



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 09:19 PM UTC

PDB ID : 5JJ1 / pdb_00005jj1
Title : Structure of the Immature Procapsid Conformation of P22 Portal Protein
Authors : Lokareddy, R.K.; Cingolani, G.
Deposited on : 2016-04-22
Resolution : 3.30 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
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

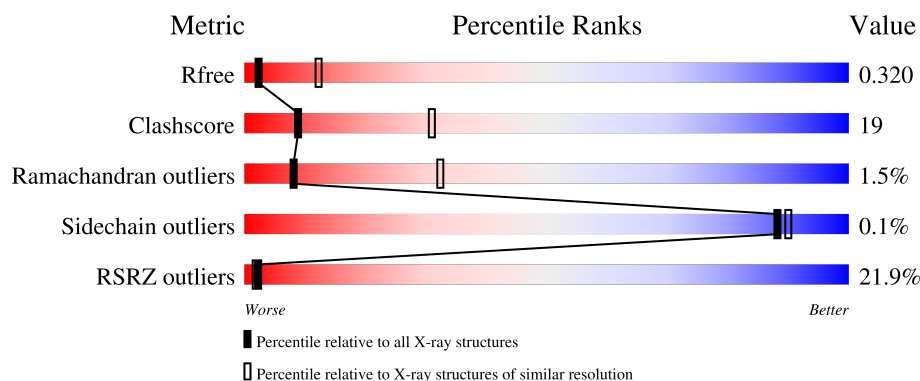
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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))
R_{free}	180053	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

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 $\leq 5\%$. 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	610	24% 61% 33% ..
1	B	610	16% 57% 36% ..
1	C	610	20% 56% 39% ..
1	D	610	25% 57% 35% ..
1	E	610	21% 58% 36% ..

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Mol	Chain	Length	Quality of chain
1	F	610	
1	G	610	
1	H	610	
1	I	610	
1	J	610	
1	K	610	
1	L	610	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 56559 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	A	585	Total	C	N	O	S	0	0	0
			4724	2976	806	921	21			
1	B	585	Total	C	N	O	S	0	0	0
			4710	2968	804	917	21			
1	C	585	Total	C	N	O	S	0	0	0
			4710	2968	804	917	21			
1	D	585	Total	C	N	O	S	0	0	0
			4723	2977	805	920	21			
1	E	585	Total	C	N	O	S	0	0	0
			4720	2974	805	920	21			
1	F	585	Total	C	N	O	S	0	0	0
			4710	2968	804	917	21			
1	G	585	Total	C	N	O	S	0	0	0
			4706	2966	804	915	21			
1	H	585	Total	C	N	O	S	0	0	0
			4710	2968	804	917	21			
1	I	585	Total	C	N	O	S	0	0	0
			4710	2968	804	917	21			
1	J	585	Total	C	N	O	S	0	0	0
			4710	2968	804	917	21			
1	K	585	Total	C	N	O	S	0	0	0
			4716	2971	805	919	21			
1	L	585	Total	C	N	O	S	0	0	0
			4710	2968	804	917	21			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	603	LEU	-	expression tag	UNP P26744
A	604	GLU	-	expression tag	UNP P26744
A	605	HIS	-	expression tag	UNP P26744
A	606	HIS	-	expression tag	UNP P26744
A	607	HIS	-	expression tag	UNP P26744

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Chain	Residue	Modelled	Actual	Comment	Reference
A	608	HIS	-	expression tag	UNP P26744
A	609	HIS	-	expression tag	UNP P26744
A	610	HIS	-	expression tag	UNP P26744
B	603	LEU	-	expression tag	UNP P26744
B	604	GLU	-	expression tag	UNP P26744
B	605	HIS	-	expression tag	UNP P26744
B	606	HIS	-	expression tag	UNP P26744
B	607	HIS	-	expression tag	UNP P26744
B	608	HIS	-	expression tag	UNP P26744
B	609	HIS	-	expression tag	UNP P26744
B	610	HIS	-	expression tag	UNP P26744
C	603	LEU	-	expression tag	UNP P26744
C	604	GLU	-	expression tag	UNP P26744
C	605	HIS	-	expression tag	UNP P26744
C	606	HIS	-	expression tag	UNP P26744
C	607	HIS	-	expression tag	UNP P26744
C	608	HIS	-	expression tag	UNP P26744
C	609	HIS	-	expression tag	UNP P26744
C	610	HIS	-	expression tag	UNP P26744
D	603	LEU	-	expression tag	UNP P26744
D	604	GLU	-	expression tag	UNP P26744
D	605	HIS	-	expression tag	UNP P26744
D	606	HIS	-	expression tag	UNP P26744
D	607	HIS	-	expression tag	UNP P26744
D	608	HIS	-	expression tag	UNP P26744
D	609	HIS	-	expression tag	UNP P26744
D	610	HIS	-	expression tag	UNP P26744
E	603	LEU	-	expression tag	UNP P26744
E	604	GLU	-	expression tag	UNP P26744
E	605	HIS	-	expression tag	UNP P26744
E	606	HIS	-	expression tag	UNP P26744
E	607	HIS	-	expression tag	UNP P26744
E	608	HIS	-	expression tag	UNP P26744
E	609	HIS	-	expression tag	UNP P26744
E	610	HIS	-	expression tag	UNP P26744
F	603	LEU	-	expression tag	UNP P26744
F	604	GLU	-	expression tag	UNP P26744
F	605	HIS	-	expression tag	UNP P26744
F	606	HIS	-	expression tag	UNP P26744
F	607	HIS	-	expression tag	UNP P26744
F	608	HIS	-	expression tag	UNP P26744
F	609	HIS	-	expression tag	UNP P26744

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Chain	Residue	Modelled	Actual	Comment	Reference
F	610	HIS	-	expression tag	UNP P26744
G	603	LEU	-	expression tag	UNP P26744
G	604	GLU	-	expression tag	UNP P26744
G	605	HIS	-	expression tag	UNP P26744
G	606	HIS	-	expression tag	UNP P26744
G	607	HIS	-	expression tag	UNP P26744
G	608	HIS	-	expression tag	UNP P26744
G	609	HIS	-	expression tag	UNP P26744
G	610	HIS	-	expression tag	UNP P26744
H	603	LEU	-	expression tag	UNP P26744
H	604	GLU	-	expression tag	UNP P26744
H	605	HIS	-	expression tag	UNP P26744
H	606	HIS	-	expression tag	UNP P26744
H	607	HIS	-	expression tag	UNP P26744
H	608	HIS	-	expression tag	UNP P26744
H	609	HIS	-	expression tag	UNP P26744
H	610	HIS	-	expression tag	UNP P26744
I	603	LEU	-	expression tag	UNP P26744
I	604	GLU	-	expression tag	UNP P26744
I	605	HIS	-	expression tag	UNP P26744
I	606	HIS	-	expression tag	UNP P26744
I	607	HIS	-	expression tag	UNP P26744
I	608	HIS	-	expression tag	UNP P26744
I	609	HIS	-	expression tag	UNP P26744
I	610	HIS	-	expression tag	UNP P26744
J	603	LEU	-	expression tag	UNP P26744
J	604	GLU	-	expression tag	UNP P26744
J	605	HIS	-	expression tag	UNP P26744
J	606	HIS	-	expression tag	UNP P26744
J	607	HIS	-	expression tag	UNP P26744
J	608	HIS	-	expression tag	UNP P26744
J	609	HIS	-	expression tag	UNP P26744
J	610	HIS	-	expression tag	UNP P26744
K	603	LEU	-	expression tag	UNP P26744
K	604	GLU	-	expression tag	UNP P26744
K	605	HIS	-	expression tag	UNP P26744
K	606	HIS	-	expression tag	UNP P26744
K	607	HIS	-	expression tag	UNP P26744
K	608	HIS	-	expression tag	UNP P26744
K	609	HIS	-	expression tag	UNP P26744
K	610	HIS	-	expression tag	UNP P26744
L	603	LEU	-	expression tag	UNP P26744

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Chain	Residue	Modelled	Actual	Comment	Reference
L	604	GLU	-	expression tag	UNP P26744
L	605	HIS	-	expression tag	UNP P26744
L	606	HIS	-	expression tag	UNP P26744
L	607	HIS	-	expression tag	UNP P26744
L	608	HIS	-	expression tag	UNP P26744
L	609	HIS	-	expression tag	UNP P26744
L	610	HIS	-	expression tag	UNP P26744

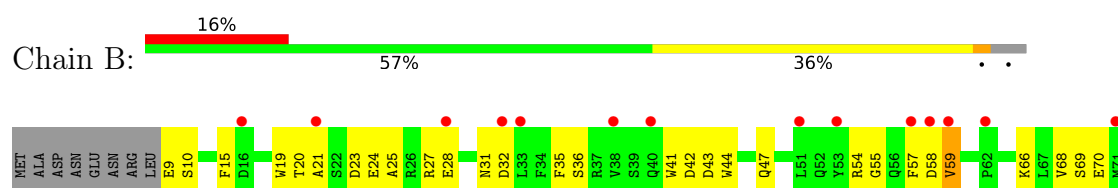
3 Residue-property plots

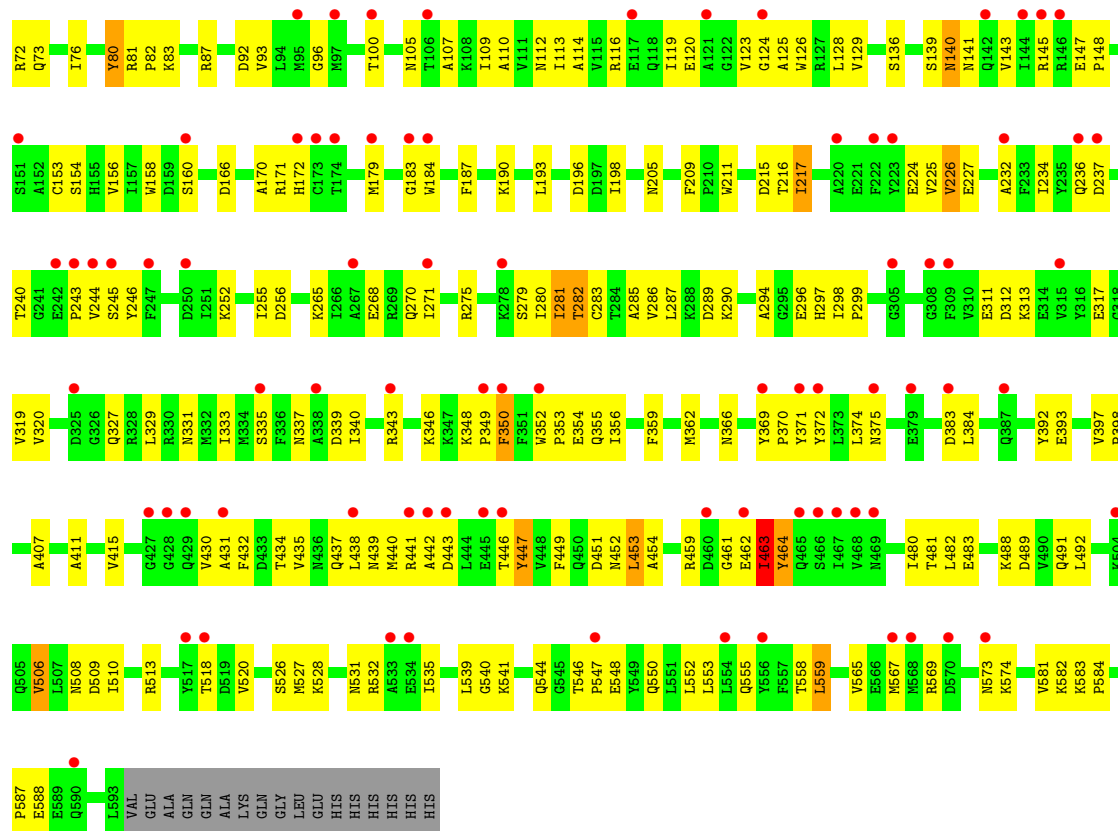
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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

