



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 16, 2021 – 08:29 PM EDT

PDB ID : 1Q57
Title : The Crystal Structure of the Bifunctional Primase-Helicase of Bacteriophage T7
Authors : Toth, E.A.; Li, Y.; Sawaya, M.R.; Cheng, Y.; Ellenberger, T.
Deposited on : 2003-08-06
Resolution : 3.45 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.23.2
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

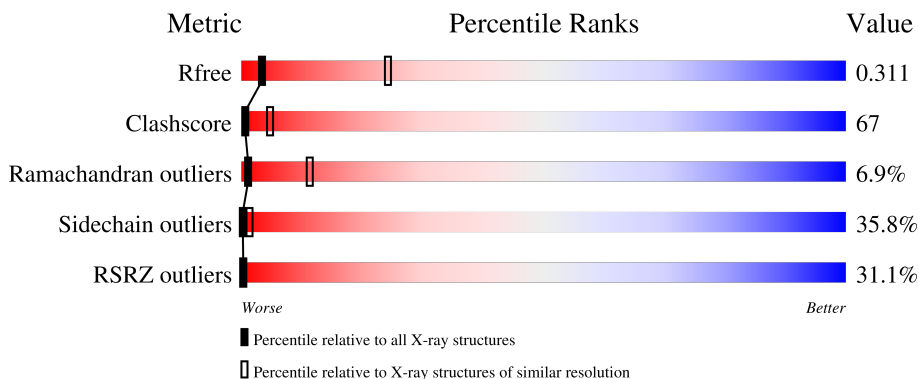
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.45 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.



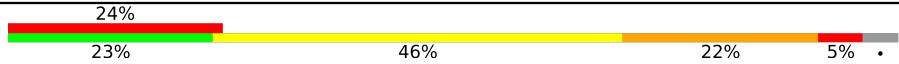
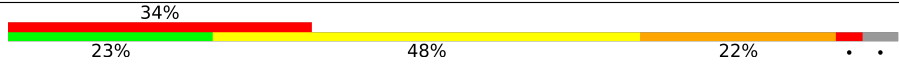
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1291 (3.52-3.40)
Clashscore	141614	1372 (3.52-3.40)
Ramachandran outliers	138981	1337 (3.52-3.40)
Sidechain outliers	138945	1338 (3.52-3.40)
RSRZ outliers	127900	1205 (3.52-3.40)

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	503	
1	B	503	
1	C	503	
1	D	503	
1	E	503	

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Mol	Chain	Length	Quality of chain
1	F	503	
1	G	503	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 26208 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called DNA primase/helicase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	483	3744	2341	657	721	25	0	0	0
1	B	483	3744	2341	657	721	25	0	0	0
1	C	483	3744	2341	657	721	25	0	0	0
1	D	483	3744	2341	657	721	25	0	0	0
1	E	483	3744	2341	657	721	25	0	0	0
1	F	483	3744	2341	657	721	25	0	0	0
1	G	483	3744	2341	657	721	25	0	0	0

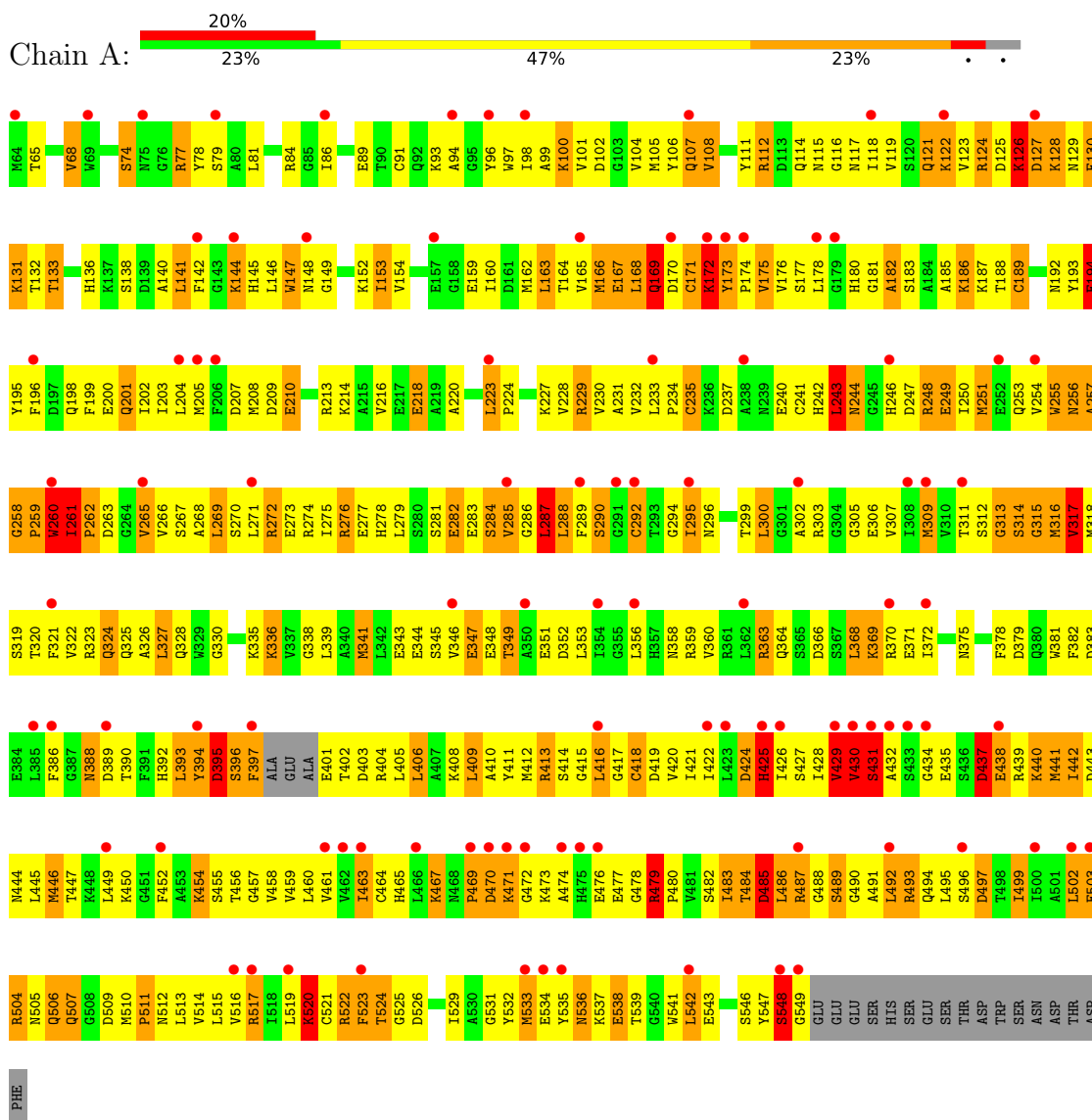
There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	317	VAL	GLY	engineered mutation	UNP P03692
A	318	MET	LYS	engineered mutation	UNP P03692
B	317	VAL	GLY	engineered mutation	UNP P03692
B	318	MET	LYS	engineered mutation	UNP P03692
C	317	VAL	GLY	engineered mutation	UNP P03692
C	318	MET	LYS	engineered mutation	UNP P03692
D	317	VAL	GLY	engineered mutation	UNP P03692
D	318	MET	LYS	engineered mutation	UNP P03692
E	317	VAL	GLY	engineered mutation	UNP P03692
E	318	MET	LYS	engineered mutation	UNP P03692
F	317	VAL	GLY	engineered mutation	UNP P03692
F	318	MET	LYS	engineered mutation	UNP P03692
G	317	VAL	GLY	engineered mutation	UNP P03692
G	318	MET	LYS	engineered mutation	UNP P03692

3 Residue-property plots

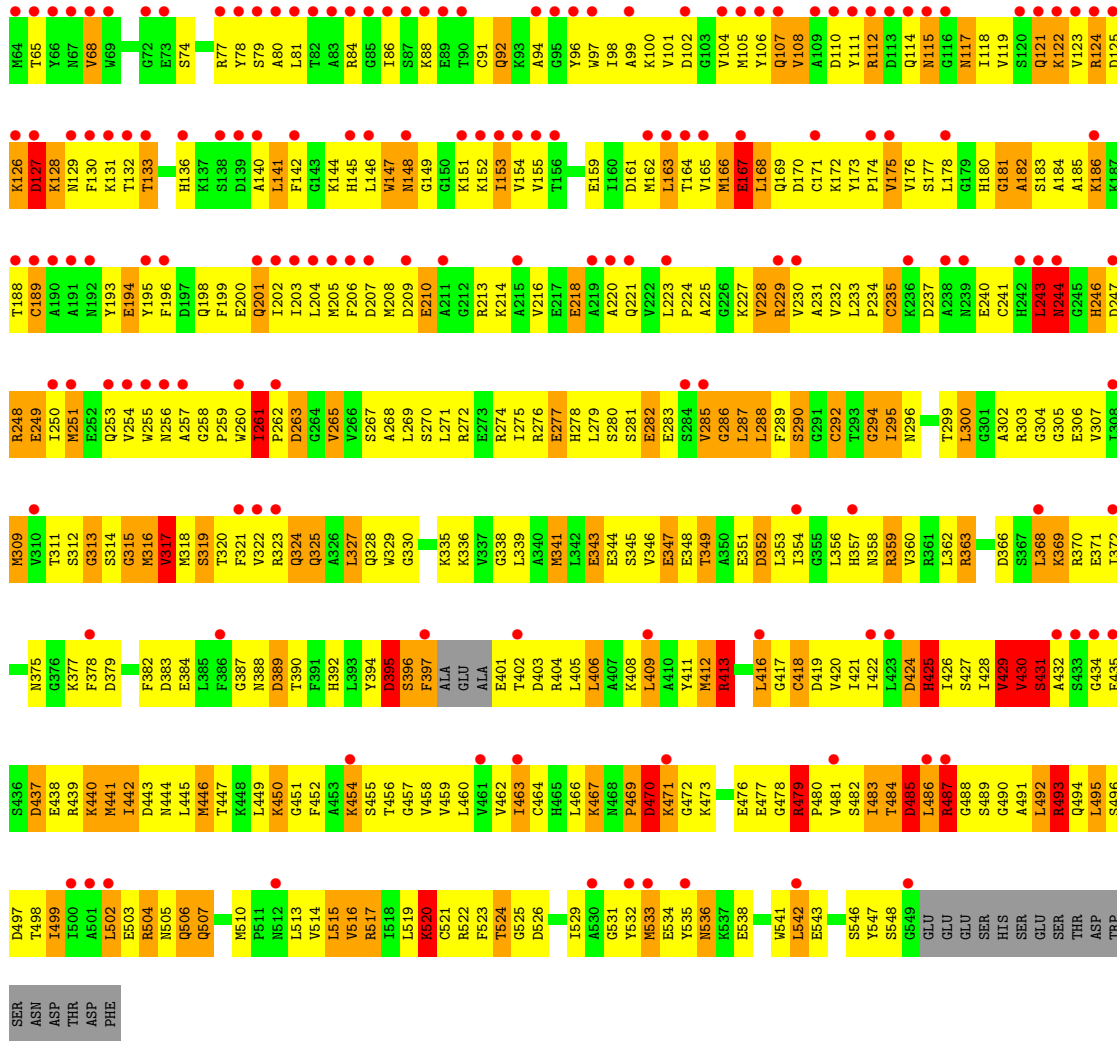
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

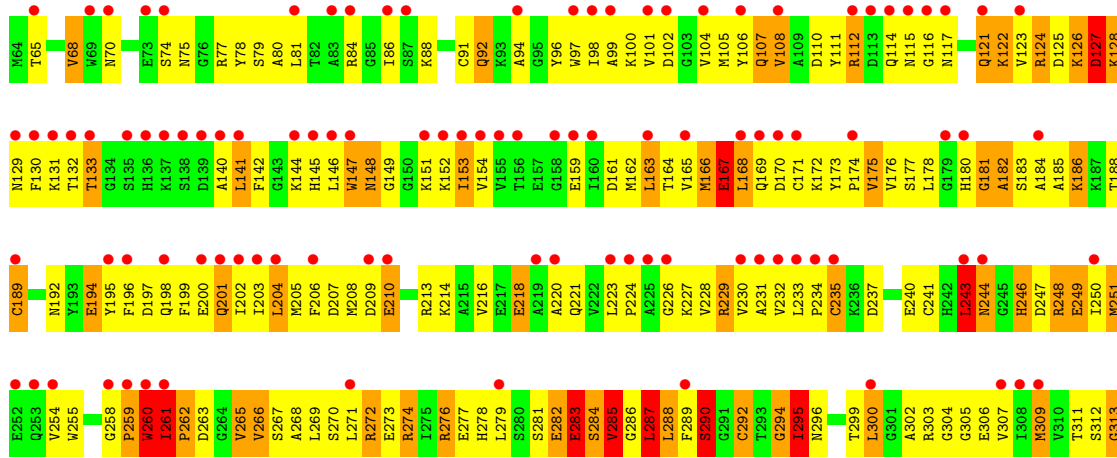
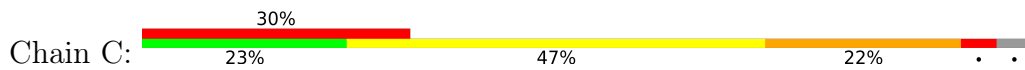


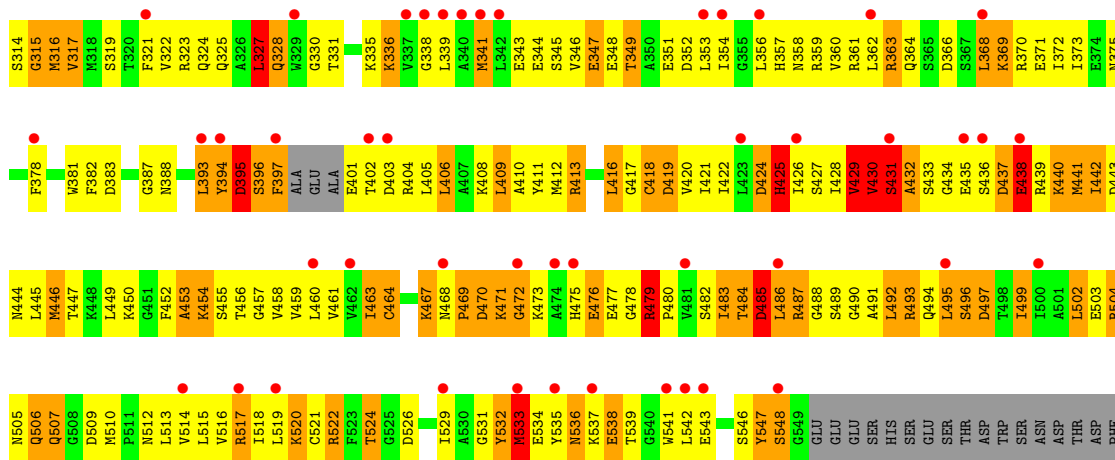
- Molecule 1: DNA primase/helicase



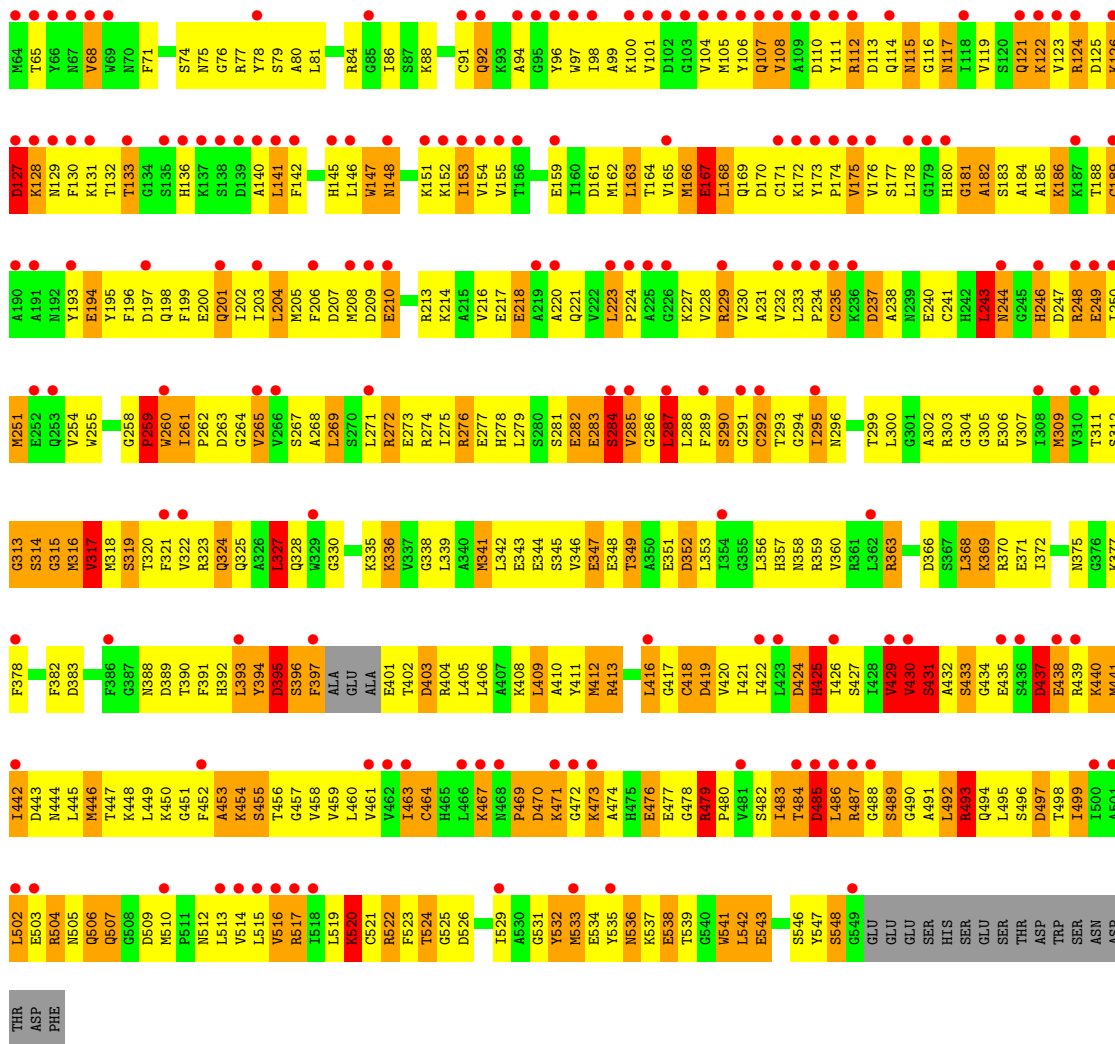
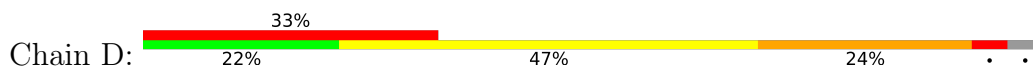


• Molecule 1: DNA primase/helicase

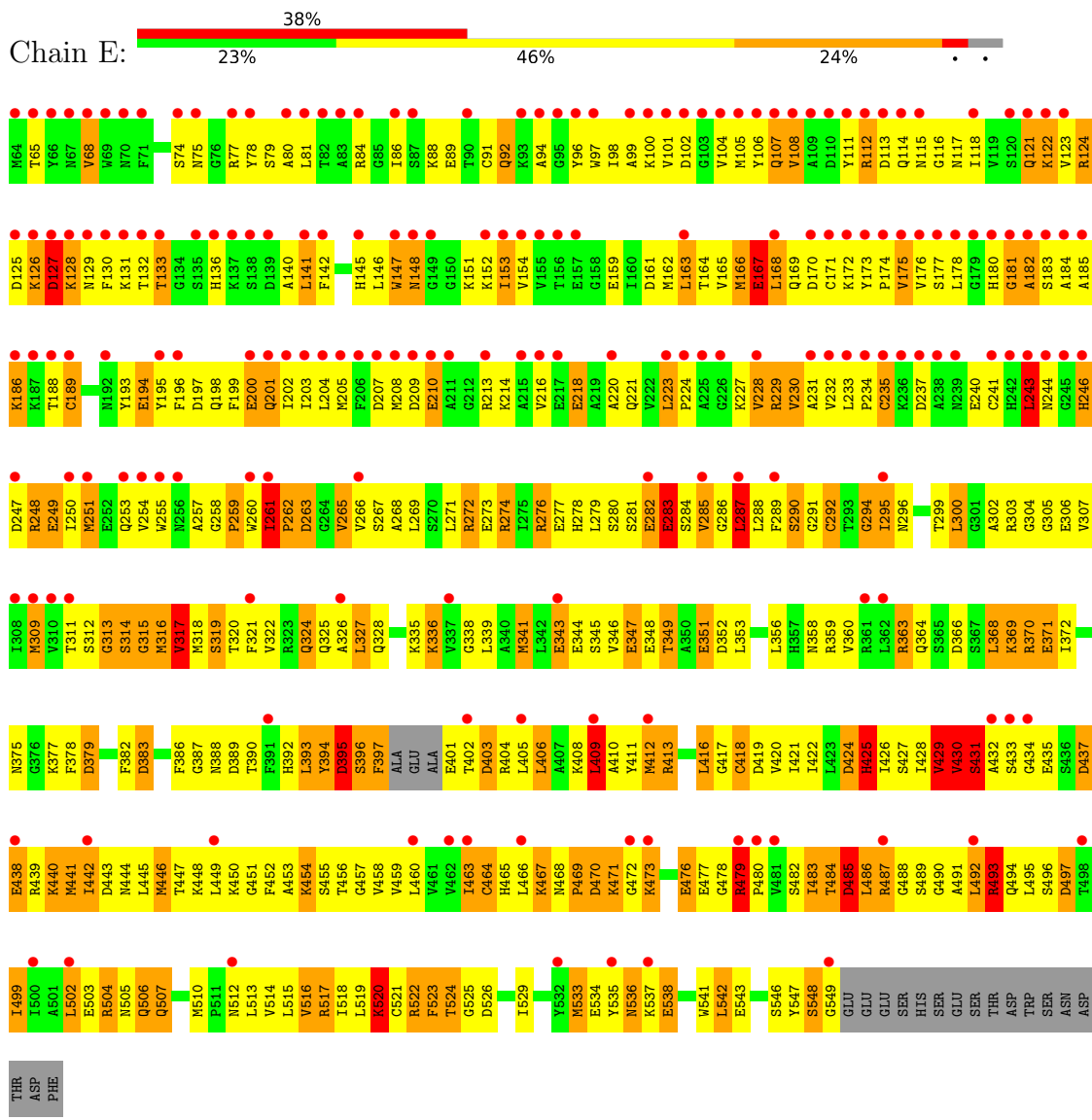




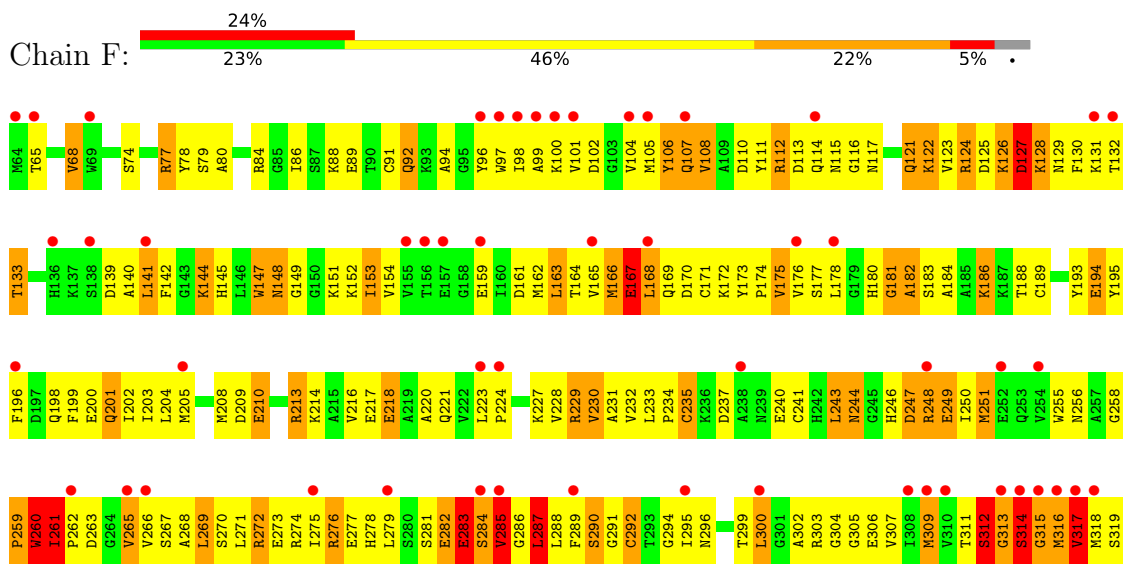
● Molecule 1: DNA primase/helicase

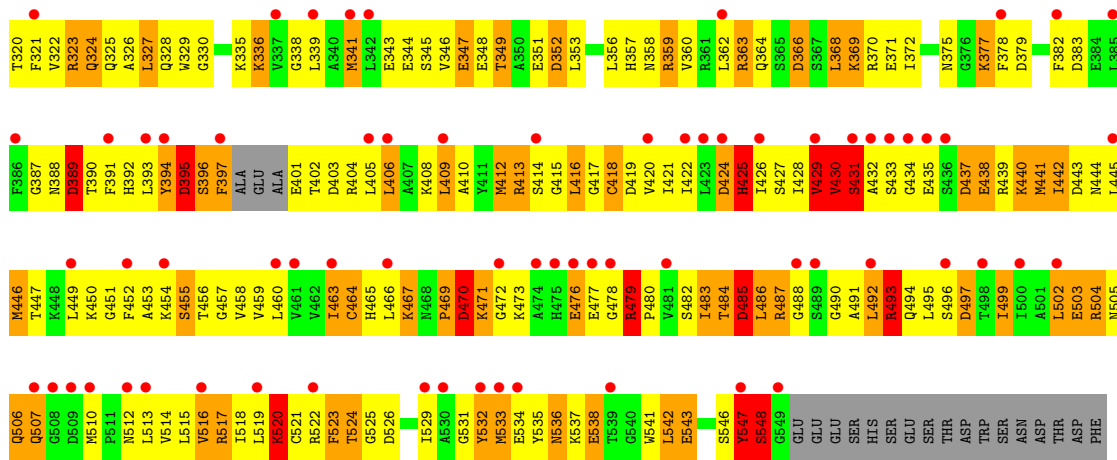


● Molecule 1: DNA primase/helicase

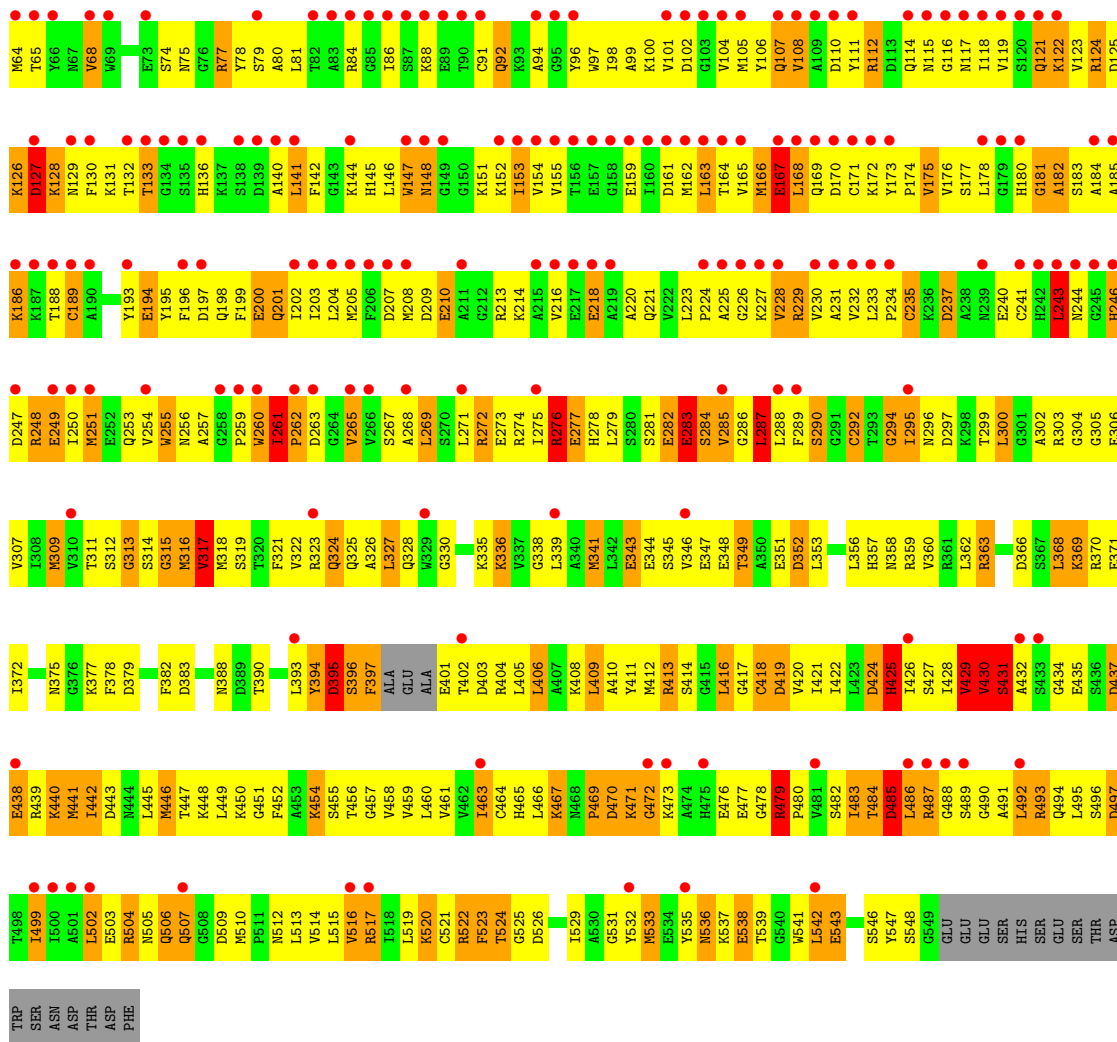


• Molecule 1: DNA primase/helicase





● Molecule 1: DNA primase/helicase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	117.18Å 171.57Å 118.58Å 90.00° 99.86° 90.00°	Depositor
Resolution (Å)	20.00 – 3.45 95.78 – 3.45	Depositor EDS
% Data completeness (in resolution range)	99.7 (20.00-3.45) 99.6 (95.78-3.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.91 (at 3.49Å)	Xtrriage
Refinement program	REFMAC 5.1.80	Depositor
R, R_{free}	0.299 , 0.326 0.284 , 0.311	Depositor DCC
R_{free} test set	3055 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	127.0	Xtrriage
Anisotropy	0.322	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 197.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.001 for l,-k,h	Xtrriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	26208	wwPDB-VP
Average B, all atoms (Å ²)	138.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.65% 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

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	0.96	5/3806 (0.1%)	1.12	33/5124 (0.6%)
1	B	0.87	2/3806 (0.1%)	1.05	35/5124 (0.7%)
1	C	0.85	5/3806 (0.1%)	1.04	33/5124 (0.6%)
1	D	0.78	2/3806 (0.1%)	1.04	33/5124 (0.6%)
1	E	0.75	1/3806 (0.0%)	1.00	33/5124 (0.6%)
1	F	0.85	1/3806 (0.0%)	1.04	32/5124 (0.6%)
1	G	0.73	1/3806 (0.0%)	1.02	36/5124 (0.7%)
All	All	0.83	17/26642 (0.1%)	1.05	235/35868 (0.7%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4
1	B	0	3
1	C	0	5
1	D	0	4
1	E	0	4
1	F	0	5
1	G	0	4
All	All	0	29

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	130	PHE	CE1-CZ	6.54	1.49	1.37
1	A	317	VAL	CB-CG2	6.50	1.66	1.52
1	F	260	TRP	CB-CG	6.18	1.61	1.50
1	B	277	GLU	CD-OE1	6.07	1.32	1.25
1	A	130	PHE	CE2-CZ	5.88	1.48	1.37
1	D	259	PRO	N-CA	5.68	1.56	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	260	TRP	CB-CG	5.52	1.60	1.50
1	C	290	SER	CA-CB	5.46	1.61	1.52
1	C	328	GLN	CB-CG	-5.40	1.38	1.52
1	D	541	TRP	CB-CG	-5.34	1.40	1.50
1	A	194	GLU	CG-CD	5.29	1.59	1.51
1	E	351	GLU	CD-OE2	5.29	1.31	1.25
1	A	364	GLN	CG-CD	5.24	1.63	1.51
1	C	438	GLU	CG-CD	5.20	1.59	1.51
1	C	290	SER	CB-OG	5.16	1.49	1.42
1	B	384	GLU	CD-OE1	5.13	1.31	1.25
1	G	261	ILE	C-N	-5.10	1.24	1.34

All (235) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	259	PRO	CA-N-CD	-13.27	92.93	111.50
1	A	262	PRO	N-CD-CG	-11.76	85.56	103.20
1	A	261	ILE	C-N-CD	-10.84	96.75	120.60
1	A	173	TYR	N-CA-CB	-10.40	91.88	110.60
1	C	167	GLU	CA-C-N	-10.27	94.60	117.20
1	D	167	GLU	CA-C-N	-10.20	94.76	117.20
1	B	167	GLU	CA-C-N	-10.19	94.79	117.20
1	G	167	GLU	CA-C-N	-10.18	94.81	117.20
1	E	167	GLU	CA-C-N	-9.95	95.31	117.20
1	F	167	GLU	CA-C-N	-9.66	95.94	117.20
1	G	395	ASP	CB-CG-OD2	9.62	126.95	118.30
1	A	172	LYS	N-CA-C	9.32	136.17	111.00
1	B	430	VAL	C-N-CA	9.21	144.72	121.70
1	D	430	VAL	C-N-CA	9.17	144.63	121.70
1	G	430	VAL	C-N-CA	9.13	144.53	121.70
1	A	430	VAL	C-N-CA	9.08	144.39	121.70
1	E	430	VAL	C-N-CA	9.05	144.33	121.70
1	F	430	VAL	C-N-CA	9.03	144.26	121.70
1	C	430	VAL	C-N-CA	8.88	143.90	121.70
1	G	261	ILE	C-N-CD	-8.84	101.15	120.60
1	D	167	GLU	O-C-N	8.73	136.67	122.70
1	C	424	ASP	CB-CG-OD2	8.63	126.06	118.30
1	D	497	ASP	CB-CG-OD2	8.10	125.59	118.30
1	E	167	GLU	O-C-N	8.09	135.64	122.70
1	B	263	ASP	CB-CG-OD2	7.98	125.48	118.30
1	B	167	GLU	O-C-N	7.91	135.35	122.70
1	D	425	HIS	CB-CA-C	7.90	126.20	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	167	GLU	O-C-N	7.86	135.27	122.70
1	G	167	GLU	O-C-N	7.85	135.26	122.70
1	F	395	ASP	CB-CG-OD2	7.82	125.33	118.30
1	D	167	GLU	C-N-CA	-7.77	102.28	121.70
1	E	430	VAL	N-CA-C	7.76	131.96	111.00
1	A	430	VAL	N-CA-C	7.69	131.77	111.00
1	A	209	ASP	CB-CG-OD2	7.67	125.21	118.30
1	A	424	ASP	CB-CG-OD2	7.66	125.19	118.30
1	C	430	VAL	N-CA-C	7.65	131.65	111.00
1	D	430	VAL	N-CA-C	7.63	131.62	111.00
1	F	497	ASP	CB-CG-OD2	7.63	125.17	118.30
1	G	424	ASP	CB-CG-OD2	7.63	125.17	118.30
1	G	167	GLU	C-N-CA	-7.63	102.63	121.70
1	B	430	VAL	N-CA-C	7.63	131.59	111.00
1	A	511	PRO	CA-N-CD	-7.62	100.84	111.50
1	G	430	VAL	N-CA-C	7.61	131.54	111.00
1	B	167	GLU	C-N-CA	-7.60	102.71	121.70
1	F	430	VAL	N-CA-C	7.60	131.51	111.00
1	C	167	GLU	C-N-CA	-7.57	102.77	121.70
1	B	383	ASP	CB-CG-OD2	7.51	125.06	118.30
1	E	167	GLU	C-N-CA	-7.49	102.99	121.70
1	B	430	VAL	CA-C-N	-7.48	100.74	117.20
1	F	167	GLU	C-N-CA	-7.33	103.39	121.70
1	C	430	VAL	CA-C-N	-7.28	101.19	117.20
1	E	430	VAL	CA-C-N	-7.27	101.21	117.20
1	D	430	VAL	CA-C-N	-7.26	101.23	117.20
1	G	430	VAL	CA-C-N	-7.25	101.25	117.20
1	B	425	HIS	CB-CA-C	7.23	124.86	110.40
1	A	207	ASP	CB-CG-OD2	7.22	124.80	118.30
1	G	263	ASP	CB-CG-OD2	7.20	124.78	118.30
1	B	425	HIS	N-CA-CB	-7.16	97.71	110.60
1	F	430	VAL	CA-C-N	-7.14	101.50	117.20
1	D	526	ASP	CB-CG-OD2	7.10	124.69	118.30
1	A	430	VAL	CA-C-N	-7.10	101.58	117.20
1	F	209	ASP	CB-CG-OD2	7.09	124.68	118.30
1	F	139	ASP	CB-CG-OD2	7.06	124.66	118.30
1	B	424	ASP	CA-C-N	-7.06	101.67	117.20
1	G	261	ILE	N-CA-C	7.06	130.05	111.00
1	E	526	ASP	CB-CG-OD2	6.99	124.59	118.30
1	D	424	ASP	CB-CG-OD2	6.97	124.58	118.30
1	D	259	PRO	N-CA-CB	6.96	111.65	103.30
1	F	424	ASP	CB-CG-OD2	6.93	124.54	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	167	GLU	O-C-N	6.92	133.77	122.70
1	E	207	ASP	CB-CG-OD2	6.88	124.49	118.30
1	A	260	TRP	CA-CB-CG	6.84	126.70	113.70
1	B	424	ASP	O-C-N	6.83	133.63	122.70
1	D	209	ASP	CB-CG-OD2	6.82	124.44	118.30
1	C	294	GLY	N-CA-C	-6.81	96.08	113.10
1	A	424	ASP	CA-C-N	-6.77	102.31	117.20
1	A	395	ASP	CB-CG-OD2	6.76	124.38	118.30
1	D	395	ASP	CB-CG-OD2	6.72	124.35	118.30
1	E	383	ASP	CB-CG-OD2	6.66	124.29	118.30
1	F	260	TRP	N-CA-C	6.63	128.90	111.00
1	C	263	ASP	CB-CG-OD2	6.54	124.19	118.30
1	C	526	ASP	CB-CG-OD2	6.52	124.17	118.30
1	D	403	ASP	CB-CG-OD2	6.50	124.16	118.30
1	E	263	ASP	CB-CG-OD2	6.47	124.12	118.30
1	B	424	ASP	CB-CG-OD2	6.42	124.07	118.30
1	B	379	ASP	CB-CG-OD2	6.38	124.05	118.30
1	E	395	ASP	CB-CG-OD2	6.36	124.02	118.30
1	A	424	ASP	O-C-N	6.32	132.81	122.70
1	D	389	ASP	CB-CG-OD2	6.27	123.94	118.30
1	F	352	ASP	CB-CG-OD2	6.25	123.93	118.30
1	C	395	ASP	CB-CG-OD2	6.24	123.91	118.30
1	C	383	ASP	CB-CG-OD2	6.23	123.91	118.30
1	E	161	ASP	CB-CG-OD2	6.23	123.90	118.30
1	B	526	ASP	CB-CG-OD2	6.21	123.89	118.30
1	B	352	ASP	CB-CG-OD2	6.17	123.85	118.30
1	F	379	ASP	CB-CG-OD2	6.12	123.81	118.30
1	B	359	ARG	NE-CZ-NH1	-6.12	117.24	120.30
1	B	413	ARG	NE-CZ-NH1	-6.07	117.27	120.30
1	C	127	ASP	CB-CG-OD2	6.07	123.76	118.30
1	B	209	ASP	CB-CG-OD2	6.07	123.76	118.30
1	B	127	ASP	CB-CG-OD2	6.06	123.76	118.30
1	D	352	ASP	CB-CG-OD2	6.03	123.73	118.30
1	E	497	ASP	CB-CG-OD2	6.03	123.72	118.30
1	C	425	HIS	CB-CA-C	6.00	122.40	110.40
1	D	207	ASP	CB-CG-OD2	5.99	123.69	118.30
1	G	425	HIS	CB-CA-C	5.98	122.36	110.40
1	E	379	ASP	CB-CG-OD2	5.98	123.68	118.30
1	F	526	ASP	CB-CG-OD2	5.97	123.67	118.30
1	G	161	ASP	CB-CG-OD2	5.95	123.66	118.30
1	D	113	ASP	CB-CG-OD2	5.95	123.65	118.30
1	G	485	ASP	CB-CG-OD2	5.94	123.65	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	497	ASP	CB-CG-OD2	5.94	123.65	118.30
1	G	262	PRO	N-CD-CG	-5.94	94.29	103.20
1	F	247	ASP	CB-CG-OD2	5.94	123.64	118.30
1	A	379	ASP	CB-CG-OD2	5.92	123.63	118.30
1	A	526	ASP	CB-CG-OD2	5.90	123.61	118.30
1	G	526	ASP	CB-CG-OD2	5.88	123.59	118.30
1	C	424	ASP	O-C-N	5.85	132.05	122.70
1	D	383	ASP	CB-CG-OD2	5.83	123.55	118.30
1	G	207	ASP	CB-CG-OD2	5.83	123.55	118.30
1	B	430	VAL	O-C-N	5.82	132.02	122.70
1	B	207	ASP	CB-CG-OD2	5.82	123.53	118.30
1	C	425	HIS	N-CA-CB	-5.81	100.14	110.60
1	D	263	ASP	CB-CG-OD2	5.79	123.51	118.30
1	E	429	VAL	C-N-CA	5.79	136.18	121.70
1	D	161	ASP	CB-CG-OD2	5.78	123.50	118.30
1	C	288	LEU	CA-CB-CG	-5.78	102.01	115.30
1	B	366	ASP	CB-CG-OD2	5.78	123.50	118.30
1	B	389	ASP	CB-CG-OD2	5.75	123.48	118.30
1	G	209	ASP	CB-CG-OD2	5.75	123.47	118.30
1	C	110	ASP	CB-CG-OD2	5.73	123.46	118.30
1	F	161	ASP	CB-CG-OD2	5.72	123.45	118.30
1	E	424	ASP	CB-CG-OD2	5.72	123.45	118.30
1	E	366	ASP	CB-CG-OD2	5.72	123.45	118.30
1	G	429	VAL	C-N-CA	5.70	135.96	121.70
1	E	424	ASP	CA-C-N	-5.70	104.66	117.20
1	E	485	ASP	CB-CG-OD2	5.69	123.42	118.30
1	C	429	VAL	C-N-CA	5.68	135.90	121.70
1	G	430	VAL	O-C-N	5.67	131.78	122.70
1	F	429	VAL	C-N-CA	5.66	135.85	121.70
1	C	424	ASP	CA-C-N	-5.66	104.75	117.20
1	A	509	ASP	CB-CG-OD2	5.64	123.38	118.30
1	C	430	VAL	O-C-N	5.63	131.72	122.70
1	G	127	ASP	CB-CG-OD2	5.62	123.36	118.30
1	A	425	HIS	CB-CA-C	5.62	121.63	110.40
1	D	110	ASP	CB-CG-OD2	5.60	123.34	118.30
1	D	430	VAL	O-C-N	5.59	131.64	122.70
1	D	127	ASP	CB-CG-OD2	5.59	123.33	118.30
1	A	263	ASP	CB-CG-OD2	5.58	123.33	118.30
1	E	197	ASP	CB-CG-OD2	5.58	123.33	118.30
1	A	429	VAL	C-N-CA	5.58	135.65	121.70
1	B	395	ASP	CB-CG-OD2	5.58	123.32	118.30
1	G	197	ASP	CB-CG-OD2	5.58	123.32	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	430	VAL	O-C-N	5.56	131.60	122.70
1	A	389	ASP	CB-CG-OD2	5.56	123.30	118.30
1	F	366	ASP	CB-CG-OD2	5.56	123.30	118.30
1	B	161	ASP	CB-CG-OD2	5.56	123.30	118.30
1	A	430	VAL	O-C-N	5.56	131.59	122.70
1	B	102	ASP	CB-CG-OD2	5.55	123.29	118.30
1	D	429	VAL	C-N-CA	5.54	135.54	121.70
1	E	209	ASP	CB-CG-OD2	5.54	123.28	118.30
1	D	197	ASP	CB-CG-OD2	5.53	123.28	118.30
1	D	437	ASP	CB-CG-OD2	5.53	123.28	118.30
1	F	470	ASP	CB-CG-OD2	5.53	123.28	118.30
1	G	110	ASP	CB-CG-OD2	5.52	123.27	118.30
1	A	497	ASP	CB-CG-OD2	5.52	123.27	118.30
1	B	485	ASP	CB-CG-OD2	5.50	123.25	118.30
1	F	127	ASP	CB-CG-OD2	5.50	123.25	118.30
1	C	497	ASP	CB-CG-OD2	5.50	123.25	118.30
1	B	429	VAL	C-N-CA	5.50	135.44	121.70
1	E	283	GLU	N-CA-C	5.47	125.78	111.00
1	D	509	ASP	CB-CG-OD2	5.46	123.22	118.30
1	B	110	ASP	CB-CG-OD2	5.44	123.19	118.30
1	E	127	ASP	CB-CG-OD2	5.43	123.19	118.30
1	F	430	VAL	O-C-N	5.43	131.38	122.70
1	E	294	GLY	N-CA-C	-5.42	99.56	113.10
1	B	288	LEU	CA-CB-CG	-5.41	102.86	115.30
1	B	294	GLY	N-CA-C	-5.38	99.64	113.10
1	F	113	ASP	CB-CG-OD2	5.38	123.14	118.30
1	C	197	ASP	CB-CG-OD2	5.36	123.12	118.30
1	G	383	ASP	CB-CG-OD2	5.35	123.12	118.30
1	F	383	ASP	CB-CG-OD2	5.35	123.11	118.30
1	G	431	SER	N-CA-C	5.34	125.42	111.00
1	E	425	HIS	N-CA-CB	-5.34	100.99	110.60
1	G	366	ASP	CB-CG-OD2	5.33	123.10	118.30
1	E	431	SER	N-CA-C	5.32	125.36	111.00
1	B	413	ARG	NE-CZ-NH2	5.31	122.96	120.30
1	E	409	LEU	CB-CG-CD2	-5.31	101.97	111.00
1	F	389	ASP	CB-CG-OD2	5.30	123.07	118.30
1	C	209	ASP	CB-CG-OD2	5.29	123.06	118.30
1	E	403	ASP	CB-CG-OD2	5.29	123.06	118.30
1	D	431	SER	N-CA-C	5.29	125.27	111.00
1	F	256	ASN	N-CA-C	5.28	125.27	111.00
1	C	533	MET	CG-SD-CE	5.28	108.64	100.20
1	G	283	GLU	CA-C-N	-5.27	105.60	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	431	SER	N-CA-C	5.25	125.17	111.00
1	E	424	ASP	O-C-N	5.25	131.09	122.70
1	F	431	SER	N-CA-C	5.24	125.16	111.00
1	A	261	ILE	N-CA-C	5.24	125.15	111.00
1	G	297	ASP	CB-CG-OD2	5.24	123.02	118.30
1	G	276	ARG	O-C-N	-5.24	114.32	122.70
1	D	237	ASP	CB-CG-OD2	5.23	123.01	118.30
1	C	207	ASP	CB-CG-OD2	5.22	123.00	118.30
1	F	110	ASP	CB-CG-OD2	5.22	123.00	118.30
1	A	437	ASP	CB-CG-OD2	5.22	123.00	118.30
1	B	470	ASP	CB-CG-OD2	5.21	122.99	118.30
1	C	431	SER	N-CA-C	5.21	125.08	111.00
1	A	172	LYS	CB-CA-C	-5.20	100.01	110.40
1	G	352	ASP	CB-CG-OD2	5.20	122.98	118.30
1	C	361	ARG	NE-CZ-NH1	-5.18	117.71	120.30
1	G	102	ASP	CB-CG-OD2	5.18	122.96	118.30
1	A	288	LEU	CA-CB-CG	-5.17	103.41	115.30
1	F	424	ASP	CA-C-N	-5.16	105.85	117.20
1	F	260	TRP	CA-C-N	-5.15	105.88	117.20
1	C	485	ASP	CB-CG-OD2	5.14	122.93	118.30
1	B	431	SER	N-CA-C	5.12	124.82	111.00
1	A	383	ASP	CB-CG-OD2	5.11	122.90	118.30
1	D	425	HIS	N-CA-CB	-5.11	101.41	110.60
1	A	485	ASP	CB-CG-OD2	5.10	122.89	118.30
1	D	433	SER	N-CA-C	5.10	124.76	111.00
1	F	266	VAL	CB-CA-C	-5.09	101.72	111.40
1	G	237	ASP	CB-CG-OD2	5.08	122.87	118.30
1	G	294	GLY	N-CA-C	-5.07	100.42	113.10
1	G	509	ASP	CB-CG-OD2	5.07	122.86	118.30
1	G	379	ASP	CB-CG-OD2	5.06	122.86	118.30
1	E	113	ASP	CB-CG-OD2	5.06	122.85	118.30
1	C	102	ASP	CB-CG-OD2	5.05	122.85	118.30
1	E	102	ASP	CB-CG-OD2	5.05	122.85	118.30
1	A	425	HIS	CA-C-N	-5.04	106.11	117.20
1	F	433	SER	N-CA-C	5.04	124.61	111.00
1	C	509	ASP	CB-CG-OD2	5.03	122.82	118.30
1	C	161	ASP	CB-CG-OD2	5.02	122.82	118.30
1	C	433	SER	N-CA-C	5.02	124.55	111.00
1	E	433	SER	N-CA-C	5.01	124.52	111.00
1	A	102	ASP	CB-CG-OD2	5.00	122.80	118.30

