



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 09:06 PM EDT

PDB ID : 7DQD / pdb_00007dqd
Title : Crystal structure of the AMP-PNP-bound mutant A(S23C)3B(N64C)3 complex from enterococcus hirae V-ATPase
Authors : Maruyama, S.; Suzuki, K.; Mizutani, K.; Imai, F.L.; Ishizuka-Katsura, Y.; Shirouzu, M.; Murata, T.
Deposited on : 2020-12-23
Resolution : 3.38 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

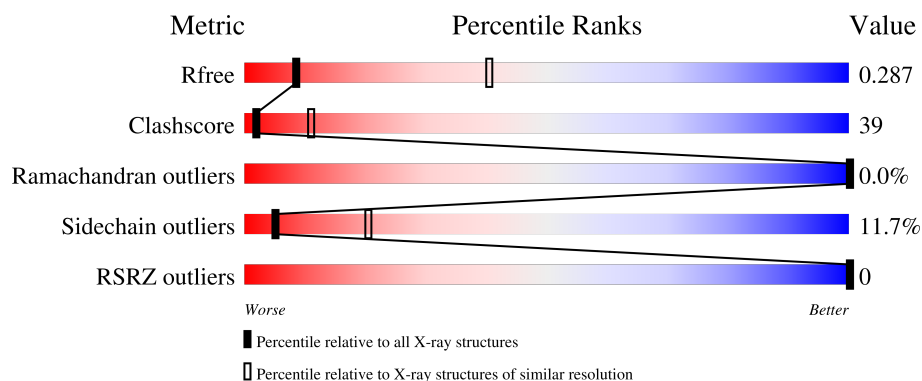
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.38 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.



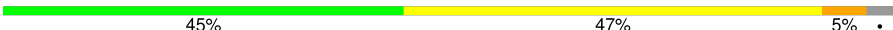
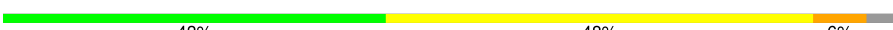
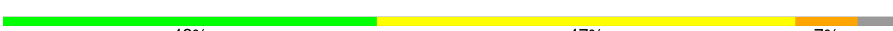
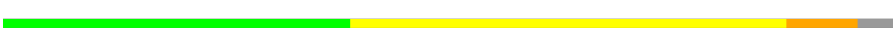
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1047 (3.42-3.34)
Clashscore	190562	1067 (3.42-3.34)
Ramachandran outliers	187476	1056 (3.42-3.34)
Sidechain outliers	187428	1056 (3.42-3.34)
RSRZ outliers	180081	1047 (3.42-3.34)

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	600	
1	B	600	
1	C	600	
1	I	600	

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Mol	Chain	Length	Quality of chain
1	J	600	 45% 47% 5% .
1	K	600	 46% 47% . .
2	D	465	 38% 50% 8% .
2	E	465	 43% 48% 6% .
2	F	465	 42% 47% 7% .
2	L	465	 39% 49% 8% .
2	M	465	 43% 46% 8% .
2	N	465	 40% 44% 8% 8%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	ANP	B	601	-	-	X	-
4	ANP	C	601	-	-	X	-
4	ANP	K	601	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 46492 atoms, of which 8 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 V-type sodium ATPase catalytic subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	584	Total	C	N	O	S	0	0	0
			4448	2789	751	883	25			
1	B	584	Total	C	N	O	S	0	0	0
			4443	2788	752	877	26			
1	C	584	Total	C	N	O	S	0	0	0
			4274	2682	728	840	24			
1	I	583	Total	C	N	O	S	0	0	0
			4291	2687	729	853	22			
1	J	584	Total	C	N	O	S	0	0	0
			4422	2781	748	866	27			
1	K	584	Total	C	N	O	S	0	0	0
			4435	2783	749	876	27			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	GLY	-	expression tag	UNP Q08636
A	-5	SER	-	expression tag	UNP Q08636
A	-4	SER	-	expression tag	UNP Q08636
A	-3	GLY	-	expression tag	UNP Q08636
A	-2	SER	-	expression tag	UNP Q08636
A	-1	SER	-	expression tag	UNP Q08636
A	0	GLY	-	expression tag	UNP Q08636
A	23	CYS	SER	engineered mutation	UNP Q08636
B	-6	GLY	-	expression tag	UNP Q08636
B	-5	SER	-	expression tag	UNP Q08636
B	-4	SER	-	expression tag	UNP Q08636
B	-3	GLY	-	expression tag	UNP Q08636
B	-2	SER	-	expression tag	UNP Q08636
B	-1	SER	-	expression tag	UNP Q08636
B	0	GLY	-	expression tag	UNP Q08636
B	23	CYS	SER	engineered mutation	UNP Q08636
C	-6	GLY	-	expression tag	UNP Q08636

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	SER	-	expression tag	UNP Q08636
C	-4	SER	-	expression tag	UNP Q08636
C	-3	GLY	-	expression tag	UNP Q08636
C	-2	SER	-	expression tag	UNP Q08636
C	-1	SER	-	expression tag	UNP Q08636
C	0	GLY	-	expression tag	UNP Q08636
C	23	CYS	SER	engineered mutation	UNP Q08636
I	-6	GLY	-	expression tag	UNP Q08636
I	-5	SER	-	expression tag	UNP Q08636
I	-4	SER	-	expression tag	UNP Q08636
I	-3	GLY	-	expression tag	UNP Q08636
I	-2	SER	-	expression tag	UNP Q08636
I	-1	SER	-	expression tag	UNP Q08636
I	0	GLY	-	expression tag	UNP Q08636
I	23	CYS	SER	engineered mutation	UNP Q08636
J	-6	GLY	-	expression tag	UNP Q08636
J	-5	SER	-	expression tag	UNP Q08636
J	-4	SER	-	expression tag	UNP Q08636
J	-3	GLY	-	expression tag	UNP Q08636
J	-2	SER	-	expression tag	UNP Q08636
J	-1	SER	-	expression tag	UNP Q08636
J	0	GLY	-	expression tag	UNP Q08636
J	23	CYS	SER	engineered mutation	UNP Q08636
K	-6	GLY	-	expression tag	UNP Q08636
K	-5	SER	-	expression tag	UNP Q08636
K	-4	SER	-	expression tag	UNP Q08636
K	-3	GLY	-	expression tag	UNP Q08636
K	-2	SER	-	expression tag	UNP Q08636
K	-1	SER	-	expression tag	UNP Q08636
K	0	GLY	-	expression tag	UNP Q08636
K	23	CYS	SER	engineered mutation	UNP Q08636

- Molecule 2 is a protein called V-type sodium ATPase subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	447	Total	C	N	O	S	0	0	0
			3383	2137	589	642	15			
2	E	453	Total	C	N	O	S	0	0	0
			3400	2152	592	643	13			
2	F	445	Total	C	N	O	S	0	0	0
			3295	2080	579	621	15			
2	L	447	Total	C	N	O	S	0	0	0
			3428	2167	591	655	15			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	M	453	Total	C	N	O	S	0	0	0
			3357	2119	586	639	13			
2	N	429	Total	C	N	O	S	0	0	0
			3162	1999	549	600	14			

There are 48 discrepancies between the modelled and reference sequences:

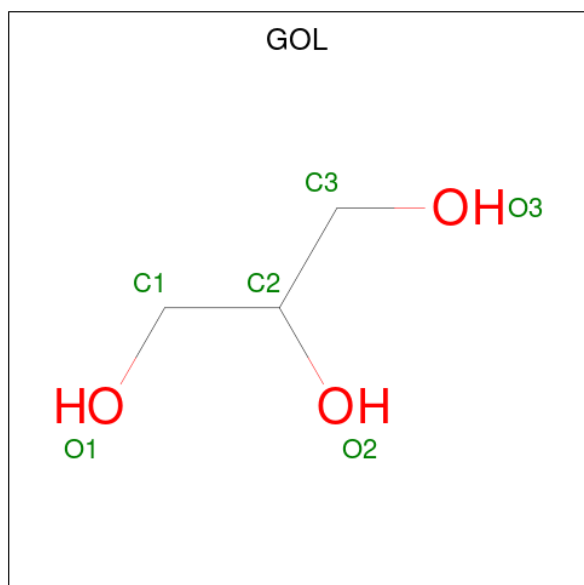
Chain	Residue	Modelled	Actual	Comment	Reference
D	-6	GLY	-	expression tag	UNP Q08637
D	-5	SER	-	expression tag	UNP Q08637
D	-4	SER	-	expression tag	UNP Q08637
D	-3	GLY	-	expression tag	UNP Q08637
D	-2	SER	-	expression tag	UNP Q08637
D	-1	SER	-	expression tag	UNP Q08637
D	0	GLY	-	expression tag	UNP Q08637
D	64	CYS	ASN	engineered mutation	UNP Q08637
E	-6	GLY	-	expression tag	UNP Q08637
E	-5	SER	-	expression tag	UNP Q08637
E	-4	SER	-	expression tag	UNP Q08637
E	-3	GLY	-	expression tag	UNP Q08637
E	-2	SER	-	expression tag	UNP Q08637
E	-1	SER	-	expression tag	UNP Q08637
E	0	GLY	-	expression tag	UNP Q08637
E	64	CYS	ASN	engineered mutation	UNP Q08637
F	-6	GLY	-	expression tag	UNP Q08637
F	-5	SER	-	expression tag	UNP Q08637
F	-4	SER	-	expression tag	UNP Q08637
F	-3	GLY	-	expression tag	UNP Q08637
F	-2	SER	-	expression tag	UNP Q08637
F	-1	SER	-	expression tag	UNP Q08637
F	0	GLY	-	expression tag	UNP Q08637
F	64	CYS	ASN	engineered mutation	UNP Q08637
L	-6	GLY	-	expression tag	UNP Q08637
L	-5	SER	-	expression tag	UNP Q08637
L	-4	SER	-	expression tag	UNP Q08637
L	-3	GLY	-	expression tag	UNP Q08637
L	-2	SER	-	expression tag	UNP Q08637
L	-1	SER	-	expression tag	UNP Q08637
L	0	GLY	-	expression tag	UNP Q08637
L	64	CYS	ASN	engineered mutation	UNP Q08637
M	-6	GLY	-	expression tag	UNP Q08637
M	-5	SER	-	expression tag	UNP Q08637

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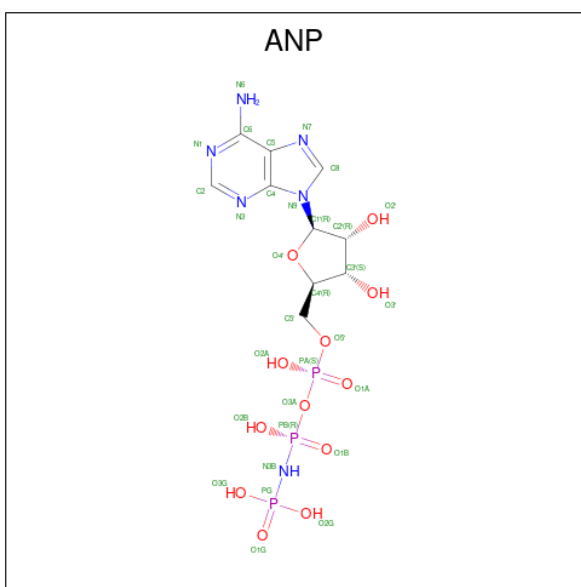
Chain	Residue	Modelled	Actual	Comment	Reference
M	-4	SER	-	expression tag	UNP Q08637
M	-3	GLY	-	expression tag	UNP Q08637
M	-2	SER	-	expression tag	UNP Q08637
M	-1	SER	-	expression tag	UNP Q08637
M	0	GLY	-	expression tag	UNP Q08637
M	64	CYS	ASN	engineered mutation	UNP Q08637
N	-6	GLY	-	expression tag	UNP Q08637
N	-5	SER	-	expression tag	UNP Q08637
N	-4	SER	-	expression tag	UNP Q08637
N	-3	GLY	-	expression tag	UNP Q08637
N	-2	SER	-	expression tag	UNP Q08637
N	-1	SER	-	expression tag	UNP Q08637
N	0	GLY	-	expression tag	UNP Q08637
N	64	CYS	ASN	engineered mutation	UNP Q08637

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	C	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	J	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	K	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Mg	0	0
			1	1		
5	C	1	Total	Mg	0	0
			1	1		
5	J	1	Total	Mg	0	0
			1	1		
5	K	1	Total	Mg	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	O	0	0
			1	1		

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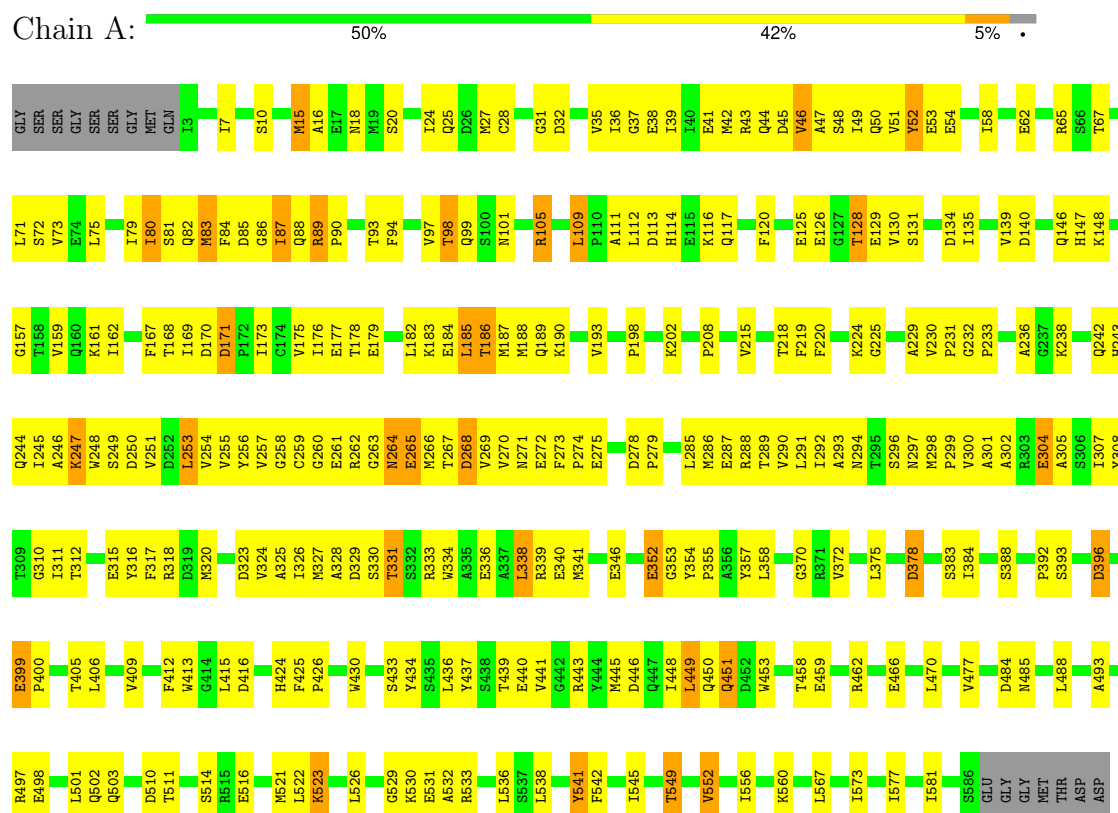
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total 1	O 1	0	0
6	C	1	Total 1	O 1	0	0
6	E	1	Total 1	O 1	0	0
6	I	2	Total 2	O 2	0	0
6	L	1	Total 1	O 1	0	0
6	M	1	Total 1	O 1	0	0
6	N	4	Total 4	O 4	0	0

3 Residue-property plots

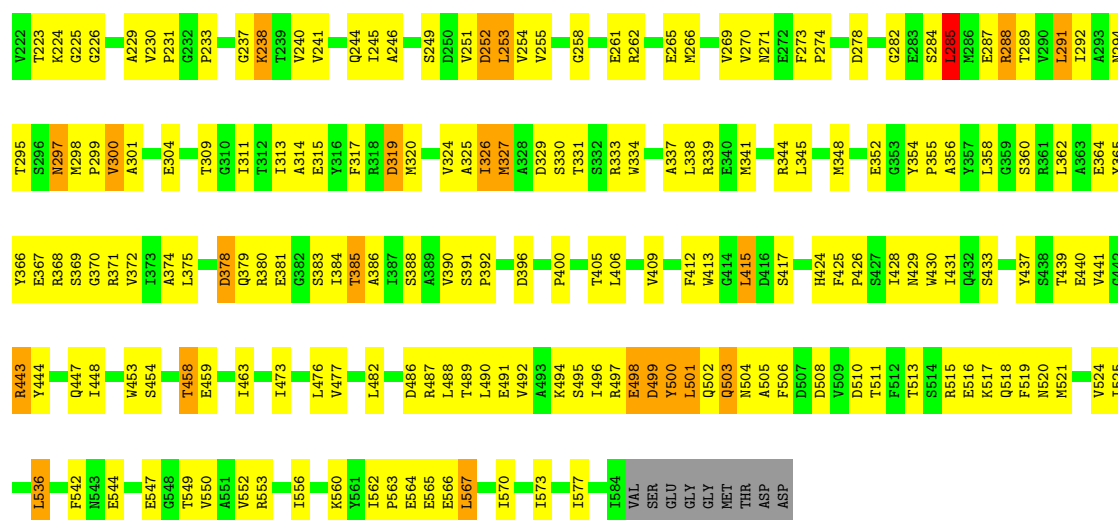
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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



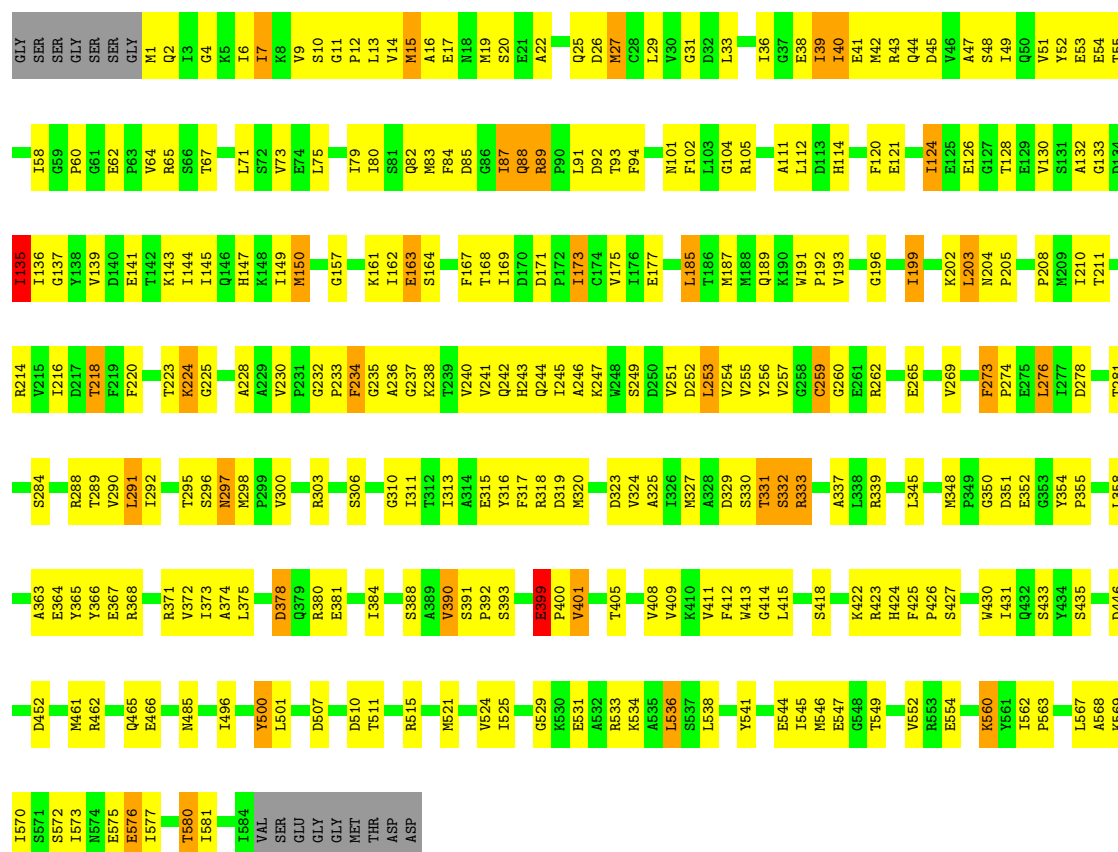
• Molecule 1: V-type sodium ATPase catalytic subunit A





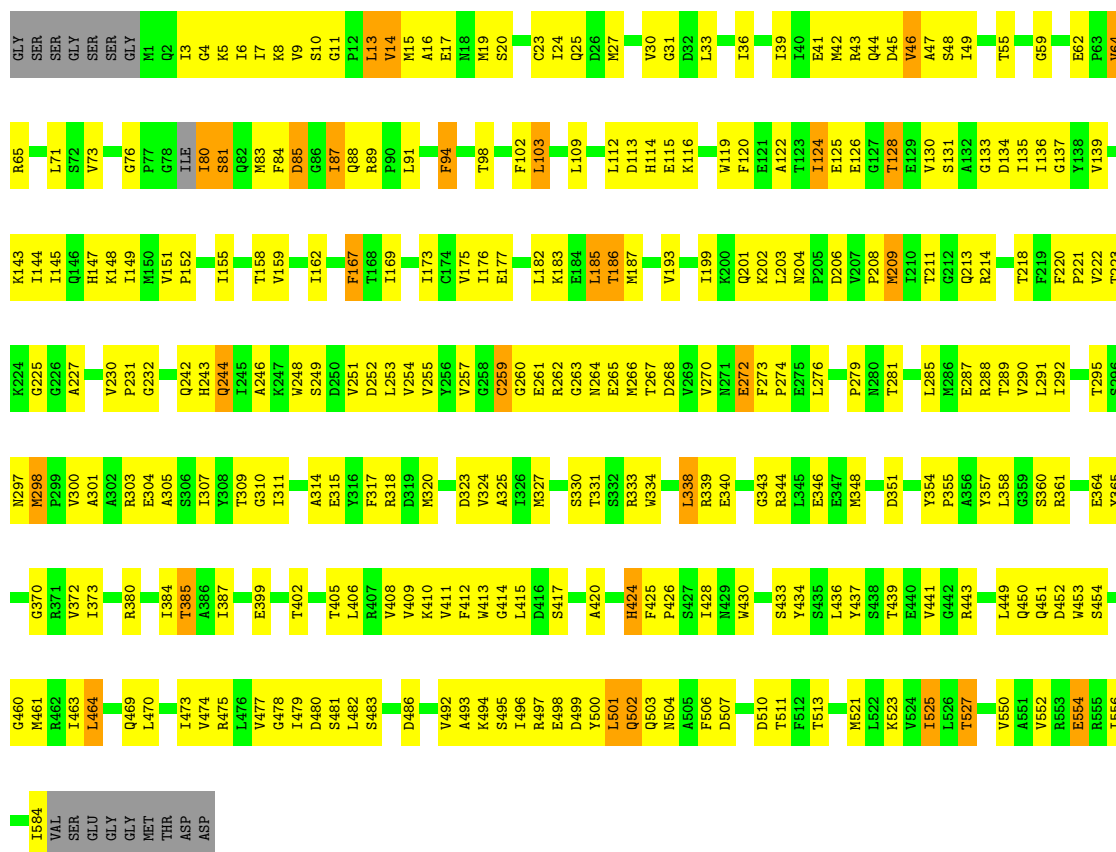
• Molecule 1: V-type sodium ATPase catalytic subunit A

Chain C: 50% 41% 6%



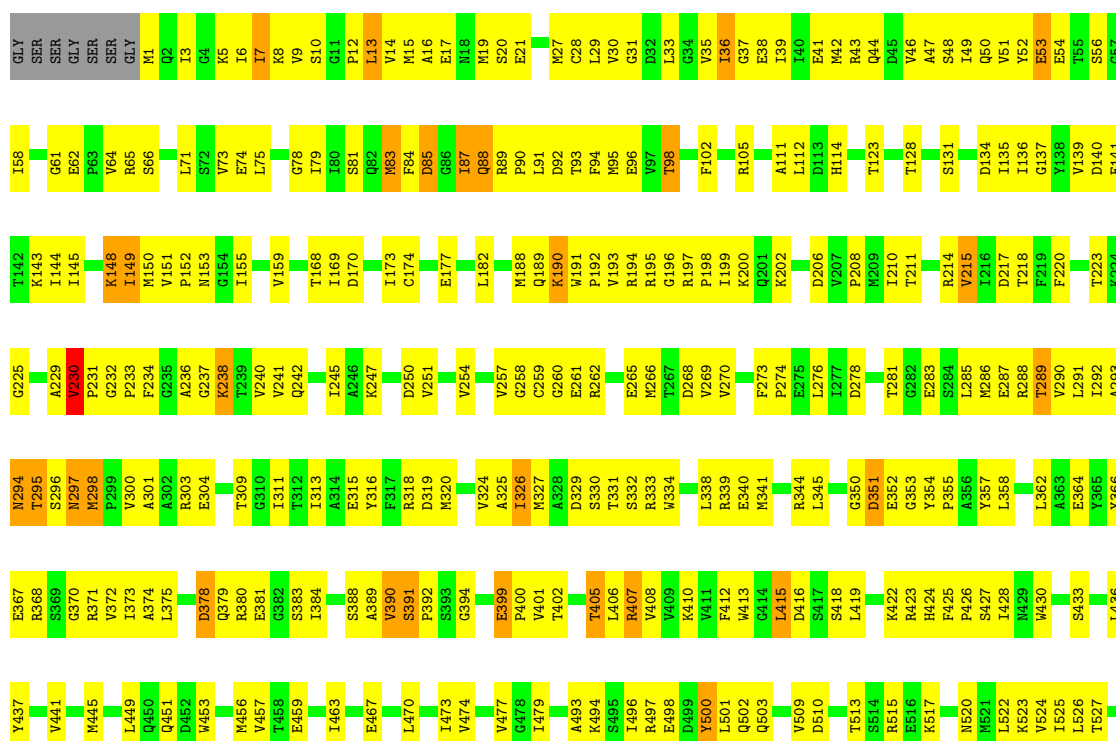
• Molecule 1: V-type sodium ATPase catalytic subunit A

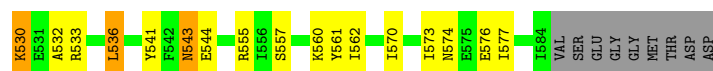
Chain I: 50% 42% 5%



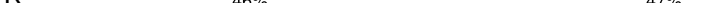
- Molecule 1: V-type sodium ATPase catalytic subunit A

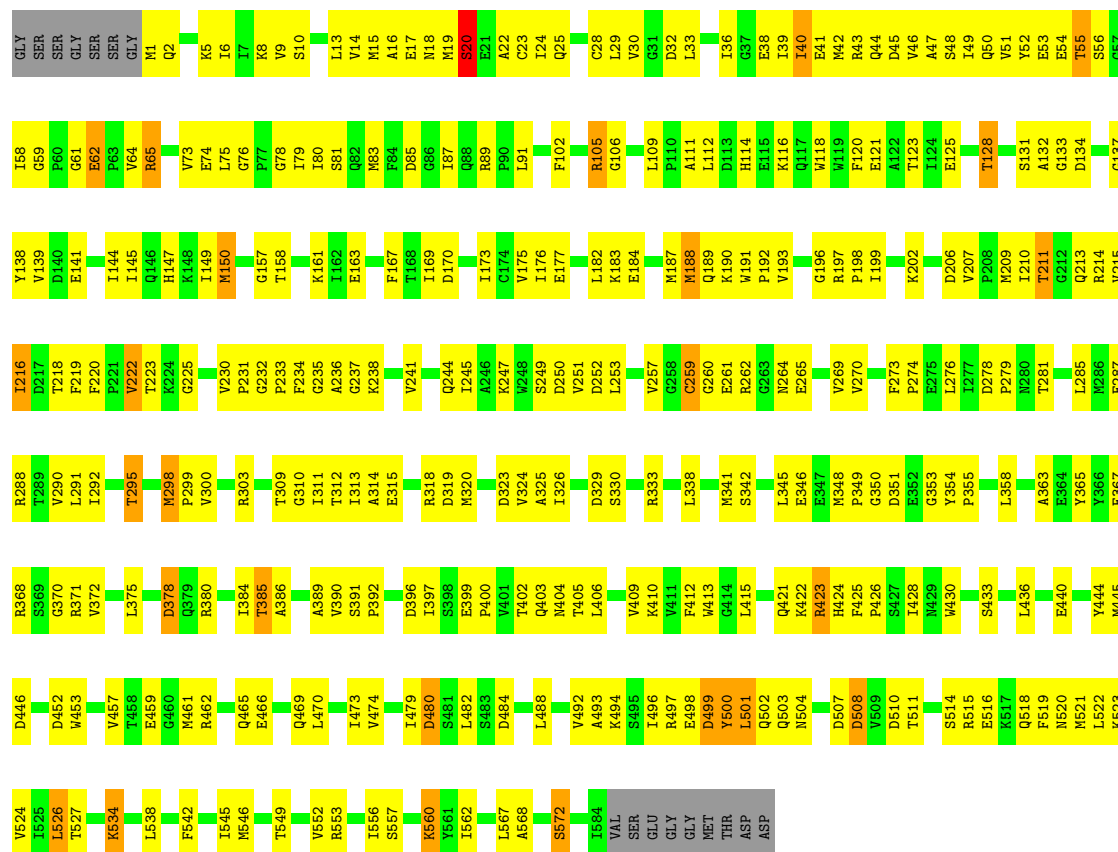
Chain J: 45% 47% 5%





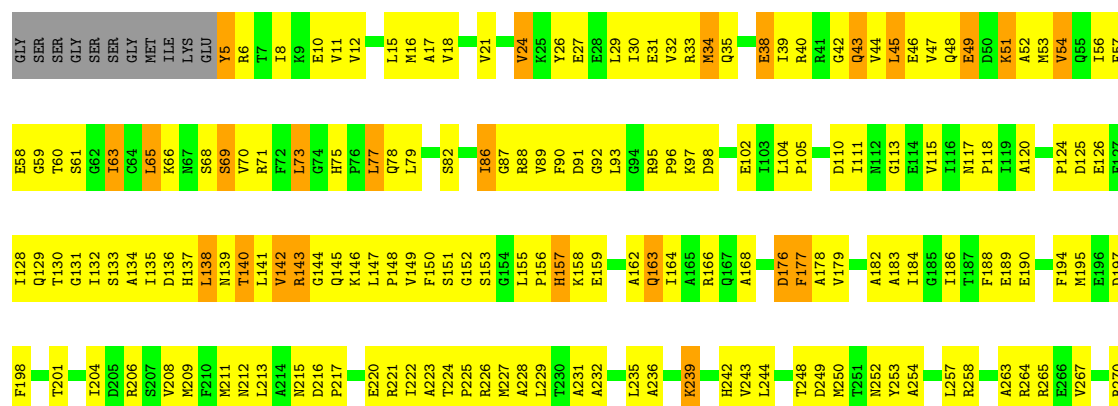
- Molecule 1: V-type sodium ATPase catalytic subunit A

Chain K:  46% 47% . .

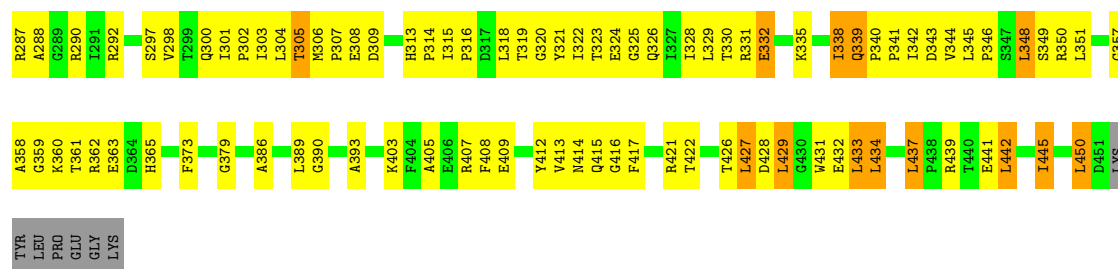


- Molecule 2: V-type sodium ATPase subunit B

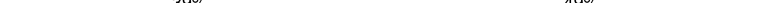
Chain D: 38% 50% 8% .

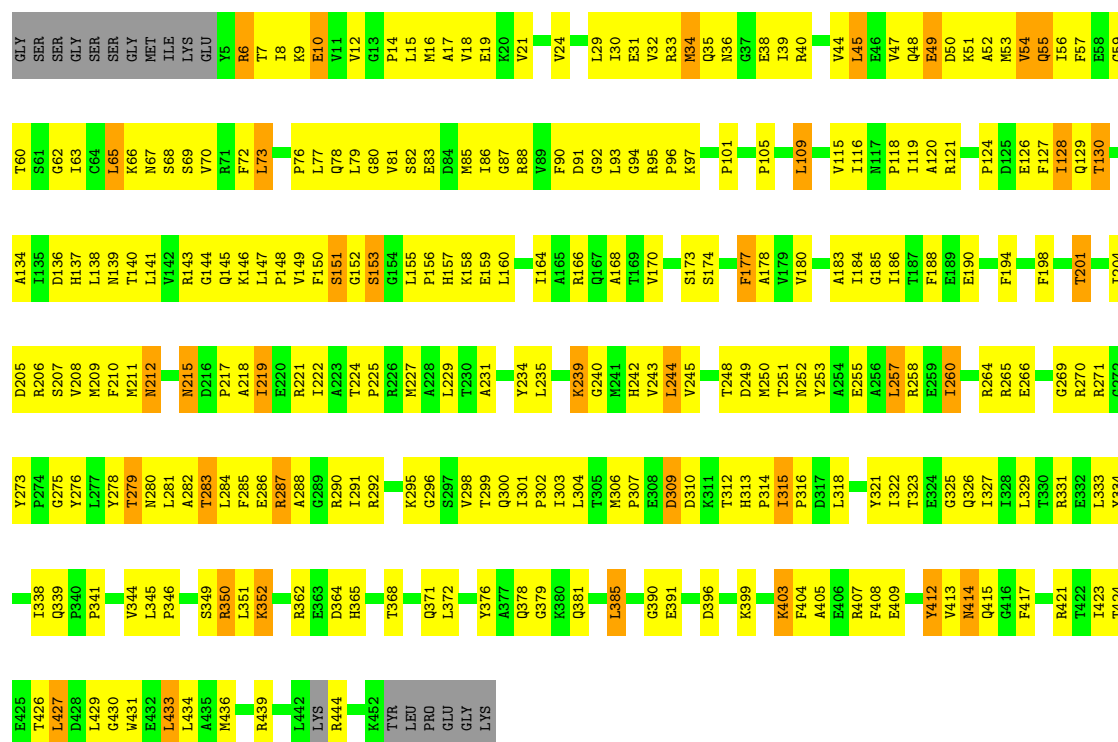




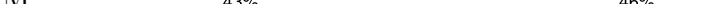


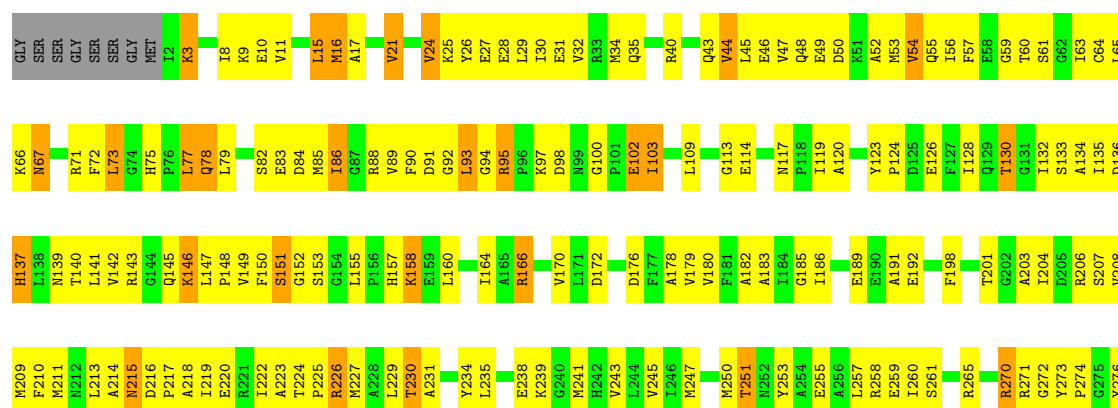
- Molecule 2: V-type sodium ATPase subunit B

Chain L:  39% 49% 8% 4%



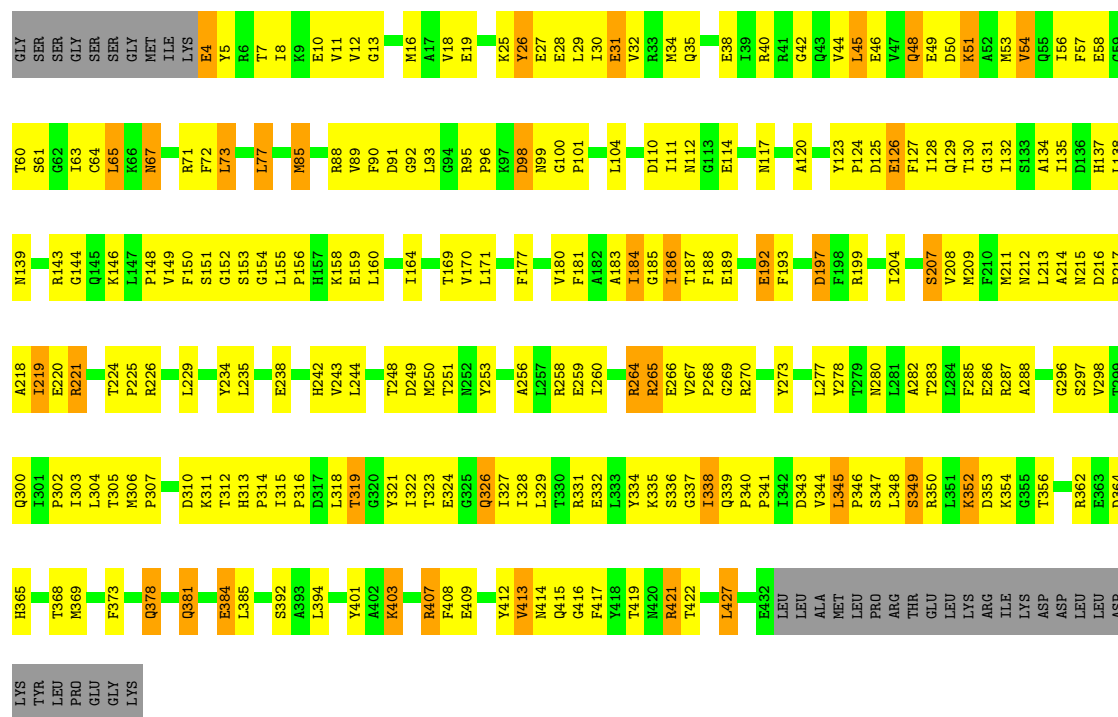
- Molecule 2: V-type sodium ATPase subunit B

Chain M:  43% 46% 8%





• Molecule 2: V-type sodium ATPase subunit B



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	117.57Å 123.38Å 230.28Å 90.00° 90.07° 90.00°	Depositor
Resolution (Å)	49.37 – 3.38 49.37 – 3.38	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.37-3.38) 99.5 (49.37-3.38)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.77 (at 3.40Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.261 , 0.286 0.261 , 0.287	Depositor DCC
R_{free} test set	4725 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	77.5	Xtriage
Anisotropy	0.202	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 91.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.069 for -k,-h,-l 0.075 for k,h,-l 0.248 for h,-k,-l	Xtriage
Reported twinning fraction	0.350 for -h,-k,l	Depositor
Outliers	0 of 91940 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	46492	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.08% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ANP, MG, GOL

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	0.26	0/4524	0.74	2/6132 (0.0%)
1	B	0.29	0/4519	0.75	3/6125 (0.0%)
1	C	0.27	0/4346	0.75	4/5903 (0.1%)
1	I	0.27	0/4361	0.78	4/5929 (0.1%)
1	J	0.33	1/4498 (0.0%)	0.80	7/6096 (0.1%)
1	K	0.27	0/4511	0.73	3/6115 (0.0%)
2	D	0.30	0/3443	0.76	4/4660 (0.1%)
2	E	0.27	0/3461	0.75	0/4693
2	F	0.27	0/3351	0.76	2/4548 (0.0%)
2	L	0.26	0/3488	0.72	0/4717
2	M	0.26	0/3413	0.72	1/4626 (0.0%)
2	N	0.30	0/3218	0.74	0/4367
All	All	0.28	1/47133 (0.0%)	0.75	30/63911 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	390	VAL	C-O	-6.05	1.17	1.24

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	87	ILE	N-CA-C	8.91	119.72	110.72
2	D	339	GLN	C-N-CD	-8.10	102.78	120.60
1	I	399	GLU	CA-C-N	6.47	125.90	118.85
1	I	399	GLU	C-N-CA	6.47	125.90	118.85
1	J	399	GLU	CA-C-N	6.44	126.36	119.28
1	J	399	GLU	C-N-CA	6.44	126.36	119.28
2	D	339	GLN	CA-C-N	6.43	142.43	127.00
2	D	339	GLN	C-N-CA	6.43	142.43	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	390	VAL	CA-C-N	-6.19	111.04	122.06
1	J	390	VAL	C-N-CA	-6.19	111.04	122.06
1	J	230	VAL	CA-C-N	5.83	127.13	119.84
1	J	230	VAL	C-N-CA	5.83	127.13	119.84
2	M	417	PHE	CB-CA-C	-5.70	110.02	116.63
1	K	562	ILE	CA-C-N	5.67	125.68	119.90
1	K	562	ILE	C-N-CA	5.67	125.68	119.90
2	D	325	GLY	N-CA-C	-5.60	105.70	112.48
1	K	20	SER	CB-CA-C	-5.55	109.68	117.23
1	J	44	GLN	CB-CA-C	-5.51	109.73	117.23
1	I	85	ASP	N-CA-C	-5.47	103.27	110.33
2	F	123	TYR	CA-C-N	5.47	126.67	119.84
2	F	123	TYR	C-N-CA	5.47	126.67	119.84
1	A	278	ASP	CA-C-N	5.46	124.92	119.24
1	A	278	ASP	C-N-CA	5.46	124.92	119.24
1	B	285	LEU	N-CA-C	5.40	116.86	110.97
1	C	567	LEU	CB-CA-C	-5.38	110.39	116.63
1	C	135	ILE	N-CA-C	5.21	117.36	108.86
1	B	289	THR	N-CA-C	5.05	117.49	109.50
1	C	399	GLU	CA-C-N	5.05	125.08	119.32
1	C	399	GLU	C-N-CA	5.05	125.08	119.32
1	B	44	GLN	CB-CA-C	-5.03	110.39	117.23

There are no chirality outliers.

There are no planarity outliers.

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	4448	0	4297	303	0
1	B	4443	0	4280	339	0
1	C	4274	0	3998	291	0
1	I	4291	0	4030	290	0
1	J	4422	0	4271	357	0
1	K	4435	0	4281	364	0
2	D	3383	0	3279	309	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	3400	0	3255	271	0
2	F	3295	0	3157	271	0
2	L	3428	0	3377	327	0
2	M	3357	0	3207	286	0
2	N	3162	0	2993	315	0
3	A	6	8	8	0	0
4	B	31	0	13	9	0
4	C	31	0	13	14	0
4	J	31	0	13	7	0
4	K	31	0	13	16	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	J	1	0	0	0	0
5	K	1	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	E	1	0	0	0	0
6	I	2	0	0	3	0
6	L	1	0	0	0	0
6	M	1	0	0	1	0
6	N	4	0	0	0	0
All	All	46484	8	44485	3512	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 39.

