23	2.17	0.44
2:b:102:PRO:HB3	2:e:109:THR:HG21	2.00	0.44
2:c:89:VAL:C	2:c:91:ALA:N	2.76	0.44
2:c:104:TYR:N	2:c:104:TYR:CD1	2.85	0.44
2:d:89:VAL:C	2:d:91:ALA:N	2.76	0.44
2:i:104:TYR:N	2:i:104:TYR:CD1	2.85	0.44
1:M:78:VAL:CG1	1:M:79:LEU:H	2.31	0.44
1:M:161:ASN:O	1:M:161:ASN:CG	2.61	0.44
1:M:236:GLN:HG3	1:M:265:LYS:HG2	1.99	0.44
1:M:528:LYS:NZ	1:M:560:LEU:HD21	2.32	0.44
1:M:577:ILE:HG12	1:M:582:LYS:CG	2.45	0.44
1:N:420:VAL:HA	1:N:428:GLY:HA2	2.00	0.44
1:O:38:VAL:HG21	1:O:324:LYS:HD2	1.99	0.44
1:O:451:ASP:O	1:O:453:LEU:N	2.51	0.44
1:R:155:HIS:CE1	1:R:204:PRO:HB2	2.52	0.44
1:S:164:LEU:HA	1:S:307:TRP:HH2	1.83	0.44
1:S:165:MSE:HG3	1:S:307:TRP:CD2	2.51	0.44
1:U:47:GLN:CG	1:U:48:TYR:H	2.30	0.44
1:U:444:LEU:O	1:U:447:TYR:N	2.49	0.44
1:V:155:HIS:CE1	1:V:204:PRO:HB2	2.52	0.44
1:V:293:ILE:HG12	1:V:294:ALA:H	1.82	0.44
1:V:387:GLN:O	1:V:389:LEU:HG	2.18	0.44
1:V:407:ALA:HB1	1:W:334:MSE:HE1	1.99	0.44
1:W:155:HIS:CE1	1:W:204:PRO:HB2	2.52	0.44
1:W:444:LEU:O	1:W:445:GLU:C	2.60	0.44
1:X:236:GLN:HG3	1:X:265:LYS:HG2	2.00	0.44
1:X:554:LEU:O	1:X:557:PHE:HB3	2.18	0.44
2:n:64:GLU:OE2	1:D:228:LYS:HG2	2.17	0.44
2:n:69:GLU:C	2:n:69:GLU:OE1	2.60	0.44
2:o:47:TRP:CD1	2:o:47:TRP:N	2.85	0.44
2:p:48:TYR:H	2:p:54:ILE:H	1.66	0.44
2:q:10:VAL:HA	2:q:15:ARG:HG2	2.00	0.44
2:r:83:VAL:HG23	2:r:84:PHE:N	2.32	0.44
2:t:30:PRO:HB2	2:t:31:GLN:H	1.59	0.44
2:v:10:VAL:HA	2:v:15:ARG:HG2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:v:83:VAL:HG23	2:v:84:PHE:N	2.31	0.44
1:A:58:ASP:O	1:A:59:VAL:HB	2.14	0.44
1:A:348:LYS:HE2	1:L:369:TYR:O	2.18	0.44
1:A:451:ASP:O	1:A:456:ALA:N	2.41	0.44
1:B:45:LEU:HD22	1:B:45:LEU:N	2.32	0.44
1:B:95:MSE:HE1	1:B:99:ARG:NH2	2.33	0.44
1:B:434:THR:O	1:B:437:GLN:HG2	2.18	0.44
1:C:273:ARG:NH2	1:C:453:LEU:HD11	2.33	0.44
1:C:293:ILE:HD13	1:C:294:ALA:N	2.31	0.44
1:C:383:ASP:CG	1:C:385:PRO:HD3	2.43	0.44
1:D:9:GLU:HG3	1:D:12:LEU:H	1.81	0.44
1:D:35:PHE:HE2	1:D:324:LYS:NZ	2.07	0.44
1:D:155:HIS:CE1	1:D:204:PRO:HB2	2.53	0.44
1:D:352:TRP:CG	1:E:376:ARG:HB2	2.53	0.44
1:E:534:GLU:O	1:E:538:LEU:HD23	2.17	0.44
1:F:47:GLN:C	1:F:48:TYR:CD2	2.95	0.44
1:F:298:ILE:HA	1:F:299:PRO:HD3	1.82	0.44
1:F:310:VAL:C	1:F:312:ASP:N	2.76	0.44
1:H:219:ILE:HD13	1:H:282:THR:HG22	2.00	0.44
1:I:9:GLU:HG3	1:I:12:LEU:H	1.81	0.44
1:I:45:LEU:HD21	1:I:328:ARG:HH21	1.82	0.44
1:I:47:GLN:C	1:I:48:TYR:CD2	2.95	0.44
1:J:219:ILE:HD13	1:J:282:THR:HG22	2.00	0.44
1:J:456:ALA:CB	1:J:509:ASP:OD2	2.65	0.44
1:K:459:ARG:HD2	1:K:459:ARG:C	2.42	0.44
1:L:248:LYS:HZ1	1:L:513:ARG:HH12	1.64	0.44
1:L:528:LYS:HD2	1:L:560:LEU:HD21	1.99	0.44
2:Y:109:THR:HG21	2:j:102:PRO:HB3	2.00	0.44
2:a:71:ASP:O	2:a:72:ASP:CB	2.65	0.44
2:a:143:THR:N	2:a:154:GLU:HA	2.32	0.44
2:f:78:GLU:O	2:f:79:GLY:C	2.59	0.44
2:i:71:ASP:O	2:i:72:ASP:CB	2.65	0.44
2:i:143:THR:N	2:i:154:GLU:HA	2.32	0.44
1:M:190:LYS:HA	1:M:190:LYS:HE3	2.00	0.44
1:M:248:LYS:HE2	1:M:513:ARG:HH12	1.83	0.44
1:N:33:LEU:HD12	1:N:34:PHE:N	2.33	0.44
1:N:34:PHE:O	1:N:37:ARG:HB2	2.17	0.44
1:N:127:ARG:HG2	1:N:147:GLU:HB2	2.00	0.44
1:O:80:TYR:OH	1:O:444:LEU:HD12	2.18	0.44
1:O:158:TRP:HD1	1:O:158:TRP:H	1.64	0.44
1:P:24:GLU:HG3	1:P:313:LYS:HE2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:236:GLN:HG3	1:P:265:LYS:HG2	2.00	0.44
3:P:718:HOH:O	1:Q:438:LEU:HD22	2.15	0.44
1:Q:135:GLN:OE1	1:R:273:ARG:HG2	2.18	0.44
1:Q:236:GLN:HG3	1:Q:265:LYS:HG2	2.00	0.44
1:R:71:MSE:CE	1:R:115:VAL:HB	2.48	0.44
1:R:372:TYR:CE2	1:X:348:LYS:HB2	2.53	0.44
1:S:330:ARG:O	1:S:334:MSE:HB2	2.17	0.44
1:S:352:TRP:O	1:S:355:GLN:HG2	2.18	0.44
1:S:510:ILE:O	1:S:513:ARG:HD2	2.18	0.44
1:U:158:TRP:H	1:U:158:TRP:HD1	1.66	0.44
1:U:360:GLU:CD	1:U:360:GLU:H	2.26	0.44
1:V:71:MSE:CE	1:V:115:VAL:HB	2.48	0.44
1:V:100:THR:HG22	1:V:138:THR:HG22	2.00	0.44
1:V:236:GLN:HG3	1:V:265:LYS:HG2	1.99	0.44
1:V:343:ARG:NH1	2:v:126:ALA:O	2.49	0.44
1:W:273:ARG:HH22	1:W:453:LEU:CD2	2.30	0.44
2:m:30:PRO:HB2	2:m:31:GLN:H	1.56	0.44
2:u:80:VAL:C	2:u:82:ALA:N	2.75	0.44
2:u:83:VAL:HG23	2:u:84:PHE:N	2.32	0.44
1:A:310:VAL:C	1:A:312:ASP:N	2.76	0.44
1:A:444:LEU:HD23	1:A:518:THR:OG1	2.18	0.44
1:B:236:GLN:HE21	1:B:265:LYS:HZ3	1.63	0.44
1:B:310:VAL:C	1:B:312:ASP:N	2.76	0.44
1:C:45:LEU:HD22	1:C:45:LEU:N	2.32	0.44
1:C:255:ILE:O	1:C:256:ASP:C	2.60	0.44
1:C:399:GLN:C	1:C:399:GLN:OE1	2.61	0.44
1:D:47:GLN:O	1:D:47:GLN:CG	2.65	0.44
1:D:94:LEU:HA	1:D:97:MSE:CE	2.37	0.44
1:E:95:MSE:HE1	1:E:99:ARG:NH2	2.33	0.44
1:E:232:ALA:N	1:E:269:ARG:O	2.50	0.44
1:E:255:ILE:O	1:E:256:ASP:C	2.60	0.44
1:E:413:LYS:HE2	1:E:413:LYS:HB3	1.74	0.44
1:F:95:MSE:HE1	1:F:99:ARG:NH2	2.33	0.44
1:F:359:PHE:HD1	2:f:129:ILE:HD11	1.81	0.44
1:F:413:LYS:HE2	1:F:413:LYS:HB3	1.74	0.44
1:G:95:MSE:HE1	1:G:99:ARG:NH2	2.33	0.44
1:G:282:THR:HG23	1:G:287:LEU:CD1	2.43	0.44
1:H:47:GLN:C	1:H:48:TYR:CD2	2.95	0.44
1:H:399:GLN:C	1:H:399:GLN:OE1	2.61	0.44
1:I:142:GLN:C	1:I:143:VAL:HG23	2.43	0.44
1:I:534:GLU:O	1:I:538:LEU:HD23	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:24:GLU:C	1:J:26:ARG:N	2.73	0.44
1:J:47:GLN:O	1:J:47:GLN:CG	2.65	0.44
1:J:444:LEU:HD23	1:J:518:THR:OG1	2.18	0.44
1:K:434:THR:O	1:K:437:GLN:HG2	2.18	0.44
1:L:15:PHE:HE2	1:L:19:TRP:HE1	1.66	0.44
2:Y:143:THR:N	2:Y:154:GLU:HA	2.32	0.44
2:Z:28:VAL:HG11	2:Z:97:ALA:HA	1.88	0.44
2:c:53:MET:HE2	2:c:92:VAL:CG1	2.20	0.44
2:c:143:THR:N	2:c:154:GLU:HA	2.32	0.44
1:M:390:ALA:CB	1:N:387:GLN:HB3	2.47	0.44
1:M:589:GLU:HA	1:M:592:TRP:HB2	1.99	0.44
1:N:101:ASP:HB3	1:N:138:THR:HG21	1.99	0.44
1:N:236:GLN:HG3	1:N:265:LYS:HG2	2.00	0.44
1:N:399:GLN:OE1	1:V:396:GLU:O	2.36	0.44
1:O:236:GLN:H	1:O:265:LYS:HB2	1.83	0.44
1:P:34:PHE:O	1:P:37:ARG:HB2	2.17	0.44
1:P:198:ILE:HA	1:P:199:PRO:HD3	1.70	0.44
1:Q:33:LEU:HD12	1:Q:34:PHE:N	2.32	0.44
1:Q:584:PRO:CG	1:Q:593:LEU:HD12	2.48	0.44
1:R:57:PHE:CD1	1:R:57:PHE:N	2.86	0.44
1:R:76:ILE:HD12	1:R:433:ASP:OD1	2.17	0.44
1:R:236:GLN:HG3	1:R:265:LYS:HG2	2.00	0.44
1:S:77:ASP:HB2	1:S:523:SER:HB2	2.00	0.44
1:S:399:GLN:OE1	1:U:396:GLU:O	2.36	0.44
1:T:35:PHE:CE1	1:T:321:ARG:NH1	2.85	0.44
1:U:78:VAL:CG1	1:U:79:LEU:H	2.31	0.44
1:U:158:TRP:N	1:U:158:TRP:HD1	2.11	0.44
1:U:293:ILE:HG12	1:U:294:ALA:H	1.83	0.44
1:U:589:GLU:HA	1:U:592:TRP:HB2	1.99	0.44
1:V:82:PRO:HB2	1:V:83:LYS:H	1.62	0.44
1:X:71:MSE:CE	1:X:115:VAL:HB	2.48	0.44
1:X:266:ILE:O	1:X:267:ALA:HB2	2.17	0.44
2:m:47:TRP:N	2:m:47:TRP:CD1	2.83	0.44
2:o:30:PRO:HB2	2:o:31:GLN:H	1.59	0.44
2:q:14:LEU:HD22	2:q:33:MET:SD	2.58	0.44
2:r:33:MET:HB3	2:r:33:MET:HE3	1.68	0.44
2:s:25:LEU:HD13	2:t:96:ALA:HB2	2.00	0.44
2:s:30:PRO:HB2	2:s:31:GLN:H	1.56	0.44
2:s:80:VAL:C	2:s:82:ALA:N	2.75	0.44
2:t:47:TRP:N	2:t:47:TRP:CD1	2.85	0.44
1:A:262:GLY:O	1:A:263:PHE:HB3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:383:ASP:CG	1:A:385:PRO:HD3	2.43	0.44
1:A:399:GLN:C	1:A:399:GLN:OE1	2.61	0.44
1:B:45:LEU:HD21	1:B:328:ARG:HH21	1.82	0.44
1:B:66:LYS:O	1:B:70:GLU:HG3	2.18	0.44
1:B:177:HIS:HE1	1:B:221:GLU:OE1	2.00	0.44
1:B:528:LYS:HZ3	1:B:560:LEU:HD21	1.81	0.44
1:C:248:LYS:HZ1	1:C:513:ARG:HH12	1.64	0.44
1:C:310:VAL:C	1:C:312:ASP:N	2.76	0.44
1:D:334:MSE:HE3	1:F:404:MSE:HE3	1.99	0.44
1:D:444:LEU:HD23	1:D:518:THR:OG1	2.18	0.44
1:D:542:THR:HA	1:D:543:PRO:HD3	1.82	0.44
1:E:35:PHE:HE1	1:E:321:ARG:NH1	2.13	0.44
1:E:35:PHE:HZ	1:E:321:ARG:NE	2.12	0.44
1:F:78:VAL:CG2	1:F:444:LEU:HD21	2.46	0.44
1:F:142:GLN:C	1:F:143:VAL:HG23	2.43	0.44
1:G:142:GLN:C	1:G:143:VAL:HG23	2.43	0.44
1:H:35:PHE:CE1	1:H:321:ARG:NH1	2.84	0.44
1:H:45:LEU:HD22	1:H:45:LEU:N	2.32	0.44
1:H:310:VAL:C	1:H:312:ASP:N	2.76	0.44
1:I:273:ARG:NH2	1:I:453:LEU:HD11	2.32	0.44
1:K:155:HIS:CE1	1:K:204:PRO:HB2	2.53	0.44
1:K:310:VAL:C	1:K:312:ASP:N	2.76	0.44
1:K:334:MSE:HE3	1:L:404:MSE:HE3	2.00	0.44
1:L:45:LEU:HD22	1:L:45:LEU:N	2.32	0.44
1:L:142:GLN:C	1:L:143:VAL:HG23	2.43	0.44
2:f:71:ASP:C	2:f:73:GLU:H	2.26	0.44
1:M:316:TYR:O	1:M:321:ARG:NH1	2.51	0.44
1:M:344:THR:O	1:M:344:THR:CG2	2.66	0.44
1:M:420:VAL:HA	1:M:428:GLY:HA2	2.00	0.44
1:N:437:GLN:HA	1:N:440:MSE:HB2	1.99	0.44
1:P:101:ASP:HB3	1:P:138:THR:HG21	1.99	0.44
1:P:265:LYS:O	1:P:266:ILE:HG12	2.18	0.44
1:P:301:VAL:HA	1:P:302:PRO:HD3	1.79	0.44
1:P:344:THR:O	1:P:344:THR:CG2	2.66	0.44
1:Q:101:ASP:HB3	1:Q:138:THR:HG21	2.00	0.44
1:Q:334:MSE:SE	1:Q:405:LEU:HD11	2.67	0.44
1:Q:344:THR:O	1:Q:344:THR:CG2	2.66	0.44
1:R:107:ALA:HA	1:R:146:ARG:HB3	1.99	0.44
1:S:29:ALA:O	1:S:33:LEU:HG	2.18	0.44
1:S:47:GLN:N	1:S:48:TYR:HD2	2.15	0.44
1:S:409:THR:O	1:S:413:LYS:HG2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:127:ARG:HG2	1:T:147:GLU:HB2	1.98	0.44
1:T:198:ILE:O	1:T:198:ILE:HG22	2.16	0.44
1:T:344:THR:O	1:T:344:THR:CG2	2.66	0.44
1:U:38:VAL:HG21	1:U:324:LYS:HD2	1.98	0.44
1:U:248:LYS:H	1:U:248:LYS:CD	2.17	0.44
1:U:387:GLN:O	1:U:389:LEU:HG	2.18	0.44
1:U:575:GLN:O	1:U:579:MSE:CG	2.65	0.44
1:V:511:ARG:HA	1:V:513:ARG:CD	2.45	0.44
1:V:577:ILE:HG12	1:V:582:LYS:CG	2.44	0.44
1:W:26:ARG:O	1:W:27:ARG:C	2.60	0.44
1:X:100:THR:HG22	1:X:138:THR:HG22	1.99	0.44
1:X:265:LYS:O	1:X:266:ILE:HG12	2.17	0.44
1:X:322:LEU:HD22	1:X:322:LEU:H	1.83	0.44
1:X:371:TYR:HE2	1:X:373:LEU:HD21	1.82	0.44
1:X:589:GLU:HA	1:X:592:TRP:HB2	1.99	0.44
2:p:49:GLN:H	2:p:53:GLY:HA3	1.83	0.44
2:p:83:VAL:HG23	2:p:84:PHE:N	2.33	0.44
2:r:113:LEU:HD23	2:r:113:LEU:HA	1.77	0.44
2:v:47:TRP:N	2:v:47:TRP:CD1	2.84	0.44
1:A:79:LEU:N	1:A:519:ASP:O	2.51	0.44
1:B:155:HIS:CE1	1:B:204:PRO:HB2	2.53	0.44
1:D:15:PHE:HE2	1:D:19:TRP:HE1	1.66	0.44
1:D:47:GLN:C	1:D:48:TYR:CD2	2.95	0.44
1:E:15:PHE:HE2	1:E:19:TRP:HE1	1.66	0.44
1:E:79:LEU:N	1:E:519:ASP:O	2.51	0.44
1:F:434:THR:O	1:F:437:GLN:HG2	2.17	0.44
1:G:66:LYS:O	1:G:70:GLU:HG3	2.18	0.44
1:G:177:HIS:HE1	1:G:221:GLU:OE1	2.00	0.44
1:H:94:LEU:HA	1:H:97:MSE:CE	2.37	0.44
1:H:273:ARG:O	1:H:274:ARG:CB	2.64	0.44
1:H:561:ASP:CB	1:I:89:ASP:HA	2.41	0.44
1:I:35:PHE:HE2	1:I:324:LYS:NZ	2.08	0.44
1:I:383:ASP:CG	1:I:385:PRO:HD3	2.43	0.44
1:J:142:GLN:C	1:J:143:VAL:HG23	2.43	0.44
1:K:251:ILE:HG23	1:K:507:LEU:HD22	1.98	0.44
1:K:528:LYS:HD2	1:K:560:LEU:HD21	1.99	0.44
1:L:58:ASP:O	1:L:59:VAL:HB	2.14	0.44
1:L:79:LEU:N	1:L:519:ASP:O	2.51	0.44
1:L:238:PRO:HG3	1:L:263:PHE:CB	2.46	0.44
2:b:89:VAL:C	2:b:91:ALA:N	2.76	0.44
2:j:150:PRO:O	2:j:151:ASN:C	2.61	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:33:LEU:HD12	1:M:34:PHE:N	2.33	0.43
1:N:190:LYS:HA	1:N:190:LYS:HE3	2.00	0.43
1:O:235:TYR:OH	1:O:252:LYS:NZ	2.50	0.43
1:P:248:LYS:HE2	1:P:513:ARG:HH12	1.83	0.43
1:P:458:ARG:HD3	1:P:458:ARG:HA	1.83	0.43
1:P:567:MSE:HE2	1:Q:554:LEU:HD22	2.00	0.43
1:P:575:GLN:O	1:P:579:MSE:CG	2.64	0.43
1:Q:349:PRO:HG3	1:Q:391:TYR:CE1	2.53	0.43
1:Q:575:GLN:O	1:Q:579:MSE:CG	2.65	0.43
1:R:34:PHE:O	1:R:37:ARG:HB2	2.18	0.43
1:S:245:SER:HG	1:S:247:PHE:HE1	1.65	0.43
1:S:390:ALA:CB	1:U:387:GLN:CB	2.96	0.43
3:S:718:HOH:O	1:T:438:LEU:HD22	2.17	0.43
1:T:35:PHE:HZ	1:T:321:ARG:NE	2.14	0.43
1:U:47:GLN:N	1:U:48:TYR:HD2	2.15	0.43
1:V:179:MSE:O	1:V:217:ILE:HD12	2.18	0.43
1:W:123:VAL:HG13	1:W:304:PHE:CE1	2.53	0.43
1:W:158:TRP:HD1	1:W:158:TRP:H	1.65	0.43
1:X:47:GLN:CG	1:X:48:TYR:H	2.28	0.43
1:X:343:ARG:H	1:X:343:ARG:HG2	1.53	0.43
2:m:83:VAL:HG23	2:m:84:PHE:N	2.32	0.43
2:o:24:THR:HG22	2:o:25:LEU:N	2.33	0.43
2:s:10:VAL:HA	2:s:15:ARG:HG2	1.99	0.43
2:s:100:THR:HG23	2:s:103:ILE:HG13	2.00	0.43
1:A:71:MSE:HE3	1:A:115:VAL:HB	2.00	0.43
1:A:127:ARG:HA	1:A:299:PRO:O	2.18	0.43
1:A:255:ILE:O	1:A:256:ASP:C	2.60	0.43
1:B:71:MSE:HE3	1:B:115:VAL:HB	2.00	0.43
1:B:142:GLN:C	1:B:143:VAL:HG23	2.43	0.43
1:B:262:GLY:O	1:B:263:PHE:HB3	2.17	0.43
1:C:142:GLN:C	1:C:143:VAL:HG23	2.43	0.43
1:C:434:THR:O	1:C:437:GLN:HG2	2.18	0.43
1:D:99:ARG:NH1	1:D:530:GLN:HE21	2.13	0.43
1:D:142:GLN:C	1:D:143:VAL:HG23	2.43	0.43
1:D:273:ARG:O	1:D:274:ARG:HB3	2.17	0.43
1:E:47:GLN:C	1:E:48:TYR:CD2	2.95	0.43
1:E:78:VAL:HG21	1:E:444:LEU:CD1	2.21	0.43
1:E:343:ARG:NH2	2:b:134:ARG:HD3	2.33	0.43
1:E:538:LEU:HB3	1:E:551:LEU:HD13	2.00	0.43
1:H:15:PHE:HE2	1:H:19:TRP:HE1	1.66	0.43
1:H:26:ARG:NH2	1:H:30:LYS:HB2	2.28	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:142:GLN:C	1:H:143:VAL:HG23	2.43	0.43
1:H:273:ARG:NH2	1:H:453:LEU:HD11	2.33	0.43
1:J:79:LEU:N	1:J:519:ASP:O	2.51	0.43
1:J:95:MSE:HE1	1:J:99:ARG:NH2	2.33	0.43
1:L:66:LYS:O	1:L:70:GLU:HG3	2.18	0.43
2:Z:43:GLN:C	2:Z:45:ALA:N	2.70	0.43
2:Z:89:VAL:C	2:Z:91:ALA:N	2.76	0.43
2:a:89:VAL:C	2:a:91:ALA:N	2.76	0.43
2:b:78:GLU:O	2:b:79:GLY:C	2.59	0.43
2:d:104:TYR:N	2:d:104:TYR:CD1	2.85	0.43
2:f:57:TYR:H	2:f:63:ILE:H	1.65	0.43
1:M:265:LYS:O	1:M:266:ILE:HG12	2.18	0.43
1:N:76:ILE:HD12	1:N:433:ASP:OD1	2.18	0.43
1:N:228:LYS:HA	1:N:228:LYS:CE	2.42	0.43
1:O:276:VAL:CG2	1:O:293:ILE:HG23	2.47	0.43
1:O:378:ASP:O	1:O:381:SER:O	2.36	0.43
1:P:584:PRO:CG	1:P:593:LEU:HD12	2.47	0.43
1:Q:266:ILE:O	1:Q:267:ALA:HB2	2.18	0.43
1:S:35:PHE:CE1	1:S:321:ARG:NH1	2.85	0.43
1:U:276:VAL:CG2	1:U:293:ILE:HG23	2.47	0.43
1:V:78:VAL:CG1	1:V:79:LEU:H	2.29	0.43
1:V:274:ARG:O	1:V:275:ARG:HD2	2.18	0.43
1:V:429:GLN:O	1:V:429:GLN:HG2	2.18	0.43
1:W:265:LYS:O	1:W:266:ILE:HG12	2.18	0.43
1:W:360:GLU:HG3	2:v:122:ARG:HB3	2.00	0.43
1:W:584:PRO:CG	1:W:593:LEU:HD12	2.48	0.43
1:X:80:TYR:OH	1:X:444:LEU:HD12	2.18	0.43
2:k:48:TYR:H	2:k:54:ILE:H	1.65	0.43
2:p:69:GLU:OE1	2:p:69:GLU:C	2.61	0.43
1:A:404:MSE:HE1	1:L:334:MSE:SE	2.67	0.43
1:B:198:ILE:HA	1:B:199:PRO:HD3	1.64	0.43
1:B:273:ARG:NH2	1:B:453:LEU:HD11	2.32	0.43
1:B:534:GLU:O	1:B:538:LEU:HD23	2.17	0.43
1:C:45:LEU:HD21	1:C:328:ARG:HH21	1.82	0.43
1:C:155:HIS:CE1	1:C:204:PRO:HB2	2.53	0.43
1:C:177:HIS:HE1	1:C:221:GLU:OE1	2.00	0.43
1:C:266:ILE:O	1:C:267:ALA:HB2	2.19	0.43
1:C:528:LYS:HD2	1:C:560:LEU:HD21	1.99	0.43
1:C:534:GLU:O	1:C:538:LEU:HD23	2.17	0.43
1:D:34:PHE:HE1	1:D:324:LYS:HZ2	1.57	0.43
1:D:35:PHE:CE1	1:D:321:ARG:NH1	2.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:79:LEU:N	1:D:519:ASP:O	2.51	0.43
1:E:155:HIS:CE1	1:E:204:PRO:HB2	2.53	0.43
1:E:273:ARG:NH2	1:E:453:LEU:HD11	2.33	0.43
1:F:82:PRO:HB2	1:F:83:LYS:H	1.58	0.43
1:F:266:ILE:O	1:F:267:ALA:HB2	2.19	0.43
1:F:542:THR:HA	1:F:543:PRO:HD3	1.82	0.43
1:G:94:LEU:HA	1:G:97:MSE:CE	2.37	0.43
1:G:155:HIS:CE1	1:G:204:PRO:HB2	2.53	0.43
1:H:47:GLN:N	1:H:47:GLN:CD	2.72	0.43
1:H:82:PRO:HB2	1:H:83:LYS:H	1.58	0.43
1:H:155:HIS:CE1	1:H:204:PRO:HB2	2.53	0.43
1:H:391:TYR:N	1:H:391:TYR:CD2	2.87	0.43
1:I:95:MSE:HE1	1:I:99:ARG:NH2	2.33	0.43
1:I:219:ILE:HD13	1:I:282:THR:HG22	2.00	0.43
1:I:255:ILE:O	1:I:256:ASP:C	2.60	0.43
1:J:79:LEU:HD23	1:J:521:GLY:HA3	2.00	0.43
1:J:262:GLY:O	1:J:263:PHE:HB3	2.17	0.43
1:J:383:ASP:CG	1:J:385:PRO:HD3	2.43	0.43
1:K:66:LYS:O	1:K:70:GLU:HG3	2.18	0.43
1:K:79:LEU:N	1:K:519:ASP:O	2.51	0.43
1:K:219:ILE:HD13	1:K:282:THR:HG22	2.00	0.43
1:K:282:THR:HG23	1:K:287:LEU:CD1	2.43	0.43
1:K:383:ASP:CG	1:K:385:PRO:HD3	2.43	0.43
1:K:444:LEU:HD23	1:K:518:THR:OG1	2.18	0.43
1:L:79:LEU:HD23	1:L:521:GLY:HA3	2.00	0.43
1:L:155:HIS:CE1	1:L:204:PRO:HB2	2.53	0.43
1:L:266:ILE:O	1:L:267:ALA:HB2	2.18	0.43
1:L:298:ILE:HA	1:L:299:PRO:HD3	1.82	0.43
1:L:444:LEU:HD23	1:L:518:THR:OG1	2.18	0.43
1:L:538:LEU:HB3	1:L:551:LEU:HD13	2.00	0.43
1:L:583:LYS:HA	1:L:584:PRO:HD3	1.85	0.43
1:M:71:MSE:HE3	1:M:115:VAL:HB	1.99	0.43
1:M:174:THR:N	3:M:705:HOH:O	2.50	0.43
1:M:340:ILE:O	1:M:344:THR:HG21	2.19	0.43
1:N:24:GLU:O	1:N:26:ARG:N	2.50	0.43
1:O:26:ARG:O	1:O:27:ARG:C	2.59	0.43
1:O:387:GLN:O	1:O:389:LEU:HG	2.19	0.43
1:O:444:LEU:O	1:O:445:GLU:C	2.62	0.43
1:P:174:THR:N	3:P:705:HOH:O	2.51	0.43
1:Q:53:TYR:OH	1:R:329:LEU:HD21	2.18	0.43
1:Q:92:ASP:OD2	1:Q:92:ASP:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:92:ASP:N	1:R:92:ASP:OD2	2.51	0.43
1:R:198:ILE:O	1:R:198:ILE:HG22	2.17	0.43
1:S:34:PHE:O	1:S:37:ARG:HB2	2.19	0.43
1:S:232:ALA:HB2	1:S:269:ARG:O	2.18	0.43
1:T:77:ASP:HB2	1:T:523:SER:HB2	1.99	0.43
1:T:123:VAL:HG13	1:T:304:PHE:CE1	2.52	0.43
1:T:236:GLN:HG3	1:T:265:LYS:HG2	2.00	0.43
1:T:589:GLU:HA	1:T:592:TRP:HB2	2.00	0.43
1:U:155:HIS:CE1	1:U:204:PRO:HB2	2.53	0.43
1:U:273:ARG:HH22	1:U:453:LEU:CD2	2.32	0.43
1:V:236:GLN:H	1:V:265:LYS:HB2	1.83	0.43
1:V:273:ARG:HH22	1:V:453:LEU:CD2	2.29	0.43
1:W:344:THR:O	1:W:344:THR:CG2	2.66	0.43
1:X:24:GLU:HG3	1:X:313:LYS:HE2	2.01	0.43
2:u:12:ALA:HB3	2:u:15:ARG:CD	2.48	0.43
1:A:528:LYS:HD2	1:A:560:LEU:HD21	1.99	0.43
1:C:71:MSE:HE3	1:C:115:VAL:HB	2.01	0.43
1:D:266:ILE:O	1:D:267:ALA:HB2	2.19	0.43
1:E:142:GLN:C	1:E:143:VAL:HG23	2.43	0.43
1:I:47:GLN:O	1:I:47:GLN:CG	2.65	0.43
1:I:139:SER:CB	1:I:455:THR:CG2	2.80	0.43
1:I:155:HIS:CE1	1:I:204:PRO:HB2	2.53	0.43
1:J:15:PHE:HE2	1:J:19:TRP:HE1	1.66	0.43
1:K:71:MSE:HE3	1:K:115:VAL:HB	2.01	0.43
1:K:266:ILE:O	1:K:267:ALA:HB2	2.19	0.43
1:L:127:ARG:HA	1:L:299:PRO:O	2.18	0.43
1:L:310:VAL:C	1:L:312:ASP:N	2.76	0.43
2:a:150:PRO:O	2:a:151:ASN:C	2.61	0.43
2:b:71:ASP:C	2:b:73:GLU:H	2.26	0.43
2:e:39:PRO:HB2	2:e:40:GLN:H	1.51	0.43
2:g:150:PRO:O	2:g:151:ASN:C	2.61	0.43
1:M:427:GLY:C	1:M:429:GLN:N	2.77	0.43
1:O:71:MSE:CE	1:O:115:VAL:HB	2.48	0.43
1:O:228:LYS:HA	1:O:228:LYS:CE	2.43	0.43
1:P:190:LYS:HE3	1:P:190:LYS:HA	2.00	0.43
1:P:420:VAL:HA	1:P:428:GLY:HA2	2.00	0.43
1:Q:164:LEU:HD22	1:Q:169:ASP:OD1	2.17	0.43
1:Q:387:GLN:CB	1:R:390:ALA:HB2	2.49	0.43
1:R:344:THR:O	1:R:344:THR:CG2	2.67	0.43
1:R:376:ARG:HB2	1:X:352:TRP:CD1	2.54	0.43
1:S:293:ILE:HG12	1:S:294:ALA:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:329:LEU:HD21	1:U:53:TYR:OH	2.17	0.43
1:V:266:ILE:O	1:V:267:ALA:HB2	2.18	0.43
1:V:352:TRP:CD1	1:W:376:ARG:HB2	2.53	0.43
1:V:387:GLN:HA	1:V:388:PRO:HD3	1.92	0.43
2:r:24:THR:HG22	2:r:25:LEU:N	2.33	0.43
2:u:59:VAL:HG22	2:u:73:HIS:O	2.18	0.43
2:u:69:GLU:OE1	2:u:69:GLU:C	2.61	0.43
1:A:95:MSE:HE1	1:A:99:ARG:NH2	2.33	0.43
1:A:99:ARG:NH1	1:A:530:GLN:HE21	2.13	0.43
1:A:155:HIS:CE1	1:A:204:PRO:HB2	2.53	0.43
1:A:343:ARG:NH2	2:Y:134:ARG:HD3	2.33	0.43
1:B:79:LEU:N	1:B:519:ASP:O	2.51	0.43
1:C:227:GLU:OE2	1:C:227:GLU:N	2.47	0.43
1:C:437:GLN:HA	1:C:440:MSE:HB2	2.01	0.43
1:D:79:LEU:HD23	1:D:521:GLY:HA3	2.00	0.43
1:F:127:ARG:HA	1:F:299:PRO:O	2.18	0.43
1:F:273:ARG:NH2	1:F:453:LEU:HD11	2.32	0.43
1:G:34:PHE:CE1	1:G:324:LYS:NZ	2.72	0.43
1:G:47:GLN:C	1:G:48:TYR:HD2	2.27	0.43
1:H:79:LEU:HD23	1:H:521:GLY:HA3	2.00	0.43
1:H:444:LEU:HD23	1:H:518:THR:OG1	2.18	0.43
1:I:79:LEU:N	1:I:519:ASP:O	2.51	0.43
1:I:229:LYS:HD2	1:I:270:GLN:HG3	2.01	0.43
1:I:266:ILE:O	1:I:267:ALA:HB2	2.19	0.43
1:I:391:TYR:CD2	1:I:391:TYR:N	2.87	0.43
1:I:437:GLN:HA	1:I:440:MSE:HB2	2.00	0.43
1:J:538:LEU:HB3	1:J:551:LEU:HD13	2.00	0.43
1:K:35:PHE:HE2	1:K:324:LYS:NZ	2.08	0.43
1:K:343:ARG:H	1:K:343:ARG:HG2	1.52	0.43
1:L:35:PHE:CZ	1:L:321:ARG:CZ	3.02	0.43
1:L:229:LYS:HD2	1:L:270:GLN:HG3	2.01	0.43
1:L:391:TYR:CD2	1:L:391:TYR:N	2.86	0.43
2:Y:150:PRO:O	2:Y:151:ASN:C	2.61	0.43
2:d:57:TYR:H	2:d:63:ILE:H	1.65	0.43
2:e:104:TYR:N	2:e:104:TYR:CD1	2.85	0.43
2:f:89:VAL:C	2:f:91:ALA:N	2.76	0.43
2:j:57:TYR:H	2:j:63:ILE:H	1.65	0.43
1:M:123:VAL:CG1	1:M:304:PHE:CE1	3.00	0.43
1:M:280:ILE:HG22	1:M:287:LEU:HD13	2.00	0.43
1:M:576:LEU:HD13	1:N:567:MSE:SE	2.68	0.43
1:N:15:PHE:CE2	1:N:19:TRP:NE1	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:266:ILE:O	1:N:267:ALA:HB2	2.19	0.43
1:N:458:ARG:HA	1:N:458:ARG:HD3	1.82	0.43
1:O:40:GLN:HE21	1:O:40:GLN:HB2	1.57	0.43
1:O:334:MSE:CG	1:P:404:MSE:HE1	2.48	0.43
1:O:369:TYR:HA	1:O:370:PRO:HD3	1.83	0.43
1:P:92:ASP:OD2	1:P:92:ASP:N	2.51	0.43
1:Q:15:PHE:CE2	1:Q:19:TRP:NE1	2.86	0.43
1:Q:343:ARG:H	1:Q:343:ARG:HG2	1.53	0.43
1:R:190:LYS:HA	1:R:190:LYS:HE3	1.99	0.43
1:R:270:GLN:OE1	1:R:270:GLN:HA	2.18	0.43
1:S:371:TYR:HE2	1:S:373:LEU:HD21	1.83	0.43
1:T:343:ARG:H	1:T:343:ARG:HG2	1.58	0.43
1:T:444:LEU:O	1:T:446:THR:N	2.50	0.43
1:U:232:ALA:HB2	1:U:269:ARG:O	2.18	0.43
1:U:236:GLN:H	1:U:265:LYS:HB2	1.83	0.43
1:V:80:TYR:OH	1:V:444:LEU:HD12	2.18	0.43
1:V:92:ASP:OD2	1:V:92:ASP:N	2.51	0.43
1:V:340:ILE:O	1:V:344:THR:HG21	2.18	0.43
1:V:437:GLN:HA	1:V:440:MSE:HB2	2.00	0.43
1:V:444:LEU:O	1:V:446:THR:N	2.51	0.43
1:W:384:LEU:HD22	1:W:384:LEU:N	2.29	0.43
1:W:413:LYS:HE2	1:W:413:LYS:HB3	1.87	0.43
1:W:589:GLU:HA	1:W:592:TRP:HB2	2.00	0.43
1:X:35:PHE:CE1	1:X:321:ARG:NH1	2.85	0.43
1:X:123:VAL:HG13	1:X:304:PHE:CE1	2.53	0.43
1:X:198:ILE:O	1:X:198:ILE:HG22	2.18	0.43
1:X:440:MSE:O	1:X:443:ASP:HB3	2.18	0.43
1:X:510:ILE:O	1:X:513:ARG:HD2	2.18	0.43
2:k:24:THR:HG22	2:k:25:LEU:N	2.33	0.43
2:n:10:VAL:HA	2:n:15:ARG:HG2	2.00	0.43
2:r:92:ALA:N	2:r:93:PRO:CD	2.81	0.43
1:A:66:LYS:O	1:A:70:GLU:HG3	2.18	0.43
1:A:252:LYS:HE3	1:A:252:LYS:O	2.19	0.43
1:A:273:ARG:NH2	1:A:453:LEU:HD11	2.33	0.43
1:A:391:TYR:CD2	1:A:391:TYR:N	2.87	0.43
1:A:437:GLN:HA	1:A:440:MSE:HB2	2.01	0.43
1:B:79:LEU:HD23	1:B:521:GLY:HA3	2.00	0.43
1:B:528:LYS:HD2	1:B:560:LEU:HD21	1.99	0.43
1:C:66:LYS:O	1:C:70:GLU:HG3	2.18	0.43
1:C:82:PRO:HB2	1:C:83:LYS:H	1.58	0.43
1:D:71:MSE:HE3	1:D:115:VAL:HB	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:82:PRO:HB2	1:E:83:LYS:H	1.58	0.43
1:E:127:ARG:HA	1:E:299:PRO:O	2.18	0.43
1:E:391:TYR:N	1:E:391:TYR:CD2	2.87	0.43
1:G:273:ARG:NH2	1:G:453:LEU:HD11	2.33	0.43
1:H:246:TYR:HD2	1:H:511:ARG:CB	2.28	0.43
1:H:343:ARG:H	1:H:343:ARG:HG2	1.52	0.43
1:I:43:ASP:N	1:I:43:ASP:OD2	2.52	0.43
1:I:78:VAL:CG2	1:I:444:LEU:HD21	2.46	0.43
1:I:378:ASP:O	1:I:381:SER:O	2.37	0.43
1:J:155:HIS:CE1	1:J:204:PRO:HB2	2.53	0.43
1:K:47:GLN:C	1:K:48:TYR:HD2	2.27	0.43
1:L:95:MSE:HE1	1:L:99:ARG:NH2	2.33	0.43
2:e:89:VAL:C	2:e:91:ALA:N	2.76	0.43
2:g:102:PRO:HB3	2:i:109:THR:HG21	1.99	0.43
1:M:345:PRO:HB2	1:M:392:TYR:CE1	2.54	0.43
1:N:26:ARG:HG3	1:N:27:ARG:N	2.32	0.43
1:N:352:TRP:CD2	1:V:376:ARG:HB2	2.53	0.43
1:P:293:ILE:HG12	1:P:294:ALA:H	1.82	0.43
1:P:380:ASN:O	1:P:381:SER:CB	2.66	0.43
1:P:542:THR:HA	1:P:543:PRO:HD3	1.88	0.43
1:Q:265:LYS:O	1:Q:266:ILE:HG12	2.18	0.43
1:R:265:LYS:O	1:R:266:ILE:HG12	2.18	0.43
1:R:334:MSE:SE	1:R:405:LEU:HD11	2.69	0.43
1:S:47:GLN:H	1:S:48:TYR:HD2	1.65	0.43
1:S:57:PHE:CD1	1:S:57:PHE:N	2.87	0.43
1:T:24:GLU:O	1:T:26:ARG:N	2.50	0.43
1:T:78:VAL:CG1	1:T:79:LEU:H	2.30	0.43
1:T:100:THR:HG22	1:T:138:THR:HG22	2.00	0.43
1:T:413:LYS:HE2	1:T:413:LYS:HB3	1.85	0.43
1:T:510:ILE:O	1:T:513:ARG:HD2	2.18	0.43
1:U:24:GLU:O	1:U:26:ARG:N	2.50	0.43
1:V:510:ILE:O	1:V:513:ARG:HD2	2.19	0.43
1:V:589:GLU:HA	1:V:592:TRP:HB2	2.00	0.43
1:X:301:VAL:HG23	1:X:439:ASN:HB3	2.01	0.43
1:X:420:VAL:HA	1:X:428:GLY:HA2	2.00	0.43
2:m:59:VAL:HG22	2:m:73:HIS:O	2.19	0.43
2:n:47:TRP:CD1	2:n:47:TRP:H	2.36	0.43
2:p:47:TRP:N	2:p:47:TRP:CD1	2.85	0.43
2:q:69:GLU:C	2:q:69:GLU:OE1	2.62	0.43
2:q:92:ALA:N	2:q:93:PRO:CD	2.82	0.43
2:r:48:TYR:H	2:r:54:ILE:H	1.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s:69:GLU:C	2:s:69:GLU:OE1	2.61	0.43
2:v:92:ALA:N	2:v:93:PRO:CD	2.82	0.43
1:A:434:THR:O	1:A:437:GLN:HG2	2.18	0.43
1:B:78:VAL:CG2	1:B:444:LEU:HD21	2.46	0.43
1:B:219:ILE:HD13	1:B:282:THR:HG22	2.00	0.43
1:C:47:GLN:C	1:C:48:TYR:HD2	2.27	0.43
1:D:95:MSE:HE1	1:D:99:ARG:NH2	2.33	0.43
1:D:127:ARG:HA	1:D:299:PRO:O	2.18	0.43
1:D:310:VAL:C	1:D:312:ASP:N	2.76	0.43
1:D:350:PHE:HE1	1:E:363:TYR:HE1	1.67	0.43
1:D:567:MSE:SE	1:F:576:LEU:HD13	2.68	0.43
1:D:598:GLN:O	1:D:601:GLN:HB2	2.19	0.43
1:E:47:GLN:C	1:E:48:TYR:HD2	2.27	0.43
1:E:382:GLY:HA2	2:c:117:LYS:NZ	2.34	0.43
1:F:35:PHE:CZ	1:F:321:ARG:CZ	3.02	0.43
1:F:155:HIS:CE1	1:F:204:PRO:HB2	2.53	0.43
1:F:219:ILE:HD13	1:F:282:THR:HG22	2.00	0.43
1:F:399:GLN:C	1:F:399:GLN:OE1	2.61	0.43
1:G:266:ILE:O	1:G:267:ALA:HB2	2.19	0.43
1:G:378:ASP:HA	2:g:118:TYR:HD2	1.83	0.43
1:H:191:TYR:HE1	1:H:278:LYS:HZ3	1.66	0.43
1:H:538:LEU:HB3	1:H:551:LEU:HD13	2.00	0.43
1:I:71:MSE:HE3	1:I:115:VAL:HB	2.00	0.43
1:I:127:ARG:HA	1:I:299:PRO:O	2.18	0.43
1:I:198:ILE:HA	1:I:199:PRO:HD3	1.64	0.43
1:K:391:TYR:N	1:K:391:TYR:CD2	2.87	0.43
1:L:71:MSE:HE3	1:L:115:VAL:HB	2.00	0.43
2:b:104:TYR:N	2:b:104:TYR:CD1	2.85	0.43
2:d:71:ASP:C	2:d:73:GLU:H	2.26	0.43
2:d:101:ALA:N	2:d:102:PRO:CD	2.82	0.43
2:e:20:ARG:C	2:e:22:ALA:N	2.74	0.43
2:f:101:ALA:N	2:f:102:PRO:CD	2.82	0.43
2:i:101:ALA:N	2:i:102:PRO:CD	2.82	0.43
2:j:89:VAL:C	2:j:91:ALA:N	2.76	0.43
1:M:245:SER:HG	1:M:247:PHE:HE1	1.60	0.43
1:M:330:ARG:O	1:M:334:MSE:HB2	2.18	0.43
1:N:34:PHE:HE1	1:N:324:LYS:HZ2	1.62	0.43
1:N:212:LEU:HD12	1:N:212:LEU:N	2.34	0.43
1:P:384:LEU:HD22	1:P:384:LEU:N	2.27	0.43
1:Q:274:ARG:O	1:Q:275:ARG:HD2	2.19	0.43
1:Q:542:THR:HA	1:Q:543:PRO:HD3	1.88	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:38:VAL:HG21	1:R:324:LYS:HD2	1.99	0.43
1:R:78:VAL:CG1	1:R:79:LEU:H	2.30	0.43
1:S:101:ASP:HB3	1:S:138:THR:HG21	2.01	0.43
1:S:431:ALA:HA	1:S:434:THR:HG22	2.01	0.43
1:T:212:LEU:N	1:T:212:LEU:HD12	2.33	0.43
1:U:198:ILE:O	1:U:198:ILE:HG22	2.17	0.43
1:U:584:PRO:CG	1:U:593:LEU:HD12	2.49	0.43
1:W:190:LYS:HA	1:W:190:LYS:HE3	2.00	0.43
2:k:69:GLU:C	2:k:69:GLU:OE1	2.60	0.43
2:r:34:GLN:C	2:r:36:ALA:H	2.27	0.43
2:r:47:TRP:N	2:r:47:TRP:CD1	2.84	0.43
2:t:24:THR:HG22	2:t:25:LEU:N	2.34	0.43
2:u:49:GLN:H	2:u:53:GLY:HA3	1.83	0.43
1:A:15:PHE:HE2	1:A:19:TRP:HE1	1.66	0.43
1:A:35:PHE:CZ	1:A:321:ARG:CZ	3.02	0.43
1:A:43:ASP:OD2	1:A:43:ASP:N	2.52	0.43
1:B:37:ARG:HA	1:B:37:ARG:HD2	1.79	0.43
1:B:212:LEU:N	1:B:212:LEU:HD12	2.34	0.43
1:B:229:LYS:HD2	1:B:270:GLN:HG3	2.01	0.43
1:B:391:TYR:N	1:B:391:TYR:CD2	2.87	0.43
1:B:437:GLN:HA	1:B:440:MSE:HB2	2.00	0.43
1:C:38:VAL:HG21	1:C:324:LYS:HD2	2.01	0.43
1:D:35:PHE:CZ	1:D:321:ARG:CZ	3.02	0.43
1:D:43:ASP:OD2	1:D:43:ASP:N	2.52	0.43
1:D:246:TYR:HD2	1:D:511:ARG:CB	2.28	0.43
1:E:598:GLN:O	1:E:601:GLN:HB2	2.19	0.43
1:F:25:ALA:O	1:F:29:ALA:CB	2.58	0.43
1:F:66:LYS:O	1:F:70:GLU:HG3	2.18	0.43
1:F:437:GLN:HA	1:F:440:MSE:HB2	2.00	0.43
1:F:538:LEU:HB3	1:F:551:LEU:HD13	2.00	0.43
1:G:24:GLU:C	1:G:26:ARG:N	2.73	0.43
1:G:79:LEU:N	1:G:519:ASP:O	2.51	0.43
1:G:219:ILE:HD13	1:G:282:THR:HG22	2.00	0.43
1:G:383:ASP:CG	1:G:385:PRO:HD3	2.43	0.43
1:G:391:TYR:CD2	1:G:391:TYR:N	2.86	0.43
1:H:95:MSE:HE1	1:H:99:ARG:NH2	2.33	0.43
1:I:79:LEU:HD23	1:I:521:GLY:HA3	2.00	0.43
1:I:80:TYR:CZ	1:I:448:VAL:HG22	2.54	0.43
1:I:413:LYS:HE2	1:I:413:LYS:HB3	1.73	0.43
1:J:45:LEU:HD21	1:J:328:ARG:HH21	1.82	0.43
1:J:266:ILE:O	1:J:267:ALA:HB2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:391:TYR:N	1:J:391:TYR:CD2	2.87	0.43
1:K:15:PHE:HE2	1:K:19:TRP:HE1	1.66	0.43
1:K:80:TYR:CZ	1:K:448:VAL:HG22	2.54	0.43
1:K:95:MSE:HE1	1:K:99:ARG:NH2	2.33	0.43
1:K:378:ASP:O	1:K:381:SER:O	2.37	0.43
1:L:378:ASP:O	1:L:381:SER:O	2.37	0.43
2:Z:20:ARG:C	2:Z:22:ALA:N	2.74	0.43
2:Z:71:ASP:C	2:Z:73:GLU:H	2.26	0.43
2:a:101:ALA:N	2:a:102:PRO:CD	2.82	0.43
2:e:101:ALA:N	2:e:102:PRO:CD	2.82	0.43
2:e:150:PRO:O	2:e:151:ASN:C	2.61	0.43
2:h:104:TYR:N	2:h:104:TYR:CD1	2.85	0.43
1:M:387:GLN:O	1:M:389:LEU:HG	2.18	0.43
1:M:395:PRO:HD2	1:O:398:PRO:HB3	2.00	0.43
1:N:179:MSE:O	1:N:217:ILE:HD12	2.19	0.43
1:N:270:GLN:OE1	1:N:270:GLN:HA	2.19	0.43
1:N:298:ILE:HA	1:N:299:PRO:HD3	1.78	0.43
1:N:316:TYR:O	1:N:321:ARG:NH1	2.52	0.43
1:O:78:VAL:CG1	1:O:79:LEU:H	2.31	0.43
1:O:180:SER:OG	1:P:161:ASN:HB3	2.19	0.43
1:O:589:GLU:HA	1:O:592:TRP:HB2	2.00	0.43
1:Q:35:PHE:CE1	1:Q:321:ARG:NH1	2.87	0.43
1:Q:589:GLU:HA	1:Q:592:TRP:HB2	2.00	0.43
1:R:158:TRP:HD1	1:R:158:TRP:H	1.65	0.43
1:R:437:GLN:HA	1:R:440:MSE:HB2	1.99	0.43
3:R:718:HOH:O	1:X:438:LEU:HD22	2.19	0.43
1:S:71:MSE:CE	1:S:115:VAL:HB	2.48	0.43
1:S:161:ASN:O	1:S:161:ASN:CG	2.61	0.43
1:T:71:MSE:CE	1:T:115:VAL:HB	2.49	0.43
1:T:340:ILE:O	1:T:344:THR:HG21	2.19	0.43
1:T:443:ASP:O	1:T:446:THR:HG22	2.19	0.43
1:U:179:MSE:O	1:U:217:ILE:HD12	2.19	0.43
1:U:340:ILE:O	1:U:344:THR:HG21	2.19	0.43
1:U:451:ASP:O	1:U:453:LEU:N	2.52	0.43
1:V:248:LYS:HE2	1:V:513:ARG:HH12	1.83	0.43
1:W:343:ARG:HD3	2:u:128:TYR:CE1	2.53	0.43
1:X:15:PHE:CE2	1:X:19:TRP:NE1	2.87	0.43
1:X:431:ALA:HA	1:X:434:THR:HG22	2.01	0.43
1:X:444:LEU:O	1:X:447:TYR:N	2.52	0.43
2:q:12:ALA:HB3	2:q:15:ARG:CD	2.49	0.43
2:q:47:TRP:N	2:q:47:TRP:CD1	2.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:r:10:VAL:HA	2:r:15:ARG:HG2	2.00	0.43
2:t:12:ALA:HB3	2:t:15:ARG:CD	2.48	0.43
2:u:84:PHE:C	2:u:84:PHE:CD2	2.96	0.43
2:u:96:ALA:HB2	2:v:25:LEU:HD13	2.01	0.43
1:A:80:TYR:CZ	1:A:448:VAL:HG22	2.54	0.43
1:A:94:LEU:HD23	1:A:94:LEU:O	2.19	0.43
1:A:266:ILE:O	1:A:267:ALA:HB2	2.19	0.43
1:B:35:PHE:CZ	1:B:321:ARG:CZ	3.02	0.43
1:B:252:LYS:O	1:B:252:LYS:HE3	2.19	0.43
1:B:371:TYR:HA	1:C:348:LYS:HB3	2.01	0.43
1:B:399:GLN:C	1:B:399:GLN:OE1	2.61	0.43
1:B:444:LEU:O	1:B:447:TYR:N	2.52	0.43
1:C:15:PHE:HE2	1:C:19:TRP:HE1	1.66	0.43
1:C:79:LEU:N	1:C:519:ASP:O	2.51	0.43
1:C:95:MSE:HE1	1:C:99:ARG:NH2	2.33	0.43
1:D:35:PHE:HZ	1:D:321:ARG:NE	2.12	0.43
1:D:378:ASP:O	1:D:381:SER:O	2.37	0.43
1:E:282:THR:HG23	1:E:287:LEU:CD1	2.44	0.43
1:E:399:GLN:C	1:E:399:GLN:OE1	2.61	0.43
1:F:378:ASP:O	1:F:381:SER:O	2.37	0.43
1:H:66:LYS:O	1:H:70:GLU:HG3	2.18	0.43
1:H:212:LEU:HD12	1:H:212:LEU:N	2.34	0.43
1:H:444:LEU:O	1:H:447:TYR:N	2.52	0.43
1:I:94:LEU:HD23	1:I:94:LEU:O	2.19	0.43
1:I:99:ARG:NH1	1:I:530:GLN:HE21	2.13	0.43
1:I:123:VAL:HG13	1:I:304:PHE:CE1	2.54	0.43
1:I:212:LEU:HD12	1:I:212:LEU:N	2.34	0.43
1:I:262:GLY:O	1:I:263:PHE:HB3	2.17	0.43
1:J:35:PHE:CZ	1:J:321:ARG:CZ	3.02	0.43
1:J:560:LEU:HD13	1:K:82:PRO:CD	2.25	0.43
1:J:583:LYS:HA	1:J:584:PRO:HD3	1.85	0.43
1:L:219:ILE:HD13	1:L:282:THR:HG22	2.00	0.43
1:L:274:ARG:HD3	1:L:296:GLU:O	2.19	0.43
2:f:78:GLU:CD	2:f:79:GLY:N	2.77	0.43
2:j:28:VAL:HG11	2:j:97:ALA:HA	1.88	0.43
2:j:71:ASP:C	2:j:73:GLU:H	2.26	0.43
1:M:543:PRO:C	1:M:545:GLY:H	2.27	0.43
1:N:164:LEU:HD22	1:N:169:ASP:OD1	2.19	0.43
1:N:191:TYR:O	1:N:288:LYS:HE2	2.19	0.43
1:N:248:LYS:H	1:N:248:LYS:CD	2.15	0.43
1:N:273:ARG:HH22	1:N:453:LEU:CD2	2.30	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:340:ILE:O	1:N:344:THR:HG21	2.19	0.43
1:O:248:LYS:HE2	1:O:513:ARG:HH12	1.83	0.43
1:P:236:GLN:H	1:P:265:LYS:HB2	1.83	0.43
1:Q:380:ASN:O	1:Q:381:SER:CB	2.67	0.43
1:R:35:PHE:CE1	1:R:321:ARG:NH1	2.86	0.43
1:R:248:LYS:HE2	1:R:513:ARG:HH12	1.84	0.43
1:R:575:GLN:O	1:R:579:MSE:CG	2.67	0.43
1:S:136:SER:N	1:S:137:PRO:HD3	2.33	0.43
1:T:53:TYR:OH	1:W:329:LEU:HD21	2.19	0.43
1:T:245:SER:HG	1:T:247:PHE:HE1	1.65	0.43
1:T:372:TYR:CE2	1:W:348:LYS:HB2	2.53	0.43
1:T:387:GLN:HA	1:T:388:PRO:HD3	1.93	0.43
1:V:164:LEU:HD22	1:V:169:ASP:OD1	2.18	0.43
1:V:174:THR:N	3:V:705:HOH:O	2.51	0.43
1:W:92:ASP:OD2	1:W:92:ASP:N	2.51	0.43
1:W:160:SER:O	1:W:161:ASN:ND2	2.45	0.43
1:W:174:THR:N	3:W:705:HOH:O	2.51	0.43
1:W:212:LEU:N	1:W:212:LEU:HD12	2.34	0.43
1:W:510:ILE:O	1:W:513:ARG:HD2	2.19	0.43
1:X:273:ARG:HH22	1:X:453:LEU:CD2	2.32	0.43
2:p:12:ALA:HB3	2:p:15:ARG:CD	2.49	0.43
2:t:83:VAL:HG23	2:t:84:PHE:N	2.33	0.43
1:A:49:THR:O	1:A:50:THR:O	2.37	0.43
1:C:219:ILE:HD13	1:C:282:THR:HG22	2.00	0.43
1:C:444:LEU:HD23	1:C:518:THR:OG1	2.18	0.43
1:D:448:VAL:C	1:D:450:GLN:H	2.27	0.43
1:E:66:LYS:O	1:E:70:GLU:HG3	2.18	0.43
1:F:229:LYS:HD2	1:F:270:GLN:HG3	2.01	0.43
1:F:598:GLN:O	1:F:601:GLN:HB2	2.19	0.43
1:G:71:MSE:HE3	1:G:115:VAL:HB	2.00	0.43
1:G:252:LYS:HE3	1:G:252:LYS:O	2.19	0.43
1:H:38:VAL:HG21	1:H:324:LYS:HD2	2.01	0.43
1:H:127:ARG:HA	1:H:299:PRO:O	2.18	0.43
1:I:35:PHE:CZ	1:I:321:ARG:CZ	3.02	0.43
1:I:47:GLN:C	1:I:48:TYR:HD2	2.27	0.43
1:J:49:THR:O	1:J:50:THR:O	2.37	0.43
1:J:66:LYS:O	1:J:70:GLU:HG3	2.18	0.43
1:J:80:TYR:CZ	1:J:448:VAL:HG22	2.54	0.43
1:J:94:LEU:O	1:J:94:LEU:HD23	2.19	0.43
1:J:399:GLN:C	1:J:399:GLN:OE1	2.61	0.43
1:K:35:PHE:CZ	1:K:321:ARG:CZ	3.02	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:182:ASN:HD22	1:L:171:ARG:HH21	1.65	0.43
1:K:274:ARG:HD3	1:K:296:GLU:O	2.19	0.43
2:Z:150:PRO:O	2:Z:151:ASN:C	2.61	0.43
2:i:78:GLU:CD	2:i:79:GLY:N	2.77	0.43
1:M:387:GLN:CB	1:O:390:ALA:CB	2.97	0.43
1:M:387:GLN:HB3	1:O:390:ALA:CB	2.49	0.43
1:N:387:GLN:O	1:N:389:LEU:HG	2.19	0.43
1:N:510:ILE:O	1:N:513:ARG:HD2	2.19	0.43
1:N:528:LYS:NZ	1:N:560:LEU:HD21	2.33	0.43
1:O:437:GLN:HA	1:O:440:MSE:HB2	2.01	0.43
1:O:528:LYS:HD2	1:O:560:LEU:HD21	2.01	0.43
1:P:158:TRP:HD1	1:P:158:TRP:H	1.66	0.43
1:Q:123:VAL:CG1	1:Q:304:PHE:CE1	3.02	0.43
1:Q:437:GLN:HA	1:Q:440:MSE:HB2	2.01	0.43
1:R:179:MSE:O	1:R:217:ILE:HD12	2.19	0.43
1:R:231:THR:CG2	1:R:249:ARG:HH11	2.31	0.43
1:S:190:LYS:HA	1:S:190:LYS:HE3	2.00	0.43
1:S:270:GLN:OE1	1:S:270:GLN:HA	2.18	0.43
1:S:567:MSE:SE	1:T:576:LEU:HD13	2.67	0.43
1:T:236:GLN:H	1:T:265:LYS:CB	2.32	0.43
1:T:262:GLY:O	1:T:263:PHE:HB3	2.19	0.43
1:T:343:ARG:NH1	2:s:126:ALA:O	2.52	0.43
1:U:171:ARG:O	1:U:224:GLU:HA	2.18	0.43
1:U:280:ILE:HD12	1:U:280:ILE:N	2.33	0.43
1:U:306:GLU:O	1:U:316:TYR:HA	2.19	0.43
1:U:364:ASP:CG	2:t:126:ALA:HB2	2.43	0.43
1:U:430:VAL:HG13	3:X:719:HOH:O	2.17	0.43
1:W:298:ILE:HA	1:W:299:PRO:HD3	1.80	0.43
2:k:49:GLN:H	2:k:53:GLY:HA3	1.83	0.43
2:o:17:LEU:HD23	2:o:17:LEU:O	2.19	0.43
2:q:48:TYR:H	2:q:54:ILE:H	1.67	0.43
2:t:92:ALA:N	2:t:93:PRO:CD	2.81	0.43
1:A:35:PHE:HZ	1:A:321:ARG:NE	2.12	0.43
1:A:38:VAL:HG21	1:A:324:LYS:HD2	2.01	0.43
1:A:139:SER:CB	1:A:455:THR:CG2	2.80	0.43
1:A:282:THR:HG23	1:A:287:LEU:CD1	2.43	0.43
1:C:79:LEU:HD23	1:C:521:GLY:HA3	2.00	0.43
1:C:80:TYR:CZ	1:C:448:VAL:HG22	2.54	0.43
1:C:198:ILE:HA	1:C:199:PRO:HD3	1.64	0.43
1:D:31:ASN:HD22	1:D:31:ASN:HA	1.62	0.43
1:D:47:GLN:C	1:D:48:TYR:HD2	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:391:TYR:CD2	1:D:391:TYR:N	2.87	0.43
1:E:79:LEU:HD23	1:E:521:GLY:HA3	2.00	0.43
1:E:94:LEU:O	1:E:94:LEU:HD23	2.19	0.43
1:F:47:GLN:C	1:F:48:TYR:HD2	2.27	0.43
1:F:79:LEU:N	1:F:519:ASP:O	2.51	0.43
1:F:252:LYS:O	1:F:252:LYS:HE3	2.19	0.43
1:F:391:TYR:CD2	1:F:391:TYR:N	2.87	0.43
1:G:94:LEU:HD23	1:G:94:LEU:O	2.19	0.43
1:G:251:ILE:HD11	1:G:275:ARG:NH2	2.34	0.43
1:G:378:ASP:O	1:G:381:SER:O	2.37	0.43
1:H:49:THR:O	1:H:50:THR:O	2.37	0.43
1:H:583:LYS:HA	1:H:584:PRO:HD3	1.85	0.43
1:I:49:THR:O	1:I:50:THR:O	2.37	0.43
1:I:448:VAL:C	1:I:450:GLN:H	2.27	0.43
1:I:583:LYS:HA	1:I:584:PRO:HD3	1.85	0.43
1:J:127:ARG:HA	1:J:299:PRO:O	2.18	0.43
1:J:274:ARG:HD3	1:J:296:GLU:O	2.19	0.43
1:J:444:LEU:O	1:J:447:TYR:N	2.52	0.43
1:K:94:LEU:O	1:K:94:LEU:HD23	2.19	0.43
1:L:49:THR:O	1:L:50:THR:O	2.37	0.43
1:L:78:VAL:HG21	1:L:444:LEU:CD1	2.21	0.43
1:L:252:LYS:HE3	1:L:252:LYS:O	2.19	0.43
2:f:20:ARG:C	2:f:22:ALA:N	2.74	0.43
2:g:71:ASP:O	2:g:72:ASP:CB	2.65	0.43
1:N:66:LYS:HZ3	1:N:420:VAL:HG21	1.84	0.42
1:O:107:ALA:HA	1:O:146:ARG:HB3	2.00	0.42
1:O:147:GLU:HA	1:O:148:PRO:HD3	1.81	0.42
1:O:179:MSE:O	1:O:217:ILE:HD12	2.19	0.42
1:O:212:LEU:N	1:O:212:LEU:HD12	2.34	0.42
1:O:274:ARG:O	1:O:275:ARG:HD2	2.19	0.42
1:P:29:ALA:O	1:P:33:LEU:HG	2.19	0.42
1:Q:76:ILE:HD12	1:Q:433:ASP:OD1	2.18	0.42
1:Q:232:ALA:HB2	1:Q:269:ARG:O	2.19	0.42
1:R:282:THR:HG23	1:R:287:LEU:CD1	2.46	0.42
1:R:306:GLU:O	1:R:316:TYR:HA	2.19	0.42
1:R:328:ARG:HB3	2:o:133:PRO:HG3	2.01	0.42
1:R:330:ARG:O	1:R:334:MSE:HB2	2.19	0.42
1:S:276:VAL:CG2	1:S:293:ILE:HG23	2.48	0.42
1:T:444:LEU:HD13	1:T:444:LEU:N	2.34	0.42
1:U:15:PHE:CE2	1:U:19:TRP:NE1	2.87	0.42
1:U:118:GLN:OE1	1:U:303:VAL:HB	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:161:ASN:O	1:V:161:ASN:CG	2.62	0.42
1:V:386:THR:CG2	1:V:389:LEU:HD21	2.49	0.42
1:W:245:SER:HG	1:W:247:PHE:HE1	1.65	0.42
1:W:575:GLN:O	1:W:579:MSE:CG	2.66	0.42
1:X:179:MSE:O	1:X:217:ILE:HD12	2.19	0.42
2:n:59:VAL:HG22	2:n:73:HIS:O	2.19	0.42
2:t:34:GLN:C	2:t:36:ALA:H	2.27	0.42
1:A:34:PHE:CE1	1:A:324:LYS:NZ	2.72	0.42
1:A:79:LEU:HD23	1:A:521:GLY:HA3	2.00	0.42
1:A:219:ILE:HD13	1:A:282:THR:HG22	2.00	0.42
1:A:538:LEU:HB3	1:A:551:LEU:HD13	2.00	0.42
1:A:579:MSE:CB	1:A:581:VAL:HG12	2.49	0.42
1:A:598:GLN:O	1:A:601:GLN:HB2	2.19	0.42
1:B:127:ARG:HA	1:B:299:PRO:O	2.18	0.42
1:B:274:ARG:HD3	1:B:296:GLU:O	2.19	0.42
1:C:123:VAL:HG13	1:C:304:PHE:CE1	2.54	0.42
1:C:212:LEU:HD12	1:C:212:LEU:N	2.34	0.42
1:C:252:LYS:O	1:C:252:LYS:HE3	2.19	0.42
1:D:38:VAL:HG21	1:D:324:LYS:HD2	2.01	0.42
1:D:80:TYR:CZ	1:D:448:VAL:HG22	2.54	0.42
1:D:123:VAL:HG13	1:D:304:PHE:CE1	2.54	0.42
1:D:229:LYS:HD2	1:D:270:GLN:HG3	2.01	0.42
1:E:219:ILE:HD13	1:E:282:THR:HG22	2.00	0.42
1:E:227:GLU:OE2	1:E:227:GLU:N	2.47	0.42
1:E:232:ALA:HB1	1:E:233:PHE:H	1.71	0.42
1:E:266:ILE:O	1:E:267:ALA:HB2	2.19	0.42
1:F:49:THR:O	1:F:50:THR:O	2.37	0.42
1:F:123:VAL:HG13	1:F:304:PHE:CE1	2.54	0.42
1:F:274:ARG:HD3	1:F:296:GLU:O	2.19	0.42
1:G:127:ARG:HA	1:G:299:PRO:O	2.18	0.42
1:G:191:TYR:HE1	1:G:278:LYS:HZ3	1.65	0.42
1:G:227:GLU:OE2	1:G:227:GLU:N	2.47	0.42
1:G:229:LYS:HD2	1:G:270:GLN:HG3	2.01	0.42
1:G:538:LEU:HB3	1:G:551:LEU:HD13	2.00	0.42
1:H:14:ARG:NE	1:H:14:ARG:CA	2.67	0.42
1:H:35:PHE:CZ	1:H:321:ARG:CZ	3.02	0.42
1:H:71:MSE:HE3	1:H:115:VAL:HB	2.00	0.42
1:H:266:ILE:O	1:H:267:ALA:HB2	2.19	0.42
1:H:437:GLN:HA	1:H:440:MSE:HB2	2.01	0.42
1:H:448:VAL:C	1:H:450:GLN:H	2.27	0.42
1:I:15:PHE:HE2	1:I:19:TRP:HE1	1.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:123:VAL:HG13	1:J:304:PHE:CE1	2.54	0.42
1:J:212:LEU:N	1:J:212:LEU:HD12	2.34	0.42
1:K:79:LEU:HD23	1:K:521:GLY:HA3	2.00	0.42
1:K:99:ARG:NH1	1:K:530:GLN:HE21	2.13	0.42
1:K:123:VAL:HG13	1:K:304:PHE:CE1	2.54	0.42
1:K:212:LEU:HD12	1:K:212:LEU:N	2.34	0.42
1:K:229:LYS:HD2	1:K:270:GLN:HG3	2.01	0.42
2:Z:78:GLU:CD	2:Z:79:GLY:N	2.77	0.42
2:g:71:ASP:C	2:g:73:GLU:H	2.26	0.42
1:M:77:ASP:HB2	1:M:523:SER:HB2	2.02	0.42
1:M:444:LEU:O	1:M:447:TYR:N	2.52	0.42
1:N:92:ASP:OD2	1:N:92:ASP:N	2.53	0.42
1:O:344:THR:O	1:O:344:THR:CG2	2.67	0.42
1:P:164:LEU:HD22	1:P:169:ASP:OD1	2.18	0.42
1:P:387:GLN:HB3	1:Q:390:ALA:CB	2.49	0.42
1:Q:371:TYR:HE2	1:Q:373:LEU:HD21	1.84	0.42
1:Q:427:GLY:C	1:Q:429:GLN:N	2.74	0.42
1:R:29:ALA:O	1:R:33:LEU:HG	2.19	0.42
1:R:266:ILE:O	1:R:267:ALA:HB2	2.19	0.42
1:R:349:PRO:HG3	1:R:391:TYR:CE1	2.54	0.42
1:S:24:GLU:O	1:S:26:ARG:N	2.50	0.42
1:S:100:THR:HG22	1:S:138:THR:HG22	2.00	0.42
1:S:589:GLU:HA	1:S:592:TRP:HB2	2.00	0.42
1:T:29:ALA:O	1:T:33:LEU:HG	2.18	0.42
1:T:161:ASN:O	1:T:161:ASN:CG	2.63	0.42
1:T:179:MSE:O	1:T:217:ILE:HD12	2.20	0.42
1:T:273:ARG:CZ	1:T:275:ARG:HE	2.31	0.42
1:T:376:ARG:HB2	1:W:352:TRP:CG	2.54	0.42
1:T:584:PRO:CG	1:T:593:LEU:HD12	2.49	0.42
1:U:57:PHE:CD1	1:U:57:PHE:N	2.87	0.42
1:V:265:LYS:O	1:V:266:ILE:HG12	2.19	0.42
1:V:344:THR:O	1:V:344:THR:CG2	2.66	0.42
1:W:29:ALA:O	1:W:33:LEU:HG	2.19	0.42
1:W:236:GLN:H	1:W:265:LYS:HB2	1.83	0.42
1:X:528:LYS:NZ	1:X:560:LEU:HD21	2.34	0.42
1:X:584:PRO:CG	1:X:593:LEU:HD12	2.49	0.42
2:n:83:VAL:HG23	2:n:84:PHE:N	2.33	0.42
2:o:67:PRO:O	2:o:68:ALA:HB2	2.19	0.42
2:p:17:LEU:O	2:p:17:LEU:HD23	2.20	0.42
2:r:64:GLU:C	2:r:66:PRO:HD2	2.44	0.42
2:v:12:ALA:HB3	2:v:15:ARG:CD	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:390:ALA:HB2	1:L:387:GLN:HG3	1.99	0.42
1:B:15:PHE:HE2	1:B:19:TRP:HE1	1.66	0.42
1:B:123:VAL:HG13	1:B:304:PHE:CE1	2.54	0.42
1:B:251:ILE:HD11	1:B:275:ARG:NH2	2.34	0.42
1:B:273:ARG:HH22	1:B:453:LEU:HD11	1.85	0.42
1:B:598:GLN:O	1:B:601:GLN:HB2	2.19	0.42
1:C:43:ASP:OD2	1:C:43:ASP:N	2.52	0.42
1:C:94:LEU:O	1:C:94:LEU:HD23	2.19	0.42
1:C:166:ASP:C	1:C:168:SER:N	2.77	0.42
1:D:94:LEU:HD23	1:D:94:LEU:O	2.19	0.42
1:D:212:LEU:N	1:D:212:LEU:HD12	2.34	0.42
1:D:252:LYS:HE3	1:D:252:LYS:O	2.19	0.42
1:D:444:LEU:O	1:D:447:TYR:N	2.52	0.42
1:E:38:VAL:HG21	1:E:324:LYS:HD2	2.01	0.42
1:E:252:LYS:O	1:E:252:LYS:HE3	2.19	0.42
1:E:273:ARG:HD2	1:E:275:ARG:HD2	2.02	0.42
1:F:79:LEU:HD23	1:F:521:GLY:HA3	2.00	0.42
1:F:251:ILE:HD11	1:F:275:ARG:NH2	2.34	0.42
1:F:448:VAL:C	1:F:450:GLN:H	2.27	0.42
1:G:52:GLN:O	2:d:147:ASN:ND2	2.52	0.42
1:H:123:VAL:HG13	1:H:304:PHE:CE1	2.54	0.42
1:I:66:LYS:O	1:I:70:GLU:HG3	2.18	0.42
1:J:43:ASP:OD2	1:J:43:ASP:N	2.52	0.42
1:J:360:GLU:HG3	2:h:131:ARG:HB3	2.02	0.42
1:J:378:ASP:O	1:J:381:SER:O	2.37	0.42
1:K:49:THR:O	1:K:50:THR:O	2.37	0.42
1:K:598:GLN:O	1:K:601:GLN:HB2	2.19	0.42
1:L:448:VAL:C	1:L:450:GLN:H	2.27	0.42
1:L:598:GLN:O	1:L:601:GLN:HB2	2.19	0.42
2:Y:78:GLU:CD	2:Y:79:GLY:N	2.77	0.42
2:Z:57:TYR:H	2:Z:63:ILE:H	1.65	0.42
2:a:78:GLU:O	2:a:79:GLY:C	2.59	0.42
2:b:101:ALA:N	2:b:102:PRO:CD	2.82	0.42
2:g:78:GLU:CD	2:g:79:GLY:N	2.77	0.42
2:h:150:PRO:O	2:h:151:ASN:C	2.61	0.42
1:M:407:ALA:HB1	1:N:334:MSE:HE1	2.00	0.42
1:O:280:ILE:HG22	1:O:287:LEU:HD13	2.02	0.42
1:O:584:PRO:CG	1:O:593:LEU:HD12	2.49	0.42
1:P:589:GLU:HA	1:P:592:TRP:HB2	2.01	0.42
1:Q:198:ILE:HA	1:Q:199:PRO:HD3	1.72	0.42
1:Q:431:ALA:HA	1:Q:434:THR:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:161:ASN:O	1:R:161:ASN:CG	2.62	0.42
1:S:280:ILE:HG22	1:S:287:LEU:HD13	2.01	0.42
1:S:584:PRO:CG	1:S:593:LEU:HD12	2.49	0.42
1:T:101:ASP:HB3	1:T:138:THR:HG21	2.01	0.42
1:T:322:LEU:HD22	1:T:322:LEU:H	1.83	0.42
1:T:578:GLN:HG2	1:T:596:ALA:CB	2.49	0.42
1:V:15:PHE:CE2	1:V:19:TRP:NE1	2.88	0.42
1:W:191:TYR:O	1:W:288:LYS:HE2	2.20	0.42
1:W:543:PRO:C	1:W:545:GLY:H	2.27	0.42
1:X:191:TYR:O	1:X:288:LYS:HE2	2.19	0.42
1:X:328:ARG:HB3	2:p:133:PRO:HG3	2.01	0.42
2:l:59:VAL:HG22	2:l:73:HIS:O	2.18	0.42
2:s:48:TYR:H	2:s:54:ILE:H	1.67	0.42
2:u:16:LYS:HZ2	2:u:16:LYS:HA	1.84	0.42
1:A:25:ALA:O	1:A:29:ALA:CB	2.58	0.42
1:A:98:TYR:C	1:A:98:TYR:CD2	2.98	0.42
1:B:26:ARG:O	1:B:27:ARG:C	2.62	0.42
1:B:47:GLN:C	1:B:48:TYR:HD2	2.27	0.42
1:B:248:LYS:H	1:B:248:LYS:CD	2.16	0.42
1:C:273:ARG:HD2	1:C:275:ARG:HD2	2.02	0.42
1:C:378:ASP:O	1:C:381:SER:O	2.37	0.42
1:D:35:PHE:HE1	1:D:321:ARG:NH1	2.13	0.42
1:D:171:ARG:HH21	1:E:182:ASN:HD22	1.65	0.42
1:D:273:ARG:HD2	1:D:275:ARG:HD2	2.01	0.42
1:F:26:ARG:NH2	1:F:30:LYS:HB2	2.28	0.42
1:F:35:PHE:HE2	1:F:324:LYS:NZ	2.08	0.42
1:F:38:VAL:HG21	1:F:324:LYS:HD2	2.01	0.42
1:F:273:ARG:HH22	1:F:453:LEU:HD11	1.85	0.42
1:G:15:PHE:HE2	1:G:19:TRP:HE1	1.66	0.42
1:G:35:PHE:CZ	1:G:321:ARG:CZ	3.02	0.42
1:G:246:TYR:HD2	1:G:511:ARG:CB	2.28	0.42
1:H:79:LEU:N	1:H:519:ASP:O	2.51	0.42
1:I:35:PHE:HE1	1:I:321:ARG:NH1	2.13	0.42
1:J:229:LYS:HD2	1:J:270:GLN:HG3	2.01	0.42
1:K:43:ASP:OD2	1:K:43:ASP:N	2.52	0.42
1:K:48:TYR:O	1:K:49:THR:CB	2.64	0.42
1:K:444:LEU:O	1:K:447:TYR:N	2.52	0.42
1:L:82:PRO:HB2	1:L:83:LYS:H	1.58	0.42
1:L:251:ILE:HD11	1:L:275:ARG:NH2	2.35	0.42
1:L:542:THR:HA	1:L:543:PRO:HD3	1.82	0.42
2:c:101:ALA:N	2:c:102:PRO:CD	2.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:d:39:PRO:HB2	2:d:40:GLN:H	1.51	0.42
2:g:101:ALA:N	2:g:102:PRO:CD	2.82	0.42
2:h:101:ALA:N	2:h:102:PRO:CD	2.82	0.42
2:i:28:VAL:HG21	2:i:96:LEU:CG	2.40	0.42
1:N:24:GLU:HG3	1:N:313:LYS:HE2	2.00	0.42
1:N:158:TRP:HH2	1:N:302:PRO:HG3	1.80	0.42
1:N:589:GLU:HA	1:N:592:TRP:HB2	2.01	0.42
1:O:123:VAL:HG13	1:O:304:PHE:CE1	2.54	0.42
1:P:444:LEU:O	1:P:447:TYR:N	2.52	0.42
1:Q:301:VAL:HA	1:Q:302:PRO:HD3	1.79	0.42
1:R:584:PRO:CG	1:R:593:LEU:HD12	2.50	0.42
1:T:437:GLN:HA	1:T:440:MSE:HB2	2.02	0.42
1:T:528:LYS:NZ	1:T:560:LEU:HD21	2.35	0.42
1:U:190:LYS:HA	1:U:190:LYS:HE3	2.00	0.42
1:U:427:GLY:C	1:U:429:GLN:N	2.77	0.42
1:V:575:GLN:O	1:V:579:MSE:CG	2.66	0.42
1:W:554:LEU:HD12	1:W:557:PHE:CD2	2.53	0.42
2:m:12:ALA:C	2:m:14:LEU:H	2.26	0.42
2:s:69:GLU:HB3	2:s:70:GLY:H	1.67	0.42
2:u:47:TRP:N	2:u:47:TRP:CD1	2.86	0.42
2:v:40:LEU:HD23	2:v:41:GLU:N	2.34	0.42
2:v:49:GLN:H	2:v:53:GLY:HA3	1.84	0.42
1:A:274:ARG:HD3	1:A:296:GLU:O	2.19	0.42
1:A:528:LYS:CD	1:A:560:LEU:HD21	2.50	0.42
1:B:378:ASP:O	1:B:381:SER:O	2.37	0.42
1:B:444:LEU:HD23	1:B:518:THR:OG1	2.18	0.42
1:C:35:PHE:CZ	1:C:321:ARG:CZ	3.02	0.42
1:C:127:ARG:HA	1:C:299:PRO:O	2.18	0.42
1:C:579:MSE:CB	1:C:581:VAL:HG12	2.49	0.42
1:E:369:TYR:HA	1:E:370:PRO:HD3	1.84	0.42
1:E:444:LEU:O	1:E:447:TYR:N	2.52	0.42
1:G:78:VAL:CG2	1:G:444:LEU:HD21	2.46	0.42
1:G:98:TYR:CD2	1:G:98:TYR:C	2.98	0.42
1:G:123:VAL:HG13	1:G:304:PHE:CE1	2.54	0.42
1:G:208:VAL:HB	1:G:209:PHE:H	1.69	0.42
1:G:552:LEU:O	1:G:556:TYR:HD2	2.03	0.42
1:G:598:GLN:O	1:G:601:GLN:HB2	2.19	0.42
1:H:251:ILE:HD11	1:H:275:ARG:NH2	2.34	0.42
1:H:528:LYS:CD	1:H:560:LEU:HD21	2.50	0.42
1:H:598:GLN:O	1:H:601:GLN:HB2	2.19	0.42
1:I:26:ARG:O	1:I:27:ARG:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:26:ARG:O	1:J:27:ARG:C	2.62	0.42
1:J:71:MSE:HE3	1:J:115:VAL:HB	2.01	0.42
1:J:251:ILE:HD11	1:J:275:ARG:NH2	2.35	0.42
1:J:448:VAL:C	1:J:450:GLN:H	2.27	0.42
1:J:556:TYR:OH	1:K:542:THR:HG21	2.20	0.42
1:J:598:GLN:O	1:J:601:GLN:HB2	2.19	0.42
1:L:579:MSE:CB	1:L:581:VAL:HG12	2.50	0.42
2:a:117:LYS:HE2	2:a:117:LYS:HB3	1.86	0.42
2:c:20:ARG:C	2:c:22:ALA:N	2.74	0.42
2:e:32:ALA:C	2:e:33:THR:CG2	2.61	0.42
2:g:28:VAL:HG11	2:g:97:ALA:HA	1.88	0.42
2:j:101:ALA:N	2:j:102:PRO:CD	2.82	0.42
1:M:35:PHE:HZ	1:M:321:ARG:NE	2.12	0.42
1:M:212:LEU:HD12	1:M:212:LEU:N	2.34	0.42
3:M:718:HOH:O	1:O:438:LEU:HD22	2.19	0.42
1:O:265:LYS:O	1:O:266:ILE:HG12	2.19	0.42
1:Q:160:SER:O	1:Q:161:ASN:ND2	2.44	0.42
1:Q:528:LYS:NZ	1:Q:560:LEU:HD21	2.34	0.42
1:R:33:LEU:HD12	1:R:34:PHE:N	2.34	0.42
1:R:54:ARG:HB2	2:p:137:GLY:HA3	2.01	0.42
1:S:543:PRO:C	1:S:545:GLY:H	2.27	0.42
1:T:34:PHE:O	1:T:37:ARG:HB2	2.19	0.42
1:T:79:LEU:N	1:T:519:ASP:O	2.53	0.42
1:U:61:ARG:CB	1:U:62:PRO:HD3	2.49	0.42
1:U:101:ASP:HB3	1:U:138:THR:HG21	2.02	0.42
1:U:236:GLN:HG3	1:U:265:LYS:HG2	2.00	0.42
1:U:443:ASP:O	1:U:446:THR:HG22	2.20	0.42
1:V:158:TRP:HH2	1:V:302:PRO:HG3	1.81	0.42
1:V:306:GLU:O	1:V:316:TYR:HA	2.19	0.42
1:W:179:MSE:O	1:W:217:ILE:HD12	2.19	0.42
1:W:306:GLU:O	1:W:316:TYR:HA	2.20	0.42
1:W:343:ARG:H	1:W:343:ARG:HG2	1.56	0.42
1:X:161:ASN:O	1:X:161:ASN:CG	2.62	0.42
1:X:280:ILE:HD12	1:X:280:ILE:N	2.34	0.42
2:r:17:LEU:HD23	2:r:17:LEU:O	2.20	0.42
2:t:80:VAL:O	2:t:82:ALA:N	2.53	0.42
2:v:19:VAL:HA	2:v:22:ASP:CB	2.47	0.42
1:A:359:PHE:HD1	2:a:129:ILE:HD11	1.84	0.42
1:A:444:LEU:O	1:A:447:TYR:N	2.52	0.42
1:B:94:LEU:O	1:B:94:LEU:HD23	2.19	0.42
1:B:266:ILE:O	1:B:267:ALA:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:579:MSE:CB	1:B:581:VAL:HG12	2.50	0.42
1:C:391:TYR:CD2	1:C:391:TYR:N	2.87	0.42
1:D:363:TYR:HE1	1:F:350:PHE:CE1	2.35	0.42
1:E:49:THR:O	1:E:50:THR:O	2.37	0.42
1:G:80:TYR:CZ	1:G:448:VAL:HG22	2.54	0.42
1:G:93:VAL:O	1:G:97:MSE:HG3	2.20	0.42
1:G:448:VAL:C	1:G:450:GLN:H	2.27	0.42
1:H:68:VAL:HG22	1:H:119:ILE:HD12	2.02	0.42
1:H:94:LEU:O	1:H:94:LEU:HD23	2.19	0.42
1:H:98:TYR:C	1:H:98:TYR:CD2	2.98	0.42
1:H:229:LYS:HD2	1:H:270:GLN:HG3	2.01	0.42
1:H:552:LEU:O	1:H:556:TYR:HD2	2.03	0.42
1:I:246:TYR:HD2	1:I:511:ARG:CB	2.28	0.42
1:I:552:LEU:O	1:I:556:TYR:HD2	2.03	0.42
1:J:47:GLN:C	1:J:48:TYR:HD2	2.27	0.42
1:J:99:ARG:NH1	1:J:530:GLN:HE21	2.13	0.42
1:J:528:LYS:CD	1:J:560:LEU:HD21	2.50	0.42
1:L:94:LEU:HD23	1:L:94:LEU:O	2.19	0.42
1:L:434:THR:HG23	1:L:435:VAL:N	2.35	0.42
1:L:437:GLN:HA	1:L:440:MSE:HB2	2.01	0.42
2:c:78:GLU:CD	2:c:79:GLY:N	2.77	0.42
2:g:78:GLU:O	2:g:79:GLY:C	2.59	0.42
2:j:78:GLU:O	2:j:79:GLY:C	2.59	0.42
1:M:40:GLN:HE21	1:M:40:GLN:HB2	1.57	0.42
1:N:280:ILE:HG22	1:N:287:LEU:HD13	2.02	0.42
1:N:301:VAL:HG23	1:N:439:ASN:HB3	2.01	0.42
1:O:92:ASP:OD2	1:O:92:ASP:N	2.52	0.42
1:P:528:LYS:NZ	1:P:560:LEU:HD21	2.34	0.42
1:Q:334:MSE:HE1	1:R:407:ALA:HB1	2.01	0.42
1:Q:378:ASP:HA	2:r:109:TYR:HD2	1.85	0.42
1:S:212:LEU:HD12	1:S:212:LEU:N	2.34	0.42
1:S:248:LYS:HE2	1:S:513:ARG:HH12	1.85	0.42
1:S:248:LYS:CG	1:S:511:ARG:HH11	2.31	0.42
1:S:427:GLY:C	1:S:429:GLN:N	2.76	0.42
1:S:554:LEU:HD21	1:U:564:GLY:CA	2.39	0.42
1:S:575:GLN:O	1:S:579:MSE:CG	2.66	0.42
1:T:92:ASP:OD2	1:T:92:ASP:N	2.52	0.42
1:T:503:GLU:HB3	1:T:508:ASN:HB3	2.02	0.42
1:U:115:VAL:HA	1:U:118:GLN:HB3	2.02	0.42
1:U:212:LEU:HD12	1:U:212:LEU:N	2.34	0.42
1:U:328:ARG:HB3	2:r:133:PRO:HG3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:344:THR:O	1:U:344:THR:CG2	2.68	0.42
1:U:369:TYR:HA	1:U:370:PRO:HD3	1.83	0.42
1:V:24:GLU:HG3	1:V:313:LYS:HE2	2.00	0.42
1:V:123:VAL:HG22	1:V:316:TYR:HE2	1.83	0.42
1:V:528:LYS:NZ	1:V:560:LEU:HD21	2.34	0.42
1:W:41:TRP:HE3	1:W:42:ASP:HB3	1.82	0.42
1:X:92:ASP:OD2	1:X:92:ASP:N	2.52	0.42
1:X:270:GLN:OE1	1:X:270:GLN:HA	2.19	0.42
1:X:543:PRO:C	1:X:545:GLY:H	2.28	0.42
2:k:126:ALA:HA	2:k:127:PRO:HD3	1.89	0.42
2:m:48:TYR:H	2:m:54:ILE:H	1.67	0.42
2:n:34:GLN:C	2:n:36:ALA:H	2.28	0.42
2:o:33:MET:HB3	2:o:33:MET:HE3	1.67	0.42
2:p:16:LYS:HE2	2:p:73:HIS:CD2	2.55	0.42
2:r:49:GLN:H	2:r:53:GLY:HA3	1.85	0.42
2:s:34:GLN:C	2:s:36:ALA:H	2.27	0.42
2:t:84:PHE:C	2:t:84:PHE:CD2	2.97	0.42
2:u:24:THR:HG22	2:u:25:LEU:N	2.34	0.42
2:u:128:TYR:HA	2:u:129:PRO:HD3	1.82	0.42
1:A:229:LYS:HD2	1:A:270:GLN:HG3	2.01	0.42
1:B:43:ASP:OD2	1:B:43:ASP:N	2.52	0.42
1:B:49:THR:O	1:B:50:THR:O	2.37	0.42
1:C:444:LEU:O	1:C:447:TYR:N	2.52	0.42
1:D:93:VAL:O	1:D:97:MSE:HG3	2.20	0.42
1:E:71:MSE:HE3	1:E:115:VAL:HB	2.01	0.42
1:E:123:VAL:HG13	1:E:304:PHE:CE1	2.54	0.42
1:E:310:VAL:C	1:E:312:ASP:N	2.76	0.42
1:F:80:TYR:CZ	1:F:448:VAL:HG22	2.54	0.42
1:F:93:VAL:O	1:F:97:MSE:HG3	2.20	0.42
1:G:444:LEU:O	1:G:447:TYR:N	2.52	0.42
1:H:93:VAL:O	1:H:97:MSE:HG3	2.20	0.42
1:J:273:ARG:HD2	1:J:275:ARG:HD2	2.02	0.42
1:K:127:ARG:HA	1:K:299:PRO:O	2.19	0.42
1:L:47:GLN:C	1:L:48:TYR:HD2	2.27	0.42
2:h:39:PRO:HB2	2:h:40:GLN:H	1.51	0.42
2:h:89:VAL:C	2:h:91:ALA:N	2.76	0.42
1:M:179:MSE:O	1:M:217:ILE:HD12	2.20	0.42
1:N:409:THR:O	1:N:413:LYS:HG2	2.20	0.42
1:O:293:ILE:HG12	1:O:294:ALA:H	1.84	0.42
1:P:77:ASP:HB2	1:P:523:SER:HB2	2.02	0.42
1:P:262:GLY:O	1:P:263:PHE:HB3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:427:GLY:C	1:P:429:GLN:N	2.76	0.42
1:Q:343:ARG:NH1	2:o:126:ALA:O	2.52	0.42
1:Q:376:ARG:HB2	1:R:352:TRP:CD1	2.55	0.42
1:Q:451:ASP:O	1:Q:453:LEU:N	2.53	0.42
1:R:80:TYR:OH	1:R:444:LEU:HD12	2.19	0.42
1:R:212:LEU:N	1:R:212:LEU:HD12	2.35	0.42
1:R:245:SER:HG	1:R:247:PHE:HE1	1.63	0.42
1:R:394:ASN:HA	1:R:395:PRO:HD3	1.93	0.42
1:R:528:LYS:HD2	1:R:560:LEU:HD21	2.02	0.42
1:R:564:GLY:HA3	1:X:535:ILE:HD11	2.00	0.42
1:R:589:GLU:HA	1:R:592:TRP:HB2	2.00	0.42
1:S:227:GLU:O	1:S:227:GLU:HG2	2.18	0.42
1:T:301:VAL:HG23	1:T:439:ASN:HB3	2.01	0.42
1:T:306:GLU:O	1:T:316:TYR:HA	2.19	0.42
1:U:191:TYR:O	1:U:288:LYS:HE2	2.19	0.42
1:U:234:ILE:HG12	1:U:267:ALA:O	2.20	0.42
1:U:444:LEU:HD13	1:U:444:LEU:N	2.34	0.42
1:V:241:GLY:O	1:V:242:GLU:C	2.63	0.42
1:V:584:PRO:CG	1:V:593:LEU:HD12	2.50	0.42
1:W:248:LYS:HE2	1:W:513:ARG:HH12	1.84	0.42
1:W:340:ILE:O	1:W:344:THR:HG21	2.20	0.42
1:W:451:ASP:O	1:W:453:LEU:N	2.52	0.42
1:X:61:ARG:CB	1:X:62:PRO:HD3	2.49	0.42
1:X:101:ASP:HB3	1:X:138:THR:HG21	2.01	0.42
1:X:248:LYS:HE2	1:X:513:ARG:HH12	1.85	0.42
1:X:306:GLU:O	1:X:316:TYR:HA	2.20	0.42
2:o:34:GLN:C	2:o:36:ALA:H	2.27	0.42
2:q:34:GLN:C	2:q:36:ALA:H	2.27	0.42
2:t:49:GLN:H	2:t:53:GLY:HA3	1.84	0.42
2:t:69:GLU:C	2:t:69:GLU:OE1	2.62	0.42
2:v:69:GLU:C	2:v:69:GLU:OE1	2.62	0.42
1:A:26:ARG:O	1:A:27:ARG:C	2.62	0.42
1:A:123:VAL:HG13	1:A:304:PHE:CE1	2.54	0.42
1:A:248:LYS:H	1:A:248:LYS:CD	2.16	0.42
1:A:251:ILE:HD11	1:A:275:ARG:NH2	2.35	0.42
1:B:332:MSE:SE	2:Y:141:MET:HA	2.69	0.42
1:B:430:VAL:HG12	1:B:431:ALA:N	2.35	0.42
1:B:528:LYS:CD	1:B:560:LEU:HD21	2.50	0.42
1:B:567:MSE:HE2	1:C:554:LEU:HD22	2.00	0.42
1:C:229:LYS:HD2	1:C:270:GLN:HG3	2.01	0.42
1:C:301:VAL:HG23	1:C:439:ASN:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:457:MSE:O	1:C:457:MSE:CG	2.63	0.42
1:C:598:GLN:O	1:C:601:GLN:HB2	2.19	0.42
1:D:561:ASP:CB	1:F:89:ASP:HA	2.43	0.42
1:E:34:PHE:CE1	1:E:324:LYS:NZ	2.72	0.42
1:E:80:TYR:CZ	1:E:448:VAL:HG22	2.54	0.42
1:E:579:MSE:CB	1:E:581:VAL:HG12	2.50	0.42
1:E:583:LYS:HA	1:E:584:PRO:HD3	1.85	0.42
1:F:26:ARG:O	1:F:27:ARG:C	2.62	0.42
1:F:98:TYR:C	1:F:98:TYR:CD2	2.98	0.42
1:F:248:LYS:HZ2	1:F:251:ILE:HD12	1.85	0.42
1:F:528:LYS:CD	1:F:560:LEU:HD21	2.50	0.42
1:G:26:ARG:O	1:G:27:ARG:C	2.63	0.42
1:G:68:VAL:HG22	1:G:119:ILE:HD12	2.02	0.42
1:H:80:TYR:CZ	1:H:448:VAL:HG22	2.54	0.42
1:H:166:ASP:C	1:H:168:SER:N	2.77	0.42
1:H:227:GLU:OE2	1:H:227:GLU:N	2.47	0.42
1:I:598:GLN:O	1:I:601:GLN:HB2	2.19	0.42
1:J:437:GLN:HA	1:J:440:MSE:HB2	2.00	0.42
1:K:35:PHE:HZ	1:K:321:ARG:NE	2.12	0.42
1:K:68:VAL:HG22	1:K:119:ILE:HD12	2.02	0.42
1:K:252:LYS:O	1:K:252:LYS:HE3	2.19	0.42
1:K:364:ASP:CG	2:j:135:ALA:HB2	2.44	0.42
1:L:48:TYR:O	1:L:49:THR:CB	2.64	0.42
1:L:53:TYR:HA	2:j:147:ASN:HD21	1.84	0.42
1:L:123:VAL:HG13	1:L:304:PHE:CE1	2.54	0.42
2:Z:104:TYR:CD1	2:Z:104:TYR:N	2.85	0.42
2:b:57:TYR:H	2:b:63:ILE:H	1.65	0.42
2:j:28:VAL:HG21	2:j:96:LEU:CG	2.40	0.42
1:M:15:PHE:CE2	1:M:19:TRP:NE1	2.88	0.42
1:M:262:GLY:O	1:M:263:PHE:HB3	2.20	0.42
1:M:578:GLN:HG2	1:M:596:ALA:CB	2.50	0.42
1:N:431:ALA:HA	1:N:434:THR:HG22	2.01	0.42
1:O:41:TRP:HE3	1:O:42:ASP:HB3	1.83	0.42
1:O:227:GLU:O	1:O:227:GLU:HG2	2.20	0.42
1:O:431:ALA:HA	1:O:434:THR:HG22	2.02	0.42
1:P:212:LEU:HD12	1:P:212:LEU:N	2.34	0.42
1:P:387:GLN:O	1:P:389:LEU:HG	2.20	0.42
1:P:443:ASP:O	1:P:446:THR:HG22	2.20	0.42
1:Q:241:GLY:O	1:Q:242:GLU:C	2.62	0.42
1:Q:372:TYR:CE2	1:R:348:LYS:HB2	2.55	0.42
1:Q:384:LEU:HD22	1:Q:384:LEU:N	2.29	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:528:LYS:HD2	1:Q:560:LEU:HD21	2.02	0.42
1:R:24:GLU:HG3	1:R:313:LYS:HE2	2.01	0.42
1:R:158:TRP:HH2	1:R:302:PRO:HG3	1.84	0.42
1:S:27:ARG:HH21	1:U:41:TRP:HE1	1.67	0.42
1:S:265:LYS:O	1:S:266:ILE:HG12	2.20	0.42
1:S:451:ASP:O	1:S:453:LEU:N	2.53	0.42
1:S:528:LYS:NZ	1:S:560:LEU:HD21	2.35	0.42
1:T:15:PHE:CE2	1:T:19:TRP:NE1	2.88	0.42
1:T:265:LYS:O	1:T:266:ILE:HG12	2.19	0.42
1:T:431:ALA:HA	1:T:434:THR:HG22	2.01	0.42
1:T:458:ARG:HD3	1:T:458:ARG:HA	1.84	0.42
1:U:503:GLU:HB3	1:U:508:ASN:HB3	2.02	0.42
1:U:528:LYS:HD2	1:U:560:LEU:HD21	2.02	0.42
1:V:158:TRP:HD1	1:V:158:TRP:H	1.66	0.42
1:V:270:GLN:OE1	1:V:270:GLN:HA	2.20	0.42
1:V:438:LEU:HD12	1:V:441:ARG:NH1	2.35	0.42
1:V:443:ASP:O	1:V:446:THR:HG22	2.20	0.42
1:V:542:THR:HA	1:V:543:PRO:HD3	1.87	0.42
1:W:437:GLN:HA	1:W:440:MSE:HB2	2.01	0.42
1:X:115:VAL:HA	1:X:118:GLN:HB3	2.02	0.42
1:X:510:ILE:HG12	1:X:511:ARG:H	1.84	0.42
2:n:24:THR:HG22	2:n:25:LEU:N	2.33	0.42
2:n:33:MET:HE3	2:n:33:MET:HB3	1.68	0.42
2:u:61:SER:HB2	2:u:67:PRO:HA	2.02	0.42
1:A:37:ARG:HA	1:A:37:ARG:HD2	1.79	0.42
1:A:47:GLN:C	1:A:48:TYR:HD2	2.27	0.42
1:C:98:TYR:CD2	1:C:98:TYR:C	2.98	0.42
1:C:147:GLU:HA	1:C:148:PRO:HD3	1.86	0.42
1:C:343:ARG:NH2	2:a:134:ARG:HD3	2.35	0.42
1:D:528:LYS:CD	1:D:560:LEU:HD21	2.50	0.42
1:E:212:LEU:HD12	1:E:212:LEU:N	2.34	0.42
1:F:71:MSE:HE3	1:F:115:VAL:HB	2.00	0.42
1:F:209:PHE:N	1:F:210:PRO:CD	2.82	0.42
1:F:552:LEU:O	1:F:556:TYR:HD2	2.03	0.42
1:G:79:LEU:HD23	1:G:521:GLY:HA3	2.00	0.42
1:G:165:MSE:HE1	1:G:435:VAL:HB	2.02	0.42
1:G:212:LEU:N	1:G:212:LEU:HD12	2.34	0.42
1:H:47:GLN:C	1:H:48:TYR:HD2	2.27	0.42
1:H:252:LYS:O	1:H:252:LYS:HE3	2.19	0.42
1:H:386:THR:HG21	1:H:389:LEU:HD21	2.02	0.42
1:I:35:PHE:HZ	1:I:321:ARG:NE	2.12	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:229:LYS:HG2	1:I:272:LYS:CG	2.50	0.42
1:I:252:LYS:O	1:I:252:LYS:HE3	2.19	0.42
1:I:369:TYR:HA	1:I:370:PRO:HD3	1.84	0.42
1:I:386:THR:HG21	1:I:389:LEU:HD21	2.02	0.42
1:I:444:LEU:O	1:I:447:TYR:N	2.52	0.42
1:J:386:THR:HG21	1:J:389:LEU:HD21	2.02	0.42
1:J:434:THR:HG23	1:J:435:VAL:N	2.35	0.42
1:L:198:ILE:HA	1:L:199:PRO:HD3	1.64	0.42
1:L:332:MSE:SE	2:h:141:MET:HA	2.70	0.42
2:b:78:GLU:CD	2:b:79:GLY:N	2.77	0.42
2:e:71:ASP:C	2:e:73:GLU:H	2.26	0.42
2:h:78:GLU:O	2:h:79:GLY:C	2.59	0.42
2:i:71:ASP:C	2:i:73:GLU:H	2.26	0.42
1:M:92:ASP:OD2	1:M:92:ASP:N	2.53	0.42
1:M:301:VAL:HG23	1:M:439:ASN:HB3	2.00	0.42
1:M:306:GLU:O	1:M:316:TYR:HA	2.19	0.42
1:N:228:LYS:O	1:N:229:LYS:HB3	2.20	0.42
1:N:301:VAL:HA	1:N:302:PRO:HD3	1.77	0.42
1:N:448:VAL:C	1:N:450:GLN:H	2.28	0.42
1:N:457:MSE:O	1:N:458:ARG:CD	2.68	0.42
1:O:245:SER:HG	1:O:247:PHE:HE1	1.64	0.42
1:O:511:ARG:HA	1:O:513:ARG:CD	2.45	0.42
1:O:599:ALA:C	1:O:600:LYS:HD2	2.45	0.42
1:P:24:GLU:O	1:P:26:ARG:N	2.51	0.42
1:P:554:LEU:HD12	1:P:557:PHE:CD2	2.52	0.42
1:Q:24:GLU:O	1:Q:26:ARG:N	2.50	0.42
1:Q:248:LYS:HE2	1:Q:513:ARG:HH12	1.84	0.42
1:Q:443:ASP:O	1:Q:446:THR:HG22	2.19	0.42
1:R:15:PHE:CE2	1:R:19:TRP:NE1	2.88	0.42
1:R:160:SER:O	1:R:161:ASN:ND2	2.46	0.42
1:S:61:ARG:CB	1:S:62:PRO:HD3	2.49	0.42
1:T:40:GLN:HE21	1:T:40:GLN:HB2	1.58	0.42
1:T:591:GLN:HA	1:T:594:VAL:CG2	2.50	0.42
3:T:719:HOH:O	1:W:430:VAL:HG13	2.18	0.42
1:U:241:GLY:O	1:U:242:GLU:C	2.63	0.42
1:V:35:PHE:CE1	1:V:321:ARG:NH1	2.86	0.42
1:V:123:VAL:HG13	1:V:304:PHE:CE1	2.55	0.42
1:V:301:VAL:HG23	1:V:439:ASN:HB3	2.01	0.42
1:V:578:GLN:HG2	1:V:596:ALA:CB	2.50	0.42
1:W:107:ALA:HA	1:W:146:ARG:HB3	2.01	0.42
1:X:311:GLU:O	1:X:312:ASP:HB2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:344:THR:O	1:X:344:THR:CG2	2.68	0.42
2:k:10:VAL:HA	2:k:15:ARG:HG2	2.01	0.42
2:l:48:TYR:H	2:l:54:ILE:H	1.65	0.42
2:m:47:TRP:CD1	2:m:47:TRP:H	2.38	0.42
2:s:59:VAL:HG22	2:s:73:HIS:O	2.18	0.42
2:t:59:VAL:HG22	2:t:73:HIS:O	2.20	0.42
1:A:212:LEU:N	1:A:212:LEU:HD12	2.34	0.42
1:C:386:THR:HG21	1:C:389:LEU:HD21	2.02	0.42
1:C:434:THR:HG23	1:C:435:VAL:N	2.35	0.42
1:C:552:LEU:O	1:C:556:TYR:HD2	2.03	0.42
1:D:49:THR:O	1:D:50:THR:O	2.37	0.42
1:D:165:MSE:HE1	1:D:435:VAL:HB	2.02	0.42
1:D:282:THR:HG23	1:D:287:LEU:CD1	2.43	0.42
1:E:35:PHE:CZ	1:E:321:ARG:CZ	3.02	0.42
1:E:43:ASP:OD2	1:E:43:ASP:N	2.52	0.42
1:E:68:VAL:HG22	1:E:119:ILE:HD12	2.02	0.42
1:E:229:LYS:HD2	1:E:270:GLN:HG3	2.01	0.42
1:E:273:ARG:HH22	1:E:453:LEU:HD11	1.85	0.42
1:E:378:ASP:O	1:E:381:SER:O	2.37	0.42
1:E:552:LEU:O	1:E:556:TYR:HD2	2.03	0.42
1:F:94:LEU:HD23	1:F:94:LEU:C	2.45	0.42
1:F:130:THR:HG23	1:F:450:GLN:NE2	2.35	0.42
1:G:528:LYS:CD	1:G:560:LEU:HD21	2.50	0.42
1:H:130:THR:HG23	1:H:450:GLN:NE2	2.35	0.42
1:H:165:MSE:HE1	1:H:435:VAL:HB	2.02	0.42
1:I:93:VAL:O	1:I:97:MSE:HG3	2.20	0.42
1:I:273:ARG:HH22	1:I:453:LEU:HD11	1.85	0.42
1:K:26:ARG:O	1:K:27:ARG:C	2.62	0.42
1:K:38:VAL:HG21	1:K:324:LYS:HD2	2.01	0.42
1:K:209:PHE:N	1:K:210:PRO:CD	2.82	0.42
1:K:229:LYS:HG2	1:K:272:LYS:CG	2.50	0.42
1:L:166:ASP:C	1:L:168:SER:N	2.77	0.42
1:L:212:LEU:N	1:L:212:LEU:HD12	2.34	0.42
2:Y:71:ASP:C	2:Y:73:GLU:H	2.26	0.42
2:Y:101:ALA:N	2:Y:102:PRO:CD	2.82	0.42
2:e:78:GLU:CD	2:e:79:GLY:N	2.77	0.42
2:g:20:ARG:C	2:g:22:ALA:N	2.74	0.42
2:g:75:PRO:HA	2:g:76:PRO:HD3	1.42	0.42
1:M:76:ILE:HD12	1:M:433:ASP:OD1	2.20	0.42
1:M:160:SER:O	1:M:161:ASN:ND2	2.45	0.42
1:M:387:GLN:HB2	1:O:390:ALA:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:431:ALA:HA	1:M:434:THR:HG22	2.02	0.42
1:N:265:LYS:O	1:N:266:ILE:HG12	2.20	0.42
1:N:280:ILE:HD12	1:N:280:ILE:N	2.35	0.42
1:N:344:THR:O	1:N:344:THR:CG2	2.67	0.42
1:O:270:GLN:HA	1:O:270:GLN:OE1	2.20	0.42
1:O:329:LEU:HD22	2:m:133:PRO:HG2	2.01	0.42
1:P:115:VAL:HA	1:P:118:GLN:HB3	2.02	0.42
1:P:591:GLN:HA	1:P:594:VAL:CG2	2.50	0.42
1:Q:266:ILE:HD13	1:Q:266:ILE:HA	1.89	0.42
1:Q:330:ARG:O	1:Q:334:MSE:HB2	2.20	0.42
1:R:232:ALA:HB2	1:R:269:ARG:O	2.19	0.42
1:S:219:ILE:HG13	1:S:220:ALA:N	2.35	0.42
1:S:306:GLU:O	1:S:316:TYR:HA	2.20	0.42
1:S:330:ARG:HD2	1:S:409:THR:CG2	2.41	0.42
1:T:54:ARG:HB2	2:s:137:GLY:HA3	2.01	0.42
1:T:190:LYS:HA	1:T:190:LYS:HE3	2.00	0.42
1:T:191:TYR:O	1:T:288:LYS:HE2	2.20	0.42
1:T:241:GLY:O	1:T:242:GLU:C	2.63	0.42
1:U:270:GLN:OE1	1:U:270:GLN:HA	2.19	0.42
1:V:76:ILE:HD12	1:V:433:ASP:OD1	2.18	0.42
1:V:212:LEU:HD12	1:V:212:LEU:N	2.35	0.42
1:V:236:GLN:H	1:V:265:LYS:CB	2.33	0.42
1:V:503:GLU:HB3	1:V:508:ASN:HB3	2.02	0.42
1:W:161:ASN:O	1:W:161:ASN:CG	2.62	0.42
1:W:280:ILE:HG22	1:W:287:LEU:HD13	2.01	0.42
1:W:528:LYS:HD2	1:W:560:LEU:HD21	2.01	0.42
1:W:542:THR:HA	1:W:543:PRO:HD3	1.87	0.42
1:X:78:VAL:CG1	1:X:79:LEU:H	2.33	0.42
1:X:380:ASN:O	1:X:381:SER:CB	2.68	0.42
2:m:67:PRO:O	2:m:68:ALA:HB2	2.19	0.42
2:p:93:PRO:HB3	2:r:100:THR:HG21	2.01	0.42
2:s:24:THR:HG22	2:s:25:LEU:N	2.34	0.42
1:A:68:VAL:HG22	1:A:119:ILE:HD12	2.02	0.42
1:A:93:VAL:O	1:A:97:MSE:HG3	2.20	0.42
1:A:130:THR:HG23	1:A:450:GLN:NE2	2.35	0.42
1:A:430:VAL:HG12	1:A:431:ALA:N	2.35	0.42
1:B:282:THR:HG23	1:B:287:LEU:CD1	2.43	0.42
1:C:68:VAL:HG22	1:C:119:ILE:HD12	2.02	0.42
1:C:229:LYS:HG2	1:C:272:LYS:CG	2.50	0.42
1:C:274:ARG:HD3	1:C:296:GLU:O	2.19	0.42
1:D:130:THR:HG23	1:D:450:GLN:NE2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:274:ARG:HD3	1:D:296:GLU:O	2.19	0.42
1:D:301:VAL:HG23	1:D:439:ASN:HB3	2.02	0.42
1:E:98:TYR:C	1:E:98:TYR:CD2	2.98	0.42
1:E:251:ILE:HD11	1:E:275:ARG:NH2	2.34	0.42
1:E:274:ARG:HD3	1:E:296:GLU:O	2.19	0.42
1:F:229:LYS:HG2	1:F:272:LYS:CG	2.50	0.42
1:F:386:THR:HG21	1:F:389:LEU:HD21	2.02	0.42
1:G:130:THR:HG23	1:G:450:GLN:NE2	2.35	0.42
1:G:265:LYS:HD2	1:G:265:LYS:HA	1.96	0.42
1:G:437:GLN:HA	1:G:440:MSE:HB2	2.01	0.42
1:H:48:TYR:O	1:H:49:THR:CB	2.64	0.42
1:H:274:ARG:HD3	1:H:296:GLU:O	2.19	0.42
1:H:434:THR:HG23	1:H:435:VAL:N	2.35	0.42
1:H:451:ASP:O	1:H:456:ALA:N	2.41	0.42
1:I:376:ARG:HB2	1:J:352:TRP:CD2	2.55	0.42
1:I:528:LYS:CD	1:I:560:LEU:HD21	2.50	0.42
1:J:35:PHE:HE1	1:J:321:ARG:NH1	2.13	0.42
1:J:301:VAL:HG23	1:J:439:ASN:HB3	2.02	0.42
1:J:567:MSE:SE	1:K:576:LEU:HD13	2.69	0.42
1:L:43:ASP:OD2	1:L:43:ASP:N	2.52	0.42
1:L:93:VAL:O	1:L:97:MSE:HG3	2.20	0.42
1:L:368:ASP:O	2:Z:134:ARG:HG3	2.20	0.42
1:L:528:LYS:CD	1:L:560:LEU:HD21	2.50	0.42
2:Z:101:ALA:N	2:Z:102:PRO:CD	2.82	0.42
2:g:124:TYR:CG	2:g:124:TYR:O	2.73	0.42
2:j:104:TYR:N	2:j:104:TYR:CD1	2.85	0.42
1:M:266:ILE:O	1:M:267:ALA:HB2	2.19	0.41
1:M:458:ARG:HD3	1:M:458:ARG:HA	1.83	0.41
1:M:575:GLN:O	1:M:579:MSE:CG	2.66	0.41
1:N:57:PHE:CD1	1:N:57:PHE:N	2.88	0.41
1:N:236:GLN:H	1:N:265:LYS:CB	2.33	0.41
1:N:241:GLY:O	1:N:242:GLU:C	2.63	0.41
1:O:24:GLU:HG3	1:O:313:LYS:HE2	2.01	0.41
1:O:298:ILE:HA	1:O:299:PRO:HD3	1.79	0.41
1:O:528:LYS:NZ	1:O:560:LEU:HD21	2.35	0.41
1:P:15:PHE:CE2	1:P:19:TRP:NE1	2.88	0.41
1:P:241:GLY:O	1:P:242:GLU:C	2.63	0.41
1:P:599:ALA:C	1:P:600:LYS:HD2	2.45	0.41
1:Q:115:VAL:HA	1:Q:118:GLN:HB3	2.02	0.41
1:Q:147:GLU:HA	1:Q:148:PRO:HD3	1.81	0.41
1:Q:543:PRO:C	1:Q:545:GLY:H	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:554:LEU:O	1:Q:557:PHE:HB3	2.20	0.41
1:R:35:PHE:HZ	1:R:321:ARG:NE	2.13	0.41
1:R:101:ASP:HB3	1:R:138:THR:HG21	2.01	0.41
1:R:301:VAL:HG23	1:R:439:ASN:HB3	2.02	0.41
1:R:380:ASN:O	1:R:381:SER:CB	2.68	0.41
1:R:384:LEU:HD22	1:R:384:LEU:N	2.33	0.41
1:S:24:GLU:HG3	1:S:313:LYS:HE2	2.02	0.41
1:S:27:ARG:NH2	1:U:41:TRP:HE1	2.18	0.41
1:S:334:MSE:HE1	1:T:407:ALA:HB1	2.02	0.41
1:T:280:ILE:N	1:T:280:ILE:HD12	2.35	0.41
1:U:511:ARG:HA	1:U:513:ARG:CD	2.47	0.41
1:U:528:LYS:NZ	1:U:560:LEU:HD21	2.34	0.41
1:U:554:LEU:HD21	1:X:564:GLY:CA	2.46	0.41
1:U:579:MSE:HB2	1:U:581:VAL:HG12	2.02	0.41
1:V:191:TYR:O	1:V:288:LYS:HE2	2.19	0.41
1:V:430:VAL:HG11	3:W:719:HOH:O	2.16	0.41
1:V:528:LYS:HD2	1:V:560:LEU:HD21	2.01	0.41
1:V:557:PHE:CE2	1:W:563:LYS:HD3	2.55	0.41
1:W:101:ASP:HB3	1:W:138:THR:HG21	2.01	0.41
1:W:262:GLY:O	1:W:263:PHE:HB3	2.21	0.41
1:W:387:GLN:H	1:W:387:GLN:HG2	1.58	0.41
2:n:49:GLN:H	2:n:53:GLY:HA3	1.84	0.41
2:q:49:GLN:H	2:q:53:GLY:HA3	1.85	0.41
2:s:64:GLU:C	2:s:66:PRO:HD2	2.45	0.41
2:t:33:MET:HE3	2:t:33:MET:HB3	1.67	0.41
2:u:10:VAL:HA	2:u:15:ARG:HG2	2.02	0.41
1:A:166:ASP:C	1:A:168:SER:N	2.77	0.41
1:A:598:GLN:HB2	1:A:601:GLN:HB3	2.02	0.41
1:B:80:TYR:CZ	1:B:448:VAL:HG22	2.54	0.41
1:B:94:LEU:HD23	1:B:94:LEU:C	2.45	0.41
1:B:130:THR:HG23	1:B:450:GLN:NE2	2.35	0.41
1:C:35:PHE:HZ	1:C:321:ARG:NE	2.12	0.41
1:C:49:THR:O	1:C:50:THR:O	2.37	0.41
1:C:568:MSE:HG3	1:E:551:LEU:CD2	2.50	0.41
1:D:68:VAL:HG22	1:D:119:ILE:HD12	2.02	0.41
1:D:229:LYS:HG2	1:D:272:LYS:CG	2.50	0.41
1:D:437:GLN:HA	1:D:440:MSE:HB2	2.01	0.41
1:E:430:VAL:HG12	1:E:431:ALA:N	2.35	0.41
1:E:434:THR:HG23	1:E:435:VAL:N	2.35	0.41
1:F:198:ILE:HA	1:F:199:PRO:HD3	1.64	0.41
1:F:273:ARG:HD2	1:F:275:ARG:HD2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:38:VAL:HG21	1:G:324:LYS:HD2	2.01	0.41
1:G:43:ASP:OD2	1:G:43:ASP:N	2.52	0.41
1:G:209:PHE:N	1:G:210:PRO:CD	2.82	0.41
1:G:229:LYS:HG2	1:G:272:LYS:CG	2.50	0.41
1:G:241:GLY:O	1:G:242:GLU:C	2.63	0.41
1:G:332:MSE:SE	2:c:141:MET:HA	2.70	0.41
1:G:434:THR:HG23	1:G:435:VAL:N	2.35	0.41
1:H:273:ARG:HH22	1:H:453:LEU:HD11	1.85	0.41
1:I:15:PHE:HE2	1:I:19:TRP:NE1	2.18	0.41
1:I:78:VAL:HG21	1:I:444:LEU:CD1	2.21	0.41
1:I:99:ARG:HH12	1:I:530:GLN:NE2	2.14	0.41
1:I:251:ILE:HD11	1:I:275:ARG:NH2	2.35	0.41
1:I:274:ARG:HD3	1:I:296:GLU:O	2.19	0.41
1:J:34:PHE:HE1	1:J:324:LYS:HZ2	1.53	0.41
1:J:93:VAL:O	1:J:97:MSE:HG3	2.20	0.41
1:J:165:MSE:HE1	1:J:435:VAL:HB	2.02	0.41
1:J:252:LYS:O	1:J:252:LYS:HE3	2.19	0.41
1:K:98:TYR:CD2	1:K:98:TYR:C	2.98	0.41
1:K:127:ARG:HG2	1:K:147:GLU:HB2	2.02	0.41
1:K:130:THR:HG23	1:K:450:GLN:NE2	2.35	0.41
1:K:430:VAL:HG12	1:K:431:ALA:N	2.35	0.41
1:K:437:GLN:HA	1:K:440:MSE:HB2	2.00	0.41
1:K:528:LYS:CD	1:K:560:LEU:HD21	2.50	0.41
1:L:98:TYR:CD2	1:L:98:TYR:C	2.98	0.41
1:L:127:ARG:HG2	1:L:147:GLU:HB2	2.02	0.41
1:L:165:MSE:HE1	1:L:435:VAL:HB	2.02	0.41
1:L:229:LYS:HG2	1:L:272:LYS:CG	2.50	0.41
1:L:273:ARG:HD2	1:L:275:ARG:HD2	2.02	0.41
1:L:282:THR:HG23	1:L:287:LEU:CD1	2.43	0.41
2:b:20:ARG:C	2:b:22:ALA:N	2.74	0.41
2:c:28:VAL:HG11	2:c:97:ALA:CA	2.42	0.41
2:c:124:TYR:O	2:c:124:TYR:CG	2.73	0.41
2:e:124:TYR:O	2:e:124:TYR:CG	2.73	0.41
2:f:124:TYR:O	2:f:124:TYR:CG	2.73	0.41
2:i:150:PRO:O	2:i:151:ASN:C	2.61	0.41
2:j:71:ASP:CB	2:j:75:PRO:HD2	2.36	0.41
1:N:430:VAL:HG11	3:V:719:HOH:O	2.19	0.41
1:P:245:SER:HG	1:P:247:PHE:HE1	1.62	0.41
1:P:280:ILE:HD12	1:P:280:ILE:N	2.35	0.41
1:P:310:VAL:HB	1:P:311:GLU:H	1.64	0.41
1:Q:301:VAL:HG23	1:Q:439:ASN:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:41:TRP:HE3	1:R:42:ASP:HB3	1.82	0.41
1:R:193:LEU:HD22	1:R:287:LEU:HB3	2.01	0.41
1:R:236:GLN:H	1:R:265:LYS:CB	2.33	0.41
1:R:340:ILE:O	1:R:344:THR:HG21	2.20	0.41
1:S:92:ASP:OD2	1:S:92:ASP:N	2.52	0.41
1:S:236:GLN:H	1:S:265:LYS:CB	2.33	0.41
1:S:241:GLY:O	1:S:242:GLU:C	2.63	0.41
1:S:273:ARG:HH22	1:S:453:LEU:CD2	2.31	0.41
1:S:457:MSE:O	1:S:458:ARG:CD	2.69	0.41
1:T:349:PRO:HB2	1:T:351:PHE:CE2	2.55	0.41
1:T:380:ASN:O	1:T:381:SER:CB	2.68	0.41
1:U:236:GLN:H	1:U:265:LYS:CB	2.33	0.41
1:U:583:LYS:HA	1:U:584:PRO:HD3	1.92	0.41
1:V:276:VAL:CG2	1:V:293:ILE:HG23	2.49	0.41
1:V:280:ILE:HD12	1:V:280:ILE:N	2.34	0.41
1:W:380:ASN:O	1:W:381:SER:CB	2.68	0.41
1:X:11:ILE:O	1:X:15:PHE:HB2	2.20	0.41
2:r:47:TRP:CD1	2:r:47:TRP:H	2.38	0.41
2:s:49:GLN:H	2:s:53:GLY:HA3	1.85	0.41
1:A:229:LYS:HG2	1:A:272:LYS:CG	2.50	0.41
1:B:93:VAL:O	1:B:97:MSE:HG3	2.20	0.41
1:B:123:VAL:HG21	1:B:153:CYS:HB3	2.02	0.41
1:B:229:LYS:HG2	1:B:272:LYS:CG	2.50	0.41
1:B:376:ARG:HB2	1:C:352:TRP:CD2	2.55	0.41
1:B:434:THR:HG23	1:B:435:VAL:N	2.35	0.41
1:C:241:GLY:O	1:C:242:GLU:C	2.63	0.41
1:D:440:MSE:O	1:D:444:LEU:CD2	2.69	0.41
1:D:552:LEU:O	1:D:556:TYR:HD2	2.03	0.41
1:F:94:LEU:HD23	1:F:94:LEU:O	2.19	0.41
1:F:212:LEU:HD12	1:F:212:LEU:N	2.34	0.41
1:F:440:MSE:O	1:F:444:LEU:CD2	2.69	0.41
1:G:528:LYS:HZ2	1:G:560:LEU:HD21	1.82	0.41
1:G:579:MSE:CB	1:G:581:VAL:HG12	2.50	0.41
1:H:26:ARG:O	1:H:27:ARG:C	2.62	0.41
1:H:378:ASP:O	1:H:381:SER:O	2.37	0.41
1:H:395:PRO:HD2	1:I:398:PRO:HB3	2.02	0.41
1:I:68:VAL:HG22	1:I:119:ILE:HD12	2.02	0.41
1:I:130:THR:HG23	1:I:450:GLN:NE2	2.35	0.41
1:J:98:TYR:C	1:J:98:TYR:CD2	2.98	0.41
1:J:130:THR:HG23	1:J:450:GLN:NE2	2.35	0.41
1:J:316:TYR:O	1:J:321:ARG:NH1	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:251:ILE:HD11	1:K:275:ARG:NH2	2.35	0.41
1:L:68:VAL:HG22	1:L:119:ILE:HD12	2.02	0.41
1:L:94:LEU:HD23	1:L:94:LEU:C	2.45	0.41
1:L:241:GLY:O	1:L:242:GLU:C	2.63	0.41
1:L:397:VAL:O	1:L:397:VAL:HG12	2.20	0.41
2:d:63:ILE:CG2	2:d:123:LEU:HB3	2.51	0.41
1:M:591:GLN:HA	1:M:594:VAL:CG2	2.50	0.41
1:N:123:VAL:HG22	1:N:316:TYR:HE2	1.84	0.41
1:N:528:LYS:HD2	1:N:560:LEU:HD21	2.03	0.41
1:O:174:THR:N	3:O:705:HOH:O	2.53	0.41
1:O:177:HIS:O	1:O:218:GLN:HA	2.21	0.41
1:O:301:VAL:HG23	1:O:439:ASN:HB3	2.02	0.41
1:O:543:PRO:C	1:O:545:GLY:H	2.28	0.41
1:P:41:TRP:HE1	1:Q:27:ARG:HH21	1.67	0.41
1:P:66:LYS:HZ3	1:P:420:VAL:HG21	1.85	0.41
1:P:147:GLU:HA	1:P:148:PRO:HD3	1.82	0.41
1:P:161:ASN:O	1:P:161:ASN:CG	2.63	0.41
1:Q:212:LEU:HD22	1:R:26:ARG:HG2	2.03	0.41
1:Q:591:GLN:HA	1:Q:594:VAL:CG2	2.50	0.41
1:R:61:ARG:CB	1:R:62:PRO:HD3	2.51	0.41
1:R:227:GLU:O	1:R:227:GLU:HG2	2.20	0.41
1:R:298:ILE:HA	1:R:299:PRO:HD3	1.78	0.41
1:R:583:LYS:HA	1:R:584:PRO:HD3	1.91	0.41
1:S:282:THR:HG23	1:S:287:LEU:CD1	2.47	0.41
1:S:511:ARG:HA	1:S:513:ARG:CD	2.47	0.41
1:S:554:LEU:HD12	1:S:557:PHE:CD2	2.53	0.41
1:T:24:GLU:HG3	1:T:313:LYS:HE2	2.02	0.41
1:T:248:LYS:HE2	1:T:513:ARG:HH12	1.85	0.41
1:T:371:TYR:HE2	1:T:373:LEU:HD21	1.85	0.41
1:U:79:LEU:N	1:U:519:ASP:O	2.53	0.41
1:U:265:LYS:O	1:U:266:ILE:HG12	2.19	0.41
1:U:413:LYS:HE2	1:U:413:LYS:HB3	1.84	0.41
1:W:227:GLU:O	1:W:227:GLU:HG2	2.20	0.41
1:W:431:ALA:HA	1:W:434:THR:HG22	2.01	0.41
1:W:457:MSE:O	1:W:458:ARG:CD	2.68	0.41
1:X:29:ALA:O	1:X:33:LEU:HG	2.19	0.41
1:X:528:LYS:HD2	1:X:560:LEU:HD21	2.02	0.41
2:p:69:GLU:HB3	2:p:70:GLY:H	1.68	0.41
2:v:17:LEU:HD23	2:v:17:LEU:O	2.20	0.41
1:A:246:TYR:HD2	1:A:511:ARG:CB	2.28	0.41
1:A:255:ILE:O	1:A:258:LEU:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:ARG:HD2	1:A:275:ARG:HD2	2.02	0.41
1:A:434:THR:HG23	1:A:435:VAL:N	2.35	0.41
1:A:568:MSE:HG3	1:B:551:LEU:CD2	2.50	0.41
1:B:157:ILE:O	1:B:157:ILE:CG1	2.69	0.41
1:B:166:ASP:C	1:B:168:SER:N	2.77	0.41
1:B:273:ARG:HD2	1:B:275:ARG:HD2	2.02	0.41
1:B:397:VAL:O	1:B:397:VAL:HG12	2.20	0.41
1:B:552:LEU:O	1:B:556:TYR:HD2	2.03	0.41
1:C:15:PHE:HE2	1:C:19:TRP:NE1	2.18	0.41
1:C:130:THR:HG23	1:C:450:GLN:NE2	2.35	0.41
1:C:251:ILE:HD11	1:C:275:ARG:NH2	2.35	0.41
1:C:448:VAL:C	1:C:450:GLN:H	2.27	0.41
1:C:528:LYS:CD	1:C:560:LEU:HD21	2.50	0.41
1:D:26:ARG:O	1:D:27:ARG:C	2.62	0.41
1:D:98:TYR:C	1:D:98:TYR:CD2	2.98	0.41
1:D:434:THR:HG23	1:D:435:VAL:N	2.35	0.41
1:E:130:THR:HG23	1:E:450:GLN:NE2	2.35	0.41
1:E:437:GLN:HA	1:E:440:MSE:HB2	2.00	0.41
1:F:241:GLY:O	1:F:242:GLU:C	2.63	0.41
1:F:434:THR:HG23	1:F:435:VAL:N	2.35	0.41
1:F:444:LEU:O	1:F:447:TYR:N	2.52	0.41
1:G:49:THR:O	1:G:50:THR:O	2.37	0.41
1:G:248:LYS:HZ1	1:G:513:ARG:HH12	1.67	0.41
1:G:274:ARG:HD3	1:G:296:GLU:O	2.19	0.41
1:H:34:PHE:HE1	1:H:324:LYS:HZ2	1.56	0.41
1:H:94:LEU:HD23	1:H:94:LEU:C	2.45	0.41
1:I:38:VAL:HG21	1:I:324:LYS:HD2	2.01	0.41
1:I:568:MSE:HG3	1:J:551:LEU:CD2	2.50	0.41
1:J:68:VAL:HG22	1:J:119:ILE:HD12	2.02	0.41
1:J:229:LYS:HG2	1:J:272:LYS:CG	2.50	0.41
1:J:241:GLY:O	1:J:242:GLU:C	2.63	0.41
1:J:579:MSE:CB	1:J:581:VAL:HG12	2.49	0.41
1:K:93:VAL:O	1:K:97:MSE:HG3	2.20	0.41
1:K:227:GLU:OE2	1:K:227:GLU:N	2.47	0.41
1:K:579:MSE:CB	1:K:581:VAL:HG12	2.50	0.41
1:L:26:ARG:O	1:L:27:ARG:C	2.62	0.41
1:L:209:PHE:N	1:L:210:PRO:CD	2.82	0.41
1:L:444:LEU:O	1:L:447:TYR:N	2.52	0.41
2:Y:28:VAL:HG11	2:Y:97:ALA:HA	1.88	0.41
2:Y:63:ILE:CG2	2:Y:123:LEU:HB3	2.51	0.41
2:Z:124:TYR:O	2:Z:124:TYR:CG	2.73	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:d:124:TYR:O	2:d:124:TYR:CG	2.73	0.41
2:h:63:ILE:CG2	2:h:123:LEU:HB3	2.51	0.41
1:M:24:GLU:N	1:M:24:GLU:OE1	2.54	0.41
1:M:293:ILE:HG12	1:M:294:ALA:H	1.85	0.41
1:M:399:GLN:OE1	1:N:396:GLU:O	2.38	0.41
1:M:438:LEU:HD12	1:M:441:ARG:NH1	2.35	0.41
1:M:528:LYS:HD2	1:M:560:LEU:HD21	2.02	0.41
1:N:310:VAL:HB	1:N:311:GLU:H	1.67	0.41
1:O:191:TYR:O	1:O:288:LYS:HE2	2.21	0.41
1:O:241:GLY:O	1:O:242:GLU:C	2.63	0.41
1:O:444:LEU:O	1:O:447:TYR:N	2.53	0.41
1:P:191:TYR:O	1:P:288:LYS:HE2	2.20	0.41
1:P:270:GLN:OE1	1:P:270:GLN:HA	2.19	0.41
1:P:371:TYR:HE2	1:P:373:LEU:HD21	1.85	0.41
1:P:372:TYR:CE2	1:Q:348:LYS:HB2	2.56	0.41
1:P:543:PRO:C	1:P:545:GLY:H	2.28	0.41
1:Q:72:ARG:HG2	1:R:434:THR:HG21	2.03	0.41
1:Q:100:THR:HG22	1:Q:138:THR:HG22	2.02	0.41
1:R:78:VAL:HG11	1:R:444:LEU:CG	2.50	0.41
1:R:241:GLY:O	1:R:242:GLU:C	2.63	0.41
1:R:387:GLN:O	1:R:389:LEU:HG	2.20	0.41
1:R:451:ASP:O	1:R:453:LEU:N	2.53	0.41
1:S:76:ILE:HD12	1:S:433:ASP:OD1	2.19	0.41
1:S:262:GLY:O	1:S:263:PHE:HB3	2.20	0.41
1:S:343:ARG:H	1:S:343:ARG:HG2	1.54	0.41
1:T:310:VAL:HB	1:T:311:GLU:H	1.70	0.41
1:T:457:MSE:O	1:T:458:ARG:CD	2.68	0.41
1:V:101:ASP:HB3	1:V:138:THR:HG21	2.01	0.41
1:W:164:LEU:HD22	1:W:169:ASP:OD1	2.20	0.41
1:W:364:ASP:CG	2:v:126:ALA:HB2	2.44	0.41
1:W:371:TYR:HE2	1:W:373:LEU:HD21	1.86	0.41
1:W:458:ARG:HD3	1:W:458:ARG:HA	1.83	0.41
1:X:66:LYS:HZ3	1:X:420:VAL:HG21	1.85	0.41
1:X:349:PRO:HG3	1:X:391:TYR:CE1	2.55	0.41
1:X:575:GLN:O	1:X:579:MSE:CG	2.68	0.41
2:k:12:ALA:HB3	2:k:15:ARG:CD	2.50	0.41
2:u:64:GLU:C	2:u:66:PRO:HD2	2.45	0.41
1:A:165:MSE:HE1	1:A:435:VAL:HB	2.02	0.41
1:A:209:PHE:N	1:A:210:PRO:CD	2.82	0.41
1:A:241:GLY:O	1:A:242:GLU:C	2.63	0.41
1:A:313:LYS:HD3	1:A:314:GLU:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:316:TYR:O	1:A:321:ARG:NH1	2.54	0.41
1:B:98:TYR:CD2	1:B:98:TYR:C	2.98	0.41
1:B:165:MSE:HE1	1:B:435:VAL:HB	2.02	0.41
1:B:316:TYR:O	1:B:321:ARG:NH1	2.53	0.41
1:B:352:TRP:HB2	1:B:355:GLN:HG2	2.03	0.41
1:C:26:ARG:O	1:C:27:ARG:C	2.62	0.41
1:D:94:LEU:HD23	1:D:94:LEU:C	2.45	0.41
1:D:316:TYR:O	1:D:321:ARG:NH1	2.54	0.41
1:D:352:TRP:HB2	1:D:355:GLN:HG2	2.03	0.41
1:D:579:MSE:CB	1:D:581:VAL:HG12	2.49	0.41
1:E:15:PHE:HE2	1:E:19:TRP:NE1	2.18	0.41
1:E:94:LEU:HD23	1:E:94:LEU:C	2.45	0.41
1:E:209:PHE:CE2	1:E:214:GLN:HG2	2.56	0.41
1:F:118:GLN:HE21	1:F:118:GLN:HB2	1.77	0.41
1:F:598:GLN:HB2	1:F:601:GLN:HB3	2.03	0.41
1:G:123:VAL:HG21	1:G:153:CYS:HB3	2.02	0.41
1:G:209:PHE:CE2	1:G:214:GLN:HG2	2.56	0.41
1:G:273:ARG:HH22	1:G:453:LEU:HD11	1.85	0.41
1:G:316:TYR:O	1:G:321:ARG:NH1	2.54	0.41
1:I:98:TYR:C	1:I:98:TYR:CD2	2.98	0.41
1:I:273:ARG:HD2	1:I:275:ARG:HD2	2.01	0.41
1:K:166:ASP:C	1:K:168:SER:N	2.77	0.41
1:K:236:GLN:HE21	1:K:265:LYS:HZ1	1.68	0.41
1:K:255:ILE:O	1:K:258:LEU:N	2.53	0.41
1:L:80:TYR:CZ	1:L:448:VAL:HG22	2.54	0.41
1:L:301:VAL:HG23	1:L:439:ASN:HB3	2.02	0.41
2:Z:56:TRP:CD1	2:Z:56:TRP:N	2.89	0.41
2:c:56:TRP:CD1	2:c:56:TRP:N	2.88	0.41
2:j:124:TYR:O	2:j:124:TYR:CG	2.73	0.41
1:M:71:MSE:CE	1:M:115:VAL:HB	2.50	0.41
1:M:164:LEU:HD22	1:M:169:ASP:OD1	2.20	0.41
1:M:301:VAL:HA	1:M:302:PRO:HD3	1.75	0.41
1:M:390:ALA:HB2	1:N:387:GLN:CB	2.50	0.41
1:N:80:TYR:OH	1:N:444:LEU:HD12	2.20	0.41
1:N:440:MSE:O	1:N:443:ASP:HB3	2.20	0.41
1:O:77:ASP:HB2	1:O:523:SER:HB2	2.02	0.41
1:O:380:ASN:O	1:O:381:SER:CB	2.69	0.41
1:P:179:MSE:O	1:P:217:ILE:HD12	2.21	0.41
1:P:266:ILE:O	1:P:267:ALA:HB2	2.18	0.41
1:P:563:LYS:HD3	1:Q:557:PHE:CE2	2.55	0.41
1:P:577:ILE:HG12	1:P:582:LYS:CG	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:328:ARG:HB3	2:n:133:PRO:HG3	2.02	0.41
1:Q:394:ASN:HA	1:Q:395:PRO:HD3	1.93	0.41
1:R:431:ALA:HA	1:R:434:THR:HG22	2.01	0.41
1:R:458:ARG:HD3	1:R:458:ARG:HA	1.83	0.41
1:S:191:TYR:O	1:S:288:LYS:HE2	2.20	0.41
1:T:387:GLN:O	1:T:389:LEU:HG	2.20	0.41
1:T:543:PRO:C	1:T:545:GLY:H	2.28	0.41
1:T:599:ALA:C	1:T:600:LYS:HD2	2.45	0.41
1:U:274:ARG:O	1:U:275:ARG:HD2	2.20	0.41
1:U:510:ILE:O	1:U:513:ARG:HD2	2.20	0.41
1:V:427:GLY:C	1:V:429:GLN:N	2.75	0.41
1:V:591:GLN:HA	1:V:594:VAL:CG2	2.51	0.41
1:W:270:GLN:OE1	1:W:270:GLN:HA	2.20	0.41
1:W:301:VAL:HG23	1:W:439:ASN:HB3	2.02	0.41
1:W:528:LYS:NZ	1:W:560:LEU:HD21	2.35	0.41
1:X:443:ASP:O	1:X:446:THR:HG22	2.21	0.41
1:X:448:VAL:C	1:X:450:GLN:H	2.29	0.41
2:m:24:THR:HG22	2:m:25:LEU:N	2.36	0.41
2:m:49:GLN:H	2:m:53:GLY:HA3	1.85	0.41
2:t:64:GLU:C	2:t:66:PRO:HD2	2.46	0.41
2:t:126:ALA:HA	2:t:127:PRO:HD3	1.90	0.41
2:v:61:SER:HB2	2:v:67:PRO:HA	2.03	0.41
1:A:15:PHE:HE2	1:A:19:TRP:NE1	2.18	0.41
1:A:94:LEU:HD23	1:A:94:LEU:C	2.45	0.41
1:A:378:ASP:O	1:A:381:SER:O	2.37	0.41
1:B:15:PHE:HE2	1:B:19:TRP:NE1	2.18	0.41
1:B:273:ARG:NH1	1:B:275:ARG:HE	2.19	0.41
1:B:276:VAL:HG23	1:B:293:ILE:HG22	2.03	0.41
1:C:99:ARG:HH12	1:C:530:GLN:NE2	2.14	0.41
1:C:598:GLN:HB2	1:C:601:GLN:HB3	2.03	0.41
1:D:386:THR:HG21	1:D:389:LEU:HD21	2.02	0.41
1:D:397:VAL:O	1:D:397:VAL:HG12	2.20	0.41
1:E:47:GLN:N	1:E:47:GLN:CD	2.72	0.41
1:E:93:VAL:O	1:E:97:MSE:HG3	2.20	0.41
1:E:165:MSE:HE1	1:E:435:VAL:HB	2.02	0.41
1:E:313:LYS:HD3	1:E:314:GLU:N	2.36	0.41
1:E:359:PHE:HD1	2:c:129:ILE:HD11	1.85	0.41
1:E:448:VAL:C	1:E:450:GLN:H	2.27	0.41
1:F:35:PHE:HZ	1:F:321:ARG:NE	2.12	0.41
1:F:166:ASP:C	1:F:168:SER:N	2.77	0.41
1:F:360:GLU:HG3	2:d:131:ARG:HB3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:166:ASP:C	1:G:168:SER:N	2.77	0.41
1:G:313:LYS:HD3	1:G:314:GLU:N	2.36	0.41
1:G:598:GLN:HB2	1:G:601:GLN:HB3	2.02	0.41
1:H:80:TYR:HB2	1:H:95:MSE:HG2	2.03	0.41
1:H:273:ARG:NH1	1:H:275:ARG:HE	2.19	0.41
1:H:301:VAL:HG23	1:H:439:ASN:HB3	2.02	0.41
1:H:310:VAL:HB	1:H:311:GLU:H	1.78	0.41
1:I:165:MSE:HE1	1:I:435:VAL:HB	2.02	0.41
1:J:198:ILE:HA	1:J:199:PRO:HD3	1.64	0.41
1:K:273:ARG:HH22	1:K:453:LEU:HD11	1.85	0.41
1:K:313:LYS:HD3	1:K:314:GLU:N	2.36	0.41
1:K:316:TYR:O	1:K:321:ARG:NH1	2.54	0.41
1:K:542:THR:HA	1:K:543:PRO:HD3	1.82	0.41
1:K:598:GLN:HB2	1:K:601:GLN:HB3	2.02	0.41
1:L:38:VAL:HG21	1:L:324:LYS:HD2	2.01	0.41
1:L:80:TYR:HB2	1:L:95:MSE:HG2	2.03	0.41
1:L:209:PHE:CE2	1:L:214:GLN:HG2	2.56	0.41
1:L:313:LYS:HD3	1:L:314:GLU:N	2.36	0.41
1:L:316:TYR:O	1:L:321:ARG:NH1	2.54	0.41
2:a:71:ASP:C	2:a:73:GLU:H	2.26	0.41
2:h:20:ARG:C	2:h:22:ALA:N	2.74	0.41
2:h:78:GLU:CD	2:h:79:GLY:N	2.77	0.41
2:i:28:VAL:CG1	2:i:97:ALA:CB	2.86	0.41
1:M:82:PRO:HB2	1:M:83:LYS:H	1.63	0.41
1:M:198:ILE:HA	1:M:199:PRO:HD3	1.70	0.41
1:M:273:ARG:HH22	1:M:453:LEU:CD2	2.31	0.41
1:M:384:LEU:HD22	1:M:384:LEU:N	2.31	0.41
1:M:451:ASP:O	1:M:453:LEU:N	2.53	0.41
1:N:78:VAL:CG1	1:N:79:LEU:H	2.31	0.41
1:N:115:VAL:HA	1:N:118:GLN:HB3	2.03	0.41
1:N:123:VAL:HG13	1:N:304:PHE:CE1	2.56	0.41
1:N:413:LYS:HE2	1:N:413:LYS:HB3	1.87	0.41
1:N:451:ASP:O	1:N:453:LEU:N	2.54	0.41
1:O:448:VAL:C	1:O:450:GLN:H	2.28	0.41
1:P:228:LYS:O	1:P:229:LYS:HB3	2.21	0.41
1:P:298:ILE:HA	1:P:299:PRO:HD3	1.77	0.41
1:P:330:ARG:O	1:P:334:MSE:HB2	2.20	0.41
1:P:528:LYS:HD2	1:P:560:LEU:HD21	2.02	0.41
1:Q:29:ALA:O	1:Q:33:LEU:HG	2.20	0.41
1:Q:65:ARG:HG2	1:R:306:GLU:OE2	2.21	0.41
1:Q:212:LEU:HD12	1:Q:212:LEU:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:236:GLN:H	1:Q:265:LYS:CB	2.33	0.41
1:Q:369:TYR:HA	1:Q:370:PRO:HD3	1.84	0.41
1:R:156:VAL:O	1:R:156:VAL:CG2	2.69	0.41
1:T:61:ARG:CB	1:T:62:PRO:HD3	2.50	0.41
1:T:126:TRP:NE1	1:T:301:VAL:HG13	2.36	0.41
1:U:92:ASP:OD2	1:U:92:ASP:N	2.53	0.41
1:U:107:ALA:HA	1:U:146:ARG:HB3	2.02	0.41
1:V:35:PHE:O	1:V:37:ARG:N	2.46	0.41
1:V:232:ALA:HB1	1:V:233:PHE:H	1.58	0.41
1:V:431:ALA:HA	1:V:434:THR:HG22	2.02	0.41
1:V:444:LEU:O	1:V:447:TYR:N	2.53	0.41
1:W:15:PHE:CE2	1:W:19:TRP:NE1	2.88	0.41
1:W:57:PHE:CD1	1:W:57:PHE:N	2.88	0.41
1:W:249:ARG:HH21	1:W:249:ARG:HD2	1.52	0.41
1:W:591:GLN:HA	1:W:594:VAL:CG2	2.50	0.41
2:m:80:VAL:O	2:m:82:ALA:N	2.54	0.41
2:o:64:GLU:C	2:o:66:PRO:HD2	2.46	0.41
1:B:38:VAL:HG21	1:B:324:LYS:HD2	2.01	0.41
1:B:68:VAL:HG22	1:B:119:ILE:HD12	2.02	0.41
1:B:209:PHE:CE2	1:B:214:GLN:HG2	2.56	0.41
1:B:313:LYS:HD3	1:B:314:GLU:N	2.36	0.41
1:C:80:TYR:HB2	1:C:95:MSE:HG2	2.03	0.41
1:C:93:VAL:O	1:C:97:MSE:HG3	2.20	0.41
1:C:265:LYS:HD2	1:C:265:LYS:HA	1.96	0.41
1:C:273:ARG:NH1	1:C:275:ARG:HE	2.19	0.41
1:C:276:VAL:HG23	1:C:293:ILE:HG22	2.03	0.41
1:C:583:LYS:HA	1:C:584:PRO:HD3	1.85	0.41
1:D:123:VAL:HG21	1:D:153:CYS:HB3	2.02	0.41
1:D:251:ILE:HD11	1:D:275:ARG:NH2	2.35	0.41
1:D:372:TYR:CD2	1:F:348:LYS:HB2	2.56	0.41
1:E:528:LYS:CD	1:E:560:LEU:HD21	2.50	0.41
1:F:43:ASP:OD2	1:F:43:ASP:N	2.52	0.41
1:F:80:TYR:HB2	1:F:95:MSE:HG2	2.03	0.41
1:F:165:MSE:HE1	1:F:435:VAL:HB	2.02	0.41
1:F:313:LYS:HD3	1:F:314:GLU:N	2.36	0.41
1:G:276:VAL:HG23	1:G:293:ILE:HG22	2.03	0.41
1:H:332:MSE:SE	2:d:141:MET:HA	2.71	0.41
1:H:579:MSE:CB	1:H:581:VAL:HG12	2.49	0.41
1:I:127:ARG:HG2	1:I:147:GLU:HB2	2.02	0.41
1:I:209:PHE:CE2	1:I:214:GLN:HG2	2.56	0.41
1:I:301:VAL:HA	1:I:302:PRO:HD3	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:316:TYR:O	1:I:321:ARG:NH1	2.54	0.41
1:J:157:ILE:O	1:J:157:ILE:CG1	2.68	0.41
1:J:236:GLN:CG	1:J:243:PRO:HB2	2.51	0.41
1:L:528:LYS:HD2	1:L:560:LEU:HD11	2.03	0.41
2:Z:63:ILE:CG2	2:Z:123:LEU:HB3	2.51	0.41
2:a:104:TYR:N	2:a:104:TYR:CD1	2.85	0.41
2:a:119:GLY:O	2:a:123:LEU:HD13	2.21	0.41
2:b:150:PRO:O	2:b:151:ASN:C	2.61	0.41
2:c:71:ASP:C	2:c:73:GLU:H	2.26	0.41
1:M:584:PRO:CG	1:M:593:LEU:HD12	2.48	0.41
1:N:107:ALA:HA	1:N:146:ARG:HB3	2.02	0.41
1:N:306:GLU:O	1:N:316:TYR:HA	2.21	0.41
1:N:387:GLN:HA	1:N:388:PRO:HD3	1.93	0.41
1:N:443:ASP:O	1:N:446:THR:HG22	2.20	0.41
1:O:159:ASP:OD2	1:O:161:ASN:N	2.51	0.41
1:O:387:GLN:HB2	1:P:390:ALA:HB2	2.03	0.41
1:O:396:GLU:O	1:P:399:GLN:OE1	2.38	0.41
1:P:156:VAL:O	1:P:156:VAL:CG2	2.69	0.41
1:P:276:VAL:CG2	1:P:293:ILE:HG23	2.50	0.41
1:P:564:GLY:O	1:Q:554:LEU:HD21	2.19	0.41
1:Q:107:ALA:HA	1:Q:146:ARG:HB3	2.03	0.41
1:R:14:ARG:NE	1:R:14:ARG:CA	2.70	0.41
1:R:231:THR:HG23	1:R:249:ARG:HE	1.85	0.41
1:R:577:ILE:HG12	1:R:582:LYS:CG	2.45	0.41
1:S:108:LYS:HD2	1:T:438:LEU:HD11	2.01	0.41
1:T:174:THR:N	3:T:705:HOH:O	2.53	0.41
1:T:369:TYR:HA	1:T:370:PRO:HD3	1.83	0.41
1:U:123:VAL:HG22	1:U:316:TYR:HE2	1.83	0.41
1:U:161:ASN:ND2	1:U:161:ASN:C	2.78	0.41
1:U:352:TRP:O	1:U:355:GLN:HG2	2.20	0.41
1:U:404:MSE:HE1	1:X:334:MSE:HG3	2.02	0.41
1:V:543:PRO:C	1:V:545:GLY:H	2.29	0.41
1:W:61:ARG:CB	1:W:62:PRO:HD3	2.50	0.41
1:W:311:GLU:H	1:W:311:GLU:HG3	1.76	0.41
1:W:352:TRP:HB2	1:W:355:GLN:HG2	2.03	0.41
1:X:227:GLU:O	1:X:227:GLU:HG2	2.20	0.41
1:X:387:GLN:O	1:X:389:LEU:HG	2.20	0.41
2:n:84:PHE:CD2	2:n:84:PHE:C	2.99	0.41
2:p:24:THR:HG22	2:p:25:LEU:N	2.35	0.41
2:q:24:THR:HG22	2:q:25:LEU:N	2.34	0.41
2:s:61:SER:HB2	2:s:67:PRO:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:u:33:MET:HB3	2:u:33:MET:HE3	1.66	0.41
2:v:48:TYR:H	2:v:54:ILE:H	1.68	0.41
1:A:301:VAL:HG23	1:A:439:ASN:HB3	2.02	0.41
1:B:127:ARG:HG2	1:B:147:GLU:HB2	2.03	0.41
1:C:397:VAL:O	1:C:397:VAL:HG12	2.20	0.41
1:D:227:GLU:OE2	1:D:227:GLU:N	2.47	0.41
1:D:241:GLY:O	1:D:242:GLU:C	2.63	0.41
1:E:166:ASP:C	1:E:168:SER:N	2.77	0.41
1:E:241:GLY:O	1:E:242:GLU:C	2.63	0.41
1:E:273:ARG:C	1:E:273:ARG:HD3	2.46	0.41
1:E:301:VAL:HG23	1:E:439:ASN:HB3	2.02	0.41
1:F:343:ARG:H	1:F:343:ARG:HG2	1.52	0.41
1:F:579:MSE:CB	1:F:581:VAL:HG12	2.49	0.41
1:G:236:GLN:CG	1:G:243:PRO:HB2	2.51	0.41
1:G:273:ARG:HD2	1:G:275:ARG:HD2	2.02	0.41
1:G:430:VAL:HG12	1:G:431:ALA:N	2.35	0.41
1:H:236:GLN:CG	1:H:243:PRO:HB2	2.51	0.41
1:H:313:LYS:HD3	1:H:314:GLU:N	2.36	0.41
1:I:273:ARG:NH1	1:I:275:ARG:HE	2.19	0.41
1:I:434:THR:HG23	1:I:435:VAL:N	2.35	0.41
1:J:15:PHE:HE2	1:J:19:TRP:NE1	2.18	0.41
1:J:567:MSE:HE2	1:K:554:LEU:HD22	2.02	0.41
1:L:301:VAL:HA	1:L:302:PRO:HD3	1.85	0.41
2:Y:119:GLY:O	2:Y:123:LEU:HD13	2.21	0.41
2:Z:135:ALA:HA	2:Z:136:PRO:HD3	1.92	0.41
2:f:103:ASP:OD1	2:g:31:ASP:HA	2.21	0.41
2:i:63:ILE:CG2	2:i:123:LEU:HB3	2.51	0.41
1:M:444:LEU:O	1:M:445:GLU:C	2.61	0.41
1:N:584:PRO:CG	1:N:593:LEU:HD12	2.49	0.41
1:O:93:VAL:O	1:O:97:MSE:HG3	2.21	0.41
1:P:123:VAL:HG13	1:P:304:PHE:CE1	2.56	0.41
1:Q:77:ASP:HB2	1:Q:523:SER:HB2	2.03	0.41
1:Q:156:VAL:O	1:Q:156:VAL:CG2	2.69	0.41
1:Q:158:TRP:HH2	1:Q:302:PRO:HG3	1.80	0.41
1:Q:262:GLY:O	1:Q:263:PHE:HB3	2.20	0.41
1:Q:340:ILE:O	1:Q:344:THR:HG21	2.21	0.41
1:Q:444:LEU:O	1:Q:447:TYR:N	2.54	0.41
1:R:276:VAL:CG2	1:R:293:ILE:HG23	2.49	0.41
1:R:438:LEU:HD12	1:R:441:ARG:NH1	2.36	0.41
1:S:280:ILE:HD12	1:S:280:ILE:N	2.35	0.41
1:S:349:PRO:HG3	1:S:391:TYR:CE1	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:266:ILE:HD13	1:T:266:ILE:HA	1.90	0.41
1:T:276:VAL:CG2	1:T:293:ILE:HG23	2.49	0.41
1:U:27:ARG:HH21	1:X:41:TRP:HE1	1.68	0.41
1:U:40:GLN:HE21	1:U:40:GLN:HB2	1.58	0.41
1:U:248:LYS:HE2	1:U:513:ARG:HH12	1.84	0.41
1:U:349:PRO:HG3	1:U:391:TYR:CE1	2.55	0.41
1:V:107:ALA:HA	1:V:146:ARG:HB3	2.03	0.41
1:V:115:VAL:HA	1:V:118:GLN:HB3	2.02	0.41
1:W:40:GLN:HE21	1:W:40:GLN:HB2	1.61	0.41
1:W:387:GLN:O	1:W:389:LEU:HG	2.20	0.41
1:X:274:ARG:O	1:X:275:ARG:HD2	2.19	0.41
1:X:343:ARG:HD3	2:r:128:TYR:CE1	2.56	0.41
1:X:457:MSE:O	1:X:458:ARG:CD	2.69	0.41
1:X:591:GLN:HA	1:X:594:VAL:CG2	2.50	0.41
2:l:24:THR:HG22	2:l:25:LEU:N	2.35	0.41
2:l:49:GLN:H	2:l:53:GLY:HA3	1.85	0.41
2:n:17:LEU:O	2:n:17:LEU:HD23	2.21	0.41
2:o:12:ALA:C	2:o:14:LEU:H	2.28	0.41
2:o:49:GLN:H	2:o:53:GLY:HA3	1.85	0.41
2:p:33:MET:HB3	2:p:33:MET:HE3	1.66	0.41
2:q:126:ALA:HA	2:q:127:PRO:HD3	1.89	0.41
2:t:16:LYS:HE2	2:t:73:HIS:CD2	2.56	0.41
2:v:67:PRO:O	2:v:68:ALA:HB2	2.20	0.41
1:A:127:ARG:HG2	1:A:147:GLU:HB2	2.02	0.41
1:A:273:ARG:HH22	1:A:453:LEU:HD11	1.85	0.41
1:A:552:LEU:O	1:A:556:TYR:HD2	2.03	0.41
1:B:236:GLN:CG	1:B:243:PRO:HB2	2.51	0.41
1:B:241:GLY:O	1:B:242:GLU:C	2.63	0.41
1:B:298:ILE:HA	1:B:299:PRO:HD3	1.82	0.41
1:C:165:MSE:HE1	1:C:435:VAL:HB	2.02	0.41
1:C:273:ARG:HD3	1:C:273:ARG:C	2.46	0.41
1:C:322:LEU:N	1:C:322:LEU:HD22	2.36	0.41
1:D:273:ARG:HH22	1:D:453:LEU:HD11	1.85	0.41
1:E:26:ARG:O	1:E:27:ARG:C	2.62	0.41
1:F:301:VAL:HG23	1:F:439:ASN:HB3	2.02	0.41
1:F:316:TYR:O	1:F:321:ARG:NH1	2.53	0.41
1:G:386:THR:HG21	1:G:389:LEU:HD21	2.02	0.41
1:I:147:GLU:HA	1:I:148:PRO:HD3	1.86	0.41
1:I:313:LYS:HD3	1:I:314:GLU:N	2.36	0.41
1:J:80:TYR:HB2	1:J:95:MSE:HG2	2.03	0.41
1:J:94:LEU:HD23	1:J:94:LEU:C	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:127:ARG:HG2	1:J:147:GLU:HB2	2.03	0.41
1:J:376:ARG:NE	1:K:354:GLU:OE2	2.51	0.41
1:J:430:VAL:HG12	1:J:431:ALA:N	2.35	0.41
1:J:528:LYS:HD2	1:J:560:LEU:HD11	2.03	0.41
1:K:236:GLN:CG	1:K:243:PRO:HB2	2.51	0.41
1:K:322:LEU:HD22	1:K:322:LEU:N	2.36	0.41
1:L:130:THR:HG23	1:L:450:GLN:NE2	2.35	0.41
1:L:386:THR:HG21	1:L:389:LEU:HD21	2.02	0.41
2:b:119:GLY:O	2:b:123:LEU:HD13	2.21	0.41
2:c:150:PRO:O	2:c:151:ASN:C	2.61	0.41
2:g:39:PRO:HB2	2:g:40:GLN:H	1.51	0.41
2:h:119:GLY:O	2:h:123:LEU:HD13	2.21	0.41
2:i:137:TYR:HA	2:i:138:PRO:HD3	1.88	0.41
2:j:63:ILE:CG2	2:j:123:LEU:HB3	2.51	0.41
2:j:78:GLU:CD	2:j:79:GLY:N	2.77	0.41
2:j:119:GLY:O	2:j:123:LEU:HD13	2.21	0.41
2:j:135:ALA:HA	2:j:136:PRO:HD3	1.92	0.41
1:M:11:ILE:O	1:M:15:PHE:HB2	2.21	0.41
1:M:101:ASP:HB3	1:M:138:THR:HG21	2.02	0.41
1:M:115:VAL:HA	1:M:118:GLN:HB3	2.02	0.41
1:M:191:TYR:O	1:M:288:LYS:HE2	2.21	0.41
1:M:227:GLU:O	1:M:227:GLU:HG2	2.21	0.41
1:M:236:GLN:H	1:M:265:LYS:CB	2.34	0.41
1:M:440:MSE:O	1:M:443:ASP:HB3	2.21	0.41
1:M:554:LEU:HD12	1:M:557:PHE:CD2	2.54	0.41
1:M:564:GLY:CA	1:O:554:LEU:HD21	2.48	0.41
1:N:123:VAL:HG23	3:N:709:HOH:O	2.21	0.41
1:N:293:ILE:HG12	1:N:294:ALA:H	1.85	0.41
1:N:311:GLU:O	1:N:312:ASP:HB2	2.21	0.41
1:N:330:ARG:O	1:N:334:MSE:HB2	2.21	0.41
1:N:349:PRO:HG3	1:N:391:TYR:CE1	2.56	0.41
1:N:360:GLU:CD	1:N:360:GLU:H	2.28	0.41
1:N:364:ASP:CG	2:m:126:ALA:HB2	2.45	0.41
1:O:103:ARG:NH1	1:P:517:TYR:HB2	2.36	0.41
1:O:330:ARG:O	1:O:334:MSE:HB2	2.20	0.41
1:O:503:GLU:HB3	1:O:508:ASN:HB3	2.03	0.41
1:O:564:GLY:HA2	1:P:554:LEU:CD2	2.43	0.41
1:O:591:GLN:HA	1:O:594:VAL:CG2	2.51	0.41
1:P:35:PHE:CE1	1:P:321:ARG:NH1	2.87	0.41
1:P:41:TRP:HE3	1:P:42:ASP:HB3	1.80	0.41
1:P:219:ILE:HG13	1:P:220:ALA:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:227:GLU:O	1:P:227:GLU:HG2	2.21	0.41
1:P:349:PRO:HG3	1:P:391:TYR:CE1	2.55	0.41
1:P:360:GLU:CD	1:P:360:GLU:H	2.29	0.41
1:P:376:ARG:HB2	1:Q:352:TRP:CG	2.56	0.41
1:P:451:ASP:O	1:P:453:LEU:N	2.54	0.41
1:P:578:GLN:HG2	1:P:596:ALA:CB	2.50	0.41
1:Q:61:ARG:CB	1:Q:62:PRO:HD3	2.50	0.41
1:Q:161:ASN:ND2	1:Q:161:ASN:C	2.78	0.41
1:Q:228:LYS:O	1:Q:229:LYS:HB3	2.21	0.41
1:Q:236:GLN:CG	1:Q:243:PRO:HB2	2.51	0.41
1:Q:387:GLN:O	1:Q:389:LEU:HG	2.21	0.41
1:Q:440:MSE:O	1:Q:443:ASP:HB3	2.21	0.41
1:R:79:LEU:N	1:R:519:ASP:O	2.53	0.41
1:R:123:VAL:HG22	1:R:316:TYR:HE2	1.84	0.41
1:R:177:HIS:O	1:R:218:GLN:HA	2.21	0.41
1:R:191:TYR:O	1:R:288:LYS:HE2	2.20	0.41
1:R:378:ASP:HA	2:q:109:TYR:HD2	1.84	0.41
1:R:427:GLY:C	1:R:429:GLN:N	2.75	0.41
1:S:387:GLN:O	1:S:389:LEU:HG	2.21	0.41
1:S:443:ASP:O	1:S:446:THR:HG22	2.20	0.41
1:T:298:ILE:HA	1:T:299:PRO:HD3	1.80	0.41
1:T:394:ASN:HA	1:T:395:PRO:HD3	1.91	0.41
1:U:24:GLU:HG3	1:U:313:LYS:HE2	2.03	0.41
1:U:35:PHE:HZ	1:U:321:ARG:NE	2.13	0.41
1:U:282:THR:HG23	1:U:287:LEU:CD1	2.46	0.41
1:U:577:ILE:HG12	1:U:582:LYS:CG	2.46	0.41
1:U:591:GLN:HA	1:U:594:VAL:CG2	2.51	0.41
1:U:599:ALA:C	1:U:600:LYS:HD2	2.45	0.41
1:V:227:GLU:O	1:V:227:GLU:HG2	2.21	0.41
1:V:228:LYS:O	1:V:229:LYS:HB3	2.21	0.41
1:V:262:GLY:O	1:V:263:PHE:HB3	2.20	0.41
1:V:298:ILE:HA	1:V:299:PRO:HD3	1.79	0.41
1:V:334:MSE:SE	1:V:405:LEU:HD11	2.71	0.41
1:W:35:PHE:O	1:W:37:ARG:N	2.46	0.41
1:W:66:LYS:HZ3	1:W:420:VAL:HG21	1.86	0.41
1:W:236:GLN:H	1:W:265:LYS:CB	2.34	0.41
1:W:241:GLY:O	1:W:242:GLU:C	2.64	0.41
1:W:274:ARG:O	1:W:275:ARG:HD2	2.21	0.41
1:W:349:PRO:HG3	1:W:391:TYR:CE1	2.56	0.41
1:W:444:LEU:O	1:W:447:TYR:N	2.53	0.41
1:W:503:GLU:HB3	1:W:508:ASN:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:78:VAL:HG11	1:X:444:LEU:CG	2.48	0.41
1:X:236:GLN:H	1:X:265:LYS:CB	2.34	0.41
1:X:241:GLY:O	1:X:242:GLU:C	2.63	0.41
1:X:360:GLU:CD	1:X:360:GLU:H	2.28	0.41
1:X:438:LEU:HD12	1:X:441:ARG:NH1	2.35	0.41
1:X:599:ALA:C	1:X:600:LYS:HD2	2.46	0.41
2:k:113:LEU:HD23	2:k:113:LEU:HA	1.79	0.41
2:l:34:GLN:C	2:l:36:ALA:H	2.28	0.41
2:l:64:GLU:C	2:l:66:PRO:HD2	2.45	0.41
2:m:40:LEU:C	2:m:40:LEU:CD2	2.92	0.41
2:m:64:GLU:C	2:m:66:PRO:HD2	2.45	0.41
2:n:12:ALA:HB3	2:n:15:ARG:CD	2.50	0.41
2:n:113:LEU:HD23	2:n:113:LEU:HA	1.76	0.41
2:p:61:SER:HB2	2:p:67:PRO:HA	2.03	0.41
2:r:12:ALA:HB3	2:r:15:ARG:CD	2.49	0.41
2:t:31:GLN:C	2:t:33:MET:N	2.79	0.41
2:v:64:GLU:C	2:v:66:PRO:HD2	2.46	0.41
1:A:236:GLN:CG	1:A:243:PRO:HB2	2.51	0.41
1:B:265:LYS:HD2	1:B:265:LYS:HA	1.96	0.41
1:B:301:VAL:HG23	1:B:439:ASN:HB3	2.02	0.41
1:B:386:THR:HG21	1:B:389:LEU:HD21	2.02	0.41
1:B:598:GLN:HB2	1:B:601:GLN:HB3	2.03	0.41
1:C:61:ARG:N	1:C:62:PRO:CD	2.84	0.41
1:C:123:VAL:HG21	1:C:153:CYS:HB3	2.02	0.41
1:C:236:GLN:CG	1:C:243:PRO:HB2	2.51	0.41
1:C:273:ARG:HH22	1:C:453:LEU:HD11	1.85	0.41
1:C:352:TRP:HB2	1:C:355:GLN:HG2	2.03	0.41
1:C:369:TYR:HA	1:C:370:PRO:HD3	1.84	0.41
1:C:383:ASP:CB	1:C:385:PRO:HD3	2.51	0.41
1:C:528:LYS:HD2	1:C:560:LEU:HD11	2.03	0.41
1:D:236:GLN:CG	1:D:243:PRO:HB2	2.51	0.41
1:D:313:LYS:HD3	1:D:314:GLU:N	2.36	0.41
1:E:80:TYR:HB2	1:E:95:MSE:HG2	2.03	0.41
1:E:276:VAL:HG23	1:E:293:ILE:HG22	2.03	0.41
1:E:298:ILE:HA	1:E:299:PRO:HD3	1.82	0.41
1:E:301:VAL:HA	1:E:302:PRO:HD3	1.84	0.41
1:E:386:THR:HG21	1:E:389:LEU:HD21	2.02	0.41
1:F:68:VAL:HG22	1:F:119:ILE:HD12	2.02	0.41
1:F:123:VAL:HG21	1:F:153:CYS:HB3	2.02	0.41
1:F:273:ARG:HD3	1:F:273:ARG:C	2.46	0.41
1:F:383:ASP:CB	1:F:385:PRO:HD3	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:430:VAL:HG12	1:F:431:ALA:N	2.35	0.41
1:F:528:LYS:HD2	1:F:560:LEU:HD11	2.03	0.41
1:G:157:ILE:O	1:G:157:ILE:CG1	2.69	0.41
1:G:310:VAL:C	1:G:312:ASP:N	2.76	0.41
1:H:43:ASP:OD2	1:H:43:ASP:N	2.52	0.41
1:H:229:LYS:HG2	1:H:272:LYS:CG	2.50	0.41
1:H:241:GLY:O	1:H:242:GLU:C	2.63	0.41
1:H:273:ARG:C	1:H:273:ARG:HD3	2.46	0.41
1:H:273:ARG:HD2	1:H:275:ARG:HD2	2.02	0.41
1:I:80:TYR:HB2	1:I:95:MSE:HG2	2.03	0.41
1:I:236:GLN:CG	1:I:243:PRO:HB2	2.51	0.41
1:I:273:ARG:C	1:I:273:ARG:HD3	2.46	0.41
1:I:598:GLN:HB2	1:I:601:GLN:HB3	2.03	0.41
1:J:38:VAL:HG21	1:J:324:LYS:HD2	2.01	0.41
1:J:61:ARG:N	1:J:62:PRO:CD	2.84	0.41
1:J:94:LEU:HA	1:J:97:MSE:CE	2.37	0.41
1:J:273:ARG:C	1:J:273:ARG:HD3	2.46	0.41
1:J:298:ILE:HA	1:J:299:PRO:HD3	1.82	0.41
1:J:313:LYS:HD3	1:J:314:GLU:N	2.36	0.41
1:J:322:LEU:HD22	1:J:322:LEU:N	2.36	0.41
1:J:397:VAL:O	1:J:397:VAL:HG12	2.20	0.41
1:J:440:MSE:O	1:J:444:LEU:CD2	2.69	0.41
1:J:552:LEU:O	1:J:556:TYR:HD2	2.03	0.41
1:K:35:PHE:HE1	1:K:321:ARG:NH1	2.13	0.41
1:K:165:MSE:HE1	1:K:435:VAL:HB	2.02	0.41
1:K:209:PHE:CE2	1:K:214:GLN:HG2	2.56	0.41
1:K:241:GLY:O	1:K:242:GLU:C	2.63	0.41
1:K:273:ARG:NH1	1:K:275:ARG:HE	2.19	0.41
1:K:359:PHE:HD1	2:Y:129:ILE:HD11	1.86	0.41
1:K:413:LYS:HE2	1:K:413:LYS:HB3	1.74	0.41
1:K:434:THR:HG23	1:K:435:VAL:N	2.35	0.41
1:K:440:MSE:O	1:K:444:LEU:CD2	2.69	0.41
1:K:552:LEU:O	1:K:556:TYR:HD2	2.03	0.41
1:L:273:ARG:HD3	1:L:273:ARG:C	2.46	0.41
2:Z:95:ASN:CG	2:Z:116:ALA:HB1	2.46	0.41
2:a:63:ILE:CG2	2:a:123:LEU:HB3	2.51	0.41
2:c:57:TYR:O	2:c:59:ASP:N	2.54	0.41
2:f:63:ILE:CG2	2:f:123:LEU:HB3	2.51	0.41
2:g:57:TYR:O	2:g:59:ASP:N	2.54	0.41
2:g:119:GLY:O	2:g:123:LEU:HD13	2.21	0.41
2:h:117:LYS:HE2	2:h:117:LYS:HB3	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:i:56:TRP:N	2:i:56:TRP:CD1	2.88	0.41
2:i:124:TYR:O	2:i:124:TYR:CG	2.73	0.41
2:j:117:LYS:HE2	2:j:117:LYS:HB3	1.86	0.41
2:j:137:TYR:HA	2:j:138:PRO:HD3	1.88	0.41
1:N:61:ARG:CB	1:N:62:PRO:HD3	2.51	0.41
1:O:349:PRO:HG3	1:O:391:TYR:CE1	2.56	0.41
1:P:340:ILE:O	1:P:344:THR:HG21	2.20	0.41
1:Q:191:TYR:O	1:Q:288:LYS:HE2	2.21	0.41
1:Q:231:THR:CG2	1:Q:249:ARG:HH11	2.32	0.41
1:Q:306:GLU:O	1:Q:316:TYR:HA	2.21	0.41
1:Q:457:MSE:O	1:Q:458:ARG:CD	2.69	0.41
1:R:198:ILE:HA	1:R:199:PRO:HD3	1.71	0.41
1:R:262:GLY:O	1:R:263:PHE:HB3	2.21	0.41
1:R:578:GLN:HG2	1:R:596:ALA:CB	2.51	0.41
1:S:107:ALA:HA	1:S:146:ARG:HB3	2.02	0.41
1:S:177:HIS:O	1:S:218:GLN:HA	2.21	0.41
1:S:210:PRO:HD2	1:S:211:TRP:CZ3	2.56	0.41
1:S:579:MSE:HB2	1:S:581:VAL:HG12	2.03	0.41
1:S:599:ALA:C	1:S:600:LYS:HD2	2.45	0.41
1:U:262:GLY:O	1:U:263:PHE:HB3	2.21	0.41
1:U:543:PRO:C	1:U:545:GLY:H	2.28	0.41
1:W:24:GLU:N	1:W:24:GLU:OE1	2.54	0.41
1:X:212:LEU:HD12	1:X:212:LEU:N	2.35	0.41
2:l:113:LEU:HD23	2:l:113:LEU:HA	1.78	0.41
2:m:16:LYS:HZ2	2:m:16:LYS:HA	1.86	0.41
2:q:64:GLU:C	2:q:66:PRO:HD2	2.46	0.41
2:q:67:PRO:O	2:q:68:ALA:HB2	2.20	0.41
2:r:16:LYS:HE2	2:r:73:HIS:CD2	2.55	0.41
2:s:47:TRP:CD1	2:s:47:TRP:H	2.39	0.41
2:t:61:SER:HB2	2:t:67:PRO:HA	2.03	0.41
2:u:34:GLN:C	2:u:36:ALA:H	2.28	0.41
1:B:78:VAL:CG1	1:B:444:LEU:HG	2.51	0.41
1:B:80:TYR:HB2	1:B:95:MSE:HG2	2.03	0.41
1:B:448:VAL:C	1:B:450:GLN:H	2.27	0.41
1:C:118:GLN:HE21	1:C:118:GLN:HB2	1.77	0.41
1:C:316:TYR:O	1:C:321:ARG:NH1	2.53	0.41
1:C:440:MSE:O	1:C:444:LEU:CD2	2.69	0.41
1:D:157:ILE:O	1:D:157:ILE:CG1	2.68	0.41
1:D:273:ARG:NH1	1:D:275:ARG:HE	2.19	0.41
1:E:383:ASP:CB	1:E:385:PRO:HD3	2.51	0.41
1:G:301:VAL:HG23	1:G:439:ASN:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:316:TYR:O	1:H:321:ARG:NH1	2.54	0.41
1:H:322:LEU:HD22	1:H:322:LEU:N	2.36	0.41
1:H:352:TRP:HB2	1:H:355:GLN:HG2	2.03	0.41
1:H:383:ASP:CB	1:H:385:PRO:HD3	2.51	0.41
1:H:430:VAL:HG12	1:H:431:ALA:N	2.35	0.41
1:I:93:VAL:HG11	1:I:458:ARG:HG2	2.03	0.41
1:I:301:VAL:HG23	1:I:439:ASN:HB3	2.02	0.41
1:I:322:LEU:N	1:I:322:LEU:HD22	2.36	0.41
1:I:383:ASP:CB	1:I:385:PRO:HD3	2.51	0.41
1:J:273:ARG:HH22	1:J:453:LEU:HD11	1.85	0.41
1:K:198:ILE:HA	1:K:199:PRO:HD3	1.64	0.41
1:L:273:ARG:HH22	1:L:453:LEU:HD11	1.85	0.41
2:Z:119:GLY:O	2:Z:123:LEU:HD13	2.21	0.41
2:a:28:VAL:HG11	2:a:97:ALA:HA	1.88	0.41
2:b:138:PRO:HD2	2:b:141:MET:HB2	2.03	0.41
2:f:95:ASN:CG	2:f:116:ALA:HB1	2.46	0.41
2:i:89:VAL:C	2:i:91:ALA:N	2.76	0.41
1:M:123:VAL:HG13	1:M:304:PHE:CE1	2.56	0.40
1:N:82:PRO:HB2	1:N:83:LYS:H	1.63	0.40
1:N:227:GLU:O	1:N:227:GLU:HG2	2.21	0.40
1:N:386:THR:CG2	1:N:389:LEU:HD21	2.51	0.40
1:N:591:GLN:HA	1:N:594:VAL:CG2	2.51	0.40
1:O:340:ILE:O	1:O:344:THR:HG21	2.22	0.40
1:P:236:GLN:H	1:P:265:LYS:CB	2.34	0.40
1:P:248:LYS:H	1:P:248:LYS:CD	2.18	0.40
1:P:511:ARG:HA	1:P:513:ARG:CD	2.46	0.40
1:Q:79:LEU:N	1:Q:519:ASP:O	2.54	0.40
1:Q:599:ALA:C	1:Q:600:LYS:HD2	2.45	0.40
1:R:310:VAL:HB	1:R:311:GLU:H	1.66	0.40
1:R:330:ARG:HD2	1:R:409:THR:CG2	2.42	0.40
1:R:543:PRO:C	1:R:545:GLY:H	2.29	0.40
1:S:80:TYR:CE1	1:S:448:VAL:CG2	3.05	0.40
1:S:179:MSE:O	1:S:217:ILE:HD12	2.21	0.40
1:S:503:GLU:HB3	1:S:508:ASN:HB3	2.03	0.40
1:T:528:LYS:HD2	1:T:560:LEU:HD21	2.02	0.40
1:U:334:MSE:SE	1:U:405:LEU:HD11	2.71	0.40
1:U:380:ASN:O	1:U:381:SER:CB	2.69	0.40
1:U:394:ASN:HA	1:U:395:PRO:HD3	1.93	0.40
1:U:457:MSE:O	1:U:458:ARG:CD	2.69	0.40
1:U:458:ARG:HD3	1:U:458:ARG:HA	1.84	0.40
1:V:251:ILE:HD11	1:V:275:ARG:HH21	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:438:LEU:HD11	1:W:108:LYS:HD2	2.02	0.40
1:V:451:ASP:O	1:V:453:LEU:N	2.54	0.40
1:W:219:ILE:HG13	1:W:220:ALA:N	2.36	0.40
1:X:370:PRO:HB2	1:X:371:TYR:CD1	2.56	0.40
2:k:80:VAL:O	2:k:82:ALA:N	2.54	0.40
2:l:108:LYS:HE2	2:l:108:LYS:HB3	1.87	0.40
2:m:12:ALA:HB3	2:m:15:ARG:CD	2.51	0.40
2:q:55:ILE:N	2:q:55:ILE:CD1	2.84	0.40
2:r:84:PHE:C	2:r:84:PHE:CD2	2.99	0.40
2:u:113:LEU:HD23	2:u:113:LEU:HA	1.78	0.40
2:v:14:LEU:HD22	2:v:33:MET:SD	2.62	0.40
2:v:34:GLN:C	2:v:36:ALA:H	2.29	0.40
1:A:209:PHE:CE2	1:A:214:GLN:HG2	2.56	0.40
1:A:273:ARG:C	1:A:273:ARG:HD3	2.46	0.40
1:B:440:MSE:O	1:B:444:LEU:CD2	2.69	0.40
1:C:94:LEU:HD23	1:C:94:LEU:C	2.45	0.40
1:C:232:ALA:HB1	1:C:233:PHE:H	1.71	0.40
1:D:209:PHE:CE2	1:D:214:GLN:HG2	2.56	0.40
1:D:322:LEU:HD22	1:D:322:LEU:N	2.36	0.40
1:D:528:LYS:HD2	1:D:560:LEU:HD11	2.03	0.40
1:D:576:LEU:HD13	1:E:567:MSE:SE	2.71	0.40
1:E:99:ARG:NH1	1:E:530:GLN:HE21	2.13	0.40
1:E:229:LYS:HG2	1:E:272:LYS:CG	2.50	0.40
1:E:322:LEU:HD22	1:E:322:LEU:N	2.36	0.40
1:E:397:VAL:O	1:E:397:VAL:HG12	2.20	0.40
1:E:440:MSE:O	1:E:444:LEU:CD2	2.69	0.40
1:F:15:PHE:HE2	1:F:19:TRP:NE1	2.18	0.40
1:F:61:ARG:N	1:F:62:PRO:CD	2.84	0.40
1:F:351:PHE:CD2	1:F:356:ILE:CD1	3.04	0.40
1:G:31:ASN:HD22	1:G:31:ASN:HA	1.62	0.40
1:G:127:ARG:HG2	1:G:147:GLU:HB2	2.03	0.40
1:G:160:SER:O	1:G:161:ASN:CG	2.64	0.40
1:G:248:LYS:HZ2	1:G:251:ILE:HD12	1.86	0.40
1:G:273:ARG:NH1	1:G:275:ARG:HE	2.19	0.40
1:G:352:TRP:HB2	1:G:355:GLN:HG2	2.03	0.40
1:H:15:PHE:HE2	1:H:19:TRP:NE1	2.18	0.40
1:H:127:ARG:HG2	1:H:147:GLU:HB2	2.02	0.40
1:H:397:VAL:O	1:H:397:VAL:HG12	2.20	0.40
1:H:440:MSE:O	1:H:444:LEU:CD2	2.69	0.40
1:I:94:LEU:HD23	1:I:94:LEU:C	2.45	0.40
1:I:123:VAL:HG21	1:I:153:CYS:HB3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:166:ASP:C	1:I:168:SER:N	2.77	0.40
1:I:352:TRP:HB2	1:I:355:GLN:HG2	2.03	0.40
1:J:35:PHE:HZ	1:J:321:ARG:NE	2.12	0.40
1:J:166:ASP:C	1:J:168:SER:N	2.77	0.40
1:J:255:ILE:O	1:J:258:LEU:N	2.53	0.40
1:K:80:TYR:HB2	1:K:95:MSE:HG2	2.03	0.40
1:K:273:ARG:HD2	1:K:275:ARG:HD2	2.02	0.40
1:K:383:ASP:CB	1:K:385:PRO:HD3	2.51	0.40
1:K:386:THR:HG21	1:K:389:LEU:HD21	2.02	0.40
1:K:448:VAL:C	1:K:450:GLN:H	2.27	0.40
1:L:35:PHE:HZ	1:L:321:ARG:NE	2.12	0.40
1:L:552:LEU:O	1:L:556:TYR:HD2	2.03	0.40
1:L:598:GLN:HB2	1:L:601:GLN:HB3	2.02	0.40
2:b:28:VAL:HG11	2:b:97:ALA:CA	2.42	0.40
2:b:95:ASN:CG	2:b:116:ALA:HB1	2.46	0.40
2:b:124:TYR:O	2:b:124:TYR:CG	2.73	0.40
2:f:57:TYR:O	2:f:59:ASP:N	2.54	0.40
2:f:150:PRO:O	2:f:151:ASN:C	2.61	0.40
2:g:138:PRO:HD2	2:g:141:MET:HB2	2.03	0.40
2:h:124:TYR:O	2:h:124:TYR:CG	2.73	0.40
2:j:56:TRP:N	2:j:56:TRP:CD1	2.88	0.40
2:j:138:PRO:HD2	2:j:141:MET:HB2	2.03	0.40
1:M:24:GLU:HG3	1:M:313:LYS:HE2	2.03	0.40
1:M:386:THR:CG2	1:M:389:LEU:HD21	2.51	0.40
1:M:457:MSE:O	1:M:458:ARG:CD	2.70	0.40
1:N:216:THR:HB	1:N:218:GLN:OE1	2.21	0.40
1:N:229:LYS:O	1:N:229:LYS:CG	2.69	0.40
1:N:248:LYS:HE2	1:N:513:ARG:HH12	1.85	0.40
1:N:360:GLU:HG3	2:m:122:ARG:HB3	2.03	0.40
1:N:503:GLU:HB3	1:N:508:ASN:HB3	2.03	0.40
1:N:583:LYS:HA	1:N:584:PRO:HD3	1.91	0.40
1:O:198:ILE:HA	1:O:199:PRO:HD3	1.69	0.40
1:O:538:LEU:HB3	1:O:551:LEU:HD13	2.02	0.40
1:P:301:VAL:HG23	1:P:439:ASN:HB3	2.02	0.40
1:P:457:MSE:O	1:P:458:ARG:CD	2.69	0.40
1:Q:210:PRO:HD2	1:Q:211:TRP:CZ3	2.56	0.40
1:Q:282:THR:HG23	1:Q:287:LEU:CD1	2.47	0.40
1:R:147:GLU:HA	1:R:148:PRO:HD3	1.80	0.40
1:R:311:GLU:O	1:R:312:ASP:HB2	2.21	0.40
1:R:599:ALA:C	1:R:600:LYS:HD2	2.46	0.40
1:S:390:ALA:CB	1:U:387:GLN:HB3	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:202:GLN:O	1:T:203:ASN:HB3	2.21	0.40
1:T:228:LYS:O	1:T:229:LYS:HB3	2.22	0.40
1:V:457:MSE:O	1:V:458:ARG:CD	2.69	0.40
1:W:310:VAL:HB	1:W:311:GLU:H	1.68	0.40
1:W:578:GLN:HG2	1:W:596:ALA:CB	2.50	0.40
1:X:54:ARG:HB2	2:r:137:GLY:HA3	2.04	0.40
1:X:177:HIS:O	1:X:218:GLN:HA	2.21	0.40
1:X:231:THR:HG23	1:X:249:ARG:HE	1.86	0.40
1:X:236:GLN:CG	1:X:243:PRO:HB2	2.51	0.40
1:X:359:PHE:C	1:X:361:HIS:N	2.80	0.40
1:X:387:GLN:HA	1:X:388:PRO:HD3	1.93	0.40
2:o:31:GLN:C	2:o:33:MET:N	2.79	0.40
2:o:81:SER:O	2:o:85:HIS:ND1	2.54	0.40
2:p:84:PHE:C	2:p:84:PHE:CD2	2.99	0.40
2:r:14:LEU:HD22	2:r:33:MET:SD	2.61	0.40
2:u:126:ALA:HA	2:u:127:PRO:HD3	1.89	0.40
1:A:61:ARG:N	1:A:62:PRO:CD	2.84	0.40
1:A:383:ASP:CB	1:A:385:PRO:HD3	2.51	0.40
1:A:397:VAL:O	1:A:397:VAL:HG12	2.20	0.40
1:A:448:VAL:C	1:A:450:GLN:H	2.27	0.40
1:A:528:LYS:HD2	1:A:560:LEU:HD11	2.03	0.40
1:A:567:MSE:HE2	1:B:554:LEU:HD22	2.03	0.40
1:B:93:VAL:HG11	1:B:458:ARG:HG2	2.03	0.40
1:B:351:PHE:CD2	1:B:356:ILE:CD1	3.04	0.40
1:C:157:ILE:O	1:C:157:ILE:CG1	2.69	0.40
1:C:351:PHE:CD2	1:C:356:ILE:CD1	3.04	0.40
1:D:61:ARG:N	1:D:62:PRO:CD	2.84	0.40
1:E:236:GLN:CG	1:E:243:PRO:HB2	2.51	0.40
1:E:352:TRP:HB2	1:E:355:GLN:HG2	2.02	0.40
1:F:276:VAL:HG23	1:F:293:ILE:HG22	2.03	0.40
1:F:561:ASP:CG	1:F:562:GLY:N	2.80	0.40
1:G:94:LEU:HD23	1:G:94:LEU:C	2.45	0.40
1:G:561:ASP:CG	1:G:562:GLY:N	2.80	0.40
1:H:123:VAL:HG21	1:H:153:CYS:HB3	2.02	0.40
1:H:160:SER:O	1:H:161:ASN:CG	2.65	0.40
1:H:209:PHE:CE2	1:H:214:GLN:HG2	2.56	0.40
1:H:528:LYS:HD2	1:H:560:LEU:HD11	2.03	0.40
1:I:293:ILE:HD13	1:I:294:ALA:H	1.86	0.40
1:J:352:TRP:HB2	1:J:355:GLN:HG2	2.03	0.40
1:K:372:TYR:CD2	1:L:348:LYS:HB2	2.55	0.40
1:K:376:ARG:HB2	1:L:352:TRP:CD1	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:123:VAL:HG21	1:L:153:CYS:HB3	2.02	0.40
1:L:322:LEU:HD22	1:L:322:LEU:N	2.36	0.40
1:L:352:TRP:HB2	1:L:355:GLN:HG2	2.03	0.40
1:L:383:ASP:CB	1:L:385:PRO:HD3	2.51	0.40
1:L:561:ASP:CG	1:L:562:GLY:N	2.80	0.40
2:Y:95:ASN:CG	2:Y:116:ALA:HB1	2.46	0.40
2:Y:124:TYR:O	2:Y:124:TYR:CG	2.73	0.40
2:c:71:ASP:CB	2:c:75:PRO:HD2	2.36	0.40
2:d:57:TYR:O	2:d:59:ASP:N	2.54	0.40
2:d:138:PRO:HD2	2:d:141:MET:HB2	2.03	0.40
2:e:63:ILE:CG2	2:e:123:LEU:HB3	2.51	0.40
2:g:104:TYR:N	2:g:104:TYR:CD1	2.85	0.40
2:h:138:PRO:HD2	2:h:141:MET:HB2	2.03	0.40
2:i:119:GLY:O	2:i:123:LEU:HD13	2.21	0.40
1:M:219:ILE:HG13	1:M:220:ALA:N	2.35	0.40
1:M:241:GLY:O	1:M:242:GLU:C	2.63	0.40
1:O:57:PHE:CD1	1:O:57:PHE:N	2.88	0.40
1:O:161:ASN:ND2	1:O:161:ASN:C	2.79	0.40
1:O:228:LYS:O	1:O:229:LYS:HB3	2.20	0.40
1:O:236:GLN:H	1:O:265:LYS:CB	2.34	0.40
1:O:440:MSE:O	1:O:443:ASP:HB3	2.22	0.40
1:O:458:ARG:HD3	1:O:458:ARG:HA	1.83	0.40
1:Q:510:ILE:HG12	1:Q:511:ARG:H	1.86	0.40
1:R:123:VAL:HG13	1:R:304:PHE:CE1	2.57	0.40
1:R:236:GLN:CG	1:R:243:PRO:HB2	2.51	0.40
1:R:360:GLU:CD	1:R:360:GLU:H	2.29	0.40
1:R:457:MSE:O	1:R:458:ARG:CD	2.69	0.40
1:R:503:GLU:HB3	1:R:508:ASN:HB3	2.03	0.40
1:S:311:GLU:O	1:S:312:ASP:HB2	2.22	0.40
1:S:343:ARG:NH1	2:t:126:ALA:O	2.52	0.40
1:U:160:SER:O	1:U:161:ASN:ND2	2.46	0.40
1:U:298:ILE:HA	1:U:299:PRO:HD3	1.77	0.40
1:W:54:ARG:HB2	2:u:137:GLY:HA3	2.04	0.40
1:X:578:GLN:HG2	1:X:596:ALA:CB	2.50	0.40
2:o:80:VAL:O	2:o:82:ALA:N	2.53	0.40
2:q:84:PHE:CD2	2:q:84:PHE:C	2.99	0.40
2:u:17:LEU:O	2:u:17:LEU:HD23	2.21	0.40
1:A:273:ARG:NH1	1:A:275:ARG:HE	2.19	0.40
1:B:35:PHE:HZ	1:B:321:ARG:NE	2.12	0.40
1:C:209:PHE:CE2	1:C:214:GLN:HG2	2.56	0.40
1:C:313:LYS:HD3	1:C:314:GLU:N	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:80:TYR:HB2	1:D:95:MSE:HG2	2.03	0.40
1:D:430:VAL:HG12	1:D:431:ALA:N	2.35	0.40
1:E:61:ARG:N	1:E:62:PRO:CD	2.84	0.40
1:E:160:SER:O	1:E:161:ASN:CG	2.64	0.40
1:E:316:TYR:O	1:E:321:ARG:NH1	2.53	0.40
1:E:528:LYS:HD2	1:E:560:LEU:HD11	2.03	0.40
1:E:598:GLN:HB2	1:E:601:GLN:HB3	2.02	0.40
1:G:40:GLN:NE2	1:G:120:GLU:OE1	2.46	0.40
1:G:383:ASP:CB	1:G:385:PRO:HD3	2.51	0.40
1:H:71:MSE:HG2	1:H:429:GLN:HG3	2.03	0.40
1:H:99:ARG:NH1	1:H:530:GLN:HE21	2.13	0.40
1:I:45:LEU:O	1:I:46:SER:HB3	2.22	0.40
1:I:71:MSE:HG2	1:I:429:GLN:HG3	2.04	0.40
1:I:542:THR:HA	1:I:543:PRO:HD3	1.82	0.40
1:I:579:MSE:CB	1:I:581:VAL:HG12	2.49	0.40
1:J:71:MSE:HG2	1:J:429:GLN:HG3	2.03	0.40
1:J:147:GLU:HA	1:J:148:PRO:HD3	1.86	0.40
1:J:598:GLN:HB2	1:J:601:GLN:HB3	2.02	0.40
1:K:93:VAL:HG11	1:K:458:ARG:HG2	2.03	0.40
1:L:293:ILE:HD13	1:L:294:ALA:H	1.87	0.40
1:L:430:VAL:HG12	1:L:431:ALA:N	2.35	0.40
2:a:95:ASN:CG	2:a:116:ALA:HB1	2.46	0.40
2:a:124:TYR:O	2:a:124:TYR:CG	2.73	0.40
2:a:138:PRO:HD2	2:a:141:MET:HB2	2.03	0.40
2:d:28:VAL:HG22	2:d:93:PHE:CA	2.52	0.40
2:e:138:PRO:HD2	2:e:141:MET:HB2	2.03	0.40
2:f:28:VAL:HG22	2:f:93:PHE:CA	2.52	0.40
2:f:138:PRO:HD2	2:f:141:MET:HB2	2.03	0.40
2:j:28:VAL:HG22	2:j:93:PHE:CA	2.52	0.40
1:M:371:TYR:CE2	1:M:373:LEU:HD21	2.56	0.40
1:M:387:GLN:CB	1:O:390:ALA:HB2	2.52	0.40
1:M:599:ALA:C	1:M:600:LYS:HD2	2.46	0.40
1:N:11:ILE:O	1:N:15:PHE:HB2	2.22	0.40
1:O:232:ALA:HB1	1:O:233:PHE:H	1.58	0.40
1:O:236:GLN:CG	1:O:243:PRO:HB2	2.51	0.40
1:O:578:GLN:HG2	1:O:596:ALA:CB	2.51	0.40
1:P:61:ARG:CB	1:P:62:PRO:HD3	2.52	0.40
1:P:306:GLU:O	1:P:316:TYR:HA	2.22	0.40
1:R:115:VAL:HA	1:R:118:GLN:HB3	2.04	0.40
1:R:280:ILE:HG22	1:R:287:LEU:HD13	2.03	0.40
1:R:444:LEU:O	1:R:447:TYR:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:160:SER:O	1:S:161:ASN:ND2	2.46	0.40
1:S:161:ASN:ND2	1:S:161:ASN:C	2.78	0.40
1:S:198:ILE:HA	1:S:199:PRO:HD3	1.71	0.40
1:S:232:ALA:HB1	1:S:233:PHE:H	1.56	0.40
1:S:328:ARG:HB3	2:q:133:PRO:HG3	2.03	0.40
1:T:164:LEU:HD22	1:T:169:ASP:OD1	2.22	0.40
1:T:227:GLU:O	1:T:227:GLU:HG2	2.20	0.40
1:T:252:LYS:O	1:T:252:LYS:HE3	2.22	0.40
1:T:386:THR:CG2	1:T:389:LEU:HD21	2.51	0.40
1:T:440:MSE:O	1:T:443:ASP:HB3	2.21	0.40
1:U:310:VAL:HB	1:U:311:GLU:H	1.66	0.40
1:U:359:PHE:C	1:U:361:HIS:N	2.79	0.40
1:V:14:ARG:NE	1:V:14:ARG:CA	2.69	0.40
1:V:177:HIS:O	1:V:218:GLN:HA	2.22	0.40
1:V:448:VAL:C	1:V:450:GLN:H	2.29	0.40
1:W:156:VAL:O	1:W:156:VAL:CG2	2.68	0.40
2:l:16:LYS:HE2	2:l:73:HIS:CD2	2.56	0.40
2:m:128:TYR:HA	2:m:129:PRO:HD3	1.84	0.40
2:o:14:LEU:HD22	2:o:33:MET:SD	2.62	0.40
2:o:19:VAL:HA	2:o:22:ASP:CB	2.48	0.40
2:o:19:VAL:HG13	2:o:84:PHE:CD2	2.57	0.40
2:o:34:GLN:C	2:o:36:ALA:N	2.80	0.40
2:p:12:ALA:C	2:p:14:LEU:H	2.30	0.40
2:v:113:LEU:HD23	2:v:113:LEU:HA	1.78	0.40
1:A:40:GLN:O	1:A:41:TRP:CB	2.55	0.40
1:A:123:VAL:HG21	1:A:153:CYS:HB3	2.02	0.40
1:A:386:THR:HG21	1:A:389:LEU:HD21	2.02	0.40
1:A:561:ASP:CG	1:A:562:GLY:N	2.80	0.40
1:B:583:LYS:HA	1:B:584:PRO:HD3	1.85	0.40
1:C:71:MSE:HG2	1:C:429:GLN:HG3	2.03	0.40
1:D:160:SER:O	1:D:161:ASN:CG	2.64	0.40
1:D:298:ILE:HA	1:D:299:PRO:HD3	1.82	0.40
1:D:368:ASP:O	2:d:134:ARG:HG3	2.21	0.40
1:E:123:VAL:HG21	1:E:153:CYS:HB3	2.02	0.40
1:E:255:ILE:O	1:E:258:LEU:N	2.53	0.40
1:E:273:ARG:NH1	1:E:275:ARG:HE	2.19	0.40
1:F:71:MSE:HG2	1:F:429:GLN:HG3	2.03	0.40
1:F:322:LEU:N	1:F:322:LEU:HD22	2.36	0.40
1:F:328:ARG:HB3	2:e:142:PRO:HG3	2.04	0.40
1:F:444:LEU:O	1:F:445:GLU:C	2.65	0.40
3:F:719:HOH:O	1:G:438:LEU:HD22	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:45:LEU:O	1:G:46:SER:HB3	2.22	0.40
1:G:273:ARG:C	1:G:273:ARG:HD3	2.46	0.40
1:G:322:LEU:N	1:G:322:LEU:HD22	2.36	0.40
1:G:528:LYS:HD2	1:G:560:LEU:HD11	2.03	0.40
1:H:35:PHE:HE2	1:H:324:LYS:NZ	2.08	0.40
1:H:37:ARG:HD2	1:H:37:ARG:HA	1.79	0.40
1:H:61:ARG:N	1:H:62:PRO:CD	2.84	0.40
1:H:102:MSE:CE	1:H:144:ILE:HD11	2.52	0.40
1:I:248:LYS:H	1:I:248:LYS:CD	2.16	0.40
1:I:430:VAL:HG12	1:I:431:ALA:N	2.35	0.40
1:I:528:LYS:HD2	1:I:560:LEU:HD11	2.03	0.40
1:J:45:LEU:O	1:J:46:SER:HB3	2.22	0.40
1:J:139:SER:CB	1:J:455:THR:CG2	2.80	0.40
1:K:45:LEU:O	1:K:46:SER:HB3	2.22	0.40
1:K:78:VAL:CG1	1:K:444:LEU:HG	2.51	0.40
1:K:160:SER:O	1:K:161:ASN:CG	2.65	0.40
1:K:371:TYR:HA	1:L:348:LYS:HB3	2.03	0.40
1:K:528:LYS:HD2	1:K:560:LEU:HD11	2.03	0.40
1:L:160:SER:O	1:L:161:ASN:CG	2.64	0.40
1:L:380:ASN:O	1:L:381:SER:CB	2.70	0.40
2:Y:28:VAL:HG22	2:Y:93:PHE:CA	2.52	0.40
2:a:28:VAL:HG22	2:a:93:PHE:CA	2.52	0.40
2:g:137:TYR:HA	2:g:138:PRO:HD3	1.88	0.40
2:h:95:ASN:CG	2:h:116:ALA:HB1	2.46	0.40
2:i:95:ASN:CG	2:i:116:ALA:HB1	2.46	0.40
1:M:251:ILE:HD11	1:M:275:ARG:HH21	1.86	0.40
1:N:210:PRO:HD2	1:N:211:TRP:CZ3	2.56	0.40
1:N:232:ALA:N	1:N:269:ARG:O	2.54	0.40
1:N:438:LEU:HD12	1:N:441:ARG:NH1	2.37	0.40
1:O:219:ILE:HG13	1:O:220:ALA:N	2.37	0.40
1:P:107:ALA:HA	1:P:146:ARG:HB3	2.03	0.40
1:P:216:THR:HB	1:P:218:GLN:OE1	2.22	0.40
1:Q:577:ILE:HG12	1:Q:582:LYS:CG	2.45	0.40
1:R:161:ASN:ND2	1:R:161:ASN:C	2.80	0.40
1:R:396:GLU:O	1:X:399:GLN:OE1	2.39	0.40
1:R:591:GLN:HA	1:R:594:VAL:CG2	2.51	0.40
1:S:301:VAL:HG23	1:S:439:ASN:HB3	2.02	0.40
1:S:514:TYR:HE2	1:U:135:GLN:NE2	2.19	0.40
3:T:719:HOH:O	1:W:430:VAL:HG11	2.17	0.40
1:U:236:GLN:CG	1:U:243:PRO:HB2	2.52	0.40
1:V:349:PRO:HG3	1:V:391:TYR:CE1	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:54:ARG:HG3	2:u:138:ASN:ND2	2.36	0.40
1:W:161:ASN:ND2	1:W:161:ASN:C	2.79	0.40
1:W:334:MSE:SE	1:W:405:LEU:HD11	2.71	0.40
1:X:210:PRO:HD2	1:X:211:TRP:CZ3	2.56	0.40
1:X:260:ASP:CA	1:X:264:ILE:HB	2.52	0.40
2:k:14:LEU:HD22	2:k:33:MET:SD	2.61	0.40
2:n:69:GLU:HB3	2:n:70:GLY:H	1.68	0.40
2:o:48:TYR:H	2:o:54:ILE:H	1.70	0.40
2:p:42:ALA:HB1	2:r:81:SER:HB3	2.03	0.40
2:r:69:GLU:HB3	2:r:70:GLY:H	1.68	0.40
1:A:352:TRP:HB2	1:A:355:GLN:HG2	2.03	0.40
1:B:61:ARG:N	1:B:62:PRO:CD	2.84	0.40
1:B:273:ARG:HD3	1:B:273:ARG:C	2.46	0.40
1:B:444:LEU:O	1:B:445:GLU:C	2.65	0.40
1:D:273:ARG:HD3	1:D:273:ARG:C	2.46	0.40
1:E:37:ARG:HD2	1:E:37:ARG:HA	1.79	0.40
1:E:127:ARG:HG2	1:E:147:GLU:HB2	2.02	0.40
1:F:127:ARG:HG2	1:F:147:GLU:HB2	2.02	0.40
1:F:160:SER:O	1:F:161:ASN:CG	2.64	0.40
1:G:35:PHE:HZ	1:G:321:ARG:NE	2.12	0.40
1:G:71:MSE:HG2	1:G:429:GLN:HG3	2.03	0.40
1:G:99:ARG:NH1	1:G:530:GLN:HE21	2.13	0.40
1:G:139:SER:CB	1:G:455:THR:CG2	2.80	0.40
1:G:440:MSE:O	1:G:444:LEU:CD2	2.69	0.40
1:H:298:ILE:HA	1:H:299:PRO:HD3	1.82	0.40
1:H:380:ASN:O	1:H:381:SER:CB	2.70	0.40
1:I:78:VAL:CG1	1:I:444:LEU:HG	2.51	0.40
1:I:160:SER:O	1:I:161:ASN:CG	2.64	0.40
1:J:99:ARG:HH12	1:J:530:GLN:NE2	2.14	0.40
1:J:123:VAL:HG21	1:J:153:CYS:HB3	2.02	0.40
1:J:246:TYR:HD2	1:J:511:ARG:CB	2.28	0.40
1:J:380:ASN:O	1:J:381:SER:CB	2.70	0.40
1:K:123:VAL:HG21	1:K:153:CYS:HB3	2.02	0.40
1:K:276:VAL:HG23	1:K:293:ILE:HG22	2.03	0.40
1:L:45:LEU:O	1:L:46:SER:HB3	2.22	0.40
1:L:102:MSE:CE	1:L:144:ILE:HD11	2.52	0.40
1:L:147:GLU:HA	1:L:148:PRO:HD3	1.86	0.40
2:Y:57:TYR:O	2:Y:59:ASP:N	2.54	0.40
2:c:63:ILE:CG2	2:c:123:LEU:HB3	2.51	0.40
2:f:56:TRP:N	2:f:56:TRP:CD1	2.88	0.40
2:g:63:ILE:CG2	2:g:123:LEU:HB3	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:h:28:VAL:HG22	2:h:93:PHE:CA	2.52	0.40
2:h:28:VAL:HG11	2:h:97:ALA:HA	1.88	0.40
2:h:56:TRP:CD1	2:h:56:TRP:N	2.88	0.40
2:j:57:TYR:O	2:j:59:ASP:N	2.54	0.40
2:j:95:ASN:CG	2:j:116:ALA:HB1	2.46	0.40