There are no chirality outliers.

All (29) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	260	TRP	Mainchain
1	A	261	ILE	Peptide
1	A	282	GLU	Peptide
1	A	396	SER	Peptide
1	B	167	GLU	Mainchain
1	B	173	TYR	Mainchain
1	B	396	SER	Peptide
1	C	167	GLU	Mainchain
1	C	173	TYR	Mainchain
1	C	282	GLU	Peptide
1	C	283	GLU	Peptide
1	C	396	SER	Peptide
1	D	167	GLU	Mainchain
1	D	173	TYR	Mainchain
1	D	282	GLU	Peptide
1	D	396	SER	Peptide
1	E	167	GLU	Mainchain
1	E	173	TYR	Mainchain
1	E	282	GLU	Peptide
1	E	396	SER	Peptide
1	F	167	GLU	Mainchain
1	F	173	TYR	Mainchain
1	F	282	GLU	Peptide
1	F	283	GLU	Peptide
1	F	396	SER	Peptide
1	G	167	GLU	Mainchain
1	G	173	TYR	Mainchain
1	G	282	GLU	Peptide
1	G	396	SER	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3744	0	3697	553	0
1	B	3744	0	3697	482	0
1	C	3744	0	3697	545	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	3744	0	3697	527	0
1	E	3744	0	3697	524	0
1	F	3744	0	3697	527	0
1	G	3744	0	3697	505	0
All	All	26208	0	25879	3503	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 67.