All (3512) 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:20:SER:HB3	1:I:45:ASP:HB2	1.25	1.16
1:K:497:ARG:HA	1:K:501:LEU:HG	1.28	1.16
1:J:9:VAL:HG21	1:J:58:ILE:HB	1.27	1.16
1:J:215:VAL:HB	1:J:501:LEU:HA	1.23	1.15
1:B:497:ARG:HA	1:B:501:LEU:HB2	1.29	1.14
1:C:10:SER:HB2	2:F:46:GLU:HG3	1.30	1.13
2:L:18:VAL:HB	2:L:52:ALA:HB3	1.25	1.12
1:K:24:ILE:HD12	1:K:41:GLU:HA	1.32	1.11
2:M:82:SER:HB3	2:M:103:ILE:HD11	1.13	1.11
1:C:577:ILE:HG22	1:C:581:ILE:HD11	1.30	1.10
1:K:232:GLY:HA3	1:K:415:LEU:HD12	1.25	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:601:ANP:H5'2	2:N:350:ARG:HD3	1.32	1.10
2:M:128:ILE:HG13	2:M:143:ARG:HG2	1.32	1.10
2:F:198:PHE:HB3	2:F:204:ILE:HB	1.25	1.09
2:N:128:ILE:HA	2:N:170:VAL:HA	1.36	1.08
1:A:264:ASN:HD21	2:D:324:GLU:HG2	1.10	1.06
2:N:338:ILE:HB	2:N:414:ASN:HD22	1.15	1.06
2:N:326:GLN:HG3	2:N:348:LEU:HB3	1.38	1.06
1:K:55:THR:HG22	1:K:58:ILE:HD12	1.39	1.05
1:K:188:MET:HE1	1:K:190:LYS:HG3	1.35	1.05
2:E:132:ILE:HG12	2:E:340:PRO:HG3	1.39	1.04
1:I:264:ASN:HB3	2:L:351:LEU:HD11	1.38	1.03
1:K:41:GLU:HG2	2:L:12:VAL:HG13	1.36	1.03
2:F:44:VAL:HG22	2:F:54:VAL:HG12	1.36	1.03
2:L:149:VAL:HA	2:L:327:ILE:HB	1.41	1.02
1:K:43:ARG:HA	2:L:10:GLU:HB3	1.38	1.02
2:E:270:ARG:HG2	2:E:271:ARG:HG2	1.38	1.01
1:K:8:LYS:HB2	2:N:48:GLN:HB3	1.39	1.01
1:B:27:MET:HE1	1:B:38:GLU:HG2	1.41	1.00
1:J:17:GLU:HA	1:J:46:VAL:HG22	1.37	1.00
1:B:202:LYS:HG2	1:B:372:VAL:HG12	1.44	1.00
2:L:6:ARG:HB3	2:L:6:ARG:HH21	1.27	1.00
1:J:392:PRO:HB3	1:J:399:GLU:HB2	1.42	1.00
1:A:39:ILE:HG12	1:A:49:ILE:HG23	1.40	0.99
1:B:11:GLY:HA2	1:B:55:THR:HG21	1.42	0.99
2:F:338:ILE:HB	2:F:414:ASN:HD22	1.29	0.98
2:F:93:LEU:HD12	2:F:95:ARG:HH22	1.28	0.98
2:E:21:VAL:HG11	2:E:52:ALA:HB2	1.43	0.97
1:J:73:VAL:HG12	1:J:88:GLN:HG3	1.46	0.97
1:J:262:ARG:NH2	2:M:321:TYR:O	1.96	0.97
1:B:13:LEU:HD22	1:B:345:LEU:HD22	1.43	0.97
1:C:83:MET:HG3	2:F:119:ILE:HD11	1.46	0.97
2:F:325:GLY:HA3	2:F:326:GLN:HG2	1.47	0.96
2:L:32:VAL:HG22	2:L:70:VAL:HG22	1.46	0.96
1:A:264:ASN:ND2	2:D:351:LEU:HD11	1.81	0.95
2:E:166:ARG:HD2	2:E:201:THR:HG21	1.48	0.95
2:D:140:THR:CB	2:D:352:LYS:HB2	1.97	0.95
1:C:135:ILE:HD11	1:C:150:MET:HA	1.48	0.95
2:D:304:LEU:HD22	2:D:315:ILE:HG22	1.51	0.93
1:B:285:LEU:CD1	1:B:288:ARG:HD2	1.98	0.93
2:E:372:LEU:HD21	2:E:412:TYR:HE1	1.33	0.92
1:B:230:VAL:HG22	1:B:413:TRP:HB2	1.50	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:249:SER:O	1:B:288:ARG:NH1	2.02	0.91
1:C:139:VAL:HG23	1:C:149:ILE:HD11	1.52	0.91
1:J:35:VAL:HB	1:J:53:GLU:HB2	1.52	0.91
1:C:572:SER:O	1:C:576:GLU:N	2.03	0.91
1:A:264:ASN:HD21	2:D:324:GLU:CG	1.82	0.91
1:A:297:ASN:HB2	2:D:286:GLU:HG3	1.53	0.90
2:M:345:LEU:HA	2:M:373:PHE:HZ	1.37	0.90
2:D:140:THR:HB	2:D:352:LYS:HB2	1.53	0.90
2:L:6:ARG:CZ	2:L:69:SER:HA	2.01	0.90
2:L:16:MET:HB2	2:L:54:VAL:HG22	1.52	0.89
2:L:148:PRO:HG2	2:L:326:GLN:HA	1.51	0.89
1:A:73:VAL:HG13	1:A:193:VAL:HG12	1.54	0.89
2:L:352:LYS:H	2:L:352:LYS:HZ3	0.93	0.89
1:J:362:LEU:HD13	1:J:405:THR:HG23	1.52	0.89
2:F:338:ILE:HB	2:F:414:ASN:ND2	1.87	0.89
2:M:145:GLN:HB2	2:M:351:LEU:HD12	1.53	0.89
1:C:202:LYS:HG3	1:C:372:VAL:HG12	1.52	0.89
2:N:91:ASP:N	2:N:95:ARG:O	2.06	0.89
2:N:44:VAL:CG2	2:N:54:VAL:HG12	2.03	0.88
1:A:24:ILE:HG22	1:A:25:GLN:HG2	1.53	0.88
2:D:29:LEU:HB2	2:D:73:LEU:HD11	1.53	0.88
1:B:208:PRO:HA	1:B:223:THR:HA	1.55	0.88
1:A:126:GLU:HG2	1:A:162:ILE:HG22	1.56	0.88
4:C:601:ANP:O3'	2:F:350:ARG:HA	1.73	0.87
1:I:318:ARG:HG3	1:I:384:ILE:HG13	1.55	0.87
1:A:215:VAL:HG23	1:A:219:PHE:HD2	1.39	0.87
2:N:152:GLY:H	2:N:155:LEU:HD12	1.36	0.87
1:J:358:LEU:HD21	1:J:401:VAL:HG22	1.56	0.87
2:N:150:PHE:HB2	2:N:328:ILE:HD13	1.56	0.87
1:C:355:PRO:HG2	1:C:358:LEU:HB2	1.57	0.86
1:J:150:MET:O	1:J:152:PRO:HD3	1.75	0.86
2:F:16:MET:HB2	2:F:54:VAL:HG23	1.57	0.86
2:N:8:ILE:HA	2:N:18:VAL:HA	1.57	0.86
1:C:73:VAL:HG12	1:C:88:GLN:HG3	1.56	0.86
2:D:362:ARG:HG3	2:D:427:LEU:HD13	1.56	0.86
2:M:179:VAL:HB	2:M:207:SER:HB3	1.58	0.86
2:N:138:LEU:HD13	2:N:344:VAL:HG11	1.55	0.86
1:I:20:SER:HA	1:I:42:MET:HE1	1.57	0.86
2:D:145:GLN:HG3	2:D:351:LEU:HD12	1.55	0.86
1:K:211:THR:HB	1:K:216:ILE:HD13	1.57	0.86
1:I:4:GLY:HA3	1:I:19:MET:HE1	1.57	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:81:SER:HB3	1:I:287:GLU:HA	1.58	0.85
2:D:128:ILE:HD11	2:D:143:ARG:HA	1.57	0.85
1:K:213:GLN:CB	1:K:216:ILE:HD11	2.05	0.85
1:K:231:PRO:HB3	1:K:390:VAL:HB	1.58	0.85
1:J:84:PHE:HB2	1:J:292:ILE:HG13	1.57	0.85
2:M:15:LEU:HD22	2:M:55:GLN:HB2	1.56	0.85
1:B:496:ILE:HG12	1:B:525:ILE:HG21	1.57	0.85
1:B:497:ARG:O	1:B:502:GLN:N	2.09	0.85
1:C:251:VAL:HG21	1:C:325:ALA:HB2	1.57	0.85
2:E:132:ILE:HG12	2:E:340:PRO:CG	2.08	0.84
2:F:152:GLY:H	2:F:155:LEU:HD12	1.41	0.84
2:N:346:PRO:HB2	2:N:347:SER:C	2.02	0.84
1:K:19:MET:HE2	1:K:39:ILE:HD13	1.59	0.84
1:K:85:ASP:OD1	1:K:89:ARG:N	2.11	0.84
1:A:231:PRO:HG2	1:A:415:LEU:H	1.40	0.84
1:B:31:GLY:HA2	1:B:62:GLU:HB3	1.58	0.84
1:A:264:ASN:ND2	2:D:324:GLU:HG2	1.91	0.84
1:C:577:ILE:HG22	1:C:581:ILE:CD1	2.07	0.84
1:C:10:SER:HB2	2:F:46:GLU:CG	2.07	0.84
2:L:278:TYR:HE1	2:L:322:ILE:HG12	1.40	0.84
1:J:6:ILE:HG23	1:J:16:ALA:HB2	1.57	0.84
1:K:231:PRO:HA	1:K:390:VAL:O	1.77	0.84
2:L:148:PRO:HA	2:L:302:PRO:HG2	1.59	0.84
2:N:282:ALA:HA	2:N:322:ILE:HG21	1.58	0.84
2:E:151:SER:O	2:E:306:MET:N	2.11	0.83
1:I:8:LYS:HB3	1:I:15:MET:HB2	1.60	0.83
2:D:179:VAL:HG22	2:D:244:LEU:HB3	1.59	0.83
2:E:29:LEU:HB3	2:E:73:LEU:HD21	1.60	0.83
2:E:35:GLN:HB3	2:E:67:ASN:HB3	1.60	0.83
1:A:497:ARG:HG2	1:A:501:LEU:HD12	1.60	0.83
1:A:27:MET:HE1	1:A:38:GLU:HG3	1.60	0.83
4:C:601:ANP:H4'	2:F:348:LEU:HD21	1.60	0.83
1:K:9:VAL:HG22	1:K:14:VAL:HG13	1.61	0.83
2:M:371:GLN:HG2	2:M:445:ILE:HD11	1.61	0.83
2:F:358:ALA:N	2:F:359:GLY:HA3	1.93	0.83
2:N:126:GLU:HB3	2:N:143:ARG:HG3	1.61	0.83
1:I:340:GLU:HG3	2:L:276:TYR:HA	1.60	0.82
1:J:415:LEU:HD22	1:J:428:ILE:HG13	1.58	0.82
2:M:82:SER:HB3	2:M:103:ILE:CD1	2.05	0.82
2:E:132:ILE:CG1	2:E:340:PRO:HG3	2.09	0.82
1:J:301:ALA:HB2	1:J:341:MET:HE3	1.61	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:214:ARG:NH1	1:K:521:MET:HE1	1.93	0.82
1:K:8:LYS:CB	2:N:48:GLN:HB3	2.10	0.82
1:A:297:ASN:CB	2:D:286:GLU:HG3	2.08	0.82
1:I:43:ARG:HB3	1:I:44:GLN:C	2.03	0.82
1:J:392:PRO:HB3	1:J:399:GLU:CB	2.09	0.82
2:M:130:THR:HG21	2:M:135:ILE:HG21	1.61	0.82
1:B:50:GLN:NE2	1:B:341:MET:SD	2.53	0.82
2:F:409:GLU:HA	2:F:413:VAL:HB	1.62	0.82
2:L:80:GLY:HA3	2:L:105:PRO:HG3	1.61	0.82
1:J:9:VAL:HG21	1:J:58:ILE:CB	2.09	0.81
1:C:39:ILE:HG12	1:C:49:ILE:HG12	1.62	0.81
2:E:124:PRO:HB3	2:E:143:ARG:O	1.79	0.81
1:I:257:VAL:HG21	1:I:310:GLY:HA3	1.62	0.81
2:M:439:ARG:NH2	2:M:451:ASP:OD2	2.13	0.81
2:N:217:PRO:HB2	2:N:220:GLU:HG3	1.61	0.81
1:I:424:HIS:CE1	1:I:501:LEU:HD22	2.15	0.81
2:N:127:PHE:O	2:N:171:LEU:N	2.13	0.81
1:A:202:LYS:HG3	1:A:372:VAL:HG12	1.62	0.81
2:L:6:ARG:HD3	2:L:70:VAL:H	1.46	0.81
2:N:338:ILE:HB	2:N:414:ASN:ND2	1.95	0.81
1:J:497:ARG:O	1:J:502:GLN:HG3	1.81	0.81
2:N:349:SER:HB3	2:N:352:LYS:HD3	1.62	0.81
1:B:83:MET:HE2	1:B:291:LEU:CD2	2.10	0.81
2:D:329:LEU:HA	2:D:342:ILE:HA	1.62	0.81
2:E:24:VAL:HG22	2:E:72:PHE:HE1	1.45	0.81
1:B:214:ARG:HB3	1:B:500:TYR:CE2	2.16	0.81
1:J:218:THR:CG2	1:J:457:VAL:HG22	2.11	0.80
2:M:85:MET:HG2	2:M:103:ILE:CD1	2.10	0.80
1:J:202:LYS:HG2	1:J:372:VAL:HG12	1.64	0.80
2:N:138:LEU:HD11	2:N:408:PHE:HZ	1.44	0.80
1:K:220:PHE:HZ	1:K:430:TRP:HA	1.46	0.80
2:N:381:GLN:HE21	2:N:381:GLN:H	1.27	0.80
1:J:144:ILE:HG13	1:J:145:ILE:HG12	1.64	0.80
2:L:155:LEU:HD13	2:L:329:LEU:HB3	1.63	0.80
1:A:497:ARG:HA	1:A:501:LEU:HB2	1.63	0.80
1:B:41:GLU:HB2	1:B:48:SER:HB3	1.64	0.80
2:E:409:GLU:HA	2:E:413:VAL:HG23	1.62	0.79
2:M:340:PRO:HD3	2:M:415:GLN:CB	2.12	0.79
2:D:44:VAL:HG22	2:D:54:VAL:HG12	1.63	0.79
1:K:74:GLU:HB2	1:K:111:ALA:HB3	1.64	0.79
2:L:250:MET:HB2	2:L:304:LEU:HB3	1.65	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:8:ILE:HD11	2:N:65:LEU:HA	1.64	0.79
1:C:40:ILE:HD12	1:C:345:LEU:HD11	1.64	0.79
1:J:295:THR:OG1	1:J:298:MET:SD	2.41	0.79
1:A:176:ILE:HD12	1:A:185:LEU:HD21	1.62	0.79
2:F:139:ASN:HB3	2:F:349:SER:HB2	1.64	0.79
1:B:298:MET:HB3	1:B:299:PRO:HD2	1.64	0.79
1:I:202:LYS:HG3	1:I:372:VAL:HG12	1.65	0.79
1:K:5:LYS:O	1:K:17:GLU:N	2.10	0.79
2:N:26:TYR:CD1	2:N:27:GLU:HG2	2.17	0.79
1:J:19:MET:HE1	1:J:64:VAL:HG11	1.65	0.79
2:M:34:MET:SD	2:M:40:ARG:NH2	2.56	0.79
2:F:325:GLY:H	2:F:350:ARG:HE	1.29	0.79
1:I:144:ILE:HG12	1:I:281:THR:HG21	1.65	0.78
1:K:497:ARG:HA	1:K:501:LEU:CG	2.12	0.78
1:I:125:GLU:O	1:I:128:THR:OG1	2.01	0.78
1:I:204:ASN:HD21	2:M:192:GLU:HG3	1.47	0.78
1:K:19:MET:HG2	1:K:47:ALA:HB3	1.64	0.78
2:D:281:LEU:HD22	2:D:285:PHE:HE2	1.49	0.78
2:L:93:LEU:HD12	2:L:95:ARG:CZ	2.14	0.78
2:M:250:MET:HB2	2:M:304:LEU:HB3	1.66	0.78
2:N:264:ARG:HG2	2:N:266:GLU:HG3	1.66	0.78
2:E:127:PHE:CZ	2:E:129:GLN:HA	2.18	0.78
1:A:220:PHE:CZ	1:A:433:SER:HB2	2.19	0.78
2:M:34:MET:HB2	2:M:40:ARG:HH21	1.49	0.78
2:D:166:ARG:HD2	2:D:201:THR:HG21	1.66	0.77
2:N:123:TYR:CD1	2:N:124:PRO:HD2	2.19	0.77
1:C:238:LYS:HG2	1:C:415:LEU:HD12	1.64	0.77
2:D:338:ILE:HG23	2:D:414:ASN:HB3	1.66	0.77
2:F:123:TYR:O	2:F:290:ARG:NH1	2.17	0.77
2:N:336:SER:HB2	2:N:337:GLY:HA2	1.66	0.77
1:A:130:VAL:HG22	1:A:157:GLY:O	1.85	0.77
1:C:300:VAL:HG12	1:C:337:ALA:HB2	1.65	0.77
2:F:77:LEU:HD23	2:F:111:ILE:HD13	1.66	0.77
2:F:93:LEU:HD12	2:F:95:ARG:NH2	1.99	0.77
1:K:262:ARG:NH2	2:N:321:TYR:O	2.16	0.77
1:B:12:PRO:HB3	1:B:344:ARG:HD2	1.65	0.77
1:K:237:GLY:CA	4:K:601:ANP:H8	2.14	0.77
2:N:129:GLN:HE22	2:N:422:THR:HA	1.48	0.77
1:B:246:ALA:HB1	1:B:254:VAL:HG11	1.65	0.77
1:K:232:GLY:CA	1:K:415:LEU:HD12	2.09	0.77
1:I:84:PHE:HB2	1:I:292:ILE:CD1	2.15	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:43:ARG:HA	2:N:10:GLU:HB2	1.65	0.77
1:J:555:ARG:HH21	1:J:573:ILE:HG12	1.50	0.77
2:M:16:MET:HE1	2:M:32:VAL:HG21	1.65	0.77
2:N:123:TYR:HD1	2:N:124:PRO:HD2	1.50	0.77
1:A:424:HIS:CE1	1:A:502:GLN:HG2	2.19	0.77
1:K:220:PHE:CZ	1:K:430:TRP:HA	2.20	0.77
1:J:232:GLY:HA3	1:J:238:LYS:HG2	1.67	0.77
1:A:264:ASN:CG	2:D:351:LEU:HD11	2.09	0.76
1:J:332:SER:OG	1:J:391:SER:N	2.18	0.76
1:K:233:PRO:HD2	1:K:236:ALA:HB2	1.67	0.76
2:M:65:LEU:H	2:M:65:LEU:HD12	1.49	0.76
1:C:577:ILE:CG2	1:C:581:ILE:HD11	2.12	0.76
1:I:497:ARG:CA	1:I:501:LEU:HB3	2.14	0.76
1:I:220:PHE:HZ	1:I:430:TRP:HA	1.48	0.76
1:I:285:LEU:HD21	1:I:288:ARG:HH21	1.50	0.76
1:I:20:SER:HB3	1:I:45:ASP:CB	2.10	0.76
1:K:5:LYS:HG3	1:K:61:GLY:HA2	1.66	0.76
2:L:6:ARG:CD	2:L:70:VAL:HB	2.16	0.76
1:K:202:LYS:HG3	1:K:372:VAL:HG12	1.68	0.76
2:N:340:PRO:HD3	2:N:416:GLY:H	1.51	0.76
1:I:80:ILE:HA	1:I:290:VAL:HG22	1.68	0.76
1:I:119:TRP:O	1:I:139:VAL:HG13	1.85	0.76
1:J:220:PHE:HB3	1:J:413:TRP:NE1	2.00	0.76
4:K:601:ANP:H5'2	2:N:350:ARG:CD	2.14	0.76
2:L:152:GLY:H	2:L:155:LEU:HD12	1.51	0.76
1:B:28:CYS:CB	1:B:66:SER:HA	2.17	0.75
2:E:29:LEU:HD11	2:E:77:LEU:HG	1.66	0.75
1:J:150:MET:HE1	1:J:319:ASP:C	2.10	0.75
2:L:14:PRO:HB2	2:L:55:GLN:HG2	1.68	0.75
2:E:55:GLN:HE22	2:E:260:ILE:HG23	1.51	0.75
2:E:153:SER:O	2:E:331:ARG:NH2	2.18	0.75
2:N:129:GLN:HB3	2:N:169:THR:H	1.50	0.75
1:B:27:MET:CE	1:B:38:GLU:HG2	2.14	0.75
1:C:214:ARG:HD2	1:C:501:LEU:H	1.49	0.75
1:J:17:GLU:CA	1:J:46:VAL:HG22	2.13	0.75
2:L:149:VAL:HB	2:L:303:ILE:HG12	1.67	0.75
2:N:138:LEU:HD11	2:N:408:PHE:CZ	2.20	0.75
2:D:158:LYS:HD3	2:D:190:GLU:HG3	1.68	0.75
1:J:220:PHE:HZ	1:J:430:TRP:HA	1.49	0.75
1:K:516:GLU:O	1:K:520:ASN:ND2	2.19	0.75
1:B:497:ARG:CA	1:B:501:LEU:HB2	2.14	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:498:GLU:HA	1:J:502:GLN:CD	2.11	0.75
1:A:38:GLU:O	1:A:50:GLN:N	2.19	0.75
1:C:149:ILE:H	1:C:149:ILE:HD12	1.52	0.75
2:E:65:LEU:H	2:E:65:LEU:HD12	1.52	0.75
1:K:410:LYS:HD3	1:K:436:LEU:HD12	1.68	0.75
2:N:148:PRO:HG3	2:N:323:THR:HG21	1.68	0.75
2:L:80:GLY:CA	2:L:105:PRO:HG3	2.16	0.75
2:N:326:GLN:CG	2:N:348:LEU:HB3	2.16	0.75
1:B:536:LEU:HD21	1:B:542:PHE:HB2	1.67	0.75
2:M:79:LEU:HB2	2:M:227:MET:HE3	1.69	0.75
2:N:77:LEU:HD11	2:N:111:ILE:HD13	1.69	0.75
2:D:140:THR:HG21	2:D:356:THR:HG23	1.69	0.74
1:I:259:CYS:SG	1:I:334:TRP:HB2	2.26	0.74
2:M:446:LYS:HE2	2:M:446:LYS:HA	1.66	0.74
1:A:264:ASN:HB2	2:D:351:LEU:CD1	2.17	0.74
1:A:536:LEU:HD21	1:A:542:PHE:HA	1.69	0.74
1:K:210:ILE:N	1:K:250:ASP:OD1	2.20	0.74
2:F:185:GLY:O	2:F:252:ASN:ND2	2.20	0.74
1:K:6:ILE:HA	1:K:16:ALA:HA	1.68	0.74
2:L:91:ASP:OD1	2:L:95:ARG:N	2.21	0.74
2:M:35:GLN:HB3	2:M:67:ASN:HB3	1.68	0.74
1:A:159:VAL:HG22	1:A:176:ILE:HG12	1.69	0.74
1:B:12:PRO:CB	1:B:344:ARG:HD2	2.18	0.74
1:K:232:GLY:HA2	1:K:415:LEU:HB2	1.69	0.74
2:E:86:ILE:HA	2:E:208:VAL:HG22	1.68	0.74
1:I:339:ARG:HB2	1:I:354:TYR:HD1	1.52	0.74
2:L:6:ARG:HB3	2:L:6:ARG:NH2	2.00	0.74
1:C:220:PHE:HZ	1:C:430:TRP:HA	1.53	0.74
1:C:568:ALA:C	1:C:570:ILE:HA	2.12	0.74
2:L:6:ARG:HG2	2:L:7:THR:N	2.02	0.74
1:A:259:CYS:CB	1:A:294:ASN:HB2	2.17	0.74
1:C:573:ILE:HG22	1:C:577:ILE:HD11	1.70	0.74
1:J:12:PRO:CD	1:J:344:ARG:HD3	2.18	0.74
1:I:83:MET:CE	2:L:119:ILE:HG21	2.18	0.74
1:B:324:VAL:HB	1:B:384:ILE:HG12	1.69	0.73
1:I:91:LEU:H	1:I:91:LEU:HD12	1.52	0.73
1:J:12:PRO:HG3	1:J:344:ARG:HD3	1.69	0.73
1:J:259:CYS:HA	1:J:294:ASN:HB3	1.68	0.73
1:K:18:ASN:ND2	1:K:20:SER:HB2	2.02	0.73
1:K:260:GLY:HA3	1:K:333:ARG:HG3	1.70	0.73
1:B:513:THR:HG23	1:B:517:LYS:HE2	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:83:MET:HE2	1:J:266:MET:HE3	1.71	0.73
1:K:43:ARG:HA	2:L:10:GLU:CB	2.18	0.73
1:A:264:ASN:HD22	2:D:351:LEU:HD11	1.51	0.73
1:B:255:VAL:HG21	1:B:314:ALA:HB2	1.70	0.73
2:D:338:ILE:HG23	2:D:414:ASN:CG	2.13	0.73
2:L:44:VAL:HG22	2:L:54:VAL:HG12	1.70	0.73
2:D:141:LEU:HD22	2:D:147:LEU:HD22	1.69	0.73
1:K:19:MET:HE3	1:K:22:ALA:HB3	1.71	0.73
1:J:215:VAL:HG23	1:J:501:LEU:HD23	1.70	0.73
1:K:213:GLN:HB2	1:K:216:ILE:HD11	1.68	0.73
2:L:8:ILE:HD13	2:L:16:MET:HE1	1.71	0.73
1:A:264:ASN:HB2	2:D:351:LEU:HD11	1.70	0.73
1:K:261:GLU:HG3	1:K:265:GLU:OE2	1.89	0.73
2:M:78:GLN:NE2	2:M:109:LEU:O	2.21	0.73
2:N:4:GLU:HB3	2:N:71:ARG:HB3	1.68	0.73
1:C:570:ILE:CB	1:C:573:ILE:HG13	2.19	0.73
2:F:45:LEU:HD22	2:F:264:ARG:NH2	2.04	0.73
1:A:38:GLU:N	1:A:50:GLN:O	2.17	0.73
1:A:43:ARG:CB	1:A:46:VAL:HG13	2.19	0.73
2:E:122:ASP:HB2	2:E:292:ARG:HG2	1.71	0.73
2:E:326:GLN:HB2	2:E:348:LEU:H	1.54	0.73
2:E:409:GLU:HA	2:E:413:VAL:CG2	2.17	0.73
1:K:19:MET:HE2	1:K:39:ILE:CD1	2.19	0.73
2:L:253:TYR:CZ	2:L:284:LEU:HD11	2.23	0.73
1:K:209:MET:SD	1:K:385:THR:HG21	2.28	0.73
2:L:352:LYS:HZ3	2:L:352:LYS:N	1.78	0.73
1:J:144:ILE:HG23	1:J:283:GLU:HG3	1.71	0.72
2:F:124:PRO:HB2	2:F:142:VAL:CG1	2.20	0.72
1:J:42:MET:SD	1:J:47:ALA:HB2	2.29	0.72
2:F:47:VAL:HG23	2:F:52:ALA:HA	1.71	0.72
2:F:139:ASN:HB3	2:F:349:SER:CB	2.18	0.72
1:C:41:GLU:OE1	1:C:43:ARG:NH1	2.21	0.72
2:F:26:TYR:CE1	2:F:27:GLU:HG2	2.24	0.72
1:I:346:GLU:O	2:M:265:ARG:NH2	2.22	0.72
1:J:233:PRO:HD2	1:J:236:ALA:CB	2.19	0.72
2:D:125:ASP:O	2:D:360:LYS:NZ	2.22	0.72
2:D:140:THR:HB	2:D:352:LYS:CB	2.19	0.72
1:I:27:MET:HE3	1:I:71:LEU:HB2	1.69	0.72
1:J:350:GLY:N	1:J:354:TYR:O	2.22	0.72
1:K:55:THR:HG22	1:K:58:ILE:CD1	2.18	0.72
2:D:338:ILE:HG23	2:D:414:ASN:CB	2.20	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:350:GLY:N	1:K:354:TYR:O	2.22	0.72
1:B:10:SER:HA	2:E:46:GLU:CB	2.20	0.72
1:K:211:THR:HB	1:K:216:ILE:CD1	2.19	0.72
1:A:338:LEU:HD22	1:A:355:PRO:HG3	1.70	0.72
2:E:131:GLY:H	2:E:167:GLN:HB3	1.53	0.72
1:J:134:ASP:O	1:J:151:VAL:HG23	1.90	0.72
1:A:262:ARG:NH2	2:D:320:GLY:O	2.22	0.72
2:D:282:ALA:C	2:D:286:GLU:HG2	2.15	0.72
1:J:12:PRO:HD3	1:J:344:ARG:HD3	1.71	0.71
1:J:215:VAL:CG1	1:J:426:PRO:HG2	2.19	0.71
1:B:35:VAL:HB	1:B:53:GLU:HB2	1.72	0.71
1:B:503:GLN:NE2	1:B:510:ASP:O	2.24	0.71
1:C:352:GLU:HB2	1:C:400:PRO:HG2	1.72	0.71
1:B:97:VAL:HG21	1:B:109:LEU:HD21	1.70	0.71
2:D:250:MET:HB2	2:D:304:LEU:HB3	1.71	0.71
1:I:177:GLU:HA	1:I:182:LEU:HA	1.71	0.71
2:L:6:ARG:HD3	2:L:70:VAL:HB	1.71	0.71
2:L:282:ALA:O	2:L:286:GLU:N	2.23	0.71
2:L:352:LYS:H	2:L:352:LYS:NZ	1.81	0.71
2:M:57:PHE:HA	2:M:219:ILE:HD13	1.70	0.71
2:N:130:THR:HG21	2:N:135:ILE:O	1.90	0.71
1:C:260:GLY:HA2	1:C:296:SER:HA	1.72	0.71
2:E:407:ARG:HG2	2:E:433:LEU:HD21	1.71	0.71
1:J:6:ILE:HD11	1:J:62:GLU:HB2	1.71	0.71
2:M:86:ILE:HA	2:M:208:VAL:HG22	1.71	0.71
1:C:295:THR:HB	1:C:297:ASN:OD1	1.90	0.71
2:E:218:ALA:HB3	2:E:260:ILE:HD11	1.72	0.71
1:J:232:GLY:CA	1:J:238:LYS:HD3	2.19	0.71
2:L:338:ILE:HG23	2:L:414:ASN:ND2	2.05	0.71
2:N:26:TYR:HD1	2:N:27:GLU:N	1.88	0.71
1:B:297:ASN:OD1	1:B:297:ASN:N	2.23	0.71
1:J:12:PRO:HD3	1:J:344:ARG:HH11	1.54	0.71
1:K:213:GLN:HB2	1:K:216:ILE:CG1	2.20	0.71
2:N:250:MET:HB2	2:N:304:LEU:HB3	1.73	0.71
1:C:36:ILE:HG23	1:C:52:TYR:HB2	1.71	0.71
1:I:148:LYS:HB2	1:I:320:MET:HE3	1.73	0.71
1:I:295:THR:H	1:I:298:MET:HG3	1.53	0.71
1:J:6:ILE:CG2	1:J:16:ALA:HB2	2.21	0.71
2:L:240:GLY:O	2:L:295:LYS:NZ	2.24	0.71
1:A:43:ARG:HB2	1:A:46:VAL:HG13	1.72	0.71
2:E:91:ASP:OD1	2:E:95:ARG:N	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:54:GLU:OE1	1:J:56:SER:N	2.22	0.71
2:L:15:LEU:HD23	2:L:55:GLN:HG3	1.72	0.71
1:A:488:LEU:HD23	1:A:533:ARG:HG3	1.73	0.71
1:B:143:LYS:H	1:B:143:LYS:HD2	1.54	0.71
2:D:111:ILE:O	2:D:287:ARG:NH2	2.24	0.71
2:F:58:GLU:OE1	2:F:58:GLU:N	2.24	0.71
1:I:39:ILE:HG12	1:I:49:ILE:HG12	1.73	0.71
1:I:507:ASP:HB3	1:I:510:ASP:HB3	1.71	0.71
1:K:500:TYR:HE2	1:K:522:LEU:HB2	1.53	0.71
2:D:146:LYS:HD3	2:D:285:PHE:O	1.91	0.70
2:D:148:PRO:HG3	2:D:323:THR:HB	1.73	0.70
2:D:198:PHE:HB3	2:D:204:ILE:HB	1.72	0.70
2:F:177:PHE:HE1	2:F:243:VAL:CA	2.04	0.70
1:I:264:ASN:CB	2:L:351:LEU:HD11	2.18	0.70
2:L:178:ALA:O	2:L:243:VAL:HA	1.90	0.70
1:C:234:PHE:HB3	2:F:321:TYR:CD2	2.26	0.70
1:I:173:ILE:HD13	1:I:187:MET:HG2	1.71	0.70
1:A:267:THR:O	1:A:271:ASN:ND2	2.23	0.70
1:B:443:ARG:NH1	1:B:443:ARG:HB2	2.06	0.70
2:D:6:ARG:HA	2:D:69:SER:HA	1.72	0.70
2:E:437:LEU:HB2	2:E:442:LEU:HD21	1.73	0.70
1:I:339:ARG:HB2	1:I:354:TYR:CD1	2.26	0.70
2:M:29:LEU:HB3	2:M:73:LEU:HD23	1.72	0.70
1:B:114:HIS:HD2	1:B:169:ILE:HD11	1.56	0.70
2:L:18:VAL:O	2:L:52:ALA:N	2.24	0.70
1:I:214:ARG:HB3	1:I:500:TYR:CZ	2.27	0.70
1:J:418:SER:O	1:J:422:LYS:HG3	1.92	0.70
1:K:298:MET:HB3	1:K:299:PRO:HD2	1.73	0.70
2:D:91:ASP:OD1	2:D:95:ARG:N	2.24	0.70
2:E:144:GLY:HA2	2:E:298:VAL:O	1.92	0.70
2:M:218:ALA:HB3	2:M:260:ILE:HD11	1.74	0.70
2:N:26:TYR:CE1	2:N:27:GLU:HG2	2.27	0.70
1:A:253:LEU:HB3	1:A:324:VAL:HG13	1.73	0.70
2:E:132:ILE:HD12	2:E:132:ILE:H	1.55	0.70
1:K:213:GLN:H	1:K:216:ILE:HD11	1.57	0.70
2:L:32:VAL:HG22	2:L:70:VAL:CG2	2.22	0.70
2:N:229:LEU:HD13	2:N:287:ARG:HG3	1.74	0.70
1:I:44:GLN:CB	1:I:45:ASP:HA	2.20	0.70
1:K:188:MET:CE	1:K:190:LYS:HG3	2.19	0.70
2:L:6:ARG:NH1	2:L:68:SER:O	2.25	0.70
2:N:129:GLN:HB3	2:N:169:THR:N	2.06	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:133:SER:HB3	2:D:426:THR:HG23	1.73	0.70
2:E:151:SER:OG	2:E:157:HIS:HB3	1.92	0.70
1:I:4:GLY:HA3	1:I:19:MET:CE	2.22	0.70
1:J:208:PRO:HA	1:J:223:THR:HA	1.74	0.70
2:N:352:LYS:O	2:N:356:THR:N	2.24	0.70
1:I:297:ASN:HB2	2:L:286:GLU:HG3	1.72	0.70
1:J:296:SER:HA	1:J:303:ARG:HH21	1.56	0.70
2:N:326:GLN:HE22	2:N:346:PRO:HB3	1.57	0.70
1:B:202:LYS:NZ	1:B:367:GLU:O	2.25	0.69
1:I:177:GLU:HG3	1:I:182:LEU:HA	1.72	0.69
1:I:497:ARG:C	1:I:501:LEU:HB3	2.17	0.69
1:J:437:TYR:OH	2:N:189:GLU:OE2	2.09	0.69
1:B:214:ARG:NH1	1:B:513:THR:OG1	2.24	0.69
2:E:45:LEU:H	2:E:45:LEU:HD22	1.56	0.69
2:F:177:PHE:CZ	2:F:244:LEU:HB2	2.27	0.69
2:N:213:LEU:H	2:N:213:LEU:HD12	1.57	0.69
2:F:86:ILE:HG22	2:F:208:VAL:HG22	1.74	0.69
1:A:41:GLU:HB2	1:A:48:SER:HB2	1.72	0.69
1:B:233:PRO:HG3	1:B:417:SER:HB2	1.74	0.69
1:I:254:VAL:H	1:I:289:THR:HG22	1.57	0.69
1:I:494:LYS:HG2	1:I:498:GLU:OE1	1.92	0.69
2:L:33:ARG:NH2	2:L:67:ASN:O	2.25	0.69
2:M:153:SER:O	2:M:331:ARG:NH2	2.25	0.69
2:M:277:LEU:HD23	2:M:318:LEU:HD12	1.75	0.69
2:M:345:LEU:HA	2:M:373:PHE:CZ	2.26	0.69
2:N:126:GLU:OE1	2:N:143:ARG:HD2	1.92	0.69
1:C:14:VAL:N	1:C:49:ILE:O	2.22	0.69
2:E:338:ILE:HG23	2:E:414:ASN:CG	2.17	0.69
1:J:406:LEU:HD21	1:J:412:PHE:CD1	2.27	0.69
2:N:138:LEU:HD13	2:N:344:VAL:CG1	2.22	0.69
1:A:36:ILE:H	1:A:36:ILE:HD12	1.56	0.69
1:A:296:SER:OG	2:D:286:GLU:OE2	2.10	0.69
1:K:150:MET:HE3	1:K:320:MET:HG2	1.73	0.69
2:N:149:VAL:HA	2:N:327:ILE:HB	1.73	0.69
2:N:378:GLN:HB3	2:N:401:TYR:CE1	2.27	0.69
2:D:325:GLY:HA2	2:D:349:SER:HA	1.75	0.69
2:F:60:THR:HA	2:F:63:ILE:HD12	1.75	0.69
1:J:415:LEU:HA	1:J:428:ILE:HA	1.73	0.69
2:N:44:VAL:HG22	2:N:54:VAL:HA	1.72	0.69
1:A:488:LEU:CD2	1:A:533:ARG:HG3	2.23	0.69
1:C:27:MET:HE2	1:C:38:GLU:HB2	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:8:LYS:HG3	2:N:48:GLN:CG	2.23	0.69
1:K:14:VAL:O	1:K:49:ILE:N	2.22	0.69
2:L:45:LEU:HD13	2:L:260:ILE:HG22	1.74	0.69
1:K:8:LYS:HG3	2:N:48:GLN:HG2	1.74	0.69
2:L:91:ASP:OD1	2:L:94:GLY:N	2.26	0.69
1:C:43:ARG:CZ	2:D:12:VAL:HG21	2.23	0.69
1:K:213:GLN:N	1:K:216:ILE:HD11	2.08	0.69
2:L:16:MET:HB2	2:L:54:VAL:CG2	2.23	0.69
1:I:297:ASN:CB	2:L:286:GLU:HG3	2.23	0.68
1:K:233:PRO:HD3	1:K:415:LEU:HB2	1.75	0.68
1:A:126:GLU:CG	1:A:162:ILE:HG22	2.23	0.68
2:F:44:VAL:HG22	2:F:54:VAL:CG1	2.17	0.68
1:I:497:ARG:HB3	1:I:501:LEU:HG	1.74	0.68
1:J:200:LYS:NZ	1:J:379:GLN:OE1	2.25	0.68
2:E:134:ALA:HB2	2:E:412:TYR:CD2	2.28	0.68
1:I:6:ILE:HG13	1:I:64:VAL:HG22	1.75	0.68
1:I:497:ARG:HA	1:I:501:LEU:HB3	1.74	0.68
2:L:313:HIS:CG	2:L:314:PRO:HD2	2.28	0.68
1:B:56:SER:HA	2:E:26:TYR:HB3	1.75	0.68
2:E:167:GLN:HG3	2:E:420:ASN:HB2	1.76	0.68
1:K:232:GLY:CA	1:K:238:LYS:HD3	2.23	0.68
1:K:241:VAL:O	1:K:245:ILE:HG12	1.92	0.68
1:B:14:VAL:N	1:B:49:ILE:O	2.25	0.68
2:E:146:LYS:HB2	2:E:324:GLU:HG2	1.74	0.68
2:F:121:ARG:NH1	2:F:288:ALA:O	2.26	0.68
2:F:408:PHE:CD1	2:F:413:VAL:HG23	2.29	0.68
1:I:291:LEU:HD23	1:I:292:ILE:N	2.09	0.68
2:L:18:VAL:CG1	2:L:21:VAL:HG11	2.22	0.68
1:K:252:ASP:H	1:K:323:ASP:HB2	1.59	0.68
1:I:20:SER:HB2	2:M:66:LYS:HZ2	1.59	0.68
1:I:497:ARG:O	1:I:501:LEU:HB3	1.92	0.68
1:A:39:ILE:CD1	1:A:49:ILE:HG12	2.24	0.68
1:B:494:LYS:HA	1:B:497:ARG:HH11	1.59	0.68
1:C:300:VAL:HG13	1:C:303:ARG:HD2	1.74	0.68
1:J:38:GLU:O	1:J:50:GLN:N	2.26	0.68
1:J:73:VAL:CG1	1:J:88:GLN:HG3	2.21	0.68
1:J:150:MET:HE1	1:J:320:MET:N	2.09	0.68
2:M:146:LYS:HB2	2:M:323:THR:O	1.94	0.68
2:N:364:ASP:CG	2:N:427:LEU:HD11	2.18	0.68
1:A:257:VAL:HG21	1:A:310:GLY:HA3	1.76	0.68
1:B:198:PRO:HB2	1:B:375:LEU:HD11	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:234:TYR:CD1	2:F:238:GLU:HG3	2.28	0.68
2:M:198:PHE:HB3	2:M:204:ILE:HB	1.76	0.68
1:I:5:LYS:NZ	1:I:17:GLU:OE2	2.27	0.68
1:J:278:ASP:O	1:J:281:THR:HG22	1.94	0.68
2:N:315:ILE:O	2:N:319:THR:OG1	2.11	0.68
1:A:264:ASN:CB	2:D:351:LEU:HD11	2.23	0.67
1:A:44:GLN:CB	1:A:45:ASP:HA	2.23	0.67
2:D:5:TYR:N	2:D:70:VAL:HB	2.08	0.67
2:D:148:PRO:O	2:D:327:ILE:HB	1.94	0.67
1:J:79:ILE:HB	1:J:112:LEU:HD21	1.76	0.67
1:K:9:VAL:HG13	1:K:14:VAL:HG22	1.76	0.67
1:B:301:ALA:HB2	1:B:341:MET:HE3	1.76	0.67
1:C:208:PRO:HA	1:C:223:THR:HA	1.75	0.67
1:J:557:SER:O	1:J:560:LYS:NZ	2.26	0.67
1:K:237:GLY:HA2	4:K:601:ANP:H8	1.75	0.67
1:A:257:VAL:HG12	1:A:258:GLY:H	1.59	0.67
1:C:211:THR:HG21	1:C:216:ILE:CG2	2.24	0.67
1:C:350:GLY:N	1:C:354:TYR:O	2.25	0.67
1:J:73:VAL:HG13	1:J:193:VAL:CG1	2.24	0.67
1:K:262:ARG:NH1	4:K:601:ANP:O2G	2.27	0.67
2:L:6:ARG:HE	2:L:8:ILE:HG13	1.58	0.67
1:A:440:GLU:HA	1:A:443:ARG:HH12	1.59	0.67
1:K:233:PRO:HD2	1:K:236:ALA:CB	2.24	0.67
2:N:92:GLY:O	2:N:93:LEU:HD23	1.95	0.67
2:N:409:GLU:HA	2:N:413:VAL:HB	1.77	0.67
1:I:135:ILE:CD1	1:I:148:LYS:HD3	2.24	0.67
1:I:338:LEU:HD22	1:I:355:PRO:HG3	1.77	0.67
1:J:232:GLY:HA3	1:J:238:LYS:CG	2.25	0.67
1:B:38:GLU:O	1:B:50:GLN:N	2.27	0.67
1:B:499:ASP:OD1	1:B:556:ILE:HG22	1.94	0.67
2:F:137:HIS:ND1	2:F:412:TYR:OH	2.28	0.67
2:F:153:SER:O	2:F:331:ARG:NH2	2.23	0.67
1:J:10:SER:CB	2:M:46:GLU:HA	2.24	0.67
1:J:218:THR:HG23	1:J:457:VAL:HG22	1.77	0.67
2:L:307:PRO:HG2	2:L:313:HIS:CE1	2.30	0.67
2:M:273:TYR:HD2	2:M:314:PRO:HG2	1.59	0.67
1:I:177:GLU:HG3	1:I:182:LEU:CA	2.24	0.67
1:A:86:GLY:H	1:A:294:ASN:HD21	1.42	0.67
2:D:125:ASP:OD1	2:D:126:GLU:HG2	1.95	0.67
1:I:84:PHE:HB2	1:I:292:ILE:HD13	1.76	0.67
1:J:13:LEU:HD21	1:J:48:SER:HB2	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:29:LEU:HD21	2:D:77:LEU:HG	1.76	0.67
2:M:152:GLY:H	2:M:155:LEU:HD12	1.60	0.67
2:N:150:PHE:HB3	2:N:306:MET:SD	2.35	0.67
2:N:185:GLY:HA2	2:N:214:ALA:HA	1.76	0.67
2:F:224:THR:HB	2:F:225:PRO:HD3	1.77	0.66
1:J:41:GLU:OE2	1:J:43:ARG:NH1	2.28	0.66
1:J:555:ARG:NH2	1:J:573:ILE:HG12	2.09	0.66
2:N:307:PRO:HG2	2:N:313:HIS:CE1	2.30	0.66
1:B:29:LEU:N	1:B:65:ARG:O	2.28	0.66
1:B:32:ASP:N	1:B:62:GLU:OE1	2.23	0.66
1:B:119:TRP:O	1:B:139:VAL:HG22	1.95	0.66
1:B:262:ARG:NH1	1:B:265:GLU:OE2	2.28	0.66
1:B:412:PHE:CD2	1:B:433:SER:HA	2.29	0.66
2:F:229:LEU:HB2	2:F:287:ARG:NH2	2.09	0.66
1:J:36:ILE:HB	1:J:52:TYR:HB2	1.78	0.66
1:J:215:VAL:CG2	1:J:501:LEU:HD23	2.23	0.66
2:N:128:ILE:HD11	2:N:143:ARG:HG2	1.77	0.66
1:A:271:ASN:OD1	2:D:292:ARG:NH2	2.27	0.66
2:E:219:ILE:H	2:E:219:ILE:HD12	1.59	0.66
1:B:253:LEU:HB3	1:B:324:VAL:HG13	1.75	0.66
2:D:282:ALA:O	2:D:286:GLU:N	2.29	0.66
2:E:93:LEU:HD12	2:E:95:ARG:NH2	2.11	0.66
2:F:313:HIS:CE1	2:F:315:ILE:HG12	2.31	0.66
1:I:39:ILE:HG21	1:I:47:ALA:HB1	1.77	0.66
1:J:27:MET:HE2	1:J:36:ILE:HG23	1.76	0.66
1:J:58:ILE:O	2:M:25:LYS:HA	1.96	0.66
1:C:300:VAL:CG2	2:F:279:THR:HG21	2.26	0.66
1:J:12:PRO:CG	1:J:344:ARG:HD3	2.26	0.66
1:K:114:HIS:ND1	1:K:170:ASP:OD1	2.29	0.66
2:M:44:VAL:HG22	2:M:54:VAL:CG1	2.26	0.66
1:A:31:GLY:HA2	1:A:62:GLU:HB3	1.77	0.66
1:B:210:ILE:HG23	1:B:515:ARG:HH21	1.60	0.66
2:D:45:LEU:HD22	2:D:264:ARG:HG3	1.77	0.66
1:J:7:ILE:HD12	1:J:8:LYS:H	1.60	0.66
1:J:497:ARG:HA	1:J:501:LEU:HD12	1.76	0.66
1:A:215:VAL:HG23	1:A:219:PHE:CD2	2.26	0.66
1:I:266:MET:HE2	2:L:118:PRO:HB3	1.75	0.66
2:N:8:ILE:HG22	2:N:18:VAL:HG22	1.77	0.66
1:B:80:ILE:HB	1:B:141:GLU:OE1	1.96	0.66
1:B:216:ILE:HD12	1:B:245:ILE:HD11	1.77	0.66
2:E:364:ASP:CB	2:E:449:LEU:HD13	2.26	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:423:ARG:NH2	2:N:352:LYS:HE3	2.09	0.66
1:C:73:VAL:HB	1:C:88:GLN:NE2	2.11	0.66
1:C:348:MET:HG3	2:D:265:ARG:HA	1.76	0.66
2:D:362:ARG:CG	2:D:427:LEU:HD13	2.25	0.66
1:J:36:ILE:O	1:J:52:TYR:N	2.29	0.66
1:J:56:SER:O	1:J:105:ARG:NH2	2.29	0.66
1:J:498:GLU:HA	1:J:502:GLN:NE2	2.11	0.66
2:N:381:GLN:H	2:N:381:GLN:NE2	1.93	0.66
1:A:339:ARG:NH2	1:A:352:GLU:O	2.25	0.66
2:D:140:THR:OG1	2:D:352:LYS:HB2	1.95	0.66
1:I:214:ARG:HD3	1:I:513:THR:OG1	1.95	0.66
1:J:79:ILE:HG13	1:J:84:PHE:CZ	2.31	0.66
1:K:230:VAL:HG13	1:K:413:TRP:HE3	1.61	0.66
2:L:6:ARG:NH2	2:L:69:SER:HA	2.10	0.66
1:A:169:ILE:O	1:A:186:THR:OG1	2.12	0.65
1:B:150:MET:HE1	1:B:319:ASP:HB3	1.78	0.65
2:D:138:LEU:HG	2:D:344:VAL:HB	1.77	0.65
1:K:237:GLY:HA3	4:K:601:ANP:H8	1.78	0.65
2:M:395:SER:OG	2:M:398:ASP:OD2	2.14	0.65
2:N:313:HIS:CE1	2:N:315:ILE:HG12	2.31	0.65
1:C:135:ILE:HG13	1:C:149:ILE:O	1.97	0.65
2:F:177:PHE:HE1	2:F:243:VAL:HA	1.61	0.65
1:K:133:GLY:O	1:K:380:ARG:NH2	2.28	0.65
2:L:6:ARG:HD3	2:L:70:VAL:N	2.11	0.65
2:M:79:LEU:HB2	2:M:227:MET:CE	2.26	0.65
2:N:415:GLN:CD	2:N:421:ARG:HD2	2.22	0.65
1:A:157:GLY:HA3	1:A:177:GLU:O	1.95	0.65
1:J:19:MET:HE1	1:J:64:VAL:CG1	2.27	0.65
1:B:12:PRO:HB3	1:B:344:ARG:CD	2.25	0.65
1:B:266:MET:HE3	1:B:291:LEU:HD21	1.79	0.65
1:C:87:ILE:HG21	1:C:89:ARG:HE	1.62	0.65
2:D:149:VAL:HB	2:D:303:ILE:HG12	1.79	0.65
1:I:297:ASN:HB2	2:L:286:GLU:OE1	1.96	0.65
2:L:325:GLY:HA3	2:L:349:SER:HA	1.79	0.65
2:E:133:SER:CB	2:E:426:THR:HG23	2.26	0.65
1:J:453:TRP:O	1:J:457:VAL:HG23	1.96	0.65
1:K:214:ARG:O	1:K:218:THR:HG22	1.95	0.65
1:K:546:MET:HE2	1:K:546:MET:HA	1.79	0.65
1:A:101:ASN:O	2:D:117:ASN:HB2	1.96	0.65
1:C:251:VAL:O	1:C:288:ARG:NH1	2.30	0.65
2:D:130:THR:OG1	2:D:136:ASP:OD1	2.14	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:138:LEU:HD21	2:F:408:PHE:HZ	1.60	0.65
2:F:339:GLN:HA	2:F:341:PRO:HD3	1.78	0.65
1:J:202:LYS:HG2	1:J:372:VAL:CG1	2.26	0.65
2:M:47:VAL:HA	2:M:52:ALA:HA	1.77	0.65
1:A:249:SER:HB3	1:A:251:VAL:HG22	1.79	0.65
1:B:304:GLU:HG3	1:B:334:TRP:HE1	1.61	0.65
2:D:338:ILE:CG2	2:D:414:ASN:HB3	2.26	0.65
1:I:251:VAL:HG21	1:I:325:ALA:HB2	1.79	0.65
2:L:409:GLU:HA	2:L:413:VAL:HB	1.79	0.65
1:A:353:GLY:HA3	2:D:270:ARG:HD3	1.77	0.65
2:E:313:HIS:HB3	2:E:316:PRO:CG	2.27	0.65
1:J:318:ARG:HD3	1:J:384:ILE:HD11	1.78	0.65
1:J:425:PHE:HA	1:J:426:PRO:C	2.22	0.65
2:D:250:MET:HE2	2:D:285:PHE:CZ	2.32	0.65
2:F:151:SER:O	2:F:306:MET:N	2.29	0.65
1:I:344:ARG:HG2	2:L:276:TYR:HB3	1.78	0.65
2:L:19:GLU:HG2	2:L:50:ASP:O	1.97	0.65
2:N:364:ASP:O	2:N:368:THR:N	2.20	0.65
1:B:246:ALA:HB2	1:B:327:MET:HG3	1.79	0.64
1:K:41:GLU:CB	2:L:12:VAL:HA	2.26	0.64
1:K:225:GLY:CA	1:K:370:GLY:HA2	2.27	0.64
2:N:138:LEU:CD1	2:N:344:VAL:HG11	2.27	0.64
1:A:105:ARG:NH1	2:D:113:GLY:O	2.28	0.64
1:B:544:GLU:OE1	1:B:544:GLU:N	2.29	0.64
2:D:130:THR:CG2	2:D:141:LEU:HD23	2.27	0.64
1:K:10:SER:HA	2:N:46:GLU:CB	2.27	0.64
1:K:235:GLY:HA2	4:K:601:ANP:H5'1	1.79	0.64
2:L:93:LEU:HD12	2:L:95:ARG:NH2	2.13	0.64
1:A:220:PHE:HZ	1:A:430:TRP:HA	1.61	0.64
1:C:87:ILE:HB	1:C:89:ARG:HG2	1.78	0.64
2:E:18:VAL:HB	2:E:52:ALA:HB3	1.79	0.64
2:E:91:ASP:OD2	2:E:93:LEU:HB2	1.97	0.64
1:I:177:GLU:HB2	1:I:182:LEU:HD23	1.79	0.64
1:K:213:GLN:HB2	1:K:216:ILE:CD1	2.28	0.64
2:L:139:ASN:HB3	2:L:349:SER:HB2	1.80	0.64
1:B:362:LEU:HD13	1:B:405:THR:HG23	1.79	0.64
1:C:73:VAL:CG1	1:C:88:GLN:HG3	2.26	0.64
1:I:415:LEU:HD23	1:I:428:ILE:HG12	1.78	0.64
1:J:232:GLY:N	1:J:238:LYS:HD3	2.12	0.64
1:K:144:ILE:HD11	1:K:288:ARG:HB3	1.77	0.64
2:M:29:LEU:HB3	2:M:73:LEU:CD2	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:152:PRO:HD2	1:B:185:LEU:HD22	1.79	0.64
1:I:159:VAL:CB	1:I:176:ILE:HG12	2.27	0.64
1:J:29:LEU:N	1:J:65:ARG:O	2.30	0.64
2:M:270:ARG:HD3	2:M:271:ARG:HG2	1.80	0.64
2:N:315:ILE:HB	2:N:316:PRO:HD3	1.78	0.64
2:N:338:ILE:CB	2:N:414:ASN:HD22	2.01	0.64
1:C:577:ILE:O	1:C:581:ILE:HG13	1.98	0.64
1:J:143:LYS:N	1:J:283:GLU:OE1	2.23	0.64
2:M:132:ILE:HD12	2:M:132:ILE:H	1.62	0.64
2:D:277:LEU:HD23	2:D:318:LEU:HD12	1.80	0.64
2:F:408:PHE:CD1	2:F:412:TYR:HB3	2.33	0.64
1:J:27:MET:SD	1:J:28:CYS:N	2.71	0.64
1:B:218:THR:HB	1:B:219:PHE:HD2	1.62	0.64
2:E:198:PHE:HB3	2:E:204:ILE:HB	1.79	0.64
1:J:189:GLN:OE1	1:J:197:ARG:NH2	2.30	0.64
2:L:18:VAL:HG12	2:L:21:VAL:HG11	1.80	0.64
2:M:406:GLU:O	2:M:410:ASN:ND2	2.25	0.64
2:E:44:VAL:HG23	2:E:53:MET:O	1.98	0.64
2:E:89:VAL:HG22	2:E:209:MET:HB2	1.79	0.64
1:J:83:MET:SD	1:J:91:LEU:HD12	2.38	0.64
1:K:42:MET:CE	2:L:65:LEU:HD11	2.27	0.64
2:N:88:ARG:NH1	2:N:101:PRO:O	2.30	0.64
1:B:13:LEU:HD21	1:B:48:SER:OG	1.97	0.64
2:F:132:ILE:HA	2:F:415:GLN:NE2	2.13	0.64
2:F:324:GLU:HA	2:F:350:ARG:HE	1.63	0.64
1:I:262:ARG:NH1	1:I:265:GLU:OE1	2.28	0.64
2:N:408:PHE:O	2:N:413:VAL:N	2.21	0.64
1:C:14:VAL:O	1:C:49:ILE:N	2.32	0.63
2:F:26:TYR:CD1	2:F:27:GLU:HG2	2.32	0.63
2:L:57:PHE:CE2	2:L:219:ILE:HD12	2.32	0.63
1:C:423:ARG:HH12	2:F:348:LEU:HB2	1.63	0.63
1:C:431:ILE:O	2:D:335:LYS:NZ	2.31	0.63
2:D:273:TYR:OH	2:D:315:ILE:HD11	1.99	0.63
2:F:258:ARG:HH21	2:F:272:GLY:HA3	1.63	0.63
1:J:8:LYS:HB2	2:M:48:GLN:CB	2.28	0.63
2:M:93:LEU:HG	2:M:95:ARG:NH2	2.13	0.63
1:B:3:ILE:HG23	1:B:64:VAL:O	1.98	0.63
1:B:300:VAL:HG22	2:E:279:THR:HG21	1.80	0.63
1:C:259:CYS:N	1:C:329:ASP:O	2.24	0.63
2:F:340:PRO:HD3	2:F:416:GLY:H	1.63	0.63
1:I:135:ILE:HD13	1:I:148:LYS:HD3	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:412:PHE:HD2	1:I:433:SER:HA	1.62	0.63
1:K:177:GLU:HA	1:K:182:LEU:HA	1.80	0.63
2:M:85:MET:HG2	2:M:103:ILE:HD12	1.80	0.63
1:B:83:MET:SD	1:B:91:LEU:HD12	2.39	0.63
1:C:531:GLU:HB3	1:C:581:ILE:HD13	1.79	0.63
2:D:222:ILE:HG23	2:D:253:TYR:CE1	2.34	0.63
2:F:251:THR:HG23	2:F:304:LEU:HB2	1.79	0.63
1:K:76:GLY:H	1:K:112:LEU:HD13	1.63	0.63
1:K:500:TYR:CE2	1:K:522:LEU:HB2	2.32	0.63
2:M:152:GLY:N	2:M:155:LEU:HD12	2.12	0.63
2:N:146:LYS:NZ	2:N:324:GLU:OE1	2.21	0.63
1:C:87:ILE:HB	1:C:89:ARG:CG	2.28	0.63
1:C:569:LYS:N	1:C:570:ILE:HA	2.14	0.63
2:E:124:PRO:HA	2:E:290:ARG:HD3	1.81	0.63
2:F:48:GLN:N	2:F:51:LYS:O	2.31	0.63
2:F:282:ALA:O	2:F:286:GLU:N	2.30	0.63
1:I:44:GLN:N	2:M:9:LYS:O	2.25	0.63
1:I:83:MET:HE3	2:L:119:ILE:HG21	1.79	0.63
2:L:302:PRO:HG3	2:L:323:THR:HG21	1.79	0.63
2:M:445:ILE:HB	2:M:450:LEU:HD21	1.81	0.63
2:N:159:GLU:N	2:N:159:GLU:OE2	2.30	0.63
1:B:241:VAL:O	1:B:245:ILE:HG12	1.98	0.63
1:B:285:LEU:HD13	1:B:288:ARG:HD2	1.81	0.63
1:C:238:LYS:HG2	1:C:415:LEU:CD1	2.27	0.63
2:D:408:PHE:HD1	2:D:412:TYR:HB3	1.62	0.63
2:F:339:GLN:CB	2:F:341:PRO:HD3	2.28	0.63
2:L:273:TYR:HE1	2:L:315:ILE:HG12	1.62	0.63
2:M:15:LEU:HA	2:M:55:GLN:HA	1.79	0.63
2:N:128:ILE:HD11	2:N:143:ARG:HA	1.80	0.63
2:N:151:SER:O	2:N:306:MET:N	2.31	0.63
2:N:152:GLY:H	2:N:155:LEU:CD1	2.11	0.63
2:F:86:ILE:HA	2:F:208:VAL:HG22	1.80	0.63
2:F:124:PRO:HB3	2:F:143:ARG:O	1.98	0.63
1:J:9:VAL:HG11	1:J:58:ILE:C	2.24	0.63
1:K:235:GLY:H	4:K:601:ANP:HNB1	1.46	0.63
2:L:403:LYS:HA	2:L:403:LYS:HE3	1.79	0.63
2:M:182:ALA:HB3	2:M:247:MET:HG2	1.81	0.63
1:A:556:ILE:HG12	1:A:573:ILE:HG21	1.80	0.63
1:B:202:LYS:HG2	1:B:372:VAL:CG1	2.25	0.63
2:E:415:GLN:O	2:E:419:THR:OG1	2.11	0.63
1:J:35:VAL:HB	1:J:53:GLU:CB	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:90:PHE:HE1	2:L:96:PRO:HB3	1.63	0.63
2:N:30:ILE:HG12	2:N:54:VAL:HB	1.80	0.63
1:C:373:ILE:HG12	1:C:381:GLU:HG2	1.80	0.63
2:D:313:HIS:ND1	2:D:314:PRO:HD2	2.13	0.63
2:E:24:VAL:HB	2:E:47:VAL:CB	2.29	0.63
2:E:91:ASP:OD2	2:E:95:ARG:NE	2.31	0.63
2:F:88:ARG:NH1	2:F:101:PRO:O	2.32	0.63
2:F:278:TYR:HB2	2:F:318:LEU:HD22	1.81	0.63
1:K:498:GLU:O	1:K:502:GLN:HB2	1.99	0.63
2:L:170:VAL:CG1	2:L:173:SER:HB3	2.28	0.63
2:M:92:GLY:O	2:M:227:MET:HG3	1.98	0.63
2:N:124:PRO:HB2	2:N:143:ARG:O	1.99	0.63
1:C:218:THR:HG21	1:C:500:TYR:CE2	2.34	0.62
2:E:150:PHE:HD2	2:E:306:MET:SD	2.21	0.62
2:F:340:PRO:HD3	2:F:416:GLY:N	2.14	0.62
1:I:6:ILE:HG13	1:I:64:VAL:CG2	2.28	0.62
1:J:297:ASN:OD1	1:J:297:ASN:N	2.26	0.62
2:L:159:GLU:OE1	2:L:159:GLU:N	2.31	0.62
2:N:134:ALA:O	2:N:138:LEU:HB2	1.98	0.62
2:N:346:PRO:O	2:N:348:LEU:HD12	1.99	0.62
1:B:58:ILE:O	2:E:25:LYS:HA	1.99	0.62
2:D:306:MET:HE1	2:D:311:LYS:HA	1.81	0.62
2:F:184:ILE:HD13	2:F:225:PRO:HG3	1.80	0.62
1:K:213:GLN:NE2	1:K:244:GLN:HB3	2.14	0.62
1:A:262:ARG:HB2	1:A:265:GLU:HB2	1.81	0.62
1:B:13:LEU:HD22	1:B:345:LEU:CD2	2.25	0.62
2:F:304:LEU:HD22	2:F:315:ILE:HG22	1.81	0.62
1:J:233:PRO:HD2	1:J:236:ALA:HB2	1.81	0.62
1:J:354:TYR:HB3	1:J:355:PRO:HD2	1.81	0.62
2:L:155:LEU:HD21	2:L:331:ARG:HA	1.81	0.62
2:N:326:GLN:NE2	2:N:346:PRO:HB3	2.15	0.62
2:N:313:HIS:ND1	2:N:315:ILE:HG12	2.14	0.62
1:A:231:PRO:CG	1:A:415:LEU:H	2.11	0.62
1:B:79:ILE:HA	1:B:112:LEU:HD22	1.82	0.62
1:B:285:LEU:HD12	1:B:285:LEU:O	1.98	0.62
1:B:352:GLU:HB3	1:B:400:PRO:HG3	1.82	0.62
1:C:235:GLY:H	4:C:601:ANP:HNB1	1.48	0.62
1:C:300:VAL:HG12	1:C:337:ALA:CB	2.28	0.62
1:J:7:ILE:HD12	1:J:8:LYS:N	2.14	0.62
2:L:152:GLY:N	2:L:155:LEU:HD12	2.13	0.62
2:L:183:ALA:HB1	2:L:186:ILE:HD13	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:327:MET:N	1:B:327:MET:SD	2.72	0.62
1:B:443:ARG:H	1:B:443:ARG:CZ	2.12	0.62
1:C:531:GLU:HB3	1:C:581:ILE:CD1	2.29	0.62
2:E:328:ILE:H	2:E:347:SER:HB3	1.64	0.62
1:J:12:PRO:HD3	1:J:344:ARG:NH1	2.14	0.62
2:L:8:ILE:HG23	2:L:17:ALA:O	1.98	0.62
2:L:250:MET:HE2	2:L:285:PHE:CZ	2.35	0.62
2:L:253:TYR:OH	2:L:280:ASN:OD1	2.14	0.62
2:N:131:GLY:O	2:N:415:GLN:NE2	2.33	0.62
1:C:295:THR:N	1:C:298:MET:SD	2.72	0.62
1:C:562:ILE:HG23	1:C:563:PRO:HD2	1.81	0.62
1:C:573:ILE:O	1:C:577:ILE:HG13	1.99	0.62
2:D:326:GLN:O	2:D:347:SER:HB2	2.00	0.62
1:I:523:LYS:O	1:I:527:THR:OG1	2.17	0.62
1:J:9:VAL:HG11	1:J:58:ILE:O	1.99	0.62
2:N:315:ILE:HB	2:N:316:PRO:CD	2.29	0.62
1:A:39:ILE:HG12	1:A:49:ILE:CG2	2.22	0.62
1:A:94:PHE:O	1:A:98:THR:OG1	2.16	0.62
2:E:132:ILE:HA	2:E:415:GLN:NE2	2.15	0.62
2:M:78:GLN:NE2	2:M:79:LEU:H	1.97	0.62
2:M:368:THR:O	2:M:372:LEU:HB2	1.99	0.62
1:A:244:GLN:OE1	1:A:511:THR:OG1	2.18	0.62
1:B:498:GLU:HA	1:B:502:GLN:HB2	1.80	0.62
1:C:75:LEU:HB2	1:C:189:GLN:HB3	1.80	0.62
2:D:222:ILE:HD11	2:D:257:LEU:HA	1.81	0.62
2:F:30:ILE:HG21	2:F:54:VAL:HG11	1.82	0.62
1:I:43:ARG:HB3	1:I:44:GLN:CA	2.30	0.62
1:J:39:ILE:HG12	1:J:49:ILE:HG12	1.80	0.62
1:K:397:ILE:O	1:K:403:GLN:NE2	2.32	0.62
1:K:445:MET:HE1	1:K:515:ARG:HD3	1.81	0.62
1:C:332:SER:HB2	1:C:391:SER:H	1.64	0.62
2:E:288:ALA:HB2	2:E:300:GLN:HG3	1.80	0.62
2:F:57:PHE:O	2:F:217:PRO:HB3	1.99	0.62
2:F:183:ALA:HB1	2:F:186:ILE:HD11	1.82	0.62
1:I:218:THR:HA	1:I:453:TRP:HZ2	1.64	0.62
1:I:230:VAL:HG22	1:I:413:TRP:HB2	1.81	0.62
1:J:208:PRO:HG3	1:J:441:VAL:HG13	1.81	0.62
1:K:318:ARG:HD3	1:K:384:ILE:HG13	1.81	0.62
2:L:138:LEU:HD23	2:L:344:VAL:HB	1.80	0.62
2:M:15:LEU:CD2	2:M:55:GLN:HG3	2.29	0.62
1:B:412:PHE:CE2	1:B:433:SER:HA	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:144:GLY:HA2	2:D:298:VAL:O	1.99	0.61
1:J:555:ARG:NH1	1:J:576:GLU:OE2	2.33	0.61
1:C:290:VAL:HG11	1:C:313:ILE:HG21	1.81	0.61
1:J:131:SER:N	1:J:134:ASP:OD2	2.32	0.61
1:K:497:ARG:HG2	1:K:501:LEU:HD12	1.81	0.61
1:K:567:LEU:N	1:K:568:ALA:HA	2.15	0.61
2:L:8:ILE:HD13	2:L:16:MET:CE	2.30	0.61
2:L:90:PHE:CE1	2:L:96:PRO:HB3	2.35	0.61
2:M:176:ASP:O	2:M:241:MET:HB2	2.01	0.61
1:A:340:GLU:OE2	2:D:279:THR:OG1	2.17	0.61
1:B:28:CYS:HB2	1:B:66:SER:HA	1.83	0.61
1:C:168:THR:HG22	1:C:171:ASP:CG	2.26	0.61
1:C:367:GLU:HG2	2:D:215:ASN:HD22	1.65	0.61
2:D:151:SER:O	2:D:305:THR:HA	2.00	0.61
2:E:338:ILE:CG2	2:E:414:ASN:HB3	2.30	0.61
1:J:81:SER:OG	1:J:287:GLU:HA	2.00	0.61
1:K:232:GLY:O	1:K:238:LYS:HD3	2.00	0.61
2:M:143:ARG:NH2	2:M:172:ASP:OD2	2.24	0.61
2:F:225:PRO:O	2:F:229:LEU:HG	2.01	0.61
1:J:258:GLY:HA3	1:J:266:MET:SD	2.41	0.61
1:K:8:LYS:HD3	1:K:10:SER:OG	1.99	0.61
1:K:213:GLN:CA	1:K:216:ILE:HD11	2.30	0.61
1:K:494:LYS:O	1:K:498:GLU:HG2	2.00	0.61
1:A:262:ARG:HH12	2:D:350:ARG:CZ	2.13	0.61
2:D:250:MET:HE2	2:D:285:PHE:HZ	1.64	0.61
2:E:128:ILE:O	2:E:129:GLN:HG3	1.99	0.61
1:I:262:ARG:H	1:I:262:ARG:HD2	1.66	0.61
1:I:439:THR:O	1:I:443:ARG:NH1	2.33	0.61
2:E:126:GLU:O	2:E:143:ARG:N	2.31	0.61
2:F:139:ASN:OD1	2:F:348:LEU:HA	2.01	0.61
2:F:151:SER:HA	2:F:329:LEU:HD12	1.83	0.61
2:F:318:LEU:O	2:F:322:ILE:HG13	2.01	0.61
2:F:325:GLY:H	2:F:350:ARG:NE	1.99	0.61
1:I:232:GLY:HA2	1:I:415:LEU:HB2	1.82	0.61
1:J:273:PHE:HB3	1:J:286:MET:HB2	1.81	0.61
2:M:78:GLN:HA	2:M:78:GLN:HE21	1.66	0.61
1:A:85:ASP:OD2	1:A:89:ARG:N	2.32	0.61
4:B:601:ANP:HNB1	2:E:350:ARG:NH2	1.99	0.61
1:C:297:ASN:OD1	1:C:297:ASN:N	2.24	0.61
2:F:26:TYR:CE1	2:F:45:LEU:HA	2.36	0.61
1:K:348:MET:HG3	2:L:265:ARG:HA	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:231:ALA:O	2:L:235:LEU:HG	2.00	0.61
2:M:21:VAL:HG12	2:M:50:ASP:O	2.01	0.61
2:N:126:GLU:CB	2:N:143:ARG:HG3	2.29	0.61