All (13) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:230:GLU:OE2	2:c:74:ASN:ND2[2_546]	1.06	1.14
1:N:230:GLU:N	2:r:64:GLU:OE2[2_455]	1.79	0.41
1:N:260:ASP:OD2	1:B:601:GLN:NE2[2_555]	1.79	0.41
1:C:250:ASP:OD2	2:c:74:ASN:OD1[2_546]	1.83	0.37
1:N:228:LYS:CG	2:r:64:GLU:OE1[2_455]	1.89	0.31
1:N:229:LYS:C	2:r:64:GLU:OE2[2_455]	1.92	0.28
1:S:249:ARG:NH1	2:v:65:ASN:CB[2_445]	1.94	0.26
1:S:249:ARG:NH2	2:v:65:ASN:ND2[2_445]	1.99	0.21
1:C:277:TYR:OH	2:c:73:GLU:CG[2_546]	2.05	0.15
1:N:262:GLY:O	1:B:594:VAL:CG1[2_555]	2.08	0.12
1:C:230:GLU:CD	2:c:74:ASN:ND2[2_546]	2.08	0.12
1:S:249:ARG:NH1	2:v:65:ASN:ND2[2_445]	2.09	0.11
1:W:249:ARG:NH1	2:g:72:ASP:CG[1_454]	2.10	0.10