All (3503) 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:G:276:ARG:HH11	1:G:276:ARG:CB	1.16	1.55
1:B:248:ARG:HH11	1:B:248:ARG:CB	1.19	1.51
1:F:260:TRP:HB2	1:F:262:PRO:CD	1.49	1.40
1:G:276:ARG:HB3	1:G:276:ARG:NH1	1.31	1.40
1:F:260:TRP:CB	1:F:262:PRO:HD2	1.56	1.35
1:B:248:ARG:NH1	1:B:248:ARG:HB3	1.38	1.33
1:B:244:ASN:HD22	1:B:244:ASN:C	1.31	1.29
1:G:220:ALA:CB	1:G:261:ILE:HG21	1.63	1.27
1:D:483:ILE:O	1:D:486:LEU:HB2	1.34	1.25
1:A:260:TRP:O	1:A:261:ILE:HG22	1.38	1.23
1:D:366:ASP:HB2	1:E:284:SER:OG	1.37	1.22
1:C:290:SER:H	1:C:325:GLN:NE2	1.37	1.22
1:B:483:ILE:O	1:B:486:LEU:HB2	1.38	1.20
1:C:260:TRP:HB2	1:C:262:PRO:HD2	1.23	1.19
1:F:483:ILE:O	1:F:486:LEU:HB2	1.41	1.18
1:E:261:ILE:H	1:E:262:PRO:CD	1.55	1.18
1:A:315:GLY:HA2	1:A:317:VAL:CG2	1.74	1.18
1:E:220:ALA:CB	1:E:261:ILE:HG21	1.74	1.17
1:A:440:LYS:HZ3	1:A:441:MET:HA	1.06	1.16
1:F:127:ASP:O	1:F:128:LYS:HB2	1.38	1.16
1:B:483:ILE:H	1:B:483:ILE:HD12	1.04	1.16
1:D:220:ALA:HB3	1:D:261:ILE:CG2	1.73	1.16
1:D:339:LEU:HB3	1:D:341:MET:CE	1.75	1.15
1:E:440:LYS:HZ3	1:E:441:MET:HA	1.05	1.15
1:D:290:SER:H	1:D:325:GLN:NE2	1.43	1.15
1:G:483:ILE:O	1:G:486:LEU:HB2	1.45	1.15
1:G:483:ILE:H	1:G:483:ILE:HD12	1.07	1.15
1:C:208:MET:HE1	1:C:232:VAL:HA	1.25	1.14
1:E:440:LYS:NZ	1:E:441:MET:HA	1.63	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:261:ILE:H	1:C:262:PRO:CD	1.55	1.14
1:D:127:ASP:O	1:D:128:LYS:HB2	1.34	1.14
1:A:208:MET:HE1	1:A:232:VAL:HA	1.30	1.14
1:E:483:ILE:O	1:E:486:LEU:HB2	1.46	1.14
1:A:220:ALA:CB	1:A:261:ILE:HD12	1.78	1.14
1:C:412:MET:HA	1:C:416:LEU:HD12	1.30	1.13
1:B:127:ASP:O	1:B:128:LYS:HB2	1.43	1.13
1:F:440:LYS:HZ3	1:F:441:MET:HA	0.97	1.13
1:F:483:ILE:HD12	1:F:483:ILE:H	1.13	1.12
1:B:208:MET:HE1	1:B:232:VAL:HA	1.31	1.12
1:A:290:SER:H	1:A:325:GLN:NE2	1.46	1.12
1:A:315:GLY:CA	1:A:317:VAL:HG23	1.79	1.12
1:E:208:MET:HE1	1:E:232:VAL:HA	1.31	1.12
1:A:126:LYS:HZ2	1:A:127:ASP:CA	1.63	1.11
1:C:440:LYS:NZ	1:C:441:MET:HA	1.65	1.11
1:B:283:GLU:CG	1:B:286:GLY:HA2	1.80	1.11
1:D:261:ILE:N	1:D:262:PRO:HD2	1.48	1.11
1:C:127:ASP:O	1:C:128:LYS:HB2	1.39	1.11
1:C:339:LEU:HB3	1:C:341:MET:CE	1.82	1.10
1:A:483:ILE:O	1:A:486:LEU:HB2	1.50	1.10
1:E:504:ARG:HD3	1:E:506:GLN:HG2	1.22	1.10
1:F:504:ARG:HD3	1:F:506:GLN:HG2	1.23	1.10
1:G:208:MET:HE1	1:G:232:VAL:HA	1.29	1.10
1:C:261:ILE:H	1:C:262:PRO:HD2	1.15	1.10
1:E:220:ALA:HB3	1:E:261:ILE:HG21	1.22	1.10
1:G:220:ALA:HB3	1:G:261:ILE:HG21	1.12	1.10
1:G:504:ARG:HD3	1:G:506:GLN:HG2	1.23	1.09
1:B:244:ASN:O	1:B:244:ASN:ND2	1.83	1.09
1:B:283:GLU:HG3	1:B:286:GLY:HA2	1.24	1.09
1:C:441:MET:HE2	1:C:441:MET:O	1.48	1.09
1:D:483:ILE:H	1:D:483:ILE:HD12	1.15	1.09
1:A:260:TRP:O	1:A:261:ILE:CG2	2.00	1.09
1:B:504:ARG:HD3	1:B:506:GLN:HG2	1.32	1.09
1:D:261:ILE:N	1:D:262:PRO:CD	2.12	1.09
1:B:283:GLU:HG3	1:B:286:GLY:CA	1.83	1.09
1:E:127:ASP:O	1:E:128:LYS:HB2	1.32	1.09
1:G:290:SER:H	1:G:325:GLN:NE2	1.48	1.09
1:C:483:ILE:H	1:C:483:ILE:HD12	1.14	1.08
1:E:370:ARG:NH1	1:E:371:GLU:HG2	1.67	1.08
1:D:220:ALA:CB	1:D:261:ILE:HG21	1.82	1.08
1:F:208:MET:HE1	1:F:232:VAL:HA	1.35	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:447:THR:HG22	1:D:495:LEU:HD21	1.29	1.08
1:B:248:ARG:CB	1:B:248:ARG:NH1	2.03	1.08
1:A:220:ALA:HB3	1:A:261:ILE:HD12	1.32	1.07
1:B:454:LYS:NZ	1:G:344:GLU:HA	1.68	1.07
1:B:483:ILE:HD12	1:B:483:ILE:N	1.62	1.07
1:D:208:MET:HE1	1:D:232:VAL:HA	1.32	1.07
1:F:283:GLU:OE2	1:F:286:GLY:HA2	1.55	1.07
1:E:253:GLN:HA	1:E:257:ALA:HB2	1.37	1.07
1:F:440:LYS:NZ	1:F:441:MET:HA	1.69	1.07
1:F:447:THR:HG22	1:F:495:LEU:HD21	1.35	1.06
1:A:315:GLY:HA2	1:A:317:VAL:HG23	1.12	1.06
1:B:290:SER:H	1:B:325:GLN:NE2	1.53	1.06
1:B:339:LEU:HB3	1:B:341:MET:CE	1.85	1.05
1:A:127:ASP:O	1:A:128:LYS:HB2	1.26	1.05
1:C:483:ILE:HD12	1:C:483:ILE:N	1.71	1.05
1:D:440:LYS:HZ3	1:D:441:MET:HA	1.16	1.05
1:E:412:MET:HA	1:E:416:LEU:HD12	1.35	1.05
1:F:290:SER:H	1:F:325:GLN:NE2	1.52	1.05
1:C:504:ARG:HD3	1:C:506:GLN:HG2	1.35	1.05
1:E:483:ILE:H	1:E:483:ILE:HD12	1.19	1.04
1:G:358:ASN:O	1:G:360:VAL:HG13	1.57	1.04
1:A:126:LYS:NZ	1:A:127:ASP:HA	1.72	1.04
1:A:504:ARG:HD3	1:A:506:GLN:HG2	1.40	1.04
1:G:483:ILE:HD12	1:G:483:ILE:N	1.72	1.04
1:B:412:MET:HA	1:B:416:LEU:HD12	1.37	1.04
1:D:440:LYS:NZ	1:D:441:MET:HA	1.71	1.04
1:D:412:MET:HA	1:D:416:LEU:HD12	1.34	1.04
1:B:229:ARG:NH2	1:B:259:PRO:HB3	1.73	1.04
1:B:447:THR:HG22	1:B:495:LEU:HD21	1.36	1.04
1:A:339:LEU:HB3	1:A:341:MET:CE	1.86	1.03
1:A:412:MET:HA	1:A:416:LEU:HD12	1.40	1.03
1:E:290:SER:H	1:E:325:GLN:NE2	1.54	1.03
1:F:412:MET:HA	1:F:416:LEU:HD12	1.36	1.03
1:D:401:GLU:HG3	1:D:431:SER:O	1.57	1.03
1:G:447:THR:HG22	1:G:495:LEU:HD21	1.37	1.03
1:A:126:LYS:HZ2	1:A:127:ASP:HA	1.20	1.03
1:C:450:LYS:CE	1:C:454:LYS:HD3	1.88	1.03
1:G:440:LYS:NZ	1:G:441:MET:HA	1.74	1.03
1:C:312:SER:HB2	1:C:502:LEU:O	1.60	1.02
1:C:450:LYS:HE2	1:C:454:LYS:HD3	1.38	1.02
1:B:483:ILE:H	1:B:483:ILE:CD1	1.72	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:440:LYS:NZ	1:B:441:MET:HA	1.73	1.02
1:A:483:ILE:HD12	1:A:483:ILE:H	1.18	1.02
1:E:450:LYS:HE2	1:E:454:LYS:HD3	1.40	1.02
1:B:440:LYS:HZ3	1:B:441:MET:HA	1.23	1.01
1:C:440:LYS:HZ3	1:C:441:MET:HA	1.11	1.01
1:C:483:ILE:O	1:C:486:LEU:HB2	1.58	1.01
1:F:339:LEU:HB3	1:F:341:MET:CE	1.89	1.01
1:A:440:LYS:NZ	1:A:441:MET:HA	1.76	1.01
1:E:339:LEU:HB3	1:E:341:MET:CE	1.90	1.01
1:G:440:LYS:HZ3	1:G:441:MET:HA	1.19	1.01
1:E:261:ILE:H	1:E:262:PRO:HD3	1.25	1.01
1:A:450:LYS:HE2	1:A:454:LYS:HD3	1.43	1.00
1:B:450:LYS:CE	1:B:454:LYS:HD3	1.91	1.00
1:B:450:LYS:HE2	1:B:454:LYS:HD3	1.43	1.00
1:A:172:LYS:O	1:A:172:LYS:CG	2.06	1.00
1:E:450:LYS:CE	1:E:454:LYS:HD3	1.91	1.00
1:D:409:LEU:HD23	1:D:421:ILE:HG21	1.44	0.99
1:G:339:LEU:HB3	1:G:341:MET:HE1	1.44	0.99
1:C:447:THR:HG22	1:C:495:LEU:HD21	1.44	0.99
1:D:260:TRP:HB2	1:D:262:PRO:CG	1.92	0.99
1:B:316:MET:HE1	1:B:535:TYR:CZ	1.98	0.99
1:A:447:THR:HG22	1:A:495:LEU:HD21	1.40	0.98
1:F:409:LEU:HD23	1:F:421:ILE:HG21	1.42	0.98
1:F:112:ARG:HB3	1:F:117:ASN:O	1.63	0.98
1:A:450:LYS:CE	1:A:454:LYS:HD3	1.92	0.98
1:E:483:ILE:HD12	1:E:483:ILE:N	1.77	0.98
1:A:259:PRO:O	1:A:260:TRP:HB3	1.64	0.98
1:F:483:ILE:HD12	1:F:483:ILE:N	1.76	0.98
1:G:412:MET:HA	1:G:416:LEU:HD12	1.41	0.98
1:G:127:ASP:O	1:G:128:LYS:HB2	1.59	0.98
1:G:483:ILE:H	1:G:483:ILE:CD1	1.78	0.97
1:G:450:LYS:HE2	1:G:454:LYS:HD3	1.44	0.97
1:A:412:MET:HE2	1:A:421:ILE:CD1	1.94	0.97
1:D:499:ILE:HG22	1:D:519:LEU:HB2	1.47	0.97
1:C:409:LEU:HD23	1:C:421:ILE:HG21	1.45	0.97
1:D:504:ARG:HD3	1:D:506:GLN:HG2	1.44	0.97
1:E:447:THR:HG22	1:E:495:LEU:HD21	1.43	0.97
1:C:483:ILE:H	1:C:483:ILE:CD1	1.78	0.97
1:A:311:THR:HA	1:A:318:MET:HE1	1.46	0.96
1:C:260:TRP:O	1:C:261:ILE:HG23	1.63	0.96
1:G:492:LEU:H	1:G:492:LEU:HD12	1.29	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:510:MET:CE	1:C:547:TYR:HE1	1.79	0.96
1:E:370:ARG:HD2	1:E:371:GLU:N	1.81	0.96
1:G:499:ILE:HG22	1:G:519:LEU:HB2	1.48	0.96
1:D:510:MET:CE	1:D:547:TYR:HE1	1.79	0.95
1:D:483:ILE:HD12	1:D:483:ILE:N	1.77	0.95
1:G:248:ARG:HB3	1:G:248:ARG:HH11	1.31	0.95
1:A:172:LYS:O	1:A:172:LYS:HG3	1.11	0.95
1:G:450:LYS:CE	1:G:454:LYS:HD3	1.96	0.95
1:E:412:MET:HA	1:E:416:LEU:CD1	1.95	0.95
1:D:492:LEU:HD12	1:D:492:LEU:H	1.32	0.95
1:E:186:LYS:HD3	1:E:218:GLU:HG3	1.48	0.95
1:C:248:ARG:HB3	1:C:248:ARG:HH11	1.29	0.95
1:A:126:LYS:HE3	1:A:127:ASP:OD1	1.66	0.95
1:A:126:LYS:HG2	1:A:127:ASP:N	1.77	0.95
1:A:127:ASP:O	1:A:128:LYS:CB	2.15	0.95
1:C:412:MET:HA	1:C:416:LEU:CD1	1.97	0.94
1:F:248:ARG:HB3	1:F:248:ARG:HH11	1.29	0.94
1:G:276:ARG:CB	1:G:276:ARG:NH1	2.02	0.94
1:C:412:MET:HE2	1:C:421:ILE:CD1	1.98	0.94
1:F:107:GLN:HB2	1:F:124:ARG:HG3	1.50	0.94
1:D:186:LYS:HD3	1:D:218:GLU:HG3	1.49	0.94
1:D:366:ASP:HB2	1:E:284:SER:CB	1.97	0.94
1:B:229:ARG:HB3	1:B:259:PRO:HA	1.49	0.94
1:B:339:LEU:HB3	1:B:341:MET:HE1	1.49	0.94
1:F:412:MET:HA	1:F:416:LEU:CD1	1.96	0.94
1:F:483:ILE:H	1:F:483:ILE:CD1	1.81	0.94
1:F:499:ILE:HG22	1:F:519:LEU:HB2	1.45	0.94
1:G:316:MET:HE1	1:G:535:TYR:CZ	2.03	0.94
1:D:97:TRP:CZ3	1:D:99:ALA:HB2	2.03	0.94
1:A:483:ILE:HD12	1:A:483:ILE:N	1.83	0.93
1:A:312:SER:HB2	1:A:502:LEU:O	1.67	0.93
1:F:450:LYS:HE2	1:F:454:LYS:HD3	1.51	0.93
1:F:309:MET:HB3	1:F:499:ILE:HD12	1.48	0.93
1:G:276:ARG:HH11	1:G:276:ARG:CG	1.82	0.93
1:B:186:LYS:HD3	1:B:218:GLU:HG3	1.48	0.93
1:E:216:VAL:HG11	1:E:230:VAL:CG2	1.99	0.93
1:G:261:ILE:O	1:G:261:ILE:HG22	1.69	0.93
1:E:409:LEU:HD23	1:E:421:ILE:HG21	1.49	0.93
1:C:186:LYS:HD3	1:C:218:GLU:HG3	1.50	0.93
1:D:260:TRP:C	1:D:262:PRO:HD2	1.89	0.93
1:G:220:ALA:HB3	1:G:261:ILE:CG2	1.99	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:186:LYS:HD3	1:F:218:GLU:HG3	1.50	0.92
1:D:312:SER:HB2	1:D:502:LEU:O	1.70	0.92
1:G:290:SER:H	1:G:325:GLN:HE21	1.16	0.92
1:C:97:TRP:CZ3	1:C:99:ALA:HB2	2.05	0.92
1:D:166:MET:HE2	1:D:171:CYS:SG	2.08	0.92
1:B:244:ASN:C	1:B:244:ASN:ND2	2.14	0.91
1:E:248:ARG:HB3	1:E:248:ARG:HH11	1.34	0.91
1:G:186:LYS:HD3	1:G:218:GLU:HG3	1.50	0.91
1:D:248:ARG:HH11	1:D:248:ARG:HB3	1.35	0.91
1:B:492:LEU:H	1:B:492:LEU:HD12	1.33	0.91
1:D:290:SER:H	1:D:325:GLN:HE21	1.14	0.91
1:F:312:SER:HB2	1:F:502:LEU:O	1.71	0.91
1:A:344:GLU:HG3	1:A:349:THR:HG22	1.53	0.91
1:D:216:VAL:HG11	1:D:230:VAL:CG2	2.01	0.91
1:B:228:VAL:HB	1:B:261:ILE:HD11	1.52	0.91
1:B:344:GLU:HG3	1:B:349:THR:HG22	1.51	0.91
1:E:483:ILE:H	1:E:483:ILE:CD1	1.83	0.91
1:E:499:ILE:HG22	1:E:519:LEU:HB2	1.53	0.90
1:B:510:MET:CE	1:B:547:TYR:HE1	1.84	0.90
1:D:412:MET:HA	1:D:416:LEU:CD1	2.00	0.90
1:E:289:PHE:H	1:E:296:ASN:HD21	1.19	0.90
1:B:282:GLU:OE2	1:B:282:GLU:HA	1.69	0.90
1:D:152:LYS:HD3	1:D:203:ILE:HD11	1.53	0.90
1:D:259:PRO:O	1:D:260:TRP:HB3	1.68	0.90
1:F:450:LYS:CE	1:F:454:LYS:HD3	2.01	0.90
1:C:290:SER:H	1:C:325:GLN:HE21	1.10	0.90
1:D:289:PHE:H	1:D:296:ASN:HD21	1.15	0.90
1:D:510:MET:CE	1:D:547:TYR:CE1	2.54	0.90
1:D:483:ILE:H	1:D:483:ILE:CD1	1.84	0.90
1:E:290:SER:H	1:E:325:GLN:HE21	1.20	0.90
1:E:469:PRO:O	1:E:470:ASP:HB2	1.71	0.90
1:F:344:GLU:HG3	1:F:349:THR:HG22	1.51	0.90
1:G:312:SER:HB2	1:G:502:LEU:O	1.72	0.90
1:A:510:MET:CE	1:A:547:TYR:CE1	2.55	0.90
1:C:261:ILE:N	1:C:262:PRO:HD2	1.84	0.90
1:C:469:PRO:O	1:C:470:ASP:HB2	1.71	0.90
1:D:260:TRP:HB2	1:D:262:PRO:HG3	1.49	0.90
1:A:186:LYS:HD3	1:A:218:GLU:HG3	1.52	0.89
1:A:499:ILE:HG22	1:A:519:LEU:HB2	1.53	0.89
1:E:97:TRP:CZ3	1:E:99:ALA:HB2	2.08	0.89
1:B:409:LEU:HD23	1:B:421:ILE:HG21	1.53	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:127:ASP:O	1:E:128:LYS:CB	2.19	0.89
1:E:261:ILE:N	1:E:262:PRO:CD	2.31	0.89
1:F:316:MET:HE1	1:F:535:TYR:CZ	2.08	0.89
1:A:97:TRP:CZ3	1:A:99:ALA:HB2	2.07	0.89
1:B:441:MET:O	1:B:441:MET:CE	2.21	0.89
1:F:546:SER:O	1:F:547:TYR:HB2	1.70	0.89
1:G:220:ALA:HB1	1:G:261:ILE:HG21	1.54	0.89
1:G:409:LEU:HD23	1:G:421:ILE:HG21	1.52	0.89
1:A:409:LEU:HD23	1:A:421:ILE:HG21	1.55	0.89
1:C:107:GLN:HB2	1:C:124:ARG:HG3	1.53	0.89
1:C:344:GLU:HG3	1:C:349:THR:HG22	1.53	0.89
1:G:510:MET:CE	1:G:547:TYR:HE1	1.86	0.89
1:E:168:LEU:HD21	1:E:247:ASP:OD2	1.72	0.89
1:G:401:GLU:HG3	1:G:431:SER:O	1.73	0.88
1:C:510:MET:CE	1:C:547:TYR:CE1	2.56	0.88
1:B:499:ILE:HG22	1:B:519:LEU:HB2	1.53	0.88
1:A:248:ARG:HB3	1:A:248:ARG:HH11	1.38	0.88
1:E:107:GLN:HB2	1:E:124:ARG:HG3	1.56	0.88
1:A:412:MET:HA	1:A:416:LEU:CD1	2.03	0.88
1:F:217:GLU:OE2	1:F:261:ILE:HG22	1.72	0.88
1:C:168:LEU:HD21	1:C:247:ASP:OD2	1.73	0.88
1:C:260:TRP:HB2	1:C:262:PRO:CD	2.04	0.88
1:E:490:GLY:HA2	1:E:493:ARG:HG3	1.56	0.88
1:C:290:SER:N	1:C:325:GLN:NE2	2.22	0.88
1:B:168:LEU:HD21	1:B:247:ASP:OD2	1.73	0.87
1:G:108:VAL:HG13	1:G:123:VAL:HG22	1.56	0.87
1:B:510:MET:CE	1:B:547:TYR:CE1	2.57	0.87
1:G:152:LYS:HD3	1:G:203:ILE:HD11	1.57	0.87
1:A:469:PRO:O	1:A:470:ASP:HB2	1.73	0.87
1:E:370:ARG:HH11	1:E:371:GLU:HG2	1.34	0.87
1:B:107:GLN:HB2	1:B:124:ARG:HG3	1.55	0.87
1:D:199:PHE:O	1:D:227:LYS:HE2	1.75	0.87
1:F:168:LEU:HD21	1:F:247:ASP:OD2	1.75	0.87
1:C:289:PHE:H	1:C:296:ASN:HD21	1.21	0.87
1:E:108:VAL:HG13	1:E:123:VAL:HG22	1.57	0.87
1:A:483:ILE:H	1:A:483:ILE:CD1	1.88	0.86
1:F:178:LEU:HB3	1:F:181:GLY:HA2	1.57	0.86
1:A:510:MET:CE	1:A:547:TYR:HE1	1.88	0.86
1:D:339:LEU:HB3	1:D:341:MET:HE1	1.55	0.86
1:G:168:LEU:HD21	1:G:247:ASP:OD2	1.74	0.86
1:A:366:ASP:HB2	1:C:285:VAL:CG2	2.05	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:412:MET:HA	1:B:416:LEU:CD1	2.04	0.86
1:D:108:VAL:HG13	1:D:123:VAL:HG22	1.57	0.86
1:E:283:GLU:HG2	1:E:284:SER:N	1.89	0.86
1:G:276:ARG:HH11	1:G:276:ARG:HB3	0.69	0.86
1:C:316:MET:HE1	1:C:535:TYR:CZ	2.09	0.86
1:D:450:LYS:HE2	1:D:454:LYS:HD3	1.58	0.86
1:F:107:GLN:CB	1:F:124:ARG:HG3	2.06	0.86
1:A:510:MET:HE3	1:A:547:TYR:HE1	1.37	0.86
1:A:290:SER:H	1:A:325:GLN:HE21	1.17	0.86
1:D:107:GLN:HB2	1:D:124:ARG:HG3	1.56	0.86
1:E:412:MET:HE2	1:E:421:ILE:CD1	2.04	0.86
1:G:216:VAL:HG11	1:G:230:VAL:CG2	2.06	0.86
1:D:166:MET:CE	1:D:171:CYS:SG	2.64	0.85
1:E:315:GLY:HA2	1:E:317:VAL:HG23	1.58	0.85
1:G:107:GLN:HB2	1:G:124:ARG:HG3	1.56	0.85
1:G:504:ARG:CD	1:G:506:GLN:HG2	2.06	0.85
1:C:166:MET:HE2	1:C:171:CYS:SG	2.17	0.85
1:C:127:ASP:O	1:C:128:LYS:CB	2.24	0.85
1:G:412:MET:HA	1:G:416:LEU:CD1	2.04	0.85
1:G:97:TRP:CZ3	1:G:99:ALA:HB2	2.12	0.85
1:C:166:MET:CE	1:C:171:CYS:SG	2.65	0.85
1:C:499:ILE:HG22	1:C:519:LEU:HB2	1.59	0.85
1:E:108:VAL:HG12	1:E:121:GLN:HG2	1.59	0.85
1:E:312:SER:HB2	1:E:502:LEU:O	1.77	0.85
1:A:251:MET:HA	1:A:251:MET:HE2	1.57	0.85
1:C:108:VAL:HG13	1:C:123:VAL:HG22	1.59	0.85
1:E:482:SER:H	1:E:485:ASP:HB2	1.41	0.85
1:B:108:VAL:HG13	1:B:123:VAL:HG22	1.56	0.84
1:D:220:ALA:HB3	1:D:261:ILE:HG21	0.88	0.84
1:G:510:MET:CE	1:G:547:TYR:CE1	2.60	0.84
1:B:490:GLY:HA2	1:B:493:ARG:HG3	1.58	0.84
1:E:413:ARG:HE	1:E:458:VAL:HB	1.43	0.84
1:D:168:LEU:HD21	1:D:247:ASP:OD2	1.75	0.84
1:F:425:HIS:CE1	1:F:427:SER:HB2	2.13	0.84
1:D:344:GLU:HG3	1:D:349:THR:HG22	1.58	0.84
1:A:482:SER:H	1:A:485:ASP:HB2	1.41	0.84
1:B:141:LEU:HD13	1:B:176:VAL:HG21	1.60	0.84
1:B:152:LYS:HD3	1:B:203:ILE:HD11	1.58	0.84
1:C:369:LYS:HG2	1:D:279:LEU:HD23	1.58	0.84
1:E:370:ARG:CD	1:E:371:GLU:N	2.41	0.84
1:G:166:MET:CE	1:G:171:CYS:SG	2.66	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:289:PHE:H	1:B:296:ASN:HD21	1.25	0.84
1:D:442:ILE:HD11	1:D:492:LEU:HD21	1.60	0.84
1:F:152:LYS:HD3	1:F:203:ILE:HD11	1.59	0.84
1:F:107:GLN:HB2	1:F:124:ARG:CG	2.08	0.83
1:F:178:LEU:CB	1:F:181:GLY:HA2	2.08	0.83
1:G:309:MET:HB3	1:G:499:ILE:HD12	1.61	0.83
1:G:199:PHE:O	1:G:227:LYS:HE2	1.77	0.83
1:G:166:MET:HE2	1:G:171:CYS:SG	2.19	0.83
1:G:482:SER:H	1:G:485:ASP:HB2	1.44	0.83
1:A:492:LEU:HD12	1:A:492:LEU:H	1.41	0.83
1:E:492:LEU:H	1:E:492:LEU:HD12	1.43	0.83
1:E:510:MET:CE	1:E:547:TYR:HE1	1.91	0.83
1:C:216:VAL:HG11	1:C:230:VAL:CG2	2.09	0.83
1:D:409:LEU:CD2	1:D:421:ILE:HG21	2.09	0.83
1:C:141:LEU:HD13	1:C:176:VAL:HG21	1.60	0.83
1:B:309:MET:HB3	1:B:499:ILE:HD12	1.59	0.83
1:F:290:SER:H	1:F:325:GLN:HE21	1.22	0.83
1:B:469:PRO:O	1:B:470:ASP:HB2	1.78	0.82
1:D:309:MET:HB3	1:D:499:ILE:HD12	1.59	0.82
1:A:220:ALA:CB	1:A:261:ILE:HG21	2.08	0.82
1:B:427:SER:HB3	1:B:487:ARG:HH12	1.43	0.82
1:D:290:SER:N	1:D:325:GLN:NE2	2.25	0.82
1:G:290:SER:N	1:G:325:GLN:NE2	2.28	0.82
1:D:289:PHE:N	1:D:296:ASN:HD21	1.76	0.82
1:B:253:GLN:HA	1:B:257:ALA:HB2	1.62	0.82
1:B:441:MET:O	1:B:441:MET:HE1	1.78	0.82
1:C:178:LEU:CB	1:C:181:GLY:HA2	2.09	0.82
1:D:338:GLY:HA3	1:D:412:MET:CE	2.10	0.82
1:D:490:GLY:HA2	1:D:493:ARG:HG3	1.59	0.82
1:G:178:LEU:CB	1:G:181:GLY:HA2	2.09	0.82
1:A:178:LEU:CB	1:A:181:GLY:HA2	2.09	0.81
1:E:405:LEU:HG	1:E:409:LEU:HD12	1.62	0.81
1:G:166:MET:HE1	1:G:171:CYS:HB3	1.58	0.81
1:C:405:LEU:HG	1:C:409:LEU:HD12	1.62	0.81
1:F:469:PRO:O	1:F:470:ASP:HB2	1.80	0.81
1:G:315:GLY:HA2	1:G:317:VAL:HG23	1.62	0.81
1:A:126:LYS:CE	1:A:127:ASP:OD1	2.28	0.81
1:C:482:SER:H	1:C:485:ASP:HB2	1.46	0.81
1:E:141:LEU:HD13	1:E:176:VAL:HG21	1.60	0.81
1:F:425:HIS:HE1	1:F:427:SER:CB	1.93	0.81
1:F:482:SER:H	1:F:485:ASP:HB2	1.45	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:LEU:O	1:A:169:GLN:HB2	1.78	0.81
1:A:510:MET:HE3	1:A:547:TYR:CE1	2.15	0.81
1:B:97:TRP:CZ3	1:B:99:ALA:HB2	2.15	0.81
1:G:339:LEU:HB3	1:G:341:MET:CE	2.10	0.81
1:A:347:GLU:OE1	1:C:274:ARG:HD2	1.81	0.81
1:C:152:LYS:HD3	1:C:203:ILE:HD11	1.63	0.81
1:D:316:MET:HE1	1:D:535:TYR:CZ	2.16	0.81
1:G:344:GLU:HG3	1:G:349:THR:HG22	1.60	0.81
1:A:253:GLN:CA	1:A:257:ALA:HB2	2.11	0.81
1:F:492:LEU:H	1:F:492:LEU:HD12	1.43	0.81
1:D:469:PRO:O	1:D:470:ASP:HB2	1.80	0.81
1:A:292:CYS:O	1:A:295:ILE:HG12	1.80	0.81
1:E:510:MET:CE	1:E:547:TYR:CE1	2.63	0.81
1:F:425:HIS:CE1	1:F:427:SER:OG	2.33	0.81
1:G:515:LEU:HD21	1:G:529:ILE:CD1	2.10	0.81
1:A:107:GLN:HB2	1:A:124:ARG:HG3	1.61	0.81
1:C:309:MET:HB3	1:C:499:ILE:HD12	1.62	0.81
1:A:141:LEU:HD11	1:A:196:PHE:CZ	2.15	0.80
1:A:229:ARG:CB	1:A:258:GLY:O	2.29	0.80
1:A:260:TRP:C	1:A:261:ILE:HG22	1.98	0.80
1:A:290:SER:N	1:A:325:GLN:NE2	2.28	0.80
1:D:178:LEU:CB	1:D:181:GLY:HA2	2.11	0.80
1:D:260:TRP:HB2	1:D:262:PRO:CD	2.10	0.80
1:C:108:VAL:HG12	1:C:121:GLN:HG2	1.62	0.80
1:C:473:LYS:HE2	1:C:479:ARG:HA	1.62	0.80
1:E:152:LYS:HD3	1:E:203:ILE:HD11	1.63	0.80
1:E:344:GLU:HG3	1:E:349:THR:HG22	1.62	0.80
1:F:108:VAL:HG13	1:F:123:VAL:HG22	1.63	0.80
1:A:229:ARG:HB2	1:A:258:GLY:O	1.81	0.80
1:B:283:GLU:CD	1:B:286:GLY:HA2	2.01	0.80
1:E:220:ALA:HB1	1:E:261:ILE:HD13	1.63	0.80
1:B:216:VAL:HG11	1:B:230:VAL:CG2	2.11	0.80
1:D:413:ARG:HE	1:D:458:VAL:HB	1.47	0.80
1:D:473:LYS:HG3	1:D:479:ARG:HB2	1.64	0.80
1:E:515:LEU:HD21	1:E:529:ILE:CD1	2.12	0.80
1:A:369:LYS:HG2	1:C:279:LEU:CD2	2.12	0.80
1:C:199:PHE:O	1:C:227:LYS:HE2	1.81	0.80
1:B:108:VAL:HG12	1:B:121:GLN:HG2	1.64	0.79
1:C:121:GLN:HB2	1:C:133:THR:OG1	1.82	0.79
1:F:283:GLU:OE2	1:F:286:GLY:CA	2.29	0.79
1:F:425:HIS:CE1	1:F:427:SER:CB	2.65	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:LEU:HD13	1:A:176:VAL:HG21	1.63	0.79
1:C:166:MET:HE1	1:C:171:CYS:HB3	1.63	0.79
1:D:141:LEU:HD11	1:D:196:PHE:CZ	2.16	0.79
1:D:412:MET:HE2	1:D:421:ILE:CD1	2.12	0.79
1:D:450:LYS:CE	1:D:454:LYS:HD3	2.12	0.79
1:A:427:SER:HB3	1:A:487:ARG:HH12	1.48	0.79
1:C:141:LEU:HD11	1:C:196:PHE:CZ	2.18	0.79
1:C:492:LEU:H	1:C:492:LEU:HD12	1.46	0.79
1:G:510:MET:HE3	1:G:547:TYR:HE1	1.45	0.79
1:A:121:GLN:HB2	1:A:133:THR:OG1	1.82	0.79
1:A:261:ILE:HG12	1:A:261:ILE:O	1.83	0.79
1:E:178:LEU:CB	1:E:181:GLY:HA2	2.13	0.79
1:A:413:ARG:HE	1:A:458:VAL:HB	1.48	0.79
1:E:411:TYR:HE1	1:F:265:VAL:HG11	1.47	0.79
1:A:199:PHE:O	1:A:227:LYS:HE2	1.83	0.79
1:D:515:LEU:HD21	1:D:529:ILE:CD1	2.13	0.79
1:F:166:MET:CE	1:F:171:CYS:SG	2.71	0.79
1:A:152:LYS:HG3	1:A:201:GLN:HG2	1.65	0.79
1:A:473:LYS:HG3	1:A:479:ARG:HB2	1.65	0.79
1:C:168:LEU:CD2	1:C:247:ASP:OD2	2.31	0.79
1:E:108:VAL:CG1	1:E:121:GLN:HG2	2.13	0.79
1:E:168:LEU:CD2	1:E:247:ASP:OD2	2.30	0.79
1:F:473:LYS:HE2	1:F:479:ARG:HA	1.64	0.79
1:G:405:LEU:HG	1:G:409:LEU:HD12	1.65	0.79
1:A:220:ALA:HB1	1:A:261:ILE:HD12	1.65	0.78
1:D:483:ILE:O	1:D:486:LEU:CB	2.25	0.78
1:F:292:CYS:O	1:F:295:ILE:HG12	1.82	0.78
1:C:107:GLN:HB2	1:C:124:ARG:CG	2.13	0.78
1:C:488:GLY:HA3	1:C:492:LEU:HD11	1.66	0.78
1:D:405:LEU:HG	1:D:409:LEU:HD12	1.64	0.78
1:E:166:MET:CE	1:E:171:CYS:SG	2.71	0.78
1:E:442:ILE:HD11	1:E:492:LEU:HD21	1.63	0.78
1:G:425:HIS:CE1	1:G:427:SER:OG	2.35	0.78
1:A:395:ASP:HB3	1:C:266:VAL:HG21	1.64	0.78
1:B:442:ILE:CD1	1:B:492:LEU:HD11	2.12	0.78
1:C:108:VAL:CG1	1:C:121:GLN:HG2	2.13	0.78
1:E:216:VAL:HG11	1:E:230:VAL:HG21	1.64	0.78
1:G:425:HIS:HE1	1:G:427:SER:OG	1.65	0.78
1:C:107:GLN:CB	1:C:124:ARG:HG3	2.12	0.78
1:E:292:CYS:O	1:E:295:ILE:HG12	1.83	0.78
1:G:141:LEU:HD13	1:G:176:VAL:HG21	1.63	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:LEU:HB3	1:A:181:GLY:HA2	1.64	0.78
1:C:339:LEU:HB3	1:C:341:MET:HE1	1.66	0.78
1:A:490:GLY:HA2	1:A:493:ARG:HG3	1.63	0.78
1:G:473:LYS:HG3	1:G:479:ARG:HB2	1.65	0.78
1:C:368:LEU:O	1:C:368:LEU:HD22	1.84	0.78
1:F:168:LEU:CD2	1:F:247:ASP:OD2	2.32	0.78
1:A:154:VAL:HB	1:A:175:VAL:HG13	1.65	0.78
1:D:153:ILE:HG13	1:D:174:PRO:HB2	1.66	0.78
1:E:473:LYS:HG3	1:E:479:ARG:HB2	1.66	0.78
1:F:378:PHE:CE2	1:G:276:ARG:HD3	2.19	0.78
1:D:321:PHE:HD2	1:D:533:MET:HE1	1.47	0.78
1:E:166:MET:HE2	1:E:171:CYS:SG	2.24	0.78
1:E:303:ARG:O	1:E:306:GLU:HG3	1.83	0.78
1:G:168:LEU:CD2	1:G:247:ASP:OD2	2.32	0.78
1:A:253:GLN:HA	1:A:257:ALA:HB2	1.67	0.77
1:B:152:LYS:HG3	1:B:201:GLN:HG2	1.65	0.77
1:A:401:GLU:HG2	1:A:402:THR:N	1.99	0.77
1:A:414:SER:HB3	1:C:226:GLY:H	1.50	0.77
1:A:126:LYS:CG	1:A:127:ASP:N	2.44	0.77
1:A:405:LEU:HG	1:A:409:LEU:HD12	1.65	0.77
1:E:290:SER:N	1:E:325:GLN:NE2	2.32	0.77
1:F:121:GLN:HB3	1:F:133:THR:HG23	1.65	0.77
1:F:504:ARG:HH21	1:F:506:GLN:HB3	1.47	0.77
1:G:108:VAL:HG12	1:G:121:GLN:HG2	1.65	0.77
1:B:168:LEU:CD2	1:B:247:ASP:OD2	2.32	0.77
1:D:259:PRO:O	1:D:260:TRP:CB	2.33	0.77
1:F:220:ALA:CB	1:F:261:ILE:HG12	2.15	0.77
1:A:339:LEU:HB3	1:A:341:MET:HE1	1.65	0.77
1:B:166:MET:CE	1:B:171:CYS:SG	2.73	0.77
1:D:283:GLU:OE2	1:D:286:GLY:HA2	1.84	0.77
1:A:425:HIS:CE1	1:A:427:SER:OG	2.37	0.77
1:B:290:SER:H	1:B:325:GLN:HE21	1.32	0.77
1:C:409:LEU:CD2	1:C:421:ILE:HG21	2.15	0.77
1:G:178:LEU:HB3	1:G:181:GLY:HA2	1.65	0.77
1:G:469:PRO:O	1:G:470:ASP:HB2	1.85	0.77
1:B:166:MET:HE2	1:B:171:CYS:SG	2.24	0.77
1:C:205:MET:HA	1:C:231:ALA:HB3	1.66	0.77
1:G:141:LEU:HD11	1:G:196:PHE:CZ	2.20	0.77
1:B:199:PHE:O	1:B:227:LYS:HE2	1.83	0.77
1:G:152:LYS:HG3	1:G:201:GLN:HG2	1.66	0.77
1:A:442:ILE:HD11	1:A:492:LEU:HD21	1.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:482:SER:H	1:B:485:ASP:HB2	1.47	0.77
1:D:127:ASP:O	1:D:128:LYS:CB	2.23	0.77
1:D:482:SER:H	1:D:485:ASP:HB2	1.48	0.77
1:C:473:LYS:HG3	1:C:479:ARG:HB2	1.66	0.77
1:D:427:SER:HB3	1:D:487:ARG:HH12	1.48	0.76
1:F:251:MET:HA	1:F:251:MET:CE	2.16	0.76
1:B:178:LEU:CB	1:B:181:GLY:HA2	2.14	0.76
1:B:321:PHE:HD2	1:B:533:MET:HE3	1.50	0.76
1:D:499:ILE:CG2	1:D:519:LEU:HB2	2.16	0.76
1:F:409:LEU:CD2	1:F:421:ILE:HG21	2.15	0.76
1:B:248:ARG:HH11	1:B:248:ARG:HB3	0.59	0.76
1:B:292:CYS:O	1:B:295:ILE:HG12	1.85	0.76
1:B:442:ILE:HD12	1:B:488:GLY:HA2	1.67	0.76
1:F:358:ASN:O	1:F:360:VAL:HG13	1.86	0.76
1:F:504:ARG:NH2	1:F:506:GLN:HB3	1.99	0.76
1:G:409:LEU:CD2	1:G:421:ILE:HG21	2.15	0.76
1:B:290:SER:N	1:B:325:GLN:NE2	2.33	0.76
1:B:473:LYS:HE2	1:B:479:ARG:HA	1.68	0.76
1:F:112:ARG:HG3	1:F:145:HIS:CD2	2.20	0.76
1:A:257:ALA:O	1:A:258:GLY:O	2.04	0.76
1:A:442:ILE:CD1	1:A:492:LEU:HD11	2.16	0.76
1:B:107:GLN:CB	1:B:124:ARG:HG3	2.14	0.76
1:F:315:GLY:HA2	1:F:317:VAL:HG23	1.66	0.76
1:E:482:SER:OG	1:E:484:THR:HG23	1.85	0.76
1:F:217:GLU:OE2	1:F:261:ILE:CG2	2.33	0.76
1:D:152:LYS:HG3	1:D:201:GLN:HG2	1.68	0.76
1:G:246:HIS:HB2	1:G:249:GLU:HB2	1.68	0.76
1:B:316:MET:HE1	1:B:535:TYR:CE2	2.21	0.75
1:B:483:ILE:O	1:B:486:LEU:CB	2.29	0.75
1:D:168:LEU:CD2	1:D:247:ASP:OD2	2.33	0.75
1:D:473:LYS:HE2	1:D:479:ARG:HA	1.68	0.75
1:G:490:GLY:HA2	1:G:493:ARG:HG3	1.67	0.75
1:D:220:ALA:CB	1:D:261:ILE:CG2	2.53	0.75
1:F:311:THR:O	1:F:312:SER:HB3	1.86	0.75
1:B:283:GLU:OE2	1:B:286:GLY:HA2	1.86	0.75
1:B:358:ASN:O	1:B:360:VAL:HG13	1.85	0.75
1:C:482:SER:OG	1:C:484:THR:HG23	1.87	0.75
1:E:261:ILE:H	1:E:262:PRO:HD2	1.47	0.75
1:F:473:LYS:HG3	1:F:479:ARG:HB2	1.66	0.75
1:G:504:ARG:HH21	1:G:506:GLN:HB3	1.52	0.75
1:E:358:ASN:O	1:E:360:VAL:HG13	1.87	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:415:GLY:HA2	1:G:226:GLY:N	2.01	0.75
1:G:442:ILE:CD1	1:G:492:LEU:HD11	2.17	0.75
1:G:482:SER:OG	1:G:484:THR:HG23	1.87	0.75
1:E:229:ARG:NH2	1:E:259:PRO:HG3	2.02	0.75
1:F:425:HIS:HE1	1:F:427:SER:OG	1.66	0.75
1:G:205:MET:HA	1:G:231:ALA:HB3	1.68	0.75
1:A:369:LYS:HG2	1:C:279:LEU:HD23	1.66	0.75
1:B:121:GLN:HB2	1:B:133:THR:OG1	1.86	0.75
1:C:442:ILE:CD1	1:C:492:LEU:HD11	2.15	0.75
1:B:121:GLN:HB3	1:B:133:THR:HG23	1.69	0.75
1:B:141:LEU:HD11	1:B:196:PHE:CZ	2.21	0.75
1:C:295:ILE:O	1:C:299:THR:HG23	1.87	0.75
1:D:303:ARG:O	1:D:306:GLU:HG3	1.86	0.75
1:B:315:GLY:HA2	1:B:317:VAL:HG23	1.69	0.75
1:F:216:VAL:HG11	1:F:230:VAL:CG2	2.17	0.75
1:F:368:LEU:HD22	1:F:368:LEU:O	1.87	0.75
1:G:289:PHE:H	1:G:296:ASN:HD21	1.34	0.74
1:A:68:VAL:HG12	1:A:121:GLN:OE1	1.86	0.74
1:E:166:MET:HE1	1:E:171:CYS:HB3	1.68	0.74
1:F:152:LYS:HG3	1:F:201:GLN:HG2	1.69	0.74
1:B:127:ASP:O	1:B:128:LYS:CB	2.30	0.74
1:B:482:SER:OG	1:B:484:THR:HG23	1.86	0.74
1:C:442:ILE:HD12	1:C:488:GLY:HA2	1.69	0.74
1:E:246:HIS:HB2	1:E:249:GLU:HB2	1.69	0.74
1:G:121:GLN:HB2	1:G:133:THR:OG1	1.87	0.74
1:A:126:LYS:HZ2	1:A:127:ASP:N	1.85	0.74
1:C:229:ARG:NH2	1:C:259:PRO:HB3	2.03	0.74
1:E:258:GLY:HA3	1:E:260:TRP:HZ3	1.52	0.74
1:G:483:ILE:O	1:G:486:LEU:CB	2.32	0.74
1:B:220:ALA:HB1	1:B:261:ILE:HD12	1.69	0.74
1:E:178:LEU:HB3	1:E:181:GLY:HA2	1.69	0.74
1:E:112:ARG:HG3	1:E:145:HIS:CD2	2.23	0.74
1:E:316:MET:HE3	1:E:535:TYR:CZ	2.22	0.74
1:F:405:LEU:HG	1:F:409:LEU:HD12	1.68	0.74
1:G:260:TRP:O	1:G:262:PRO:HD2	1.87	0.74
1:G:412:MET:HE2	1:G:421:ILE:CD1	2.18	0.74
1:A:261:ILE:O	1:A:261:ILE:CG1	2.34	0.74
1:B:108:VAL:CG1	1:B:121:GLN:HG2	2.18	0.74
1:B:368:LEU:O	1:B:368:LEU:HD22	1.88	0.74
1:D:205:MET:HA	1:D:231:ALA:HB3	1.70	0.74
1:E:473:LYS:HE2	1:E:479:ARG:HA	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:107:GLN:CB	1:G:124:ARG:HG3	2.18	0.74
1:D:178:LEU:HB3	1:D:181:GLY:HA2	1.70	0.74
1:E:107:GLN:CB	1:E:124:ARG:HG3	2.17	0.74
1:F:372:ILE:HA	1:F:375:ASN:OD1	1.87	0.74
1:F:499:ILE:CG2	1:F:519:LEU:HB2	2.18	0.74
1:D:141:LEU:HD13	1:D:176:VAL:HG21	1.69	0.74
1:A:510:MET:HE2	1:A:513:LEU:HD22	1.68	0.73
1:C:446:MET:HE3	1:C:492:LEU:HA	1.70	0.73
1:E:420:VAL:HG22	1:E:459:VAL:HB	1.68	0.73
1:B:166:MET:HE1	1:B:171:CYS:HB3	1.70	0.73
1:B:289:PHE:N	1:B:296:ASN:HD21	1.86	0.73
1:B:450:LYS:CE	1:B:454:LYS:CD	2.66	0.73
1:C:251:MET:HE2	1:C:251:MET:HA	1.68	0.73
1:C:413:ARG:HE	1:C:458:VAL:HB	1.53	0.73
1:E:322:VAL:HG21	1:E:463:ILE:HD11	1.70	0.73
1:E:411:TYR:CE1	1:F:262:PRO:HB3	2.23	0.73
1:B:510:MET:HE3	1:B:547:TYR:HE1	1.51	0.73
1:C:372:ILE:HA	1:C:375:ASN:OD1	1.89	0.73
1:D:311:THR:O	1:D:312:SER:HB3	1.88	0.73
1:E:261:ILE:N	1:E:262:PRO:HD2	2.02	0.73
1:F:366:ASP:HB2	1:G:284:SER:CB	2.17	0.73
1:A:425:HIS:CE1	1:A:465:HIS:CG	2.76	0.73
1:B:229:ARG:HH21	1:B:259:PRO:HB3	1.52	0.73
1:C:229:ARG:CZ	1:C:259:PRO:HB3	2.18	0.73
1:F:389:ASP:HA	1:G:269:LEU:CD2	2.17	0.73
1:A:289:PHE:H	1:A:296:ASN:HD21	1.35	0.73
1:A:368:LEU:O	1:A:368:LEU:HD22	1.88	0.73
1:B:186:LYS:HD3	1:B:218:GLU:CG	2.19	0.73
1:C:152:LYS:HG3	1:C:201:GLN:HG2	1.71	0.73
1:C:369:LYS:HG2	1:D:279:LEU:CD2	2.17	0.73
1:E:199:PHE:O	1:E:227:LYS:HE2	1.89	0.73
1:E:409:LEU:CD2	1:E:421:ILE:HG21	2.17	0.73
1:A:256:ASN:OD1	1:A:257:ALA:N	2.21	0.73
1:F:295:ILE:O	1:F:299:THR:HG23	1.87	0.73
1:E:368:LEU:HD22	1:E:372:ILE:HG23	1.68	0.73
1:G:111:TYR:CE2	1:G:142:PHE:HB2	2.23	0.73
1:C:515:LEU:HD21	1:C:529:ILE:CD1	2.19	0.73
1:D:108:VAL:HG12	1:D:121:GLN:HG2	1.68	0.73
1:F:515:LEU:HD21	1:F:529:ILE:CD1	2.18	0.73
1:F:321:PHE:HD2	1:F:533:MET:HE3	1.54	0.73
1:F:504:ARG:CD	1:F:506:GLN:HG2	2.11	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:427:SER:HB3	1:G:487:ARG:HH12	1.53	0.73
1:A:112:ARG:HG3	1:A:145:HIS:CD2	2.23	0.73
1:E:121:GLN:HB2	1:E:133:THR:OG1	1.88	0.73
1:F:248:ARG:HB3	1:F:248:ARG:NH1	2.04	0.73
1:G:413:ARG:HE	1:G:458:VAL:HB	1.53	0.73
1:A:104:VAL:HG12	1:A:106:TYR:CE1	2.24	0.72
1:A:358:ASN:O	1:A:360:VAL:HG13	1.88	0.72
1:D:217:GLU:OE2	1:D:261:ILE:HA	1.89	0.72
1:A:488:GLY:HA3	1:A:492:LEU:HD11	1.71	0.72
1:B:488:GLY:HA3	1:B:492:LEU:HD11	1.71	0.72
1:E:152:LYS:HG3	1:E:201:GLN:HG2	1.70	0.72
1:F:290:SER:N	1:F:325:GLN:NE2	2.32	0.72
1:C:248:ARG:HB3	1:C:248:ARG:NH1	2.04	0.72
1:E:442:ILE:CD1	1:E:492:LEU:HD11	2.19	0.72
1:A:446:MET:HE2	1:A:492:LEU:HB3	1.71	0.72
1:B:248:ARG:HH11	1:B:248:ARG:HB2	1.45	0.72
1:B:205:MET:HA	1:B:231:ALA:HB3	1.71	0.72
1:D:358:ASN:O	1:D:360:VAL:HG13	1.89	0.72
1:C:246:HIS:HB2	1:C:249:GLU:HB2	1.71	0.72
1:D:154:VAL:HB	1:D:175:VAL:HG13	1.71	0.72
1:E:289:PHE:N	1:E:296:ASN:HD21	1.87	0.72
1:F:389:ASP:HA	1:G:269:LEU:HD23	1.70	0.72
1:A:253:GLN:O	1:A:257:ALA:HB2	1.90	0.72
1:C:94:ALA:HB1	1:C:162:MET:HE3	1.72	0.72
1:C:261:ILE:N	1:C:262:PRO:CD	2.35	0.72
1:C:268:ALA:HA	1:C:271:LEU:CD1	2.19	0.72
1:C:490:GLY:HA2	1:C:493:ARG:HG3	1.70	0.72
1:E:321:PHE:HD2	1:E:533:MET:HE3	1.53	0.72
1:E:488:GLY:HA3	1:E:492:LEU:HD11	1.72	0.72
1:A:409:LEU:CD2	1:A:421:ILE:HG21	2.20	0.72
1:B:467:LYS:HE3	1:B:486:LEU:O	1.90	0.72
1:D:121:GLN:HB2	1:D:133:THR:OG1	1.90	0.72
1:E:141:LEU:HD11	1:E:196:PHE:CZ	2.25	0.72
1:E:425:HIS:CE1	1:E:427:SER:OG	2.43	0.72
1:F:108:VAL:HG12	1:F:121:GLN:HG2	1.71	0.72
1:F:268:ALA:HA	1:F:271:LEU:CD1	2.19	0.72
1:F:316:MET:HE1	1:F:535:TYR:CE2	2.24	0.72
1:A:467:LYS:HE3	1:A:486:LEU:O	1.89	0.72
1:B:260:TRP:O	1:B:261:ILE:HG12	1.90	0.72
1:B:447:THR:HG22	1:B:495:LEU:CD2	2.18	0.72
1:B:454:LYS:HZ2	1:G:344:GLU:HA	1.53	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:290:SER:H	1:C:325:GLN:HE22	1.33	0.72
1:C:536:ASN:HD22	1:C:538:GLU:H	1.36	0.72
1:D:351:GLU:OE1	1:E:278:HIS:CD2	2.43	0.72
1:D:488:GLY:HA3	1:D:492:LEU:HD11	1.71	0.72
1:G:499:ILE:CG2	1:G:519:LEU:HB2	2.19	0.72
1:B:112:ARG:HG3	1:B:145:HIS:CD2	2.25	0.71
1:D:510:MET:HE3	1:D:547:TYR:HE1	1.52	0.71
1:E:104:VAL:HG12	1:E:106:TYR:CE1	2.24	0.71
1:F:442:ILE:HD11	1:F:492:LEU:HD21	1.71	0.71
1:F:483:ILE:O	1:F:486:LEU:CB	2.32	0.71
1:A:366:ASP:HB2	1:C:285:VAL:HG23	1.72	0.71
1:A:412:MET:CE	1:A:421:ILE:CD1	2.67	0.71
1:C:178:LEU:HB3	1:C:181:GLY:HA2	1.71	0.71
1:C:521:CYS:SG	1:C:524:THR:HG23	2.30	0.71
1:F:104:VAL:HG12	1:F:106:TYR:CE1	2.24	0.71
1:F:339:LEU:HB3	1:F:341:MET:HE1	1.73	0.71
1:A:442:ILE:HD12	1:A:488:GLY:HA2	1.72	0.71
1:F:251:MET:HA	1:F:251:MET:HE2	1.73	0.71
1:G:104:VAL:HG12	1:G:106:TYR:CE1	2.24	0.71
1:G:292:CYS:O	1:G:295:ILE:HG12	1.91	0.71
1:G:504:ARG:NH2	1:G:506:GLN:HB3	2.03	0.71
1:A:372:ILE:HA	1:A:375:ASN:OD1	1.90	0.71
1:C:504:ARG:CD	1:C:506:GLN:HG2	2.18	0.71
1:D:246:HIS:HB2	1:D:249:GLU:HB2	1.73	0.71
1:A:251:MET:HA	1:A:251:MET:CE	2.20	0.71
1:F:482:SER:OG	1:F:484:THR:HG23	1.91	0.71
1:B:107:GLN:HB2	1:B:124:ARG:CG	2.20	0.71
1:B:178:LEU:HB3	1:B:181:GLY:HA2	1.71	0.71
1:E:504:ARG:CD	1:E:506:GLN:HG2	2.12	0.71
1:F:229:ARG:HB2	1:F:258:GLY:O	1.90	0.71
1:F:366:ASP:HB2	1:G:284:SER:HB2	1.70	0.71
1:A:312:SER:N	1:A:318:MET:HE2	2.05	0.71
1:B:321:PHE:CD2	1:B:533:MET:HE3	2.25	0.71
1:F:122:LYS:HE2	1:F:159:GLU:OE1	1.90	0.71
1:A:86:ILE:HG21	1:A:163:LEU:HD12	1.73	0.71
1:B:246:HIS:HB2	1:B:249:GLU:HB2	1.71	0.71
1:B:473:LYS:HG3	1:B:479:ARG:HB2	1.72	0.71
1:C:121:GLN:HB3	1:C:133:THR:HG23	1.73	0.71
1:C:441:MET:CE	1:C:444:ASN:HB3	2.20	0.71
1:E:467:LYS:HE3	1:E:486:LEU:O	1.89	0.71
1:F:289:PHE:H	1:F:296:ASN:HD21	1.39	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:186:LYS:HD3	1:C:218:GLU:CG	2.20	0.71
1:D:292:CYS:O	1:D:295:ILE:HG12	1.91	0.71
1:D:369:LYS:HG2	1:E:279:LEU:CD2	2.21	0.71
1:F:229:ARG:CB	1:F:258:GLY:O	2.39	0.71
1:G:248:ARG:HB3	1:G:248:ARG:NH1	2.04	0.71
1:A:246:HIS:HB2	1:A:249:GLU:HB2	1.73	0.70
1:G:154:VAL:HB	1:G:175:VAL:HG13	1.73	0.70
1:G:228:VAL:HB	1:G:261:ILE:CD1	2.21	0.70
1:B:442:ILE:HD12	1:B:488:GLY:CA	2.21	0.70
1:D:447:THR:CG2	1:D:495:LEU:HD21	2.17	0.70