1:A:86:GLY:HA3	1:A:302:ALA:O	2.00	0.61
1:B:273:PHE:HB2	1:B:274:PRO:HD3	1.83	0.61
2:D:326:GLN:C	2:D:347:SER:HB2	2.24	0.61
2:E:28:GLU:O	2:E:44:VAL:HG12	2.01	0.61
2:F:86:ILE:HG22	2:F:208:VAL:CG2	2.31	0.61
1:J:9:VAL:HA	1:J:14:VAL:HG13	1.83	0.61
1:J:257:VAL:HG22	1:J:292:ILE:HB	1.82	0.61
1:A:262:ARG:O	1:A:266:MET:N	2.29	0.61
1:B:355:PRO:HG2	1:B:358:LEU:HB2	1.83	0.61
1:C:51:VAL:HG21	1:C:55:THR:HG23	1.83	0.61
2:D:21:VAL:HG21	2:D:52:ALA:HB2	1.83	0.61
2:E:34:MET:SD	2:E:63:ILE:HG12	2.41	0.61
1:J:16:ALA:C	1:J:46:VAL:HG13	2.25	0.61
1:J:36:ILE:N	1:J:53:GLU:OE1	2.27	0.61
2:L:29:LEU:HD11	2:L:77:LEU:HD23	1.83	0.61
2:D:92:GLY:HA3	2:D:224:THR:HG22	1.83	0.61
2:D:139:ASN:HB3	2:D:349:SER:HB2	1.82	0.61
1:I:483:SER:OG	1:I:486:ASP:OD1	2.19	0.61
1:I:501:LEU:HD12	1:I:502:GLN:HG2	1.83	0.61
1:J:496:ILE:HA	1:J:525:ILE:HD13	1.81	0.61
1:K:55:THR:CG2	1:K:58:ILE:HD12	2.25	0.61
1:K:238:LYS:HG2	1:K:415:LEU:HD12	1.82	0.61
2:L:396:ASP:O	2:L:399:LYS:HE2	2.01	0.61
2:M:357:GLY:HA2	2:M:363:GLU:HA	1.83	0.61
1:A:80:ILE:H	1:A:80:ILE:HD12	1.65	0.60
1:A:304:GLU:O	1:A:334:TRP:NE1	2.32	0.60
1:J:73:VAL:HG13	1:J:193:VAL:HG11	1.82	0.60
1:J:234:PHE:HZ	2:M:311:LYS:HD3	1.66	0.60
1:K:53:GLU:HG2	1:K:106:GLY:H	1.65	0.60
2:N:188:PHE:O	2:N:192:GLU:N	2.34	0.60
1:A:218:THR:HG23	1:A:453:TRP:CZ2	2.36	0.60
1:A:231:PRO:HG2	1:A:415:LEU:N	2.14	0.60
1:B:262:ARG:NH2	2:E:321:TYR:O	2.35	0.60
1:C:114:HIS:O	1:C:168:THR:OG1	2.18	0.60
2:D:18:VAL:O	2:D:52:ALA:N	2.32	0.60
2:D:125:ASP:OD1	2:D:126:GLU:N	2.33	0.60
1:K:209:MET:HE3	1:K:211:THR:HG23	1.83	0.60
1:K:257:VAL:HG21	1:K:310:GLY:HA3	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:149:VAL:HB	2:M:303:ILE:HG12	1.82	0.60
1:C:101:ASN:O	2:F:117:ASN:HB2	2.01	0.60
2:D:148:PRO:HG3	2:D:323:THR:CB	2.30	0.60
2:D:356:THR:HA	2:D:361:THR:OG1	2.01	0.60
1:J:562:ILE:HD12	1:J:570:ILE:HG12	1.83	0.60
1:K:42:MET:HG2	1:K:47:ALA:HB2	1.83	0.60
2:L:18:VAL:HG12	2:L:21:VAL:CG1	2.31	0.60
2:N:226:ARG:NH2	2:N:253:TYR:OH	2.34	0.60
1:C:255:VAL:N	1:C:325:ALA:O	2.27	0.60
1:C:529:GLY:O	1:C:533:ARG:HB2	2.02	0.60
2:E:73:LEU:HD13	2:E:75:HIS:CE1	2.37	0.60
2:E:376:TYR:OH	2:E:409:GLU:OE2	2.18	0.60
1:I:244:GLN:OE1	1:I:511:THR:OG1	2.19	0.60
1:J:215:VAL:HG11	1:J:426:PRO:HG2	1.83	0.60
2:L:6:ARG:HD2	2:L:70:VAL:HB	1.83	0.60
2:M:343:ASP:O	2:M:347:SER:OG	2.19	0.60
1:C:41:GLU:HB2	2:D:12:VAL:HA	1.81	0.60
1:C:202:LYS:HB3	2:D:188:PHE:CZ	2.36	0.60
1:C:269:VAL:O	1:C:273:PHE:HB2	2.01	0.60
2:L:9:LYS:HG3	2:L:19:GLU:HG3	1.83	0.60
2:N:177:PHE:HA	2:N:242:HIS:HB2	1.82	0.60
1:A:266:MET:HE2	2:D:118:PRO:HB3	1.84	0.60
1:B:27:MET:HE1	1:B:38:GLU:CG	2.26	0.60
1:C:135:ILE:HD11	1:C:150:MET:CA	2.26	0.60
2:E:89:VAL:CG1	2:E:211:MET:HG2	2.31	0.60
1:J:85:ASP:OD1	1:J:89:ARG:N	2.30	0.60
4:J:601:ANP:O2G	2:M:321:TYR:O	2.20	0.60
1:K:29:LEU:HD13	1:K:65:ARG:HH21	1.66	0.60
2:L:32:VAL:CG2	2:L:70:VAL:HG22	2.27	0.60
2:L:45:LEU:HD21	2:L:55:GLN:HB2	1.84	0.60
1:B:371:ARG:NH1	1:B:381:GLU:OE2	2.35	0.60
2:D:159:GLU:OE1	2:D:159:GLU:N	2.33	0.60
2:F:21:VAL:HG21	2:F:52:ALA:HB2	1.83	0.60
2:F:408:PHE:HD1	2:F:412:TYR:HB3	1.66	0.60
1:J:240:VAL:HG23	4:J:601:ANP:O2A	2.02	0.60
1:C:39:ILE:HG12	1:C:49:ILE:CG1	2.32	0.60
1:C:235:GLY:HA2	4:C:601:ANP:H5'1	1.82	0.60
1:C:238:LYS:NZ	4:C:601:ANP:O2B	2.34	0.60
2:F:177:PHE:HD1	2:F:178:ALA:N	2.00	0.60
1:J:36:ILE:HG22	1:J:52:TYR:CD1	2.37	0.60
1:C:241:VAL:O	1:C:245:ILE:HG12	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:134:ALA:HA	2:E:412:TYR:CE2	2.37	0.60
2:E:250:MET:HB2	2:E:304:LEU:HB3	1.84	0.60
2:F:217:PRO:HB2	2:F:220:GLU:HB2	1.82	0.60
2:F:328:ILE:O	2:F:342:ILE:HG23	2.01	0.60
1:J:39:ILE:HG12	1:J:49:ILE:HG23	1.84	0.60
1:K:262:ARG:NH2	2:N:350:ARG:HH12	1.99	0.60
2:M:89:VAL:HG22	2:M:209:MET:HB2	1.83	0.60
1:A:25:GLN:HG3	2:E:61:SER:HA	1.84	0.60
1:B:500:TYR:OH	1:B:518:GLN:HA	2.01	0.60
1:C:120:PHE:CD1	1:C:173:ILE:HD11	2.37	0.60
1:C:251:VAL:HG12	1:C:323:ASP:HB3	1.83	0.60
1:I:301:ALA:O	1:I:305:ALA:N	2.35	0.60
1:J:31:GLY:HA2	1:J:62:GLU:HB3	1.84	0.60
1:J:237:GLY:HA3	4:J:601:ANP:H8	1.84	0.60
1:J:424:HIS:NE2	1:J:502:GLN:HG2	2.17	0.60
2:N:8:ILE:HD11	2:N:65:LEU:CA	2.31	0.60
2:D:65:LEU:HD12	2:D:66:LYS:H	1.67	0.59
1:K:232:GLY:C	1:K:238:LYS:HD3	2.26	0.59
1:K:238:LYS:NZ	4:K:601:ANP:O1G	2.25	0.59
2:L:57:PHE:HE2	2:L:219:ILE:HD12	1.66	0.59
2:M:224:THR:HB	2:M:225:PRO:HD3	1.84	0.59
2:D:89:VAL:HG22	2:D:209:MET:HB2	1.83	0.59
2:E:90:PHE:HA	2:E:96:PRO:HA	1.84	0.59
1:I:6:ILE:HA	1:I:16:ALA:HA	1.84	0.59
1:K:18:ASN:HD21	1:K:20:SER:HB2	1.67	0.59
1:K:238:LYS:HG2	1:K:415:LEU:CD1	2.32	0.59
1:A:39:ILE:CG1	1:A:49:ILE:HG23	2.25	0.59
1:B:521:MET:CE	1:B:560:LYS:HB3	2.31	0.59
1:C:84:PHE:HB2	1:C:292:ILE:HG13	1.85	0.59
2:D:88:ARG:NE	2:D:98:ASP:OD2	2.32	0.59
2:E:29:LEU:HB2	2:E:73:LEU:HD11	1.83	0.59
1:I:169:ILE:O	1:I:186:THR:OG1	2.16	0.59
1:I:351:ASP:OD1	2:M:258:ARG:NH1	2.30	0.59
1:B:550:VAL:HG12	1:B:553:ARG:NH2	2.18	0.59
1:C:132:ALA:O	1:C:375:LEU:HB3	2.02	0.59
2:D:137:HIS:HA	2:D:365:HIS:NE2	2.17	0.59
2:E:345:LEU:HB2	2:E:346:PRO:HD3	1.83	0.59
1:K:459:GLU:OE2	1:K:462:ARG:NH1	2.36	0.59
2:M:40:ARG:HG2	2:M:56:ILE:HG21	1.84	0.59
2:M:270:ARG:HD3	2:M:271:ARG:CG	2.32	0.59
2:D:176:ASP:HB3	2:D:206:ARG:HD2	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:20:SER:CB	1:I:45:ASP:HB2	2.18	0.59
1:J:532:ALA:O	1:J:536:LEU:N	2.35	0.59
2:M:226:ARG:HA	2:M:229:LEU:HD12	1.83	0.59
2:N:10:GLU:HA	2:N:65:LEU:HD13	1.84	0.59
1:B:497:ARG:HA	1:B:501:LEU:CB	2.19	0.59
2:F:29:LEU:HD23	2:F:73:LEU:HD23	1.84	0.59
2:M:223:ALA:O	2:M:227:MET:HG2	2.02	0.59
1:B:12:PRO:HB2	1:B:344:ARG:CB	2.33	0.59
1:B:83:MET:HE2	1:B:291:LEU:HD22	1.82	0.59
1:B:240:VAL:HG23	4:B:601:ANP:O2A	2.02	0.59
1:B:565:GLU:OE1	1:B:565:GLU:N	2.27	0.59
4:B:601:ANP:H5'2	2:E:350:ARG:HD3	1.84	0.59
2:D:282:ALA:O	2:D:286:GLU:HG2	2.02	0.59
2:D:315:ILE:HB	2:D:316:PRO:HD3	1.85	0.59
2:E:339:GLN:O	2:E:414:ASN:HB2	2.02	0.59
2:F:89:VAL:HG22	2:F:209:MET:HB2	1.84	0.59
2:F:339:GLN:HA	2:F:341:PRO:CD	2.33	0.59
1:I:87:ILE:N	1:I:88:GLN:HA	2.17	0.59
1:I:255:VAL:N	1:I:325:ALA:O	2.31	0.59
1:I:424:HIS:O	1:I:425:PHE:HD1	1.86	0.59
1:I:497:ARG:O	1:I:501:LEU:N	2.36	0.59
1:J:318:ARG:HB2	1:J:384:ILE:HD11	1.84	0.59
1:K:75:LEU:O	1:K:188:MET:HA	2.02	0.59
1:K:244:GLN:NE2	1:K:511:THR:OG1	2.31	0.59
2:N:57:PHE:HD1	2:N:219:ILE:HB	1.67	0.59
2:N:98:ASP:OD1	2:N:100:GLY:N	2.35	0.59
2:N:341:PRO:HD2	2:N:417:PHE:CZ	2.37	0.59
1:J:8:LYS:HD3	2:M:48:GLN:CB	2.33	0.59
1:K:24:ILE:CD1	1:K:41:GLU:HA	2.19	0.59
1:K:230:VAL:HG23	1:K:389:ALA:HA	1.84	0.59
1:K:230:VAL:CG1	1:K:413:TRP:HE3	2.15	0.59
1:K:424:HIS:CD2	1:K:502:GLN:HG2	2.38	0.59
2:N:89:VAL:HG22	2:N:209:MET:HB2	1.84	0.59
1:A:39:ILE:HD13	1:A:49:ILE:HG12	1.85	0.59
1:A:117:GLN:HG2	1:A:168:THR:HG22	1.85	0.59
1:B:354:TYR:HB3	1:B:355:PRO:HD2	1.85	0.59
1:C:83:MET:HG3	2:F:119:ILE:CD1	2.27	0.59
1:C:393:SER:H	1:C:399:GLU:HG3	1.67	0.59
2:E:29:LEU:CB	2:E:73:LEU:HD11	2.33	0.59
2:E:357:GLY:N	2:E:358:ALA:HA	2.17	0.59
1:I:7:ILE:HB	2:L:49:GLU:CG	2.31	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:175:VAL:HG12	1:I:182:LEU:HD22	1.85	0.59
1:A:231:PRO:HD3	1:A:413:TRP:O	2.03	0.59
1:B:562:ILE:HD12	1:B:570:ILE:HG12	1.85	0.59
2:F:325:GLY:O	2:F:349:SER:HA	2.02	0.59
1:J:8:LYS:HG2	1:J:10:SER:H	1.67	0.59
2:L:87:GLY:HA2	2:L:204:ILE:O	2.03	0.59
2:L:350:ARG:N	2:L:352:LYS:HZ1	2.00	0.59
2:L:423:ILE:O	2:L:427:LEU:HG	2.03	0.59
2:N:183:ALA:HB3	2:N:211:MET:HA	1.85	0.59
1:C:1:MET:HG2	1:C:2:GLN:H	1.66	0.58
2:F:213:LEU:N	2:F:216:ASP:OD2	2.36	0.58
2:L:90:PHE:O	2:L:210:PHE:HA	2.03	0.58
2:L:244:LEU:HD12	2:L:299:THR:HB	1.84	0.58
1:A:357:TYR:HB3	2:E:259:GLU:HG3	1.85	0.58
1:B:285:LEU:HD11	1:B:288:ARG:HD2	1.84	0.58
1:C:19:MET:HE2	1:C:64:VAL:CG1	2.33	0.58
1:C:124:ILE:CG2	1:C:136:ILE:HB	2.33	0.58
2:D:48:GLN:HB2	2:D:51:LYS:HG2	1.85	0.58
2:D:315:ILE:HB	2:D:316:PRO:CD	2.32	0.58
2:F:97:LYS:HE2	2:F:211:MET:HB2	1.85	0.58
2:F:285:PHE:CE2	2:F:319:THR:HG23	2.37	0.58
2:F:340:PRO:HA	2:F:417:PHE:CE1	2.37	0.58
1:J:27:MET:CE	1:J:36:ILE:HG23	2.33	0.58
1:J:238:LYS:HE3	4:J:601:ANP:O2B	2.03	0.58
1:A:42:MET:SD	1:A:47:ALA:HB2	2.42	0.58
2:L:325:GLY:CA	2:L:349:SER:HA	2.33	0.58
2:M:48:GLN:HA	2:M:49:GLU:C	2.28	0.58
2:M:183:ALA:HB3	2:M:211:MET:HA	1.85	0.58
2:N:153:SER:O	2:N:331:ARG:NH2	2.35	0.58
1:A:440:GLU:HA	1:A:443:ARG:NH1	2.19	0.58
1:B:15:MET:HA	1:B:47:ALA:O	2.04	0.58
1:B:495:SER:O	1:B:499:ASP:HB2	2.04	0.58
1:B:497:ARG:HA	1:B:501:LEU:HD13	1.85	0.58
1:B:565:GLU:H	1:B:565:GLU:CD	2.10	0.58
1:I:9:VAL:HB	2:L:47:VAL:HG22	1.86	0.58
1:K:41:GLU:CG	2:L:12:VAL:HG13	2.22	0.58
2:N:137:HIS:HA	2:N:365:HIS:CD2	2.38	0.58
1:C:251:VAL:HG21	1:C:325:ALA:CB	2.32	0.58
2:E:82:SER:O	2:E:85:MET:HB2	2.04	0.58
2:F:181:PHE:HD2	2:F:209:MET:HE3	1.67	0.58
2:L:124:PRO:HB3	2:L:143:ARG:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:169:ILE:O	1:B:186:THR:HB	2.03	0.58
1:B:441:VAL:N	1:B:443:ARG:HH22	2.01	0.58
2:F:34:MET:SD	2:F:63:ILE:HG12	2.43	0.58
2:F:124:PRO:HB2	2:F:142:VAL:HG12	1.83	0.58
1:K:264:ASN:ND2	2:N:324:GLU:OE1	2.36	0.58
1:K:278:ASP:HB3	1:K:281:THR:HG21	1.84	0.58
2:M:166:ARG:HD2	2:M:201:THR:HG21	1.86	0.58
2:N:44:VAL:HG13	2:N:53:MET:O	2.04	0.58
1:A:545:ILE:O	1:A:549:THR:OG1	2.18	0.58
2:D:60:THR:HA	2:D:63:ILE:HD13	1.85	0.58
2:D:86:ILE:HD13	2:D:208:VAL:HG23	1.85	0.58
2:D:111:ILE:HG21	2:D:227:MET:HG2	1.84	0.58
2:D:140:THR:HB	2:D:352:LYS:CA	2.33	0.58
1:I:84:PHE:HB3	1:I:88:GLN:CB	2.33	0.58
1:J:261:GLU:HB3	1:J:265:GLU:OE1	2.03	0.58
1:K:214:ARG:NH2	1:K:510:ASP:OD1	2.36	0.58
1:K:222:VAL:HG22	1:K:413:TRP:CZ2	2.39	0.58
2:L:126:GLU:HB2	2:L:143:ARG:HD2	1.84	0.58
2:L:345:LEU:HB2	2:L:346:PRO:HD3	1.84	0.58
2:N:45:LEU:HD13	2:N:45:LEU:H	1.67	0.58
1:A:297:ASN:HB2	2:D:286:GLU:CG	2.32	0.58
1:C:576:GLU:O	1:C:580:THR:OG1	2.20	0.58
2:F:160:LEU:HD22	2:F:342:ILE:HD11	1.85	0.58
1:J:6:ILE:CD1	1:J:62:GLU:HB2	2.34	0.58
1:K:49:ILE:HD11	1:K:64:VAL:HG11	1.86	0.58
1:K:499:ASP:OD2	1:K:557:SER:HA	2.02	0.58
2:L:407:ARG:HD3	2:L:436:MET:HE1	1.85	0.58
2:M:324:GLU:CB	2:M:350:ARG:HD2	2.34	0.58
2:N:313:HIS:CG	2:N:314:PRO:HD2	2.39	0.58
1:A:311:ILE:O	1:A:315:GLU:HG3	2.04	0.58
1:A:393:SER:HB2	2:D:321:TYR:HE1	1.69	0.58
1:B:27:MET:HE1	1:B:52:TYR:HE2	1.68	0.58
1:C:546:MET:O	1:C:549:THR:OG1	2.22	0.58
2:D:153:SER:O	2:D:331:ARG:NH2	2.30	0.58
2:D:156:PRO:HG3	2:D:334:TYR:CE1	2.39	0.58
2:E:93:LEU:HD12	2:E:95:ARG:HH22	1.67	0.58
2:F:15:LEU:HD12	2:F:55:GLN:HG3	1.84	0.58
1:I:225:GLY:HA2	1:I:384:ILE:O	2.03	0.58
1:K:145:ILE:HD11	1:K:252:ASP:O	2.04	0.58
2:L:146:LYS:HD3	2:L:285:PHE:O	2.04	0.58
2:N:264:ARG:HG2	2:N:266:GLU:CG	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:409:GLU:O	2:E:413:VAL:HB	2.04	0.58
1:J:128:THR:H	1:J:159:VAL:CB	2.17	0.58
1:K:49:ILE:CD1	1:K:64:VAL:HG11	2.34	0.58
2:L:198:PHE:HB3	2:L:204:ILE:HB	1.85	0.58
2:L:278:TYR:CE1	2:L:322:ILE:HG12	2.29	0.58
2:N:183:ALA:HB3	2:N:212:ASN:H	1.69	0.58
1:A:83:MET:HE1	1:A:270:VAL:HG13	1.85	0.57
1:B:209:MET:HB2	1:B:224:LYS:HD3	1.86	0.57
2:D:254:ALA:HB1	2:D:273:TYR:CE1	2.38	0.57
1:I:43:ARG:HB2	1:I:46:VAL:O	2.04	0.57
1:J:415:LEU:HD23	1:J:415:LEU:N	2.18	0.57
1:K:76:GLY:N	1:K:112:LEU:HD13	2.18	0.57
2:L:8:ILE:HD11	2:L:70:VAL:HG23	1.86	0.57
2:M:8:ILE:CB	2:M:65:LEU:HB3	2.34	0.57
2:M:255:GLU:O	2:M:258:ARG:HG2	2.03	0.57
1:C:29:LEU:N	1:C:65:ARG:O	2.37	0.57
2:D:78:GLN:HG2	2:D:110:ASP:HA	1.85	0.57
2:F:408:PHE:O	2:F:413:VAL:N	2.19	0.57
1:I:330:SER:HB3	1:I:333:ARG:HG2	1.84	0.57
1:J:38:GLU:OE1	1:J:194:ARG:NH2	2.31	0.57
2:L:91:ASP:OD2	2:L:93:LEU:HB2	2.03	0.57
1:B:374:ALA:HB3	1:B:380:ARG:HG2	1.86	0.57
1:C:62:GLU:OE2	2:F:25:LYS:NZ	2.34	0.57
2:F:422:THR:O	2:F:426:THR:OG1	2.20	0.57
1:J:197:ARG:HG3	1:J:315:GLU:HB3	1.85	0.57
1:J:220:PHE:HB3	1:J:413:TRP:HE1	1.67	0.57
1:K:14:VAL:HB	1:K:49:ILE:HB	1.85	0.57
1:K:157:GLY:HA3	1:K:177:GLU:O	2.04	0.57
2:M:386:ALA:O	2:M:390:GLY:N	2.37	0.57
1:B:2:GLN:NE2	1:B:18:ASN:O	2.37	0.57
2:D:31:GLU:O	2:D:71:ARG:N	2.37	0.57
2:E:24:VAL:HG22	2:E:72:PHE:CE1	2.33	0.57
1:I:248:TRP:CZ3	1:I:279:PRO:HG2	2.39	0.57
1:I:420:ALA:HA	1:I:425:PHE:HE1	1.70	0.57
1:J:340:GLU:OE2	1:J:344:ARG:NE	2.35	0.57
2:L:148:PRO:CA	2:L:302:PRO:HG2	2.32	0.57
1:B:218:THR:HB	1:B:219:PHE:CD2	2.39	0.57
2:E:137:HIS:ND1	2:E:412:TYR:OH	2.37	0.57
2:F:34:MET:HE1	2:F:40:ARG:HD2	1.87	0.57
1:K:42:MET:CG	1:K:47:ALA:HB2	2.34	0.57
1:K:139:VAL:O	1:K:147:HIS:HB3	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:229:LEU:HD13	2:L:287:ARG:HD3	1.86	0.57
2:M:29:LEU:HB2	2:M:75:HIS:O	2.04	0.57
2:N:148:PRO:HB2	2:N:150:PHE:HE1	1.68	0.57
2:N:242:HIS:ND1	2:N:296:GLY:HA2	2.20	0.57
1:B:42:MET:HG2	2:F:65:LEU:HD21	1.85	0.57
1:C:378:ASP:HB2	1:C:380:ARG:HH21	1.70	0.57
2:L:6:ARG:HD3	2:L:70:VAL:CB	2.34	0.57
2:L:143:ARG:HD3	2:L:290:ARG:HH11	1.69	0.57
2:M:350:ARG:C	2:M:351:LEU:HD23	2.29	0.57
1:A:256:TYR:CE2	1:A:269:VAL:HG11	2.39	0.57
1:B:258:GLY:N	1:B:292:ILE:O	2.33	0.57
1:B:563:PRO:HB2	1:B:566:GLU:HG3	1.86	0.57
1:C:485:ASN:O	1:C:533:ARG:NH1	2.31	0.57
2:E:166:ARG:HH22	2:E:418:TYR:HA	1.70	0.57
2:E:185:GLY:O	2:E:252:ASN:ND2	2.38	0.57
2:E:339:GLN:HB3	2:E:417:PHE:CZ	2.40	0.57
2:E:372:LEU:CD2	2:E:412:TYR:HE1	2.12	0.57
1:I:493:ALA:O	1:I:497:ARG:HG3	2.04	0.57
1:J:260:GLY:HA3	1:J:333:ARG:HG3	1.87	0.57
1:K:79:ILE:HA	1:K:112:LEU:HD21	1.86	0.57
1:K:492:VAL:O	1:K:496:ILE:HG13	2.05	0.57
2:N:35:GLN:NE2	2:N:64:CYS:SG	2.78	0.57
1:C:257:VAL:HG21	1:C:310:GLY:HA3	1.85	0.57
2:D:18:VAL:HB	2:D:52:ALA:HB3	1.87	0.57
2:E:218:ALA:O	2:E:222:ILE:HG12	2.05	0.57
1:K:19:MET:HE3	1:K:22:ALA:CB	2.34	0.57
1:A:120:PHE:CE2	1:A:173:ILE:HD12	2.39	0.57
1:A:232:GLY:N	1:A:233:PRO:HD3	2.20	0.57
1:A:497:ARG:HA	1:A:501:LEU:HD12	1.86	0.57
1:C:234:PHE:HD1	1:C:234:PHE:H	1.50	0.57
2:E:57:PHE:HA	2:E:219:ILE:HD13	1.86	0.57
1:I:242:GLN:HA	1:I:327:MET:HE1	1.87	0.57
1:J:229:ALA:C	1:J:231:PRO:HD3	2.30	0.57
1:J:281:THR:HG23	1:J:283:GLU:H	1.68	0.57
2:L:141:LEU:HD13	2:L:147:LEU:HD22	1.86	0.57
2:L:209:MET:HE2	2:L:211:MET:HE2	1.87	0.57
1:B:254:VAL:HG13	1:B:327:MET:SD	2.45	0.57
1:J:262:ARG:HH21	2:M:350:ARG:NH1	2.03	0.57
1:J:392:PRO:HA	1:J:399:GLU:HG3	1.85	0.57
1:K:206:ASP:HB2	1:K:440:GLU:OE2	2.05	0.57
1:K:501:LEU:N	1:K:501:LEU:HD23	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:150:PHE:CB	2:L:306:MET:HE3	2.35	0.57
2:N:110:ASP:OD2	2:N:112:ASN:ND2	2.35	0.57
2:N:378:GLN:O	2:N:378:GLN:NE2	2.29	0.57
1:A:538:LEU:C	1:A:538:LEU:HD12	2.29	0.56
1:B:216:ILE:HD12	1:B:245:ILE:CD1	2.35	0.56
2:D:164:ILE:O	2:D:168:ALA:N	2.38	0.56
2:D:166:ARG:NH1	2:D:197:ASP:OD2	2.33	0.56
2:F:273:TYR:CD2	2:F:314:PRO:HG2	2.40	0.56
2:F:325:GLY:HA3	2:F:326:GLN:CG	2.28	0.56
1:I:209:MET:SD	1:I:385:THR:HG21	2.44	0.56
1:J:30:VAL:O	1:J:35:VAL:HG22	2.05	0.56
1:J:196:GLY:HA2	1:J:368:ARG:NH1	2.20	0.56
1:J:254:VAL:HB	1:J:289:THR:HG23	1.86	0.56
1:K:238:LYS:HG3	4:K:601:ANP:O2B	2.05	0.56
1:K:422:LYS:O	1:K:423:ARG:HB2	2.05	0.56
1:A:220:PHE:CZ	1:A:430:TRP:HA	2.40	0.56
1:C:262:ARG:NH1	4:C:601:ANP:O3G	2.29	0.56
2:D:29:LEU:HB2	2:D:73:LEU:CD1	2.29	0.56
2:D:177:PHE:O	2:D:206:ARG:NE	2.38	0.56
2:E:438:PRO:HG2	2:E:441:GLU:HB2	1.86	0.56
2:F:250:MET:HB2	2:F:304:LEU:HB3	1.85	0.56
4:J:601:ANP:HNB1	2:M:350:ARG:NH2	2.04	0.56
1:K:259:CYS:O	1:K:330:SER:N	2.32	0.56
2:N:132:ILE:HA	2:N:415:GLN:OE1	2.04	0.56
1:A:10:SER:CB	2:D:46:GLU:HG3	2.34	0.56
1:A:39:ILE:HG21	1:A:47:ALA:HB1	1.87	0.56
1:A:73:VAL:HG13	1:A:193:VAL:CG1	2.31	0.56
1:A:263:GLY:O	1:A:267:THR:OG1	2.19	0.56
1:B:28:CYS:SG	1:B:49:ILE:HD13	2.45	0.56
1:B:356:ALA:HB1	2:F:258:ARG:HG3	1.88	0.56
1:B:504:ASN:N	1:B:510:ASP:OD2	2.31	0.56
1:C:300:VAL:HG13	1:C:303:ARG:CD	2.35	0.56
2:D:270:ARG:HG2	2:D:271:ARG:HG2	1.87	0.56
2:E:226:ARG:O	2:E:230:THR:OG1	2.23	0.56
2:E:443:LYS:NZ	2:E:443:LYS:HB2	2.20	0.56
2:F:138:LEU:HD13	2:F:344:VAL:HB	1.87	0.56
1:J:148:LYS:C	1:J:149:ILE:HD13	2.30	0.56
1:J:259:CYS:HA	1:J:294:ASN:CB	2.35	0.56
1:K:59:GLY:O	1:K:62:GLU:HB2	2.05	0.56
1:K:262:ARG:HH12	4:K:601:ANP:PG	2.27	0.56
1:K:500:TYR:HB3	1:K:501:LEU:HD23	1.85	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:6:ARG:CD	2:L:70:VAL:H	2.18	0.56
2:L:371:GLN:OE1	2:L:444:ARG:N	2.38	0.56
2:M:141:LEU:HD13	2:M:147:LEU:HB2	1.87	0.56
2:M:183:ALA:HB1	2:M:186:ILE:CD1	2.35	0.56
2:M:309:ASP:OD1	2:M:331:ARG:NH1	2.38	0.56
2:N:30:ILE:HG21	2:N:54:VAL:HG11	1.86	0.56
1:I:410:LYS:HB3	1:I:436:LEU:HB2	1.87	0.56
1:J:28:CYS:CB	1:J:66:SER:HA	2.35	0.56
1:J:114:HIS:ND1	1:J:170:ASP:OD1	2.38	0.56
1:J:333:ARG:HD2	2:M:278:TYR:CE1	2.41	0.56
1:K:120:PHE:CE2	1:K:137:GLY:HA3	2.40	0.56
1:K:213:GLN:H	1:K:216:ILE:CD1	2.18	0.56
1:K:260:GLY:HA3	1:K:333:ARG:CG	2.33	0.56
2:L:79:LEU:HD13	2:L:227:MET:HE1	1.88	0.56
2:M:15:LEU:HD22	2:M:55:GLN:CB	2.31	0.56
1:A:113:ASP:OD1	1:A:116:LYS:N	2.38	0.56
1:B:425:PHE:HB3	1:B:426:PRO:HA	1.88	0.56
2:D:77:LEU:HB3	2:D:111:ILE:HD13	1.86	0.56
2:D:156:PRO:HD3	2:D:334:TYR:CD2	2.41	0.56
2:E:90:PHE:CD1	2:E:96:PRO:HG3	2.40	0.56
2:E:132:ILE:HA	2:E:415:GLN:CD	2.30	0.56
1:J:428:ILE:H	1:J:428:ILE:HD12	1.70	0.56
2:N:378:GLN:HA	2:N:381:GLN:HE22	1.70	0.56
1:C:203:LEU:HD21	1:C:373:ILE:HG13	1.87	0.56
1:C:259:CYS:SG	1:C:306:SER:OG	2.64	0.56
2:D:78:GLN:NE2	2:D:110:ASP:OD1	2.35	0.56
1:I:43:ARG:HA	1:I:43:ARG:NE	2.21	0.56
1:I:261:GLU:HB3	1:I:266:MET:HG2	1.87	0.56
1:J:378:ASP:N	1:J:378:ASP:OD1	2.39	0.56
1:K:499:ASP:N	1:K:499:ASP:OD1	2.38	0.56
2:L:166:ARG:HD2	2:L:201:THR:HG21	1.88	0.56
2:M:315:ILE:HB	2:M:316:PRO:HD3	1.88	0.56
1:A:114:HIS:O	1:A:168:THR:HB	2.06	0.56
1:B:221:PRO:HG2	1:B:441:VAL:HG21	1.87	0.56
1:B:437:TYR:O	1:B:441:VAL:HG23	2.05	0.56
1:C:324:VAL:O	1:C:384:ILE:HA	2.05	0.56
2:E:4:GLU:HA	2:E:71:ARG:HA	1.86	0.56
2:F:315:ILE:HB	2:F:316:PRO:HD3	1.87	0.56
1:I:23:CYS:SG	2:M:64:CYS:HB2	2.45	0.56
1:K:218:THR:HG21	1:K:500:TYR:CE1	2.41	0.56
2:L:184:ILE:HA	2:L:212:ASN:HB2	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:158:LYS:CD	2:M:158:LYS:H	2.17	0.56
2:N:35:GLN:HB3	2:N:67:ASN:HB2	1.88	0.56
2:N:144:GLY:HA2	2:N:298:VAL:O	2.05	0.56
2:N:213:LEU:HB2	2:N:216:ASP:OD1	2.04	0.56
1:B:28:CYS:HB3	1:B:66:SER:HA	1.87	0.56
1:C:199:ILE:HG21	1:C:372:VAL:HG21	1.86	0.56
1:I:204:ASN:ND2	2:M:192:GLU:HG3	2.19	0.56
1:I:478:GLY:O	1:I:481:SER:OG	2.16	0.56
1:J:12:PRO:HG3	1:J:344:ARG:CD	2.35	0.56
1:J:503:GLN:NE2	1:J:510:ASP:O	2.38	0.56
1:B:214:ARG:HD2	1:B:500:TYR:CE2	2.41	0.56
1:B:220:PHE:HZ	1:B:430:TRP:HA	1.70	0.56
1:C:230:VAL:HG22	1:C:413:TRP:HE3	1.70	0.56
1:I:42:MET:HE2	2:M:65:LEU:HD13	1.87	0.56
1:K:16:ALA:O	1:K:46:VAL:HG13	2.06	0.56
2:M:446:LYS:O	2:M:450:LEU:HG	2.06	0.56
1:A:215:VAL:HA	1:A:219:PHE:CD2	2.40	0.56
1:B:285:LEU:HD12	1:B:285:LEU:C	2.31	0.56
1:B:378:ASP:N	1:B:378:ASP:OD1	2.38	0.56
2:F:158:LYS:HG2	2:F:190:GLU:HB3	1.88	0.56
1:I:412:PHE:CD2	1:I:433:SER:HA	2.41	0.56
1:J:374:ALA:N	1:J:380:ARG:O	2.35	0.56
1:K:319:ASP:O	1:K:380:ARG:NH1	2.38	0.56
2:L:16:MET:N	2:L:54:VAL:O	2.36	0.56
2:M:24:VAL:HG22	2:M:72:PHE:CE2	2.41	0.56
1:A:462:ARG:O	1:A:466:GLU:HB2	2.07	0.55
1:C:244:GLN:OE1	1:C:511:THR:OG1	2.24	0.55
2:D:58:GLU:OE1	2:D:58:GLU:N	2.34	0.55
2:E:149:VAL:HA	2:E:327:ILE:HB	1.88	0.55
2:F:171:LEU:H	2:F:171:LEU:HD12	1.72	0.55
1:I:355:PRO:HG2	1:I:358:LEU:HB2	1.88	0.55
2:L:130:THR:H	2:L:136:ASP:CG	2.14	0.55
2:L:150:PHE:HB3	2:L:306:MET:HE3	1.87	0.55
2:M:21:VAL:HG13	2:M:24:VAL:HG21	1.87	0.55
2:N:129:GLN:NE2	2:N:422:THR:HA	2.19	0.55
1:B:482:LEU:HD22	1:B:490:LEU:HD11	1.88	0.55
1:C:39:ILE:CG1	1:C:49:ILE:HG12	2.35	0.55
1:C:163:GLU:OE2	1:C:173:ILE:HB	2.07	0.55
2:D:86:ILE:HA	2:D:208:VAL:HG22	1.88	0.55
2:D:92:GLY:CA	2:D:224:THR:HG22	2.36	0.55
2:F:161:ALA:HB2	2:F:303:ILE:HD11	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:339:GLN:HA	2:F:341:PRO:N	2.21	0.55
1:A:215:VAL:O	1:A:219:PHE:HB2	2.06	0.55
1:C:425:PHE:HA	1:C:426:PRO:C	2.31	0.55
2:D:184:ILE:O	2:D:252:ASN:ND2	2.34	0.55
2:D:226:ARG:HG2	2:D:284:LEU:HD21	1.87	0.55
1:J:218:THR:HG22	1:J:457:VAL:HG22	1.89	0.55
2:L:34:MET:SD	2:L:63:ILE:HG12	2.47	0.55
2:M:333:LEU:HD21	2:M:409:GLU:OE2	2.07	0.55
2:N:130:THR:HB	2:N:135:ILE:HB	1.89	0.55
2:N:180:VAL:HG22	2:N:208:VAL:HB	1.88	0.55
1:B:41:GLU:HA	2:F:12:VAL:CB	2.36	0.55
2:D:144:GLY:CA	2:D:289:GLY:HA2	2.37	0.55
2:D:325:GLY:CA	2:D:349:SER:HA	2.37	0.55
1:I:218:THR:HA	1:I:453:TRP:CZ2	2.42	0.55
1:K:85:ASP:OD2	1:K:89:ARG:HB2	2.06	0.55
1:K:218:THR:HB	1:K:453:TRP:HZ2	1.70	0.55
1:K:568:ALA:O	1:K:572:SER:OG	2.24	0.55
1:B:341:MET:O	1:B:345:LEU:HG	2.06	0.55
1:B:364:GLU:HG2	2:F:215:ASN:HA	1.87	0.55
1:B:494:LYS:HA	1:B:497:ARG:HD3	1.87	0.55
1:C:141:GLU:OE2	1:C:147:HIS:ND1	2.28	0.55
1:C:318:ARG:HD3	1:C:384:ILE:HD11	1.89	0.55
2:D:224:THR:OG1	2:D:225:PRO:HD3	2.07	0.55
1:I:41:GLU:HB2	1:I:48:SER:HB2	1.89	0.55
1:J:58:ILE:CG2	1:J:62:GLU:HG3	2.36	0.55
1:J:318:ARG:HD3	1:J:384:ILE:CD1	2.36	0.55
2:L:18:VAL:HG11	2:L:21:VAL:HG11	1.88	0.55
1:A:541:TYR:O	1:A:545:ILE:HG13	2.06	0.55
1:B:167:PHE:CD2	1:B:173:ILE:HG21	2.41	0.55
2:D:222:ILE:O	2:D:225:PRO:HD2	2.05	0.55
2:E:313:HIS:HB3	2:E:316:PRO:CD	2.36	0.55
2:F:161:ALA:HB1	2:F:246:ILE:HG21	1.88	0.55
1:I:84:PHE:HA	1:I:89:ARG:O	2.06	0.55
1:J:500:TYR:HE2	1:J:522:LEU:HD22	1.72	0.55
1:K:6:ILE:HG13	1:K:62:GLU:O	2.06	0.55
1:A:54:GLU:HB2	1:A:105:ARG:HH21	1.72	0.55
1:A:125:GLU:O	1:A:128:THR:OG1	2.24	0.55
1:A:291:LEU:HD23	1:A:292:ILE:N	2.21	0.55
1:A:522:LEU:O	1:A:526:LEU:HG	2.06	0.55
1:B:425:PHE:HA	1:B:426:PRO:C	2.32	0.55
1:B:494:LYS:HA	1:B:497:ARG:NH1	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:144:GLY:HA2	2:F:298:VAL:O	2.05	0.55
1:I:71:LEU:O	1:I:193:VAL:HG22	2.07	0.55
1:J:202:LYS:HE2	1:J:372:VAL:HG11	1.88	0.55
2:L:33:ARG:N	2:L:69:SER:O	2.25	0.55
2:N:224:THR:HB	2:N:225:PRO:HD3	1.87	0.55
1:A:114:HIS:ND1	1:A:170:ASP:OD2	2.38	0.55
2:D:285:PHE:CE1	2:D:302:PRO:HB3	2.42	0.55
2:E:182:ALA:HB3	2:E:247:MET:HG3	1.88	0.55
1:I:177:GLU:HB2	1:I:182:LEU:CD2	2.37	0.55
1:K:144:ILE:HG13	1:K:145:ILE:HG13	1.88	0.55
2:N:288:ALA:HB1	2:N:298:VAL:O	2.06	0.55
1:A:224:LYS:NZ	1:A:250:ASP:OD1	2.36	0.55
1:A:264:ASN:HB2	2:D:351:LEU:HD13	1.88	0.55
2:F:50:ASP:C	2:F:51:LYS:HG2	2.31	0.55
2:F:158:LYS:H	2:F:158:LYS:HD2	1.71	0.55
1:J:43:ARG:HA	2:N:10:GLU:CB	2.36	0.55
1:J:71:LEU:O	1:J:193:VAL:HG22	2.06	0.55
1:J:230:VAL:N	1:J:231:PRO:HD3	2.22	0.55
1:K:423:ARG:HG3	2:N:373:PHE:CG	2.41	0.55
2:N:34:MET:HE1	2:N:63:ILE:HG12	1.89	0.55
2:N:183:ALA:O	2:N:212:ASN:HB3	2.06	0.55
2:N:364:ASP:OD2	2:N:427:LEU:HD11	2.06	0.55
1:A:285:LEU:O	1:A:285:LEU:HD23	2.07	0.55
1:B:82:GLN:NE2	1:B:92:ASP:OD2	2.39	0.55
1:B:516:GLU:OE1	1:B:516:GLU:N	2.40	0.55
1:C:120:PHE:CE1	1:C:173:ILE:HD11	2.42	0.55
1:K:237:GLY:HA3	4:K:601:ANP:C8	2.36	0.55
1:K:290:VAL:HG11	1:K:313:ILE:HG21	1.87	0.55
2:L:148:PRO:O	2:L:327:ILE:N	2.36	0.55
2:L:222:ILE:CD1	2:L:260:ILE:HD11	2.37	0.55
2:N:328:ILE:HG13	2:N:346:PRO:CG	2.36	0.55
1:A:175:VAL:HG22	1:A:184:GLU:HG2	1.88	0.54
1:B:496:ILE:HG22	1:B:501:LEU:HD12	1.88	0.54
1:C:7:ILE:O	2:F:49:GLU:HA	2.07	0.54
1:C:31:GLY:HA2	1:C:62:GLU:HB3	1.89	0.54
1:C:80:ILE:HG23	1:C:290:VAL:HG22	1.89	0.54
1:I:177:GLU:CB	1:I:182:LEU:HD23	2.36	0.54
1:I:285:LEU:HD13	1:I:285:LEU:O	2.06	0.54
1:I:357:TYR:HB3	2:M:259:GLU:HG3	1.89	0.54
1:J:79:ILE:HG13	1:J:84:PHE:HZ	1.70	0.54
1:J:202:LYS:HB2	2:N:188:PHE:CZ	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:530:LYS:NZ	1:J:530:LYS:HB3	2.23	0.54
2:M:283:THR:O	2:M:287:ARG:HG2	2.07	0.54
2:N:339:GLN:O	2:N:414:ASN:HB3	2.07	0.54
2:N:347:SER:HB2	2:N:373:PHE:CE1	2.42	0.54
1:B:14:VAL:O	1:B:49:ILE:N	2.31	0.54
1:C:43:ARG:NH2	2:D:12:VAL:HG21	2.22	0.54
2:D:149:VAL:HA	2:D:327:ILE:HB	1.89	0.54
2:F:160:LEU:CD2	2:F:342:ILE:HD11	2.37	0.54
1:I:83:MET:SD	1:I:270:VAL:HG13	2.48	0.54
1:I:83:MET:HE1	2:L:119:ILE:HG21	1.89	0.54
1:J:135:ILE:HA	1:J:149:ILE:O	2.07	0.54
1:J:338:LEU:HB3	1:J:355:PRO:HG3	1.89	0.54
2:N:181:PHE:HB3	2:N:209:MET:SD	2.47	0.54
1:A:202:LYS:HG3	1:A:372:VAL:CG1	2.35	0.54
1:A:254:VAL:N	1:A:289:THR:OG1	2.34	0.54
1:A:536:LEU:HG	1:A:545:ILE:HD12	1.88	0.54
1:B:11:GLY:N	1:B:12:PRO:HD2	2.22	0.54
1:B:230:VAL:HA	1:B:413:TRP:O	2.07	0.54
1:C:73:VAL:HB	1:C:88:GLN:CD	2.31	0.54
1:C:211:THR:HB	1:C:245:ILE:HD12	1.89	0.54
1:J:262:ARG:NH2	4:J:601:ANP:O2G	2.39	0.54
1:J:410:LYS:HD3	1:J:437:TYR:CE1	2.42	0.54
1:K:81:SER:OG	1:K:287:GLU:HA	2.06	0.54
1:K:514:SER:O	1:K:518:GLN:HG3	2.07	0.54
2:L:350:ARG:O	2:L:351:LEU:HD23	2.08	0.54
2:M:178:ALA:HB3	2:M:243:VAL:HG22	1.89	0.54
1:A:75:LEU:O	1:A:189:GLN:N	2.26	0.54
1:B:7:ILE:O	2:E:48:GLN:HA	2.08	0.54
1:B:453:TRP:HZ3	1:B:519:PHE:HA	1.71	0.54
1:C:79:ILE:HA	1:C:112:LEU:HD21	1.89	0.54
2:D:249:ASP:OD1	2:D:304:LEU:HA	2.08	0.54
2:F:407:ARG:HB2	2:F:433:LEU:HD11	1.89	0.54
1:B:440:GLU:C	1:B:443:ARG:HH22	2.15	0.54
1:C:249:SER:HB3	1:C:251:VAL:HG22	1.88	0.54
2:D:15:LEU:HD11	2:D:263:ALA:HB1	1.89	0.54
2:E:372:LEU:HD21	2:E:412:TYR:CE1	2.25	0.54
2:E:405:ALA:O	2:E:409:GLU:HG3	2.08	0.54
2:F:421:ARG:CZ	2:F:429:LEU:HD13	2.38	0.54
1:I:25:GLN:HG3	2:M:61:SER:OG	2.07	0.54
1:I:83:MET:HE1	2:L:119:ILE:CG2	2.37	0.54
1:J:14:VAL:HG23	1:J:51:VAL:CG2	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:16:ALA:HB3	1:J:19:MET:HE2	1.88	0.54
2:L:6:ARG:HD3	2:L:70:VAL:CA	2.37	0.54
2:L:349:SER:HB3	2:L:352:LYS:HZ2	1.73	0.54
2:N:44:VAL:HG22	2:N:54:VAL:CA	2.35	0.54
2:N:339:GLN:HA	2:N:341:PRO:HD3	1.89	0.54
2:N:346:PRO:C	2:N:348:LEU:HB2	2.33	0.54
1:B:220:PHE:CZ	1:B:430:TRP:HA	2.42	0.54
1:B:254:VAL:HA	1:B:325:ALA:O	2.07	0.54
1:C:83:MET:HE3	1:C:91:LEU:HD12	1.90	0.54
2:D:158:LYS:HG3	2:D:194:PHE:CE1	2.42	0.54
2:E:438:PRO:HG2	2:E:441:GLU:CG	2.38	0.54
1:I:31:GLY:HA2	1:I:62:GLU:HB3	1.89	0.54
1:J:304:GLU:HG3	1:J:334:TRP:HE1	1.71	0.54
1:K:211:THR:CB	1:K:216:ILE:CD1	2.85	0.54
2:L:151:SER:OG	2:L:329:LEU:HD22	2.08	0.54
1:B:39:ILE:HG12	1:B:49:ILE:HG12	1.90	0.54
1:B:114:HIS:CD2	1:B:169:ILE:HD11	2.40	0.54
2:E:149:VAL:HB	2:E:303:ILE:HG12	1.88	0.54
2:F:26:TYR:CD1	2:F:27:GLU:N	2.75	0.54
2:F:233:GLU:HB3	2:F:237:TYR:CE1	2.42	0.54
1:J:352:GLU:CB	1:J:400:PRO:HG3	2.38	0.54
1:K:552:VAL:O	1:K:556:ILE:HG13	2.08	0.54
2:L:333:LEU:O	2:L:338:ILE:HB	2.08	0.54
2:M:439:ARG:NH2	2:M:450:LEU:HB2	2.22	0.54
2:N:339:GLN:HB3	2:N:417:PHE:CE2	2.42	0.54
1:A:43:ARG:HB3	1:A:44:GLN:C	2.33	0.54
1:A:424:HIS:CE1	1:A:501:LEU:HB3	2.43	0.54
1:A:503:GLN:NE2	1:A:510:ASP:O	2.35	0.54
1:B:348:MET:HE2	2:F:265:ARG:HG3	1.90	0.54
1:B:392:PRO:HB2	1:B:396:ASP:O	2.08	0.54
1:C:297:ASN:ND2	2:F:115:VAL:HG13	2.23	0.54
2:D:45:LEU:HD13	2:D:264:ARG:HG2	1.90	0.54
2:D:273:TYR:CZ	2:D:313:HIS:HE1	2.26	0.54
2:E:313:HIS:CD2	2:E:314:PRO:HD2	2.43	0.54
2:F:44:VAL:CG2	2:F:54:VAL:HG12	2.25	0.54
1:J:262:ARG:HH21	2:M:350:ARG:HH12	1.54	0.54
1:K:2:GLN:HE22	1:K:20:SER:CB	2.21	0.54
1:K:144:ILE:HG21	1:K:281:THR:HB	1.90	0.54
1:K:209:MET:HE3	1:K:211:THR:CG2	2.37	0.54
1:K:295:THR:N	1:K:298:MET:HG3	2.22	0.54
2:L:222:ILE:HD13	2:L:260:ILE:HD11	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:225:GLY:HA2	1:B:384:ILE:O	2.08	0.54
1:B:278:ASP:O	1:B:282:GLY:HA3	2.07	0.54
2:D:213:LEU:O	2:D:216:ASP:HB2	2.08	0.54
2:D:345:LEU:N	2:D:346:PRO:HD2	2.23	0.54
2:E:212:ASN:OD1	2:E:221:ARG:HA	2.08	0.54
1:J:92:ASP:OD1	1:J:93:THR:N	2.40	0.54
1:K:41:GLU:OE1	2:L:12:VAL:HG22	2.08	0.54
1:K:326:ILE:HG23	1:K:386:ALA:HA	1.90	0.54
1:K:412:PHE:CD2	1:K:433:SER:HA	2.42	0.54
2:L:49:GLU:H	2:L:49:GLU:CD	2.16	0.54
2:L:137:HIS:O	2:L:137:HIS:ND1	2.39	0.54
2:L:180:VAL:HB	2:L:245:VAL:HG22	1.90	0.54
2:M:315:ILE:O	2:M:319:THR:OG1	2.23	0.54
2:M:318:LEU:O	2:M:321:TYR:HB2	2.08	0.54
2:N:408:PHE:CD2	2:N:413:VAL:HG23	2.43	0.54
1:A:173:ILE:HG21	1:A:187:MET:HE3	1.90	0.54
1:B:439:THR:O	1:B:443:ARG:NH2	2.41	0.54
1:C:414:GLY:C	1:C:415:LEU:HD23	2.33	0.54
2:E:32:VAL:HG22	2:E:70:VAL:HG22	1.89	0.54
2:E:309:ASP:OD2	2:E:331:ARG:NH1	2.41	0.54
1:I:415:LEU:CD2	1:I:428:ILE:HG12	2.37	0.54
1:J:202:LYS:NZ	1:J:367:GLU:O	2.28	0.54
1:J:301:ALA:HB2	1:J:341:MET:CE	2.35	0.54
1:J:324:VAL:O	1:J:384:ILE:HA	2.08	0.54
2:M:394:LEU:O	2:M:399:LYS:NZ	2.30	0.54
2:N:148:PRO:HG3	2:N:323:THR:CG2	2.37	0.54
1:A:16:ALA:O	1:A:46:VAL:HA	2.08	0.53
1:B:101:ASN:O	2:E:117:ASN:HB2	2.08	0.53
1:C:92:ASP:OD1	1:C:93:THR:N	2.41	0.53
1:C:300:VAL:CG1	1:C:303:ARG:HD2	2.38	0.53
2:D:138:LEU:HG	2:D:344:VAL:CG1	2.39	0.53
2:D:357:GLY:N	2:D:361:THR:OG1	2.41	0.53
2:F:16:MET:N	2:F:54:VAL:O	2.35	0.53
2:F:270:ARG:HG2	2:F:271:ARG:HG2	1.90	0.53
1:I:202:LYS:HG3	1:I:372:VAL:CG1	2.37	0.53
1:I:214:ARG:NH2	1:I:503:GLN:HG3	2.23	0.53
4:K:601:ANP:O3'	2:N:350:ARG:HA	2.08	0.53
2:L:170:VAL:HG11	2:L:173:SER:HB3	1.89	0.53
2:M:15:LEU:N	2:M:15:LEU:HD23	2.23	0.53
2:N:30:ILE:HG12	2:N:54:VAL:CB	2.37	0.53
2:N:283:THR:O	2:N:287:ARG:HG2	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:135:ILE:HD13	1:A:148:LYS:HD3	1.89	0.53
2:D:152:GLY:H	2:D:155:LEU:HD12	1.72	0.53
1:I:221:PRO:HB2	1:I:441:VAL:HG21	1.89	0.53
1:K:446:ASP:OD1	1:K:452:ASP:HA	2.08	0.53
1:K:498:GLU:HA	1:K:502:GLN:HG3	1.90	0.53
2:M:315:ILE:HB	2:M:316:PRO:CD	2.38	0.53
2:N:30:ILE:HG13	2:N:42:GLY:O	2.08	0.53
2:N:332:GLU:HA	2:N:335:LYS:HE3	1.89	0.53
1:A:437:TYR:OH	2:E:189:GLU:OE2	2.20	0.53
1:I:20:SER:HA	1:I:42:MET:CE	2.34	0.53
1:I:24:ILE:HG13	2:M:11:VAL:HG11	1.89	0.53
1:I:120:PHE:CE2	1:I:122:ALA:HB2	2.44	0.53
1:J:94:PHE:O	1:J:98:THR:OG1	2.26	0.53
1:K:318:ARG:HD3	1:K:384:ILE:CD1	2.38	0.53
2:L:339:GLN:HA	2:L:341:PRO:HD3	1.90	0.53
2:M:261:SER:HB2	2:M:276:TYR:OH	2.09	0.53
2:D:362:ARG:HB2	2:D:427:LEU:HD13	1.90	0.53
1:J:38:GLU:HB2	1:J:50:GLN:HB2	1.90	0.53
1:K:484:ASP:HB3	1:K:542:PHE:HB2	1.91	0.53
2:L:6:ARG:NH1	2:L:69:SER:HA	2.23	0.53
2:N:57:PHE:O	2:N:217:PRO:HB3	2.08	0.53
1:A:378:ASP:N	1:A:378:ASP:OD1	2.42	0.53
1:B:238:LYS:HG2	1:B:415:LEU:HD13	1.89	0.53
1:C:144:ILE:HG23	1:C:145:ILE:HG12	1.90	0.53
2:F:315:ILE:HB	2:F:316:PRO:CD	2.39	0.53
2:L:153:SER:O	2:L:331:ARG:NH1	2.42	0.53
2:L:273:TYR:CE1	2:L:315:ILE:HG12	2.42	0.53
2:M:44:VAL:HG22	2:M:54:VAL:HG12	1.90	0.53
2:M:307:PRO:HG2	2:M:313:HIS:CD2	2.43	0.53
2:N:28:GLU:OE2	2:N:72:PHE:HB3	2.08	0.53
1:B:80:ILE:HD12	1:B:317:PHE:CZ	2.44	0.53
1:C:10:SER:CB	2:F:46:GLU:HG3	2.22	0.53
1:C:300:VAL:HG22	2:F:279:THR:HG21	1.90	0.53
2:F:309:ASP:OD2	2:F:331:ARG:NH1	2.42	0.53
2:F:325:GLY:N	2:F:350:ARG:HE	2.01	0.53
1:J:92:ASP:O	1:J:96:GLU:HG2	2.09	0.53
2:L:143:ARG:HD3	2:L:290:ARG:NH1	2.23	0.53
2:N:48:GLN:O	2:N:51:LYS:N	2.38	0.53
1:C:329:ASP:OD1	1:C:330:SER:HB2	2.08	0.53
1:C:552:VAL:HG23	1:C:576:GLU:HG2	1.90	0.53
2:D:27:GLU:O	2:D:43:GLN:NE2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:34:MET:HG3	2:E:38:GLU:HB3	1.90	0.53
2:F:149:VAL:HB	2:F:303:ILE:HG12	1.91	0.53
1:I:298:MET:HA	1:I:298:MET:HE2	1.90	0.53
1:I:405:THR:O	1:I:409:VAL:HG22	2.08	0.53
1:J:463:ILE:HG22	1:J:493:ALA:HB2	1.91	0.53
1:K:213:GLN:CG	1:K:216:ILE:HD11	2.39	0.53
1:K:479:ILE:CG2	2:N:394:LEU:HA	2.38	0.53
4:K:601:ANP:C5'	2:N:350:ARG:HD3	2.21	0.53
2:N:148:PRO:HB2	2:N:150:PHE:CE1	2.43	0.53
1:C:446:ASP:CB	1:C:452:ASP:HA	2.39	0.53
2:E:5:TYR:O	2:E:70:VAL:N	2.30	0.53
2:E:91:ASP:OD1	2:E:95:ARG:HG3	2.09	0.53
2:E:148:PRO:O	2:E:327:ILE:HB	2.08	0.53
2:E:213:LEU:HB3	2:E:215:ASN:OD1	2.08	0.53
1:I:408:VAL:HG23	1:I:409:VAL:HG13	1.90	0.53
1:J:38:GLU:HG2	1:J:52:TYR:CZ	2.43	0.53
1:K:79:ILE:CA	1:K:112:LEU:HD21	2.38	0.53
1:K:260:GLY:CA	1:K:333:ARG:HG3	2.38	0.53
1:A:392:PRO:HB3	1:A:399:GLU:CD	2.34	0.53
1:A:424:HIS:ND1	1:A:502:GLN:HG2	2.24	0.53
2:D:29:LEU:CB	2:D:73:LEU:HD21	2.39	0.53
2:E:329:LEU:HD22	2:E:341:PRO:O	2.08	0.53
2:E:338:ILE:HG22	2:E:414:ASN:HB3	1.91	0.53
1:J:149:ILE:HD13	1:J:149:ILE:N	2.23	0.53
1:J:236:ALA:HB1	1:J:415:LEU:HD12	1.90	0.53
1:J:300:VAL:CG2	2:M:279:THR:HG21	2.38	0.53
1:K:378:ASP:OD1	1:K:378:ASP:N	2.41	0.53
1:K:425:PHE:HA	1:K:426:PRO:C	2.33	0.53
2:L:235:LEU:HA	2:L:239:LYS:HB2	1.90	0.53
2:M:135:ILE:O	2:M:140:THR:HA	2.09	0.53
2:N:13:GLY:O	2:N:60:THR:OG1	2.19	0.53
1:A:43:ARG:CG	1:A:46:VAL:HG13	2.39	0.53
1:A:177:GLU:HG3	1:A:182:LEU:HD23	1.91	0.53
2:D:212:ASN:OD1	2:D:221:ARG:HG3	2.09	0.53
2:E:26:TYR:CE2	2:E:27:GLU:HG3	2.44	0.53
2:E:127:PHE:HZ	2:E:136:ASP:CB	2.22	0.53
2:F:255:GLU:O	2:F:258:ARG:HG2	2.09	0.53
1:I:175:VAL:CG1	1:I:182:LEU:HD22	2.39	0.53
1:J:218:THR:HG1	1:J:500:TYR:HH	1.54	0.53
1:J:259:CYS:O	1:J:330:SER:N	2.37	0.53
1:K:51:VAL:HG21	1:K:55:THR:HG23	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:92:GLY:O	2:L:227:MET:HE2	2.10	0.53
2:M:17:ALA:HA	2:M:53:MET:HA	1.91	0.53
2:M:446:LYS:HB3	2:M:448:ASP:OD1	2.08	0.53
1:A:188:MET:HE1	1:A:190:LYS:NZ	2.25	0.52
1:A:425:PHE:O	1:A:503:GLN:N	2.22	0.52
1:B:515:ARG:HA	1:B:518:GLN:HG3	1.91	0.52
2:D:40:ARG:NH1	2:D:59:GLY:O	2.40	0.52
2:D:415:GLN:HB3	2:D:421:ARG:NH1	2.23	0.52
2:F:278:TYR:CE1	2:F:322:ILE:HG12	2.44	0.52
2:F:358:ALA:N	2:F:359:GLY:CA	2.69	0.52
1:J:50:GLN:HE21	1:J:345:LEU:CD1	2.22	0.52
1:K:214:ARG:NH1	1:K:499:ASP:O	2.42	0.52
2:L:9:LYS:HG3	2:L:19:GLU:CG	2.39	0.52
2:M:78:GLN:NE2	2:M:78:GLN:HA	2.24	0.52
2:M:82:SER:CB	2:M:103:ILE:HD11	2.09	0.52
1:A:285:LEU:O	1:A:288:ARG:HG2	2.09	0.52
1:A:297:ASN:CG	2:D:286:GLU:HG3	2.34	0.52
1:B:491:GLU:HG3	1:B:542:PHE:HZ	1.74	0.52
2:D:407:ARG:HD3	2:D:436:MET:HE1	1.91	0.52
2:E:183:ALA:HB1	2:E:186:ILE:HD11	1.90	0.52
2:F:339:GLN:CA	2:F:341:PRO:HD3	2.38	0.52
1:I:208:PRO:HA	1:I:223:THR:HA	1.90	0.52
1:K:211:THR:OG1	1:K:216:ILE:HD12	2.09	0.52
2:L:79:LEU:HD13	2:L:227:MET:CE	2.40	0.52
2:L:257:LEU:HA	2:L:260:ILE:CD1	2.39	0.52
2:L:349:SER:C	2:L:352:LYS:HZ1	2.16	0.52
1:A:20:SER:HA	1:A:42:MET:CE	2.40	0.52
1:A:523:LYS:HA	1:A:523:LYS:HE3	1.92	0.52
1:B:29:LEU:HD23	1:B:65:ARG:HB2	1.90	0.52
2:D:220:GLU:O	2:D:224:THR:HG23	2.08	0.52
1:J:406:LEU:HD21	1:J:412:PHE:HB2	1.91	0.52
2:L:283:THR:HA	2:L:286:GLU:HB2	1.91	0.52
2:M:60:THR:OG1	2:M:63:ILE:HD12	2.09	0.52
2:M:82:SER:O	2:M:85:MET:HG3	2.09	0.52
2:M:147:LEU:O	2:M:302:PRO:HD2	2.09	0.52
2:N:67:ASN:OD1	2:N:67:ASN:N	2.42	0.52
1:A:140:ASP:OD1	1:A:146:GLN:HG3	2.09	0.52
1:A:323:ASP:OD1	1:A:383:SER:OG	2.28	0.52
1:A:445:MET:HG3	1:A:453:TRP:CE3	2.45	0.52
1:A:577:ILE:O	1:A:581:ILE:HG12	2.09	0.52
2:D:38:GLU:OE2	2:D:40:ARG:NE	2.33	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:56:ILE:HG22	2:E:59:GLY:H	1.75	0.52
2:E:423:ILE:O	2:E:427:LEU:HG	2.09	0.52
1:K:29:LEU:HB2	1:K:65:ARG:HE	1.74	0.52
2:L:30:ILE:HD12	2:L:30:ILE:O	2.10	0.52
2:M:235:LEU:HB2	2:M:243:VAL:HG21	1.91	0.52
2:M:388:VAL:HG13	2:M:389:LEU:HG	1.92	0.52
1:A:15:MET:HA	1:A:47:ALA:O	2.09	0.52
1:B:36:ILE:HD12	1:B:87:ILE:HD13	1.91	0.52
1:B:83:MET:HE3	2:E:119:ILE:HD11	1.92	0.52
1:J:355:PRO:HG2	1:J:358:LEU:HB2	1.90	0.52
1:K:392:PRO:HB3	1:K:396:ASP:O	2.08	0.52
2:L:33:ARG:HB3	2:L:69:SER:OG	2.09	0.52
2:L:339:GLN:N	2:L:414:ASN:HD21	2.07	0.52
2:M:57:PHE:CE2	2:M:219:ILE:HG21	2.45	0.52
2:M:324:GLU:C	2:M:350:ARG:HD2	2.34	0.52
2:N:347:SER:HB3	2:N:348:LEU:HA	1.91	0.52
1:A:43:ARG:HB3	1:A:44:GLN:CA	2.40	0.52
1:B:251:VAL:HG21	1:B:325:ALA:HB3	1.90	0.52
1:B:547:GLU:HA	1:B:550:VAL:HG13	1.92	0.52
1:C:573:ILE:HG22	1:C:577:ILE:CD1	2.38	0.52
1:I:340:GLU:O	1:I:344:ARG:HG3	2.10	0.52
1:K:59:GLY:HA3	2:N:25:LYS:HD3	1.92	0.52
1:K:500:TYR:HE2	1:K:522:LEU:CB	2.20	0.52
2:M:79:LEU:HD13	2:M:94:GLY:HA3	1.91	0.52
2:M:91:ASP:CG	2:M:95:ARG:HG2	2.34	0.52
2:M:91:ASP:OD1	2:M:95:ARG:HG2	2.10	0.52
2:M:277:LEU:O	2:M:281:LEU:HB2	2.10	0.52
2:N:304:LEU:HD22	2:N:315:ILE:HG22	1.91	0.52
1:A:52:TYR:CB	1:A:299:PRO:HB3	2.40	0.52
1:C:71:LEU:HD23	1:C:193:VAL:HG21	1.91	0.52
1:C:331:THR:CG2	1:C:390:VAL:HG22	2.39	0.52
2:E:6:ARG:HA	2:E:69:SER:HA	1.92	0.52
2:F:142:VAL:HG21	2:F:351:LEU:HB3	1.90	0.52
1:I:43:ARG:HG2	1:I:46:VAL:HG13	1.91	0.52
1:I:139:VAL:O	1:I:147:HIS:HB3	2.09	0.52
1:J:84:PHE:O	1:J:292:ILE:HG23	2.09	0.52
1:K:32:ASP:H	1:K:62:GLU:HG2	1.74	0.52
2:L:120:ALA:O	2:L:292:ARG:HB2	2.10	0.52
2:M:231:ALA:O	2:M:235:LEU:HG	2.10	0.52
2:N:328:ILE:HG13	2:N:346:PRO:HG3	1.91	0.52
2:N:378:GLN:HB3	2:N:401:TYR:CD1	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:488:LEU:O	1:B:492:VAL:HG23	2.09	0.52
2:D:138:LEU:HG	2:D:344:VAL:CB	2.40	0.52
2:E:224:THR:HB	2:E:225:PRO:HD3	1.92	0.52
2:E:284:LEU:HD12	2:E:285:PHE:H	1.75	0.52
2:E:372:LEU:HD13	2:E:434:LEU:HG	1.91	0.52
2:F:65:LEU:N	2:F:65:LEU:HD23	2.24	0.52
2:F:215:ASN:OD1	2:F:215:ASN:N	2.40	0.52
1:I:42:MET:HG3	2:M:65:LEU:HD11	1.91	0.52
1:I:255:VAL:HG12	1:I:257:VAL:HG23	1.92	0.52
1:J:232:GLY:O	1:J:238:LYS:HD3	2.09	0.52
1:K:230:VAL:HG23	1:K:389:ALA:CB	2.40	0.52
1:K:522:LEU:O	1:K:526:LEU:HB2	2.09	0.52
2:N:11:VAL:HG22	2:N:16:MET:HG3	1.92	0.52
1:A:75:LEU:HB3	1:A:316:TYR:CD2	2.44	0.52
1:B:19:MET:HE2	1:B:19:MET:HA	1.92	0.52
1:B:83:MET:HE2	1:B:291:LEU:HD23	1.92	0.52
1:B:230:VAL:HG13	1:B:413:TRP:O	2.10	0.52
1:B:339:ARG:NH2	2:E:275:GLY:O	2.43	0.52
1:C:367:GLU:HG2	2:D:215:ASN:ND2	2.24	0.52
1:C:412:PHE:CD2	1:C:433:SER:HA	2.45	0.52
2:D:8:ILE:HD13	2:D:16:MET:HE3	1.92	0.52
2:E:6:ARG:CZ	2:L:290:ARG:HH21	2.23	0.52
2:F:324:GLU:HA	2:F:350:ARG:NE	2.24	0.52
1:J:210:ILE:O	1:J:210:ILE:HG13	2.10	0.52
1:J:231:PRO:HA	1:J:390:VAL:O	2.10	0.52
1:J:300:VAL:HG22	2:M:279:THR:HG21	1.91	0.52
1:K:444:TYR:HE2	1:K:515:ARG:HH12	1.58	0.52
2:L:18:VAL:O	2:L:51:LYS:HA	2.10	0.52
2:N:98:ASP:N	2:N:99:ASN:HA	2.25	0.52
2:N:269:GLY:N	2:N:273:TYR:O	2.31	0.52
1:A:225:GLY:HA2	1:A:384:ILE:O	2.09	0.52
1:A:315:GLU:HG2	1:A:318:ARG:HH21	1.74	0.52
1:A:330:SER:HB3	1:A:333:ARG:HG3	1.92	0.52
1:C:161:LYS:HE3	1:C:175:VAL:CG2	2.40	0.52
1:C:573:ILE:CG2	1:C:577:ILE:HD11	2.39	0.52
2:D:29:LEU:HD11	2:D:77:LEU:HA	1.91	0.52
2:D:184:ILE:HD13	2:D:225:PRO:HG3	1.92	0.52
2:E:30:ILE:HD11	2:E:42:GLY:HA3	1.92	0.52
2:F:413:VAL:HG12	2:F:414:ASN:CG	2.35	0.52
1:I:33:LEU:H	1:I:33:LEU:HD12	1.75	0.52
1:J:144:ILE:HD11	1:J:288:ARG:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:147:LEU:HB3	2:M:301:ILE:HG12	1.90	0.52
1:A:120:PHE:HA	1:A:139:VAL:HG22	1.91	0.51
1:B:443:ARG:HB2	1:B:443:ARG:HH11	1.74	0.51
1:B:497:ARG:HA	1:B:501:LEU:CD1	2.40	0.51
1:C:552:VAL:CG2	1:C:576:GLU:HG2	2.41	0.51
2:D:33:ARG:N	2:D:69:SER:O	2.24	0.51
2:E:195:MET:HG2	2:E:209:MET:HE1	1.92	0.51
1:I:370:GLY:H	1:I:384:ILE:HB	1.75	0.51
1:J:494:LYS:O	1:J:498:GLU:HG2	2.10	0.51
1:K:213:GLN:HE22	1:K:244:GLN:HE21	1.57	0.51
1:K:234:PHE:HZ	2:N:311:LYS:HD2	1.75	0.51
1:K:262:ARG:CZ	2:N:350:ARG:HH12	2.22	0.51
2:L:222:ILE:HG23	2:L:253:TYR:CE1	2.44	0.51
2:M:270:ARG:O	2:M:271:ARG:HB2	2.09	0.51
1:A:261:GLU:CB	1:A:266:MET:HG2	2.40	0.51
1:A:340:GLU:HG3	2:D:276:TYR:HA	1.92	0.51
2:D:162:ALA:O	2:D:166:ARG:HG3	2.11	0.51
2:E:29:LEU:HD23	2:E:42:GLY:O	2.10	0.51
2:E:326:GLN:HB2	2:E:347:SER:HA	1.91	0.51
2:F:24:VAL:HG22	2:F:72:PHE:HE2	1.75	0.51
2:F:177:PHE:CE1	2:F:244:LEU:N	2.78	0.51
1:I:425:PHE:HA	1:I:426:PRO:C	2.34	0.51
1:J:285:LEU:O	1:J:285:LEU:HD23	2.11	0.51
1:K:54:GLU:HB2	1:K:105:ARG:HD3	1.90	0.51