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	5
1	B	565/602 (94%)	434 (77%)	87 (15%)	44 (8%)	1	4
1	C	565/602 (94%)	434 (77%)	87 (15%)	44 (8%)	1	4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	5
1	E	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	5
1	F	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	5
1	G	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	5
1	H	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	5
1	I	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	5
1	J	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	5
1	K	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	5
1	L	565/602 (94%)	434 (77%)	87 (15%)	44 (8%)	1	4
1	M	565/602 (94%)	446 (79%)	81 (14%)	38 (7%)	1	6
1	N	565/602 (94%)	447 (79%)	79 (14%)	39 (7%)	1	6
1	O	565/602 (94%)	447 (79%)	80 (14%)	38 (7%)	1	6
1	P	565/602 (94%)	448 (79%)	79 (14%)	38 (7%)	1	6
1	Q	565/602 (94%)	447 (79%)	79 (14%)	39 (7%)	1	6
1	R	565/602 (94%)	448 (79%)	79 (14%)	38 (7%)	1	6
1	S	565/602 (94%)	443 (78%)	83 (15%)	39 (7%)	1	6
1	T	565/602 (94%)	446 (79%)	81 (14%)	38 (7%)	1	6
1	U	565/602 (94%)	447 (79%)	79 (14%)	39 (7%)	1	6
1	V	565/602 (94%)	445 (79%)	82 (14%)	38 (7%)	1	6
1	W	565/602 (94%)	448 (79%)	78 (14%)	39 (7%)	1	6
1	X	565/602 (94%)	448 (79%)	78 (14%)	39 (7%)	1	6
2	Y	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	0	3
2	Z	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	0	3
2	a	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	0	3
2	b	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	0	3
2	c	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	0	3
2	d	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	0	3
2	e	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	0	3
2	f	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	0	3
2	g	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	0	3
2	h	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	0	3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	i	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	0	3
2	j	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	0	3
2	k	143/166 (86%)	115 (80%)	17 (12%)	11 (8%)	1	5
2	l	143/166 (86%)	114 (80%)	18 (13%)	11 (8%)	1	5
2	m	143/166 (86%)	115 (80%)	18 (13%)	10 (7%)	1	6
2	n	143/166 (86%)	114 (80%)	18 (13%)	11 (8%)	1	5
2	o	143/166 (86%)	115 (80%)	17 (12%)	11 (8%)	1	5
2	p	143/166 (86%)	115 (80%)	17 (12%)	11 (8%)	1	5
2	q	143/166 (86%)	113 (79%)	19 (13%)	11 (8%)	1	5
2	r	143/166 (86%)	114 (80%)	18 (13%)	11 (8%)	1	5
2	s	143/166 (86%)	114 (80%)	18 (13%)	11 (8%)	1	5
2	t	143/166 (86%)	113 (79%)	19 (13%)	11 (8%)	1	5
2	u	143/166 (86%)	114 (80%)	18 (13%)	11 (8%)	1	5
2	v	143/166 (86%)	114 (80%)	19 (13%)	10 (7%)	1	6
All	All	17004/18432 (92%)	13318 (78%)	2419 (14%)	1267 (8%)	1	5

All (1267) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	M	82	PRO
1	M	263	PHE
1	M	294	ALA
1	M	462	GLU
1	M	514	TYR
1	M	561	ASP
1	M	586	THR
1	M	588	GLU
1	N	82	PRO
1	N	263	PHE
1	N	294	ALA
1	N	462	GLU
1	N	514	TYR
1	N	561	ASP
1	N	586	THR
1	N	588	GLU
1	O	82	PRO
1	O	263	PHE

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Mol	Chain	Res	Type
1	O	294	ALA
1	O	462	GLU
1	O	514	TYR
1	O	561	ASP
1	O	586	THR
1	O	588	GLU
1	P	82	PRO
1	P	263	PHE
1	P	294	ALA
1	P	462	GLU
1	P	514	TYR
1	P	561	ASP
1	P	586	THR
1	P	588	GLU
1	Q	82	PRO
1	Q	263	PHE
1	Q	294	ALA
1	Q	462	GLU
1	Q	514	TYR
1	Q	561	ASP
1	Q	586	THR
1	Q	588	GLU
1	R	82	PRO
1	R	263	PHE
1	R	294	ALA
1	R	462	GLU
1	R	514	TYR
1	R	561	ASP
1	R	586	THR
1	R	588	GLU
1	S	82	PRO
1	S	263	PHE
1	S	294	ALA
1	S	462	GLU
1	S	514	TYR
1	S	561	ASP
1	S	586	THR
1	S	588	GLU
1	T	82	PRO
1	T	263	PHE
1	T	294	ALA
1	T	462	GLU

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Mol	Chain	Res	Type
1	T	514	TYR
1	T	561	ASP
1	T	586	THR
1	T	588	GLU
1	U	82	PRO
1	U	263	PHE
1	U	294	ALA
1	U	462	GLU
1	U	514	TYR
1	U	561	ASP
1	U	586	THR
1	U	588	GLU
1	V	82	PRO
1	V	263	PHE
1	V	294	ALA
1	V	462	GLU
1	V	514	TYR
1	V	561	ASP
1	V	586	THR
1	V	588	GLU
1	W	82	PRO
1	W	263	PHE
1	W	294	ALA
1	W	462	GLU
1	W	514	TYR
1	W	561	ASP
1	W	586	THR
1	W	588	GLU
1	X	82	PRO
1	X	263	PHE
1	X	294	ALA
1	X	462	GLU
1	X	514	TYR
1	X	561	ASP
1	X	586	THR
1	X	588	GLU
2	k	25	LEU
2	k	30	PRO
2	k	123	ALA
2	l	25	LEU
2	l	30	PRO
2	l	123	ALA

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Mol	Chain	Res	Type
2	m	25	LEU
2	m	30	PRO
2	m	123	ALA
2	n	25	LEU
2	n	30	PRO
2	n	123	ALA
2	o	25	LEU
2	o	30	PRO
2	o	123	ALA
2	p	25	LEU
2	p	30	PRO
2	p	123	ALA
2	q	25	LEU
2	q	30	PRO
2	q	123	ALA
2	r	25	LEU
2	r	30	PRO
2	r	123	ALA
2	s	25	LEU
2	s	30	PRO
2	s	123	ALA
2	t	25	LEU
2	t	30	PRO
2	t	123	ALA
2	u	25	LEU
2	u	30	PRO
2	u	123	ALA
2	v	25	LEU
2	v	30	PRO
2	v	123	ALA
1	A	41	TRP
1	A	50	THR
1	A	59	VAL
1	A	82	PRO
1	A	159	ASP
1	A	208	VAL
1	A	256	ASP
1	A	263	PHE
1	A	294	ALA
1	A	387	GLN
1	A	462	GLU
1	A	504	LYS

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Mol	Chain	Res	Type
1	A	514	TYR
1	A	561	ASP
1	A	586	THR
1	B	41	TRP
1	B	50	THR
1	B	59	VAL
1	B	82	PRO
1	B	159	ASP
1	B	208	VAL
1	B	256	ASP
1	B	263	PHE
1	B	294	ALA
1	B	387	GLN
1	B	462	GLU
1	B	504	LYS
1	B	514	TYR
1	B	561	ASP
1	B	586	THR
1	C	41	TRP
1	C	50	THR
1	C	59	VAL
1	C	82	PRO
1	C	159	ASP
1	C	208	VAL
1	C	256	ASP
1	C	263	PHE
1	C	294	ALA
1	C	387	GLN
1	C	462	GLU
1	C	504	LYS
1	C	514	TYR
1	C	561	ASP
1	C	586	THR
1	D	41	TRP
1	D	50	THR
1	D	59	VAL
1	D	82	PRO
1	D	159	ASP
1	D	208	VAL
1	D	256	ASP
1	D	263	PHE
1	D	294	ALA

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Mol	Chain	Res	Type
1	D	387	GLN
1	D	462	GLU
1	D	504	LYS
1	D	514	TYR
1	D	561	ASP
1	D	586	THR
1	E	41	TRP
1	E	50	THR
1	E	59	VAL
1	E	82	PRO
1	E	159	ASP
1	E	208	VAL
1	E	256	ASP
1	E	263	PHE
1	E	294	ALA
1	E	387	GLN
1	E	462	GLU
1	E	504	LYS
1	E	514	TYR
1	E	561	ASP
1	E	586	THR
1	F	41	TRP
1	F	50	THR
1	F	59	VAL
1	F	82	PRO
1	F	159	ASP
1	F	208	VAL
1	F	256	ASP
1	F	263	PHE
1	F	294	ALA
1	F	387	GLN
1	F	462	GLU
1	F	504	LYS
1	F	514	TYR
1	F	561	ASP
1	F	586	THR
1	G	41	TRP
1	G	50	THR
1	G	59	VAL
1	G	82	PRO
1	G	159	ASP
1	G	208	VAL

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Mol	Chain	Res	Type
1	G	256	ASP
1	G	263	PHE
1	G	294	ALA
1	G	387	GLN
1	G	462	GLU
1	G	504	LYS
1	G	514	TYR
1	G	561	ASP
1	G	586	THR
1	H	41	TRP
1	H	50	THR
1	H	59	VAL
1	H	82	PRO
1	H	159	ASP
1	H	208	VAL
1	H	256	ASP
1	H	263	PHE
1	H	294	ALA
1	H	387	GLN
1	H	462	GLU
1	H	504	LYS
1	H	514	TYR
1	H	561	ASP
1	H	586	THR
1	I	41	TRP
1	I	50	THR
1	I	59	VAL
1	I	82	PRO
1	I	159	ASP
1	I	208	VAL
1	I	256	ASP
1	I	263	PHE
1	I	294	ALA
1	I	387	GLN
1	I	462	GLU
1	I	504	LYS
1	I	514	TYR
1	I	561	ASP
1	I	586	THR
1	J	41	TRP
1	J	50	THR
1	J	59	VAL

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Mol	Chain	Res	Type
1	J	82	PRO
1	J	159	ASP
1	J	208	VAL
1	J	256	ASP
1	J	263	PHE
1	J	294	ALA
1	J	387	GLN
1	J	462	GLU
1	J	504	LYS
1	J	514	TYR
1	J	561	ASP
1	J	586	THR
1	K	41	TRP
1	K	50	THR
1	K	59	VAL
1	K	82	PRO
1	K	208	VAL
1	K	256	ASP
1	K	263	PHE
1	K	294	ALA
1	K	387	GLN
1	K	462	GLU
1	K	504	LYS
1	K	514	TYR
1	K	561	ASP
1	K	586	THR
1	L	41	TRP
1	L	50	THR
1	L	59	VAL
1	L	82	PRO
1	L	159	ASP
1	L	208	VAL
1	L	256	ASP
1	L	263	PHE
1	L	294	ALA
1	L	387	GLN
1	L	462	GLU
1	L	504	LYS
1	L	514	TYR
1	L	561	ASP
1	L	586	THR
2	Y	33	THR

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Mol	Chain	Res	Type
2	Y	39	PRO
2	Y	75	PRO
2	Y	76	PRO
2	Y	133	LYS
2	Z	33	THR
2	Z	39	PRO
2	Z	75	PRO
2	Z	76	PRO
2	Z	133	LYS
2	a	33	THR
2	a	39	PRO
2	a	75	PRO
2	a	76	PRO
2	a	133	LYS
2	b	33	THR
2	b	39	PRO
2	b	75	PRO
2	b	76	PRO
2	b	133	LYS
2	c	33	THR
2	c	39	PRO
2	c	75	PRO
2	c	76	PRO
2	c	133	LYS
2	d	33	THR
2	d	39	PRO
2	d	75	PRO
2	d	76	PRO
2	d	133	LYS
2	e	33	THR
2	e	39	PRO
2	e	75	PRO
2	e	76	PRO
2	e	133	LYS
2	f	33	THR
2	f	39	PRO
2	f	75	PRO
2	f	76	PRO
2	f	133	LYS
2	g	33	THR
2	g	39	PRO
2	g	75	PRO

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Mol	Chain	Res	Type
2	g	76	PRO
2	g	133	LYS
2	h	33	THR
2	h	39	PRO
2	h	75	PRO
2	h	76	PRO
2	h	133	LYS
2	i	33	THR
2	i	39	PRO
2	i	75	PRO
2	i	76	PRO
2	i	133	LYS
2	j	33	THR
2	j	39	PRO
2	j	75	PRO
2	j	76	PRO
2	j	133	LYS
1	M	25	ALA
1	M	159	ASP
1	M	205	ASN
1	M	267	ALA
1	M	500	ALA
1	N	25	ALA
1	N	159	ASP
1	N	205	ASN
1	N	267	ALA
1	N	295	GLY
1	N	500	ALA
1	N	513	ARG
1	O	25	ALA
1	O	76	ILE
1	O	159	ASP
1	O	205	ASN
1	O	267	ALA
1	O	295	GLY
1	O	500	ALA
1	O	513	ARG
1	P	25	ALA
1	P	49	THR
1	P	159	ASP
1	P	205	ASN
1	P	267	ALA

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Mol	Chain	Res	Type
1	P	500	ALA
1	P	513	ARG
1	Q	25	ALA
1	Q	159	ASP
1	Q	205	ASN
1	Q	267	ALA
1	Q	500	ALA
1	R	25	ALA
1	R	159	ASP
1	R	205	ASN
1	R	267	ALA
1	R	295	GLY
1	R	500	ALA
1	S	25	ALA
1	S	49	THR
1	S	159	ASP
1	S	205	ASN
1	S	267	ALA
1	S	295	GLY
1	S	500	ALA
1	S	513	ARG
1	T	25	ALA
1	T	159	ASP
1	T	205	ASN
1	T	267	ALA
1	T	500	ALA
1	T	513	ARG
1	U	25	ALA
1	U	159	ASP
1	U	205	ASN
1	U	267	ALA
1	U	295	GLY
1	U	500	ALA
1	U	513	ARG
1	V	25	ALA
1	V	159	ASP
1	V	205	ASN
1	V	267	ALA
1	V	295	GLY
1	V	500	ALA
1	W	25	ALA
1	W	159	ASP

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Mol	Chain	Res	Type
1	W	205	ASN
1	W	267	ALA
1	W	295	GLY
1	W	500	ALA
1	X	25	ALA
1	X	76	ILE
1	X	159	ASP
1	X	205	ASN
1	X	267	ALA
1	X	295	GLY
1	X	500	ALA
2	k	66	PRO
2	k	69	GLU
2	k	124	LYS
2	k	149	PHE
2	l	66	PRO
2	l	69	GLU
2	l	124	LYS
2	l	131	ARG
2	l	149	PHE
2	m	66	PRO
2	m	124	LYS
2	m	149	PHE
2	n	66	PRO
2	n	124	LYS
2	n	131	ARG
2	n	149	PHE
2	o	66	PRO
2	o	124	LYS
2	o	149	PHE
2	p	66	PRO
2	p	124	LYS
2	p	149	PHE
2	q	66	PRO
2	q	69	GLU
2	q	124	LYS
2	q	149	PHE
2	r	66	PRO
2	r	69	GLU
2	r	124	LYS
2	r	131	ARG
2	r	149	PHE

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Mol	Chain	Res	Type
2	s	66	PRO
2	s	124	LYS
2	s	149	PHE
2	t	66	PRO
2	t	124	LYS
2	t	149	PHE
2	u	66	PRO
2	u	69	GLU
2	u	124	LYS
2	u	149	PHE
2	v	66	PRO
2	v	69	GLU
2	v	124	LYS
2	v	149	PHE
1	A	267	ALA
1	A	381	SER
1	A	388	PRO
1	A	588	GLU
1	B	267	ALA
1	B	381	SER
1	B	388	PRO
1	B	588	GLU
1	C	267	ALA
1	C	381	SER
1	C	388	PRO
1	C	588	GLU
1	D	267	ALA
1	D	381	SER
1	D	388	PRO
1	D	588	GLU
1	E	267	ALA
1	E	381	SER
1	E	388	PRO
1	E	588	GLU
1	F	267	ALA
1	F	381	SER
1	F	388	PRO
1	F	588	GLU
1	G	267	ALA
1	G	381	SER
1	G	388	PRO
1	G	588	GLU

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Mol	Chain	Res	Type
1	H	267	ALA
1	H	381	SER
1	H	388	PRO
1	H	588	GLU
1	I	267	ALA
1	I	381	SER
1	I	388	PRO
1	I	588	GLU
1	J	267	ALA
1	J	381	SER
1	J	388	PRO
1	J	588	GLU
1	K	159	ASP
1	K	267	ALA
1	K	381	SER
1	K	388	PRO
1	K	588	GLU
1	L	267	ALA
1	L	381	SER
1	L	388	PRO
1	L	588	GLU
2	Y	80	ASP
2	Y	132	ALA
2	Y	140	ARG
2	Y	158	PHE
2	Z	80	ASP
2	Z	132	ALA
2	Z	140	ARG
2	Z	158	PHE
2	a	80	ASP
2	a	132	ALA
2	a	140	ARG
2	a	158	PHE
2	b	80	ASP
2	b	132	ALA
2	b	140	ARG
2	b	158	PHE
2	c	80	ASP
2	c	132	ALA
2	c	140	ARG
2	c	158	PHE
2	d	80	ASP

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Mol	Chain	Res	Type
2	d	132	ALA
2	d	140	ARG
2	d	158	PHE
2	e	80	ASP
2	e	132	ALA
2	e	140	ARG
2	e	158	PHE
2	f	80	ASP
2	f	132	ALA
2	f	140	ARG
2	f	158	PHE
2	g	80	ASP
2	g	132	ALA
2	g	140	ARG
2	g	158	PHE
2	h	80	ASP
2	h	132	ALA
2	h	140	ARG
2	h	158	PHE
2	i	80	ASP
2	i	132	ALA
2	i	140	ARG
2	i	158	PHE
2	j	80	ASP
2	j	132	ALA
2	j	140	ARG
2	j	158	PHE
1	M	8	LEU
1	M	49	THR
1	M	76	ILE
1	M	210	PRO
1	M	216	THR
1	M	295	GLY
1	M	302	PRO
1	M	381	SER
1	M	388	PRO
1	M	452	ASN
1	M	513	ARG
1	N	8	LEU
1	N	49	THR
1	N	76	ILE
1	N	210	PRO

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Mol	Chain	Res	Type
1	N	216	THR
1	N	302	PRO
1	N	388	PRO
1	N	457	MSE
1	O	8	LEU
1	O	49	THR
1	O	210	PRO
1	O	216	THR
1	O	302	PRO
1	O	381	SER
1	O	388	PRO
1	O	452	ASN
1	O	457	MSE
1	P	8	LEU
1	P	76	ILE
1	P	210	PRO
1	P	216	THR
1	P	295	GLY
1	P	302	PRO
1	P	381	SER
1	P	388	PRO
1	P	452	ASN
1	P	457	MSE
1	Q	8	LEU
1	Q	49	THR
1	Q	76	ILE
1	Q	210	PRO
1	Q	216	THR
1	Q	295	GLY
1	Q	302	PRO
1	Q	381	SER
1	Q	388	PRO
1	Q	457	MSE
1	Q	513	ARG
1	R	8	LEU
1	R	49	THR
1	R	76	ILE
1	R	210	PRO
1	R	216	THR
1	R	302	PRO
1	R	388	PRO
1	R	457	MSE

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Mol	Chain	Res	Type
1	R	513	ARG
1	S	8	LEU
1	S	76	ILE
1	S	210	PRO
1	S	216	THR
1	S	302	PRO
1	S	381	SER
1	S	388	PRO
1	S	452	ASN
1	S	457	MSE
1	T	8	LEU
1	T	49	THR
1	T	76	ILE
1	T	210	PRO
1	T	216	THR
1	T	295	GLY
1	T	302	PRO
1	T	381	SER
1	T	388	PRO
1	T	452	ASN
1	U	8	LEU
1	U	49	THR
1	U	76	ILE
1	U	210	PRO
1	U	216	THR
1	U	302	PRO
1	U	388	PRO
1	U	452	ASN
1	V	8	LEU
1	V	36	SER
1	V	49	THR
1	V	76	ILE
1	V	210	PRO
1	V	216	THR
1	V	302	PRO
1	V	388	PRO
1	V	513	ARG
1	W	8	LEU
1	W	49	THR
1	W	76	ILE
1	W	210	PRO
1	W	216	THR

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Mol	Chain	Res	Type
1	W	302	PRO
1	W	388	PRO
1	W	452	ASN
1	W	457	MSE
1	W	513	ARG
1	X	8	LEU
1	X	49	THR
1	X	210	PRO
1	X	216	THR
1	X	302	PRO
1	X	381	SER
1	X	388	PRO
1	X	457	MSE
1	X	513	ARG
2	k	131	ARG
2	m	69	GLU
2	m	131	ARG
2	n	69	GLU
2	o	69	GLU
2	o	131	ARG
2	p	69	GLU
2	p	131	ARG
2	q	131	ARG
2	s	69	GLU
2	s	131	ARG
2	t	69	GLU
2	t	131	ARG
2	u	131	ARG
2	v	131	ARG
1	A	26	ARG
1	A	36	SER
1	A	205	ASN
1	A	262	GLY
1	B	26	ARG
1	B	36	SER
1	B	205	ASN
1	B	262	GLY
1	C	26	ARG
1	C	36	SER
1	C	205	ASN
1	C	262	GLY
1	D	26	ARG

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Mol	Chain	Res	Type
1	D	36	SER
1	D	205	ASN
1	D	262	GLY
1	E	26	ARG
1	E	36	SER
1	E	205	ASN
1	E	262	GLY
1	F	26	ARG
1	F	36	SER
1	F	205	ASN
1	F	262	GLY
1	G	26	ARG
1	G	36	SER
1	G	205	ASN
1	G	262	GLY
1	H	26	ARG
1	H	36	SER
1	H	205	ASN
1	H	262	GLY
1	I	26	ARG
1	I	36	SER
1	I	205	ASN
1	I	262	GLY
1	J	26	ARG
1	J	36	SER
1	J	205	ASN
1	J	262	GLY
1	K	26	ARG
1	K	36	SER
1	K	205	ASN
1	K	262	GLY
1	L	26	ARG
1	L	36	SER
1	L	205	ASN
1	L	262	GLY
2	Y	54	ALA
2	Y	78	GLU
2	Z	54	ALA
2	Z	78	GLU
2	a	54	ALA
2	a	78	GLU
2	b	54	ALA

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Mol	Chain	Res	Type
2	b	78	GLU
2	c	54	ALA
2	c	78	GLU
2	d	54	ALA
2	d	78	GLU
2	e	54	ALA
2	e	78	GLU
2	f	54	ALA
2	f	78	GLU
2	g	54	ALA
2	g	78	GLU
2	h	54	ALA
2	h	78	GLU
2	i	54	ALA
2	i	78	GLU
2	j	54	ALA
2	j	78	GLU
1	M	192	ASP
1	M	198	ILE
1	M	244	VAL
1	M	457	MSE
1	M	583	LYS
1	N	36	SER
1	N	192	ASP
1	N	198	ILE
1	N	244	VAL
1	N	381	SER
1	N	452	ASN
1	N	583	LYS
1	O	36	SER
1	O	192	ASP
1	O	198	ILE
1	O	244	VAL
1	O	508	ASN
1	O	583	LYS
1	P	192	ASP
1	P	198	ILE
1	P	244	VAL
1	P	583	LYS
1	Q	36	SER
1	Q	192	ASP
1	Q	198	ILE

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Mol	Chain	Res	Type
1	Q	244	VAL
1	Q	452	ASN
1	Q	583	LYS
1	R	36	SER
1	R	198	ILE
1	R	244	VAL
1	R	381	SER
1	R	452	ASN
1	R	583	LYS
1	S	36	SER
1	S	192	ASP
1	S	198	ILE
1	S	244	VAL
1	S	450	GLN
1	S	583	LYS
1	T	192	ASP
1	T	198	ILE
1	T	244	VAL
1	T	457	MSE
1	T	583	LYS
1	U	36	SER
1	U	192	ASP
1	U	198	ILE
1	U	244	VAL
1	U	381	SER
1	U	457	MSE
1	U	583	LYS
1	V	192	ASP
1	V	198	ILE
1	V	244	VAL
1	V	381	SER
1	V	452	ASN
1	V	457	MSE
1	V	583	LYS
1	W	36	SER
1	W	192	ASP
1	W	198	ILE
1	W	244	VAL
1	W	381	SER
1	W	583	LYS
1	X	36	SER
1	X	192	ASP

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Mol	Chain	Res	Type
1	X	198	ILE
1	X	244	VAL
1	X	452	ASN
1	X	583	LYS
2	k	132	MET
2	l	132	MET
2	m	132	MET
2	n	132	MET
2	o	132	MET
2	p	132	MET
2	q	132	MET
2	r	132	MET
2	s	132	MET
2	t	132	MET
2	u	132	MET
2	v	132	MET
1	A	161	ASN
1	A	198	ILE
1	A	209	PHE
1	A	216	THR
1	A	244	VAL
1	A	253	ASP
1	A	380	ASN
1	A	583	LYS
1	B	161	ASN
1	B	198	ILE
1	B	209	PHE
1	B	216	THR
1	B	244	VAL
1	B	253	ASP
1	B	380	ASN
1	B	583	LYS
1	C	161	ASN
1	C	198	ILE
1	C	209	PHE
1	C	216	THR
1	C	244	VAL
1	C	253	ASP
1	C	380	ASN
1	C	583	LYS
1	D	161	ASN
1	D	198	ILE

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Mol	Chain	Res	Type
1	D	209	PHE
1	D	216	THR
1	D	244	VAL
1	D	253	ASP
1	D	380	ASN
1	D	583	LYS
1	E	161	ASN
1	E	198	ILE
1	E	209	PHE
1	E	216	THR
1	E	244	VAL
1	E	253	ASP
1	E	380	ASN
1	E	583	LYS
1	F	161	ASN
1	F	198	ILE
1	F	209	PHE
1	F	216	THR
1	F	244	VAL
1	F	253	ASP
1	F	380	ASN
1	F	583	LYS
1	G	161	ASN
1	G	198	ILE
1	G	209	PHE
1	G	216	THR
1	G	244	VAL
1	G	253	ASP
1	G	380	ASN
1	G	583	LYS
1	H	161	ASN
1	H	198	ILE
1	H	209	PHE
1	H	216	THR
1	H	244	VAL
1	H	253	ASP
1	H	380	ASN
1	H	583	LYS
1	I	161	ASN
1	I	198	ILE
1	I	209	PHE
1	I	216	THR

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Mol	Chain	Res	Type
1	I	244	VAL
1	I	253	ASP
1	I	380	ASN
1	I	583	LYS
1	J	161	ASN
1	J	198	ILE
1	J	209	PHE
1	J	216	THR
1	J	244	VAL
1	J	253	ASP
1	J	380	ASN
1	J	583	LYS
1	K	161	ASN
1	K	198	ILE
1	K	209	PHE
1	K	216	THR
1	K	244	VAL
1	K	253	ASP
1	K	380	ASN
1	K	583	LYS
1	L	161	ASN
1	L	198	ILE
1	L	209	PHE
1	L	216	THR
1	L	244	VAL
1	L	253	ASP
1	L	380	ASN
1	L	583	LYS
2	Y	141	MET
2	Y	149	PHE
2	Z	141	MET
2	Z	149	PHE
2	a	141	MET
2	a	149	PHE
2	b	141	MET
2	b	149	PHE
2	c	141	MET
2	c	149	PHE
2	d	141	MET
2	d	149	PHE
2	e	141	MET
2	e	149	PHE

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Mol	Chain	Res	Type
2	f	141	MET
2	f	149	PHE
2	g	141	MET
2	g	149	PHE
2	h	141	MET
2	h	149	PHE
2	i	141	MET
2	i	149	PHE
2	j	141	MET
2	j	149	PHE
1	M	36	SER
1	M	344	THR
1	M	450	GLN
1	M	508	ASN
1	N	262	GLY
1	N	344	THR
1	N	508	ASN
1	O	217	ILE
1	O	344	THR
1	P	445	GLU
1	P	450	GLN
1	P	508	ASN
1	Q	262	GLY
1	Q	450	GLN
1	Q	508	ASN
1	R	192	ASP
1	R	217	ILE
1	R	450	GLN
1	R	508	ASN
1	S	445	GLU
1	S	508	ASN
1	T	36	SER
1	T	217	ILE
1	T	262	GLY
1	T	450	GLN
1	T	508	ASN
1	U	262	GLY
1	U	344	THR
1	U	445	GLU
1	U	450	GLN
1	U	508	ASN
1	V	344	THR

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Mol	Chain	Res	Type
1	V	450	GLN
1	V	508	ASN
1	W	217	ILE
1	W	344	THR
1	W	450	GLN
1	W	508	ASN
1	X	344	THR
1	X	445	GLU
1	X	508	ASN
2	k	44	MET
2	l	44	MET
2	n	44	MET
2	p	44	MET
2	q	44	MET
2	r	44	MET
1	A	76	ILE
1	A	192	ASP
1	A	206	ASP
1	A	232	ALA
1	A	295	GLY
1	A	302	PRO
1	B	76	ILE
1	B	192	ASP
1	B	206	ASP
1	B	232	ALA
1	B	295	GLY
1	B	302	PRO
1	C	76	ILE
1	C	192	ASP
1	C	206	ASP
1	C	232	ALA
1	C	295	GLY
1	C	302	PRO
1	D	76	ILE
1	D	192	ASP
1	D	232	ALA
1	D	295	GLY
1	D	302	PRO
1	E	76	ILE
1	E	192	ASP
1	E	206	ASP
1	E	232	ALA

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Mol	Chain	Res	Type
1	E	295	GLY
1	E	302	PRO
1	F	76	ILE
1	F	192	ASP
1	F	206	ASP
1	F	232	ALA
1	F	295	GLY
1	F	302	PRO
1	G	76	ILE
1	G	192	ASP
1	G	206	ASP
1	G	232	ALA
1	G	295	GLY
1	G	302	PRO
1	H	76	ILE
1	H	192	ASP
1	H	206	ASP
1	H	232	ALA
1	H	295	GLY
1	H	302	PRO
1	I	76	ILE
1	I	192	ASP
1	I	232	ALA
1	I	295	GLY
1	I	302	PRO
1	J	76	ILE
1	J	192	ASP
1	J	206	ASP
1	J	232	ALA
1	J	295	GLY
1	J	302	PRO
1	K	76	ILE
1	K	192	ASP
1	K	206	ASP
1	K	232	ALA
1	K	295	GLY
1	K	302	PRO
1	L	76	ILE
1	L	192	ASP
1	L	206	ASP
1	L	232	ALA
1	L	295	GLY

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Mol	Chain	Res	Type
1	L	302	PRO
1	M	203	ASN
1	M	217	ILE
1	M	262	GLY
1	M	397	VAL
1	N	203	ASN
1	N	217	ILE
1	N	445	GLU
1	N	450	GLN
1	O	203	ASN
1	O	262	GLY
1	O	397	VAL
1	O	450	GLN
1	P	203	ASN
1	P	262	GLY
1	P	344	THR
1	Q	203	ASN
1	Q	217	ILE
1	Q	344	THR
1	Q	397	VAL
1	Q	498	ASP
1	R	203	ASN
1	R	262	GLY
1	R	344	THR
1	R	397	VAL
1	S	203	ASN
1	S	217	ILE
1	S	262	GLY
1	T	203	ASN
1	T	344	THR
1	U	203	ASN
1	U	217	ILE
1	V	203	ASN
1	V	217	ILE
1	V	262	GLY
1	W	203	ASN
1	W	262	GLY
1	W	445	GLU
1	X	203	ASN
1	X	217	ILE
1	X	262	GLY
1	X	397	VAL

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Mol	Chain	Res	Type
1	X	450	GLN
2	o	44	MET
2	s	44	MET
2	t	44	MET
2	u	44	MET
1	A	311	GLU
1	A	384	LEU
1	B	311	GLU
1	B	384	LEU
1	B	507	LEU
1	C	311	GLU
1	C	384	LEU
1	C	507	LEU
1	D	206	ASP
1	D	311	GLU
1	D	384	LEU
1	E	311	GLU
1	E	384	LEU
1	F	311	GLU
1	F	384	LEU
1	G	311	GLU
1	G	384	LEU
1	H	311	GLU
1	H	384	LEU
1	I	206	ASP
1	I	311	GLU
1	I	384	LEU
1	J	311	GLU
1	J	384	LEU
1	K	311	GLU
1	K	384	LEU
1	L	311	GLU
1	L	384	LEU
1	L	507	LEU
1	N	397	VAL
1	P	217	ILE
1	S	344	THR
1	S	397	VAL
1	T	397	VAL
1	V	397	VAL
1	W	397	VAL
2	k	140	PHE

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Mol	Chain	Res	Type
2	l	140	PHE
2	m	140	PHE
2	n	140	PHE
2	s	140	PHE
2	t	140	PHE
2	v	140	PHE
1	A	203	ASN
1	B	203	ASN
1	C	203	ASN
1	D	203	ASN
1	E	203	ASN
1	F	203	ASN
1	G	203	ASN
1	H	203	ASN
1	I	203	ASN
1	J	203	ASN
1	K	203	ASN
1	L	203	ASN
1	P	397	VAL
2	o	140	PHE
2	p	140	PHE
2	q	140	PHE
2	r	140	PHE
2	u	140	PHE
1	A	385	PRO
1	A	427	GLY
1	B	385	PRO
1	B	427	GLY
1	C	385	PRO
1	C	427	GLY
1	D	385	PRO
1	D	427	GLY
1	E	385	PRO
1	E	427	GLY
1	F	385	PRO
1	F	427	GLY
1	G	385	PRO
1	G	427	GLY
1	H	385	PRO
1	H	427	GLY
1	I	385	PRO
1	I	427	GLY

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Mol	Chain	Res	Type
1	J	385	PRO
1	J	427	GLY
1	K	385	PRO
1	K	427	GLY
1	L	385	PRO
1	L	427	GLY
1	U	397	VAL
1	M	310	VAL
1	N	310	VAL
1	O	310	VAL
1	P	310	VAL
1	Q	310	VAL
1	R	310	VAL
1	S	310	VAL
1	T	310	VAL
1	U	310	VAL
1	V	310	VAL
1	W	310	VAL
1	X	310	VAL
1	A	210	PRO
1	B	210	PRO
1	C	210	PRO
1	D	210	PRO
1	E	210	PRO
1	F	210	PRO
1	G	210	PRO
1	H	210	PRO
1	I	210	PRO
1	J	210	PRO
1	K	210	PRO
1	L	210	PRO

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	483/510 (95%)	409 (85%)	74 (15%)	3	12
1	B	483/510 (95%)	409 (85%)	74 (15%)	3	12
1	C	483/510 (95%)	409 (85%)	74 (15%)	3	12
1	D	483/510 (95%)	409 (85%)	74 (15%)	3	12
1	E	483/510 (95%)	409 (85%)	74 (15%)	3	12
1	F	483/510 (95%)	409 (85%)	74 (15%)	3	12
1	G	483/510 (95%)	409 (85%)	74 (15%)	3	12
1	H	483/510 (95%)	409 (85%)	74 (15%)	3	12
1	I	483/510 (95%)	409 (85%)	74 (15%)	3	12
1	J	483/510 (95%)	409 (85%)	74 (15%)	3	12
1	K	483/510 (95%)	409 (85%)	74 (15%)	3	12
1	L	483/510 (95%)	409 (85%)	74 (15%)	3	12
1	M	485/510 (95%)	413 (85%)	72 (15%)	3	13
1	N	485/510 (95%)	414 (85%)	71 (15%)	3	14
1	O	485/510 (95%)	414 (85%)	71 (15%)	3	14
1	P	485/510 (95%)	413 (85%)	72 (15%)	3	13
1	Q	485/510 (95%)	413 (85%)	72 (15%)	3	13
1	R	485/510 (95%)	413 (85%)	72 (15%)	3	13
1	S	485/510 (95%)	413 (85%)	72 (15%)	3	13
1	T	485/510 (95%)	412 (85%)	73 (15%)	3	13
1	U	485/510 (95%)	412 (85%)	73 (15%)	3	13
1	V	485/510 (95%)	413 (85%)	72 (15%)	3	13
1	W	485/510 (95%)	412 (85%)	73 (15%)	3	13
1	X	485/510 (95%)	412 (85%)	73 (15%)	3	13
2	Y	98/132 (74%)	83 (85%)	15 (15%)	3	12
2	Z	98/132 (74%)	83 (85%)	15 (15%)	3	12
2	a	98/132 (74%)	83 (85%)	15 (15%)	3	12
2	b	98/132 (74%)	83 (85%)	15 (15%)	3	12
2	c	98/132 (74%)	83 (85%)	15 (15%)	3	12
2	d	98/132 (74%)	83 (85%)	15 (15%)	3	12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	e	98/132 (74%)	83 (85%)	15 (15%)	3 12
2	f	98/132 (74%)	83 (85%)	15 (15%)	3 12
2	g	98/132 (74%)	83 (85%)	15 (15%)	3 12
2	h	98/132 (74%)	83 (85%)	15 (15%)	3 12
2	i	98/132 (74%)	83 (85%)	15 (15%)	3 12
2	j	98/132 (74%)	83 (85%)	15 (15%)	3 12
2	k	100/132 (76%)	85 (85%)	15 (15%)	3 13
2	l	100/132 (76%)	84 (84%)	16 (16%)	2 11
2	m	100/132 (76%)	85 (85%)	15 (15%)	3 13
2	n	100/132 (76%)	85 (85%)	15 (15%)	3 13
2	o	100/132 (76%)	84 (84%)	16 (16%)	2 11
2	p	100/132 (76%)	85 (85%)	15 (15%)	3 13
2	q	100/132 (76%)	85 (85%)	15 (15%)	3 13
2	r	100/132 (76%)	85 (85%)	15 (15%)	3 13
2	s	100/132 (76%)	85 (85%)	15 (15%)	3 13
2	t	100/132 (76%)	85 (85%)	15 (15%)	3 13
2	u	100/132 (76%)	83 (83%)	17 (17%)	2 9
2	v	100/132 (76%)	84 (84%)	16 (16%)	2 11
All	All	13992/15408 (91%)	11873 (85%)	2119 (15%)	3 13

All (2119) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	M	14	ARG
1	M	24	GLU
1	M	30	LYS
1	M	31	ASN
1	M	33	LEU
1	M	40	GLN
1	M	42	ASP
1	M	45	LEU
1	M	47	GLN
1	M	49	THR
1	M	50	THR
1	M	56	GLN
1	M	59	VAL

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Mol	Chain	Res	Type
1	M	79	LEU
1	M	94	LEU
1	M	101	ASP
1	M	123	VAL
1	M	133	GLU
1	M	135	GLN
1	M	144	ILE
1	M	156	VAL
1	M	157	ILE
1	M	158	TRP
1	M	161	ASN
1	M	164	LEU
1	M	165	MSE
1	M	174	THR
1	M	175	VAL
1	M	190	LYS
1	M	202	GLN
1	M	217	ILE
1	M	218	GLN
1	M	225	VAL
1	M	226	VAL
1	M	228	LYS
1	M	231	THR
1	M	234	ILE
1	M	246	TYR
1	M	248	LYS
1	M	266	ILE
1	M	270	GLN
1	M	279	SER
1	M	286	VAL
1	M	293	ILE
1	M	298	ILE
1	M	301	VAL
1	M	310	VAL
1	M	311	GLU
1	M	315	VAL
1	M	327	GLN
1	M	343	ARG
1	M	356	ILE
1	M	359	PHE
1	M	360	GLU
1	M	378	ASP