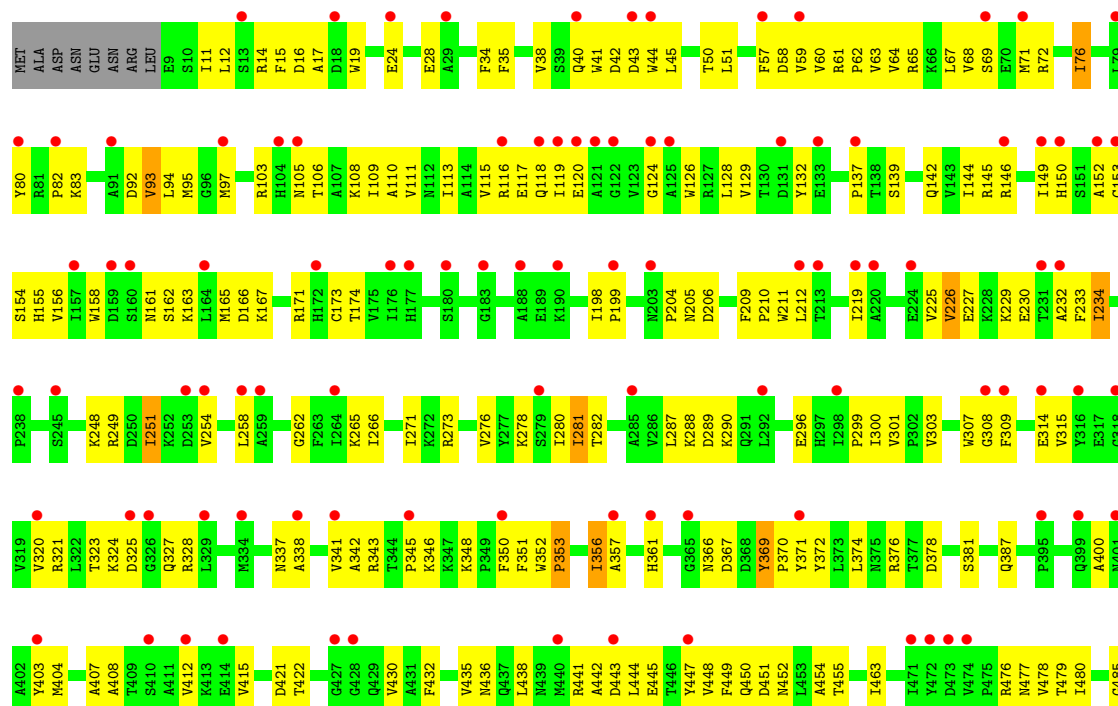


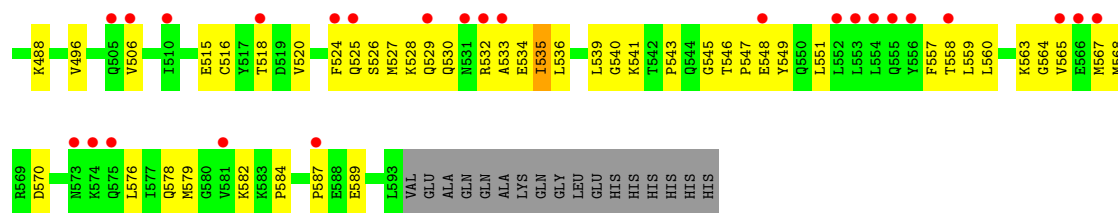
• Molecule 1: Portal protein



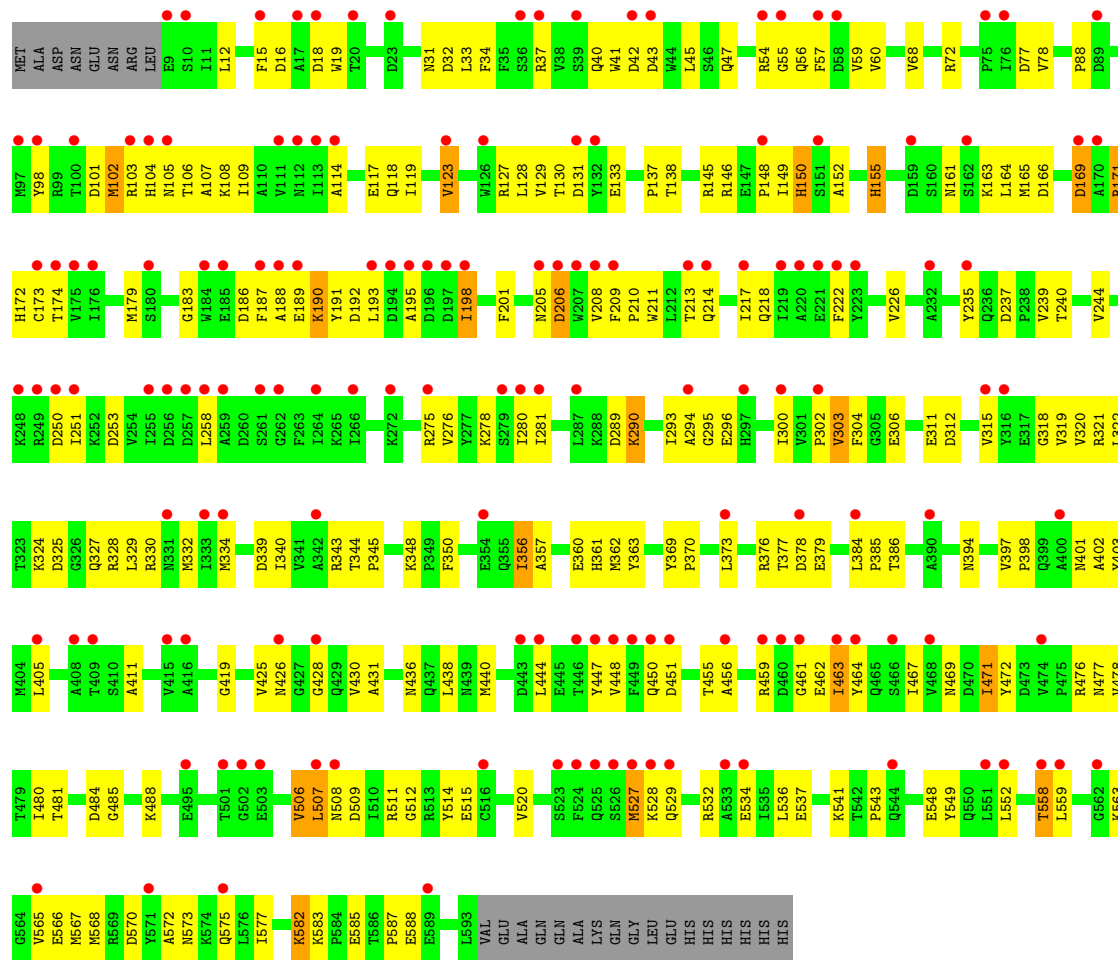


● Molecule 1: Portal protein

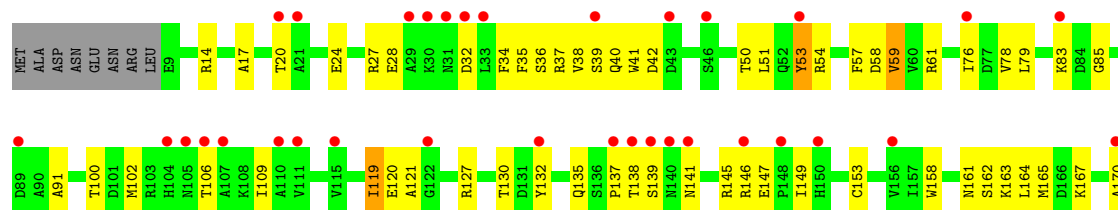


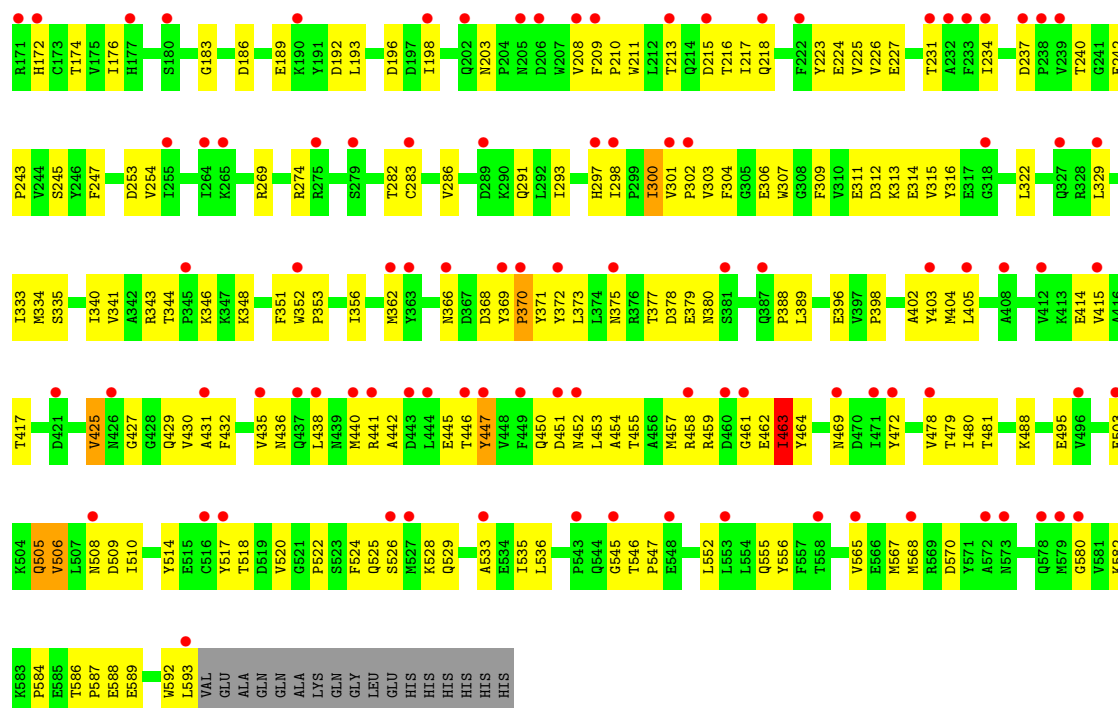


• Molecule 1: Portal protein

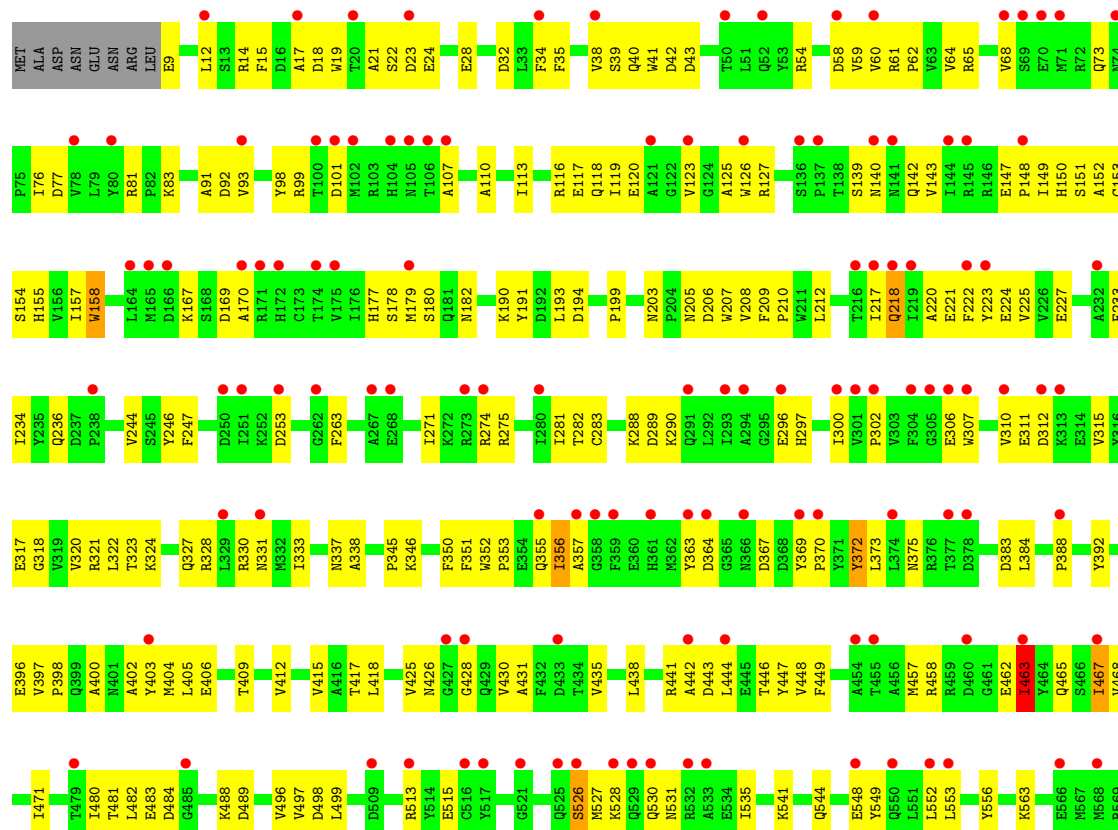


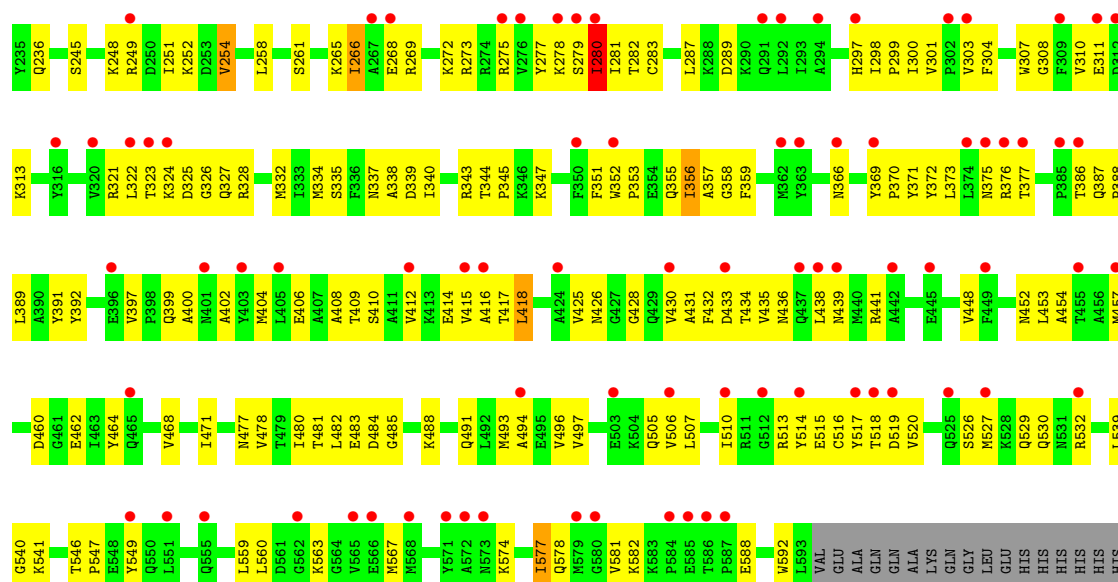
• Molecule 1: Portal protein



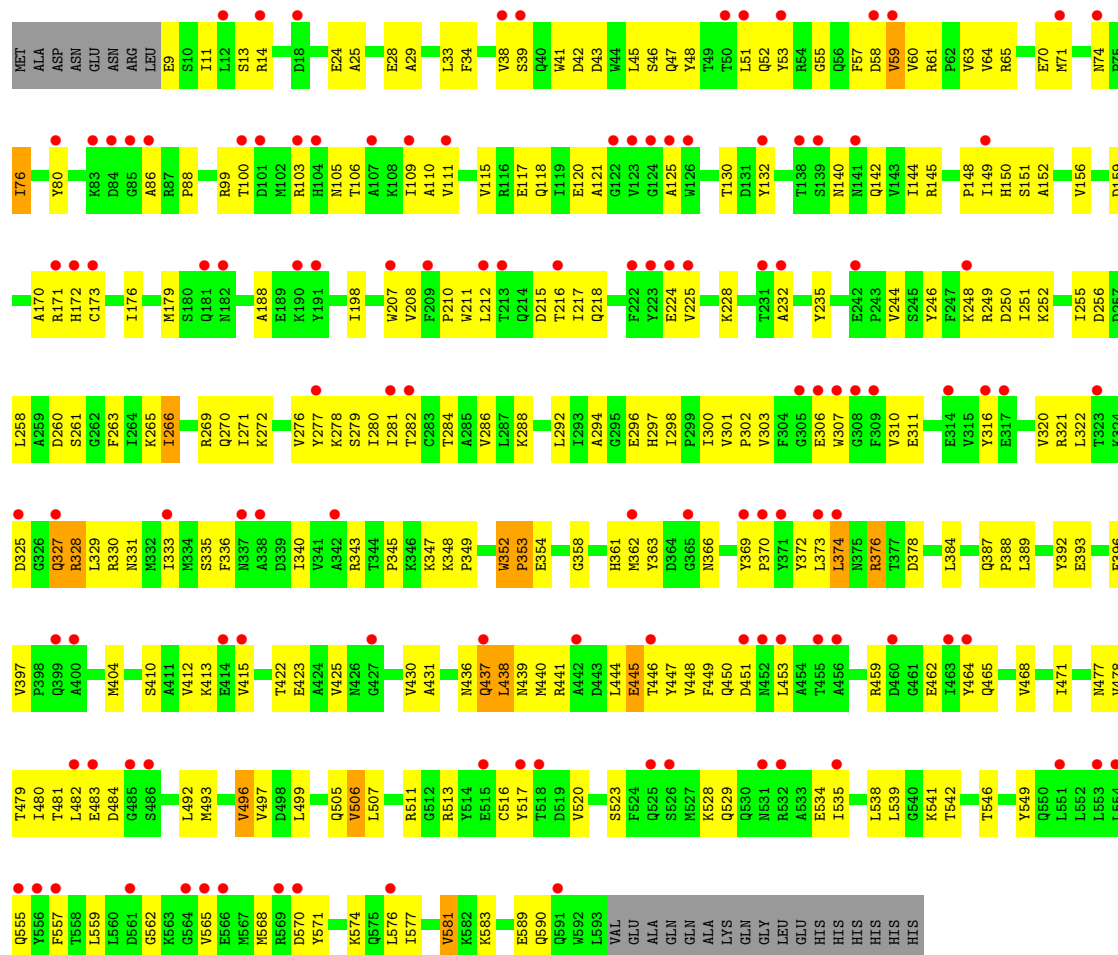


• Molecule 1: Portal protein

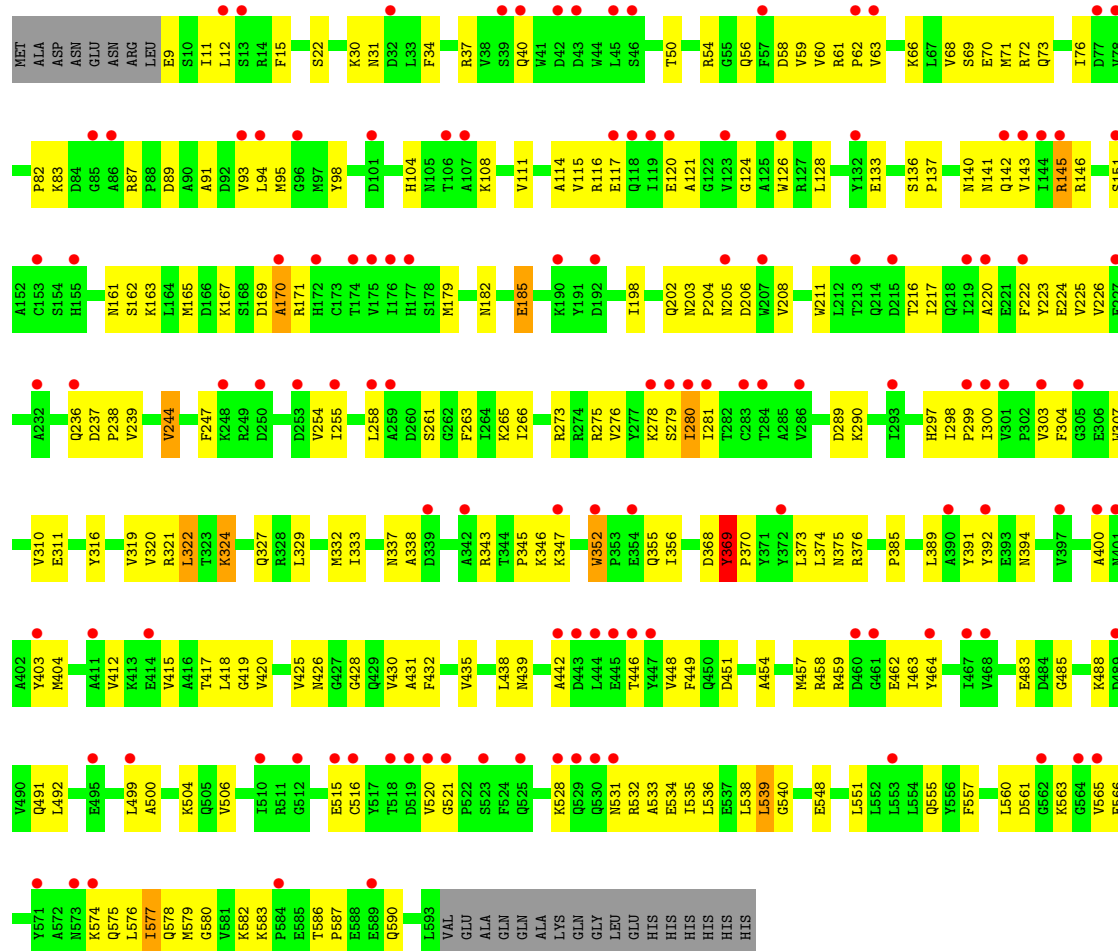




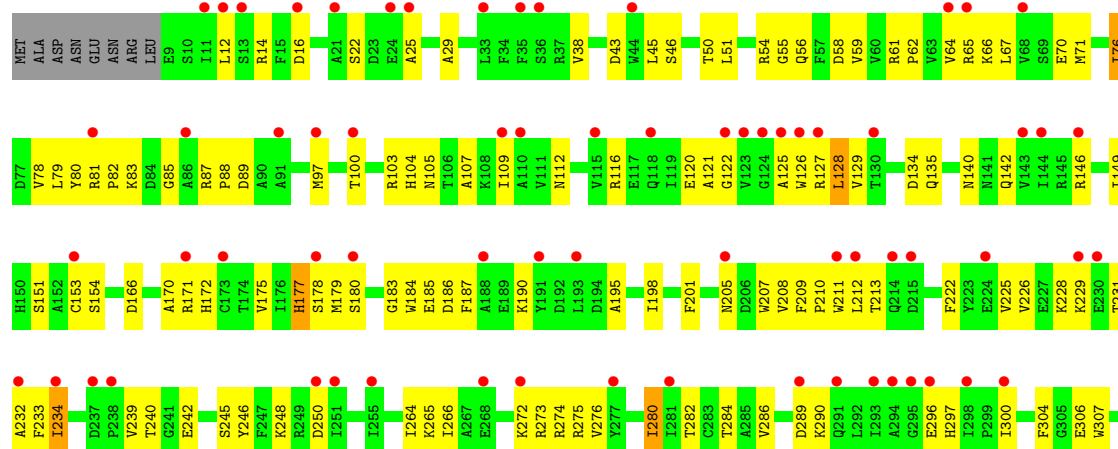
• Molecule 1: Portal protein

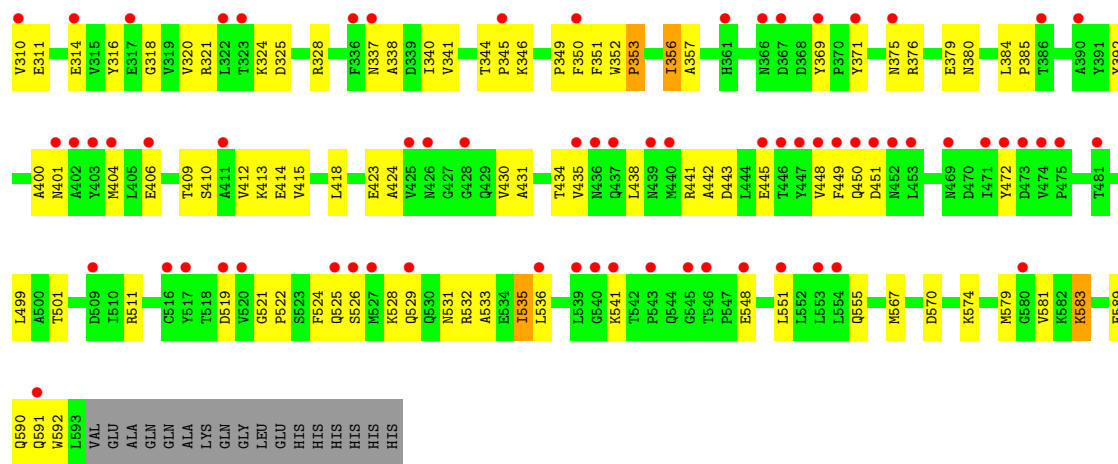


• Molecule 1: Portal protein

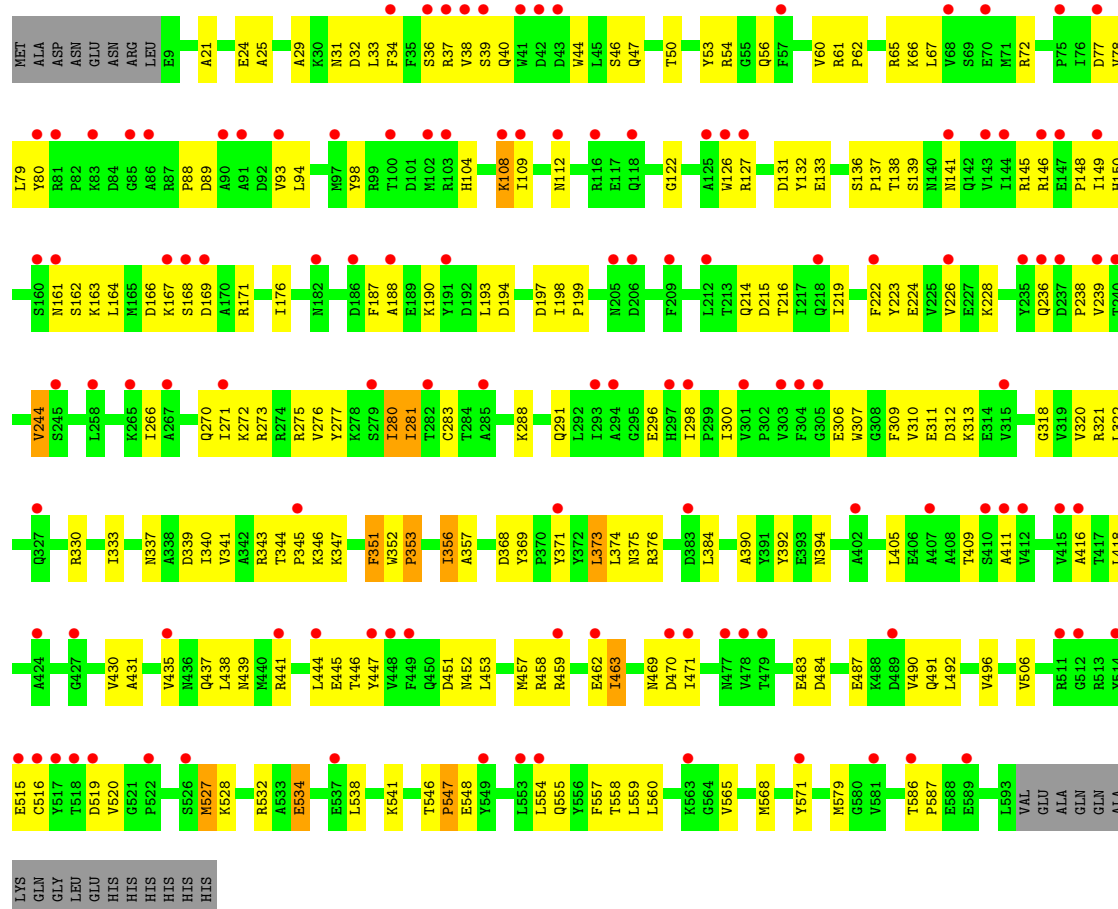


• Molecule 1: Portal protein





• Molecule 1: Portal protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 42	Depositor
Cell constants a, b, c, α , β , γ	316.81Å 316.81Å 138.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 3.30 15.00 – 3.30	Depositor EDS
% Data completeness (in resolution range)	85.0 (15.00-3.30) 84.1 (15.00-3.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.84 (at 3.33Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.295 , 0.315 0.310 , 0.320	Depositor DCC
R_{free} test set	1737 reflections (0.84%)	wwPDB-VP
Wilson B-factor (Å ²)	91.0	Xtriage
Anisotropy	0.292	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.00 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.078 for h,-k,-l	Xtriage
Reported twinning fraction	0.502 for H, K, L 0.498 for -H, K, -L	Depositor
Outliers	15 of 175831 reflections (0.009%)	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	56559	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.61% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	0.20	0/4826	0.58	0/6550
1	B	0.26	1/4812 (0.0%)	0.65	6/6533 (0.1%)
1	C	0.25	1/4812 (0.0%)	0.61	0/6533
1	D	0.23	0/4825	0.63	5/6550 (0.1%)
1	E	0.22	1/4822 (0.0%)	0.57	0/6546
1	F	0.21	0/4812	0.59	3/6533 (0.0%)
1	G	0.30	1/4808 (0.0%)	0.68	11/6528 (0.2%)
1	H	0.22	1/4812 (0.0%)	0.57	0/6533
1	I	0.24	0/4812	0.63	4/6533 (0.1%)
1	J	0.25	1/4812 (0.0%)	0.60	0/6533
1	K	0.20	0/4818	0.60	3/6541 (0.0%)
1	L	0.20	0/4812	0.59	1/6533 (0.0%)
All	All	0.23	6/57783 (0.0%)	0.61	33/78446 (0.0%)

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	5
1	B	0	6
1	C	0	8
1	D	0	11
1	E	0	9
1	F	0	10
1	G	0	7
1	H	0	8
1	I	0	8
1	J	0	10
1	K	0	7
1	L	0	7
All	All	0	96

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	348	LYS	C-N	8.29	1.53	1.33
1	E	203	ASN	C-N	6.90	1.50	1.33
1	H	352	TRP	C-N	6.83	1.49	1.33
1	J	203	ASN	C-N	6.11	1.48	1.33
1	B	80	TYR	C-N	5.85	1.45	1.33
1	G	353	PRO	N-CD	5.08	1.54	1.47

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	470	ASP	N-CA-C	12.72	128.03	111.75
1	G	240	THR	N-CA-C	10.54	122.52	111.14
1	G	471	ILE	N-CA-C	-9.04	105.12	113.71
1	I	484	ASP	N-CA-C	8.84	121.72	111.11
1	D	150	HIS	N-CA-C	8.20	121.03	111.02
1	L	108	LYS	N-CA-C	8.17	119.87	110.97
1	D	155	HIS	N-CA-C	7.79	124.14	111.37
1	K	350	PHE	N-CA-C	7.78	121.61	108.23
1	D	192	ASP	N-CA-CB	-7.29	97.92	110.17
1	F	527	MET	N-CA-C	-6.69	100.67	111.04
1	B	283	CYS	N-CA-C	6.57	118.52	111.36
1	I	252	LYS	N-CA-C	6.54	120.36	112.38
1	D	169	ASP	N-CA-C	6.50	118.05	110.97
1	G	470	ASP	CB-CA-C	-6.41	98.03	110.46
1	F	463	ILE	CB-CA-C	-6.16	101.19	111.29
1	D	290	LYS	N-CA-C	6.09	119.64	111.24
1	G	471	ILE	N-CA-CB	5.99	120.79	111.57
1	G	348	LYS	CA-C-N	-5.79	112.60	119.84
1	G	348	LYS	C-N-CA	-5.79	112.60	119.84
1	B	55	GLY	N-CA-C	5.68	126.65	113.18
1	G	239	VAL	N-CA-C	5.59	120.96	109.34
1	I	328	ARG	N-CA-C	-5.36	105.84	112.38
1	B	350	PHE	N-CA-C	5.34	116.96	108.79
1	K	97	MET	N-CA-C	5.31	117.49	111.02
1	G	352	TRP	CA-C-N	-5.28	113.25	119.84
1	G	352	TRP	C-N-CA	-5.28	113.25	119.84
1	I	484	ASP	CB-CA-C	-5.27	102.38	110.81
1	G	349	PRO	CA-N-CD	-5.14	104.81	112.00
1	B	281	ILE	N-CA-C	5.10	116.06	108.46
1	F	101	ASP	CB-CA-C	-5.09	110.69	116.54
1	K	55	GLY	N-CA-C	5.07	122.29	115.00
1	B	463	ILE	CB-CA-C	-5.05	103.00	111.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	464	TYR	N-CA-C	-5.03	106.28	112.72

There are no chirality outliers.

All (96) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	13	SER	Peptide
1	A	177	HIS	Peptide
1	A	264	ILE	Peptide
1	A	352	TRP	Peptide
1	A	527	MET	Peptide
1	B	139	SER	Peptide
1	B	372	TYR	Peptide
1	B	41	TRP	Peptide
1	B	447	TYR	Peptide
1	B	54	ARG	Peptide
1	B	559	LEU	Peptide
1	C	212	LEU	Peptide
1	C	226	VAL	Peptide
1	C	233	PHE	Peptide
1	C	369	TYR	Peptide
1	C	51	LEU	Peptide
1	C	587	PRO	Peptide
1	C	92	ASP	Peptide
1	C	93	VAL	Peptide
1	D	102	MET	Peptide
1	D	171	ARG	Peptide
1	D	191	TYR	Peptide
1	D	198	ILE	Peptide
1	D	206	ASP	Peptide
1	D	294	ALA	Peptide
1	D	511	ARG	Peptide
1	D	520	VAL	Peptide
1	D	527	MET	Peptide
1	D	558	THR	Peptide
1	D	582	LYS	Peptide
1	E	352	TRP	Peptide
1	E	370	PRO	Peptide
1	E	446	THR	Peptide
1	E	447	TYR	Peptide
1	E	452	ASN	Peptide
1	E	505	GLN	Peptide

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Mol	Chain	Res	Type	Group
1	E	53	TYR	Peptide
1	E	588	GLU	Peptide
1	E	79	LEU	Peptide
1	F	158	TRP	Peptide
1	F	167	LYS	Peptide
1	F	177	HIS	Peptide
1	F	218	GLN	Sidechain
1	F	315	VAL	Peptide
1	F	363	TYR	Peptide
1	F	364	ASP	Peptide
1	F	372	TYR	Peptide
1	F	526	SER	Peptide
1	F	574	LYS	Peptide
1	G	313	LYS	Peptide
1	G	363	TYR	Peptide
1	G	368	ASP	Peptide
1	G	45	LEU	Peptide
1	G	47	GLN	Peptide
1	G	526	SER	Peptide
1	G	79	LEU	Peptide
1	H	126	TRP	Peptide
1	H	150	HIS	Peptide
1	H	159	ASP	Peptide
1	H	272	LYS	Peptide
1	H	280	ILE	Peptide
1	H	344	THR	Peptide
1	H	345	PRO	Peptide
1	H	530	GLN	Peptide
1	I	327	GLN	Sidechain
1	I	352	TRP	Peptide
1	I	376	ARG	Peptide
1	I	388	PRO	Peptide
1	I	41	TRP	Peptide
1	I	437	GLN	Sidechain
1	I	438	LEU	Peptide
1	I	445	GLU	Peptide
1	J	143	VAL	Peptide
1	J	145	ARG	Peptide
1	J	151	SER	Peptide
1	J	185	GLU	Peptide
1	J	322	LEU	Peptide
1	J	352	TRP	Peptide

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Mol	Chain	Res	Type	Group
1	J	368	ASP	Peptide
1	J	369	TYR	Peptide
1	J	454	ALA	Peptide
1	J	483	GLU	Peptide
1	K	128	LEU	Peptide
1	K	177	HIS	Peptide
1	K	201	PHE	Peptide
1	K	410	SER	Peptide
1	K	472	TYR	Peptide
1	K	526	SER	Peptide
1	K	583	LYS	Peptide
1	L	351	PHE	Peptide
1	L	368	ASP	Peptide
1	L	373	LEU	Peptide
1	L	527	MET	Peptide
1	L	534	GLU	Peptide
1	L	547	PRO	Peptide
1	L	579	MET	Peptide

5.2 Too-close contacts

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	4724	0	4562	162	0
1	B	4710	0	4536	189	0
1	C	4710	0	4536	218	0
1	D	4723	0	4562	201	0
1	E	4720	0	4553	190	0
1	F	4710	0	4536	184	0
1	G	4706	0	4532	174	0
1	H	4710	0	4536	200	0
1	I	4710	0	4536	214	0
1	J	4710	0	4536	180	0
1	K	4716	0	4547	177	0
1	L	4710	0	4536	158	0
All	All	56559	0	54508	2061	0

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 19.