1:K:120:PHE:CZ	1:K:173:ILE:HD12	2.44	0.51
1:K:149:ILE:HD12	1:K:149:ILE:N	2.25	0.51
1:K:503:GLN:NE2	1:K:510:ASP:O	2.33	0.51
2:M:437:LEU:HB2	2:M:442:LEU:HD21	1.93	0.51
2:N:4:GLU:HB3	2:N:71:ARG:CB	2.36	0.51
1:A:20:SER:HB3	1:A:45:ASP:HB3	1.92	0.51
1:B:39:ILE:HG12	1:B:49:ILE:HG23	1.91	0.51
1:C:169:ILE:HG23	1:C:187:MET:HB2	1.91	0.51
2:D:225:PRO:O	2:D:229:LEU:HG	2.11	0.51
2:D:409:GLU:HA	2:D:413:VAL:CG2	2.40	0.51
2:F:26:TYR:HE1	2:F:45:LEU:HA	1.73	0.51
1:J:522:LEU:HG	1:J:526:LEU:HD11	1.93	0.51
1:K:508:ASP:N	1:K:508:ASP:OD1	2.43	0.51
2:L:31:GLU:O	2:L:70:VAL:HA	2.11	0.51
2:M:21:VAL:HG22	2:M:72:PHE:HZ	1.75	0.51
2:M:132:ILE:HG22	2:M:134:ALA:H	1.75	0.51
2:M:226:ARG:HH11	2:M:284:LEU:HD21	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:32:VAL:N	2:N:40:ARG:O	2.37	0.51
2:N:88:ARG:HH22	2:N:96:PRO:HB3	1.74	0.51
1:A:521:MET:CE	1:A:560:LYS:HB3	2.40	0.51
1:C:366:TYR:OH	1:C:388:SER:HB2	2.10	0.51
2:D:223:ALA:O	2:D:227:MET:HG3	2.10	0.51
2:E:325:GLY:N	2:E:350:ARG:HG2	2.26	0.51
1:I:20:SER:HB2	2:M:66:LYS:NZ	2.23	0.51
1:J:374:ALA:HB3	1:J:380:ARG:HG2	1.92	0.51
1:K:421:GLN:HB3	2:N:345:LEU:O	2.10	0.51
2:L:249:ASP:OD1	2:L:304:LEU:HA	2.11	0.51
2:N:44:VAL:HG21	2:N:54:VAL:HG12	1.85	0.51
2:N:338:ILE:HG22	2:N:414:ASN:HB2	1.93	0.51
1:C:149:ILE:HD12	1:C:149:ILE:N	2.22	0.51
1:C:278:ASP:HB3	1:C:281:THR:HG21	1.91	0.51
2:D:138:LEU:CG	2:D:344:VAL:HB	2.41	0.51
1:I:254:VAL:O	1:I:289:THR:HB	2.10	0.51
1:K:225:GLY:O	1:K:370:GLY:HA2	2.10	0.51
1:K:259:CYS:N	1:K:329:ASP:O	2.43	0.51
2:L:14:PRO:HB2	2:L:55:GLN:CG	2.38	0.51
2:L:338:ILE:HG23	2:L:414:ASN:CG	2.35	0.51
2:M:21:VAL:CG1	2:M:24:VAL:HG21	2.40	0.51
2:M:88:ARG:NE	2:M:98:ASP:OD2	2.34	0.51
2:N:88:ARG:NH2	2:N:96:PRO:HB3	2.26	0.51
2:N:258:ARG:HD2	2:N:273:TYR:CE1	2.45	0.51
1:C:12:PRO:O	1:C:51:VAL:HG22	2.11	0.51
1:C:415:LEU:HD22	1:C:427:SER:O	2.09	0.51
1:C:423:ARG:NH1	2:F:348:LEU:HB2	2.26	0.51
2:F:338:ILE:O	2:F:341:PRO:HB3	2.11	0.51
1:I:424:HIS:C	1:I:425:PHE:HD1	2.18	0.51
1:J:236:ALA:CB	1:J:415:LEU:HD12	2.40	0.51
1:K:215:VAL:HG23	1:K:216:ILE:N	2.25	0.51
2:L:128:ILE:HD11	2:L:143:ARG:HA	1.92	0.51
1:C:295:THR:OG1	1:C:298:MET:SD	2.58	0.51
2:E:29:LEU:CD1	2:E:77:LEU:HG	2.36	0.51
2:E:93:LEU:HD12	2:E:95:ARG:CZ	2.40	0.51
1:I:199:ILE:HG21	1:I:372:VAL:HG21	1.93	0.51
1:I:232:GLY:HA3	1:I:415:LEU:HD12	1.92	0.51
1:I:439:THR:HG22	1:I:443:ARG:HH12	1.75	0.51
1:I:521:MET:O	1:I:525:ILE:HG13	2.11	0.51
1:K:41:GLU:HB2	2:L:12:VAL:HA	1.91	0.51
2:M:179:VAL:O	2:M:207:SER:HA	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:273:TYR:CD2	2:M:314:PRO:HG2	2.42	0.51
2:N:35:GLN:OE1	2:N:35:GLN:N	2.26	0.51
2:N:40:ARG:HD3	2:N:58:GLU:HB2	1.91	0.51
2:N:135:ILE:HA	2:N:139:ASN:HB2	1.92	0.51
1:A:497:ARG:CG	1:A:501:LEU:HD12	2.38	0.51
2:D:278:TYR:HE1	2:D:322:ILE:HG12	1.76	0.51
2:E:132:ILE:HD12	2:E:132:ILE:N	2.25	0.51
2:E:338:ILE:HG23	2:E:414:ASN:HB3	1.92	0.51
2:F:24:VAL:HG22	2:F:72:PHE:CE2	2.46	0.51
2:F:242:HIS:HA	2:F:297:SER:H	1.76	0.51
2:F:339:GLN:HB3	2:F:341:PRO:HD3	1.92	0.51
1:I:59:GLY:O	1:I:62:GLU:HG3	2.11	0.51
1:I:203:LEU:HD11	1:I:373:ILE:HG13	1.92	0.51
1:I:497:ARG:HA	1:I:501:LEU:CB	2.38	0.51
1:J:215:VAL:HG11	1:J:426:PRO:CG	2.40	0.51
1:J:419:LEU:HD23	1:J:422:LYS:HD2	1.93	0.51
1:K:191:TRP:HD1	1:K:312:THR:HG23	1.76	0.51
1:K:259:CYS:O	1:K:333:ARG:HG3	2.11	0.51
2:L:310:ASP:OD2	2:L:312:THR:OG1	2.29	0.51
2:L:329:LEU:HG	2:L:341:PRO:O	2.11	0.51
1:A:445:MET:O	1:A:449:LEU:HB2	2.10	0.51
1:A:484:ASP:OD2	1:A:484:ASP:N	2.43	0.51
1:B:214:ARG:HD2	1:B:500:TYR:HE2	1.76	0.51
1:B:252:ASP:OD2	1:B:252:ASP:N	2.43	0.51
1:C:75:LEU:O	1:C:189:GLN:N	2.43	0.51
1:C:233:PRO:HA	2:F:321:TYR:OH	2.11	0.51
2:E:149:VAL:HG22	2:E:327:ILE:HG21	1.92	0.51
2:E:283:THR:O	2:E:287:ARG:HG2	2.10	0.51
1:I:145:ILE:HG13	1:I:253:LEU:HD11	1.93	0.51
1:I:470:LEU:O	1:I:474:VAL:HG23	2.10	0.51
2:L:130:THR:N	2:L:136:ASP:OD2	2.44	0.51
2:L:151:SER:OG	2:L:157:HIS:HB3	2.11	0.51
2:M:102:GLU:H	2:M:102:GLU:CD	2.14	0.51
2:M:304:LEU:HD22	2:M:315:ILE:HG22	1.92	0.51
2:N:248:THR:HB	2:N:303:ILE:HB	1.92	0.51
1:A:257:VAL:HG12	1:A:258:GLY:N	2.23	0.51
2:D:32:VAL:HG22	2:D:70:VAL:HG22	1.92	0.51
2:D:90:PHE:HA	2:D:96:PRO:HA	1.92	0.51
2:F:403:LYS:O	2:F:407:ARG:HG3	2.11	0.51
1:J:497:ARG:HA	1:J:501:LEU:CD1	2.41	0.51
1:K:202:LYS:HB3	2:L:188:PHE:CE2	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:233:PRO:CD	1:K:236:ALA:HB2	2.38	0.51
2:M:119:ILE:O	2:M:292:ARG:NH1	2.44	0.51
1:A:264:ASN:HD21	2:D:324:GLU:CD	2.19	0.50
1:B:15:MET:HA	1:B:48:SER:HA	1.93	0.50
1:C:41:GLU:OE2	2:D:12:VAL:HG13	2.11	0.50
1:C:60:PRO:HD3	2:F:47:VAL:HG11	1.93	0.50
1:C:210:ILE:HD11	1:C:515:ARG:HH21	1.76	0.50
2:E:57:PHE:CE2	2:E:219:ILE:HG21	2.46	0.50
1:I:307:ILE:HB	1:I:365:TYR:CE1	2.45	0.50
1:J:247:LYS:HA	1:J:285:LEU:HD11	1.93	0.50
1:K:41:GLU:HB3	2:L:12:VAL:HA	1.93	0.50
1:K:42:MET:HE2	2:L:65:LEU:HD11	1.93	0.50
2:L:345:LEU:HB2	2:L:346:PRO:CD	2.41	0.50
2:L:429:LEU:O	2:L:433:LEU:HG	2.11	0.50
1:A:271:ASN:O	1:A:275:GLU:HG2	2.11	0.50
1:B:292:ILE:HD11	1:B:313:ILE:HD12	1.92	0.50
1:B:406:LEU:HD21	1:B:412:PHE:CD1	2.47	0.50
2:F:133:SER:OG	2:F:426:THR:HG23	2.11	0.50
1:I:264:ASN:ND2	2:L:145:GLN:HA	2.25	0.50
1:J:188:MET:HG2	1:J:189:GLN:N	2.27	0.50
1:K:355:PRO:HG2	1:K:358:LEU:HB2	1.92	0.50
1:K:453:TRP:HZ3	1:K:519:PHE:HA	1.77	0.50
1:A:497:ARG:O	1:A:501:LEU:HB2	2.11	0.50
1:B:54:GLU:HB3	1:B:105:ARG:HH11	1.77	0.50
1:C:149:ILE:H	1:C:149:ILE:CD1	2.23	0.50
1:C:425:PHE:HB3	4:C:601:ANP:C6	2.41	0.50
2:E:152:GLY:O	2:E:155:LEU:HB2	2.11	0.50
2:F:126:GLU:H	2:F:142:VAL:CG1	2.25	0.50
2:F:126:GLU:H	2:F:142:VAL:HG12	1.76	0.50
2:F:133:SER:HB2	2:F:415:GLN:OE1	2.11	0.50
1:I:139:VAL:HG21	1:I:149:ILE:HD11	1.92	0.50
1:J:331:THR:HG21	1:J:388:SER:HB2	1.93	0.50
1:K:73:VAL:HG11	1:K:309:THR:HG23	1.93	0.50
2:L:185:GLY:O	2:L:252:ASN:ND2	2.44	0.50
2:M:124:PRO:HB3	2:M:143:ARG:O	2.12	0.50
1:A:485:ASN:OD1	1:A:533:ARG:NH1	2.44	0.50
1:A:532:ALA:O	1:A:536:LEU:HB2	2.11	0.50
1:B:429:ASN:O	1:B:433:SER:OG	2.26	0.50
2:D:16:MET:N	2:D:54:VAL:O	2.39	0.50
2:D:159:GLU:O	2:D:163:GLN:HB2	2.12	0.50
2:D:235:LEU:HA	2:D:239:LYS:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:408:PHE:CD1	2:D:412:TYR:HB3	2.46	0.50
2:E:21:VAL:HG11	2:E:52:ALA:CB	2.29	0.50
1:I:479:ILE:HG13	1:I:480:ASP:N	2.26	0.50
1:J:390:VAL:O	1:J:392:PRO:HD3	2.11	0.50
1:K:87:ILE:HD11	1:K:89:ARG:NH2	2.26	0.50
1:K:269:VAL:HG11	1:K:291:LEU:HD21	1.93	0.50
2:L:251:THR:O	2:L:255:GLU:HG2	2.11	0.50
2:M:130:THR:OG1	2:M:135:ILE:HB	2.12	0.50
2:M:150:PHE:CZ	2:M:319:THR:HB	2.46	0.50
1:A:38:GLU:HB2	1:A:52:TYR:OH	2.11	0.50
1:A:208:PRO:CG	1:A:441:VAL:HG13	2.42	0.50
1:A:493:ALA:O	1:A:497:ARG:HG3	2.12	0.50
1:K:28:CYS:SG	1:K:39:ILE:HD11	2.51	0.50
1:K:211:THR:CB	1:K:216:ILE:HD12	2.41	0.50
2:M:16:MET:HE1	2:M:32:VAL:CG2	2.37	0.50
2:M:126:GLU:O	2:M:142:VAL:HG13	2.11	0.50
2:M:151:SER:O	2:M:305:THR:HA	2.12	0.50
1:A:266:MET:SD	1:A:293:ALA:HB1	2.52	0.50
1:B:119:TRP:HE1	1:B:121:GLU:HB2	1.76	0.50
1:B:173:ILE:HD13	1:B:173:ILE:H	1.77	0.50
1:B:285:LEU:CD1	1:B:288:ARG:CD	2.83	0.50
1:B:520:ASN:O	1:B:524:VAL:HG23	2.12	0.50
1:B:521:MET:HE1	1:B:560:LYS:HB3	1.92	0.50
2:D:34:MET:HE1	2:D:40:ARG:HG3	1.92	0.50
2:E:338:ILE:HG23	2:E:414:ASN:CB	2.42	0.50
1:I:460:GLY:O	1:I:464:LEU:HD12	2.11	0.50
1:J:273:PHE:HB2	1:J:274:PRO:HD3	1.94	0.50
1:K:176:ILE:N	1:K:183:LYS:O	2.41	0.50
1:K:222:VAL:HG22	1:K:413:TRP:HZ2	1.76	0.50
2:L:315:ILE:HB	2:L:316:PRO:HD3	1.93	0.50
2:L:339:GLN:HB2	2:L:417:PHE:CZ	2.46	0.50
2:N:92:GLY:C	2:N:93:LEU:HD23	2.35	0.50
2:N:256:ALA:O	2:N:260:ILE:HG12	2.11	0.50
1:A:218:THR:HA	1:A:453:TRP:CH2	2.47	0.50
1:A:257:VAL:O	1:A:328:ALA:HA	2.11	0.50
1:B:78:GLY:H	1:B:141:GLU:CD	2.20	0.50
2:F:339:GLN:O	2:F:416:GLY:N	2.45	0.50
1:J:198:PRO:HB2	1:J:375:LEU:HD11	1.93	0.50
1:K:22:ALA:O	1:K:42:MET:SD	2.70	0.50
1:K:230:VAL:HG23	1:K:389:ALA:CA	2.41	0.50
2:M:147:LEU:C	2:M:302:PRO:HD2	2.37	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:213:GLN:HG3	1:B:245:ILE:CD1	2.42	0.50
1:C:168:THR:HG22	1:C:171:ASP:OD2	2.12	0.50
1:C:185:LEU:O	1:C:185:LEU:HD12	2.12	0.50
1:C:331:THR:HG21	1:C:390:VAL:HG22	1.94	0.50
1:J:58:ILE:HG22	1:J:62:GLU:HG3	1.93	0.50
1:J:333:ARG:HD3	1:J:333:ARG:N	2.26	0.50
1:K:173:ILE:HD13	1:K:187:MET:HG2	1.94	0.50
1:K:225:GLY:HA3	1:K:371:ARG:N	2.27	0.50
1:K:314:ALA:HB1	1:K:324:VAL:HG11	1.93	0.50
2:L:40:ARG:NH1	2:L:59:GLY:O	2.45	0.50
2:L:269:GLY:N	2:L:273:TYR:O	2.44	0.50
2:M:219:ILE:O	2:M:223:ALA:N	2.45	0.50
2:N:329:LEU:HD22	2:N:341:PRO:O	2.12	0.50
1:A:18:ASN:N	1:A:45:ASP:OD1	2.43	0.50
1:B:504:ASN:OD1	1:B:506:PHE:HB2	2.12	0.50
2:D:139:ASN:HB3	2:D:349:SER:CB	2.41	0.50
2:D:270:ARG:NH1	2:D:270:ARG:HB3	2.27	0.50
1:J:37:GLY:HA3	1:J:50:GLN:O	2.12	0.50
1:J:95:MET:SD	2:M:120:ALA:HB2	2.52	0.50
1:K:480:ASP:OD2	1:K:480:ASP:N	2.44	0.50
2:M:88:ARG:NH2	2:M:100:GLY:O	2.45	0.50
2:N:347:SER:N	2:N:348:LEU:CA	2.75	0.50
1:C:41:GLU:CD	2:D:12:VAL:HG13	2.37	0.49
1:C:54:GLU:O	1:C:105:ARG:NH1	2.45	0.49
2:F:434:LEU:HD13	2:F:434:LEU:H	1.77	0.49
1:I:13:LEU:HG	1:I:14:VAL:N	2.26	0.49
1:I:84:PHE:HB2	1:I:292:ILE:HD12	1.93	0.49
1:J:42:MET:HG3	2:N:65:LEU:HD11	1.92	0.49
1:J:78:GLY:H	1:J:141:GLU:CD	2.20	0.49
1:K:197:ARG:NE	1:K:319:ASP:OD2	2.32	0.49
1:K:311:ILE:HB	1:K:365:TYR:HE1	1.76	0.49
2:L:183:ALA:HB1	2:L:186:ILE:CD1	2.41	0.49
1:B:41:GLU:OE2	1:B:43:ARG:NH1	2.36	0.49
1:B:226:GLY:H	1:B:385:THR:HG23	1.77	0.49
1:B:300:VAL:CG2	2:E:279:THR:HG21	2.42	0.49
1:C:79:ILE:HG13	1:C:84:PHE:CE2	2.47	0.49
2:D:32:VAL:HG21	2:D:56:ILE:HD11	1.94	0.49
2:E:146:LYS:HD2	2:E:323:THR:HA	1.94	0.49
2:F:47:VAL:HG23	2:F:52:ALA:CA	2.41	0.49
1:I:260:GLY:O	1:I:333:ARG:HG3	2.12	0.49
1:I:297:ASN:HB2	2:L:286:GLU:CG	2.40	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:318:ARG:CB	1:J:384:ILE:HD11	2.42	0.49
1:K:6:ILE:HG21	1:K:9:VAL:CG2	2.41	0.49
1:K:230:VAL:HG23	1:K:389:ALA:HB2	1.94	0.49
2:M:213:LEU:N	2:M:216:ASP:OD2	2.45	0.49
1:A:340:GLU:HG3	2:D:275:GLY:O	2.11	0.49
1:A:412:PHE:HD1	1:A:434:TYR:CE2	2.29	0.49
1:A:536:LEU:HD21	1:A:542:PHE:CA	2.41	0.49
1:C:130:VAL:HG22	1:C:157:GLY:O	2.12	0.49
2:E:122:ASP:OD1	2:E:123:TYR:N	2.45	0.49
2:E:379:GLY:HA3	2:E:405:ALA:HB2	1.93	0.49
1:J:423:ARG:HG2	2:M:348:LEU:HD13	1.95	0.49
1:K:114:HIS:ND1	1:K:169:ILE:HD11	2.27	0.49
1:K:523:LYS:O	1:K:527:THR:N	2.42	0.49
2:M:34:MET:HB2	2:M:40:ARG:NH2	2.23	0.49
2:M:285:PHE:HA	2:M:300:GLN:HE22	1.77	0.49
2:N:347:SER:N	2:N:348:LEU:HB2	2.27	0.49
1:A:86:GLY:N	1:A:294:ASN:HD21	2.10	0.49
1:B:284:SER:O	1:B:287:GLU:HB2	2.12	0.49
1:B:371:ARG:HG3	1:B:383:SER:HB3	1.94	0.49
1:C:6:ILE:HG21	1:C:9:VAL:HG22	1.93	0.49
1:C:27:MET:SD	1:C:36:ILE:HD11	2.52	0.49
1:C:240:VAL:O	1:C:244:GLN:HG2	2.12	0.49
1:C:315:GLU:OE1	1:C:368:ARG:NH2	2.42	0.49
1:C:408:VAL:HG23	1:C:409:VAL:HG13	1.93	0.49
2:D:147:LEU:O	2:D:301:ILE:HA	2.12	0.49
2:E:35:GLN:CD	2:E:35:GLN:H	2.21	0.49
2:F:150:PHE:HB3	2:F:306:MET:SD	2.52	0.49
2:F:198:PHE:CB	2:F:204:ILE:HB	2.19	0.49
1:J:8:LYS:O	1:J:14:VAL:HG13	2.12	0.49
1:J:28:CYS:HB3	1:J:66:SER:HA	1.93	0.49
1:J:102:PHE:HB3	2:M:114:GLU:HB3	1.93	0.49
1:J:269:VAL:HG11	1:J:291:LEU:HD21	1.94	0.49
1:J:352:GLU:HB3	1:J:400:PRO:HG3	1.94	0.49
1:K:202:LYS:HB3	2:L:188:PHE:CZ	2.47	0.49
1:K:202:LYS:HD3	2:L:188:PHE:CG	2.47	0.49
1:K:470:LEU:O	1:K:474:VAL:HG23	2.12	0.49
2:L:57:PHE:HB3	2:L:217:PRO:HG2	1.95	0.49
2:M:29:LEU:CD1	2:M:77:LEU:HA	2.42	0.49
2:M:60:THR:HA	2:M:63:ILE:HD12	1.93	0.49
2:M:93:LEU:HG	2:M:95:ARG:HH21	1.78	0.49
2:N:91:ASP:CB	2:N:95:ARG:HB2	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:129:GLN:HB3	2:N:169:THR:CB	2.42	0.49
1:A:28:CYS:SG	1:A:39:ILE:HD11	2.52	0.49
1:B:27:MET:SD	1:B:38:GLU:HG2	2.52	0.49
1:B:315:GLU:OE2	1:B:368:ARG:HB3	2.12	0.49
2:E:34:MET:HB2	2:E:36:ASN:OD1	2.12	0.49
2:E:93:LEU:HD12	2:E:95:ARG:NH1	2.27	0.49
2:E:281:LEU:HA	2:E:284:LEU:HD11	1.95	0.49
2:E:448:ASP:OD1	2:E:449:LEU:N	2.46	0.49
2:F:133:SER:H	2:F:415:GLN:CD	2.19	0.49
2:F:177:PHE:HE1	2:F:243:VAL:C	2.20	0.49
2:F:179:VAL:HG22	2:F:244:LEU:HB3	1.94	0.49
2:F:186:ILE:HB	2:F:190:GLU:OE1	2.12	0.49
2:F:326:GLN:HB2	2:F:348:LEU:N	2.27	0.49
1:I:213:GLN:NE2	1:I:244:GLN:HB3	2.28	0.49
1:I:262:ARG:NE	2:L:321:TYR:O	2.45	0.49
1:J:265:GLU:O	1:J:269:VAL:HG23	2.12	0.49
1:J:459:GLU:O	1:J:463:ILE:HG13	2.12	0.49
1:K:116:LYS:HD3	1:K:118:TRP:CZ2	2.48	0.49
1:K:247:LYS:HD2	1:K:276:LEU:HD13	1.94	0.49
2:L:206:ARG:O	2:L:206:ARG:HG2	2.12	0.49
2:N:129:GLN:HB3	2:N:169:THR:CA	2.42	0.49
1:B:56:SER:CA	2:E:26:TYR:HD2	2.26	0.49
1:B:85:ASP:OD1	1:B:89:ARG:N	2.27	0.49
1:B:301:ALA:HB2	1:B:341:MET:CE	2.41	0.49
2:E:76:PRO:O	2:E:78:GLN:HG3	2.13	0.49
2:E:183:ALA:O	2:E:212:ASN:HB2	2.12	0.49
2:E:324:GLU:HB2	2:E:350:ARG:O	2.13	0.49
2:F:428:ASP:O	2:F:432:GLU:HG3	2.12	0.49
1:I:91:LEU:HD12	1:I:91:LEU:N	2.25	0.49
1:I:144:ILE:HG21	1:I:288:ARG:HD3	1.94	0.49
1:B:19:MET:N	1:B:45:ASP:O	2.25	0.49
1:B:30:VAL:O	1:B:35:VAL:HG22	2.13	0.49
2:D:57:PHE:HB3	2:D:217:PRO:HG2	1.94	0.49
2:D:132:ILE:HG22	2:D:134:ALA:N	2.27	0.49
1:J:285:LEU:O	1:J:288:ARG:HG3	2.12	0.49
1:K:5:LYS:HG3	1:K:61:GLY:CA	2.40	0.49
1:K:245:ILE:HG22	1:K:249:SER:OG	2.12	0.49
2:L:60:THR:HA	2:L:63:ILE:HD12	1.94	0.49
2:M:183:ALA:HB1	2:M:186:ILE:HD11	1.95	0.49
1:A:130:VAL:HG22	1:A:157:GLY:H	1.77	0.49
1:A:245:ILE:O	1:A:249:SER:OG	2.19	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:498:GLU:HA	1:A:502:GLN:HG3	1.94	0.49
2:E:326:GLN:HG2	2:E:348:LEU:O	2.11	0.49
1:I:158:THR:C	1:I:176:ILE:HG23	2.36	0.49
1:I:297:ASN:HB3	2:L:115:VAL:HG13	1.94	0.49
1:I:479:ILE:O	1:I:482:LEU:HG	2.12	0.49
1:I:550:VAL:O	1:I:554:GLU:HB2	2.12	0.49
1:J:75:LEU:HD13	1:J:316:TYR:HB2	1.94	0.49
1:K:16:ALA:O	1:K:46:VAL:HG22	2.13	0.49
2:L:10:GLU:H	2:L:17:ALA:HB3	1.76	0.49
2:N:117:ASN:HB3	2:N:120:ALA:HB3	1.95	0.49
2:N:183:ALA:CB	2:N:186:ILE:HD11	2.42	0.49
2:N:415:GLN:OE1	2:N:421:ARG:HD2	2.12	0.49
1:A:25:GLN:N	1:A:39:ILE:O	2.38	0.49
1:A:83:MET:CE	1:A:270:VAL:HG13	2.42	0.49
1:B:16:ALA:HB3	1:B:19:MET:HG3	1.95	0.49
1:B:20:SER:HB3	1:B:45:ASP:HA	1.94	0.49
1:B:225:GLY:O	1:B:370:GLY:HA2	2.12	0.49
1:C:225:GLY:HA2	1:C:384:ILE:O	2.13	0.49
2:D:178:ALA:O	2:D:243:VAL:HA	2.13	0.49
2:E:43:GLN:HB2	2:E:57:PHE:HE2	1.78	0.49
2:E:255:GLU:O	2:E:258:ARG:HG2	2.11	0.49
2:F:117:ASN:HB3	2:F:120:ALA:HB3	1.94	0.49
1:I:24:ILE:HG22	1:I:25:GLN:HG2	1.94	0.49
1:I:340:GLU:OE2	2:L:279:THR:OG1	2.25	0.49
1:J:425:PHE:HA	1:J:427:SER:N	2.28	0.49
1:K:237:GLY:HA2	4:K:601:ANP:PA	2.53	0.49
2:M:304:LEU:HD21	2:M:319:THR:OG1	2.12	0.49
2:N:235:LEU:HB2	2:N:243:VAL:HG21	1.95	0.49
1:A:97:VAL:HG11	1:A:109:LEU:HD21	1.95	0.49
1:B:49:ILE:HG22	1:B:50:GLN:O	2.12	0.49
1:B:238:LYS:HE2	1:B:391:SER:HB3	1.94	0.49
1:I:300:VAL:O	1:I:304:GLU:N	2.42	0.49
2:M:448:ASP:OD1	2:M:449:LEU:N	2.46	0.49
2:N:349:SER:HB3	2:N:352:LYS:CD	2.39	0.49
1:A:215:VAL:CG2	1:A:219:PHE:HD2	2.18	0.48
1:A:232:GLY:N	1:A:233:PRO:CD	2.76	0.48
1:A:516:GLU:HB2	1:A:567:LEU:HD21	1.95	0.48
1:B:330:SER:HB3	1:B:333:ARG:HG2	1.95	0.48
1:C:19:MET:HE2	1:C:64:VAL:HG12	1.95	0.48
1:C:521:MET:O	1:C:525:ILE:HG13	2.13	0.48
2:D:77:LEU:HD21	2:D:93:LEU:HD22	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:177:GLU:HA	1:J:182:LEU:HA	1.95	0.48
1:J:202:LYS:HE2	1:J:372:VAL:CG1	2.43	0.48
1:A:39:ILE:HG12	1:A:49:ILE:HG12	1.94	0.48
1:A:120:PHE:HB2	1:A:187:MET:CE	2.43	0.48
1:A:159:VAL:HG22	1:A:176:ILE:CG1	2.40	0.48
1:A:251:VAL:HG21	1:A:325:ALA:CB	2.44	0.48
1:B:231:PRO:CD	1:B:412:PHE:HE1	2.26	0.48
1:B:253:LEU:HB2	1:B:324:VAL:HG22	1.94	0.48
1:B:258:GLY:O	1:B:294:ASN:N	2.38	0.48
1:C:211:THR:HG21	1:C:216:ILE:HG22	1.95	0.48
2:D:132:ILE:HG22	2:D:134:ALA:H	1.77	0.48
2:D:150:PHE:HB2	2:D:328:ILE:HD13	1.95	0.48
2:E:183:ALA:HB1	2:E:186:ILE:CD1	2.43	0.48
1:J:232:GLY:C	1:J:238:LYS:HD3	2.38	0.48
1:J:303:ARG:NH2	2:M:279:THR:HG22	2.28	0.48
1:K:38:GLU:N	1:K:50:GLN:O	2.37	0.48
1:K:121:GLU:HB3	1:K:138:TYR:CZ	2.49	0.48
1:K:400:PRO:O	1:K:404:ASN:ND2	2.28	0.48
2:L:81:VAL:HB	2:L:234:TYR:CD2	2.48	0.48
2:L:315:ILE:HB	2:L:316:PRO:CD	2.43	0.48
2:N:31:GLU:OE1	2:N:71:ARG:NH2	2.46	0.48
2:N:130:THR:HG21	2:N:135:ILE:HG22	1.94	0.48
2:N:346:PRO:N	2:N:347:SER:HA	2.27	0.48
1:A:130:VAL:CG2	1:A:157:GLY:H	2.26	0.48
1:C:39:ILE:HG23	1:C:48:SER:C	2.37	0.48
2:D:29:LEU:HB2	2:D:73:LEU:HD21	1.95	0.48
2:E:81:VAL:HG11	2:E:234:TYR:CG	2.48	0.48
2:E:109:LEU:HD13	2:E:230:THR:HG22	1.94	0.48
2:E:235:LEU:O	2:E:239:LYS:HB2	2.13	0.48
2:F:175:ASP:HA	2:F:176:ASP:C	2.38	0.48
2:F:235:LEU:O	2:F:240:GLY:N	2.47	0.48
1:I:318:ARG:HG3	1:I:384:ILE:CG1	2.33	0.48
1:K:20:SER:O	1:K:42:MET:HE3	2.13	0.48
1:K:30:VAL:HG13	1:K:64:VAL:HG22	1.95	0.48
1:K:214:ARG:HH12	1:K:521:MET:HE1	1.71	0.48
1:K:245:ILE:O	1:K:249:SER:N	2.47	0.48
2:L:6:ARG:NH2	2:L:69:SER:CA	2.76	0.48
2:L:412:TYR:C	2:L:412:TYR:CD2	2.91	0.48
2:M:155:LEU:O	2:M:157:HIS:ND1	2.47	0.48
2:M:203:ALA:HA	2:M:206:ARG:NH1	2.28	0.48
2:N:347:SER:N	2:N:348:LEU:HA	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:396:ASP:N	1:A:396:ASP:OD2	2.47	0.48
1:B:265:GLU:O	1:B:269:VAL:HG23	2.13	0.48
1:B:270:VAL:O	1:B:274:PRO:HG2	2.13	0.48
1:B:297:ASN:ND2	2:E:115:VAL:HG13	2.27	0.48
1:B:311:ILE:HB	1:B:365:TYR:HE1	1.77	0.48
1:C:290:VAL:HG21	1:C:317:PHE:HE2	1.77	0.48
2:E:43:GLN:HB2	2:E:57:PHE:CE2	2.49	0.48
2:F:325:GLY:C	2:F:349:SER:HA	2.38	0.48
1:I:10:SER:HB3	1:I:13:LEU:O	2.13	0.48
2:L:140:THR:OG1	2:L:352:LYS:HB2	2.13	0.48
2:N:248:THR:HA	2:N:249:ASP:HA	1.56	0.48
2:N:310:ASP:OD2	2:N:312:THR:OG1	2.26	0.48
1:A:120:PHE:HB2	1:A:187:MET:HE1	1.95	0.48
1:A:274:PRO:HG3	1:A:286:MET:HE2	1.94	0.48
1:A:497:ARG:HA	1:A:501:LEU:CB	2.40	0.48
1:B:14:VAL:HG21	1:B:51:VAL:HG21	1.95	0.48
1:B:231:PRO:HD2	1:B:413:TRP:O	2.14	0.48
1:C:33:LEU:H	1:C:33:LEU:HD12	1.78	0.48
1:C:121:GLU:HA	1:C:164:SER:OG	2.13	0.48
2:D:141:LEU:HD12	2:D:145:GLN:OE1	2.12	0.48
2:D:254:ALA:O	2:D:258:ARG:HG3	2.14	0.48
2:F:166:ARG:HD2	2:F:201:THR:HG21	1.96	0.48
2:F:345:LEU:N	2:F:346:PRO:HD2	2.28	0.48
1:I:103:LEU:HD22	1:I:298:MET:HE1	1.96	0.48
1:I:231:PRO:HG3	1:I:412:PHE:CZ	2.49	0.48
1:I:254:VAL:HG22	1:I:325:ALA:HB3	1.96	0.48
1:J:242:GLN:OE1	1:J:329:ASP:HB2	2.13	0.48
1:K:41:GLU:CD	2:L:12:VAL:HG22	2.38	0.48
1:K:191:TRP:CE3	1:K:192:PRO:HD2	2.49	0.48
2:L:32:VAL:HG13	2:L:70:VAL:HG22	1.96	0.48
2:L:88:ARG:NH1	2:L:101:PRO:O	2.46	0.48
2:L:146:LYS:HA	2:L:300:GLN:O	2.12	0.48
2:L:282:ALA:HA	2:L:322:ILE:HG21	1.96	0.48
2:M:15:LEU:HD23	2:M:55:GLN:HG3	1.94	0.48
1:B:517:LYS:HD3	1:B:564:GLU:OE2	2.13	0.48
1:C:133:GLY:O	1:C:380:ARG:NH1	2.40	0.48
2:D:390:GLY:HA2	2:D:391:GLU:HA	1.54	0.48
2:F:46:GLU:HG2	2:F:47:VAL:N	2.28	0.48
2:F:91:ASP:OD1	2:F:94:GLY:N	2.47	0.48
2:F:251:THR:HG22	2:F:315:ILE:HG21	1.96	0.48
1:K:132:ALA:O	1:K:375:LEU:HB3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:349:SER:HB3	2:L:352:LYS:NZ	2.29	0.48
2:M:274:PRO:HB3	2:M:276:TYR:CE2	2.49	0.48
2:N:32:VAL:HG21	2:N:56:ILE:HD12	1.95	0.48
2:N:146:LYS:HG2	2:N:285:PHE:O	2.12	0.48
1:C:150:MET:HE1	1:C:320:MET:HA	1.96	0.48
1:C:237:GLY:O	1:C:241:VAL:HG23	2.14	0.48
2:D:30:ILE:N	2:D:42:GLY:O	2.41	0.48
2:D:222:ILE:HG22	2:D:226:ARG:HH21	1.78	0.48
2:F:26:TYR:O	2:F:27:GLU:HB2	2.14	0.48
2:F:150:PHE:O	2:F:329:LEU:HD12	2.14	0.48
1:K:8:LYS:CG	2:N:48:GLN:HB3	2.44	0.48
2:L:219:ILE:HA	2:L:222:ILE:HD12	1.94	0.48
2:M:90:PHE:O	2:M:210:PHE:HA	2.14	0.48
2:M:180:VAL:HB	2:M:245:VAL:HG22	1.96	0.48
2:N:29:LEU:HD12	2:N:42:GLY:O	2.13	0.48
1:A:531:GLU:HB3	1:A:581:ILE:HG13	1.95	0.48
1:B:12:PRO:HB2	1:B:344:ARG:HB3	1.95	0.48
1:C:14:VAL:HG23	1:C:51:VAL:HG13	1.95	0.48
1:C:568:ALA:O	1:C:570:ILE:HA	2.12	0.48
1:K:55:THR:O	2:N:26:TYR:HB3	2.14	0.48
2:L:257:LEU:HA	2:L:260:ILE:HD11	1.95	0.48
2:L:412:TYR:C	2:L:412:TYR:HD2	2.21	0.48
1:A:497:ARG:CA	1:A:501:LEU:HB2	2.40	0.48
1:B:190:LYS:HB2	1:B:190:LYS:NZ	2.28	0.48
1:B:196:GLY:HA2	1:B:368:ARG:CZ	2.43	0.48
1:B:443:ARG:O	1:B:447:GLN:HB2	2.14	0.48
1:C:11:GLY:O	1:C:55:THR:OG1	2.24	0.48
1:C:274:PRO:HA	1:C:284:SER:HB2	1.96	0.48
2:F:16:MET:HB2	2:F:54:VAL:CG2	2.37	0.48
2:F:33:ARG:HD2	2:F:71:ARG:HD3	1.96	0.48
1:I:6:ILE:CG1	1:I:64:VAL:HG22	2.44	0.48
1:K:199:ILE:HG21	1:K:372:VAL:HG21	1.95	0.48
1:K:231:PRO:CA	1:K:390:VAL:O	2.56	0.48
1:B:27:MET:HE3	1:B:37:GLY:O	2.13	0.48
1:B:27:MET:C	1:B:67:THR:HG1	2.22	0.48
1:B:120:PHE:HB2	1:B:187:MET:CE	2.43	0.48
1:C:85:ASP:OD1	1:C:89:ARG:N	2.46	0.48
1:C:120:PHE:CE2	1:C:137:GLY:HA3	2.49	0.48
2:D:88:ARG:HH12	2:D:102:GLU:CB	2.27	0.48
2:D:409:GLU:HA	2:D:413:VAL:HB	1.95	0.48
2:F:273:TYR:CE2	2:F:314:PRO:HG2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:253:LEU:HG	1:I:317:PHE:CD1	2.49	0.48
1:J:41:GLU:CD	2:N:12:VAL:HG13	2.39	0.48
1:J:339:ARG:HG3	1:J:353:GLY:O	2.14	0.48
1:J:513:THR:HG23	1:J:517:LYS:HG2	1.95	0.48
1:K:6:ILE:CG1	1:K:64:VAL:HG23	2.43	0.48
1:K:175:VAL:HA	1:K:184:GLU:HA	1.95	0.48
1:K:251:VAL:HG11	1:K:325:ALA:HB2	1.96	0.48
2:L:10:GLU:HA	2:L:65:LEU:HD23	1.96	0.48
2:N:27:GLU:HA	2:N:27:GLU:OE2	2.13	0.48
2:N:34:MET:SD	2:N:63:ILE:HG12	2.53	0.48
2:N:130:THR:HG21	2:N:135:ILE:C	2.39	0.48
2:N:185:GLY:CA	2:N:214:ALA:HA	2.41	0.48
1:B:352:GLU:CB	1:B:400:PRO:HG3	2.44	0.47
1:C:27:MET:O	1:C:67:THR:OG1	2.30	0.47
2:D:131:GLY:C	2:D:132:ILE:HD12	2.39	0.47
2:E:440:THR:O	2:E:443:LYS:HG3	2.14	0.47
2:F:282:ALA:HA	2:F:322:ILE:HG21	1.96	0.47
2:F:379:GLY:HA3	2:F:405:ALA:HB2	1.96	0.47
1:I:114:HIS:ND1	1:I:169:ILE:HD11	2.29	0.47
1:I:253:LEU:HD12	1:I:288:ARG:O	2.14	0.47
1:J:373:ILE:HD13	1:J:381:GLU:HB2	1.95	0.47
1:J:373:ILE:HD13	1:J:381:GLU:HG3	1.96	0.47
2:L:90:PHE:HE1	2:L:96:PRO:CB	2.27	0.47
2:L:334:TYR:HB2	2:L:341:PRO:HG3	1.96	0.47
2:M:15:LEU:HD22	2:M:55:GLN:HG3	1.97	0.47
2:M:21:VAL:HG13	2:M:24:VAL:CG2	2.44	0.47
2:N:126:GLU:HG2	2:N:143:ARG:HG3	1.94	0.47
2:N:352:LYS:H	2:N:352:LYS:HG2	1.36	0.47
1:B:304:GLU:HA	1:B:334:TRP:CD1	2.48	0.47
1:C:139:VAL:HG23	1:C:149:ILE:CD1	2.33	0.47
1:C:211:THR:HG21	1:C:216:ILE:HG21	1.96	0.47
2:D:249:ASP:HB3	2:D:252:ASN:ND2	2.28	0.47
1:I:43:ARG:CG	1:I:46:VAL:HG13	2.44	0.47
1:J:19:MET:CE	1:J:64:VAL:HG11	2.40	0.47
2:M:3:LYS:NZ	2:M:3:LYS:HB2	2.28	0.47
2:M:137:HIS:NE2	2:M:365:HIS:O	2.47	0.47
1:B:237:GLY:HA2	4:B:601:ANP:PA	2.54	0.47
1:C:205:PRO:HB2	1:C:224:LYS:O	2.14	0.47
1:C:253:LEU:O	1:C:325:ALA:N	2.46	0.47
2:D:132:ILE:HB	2:D:135:ILE:HG13	1.96	0.47
1:K:2:GLN:OE1	1:K:20:SER:HB3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:549:THR:O	1:K:553:ARG:HG3	2.14	0.47
2:M:28:GLU:O	2:M:44:VAL:HG23	2.15	0.47
2:N:34:MET:HG3	2:N:38:GLU:HB3	1.96	0.47
2:N:188:PHE:CZ	2:N:192:GLU:HG2	2.49	0.47
1:A:219:PHE:HE2	1:A:501:LEU:HD23	1.79	0.47
1:C:374:ALA:HB3	1:C:380:ARG:HG2	1.97	0.47
2:D:137:HIS:CE1	2:D:368:THR:HB	2.49	0.47
2:E:396:ASP:HA	2:E:399:LYS:HG3	1.94	0.47
2:F:30:ILE:HG22	2:F:72:PHE:CD1	2.50	0.47
2:F:155:LEU:HD13	2:F:329:LEU:HB3	1.97	0.47
2:F:273:TYR:HB3	2:F:277:LEU:HD22	1.95	0.47
2:F:439:ARG:CG	2:F:450:LEU:HD13	2.45	0.47
1:I:159:VAL:HA	1:I:176:ILE:HA	1.96	0.47
1:I:177:GLU:HG3	1:I:182:LEU:N	2.29	0.47
1:I:249:SER:HB3	1:I:251:VAL:HG22	1.95	0.47
1:I:253:LEU:HG	1:I:317:PHE:HD1	1.79	0.47
1:J:415:LEU:CD2	1:J:428:ILE:HG13	2.38	0.47
1:K:479:ILE:HG22	2:N:394:LEU:HA	1.95	0.47
2:L:128:ILE:HD13	2:L:177:PHE:CZ	2.50	0.47
2:N:137:HIS:HB3	2:N:412:TYR:OH	2.15	0.47
1:A:317:PHE:HA	1:A:320:MET:SD	2.54	0.47
1:B:27:MET:CE	1:B:52:TYR:HE2	2.27	0.47
1:B:179:GLU:OE2	1:B:180:GLN:N	2.46	0.47
1:C:204:ASN:ND2	2:D:189:GLU:HA	2.29	0.47
2:E:17:ALA:HA	2:E:52:ALA:O	2.15	0.47
2:E:326:GLN:N	2:E:348:LEU:O	2.47	0.47
2:F:229:LEU:HD22	2:F:300:GLN:OE1	2.14	0.47
1:I:343:GLY:HA3	2:L:275:GLY:HA3	1.97	0.47
2:M:376:TYR:OH	2:M:409:GLU:OE2	2.32	0.47
1:A:254:VAL:C	1:A:289:THR:HG21	2.40	0.47
1:B:11:GLY:N	1:B:12:PRO:CD	2.78	0.47
1:B:415:LEU:HG	1:B:428:ILE:HD13	1.96	0.47
1:C:378:ASP:OD1	1:C:378:ASP:N	2.46	0.47
1:C:524:VAL:HG13	1:C:573:ILE:HG21	1.94	0.47
2:D:79:LEU:HB2	2:D:227:MET:HE2	1.97	0.47
2:D:231:ALA:O	2:D:235:LEU:HG	2.15	0.47
2:E:217:PRO:HD2	2:E:220:GLU:OE2	2.15	0.47
2:F:147:LEU:O	2:F:301:ILE:HA	2.14	0.47
1:I:73:VAL:CG1	1:I:309:THR:HG23	2.44	0.47
1:I:584:ILE:O	1:I:584:ILE:HG22	2.14	0.47
2:L:242:HIS:HD2	2:L:296:GLY:HA2	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:32:VAL:HG21	2:M:56:ILE:HD11	1.96	0.47
2:M:40:ARG:CG	2:M:56:ILE:HG21	2.44	0.47
2:N:306:MET:HE3	2:N:310:ASP:C	2.39	0.47
2:N:340:PRO:HB3	2:N:417:PHE:CE1	2.49	0.47
1:A:7:ILE:O	2:D:49:GLU:HG2	2.14	0.47
1:A:39:ILE:HA	1:A:49:ILE:HA	1.97	0.47
1:A:225:GLY:HA3	1:A:370:GLY:HA2	1.96	0.47
1:A:274:PRO:HA	1:A:286:MET:HG2	1.97	0.47
1:B:16:ALA:O	1:B:46:VAL:HA	2.15	0.47
1:B:73:VAL:HG13	1:B:193:VAL:HG12	1.97	0.47
1:B:193:VAL:HG11	1:B:309:THR:HG22	1.96	0.47
1:B:244:GLN:OE1	1:B:511:THR:OG1	2.30	0.47
1:B:362:LEU:HD13	1:B:405:THR:CG2	2.43	0.47
1:C:238:LYS:HG3	4:C:601:ANP:O2B	2.15	0.47
2:D:61:SER:O	2:D:63:ILE:HD12	2.15	0.47
2:D:132:ILE:HD11	2:D:163:GLN:NE2	2.30	0.47
2:D:141:LEU:HD22	2:D:147:LEU:CD2	2.41	0.47
2:D:152:GLY:N	2:D:155:LEU:HD12	2.28	0.47
2:E:95:ARG:HG2	2:E:95:ARG:HH11	1.78	0.47
2:E:423:ILE:HG13	2:E:427:LEU:HD11	1.97	0.47
2:F:111:ILE:HG13	2:F:112:ASN:N	2.29	0.47
2:F:157:HIS:CD2	2:F:158:LYS:HG3	2.50	0.47
1:I:252:ASP:HB2	1:I:253:LEU:HD22	1.97	0.47
1:I:501:LEU:HD13	1:I:502:GLN:N	2.30	0.47
1:J:139:VAL:HG12	1:J:140:ASP:N	2.29	0.47
1:J:150:MET:CE	1:J:320:MET:HG2	2.45	0.47
1:J:225:GLY:O	1:J:370:GLY:HA2	2.15	0.47
2:L:147:LEU:HB3	2:L:301:ILE:HG12	1.96	0.47
2:L:158:LYS:HG3	2:L:194:PHE:CZ	2.49	0.47
2:M:146:LYS:HD3	2:M:285:PHE:O	2.15	0.47
1:A:308:TYR:O	1:A:312:THR:OG1	2.28	0.47
1:C:216:ILE:HD12	1:C:245:ILE:HD11	1.96	0.47
2:D:10:GLU:H	2:D:17:ALA:HB3	1.80	0.47
2:E:86:ILE:HD13	2:E:208:VAL:CG2	2.44	0.47
1:I:6:ILE:CD1	1:I:30:VAL:HG13	2.45	0.47
1:I:134:ASP:O	1:I:151:VAL:HG23	2.15	0.47
1:I:266:MET:HE1	1:I:270:VAL:CG2	2.44	0.47
1:I:552:VAL:O	1:I:556:ILE:HG13	2.15	0.47
1:K:202:LYS:CG	1:K:372:VAL:HG12	2.42	0.47
1:K:259:CYS:SG	1:K:303:ARG:HB3	2.55	0.47
1:K:278:ASP:CG	1:K:279:PRO:HD2	2.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:244:LEU:HA	2:L:299:THR:O	2.14	0.47
2:M:109:LEU:O	2:M:230:THR:HG21	2.15	0.47
2:M:137:HIS:HE1	2:M:368:THR:OG1	1.98	0.47
1:A:90:PRO:HD3	1:A:111:ALA:HA	1.96	0.47
1:A:436:LEU:HD12	1:A:436:LEU:H	1.80	0.47
1:A:552:VAL:O	1:A:556:ILE:HG13	2.14	0.47
2:E:163:GLN:O	2:E:167:GLN:HB2	2.13	0.47
2:F:163:GLN:HA	2:F:166:ARG:NH1	2.30	0.47
1:I:122:ALA:HA	1:I:137:GLY:HA3	1.97	0.47
1:I:340:GLU:OE1	2:L:278:TYR:HB3	2.15	0.47
1:J:74:GLU:HB2	1:J:111:ALA:HB3	1.97	0.47
1:J:84:PHE:O	1:J:293:ALA:N	2.47	0.47
1:K:6:ILE:HG21	1:K:9:VAL:HG23	1.97	0.47
1:K:18:ASN:ND2	1:K:18:ASN:O	2.44	0.47
1:K:507:ASP:HB3	1:K:510:ASP:HB3	1.96	0.47
2:M:324:GLU:CB	2:M:350:ARG:HB2	2.44	0.47
2:N:341:PRO:HD2	2:N:417:PHE:HZ	1.78	0.47
1:A:71:LEU:O	1:A:193:VAL:HG22	2.14	0.47
1:A:248:TRP:CZ3	1:A:279:PRO:HG2	2.50	0.47
1:B:499:ASP:CG	1:B:556:ILE:HG22	2.41	0.47
1:C:7:ILE:HB	2:F:49:GLU:CB	2.45	0.47
1:C:102:PHE:HB3	2:F:114:GLU:HB2	1.97	0.47
2:D:32:VAL:HG22	2:D:70:VAL:HG13	1.97	0.47
2:D:148:PRO:HG2	2:D:325:GLY:O	2.15	0.47
2:E:78:GLN:HG2	2:E:110:ASP:HA	1.97	0.47
2:E:357:GLY:N	2:E:358:ALA:CA	2.77	0.47
1:I:262:ARG:O	1:I:266:MET:HB2	2.15	0.47
1:J:9:VAL:CG2	1:J:58:ILE:HB	2.21	0.47
1:J:364:GLU:HG2	2:N:215:ASN:HB2	1.96	0.47
1:K:33:LEU:HD22	1:K:106:GLY:HA3	1.97	0.47
2:L:381:GLN:O	2:L:385:LEU:N	2.39	0.47
2:M:219:ILE:H	2:M:219:ILE:HD12	1.80	0.47
2:M:222:ILE:HG23	2:M:253:TYR:CE1	2.50	0.47
2:M:235:LEU:O	2:M:239:LYS:HB2	2.14	0.47
2:M:257:LEU:HD21	2:M:276:TYR:HE1	1.80	0.47
2:N:98:ASP:CG	2:N:99:ASN:HA	2.40	0.47
1:A:268:ASP:O	1:A:272:GLU:HB2	2.16	0.46
1:A:346:GLU:HG2	2:D:267:VAL:HB	1.97	0.46
1:C:7:ILE:HG23	1:C:17:GLU:HB2	1.97	0.46
1:C:44:GLN:CG	1:C:45:ASP:H	2.28	0.46
2:D:353:ASP:HA	2:D:356:THR:HG1	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:143:ARG:HH21	2:E:170:VAL:HG12	1.80	0.46
2:E:160:LEU:O	2:E:164:ILE:HG13	2.14	0.46
2:F:345:LEU:HA	2:F:373:PHE:CZ	2.50	0.46
1:J:114:HIS:O	1:J:168:THR:HB	2.15	0.46
1:J:232:GLY:CA	1:J:415:LEU:HG	2.44	0.46
1:J:371:ARG:HA	1:J:383:SER:HA	1.97	0.46
1:K:29:LEU:HB2	1:K:65:ARG:HG3	1.95	0.46
1:K:265:GLU:O	1:K:269:VAL:HG23	2.14	0.46
2:L:155:LEU:CD1	2:L:329:LEU:HB3	2.38	0.46
2:L:258:ARG:HD2	2:L:273:TYR:HD2	1.80	0.46
2:L:318:LEU:O	2:L:322:ILE:HG13	2.15	0.46
2:M:258:ARG:HH21	2:M:272:GLY:HA3	1.80	0.46
2:N:345:LEU:N	2:N:346:PRO:CD	2.78	0.46
1:A:262:ARG:NE	2:D:321:TYR:O	2.48	0.46
1:A:336:GLU:OE2	1:A:339:ARG:HD2	2.16	0.46
1:B:214:ARG:CB	1:B:500:TYR:CE2	2.95	0.46
1:B:251:VAL:HG21	1:B:325:ALA:CB	2.45	0.46
1:C:220:PHE:HB3	1:C:435:SER:HB2	1.96	0.46
1:C:243:HIS:O	1:C:247:LYS:HD2	2.15	0.46
2:E:343:ASP:O	2:E:347:SER:OG	2.32	0.46
2:F:88:ARG:NH2	2:F:98:ASP:OD1	2.48	0.46
2:F:442:LEU:HD12	2:F:445:ILE:HD11	1.96	0.46
1:I:314:ALA:HB1	1:I:324:VAL:HG11	1.98	0.46
1:K:534:LYS:NZ	1:K:534:LYS:HB2	2.30	0.46
2:L:6:ARG:HE	2:L:8:ILE:CG1	2.28	0.46
2:L:44:VAL:HG13	2:L:53:MET:O	2.15	0.46
2:L:134:ALA:O	2:L:138:LEU:HB2	2.15	0.46
2:M:209:MET:HE2	2:M:211:MET:SD	2.55	0.46
1:C:256:TYR:HB3	1:C:291:LEU:HD12	1.96	0.46
1:C:405:THR:O	1:C:409:VAL:HG22	2.14	0.46
2:D:44:VAL:HG11	2:D:47:VAL:CG1	2.46	0.46
2:E:325:GLY:HA2	2:E:350:ARG:HG2	1.97	0.46
2:E:350:ARG:HA	2:E:351:LEU:HA	1.57	0.46
2:F:29:LEU:HD12	2:F:42:GLY:O	2.16	0.46
1:I:449:LEU:O	1:I:451:GLN:NE2	2.44	0.46
1:J:206:ASP:OD1	1:J:206:ASP:N	2.47	0.46
1:K:78:GLY:H	1:K:141:GLU:CD	2.21	0.46
2:L:9:LYS:HD2	2:L:19:GLU:HG3	1.95	0.46
2:L:253:TYR:CE1	2:L:284:LEU:HD11	2.50	0.46
2:L:350:ARG:C	2:L:351:LEU:HD23	2.41	0.46
1:A:43:ARG:HB3	1:A:44:GLN:HA	1.95	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:86:GLY:H	1:A:294:ASN:ND2	2.11	0.46
1:B:102:PHE:HB3	2:E:114:GLU:HB3	1.97	0.46
1:B:496:ILE:HA	1:B:525:ILE:HD13	1.98	0.46
1:C:496:ILE:O	1:C:500:TYR:N	2.38	0.46
2:D:35:GLN:CD	2:D:35:GLN:H	2.23	0.46
2:D:63:ILE:HG23	2:D:68:SER:OG	2.14	0.46
2:E:5:TYR:CZ	2:E:21:VAL:HG23	2.51	0.46
2:E:183:ALA:HB3	2:E:211:MET:HA	1.98	0.46
2:E:340:PRO:HD2	2:E:414:ASN:HA	1.97	0.46
1:I:307:ILE:HD11	1:I:334:TRP:CE2	2.51	0.46
1:I:463:ILE:HG22	1:I:493:ALA:HB2	1.97	0.46
1:J:16:ALA:HB3	1:J:19:MET:CE	2.45	0.46
1:J:357:TYR:HB3	2:N:259:GLU:CD	2.40	0.46
2:L:150:PHE:CG	2:L:306:MET:HE3	2.50	0.46
2:M:226:ARG:NH1	2:M:284:LEU:HD21	2.30	0.46
2:M:324:GLU:HA	2:M:350:ARG:HH11	1.79	0.46
2:M:408:PHE:HD1	2:M:412:TYR:HB3	1.81	0.46
2:N:204:ILE:O	2:N:207:SER:OG	2.33	0.46
1:B:94:PHE:HZ	1:B:104:GLY:H	1.63	0.46
2:D:45:LEU:HB2	2:D:264:ARG:HD3	1.97	0.46
1:I:133:GLY:O	1:I:380:ARG:NH2	2.45	0.46
2:M:133:SER:OG	2:M:412:TYR:O	2.33	0.46
1:B:92:ASP:OD1	1:B:93:THR:N	2.49	0.46
1:J:473:ILE:O	1:J:477:VAL:HG22	2.16	0.46
1:K:415:LEU:CD2	1:K:428:ILE:HG12	2.45	0.46
1:K:479:ILE:HA	1:K:482:LEU:HD13	1.97	0.46
2:L:127:PHE:CE1	2:L:140:THR:HB	2.51	0.46
2:L:345:LEU:N	2:L:346:PRO:HD2	2.30	0.46
2:N:26:TYR:O	2:N:27:GLU:HB2	2.15	0.46
2:N:88:ARG:HH22	2:N:96:PRO:CB	2.29	0.46
2:N:419:THR:HG22	2:N:421:ARG:HG3	1.97	0.46
1:A:39:ILE:CG1	1:A:49:ILE:HG12	2.45	0.46
1:A:466:GLU:O	1:A:470:LEU:HG	2.15	0.46
1:B:254:VAL:HG23	1:B:288:ARG:NH2	2.31	0.46
1:B:337:ALA:O	1:B:341:MET:HG2	2.15	0.46
1:C:232:GLY:O	1:C:392:PRO:HD2	2.14	0.46
2:D:32:VAL:HA	2:D:70:VAL:HA	1.98	0.46
2:D:306:MET:CE	2:D:311:LYS:HA	2.44	0.46
1:J:137:GLY:O	1:J:149:ILE:HG12	2.15	0.46
1:K:213:GLN:HB2	1:K:216:ILE:HG12	1.95	0.46
1:K:329:ASP:HA	1:K:330:SER:HA	1.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:340:PRO:HD3	2:N:416:GLY:N	2.27	0.46
1:B:285:LEU:HD11	1:B:288:ARG:CD	2.43	0.46
1:C:26:ASP:O	1:C:39:ILE:HD12	2.16	0.46
1:C:318:ARG:CB	1:C:384:ILE:HD11	2.45	0.46
2:E:34:MET:HG2	2:E:38:GLU:O	2.16	0.46
1:I:42:MET:SD	1:I:47:ALA:HB2	2.56	0.46
1:I:94:PHE:O	1:I:98:THR:OG1	2.27	0.46
1:I:120:PHE:CE1	1:I:173:ILE:HD12	2.51	0.46
1:J:5:LYS:HD2	1:J:61:GLY:HA2	1.97	0.46
1:J:251:VAL:HG21	1:J:325:ALA:CB	2.45	0.46
1:J:351:ASP:OD2	1:J:351:ASP:N	2.48	0.46
1:K:9:VAL:HG21	1:K:58:ILE:CG2	2.46	0.46
1:K:213:GLN:HG2	1:K:216:ILE:HD11	1.97	0.46
2:L:121:ARG:NH1	2:L:288:ALA:O	2.41	0.46
2:L:144:GLY:HA2	2:L:298:VAL:O	2.15	0.46
2:L:212:ASN:OD1	2:L:224:THR:OG1	2.12	0.46
2:M:239:LYS:HB2	2:M:241:MET:HG2	1.97	0.46
2:M:409:GLU:HA	2:M:413:VAL:CG2	2.46	0.46
2:N:32:VAL:O	2:N:40:ARG:N	2.44	0.46
2:N:336:SER:HB2	2:N:337:GLY:CA	2.41	0.46
2:N:381:GLN:HA	2:N:384:GLU:CG	2.46	0.46
1:B:331:THR:HG23	1:B:390:VAL:HG22	1.97	0.46
1:B:437:TYR:OH	2:F:189:GLU:OE1	2.32	0.46
1:B:549:THR:O	1:B:552:VAL:HG12	2.16	0.46
4:B:601:ANP:O1A	4:B:601:ANP:N3B	2.49	0.46
4:B:601:ANP:O3'	2:E:350:ARG:HB2	2.16	0.46
1:C:161:LYS:HE3	1:C:175:VAL:HG23	1.98	0.46
1:C:234:PHE:CD1	1:C:234:PHE:N	2.80	0.46
2:D:93:LEU:HD21	2:D:220:GLU:HG2	1.98	0.46
2:D:313:HIS:CE1	2:D:314:PRO:HD2	2.51	0.46
2:E:225:PRO:O	2:E:229:LEU:HG	2.16	0.46
1:I:103:LEU:N	2:L:115:VAL:O	2.39	0.46
1:I:262:ARG:HD2	1:I:262:ARG:N	2.31	0.46
1:J:436:LEU:HD21	2:N:154:GLY:O	2.15	0.46
1:K:44:GLN:N	2:L:10:GLU:HG2	2.31	0.46
2:L:136:ASP:O	2:L:140:THR:HG22	2.16	0.46
2:L:430:GLY:O	2:L:434:LEU:HB2	2.15	0.46
2:M:30:ILE:HG21	2:M:54:VAL:HG11	1.98	0.46
2:M:222:ILE:HD11	2:M:257:LEU:HA	1.98	0.46
2:N:129:GLN:H	2:N:169:THR:C	2.24	0.46
1:A:37:GLY:HA3	1:A:51:VAL:HG22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:242:GLN:HA	1:A:327:MET:HE1	1.98	0.46
1:B:200:LYS:NZ	1:B:379:GLN:OE1	2.49	0.46
2:D:282:ALA:HA	2:D:322:ILE:HG21	1.98	0.46
2:E:79:LEU:HD21	2:E:85:MET:HE1	1.98	0.46
2:E:95:ARG:HG3	2:E:95:ARG:H	1.58	0.46
2:E:127:PHE:CE2	2:E:129:GLN:HA	2.51	0.46
1:I:91:LEU:HB2	2:L:119:ILE:HD13	1.98	0.46
1:I:501:LEU:HD13	1:I:501:LEU:C	2.41	0.46
1:J:73:VAL:HG11	1:J:309:THR:HG23	1.97	0.46
2:L:30:ILE:HG12	2:L:54:VAL:HB	1.97	0.46
2:M:351:LEU:HD23	2:M:351:LEU:N	2.31	0.46
2:N:88:ARG:NH2	2:N:100:GLY:H	2.14	0.46
2:N:151:SER:OG	2:N:155:LEU:HB2	2.15	0.46
2:N:336:SER:N	2:N:337:GLY:HA2	2.31	0.46
1:A:288:ARG:C	1:A:289:THR:HG1	2.23	0.45
1:B:230:VAL:HG12	1:B:415:LEU:CD1	2.46	0.45
1:C:214:ARG:NH2	1:C:560:LYS:HB2	2.31	0.45
2:D:183:ALA:HB1	2:D:186:ILE:CD1	2.46	0.45
2:E:60:THR:HA	2:E:63:ILE:HD12	1.98	0.45
2:E:339:GLN:HA	2:E:341:PRO:HD3	1.98	0.45
2:F:35:GLN:H	2:F:35:GLN:CD	2.23	0.45
1:I:214:ARG:HG2	1:I:513:THR:HB	1.97	0.45
1:I:220:PHE:HB3	1:I:413:TRP:HE1	1.80	0.45
2:D:281:LEU:HD22	2:D:285:PHE:CE2	2.39	0.45
2:D:408:PHE:HE1	2:D:412:TYR:CD2	2.34	0.45
1:I:83:MET:CE	2:L:119:ILE:CG2	2.90	0.45
1:I:243:HIS:HB3	1:I:276:LEU:HD11	1.99	0.45
1:I:469:GLN:O	1:I:473:ILE:HG13	2.16	0.45
1:J:13:LEU:HD12	1:J:50:GLN:N	2.31	0.45
1:J:15:MET:HG2	1:J:48:SER:HA	1.99	0.45
1:J:16:ALA:O	1:J:46:VAL:HA	2.17	0.45
1:J:329:ASP:HA	1:J:330:SER:HA	1.50	0.45
1:J:366:TYR:OH	1:J:388:SER:OG	2.15	0.45
1:J:419:LEU:HA	1:J:422:LYS:HD2	1.97	0.45
1:J:445:MET:SD	1:J:515:ARG:NH1	2.89	0.45
1:K:83:MET:SD	1:K:91:LEU:HD12	2.57	0.45
1:K:102:PHE:HB3	2:N:114:GLU:HB2	1.98	0.45
2:L:14:PRO:O	2:L:55:GLN:HA	2.16	0.45
2:L:34:MET:HE3	2:L:62:GLY:O	2.17	0.45
2:L:149:VAL:HG22	2:L:327:ILE:HG13	1.97	0.45
2:L:264:ARG:HB3	2:L:266:GLU:HG3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:29:LEU:O	2:N:73:LEU:HB2	2.15	0.45
2:N:34:MET:HE3	2:N:40:ARG:CZ	2.45	0.45
2:N:85:MET:HG2	2:N:90:PHE:CZ	2.51	0.45
2:N:129:GLN:CB	2:N:169:THR:CB	2.94	0.45
1:A:307:ILE:HG13	1:A:308:TYR:N	2.30	0.45
1:B:15:MET:HG2	1:B:48:SER:OG	2.17	0.45
1:B:152:PRO:CD	1:B:185:LEU:HD22	2.46	0.45
1:B:214:ARG:HG3	1:B:500:TYR:O	2.15	0.45
1:C:230:VAL:CG2	1:C:413:TRP:HE3	2.30	0.45
1:C:247:LYS:HE2	1:C:276:LEU:CD1	2.46	0.45
1:C:257:VAL:HG22	1:C:292:ILE:HD13	1.98	0.45
2:D:21:VAL:HB	2:D:24:VAL:HG21	1.98	0.45
2:D:26:TYR:CE2	2:D:27:GLU:HG3	2.51	0.45
2:E:260:ILE:O	2:E:264:ARG:HG3	2.17	0.45
1:I:273:PHE:HB3	1:I:274:PRO:HD3	1.97	0.45
2:L:18:VAL:HG11	2:L:72:PHE:CZ	2.51	0.45
2:L:44:VAL:HG22	2:L:54:VAL:CG1	2.45	0.45
2:M:134:ALA:O	2:M:139:ASN:N	2.46	0.45
1:A:131:SER:N	1:A:134:ASP:OD2	2.36	0.45
1:A:220:PHE:CE1	1:A:433:SER:HB2	2.51	0.45
1:B:412:PHE:O	1:B:433:SER:HB2	2.17	0.45
1:B:454:SER:O	1:B:458:THR:OG1	2.35	0.45
1:B:573:ILE:O	1:B:577:ILE:HG13	2.16	0.45
1:C:75:LEU:HD13	1:C:316:TYR:CG	2.51	0.45
1:C:237:GLY:HA2	4:C:601:ANP:O2A	2.16	0.45
1:C:246:ALA:HB1	1:C:254:VAL:HG11	1.98	0.45
1:C:300:VAL:HG13	1:C:303:ARG:NE	2.31	0.45
2:D:132:ILE:CG2	2:D:135:ILE:HG13	2.47	0.45
2:E:184:ILE:HD13	2:E:225:PRO:HG3	1.98	0.45
2:F:160:LEU:O	2:F:164:ILE:HG13	2.17	0.45
2:F:360:LYS:CB	2:F:361:THR:HA	2.46	0.45
1:J:237:GLY:HA2	4:J:601:ANP:O2A	2.16	0.45
1:K:123:THR:HG22	1:K:137:GLY:HA2	1.98	0.45
2:M:97:LYS:NZ	6:M:501:HOH:O	2.49	0.45
2:M:126:GLU:O	2:M:143:ARG:HG3	2.16	0.45
2:M:142:VAL:O	2:M:145:GLN:HB3	2.17	0.45
2:M:185:GLY:HA2	2:M:214:ALA:HA	1.99	0.45
1:A:300:VAL:HG21	1:A:341:MET:HG2	1.98	0.45
1:B:71:LEU:O	1:B:193:VAL:HG22	2.16	0.45
1:B:197:ARG:HA	1:B:198:PRO:HD3	1.85	0.45
1:B:329:ASP:HA	1:B:330:SER:HA	1.54	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:443:ARG:HB2	1:B:443:ARG:CZ	2.47	0.45
1:C:228:ALA:HA	1:C:411:VAL:HB	1.99	0.45
1:C:339:ARG:NH2	2:F:275:GLY:O	2.50	0.45
2:D:48:GLN:N	2:D:51:LYS:O	2.49	0.45
2:D:273:TYR:HD1	2:D:277:LEU:HD22	1.82	0.45
2:E:77:LEU:HB3	2:E:111:ILE:HD13	1.99	0.45
2:F:195:MET:SD	2:F:209:MET:HE1	2.56	0.45
1:J:51:VAL:HG12	1:J:53:GLU:O	2.17	0.45
1:J:90:PRO:HG2	1:J:93:THR:HB	1.97	0.45
1:J:123:THR:HG22	1:J:137:GLY:HA2	1.99	0.45
1:J:290:VAL:HG11	1:J:313:ILE:HG21	1.99	0.45
1:J:509:VAL:HG11	1:J:561:TYR:O	2.17	0.45
1:K:29:LEU:CB	1:K:65:ARG:HE	2.30	0.45
1:K:191:TRP:CD2	1:K:192:PRO:HD2	2.51	0.45
2:L:160:LEU:O	2:L:164:ILE:HG13	2.17	0.45
2:L:215:ASN:OD1	2:L:215:ASN:N	2.44	0.45
2:M:34:MET:SD	2:M:63:ILE:HG12	2.56	0.45
2:M:150:PHE:HZ	2:M:319:THR:HB	1.81	0.45
2:N:143:ARG:HH22	2:N:242:HIS:CD2	2.34	0.45
1:A:43:ARG:HA	1:A:43:ARG:CZ	2.47	0.45
1:A:58:ILE:HG23	1:A:62:GLU:HG3	1.98	0.45
1:B:221:PRO:CB	1:B:441:VAL:HG11	2.46	0.45
1:B:492:VAL:O	1:B:496:ILE:HG13	2.16	0.45
1:C:44:GLN:HG3	1:C:45:ASP:H	1.81	0.45
1:C:240:VAL:HG23	4:C:601:ANP:O2A	2.17	0.45
2:D:195:MET:HG3	2:D:211:MET:HE3	1.99	0.45
2:E:184:ILE:CD1	2:E:225:PRO:HG3	2.47	0.45
2:E:313:HIS:HB3	2:E:316:PRO:HG3	1.99	0.45
2:F:248:THR:HA	2:F:249:ASP:HA	1.51	0.45
2:F:285:PHE:HB2	2:F:322:ILE:HG21	1.98	0.45
1:I:102:PHE:HD1	2:L:116:ILE:HG12	1.82	0.45
1:J:9:VAL:HG22	1:J:9:VAL:O	2.17	0.45
1:J:259:CYS:N	1:J:329:ASP:O	2.49	0.45
1:K:120:PHE:HE2	1:K:137:GLY:HA3	1.80	0.45
2:L:39:ILE:HD12	2:L:39:ILE:N	2.32	0.45
2:M:160:LEU:O	2:M:164:ILE:HG13	2.17	0.45
2:N:234:TYR:CD1	2:N:238:GLU:HG3	2.51	0.45
1:B:231:PRO:CG	1:B:412:PHE:HE1	2.30	0.45
1:C:259:CYS:O	1:C:333:ARG:HG3	2.17	0.45
1:C:462:ARG:O	1:C:466:GLU:HG3	2.17	0.45
2:D:151:SER:HB2	2:D:329:LEU:HD22	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:362:ARG:CB	2:D:427:LEU:HD13	2.45	0.45
2:E:178:ALA:HB2	2:E:241:MET:HE2	1.98	0.45
2:E:315:ILE:N	2:E:316:PRO:HD2	2.32	0.45