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Mol	Chain	Res	Type
1	M	384	LEU
1	M	387	GLN
1	M	389	LEU
1	M	405	LEU
1	M	430	VAL
1	M	433	ASP
1	M	438	LEU
1	M	444	LEU
1	M	455	THR
1	M	510	ILE
1	M	513	ARG
1	M	518	THR
1	M	541	LYS
1	M	546	THR
1	M	558	THR
1	M	592	TRP
1	M	593	LEU
1	N	14	ARG
1	N	24	GLU
1	N	30	LYS
1	N	31	ASN
1	N	33	LEU
1	N	40	GLN
1	N	42	ASP
1	N	45	LEU
1	N	47	GLN
1	N	49	THR
1	N	50	THR
1	N	56	GLN
1	N	59	VAL
1	N	79	LEU
1	N	94	LEU
1	N	101	ASP
1	N	123	VAL
1	N	133	GLU
1	N	135	GLN
1	N	144	ILE
1	N	145	ARG
1	N	156	VAL
1	N	157	ILE
1	N	158	TRP
1	N	161	ASN

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Mol	Chain	Res	Type
1	N	164	LEU
1	N	165	MSE
1	N	174	THR
1	N	175	VAL
1	N	190	LYS
1	N	202	GLN
1	N	217	ILE
1	N	218	GLN
1	N	225	VAL
1	N	226	VAL
1	N	228	LYS
1	N	231	THR
1	N	234	ILE
1	N	246	TYR
1	N	248	LYS
1	N	266	ILE
1	N	270	GLN
1	N	286	VAL
1	N	293	ILE
1	N	298	ILE
1	N	301	VAL
1	N	310	VAL
1	N	311	GLU
1	N	315	VAL
1	N	327	GLN
1	N	343	ARG
1	N	356	ILE
1	N	359	PHE
1	N	360	GLU
1	N	378	ASP
1	N	384	LEU
1	N	387	GLN
1	N	389	LEU
1	N	405	LEU
1	N	430	VAL
1	N	433	ASP
1	N	444	LEU
1	N	455	THR
1	N	510	ILE
1	N	513	ARG
1	N	518	THR
1	N	541	LYS

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Mol	Chain	Res	Type
1	N	546	THR
1	N	558	THR
1	N	592	TRP
1	N	593	LEU
1	O	14	ARG
1	O	24	GLU
1	O	30	LYS
1	O	31	ASN
1	O	33	LEU
1	O	40	GLN
1	O	42	ASP
1	O	45	LEU
1	O	47	GLN
1	O	49	THR
1	O	50	THR
1	O	56	GLN
1	O	59	VAL
1	O	79	LEU
1	O	94	LEU
1	O	101	ASP
1	O	123	VAL
1	O	133	GLU
1	O	135	GLN
1	O	144	ILE
1	O	145	ARG
1	O	156	VAL
1	O	157	ILE
1	O	158	TRP
1	O	161	ASN
1	O	164	LEU
1	O	165	MSE
1	O	174	THR
1	O	175	VAL
1	O	190	LYS
1	O	202	GLN
1	O	217	ILE
1	O	218	GLN
1	O	225	VAL
1	O	226	VAL
1	O	228	LYS
1	O	231	THR
1	O	234	ILE

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Mol	Chain	Res	Type
1	O	246	TYR
1	O	248	LYS
1	O	266	ILE
1	O	270	GLN
1	O	286	VAL
1	O	293	ILE
1	O	298	ILE
1	O	301	VAL
1	O	310	VAL
1	O	311	GLU
1	O	315	VAL
1	O	327	GLN
1	O	343	ARG
1	O	356	ILE
1	O	359	PHE
1	O	360	GLU
1	O	378	ASP
1	O	384	LEU
1	O	387	GLN
1	O	389	LEU
1	O	405	LEU
1	O	430	VAL
1	O	433	ASP
1	O	444	LEU
1	O	455	THR
1	O	510	ILE
1	O	513	ARG
1	O	518	THR
1	O	541	LYS
1	O	546	THR
1	O	558	THR
1	O	592	TRP
1	O	593	LEU
1	P	14	ARG
1	P	24	GLU
1	P	30	LYS
1	P	31	ASN
1	P	33	LEU
1	P	40	GLN
1	P	42	ASP
1	P	45	LEU
1	P	47	GLN

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Mol	Chain	Res	Type
1	P	49	THR
1	P	50	THR
1	P	56	GLN
1	P	59	VAL
1	P	79	LEU
1	P	94	LEU
1	P	101	ASP
1	P	123	VAL
1	P	133	GLU
1	P	135	GLN
1	P	144	ILE
1	P	145	ARG
1	P	156	VAL
1	P	157	ILE
1	P	158	TRP
1	P	161	ASN
1	P	164	LEU
1	P	165	MSE
1	P	174	THR
1	P	175	VAL
1	P	190	LYS
1	P	202	GLN
1	P	217	ILE
1	P	218	GLN
1	P	225	VAL
1	P	226	VAL
1	P	228	LYS
1	P	231	THR
1	P	234	ILE
1	P	246	TYR
1	P	248	LYS
1	P	266	ILE
1	P	270	GLN
1	P	286	VAL
1	P	293	ILE
1	P	298	ILE
1	P	301	VAL
1	P	310	VAL
1	P	311	GLU
1	P	315	VAL
1	P	327	GLN
1	P	343	ARG

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Mol	Chain	Res	Type
1	P	356	ILE
1	P	359	PHE
1	P	360	GLU
1	P	378	ASP
1	P	384	LEU
1	P	387	GLN
1	P	389	LEU
1	P	405	LEU
1	P	430	VAL
1	P	433	ASP
1	P	438	LEU
1	P	444	LEU
1	P	455	THR
1	P	510	ILE
1	P	513	ARG
1	P	518	THR
1	P	541	LYS
1	P	546	THR
1	P	558	THR
1	P	592	TRP
1	P	593	LEU
1	Q	14	ARG
1	Q	24	GLU
1	Q	30	LYS
1	Q	31	ASN
1	Q	33	LEU
1	Q	40	GLN
1	Q	42	ASP
1	Q	45	LEU
1	Q	47	GLN
1	Q	49	THR
1	Q	50	THR
1	Q	56	GLN
1	Q	59	VAL
1	Q	79	LEU
1	Q	94	LEU
1	Q	101	ASP
1	Q	123	VAL
1	Q	133	GLU
1	Q	135	GLN
1	Q	144	ILE
1	Q	145	ARG

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Mol	Chain	Res	Type
1	Q	156	VAL
1	Q	157	ILE
1	Q	158	TRP
1	Q	161	ASN
1	Q	164	LEU
1	Q	165	MSE
1	Q	174	THR
1	Q	175	VAL
1	Q	190	LYS
1	Q	202	GLN
1	Q	217	ILE
1	Q	218	GLN
1	Q	225	VAL
1	Q	226	VAL
1	Q	228	LYS
1	Q	231	THR
1	Q	234	ILE
1	Q	246	TYR
1	Q	248	LYS
1	Q	266	ILE
1	Q	270	GLN
1	Q	286	VAL
1	Q	293	ILE
1	Q	298	ILE
1	Q	301	VAL
1	Q	310	VAL
1	Q	311	GLU
1	Q	315	VAL
1	Q	327	GLN
1	Q	343	ARG
1	Q	356	ILE
1	Q	359	PHE
1	Q	360	GLU
1	Q	378	ASP
1	Q	384	LEU
1	Q	387	GLN
1	Q	389	LEU
1	Q	405	LEU
1	Q	430	VAL
1	Q	433	ASP
1	Q	444	LEU
1	Q	446	THR

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Mol	Chain	Res	Type
1	Q	455	THR
1	Q	510	ILE
1	Q	513	ARG
1	Q	518	THR
1	Q	541	LYS
1	Q	546	THR
1	Q	558	THR
1	Q	592	TRP
1	Q	593	LEU
1	R	14	ARG
1	R	24	GLU
1	R	30	LYS
1	R	31	ASN
1	R	33	LEU
1	R	40	GLN
1	R	42	ASP
1	R	45	LEU
1	R	47	GLN
1	R	49	THR
1	R	50	THR
1	R	56	GLN
1	R	59	VAL
1	R	79	LEU
1	R	94	LEU
1	R	101	ASP
1	R	123	VAL
1	R	133	GLU
1	R	135	GLN
1	R	144	ILE
1	R	145	ARG
1	R	156	VAL
1	R	157	ILE
1	R	158	TRP
1	R	161	ASN
1	R	164	LEU
1	R	165	MSE
1	R	174	THR
1	R	175	VAL
1	R	190	LYS
1	R	202	GLN
1	R	217	ILE
1	R	218	GLN

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Mol	Chain	Res	Type
1	R	225	VAL
1	R	226	VAL
1	R	228	LYS
1	R	231	THR
1	R	234	ILE
1	R	246	TYR
1	R	248	LYS
1	R	266	ILE
1	R	270	GLN
1	R	286	VAL
1	R	293	ILE
1	R	298	ILE
1	R	301	VAL
1	R	310	VAL
1	R	311	GLU
1	R	315	VAL
1	R	327	GLN
1	R	343	ARG
1	R	356	ILE
1	R	359	PHE
1	R	360	GLU
1	R	378	ASP
1	R	384	LEU
1	R	387	GLN
1	R	389	LEU
1	R	405	LEU
1	R	430	VAL
1	R	433	ASP
1	R	438	LEU
1	R	444	LEU
1	R	455	THR
1	R	510	ILE
1	R	513	ARG
1	R	518	THR
1	R	541	LYS
1	R	546	THR
1	R	558	THR
1	R	592	TRP
1	R	593	LEU
1	S	14	ARG
1	S	24	GLU
1	S	30	LYS

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Mol	Chain	Res	Type
1	S	31	ASN
1	S	33	LEU
1	S	40	GLN
1	S	42	ASP
1	S	45	LEU
1	S	47	GLN
1	S	49	THR
1	S	50	THR
1	S	56	GLN
1	S	59	VAL
1	S	79	LEU
1	S	94	LEU
1	S	101	ASP
1	S	123	VAL
1	S	133	GLU
1	S	135	GLN
1	S	144	ILE
1	S	145	ARG
1	S	156	VAL
1	S	157	ILE
1	S	158	TRP
1	S	161	ASN
1	S	164	LEU
1	S	165	MSE
1	S	174	THR
1	S	175	VAL
1	S	190	LYS
1	S	202	GLN
1	S	217	ILE
1	S	218	GLN
1	S	225	VAL
1	S	226	VAL
1	S	228	LYS
1	S	231	THR
1	S	234	ILE
1	S	246	TYR
1	S	248	LYS
1	S	266	ILE
1	S	270	GLN
1	S	286	VAL
1	S	293	ILE
1	S	298	ILE

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Mol	Chain	Res	Type
1	S	301	VAL
1	S	310	VAL
1	S	311	GLU
1	S	315	VAL
1	S	327	GLN
1	S	343	ARG
1	S	356	ILE
1	S	359	PHE
1	S	360	GLU
1	S	378	ASP
1	S	384	LEU
1	S	387	GLN
1	S	389	LEU
1	S	405	LEU
1	S	430	VAL
1	S	433	ASP
1	S	444	LEU
1	S	446	THR
1	S	455	THR
1	S	510	ILE
1	S	513	ARG
1	S	518	THR
1	S	541	LYS
1	S	546	THR
1	S	558	THR
1	S	592	TRP
1	S	593	LEU
1	T	14	ARG
1	T	24	GLU
1	T	30	LYS
1	T	31	ASN
1	T	33	LEU
1	T	40	GLN
1	T	42	ASP
1	T	45	LEU
1	T	47	GLN
1	T	49	THR
1	T	50	THR
1	T	56	GLN
1	T	59	VAL
1	T	69	SER
1	T	79	LEU

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Mol	Chain	Res	Type
1	T	94	LEU
1	T	101	ASP
1	T	123	VAL
1	T	133	GLU
1	T	135	GLN
1	T	144	ILE
1	T	156	VAL
1	T	157	ILE
1	T	158	TRP
1	T	161	ASN
1	T	164	LEU
1	T	165	MSE
1	T	174	THR
1	T	175	VAL
1	T	190	LYS
1	T	202	GLN
1	T	217	ILE
1	T	218	GLN
1	T	225	VAL
1	T	226	VAL
1	T	228	LYS
1	T	231	THR
1	T	234	ILE
1	T	246	TYR
1	T	248	LYS
1	T	266	ILE
1	T	270	GLN
1	T	279	SER
1	T	286	VAL
1	T	293	ILE
1	T	298	ILE
1	T	301	VAL
1	T	310	VAL
1	T	311	GLU
1	T	315	VAL
1	T	327	GLN
1	T	343	ARG
1	T	356	ILE
1	T	359	PHE
1	T	360	GLU
1	T	378	ASP
1	T	384	LEU

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Mol	Chain	Res	Type
1	T	387	GLN
1	T	389	LEU
1	T	405	LEU
1	T	430	VAL
1	T	433	ASP
1	T	444	LEU
1	T	446	THR
1	T	455	THR
1	T	510	ILE
1	T	513	ARG
1	T	518	THR
1	T	541	LYS
1	T	546	THR
1	T	558	THR
1	T	592	TRP
1	T	593	LEU
1	U	14	ARG
1	U	24	GLU
1	U	30	LYS
1	U	31	ASN
1	U	33	LEU
1	U	40	GLN
1	U	42	ASP
1	U	45	LEU
1	U	47	GLN
1	U	49	THR
1	U	50	THR
1	U	56	GLN
1	U	59	VAL
1	U	79	LEU
1	U	94	LEU
1	U	101	ASP
1	U	123	VAL
1	U	133	GLU
1	U	135	GLN
1	U	144	ILE
1	U	145	ARG
1	U	156	VAL
1	U	157	ILE
1	U	158	TRP
1	U	161	ASN
1	U	164	LEU

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Mol	Chain	Res	Type
1	U	165	MSE
1	U	174	THR
1	U	175	VAL
1	U	190	LYS
1	U	202	GLN
1	U	217	ILE
1	U	218	GLN
1	U	225	VAL
1	U	226	VAL
1	U	228	LYS
1	U	231	THR
1	U	234	ILE
1	U	246	TYR
1	U	248	LYS
1	U	266	ILE
1	U	270	GLN
1	U	286	VAL
1	U	293	ILE
1	U	298	ILE
1	U	301	VAL
1	U	310	VAL
1	U	311	GLU
1	U	315	VAL
1	U	327	GLN
1	U	343	ARG
1	U	356	ILE
1	U	359	PHE
1	U	360	GLU
1	U	378	ASP
1	U	384	LEU
1	U	387	GLN
1	U	389	LEU
1	U	405	LEU
1	U	430	VAL
1	U	433	ASP
1	U	438	LEU
1	U	444	LEU
1	U	446	THR
1	U	455	THR
1	U	510	ILE
1	U	513	ARG
1	U	518	THR

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Mol	Chain	Res	Type
1	U	541	LYS
1	U	546	THR
1	U	558	THR
1	U	592	TRP
1	U	593	LEU
1	V	14	ARG
1	V	24	GLU
1	V	30	LYS
1	V	31	ASN
1	V	33	LEU
1	V	40	GLN
1	V	42	ASP
1	V	45	LEU
1	V	47	GLN
1	V	49	THR
1	V	50	THR
1	V	56	GLN
1	V	59	VAL
1	V	79	LEU
1	V	94	LEU
1	V	101	ASP
1	V	123	VAL
1	V	133	GLU
1	V	135	GLN
1	V	144	ILE
1	V	156	VAL
1	V	157	ILE
1	V	158	TRP
1	V	161	ASN
1	V	164	LEU
1	V	165	MSE
1	V	174	THR
1	V	175	VAL
1	V	190	LYS
1	V	202	GLN
1	V	217	ILE
1	V	218	GLN
1	V	225	VAL
1	V	226	VAL
1	V	228	LYS
1	V	231	THR
1	V	234	ILE

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Mol	Chain	Res	Type
1	V	246	TYR
1	V	248	LYS
1	V	266	ILE
1	V	270	GLN
1	V	286	VAL
1	V	293	ILE
1	V	298	ILE
1	V	301	VAL
1	V	310	VAL
1	V	311	GLU
1	V	315	VAL
1	V	327	GLN
1	V	343	ARG
1	V	356	ILE
1	V	359	PHE
1	V	360	GLU
1	V	378	ASP
1	V	384	LEU
1	V	387	GLN
1	V	389	LEU
1	V	405	LEU
1	V	430	VAL
1	V	433	ASP
1	V	438	LEU
1	V	444	LEU
1	V	446	THR
1	V	455	THR
1	V	510	ILE
1	V	513	ARG
1	V	518	THR
1	V	541	LYS
1	V	546	THR
1	V	558	THR
1	V	592	TRP
1	V	593	LEU
1	W	14	ARG
1	W	24	GLU
1	W	30	LYS
1	W	31	ASN
1	W	33	LEU
1	W	40	GLN
1	W	42	ASP

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Mol	Chain	Res	Type
1	W	45	LEU
1	W	47	GLN
1	W	49	THR
1	W	50	THR
1	W	56	GLN
1	W	59	VAL
1	W	79	LEU
1	W	94	LEU
1	W	101	ASP
1	W	123	VAL
1	W	133	GLU
1	W	135	GLN
1	W	144	ILE
1	W	145	ARG
1	W	156	VAL
1	W	157	ILE
1	W	158	TRP
1	W	161	ASN
1	W	164	LEU
1	W	165	MSE
1	W	174	THR
1	W	175	VAL
1	W	190	LYS
1	W	202	GLN
1	W	217	ILE
1	W	218	GLN
1	W	225	VAL
1	W	226	VAL
1	W	228	LYS
1	W	231	THR
1	W	234	ILE
1	W	246	TYR
1	W	248	LYS
1	W	266	ILE
1	W	270	GLN
1	W	286	VAL
1	W	293	ILE
1	W	298	ILE
1	W	301	VAL
1	W	310	VAL
1	W	311	GLU
1	W	315	VAL

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Mol	Chain	Res	Type
1	W	327	GLN
1	W	343	ARG
1	W	356	ILE
1	W	359	PHE
1	W	360	GLU
1	W	378	ASP
1	W	384	LEU
1	W	387	GLN
1	W	389	LEU
1	W	405	LEU
1	W	430	VAL
1	W	433	ASP
1	W	438	LEU
1	W	444	LEU
1	W	446	THR
1	W	455	THR
1	W	510	ILE
1	W	513	ARG
1	W	518	THR
1	W	541	LYS
1	W	546	THR
1	W	558	THR
1	W	592	TRP
1	W	593	LEU
1	X	14	ARG
1	X	24	GLU
1	X	30	LYS
1	X	31	ASN
1	X	33	LEU
1	X	40	GLN
1	X	42	ASP
1	X	45	LEU
1	X	47	GLN
1	X	49	THR
1	X	50	THR
1	X	56	GLN
1	X	59	VAL
1	X	79	LEU
1	X	94	LEU
1	X	101	ASP
1	X	123	VAL
1	X	133	GLU

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Mol	Chain	Res	Type
1	X	135	GLN
1	X	144	ILE
1	X	145	ARG
1	X	156	VAL
1	X	157	ILE
1	X	158	TRP
1	X	161	ASN
1	X	164	LEU
1	X	165	MSE
1	X	174	THR
1	X	175	VAL
1	X	190	LYS
1	X	202	GLN
1	X	217	ILE
1	X	218	GLN
1	X	225	VAL
1	X	226	VAL
1	X	228	LYS
1	X	231	THR
1	X	234	ILE
1	X	246	TYR
1	X	248	LYS
1	X	266	ILE
1	X	270	GLN
1	X	286	VAL
1	X	293	ILE
1	X	298	ILE
1	X	301	VAL
1	X	310	VAL
1	X	311	GLU
1	X	315	VAL
1	X	327	GLN
1	X	343	ARG
1	X	356	ILE
1	X	359	PHE
1	X	360	GLU
1	X	378	ASP
1	X	384	LEU
1	X	387	GLN
1	X	389	LEU
1	X	405	LEU
1	X	430	VAL

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Mol	Chain	Res	Type
1	X	433	ASP
1	X	438	LEU
1	X	444	LEU
1	X	446	THR
1	X	455	THR
1	X	510	ILE
1	X	513	ARG
1	X	518	THR
1	X	541	LYS
1	X	546	THR
1	X	558	THR
1	X	592	TRP
1	X	593	LEU
2	k	14	LEU
2	k	16	LYS
2	k	27	ASP
2	k	29	GLU
2	k	33	MET
2	k	37	VAL
2	k	39	ASP
2	k	56	THR
2	k	63	ASP
2	k	69	GLU
2	k	71	ASP
2	k	87	LEU
2	k	130	SER
2	k	131	ARG
2	k	136	SER
2	l	14	LEU
2	l	16	LYS
2	l	27	ASP
2	l	29	GLU
2	l	33	MET
2	l	37	VAL
2	l	39	ASP
2	l	56	THR
2	l	63	ASP
2	l	69	GLU
2	l	71	ASP
2	l	87	LEU
2	l	100	THR
2	l	130	SER

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Mol	Chain	Res	Type
2	l	131	ARG
2	l	136	SER
2	m	14	LEU
2	m	16	LYS
2	m	27	ASP
2	m	29	GLU
2	m	33	MET
2	m	37	VAL
2	m	39	ASP
2	m	56	THR
2	m	63	ASP
2	m	69	GLU
2	m	71	ASP
2	m	87	LEU
2	m	130	SER
2	m	131	ARG
2	m	136	SER
2	n	14	LEU
2	n	16	LYS
2	n	27	ASP
2	n	29	GLU
2	n	33	MET
2	n	37	VAL
2	n	39	ASP
2	n	56	THR
2	n	63	ASP
2	n	69	GLU
2	n	71	ASP
2	n	87	LEU
2	n	130	SER
2	n	131	ARG
2	n	136	SER
2	o	14	LEU
2	o	16	LYS
2	o	27	ASP
2	o	29	GLU
2	o	33	MET
2	o	37	VAL
2	o	39	ASP
2	o	56	THR
2	o	63	ASP
2	o	69	GLU

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Mol	Chain	Res	Type
2	o	71	ASP
2	o	87	LEU
2	o	100	THR
2	o	130	SER
2	o	131	ARG
2	o	136	SER
2	p	14	LEU
2	p	16	LYS
2	p	27	ASP
2	p	29	GLU
2	p	33	MET
2	p	37	VAL
2	p	39	ASP
2	p	56	THR
2	p	63	ASP
2	p	69	GLU
2	p	71	ASP
2	p	87	LEU
2	p	130	SER
2	p	131	ARG
2	p	136	SER
2	q	14	LEU
2	q	16	LYS
2	q	27	ASP
2	q	29	GLU
2	q	33	MET
2	q	37	VAL
2	q	39	ASP
2	q	56	THR
2	q	63	ASP
2	q	69	GLU
2	q	71	ASP
2	q	87	LEU
2	q	130	SER
2	q	131	ARG
2	q	136	SER
2	r	14	LEU
2	r	16	LYS
2	r	27	ASP
2	r	29	GLU
2	r	33	MET
2	r	37	VAL

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Mol	Chain	Res	Type
2	r	39	ASP
2	r	56	THR
2	r	63	ASP
2	r	69	GLU
2	r	71	ASP
2	r	87	LEU
2	r	130	SER
2	r	131	ARG
2	r	136	SER
2	s	14	LEU
2	s	16	LYS
2	s	27	ASP
2	s	29	GLU
2	s	33	MET
2	s	37	VAL
2	s	39	ASP
2	s	56	THR
2	s	63	ASP
2	s	69	GLU
2	s	71	ASP
2	s	87	LEU
2	s	130	SER
2	s	131	ARG
2	s	136	SER
2	t	14	LEU
2	t	16	LYS
2	t	27	ASP
2	t	29	GLU
2	t	33	MET
2	t	37	VAL
2	t	39	ASP
2	t	56	THR
2	t	63	ASP
2	t	69	GLU
2	t	71	ASP
2	t	87	LEU
2	t	130	SER
2	t	131	ARG
2	t	136	SER
2	u	14	LEU
2	u	16	LYS
2	u	24	THR

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Mol	Chain	Res	Type
2	u	27	ASP
2	u	29	GLU
2	u	33	MET
2	u	37	VAL
2	u	39	ASP
2	u	56	THR
2	u	63	ASP
2	u	69	GLU
2	u	71	ASP
2	u	87	LEU
2	u	100	THR
2	u	130	SER
2	u	131	ARG
2	u	136	SER
2	v	14	LEU
2	v	16	LYS
2	v	17	LEU
2	v	27	ASP
2	v	29	GLU
2	v	33	MET
2	v	37	VAL
2	v	39	ASP
2	v	56	THR
2	v	63	ASP
2	v	69	GLU
2	v	71	ASP
2	v	87	LEU
2	v	130	SER
2	v	131	ARG
2	v	136	SER
1	A	14	ARG
1	A	24	GLU
1	A	30	LYS
1	A	31	ASN
1	A	33	LEU
1	A	37	ARG
1	A	42	ASP
1	A	43	ASP
1	A	45	LEU
1	A	56	GLN
1	A	79	LEU
1	A	115	VAL

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Mol	Chain	Res	Type
1	A	118	GLN
1	A	123	VAL
1	A	133	GLU
1	A	135	GLN
1	A	144	ILE
1	A	145	ARG
1	A	156	VAL
1	A	157	ILE
1	A	158	TRP
1	A	161	ASN
1	A	164	LEU
1	A	168	SER
1	A	174	THR
1	A	190	LYS
1	A	201	PHE
1	A	202	GLN
1	A	208	VAL
1	A	209	PHE
1	A	217	ILE
1	A	218	GLN
1	A	226	VAL
1	A	229	LYS
1	A	234	ILE
1	A	246	TYR
1	A	248	LYS
1	A	265	LYS
1	A	266	ILE
1	A	286	VAL
1	A	287	LEU
1	A	293	ILE
1	A	301	VAL
1	A	310	VAL
1	A	315	VAL
1	A	325	ASP
1	A	327	GLN
1	A	343	ARG
1	A	356	ILE
1	A	359	PHE
1	A	360	GLU
1	A	384	LEU
1	A	386	THR
1	A	387	GLN

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Mol	Chain	Res	Type
1	A	389	LEU
1	A	405	LEU
1	A	422	THR
1	A	430	VAL
1	A	432	PHE
1	A	438	LEU
1	A	444	LEU
1	A	507	LEU
1	A	513	ARG
1	A	518	THR
1	A	529	GLN
1	A	541	LYS
1	A	546	THR
1	A	555	GLN
1	A	558	THR
1	A	565	VAL
1	A	581	VAL
1	A	592	TRP
1	A	593	LEU
1	A	597	GLN
1	B	14	ARG
1	B	24	GLU
1	B	30	LYS
1	B	31	ASN
1	B	33	LEU
1	B	37	ARG
1	B	42	ASP
1	B	43	ASP
1	B	45	LEU
1	B	56	GLN
1	B	79	LEU
1	B	115	VAL
1	B	118	GLN
1	B	123	VAL
1	B	133	GLU
1	B	135	GLN
1	B	144	ILE
1	B	145	ARG
1	B	156	VAL
1	B	157	ILE
1	B	158	TRP
1	B	161	ASN

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Mol	Chain	Res	Type
1	B	164	LEU
1	B	168	SER
1	B	174	THR
1	B	190	LYS
1	B	201	PHE
1	B	202	GLN
1	B	208	VAL
1	B	209	PHE
1	B	217	ILE
1	B	218	GLN
1	B	226	VAL
1	B	229	LYS
1	B	234	ILE
1	B	246	TYR
1	B	248	LYS
1	B	265	LYS
1	B	266	ILE
1	B	286	VAL
1	B	287	LEU
1	B	293	ILE
1	B	301	VAL
1	B	310	VAL
1	B	315	VAL
1	B	325	ASP
1	B	327	GLN
1	B	343	ARG
1	B	356	ILE
1	B	359	PHE
1	B	360	GLU
1	B	384	LEU
1	B	386	THR
1	B	387	GLN
1	B	389	LEU
1	B	405	LEU
1	B	422	THR
1	B	430	VAL
1	B	432	PHE
1	B	438	LEU
1	B	444	LEU
1	B	507	LEU
1	B	513	ARG
1	B	518	THR

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Mol	Chain	Res	Type
1	B	529	GLN
1	B	541	LYS
1	B	546	THR
1	B	555	GLN
1	B	558	THR
1	B	565	VAL
1	B	581	VAL
1	B	592	TRP
1	B	593	LEU
1	B	597	GLN
1	C	14	ARG
1	C	24	GLU
1	C	30	LYS
1	C	31	ASN
1	C	33	LEU
1	C	37	ARG
1	C	42	ASP
1	C	43	ASP
1	C	45	LEU
1	C	56	GLN
1	C	79	LEU
1	C	115	VAL
1	C	118	GLN
1	C	123	VAL
1	C	133	GLU
1	C	135	GLN
1	C	144	ILE
1	C	145	ARG
1	C	156	VAL
1	C	157	ILE
1	C	158	TRP
1	C	161	ASN
1	C	164	LEU
1	C	168	SER
1	C	174	THR
1	C	190	LYS
1	C	201	PHE
1	C	202	GLN
1	C	208	VAL
1	C	209	PHE
1	C	217	ILE
1	C	218	GLN

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Mol	Chain	Res	Type
1	C	226	VAL
1	C	229	LYS
1	C	234	ILE
1	C	246	TYR
1	C	248	LYS
1	C	265	LYS
1	C	266	ILE
1	C	286	VAL
1	C	287	LEU
1	C	293	ILE
1	C	301	VAL
1	C	310	VAL
1	C	315	VAL
1	C	325	ASP
1	C	327	GLN
1	C	343	ARG
1	C	356	ILE
1	C	359	PHE
1	C	360	GLU
1	C	384	LEU
1	C	386	THR
1	C	387	GLN
1	C	389	LEU
1	C	405	LEU
1	C	422	THR
1	C	430	VAL
1	C	432	PHE
1	C	438	LEU
1	C	444	LEU
1	C	507	LEU
1	C	513	ARG
1	C	518	THR
1	C	529	GLN
1	C	541	LYS
1	C	546	THR
1	C	555	GLN
1	C	558	THR
1	C	565	VAL
1	C	581	VAL
1	C	592	TRP
1	C	593	LEU
1	C	597	GLN

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Mol	Chain	Res	Type
1	D	14	ARG
1	D	24	GLU
1	D	30	LYS
1	D	31	ASN
1	D	33	LEU
1	D	37	ARG
1	D	42	ASP
1	D	43	ASP
1	D	45	LEU
1	D	56	GLN
1	D	79	LEU
1	D	115	VAL
1	D	118	GLN
1	D	123	VAL
1	D	133	GLU
1	D	135	GLN
1	D	144	ILE
1	D	145	ARG
1	D	156	VAL
1	D	157	ILE
1	D	158	TRP
1	D	161	ASN
1	D	164	LEU
1	D	168	SER
1	D	174	THR
1	D	190	LYS
1	D	201	PHE
1	D	202	GLN
1	D	208	VAL
1	D	209	PHE
1	D	217	ILE
1	D	218	GLN
1	D	226	VAL
1	D	229	LYS
1	D	234	ILE
1	D	246	TYR
1	D	248	LYS
1	D	265	LYS
1	D	266	ILE
1	D	286	VAL
1	D	287	LEU
1	D	293	ILE

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Mol	Chain	Res	Type
1	D	301	VAL
1	D	310	VAL
1	D	315	VAL
1	D	325	ASP
1	D	327	GLN
1	D	343	ARG
1	D	356	ILE
1	D	359	PHE
1	D	360	GLU
1	D	384	LEU
1	D	386	THR
1	D	387	GLN
1	D	389	LEU
1	D	405	LEU
1	D	422	THR
1	D	430	VAL
1	D	432	PHE
1	D	438	LEU
1	D	444	LEU
1	D	507	LEU
1	D	513	ARG
1	D	518	THR
1	D	529	GLN
1	D	541	LYS
1	D	546	THR
1	D	555	GLN
1	D	558	THR
1	D	565	VAL
1	D	581	VAL
1	D	592	TRP
1	D	593	LEU
1	D	597	GLN
1	E	14	ARG
1	E	24	GLU
1	E	30	LYS
1	E	31	ASN
1	E	33	LEU
1	E	37	ARG
1	E	42	ASP
1	E	43	ASP
1	E	45	LEU
1	E	56	GLN

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Mol	Chain	Res	Type
1	E	79	LEU
1	E	115	VAL
1	E	118	GLN
1	E	123	VAL
1	E	133	GLU
1	E	135	GLN
1	E	144	ILE
1	E	145	ARG
1	E	156	VAL
1	E	157	ILE
1	E	158	TRP
1	E	161	ASN
1	E	164	LEU
1	E	168	SER
1	E	174	THR
1	E	190	LYS
1	E	201	PHE
1	E	202	GLN
1	E	208	VAL
1	E	209	PHE
1	E	217	ILE
1	E	218	GLN
1	E	226	VAL
1	E	229	LYS
1	E	234	ILE
1	E	246	TYR
1	E	248	LYS
1	E	265	LYS
1	E	266	ILE
1	E	286	VAL
1	E	287	LEU
1	E	293	ILE
1	E	301	VAL
1	E	310	VAL
1	E	315	VAL
1	E	325	ASP
1	E	327	GLN
1	E	343	ARG
1	E	356	ILE
1	E	359	PHE
1	E	360	GLU
1	E	384	LEU

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Mol	Chain	Res	Type
1	E	386	THR
1	E	387	GLN
1	E	389	LEU
1	E	405	LEU
1	E	422	THR
1	E	430	VAL
1	E	432	PHE
1	E	438	LEU
1	E	444	LEU
1	E	507	LEU
1	E	513	ARG
1	E	518	THR
1	E	529	GLN
1	E	541	LYS
1	E	546	THR
1	E	555	GLN
1	E	558	THR
1	E	565	VAL
1	E	581	VAL
1	E	592	TRP
1	E	593	LEU
1	E	597	GLN
1	F	14	ARG
1	F	24	GLU
1	F	30	LYS
1	F	31	ASN
1	F	33	LEU
1	F	37	ARG
1	F	42	ASP
1	F	43	ASP
1	F	45	LEU
1	F	56	GLN
1	F	79	LEU
1	F	115	VAL
1	F	118	GLN
1	F	123	VAL
1	F	133	GLU
1	F	135	GLN
1	F	144	ILE
1	F	145	ARG
1	F	156	VAL
1	F	157	ILE

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Mol	Chain	Res	Type
1	F	158	TRP
1	F	161	ASN
1	F	164	LEU
1	F	168	SER
1	F	174	THR
1	F	190	LYS
1	F	201	PHE
1	F	202	GLN
1	F	208	VAL
1	F	209	PHE
1	F	217	ILE
1	F	218	GLN
1	F	226	VAL
1	F	229	LYS
1	F	234	ILE
1	F	246	TYR
1	F	248	LYS
1	F	265	LYS
1	F	266	ILE
1	F	286	VAL
1	F	287	LEU
1	F	293	ILE
1	F	301	VAL
1	F	310	VAL
1	F	315	VAL
1	F	325	ASP
1	F	327	GLN
1	F	343	ARG
1	F	356	ILE
1	F	359	PHE
1	F	360	GLU
1	F	384	LEU
1	F	386	THR
1	F	387	GLN
1	F	389	LEU
1	F	405	LEU
1	F	422	THR
1	F	430	VAL
1	F	432	PHE
1	F	438	LEU
1	F	444	LEU
1	F	507	LEU

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Mol	Chain	Res	Type
1	F	513	ARG
1	F	518	THR
1	F	529	GLN
1	F	541	LYS
1	F	546	THR
1	F	555	GLN
1	F	558	THR
1	F	565	VAL
1	F	581	VAL
1	F	592	TRP
1	F	593	LEU
1	F	597	GLN
1	G	14	ARG
1	G	24	GLU
1	G	30	LYS
1	G	31	ASN
1	G	33	LEU
1	G	37	ARG
1	G	42	ASP
1	G	43	ASP
1	G	45	LEU
1	G	56	GLN
1	G	79	LEU
1	G	115	VAL
1	G	118	GLN
1	G	123	VAL
1	G	133	GLU
1	G	135	GLN
1	G	144	ILE
1	G	145	ARG
1	G	156	VAL
1	G	157	ILE
1	G	158	TRP
1	G	161	ASN
1	G	164	LEU
1	G	168	SER
1	G	174	THR
1	G	190	LYS
1	G	201	PHE
1	G	202	GLN
1	G	208	VAL
1	G	209	PHE

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Mol	Chain	Res	Type
1	G	217	ILE
1	G	218	GLN
1	G	226	VAL
1	G	229	LYS
1	G	234	ILE
1	G	246	TYR
1	G	248	LYS
1	G	265	LYS
1	G	266	ILE
1	G	286	VAL
1	G	287	LEU
1	G	293	ILE
1	G	301	VAL
1	G	310	VAL
1	G	315	VAL
1	G	325	ASP
1	G	327	GLN
1	G	343	ARG
1	G	356	ILE
1	G	359	PHE
1	G	360	GLU
1	G	384	LEU
1	G	386	THR
1	G	387	GLN
1	G	389	LEU
1	G	405	LEU
1	G	422	THR
1	G	430	VAL
1	G	432	PHE
1	G	438	LEU
1	G	444	LEU
1	G	507	LEU
1	G	513	ARG
1	G	518	THR
1	G	529	GLN
1	G	541	LYS
1	G	546	THR
1	G	555	GLN
1	G	558	THR
1	G	565	VAL
1	G	581	VAL
1	G	592	TRP

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Mol	Chain	Res	Type
1	G	593	LEU
1	G	597	GLN
1	H	14	ARG
1	H	24	GLU
1	H	30	LYS
1	H	31	ASN
1	H	33	LEU
1	H	37	ARG
1	H	42	ASP
1	H	43	ASP
1	H	45	LEU
1	H	56	GLN
1	H	79	LEU
1	H	115	VAL
1	H	118	GLN
1	H	123	VAL
1	H	133	GLU
1	H	135	GLN
1	H	144	ILE
1	H	145	ARG
1	H	156	VAL
1	H	157	ILE
1	H	158	TRP
1	H	161	ASN
1	H	164	LEU
1	H	168	SER
1	H	174	THR
1	H	190	LYS
1	H	201	PHE
1	H	202	GLN
1	H	208	VAL
1	H	209	PHE
1	H	217	ILE
1	H	218	GLN
1	H	226	VAL
1	H	229	LYS
1	H	234	ILE
1	H	246	TYR
1	H	248	LYS
1	H	265	LYS
1	H	266	ILE
1	H	286	VAL

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Mol	Chain	Res	Type
1	H	287	LEU
1	H	293	ILE
1	H	301	VAL
1	H	310	VAL
1	H	315	VAL
1	H	325	ASP
1	H	327	GLN
1	H	343	ARG
1	H	356	ILE
1	H	359	PHE
1	H	360	GLU
1	H	384	LEU
1	H	386	THR
1	H	387	GLN
1	H	389	LEU
1	H	405	LEU
1	H	422	THR
1	H	430	VAL
1	H	432	PHE
1	H	438	LEU
1	H	444	LEU
1	H	507	LEU
1	H	513	ARG
1	H	518	THR
1	H	529	GLN
1	H	541	LYS
1	H	546	THR
1	H	555	GLN
1	H	558	THR
1	H	565	VAL
1	H	581	VAL
1	H	592	TRP
1	H	593	LEU
1	H	597	GLN
1	I	14	ARG
1	I	24	GLU
1	I	30	LYS
1	I	31	ASN
1	I	33	LEU
1	I	37	ARG
1	I	42	ASP
1	I	43	ASP

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Mol	Chain	Res	Type
1	I	45	LEU
1	I	56	GLN
1	I	79	LEU
1	I	115	VAL
1	I	118	GLN
1	I	123	VAL
1	I	133	GLU
1	I	135	GLN
1	I	144	ILE
1	I	145	ARG
1	I	156	VAL
1	I	157	ILE
1	I	158	TRP
1	I	161	ASN
1	I	164	LEU
1	I	168	SER
1	I	174	THR
1	I	190	LYS
1	I	201	PHE
1	I	202	GLN
1	I	208	VAL
1	I	209	PHE
1	I	217	ILE
1	I	218	GLN
1	I	226	VAL
1	I	229	LYS
1	I	234	ILE
1	I	246	TYR
1	I	248	LYS
1	I	265	LYS
1	I	266	ILE
1	I	286	VAL
1	I	287	LEU
1	I	293	ILE
1	I	301	VAL
1	I	310	VAL
1	I	315	VAL
1	I	325	ASP
1	I	327	GLN
1	I	343	ARG
1	I	356	ILE
1	I	359	PHE

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Mol	Chain	Res	Type
1	I	360	GLU
1	I	384	LEU
1	I	386	THR
1	I	387	GLN
1	I	389	LEU
1	I	405	LEU
1	I	422	THR
1	I	430	VAL
1	I	432	PHE
1	I	438	LEU
1	I	444	LEU
1	I	507	LEU
1	I	513	ARG
1	I	518	THR
1	I	529	GLN
1	I	541	LYS
1	I	546	THR
1	I	555	GLN
1	I	558	THR
1	I	565	VAL
1	I	581	VAL
1	I	592	TRP
1	I	593	LEU
1	I	597	GLN
1	J	14	ARG
1	J	24	GLU
1	J	30	LYS
1	J	31	ASN
1	J	33	LEU
1	J	37	ARG
1	J	42	ASP
1	J	43	ASP
1	J	45	LEU
1	J	56	GLN
1	J	79	LEU
1	J	115	VAL
1	J	118	GLN
1	J	123	VAL
1	J	133	GLU
1	J	135	GLN
1	J	144	ILE
1	J	145	ARG

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Mol	Chain	Res	Type
1	J	156	VAL
1	J	157	ILE
1	J	158	TRP
1	J	161	ASN
1	J	164	LEU
1	J	168	SER
1	J	174	THR
1	J	190	LYS
1	J	201	PHE
1	J	202	GLN
1	J	208	VAL
1	J	209	PHE
1	J	217	ILE
1	J	218	GLN
1	J	226	VAL
1	J	229	LYS
1	J	234	ILE
1	J	246	TYR
1	J	248	LYS
1	J	265	LYS
1	J	266	ILE
1	J	286	VAL
1	J	287	LEU
1	J	293	ILE
1	J	301	VAL
1	J	310	VAL
1	J	315	VAL
1	J	325	ASP
1	J	327	GLN
1	J	343	ARG
1	J	356	ILE
1	J	359	PHE
1	J	360	GLU
1	J	384	LEU
1	J	386	THR
1	J	387	GLN
1	J	389	LEU
1	J	405	LEU
1	J	422	THR
1	J	430	VAL
1	J	432	PHE
1	J	438	LEU

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Mol	Chain	Res	Type
1	J	444	LEU
1	J	507	LEU
1	J	513	ARG
1	J	518	THR
1	J	529	GLN
1	J	541	LYS
1	J	546	THR
1	J	555	GLN
1	J	558	THR
1	J	565	VAL
1	J	581	VAL
1	J	592	TRP
1	J	593	LEU
1	J	597	GLN
1	K	14	ARG
1	K	24	GLU
1	K	30	LYS
1	K	31	ASN
1	K	33	LEU
1	K	37	ARG
1	K	42	ASP
1	K	43	ASP
1	K	45	LEU
1	K	56	GLN
1	K	79	LEU
1	K	115	VAL
1	K	118	GLN
1	K	123	VAL
1	K	133	GLU
1	K	135	GLN
1	K	144	ILE
1	K	145	ARG
1	K	156	VAL
1	K	157	ILE
1	K	158	TRP
1	K	161	ASN
1	K	164	LEU
1	K	168	SER
1	K	174	THR
1	K	190	LYS
1	K	201	PHE
1	K	202	GLN

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Mol	Chain	Res	Type
1	K	208	VAL
1	K	209	PHE
1	K	217	ILE
1	K	218	GLN
1	K	226	VAL
1	K	229	LYS
1	K	234	ILE
1	K	246	TYR
1	K	248	LYS
1	K	265	LYS
1	K	266	ILE
1	K	286	VAL
1	K	287	LEU
1	K	293	ILE
1	K	301	VAL
1	K	310	VAL
1	K	315	VAL
1	K	325	ASP
1	K	327	GLN
1	K	343	ARG
1	K	356	ILE
1	K	359	PHE
1	K	360	GLU
1	K	384	LEU
1	K	386	THR
1	K	387	GLN
1	K	389	LEU
1	K	405	LEU
1	K	422	THR
1	K	430	VAL
1	K	432	PHE
1	K	438	LEU
1	K	444	LEU
1	K	507	LEU
1	K	513	ARG
1	K	518	THR
1	K	529	GLN
1	K	541	LYS
1	K	546	THR
1	K	555	GLN
1	K	558	THR
1	K	565	VAL

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Mol	Chain	Res	Type
1	K	581	VAL
1	K	592	TRP
1	K	593	LEU
1	K	597	GLN
1	L	14	ARG
1	L	24	GLU
1	L	30	LYS
1	L	31	ASN
1	L	33	LEU
1	L	37	ARG
1	L	42	ASP
1	L	43	ASP
1	L	45	LEU
1	L	56	GLN
1	L	79	LEU
1	L	115	VAL
1	L	118	GLN
1	L	123	VAL
1	L	133	GLU
1	L	135	GLN
1	L	144	ILE
1	L	145	ARG
1	L	156	VAL
1	L	157	ILE
1	L	158	TRP
1	L	161	ASN
1	L	164	LEU
1	L	168	SER
1	L	174	THR
1	L	190	LYS
1	L	201	PHE
1	L	202	GLN
1	L	208	VAL
1	L	209	PHE
1	L	217	ILE
1	L	218	GLN
1	L	226	VAL
1	L	229	LYS
1	L	234	ILE
1	L	246	TYR
1	L	248	LYS
1	L	265	LYS

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Mol	Chain	Res	Type
1	L	266	ILE
1	L	286	VAL
1	L	287	LEU
1	L	293	ILE
1	L	301	VAL
1	L	310	VAL
1	L	315	VAL
1	L	325	ASP
1	L	327	GLN
1	L	343	ARG
1	L	356	ILE
1	L	359	PHE
1	L	360	GLU
1	L	384	LEU
1	L	386	THR
1	L	387	GLN
1	L	389	LEU
1	L	405	LEU
1	L	422	THR
1	L	430	VAL
1	L	432	PHE
1	L	438	LEU
1	L	444	LEU
1	L	507	LEU
1	L	513	ARG
1	L	518	THR
1	L	529	GLN
1	L	541	LYS
1	L	546	THR
1	L	555	GLN
1	L	558	THR
1	L	565	VAL
1	L	581	VAL
1	L	592	TRP
1	L	593	LEU
1	L	597	GLN
2	Y	26	LEU
2	Y	42	MET
2	Y	46	VAL
2	Y	49	LEU
2	Y	52	MET
2	Y	53	MET

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Mol	Chain	Res	Type
2	Y	78	GLU
2	Y	80	ASP
2	Y	90	SER
2	Y	96	LEU
2	Y	113	ILE
2	Y	139	SER
2	Y	140	ARG
2	Y	145	SER
2	Y	147	ASN
2	Z	26	LEU
2	Z	42	MET
2	Z	46	VAL
2	Z	49	LEU
2	Z	52	MET
2	Z	53	MET
2	Z	78	GLU
2	Z	80	ASP
2	Z	90	SER
2	Z	96	LEU
2	Z	113	ILE
2	Z	139	SER
2	Z	140	ARG
2	Z	145	SER
2	Z	147	ASN
2	a	26	LEU
2	a	42	MET
2	a	46	VAL
2	a	49	LEU
2	a	52	MET
2	a	53	MET
2	a	78	GLU
2	a	80	ASP
2	a	90	SER
2	a	96	LEU
2	a	113	ILE
2	a	139	SER
2	a	140	ARG
2	a	145	SER
2	a	147	ASN
2	b	26	LEU
2	b	42	MET
2	b	46	VAL

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Mol	Chain	Res	Type
2	b	49	LEU
2	b	52	MET
2	b	53	MET
2	b	78	GLU
2	b	80	ASP
2	b	90	SER
2	b	96	LEU
2	b	113	ILE
2	b	139	SER
2	b	140	ARG
2	b	145	SER
2	b	147	ASN
2	c	26	LEU
2	c	42	MET
2	c	46	VAL
2	c	49	LEU
2	c	52	MET
2	c	53	MET
2	c	78	GLU
2	c	80	ASP
2	c	90	SER
2	c	96	LEU
2	c	113	ILE
2	c	139	SER
2	c	140	ARG
2	c	145	SER
2	c	147	ASN
2	d	26	LEU
2	d	42	MET
2	d	46	VAL
2	d	49	LEU
2	d	52	MET
2	d	53	MET
2	d	78	GLU
2	d	80	ASP
2	d	90	SER
2	d	96	LEU
2	d	113	ILE
2	d	139	SER
2	d	140	ARG
2	d	145	SER
2	d	147	ASN

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Mol	Chain	Res	Type
2	e	26	LEU
2	e	42	MET
2	e	46	VAL
2	e	49	LEU
2	e	52	MET
2	e	53	MET
2	e	78	GLU
2	e	80	ASP
2	e	90	SER
2	e	96	LEU
2	e	113	ILE
2	e	139	SER
2	e	140	ARG
2	e	145	SER
2	e	147	ASN
2	f	26	LEU
2	f	42	MET
2	f	46	VAL
2	f	49	LEU
2	f	52	MET
2	f	53	MET
2	f	78	GLU
2	f	80	ASP
2	f	90	SER
2	f	96	LEU
2	f	113	ILE
2	f	139	SER
2	f	140	ARG
2	f	145	SER
2	f	147	ASN
2	g	26	LEU
2	g	42	MET
2	g	46	VAL
2	g	49	LEU
2	g	52	MET
2	g	53	MET
2	g	78	GLU
2	g	80	ASP
2	g	90	SER
2	g	96	LEU
2	g	113	ILE
2	g	139	SER

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Mol	Chain	Res	Type
2	g	140	ARG
2	g	145	SER
2	g	147	ASN
2	h	26	LEU
2	h	42	MET
2	h	46	VAL
2	h	49	LEU
2	h	52	MET
2	h	53	MET
2	h	78	GLU
2	h	80	ASP
2	h	90	SER
2	h	96	LEU
2	h	113	ILE
2	h	139	SER
2	h	140	ARG
2	h	145	SER
2	h	147	ASN
2	i	26	LEU
2	i	42	MET
2	i	46	VAL
2	i	49	LEU
2	i	52	MET
2	i	53	MET
2	i	78	GLU
2	i	80	ASP
2	i	90	SER
2	i	96	LEU
2	i	113	ILE
2	i	139	SER
2	i	140	ARG
2	i	145	SER
2	i	147	ASN
2	j	26	LEU
2	j	42	MET
2	j	46	VAL
2	j	49	LEU
2	j	52	MET
2	j	53	MET
2	j	78	GLU
2	j	80	ASP
2	j	90	SER

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Mol	Chain	Res	Type
2	j	96	LEU
2	j	113	ILE
2	j	139	SER
2	j	140	ARG
2	j	145	SER
2	j	147	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (447) such sidechains are listed below:

Mol	Chain	Res	Type
1	M	31	ASN
1	M	40	GLN
1	M	74	ASN
1	M	104	HIS
1	M	142	GLN
1	M	150	HIS
1	M	203	ASN
1	M	218	GLN
1	M	297	HIS
1	M	375	ASN
1	M	450	GLN
1	M	508	ASN
1	M	573	ASN
1	M	575	GLN
1	N	31	ASN
1	N	40	GLN
1	N	74	ASN
1	N	104	HIS
1	N	150	HIS
1	N	203	ASN
1	N	218	GLN
1	N	297	HIS
1	N	508	ASN
1	N	575	GLN
1	O	31	ASN
1	O	40	GLN
1	O	74	ASN
1	O	104	HIS
1	O	135	GLN
1	O	142	GLN
1	O	150	HIS
1	O	203	ASN

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Mol	Chain	Res	Type
1	O	218	GLN
1	O	297	HIS
1	O	508	ASN
1	O	575	GLN
1	P	31	ASN
1	P	40	GLN
1	P	74	ASN
1	P	104	HIS
1	P	142	GLN
1	P	150	HIS
1	P	203	ASN
1	P	218	GLN
1	P	297	HIS
1	P	508	ASN
1	P	575	GLN
1	Q	31	ASN
1	Q	40	GLN
1	Q	74	ASN
1	Q	104	HIS
1	Q	142	GLN
1	Q	203	ASN
1	Q	218	GLN
1	Q	291	GLN
1	Q	297	HIS
1	Q	508	ASN
1	Q	575	GLN
1	R	31	ASN
1	R	40	GLN
1	R	74	ASN
1	R	104	HIS
1	R	150	HIS
1	R	203	ASN
1	R	218	GLN
1	R	297	HIS
1	R	450	GLN
1	R	508	ASN
1	R	573	ASN
1	R	575	GLN
1	S	31	ASN
1	S	40	GLN
1	S	74	ASN
1	S	104	HIS

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Mol	Chain	Res	Type
1	S	135	GLN
1	S	142	GLN
1	S	203	ASN
1	S	218	GLN
1	S	291	GLN
1	S	297	HIS
1	S	508	ASN
1	S	575	GLN
1	T	31	ASN
1	T	40	GLN
1	T	74	ASN
1	T	104	HIS
1	T	142	GLN
1	T	150	HIS
1	T	155	HIS
1	T	203	ASN
1	T	218	GLN
1	T	297	HIS
1	T	508	ASN
1	T	573	ASN
1	T	575	GLN
1	U	31	ASN
1	U	40	GLN
1	U	104	HIS
1	U	135	GLN
1	U	142	GLN
1	U	150	HIS
1	U	203	ASN
1	U	218	GLN
1	U	291	GLN
1	U	297	HIS
1	U	508	ASN
1	U	575	GLN
1	V	31	ASN
1	V	40	GLN
1	V	74	ASN
1	V	104	HIS
1	V	142	GLN
1	V	203	ASN
1	V	218	GLN
1	V	291	GLN
1	V	297	HIS

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Mol	Chain	Res	Type
1	V	508	ASN
1	V	575	GLN
1	W	40	GLN
1	W	74	ASN
1	W	104	HIS
1	W	142	GLN
1	W	203	ASN
1	W	218	GLN
1	W	291	GLN
1	W	297	HIS
1	W	375	ASN
1	W	508	ASN
1	W	575	GLN
1	X	31	ASN
1	X	40	GLN
1	X	74	ASN
1	X	104	HIS
1	X	142	GLN
1	X	203	ASN
1	X	218	GLN
1	X	291	GLN
1	X	297	HIS
1	X	508	ASN
1	X	575	GLN
2	l	138	ASN
2	m	138	ASN
2	p	138	ASN
2	q	138	ASN
2	r	138	ASN
2	s	138	ASN
2	t	138	ASN
2	u	138	ASN
2	v	138	ASN
1	A	31	ASN
1	A	56	GLN
1	A	73	GLN
1	A	74	ASN
1	A	112	ASN
1	A	118	GLN
1	A	135	GLN
1	A	155	HIS
1	A	161	ASN

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Mol	Chain	Res	Type
1	A	177	HIS
1	A	182	ASN
1	A	202	GLN
1	A	214	GLN
1	A	218	GLN
1	A	236	GLN
1	A	291	GLN
1	A	297	HIS
1	A	337	ASN
1	A	439	ASN
1	A	529	GLN
1	A	530	GLN
1	A	555	GLN
1	A	597	GLN
1	B	31	ASN
1	B	56	GLN
1	B	73	GLN
1	B	74	ASN
1	B	112	ASN
1	B	118	GLN
1	B	135	GLN
1	B	161	ASN
1	B	177	HIS
1	B	182	ASN
1	B	202	GLN
1	B	214	GLN
1	B	218	GLN
1	B	236	GLN
1	B	291	GLN
1	B	297	HIS
1	B	337	ASN
1	B	375	ASN
1	B	439	ASN
1	B	529	GLN
1	B	530	GLN
1	B	555	GLN
1	B	597	GLN
1	C	31	ASN
1	C	56	GLN
1	C	73	GLN
1	C	74	ASN
1	C	112	ASN

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Mol	Chain	Res	Type
1	C	118	GLN
1	C	135	GLN
1	C	161	ASN
1	C	177	HIS
1	C	182	ASN
1	C	202	GLN
1	C	214	GLN
1	C	218	GLN
1	C	236	GLN
1	C	291	GLN
1	C	297	HIS
1	C	337	ASN
1	C	439	ASN
1	C	450	GLN
1	C	529	GLN
1	C	530	GLN
1	C	555	GLN
1	C	597	GLN
1	D	31	ASN
1	D	56	GLN
1	D	73	GLN
1	D	74	ASN
1	D	112	ASN
1	D	118	GLN
1	D	135	GLN
1	D	161	ASN
1	D	177	HIS
1	D	182	ASN
1	D	202	GLN
1	D	214	GLN
1	D	218	GLN
1	D	236	GLN
1	D	291	GLN
1	D	297	HIS
1	D	337	ASN
1	D	375	ASN
1	D	439	ASN
1	D	450	GLN
1	D	529	GLN
1	D	530	GLN
1	D	555	GLN
1	D	597	GLN

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Mol	Chain	Res	Type
1	E	31	ASN
1	E	56	GLN
1	E	73	GLN
1	E	74	ASN
1	E	112	ASN
1	E	118	GLN
1	E	135	GLN
1	E	161	ASN
1	E	177	HIS
1	E	182	ASN
1	E	202	GLN
1	E	214	GLN
1	E	218	GLN
1	E	236	GLN
1	E	291	GLN
1	E	297	HIS
1	E	337	ASN
1	E	439	ASN
1	E	529	GLN
1	E	530	GLN
1	E	555	GLN
1	E	597	GLN
1	F	31	ASN
1	F	56	GLN
1	F	73	GLN
1	F	74	ASN
1	F	112	ASN
1	F	118	GLN
1	F	135	GLN
1	F	161	ASN
1	F	177	HIS
1	F	182	ASN
1	F	202	GLN
1	F	214	GLN
1	F	218	GLN
1	F	236	GLN
1	F	291	GLN
1	F	297	HIS
1	F	337	ASN
1	F	439	ASN
1	F	450	GLN
1	F	529	GLN

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Mol	Chain	Res	Type
1	F	530	GLN
1	F	555	GLN
1	F	575	GLN
1	F	597	GLN
1	G	31	ASN
1	G	56	GLN
1	G	73	GLN
1	G	74	ASN
1	G	112	ASN
1	G	118	GLN
1	G	135	GLN
1	G	161	ASN
1	G	177	HIS
1	G	182	ASN
1	G	202	GLN
1	G	214	GLN
1	G	218	GLN
1	G	236	GLN
1	G	291	GLN
1	G	297	HIS
1	G	337	ASN
1	G	439	ASN
1	G	450	GLN
1	G	529	GLN
1	G	530	GLN
1	G	555	GLN
1	G	597	GLN
1	H	31	ASN
1	H	56	GLN
1	H	73	GLN
1	H	74	ASN
1	H	112	ASN
1	H	118	GLN
1	H	135	GLN
1	H	161	ASN
1	H	177	HIS
1	H	182	ASN
1	H	202	GLN
1	H	214	GLN
1	H	218	GLN
1	H	236	GLN
1	H	291	GLN

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Mol	Chain	Res	Type
1	H	297	HIS
1	H	337	ASN
1	H	439	ASN
1	H	450	GLN
1	H	529	GLN
1	H	530	GLN
1	H	555	GLN
1	H	597	GLN
1	I	31	ASN
1	I	56	GLN
1	I	73	GLN
1	I	74	ASN
1	I	112	ASN
1	I	118	GLN
1	I	135	GLN
1	I	161	ASN
1	I	177	HIS
1	I	182	ASN
1	I	202	GLN
1	I	214	GLN
1	I	218	GLN
1	I	236	GLN
1	I	291	GLN
1	I	297	HIS
1	I	337	ASN
1	I	439	ASN
1	I	450	GLN
1	I	529	GLN
1	I	530	GLN
1	I	555	GLN
1	I	597	GLN
1	J	31	ASN
1	J	56	GLN
1	J	73	GLN
1	J	74	ASN
1	J	112	ASN
1	J	118	GLN
1	J	135	GLN
1	J	161	ASN
1	J	177	HIS
1	J	182	ASN
1	J	202	GLN

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Mol	Chain	Res	Type
1	J	214	GLN
1	J	218	GLN
1	J	236	GLN
1	J	291	GLN
1	J	297	HIS
1	J	337	ASN
1	J	439	ASN
1	J	529	GLN
1	J	530	GLN
1	J	555	GLN
1	J	597	GLN
1	K	31	ASN
1	K	56	GLN
1	K	73	GLN
1	K	74	ASN
1	K	112	ASN
1	K	118	GLN
1	K	135	GLN
1	K	161	ASN
1	K	177	HIS
1	K	182	ASN
1	K	202	GLN
1	K	214	GLN
1	K	218	GLN
1	K	236	GLN
1	K	291	GLN
1	K	297	HIS
1	K	337	ASN
1	K	439	ASN
1	K	450	GLN
1	K	529	GLN
1	K	530	GLN
1	K	555	GLN
1	K	597	GLN
1	L	31	ASN
1	L	56	GLN
1	L	73	GLN
1	L	74	ASN
1	L	112	ASN
1	L	118	GLN
1	L	135	GLN
1	L	161	ASN

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Mol	Chain	Res	Type
1	L	177	HIS
1	L	182	ASN
1	L	202	GLN
1	L	214	GLN
1	L	218	GLN
1	L	236	GLN
1	L	291	GLN
1	L	297	HIS
1	L	337	ASN
1	L	439	ASN
1	L	450	GLN
1	L	529	GLN
1	L	530	GLN
1	L	555	GLN
1	L	597	GLN
2	Y	94	HIS
2	Y	126	GLN
2	Z	94	HIS
2	Z	126	GLN
2	a	94	HIS
2	a	126	GLN
2	b	94	HIS
2	b	126	GLN
2	c	94	HIS
2	c	126	GLN
2	d	94	HIS
2	e	94	HIS
2	e	126	GLN
2	f	94	HIS
2	g	94	HIS
2	g	126	GLN
2	h	94	HIS
2	h	126	GLN
2	i	94	HIS
2	i	126	GLN
2	j	94	HIS
2	j	126	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	552/602 (91%)	2.87	373 (67%)	0	0	22, 84, 246, 379	0
1	B	552/602 (91%)	2.80	368 (66%)	0	0	23, 85, 246, 379	0
1	C	552/602 (91%)	2.82	376 (68%)	0	0	26, 84, 246, 379	0
1	D	552/602 (91%)	2.66	352 (63%)	0	0	25, 84, 246, 379	0
1	E	552/602 (91%)	2.74	357 (64%)	0	0	25, 84, 246, 379	0
1	F	552/602 (91%)	2.73	358 (64%)	0	0	25, 84, 246, 379	0
1	G	552/602 (91%)	2.79	360 (65%)	0	0	30, 84, 246, 379	0
1	H	552/602 (91%)	2.66	341 (61%)	0	0	26, 86, 246, 379	0
1	I	552/602 (91%)	2.80	378 (68%)	0	0	31, 88, 246, 379	0
1	J	552/602 (91%)	3.06	397 (71%)	0	0	33, 96, 246, 379	0
1	K	552/602 (91%)	2.99	393 (71%)	0	0	26, 88, 245, 379	0
1	L	552/602 (91%)	3.01	391 (70%)	0	0	24, 87, 246, 379	0
1	M	552/602 (91%)	2.34	298 (53%)	0	0	15, 70, 209, 327	0
1	N	551/602 (91%)	2.41	304 (55%)	0	0	18, 69, 209, 327	0
1	O	552/602 (91%)	2.49	316 (57%)	0	0	15, 69, 209, 326	0
1	P	552/602 (91%)	2.50	309 (55%)	0	0	15, 70, 209, 327	0
1	Q	552/602 (91%)	2.47	317 (57%)	0	0	15, 69, 209, 326	0
1	R	550/602 (91%)	2.55	322 (58%)	0	0	17, 69, 209, 327	0
1	S	552/602 (91%)	2.37	284 (51%)	0	0	19, 70, 209, 326	0
1	T	552/602 (91%)	2.35	303 (54%)	0	0	15, 70, 208, 326	0
1	U	552/602 (91%)	2.59	338 (61%)	0	0	17, 69, 209, 327	0
1	V	552/602 (91%)	2.42	312 (56%)	0	0	18, 70, 209, 327	0
1	W	552/602 (91%)	2.51	312 (56%)	0	0	17, 70, 209, 326	0
1	X	552/602 (91%)	2.45	322 (58%)	0	0	14, 69, 209, 326	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
2	Y	146/166 (87%)	2.72	99 (67%) 0 0	38, 75, 221, 304	0
2	Z	146/166 (87%)	2.76	102 (69%) 0 0	37, 73, 222, 304	0
2	a	146/166 (87%)	2.61	87 (59%) 0 0	37, 77, 221, 304	0
2	b	146/166 (87%)	2.71	94 (64%) 0 0	39, 72, 221, 304	0
2	c	146/166 (87%)	2.93	109 (74%) 0 0	39, 72, 222, 305	0
2	d	146/166 (87%)	2.98	106 (72%) 0 0	35, 72, 222, 304	0
2	e	146/166 (87%)	2.69	91 (62%) 0 0	37, 73, 220, 304	0
2	f	146/166 (87%)	2.94	109 (74%) 0 0	39, 74, 222, 304	0
2	g	146/166 (87%)	3.02	101 (69%) 0 0	44, 75, 221, 304	0
2	h	146/166 (87%)	2.82	102 (69%) 0 0	38, 75, 221, 305	0
2	i	146/166 (87%)	3.03	106 (72%) 0 0	40, 75, 221, 304	0
2	j	146/166 (87%)	2.83	103 (70%) 0 0	36, 75, 222, 305	0
2	k	145/166 (87%)	2.29	74 (51%) 0 0	25, 57, 204, 314	0
2	l	145/166 (87%)	2.40	84 (57%) 0 0	28, 56, 204, 314	0
2	m	145/166 (87%)	2.35	75 (51%) 0 0	30, 59, 203, 314	0
2	n	145/166 (87%)	2.69	88 (60%) 0 0	23, 55, 204, 314	0
2	o	145/166 (87%)	2.41	85 (58%) 0 0	26, 57, 204, 314	0
2	p	145/166 (87%)	2.30	77 (53%) 0 0	27, 57, 204, 314	0
2	q	145/166 (87%)	2.41	78 (53%) 0 0	29, 58, 204, 314	0
2	r	145/166 (87%)	2.27	72 (49%) 0 0	26, 57, 205, 314	0
2	s	145/166 (87%)	2.10	63 (43%) 0 1	30, 58, 204, 314	0
2	t	145/166 (87%)	2.17	66 (45%) 0 0	31, 58, 204, 314	0
2	u	145/166 (87%)	2.12	63 (43%) 0 1	30, 58, 204, 314	0
2	v	145/166 (87%)	2.23	75 (51%) 0 0	29, 57, 204, 314	0
All	All	16737/18432 (90%)	2.63	10290 (61%) 0 0	14, 76, 228, 379	0

All (10290) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	c	28	VAL	16.7
1	E	32	ASP	15.0
1	F	32	ASP	14.7
1	L	183	GLY	13.9
1	E	13	SER	12.8

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Mol	Chain	Res	Type	RSRZ
1	C	564	GLY	12.2
1	D	170	ALA	11.8
1	E	35	PHE	11.6
1	T	439	ASN	11.6
1	B	417	THR	11.6
2	e	28	VAL	11.5
1	N	564	GLY	11.2
1	D	32	ASP	11.0
1	A	183	GLY	10.9
1	C	32	ASP	10.9
1	H	564	GLY	10.7
1	C	260	ASP	10.6
1	F	564	GLY	10.5
1	M	564	GLY	10.5
1	L	25	ALA	10.3
1	G	564	GLY	10.3
2	q	94	ASP	10.0
1	W	564	GLY	10.0
1	C	248	LYS	9.9
1	D	25	ALA	9.9
1	S	32	ASP	9.8
1	J	25	ALA	9.8
1	A	42	ASP	9.7
1	Q	173	CYS	9.7
1	C	41	TRP	9.6
2	g	153	ASN	9.5
1	B	564	GLY	9.5
2	q	39	ASP	9.4
1	C	434	THR	9.4
1	V	564	GLY	9.3
2	m	144	ASN	9.3
1	B	25	ALA	9.3
1	M	523	SER	9.3
2	q	145	GLU	9.2
1	G	186	ASP	9.2
1	J	437	GLN	9.2
1	N	456	ALA	9.1
1	X	564	GLY	9.1
1	O	173	CYS	9.1
1	J	252	LYS	9.1
1	K	25	ALA	9.0
1	P	439	ASN	9.0

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Mol	Chain	Res	Type	RSRZ
1	L	173	CYS	8.9
1	O	564	GLY	8.8
1	F	565	VAL	8.8
2	p	145	GLU	8.8
1	J	456	ALA	8.7
1	G	28	GLU	8.7
1	J	410	SER	8.7
1	C	25	ALA	8.6
1	H	32	ASP	8.6
1	U	449	PHE	8.6
1	A	41	TRP	8.5
1	Q	564	GLY	8.5
1	T	32	ASP	8.5
1	A	246	TYR	8.5
1	J	253	ASP	8.5
1	X	449	PHE	8.5
1	J	162	SER	8.5
1	E	25	ALA	8.4
1	J	23	ASP	8.4
1	I	564	GLY	8.4
1	E	564	GLY	8.3
1	D	13	SER	8.3
1	G	456	ALA	8.3
2	u	145	GLU	8.3
1	R	254	VAL	8.3
1	E	41	TRP	8.3
1	I	173	CYS	8.3
1	D	548	GLU	8.3
1	L	564	GLY	8.2
1	G	25	ALA	8.2
1	B	32	ASP	8.2
1	B	13	SER	8.2
1	P	183	GLY	8.1
2	p	39	ASP	8.1
1	Q	15	PHE	8.1
1	L	281	ILE	8.0
2	b	28	VAL	8.0
1	R	564	GLY	8.0
1	A	25	ALA	8.0
2	n	79	ALA	8.0
2	f	153	ASN	8.0
1	E	204	PRO	8.0

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Mol	Chain	Res	Type	RSRZ
1	J	563	LYS	8.0
1	O	439	ASN	7.9
1	O	25	ALA	7.9
1	H	451	ASP	7.9
1	J	564	GLY	7.9
1	A	563	LYS	7.9
1	D	564	GLY	7.9
1	L	15	PHE	7.9
2	n	39	ASP	7.9
1	J	346	LYS	7.9
2	a	28	VAL	7.8
1	U	25	ALA	7.8
1	X	547	PRO	7.8
1	T	35	PHE	7.8
1	A	32	ASP	7.8
1	H	560	LEU	7.8
1	K	560	LEU	7.8
1	Q	439	ASN	7.8
1	W	439	ASN	7.8
1	K	439	ASN	7.8
1	J	130	THR	7.7
1	I	331	ASN	7.7
1	G	556	TYR	7.7
1	U	564	GLY	7.7
1	E	549	TYR	7.7
1	A	564	GLY	7.7
2	n	145	GLU	7.7
1	E	58	ASP	7.7
1	L	156	VAL	7.7
1	K	31	ASN	7.6
1	K	450	GLN	7.6
1	F	556	TYR	7.6
1	G	213	THR	7.6
1	W	136	SER	7.6
1	D	159	ASP	7.6
1	P	444	LEU	7.6
1	R	456	ALA	7.6
2	n	144	ASN	7.6
1	I	115	VAL	7.6
1	C	72	ARG	7.6
1	S	173	CYS	7.5
1	E	456	ALA	7.5

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Mol	Chain	Res	Type	RSRZ
1	S	35	PHE	7.5
1	K	32	ASP	7.5
2	l	92	ALA	7.5
1	X	439	ASN	7.5
1	G	563	LYS	7.5
2	s	145	GLU	7.5
1	C	15	PHE	7.5
1	B	563	LYS	7.5
1	N	250	ASP	7.5
1	R	89	ASP	7.5
2	k	39	ASP	7.5
2	l	39	ASP	7.5
1	C	219	ILE	7.4
1	V	136	SER	7.4
1	K	281	ILE	7.4
1	Q	168	SER	7.4
1	C	335	SER	7.4
1	O	15	PHE	7.4
2	f	37	VAL	7.4
1	F	25	ALA	7.4
2	s	39	ASP	7.4
2	u	39	ASP	7.4
1	L	602	GLY	7.3
1	A	338	ALA	7.3
1	G	29	ALA	7.3
1	G	31	ASN	7.3
1	N	560	LEU	7.3
1	O	563	LYS	7.3
1	E	324	LYS	7.3
1	K	13	SER	7.3
1	D	29	ALA	7.3
1	P	246	TYR	7.3
1	S	400	ALA	7.3
1	S	434	THR	7.3
1	L	188	ALA	7.3
1	V	31	ASN	7.3
1	G	177	HIS	7.3
1	K	420	VAL	7.3
2	q	28	VAL	7.3
1	H	114	ALA	7.3
2	h	155	TRP	7.3
2	d	28	VAL	7.3

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Mol	Chain	Res	Type	RSRZ
1	V	400	ALA	7.3
1	T	99	ARG	7.3
1	A	339	ASP	7.2
1	B	42	ASP	7.2
1	I	449	PHE	7.2
1	X	173	CYS	7.2
1	A	186	ASP	7.2
1	R	173	CYS	7.2
1	S	437	GLN	7.2
2	b	49	LEU	7.2
1	G	183	GLY	7.2
1	J	173	CYS	7.2
1	Q	255	ILE	7.2
1	S	41	TRP	7.2
1	W	162	SER	7.2
1	H	523	SER	7.2
1	K	444	LEU	7.2
1	M	253	ASP	7.1
1	K	433	ASP	7.1
1	B	41	TRP	7.1
2	e	155	TRP	7.1
1	C	204	PRO	7.1
1	K	434	THR	7.1
1	Q	169	ASP	7.1
1	Q	50	THR	7.1
1	S	50	THR	7.1
2	i	28	VAL	7.1
2	n	62	ASP	7.1
2	o	146	TRP	7.1
1	A	28	GLU	7.1
1	N	20	THR	7.1
1	H	49	THR	7.1
1	L	444	LEU	7.1
1	Q	25	ALA	7.1
1	U	15	PHE	7.1
1	L	560	LEU	7.1
1	G	114	ALA	7.1
2	i	110	ALA	7.1
1	U	99	ARG	7.1
1	I	451	ASP	7.0
1	G	33	LEU	7.0
2	q	75	LEU	7.0

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Mol	Chain	Res	Type	RSRZ
2	g	148	SER	7.0
1	P	50	THR	7.0
2	r	39	ASP	7.0
1	U	346	LYS	7.0
1	M	169	ASP	7.0
1	N	169	ASP	7.0
2	n	22	ASP	7.0
2	j	31	ASP	7.0
1	M	451	ASP	7.0
2	t	39	ASP	7.0
1	I	563	LYS	7.0
1	E	556	TYR	7.0
1	L	445	GLU	7.0
1	R	516	CYS	7.0
1	K	437	GLN	7.0
1	V	449	PHE	7.0
1	S	564	GLY	6.9
1	P	445	GLU	6.9
1	P	38	VAL	6.9
1	F	183	GLY	6.9
1	U	11	ILE	6.9
1	T	41	TRP	6.9
1	D	28	GLU	6.9
1	H	541	LYS	6.9
1	V	558	THR	6.9
1	K	174	THR	6.9
1	R	188	ALA	6.9
1	S	293	ILE	6.9
1	L	420	VAL	6.9
1	J	436	ASN	6.9
2	o	110	GLY	6.9
1	A	312	ASP	6.9
1	S	25	ALA	6.9
1	C	563	LYS	6.9
1	I	437	GLN	6.9
1	G	293	ILE	6.9
1	W	169	ASP	6.9
2	r	94	ASP	6.9
1	A	559	LEU	6.9
1	K	550	GLN	6.8
2	Z	62	GLY	6.8
1	C	264	ILE	6.8

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Mol	Chain	Res	Type	RSRZ
2	n	28	VAL	6.8
1	T	162	SER	6.8
1	D	173	CYS	6.8
1	N	28	GLU	6.8
2	j	154	GLU	6.8
1	A	50	THR	6.8
1	V	183	GLY	6.8
1	W	230	GLU	6.8
1	G	433	ASP	6.8
1	I	28	GLU	6.8
1	Q	449	PHE	6.8
1	E	563	LYS	6.8
1	R	50	THR	6.8
1	T	549	TYR	6.8
1	N	173	CYS	6.8
1	G	378	ASP	6.8
1	U	417	THR	6.8
2	d	77	ALA	6.8
1	F	563	LYS	6.8
1	K	252	LYS	6.8
2	k	9	LEU	6.7
1	R	25	ALA	6.7
1	R	437	GLN	6.7
1	A	225	VAL	6.7
1	W	563	LYS	6.7
1	E	15	PHE	6.7
2	r	145	GLU	6.7
1	Q	444	LEU	6.7
1	T	339	ASP	6.7
1	L	28	GLU	6.7
2	l	14	LEU	6.7
1	K	38	VAL	6.7
1	W	133	GLU	6.7
2	i	155	TRP	6.7
1	N	400	ALA	6.7
1	W	259	ALA	6.7
1	D	248	LYS	6.7
1	I	407	ALA	6.7
1	J	108	LYS	6.7
1	C	58	ASP	6.7
2	k	94	ASP	6.7
1	O	130	THR	6.7

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Mol	Chain	Res	Type	RSRZ
1	P	20	THR	6.7
1	A	417	THR	6.7
1	C	99	ARG	6.7
1	U	50	THR	6.6
1	L	41	TRP	6.6
2	a	47	ASP	6.6
1	Q	560	LEU	6.6
1	V	565	VAL	6.6
2	k	144	ASN	6.6
2	u	144	ASN	6.6
1	X	443	ASP	6.6
1	C	293	ILE	6.6
1	H	325	ASP	6.6
1	H	563	LYS	6.6
1	R	38	VAL	6.6
2	h	90	SER	6.6
1	X	248	LYS	6.6
1	B	248	LYS	6.6
1	O	253	ASP	6.6
1	E	339	ASP	6.6
1	J	451	ASP	6.6
1	K	18	ASP	6.6
1	B	371	TYR	6.6
1	U	70	GLU	6.6
1	F	360	GLU	6.6
1	G	137	PRO	6.6
1	R	32	ASP	6.6
1	S	549	TYR	6.6
1	Q	346	LYS	6.5
1	H	248	LYS	6.5
1	B	35	PHE	6.5
1	L	335	SER	6.5
1	T	564	GLY	6.5
2	Y	48	ASP	6.5
1	F	388	PRO	6.5
2	r	28	VAL	6.5
1	N	220	ALA	6.5
1	G	400	ALA	6.5
2	a	21	ALA	6.5
1	C	437	GLN	6.5
1	D	254	VAL	6.5
2	i	88	ALA	6.5

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Mol	Chain	Res	Type	RSRZ
1	F	589	GLU	6.5
2	t	145	GLU	6.5
1	N	23	ASP	6.5
2	Z	103	ASP	6.5
1	A	592	TRP	6.5
1	D	41	TRP	6.5
1	J	264	ILE	6.5
2	h	58	GLN	6.5
1	U	248	LYS	6.5
1	L	29	ALA	6.5
1	R	560	LEU	6.5
1	H	237	ASP	6.5
1	N	31	ASN	6.4
1	F	259	ALA	6.4
1	L	174	THR	6.4
1	W	12	LEU	6.4
1	G	576	LEU	6.4
1	E	173	CYS	6.4
1	I	108	LYS	6.4
1	G	560	LEU	6.4
1	H	452	ASN	6.4
2	d	65	THR	6.4
1	D	162	SER	6.4
1	F	136	SER	6.4
1	S	28	GLU	6.4
1	C	547	PRO	6.4
1	K	367	ASP	6.4
1	W	25	ALA	6.4
2	e	24	ARG	6.4
1	N	240	THR	6.4
1	K	130	THR	6.4
1	C	35	PHE	6.4
1	K	15	PHE	6.4
2	b	53	MET	6.4
1	C	312	ASP	6.4
2	e	48	ASP	6.4
1	H	173	CYS	6.4
1	Q	31	ASN	6.4
1	E	50	THR	6.4
1	J	174	THR	6.4
2	l	144	ASN	6.4
1	J	447	TYR	6.4

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Mol	Chain	Res	Type	RSRZ
1	H	456	ALA	6.3
1	K	387	GLN	6.3
1	S	248	LYS	6.3
1	L	248	LYS	6.3
1	U	173	CYS	6.3
1	H	161	ASN	6.3
1	B	553	LEU	6.3
1	D	437	GLN	6.3
1	J	450	GLN	6.3
1	W	556	TYR	6.3
1	C	439	ASN	6.3
2	q	14	LEU	6.3
1	G	168	SER	6.3
1	H	25	ALA	6.3
1	L	17	ALA	6.3
2	s	81	SER	6.3
1	P	281	ILE	6.3
1	J	157	ILE	6.3
1	Q	159	ASP	6.3
1	A	443	ASP	6.3
1	C	92	ASP	6.3
1	R	240	THR	6.3
1	J	38	VAL	6.3
1	B	556	TYR	6.3
1	M	173	CYS	6.3
1	J	24	GLU	6.3
1	O	6	ASN	6.3
1	G	136	SER	6.3
2	q	53	GLY	6.3
1	D	58	ASP	6.3
1	O	543	PRO	6.3
1	L	403	TYR	6.3
1	M	439	ASN	6.3
1	U	439	ASN	6.3
1	C	550	GLN	6.3
2	c	48	ASP	6.2
1	K	410	SER	6.2
2	Y	53	MET	6.2
1	R	445	GLU	6.2
1	D	547	PRO	6.2
1	L	285	ALA	6.2
2	s	94	ASP	6.2

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Mol	Chain	Res	Type	RSRZ
2	v	39	ASP	6.2
1	J	10	SER	6.2
1	N	115	VAL	6.2
1	J	444	LEU	6.2
1	N	601	GLN	6.2
1	P	387	GLN	6.2
1	Q	437	GLN	6.2
1	X	346	LYS	6.2
1	E	547	PRO	6.2
1	G	518	THR	6.2
1	J	107	ALA	6.2
1	K	386	THR	6.2
1	N	445	GLU	6.2
1	F	561	ASP	6.2
1	L	77	ASP	6.2
2	a	24	ARG	6.2
1	L	271	ILE	6.2
1	I	31	ASN	6.2
2	m	14	LEU	6.2
1	U	386	THR	6.2
1	W	50	THR	6.2
2	n	66	PRO	6.2
1	U	55	GLY	6.2
1	X	35	PHE	6.2
1	B	565	VAL	6.2
1	E	439	ASN	6.2
1	H	41	TRP	6.2
1	T	13	SER	6.2
1	F	387	GLN	6.2
1	G	450	GLN	6.2
2	h	21	ALA	6.2
1	V	246	TYR	6.2
1	U	159	ASP	6.2
1	U	263	PHE	6.2
1	J	247	PHE	6.2
2	n	14	LEU	6.2
2	n	25	LEU	6.2
2	m	28	VAL	6.1
1	P	180	SER	6.1
1	W	279	SER	6.1
1	A	245	SER	6.1
1	K	563	LYS	6.1