All (2061) 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)
1:I:297:HIS:HB3	1:I:450:GLN:OE1	1.30	1.26
1:I:447:TYR:OH	1:I:513:ARG:CD	1.88	1.21
1:I:447:TYR:OH	1:I:513:ARG:HD2	0.93	1.08
1:B:282:THR:OG1	1:B:285:ALA:O	1.85	0.95
1:I:297:HIS:CB	1:I:450:GLN:OE1	2.16	0.93
1:A:532:ARG:NH2	1:A:558:THR:OG1	2.02	0.93
1:D:290:LYS:HG3	1:D:290:LYS:O	1.69	0.91
1:I:446:THR:H	1:I:448:VAL:HG23	1.37	0.89
1:G:346:LYS:NZ	1:G:348:LYS:HG3	1.89	0.87
1:G:586:THR:OG1	1:G:589:GLU:OE2	1.92	0.87
1:A:457:MET:SD	1:A:505:GLN:NE2	2.47	0.86
1:G:235:TYR:O	1:G:236:GLN:HG2	1.76	0.84
1:L:44:TRP:O	1:L:47:GLN:NE2	2.09	0.84
1:H:337:ASN:OD1	1:H:338:ALA:N	2.11	0.84
1:H:178:SER:O	1:H:218:GLN:NE2	2.11	0.83
1:B:281:ILE:O	1:B:282:THR:OG1	1.96	0.83
1:C:42:ASP:OD2	1:C:44:TRP:NE1	2.12	0.83
1:I:297:HIS:ND1	1:I:450:GLN:HB2	1.94	0.83
1:L:131:ASP:OD2	1:L:291:GLN:NE2	2.11	0.83
1:B:532:ARG:NH2	1:B:558:THR:OG1	2.12	0.82
1:H:248:LYS:NZ	1:I:188:ALA:O	2.12	0.82
1:I:447:TYR:CZ	1:I:513:ARG:HD2	2.12	0.81
1:I:451:ASP:HB3	1:I:506:VAL:CA	2.10	0.81
1:E:237:ASP:OD2	1:E:240:THR:OG1	1.99	0.79
1:J:574:LYS:O	1:J:590:GLN:NE2	2.16	0.79
1:E:130:THR:OG1	1:E:189:GLU:OE2	2.01	0.78
1:K:414:GLU:OE2	1:L:330:ARG:NH2	2.17	0.78
1:I:327:GLN:HA	1:I:329:LEU:HG	1.65	0.78
1:B:463:ILE:O	1:B:463:ILE:HG22	1.83	0.78
1:J:343:ARG:NH1	1:L:369:TYR:OH	2.17	0.78
1:G:394:ASN:OD1	1:H:391:TYR:OH	2.01	0.77
1:L:104:HIS:O	1:L:145:ARG:NH1	2.17	0.77
1:J:208:VAL:O	1:J:211:TRP:NE1	2.17	0.77
1:C:325:ASP:HA	1:C:328:ARG:HG2	1.67	0.77
1:I:9:GLU:O	1:I:13:SER:OG	2.02	0.77
1:G:541:LYS:NZ	1:H:532:ARG:O	2.15	0.76
1:A:71:MET:SD	1:A:118:GLN:NE2	2.57	0.76
1:D:54:ARG:NE	1:D:334:MET:SD	2.60	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:321:ARG:O	1:J:56:GLN:NE2	2.18	0.75
1:G:141:ASN:ND2	1:G:451:ASP:OD1	2.18	0.75
1:F:81:ARG:NH1	1:F:515:GLU:O	2.20	0.74
1:F:463:ILE:HG22	1:F:463:ILE:O	1.87	0.74
1:C:545:GLY:O	1:C:549:TYR:N	2.20	0.74
1:G:549:TYR:O	1:G:553:LEU:N	2.20	0.74
1:A:478:VAL:O	1:A:479:THR:OG1	2.04	0.74
1:D:173:CYS:SG	1:D:174:THR:N	2.58	0.74
1:I:105:ASN:OD1	1:I:145:ARG:NH1	2.21	0.74
1:C:447:TYR:OH	1:C:516:CYS:O	2.05	0.73
1:D:476:ARG:HG2	1:D:477:ASN:H	1.53	0.73
1:E:54:ARG:NH2	1:E:335:SER:OG	2.20	0.73
1:L:137:PRO:O	1:L:138:THR:OG1	2.06	0.73
1:E:161:ASN:OD1	1:E:163:LYS:N	2.21	0.73
1:F:77:ASP:OD1	1:F:98:TYR:OH	2.07	0.73
1:F:317:GLU:O	1:F:321:ARG:NH1	2.22	0.73
1:H:42:ASP:OD2	1:H:44:TRP:NE1	2.22	0.73
1:J:579:MET:SD	1:K:574:LYS:NZ	2.56	0.73
1:I:447:TYR:HH	1:I:513:ARG:HD2	1.47	0.73
1:A:130:THR:HG21	1:A:186:ASP:HB2	1.71	0.72
1:B:451:ASP:OD1	1:B:506:VAL:N	2.23	0.72
1:D:149:ILE:HG22	1:D:150:HIS:H	1.54	0.72
1:A:392:TYR:HA	1:B:349:PRO:HG2	1.71	0.72
1:E:37:ARG:NH1	1:E:42:ASP:OD2	2.23	0.72
1:I:159:ASP:OD1	1:J:182:ASN:ND2	2.22	0.71
1:J:15:PHE:HA	1:J:281:ILE:HD11	1.70	0.71
1:I:555:GLN:NE2	1:J:563:LYS:O	2.23	0.71
1:D:198:ILE:HB	1:D:217:ILE:HD12	1.72	0.71
1:K:511:ARG:NH2	1:L:141:ASN:OD1	2.23	0.71
1:E:458:ARG:NH1	1:E:503:GLU:O	2.22	0.71
1:E:369:TYR:HB3	1:E:370:PRO:HD2	1.73	0.71
1:F:430:VAL:HG12	1:F:431:ALA:H	1.56	0.71
1:I:480:ILE:HG22	1:I:481:THR:H	1.54	0.71
1:E:488:LYS:NZ	1:E:495:GLU:OE2	2.17	0.71
1:F:352:TRP:NE1	1:F:375:ASN:O	2.24	0.71
1:D:319:VAL:O	1:E:61:ARG:NH1	2.24	0.70
1:C:149:ILE:HG22	1:C:150:HIS:H	1.57	0.70
1:D:345:PRO:O	1:D:348:LYS:NZ	2.25	0.70
1:I:451:ASP:HB3	1:I:506:VAL:N	2.07	0.70
1:J:223:TYR:O	1:J:279:SER:OG	2.09	0.70
1:L:161:ASN:ND2	1:L:169:ASP:OD2	2.23	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:237:ASP:OD2	1:J:261:SER:OG	2.08	0.70
1:F:574:LYS:NZ	1:F:589:GLU:OE2	2.24	0.70
1:D:340:ILE:O	1:D:344:THR:OG1	2.10	0.70
1:B:451:ASP:OD2	1:B:513:ARG:NH1	2.25	0.69
1:F:337:ASN:OD1	1:F:338:ALA:N	2.24	0.69
1:I:316:TYR:O	1:J:40:GLN:NE2	2.21	0.69
1:G:88:PRO:HA	1:G:91:ALA:HB3	1.75	0.69
1:G:510:ILE:HG22	1:G:511:ARG:H	1.58	0.69
1:J:222:PHE:HB2	1:J:280:ILE:HG12	1.75	0.69
1:K:25:ALA:HA	1:K:29:ALA:HB3	1.75	0.69
1:J:133:GLU:OE2	1:J:140:ASN:ND2	2.25	0.69
1:L:280:ILE:O	1:L:281:ILE:HG22	1.91	0.69
1:E:461:GLY:O	1:E:462:GLU:HB2	1.92	0.69
1:E:526:SER:OG	1:F:563:LYS:NZ	2.26	0.68
1:I:297:HIS:HD1	1:I:450:GLN:HB2	1.56	0.68
1:G:530:GLN:HA	1:G:533:ALA:HB2	1.73	0.68
1:I:570:ASP:OD1	1:I:571:TYR:N	2.26	0.68
1:G:342:ALA:O	1:H:366:ASN:ND2	2.25	0.68
1:E:127:ARG:NH2	1:E:176:ILE:O	2.25	0.68
1:B:339:ASP:O	1:B:343:ARG:NH1	2.27	0.68
1:E:170:ALA:N	1:E:226:VAL:O	2.26	0.68
1:K:337:ASN:OD1	1:K:338:ALA:N	2.27	0.68
1:L:538:LEU:O	1:L:541:LYS:NZ	2.27	0.68
1:L:558:THR:O	1:L:560:LEU:N	2.27	0.67
1:B:443:ASP:OD2	1:B:446:THR:OG1	2.08	0.67
1:H:118:GLN:OE1	1:H:436:ASN:ND2	2.27	0.67
1:H:425:VAL:HG12	1:H:426:ASN:H	1.57	0.67
1:L:24:GLU:OE2	1:L:313:LYS:NZ	2.28	0.67
1:A:128:LEU:O	1:A:131:ASP:N	2.27	0.67
1:D:300:ILE:HG22	1:D:302:PRO:HD3	1.76	0.67
1:J:310:VAL:HG13	1:J:311:GLU:H	1.59	0.67
1:H:236:GLN:OE1	1:H:245:SER:OG	2.13	0.67
1:K:179:MET:O	1:K:180:SER:OG	2.08	0.67
1:H:321:ARG:NH1	1:I:55:GLY:O	2.23	0.67
1:H:477:ASN:OD1	1:H:478:VAL:N	2.26	0.67
1:C:14:ARG:NH2	1:C:278:LYS:O	2.28	0.66
1:L:25:ALA:O	1:L:29:ALA:N	2.25	0.66
1:C:232:ALA:HB2	1:C:248:LYS:HA	1.77	0.66
1:G:337:ASN:OD1	1:G:338:ALA:N	2.28	0.66
1:K:51:LEU:O	1:K:54:ARG:NH1	2.27	0.66
1:L:457:MET:HG3	1:L:458:ARG:H	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:570:ASP:OD1	1:F:571:TYR:N	2.29	0.66
1:I:171:ARG:HG2	1:I:224:GLU:HB3	1.76	0.66
1:K:50:THR:OG1	1:K:54:ARG:NH1	2.29	0.66
1:H:70:GLU:O	1:H:73:GLN:NE2	2.27	0.66
1:I:447:TYR:HE1	1:I:513:ARG:HG2	1.60	0.66
1:B:569:ARG:O	1:B:574:LYS:NZ	2.24	0.66
1:C:324:LYS:CD	1:D:57:PHE:HA	2.26	0.66
1:H:323:THR:OG1	1:H:414:GLU:OE1	2.14	0.66
1:L:32:ASP:OD1	1:L:122:GLY:N	2.29	0.65
1:B:57:PHE:HZ	1:B:327:GLN:HB3	1.61	0.65
1:B:280:ILE:HG13	1:B:281:ILE:H	1.61	0.65
1:E:427:GLY:N	1:E:429:GLN:OE1	2.28	0.65
1:J:120:GLU:O	1:J:316:TYR:OH	2.13	0.65
1:E:414:GLU:O	1:E:417:THR:OG1	2.13	0.65
1:J:533:ALA:N	1:J:534:GLU:OE1	2.29	0.65
1:K:12:LEU:HB3	1:K:16:ASP:HB2	1.77	0.65
1:D:425:VAL:HG12	1:D:426:ASN:H	1.61	0.65
1:B:583:LYS:HD3	1:C:563:LYS:HB3	1.79	0.65
1:F:253:ASP:HB3	1:G:293:ILE:HD12	1.77	0.65
1:I:448:VAL:HG13	1:I:517:TYR:OH	1.96	0.65
1:K:103:ARG:HG2	1:K:104:HIS:H	1.60	0.65
1:G:375:ASN:OD1	1:G:376:ARG:N	2.30	0.65
1:H:559:LEU:HD12	1:H:560:LEU:N	2.12	0.65
1:J:117:GLU:HG3	1:J:121:ALA:HB3	1.78	0.65
1:J:216:THR:HG22	1:J:217:ILE:H	1.61	0.65
1:K:146:ARG:NH2	1:K:443:ASP:OD1	2.29	0.65
1:L:435:VAL:O	1:L:439:ASN:ND2	2.30	0.65
1:D:208:VAL:HG12	1:D:210:PRO:HD2	1.78	0.65
1:E:83:LYS:HG2	1:E:85:GLY:H	1.61	0.65
1:F:425:VAL:HG12	1:F:426:ASN:H	1.61	0.65
1:I:448:VAL:HG13	1:I:517:TYR:CZ	2.32	0.65
1:L:452:ASN:OD1	1:L:453:LEU:N	2.30	0.65
1:B:234:ILE:HG22	1:B:265:LYS:HE2	1.79	0.65
1:J:425:VAL:HG12	1:J:426:ASN:H	1.61	0.65
1:G:456:ALA:HB1	1:G:460:ASP:H	1.62	0.64
1:I:271:ILE:HG22	1:I:272:LYS:H	1.62	0.64
1:K:186:ASP:OD1	1:K:187:PHE:N	2.30	0.64
1:D:201:PHE:O	1:D:218:GLN:NE2	2.30	0.64
1:E:165:MET:HA	1:E:167:LYS:HD3	1.79	0.64
1:G:572:ALA:HB1	1:G:582:LYS:HD2	1.78	0.64
1:C:535:ILE:HG23	1:C:536:LEU:H	1.61	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:346:LYS:HZ2	1:G:348:LYS:HG3	1.62	0.64
1:K:310:VAL:HG12	1:K:311:GLU:HG2	1.79	0.64
1:C:369:TYR:HB3	1:C:371:TYR:HD2	1.63	0.64
1:L:21:ALA:O	1:L:313:LYS:NZ	2.30	0.64
1:A:443:ASP:OD1	1:A:444:LEU:N	2.31	0.64
1:K:126:TRP:HE1	1:K:146:ARG:HD3	1.63	0.64
1:J:352:TRP:HB3	1:J:374:LEU:HD22	1.80	0.64
1:C:171:ARG:NH2	1:C:296:GLU:OE1	2.31	0.64
1:A:203:ASN:OD1	1:A:204:PRO:HD2	1.98	0.63
1:B:36:SER:OG	1:B:120:GLU:O	2.15	0.63
1:C:65:ARG:NH1	1:C:69:SER:OG	2.31	0.63
1:G:346:LYS:HZ1	1:G:348:LYS:HG3	1.62	0.63
1:J:225:VAL:HG23	1:J:280:ILE:HA	1.80	0.63
1:H:172:HIS:ND1	1:H:172:HIS:O	2.30	0.63
1:J:223:TYR:C	1:J:280:ILE:HB	2.24	0.63
1:L:164:LEU:O	1:L:171:ARG:NH1	2.32	0.63
1:E:458:ARG:HH12	1:E:505:GLN:HG3	1.63	0.63
1:J:337:ASN:OD1	1:J:338:ALA:N	2.29	0.63
1:I:482:LEU:HG	1:I:483:GLU:H	1.64	0.63
1:J:457:MET:HG3	1:J:458:ARG:H	1.62	0.63
1:K:533:ALA:O	1:K:541:LYS:NZ	2.30	0.63
1:G:583:LYS:HB2	1:H:567:MET:HG2	1.81	0.63
1:F:467:ILE:HG22	1:F:468:VAL:HG23	1.81	0.63
1:B:216:THR:HG22	1:B:217:ILE:H	1.63	0.63
1:G:129:VAL:HG13	1:G:130:THR:HG23	1.81	0.63
1:I:297:HIS:HD1	1:I:450:GLN:CB	2.11	0.63
1:J:225:VAL:HG12	1:J:226:VAL:HG22	1.81	0.63
1:B:58:ASP:O	1:B:59:VAL:HG12	1.98	0.63
1:C:366:ASN:OD1	1:C:367:ASP:N	2.30	0.63
1:B:9:GLU:HG2	1:B:10:SER:H	1.64	0.62
1:C:248:LYS:O	1:C:249:ARG:HG2	1.99	0.62
1:G:547:PRO:HD2	1:H:549:TYR:HB2	1.80	0.62
1:H:441:ARG:NH2	1:H:517:TYR:O	2.31	0.62
1:J:11:ILE:O	1:J:278:LYS:NZ	2.31	0.62
1:I:451:ASP:HB3	1:I:506:VAL:CB	2.29	0.62
1:K:46:SER:OG	1:K:328:ARG:NH1	2.32	0.62
1:G:480:ILE:HG22	1:G:481:THR:H	1.63	0.62
1:J:289:ASP:OD1	1:J:290:LYS:N	2.32	0.62
1:L:375:ASN:OD1	1:L:376:ARG:N	2.31	0.62
1:A:167:LYS:HE2	1:A:169:ASP:HB2	1.80	0.62
1:E:138:THR:HG22	1:E:139:SER:H	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:118:GLN:HA	1:F:123:VAL:HG22	1.82	0.62
1:F:234:ILE:HD13	1:F:247:PHE:HB2	1.81	0.62
1:G:425:VAL:HG12	1:G:426:ASN:H	1.64	0.62
1:H:435:VAL:O	1:H:438:LEU:HB3	2.00	0.62
1:C:258:LEU:HD23	1:C:262:GLY:HA3	1.82	0.62
1:I:47:GLN:HG2	1:I:48:TYR:H	1.65	0.62
1:I:589:GLU:HG2	1:I:590:GLN:H	1.64	0.62
1:K:140:ASN:OD1	1:K:142:GLN:HB2	2.00	0.62
1:D:105:ASN:OD1	1:D:106:THR:N	2.33	0.62
1:F:355:GLN:HG2	1:F:373:LEU:HD11	1.82	0.62
1:L:62:PRO:O	1:L:66:LYS:NZ	2.33	0.62
1:K:226:VAL:O	1:K:226:VAL:HG12	1.99	0.62
1:F:179:MET:O	1:F:180:SER:OG	2.15	0.62
1:H:406:GLU:HA	1:H:409:THR:HG23	1.82	0.62
1:L:271:ILE:HG22	1:L:272:LYS:HG3	1.81	0.62
1:E:458:ARG:HG3	1:E:459:ARG:H	1.65	0.61
1:G:383:ASP:O	1:G:384:LEU:HD12	1.98	0.61
1:G:141:ASN:O	1:G:142:GLN:HG3	2.00	0.61
1:C:11:ILE:HG12	1:C:14:ARG:HE	1.65	0.61
1:C:543:PRO:HD3	1:D:532:ARG:HH22	1.64	0.61
1:D:290:LYS:O	1:D:290:LYS:CG	2.43	0.61
1:I:265:LYS:O	1:I:266:ILE:HG22	2.00	0.61
1:G:352:TRP:O	1:G:354:GLU:OE1	2.18	0.61
1:J:329:LEU:HA	1:J:332:MET:HB2	1.81	0.61
1:D:345:PRO:HB3	1:D:348:LYS:HE2	1.82	0.61
1:G:146:ARG:HG2	1:G:147:GLU:H	1.66	0.61
1:I:171:ARG:HD2	1:I:298:ILE:HD12	1.83	0.61
1:E:146:ARG:HH12	1:E:440:MET:HA	1.65	0.61
1:C:559:LEU:HD23	1:C:565:VAL:HG13	1.83	0.61
1:H:417:THR:OG1	1:I:65:ARG:NH1	2.34	0.61
1:J:258:LEU:HD22	1:J:263:PHE:HB3	1.82	0.61
1:A:322:LEU:HD11	1:A:411:ALA:HB1	1.81	0.61
1:E:312:ASP:OD1	1:E:313:LYS:N	2.34	0.61
1:F:544:GLN:OE1	1:G:544:GLN:NE2	2.34	0.61
1:B:312:ASP:OD2	1:C:211:TRP:NE1	2.19	0.60
1:B:215:ASP:OD1	1:B:216:THR:N	2.34	0.60
1:C:68:VAL:HA	1:C:71:MET:HB2	1.83	0.60
1:J:116:ARG:NH1	1:J:120:GLU:OE1	2.34	0.60
1:K:120:GLU:HG2	1:K:121:ALA:H	1.66	0.60
1:A:43:ASP:OD1	1:A:43:ASP:N	2.34	0.60
1:F:311:GLU:HG2	1:F:312:ASP:H	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:462:GLU:HG2	1:F:463:ILE:HG12	1.83	0.60
1:B:362:MET:HG2	1:B:366:ASN:HD21	1.67	0.60
1:E:231:THR:O	1:E:269:ARG:NH1	2.35	0.60
1:L:127:ARG:HB2	1:L:149:ILE:HA	1.83	0.60
1:H:34:PHE:HA	1:H:37:ARG:HG2	1.83	0.60
1:H:149:ILE:HG13	1:H:150:HIS:H	1.66	0.60
1:H:515:GLU:HG3	1:H:516:CYS:H	1.66	0.60
1:K:228:LYS:O	1:K:275:ARG:NH2	2.35	0.60
1:A:33:LEU:O	1:A:37:ARG:N	2.34	0.60
1:G:235:TYR:O	1:G:236:GLN:CG	2.50	0.60
1:B:573:ASN:OD1	1:B:574:LYS:NZ	2.34	0.60
1:I:336:PHE:HA	1:I:340:ILE:HG22	1.82	0.60
1:L:463:ILE:O	1:L:463:ILE:HG22	2.01	0.60
1:B:96:GLY:O	1:B:141:ASN:ND2	2.33	0.60
1:D:318:GLY:H	1:D:321:ARG:HH12	1.48	0.60
1:F:383:ASP:O	1:F:384:LEU:HD12	2.00	0.60
1:G:528:LYS:HE2	1:G:554:LEU:HD11	1.83	0.60
1:J:87:ARG:HG2	1:J:89:ASP:H	1.67	0.60
1:B:452:ASN:O	1:B:459:ARG:NH1	2.34	0.60
1:A:405:LEU:O	1:A:409:THR:OG1	2.16	0.59
1:D:59:VAL:HG23	1:D:60:VAL:HG23	1.84	0.59
1:E:132:TYR:CE1	1:E:453:LEU:HD21	2.37	0.59
1:F:396:GLU:HG2	1:F:397:VAL:HG23	1.84	0.59
1:L:356:ILE:HG22	1:L:357:ALA:H	1.67	0.59
1:G:260:ASP:OD1	1:G:261:SER:N	2.35	0.59
1:I:42:ASP:OD1	1:I:43:ASP:N	2.33	0.59
1:K:175:VAL:HG23	1:K:177:HIS:CE1	2.37	0.59
1:D:376:ARG:NH1	1:D:377:THR:O	2.36	0.59
1:E:442:ALA:HA	1:E:445:GLU:HB2	1.84	0.59
1:C:321:ARG:O	1:D:56:GLN:NE2	2.35	0.59
1:G:280:ILE:HG12	1:G:288:LYS:HD3	1.83	0.59
1:H:248:LYS:O	1:H:249:ARG:HG2	2.02	0.59
1:H:287:LEU:HD23	1:H:289:ASP:H	1.67	0.59
1:L:36:SER:O	1:L:40:GLN:N	2.34	0.59
1:B:527:MET:HG3	1:B:528:LYS:H	1.67	0.59
1:B:541:LYS:HA	1:C:539:LEU:HD11	1.84	0.59
1:E:27:ARG:HG2	1:E:313:LYS:HD3	1.83	0.59
1:B:153:CYS:SG	1:B:154:SER:N	2.75	0.59
1:D:572:ALA:HA	1:D:575:GLN:HE22	1.67	0.59
1:E:478:VAL:HG12	1:E:479:THR:H	1.67	0.59
1:J:369:TYR:HB3	1:J:370:PRO:HD3	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:430:VAL:HG12	1:B:432:PHE:H	1.67	0.59
1:C:337:ASN:OD1	1:C:338:ALA:N	2.35	0.59
1:D:328:ARG:NE	1:E:53:TYR:OH	2.36	0.59
1:H:205:ASN:HB2	1:H:209:PHE:HA	1.84	0.59
1:L:167:LYS:NZ	1:L:296:GLU:O	2.35	0.59
1:A:231:THR:HG23	1:A:232:ALA:H	1.66	0.59
1:G:292:LEU:O	1:G:293:ILE:HD13	2.03	0.59
1:J:491:GLN:HG2	1:J:492:LEU:H	1.68	0.59
1:A:208:VAL:HG22	1:A:210:PRO:HD3	1.84	0.59
1:B:110:ALA:HB3	1:B:145:ARG:HH12	1.66	0.59
1:D:88:PRO:HG2	1:D:585:GLU:HB2	1.84	0.59
1:F:528:LYS:HZ1	1:G:564:GLY:CA	2.16	0.59
1:I:329:LEU:HD22	1:I:404:MET:HB3	1.84	0.59
1:I:437:GLN:NE2	1:I:520:VAL:HG13	2.18	0.59
1:C:441:ARG:NH2	1:D:105:ASN:OD1	2.35	0.58
1:I:448:VAL:HG13	1:I:517:TYR:CE1	2.38	0.58
1:B:81:ARG:HH12	1:B:518:THR:HA	1.69	0.58
1:B:535:ILE:HG22	1:B:539:LEU:HD13	1.84	0.58
1:J:319:VAL:HG23	1:J:320:VAL:H	1.67	0.58
1:J:528:LYS:HD3	1:J:531:ASN:HB3	1.85	0.58
1:F:199:PRO:HG2	1:F:218:GLN:HE21	1.68	0.58
1:H:165:MET:HG3	1:H:438:LEU:HD21	1.85	0.58
1:K:418:LEU:HA	1:L:66:LYS:HG2	1.84	0.58
1:E:58:ASP:O	1:E:59:VAL:HG22	2.03	0.58
1:E:340:ILE:O	1:E:344:THR:N	2.36	0.58
1:F:443:ASP:O	1:F:446:THR:OG1	2.21	0.58
1:G:44:TRP:CD1	1:G:47:GLN:HG2	2.38	0.58
1:G:81:ARG:HH12	1:H:563:LYS:HB2	1.69	0.58
1:H:63:VAL:HG13	1:H:415:VAL:HG11	1.83	0.58
1:D:289:ASP:OD1	1:D:290:LYS:N	2.36	0.58
1:G:163:LYS:HG2	1:H:149:ILE:HG22	1.85	0.58
1:H:323:THR:HG23	1:H:412:VAL:HG13	1.84	0.58
1:H:480:ILE:HG13	1:H:481:THR:H	1.67	0.58
1:L:483:GLU:HG2	1:L:484:ASP:H	1.68	0.58
1:A:400:ALA:HB3	1:A:404:MET:HE3	1.85	0.58
1:D:15:PHE:HZ	1:D:19:TRP:HE3	1.51	0.58
1:D:104:HIS:NE2	1:D:145:ARG:O	2.37	0.58
1:L:534:GLU:OE1	1:L:534:GLU:N	2.36	0.58
1:B:224:GLU:HB2	1:B:227:GLU:HG2	1.86	0.58
1:G:100:THR:OG1	1:G:103:ARG:NH2	2.36	0.58
1:I:130:THR:HG22	1:I:132:TYR:H	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:215:ASP:OD1	1:I:216:THR:N	2.36	0.58
1:J:141:ASN:OD1	1:J:141:ASN:O	2.21	0.58
1:I:111:VAL:HG22	1:I:439:ASN:HD21	1.69	0.58
1:J:265:LYS:O	1:J:266:ILE:HG22	2.04	0.58
1:A:353:PRO:HB3	1:A:356:ILE:HB	1.86	0.58
1:B:482:LEU:HG	1:B:483:GLU:H	1.67	0.58
1:E:378:ASP:OD1	1:E:379:GLU:N	2.37	0.58
1:K:525:GLN:N	1:K:529:GLN:OE1	2.32	0.58
1:G:231:THR:HG23	1:G:232:ALA:H	1.67	0.58
1:J:577:ILE:HG23	1:J:578:GLN:H	1.69	0.58
1:F:221:GLU:HB2	1:F:288:LYS:HE2	1.86	0.57
1:F:480:ILE:HG13	1:F:481:THR:H	1.69	0.57
1:H:356:ILE:HG12	1:H:357:ALA:H	1.69	0.57
1:K:58:ASP:OD2	1:K:61:ARG:NH1	2.37	0.57
1:D:558:THR:OG1	1:D:565:VAL:HG11	2.04	0.57
1:G:456:ALA:HB1	1:G:460:ASP:N	2.19	0.57
1:H:457:MET:HG2	1:H:505:GLN:HA	1.87	0.57
1:K:379:GLU:HG3	1:K:380:ASN:H	1.69	0.57
1:D:401:ASN:HD22	1:D:405:LEU:HB2	1.68	0.57
1:E:425:VAL:HG13	1:E:536:LEU:HD21	1.86	0.57
1:G:328:ARG:HG2	1:G:329:LEU:H	1.69	0.57
1:I:269:ARG:HG2	1:I:270:GLN:H	1.68	0.57
1:K:356:ILE:HG13	1:K:357:ALA:N	2.20	0.57
1:F:125:ALA:HB3	1:F:149:ILE:HG13	1.85	0.57
1:H:51:LEU:HG	1:H:52:GLN:H	1.70	0.57
1:I:34:PHE:HB3	1:I:38:VAL:HG23	1.86	0.57
1:A:462:GLU:C	1:A:463:ILE:HG13	2.30	0.57
1:A:340:ILE:HD13	1:B:346:LYS:HD3	1.86	0.57
1:B:20:THR:O	1:B:24:GLU:N	2.33	0.57
1:B:383:ASP:O	1:B:384:LEU:HD12	2.04	0.57
1:K:67:LEU:HA	1:K:70:GLU:HB2	1.86	0.57
1:H:62:PRO:O	1:H:66:LYS:NZ	2.38	0.57
1:J:128:LEU:HD11	1:J:299:PRO:HB2	1.87	0.57
1:A:112:ASN:O	1:A:116:ARG:NH1	2.38	0.57
1:B:82:PRO:HB3	1:C:563:LYS:HG3	1.86	0.57
1:C:289:ASP:OD1	1:C:290:LYS:N	2.38	0.57
1:D:15:PHE:HA	1:D:18:ASP:HB2	1.87	0.57
1:J:532:ARG:HH21	1:J:535:ILE:HG23	1.69	0.57
1:F:356:ILE:HG23	1:F:357:ALA:H	1.68	0.57
1:K:280:ILE:O	1:K:280:ILE:HG22	2.04	0.57
1:A:527:MET:HG3	1:A:559:LEU:HA	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:567:MET:HA	1:C:570:ASP:HB2	1.87	0.57
1:J:448:VAL:HG23	1:J:449:PHE:H	1.69	0.57
1:K:229:LYS:HD2	1:K:273:ARG:HH21	1.70	0.57
1:L:164:LEU:HD21	1:L:166:ASP:HB3	1.87	0.57
1:F:465:GLN:O	1:F:467:ILE:HG12	2.05	0.56
1:G:549:TYR:HA	1:G:552:LEU:HB2	1.87	0.56
1:K:340:ILE:O	1:K:344:THR:HG23	2.05	0.56
1:L:149:ILE:HG13	1:L:150:HIS:H	1.69	0.56
1:C:128:LEU:HD13	1:C:146:ARG:HE	1.69	0.56
1:C:167:LYS:HE2	1:C:445:GLU:HB3	1.86	0.56
1:H:167:LYS:HE3	1:H:169:ASP:HB2	1.85	0.56
1:B:546:THR:HB	1:B:547:PRO:HD3	1.85	0.56
1:F:369:TYR:HB2	1:F:370:PRO:HD3	1.86	0.56
1:I:140:ASN:OD1	1:I:142:GLN:NE2	2.38	0.56
1:J:346:LYS:HG3	1:K:369:TYR:HD2	1.71	0.56
1:F:351:PHE:HB2	1:F:388:PRO:HG2	1.88	0.56
1:J:142:GLN:N	1:J:142:GLN:OE1	2.39	0.56
1:C:323:THR:OG1	1:C:324:LYS:N	2.36	0.56
1:D:348:LYS:HD2	1:E:370:PRO:HB3	1.88	0.56
1:J:575:GLN:OE1	1:J:575:GLN:N	2.35	0.56
1:A:384:LEU:HD12	1:B:384:LEU:HG	1.86	0.56
1:C:161:ASN:O	1:C:162:SER:OG	2.23	0.56
1:I:58:ASP:O	1:I:59:VAL:HG12	2.05	0.56
1:I:523:SER:O	1:I:529:GLN:NE2	2.38	0.56
1:A:118:GLN:HG3	1:A:119:ILE:HD12	1.86	0.56
1:A:476:ARG:HG2	1:A:477:ASN:H	1.69	0.56
1:C:166:ASP:OD1	1:C:167:LYS:N	2.38	0.56
1:C:230:GLU:HG3	1:C:248:LYS:HD2	1.88	0.56
1:C:324:LYS:HD3	1:D:57:PHE:HA	1.87	0.56
1:E:127:ARG:HD2	1:E:149:ILE:HD12	1.88	0.56
1:I:156:VAL:HG22	1:I:176:ILE:HG23	1.87	0.56
1:J:280:ILE:HG13	1:J:281:ILE:N	2.20	0.56
1:L:280:ILE:HG12	1:L:281:ILE:H	1.71	0.56
1:D:534:GLU:O	1:D:537:GLU:N	2.35	0.56
1:L:351:PHE:HA	1:L:353:PRO:HD2	1.88	0.56
1:L:445:GLU:OE1	1:L:446:THR:HG23	2.06	0.56
1:C:356:ILE:HG12	1:C:357:ALA:H	1.71	0.56
1:F:157:ILE:HG22	1:F:158:TRP:H	1.70	0.56
1:F:320:VAL:O	1:F:324:LYS:NZ	2.29	0.56
1:H:34:PHE:HZ	1:H:45:LEU:HD21	1.70	0.56
1:J:297:HIS:NE2	1:J:451:ASP:O	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:125:ALA:H	1:K:149:ILE:HG12	1.70	0.56
1:L:33:LEU:HD23	1:L:37:ARG:HH12	1.70	0.56
1:L:215:ASP:O	1:L:216:THR:OG1	2.20	0.56
1:D:118:GLN:OE1	1:D:436:ASN:ND2	2.38	0.56
1:D:205:ASN:OD1	1:D:206:ASP:N	2.38	0.56
1:E:547:PRO:HG2	1:F:553:LEU:HD11	1.88	0.56
1:G:11:ILE:HD12	1:G:278:LYS:HZ3	1.70	0.56
1:E:451:ASP:OD1	1:E:458:ARG:NH2	2.39	0.55
1:G:389:LEU:HB2	1:H:389:LEU:HD21	1.88	0.55
1:I:441:ARG:HD3	1:I:444:LEU:HB3	1.88	0.55
1:K:375:ASN:OD1	1:K:376:ARG:N	2.39	0.55
1:A:68:VAL:HG11	1:L:431:ALA:HB2	1.88	0.55
1:C:120:GLU:OE1	1:C:120:GLU:N	2.40	0.55
1:D:171:ARG:NH1	1:D:173:CYS:H	2.04	0.55
1:L:469:ASN:OD1	1:L:470:ASP:N	2.40	0.55
1:A:452:ASN:ND2	1:A:506:VAL:O	2.40	0.55
1:E:322:LEU:HD22	1:F:59:VAL:HB	1.89	0.55
1:I:25:ALA:HA	1:I:28:GLU:HB2	1.89	0.55
1:C:117:GLU:OE1	1:C:117:GLU:N	2.37	0.55
1:F:438:LEU:HD21	1:G:109:ILE:HG21	1.89	0.55
1:G:113:ILE:HD11	1:G:148:PRO:HB2	1.88	0.55
1:K:222:PHE:O	1:K:280:ILE:HG23	2.04	0.55
1:A:106:THR:HA	1:A:109:ILE:HG22	1.89	0.55
1:A:352:TRP:HE1	1:A:376:ARG:HH12	1.54	0.55
1:C:12:LEU:HD23	1:C:16:ASP:HB2	1.89	0.55
1:C:421:ASP:OD1	1:C:422:THR:N	2.37	0.55
1:I:477:ASN:OD1	1:I:478:VAL:N	2.39	0.55
1:A:81:ARG:HE	1:A:517:TYR:HB3	1.71	0.55
1:B:82:PRO:O	1:B:83:LYS:HG3	2.06	0.55
1:B:480:ILE:HG13	1:B:481:THR:H	1.69	0.55
1:B:526:SER:HB3	1:C:560:LEU:HD22	1.89	0.55
1:D:77:ASP:OD1	1:D:78:VAL:N	2.40	0.55
1:D:213:THR:O	1:D:214:GLN:HG2	2.07	0.55
1:E:415:VAL:HG11	1:F:59:VAL:HG23	1.89	0.55
1:F:142:GLN:O	1:F:143:VAL:HG13	2.06	0.55
1:H:369:TYR:HB2	1:H:370:PRO:HD3	1.88	0.55
1:I:431:ALA:HB2	1:J:72:ARG:HH22	1.71	0.55
1:I:541:LYS:HD3	1:J:532:ARG:NH2	2.21	0.55
1:J:347:LYS:HG2	1:J:391:TYR:CZ	2.42	0.55
1:D:306:GLU:OE2	1:D:315:VAL:N	2.39	0.55
1:H:15:PHE:HB3	1:H:281:ILE:HG21	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:298:ILE:O	1:H:298:ILE:HD12	2.07	0.55
1:C:83:LYS:N	1:C:515:GLU:OE2	2.36	0.55
1:C:199:PRO:HD2	1:C:219:ILE:HA	1.88	0.55
1:F:42:ASP:OD1	1:F:43:ASP:N	2.39	0.55
1:G:443:ASP:O	1:G:446:THR:OG1	2.24	0.55
1:I:251:ILE:HG22	1:I:251:ILE:O	2.06	0.55
1:I:478:VAL:O	1:I:479:THR:HG23	2.07	0.55
1:L:39:SER:HB2	1:L:320:VAL:HG21	1.89	0.55
1:L:77:ASP:OD1	1:L:78:VAL:N	2.39	0.55
1:L:228:LYS:O	1:L:273:ARG:NH2	2.28	0.55
1:C:205:ASN:HD22	1:C:209:PHE:HB3	1.71	0.55
1:E:343:ARG:NH1	1:E:343:ARG:O	2.38	0.55
1:F:208:VAL:HG23	1:F:210:PRO:HD3	1.89	0.55
1:J:438:LEU:HD22	1:K:109:ILE:HG21	1.88	0.55
1:F:225:VAL:HG11	1:F:281:ILE:HD11	1.89	0.55
1:K:231:THR:HG23	1:K:232:ALA:H	1.69	0.55
1:A:25:ALA:HA	1:A:29:ALA:HB3	1.89	0.54
1:D:480:ILE:HG13	1:D:481:THR:H	1.73	0.54
1:E:301:VAL:N	1:E:302:PRO:HD3	2.22	0.54
1:F:310:VAL:HG23	1:F:311:GLU:H	1.72	0.54
1:F:322:LEU:HD22	1:F:415:VAL:HB	1.89	0.54
1:G:80:TYR:HE1	1:G:444:LEU:HD21	1.71	0.54
1:H:546:THR:HB	1:H:547:PRO:HD3	1.89	0.54
1:K:228:LYS:HZ1	1:L:188:ALA:HB3	1.72	0.54
1:B:15:PHE:O	1:B:19:TRP:N	2.38	0.54
1:B:25:ALA:HA	1:B:28:GLU:HG2	1.89	0.54
1:B:289:ASP:OD1	1:B:290:LYS:N	2.40	0.54
1:B:337:ASN:O	1:B:340:ILE:N	2.39	0.54
1:E:208:VAL:HG13	1:E:209:PHE:H	1.72	0.54
1:E:329:LEU:HD21	1:E:404:MET:HB2	1.89	0.54
1:E:546:THR:HB	1:E:547:PRO:HD3	1.90	0.54
1:K:296:GLU:HG3	1:K:297:HIS:ND1	2.22	0.54
1:L:390:ALA:O	1:L:394:ASN:ND2	2.40	0.54
1:A:297:HIS:HB2	1:A:446:THR:HB	1.89	0.54
1:E:141:ASN:OD1	1:E:455:THR:OG1	2.22	0.54
1:F:58:ASP:O	1:F:59:VAL:HG12	2.07	0.54
1:F:448:VAL:O	1:F:513:ARG:NH1	2.38	0.54
1:G:247:PHE:CE2	1:H:191:TYR:HA	2.43	0.54
1:G:309:PHE:HA	1:G:314:GLU:OE2	2.07	0.54
1:H:491:GLN:NE2	1:H:588:GLU:HA	2.22	0.54
1:H:577:ILE:HG23	1:H:578:GLN:H	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:151:SER:OG	1:I:152:ALA:N	2.40	0.54
1:I:581:VAL:HG23	1:I:583:LYS:H	1.72	0.54
1:J:321:ARG:H	1:K:61:ARG:HH22	1.54	0.54
1:A:190:LYS:HG3	1:A:191:TYR:H	1.73	0.54
1:D:332:MET:HE1	1:E:341:VAL:HB	1.89	0.54
1:F:126:TRP:HA	1:F:148:PRO:HA	1.90	0.54
1:K:38:VAL:HG21	1:K:321:ARG:HB2	1.89	0.54
1:A:249:ARG:HA	1:B:190:LYS:HE2	1.89	0.54
1:D:102:MET:HE2	1:D:108:LYS:HE2	1.88	0.54
1:G:535:ILE:HG13	1:G:536:LEU:H	1.73	0.54
1:H:116:ARG:HG2	1:H:117:GLU:N	2.22	0.54
1:H:126:TRP:CZ2	1:H:152:ALA:HB3	2.43	0.54
1:H:322:LEU:HD22	1:H:414:GLU:HG3	1.88	0.54
1:I:430:VAL:HG22	1:I:431:ALA:H	1.73	0.54
1:L:127:ARG:HH11	1:L:150:HIS:HB2	1.72	0.54
1:B:463:ILE:O	1:B:463:ILE:CG2	2.55	0.54
1:C:82:PRO:HA	1:C:515:GLU:HG3	1.88	0.54
1:C:324:LYS:HG2	1:D:56:GLN:HB3	1.89	0.54
1:D:319:VAL:HG23	1:D:320:VAL:HG23	1.89	0.54
1:E:430:VAL:HG12	1:E:431:ALA:H	1.72	0.54
1:L:527:MET:HE1	1:L:558:THR:O	2.08	0.54
1:F:449:PHE:O	1:F:513:ARG:NH2	2.40	0.54
1:K:64:VAL:HG12	1:K:320:VAL:HG12	1.90	0.54
1:K:79:LEU:HD13	1:K:525:GLN:HG3	1.90	0.54
1:K:325:ASP:HA	1:L:56:GLN:HB3	1.90	0.54
1:E:14:ARG:NH1	1:E:225:VAL:HG22	2.22	0.54
1:I:447:TYR:HA	1:I:450:GLN:O	2.07	0.54
1:K:107:ALA:HB1	1:K:146:ARG:HG2	1.90	0.54
1:B:312:ASP:CG	1:B:313:LYS:H	2.16	0.54
1:D:152:ALA:O	1:D:155:HIS:ND1	2.41	0.54
1:G:418:LEU:HD23	1:G:430:VAL:HG21	1.90	0.54
1:G:484:ASP:OD1	1:G:485:GLY:N	2.40	0.54
1:H:265:LYS:O	1:H:266:ILE:HG13	2.07	0.54
1:G:356:ILE:HG23	1:G:357:ALA:H	1.74	0.54
1:H:67:LEU:HD21	1:H:416:ALA:HA	1.89	0.54
1:J:91:ALA:HA	1:J:95:MET:HG3	1.90	0.54
1:A:353:PRO:HB3	1:A:356:ILE:HD13	1.90	0.53
1:A:452:ASN:OD1	1:A:508:ASN:ND2	2.39	0.53
1:C:438:LEU:O	1:C:442:ALA:N	2.41	0.53
1:D:104:HIS:CE1	1:D:107:ALA:HB3	2.43	0.53
1:F:19:TRP:O	1:F:22:SER:OG	2.22	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:222:PHE:HD1	1:J:280:ILE:HG21	1.73	0.53
1:K:400:ALA:O	1:K:404:MET:N	2.29	0.53
1:D:447:TYR:OH	1:D:515:GLU:OE1	2.19	0.53
1:G:529:GLN:O	1:G:533:ALA:N	2.41	0.53
1:H:59:VAL:O	1:H:327:GLN:NE2	2.42	0.53
1:A:251:ILE:HD13	1:B:294:ALA:HA	1.89	0.53
1:A:548:GLU:O	1:A:552:LEU:HB2	2.09	0.53
1:B:114:ALA:HB1	1:B:124:GLY:HA2	1.89	0.53
1:G:191:TYR:OH	1:G:197:ASP:OD1	2.25	0.53
1:G:392:TYR:O	1:H:347:LYS:HG2	2.08	0.53
1:H:347:LYS:O	1:I:369:TYR:OH	2.27	0.53
1:I:431:ALA:HA	1:J:72:ARG:HH12	1.73	0.53
1:J:430:VAL:HG22	1:J:431:ALA:H	1.73	0.53
1:D:577:ILE:HD11	1:E:593:LEU:HD22	1.91	0.53
1:E:514:TYR:HE1	1:E:517:TYR:HB2	1.73	0.53
1:F:21:ALA:O	1:F:24:GLU:HG2	2.08	0.53
1:H:310:VAL:HG23	1:H:311:GLU:H	1.72	0.53
1:K:166:ASP:OD1	1:K:441:ARG:NH2	2.41	0.53
1:L:222:PHE:CG	1:L:281:ILE:HG21	2.43	0.53
1:F:498:ASP:OD1	1:F:499:LEU:N	2.42	0.53
1:J:528:LYS:NZ	1:J:557:PHE:O	2.36	0.53
1:K:14:ARG:HH11	1:K:226:VAL:HG21	1.73	0.53
1:B:268:GLU:H	1:B:270:GLN:HE22	1.56	0.53
1:C:448:VAL:HG23	1:C:449:PHE:H	1.74	0.53
1:E:396:GLU:HG2	1:E:396:GLU:O	2.08	0.53
1:F:535:ILE:HD12	1:F:541:LYS:HB2	1.91	0.53
1:B:184:TRP:HB3	1:B:187:PHE:CE2	2.43	0.53
1:B:354:GLU:HB3	1:B:374:LEU:HA	1.90	0.53
1:D:187:PHE:O	1:D:190:LYS:N	2.41	0.53
1:D:394:ASN:HD22	1:E:389:LEU:HD11	1.74	0.53
1:F:288:LYS:H	1:F:288:LYS:HD2	1.72	0.53
1:G:431:ALA:O	1:G:434:THR:OG1	2.26	0.53
1:H:510:ILE:O	1:H:510:ILE:HG22	2.09	0.53
1:J:22:SER:OG	1:J:202:GLN:OE1	2.17	0.53
1:J:327:GLN:OE1	1:J:327:GLN:N	2.41	0.53
1:C:400:ALA:HB2	1:D:398:PRO:HG2	1.91	0.53
1:C:477:ASN:OD1	1:C:478:VAL:N	2.42	0.53
1:D:484:ASP:H	1:D:488:LYS:CE	2.22	0.53
1:H:457:MET:HE2	1:H:460:ASP:HA	1.91	0.53
1:I:100:THR:HA	1:I:103:ARG:HH21	1.74	0.53
1:K:384:LEU:HB3	1:K:385:PRO:HD2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:223:TYR:CD2	1:L:224:GLU:HG2	2.44	0.53
1:B:558:THR:HG22	1:B:559:LEU:HD13	1.91	0.53
1:D:37:ARG:NH1	1:D:43:ASP:O	2.41	0.53
1:D:102:MET:O	1:D:103:ARG:NH1	2.37	0.53
1:D:130:THR:HG23	1:D:293:ILE:HG23	1.89	0.53
1:D:378:ASP:OD1	1:D:379:GLU:N	2.39	0.53
1:E:37:ARG:O	1:E:42:ASP:N	2.42	0.53
1:F:457:MET:HG3	1:F:458:ARG:H	1.73	0.53
1:G:437:GLN:NE2	1:G:518:THR:OG1	2.42	0.53
1:G:532:ARG:HH21	1:G:556:TYR:HA	1.73	0.53
1:I:451:ASP:HB3	1:I:506:VAL:HA	1.91	0.53
1:B:520:VAL:O	1:C:105:ASN:ND2	2.42	0.53
1:J:50:THR:OG1	1:J:54:ARG:NH1	2.42	0.53
1:J:108:LYS:HZ1	1:J:145:ARG:HD3	1.72	0.53
1:J:275:ARG:HG2	1:J:276:VAL:H	1.73	0.53
1:J:276:VAL:HG12	1:J:278:LYS:H	1.74	0.53
1:L:236:GLN:HG3	1:L:238:PRO:HD3	1.91	0.53
1:I:172:HIS:NE2	1:I:300:ILE:O	2.31	0.52
1:K:61:ARG:HA	1:K:64:VAL:HG22	1.91	0.52
1:L:298:ILE:HD13	1:L:300:ILE:O	2.09	0.52
1:L:418:LEU:HD21	1:L:430:VAL:HG11	1.91	0.52
1:B:225:VAL:O	1:B:226:VAL:HG22	2.08	0.52
1:D:59:VAL:HB	1:D:324:LYS:HE3	1.90	0.52
1:D:345:PRO:CB	1:D:348:LYS:HE2	2.39	0.52
1:G:546:THR:HB	1:G:547:PRO:HD3	1.90	0.52
1:I:376:ARG:NH2	1:I:378:ASP:OD2	2.39	0.52
1:L:371:TYR:HE1	1:L:373:LEU:HD21	1.73	0.52
1:A:43:ASP:OD1	1:A:54:ARG:HD3	2.09	0.52
1:C:126:TRP:HA	1:C:149:ILE:HD12	1.89	0.52
1:I:80:TYR:HB2	1:I:516:CYS:HB3	1.91	0.52
1:I:373:LEU:O	1:I:373:LEU:HD23	2.09	0.52
1:K:280:ILE:O	1:K:280:ILE:CG2	2.57	0.52
1:K:296:GLU:HB2	1:K:451:ASP:OD1	2.09	0.52
1:D:187:PHE:CE1	1:D:190:LYS:HD3	2.43	0.52
1:D:222:PHE:CD2	1:D:280:ILE:HG12	2.45	0.52
1:F:571:TYR:HA	1:F:574:LYS:HE2	1.91	0.52
1:H:430:VAL:HG22	1:H:431:ALA:H	1.74	0.52
1:J:369:TYR:HB3	1:J:370:PRO:CD	2.39	0.52
1:K:352:TRP:N	1:K:353:PRO:HD3	2.24	0.52
1:L:353:PRO:HB3	1:L:373:LEU:HD22	1.90	0.52
1:L:532:ARG:NH2	1:L:555:GLN:OE1	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:74:ASN:ND2	1:H:433:ASP:OD1	2.41	0.52
1:K:442:ALA:HA	1:K:445:GLU:HG2	1.91	0.52
1:L:534:GLU:HG2	1:L:534:GLU:O	2.10	0.52
1:A:237:ASP:N	1:A:238:PRO:HD3	2.25	0.52
1:A:348:LYS:HB3	1:B:369:TYR:HB2	1.91	0.52
1:C:478:VAL:C	1:C:479:THR:HG1	2.17	0.52
1:D:527:MET:HB3	1:D:559:LEU:HD13	1.92	0.52
1:K:170:ALA:HB2	1:K:297:HIS:HB3	1.90	0.52
1:B:107:ALA:HB1	1:B:145:ARG:HD3	1.92	0.52
1:D:239:VAL:HG13	1:D:240:THR:H	1.74	0.52
1:E:163:LYS:HE2	1:F:150:HIS:CE1	2.44	0.52
1:F:300:ILE:HG22	1:F:302:PRO:HD2	1.91	0.52
1:I:172:HIS:NE2	1:I:300:ILE:HG23	2.25	0.52
1:J:104:HIS:HB3	1:J:145:ARG:HD2	1.91	0.52
1:B:491:GLN:HG2	1:B:492:LEU:HD22	1.90	0.52
1:C:155:HIS:NE2	1:C:204:PRO:HD2	2.25	0.52
1:D:537:GLU:O	1:D:541:LYS:NZ	2.42	0.52
1:I:589:GLU:HG2	1:I:590:GLN:N	2.24	0.52
1:K:434:THR:OG1	1:L:72:ARG:NH2	2.43	0.52
1:L:281:ILE:HG23	1:L:281:ILE:O	2.10	0.52
1:C:111:VAL:O	1:C:115:VAL:HG23	2.10	0.52
1:C:309:PHE:HZ	1:C:315:VAL:O	1.92	0.52
1:D:506:VAL:HG12	1:D:507:LEU:N	2.25	0.52
1:H:34:PHE:CD1	1:H:37:ARG:HD3	2.45	0.52
1:I:297:HIS:CE1	1:I:450:GLN:HB2	2.44	0.52
1:A:286:VAL:HG23	1:A:288:LYS:HG3	1.92	0.52
1:E:57:PHE:HB2	1:E:334:MET:HE1	1.92	0.52
1:E:353:PRO:HB3	1:E:356:ILE:HD13	1.92	0.52
1:H:281:ILE:O	1:H:282:THR:OG1	2.26	0.52
1:J:31:ASN:HA	1:J:34:PHE:HB2	1.91	0.52
1:K:320:VAL:HG23	1:K:321:ARG:H	1.74	0.52
1:L:238:PRO:HG2	1:L:239:VAL:HG23	1.92	0.52
1:C:526:SER:OG	1:C:527:MET:N	2.43	0.51
1:D:209:PHE:CD1	1:D:210:PRO:HD3	2.45	0.51
1:E:208:VAL:HG22	1:E:210:PRO:HD3	1.92	0.51
1:F:127:ARG:N	1:F:147:GLU:O	2.43	0.51
1:I:345:PRO:HB2	1:I:347:LYS:HG3	1.92	0.51
1:A:76:ILE:O	1:A:76:ILE:HG22	2.10	0.51
1:B:234:ILE:HG23	1:B:246:TYR:CD1	2.45	0.51
1:C:361:HIS:ND1	1:C:361:HIS:O	2.44	0.51
1:D:384:LEU:O	1:D:386:THR:N	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:522:PRO:HB2	1:E:524:PHE:CD2	2.45	0.51
1:F:190:LYS:HG2	1:F:191:TYR:H	1.75	0.51
1:K:76:ILE:HD12	1:K:521:GLY:O	2.09	0.51
1:L:40:GLN:HA	1:L:60:VAL:HG21	1.91	0.51
1:A:251:ILE:HG21	1:B:294:ALA:HB2	1.93	0.51
1:A:331:ASN:O	1:A:335:SER:N	2.39	0.51
1:D:45:LEU:N	1:D:47:GLN:OE1	2.43	0.51
1:E:379:GLU:HG2	1:E:380:ASN:H	1.75	0.51
1:F:571:TYR:O	1:F:574:LYS:HG2	2.10	0.51
1:G:28:GLU:O	1:G:32:ASP:N	2.42	0.51
1:H:268:GLU:HG2	1:H:269:ARG:HG2	1.93	0.51
1:K:43:ASP:O	1:K:45:LEU:HG	2.09	0.51
1:B:70:GLU:O	1:B:73:GLN:NE2	2.42	0.51
1:B:100:THR:HG22	1:B:141:ASN:HD21	1.75	0.51
1:F:306:GLU:O	1:F:307:TRP:HD1	1.93	0.51
1:H:163:LYS:HB3	1:H:167:LYS:HD2	1.92	0.51
1:I:39:SER:OG	1:I:120:GLU:OE2	2.28	0.51
1:I:492:LEU:HD13	1:I:493:MET:H	1.75	0.51
1:J:520:VAL:HG22	1:J:521:GLY:H	1.75	0.51
1:K:250:ASP:OD2	1:L:291:GLN:NE2	2.44	0.51
1:K:297:HIS:O	1:K:450:GLN:NE2	2.43	0.51
1:K:356:ILE:HG23	1:K:357:ALA:H	1.74	0.51
1:L:471:ILE:HG12	1:L:496:VAL:HG12	1.91	0.51
1:A:112:ASN:OD1	1:A:116:ARG:NH1	2.41	0.51
1:A:459:ARG:O	1:A:463:ILE:N	2.43	0.51
1:D:356:ILE:HG23	1:E:372:TYR:CE1	2.46	0.51
1:F:346:LYS:HB3	1:G:366:ASN:ND2	2.25	0.51
1:H:581:VAL:HG12	1:H:582:LYS:HD2	1.93	0.51
1:I:63:VAL:HG23	1:I:64:VAL:HG23	1.93	0.51
1:B:140:ASN:HA	1:B:454:ALA:HA	1.92	0.51
1:D:356:ILE:HG22	1:D:357:ALA:N	2.26	0.51
1:G:81:ARG:HD2	1:G:82:PRO:HD2	1.93	0.51