2:F:357:GLY:C	2:F:359:GLY:HA3	2.40	0.45
1:I:211:THR:C	1:I:213:GLN:H	2.24	0.45
1:I:304:GLU:O	1:I:334:TRP:NE1	2.49	0.45
1:J:3:ILE:HG23	1:J:64:VAL:O	2.16	0.45
1:J:19:MET:HG3	1:J:19:MET:O	2.17	0.45
1:J:331:THR:HG22	1:J:389:ALA:O	2.17	0.45
1:K:406:LEU:HA	1:K:409:VAL:HG22	1.98	0.45
2:L:65:LEU:HD12	2:L:65:LEU:N	2.31	0.45
2:L:273:TYR:CD1	2:L:314:PRO:HB2	2.52	0.45
1:A:79:ILE:O	1:A:290:VAL:HG22	2.17	0.45
1:A:446:ASP:OD1	1:A:453:TRP:N	2.47	0.45
1:C:236:ALA:O	1:C:427:SER:OG	2.20	0.45
1:C:247:LYS:HE2	1:C:276:LEU:HD11	1.99	0.45
2:D:57:PHE:HB3	2:D:217:PRO:CG	2.47	0.45
2:D:236:ALA:O	2:D:296:GLY:HA3	2.17	0.45
2:E:273:TYR:CE1	2:E:315:ILE:HD11	2.52	0.45
1:J:428:ILE:HD12	1:J:428:ILE:N	2.31	0.45
1:K:220:PHE:HZ	1:K:430:TRP:CA	2.23	0.45
2:L:408:PHE:O	2:L:413:VAL:HG23	2.17	0.45
2:M:276:TYR:O	2:M:280:ASN:N	2.28	0.45
2:N:89:VAL:CG1	2:N:211:MET:HG2	2.47	0.45
2:N:319:THR:HG22	2:N:323:THR:HG21	1.99	0.45
1:A:82:GLN:NE2	1:A:93:THR:OG1	2.50	0.45
1:A:251:VAL:HG12	1:A:323:ASP:HB3	1.99	0.45
1:A:324:VAL:O	1:A:384:ILE:HA	2.17	0.45
1:B:82:GLN:HB3	1:B:84:PHE:CZ	2.51	0.45
1:C:22:ALA:O	1:C:42:MET:HE1	2.16	0.45
1:C:157:GLY:HA3	1:C:177:GLU:O	2.16	0.45
1:C:533:ARG:HD2	1:C:536:LEU:CD1	2.46	0.45
2:D:334:TYR:HB2	2:D:341:PRO:CB	2.46	0.45
2:E:126:GLU:C	2:E:143:ARG:HG3	2.42	0.45
2:F:148:PRO:HG3	2:F:323:THR:OG1	2.17	0.45
2:F:320:GLY:O	2:F:350:ARG:NH2	2.50	0.45
2:F:439:ARG:HD3	2:F:450:LEU:HD13	1.99	0.45
1:J:407:ARG:HG2	1:J:408:VAL:N	2.31	0.45
1:K:245:ILE:O	1:K:249:SER:OG	2.32	0.45
2:L:14:PRO:O	2:L:56:ILE:N	2.36	0.45
2:L:141:LEU:HD21	2:L:244:LEU:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:227:MET:HE3	2:L:227:MET:HB3	1.74	0.45
2:M:11:VAL:HG23	2:M:65:LEU:CD2	2.46	0.45
2:M:21:VAL:CG2	2:M:72:PHE:HZ	2.28	0.45
2:M:120:ALA:O	2:M:292:ARG:HB2	2.17	0.45
1:B:36:ILE:CD1	1:B:87:ILE:HG21	2.47	0.45
1:B:199:ILE:HG21	1:B:372:VAL:HG21	1.99	0.45
1:C:214:ARG:HH22	1:C:560:LYS:HB2	1.82	0.45
1:C:278:ASP:HB3	1:C:281:THR:CG2	2.47	0.45
2:D:30:ILE:HD12	2:D:30:ILE:O	2.17	0.45
2:D:56:ILE:HG22	2:D:59:GLY:H	1.82	0.45
2:D:140:THR:HB	2:D:352:LYS:HA	1.99	0.45
2:E:6:ARG:NE	2:L:290:ARG:HH21	2.15	0.45
2:E:79:LEU:HD23	2:E:81:VAL:HG22	1.99	0.45
2:F:86:ILE:HB	2:F:206:ARG:O	2.17	0.45
2:F:213:LEU:HG	2:F:216:ASP:OD2	2.16	0.45
1:I:268:ASP:O	1:I:272:GLU:HB2	2.17	0.45
1:I:360:SER:O	1:I:364:GLU:HG3	2.16	0.45
1:J:13:LEU:HD11	1:J:48:SER:C	2.42	0.45
1:K:18:ASN:HA	1:K:45:ASP:O	2.17	0.45
1:K:318:ARG:HD3	1:K:384:ILE:CG1	2.45	0.45
1:K:493:ALA:O	1:K:497:ARG:HG3	2.17	0.45
2:L:35:GLN:H	2:L:35:GLN:CD	2.25	0.45
2:M:226:ARG:HD3	2:M:284:LEU:CD2	2.47	0.45
2:M:340:PRO:HA	2:M:341:PRO:HD3	1.90	0.45
1:A:188:MET:SD	1:A:190:LYS:HG3	2.57	0.44
1:B:85:ASP:OD2	1:B:89:ARG:HB2	2.17	0.44
1:B:261:GLU:OE2	1:B:330:SER:N	2.50	0.44
1:C:318:ARG:HB2	1:C:384:ILE:HD11	1.99	0.44
1:C:572:SER:O	1:C:575:GLU:N	2.49	0.44
2:D:29:LEU:CB	2:D:73:LEU:HD11	2.35	0.44
2:D:433:LEU:HA	2:D:436:MET:HE3	1.99	0.44
2:E:85:MET:HG2	2:E:90:PHE:CZ	2.52	0.44
2:E:178:ALA:HB3	2:E:243:VAL:HG22	1.99	0.44
1:I:251:VAL:HG12	1:I:323:ASP:HB3	1.98	0.44
1:I:327:MET:HA	1:I:387:ILE:O	2.16	0.44
1:I:348:MET:HG3	2:M:265:ARG:HA	1.99	0.44
1:J:220:PHE:CZ	1:J:430:TRP:HA	2.40	0.44
1:J:234:PHE:HZ	2:M:311:LYS:CD	2.28	0.44
1:J:285:LEU:O	1:J:289:THR:OG1	2.35	0.44
1:K:292:ILE:HD12	1:K:292:ILE:N	2.32	0.44
2:L:415:GLN:HG2	2:L:421:ARG:HD2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:85:MET:HG2	2:M:103:ILE:HD11	1.96	0.44
2:N:130:THR:CG2	2:N:135:ILE:HG22	2.46	0.44
1:A:73:VAL:HA	1:A:88:GLN:OE1	2.18	0.44
1:A:167:PHE:CD2	1:A:173:ILE:HG22	2.53	0.44
1:A:262:ARG:HG2	2:D:324:GLU:HG3	2.00	0.44
1:C:196:GLY:HA2	1:C:368:ARG:NH2	2.33	0.44
1:C:214:ARG:HB3	1:C:500:TYR:CD1	2.53	0.44
1:C:300:VAL:HG13	1:C:303:ARG:CZ	2.47	0.44
2:E:438:PRO:HG2	2:E:441:GLU:CB	2.47	0.44
1:I:348:MET:CG	2:M:265:ARG:HA	2.47	0.44
2:L:73:LEU:HD12	2:L:73:LEU:HA	1.74	0.44
2:L:83:GLU:CD	2:L:239:LYS:HD2	2.42	0.44
2:L:339:GLN:C	2:L:414:ASN:HD21	2.25	0.44
2:M:24:VAL:HG22	2:M:72:PHE:CZ	2.53	0.44
2:M:158:LYS:H	2:M:158:LYS:HD3	1.82	0.44
2:M:371:GLN:NE2	2:M:442:LEU:HA	2.32	0.44
2:M:372:LEU:HD23	2:M:412:TYR:HE2	1.82	0.44
2:N:148:PRO:HG3	2:N:323:THR:CB	2.48	0.44
1:A:43:ARG:N	1:A:46:VAL:O	2.51	0.44
1:A:424:HIS:HE1	1:A:502:GLN:HG2	1.77	0.44
1:B:430:TRP:CD1	1:B:431:ILE:HG12	2.51	0.44
1:B:487:ARG:HA	1:B:490:LEU:HD12	1.99	0.44
2:D:291:ILE:HB	2:D:294:LEU:HD12	1.98	0.44
2:F:282:ALA:O	2:F:286:GLU:HG2	2.17	0.44
1:J:202:LYS:HB2	2:N:188:PHE:CE1	2.53	0.44
1:J:232:GLY:HA2	1:J:415:LEU:HG	1.98	0.44
2:L:173:SER:O	2:L:174:SER:HB3	2.18	0.44
2:L:183:ALA:O	2:L:212:ASN:N	2.47	0.44
2:M:40:ARG:NE	2:M:63:ILE:HD11	2.31	0.44
2:M:324:GLU:O	2:M:350:ARG:HD2	2.18	0.44
2:N:32:VAL:HB	2:N:40:ARG:HB3	1.99	0.44
1:A:81:SER:OG	1:A:287:GLU:HA	2.17	0.44
1:A:329:ASP:HA	1:A:330:SER:HA	1.51	0.44
1:C:521:MET:HE1	1:C:560:LYS:HB3	2.00	0.44
2:E:235:LEU:HB2	2:E:243:VAL:HG21	1.99	0.44
2:F:307:PRO:HG3	2:F:313:HIS:CE1	2.52	0.44
1:I:3:ILE:HD12	1:I:3:ILE:N	2.33	0.44
1:I:424:HIS:NE2	1:I:501:LEU:HD22	2.33	0.44
1:J:36:ILE:HD12	1:J:87:ILE:HG22	1.99	0.44
1:J:37:GLY:HA2	1:J:52:TYR:H	1.83	0.44
1:K:52:TYR:O	1:K:299:PRO:HB3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:214:ARG:HH22	1:K:560:LYS:HD3	1.82	0.44
2:L:29:LEU:HB3	2:L:73:LEU:HD23	1.98	0.44
2:L:87:GLY:HA3	2:L:205:ASP:HA	1.97	0.44
2:M:8:ILE:O	2:M:65:LEU:HB3	2.18	0.44
2:M:147:LEU:O	2:M:301:ILE:HG23	2.18	0.44
2:M:183:ALA:HB1	2:M:186:ILE:HD13	2.00	0.44
2:M:384:GLU:O	2:M:387:VAL:HG22	2.18	0.44
1:A:139:VAL:O	1:A:147:HIS:HB3	2.17	0.44
1:B:102:PHE:HB3	2:E:114:GLU:CB	2.48	0.44
1:B:549:THR:O	1:B:553:ARG:HG3	2.18	0.44
1:C:273:PHE:HE2	1:C:289:THR:HG21	1.82	0.44
2:D:157:HIS:HD2	2:D:158:LYS:N	2.15	0.44
2:D:176:ASP:HB3	2:D:206:ARG:CD	2.48	0.44
2:E:131:GLY:N	2:E:167:GLN:HB3	2.29	0.44
2:E:284:LEU:HD13	2:E:285:PHE:CD1	2.53	0.44
2:E:430:GLY:O	2:E:434:LEU:HB2	2.18	0.44
1:I:7:ILE:HB	2:L:49:GLU:HG2	1.98	0.44
1:I:43:ARG:HA	1:I:43:ARG:HE	1.82	0.44
1:I:94:PHE:CD1	1:I:109:LEU:HD12	2.52	0.44
1:I:257:VAL:HA	1:I:292:ILE:HB	2.00	0.44
1:J:20:SER:HA	1:J:42:MET:HE2	1.99	0.44
1:J:532:ALA:O	1:J:536:LEU:HB2	2.17	0.44
1:K:36:ILE:HG22	1:K:53:GLU:OE2	2.18	0.44
1:K:405:THR:O	1:K:409:VAL:HG22	2.18	0.44
2:L:33:ARG:O	2:L:69:SER:N	2.46	0.44
2:L:270:ARG:HB3	2:L:270:ARG:HH11	1.82	0.44
2:N:213:LEU:HD12	2:N:213:LEU:N	2.30	0.44
1:A:20:SER:HA	1:A:42:MET:HE2	2.00	0.44
1:A:43:ARG:N	1:A:44:GLN:HA	2.32	0.44
1:A:72:SER:HA	1:A:193:VAL:HG13	1.99	0.44
1:A:218:THR:HA	1:A:453:TRP:CZ2	2.52	0.44
1:A:315:GLU:HA	1:A:384:ILE:HD11	1.98	0.44
1:B:118:TRP:CZ3	1:B:141:GLU:HA	2.52	0.44
1:B:459:GLU:O	1:B:463:ILE:HG13	2.18	0.44
1:C:75:LEU:N	1:C:189:GLN:O	2.47	0.44
1:C:94:PHE:HZ	1:C:104:GLY:H	1.66	0.44
1:C:330:SER:HB3	1:C:333:ARG:HG2	1.99	0.44
2:F:57:PHE:HA	2:F:219:ILE:CB	2.48	0.44
2:F:251:THR:HG21	2:F:305:THR:O	2.17	0.44
2:F:282:ALA:HA	2:F:322:ILE:CG2	2.47	0.44
1:K:560:LYS:H	1:K:560:LYS:HG3	1.56	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:250:MET:HE2	2:N:285:PHE:CZ	2.52	0.44
1:B:324:VAL:O	1:B:384:ILE:HA	2.18	0.44
1:C:363:ALA:O	1:C:367:GLU:HB2	2.18	0.44
2:D:132:ILE:HD13	2:D:135:ILE:HD12	2.00	0.44
2:D:345:LEU:HD21	2:D:376:TYR:CE2	2.52	0.44
2:E:34:MET:CG	2:E:38:GLU:HB3	2.48	0.44
2:F:179:VAL:HG13	2:F:244:LEU:HD23	1.99	0.44
1:I:19:MET:HE1	1:I:64:VAL:HB	1.99	0.44
1:I:338:LEU:HD11	1:I:361:ARG:HG3	2.00	0.44
1:J:214:ARG:CD	1:J:513:THR:HG21	2.48	0.44
1:K:89:ARG:HD3	1:K:109:LEU:H	1.81	0.44
1:K:237:GLY:O	1:K:241:VAL:HG23	2.17	0.44
1:K:342:SER:HA	1:K:345:LEU:HD12	2.00	0.44
2:L:349:SER:CB	2:L:352:LYS:HZ2	2.31	0.44
2:M:339:GLN:HA	2:M:340:PRO:C	2.42	0.44
2:N:427:LEU:O	2:N:427:LEU:HD13	2.17	0.44
1:A:82:GLN:HB3	1:A:84:PHE:CZ	2.53	0.44
1:A:285:LEU:CD2	1:A:288:ARG:HD3	2.47	0.44
1:B:12:PRO:CB	1:B:344:ARG:CD	2.90	0.44
1:B:126:GLU:OE2	1:B:161:LYS:HA	2.17	0.44
1:B:238:LYS:H	1:B:238:LYS:HG3	1.60	0.44
1:B:565:GLU:O	1:B:567:LEU:HD23	2.18	0.44
1:C:418:SER:O	1:C:422:LYS:HD2	2.17	0.44
2:E:162:ALA:O	2:E:166:ARG:HG3	2.18	0.44
2:F:362:ARG:CB	2:F:427:LEU:HD21	2.48	0.44
1:I:120:PHE:CZ	1:I:173:ILE:HD12	2.52	0.44
1:J:29:LEU:H	1:J:29:LEU:HD22	1.83	0.44
2:L:137:HIS:HD2	2:L:426:THR:HG22	1.81	0.44
2:L:153:SER:HB3	2:L:331:ARG:NH2	2.32	0.44
2:L:404:PHE:HE1	2:L:434:LEU:HA	1.83	0.44
2:M:29:LEU:O	2:M:73:LEU:HB2	2.18	0.44
2:N:339:GLN:HA	2:N:341:PRO:CD	2.48	0.44
1:B:8:LYS:HG3	1:B:15:MET:HE3	1.98	0.44
1:B:11:GLY:CA	1:B:55:THR:HG21	2.29	0.44
1:B:360:SER:O	1:B:364:GLU:HG3	2.17	0.44
2:D:32:VAL:HG13	2:D:70:VAL:HG22	2.00	0.44
2:D:44:VAL:HG11	2:D:47:VAL:HG13	1.99	0.44
2:D:325:GLY:HA2	2:D:348:LEU:O	2.18	0.44
2:E:313:HIS:CG	2:E:314:PRO:HD2	2.53	0.44
2:F:48:GLN:HB2	2:F:53:MET:HE2	1.99	0.44
2:F:325:GLY:HA2	2:F:326:GLN:HA	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:214:ARG:HG3	1:I:503:GLN:OE1	2.18	0.44
1:I:298:MET:HE3	2:L:115:VAL:HG11	2.00	0.44
1:J:30:VAL:O	1:J:35:VAL:N	2.48	0.44
1:K:147:HIS:CE1	1:K:320:MET:HE1	2.53	0.44
2:L:65:LEU:HD12	2:L:66:LYS:H	1.83	0.44
2:L:109:LEU:H	2:L:109:LEU:HD12	1.82	0.44
2:L:121:ARG:NH2	2:L:286:GLU:O	2.43	0.44
2:L:183:ALA:HA	2:L:248:THR:O	2.17	0.44
2:L:234:TYR:OH	2:L:239:LYS:NZ	2.36	0.44
2:M:48:GLN:CB	2:M:49:GLU:HA	2.47	0.44
2:N:34:MET:CG	2:N:38:GLU:HB3	2.47	0.44
2:N:155:LEU:CD1	2:N:329:LEU:HB2	2.48	0.44
1:A:42:MET:HG3	2:E:65:LEU:HD11	2.00	0.43
1:A:246:ALA:CB	1:A:254:VAL:HG11	2.48	0.43
1:A:255:VAL:HB	1:A:326:ILE:HA	2.00	0.43
1:A:273:PHE:HB3	1:A:274:PRO:HD3	1.99	0.43
1:B:271:ASN:C	1:B:274:PRO:HD2	2.43	0.43
1:B:406:LEU:HA	1:B:409:VAL:HG22	2.00	0.43
1:B:482:LEU:H	1:B:482:LEU:HD12	1.83	0.43
1:C:500:TYR:HD1	1:C:500:TYR:HA	1.72	0.43
2:E:20:LYS:HD3	2:L:292:ARG:NH1	2.33	0.43
2:E:134:ALA:HB2	2:E:412:TYR:O	2.18	0.43
2:F:258:ARG:HH21	2:F:272:GLY:CA	2.30	0.43
1:I:437:TYR:O	1:I:441:VAL:HG23	2.18	0.43
1:J:424:HIS:HE1	1:J:502:GLN:HB3	1.82	0.43
2:M:40:ARG:HD3	2:M:59:GLY:O	2.17	0.43
1:A:536:LEU:HD23	1:A:536:LEU:HA	1.84	0.43
1:B:246:ALA:HB2	1:B:327:MET:CG	2.48	0.43
2:D:345:LEU:HA	2:D:373:PHE:CZ	2.53	0.43
2:E:18:VAL:O	2:E:52:ALA:N	2.45	0.43
2:F:260:ILE:CG2	2:F:264:ARG:HH21	2.31	0.43
2:F:300:GLN:C	2:F:302:PRO:HD3	2.44	0.43
1:I:119:TRP:HA	1:I:119:TRP:CE3	2.54	0.43
1:I:402:THR:O	1:I:406:LEU:HG	2.18	0.43
1:J:35:VAL:CB	1:J:53:GLU:HB2	2.35	0.43
1:K:207:VAL:O	1:K:223:THR:HA	2.18	0.43
1:K:210:ILE:CG1	1:K:515:ARG:HH21	2.31	0.43
2:L:218:ALA:HA	2:L:221:ARG:HE	1.81	0.43
2:L:390:GLY:HA2	2:L:391:GLU:HA	1.70	0.43
2:L:405:ALA:O	2:L:409:GLU:HG3	2.18	0.43
2:M:251:THR:OG1	2:M:305:THR:N	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:372:LEU:HD12	2:M:372:LEU:HA	1.86	0.43
1:A:229:ALA:HA	1:A:388:SER:O	2.18	0.43
1:B:491:GLU:OE1	1:B:494:LYS:NZ	2.35	0.43
2:D:124:PRO:HB2	2:D:142:VAL:HB	2.01	0.43
2:E:123:TYR:HA	2:E:124:PRO:HD3	1.89	0.43
2:E:178:ALA:O	2:E:243:VAL:HA	2.19	0.43
2:E:354:LYS:HA	2:E:355:GLY:HA2	1.50	0.43
2:E:423:ILE:HG23	2:E:424:THR:N	2.32	0.43
2:F:362:ARG:CB	2:F:365:HIS:HB2	2.48	0.43
2:L:158:LYS:HD3	2:L:190:GLU:HG2	2.00	0.43
2:M:218:ALA:O	2:M:222:ILE:HG13	2.19	0.43
1:A:202:LYS:HA	1:A:372:VAL:HG12	1.99	0.43
1:A:529:GLY:O	1:A:533:ARG:HB2	2.18	0.43
1:B:82:GLN:HE22	1:B:92:ASP:CG	2.27	0.43
1:C:424:HIS:NE2	1:C:501:LEU:O	2.52	0.43
2:D:73:LEU:HB2	2:D:75:HIS:CE1	2.53	0.43
2:E:16:MET:HE1	2:E:32:VAL:HG21	2.00	0.43
2:E:33:ARG:HH12	2:E:71:ARG:HE	1.65	0.43
2:F:30:ILE:HG22	2:F:72:PHE:HD1	1.84	0.43
2:F:57:PHE:HB3	2:F:220:GLU:N	2.33	0.43
1:K:469:GLN:O	1:K:473:ILE:HG13	2.18	0.43
1:K:545:ILE:O	1:K:549:THR:OG1	2.30	0.43
2:M:130:THR:HG21	2:M:135:ILE:CG2	2.41	0.43
2:M:229:LEU:HD22	2:M:287:ARG:HG3	1.99	0.43
2:N:26:TYR:CD1	2:N:26:TYR:C	2.97	0.43
2:N:328:ILE:CG1	2:N:346:PRO:HG2	2.48	0.43
1:A:208:PRO:HG3	1:A:441:VAL:HG13	2.00	0.43
1:C:364:GLU:O	1:C:368:ARG:HG3	2.18	0.43
2:D:345:LEU:HD21	2:D:376:TYR:CD2	2.53	0.43
2:E:18:VAL:N	2:E:52:ALA:O	2.37	0.43
2:E:364:ASP:CB	2:E:449:LEU:HD22	2.49	0.43
2:F:258:ARG:NH2	2:F:272:GLY:HA3	2.33	0.43
2:F:313:HIS:CD2	2:F:314:PRO:HD2	2.54	0.43
1:I:124:ILE:O	1:I:162:ILE:HG21	2.18	0.43
1:K:278:ASP:HB3	1:K:281:THR:CG2	2.48	0.43
1:K:521:MET:HE2	1:K:521:MET:HB3	1.81	0.43
2:L:82:SER:O	2:L:85:MET:HG2	2.19	0.43
2:L:137:HIS:CD2	2:L:426:THR:HG22	2.53	0.43
2:L:364:ASP:HB2	2:L:431:TRP:HZ2	1.84	0.43
2:M:279:THR:O	2:M:283:THR:HG23	2.18	0.43
1:A:43:ARG:HG2	1:A:46:VAL:HG13	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:324:VAL:HG12	1:A:325:ALA:N	2.33	0.43
1:B:214:ARG:HB3	1:B:500:TYR:CZ	2.53	0.43
1:B:261:GLU:HG2	1:B:329:ASP:O	2.17	0.43
1:C:4:GLY:O	1:C:64:VAL:HG23	2.19	0.43
1:C:9:VAL:HG11	1:C:58:ILE:HB	2.01	0.43
1:C:20:SER:HB3	1:C:45:ASP:HA	2.01	0.43
1:C:242:GLN:OE1	1:C:329:ASP:HB2	2.19	0.43
2:D:148:PRO:HG3	2:D:323:THR:OG1	2.18	0.43
2:E:290:ARG:HG3	2:E:297:SER:HB3	2.01	0.43
2:F:124:PRO:HB2	2:F:142:VAL:HG11	1.96	0.43
2:F:197:ASP:O	2:F:201:THR:HG23	2.17	0.43
1:I:246:ALA:CB	1:I:254:VAL:HG11	2.48	0.43
1:I:262:ARG:HH12	2:L:350:ARG:CZ	2.31	0.43
1:J:315:GLU:OE2	1:J:368:ARG:HB3	2.18	0.43
1:J:392:PRO:HG3	1:J:402:THR:OG1	2.19	0.43
1:K:209:MET:N	1:K:222:VAL:O	2.37	0.43
1:K:351:ASP:OD2	1:K:351:ASP:N	2.50	0.43
2:L:21:VAL:HG21	2:L:52:ALA:HB2	2.00	0.43
2:M:21:VAL:HG22	2:M:72:PHE:CZ	2.53	0.43
2:N:45:LEU:HD22	2:N:46:GLU:H	1.83	0.43
2:N:242:HIS:HA	2:N:297:SER:H	1.84	0.43
2:N:381:GLN:HA	2:N:384:GLU:HG3	2.01	0.43
1:A:20:SER:HA	1:A:42:MET:HE1	2.01	0.43
1:A:85:ASP:OD2	1:A:88:GLN:N	2.51	0.43
1:A:266:MET:HE1	1:A:270:VAL:HG21	2.00	0.43
1:B:79:ILE:HB	1:B:112:LEU:CD1	2.48	0.43
1:B:191:TRP:CG	1:B:192:PRO:HD2	2.53	0.43
1:B:209:MET:HE2	1:B:251:VAL:HG11	2.01	0.43
1:B:366:TYR:O	1:B:369:SER:OG	2.36	0.43
1:B:425:PHE:HB2	4:B:601:ANP:N6	2.33	0.43
2:D:48:GLN:CB	2:D:51:LYS:HG2	2.47	0.43
2:D:129:GLN:O	2:D:168:ALA:HA	2.19	0.43
2:E:167:GLN:HG3	2:E:420:ASN:CB	2.48	0.43
2:F:437:LEU:HD23	2:F:441:GLU:OE2	2.19	0.43
1:I:33:LEU:HD12	1:I:33:LEU:N	2.34	0.43
1:J:50:GLN:HE21	1:J:345:LEU:HD11	1.83	0.43
1:J:79:ILE:HG13	1:J:84:PHE:CE2	2.54	0.43
1:J:295:THR:O	1:J:298:MET:HB2	2.18	0.43
1:J:362:LEU:O	1:J:366:TYR:HD2	2.02	0.43
1:K:41:GLU:O	1:K:47:ALA:HB1	2.19	0.43
2:L:6:ARG:NH2	2:L:6:ARG:CB	2.77	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:9:LYS:HG3	2:L:19:GLU:CD	2.44	0.43
2:M:113:GLY:HA3	2:M:287:ARG:NH1	2.33	0.43
2:M:130:THR:HB	2:M:135:ILE:HD12	2.01	0.43
2:N:213:LEU:H	2:N:213:LEU:CD1	2.30	0.43
1:A:198:PRO:HB2	1:A:375:LEU:HD11	2.01	0.43
1:A:297:ASN:ND2	2:D:115:VAL:HG13	2.33	0.43
1:A:352:GLU:HB2	1:A:400:PRO:HG2	2.00	0.43
1:B:29:LEU:HD12	1:B:34:GLY:O	2.17	0.43
1:B:215:VAL:HG11	1:B:426:PRO:HG2	1.99	0.43
1:B:229:ALA:HA	1:B:388:SER:O	2.19	0.43
1:B:258:GLY:HA3	1:B:266:MET:SD	2.59	0.43
1:C:256:TYR:CD1	1:C:327:MET:HB2	2.53	0.43
2:D:232:ALA:HB1	2:D:243:VAL:HG11	2.00	0.43
2:D:313:HIS:CG	2:D:314:PRO:HD2	2.54	0.43
2:E:285:PHE:CE2	2:E:319:THR:HG23	2.54	0.43
1:I:16:ALA:HB1	1:I:64:VAL:HG21	2.01	0.43
1:I:185:LEU:N	1:I:185:LEU:HD23	2.34	0.43
1:I:295:THR:H	1:I:298:MET:CG	2.26	0.43
1:J:401:VAL:O	1:J:405:THR:OG1	2.28	0.43
1:J:498:GLU:O	1:J:502:GLN:HB2	2.19	0.43
1:K:9:VAL:HG21	1:K:58:ILE:HG21	2.01	0.43
1:K:131:SER:N	1:K:134:ASP:OD2	2.32	0.43
1:K:392:PRO:HA	1:K:399:GLU:CD	2.43	0.43
2:M:11:VAL:HG23	2:M:65:LEU:HD23	2.00	0.43
2:M:147:LEU:O	2:M:301:ILE:HA	2.18	0.43
2:N:34:MET:HE1	2:N:63:ILE:CD1	2.49	0.43
2:N:126:GLU:CG	2:N:143:ARG:HG3	2.49	0.43
2:N:186:ILE:H	2:N:186:ILE:HG12	1.64	0.43
2:N:403:LYS:O	2:N:407:ARG:HG3	2.17	0.43
1:A:98:THR:O	1:A:99:GLN:HB2	2.18	0.43
1:A:405:THR:O	1:A:409:VAL:HG22	2.19	0.43
1:B:209:MET:HG2	1:B:210:ILE:N	2.33	0.43
1:B:237:GLY:N	4:B:601:ANP:O3A	2.47	0.43
1:B:245:ILE:O	1:B:249:SER:OG	2.18	0.43
1:B:292:ILE:HD12	1:B:292:ILE:N	2.34	0.43
1:C:39:ILE:HG23	1:C:48:SER:O	2.19	0.43
1:C:292:ILE:HD12	1:C:292:ILE:N	2.33	0.43
2:E:306:MET:HG2	2:E:310:ASP:O	2.17	0.43
1:I:145:ILE:HG13	1:I:253:LEU:CD1	2.48	0.43
1:I:263:GLY:O	1:I:267:THR:OG1	2.28	0.43
1:J:19:MET:HE3	1:J:49:ILE:HD11	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:199:ILE:HG21	1:J:372:VAL:HG21	1.99	0.43
1:A:84:PHE:CE2	1:A:290:VAL:HG13	2.54	0.43
1:A:266:MET:HE1	1:A:270:VAL:CG2	2.48	0.43
1:A:426:PRO:HD2	1:A:501:LEU:O	2.19	0.43
1:A:532:ALA:O	1:A:536:LEU:N	2.50	0.43
1:B:315:GLU:OE2	1:B:368:ARG:NE	2.52	0.43
2:D:163:GLN:HG3	2:D:417:PHE:HD1	1.83	0.43
2:E:356:THR:HA	2:E:357:GLY:C	2.44	0.43
2:E:434:LEU:HD22	2:E:442:LEU:HD22	2.00	0.43
2:F:175:ASP:N	2:F:176:ASP:CB	2.82	0.43
2:F:177:PHE:CE1	2:F:243:VAL:C	2.96	0.43
1:I:254:VAL:H	1:I:289:THR:CG2	2.27	0.43
1:J:37:GLY:N	1:J:52:TYR:HD1	2.16	0.43
1:J:88:GLN:OE1	1:J:111:ALA:HB1	2.19	0.43
1:J:406:LEU:HD21	1:J:412:PHE:CG	2.54	0.43
1:K:209:MET:HE2	1:K:222:VAL:HB	2.00	0.43
1:K:237:GLY:N	4:K:601:ANP:O3A	2.49	0.43
2:M:128:ILE:HG13	2:M:143:ARG:CG	2.24	0.43
2:N:7:THR:O	2:N:19:GLU:HG2	2.19	0.43
2:N:29:LEU:HD13	2:N:77:LEU:HB3	2.00	0.43
2:N:130:THR:O	2:N:132:ILE:HD12	2.19	0.43
2:N:156:PRO:HD3	2:N:334:TYR:CE1	2.54	0.43
2:N:199:ARG:HA	2:N:204:ILE:HG21	2.01	0.43
2:N:362:ARG:O	2:N:365:HIS:HB3	2.18	0.43
1:A:219:PHE:HE2	1:A:501:LEU:CD2	2.32	0.42
2:D:16:MET:HB2	2:D:54:VAL:HG22	2.01	0.42
2:D:159:GLU:HB3	2:D:417:PHE:CG	2.54	0.42
2:D:408:PHE:O	2:D:413:VAL:HG23	2.19	0.42
2:E:439:ARG:HH22	2:E:451:ASP:CG	2.26	0.42
2:F:45:LEU:H	2:F:45:LEU:HG	1.55	0.42
2:F:86:ILE:CA	2:F:208:VAL:HG22	2.48	0.42
1:I:136:ILE:CG1	1:I:137:GLY:N	2.81	0.42
1:J:150:MET:HE2	1:J:320:MET:HG2	1.99	0.42
1:J:211:THR:HB	1:J:245:ILE:CD1	2.49	0.42
1:J:326:ILE:HD13	1:J:326:ILE:C	2.43	0.42
1:K:24:ILE:HG21	2:L:60:THR:HG23	2.01	0.42
2:L:90:PHE:CD1	2:L:96:PRO:HA	2.54	0.42
2:L:224:THR:HB	2:L:225:PRO:HD3	2.00	0.42
2:L:250:MET:HE2	2:L:285:PHE:CE1	2.54	0.42
2:M:186:ILE:HD12	2:M:191:ALA:HA	2.01	0.42
2:M:213:LEU:HB3	2:M:215:ASN:OD1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:92:GLY:HA3	2:N:220:GLU:OE1	2.18	0.42
2:N:251:THR:HG23	2:N:315:ILE:HG13	2.01	0.42
1:A:238:LYS:HE2	1:A:238:LYS:HB3	1.93	0.42
1:A:256:TYR:HB3	1:A:291:LEU:HG	2.01	0.42
1:B:153:ASN:HB2	1:B:191:TRP:HZ3	1.84	0.42
1:B:338:LEU:HB3	1:B:355:PRO:HG3	2.01	0.42
1:C:461:MET:O	1:C:465:GLN:HG3	2.19	0.42
2:D:130:THR:HG23	2:D:141:LEU:HD23	2.01	0.42
2:D:282:ALA:HA	2:D:322:ILE:HD13	2.01	0.42
2:D:339:GLN:C	2:D:414:ASN:HB2	2.44	0.42
2:E:151:SER:O	2:E:305:THR:HA	2.19	0.42
2:E:345:LEU:HB2	2:E:346:PRO:CD	2.47	0.42
2:F:21:VAL:HB	2:F:24:VAL:HG21	2.00	0.42
2:F:66:LYS:HB3	2:F:66:LYS:HE3	1.77	0.42
2:F:212:ASN:OD1	2:F:221:ARG:HG2	2.19	0.42
1:I:173:ILE:HG22	6:I:601:HOH:O	2.18	0.42
1:I:424:HIS:O	1:I:424:HIS:CG	2.71	0.42
1:I:492:VAL:O	1:I:496:ILE:HG13	2.20	0.42
1:K:311:ILE:O	1:K:315:GLU:HG3	2.19	0.42
1:K:338:LEU:HB3	1:K:355:PRO:HG3	2.00	0.42
1:K:402:THR:O	1:K:406:LEU:HG	2.18	0.42
2:L:6:ARG:NE	2:L:8:ILE:HG13	2.29	0.42
2:L:151:SER:CB	2:L:157:HIS:HB3	2.49	0.42
2:M:31:GLU:HB3	2:M:71:ARG:HB2	2.01	0.42
2:N:139:ASN:HA	2:N:349:SER:HB2	2.00	0.42
2:N:180:VAL:N	2:N:244:LEU:O	2.35	0.42
2:N:277:LEU:HD23	2:N:318:LEU:HD12	2.01	0.42
1:C:210:ILE:HD11	1:C:515:ARG:NH2	2.34	0.42
1:C:237:GLY:HA2	4:C:601:ANP:PA	2.59	0.42
1:C:257:VAL:HG11	1:C:306:SER:O	2.20	0.42
2:E:30:ILE:HG13	2:E:42:GLY:C	2.44	0.42
2:E:45:LEU:HD13	2:E:45:LEU:N	2.35	0.42
2:E:372:LEU:HD12	2:E:404:PHE:HZ	1.84	0.42
2:F:77:LEU:O	2:F:111:ILE:HG23	2.19	0.42
2:F:445:ILE:HD13	2:F:445:ILE:H	1.83	0.42
1:I:222:VAL:HB	1:I:411:VAL:HG21	2.00	0.42
1:J:33:LEU:HD13	1:J:105:ARG:HB2	2.02	0.42
1:K:58:ILE:O	2:N:25:LYS:HA	2.19	0.42
1:K:59:GLY:CA	2:N:25:LYS:HD3	2.50	0.42
1:K:197:ARG:HA	1:K:198:PRO:HD3	1.86	0.42
2:L:97:LYS:HE2	2:L:97:LYS:HB3	1.71	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:408:PHE:CD1	2:M:408:PHE:C	2.97	0.42
2:N:34:MET:CE	2:N:63:ILE:HG12	2.49	0.42
1:A:262:ARG:HG2	2:D:322:ILE:O	2.19	0.42
1:A:406:LEU:HA	1:A:409:VAL:HG22	2.00	0.42
1:A:425:PHE:N	1:A:425:PHE:CD1	2.88	0.42
1:B:83:MET:CE	2:E:119:ILE:HD11	2.50	0.42
2:D:135:ILE:O	2:D:135:ILE:HG22	2.20	0.42
2:D:157:HIS:HD2	2:D:158:LYS:H	1.68	0.42
2:F:358:ALA:HA	2:F:363:GLU:HA	2.00	0.42
1:K:507:ASP:HB3	1:K:510:ASP:CB	2.49	0.42
2:L:141:LEU:HD13	2:L:147:LEU:HB2	2.01	0.42
2:M:26:TYR:O	2:M:27:GLU:HB2	2.18	0.42
2:M:91:ASP:OD2	2:M:93:LEU:HB2	2.20	0.42
2:M:219:ILE:HD11	2:M:260:ILE:HD12	2.00	0.42
2:M:285:PHE:CE1	2:M:302:PRO:HB3	2.54	0.42
2:N:45:LEU:HD22	2:N:45:LEU:N	2.34	0.42
2:N:199:ARG:HA	2:N:204:ILE:CG2	2.49	0.42
2:N:378:GLN:CA	2:N:381:GLN:HE22	2.32	0.42
1:B:215:VAL:CG1	1:B:426:PRO:HG2	2.49	0.42
1:B:326:ILE:O	1:B:386:ALA:HA	2.19	0.42
1:C:562:ILE:H	1:C:562:ILE:HD12	1.84	0.42
2:D:29:LEU:HB3	2:D:73:LEU:HD21	2.02	0.42
2:E:318:LEU:O	2:E:322:ILE:HG13	2.19	0.42
2:F:32:VAL:HG21	2:F:56:ILE:HD12	2.01	0.42
2:F:139:ASN:HB3	2:F:349:SER:HB3	2.01	0.42
2:F:161:ALA:HB2	2:F:303:ILE:CD1	2.49	0.42
2:F:342:ILE:HG22	2:F:343:ASP:O	2.20	0.42
1:I:80:ILE:HG22	1:I:81:SER:H	1.84	0.42
1:I:155:ILE:HD12	1:I:183:LYS:HG2	2.01	0.42
1:J:47:ALA:O	1:J:49:ILE:HG13	2.20	0.42
1:J:73:VAL:O	1:J:73:VAL:HG23	2.20	0.42
1:J:190:LYS:HB2	1:J:190:LYS:NZ	2.34	0.42
1:J:311:ILE:HG23	1:J:368:ARG:HH21	1.84	0.42
1:J:415:LEU:HD23	1:J:415:LEU:H	1.83	0.42
1:K:33:LEU:CD2	1:K:106:GLY:HA3	2.49	0.42
1:K:54:GLU:CB	1:K:105:ARG:HD3	2.48	0.42
2:L:376:TYR:CD1	2:L:408:PHE:HD2	2.37	0.42
2:M:15:LEU:HD22	2:M:55:GLN:CG	2.50	0.42
2:M:396:ASP:HA	2:M:399:LYS:HG3	2.01	0.42
2:M:446:LYS:HA	2:M:446:LYS:CE	2.38	0.42
2:N:129:GLN:HE22	2:N:422:THR:CA	2.26	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:409:GLU:HA	2:N:413:VAL:CB	2.49	0.42
1:A:168:THR:OG1	1:A:171:ASP:OD2	2.23	0.42
1:B:56:SER:HA	2:E:26:TYR:HD2	1.84	0.42
1:B:238:LYS:HG2	1:B:415:LEU:CD1	2.50	0.42
1:B:505:ALA:O	1:B:511:THR:HB	2.20	0.42
1:C:329:ASP:HA	1:C:330:SER:HA	1.58	0.42
2:E:391:GLU:O	2:E:399:LYS:NZ	2.50	0.42
2:F:86:ILE:CG2	2:F:208:VAL:HG22	2.46	0.42
2:F:229:LEU:O	2:F:233:GLU:N	2.40	0.42
1:J:292:ILE:HD12	1:J:292:ILE:N	2.35	0.42
1:J:352:GLU:HB2	1:J:400:PRO:HG3	2.02	0.42
2:L:9:LYS:C	2:L:10:GLU:HG3	2.44	0.42
2:L:34:MET:HB3	2:L:36:ASN:OD1	2.19	0.42
2:L:76:PRO:O	2:L:78:GLN:HG3	2.20	0.42
2:M:29:LEU:HD11	2:M:77:LEU:HD23	2.02	0.42
1:A:20:SER:HB3	1:A:45:ASP:CB	2.49	0.42
1:A:35:VAL:HB	1:A:53:GLU:HB2	2.02	0.42
1:B:27:MET:SD	1:B:71:LEU:HB2	2.59	0.42
1:B:309:THR:O	1:B:313:ILE:HG13	2.19	0.42
1:B:564:GLU:N	1:B:565:GLU:OE1	2.52	0.42
1:C:80:ILE:HG13	1:C:141:GLU:OE1	2.20	0.42
1:C:399:GLU:HA	1:C:400:PRO:HD3	1.90	0.42
2:D:39:ILE:HD12	2:D:39:ILE:N	2.34	0.42
2:D:324:GLU:CD	2:D:324:GLU:N	2.77	0.42
2:E:77:LEU:O	2:E:111:ILE:HG23	2.20	0.42
2:E:112:ASN:O	2:E:287:ARG:NH1	2.53	0.42
1:I:251:VAL:HG11	1:I:385:THR:OG1	2.20	0.42
1:J:456:MET:HB3	1:J:526:LEU:HD11	2.01	0.42
1:J:543:ASN:OD1	1:J:543:ASN:N	2.52	0.42
1:K:504:ASN:N	1:K:510:ASP:OD2	2.39	0.42
2:L:44:VAL:HG11	2:L:47:VAL:HG12	2.02	0.42
2:L:129:GLN:O	2:L:168:ALA:HA	2.20	0.42
2:M:124:PRO:HG2	2:M:351:LEU:CD1	2.49	0.42
2:M:219:ILE:HD12	2:M:219:ILE:N	2.35	0.42
2:M:306:MET:HA	2:M:307:PRO:HD3	1.76	0.42
2:M:372:LEU:CD2	2:M:412:TYR:HE2	2.33	0.42
2:N:278:TYR:CE1	2:N:322:ILE:HG12	2.54	0.42
2:N:300:GLN:C	2:N:302:PRO:HD3	2.45	0.42
1:A:42:MET:HE3	1:A:42:MET:HB3	1.90	0.42
1:B:1:MET:HG2	1:B:2:GLN:H	1.85	0.42
1:B:29:LEU:O	1:B:64:VAL:HG13	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:237:GLY:HA2	4:C:601:ANP:H8	2.01	0.42
2:D:30:ILE:HG13	2:D:42:GLY:O	2.18	0.42
2:D:343:ASP:HB3	2:D:346:PRO:CD	2.49	0.42
2:E:273:TYR:OH	2:E:315:ILE:HD11	2.19	0.42
1:J:394:GLY:N	2:M:317:ASP:OD2	2.35	0.42
1:J:467:GLU:OE2	1:J:497:ARG:NH1	2.53	0.42
1:J:470:LEU:O	1:J:474:VAL:HG23	2.20	0.42
1:K:29:LEU:O	1:K:65:ARG:HG3	2.20	0.42
1:K:349:PRO:HB2	1:K:353:GLY:HA2	2.02	0.42
1:K:461:MET:HE1	1:K:465:GLN:HG3	2.02	0.42
2:L:8:ILE:HA	2:L:17:ALA:O	2.20	0.42
2:M:29:LEU:HD11	2:M:77:LEU:HA	2.02	0.42
2:N:134:ALA:O	2:N:139:ASN:N	2.52	0.42
2:N:137:HIS:O	2:N:369:MET:HE2	2.20	0.42
2:N:345:LEU:HA	2:N:345:LEU:HD12	1.75	0.42
1:A:130:VAL:HG11	1:A:176:ILE:HD13	2.01	0.42
1:A:331:THR:HG21	1:A:388:SER:HB3	2.02	0.42
1:C:257:VAL:HG13	1:C:292:ILE:HB	2.01	0.42
2:D:117:ASN:HB3	2:D:120:ALA:HB3	2.02	0.42
2:D:331:ARG:O	2:D:335:LYS:HB2	2.20	0.42
2:F:175:ASP:CA	2:F:176:ASP:C	2.93	0.42
1:I:84:PHE:C	1:I:91:LEU:HD11	2.45	0.42
1:I:206:ASP:OD2	1:I:206:ASP:N	2.52	0.42
1:I:295:THR:O	1:I:303:ARG:HD3	2.19	0.42
1:J:83:MET:SD	1:J:293:ALA:HB2	2.60	0.42
1:K:2:GLN:HE22	1:K:20:SER:HB3	1.85	0.42
1:K:341:MET:O	1:K:345:LEU:HG	2.19	0.42
2:L:286:GLU:OE2	2:L:286:GLU:HA	2.19	0.42
2:L:379:GLY:HA3	2:L:405:ALA:HB2	2.02	0.42
2:M:113:GLY:HA3	2:M:287:ARG:HH12	1.85	0.42
2:M:217:PRO:HB2	2:M:220:GLU:HG3	2.01	0.42
1:A:424:HIS:NE2	1:A:501:LEU:HB3	2.35	0.42
1:B:18:ASN:HA	1:B:45:ASP:HB2	2.02	0.42
1:B:120:PHE:N	1:B:165:GLY:O	2.47	0.42
1:B:148:LYS:O	1:B:320:MET:HE2	2.19	0.42
1:B:254:VAL:CG2	1:B:288:ARG:NH2	2.82	0.42
1:C:54:GLU:HB2	1:C:105:ARG:CD	2.50	0.42
1:C:126:GLU:HG3	1:C:162:ILE:HG22	2.02	0.42
1:J:49:ILE:HG22	1:J:50:GLN:O	2.20	0.42
1:J:230:VAL:HG23	1:J:389:ALA:HA	2.02	0.42
1:J:241:VAL:O	1:J:245:ILE:HG12	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:218:THR:HG23	1:K:219:PHE:CD2	2.54	0.42
1:K:262:ARG:NH2	2:N:350:ARG:NH1	2.67	0.42
2:L:156:PRO:HG3	2:L:334:TYR:CE1	2.55	0.42
2:M:325:GLY:HA3	2:M:348:LEU:O	2.20	0.42
2:N:193:PHE:O	2:N:197:ASP:HB2	2.19	0.42
1:A:449:LEU:O	1:A:450:GLN:HB2	2.20	0.41
1:B:473:ILE:O	1:B:477:VAL:HG22	2.19	0.41
1:C:135:ILE:HA	1:C:135:ILE:HD13	1.62	0.41
2:D:155:LEU:HD21	2:D:331:ARG:HG2	2.01	0.41
2:F:210:PHE:CD2	2:F:228:ALA:HA	2.54	0.41
1:I:262:ARG:HD3	1:I:265:GLU:OE1	2.20	0.41
1:K:167:PHE:HD2	1:K:173:ILE:HG22	1.85	0.41
1:K:247:LYS:HD2	1:K:276:LEU:CD1	2.50	0.41
1:K:500:TYR:C	1:K:501:LEU:HD23	2.45	0.41
2:L:21:VAL:CG2	2:L:24:VAL:HG21	2.49	0.41
2:L:148:PRO:HG3	2:L:323:THR:OG1	2.19	0.41
2:N:130:THR:CB	2:N:135:ILE:HB	2.49	0.41
2:N:328:ILE:HB	2:N:346:PRO:HG2	2.02	0.41
1:A:52:TYR:CD2	1:A:299:PRO:HB3	2.55	0.41
1:A:255:VAL:N	1:A:325:ALA:O	2.41	0.41
1:B:114:HIS:HA	1:B:169:ILE:HG12	2.01	0.41
1:C:79:ILE:HG13	1:C:84:PHE:CZ	2.55	0.41
2:D:182:ALA:HB2	2:D:228:ALA:HB2	2.02	0.41
2:D:279:THR:O	2:D:283:THR:OG1	2.37	0.41
2:E:91:ASP:OD1	2:E:94:GLY:N	2.53	0.41
2:E:163:GLN:NE2	2:E:416:GLY:O	2.46	0.41
2:E:328:ILE:HG13	2:E:346:PRO:HB2	2.01	0.41
2:E:422:THR:OG1	2:E:425:GLU:HG3	2.19	0.41
1:I:39:ILE:CG2	1:I:47:ALA:HB1	2.49	0.41
1:I:499:ASP:OD2	1:I:525:ILE:HG12	2.20	0.41
1:K:56:SER:HB2	2:N:27:GLU:HG3	2.02	0.41
1:K:206:ASP:HB2	1:K:440:GLU:CD	2.44	0.41
1:K:232:GLY:N	1:K:238:LYS:HD3	2.33	0.41
1:K:488:LEU:O	1:K:492:VAL:HG23	2.20	0.41
2:M:345:LEU:HG	2:M:373:PHE:HE2	1.85	0.41
2:N:326:GLN:HE21	2:N:326:GLN:HB2	1.56	0.41
1:A:251:VAL:O	1:A:288:ARG:NH2	2.53	0.41
1:B:211:THR:HB	1:B:245:ILE:HD12	2.03	0.41
1:C:6:ILE:HA	1:C:16:ALA:HA	2.03	0.41
1:C:15:MET:HA	1:C:47:ALA:O	2.20	0.41
1:C:120:PHE:HE2	1:C:137:GLY:HA3	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:82:SER:HB2	2:D:104:LEU:CB	2.50	0.41
2:D:88:ARG:NH1	2:D:102:GLU:CB	2.83	0.41
2:E:132:ILE:H	2:E:132:ILE:CD1	2.30	0.41
2:F:386:ALA:O	2:F:390:GLY:N	2.53	0.41
1:I:221:PRO:O	1:I:437:TYR:HB2	2.20	0.41
1:J:191:TRP:CD2	1:J:192:PRO:HD2	2.55	0.41
1:J:197:ARG:HH11	1:J:316:TYR:HA	1.84	0.41
1:J:262:ARG:NH2	2:M:350:ARG:NH1	2.67	0.41
1:J:304:GLU:HG3	1:J:334:TRP:NE1	2.35	0.41
1:K:215:VAL:HG22	1:K:426:PRO:HG2	2.02	0.41
2:L:147:LEU:O	2:L:301:ILE:HG23	2.20	0.41
2:N:40:ARG:HG3	2:N:58:GLU:OE1	2.20	0.41
1:B:84:PHE:HB3	1:B:88:GLN:C	2.45	0.41
1:B:214:ARG:NH2	1:B:510:ASP:OD1	2.53	0.41
1:B:233:PRO:HG3	1:B:417:SER:CB	2.47	0.41
1:C:191:TRP:CD2	1:C:192:PRO:HD2	2.56	0.41
1:C:348:MET:CG	2:D:265:ARG:HA	2.47	0.41
1:C:560:LYS:H	1:C:560:LYS:HG3	1.58	0.41
2:D:34:MET:CG	2:D:63:ILE:HG13	2.51	0.41
2:D:206:ARG:O	2:D:206:ARG:HG2	2.21	0.41
2:F:332:GLU:HA	2:F:335:LYS:HG2	2.02	0.41
1:I:36:ILE:H	1:I:36:ILE:HD12	1.84	0.41
1:I:167:PHE:HB2	6:I:601:HOH:O	2.20	0.41
1:I:262:ARG:O	1:I:266:MET:N	2.38	0.41
1:J:573:ILE:O	1:J:577:ILE:HG13	2.21	0.41
1:K:75:LEU:H	1:K:188:MET:HE3	1.85	0.41
1:K:415:LEU:HD21	1:K:428:ILE:HG12	2.02	0.41
1:K:494:LYS:HA	1:K:497:ARG:HD3	2.01	0.41
2:M:60:THR:HA	2:M:63:ILE:CD1	2.50	0.41
2:M:273:TYR:HA	2:M:274:PRO:HD3	1.89	0.41
2:N:218:ALA:HA	2:N:221:ARG:HG3	2.01	0.41
2:N:307:PRO:HB2	2:N:313:HIS:CD2	2.55	0.41
2:N:343:ASP:O	2:N:346:PRO:HD2	2.20	0.41
1:A:243:HIS:O	1:A:247:LYS:HG2	2.19	0.41
1:A:301:ALA:O	1:A:305:ALA:N	2.43	0.41
1:B:72:SER:HA	1:B:193:VAL:HG13	2.03	0.41
1:B:75:LEU:O	1:B:188:MET:HA	2.20	0.41
1:B:266:MET:CE	1:B:291:LEU:HD21	2.48	0.41
2:D:248:THR:HA	2:D:249:ASP:HA	1.73	0.41
2:E:191:ALA:O	2:E:195:MET:HG3	2.19	0.41
2:F:30:ILE:HG13	2:F:42:GLY:C	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:151:SER:HB2	2:F:157:HIS:HB3	2.02	0.41
1:I:231:PRO:HD2	1:I:414:GLY:HA2	2.03	0.41
1:I:437:TYR:OH	2:M:189:GLU:OE1	2.37	0.41
1:I:504:ASN:OD1	1:I:506:PHE:HB2	2.20	0.41
1:J:220:PHE:CZ	1:J:433:SER:HB2	2.55	0.41
1:J:424:HIS:O	1:J:427:SER:HB3	2.21	0.41
1:K:214:ARG:HH21	1:K:503:GLN:HG3	1.86	0.41
1:K:273:PHE:HB2	1:K:274:PRO:HD3	2.01	0.41
2:L:225:PRO:O	2:L:229:LEU:HG	2.20	0.41
2:M:148:PRO:HA	2:M:302:PRO:HG2	2.03	0.41
2:M:335:LYS:HE2	2:M:335:LYS:HB3	1.89	0.41
2:N:29:LEU:HD23	2:N:73:LEU:HD23	2.01	0.41
2:N:89:VAL:HG22	2:N:209:MET:CB	2.50	0.41
1:A:219:PHE:CE2	1:A:501:LEU:CD2	3.03	0.41
1:A:449:LEU:C	1:A:451:GLN:H	2.27	0.41
1:B:116:LYS:HG2	1:B:118:TRP:NE1	2.35	0.41
1:C:202:LYS:HG3	1:C:372:VAL:CG1	2.38	0.41
1:C:311:ILE:HB	1:C:365:TYR:HE1	1.85	0.41
1:C:318:ARG:NH2	1:C:319:ASP:OD1	2.39	0.41
2:E:213:LEU:HB2	2:E:216:ASP:OD1	2.20	0.41
2:F:42:GLY:HA2	2:F:57:PHE:CE2	2.56	0.41
2:F:264:ARG:HD2	2:F:266:GLU:OE2	2.21	0.41
2:F:442:LEU:HD23	2:F:442:LEU:N	2.35	0.41
1:J:114:HIS:HA	1:J:169:ILE:HG12	2.03	0.41
1:J:144:ILE:HG13	1:J:145:ILE:N	2.36	0.41
1:J:296:SER:CA	1:J:303:ARG:HH21	2.28	0.41
1:J:523:LYS:HA	1:J:526:LEU:HD12	2.03	0.41
1:J:562:ILE:HB	1:J:570:ILE:HD11	2.02	0.41
1:K:188:MET:C	1:K:188:MET:HE2	2.45	0.41
1:K:214:ARG:HH11	1:K:521:MET:HE1	1.77	0.41
1:K:225:GLY:C	1:K:370:GLY:HA2	2.45	0.41
2:L:309:ASP:CG	2:L:331:ARG:HE	2.28	0.41
2:M:411:GLU:OE1	2:M:411:GLU:N	2.53	0.41
1:A:219:PHE:CE2	1:A:501:LEU:HD21	2.56	0.41
1:A:246:ALA:HB1	1:A:254:VAL:HG11	2.01	0.41
1:B:56:SER:N	2:E:26:TYR:HD2	2.19	0.41
1:B:167:PHE:CE2	1:B:173:ILE:HG21	2.56	0.41
1:B:273:PHE:N	1:B:274:PRO:CD	2.83	0.41
1:C:242:GLN:HG2	1:C:327:MET:HE3	2.03	0.41
1:C:265:GLU:O	1:C:269:VAL:HG23	2.21	0.41
1:C:534:LYS:O	1:C:538:LEU:HG	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:151:SER:OG	2:D:155:LEU:HB2	2.20	0.41
2:E:73:LEU:HD13	2:E:75:HIS:ND1	2.36	0.41
2:E:82:SER:HB2	2:E:103:ILE:HD11	2.02	0.41
2:E:122:ASP:N	2:E:290:ARG:O	2.39	0.41
2:E:166:ARG:HD3	2:E:197:ASP:OD2	2.19	0.41
2:F:431:TRP:CH2	2:F:445:ILE:HG21	2.56	0.41
1:J:574:ASN:OD1	1:J:574:ASN:N	2.54	0.41
1:K:211:THR:O	1:K:245:ILE:HD13	2.20	0.41
1:K:225:GLY:HA2	1:K:384:ILE:O	2.21	0.41
1:K:233:PRO:CD	1:K:415:LEU:HB2	2.48	0.41
1:K:311:ILE:HB	1:K:365:TYR:CE1	2.54	0.41
1:K:315:GLU:HA	1:K:384:ILE:HD11	2.02	0.41
1:B:6:ILE:O	1:B:60:PRO:HA	2.20	0.41
1:B:513:THR:HG22	1:B:518:GLN:HG2	2.02	0.41
1:C:88:GLN:OE1	1:C:111:ALA:HB1	2.20	0.41
1:C:238:LYS:HE2	1:C:238:LYS:HB2	1.92	0.41
1:C:278:ASP:O	1:C:281:THR:OG1	2.26	0.41
1:C:541:TYR:HB2	1:C:544:GLU:HG3	2.01	0.41
2:D:21:VAL:HB	2:D:24:VAL:CG2	2.51	0.41
2:D:87:GLY:HA2	2:D:204:ILE:O	2.21	0.41
2:D:128:ILE:HD11	2:D:143:ARG:CA	2.40	0.41
2:D:177:PHE:CE2	2:D:242:HIS:HB3	2.56	0.41
2:E:244:LEU:HD12	2:E:299:THR:HB	2.02	0.41
2:F:141:LEU:HD12	2:F:147:LEU:HB2	2.03	0.41
2:F:313:HIS:HA	2:F:314:PRO:HD3	1.93	0.41
2:F:339:GLN:O	2:F:414:ASN:HB3	2.20	0.41
1:I:11:GLY:HA2	1:I:55:THR:OG1	2.21	0.41
1:I:94:PHE:HA	1:I:109:LEU:HD12	2.02	0.41
1:I:311:ILE:O	1:I:315:GLU:HG3	2.21	0.41
1:I:412:PHE:HB2	1:I:434:TYR:CE2	2.55	0.41
1:K:6:ILE:HG12	1:K:64:VAL:HG23	2.02	0.41
1:K:196:GLY:HA2	1:K:368:ARG:NH2	2.36	0.41
1:K:219:PHE:CE1	1:K:457:VAL:HG13	2.56	0.41
1:K:219:PHE:CE1	1:K:461:MET:HG2	2.56	0.41
2:M:16:MET:CE	2:M:32:VAL:HG21	2.45	0.41
2:M:151:SER:OG	2:M:157:HIS:HB3	2.21	0.41
2:N:111:ILE:HB	2:N:226:ARG:HB3	2.02	0.41
1:A:176:ILE:N	1:A:183:LYS:O	2.50	0.41
1:A:425:PHE:N	1:A:425:PHE:HD1	2.18	0.41
1:B:500:TYR:HD2	1:B:500:TYR:HA	1.69	0.41
1:C:27:MET:CE	1:C:38:GLU:HB2	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:39:ILE:HG13	1:C:49:ILE:HG23	2.03	0.41
4:C:601:ANP:HNB1	2:F:350:ARG:NH1	2.17	0.41
2:D:34:MET:HE1	2:D:40:ARG:CG	2.51	0.41
2:D:124:PRO:HB3	2:D:143:ARG:O	2.20	0.41
2:D:281:LEU:HD23	2:D:281:LEU:HA	1.97	0.41
2:E:256:ALA:O	2:E:260:ILE:HG12	2.20	0.41
2:E:339:GLN:HB3	2:E:417:PHE:CE1	2.56	0.41
2:E:345:LEU:N	2:E:346:PRO:HD2	2.36	0.41
2:E:431:TRP:HZ3	2:E:450:LEU:HD23	1.86	0.41
2:F:183:ALA:HB1	2:F:186:ILE:CD1	2.49	0.41
2:F:389:LEU:CB	2:F:393:ALA:HB3	2.50	0.41
2:F:450:LEU:H	2:F:450:LEU:HG	1.61	0.41
1:I:85:ASP:C	1:I:87:ILE:H	2.27	0.41
1:I:126:GLU:HG2	1:I:162:ILE:HG22	2.03	0.41
1:I:152:PRO:HG3	6:I:602:HOH:O	2.20	0.41
1:J:237:GLY:O	1:J:241:VAL:HG23	2.21	0.41
1:J:268:ASP:HB2	2:M:123:TYR:CE1	2.56	0.41
1:J:270:VAL:O	1:J:274:PRO:HG2	2.21	0.41
1:J:373:ILE:HD13	1:J:381:GLU:CG	2.51	0.41
1:K:1:MET:HB3	1:K:2:GLN:H	1.65	0.41
1:K:24:ILE:HG23	1:K:40:ILE:O	2.21	0.41
1:K:29:LEU:CD1	1:K:65:ARG:HH21	2.34	0.41
1:K:285:LEU:HD12	1:K:285:LEU:C	2.46	0.41
2:L:170:VAL:HG13	2:L:173:SER:HB3	2.03	0.41
2:L:183:ALA:O	2:L:212:ASN:HB2	2.20	0.41
2:M:65:LEU:H	2:M:65:LEU:CD1	2.25	0.41
2:M:117:ASN:HB3	2:M:120:ALA:HB3	2.02	0.41
2:M:345:LEU:N	2:M:346:PRO:HD2	2.36	0.41
2:N:34:MET:HE1	2:N:63:ILE:CG1	2.50	0.41
2:N:128:ILE:HD11	2:N:143:ARG:CA	2.50	0.41
2:N:265:ARG:HB2	2:N:265:ARG:HH11	1.85	0.41
2:N:319:THR:HG22	2:N:323:THR:CG2	2.51	0.41
2:N:427:LEU:HA	2:N:427:LEU:HD22	1.82	0.41
1:A:10:SER:CB	2:D:46:GLU:HB2	2.50	0.41
1:A:236:ALA:HB1	1:A:415:LEU:HB3	2.02	0.41
1:A:339:ARG:HD3	2:D:270:ARG:HH12	1.86	0.41
1:B:44:GLN:HG3	2:F:9:LYS:O	2.21	0.41
1:C:401:VAL:O	1:C:405:THR:N	2.47	0.41
1:C:541:TYR:O	1:C:545:ILE:HG13	2.21	0.41
2:D:26:TYR:HE1	2:D:45:LEU:HA	1.86	0.41
2:E:24:VAL:O	2:E:25:LYS:HD3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:177:GLU:CD	1:I:182:LEU:HG	2.45	0.41
1:J:21:GLU:CD	1:J:21:GLU:H	2.29	0.41
1:J:152:PRO:HA	1:J:153:ASN:HA	1.37	0.41
1:K:318:ARG:CD	1:K:384:ILE:HG13	2.48	0.41
2:L:180:VAL:O	2:L:245:VAL:HG13	2.21	0.41
2:L:180:VAL:HG13	2:L:208:VAL:HB	2.02	0.41
2:M:16:MET:O	2:M:54:VAL:N	2.34	0.41
2:M:234:TYR:CD1	2:M:238:GLU:HG3	2.56	0.41
2:N:188:PHE:O	2:N:192:GLU:HB2	2.21	0.41
1:A:230:VAL:HG22	1:A:413:TRP:HE3	1.85	0.40
4:C:601:ANP:H8	4:C:601:ANP:O5'	2.20	0.40
2:D:158:LYS:HG3	2:D:194:PHE:CZ	2.56	0.40
2:D:403:LYS:HA	2:D:403:LYS:HD2	1.94	0.40
2:E:315:ILE:H	2:E:315:ILE:HG13	1.63	0.40
2:E:434:LEU:HD22	2:E:442:LEU:CD2	2.51	0.40
2:F:151:SER:CA	2:F:329:LEU:HD12	2.47	0.40
1:I:227:ALA:HB3	1:I:409:VAL:HG12	2.03	0.40
1:I:324:VAL:O	1:I:385:THR:N	2.33	0.40
1:J:214:ARG:HD3	1:J:513:THR:HG21	2.02	0.40
1:J:406:LEU:CD2	1:J:412:PHE:HB2	2.51	0.40
1:J:520:ASN:O	1:J:524:VAL:HG23	2.21	0.40
1:K:315:GLU:CD	1:K:368:ARG:HH21	2.27	0.40
2:L:116:ILE:HG21	2:L:291:ILE:HD12	2.02	0.40
2:L:156:PRO:HD3	2:L:334:TYR:CD1	2.56	0.40
2:L:281:LEU:HD23	2:L:281:LEU:HA	1.90	0.40
2:N:32:VAL:HG21	2:N:56:ILE:CD1	2.51	0.40
1:A:85:ASP:OD2	1:A:87:ILE:HG13	2.22	0.40
1:A:294:ASN:HB3	1:A:298:MET:HG3	2.04	0.40
1:A:354:TYR:HB3	1:A:358:LEU:HD22	2.04	0.40
1:B:497:ARG:CA	1:B:501:LEU:HD13	2.52	0.40
1:C:4:GLY:O	1:C:64:VAL:N	2.53	0.40
1:C:205:PRO:HB3	1:C:371:ARG:CB	2.52	0.40
1:C:507:ASP:OD2	1:C:510:ASP:N	2.54	0.40
2:D:44:VAL:HG13	2:D:53:MET:O	2.21	0.40
2:D:147:LEU:HA	2:D:148:PRO:HD3	1.83	0.40
2:E:117:ASN:HA	2:E:118:PRO:HD3	1.98	0.40
2:E:338:ILE:HG23	2:E:414:ASN:OD1	2.19	0.40
2:F:159:GLU:HG3	2:F:193:PHE:CZ	2.56	0.40
1:I:73:VAL:HG11	1:I:309:THR:HG23	2.02	0.40
1:J:449:LEU:C	1:J:451:GLN:H	2.29	0.40
1:K:38:GLU:OE2	1:K:52:TYR:OH	2.34	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:363:ALA:O	1:K:367:GLU:HB2	2.20	0.40
1:K:479:ILE:HG21	2:N:394:LEU:HA	2.03	0.40
1:K:500:TYR:CE2	1:K:522:LEU:HD13	2.56	0.40
2:N:49:GLU:HA	2:N:50:ASP:HA	1.67	0.40
2:N:150:PHE:N	2:N:150:PHE:CD1	2.90	0.40
2:N:184:ILE:HD12	2:N:184:ILE:N	2.37	0.40
2:N:267:VAL:HA	2:N:268:PRO:HD3	1.95	0.40
1:A:80:ILE:HA	1:A:290:VAL:HG22	2.03	0.40
1:A:88:GLN:HG2	1:A:88:GLN:O	2.21	0.40
1:A:112:LEU:HD12	1:A:188:MET:HG2	2.03	0.40
1:A:459:GLU:OE2	1:A:462:ARG:NH2	2.46	0.40
1:B:79:ILE:HG13	1:B:112:LEU:HD21	2.03	0.40
1:B:221:PRO:CG	1:B:441:VAL:HG21	2.51	0.40
2:D:345:LEU:HA	2:D:373:PHE:CE1	2.56	0.40
2:E:146:LYS:HE2	2:E:324:GLU:HG2	2.03	0.40
2:F:339:GLN:HB3	2:F:340:PRO:HA	2.03	0.40
1:I:76:GLY:H	1:I:112:LEU:CD1	2.34	0.40
1:I:122:ALA:HB1	1:I:162:ILE:HD11	2.03	0.40
1:I:449:LEU:O	1:I:450:GLN:HB2	2.20	0.40
1:J:123:THR:HG22	1:J:136:ILE:C	2.46	0.40
1:K:351:ASP:OD2	2:L:258:ARG:NH2	2.54	0.40
2:M:130:THR:CB	2:M:135:ILE:HB	2.52	0.40
2:N:44:VAL:HG22	2:N:54:VAL:HG12	1.93	0.40
2:N:160:LEU:O	2:N:164:ILE:HG13	2.21	0.40
2:N:318:LEU:HD23	2:N:318:LEU:HA	1.93	0.40
1:A:259:CYS:HA	1:A:260:GLY:HA2	1.76	0.40
1:B:208:PRO:HD2	1:B:444:TYR:CD2	2.56	0.40
1:B:262:ARG:NH2	4:B:601:ANP:O3G	2.39	0.40
1:C:36:ILE:CD1	1:C:87:ILE:HG23	2.52	0.40
1:C:351:ASP:O	1:C:352:GLU:HB2	2.20	0.40
2:D:307:PRO:HG2	2:D:313:HIS:CE1	2.57	0.40
2:D:313:HIS:O	2:D:317:ASP:HB2	2.21	0.40
2:D:343:ASP:HB3	2:D:346:PRO:CG	2.52	0.40
1:I:244:GLN:OE1	1:I:248:TRP:NE1	2.38	0.40
1:J:58:ILE:HG23	1:J:62:GLU:HG3	2.02	0.40
1:J:84:PHE:O	1:J:292:ILE:HA	2.21	0.40
1:K:73:VAL:HG13	1:K:193:VAL:HG12	2.04	0.40
2:N:158:LYS:HB2	2:N:158:LYS:HE3	1.80	0.40
2:N:354:LYS:HD3	2:N:354:LYS:HA	1.84	0.40
1:B:79:ILE:HB	1:B:112:LEU:HD13	2.04	0.40
1:B:482:LEU:HD23	1:B:486:ASP:HB3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:533:ARG:HD2	1:C:536:LEU:HD11	2.02	0.40
2:D:225:PRO:CB	2:D:284:LEU:HD13	2.52	0.40
2:D:340:PRO:HA	2:D:341:PRO:HD3	1.87	0.40
2:D:351:LEU:HB3	2:D:354:LYS:HD2	2.02	0.40
2:D:362:ARG:O	2:D:365:HIS:HB2	2.20	0.40
2:E:34:MET:N	2:E:38:GLU:O	2.41	0.40
2:E:155:LEU:O	2:E:157:HIS:ND1	2.54	0.40
2:F:143:ARG:CZ	2:F:170:VAL:HG21	2.51	0.40
2:F:285:PHE:HB2	2:F:322:ILE:CG2	2.52	0.40
1:I:113:ASP:OD2	1:I:116:LYS:N	2.51	0.40
1:J:233:PRO:HD3	1:J:415:LEU:O	2.21	0.40
1:J:358:LEU:O	1:J:362:LEU:HG	2.20	0.40
1:K:125:GLU:O	1:K:128:THR:OG1	2.39	0.40
1:K:232:GLY:H	1:K:238:LYS:CD	2.34	0.40
2:L:362:ARG:O	2:L:365:HIS:HB3	2.21	0.40
2:N:347:SER:H	2:N:348:LEU:HA	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	582/600 (97%)	579 (100%)	3 (0%)	0	100	100
1	B	582/600 (97%)	570 (98%)	12 (2%)	0	100	100
1	C	582/600 (97%)	569 (98%)	13 (2%)	0	100	100
1	I	579/600 (96%)	570 (98%)	9 (2%)	0	100	100
1	J	582/600 (97%)	572 (98%)	10 (2%)	0	100	100
1	K	582/600 (97%)	572 (98%)	10 (2%)	0	100	100
2	D	443/465 (95%)	441 (100%)	1 (0%)	1 (0%)	43	70