1:G:268:ALA:HA	1:G:271:LEU:CD1	2.21	0.70
1:G:220:ALA:CB	1:G:261:ILE:CG2	2.58	0.70
1:B:499:ILE:CG2	1:B:519:LEU:HB2	2.21	0.70
1:C:111:TYR:CE2	1:C:142:PHE:HB2	2.26	0.70
1:C:289:PHE:N	1:C:296:ASN:HD21	1.86	0.70
1:D:107:GLN:CB	1:D:124:ARG:HG3	2.20	0.70
1:D:121:GLN:HB3	1:D:133:THR:HG23	1.73	0.70
1:E:490:GLY:CA	1:E:493:ARG:HG3	2.21	0.70
1:B:442:ILE:HD11	1:B:492:LEU:HD21	1.74	0.70
1:E:229:ARG:HA	1:E:259:PRO:HA	1.74	0.70
1:A:424:ASP:OD2	1:A:425:HIS:HB2	1.92	0.70
1:B:154:VAL:HB	1:B:175:VAL:HG13	1.73	0.70
1:C:112:ARG:HG3	1:C:145:HIS:CD2	2.25	0.70
1:D:216:VAL:HG11	1:D:230:VAL:HG21	1.72	0.70
1:F:424:ASP:OD2	1:F:425:HIS:HB2	1.90	0.70
1:G:368:LEU:O	1:G:368:LEU:HD22	1.92	0.70
1:C:420:VAL:HG22	1:C:459:VAL:HB	1.74	0.70
1:D:79:SER:H	1:D:98:ILE:HD13	1.56	0.70
1:D:504:ARG:NH2	1:D:506:GLN:HB3	2.06	0.70
1:F:259:PRO:O	1:F:260:TRP:HB3	1.89	0.70
1:G:166:MET:CE	1:G:171:CYS:CB	2.69	0.70
1:G:473:LYS:HE2	1:G:479:ARG:HA	1.74	0.70
1:A:216:VAL:HG11	1:A:230:VAL:CG2	2.22	0.70
1:B:536:ASN:HD22	1:B:538:GLU:H	1.40	0.70
1:D:111:TYR:CE2	1:D:142:PHE:HB2	2.26	0.70
1:G:467:LYS:HE3	1:G:486:LEU:O	1.91	0.70
1:B:405:LEU:HG	1:B:409:LEU:HD12	1.74	0.70
1:E:321:PHE:CD2	1:E:533:MET:HE3	2.27	0.70
1:F:130:PHE:HB2	1:G:64:MET:CA	2.21	0.70
1:B:278:HIS:CD2	1:G:351:GLU:OE1	2.45	0.70
1:D:490:GLY:CA	1:D:493:ARG:HG3	2.22	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:347:GLU:O	1:E:351:GLU:HG3	1.92	0.70
1:E:413:ARG:O	1:E:417:GLY:HA2	1.91	0.70
1:A:312:SER:N	1:A:318:MET:CE	2.54	0.69
1:A:515:LEU:HD21	1:A:529:ILE:CD1	2.22	0.69
1:D:194:GLU:CD	1:D:194:GLU:H	1.92	0.69
1:E:107:GLN:HB2	1:E:124:ARG:CG	2.21	0.69
1:F:97:TRP:CZ3	1:F:99:ALA:HB2	2.26	0.69
1:F:141:LEU:HD13	1:F:176:VAL:HG21	1.73	0.69
1:F:378:PHE:CD2	1:G:276:ARG:CD	2.75	0.69
1:A:268:ALA:HA	1:A:271:LEU:CD1	2.22	0.69
1:B:441:MET:HE2	1:B:444:ASN:HB3	1.73	0.69
1:F:96:TYR:HE2	1:F:107:GLN:HE21	1.39	0.69
1:F:488:GLY:HA3	1:F:492:LEU:HD11	1.72	0.69
1:D:186:LYS:HD3	1:D:218:GLU:CG	2.23	0.69
1:E:392:HIS:ND1	1:F:267:SER:CB	2.56	0.69
1:F:141:LEU:HD11	1:F:196:PHE:CZ	2.27	0.69
1:A:473:LYS:HE2	1:A:479:ARG:HA	1.73	0.69
1:A:499:ILE:CG2	1:A:519:LEU:HB2	2.23	0.69
1:B:338:GLY:HA3	1:B:412:MET:CE	2.23	0.69
1:D:321:PHE:CD2	1:D:533:MET:HE1	2.26	0.69
1:E:499:ILE:CG2	1:E:519:LEU:HB2	2.21	0.69
1:G:112:ARG:HG3	1:G:145:HIS:CD2	2.27	0.69
1:D:315:GLY:HA2	1:D:317:VAL:HG23	1.73	0.69
1:G:167:GLU:C	1:G:169:GLN:N	2.46	0.69
1:G:424:ASP:OD2	1:G:425:HIS:HB2	1.92	0.69
1:B:394:TYR:HE1	1:B:396:SER:HB2	1.57	0.69
1:D:347:GLU:OE1	1:E:274:ARG:HD2	1.93	0.69
1:E:427:SER:HB3	1:E:487:ARG:HH12	1.56	0.69
1:F:108:VAL:CG1	1:F:121:GLN:HG2	2.22	0.69
1:C:288:LEU:N	1:C:288:LEU:HD12	2.08	0.69
1:C:412:MET:CA	1:C:416:LEU:HD12	2.18	0.69
1:E:141:LEU:HD13	1:E:176:VAL:CG2	2.22	0.69
1:F:220:ALA:HB1	1:F:261:ILE:HG12	1.73	0.69
1:F:412:MET:CA	1:F:416:LEU:HD12	2.19	0.69
1:G:108:VAL:CG1	1:G:121:GLN:HG2	2.22	0.69
1:B:490:GLY:CA	1:B:493:ARG:HG3	2.23	0.69
1:C:178:LEU:HB2	1:C:181:GLY:HA2	1.74	0.69
1:D:536:ASN:HD22	1:D:538:GLU:H	1.40	0.69
1:E:372:ILE:HA	1:E:375:ASN:OD1	1.91	0.69
1:F:112:ARG:CB	1:F:117:ASN:O	2.38	0.69
1:G:338:GLY:HA3	1:G:412:MET:CE	2.23	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:316:MET:HE3	1:A:535:TYR:CZ	2.28	0.69
1:B:86:ILE:HG21	1:B:163:LEU:HD12	1.73	0.69
1:C:305:GLY:O	1:C:454:LYS:HD2	1.93	0.69
1:A:111:TYR:CE2	1:A:142:PHE:HB2	2.28	0.69
1:A:205:MET:HA	1:A:231:ALA:HB3	1.73	0.69
1:A:309:MET:HB3	1:A:499:ILE:HD12	1.75	0.69
1:A:311:THR:O	1:A:312:SER:HB3	1.92	0.69
1:A:450:LYS:CE	1:A:454:LYS:CD	2.71	0.69
1:B:79:SER:H	1:B:98:ILE:HD13	1.58	0.69
1:C:104:VAL:HG12	1:C:106:TYR:CE1	2.28	0.69
1:C:425:HIS:CE1	1:C:427:SER:OG	2.46	0.69
1:E:248:ARG:HB3	1:E:248:ARG:NH1	2.07	0.69
1:F:86:ILE:HG21	1:F:163:LEU:HD12	1.75	0.69
1:F:154:VAL:HB	1:F:175:VAL:HG13	1.75	0.69
1:F:166:MET:HE3	1:F:171:CYS:SG	2.33	0.69
1:B:504:ARG:HH21	1:B:506:GLN:HB3	1.58	0.68
1:E:186:LYS:HD3	1:E:218:GLU:CG	2.22	0.68
1:G:295:ILE:O	1:G:299:THR:HG23	1.92	0.68
1:D:108:VAL:CG1	1:D:121:GLN:HG2	2.22	0.68
1:F:309:MET:HB3	1:F:499:ILE:CD1	2.21	0.68
1:B:413:ARG:HE	1:B:458:VAL:HB	1.58	0.68
1:B:504:ARG:NH2	1:B:506:GLN:HB3	2.08	0.68
1:C:141:LEU:HD13	1:C:176:VAL:CG2	2.23	0.68
1:G:311:THR:O	1:G:312:SER:HB3	1.92	0.68
1:A:108:VAL:HG13	1:A:123:VAL:HG22	1.76	0.68
1:A:124:ARG:CZ	1:A:126:LYS:HA	2.23	0.68
1:A:275:ILE:HD12	1:B:382:PHE:HE1	1.57	0.68
1:A:496:SER:O	1:A:520:LYS:HE2	1.93	0.68
1:B:96:TYR:HE2	1:B:107:GLN:HE21	1.39	0.68
1:A:186:LYS:HD3	1:A:218:GLU:CG	2.22	0.68
1:B:283:GLU:CG	1:B:286:GLY:CA	2.56	0.68
1:B:372:ILE:HA	1:B:375:ASN:OD1	1.94	0.68
1:C:290:SER:N	1:C:325:GLN:HE21	1.87	0.68
1:E:351:GLU:OE1	1:F:278:HIS:CD2	2.46	0.68
1:F:394:TYR:HE1	1:F:396:SER:HB2	1.59	0.68
1:G:107:GLN:HB2	1:G:124:ARG:CG	2.24	0.68
1:G:186:LYS:HD3	1:G:218:GLU:CG	2.24	0.68
1:G:368:LEU:HD22	1:G:372:ILE:HG23	1.75	0.68
1:A:394:TYR:HE1	1:A:396:SER:HB2	1.58	0.68
1:B:504:ARG:CD	1:B:506:GLN:HG2	2.16	0.68
1:C:368:LEU:HD22	1:C:372:ILE:HG23	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:424:ASP:OD2	1:C:425:HIS:HB2	1.94	0.68
1:E:339:LEU:HB3	1:E:341:MET:HE2	1.76	0.68
1:F:427:SER:HB3	1:F:487:ARG:HH12	1.58	0.68
1:G:141:LEU:HD13	1:G:176:VAL:CG2	2.24	0.68
1:B:141:LEU:HD13	1:B:176:VAL:CG2	2.22	0.68
1:D:167:GLU:C	1:D:169:GLN:N	2.44	0.68
1:G:78:TYR:CD2	1:G:92:GLN:HG2	2.28	0.68
1:A:74:SER:HB2	1:A:99:ALA:HB1	1.76	0.68
1:C:166:MET:CE	1:C:171:CYS:CB	2.72	0.68
1:C:510:MET:HE3	1:C:547:TYR:HE1	1.56	0.68
1:D:104:VAL:HG12	1:D:106:TYR:CE1	2.29	0.68
1:D:504:ARG:HH21	1:D:506:GLN:HB3	1.56	0.68
1:E:394:TYR:HE1	1:E:396:SER:HB2	1.59	0.68
1:E:401:GLU:HG2	1:E:402:THR:N	2.08	0.68
1:F:260:TRP:HB2	1:F:262:PRO:HD2	0.71	0.68
1:G:488:GLY:HA3	1:G:492:LEU:HD11	1.76	0.68
1:C:167:GLU:C	1:C:169:GLN:N	2.48	0.68
1:D:166:MET:HE1	1:D:171:CYS:HB3	1.75	0.68
1:E:309:MET:HB3	1:E:499:ILE:HD12	1.75	0.68
1:A:169:GLN:HE22	1:A:254:VAL:HG11	1.58	0.68
1:C:292:CYS:O	1:C:295:ILE:HG12	1.93	0.68
1:E:202:ILE:HD13	1:E:223:LEU:HD22	1.76	0.68
1:F:260:TRP:CG	1:F:262:PRO:HD2	2.27	0.68
1:F:413:ARG:HE	1:F:458:VAL:HB	1.58	0.68
1:G:312:SER:O	1:G:313:GLY:O	2.12	0.68
1:A:504:ARG:CD	1:A:506:GLN:HG2	2.22	0.67
1:C:78:TYR:CE1	1:C:97:TRP:HB3	2.29	0.67
1:D:295:ILE:O	1:D:299:THR:HG23	1.93	0.67
1:E:167:GLU:C	1:E:169:GLN:N	2.47	0.67
1:E:412:MET:CA	1:E:416:LEU:HD12	2.19	0.67
1:F:167:GLU:C	1:F:169:GLN:N	2.46	0.67
1:F:307:VAL:O	1:F:307:VAL:HG12	1.95	0.67
1:B:251:MET:HE2	1:B:251:MET:HA	1.76	0.67
1:D:368:LEU:O	1:D:368:LEU:HD22	1.94	0.67
1:F:153:ILE:HG13	1:F:174:PRO:HB2	1.77	0.67
1:A:108:VAL:HG12	1:A:121:GLN:HG2	1.74	0.67
1:B:260:TRP:C	1:B:261:ILE:HG12	2.14	0.67
1:D:290:SER:N	1:D:325:GLN:HE21	1.90	0.67
1:E:370:ARG:HD2	1:E:371:GLU:H	1.53	0.67
1:F:490:GLY:HA2	1:F:493:ARG:HG3	1.76	0.67
1:G:84:ARG:HA	1:G:243:LEU:HD21	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:96:TYR:HE2	1:C:107:GLN:HE21	1.43	0.67
1:F:127:ASP:O	1:F:128:LYS:CB	2.26	0.67
1:G:121:GLN:HB3	1:G:133:THR:HG23	1.74	0.67
1:A:126:LYS:NZ	1:A:127:ASP:CA	2.40	0.67
1:A:261:ILE:O	1:A:261:ILE:CD1	2.43	0.67
1:B:94:ALA:HB1	1:B:162:MET:HE3	1.76	0.67
1:C:194:GLU:H	1:C:194:GLU:CD	1.95	0.67
1:D:230:VAL:HG11	1:D:260:TRP:HE1	1.59	0.67
1:E:311:THR:O	1:E:312:SER:HB3	1.94	0.67
1:F:389:ASP:H	1:G:269:LEU:HD21	1.59	0.67
1:G:68:VAL:HG12	1:G:121:GLN:OE1	1.95	0.67
1:G:86:ILE:HG21	1:G:163:LEU:HD12	1.75	0.67
1:G:283:GLU:HG2	1:G:284:SER:N	2.10	0.67
1:G:303:ARG:O	1:G:306:GLU:HG3	1.93	0.67
1:G:420:VAL:HG22	1:G:459:VAL:HB	1.77	0.67
1:C:306:GLU:HA	1:C:497:ASP:OD2	1.95	0.67
1:D:86:ILE:HG21	1:D:163:LEU:HD12	1.76	0.67
1:G:287:LEU:HD11	1:G:335:LYS:HG3	1.77	0.67
1:B:167:GLU:C	1:B:169:GLN:N	2.46	0.67
1:C:294:GLY:O	1:C:295:ILE:C	2.29	0.67
1:C:339:LEU:HB3	1:C:341:MET:HE3	1.72	0.67
1:C:425:HIS:HE1	1:C:427:SER:OG	1.76	0.67
1:D:107:GLN:HB2	1:D:124:ARG:CG	2.25	0.67
1:E:121:GLN:HB3	1:E:133:THR:HG23	1.75	0.67
1:E:276:ARG:HG2	1:E:276:ARG:HH11	1.58	0.67
1:E:442:ILE:HD12	1:E:488:GLY:HA2	1.76	0.67
1:F:382:PHE:HE1	1:G:275:ILE:HD12	1.59	0.67
1:C:220:ALA:HB1	1:C:261:ILE:HD12	1.76	0.67
1:F:442:ILE:CD1	1:F:492:LEU:HD11	2.25	0.67
1:C:315:GLY:HA2	1:C:317:VAL:HG23	1.76	0.67
1:F:199:PHE:O	1:F:227:LYS:HE2	1.95	0.67
1:F:394:TYR:CE2	1:F:405:LEU:HD12	2.29	0.67
1:A:169:GLN:O	1:A:170:ASP:HB2	1.94	0.67
1:C:338:GLY:HA3	1:C:412:MET:CE	2.24	0.67
1:D:78:TYR:CD2	1:D:92:GLN:HG2	2.30	0.67
1:E:338:GLY:HA3	1:E:412:MET:CE	2.25	0.67
1:A:94:ALA:HB1	1:A:162:MET:HE3	1.77	0.66
1:A:107:GLN:CB	1:A:124:ARG:HG3	2.25	0.66
1:B:229:ARG:HB2	1:B:258:GLY:O	1.95	0.66
1:E:205:MET:HA	1:E:231:ALA:HB3	1.77	0.66
1:B:439:ARG:O	1:B:442:ILE:HG22	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:412:MET:CE	1:E:421:ILE:CD1	2.73	0.66
1:F:246:HIS:HB2	1:F:249:GLU:HB2	1.76	0.66
1:G:305:GLY:O	1:G:454:LYS:HD2	1.95	0.66
1:A:260:TRP:O	1:A:261:ILE:HG23	1.94	0.66
1:B:450:LYS:HE2	1:B:454:LYS:CD	2.23	0.66
1:C:344:GLU:OE1	1:C:349:THR:HB	1.94	0.66
1:D:289:PHE:H	1:D:296:ASN:ND2	1.90	0.66
1:D:447:THR:HG22	1:D:495:LEU:CD2	2.16	0.66
1:B:78:TYR:CE1	1:B:97:TRP:HB3	2.31	0.66
1:B:283:GLU:HG3	1:B:286:GLY:N	2.11	0.66
1:E:425:HIS:HE1	1:E:427:SER:OG	1.76	0.66
1:G:515:LEU:HD21	1:G:529:ILE:HD11	1.78	0.66
1:A:261:ILE:O	1:A:261:ILE:HD13	1.95	0.66
1:C:467:LYS:HE3	1:C:486:LEU:O	1.95	0.66
1:D:268:ALA:HA	1:D:271:LEU:CD1	2.24	0.66
1:E:339:LEU:HB3	1:E:341:MET:HE1	1.76	0.66
1:F:338:GLY:HA3	1:F:412:MET:CE	2.25	0.66
1:G:289:PHE:N	1:G:296:ASN:HD21	1.92	0.66
1:G:504:ARG:HD3	1:G:506:GLN:CG	2.15	0.66
1:A:401:GLU:HG2	1:A:402:THR:H	1.59	0.66
1:E:387:GLY:HA2	1:F:269:LEU:HD11	1.77	0.66
1:F:420:VAL:HG22	1:F:459:VAL:HB	1.78	0.66
1:B:484:THR:C	1:B:486:LEU:H	1.96	0.66
1:D:307:VAL:HG12	1:D:307:VAL:O	1.95	0.66
1:E:295:ILE:O	1:E:299:THR:HG23	1.95	0.66
1:A:79:SER:H	1:A:98:ILE:HD13	1.61	0.66
1:C:311:THR:O	1:C:312:SER:HB3	1.94	0.66
1:D:216:VAL:HG11	1:D:230:VAL:HG22	1.77	0.66
1:D:439:ARG:O	1:D:442:ILE:HG22	1.95	0.66
1:E:305:GLY:O	1:E:454:LYS:HD2	1.95	0.66
1:E:411:TYR:CE1	1:F:265:VAL:HG11	2.29	0.66
1:B:194:GLU:CD	1:B:194:GLU:H	1.97	0.66
1:C:394:TYR:CE2	1:C:405:LEU:HD12	2.30	0.66
1:F:162:MET:SD	1:F:166:MET:HG3	2.36	0.66
1:B:409:LEU:CD2	1:B:421:ILE:HG21	2.23	0.65
1:D:147:TRP:CG	1:D:174:PRO:HB3	2.31	0.65
1:D:261:ILE:H	1:D:262:PRO:CD	2.08	0.65
1:F:439:ARG:O	1:F:442:ILE:HG22	1.95	0.65
1:F:476:GLU:H	1:F:476:GLU:CD	2.00	0.65
1:G:394:TYR:HE1	1:G:396:SER:HB2	1.60	0.65
1:A:496:SER:HB2	1:A:499:ILE:HD11	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:420:VAL:HG22	1:B:459:VAL:HB	1.78	0.65
1:B:427:SER:HB3	1:B:487:ARG:NH1	2.10	0.65
1:C:442:ILE:HD12	1:C:488:GLY:CA	2.27	0.65
1:C:499:ILE:CG2	1:C:519:LEU:HB2	2.25	0.65
1:E:223:LEU:HD23	1:E:224:PRO:HD2	1.77	0.65
1:G:346:VAL:HB	1:G:395:ASP:HB2	1.78	0.65
1:A:124:ARG:HD3	1:A:125:ASP:C	2.16	0.65
1:A:289:PHE:N	1:A:296:ASN:HD21	1.94	0.65
1:D:78:TYR:CE1	1:D:97:TRP:HB3	2.32	0.65
1:D:248:ARG:HB3	1:D:248:ARG:NH1	2.08	0.65
1:E:322:VAL:CG2	1:E:463:ILE:HD11	2.27	0.65
1:B:424:ASP:OD2	1:B:425:HIS:HB2	1.96	0.65
1:D:152:LYS:HD3	1:D:203:ILE:CD1	2.24	0.65
1:D:178:LEU:HB2	1:D:181:GLY:HA2	1.78	0.65
1:B:441:MET:O	1:B:441:MET:HE2	1.95	0.65
1:C:476:GLU:CD	1:C:476:GLU:H	1.98	0.65
1:D:424:ASP:OD2	1:D:425:HIS:HB2	1.96	0.65
1:E:111:TYR:CE2	1:E:142:PHE:HB2	2.31	0.65
1:F:107:GLN:CB	1:F:124:ARG:CG	2.71	0.65
1:F:111:TYR:CE2	1:F:142:PHE:HB2	2.32	0.65
1:A:208:MET:HE1	1:A:232:VAL:CA	2.19	0.65
1:A:295:ILE:O	1:A:299:THR:HG23	1.96	0.65
1:C:358:ASN:O	1:C:360:VAL:HG13	1.96	0.65
1:C:490:GLY:CA	1:C:493:ARG:HG3	2.27	0.65
1:E:478:GLY:HA3	1:E:505:ASN:HB2	1.79	0.65
1:G:79:SER:H	1:G:98:ILE:HD13	1.60	0.65
1:B:441:MET:HE1	1:B:445:LEU:H	1.61	0.65
1:E:86:ILE:HG21	1:E:163:LEU:HD12	1.77	0.65
1:E:389:ASP:HA	1:F:269:LEU:HD23	1.77	0.65
1:F:260:TRP:HB2	1:F:262:PRO:HD3	1.69	0.65
1:F:321:PHE:CD2	1:F:533:MET:HE3	2.31	0.65
1:B:104:VAL:HG12	1:B:106:TYR:CE1	2.32	0.65
1:B:312:SER:O	1:B:313:GLY:O	2.15	0.65
1:D:517:ARG:HB3	1:D:519:LEU:CD1	2.27	0.65
1:G:96:TYR:HE2	1:G:107:GLN:HE21	1.43	0.65
1:G:442:ILE:HD11	1:G:492:LEU:HD21	1.78	0.65
1:D:394:TYR:HE1	1:D:396:SER:HB2	1.61	0.65
1:A:108:VAL:CG1	1:A:121:GLN:HG2	2.26	0.65
1:D:166:MET:CE	1:D:171:CYS:CB	2.75	0.65
1:D:366:ASP:HB2	1:E:284:SER:HG	1.59	0.65
1:E:216:VAL:CG1	1:E:230:VAL:CG2	2.74	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:414:SER:CB	1:C:226:GLY:H	2.10	0.64
1:C:78:TYR:CD2	1:C:92:GLN:HG2	2.31	0.64
1:C:425:HIS:CE1	1:C:427:SER:HB2	2.32	0.64
1:F:476:GLU:HB3	1:F:506:GLN:OE1	1.97	0.64
1:A:412:MET:CA	1:A:416:LEU:HD12	2.24	0.64
1:A:442:ILE:HD12	1:A:488:GLY:CA	2.27	0.64
1:B:68:VAL:HG12	1:B:121:GLN:OE1	1.97	0.64
1:B:248:ARG:NH1	1:B:248:ARG:HB2	2.04	0.64
1:D:344:GLU:CG	1:D:349:THR:HG22	2.25	0.64
1:E:154:VAL:HB	1:E:175:VAL:HG13	1.79	0.64
1:F:289:PHE:N	1:F:296:ASN:HD21	1.93	0.64
1:G:442:ILE:HD12	1:G:488:GLY:HA2	1.79	0.64
1:A:107:GLN:HB2	1:A:124:ARG:CG	2.28	0.64
1:A:414:SER:HB3	1:C:226:GLY:N	2.11	0.64
1:B:262:PRO:HB2	1:B:265:VAL:HG12	1.77	0.64
1:C:412:MET:HE2	1:C:421:ILE:HD13	1.80	0.64
1:C:427:SER:HB3	1:C:487:ARG:HH12	1.62	0.64
1:G:490:GLY:CA	1:G:493:ARG:HG3	2.27	0.64
1:C:344:GLU:HA	1:D:454:LYS:NZ	2.12	0.64
1:C:401:GLU:HB3	1:C:404:ARG:HB3	1.80	0.64
1:D:312:SER:CB	1:D:502:LEU:O	2.44	0.64
1:E:504:ARG:HH21	1:E:506:GLN:HB3	1.63	0.64
1:D:339:LEU:HB3	1:D:341:MET:HE3	1.76	0.64
1:D:452:PHE:O	1:D:456:THR:HG23	1.97	0.64
1:E:439:ARG:O	1:E:442:ILE:HG22	1.97	0.64
1:F:121:GLN:HB2	1:F:133:THR:OG1	1.96	0.64
1:F:121:GLN:CB	1:F:133:THR:HG23	2.27	0.64
1:F:496:SER:O	1:F:520:LYS:HE2	1.98	0.64
1:A:78:TYR:CE1	1:A:97:TRP:HB3	2.33	0.64
1:A:303:ARG:O	1:A:306:GLU:HG3	1.97	0.64
1:B:111:TYR:CE2	1:B:142:PHE:HB2	2.32	0.64
1:B:515:LEU:HD21	1:B:529:ILE:CD1	2.28	0.64
1:C:79:SER:H	1:C:98:ILE:HD13	1.62	0.64
1:C:216:VAL:HG11	1:C:230:VAL:HG22	1.80	0.64
1:F:412:MET:HE2	1:F:421:ILE:CD1	2.27	0.64
1:A:278:HIS:CD2	1:B:351:GLU:OE1	2.51	0.64
1:C:154:VAL:HB	1:C:175:VAL:HG13	1.79	0.64
1:D:74:SER:HB2	1:D:99:ALA:HB1	1.80	0.64
1:A:194:GLU:H	1:A:194:GLU:CD	1.99	0.64
1:A:480:PRO:HA	1:A:503:GLU:CD	2.18	0.64
1:A:536:ASN:HD22	1:A:538:GLU:H	1.45	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:446:MET:HE3	1:D:492:LEU:HA	1.78	0.64
1:D:476:GLU:HB3	1:D:506:GLN:OE1	1.97	0.64
1:F:303:ARG:O	1:F:306:GLU:HG3	1.97	0.64
1:A:130:PHE:O	1:A:131:LYS:HG3	1.98	0.64
1:A:145:HIS:CE1	1:A:146:LEU:HD23	2.33	0.64
1:A:248:ARG:HB3	1:A:248:ARG:NH1	2.10	0.64
1:A:490:GLY:CA	1:A:493:ARG:HG3	2.27	0.64
1:D:496:SER:O	1:D:520:LYS:HE2	1.98	0.64
1:E:78:TYR:CD2	1:E:92:GLN:HG2	2.32	0.64
1:F:208:MET:HE1	1:F:232:VAL:CA	2.22	0.64
1:G:356:LEU:HD12	1:G:541:TRP:NE1	2.13	0.64
1:G:510:MET:HE3	1:G:547:TYR:CE1	2.27	0.64
1:C:504:ARG:HH21	1:C:506:GLN:HB3	1.63	0.64
1:E:84:ARG:HA	1:E:243:LEU:HD21	1.80	0.64
1:E:389:ASP:H	1:F:269:LEU:HD21	1.63	0.64
1:E:504:ARG:NH2	1:E:506:GLN:HB3	2.13	0.64
1:F:79:SER:H	1:F:98:ILE:HD13	1.63	0.64
1:F:84:ARG:HA	1:F:243:LEU:HD21	1.80	0.64
1:A:517:ARG:HB3	1:A:519:LEU:CD1	2.28	0.63
1:F:261:ILE:H	1:F:262:PRO:CD	2.11	0.63
1:F:283:GLU:CD	1:F:286:GLY:HA2	2.18	0.63
1:F:446:MET:HE2	1:F:492:LEU:HB3	1.80	0.63
1:G:316:MET:HE1	1:G:535:TYR:CE2	2.33	0.63
1:A:446:MET:HE3	1:A:492:LEU:HA	1.79	0.63
1:B:356:LEU:HD12	1:B:541:TRP:NE1	2.13	0.63
1:B:480:PRO:HA	1:B:503:GLU:OE1	1.99	0.63
1:C:287:LEU:HD11	1:C:335:LYS:HG3	1.79	0.63
1:D:84:ARG:HA	1:D:243:LEU:HD21	1.80	0.63
1:D:321:PHE:CD2	1:D:533:MET:CE	2.81	0.63
1:E:424:ASP:OD2	1:E:425:HIS:HB2	1.98	0.63
1:G:152:LYS:HD3	1:G:203:ILE:CD1	2.28	0.63
1:B:166:MET:CE	1:B:171:CYS:CB	2.77	0.63
1:C:303:ARG:O	1:C:306:GLU:HG3	1.97	0.63
1:B:346:VAL:HB	1:B:395:ASP:HB2	1.80	0.63
1:D:216:VAL:CG1	1:D:230:VAL:CG2	2.77	0.63
1:G:216:VAL:HG11	1:G:230:VAL:HG22	1.81	0.63
1:G:413:ARG:O	1:G:417:GLY:HA2	1.99	0.63
1:A:504:ARG:HH21	1:A:506:GLN:HG2	1.64	0.63
1:E:441:MET:HE2	1:E:444:ASN:HB3	1.81	0.63
1:F:216:VAL:HG11	1:F:230:VAL:HG21	1.80	0.63
1:G:152:LYS:HG3	1:G:201:GLN:CG	2.29	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:147:TRP:CG	1:B:174:PRO:HB3	2.34	0.63
1:D:141:LEU:HD13	1:D:176:VAL:CG2	2.28	0.63
1:B:285:VAL:HG22	1:B:300:LEU:HD11	1.81	0.63
1:C:411:TYR:OH	1:D:260:TRP:CB	2.46	0.63
1:F:94:ALA:HB1	1:F:162:MET:HE3	1.80	0.63
1:G:290:SER:N	1:G:325:GLN:HE21	1.91	0.63
1:C:510:MET:HE2	1:C:547:TYR:HE1	1.60	0.63
1:A:269:LEU:HD11	1:B:387:GLY:HA2	1.80	0.63
1:C:496:SER:O	1:C:520:LYS:HE2	1.98	0.63
1:D:369:LYS:HG2	1:E:279:LEU:HD22	1.81	0.63
1:F:446:MET:HE3	1:F:492:LEU:HA	1.80	0.63
1:A:253:GLN:O	1:A:257:ALA:CB	2.47	0.62
1:B:454:LYS:HZ1	1:G:344:GLU:HA	1.60	0.62
1:C:446:MET:HE2	1:C:492:LEU:HB3	1.81	0.62
1:E:229:ARG:HB3	1:E:259:PRO:HB3	1.80	0.62
1:F:486:LEU:HB3	1:F:493:ARG:HD2	1.80	0.62
1:G:283:GLU:O	1:G:303:ARG:HG2	1.98	0.62
1:A:141:LEU:HD11	1:A:196:PHE:HZ	1.64	0.62
1:A:220:ALA:HB3	1:A:261:ILE:HG21	1.80	0.62
1:B:412:MET:HE2	1:B:421:ILE:CD1	2.29	0.62
1:C:259:PRO:O	1:C:260:TRP:HB3	1.99	0.62
1:F:517:ARG:HB3	1:F:519:LEU:CD1	2.29	0.62
1:D:486:LEU:HB3	1:D:493:ARG:HD2	1.81	0.62
1:B:352:ASP:CG	1:B:363:ARG:HD3	2.20	0.62
1:E:166:MET:CE	1:E:171:CYS:CB	2.77	0.62
1:F:504:ARG:HH21	1:F:506:GLN:CB	2.13	0.62
1:A:290:SER:N	1:A:325:GLN:HE21	1.92	0.62
1:A:521:CYS:SG	1:A:524:THR:HG23	2.39	0.62
1:B:312:SER:HB2	1:B:502:LEU:O	1.99	0.62
1:C:111:TYR:CZ	1:C:142:PHE:HB2	2.35	0.62
1:C:152:LYS:HG3	1:C:201:GLN:CG	2.29	0.62
1:C:441:MET:O	1:C:441:MET:CE	2.36	0.62
1:D:152:LYS:HG3	1:D:201:GLN:CG	2.28	0.62
1:D:316:MET:HE1	1:D:535:TYR:CE2	2.34	0.62
1:E:411:TYR:OH	1:F:262:PRO:HG3	1.99	0.62
1:F:194:GLU:H	1:F:194:GLU:CD	2.01	0.62
1:F:290:SER:N	1:F:325:GLN:HE21	1.96	0.62
1:F:346:VAL:HB	1:F:395:ASP:HB2	1.80	0.62
1:A:412:MET:HE2	1:A:421:ILE:HD11	1.80	0.62
1:C:421:ILE:HB	1:C:460:LEU:HD12	1.81	0.62
1:D:339:LEU:HB3	1:D:341:MET:HE2	1.78	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:216:VAL:HG11	1:G:230:VAL:HG21	1.79	0.62
1:G:344:GLU:CG	1:G:349:THR:HG22	2.28	0.62
1:A:482:SER:OG	1:A:484:THR:HG23	2.00	0.62
1:B:152:LYS:HG3	1:B:201:GLN:CG	2.29	0.62
1:B:295:ILE:O	1:B:299:THR:HG23	2.00	0.62
1:D:68:VAL:HG12	1:D:121:GLN:OE1	2.00	0.62
1:E:262:PRO:HB2	1:E:265:VAL:HG12	1.81	0.62
1:F:401:GLU:HG3	1:F:431:SER:O	1.99	0.62
1:D:346:VAL:HB	1:D:395:ASP:HB2	1.82	0.62
1:D:504:ARG:CD	1:D:506:GLN:HG2	2.26	0.62
1:E:251:MET:HE2	1:E:251:MET:HA	1.82	0.62
1:E:307:VAL:O	1:E:307:VAL:HG12	1.99	0.62
1:F:68:VAL:HG12	1:F:121:GLN:OE1	1.99	0.62
1:G:496:SER:HB2	1:G:499:ILE:HD11	1.79	0.62
1:A:318:MET:SD	1:A:463:ILE:CD1	2.88	0.62
1:C:251:MET:HA	1:C:251:MET:CE	2.29	0.62
1:C:345:SER:O	1:C:349:THR:CG2	2.48	0.62
1:D:112:ARG:HG3	1:D:145:HIS:CD2	2.34	0.62
1:E:96:TYR:HE2	1:E:107:GLN:HE21	1.47	0.62
1:E:194:GLU:CD	1:E:194:GLU:H	2.02	0.62
1:E:478:GLY:CA	1:E:505:ASN:HB2	2.30	0.62
1:G:178:LEU:HB2	1:G:181:GLY:HA2	1.80	0.62
1:G:322:VAL:HG21	1:G:463:ILE:HD11	1.80	0.62
1:B:309:MET:HB3	1:B:499:ILE:CD1	2.30	0.62
1:C:312:SER:CB	1:C:502:LEU:O	2.42	0.62
1:B:78:TYR:CD2	1:B:92:GLN:HG2	2.34	0.61
1:B:253:GLN:CA	1:B:257:ALA:HB2	2.30	0.61
1:B:471:LYS:HB3	1:B:479:ARG:NH1	2.15	0.61
1:D:482:SER:OG	1:D:484:THR:HG23	1.99	0.61
1:F:205:MET:HA	1:F:231:ALA:HB3	1.81	0.61
1:G:223:LEU:HD23	1:G:224:PRO:HD2	1.81	0.61
1:A:312:SER:H	1:A:318:MET:CE	2.12	0.61
1:A:504:ARG:NH2	1:A:506:GLN:HB3	2.15	0.61
1:B:303:ARG:O	1:B:306:GLU:HG3	1.99	0.61
1:B:322:VAL:HG21	1:B:463:ILE:HD11	1.80	0.61
1:B:368:LEU:HD22	1:B:372:ILE:HG23	1.82	0.61
1:D:447:THR:HA	1:D:495:LEU:HD23	1.82	0.61
1:D:476:GLU:H	1:D:476:GLU:CD	2.03	0.61
1:E:79:SER:H	1:E:98:ILE:HD13	1.64	0.61
1:G:504:ARG:HH21	1:G:506:GLN:CB	2.12	0.61
1:A:152:LYS:HG3	1:A:201:GLN:CG	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:394:TYR:CE2	1:A:408:LYS:HD2	2.36	0.61
1:B:186:LYS:CD	1:B:218:GLU:HG3	2.27	0.61
1:C:309:MET:HB3	1:C:499:ILE:CD1	2.30	0.61
1:C:344:GLU:HB2	1:C:348:GLU:OE2	2.00	0.61
1:D:217:GLU:HA	1:D:261:ILE:HG22	1.82	0.61
1:D:412:MET:CA	1:D:416:LEU:HD12	2.21	0.61
1:E:440:LYS:HE2	1:E:440:LYS:O	1.99	0.61
1:G:401:GLU:HG2	1:G:402:THR:H	1.64	0.61
1:A:394:TYR:CD1	1:A:394:TYR:C	2.74	0.61
1:D:372:ILE:HA	1:D:375:ASN:OD1	1.99	0.61
1:A:84:ARG:HA	1:A:243:LEU:HD21	1.81	0.61
1:A:256:ASN:OD1	1:A:256:ASN:C	2.36	0.61
1:A:322:VAL:HG21	1:A:463:ILE:HD11	1.82	0.61
1:A:439:ARG:O	1:A:442:ILE:HG22	1.99	0.61
1:C:84:ARG:HA	1:C:243:LEU:HD21	1.83	0.61
1:C:442:ILE:HD11	1:C:492:LEU:HD11	1.82	0.61
1:C:450:LYS:CE	1:C:454:LYS:CD	2.73	0.61
1:D:305:GLY:O	1:D:454:LYS:HD2	2.01	0.61
1:E:78:TYR:CE1	1:E:97:TRP:HB3	2.36	0.61
1:E:442:ILE:HD12	1:E:488:GLY:CA	2.31	0.61
1:E:450:LYS:CE	1:E:454:LYS:CD	2.72	0.61
1:F:406:LEU:HD21	1:F:449:LEU:HD23	1.81	0.61
1:G:127:ASP:O	1:G:128:LYS:CB	2.39	0.61
1:G:406:LEU:HD21	1:G:449:LEU:HD23	1.82	0.61
1:A:305:GLY:O	1:A:454:LYS:HD2	2.00	0.61
1:B:202:ILE:HD13	1:B:223:LEU:HD22	1.81	0.61
1:B:394:TYR:CE2	1:B:405:LEU:HD12	2.35	0.61
1:E:147:TRP:CG	1:E:174:PRO:HB3	2.36	0.61
1:E:258:GLY:HA3	1:E:260:TRP:CZ3	2.35	0.61
1:E:287:LEU:HD11	1:E:335:LYS:HG3	1.82	0.61
1:E:345:SER:O	1:E:349:THR:CG2	2.49	0.61
1:E:521:CYS:SG	1:E:524:THR:HG23	2.40	0.61
1:F:148:ASN:HD22	1:F:198:GLN:HE22	1.46	0.61
1:G:324:GLN:HE22	1:G:542:LEU:H	1.47	0.61
1:B:195:TYR:O	1:B:198:GLN:HB2	2.01	0.61
1:B:372:ILE:HG13	1:B:378:PHE:HB2	1.81	0.61
1:E:153:ILE:HG13	1:E:174:PRO:HB2	1.81	0.61
1:E:370:ARG:HH11	1:E:371:GLU:CG	2.09	0.61
1:F:112:ARG:HD2	1:F:145:HIS:CE1	2.35	0.61
1:F:442:ILE:HD12	1:F:488:GLY:HA2	1.80	0.61
1:G:78:TYR:CE1	1:G:97:TRP:HB3	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:251:MET:HE2	1:G:251:MET:HA	1.83	0.61
1:G:478:GLY:HA3	1:G:505:ASN:HB2	1.81	0.61
1:D:202:ILE:HD13	1:D:223:LEU:HD22	1.82	0.61
1:E:220:ALA:HB3	1:E:261:ILE:CG2	2.14	0.61
1:G:439:ARG:O	1:G:442:ILE:HG22	2.00	0.61
1:B:216:VAL:HG11	1:B:230:VAL:HG21	1.81	0.61
1:C:425:HIS:CE1	1:C:427:SER:CB	2.84	0.61
1:D:208:MET:HE1	1:D:232:VAL:CA	2.21	0.61
1:F:229:ARG:HB3	1:F:259:PRO:HA	1.82	0.61
1:A:338:GLY:HA3	1:A:412:MET:CE	2.30	0.61
1:B:510:MET:HE3	1:B:547:TYR:CE1	2.31	0.61
1:E:68:VAL:HG12	1:E:121:GLN:OE1	2.01	0.61
1:A:482:SER:N	1:A:485:ASP:HB2	2.15	0.60
1:G:484:THR:C	1:G:486:LEU:H	2.04	0.60
1:A:178:LEU:HB2	1:A:181:GLY:HA2	1.82	0.60
1:B:251:MET:HA	1:B:251:MET:CE	2.31	0.60
1:C:166:MET:CE	1:C:171:CYS:HB3	2.31	0.60
1:C:401:GLU:CG	1:C:402:THR:H	2.14	0.60
1:D:96:TYR:HE2	1:D:107:GLN:HE21	1.46	0.60
1:F:378:PHE:CE2	1:G:276:ARG:CD	2.83	0.60
1:A:220:ALA:CB	1:A:261:ILE:CG2	2.77	0.60
1:C:413:ARG:O	1:C:417:GLY:HA2	2.01	0.60
1:C:531:GLY:C	1:C:532:TYR:CD1	2.74	0.60
1:C:536:ASN:HD21	1:C:538:GLU:CB	2.14	0.60
1:D:338:GLY:HA3	1:D:412:MET:HE1	1.82	0.60
1:G:261:ILE:O	1:G:261:ILE:CG2	2.46	0.60
1:A:344:GLU:HB2	1:A:348:GLU:OE2	2.02	0.60
1:C:124:ARG:HD3	1:C:125:ASP:C	2.22	0.60
1:C:437:ASP:OD1	1:C:439:ARG:HB2	2.01	0.60
1:C:478:GLY:HA3	1:C:505:ASN:HB2	1.81	0.60
1:D:121:GLN:CB	1:D:133:THR:HG23	2.31	0.60
1:D:413:ARG:NE	1:D:458:VAL:HB	2.16	0.60
1:D:520:LYS:HG3	1:D:521:CYS:N	2.16	0.60
1:F:276:ARG:HG2	1:F:276:ARG:HH11	1.66	0.60
1:G:166:MET:CE	1:G:171:CYS:HB3	2.27	0.60
1:G:517:ARG:HB3	1:G:519:LEU:CD1	2.32	0.60
1:A:311:THR:CA	1:A:318:MET:HE1	2.28	0.60
1:B:141:LEU:HD11	1:B:196:PHE:HZ	1.65	0.60
1:F:421:ILE:HB	1:F:460:LEU:HD12	1.83	0.60
1:G:401:GLU:HG2	1:G:402:THR:N	2.16	0.60
1:B:121:GLN:CB	1:B:133:THR:HG23	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:504:ARG:NH2	1:C:506:GLN:HB3	2.17	0.60
1:B:477:GLU:HG3	1:B:507:GLN:NE2	2.15	0.60
1:D:145:HIS:CE1	1:D:146:LEU:HD23	2.37	0.60
1:D:442:ILE:CD1	1:D:492:LEU:HD11	2.31	0.60
1:E:486:LEU:HB3	1:E:493:ARG:HD2	1.84	0.60
1:E:502:LEU:HD12	1:E:502:LEU:N	2.16	0.60
1:G:208:MET:HE1	1:G:232:VAL:CA	2.20	0.60
1:D:338:GLY:HA3	1:D:412:MET:HE3	1.84	0.60
1:E:446:MET:HE2	1:E:492:LEU:HB3	1.82	0.60
1:F:486:LEU:HD12	1:F:493:ARG:CD	2.32	0.60
1:G:111:TYR:CZ	1:G:142:PHE:HB2	2.36	0.60
1:G:268:ALA:HA	1:G:271:LEU:HD13	1.82	0.60
1:B:478:GLY:HA3	1:B:505:ASN:HB2	1.83	0.60
1:C:477:GLU:HG3	1:C:507:GLN:NE2	2.17	0.60
1:F:223:LEU:HD23	1:F:224:PRO:HD2	1.83	0.60
1:F:260:TRP:C	1:F:261:ILE:HG13	2.23	0.60
1:G:94:ALA:HB1	1:G:162:MET:HE3	1.83	0.60
1:A:294:GLY:O	1:A:295:ILE:C	2.39	0.60
1:C:208:MET:HE1	1:C:232:VAL:CA	2.16	0.60
1:G:194:GLU:CD	1:G:194:GLU:H	2.04	0.60
1:G:307:VAL:HG12	1:G:307:VAL:O	2.01	0.60
1:A:141:LEU:HD13	1:A:176:VAL:CG2	2.32	0.59
1:A:229:ARG:HB3	1:A:258:GLY:O	2.01	0.59
1:A:287:LEU:HD11	1:A:335:LYS:HG3	1.83	0.59
1:A:306:GLU:HA	1:A:497:ASP:OD2	2.02	0.59
1:A:480:PRO:HA	1:A:503:GLU:OE1	2.01	0.59
1:A:482:SER:H	1:A:485:ASP:CB	2.14	0.59
1:D:287:LEU:HD11	1:D:335:LYS:HG3	1.84	0.59
1:D:478:GLY:HA3	1:D:505:ASN:HB2	1.85	0.59
1:E:510:MET:HE2	1:E:547:TYR:HE1	1.67	0.59
1:G:303:ARG:CZ	1:G:523:PHE:CD1	2.85	0.59
1:G:326:ALA:HB2	1:G:422:ILE:HD12	1.84	0.59
1:G:372:ILE:HA	1:G:375:ASN:OD1	2.01	0.59
1:C:442:ILE:HD11	1:C:492:LEU:HD21	1.83	0.59
1:C:510:MET:HE3	1:C:547:TYR:CE1	2.34	0.59
1:D:141:LEU:HD11	1:D:196:PHE:HZ	1.63	0.59
1:A:96:TYR:HE2	1:A:107:GLN:HE21	1.49	0.59
1:A:410:ALA:HA	1:A:452:PHE:CE1	2.38	0.59
1:B:152:LYS:HD3	1:B:203:ILE:CD1	2.30	0.59
1:B:484:THR:O	1:B:486:LEU:N	2.35	0.59
1:C:441:MET:HE2	1:C:444:ASN:HB3	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:178:LEU:HB2	1:E:181:GLY:HA2	1.83	0.59
1:F:368:LEU:HD22	1:F:372:ILE:HG23	1.85	0.59
1:B:442:ILE:HD11	1:B:492:LEU:HD11	1.83	0.59
1:C:107:GLN:CB	1:C:124:ARG:CG	2.78	0.59
1:C:162:MET:SD	1:C:166:MET:HG3	2.42	0.59
1:C:473:LYS:HE2	1:C:479:ARG:CA	2.31	0.59
1:C:473:LYS:CG	1:C:479:ARG:HB2	2.32	0.59
1:D:521:CYS:O	1:D:525:GLY:N	2.33	0.59
1:E:441:MET:CE	1:E:444:ASN:HB3	2.32	0.59
1:B:486:LEU:HB3	1:B:493:ARG:HD2	1.84	0.59
1:C:216:VAL:HG11	1:C:230:VAL:HG21	1.83	0.59
1:C:366:ASP:HB2	1:D:284:SER:OG	2.03	0.59
1:D:424:ASP:O	1:D:425:HIS:HB3	2.01	0.59
1:E:251:MET:HA	1:E:251:MET:CE	2.33	0.59
1:F:366:ASP:CB	1:G:284:SER:OG	2.50	0.59
1:F:546:SER:O	1:F:547:TYR:CB	2.42	0.59
1:A:288:LEU:N	1:A:288:LEU:HD12	2.18	0.59
1:A:476:GLU:H	1:A:476:GLU:CD	2.06	0.59
1:B:440:LYS:HE2	1:B:440:LYS:O	2.02	0.59
1:C:316:MET:HE1	1:C:535:TYR:CE2	2.37	0.59
1:D:290:SER:H	1:D:325:GLN:HE22	1.44	0.59
1:D:291:GLY:O	1:D:292:CYS:HB2	2.03	0.59
1:G:202:ILE:HD13	1:G:223:LEU:HD22	1.83	0.59
1:A:168:LEU:HD22	1:A:247:ASP:OD2	2.03	0.59
1:A:216:VAL:HG11	1:A:230:VAL:HG21	1.83	0.59
1:A:344:GLU:CG	1:A:349:THR:HG22	2.30	0.59
1:C:74:SER:HB2	1:C:99:ALA:HB1	1.83	0.59
1:C:152:LYS:HD3	1:C:203:ILE:CD1	2.30	0.59
1:C:440:LYS:HE2	1:C:440:LYS:O	2.02	0.59
1:D:366:ASP:CB	1:E:284:SER:OG	2.31	0.59
1:E:186:LYS:CD	1:E:218:GLU:HG3	2.28	0.59
1:E:306:GLU:HA	1:E:497:ASP:OD2	2.02	0.59
1:E:383:ASP:OD1	1:F:272:ARG:NH2	2.34	0.59
1:F:382:PHE:CE1	1:G:272:ARG:HA	2.38	0.59
1:B:84:ARG:HA	1:B:243:LEU:HD21	1.84	0.59
1:B:288:LEU:HD12	1:B:288:LEU:N	2.18	0.59
1:B:521:CYS:SG	1:B:524:THR:HG23	2.43	0.59
1:C:141:LEU:HD11	1:C:196:PHE:HZ	1.65	0.59
1:D:442:ILE:HD11	1:D:492:LEU:CD2	2.31	0.59
1:D:480:PRO:HA	1:D:503:GLU:OE1	2.03	0.59
1:E:124:ARG:HD3	1:E:125:ASP:C	2.23	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:229:ARG:CZ	1:E:259:PRO:HB3	2.32	0.59
1:G:220:ALA:CB	1:G:261:ILE:HD13	2.32	0.59
1:B:285:VAL:O	1:B:285:VAL:HG12	2.03	0.59
1:B:471:LYS:HB3	1:B:479:ARG:HH11	1.68	0.59
1:B:484:THR:C	1:B:486:LEU:N	2.56	0.59
1:C:223:LEU:HD23	1:C:224:PRO:HD2	1.84	0.59
1:E:394:TYR:CE2	1:E:405:LEU:HD12	2.38	0.59
1:A:166:MET:HG2	1:A:175:VAL:CG2	2.33	0.59
1:E:389:ASP:H	1:F:269:LEU:CD2	2.16	0.59
1:F:450:LYS:CE	1:F:454:LYS:CD	2.79	0.59
1:A:394:TYR:CE2	1:A:405:LEU:HD12	2.39	0.58
1:A:421:ILE:HB	1:A:460:LEU:HD12	1.84	0.58
1:B:178:LEU:HB2	1:B:181:GLY:HA2	1.83	0.58
1:C:261:ILE:H	1:C:262:PRO:HD3	1.59	0.58
1:C:321:PHE:HD2	1:C:533:MET:HE3	1.67	0.58
1:C:536:ASN:HD22	1:C:536:ASN:C	2.06	0.58
1:D:251:MET:CE	1:D:251:MET:HA	2.33	0.58
1:G:141:LEU:HD11	1:G:196:PHE:HZ	1.68	0.58
1:A:480:PRO:HA	1:A:503:GLU:OE2	2.03	0.58
1:C:86:ILE:HG21	1:C:163:LEU:HD12	1.83	0.58
1:C:229:ARG:HA	1:C:259:PRO:HA	1.84	0.58
1:C:517:ARG:HB3	1:C:519:LEU:CD1	2.33	0.58
1:D:394:TYR:CD1	1:D:394:TYR:C	2.76	0.58
1:D:515:LEU:HD21	1:D:529:ILE:HD11	1.85	0.58
1:F:124:ARG:HD3	1:F:125:ASP:C	2.23	0.58
1:F:366:ASP:HB2	1:G:284:SER:OG	2.03	0.58
1:F:413:ARG:HH21	1:F:458:VAL:N	2.01	0.58
1:G:442:ILE:HD12	1:G:488:GLY:CA	2.32	0.58
1:A:253:GLN:C	1:A:257:ALA:HB2	2.23	0.58
1:A:366:ASP:CB	1:C:285:VAL:CG2	2.79	0.58
1:C:496:SER:HB2	1:C:499:ILE:HD11	1.84	0.58
1:D:186:LYS:CD	1:D:218:GLU:HG3	2.29	0.58
1:D:440:LYS:CE	1:D:441:MET:HA	2.33	0.58
1:D:467:LYS:HE3	1:D:486:LEU:O	2.03	0.58
1:E:425:HIS:CE1	1:E:427:SER:CB	2.86	0.58
1:F:356:LEU:HD12	1:F:541:TRP:NE1	2.18	0.58
1:F:413:ARG:O	1:F:417:GLY:HA2	2.02	0.58
1:A:181:GLY:O	1:A:182:ALA:C	2.40	0.58
1:B:229:ARG:CB	1:B:259:PRO:HA	2.29	0.58
1:D:309:MET:HB3	1:D:499:ILE:CD1	2.33	0.58
1:F:480:PRO:HA	1:F:503:GLU:CD	2.22	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:121:GLN:CB	1:G:133:THR:HG23	2.34	0.58
1:A:121:GLN:HB3	1:A:133:THR:HG23	1.85	0.58
1:A:369:LYS:HG2	1:C:279:LEU:HD22	1.85	0.58
1:A:401:GLU:HG3	1:A:431:SER:O	2.04	0.58
1:B:166:MET:CE	1:B:171:CYS:HB3	2.33	0.58
1:C:230:VAL:N	1:C:258:GLY:O	2.35	0.58
1:C:480:PRO:HA	1:C:503:GLU:OE1	2.03	0.58
1:C:536:ASN:ND2	1:C:538:GLU:H	2.01	0.58
1:E:152:LYS:HD3	1:E:203:ILE:CD1	2.31	0.58
1:E:227:LYS:O	1:E:229:ARG:HD2	2.03	0.58
1:E:471:LYS:HB3	1:E:479:ARG:NH1	2.18	0.58
1:F:124:ARG:CZ	1:F:126:LYS:HA	2.34	0.58
1:F:261:ILE:O	1:F:263:ASP:N	2.36	0.58
1:F:322:VAL:CG1	1:F:422:ILE:HG21	2.33	0.58
1:F:344:GLU:CG	1:F:349:THR:HG22	2.28	0.58
1:G:262:PRO:HB2	1:G:265:VAL:HG12	1.85	0.58
1:E:496:SER:O	1:E:520:LYS:HE2	2.04	0.58
1:F:141:LEU:HD11	1:F:196:PHE:HZ	1.69	0.58
1:G:321:PHE:HD2	1:G:533:MET:HE1	1.68	0.58
1:A:195:TYR:O	1:A:198:GLN:HB2	2.03	0.58
1:A:412:MET:HE2	1:A:421:ILE:HD12	1.81	0.58
1:A:452:PHE:O	1:A:456:THR:HG23	2.04	0.58
1:B:166:MET:HG2	1:B:175:VAL:HG23	1.85	0.58
1:C:202:ILE:HD13	1:C:223:LEU:HD22	1.84	0.58
1:C:492:LEU:H	1:C:492:LEU:CD1	2.17	0.58
1:C:520:LYS:HG3	1:C:521:CYS:N	2.14	0.58
1:C:536:ASN:ND2	1:C:538:GLU:CB	2.67	0.58
1:D:322:VAL:CG2	1:D:463:ILE:HD11	2.34	0.58
1:D:484:THR:C	1:D:486:LEU:H	2.07	0.58
1:F:86:ILE:HD12	1:F:163:LEU:HB3	1.85	0.58
1:F:394:TYR:CD1	1:F:394:TYR:C	2.77	0.58
1:F:452:PHE:O	1:F:456:THR:HG23	2.03	0.58
1:F:478:GLY:HA3	1:F:505:ASN:HB2	1.85	0.58
1:B:494:GLN:HE21	1:G:428:ILE:HG13	1.69	0.58
1:D:145:HIS:CE1	1:D:146:LEU:CD2	2.87	0.58
1:D:413:ARG:HH21	1:D:458:VAL:N	2.01	0.58
1:D:499:ILE:CG2	1:D:519:LEU:CB	2.82	0.58
1:E:152:LYS:HG3	1:E:201:GLN:CG	2.34	0.58
1:E:202:ILE:HD13	1:E:223:LEU:CD2	2.33	0.58
1:E:268:ALA:HA	1:E:271:LEU:CD1	2.34	0.58
1:E:382:PHE:HE1	1:F:275:ILE:HD12	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:490:GLY:CA	1:F:493:ARG:HG3	2.34	0.58
1:A:145:HIS:CE1	1:A:146:LEU:CD2	2.86	0.58
1:B:268:ALA:HA	1:B:271:LEU:CD1	2.34	0.58
1:B:285:VAL:CG1	1:B:288:LEU:HD21	2.34	0.58
1:B:322:VAL:CG2	1:B:463:ILE:HD11	2.33	0.58
1:B:494:GLN:NE2	1:G:428:ILE:HG13	2.19	0.58
1:D:368:LEU:HD22	1:D:372:ILE:HG23	1.85	0.58
1:D:492:LEU:HD12	1:D:492:LEU:N	2.12	0.58
1:E:425:HIS:CE1	1:E:427:SER:HB2	2.38	0.58
1:E:442:ILE:HD11	1:E:492:LEU:CD2	2.34	0.58
1:F:378:PHE:HE2	1:G:276:ARG:HD3	1.66	0.58