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Mol	Chain	Res	Type	RSRZ
1	I	254	VAL	6.1
1	J	428	GLY	6.1
1	G	451	ASP	6.1
2	g	90	SER	6.1
1	T	240	THR	6.1
1	R	549	TYR	6.1
1	E	193	LEU	6.1
1	L	449	PHE	6.1
2	t	28	VAL	6.1
2	v	28	VAL	6.1
1	G	41	TRP	6.1
1	V	182	ASN	6.1
2	s	144	ASN	6.1
1	C	313	LYS	6.1
1	I	346	LYS	6.1
1	I	180	SER	6.1
1	U	138	THR	6.1
1	J	50	THR	6.1
1	U	35	PHE	6.1
1	M	32	ASP	6.1
1	X	339	ASP	6.1
2	g	31	ASP	6.1
1	S	259	ALA	6.1
1	I	357	ALA	6.1
1	K	456	ALA	6.1
2	i	58	GLN	6.1
1	D	10	SER	6.1
1	G	32	ASP	6.1
2	b	24	ARG	6.0
1	A	173	CYS	6.0
1	E	558	THR	6.0
1	G	173	CYS	6.0
1	K	447	TYR	6.0
1	L	246	TYR	6.0
1	O	407	ALA	6.0
1	W	110	ALA	6.0
1	W	408	ALA	6.0
1	I	232	ALA	6.0
1	J	533	ALA	6.0
2	c	77	ALA	6.0
1	X	77	ASP	6.0
1	B	260	ASP	6.0

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Mol	Chain	Res	Type	RSRZ
1	L	8	LEU	6.0
2	t	14	LEU	6.0
1	L	205	ASN	6.0
1	G	565	VAL	6.0
2	h	53	MET	6.0
1	M	50	THR	6.0
1	V	248	LYS	6.0
1	J	516	CYS	6.0
1	N	509	ASP	6.0
1	P	42	ASP	6.0
1	X	42	ASP	6.0
1	A	58	ASP	6.0
1	B	196	ASP	6.0
1	M	252	LYS	6.0
1	A	185	GLU	6.0
1	L	50	THR	6.0
1	L	178	SER	6.0
1	Q	283	CYS	6.0
1	P	29	ALA	6.0
1	F	456	ALA	6.0
1	S	507	LEU	6.0
1	H	33	LEU	6.0
2	d	84	LEU	6.0
2	i	49	LEU	6.0
1	V	388	PRO	6.0
1	W	387	GLN	6.0
1	L	388	PRO	6.0
1	B	449	PHE	6.0
1	H	23	ASP	6.0
1	I	84	ASP	6.0
1	K	159	ASP	6.0
1	K	284	THR	6.0
1	I	99	ARG	6.0
2	p	14	LEU	6.0
2	k	28	VAL	6.0
1	G	426	ASN	6.0
1	B	549	TYR	6.0
2	d	134	ARG	6.0
1	X	41	TRP	5.9
2	t	89	CYS	5.9
1	M	449	PHE	5.9
1	W	388	PRO	5.9

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Mol	Chain	Res	Type	RSRZ
1	E	248	LYS	5.9
1	K	547	PRO	5.9
1	H	312	ASP	5.9
1	O	507	LEU	5.9
1	T	193	LEU	5.9
1	U	264	ILE	5.9
1	V	293	ILE	5.9
1	B	409	THR	5.9
2	i	24	ARG	5.9
1	D	294	ALA	5.9
1	P	563	LYS	5.9
1	R	410	SER	5.9
1	N	41	TRP	5.9
1	C	430	VAL	5.9
1	B	199	PRO	5.9
1	F	449	PHE	5.9
1	K	173	CYS	5.9
1	W	445	GLU	5.9
1	D	84	ASP	5.9
1	D	549	TYR	5.9
1	F	16	ASP	5.9
1	J	21	ALA	5.9
1	J	138	THR	5.9
1	L	282	THR	5.9
1	L	344	THR	5.9
2	j	153	ASN	5.9
1	D	563	LYS	5.9
1	E	279	SER	5.9
1	F	13	SER	5.9
1	G	449	PHE	5.9
2	n	110	GLY	5.9
1	P	144	ILE	5.9
1	U	418	LEU	5.9
1	J	271	ILE	5.9
1	K	144	ILE	5.9
1	N	325	ASP	5.9
1	B	346	LYS	5.9
2	o	148	TYR	5.9
2	o	144	ASN	5.9
2	i	52	MET	5.9
1	O	41	TRP	5.9
1	C	259	ALA	5.9

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Mol	Chain	Res	Type	RSRZ
2	h	110	ALA	5.9
1	W	284	THR	5.9
1	C	409	THR	5.9
1	D	439	ASN	5.9
1	K	84	ASP	5.9
2	u	86	ASN	5.9
2	i	48	ASP	5.9
1	P	15	PHE	5.9
1	U	41	TRP	5.9
1	W	139	SER	5.9
1	A	8	LEU	5.9
1	I	248	LYS	5.9
1	E	259	ALA	5.9
2	g	154	GLU	5.9
1	J	254	VAL	5.8
1	N	449	PHE	5.8
1	R	443	ASP	5.8
1	L	203	ASN	5.8
1	B	33	LEU	5.8
2	t	97	LEU	5.8
1	S	563	LYS	5.8
1	E	170	ALA	5.8
2	j	108	ALA	5.8
1	D	445	GLU	5.8
1	D	99	ARG	5.8
1	F	240	THR	5.8
1	H	35	PHE	5.8
1	P	436	ASN	5.8
1	H	159	ASP	5.8
1	L	18	ASP	5.8
1	K	210	PRO	5.8
1	E	538	LEU	5.8
2	m	75	LEU	5.8
1	T	122	GLY	5.8
1	I	293	ILE	5.8
1	D	450	GLN	5.8
1	E	437	GLN	5.8
1	E	139	SER	5.8
1	C	91	ALA	5.8
1	J	121	ALA	5.8
2	s	28	VAL	5.8
1	M	99	ARG	5.8

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Mol	Chain	Res	Type	RSRZ
1	B	99	ARG	5.8
1	O	449	PHE	5.8
1	Q	246	TYR	5.8
1	V	50	THR	5.8
1	F	282	THR	5.8
1	N	248	LYS	5.8
1	N	159	ASP	5.8
1	S	451	ASP	5.8
1	E	159	ASP	5.8
2	j	48	ASP	5.8
2	j	100	ILE	5.8
2	g	101	ALA	5.8
1	J	335	SER	5.8
1	P	93	VAL	5.8
2	h	121	GLU	5.8
1	L	447	TYR	5.8
1	T	19	TRP	5.8
1	C	42	ASP	5.8
2	g	73	GLU	5.8
2	i	87	SER	5.8
1	H	449	PHE	5.8
1	L	346	LYS	5.8
1	R	246	TYR	5.8
2	f	84	LEU	5.8
1	O	50	THR	5.8
1	K	50	THR	5.8
1	L	417	THR	5.8
1	Q	75	PRO	5.8
1	R	439	ASN	5.8
1	S	592	TRP	5.8
1	D	101	ASP	5.7
1	B	437	GLN	5.7
1	A	560	LEU	5.7
1	V	542	THR	5.7
1	L	20	THR	5.7
2	d	138	PRO	5.7
1	W	41	TRP	5.7
1	J	184	TRP	5.7
1	E	205	ASN	5.7
1	J	331	ASN	5.7
1	B	383	ASP	5.7
1	C	565	VAL	5.7

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Mol	Chain	Res	Type	RSRZ
1	D	449	PHE	5.7
1	F	28	GLU	5.7
1	J	445	GLU	5.7
2	o	145	GLU	5.7
2	g	123	LEU	5.7
2	e	99	ARG	5.7
1	F	41	TRP	5.7
1	S	439	ASN	5.7
1	K	399	GLN	5.7
1	I	192	ASP	5.7
1	S	15	PHE	5.7
1	T	180	SER	5.7
1	W	219	ILE	5.7
1	A	139	SER	5.7
1	H	27	ARG	5.7
1	B	318	GLY	5.7
1	V	195	ALA	5.7
1	B	259	ALA	5.7
1	F	313	LYS	5.7
1	O	557	PHE	5.7
1	L	194	ASP	5.7
1	L	549	TYR	5.7
1	N	388	PRO	5.7
1	V	168	SER	5.7
1	I	448	VAL	5.7
1	D	592	TRP	5.7
1	S	153	CYS	5.7
1	C	263	PHE	5.7
1	I	439	ASN	5.7
1	G	159	ASP	5.7
1	K	58	ASP	5.7
2	o	39	ASP	5.7
2	b	99	ARG	5.7
2	e	107	GLU	5.7
1	E	219	ILE	5.7
1	R	388	PRO	5.6
1	O	254	VAL	5.6
1	P	550	GLN	5.6
2	c	98	CYS	5.6
1	C	401	ASN	5.6
1	K	230	GLU	5.6
1	L	76	ILE	5.6

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Mol	Chain	Res	Type	RSRZ
1	E	84	ASP	5.6
1	G	561	ASP	5.6
2	o	22	ASP	5.6
1	W	246	TYR	5.6
1	P	25	ALA	5.6
1	A	107	ALA	5.6
1	J	115	VAL	5.6
2	e	53	MET	5.6
2	g	37	VAL	5.6
1	O	8	LEU	5.6
1	C	538	LEU	5.6
1	T	15	PHE	5.6
1	I	41	TRP	5.6
2	n	146	TRP	5.6
1	Q	450	GLN	5.6
1	K	280	ILE	5.6
1	K	510	ILE	5.6
2	u	95	TYR	5.6
1	E	220	ALA	5.6
2	g	21	ALA	5.6
1	R	418	LEU	5.6
1	A	418	LEU	5.6
2	r	25	LEU	5.6
2	b	84	LEU	5.6
2	g	122	LEU	5.6
2	Z	90	SER	5.6
1	R	255	ILE	5.6
1	F	255	ILE	5.6
1	K	406	GLU	5.6
1	E	203	ASN	5.6
1	L	31	ASN	5.6
2	Y	74	ASN	5.6
1	E	82	PRO	5.6
1	Q	17	ALA	5.6
1	R	253	ASP	5.6
1	V	186	ASP	5.6
1	W	58	ASP	5.6
1	I	456	ALA	5.6
1	L	89	ASP	5.6
1	P	33	LEU	5.6
2	Z	99	ARG	5.6
1	M	263	PHE	5.6

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Mol	Chain	Res	Type	RSRZ
1	A	449	PHE	5.6
1	Q	245	SER	5.6
1	R	28	GLU	5.6
1	V	230	GLU	5.6
1	D	539	LEU	5.6
2	u	14	LEU	5.6
1	A	256	ASP	5.6
2	f	48	ASP	5.6
1	P	346	LYS	5.6
1	B	108	LYS	5.6
1	I	50	THR	5.6
1	I	264	ILE	5.6
1	W	437	GLN	5.5
1	A	327	GLN	5.5
1	R	230	GLU	5.5
1	C	315	VAL	5.5
1	N	25	ALA	5.5
1	O	99	ARG	5.5
1	Q	572	ALA	5.5
1	H	400	ALA	5.5
1	L	337	ASN	5.5
1	A	248	LYS	5.5
2	m	22	ASP	5.5
1	L	409	THR	5.5
2	e	90	SER	5.5
2	l	34	GLN	5.5
1	W	28	GLU	5.5
1	U	79	LEU	5.5
1	J	438	LEU	5.5
2	a	37	VAL	5.5
1	M	388	PRO	5.5
1	T	183	GLY	5.5
1	J	210	PRO	5.5
1	B	574	LYS	5.5
1	C	556	TYR	5.5
1	K	449	PHE	5.5
1	T	264	ILE	5.5
1	U	134	ASP	5.5
1	X	32	ASP	5.5
1	I	213	THR	5.5
1	L	339	ASP	5.5
2	b	35	THR	5.5

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Mol	Chain	Res	Type	RSRZ
1	B	335	SER	5.5
1	L	450	GLN	5.5
1	O	406	GLU	5.5
1	W	456	ALA	5.5
1	B	547	PRO	5.5
1	E	199	PRO	5.5
1	E	346	LYS	5.5
1	N	263	PHE	5.5
1	J	549	TYR	5.5
1	U	293	ILE	5.5
1	M	213	THR	5.5
1	S	58	ASP	5.5
1	B	240	THR	5.5
1	C	153	CYS	5.5
1	V	41	TRP	5.5
1	F	44	TRP	5.5
1	A	315	VAL	5.5
2	k	16	LYS	5.5
2	v	33	MET	5.5
2	j	53	MET	5.5
2	f	45	ALA	5.5
1	R	35	PHE	5.5
2	p	144	ASN	5.5
2	i	153	ASN	5.5
1	R	58	ASP	5.5
1	E	153	CYS	5.5
1	H	197	ASP	5.5
1	U	208	VAL	5.5
2	v	16	LYS	5.5
1	G	73	GLN	5.5
1	L	437	GLN	5.5
1	L	408	ALA	5.5
1	B	70	GLU	5.5
2	d	83	GLY	5.5
1	C	157	ILE	5.5
1	D	514	TYR	5.5
1	K	246	TYR	5.5
1	P	248	LYS	5.4
1	S	346	LYS	5.4
1	N	451	ASP	5.4
1	K	320	VAL	5.4
2	d	31	ASP	5.4

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Mol	Chain	Res	Type	RSRZ
1	P	385	PRO	5.4
1	X	385	PRO	5.4
1	A	410	SER	5.4
2	p	91	ILE	5.4
1	K	346	LYS	5.4
1	A	94	LEU	5.4
2	b	153	ASN	5.4
1	Q	38	VAL	5.4
2	r	134	THR	5.4
2	j	143	THR	5.4
1	R	256	ASP	5.4
1	A	259	ALA	5.4
2	j	155	TRP	5.4
1	F	173	CYS	5.4
1	A	57	PHE	5.4
2	p	141	PRO	5.4
1	Q	76	ILE	5.4
1	W	144	ILE	5.4
2	b	90	SER	5.4
1	M	563	LYS	5.4
1	X	563	LYS	5.4
1	B	559	LEU	5.4
1	C	539	LEU	5.4
1	N	254	VAL	5.4
1	V	213	THR	5.4
1	U	592	TRP	5.4
1	J	41	TRP	5.4
2	n	92	ALA	5.4
1	M	387	GLN	5.4
1	P	437	GLN	5.4
1	V	32	ASP	5.4
1	A	437	GLN	5.4
1	H	308	GLY	5.4
1	P	173	CYS	5.4
1	P	224	GLU	5.4
1	R	199	PRO	5.4
1	R	296	GLU	5.4
1	C	385	PRO	5.4
1	C	249	ARG	5.4
1	E	293	ILE	5.4
1	F	160	SER	5.4
1	K	10	SER	5.4

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Mol	Chain	Res	Type	RSRZ
1	K	160	SER	5.4
1	O	556	TYR	5.4
1	G	292	LEU	5.4
1	I	373	LEU	5.4
1	O	156	VAL	5.4
1	L	38	VAL	5.4
2	g	52	MET	5.4
1	R	540	GLY	5.4
1	B	602	GLY	5.4
1	E	14	ARG	5.4
1	H	510	ILE	5.4
2	o	91	ILE	5.4
2	j	44	ASP	5.4
1	T	8	LEU	5.4
2	a	148	SER	5.4
1	C	549	TYR	5.4
1	I	447	TYR	5.4
1	D	244	VAL	5.4
1	G	420	VAL	5.4
1	J	220	ALA	5.4
2	h	45	ALA	5.4
1	V	439	ASN	5.4
1	W	31	ASN	5.4
1	D	31	ASN	5.4
1	X	461	GLY	5.4
1	E	19	TRP	5.4
1	V	387	GLN	5.4
1	J	144	ILE	5.4
1	K	288	LYS	5.4
1	O	28	GLU	5.3
1	F	197	ASP	5.3
1	M	559	LEU	5.3
1	M	560	LEU	5.3
1	E	444	LEU	5.3
2	Y	98	CYS	5.3
2	i	122	LEU	5.3
2	f	53	MET	5.3
1	A	29	ALA	5.3
1	I	195	ALA	5.3
1	O	558	THR	5.3
2	l	26	THR	5.3
2	t	118	THR	5.3

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Mol	Chain	Res	Type	RSRZ
2	v	145	GLU	5.3
1	A	43	ASP	5.3
1	T	38	VAL	5.3
1	D	188	ALA	5.3
1	H	91	ALA	5.3
1	H	259	ALA	5.3
1	Q	213	THR	5.3
1	E	280	ILE	5.3
1	U	426	ASN	5.3
1	E	387	GLN	5.3
1	M	507	LEU	5.3
1	V	28	GLU	5.3
1	A	296	GLU	5.3
1	H	396	GLU	5.3
2	r	14	LEU	5.3
1	U	303	VAL	5.3
1	F	186	ASP	5.3
1	N	99	ARG	5.3
1	E	99	ARG	5.3
1	T	25	ALA	5.3
1	U	121	ALA	5.3
1	U	279	SER	5.3
1	J	195	ALA	5.3
2	d	15	LYS	5.3
1	Q	434	THR	5.3
1	T	219	ILE	5.3
2	j	112	ILE	5.3
1	U	538	LEU	5.3
1	V	560	LEU	5.3
2	u	9	LEU	5.3
1	J	399	GLN	5.3
1	R	337	ASN	5.3
1	A	337	ASN	5.3
1	B	573	ASN	5.3
1	D	38	VAL	5.3
1	D	420	VAL	5.3
1	I	63	VAL	5.3
1	L	448	VAL	5.3
1	D	14	ARG	5.3
1	P	253	ASP	5.3
2	c	17	ASP	5.3
2	f	31	ASP	5.3

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Mol	Chain	Res	Type	RSRZ
1	G	267	ALA	5.3
2	p	119	ALA	5.3
1	A	157	ILE	5.3
1	B	139	SER	5.3
1	G	264	ILE	5.3
2	n	21	SER	5.3
1	A	547	PRO	5.3
1	V	592	TRP	5.3
1	I	387	GLN	5.3
2	b	154	GLU	5.3
1	T	115	VAL	5.3
1	G	254	VAL	5.3
1	A	99	ARG	5.3
1	E	313	LYS	5.3
1	O	549	TYR	5.3
1	J	159	ASP	5.3
2	b	48	ASP	5.3
2	f	44	ASP	5.3
2	j	94	HIS	5.3
2	e	113	ILE	5.3
1	S	212	LEU	5.2
1	S	553	LEU	5.2
1	A	69	SER	5.2
1	J	183	GLY	5.2
1	J	279	SER	5.2
2	e	49	LEU	5.2
1	K	344	THR	5.2
1	P	41	TRP	5.2
1	Q	387	GLN	5.2
1	R	387	GLN	5.2
2	j	58	GLN	5.2
2	g	111	LYS	5.2
1	P	31	ASN	5.2
1	W	188	ALA	5.2
1	X	411	ALA	5.2
2	m	92	ALA	5.2
1	A	172	HIS	5.2
1	L	155	HIS	5.2
1	I	212	LEU	5.2
2	r	75	LEU	5.2
1	T	50	THR	5.2
1	U	178	SER	5.2

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Mol	Chain	Res	Type	RSRZ
1	V	586	THR	5.2
1	B	385	PRO	5.2
2	Y	143	THR	5.2
1	T	541	LYS	5.2
1	W	290	LYS	5.2
1	D	30	LYS	5.2
1	E	541	LYS	5.2
1	M	445	GLU	5.2
1	P	230	GLU	5.2
1	K	28	GLU	5.2
1	R	408	ALA	5.2
2	c	132	ALA	5.2
1	P	549	TYR	5.2
1	B	219	ILE	5.2
1	I	371	TYR	5.2
1	L	329	LEU	5.2
2	a	49	LEU	5.2
1	S	77	ASP	5.2
1	C	378	ASP	5.2
1	L	32	ASP	5.2
2	Z	48	ASP	5.2
2	d	103	ASP	5.2
1	X	99	ARG	5.2
1	O	208	VAL	5.2
1	A	335	SER	5.2
1	F	50	THR	5.2
2	m	19	VAL	5.2
1	U	135	GLN	5.2
1	X	437	GLN	5.2
2	p	146	TRP	5.2
1	W	29	ALA	5.2
1	K	29	ALA	5.2
1	S	94	LEU	5.2
1	K	549	TYR	5.2
2	i	124	TYR	5.2
2	j	99	ARG	5.2
1	B	84	ASP	5.2
1	A	156	VAL	5.2
1	D	64	VAL	5.2
1	J	448	VAL	5.2
2	Y	37	VAL	5.2
1	C	213	THR	5.2

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Mol	Chain	Res	Type	RSRZ
1	O	450	GLN	5.2
1	B	160	SER	5.2
1	J	354	GLU	5.2
2	i	55	GLU	5.2
1	V	456	ALA	5.2
1	K	407	ALA	5.2
2	d	22	ALA	5.2
1	S	380	ASN	5.2
1	D	112	ASN	5.2
2	g	104	TYR	5.2
1	F	108	LYS	5.2
1	I	252	LYS	5.2
1	S	547	PRO	5.2
1	F	92	ASP	5.2
1	C	50	THR	5.2
1	J	434	THR	5.2
1	M	41	TRP	5.2
1	P	279	SER	5.2
1	D	259	ALA	5.2
1	B	554	LEU	5.1
1	D	444	LEU	5.1
1	S	99	ARG	5.1
1	G	313	LYS	5.1
2	i	111	LYS	5.1
1	C	337	ASN	5.1
1	R	183	GLY	5.1
1	F	235	TYR	5.1
1	O	63	VAL	5.1
1	O	237	ASP	5.1
1	T	43	ASP	5.1
2	m	35	ASP	5.1
1	A	529	GLN	5.1
2	a	155	TRP	5.1
1	O	12	LEU	5.1
1	I	356	ILE	5.1
1	W	173	CYS	5.1
1	F	359	PHE	5.1
1	J	449	PHE	5.1
1	N	439	ASN	5.1
1	V	161	ASN	5.1
1	V	547	PRO	5.1
2	m	133	PRO	5.1

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Mol	Chain	Res	Type	RSRZ
1	N	32	ASP	5.1
1	P	169	ASP	5.1
1	P	213	THR	5.1
1	R	561	ASP	5.1
1	A	409	THR	5.1
1	C	339	ASP	5.1
1	E	260	ASP	5.1
1	G	216	THR	5.1
1	G	519	ASP	5.1
2	l	35	ASP	5.1
2	j	115	THR	5.1
1	R	572	ALA	5.1
1	W	418	LEU	5.1
1	K	33	LEU	5.1
2	n	103	ILE	5.1
2	v	119	ALA	5.1
2	Y	97	ALA	5.1
2	Z	58	GLN	5.1
1	G	248	LYS	5.1
1	G	346	LYS	5.1
1	V	180	SER	5.1
1	O	183	GLY	5.1
1	K	123	VAL	5.1
1	O	405	LEU	5.1
1	C	552	LEU	5.1
1	K	108	LYS	5.1
2	Z	24	ARG	5.1
1	T	281	ILE	5.1
1	C	170	ALA	5.1
1	L	144	ILE	5.1
1	L	213	THR	5.1
2	b	45	ALA	5.1
1	T	445	GLU	5.1
1	G	250	ASP	5.1
1	J	443	ASP	5.1
1	K	451	ASP	5.1
2	Z	31	ASP	5.1
2	a	154	GLU	5.1
2	c	154	GLU	5.1
2	g	44	ASP	5.1
1	J	22	SER	5.1
1	H	115	VAL	5.1

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Mol	Chain	Res	Type	RSRZ
2	g	118	TYR	5.1
1	D	161	ASN	5.1
1	G	547	PRO	5.1
1	K	141	ASN	5.1
2	v	144	ASN	5.1
2	d	85	ARG	5.1
1	I	25	ALA	5.1
1	P	386	THR	5.1
1	X	138	THR	5.1
1	F	213	THR	5.1
1	J	409	THR	5.1
1	C	28	GLU	5.1
1	K	548	GLU	5.1
1	P	443	ASP	5.1
1	W	192	ASP	5.1
1	J	197	ASP	5.1
1	P	420	VAL	5.1
1	H	180	SER	5.1
1	I	129	VAL	5.1
1	S	556	TYR	5.1
1	B	191	TYR	5.1
1	M	373	LEU	5.1
1	O	331	ASN	5.1
1	F	413	LYS	5.1
1	B	212	LEU	5.1
1	G	439	ASN	5.1
2	r	144	ASN	5.1
2	t	144	ASN	5.1
1	M	357	ALA	5.0
1	R	29	ALA	5.0
1	W	264	ILE	5.0
1	D	264	ILE	5.0
1	F	152	ALA	5.0
1	I	281	ILE	5.0
1	J	298	ILE	5.0
1	Q	515	GLU	5.0
1	G	437	GLN	5.0
1	G	537	GLU	5.0
2	c	58	GLN	5.0
1	M	421	ASP	5.0
1	R	383	ASP	5.0
1	R	547	PRO	5.0

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Mol	Chain	Res	Type	RSRZ
1	X	212	LEU	5.0
1	J	374	LEU	5.0
2	r	141	PRO	5.0
1	G	161	ASN	5.0
1	H	251	ILE	5.0
1	H	331	ASN	5.0
1	J	281	ILE	5.0
1	F	107	ALA	5.0
1	H	416	ALA	5.0
1	J	17	ALA	5.0
1	L	456	ALA	5.0
1	O	445	GLU	5.0
1	S	240	THR	5.0
1	T	530	GLN	5.0
1	F	592	TRP	5.0
1	J	344	THR	5.0
2	g	58	GLN	5.0
1	X	565	VAL	5.0
1	N	498	ASP	5.0
1	Q	18	ASP	5.0
1	Q	183	GLY	5.0
1	A	346	LYS	5.0
2	Y	99	ARG	5.0
1	T	246	TYR	5.0
1	D	12	LEU	5.0
1	U	204	PRO	5.0
1	J	543	PRO	5.0
1	B	109	ILE	5.0
2	m	20	ALA	5.0
2	p	88	ALA	5.0
1	R	187	PHE	5.0
1	T	263	PHE	5.0
1	E	263	PHE	5.0
1	F	247	PHE	5.0
1	T	20	THR	5.0
1	X	296	GLU	5.0
1	B	314	GLU	5.0
1	E	28	GLU	5.0
1	K	41	TRP	5.0
2	p	28	VAL	5.0
1	M	318	GLY	5.0
1	K	14	ARG	5.0

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Mol	Chain	Res	Type	RSRZ
1	A	519	ASP	5.0
1	C	43	ASP	5.0
1	L	33	LEU	5.0
1	M	172	HIS	5.0
1	B	398	PRO	5.0
2	v	32	SER	5.0
2	i	21	ALA	5.0
2	s	89	CYS	5.0
1	X	103	ARG	5.0
1	B	592	TRP	5.0
1	G	445	GLU	5.0
2	f	58	GLN	5.0
2	i	121	GLU	5.0
1	T	305	GLY	5.0
2	f	49	LEU	5.0
1	W	101	ASP	5.0
2	m	39	ASP	5.0
2	h	44	ASP	5.0
1	U	98	TYR	5.0
1	B	510	ILE	5.0
1	I	388	PRO	5.0
2	g	57	TYR	5.0
1	J	180	SER	5.0
2	h	22	ALA	5.0
1	V	35	PHE	5.0
1	O	108	LYS	5.0
1	A	565	VAL	5.0
1	B	105	ASN	5.0
1	E	565	VAL	5.0
1	L	182	ASN	5.0
1	Q	406	GLU	5.0
1	W	73	GLN	5.0
1	E	240	THR	5.0
1	G	592	TRP	5.0
1	I	592	TRP	5.0
2	d	50	GLU	5.0
1	U	12	LEU	5.0
1	Q	281	ILE	4.9
1	L	370	PRO	4.9
2	n	91	ILE	4.9
1	P	18	ASP	4.9
1	Q	172	HIS	4.9

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Mol	Chain	Res	Type	RSRZ
1	S	260	ASP	4.9
2	f	103	ASP	4.9
1	A	408	ALA	4.9
1	C	190	LYS	4.9
1	C	410	SER	4.9
1	D	39	SER	4.9
1	A	123	VAL	4.9
2	o	19	VAL	4.9
1	P	450	GLN	4.9
1	T	153	CYS	4.9
1	C	379	GLU	4.9
1	P	560	LEU	4.9
1	Q	41	TRP	4.9
1	E	354	GLU	4.9
2	k	145	GLU	4.9
1	K	128	LEU	4.9
2	v	14	LEU	4.9
2	a	84	LEU	4.9
1	M	251	ILE	4.9
1	N	210	PRO	4.9
1	P	449	PHE	4.9
1	Q	272	LYS	4.9
1	T	169	ASP	4.9
1	V	92	ASP	4.9
1	W	222	PHE	4.9
1	C	346	LYS	4.9
1	H	89	ASP	4.9
1	F	315	VAL	4.9
1	K	279	SER	4.9
1	N	507	LEU	4.9
1	U	444	LEU	4.9
1	U	559	LEU	4.9
1	V	295	GLY	4.9
1	L	434	THR	4.9
2	Z	16	GLY	4.9
2	h	154	GLU	4.9
1	A	377	THR	4.9
1	M	293	ILE	4.9
2	n	133	PRO	4.9
2	q	66	PRO	4.9
2	h	142	PRO	4.9
1	D	108	LYS	4.9

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Mol	Chain	Res	Type	RSRZ
1	F	248	LYS	4.9
1	K	121	ALA	4.9
2	h	108	ALA	4.9
1	A	549	TYR	4.9
2	j	124	TYR	4.9
1	L	58	ASP	4.9
2	Y	17	ASP	4.9
1	P	115	VAL	4.9
1	W	420	VAL	4.9
1	F	420	VAL	4.9
1	R	335	SER	4.9
1	U	335	SER	4.9
1	F	168	SER	4.9
1	I	538	LEU	4.9
2	s	14	LEU	4.9
2	Y	70	SER	4.9
1	V	450	GLN	4.9
1	A	354	GLU	4.9
1	U	157	ILE	4.9
1	X	333	ILE	4.9
1	I	217	ILE	4.9
1	J	280	ILE	4.9
1	A	407	ALA	4.9
1	A	38	VAL	4.9
1	J	341	VAL	4.9
2	u	28	VAL	4.9
1	R	197	ASP	4.9
1	V	192	ASP	4.9
1	X	383	ASP	4.9
1	B	169	ASP	4.9
1	C	451	ASP	4.9
2	l	22	ASP	4.9
2	c	31	ASP	4.9
2	g	17	ASP	4.9
1	S	335	SER	4.9
1	U	525	GLN	4.9
1	R	563	LYS	4.9
1	I	216	THR	4.9
1	F	31	ASN	4.9
1	G	182	ASN	4.9
1	V	516	CYS	4.9
1	R	449	PHE	4.9

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Mol	Chain	Res	Type	RSRZ
1	G	155	HIS	4.9
1	H	420	VAL	4.9
1	T	258	LEU	4.9
2	j	49	LEU	4.9
1	M	159	ASP	4.9
1	O	451	ASP	4.9
1	I	131	ASP	4.9
2	m	70	GLY	4.8
1	N	136	SER	4.8
1	N	387	GLN	4.8
1	C	13	SER	4.8
2	Z	154	GLU	4.8
1	D	19	TRP	4.8
1	L	240	THR	4.8
2	q	144	ASN	4.8
1	X	199	PRO	4.8
1	E	420	VAL	4.8
1	X	576	LEU	4.8
1	D	33	LEU	4.8
1	J	246	TYR	4.8
2	q	25	LEU	4.8
1	N	563	LYS	4.8
1	R	346	LYS	4.8
1	U	101	ASP	4.8
1	W	159	ASP	4.8
1	D	134	ASP	4.8
1	F	234	ILE	4.8
1	I	32	ASP	4.8
1	K	192	ASP	4.8
1	K	264	ILE	4.8
2	n	94	ASP	4.8
1	D	314	GLU	4.8
1	G	379	GLU	4.8
1	U	211	TRP	4.8
1	W	291	GLN	4.8
1	W	450	GLN	4.8
1	D	200	SER	4.8
1	F	558	THR	4.8
1	H	50	THR	4.8
1	O	456	ALA	4.8
1	E	449	PHE	4.8
2	e	22	ALA	4.8

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Mol	Chain	Res	Type	RSRZ
2	d	151	ASN	4.8
1	P	438	LEU	4.8
1	G	315	VAL	4.8
2	d	99	ARG	4.8
1	P	318	GLY	4.8
1	V	234	ILE	4.8
1	B	293	ILE	4.8
1	B	463	ILE	4.8
1	B	580	GLY	4.8
1	V	445	GLU	4.8
2	c	44	ASP	4.8
2	f	17	ASP	4.8
2	g	48	ASP	4.8
2	b	155	TRP	4.8
1	Q	240	THR	4.8
1	X	557	PHE	4.8
1	A	174	THR	4.8
1	I	558	THR	4.8
1	J	400	ALA	4.8
1	K	338	ALA	4.8
2	s	139	SER	4.8
2	Y	139	SER	4.8
2	g	33	THR	4.8
2	i	45	ALA	4.8
1	A	204	PRO	4.8
1	O	380	ASN	4.8
1	O	452	ASN	4.8
1	T	507	LEU	4.8
1	A	33	LEU	4.8
1	A	254	VAL	4.8
1	J	94	LEU	4.8
1	J	128	LEU	4.8
1	J	320	VAL	4.8
1	C	380	ASN	4.8
1	F	439	ASN	4.8
1	J	205	ASN	4.8
1	J	439	ASN	4.8
1	J	507	LEU	4.8
1	L	94	LEU	4.8
2	q	44	MET	4.8
1	S	246	TYR	4.8
1	U	549	TYR	4.8

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Mol	Chain	Res	Type	RSRZ
1	C	191	TYR	4.8
1	J	248	LYS	4.8
1	K	391	TYR	4.8
2	j	111	LYS	4.8
1	X	109	ILE	4.8
1	K	445	GLU	4.8
1	M	197	ASP	4.8
1	O	270	GLN	4.8
1	P	159	ASP	4.8
1	W	170	ALA	4.8
1	X	92	ASP	4.8
1	C	237	ASP	4.8
1	D	408	ALA	4.8
1	D	550	GLN	4.8
1	J	16	ASP	4.8
2	a	48	ASP	4.8
2	b	31	ASP	4.8
1	J	15	PHE	4.8
2	Y	69	PHE	4.8
1	O	455	THR	4.8
1	M	33	LEU	4.8
1	M	115	VAL	4.8
1	P	8	LEU	4.8
1	T	547	PRO	4.8
1	B	94	LEU	4.8
1	O	248	LYS	4.8
1	T	248	LYS	4.8
1	N	459	ARG	4.8
1	U	337	ASN	4.8
1	B	205	ASN	4.8
1	D	531	ASN	4.8
1	I	27	ARG	4.8
1	D	371	TYR	4.8
1	S	251	ILE	4.8
1	U	510	ILE	4.8
1	J	11	ILE	4.8
1	A	445	GLU	4.8
1	D	230	GLU	4.8
2	Y	154	GLU	4.8
2	e	50	GLU	4.8
1	M	35	PHE	4.8
1	W	263	PHE	4.8

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Mol	Chain	Res	Type	RSRZ
1	I	121	ALA	4.8
2	n	96	ALA	4.8
1	R	192	ASP	4.8
1	U	32	ASP	4.8
1	E	592	TRP	4.8
1	F	12	LEU	4.8
1	G	194	ASP	4.8
1	J	33	LEU	4.8
1	K	19	TRP	4.8
1	L	19	TRP	4.8
2	g	155	TRP	4.8
1	M	558	THR	4.8
1	R	100	THR	4.8
1	T	204	PRO	4.8
1	A	62	PRO	4.8
1	D	543	PRO	4.8
1	G	303	VAL	4.8
1	K	448	VAL	4.8
2	Z	37	VAL	4.8
2	h	37	VAL	4.8
1	Q	563	LYS	4.8
1	L	541	LYS	4.8
2	c	90	SER	4.8
1	J	99	ARG	4.8
2	g	24	ARG	4.8
2	c	94	HIS	4.7
1	U	251	ILE	4.7
1	C	371	TYR	4.7
1	N	283	CYS	4.7
1	X	407	ALA	4.7
1	C	79	LEU	4.7
1	D	15	PHE	4.7
2	r	119	ALA	4.7
1	E	450	GLN	4.7
1	H	559	LEU	4.7
2	v	25	LEU	4.7
1	W	592	TRP	4.7
1	D	319	VAL	4.7
1	W	210	PRO	4.7
1	I	215	ASP	4.7
1	J	312	ASP	4.7
2	d	53	MET	4.7

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Mol	Chain	Res	Type	RSRZ
1	G	178	SER	4.7
2	Z	63	ILE	4.7
1	I	549	TYR	4.7
1	A	545	GLY	4.7
1	P	12	LEU	4.7
1	U	400	ALA	4.7
1	R	252	LYS	4.7
1	X	263	PHE	4.7
1	C	173	CYS	4.7
1	C	553	LEU	4.7
1	D	222	PHE	4.7
1	I	259	ALA	4.7
1	J	28	GLU	4.7
1	J	313	LYS	4.7
2	q	40	LEU	4.7
1	R	99	ARG	4.7
1	F	450	GLN	4.7
1	F	530	GLN	4.7
1	P	364	ASP	4.7
1	K	42	ASP	4.7
2	q	8	ASP	4.7
2	Z	17	ASP	4.7
1	O	410	SER	4.7
1	U	139	SER	4.7
1	I	113	ILE	4.7
1	J	293	ILE	4.7
1	M	452	ASN	4.7
1	V	380	ASN	4.7
1	W	112	ASN	4.7
1	Q	33	LEU	4.7
1	H	108	LYS	4.7
1	I	431	ALA	4.7
1	I	560	LEU	4.7
1	J	442	ALA	4.7
1	L	563	LYS	4.7
1	J	420	VAL	4.7
1	L	520	VAL	4.7
2	s	146	TRP	4.7
2	v	146	TRP	4.7
2	i	56	TRP	4.7
2	g	115	THR	4.7
1	P	76	ILE	4.7

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Mol	Chain	Res	Type	RSRZ
1	R	339	ASP	4.7
1	T	58	ASP	4.7
1	J	300	ILE	4.7
2	e	63	ILE	4.7
1	F	104	HIS	4.7
1	L	172	HIS	4.7
1	B	151	SER	4.7
2	i	118	TYR	4.7
1	S	528	LYS	4.7
1	X	560	LEU	4.7
1	A	182	ASN	4.7
1	A	528	LYS	4.7
1	L	322	LEU	4.7
1	R	37	ARG	4.7
1	U	338	ALA	4.7
1	X	25	ALA	4.7
2	a	45	ALA	4.7
1	M	78	VAL	4.7
1	M	437	GLN	4.7
1	P	199	PRO	4.7
1	N	592	TRP	4.7
1	M	109	ILE	4.7
1	N	213	THR	4.7
1	D	542	THR	4.7
1	I	518	THR	4.7
2	s	26	THR	4.7
2	b	63	ILE	4.7
1	N	260	ASP	4.7
1	U	92	ASP	4.7
1	M	122	GLY	4.7
1	F	346	LYS	4.7
1	I	541	LYS	4.7
1	N	458	ARG	4.7
1	P	410	SER	4.7
1	P	526	SER	4.7
1	X	139	SER	4.7
1	X	507	LEU	4.7
1	E	8	LEU	4.7
1	L	168	SER	4.7
2	j	123	LEU	4.7
1	W	380	ASN	4.7
1	X	91	ALA	4.7

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Mol	Chain	Res	Type	RSRZ
1	A	331	ASN	4.7
2	b	51	ALA	4.7
2	e	110	ALA	4.7
1	F	435	VAL	4.7
2	a	53	MET	4.7
1	G	296	GLU	4.7
1	H	133	GLU	4.7
2	d	38	GLU	4.7
1	A	387	GLN	4.6
1	F	218	GLN	4.6
1	O	251	ILE	4.6
1	C	271	ILE	4.6
2	Y	100	ILE	4.6
1	J	20	THR	4.6
1	W	346	LYS	4.6
1	O	159	ASP	4.6
1	P	458	ARG	4.6
1	R	312	ASP	4.6
1	W	32	ASP	4.6
1	H	99	ARG	4.6
2	k	62	ASP	4.6
2	Y	24	ARG	4.6
2	Y	96	LEU	4.6
1	A	403	TYR	4.6
1	K	403	TYR	4.6
2	g	124	TYR	4.6
1	B	456	ALA	4.6
1	I	114	ALA	4.6
1	J	63	VAL	4.6
2	h	88	ALA	4.6
1	V	203	ASN	4.6
1	A	439	ASN	4.6
1	H	380	ASN	4.6
2	o	138	ASN	4.6
1	X	28	GLU	4.6
1	A	398	PRO	4.6
2	c	142	PRO	4.6
1	P	291	GLN	4.6
2	v	31	GLN	4.6
1	S	558	THR	4.6
1	B	282	THR	4.6
2	d	14	THR	4.6

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Mol	Chain	Res	Type	RSRZ
1	P	212	LEU	4.6
1	B	8	LEU	4.6
1	J	12	LEU	4.6
1	K	12	LEU	4.6
2	a	123	LEU	4.6
1	M	220	ALA	4.6
1	R	565	VAL	4.6
1	A	456	ALA	4.6
1	E	312	ASP	4.6
2	n	148	TYR	4.6
2	v	42	ALA	4.6
2	a	17	ASP	4.6
2	g	32	ALA	4.6
2	g	103	ASP	4.6
2	h	48	ASP	4.6
2	j	37	VAL	4.6
1	P	337	ASN	4.6
1	U	380	ASN	4.6
1	F	375	ASN	4.6
1	M	189	GLU	4.6
1	O	230	GLU	4.6
1	U	317	GLU	4.6
1	A	406	GLU	4.6
1	F	385	PRO	4.6
2	q	141	PRO	4.6
1	N	530	GLN	4.6
1	E	264	ILE	4.6
1	R	507	LEU	4.6
1	A	216	THR	4.6
1	B	344	THR	4.6
1	F	295	GLY	4.6
1	I	172	HIS	4.6
1	M	63	VAL	4.6
1	N	557	PHE	4.6
1	S	338	ALA	4.6
1	X	15	PHE	4.6
1	X	188	ALA	4.6
1	B	319	VAL	4.6
1	I	123	VAL	4.6
1	J	285	ALA	4.6
1	J	407	ALA	4.6
1	K	17	ALA	4.6

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Mol	Chain	Res	Type	RSRZ
1	F	246	TYR	4.6
1	A	237	ASP	4.6
1	O	346	LYS	4.6
1	W	293	ILE	4.6
1	H	182	ASN	4.6
1	I	353	PRO	4.6
1	I	406	GLU	4.6
1	K	185	GLU	4.6
1	K	436	ASN	4.6
2	m	104	ILE	4.6
2	b	78	GLU	4.6
1	R	459	ARG	4.6
1	X	387	GLN	4.6
1	E	530	GLN	4.6
1	J	126	TRP	4.6
1	T	284	THR	4.6
1	V	455	THR	4.6
1	A	323	THR	4.6
1	L	558	THR	4.6
1	N	326	GLY	4.6
1	N	540	GLY	4.6
1	U	122	GLY	4.6
1	L	502	GLY	4.6
1	C	357	ALA	4.6
1	J	123	VAL	4.6
2	i	101	ALA	4.6
1	N	313	LYS	4.6
2	i	31	ASP	4.6
1	Q	587	PRO	4.6
1	R	251	ILE	4.6
1	U	385	PRO	4.6
1	X	577	ILE	4.6
1	H	445	GLU	4.6
1	B	439	ASN	4.6
1	D	418	LEU	4.6
2	d	49	LEU	4.6
1	P	19	TRP	4.6
1	O	213	THR	4.6
1	A	138	THR	4.6
1	C	377	THR	4.6
1	I	602	GLY	4.6
2	f	33	THR	4.6

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Mol	Chain	Res	Type	RSRZ
1	V	38	VAL	4.6
1	W	449	PHE	4.6
1	H	195	ALA	4.6
1	I	110	ALA	4.6
2	o	92	ALA	4.6
2	b	37	VAL	4.6
1	X	571	TYR	4.5
1	H	556	TYR	4.5
1	J	163	LYS	4.5
1	Q	32	ASP	4.5
1	V	333	ILE	4.5
1	G	99	ARG	4.5
1	A	383	ASP	4.5
1	B	159	ASP	4.5
1	H	561	ASP	4.5
1	L	101	ASP	4.5
1	N	385	PRO	4.5
1	G	210	PRO	4.5
1	R	212	LEU	4.5
1	U	33	LEU	4.5
1	W	13	SER	4.5
1	B	379	GLU	4.5
1	H	314	GLU	4.5
1	F	258	LEU	4.5
1	J	164	LEU	4.5
2	u	25	LEU	4.5
2	f	87	SER	4.5
2	g	18	LEU	4.5
1	X	31	ASN	4.5
1	E	550	GLN	4.5
1	K	375	ASN	4.5
2	a	58	GLN	4.5
1	O	38	VAL	4.5
1	U	78	VAL	4.5
1	U	326	GLY	4.5
1	Q	408	ALA	4.5
1	V	25	ALA	4.5
1	V	121	ALA	4.5
1	X	240	THR	4.5
1	B	15	PHE	4.5
1	E	239	VAL	4.5
1	F	35	PHE	4.5

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Mol	Chain	Res	Type	RSRZ
1	I	107	ALA	4.5
1	I	524	PHE	4.5
2	f	27	GLY	4.5
2	a	22	ALA	4.5
1	H	313	LYS	4.5
1	H	403	TYR	4.5
1	I	403	TYR	4.5
2	d	57	TYR	4.5
2	f	99	ARG	4.5
2	h	24	ARG	4.5
1	D	281	ILE	4.5
1	K	271	ILE	4.5
1	Q	199	PRO	4.5
1	O	32	ASP	4.5
1	Q	77	ASP	4.5
1	Q	192	ASP	4.5
1	Q	433	ASP	4.5
1	S	8	LEU	4.5
1	X	58	ASP	4.5
1	A	258	LEU	4.5
1	B	445	GLU	4.5
1	F	84	ASP	4.5
1	L	185	GLU	4.5
2	r	38	ASP	4.5
2	t	29	GLU	4.5
2	a	96	LEU	4.5
2	f	122	LEU	4.5
2	g	152	LEU	4.5
1	U	47	GLN	4.5
1	J	47	GLN	4.5
1	F	161	ASN	4.5
2	b	95	ASN	4.5
1	M	15	PHE	4.5
1	D	239	VAL	4.5
1	E	60	VAL	4.5
1	G	239	VAL	4.5
1	K	565	VAL	4.5
1	P	533	ALA	4.5
2	c	93	PHE	4.5
1	D	313	LYS	4.5
1	G	130	THR	4.5
2	b	143	THR	4.5

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Mol	Chain	Res	Type	RSRZ
1	J	172	HIS	4.5
1	M	517	TYR	4.5
1	Q	549	TYR	4.5
1	S	535	ILE	4.5
1	U	556	TYR	4.5
1	A	219	ILE	4.5
2	u	55	ILE	4.5
1	B	353	PRO	4.5
1	E	507	LEU	4.5
2	e	154	GLU	4.5
2	f	38	GLU	4.5
1	P	186	ASP	4.5
1	V	561	ASP	4.5
1	F	433	ASP	4.5
1	G	421	ASP	4.5
1	H	42	ASP	4.5
1	L	42	ASP	4.5
1	T	529	GLN	4.5
1	D	387	GLN	4.5
1	O	115	VAL	4.5
1	E	38	VAL	4.5
2	l	19	VAL	4.5
1	P	375	ASN	4.5
1	X	96	GLY	4.5
1	K	408	ALA	4.5
2	Z	53	MET	4.5
1	T	558	THR	4.5
1	B	249	ARG	4.5
1	E	216	THR	4.5
2	b	65	THR	4.5
1	Q	556	TYR	4.5
1	H	371	TYR	4.5
1	P	374	LEU	4.5
1	C	551	LEU	4.5
1	D	8	LEU	4.5
1	I	559	LEU	4.5
2	l	66	PRO	4.5
1	J	185	GLU	4.5
1	J	548	GLU	4.5
1	K	516	CYS	4.5
2	i	50	GLU	4.5
1	C	252	LYS	4.5

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Mol	Chain	Res	Type	RSRZ
1	P	84	ASP	4.5
1	S	42	ASP	4.5
1	C	77	ASP	4.5
1	C	578	GLN	4.5
1	E	448	VAL	4.5
1	I	237	ASP	4.5
2	Y	44	ASP	4.5
1	Q	160	SER	4.5
1	Q	410	SER	4.5
1	R	15	PHE	4.5
1	E	57	PHE	4.5
1	H	335	SER	4.5
1	K	233	PHE	4.5
1	C	592	TRP	4.5
1	L	220	ALA	4.5
2	c	97	ALA	4.5
1	X	452	ASN	4.5
1	B	531	ASN	4.5
1	D	205	ASN	4.5
2	Z	153	ASN	4.5
1	X	546	THR	4.5
1	C	20	THR	4.5
1	K	240	THR	4.5
1	O	271	ILE	4.5
1	T	539	LEU	4.5
1	C	559	LEU	4.5
2	n	17	LEU	4.5
1	C	210	PRO	4.5
1	P	252	LYS	4.5
1	T	313	LYS	4.5
1	W	224	GLU	4.5
1	T	64	VAL	4.5
1	V	420	VAL	4.5
2	o	28	VAL	4.5
1	A	247	PHE	4.5
1	X	572	ALA	4.4
1	C	101	ASP	4.4
1	E	451	ASP	4.4
1	F	308	GLY	4.4
1	J	42	ASP	4.4
2	n	23	ALA	4.4
2	r	13	ALA	4.4

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Mol	Chain	Res	Type	RSRZ
2	f	21	ALA	4.4
1	C	381	SER	4.4
1	L	36	SER	4.4
1	X	50	THR	4.4
1	X	217	ILE	4.4
1	X	409	THR	4.4
2	i	65	THR	4.4
1	Q	553	LEU	4.4
1	E	212	LEU	4.4
1	L	193	LEU	4.4
2	l	17	LEU	4.4
2	r	148	TYR	4.4
1	M	313	LYS	4.4
1	T	563	LYS	4.4
1	U	199	PRO	4.4
1	H	210	PRO	4.4
2	j	150	PRO	4.4
1	S	230	GLU	4.4
1	T	532	ARG	4.4
1	X	38	VAL	4.4
1	M	34	PHE	4.4
1	R	195	ALA	4.4
1	W	91	ALA	4.4
1	B	550	GLN	4.4
1	G	562	GLY	4.4
1	H	327	GLN	4.4
1	K	195	ALA	4.4
2	f	16	GLY	4.4
1	V	153	CYS	4.4
1	O	197	ASP	4.4
1	S	196	ASP	4.4
1	H	592	TRP	4.4
1	J	433	ASP	4.4
1	M	510	ILE	4.4
1	N	335	SER	4.4
1	O	255	ILE	4.4
1	U	212	LEU	4.4
1	M	240	THR	4.4
1	V	205	ASN	4.4
2	b	156	HIS	4.4
1	R	235	TYR	4.4
1	P	129	VAL	4.4

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Mol	Chain	Res	Type	RSRZ
1	T	565	VAL	4.4
1	X	208	VAL	4.4
1	L	123	VAL	4.4
1	V	585	GLU	4.4
1	C	227	GLU	4.4
1	H	28	GLU	4.4
2	f	52	MET	4.4
1	W	502	GLY	4.4
2	s	110	GLY	4.4
1	M	212	LEU	4.4
1	S	12	LEU	4.4
1	C	212	LEU	4.4
1	F	560	LEU	4.4
1	H	283	CYS	4.4
1	H	378	ASP	4.4
2	l	38	ASP	4.4
2	b	17	ASP	4.4
2	i	44	ASP	4.4
1	Q	20	THR	4.4
1	W	541	LYS	4.4
1	F	380	ASN	4.4
1	H	172	HIS	4.4
1	I	151	SER	4.4
2	u	81	SER	4.4
1	X	213	THR	4.4
1	A	501	THR	4.4
1	B	377	THR	4.4
1	D	240	THR	4.4
1	K	558	THR	4.4
2	k	86	ASN	4.4
1	P	103	ARG	4.4
1	Q	14	ARG	4.4
1	C	98	TYR	4.4
1	E	273	ARG	4.4
2	j	24	ARG	4.4
1	J	345	PRO	4.4
2	r	133	PRO	4.4
2	t	19	VAL	4.4
1	M	557	PHE	4.4
1	Q	28	GLU	4.4
1	Q	201	PHE	4.4
1	S	557	PHE	4.4

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Mol	Chain	Res	Type	RSRZ
1	K	21	ALA	4.4
1	L	259	ALA	4.4
2	h	101	ALA	4.4
2	j	45	ALA	4.4
1	A	96	GLY	4.4
1	H	540	GLY	4.4
1	Q	142	GLN	4.4
1	D	52	GLN	4.4
1	Q	12	LEU	4.4
1	R	79	LEU	4.4
1	V	507	LEU	4.4
1	W	258	LEU	4.4
1	B	560	LEU	4.4
1	K	507	LEU	4.4
2	b	106	LEU	4.4
1	S	19	TRP	4.4
2	Z	155	TRP	4.4
1	B	324	LYS	4.4
2	i	117	LYS	4.4
1	R	364	ASP	4.4
1	X	172	HIS	4.4
1	C	186	ASP	4.4
1	L	516	CYS	4.4
2	r	35	ASP	4.4
1	O	174	THR	4.4
1	R	178	SER	4.4
1	R	213	THR	4.4
1	U	455	THR	4.4
1	A	279	SER	4.4
1	B	178	SER	4.4
1	C	386	THR	4.4
1	G	103	ARG	4.4
1	I	335	SER	4.4
1	I	344	THR	4.4
2	s	90	ARG	4.4
2	i	90	SER	4.4
1	R	31	ASN	4.4
1	T	366	ASN	4.4
1	S	48	TYR	4.4
1	T	210	PRO	4.4
1	D	225	VAL	4.4
1	F	254	VAL	4.4

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Mol	Chain	Res	Type	RSRZ
1	G	371	TYR	4.4
2	Y	92	VAL	4.4
2	Y	150	PRO	4.4
2	b	67	TYR	4.4
1	B	557	PHE	4.4
1	N	416	ALA	4.4
1	W	406	GLU	4.4
1	B	28	GLU	4.4
1	E	408	ALA	4.4
2	n	13	ALA	4.4
2	e	78	GLU	4.4
1	S	96	GLY	4.4
1	S	559	LEU	4.4
1	X	8	LEU	4.4
1	M	248	LYS	4.4
1	M	504	LYS	4.4
1	M	530	GLN	4.4
1	P	541	LYS	4.4
1	A	76	ILE	4.4
1	J	560	LEU	4.4
2	s	9	LEU	4.4
1	C	19	TRP	4.4
1	F	361	HIS	4.4
2	o	147	HIS	4.4
1	P	240	THR	4.4
1	U	561	ASP	4.4
1	W	240	THR	4.4
1	G	92	ASP	4.4
1	J	18	ASP	4.4
2	q	72	ASP	4.4
1	M	111	VAL	4.4
1	O	205	ASN	4.4
1	W	371	TYR	4.4
1	D	370	PRO	4.4
1	H	439	ASN	4.4
1	K	388	PRO	4.4
2	Y	153	ASN	4.4
2	a	46	VAL	4.4
2	g	74	ASN	4.4
2	g	150	PRO	4.4
1	W	432	PHE	4.3
1	L	57	PHE	4.3

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Mol	Chain	Res	Type	RSRZ
1	Q	86	ALA	4.3
1	U	294	ALA	4.3
1	N	576	LEU	4.3
1	R	329	LEU	4.3
1	A	122	GLY	4.3
2	d	78	GLU	4.3
1	L	418	LEU	4.3
2	m	9	LEU	4.3
1	M	264	ILE	4.3
1	Q	510	ILE	4.3
1	I	149	ILE	4.3
1	K	300	ILE	4.3
2	g	117	LYS	4.3
1	O	437	GLN	4.3
1	P	592	TRP	4.3
1	L	184	TRP	4.3
1	V	104	HIS	4.3
1	N	130	THR	4.3
1	N	378	ASP	4.3
1	T	60	VAL	4.3
1	U	166	ASP	4.3
1	U	312	ASP	4.3
1	W	186	ASP	4.3
1	J	153	CYS	4.3
1	J	364	ASP	4.3
2	n	35	ASP	4.3
1	U	388	PRO	4.3
1	Q	263	PHE	4.3
1	S	205	ASN	4.3
1	U	160	SER	4.3
1	U	34	PHE	4.3
1	U	105	ASN	4.3
1	J	182	ASN	4.3
1	J	337	ASN	4.3
1	L	13	SER	4.3
1	X	549	TYR	4.3
1	G	263	PHE	4.3
2	c	104	TYR	4.3
1	R	91	ALA	4.3
1	S	91	ALA	4.3
2	k	82	ALA	4.3
2	k	123	ALA	4.3

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Mol	Chain	Res	Type	RSRZ
1	O	228	LYS	4.3
1	K	438	LEU	4.3
1	K	538	LEU	4.3
2	s	97	LEU	4.3
2	t	16	LYS	4.3
1	N	251	ILE	4.3
1	Q	221	GLU	4.3
1	R	264	ILE	4.3
1	R	340	ILE	4.3
1	B	113	ILE	4.3
1	C	406	GLU	4.3
1	G	219	ILE	4.3
2	d	63	ILE	4.3
1	X	550	GLN	4.3
1	G	211	TRP	4.3
1	H	211	TRP	4.3
1	S	93	VAL	4.3
1	K	254	VAL	4.3
2	l	28	VAL	4.3
1	N	138	THR	4.3
1	B	50	THR	4.3
2	h	143	THR	4.3
1	K	385	PRO	4.3
1	Q	259	ALA	4.3
1	T	39	SER	4.3
1	X	279	SER	4.3
1	D	516	CYS	4.3
1	I	169	ASP	4.3
1	K	43	ASP	4.3
1	K	253	ASP	4.3
1	E	105	ASN	4.3
1	H	160	SER	4.3
1	F	453	LEU	4.3
1	H	220	ALA	4.3
1	J	394	ASN	4.3
1	L	245	SER	4.3
1	L	438	LEU	4.3
2	n	143	LEU	4.3
2	r	92	ALA	4.3
2	s	25	LEU	4.3
2	u	123	ALA	4.3
2	v	68	ALA	4.3

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Mol	Chain	Res	Type	RSRZ
2	h	117	LYS	4.3
1	Q	329	LEU	4.3
2	c	49	LEU	4.3
1	K	545	GLY	4.3
2	t	137	GLY	4.3
1	P	99	ARG	4.3
1	S	548	GLU	4.3
1	G	81	ARG	4.3
1	I	441	ARG	4.3
2	v	46	GLU	4.3
2	b	121	GLU	4.3
1	R	550	GLN	4.3
1	F	239	VAL	4.3
1	G	448	VAL	4.3
1	H	397	VAL	4.3
1	O	163	LYS	4.3
1	R	248	LYS	4.3
1	V	557	PHE	4.3
1	V	563	LYS	4.3
1	C	449	PHE	4.3
1	D	50	THR	4.3
1	G	20	THR	4.3
1	J	359	PHE	4.3
1	J	432	PHE	4.3
1	L	543	PRO	4.3
2	b	33	THR	4.3
1	P	121	ALA	4.3
1	F	33	LEU	4.3
1	I	552	LEU	4.3
1	J	538	LEU	4.3
2	h	23	LEU	4.3
1	B	192	ASP	4.3
1	B	451	ASP	4.3
1	G	169	ASP	4.3
1	Q	200	SER	4.3
1	W	153	CYS	4.3
1	R	96	GLY	4.3
1	J	452	ASN	4.3
1	L	436	ASN	4.3
1	P	354	GLU	4.3
1	J	230	GLU	4.3
1	S	550	GLN	4.3

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Mol	Chain	Res	Type	RSRZ
1	T	387	GLN	4.3
1	J	525	GLN	4.3
1	P	254	VAL	4.3
1	Q	420	VAL	4.3
1	S	38	VAL	4.3
1	B	123	VAL	4.3
1	C	420	VAL	4.3
2	g	56	TRP	4.3
1	U	172	HIS	4.3
1	G	172	HIS	4.3
1	T	57	PHE	4.3
1	D	558	THR	4.3
1	G	329	LEU	4.3
1	J	547	PRO	4.3
1	L	199	PRO	4.3
1	L	353	PRO	4.3
2	l	133	PRO	4.3
2	n	26	THR	4.3
2	i	109	THR	4.3
2	m	23	ALA	4.3
2	c	24	ARG	4.3
2	j	116	ALA	4.3
1	N	264	ILE	4.3
1	O	109	ILE	4.3
1	R	217	ILE	4.3
1	R	577	ILE	4.3
1	U	219	ILE	4.3
1	Q	443	ASP	4.3
1	U	260	ASP	4.3
1	U	451	ASP	4.3
1	D	339	ASP	4.3
1	E	186	ASP	4.3
1	G	326	GLY	4.3
1	H	186	ASP	4.3
1	I	159	ASP	4.3
1	I	253	ASP	4.3
2	u	8	ASP	4.3
2	Z	144	GLY	4.3
1	U	205	ASN	4.3
1	W	160	SER	4.3
1	P	28	GLU	4.3
1	E	589	GLU	4.3

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Mol	Chain	Res	Type	RSRZ
1	K	396	GLU	4.3
2	c	78	GLU	4.3
1	B	38	VAL	4.3
1	C	594	VAL	4.3
1	O	592	TRP	4.2
1	E	108	LYS	4.2
1	Q	187	PHE	4.2
1	R	8	LEU	4.2
1	U	507	LEU	4.2
1	W	560	LEU	4.2
1	X	210	PRO	4.2
1	C	94	LEU	4.2
2	r	97	LEU	4.2
2	Z	49	LEU	4.2
1	H	532	ARG	4.2
1	L	14	ARG	4.2
1	Q	386	THR	4.2
1	R	259	ALA	4.2
1	S	264	ILE	4.2
1	B	298	ILE	4.2
1	I	198	ILE	4.2
2	f	65	THR	4.2
1	N	602	GLY	4.2
1	O	517	TYR	4.2
1	A	502	GLY	4.2
1	J	382	GLY	4.2
1	O	16	ASP	4.2
1	P	433	ASP	4.2
1	U	215	ASP	4.2
1	U	289	ASP	4.2
1	A	31	ASN	4.2
1	B	58	ASP	4.2
1	E	215	ASP	4.2
1	I	13	SER	4.2
1	K	401	ASN	4.2
2	t	94	ASP	4.2
1	C	523	SER	4.2
1	E	36	SER	4.2
1	O	252	LYS	4.2
1	Q	541	LYS	4.2
1	B	541	LYS	4.2
1	O	239	VAL	4.2

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Mol	Chain	Res	Type	RSRZ
1	R	142	GLN	4.2
1	T	504	LYS	4.2
1	G	291	GLN	4.2
1	K	135	GLN	4.2
1	L	142	GLN	4.2
1	L	387	GLN	4.2
1	R	444	LEU	4.2
1	W	507	LEU	4.2
1	A	103	ARG	4.2
1	B	187	PHE	4.2
1	C	350	PHE	4.2
1	E	557	PHE	4.2
1	H	8	LEU	4.2
1	I	309	PHE	4.2
2	k	25	LEU	4.2
1	V	395	PRO	4.2
1	O	356	ILE	4.2
2	a	32	ALA	4.2
1	V	446	THR	4.2
1	L	501	THR	4.2
2	l	134	THR	4.2
2	a	143	THR	4.2
2	d	115	THR	4.2
1	A	580	GLY	4.2
1	F	191	TYR	4.2
1	H	246	TYR	4.2
2	i	57	TYR	4.2
1	T	230	GLU	4.2
1	L	230	GLU	4.2
1	N	105	ASN	4.2
1	Q	84	ASP	4.2
1	R	101	ASP	4.2
1	X	312	ASP	4.2
1	Q	335	SER	4.2
1	T	178	SER	4.2
1	B	526	SER	4.2
1	C	139	SER	4.2
1	D	346	LYS	4.2
1	G	253	ASP	4.2
1	I	197	ASP	4.2
1	K	140	ASN	4.2
1	K	339	ASP	4.2

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Mol	Chain	Res	Type	RSRZ
1	L	364	ASP	4.2
2	l	16	LYS	4.2
2	o	35	ASP	4.2
2	a	44	ASP	4.2
1	E	261	SER	4.2
1	I	410	SER	4.2
2	t	139	SER	4.2
2	e	95	ASN	4.2
1	G	64	VAL	4.2
1	G	208	VAL	4.2
1	J	142	GLN	4.2
1	O	373	LEU	4.2
1	R	249	ARG	4.2
1	B	418	LEU	4.2
1	F	552	LEU	4.2
1	I	128	LEU	4.2
1	J	72	ARG	4.2
1	W	57	PHE	4.2
1	H	263	PHE	4.2
1	J	187	PHE	4.2
1	K	57	PHE	4.2
1	O	172	HIS	4.2
1	M	356	ILE	4.2
1	U	91	ALA	4.2
1	F	293	ILE	4.2
2	Y	116	ALA	4.2
2	t	53	GLY	4.2
1	A	98	TYR	4.2
1	B	80	TYR	4.2
2	d	104	TYR	4.2
2	f	124	TYR	4.2
2	b	117	LYS	4.2
1	M	589	GLU	4.2
1	L	503	GLU	4.2
1	Q	565	VAL	4.2
1	O	31	ASN	4.2
1	O	335	SER	4.2
1	V	215	ASP	4.2
1	X	159	ASP	4.2
1	X	410	SER	4.2
1	A	77	ASP	4.2
1	A	180	SER	4.2

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Mol	Chain	Res	Type	RSRZ
1	B	325	ASP	4.2
1	G	111	VAL	4.2
1	C	531	ASN	4.2
1	H	253	ASP	4.2
1	J	32	ASP	4.2
2	Y	31	ASP	4.2
1	S	578	GLN	4.2
1	W	551	LEU	4.2
1	B	173	CYS	4.2
1	E	551	LEU	4.2
1	H	128	LEU	4.2
1	K	79	LEU	4.2
1	K	418	LEU	4.2
2	h	122	LEU	4.2
1	C	304	PHE	4.2
1	J	222	PHE	4.2
1	M	107	ALA	4.2
1	M	543	PRO	4.2
1	P	11	ILE	4.2
1	R	338	ALA	4.2
1	D	219	ILE	4.2
1	I	255	ILE	4.2
1	K	454	ALA	4.2
1	T	30	LYS	4.2
1	A	518	THR	4.2
1	E	20	THR	4.2
1	I	240	THR	4.2
2	g	27	GLY	4.2
1	L	313	LYS	4.2
2	g	125	LYS	4.2
2	g	143	THR	4.2
1	B	571	TYR	4.2
1	J	392	TYR	4.2
1	J	556	TYR	4.2
1	T	28	GLU	4.2
1	T	208	VAL	4.2
1	U	120	GLU	4.2
1	W	239	VAL	4.2
1	H	448	VAL	4.2
2	Z	19	VAL	4.2
2	f	154	GLU	4.2
2	g	85	ARG	4.2

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Mol	Chain	Res	Type	RSRZ
2	i	99	ARG	4.2
1	N	12	LEU	4.2
1	O	538	LEU	4.2
1	F	212	LEU	4.2
2	f	34	LEU	4.2
2	h	123	LEU	4.2
1	V	160	SER	4.2
1	E	160	SER	4.2
1	G	180	SER	4.2
1	I	561	ASP	4.2
1	K	112	ASN	4.2
2	Z	148	SER	4.2
2	b	44	ASP	4.2
1	H	304	PHE	4.2
2	f	90	SER	4.2
1	W	516	CYS	4.2
1	T	599	ALA	4.2
1	A	271	ILE	4.2
1	C	442	ALA	4.2
1	F	114	ALA	4.2
1	G	266	ILE	4.2
1	K	188	ALA	4.2
1	L	21	ALA	4.2
1	L	264	ILE	4.2
2	r	20	ALA	4.2
1	O	388	PRO	4.2
2	e	142	PRO	4.2
2	j	117	LYS	4.2
1	L	85	GLY	4.2
1	D	216	THR	4.2
2	h	115	THR	4.2
1	N	87	ARG	4.2
1	N	420	VAL	4.1
1	P	320	VAL	4.1
1	S	72	ARG	4.2
1	A	520	VAL	4.1
1	M	28	GLU	4.1
1	I	548	GLU	4.1
2	l	145	GLU	4.1
1	R	325	ASP	4.1
1	S	31	ASN	4.1
1	M	25	ALA	4.1

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Mol	Chain	Res	Type	RSRZ
1	U	381	SER	4.1
1	X	186	ASP	4.1
1	E	140	ASN	4.1
1	I	105	ASN	4.1
1	I	519	ASP	4.1
1	J	375	ASN	4.1
1	E	298	ILE	4.1
1	H	293	ILE	4.1
1	K	89	ASP	4.1
2	f	151	ASN	4.1
1	L	157	ILE	4.1
2	h	31	ASP	4.1
2	l	79	ALA	4.1
2	Y	128	ALA	4.1
2	Z	45	ALA	4.1
2	i	112	ILE	4.1
1	K	62	PRO	4.1
2	u	146	TRP	4.1
1	V	173	CYS	4.1
1	W	228	LYS	4.1
1	D	541	LYS	4.1
2	o	85	HIS	4.1
2	p	66	PRO	4.1
2	i	98	CYS	4.1
1	R	409	THR	4.1
1	D	275	ARG	4.1
1	J	106	THR	4.1
1	J	213	THR	4.1
1	R	276	VAL	4.1
1	A	420	VAL	4.1
1	H	208	VAL	4.1
1	F	8	LEU	4.1
1	I	33	LEU	4.1
2	j	152	LEU	4.1
1	Q	445	GLU	4.1
1	S	445	GLU	4.1
1	X	133	GLU	4.1
1	X	230	GLU	4.1
1	P	109	ILE	4.1
1	S	219	ILE	4.1
1	A	300	ILE	4.1
1	F	340	ILE	4.1

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Mol	Chain	Res	Type	RSRZ
1	H	264	ILE	4.1
1	L	550	GLN	4.1
2	k	91	ILE	4.1
2	d	100	ILE	4.1
1	M	259	ALA	4.1
1	M	380	ASN	4.1
1	M	456	ALA	4.1
1	D	290	LYS	4.1
1	F	260	ASP	4.1
1	I	436	ASN	4.1
2	u	82	ALA	4.1
2	c	51	ALA	4.1
1	M	77	ASP	4.1
1	M	509	ASP	4.1
1	M	398	PRO	4.1
1	U	151	SER	4.1
1	W	199	PRO	4.1
1	A	160	SER	4.1
1	J	237	ASP	4.1
1	C	199	PRO	4.1
1	K	44	TRP	4.1
2	l	141	PRO	4.1
2	Z	75	PRO	4.1
2	a	90	SER	4.1
2	j	41	SER	4.1
1	K	155	HIS	4.1
1	T	173	CYS	4.1
1	A	249	ARG	4.1
1	C	26	ARG	4.1
1	J	419	GLY	4.1
2	f	146	GLY	4.1
1	S	63	VAL	4.1
1	V	497	VAL	4.1
1	A	240	THR	4.1
1	G	50	THR	4.1
1	G	455	THR	4.1
2	i	143	THR	4.1
1	O	559	LEU	4.1
1	Q	418	LEU	4.1
1	G	549	TYR	4.1
2	o	14	LEU	4.1
2	i	23	LEU	4.1

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Mol	Chain	Res	Type	RSRZ
1	S	414	GLU	4.1
1	A	9	GLU	4.1
1	I	227	GLU	4.1
1	I	354	GLU	4.1
1	L	432	PHE	4.1
1	P	266	ILE	4.1
1	X	340	ILE	4.1
1	A	333	ILE	4.1
1	K	535	ILE	4.1
1	L	66	LYS	4.1
2	i	125	LYS	4.1
1	M	431	ALA	4.1
1	S	596	ALA	4.1
1	B	575	GLN	4.1
2	m	119	ALA	4.1
1	S	210	PRO	4.1
1	U	547	PRO	4.1
1	F	182	ASN	4.1
1	G	388	PRO	4.1
1	E	250	ASP	4.1
1	I	44	TRP	4.1
2	m	150	PRO	4.1
2	c	76	PRO	4.1
1	N	433	ASP	4.1
1	Q	325	ASP	4.1
1	T	215	ASP	4.1
1	U	509	ASP	4.1
1	W	171	ARG	4.1
2	a	99	ARG	4.1
2	c	155	TRP	4.1
1	P	419	GLY	4.1
1	M	444	LEU	4.1
1	O	420	VAL	4.1
1	S	329	LEU	4.1
1	U	153	CYS	4.1
1	W	38	VAL	4.1
1	A	208	VAL	4.1
1	F	153	CYS	4.1
1	O	323	THR	4.1
1	Q	518	THR	4.1
1	B	174	THR	4.1
1	B	284	THR	4.1

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Mol	Chain	Res	Type	RSRZ
1	B	403	TYR	4.1
2	c	65	THR	4.1
2	c	52	MET	4.1
1	M	230	GLU	4.1
1	R	541	LYS	4.1
1	S	263	PHE	4.1
1	S	541	LYS	4.1
1	V	167	LYS	4.1
1	D	406	GLU	4.1
1	V	263	PHE	4.1
2	g	113	ILE	4.1
2	j	113	ILE	4.1
1	M	424	ALA	4.1
2	m	96	ALA	4.1
2	n	101	ALA	4.1
1	U	103	ARG	4.1
1	E	27	ARG	4.1
1	G	441	ARG	4.1
2	k	90	ARG	4.1
2	h	20	ARG	4.1
1	R	205	ASN	4.1
1	K	361	HIS	4.1
2	f	83	GLY	4.1
2	h	94	HIS	4.1
1	P	421	ASP	4.1
1	V	451	ASP	4.1
1	E	368	ASP	4.1
2	k	139	SER	4.1
2	n	63	ASP	4.1
1	M	164	LEU	4.1
1	N	8	LEU	4.1
1	S	576	LEU	4.1
1	G	374	LEU	4.1
2	f	28	VAL	4.1
2	g	28	VAL	4.1
2	i	37	VAL	4.1
2	i	123	LEU	4.1
1	P	446	THR	4.1
1	V	283	CYS	4.1
1	P	517	TYR	4.1
1	G	369	TYR	4.1
1	I	106	THR	4.1

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Mol	Chain	Res	Type	RSRZ
1	V	313	LYS	4.1
2	k	102	LYS	4.1
2	f	117	LYS	4.1
1	N	293	ILE	4.1
1	R	144	ILE	4.1
1	R	242	GLU	4.1
1	S	534	GLU	4.1
1	T	293	ILE	4.1
1	V	360	GLU	4.1
1	X	445	GLU	4.1
1	D	57	PHE	4.1
1	F	503	GLU	4.1
1	V	267	ALA	4.1
2	b	21	ALA	4.1
1	D	274	ARG	4.1
2	g	99	ARG	4.1
1	T	550	GLN	4.1
1	K	591	GLN	4.1
2	r	49	GLN	4.1
1	I	345	PRO	4.1
2	i	142	PRO	4.1
1	H	104	HIS	4.1
2	g	16	GLY	4.1
1	Q	182	ASN	4.0
1	U	554	LEU	4.0
1	F	203	ASN	4.0
1	I	565	VAL	4.0
2	Y	49	LEU	4.0
1	O	13	SER	4.0
1	Q	22	SER	4.0
1	R	245	SER	4.0
1	A	159	ASP	4.0
1	D	215	ASP	4.0
1	L	206	ASP	4.0
2	e	87	SER	4.0
1	S	190	LYS	4.0
1	W	248	LYS	4.0
2	q	132	MET	4.0
1	R	138	THR	4.0
1	V	240	THR	4.0
2	l	106	THR	4.0
2	s	24	THR	4.0

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Mol	Chain	Res	Type	RSRZ
1	W	557	PHE	4.0
1	C	280	ILE	4.0
1	F	222	PHE	4.0
1	G	516	CYS	4.0
1	J	333	ILE	4.0
2	u	89	CYS	4.0
1	K	227	GLU	4.0
1	N	114	ALA	4.0
1	Q	431	ALA	4.0
1	A	328	ARG	4.0
1	K	411	ALA	4.0
1	L	103	ARG	4.0
2	h	99	ARG	4.0
2	j	114	ALA	4.0
1	U	387	GLN	4.0
1	U	399	GLN	4.0
1	W	530	GLN	4.0
1	B	202	GLN	4.0
1	H	450	GLN	4.0
1	J	387	GLN	4.0
2	Y	94	HIS	4.0
1	M	105	ASN	4.0
1	W	582	LYS	4.0
1	X	528	LYS	4.0
1	E	272	LYS	4.0
2	v	102	LYS	4.0
2	c	153	ASN	4.0
2	e	111	LYS	4.0
1	O	42	ASP	4.0
1	P	16	ASP	4.0
1	R	42	ASP	4.0
1	C	180	SER	4.0
2	q	78	SER	4.0
2	t	136	SER	4.0
1	S	213	THR	4.0
1	V	34	PHE	4.0
1	C	535	ILE	4.0
1	E	144	ILE	4.0
1	J	558	THR	4.0
1	S	441	ARG	4.0
1	J	532	ARG	4.0
1	U	445	GLU	4.0

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Mol	Chain	Res	Type	RSRZ
2	c	22	ALA	4.0
2	j	101	ALA	4.0
1	M	210	PRO	4.0
1	N	202	GLN	4.0
1	O	118	GLN	4.0
1	Q	438	LEU	4.0
1	R	539	LEU	4.0
1	R	584	PRO	4.0
1	T	388	PRO	4.0
1	U	539	LEU	4.0
1	V	385	PRO	4.0
1	C	398	PRO	4.0
1	F	429	GLN	4.0
1	H	137	PRO	4.0
1	H	437	GLN	4.0
1	K	56	GLN	4.0
1	L	212	LEU	4.0
2	f	75	PRO	4.0
1	P	448	VAL	4.0
1	S	504	LYS	4.0
1	V	346	LYS	4.0
1	C	278	LYS	4.0
1	G	427	GLY	4.0
1	I	341	VAL	4.0
2	e	37	VAL	4.0
2	d	52	MET	4.0
1	P	205	ASN	4.0
2	d	95	ASN	4.0
1	N	333	ILE	4.0
1	P	192	ASP	4.0
1	Q	42	ASP	4.0
1	Q	557	PHE	4.0
1	V	159	ASP	4.0
1	W	43	ASP	4.0
1	X	335	SER	4.0
1	X	459	ARG	4.0
1	A	18	ASP	4.0
1	D	196	ASP	4.0
1	D	245	SER	4.0
1	K	16	ASP	4.0
1	L	201	PHE	4.0
1	L	300	ILE	4.0

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Mol	Chain	Res	Type	RSRZ
2	o	81	SER	4.0
2	c	148	SER	4.0
2	d	48	ASP	4.0
2	d	90	SER	4.0
1	Q	174	THR	4.0
1	U	80	TYR	4.0
1	D	434	THR	4.0
1	H	417	THR	4.0
1	I	517	TYR	4.0
1	K	392	TYR	4.0
2	c	115	THR	4.0
2	d	118	TYR	4.0
1	X	121	ALA	4.0
1	B	596	ALA	4.0
1	G	357	ALA	4.0
1	K	24	GLU	4.0
2	Z	51	ALA	4.0
2	a	51	ALA	4.0
2	h	116	ALA	4.0
1	V	418	LEU	4.0
1	O	530	GLN	4.0
1	S	385	PRO	4.0
1	S	552	LEU	4.0
1	H	387	GLN	4.0
1	K	543	PRO	4.0
2	v	17	LEU	4.0
2	f	111	LYS	4.0
1	U	124	GLY	4.0
1	H	305	GLY	4.0
2	r	53	GLY	4.0
1	R	41	TRP	4.0
1	G	14	ARG	4.0
1	R	271	ILE	4.0
1	H	309	PHE	4.0
1	L	255	ILE	4.0
2	p	103	ILE	4.0
2	f	100	ILE	4.0
1	M	237	ASP	4.0
1	N	42	ASP	4.0
1	O	180	SER	4.0
1	P	250	ASP	4.0
1	W	197	ASP	4.0

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Mol	Chain	Res	Type	RSRZ
1	N	17	ALA	4.0
1	P	408	ALA	4.0
1	W	446	THR	4.0
1	A	166	ASP	4.0
1	A	215	ASP	4.0
1	B	92	ASP	4.0
1	E	386	THR	4.0
1	E	455	THR	4.0
1	F	139	SER	4.0
1	J	86	ALA	4.0
1	K	371	TYR	4.0
1	L	371	TYR	4.0
1	L	410	SER	4.0
2	k	35	ASP	4.0
2	s	22	ASP	4.0
2	Z	44	ASP	4.0
2	d	17	ASP	4.0
2	g	105	ALA	4.0
2	j	54	ALA	4.0
2	j	128	ALA	4.0
1	W	589	GLU	4.0
1	O	504	LYS	4.0
1	O	560	LEU	4.0
1	U	563	LYS	4.0
1	V	258	LEU	4.0
1	W	405	LEU	4.0
1	W	552	LEU	4.0
1	B	258	LEU	4.0
1	M	129	VAL	4.0
1	M	204	PRO	4.0
1	O	516	CYS	4.0
1	R	385	PRO	4.0
1	A	385	PRO	4.0
1	O	387	GLN	4.0
1	R	218	GLN	4.0
1	C	38	VAL	4.0
2	n	89	CYS	4.0
1	I	555	GLN	4.0
2	d	144	GLY	4.0
1	M	524	PHE	4.0
1	J	535	ILE	4.0
2	h	113	ILE	4.0

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Mol	Chain	Res	Type	RSRZ
1	T	182	ASN	4.0
1	X	331	ASN	4.0
2	h	147	ASN	4.0
1	N	431	ALA	4.0
1	U	259	ALA	4.0
1	A	599	ALA	4.0
1	E	213	THR	4.0
1	E	371	TYR	4.0
2	b	32	ALA	4.0
1	P	422	THR	4.0
1	L	379	GLU	4.0
2	m	145	GLU	4.0
2	q	61	SER	4.0
2	d	137	TYR	4.0
2	d	157	TYR	4.0
2	e	104	TYR	4.0
1	T	237	ASP	4.0
1	U	77	ASP	4.0
1	V	378	ASP	4.0
1	H	589	GLU	4.0
1	I	250	ASP	4.0
1	J	166	ASP	4.0
2	h	65	THR	4.0
1	X	242	GLU	4.0
1	J	534	GLU	4.0
1	M	405	LEU	4.0
1	T	593	LEU	4.0
1	U	560	LEU	4.0
1	H	552	LEU	4.0
1	K	551	LEU	4.0
2	o	87	LEU	4.0
1	N	543	PRO	3.9
1	A	397	VAL	3.9
1	D	506	VAL	3.9
2	t	83	VAL	3.9
2	e	150	PRO	3.9
2	j	92	VAL	3.9
1	U	437	GLN	3.9
1	G	135	GLN	3.9
1	G	505	GLN	3.9
1	B	61	ARG	3.9
1	A	19	TRP	3.9