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	451/465 (97%)	447 (99%)	4 (1%)	0	100	100
2	F	443/465 (95%)	438 (99%)	5 (1%)	0	100	100
2	L	443/465 (95%)	435 (98%)	8 (2%)	0	100	100
2	M	451/465 (97%)	441 (98%)	10 (2%)	0	100	100
2	N	427/465 (92%)	411 (96%)	16 (4%)	0	100	100
All	All	6147/6390 (96%)	6045 (98%)	101 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	105	PRO

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	471/511 (92%)	425 (90%)	46 (10%)	7	27
1	B	465/511 (91%)	410 (88%)	55 (12%)	5	20
1	C	420/511 (82%)	373 (89%)	47 (11%)	6	21
1	I	430/511 (84%)	389 (90%)	41 (10%)	8	29
1	J	461/511 (90%)	415 (90%)	46 (10%)	7	26
1	K	467/511 (91%)	422 (90%)	45 (10%)	8	28
2	D	337/387 (87%)	291 (86%)	46 (14%)	3	15
2	E	329/387 (85%)	294 (89%)	35 (11%)	6	23
2	F	317/387 (82%)	275 (87%)	42 (13%)	4	16
2	L	354/387 (92%)	308 (87%)	46 (13%)	4	16
2	M	323/387 (84%)	274 (85%)	49 (15%)	3	11
2	N	300/387 (78%)	251 (84%)	49 (16%)	2	10
All	All	4674/5388 (87%)	4127 (88%)	547 (12%)	5	20