1:I:140:ASN:O	1:I:142:GLN:NE2	2.44	0.51
1:I:232:ALA:O	1:I:248:LYS:HE2	2.11	0.51
1:J:128:LEU:H	1:J:300:ILE:HG22	1.75	0.51
1:J:419:GLY:HA3	1:J:428:GLY:HA2	1.92	0.51
1:B:110:ALA:O	1:B:112:ASN:ND2	2.44	0.51
1:B:236:GLN:HB2	1:B:246:TYR:CE1	2.45	0.51
1:B:355:GLN:HB3	1:B:371:TYR:HE2	1.75	0.51
1:C:412:VAL:O	1:C:415:VAL:HG12	2.10	0.51
1:F:227:GLU:HA	1:F:275:ARG:HH22	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:80:TYR:CE1	1:G:444:LEU:HD21	2.46	0.51
1:I:447:TYR:CE1	1:I:513:ARG:HG2	2.44	0.51
1:I:528:LYS:HE2	1:J:563:LYS:HB3	1.93	0.51
1:J:531:ASN:ND2	1:J:555:GLN:HB3	2.26	0.51
1:J:538:LEU:C	1:J:539:LEU:HD13	2.35	0.51
1:C:281:ILE:O	1:C:281:ILE:HG22	2.10	0.51
1:D:127:ARG:HA	1:D:300:ILE:HG23	1.93	0.51
1:D:430:VAL:HG22	1:D:431:ALA:H	1.75	0.51
1:E:432:PHE:HA	1:E:435:VAL:HB	1.92	0.51
1:G:151:SER:OG	1:G:152:ALA:N	2.41	0.51
1:G:387:GLN:HG3	1:G:389:LEU:HD12	1.93	0.51
1:I:358:GLY:H	1:I:362:MET:HE1	1.75	0.51
1:I:396:GLU:HG3	1:I:397:VAL:HG22	1.92	0.51
1:J:531:ASN:OD1	1:J:531:ASN:O	2.29	0.51
1:B:281:ILE:HG22	1:B:282:THR:HG23	1.93	0.51
1:H:26:ARG:HG2	1:H:27:ARG:H	1.75	0.51
1:J:304:PHE:O	1:J:439:ASN:ND2	2.33	0.51
1:K:430:VAL:HG12	1:K:431:ALA:H	1.75	0.51
1:B:129:VAL:HG13	1:B:143:VAL:HG13	1.93	0.51
1:E:315:VAL:HG12	1:E:316:TYR:CD2	2.46	0.51
1:H:94:LEU:O	1:H:94:LEU:HD13	2.10	0.51
1:H:322:LEU:HD23	1:I:59:VAL:HG23	1.93	0.51
1:I:374:LEU:H	1:I:374:LEU:HD13	1.76	0.51
1:J:225:VAL:HG23	1:J:280:ILE:CA	2.41	0.51
1:A:242:GLU:N	1:A:243:PRO:HD3	2.26	0.50
1:B:236:GLN:HB2	1:B:246:TYR:CD1	2.46	0.50
1:B:461:GLY:O	1:B:462:GLU:HG2	2.10	0.50
1:C:165:MET:O	1:C:166:ASP:OD1	2.29	0.50
1:C:320:VAL:O	1:C:320:VAL:HG12	2.11	0.50
1:E:351:PHE:C	1:E:353:PRO:HD3	2.36	0.50
1:E:586:THR:HA	1:E:589:GLU:HB2	1.92	0.50
1:F:15:PHE:CE1	1:F:283:CYS:HB2	2.46	0.50
1:I:330:ARG:O	1:I:333:ILE:HG12	2.11	0.50
1:J:373:LEU:O	1:J:374:LEU:HD23	2.11	0.50
1:K:70:GLU:HG2	1:K:71:MET:HG3	1.93	0.50
1:A:388:PRO:HB3	1:B:352:TRP:CE3	2.46	0.50
1:B:170:ALA:HB2	1:B:227:GLU:HB2	1.94	0.50
1:C:15:PHE:HZ	1:C:225:VAL:HG11	1.75	0.50
1:C:163:LYS:NZ	1:C:314:GLU:OE2	2.38	0.50
1:D:161:ASN:OD1	1:D:163:LYS:NZ	2.21	0.50
1:D:324:LYS:HD2	1:D:327:GLN:HB2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:173:CYS:HB2	1:G:301:VAL:HA	1.92	0.50
1:H:386:THR:HG22	1:H:388:PRO:HD3	1.92	0.50
1:I:448:VAL:CG1	1:I:517:TYR:CE1	2.95	0.50
1:K:423:GLU:CD	1:K:536:LEU:HD12	2.36	0.50
1:L:199:PRO:HB3	1:L:283:CYS:HB3	1.93	0.50
1:L:244:VAL:O	1:L:244:VAL:HG12	2.11	0.50
1:A:59:VAL:HG22	1:L:322:LEU:HD22	1.92	0.50
1:A:126:TRP:CD1	1:A:300:ILE:HG23	2.46	0.50
1:B:21:ALA:HA	1:B:24:GLU:HG2	1.93	0.50
1:B:298:ILE:N	1:B:299:PRO:HD3	2.26	0.50
1:B:337:ASN:HA	1:B:340:ILE:HG22	1.92	0.50
1:F:296:GLU:HG3	1:F:297:HIS:N	2.26	0.50
1:G:143:VAL:O	1:G:144:ILE:HG23	2.11	0.50
1:E:529:GLN:O	1:E:533:ALA:N	2.44	0.50
1:H:408:ALA:HB1	1:H:412:VAL:HG23	1.94	0.50
1:I:260:ASP:OD1	1:I:261:SER:N	2.44	0.50
1:J:329:LEU:O	1:J:333:ILE:N	2.43	0.50
1:K:346:LYS:HG3	1:L:369:TYR:HB3	1.94	0.50
1:A:112:ASN:O	1:A:115:VAL:HG22	2.11	0.50
1:A:160:SER:OG	1:A:167:LYS:NZ	2.44	0.50
1:B:232:ALA:O	1:B:234:ILE:HG12	2.11	0.50
1:C:80:TYR:HB3	1:C:516:CYS:HB2	1.92	0.50
1:C:546:THR:CG2	1:C:547:PRO:HD3	2.41	0.50
1:E:312:ASP:CG	1:E:313:LYS:H	2.18	0.50
1:F:496:VAL:HG23	1:F:497:VAL:H	1.76	0.50
1:G:222:PHE:O	1:G:280:ILE:HG22	2.12	0.50
1:H:418:LEU:HD21	1:H:428:GLY:O	2.11	0.50
1:I:255:ILE:HG22	1:I:256:ASP:N	2.26	0.50
1:J:71:MET:HE1	1:J:115:VAL:HG21	1.93	0.50
1:J:205:ASN:O	1:J:206:ASP:OD1	2.29	0.50
1:K:529:GLN:O	1:K:532:ARG:O	2.29	0.50
1:L:554:LEU:HA	1:L:557:PHE:CE2	2.47	0.50
1:B:431:ALA:O	1:B:434:THR:HG22	2.11	0.50
1:C:58:ASP:O	1:C:59:VAL:HG12	2.12	0.50
1:D:98:TYR:HA	1:D:101:ASP:CG	2.37	0.50
1:I:412:VAL:O	1:I:415:VAL:HG12	2.12	0.50
1:L:164:LEU:HD22	1:L:168:SER:HB3	1.93	0.50
1:C:528:LYS:HB3	1:C:532:ARG:HH12	1.76	0.50
1:G:309:PHE:H	1:H:116:ARG:NH2	2.10	0.50
1:G:372:TYR:O	1:G:373:LEU:HB2	2.11	0.50
1:G:455:THR:HG23	1:G:456:ALA:H	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:397:VAL:O	1:H:399:GLN:N	2.45	0.50
1:A:126:TRP:HE1	1:A:128:LEU:HD11	1.77	0.50
1:D:340:ILE:HA	1:D:344:THR:HG23	1.94	0.50
1:D:570:ASP:OD1	1:D:573:ASN:ND2	2.29	0.50
1:E:306:GLU:OE1	1:E:306:GLU:N	2.45	0.50
1:G:110:ALA:HB1	1:G:148:PRO:HD3	1.93	0.50
1:H:355:GLN:O	1:H:356:ILE:HG22	2.12	0.50
1:H:410:SER:O	1:H:414:GLU:N	2.42	0.50
1:K:531:ASN:OD1	1:K:532:ARG:N	2.42	0.50
1:C:173:CYS:HA	1:C:225:VAL:HG12	1.94	0.50
1:D:237:ASP:HB2	1:D:258:LEU:HD13	1.94	0.50
1:D:484:ASP:HB2	1:D:488:LYS:HZ1	1.76	0.50
1:G:58:ASP:HB2	1:G:61:ARG:HH12	1.76	0.50
1:G:233:PHE:O	1:G:234:ILE:HB	2.12	0.50
1:G:405:LEU:O	1:G:409:THR:OG1	2.24	0.50
1:H:323:THR:O	1:H:327:GLN:N	2.42	0.50
1:I:438:LEU:HD22	1:I:440:MET:HB2	1.94	0.50
1:J:98:TYR:HH	1:J:516:CYS:HG	1.59	0.50
1:J:442:ALA:HA	1:K:104:HIS:CE1	2.47	0.50
1:A:28:GLU:HG3	1:A:313:LYS:HD2	1.94	0.49
1:J:223:TYR:CD2	1:J:224:GLU:HB3	2.47	0.49
1:B:348:LYS:HE3	1:B:350:PHE:HZ	1.77	0.49
1:C:24:GLU:HA	1:C:28:GLU:HB3	1.93	0.49
1:C:132:TYR:HE1	1:C:455:THR:HG23	1.77	0.49
1:C:485:GLY:O	1:C:488:LYS:NZ	2.38	0.49
1:C:541:LYS:O	1:D:532:ARG:NH1	2.44	0.49
1:C:589:GLU:OE1	1:C:589:GLU:N	2.45	0.49
1:D:123:VAL:HG11	1:D:155:HIS:CG	2.47	0.49
1:D:250:ASP:OD2	1:E:189:GLU:HG3	2.11	0.49
1:E:529:GLN:HB3	1:E:533:ALA:HB2	1.92	0.49
1:G:537:GLU:OE1	1:G:541:LYS:NZ	2.45	0.49
1:H:193:LEU:HD23	1:H:195:ALA:H	1.77	0.49
1:H:397:VAL:O	1:H:399:GLN:OE1	2.30	0.49
1:I:76:ILE:HD13	1:I:437:GLN:HG3	1.93	0.49
1:I:562:GLY:H	1:I:565:VAL:HB	1.77	0.49
1:L:21:ALA:HB1	1:L:313:LYS:HD3	1.93	0.49
1:A:80:TYR:HD1	1:A:516:CYS:HB3	1.76	0.49
1:D:15:PHE:HB2	1:D:281:ILE:HD12	1.93	0.49
1:G:291:GLN:O	1:G:292:LEU:HB2	2.13	0.49
1:F:323:THR:HG22	1:F:327:GLN:HG3	1.93	0.49
1:F:351:PHE:C	1:F:353:PRO:HD3	2.38	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:448:VAL:HG23	1:H:515:GLU:HB3	1.93	0.49
1:H:514:TYR:CZ	1:I:103:ARG:HD2	2.48	0.49
1:H:527:MET:O	1:H:529:GLN:N	2.46	0.49
1:I:11:ILE:HA	1:I:277:TYR:CE2	2.48	0.49
1:I:352:TRP:O	1:I:374:LEU:HB3	2.12	0.49
1:A:105:ASN:HB3	1:L:438:LEU:HD23	1.93	0.49
1:B:128:LEU:HD13	1:B:129:VAL:N	2.28	0.49
1:D:118:GLN:HG3	1:D:119:ILE:HD12	1.92	0.49
1:D:251:ILE:HG21	1:E:293:ILE:HG21	1.94	0.49
1:F:193:LEU:HD23	1:F:194:ASP:N	2.27	0.49
1:F:350:PHE:HE1	1:G:374:LEU:HB2	1.78	0.49
1:G:155:HIS:CD2	1:G:204:PRO:HD3	2.47	0.49
1:I:492:LEU:HD13	1:I:493:MET:N	2.27	0.49
1:J:300:ILE:O	1:J:300:ILE:HG13	2.13	0.49
1:B:441:ARG:NH1	1:B:518:THR:O	2.46	0.49
1:D:477:ASN:OD1	1:D:478:VAL:N	2.46	0.49
1:F:92:ASP:OD1	1:F:93:VAL:N	2.46	0.49
1:H:99:ARG:NH1	1:H:103:ARG:HE	2.11	0.49
1:H:116:ARG:NH1	1:H:151:SER:HB2	2.28	0.49
1:K:170:ALA:O	1:K:172:HIS:ND1	2.46	0.49
1:K:233:PHE:O	1:K:234:ILE:HG22	2.12	0.49
1:L:78:VAL:HB	1:L:519:ASP:HB3	1.94	0.49
1:A:222:PHE:CD2	1:A:279:SER:HB3	2.48	0.49
1:A:479:THR:HG22	1:A:480:ILE:N	2.28	0.49
1:B:270:GLN:O	1:B:271:ILE:HD13	2.13	0.49
1:B:271:ILE:HD12	1:B:275:ARG:NH2	2.28	0.49
1:D:165:MET:HE2	1:E:147:GLU:HG2	1.95	0.49
1:D:527:MET:H	1:D:529:GLN:HG2	1.77	0.49
1:E:234:ILE:HG23	1:E:247:PHE:CE2	2.48	0.49
1:I:331:ASN:O	1:I:335:SER:N	2.45	0.49
1:J:70:GLU:OE2	1:J:428:GLY:HA3	2.13	0.49
1:A:552:LEU:HA	1:A:555:GLN:HG2	1.95	0.49
1:B:340:ILE:HG13	1:B:343:ARG:HB2	1.94	0.49
1:C:144:ILE:HG12	1:C:145:ARG:H	1.78	0.49
1:C:438:LEU:O	1:C:441:ARG:N	2.46	0.49
1:D:123:VAL:HG21	1:D:155:HIS:CE1	2.47	0.49
1:F:482:LEU:O	1:F:483:GLU:HG2	2.13	0.49
1:G:68:VAL:HG21	1:G:116:ARG:HH12	1.77	0.49
1:G:83:LYS:HG2	1:G:84:ASP:H	1.77	0.49
1:G:483:GLU:O	1:G:484:ASP:OD1	2.30	0.49
1:I:149:ILE:HG22	1:I:150:HIS:H	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:34:PHE:HA	1:J:37:ARG:HG2	1.95	0.49
1:D:123:VAL:HG13	1:D:303:VAL:HG22	1.95	0.49
1:E:216:THR:O	1:E:218:GLN:NE2	2.45	0.49
1:I:255:ILE:HD13	1:I:258:LEU:HD23	1.94	0.49
1:J:310:VAL:O	1:K:151:SER:OG	2.29	0.49
1:A:127:ARG:HH21	1:A:178:SER:H	1.60	0.49
1:C:400:ALA:O	1:C:403:TYR:N	2.44	0.49
1:E:369:TYR:HB3	1:E:370:PRO:CD	2.41	0.49
1:F:15:PHE:O	1:F:18:ASP:HB2	2.13	0.49
1:G:82:PRO:HB3	1:G:516:CYS:SG	2.53	0.49
1:I:441:ARG:O	1:I:444:LEU:HD23	2.13	0.49
1:K:65:ARG:HE	1:K:66:LYS:HE2	1.77	0.49
1:A:124:GLY:HA3	1:A:152:ALA:HB3	1.95	0.48
1:B:21:ALA:O	1:B:24:GLU:HG2	2.13	0.48
1:C:165:MET:HE1	1:C:303:VAL:HA	1.95	0.48
1:H:35:PHE:HD1	1:H:121:ALA:HA	1.78	0.48
1:I:250:ASP:OD1	1:I:250:ASP:N	2.46	0.48
1:I:534:GLU:OE1	1:I:542:THR:OG1	2.29	0.48
1:J:68:VAL:HG13	1:J:69:SER:H	1.78	0.48
1:A:177:HIS:ND1	1:A:183:GLY:O	2.45	0.48
1:A:226:VAL:HG12	1:A:227:GLU:HG3	1.95	0.48
1:K:239:VAL:HG12	1:K:240:THR:N	2.28	0.48
1:K:239:VAL:HG12	1:K:240:THR:H	1.78	0.48
1:K:423:GLU:CD	1:K:424:ALA:H	2.20	0.48
1:B:184:TRP:HB3	1:B:187:PHE:HE2	1.78	0.48
1:B:205:ASN:HD21	1:B:209:PHE:HA	1.77	0.48
1:B:279:SER:HB3	1:B:286:VAL:HG21	1.94	0.48
1:D:123:VAL:HG21	1:D:155:HIS:NE2	2.28	0.48
1:E:34:PHE:HB3	1:E:38:VAL:HG23	1.95	0.48
1:H:13:SER:OG	1:H:278:LYS:HG3	2.13	0.48
1:H:539:LEU:HD23	1:H:540:GLY:H	1.77	0.48
1:I:327:GLN:HA	1:I:329:LEU:CG	2.41	0.48
1:K:127:ARG:HD2	1:K:177:HIS:CG	2.48	0.48
1:L:340:ILE:HG22	1:L:343:ARG:HB3	1.94	0.48
1:A:79:LEU:HD13	1:A:440:MET:HE1	1.94	0.48
1:A:375:ASN:OD1	1:A:376:ARG:N	2.46	0.48
1:A:503:GLU:N	1:A:503:GLU:OE1	2.45	0.48
1:C:265:LYS:O	1:C:266:ILE:HG22	2.14	0.48
1:C:557:PHE:HB2	1:C:568:MET:HG3	1.95	0.48
1:D:436:ASN:O	1:D:436:ASN:OD1	2.31	0.48
1:D:534:GLU:O	1:D:536:LEU:N	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:57:PHE:O	1:E:59:VAL:HG13	2.13	0.48
1:E:282:THR:HG22	1:E:283:CYS:N	2.28	0.48
1:E:362:MET:HE1	1:E:373:LEU:HB3	1.94	0.48
1:E:430:VAL:HG12	1:E:431:ALA:N	2.29	0.48
1:E:450:GLN:OE1	1:E:450:GLN:N	2.45	0.48
1:F:43:ASP:HB2	1:F:328:ARG:NH2	2.29	0.48
1:F:118:GLN:HG3	1:F:119:ILE:HD12	1.95	0.48
1:F:153:CYS:SG	1:F:154:SER:N	2.86	0.48
1:G:161:ASN:OD1	1:G:162:SER:N	2.35	0.48
1:H:506:VAL:HA	1:H:513:ARG:HH21	1.79	0.48
1:K:225:VAL:HG22	1:K:226:VAL:HG23	1.96	0.48
1:K:413:LYS:HG3	1:K:414:GLU:HG3	1.96	0.48
1:A:225:VAL:HG22	1:A:226:VAL:HG23	1.95	0.48
1:B:441:ARG:HG3	1:C:105:ASN:HB3	1.94	0.48
1:C:94:LEU:O	1:C:97:MET:N	2.43	0.48
1:D:471:ILE:HG23	1:D:472:TYR:H	1.79	0.48
1:F:281:ILE:O	1:F:282:THR:OG1	2.24	0.48
1:G:499:LEU:HD13	1:G:500:ALA:N	2.29	0.48
1:I:340:ILE:O	1:I:343:ARG:HG2	2.14	0.48
1:L:266:ILE:O	1:L:266:ILE:HG12	2.13	0.48
1:C:249:ARG:NH2	1:C:251:ILE:HD11	2.29	0.48
1:D:329:LEU:HA	1:D:332:MET:HB2	1.95	0.48
1:D:360:GLU:HG2	1:D:361:HIS:ND1	2.28	0.48
1:E:333:ILE:O	1:E:333:ILE:HG22	2.13	0.48
1:F:212:LEU:HD12	1:F:212:LEU:O	2.13	0.48
1:H:321:ARG:NH2	1:I:58:ASP:OD2	2.47	0.48
1:H:527:MET:O	1:H:527:MET:HG3	2.13	0.48
1:J:400:ALA:HB1	1:J:404:MET:HE3	1.96	0.48
1:K:109:ILE:HD12	1:K:112:ASN:HB2	1.95	0.48
1:K:116:ARG:NH1	1:K:120:GLU:HG3	2.28	0.48
1:L:462:GLU:O	1:L:463:ILE:HB	2.14	0.48
1:D:172:HIS:ND1	1:D:302:PRO:HG2	2.27	0.48
1:D:403:TYR:OH	1:E:398:PRO:HB2	2.13	0.48
1:F:99:ARG:O	1:F:99:ARG:HG2	2.13	0.48
1:G:263:PHE:HB3	1:G:265:LYS:HG3	1.96	0.48
1:I:310:VAL:HG13	1:I:311:GLU:H	1.78	0.48
1:I:322:LEU:HD12	1:J:61:ARG:HH11	1.79	0.48
1:I:438:LEU:HD11	1:I:520:VAL:HG21	1.96	0.48
1:K:187:PHE:O	1:K:190:LYS:N	2.33	0.48
1:B:319:VAL:HG23	1:B:320:VAL:HG13	1.96	0.48
1:C:533:ALA:O	1:C:535:ILE:HG22	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:428:GLY:O	1:F:430:VAL:HG23	2.13	0.48
1:I:277:TYR:CE2	1:I:279:SER:HB2	2.48	0.48
1:I:447:TYR:CE1	1:I:513:ARG:CG	2.97	0.48
1:J:169:ASP:C	1:J:171:ARG:H	2.22	0.48
1:A:479:THR:HG22	1:A:480:ILE:H	1.78	0.48
1:C:548:GLU:O	1:C:551:LEU:HB3	2.13	0.48
1:D:253:ASP:HB3	1:E:293:ILE:HG23	1.95	0.48
1:E:24:GLU:HB3	1:E:28:GLU:HB3	1.96	0.48
1:E:172:HIS:HB2	1:E:300:ILE:HG21	1.96	0.48
1:G:548:GLU:O	1:G:551:LEU:HB3	2.14	0.48
1:H:92:ASP:OD1	1:H:92:ASP:N	2.45	0.48
1:J:432:PHE:O	1:J:435:VAL:HG22	2.14	0.48
1:L:437:GLN:HG2	1:L:520:VAL:HG11	1.96	0.48
1:B:225:VAL:HG22	1:B:226:VAL:HG13	1.96	0.48
1:C:532:ARG:HE	1:C:558:THR:HG23	1.78	0.48
1:D:295:GLY:HA3	1:D:450:GLN:HG3	1.96	0.48
1:E:198:ILE:HG23	1:E:198:ILE:O	2.13	0.48
1:F:488:LYS:HG3	1:F:489:ASP:H	1.77	0.48
1:H:26:ARG:HH21	1:H:28:GLU:HB2	1.78	0.48
1:H:265:LYS:C	1:H:266:ILE:HG13	2.39	0.48
1:H:430:VAL:HG13	1:H:432:PHE:H	1.78	0.48
1:H:526:SER:HA	1:I:559:LEU:HD21	1.95	0.48
1:I:60:VAL:HG11	1:I:320:VAL:HG13	1.95	0.48
1:I:118:GLN:NE2	1:I:436:ASN:OD1	2.47	0.48
1:I:306:GLU:C	1:I:307:TRP:HD1	2.22	0.48
1:J:389:LEU:O	1:J:391:TYR:HD2	1.97	0.48
1:A:74:ASN:OD1	1:A:523:SER:OG	2.24	0.47
1:A:80:TYR:N	1:A:517:TYR:O	2.47	0.47
1:A:291:GLN:O	1:A:292:LEU:HB2	2.13	0.47
1:C:94:LEU:HD12	1:C:95:MET:N	2.29	0.47
1:D:31:ASN:OD1	1:D:32:ASP:N	2.47	0.47
1:E:282:THR:HG22	1:E:283:CYS:H	1.79	0.47
1:E:458:ARG:HD3	1:E:503:GLU:OE1	2.13	0.47
1:J:448:VAL:HG12	1:J:516:CYS:HB2	1.96	0.47
1:A:212:LEU:HD12	1:A:213:THR:N	2.28	0.47
1:B:509:ASP:HB3	1:C:137:PRO:O	2.15	0.47
1:D:114:ALA:HB2	1:D:148:PRO:HG3	1.95	0.47
1:D:461:GLY:C	1:D:463:ILE:H	2.22	0.47
1:E:35:PHE:CG	1:E:36:SER:N	2.82	0.47
1:E:36:SER:HA	1:E:39:SER:HB3	1.96	0.47
1:G:324:LYS:HB2	1:H:54:ARG:NH1	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:448:VAL:HG23	1:K:449:PHE:H	1.78	0.47
1:B:123:VAL:HG12	1:B:124:GLY:H	1.77	0.47
1:C:128:LEU:HB2	1:C:146:ARG:HG2	1.96	0.47
1:D:508:ASN:OD1	1:D:509:ASP:N	2.47	0.47
1:E:582:LYS:O	1:E:584:PRO:HD3	2.15	0.47
1:F:14:ARG:HB3	1:F:281:ILE:HD13	1.95	0.47
1:F:206:ASP:O	1:F:207:TRP:CD1	2.68	0.47
1:H:249:ARG:NH1	1:H:251:ILE:O	2.47	0.47
1:L:54:ARG:NH2	1:L:339:ASP:OD1	2.47	0.47
1:A:322:LEU:HB3	1:A:415:VAL:HG21	1.96	0.47
1:B:123:VAL:HG12	1:B:124:GLY:N	2.30	0.47
1:B:329:LEU:O	1:B:333:ILE:HG12	2.15	0.47
1:F:430:VAL:HG12	1:F:431:ALA:N	2.28	0.47
1:G:324:LYS:HB2	1:H:54:ARG:HH12	1.79	0.47
1:I:14:ARG:HB3	1:I:281:ILE:HG22	1.96	0.47
1:J:58:ASP:OD2	1:J:61:ARG:NH1	2.32	0.47
1:J:400:ALA:HA	1:J:403:TYR:CE2	2.49	0.47
1:L:318:GLY:O	1:L:321:ARG:NH1	2.48	0.47
1:A:187:PHE:O	1:A:190:LYS:NZ	2.40	0.47
1:A:327:GLN:OE1	1:A:327:GLN:N	2.48	0.47
1:B:68:VAL:HG21	1:B:116:ARG:HE	1.78	0.47
1:B:587:PRO:O	1:B:588:GLU:HG3	2.14	0.47
1:C:173:CYS:SG	1:C:174:THR:N	2.88	0.47
1:F:552:LEU:HD12	1:F:556:TYR:CE2	2.49	0.47
1:G:35:PHE:HB2	1:G:121:ALA:HA	1.96	0.47
1:G:480:ILE:HG22	1:G:481:THR:N	2.26	0.47
1:H:307:TRP:CG	1:H:308:GLY:H	2.33	0.47
1:I:362:MET:HG3	1:I:363:TYR:CD2	2.49	0.47
1:I:372:TYR:CG	1:I:372:TYR:O	2.68	0.47
1:I:448:VAL:CG2	1:I:517:TYR:HE1	2.26	0.47
1:L:25:ALA:HB1	1:L:29:ALA:HB2	1.96	0.47
1:C:271:ILE:HD11	1:C:273:ARG:HH11	1.78	0.47
1:D:369:TYR:HB3	1:D:370:PRO:HD3	1.96	0.47
1:E:37:ARG:HA	1:E:41:TRP:HB2	1.95	0.47
1:E:351:PHE:HB2	1:E:388:PRO:HD3	1.96	0.47
1:H:518:THR:HG22	1:H:519:ASP:H	1.80	0.47
1:I:325:ASP:H	1:J:56:GLN:HG2	1.80	0.47
1:B:434:THR:HA	1:B:437:GLN:OE1	2.15	0.47
1:C:109:ILE:HG13	1:C:110:ALA:N	2.29	0.47
1:C:579:MET:HE1	1:C:584:PRO:HD3	1.97	0.47
1:D:169:ASP:OD1	1:D:169:ASP:N	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:211:TRP:HE1	1:D:213:THR:C	2.23	0.47
1:E:158:TRP:CZ2	1:E:174:THR:HG21	2.49	0.47
1:E:165:MET:HG3	1:E:304:PHE:HA	1.96	0.47
1:F:61:ARG:HD2	1:F:65:ARG:HD2	1.96	0.47
1:F:246:TYR:OH	1:F:274:ARG:NH2	2.48	0.47
1:F:397:VAL:N	1:F:398:PRO:HD3	2.30	0.47
1:G:395:PRO:HB2	1:G:397:VAL:HG23	1.96	0.47
1:H:117:GLU:HB3	1:H:121:ALA:HB3	1.95	0.47
1:H:328:ARG:O	1:H:332:MET:HG2	2.15	0.47
1:H:400:ALA:HB1	1:H:404:MET:HE3	1.96	0.47
1:H:414:GLU:HG2	1:H:415:VAL:HG13	1.96	0.47
1:I:546:THR:O	1:I:549:TYR:HD2	1.98	0.47
1:J:273:ARG:HH11	1:J:275:ARG:HH22	1.62	0.47
1:K:242:GLU:HB3	1:K:245:SER:HA	1.97	0.47
1:L:44:TRP:CZ2	1:L:46:SER:HB2	2.50	0.47
1:A:538:LEU:HD13	1:A:541:LYS:HZ1	1.80	0.47
1:B:558:THR:O	1:B:559:LEU:HD12	2.15	0.47
1:C:576:LEU:O	1:C:578:GLN:N	2.48	0.47
1:D:403:TYR:CZ	1:E:402:ALA:HB2	2.50	0.47
1:F:444:LEU:O	1:F:448:VAL:HG12	2.15	0.47
1:G:293:ILE:O	1:G:295:GLY:O	2.32	0.47
1:K:22:SER:HA	1:K:25:ALA:HB2	1.96	0.47
1:A:175:VAL:HG21	1:A:300:ILE:HD13	1.97	0.47
1:F:125:ALA:HB1	1:F:302:PRO:HB3	1.96	0.47
1:G:64:VAL:O	1:G:68:VAL:HG13	2.14	0.47
1:H:325:ASP:HB3	1:H:328:ARG:HE	1.80	0.47
1:I:328:ARG:O	1:I:328:ARG:HG2	2.14	0.47
1:J:63:VAL:HG11	1:J:321:ARG:HD3	1.97	0.47
1:J:82:PRO:HB2	1:J:515:GLU:HG2	1.97	0.47
1:J:412:VAL:HA	1:J:415:VAL:HG12	1.95	0.47
1:J:560:LEU:HG	1:J:561:ASP:H	1.79	0.47
1:K:499:LEU:HB3	1:K:501:THR:HG22	1.97	0.47
1:C:534:GLU:OE2	1:C:539:LEU:HG	2.16	0.47
1:D:462:GLU:OE1	1:D:464:TYR:HB2	2.15	0.47
1:D:527:MET:O	1:D:528:LYS:HB2	2.14	0.47
1:E:348:LYS:HE3	1:F:370:PRO:O	2.15	0.47
1:F:9:GLU:N	1:F:9:GLU:OE1	2.47	0.47
1:F:330:ARG:O	1:F:333:ILE:HG12	2.15	0.47
1:H:42:ASP:OD1	1:H:43:ASP:N	2.40	0.47
1:H:279:SER:O	1:H:280:ILE:C	2.56	0.47
1:I:322:LEU:HD12	1:J:61:ARG:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:451:ASP:CG	1:I:506:VAL:H	2.23	0.47
1:J:30:LYS:HG2	1:J:34:PHE:CZ	2.50	0.47
1:J:63:VAL:HG21	1:J:321:ARG:NH2	2.30	0.47
1:K:280:ILE:HG21	1:K:286:VAL:HG11	1.96	0.47
1:K:567:MET:HA	1:K:570:ASP:HB3	1.96	0.47
1:A:128:LEU:O	1:A:129:VAL:C	2.58	0.46
1:C:162:SER:O	1:C:307:TRP:NE1	2.48	0.46
1:C:165:MET:HE3	1:C:307:TRP:HH2	1.80	0.46
1:D:319:VAL:C	1:E:61:ARG:HH12	2.17	0.46
1:D:455:THR:OG1	1:D:456:ALA:N	2.45	0.46
1:E:53:TYR:CD2	1:E:53:TYR:O	2.68	0.46
1:E:462:GLU:C	1:E:463:ILE:HG13	2.40	0.46
1:G:53:TYR:HE2	1:G:339:ASP:HB2	1.80	0.46
1:G:105:ASN:O	1:G:106:THR:HG22	2.14	0.46
1:G:328:ARG:HG2	1:G:329:LEU:N	2.29	0.46
1:J:565:VAL:HG12	1:J:565:VAL:O	2.15	0.46
1:K:59:VAL:O	1:K:59:VAL:HG12	2.13	0.46
1:L:271:ILE:HG22	1:L:272:LYS:N	2.30	0.46
1:L:418:LEU:HD21	1:L:430:VAL:HG21	1.97	0.46
1:A:574:LYS:H	1:A:577:ILE:HG23	1.80	0.46
1:B:452:ASN:C	1:B:459:ARG:HH12	2.22	0.46
1:C:206:ASP:OD1	1:C:210:PRO:HD3	2.15	0.46
1:C:441:ARG:C	1:C:443:ASP:H	2.22	0.46
1:E:432:PHE:HB3	1:E:436:ASN:HD22	1.81	0.46
1:F:12:LEU:O	1:F:12:LEU:HD12	2.15	0.46
1:G:72:ARG:HH21	1:G:116:ARG:HH21	1.64	0.46
1:I:249:ARG:HH21	1:I:251:ILE:HB	1.80	0.46
1:J:34:PHE:HD1	1:J:37:ARG:HD3	1.81	0.46
1:K:212:LEU:O	1:K:213:THR:HG22	2.15	0.46
1:B:296:GLU:N	1:B:296:GLU:OE1	2.47	0.46
1:B:541:LYS:HD3	1:C:534:GLU:CD	2.41	0.46
1:D:356:ILE:HG22	1:D:357:ALA:H	1.81	0.46
1:E:306:GLU:HG2	1:E:306:GLU:O	2.16	0.46
1:E:528:LYS:NZ	1:E:555:GLN:O	2.45	0.46
1:F:14:ARG:HD2	1:F:17:ALA:HB3	1.97	0.46
1:F:236:GLN:HG2	1:F:263:PHE:CE1	2.51	0.46
1:G:432:PHE:O	1:G:435:VAL:HG12	2.16	0.46
1:H:84:ASP:HB2	1:I:99:ARG:HD2	1.97	0.46
1:H:124:GLY:HA2	1:H:303:VAL:H	1.80	0.46
1:K:318:GLY:O	1:L:61:ARG:NH1	2.48	0.46
1:K:583:LYS:NZ	1:L:565:VAL:HA	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:193:LEU:HD12	1:L:194:ASP:H	1.80	0.46
1:A:83:LYS:HG2	1:A:84:ASP:H	1.81	0.46
1:B:489:ASP:HB3	1:B:588:GLU:OE1	2.15	0.46
1:C:113:ILE:HB	1:C:116:ARG:HH12	1.81	0.46
1:E:510:ILE:HG23	1:E:510:ILE:O	2.16	0.46
1:I:29:ALA:O	1:I:33:LEU:N	2.49	0.46
1:I:179:MET:SD	1:I:212:LEU:HB3	2.56	0.46
1:I:538:LEU:C	1:I:539:LEU:HD12	2.40	0.46
1:J:280:ILE:HG23	1:J:281:ILE:H	1.80	0.46
1:K:320:VAL:HG23	1:K:321:ARG:N	2.30	0.46
1:L:193:LEU:HD12	1:L:194:ASP:N	2.31	0.46
1:L:515:GLU:HG3	1:L:516:CYS:H	1.81	0.46
1:L:559:LEU:HG	1:L:568:MET:HE1	1.96	0.46
1:A:61:ARG:NH1	1:L:321:ARG:HD2	2.31	0.46
1:A:352:TRP:HE3	1:L:392:TYR:OH	1.99	0.46
1:B:69:SER:HA	1:B:72:ARG:HH11	1.79	0.46
1:B:531:ASN:ND2	1:B:555:GLN:O	2.49	0.46
1:D:42:ASP:HB3	1:D:55:GLY:HA2	1.96	0.46
1:E:368:ASP:CG	1:E:369:TYR:H	2.23	0.46
1:F:327:GLN:O	1:F:330:ARG:HG2	2.16	0.46
1:F:535:ILE:O	1:F:541:LYS:NZ	2.41	0.46
1:H:126:TRP:H	1:H:148:PRO:HB3	1.80	0.46
1:I:125:ALA:HB2	1:I:303:VAL:HG23	1.97	0.46
1:D:188:ALA:C	1:D:190:LYS:H	2.22	0.46
1:E:545:GLY:HA2	1:F:549:TYR:HD1	1.81	0.46
1:H:127:ARG:HH22	1:H:149:ILE:HD11	1.80	0.46
1:H:149:ILE:HG13	1:H:150:HIS:N	2.29	0.46
1:H:323:THR:HG22	1:H:327:GLN:HG2	1.97	0.46
1:H:577:ILE:HG23	1:H:578:GLN:N	2.30	0.46
1:I:142:GLN:HE21	1:I:453:LEU:HB3	1.81	0.46
1:J:111:VAL:HA	1:J:114:ALA:HB3	1.98	0.46
1:K:282:THR:HG22	1:K:284:THR:H	1.81	0.46
1:C:287:LEU:HD12	1:C:287:LEU:O	2.15	0.46
1:E:170:ALA:HA	1:E:227:GLU:HB3	1.97	0.46
1:E:362:MET:HG3	1:E:371:TYR:CG	2.50	0.46
1:F:169:ASP:OD2	1:G:185:GLU:HB3	2.16	0.46
1:F:223:TYR:CE1	1:F:224:GLU:HG2	2.51	0.46
1:F:548:GLU:O	1:F:552:LEU:HB2	2.15	0.46
1:I:310:VAL:HG13	1:I:311:GLU:N	2.31	0.46
1:J:346:LYS:HG3	1:K:369:TYR:CD2	2.50	0.46
1:K:522:PRO:HD2	1:K:524:PHE:HE2	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:513:ARG:O	1:A:514:TYR:HB2	2.16	0.46
1:B:216:THR:O	1:B:217:ILE:HG22	2.15	0.46
1:C:308:GLY:O	1:C:309:PHE:CG	2.69	0.46
1:E:215:ASP:OD1	1:E:216:THR:N	2.48	0.46
1:F:139:SER:OG	1:F:140:ASN:N	2.47	0.46
1:F:180:SER:HB3	1:F:182:ASN:H	1.81	0.46
1:F:323:THR:HA	1:F:412:VAL:HG12	1.97	0.46
1:H:249:ARG:HH12	1:H:254:VAL:HB	1.80	0.46
1:H:323:THR:O	1:H:326:GLY:N	2.48	0.46
1:J:321:ARG:HG3	1:J:322:LEU:H	1.81	0.46
1:K:345:PRO:O	1:K:392:TYR:OH	2.32	0.46
1:L:36:SER:HA	1:L:39:SER:HB3	1.98	0.46
1:B:42:ASP:CG	1:B:43:ASP:H	2.24	0.46
1:B:179:MET:HB3	1:B:183:GLY:HA3	1.97	0.46
1:B:518:THR:HG23	1:B:520:VAL:H	1.81	0.46
1:C:15:PHE:CZ	1:C:225:VAL:HG11	2.51	0.46
1:D:128:LEU:HD23	1:D:129:VAL:O	2.16	0.46
1:E:300:ILE:O	1:E:300:ILE:HG22	2.15	0.46
1:E:309:PHE:HE1	1:F:151:SER:H	1.62	0.46
1:F:322:LEU:HD12	1:F:323:THR:OG1	2.16	0.46
1:H:249:ARG:HH11	1:H:252:LYS:C	2.23	0.46
1:H:574:LYS:O	1:H:592:TRP:NE1	2.49	0.46
1:I:110:ALA:HB1	1:I:148:PRO:HD2	1.98	0.46
1:I:496:VAL:HG13	1:I:497:VAL:N	2.31	0.46
1:I:557:PHE:CE2	1:I:568:MET:HE3	2.51	0.46
1:K:297:HIS:C	1:K:450:GLN:HE21	2.24	0.46
1:L:463:ILE:O	1:L:463:ILE:CG2	2.64	0.46
1:A:74:ASN:O	1:A:76:ILE:HG13	2.16	0.46
1:A:132:TYR:O	1:A:133:GLU:HG2	2.16	0.46
1:A:425:VAL:HG12	1:A:536:LEU:HD22	1.98	0.46
1:A:582:LYS:O	1:A:583:LYS:HD2	2.16	0.46
1:B:407:ALA:O	1:B:411:ALA:HB2	2.16	0.46
1:C:249:ARG:HD3	1:D:189:GLU:HG2	1.98	0.46
1:C:543:PRO:HG2	1:C:548:GLU:OE1	2.16	0.46
1:F:206:ASP:O	1:F:207:TRP:CG	2.69	0.46
1:F:327:GLN:O	1:F:331:ASN:ND2	2.48	0.46
1:F:438:LEU:O	1:F:441:ARG:HG2	2.16	0.46
1:G:99:ARG:O	1:G:103:ARG:HB2	2.15	0.46
1:G:110:ALA:CB	1:G:147:GLU:HA	2.44	0.46
1:G:128:LEU:H	1:G:300:ILE:CG2	2.29	0.46
1:G:330:ARG:O	1:G:333:ILE:HG12	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:592:TRP:O	1:G:593:LEU:C	2.59	0.46
1:H:172:HIS:CE1	1:H:175:VAL:HG22	2.51	0.46
1:I:45:LEU:HD12	1:I:46:SER:N	2.31	0.46
1:J:577:ILE:HG13	1:J:578:GLN:N	2.31	0.46
1:L:373:LEU:HD12	1:L:374:LEU:N	2.31	0.46
1:A:193:LEU:C	1:A:195:ALA:H	2.24	0.45
1:C:249:ARG:HH21	1:C:251:ILE:HD11	1.80	0.45
1:C:518:THR:HG23	1:C:520:VAL:HG23	1.98	0.45
1:D:163:LYS:HD2	1:E:149:ILE:HG12	1.98	0.45
1:E:509:ASP:O	1:E:510:ILE:C	2.60	0.45
1:F:40:GLN:HB3	1:F:41:TRP:HE3	1.81	0.45
1:H:57:PHE:O	1:H:59:VAL:HG13	2.15	0.45
1:J:60:VAL:HA	1:J:321:ARG:HH12	1.81	0.45
1:J:179:MET:CE	1:J:204:PRO:HD3	2.46	0.45
1:J:392:TYR:O	1:J:392:TYR:CG	2.70	0.45
1:A:337:ASN:HA	1:A:340:ILE:HG22	1.98	0.45
1:A:536:LEU:HD12	1:A:536:LEU:O	2.16	0.45
1:A:558:THR:HG22	1:A:559:LEU:HG	1.98	0.45
1:C:171:ARG:HG3	1:C:227:GLU:HA	1.99	0.45
1:C:280:ILE:HG23	1:C:281:ILE:H	1.81	0.45
1:C:535:ILE:HG23	1:C:536:LEU:N	2.31	0.45
1:E:164:LEU:HD11	1:F:107:ALA:HB1	1.97	0.45
1:E:306:GLU:C	1:E:307:TRP:HD1	2.24	0.45
1:G:163:LYS:HE2	1:H:149:ILE:HB	1.98	0.45
1:G:171:ARG:O	1:G:171:ARG:HG2	2.16	0.45
1:H:356:ILE:HD11	1:I:372:TYR:CE2	2.52	0.45
1:H:559:LEU:HD13	1:H:560:LEU:O	2.16	0.45
1:I:117:GLU:O	1:I:121:ALA:N	2.36	0.45
1:K:134:ASP:OD1	1:K:135:GLN:N	2.48	0.45
1:L:47:GLN:HB3	1:L:50:THR:HG21	1.98	0.45
1:L:546:THR:OG1	1:L:547:PRO:HD3	2.16	0.45
1:B:112:ASN:OD1	1:B:113:ILE:N	2.50	0.45
1:B:437:GLN:HA	1:B:440:MET:HG2	1.98	0.45
1:D:401:ASN:ND2	1:D:405:LEU:HB2	2.30	0.45
1:E:211:TRP:CD1	1:E:213:THR:H	2.34	0.45
1:F:438:LEU:HD11	1:G:109:ILE:HG22	1.99	0.45
1:G:88:PRO:HG3	1:H:563:LYS:HZ3	1.81	0.45
1:G:169:ASP:O	1:G:171:ARG:N	2.49	0.45
1:I:198:ILE:HD12	1:I:217:ILE:HA	1.98	0.45
1:I:437:GLN:NE2	1:I:520:VAL:CG1	2.79	0.45
1:L:306:GLU:O	1:L:307:TRP:HD1	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:330:ARG:HA	1:L:333:ILE:HD12	1.98	0.45
1:A:337:ASN:OD1	1:A:338:ALA:N	2.49	0.45
1:C:525:GLN:HB2	1:C:529:GLN:OE1	2.17	0.45
1:D:37:ARG:HH22	1:D:43:ASP:HA	1.82	0.45
1:D:329:LEU:O	1:D:332:MET:HB2	2.15	0.45
1:D:451:ASP:HB3	1:D:506:VAL:H	1.82	0.45
1:E:161:ASN:OD1	1:E:162:SER:N	2.50	0.45
1:E:403:TYR:OH	1:F:402:ALA:O	2.24	0.45
1:G:430:VAL:HG12	1:G:431:ALA:H	1.82	0.45
1:H:140:ASN:OD1	1:H:142:GLN:NE2	2.49	0.45
1:H:417:THR:O	1:H:418:LEU:HB2	2.16	0.45
1:I:144:ILE:HG22	1:I:145:ARG:N	2.31	0.45
1:K:280:ILE:HD12	1:K:286:VAL:HG21	1.97	0.45
1:A:21:ALA:HA	1:A:24:GLU:HG2	1.98	0.45
1:A:581:VAL:O	1:A:581:VAL:HG12	2.16	0.45
1:B:320:VAL:HG23	1:B:320:VAL:O	2.16	0.45
1:C:35:PHE:HZ	1:C:321:ARG:NH2	2.14	0.45
1:E:346:LYS:HD2	1:F:367:ASP:HB3	1.98	0.45
1:F:531:ASN:HB3	1:G:556:TYR:HE2	1.82	0.45
1:K:205:ASN:O	1:K:207:TRP:HE3	2.00	0.45
1:L:108:LYS:HG3	1:L:109:ILE:H	1.80	0.45
1:A:145:ARG:NH2	1:A:441:ARG:HE	2.15	0.45
1:A:232:ALA:O	1:A:234:ILE:HG12	2.16	0.45
1:C:61:ARG:N	1:C:62:PRO:HD3	2.32	0.45
1:C:387:GLN:OE1	1:D:385:PRO:HB3	2.17	0.45
1:D:164:LEU:HD12	1:E:147:GLU:OE1	2.17	0.45
1:D:350:PHE:HE1	1:D:363:TYR:HD2	1.63	0.45
1:E:311:GLU:O	1:E:312:ASP:OD1	2.34	0.45
1:F:91:ALA:O	1:F:92:ASP:OD1	2.35	0.45
1:F:322:LEU:HD12	1:F:323:THR:N	2.31	0.45
1:F:443:ASP:O	1:F:447:TYR:HD2	2.00	0.45
1:G:309:PHE:HB2	1:H:116:ARG:HH12	1.81	0.45
1:G:392:TYR:OH	1:H:351:PHE:HB3	2.17	0.45
1:G:462:GLU:O	1:G:463:ILE:HG22	2.17	0.45
1:I:276:VAL:O	1:I:278:LYS:NZ	2.47	0.45
1:J:280:ILE:HG13	1:J:281:ILE:H	1.81	0.45
1:J:579:MET:HE2	1:K:570:ASP:OD2	2.16	0.45
1:K:289:ASP:CG	1:K:290:LYS:H	2.24	0.45
1:K:528:LYS:HZ1	1:K:555:GLN:C	2.25	0.45
1:K:579:MET:HE3	1:K:581:VAL:HG12	1.98	0.45
1:L:88:PRO:O	1:L:89:ASP:OD1	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:270:GLN:O	1:L:271:ILE:HG13	2.17	0.45
1:A:458:ARG:O	1:A:459:ARG:HG3	2.16	0.45
1:B:431:ALA:HB2	1:C:72:ARG:NH2	2.32	0.45
1:C:346:LYS:NZ	1:D:363:TYR:OH	2.50	0.45
1:E:145:ARG:NH2	1:E:147:GLU:OE2	2.49	0.45
1:F:34:PHE:O	1:F:38:VAL:HG22	2.17	0.45
1:F:169:ASP:OD1	1:F:170:ALA:N	2.41	0.45
1:F:400:ALA:O	1:F:404:MET:HG3	2.16	0.45
1:H:172:HIS:HB2	1:H:298:ILE:HD13	1.98	0.45
1:H:258:LEU:O	1:H:261:SER:OG	2.30	0.45
1:H:494:ALA:HB1	1:H:497:VAL:HG22	1.99	0.45
1:I:198:ILE:HG23	1:I:218:GLN:H	1.81	0.45
1:J:485:GLY:HA3	1:J:488:LYS:HE2	1.99	0.45
1:L:280:ILE:HG23	1:L:281:ILE:H	1.80	0.45
1:L:491:GLN:HG3	1:L:492:LEU:HD13	1.99	0.45
1:A:135:GLN:OE1	1:A:135:GLN:N	2.49	0.45
1:B:156:VAL:HG22	1:B:158:TRP:HE1	1.81	0.45
1:B:196:ASP:HB3	1:B:198:ILE:HG13	1.99	0.45
1:D:485:GLY:O	1:D:488:LYS:NZ	2.31	0.45
1:E:50:THR:O	1:E:51:LEU:HD12	2.17	0.45
1:F:468:VAL:O	1:F:468:VAL:HG12	2.17	0.45
1:I:14:ARG:O	1:I:281:ILE:HB	2.17	0.45
1:I:263:PHE:HE2	1:I:265:LYS:HB2	1.82	0.45
1:I:422:THR:O	1:I:423:GLU:HG2	2.16	0.45
1:J:58:ASP:O	1:J:59:VAL:HG22	2.17	0.45
1:J:198:ILE:HA	1:J:217:ILE:HG23	1.98	0.45
1:K:589:GLU:HG2	1:K:590:GLN:H	1.81	0.45
1:B:147:GLU:HG2	1:B:148:PRO:O	2.16	0.45
1:C:44:TRP:CD1	1:C:50:THR:HG21	2.51	0.45
1:C:356:ILE:HG23	1:C:357:ALA:N	2.32	0.45
1:C:374:LEU:HD23	1:C:376:ARG:HH22	1.81	0.45
1:D:325:ASP:OD1	1:E:53:TYR:OH	2.34	0.45
1:E:223:TYR:CD1	1:E:291:GLN:HB2	2.52	0.45
1:E:469:ASN:OD1	1:E:472:TYR:HB2	2.17	0.45
1:F:24:GLU:HB2	1:F:28:GLU:HB2	1.98	0.45
1:G:53:TYR:CE2	1:G:339:ASP:HB2	2.52	0.45
1:G:390:ALA:O	1:G:391:TYR:HB2	2.17	0.45
1:I:272:LYS:O	1:I:272:LYS:HG3	2.16	0.45
1:I:292:LEU:HD21	1:I:294:ALA:O	2.17	0.45
1:K:274:ARG:HH12	1:K:276:VAL:HG22	1.82	0.45
1:A:257:ASP:OD1	1:A:257:ASP:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:158:TRP:CD1	1:B:172:HIS:CE1	3.04	0.45
1:B:331:ASN:O	1:B:335:SER:OG	2.23	0.45
1:D:12:LEU:HD21	1:D:16:ASP:HB2	1.98	0.45
1:D:198:ILE:HG23	1:D:198:ILE:O	2.16	0.45
1:E:121:ALA:HB3	1:E:153:CYS:HB3	1.99	0.45
1:E:208:VAL:HG13	1:E:209:PHE:N	2.32	0.45
1:F:467:ILE:HG22	1:F:468:VAL:N	2.32	0.45
1:K:297:HIS:C	1:K:450:GLN:NE2	2.75	0.45
1:L:138:THR:HG22	1:L:139:SER:N	2.32	0.45
1:L:280:ILE:HG12	1:L:281:ILE:N	2.32	0.45
1:L:352:TRP:N	1:L:353:PRO:CD	2.80	0.45
1:B:236:GLN:HG3	1:B:237:ASP:OD1	2.17	0.44
1:D:451:ASP:OD2	1:D:459:ARG:NH2	2.42	0.44
1:E:106:THR:O	1:E:109:ILE:HG22	2.17	0.44
1:E:438:LEU:O	1:E:441:ARG:NH2	2.50	0.44
1:E:440:MET:HG3	1:E:440:MET:O	2.17	0.44
1:E:552:LEU:HA	1:E:556:TYR:CE2	2.52	0.44
1:F:589:GLU:HG3	1:F:591:GLN:HE22	1.82	0.44
1:G:355:GLN:O	1:G:356:ILE:HG22	2.17	0.44
1:H:273:ARG:HD3	1:H:275:ARG:HE	1.81	0.44
1:H:468:VAL:HG12	1:H:468:VAL:O	2.17	0.44
1:H:541:LYS:HE2	1:I:535:ILE:HG12	1.99	0.44
1:I:425:VAL:HG13	1:I:425:VAL:O	2.17	0.44
1:J:356:ILE:HD11	1:K:371:TYR:O	2.18	0.44
1:K:346:LYS:HB3	1:L:371:TYR:HE2	1.81	0.44
1:A:161:ASN:HB2	1:A:167:LYS:HZ2	1.83	0.44
1:B:166:ASP:OD2	1:B:443:ASP:HA	2.18	0.44
1:B:441:ARG:NH2	1:B:518:THR:O	2.51	0.44
1:C:308:GLY:O	1:C:309:PHE:CD2	2.70	0.44
1:C:530:GLN:HA	1:C:533:ALA:HB2	1.99	0.44
1:F:110:ALA:O	1:F:113:ILE:HG22	2.17	0.44
1:G:223:TYR:CD2	1:G:224:GLU:HG3	2.52	0.44
1:I:70:GLU:OE1	1:I:70:GLU:N	2.48	0.44
1:I:352:TRP:NE1	1:I:376:ARG:HD2	2.33	0.44
1:I:459:ARG:HG3	1:I:462:GLU:HG2	1.98	0.44
1:J:582:LYS:O	1:J:583:LYS:C	2.61	0.44
1:K:184:TRP:HD1	1:K:187:PHE:CE2	2.35	0.44
1:B:170:ALA:O	1:B:171:ARG:HG2	2.17	0.44
1:B:581:VAL:HG12	1:B:582:LYS:N	2.32	0.44
1:C:350:PHE:CE1	1:C:353:PRO:HG3	2.53	0.44
1:C:407:ALA:HB1	1:D:330:ARG:HH12	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:479:THR:HG22	1:C:480:ILE:N	2.32	0.44
1:G:527:MET:HG3	1:G:527:MET:O	2.17	0.44
1:H:278:LYS:HD2	1:H:281:ILE:HD11	1.99	0.44
1:J:566:GLU:OE1	1:J:566:GLU:N	2.48	0.44
1:K:548:GLU:HA	1:K:551:LEU:HB3	1.98	0.44
1:L:136:SER:N	1:L:137:PRO:HD3	2.32	0.44
1:L:164:LEU:H	1:L:171:ARG:HH22	1.65	0.44
1:B:350:PHE:CZ	1:C:372:TYR:CE2	3.06	0.44
1:C:280:ILE:C	1:C:282:THR:H	2.26	0.44
1:C:476:ARG:HG3	1:C:477:ASN:N	2.33	0.44
1:D:209:PHE:CG	1:D:210:PRO:HD3	2.52	0.44
1:E:83:LYS:HE3	1:E:85:GLY:HA3	2.00	0.44
1:E:196:ASP:O	1:E:198:ILE:HG22	2.17	0.44
1:F:415:VAL:HG12	1:F:415:VAL:O	2.17	0.44
1:G:251:ILE:HG13	1:G:253:ASP:H	1.82	0.44
1:H:453:LEU:HD23	1:H:454:ALA:H	1.82	0.44
1:I:505:GLN:C	1:I:507:LEU:H	2.26	0.44
1:J:254:VAL:HG23	1:J:255:ILE:N	2.33	0.44
1:J:355:GLN:O	1:J:356:ILE:C	2.59	0.44
1:L:36:SER:O	1:L:39:SER:N	2.50	0.44
1:L:487:GLU:O	1:L:490:VAL:HG12	2.17	0.44