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Mol	Chain	Res	Type	RSRZ
1	D	172	HIS	3.9
1	N	201	PHE	3.9
1	G	300	ILE	3.9
1	G	524	PHE	3.9
1	K	76	ILE	3.9
1	T	91	ALA	3.9
1	O	246	TYR	3.9
1	V	452	ASN	3.9
1	C	108	LYS	3.9
1	H	528	LYS	3.9
1	A	444	LEU	3.9
1	B	551	LEU	3.9
1	D	556	TYR	3.9
1	M	227	GLU	3.9
1	N	133	GLU	3.9
1	N	409	THR	3.9
1	S	417	THR	3.9
1	T	538	LEU	3.9
1	E	548	GLU	3.9
1	F	106	THR	3.9
1	K	94	LEU	3.9
1	G	589	GLU	3.9
1	K	323	THR	3.9
2	b	122	LEU	3.9
1	S	117	GLU	3.9
1	L	515	GLU	3.9
2	Y	78	GLU	3.9
1	P	32	ASP	3.9
1	P	339	ASP	3.9
1	W	367	ASP	3.9
1	C	383	ASP	3.9
1	F	367	ASP	3.9
2	Y	71	ASP	3.9
1	U	254	VAL	3.9
1	J	60	VAL	3.9
1	H	328	ARG	3.9
1	K	345	PRO	3.9
2	o	141	PRO	3.9
1	Q	602	GLY	3.9
1	K	564	GLY	3.9
1	B	387	GLN	3.9
1	E	251	ILE	3.9

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Mol	Chain	Res	Type	RSRZ
1	Q	19	TRP	3.9
1	H	34	PHE	3.9
1	J	44	TRP	3.9
1	M	500	ALA	3.9
1	Q	442	ALA	3.9
1	B	107	ALA	3.9
1	H	346	LYS	3.9
1	H	431	ALA	3.9
1	I	220	ALA	3.9
1	I	400	ALA	3.9
2	v	23	ALA	3.9
2	Y	21	ALA	3.9
2	e	45	ALA	3.9
1	M	258	LEU	3.9
1	T	373	LEU	3.9
1	T	444	LEU	3.9
1	E	552	LEU	3.9
1	J	212	LEU	3.9
2	h	34	LEU	3.9
1	Q	230	GLU	3.9
1	W	213	THR	3.9
1	W	375	ASN	3.9
1	X	105	ASN	3.9
1	A	6	ASN	3.9
1	I	537	GLU	3.9
1	J	6	ASN	3.9
2	s	138	ASN	3.9
2	u	148	TYR	3.9
1	B	414	GLU	3.9
1	B	434	THR	3.9
2	j	151	ASN	3.9
1	E	225	VAL	3.9
1	I	239	VAL	3.9
2	Y	68	VAL	3.9
1	T	443	ASP	3.9
1	G	197	ASP	3.9
1	L	197	ASP	3.9
2	l	78	SER	3.9
2	t	35	ASP	3.9
2	a	145	SER	3.9
2	e	17	ASP	3.9
1	P	545	GLY	3.9

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Mol	Chain	Res	Type	RSRZ
1	K	199	PRO	3.9
1	L	241	GLY	3.9
2	c	42	MET	3.9
1	O	73	GLN	3.9
1	H	590	GLN	3.9
1	I	399	GLN	3.9
1	L	575	GLN	3.9
2	l	104	ILE	3.9
1	P	557	PHE	3.9
2	n	85	HIS	3.9
1	V	44	TRP	3.9
2	m	146	TRP	3.9
1	O	416	ALA	3.9
1	O	444	LEU	3.9
1	X	539	LEU	3.9
1	E	12	LEU	3.9
1	K	8	LEU	3.9
1	L	357	ALA	3.9
2	f	23	LEU	3.9
1	O	320	VAL	3.9
1	V	208	VAL	3.9
1	S	401	ASN	3.9
1	V	216	THR	3.9
1	B	420	VAL	3.9
1	E	445	GLU	3.9
1	F	581	VAL	3.9
1	F	586	THR	3.9
1	H	72	ARG	3.9
1	J	14	ARG	3.9
2	m	115	TYR	3.9
2	Z	67	TYR	3.9
1	A	141	ASN	3.9
1	C	100	THR	3.9
2	Z	151	ASN	3.9
2	j	78	GLU	3.9
1	Q	547	PRO	3.9
1	H	385	PRO	3.9
1	O	84	ASP	3.9
1	S	312	ASP	3.9
1	T	260	ASP	3.9
1	H	92	ASP	3.9
1	J	13	SER	3.9

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Mol	Chain	Res	Type	RSRZ
1	K	166	ASP	3.9
1	K	540	GLY	3.9
1	L	16	ASP	3.9
2	q	71	ASP	3.9
1	R	575	GLN	3.9
1	A	281	ILE	3.9
1	F	264	ILE	3.9
1	G	387	GLN	3.9
1	C	541	LYS	3.9
1	K	350	PHE	3.9
1	L	350	PHE	3.9
1	X	259	ALA	3.9
1	D	538	LEU	3.9
1	I	553	LEU	3.9
1	L	195	ALA	3.9
2	o	96	ALA	3.9
2	q	143	LEU	3.9
1	W	26	ARG	3.9
1	I	376	ARG	3.9
1	J	249	ARG	3.9
1	N	38	VAL	3.9
1	G	506	VAL	3.9
1	I	397	VAL	3.9
2	h	92	VAL	3.9
1	U	371	TYR	3.9
1	A	495	GLU	3.9
1	B	227	GLU	3.9
1	F	542	THR	3.9
1	G	138	THR	3.9
1	H	70	GLU	3.9
1	Q	210	PRO	3.9
1	X	205	ASN	3.9
1	B	204	PRO	3.9
1	K	337	ASN	3.9
1	L	141	ASN	3.9
2	v	141	PRO	3.9
2	c	53	MET	3.9
1	M	42	ASP	3.9
1	O	324	LYS	3.9
1	R	333	ILE	3.9
1	V	356	ILE	3.9
1	E	255	ILE	3.9

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Mol	Chain	Res	Type	RSRZ
1	J	186	ASP	3.9
1	L	367	ASP	3.9
2	v	8	ASP	3.9
2	Y	103	ASP	3.9
2	h	63	ILE	3.9
1	T	56	GLN	3.9
1	T	598	GLN	3.9
1	W	247	PHE	3.9
1	D	432	PHE	3.9
1	K	187	PHE	3.9
1	N	177	HIS	3.9
2	i	94	HIS	3.9
1	U	453	LEU	3.9
1	V	551	LEU	3.9
1	A	538	LEU	3.9
1	E	554	LEU	3.9
1	I	405	LEU	3.9
2	t	17	LEU	3.9
1	M	400	ALA	3.9
1	C	411	ALA	3.9
1	K	285	ALA	3.9
1	K	390	ALA	3.9
1	K	249	ARG	3.8
2	r	76	ARG	3.8
2	t	90	ARG	3.8
1	W	435	VAL	3.8
1	L	315	VAL	3.8
1	U	316	TYR	3.8
1	O	284	THR	3.8
1	U	213	THR	3.8
1	A	379	GLU	3.8
1	E	377	THR	3.8
1	E	546	THR	3.8
1	F	423	GLU	3.8
1	I	392	TYR	3.8
1	J	306	GLU	3.8
1	J	363	TYR	3.8
1	L	369	TYR	3.8
1	G	409	THR	3.8
1	K	20	THR	3.8
1	M	346	LYS	3.8
1	O	385	PRO	3.8

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Mol	Chain	Res	Type	RSRZ
1	T	199	PRO	3.8
1	B	96	GLY	3.8
1	T	161	ASN	3.8
1	B	264	ILE	3.8
1	B	288	LYS	3.8
1	B	502	GLY	3.8
1	C	345	PRO	3.8
1	J	388	PRO	3.8
2	Y	159	PRO	3.8
1	B	157	ILE	3.8
1	G	176	ILE	3.8
1	I	251	ILE	3.8
1	I	535	ILE	3.8
2	Z	112	ILE	3.8
2	a	100	ILE	3.8
2	e	151	ASN	3.8
2	i	63	ILE	3.8
1	P	178	SER	3.8
1	A	187	PHE	3.8
1	A	233	PHE	3.8
1	Q	253	ASP	3.8
1	S	245	SER	3.8
1	S	279	SER	3.8
1	T	279	SER	3.8
1	U	58	ASP	3.8
1	D	250	ASP	3.8
1	D	312	ASP	3.8
1	D	433	ASP	3.8
1	F	52	GLN	3.8
2	a	126	GLN	3.8
1	O	33	LEU	3.8
1	B	507	LEU	3.8
2	h	26	LEU	3.8
1	O	441	ARG	3.8
1	Q	459	ARG	3.8
1	Q	533	ALA	3.8
1	R	172	HIS	3.8
1	R	184	TRP	3.8
1	T	592	TRP	3.8
1	W	338	ALA	3.8
1	D	91	ALA	3.8
1	J	431	ALA	3.8

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Mol	Chain	Res	Type	RSRZ
1	J	454	ALA	3.8
1	K	431	ALA	3.8
2	m	107	ALA	3.8
2	i	116	ALA	3.8
1	H	93	VAL	3.8
1	K	244	VAL	3.8
1	P	283	CYS	3.8
1	M	108	LYS	3.8
1	R	313	LYS	3.8
1	T	371	TYR	3.8
1	W	98	TYR	3.8
1	B	246	TYR	3.8
1	C	314	GLU	3.8
1	F	403	TYR	3.8
1	J	348	LYS	3.8
2	l	115	TYR	3.8
2	d	55	GLU	3.8
2	h	125	LYS	3.8
1	O	510	ILE	3.8
1	A	11	ILE	3.8
1	B	210	PRO	3.8
1	J	238	PRO	3.8
1	K	353	PRO	3.8
1	L	284	THR	3.8
2	t	24	THR	3.8
2	a	65	THR	3.8
2	h	109	THR	3.8
2	u	104	ILE	3.8
1	P	263	PHE	3.8
1	Q	436	ASN	3.8
1	T	449	PHE	3.8
1	F	57	PHE	3.8
1	M	291	GLN	3.8
1	N	258	LEU	3.8
1	P	94	LEU	3.8
1	A	212	LEU	3.8
1	Q	441	ARG	3.8
1	N	421	ASP	3.8
1	P	21	ALA	3.8
1	U	367	ASP	3.8
1	V	250	ASP	3.8
1	X	451	ASP	3.8

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Mol	Chain	Res	Type	RSRZ
1	D	160	SER	3.8
1	I	72	ARG	3.8
1	J	511	ARG	3.8
2	t	81	SER	3.8
1	C	408	ALA	3.8
1	J	114	ALA	3.8
2	l	96	ALA	3.8
2	Z	82	HIS	3.8
2	c	128	ALA	3.8
2	g	45	ALA	3.8
1	A	158	TRP	3.8
1	O	111	VAL	3.8
1	S	565	VAL	3.8
1	W	412	VAL	3.8
1	W	565	VAL	3.8
1	X	123	VAL	3.8
1	G	123	VAL	3.8
2	d	92	VAL	3.8
1	D	504	LYS	3.8
2	i	53	MET	3.8
1	A	230	GLU	3.8
1	B	535	ILE	3.8
1	C	534	GLU	3.8
1	H	227	GLU	3.8
1	K	354	GLU	3.8
1	L	326	GLY	3.8
2	v	57	GLY	3.8
2	b	38	GLU	3.8
2	b	55	GLU	3.8
1	S	216	THR	3.8
1	U	434	THR	3.8
1	I	284	THR	3.8
1	J	350	PHE	3.8
1	C	418	LEU	3.8
1	D	103	ARG	3.8
1	C	327	GLN	3.8
2	g	126	GLN	3.8
1	N	29	ALA	3.8
1	Q	29	ALA	3.8
1	T	259	ALA	3.8
1	G	259	ALA	3.8
1	K	442	ALA	3.8

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Mol	Chain	Res	Type	RSRZ
1	L	107	ALA	3.8
2	d	116	ALA	3.8
2	i	51	ALA	3.8
1	N	77	ASP	3.8
1	O	192	ASP	3.8
1	Q	367	ASP	3.8
1	W	134	ASP	3.8
1	B	172	HIS	3.8
1	E	162	SER	3.8
1	F	18	ASP	3.8
1	G	260	ASP	3.8
1	M	420	VAL	3.8
1	R	315	VAL	3.8
1	U	565	VAL	3.8
1	V	225	VAL	3.8
1	X	592	TRP	3.8
1	C	319	VAL	3.8
1	K	184	TRP	3.8
2	h	89	VAL	3.8
1	W	313	LYS	3.8
1	C	163	LYS	3.8
1	F	583	LYS	3.8
2	j	52	MET	3.8
1	R	503	GLU	3.8
1	S	11	ILE	3.8
1	V	354	GLU	3.8
1	A	371	TYR	3.8
1	F	251	ILE	3.8
1	I	298	ILE	3.8
1	K	176	ILE	3.8
1	E	370	PRO	3.8
1	K	414	GLU	3.8
2	l	18	GLY	3.8
2	v	115	TYR	3.8
2	h	124	TYR	3.8
1	M	455	THR	3.8
1	P	35	PHE	3.8
1	Q	258	LEU	3.8
1	F	374	LEU	3.8
1	G	304	PHE	3.8
1	H	87	ARG	3.8
1	H	213	THR	3.8

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Mol	Chain	Res	Type	RSRZ
1	I	8	LEU	3.8
1	I	14	ARG	3.8
2	k	14	LEU	3.8
2	d	123	LEU	3.8
1	M	232	ALA	3.8
1	R	573	ASN	3.8
1	W	205	ASN	3.8
1	X	597	GLN	3.8
1	H	399	GLN	3.8
2	c	29	ALA	3.8
2	d	153	ASN	3.8
1	A	244	VAL	3.8
1	F	39	SER	3.8
1	F	162	SER	3.8
1	K	154	SER	3.8
1	M	18	ASP	3.8
1	N	197	ASP	3.8
1	T	159	ASP	3.8
1	U	237	ASP	3.8
1	V	197	ASP	3.8
1	W	253	ASP	3.8
1	B	570	ASP	3.8
1	K	368	ASP	3.8
1	K	443	ASP	3.8
2	t	146	TRP	3.8
1	N	219	ILE	3.8
1	P	300	ILE	3.8
1	T	251	ILE	3.8
1	F	144	ILE	3.8
1	S	602	GLY	3.8
1	C	241	GLY	3.8
1	P	538	LEU	3.8
1	S	593	LEU	3.8
1	T	385	PRO	3.8
1	E	230	GLU	3.8
1	G	72	ARG	3.8
1	E	373	LEU	3.8
1	G	543	PRO	3.8
1	J	371	TYR	3.8
1	H	551	LEU	3.8
1	J	553	LEU	3.8
1	K	329	LEU	3.8

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Mol	Chain	Res	Type	RSRZ
1	L	75	PRO	3.8
1	L	513	ARG	3.8
2	k	125	ARG	3.8
1	B	593	LEU	3.8
1	C	329	LEU	3.8
1	G	557	PHE	3.8
1	I	247	PHE	3.8
2	r	40	LEU	3.8
1	U	174	THR	3.8
1	F	20	THR	3.8
2	p	134	THR	3.8
2	b	98	CYS	3.8
2	d	98	CYS	3.8
1	P	442	ALA	3.7
1	B	572	ALA	3.7
1	K	357	ALA	3.7
1	L	400	ALA	3.7
2	u	23	ALA	3.7
2	Z	21	ALA	3.7
2	e	29	ALA	3.7
2	f	101	ALA	3.7
1	R	270	GLN	3.7
1	A	429	GLN	3.7
1	X	401	ASN	3.7
1	O	155	HIS	3.7
1	O	448	VAL	3.7
1	H	252	LYS	3.7
2	Z	61	LYS	3.7
2	e	147	ASN	3.7
1	P	69	SER	3.7
1	X	184	TRP	3.7
2	r	146	TRP	3.7
2	h	56	TRP	3.7
2	j	148	SER	3.7
1	N	131	ASP	3.7
1	Q	197	ASP	3.7
1	G	383	ASP	3.7
1	H	509	ASP	3.7
1	J	134	ASP	3.7
2	m	8	ASP	3.7
2	e	31	ASP	3.7
1	W	280	ILE	3.7

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Mol	Chain	Res	Type	RSRZ
1	W	281	ILE	3.7
1	Q	8	LEU	3.7
1	S	560	LEU	3.7
1	X	51	LEU	3.7
1	C	384	LEU	3.7
1	E	227	GLU	3.7
1	F	117	GLU	3.7
1	F	210	PRO	3.7
2	Z	123	LEU	3.7
2	c	84	LEU	3.7
2	e	76	PRO	3.7
2	i	152	LEU	3.7
1	N	495	GLU	3.7
1	R	557	PHE	3.7
1	F	233	PHE	3.7
1	H	185	GLU	3.7
1	J	263	PHE	3.7
1	J	403	TYR	3.7
1	L	98	TYR	3.7
1	Q	409	THR	3.7
1	G	377	THR	3.7
2	u	56	THR	3.7
1	O	121	ALA	3.7
1	A	574	LYS	3.7
1	K	290	LYS	3.7
2	Y	108	ALA	3.7
1	B	208	VAL	3.7
1	C	68	VAL	3.7
1	E	202	GLN	3.7
1	G	63	VAL	3.7
1	H	506	VAL	3.7
1	I	38	VAL	3.7
1	A	155	HIS	3.7
1	G	112	ASN	3.7
1	A	146	ARG	3.7
1	A	264	ILE	3.7
1	A	275	ARG	3.7
1	E	281	ILE	3.7
1	J	119	ILE	3.7
1	K	168	SER	3.7
1	K	513	ARG	3.7
1	M	312	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
1	O	325	ASP	3.7
1	F	166	ASP	3.7
1	G	312	ASP	3.7
1	I	256	ASP	3.7
1	I	312	ASP	3.7
1	K	312	ASP	3.7
2	l	62	ASP	3.7
2	d	71	ASP	3.7
1	M	79	LEU	3.7
2	i	27	GLY	3.7
1	U	557	PHE	3.7
1	O	548	GLU	3.7
1	S	199	PRO	3.7
1	A	395	PRO	3.7
1	X	246	TYR	3.7
2	n	48	TYR	3.7
2	q	48	TYR	3.7
2	c	50	GLU	3.7
1	M	138	THR	3.7
1	P	228	LYS	3.7
1	U	240	THR	3.7
1	W	108	LYS	3.7
1	B	190	LYS	3.7
1	H	446	THR	3.7
2	c	15	LYS	3.7
2	h	120	LYS	3.7
1	O	110	ALA	3.7
1	R	107	ALA	3.7
1	X	456	ALA	3.7
1	B	91	ALA	3.7
2	o	99	ALA	3.7
2	Z	101	ALA	3.7
1	P	111	VAL	3.7
1	S	276	VAL	3.7
1	T	420	VAL	3.7
1	B	520	VAL	3.7
1	X	153	CYS	3.7
1	D	218	GLN	3.7
2	j	98	CYS	3.7
1	O	177	HIS	3.7
1	D	72	ARG	3.7
2	a	153	ASN	3.7

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Mol	Chain	Res	Type	RSRZ
1	P	510	ILE	3.7
1	C	217	ILE	3.7
1	C	281	ILE	3.7
1	F	211	TRP	3.7
1	F	333	ILE	3.7
1	O	552	LEU	3.7
1	P	373	LEU	3.7
1	S	418	LEU	3.7
1	V	212	LEU	3.7
1	W	373	LEU	3.7
1	W	538	LEU	3.7
1	W	539	LEU	3.7
1	E	326	GLY	3.7
1	E	383	ASP	3.7
1	F	580	GLY	3.7
1	F	602	GLY	3.7
1	G	206	ASP	3.7
1	G	540	GLY	3.7
1	K	335	SER	3.7
2	i	86	SER	3.7
2	i	148	SER	3.7
1	Q	101	ASP	3.7
1	V	498	ASP	3.7
1	W	364	ASP	3.7
1	B	43	ASP	3.7
1	L	209	PHE	3.7
2	l	94	ASP	3.7
2	t	38	ASP	3.7
2	g	71	ASP	3.7
1	O	210	PRO	3.7
1	V	210	PRO	3.7
1	P	288	LYS	3.7
1	W	191	TYR	3.7
2	h	118	TYR	3.7
2	i	25	LYS	3.7
1	N	121	ALA	3.7
1	A	220	ALA	3.7
1	B	20	THR	3.7
1	C	431	ALA	3.7
1	L	431	ALA	3.7
2	a	115	THR	3.7
2	e	33	THR	3.7

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Mol	Chain	Res	Type	RSRZ
1	Q	254	VAL	3.7
1	M	327	GLN	3.7
1	R	14	ARG	3.7
1	R	47	GLN	3.7
1	S	525	GLN	3.7
1	W	327	GLN	3.7
1	X	270	GLN	3.7
1	G	532	ARG	3.7
1	L	249	ARG	3.7
1	R	283	CYS	3.7
2	d	82	HIS	3.7
1	H	198	ILE	3.7
2	l	103	ILE	3.7
2	o	103	ILE	3.7
1	W	331	ASN	3.7
1	A	184	TRP	3.7
1	A	576	LEU	3.7
1	B	184	TRP	3.7
1	B	193	LEU	3.7
1	E	508	ASN	3.7
1	L	331	ASN	3.7
2	e	26	LEU	3.7
1	J	504	LYS	3.7
1	L	504	LYS	3.7
2	q	60	PHE	3.7
1	U	75	PRO	3.7
1	G	162	SER	3.7
1	G	385	PRO	3.7
2	l	81	SER	3.7
2	a	86	SER	3.7
1	N	383	ASP	3.7
1	Q	548	GLU	3.7
1	F	257	ASP	3.7
1	H	53	TYR	3.7
1	J	317	GLU	3.7
1	L	215	ASP	3.7
1	L	433	ASP	3.7
2	a	118	TYR	3.7
1	X	338	ALA	3.7
1	C	86	ALA	3.7
1	F	424	ALA	3.7
2	d	97	ALA	3.7

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Mol	Chain	Res	Type	RSRZ
1	Q	123	VAL	3.7
1	V	386	THR	3.7
1	B	581	VAL	3.7
1	J	239	VAL	3.7
1	J	446	THR	3.7
1	L	78	VAL	3.7
1	N	591	GLN	3.7
1	A	575	GLN	3.7
1	D	529	GLN	3.7
1	F	590	GLN	3.7
2	q	49	GLN	3.7
1	X	266	ILE	3.7
1	E	198	ILE	3.7
1	J	356	ILE	3.7
1	L	361	HIS	3.7
1	N	33	LEU	3.7
1	F	538	LEU	3.7
2	m	97	LEU	3.7
2	o	17	LEU	3.7
1	S	337	ASN	3.7
1	B	44	TRP	3.7
1	C	205	ASN	3.7
1	F	30	LYS	3.7
1	G	44	TRP	3.7
1	J	541	LYS	3.7
1	K	313	LYS	3.7
1	K	331	ASN	3.7
2	c	74	ASN	3.7
2	g	25	LYS	3.7
1	L	233	PHE	3.7
1	G	62	PRO	3.6
1	K	398	PRO	3.6
2	o	112	GLU	3.6
2	p	81	SER	3.6
1	O	53	TYR	3.6
1	O	312	ASP	3.6
1	P	107	ALA	3.6
1	S	339	ASP	3.6
1	T	220	ALA	3.6
1	V	259	ALA	3.6
1	X	195	ALA	3.6
1	A	572	ALA	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	315	VAL	3.6
1	C	400	ALA	3.6
1	C	433	ASP	3.6
1	G	58	ASP	3.6
1	I	246	TYR	3.6
2	k	10	VAL	3.6
2	s	88	ALA	3.6
2	Y	67	TYR	3.6
2	a	97	ALA	3.6
2	g	78	GLU	3.6
1	J	506	VAL	3.6
1	A	27	ARG	3.6
1	C	459	ARG	3.6
1	V	138	THR	3.6
1	X	558	THR	3.6
1	C	49	THR	3.6
2	q	24	THR	3.6
1	W	591	GLN	3.6
1	X	94	LEU	3.6
1	B	333	ILE	3.6
1	B	450	GLN	3.6
1	I	418	LEU	3.6
1	J	251	ILE	3.6
1	K	539	LEU	3.6
2	p	87	LEU	3.6
1	E	172	HIS	3.6
1	W	30	LYS	3.6
2	d	125	LYS	3.6
1	M	211	TRP	3.6
1	M	331	ASN	3.6
1	O	337	ASN	3.6
1	W	326	GLY	3.6
1	D	295	GLY	3.6
1	H	516	CYS	3.6
1	I	359	PHE	3.6
1	H	394	ASN	3.6
1	E	210	PRO	3.6
1	H	388	PRO	3.6
2	m	141	PRO	3.6
1	M	397	VAL	3.6
1	Q	407	ALA	3.6
1	N	235	TYR	3.6

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Mol	Chain	Res	Type	RSRZ
1	X	22	SER	3.6
1	X	224	GLU	3.6
1	C	230	GLU	3.6
1	H	306	GLU	3.6
1	I	314	GLU	3.6
2	r	83	VAL	3.6
2	s	123	ALA	3.6
2	c	46	VAL	3.6
2	g	110	ALA	3.6
2	s	148	TYR	3.6
2	v	48	TYR	3.6
2	f	137	TYR	3.6
1	O	367	ASP	3.6
1	S	378	ASP	3.6
1	D	16	ASP	3.6
1	D	451	ASP	3.6
1	H	260	ASP	3.6
2	o	94	ASP	3.6
2	v	35	ASP	3.6
1	P	409	THR	3.6
1	S	455	THR	3.6
1	H	138	THR	3.6
2	m	26	THR	3.6
2	n	56	THR	3.6
2	Y	65	THR	3.6
2	f	143	THR	3.6
1	P	251	ILE	3.6
1	C	287	LEU	3.6
1	D	536	LEU	3.6
1	F	266	ILE	3.6
2	n	104	ILE	3.6
2	Y	123	LEU	3.6
1	R	528	LYS	3.6
1	V	505	GLN	3.6
1	F	582	LYS	3.6
1	L	252	LYS	3.6
1	J	361	HIS	3.6
1	D	263	PHE	3.6
1	F	557	PHE	3.6
1	E	262	GLY	3.6
1	O	182	ASN	3.6
1	R	370	PRO	3.6

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Mol	Chain	Res	Type	RSRZ
1	G	587	PRO	3.6
1	I	380	ASN	3.6
1	J	148	PRO	3.6
2	r	150	PRO	3.6
2	h	153	ASN	3.6
1	N	267	ALA	3.6
1	O	86	ALA	3.6
1	U	581	VAL	3.6
1	V	301	VAL	3.6
1	X	408	ALA	3.6
1	A	267	ALA	3.6
1	B	29	ALA	3.6
1	J	68	VAL	3.6
1	K	286	VAL	3.6
1	L	397	VAL	3.6
1	L	430	VAL	3.6
2	o	23	ALA	3.6
2	p	23	ALA	3.6
1	S	70	GLU	3.6
1	F	133	GLU	3.6
1	H	537	GLU	3.6
2	n	112	GLU	3.6
2	c	107	GLU	3.6
1	U	277	TYR	3.6
1	M	180	SER	3.6
1	J	526	SER	3.6
1	R	194	ASP	3.6
1	R	206	ASP	3.6
1	X	206	ASP	3.6
1	E	196	ASP	3.6
1	F	159	ASP	3.6
1	J	84	ASP	3.6
1	J	339	ASP	3.6
1	L	460	ASP	3.6
2	u	94	ASP	3.6
2	Z	152	LEU	3.6
2	d	80	ASP	3.6
1	N	228	LYS	3.6
1	W	76	ILE	3.6
1	C	240	THR	3.6
1	K	340	ILE	3.6
2	g	26	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	S	450	GLN	3.6
1	V	73	GLN	3.6
2	b	126	GLN	3.6
1	Q	233	PHE	3.6
1	O	540	GLY	3.6
1	P	564	GLY	3.6
1	I	183	GLY	3.6
2	d	16	GLY	3.6
1	L	99	ARG	3.6
1	L	459	ARG	3.6
1	Q	385	PRO	3.6
2	o	93	PRO	3.6
1	M	342	ALA	3.6
1	N	565	VAL	3.6
1	P	456	ALA	3.6
1	S	129	VAL	3.6
1	E	107	ALA	3.6
1	E	411	ALA	3.6
1	F	38	VAL	3.6
1	K	143	VAL	3.6
2	u	99	ALA	3.6
2	g	19	VAL	3.6
1	Q	153	CYS	3.6
1	B	31	ASN	3.6
1	B	140	ASN	3.6
1	G	331	ASN	3.6
1	L	227	GLU	3.6
2	j	55	GLU	3.6
1	T	556	TYR	3.6
1	X	98	TYR	3.6
1	E	536	LEU	3.6
1	E	539	LEU	3.6
1	I	444	LEU	3.6
1	J	8	LEU	3.6
1	K	51	LEU	3.6
1	K	583	LYS	3.6
1	L	571	TYR	3.6
1	R	258	LEU	3.6
1	D	438	LEU	3.6
1	R	13	SER	3.6
1	R	300	ILE	3.6
1	S	538	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	L	510	ILE	3.6
2	u	143	LEU	3.6
2	f	123	LEU	3.6
1	F	180	SER	3.6
1	G	39	SER	3.6
2	n	78	SER	3.6
1	M	367	ASP	3.6
1	O	20	THR	3.6
1	R	421	ASP	3.6
1	R	519	ASP	3.6
1	U	84	ASP	3.6
1	V	518	THR	3.6
1	W	451	ASP	3.6
1	F	237	ASP	3.6
1	G	131	ASP	3.6
1	I	174	THR	3.6
1	J	421	ASP	3.6
1	K	325	ASP	3.6
2	Z	14	THR	3.6
2	Z	143	THR	3.6
1	M	505	GLN	3.6
1	A	56	GLN	3.6
1	E	555	GLN	3.6
1	H	578	GLN	3.6
1	L	270	GLN	3.6
1	I	104	HIS	3.6
1	J	57	PHE	3.6
1	P	441	ARG	3.6
1	U	273	ARG	3.6
1	C	96	GLY	3.6
1	J	269	ARG	3.6
2	f	24	ARG	3.6
1	V	211	TRP	3.6
1	M	121	ALA	3.6
1	N	62	PRO	3.6
1	O	500	ALA	3.6
1	Q	220	ALA	3.6
1	R	64	VAL	3.6
1	V	111	VAL	3.6
1	W	370	PRO	3.6
1	W	385	PRO	3.6
1	A	345	PRO	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	121	ALA	3.6
1	G	195	ALA	3.6
1	G	301	VAL	3.6
1	I	416	ALA	3.6
1	J	303	VAL	3.6
2	c	21	ALA	3.6
1	M	31	ASN	3.6
1	S	120	GLU	3.6
1	U	108	LYS	3.6
1	D	426	ASN	3.6
1	E	418	LEU	3.6
1	E	566	GLU	3.6
1	F	531	ASN	3.6
1	H	379	GLU	3.6
1	K	205	ASN	3.6
1	V	539	LEU	3.6
1	V	576	LEU	3.6
1	M	577	ILE	3.6
1	N	98	TYR	3.6
1	N	266	ILE	3.6
1	R	277	TYR	3.6
1	W	48	TYR	3.6
1	X	418	LEU	3.6
1	A	552	LEU	3.6
2	l	143	LEU	3.6
2	n	87	LEU	3.6
2	q	46	GLU	3.6
2	Y	23	LEU	3.6
2	b	50	GLU	3.6
2	Z	57	TYR	3.6
2	h	49	LEU	3.6
1	X	271	ILE	3.6
1	B	251	ILE	3.6
1	D	280	ILE	3.6
1	K	298	ILE	3.6
2	j	67	TYR	3.6
1	S	381	SER	3.6
1	T	410	SER	3.6
1	B	200	SER	3.6
1	F	178	SER	3.6
1	G	323	THR	3.6
1	I	178	SER	3.6

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Mol	Chain	Res	Type	RSRZ
1	L	139	SER	3.6
1	L	216	THR	3.6
2	j	109	THR	3.6
1	R	237	ASP	3.6
1	C	166	ASP	3.6
1	G	215	ASP	3.6
1	K	186	ASP	3.6
1	T	14	ARG	3.5
1	U	601	GLN	3.5
1	B	597	GLN	3.5
1	E	187	PHE	3.5
1	I	263	PHE	3.5
1	K	172	HIS	3.5
1	T	502	GLY	3.5
1	A	326	GLY	3.5
1	F	241	GLY	3.5
1	J	562	GLY	3.5
2	s	74	GLY	3.5
1	N	137	PRO	3.5
1	U	38	VAL	3.5
1	X	111	VAL	3.5
1	X	156	VAL	3.5
1	H	63	VAL	3.5
1	J	62	PRO	3.5
1	K	415	VAL	3.5
1	L	415	VAL	3.5
1	L	587	PRO	3.5
2	k	146	TRP	3.5
2	o	66	PRO	3.5
2	f	92	VAL	3.5
1	Q	21	ALA	3.5
1	U	195	ALA	3.5
1	Q	228	LYS	3.5
1	S	108	LYS	3.5
1	F	541	LYS	3.5
1	K	272	LYS	3.5
2	Z	15	LYS	3.5
1	W	559	LEU	3.5
1	B	12	LEU	3.5
1	J	67	LEU	3.5
2	k	75	LEU	3.5
2	m	143	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
2	g	53	MET	3.5
2	h	152	LEU	3.5
1	P	534	GLU	3.5
1	P	537	GLU	3.5
1	A	70	GLU	3.5
1	N	556	TYR	3.5
1	R	531	ASN	3.5
1	G	311	GLU	3.5
1	K	333	ILE	3.5
1	L	24	GLU	3.5
1	L	251	ILE	3.5
1	L	333	ILE	3.5
2	n	138	ASN	3.5
2	r	46	GLU	3.5
2	h	64	ILE	3.5
2	h	100	ILE	3.5
2	i	154	GLU	3.5
1	R	556	TYR	3.5
1	F	369	TYR	3.5
1	F	391	TYR	3.5
1	K	235	TYR	3.5
2	Z	118	TYR	3.5
1	A	283	CYS	3.5
1	P	13	SER	3.5
1	P	434	THR	3.5
1	Q	139	SER	3.5
1	U	20	THR	3.5
1	A	26	ARG	3.5
1	B	323	THR	3.5
1	G	381	SER	3.5
1	H	240	THR	3.5
1	H	518	THR	3.5
1	I	130	THR	3.5
1	I	557	PHE	3.5
1	K	36	SER	3.5
2	v	118	THR	3.5
2	Z	70	SER	3.5
2	c	14	THR	3.5
1	C	247	PHE	3.5
1	O	256	ASP	3.5
1	B	270	GLN	3.5
1	C	215	ASP	3.5

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Mol	Chain	Res	Type	RSRZ
1	D	421	ASP	3.5
1	I	591	GLN	3.5
1	F	177	HIS	3.5
1	G	361	HIS	3.5
2	c	66	GLY	3.5
2	d	62	GLY	3.5
2	e	156	HIS	3.5
1	N	594	VAL	3.5
1	B	254	VAL	3.5
1	F	167	LYS	3.5
1	H	64	VAL	3.5
1	L	152	ALA	3.5
2	o	36	ALA	3.5
2	Y	111	LYS	3.5
2	f	89	VAL	3.5
1	O	17	ALA	3.5
1	O	267	ALA	3.5
1	O	547	PRO	3.5
1	R	442	ALA	3.5
1	V	184	TRP	3.5
1	A	44	TRP	3.5
1	D	126	TRP	3.5
1	F	62	PRO	3.5
1	H	522	PRO	3.5
1	I	86	ALA	3.5
2	p	133	PRO	3.5
2	c	75	PRO	3.5
2	e	51	ALA	3.5
1	W	329	LEU	3.5
1	X	559	LEU	3.5
1	B	552	LEU	3.5
1	F	389	LEU	3.5
2	g	23	LEU	3.5
1	S	577	ILE	3.5
1	X	510	ILE	3.5
1	D	298	ILE	3.5
1	D	537	GLU	3.5
1	E	414	GLU	3.5
1	J	314	GLU	3.5
2	Y	50	GLU	3.5
2	f	78	GLU	3.5
1	U	74	ASN	3.5

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Mol	Chain	Res	Type	RSRZ
1	V	556	TYR	3.5
1	C	508	ASN	3.5
1	I	401	ASN	3.5
1	J	31	ASN	3.5
1	K	191	TYR	3.5
2	q	142	ASN	3.5
2	s	95	TYR	3.5
2	c	147	ASN	3.5
2	f	104	TYR	3.5
1	Q	273	ARG	3.5
1	W	99	ARG	3.5
2	c	99	ARG	3.5
1	W	283	CYS	3.5
1	J	283	CYS	3.5
2	o	89	CYS	3.5
1	E	542	THR	3.5
1	G	49	THR	3.5
2	l	100	THR	3.5
2	r	149	PHE	3.5
2	Y	14	THR	3.5
2	a	69	PHE	3.5
2	f	115	THR	3.5
1	N	578	GLN	3.5
1	I	505	GLN	3.5
1	L	202	GLN	3.5
2	v	81	SER	3.5
1	M	101	ASP	3.5
1	V	172	HIS	3.5
1	N	239	VAL	3.5
1	U	420	VAL	3.5
1	W	42	ASP	3.5
1	X	101	ASP	3.5
1	X	570	ASP	3.5
1	C	443	ASP	3.5
1	C	540	GLY	3.5
1	F	256	ASP	3.5
1	G	38	VAL	3.5
1	H	229	LYS	3.5
2	p	85	HIS	3.5
2	Z	47	ASP	3.5
2	Z	94	HIS	3.5
1	B	594	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
1	D	565	VAL	3.5
1	J	111	VAL	3.5
2	c	25	LYS	3.5
1	O	400	ALA	3.5
1	U	285	ALA	3.5
1	E	195	ALA	3.5
2	k	36	ALA	3.5
2	k	119	ALA	3.5
2	c	116	ALA	3.5
1	M	554	LEU	3.5
1	U	553	LEU	3.5
1	I	547	PRO	3.5
1	L	385	PRO	3.5
2	o	143	LEU	3.5
2	j	23	LEU	3.5
1	X	76	ILE	3.5
1	I	119	ILE	3.5
2	m	91	ILE	3.5
2	f	113	ILE	3.5
1	R	26	ARG	3.5
1	S	589	GLU	3.5
1	U	379	GLU	3.5
1	V	379	GLU	3.5
1	X	185	GLU	3.5
1	A	224	GLU	3.5
1	C	306	GLU	3.5
1	E	515	GLU	3.5
1	F	445	GLU	3.5
1	K	441	ARG	3.5
2	d	24	ARG	3.5
1	M	549	TYR	3.5
1	N	371	TYR	3.5
1	G	98	TYR	3.5
1	K	514	TYR	3.5
1	L	392	TYR	3.5
2	b	118	TYR	3.5
2	f	57	TYR	3.5
1	J	380	ASN	3.5
1	L	531	ASN	3.5
1	O	187	PHE	3.5
1	Q	34	PHE	3.5
1	W	359	PHE	3.5

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Mol	Chain	Res	Type	RSRZ
1	X	57	PHE	3.5
1	A	524	PHE	3.5
1	F	209	PHE	3.5
1	F	263	PHE	3.5
1	K	557	PHE	3.5
2	v	84	PHE	3.5
1	U	528	LYS	3.5
1	J	229	LYS	3.5
1	K	283	CYS	3.5
2	l	116	LYS	3.5
2	u	106	THR	3.5
2	i	115	THR	3.5
1	P	135	GLN	3.5
1	T	59	VAL	3.5
1	U	155	HIS	3.5
1	A	261	SER	3.5
1	B	381	SER	3.5
1	C	85	GLY	3.5
1	C	208	VAL	3.5
1	C	254	VAL	3.5
1	E	505	GLN	3.5
1	G	530	GLN	3.5
1	I	202	GLN	3.5
1	I	319	VAL	3.5
1	J	56	GLN	3.5
1	K	291	GLN	3.5
1	K	301	VAL	3.5
1	L	291	GLN	3.5
1	L	591	GLN	3.5
2	p	32	SER	3.5
2	p	130	SER	3.5
2	Z	66	GLY	3.5
2	d	30	SER	3.5
2	g	30	SER	3.5
1	M	8	LEU	3.5
1	O	89	ASP	3.5
1	O	166	ASP	3.5
1	O	186	ASP	3.5
1	O	453	LEU	3.5
1	C	560	LEU	3.5
1	D	253	ASP	3.5
1	D	596	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
1	G	110	ALA	3.5
1	J	561	ASP	3.5
1	K	421	ASP	3.5
2	p	92	ALA	3.5
2	q	42	ALA	3.5
1	U	398	PRO	3.5
1	U	576	LEU	3.5
1	B	329	LEU	3.5
2	u	62	ASP	3.5
1	I	370	PRO	3.5
1	J	88	PRO	3.5
1	L	547	PRO	3.5
2	k	66	PRO	3.5
2	a	122	LEU	3.5
2	e	122	LEU	3.5
1	N	19	TRP	3.5
1	P	184	TRP	3.5
1	S	255	ILE	3.5
1	T	144	ILE	3.5
2	l	91	ILE	3.5
2	Z	113	ILE	3.5
2	g	63	ILE	3.5
1	G	27	ARG	3.5
1	M	406	GLU	3.5
1	B	566	GLU	3.5
1	I	147	GLU	3.5
2	Y	73	GLU	3.5
1	U	571	TYR	3.5
1	B	517	TYR	3.5
1	D	235	TYR	3.5
1	F	371	TYR	3.5
1	M	541	LYS	3.5
1	A	35	PHE	3.5
1	N	380	ASN	3.5
1	N	541	LYS	3.5
1	B	337	ASN	3.5
1	K	541	LYS	3.5
1	L	272	LYS	3.5
1	L	439	ASN	3.5
2	t	142	ASN	3.5
1	N	386	THR	3.5
1	W	434	THR	3.5

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Mol	Chain	Res	Type	RSRZ
1	X	434	THR	3.5
1	B	415	VAL	3.5
1	P	516	CYS	3.5
1	S	580	GLY	3.5
1	S	594	VAL	3.5
1	E	254	VAL	3.5
1	H	315	VAL	3.5
1	Q	429	GLN	3.5
1	U	118	GLN	3.5
1	W	52	GLN	3.5
1	F	578	GLN	3.5
1	L	47	GLN	3.5
2	m	49	GLN	3.5
1	P	110	ALA	3.5
1	P	195	ALA	3.5
1	W	431	ALA	3.5
1	W	553	LEU	3.5
1	A	411	ALA	3.5
1	A	553	LEU	3.5
1	B	442	ALA	3.5
1	D	212	LEU	3.5
1	E	94	LEU	3.5
1	E	329	LEU	3.5
1	I	160	SER	3.5
1	I	374	LEU	3.5
1	J	357	ALA	3.5
1	K	553	LEU	3.5
2	k	107	ALA	3.5
2	l	139	SER	3.5
2	o	13	ALA	3.5
2	v	139	SER	3.5
2	Y	90	SER	3.5
2	d	148	SER	3.5
2	e	139	SER	3.5
2	f	30	SER	3.5
2	g	22	ALA	3.5
2	g	84	LEU	3.5
2	j	97	ALA	3.5
1	Q	299	PRO	3.5
1	X	204	PRO	3.5
1	D	210	PRO	3.5
1	H	345	PRO	3.5

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Mol	Chain	Res	Type	RSRZ
1	I	395	PRO	3.5
1	J	75	PRO	3.5
1	K	370	PRO	3.5
2	h	75	PRO	3.5
1	S	101	ASP	3.5
1	T	433	ASP	3.5
1	Q	26	ARG	3.5
1	X	19	TRP	3.5
1	X	264	ILE	3.5
1	J	325	ASP	3.5
2	p	38	ASP	3.5
2	q	50	ASP	3.5
2	v	94	ASP	3.5
1	B	103	ARG	3.5
1	F	19	TRP	3.5
1	F	569	ARG	3.5
1	O	185	GLU	3.4
1	T	588	GLU	3.4
1	E	314	GLU	3.4
1	E	379	GLU	3.4
1	G	185	GLU	3.4
2	k	46	GLU	3.4
2	Z	55	GLU	3.4
1	V	252	LYS	3.4
1	A	324	LYS	3.4
1	H	57	PHE	3.4
2	Z	69	PHE	3.4
1	P	401	ASN	3.4
1	C	78	VAL	3.4
1	H	565	VAL	3.4
1	J	319	VAL	3.4
1	L	380	ASN	3.4
2	h	151	ASN	3.4
1	N	518	THR	3.4
1	O	428	GLY	3.4
1	M	590	GLN	3.4
1	O	212	LEU	3.4
1	P	216	THR	3.4
1	P	505	GLN	3.4
1	Q	338	ALA	3.4
1	R	416	ALA	3.4
1	S	533	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
1	W	322	LEU	3.4
1	X	329	LEU	3.4
1	C	231	THR	3.4
1	C	417	THR	3.4
1	E	258	LEU	3.4
1	E	438	LEU	3.4
1	F	386	THR	3.4
2	a	16	GLY	3.4
1	T	361	HIS	3.4
1	B	601	GLN	3.4
1	C	438	LEU	3.4
1	H	135	GLN	3.4
2	p	12	ALA	3.4
1	F	516	CYS	3.4
1	N	532	ARG	3.4
1	O	261	SER	3.4
1	Q	458	ARG	3.4
1	X	75	PRO	3.4
1	C	251	ILE	3.4
1	C	388	PRO	3.4
1	D	171	ARG	3.4
1	E	136	SER	3.4
1	E	245	SER	3.4
1	E	328	ARG	3.4
1	H	39	SER	3.4
1	H	381	SER	3.4
2	d	70	SER	3.4
1	M	433	ASP	3.4
1	N	312	ASP	3.4
1	N	367	ASP	3.4
1	P	58	ASP	3.4
1	P	215	ASP	3.4
1	P	383	ASP	3.4
1	Q	134	ASP	3.4
1	Q	364	ASP	3.4
1	S	367	ASP	3.4
1	C	197	ASP	3.4
1	F	289	ASP	3.4
1	G	166	ASP	3.4
1	I	166	ASP	3.4
1	I	421	ASP	3.4
1	K	23	ASP	3.4

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Mol	Chain	Res	Type	RSRZ
1	K	364	ASP	3.4
1	L	134	ASP	3.4
1	L	196	ASP	3.4
1	L	561	ASP	3.4
1	Q	229	LYS	3.4
1	L	108	LYS	3.4
1	U	354	GLU	3.4
1	V	515	GLU	3.4
1	B	317	GLU	3.4
1	B	354	GLU	3.4
1	C	133	GLU	3.4
1	C	354	GLU	3.4
1	F	227	GLU	3.4
2	s	98	GLU	3.4
2	f	55	GLU	3.4
1	A	432	PHE	3.4
1	D	447	TYR	3.4
2	Z	157	TYR	3.4
2	b	157	TYR	3.4
2	d	124	TYR	3.4
1	O	303	VAL	3.4
1	Q	64	VAL	3.4
1	S	208	VAL	3.4
1	A	239	VAL	3.4
1	I	420	VAL	3.4
1	K	412	VAL	3.4
1	M	292	LEU	3.4
1	T	576	LEU	3.4
1	U	552	LEU	3.4
1	V	559	LEU	3.4
1	W	212	LEU	3.4
1	F	287	LEU	3.4
1	H	512	GLY	3.4
1	K	74	ASN	3.4
1	K	212	LEU	3.4
1	K	405	LEU	3.4
1	M	417	THR	3.4
1	N	377	THR	3.4
1	T	216	THR	3.4
1	N	47	GLN	3.4
1	O	114	ALA	3.4
1	R	327	GLN	3.4

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Mol	Chain	Res	Type	RSRZ
1	X	125	ALA	3.4
1	X	518	THR	3.4
1	B	518	THR	3.4
2	n	86	ASN	3.4
1	A	40	GLN	3.4
1	C	456	ALA	3.4
1	C	591	GLN	3.4
2	e	97	ALA	3.4
1	R	88	PRO	3.4
1	W	234	ILE	3.4
1	A	199	PRO	3.4
1	L	302	PRO	3.4
2	r	93	PRO	3.4
2	t	66	PRO	3.4
2	Z	138	PRO	3.4
2	j	75	PRO	3.4
1	Q	516	CYS	3.4
1	B	153	CYS	3.4
1	S	526	SER	3.4
1	T	160	SER	3.4
1	V	335	SER	3.4
2	k	81	SER	3.4
2	m	61	SER	3.4
2	n	81	SER	3.4
2	q	32	SER	3.4
2	v	130	SER	3.4
1	M	163	LYS	3.4
1	P	108	LYS	3.4
1	U	19	TRP	3.4
1	A	313	LYS	3.4
1	L	44	TRP	3.4
1	P	451	ASP	3.4
1	S	253	ASP	3.4
1	C	159	ASP	3.4
1	G	43	ASP	3.4
1	I	58	ASP	3.4
1	N	117	GLU	3.4
1	O	263	PHE	3.4
1	V	227	GLU	3.4
1	C	595	GLU	3.4
1	J	5	GLU	3.4
1	K	247	PHE	3.4

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Mol	Chain	Res	Type	RSRZ
1	L	336	PHE	3.4
1	L	406	GLU	3.4
2	c	55	GLU	3.4
1	S	571	TYR	3.4
1	L	80	TYR	3.4
2	h	57	TYR	3.4
1	N	315	VAL	3.4
1	O	129	VAL	3.4
1	D	208	VAL	3.4
1	K	60	VAL	3.4
1	O	554	LEU	3.4
1	R	553	LEU	3.4
1	F	418	LEU	3.4
1	F	553	LEU	3.4
1	M	458	ARG	3.4
1	T	65	ARG	3.4
1	C	103	ARG	3.4
1	C	328	ARG	3.4
1	D	358	GLY	3.4
1	G	17	ALA	3.4
1	H	441	ARG	3.4
1	L	116	ARG	3.4
1	L	121	ALA	3.4
2	k	42	ALA	3.4
2	q	13	ALA	3.4
2	Y	32	ALA	3.4
2	Z	85	ARG	3.4
2	f	85	ARG	3.4
1	N	356	ILE	3.4
1	N	505	GLN	3.4
1	Q	333	ILE	3.4
1	Q	535	ILE	3.4
1	S	387	GLN	3.4
1	T	437	GLN	3.4
1	A	73	GLN	3.4
1	A	452	ASN	3.4
1	A	573	ASN	3.4
1	B	213	THR	3.4
1	D	138	THR	3.4
1	F	505	GLN	3.4
1	H	377	THR	3.4
1	I	47	GLN	3.4

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Mol	Chain	Res	Type	RSRZ
1	I	112	ASN	3.4
1	I	142	GLN	3.4
1	K	518	THR	3.4
2	l	24	THR	3.4
2	m	44	MET	3.4
1	D	530	GLN	3.4
2	t	54	ILE	3.4
2	d	58	GLN	3.4
2	i	113	ILE	3.4
1	P	388	PRO	3.4
1	S	584	PRO	3.4
2	t	141	PRO	3.4
1	O	528	LYS	3.4
1	Q	248	LYS	3.4
2	j	25	LYS	3.4
1	P	39	SER	3.4
1	R	44	TRP	3.4
1	R	200	SER	3.4
1	X	211	TRP	3.4
1	C	69	SER	3.4
1	H	44	TRP	3.4
1	O	433	ASP	3.4
1	B	519	ASP	3.4
1	C	16	ASP	3.4
1	M	70	GLU	3.4
1	R	224	GLU	3.4
1	S	449	PHE	3.4
1	H	15	PHE	3.4
1	H	256	ASP	3.4
1	L	260	ASP	3.4
2	o	149	PHE	3.4
1	M	128	LEU	3.4
1	T	319	VAL	3.4
1	T	438	LEU	3.4
1	U	93	VAL	3.4
1	U	191	TYR	3.4
1	V	98	TYR	3.4
1	W	225	VAL	3.4
1	W	581	VAL	3.4
1	A	329	LEU	3.4
1	A	369	TYR	3.4
1	B	64	VAL	3.4

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Mol	Chain	Res	Type	RSRZ
1	D	403	TYR	3.4
1	I	292	LEU	3.4
1	K	341	VAL	3.4
1	K	536	LEU	3.4
1	L	258	LEU	3.4
1	L	539	LEU	3.4
2	k	19	VAL	3.4
2	c	157	TYR	3.4
2	f	152	LEU	3.4
2	h	96	LEU	3.4
1	P	14	ARG	3.4
1	D	26	ARG	3.4
1	E	171	ARG	3.4
1	G	249	ARG	3.4
1	L	72	ARG	3.4
1	L	269	ARG	3.4
1	M	91	ALA	3.4
1	T	21	ALA	3.4
1	V	122	GLY	3.4
1	D	456	ALA	3.4
1	F	122	GLY	3.4
1	I	85	GLY	3.4
1	K	533	ALA	3.4
1	L	572	ALA	3.4
2	v	99	ALA	3.4
1	Q	271	ILE	3.4
1	V	264	ILE	3.4
1	B	119	ILE	3.4
1	M	118	GLN	3.4
1	R	386	THR	3.4
1	R	401	ASN	3.4
1	R	504	LYS	3.4
1	T	380	ASN	3.4
1	A	550	GLN	3.4
1	C	172	HIS	3.4
1	C	344	THR	3.4
1	E	535	ILE	3.4
1	H	386	THR	3.4
1	I	11	ILE	3.4
2	k	54	ILE	3.4
2	a	113	ILE	3.4
2	c	63	ILE	3.4

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Mol	Chain	Res	Type	RSRZ
1	W	204	PRO	3.4
1	X	148	PRO	3.4
1	A	205	ASN	3.4
1	F	205	ASN	3.4
1	F	437	GLN	3.4
1	I	204	PRO	3.4
1	J	349	PRO	3.4
1	J	584	PRO	3.4
2	d	117	LYS	3.4
2	e	153	ASN	3.4
2	g	75	PRO	3.4
2	h	111	LYS	3.4
1	E	184	TRP	3.4
1	X	201	PHE	3.4
1	A	526	SER	3.4
1	B	34	PHE	3.4
1	C	187	PHE	3.4
1	I	162	SER	3.4
1	L	154	SER	3.4
2	Y	86	SER	3.4
2	a	70	SER	3.4
2	f	98	CYS	3.4
1	P	405	LEU	3.4
1	Q	59	VAL	3.4
1	R	18	ASP	3.4
1	R	156	VAL	3.4
1	S	134	ASP	3.4
1	T	101	ASP	3.4
1	V	253	ASP	3.4
1	X	147	GLU	3.4
1	X	384	LEU	3.4
1	A	72	ARG	3.4
1	B	576	LEU	3.4
1	D	559	LEU	3.4
1	H	9	GLU	3.4
1	E	72	ARG	3.4
1	G	275	ARG	3.4
1	H	258	LEU	3.4
1	I	143	VAL	3.4
1	J	406	GLU	3.4
1	J	441	ARG	3.4
1	K	509	ASP	3.4

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Mol	Chain	Res	Type	RSRZ
1	L	111	VAL	3.4
2	t	114	LEU	3.4
2	u	98	GLU	3.4
2	v	83	VAL	3.4
2	Z	23	LEU	3.4
2	a	23	LEU	3.4
2	a	71	ASP	3.4
1	U	372	TYR	3.4
1	G	235	TYR	3.4
1	H	571	TYR	3.4
1	A	124	GLY	3.4
1	B	114	ALA	3.4
1	D	424	ALA	3.4
1	J	259	ALA	3.4
2	i	135	ALA	3.4
1	U	271	ILE	3.4
1	E	278	LYS	3.4
1	H	300	ILE	3.4
1	N	437	GLN	3.4
1	X	501	THR	3.4
1	A	100	THR	3.4
1	C	216	THR	3.4
1	E	174	THR	3.4
1	G	446	THR	3.4
1	J	302	PRO	3.4
1	K	355	GLN	3.4
2	u	133	PRO	3.4
2	b	94	HIS	3.4
2	e	94	HIS	3.4
1	J	161	ASN	3.3
2	m	142	ASN	3.3
1	M	19	TRP	3.3
1	O	103	ARG	3.3
1	Q	27	ARG	3.3
1	A	79	LEU	3.3
1	D	94	LEU	3.3
1	M	396	GLU	3.3
1	Q	175	VAL	3.3
1	T	343	ARG	3.3
1	U	14	ARG	3.3
1	U	164	LEU	3.3
1	W	317	GLU	3.3

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Mol	Chain	Res	Type	RSRZ
1	D	430	VAL	3.3
1	F	46	SER	3.3
1	H	444	LEU	3.3
1	J	321	ARG	3.3
2	Z	46	VAL	3.3
2	f	20	ARG	3.3
1	I	589	GLU	3.3
2	n	64	GLU	3.3
2	v	69	GLU	3.3
2	g	139	SER	3.3
1	M	260	ASP	3.3
1	N	58	ASP	3.3
1	W	260	ASP	3.3
1	D	42	ASP	3.3
1	K	561	ASP	3.3
1	L	186	ASP	3.3
1	O	431	ALA	3.3
1	S	514	TYR	3.3
1	S	324	LYS	3.3
1	U	411	ALA	3.3
1	C	403	TYR	3.3
1	E	114	ALA	3.3
1	F	195	ALA	3.3
1	H	98	TYR	3.3
2	k	115	TYR	3.3
2	a	67	TYR	3.3
2	b	146	GLY	3.3
2	e	124	TYR	3.3
1	U	217	ILE	3.3
1	C	76	ILE	3.3
1	G	340	ILE	3.3
1	N	550	GLN	3.3
1	R	20	THR	3.3
1	S	20	THR	3.3
1	T	542	THR	3.3
1	V	199	PRO	3.3
1	X	388	PRO	3.3
1	D	388	PRO	3.3
1	H	238	PRO	3.3
1	I	377	THR	3.3
1	I	543	PRO	3.3
1	K	446	THR	3.3

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Mol	Chain	Res	Type	RSRZ
1	K	455	THR	3.3
1	L	345	PRO	3.3
2	h	126	GLN	3.3
2	j	65	THR	3.3
1	V	531	ASN	3.3
1	B	331	ASN	3.3
1	L	74	ASN	3.3
1	O	171	ARG	3.3
1	U	458	ARG	3.3
1	U	459	ARG	3.3
1	G	57	PHE	3.3
1	L	35	PHE	3.3
1	M	538	LEU	3.3
1	R	453	LEU	3.3
1	T	12	LEU	3.3
1	C	576	LEU	3.3
2	l	146	TRP	3.3
1	H	111	VAL	3.3
2	o	83	VAL	3.3
2	p	75	LEU	3.3
1	R	189	GLU	3.3
1	S	133	GLU	3.3
1	T	117	GLU	3.3
1	W	306	GLU	3.3
1	C	360	GLU	3.3
1	D	242	GLU	3.3
1	G	588	GLU	3.3
1	H	117	GLU	3.3
1	J	117	GLU	3.3
2	t	46	GLU	3.3
2	t	69	GLU	3.3
1	P	190	LYS	3.3
1	U	163	LYS	3.3
1	C	162	SER	3.3
1	F	10	SER	3.3
1	F	245	SER	3.3
2	k	108	LYS	3.3
2	s	6	LYS	3.3
2	f	148	SER	3.3
1	M	407	ALA	3.3
1	N	16	ASP	3.3
1	O	144	ILE	3.3

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Mol	Chain	Res	Type	RSRZ
1	O	305	GLY	3.3
1	O	340	ILE	3.3
1	P	114	ALA	3.3
1	S	217	ILE	3.3
1	S	572	ALA	3.3
1	E	232	ALA	3.3
1	E	305	GLY	3.3
1	F	217	ILE	3.3
1	G	285	ALA	3.3
1	F	312	ASP	3.3
1	G	77	ASP	3.3
1	G	447	TYR	3.3
1	I	294	ALA	3.3
1	J	369	TYR	3.3
1	L	110	ALA	3.3
2	Z	98	CYS	3.3
1	S	433	ASP	3.3
1	T	250	ASP	3.3
1	U	577	ILE	3.3
1	V	540	GLY	3.3
1	L	383	ASP	3.3
2	Y	79	GLY	3.3
2	a	29	ALA	3.3
2	c	32	ALA	3.3
1	W	23	ASP	3.3
1	B	339	ASP	3.3
1	H	43	ASP	3.3
1	H	77	ASP	3.3
1	H	383	ASP	3.3
1	L	84	ASP	3.3
2	a	80	ASP	3.3
2	h	146	GLY	3.3
1	N	118	GLN	3.3
1	N	542	THR	3.3
1	T	591	GLN	3.3
1	A	104	HIS	3.3
1	D	353	PRO	3.3
1	H	547	PRO	3.3
1	I	135	GLN	3.3
1	L	399	GLN	3.3
2	m	66	PRO	3.3
2	s	141	PRO	3.3

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Mol	Chain	Res	Type	RSRZ
2	Y	126	GLN	3.3
2	c	102	PRO	3.3
2	d	150	PRO	3.3
2	f	138	PRO	3.3
1	K	216	THR	3.3
1	E	532	ARG	3.3
1	F	99	ARG	3.3
1	I	328	ARG	3.3
1	K	103	ARG	3.3
1	N	79	LEU	3.3
1	N	203	ASN	3.3
1	S	554	LEU	3.3
1	W	15	PHE	3.3
1	A	401	ASN	3.3
1	A	405	LEU	3.3
1	C	222	PHE	3.3
1	D	258	LEU	3.3
1	F	507	LEU	3.3
1	I	74	ASN	3.3
1	J	389	LEU	3.3
1	J	531	ASN	3.3
1	K	201	PHE	3.3
2	n	9	LEU	3.3
2	Y	84	LEU	3.3
1	O	175	VAL	3.3
1	Q	208	VAL	3.3
1	Q	592	TRP	3.3
1	X	341	VAL	3.3
1	F	184	TRP	3.3
1	K	129	VAL	3.3
2	u	83	VAL	3.3
2	i	68	VAL	3.3
1	B	504	LYS	3.3
2	m	16	LYS	3.3
1	R	379	GLU	3.3
1	G	5	GLU	3.3
1	J	120	GLU	3.3
2	s	41	GLU	3.3
1	M	114	ALA	3.3
1	N	109	ILE	3.3
1	R	463	ILE	3.3
1	S	356	ILE	3.3

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Mol	Chain	Res	Type	RSRZ
1	U	572	ALA	3.3
1	V	411	ALA	3.3
1	E	295	GLY	3.3
1	G	580	GLY	3.3
1	T	283	CYS	3.3
1	D	246	TYR	3.3
1	L	517	TYR	3.3
1	P	367	ASP	3.3
1	R	77	ASP	3.3
1	T	451	ASP	3.3
1	U	196	ASP	3.3
1	D	237	ASP	3.3
1	H	250	ASP	3.3
1	J	367	ASP	3.3
1	K	237	ASP	3.3
1	L	312	ASP	3.3
2	q	35	ASP	3.3
2	r	62	ASP	3.3
2	r	66	PRO	3.3
1	S	386	THR	3.3
1	U	171	ARG	3.3
1	V	103	ARG	3.3
1	X	284	THR	3.3
1	D	575	GLN	3.3
1	I	434	THR	3.3
1	L	104	HIS	3.3
2	v	85	HIS	3.3
2	h	33	THR	3.3
1	N	164	LEU	3.3
1	P	539	LEU	3.3
1	S	551	LEU	3.3
1	T	34	PHE	3.3
1	D	329	LEU	3.3
1	E	247	PHE	3.3
1	G	418	LEU	3.3
1	I	438	LEU	3.3
1	L	187	PHE	3.3
2	c	34	LEU	3.3
1	O	313	LYS	3.3
1	P	504	LYS	3.3
1	T	288	LYS	3.3
1	X	108	LYS	3.3

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Mol	Chain	Res	Type	RSRZ
1	X	412	VAL	3.3
1	A	108	LYS	3.3
1	C	244	VAL	3.3
1	H	341	VAL	3.3
1	H	435	VAL	3.3
1	I	301	VAL	3.3
1	K	208	VAL	3.3
2	v	59	VAL	3.3
1	G	375	ASN	3.3
1	J	105	ASN	3.3
1	Q	379	GLU	3.3
1	U	24	GLU	3.3
1	G	220	ALA	3.3
1	G	342	ALA	3.3
1	I	423	GLU	3.3
1	K	157	ILE	3.3
1	K	224	GLU	3.3
2	h	141	MET	3.3
1	X	86	ALA	3.3
1	B	188	ALA	3.3
1	D	152	ALA	3.3
1	D	293	ILE	3.3
1	E	21	ALA	3.3
2	u	54	ILE	3.3
2	b	27	GLY	3.3
1	C	160	SER	3.3
1	C	178	SER	3.3
1	E	69	SER	3.3
1	G	335	SER	3.3
1	H	549	TYR	3.3
1	I	556	TYR	3.3
1	J	154	SER	3.3
2	Y	41	SER	3.3
2	i	139	SER	3.3
2	j	90	SER	3.3
1	I	89	ASP	3.3
1	L	509	ASP	3.3
2	k	22	ASP	3.3
1	U	210	PRO	3.3
1	G	238	PRO	3.3
2	n	125	ARG	3.3
2	q	90	ARG	3.3

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Mol	Chain	Res	Type	RSRZ
1	P	118	GLN	3.3
1	N	35	PHE	3.3
1	S	453	LEU	3.3
1	S	530	GLN	3.3
1	T	291	GLN	3.3
1	A	213	THR	3.3
1	C	67	LEU	3.3
1	F	202	GLN	3.3
2	g	94	HIS	3.3
1	I	35	PHE	3.3
1	P	582	LYS	3.3
1	U	175	VAL	3.3
1	V	93	VAL	3.3
1	X	506	VAL	3.3
1	B	528	LYS	3.3
1	C	60	VAL	3.3
2	l	102	LYS	3.3
1	H	531	ASN	3.3
1	J	211	TRP	3.3
1	R	219	ILE	3.3
1	W	198	ILE	3.3
1	C	144	ILE	3.3
1	D	255	ILE	3.3
1	F	267	ALA	3.3
1	F	588	GLU	3.3
1	G	534	GLU	3.3
1	I	454	ALA	3.3
1	J	76	ILE	3.3
1	K	109	ILE	3.3
1	L	454	ALA	3.3
2	k	103	ILE	3.3
2	r	91	ILE	3.3
2	c	113	ILE	3.3
2	e	121	GLU	3.3
2	f	22	ALA	3.3
1	D	540	GLY	3.3
1	L	235	TYR	3.2
1	L	274	ARG	3.2
1	L	391	TYR	3.2
2	l	128	TYR	3.2
1	P	160	SER	3.2
1	Q	10	SER	3.2

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Mol	Chain	Res	Type	RSRZ
1	Q	13	SER	3.2
1	V	526	SER	3.2
1	F	410	SER	3.2
1	G	151	SER	3.2
2	m	130	SER	3.2
2	j	87	SER	3.2
1	V	584	PRO	3.2
2	k	141	PRO	3.2
2	b	76	PRO	3.2
2	d	159	PRO	3.2
2	f	76	PRO	3.2
1	M	84	ASP	3.2
1	M	453	LEU	3.2
1	P	77	ASP	3.2
1	P	193	LEU	3.2
1	Q	561	ASP	3.2
1	Q	570	ASP	3.2
1	B	292	LEU	3.2
1	O	201	PHE	3.2
1	R	34	PHE	3.2
1	R	155	HIS	3.2
1	S	209	PHE	3.2
1	W	504	LYS	3.2
1	C	325	ASP	3.2
1	K	197	ASP	3.2
2	s	27	ASP	3.2
2	Y	26	LEU	3.2
2	a	59	ASP	3.2
2	d	34	LEU	3.2
2	j	26	LEU	3.2
1	A	15	PHE	3.2
1	B	336	PHE	3.2
1	C	336	PHE	3.2
1	K	202	GLN	3.2
2	r	60	PHE	3.2
1	M	586	THR	3.2
1	W	216	THR	3.2
1	D	156	VAL	3.2
1	D	323	THR	3.2
1	D	435	VAL	3.2
1	F	93	VAL	3.2
1	F	123	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	I	208	VAL	3.2
1	I	581	VAL	3.2
1	J	412	VAL	3.2
1	J	518	THR	3.2
2	u	37	VAL	3.2
2	Y	109	THR	3.2
2	g	14	THR	3.2
2	j	28	VAL	3.2
1	N	107	ALA	3.2
1	P	264	ILE	3.2
1	E	217	ILE	3.2
1	F	352	TRP	3.2
1	H	11	ILE	3.2
2	c	141	MET	3.2
1	R	90	ALA	3.2
1	R	121	ALA	3.2
1	B	357	ALA	3.2
1	I	17	ALA	3.2
1	J	416	ALA	3.2
2	n	142	ASN	3.2
2	s	96	ALA	3.2
2	u	88	ALA	3.2
2	d	74	ASN	3.2
2	f	105	ALA	3.2
2	g	29	ALA	3.2
2	j	32	ALA	3.2
1	M	117	GLU	3.2
1	Q	545	GLY	3.2
1	S	311	GLU	3.2
1	A	24	GLU	3.2
1	A	147	GLU	3.2
2	n	135	GLY	3.2
2	f	121	GLU	3.2
2	i	119	GLY	3.2
1	O	249	ARG	3.2
1	F	103	ARG	3.2
1	I	249	ARG	3.2
1	K	116	ARG	3.2
1	L	328	ARG	3.2
2	q	125	ARG	3.2
1	M	48	TYR	3.2
1	I	53	TYR	3.2

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Mol	Chain	Res	Type	RSRZ
1	N	162	SER	3.2
1	P	128	LEU	3.2
1	P	389	LEU	3.2
1	V	552	LEU	3.2
1	B	261	SER	3.2
1	B	395	PRO	3.2
1	B	538	LEU	3.2
1	C	528	LYS	3.2
1	G	199	PRO	3.2
1	G	528	LYS	3.2
1	H	178	SER	3.2
1	J	288	LYS	3.2
1	J	324	LYS	3.2
1	K	67	LEU	3.2
2	p	40	LEU	3.2
2	r	9	LEU	3.2
2	d	87	SER	3.2
2	e	117	LYS	3.2
2	j	15	LYS	3.2
1	M	93	VAL	3.2
1	O	341	VAL	3.2
1	S	197	ASP	3.2
1	T	594	VAL	3.2
1	U	16	ASP	3.2
1	U	250	ASP	3.2
1	U	570	ASP	3.2
1	V	276	VAL	3.2
1	W	177	HIS	3.2
1	B	57	PHE	3.2
1	D	247	PHE	3.2
1	L	359	PHE	3.2
1	X	529	GLN	3.2
1	D	310	VAL	3.2
1	F	591	GLN	3.2
1	G	429	GLN	3.2
1	H	519	ASP	3.2
1	K	239	VAL	3.2
2	q	62	ASP	3.2
2	q	83	VAL	3.2
2	a	31	ASP	3.2
2	e	47	ASP	3.2
2	h	98	CYS	3.2

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Mol	Chain	Res	Type	RSRZ
2	j	47	ASP	3.2
1	M	49	THR	3.2
1	N	455	THR	3.2
1	S	138	THR	3.2
1	V	174	THR	3.2
1	K	409	THR	3.2
2	n	100	THR	3.2
2	c	33	THR	3.2
1	O	293	ILE	3.2
1	P	271	ILE	3.2
1	X	463	ILE	3.2
1	H	119	ILE	3.2
1	J	255	ILE	3.2
2	a	63	ILE	3.2
1	N	259	ALA	3.2
1	O	411	ALA	3.2
1	U	158	TRP	3.2
2	l	126	ALA	3.2
2	t	13	ALA	3.2
2	c	108	ALA	3.2
2	d	56	TRP	3.2
1	N	503	GLU	3.2
1	N	589	GLU	3.2
1	P	426	ASN	3.2
1	P	548	GLU	3.2
1	V	317	GLU	3.2
1	X	337	ASN	3.2
1	B	589	GLU	3.2
1	H	275	ARG	3.2
1	H	317	GLU	3.2
1	I	268	GLU	3.2
1	L	376	ARG	3.2
2	g	151	ASN	3.2
1	M	528	LYS	3.2
1	R	98	TYR	3.2
1	T	212	LEU	3.2
1	V	12	LEU	3.2
1	W	287	LEU	3.2
1	E	290	LYS	3.2
1	F	53	TYR	3.2
1	G	12	LEU	3.2
1	J	278	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
1	K	164	LEU	3.2
1	K	593	LEU	3.2
2	t	113	LEU	3.2
2	e	118	TYR	3.2
2	o	150	PRO	3.2
2	Z	102	PRO	3.2
1	T	526	SER	3.2
1	W	200	SER	3.2
1	A	336	PHE	3.2
1	G	35	PHE	3.2
1	H	136	SER	3.2
2	m	77	SER	3.2
2	u	139	SER	3.2
2	Z	158	PHE	3.2
2	e	92	VAL	3.2
2	h	139	SER	3.2
2	i	69	PHE	3.2
1	M	202	GLN	3.2
1	P	47	GLN	3.2
1	S	47	GLN	3.2
1	W	529	GLN	3.2
1	A	399	GLN	3.2
1	L	505	GLN	3.2
1	L	578	GLN	3.2
1	N	50	THR	3.2
1	N	516	CYS	3.2
1	P	23	ASP	3.2
1	R	215	ASP	3.2
1	T	84	ASP	3.2
1	V	77	ASP	3.2
1	V	377	THR	3.2
1	W	256	ASP	3.2
1	W	558	THR	3.2
1	X	325	ASP	3.2
1	C	519	ASP	3.2
1	E	138	THR	3.2
1	F	43	ASP	3.2
1	F	325	ASP	3.2
1	I	231	THR	3.2
1	I	417	THR	3.2
1	J	250	ASP	3.2
1	L	237	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
2	o	8	ASP	3.2
2	a	33	THR	3.2
1	O	157	ILE	3.2
1	O	264	ILE	3.2
1	O	535	ILE	3.2
1	Q	144	ILE	3.2
1	Q	234	ILE	3.2
1	U	266	ILE	3.2
1	X	300	ILE	3.2
1	B	76	ILE	3.2
2	a	52	MET	3.2
2	d	42	MET	3.2
1	N	441	ARG	3.2
1	O	7	ARG	3.2
1	V	110	ALA	3.2
1	H	29	ALA	3.2
1	H	110	ALA	3.2
1	H	407	ALA	3.2
1	I	424	ALA	3.2
2	o	12	ALA	3.2
2	Y	85	ARG	3.2
2	Z	32	ALA	3.2
2	d	45	ALA	3.2
2	f	51	ALA	3.2
1	D	602	GLY	3.2
1	S	354	GLU	3.2
1	N	108	LYS	3.2
1	O	105	ASN	3.2
1	O	541	LYS	3.2
1	P	112	ASN	3.2
1	S	228	LYS	3.2
1	X	228	LYS	3.2
1	C	288	LYS	3.2
1	G	436	ASN	3.2
1	I	288	LYS	3.2
1	K	161	ASN	3.2
1	T	418	LEU	3.2
1	F	539	LEU	3.2
1	I	94	LEU	3.2
2	e	123	LEU	3.2
1	B	98	TYR	3.2
1	E	53	TYR	3.2

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Mol	Chain	Res	Type	RSRZ
1	H	447	TYR	3.2
2	t	148	TYR	3.2
1	O	370	PRO	3.2
1	B	543	PRO	3.2
1	M	208	VAL	3.2
1	N	304	PHE	3.2
1	L	557	PHE	3.2
2	u	66	PRO	3.2
2	d	76	PRO	3.2
1	R	175	VAL	3.2
1	C	239	VAL	3.2
1	F	506	VAL	3.2
1	J	208	VAL	3.2
1	S	361	HIS	3.2
1	V	550	GLN	3.2
1	W	550	GLN	3.2
1	D	429	GLN	3.2
1	E	523	SER	3.2
1	G	40	GLN	3.2
1	J	135	GLN	3.2
1	A	386	THR	3.2
1	M	325	ASP	3.2
1	N	144	ILE	3.2
1	N	237	ASP	3.2
1	S	509	ASP	3.2
1	U	255	ILE	3.2
1	U	519	ASP	3.2
1	W	433	ASP	3.2
1	X	169	ASP	3.2
1	B	217	ILE	3.2
1	B	513	ARG	3.2
1	C	356	ILE	3.2
1	F	459	ARG	3.2
1	G	256	ASP	3.2
1	H	14	ARG	3.2
1	H	409	THR	3.2
1	I	157	ILE	3.2
1	I	455	THR	3.2
1	L	377	THR	3.2
2	t	26	THR	3.2
1	E	16	ASP	3.2
1	L	256	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
2	p	94	ASP	3.2
2	q	91	ILE	3.2
1	S	121	ALA	3.2
1	S	516	CYS	3.2
1	B	400	ALA	3.2
2	l	20	ALA	3.2
2	Y	51	ALA	3.2
2	d	51	ALA	3.2
2	e	21	ALA	3.2
2	h	54	ALA	3.2
1	X	288	LYS	3.2
1	A	228	LYS	3.2
1	C	308	GLY	3.2
1	E	602	GLY	3.2
1	F	305	GLY	3.2
1	G	122	GLY	3.2
1	H	241	GLY	3.2
2	b	111	LYS	3.2
1	M	552	LEU	3.2
1	N	418	LEU	3.2
1	Q	212	LEU	3.2
1	R	33	LEU	3.2
1	S	9	GLU	3.2
1	S	258	LEU	3.2
1	V	70	GLU	3.2
1	J	287	LEU	3.2
1	K	322	LEU	3.2
2	p	114	LEU	3.2
2	Y	121	GLU	3.2
2	b	26	LEU	3.2
2	f	26	LEU	3.2
2	i	34	LEU	3.2
1	X	380	ASN	3.2
1	A	74	ASN	3.2
1	F	6	ASN	3.2
1	K	182	ASN	3.2
1	L	401	ASN	3.2
2	u	65	ASN	3.2
1	U	447	TYR	3.2
1	P	301	VAL	3.2
1	Q	543	PRO	3.2
1	T	412	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	T	557	PHE	3.2
1	V	254	VAL	3.2
1	X	276	VAL	3.2
1	X	448	VAL	3.2
1	L	398	PRO	3.2
2	k	150	PRO	3.2
2	c	89	VAL	3.2
1	N	399	GLN	3.2
1	Q	264	ILE	3.2
1	V	99	ARG	3.2
1	X	104	HIS	3.2
1	G	145	ARG	3.2
1	I	321	ARG	3.2
1	K	177	HIS	3.2
1	R	136	SER	3.2
1	R	591	GLN	3.2
1	T	450	GLN	3.2
1	V	181	GLN	3.2
1	W	56	GLN	3.2
1	W	218	GLN	3.2
1	B	327	GLN	3.2
1	B	578	GLN	3.2
1	C	505	GLN	3.2
1	C	530	GLN	3.2
1	K	142	GLN	3.2
1	L	601	GLN	3.2
2	b	52	MET	3.2
2	f	129	ILE	3.2
2	i	43	GLN	3.2
1	N	408	ALA	3.2
1	N	586	THR	3.2
1	O	240	THR	3.2
1	O	518	THR	3.2
1	P	170	ALA	3.2
1	T	138	THR	3.2
1	V	220	ALA	3.2
1	B	106	THR	3.2
1	K	110	ALA	3.2
1	K	267	ALA	3.2
1	L	49	THR	3.2
2	p	107	ALA	3.2
2	p	118	THR	3.2

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Mol	Chain	Res	Type	RSRZ
2	g	116	ALA	3.2
1	S	368	ASP	3.1
1	U	288	LYS	3.1
1	V	18	ASP	3.1
1	V	383	ASP	3.1
1	A	92	ASP	3.1
1	B	30	LYS	3.1
1	B	77	ASP	3.1
1	H	84	ASP	3.1
1	J	131	ASP	3.1
2	d	44	ASP	3.1
2	e	44	ASP	3.1
1	J	602	GLY	3.1
1	L	283	CYS	3.1
1	K	126	TRP	3.1
2	e	152	LEU	3.1
1	T	548	GLU	3.1
1	T	585	GLU	3.1
1	V	588	GLU	3.1
1	X	354	GLU	3.1
1	D	227	GLU	3.1
1	F	354	GLU	3.1
1	V	331	ASN	3.1
1	N	514	TYR	3.1
1	Q	156	VAL	3.1
1	Q	244	VAL	3.1
1	W	34	PHE	3.1
1	W	201	PHE	3.1
1	W	531	ASN	3.1
1	B	78	VAL	3.1
1	E	531	ASN	3.1
1	F	397	VAL	3.1
1	H	38	VAL	3.1
1	I	452	ASN	3.1
1	K	394	ASN	3.1
2	Z	74	ASN	3.1
2	f	147	ASN	3.1
1	Q	388	PRO	3.1
1	V	543	PRO	3.1
2	h	157	TYR	3.1
1	S	513	ARG	3.1
1	F	249	ARG	3.1

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Mol	Chain	Res	Type	RSRZ
1	S	144	ILE	3.1
1	B	104	HIS	3.1
1	B	149	ILE	3.1
1	B	281	ILE	3.1
1	D	535	ILE	3.1
1	G	144	ILE	3.1
1	N	450	GLN	3.1
1	X	47	GLN	3.1
1	H	550	GLN	3.1
1	M	20	THR	3.1
1	M	29	ALA	3.1
1	M	106	THR	3.1
1	O	446	THR	3.1
1	W	22	SER	3.1
1	W	106	THR	3.1
1	W	125	ALA	3.1
1	X	386	THR	3.1
1	A	434	THR	3.1
1	A	523	SER	3.1
1	A	546	THR	3.1
1	B	195	ALA	3.1
1	C	174	THR	3.1
1	C	279	SER	3.1
1	C	533	ALA	3.1
1	I	163	LYS	3.1
1	I	228	LYS	3.1
1	I	313	LYS	3.1
1	D	446	THR	3.1
1	G	106	THR	3.1
1	G	231	THR	3.1
1	L	180	SER	3.1
1	L	323	THR	3.1
2	l	105	ALA	3.1
2	d	143	THR	3.1
2	h	145	SER	3.1
2	j	22	ALA	3.1
1	P	134	ASP	3.1
1	T	329	LEU	3.1
1	U	51	LEU	3.1
1	W	312	ASP	3.1
1	X	498	ASP	3.1
1	A	593	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	55	GLY	3.1
1	B	308	GLY	3.1
1	K	131	ASP	3.1
1	L	427	GLY	3.1
2	n	8	ASP	3.1
1	N	207	TRP	3.1
1	C	158	TRP	3.1
1	L	592	TRP	3.1
1	N	354	GLU	3.1
1	U	9	GLU	3.1
1	V	185	GLU	3.1
1	B	120	GLU	3.1
1	R	420	VAL	3.1
1	T	78	VAL	3.1
1	D	187	PHE	3.1
2	c	19	VAL	3.1
1	N	452	ASN	3.1
1	N	508	ASN	3.1
1	P	371	TYR	3.1
1	U	573	ASN	3.1
1	A	388	PRO	3.1
1	B	299	PRO	3.1
1	E	191	TYR	3.1
1	E	369	TYR	3.1
1	F	199	PRO	3.1
1	G	146	ARG	3.1
1	G	345	PRO	3.1
1	H	205	ASN	3.1
1	H	436	ASN	3.1
1	J	98	TYR	3.1
1	J	223	TYR	3.1
1	K	458	ARG	3.1
1	L	191	TYR	3.1
2	k	93	PRO	3.1
2	g	67	TYR	3.1
2	g	142	PRO	3.1
2	i	102	PRO	3.1
2	i	147	ASN	3.1
2	j	102	PRO	3.1
1	W	266	ILE	3.1
1	D	76	ILE	3.1
1	O	361	HIS	3.1