All (547) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	MET
1	A	32	ASP
1	A	46	VAL
1	A	52	TYR
1	A	65	ARG
1	A	67	THR
1	A	80	ILE
1	A	83	MET
1	A	87	ILE
1	A	89	ARG
1	A	98	THR
1	A	105	ARG
1	A	109	LEU
1	A	128	THR
1	A	129	GLU
1	A	161	LYS
1	A	171	ASP
1	A	178	THR
1	A	179	GLU
1	A	185	LEU
1	A	186	THR
1	A	247	LYS
1	A	253	LEU
1	A	264	ASN
1	A	265	GLU
1	A	268	ASP
1	A	304	GLU
1	A	331	THR
1	A	338	LEU
1	A	352	GLU
1	A	378	ASP
1	A	396	ASP
1	A	399	GLU
1	A	416	ASP
1	A	439	THR
1	A	448	ILE
1	A	449	LEU
1	A	451	GLN
1	A	458	THR
1	A	477	VAL
1	A	514	SER
1	A	523	LYS

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Mol	Chain	Res	Type
1	A	530	LYS
1	A	541	TYR
1	A	549	THR
1	A	552	VAL
1	B	3	ILE
1	B	8	LYS
1	B	19	MET
1	B	21	GLU
1	B	25	GLN
1	B	38	GLU
1	B	42	MET
1	B	54	GLU
1	B	67	THR
1	B	72	SER
1	B	80	ILE
1	B	88	GLN
1	B	139	VAL
1	B	140	ASP
1	B	141	GLU
1	B	143	LYS
1	B	147	HIS
1	B	148	LYS
1	B	150	MET
1	B	173	ILE
1	B	179	GLU
1	B	183	LYS
1	B	185	LEU
1	B	190	LYS
1	B	214	ARG
1	B	216	ILE
1	B	238	LYS
1	B	252	ASP
1	B	253	LEU
1	B	285	LEU
1	B	288	ARG
1	B	291	LEU
1	B	295	THR
1	B	297	ASN
1	B	300	VAL
1	B	319	ASP
1	B	326	ILE
1	B	327	MET