1:A:557:PHE:HB3	1:A:568:MET:SD	2.57	0.44
1:B:252:LYS:NZ	1:B:256:ASP:OD1	2.45	0.44
1:B:447:TYR:HB2	1:B:449:PHE:H	1.82	0.44
1:B:544:GLN:NE2	1:B:552:LEU:HD12	2.33	0.44
1:C:108:LYS:O	1:C:109:ILE:C	2.60	0.44
1:C:206:ASP:OD1	1:C:206:ASP:N	2.51	0.44
1:C:280:ILE:HA	1:C:288:LYS:HE3	2.00	0.44
1:C:435:VAL:O	1:C:438:LEU:HD13	2.17	0.44
1:C:444:LEU:HD21	1:D:105:ASN:ND2	2.33	0.44
1:C:449:PHE:CD2	1:C:450:GLN:HG2	2.53	0.44
1:D:362:MET:HG3	1:D:373:LEU:HD21	1.99	0.44
1:D:440:MET:HG2	1:E:106:THR:HG22	1.98	0.44
1:E:402:ALA:HA	1:E:405:LEU:HG	1.99	0.44
1:E:447:TYR:HB3	1:E:450:GLN:OE1	2.16	0.44
1:G:94:LEU:HA	1:G:97:MET:HE3	1.98	0.44
1:I:149:ILE:HG22	1:I:150:HIS:N	2.31	0.44
1:K:209:PHE:N	1:K:210:PRO:HD3	2.33	0.44
1:L:112:ASN:OD1	1:L:112:ASN:C	2.61	0.44
1:A:87:ARG:HG3	1:A:88:PRO:HD2	1.99	0.44
1:A:436:ASN:HA	1:A:439:ASN:OD1	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:539:LEU:HG	1:B:540:GLY:H	1.81	0.44
1:C:61:ARG:HG3	1:C:320:VAL:HG11	1.98	0.44
1:C:63:VAL:HG22	1:C:67:LEU:HD13	1.99	0.44
1:C:341:VAL:HG23	1:C:342:ALA:N	2.33	0.44
1:C:343:ARG:C	1:C:345:PRO:HD3	2.43	0.44
1:C:560:LEU:O	1:C:565:VAL:HG11	2.17	0.44
1:D:276:VAL:HG11	1:D:278:LYS:HE3	2.00	0.44
1:D:419:GLY:HA3	1:D:428:GLY:HA2	1.98	0.44
1:F:92:ASP:CG	1:F:93:VAL:H	2.25	0.44
1:H:299:PRO:O	1:H:301:VAL:HG23	2.18	0.44
1:H:356:ILE:HG23	1:H:357:ALA:N	2.33	0.44
1:H:462:GLU:O	1:H:464:TYR:HD2	2.01	0.44
1:I:28:GLU:HG3	1:I:29:ALA:H	1.83	0.44
1:I:384:LEU:HD11	1:J:385:PRO:HD3	1.99	0.44
1:I:496:VAL:HG13	1:I:497:VAL:H	1.82	0.44
1:I:496:VAL:HG22	1:I:497:VAL:H	1.82	0.44
1:K:211:TRP:CD1	1:K:212:LEU:HG	2.53	0.44
1:K:438:LEU:HD12	1:K:441:ARG:HH11	1.83	0.44
1:L:310:VAL:HG13	1:L:311:GLU:H	1.82	0.44
1:A:75:PRO:HD2	1:A:523:SER:OG	2.18	0.44
1:C:17:ALA:HA	1:C:19:TRP:CE3	2.53	0.44
1:C:165:MET:HE3	1:C:307:TRP:CH2	2.53	0.44
1:C:438:LEU:HD12	1:C:441:ARG:NH1	2.33	0.44
1:D:311:GLU:HG2	1:D:312:ASP:H	1.83	0.44
1:D:541:LYS:C	1:D:543:PRO:HD3	2.43	0.44
1:F:345:PRO:O	1:G:366:ASN:ND2	2.51	0.44
1:J:136:SER:N	1:J:137:PRO:HD3	2.32	0.44
1:J:375:ASN:OD1	1:J:376:ARG:N	2.48	0.44
1:K:128:LEU:HB3	1:K:300:ILE:HG22	1.99	0.44
1:L:280:ILE:HG23	1:L:281:ILE:N	2.33	0.44
1:B:27:ARG:O	1:B:31:ASN:N	2.37	0.44
1:B:119:ILE:HG23	1:B:120:GLU:H	1.82	0.44
1:C:82:PRO:HD2	1:D:563:LYS:HE2	2.00	0.44
1:C:229:LYS:HD2	1:C:296:GLU:OE2	2.18	0.44
1:C:496:VAL:O	1:C:496:VAL:HG12	2.18	0.44
1:D:145:ARG:HG2	1:D:146:ARG:HG3	1.98	0.44
1:F:113:ILE:HD11	1:F:116:ARG:CZ	2.48	0.44
1:H:67:LEU:HD11	1:H:416:ALA:HA	2.00	0.44
1:H:280:ILE:HG23	1:H:280:ILE:O	2.18	0.44
1:J:70:GLU:OE1	1:J:73:GLN:NE2	2.50	0.44
1:K:535:ILE:HG22	1:K:536:LEU:H	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:34:PHE:O	1:L:38:VAL:HG22	2.17	0.44
1:L:149:ILE:HG12	1:L:176:ILE:O	2.18	0.44
1:A:423:GLU:HG3	1:A:424:ALA:N	2.32	0.44
1:A:458:ARG:HG2	1:A:462:GLU:HG2	2.00	0.44
1:D:211:TRP:HE1	1:D:214:GLN:HG2	1.83	0.44
1:D:322:LEU:HD13	1:D:411:ALA:HB1	1.99	0.44
1:D:459:ARG:O	1:D:462:GLU:N	2.40	0.44
1:E:297:HIS:CE1	1:E:508:ASN:HB3	2.52	0.44
1:F:23:ASP:OD1	1:F:24:GLU:N	2.51	0.44
1:F:54:ARG:NH1	1:F:331:ASN:O	2.51	0.44
1:F:152:ALA:HA	1:F:155:HIS:CE1	2.52	0.44
1:F:244:VAL:HG13	1:F:244:VAL:O	2.18	0.44
1:F:417:THR:O	1:F:418:LEU:HD12	2.17	0.44
1:H:372:TYR:OH	1:H:375:ASN:OD1	2.18	0.44
1:H:436:ASN:ND2	1:H:439:ASN:OD1	2.35	0.44
1:H:488:LYS:HD2	1:H:493:MET:HE3	2.00	0.44
1:I:144:ILE:CG2	1:I:145:ARG:N	2.81	0.44
1:K:171:ARG:HE	1:K:226:VAL:H	1.64	0.44
1:K:451:ASP:OD1	1:K:451:ASP:O	2.36	0.44
1:A:146:ARG:HH12	1:A:441:ARG:CZ	2.30	0.43
1:E:545:GLY:HA2	1:F:549:TYR:CD1	2.53	0.43
1:G:112:ASN:O	1:G:115:VAL:HG22	2.17	0.43
1:H:126:TRP:CE2	1:H:152:ALA:HB3	2.53	0.43
1:K:198:ILE:O	1:K:198:ILE:HG23	2.18	0.43
1:K:351:PHE:O	1:K:352:TRP:HD1	2.01	0.43
1:L:275:ARG:HG2	1:L:276:VAL:N	2.32	0.43
1:B:439:ASN:HA	1:B:442:ALA:HB2	2.00	0.43
1:E:438:LEU:O	1:E:441:ARG:NE	2.50	0.43
1:E:462:GLU:C	1:E:464:TYR:H	2.25	0.43
1:F:14:ARG:O	1:F:17:ALA:HB3	2.18	0.43
1:F:65:ARG:HA	1:F:68:VAL:HG22	2.00	0.43
1:F:350:PHE:HZ	1:G:374:LEU:HD13	1.83	0.43
1:F:373:LEU:HD12	1:F:373:LEU:O	2.18	0.43
1:G:459:ARG:HG3	1:G:459:ARG:O	2.19	0.43
1:G:526:SER:HA	1:G:529:GLN:HB3	1.99	0.43
1:G:538:LEU:HB3	1:G:539:LEU:H	1.64	0.43
1:H:32:ASP:O	1:H:35:PHE:HD2	2.01	0.43
1:H:402:ALA:O	1:H:406:GLU:HG2	2.17	0.43
1:H:484:ASP:CG	1:H:485:GLY:H	2.25	0.43
1:J:322:LEU:O	1:J:324:LYS:N	2.51	0.43
1:J:457:MET:HE2	1:J:458:ARG:HG2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:548:GLU:O	1:J:551:LEU:N	2.51	0.43
1:J:576:LEU:HB3	1:J:580:GLY:H	1.83	0.43
1:K:273:ARG:HA	1:K:273:ARG:HD3	1.81	0.43
1:K:555:GLN:OE1	1:K:555:GLN:N	2.50	0.43
1:A:208:VAL:HG13	1:A:209:PHE:N	2.33	0.43
1:A:437:GLN:HB2	1:B:109:ILE:HD11	2.00	0.43
1:B:87:ARG:HG3	1:B:87:ARG:O	2.18	0.43
1:B:234:ILE:HG23	1:B:246:TYR:CE1	2.53	0.43
1:B:354:GLU:HB2	1:B:375:ASN:H	1.83	0.43
1:C:17:ALA:HA	1:C:19:TRP:CZ3	2.53	0.43
1:D:320:VAL:O	1:D:320:VAL:HG12	2.17	0.43
1:D:397:VAL:O	1:D:397:VAL:HG13	2.19	0.43
1:E:17:ALA:O	1:E:20:THR:OG1	2.21	0.43
1:E:32:ASP:O	1:E:35:PHE:CD2	2.71	0.43
1:F:467:ILE:HG22	1:F:468:VAL:H	1.83	0.43
1:G:44:TRP:CG	1:G:45:LEU:N	2.86	0.43
1:H:434:THR:HG22	1:H:520:VAL:HG21	1.99	0.43
1:I:24:GLU:HG3	1:I:24:GLU:O	2.18	0.43
1:J:418:LEU:HA	1:K:66:LYS:NZ	2.33	0.43
1:L:353:PRO:HA	1:L:373:LEU:HB2	2.00	0.43
1:B:584:PRO:HD3	1:C:567:MET:HE1	2.01	0.43
1:C:69:SER:HA	1:C:72:ARG:NH1	2.32	0.43
1:C:309:PHE:CE2	1:C:314:GLU:HA	2.53	0.43
1:C:337:ASN:O	1:C:341:VAL:HG22	2.19	0.43
1:C:403:TYR:CE1	1:D:402:ALA:HA	2.54	0.43
1:C:532:ARG:HE	1:C:558:THR:CG2	2.31	0.43
1:D:179:MET:HE1	1:D:214:GLN:OE1	2.18	0.43
1:D:183:GLY:HA2	1:D:186:ASP:HB2	2.00	0.43
1:E:303:VAL:O	1:E:303:VAL:HG13	2.18	0.43
1:G:41:TRP:CD1	1:G:42:ASP:H	2.35	0.43
1:G:234:ILE:HG23	1:G:235:TYR:HB3	2.00	0.43
1:G:266:ILE:HG23	1:G:266:ILE:O	2.18	0.43
1:G:306:GLU:O	1:G:307:TRP:HD1	2.01	0.43
1:G:444:LEU:HD22	1:G:517:TYR:CE1	2.54	0.43
1:G:474:VAL:HG13	1:G:475:PRO:HD2	2.00	0.43
1:H:273:ARG:HD3	1:H:275:ARG:NE	2.33	0.43
1:I:279:SER:O	1:I:280:ILE:HG12	2.18	0.43
1:I:280:ILE:HD13	1:I:288:LYS:HE2	2.01	0.43
1:J:63:VAL:O	1:J:66:LYS:HB2	2.18	0.43
1:J:499:LEU:HD12	1:J:500:ALA:H	1.83	0.43
1:K:441:ARG:O	1:K:445:GLU:N	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:451:ASP:OD1	1:L:453:LEU:HG	2.18	0.43
1:B:299:PRO:HA	1:B:443:ASP:OD1	2.18	0.43
1:C:546:THR:HA	1:C:549:TYR:HB2	2.01	0.43
1:D:328:ARG:O	1:D:332:MET:HG2	2.18	0.43
1:D:484:ASP:H	1:D:488:LYS:HE3	1.83	0.43
1:E:40:GLN:HG3	1:E:41:TRP:CD1	2.53	0.43
1:F:488:LYS:HG3	1:F:489:ASP:N	2.34	0.43
1:I:211:TRP:HE3	1:I:212:LEU:HD22	1.84	0.43
1:J:298:ILE:HG23	1:J:298:ILE:O	2.18	0.43
1:J:446:THR:O	1:J:446:THR:HG22	2.19	0.43
1:K:412:VAL:HA	1:K:415:VAL:HB	2.01	0.43
1:L:405:LEU:O	1:L:409:THR:N	2.39	0.43
1:A:124:GLY:HA2	1:A:155:HIS:HE2	1.83	0.43
1:A:186:ASP:HA	1:A:189:GLU:HG3	1.99	0.43
1:A:353:PRO:CB	1:A:356:ILE:HB	2.47	0.43
1:A:554:LEU:HD21	1:A:581:VAL:HG11	2.01	0.43
1:C:15:PHE:HD2	1:C:281:ILE:HG12	1.84	0.43
1:C:128:LEU:HG	1:C:300:ILE:HD13	2.00	0.43
1:C:478:VAL:O	1:C:479:THR:OG1	2.36	0.43
1:D:34:PHE:HA	1:D:37:ARG:HG2	2.00	0.43
1:E:161:ASN:OD1	1:E:161:ASN:C	2.61	0.43
1:E:254:VAL:HG12	1:E:254:VAL:O	2.19	0.43
1:E:415:VAL:O	1:E:415:VAL:HG12	2.18	0.43
1:F:355:GLN:O	1:F:356:ILE:HG22	2.19	0.43
1:F:484:ASP:OD1	1:F:488:LYS:HE2	2.19	0.43
1:J:165:MET:O	1:J:167:LYS:HG3	2.18	0.43
1:J:238:PRO:O	1:J:239:VAL:HG22	2.19	0.43
1:J:320:VAL:HB	1:J:321:ARG:HH21	1.83	0.43
1:J:539:LEU:CD2	1:J:540:GLY:H	2.32	0.43
1:L:457:MET:HG2	1:L:459:ARG:NH2	2.34	0.43
1:L:547:PRO:HG2	1:L:548:GLU:HG3	2.00	0.43
1:L:586:THR:OG1	1:L:587:PRO:HD2	2.18	0.43
1:B:66:LYS:O	1:B:69:SER:HB2	2.19	0.43
1:B:92:ASP:OD1	1:B:93:VAL:N	2.51	0.43
1:B:217:ILE:O	1:B:217:ILE:HG23	2.18	0.43
1:C:64:VAL:HG22	1:C:119:ILE:HG21	2.00	0.43
1:C:106:THR:O	1:C:109:ILE:HG12	2.19	0.43
1:E:362:MET:HG3	1:E:371:TYR:CB	2.48	0.43
1:E:375:ASN:OD1	1:E:377:THR:HG23	2.18	0.43
1:F:203:ASN:OD1	1:F:205:ASN:ND2	2.52	0.43
1:H:214:GLN:O	1:H:216:THR:HG23	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:161:ASN:O	1:J:162:SER:OG	2.28	0.43
1:K:81:ARG:HG2	1:K:519:ASP:HB3	2.00	0.43
1:K:183:GLY:C	1:K:185:GLU:N	2.76	0.43
1:K:338:ALA:HA	1:K:341:VAL:HG22	2.01	0.43
1:K:345:PRO:HB2	1:L:371:TYR:CE2	2.54	0.43
1:K:435:VAL:HG23	1:L:108:LYS:HB2	1.99	0.43
1:L:61:ARG:O	1:L:65:ARG:HG2	2.19	0.43
1:A:281:ILE:HG23	1:A:281:ILE:O	2.19	0.43
1:C:128:LEU:HB2	1:C:146:ARG:CG	2.49	0.43
1:D:98:TYR:CZ	1:D:444:LEU:HG	2.53	0.43
1:D:339:ASP:O	1:D:343:ARG:HB3	2.17	0.43
1:D:448:VAL:HG13	1:D:448:VAL:O	2.19	0.43
1:D:548:GLU:O	1:D:552:LEU:HG	2.19	0.43
1:D:582:LYS:HG3	1:D:583:LYS:N	2.33	0.43
1:E:297:HIS:O	1:E:298:ILE:HD13	2.19	0.43
1:F:317:GLU:HB3	1:F:321:ARG:HD3	2.01	0.43
1:G:461:GLY:C	1:G:463:ILE:H	2.26	0.43
1:H:47:GLN:HA	1:I:53:TYR:OH	2.18	0.43
1:I:58:ASP:CG	1:I:59:VAL:H	2.26	0.43
1:I:225:VAL:CG2	1:I:278:LYS:HD2	2.48	0.43
1:I:296:GLU:HG3	1:I:296:GLU:O	2.19	0.43
1:I:354:GLU:HB2	1:I:373:LEU:CD2	2.49	0.43
1:J:9:GLU:OE1	1:J:9:GLU:N	2.52	0.43
1:J:392:TYR:CE2	1:K:349:PRO:HB3	2.54	0.43
1:K:591:GLN:HG2	1:K:592:TRP:H	1.83	0.43
1:L:132:TYR:CG	1:L:133:GLU:N	2.87	0.43
1:L:337:ASN:OD1	1:L:337:ASN:N	2.52	0.43
1:A:102:MET:HA	1:A:108:LYS:HD3	2.00	0.43
1:A:339:ASP:HA	1:A:342:ALA:HB3	2.01	0.43
1:B:205:ASN:OD1	1:B:211:TRP:NE1	2.36	0.43
1:C:109:ILE:O	1:C:113:ILE:HG12	2.19	0.43
1:C:280:ILE:HG23	1:C:281:ILE:N	2.34	0.43
1:C:321:ARG:NH1	1:D:41:TRP:HE1	2.16	0.43
1:D:68:VAL:O	1:D:72:ARG:HB3	2.19	0.43
1:D:512:GLY:H	1:D:514:TYR:HD2	1.65	0.43
1:E:119:ILE:HG22	1:E:120:GLU:H	1.83	0.43
1:F:81:ARG:O	1:F:83:LYS:NZ	2.48	0.43
1:I:207:TRP:CD1	1:I:208:VAL:HG23	2.53	0.43
1:I:541:LYS:HD3	1:J:532:ARG:HH22	1.84	0.43
1:J:534:GLU:O	1:J:536:LEU:N	2.52	0.43
1:K:76:ILE:HG23	1:K:76:ILE:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:266:ILE:O	1:K:266:ILE:HG23	2.18	0.43
1:A:391:TYR:CE2	1:B:349:PRO:HG3	2.54	0.43
1:B:296:GLU:O	1:B:296:GLU:HG2	2.19	0.43
1:C:93:VAL:O	1:C:93:VAL:HG12	2.19	0.43
1:C:171:ARG:HG3	1:C:227:GLU:H	1.84	0.43
1:D:235:TYR:HD2	1:D:258:LEU:H	1.67	0.43
1:E:274:ARG:O	1:E:274:ARG:HG3	2.19	0.43
1:E:362:MET:HE2	1:E:371:TYR:HB2	1.99	0.43
1:F:322:LEU:HD13	1:F:412:VAL:O	2.19	0.43
1:F:468:VAL:O	1:F:471:ILE:HD12	2.18	0.43
1:F:553:LEU:HD23	1:F:573:ASN:ND2	2.34	0.43
1:G:127:ARG:H	1:G:146:ARG:HH22	1.67	0.43
1:G:241:GLY:C	1:G:243:PRO:HD3	2.44	0.43
1:G:331:ASN:O	1:G:334:MET:HB2	2.19	0.43
1:H:387:GLN:HG3	1:H:389:LEU:HD13	2.01	0.43
1:I:348:LYS:HG3	1:I:348:LYS:O	2.19	0.43
1:I:576:LEU:HG	1:I:581:VAL:HG12	2.01	0.43
1:J:116:ARG:NH2	1:J:120:GLU:OE2	2.47	0.43
1:J:400:ALA:HA	1:J:403:TYR:CZ	2.54	0.43
1:L:126:TRP:HA	1:L:148:PRO:HA	2.00	0.43
1:L:187:PHE:CE2	1:L:219:ILE:HG21	2.54	0.43
1:L:527:MET:CE	1:L:528:LYS:H	2.32	0.43
1:A:496:VAL:HG13	1:A:497:VAL:N	2.34	0.42
1:B:32:ASP:OD2	1:B:154:SER:HB3	2.19	0.42
1:C:34:PHE:HZ	1:C:45:LEU:HD21	1.83	0.42
1:C:156:VAL:HG13	1:C:158:TRP:CE2	2.54	0.42
1:F:35:PHE:HB3	1:F:120:GLU:O	2.19	0.42
1:F:40:GLN:HB3	1:F:41:TRP:CE3	2.54	0.42
1:F:233:PHE:CE2	1:F:271:ILE:HD12	2.54	0.42
1:F:575:GLN:HG3	1:F:576:LEU:H	1.84	0.42
1:H:80:TYR:CD1	1:H:80:TYR:O	2.72	0.42
1:I:51:LEU:HG	1:I:52:GLN:H	1.83	0.42
1:I:246:TYR:O	1:I:246:TYR:CG	2.72	0.42
1:I:255:ILE:HG22	1:I:256:ASP:H	1.84	0.42
1:K:187:PHE:HB2	1:K:190:LYS:HB2	2.00	0.42
1:K:337:ASN:HA	1:K:340:ILE:HG22	2.00	0.42
1:L:67:LEU:HD21	1:L:416:ALA:O	2.19	0.42
1:A:179:MET:N	1:A:218:GLN:OE1	2.36	0.42
1:A:296:GLU:OE1	1:A:450:GLN:HB3	2.19	0.42
1:B:240:THR:O	1:B:240:THR:HG22	2.18	0.42
1:C:559:LEU:O	1:C:560:LEU:HD12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:54:ARG:NH2	1:F:331:ASN:O	2.49	0.42
1:F:528:LYS:HZ1	1:G:564:GLY:HA3	1.84	0.42
1:H:106:THR:OG1	1:H:145:ARG:NH2	2.35	0.42
1:H:324:LYS:O	1:H:327:GLN:HB2	2.19	0.42
1:I:277:TYR:CZ	1:I:279:SER:HB2	2.54	0.42
1:I:286:VAL:HG23	1:I:288:LYS:HD3	2.01	0.42
1:I:447:TYR:CD1	1:I:447:TYR:O	2.72	0.42
1:I:589:GLU:OE1	1:I:589:GLU:N	2.39	0.42
1:J:185:GLU:O	1:J:185:GLU:HG2	2.19	0.42
1:J:417:THR:O	1:J:418:LEU:HD12	2.18	0.42
1:K:306:GLU:HG3	1:K:316:TYR:OH	2.19	0.42
1:L:31:ASN:HA	1:L:34:PHE:HB2	2.01	0.42
1:A:339:ASP:OD1	1:A:343:ARG:NH1	2.52	0.42
1:A:397:VAL:O	1:A:397:VAL:HG13	2.19	0.42
1:B:126:TRP:CZ3	1:B:128:LEU:HB2	2.54	0.42
1:B:160:SER:HB2	1:B:171:ARG:HE	1.83	0.42
1:C:65:ARG:NH1	1:C:65:ARG:O	2.45	0.42
1:C:539:LEU:HD23	1:C:540:GLY:N	2.34	0.42
1:D:33:LEU:O	1:D:37:ARG:HG2	2.18	0.42
1:D:60:VAL:O	1:D:60:VAL:HG12	2.18	0.42
1:D:401:ASN:ND2	1:D:401:ASN:O	2.53	0.42
1:H:517:TYR:CD1	1:I:103:ARG:HD3	2.55	0.42
1:I:74:ASN:O	1:I:76:ILE:HD12	2.19	0.42
1:I:173:CYS:HA	1:I:225:VAL:HG12	2.00	0.42
1:I:392:TYR:CG	1:I:393:GLU:N	2.87	0.42
1:J:548:GLU:O	1:J:548:GLU:HG2	2.19	0.42
1:K:208:VAL:C	1:K:210:PRO:HD3	2.44	0.42
1:L:98:TYR:HE1	1:L:447:TYR:CG	2.38	0.42
1:A:169:ASP:OD1	1:A:170:ALA:N	2.49	0.42
1:A:240:THR:HG22	1:A:240:THR:O	2.20	0.42
1:A:350:PHE:HA	1:A:353:PRO:HD2	2.02	0.42
1:A:369:TYR:HB2	1:A:370:PRO:HD3	2.00	0.42
1:B:280:ILE:HG13	1:B:281:ILE:N	2.32	0.42
1:B:354:GLU:HG3	1:B:354:GLU:O	2.19	0.42
1:B:527:MET:CG	1:B:528:LYS:H	2.30	0.42
1:B:583:LYS:HE2	1:C:563:LYS:HD2	2.00	0.42
1:B:583:LYS:N	1:C:564:GLY:HA3	2.35	0.42
1:D:98:TYR:HA	1:D:101:ASP:OD1	2.19	0.42
1:E:506:VAL:HG21	1:E:510:ILE:HG21	2.01	0.42
1:E:567:MET:HG3	1:E:570:ASP:HB2	2.00	0.42
1:G:309:PHE:HB3	1:H:150:HIS:NE2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:347:LYS:HG2	1:G:393:GLU:HG3	2.00	0.42
1:H:81:ARG:HD3	1:H:517:TYR:HB2	2.02	0.42
1:J:586:THR:N	1:J:587:PRO:HD3	2.35	0.42
1:K:171:ARG:NE	1:K:226:VAL:H	2.17	0.42
1:K:304:PHE:CZ	1:K:307:TRP:HB2	2.54	0.42
1:K:532:ARG:HG3	1:K:541:LYS:HG3	2.01	0.42
1:B:35:PHE:CZ	1:B:317:GLU:HG3	2.54	0.42
1:B:544:GLN:HA	1:B:548:GLU:OE1	2.19	0.42
1:C:403:TYR:OH	1:D:401:ASN:HB3	2.20	0.42
1:C:463:ILE:HG22	1:C:463:ILE:O	2.18	0.42
1:D:348:LYS:HA	1:D:348:LYS:HD3	1.74	0.42
1:E:100:THR:HA	1:E:102:MET:HG2	2.01	0.42
1:E:297:HIS:CE1	1:E:451:ASP:H	2.37	0.42
1:E:463:ILE:O	1:E:463:ILE:HG22	2.19	0.42
1:E:505:GLN:C	1:E:506:VAL:HG22	2.45	0.42
1:E:518:THR:OG1	1:E:520:VAL:HG23	2.19	0.42
1:H:32:ASP:O	1:H:34:PHE:N	2.53	0.42
1:H:310:VAL:O	1:H:311:GLU:HB2	2.20	0.42
1:I:464:TYR:HE1	1:I:465:GLN:HE21	1.68	0.42
1:J:165:MET:HB3	1:J:307:TRP:CH2	2.54	0.42
1:K:116:ARG:O	1:K:120:GLU:HB2	2.19	0.42
1:K:153:CYS:SG	1:K:154:SER:N	2.90	0.42
1:K:423:GLU:CD	1:K:424:ALA:N	2.77	0.42
1:K:451:ASP:OD1	1:K:451:ASP:C	2.62	0.42
1:L:341:VAL:O	1:L:344:THR:OG1	2.34	0.42
1:A:11:ILE:HG22	1:A:11:ILE:O	2.19	0.42
1:A:212:LEU:O	1:A:214:GLN:HG3	2.19	0.42
1:B:286:VAL:C	1:B:287:LEU:HD12	2.45	0.42
1:D:164:LEU:HG	1:D:166:ASP:O	2.20	0.42
1:E:340:ILE:O	1:E:344:THR:HG23	2.19	0.42
1:H:106:THR:HG1	1:H:145:ARG:HH21	1.61	0.42
1:H:127:ARG:NH2	1:H:149:ILE:HD11	2.33	0.42
1:H:297:HIS:O	1:H:298:ILE:HG13	2.20	0.42
1:L:162:SER:O	1:L:163:LYS:HB2	2.20	0.42
1:L:441:ARG:HG3	1:L:444:LEU:HB3	2.02	0.42
1:A:180:SER:C	1:A:183:GLY:H	2.28	0.42
1:B:397:VAL:O	1:B:398:PRO:C	2.63	0.42
1:B:462:GLU:C	1:B:464:TYR:H	2.26	0.42
1:C:254:VAL:O	1:C:254:VAL:HG12	2.19	0.42
1:D:239:VAL:HG13	1:D:240:THR:N	2.35	0.42
1:D:275:ARG:HH21	1:D:290:LYS:HD3	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:535:ILE:HG13	1:E:536:LEU:H	1.84	0.42
1:F:43:ASP:HB2	1:F:328:ARG:HH22	1.85	0.42
1:G:476:ARG:HG2	1:G:477:ASN:H	1.83	0.42
1:H:165:MET:HE1	1:H:304:PHE:H	1.85	0.42
1:I:306:GLU:O	1:I:307:TRP:HD1	2.03	0.42
1:I:370:PRO:HB2	1:I:372:TYR:CD2	2.55	0.42
1:I:574:LYS:O	1:I:577:ILE:HG23	2.20	0.42
1:K:87:ARG:HB2	1:K:88:PRO:HD2	2.02	0.42
1:K:177:HIS:O	1:K:178:SER:OG	2.26	0.42
1:K:184:TRP:HB3	1:K:187:PHE:CZ	2.55	0.42
1:L:571:TYR:CG	1:L:571:TYR:O	2.73	0.42
1:A:264:ILE:O	1:A:266:ILE:HD12	2.20	0.42
1:A:346:LYS:HG3	1:B:369:TYR:HB3	2.01	0.42
1:A:352:TRP:N	1:A:353:PRO:CD	2.82	0.42
1:A:503:GLU:HG2	1:A:504:LYS:O	2.19	0.42
1:B:296:GLU:O	1:B:297:HIS:ND1	2.53	0.42
1:C:351:PHE:HB3	1:C:352:TRP:CE3	2.55	0.42
1:C:582:LYS:HG2	1:D:566:GLU:HB2	2.01	0.42
1:E:132:TYR:OH	1:E:137:PRO:HG2	2.20	0.42
1:E:517:TYR:CD2	1:E:518:THR:HG22	2.55	0.42
1:F:350:PHE:HB2	1:F:353:PRO:HG2	2.01	0.42
1:F:356:ILE:HG23	1:F:357:ALA:N	2.34	0.42
1:G:44:TRP:CG	1:G:45:LEU:H	2.37	0.42
1:G:248:LYS:NZ	1:H:188:ALA:O	2.37	0.42
1:G:348:LYS:HE2	1:G:350:PHE:HB2	2.01	0.42
1:G:430:VAL:HG12	1:G:431:ALA:N	2.35	0.42
1:H:356:ILE:HG12	1:H:357:ALA:N	2.33	0.42
1:H:471:ILE:HD13	1:H:496:VAL:HA	2.01	0.42
1:J:126:TRP:NE1	1:J:146:ARG:HB2	2.35	0.42
1:J:170:ALA:O	1:J:171:ARG:HB2	2.20	0.42
1:J:345:PRO:HB3	1:K:371:TYR:OH	2.20	0.42
1:K:324:LYS:HD3	1:L:53:TYR:OH	2.20	0.42
1:A:28:GLU:OE2	1:A:31:ASN:ND2	2.52	0.42
1:A:111:VAL:O	1:A:115:VAL:HG13	2.19	0.42
1:A:329:LEU:HD12	1:A:330:ARG:N	2.35	0.42
1:C:345:PRO:O	1:C:346:LYS:C	2.63	0.42
1:C:352:TRP:O	1:C:352:TRP:CD1	2.73	0.42
1:C:408:ALA:O	1:C:412:VAL:HG23	2.20	0.42
1:D:463:ILE:O	1:D:463:ILE:HG22	2.20	0.42
1:E:91:ALA:HA	1:E:457:MET:HE1	2.02	0.42
1:F:61:ARG:O	1:F:64:VAL:HG12	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:406:GLU:O	1:F:409:THR:OG1	2.29	0.42
1:G:31:ASN:O	1:G:34:PHE:HD2	2.03	0.42
1:H:109:ILE:O	1:H:111:VAL:N	2.53	0.42
1:H:282:THR:HG22	1:H:283:CYS:N	2.35	0.42
1:I:111:VAL:O	1:I:115:VAL:HG23	2.20	0.42
1:I:345:PRO:HB3	1:I:392:TYR:CZ	2.54	0.42
1:I:387:GLN:HB3	1:I:389:LEU:HD13	2.01	0.42
1:K:324:LYS:HG3	1:L:56:GLN:O	2.19	0.42
1:B:43:ASP:C	1:B:44:TRP:CD1	2.98	0.42
1:B:43:ASP:HB3	1:B:47:GLN:HE22	1.84	0.42
1:B:453:LEU:CD1	1:B:453:LEU:H	2.33	0.42
1:C:378:ASP:HB2	1:C:381:SER:HB3	2.02	0.42
1:D:12:LEU:HG	1:D:15:PHE:HB3	2.00	0.42
1:D:109:ILE:HG22	1:D:109:ILE:O	2.19	0.42
1:D:567:MET:HG2	1:D:568:MET:N	2.33	0.42
1:E:183:GLY:O	1:E:186:ASP:HB2	2.20	0.42
1:E:192:ASP:OD1	1:E:193:LEU:N	2.52	0.42
1:E:506:VAL:HG23	1:E:508:ASN:H	1.83	0.42
1:G:156:VAL:HG13	1:G:176:ILE:HD12	2.02	0.42
1:H:358:GLY:O	1:H:359:PHE:C	2.62	0.42
1:K:66:LYS:O	1:K:70:GLU:N	2.52	0.42
1:L:527:MET:HG3	1:L:528:LYS:N	2.35	0.42
1:L:558:THR:HG23	1:L:559:LEU:N	2.34	0.42
1:B:435:VAL:O	1:B:438:LEU:HG	2.20	0.41
1:C:76:ILE:O	1:C:76:ILE:HG22	2.19	0.41
1:C:441:ARG:C	1:C:443:ASP:N	2.78	0.41
1:C:444:LEU:HD21	1:D:105:ASN:HD21	1.84	0.41
1:C:451:ASP:OD1	1:C:452:ASN:N	2.53	0.41
1:G:107:ALA:HB1	1:G:145:ARG:O	2.20	0.41
1:H:63:VAL:HG22	1:H:415:VAL:HG21	2.01	0.41
1:H:104:HIS:CE1	1:H:105:ASN:HD22	2.38	0.41
1:H:332:MET:O	1:H:335:SER:HB3	2.20	0.41
1:K:107:ALA:HB2	1:K:146:ARG:O	2.20	0.41
1:K:551:LEU:O	1:K:555:GLN:HB2	2.20	0.41
1:L:164:LEU:H	1:L:171:ARG:HH12	1.66	0.41
1:L:276:VAL:CG2	1:L:277:TYR:HD2	2.33	0.41
1:L:288:LYS:NZ	1:L:291:GLN:OE1	2.41	0.41
1:L:311:GLU:HG2	1:L:312:ASP:N	2.35	0.41
1:A:77:ASP:OD2	1:A:525:GLN:NE2	2.53	0.41
1:A:376:ARG:HD2	1:L:384:LEU:HD21	2.02	0.41
1:B:255:ILE:O	1:B:255:ILE:HG22	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:353:PRO:HA	1:B:374:LEU:HG	2.01	0.41
1:D:172:HIS:CE1	1:D:303:VAL:HB	2.55	0.41
1:E:165:MET:HB2	1:E:304:PHE:HA	2.03	0.41
1:G:230:GLU:HG2	1:G:248:LYS:HG2	2.02	0.41
1:I:410:SER:HA	1:I:413:LYS:HG2	2.02	0.41
1:I:447:TYR:HB2	1:I:451:ASP:HA	2.01	0.41
1:J:280:ILE:HG23	1:J:281:ILE:N	2.34	0.41
1:A:68:VAL:HA	1:A:71:MET:HG2	2.01	0.41
1:A:109:ILE:HG13	1:A:112:ASN:HB3	2.03	0.41
1:A:193:LEU:C	1:A:195:ALA:N	2.77	0.41
1:A:320:VAL:HG12	1:A:324:LYS:HD2	2.02	0.41
1:C:226:VAL:O	1:C:226:VAL:HG13	2.19	0.41
1:C:341:VAL:HG23	1:C:342:ALA:H	1.85	0.41
1:C:343:ARG:O	1:C:345:PRO:HD3	2.20	0.41
1:C:532:ARG:HH21	1:C:558:THR:HA	1.84	0.41
1:C:558:THR:HG22	1:C:559:LEU:N	2.35	0.41
1:D:345:PRO:HB3	1:D:348:LYS:CE	2.50	0.41
1:E:242:GLU:N	1:E:243:PRO:HD3	2.35	0.41
1:E:282:THR:HG21	1:E:286:VAL:HG13	2.03	0.41
1:E:297:HIS:HB3	1:E:450:GLN:HG3	2.01	0.41
1:F:209:PHE:N	1:F:210:PRO:HD3	2.36	0.41
1:F:442:ALA:O	1:F:446:THR:HG23	2.20	0.41
1:H:452:ASN:OD1	1:H:452:ASN:N	2.53	0.41
1:I:581:VAL:HG23	1:I:583:LYS:N	2.34	0.41
1:J:266:ILE:HG23	1:J:266:ILE:O	2.20	0.41
1:J:324:LYS:HB2	1:K:56:GLN:OE1	2.20	0.41
1:J:459:ARG:CZ	1:J:504:LYS:HA	2.50	0.41
1:A:128:LEU:O	1:A:130:THR:N	2.53	0.41
1:A:511:ARG:HE	1:B:136:SER:HB3	1.85	0.41
1:B:20:THR:HA	1:B:23:ASP:HB3	2.02	0.41
1:B:66:LYS:HD2	1:B:66:LYS:N	2.35	0.41
1:B:392:TYR:O	1:B:393:GLU:HG3	2.20	0.41
1:C:118:GLN:OE1	1:C:432:PHE:HB3	2.21	0.41
1:C:124:GLY:HA3	1:C:152:ALA:HB3	2.01	0.41
1:C:132:TYR:CE1	1:C:455:THR:HG23	2.55	0.41
1:C:139:SER:O	1:C:142:GLN:NE2	2.51	0.41
1:C:524:PHE:HB2	1:C:530:GLN:HB2	2.02	0.41
1:E:580:GLY:HA3	1:F:571:TYR:CE1	2.54	0.41
1:E:592:TRP:C	1:E:593:LEU:HD12	2.45	0.41
1:F:32:ASP:HA	1:F:35:PHE:HB2	2.03	0.41
1:F:61:ARG:O	1:F:62:PRO:C	2.64	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:220:ALA:O	1:F:288:LYS:NZ	2.48	0.41
1:F:289:ASP:OD1	1:F:290:LYS:N	2.53	0.41
1:F:528:LYS:HZ1	1:G:564:GLY:H	1.67	0.41
1:G:61:ARG:N	1:G:62:PRO:CD	2.82	0.41
1:G:156:VAL:HG12	1:G:158:TRP:CE3	2.55	0.41
1:I:170:ALA:HA	1:I:228:LYS:HE3	2.01	0.41
1:K:184:TRP:NE1	1:K:195:ALA:HB1	2.35	0.41
1:K:240:THR:O	1:K:240:THR:HG22	2.20	0.41
1:L:322:LEU:HD11	1:L:411:ALA:HB1	2.02	0.41
1:A:155:HIS:CE1	1:A:156:VAL:HG12	2.55	0.41
1:A:386:THR:HB	1:B:352:TRP:CH2	2.56	0.41
1:C:234:ILE:HG13	1:C:234:ILE:O	2.20	0.41
1:C:356:ILE:HG23	1:C:357:ALA:H	1.85	0.41
1:D:137:PRO:C	1:D:138:THR:HG1	2.20	0.41
1:D:343:ARG:O	1:E:366:ASN:ND2	2.53	0.41
1:D:549:TYR:HA	1:D:552:LEU:HD12	2.02	0.41
1:E:224:GLU:OE1	1:E:226:VAL:N	2.52	0.41
1:F:528:LYS:HZ1	1:G:564:GLY:N	2.18	0.41
1:G:48:TYR:O	1:G:49:THR:C	2.62	0.41
1:G:234:ILE:HG13	1:G:235:TYR:N	2.35	0.41
1:H:441:ARG:HH21	1:H:516:CYS:HB3	1.86	0.41
1:H:481:THR:O	1:H:482:LEU:HD12	2.20	0.41
1:I:86:ALA:O	1:I:88:PRO:HD3	2.19	0.41
1:K:59:VAL:O	1:K:62:PRO:HD2	2.20	0.41
1:K:179:MET:C	1:K:180:SER:HG	2.11	0.41
1:K:311:GLU:O	1:K:314:GLU:OE2	2.39	0.41
1:B:508:ASN:O	1:B:510:ILE:HG12	2.20	0.41
1:C:38:VAL:HB	1:C:60:VAL:HB	2.02	0.41
1:C:40:GLN:HG2	1:C:41:TRP:N	2.36	0.41
1:C:432:PHE:HB3	1:C:436:ASN:ND2	2.36	0.41
1:D:189:GLU:C	1:D:190:LYS:O	2.63	0.41
1:D:211:TRP:NE1	1:D:214:GLN:HG2	2.35	0.41
1:D:332:MET:HE1	1:E:341:VAL:CG2	2.51	0.41
1:D:332:MET:HE3	1:D:332:MET:HB3	1.86	0.41
1:D:471:ILE:HG23	1:D:472:TYR:N	2.36	0.41
1:E:234:ILE:HG21	1:E:245:SER:O	2.20	0.41
1:F:222:PHE:HD2	1:F:225:VAL:HG22	1.85	0.41
1:G:16:ASP:O	1:G:20:THR:HG23	2.21	0.41
1:G:310:VAL:N	1:G:314:GLU:OE1	2.54	0.41
1:H:15:PHE:HB3	1:H:281:ILE:CG2	2.49	0.41
1:I:106:THR:O	1:I:109:ILE:HG22	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:144:ILE:HD13	1:I:445:GLU:O	2.21	0.41
1:I:279:SER:O	1:I:280:ILE:CG1	2.68	0.41
1:I:353:PRO:O	1:I:354:GLU:C	2.63	0.41
1:I:449:PHE:HE1	1:I:511:ARG:NH2	2.19	0.41
1:J:93:VAL:HG12	1:J:94:LEU:HD12	2.02	0.41
1:K:105:ASN:HD21	1:K:107:ALA:HB3	1.85	0.41
1:A:459:ARG:O	1:A:462:GLU:N	2.54	0.41
1:A:550:GLN:O	1:A:553:LEU:HB3	2.20	0.41
1:B:311:GLU:O	1:B:312:ASP:OD1	2.39	0.41
1:C:57:PHE:HB2	1:C:327:GLN:NE2	2.35	0.41
1:D:188:ALA:C	1:D:190:LYS:N	2.79	0.41
1:E:314:GLU:HG2	1:E:314:GLU:O	2.21	0.41
1:F:73:GLN:HG3	1:F:73:GLN:O	2.21	0.41
1:G:444:LEU:HD22	1:G:517:TYR:CD1	2.55	0.41
1:H:11:ILE:HG23	1:H:277:TYR:HB3	2.02	0.41
1:H:351:PHE:C	1:H:353:PRO:HD3	2.45	0.41
1:I:58:ASP:OD2	1:I:61:ARG:NH2	2.53	0.41
1:J:83:LYS:HD3	1:K:100:THR:HG22	2.02	0.41
1:J:163:LYS:O	1:J:307:TRP:NE1	2.53	0.41
1:J:220:ALA:HB3	1:J:222:PHE:HE2	1.85	0.41
1:J:258:LEU:HD23	1:J:258:LEU:O	2.20	0.41
1:K:83:LYS:HG3	1:K:85:GLY:H	1.86	0.41
1:K:213:THR:HG23	1:K:213:THR:O	2.19	0.41
1:L:126:TRP:CZ2	1:L:146:ARG:HA	2.55	0.41
1:A:93:VAL:O	1:A:93:VAL:HG12	2.21	0.41
1:A:541:LYS:HD3	1:A:541:LYS:HA	1.90	0.41
1:C:128:LEU:HD12	1:C:128:LEU:O	2.20	0.41
1:C:153:CYS:SG	1:C:154:SER:N	2.93	0.41
1:D:114:ALA:O	1:D:117:GLU:HG2	2.20	0.41
1:E:58:ASP:OD2	1:E:61:ARG:NH2	2.54	0.41
1:E:135:GLN:O	1:E:137:PRO:HD3	2.20	0.41
1:E:172:HIS:CE1	1:E:174:THR:O	2.73	0.41
1:F:39:SER:O	1:F:60:VAL:HG11	2.20	0.41
1:F:405:LEU:O	1:F:409:THR:HG23	2.21	0.41
1:G:564:GLY:O	1:G:567:MET:HG3	2.20	0.41
1:H:26:ARG:HH22	1:H:313:LYS:HE3	1.85	0.41
1:H:146:ARG:HD3	1:H:300:ILE:HA	2.02	0.41
1:H:227:GLU:OE2	1:H:229:LYS:HB2	2.21	0.41
1:H:507:LEU:H	1:H:513:ARG:HE	1.67	0.41
1:I:34:PHE:O	1:I:38:VAL:N	2.48	0.41
1:I:354:GLU:HB2	1:I:373:LEU:HD22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:361:HIS:NE2	1:I:366:ASN:HB3	2.35	0.41
1:J:244:VAL:O	1:J:244:VAL:HG13	2.21	0.41
1:A:151:SER:OG	1:L:309:PHE:N	2.47	0.41
1:A:268:GLU:O	1:A:269:ARG:NH1	2.52	0.41
1:A:323:THR:HA	1:A:327:GLN:NE2	2.35	0.41
1:B:125:ALA:H	1:B:148:PRO:HB3	1.86	0.41
1:B:243:PRO:C	1:B:245:SER:H	2.29	0.41
1:B:565:VAL:HG12	1:B:565:VAL:O	2.21	0.41
1:C:126:TRP:CD1	1:C:128:LEU:HD23	2.56	0.41
1:C:400:ALA:HB1	1:C:404:MET:HE3	2.03	0.41
1:D:40:GLN:HG3	1:D:41:TRP:HE3	1.85	0.41
1:D:131:ASP:O	1:D:133:GLU:HG3	2.21	0.41
1:D:304:PHE:CD2	1:D:438:LEU:HD22	2.56	0.41
1:E:454:ALA:HA	1:E:459:ARG:HH12	1.86	0.41
1:F:117:GLU:OE1	1:F:117:GLU:N	2.49	0.41
1:G:58:ASP:O	1:G:59:VAL:HG12	2.21	0.41
1:G:135:GLN:O	1:G:136:SER:OG	2.36	0.41
1:G:356:ILE:HG23	1:G:357:ALA:N	2.35	0.41
1:H:337:ASN:O	1:H:340:ILE:HG13	2.21	0.41
1:I:327:GLN:C	1:I:329:LEU:N	2.77	0.41
1:I:468:VAL:HG13	1:I:471:ILE:HD12	2.01	0.41
1:J:394:ASN:OD1	1:J:394:ASN:N	2.54	0.41
1:K:121:ALA:O	1:K:122:GLY:C	2.64	0.41
1:K:430:VAL:HG12	1:K:431:ALA:N	2.34	0.41
1:L:79:LEU:O	1:L:79:LEU:HD12	2.21	0.41
1:L:347:LYS:HD2	1:L:347:LYS:N	2.36	0.41
1:A:300:ILE:O	1:A:300:ILE:CG2	2.69	0.41
1:A:441:ARG:HG3	1:A:442:ALA:H	1.86	0.41
1:B:488:LYS:HG2	1:B:489:ASP:N	2.36	0.41
1:C:15:PHE:CD2	1:C:281:ILE:HG12	2.55	0.41
1:C:351:PHE:C	1:C:353:PRO:HD3	2.46	0.41
1:D:332:MET:HE1	1:E:341:VAL:CB	2.50	0.41
1:F:392:TYR:OH	1:G:351:PHE:O	2.32	0.41
1:H:334:MET:HA	1:H:337:ASN:OD1	2.21	0.41
1:H:431:ALA:HB2	1:I:71:MET:HE1	2.02	0.41
1:J:12:LEU:HG	1:J:15:PHE:HB3	2.03	0.41
1:J:61:ARG:N	1:J:62:PRO:HD2	2.35	0.41
1:J:462:GLU:C	1:J:464:TYR:H	2.29	0.41
1:K:87:ARG:HG3	1:K:89:ASP:OD1	2.21	0.41
1:K:321:ARG:HD2	1:K:324:LYS:HB3	2.03	0.41
1:L:197:ASP:OD1	1:L:198:ILE:N	2.43	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:237:ASP:O	1:A:242:GLU:HG3	2.20	0.40
1:A:551:LEU:HD22	1:B:567:MET:HG3	2.03	0.40
1:B:369:TYR:O	1:B:370:PRO:C	2.64	0.40
1:C:132:TYR:CZ	1:C:454:ALA:HB1	2.56	0.40
1:C:165:MET:HE2	1:C:165:MET:HA	2.02	0.40
1:C:299:PRO:O	1:C:301:VAL:HG23	2.21	0.40
1:E:224:GLU:OE1	1:E:227:GLU:N	2.54	0.40
1:E:480:ILE:HG13	1:E:481:THR:H	1.85	0.40
1:F:526:SER:HB2	1:F:530:GLN:CG	2.50	0.40
1:G:376:ARG:O	1:G:376:ARG:HG2	2.21	0.40
1:H:339:ASP:O	1:H:343:ARG:HG2	2.20	0.40
1:H:371:TYR:CE2	1:H:373:LEU:HD12	2.56	0.40
1:H:541:LYS:HB3	1:I:535:ILE:HG21	2.03	0.40
1:I:565:VAL:HG12	1:I:565:VAL:O	2.21	0.40
1:J:108:LYS:O	1:J:111:VAL:HG22	2.21	0.40
1:L:93:VAL:HG23	1:L:94:LEU:N	2.37	0.40
1:A:528:LYS:HB3	1:A:532:ARG:HB2	2.03	0.40
1:B:441:ARG:NH2	1:C:103:ARG:O	2.54	0.40
1:C:445:GLU:O	1:C:449:PHE:N	2.54	0.40
1:D:467:ILE:C	1:D:469:ASN:N	2.78	0.40
1:D:566:GLU:N	1:D:566:GLU:OE1	2.54	0.40
1:F:352:TRP:HE1	1:F:375:ASN:C	2.28	0.40
1:F:403:TYR:HA	1:F:406:GLU:OE1	2.21	0.40
1:G:336:PHE:CZ	1:G:397:VAL:HG22	2.56	0.40
1:H:155:HIS:O	1:H:157:ILE:HD12	2.21	0.40
1:H:483:GLU:O	1:H:484:ASP:OD1	2.38	0.40
1:I:235:TYR:OH	1:I:249:ARG:NH1	2.54	0.40
1:J:58:ASP:OD1	1:J:58:ASP:N	2.52	0.40
1:J:420:VAL:O	1:J:426:ASN:ND2	2.48	0.40
1:J:430:VAL:HG13	1:J:432:PHE:H	1.85	0.40
1:K:272:LYS:HG3	1:K:272:LYS:O	2.21	0.40
1:K:406:GLU:HA	1:K:409:THR:HB	2.03	0.40
1:L:80:TYR:CE2	1:L:98:TYR:HB3	2.56	0.40
1:L:214:GLN:O	1:L:216:THR:HG23	2.21	0.40
1:A:292:LEU:HD21	1:A:295:GLY:H	1.86	0.40
1:A:574:LYS:HB2	1:A:576:LEU:HB3	2.03	0.40
1:B:320:VAL:HG11	1:B:415:VAL:HB	2.02	0.40
1:B:354:GLU:H	1:B:374:LEU:HG	1.85	0.40
1:B:359:PHE:CZ	1:B:362:MET:HE3	2.55	0.40
1:B:539:LEU:CG	1:B:540:GLY:H	2.34	0.40
1:C:80:TYR:C	1:C:516:CYS:HB2	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:198:ILE:O	1:C:198:ILE:HG22	2.20	0.40
1:D:193:LEU:HD12	1:D:195:ALA:H	1.86	0.40
1:D:296:GLU:OE1	1:D:296:GLU:N	2.54	0.40
1:E:226:VAL:HG23	1:E:227:GLU:H	1.86	0.40
1:E:565:VAL:HB	1:E:568:MET:HE3	2.04	0.40
1:F:318:GLY:O	1:F:321:ARG:HG3	2.21	0.40
1:G:280:ILE:HG12	1:G:288:LYS:CD	2.49	0.40
1:G:280:ILE:HG21	1:G:288:LYS:HE2	2.03	0.40
1:H:72:ARG:NH1	1:H:112:ASN:OD1	2.54	0.40
1:H:123:VAL:HG13	1:H:303:VAL:HG23	2.04	0.40
1:H:488:LYS:NZ	1:H:491:GLN:HA	2.37	0.40
1:J:58:ASP:CG	1:J:59:VAL:H	2.29	0.40
1:J:236:GLN:HG3	1:J:247:PHE:CZ	2.57	0.40
1:J:321:ARG:HH11	1:J:327:GLN:HE21	1.67	0.40
1:J:403:TYR:OH	1:K:401:ASN:ND2	2.54	0.40
1:K:264:ILE:HG12	1:K:265:LYS:H	1.86	0.40
1:B:156:VAL:O	1:B:156:VAL:HG13	2.21	0.40
1:C:126:TRP:NE1	1:C:128:LEU:HD23	2.36	0.40
1:C:430:VAL:HG13	1:C:432:PHE:HB2	2.04	0.40
1:C:546:THR:HG23	1:C:547:PRO:HD3	2.03	0.40
1:D:123:VAL:HB	1:D:152:ALA:HB1	2.04	0.40
1:E:78:VAL:HG12	1:E:525:GLN:HA	2.04	0.40
1:F:370:PRO:HG2	1:F:372:TYR:CZ	2.56	0.40
1:G:57:PHE:HB3	1:G:331:ASN:OD1	2.22	0.40
1:G:249:ARG:HD3	1:G:252:LYS:HG2	2.03	0.40
1:G:552:LEU:C	1:G:555:GLN:H	2.29	0.40
1:H:372:TYR:CG	1:H:373:LEU:N	2.90	0.40
1:H:376:ARG:O	1:H:377:THR:C	2.64	0.40
1:I:282:THR:HG22	1:I:284:THR:H	1.86	0.40
1:I:301:VAL:HG12	1:I:302:PRO:O	2.22	0.40
1:J:63:VAL:CG2	1:J:320:VAL:HG11	2.52	0.40
1:K:80:TYR:CE2	1:K:82:PRO:HG3	2.56	0.40
1:K:248:LYS:HD3	1:L:190:LYS:O	2.22	0.40
1:L:126:TRP:HZ2	1:L:146:ARG:HA	1.86	0.40
1:L:345:PRO:O	1:L:346:LYS:HB2	2.21	0.40
1:A:520:VAL:HG11	1:B:105:ASN:ND2	2.36	0.40
1:B:80:TYR:CE2	1:C:563:LYS:HE3	2.57	0.40
1:B:550:GLN:O	1:B:553:LEU:HD13	2.21	0.40
1:C:42:ASP:CG	1:C:43:ASP:H	2.30	0.40
1:D:582:LYS:HG3	1:D:583:LYS:HG2	2.04	0.40
1:D:587:PRO:HB2	1:D:588:GLU:OE1	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:253:ASP:CG	1:E:254:VAL:HG23	2.47	0.40
1:F:59:VAL:HG13	1:F:59:VAL:O	2.22	0.40
1:F:306:GLU:HG2	1:F:435:VAL:HG21	2.04	0.40
1:H:169:ASP:CG	1:H:170:ALA:H	2.29	0.40
1:H:392:TYR:HB2	1:I:349:PRO:HB3	2.03	0.40
1:H:577:ILE:HG13	1:H:578:GLN:N	2.36	0.40
1:I:14:ARG:HH22	1:I:225:VAL:CG2	2.35	0.40
1:I:249:ARG:NH2	1:I:251:ILE:HB	2.37	0.40
1:J:60:VAL:O	1:J:60:VAL:HG12	2.21	0.40
1:J:124:GLY:O	1:J:303:VAL:N	2.54	0.40
1:K:78:VAL:HG12	1:K:524:PHE:O	2.22	0.40
1:K:246:TYR:CE2	1:K:272:LYS:HD2	2.57	0.40
1:K:352:TRP:N	1:K:353:PRO:CD	2.84	0.40
1:L:198:ILE:O	1:L:198:ILE:HG23	2.22	0.40