1:G:510:MET:HE2	1:G:513:LEU:HD22	1.85	0.58
1:A:91:CYS:HB3	1:A:96:TYR:O	2.04	0.58
1:C:405:LEU:HG	1:C:409:LEU:CD1	2.32	0.58
1:D:369:LYS:HG2	1:E:279:LEU:HD23	1.85	0.58
1:F:78:TYR:CE1	1:F:97:TRP:HB3	2.39	0.58
1:F:467:LYS:HE3	1:F:486:LEU:O	2.04	0.58
1:A:510:MET:HB3	1:A:513:LEU:HB2	1.86	0.57
1:F:442:ILE:HD12	1:F:488:GLY:CA	2.34	0.57
1:F:496:SER:HB2	1:F:499:ILE:HD11	1.86	0.57
1:A:279:LEU:HD23	1:B:369:LYS:HG2	1.87	0.57
1:A:504:ARG:HH21	1:A:506:GLN:HB3	1.69	0.57
1:B:427:SER:CB	1:B:487:ARG:HH12	2.15	0.57
1:E:394:TYR:C	1:E:394:TYR:CD1	2.77	0.57
1:F:166:MET:HG2	1:F:175:VAL:CG2	2.34	0.57
1:A:346:VAL:CG2	1:C:271:LEU:HD21	2.34	0.57
1:A:368:LEU:HD22	1:A:372:ILE:HG23	1.86	0.57
1:A:413:ARG:NE	1:A:458:VAL:HB	2.18	0.57
1:B:153:ILE:HG13	1:B:174:PRO:HB2	1.86	0.57
1:B:321:PHE:CD2	1:B:533:MET:CE	2.86	0.57
1:C:344:GLU:CG	1:C:349:THR:HG22	2.30	0.57
1:F:195:TYR:O	1:F:198:GLN:HB2	2.04	0.57
1:G:322:VAL:CG2	1:G:463:ILE:HD11	2.33	0.57
1:A:290:SER:H	1:A:325:GLN:HE22	1.46	0.57
1:A:401:GLU:HB3	1:A:404:ARG:HB3	1.87	0.57
1:C:346:VAL:HB	1:C:395:ASP:HB2	1.87	0.57
1:C:351:GLU:OE1	1:D:278:HIS:CD2	2.58	0.57
1:D:440:LYS:HE2	1:D:440:LYS:O	2.04	0.57
1:E:166:MET:CE	1:E:171:CYS:HB3	2.35	0.57
1:E:510:MET:HE3	1:E:547:TYR:HE1	1.68	0.57
1:F:499:ILE:CG2	1:F:519:LEU:CB	2.81	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:VAL:HG21	1:A:254:VAL:HG22	1.86	0.57
1:B:151:LYS:HG2	1:B:200:GLU:OE2	2.05	0.57
1:C:186:LYS:CD	1:C:218:GLU:HG3	2.29	0.57
1:G:124:ARG:HD3	1:G:125:ASP:C	2.24	0.57
1:G:339:LEU:CB	1:G:341:MET:HE1	2.28	0.57
1:A:312:SER:CB	1:A:502:LEU:O	2.47	0.57
1:B:480:PRO:HA	1:B:503:GLU:CD	2.24	0.57
1:D:322:VAL:HG21	1:D:463:ILE:HD11	1.86	0.57
1:D:421:ILE:HB	1:D:460:LEU:HD12	1.87	0.57
1:D:477:GLU:HG3	1:D:507:GLN:NE2	2.18	0.57
1:D:480:PRO:HA	1:D:503:GLU:CD	2.24	0.57
1:E:283:GLU:CG	1:E:284:SER:N	2.64	0.57
1:E:437:ASP:OD1	1:E:439:ARG:HB2	2.04	0.57
1:G:312:SER:CB	1:G:502:LEU:O	2.50	0.57
1:A:122:LYS:HE2	1:A:159:GLU:OE1	2.04	0.57
1:A:414:SER:HB3	1:C:226:GLY:CA	2.34	0.57
1:B:166:MET:HG2	1:B:175:VAL:CG2	2.35	0.57
1:C:229:ARG:NH2	1:C:259:PRO:CB	2.68	0.57
1:C:289:PHE:H	1:C:296:ASN:ND2	1.99	0.57
1:D:347:GLU:CD	1:E:274:ARG:HD2	2.24	0.57
1:E:94:ALA:HB1	1:E:162:MET:HE3	1.87	0.57
1:E:141:LEU:CD1	1:E:176:VAL:HG21	2.34	0.57
1:E:338:GLY:HA3	1:E:412:MET:HE3	1.87	0.57
1:E:401:GLU:CG	1:E:402:THR:N	2.66	0.57
1:E:413:ARG:NE	1:E:458:VAL:HB	2.15	0.57
1:G:153:ILE:HG13	1:G:174:PRO:HB2	1.86	0.57
1:G:216:VAL:CG1	1:G:230:VAL:CG2	2.82	0.57
1:G:446:MET:HE2	1:G:492:LEU:HB3	1.85	0.57
1:B:287:LEU:HD11	1:B:335:LYS:HG3	1.87	0.57
1:C:480:PRO:HA	1:C:503:GLU:CD	2.24	0.57
1:E:386:PHE:O	1:F:269:LEU:HD21	2.04	0.57
1:E:480:PRO:HA	1:E:503:GLU:OE1	2.05	0.57
1:F:437:ASP:OD1	1:F:439:ARG:HB2	2.04	0.57
1:F:447:THR:HG22	1:F:495:LEU:CD2	2.22	0.57
1:A:478:GLY:HA3	1:A:505:ASN:HB2	1.85	0.57
1:A:510:MET:CE	1:A:513:LEU:HD22	2.34	0.57
1:D:413:ARG:O	1:D:417:GLY:HA2	2.05	0.57
1:D:473:LYS:CG	1:D:479:ARG:HB2	2.32	0.57
1:E:141:LEU:HD11	1:E:196:PHE:HZ	1.69	0.57
1:F:536:ASN:HD22	1:F:538:GLU:H	1.53	0.57
1:G:74:SER:HB2	1:G:99:ALA:HB1	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:401:GLU:CG	1:G:431:SER:O	2.50	0.57
1:A:346:VAL:HB	1:A:395:ASP:HB2	1.87	0.57
1:B:74:SER:HB3	1:B:101:VAL:HG22	1.87	0.57
1:B:241:CYS:HB2	1:B:250:ILE:HD11	1.85	0.57
1:C:441:MET:HE3	1:C:444:ASN:HB3	1.87	0.57
1:D:427:SER:HB3	1:D:487:ARG:NH1	2.19	0.57
1:G:251:MET:HA	1:G:251:MET:CE	2.35	0.57
1:A:402:THR:HG23	1:A:403:ASP:H	1.70	0.56
1:A:413:ARG:O	1:A:417:GLY:HA2	2.05	0.56
1:B:223:LEU:HD23	1:B:224:PRO:HD2	1.86	0.56
1:B:452:PHE:O	1:B:456:THR:HG23	2.04	0.56
1:E:471:LYS:HB3	1:E:479:ARG:HH11	1.69	0.56
1:F:486:LEU:HD12	1:F:493:ARG:CG	2.35	0.56
1:A:259:PRO:O	1:A:259:PRO:CD	2.53	0.56
1:A:446:MET:CE	1:A:492:LEU:HA	2.35	0.56
1:B:438:GLU:O	1:B:442:ILE:HG22	2.05	0.56
1:C:532:TYR:CD1	1:C:532:TYR:N	2.73	0.56
1:E:122:LYS:HE2	1:E:159:GLU:OE1	2.05	0.56
1:E:424:ASP:O	1:E:425:HIS:HB3	2.05	0.56
1:E:480:PRO:HA	1:E:503:GLU:CD	2.26	0.56
1:E:486:LEU:HD13	1:E:487:ARG:O	2.05	0.56
1:F:186:LYS:HD3	1:F:218:GLU:CG	2.30	0.56
1:F:369:LYS:HG2	1:G:279:LEU:HD23	1.88	0.56
1:G:74:SER:HB3	1:G:101:VAL:HG22	1.87	0.56
1:G:186:LYS:CD	1:G:218:GLU:HG3	2.30	0.56
1:G:438:GLU:O	1:G:442:ILE:HG22	2.05	0.56
1:G:484:THR:C	1:G:486:LEU:N	2.58	0.56
1:A:307:VAL:O	1:A:307:VAL:HG12	2.05	0.56
1:A:313:GLY:O	1:A:315:GLY:N	2.38	0.56
1:A:477:GLU:HG3	1:A:507:GLN:NE2	2.21	0.56
1:A:496:SER:CB	1:A:499:ILE:HD11	2.34	0.56
1:B:74:SER:HB2	1:B:99:ALA:HB1	1.87	0.56
1:C:322:VAL:CG1	1:C:422:ILE:HG21	2.35	0.56
1:C:424:ASP:O	1:C:425:HIS:HB3	2.06	0.56
1:C:473:LYS:CE	1:C:479:ARG:HA	2.34	0.56
1:E:216:VAL:HG11	1:E:230:VAL:HG22	1.83	0.56
1:E:368:LEU:HD22	1:E:368:LEU:O	2.05	0.56
1:E:483:ILE:O	1:E:486:LEU:CB	2.38	0.56
1:E:515:LEU:HD21	1:E:529:ILE:HD11	1.86	0.56
1:F:482:SER:N	1:F:485:ASP:HB2	2.19	0.56
1:G:151:LYS:HG2	1:G:200:GLU:OE2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:447:THR:HA	1:G:495:LEU:HD23	1.87	0.56
1:G:477:GLU:HG3	1:G:507:GLN:NE2	2.19	0.56
1:G:499:ILE:CG2	1:G:519:LEU:CB	2.83	0.56
1:A:166:MET:HG2	1:A:175:VAL:HG23	1.88	0.56
1:A:345:SER:O	1:A:349:THR:HG23	2.05	0.56
1:A:442:ILE:HD11	1:A:492:LEU:HD11	1.88	0.56
1:D:442:ILE:HD12	1:D:488:GLY:HA2	1.88	0.56
1:E:121:GLN:CB	1:E:133:THR:HG23	2.36	0.56
1:E:233:LEU:HD22	1:E:241:CYS:SG	2.45	0.56
1:E:276:ARG:HH11	1:E:276:ARG:CG	2.18	0.56
1:E:401:GLU:HB3	1:E:404:ARG:HB3	1.86	0.56
1:E:405:LEU:HG	1:E:409:LEU:CD1	2.33	0.56
1:F:473:LYS:CG	1:F:479:ARG:HB2	2.33	0.56
1:A:486:LEU:HB3	1:A:493:ARG:HD2	1.86	0.56
1:B:216:VAL:HG11	1:B:230:VAL:HG22	1.85	0.56
1:C:154:VAL:HG21	1:C:254:VAL:HG22	1.87	0.56
1:C:364:GLN:HA	1:D:523:PHE:CZ	2.40	0.56
1:C:394:TYR:C	1:C:394:TYR:CD1	2.78	0.56
1:E:229:ARG:NH2	1:E:259:PRO:CG	2.68	0.56
1:F:181:GLY:O	1:F:182:ALA:C	2.43	0.56
1:G:446:MET:HE3	1:G:492:LEU:HA	1.87	0.56
1:A:369:LYS:CG	1:C:279:LEU:CD2	2.83	0.56
1:B:229:ARG:CZ	1:B:259:PRO:HB3	2.35	0.56
1:B:316:MET:CE	1:B:535:TYR:CE2	2.88	0.56
1:C:68:VAL:HG12	1:C:121:GLN:OE1	2.04	0.56
1:C:229:ARG:NE	1:C:259:PRO:HB3	2.20	0.56
1:C:328:GLN:HA	1:C:331:THR:OG1	2.05	0.56
1:D:262:PRO:HB2	1:D:265:VAL:HG12	1.86	0.56
1:E:322:VAL:HG21	1:E:463:ILE:CD1	2.35	0.56
1:E:336:LYS:HB3	1:E:418:CYS:HB3	1.88	0.56
1:G:486:LEU:HB3	1:G:493:ARG:HD2	1.87	0.56
1:C:546:SER:O	1:C:547:TYR:HB2	2.05	0.56
1:D:205:MET:HG3	1:D:231:ALA:CB	2.35	0.56
1:F:178:LEU:HB2	1:F:181:GLY:HA2	1.87	0.56
1:F:268:ALA:HA	1:F:271:LEU:HD12	1.88	0.56
1:B:343:GLU:OE1	1:B:343:GLU:HA	2.06	0.56
1:C:151:LYS:HG2	1:C:200:GLU:OE2	2.05	0.56
1:C:488:GLY:HA3	1:C:492:LEU:CD1	2.36	0.56
1:D:94:ALA:HB1	1:D:162:MET:HE3	1.88	0.56
1:E:359:ARG:HD3	1:E:541:TRP:NE1	2.20	0.56
1:F:152:LYS:HD3	1:F:203:ILE:CD1	2.33	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:515:LEU:HD21	1:F:529:ILE:HD11	1.87	0.56
1:G:336:LYS:HB3	1:G:418:CYS:HA	1.87	0.56
1:G:473:LYS:CG	1:G:479:ARG:HB2	2.34	0.56
1:A:473:LYS:CG	1:A:479:ARG:HB2	2.35	0.56
1:A:499:ILE:CG2	1:A:519:LEU:CB	2.84	0.56
1:B:424:ASP:O	1:B:425:HIS:HB3	2.06	0.56
1:C:369:LYS:CG	1:D:279:LEU:CD2	2.84	0.56
1:C:478:GLY:CA	1:C:505:ASN:HB2	2.34	0.56
1:D:347:GLU:OE2	1:E:274:ARG:HD2	2.06	0.56
1:E:74:SER:HB2	1:E:99:ALA:HB1	1.88	0.56
1:E:477:GLU:HG3	1:E:507:GLN:NE2	2.20	0.56
1:F:471:LYS:HB3	1:F:479:ARG:NH1	2.21	0.56
1:A:442:ILE:HD11	1:A:492:LEU:CD2	2.35	0.56
1:B:124:ARG:HD3	1:B:125:ASP:C	2.27	0.56
1:C:382:PHE:HE1	1:D:275:ILE:HD12	1.71	0.56
1:C:413:ARG:HH21	1:C:458:VAL:N	2.03	0.56
1:E:428:ILE:H	1:E:428:ILE:HD12	1.71	0.56
1:A:427:SER:HB3	1:A:487:ARG:NH1	2.18	0.55
1:D:195:TYR:O	1:D:198:GLN:HB2	2.05	0.55
1:D:369:LYS:CG	1:E:279:LEU:HD22	2.35	0.55
1:E:394:TYR:HE1	1:E:396:SER:CB	2.19	0.55
1:F:152:LYS:HG3	1:F:201:GLN:CG	2.34	0.55
1:G:515:LEU:HD21	1:G:529:ILE:HD12	1.89	0.55
1:A:268:ALA:HA	1:A:271:LEU:HD13	1.87	0.55
1:A:351:GLU:HB2	1:A:363:ARG:HD2	1.88	0.55
1:C:439:ARG:O	1:C:442:ILE:HG22	2.06	0.55
1:D:276:ARG:HG2	1:D:276:ARG:HH11	1.69	0.55
1:E:312:SER:CB	1:E:502:LEU:O	2.53	0.55
1:E:473:LYS:CG	1:E:479:ARG:HB2	2.35	0.55
1:E:504:ARG:HH21	1:E:506:GLN:CB	2.19	0.55
1:F:74:SER:HB3	1:F:101:VAL:HG22	1.88	0.55
1:F:389:ASP:CA	1:G:269:LEU:HD23	2.36	0.55
1:A:229:ARG:HB3	1:A:259:PRO:HA	1.88	0.55
1:A:429:VAL:HG23	1:A:430:VAL:H	1.71	0.55
1:A:521:CYS:O	1:A:525:GLY:N	2.34	0.55
1:C:322:VAL:CG2	1:C:463:ILE:HD11	2.37	0.55
1:C:438:GLU:O	1:C:442:ILE:HG22	2.06	0.55
1:C:471:LYS:HB3	1:C:479:ARG:NH1	2.21	0.55
1:D:429:VAL:HG23	1:D:430:VAL:H	1.71	0.55
1:F:141:LEU:HD13	1:F:176:VAL:CG2	2.35	0.55
1:G:482:SER:N	1:G:485:ASP:HB2	2.19	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:318:MET:SD	1:A:463:ILE:HD12	2.46	0.55
1:B:345:SER:O	1:B:349:THR:HG23	2.06	0.55
1:B:351:GLU:HB2	1:B:363:ARG:HD2	1.89	0.55
1:C:366:ASP:CA	1:D:284:SER:OG	2.55	0.55
1:D:471:LYS:HB3	1:D:479:ARG:NH1	2.22	0.55
1:E:195:TYR:O	1:E:198:GLN:HB2	2.06	0.55
1:F:262:PRO:HB2	1:F:265:VAL:HG12	1.88	0.55
1:F:480:PRO:HA	1:F:503:GLU:OE1	2.05	0.55
1:C:166:MET:HE1	1:C:171:CYS:CB	2.32	0.55
1:D:261:ILE:N	1:D:262:PRO:HD3	2.17	0.55
1:D:510:MET:HE3	1:D:547:TYR:CE1	2.33	0.55
1:D:536:ASN:ND2	1:D:538:GLU:H	2.04	0.55
1:E:499:ILE:CG2	1:E:519:LEU:CB	2.84	0.55
1:F:478:GLY:CA	1:F:505:ASN:HB2	2.37	0.55
1:A:359:ARG:HD3	1:A:541:TRP:NE1	2.22	0.55
1:A:405:LEU:HG	1:A:409:LEU:CD1	2.34	0.55
1:B:111:TYR:CZ	1:B:142:PHE:HB2	2.42	0.55
1:C:216:VAL:CG1	1:C:230:VAL:CG2	2.84	0.55
1:E:205:MET:HG3	1:E:231:ALA:CB	2.36	0.55
1:E:290:SER:N	1:E:325:GLN:HE21	1.97	0.55
1:F:321:PHE:CD2	1:F:533:MET:CE	2.88	0.55
1:F:352:ASP:CG	1:F:363:ARG:HD3	2.26	0.55
1:F:477:GLU:HG3	1:F:507:GLN:NE2	2.21	0.55
1:G:147:TRP:CG	1:G:174:PRO:HB3	2.42	0.55
1:G:442:ILE:HD11	1:G:492:LEU:HD11	1.89	0.55
1:A:243:LEU:O	1:A:244:ASN:O	2.25	0.55
1:A:454:LYS:HE3	1:A:522:ARG:HH22	1.72	0.55
1:B:122:LYS:HE2	1:B:159:GLU:OE1	2.07	0.55
1:B:312:SER:CB	1:B:502:LEU:O	2.55	0.55
1:B:412:MET:CA	1:B:416:LEU:HD12	2.24	0.55
1:C:515:LEU:HD21	1:C:529:ILE:HD11	1.89	0.55
1:D:74:SER:HB3	1:D:101:VAL:HG22	1.89	0.55
1:D:229:ARG:CB	1:D:258:GLY:O	2.55	0.55
1:D:352:ASP:CG	1:D:363:ARG:HD3	2.26	0.55
1:D:496:SER:HB2	1:D:499:ILE:HD11	1.87	0.55
1:E:154:VAL:HG21	1:E:254:VAL:HG22	1.88	0.55
1:F:392:HIS:ND1	1:G:267:SER:HB2	2.21	0.55
1:G:122:LYS:HE2	1:G:159:GLU:OE1	2.06	0.55
1:G:229:ARG:NH2	1:G:259:PRO:HG3	2.21	0.55
1:G:405:LEU:HG	1:G:409:LEU:CD1	2.36	0.55
1:B:205:MET:HG3	1:B:231:ALA:CB	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:322:VAL:HG21	1:C:463:ILE:HD11	1.89	0.55
1:D:360:VAL:HG23	1:D:360:VAL:O	2.07	0.55
1:E:74:SER:HB3	1:E:101:VAL:HG22	1.87	0.55
1:E:165:VAL:HB	1:E:175:VAL:HG11	1.89	0.55
1:E:401:GLU:CG	1:E:402:THR:H	2.19	0.55
1:E:484:THR:C	1:E:486:LEU:H	2.10	0.55
1:F:202:ILE:HD13	1:F:223:LEU:HD22	1.89	0.55
1:G:352:ASP:CG	1:G:363:ARG:HD3	2.27	0.55
1:G:447:THR:HG22	1:G:495:LEU:CD2	2.26	0.55
1:A:162:MET:HG2	1:A:175:VAL:HB	1.89	0.55
1:A:162:MET:SD	1:A:166:MET:HG3	2.46	0.55
1:E:369:LYS:HG2	1:F:279:LEU:CD2	2.37	0.55
1:E:440:LYS:HE2	1:E:440:LYS:C	2.27	0.55
1:E:504:ARG:HH21	1:E:506:GLN:HG2	1.71	0.55
1:A:126:LYS:NZ	1:A:127:ASP:OD1	2.40	0.55
1:A:276:ARG:HG2	1:A:276:ARG:HH11	1.71	0.55
1:C:121:GLN:HB2	1:C:133:THR:HG1	1.71	0.55
1:D:442:ILE:HD12	1:D:488:GLY:CA	2.36	0.55
1:E:438:GLU:O	1:E:442:ILE:HG22	2.07	0.55
1:E:476:GLU:CD	1:E:476:GLU:H	2.09	0.55
1:F:260:TRP:CB	1:F:262:PRO:CD	2.44	0.55
1:F:336:LYS:HB3	1:F:418:CYS:HA	1.89	0.55
1:F:471:LYS:HB3	1:F:479:ARG:HH11	1.72	0.55
1:A:322:VAL:CG2	1:A:463:ILE:HD11	2.37	0.54
1:A:352:ASP:CG	1:A:363:ARG:HD3	2.27	0.54
1:A:395:ASP:HB3	1:C:266:VAL:CG2	2.36	0.54
1:A:425:HIS:HE1	1:A:465:HIS:HB2	1.71	0.54
1:A:441:MET:CE	1:A:444:ASN:HB3	2.37	0.54
1:C:512:ASN:HD21	1:C:537:LYS:HE3	1.71	0.54
1:D:91:CYS:HB3	1:D:96:TYR:O	2.07	0.54
1:D:440:LYS:HE2	1:D:440:LYS:C	2.28	0.54
1:D:510:MET:HE2	1:D:513:LEU:HD22	1.89	0.54
1:E:126:LYS:HG2	1:E:127:ASP:H	1.72	0.54
1:E:440:LYS:CE	1:E:441:MET:HA	2.36	0.54
1:A:79:SER:H	1:A:98:ILE:CD1	2.20	0.54
1:A:402:THR:HG23	1:A:403:ASP:N	2.22	0.54
1:A:420:VAL:HG22	1:A:459:VAL:HB	1.88	0.54
1:B:504:ARG:HH21	1:B:506:GLN:CB	2.20	0.54
1:C:338:GLY:HA3	1:C:412:MET:HE3	1.88	0.54
1:D:126:LYS:HG2	1:D:127:ASP:H	1.73	0.54
1:D:359:ARG:HD3	1:D:541:TRP:NE1	2.20	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:229:ARG:NE	1:E:259:PRO:HB3	2.22	0.54
1:E:303:ARG:CZ	1:E:523:PHE:CD1	2.90	0.54
1:E:412:MET:CE	1:E:421:ILE:HD13	2.36	0.54
1:E:429:VAL:HG23	1:E:430:VAL:H	1.72	0.54
1:F:521:CYS:SG	1:F:524:THR:HG23	2.47	0.54
1:A:259:PRO:O	1:A:259:PRO:HD2	2.08	0.54
1:B:275:ILE:HD12	1:G:382:PHE:HE1	1.72	0.54
1:B:303:ARG:CZ	1:B:523:PHE:CD1	2.90	0.54
1:C:260:TRP:C	1:C:261:ILE:HD13	2.27	0.54
1:C:283:GLU:CD	1:C:286:GLY:HA2	2.27	0.54
1:D:142:PHE:CE2	1:D:162:MET:HE3	2.42	0.54
1:D:288:LEU:HD12	1:D:288:LEU:N	2.21	0.54
1:F:91:CYS:HB3	1:F:96:TYR:O	2.07	0.54
1:B:344:GLU:CG	1:B:349:THR:HG22	2.29	0.54
1:B:521:CYS:O	1:B:525:GLY:N	2.35	0.54
1:C:352:ASP:CG	1:C:363:ARG:HD3	2.27	0.54
1:D:484:THR:C	1:D:486:LEU:N	2.59	0.54
1:D:521:CYS:SG	1:D:524:THR:HG23	2.48	0.54
1:E:321:PHE:CD2	1:E:533:MET:CE	2.90	0.54
1:F:286:GLY:O	1:F:302:ALA:N	2.41	0.54
1:G:429:VAL:HG23	1:G:430:VAL:H	1.72	0.54
1:A:232:VAL:O	1:A:232:VAL:HG12	2.06	0.54
1:A:318:MET:SD	1:A:463:ILE:HD13	2.47	0.54
1:B:141:LEU:CD1	1:B:176:VAL:HG21	2.34	0.54
1:B:397:PHE:CD1	1:B:397:PHE:C	2.80	0.54
1:C:268:ALA:HA	1:C:271:LEU:HD12	1.90	0.54
1:C:486:LEU:HB3	1:C:493:ARG:HD2	1.90	0.54
1:E:346:VAL:HB	1:E:395:ASP:HB2	1.88	0.54
1:E:496:SER:HB2	1:E:499:ILE:HD11	1.90	0.54
1:E:502:LEU:HD12	1:E:502:LEU:H	1.72	0.54
1:E:546:SER:O	1:E:547:TYR:HB2	2.07	0.54
1:F:74:SER:HB2	1:F:99:ALA:HB1	1.90	0.54
1:F:440:LYS:O	1:F:440:LYS:HE2	2.07	0.54
1:G:480:PRO:HA	1:G:503:GLU:CD	2.28	0.54
1:G:521:CYS:SG	1:G:524:THR:HG23	2.48	0.54
1:A:112:ARG:NH2	1:A:118:ILE:HD11	2.23	0.54
1:C:536:ASN:HD21	1:C:538:GLU:HB2	1.71	0.54
1:E:151:LYS:HG2	1:E:200:GLU:OE2	2.08	0.54
1:E:318:MET:CE	1:E:465:HIS:CD2	2.91	0.54
1:G:233:LEU:HD22	1:G:241:CYS:SG	2.48	0.54
1:G:478:GLY:CA	1:G:505:ASN:HB2	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:443:ASP:HA	1:A:491:ALA:CB	2.38	0.54
1:B:265:VAL:HG11	1:G:411:TYR:HE1	1.73	0.54
1:B:421:ILE:HB	1:B:460:LEU:HD12	1.90	0.54
1:C:122:LYS:HE3	1:C:130:PHE:CE2	2.43	0.54
1:C:317:VAL:HG21	1:C:504:ARG:HD2	1.90	0.54
1:C:484:THR:C	1:C:486:LEU:H	2.09	0.54
1:D:223:LEU:HD23	1:D:224:PRO:HD2	1.90	0.54
1:D:536:ASN:ND2	1:D:538:GLU:CB	2.71	0.54
1:E:343:GLU:OE1	1:E:343:GLU:HA	2.07	0.54
1:E:521:CYS:O	1:E:525:GLY:N	2.34	0.54
1:F:233:LEU:HD22	1:F:241:CYS:SG	2.48	0.54
1:F:241:CYS:HB2	1:F:250:ILE:HD11	1.90	0.54
1:F:320:THR:HG22	1:F:324:GLN:NE2	2.23	0.54
1:B:447:THR:HA	1:B:495:LEU:HD23	1.90	0.54
1:C:351:GLU:HB2	1:C:363:ARG:HD2	1.90	0.54
1:C:394:TYR:HE1	1:C:396:SER:HB2	1.73	0.54
1:C:482:SER:H	1:C:485:ASP:CB	2.19	0.54
1:E:241:CYS:HB2	1:E:250:ILE:HD11	1.89	0.54
1:E:382:PHE:CE1	1:F:272:ARG:HA	2.43	0.54
1:E:392:HIS:ND1	1:F:267:SER:HB2	2.23	0.54
1:E:536:ASN:HD22	1:E:538:GLU:H	1.56	0.54
1:F:186:LYS:CD	1:F:218:GLU:HG3	2.32	0.54
1:F:294:GLY:O	1:F:295:ILE:C	2.42	0.54
1:F:369:LYS:HG2	1:G:279:LEU:CD2	2.37	0.54
1:C:153:ILE:HG13	1:C:174:PRO:HB2	1.89	0.54
1:C:429:VAL:HG23	1:C:430:VAL:H	1.72	0.54
1:D:124:ARG:HD3	1:D:125:ASP:C	2.28	0.54
1:D:471:LYS:HB3	1:D:479:ARG:HH11	1.72	0.54
1:D:487:ARG:O	1:D:493:ARG:HD3	2.08	0.54
1:E:512:ASN:HD21	1:E:537:LYS:HE3	1.73	0.54
1:F:111:TYR:CZ	1:F:142:PHE:HB2	2.43	0.54
1:F:446:MET:CE	1:F:492:LEU:HA	2.38	0.54
1:A:347:GLU:O	1:A:351:GLU:HG3	2.08	0.54
1:B:164:THR:O	1:B:167:GLU:HB2	2.08	0.54
1:C:145:HIS:CE1	1:C:146:LEU:CD2	2.91	0.54
1:C:166:MET:HG2	1:C:175:VAL:HG23	1.90	0.54
1:C:208:MET:CE	1:C:232:VAL:HA	2.18	0.54
1:C:411:TYR:CZ	1:D:262:PRO:HD3	2.42	0.54
1:E:401:GLU:HG2	1:E:402:THR:H	1.71	0.54
1:G:166:MET:HG2	1:G:175:VAL:HG23	1.90	0.54
1:G:227:LYS:O	1:G:229:ARG:HD2	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:LYS:HD3	1:A:203:ILE:HD11	1.90	0.53
1:A:347:GLU:CD	1:C:274:ARG:HD2	2.28	0.53
1:A:351:GLU:OE1	1:C:278:HIS:CD2	2.62	0.53
1:A:437:ASP:OD1	1:A:439:ARG:HB2	2.07	0.53
1:A:447:THR:CG2	1:A:495:LEU:HD21	2.27	0.53
1:C:195:TYR:O	1:C:198:GLN:HB2	2.08	0.53
1:D:111:TYR:CZ	1:D:142:PHE:HB2	2.43	0.53
1:D:294:GLY:O	1:D:295:ILE:C	2.44	0.53
1:E:320:THR:HG22	1:E:324:GLN:NE2	2.23	0.53
1:E:515:LEU:HD21	1:E:529:ILE:HD12	1.91	0.53
1:F:499:ILE:HG22	1:F:519:LEU:CB	2.27	0.53
1:G:241:CYS:HB2	1:G:250:ILE:HD11	1.89	0.53
1:G:311:THR:OG1	1:G:466:LEU:HD21	2.07	0.53
1:G:450:LYS:CE	1:G:454:LYS:CD	2.81	0.53
1:G:471:LYS:HB3	1:G:479:ARG:NH1	2.23	0.53
1:G:492:LEU:HD12	1:G:492:LEU:N	2.12	0.53
1:B:397:PHE:C	1:B:397:PHE:HD1	2.11	0.53
1:B:429:VAL:HG23	1:B:430:VAL:H	1.73	0.53
1:C:147:TRP:CG	1:C:174:PRO:HB3	2.42	0.53
1:C:347:GLU:O	1:C:351:GLU:HG3	2.09	0.53
1:C:356:LEU:HD12	1:C:541:TRP:NE1	2.23	0.53
1:D:372:ILE:HG13	1:D:378:PHE:HB2	1.89	0.53
1:D:401:GLU:HG2	1:D:402:THR:H	1.73	0.53
1:F:372:ILE:HG13	1:F:378:PHE:HB2	1.90	0.53
1:G:510:MET:HB3	1:G:513:LEU:HB2	1.90	0.53
1:B:413:ARG:O	1:B:417:GLY:HA2	2.08	0.53
1:C:486:LEU:HD12	1:C:493:ARG:CD	2.38	0.53
1:D:166:MET:CE	1:D:171:CYS:HB3	2.37	0.53
1:D:230:VAL:HB	1:D:260:TRP:NE1	2.22	0.53
1:D:437:ASP:OD1	1:D:439:ARG:HB2	2.08	0.53
1:D:510:MET:HE1	1:D:547:TYR:CE1	2.44	0.53
1:D:536:ASN:HD21	1:D:538:GLU:CB	2.20	0.53
1:E:440:LYS:NZ	1:E:441:MET:CA	2.55	0.53
1:E:504:ARG:HD3	1:E:506:GLN:CG	2.16	0.53
1:B:86:ILE:HG21	1:B:163:LEU:CD1	2.38	0.53
1:B:235:CYS:CB	1:B:240:GLU:HG2	2.39	0.53
1:B:441:MET:CE	1:B:445:LEU:H	2.21	0.53
1:C:268:ALA:HA	1:C:271:LEU:HD13	1.90	0.53
1:C:471:LYS:HB3	1:C:479:ARG:HH11	1.72	0.53
1:D:217:GLU:OE2	1:D:261:ILE:CA	2.54	0.53
1:D:306:GLU:HA	1:D:497:ASP:OD2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:318:MET:SD	1:D:463:ILE:HG23	2.48	0.53
1:G:141:LEU:CD1	1:G:176:VAL:HG21	2.36	0.53
1:G:338:GLY:HA3	1:G:412:MET:HE1	1.90	0.53
1:G:394:TYR:CD1	1:G:394:TYR:C	2.82	0.53
1:A:356:LEU:HD12	1:A:541:TRP:NE1	2.24	0.53
1:B:246:HIS:HB3	1:B:249:GLU:OE1	2.09	0.53
1:D:345:SER:O	1:D:349:THR:CG2	2.56	0.53
1:D:345:SER:O	1:D:349:THR:HG23	2.08	0.53
1:D:512:ASN:HD21	1:D:537:LYS:HE3	1.73	0.53
1:E:517:ARG:HB3	1:E:519:LEU:CD1	2.38	0.53
1:F:78:TYR:CD2	1:F:92:GLN:HG2	2.43	0.53
1:F:305:GLY:O	1:F:454:LYS:HD2	2.09	0.53
1:F:496:SER:CB	1:F:499:ILE:HD11	2.39	0.53
1:G:412:MET:CA	1:G:416:LEU:HD12	2.28	0.53
1:B:307:VAL:O	1:B:307:VAL:HG12	2.07	0.53
1:B:322:VAL:HG21	1:B:463:ILE:CG1	2.38	0.53
1:B:345:SER:O	1:B:349:THR:CG2	2.56	0.53
1:B:439:ARG:HG2	1:B:489:SER:OG	2.09	0.53
1:B:546:SER:O	1:B:547:TYR:HB2	2.08	0.53
1:E:447:THR:HA	1:E:495:LEU:HD23	1.90	0.53
1:F:447:THR:HA	1:F:495:LEU:HD23	1.90	0.53
1:G:256:ASN:O	1:G:256:ASN:ND2	2.42	0.53
1:A:166:MET:O	1:A:171:CYS:HB3	2.08	0.53
1:A:235:CYS:CB	1:A:240:GLU:HG2	2.39	0.53
1:B:154:VAL:HG21	1:B:254:VAL:HG22	1.90	0.53
1:B:445:LEU:HD12	1:B:445:LEU:O	2.09	0.53
1:C:121:GLN:CB	1:C:133:THR:HG23	2.39	0.53
1:C:401:GLU:CG	1:C:402:THR:N	2.71	0.53
1:C:440:LYS:HE2	1:C:440:LYS:C	2.28	0.53
1:E:152:LYS:O	1:E:174:PRO:HD2	2.08	0.53
1:E:164:THR:O	1:E:167:GLU:HB2	2.09	0.53
1:E:166:MET:HG2	1:E:175:VAL:HG23	1.91	0.53
1:F:126:LYS:HG2	1:F:127:ASP:H	1.73	0.53
1:F:441:MET:CE	1:F:444:ASN:HB3	2.39	0.53
1:G:86:ILE:HG21	1:G:163:LEU:CD1	2.38	0.53
1:G:343:GLU:OE1	1:G:343:GLU:HA	2.09	0.53
1:A:321:PHE:HD2	1:A:533:MET:HE3	1.74	0.53
1:A:504:ARG:HH21	1:A:506:GLN:CG	2.21	0.53
1:A:510:MET:HB2	1:A:513:LEU:HB3	1.91	0.53
1:B:91:CYS:HB3	1:B:96:TYR:O	2.09	0.53
1:C:382:PHE:CE1	1:D:272:ARG:HA	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:241:CYS:HB2	1:D:250:ILE:HD11	1.91	0.53
1:D:486:LEU:HD12	1:D:493:ARG:CD	2.38	0.53
1:D:504:ARG:HH21	1:D:506:GLN:CB	2.21	0.53
1:E:312:SER:O	1:E:313:GLY:O	2.26	0.53
1:F:286:GLY:O	1:F:287:LEU:O	2.27	0.53
1:A:168:LEU:HD12	1:A:251:MET:HE3	1.90	0.53
1:A:234:PRO:HG2	1:A:249:GLU:HG2	1.91	0.53
1:A:324:GLN:OE1	1:A:541:TRP:CE3	2.61	0.53
1:A:343:GLU:OE1	1:A:343:GLU:HA	2.09	0.53
1:B:536:ASN:ND2	1:B:538:GLU:H	2.07	0.53
1:C:314:SER:O	1:C:315:GLY:C	2.47	0.53
1:C:406:LEU:HD21	1:C:449:LEU:HD23	1.89	0.53
1:D:180:HIS:HB2	1:D:184:ALA:HB3	1.91	0.53
1:D:322:VAL:HG21	1:D:463:ILE:CG1	2.39	0.53
1:D:394:TYR:CE2	1:D:405:LEU:HD12	2.44	0.53
1:E:86:ILE:HG21	1:E:163:LEU:CD1	2.39	0.53
1:G:476:GLU:H	1:G:476:GLU:CD	2.11	0.53
1:A:164:THR:O	1:A:167:GLU:HB2	2.09	0.53
1:A:496:SER:O	1:A:520:LYS:CE	2.56	0.53
1:B:294:GLY:O	1:B:295:ILE:C	2.46	0.53
1:D:232:VAL:O	1:D:232:VAL:HG12	2.07	0.53
1:E:114:GLN:NE2	1:E:195:TYR:HD1	2.07	0.53
1:F:125:ASP:OD1	1:F:129:ASN:HB2	2.08	0.53
1:A:259:PRO:O	1:A:260:TRP:CB	2.46	0.52
1:A:262:PRO:HB2	1:A:265:VAL:HG12	1.90	0.52
1:B:114:GLN:NE2	1:B:195:TYR:HD1	2.07	0.52
1:B:152:LYS:O	1:B:174:PRO:HD2	2.09	0.52
1:B:216:VAL:CG1	1:B:230:VAL:CG2	2.85	0.52
1:C:411:TYR:OH	1:D:260:TRP:HA	2.09	0.52
1:D:515:LEU:HD21	1:D:529:ILE:HD12	1.90	0.52
1:E:386:PHE:O	1:F:269:LEU:CD2	2.58	0.52
1:E:510:MET:HE2	1:E:547:TYR:CE1	2.43	0.52
1:F:343:GLU:OE1	1:F:343:GLU:HA	2.09	0.52
1:G:145:HIS:CE1	1:G:146:LEU:CD2	2.92	0.52
1:G:412:MET:CE	1:G:421:ILE:CD1	2.87	0.52
1:G:471:LYS:HB3	1:G:479:ARG:HH11	1.74	0.52
1:A:347:GLU:CD	1:C:274:ARG:HG2	2.30	0.52
1:B:126:LYS:HG2	1:B:127:ASP:H	1.74	0.52
1:B:359:ARG:HD3	1:B:541:TRP:NE1	2.23	0.52
1:C:106:TYR:HB3	1:C:123:VAL:HG12	1.91	0.52
1:C:445:LEU:HD12	1:C:445:LEU:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:484:THR:C	1:E:486:LEU:N	2.62	0.52
1:F:86:ILE:HG21	1:F:163:LEU:CD1	2.39	0.52
1:F:268:ALA:HA	1:F:271:LEU:HD13	1.91	0.52
1:F:338:GLY:HA3	1:F:412:MET:HE3	1.90	0.52
1:G:145:HIS:CE1	1:G:146:LEU:HD23	2.44	0.52
1:G:166:MET:HE3	1:G:171:CYS:HA	1.91	0.52
1:G:487:ARG:O	1:G:493:ARG:HD3	2.09	0.52
1:A:74:SER:HB3	1:A:101:VAL:HG22	1.90	0.52
1:A:344:GLU:OE1	1:A:349:THR:HB	2.10	0.52
1:A:536:ASN:ND2	1:A:538:GLU:H	2.08	0.52
1:B:536:ASN:ND2	1:B:538:GLU:CB	2.72	0.52
1:C:145:HIS:CE1	1:C:146:LEU:HD23	2.45	0.52
1:D:122:LYS:HE3	1:D:130:PHE:CE2	2.45	0.52
1:D:230:VAL:HG11	1:D:260:TRP:NE1	2.24	0.52
1:E:232:VAL:HG12	1:E:232:VAL:O	2.08	0.52
1:E:345:SER:O	1:E:349:THR:HG23	2.08	0.52
1:F:267:SER:O	1:F:270:SER:OG	2.26	0.52
1:G:492:LEU:H	1:G:492:LEU:CD1	2.05	0.52
1:A:74:SER:HB3	1:A:101:VAL:CG2	2.40	0.52
1:A:394:TYR:HE1	1:A:396:SER:CB	2.21	0.52
1:A:412:MET:HG2	1:C:265:VAL:HG21	1.92	0.52
1:B:478:GLY:CA	1:B:505:ASN:HB2	2.39	0.52
1:C:141:LEU:CD1	1:C:176:VAL:HG21	2.35	0.52
1:C:273:GLU:OE2	1:C:276:ARG:NH1	2.42	0.52
1:D:344:GLU:OE1	1:D:349:THR:HB	2.10	0.52
1:E:410:ALA:HA	1:E:452:PHE:CE1	2.44	0.52
1:E:482:SER:H	1:E:485:ASP:CB	2.17	0.52
1:F:359:ARG:HD3	1:F:541:TRP:NE1	2.25	0.52
1:G:166:MET:HG2	1:G:175:VAL:CG2	2.39	0.52
1:G:294:GLY:O	1:G:295:ILE:C	2.46	0.52
1:G:344:GLU:OE1	1:G:349:THR:HB	2.09	0.52
1:A:147:TRP:CG	1:A:174:PRO:HB3	2.45	0.52
1:B:229:ARG:CB	1:B:258:GLY:O	2.58	0.52
1:F:347:GLU:O	1:F:351:GLU:HG3	2.09	0.52
1:F:401:GLU:CG	1:F:431:SER:O	2.57	0.52
1:F:445:LEU:CD1	1:F:449:LEU:HG	2.39	0.52
1:G:205:MET:HG3	1:G:231:ALA:CB	2.39	0.52
1:A:205:MET:HG3	1:A:231:ALA:CB	2.40	0.52
1:A:478:GLY:CA	1:A:505:ASN:HB2	2.40	0.52
1:B:290:SER:N	1:B:325:GLN:HE21	2.02	0.52
1:B:487:ARG:O	1:B:493:ARG:HD3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:447:THR:HA	1:C:495:LEU:HD23	1.91	0.52
1:C:510:MET:HE2	1:C:547:TYR:CE1	2.39	0.52
1:C:510:MET:CB	1:C:513:LEU:HB2	2.39	0.52
1:D:318:MET:SD	1:D:463:ILE:CD1	2.98	0.52
1:F:440:LYS:CE	1:F:441:MET:HA	2.39	0.52
1:G:140:ALA:O	1:G:141:LEU:HD23	2.10	0.52
1:G:300:LEU:HB3	1:G:303:ARG:HH12	1.74	0.52
1:A:428:ILE:HD12	1:A:428:ILE:H	1.75	0.52
1:A:536:ASN:HD21	1:A:538:GLU:CB	2.23	0.52
1:B:140:ALA:O	1:B:141:LEU:HD23	2.10	0.52
1:B:162:MET:SD	1:B:166:MET:HG3	2.49	0.52
1:B:338:GLY:HA3	1:B:412:MET:HE1	1.91	0.52
1:B:362:LEU:HD12	1:B:362:LEU:O	2.10	0.52
1:C:122:LYS:HE2	1:C:159:GLU:OE1	2.10	0.52
1:C:140:ALA:O	1:C:141:LEU:HD23	2.10	0.52
1:D:341:MET:SD	1:D:424:ASP:HB2	2.50	0.52
1:D:359:ARG:HD3	1:D:541:TRP:HE1	1.75	0.52
1:E:486:LEU:HD12	1:E:493:ARG:CD	2.39	0.52
1:G:114:GLN:NE2	1:G:195:TYR:HD1	2.07	0.52
1:A:233:LEU:HD22	1:A:241:CYS:SG	2.50	0.52
1:B:352:ASP:OD2	1:B:363:ARG:NH1	2.43	0.52
1:B:439:ARG:O	1:B:442:ILE:CG2	2.57	0.52
1:B:440:LYS:HE2	1:B:440:LYS:C	2.30	0.52
1:C:322:VAL:HG21	1:C:463:ILE:CG1	2.40	0.52
1:D:164:THR:O	1:D:167:GLU:HB2	2.09	0.52
1:D:318:MET:SD	1:D:463:ILE:HD13	2.50	0.52
1:E:91:CYS:HB3	1:E:96:TYR:O	2.10	0.52
1:F:287:LEU:HD11	1:F:335:LYS:HG3	1.92	0.52
1:F:324:GLN:HE22	1:F:542:LEU:H	1.58	0.52
1:G:440:LYS:HE2	1:G:440:LYS:O	2.10	0.52
1:G:447:THR:CG2	1:G:495:LEU:HD21	2.27	0.52
1:A:321:PHE:CD2	1:A:533:MET:CE	2.93	0.52
1:B:304:GLY:HA2	1:B:459:VAL:HG22	1.92	0.52
1:B:305:GLY:O	1:B:454:LYS:HD2	2.10	0.52
1:B:311:THR:O	1:B:312:SER:HB3	2.10	0.52
1:C:321:PHE:CD2	1:C:533:MET:HE3	2.44	0.52
1:C:345:SER:O	1:C:349:THR:HG23	2.10	0.52
1:C:410:ALA:HA	1:C:452:PHE:CE1	2.45	0.52
1:C:504:ARG:HH21	1:C:506:GLN:HG2	1.73	0.52
1:E:140:ALA:O	1:E:141:LEU:HD23	2.10	0.52
1:E:234:PRO:CG	1:E:249:GLU:HG2	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:288:LEU:HD12	1:G:288:LEU:N	2.25	0.52
1:G:536:ASN:HD22	1:G:538:GLU:H	1.56	0.52
1:A:324:GLN:HE22	1:A:542:LEU:H	1.58	0.52
1:A:345:SER:O	1:A:349:THR:CG2	2.58	0.52
1:A:413:ARG:HH21	1:A:458:VAL:N	2.08	0.52
1:B:488:GLY:HA3	1:B:492:LEU:CD1	2.38	0.52
1:B:499:ILE:CG2	1:B:519:LEU:CB	2.87	0.52
1:B:536:ASN:HD21	1:B:538:GLU:CB	2.22	0.52
1:C:126:LYS:HG2	1:C:127:ASP:H	1.73	0.52
1:C:229:ARG:HB3	1:C:259:PRO:HA	1.91	0.52
1:C:276:ARG:HG2	1:C:276:ARG:HH11	1.75	0.52
1:C:359:ARG:HD3	1:C:541:TRP:NE1	2.25	0.52
1:D:322:VAL:CG1	1:D:422:ILE:HG21	2.40	0.52
1:F:378:PHE:CD2	1:G:276:ARG:HD3	2.40	0.52
1:F:413:ARG:NE	1:F:458:VAL:HB	2.24	0.52
1:F:517:ARG:HB3	1:F:519:LEU:HD13	1.92	0.52
1:G:372:ILE:HG13	1:G:378:PHE:HB2	1.91	0.52
1:G:496:SER:O	1:G:520:LYS:HE2	2.09	0.52
1:A:338:GLY:HA3	1:A:412:MET:HE3	1.92	0.51
1:A:471:LYS:HB3	1:A:479:ARG:NH1	2.24	0.51
1:B:324:GLN:HE22	1:B:542:LEU:H	1.56	0.51
1:C:446:MET:O	1:C:449:LEU:HB2	2.10	0.51
1:F:378:PHE:CD2	1:G:276:ARG:HD2	2.44	0.51
1:F:394:TYR:HE1	1:F:396:SER:CB	2.21	0.51
1:G:106:TYR:HB3	1:G:123:VAL:HG12	1.92	0.51
1:G:154:VAL:HG21	1:G:254:VAL:HG22	1.91	0.51
1:A:406:LEU:HD21	1:A:449:LEU:HD23	1.93	0.51
1:B:394:TYR:CD1	1:B:394:TYR:C	2.83	0.51
1:B:486:LEU:HD12	1:B:493:ARG:CD	2.40	0.51
1:B:496:SER:O	1:B:520:LYS:HE2	2.10	0.51
1:C:125:ASP:OD1	1:C:129:ASN:HB2	2.10	0.51
1:C:227:LYS:O	1:C:229:ARG:HD2	2.10	0.51
1:C:510:MET:HB2	1:C:513:LEU:CB	2.39	0.51
1:E:148:ASN:HD22	1:E:198:GLN:HE22	1.58	0.51
1:E:289:PHE:H	1:E:296:ASN:ND2	1.96	0.51
1:E:322:VAL:HG21	1:E:463:ILE:CG1	2.40	0.51
1:F:232:VAL:O	1:F:232:VAL:HG12	2.09	0.51
1:F:322:VAL:HG21	1:F:463:ILE:HD11	1.92	0.51
1:F:484:THR:C	1:F:486:LEU:H	2.13	0.51
1:G:421:ILE:HB	1:G:460:LEU:HD12	1.92	0.51
1:A:220:ALA:HB3	1:A:261:ILE:CD1	2.23	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:471:LYS:HB3	1:A:479:ARG:HH11	1.75	0.51
1:B:440:LYS:CE	1:B:441:MET:HA	2.41	0.51
1:C:166:MET:HG2	1:C:175:VAL:CG2	2.41	0.51
1:C:504:ARG:HH21	1:C:506:GLN:CB	2.24	0.51
1:D:260:TRP:HB2	1:D:262:PRO:HD2	1.87	0.51
1:E:111:TYR:CZ	1:E:142:PHE:HB2	2.44	0.51
1:E:309:MET:HB3	1:E:499:ILE:CD1	2.40	0.51
1:F:162:MET:HG2	1:F:175:VAL:HB	1.92	0.51
1:F:362:LEU:HD12	1:F:362:LEU:O	2.11	0.51
1:F:401:GLU:HB3	1:F:404:ARG:HB3	1.92	0.51
1:F:429:VAL:HG23	1:F:430:VAL:H	1.75	0.51
1:F:482:SER:H	1:F:485:ASP:CB	2.20	0.51
1:G:180:HIS:HB2	1:G:184:ALA:HB3	1.92	0.51
1:G:195:TYR:O	1:G:198:GLN:HB2	2.09	0.51
1:G:504:ARG:HH21	1:G:506:GLN:HG2	1.74	0.51
1:A:520:LYS:HG3	1:A:521:CYS:N	2.24	0.51
1:C:387:GLY:HA2	1:D:269:LEU:HD11	1.91	0.51
1:C:428:ILE:H	1:C:428:ILE:HD12	1.75	0.51
1:D:369:LYS:CG	1:E:279:LEU:CD2	2.88	0.51
1:D:382:PHE:CE1	1:E:272:ARG:HA	2.45	0.51
1:D:517:ARG:HB3	1:D:519:LEU:HD13	1.92	0.51
1:E:533:MET:HB3	1:E:543:GLU:O	2.11	0.51
1:F:412:MET:CE	1:F:421:ILE:CD1	2.87	0.51
1:F:447:THR:CG2	1:F:495:LEU:HD21	2.25	0.51
1:G:309:MET:HB3	1:G:499:ILE:CD1	2.39	0.51
1:A:265:VAL:HG11	1:B:411:TYR:HE1	1.76	0.51
1:C:484:THR:C	1:C:486:LEU:N	2.64	0.51
1:D:336:LYS:HB3	1:D:418:CYS:HA	1.92	0.51
1:E:162:MET:SD	1:E:166:MET:HG3	2.50	0.51
1:E:402:THR:HG23	1:E:403:ASP:N	2.25	0.51
1:G:437:ASP:OD1	1:G:439:ARG:HB2	2.09	0.51
1:A:339:LEU:HB3	1:A:341:MET:HE2	1.84	0.51
1:B:106:TYR:HB3	1:B:123:VAL:HG12	1.93	0.51
1:B:401:GLU:HG2	1:B:402:THR:N	2.26	0.51
1:D:86:ILE:HG21	1:D:163:LEU:CD1	2.40	0.51
1:E:359:ARG:HD3	1:E:541:TRP:HE1	1.76	0.51
1:E:482:SER:N	1:E:485:ASP:HB2	2.19	0.51
1:G:78:TYR:CG	1:G:92:GLN:HG2	2.45	0.51
1:A:234:PRO:CG	1:A:249:GLU:HG2	2.40	0.51
1:A:346:VAL:HG13	1:C:271:LEU:CD2	2.40	0.51
1:A:414:SER:HB3	1:C:226:GLY:HA3	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:401:GLU:HG3	1:B:431:SER:O	2.10	0.51
1:C:164:THR:O	1:C:167:GLU:HB2	2.11	0.51
1:C:166:MET:HE3	1:C:171:CYS:HA	1.91	0.51
1:D:80:ALA:HB2	1:D:88:LYS:HB2	1.92	0.51
1:D:510:MET:HE2	1:D:547:TYR:CE1	2.44	0.51
1:F:402:THR:HG23	1:F:403:ASP:N	2.26	0.51
1:F:547:TYR:CD2	1:F:548:SER:N	2.79	0.51
1:G:306:GLU:HA	1:G:497:ASP:OD2	2.10	0.51
1:A:445:LEU:CD1	1:A:449:LEU:HG	2.41	0.51
1:B:492:LEU:H	1:B:492:LEU:CD1	2.05	0.51
1:C:74:SER:HB3	1:C:101:VAL:HG22	1.92	0.51
1:C:235:CYS:CB	1:C:240:GLU:HG2	2.40	0.51
1:C:286:GLY:O	1:C:302:ALA:N	2.44	0.51
1:C:411:TYR:OH	1:D:260:TRP:CA	2.59	0.51
1:C:486:LEU:HD22	1:C:487:ARG:H	1.76	0.51
1:D:166:MET:HE3	1:D:171:CYS:HA	1.93	0.51
1:E:421:ILE:HB	1:E:460:LEU:HD12	1.92	0.51
1:F:306:GLU:HA	1:F:497:ASP:OD2	2.11	0.51
1:F:313:GLY:O	1:F:315:GLY:N	2.44	0.51
1:G:91:CYS:HB3	1:G:96:TYR:O	2.11	0.51
1:G:402:THR:HG23	1:G:403:ASP:N	2.26	0.51
1:A:346:VAL:HG22	1:C:271:LEU:HD21	1.91	0.51
1:B:107:GLN:CB	1:B:124:ARG:CG	2.84	0.51
1:C:91:CYS:HB3	1:C:96:TYR:O	2.11	0.51
1:C:411:TYR:OH	1:D:260:TRP:HB3	2.11	0.51
1:E:107:GLN:CB	1:E:124:ARG:CG	2.87	0.51
1:F:339:LEU:HB3	1:F:341:MET:HE3	1.87	0.51
1:G:126:LYS:HG2	1:G:127:ASP:H	1.76	0.51
1:B:450:LYS:NZ	1:B:454:LYS:HD3	2.25	0.51
1:D:112:ARG:HD3	1:D:116:GLY:O	2.11	0.51
1:D:122:LYS:HE2	1:D:159:GLU:OE1	2.11	0.51
1:D:165:VAL:HB	1:D:175:VAL:HG11	1.91	0.51
1:D:251:MET:HA	1:D:251:MET:HE2	1.93	0.51
1:D:268:ALA:HA	1:D:271:LEU:HD12	1.91	0.51
1:D:394:TYR:HE1	1:D:396:SER:CB	2.22	0.51
1:E:446:MET:HE3	1:E:492:LEU:HA	1.93	0.51
1:F:424:ASP:O	1:F:425:HIS:HB3	2.10	0.51
1:G:165:VAL:HB	1:G:175:VAL:HG11	1.92	0.51
1:G:276:ARG:NH1	1:G:276:ARG:CG	2.48	0.51
1:G:321:PHE:CD2	1:G:533:MET:HE1	2.46	0.51
1:G:351:GLU:HB2	1:G:363:ARG:HD2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:413:ARG:NE	1:G:458:VAL:HB	2.24	0.51
1:B:208:MET:HE1	1:B:232:VAL:CA	2.22	0.50
1:B:233:LEU:HD22	1:B:241:CYS:SG	2.51	0.50
1:C:463:ILE:CG2	1:C:464:CYS:N	2.74	0.50
1:C:536:ASN:ND2	1:C:538:GLU:HB2	2.26	0.50
1:D:401:GLU:HB3	1:D:404:ARG:HB3	1.92	0.50
1:D:478:GLY:CA	1:D:505:ASN:HB2	2.40	0.50
1:E:125:ASP:OD1	1:E:129:ASN:HB2	2.11	0.50
1:E:379:ASP:OD1	1:F:276:ARG:NH2	2.42	0.50
1:F:180:HIS:HB2	1:F:184:ALA:HB3	1.93	0.50
1:F:304:GLY:HA2	1:F:459:VAL:HG22	1.92	0.50
1:F:389:ASP:CA	1:G:269:LEU:CD2	2.87	0.50
1:A:286:GLY:O	1:A:302:ALA:N	2.44	0.50
1:B:279:LEU:HD23	1:G:369:LYS:HG2	1.94	0.50
1:C:330:GLY:HA2	1:C:335:LYS:O	2.12	0.50