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Mol	Chain	Res	Type
1	B	378	ASP
1	B	385	THR
1	B	415	LEU
1	B	424	HIS
1	B	443	ARG
1	B	448	ILE
1	B	458	THR
1	B	476	LEU
1	B	489	THR
1	B	498	GLU
1	B	499	ASP
1	B	500	TYR
1	B	501	LEU
1	B	503	GLN
1	B	508	ASP
1	B	536	LEU
1	B	567	LEU
1	C	7	ILE
1	C	13	LEU
1	C	15	MET
1	C	25	GLN
1	C	27	MET
1	C	39	ILE
1	C	40	ILE
1	C	53	GLU
1	C	82	GLN
1	C	87	ILE
1	C	88	GLN
1	C	89	ARG
1	C	124	ILE
1	C	128	THR
1	C	135	ILE
1	C	143	LYS
1	C	150	MET
1	C	163	GLU
1	C	167	PHE
1	C	173	ILE
1	C	185	LEU
1	C	199	ILE
1	C	203	LEU
1	C	218	THR
1	C	224	LYS

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Mol	Chain	Res	Type
1	C	234	PHE
1	C	252	ASP
1	C	253	LEU
1	C	259	CYS
1	C	273	PHE
1	C	276	LEU
1	C	291	LEU
1	C	297	ASN
1	C	331	THR
1	C	332	SER
1	C	333	ARG
1	C	378	ASP
1	C	390	VAL
1	C	399	GLU
1	C	401	VAL
1	C	500	TYR
1	C	536	LEU
1	C	547	GLU
1	C	554	GLU
1	C	560	LYS
1	C	576	GLU
1	C	580	THR
2	D	5	TYR
2	D	11	VAL
2	D	24	VAL
2	D	34	MET
2	D	38	GLU
2	D	43	GLN
2	D	45	LEU
2	D	49	GLU
2	D	51	LYS
2	D	54	VAL
2	D	63	ILE
2	D	65	LEU
2	D	69	SER
2	D	73	LEU
2	D	77	LEU
2	D	86	ILE
2	D	97	LYS
2	D	138	LEU
2	D	140	THR
2	D	142	VAL

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Mol	Chain	Res	Type
2	D	143	ARG
2	D	157	HIS
2	D	163	GLN
2	D	176	ASP
2	D	177	PHE
2	D	239	LYS
2	D	279	THR
2	D	280	ASN
2	D	283	THR
2	D	287	ARG
2	D	324	GLU
2	D	330	THR
2	D	332	GLU
2	D	335	LYS
2	D	339	GLN
2	D	343	ASP
2	D	345	LEU
2	D	348	LEU
2	D	360	LYS
2	D	362	ARG
2	D	370	ASN
2	D	401	TYR
2	D	414	ASN
2	D	415	GLN
2	D	432	GLU
2	D	442	LEU
2	E	6	ARG
2	E	33	ARG
2	E	43	GLN
2	E	45	LEU
2	E	73	LEU
2	E	77	LEU
2	E	79	LEU
2	E	82	SER
2	E	84	ASP
2	E	86	ILE
2	E	95	ARG
2	E	103	ILE
2	E	104	LEU
2	E	109	LEU
2	E	129	GLN
2	E	153	SER

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Mol	Chain	Res	Type
2	E	158	LYS
2	E	167	GLN
2	E	170	VAL
2	E	187	THR
2	E	212	ASN
2	E	215	ASN
2	E	230	THR
2	E	271	ARG
2	E	284	LEU
2	E	290	ARG
2	E	295	LYS
2	E	306	MET
2	E	339	GLN
2	E	342	ILE
2	E	419	THR
2	E	421	ARG
2	E	434	LEU
2	E	443	LYS
2	E	444	ARG
2	F	9	LYS
2	F	31	GLU
2	F	44	VAL
2	F	45	LEU
2	F	50	ASP
2	F	60	THR
2	F	61	SER
2	F	65	LEU
2	F	71	ARG
2	F	73	LEU
2	F	86	ILE
2	F	97	LYS
2	F	133	SER
2	F	136	ASP
2	F	142	VAL
2	F	147	LEU
2	F	171	LEU
2	F	187	THR
2	F	190	GLU
2	F	192	GLU
2	F	207	SER
2	F	208	VAL
2	F	213	LEU

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Mol	Chain	Res	Type
2	F	215	ASN
2	F	220	GLU
2	F	257	LEU
2	F	292	ARG
2	F	305	THR
2	F	308	GLU
2	F	330	THR
2	F	332	GLU
2	F	338	ILE
2	F	339	GLN
2	F	348	LEU
2	F	427	LEU
2	F	429	LEU
2	F	433	LEU
2	F	434	LEU
2	F	437	LEU
2	F	442	LEU
2	F	445	ILE
2	F	450	LEU
1	I	13	LEU
1	I	14	VAL
1	I	46	VAL
1	I	64	VAL
1	I	65	ARG
1	I	80	ILE
1	I	81	SER
1	I	94	PHE
1	I	103	LEU
1	I	115	GLU
1	I	124	ILE
1	I	128	THR
1	I	130	VAL
1	I	131	SER
1	I	143	LYS
1	I	167	PHE
1	I	185	LEU
1	I	186	THR
1	I	201	GLN
1	I	209	MET
1	I	244	GLN
1	I	259	CYS
1	I	272	GLU

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Mol	Chain	Res	Type
1	I	298	MET
1	I	331	THR
1	I	338	LEU
1	I	385	THR
1	I	417	SER
1	I	424	HIS
1	I	452	ASP
1	I	454	SER
1	I	461	MET
1	I	464	LEU
1	I	475	ARG
1	I	477	VAL
1	I	495	SER
1	I	501	LEU
1	I	502	GLN
1	I	525	ILE
1	I	527	THR
1	I	554	GLU
1	J	1	MET
1	J	7	ILE
1	J	13	LEU
1	J	36	ILE
1	J	53	GLU
1	J	83	MET
1	J	85	ASP
1	J	87	ILE
1	J	88	GLN
1	J	98	THR
1	J	148	LYS
1	J	149	ILE
1	J	155	ILE
1	J	173	ILE
1	J	174	CYS
1	J	190	LYS
1	J	195	ARG
1	J	215	VAL
1	J	217	ASP
1	J	230	VAL
1	J	238	LYS
1	J	250	ASP
1	J	276	LEU
1	J	289	THR

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Mol	Chain	Res	Type
1	J	294	ASN
1	J	295	THR
1	J	297	ASN
1	J	298	MET
1	J	326	ILE
1	J	327	MET
1	J	351	ASP
1	J	378	ASP
1	J	391	SER
1	J	405	THR
1	J	407	ARG
1	J	415	LEU
1	J	416	ASP
1	J	479	ILE
1	J	500	TYR
1	J	527	THR
1	J	530	LYS
1	J	533	ARG
1	J	536	LEU
1	J	541	TYR
1	J	543	ASN
1	J	544	GLU
1	K	13	LEU
1	K	15	MET
1	K	20	SER
1	K	23	CYS
1	K	25	GLN
1	K	40	ILE
1	K	48	SER
1	K	55	THR
1	K	62	GLU
1	K	65	ARG
1	K	80	ILE
1	K	105	ARG
1	K	128	THR
1	K	150	MET
1	K	158	THR
1	K	161	LYS
1	K	163	GLU
1	K	188	MET
1	K	189	GLN
1	K	211	THR

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Mol	Chain	Res	Type
1	K	216	ILE
1	K	222	VAL
1	K	253	LEU
1	K	259	CYS
1	K	270	VAL
1	K	295	THR
1	K	298	MET
1	K	300	VAL
1	K	346	GLU
1	K	378	ASP
1	K	385	THR
1	K	391	SER
1	K	423	ARG
1	K	466	GLU
1	K	480	ASP
1	K	499	ASP
1	K	500	TYR
1	K	501	LEU
1	K	508	ASP
1	K	524	VAL
1	K	526	LEU
1	K	534	LYS
1	K	538	LEU
1	K	560	LYS
1	K	572	SER
2	L	6	ARG
2	L	10	GLU
2	L	34	MET
2	L	38	GLU
2	L	45	LEU
2	L	48	GLN
2	L	49	GLU
2	L	54	VAL
2	L	55	GLN
2	L	65	LEU
2	L	73	LEU
2	L	86	ILE
2	L	109	LEU
2	L	128	ILE
2	L	130	THR
2	L	151	SER
2	L	153	SER

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Mol	Chain	Res	Type
2	L	177	PHE
2	L	201	THR
2	L	207	SER
2	L	212	ASN
2	L	215	ASN
2	L	219	ILE
2	L	239	LYS
2	L	244	LEU
2	L	257	LEU
2	L	260	ILE
2	L	271	ARG
2	L	279	THR
2	L	283	THR
2	L	287	ARG
2	L	309	ASP
2	L	315	ILE
2	L	350	ARG
2	L	352	LYS
2	L	368	THR
2	L	372	LEU
2	L	378	GLN
2	L	385	LEU
2	L	403	LYS
2	L	412	TYR
2	L	414	ASN
2	L	424	THR
2	L	427	LEU
2	L	433	LEU
2	L	439	ARG
2	M	3	LYS
2	M	10	GLU
2	M	15	LEU
2	M	16	MET
2	M	21	VAL
2	M	24	VAL
2	M	43	GLN
2	M	44	VAL
2	M	45	LEU
2	M	54	VAL
2	M	67	ASN
2	M	73	LEU
2	M	77	LEU

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Mol	Chain	Res	Type
2	M	78	GLN
2	M	83	GLU
2	M	84	ASP
2	M	86	ILE
2	M	93	LEU
2	M	95	ARG
2	M	102	GLU
2	M	103	ILE
2	M	130	THR
2	M	136	ASP
2	M	137	HIS
2	M	146	LYS
2	M	151	SER
2	M	158	LYS
2	M	166	ARG
2	M	170	VAL
2	M	215	ASN
2	M	226	ARG
2	M	230	THR
2	M	251	THR
2	M	270	ARG
2	M	281	LEU
2	M	304	LEU
2	M	305	THR
2	M	306	MET
2	M	319	THR
2	M	339	GLN
2	M	351	LEU
2	M	368	THR
2	M	380	LYS
2	M	381	GLN
2	M	385	LEU
2	M	396	ASP
2	M	444	ARG
2	M	445	ILE
2	M	446	LYS
2	N	4	GLU
2	N	5	TYR
2	N	26	TYR
2	N	31	GLU
2	N	45	LEU
2	N	48	GLN

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Mol	Chain	Res	Type
2	N	51	LYS
2	N	54	VAL
2	N	61	SER
2	N	65	LEU
2	N	67	ASN
2	N	73	LEU
2	N	77	LEU
2	N	85	MET
2	N	98	ASP
2	N	104	LEU
2	N	125	ASP
2	N	126	GLU
2	N	184	ILE
2	N	186	ILE
2	N	187	THR
2	N	192	GLU
2	N	197	ASP
2	N	207	SER
2	N	219	ILE
2	N	221	ARG
2	N	264	ARG
2	N	265	ARG
2	N	270	ARG
2	N	280	ASN
2	N	286	GLU
2	N	305	THR
2	N	319	THR
2	N	326	GLN
2	N	338	ILE
2	N	345	LEU
2	N	349	SER
2	N	352	LYS
2	N	353	ASP
2	N	378	GLN
2	N	381	GLN
2	N	384	GLU
2	N	385	LEU
2	N	392	SER
2	N	403	LYS
2	N	407	ARG
2	N	413	VAL
2	N	421	ARG

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Mol	Chain	Res	Type
2	N	427	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	213	GLN
1	A	264	ASN
1	A	403	GLN
1	B	147	HIS
1	B	503	GLN
1	C	50	GLN
1	C	99	GLN
2	D	157	HIS
2	D	163	GLN
2	D	167	GLN
2	D	215	ASN
2	D	313	HIS
2	D	339	GLN
2	D	370	ASN
2	D	414	ASN
2	E	55	GLN
2	E	112	ASN
2	F	300	GLN
2	F	410	ASN
1	I	101	ASN
1	I	243	HIS
1	I	264	ASN
1	I	424	HIS
1	J	50	GLN
1	J	146	GLN
1	K	117	GLN
1	K	153	ASN
1	K	213	GLN
1	K	294	ASN
2	L	163	GLN
2	L	370	ASN
2	L	414	ASN
2	M	43	GLN
2	M	137	HIS
2	M	280	ASN
2	N	129	GLN
2	N	252	ASN

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Mol	Chain	Res	Type
2	N	365	HIS
2	N	414	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 9 ligands modelled in this entry, 4 are monoatomic - leaving 5 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
4	ANP	B	601	5	33,33,33	0.95	4 (12%)	45,52,52	0.71	1 (2%)
3	GOL	A	601	-	5,5,5	0.37	0	5,5,5	0.17	0
4	ANP	J	601	5	33,33,33	0.97	4 (12%)	45,52,52	0.70	2 (4%)
4	ANP	K	601	5	33,33,33	0.94	4 (12%)	45,52,52	0.59	0
4	ANP	C	601	5	33,33,33	0.93	4 (12%)	45,52,52	0.81	1 (2%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ANP	B	601	5	-	3/18/38/38	0/3/3/3
3	GOL	A	601	-	-	2/4/4/4	-
4	ANP	J	601	5	-	5/18/38/38	0/3/3/3
4	ANP	K	601	5	-	3/18/38/38	0/3/3/3
4	ANP	C	601	5	-	1/18/38/38	0/3/3/3

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	J	601	ANP	PG-N3B	2.75	1.70	1.63
4	C	601	ANP	PG-O1G	2.61	1.50	1.46
4	K	601	ANP	PG-O1G	2.57	1.50	1.46
4	B	601	ANP	PG-O1G	2.54	1.50	1.46
4	B	601	ANP	PB-O3A	-2.52	1.55	1.59
4	C	601	ANP	PG-N3B	2.52	1.69	1.63
4	B	601	ANP	PB-O1B	2.48	1.49	1.46
4	K	601	ANP	PB-O1B	2.46	1.49	1.46
4	K	601	ANP	PB-O3A	-2.45	1.56	1.59
4	J	601	ANP	PB-O3A	-2.45	1.56	1.59
4	B	601	ANP	PG-N3B	2.42	1.69	1.63
4	K	601	ANP	PG-N3B	2.41	1.69	1.63
4	J	601	ANP	PG-O1G	2.35	1.49	1.46
4	J	601	ANP	PB-O1B	2.35	1.49	1.46
4	C	601	ANP	PB-O3A	-2.22	1.56	1.59
4	C	601	ANP	PB-O1B	2.18	1.49	1.46

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	J	601	ANP	O2G-PG-O1G	-2.35	107.55	113.45
4	C	601	ANP	C3'-C2'-C1'	2.23	105.68	101.46
4	J	601	ANP	C3'-C2'-C1'	2.14	105.52	101.46
4	B	601	ANP	C3'-C2'-C1'	2.12	105.48	101.46

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	GOL	C1-C2-C3-O3
3	A	601	GOL	O2-C2-C3-O3
4	B	601	ANP	PB-N3B-PG-O1G

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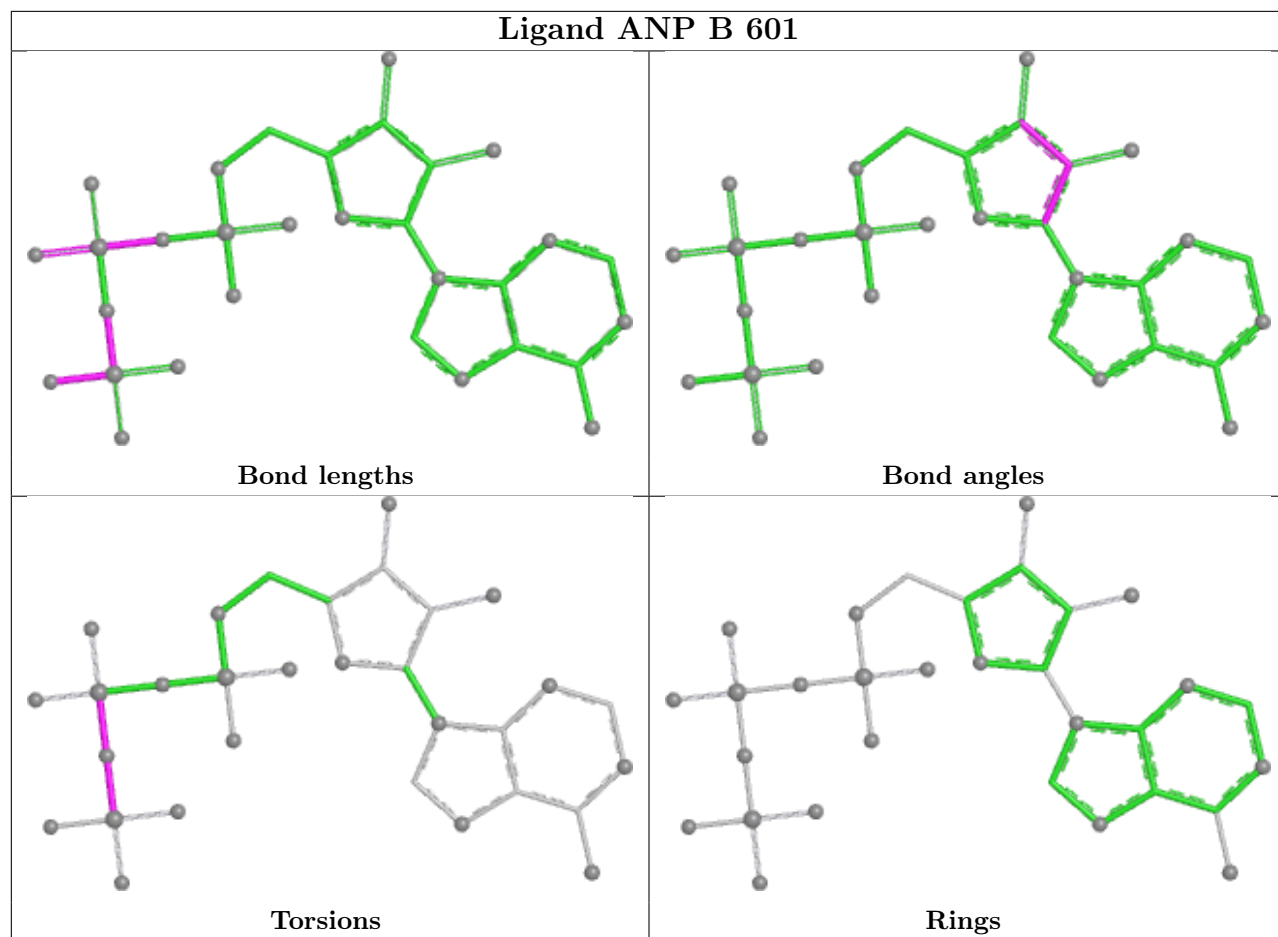
Mol	Chain	Res	Type	Atoms
4	B	601	ANP	PG-N3B-PB-O1B
4	B	601	ANP	PG-N3B-PB-O3A
4	C	601	ANP	PB-N3B-PG-O1G
4	J	601	ANP	PB-N3B-PG-O1G
4	J	601	ANP	C5'-O5'-PA-O3A
4	K	601	ANP	PB-N3B-PG-O1G
4	J	601	ANP	O4'-C4'-C5'-O5'
4	K	601	ANP	O4'-C4'-C5'-O5'
4	J	601	ANP	PG-N3B-PB-O1B
4	K	601	ANP	C3'-C4'-C5'-O5'
4	J	601	ANP	C3'-C4'-C5'-O5'

There are no ring outliers.

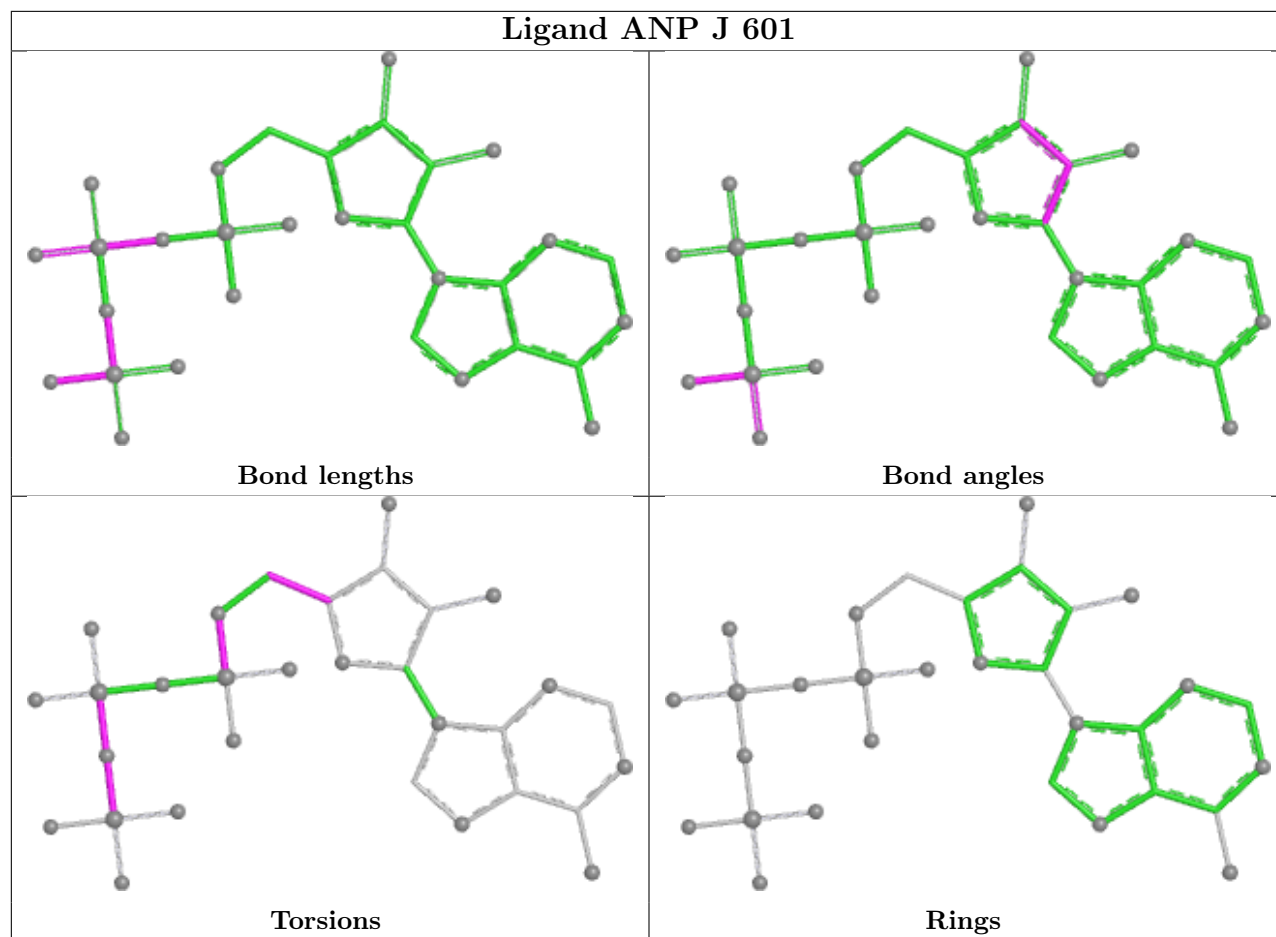
4 monomers are involved in 46 short contacts:

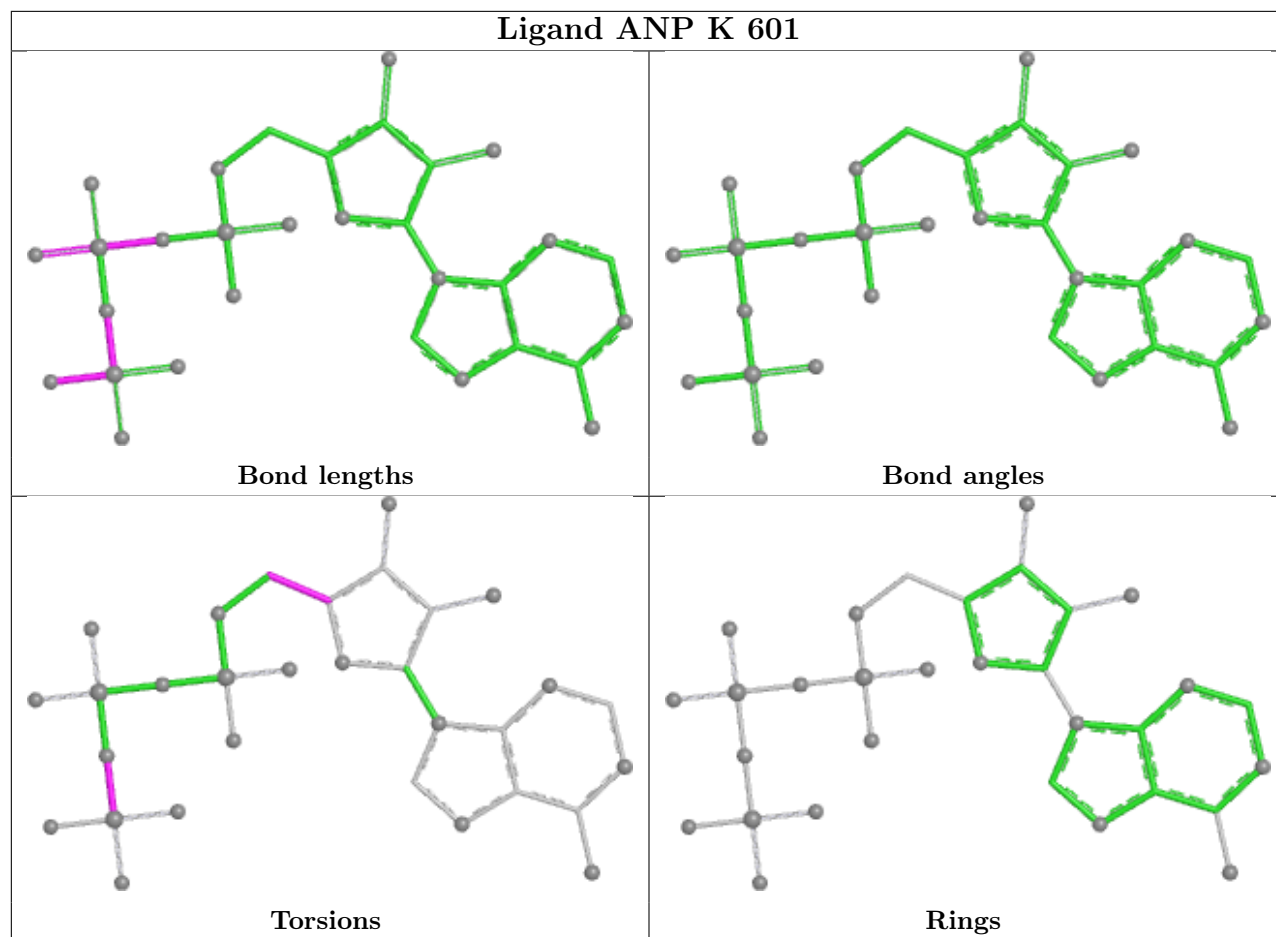
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	601	ANP	9	0
4	J	601	ANP	7	0
4	K	601	ANP	16	0
4	C	601	ANP	14	0

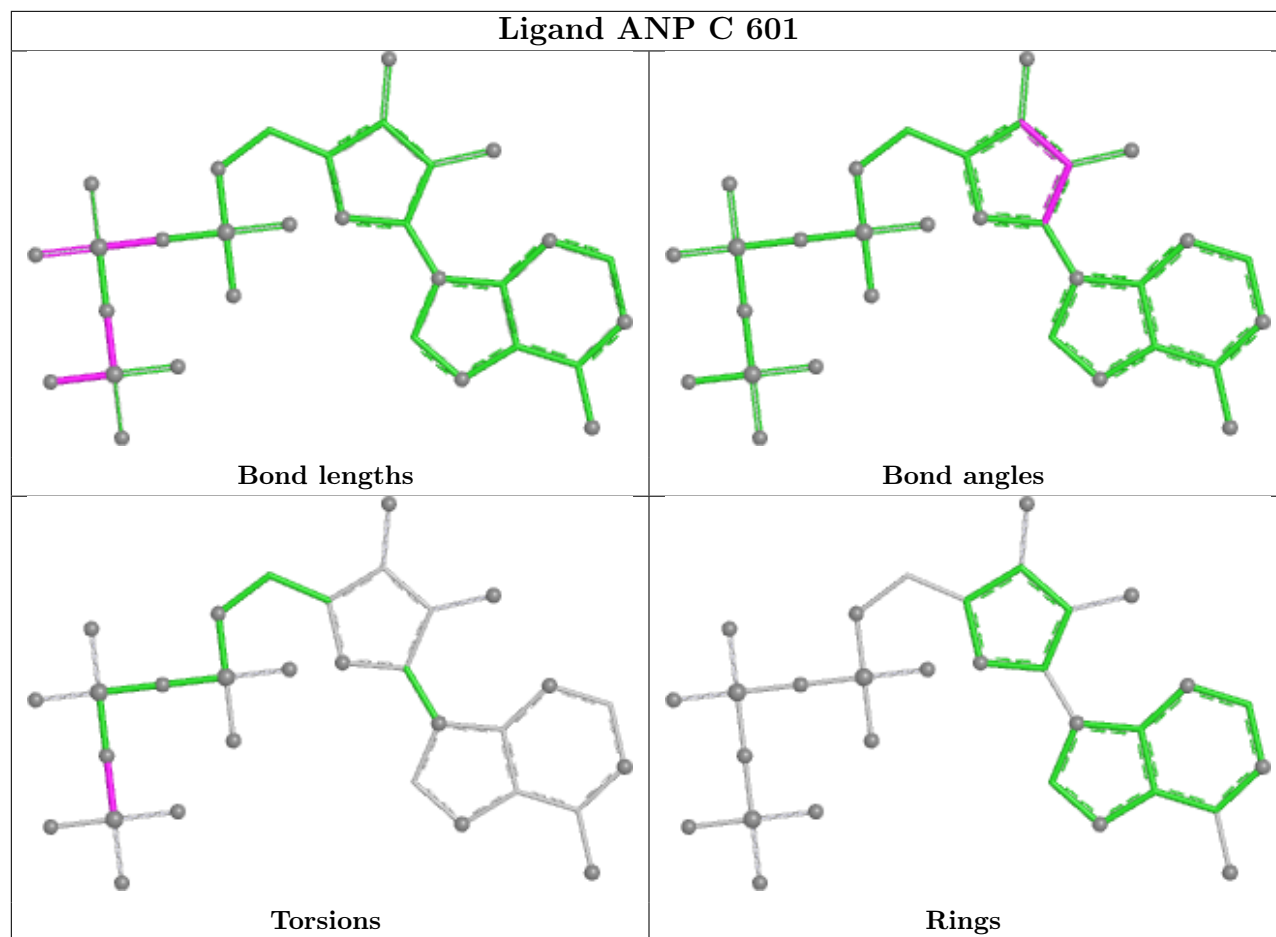
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



Ligand ANP J 601







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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	584/600 (97%)	-0.91	0 100 100	42, 77, 103, 125	0
1	B	584/600 (97%)	-0.98	0 100 100	37, 72, 98, 116	0
1	C	584/600 (97%)	-0.84	0 100 100	39, 80, 129, 154	0
1	I	583/600 (97%)	-0.92	0 100 100	38, 72, 100, 125	0
1	J	584/600 (97%)	-0.76	0 100 100	66, 92, 117, 151	0
1	K	584/600 (97%)	-0.96	0 100 100	34, 69, 105, 178	0
2	D	447/465 (96%)	-0.92	0 100 100	45, 78, 112, 131	0
2	E	453/465 (97%)	-0.90	0 100 100	49, 73, 107, 135	0
2	F	445/465 (95%)	-0.88	0 100 100	44, 75, 121, 154	0
2	L	447/465 (96%)	-0.95	0 100 100	37, 70, 122, 153	0
2	M	453/465 (97%)	-0.75	0 100 100	52, 90, 130, 150	0
2	N	429/465 (92%)	-0.77	0 100 100	51, 93, 128, 168	0
All	All	6177/6390 (96%)	-0.88	0 100 100	34, 78, 117, 178	0

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates [i](#)

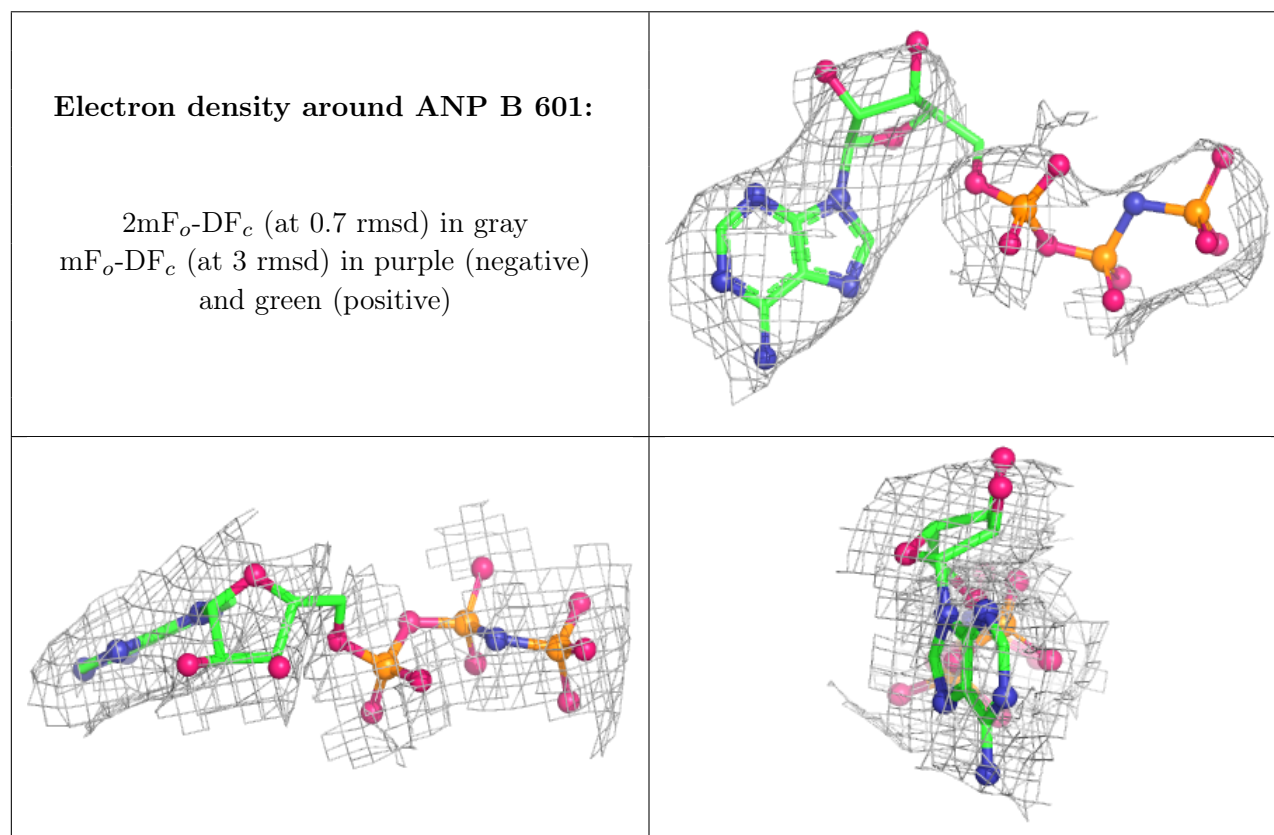
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

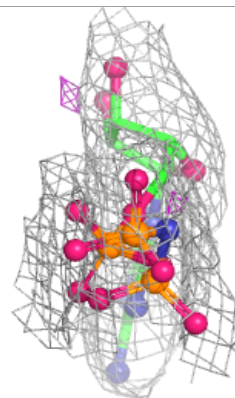
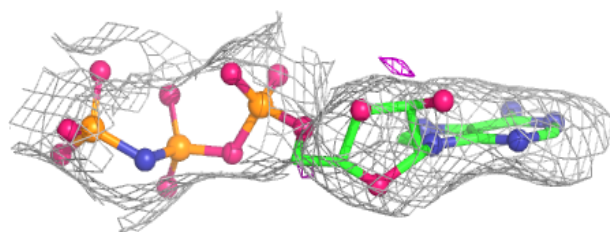
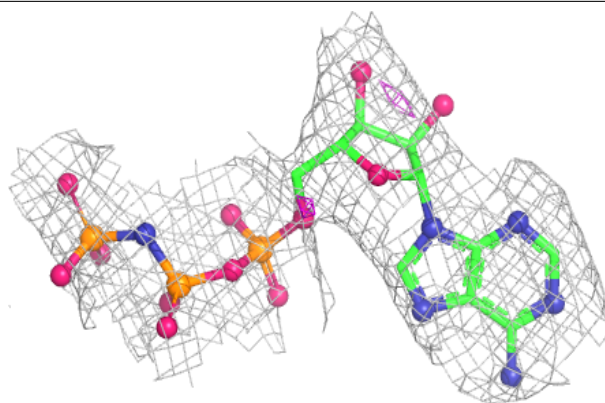
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	GOL	A	601	6/6	0.99	0.04	11,13,16,16	0
4	ANP	B	601	31/31	0.99	0.04	19,28,45,45	0
4	ANP	C	601	31/31	0.99	0.04	28,34,99,113	0
4	ANP	J	601	31/31	0.99	0.04	29,47,58,71	0
4	ANP	K	601	31/31	0.99	0.05	29,45,69,85	0
5	MG	C	602	1/1	0.99	0.04	49,49,49,49	0
5	MG	K	602	1/1	0.99	0.03	27,27,27,27	0
5	MG	J	602	1/1	1.00	0.03	26,26,26,26	0
5	MG	B	602	1/1	1.00	0.02	8,8,8,8	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

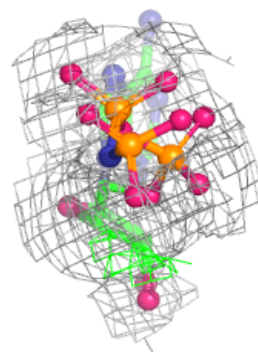
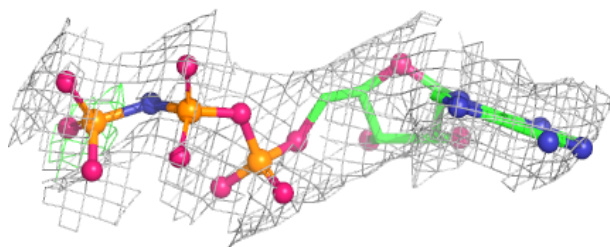
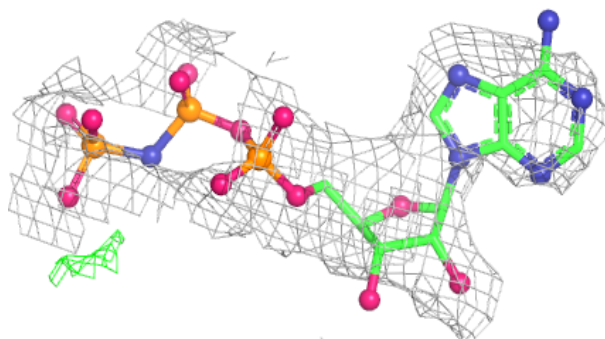


Electron density around ANP C 601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

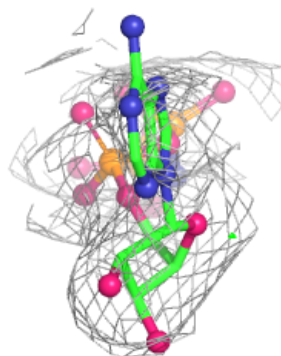
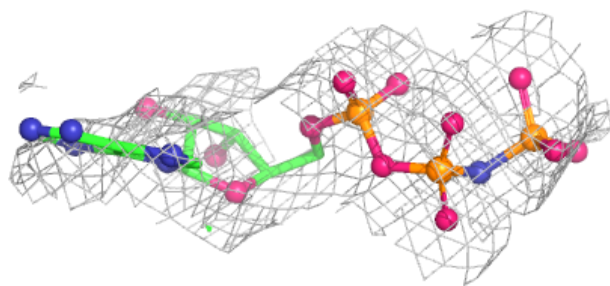
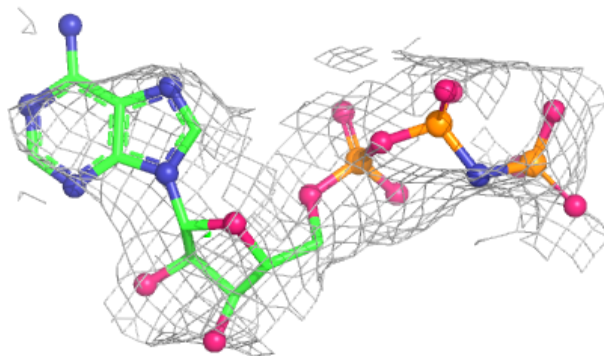
**Electron density around ANP J 601:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ANP K 601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.