There are no symmetry-related clashes.

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	583/610 (96%)	461 (79%)	115 (20%)	7 (1%)	10	37
1	B	583/610 (96%)	461 (79%)	112 (19%)	10 (2%)	7	30
1	C	583/610 (96%)	442 (76%)	130 (22%)	11 (2%)	6	28
1	D	583/610 (96%)	451 (77%)	123 (21%)	9 (2%)	8	32
1	E	583/610 (96%)	454 (78%)	120 (21%)	9 (2%)	8	32
1	F	583/610 (96%)	448 (77%)	129 (22%)	6 (1%)	12	40
1	G	583/610 (96%)	438 (75%)	135 (23%)	10 (2%)	7	30
1	H	583/610 (96%)	440 (76%)	134 (23%)	9 (2%)	8	32
1	I	583/610 (96%)	436 (75%)	137 (24%)	10 (2%)	7	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	J	583/610 (96%)	443 (76%)	132 (23%)	8 (1%)	9	33
1	K	583/610 (96%)	455 (78%)	121 (21%)	7 (1%)	10	37
1	L	583/610 (96%)	450 (77%)	125 (21%)	8 (1%)	9	33
All	All	6996/7320 (96%)	5379 (77%)	1513 (22%)	104 (2%)	8	32

All (104) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	59	VAL
1	B	226	VAL
1	B	244	VAL
1	B	282	THR
1	C	281	ILE
1	D	463	ILE
1	E	463	ILE
1	F	76	ILE
1	I	506	VAL
1	J	463	ILE
1	J	506	VAL
1	L	244	VAL
1	L	463	ILE
1	C	370	PRO
1	C	506	VAL
1	E	59	VAL
1	E	300	ILE
1	E	506	VAL
1	G	234	ILE
1	I	59	VAL
1	I	210	PRO
1	I	581	VAL
1	J	170	ALA
1	K	280	ILE
1	B	506	VAL
1	D	356	ILE
1	F	467	ILE
1	H	254	VAL
1	H	356	ILE
1	I	496	VAL
1	K	535	ILE
1	A	144	ILE
1	A	226	VAL