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Mol	Chain	Res	Type	RSRZ
1	T	346	LYS	3.1
1	F	219	ILE	3.1
1	O	29	ALA	3.1
1	P	400	ALA	3.1
1	Q	599	ALA	3.1
1	S	114	ALA	3.1
1	W	47	GLN	3.1
1	D	135	GLN	3.1
1	E	355	GLN	3.1
1	K	118	GLN	3.1
1	L	338	ALA	3.1
2	n	105	ALA	3.1
2	i	22	ALA	3.1
2	i	29	ALA	3.1
1	V	106	THR	3.1
1	V	282	THR	3.1
1	A	282	THR	3.1
1	M	139	SER	3.1
1	O	128	LEU	3.1
1	O	417	THR	3.1
1	S	405	LEU	3.1
1	E	410	SER	3.1
1	H	329	LEU	3.1
1	K	287	LEU	3.1
2	p	143	LEU	3.1
2	b	115	THR	3.1
1	V	178	SER	3.1
1	W	540	GLY	3.1
2	Z	86	SER	3.1
2	g	87	SER	3.1
2	j	86	SER	3.1
1	M	194	ASP	3.1
1	O	23	ASP	3.1
1	P	197	ASP	3.1
1	U	421	ASP	3.1
1	V	509	ASP	3.1
1	A	101	ASP	3.1
1	A	325	ASP	3.1
1	F	77	ASP	3.1
1	G	237	ASP	3.1
1	H	58	ASP	3.1
1	L	92	ASP	3.1

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Mol	Chain	Res	Type	RSRZ
2	h	103	ASP	3.1
1	N	24	GLU	3.1
1	P	296	GLU	3.1
1	R	70	GLU	3.1
1	T	314	GLU	3.1
1	W	585	GLU	3.1
1	C	566	GLU	3.1
1	K	9	GLU	3.1
1	L	317	GLU	3.1
2	Z	78	GLU	3.1
2	d	154	GLU	3.1
2	h	50	GLU	3.1
1	N	448	VAL	3.1
1	P	201	PHE	3.1
1	Q	412	VAL	3.1
1	Q	435	VAL	3.1
1	W	254	VAL	3.1
1	F	187	PHE	3.1
1	H	247	PHE	3.1
1	I	57	PHE	3.1
1	J	286	VAL	3.1
1	L	320	VAL	3.1
2	l	80	VAL	3.1
2	c	37	VAL	3.1
1	S	274	ARG	3.1
1	A	14	ARG	3.1
1	B	72	ARG	3.1
1	D	513	ARG	3.1
1	A	353	PRO	3.1
2	o	133	PRO	3.1
2	Y	142	PRO	3.1
1	M	113	ILE	3.1
1	M	198	ILE	3.1
1	M	219	ILE	3.1
1	R	198	ILE	3.1
1	T	531	ASN	3.1
1	W	203	ASN	3.1
1	X	144	ILE	3.1
1	A	298	ILE	3.1
1	G	252	LYS	3.1
1	K	163	LYS	3.1
2	k	43	MET	3.1

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Mol	Chain	Res	Type	RSRZ
1	P	259	ALA	3.1
1	Q	110	ALA	3.1
1	W	361	HIS	3.1
1	S	505	GLN	3.1
1	T	411	ALA	3.1
1	D	402	ALA	3.1
1	F	529	GLN	3.1
1	I	118	GLN	3.1
1	J	29	ALA	3.1
2	f	128	ALA	3.1
2	h	97	ALA	3.1
1	Q	405	LEU	3.1
1	V	164	LEU	3.1
1	E	287	LEU	3.1
1	F	373	LEU	3.1
1	F	551	LEU	3.1
1	H	212	LEU	3.1
1	I	12	LEU	3.1
1	J	576	LEU	3.1
2	l	9	LEU	3.1
2	p	25	LEU	3.1
2	e	34	LEU	3.1
1	O	434	THR	3.1
1	O	502	GLY	3.1
1	D	282	THR	3.1
1	E	130	THR	3.1
2	t	134	THR	3.1
1	I	10	SER	3.1
2	m	81	SER	3.1
2	m	139	SER	3.1
2	Y	148	SER	3.1
2	Z	139	SER	3.1
2	i	130	SER	3.1
1	M	459	ARG	3.1
1	O	421	ASP	3.1
1	O	520	VAL	3.1
1	P	143	VAL	3.1
1	P	166	ASP	3.1
1	P	432	PHE	3.1
1	Q	115	VAL	3.1
1	R	451	ASP	3.1
1	S	215	ASP	3.1

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Mol	Chain	Res	Type	RSRZ
1	T	368	ASP	3.1
1	U	72	ARG	3.1
1	V	289	ASP	3.1
1	W	215	ASP	3.1
1	W	443	ASP	3.1
1	X	26	ARG	3.1
1	A	196	ASP	3.1
1	B	230	GLU	3.1
1	C	7	ARG	3.1
1	E	435	VAL	3.1
1	H	230	GLU	3.1
1	K	360	GLU	3.1
1	L	43	ASP	3.1
2	o	80	VAL	3.1
1	S	204	PRO	3.1
1	U	541	LYS	3.1
1	A	30	LYS	3.1
1	A	541	LYS	3.1
1	B	388	PRO	3.1
1	E	395	PRO	3.1
1	G	153	CYS	3.1
2	o	16	LYS	3.1
2	q	93	PRO	3.1
2	e	25	LYS	3.1
1	Q	219	ILE	3.1
1	T	76	ILE	3.1
1	A	293	ILE	3.1
1	C	571	TYR	3.1
1	E	235	TYR	3.1
1	G	517	TYR	3.1
1	I	266	ILE	3.1
2	g	100	ILE	3.1
1	T	508	ASN	3.1
1	F	74	ASN	3.1
2	i	151	ASN	3.1
1	N	195	ALA	3.1
1	T	170	ALA	3.1
1	B	599	ALA	3.1
1	E	431	ALA	3.1
1	F	599	ALA	3.1
2	b	110	ALA	3.1
2	d	128	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
1	M	450	GLN	3.1
1	U	327	GLN	3.1
1	U	450	GLN	3.1
1	W	593	LEU	3.1
1	G	322	LEU	3.1
1	H	40	GLN	3.1
1	H	591	GLN	3.1
1	I	450	GLN	3.1
1	K	193	LEU	3.1
1	L	593	LEU	3.1
2	Z	106	LEU	3.1
2	g	49	LEU	3.1
1	Q	323	THR	3.1
1	R	106	THR	3.1
1	U	558	THR	3.1
1	U	602	GLY	3.1
1	X	382	GLY	3.1
1	B	216	THR	3.1
1	D	20	THR	3.1
1	F	446	THR	3.1
1	G	382	GLY	3.1
1	H	558	THR	3.1
1	J	231	THR	3.1
2	r	100	THR	3.1
2	c	143	THR	3.1
1	B	26	ARG	3.1
1	H	459	ARG	3.1
2	h	85	ARG	3.1
1	N	208	VAL	3.1
1	V	448	VAL	3.1
1	W	261	SER	3.1
1	X	200	SER	3.1
1	A	430	VAL	3.1
1	H	123	VAL	3.1
1	I	111	VAL	3.1
1	J	435	VAL	3.1
2	e	130	SER	3.1
2	f	19	VAL	3.1
1	O	189	GLU	3.1
1	T	515	GLU	3.1
1	W	211	TRP	3.1
1	W	278	LYS	3.1

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Mol	Chain	Res	Type	RSRZ
1	X	190	LYS	3.1
1	X	227	GLU	3.1
1	B	185	GLU	3.1
1	C	117	GLU	3.1
1	C	224	GLU	3.1
1	E	406	GLU	3.1
1	E	534	GLU	3.1
1	F	15	PHE	3.1
1	D	288	LYS	3.1
1	A	561	ASP	3.1
1	B	509	ASP	3.1
2	i	71	ASP	3.1
1	M	385	PRO	3.1
1	P	204	PRO	3.1
1	X	149	ILE	3.1
1	D	144	ILE	3.1
1	G	217	ILE	3.1
1	H	217	ILE	3.1
1	I	148	PRO	3.1
2	j	157	TYR	3.1
1	O	539	LEU	3.0
1	P	411	ALA	3.0
1	R	452	ASN	3.0
1	S	531	ASN	3.0
1	T	426	ASN	3.0
1	X	444	LEU	3.0
1	B	536	LEU	3.0
1	D	150	HIS	3.0
1	D	337	ASN	3.0
1	D	572	ALA	3.0
1	F	110	ALA	3.0
1	G	416	ALA	3.0
1	G	507	LEU	3.0
1	H	121	ALA	3.0
1	J	329	LEU	3.0
1	K	107	ALA	3.0
1	L	402	ALA	3.0
2	l	65	ASN	3.0
2	p	36	ALA	3.0
2	t	88	ALA	3.0
2	a	34	LEU	3.0
2	e	84	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
2	e	96	LEU	3.0
2	e	105	ALA	3.0
2	j	122	LEU	3.0
1	V	177	HIS	3.0
1	U	550	GLN	3.0
1	X	218	GLN	3.0
1	F	40	GLN	3.0
1	G	399	GLN	3.0
1	J	505	GLN	3.0
1	J	544	GLN	3.0
1	L	441	ARG	3.0
2	Z	83	GLY	3.0
2	a	146	GLY	3.0
1	S	542	THR	3.0
1	J	417	THR	3.0
1	L	518	THR	3.0
2	Z	109	THR	3.0
1	R	412	VAL	3.0
1	A	115	VAL	3.0
1	E	63	VAL	3.0
1	L	239	VAL	3.0
1	N	209	PHE	3.0
1	O	524	PHE	3.0
1	P	187	PHE	3.0
1	Q	432	PHE	3.0
1	R	66	LYS	3.0
1	A	351	PHE	3.0
1	K	222	PHE	3.0
1	K	248	LYS	3.0
1	L	222	PHE	3.0
2	l	60	PHE	3.0
1	O	595	GLU	3.0
1	P	335	SER	3.0
1	T	69	SER	3.0
1	B	158	TRP	3.0
1	C	307	TRP	3.0
1	E	462	GLU	3.0
1	F	406	GLU	3.0
1	G	160	SER	3.0
1	J	588	GLU	3.0
2	l	21	SER	3.0
2	Y	55	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
2	e	148	SER	3.0
2	g	121	GLU	3.0
2	h	55	GLU	3.0
1	O	219	ILE	3.0
1	R	398	PRO	3.0
1	S	271	ILE	3.0
1	S	388	PRO	3.0
1	U	535	ILE	3.0
1	D	11	ILE	3.0
1	D	271	ILE	3.0
1	G	398	PRO	3.0
2	m	103	ILE	3.0
2	Y	112	ILE	3.0
2	i	129	ILE	3.0
1	M	250	ASP	3.0
1	N	561	ASP	3.0
1	X	433	ASP	3.0
1	A	433	ASP	3.0
1	A	451	ASP	3.0
1	B	367	ASP	3.0
1	D	186	ASP	3.0
1	D	197	ASP	3.0
1	D	325	ASP	3.0
1	E	509	ASP	3.0
1	F	451	ASP	3.0
2	q	38	ASP	3.0
2	h	80	ASP	3.0
1	Q	514	TYR	3.0
1	S	369	TYR	3.0
1	W	235	TYR	3.0
1	D	53	TYR	3.0
1	D	571	TYR	3.0
1	F	549	TYR	3.0
2	g	137	TYR	3.0
1	R	407	ALA	3.0
1	S	373	LEU	3.0
1	V	152	ALA	3.0
1	V	405	LEU	3.0
1	X	553	LEU	3.0
1	E	267	ALA	3.0
1	E	338	ALA	3.0
1	G	539	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
1	H	418	LEU	3.0
1	H	453	LEU	3.0
1	I	287	LEU	3.0
1	K	374	LEU	3.0
1	L	553	LEU	3.0
2	n	114	LEU	3.0
2	i	128	ALA	3.0
1	O	459	ARG	3.0
1	U	452	ASN	3.0
1	O	505	GLN	3.0
1	S	103	ARG	3.0
1	T	441	ARG	3.0
1	A	441	ARG	3.0
1	B	401	ASN	3.0
1	E	401	ASN	3.0
1	F	436	ASN	3.0
1	F	452	ASN	3.0
1	I	532	ARG	3.0
1	K	380	ASN	3.0
1	L	394	ASN	3.0
2	j	85	ARG	3.0
2	j	95	ASN	3.0
1	Q	427	GLY	3.0
1	T	540	GLY	3.0
1	U	591	GLN	3.0
1	X	318	GLY	3.0
1	B	47	GLN	3.0
1	N	284	THR	3.0
1	R	228	LYS	3.0
1	S	348	LYS	3.0
1	V	435	VAL	3.0
1	W	208	VAL	3.0
1	X	174	THR	3.0
1	B	100	THR	3.0
1	C	63	VAL	3.0
1	I	64	VAL	3.0
1	I	175	VAL	3.0
1	J	143	VAL	3.0
1	L	386	THR	3.0
2	b	46	VAL	3.0
2	j	14	THR	3.0
1	O	35	PHE	3.0

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Mol	Chain	Res	Type	RSRZ
1	P	209	PHE	3.0
1	V	359	PHE	3.0
1	A	350	PHE	3.0
1	H	222	PHE	3.0
1	I	222	PHE	3.0
1	O	503	GLU	3.0
1	U	589	GLU	3.0
1	V	224	GLU	3.0
1	E	588	GLU	3.0
1	G	158	TRP	3.0
1	H	595	GLU	3.0
1	I	595	GLU	3.0
1	K	70	GLU	3.0
1	L	189	GLU	3.0
1	L	414	GLU	3.0
2	p	46	GLU	3.0
1	M	10	SER	3.0
1	M	151	SER	3.0
1	W	251	ILE	3.0
1	A	217	ILE	3.0
1	E	526	SER	3.0
1	L	39	SER	3.0
1	U	584	PRO	3.0
1	D	199	PRO	3.0
1	J	299	PRO	3.0
2	c	150	PRO	3.0
1	N	215	ASP	3.0
1	Q	186	ASP	3.0
1	U	593	LEU	3.0
1	R	48	TYR	3.0
1	T	338	ALA	3.0
1	A	392	TYR	3.0
1	A	421	ASP	3.0
1	B	561	ASP	3.0
1	C	373	LEU	3.0
1	X	80	TYR	3.0
1	C	421	ASP	3.0
1	J	258	LEU	3.0
2	j	96	LEU	3.0
1	D	431	ALA	3.0
1	E	447	TYR	3.0
1	H	267	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
1	J	408	ALA	3.0
1	K	416	ALA	3.0
2	l	123	ALA	3.0
2	m	82	ALA	3.0
2	b	91	ALA	3.0
1	L	511	ARG	3.0
1	Q	361	HIS	3.0
1	D	361	HIS	3.0
1	U	31	ASN	3.0
1	U	73	GLN	3.0
1	V	112	ASN	3.0
1	B	122	GLY	3.0
1	B	290	LYS	3.0
1	B	530	GLN	3.0
1	C	229	LYS	3.0
1	F	550	GLN	3.0
1	G	202	GLN	3.0
1	H	508	ASN	3.0
1	J	528	LYS	3.0
1	K	528	LYS	3.0
1	L	181	GLN	3.0
2	m	116	LYS	3.0
2	j	125	LYS	3.0
2	j	147	ASN	3.0
1	Q	68	VAL	3.0
1	T	239	VAL	3.0
1	W	415	VAL	3.0
1	A	276	VAL	3.0
1	C	303	VAL	3.0
1	A	558	THR	3.0
1	I	15	PHE	3.0
1	K	213	THR	3.0
1	K	282	THR	3.0
1	M	379	GLU	3.0
1	P	70	GLU	3.0
1	R	185	GLU	3.0
1	S	406	GLU	3.0
1	T	406	GLU	3.0
1	T	503	GLU	3.0
1	E	495	GLU	3.0
1	F	5	GLU	3.0
1	G	126	TRP	3.0

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Mol	Chain	Res	Type	RSRZ
1	G	306	GLU	3.0
1	I	211	TRP	3.0
1	I	510	ILE	3.0
1	L	396	GLU	3.0
2	b	113	ILE	3.0
2	c	129	ILE	3.0
2	n	141	PRO	3.0
2	p	150	PRO	3.0
2	u	141	PRO	3.0
1	M	12	LEU	3.0
1	N	69	SER	3.0
1	F	51	LEU	3.0
1	J	381	SER	3.0
1	J	536	LEU	3.0
1	L	12	LEU	3.0
2	n	77	SER	3.0
2	r	143	LEU	3.0
1	M	17	ALA	3.0
1	N	90	ALA	3.0
1	N	152	ALA	3.0
1	T	103	ARG	3.0
1	V	14	ARG	3.0
1	W	14	ARG	3.0
1	X	372	TYR	3.0
1	A	511	ARG	3.0
1	B	411	ALA	3.0
1	D	48	TYR	3.0
1	G	86	ALA	3.0
1	G	372	TYR	3.0
2	k	148	TYR	3.0
2	l	23	ALA	3.0
2	Z	108	ALA	3.0
1	S	43	ASP	3.0
1	T	23	ASP	3.0
1	T	257	ASP	3.0
1	D	378	ASP	3.0
1	E	561	ASP	3.0
2	l	8	ASP	3.0
2	Z	80	ASP	3.0
1	S	313	LYS	3.0
1	B	252	LYS	3.0
1	G	582	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	I	348	LYS	3.0
2	n	102	LYS	3.0
2	Y	117	LYS	3.0
1	P	305	GLY	3.0
1	N	78	VAL	3.0
1	N	129	VAL	3.0
1	P	506	VAL	3.0
1	R	244	VAL	3.0
1	R	506	VAL	3.0
1	S	56	GLN	3.0
1	S	555	GLN	3.0
1	V	68	VAL	3.0
1	W	60	VAL	3.0
1	A	181	GLN	3.0
1	B	540	GLY	3.0
1	F	355	GLN	3.0
1	F	521	GLY	3.0
1	K	47	GLN	3.0
1	K	562	GLY	3.0
1	L	382	GLY	3.0
1	G	225	VAL	3.0
1	G	496	VAL	3.0
1	L	303	VAL	3.0
2	i	126	GLN	3.0
1	D	182	ASN	3.0
1	G	205	ASN	3.0
1	J	141	ASN	3.0
2	b	147	ASN	3.0
1	N	34	PHE	3.0
1	P	34	PHE	3.0
1	T	247	PHE	3.0
1	V	247	PHE	3.0
1	B	558	THR	3.0
1	T	217	ILE	3.0
1	V	109	ILE	3.0
2	Y	113	ILE	3.0
1	O	584	PRO	3.0
1	P	210	PRO	3.0
1	Q	193	LEU	3.0
1	S	296	GLU	3.0
1	A	12	LEU	3.0
1	C	184	TRP	3.0

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Mol	Chain	Res	Type	RSRZ
1	J	242	GLU	3.0
2	p	98	GLU	3.0
2	n	93	PRO	3.0
2	s	40	LEU	3.0
2	Y	34	LEU	3.0
2	b	123	LEU	3.0
2	f	155	TRP	3.0
1	G	82	PRO	3.0
1	H	398	PRO	3.0
2	d	39	PRO	3.0
2	e	138	PRO	3.0
1	D	61	ARG	3.0
1	D	343	ARG	3.0
1	G	513	ARG	3.0
1	I	511	ARG	3.0
1	J	459	ARG	3.0
1	M	178	SER	3.0
1	O	107	ALA	3.0
1	P	338	ALA	3.0
1	R	411	ALA	3.0
1	V	424	ALA	3.0
1	X	36	SER	3.0
1	E	10	SER	3.0
1	E	572	ALA	3.0
1	H	408	ALA	3.0
1	J	411	ALA	3.0
1	L	407	ALA	3.0
1	L	411	ALA	3.0
2	r	36	ALA	3.0
2	e	70	SER	3.0
1	M	246	TYR	3.0
1	N	167	LYS	3.0
1	Q	252	LYS	3.0
1	W	372	TYR	3.0
1	E	246	TYR	3.0
2	n	16	LYS	3.0
1	N	519	ASP	3.0
1	O	561	ASP	3.0
1	R	186	ASP	3.0
1	T	256	ASP	3.0
1	X	84	ASP	3.0
1	E	42	ASP	3.0

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Mol	Chain	Res	Type	RSRZ
1	E	169	ASP	3.0
1	K	215	ASP	3.0
1	N	435	VAL	3.0
1	O	122	GLY	3.0
1	R	115	VAL	3.0
1	S	122	GLY	3.0
1	W	341	VAL	3.0
1	D	303	VAL	3.0
1	F	358	GLY	3.0
1	K	435	VAL	3.0
2	q	37	VAL	3.0
1	A	355	GLN	3.0
1	G	550	GLN	3.0
2	s	34	GLN	3.0
1	U	401	ASN	3.0
1	V	337	ASN	3.0
1	V	401	ASN	3.0
1	A	161	ASN	3.0
1	A	426	ASN	3.0
1	C	31	ASN	3.0
1	G	203	ASN	3.0
1	G	283	CYS	3.0
2	o	86	ASN	3.0
1	O	422	THR	3.0
1	O	463	ILE	3.0
1	U	100	THR	3.0
1	B	255	ILE	3.0
1	D	377	THR	3.0
1	G	586	THR	3.0
1	J	219	ILE	3.0
1	K	49	THR	3.0
1	K	119	ILE	3.0
2	s	106	THR	3.0
1	R	593	LEU	2.9
1	S	536	LEU	2.9
1	S	539	LEU	2.9
1	V	373	LEU	2.9
1	I	554	LEU	2.9
1	M	145	ARG	2.9
1	M	587	PRO	2.9
1	O	204	PRO	2.9
1	U	534	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	X	353	PRO	2.9
1	A	330	ARG	2.9
1	B	370	PRO	2.9
1	B	441	ARG	2.9
1	C	317	GLU	2.9
1	D	44	TRP	2.9
1	D	158	TRP	2.9
1	D	354	GLU	2.9
1	D	379	GLU	2.9
1	E	311	GLU	2.9
1	F	230	GLU	2.9
1	G	204	PRO	2.9
1	H	360	GLU	2.9
1	H	513	ARG	2.9
1	J	513	ARG	2.9
2	p	112	GLU	2.9
2	q	29	GLU	2.9
2	b	150	PRO	2.9
2	h	102	PRO	2.9
1	P	17	ALA	2.9
1	Q	288	LYS	2.9
1	U	30	LYS	2.9
1	U	188	ALA	2.9
1	U	533	ALA	2.9
1	W	152	ALA	2.9
1	A	188	ALA	2.9
1	G	121	ALA	2.9
1	I	408	ALA	2.9
1	J	110	ALA	2.9
1	K	220	ALA	2.9
1	L	324	LYS	2.9
1	L	424	ALA	2.9
2	p	16	LYS	2.9
2	a	101	ALA	2.9
2	c	111	LYS	2.9
2	h	128	ALA	2.9
1	P	235	TYR	2.9
1	Q	371	TYR	2.9
1	A	46	SER	2.9
1	F	316	TYR	2.9
1	L	160	SER	2.9
2	s	78	SER	2.9

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Mol	Chain	Res	Type	RSRZ
2	b	86	SER	2.9
2	h	86	SER	2.9
1	M	561	ASP	2.9
1	P	498	ASP	2.9
1	Q	519	ASP	2.9
1	R	104	HIS	2.9
1	S	496	VAL	2.9
1	S	16	ASP	2.9
1	V	419	GLY	2.9
1	W	561	ASP	2.9
1	C	177	HIS	2.9
1	K	63	VAL	2.9
1	F	192	ASP	2.9
2	m	94	ASP	2.9
2	i	17	ASP	2.9
2	i	60	GLY	2.9
2	i	80	ASP	2.9
1	O	52	GLN	2.9
1	P	247	PHE	2.9
1	Q	118	GLN	2.9
1	T	118	GLN	2.9
1	B	40	GLN	2.9
1	B	118	GLN	2.9
1	C	47	GLN	2.9
1	C	202	GLN	2.9
1	J	530	GLN	2.9
1	K	429	GLN	2.9
2	p	49	GLN	2.9
1	T	356	ILE	2.9
1	U	149	ILE	2.9
1	X	119	ILE	2.9
1	X	251	ILE	2.9
1	L	340	ILE	2.9
2	d	64	ILE	2.9
1	U	94	LEU	2.9
1	F	513	ARG	2.9
1	G	128	LEU	2.9
1	G	559	LEU	2.9
1	J	240	THR	2.9
1	L	79	LEU	2.9
2	k	143	LEU	2.9
2	t	25	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
2	u	90	ARG	2.9
1	S	211	TRP	2.9
1	T	582	LYS	2.9
1	W	515	GLU	2.9
1	A	299	PRO	2.9
1	C	137	PRO	2.9
1	D	278	LYS	2.9
1	F	290	LYS	2.9
1	J	398	PRO	2.9
1	K	120	GLU	2.9
1	K	299	PRO	2.9
1	L	120	GLU	2.9
1	L	158	TRP	2.9
2	p	69	GLU	2.9
2	Y	155	TRP	2.9
2	a	111	LYS	2.9
2	b	142	PRO	2.9
2	f	102	PRO	2.9
1	M	110	ALA	2.9
1	N	21	ALA	2.9
1	T	456	ALA	2.9
1	C	29	ALA	2.9
2	b	105	ALA	2.9
2	f	116	ALA	2.9
2	j	21	ALA	2.9
1	P	571	TYR	2.9
1	Q	98	TYR	2.9
1	M	38	VAL	2.9
1	Q	63	VAL	2.9
1	S	261	SER	2.9
1	T	447	TYR	2.9
1	R	123	VAL	2.9
1	R	341	VAL	2.9
1	S	420	VAL	2.9
1	V	523	SER	2.9
1	F	372	TYR	2.9
1	H	80	TYR	2.9
1	I	372	TYR	2.9
1	J	178	SER	2.9
2	Y	89	VAL	2.9
2	d	86	SER	2.9
2	f	46	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
2	j	139	SER	2.9
1	A	241	GLY	2.9
1	C	305	GLY	2.9
2	p	53	GLY	2.9
2	q	137	GLY	2.9
1	B	247	PHE	2.9
1	D	359	PHE	2.9
1	G	15	PHE	2.9
1	I	150	HIS	2.9
2	r	85	HIS	2.9
2	c	82	HIS	2.9
1	O	399	GLN	2.9
1	P	429	GLN	2.9
1	Q	149	ILE	2.9
1	V	251	ILE	2.9
1	V	530	GLN	2.9
1	W	16	ASP	2.9
1	W	77	ASP	2.9
1	X	367	ASP	2.9
1	X	525	GLN	2.9
1	E	367	ASP	2.9
1	G	84	ASP	2.9
1	G	289	ASP	2.9
1	G	498	ASP	2.9
1	I	18	ASP	2.9
1	L	169	ASP	2.9
1	L	368	ASP	2.9
1	B	271	ILE	2.9
2	b	58	GLN	2.9
2	c	112	ILE	2.9
2	j	126	GLN	2.9
1	Q	384	LEU	2.9
1	R	576	LEU	2.9
1	U	329	LEU	2.9
1	W	458	ARG	2.9
1	C	554	LEU	2.9
1	F	536	LEU	2.9
1	I	539	LEU	2.9
1	K	330	ARG	2.9
2	Z	140	ARG	2.9
1	N	337	ASN	2.9
1	P	74	ASN	2.9

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Mol	Chain	Res	Type	RSRZ
1	Q	324	LYS	2.9
1	T	516	CYS	2.9
1	U	112	ASN	2.9
1	C	228	LYS	2.9
1	F	216	THR	2.9
1	H	542	THR	2.9
1	L	153	CYS	2.9
1	L	231	THR	2.9
2	e	98	CYS	2.9
1	C	349	PRO	2.9
1	M	170	ALA	2.9
1	P	503	GLU	2.9
1	P	547	PRO	2.9
1	O	307	TRP	2.9
1	O	338	ALA	2.9
1	R	267	ALA	2.9
1	S	379	GLU	2.9
2	b	102	PRO	2.9
2	g	138	PRO	2.9
1	V	107	ALA	2.9
1	X	416	ALA	2.9
1	B	408	ALA	2.9
1	C	294	ALA	2.9
1	E	126	TRP	2.9
1	H	19	TRP	2.9
1	I	91	ALA	2.9
2	r	88	ALA	2.9
2	e	101	ALA	2.9
1	O	363	TYR	2.9
1	P	556	TYR	2.9
1	R	191	TYR	2.9
1	S	60	VAL	2.9
1	U	425	VAL	2.9
1	V	320	VAL	2.9
1	X	303	VAL	2.9
1	X	371	TYR	2.9
1	E	315	VAL	2.9
1	F	98	TYR	2.9
1	F	514	TYR	2.9
1	G	53	TYR	2.9
1	J	310	VAL	2.9
2	l	109	TYR	2.9

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Mol	Chain	Res	Type	RSRZ
1	R	160	SER	2.9
1	V	365	GLY	2.9
1	A	136	SER	2.9
1	I	427	GLY	2.9
1	E	177	HIS	2.9
1	K	209	PHE	2.9
2	a	139	SER	2.9
1	Q	155	HIS	2.9
1	T	177	HIS	2.9
2	a	94	HIS	2.9
1	N	198	ILE	2.9
1	N	234	ILE	2.9
1	O	555	GLN	2.9
1	Q	249	ARG	2.9
1	Q	532	ARG	2.9
1	S	511	ARG	2.9
1	T	535	ILE	2.9
1	U	176	ILE	2.9
1	R	12	LEU	2.9
1	R	181	GLN	2.9
1	T	505	GLN	2.9
1	U	532	ARG	2.9
1	V	269	ARG	2.9
1	W	453	LEU	2.9
1	X	12	LEU	2.9
1	B	274	ARG	2.9
1	E	113	ILE	2.9
1	E	157	ILE	2.9
1	H	463	ILE	2.9
1	K	11	ILE	2.9
1	K	234	ILE	2.9
1	L	217	ILE	2.9
1	D	291	GLN	2.9
1	E	453	LEU	2.9
1	G	444	LEU	2.9
2	l	25	LEU	2.9
2	m	76	ARG	2.9
2	s	113	LEU	2.9
2	u	34	GLN	2.9
2	b	34	LEU	2.9
2	f	134	ARG	2.9
1	P	509	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	V	325	ASP	2.9
1	V	367	ASP	2.9
1	V	433	ASP	2.9
1	X	256	ASP	2.9
1	B	313	LYS	2.9
1	D	169	ASP	2.9
1	E	433	ASP	2.9
1	H	66	LYS	2.9
1	H	134	ASP	2.9
1	K	229	LYS	2.9
1	L	378	ASP	2.9
1	M	88	PRO	2.9
1	O	424	ALA	2.9
1	Q	70	GLU	2.9
1	S	402	ALA	2.9
1	S	424	ALA	2.9
1	U	224	GLU	2.9
1	U	442	ALA	2.9
1	U	454	ALA	2.9
1	W	195	ALA	2.9
1	X	366	ASN	2.9
1	B	455	THR	2.9
1	G	105	ASN	2.9
1	G	380	ASN	2.9
1	I	302	PRO	2.9
1	I	337	ASN	2.9
1	I	394	ASN	2.9
1	K	106	THR	2.9
2	Z	65	THR	2.9
2	i	35	THR	2.9
1	A	414	GLU	2.9
1	A	424	ALA	2.9
1	D	385	PRO	2.9
1	D	515	GLU	2.9
1	E	117	GLU	2.9
1	F	379	GLU	2.9
1	J	338	ALA	2.9
1	J	385	PRO	2.9
1	J	595	GLU	2.9
2	k	13	ALA	2.9
2	m	46	GLU	2.9
2	v	36	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
2	v	133	PRO	2.9
2	c	159	PRO	2.9
2	d	75	PRO	2.9
2	g	114	ALA	2.9
2	h	150	PRO	2.9
2	j	142	PRO	2.9
1	H	158	TRP	2.9
1	J	158	TRP	2.9
2	j	56	TRP	2.9
1	P	435	VAL	2.9
1	U	239	VAL	2.9
1	U	435	VAL	2.9
1	U	497	VAL	2.9
1	D	412	VAL	2.9
1	E	64	VAL	2.9
1	G	435	VAL	2.9
1	H	276	VAL	2.9
1	M	602	GLY	2.9
1	Q	85	GLY	2.9
1	U	308	GLY	2.9
1	M	14	ARG	2.9
1	Q	72	ARG	2.9
1	Q	209	PHE	2.9
1	U	96	GLY	2.9
1	T	26	ARG	2.9
1	T	61	ARG	2.9
1	U	336	PHE	2.9
1	V	222	PHE	2.9
1	D	318	GLY	2.9
1	I	382	GLY	2.9
1	K	363	TYR	2.9
2	v	58	TYR	2.9
1	H	350	PHE	2.9
2	h	119	GLY	2.9
1	V	513	ARG	2.9
1	H	376	ARG	2.9
1	J	145	ARG	2.9
2	n	76	ARG	2.9
2	o	15	ARG	2.9
2	c	131	ARG	2.9
1	M	255	ILE	2.9
1	N	405	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	O	198	ILE	2.9
1	Q	164	LEU	2.9
1	W	66	LYS	2.9
1	W	193	LEU	2.9
1	A	229	LYS	2.9
1	D	322	LEU	2.9
1	D	593	LEU	2.9
1	F	384	LEU	2.9
1	L	535	ILE	2.9
2	n	121	SER	2.9
2	Z	156	HIS	2.9
1	L	348	LYS	2.9
1	O	429	GLN	2.9
1	T	40	GLN	2.9
1	L	327	GLN	2.9
1	L	429	GLN	2.9
1	N	84	ASP	2.9
1	N	253	ASP	2.9
1	Q	260	ASP	2.9
1	U	169	ASP	2.9
1	D	256	ASP	2.9
1	E	43	ASP	2.9
1	E	89	ASP	2.9
1	G	443	ASP	2.9
1	J	383	ASP	2.9
1	K	378	ASP	2.9
1	L	443	ASP	2.9
1	L	451	ASP	2.9
2	n	71	ASP	2.9
1	M	416	ALA	2.9
1	O	386	THR	2.9
1	P	431	ALA	2.9
1	R	75	PRO	2.9
1	S	442	ALA	2.9
1	T	386	THR	2.9
1	T	395	PRO	2.9
1	A	121	ALA	2.9
1	A	210	PRO	2.9
1	B	431	ALA	2.9
1	B	501	THR	2.9
1	D	302	PRO	2.9
1	H	342	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
1	L	90	ALA	2.9
1	L	442	ALA	2.9
2	m	106	THR	2.9
2	n	126	ALA	2.9
2	r	24	THR	2.9
2	c	45	ALA	2.9
2	h	132	ALA	2.9
1	P	331	ASN	2.9
1	S	141	ASN	2.9
1	U	221	GLU	2.9
1	V	133	GLU	2.9
1	C	24	GLU	2.9
1	E	112	ASN	2.9
1	F	120	GLU	2.9
2	r	65	ASN	2.9
1	K	211	TRP	2.9
1	N	111	VAL	2.9
1	D	153	CYS	2.9
1	E	516	CYS	2.9
1	H	78	VAL	2.9
1	O	26	ARG	2.9
1	Q	305	GLY	2.9
1	R	447	TYR	2.9
1	W	295	GLY	2.9
1	C	273	ARG	2.9
1	D	441	ARG	2.9
1	E	183	GLY	2.9
1	H	321	ARG	2.9
1	H	326	GLY	2.9
1	J	328	ARG	2.9
1	K	369	TYR	2.9
2	u	58	TYR	2.9
2	v	95	TYR	2.9
1	M	438	LEU	2.9
1	T	108	LYS	2.9
1	U	109	ILE	2.9
1	U	504	LYS	2.9
1	A	193	LEU	2.9
1	C	12	LEU	2.9
1	F	163	LYS	2.9
1	G	272	LYS	2.9
1	H	347	LYS	2.9

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Mol	Chain	Res	Type	RSRZ
2	u	40	LEU	2.9
2	b	141	MET	2.9
2	d	94	HIS	2.8
2	e	52	MET	2.9
2	h	25	LYS	2.9
1	C	104	HIS	2.8
1	Q	178	SER	2.8
1	R	69	SER	2.8
1	B	279	SER	2.8
1	H	47	GLN	2.8
1	H	200	SER	2.8
1	J	270	GLN	2.8
1	J	550	GLN	2.8
1	K	69	SER	2.8
1	K	162	SER	2.8
1	M	90	ALA	2.8
1	O	443	ASP	2.8
1	P	500	ALA	2.8
1	R	166	ASP	2.8
1	S	237	ASP	2.8
1	U	339	ASP	2.8
1	W	339	ASP	2.8
1	A	431	ALA	2.8
1	B	16	ASP	2.8
1	C	23	ASP	2.8
1	M	386	THR	2.8
1	N	547	PRO	2.8
1	Q	584	PRO	2.8
1	U	29	ALA	2.8
1	R	501	THR	2.8
1	B	75	PRO	2.8
1	C	110	ALA	2.8
1	C	206	ASP	2.8
1	F	58	ASP	2.8
1	G	367	ASP	2.8
1	I	383	ASP	2.8
2	p	13	ALA	2.8
2	f	159	PRO	2.8
2	j	29	ALA	2.8
1	G	284	THR	2.8
2	d	33	THR	2.8
2	j	127	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	N	360	GLU	2.8
1	O	24	GLU	2.8
1	U	414	GLU	2.8
1	C	9	GLU	2.8
1	G	495	GLU	2.8
1	L	9	GLU	2.8
2	q	69	GLU	2.8
2	g	38	GLU	2.8
2	i	73	GLU	2.8
1	M	565	VAL	2.8
1	P	126	TRP	2.8
1	Q	74	ASN	2.8
1	R	239	VAL	2.8
1	T	205	ASN	2.8
1	V	581	VAL	2.8
1	X	140	ASN	2.8
1	A	303	VAL	2.8
1	A	320	VAL	2.8
1	B	352	TRP	2.8
1	E	44	TRP	2.8
1	E	594	VAL	2.8
1	F	126	TRP	2.8
1	G	531	ASN	2.8
1	H	105	ASN	2.8
1	L	68	VAL	2.8
2	s	86	ASN	2.8
2	b	151	ASN	2.8
1	M	441	ARG	2.8
1	O	458	ARG	2.8
1	U	61	ARG	2.8
1	N	350	PHE	2.8
1	R	201	PHE	2.8
1	W	336	PHE	2.8
1	C	167	LYS	2.8
1	C	557	PHE	2.8
1	D	35	PHE	2.8
1	M	556	TYR	2.8
1	P	67	LEU	2.8
1	S	193	LEU	2.8
1	T	234	ILE	2.8
1	X	219	ILE	2.8
1	A	571	TYR	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	389	LEU	2.8
1	E	51	LEU	2.8
1	G	359	PHE	2.8
1	E	271	ILE	2.8
1	F	329	LEU	2.8
1	J	453	LEU	2.8
1	K	359	PHE	2.8
2	a	106	LEU	2.8
2	d	69	PHE	2.8
1	G	149	ILE	2.8
1	G	356	ILE	2.8
1	I	571	TYR	2.8
1	J	53	TYR	2.8
2	q	54	ILE	2.8
2	c	57	TYR	2.8
2	c	100	ILE	2.8
1	B	150	HIS	2.8
1	G	104	HIS	2.8
1	L	177	HIS	2.8
1	Q	591	GLN	2.8
1	V	52	GLN	2.8
1	V	162	SER	2.8
1	F	335	SER	2.8
1	G	47	GLN	2.8
1	K	200	SER	2.8
2	m	78	SER	2.8
1	P	407	ALA	2.8
1	Q	114	ALA	2.8
1	S	500	ALA	2.8
1	T	572	ALA	2.8
1	J	424	ALA	2.8
2	q	119	ALA	2.8
1	R	204	PRO	2.8
1	A	238	PRO	2.8
1	E	398	PRO	2.8
1	G	395	PRO	2.8
1	L	210	PRO	2.8
2	Z	150	PRO	2.8
1	N	194	ASP	2.8
1	N	216	THR	2.8
1	N	256	ASP	2.8
1	O	131	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
1	O	519	ASP	2.8
1	O	586	THR	2.8
1	S	159	ASP	2.8
1	T	455	THR	2.8
1	U	378	ASP	2.8
1	C	250	ASP	2.8
1	D	18	ASP	2.8
1	E	23	ASP	2.8
1	F	101	ASP	2.8
1	H	101	ASP	2.8
1	F	314	GLU	2.8
1	H	106	THR	2.8
1	I	101	ASP	2.8
1	R	103	ARG	2.8
1	S	64	VAL	2.8
1	W	534	GLU	2.8
1	D	24	GLU	2.8
1	D	117	GLU	2.8
1	H	254	VAL	2.8
1	H	594	VAL	2.8
1	I	396	GLU	2.8
2	c	68	VAL	2.8
2	d	19	VAL	2.8
1	Q	184	TRP	2.8
1	V	19	TRP	2.8
1	B	211	TRP	2.8
1	G	19	TRP	2.8
1	N	346	LYS	2.8
1	R	331	ASN	2.8
1	U	366	ASN	2.8
1	D	272	LYS	2.8
1	L	161	ASN	2.8
2	Z	111	LYS	2.8
2	h	95	ASN	2.8
1	O	418	LEU	2.8
1	S	540	GLY	2.8
1	T	11	ILE	2.8
1	T	201	PHE	2.8
1	V	144	ILE	2.8
1	W	356	ILE	2.8
1	X	157	ILE	2.8
1	A	463	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	507	LEU	2.8
1	B	183	GLY	2.8
1	B	222	PHE	2.8
1	C	444	LEU	2.8
1	D	562	GLY	2.8
1	E	233	PHE	2.8
1	E	593	LEU	2.8
1	F	562	GLY	2.8
1	G	577	ILE	2.8
2	p	149	PHE	2.8
2	c	16	GLY	2.8
1	N	48	TYR	2.8
1	Q	447	TYR	2.8
1	T	372	TYR	2.8
1	U	246	TYR	2.8
1	G	514	TYR	2.8
1	H	369	TYR	2.8
1	H	392	TYR	2.8
1	I	283	CYS	2.8
2	a	57	TYR	2.8
2	b	104	TYR	2.8
1	L	297	HIS	2.8
1	B	429	GLN	2.8
2	Y	58	GLN	2.8
1	N	46	SER	2.8
1	N	188	ALA	2.8
1	N	357	ALA	2.8
1	B	410	SER	2.8
1	C	416	ALA	2.8
1	F	29	ALA	2.8
1	H	90	ALA	2.8
1	K	245	SER	2.8
2	o	21	SER	2.8
1	W	137	PRO	2.8
1	X	584	PRO	2.8
1	A	584	PRO	2.8
1	B	275	ARG	2.8
1	I	116	ARG	2.8
2	f	150	PRO	2.8
1	M	276	VAL	2.8
1	M	341	VAL	2.8
1	M	377	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	64	VAL	2.8
1	C	276	VAL	2.8
1	D	581	VAL	2.8
1	O	290	LYS	2.8
1	P	325	ASP	2.8
1	R	282	THR	2.8
1	R	284	THR	2.8
1	R	397	VAL	2.8
1	R	24	GLU	2.8
1	R	348	LYS	2.8
1	U	284	THR	2.8
1	E	229	LYS	2.8
1	E	288	LYS	2.8
1	E	446	THR	2.8
1	F	417	THR	2.8
1	F	425	VAL	2.8
1	K	430	VAL	2.8
1	L	208	VAL	2.8
1	L	565	VAL	2.8
2	o	10	VAL	2.8
1	V	23	ASP	2.8
1	A	84	ASP	2.8
1	A	192	ASP	2.8
1	E	537	GLU	2.8
1	F	66	LYS	2.8
1	F	252	LYS	2.8
2	o	100	THR	2.8
2	q	112	GLU	2.8
2	s	8	ASP	2.8
2	Z	33	THR	2.8
2	g	120	LYS	2.8
1	M	576	LEU	2.8
1	P	44	TRP	2.8
1	P	576	LEU	2.8
1	S	444	LEU	2.8
1	T	559	LEU	2.8
1	V	8	LEU	2.8
1	V	538	LEU	2.8
1	X	158	TRP	2.8
1	G	352	TRP	2.8
1	I	19	TRP	2.8
1	K	158	TRP	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	263	PHE	2.8
2	u	75	LEU	2.8
2	a	26	LEU	2.8
2	i	26	LEU	2.8
1	S	419	GLY	2.8
1	C	340	ILE	2.8
1	D	262	GLY	2.8
1	L	219	ILE	2.8
1	L	419	GLY	2.8
1	L	452	ASN	2.8
2	v	74	GLY	2.8
1	I	223	TYR	2.8
1	L	372	TYR	2.8
1	A	153	CYS	2.8
1	H	153	CYS	2.8
2	f	156	HIS	2.8
1	R	21	ALA	2.8
1	T	52	GLN	2.8
1	T	424	ALA	2.8
1	V	429	GLN	2.8
1	X	450	GLN	2.8
1	A	591	GLN	2.8
1	I	152	ALA	2.8
1	I	327	GLN	2.8
1	K	400	ALA	2.8
2	l	42	ALA	2.8
2	v	123	ALA	2.8
2	d	126	GLN	2.8
2	e	114	ALA	2.8
1	O	321	ARG	2.8
1	T	116	ARG	2.8
1	J	103	ARG	2.8
2	r	90	ARG	2.8
1	P	412	VAL	2.8
1	S	252	LYS	2.8
1	U	276	VAL	2.8
1	B	345	PRO	2.8
1	C	156	VAL	2.8
1	C	448	VAL	2.8
1	F	204	PRO	2.8
1	I	320	VAL	2.8
1	I	506	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
1	J	583	LYS	2.8
1	L	62	PRO	2.8
2	e	46	VAL	2.8
2	f	139	SER	2.8
1	M	296	GLU	2.8
1	T	589	GLU	2.8
1	C	546	THR	2.8
1	F	193	LEU	2.8
1	F	518	THR	2.8
1	I	542	THR	2.8
2	n	113	LEU	2.8
2	n	134	THR	2.8
2	o	25	LEU	2.8
2	Y	35	THR	2.8
1	Q	43	ASP	2.8
1	Q	166	ASP	2.8
1	R	260	ASP	2.8
1	T	192	ASP	2.8
1	U	209	PHE	2.8
1	V	432	PHE	2.8
1	X	166	ASP	2.8
1	A	257	ASP	2.8
1	A	367	ASP	2.8
1	E	300	ILE	2.8
1	G	134	ASP	2.8
1	H	209	PHE	2.8
1	J	109	ILE	2.8
1	L	34	PHE	2.8
1	L	325	ASP	2.8
2	u	35	ASP	2.8
2	Y	63	ILE	2.8
2	d	59	ASP	2.8
2	e	103	ASP	2.8
1	Q	326	GLY	2.8
1	D	419	GLY	2.8
1	R	380	ASN	2.8
1	T	105	ASN	2.8
1	T	203	ASN	2.8
1	D	74	ASN	2.8
1	E	31	ASN	2.8
1	G	452	ASN	2.8
2	g	147	ASN	2.8

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Mol	Chain	Res	Type	RSRZ
1	O	371	TYR	2.8
1	C	48	TYR	2.8
1	I	514	TYR	2.8
1	J	391	TYR	2.8
2	o	48	TYR	2.8
2	p	148	TYR	2.8
1	N	172	HIS	2.8
1	P	155	HIS	2.8
1	P	81	ARG	2.8
1	W	275	ARG	2.8
1	O	591	GLN	2.8
1	S	181	GLN	2.8
1	W	596	ALA	2.8
1	X	65	ARG	2.8
1	X	110	ALA	2.8
1	D	17	ALA	2.8
1	E	181	GLN	2.8
1	F	118	GLN	2.8
1	F	125	ALA	2.8
1	H	118	GLN	2.8
1	K	125	ALA	2.8
2	n	90	ARG	2.8
2	p	34	GLN	2.8
2	s	119	ALA	2.8
2	Z	134	ARG	2.8
2	a	43	GLN	2.8
2	g	77	ALA	2.8
2	i	105	ALA	2.8
1	V	66	LYS	2.8
1	L	229	LYS	2.8
1	M	239	VAL	2.8
1	O	587	PRO	2.8
1	A	111	VAL	2.8
1	B	276	VAL	2.8
1	F	59	VAL	2.8
1	F	299	PRO	2.8
1	G	244	VAL	2.8
1	I	435	VAL	2.8
1	L	412	VAL	2.8
2	d	89	VAL	2.8
1	N	261	SER	2.8
1	S	438	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	T	67	LEU	2.8
1	U	405	LEU	2.8
1	X	151	SER	2.8
1	A	374	LEU	2.8
1	B	523	SER	2.8
1	C	193	LEU	2.8
1	C	507	LEU	2.8
1	D	410	SER	2.8
1	D	553	LEU	2.8
1	I	168	SER	2.8
1	L	389	LEU	2.8
2	d	139	SER	2.8
2	g	41	SER	2.8
1	M	354	GLU	2.8
1	P	185	GLU	2.8
1	U	133	GLU	2.8
1	N	463	ILE	2.8
1	O	266	ILE	2.8
1	P	417	THR	2.8
1	U	377	THR	2.8
1	W	417	THR	2.8
1	H	354	GLU	2.8
1	I	9	GLU	2.8
1	K	515	GLU	2.8
1	B	432	PHE	2.7
1	D	251	ILE	2.8
1	D	350	PHE	2.7
1	F	157	ILE	2.8
1	G	11	ILE	2.8
1	G	234	ILE	2.8
1	G	432	PHE	2.7
1	J	34	PHE	2.7
1	J	266	ILE	2.8
2	q	149	PHE	2.7
2	b	69	PHE	2.7
1	W	44	TRP	2.7
2	t	44	MET	2.7
1	P	89	ASP	2.7
1	P	289	ASP	2.7
1	P	312	ASP	2.7
1	V	89	ASP	2.7
1	V	194	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	V	206	ASP	2.7
1	X	43	ASP	2.7
1	X	131	ASP	2.7
1	C	253	ASP	2.7
1	C	461	GLY	2.7
1	D	23	ASP	2.7
1	L	540	GLY	2.7
1	H	31	ASN	2.7
2	m	138	ASN	2.7
1	N	191	TYR	2.7
1	R	403	TYR	2.7
1	E	403	TYR	2.7
1	L	48	TYR	2.7
1	L	277	TYR	2.7
1	L	363	TYR	2.7
2	m	148	TYR	2.7
2	q	95	TYR	2.7
1	M	376	ARG	2.7
1	X	249	ARG	2.7
2	s	85	HIS	2.7
2	v	131	ARG	2.7
2	f	82	HIS	2.7
1	P	424	ALA	2.7
1	P	596	ALA	2.7
1	Q	107	ALA	2.7
1	R	232	ALA	2.7
1	R	357	ALA	2.7
1	A	402	ALA	2.7
1	D	400	ALA	2.7
1	E	110	ALA	2.7
1	I	442	ALA	2.7
2	q	16	LYS	2.7
2	t	20	ALA	2.7
2	a	128	ALA	2.7
2	e	32	ALA	2.7
2	i	32	ALA	2.7
1	N	397	VAL	2.7
1	O	319	VAL	2.7
1	P	303	VAL	2.7
1	Q	270	GLN	2.7
1	U	496	VAL	2.7
1	B	244	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	142	GLN	2.7
1	D	598	GLN	2.7
1	G	93	VAL	2.7
1	K	319	VAL	2.7
1	M	547	PRO	2.7
1	U	587	PRO	2.7
1	F	395	PRO	2.7
1	J	395	PRO	2.7
2	g	76	PRO	2.7
1	R	405	LEU	2.7
1	C	389	LEU	2.7
1	H	576	LEU	2.7
1	J	552	LEU	2.7
1	L	576	LEU	2.7
2	u	17	LEU	2.7
1	V	39	SER	2.7
1	V	209	PHE	2.7
1	V	340	ILE	2.7
1	N	434	THR	2.7
1	P	406	GLU	2.7
1	R	354	GLU	2.7
1	R	586	THR	2.7
1	S	147	GLU	2.7
1	V	534	GLU	2.7
1	W	335	SER	2.7
1	C	209	PHE	2.7
1	D	198	ILE	2.7
1	F	22	SER	2.7
1	F	396	GLU	2.7
1	H	266	ILE	2.7
1	I	233	PHE	2.7
1	I	300	ILE	2.7
1	K	217	ILE	2.7
2	u	32	SER	2.7
2	b	139	SER	2.7
2	c	41	SER	2.7
2	f	70	SER	2.7
2	j	158	PHE	2.7
1	X	106	THR	2.7
1	C	518	THR	2.7
1	C	558	THR	2.7
2	m	134	THR	2.7

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Mol	Chain	Res	Type	RSRZ
1	T	96	GLY	2.7
1	J	427	GLY	2.7
1	J	592	TRP	2.7
1	O	58	ASP	2.7
1	O	77	ASP	2.7
1	S	84	ASP	2.7
1	T	421	ASP	2.7
1	U	325	ASP	2.7
1	A	169	ASP	2.7
1	E	101	ASP	2.7
1	E	325	ASP	2.7
1	H	196	ASP	2.7
2	j	71	ASP	2.7
1	R	458	ARG	2.7
1	U	7	ARG	2.7
1	E	343	ARG	2.7
1	M	132	TYR	2.7
1	P	313	LYS	2.7
1	S	371	TYR	2.7
1	V	514	TYR	2.7
1	W	426	ASN	2.7
1	W	436	ASN	2.7
1	A	235	TYR	2.7
1	A	380	ASN	2.7
1	A	391	TYR	2.7
1	J	167	LYS	2.7
2	r	16	LYS	2.7
2	v	148	TYR	2.7
2	e	157	TYR	2.7
2	j	57	TYR	2.7
1	O	442	ALA	2.7
1	B	90	ALA	2.7
1	H	361	HIS	2.7
2	r	99	ALA	2.7
2	Y	45	ALA	2.7
2	i	108	ALA	2.7
1	M	123	VAL	2.7
1	M	254	VAL	2.7
1	P	341	VAL	2.7
1	P	530	GLN	2.7
1	U	68	VAL	2.7
1	U	156	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	V	64	VAL	2.7
1	V	115	VAL	2.7
1	X	59	VAL	2.7
1	X	64	VAL	2.7
1	A	59	VAL	2.7
1	C	387	GLN	2.7
1	H	303	VAL	2.7
2	q	19	VAL	2.7
2	r	10	VAL	2.7
1	N	243	PRO	2.7
1	N	287	LEU	2.7
1	R	153	CYS	2.7
1	V	128	LEU	2.7
1	V	193	LEU	2.7
1	W	444	LEU	2.7
1	X	299	PRO	2.7
1	X	398	PRO	2.7
1	C	499	LEU	2.7
1	F	543	PRO	2.7
1	I	536	LEU	2.7
1	L	128	LEU	2.7
2	Y	152	LEU	2.7
2	Z	26	LEU	2.7
1	M	201	PHE	2.7
1	O	234	ILE	2.7
1	R	432	PHE	2.7
1	T	280	ILE	2.7
1	V	233	PHE	2.7
1	A	176	ILE	2.7
1	A	251	ILE	2.7
1	C	255	ILE	2.7
1	C	300	ILE	2.7
1	L	263	PHE	2.7
2	m	43	MET	2.7
1	O	133	GLU	2.7
1	T	317	GLU	2.7
1	T	534	GLU	2.7
1	V	306	GLU	2.7
1	D	589	GLU	2.7
1	G	24	GLU	2.7
1	I	230	GLU	2.7
2	v	29	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
1	P	282	THR	2.7
1	Q	344	THR	2.7
1	W	39	SER	2.7
1	B	180	SER	2.7
1	C	586	THR	2.7
1	D	261	SER	2.7
1	E	180	SER	2.7
1	F	138	THR	2.7
1	G	295	GLY	2.7
1	G	386	THR	2.7
1	H	20	THR	2.7
1	H	216	THR	2.7
1	I	20	THR	2.7
1	I	245	SER	2.7
1	J	545	GLY	2.7
1	L	200	SER	2.7
1	L	279	SER	2.7
2	m	24	THR	2.7
2	m	53	GLY	2.7
1	T	44	TRP	2.7
1	W	126	TRP	2.7
1	M	103	ARG	2.7
1	B	328	ARG	2.7
1	G	61	ARG	2.7
2	p	90	ARG	2.7
1	Q	504	LYS	2.7
1	L	528	LYS	2.7
1	L	574	LYS	2.7
2	d	111	LYS	2.7
1	N	92	ASP	2.7
1	T	509	ASP	2.7
1	X	421	ASP	2.7
1	X	561	ASP	2.7
1	B	131	ASP	2.7
1	B	312	ASP	2.7
1	K	383	ASP	2.7
2	m	62	ASP	2.7
1	M	98	TYR	2.7
1	Q	48	TYR	2.7
1	U	392	TYR	2.7
1	U	514	TYR	2.7
1	X	556	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
1	I	98	TYR	2.7
2	p	48	TYR	2.7
1	N	86	ALA	2.7
1	R	361	HIS	2.7
1	R	424	ALA	2.7
1	U	110	ALA	2.7
1	U	508	ASN	2.7
1	V	188	ALA	2.7
1	W	161	ASN	2.7
1	X	6	ASN	2.7
1	X	431	ALA	2.7
1	X	442	ALA	2.7
1	A	416	ALA	2.7
1	A	508	ASN	2.7
1	J	170	ALA	2.7
1	K	203	ASN	2.7
2	p	86	ASN	2.7
2	q	99	ALA	2.7
1	N	581	VAL	2.7
1	V	239	VAL	2.7
1	D	594	VAL	2.7
1	G	310	VAL	2.7
1	G	497	VAL	2.7
1	L	341	VAL	2.7
1	Q	536	LEU	2.7
1	Q	538	LEU	2.7
1	R	438	LEU	2.7
1	T	94	LEU	2.7
1	D	128	LEU	2.7
1	G	8	LEU	2.7
1	L	507	LEU	2.7
2	s	114	LEU	2.7
2	c	152	LEU	2.7
1	P	529	GLN	2.7
1	X	578	GLN	2.7
1	E	52	GLN	2.7
1	J	202	GLN	2.7
1	K	270	GLN	2.7
2	e	58	GLN	2.7
2	i	75	PRO	2.7
1	M	209	PHE	2.7
1	O	281	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
1	U	304	PHE	2.7
1	B	11	ILE	2.7
1	D	157	ILE	2.7
1	E	350	PHE	2.7
1	I	109	ILE	2.7
1	J	149	ILE	2.7
1	N	296	GLU	2.7
1	P	133	GLU	2.7
1	R	406	GLU	2.7
1	W	360	GLU	2.7
1	K	317	GLU	2.7
1	L	534	GLU	2.7
1	O	72	ARG	2.7
1	W	27	ARG	2.7
1	A	274	ARG	2.7
1	E	513	ARG	2.7
2	i	16	GLY	2.7
1	D	417	THR	2.7
1	I	409	THR	2.7
1	J	386	THR	2.7
2	q	100	THR	2.7
2	a	109	THR	2.7
2	a	127	THR	2.7
2	c	117	LYS	2.7
2	f	14	THR	2.7
2	j	134	ARG	2.7
1	N	180	SER	2.7
1	T	261	SER	2.7
1	F	36	SER	2.7
1	F	154	SER	2.7
2	o	77	SER	2.7
2	d	130	SER	2.7
1	Q	424	ALA	2.7
1	S	431	ALA	2.7
1	V	312	ASP	2.7
1	V	391	TYR	2.7
1	V	443	ASP	2.7
1	A	277	TYR	2.7
1	B	89	ASP	2.7
1	E	294	ALA	2.7
1	F	42	ASP	2.7
1	F	447	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
1	G	325	ASP	2.7
1	G	403	TYR	2.7
1	H	107	ALA	2.7
1	H	372	TYR	2.7
1	H	391	TYR	2.7
1	H	514	TYR	2.7
1	I	342	ALA	2.7
1	I	369	TYR	2.7
1	K	294	ALA	2.7
2	l	148	TYR	2.7
2	q	63	ASP	2.7
2	t	96	ALA	2.7
2	g	72	ASP	2.7
2	j	88	ALA	2.7
1	M	156	VAL	2.7
1	M	506	VAL	2.7
1	V	63	VAL	2.7
1	P	105	ASN	2.7
1	P	258	LEU	2.7
1	R	389	LEU	2.7
1	T	225	VAL	2.7
1	T	292	LEU	2.7
1	X	531	ASN	2.7
1	A	539	LEU	2.7
1	B	405	LEU	2.7
1	D	507	LEU	2.7
1	F	412	VAL	2.7
1	G	212	LEU	2.7
1	H	68	VAL	2.7
1	I	329	LEU	2.7
1	K	111	VAL	2.7
2	a	147	ASN	2.7
1	N	204	PRO	2.7
1	R	76	ILE	2.7
1	T	266	ILE	2.7
1	V	587	PRO	2.7
1	A	202	GLN	2.7
1	C	370	PRO	2.7
1	J	82	PRO	2.7
2	r	103	ILE	2.7
1	I	350	PHE	2.7
1	P	249	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
1	W	103	ARG	2.7
1	W	249	ARG	2.7
1	E	249	ARG	2.7
1	O	5	GLU	2.7
1	T	55	GLY	2.7
1	V	147	GLU	2.7
1	W	252	LYS	2.7
1	A	583	LYS	2.7
2	n	41	GLU	2.7
2	t	112	GLU	2.7
2	c	144	GLY	2.7
2	j	50	GLU	2.7
2	j	107	GLU	2.7
1	S	100	THR	2.7
1	X	377	THR	2.7
1	C	455	THR	2.7
1	D	213	THR	2.7
2	Z	115	THR	2.7
2	e	14	THR	2.7
1	R	592	TRP	2.7
1	T	184	TRP	2.7
2	o	47	TRP	2.7
2	Z	56	TRP	2.7
1	Q	69	SER	2.7
1	T	36	SER	2.7
1	W	107	ALA	2.7
1	D	442	ALA	2.7
1	F	572	ALA	2.7
1	I	599	ALA	2.7
1	K	259	ALA	2.7
1	M	319	VAL	2.7
1	O	276	VAL	2.7
1	V	571	TYR	2.7
1	X	239	VAL	2.7
1	C	453	LEU	2.7
1	E	45	LEU	2.7
1	F	128	LEU	2.7
1	G	571	TYR	2.7
1	G	581	VAL	2.7
1	G	593	LEU	2.7
1	H	389	LEU	2.7
1	J	430	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
2	s	19	VAL	2.7
2	Z	122	LEU	2.7
2	b	92	VAL	2.7
2	c	123	LEU	2.7
2	d	37	VAL	2.7
1	Q	312	ASP	2.7
1	B	155	HIS	2.7
1	C	297	HIS	2.7
1	E	134	ASP	2.7
1	I	77	ASP	2.7
1	I	155	HIS	2.7
1	U	331	ASN	2.7
1	C	112	ASN	2.7
2	k	142	ASN	2.7
1	S	157	ILE	2.6
1	V	82	PRO	2.6
1	V	217	ILE	2.6
1	W	109	ILE	2.6
1	N	15	PHE	2.6
1	O	202	GLN	2.6
1	U	218	GLN	2.6
1	N	249	ARG	2.6
1	R	27	ARG	2.6
1	S	459	ARG	2.6
1	T	458	ARG	2.6
1	V	15	PHE	2.6
1	V	47	GLN	2.6
1	V	142	GLN	2.6
1	A	137	PRO	2.6
1	B	300	ILE	2.6
1	B	201	PHE	2.6
1	C	525	GLN	2.6
1	J	587	PRO	2.6
1	L	56	GLN	2.6
1	L	118	GLN	2.6
1	W	532	ARG	2.6
1	F	61	ARG	2.6
2	p	76	ARG	2.6
1	Q	528	LYS	2.6
1	T	528	LYS	2.6
1	E	83	LYS	2.6
1	F	190	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	L	190	LYS	2.6
1	N	308	GLY	2.6
1	R	305	GLY	2.6
1	U	595	GLU	2.6
1	C	414	GLU	2.6
1	F	515	GLU	2.6
2	m	112	GLU	2.6
2	p	7	GLY	2.6
2	b	16	GLY	2.6
2	b	144	GLY	2.6
1	N	422	THR	2.6
1	Q	282	THR	2.6
1	R	518	THR	2.6
1	W	386	THR	2.6
1	F	377	THR	2.6
1	G	282	THR	2.6
1	G	501	THR	2.6
1	G	558	THR	2.6
1	H	455	THR	2.6
2	c	109	THR	2.6
2	n	47	TRP	2.6
1	M	320	VAL	2.6
1	M	412	VAL	2.6
1	N	539	LEU	2.6
1	O	143	VAL	2.6
1	O	381	SER	2.6
1	P	565	VAL	2.6
1	Q	60	VAL	2.6
1	Q	121	ALA	2.6
1	R	154	SER	2.6
1	V	78	VAL	2.6
1	V	506	VAL	2.6
1	W	46	SER	2.6
1	X	397	VAL	2.6
1	A	294	ALA	2.6
1	C	8	LEU	2.6
1	C	407	ALA	2.6
1	D	51	LEU	2.6
1	D	338	ALA	2.6
1	E	178	SER	2.6
1	E	286	VAL	2.6
1	F	244	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	G	69	SER	2.6
1	I	45	LEU	2.6
1	K	152	ALA	2.6
2	n	19	VAL	2.6
2	p	20	ALA	2.6
2	v	20	ALA	2.6
2	Z	84	LEU	2.6
2	c	130	SER	2.6
2	d	122	LEU	2.6
1	O	447	TYR	2.6
1	Q	571	TYR	2.6
1	C	235	TYR	2.6
1	L	514	TYR	2.6
2	l	95	TYR	2.6
2	h	104	TYR	2.6
2	t	147	HIS	2.6
2	v	73	HIS	2.6
1	O	383	ASP	2.6
1	Q	421	ASP	2.6
1	R	11	ILE	2.6
1	T	561	ASP	2.6
1	U	433	ASP	2.6
1	V	166	ASP	2.6
1	A	113	ILE	2.6
1	B	253	ASP	2.6
1	C	570	ASP	2.6
1	D	443	ASP	2.6
1	F	368	ASP	2.6
1	F	383	ASP	2.6
1	I	194	ASP	2.6
2	l	50	ASP	2.6
2	q	22	ASP	2.6
2	r	8	ASP	2.6
2	r	54	ILE	2.6
2	Y	47	ASP	2.6
1	M	87	ARG	2.6
1	N	199	PRO	2.6
1	V	72	ARG	2.6
1	X	14	ARG	2.6
1	M	218	GLN	2.6
1	N	135	GLN	2.6
1	N	205	ASN	2.6

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Mol	Chain	Res	Type	RSRZ
1	N	574	LYS	2.6
1	R	135	GLN	2.6
1	X	34	PHE	2.6
1	A	105	ASN	2.6
1	A	209	PHE	2.6
1	B	273	ARG	2.6
1	B	304	PHE	2.6
1	C	57	PHE	2.6
1	F	353	PRO	2.6
1	H	88	PRO	2.6
1	I	73	GLN	2.6
1	I	324	LYS	2.6
1	J	61	ARG	2.6
1	L	61	ARG	2.6
2	l	43	MET	2.6
2	m	93	PRO	2.6
2	p	116	LYS	2.6
2	Y	75	PRO	2.6
2	f	142	PRO	2.6
1	D	40	GLN	2.6
1	D	202	GLN	2.6
1	D	591	GLN	2.6
1	I	428	GLY	2.6
2	o	135	GLY	2.6
1	M	314	GLU	2.6
1	O	9	GLU	2.6
1	O	354	GLU	2.6
1	P	117	GLU	2.6
1	S	595	GLU	2.6
1	B	360	GLU	2.6
1	G	117	GLU	2.6
2	m	98	GLU	2.6
2	o	46	GLU	2.6
2	c	38	GLU	2.6
1	M	518	THR	2.6
1	W	323	THR	2.6
1	X	216	THR	2.6
1	F	409	THR	2.6
1	L	586	THR	2.6
2	q	134	THR	2.6
2	b	14	THR	2.6
2	g	109	THR	2.6

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Mol	Chain	Res	Type	RSRZ
1	U	184	TRP	2.6
1	N	93	VAL	2.6
1	N	123	VAL	2.6
1	N	506	VAL	2.6
1	N	552	LEU	2.6
1	O	496	VAL	2.6
1	Q	232	ALA	2.6
1	Q	496	VAL	2.6
1	R	448	VAL	2.6
1	S	110	ALA	2.6
1	T	29	ALA	2.6
1	T	506	VAL	2.6
1	U	8	LEU	2.6
1	U	424	ALA	2.6
1	U	520	VAL	2.6
1	V	33	LEU	2.6
1	V	412	VAL	2.6
1	X	497	VAL	2.6
1	X	552	LEU	2.6
1	G	258	LEU	2.6
1	K	592	TRP	2.6
1	A	454	ALA	2.6
1	B	152	ALA	2.6
1	J	390	ALA	2.6
1	L	164	LEU	2.6
2	o	113	LEU	2.6
2	u	87	LEU	2.6
2	Z	116	ALA	2.6
2	f	132	ALA	2.6
2	j	135	ALA	2.6
1	P	200	SER	2.6
1	V	69	SER	2.6
1	W	178	SER	2.6
1	A	200	SER	2.6
1	B	154	SER	2.6
1	H	10	SER	2.6
1	I	39	SER	2.6
1	J	160	SER	2.6
1	J	245	SER	2.6
1	M	371	TYR	2.6
1	U	48	TYR	2.6
1	E	104	HIS	2.6