1:C:536:ASN:C	1:C:538:GLU:H	2.13	0.50
1:D:425:HIS:CE1	1:D:427:SER:OG	2.64	0.50
1:D:473:LYS:CE	1:D:479:ARG:HA	2.39	0.50
1:E:392:HIS:CE1	1:F:267:SER:HB2	2.45	0.50
1:F:168:LEU:HD11	1:F:250:ILE:HD12	1.92	0.50
1:F:205:MET:HG3	1:F:231:ALA:CB	2.41	0.50
1:F:322:VAL:HG21	1:F:463:ILE:CG1	2.42	0.50
1:G:321:PHE:CD2	1:G:533:MET:CE	2.94	0.50
1:G:425:HIS:CE1	1:G:427:SER:CB	2.94	0.50
1:A:326:ALA:HB2	1:A:422:ILE:HD12	1.92	0.50
1:B:166:MET:HE3	1:B:171:CYS:HA	1.94	0.50
1:B:402:THR:HG23	1:B:403:ASP:N	2.26	0.50
1:B:482:SER:N	1:B:485:ASP:HB2	2.22	0.50
1:C:168:LEU:HD11	1:C:250:ILE:HD12	1.92	0.50
1:C:401:GLU:N	1:C:404:ARG:HD2	2.26	0.50
1:D:168:LEU:HD11	1:D:250:ILE:HD12	1.93	0.50
1:D:412:MET:CE	1:D:421:ILE:CD1	2.86	0.50
1:D:463:ILE:CG2	1:D:464:CYS:N	2.74	0.50
1:D:482:SER:H	1:D:485:ASP:CB	2.23	0.50
1:E:311:THR:OG1	1:E:466:LEU:HD21	2.11	0.50
1:F:521:CYS:O	1:F:525:GLY:N	2.38	0.50
1:G:80:ALA:HB2	1:G:88:LYS:HB2	1.93	0.50
1:G:220:ALA:HB2	1:G:261:ILE:HD13	1.94	0.50
1:G:322:VAL:HG21	1:G:463:ILE:CG1	2.41	0.50
1:A:318:MET:SD	1:A:463:ILE:HG23	2.52	0.50
1:B:80:ALA:HB2	1:B:88:LYS:HB2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:112:ARG:HD2	1:B:145:HIS:CE1	2.46	0.50
1:B:427:SER:CB	1:B:487:ARG:NH1	2.74	0.50
1:C:443:ASP:HA	1:C:491:ALA:CB	2.42	0.50
1:E:180:HIS:HB2	1:E:184:ALA:HB3	1.93	0.50
1:F:387:GLY:HA2	1:G:269:LEU:HD11	1.92	0.50
1:F:439:ARG:O	1:F:442:ILE:CG2	2.59	0.50
1:F:487:ARG:O	1:F:493:ARG:HD3	2.11	0.50
1:G:148:ASN:HD22	1:G:198:GLN:HE22	1.58	0.50
1:G:502:LEU:N	1:G:502:LEU:HD12	2.27	0.50
1:G:504:ARG:HH21	1:G:506:GLN:CG	2.25	0.50
1:B:79:SER:H	1:B:98:ILE:CD1	2.23	0.50
1:D:351:GLU:HB2	1:D:363:ARG:HD2	1.93	0.50
1:D:484:THR:O	1:D:486:LEU:N	2.45	0.50
1:E:74:SER:HB3	1:E:101:VAL:CG2	2.42	0.50
1:F:311:THR:O	1:F:502:LEU:HD12	2.11	0.50
1:F:473:LYS:CE	1:F:479:ARG:HA	2.36	0.50
1:G:168:LEU:HD11	1:G:250:ILE:HD12	1.93	0.50
1:G:202:ILE:HD13	1:G:223:LEU:CD2	2.41	0.50
1:G:260:TRP:C	1:G:262:PRO:HD2	2.32	0.50
1:G:358:ASN:O	1:G:360:VAL:CG1	2.47	0.50
1:G:480:PRO:HA	1:G:503:GLU:OE2	2.11	0.50
1:A:186:LYS:CD	1:A:218:GLU:HG3	2.32	0.50
1:A:447:THR:HA	1:A:495:LEU:HD23	1.93	0.50
1:A:502:LEU:HD12	1:A:502:LEU:N	2.27	0.50
1:B:165:VAL:HB	1:B:175:VAL:HG11	1.94	0.50
1:C:413:ARG:HH21	1:C:457:GLY:C	2.14	0.50
1:D:261:ILE:H	1:D:262:PRO:HD3	1.75	0.50
1:D:445:LEU:CD1	1:D:449:LEU:HG	2.42	0.50
1:F:322:VAL:CG2	1:F:463:ILE:HD11	2.42	0.50
1:F:345:SER:O	1:F:349:THR:HG23	2.11	0.50
1:F:410:ALA:HA	1:F:452:PHE:CE1	2.47	0.50
1:G:410:ALA:HA	1:G:452:PHE:CE1	2.45	0.50
1:A:425:HIS:HE1	1:A:427:SER:OG	1.90	0.50
1:B:234:PRO:HG2	1:B:249:GLU:HG2	1.94	0.50
1:B:314:SER:O	1:B:315:GLY:C	2.49	0.50
1:C:114:GLN:NE2	1:C:195:TYR:HD1	2.10	0.50
1:D:343:GLU:OE1	1:D:343:GLU:HA	2.11	0.50
1:D:441:MET:CE	1:D:444:ASN:HB3	2.41	0.50
1:E:510:MET:HE3	1:E:547:TYR:CE1	2.43	0.50
1:F:473:LYS:HE2	1:F:479:ARG:CA	2.38	0.50
1:F:480:PRO:HA	1:F:503:GLU:OE2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:504:ARG:HH21	1:A:506:GLN:CB	2.23	0.50
1:C:162:MET:HG2	1:C:175:VAL:HB	1.92	0.50
1:E:81:LEU:HG	1:E:91:CYS:SG	2.52	0.50
1:E:112:ARG:HD2	1:E:145:HIS:CE1	2.47	0.50
1:F:316:MET:CE	1:F:535:TYR:CE2	2.94	0.50
1:F:441:MET:HE1	1:F:444:ASN:HB3	1.93	0.50
1:F:442:ILE:HD11	1:F:492:LEU:CD2	2.41	0.50
1:G:74:SER:HB3	1:G:101:VAL:CG2	2.42	0.50
1:G:86:ILE:HD12	1:G:163:LEU:HB3	1.93	0.50
1:B:502:LEU:N	1:B:502:LEU:HD12	2.27	0.50
1:C:336:LYS:HB3	1:C:418:CYS:HA	1.92	0.50
1:D:441:MET:HE1	1:D:445:LEU:N	2.27	0.50
1:D:450:LYS:O	1:D:453:ALA:HB3	2.12	0.50
1:F:168:LEU:HD22	1:F:247:ASP:OD2	2.12	0.50
1:F:443:ASP:HA	1:F:491:ALA:CB	2.41	0.50
1:B:227:LYS:O	1:B:229:ARG:HD2	2.11	0.49
1:C:515:LEU:HD21	1:C:529:ILE:HD12	1.93	0.49
1:D:114:GLN:NE2	1:D:195:TYR:HD1	2.10	0.49
1:D:480:PRO:HA	1:D:503:GLU:OE2	2.12	0.49
1:E:246:HIS:HB3	1:E:249:GLU:OE1	2.12	0.49
1:F:486:LEU:HD22	1:F:487:ARG:H	1.77	0.49
1:G:232:VAL:O	1:G:232:VAL:HG12	2.12	0.49
1:G:288:LEU:HD12	1:G:288:LEU:H	1.77	0.49
1:G:295:ILE:HD12	1:G:516:VAL:HG11	1.94	0.49
1:G:486:LEU:HD12	1:G:493:ARG:CD	2.42	0.49
1:A:321:PHE:CD2	1:A:533:MET:HE3	2.48	0.49
1:A:536:ASN:ND2	1:A:538:GLU:CB	2.75	0.49
1:B:122:LYS:HE3	1:B:130:PHE:CE2	2.47	0.49
1:B:510:MET:HE2	1:B:547:TYR:CE1	2.47	0.49
1:D:286:GLY:O	1:D:302:ALA:N	2.45	0.49
1:D:499:ILE:HG22	1:D:519:LEU:CB	2.31	0.49
1:E:235:CYS:CB	1:E:240:GLU:HG2	2.41	0.49
1:F:401:GLU:HG2	1:F:402:THR:N	2.26	0.49
1:G:344:GLU:HB2	1:G:348:GLU:OE2	2.11	0.49
1:G:413:ARG:HH21	1:G:458:VAL:N	2.10	0.49
1:G:510:MET:CB	1:G:513:LEU:HB2	2.42	0.49
1:A:515:LEU:HD21	1:A:529:ILE:HD11	1.94	0.49
1:B:234:PRO:CG	1:B:249:GLU:HG2	2.42	0.49
1:C:304:GLY:HA2	1:C:459:VAL:HG22	1.94	0.49
1:C:412:MET:CE	1:C:421:ILE:CD1	2.81	0.49
1:D:78:TYR:CG	1:D:92:GLN:HG2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:79:SER:H	1:D:98:ILE:CD1	2.24	0.49
1:D:482:SER:N	1:D:485:ASP:HB2	2.22	0.49
1:E:122:LYS:HE3	1:E:130:PHE:CE2	2.47	0.49
1:E:166:MET:HG2	1:E:175:VAL:CG2	2.41	0.49
1:E:389:ASP:CA	1:F:269:LEU:HD23	2.43	0.49
1:E:392:HIS:ND1	1:F:267:SER:HB3	2.27	0.49
1:F:330:GLY:HA2	1:F:335:LYS:O	2.12	0.49
1:F:440:LYS:HE2	1:F:440:LYS:C	2.32	0.49
1:G:480:PRO:HA	1:G:503:GLU:OE1	2.12	0.49
1:G:492:LEU:C	1:G:494:GLN:N	2.66	0.49
1:A:112:ARG:HD3	1:A:116:GLY:O	2.12	0.49
1:C:259:PRO:O	1:C:260:TRP:CB	2.60	0.49
1:D:397:PHE:CD1	1:D:397:PHE:C	2.86	0.49
1:E:86:ILE:HD12	1:E:163:LEU:HB3	1.94	0.49
1:E:258:GLY:CA	1:E:260:TRP:HZ3	2.23	0.49
1:E:316:MET:HE3	1:E:535:TYR:CE2	2.47	0.49
1:A:272:ARG:HA	1:B:382:PHE:CE1	2.48	0.49
1:A:346:VAL:HG23	1:A:393:LEU:HB2	1.94	0.49
1:A:492:LEU:C	1:A:494:GLN:N	2.65	0.49
1:B:445:LEU:CD1	1:B:449:LEU:HG	2.42	0.49
1:C:165:VAL:HB	1:C:175:VAL:HG11	1.93	0.49
1:C:205:MET:HG3	1:C:231:ALA:CB	2.42	0.49
1:C:372:ILE:HG13	1:C:378:PHE:HB2	1.94	0.49
1:C:487:ARG:O	1:C:493:ARG:HD3	2.13	0.49
1:E:112:ARG:HD3	1:E:116:GLY:O	2.12	0.49
1:F:344:GLU:HB2	1:F:348:GLU:OE2	2.13	0.49
1:F:510:MET:HE2	1:F:513:LEU:HD22	1.93	0.49
1:G:345:SER:O	1:G:349:THR:HG23	2.13	0.49
1:G:397:PHE:CD1	1:G:397:PHE:C	2.86	0.49
1:A:330:GLY:HA2	1:A:335:LYS:O	2.13	0.49
1:A:358:ASN:ND2	1:A:381:TRP:CE2	2.81	0.49
1:A:512:ASN:HD21	1:A:537:LYS:HE3	1.77	0.49
1:B:74:SER:HB3	1:B:101:VAL:CG2	2.42	0.49
1:C:413:ARG:NE	1:C:458:VAL:HB	2.24	0.49
1:D:205:MET:HG3	1:D:231:ALA:HB1	1.94	0.49
1:D:536:ASN:HD21	1:D:538:GLU:HB2	1.77	0.49
1:F:318:MET:SD	1:F:463:ILE:HG23	2.52	0.49
1:F:425:HIS:CD2	1:F:465:HIS:CE1	3.01	0.49
1:A:369:LYS:CG	1:C:279:LEU:HD22	2.41	0.49
1:A:372:ILE:HG13	1:A:378:PHE:HB2	1.95	0.49
1:A:397:PHE:CD1	1:A:397:PHE:C	2.86	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:167:GLU:C	1:B:169:GLN:H	2.15	0.49
1:B:322:VAL:HG21	1:B:463:ILE:CD1	2.43	0.49
1:B:504:ARG:HH21	1:B:506:GLN:HG2	1.77	0.49
1:C:260:TRP:N	1:C:260:TRP:HE3	2.10	0.49
1:D:425:HIS:CE1	1:D:427:SER:HB2	2.48	0.49
1:A:312:SER:O	1:A:313:GLY:O	2.31	0.49
1:C:536:ASN:OD1	1:C:539:THR:HG23	2.12	0.49
1:D:235:CYS:CB	1:D:240:GLU:HG2	2.43	0.49
1:D:401:GLU:CG	1:D:431:SER:O	2.44	0.49
1:E:439:ARG:O	1:E:442:ILE:CG2	2.61	0.49
1:A:440:LYS:HE2	1:A:440:LYS:O	2.13	0.49
1:B:202:ILE:HD13	1:B:223:LEU:CD2	2.42	0.49
1:B:322:VAL:CG1	1:B:422:ILE:HG21	2.43	0.49
1:B:437:ASP:OD1	1:B:439:ARG:HB2	2.13	0.49
1:C:112:ARG:HD3	1:C:116:GLY:O	2.12	0.49
1:C:382:PHE:C	1:C:382:PHE:CD2	2.86	0.49
1:D:360:VAL:O	1:D:360:VAL:CG2	2.59	0.49
1:E:80:ALA:HB2	1:E:88:LYS:HB2	1.93	0.49
1:E:168:LEU:HD11	1:E:250:ILE:HD12	1.94	0.49
1:E:389:ASP:HA	1:F:269:LEU:CD2	2.43	0.49
1:F:438:GLU:O	1:F:442:ILE:HG22	2.12	0.49
1:G:316:MET:CE	1:G:535:TYR:CE2	2.96	0.49
1:G:427:SER:HB3	1:G:487:ARG:NH1	2.25	0.49
1:G:473:LYS:CE	1:G:479:ARG:HA	2.42	0.49
1:B:279:LEU:CD2	1:G:369:LYS:HG2	2.42	0.49
1:C:412:MET:CE	1:C:421:ILE:HD13	2.42	0.49
1:C:440:LYS:CE	1:C:441:MET:HA	2.43	0.49
1:D:229:ARG:HB2	1:D:258:GLY:O	2.13	0.49
1:D:271:LEU:O	1:D:272:ARG:C	2.51	0.49
1:E:441:MET:HE1	1:E:445:LEU:N	2.28	0.49
1:E:452:PHE:O	1:E:456:THR:HG23	2.12	0.49
1:F:392:HIS:ND1	1:G:267:SER:CB	2.75	0.49
1:G:229:ARG:HH21	1:G:259:PRO:HG3	1.78	0.49
1:A:346:VAL:HG22	1:C:271:LEU:CD2	2.42	0.48
1:B:401:GLU:CG	1:B:402:THR:N	2.75	0.48
1:C:510:MET:HE2	1:C:513:LEU:HD22	1.94	0.48
1:E:234:PRO:HG2	1:E:249:GLU:HG2	1.95	0.48
1:E:397:PHE:CD1	1:E:397:PHE:C	2.87	0.48
1:F:140:ALA:O	1:F:141:LEU:HD23	2.12	0.48
1:F:443:ASP:HA	1:F:491:ALA:HB3	1.95	0.48
1:B:228:VAL:CB	1:B:261:ILE:HD11	2.36	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:401:GLU:HB3	1:B:404:ARG:HB3	1.94	0.48
1:B:405:LEU:HG	1:B:409:LEU:CD1	2.42	0.48
1:C:482:SER:N	1:C:485:ASP:HB2	2.22	0.48
1:D:167:GLU:C	1:D:169:GLN:H	2.13	0.48
1:D:486:LEU:HD12	1:D:493:ARG:CG	2.43	0.48
1:D:496:SER:CB	1:D:499:ILE:HD11	2.43	0.48
1:E:204:LEU:HD23	1:E:204:LEU:N	2.27	0.48
1:E:326:ALA:HB2	1:E:422:ILE:HD12	1.95	0.48
1:E:370:ARG:CD	1:E:370:ARG:C	2.81	0.48
1:F:220:ALA:HB3	1:F:261:ILE:HG12	1.92	0.48
1:G:168:LEU:HD22	1:G:247:ASP:OD2	2.13	0.48
1:A:185:ALA:O	1:A:189:CYS:HB2	2.12	0.48
1:A:469:PRO:O	1:A:470:ASP:CB	2.54	0.48
1:B:510:MET:HE2	1:B:547:TYR:HE1	1.74	0.48
1:C:262:PRO:HB2	1:C:265:VAL:HG12	1.94	0.48
1:C:345:SER:O	1:C:349:THR:HG22	2.13	0.48
1:C:531:GLY:C	1:C:532:TYR:HD1	2.16	0.48
1:D:230:VAL:HB	1:D:260:TRP:CE2	2.48	0.48
1:D:438:GLU:O	1:D:442:ILE:HG22	2.13	0.48
1:D:439:ARG:O	1:D:442:ILE:CG2	2.60	0.48
1:D:492:LEU:C	1:D:494:GLN:N	2.66	0.48
1:D:510:MET:HE2	1:D:547:TYR:HE1	1.67	0.48
1:E:439:ARG:HG2	1:E:489:SER:OG	2.13	0.48
1:E:454:LYS:HE3	1:E:522:ARG:HH22	1.78	0.48
1:F:153:ILE:HG13	1:F:174:PRO:CB	2.43	0.48
1:G:267:SER:O	1:G:271:LEU:HD12	2.14	0.48
1:G:359:ARG:HD3	1:G:541:TRP:NE1	2.28	0.48
1:G:443:ASP:HA	1:G:491:ALA:CB	2.42	0.48
1:A:279:LEU:CD2	1:B:369:LYS:HG2	2.43	0.48
1:B:536:ASN:HD21	1:B:538:GLU:HB3	1.78	0.48
1:C:229:ARG:NH2	1:C:259:PRO:HG3	2.27	0.48
1:A:121:GLN:HB2	1:A:133:THR:HG1	1.77	0.48
1:A:255:TRP:O	1:A:256:ASN:OD1	2.31	0.48
1:A:484:THR:C	1:A:486:LEU:N	2.66	0.48
1:B:289:PHE:HA	1:B:325:GLN:HE21	1.77	0.48
1:D:185:ALA:O	1:D:189:CYS:HB2	2.13	0.48
1:D:447:THR:HA	1:D:495:LEU:CD2	2.42	0.48
1:E:253:GLN:CA	1:E:257:ALA:HB2	2.25	0.48
1:E:294:GLY:O	1:E:295:ILE:C	2.49	0.48
1:F:405:LEU:HG	1:F:409:LEU:CD1	2.41	0.48
1:F:441:MET:HE1	1:F:445:LEU:N	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:162:MET:HG2	1:G:175:VAL:HB	1.96	0.48
1:G:235:CYS:CB	1:G:240:GLU:HG2	2.43	0.48
1:G:402:THR:HG23	1:G:403:ASP:H	1.79	0.48
1:A:122:LYS:HE3	1:A:130:PHE:CE2	2.48	0.48
1:A:126:LYS:HZ2	1:A:127:ASP:CB	2.22	0.48
1:A:216:VAL:CG1	1:A:230:VAL:CG2	2.90	0.48
1:B:309:MET:CE	1:B:462:VAL:HG12	2.44	0.48
1:D:106:TYR:HB3	1:D:123:VAL:HG12	1.95	0.48
1:D:312:SER:O	1:D:313:GLY:O	2.30	0.48
1:E:492:LEU:C	1:E:494:GLN:N	2.65	0.48
1:F:289:PHE:HA	1:F:325:GLN:HE21	1.78	0.48
1:F:351:GLU:OE1	1:G:278:HIS:CD2	2.66	0.48
1:G:330:GLY:HA2	1:G:335:LYS:O	2.14	0.48
1:G:394:TYR:CE2	1:G:405:LEU:HD12	2.49	0.48
1:G:499:ILE:HG22	1:G:519:LEU:CB	2.31	0.48
1:A:267:SER:O	1:A:270:SER:OG	2.27	0.48
1:A:268:ALA:HA	1:A:271:LEU:HD12	1.94	0.48
1:A:510:MET:CB	1:A:513:LEU:HB2	2.43	0.48
1:C:358:ASN:C	1:C:359:ARG:HG2	2.32	0.48
1:C:360:VAL:HG23	1:C:360:VAL:O	2.13	0.48
1:D:404:ARG:O	1:D:408:LYS:HG2	2.14	0.48
1:E:121:GLN:HB2	1:E:133:THR:HG1	1.77	0.48
1:E:443:ASP:HA	1:E:491:ALA:CB	2.44	0.48
1:F:114:GLN:HG3	1:F:144:LYS:HE2	1.96	0.48
1:G:246:HIS:HB3	1:G:249:GLU:OE1	2.14	0.48
1:G:419:ASP:OD2	1:G:419:ASP:N	2.47	0.48
1:A:149:GLY:O	1:A:199:PHE:CE2	2.67	0.48
1:A:427:SER:CB	1:A:487:ARG:HH12	2.21	0.48
1:A:438:GLU:O	1:A:442:ILE:HG22	2.12	0.48
1:B:81:LEU:HG	1:B:91:CYS:SG	2.53	0.48
1:B:86:ILE:HD12	1:B:163:LEU:HB3	1.96	0.48
1:C:368:LEU:CD2	1:C:372:ILE:HG23	2.43	0.48
1:D:121:GLN:HB2	1:D:133:THR:HG1	1.79	0.48
1:D:202:ILE:HD13	1:D:223:LEU:CD2	2.44	0.48
1:D:230:VAL:HG12	1:D:260:TRP:CZ2	2.49	0.48
1:D:338:GLY:CA	1:D:412:MET:CE	2.90	0.48
1:G:164:THR:O	1:G:167:GLU:HB2	2.14	0.48
1:G:521:CYS:O	1:G:525:GLY:N	2.38	0.48
1:B:145:HIS:CE1	1:B:146:LEU:HD23	2.49	0.48
1:C:168:LEU:HD22	1:C:247:ASP:OD2	2.11	0.48
1:C:234:PRO:CG	1:C:249:GLU:HG2	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:353:LEU:HD23	1:C:353:LEU:HA	1.72	0.48
1:C:359:ARG:HD3	1:C:541:TRP:HE1	1.79	0.48
1:C:480:PRO:HA	1:C:503:GLU:OE2	2.14	0.48
1:D:420:VAL:HG22	1:D:459:VAL:HB	1.96	0.48
1:E:336:LYS:HB3	1:E:418:CYS:HA	1.95	0.48
1:F:446:MET:O	1:F:449:LEU:HB2	2.14	0.48
1:G:445:LEU:CD1	1:G:449:LEU:HG	2.43	0.48
1:A:303:ARG:CZ	1:A:523:PHE:CD1	2.97	0.48
1:A:517:ARG:HB3	1:A:519:LEU:HD13	1.95	0.48
1:B:162:MET:HG2	1:B:175:VAL:HB	1.93	0.48
1:C:446:MET:CE	1:C:492:LEU:HA	2.40	0.48
1:C:479:ARG:HA	1:C:480:PRO:HD3	1.76	0.48
1:C:510:MET:HB2	1:C:513:LEU:HB2	1.95	0.48
1:E:291:GLY:O	1:E:292:CYS:HB2	2.13	0.48
1:F:492:LEU:C	1:F:494:GLN:N	2.67	0.48
1:G:452:PHE:O	1:G:456:THR:HG23	2.14	0.48
1:G:536:ASN:HD22	1:G:536:ASN:C	2.17	0.48
1:A:114:GLN:NE2	1:A:195:TYR:HD1	2.11	0.47
1:A:322:VAL:CG1	1:A:422:ILE:HG21	2.43	0.47
1:B:306:GLU:HA	1:B:497:ASP:OD2	2.13	0.47
1:B:327:LEU:HD11	1:B:357:HIS:HA	1.96	0.47
1:B:344:GLU:HB2	1:B:348:GLU:OE2	2.14	0.47
1:C:452:PHE:O	1:C:456:THR:HG23	2.14	0.47
1:D:492:LEU:H	1:D:492:LEU:CD1	2.06	0.47
1:E:300:LEU:HB3	1:E:303:ARG:HH12	1.79	0.47
1:E:504:ARG:HH21	1:E:506:GLN:CG	2.26	0.47
1:F:166:MET:HG2	1:F:175:VAL:HG23	1.94	0.47
1:G:162:MET:SD	1:G:166:MET:HG3	2.54	0.47
1:G:345:SER:O	1:G:349:THR:CG2	2.62	0.47
1:G:394:TYR:HE1	1:G:396:SER:CB	2.27	0.47
1:G:512:ASN:HD21	1:G:537:LYS:HE3	1.78	0.47
1:A:467:LYS:H	1:A:467:LYS:HG3	1.53	0.47
1:B:125:ASP:OD1	1:B:129:ASN:HB2	2.14	0.47
1:B:288:LEU:HD12	1:B:288:LEU:H	1.79	0.47
1:B:478:GLY:O	1:B:479:ARG:C	2.51	0.47
1:C:248:ARG:O	1:C:248:ARG:HG2	2.14	0.47
1:C:486:LEU:HD13	1:C:487:ARG:O	2.14	0.47
1:D:86:ILE:HD12	1:D:163:LEU:HB3	1.96	0.47
1:D:154:VAL:HG21	1:D:254:VAL:HG22	1.96	0.47
1:D:411:TYR:HE1	1:E:265:VAL:HG11	1.78	0.47
1:E:344:GLU:HB2	1:E:348:GLU:OE2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:486:LEU:HD12	1:E:493:ARG:CG	2.44	0.47
1:F:77:ARG:HE	1:F:77:ARG:HB2	1.49	0.47
1:F:106:TYR:HB3	1:F:123:VAL:HG12	1.96	0.47
1:F:312:SER:O	1:F:313:GLY:O	2.32	0.47
1:F:486:LEU:HB3	1:F:493:ARG:CD	2.44	0.47
1:G:234:PRO:CG	1:G:249:GLU:HG2	2.44	0.47
1:A:111:TYR:CZ	1:A:142:PHE:HB2	2.48	0.47
1:A:180:HIS:CD2	1:A:180:HIS:N	2.81	0.47
1:B:148:ASN:HD22	1:B:198:GLN:HE22	1.62	0.47
1:B:402:THR:HG23	1:B:403:ASP:H	1.79	0.47
1:B:496:SER:HB2	1:B:499:ILE:HD11	1.96	0.47
1:C:148:ASN:HD22	1:C:198:GLN:HE22	1.61	0.47
1:D:397:PHE:C	1:D:397:PHE:HD1	2.17	0.47
1:D:419:ASP:OD2	1:D:419:ASP:N	2.47	0.47
1:E:106:TYR:HB3	1:E:123:VAL:HG12	1.95	0.47
1:E:480:PRO:HA	1:E:503:GLU:OE2	2.14	0.47
1:F:265:VAL:HG12	1:F:265:VAL:O	2.14	0.47
1:G:439:ARG:O	1:G:442:ILE:CG2	2.62	0.47
1:G:513:LEU:HD12	1:G:533:MET:O	2.15	0.47
1:G:533:MET:HB3	1:G:543:GLU:O	2.14	0.47
1:A:126:LYS:NZ	1:A:127:ASP:CB	2.76	0.47
1:A:140:ALA:O	1:A:141:LEU:HD23	2.15	0.47
1:A:336:LYS:HB3	1:A:418:CYS:HA	1.96	0.47
1:B:287:LEU:HD23	1:B:329:TRP:CE2	2.49	0.47
1:B:347:GLU:O	1:B:351:GLU:HG3	2.13	0.47
1:B:440:LYS:O	1:B:443:ASP:HB2	2.15	0.47
1:B:520:LYS:HG3	1:B:521:CYS:N	2.24	0.47
1:D:151:LYS:HG2	1:D:200:GLU:OE2	2.13	0.47
1:D:268:ALA:HA	1:D:271:LEU:HD13	1.95	0.47
1:E:78:TYR:CG	1:E:92:GLN:HG2	2.50	0.47
1:E:146:LEU:HB2	1:E:147:TRP:CE2	2.50	0.47
1:E:510:MET:HB3	1:E:513:LEU:HB2	1.96	0.47
1:F:428:ILE:HD12	1:F:428:ILE:H	1.80	0.47
1:F:445:LEU:HD12	1:F:445:LEU:O	2.13	0.47
1:G:353:LEU:HA	1:G:353:LEU:HD23	1.71	0.47
1:A:168:LEU:HB2	1:A:251:MET:HE1	1.97	0.47
1:A:442:ILE:HD11	1:A:492:LEU:CG	2.44	0.47
1:A:499:ILE:HG22	1:A:499:ILE:O	2.15	0.47
1:B:480:PRO:HA	1:B:503:GLU:OE2	2.15	0.47
1:D:344:GLU:HB2	1:D:348:GLU:OE2	2.14	0.47
1:F:401:GLU:CG	1:F:402:THR:N	2.77	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:492:LEU:HD12	1:F:492:LEU:N	2.21	0.47
1:G:112:ARG:HD3	1:G:116:GLY:O	2.14	0.47
1:G:220:ALA:HB1	1:G:261:ILE:CG2	2.37	0.47
1:G:484:THR:O	1:G:486:LEU:N	2.47	0.47
1:G:486:LEU:HD22	1:G:487:ARG:H	1.79	0.47
1:A:223:LEU:HD23	1:A:224:PRO:HD2	1.96	0.47
1:A:412:MET:CE	1:A:421:ILE:HD12	2.40	0.47
1:A:482:SER:O	1:A:485:ASP:CB	2.62	0.47
1:B:205:MET:HG3	1:B:231:ALA:HB1	1.95	0.47
1:B:283:GLU:CG	1:B:283:GLU:O	2.62	0.47
1:B:316:MET:HE1	1:B:535:TYR:OH	2.14	0.47
1:B:517:ARG:HB3	1:B:519:LEU:CD1	2.45	0.47
1:C:81:LEU:HG	1:C:91:CYS:SG	2.54	0.47
1:D:168:LEU:HD22	1:D:247:ASP:OD2	2.15	0.47
1:D:536:ASN:HD22	1:D:536:ASN:C	2.16	0.47
1:E:228:VAL:CG2	1:E:261:ILE:HD11	2.45	0.47
1:F:167:GLU:C	1:F:169:GLN:H	2.15	0.47
1:F:413:ARG:HH21	1:F:457:GLY:C	2.18	0.47
1:A:152:LYS:NZ	1:A:256:ASN:H	2.13	0.47
1:A:235:CYS:HB2	1:A:240:GLU:HG2	1.96	0.47
1:A:248:ARG:O	1:A:248:ARG:HG2	2.14	0.47
1:A:487:ARG:O	1:A:493:ARG:HD3	2.14	0.47
1:B:476:GLU:CD	1:B:476:GLU:H	2.18	0.47
1:B:492:LEU:C	1:B:494:GLN:N	2.68	0.47
1:C:153:ILE:O	1:C:153:ILE:HG23	2.14	0.47
1:C:202:ILE:HD13	1:C:223:LEU:CD2	2.44	0.47
1:C:419:ASP:OD2	1:C:419:ASP:N	2.47	0.47
1:C:499:ILE:CG2	1:C:519:LEU:CB	2.93	0.47
1:D:74:SER:HB3	1:D:101:VAL:CG2	2.45	0.47
1:D:233:LEU:HD22	1:D:241:CYS:SG	2.54	0.47
1:D:382:PHE:CZ	1:E:272:ARG:HB2	2.50	0.47
1:D:446:MET:HE2	1:D:492:LEU:HB3	1.96	0.47
1:D:510:MET:CE	1:D:513:LEU:HD22	2.44	0.47
1:E:260:TRP:O	1:E:261:ILE:CG1	2.63	0.47
1:E:315:GLY:HA2	1:E:317:VAL:CG2	2.39	0.47
1:E:324:GLN:HE22	1:E:542:LEU:H	1.63	0.47
1:F:163:LEU:N	1:F:163:LEU:HD23	2.30	0.47
1:F:273:GLU:OE2	1:F:276:ARG:NH1	2.48	0.47
1:F:368:LEU:HD22	1:F:368:LEU:C	2.35	0.47
1:F:463:ILE:CG2	1:F:464:CYS:N	2.78	0.47
1:G:125:ASP:OD1	1:G:129:ASN:HB2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:326:ALA:HB2	1:G:422:ILE:CD1	2.44	0.47
1:G:463:ILE:CG2	1:G:464:CYS:N	2.78	0.47
1:A:169:GLN:HE22	1:A:254:VAL:CG1	2.27	0.47
1:A:484:THR:C	1:A:486:LEU:H	2.18	0.47
1:B:78:TYR:CG	1:B:92:GLN:HG2	2.49	0.47
1:B:413:ARG:NE	1:B:458:VAL:HB	2.28	0.47
1:C:476:GLU:CD	1:C:476:GLU:N	2.68	0.47
1:D:536:ASN:ND2	1:D:538:GLU:HB2	2.30	0.47
1:E:223:LEU:CD2	1:E:224:PRO:HD2	2.42	0.47
1:F:164:THR:O	1:F:167:GLU:HB2	2.15	0.47
1:F:484:THR:C	1:F:486:LEU:N	2.67	0.47
1:F:486:LEU:HD12	1:F:493:ARG:HG2	1.97	0.47
1:A:273:GLU:OE2	1:A:276:ARG:NH1	2.47	0.47
1:A:397:PHE:C	1:A:397:PHE:HD1	2.18	0.47
1:A:542:LEU:HD12	1:A:542:LEU:HA	1.60	0.47
1:B:353:LEU:HD23	1:B:353:LEU:HA	1.69	0.47
1:C:194:GLU:CD	1:C:194:GLU:N	2.67	0.47
1:C:205:MET:HG3	1:C:231:ALA:HB1	1.97	0.47
1:C:486:LEU:HD12	1:C:493:ARG:CG	2.45	0.47
1:D:230:VAL:CB	1:D:260:TRP:NE1	2.78	0.47
1:F:166:MET:HG2	1:F:175:VAL:HG21	1.97	0.47
1:F:216:VAL:CG1	1:F:230:VAL:CG2	2.93	0.47
1:F:311:THR:OG1	1:F:466:LEU:HD21	2.15	0.47
1:F:322:VAL:HG11	1:F:422:ILE:HG21	1.97	0.47
1:G:493:ARG:H	1:G:493:ARG:HG2	1.47	0.47
1:A:322:VAL:HG21	1:A:463:ILE:CG1	2.44	0.47
1:A:440:LYS:CE	1:A:441:MET:HA	2.42	0.47
1:A:486:LEU:HD12	1:A:493:ARG:CD	2.45	0.47
1:B:145:HIS:CE1	1:B:146:LEU:CD2	2.97	0.47
1:B:168:LEU:HD11	1:B:250:ILE:HD12	1.96	0.47
1:B:220:ALA:HB1	1:B:261:ILE:CD1	2.41	0.47
1:C:288:LEU:HD12	1:C:288:LEU:H	1.77	0.47
1:C:339:LEU:CB	1:C:341:MET:HE1	2.42	0.47
1:C:369:LYS:HZ2	1:D:284:SER:H	1.62	0.47
1:D:283:GLU:OE2	1:D:286:GLY:CA	2.60	0.47
1:E:162:MET:HG2	1:E:175:VAL:HB	1.96	0.47
1:E:268:ALA:HA	1:E:271:LEU:HD13	1.96	0.47
1:E:372:ILE:HG13	1:E:378:PHE:HB2	1.95	0.47
1:F:151:LYS:HG2	1:F:200:GLU:OE2	2.14	0.47
1:F:292:CYS:HB3	1:F:295:ILE:CG1	2.45	0.47
1:F:441:MET:HE1	1:F:445:LEU:H	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:518:ILE:HD13	1:F:518:ILE:HA	1.79	0.47
1:G:81:LEU:HG	1:G:91:CYS:SG	2.54	0.47
1:A:246:HIS:HB3	1:A:249:GLU:OE1	2.14	0.46
1:A:288:LEU:HD12	1:A:288:LEU:H	1.80	0.46
1:C:78:TYR:CG	1:C:92:GLN:HG2	2.49	0.46
1:C:79:SER:H	1:C:98:ILE:CD1	2.28	0.46
1:D:314:SER:O	1:D:315:GLY:C	2.53	0.46
1:E:326:ALA:HB2	1:E:422:ILE:CD1	2.45	0.46
1:E:327:LEU:HA	1:E:327:LEU:HD23	1.44	0.46
1:E:369:LYS:HG2	1:F:279:LEU:HD22	1.97	0.46
1:F:124:ARG:HD3	1:F:125:ASP:CA	2.45	0.46
1:F:345:SER:O	1:F:349:THR:CG2	2.63	0.46
1:G:397:PHE:C	1:G:397:PHE:HD1	2.18	0.46
1:G:510:MET:HE2	1:G:547:TYR:CE1	2.50	0.46
1:A:126:LYS:NZ	1:A:127:ASP:CG	2.68	0.46
1:A:394:TYR:C	1:A:394:TYR:HD1	2.18	0.46
1:A:414:SER:CB	1:C:226:GLY:N	2.76	0.46
1:C:246:HIS:HB3	1:C:249:GLU:OE1	2.14	0.46
1:C:251:MET:CE	1:C:251:MET:CA	2.92	0.46
1:C:307:VAL:O	1:C:307:VAL:HG12	2.14	0.46
1:D:450:LYS:HA	1:D:450:LYS:HD2	1.69	0.46
1:E:344:GLU:CG	1:E:349:THR:HG22	2.40	0.46
1:F:312:SER:CB	1:F:502:LEU:O	2.54	0.46
1:F:353:LEU:HD23	1:F:353:LEU:HA	1.65	0.46
1:F:510:MET:HB3	1:F:513:LEU:HB2	1.97	0.46
1:G:253:GLN:O	1:G:257:ALA:HB2	2.16	0.46
1:G:322:VAL:HG21	1:G:463:ILE:CD1	2.43	0.46
1:G:496:SER:CB	1:G:499:ILE:HD11	2.45	0.46
1:A:486:LEU:HD13	1:A:487:ARG:O	2.15	0.46
1:B:114:GLN:HG3	1:B:144:LYS:HE2	1.97	0.46
1:B:267:SER:O	1:B:270:SER:OG	2.31	0.46
1:B:443:ASP:HA	1:B:491:ALA:HB3	1.97	0.46
1:C:86:ILE:HG21	1:C:163:LEU:CD1	2.45	0.46
1:C:166:MET:O	1:C:171:CYS:SG	2.69	0.46
1:E:168:LEU:HD22	1:E:247:ASP:OD2	2.12	0.46
1:E:413:ARG:HH21	1:E:458:VAL:N	2.13	0.46
1:F:205:MET:HG3	1:F:231:ALA:HB1	1.97	0.46
1:F:229:ARG:HB3	1:F:258:GLY:O	2.14	0.46
1:F:326:ALA:HB2	1:F:422:ILE:HD12	1.97	0.46
1:F:344:GLU:OE1	1:F:349:THR:HB	2.15	0.46
1:G:220:ALA:HB1	1:G:261:ILE:HD13	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:300:LEU:HB3	1:G:303:ARG:NH1	2.29	0.46
1:G:429:VAL:HG13	1:G:438:GLU:OE1	2.15	0.46
1:G:482:SER:H	1:G:485:ASP:CB	2.19	0.46
1:G:531:GLY:C	1:G:532:TYR:CD1	2.88	0.46
1:A:382:PHE:C	1:A:382:PHE:CD2	2.88	0.46
1:A:536:ASN:OD1	1:A:539:THR:HG23	2.15	0.46
1:C:513:LEU:HD12	1:C:533:MET:O	2.16	0.46
1:E:313:GLY:O	1:E:315:GLY:N	2.48	0.46
1:E:316:MET:O	1:E:319:SER:N	2.48	0.46
1:E:411:TYR:CD1	1:E:411:TYR:C	2.89	0.46
1:E:492:LEU:C	1:E:494:GLN:H	2.18	0.46
1:F:427:SER:HB3	1:F:487:ARG:NH1	2.29	0.46
1:G:136:HIS:CD2	1:G:180:HIS:CE1	3.03	0.46
1:G:304:GLY:HA2	1:G:459:VAL:HG22	1.96	0.46
1:A:160:ILE:O	1:A:163:LEU:HB2	2.16	0.46
1:B:394:TYR:HE1	1:B:396:SER:CB	2.26	0.46
1:E:295:ILE:HD12	1:E:516:VAL:HG11	1.98	0.46
1:E:353:LEU:HD23	1:E:353:LEU:HA	1.65	0.46
1:E:406:LEU:HD21	1:E:449:LEU:HD23	1.98	0.46
1:F:311:THR:O	1:F:312:SER:CB	2.59	0.46
1:F:486:LEU:HD13	1:F:487:ARG:O	2.15	0.46
1:F:512:ASN:HD21	1:F:537:LYS:HE3	1.79	0.46
1:G:404:ARG:O	1:G:408:LYS:HG2	2.16	0.46
1:A:241:CYS:HB2	1:A:250:ILE:HD11	1.97	0.46
1:A:322:VAL:HG21	1:A:463:ILE:CD1	2.46	0.46
1:B:300:LEU:O	1:B:300:LEU:CD1	2.64	0.46
1:C:412:MET:HE2	1:C:421:ILE:HD12	1.90	0.46
1:C:473:LYS:CD	1:C:479:ARG:HB2	2.46	0.46
1:D:162:MET:HG2	1:D:175:VAL:HB	1.98	0.46
1:D:205:MET:SD	1:D:238:ALA:HB2	2.56	0.46
1:D:401:GLU:N	1:D:404:ARG:HD2	2.31	0.46
1:F:79:SER:H	1:F:98:ILE:CD1	2.27	0.46
1:G:114:GLN:HG3	1:G:144:LYS:HE2	1.98	0.46
1:G:234:PRO:HG2	1:G:249:GLU:HG2	1.98	0.46
1:G:271:LEU:O	1:G:272:ARG:C	2.53	0.46
1:G:486:LEU:HD13	1:G:487:ARG:O	2.15	0.46
1:A:243:LEU:O	1:A:244:ASN:C	2.53	0.46
1:A:443:ASP:HA	1:A:491:ALA:HB3	1.97	0.46
1:D:125:ASP:OD1	1:D:129:ASN:HB2	2.15	0.46
1:D:276:ARG:HH11	1:D:276:ARG:CG	2.29	0.46
1:D:442:ILE:HD11	1:D:492:LEU:CG	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:142:PHE:CE2	1:E:162:MET:HE3	2.51	0.46
1:E:205:MET:HG3	1:E:231:ALA:HB1	1.97	0.46
1:E:322:VAL:CG1	1:E:422:ILE:HG21	2.45	0.46
1:E:402:THR:HG23	1:E:403:ASP:H	1.80	0.46
1:E:487:ARG:O	1:E:493:ARG:HD3	2.15	0.46
1:F:170:ASP:O	1:F:172:LYS:HG3	2.16	0.46
1:G:167:GLU:C	1:G:169:GLN:H	2.15	0.46
1:G:311:THR:O	1:G:502:LEU:HD12	2.16	0.46
1:G:327:LEU:HD23	1:G:327:LEU:HA	1.55	0.46
1:G:339:LEU:HD22	1:G:341:MET:HE1	1.97	0.46
1:A:152:LYS:O	1:A:174:PRO:HD2	2.16	0.46
1:A:154:VAL:HB	1:A:175:VAL:CG1	2.43	0.46
1:B:289:PHE:H	1:B:296:ASN:ND2	2.04	0.46
1:B:504:ARG:HH21	1:B:506:GLN:CG	2.29	0.46
1:C:327:LEU:HD11	1:C:357:HIS:HA	1.98	0.46
1:C:368:LEU:HD22	1:C:368:LEU:C	2.36	0.46
1:C:425:HIS:HE1	1:C:427:SER:CB	2.27	0.46
1:D:140:ALA:O	1:D:141:LEU:HD23	2.15	0.46
1:E:167:GLU:C	1:E:169:GLN:H	2.16	0.46
1:E:351:GLU:HB2	1:E:363:ARG:HD2	1.98	0.46
1:E:413:ARG:HH21	1:E:457:GLY:C	2.19	0.46
1:F:213:ARG:NE	1:F:213:ARG:HA	2.30	0.46
1:F:451:GLY:O	1:F:455:SER:HB3	2.16	0.46
1:F:467:LYS:H	1:F:467:LYS:HG3	1.50	0.46
1:G:205:MET:HG3	1:G:231:ALA:HB1	1.98	0.46
1:A:488:GLY:HA3	1:A:492:LEU:CD1	2.42	0.46
1:B:442:ILE:HD11	1:B:492:LEU:CD2	2.45	0.46
1:C:312:SER:O	1:C:313:GLY:O	2.34	0.46
1:D:283:GLU:CD	1:D:286:GLY:HA2	2.36	0.46
1:D:324:GLN:HE22	1:D:542:LEU:H	1.63	0.46
1:E:450:LYS:HD2	1:E:450:LYS:HA	1.68	0.46
1:F:80:ALA:HB2	1:F:88:LYS:HB2	1.97	0.46
1:F:223:LEU:CD2	1:F:224:PRO:HD2	2.46	0.46
1:F:351:GLU:HB2	1:F:363:ARG:HD2	1.98	0.46
1:G:228:VAL:HB	1:G:261:ILE:HD13	1.97	0.46
1:A:146:LEU:HB2	1:A:147:TRP:CE2	2.51	0.46
1:A:441:MET:HE2	1:A:444:ASN:HB3	1.97	0.46
1:B:510:MET:HB2	1:B:513:LEU:CB	2.46	0.46
1:C:241:CYS:HB2	1:C:250:ILE:HD11	1.98	0.46
1:D:391:PHE:C	1:D:392:HIS:CD2	2.89	0.46
1:D:446:MET:CE	1:D:492:LEU:HA	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:476:GLU:CD	1:D:476:GLU:N	2.70	0.46
1:F:194:GLU:CD	1:F:194:GLU:N	2.66	0.46
1:F:248:ARG:O	1:F:248:ARG:HG2	2.15	0.46
1:F:510:MET:CB	1:F:513:LEU:HB2	2.45	0.46
1:G:81:LEU:HD11	1:G:96:TYR:CD2	2.51	0.46
1:G:440:LYS:CE	1:G:441:MET:HA	2.43	0.46
1:G:446:MET:CE	1:G:492:LEU:HA	2.46	0.46
1:A:314:SER:O	1:A:315:GLY:C	2.54	0.45
1:A:360:VAL:HG23	1:A:360:VAL:O	2.16	0.45
1:B:401:GLU:CG	1:B:402:THR:H	2.29	0.45
1:B:406:LEU:HD21	1:B:449:LEU:HD23	1.97	0.45
1:B:451:GLY:O	1:B:452:PHE:C	2.54	0.45
1:C:80:ALA:HB2	1:C:88:LYS:HB2	1.98	0.45
1:C:180:HIS:HB2	1:C:184:ALA:HB3	1.98	0.45
1:C:223:LEU:CD2	1:C:224:PRO:HD2	2.46	0.45
1:C:476:GLU:HB3	1:C:506:GLN:OE1	2.16	0.45
1:D:216:VAL:CG1	1:D:230:VAL:HG22	2.45	0.45
1:D:471:LYS:HA	1:D:471:LYS:HD2	1.60	0.45
1:F:271:LEU:O	1:F:272:ARG:C	2.53	0.45
1:F:402:THR:HG23	1:F:403:ASP:H	1.81	0.45
1:B:517:ARG:CZ	1:B:529:ILE:HD11	2.46	0.45
1:C:234:PRO:HG2	1:C:249:GLU:HG2	1.98	0.45
1:C:454:LYS:HE3	1:C:522:ARG:HH22	1.82	0.45
1:D:148:ASN:HD22	1:D:198:GLN:HE22	1.63	0.45
1:F:327:LEU:HD23	1:F:327:LEU:HA	1.55	0.45
1:F:397:PHE:CD1	1:F:397:PHE:C	2.90	0.45
1:F:478:GLY:O	1:F:479:ARG:C	2.54	0.45
1:G:269:LEU:HA	1:G:269:LEU:HD13	1.48	0.45
1:A:153:ILE:HG23	1:A:153:ILE:O	2.16	0.45
1:A:193:TYR:CE1	1:A:224:PRO:HA	2.51	0.45
1:B:112:ARG:NH2	1:B:118:ILE:HD11	2.31	0.45
1:B:401:GLU:CG	1:B:431:SER:O	2.64	0.45
1:C:327:LEU:HA	1:C:327:LEU:HD23	1.59	0.45
1:C:402:THR:HG23	1:C:403:ASP:N	2.31	0.45
1:D:181:GLY:O	1:D:182:ALA:C	2.55	0.45
1:D:193:TYR:CE1	1:D:224:PRO:HA	2.52	0.45
1:D:346:VAL:HG13	1:E:271:LEU:CD2	2.47	0.45
1:D:427:SER:CB	1:D:487:ARG:HH12	2.22	0.45
1:D:443:ASP:HA	1:D:491:ALA:CB	2.47	0.45
1:F:124:ARG:HD3	1:F:125:ASP:N	2.31	0.45
1:G:181:GLY:O	1:G:182:ALA:C	2.54	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:506:GLN:H	1:G:506:GLN:HG3	1.56	0.45
1:G:517:ARG:HB3	1:G:519:LEU:HD13	1.96	0.45
1:A:439:ARG:O	1:A:442:ILE:CG2	2.62	0.45
1:A:450:LYS:HA	1:A:450:LYS:HD2	1.61	0.45
1:A:491:ALA:O	1:A:495:LEU:N	2.46	0.45
1:B:232:VAL:O	1:B:232:VAL:HG12	2.14	0.45
1:B:413:ARG:HH21	1:B:457:GLY:C	2.18	0.45
1:B:486:LEU:HD12	1:B:493:ARG:CG	2.47	0.45
1:C:397:PHE:C	1:C:397:PHE:CD1	2.89	0.45
1:C:532:TYR:N	1:C:532:TYR:HD1	2.14	0.45
1:D:267:SER:O	1:D:271:LEU:HD12	2.17	0.45
1:D:307:VAL:O	1:D:307:VAL:CG1	2.64	0.45
1:E:193:TYR:CE1	1:E:224:PRO:HA	2.52	0.45
1:E:314:SER:O	1:E:315:GLY:C	2.54	0.45
1:F:243:LEU:O	1:F:244:ASN:C	2.55	0.45
1:F:440:LYS:NZ	1:F:441:MET:CA	2.60	0.45
1:G:112:ARG:HD2	1:G:145:HIS:CE1	2.51	0.45
1:G:314:SER:O	1:G:315:GLY:C	2.55	0.45
1:A:168:LEU:HD12	1:A:251:MET:CE	2.46	0.45
1:A:359:ARG:HD3	1:A:541:TRP:HE1	1.80	0.45
1:A:441:MET:HE3	1:A:444:ASN:HB3	1.98	0.45
1:B:265:VAL:HG11	1:G:411:TYR:CE1	2.52	0.45
1:B:311:THR:OG1	1:B:466:LEU:HD21	2.16	0.45
1:B:492:LEU:HD12	1:B:492:LEU:N	2.16	0.45
1:C:124:ARG:HD3	1:C:125:ASP:N	2.32	0.45
1:C:167:GLU:C	1:C:169:GLN:H	2.17	0.45
1:C:496:SER:O	1:C:520:LYS:CE	2.63	0.45
1:D:502:LEU:N	1:D:502:LEU:HD12	2.31	0.45
1:D:536:ASN:OD1	1:D:539:THR:HG23	2.17	0.45
1:E:220:ALA:HB1	1:E:261:ILE:HG21	1.87	0.45
1:E:248:ARG:HG2	1:E:248:ARG:O	2.16	0.45
1:E:345:SER:O	1:E:349:THR:HG22	2.16	0.45
1:E:356:LEU:HD12	1:E:541:TRP:NE1	2.32	0.45
1:E:482:SER:CB	1:E:484:THR:HG23	2.46	0.45
1:F:267:SER:O	1:F:271:LEU:HD12	2.16	0.45
1:F:389:ASP:H	1:G:269:LEU:CD2	2.29	0.45
1:F:504:ARG:HH21	1:F:506:GLN:HG2	1.82	0.45
1:G:121:GLN:HB2	1:G:133:THR:HG1	1.81	0.45
1:G:122:LYS:HE3	1:G:130:PHE:CE2	2.52	0.45
1:A:289:PHE:HA	1:A:325:GLN:HE21	1.82	0.45
1:C:321:PHE:CD2	1:C:533:MET:CE	3.00	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:450:LYS:O	1:C:453:ALA:HB3	2.16	0.45
1:C:467:LYS:H	1:C:467:LYS:HG3	1.36	0.45
1:E:288:LEU:HD12	1:E:288:LEU:N	2.31	0.45
1:E:371:GLU:OE1	1:E:375:ASN:ND2	2.49	0.45
1:E:401:GLU:CB	1:E:431:SER:O	2.65	0.45
1:F:303:ARG:HB2	1:F:306:GLU:CD	2.37	0.45
1:F:515:LEU:HD21	1:F:529:ILE:HD12	1.95	0.45
1:G:261:ILE:N	1:G:262:PRO:HD2	2.30	0.45
1:A:267:SER:CB	1:B:392:HIS:ND1	2.80	0.45
1:A:483:ILE:O	1:A:486:LEU:CB	2.41	0.45
1:B:359:ARG:HD3	1:B:541:TRP:HE1	1.81	0.45
1:C:124:ARG:C	1:C:124:ARG:CD	2.84	0.45
1:C:294:GLY:O	1:C:296:ASN:N	2.49	0.45
1:C:473:LYS:HE2	1:C:479:ARG:CB	2.46	0.45
1:C:518:ILE:HD13	1:C:518:ILE:HA	1.76	0.45
1:D:142:PHE:CE2	1:D:162:MET:CE	2.99	0.45
1:D:246:HIS:HB3	1:D:249:GLU:OE1	2.17	0.45
1:D:410:ALA:HA	1:D:452:PHE:CE1	2.51	0.45
1:E:300:LEU:HB3	1:E:303:ARG:NH1	2.32	0.45
1:E:320:THR:HG22	1:E:324:GLN:HE21	1.82	0.45
1:E:344:GLU:OE1	1:E:349:THR:HB	2.16	0.45
1:F:112:ARG:HB3	1:F:117:ASN:C	2.34	0.45
1:G:248:ARG:HG2	1:G:248:ARG:O	2.15	0.45
1:G:324:GLN:NE2	1:G:542:LEU:H	2.14	0.45
1:G:486:LEU:HD12	1:G:493:ARG:CG	2.47	0.45
1:A:446:MET:HB3	1:A:491:ALA:HB1	1.99	0.45
1:B:450:LYS:HE3	1:B:454:LYS:CD	2.45	0.45
1:C:316:MET:CE	1:C:535:TYR:CE2	3.00	0.45
1:D:234:PRO:CG	1:D:249:GLU:HG2	2.47	0.45
1:D:321:PHE:CE2	1:D:533:MET:HE2	2.52	0.45
1:D:510:MET:HB2	1:D:513:LEU:HB3	1.98	0.45
1:D:531:GLY:C	1:D:532:TYR:CD1	2.90	0.45
1:E:229:ARG:HB3	1:E:259:PRO:CB	2.46	0.45
1:E:548:SER:HB3	1:E:549:GLY:H	1.61	0.45
1:F:251:MET:CE	1:F:251:MET:CA	2.92	0.45
1:F:276:ARG:HH11	1:F:276:ARG:CG	2.28	0.45
1:F:504:ARG:HH21	1:F:506:GLN:CG	2.30	0.45
1:A:413:ARG:O	1:A:413:ARG:HD2	2.17	0.45
1:A:492:LEU:HD12	1:A:492:LEU:N	2.21	0.45
1:B:510:MET:HE2	1:B:513:LEU:HD22	1.97	0.45
1:B:531:GLY:C	1:B:532:TYR:CD1	2.90	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:243:LEU:O	1:C:244:ASN:O	2.35	0.45
1:C:258:GLY:HA2	1:C:259:PRO:HD3	1.78	0.45
1:C:401:GLU:OE2	1:C:432:ALA:HB2	2.17	0.45
1:D:230:VAL:CG1	1:D:260:TRP:NE1	2.80	0.45
1:E:145:HIS:CE1	1:E:146:LEU:HD23	2.52	0.45
1:F:243:LEU:O	1:F:244:ASN:O	2.34	0.45
1:F:288:LEU:N	1:F:288:LEU:HD12	2.32	0.45
1:G:286:GLY:O	1:G:302:ALA:N	2.49	0.45
1:G:473:LYS:HE2	1:G:479:ARG:CA	2.46	0.45
1:A:292:CYS:HB3	1:A:295:ILE:CG1	2.47	0.45
1:A:450:LYS:HE2	1:A:454:LYS:CD	2.30	0.45
1:A:479:ARG:HA	1:A:480:PRO:HD3	1.85	0.45
1:B:312:SER:N	1:B:318:MET:HE2	2.32	0.45
1:B:368:LEU:HD22	1:B:368:LEU:C	2.38	0.45
1:C:114:GLN:HG3	1:C:144:LYS:HE2	1.99	0.45
1:C:364:GLN:HG3	1:D:523:PHE:CZ	2.52	0.45
1:D:166:MET:HG2	1:D:175:VAL:HG23	1.99	0.45
1:D:194:GLU:CD	1:D:194:GLU:N	2.64	0.45
1:D:493:ARG:H	1:D:493:ARG:HG2	1.40	0.45
1:E:447:THR:CG2	1:E:495:LEU:HD21	2.31	0.45
1:E:493:ARG:H	1:E:493:ARG:HG2	1.41	0.45
1:E:510:MET:HB2	1:E:513:LEU:HB3	1.98	0.45
1:E:542:LEU:HA	1:E:542:LEU:HD12	1.56	0.45