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Mol	Chain	Res	Type
1	A	353	PRO
1	B	356	ILE
1	B	463	ILE
1	C	356	ILE
1	C	535	ILE
1	D	190	LYS
1	D	506	VAL
1	E	119	ILE
1	E	425	VAL
1	F	356	ILE
1	G	338	ALA
1	G	356	ILE
1	G	506	VAL
1	G	535	ILE
1	H	577	ILE
1	J	280	ILE
1	J	577	ILE
1	K	356	ILE
1	L	226	VAL
1	L	280	ILE
1	L	281	ILE
1	L	356	ILE
1	L	506	VAL
1	B	140	ASN
1	G	370	PRO
1	G	388	PRO
1	H	418	LEU
1	I	57	PHE
1	I	353	PRO
1	A	463	ILE
1	C	129	VAL
1	F	178	SER
1	F	217	ILE
1	K	129	VAL
1	K	353	PRO
1	D	226	VAL
1	D	244	VAL
1	F	463	ILE
1	H	76	ILE
1	J	76	ILE
1	J	244	VAL
1	J	369	TYR

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Mol	Chain	Res	Type
1	K	76	ILE
1	L	353	PRO
1	B	76	ILE
1	C	76	ILE
1	C	234	ILE
1	C	353	PRO
1	D	303	VAL
1	E	76	ILE
1	I	76	ILE
1	I	244	VAL
1	K	234	ILE
1	A	217	ILE
1	C	276	VAL
1	D	471	ILE
1	H	234	ILE
1	A	480	ILE
1	C	251	ILE
1	D	123	VAL
1	E	217	ILE
1	E	587	PRO
1	G	217	ILE
1	G	497	VAL
1	H	217	ILE
1	H	266	ILE
1	H	280	ILE
1	I	266	ILE
1	A	76	ILE
1	B	217	ILE
1	G	463	ILE

5.3.2 Protein sidechains ⓘ

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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	512/536 (96%)	512 (100%)	0	100	100
1	B	508/536 (95%)	506 (100%)	2 (0%)	84	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	508/536 (95%)	508 (100%)	0	100	100
1	D	512/536 (96%)	511 (100%)	1 (0%)	87	88
1	E	511/536 (95%)	510 (100%)	1 (0%)	87	88
1	F	508/536 (95%)	508 (100%)	0	100	100
1	G	507/536 (95%)	506 (100%)	1 (0%)	87	88
1	H	508/536 (95%)	508 (100%)	0	100	100
1	I	508/536 (95%)	506 (100%)	2 (0%)	84	84
1	J	508/536 (95%)	506 (100%)	2 (0%)	84	84
1	K	510/536 (95%)	510 (100%)	0	100	100
1	L	508/536 (95%)	508 (100%)	0	100	100
All	All	6108/6432 (95%)	6099 (100%)	9 (0%)	88	90

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	193	LEU
1	B	453	LEU
1	D	507	LEU
1	E	463	ILE
1	G	351	PHE
1	I	374	LEU
1	I	499	LEU
1	J	324	LYS
1	J	539	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (50) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	GLN
1	A	150	HIS
1	B	40	GLN
1	B	74	ASN
1	B	141	ASN
1	B	172	HIS
1	B	436	ASN
1	B	465	GLN
1	C	401	ASN

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Mol	Chain	Res	Type
1	C	591	GLN
1	D	74	ASN
1	D	118	GLN
1	D	135	GLN
1	D	142	GLN
1	D	401	ASN
1	D	436	ASN
1	D	531	ASN
1	E	181	GLN
1	E	182	ASN
1	E	366	ASN
1	E	394	ASN
1	E	436	ASN
1	E	505	GLN
1	E	525	GLN
1	F	52	GLN
1	F	73	GLN
1	F	150	HIS
1	F	205	ASN
1	F	218	GLN
1	F	439	ASN
1	F	452	ASN
1	F	525	GLN
1	G	155	HIS
1	G	236	GLN
1	G	366	ASN
1	G	437	GLN
1	G	525	GLN
1	H	202	GLN
1	H	469	ASN
1	I	401	ASN
1	I	437	GLN
1	I	544	GLN
1	J	426	ASN
1	J	450	GLN
1	J	591	GLN
1	K	450	GLN
1	K	469	ASN
1	L	40	GLN
1	L	150	HIS
1	L	331	ASN

5.3.3 RNA [i](#)

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, 95th 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	585/610 (95%)	1.31	145 (24%) 2 1	16, 65, 94, 113	0
1	B	585/610 (95%)	1.15	96 (16%) 4 4	19, 62, 89, 109	0
1	C	585/610 (95%)	1.21	124 (21%) 2 2	19, 61, 91, 130	0
1	D	585/610 (95%)	1.43	155 (26%) 1 1	21, 66, 97, 184	0
1	E	585/610 (95%)	1.32	128 (21%) 2 2	19, 63, 98, 205	0
1	F	585/610 (95%)	1.24	128 (21%) 2 2	22, 60, 94, 142	0
1	G	585/610 (95%)	1.18	111 (18%) 3 3	18, 59, 92, 136	0
1	H	585/610 (95%)	1.30	145 (24%) 2 1	20, 62, 93, 117	0
1	I	585/610 (95%)	1.25	121 (20%) 2 2	19, 66, 99, 192	0
1	J	585/610 (95%)	1.29	124 (21%) 2 2	21, 65, 97, 142	0
1	K	585/610 (95%)	1.29	137 (23%) 2 2	27, 67, 100, 132	0
1	L	585/610 (95%)	1.29	123 (21%) 2 2	21, 64, 102, 156	0
All	All	7020/7320 (95%)	1.27	1537 (21%) 2 2	16, 63, 96, 205	0

All (1537) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	232	ALA	22.8
1	C	574	LYS	16.2
1	H	572	ALA	14.7
1	D	220	ALA	13.2
1	L	516	CYS	12.6
1	F	302	PRO	11.3
1	D	526	SER	11.0
1	J	118	GLN	10.2
1	B	245	SER	10.1
1	K	527	MET	9.9
1	G	461	GLY	9.8

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Mol	Chain	Res	Type	RSRZ
1	H	151	SER	9.3
1	K	526	SER	9.3
1	E	238	PRO	9.2
1	D	524	PHE	9.1
1	K	36	SER	9.0
1	K	435	VAL	8.7
1	A	447	TYR	8.6
1	I	564	GLY	8.5
1	E	107	ALA	8.4
1	J	219	ILE	8.3
1	G	13	SER	8.3
1	D	460	ASP	8.2
1	F	267	ALA	8.2
1	D	558	THR	8.1
1	D	255	ILE	8.1
1	D	259	ALA	7.9
1	E	233	PHE	7.8
1	K	404	MET	7.8
1	F	305	GLY	7.8
1	D	516	CYS	7.7
1	G	175	VAL	7.5
1	C	43	ASP	7.4
1	L	168	SER	7.3
1	A	526	SER	7.3
1	E	437	GLN	7.3
1	J	531	ASN	7.2
1	C	231	THR	7.1
1	L	553	LEU	7.1
1	A	203	ASN	7.1
1	L	226	VAL	7.1
1	F	403	TYR	7.1
1	E	231	THR	7.1
1	B	95	MET	7.0
1	E	516	CYS	7.0
1	E	237	ASP	7.0
1	L	125	ALA	6.9
1	A	183	GLY	6.9
1	L	147	GLU	6.9
1	K	337	ASN	6.8
1	A	448	VAL	6.8
1	I	455	THR	6.7
1	L	80	TYR	6.6

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Mol	Chain	Res	Type	RSRZ
1	L	294	ALA	6.6
1	L	161	ASN	6.6
1	D	333	ILE	6.5
1	I	84	ASP	6.5
1	G	39	SER	6.4
1	J	460	ASP	6.4
1	E	460	ASP	6.4
1	H	64	VAL	6.4
1	A	318	GLY	6.3
1	I	122	GLY	6.3
1	J	443	ASP	6.3
1	A	296	GLU	6.3
1	F	71	MET	6.3
1	L	258	LEU	6.2
1	H	125	ALA	6.2
1	D	502	GLY	6.2
1	I	138	THR	6.1
1	F	460	ASP	6.1
1	K	294	ALA	6.1
1	J	293	ILE	6.1
1	D	507	LEU	6.1
1	K	100	THR	6.0
1	C	309	PHE	6.0
1	H	433	ASP	5.9
1	H	322	LEU	5.9
1	I	103	ARG	5.9
1	K	281	ILE	5.9
1	D	426	ASN	5.9
1	J	283	CYS	5.8
1	G	124	GLY	5.8
1	H	22	SER	5.8
1	C	506	VAL	5.7
1	K	153	CYS	5.7
1	A	439	ASN	5.7
1	B	160	SER	5.7
1	D	174	THR	5.7
1	B	350	PHE	5.6
1	I	141	ASN	5.6
1	L	240	THR	5.6
1	H	430	VAL	5.6
1	K	475	PRO	5.5
1	G	566	GLU	5.5

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Mol	Chain	Res	Type	RSRZ
1	I	231	THR	5.5
1	L	188	ALA	5.5
1	A	523	SER	5.5
1	I	442	ALA	5.5
1	J	43	ASP	5.4
1	A	46	SER	5.4
1	A	522	PRO	5.4
1	K	124	GLY	5.4
1	B	462	GLU	5.4
1	G	475	PRO	5.4
1	D	408	ALA	5.4
1	D	416	ALA	5.4
1	C	183	GLY	5.4
1	G	238	PRO	5.4
1	D	10	SER	5.3
1	D	258	LEU	5.3
1	C	105	ASN	5.3
1	J	86	ALA	5.3
1	H	85	GLY	5.2
1	D	195	ALA	5.2
1	G	107	ALA	5.2
1	D	294	ALA	5.2
1	G	453	LEU	5.2
1	H	580	GLY	5.2
1	G	12	LEU	5.2
1	B	383	ASP	5.2
1	C	91	ALA	5.2
1	K	336	PHE	5.1
1	B	305	GLY	5.1
1	D	316	TYR	5.1
1	B	220	ALA	5.1
1	K	426	ASN	5.1
1	F	126	TRP	5.1
1	J	279	SER	5.1
1	B	466	SER	5.1
1	H	565	VAL	5.1
1	D	552	LEU	5.1
1	B	442	ALA	5.0
1	F	268	GLU	5.0
1	E	318	GLY	5.0
1	E	435	VAL	5.0
1	H	279	SER	5.0

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Mol	Chain	Res	Type	RSRZ
1	C	525	GLN	5.0
1	C	326	GLY	5.0
1	K	436	ASN	5.0
1	A	396	GLU	5.0
1	E	255	ILE	4.9
1	C	172	HIS	4.9
1	E	213	THR	4.9
1	F	442	ALA	4.9
1	I	483	GLU	4.9
1	J	280	ILE	4.9
1	H	130	THR	4.9
1	L	112	ASN	4.9
1	C	553	LEU	4.8
1	G	11	ILE	4.8
1	H	149	ILE	4.8
1	C	13	SER	4.8
1	J	530	GLN	4.8
1	E	302	PRO	4.8
1	C	259	ALA	4.8
1	G	322	LEU	4.8
1	D	197	ASP	4.8
1	D	250	ASP	4.8
1	J	520	VAL	4.8
1	B	445	GLU	4.7
1	E	156	VAL	4.7
1	A	508	ASN	4.7
1	B	21	ALA	4.7
1	C	164	LEU	4.7
1	J	143	VAL	4.7
1	A	126	TRP	4.7
1	J	461	GLY	4.7
1	C	401	ASN	4.7
1	D	193	LEU	4.6
1	F	301	VAL	4.6
1	H	21	ALA	4.6
1	L	448	VAL	4.6
1	C	518	THR	4.6
1	I	85	GLY	4.6
1	H	566	GLU	4.6
1	J	510	ILE	4.6
1	H	226	VAL	4.6
1	I	535	ILE	4.6

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Mol	Chain	Res	Type	RSRZ
1	B	387	GLN	4.6
1	H	291	GLN	4.6
1	I	525	GLN	4.6
1	J	564	GLY	4.6
1	J	565	VAL	4.6
1	A	440	MET	4.6
1	L	517	TYR	4.6
1	H	249	ARG	4.6
1	A	272	LYS	4.5
1	K	447	TYR	4.5
1	C	395	PRO	4.5
1	E	329	LEU	4.5
1	E	545	GLY	4.5
1	I	50	THR	4.5
1	A	146	ARG	4.5
1	I	576	LEU	4.5
1	L	444	LEU	4.5
1	G	241	GLY	4.5
1	D	217	ILE	4.5
1	G	460	ASP	4.5
1	G	200	SER	4.5
1	H	506	VAL	4.5
1	D	55	GLY	4.5
1	I	242	GLU	4.5
1	A	262	GLY	4.5
1	K	403	TYR	4.5
1	F	530	GLN	4.5
1	K	65	ARG	4.5
1	A	570	ASP	4.4
1	F	74	ASN	4.4
1	L	212	LEU	4.4
1	E	301	VAL	4.4
1	C	533	ALA	4.4
1	I	125	ALA	4.4
1	I	338	ALA	4.4
1	E	139	SER	4.4
1	I	171	ARG	4.4
1	D	219	ILE	4.4
1	J	495	GLU	4.4
1	F	370	PRO	4.4
1	E	209	PHE	4.4
1	J	445	GLU	4.4

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Mol	Chain	Res	Type	RSRZ
1	K	390	ALA	4.4
1	I	308	GLY	4.4
1	J	174	THR	4.4
1	D	400	ALA	4.3
1	K	361	HIS	4.3
1	F	101	ASP	4.3
1	G	42	ASP	4.3
1	J	13	SER	4.3
1	L	526	SER	4.3
1	I	437	GLN	4.3
1	C	160	SER	4.3
1	K	295	GLY	4.3
1	C	82	PRO	4.3
1	K	21	ALA	4.3
1	L	235	TYR	4.3
1	K	451	ASP	4.3
1	L	42	ASP	4.3
1	D	279	SER	4.3
1	D	529	GLN	4.3
1	F	307	TRP	4.2
1	C	79	LEU	4.2
1	E	279	SER	4.2
1	L	236	GLN	4.2
1	K	322	LEU	4.2
1	K	539	LEU	4.2
1	L	304	PHE	4.2
1	A	460	ASP	4.2
1	G	173	CYS	4.2
1	L	265	LYS	4.2
1	G	96	GLY	4.2
1	I	414	GLU	4.2
1	D	559	LEU	4.2
1	C	555	GLN	4.2
1	L	245	SER	4.2
1	C	125	ALA	4.2
1	J	512	GLY	4.2
1	B	223	TYR	4.2
1	I	556	TYR	4.2
1	L	279	SER	4.1
1	H	518	THR	4.1
1	I	39	SER	4.1
1	F	358	GLY	4.1

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Mol	Chain	Res	Type	RSRZ
1	F	580	GLY	4.1
1	F	293	ILE	4.1
1	B	573	ASN	4.1
1	C	122	GLY	4.1
1	E	30	LYS	4.1
1	A	388	PRO	4.1
1	L	345	PRO	4.1
1	J	46	SER	4.1
1	I	126	TRP	4.1
1	H	375	ASN	4.0
1	A	364	ASP	4.0
1	G	97	MET	4.0
1	A	417	THR	4.0
1	H	512	GLY	4.0
1	H	309	PHE	4.0
1	H	403	TYR	4.0
1	G	188	ALA	4.0
1	E	298	ILE	4.0
1	I	282	THR	4.0
1	L	571	TYR	4.0
1	J	12	LEU	4.0
1	I	565	VAL	4.0
1	B	100	THR	4.0
1	D	18	ASP	4.0
1	G	558	THR	4.0
1	J	39	SER	4.0
1	J	444	LEU	4.0
1	D	9	GLU	4.0
1	H	142	GLN	3.9
1	C	104	HIS	3.9
1	D	105	ASN	3.9
1	D	248	LYS	3.9
1	A	481	THR	3.9
1	G	534	GLU	3.9
1	L	36	SER	3.9
1	C	474	VAL	3.9
1	A	582	LYS	3.9
1	J	190	LYS	3.9
1	E	138	THR	3.9
1	I	515	GLU	3.9
1	C	220	ALA	3.9
1	F	553	LEU	3.9

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Mol	Chain	Res	Type	RSRZ
1	H	517	TYR	3.9
1	K	291	GLN	3.9
1	K	193	LEU	3.9
1	L	38	VAL	3.9
1	C	149	ILE	3.9
1	J	144	ILE	3.9
1	B	590	GLN	3.9
1	A	106	THR	3.8
1	F	102	MET	3.8
1	D	562	GLY	3.8
1	B	325	ASP	3.8
1	E	33	LEU	3.8
1	D	104	HIS	3.8
1	J	145	ARG	3.8
1	G	301	VAL	3.8
1	H	311	GLU	3.8
1	C	318	GLY	3.8
1	D	213	THR	3.8
1	G	47	GLN	3.8
1	G	43	ASP	3.8
1	L	206	ASP	3.8
1	D	428	GLY	3.8
1	H	503	GLU	3.8
1	J	232	ALA	3.8
1	B	570	ASP	3.8
1	D	185	GLU	3.8
1	H	584	PRO	3.8
1	E	508	ASN	3.8
1	L	97	MET	3.8
1	F	144	ILE	3.8
1	A	391	TYR	3.8
1	L	116	ARG	3.8
1	F	294	ALA	3.7
1	D	272	LYS	3.7
1	D	525	GLN	3.7
1	L	205	ASN	3.7
1	I	139	SER	3.7
1	H	510	ILE	3.7
1	H	99	ARG	3.7
1	B	369	TYR	3.7
1	C	238	PRO	3.7
1	G	472	TYR	3.7

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Mol	Chain	Res	Type	RSRZ
1	L	447	TYR	3.7
1	F	20	THR	3.7
1	J	77	ASP	3.7
1	I	209	PHE	3.7
1	I	557	PHE	3.7
1	A	107	ALA	3.7
1	E	110	ALA	3.7
1	H	416	ALA	3.7
1	A	520	VAL	3.7
1	J	142	GLN	3.7
1	B	568	MET	3.7
1	H	275	ARG	3.7
1	D	113	ILE	3.7
1	G	266	ILE	3.7
1	L	149	ILE	3.7
1	H	13	SER	3.7
1	A	16	ASP	3.7
1	H	131	ASP	3.7
1	I	309	PHE	3.7
1	I	485	GLY	3.7
1	K	540	GLY	3.7
1	G	306	GLU	3.7
1	K	448	VAL	3.7
1	L	412	VAL	3.7
1	D	249	ARG	3.7
1	F	217	ILE	3.7
1	G	292	LEU	3.7
1	I	374	LEU	3.7
1	A	521	GLY	3.7
1	D	235	TYR	3.7
1	E	403	TYR	3.7
1	D	315	VAL	3.7
1	D	409	THR	3.7
1	J	468	VAL	3.7
1	B	146	ARG	3.7
1	C	471	ILE	3.7
1	B	554	LEU	3.7
1	K	229	LYS	3.7
1	F	433	ASP	3.6
1	I	460	ASP	3.6
1	J	301	VAL	3.6
1	F	12	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	I	555	GLN	3.6
1	I	207	TRP	3.6
1	C	447	TYR	3.6
1	E	412	VAL	3.6
1	I	224	GLU	3.6
1	L	68	VAL	3.6
1	L	410	SER	3.6
1	L	549	TYR	3.6
1	A	32	ASP	3.6
1	A	368	ASP	3.6
1	E	443	ASP	3.6
1	K	289	ASP	3.6
1	L	441	ARG	3.6
1	D	447	TYR	3.6
1	I	58	ASP	3.6
1	D	251	ILE	3.6
1	H	350	PHE	3.6
1	L	81	ARG	3.6
1	D	448	VAL	3.6
1	H	445	GLU	3.6
1	I	526	SER	3.6
1	A	225	VAL	3.6
1	C	232	ALA	3.6
1	C	224	GLU	3.6
1	I	554	LEU	3.6
1	B	467	ILE	3.6
1	E	180	SER	3.6
1	F	100	THR	3.6
1	G	36	SER	3.6
1	H	377	THR	3.6
1	C	159	ASP	3.6
1	J	175	VAL	3.5
1	G	170	ALA	3.5
1	I	232	ALA	3.5
1	F	140	ASN	3.5
1	G	463	ILE	3.5
1	A	130	THR	3.5
1	A	486	SER	3.5
1	B	518	THR	3.5
1	C	116	ARG	3.5
1	G	532	ARG	3.5
1	F	304	PHE	3.5

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Mol	Chain	Res	Type	RSRZ
1	D	196	ASP	3.5
1	F	172	HIS	3.5
1	G	148	PRO	3.5
1	I	191	TYR	3.5
1	A	518	THR	3.5
1	F	136	SER	3.5
1	H	56	GLN	3.5
1	H	124	GLY	3.5
1	F	533	ALA	3.5
1	D	76	ILE	3.5
1	H	376	ARG	3.5
1	K	268	GLU	3.5
1	I	369	TYR	3.5
1	G	439	ASN	3.5
1	I	74	ASN	3.5
1	G	201	PHE	3.5
1	C	153	CYS	3.5
1	B	124	GLY	3.5
1	L	146	ARG	3.5
1	L	209	PHE	3.5
1	E	461	GLY	3.5
1	H	302	PRO	3.5
1	C	176	ILE	3.5
1	E	89	ASP	3.5
1	D	461	GLY	3.4
1	B	121	ALA	3.4
1	G	259	ALA	3.4
1	F	528	LYS	3.4
1	L	191	TYR	3.4
1	H	208	VAL	3.4
1	A	453	LEU	3.4
1	H	141	ASN	3.4
1	I	452	ASN	3.4
1	F	17	ALA	3.4
1	F	532	ARG	3.4
1	I	281	ILE	3.4
1	J	153	CYS	3.4
1	J	347	LYS	3.4
1	G	187	PHE	3.4
1	B	517	TYR	3.4
1	A	397	VAL	3.4
1	I	123	VAL	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	438	LEU	3.4
1	C	554	LEU	3.4
1	I	373	LEU	3.4
1	K	428	GLY	3.4
1	C	399	GLN	3.4
1	F	467	ILE	3.4
1	L	57	PHE	3.4
1	E	593	LEU	3.4
1	F	175	VAL	3.4
1	K	12	LEU	3.4
1	A	342	ALA	3.4
1	G	21	ALA	3.4
1	G	567	MET	3.4
1	F	388	PRO	3.4
1	E	438	LEU	3.4
1	E	553	LEU	3.4
1	L	305	GLY	3.4
1	F	137	PRO	3.4
1	I	172	HIS	3.4
1	K	446	THR	3.4
1	L	118	GLN	3.4
1	A	127	ARG	3.3
1	L	462	GLU	3.3
1	J	101	ASP	3.3
1	K	16	ASP	3.3
1	L	237	ASP	3.3
1	J	119	ILE	3.3
1	E	177	HIS	3.3
1	F	216	THR	3.3
1	H	118	GLN	3.3
1	L	581	VAL	3.3
1	C	365	GLY	3.3
1	D	98	TYR	3.3
1	E	572	ALA	3.3
1	H	217	ILE	3.3
1	H	294	ALA	3.3
1	J	42	ASP	3.3
1	A	446	THR	3.3
1	C	177	HIS	3.3
1	I	213	THR	3.3
1	C	573	ASN	3.3
1	J	401	ASN	3.3