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Mol	Chain	Res	Type	RSRZ
1	E	277	TYR	2.6
1	H	316	TYR	2.6
1	I	48	TYR	2.6
1	J	517	TYR	2.6
1	O	116	ARG	2.6
1	O	119	ILE	2.6
1	P	26	ARG	2.6
1	P	72	ARG	2.6
1	Q	99	ARG	2.6
1	Q	280	ILE	2.6
1	T	510	ILE	2.6
1	V	504	LYS	2.6
1	W	269	ARG	2.6
1	W	528	LYS	2.6
1	A	376	ARG	2.6
1	B	65	ARG	2.6
1	C	119	ILE	2.6
1	E	441	ARG	2.6
1	F	27	ARG	2.6
1	J	510	ILE	2.6
1	K	99	ARG	2.6
2	e	120	LYS	2.6
2	h	156	HIS	2.6
2	i	100	ILE	2.6
1	P	359	PHE	2.6
1	R	62	PRO	2.6
1	D	351	PHE	2.6
1	G	336	PHE	2.6
2	e	69	PHE	2.6
2	j	42	MET	2.6
1	O	169	ASP	2.6
1	T	312	ASP	2.6
1	V	16	ASP	2.6
1	V	131	ASP	2.6
1	W	84	ASP	2.6
1	M	205	ASN	2.6
1	O	327	GLN	2.6
1	Q	58	ASP	2.6
1	P	182	ASN	2.6
1	Q	337	ASN	2.6
1	X	40	GLN	2.6
1	A	260	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	399	GLN	2.6
1	E	253	ASP	2.6
1	I	260	ASP	2.6
2	c	103	ASP	2.6
2	f	72	ASP	2.6
1	C	366	ASN	2.6
1	G	366	ASN	2.6
1	R	124	GLY	2.6
1	H	461	GLY	2.6
1	K	122	GLY	2.6
1	P	317	GLU	2.6
1	R	588	GLU	2.6
1	T	296	GLU	2.6
1	T	379	GLU	2.6
1	W	9	GLU	2.6
1	D	534	GLU	2.6
1	F	189	GLU	2.6
1	G	227	GLU	2.6
1	I	5	GLU	2.6
1	I	379	GLU	2.6
1	J	221	GLU	2.6
1	J	495	GLU	2.6
2	Z	50	GLU	2.6
2	h	78	GLU	2.6
2	j	121	GLU	2.6
1	N	444	LEU	2.6
1	N	559	LEU	2.6
1	P	329	LEU	2.6
1	O	19	TRP	2.6
1	P	402	ALA	2.6
1	R	342	ALA	2.6
1	T	213	THR	2.6
1	T	435	VAL	2.6
1	T	533	ALA	2.6
1	U	216	THR	2.6
1	H	12	LEU	2.6
1	E	533	ALA	2.6
1	F	121	ALA	2.6
1	G	338	ALA	2.6
1	G	341	VAL	2.6
1	I	386	THR	2.6
1	K	115	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	K	501	THR	2.6
1	L	416	ALA	2.6
2	m	13	ALA	2.6
2	o	26	THR	2.6
2	t	40	LEU	2.6
2	o	101	ALA	2.6
2	o	107	ALA	2.6
2	u	26	THR	2.6
2	b	152	LEU	2.6
2	h	28	VAL	2.6
2	i	33	THR	2.6
2	j	33	THR	2.6
2	j	34	LEU	2.6
1	U	448	VAL	2.6
1	W	59	VAL	2.6
1	B	60	VAL	2.6
1	B	307	TRP	2.6
1	B	341	VAL	2.6
1	D	415	VAL	2.6
2	e	128	ALA	2.6
2	g	98	CYS	2.6
1	X	81	ARG	2.6
1	C	274	ARG	2.6
1	M	300	ILE	2.6
1	N	252	LYS	2.6
1	E	321	ARG	2.6
1	F	272	LYS	2.6
1	L	26	ARG	2.6
2	o	90	ARG	2.6
1	P	280	ILE	2.6
1	V	510	ILE	2.6
1	B	168	SER	2.6
1	C	266	ILE	2.6
1	F	200	SER	2.6
1	K	39	SER	2.6
1	K	571	TYR	2.6
2	p	78	SER	2.6
2	a	156	HIS	2.6
2	b	148	SER	2.6
2	i	70	SER	2.6
1	M	57	PHE	2.6
1	T	543	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
1	U	222	PHE	2.6
1	X	187	PHE	2.6
1	O	218	GLN	2.6
1	O	544	GLN	2.6
1	R	291	GLN	2.6
1	T	92	ASP	2.6
1	U	498	ASP	2.6
1	U	505	GLN	2.6
1	W	421	ASP	2.6
1	W	429	GLN	2.6
1	C	399	GLN	2.6
1	C	498	ASP	2.6
1	F	250	ASP	2.6
1	H	291	GLN	2.6
1	H	367	ASP	2.6
1	I	525	GLN	2.6
1	J	429	GLN	2.6
2	m	38	ASP	2.6
2	i	103	ASP	2.6
1	M	531	ASN	2.6
1	N	531	ASN	2.6
1	O	382	GLY	2.6
1	R	141	ASN	2.6
1	R	365	GLY	2.6
1	V	6	ASN	2.6
1	V	366	ASN	2.6
1	W	337	ASN	2.6
1	X	203	ASN	2.6
1	D	375	ASN	2.6
1	H	112	ASN	2.6
1	H	419	GLY	2.6
2	n	18	GLY	2.6
2	b	66	GLY	2.6
1	N	534	GLU	2.6
1	O	499	LEU	2.6
1	P	322	LEU	2.6
1	P	552	LEU	2.6
1	Q	322	LEU	2.6
1	V	5	GLU	2.6
1	X	189	GLU	2.6
1	A	503	GLU	2.6
1	D	360	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	503	GLU	2.6
1	G	317	GLU	2.6
1	G	360	GLU	2.6
1	G	595	GLU	2.6
2	m	25	LEU	2.6
2	o	114	LEU	2.6
2	a	121	GLU	2.6
1	M	195	ALA	2.6
1	M	411	ALA	2.6
1	N	496	VAL	2.6
1	Q	506	VAL	2.6
1	X	115	VAL	2.6
1	M	116	ARG	2.6
1	N	569	ARG	2.6
1	P	174	THR	2.6
1	Q	558	THR	2.6
1	U	232	ALA	2.6
1	U	409	THR	2.6
1	W	455	THR	2.6
1	X	29	ALA	2.6
1	O	167	LYS	2.6
1	P	459	ARG	2.6
1	W	184	TRP	2.6
1	X	231	THR	2.6
1	A	344	THR	2.6
1	C	494	ALA	2.6
1	J	226	VAL	2.6
1	F	116	ARG	2.6
1	I	138	THR	2.6
1	K	417	THR	2.6
1	L	390	ALA	2.6
2	l	82	ALA	2.6
2	a	54	ALA	2.6
2	c	101	ALA	2.6
2	f	91	ALA	2.6
1	X	569	ARG	2.6
1	B	376	ARG	2.6
1	H	583	LYS	2.6
1	K	30	LYS	2.6
1	K	190	LYS	2.6
2	o	111	LYS	2.6
1	M	516	CYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	P	234	ILE	2.6
1	I	516	CYS	2.6
1	L	109	ILE	2.6
2	f	112	ILE	2.6
1	N	246	TYR	2.6
1	M	522	PRO	2.6
1	W	69	SER	2.6
1	W	209	PHE	2.6
1	C	53	TYR	2.6
1	X	160	SER	2.6
1	F	151	SER	2.6
1	J	155	HIS	2.6
1	L	204	PRO	2.6
2	t	77	SER	2.6
2	Z	30	SER	2.6
2	d	158	PHE	2.6
1	H	543	PRO	2.6
1	I	199	PRO	2.6
2	f	86	SER	2.6
1	P	40	GLN	2.6
1	R	597	GLN	2.6
1	V	437	GLN	2.6
1	B	181	GLN	2.6
1	H	202	GLN	2.6
1	N	43	ASP	2.6
1	O	161	ASN	2.6
1	P	43	ASP	2.6
1	Q	23	ASP	2.6
1	Q	203	ASN	2.6
1	R	433	ASP	2.6
1	T	186	ASP	2.6
1	F	394	ASN	2.6
1	G	196	ASP	2.6
1	G	308	GLY	2.6
2	k	38	ASP	2.6
2	n	50	ASP	2.6
2	o	137	GLY	2.6
1	C	141	ASN	2.6
1	G	394	ASN	2.6
1	I	205	ASN	2.6
1	K	105	ASN	2.6
2	p	62	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
2	p	142	ASN	2.6
2	s	35	ASP	2.6
1	N	128	LEU	2.6
1	U	438	LEU	2.6
1	G	552	LEU	2.6
1	H	538	LEU	2.6
1	L	551	LEU	2.6
2	e	23	LEU	2.6
1	F	24	GLU	2.6
1	G	224	GLU	2.6
1	H	120	GLU	2.6
1	I	117	GLU	2.6
1	I	296	GLU	2.6
1	J	537	GLU	2.6
1	K	462	GLU	2.6
1	N	407	ALA	2.6
1	O	220	ALA	2.6
1	P	513	ARG	2.6
1	T	156	VAL	2.6
1	Q	66	LYS	2.6
1	R	288	LYS	2.6
1	R	600	LYS	2.6
1	X	27	ARG	2.6
1	X	152	ALA	2.6
1	X	275	ARG	2.6
1	A	412	VAL	2.6
1	B	14	ARG	2.6
1	B	116	ARG	2.6
1	B	225	VAL	2.6
1	D	143	VAL	2.6
1	G	276	VAL	2.6
1	G	520	VAL	2.6
1	E	252	LYS	2.6
1	H	330	ARG	2.6
1	I	125	ALA	2.6
1	I	156	VAL	2.6
1	H	413	LYS	2.6
1	K	500	ALA	2.6
1	K	511	ARG	2.6
2	k	15	ARG	2.6
2	n	36	ALA	2.6
2	o	82	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
2	r	82	ALA	2.6
2	t	105	ALA	2.6
1	M	446	THR	2.6
1	R	417	THR	2.6
1	A	126	TRP	2.5
1	A	211	TRP	2.5
2	s	56	THR	2.6
2	f	56	TRP	2.5
1	M	463	ILE	2.5
1	Q	300	ILE	2.5
1	S	198	ILE	2.5
1	V	113	ILE	2.5
1	A	280	ILE	2.5
1	F	281	ILE	2.5
1	G	510	ILE	2.5
1	H	113	ILE	2.5
1	K	219	ILE	2.5
2	k	104	ILE	2.5
2	r	104	ILE	2.5
1	D	233	PHE	2.5
1	S	172	HIS	2.5
1	U	235	TYR	2.5
1	V	48	TYR	2.5
1	X	150	HIS	2.5
1	B	361	HIS	2.5
1	K	48	TYR	2.5
1	Q	204	PRO	2.5
1	D	148	PRO	2.5
1	E	543	PRO	2.5
1	K	75	PRO	2.5
2	t	30	PRO	2.5
2	b	39	PRO	2.5
2	b	75	PRO	2.5
1	W	381	SER	2.5
1	D	36	SER	2.5
1	K	523	SER	2.5
2	c	87	SER	2.5
2	f	41	SER	2.5
1	M	555	GLN	2.5
1	P	122	GLY	2.5
1	R	262	GLY	2.5
1	X	124	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	218	GLN	2.5
1	D	578	GLN	2.5
1	E	540	GLY	2.5
1	F	427	GLY	2.5
1	H	382	GLY	2.5
1	H	555	GLN	2.5
1	I	355	GLN	2.5
1	I	544	GLN	2.5
1	I	550	GLN	2.5
1	L	355	GLN	2.5
2	b	40	GLN	2.5
1	P	418	LEU	2.5
1	R	67	LEU	2.5
1	U	551	LEU	2.5
1	A	67	LEU	2.5
1	A	551	LEU	2.5
1	B	384	LEU	2.5
1	K	554	LEU	2.5
2	o	40	LEU	2.5
2	t	9	LEU	2.5
1	O	250	ASP	2.5
1	O	401	ASN	2.5
1	R	367	ASP	2.5
1	R	378	ASP	2.5
1	V	459	ARG	2.5
1	N	170	ALA	2.5
1	S	170	ALA	2.5
1	T	442	ALA	2.5
1	W	379	GLU	2.5
1	A	167	LYS	2.5
1	A	301	VAL	2.5
1	B	81	ARG	2.5
1	C	182	ASN	2.5
1	D	194	ASP	2.5
1	A	588	GLU	2.5
1	D	120	GLU	2.5
1	E	30	LYS	2.5
1	F	72	ARG	2.5
1	F	331	ASN	2.5
1	G	257	ASP	2.5
1	H	163	LYS	2.5
1	I	306	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	J	83	LYS	2.5
1	J	93	VAL	2.5
1	J	156	VAL	2.5
1	J	315	VAL	2.5
1	K	169	ASP	2.5
1	K	175	VAL	2.5
1	K	273	ARG	2.5
1	L	105	ASN	2.5
2	k	83	VAL	2.5
2	l	142	ASN	2.5
2	e	59	ASP	2.5
2	e	131	ARG	2.5
1	X	402	ALA	2.5
1	F	416	ALA	2.5
1	H	17	ALA	2.5
1	H	442	ALA	2.5
1	L	588	GLU	2.5
2	n	88	ALA	2.5
2	o	119	ALA	2.5
2	r	41	GLU	2.5
2	u	29	GLU	2.5
2	v	12	ALA	2.5
2	Y	110	ALA	2.5
2	a	105	ALA	2.5
1	O	217	ILE	2.5
1	R	281	ILE	2.5
1	R	535	ILE	2.5
1	X	207	TRP	2.5
1	D	386	THR	2.5
1	E	11	ILE	2.5
1	H	434	THR	2.5
1	J	455	THR	2.5
1	L	113	ILE	2.5
2	p	54	ILE	2.5
2	Y	115	THR	2.5
2	h	112	ILE	2.5
2	i	141	MET	2.5
1	A	222	PHE	2.5
1	A	557	PHE	2.5
1	F	336	PHE	2.5
1	S	104	HIS	2.5
1	T	98	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
1	T	587	PRO	2.5
1	A	75	PRO	2.5
1	C	361	HIS	2.5
1	J	235	TYR	2.5
1	M	305	GLY	2.5
1	N	329	LEU	2.5
1	N	382	GLY	2.5
1	Q	279	SER	2.5
1	S	136	SER	2.5
1	N	429	GLN	2.5
1	V	287	LEU	2.5
1	X	308	GLY	2.5
1	A	13	SER	2.5
1	A	461	GLY	2.5
1	C	245	SER	2.5
1	D	151	SER	2.5
1	E	322	LEU	2.5
1	E	525	GLN	2.5
1	E	529	GLN	2.5
1	F	593	LEU	2.5
1	H	373	LEU	2.5
2	k	32	SER	2.5
2	k	61	SER	2.5
2	m	21	SER	2.5
2	o	78	SER	2.5
2	Z	126	GLN	2.5
2	c	26	LEU	2.5
2	h	148	SER	2.5
1	C	270	GLN	2.5
1	I	578	GLN	2.5
1	S	249	ARG	2.5
1	T	27	ARG	2.5
1	T	459	ARG	2.5
1	X	273	ARG	2.5
1	E	167	LYS	2.5
1	F	14	ARG	2.5
1	G	541	LYS	2.5
1	H	190	LYS	2.5
1	K	459	ARG	2.5
2	t	15	ARG	2.5
2	Y	131	ARG	2.5
2	a	140	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
2	i	20	ARG	2.5
1	P	496	VAL	2.5
1	Q	78	VAL	2.5
1	T	143	VAL	2.5
1	U	226	VAL	2.5
1	U	286	VAL	2.5
1	X	594	VAL	2.5
1	C	581	VAL	2.5
1	I	520	VAL	2.5
2	q	59	VAL	2.5
2	i	19	VAL	2.5
1	M	16	ASP	2.5
1	M	92	ASP	2.5
1	N	196	ASP	2.5
1	N	331	ASN	2.5
1	O	196	ASP	2.5
1	O	215	ASP	2.5
1	P	256	ASP	2.5
1	Q	9	GLU	2.5
1	Q	354	GLU	2.5
1	S	436	ASN	2.5
1	T	367	ASP	2.5
1	X	360	GLU	2.5
1	X	573	ASN	2.5
1	A	232	ALA	2.5
1	B	206	ASP	2.5
1	E	454	ALA	2.5
1	G	133	GLU	2.5
1	G	454	ALA	2.5
1	H	169	ASP	2.5
1	I	189	GLU	2.5
1	K	311	GLU	2.5
2	o	79	ALA	2.5
2	s	23	ALA	2.5
2	t	22	ASP	2.5
2	t	65	ASN	2.5
2	v	112	GLU	2.5
2	g	59	ASP	2.5
1	P	293	ILE	2.5
1	P	333	ILE	2.5
1	A	284	THR	2.5
1	B	19	TRP	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	546	THR	2.5
1	C	446	THR	2.5
1	H	126	TRP	2.5
1	H	323	THR	2.5
1	J	49	THR	2.5
2	n	44	MET	2.5
2	p	106	THR	2.5
2	a	14	THR	2.5
2	e	143	THR	2.5
1	U	309	PHE	2.5
1	D	34	PHE	2.5
2	f	93	PHE	2.5
1	N	238	PRO	2.5
1	P	398	PRO	2.5
1	Q	243	PRO	2.5
1	A	177	HIS	2.5
1	A	543	PRO	2.5
1	G	246	TYR	2.5
1	I	385	PRO	2.5
2	p	30	PRO	2.5
2	f	157	TYR	2.5
1	M	249	ARG	2.5
1	Q	190	LYS	2.5
1	T	330	ARG	2.5
1	V	453	LEU	2.5
1	T	602	GLY	2.5
1	U	26	ARG	2.5
1	V	458	ARG	2.5
1	V	583	LYS	2.5
1	X	146	ARG	2.5
1	C	54	ARG	2.5
1	C	511	ARG	2.5
1	D	27	ARG	2.5
1	D	145	ARG	2.5
1	D	190	LYS	2.5
1	E	190	LYS	2.5
1	E	553	LEU	2.5
1	F	322	LEU	2.5
1	G	30	LYS	2.5
1	I	167	LYS	2.5
2	p	113	LEU	2.5
2	d	18	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
2	m	18	GLY	2.5
1	M	47	GLN	2.5
1	O	178	SER	2.5
1	Q	154	SER	2.5
1	R	139	SER	2.5
1	R	523	SER	2.5
1	E	214	GLN	2.5
1	I	52	GLN	2.5
1	I	154	SER	2.5
1	I	291	GLN	2.5
1	J	291	GLN	2.5
2	d	41	SER	2.5
1	P	156	VAL	2.5
1	R	301	VAL	2.5
1	C	226	VAL	2.5
1	N	390	ALA	2.5
1	O	170	ALA	2.5
1	Q	125	ALA	2.5
1	T	285	ALA	2.5
1	V	29	ALA	2.5
2	p	79	ALA	2.5
2	c	91	ALA	2.5
2	e	91	ALA	2.5
2	e	116	ALA	2.5
2	f	88	ALA	2.5
2	h	32	ALA	2.5
1	R	227	GLU	2.5
1	B	406	GLU	2.5
1	C	462	GLU	2.5
1	F	296	GLU	2.5
1	G	414	GLU	2.5
1	L	133	GLU	2.5
2	a	55	GLU	2.5
1	M	215	ASP	2.5
1	N	510	ILE	2.5
1	O	112	ASN	2.5
1	S	561	ASP	2.5
1	T	325	ASP	2.5
1	U	298	ILE	2.5
1	W	255	ILE	2.5
1	W	394	ASN	2.5
1	A	109	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	340	ILE	2.5
1	A	364	ASP	2.5
1	B	101	ASP	2.5
1	E	77	ASP	2.5
1	F	113	ILE	2.5
1	F	134	ASP	2.5
1	H	144	ILE	2.5
1	J	58	ASP	2.5
1	L	159	ASP	2.5
2	c	59	ASP	2.5
2	c	95	ASN	2.5
2	f	59	ASP	2.5
1	O	211	TRP	2.5
1	T	422	THR	2.5
1	U	207	TRP	2.5
1	U	247	PHE	2.5
1	W	138	THR	2.5
1	X	336	PHE	2.5
1	B	586	THR	2.5
1	K	35	PHE	2.5
2	Y	56	TRP	2.5
2	g	127	THR	2.5
1	Q	290	LYS	2.5
1	R	441	ARG	2.5
1	S	14	ARG	2.5
1	U	53	TYR	2.5
1	V	116	ARG	2.5
1	X	48	TYR	2.5
1	A	517	TYR	2.5
1	E	292	LEU	2.5
1	E	392	TYR	2.5
1	G	191	TYR	2.5
1	G	458	ARG	2.5
1	G	459	ARG	2.5
1	H	223	TYR	2.5
1	H	587	PRO	2.5
2	l	93	PRO	2.5
2	Z	159	PRO	2.5
2	a	25	LYS	2.5
2	b	124	TYR	2.5
2	j	159	PRO	2.5
1	C	37	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
1	J	418	LEU	2.5
1	K	532	ARG	2.5
2	o	131	ARG	2.5
2	r	102	LYS	2.5
2	s	16	LYS	2.5
1	N	580	GLY	2.5
1	S	326	GLY	2.5
1	B	419	GLY	2.5
2	u	7	GLY	2.5
1	M	64	VAL	2.5
1	M	142	GLN	2.5
1	O	236	GLN	2.5
1	O	525	GLN	2.5
1	P	181	GLN	2.5
1	P	520	VAL	2.5
1	R	525	GLN	2.5
1	U	123	VAL	2.5
1	V	118	GLN	2.5
1	V	525	GLN	2.5
1	A	581	VAL	2.5
1	B	303	VAL	2.5
1	D	276	VAL	2.5
1	D	301	VAL	2.5
1	E	115	VAL	2.5
1	I	530	GLN	2.5
1	J	78	VAL	2.5
1	J	520	VAL	2.5
1	K	156	VAL	2.5
1	L	115	VAL	2.5
1	L	435	VAL	2.5
2	i	46	VAL	2.5
1	O	294	ALA	2.5
1	P	10	SER	2.5
1	Q	170	ALA	2.5
1	Q	416	ALA	2.5
1	R	431	ALA	2.5
1	V	294	ALA	2.5
1	W	424	ALA	2.5
1	X	107	ALA	2.5
1	D	267	ALA	2.5
1	F	411	ALA	2.5
1	F	454	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
1	H	526	SER	2.5
2	k	78	SER	2.5
2	l	107	ALA	2.5
2	q	96	ALA	2.5
2	Y	132	ALA	2.5
2	a	98	CYS	2.5
2	e	145	SER	2.5
1	N	221	GLU	2.5
1	N	393	GLU	2.5
1	P	379	GLU	2.5
1	P	463	ILE	2.5
1	Q	588	GLU	2.5
1	W	189	GLU	2.5
1	W	503	GLU	2.5
1	F	510	ILE	2.5
1	J	360	GLU	2.5
1	L	298	ILE	2.5
1	L	495	GLU	2.5
2	c	121	GLU	2.5
1	M	426	ASN	2.5
1	N	112	ASN	2.5
1	Q	339	ASP	2.5
1	R	203	ASN	2.5
1	S	166	ASP	2.5
1	S	325	ASP	2.5
1	T	18	ASP	2.5
1	B	74	ASN	2.5
1	B	186	ASP	2.5
1	B	426	ASN	2.5
1	D	380	ASN	2.5
1	E	92	ASP	2.5
1	H	359	PHE	2.5
1	I	375	ASN	2.5
1	L	519	ASP	2.5
2	Z	72	ASP	2.5
2	b	71	ASP	2.5
2	h	59	ASP	2.5
2	j	59	ASP	2.5
1	L	100	THR	2.5
2	k	118	THR	2.5
1	Q	313	LYS	2.5
1	Q	539	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	T	453	LEU	2.5
1	T	513	ARG	2.5
1	U	275	ARG	2.5
1	V	81	ARG	2.5
1	G	171	ARG	2.5
1	H	228	LYS	2.5
1	L	532	ARG	2.5
2	k	76	ARG	2.5
2	m	131	ARG	2.5
2	o	108	LYS	2.5
2	q	52	LYS	2.5
1	U	62	PRO	2.5
1	W	353	PRO	2.5
1	W	543	PRO	2.5
1	X	395	PRO	2.5
1	B	137	PRO	2.5
1	C	243	PRO	2.5
1	C	353	PRO	2.5
1	F	370	PRO	2.5
1	F	405	LEU	2.5
1	H	299	PRO	2.5
1	J	292	LEU	2.5
1	J	322	LEU	2.5
2	o	67	PRO	2.5
2	p	93	PRO	2.5
2	q	113	LEU	2.5
2	u	129	PRO	2.5
2	Y	102	PRO	2.5
1	V	361	HIS	2.5
1	C	246	TYR	2.5
2	e	67	TYR	2.5
2	h	67	TYR	2.5
1	O	427	GLY	2.5
1	V	580	GLY	2.5
1	W	183	GLY	2.5
1	W	602	GLY	2.5
1	C	502	GLY	2.5
1	F	540	GLY	2.5
1	H	55	GLY	2.5
2	s	70	GLY	2.5
2	j	27	GLY	2.5
1	M	448	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	520	VAL	2.5
1	E	276	VAL	2.5
1	E	319	VAL	2.5
1	G	68	VAL	2.5
1	K	520	VAL	2.5
1	L	63	VAL	2.5
2	g	46	VAL	2.5
1	G	575	GLN	2.5
1	H	505	GLN	2.5
1	J	236	GLN	2.5
1	L	598	GLN	2.5
2	l	49	GLN	2.5
2	f	40	GLN	2.5
1	U	220	ALA	2.4
1	V	454	ALA	2.4
1	C	114	ALA	2.4
1	F	357	ALA	2.4
1	F	431	ALA	2.4
2	q	20	ALA	2.4
2	u	107	ALA	2.4
2	e	132	ALA	2.4
1	N	577	ILE	2.4
1	Q	298	ILE	2.4
1	Q	356	ILE	2.4
1	W	151	SER	2.4
1	A	22	SER	2.4
1	B	283	CYS	2.4
1	C	149	ILE	2.4
1	H	356	ILE	2.4
1	M	306	GLU	2.4
1	M	503	GLU	2.4
1	O	534	GLU	2.4
1	V	589	GLU	2.4
1	W	414	GLU	2.4
1	X	396	GLU	2.4
1	I	588	GLU	2.4
2	o	132	MET	2.4
2	q	43	MET	2.4
2	u	64	GLU	2.4
2	k	149	PHE	2.4
1	M	161	ASN	2.4
1	N	81	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	M	422	THR	2.4
1	N	166	ASP	2.4
1	P	519	ASP	2.4
1	Q	256	ASP	2.4
1	S	508	ASN	2.4
1	S	532	ARG	2.4
1	U	190	LYS	2.4
1	W	383	ASP	2.4
1	W	509	ASP	2.4
1	X	513	ARG	2.4
1	M	551	LEU	2.4
1	Q	373	LEU	2.4
1	S	501	THR	2.4
1	X	499	LEU	2.4
1	A	49	THR	2.4
1	A	250	ASP	2.4
1	B	182	ASN	2.4
1	B	421	ASP	2.4
1	B	433	ASP	2.4
1	C	561	ASP	2.4
1	D	401	ASN	2.4
1	E	443	ASP	2.4
1	E	519	ASP	2.4
1	F	194	ASP	2.4
1	G	376	ARG	2.4
1	H	337	ASN	2.4
1	I	229	LYS	2.4
1	J	112	ASN	2.4
1	G	240	THR	2.4
1	J	169	ASP	2.4
1	J	215	ASP	2.4
1	K	231	THR	2.4
1	K	257	ASP	2.4
1	L	421	ASP	2.4
2	r	63	ASP	2.4
2	Y	147	ASN	2.4
2	f	71	ASP	2.4
2	f	125	LYS	2.4
1	C	138	THR	2.4
2	i	72	ASP	2.4
1	D	193	LEU	2.4
1	J	554	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	R	82	PRO	2.4
1	D	243	PRO	2.4
1	I	210	PRO	2.4
1	I	349	PRO	2.4
1	O	277	TYR	2.4
1	T	150	HIS	2.4
1	M	428	GLY	2.4
1	N	68	VAL	2.4
1	P	63	VAL	2.4
1	Q	111	VAL	2.4
1	E	78	VAL	2.4
1	I	540	GLY	2.4
2	r	70	GLY	2.4
2	u	135	GLY	2.4
1	O	550	GLN	2.4
1	Q	152	ALA	2.4
1	T	555	GLN	2.4
1	W	505	GLN	2.4
1	A	142	GLN	2.4
1	C	424	ALA	2.4
1	E	270	GLN	2.4
1	F	86	ALA	2.4
1	F	408	ALA	2.4
1	G	152	ALA	2.4
1	H	357	ALA	2.4
1	I	56	GLN	2.4
1	I	429	GLN	2.4
1	J	267	ALA	2.4
1	J	596	ALA	2.4
1	K	424	ALA	2.4
2	t	42	ALA	2.4
1	N	217	ILE	2.4
1	P	255	ILE	2.4
1	Q	217	ILE	2.4
1	U	119	ILE	2.4
1	W	340	ILE	2.4
1	J	113	ILE	2.4
1	J	577	ILE	2.4
1	K	463	ILE	2.4
2	u	120	ILE	2.4
1	P	245	SER	2.4
1	T	133	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	U	5	GLU	2.4
1	V	117	GLU	2.4
1	W	242	GLU	2.4
1	C	495	GLU	2.4
1	F	537	GLU	2.4
1	H	268	GLU	2.4
1	J	566	GLU	2.4
1	L	70	GLU	2.4
1	L	242	GLU	2.4
2	q	139	SER	2.4
2	i	30	SER	2.4
1	X	309	PHE	2.4
1	B	272	LYS	2.4
1	B	350	PHE	2.4
1	C	524	PHE	2.4
1	E	511	ARG	2.4
1	G	413	LYS	2.4
1	H	116	ARG	2.4
1	J	116	ARG	2.4
1	K	167	LYS	2.4
2	f	158	PHE	2.4
1	V	274	ARG	2.4
1	C	14	ARG	2.4
1	C	532	ARG	2.4
2	a	131	ARG	2.4
2	i	120	LYS	2.4
1	M	539	LEU	2.4
1	P	79	LEU	2.4
1	R	94	LEU	2.4
1	B	438	LEU	2.4
1	B	453	LEU	2.4
1	E	576	LEU	2.4
1	G	193	LEU	2.4
2	c	96	LEU	2.4
1	N	158	TRP	2.4
1	O	436	ASN	2.4
1	Q	105	ASN	2.4
1	S	161	ASN	2.4
1	V	375	ASN	2.4
1	W	20	THR	2.4
1	C	207	TRP	2.4
2	u	138	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
2	c	151	ASN	2.4
1	A	253	ASP	2.4
1	B	215	ASP	2.4
1	D	192	ASP	2.4
1	E	18	ASP	2.4
1	E	131	ASP	2.4
1	H	166	ASP	2.4
2	p	71	ASP	2.4
1	P	543	PRO	2.4
1	T	62	PRO	2.4
1	U	353	PRO	2.4
1	H	75	PRO	2.4
1	J	204	PRO	2.4
2	v	30	PRO	2.4
2	f	39	PRO	2.4
1	M	155	HIS	2.4
1	N	571	TYR	2.4
1	P	104	HIS	2.4
1	P	447	TYR	2.4
1	S	303	VAL	2.4
1	W	53	TYR	2.4
1	A	361	HIS	2.4
1	B	48	TYR	2.4
1	C	80	TYR	2.4
1	D	369	TYR	2.4
1	D	391	TYR	2.4
1	E	96	GLY	2.4
1	I	315	VAL	2.4
1	I	363	TYR	2.4
2	r	109	TYR	2.4
1	M	149	ILE	2.4
1	R	17	ALA	2.4
1	X	400	ALA	2.4
1	C	572	ALA	2.4
1	Q	52	GLN	2.4
1	R	40	GLN	2.4
1	R	450	GLN	2.4
1	R	505	GLN	2.4
1	S	281	ILE	2.4
1	S	591	GLN	2.4
1	U	270	GLN	2.4
1	X	399	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	118	GLN	2.4
1	A	525	GLN	2.4
1	B	525	GLN	2.4
1	C	236	GLN	2.4
1	C	577	ILE	2.4
2	p	99	ALA	2.4
2	Z	100	ILE	2.4
2	d	135	ALA	2.4
2	i	97	ALA	2.4
1	M	120	GLU	2.4
1	M	268	GLU	2.4
1	N	513	ARG	2.4
1	P	242	GLU	2.4
1	R	269	ARG	2.4
1	R	275	ARG	2.4
1	R	290	LYS	2.4
1	Q	566	GLU	2.4
1	W	330	ARG	2.4
1	F	330	ARG	2.4
1	K	324	LYS	2.4
1	L	275	ARG	2.4
1	L	600	LYS	2.4
1	C	359	PHE	2.4
1	C	445	GLU	2.4
1	D	133	GLU	2.4
1	G	222	PHE	2.4
1	I	120	GLU	2.4
1	J	396	GLU	2.4
1	J	557	PHE	2.4
2	l	64	GLU	2.4
2	s	46	GLU	2.4
1	O	151	SER	2.4
1	V	36	SER	2.4
1	E	39	SER	2.4
1	K	151	SER	2.4
1	K	178	SER	2.4
2	j	30	SER	2.4
1	O	536	LEU	2.4
1	P	164	LEU	2.4
1	Q	128	LEU	2.4
1	R	536	LEU	2.4
1	W	8	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	X	258	LEU	2.4
1	D	551	LEU	2.4
1	G	389	LEU	2.4
1	G	499	LEU	2.4
1	K	453	LEU	2.4
2	k	17	LEU	2.4
2	f	18	LEU	2.4
1	O	126	TRP	2.4
1	N	401	ASN	2.4
1	P	452	ASN	2.4
1	T	586	THR	2.4
1	U	299	PRO	2.4
1	B	380	ASN	2.4
1	E	366	ASN	2.4
1	G	542	THR	2.4
1	L	106	THR	2.4
2	q	30	PRO	2.4
2	a	39	PRO	2.4
2	d	127	THR	2.4
1	O	565	VAL	2.4
1	P	208	VAL	2.4
1	R	435	VAL	2.4
1	S	92	ASP	2.4
1	W	257	ASP	2.4
1	X	289	ASP	2.4
1	C	435	VAL	2.4
1	D	260	ASP	2.4
1	E	256	ASP	2.4
1	E	289	ASP	2.4
1	F	303	VAL	2.4
1	I	325	ASP	2.4
1	J	519	ASP	2.4
1	J	565	VAL	2.4
1	L	244	VAL	2.4
2	n	80	VAL	2.4
2	t	71	ASP	2.4
2	j	89	VAL	2.4
1	N	361	HIS	2.4
1	S	235	TYR	2.4
1	V	191	TYR	2.4
1	X	326	GLY	2.4
1	B	241	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	326	GLY	2.4
1	C	602	GLY	2.4
1	F	132	TYR	2.4
1	H	155	HIS	2.4
1	I	419	GLY	2.4
1	K	419	GLY	2.4
1	K	556	TYR	2.4
2	q	135	GLY	2.4
2	c	118	TYR	2.4
1	Q	11	ILE	2.4
1	R	113	ILE	2.4
1	R	510	ILE	2.4
1	T	577	ILE	2.4
1	U	300	ILE	2.4
1	A	535	ILE	2.4
1	E	333	ILE	2.4
1	H	424	ALA	2.4
1	L	356	ILE	2.4
2	o	88	ALA	2.4
2	b	129	ILE	2.4
2	d	101	ALA	2.4
1	M	544	GLN	2.4
1	P	528	LYS	2.4
1	P	583	LYS	2.4
1	T	575	GLN	2.4
1	B	135	GLN	2.4
1	R	328	ARG	2.4
1	S	269	ARG	2.4
1	V	569	ARG	2.4
1	X	37	ARG	2.4
1	B	511	ARG	2.4
1	C	61	ARG	2.4
1	E	61	ARG	2.4
1	G	328	ARG	2.4
1	H	324	LYS	2.4
1	L	145	ARG	2.4
2	Y	134	ARG	2.4
2	d	140	ARG	2.4
1	R	247	PHE	2.4
1	T	187	PHE	2.4
1	W	35	PHE	2.4
1	X	209	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
1	E	222	PHE	2.4
1	G	247	PHE	2.4
1	J	336	PHE	2.4
1	K	432	PHE	2.4
2	t	149	PHE	2.4
1	N	595	GLU	2.4
1	T	227	GLU	2.4
1	T	306	GLU	2.4
1	U	311	GLU	2.4
1	U	588	GLU	2.4
1	B	306	GLU	2.4
1	B	595	GLU	2.4
1	D	9	GLU	2.4
1	D	405	LEU	2.4
1	E	384	LEU	2.4
1	G	314	GLU	2.4
1	L	67	LEU	2.4
1	L	554	LEU	2.4
2	a	78	GLU	2.4
2	d	23	LEU	2.4
2	e	38	GLU	2.4
2	f	50	GLU	2.4
1	S	162	SER	2.4
1	D	168	SER	2.4
2	l	89	CYS	2.4
1	F	349	PRO	2.4
1	L	137	PRO	2.4
2	q	146	TRP	2.4
1	M	415	VAL	2.4
1	Q	216	THR	2.4
1	T	244	VAL	2.4
1	W	518	THR	2.4
1	H	422	THR	2.4
1	K	64	VAL	2.4
2	n	106	THR	2.4
2	p	80	VAL	2.4
2	s	83	VAL	2.4
2	v	100	THR	2.4
2	i	92	VAL	2.4
2	i	159	PRO	2.4
1	M	498	ASP	2.4
1	O	365	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	P	237	ASP	2.4
1	Q	383	ASP	2.4
1	Q	451	ASP	2.4
1	U	295	GLY	2.4
1	W	166	ASP	2.4
1	X	215	ASP	2.4
1	A	295	GLY	2.4
1	B	112	ASN	2.4
1	H	602	GLY	2.4
1	E	149	ILE	2.4
1	F	76	ILE	2.4
1	H	235	TYR	2.4
1	I	16	ASP	2.4
1	K	98	TYR	2.4
1	L	23	ASP	2.4
1	L	250	ASP	2.4
2	l	110	GLY	2.4
2	n	38	ASP	2.4
1	N	110	ALA	2.4
1	O	76	ILE	2.4
1	P	86	ALA	2.4
1	S	195	ALA	2.4
1	U	340	ILE	2.4
1	W	572	ALA	2.4
1	A	596	ALA	2.4
1	I	188	ALA	2.4
2	o	105	ALA	2.4
2	q	45	ALA	2.4
2	v	88	ALA	2.4
2	Z	128	ALA	2.4
2	e	77	ALA	2.4
2	h	135	ALA	2.4
1	R	30	LYS	2.4
1	U	290	LYS	2.4
1	V	541	LYS	2.4
1	W	163	LYS	2.4
1	B	228	LYS	2.4
1	E	504	LYS	2.4
2	o	102	LYS	2.4
2	p	108	LYS	2.4
2	Z	125	LYS	2.4
1	M	72	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	N	269	ARG	2.4
1	A	81	ARG	2.4
1	J	171	ARG	2.4
1	K	72	ARG	2.4
2	f	140	ARG	2.4
1	M	525	GLN	2.4
1	P	327	GLN	2.4
1	A	530	GLN	2.4
1	D	47	GLN	2.4
1	J	118	GLN	2.4
1	K	525	GLN	2.4
1	U	57	PHE	2.4
1	E	34	PHE	2.4
1	O	67	LEU	2.4
1	T	551	LEU	2.4
1	V	322	LEU	2.4
1	V	553	LEU	2.4
1	F	554	LEU	2.4
1	F	576	LEU	2.4
1	G	51	LEU	2.4
1	H	405	LEU	2.4
1	J	51	LEU	2.4
1	K	45	LEU	2.4
1	L	374	LEU	2.4
1	Q	189	GLU	2.4
1	S	242	GLU	2.4
1	A	534	GLU	2.4
1	B	423	GLU	2.4
1	C	515	GLU	2.4
1	D	224	GLU	2.4
1	G	9	GLU	2.4
2	l	29	GLU	2.4
1	P	36	SER	2.4
1	P	381	SER	2.4
1	S	69	SER	2.4
1	V	279	SER	2.4
1	M	584	PRO	2.4
1	R	543	PRO	2.4
1	S	82	PRO	2.4
1	T	211	TRP	2.4
1	V	204	PRO	2.4
1	X	225	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	435	VAL	2.4
1	C	211	TRP	2.4
1	E	385	PRO	2.4
1	F	111	VAL	2.4
1	H	415	VAL	2.4
1	I	60	VAL	2.4
1	I	207	TRP	2.4
1	L	59	VAL	2.4
1	L	254	VAL	2.4
2	m	89	CYS	2.4
2	v	129	PRO	2.4
2	Z	89	VAL	2.4
1	A	382	GLY	2.3
1	D	428	GLY	2.3
1	E	122	GLY	2.3
1	I	305	GLY	2.3
1	K	318	GLY	2.3
2	q	18	GLY	2.3
1	N	426	ASN	2.3
1	O	394	ASN	2.3
1	N	549	TYR	2.3
1	P	269	ARG	2.3
1	R	152	ALA	2.3
1	R	400	ALA	2.3
1	S	105	ASN	2.3
1	U	416	ALA	2.3
1	V	572	ALA	2.3
1	X	155	HIS	2.3
1	V	84	ASP	2.3
1	V	249	ARG	2.3
1	X	274	ARG	2.3
1	X	424	ALA	2.3
1	X	535	ILE	2.3
1	E	266	ILE	2.3
1	G	228	LYS	2.3
1	E	376	ARG	2.3
1	G	80	TYR	2.3
1	G	251	ILE	2.3
1	H	176	ILE	2.3
1	I	347	LYS	2.3
1	I	494	ALA	2.3
1	I	531	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
1	J	90	ALA	2.3
1	K	504	LYS	2.3
1	K	577	ILE	2.3
1	L	176	ILE	2.3
2	l	36	ALA	2.3
2	p	96	ALA	2.3
1	D	257	ASP	2.3
1	I	43	ASP	2.3
1	K	134	ASP	2.3
2	q	109	TYR	2.3
2	Y	80	ASP	2.3
2	Z	71	ASP	2.3
2	Z	104	TYR	2.3
2	b	103	ASP	2.3
2	h	71	ASP	2.3
1	Q	135	GLN	2.3
1	T	202	GLN	2.3
1	T	554	LEU	2.3
1	W	598	GLN	2.3
1	A	263	PHE	2.3
1	F	444	LEU	2.3
1	H	557	PHE	2.3
1	I	336	PHE	2.3
1	L	218	GLN	2.3
2	l	114	LEU	2.3
2	v	9	LEU	2.3
2	c	122	LEU	2.3
2	g	34	LEU	2.3
1	Q	117	GLU	2.3
1	U	296	GLU	2.3
1	V	503	GLU	2.3
1	X	306	GLU	2.3
1	X	393	GLU	2.3
1	A	317	GLU	2.3
1	C	548	GLU	2.3
1	E	133	GLU	2.3
1	K	5	GLU	2.3
1	K	589	GLU	2.3
2	o	98	GLU	2.3
2	Z	121	GLU	2.3
2	i	78	GLU	2.3
1	Q	448	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	R	415	VAL	2.3
1	U	397	VAL	2.3
1	U	594	VAL	2.3
1	V	244	VAL	2.3
1	D	59	VAL	2.3
1	D	286	VAL	2.3
1	H	244	VAL	2.3
2	a	92	VAL	2.3
2	j	68	VAL	2.3
1	M	137	PRO	2.3
1	M	162	SER	2.3
1	X	178	SER	2.3
1	B	62	PRO	2.3
1	D	381	SER	2.3
1	K	22	SER	2.3
1	L	162	SER	2.3
1	L	238	PRO	2.3
2	v	136	SER	2.3
2	Z	142	PRO	2.3
2	a	75	PRO	2.3
2	d	142	PRO	2.3
1	N	582	LYS	2.3
1	N	72	ARG	2.3
1	S	241	GLY	2.3
1	T	290	LYS	2.3
1	T	419	GLY	2.3
1	N	113	ILE	2.3
1	P	532	ARG	2.3
1	U	422	THR	2.3
1	A	20	THR	2.3
1	B	27	ARG	2.3
1	C	87	ARG	2.3
1	C	326	GLY	2.3
1	D	308	GLY	2.3
1	D	502	GLY	2.3
1	E	428	GLY	2.3
1	H	504	LYS	2.3
1	J	228	LYS	2.3
1	E	407	ALA	2.3
1	F	91	ALA	2.3
1	H	298	ILE	2.3
1	H	458	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	I	54	ARG	2.3
1	K	382	GLY	2.3
2	n	124	LYS	2.3
1	O	188	ALA	2.3
1	Q	157	ILE	2.3
1	X	170	ALA	2.3
1	X	255	ILE	2.3
2	p	125	ARG	2.3
2	o	20	ALA	2.3
2	r	55	ILE	2.3
2	d	129	ILE	2.3
2	e	35	THR	2.3
1	W	172	HIS	2.3
1	B	338	ALA	2.3
1	D	155	HIS	2.3
1	J	150	HIS	2.3
1	J	297	HIS	2.3
2	u	85	HIS	2.3
1	M	514	TYR	2.3
1	N	141	ASN	2.3
1	O	48	TYR	2.3
1	P	403	TYR	2.3
1	Q	112	ASN	2.3
1	W	517	TYR	2.3
1	X	74	ASN	2.3
1	B	316	TYR	2.3
1	E	98	TYR	2.3
1	I	391	TYR	2.3
1	I	573	ASN	2.3
1	L	223	TYR	2.3
1	L	508	ASN	2.3
2	l	44	MET	2.3
2	v	86	ASN	2.3
1	M	443	ASP	2.3
1	P	561	ASP	2.3
1	Q	368	ASP	2.3
1	D	89	ASP	2.3
1	M	553	LEU	2.3
1	O	553	LEU	2.3
1	X	322	LEU	2.3
1	O	47	GLN	2.3
1	P	336	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
1	S	202	GLN	2.3
1	T	209	PHE	2.3
1	E	374	LEU	2.3
1	F	559	LEU	2.3
1	F	525	GLN	2.3
1	G	201	PHE	2.3
1	I	34	PHE	2.3
1	J	309	PHE	2.3
1	J	384	LEU	2.3
2	u	117	GLN	2.3
2	Y	149	PHE	2.3
2	j	18	LEU	2.3
1	A	597	GLN	2.3
1	C	555	GLN	2.3
1	E	40	GLN	2.3
2	f	126	GLN	2.3
1	O	306	GLU	2.3
1	O	314	GLU	2.3
1	Q	224	GLU	2.3
1	Q	537	GLU	2.3
1	R	462	GLU	2.3
1	W	24	GLU	2.3
1	X	423	GLU	2.3
1	A	5	GLU	2.3
1	D	462	GLU	2.3
1	H	147	GLU	2.3
1	N	64	VAL	2.3
1	O	78	VAL	2.3
1	C	175	VAL	2.3
1	F	594	VAL	2.3
1	G	320	VAL	2.3
1	I	430	VAL	2.3
1	L	506	VAL	2.3
2	g	89	VAL	2.3
1	M	582	LYS	2.3
1	R	83	LYS	2.3
1	S	288	LYS	2.3
1	V	413	LYS	2.3
1	C	504	LYS	2.3
2	o	6	LYS	2.3
1	N	88	PRO	2.3
1	P	587	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	T	273	ARG	2.3
1	T	584	PRO	2.3
1	X	145	ARG	2.3
1	H	511	ARG	2.3
1	J	370	PRO	2.3
2	s	150	PRO	2.3
1	O	419	GLY	2.3
1	Q	158	TRP	2.3
1	S	266	ILE	2.3
1	V	219	ILE	2.3
1	V	266	ILE	2.3
1	M	188	ALA	2.3
1	M	572	ALA	2.3
1	N	36	SER	2.3
1	O	599	ALA	2.3
1	Q	91	ALA	2.3
1	R	174	THR	2.3
1	T	500	ALA	2.3
1	U	69	SER	2.3
1	U	114	ALA	2.3
1	U	170	ALA	2.3
1	W	442	ALA	2.3
1	X	100	THR	2.3
1	A	231	THR	2.3
1	B	138	THR	2.3
1	B	220	ALA	2.3
1	D	69	SER	2.3
1	F	356	ILE	2.3
1	H	340	ILE	2.3
1	I	184	TRP	2.3
1	J	19	TRP	2.3
1	E	599	ALA	2.3
1	F	174	THR	2.3
1	F	400	ALA	2.3
1	G	442	ALA	2.3
1	J	125	ALA	2.3
1	J	200	SER	2.3
1	L	577	ILE	2.3
2	l	47	TRP	2.3
2	r	81	SER	2.3
2	s	47	TRP	2.3
2	Z	60	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
2	Z	105	ALA	2.3
2	a	30	SER	2.3
2	g	119	GLY	2.3
2	j	129	ILE	2.3
1	J	377	THR	2.3
2	m	105	ALA	2.3
2	n	42	ALA	2.3
2	h	105	ALA	2.3
1	C	155	HIS	2.3
2	v	43	MET	2.3
1	M	235	TYR	2.3
1	Q	517	TYR	2.3
1	V	53	TYR	2.3
1	W	447	TYR	2.3
1	A	191	TYR	2.3
1	D	392	TYR	2.3
2	k	58	TYR	2.3
2	m	95	TYR	2.3
2	p	58	TYR	2.3
2	Y	118	TYR	2.3
2	j	118	TYR	2.3
1	S	6	ASN	2.3
1	S	287	LEU	2.3
1	V	394	ASN	2.3
1	A	554	LEU	2.3
1	C	536	LEU	2.3
1	L	366	ASN	2.3
1	L	405	LEU	2.3
2	Y	122	LEU	2.3
1	U	187	PHE	2.3
1	D	524	PHE	2.3
1	L	247	PHE	2.3
2	l	140	PHE	2.3
1	Q	250	ASP	2.3
1	S	421	ASP	2.3
1	T	42	ASP	2.3
1	A	16	ASP	2.3
1	E	257	ASP	2.3
1	F	169	ASP	2.3
1	I	186	ASP	2.3
1	K	260	ASP	2.3
1	O	578	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
1	S	40	GLN	2.3
1	C	118	GLN	2.3
1	G	236	GLN	2.3
1	K	597	GLN	2.3
2	c	43	GLN	2.3
1	P	306	GLU	2.3
1	Q	185	GLU	2.3
1	S	185	GLU	2.3
1	V	566	GLU	2.3
1	A	462	GLU	2.3
1	H	406	GLU	2.3
1	I	445	GLU	2.3
1	L	224	GLU	2.3
2	l	46	GLU	2.3
1	M	520	VAL	2.3
1	U	506	VAL	2.3
1	X	324	LYS	2.3
1	D	228	LYS	2.3
1	D	252	LYS	2.3
1	E	244	VAL	2.3
1	E	583	LYS	2.3
1	J	347	LYS	2.3
1	K	68	VAL	2.3
2	a	15	LYS	2.3
2	j	46	VAL	2.3
1	P	328	ARG	2.3
1	B	569	ARG	2.3
1	E	459	ARG	2.3
1	X	345	PRO	2.3
1	H	109	ILE	2.3
1	H	395	PRO	2.3
1	I	176	ILE	2.3
1	I	398	PRO	2.3
2	t	150	PRO	2.3
2	g	159	PRO	2.3
1	W	122	GLY	2.3
1	I	352	TRP	2.3
1	J	122	GLY	2.3
2	k	135	GLY	2.3
2	s	18	GLY	2.3
2	b	83	GLY	2.3
2	e	144	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	N	454	ALA	2.3
1	R	402	ALA	2.3
1	E	91	ALA	2.3
2	Y	101	ALA	2.3
2	h	29	ALA	2.3
1	M	231	THR	2.3
1	N	417	THR	2.3
1	Q	39	SER	2.3
1	S	22	SER	2.3
1	S	180	SER	2.3
1	U	106	THR	2.3
1	V	20	THR	2.3
1	X	455	THR	2.3
1	D	136	SER	2.3
1	D	523	SER	2.3
1	K	526	SER	2.3
2	t	100	THR	2.3
1	U	258	LEU	2.3
1	V	374	LEU	2.3
1	W	438	LEU	2.3
1	X	67	LEU	2.3
1	D	499	LEU	2.3
2	k	147	HIS	2.3
2	l	113	LEU	2.3
2	v	75	LEU	2.3
2	v	147	HIS	2.3
1	Q	223	TYR	2.3
1	B	447	TYR	2.3
1	J	48	TYR	2.3
1	Q	35	PHE	2.3
1	V	336	PHE	2.3
1	X	233	PHE	2.3
1	A	201	PHE	2.3
1	D	336	PHE	2.3
1	H	432	PHE	2.3
2	p	60	PHE	2.3
1	M	112	ASN	2.3
1	T	112	ASN	2.3
1	T	375	ASN	2.3
1	E	337	ASN	2.3
1	F	112	ASN	2.3
1	F	140	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
1	G	508	ASN	2.3
2	u	142	ASN	2.3
1	Q	47	GLN	2.3
1	Q	89	ASP	2.3
1	Q	215	ASP	2.3
1	R	196	ASP	2.3
1	S	601	GLN	2.3
1	T	383	ASP	2.3
1	V	368	ASP	2.3
1	X	118	GLN	2.3
1	C	289	ASP	2.3
1	D	142	GLN	2.3
1	E	291	GLN	2.3
1	F	215	ASP	2.3
1	F	327	GLN	2.3
1	F	364	ASP	2.3
1	G	89	ASP	2.3
1	H	368	ASP	2.3
1	I	42	ASP	2.3
1	I	218	GLN	2.3
1	J	601	GLN	2.3
2	u	22	ASP	2.3
2	Y	59	ASP	2.3
2	j	80	ASP	2.3
1	N	528	LYS	2.3
1	O	583	LYS	2.3
1	B	278	LYS	2.3
1	G	278	LYS	2.3
1	J	290	LYS	2.3
1	R	532	ARG	2.3
1	S	328	ARG	2.3
1	U	249	ARG	2.3
1	V	60	VAL	2.3
1	W	314	GLU	2.3
1	W	354	GLU	2.3
1	X	116	ARG	2.3
1	C	341	VAL	2.3
1	F	225	VAL	2.3
1	F	306	GLU	2.3
1	H	274	ARG	2.3
1	I	310	VAL	2.3
1	K	379	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	L	273	ARG	2.3
2	Y	38	GLU	2.3
1	P	356	ILE	2.3
1	V	157	ILE	2.3
1	D	119	ILE	2.3
1	E	587	PRO	2.3
1	F	243	PRO	2.3
1	F	587	PRO	2.3
1	G	349	PRO	2.3
1	K	148	PRO	2.3
2	q	104	ILE	2.3
2	v	55	ILE	2.3
2	j	63	ILE	2.3
1	Q	540	GLY	2.3
1	S	411	ALA	2.3
1	T	596	ALA	2.3
1	U	402	ALA	2.3
1	U	428	GLY	2.3
1	A	17	ALA	2.3
1	A	512	GLY	2.3
1	D	125	ALA	2.3
1	F	124	GLY	2.3
1	F	294	ALA	2.3
1	I	338	ALA	2.3
1	J	318	GLY	2.3
2	s	13	ALA	2.3
2	s	44	MET	2.3
2	Z	22	ALA	2.3
2	h	114	ALA	2.3
1	N	211	TRP	2.3
1	Q	207	TRP	2.3
1	R	19	TRP	2.3
1	W	19	TRP	2.3
1	K	207	TRP	2.3
1	M	130	THR	2.3
1	O	258	LEU	2.3
1	O	542	THR	2.3
1	Q	417	THR	2.3
1	W	542	THR	2.3
1	D	100	THR	2.3
1	D	576	LEU	2.3
1	E	422	THR	2.3

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Mol	Chain	Res	Type	RSRZ
1	H	501	THR	2.3
1	I	49	THR	2.3
1	J	284	THR	2.3
1	K	373	LEU	2.3
2	n	147	HIS	2.3
1	N	523	SER	2.3
1	O	309	PHE	2.3
1	R	263	PHE	2.3
1	R	371	TYR	2.3
1	R	524	PHE	2.3
1	E	168	SER	2.3
1	H	13	SER	2.3
1	I	261	SER	2.3
1	T	48	TYR	2.3
2	Y	158	PHE	2.3
2	h	158	PHE	2.3
1	Q	205	ASN	2.3
1	M	597	GLN	2.3
1	P	525	GLN	2.3
1	T	525	GLN	2.3
1	U	228	LYS	2.3
1	X	582	LYS	2.3
1	A	190	LYS	2.3
1	C	74	ASN	2.3
1	D	366	ASN	2.3
1	D	436	ASN	2.3
1	E	182	ASN	2.3
1	F	337	ASN	2.3
1	H	375	ASN	2.3
1	V	441	ARG	2.3
1	W	513	ARG	2.3
1	A	218	GLN	2.3
1	C	355	GLN	2.3
1	C	529	GLN	2.3
1	D	597	GLN	2.3
1	E	575	GLN	2.3
1	H	142	GLN	2.3
1	I	40	GLN	2.3
1	K	66	LYS	2.3
1	N	244	VAL	2.3
1	O	18	ASP	2.3
1	S	397	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	T	77	ASP	2.3
1	T	254	VAL	2.3
1	U	319	VAL	2.3
1	B	63	VAL	2.3
1	B	443	ASP	2.3
1	D	77	ASP	2.3
1	E	93	VAL	2.3
1	E	237	ASP	2.3
1	E	520	VAL	2.3
1	F	341	VAL	2.3
1	H	16	ASP	2.3
2	Y	72	ASP	2.3
1	M	360	GLU	2.2
1	Q	133	GLU	2.2
1	T	242	GLU	2.2
1	G	189	GLU	2.2
1	I	311	GLU	2.2
1	K	133	GLU	2.2
1	K	296	GLU	2.2
1	X	293	ILE	2.2
1	G	109	ILE	2.2
1	K	149	ILE	2.2
2	k	55	ILE	2.2
2	f	64	ILE	2.2
1	O	545	GLY	2.2
1	R	238	PRO	2.2
1	S	232	ALA	2.2
1	T	121	ALA	2.2
1	V	382	GLY	2.2
1	X	122	GLY	2.2
1	A	522	PRO	2.2
1	A	562	GLY	2.2
1	D	55	GLY	2.2
1	D	238	PRO	2.2
1	H	353	PRO	2.2
1	I	587	PRO	2.2
2	q	70	GLY	2.2
2	r	23	ALA	2.2
2	u	18	GLY	2.2
2	b	138	PRO	2.2
2	c	138	PRO	2.2
2	b	132	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
2	d	66	GLY	2.2
2	f	136	PRO	2.2
2	i	138	PRO	2.2
1	A	21	ALA	2.2
1	E	342	ALA	2.2
1	E	400	ALA	2.2
2	d	141	MET	2.2
2	f	77	ALA	2.2
1	C	164	LEU	2.2
1	H	292	LEU	2.2
1	L	536	LEU	2.2
2	r	114	LEU	2.2
1	M	309	PHE	2.2
1	P	138	THR	2.2
1	X	177	HIS	2.2
2	o	118	THR	2.2
2	e	82	HIS	2.2
2	j	93	PHE	2.2
1	N	66	LYS	2.2
1	N	381	SER	2.2
1	N	504	LYS	2.2
1	R	324	LYS	2.2
1	T	252	LYS	2.2
1	T	272	LYS	2.2
1	X	30	LYS	2.2
1	X	69	SER	2.2
1	X	163	LYS	2.2
1	G	261	SER	2.2
1	I	582	LYS	2.2
1	L	151	SER	2.2
2	k	111	LYS	2.2
2	Y	57	TYR	2.2
1	Q	103	ARG	2.2
1	X	458	ARG	2.2
1	A	171	ARG	2.2
1	A	269	ARG	2.2
1	A	569	ARG	2.2
1	I	513	ARG	2.2
1	K	328	ARG	2.2
1	M	581	VAL	2.2
1	Q	129	VAL	2.2
1	R	182	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
1	R	214	GLN	2.2
1	S	78	VAL	2.2
1	U	310	VAL	2.2
1	A	60	VAL	2.2
1	B	226	VAL	2.2
1	C	161	ASN	2.2
1	E	161	ASN	2.2
1	G	218	GLN	2.2
1	L	40	GLN	2.2
1	L	135	GLN	2.2
1	L	581	VAL	2.2
2	Y	19	VAL	2.2
2	Y	151	ASN	2.2
2	Z	92	VAL	2.2
1	O	120	GLU	2.2
1	P	368	ASP	2.2
1	S	250	ASP	2.2
1	U	566	GLU	2.2
1	W	378	ASP	2.2
1	A	227	GLU	2.2
1	A	314	GLU	2.2
1	A	396	GLU	2.2
1	B	393	GLU	2.2
1	F	185	GLU	2.2
1	G	354	GLU	2.2
1	I	414	GLU	2.2
1	J	9	GLU	2.2
1	J	378	ASP	2.2
1	K	256	ASP	2.2
2	l	98	GLU	2.2
2	o	50	ASP	2.2
2	r	27	ASP	2.2
2	s	29	GLU	2.2
2	v	22	ASP	2.2
2	d	72	ASP	2.2
1	T	255	ILE	2.2
1	G	113	ILE	2.2
1	G	333	ILE	2.2
1	H	157	ILE	2.2
1	I	144	ILE	2.2
1	L	293	ILE	2.2
1	N	91	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	O	522	PRO	2.2
1	P	82	PRO	2.2
1	S	349	PRO	2.2
1	Q	593	LEU	2.2
1	S	512	GLY	2.2
1	U	373	LEU	2.2
1	W	124	GLY	2.2
1	W	267	ALA	2.2
1	A	357	ALA	2.2
1	B	238	PRO	2.2
1	G	431	ALA	2.2
1	I	507	LEU	2.2
1	J	152	ALA	2.2
1	J	373	LEU	2.2
1	K	580	GLY	2.2
2	l	12	ALA	2.2
2	t	43	MET	2.2
2	v	114	LEU	2.2
2	v	126	ALA	2.2
2	v	132	MET	2.2
2	a	138	PRO	2.2
1	W	374	LEU	2.2
1	W	554	LEU	2.2
1	D	373	LEU	2.2
1	D	453	LEU	2.2
1	D	552	LEU	2.2
2	d	21	ALA	2.2
2	d	88	ALA	2.2
2	g	62	GLY	2.2
1	N	44	TRP	2.2
1	T	126	TRP	2.2
1	O	432	PHE	2.2
1	Q	422	THR	2.2
1	R	272	LYS	2.2
1	V	348	LYS	2.2
1	W	155	HIS	2.2
1	X	422	THR	2.2
1	X	541	LYS	2.2
1	A	422	THR	2.2
1	A	455	THR	2.2
1	B	163	LYS	2.2
1	F	228	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	G	187	PHE	2.2
1	K	336	PHE	2.2
1	H	174	THR	2.2
1	I	323	THR	2.2
1	J	282	THR	2.2
1	J	542	THR	2.2
1	L	583	LYS	2.2
2	o	134	THR	2.2
2	s	134	THR	2.2
1	N	447	TYR	2.2
1	O	235	TYR	2.2
1	S	98	TYR	2.2
1	U	328	ARG	2.2
1	V	517	TYR	2.2
1	W	116	ARG	2.2
1	A	48	TYR	2.2
1	A	61	ARG	2.2
1	E	48	TYR	2.2
1	E	223	TYR	2.2
1	K	26	ARG	2.2
2	k	95	TYR	2.2
2	k	128	TYR	2.2
2	o	115	TYR	2.2
2	q	58	TYR	2.2
2	b	85	ARG	2.2
2	i	85	ARG	2.2
2	i	134	ARG	2.2
1	S	36	SER	2.2
2	Z	41	SER	2.2
2	c	70	SER	2.2
2	j	70	SER	2.2
1	P	64	VAL	2.2
1	R	520	VAL	2.2
1	S	254	VAL	2.2
1	U	341	VAL	2.2
1	U	412	VAL	2.2
1	V	315	VAL	2.2
1	X	254	VAL	2.2
1	X	496	VAL	2.2
1	B	111	VAL	2.2
1	C	301	VAL	2.2
1	E	412	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	G	397	VAL	2.2
1	K	581	VAL	2.2
2	k	37	VAL	2.2
1	S	270	GLN	2.2
1	T	47	GLN	2.2
1	X	142	GLN	2.2
1	A	450	GLN	2.2
1	B	591	GLN	2.2
1	C	40	GLN	2.2
1	D	555	GLN	2.2
1	E	429	GLN	2.2
2	g	40	GLN	2.2
1	O	531	ASN	2.2
1	S	203	ASN	2.2
1	E	394	ASN	2.2
1	M	414	GLU	2.2
1	C	185	GLU	2.2
1	E	24	GLU	2.2
1	H	534	GLU	2.2
1	I	234	ILE	2.2
1	I	271	ILE	2.2
1	J	379	GLU	2.2
2	k	29	GLU	2.2
2	o	120	ILE	2.2
2	t	98	GLU	2.2
2	v	54	ILE	2.2
2	Z	64	ILE	2.2
2	i	38	GLU	2.2
1	O	101	ASP	2.2
1	V	260	ASP	2.2
1	M	243	PRO	2.2
1	N	398	PRO	2.2
1	O	438	LEU	2.2
1	P	453	LEU	2.2
1	Q	559	LEU	2.2
1	Q	576	LEU	2.2
1	R	596	ALA	2.2
1	S	79	LEU	2.2
1	T	134	ASP	2.2
1	T	197	ASP	2.2
1	T	114	ALA	2.2
1	T	416	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	U	382	GLY	2.2
1	U	407	ALA	2.2
1	V	96	GLY	2.2
1	W	384	LEU	2.2
1	X	79	LEU	2.2
1	A	438	LEU	2.2
1	A	453	LEU	2.2
1	C	18	ASP	2.2
1	B	294	ALA	2.2
1	B	389	LEU	2.2
1	C	509	ASP	2.2
1	F	498	ASP	2.2
1	G	373	LEU	2.2
1	I	384	LEU	2.2
1	J	43	ASP	2.2
1	J	509	ASP	2.2
1	L	253	ASP	2.2
2	k	63	ASP	2.2
2	l	71	ASP	2.2
1	L	580	GLY	2.2
2	l	132	MET	2.2
2	p	33	MET	2.2
2	t	143	LEU	2.2
2	v	63	ASP	2.2
1	C	402	ALA	2.2
1	J	188	ALA	2.2
1	K	395	PRO	2.2
2	n	107	ALA	2.2
2	v	87	LEU	2.2
2	Y	138	PRO	2.2
2	d	102	PRO	2.2
2	e	83	GLY	2.2
2	g	135	ALA	2.2
2	h	77	ALA	2.2
1	U	265	LYS	2.2
1	C	348	LYS	2.2
2	c	125	LYS	2.2
1	R	57	PHE	2.2
1	J	304	PHE	2.2
2	i	158	PHE	2.2
1	A	459	ARG	2.2
1	C	513	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	E	65	ARG	2.2
1	E	116	ARG	2.2
1	L	54	ARG	2.2
2	h	140	ARG	2.2
1	M	216	THR	2.2
1	O	409	THR	2.2
1	Q	106	THR	2.2
1	S	284	THR	2.2
1	U	297	HIS	2.2
1	C	501	THR	2.2
1	D	455	THR	2.2
1	E	150	HIS	2.2
2	k	56	THR	2.2
2	v	134	THR	2.2
2	h	14	THR	2.2
1	T	235	TYR	2.2
2	n	58	TYR	2.2
1	Q	303	VAL	2.2
1	U	60	VAL	2.2
1	X	226	VAL	2.2
1	C	123	VAL	2.2
1	E	415	VAL	2.2
2	p	83	VAL	2.2
2	Z	68	VAL	2.2
2	g	68	VAL	2.2
2	h	46	VAL	2.2
1	V	154	SER	2.2
1	C	136	SER	2.2
1	D	139	SER	2.2
1	D	526	SER	2.2
2	n	130	SER	2.2
2	u	77	SER	2.2
2	v	121	SER	2.2
1	U	355	GLN	2.2
1	U	530	GLN	2.2
1	W	597	GLN	2.2
1	K	529	GLN	2.2
1	P	157	ILE	2.2
1	S	113	ILE	2.2
1	U	76	ILE	2.2
1	V	577	ILE	2.2
1	W	577	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	E	176	ILE	2.2
1	J	198	ILE	2.2
2	g	112	ILE	2.2
2	i	64	ILE	2.2
1	N	230	GLU	2.2
1	O	366	ASN	2.2
1	P	495	GLU	2.2
1	S	366	ASN	2.2
1	T	401	ASN	2.2
1	A	384	LEU	2.2
1	B	133	GLU	2.2
1	B	161	ASN	2.2
1	W	67	LEU	2.2
1	C	537	GLU	2.2
1	E	331	ASN	2.2
1	H	24	GLU	2.2
1	I	133	GLU	2.2
1	I	161	ASN	2.2
1	I	426	ASN	2.2
2	l	112	GLU	2.2
2	v	142	ASN	2.2
1	K	258	LEU	2.2
2	q	97	LEU	2.2
2	j	38	GLU	2.2
1	P	584	PRO	2.2
1	Q	428	GLY	2.2
1	Q	456	ALA	2.2
1	R	220	ALA	2.2
1	R	587	PRO	2.2
1	S	86	ALA	2.2
1	X	90	ALA	2.2
1	X	114	ALA	2.2
1	C	599	ALA	2.2
2	l	13	ALA	2.2
2	m	135	GLY	2.2
2	o	123	ALA	2.2
2	f	141	MET	2.2
1	E	137	PRO	2.2
1	F	419	GLY	2.2
1	F	545	GLY	2.2
1	I	522	PRO	2.2
1	K	302	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	K	587	PRO	2.2
1	N	600	LYS	2.2
1	R	43	ASP	2.2
1	S	519	ASP	2.2
1	U	83	LYS	2.2
1	V	256	ASP	2.2
1	X	413	LYS	2.2
1	B	250	ASP	2.2
1	D	561	ASP	2.2
1	G	42	ASP	2.2
1	K	582	LYS	2.2
2	j	17	ASP	2.2
1	M	27	ARG	2.2
1	Q	247	PHE	2.2
1	T	511	ARG	2.2
1	D	557	PHE	2.2
1	F	145	ARG	2.2
1	F	511	ARG	2.2
1	I	269	ARG	2.2
2	s	122	ARG	2.2
2	a	85	ARG	2.2
1	V	207	TRP	2.2
1	H	184	TRP	2.2
1	N	100	THR	2.2
1	T	417	THR	2.2
1	F	422	THR	2.2
1	H	586	THR	2.2
2	t	85	HIS	2.2
2	Y	33	THR	2.2
2	d	156	HIS	2.2
2	g	82	HIS	2.2
1	N	303	VAL	2.2
1	N	403	TYR	2.2
1	O	392	TYR	2.2
1	O	506	VAL	2.2
1	Q	320	VAL	2.2
1	S	372	TYR	2.2
1	S	412	VAL	2.2
1	V	223	TYR	2.2
1	A	80	TYR	2.2
1	B	412	VAL	2.2
1	C	225	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	E	156	VAL	2.2
1	E	303	VAL	2.2
1	H	581	VAL	2.2
1	K	372	TYR	2.2
2	Z	28	VAL	2.2
2	i	67	TYR	2.2
2	i	157	TYR	2.2
1	M	381	SER	2.2
1	O	601	GLN	2.2
1	Q	56	GLN	2.2
1	Q	181	GLN	2.2
1	W	10	SER	2.2
1	X	113	ILE	2.2
1	X	180	SER	2.2
1	B	198	ILE	2.2
1	B	340	ILE	2.2
1	F	463	ILE	2.2
1	I	76	ILE	2.2
1	K	530	GLN	2.2
1	K	578	GLN	2.2
2	o	31	GLN	2.2
2	o	54	ILE	2.2
2	o	104	ILE	2.2
2	Y	87	SER	2.2
2	f	63	ILE	2.2
1	O	329	LEU	2.2
1	T	552	LEU	2.2
1	C	322	LEU	2.2
1	G	551	LEU	2.2
1	I	499	LEU	2.2
1	L	292	LEU	2.2
2	t	75	LEU	2.2
1	O	195	ALA	2.2
1	P	585	GLU	2.2
1	Q	503	GLU	2.2
1	R	117	GLU	2.2
1	W	595	GLU	2.2
1	P	349	PRO	2.2
1	Q	382	GLY	2.2
1	R	108	LYS	2.2
1	S	29	ALA	2.2
1	T	17	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	U	227	GLU	2.2
1	R	326	GLY	2.2
1	U	348	LYS	2.2
1	X	232	ALA	2.2
1	X	583	LYS	2.2
1	B	267	ALA	2.2
1	B	366	ASN	2.2
1	C	105	ASN	2.2
1	D	533	ALA	2.2
1	E	29	ALA	2.2
1	G	70	GLU	2.2
1	E	413	LYS	2.2
1	F	278	LYS	2.2
1	F	504	LYS	2.2
1	G	232	ALA	2.2
1	G	294	ALA	2.2
1	I	185	GLU	2.2
1	J	147	GLU	2.2
1	K	426	ASN	2.2
2	k	23	ALA	2.2
2	l	138	ASN	2.2
2	m	123	ALA	2.2
2	r	64	GLU	2.2
2	u	36	ALA	2.2
2	d	29	ALA	2.2
2	c	79	GLY	2.2
2	f	25	LYS	2.2
2	g	128	ALA	2.2
1	D	241	GLY	2.2
1	D	427	GLY	2.2
1	J	326	GLY	2.2
2	s	93	PRO	2.2
1	O	27	ARG	2.2
1	O	513	ARG	2.2
1	T	7	ARG	2.2
1	X	7	ARG	2.2
1	J	37	ARG	2.2
1	K	61	ARG	2.2
2	n	15	ARG	2.2
1	S	443	ASP	2.2
1	T	89	ASP	2.2
1	T	519	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	W	237	ASP	2.2
1	X	222	PHE	2.2
1	X	247	PHE	2.2
1	X	250	ASP	2.2
1	E	359	PHE	2.2
1	F	443	ASP	2.2
2	l	63	ASP	2.2
2	s	38	ASP	2.2
1	D	207	TRP	2.2
1	P	361	HIS	2.2
1	E	297	HIS	2.2
1	O	301	VAL	2.1
1	Q	301	VAL	2.1
1	R	303	VAL	2.1
1	W	586	THR	2.1
1	W	594	VAL	2.1
1	X	581	VAL	2.1
1	A	448	VAL	2.1
1	C	93	VAL	2.1
1	C	397	VAL	2.1
1	D	130	THR	2.1
1	G	115	VAL	2.1
1	J	175	VAL	2.1
1	J	415	VAL	2.1
2	m	118	THR	2.1
2	q	26	THR	2.1
2	u	134	THR	2.1
2	c	127	THR	2.1
2	j	35	THR	2.1
1	Q	369	TYR	2.1
1	R	316	TYR	2.1
1	C	392	TYR	2.1
2	Y	104	TYR	2.1
2	c	124	TYR	2.1
1	X	176	ILE	2.1
1	B	176	ILE	2.1
1	C	11	ILE	2.1
1	N	291	GLN	2.1
1	V	389	LEU	2.1
1	A	51	LEU	2.1
1	E	47	GLN	2.1
1	E	405	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	E	499	LEU	2.1
1	H	94	LEU	2.1
1	M	86	ALA	2.1
1	O	162	SER	2.1
1	O	200	SER	2.1
1	R	526	SER	2.1
1	T	163	LYS	2.1
1	E	335	SER	2.1
1	G	290	LYS	2.1
1	G	348	LYS	2.1
1	I	30	LYS	2.1
2	s	43	MET	2.1
2	h	52	MET	2.1
1	M	311	GLU	2.1
1	N	338	ALA	2.1
1	O	379	GLU	2.1
1	U	152	ALA	2.1
1	M	238	PRO	2.1
1	O	14	ARG	2.1
1	O	511	ARG	2.1
1	O	589	GLU	2.1
1	P	120	GLU	2.1
1	P	127	ARG	2.1
1	Q	321	ARG	2.1
1	U	230	GLU	2.1
1	X	61	ARG	2.1
1	X	414	GLU	2.1
1	A	242	GLU	2.1
1	C	338	ALA	2.1
1	E	424	ALA	2.1
2	n	29	GLU	2.1
2	Z	29	ALA	2.1
2	j	110	ALA	2.1
1	C	382	GLY	2.1
1	G	602	GLY	2.1
1	H	54	ARG	2.1
1	K	146	ARG	2.1
2	n	131	ARG	2.1
2	v	135	GLY	2.1
2	Y	144	GLY	2.1
1	R	426	ASN	2.1
1	R	436	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	394	ASN	2.1
1	E	573	ASN	2.1
1	T	233	PHE	2.1
2	g	93	PHE	2.1
1	M	153	CYS	2.1
1	M	519	ASP	2.1
1	N	257	ASP	2.1
1	N	570	ASP	2.1
1	R	159	ASP	2.1
1	U	18	ASP	2.1
1	B	256	ASP	2.1
1	H	257	ASP	2.1
2	k	8	ASP	2.1
2	m	27	ASP	2.1
2	p	35	ASP	2.1
2	c	72	ASP	2.1
2	i	47	ASP	2.1
1	M	497	VAL	2.1
1	S	239	VAL	2.1
1	T	341	VAL	2.1
1	V	303	VAL	2.1
1	V	425	VAL	2.1
1	W	286	VAL	2.1
1	B	425	VAL	2.1
1	C	44	TRP	2.1
1	D	341	VAL	2.1
1	E	361	HIS	2.1
1	K	397	VAL	2.1
1	N	446	THR	2.1
1	P	518	THR	2.1
1	K	138	THR	2.1
2	k	134	THR	2.1
1	N	363	TYR	2.1
1	P	219	ILE	2.1
1	Q	176	ILE	2.1
1	Q	251	ILE	2.1
1	R	391	TYR	2.1
1	B	235	TYR	2.1
1	B	277	TYR	2.1
1	C	369	TYR	2.1
1	G	198	ILE	2.1
1	H	219	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	I	80	TYR	2.1
1	K	316	TYR	2.1
2	m	58	TYR	2.1
2	r	58	TYR	2.1
2	Y	157	TYR	2.1
2	d	67	TYR	2.1
1	N	212	LEU	2.1
1	N	322	LEU	2.1
1	P	507	LEU	2.1
1	Q	507	LEU	2.1
1	R	374	LEU	2.1
1	U	313	LYS	2.1
1	X	373	LEU	2.1
1	X	593	LEU	2.1
1	F	83	LYS	2.1
1	G	324	LYS	2.1
1	J	559	LEU	2.1
1	K	389	LEU	2.1
2	k	114	LEU	2.1
2	Y	125	LYS	2.1
1	P	555	GLN	2.1
1	Q	578	GLN	2.1
1	R	56	GLN	2.1
1	T	142	GLN	2.1
1	U	202	GLN	2.1
1	X	291	GLN	2.1
1	X	327	GLN	2.1
1	X	429	GLN	2.1
1	B	73	GLN	2.1
1	E	142	GLN	2.1
1	F	142	GLN	2.1
1	H	355	GLN	2.1
2	k	44	MET	2.1
1	M	454	ALA	2.1
1	Q	7	ARG	2.1
1	S	107	ALA	2.1
1	X	21	ALA	2.1
1	D	532	ARG	2.1
1	E	90	ALA	2.1
1	F	441	ARG	2.1
1	G	408	ALA	2.1
1	I	29	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	K	269	ARG	2.1
1	L	27	ARG	2.1
1	L	596	ALA	2.1
2	k	131	ARG	2.1
2	l	90	ARG	2.1
2	p	131	ARG	2.1
2	c	85	ARG	2.1
1	N	185	GLU	2.1
1	O	199	PRO	2.1
1	S	13	SER	2.1
1	S	154	SER	2.1
1	U	526	SER	2.1
1	U	580	GLY	2.1
1	W	305	GLY	2.1
1	A	423	GLU	2.1
1	B	88	PRO	2.1
1	C	543	PRO	2.1
1	D	414	GLU	2.1
1	E	22	SER	2.1
1	G	515	GLU	2.1
1	I	200	SER	2.1
1	I	495	GLU	2.1
1	J	39	SER	2.1
1	K	117	GLU	2.1
1	K	588	GLU	2.1
1	L	69	SER	2.1
2	q	133	PRO	2.1
2	r	30	PRO	2.1
1	T	436	ASN	2.1
1	U	203	ASN	2.1
1	D	203	ASN	2.1
1	F	34	PHE	2.1
1	F	351	PHE	2.1
1	I	432	PHE	2.1
2	n	65	ASN	2.1
2	h	74	ASN	2.1
1	M	383	ASP	2.1
1	N	134	ASP	2.1
1	P	207	TRP	2.1
1	Q	581	VAL	2.1
1	S	68	VAL	2.1
1	S	581	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	V	415	VAL	2.1
1	X	420	VAL	2.1
1	C	89	ASP	2.1
1	C	412	VAL	2.1
1	F	63	VAL	2.1
1	H	496	VAL	2.1
1	J	64	VAL	2.1
1	J	77	ASP	2.1
2	a	36	ASP	2.1
2	a	81	ASP	2.1
2	c	56	TRP	2.1
2	c	92	VAL	2.1
1	N	104	HIS	2.1
2	q	85	HIS	2.1
2	b	82	HIS	2.1
1	M	94	LEU	2.1
1	N	278	LYS	2.1
1	N	344	THR	2.1
1	P	130	THR	2.1
1	P	535	ILE	2.1
1	U	446	THR	2.1
1	W	217	ILE	2.1
1	A	144	ILE	2.1
1	M	447	TYR	2.1
1	N	389	LEU	2.1
1	Q	552	LEU	2.1
1	S	517	TYR	2.1
1	T	571	TYR	2.1
1	U	67	LEU	2.1
1	V	235	TYR	2.1
1	A	272	LYS	2.1
1	C	422	THR	2.1
1	D	106	THR	2.1
1	D	231	THR	2.1
2	Z	117	LYS	2.1
2	c	35	THR	2.1
2	h	129	ILE	2.1
1	M	513	ARG	2.1
1	U	274	ARG	2.1
1	U	513	ARG	2.1
1	B	7	ARG	2.1
1	E	81	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	I	145	ARG	2.1
2	n	132	MET	2.1
2	u	125	ARG	2.1
1	N	442	ALA	2.1
1	V	494	ALA	2.1
1	W	555	GLN	2.1
1	X	530	GLN	2.1
1	C	121	ALA	2.1
1	D	56	GLN	2.1
1	E	17	ALA	2.1
1	F	170	ALA	2.1
1	H	294	ALA	2.1
1	J	529	GLN	2.1
2	n	12	ALA	2.1
2	r	34	GLN	2.1
2	b	128	ALA	2.1
2	c	40	GLN	2.1
2	j	43	GLN	2.1
1	M	185	GLU	2.1
1	M	326	GLY	2.1
1	N	406	GLU	2.1
1	P	227	GLU	2.1
1	Q	24	GLU	2.1
1	R	120	GLU	2.1
1	T	70	GLU	2.1
1	V	495	GLU	2.1
1	W	566	GLU	2.1
1	A	358	GLY	2.1
1	C	82	PRO	2.1
1	C	183	GLY	2.1
1	D	398	PRO	2.1
1	D	545	GLY	2.1
1	E	189	GLU	2.1
1	F	96	GLY	2.1
1	H	5	GLU	2.1
1	I	241	GLY	2.1
1	K	189	GLU	2.1
1	K	268	GLU	2.1
1	L	589	GLU	2.1
2	k	30	PRO	2.1
2	n	57	GLY	2.1
2	s	112	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
2	Z	73	GLU	2.1
2	h	79	GLY	2.1
1	N	336	PHE	2.1
1	O	245	SER	2.1
1	W	154	SER	2.1
1	A	381	SER	2.1
1	G	209	PHE	2.1
1	I	209	PHE	2.1
2	r	136	SER	2.1
1	Q	366	ASN	2.1
1	W	401	ASN	2.1
1	A	366	ASN	2.1
1	C	573	ASN	2.1
1	G	337	ASN	2.1
2	Z	95	ASN	2.1
1	N	415	VAL	2.1
1	O	415	VAL	2.1
1	R	208	VAL	2.1
1	T	310	VAL	2.1
1	X	175	VAL	2.1
1	F	448	VAL	2.1
2	l	10	VAL	2.1
1	M	43	ASP	2.1
1	M	119	ILE	2.1
1	M	144	ILE	2.1
1	N	364	ASP	2.1
1	O	289	ASP	2.1
1	O	509	ASP	2.1
1	T	172	HIS	2.1
1	T	352	TRP	2.1
1	T	600	LYS	2.1
1	R	128	LEU	2.1
1	U	198	ILE	2.1
1	V	169	ASP	2.1
1	V	570	ASP	2.1
1	B	347	LYS	2.1
1	B	234	ILE	2.1
1	C	84	ASP	2.1
1	C	367	ASP	2.1
1	E	163	LYS	2.1
1	F	155	HIS	2.1
1	F	229	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	I	361	HIS	2.1
1	J	196	ASP	2.1
1	J	272	LYS	2.1
1	L	265	LYS	2.1
2	p	102	LYS	2.1
2	t	47	TRP	2.1
1	G	553	LEU	2.1
1	J	405	LEU	2.1
2	Z	18	LEU	2.1
2	b	23	LEU	2.1
1	N	14	ARG	2.1
1	P	511	ARG	2.1
1	Q	328	ARG	2.1
1	W	377	THR	2.1
1	X	532	ARG	2.1
1	H	546	THR	2.1
1	J	343	ARG	2.1
1	V	549	TYR	2.1
1	D	517	TYR	2.1
2	k	106	THR	2.1
2	p	100	THR	2.1
2	n	43	MET	2.1
2	p	115	TYR	2.1
2	e	115	THR	2.1
1	N	411	ALA	2.1
1	S	188	ALA	2.1
1	V	232	ALA	2.1
1	B	342	ALA	2.1
1	D	121	ALA	2.1
2	q	23	ALA	2.1
2	q	88	ALA	2.1
2	r	96	ALA	2.1
2	s	42	ALA	2.1
2	b	101	ALA	2.1
1	P	202	GLN	2.1
1	U	575	GLN	2.1
1	V	135	GLN	2.1
1	E	135	GLN	2.1
1	I	214	GLN	2.1
2	t	117	GLN	2.1
1	N	295	GLY	2.1
1	B	382	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	428	GLY	2.1
1	D	365	GLY	2.1
1	M	247	PHE	2.1
1	M	304	PHE	2.1
1	O	34	PHE	2.1
1	S	359	PHE	2.1
1	T	359	PHE	2.1
1	X	495	GLU	2.1
1	X	543	PRO	2.1
1	B	537	GLU	2.1
1	C	88	PRO	2.1
1	C	233	PHE	2.1
1	F	137	PRO	2.1
1	F	224	GLU	2.1
2	g	136	PRO	2.1
2	i	107	GLU	2.1
1	M	36	SER	2.1
1	U	154	SER	2.1
2	b	70	SER	2.1
1	W	320	VAL	2.1
1	B	68	VAL	2.1
1	C	506	VAL	2.1
1	D	315	VAL	2.1
1	D	320	VAL	2.1
1	D	448	VAL	2.1
1	G	78	VAL	2.1
1	J	301	VAL	2.1
1	W	74	ASN	2.1
1	D	508	ASN	2.1
1	D	528	LYS	2.1
1	G	190	LYS	2.1
1	H	426	ASN	2.1
1	I	6	ASN	2.1
2	m	86	ASN	2.1
2	n	108	LYS	2.1
2	b	25	LYS	2.1
1	M	81	ARG	2.1
1	Q	145	ARG	2.1
1	Q	266	ILE	2.1
1	S	184	TRP	2.1
1	T	274	ARG	2.1
1	V	329	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	V	463	ILE	2.1
1	X	297	HIS	2.1
1	A	116	ARG	2.1
1	A	577	ILE	2.1
1	C	198	ILE	2.1
1	F	109	ILE	2.1
1	G	463	ILE	2.1
1	H	384	LEU	2.1
1	I	453	LEU	2.1
1	L	321	ARG	2.1
2	m	125	ARG	2.1
2	v	143	LEU	2.1
2	d	26	LEU	2.1
1	O	570	ASP	2.1
1	C	134	ASP	2.1
1	H	498	ASP	2.1
1	K	77	ASP	2.1
1	M	80	TYR	2.1
1	M	223	TYR	2.1
1	U	369	TYR	2.1
1	W	130	THR	2.1
1	W	549	TYR	2.1
1	X	20	THR	2.1
1	B	231	THR	2.1
2	u	44	MET	2.1
1	J	514	TYR	2.1
2	n	115	TYR	2.1
2	v	56	THR	2.1
2	c	67	TYR	2.1
2	i	104	TYR	2.1
1	Q	494	ALA	2.1
1	T	267	ALA	2.1
1	U	125	ALA	2.1
1	V	114	ALA	2.1
1	C	267	ALA	2.1
1	D	357	ALA	2.1
1	E	442	ALA	2.1
1	J	402	ALA	2.1
1	K	402	ALA	2.1
2	r	107	ALA	2.1
2	b	97	ALA	2.1
2	j	132	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	M	419	GLY	2.1
1	R	590	GLN	2.1
1	U	419	GLY	2.1
1	U	555	GLN	2.1
1	V	555	GLN	2.1
1	C	122	GLY	2.1
1	D	122	GLY	2.1
1	F	365	GLY	2.1
1	F	575	GLN	2.1
1	G	305	GLY	2.1
1	J	540	GLY	2.1
1	L	521	GLY	2.1
2	m	137	GLY	2.1
2	h	40	GLN	2.1
2	h	83	GLY	2.1
1	M	24	GLU	2.1
1	M	534	GLU	2.1
1	X	70	GLU	2.1
1	D	189	GLU	2.1
1	G	34	PHE	2.1
2	m	29	GLU	2.1
1	S	320	VAL	2.0
1	S	430	VAL	2.0
1	W	448	VAL	2.0
1	C	425	VAL	2.0
1	E	208	VAL	2.0
1	I	594	VAL	2.0
1	L	93	VAL	2.0
2	b	15	LYS	2.0
2	b	120	LYS	2.0
2	f	133	LYS	2.0
1	U	180	SER	2.0
1	B	36	SER	2.0
1	D	154	SER	2.0
2	o	139	SER	2.0
2	r	78	SER	2.0
2	s	130	SER	2.0
2	a	41	SER	2.0
2	h	30	SER	2.0
1	T	171	ARG	2.0
1	V	146	ARG	2.0
1	V	255	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
1	W	576	LEU	2.0
1	C	171	ARG	2.0
1	E	389	LEU	2.0
1	E	436	ASN	2.0
1	G	274	ARG	2.0
1	G	280	ILE	2.0
1	I	576	LEU	2.0
1	L	81	ARG	2.0
1	L	140	ASN	2.0
2	q	17	LEU	2.0
2	v	122	ARG	2.0
2	Y	64	ILE	2.0
2	b	64	ILE	2.0
1	W	207	TRP	2.0
1	D	184	TRP	2.0
1	K	352	TRP	2.0
2	f	94	HIS	2.0
1	M	542	THR	2.0
1	O	106	THR	2.0
1	Q	132	TYR	2.0
1	R	49	THR	2.0
1	S	294	ALA	2.0
1	U	500	ALA	2.0
1	U	599	ALA	2.0
1	V	17	ALA	2.0
1	W	416	ALA	2.0
1	W	494	ALA	2.0
1	A	556	TYR	2.0
1	D	43	ASP	2.0
1	D	411	ALA	2.0
1	E	194	ASP	2.0
1	J	80	TYR	2.0
1	J	372	TYR	2.0
1	K	519	ASP	2.0
1	L	166	ASP	2.0
2	k	72	ASP	2.0
2	l	27	ASP	2.0
2	o	109	TYR	2.0
2	q	27	ASP	2.0
2	r	22	ASP	2.0
2	r	106	THR	2.0
2	t	8	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
2	v	106	THR	2.0
2	a	35	THR	2.0
2	c	81	ASP	2.0
2	d	36	ASP	2.0
2	e	57	TYR	2.0
2	f	32	ALA	2.0
2	f	35	THR	2.0
2	g	157	TYR	2.0
1	N	427	GLY	2.0
1	N	502	GLY	2.0
1	N	349	PRO	2.0
1	R	304	PHE	2.0
1	T	326	GLY	2.0
1	U	142	GLN	2.0
1	V	309	PHE	2.0
1	W	187	PHE	2.0
1	A	47	GLN	2.0
1	A	544	GLN	2.0
1	B	427	GLY	2.0
1	D	544	GLN	2.0
1	E	318	GLY	2.0
1	I	326	GLY	2.0
1	K	52	GLN	2.0
1	L	562	GLY	2.0
2	f	43	GLN	2.0
1	D	204	PRO	2.0
1	K	238	PRO	2.0
2	e	75	PRO	2.0
1	N	583	LYS	2.0
1	C	120	GLU	2.0
1	D	163	LYS	2.0
1	G	120	GLU	2.0
1	I	290	LYS	2.0
1	K	83	LYS	2.0
1	L	311	GLU	2.0
1	M	60	VAL	2.0
1	M	175	VAL	2.0
1	Q	520	VAL	2.0
1	R	59	VAL	2.0
1	R	78	VAL	2.0
1	W	506	VAL	2.0
1	G	175	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
2	r	19	VAL	2.0
1	P	274	ARG	2.0
1	Q	287	LEU	2.0
1	I	61	ARG	2.0
1	I	273	ARG	2.0
2	m	114	LEU	2.0
2	r	87	LEU	2.0
2	Y	140	ARG	2.0
2	g	20	ARG	2.0
1	M	217	ILE	2.0
1	O	168	SER	2.0
1	R	46	SER	2.0
1	T	119	ILE	2.0
1	W	11	ILE	2.0
1	A	151	SER	2.0
1	B	10	SER	2.0
1	C	526	SER	2.0
1	G	200	SER	2.0
2	a	64	ILE	2.0
2	e	129	ILE	2.0
1	M	375	ASN	2.0
1	M	401	ASN	2.0
1	M	436	ASN	2.0
1	Q	141	ASN	2.0
1	E	426	ASN	2.0
1	I	508	ASN	2.0
1	J	140	ASN	2.0
1	K	508	ASN	2.0
2	t	86	ASN	2.0
1	R	211	TRP	2.0
1	U	361	HIS	2.0
1	X	361	HIS	2.0
1	H	207	TRP	2.0
2	b	42	MET	2.0
1	M	152	ALA	2.0
1	O	216	THR	2.0
1	P	344	THR	2.0
1	Q	455	THR	2.0
1	S	267	ALA	2.0
1	C	220	ALA	2.0
1	C	316	TYR	2.0
1	D	409	THR	2.0

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Mol	Chain	Res	Type	RSRZ
1	D	416	ALA	2.0
1	F	501	THR	2.0
1	H	500	ALA	2.0
1	L	556	TYR	2.0
2	l	56	THR	2.0
2	p	105	ALA	2.0
2	p	123	ALA	2.0
2	t	92	ALA	2.0
2	c	88	ALA	2.0
2	g	132	ALA	2.0
1	B	392	TYR	2.0
1	J	132	TYR	2.0
1	K	517	TYR	2.0
1	U	383	ASP	2.0
1	B	237	ASP	2.0
1	I	257	ASP	2.0
2	s	71	ASP	2.0
2	Y	36	ASP	2.0
2	a	103	ASP	2.0
1	O	602	GLY	2.0
1	R	122	GLY	2.0
1	S	247	PHE	2.0
1	V	201	PHE	2.0
1	W	428	GLY	2.0
1	B	524	PHE	2.0
1	E	427	GLY	2.0
1	F	350	PHE	2.0
2	n	137	GLY	2.0
2	Y	66	GLY	2.0
2	e	16	GLY	2.0
2	g	83	GLY	2.0
1	M	228	LYS	2.0
1	O	353	PRO	2.0
1	P	52	GLN	2.0
1	P	243	PRO	2.0
1	Q	108	LYS	2.0
1	Q	398	PRO	2.0
1	R	522	PRO	2.0
1	R	574	LYS	2.0
1	S	597	GLN	2.0
1	T	190	LYS	2.0
1	V	353	PRO	2.0

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Mol	Chain	Res	Type	RSRZ
1	V	591	GLN	2.0
1	A	66	LYS	2.0
1	A	88	PRO	2.0
1	A	370	PRO	2.0
1	C	272	LYS	2.0
1	C	291	GLN	2.0
1	D	413	LYS	2.0
1	J	265	LYS	2.0
1	J	353	PRO	2.0
2	v	150	PRO	2.0
1	M	425	VAL	2.0
1	N	379	GLU	2.0
1	O	117	GLU	2.0
1	N	274	ARG	2.0
1	R	116	ARG	2.0
1	R	145	ARG	2.0
1	R	320	VAL	2.0
1	T	537	GLU	2.0
1	W	397	VAL	2.0
1	X	379	GLU	2.0
1	B	496	VAL	2.0
1	C	70	GLU	2.0
1	C	311	GLU	2.0
1	I	503	GLU	2.0
1	J	296	GLU	2.0
1	K	303	VAL	2.0
2	i	140	ARG	2.0
1	P	384	LEU	2.0
1	U	292	LEU	2.0
1	X	33	LEU	2.0
1	C	258	LEU	2.0
2	c	23	LEU	2.0
1	Q	109	ILE	2.0
1	F	577	ILE	2.0
1	J	340	ILE	2.0
1	K	356	ILE	2.0
2	d	113	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.