1:F:382:PHE:C	1:F:382:PHE:CD2	2.91	0.45
1:G:427:SER:CB	1:G:487:ARG:HH12	2.26	0.45
1:A:106:TYR:HB3	1:A:123:VAL:HG12	1.99	0.44
1:A:130:PHE:O	1:A:131:LYS:CG	2.64	0.44
1:A:412:MET:CE	1:A:421:ILE:HD13	2.44	0.44
1:A:441:MET:HE2	1:A:445:LEU:N	2.32	0.44
1:A:486:LEU:HD22	1:A:487:ARG:H	1.83	0.44
1:A:515:LEU:HD21	1:A:529:ILE:HD12	1.99	0.44
1:B:194:GLU:CD	1:B:194:GLU:N	2.70	0.44
1:B:510:MET:CB	1:B:513:LEU:HB2	2.46	0.44
1:C:346:VAL:HG23	1:C:393:LEU:HB2	1.99	0.44
1:C:504:ARG:HH21	1:C:506:GLN:CG	2.29	0.44
1:D:499:ILE:HG22	1:D:499:ILE:O	2.17	0.44
1:D:506:GLN:H	1:D:506:GLN:HG3	1.49	0.44
1:E:447:THR:O	1:E:448:LYS:C	2.56	0.44
1:F:425:HIS:HE1	1:F:427:SER:HB2	1.60	0.44
1:F:533:MET:HB3	1:F:543:GLU:O	2.17	0.44
1:F:536:ASN:ND2	1:F:538:GLU:CB	2.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:223:LEU:CD2	1:G:224:PRO:HD2	2.47	0.44
1:A:138:SER:HB3	1:A:187:LYS:HD3	1.99	0.44
1:B:496:SER:CB	1:B:499:ILE:HD11	2.47	0.44
1:C:427:SER:CB	1:C:487:ARG:HH12	2.30	0.44
1:D:303:ARG:CZ	1:D:523:PHE:CD1	3.00	0.44
1:D:496:SER:O	1:D:520:LYS:CE	2.65	0.44
1:E:185:ALA:O	1:E:189:CYS:HB2	2.17	0.44
1:E:276:ARG:CG	1:E:276:ARG:NH1	2.76	0.44
1:E:484:THR:O	1:E:486:LEU:N	2.50	0.44
1:F:235:CYS:CB	1:F:240:GLU:HG2	2.46	0.44
1:F:491:ALA:O	1:F:495:LEU:N	2.48	0.44
1:F:496:SER:O	1:F:520:LYS:CE	2.65	0.44
1:G:439:ARG:HG2	1:G:489:SER:OG	2.16	0.44
1:A:77:ARG:HE	1:A:77:ARG:HB2	1.60	0.44
1:A:320:THR:HG22	1:A:324:GLN:NE2	2.32	0.44
1:A:392:HIS:ND1	1:C:267:SER:HB2	2.32	0.44
1:C:482:SER:CB	1:C:484:THR:HG23	2.47	0.44
1:D:321:PHE:CD2	1:D:533:MET:HE2	2.52	0.44
1:D:401:GLU:HB2	1:D:404:ARG:NH2	2.32	0.44
1:E:260:TRP:C	1:E:261:ILE:HG13	2.37	0.44
1:F:74:SER:HB3	1:F:101:VAL:CG2	2.47	0.44
1:F:492:LEU:C	1:F:494:GLN:H	2.21	0.44
1:F:510:MET:HB2	1:F:513:LEU:HB3	1.98	0.44
1:F:516:VAL:HG23	1:F:531:GLY:O	2.17	0.44
1:G:443:ASP:HA	1:G:491:ALA:HB3	1.99	0.44
1:A:121:GLN:CB	1:A:133:THR:HG23	2.48	0.44
1:A:220:ALA:HB1	1:A:261:ILE:CG2	2.47	0.44
1:A:510:MET:HB2	1:A:513:LEU:CB	2.47	0.44
1:C:362:LEU:O	1:C:362:LEU:HD12	2.17	0.44
1:D:368:LEU:HD22	1:D:368:LEU:C	2.36	0.44
1:D:510:MET:CB	1:D:513:LEU:HB2	2.47	0.44
1:D:513:LEU:HD11	1:D:532:TYR:HB3	1.99	0.44
1:E:318:MET:HE3	1:E:465:HIS:CD2	2.52	0.44
1:F:106:TYR:N	1:F:106:TYR:CD1	2.85	0.44
1:F:107:GLN:H	1:F:124:ARG:HG3	1.82	0.44
1:F:234:PRO:CG	1:F:249:GLU:HG2	2.48	0.44
1:F:259:PRO:O	1:F:259:PRO:CG	2.64	0.44
1:F:404:ARG:O	1:F:408:LYS:HG2	2.16	0.44
1:F:532:TYR:N	1:F:532:TYR:CD1	2.85	0.44
1:A:440:LYS:HE2	1:A:440:LYS:C	2.38	0.44
1:B:136:HIS:CD2	1:B:180:HIS:CE1	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:493:ARG:H	1:B:493:ARG:HG2	1.43	0.44
1:B:510:MET:HB2	1:B:513:LEU:HB3	2.00	0.44
1:C:220:ALA:HB3	1:C:261:ILE:HG21	2.00	0.44
1:C:271:LEU:O	1:C:272:ARG:C	2.54	0.44
1:C:440:LYS:HZ2	1:C:441:MET:HA	1.70	0.44
1:D:78:TYR:O	1:D:88:LYS:HG3	2.17	0.44
1:E:408:LYS:O	1:E:412:MET:HG3	2.18	0.44
1:F:510:MET:HB2	1:F:513:LEU:CB	2.47	0.44
1:G:185:ALA:O	1:G:189:CYS:HB2	2.18	0.44
1:G:401:GLU:HB3	1:G:404:ARG:HB3	2.00	0.44
1:A:100:LYS:HD3	1:A:105:MET:HB2	1.99	0.44
1:A:202:ILE:HD13	1:A:223:LEU:HD22	2.00	0.44
1:A:440:LYS:O	1:A:443:ASP:HB2	2.17	0.44
1:A:536:ASN:C	1:A:538:GLU:H	2.21	0.44
1:A:546:SER:O	1:A:547:TYR:HB2	2.17	0.44
1:B:180:HIS:CD2	1:B:180:HIS:N	2.85	0.44
1:B:536:ASN:ND2	1:B:538:GLU:HB3	2.32	0.44
1:C:517:ARG:HB3	1:C:519:LEU:HD13	1.99	0.44
1:D:204:LEU:HD13	1:D:206:PHE:CZ	2.53	0.44
1:D:408:LYS:NZ	1:E:263:ASP:C	2.71	0.44
1:D:532:TYR:CD1	1:D:532:TYR:N	2.85	0.44
1:E:79:SER:H	1:E:98:ILE:CD1	2.29	0.44
1:E:463:ILE:CG2	1:E:464:CYS:N	2.79	0.44
1:E:488:GLY:HA3	1:E:492:LEU:CD1	2.44	0.44
1:G:152:LYS:O	1:G:174:PRO:HD2	2.17	0.44
1:G:315:GLY:HA2	1:G:317:VAL:CG2	2.42	0.44
1:A:336:LYS:HB3	1:A:418:CYS:HB3	1.98	0.44
1:D:227:LYS:O	1:D:229:ARG:HD2	2.18	0.44
1:D:295:ILE:HD12	1:D:516:VAL:HG11	1.97	0.44
1:D:304:GLY:HA2	1:D:459:VAL:HG22	1.98	0.44
1:D:395:ASP:HB3	1:E:266:VAL:HG21	2.00	0.44
1:D:486:LEU:HB3	1:D:493:ARG:CD	2.45	0.44
1:E:304:GLY:HA2	1:E:459:VAL:HG22	1.98	0.44
1:E:352:ASP:CG	1:E:363:ARG:HD3	2.38	0.44
1:E:440:LYS:O	1:E:443:ASP:HB2	2.18	0.44
1:F:339:LEU:HB3	1:F:341:MET:HE2	1.86	0.44
1:G:193:TYR:CE1	1:G:224:PRO:HA	2.53	0.44
1:G:362:LEU:HD12	1:G:362:LEU:O	2.17	0.44
1:A:321:PHE:CE2	1:A:533:MET:HE1	2.53	0.44
1:A:510:MET:CE	1:A:513:LEU:CD2	2.95	0.44
1:C:327:LEU:HB3	1:C:328:GLN:H	1.70	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:406:LEU:HD13	1:C:406:LEU:HA	1.80	0.44
1:C:409:LEU:HD23	1:C:421:ILE:CG2	2.33	0.44
1:D:96:TYR:CE2	1:D:107:GLN:HG2	2.53	0.44
1:D:447:THR:O	1:D:448:LYS:C	2.56	0.44
1:D:498:THR:C	1:D:499:ILE:HD13	2.37	0.44
1:E:286:GLY:O	1:E:302:ALA:N	2.51	0.44
1:E:492:LEU:O	1:E:494:GLN:N	2.51	0.44
1:F:531:GLY:C	1:F:532:TYR:CD1	2.92	0.44
1:G:300:LEU:HA	1:G:300:LEU:HD22	1.54	0.44
1:G:338:GLY:HA3	1:G:412:MET:HE3	2.00	0.44
1:G:339:LEU:HD13	1:G:341:MET:CE	2.48	0.44
1:G:488:GLY:HA3	1:G:492:LEU:CD1	2.46	0.44
1:A:136:HIS:CD2	1:A:180:HIS:CE1	3.05	0.44
1:A:251:MET:CE	1:A:251:MET:CA	2.92	0.44
1:A:316:MET:CE	1:A:535:TYR:CZ	3.00	0.44
1:A:401:GLU:CG	1:A:402:THR:N	2.76	0.44
1:A:425:HIS:CE1	1:A:465:HIS:HB2	2.50	0.44
1:A:473:LYS:CE	1:A:479:ARG:HA	2.44	0.44
1:B:208:MET:CE	1:B:232:VAL:HA	2.22	0.44
1:B:283:GLU:OE2	1:B:286:GLY:CA	2.61	0.44
1:B:320:THR:HG22	1:B:324:GLN:NE2	2.33	0.44
1:C:124:ARG:HD3	1:C:125:ASP:CA	2.47	0.44
1:D:155:VAL:HG12	1:D:206:PHE:HE2	1.83	0.44
1:D:322:VAL:HG21	1:D:463:ILE:CD1	2.47	0.44
1:D:347:GLU:OE2	1:E:274:ARG:CD	2.66	0.44
1:D:405:LEU:HG	1:D:409:LEU:CD1	2.42	0.44
1:E:370:ARG:HH12	1:E:371:GLU:HG2	1.71	0.44
1:F:401:GLU:CG	1:F:402:THR:H	2.30	0.44
1:F:412:MET:HE2	1:F:412:MET:HB3	1.53	0.44
1:G:228:VAL:HB	1:G:261:ILE:HD12	1.99	0.44
1:G:450:LYS:HD2	1:G:450:LYS:HA	1.67	0.44
1:G:510:MET:HB2	1:G:513:LEU:HB3	2.00	0.44
1:A:122:LYS:HE3	1:A:130:PHE:HE2	1.81	0.43
1:A:125:ASP:OD1	1:A:129:ASN:HB2	2.18	0.43
1:A:169:GLN:O	1:A:170:ASP:CB	2.63	0.43
1:A:493:ARG:H	1:A:493:ARG:HG2	1.40	0.43
1:A:519:LEU:O	1:A:520:LYS:CB	2.66	0.43
1:B:251:MET:CE	1:B:251:MET:CA	2.96	0.43
1:B:401:GLU:CA	1:B:430:VAL:O	2.66	0.43
1:B:450:LYS:HA	1:B:450:LYS:HD2	1.67	0.43
1:C:233:LEU:HD22	1:C:241:CYS:SG	2.58	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:513:LEU:HD11	1:C:532:TYR:HB3	2.00	0.43
1:D:145:HIS:CE1	1:D:146:LEU:HD21	2.52	0.43
1:E:181:GLY:O	1:E:182:ALA:C	2.57	0.43
1:E:338:GLY:O	1:E:421:ILE:HA	2.18	0.43
1:E:363:ARG:H	1:E:363:ARG:HG2	1.66	0.43
1:G:492:LEU:C	1:G:494:GLN:H	2.19	0.43
1:B:428:ILE:H	1:B:428:ILE:HD12	1.83	0.43
1:C:235:CYS:HB2	1:C:240:GLU:HG2	2.00	0.43
1:D:319:SER:O	1:D:323:ARG:HB2	2.18	0.43
1:D:342:LEU:N	1:D:342:LEU:HD23	2.32	0.43
1:D:346:VAL:HG23	1:D:393:LEU:HB2	2.00	0.43
1:D:356:LEU:HD12	1:D:541:TRP:NE1	2.33	0.43
1:E:112:ARG:NH2	1:E:118:ILE:HD11	2.33	0.43
1:E:273:GLU:OE2	1:E:276:ARG:NH1	2.50	0.43
1:E:318:MET:HE1	1:E:465:HIS:CD2	2.53	0.43
1:E:443:ASP:HA	1:E:491:ALA:HB3	2.00	0.43
1:E:451:GLY:O	1:E:452:PHE:C	2.57	0.43
1:F:287:LEU:HD23	1:F:329:TRP:CE2	2.53	0.43
1:F:473:LYS:CD	1:F:479:ARG:HB2	2.48	0.43
1:F:492:LEU:O	1:F:494:GLN:N	2.52	0.43
1:G:406:LEU:HD13	1:G:406:LEU:HA	1.81	0.43
1:G:471:LYS:HD2	1:G:472:GLY:N	2.33	0.43
1:G:546:SER:O	1:G:547:TYR:HB2	2.18	0.43
1:A:141:LEU:HG	1:A:192:ASN:ND2	2.34	0.43
1:A:450:LYS:NZ	1:A:454:LYS:HD3	2.31	0.43
1:B:121:GLN:HB2	1:B:133:THR:HG1	1.78	0.43
1:B:446:MET:HE3	1:B:492:LEU:HA	2.00	0.43
1:B:486:LEU:HD23	1:B:486:LEU:HA	1.71	0.43
1:C:181:GLY:O	1:C:182:ALA:C	2.56	0.43
1:C:336:LYS:HB3	1:C:418:CYS:HB3	2.00	0.43
1:C:373:ILE:HD11	1:D:279:LEU:HB2	2.00	0.43
1:D:352:ASP:OD2	1:D:363:ARG:HD3	2.17	0.43
1:D:425:HIS:CE1	1:D:427:SER:CB	3.01	0.43
1:E:404:ARG:O	1:E:408:LYS:HG2	2.18	0.43
1:E:412:MET:HE2	1:E:412:MET:HB3	1.64	0.43
1:E:536:ASN:ND2	1:E:538:GLU:H	2.17	0.43
1:F:112:ARG:HD3	1:F:116:GLY:O	2.18	0.43
1:F:368:LEU:HD23	1:F:368:LEU:HA	1.69	0.43
1:F:391:PHE:C	1:F:392:HIS:CD2	2.91	0.43
1:G:80:ALA:HB2	1:G:88:LYS:N	2.33	0.43
1:G:255:TRP:O	1:G:256:ASN:C	2.57	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:415:GLY:N	1:C:226:GLY:HA3	2.34	0.43
1:A:536:ASN:HD22	1:A:536:ASN:C	2.20	0.43
1:B:180:HIS:HB2	1:B:184:ALA:HB3	1.99	0.43
1:B:193:TYR:CE1	1:B:224:PRO:HA	2.53	0.43
1:B:319:SER:O	1:B:323:ARG:HB2	2.18	0.43
1:B:440:LYS:HZ3	1:B:444:ASN:HB3	1.82	0.43
1:C:358:ASN:ND2	1:C:381:TRP:CE2	2.87	0.43
1:C:483:ILE:O	1:C:486:LEU:CB	2.48	0.43
1:D:283:GLU:O	1:D:283:GLU:HG2	2.16	0.43
1:D:402:THR:HG23	1:D:403:ASP:N	2.33	0.43
1:D:473:LYS:HE2	1:D:479:ARG:CA	2.42	0.43
1:E:445:LEU:HD12	1:E:445:LEU:O	2.17	0.43
1:F:107:GLN:HB3	1:F:124:ARG:CG	2.49	0.43
1:F:314:SER:O	1:F:315:GLY:C	2.56	0.43
1:F:378:PHE:HD2	1:G:276:ARG:HD2	1.83	0.43
1:F:535:TYR:CE1	1:F:537:LYS:HA	2.53	0.43
1:G:496:SER:O	1:G:520:LYS:CE	2.66	0.43
1:B:503:GLU:HG3	1:B:515:LEU:CD2	2.48	0.43
1:C:397:PHE:C	1:C:397:PHE:HD1	2.21	0.43
1:C:450:LYS:HE3	1:C:454:LYS:CD	2.48	0.43
1:C:506:GLN:H	1:C:506:GLN:HG3	1.56	0.43
1:D:330:GLY:HA2	1:D:335:LYS:O	2.18	0.43
1:D:440:LYS:O	1:D:443:ASP:HB2	2.19	0.43
1:D:510:MET:HB2	1:D:513:LEU:CB	2.48	0.43
1:E:229:ARG:CA	1:E:259:PRO:HA	2.46	0.43
1:E:447:THR:HA	1:E:495:LEU:CD2	2.48	0.43
1:E:510:MET:CB	1:E:513:LEU:HB2	2.48	0.43
1:F:322:VAL:HG11	1:F:422:ILE:CG2	2.47	0.43
1:F:476:GLU:CD	1:F:476:GLU:N	2.69	0.43
1:G:289:PHE:HA	1:G:325:GLN:HE21	1.84	0.43
1:G:321:PHE:CE2	1:G:533:MET:HE2	2.53	0.43
1:G:478:GLY:O	1:G:479:ARG:C	2.57	0.43
1:A:414:SER:C	1:C:226:GLY:HA3	2.39	0.43
1:A:441:MET:HE2	1:A:445:LEU:H	1.83	0.43
1:B:285:VAL:HG22	1:B:300:LEU:CD1	2.47	0.43
1:C:185:ALA:O	1:C:189:CYS:HB2	2.18	0.43
1:C:429:VAL:HG13	1:C:438:GLU:OE1	2.19	0.43
1:C:439:ARG:O	1:C:442:ILE:CG2	2.67	0.43
1:D:320:THR:HG22	1:D:324:GLN:NE2	2.34	0.43
1:D:324:GLN:OE1	1:D:541:TRP:CE3	2.71	0.43
1:D:338:GLY:CA	1:D:412:MET:HE1	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:430:VAL:O	1:E:430:VAL:HG12	2.18	0.43
1:E:446:MET:CE	1:E:492:LEU:HA	2.48	0.43
1:E:486:LEU:HB3	1:E:493:ARG:CD	2.48	0.43
1:G:442:ILE:HD11	1:G:492:LEU:CD2	2.47	0.43
1:A:492:LEU:C	1:A:494:GLN:H	2.21	0.43
1:B:204:LEU:HD13	1:B:206:PHE:CZ	2.54	0.43
1:B:286:GLY:O	1:B:302:ALA:O	2.35	0.43
1:B:312:SER:HB3	1:B:502:LEU:H	1.83	0.43
1:B:492:LEU:O	1:B:494:GLN:N	2.52	0.43
1:C:122:LYS:HE3	1:C:130:PHE:HE2	1.81	0.43
1:C:440:LYS:O	1:C:443:ASP:HB2	2.19	0.43
1:D:81:LEU:HG	1:D:91:CYS:SG	2.59	0.43
1:D:141:LEU:CD1	1:D:176:VAL:HG21	2.43	0.43
1:D:147:TRP:CD2	1:D:174:PRO:HB3	2.54	0.43
1:D:220:ALA:HB1	1:D:261:ILE:HG12	2.01	0.43
1:D:441:MET:HE1	1:D:445:LEU:H	1.82	0.43
1:E:136:HIS:CD2	1:E:180:HIS:CE1	3.06	0.43
1:E:153:ILE:HG23	1:E:153:ILE:O	2.18	0.43
1:E:397:PHE:C	1:E:397:PHE:HD1	2.21	0.43
1:F:193:TYR:CE1	1:F:224:PRO:HA	2.54	0.43
1:F:536:ASN:HD21	1:F:538:GLU:CB	2.32	0.43
1:G:124:ARG:HD3	1:G:125:ASP:O	2.19	0.43
1:A:105:MET:O	1:A:105:MET:HG2	2.18	0.43
1:A:114:GLN:HG3	1:A:144:LYS:HE2	2.01	0.43
1:A:321:PHE:CD2	1:A:533:MET:HE1	2.53	0.43
1:A:401:GLU:N	1:A:404:ARG:HD2	2.34	0.43
1:B:248:ARG:NH1	1:B:248:ARG:CG	2.70	0.43
1:B:510:MET:HE1	1:B:547:TYR:CE1	2.50	0.43
1:C:260:TRP:O	1:C:261:ILE:HD13	2.19	0.43
1:C:427:SER:HB3	1:C:487:ARG:NH1	2.33	0.43
1:C:442:ILE:HD11	1:C:492:LEU:CD1	2.47	0.43
1:E:412:MET:HE2	1:E:421:ILE:HD11	1.93	0.43
1:F:122:LYS:HE3	1:F:130:PHE:CE2	2.53	0.43
1:F:149:GLY:O	1:F:199:PHE:CE2	2.71	0.43
1:F:285:VAL:HG13	1:F:300:LEU:CD1	2.49	0.43
1:F:320:THR:HG22	1:F:324:GLN:HE21	1.84	0.43
1:F:366:ASP:CB	1:G:284:SER:CB	2.92	0.43
1:F:440:LYS:O	1:F:443:ASP:HB2	2.18	0.43
1:C:149:GLY:O	1:C:199:PHE:CE2	2.72	0.43
1:C:360:VAL:O	1:C:360:VAL:CG2	2.67	0.43
1:C:364:GLN:HA	1:D:523:PHE:HZ	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:322:VAL:HG11	1:D:422:ILE:HG21	2.01	0.43
1:E:145:HIS:CE1	1:E:146:LEU:CD2	3.02	0.43
1:F:450:LYS:HA	1:F:450:LYS:HD2	1.72	0.43
1:G:268:ALA:HA	1:G:271:LEU:HD12	1.98	0.43
1:G:413:ARG:HH21	1:G:457:GLY:C	2.22	0.43
1:G:425:HIS:NE2	1:G:465:HIS:ND1	2.66	0.43
1:G:428:ILE:H	1:G:428:ILE:HD12	1.83	0.43
1:G:536:ASN:ND2	1:G:538:GLU:H	2.16	0.43
1:A:208:MET:CE	1:A:232:VAL:HA	2.22	0.43
1:A:216:VAL:HG11	1:A:230:VAL:HG22	1.99	0.43
1:A:327:LEU:HA	1:A:327:LEU:HD23	1.43	0.43
1:A:413:ARG:HH21	1:A:457:GLY:C	2.22	0.43
1:A:427:SER:CB	1:A:487:ARG:NH1	2.81	0.43
1:A:510:MET:CB	1:A:513:LEU:CB	2.97	0.43
1:B:344:GLU:OE1	1:B:349:THR:HB	2.19	0.43
1:C:208:MET:CE	1:C:233:LEU:H	2.32	0.43
1:C:441:MET:CE	1:C:445:LEU:H	2.32	0.43
1:D:251:MET:CE	1:D:251:MET:CA	2.97	0.43
1:D:441:MET:HE1	1:D:444:ASN:HB3	2.00	0.43
1:E:251:MET:CE	1:E:251:MET:CA	2.97	0.43
1:E:368:LEU:CD2	1:E:372:ILE:HG23	2.43	0.43
1:E:401:GLU:HG3	1:E:431:SER:O	2.19	0.43
1:E:442:ILE:HD11	1:E:492:LEU:HD11	1.95	0.43
1:E:517:ARG:CG	1:E:517:ARG:HH11	2.30	0.43
1:F:318:MET:SD	1:F:463:ILE:HD13	2.59	0.43
1:G:536:ASN:OD1	1:G:539:THR:HG23	2.19	0.43
1:A:265:VAL:HG21	1:B:412:MET:HG2	2.01	0.42
1:A:450:LYS:HE3	1:A:454:LYS:CD	2.47	0.42
1:B:181:GLY:O	1:B:182:ALA:C	2.57	0.42
1:B:248:ARG:O	1:B:248:ARG:HG2	2.19	0.42
1:B:536:ASN:HD22	1:B:536:ASN:C	2.21	0.42
1:C:145:HIS:CE1	1:C:146:LEU:HD21	2.53	0.42
1:C:290:SER:N	1:C:325:GLN:HE22	2.03	0.42
1:C:442:ILE:HD11	1:C:492:LEU:CG	2.48	0.42
1:C:491:ALA:O	1:C:495:LEU:N	2.47	0.42
1:E:122:LYS:HE3	1:E:130:PHE:HE2	1.84	0.42
1:E:449:LEU:O	1:E:452:PHE:HB3	2.18	0.42
1:F:382:PHE:CZ	1:G:272:ARG:HA	2.54	0.42
1:G:327:LEU:HD11	1:G:357:HIS:HA	2.00	0.42
1:G:424:ASP:O	1:G:425:HIS:HB3	2.19	0.42
1:A:145:HIS:CE1	1:A:146:LEU:HD21	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:346:VAL:CG1	1:C:271:LEU:HD21	2.50	0.42
1:A:401:GLU:CB	1:A:431:SER:O	2.67	0.42
1:B:473:LYS:HE2	1:B:479:ARG:CA	2.44	0.42
1:C:86:ILE:HD12	1:C:163:LEU:HB3	2.02	0.42
1:C:427:SER:HB2	1:D:494:GLN:HE22	1.84	0.42
1:C:510:MET:CE	1:C:513:LEU:HD22	2.49	0.42
1:D:317:VAL:HG21	1:D:504:ARG:HD2	2.01	0.42
1:D:327:LEU:HA	1:D:327:LEU:HD23	1.47	0.42
1:D:440:LYS:NZ	1:D:441:MET:HG2	2.34	0.42
1:E:81:LEU:HD11	1:E:96:TYR:CD2	2.54	0.42
1:E:178:LEU:HD23	1:E:178:LEU:HA	1.83	0.42
1:E:411:TYR:CZ	1:F:262:PRO:HB3	2.52	0.42
1:E:445:LEU:CD1	1:E:449:LEU:HG	2.49	0.42
1:E:479:ARG:HA	1:E:480:PRO:HD3	1.83	0.42
1:E:520:LYS:HG3	1:E:521:CYS:N	2.25	0.42
1:F:180:HIS:CD2	1:F:180:HIS:N	2.87	0.42
1:F:285:VAL:HA	1:F:300:LEU:HD12	2.00	0.42
1:G:440:LYS:HE2	1:G:440:LYS:C	2.39	0.42
1:A:313:GLY:C	1:A:315:GLY:N	2.71	0.42
1:B:170:ASP:O	1:B:172:LYS:HG3	2.20	0.42
1:B:336:LYS:HB3	1:B:418:CYS:HA	2.00	0.42
1:B:476:GLU:HB3	1:B:506:GLN:OE1	2.19	0.42
1:C:146:LEU:HB2	1:C:147:TRP:CE2	2.54	0.42
1:C:204:LEU:HD13	1:C:206:PHE:CZ	2.54	0.42
1:D:290:SER:N	1:D:325:GLN:HE22	2.08	0.42
1:D:311:THR:O	1:D:502:LEU:HD12	2.18	0.42
1:D:413:ARG:HH21	1:D:457:GLY:C	2.22	0.42
1:D:542:LEU:HD12	1:D:542:LEU:HA	1.56	0.42
1:E:441:MET:HE1	1:E:445:LEU:H	1.84	0.42
1:E:518:ILE:HA	1:E:518:ILE:HD13	1.75	0.42
1:F:303:ARG:CZ	1:F:523:PHE:CD1	3.02	0.42
1:F:401:GLU:HG2	1:F:402:THR:H	1.85	0.42
1:F:442:ILE:HD11	1:F:492:LEU:CG	2.49	0.42
1:A:168:LEU:O	1:A:169:GLN:CB	2.55	0.42
1:A:406:LEU:HA	1:A:406:LEU:HD13	1.74	0.42
1:A:499:ILE:HG22	1:A:519:LEU:CB	2.34	0.42
1:A:510:MET:HE2	1:A:547:TYR:CE1	2.51	0.42
1:D:220:ALA:CB	1:D:261:ILE:HG23	2.47	0.42
1:D:412:MET:HE2	1:D:421:ILE:HD12	1.97	0.42
1:D:482:SER:O	1:D:485:ASP:CB	2.68	0.42
1:E:267:SER:O	1:E:271:LEU:HD12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:442:ILE:HD11	1:E:492:LEU:CG	2.48	0.42
1:F:322:VAL:CG1	1:F:422:ILE:HD13	2.49	0.42
1:A:141:LEU:CD1	1:A:176:VAL:HG21	2.43	0.42
1:A:339:LEU:HB3	1:A:341:MET:HE3	1.88	0.42
1:A:445:LEU:O	1:A:446:MET:C	2.58	0.42
1:B:114:GLN:NE2	1:B:195:TYR:CD1	2.88	0.42
1:B:235:CYS:HB2	1:B:240:GLU:HG2	2.01	0.42
1:C:443:ASP:HA	1:C:491:ALA:HB3	2.00	0.42
1:D:492:LEU:C	1:D:494:GLN:H	2.22	0.42
1:F:121:GLN:HB3	1:F:133:THR:CG2	2.45	0.42
1:F:178:LEU:HB3	1:F:181:GLY:CA	2.40	0.42
1:F:513:LEU:HD12	1:F:533:MET:O	2.18	0.42
1:G:124:ARG:CZ	1:G:126:LYS:HA	2.49	0.42
1:G:520:LYS:HG3	1:G:521:CYS:N	2.30	0.42
1:A:300:LEU:HD22	1:A:300:LEU:HA	1.78	0.42
1:A:401:GLU:CA	1:A:430:VAL:O	2.67	0.42
1:A:536:ASN:HD21	1:A:538:GLU:HB2	1.83	0.42
1:B:263:ASP:C	1:G:408:LYS:NZ	2.73	0.42
1:B:406:LEU:HA	1:B:406:LEU:HD13	1.59	0.42
1:C:121:GLN:HB3	1:C:133:THR:CG2	2.47	0.42
1:C:124:ARG:CZ	1:C:126:LYS:HA	2.50	0.42
1:C:141:LEU:HG	1:C:192:ASN:ND2	2.34	0.42
1:C:339:LEU:HB3	1:C:341:MET:HE2	1.88	0.42
1:D:107:GLN:CB	1:D:124:ARG:CG	2.93	0.42
1:D:289:PHE:HA	1:D:325:GLN:HE21	1.84	0.42
1:D:444:ASN:OD1	1:D:448:LYS:HE3	2.19	0.42
1:D:546:SER:O	1:D:547:TYR:HB2	2.20	0.42
1:E:114:GLN:NE2	1:E:195:TYR:CD1	2.87	0.42
1:F:217:GLU:OE2	1:F:261:ILE:HG23	2.18	0.42
1:G:153:ILE:HG23	1:G:153:ILE:O	2.20	0.42
1:A:124:ARG:CD	1:A:125:ASP:C	2.86	0.42
1:A:229:ARG:NH2	1:A:259:PRO:HB3	2.34	0.42
1:A:352:ASP:OD2	1:A:363:ARG:HD3	2.20	0.42
1:C:74:SER:HB3	1:C:101:VAL:CG2	2.50	0.42
1:C:344:GLU:OE1	1:C:349:THR:CB	2.66	0.42
1:C:510:MET:HB2	1:C:513:LEU:HB3	2.00	0.42
1:D:115:ASN:HB3	1:D:117:ASN:HD21	1.84	0.42
1:D:347:GLU:O	1:D:351:GLU:HG3	2.20	0.42
1:D:486:LEU:HD22	1:D:487:ARG:H	1.85	0.42
1:E:341:MET:SD	1:E:424:ASP:HB2	2.59	0.42
1:E:429:VAL:HG13	1:E:438:GLU:OE1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:486:LEU:HD22	1:E:487:ARG:H	1.85	0.42
1:E:517:ARG:CZ	1:E:529:ILE:HD11	2.50	0.42
1:F:260:TRP:CD1	1:F:262:PRO:HD2	2.55	0.42
1:G:363:ARG:H	1:G:363:ARG:HG2	1.55	0.42
1:G:382:PHE:C	1:G:382:PHE:CD2	2.92	0.42
1:G:445:LEU:HD12	1:G:445:LEU:O	2.19	0.42
1:G:451:GLY:O	1:G:452:PHE:C	2.58	0.42
1:C:70:ASN:HD22	1:C:70:ASN:HA	1.69	0.42
1:E:427:SER:HB3	1:E:487:ARG:NH1	2.28	0.42
1:E:536:ASN:HD22	1:E:536:ASN:C	2.23	0.42
1:F:356:LEU:HD12	1:F:541:TRP:CD1	2.54	0.42
1:F:362:LEU:HD12	1:F:362:LEU:C	2.40	0.42
1:F:415:GLY:HA2	1:G:226:GLY:H	1.82	0.42
1:A:269:LEU:HD21	1:B:389:ASP:H	1.84	0.42
1:B:248:ARG:HD2	1:B:249:GLU:OE2	2.20	0.42
1:B:404:ARG:O	1:B:408:LYS:HG2	2.19	0.42
1:B:429:VAL:HG13	1:B:438:GLU:OE1	2.19	0.42
1:C:233:LEU:CD2	1:C:250:ILE:HG12	2.50	0.42
1:C:401:GLU:HG3	1:C:431:SER:O	2.20	0.42
1:D:347:GLU:CD	1:E:274:ARG:HG2	2.40	0.42
1:D:451:GLY:O	1:D:455:SER:HB3	2.19	0.42
1:D:536:ASN:C	1:D:538:GLU:H	2.22	0.42
1:E:229:ARG:HB3	1:E:259:PRO:CA	2.50	0.42
1:E:368:LEU:HD22	1:E:372:ILE:CG2	2.46	0.42
1:E:478:GLY:O	1:E:479:ARG:C	2.58	0.42
1:F:165:VAL:HB	1:F:175:VAL:HG11	2.02	0.42
1:F:307:VAL:HG12	1:F:496:SER:HA	2.01	0.42
1:F:488:GLY:HA3	1:F:492:LEU:CD1	2.45	0.42
1:G:440:LYS:NZ	1:G:441:MET:HG2	2.35	0.42
1:A:242:HIS:O	1:A:244:ASN:N	2.53	0.42
1:A:368:LEU:HD22	1:A:368:LEU:C	2.33	0.42
1:A:440:LYS:NZ	1:A:441:MET:HG2	2.34	0.42
1:B:401:GLU:CB	1:B:431:SER:O	2.68	0.42
1:B:479:ARG:HA	1:B:480:PRO:HD3	1.85	0.42
1:B:482:SER:H	1:B:485:ASP:CB	2.23	0.42
1:C:204:LEU:N	1:C:204:LEU:HD23	2.35	0.42
1:C:442:ILE:HD11	1:C:492:LEU:CD2	2.49	0.42
1:C:536:ASN:C	1:C:538:GLU:N	2.73	0.42
1:D:259:PRO:O	1:D:260:TRP:CE3	2.72	0.42
1:D:492:LEU:O	1:D:494:GLN:N	2.53	0.42
1:E:124:ARG:HD3	1:E:125:ASP:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:370:ARG:HD2	1:E:371:GLU:CA	2.49	0.42
1:F:378:PHE:CE2	1:G:276:ARG:CG	3.03	0.42
1:F:442:ILE:HD11	1:F:492:LEU:HD11	1.98	0.42
1:G:77:ARG:HE	1:G:77:ARG:HB2	1.61	0.42
1:G:170:ASP:O	1:G:172:LYS:HG3	2.20	0.42
1:G:307:VAL:HG22	1:G:460:LEU:HB3	2.02	0.42
1:B:122:LYS:HE3	1:B:130:PHE:HE2	1.85	0.41
1:B:542:LEU:HD12	1:B:542:LEU:HA	1.64	0.41
1:C:267:SER:O	1:C:270:SER:OG	2.28	0.41
1:C:322:VAL:HG21	1:C:463:ILE:CD1	2.49	0.41
1:C:366:ASP:CB	1:D:284:SER:OG	2.67	0.41
1:C:504:ARG:HD3	1:C:506:GLN:CG	2.26	0.41
1:E:208:MET:HE1	1:E:232:VAL:CA	2.23	0.41
1:E:447:THR:HG22	1:E:495:LEU:CD2	2.31	0.41
1:E:496:SER:O	1:E:520:LYS:CE	2.67	0.41
1:F:259:PRO:O	1:F:260:TRP:CB	2.58	0.41
1:F:285:VAL:HA	1:F:300:LEU:CD1	2.49	0.41
1:F:295:ILE:HD12	1:F:516:VAL:HG11	2.02	0.41
1:F:397:PHE:C	1:F:397:PHE:HD1	2.22	0.41
1:F:482:SER:CB	1:F:484:THR:HG23	2.49	0.41
1:F:536:ASN:HD22	1:F:536:ASN:C	2.22	0.41
1:G:425:HIS:CE1	1:G:427:SER:HB2	2.55	0.41
1:G:517:ARG:CZ	1:G:529:ILE:HD11	2.50	0.41
1:G:532:TYR:CD1	1:G:532:TYR:N	2.88	0.41
1:A:173:TYR:CD1	1:A:173:TYR:N	2.88	0.41
1:A:276:ARG:HH11	1:A:276:ARG:CG	2.30	0.41
1:A:492:LEU:H	1:A:492:LEU:CD1	2.13	0.41
1:B:106:TYR:HB3	1:B:123:VAL:CG1	2.50	0.41
1:B:185:ALA:O	1:B:189:CYS:HB2	2.19	0.41
1:B:324:GLN:OE1	1:B:541:TRP:CE3	2.73	0.41
1:B:486:LEU:HB3	1:B:493:ARG:CD	2.50	0.41
1:C:229:ARG:NH2	1:C:259:PRO:CG	2.83	0.41
1:C:369:LYS:NZ	1:D:284:SER:H	2.19	0.41
1:C:440:LYS:NZ	1:C:441:MET:CA	2.58	0.41
1:D:152:LYS:O	1:D:174:PRO:HD2	2.19	0.41
1:D:445:LEU:O	1:D:445:LEU:HD12	2.20	0.41
1:E:170:ASP:O	1:E:172:LYS:HG3	2.20	0.41
1:F:147:TRP:CE2	1:F:174:PRO:HA	2.55	0.41
1:F:366:ASP:HA	1:G:284:SER:OG	2.20	0.41
1:F:414:SER:O	1:G:225:ALA:HB1	2.19	0.41
1:G:272:ARG:CG	1:G:273:GLU:N	2.81	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:284:SER:O	1:G:300:LEU:HD12	2.19	0.41
1:A:166:MET:HG2	1:A:175:VAL:HG21	2.02	0.41
1:A:173:TYR:HA	1:A:174:PRO:HD3	1.94	0.41
1:A:267:SER:O	1:A:271:LEU:HD12	2.20	0.41
1:A:424:ASP:HA	1:A:463:ILE:HB	2.01	0.41
1:A:548:SER:HB3	1:A:549:GLY:H	1.60	0.41
1:B:81:LEU:HD12	1:B:86:ILE:HB	2.02	0.41
1:B:204:LEU:N	1:B:204:LEU:HD23	2.36	0.41
1:B:262:PRO:CB	1:B:265:VAL:HG12	2.49	0.41
1:B:283:GLU:HG3	1:B:283:GLU:O	2.20	0.41
1:B:330:GLY:HA2	1:B:335:LYS:O	2.20	0.41
1:C:402:THR:HG23	1:C:403:ASP:H	1.85	0.41
1:C:447:THR:HG22	1:C:495:LEU:CD2	2.32	0.41
1:D:129:ASN:OD1	1:E:89:GLU:OE1	2.38	0.41
1:D:533:MET:HB3	1:D:543:GLU:O	2.20	0.41
1:E:346:VAL:HG23	1:E:393:LEU:HB2	2.02	0.41
1:F:360:VAL:O	1:F:360:VAL:HG23	2.20	0.41
1:F:412:MET:HA	1:F:416:LEU:HD11	1.96	0.41
1:F:486:LEU:HD22	1:F:487:ARG:N	2.35	0.41
1:G:81:LEU:HD22	1:G:107:GLN:NE2	2.35	0.41
1:A:227:LYS:O	1:A:229:ARG:HD2	2.21	0.41
1:A:347:GLU:OE2	1:C:274:ARG:HD2	2.21	0.41
1:A:368:LEU:HD23	1:A:368:LEU:HA	1.67	0.41
1:B:283:GLU:O	1:B:286:GLY:N	2.53	0.41
1:B:286:GLY:O	1:B:287:LEU:CB	2.68	0.41
1:C:170:ASP:O	1:C:172:LYS:HG3	2.20	0.41
1:C:180:HIS:CD2	1:C:180:HIS:N	2.88	0.41
1:C:216:VAL:CG1	1:C:230:VAL:HG22	2.47	0.41
1:C:366:ASP:HA	1:D:284:SER:OG	2.21	0.41
1:C:442:ILE:HG23	1:C:443:ASP:N	2.35	0.41
1:C:477:GLU:HG3	1:C:507:GLN:HE22	1.86	0.41
1:D:313:GLY:O	1:D:315:GLY:N	2.53	0.41
1:E:411:TYR:O	1:E:411:TYR:CG	2.73	0.41
1:E:450:LYS:HE3	1:E:454:LYS:CD	2.48	0.41
1:E:513:LEU:HD12	1:E:533:MET:O	2.20	0.41
1:E:517:ARG:CG	1:E:517:ARG:NH1	2.82	0.41
1:F:375:ASN:CG	1:F:377:LYS:HG3	2.40	0.41
1:G:145:HIS:CE1	1:G:146:LEU:HD21	2.55	0.41
1:G:318:MET:SD	1:G:463:ILE:HG23	2.60	0.41
1:A:165:VAL:HB	1:A:175:VAL:HG11	2.03	0.41
1:A:439:ARG:HG2	1:A:489:SER:OG	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:447:THR:HA	1:A:495:LEU:CD2	2.50	0.41
1:A:529:ILE:HD13	1:A:529:ILE:HA	1.88	0.41
1:A:531:GLY:C	1:A:532:TYR:CD1	2.94	0.41
1:A:533:MET:HB3	1:A:543:GLU:O	2.20	0.41
1:B:253:GLN:O	1:B:257:ALA:HB2	2.21	0.41
1:B:311:THR:O	1:B:312:SER:CB	2.68	0.41
1:B:363:ARG:H	1:B:363:ARG:HG2	1.52	0.41
1:B:492:LEU:C	1:B:494:GLN:H	2.24	0.41
1:B:498:THR:C	1:B:499:ILE:HD13	2.40	0.41
1:C:97:TRP:HZ3	1:C:99:ALA:HB2	1.76	0.41
1:C:178:LEU:HA	1:C:178:LEU:HD23	1.81	0.41
1:D:147:TRP:CE2	1:D:174:PRO:HA	2.55	0.41
1:D:486:LEU:HD13	1:D:487:ARG:O	2.20	0.41
1:D:536:ASN:HD21	1:D:538:GLU:HB3	1.86	0.41
1:F:234:PRO:HG2	1:F:249:GLU:HG2	2.02	0.41
1:F:300:LEU:HD22	1:F:300:LEU:HA	1.79	0.41
1:G:233:LEU:CD2	1:G:250:ILE:HG12	2.50	0.41
1:G:276:ARG:O	1:G:277:GLU:C	2.58	0.41
1:G:442:ILE:HD11	1:G:492:LEU:CG	2.51	0.41
1:A:229:ARG:HA	1:A:259:PRO:HA	2.02	0.41
1:B:309:MET:HE2	1:B:462:VAL:HG12	2.02	0.41
1:C:296:ASN:O	1:C:300:LEU:N	2.35	0.41
1:D:353:LEU:HA	1:D:353:LEU:HD23	1.56	0.41
1:D:401:GLU:HB2	1:D:404:ARG:HH21	1.85	0.41
1:F:101:VAL:HG12	1:F:102:ASP:OD2	2.20	0.41
1:F:404:ARG:HH21	1:F:404:ARG:CB	2.33	0.41
1:G:294:GLY:C	1:G:296:ASN:N	2.74	0.41
1:G:317:VAL:HG21	1:G:504:ARG:HD2	2.02	0.41
1:G:517:ARG:HG3	1:G:529:ILE:HD13	2.03	0.41
1:A:353:LEU:HA	1:A:353:LEU:HD23	1.59	0.41
1:A:411:TYR:CD1	1:A:411:TYR:C	2.92	0.41
1:A:430:VAL:O	1:A:430:VAL:HG12	2.20	0.41
1:A:473:LYS:HE2	1:A:479:ARG:CA	2.47	0.41
1:B:115:ASN:HB3	1:B:117:ASN:HD21	1.85	0.41
1:B:147:TRP:CD2	1:B:174:PRO:HB3	2.54	0.41
1:B:155:VAL:HG22	1:B:176:VAL:CG2	2.51	0.41
1:C:81:LEU:HD11	1:C:96:TYR:CD2	2.55	0.41
1:C:338:GLY:HA3	1:C:412:MET:HE1	2.02	0.41
1:C:493:ARG:H	1:C:493:ARG:HG2	1.43	0.41
1:C:529:ILE:HD13	1:C:529:ILE:HA	1.80	0.41
1:D:136:HIS:CD2	1:D:180:HIS:CE1	3.07	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:223:LEU:CD2	1:D:224:PRO:HD2	2.51	0.41
1:D:499:ILE:HG21	1:D:519:LEU:CB	2.50	0.41
1:D:510:MET:HB3	1:D:513:LEU:HB2	2.02	0.41
1:E:233:LEU:CD2	1:E:250:ILE:HG12	2.50	0.41
1:E:260:TRP:O	1:E:261:ILE:HG12	2.20	0.41
1:E:260:TRP:C	1:E:261:ILE:CG1	2.88	0.41
1:E:370:ARG:CD	1:E:371:GLU:CA	2.99	0.41
1:E:427:SER:CB	1:E:487:ARG:HH12	2.27	0.41
1:E:450:LYS:NZ	1:E:454:LYS:HD3	2.35	0.41
1:F:471:LYS:HA	1:F:471:LYS:HD2	1.61	0.41
1:F:486:LEU:HD23	1:F:486:LEU:HA	1.77	0.41
1:G:324:GLN:HE22	1:G:542:LEU:HB2	1.84	0.41
1:A:265:VAL:C	1:A:266:VAL:HG23	2.41	0.41
1:A:347:GLU:OE2	1:C:274:ARG:HG2	2.21	0.41
1:A:386:PHE:O	1:A:388:ASN:N	2.50	0.41
1:A:486:LEU:HB3	1:A:493:ARG:CD	2.51	0.41
1:B:225:ALA:HB1	1:G:414:SER:CB	2.50	0.41
1:B:233:LEU:CD2	1:B:250:ILE:HG12	2.50	0.41
1:B:261:ILE:H	1:B:262:PRO:CD	2.34	0.41
1:B:268:ALA:HA	1:B:271:LEU:HD12	2.01	0.41
1:B:413:ARG:HA	1:B:413:ARG:HD3	1.92	0.41
1:C:106:TYR:HB3	1:C:123:VAL:CG1	2.50	0.41
1:D:443:ASP:HA	1:D:491:ALA:HB3	2.03	0.41
1:D:478:GLY:O	1:D:479:ARG:C	2.59	0.41
1:E:124:ARG:CZ	1:E:126:LYS:HA	2.51	0.41
1:F:251:MET:HA	1:F:251:MET:HE3	1.98	0.41
1:F:409:LEU:HD23	1:F:421:ILE:CG2	2.32	0.41
1:F:503:GLU:CD	1:F:517:ARG:HE	2.24	0.41
1:G:216:VAL:CG1	1:G:230:VAL:HG22	2.49	0.41
1:G:510:MET:HB2	1:G:513:LEU:CB	2.50	0.41
1:A:81:LEU:HD11	1:A:96:TYR:CD2	2.56	0.41
1:A:152:LYS:HZ2	1:A:256:ASN:H	1.68	0.41
1:A:262:PRO:HB3	1:B:411:TYR:CE1	2.56	0.41
1:A:499:ILE:HD12	1:A:499:ILE:HA	1.83	0.41
1:A:503:GLU:HG3	1:A:515:LEU:CD2	2.51	0.41
1:B:121:GLN:CB	1:B:133:THR:CG2	2.98	0.41
1:B:223:LEU:CD2	1:B:224:PRO:HD2	2.50	0.41
1:B:440:LYS:NZ	1:B:441:MET:CA	2.64	0.41
1:B:503:GLU:HG3	1:B:515:LEU:HD23	2.02	0.41
1:B:515:LEU:HD21	1:B:529:ILE:HD12	2.03	0.41
1:C:229:ARG:HH21	1:C:259:PRO:CB	2.32	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:394:TYR:HE1	1:C:396:SER:CB	2.32	0.41
1:C:445:LEU:CD1	1:C:449:LEU:HG	2.51	0.41
1:C:446:MET:HB3	1:C:491:ALA:HB1	2.03	0.41
1:C:469:PRO:HD3	1:C:475:HIS:HE1	1.86	0.41
1:D:112:ARG:HD2	1:D:145:HIS:CE1	2.55	0.41
1:D:200:GLU:O	1:D:227:LYS:HE3	2.21	0.41
1:D:243:LEU:O	1:D:244:ASN:O	2.37	0.41
1:D:273:GLU:OE2	1:D:276:ARG:NH1	2.53	0.41
1:D:327:LEU:HD11	1:D:357:HIS:HA	2.03	0.41
1:D:454:LYS:HE3	1:D:522:ARG:HH22	1.85	0.41
1:D:504:ARG:HH21	1:D:506:GLN:HG2	1.86	0.41
1:E:124:ARG:HD3	1:E:125:ASP:N	2.35	0.41
1:E:235:CYS:HB2	1:E:240:GLU:HG2	2.03	0.41
1:E:401:GLU:N	1:E:430:VAL:O	2.54	0.41
1:E:473:LYS:HE2	1:E:479:ARG:CA	2.43	0.41
1:F:204:LEU:HD23	1:F:204:LEU:N	2.36	0.41
1:F:291:GLY:O	1:F:292:CYS:HB2	2.21	0.41
1:F:321:PHE:CE2	1:F:533:MET:HE1	2.56	0.41
1:F:427:SER:CB	1:F:487:ARG:HH12	2.30	0.41
1:A:152:LYS:HD3	1:A:203:ILE:CD1	2.51	0.41
1:A:265:VAL:CG2	1:B:412:MET:HG2	2.51	0.41
1:B:413:ARG:HH21	1:B:458:VAL:N	2.19	0.41
1:C:322:VAL:HG11	1:C:422:ILE:CG2	2.51	0.41
1:C:341:MET:HE2	1:C:341:MET:N	2.35	0.41
1:C:484:THR:O	1:C:486:LEU:N	2.54	0.41
1:E:216:VAL:CG1	1:E:230:VAL:HG22	2.49	0.41
1:E:228:VAL:HG23	1:E:261:ILE:HD11	2.01	0.41
1:E:303:ARG:HB2	1:E:306:GLU:CD	2.42	0.41
1:E:476:GLU:CD	1:E:476:GLU:N	2.74	0.41
1:E:499:ILE:HG21	1:E:519:LEU:CB	2.51	0.41
1:F:78:TYR:CG	1:F:92:GLN:HG2	2.55	0.41
1:F:327:LEU:HD11	1:F:357:HIS:HA	2.03	0.41
1:G:204:LEU:N	1:G:204:LEU:HD23	2.35	0.41
1:G:321:PHE:CD2	1:G:533:MET:HE2	2.55	0.41
1:G:336:LYS:HB3	1:G:418:CYS:HB3	2.03	0.41
1:G:447:THR:O	1:G:448:LYS:C	2.60	0.41
1:A:446:MET:O	1:A:449:LEU:HB2	2.20	0.40
1:B:467:LYS:H	1:B:467:LYS:HG3	1.50	0.40
1:D:260:TRP:CB	1:D:262:PRO:HG3	2.35	0.40
1:A:482:SER:O	1:A:485:ASP:HB2	2.21	0.40
1:A:492:LEU:O	1:A:494:GLN:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:295:ILE:HD12	1:B:516:VAL:HG11	2.04	0.40
1:C:478:GLY:O	1:C:479:ARG:C	2.60	0.40
1:F:323:ARG:O	1:F:326:ALA:HB3	2.22	0.40
1:F:338:GLY:HA2	1:F:392:HIS:O	2.21	0.40
1:F:401:GLU:N	1:F:404:ARG:HD2	2.36	0.40
1:G:114:GLN:NE2	1:G:195:TYR:CD1	2.88	0.40
1:G:155:VAL:HG22	1:G:176:VAL:CG2	2.51	0.40
1:G:285:VAL:HA	1:G:300:LEU:CD1	2.51	0.40
1:G:447:THR:HA	1:G:495:LEU:CD2	2.50	0.40
1:G:492:LEU:O	1:G:494:GLN:N	2.53	0.40
1:A:478:GLY:O	1:A:479:ARG:C	2.60	0.40
1:A:536:ASN:HD21	1:A:538:GLU:HB3	1.86	0.40
1:B:80:ALA:HB2	1:B:88:LYS:N	2.36	0.40
1:B:168:LEU:HD22	1:B:247:ASP:OD2	2.15	0.40
1:B:440:LYS:HZ2	1:B:441:MET:HA	1.76	0.40
1:C:229:ARG:HH21	1:C:259:PRO:HB3	1.82	0.40
1:C:492:LEU:C	1:C:494:GLN:N	2.73	0.40
1:D:292:CYS:O	1:D:293:THR:C	2.60	0.40
1:D:442:ILE:HG23	1:D:443:ASP:N	2.36	0.40
1:F:502:LEU:HD12	1:F:502:LEU:N	2.35	0.40
1:F:542:LEU:HA	1:F:542:LEU:HD12	1.63	0.40
1:G:251:MET:CE	1:G:251:MET:CA	2.99	0.40
1:G:322:VAL:CG1	1:G:422:ILE:HG21	2.51	0.40
1:G:482:SER:CB	1:G:484:THR:HG23	2.51	0.40
1:G:495:LEU:N	1:G:495:LEU:CD1	2.84	0.40
1:G:504:ARG:CG	1:G:506:GLN:HG2	2.51	0.40
1:A:471:LYS:HA	1:A:471:LYS:HD2	1.64	0.40
1:A:536:ASN:ND2	1:A:538:GLU:HB2	2.36	0.40
1:B:81:LEU:HD22	1:B:107:GLN:NE2	2.36	0.40
1:B:149:GLY:O	1:B:199:PHE:CE2	2.75	0.40
1:B:300:LEU:O	1:B:300:LEU:HD13	2.21	0.40
1:C:152:LYS:O	1:C:174:PRO:HD2	2.21	0.40
1:C:232:VAL:O	1:C:232:VAL:HG12	2.20	0.40
1:C:401:GLU:HG2	1:C:402:THR:H	1.86	0.40
1:C:408:LYS:O	1:C:412:MET:HG3	2.21	0.40
1:C:471:LYS:HD2	1:C:472:GLY:N	2.36	0.40
1:C:502:LEU:N	1:C:502:LEU:HD12	2.37	0.40
1:C:536:ASN:HD21	1:C:538:GLU:HB3	1.83	0.40
1:D:74:SER:O	1:D:76:GLY:N	2.54	0.40
1:D:170:ASP:O	1:D:172:LYS:HG3	2.20	0.40
1:D:248:ARG:O	1:D:248:ARG:HG2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:318:MET:SD	1:D:463:ILE:HD12	2.61	0.40
1:D:346:VAL:CB	1:D:395:ASP:HB2	2.50	0.40
1:D:536:ASN:C	1:D:538:GLU:N	2.75	0.40
1:E:386:PHE:HB3	1:F:269:LEU:HD13	2.03	0.40
1:F:121:GLN:CB	1:F:133:THR:CG2	2.99	0.40
1:F:322:VAL:HG21	1:F:463:ILE:CD1	2.52	0.40
1:F:429:VAL:HG13	1:F:438:GLU:OE1	2.22	0.40
1:F:430:VAL:HG12	1:F:430:VAL:O	2.21	0.40
1:F:447:THR:HA	1:F:495:LEU:CD2	2.52	0.40
1:G:79:SER:H	1:G:98:ILE:CD1	2.29	0.40
1:G:413:ARG:HA	1:G:413:ARG:HD3	1.86	0.40
1:A:126:LYS:CE	1:A:127:ASP:CG	2.90	0.40
1:A:166:MET:C	1:A:171:CYS:HB3	2.42	0.40
1:A:294:GLY:C	1:A:296:ASN:N	2.72	0.40
1:A:324:GLN:OE1	1:A:541:TRP:HE3	2.05	0.40
1:B:481:VAL:HG13	1:B:503:GLU:OE2	2.20	0.40
1:C:276:ARG:HH11	1:C:276:ARG:CG	2.34	0.40
1:C:443:ASP:O	1:C:447:THR:HG23	2.22	0.40
1:C:510:MET:HE1	1:C:547:TYR:CE1	2.52	0.40
1:D:122:LYS:HE3	1:D:130:PHE:HE2	1.86	0.40
1:D:427:SER:CB	1:D:487:ARG:NH1	2.84	0.40
1:D:439:ARG:HG2	1:D:489:SER:OG	2.21	0.40
1:E:80:ALA:HB2	1:E:88:LYS:N	2.36	0.40
1:E:180:HIS:CD2	1:E:180:HIS:N	2.89	0.40
1:E:345:SER:OG	1:E:347:GLU:HG2	2.21	0.40
1:E:405:LEU:HD21	1:E:409:LEU:HD11	2.04	0.40
1:G:112:ARG:NH2	1:G:118:ILE:HD11	2.36	0.40
1:G:339:LEU:HD22	1:G:341:MET:CE	2.51	0.40
1:G:445:LEU:HD11	1:G:449:LEU:HG	2.03	0.40
1:G:454:LYS:HE3	1:G:522:ARG:HH22	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [\(i\)](#)