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Mol	Chain	Res	Type	RSRZ
1	H	267	ALA	3.3
1	I	107	ALA	3.3
1	I	124	GLY	3.3
1	J	342	ALA	3.3
1	L	402	ALA	3.3
1	C	146	ARG	3.3
1	E	218	GLN	3.3
1	K	529	GLN	3.3
1	F	552	LEU	3.3
1	H	551	LEU	3.3
1	F	310	VAL	3.3
1	H	412	VAL	3.3
1	H	439	ASN	3.3
1	B	534	GLU	3.3
1	D	281	ILE	3.3
1	B	243	PRO	3.3
1	I	212	LEU	3.3
1	K	536	LEU	3.3
1	E	573	ASN	3.3
1	K	44	TRP	3.3
1	K	375	ASN	3.3
1	K	469	ASN	3.3
1	C	567	MET	3.3
1	E	503	GLU	3.3
1	D	169	ASP	3.2
1	I	12	LEU	3.2
1	L	297	HIS	3.2
1	F	50	THR	3.2
1	A	281	ILE	3.2
1	H	29	ALA	3.2
1	A	295	GLY	3.2
1	A	569	ARG	3.2
1	K	369	TYR	3.2
1	A	299	PRO	3.2
1	A	73	GLN	3.2
1	C	18	ASP	3.2
1	E	215	ASP	3.2
1	J	529	GLN	3.2
1	E	21	ALA	3.2
1	I	307	TRP	3.2
1	F	70	GLU	3.2
1	H	53	TYR	3.2

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Mol	Chain	Res	Type	RSRZ
1	K	541	LYS	3.2
1	L	554	LEU	3.2
1	B	244	VAL	3.2
1	E	526	SER	3.2
1	H	68	VAL	3.2
1	H	225	VAL	3.2
1	A	177	HIS	3.2
1	F	312	ASP	3.2
1	I	561	ASP	3.2
1	H	127	ARG	3.2
1	J	207	TRP	3.2
1	B	53	TYR	3.2
1	A	36	SER	3.2
1	E	381	SER	3.2
1	E	446	THR	3.2
1	D	257	ASP	3.2
1	L	37	ARG	3.2
1	A	574	LYS	3.2
1	D	528	LYS	3.2
1	F	262	GLY	3.2
1	C	133	GLU	3.2
1	G	469	ASN	3.2
1	H	549	TYR	3.2
1	K	472	TYR	3.2
1	B	349	PRO	3.2
1	I	225	VAL	3.2
1	B	179	MET	3.2
1	C	529	GLN	3.2
1	I	181	GLN	3.2
1	A	572	ALA	3.2
1	D	232	ALA	3.2
1	F	107	ALA	3.2
1	J	446	THR	3.2
1	D	551	LEU	3.1
1	F	566	GLU	3.1
1	J	515	GLU	3.1
1	F	141	ASN	3.1
1	E	148	PRO	3.1
1	G	98	TYR	3.1
1	E	104	HIS	3.1
1	J	220	ALA	3.1
1	L	100	THR	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	451	ASP	3.1
1	D	405	LEU	3.1
1	E	32	ASP	3.1
1	H	79	LEU	3.1
1	J	215	ASP	3.1
1	J	553	LEU	3.1
1	J	120	GLU	3.1
1	K	296	GLU	3.1
1	H	123	VAL	3.1
1	C	472	TYR	3.1
1	F	165	MET	3.1
1	J	278	LYS	3.1
1	J	300	ILE	3.1
1	K	293	ILE	3.1
1	H	91	ALA	3.1
1	B	174	THR	3.1
1	E	46	SER	3.1
1	C	443	ASP	3.1
1	D	206	ASP	3.1
1	J	516	CYS	3.1
1	K	68	VAL	3.1
1	F	517	TYR	3.1
1	I	182	ASN	3.1
1	A	525	GLN	3.1
1	C	292	LEU	3.1
1	F	164	LEU	3.1
1	B	247	PHE	3.1
1	K	548	GLU	3.1
1	G	199	PRO	3.1
1	C	371	TYR	3.1
1	L	144	ILE	3.1
1	L	411	ALA	3.1
1	E	405	LEU	3.1
1	C	308	GLY	3.1
1	I	216	THR	3.1
1	F	145	ARG	3.1
1	I	532	ARG	3.1
1	C	69	SER	3.1
1	D	466	SER	3.1
1	L	435	VAL	3.1
1	J	155	HIS	3.0
1	G	174	THR	3.0

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Mol	Chain	Res	Type	RSRZ
1	K	130	THR	3.0
1	G	115	VAL	3.0
1	J	286	VAL	3.0
1	K	123	VAL	3.0
1	B	151	SER	3.0
1	K	317	GLU	3.0
1	C	264	ILE	3.0
1	E	206	ASP	3.0
1	I	101	ASP	3.0
1	D	173	CYS	3.0
1	F	121	ALA	3.0
1	A	361	HIS	3.0
1	C	532	ARG	3.0
1	E	580	GLY	3.0
1	I	190	LYS	3.0
1	A	350	PHE	3.0
1	H	28	GLU	3.0
1	L	293	ILE	3.0
1	A	322	LEU	3.0
1	A	443	ASP	3.0
1	C	325	ASP	3.0
1	E	132	TYR	3.0
1	H	134	ASP	3.0
1	H	312	ASP	3.0
1	L	511	ARG	3.0
1	F	427	GLY	3.0
1	I	365	GLY	3.0
1	K	545	GLY	3.0
1	E	565	VAL	3.0
1	G	123	VAL	3.0
1	H	323	THR	3.0
1	C	71	MET	3.0
1	F	238	PRO	3.0
1	D	132	TYR	3.0
1	J	259	ALA	3.0
1	K	125	ALA	3.0
1	J	192	ASP	3.0
1	B	427	GLY	3.0
1	G	183	GLY	3.0
1	G	562	GLY	3.0
1	J	40	GLN	3.0
1	J	93	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	531	ASN	3.0
1	D	508	ASN	3.0
1	I	531	ASN	3.0
1	B	106	THR	3.0
1	K	386	THR	3.0
1	I	566	GLU	3.0
1	E	370	PRO	3.0
1	A	17	ALA	3.0
1	J	571	TYR	3.0
1	A	131	ASP	3.0
1	D	42	ASP	3.0
1	A	78	VAL	3.0
1	C	341	VAL	3.0
1	I	591	GLN	3.0
1	H	153	CYS	3.0
1	J	518	THR	3.0
1	H	352	TRP	2.9
1	D	533	ALA	2.9
1	F	232	ALA	2.9
1	I	223	TYR	2.9
1	J	305	GLY	2.9
1	C	505	GLN	2.9
1	F	525	GLN	2.9
1	E	106	THR	2.9
1	G	14	ARG	2.9
1	K	445	GLU	2.9
1	H	424	ALA	2.9
1	E	53	TYR	2.9
1	D	123	VAL	2.9
1	E	496	VAL	2.9
1	F	93	VAL	2.9
1	H	111	VAL	2.9
1	B	172	HIS	2.9
1	A	509	ASP	2.9
1	E	289	ASP	2.9
1	J	339	ASP	2.9
1	L	489	ASP	2.9
1	D	334	MET	2.9
1	E	441	ARG	2.9
1	D	205	ASN	2.9
1	G	436	ASN	2.9
1	E	29	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
1	J	447	TYR	2.9
1	G	22	SER	2.9
1	F	104	HIS	2.9
1	C	118	GLN	2.9
1	D	103	ARG	2.9
1	F	300	ILE	2.9
1	I	453	LEU	2.9
1	B	469	ASN	2.9
1	I	86	ALA	2.9
1	I	173	CYS	2.9
1	B	222	PHE	2.9
1	C	124	GLY	2.9
1	F	34	PHE	2.9
1	K	449	PHE	2.9
1	C	150	HIS	2.9
1	E	234	ILE	2.9
1	G	467	ILE	2.9
1	G	568	MET	2.9
1	H	109	ILE	2.9
1	H	280	ILE	2.9
1	I	104	HIS	2.9
1	J	523	SER	2.9
1	K	251	ILE	2.9
1	E	283	CYS	2.9
1	F	68	VAL	2.9
1	G	468	VAL	2.9
1	G	565	VAL	2.9
1	E	122	GLY	2.9
1	E	517	TYR	2.9
1	A	333	ILE	2.9
1	A	536	LEU	2.9
1	I	83	LYS	2.9
1	F	253	ASP	2.8
1	G	32	ASP	2.8
1	K	367	ASP	2.8
1	F	455	THR	2.8
1	A	31	ASN	2.8
1	C	412	VAL	2.8
1	E	415	VAL	2.8
1	B	504	LYS	2.8
1	E	222	PHE	2.8
1	K	277	TYR	2.8

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Mol	Chain	Res	Type	RSRZ
1	K	517	TYR	2.8
1	K	13	SER	2.8
1	B	32	ASP	2.8
1	E	239	VAL	2.8
1	G	117	GLU	2.8
1	L	126	TRP	2.8
1	A	105	ASN	2.8
1	D	198	ILE	2.8
1	F	521	GLY	2.8
1	G	300	ILE	2.8
1	H	562	GLY	2.8
1	I	482	LEU	2.8
1	F	179	MET	2.8
1	C	556	TYR	2.8
1	L	239	VAL	2.8
1	L	282	THR	2.8
1	K	212	LEU	2.8
1	B	144	ILE	2.8
1	B	375	ASN	2.8
1	F	366	ASN	2.8
1	I	277	TYR	2.8
1	J	172	HIS	2.8
1	D	342	ALA	2.8
1	B	441	ARG	2.8
1	B	59	VAL	2.8
1	A	184	TRP	2.8
1	B	71	MET	2.8
1	K	144	ILE	2.8
1	L	85	GLY	2.8
1	E	170	ALA	2.8
1	H	90	ALA	2.8
1	L	218	GLN	2.8
1	D	151	SER	2.8
1	B	271	ILE	2.8
1	D	449	PHE	2.7
1	E	449	PHE	2.7
1	G	333	ILE	2.8
1	J	284	THR	2.8
1	K	440	MET	2.7
1	H	573	ASN	2.7
1	A	98	TYR	2.7
1	I	14	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
1	I	248	LYS	2.7
1	E	578	GLN	2.7
1	G	111	VAL	2.7
1	A	24	GLU	2.7
1	C	97	MET	2.7
1	D	256	ASP	2.7
1	G	275	ARG	2.7
1	A	205	ASN	2.7
1	C	190	LYS	2.7
1	F	571	TYR	2.7
1	G	112	ASN	2.7
1	J	303	VAL	2.7
1	K	214	GLN	2.7
1	L	143	VAL	2.7
1	L	415	VAL	2.7
1	B	173	CYS	2.7
1	C	524	PHE	2.7
1	C	24	GLU	2.7
1	L	515	GLU	2.7
1	E	558	THR	2.7
1	J	85	GLY	2.7
1	J	126	TRP	2.7
1	D	297	HIS	2.7
1	E	366	ASN	2.7
1	E	431	ALA	2.7
1	E	208	VAL	2.7
1	I	370	PRO	2.7
1	L	522	PRO	2.7
1	C	440	MET	2.7
1	K	350	PHE	2.7
1	D	534	GLU	2.7
1	I	100	THR	2.7
1	F	526	SER	2.7
1	G	410	SER	2.7
1	A	152	ALA	2.7
1	C	357	ALA	2.7
1	D	58	ASP	2.7
1	D	170	ALA	2.7
1	E	472	TYR	2.7
1	K	411	ALA	2.7
1	K	64	VAL	2.7
1	J	62	PRO	2.7

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Mol	Chain	Res	Type	RSRZ
1	K	109	ILE	2.7
1	A	445	GLU	2.7
1	K	272	LYS	2.7
1	K	126	TRP	2.7
1	K	180	SER	2.7
1	F	454	ALA	2.7
1	B	438	LEU	2.7
1	J	63	VAL	2.7
1	G	297	HIS	2.7
1	J	519	ASP	2.7
1	L	186	ASP	2.7
1	F	273	ARG	2.6
1	A	190	LYS	2.6
1	J	562	GLY	2.6
1	L	512	GLY	2.6
1	F	106	THR	2.6
1	E	444	LEU	2.6
1	I	551	LEU	2.6
1	L	301	VAL	2.6
1	E	372	TYR	2.6
1	B	58	ASP	2.6
1	B	237	ASP	2.6
1	C	253	ASP	2.6
1	G	131	ASP	2.6
1	G	378	ASP	2.6
1	H	89	ASP	2.6
1	D	459	ARG	2.6
1	E	171	ARG	2.6
1	F	589	GLU	2.6
1	K	224	GLU	2.6
1	F	586	THR	2.6
1	G	240	THR	2.6
1	G	377	THR	2.6
1	I	446	THR	2.6
1	K	211	TRP	2.6
1	A	25	ALA	2.6
1	G	454	ALA	2.6
1	C	279	SER	2.6
1	D	36	SER	2.6
1	D	261	SER	2.6
1	A	80	TYR	2.6
1	D	280	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
1	I	569	ARG	2.6
1	L	459	ARG	2.6
1	D	302	PRO	2.6
1	E	527	MET	2.6
1	J	222	PHE	2.6
1	D	451	ASP	2.6
1	J	205	ASN	2.6
1	J	236	GLN	2.6
1	J	573	ASN	2.6
1	B	117	GLU	2.6
1	C	552	LEU	2.6
1	B	267	ALA	2.6
1	B	431	ALA	2.6
1	C	338	ALA	2.6
1	E	20	THR	2.6
1	J	170	ALA	2.6
1	J	352	TRP	2.6
1	J	397	VAL	2.6
1	A	464	TYR	2.6
1	K	11	ILE	2.6
1	L	39	SER	2.6
1	L	514	TYR	2.6
1	C	57	PHE	2.6
1	E	137	PRO	2.6
1	H	555	GLN	2.6
1	K	525	GLN	2.6
1	L	169	ASP	2.6
1	A	436	ASN	2.6
1	I	427	GLY	2.6
1	A	67	LEU	2.6
1	I	51	LEU	2.6
1	K	551	LEU	2.6
1	E	111	VAL	2.6
1	F	170	ALA	2.6
1	I	111	VAL	2.6
1	K	310	VAL	2.6
1	B	184	TRP	2.6
1	C	361	HIS	2.6
1	D	523	SER	2.6
1	E	172	HIS	2.6
1	G	172	HIS	2.6
1	F	52	GLN	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	308	GLY	2.6
1	B	250	ASP	2.6
1	G	237	ASP	2.6
1	K	237	ASP	2.6
1	L	141	ASN	2.6
1	A	538	LEU	2.6
1	A	185	GLU	2.6
1	B	379	GLU	2.6
1	D	503	GLU	2.6
1	C	152	ALA	2.6
1	D	208	VAL	2.6
1	D	565	VAL	2.6
1	E	115	VAL	2.6
1	H	38	VAL	2.6
1	H	442	ALA	2.6
1	J	78	VAL	2.6
1	K	171	ARG	2.6
1	D	501	THR	2.6
1	F	377	THR	2.6
1	J	213	THR	2.6
1	L	518	THR	2.6
1	H	113	ILE	2.5
1	H	234	ILE	2.5
1	I	463	ILE	2.5
1	E	579	MET	2.5
1	D	450	GLN	2.5
1	G	218	GLN	2.5
1	K	450	GLN	2.5
1	F	374	LEU	2.5
1	A	208	VAL	2.5
1	E	426	ASN	2.5
1	E	452	ASN	2.5
1	L	77	ASP	2.5
1	L	478	VAL	2.5
1	E	533	ALA	2.5
1	K	402	ALA	2.5
1	L	589	GLU	2.5
1	A	138	THR	2.5
1	D	207	TRP	2.5
1	G	34	PHE	2.5
1	C	316	TYR	2.5
1	H	363	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
1	I	132	TYR	2.5
1	D	287	LEU	2.5
1	I	327	GLN	2.5
1	A	171	ARG	2.5
1	B	315	VAL	2.5
1	F	60	VAL	2.5
1	C	29	ALA	2.5
1	I	314	GLU	2.5
1	J	253	ASP	2.5
1	K	452	ASN	2.5
1	L	407	ALA	2.5
1	D	300	ILE	2.5
1	E	198	ILE	2.5
1	A	307	TRP	2.5
1	D	15	PHE	2.5
1	C	137	PRO	2.5
1	C	403	TYR	2.5
1	D	148	PRO	2.5
1	H	297	HIS	2.5
1	J	464	TYR	2.5
1	H	374	LEU	2.5
1	I	553	LEU	2.5
1	K	453	LEU	2.5
1	K	425	VAL	2.5
1	G	121	ALA	2.5
1	H	152	ALA	2.5
1	I	456	ALA	2.5
1	C	314	GLU	2.5
1	C	219	ILE	2.5
1	J	32	ASP	2.5
1	E	440	MET	2.5
1	D	20	THR	2.5
1	F	174	THR	2.5
1	H	126	TRP	2.5
1	A	302	PRO	2.5
1	H	292	LEU	2.5
1	J	248	LYS	2.5
1	B	308	GLY	2.5
1	F	591	GLN	2.5
1	G	236	GLN	2.5
1	H	465	GLN	2.5
1	K	520	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	180	SER	2.5
1	A	533	ALA	2.5
1	D	180	SER	2.5
1	A	534	GLU	2.5
1	J	354	GLU	2.5
1	L	537	GLU	2.5
1	D	97	MET	2.5
1	J	489	ASP	2.5
1	H	324	LYS	2.5
1	B	33	LEU	2.5
1	G	373	LEU	2.5
1	A	369	TYR	2.5
1	I	517	TYR	2.5
1	J	392	TYR	2.5
1	B	429	GLN	2.5
1	H	52	GLN	2.5
1	H	114	ALA	2.4
1	J	411	ALA	2.4
1	A	245	SER	2.4
1	F	516	CYS	2.4
1	C	334	MET	2.4
1	D	189	GLU	2.4
1	G	120	GLU	2.4
1	G	462	GLU	2.4
1	H	568	MET	2.4
1	J	227	GLU	2.4
1	L	449	PHE	2.4
1	A	145	ARG	2.4
1	D	194	ASP	2.4
1	K	215	ASP	2.4
1	A	128	LEU	2.4
1	D	373	LEU	2.4
1	J	258	LEU	2.4
1	H	587	PRO	2.4
1	E	150	HIS	2.4
1	H	191	TYR	2.4
1	L	371	TYR	2.4
1	G	308	GLY	2.4
1	J	255	ILE	2.4
1	D	162	SER	2.4
1	I	486	SER	2.4
1	L	108	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	K	553	LEU	2.4
1	A	44	TRP	2.4
1	A	461	GLY	2.4
1	C	254	VAL	2.4
1	F	123	VAL	2.4
1	G	478	VAL	2.4
1	K	143	VAL	2.4
1	K	580	GLY	2.4
1	A	442	ALA	2.4
1	J	467	ILE	2.4
1	K	25	ALA	2.4
1	A	530	GLN	2.4
1	A	544	GLN	2.4
1	F	550	GLN	2.4
1	A	351	PHE	2.4
1	D	54	ARG	2.4
1	E	275	ARG	2.4
1	H	227	GLU	2.4
1	L	222	PHE	2.4
1	C	180	SER	2.4
1	K	173	CYS	2.4
1	D	184	TRP	2.4
1	A	452	ASN	2.4
1	F	23	ASP	2.4
1	H	320	VAL	2.4
1	I	451	ASP	2.4
1	A	122	GLY	2.4
1	E	297	HIS	2.4
1	E	363	TYR	2.4
1	G	293	ILE	2.4
1	J	400	ALA	2.4
1	F	568	MET	2.4
1	I	399	GLN	2.4
1	C	258	LEU	2.4
1	C	329	LEU	2.4
1	E	548	GLU	2.4
1	I	317	GLU	2.4
1	J	45	LEU	2.4
1	B	352	TRP	2.4
1	F	38	VAL	2.4
1	G	446	THR	2.4
1	G	455	THR	2.4

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Mol	Chain	Res	Type	RSRZ
1	H	62	PRO	2.4
1	A	141	ASN	2.4
1	E	375	ASN	2.4
1	A	198	ILE	2.4
1	A	390	ALA	2.4
1	G	298	ILE	2.4
1	E	146	ARG	2.4
1	B	57	PHE	2.4
1	I	222	PHE	2.4
1	A	178	SER	2.4
1	L	41	TRP	2.4
1	C	213	THR	2.3
1	I	518	THR	2.3
1	A	91	ALA	2.3
1	B	338	ALA	2.3
1	D	114	ALA	2.3
1	E	205	ASN	2.3
1	H	140	ASN	2.3
1	B	556	TYR	2.3
1	H	98	TYR	2.3
1	H	519	ASP	2.3
1	I	316	TYR	2.3
1	K	234	ILE	2.3
1	B	97	MET	2.3
1	E	568	MET	2.3
1	B	465	GLN	2.3
1	F	291	GLN	2.3
1	F	296	GLU	2.3
1	K	115	VAL	2.3
1	A	124	GLY	2.3
1	C	558	THR	2.3
1	J	574	LYS	2.3
1	C	121	ALA	2.3
1	E	471	ILE	2.3
1	K	91	ALA	2.3
1	E	469	ASN	2.3
1	L	383	ASP	2.3
1	J	57	PHE	2.3
1	J	499	LEU	2.3
1	F	529	GLN	2.3
1	F	306	GLU	2.3
1	K	24	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	K	314	GLU	2.3
1	A	59	VAL	2.3
1	J	123	VAL	2.3
1	K	474	VAL	2.3
1	G	83	LYS	2.3
1	G	346	LYS	2.3
1	C	345	PRO	2.3
1	J	299	PRO	2.3
1	L	75	PRO	2.3
1	A	39	SER	2.3
1	A	144	ILE	2.3
1	C	510	ILE	2.3
1	H	178	SER	2.3
1	I	305	GLY	2.3
1	L	109	ILE	2.3
1	K	110	ALA	2.3
1	L	586	THR	2.3
1	D	527	MET	2.3
1	J	177	HIS	2.3
1	D	464	TYR	2.3
1	J	94	LEU	2.3
1	K	554	LEU	2.3
1	F	250	ASP	2.3
1	F	570	ASP	2.3
1	K	473	ASP	2.3
1	K	519	ASP	2.3
1	C	575	GLN	2.3
1	G	40	GLN	2.3
1	K	591	GLN	2.3
1	G	360	GLU	2.3
1	E	478	VAL	2.3
1	K	122	GLY	2.3
1	K	471	ILE	2.3
1	D	188	ALA	2.3
1	D	390	ALA	2.3
1	H	107	ALA	2.3
1	B	446	THR	2.3
1	G	151	SER	2.3
1	K	481	THR	2.3
1	H	438	LEU	2.3
1	H	132	TYR	2.3
1	I	53	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	16	ASP	2.3
1	G	52	GLN	2.3
1	E	190	LYS	2.3
1	I	306	GLU	2.3
1	L	103	ARG	2.3
1	A	463	ILE	2.3
1	L	271	ILE	2.3
1	L	86	ALA	2.3
1	L	91	ALA	2.3
1	L	285	ALA	2.3
1	L	416	ALA	2.3
1	L	427	GLY	2.3
1	D	444	LEU	2.3
1	B	309	PHE	2.3
1	C	203	ASN	2.3
1	A	81	ARG	2.3
1	E	387	GLN	2.3
1	H	190	LYS	2.3
1	C	473	ASP	2.3
1	C	565	VAL	2.3
1	D	415	VAL	2.3
1	J	117	GLU	2.2
1	A	587	PRO	2.2
1	H	122	GLY	2.2
1	H	494	ALA	2.2
1	J	107	ALA	2.2
1	F	329	LEU	2.2
1	F	444	LEU	2.2
1	L	479	THR	2.2
1	H	514	TYR	2.2
1	J	132	TYR	2.2
1	J	403	TYR	2.2
1	F	513	ARG	2.2
1	L	127	ARG	2.2
1	C	59	VAL	2.2
1	D	175	VAL	2.2
1	D	214	GLN	2.2
1	H	525	GLN	2.2
1	K	437	GLN	2.2
1	A	166	ASP	2.2
1	D	23	ASP	2.2
1	D	43	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	159	ASP	2.2
1	E	43	ASP	2.2
1	G	109	ILE	2.2
1	G	280	ILE	2.2
1	A	395	PRO	2.2
1	F	428	GLY	2.2
1	G	365	GLY	2.2
1	H	212	LEU	2.2
1	K	188	ALA	2.2
1	C	44	TRP	2.2
1	E	352	TRP	2.2
1	D	100	THR	2.2
1	F	313	LYS	2.2
1	F	361	HIS	2.2
1	H	386	THR	2.2
1	A	556	TYR	2.2
1	F	363	TYR	2.2
1	H	37	ARG	2.2
1	H	316	TYR	2.2
1	K	371	TYR	2.2
1	B	38	VAL	2.2
1	L	315	VAL	2.2
1	B	40	GLN	2.2
1	B	236	GLN	2.2
1	B	28	GLU	2.2
1	C	157	ILE	2.2
1	D	463	ILE	2.2
1	D	589	GLU	2.2
1	E	76	ILE	2.2
1	L	298	ILE	2.2
1	A	92	ASP	2.2
1	D	131	ASP	2.2
1	E	451	ASP	2.2
1	H	84	ASP	2.2
1	J	521	GLY	2.2
1	K	97	MET	2.2
1	L	43	ASP	2.2
1	D	262	GLY	2.2
1	K	345	PRO	2.2
1	L	424	ALA	2.2
1	B	278	LYS	2.2
1	C	350	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	G	336	PHE	2.2
1	D	37	ARG	2.2
1	K	146	ARG	2.2
1	J	106	THR	2.2
1	H	571	TYR	2.2
1	I	371	TYR	2.2
1	H	276	VAL	2.2
1	E	39	SER	2.2
1	E	264	ILE	2.2
1	A	444	LEU	2.2
1	A	503	GLU	2.2
1	B	242	GLU	2.2
1	G	296	GLU	2.2
1	B	428	GLY	2.2
1	G	299	PRO	2.2
1	G	564	GLY	2.2
1	I	400	ALA	2.2
1	B	443	ASP	2.2
1	C	131	ASP	2.2
1	D	378	ASP	2.2
1	F	58	ASP	2.2
1	H	206	ASP	2.2
1	B	145	ARG	2.2
1	K	323	THR	2.2
1	E	447	TYR	2.2
1	I	415	VAL	2.2
1	F	280	ILE	2.2
1	K	300	ILE	2.2
1	H	405	LEU	2.2
1	C	120	GLU	2.2
1	D	112	ASN	2.2
1	H	188	ALA	2.2
1	B	547	PRO	2.2
1	C	199	PRO	2.2
1	F	148	PRO	2.2
1	H	278	LYS	2.2
1	K	543	PRO	2.2
1	E	458	ARG	2.2
1	H	116	ARG	2.2
1	A	449	PHE	2.2
1	D	209	PHE	2.2
1	D	443	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	F	364	ASP	2.2
1	F	378	ASP	2.2
1	H	449	PHE	2.2
1	K	35	PHE	2.2
1	D	126	TRP	2.2
1	A	323	THR	2.1
1	C	581	VAL	2.1
1	D	111	VAL	2.1
1	F	78	VAL	2.1
1	G	38	VAL	2.1
1	G	100	THR	2.1
1	H	303	VAL	2.1
1	A	392	TYR	2.1
1	F	223	TYR	2.1
1	I	80	TYR	2.1
1	F	251	ILE	2.1
1	I	109	ILE	2.1
1	I	149	ILE	2.1
1	A	51	LEU	2.1
1	D	384	LEU	2.1
1	F	218	GLN	2.1
1	L	327	GLN	2.1
1	J	528	LYS	2.1
1	K	178	SER	2.1
1	L	160	SER	2.1
1	L	167	LYS	2.1
1	C	188	ALA	2.1
1	G	268	GLU	2.1
1	H	171	ARG	2.1
1	H	585	GLU	2.1
1	L	70	GLU	2.1
1	C	587	PRO	2.1
1	E	345	PRO	2.1
1	F	105	ASN	2.1
1	H	366	ASN	2.1
1	H	401	ASN	2.1
1	J	584	PRO	2.1
1	A	339	ASP	2.1
1	D	89	ASP	2.1
1	H	415	VAL	2.1
1	D	446	THR	2.1
1	G	386	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	H	455	THR	2.1
1	I	323	THR	2.1
1	B	372	TYR	2.1
1	D	176	ILE	2.1
1	I	464	TYR	2.1
1	J	176	ILE	2.1
1	A	450	GLN	2.1
1	D	544	GLN	2.1
1	D	575	GLN	2.1
1	F	355	GLN	2.1
1	H	362	MET	2.1
1	H	437	GLN	2.1
1	D	17	ALA	2.1
1	J	442	ALA	2.1
1	A	241	GLY	2.1
1	A	466	SER	2.1
1	C	410	SER	2.1
1	D	39	SER	2.1
1	H	36	SER	2.1
1	H	268	GLU	2.1
1	J	151	SER	2.1
1	E	140	ASN	2.1
1	E	141	ASN	2.1
1	F	222	PHE	2.1
1	F	359	PHE	2.1
1	G	309	PHE	2.1
1	L	477	ASN	2.1
1	A	111	VAL	2.1
1	I	59	VAL	2.1
1	L	470	ASP	2.1
1	F	219	ILE	2.1
1	F	479	THR	2.1
1	G	106	THR	2.1
1	G	323	THR	2.1
1	I	333	ILE	2.1
1	B	371	TYR	2.1
1	C	80	TYR	2.1
1	D	223	TYR	2.1
1	K	191	TYR	2.1
1	H	527	MET	2.1
1	A	357	ALA	2.1
1	B	142	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	543	PRO	2.1
1	F	485	GLY	2.1
1	J	589	GLU	2.1
1	A	279	SER	2.1
1	F	69	SER	2.1
1	E	31	ASN	2.1
1	L	182	ASN	2.1
1	D	468	VAL	2.1
1	A	519	ASP	2.1
1	A	535	ILE	2.1
1	C	298	ILE	2.1
1	F	166	ASP	2.1
1	G	94	LEU	2.1
1	H	176	ILE	2.1
1	K	509	ASP	2.1
1	F	171	ARG	2.1
1	K	127	ARG	2.1
1	B	567	MET	2.1
1	G	391	TYR	2.1
1	I	71	MET	2.1
1	B	533	ALA	2.1
1	C	285	ALA	2.1
1	I	342	ALA	2.1
1	J	390	ALA	2.1
1	K	232	ALA	2.1
1	L	267	ALA	2.1
1	A	529	GLN	2.1
1	E	202	GLN	2.1
1	A	222	PHE	2.1
1	B	62	PRO	2.1
1	C	414	GLU	2.1
1	D	221	GLU	2.1
1	F	548	GLU	2.1
1	H	385	PRO	2.1
1	K	230	GLU	2.1
1	C	245	SER	2.1
1	C	320	VAL	2.1
1	D	474	VAL	2.1
1	E	265	LYS	2.1
1	I	337	ASN	2.1
1	K	439	ASN	2.1
1	L	563	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	297	HIS	2.1
1	B	343	ARG	2.1
1	K	33	LEU	2.1
1	A	470	ASP	2.1
1	E	362	MET	2.1
1	F	509	ASP	2.1
1	I	18	ASP	2.1
1	I	325	ASP	2.1
1	I	362	MET	2.1
1	K	516	CYS	2.1
1	K	546	THR	2.1
1	L	102	MET	2.1
1	E	369	TYR	2.1
1	B	232	ALA	2.1
1	D	456	ALA	2.1
1	F	357	ALA	2.1
1	B	183	GLY	2.1
1	C	40	GLN	2.1
1	C	428	GLY	2.1
1	K	118	GLN	2.1
1	A	548	GLU	2.1
1	D	187	PHE	2.1
1	D	354	GLU	2.1
1	E	543	PRO	2.1
1	I	38	VAL	2.0
1	L	303	VAL	2.0
1	B	335	SER	2.0
1	C	119	ILE	2.0
1	C	531	ASN	2.0
1	D	275	ARG	2.0
1	D	331	ASN	2.0
1	F	331	ASN	2.0
1	G	105	ASN	2.0
1	H	105	ASN	2.0
1	K	81	ARG	2.0
1	K	205	ASN	2.0
1	K	401	ASN	2.0
1	L	471	ILE	2.0
1	A	223	TYR	2.0
1	A	363	TYR	2.0
1	E	408	ALA	2.0
1	E	421	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
1	H	50	THR	2.0
1	H	106	THR	2.0
1	I	570	ASP	2.0
1	J	372	TYR	2.0
1	K	250	ASP	2.0
1	L	519	ASP	2.0
1	A	85	GLY	2.0
1	D	75	PRO	2.0
1	D	222	PHE	2.0
1	J	96	GLY	2.0
1	K	238	PRO	2.0
1	C	548	GLU	2.0
1	D	495	GLU	2.0
1	H	396	GLU	2.0
1	J	414	GLU	2.0
1	K	406	GLU	2.0
1	L	83	LYS	2.0
1	A	497	VAL	2.0
1	A	506	VAL	2.0
1	L	93	VAL	2.0
1	B	51	LEU	2.0
1	G	258	LEU	2.0
1	H	103	ARG	2.0
1	H	532	ARG	2.0
1	D	264	ILE	2.0
1	F	463	ILE	2.0
1	G	523	SER	2.0
1	J	281	ILE	2.0
1	K	255	ILE	2.0
1	E	105	ASN	2.0
1	H	457	MET	2.0
1	H	579	MET	2.0
1	K	366	ASN	2.0
1	H	369	TYR	2.0
1	H	586	THR	2.0
1	K	86	ALA	2.0
1	L	90	ALA	2.0
1	D	571	TYR	2.0
1	F	80	TYR	2.0
1	F	369	TYR	2.0
1	B	460	ASP	2.0
1	G	197	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
1	J	250	ASP	2.0
1	A	524	PHE	2.0
1	C	427	GLY	2.0
1	D	57	PHE	2.0
1	L	34	PHE	2.0
1	E	83	LYS	2.0
1	E	327	GLN	2.0
1	J	525	GLN	2.0
1	B	468	VAL	2.0
1	C	566	GLU	2.0
1	F	274	ARG	2.0
1	C	212	LEU	2.0
1	D	266	ILE	2.0
1	K	298	ILE	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.