5.3.1 Protein backbone [\(i\)](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	479/503 (95%)	377 (79%)	68 (14%)	34 (7%)	1	11
1	B	479/503 (95%)	384 (80%)	65 (14%)	30 (6%)	1	13
1	C	479/503 (95%)	385 (80%)	57 (12%)	37 (8%)	1	9
1	D	479/503 (95%)	377 (79%)	66 (14%)	36 (8%)	1	10
1	E	479/503 (95%)	381 (80%)	65 (14%)	33 (7%)	1	11
1	F	479/503 (95%)	380 (79%)	63 (13%)	36 (8%)	1	10
1	G	479/503 (95%)	386 (81%)	67 (14%)	26 (5%)	2	16
All	All	3353/3521 (95%)	2670 (80%)	451 (14%)	232 (7%)	1	11

All (232) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	128	LYS
1	A	182	ALA
1	A	244	ASN
1	A	258	GLY
1	A	261	ILE
1	A	432	ALA
1	B	128	LYS
1	B	182	ALA
1	B	244	ASN
1	B	261	ILE
1	B	313	GLY
1	B	429	VAL
1	B	432	ALA
1	C	128	LYS
1	C	182	ALA
1	C	244	ASN
1	C	261	ILE
1	C	284	SER
1	C	315	GLY
1	C	327	LEU
1	C	429	VAL
1	C	432	ALA
1	D	128	LYS
1	D	182	ALA
1	D	244	ASN
1	D	284	SER

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Mol	Chain	Res	Type
1	D	432	ALA
1	E	128	LYS
1	E	182	ALA
1	E	244	ASN
1	E	261	ILE
1	E	425	HIS
1	E	432	ALA
1	F	128	LYS
1	F	182	ALA
1	F	244	ASN
1	F	259	PRO
1	F	261	ILE
1	F	284	SER
1	F	425	HIS
1	F	429	VAL
1	F	432	ALA
1	G	128	LYS
1	G	182	ALA
1	G	244	ASN
1	G	261	ILE
1	G	313	GLY
1	G	429	VAL
1	G	432	ALA
1	A	126	LYS
1	A	169	GLN
1	A	171	CYS
1	A	210	GLU
1	A	257	ALA
1	A	287	LEU
1	A	292	CYS
1	A	313	GLY
1	A	314	SER
1	A	315	GLY
1	A	425	HIS
1	A	429	VAL
1	A	472	GLY
1	B	168	LEU
1	B	210	GLU
1	B	243	LEU
1	B	315	GLY
1	B	425	HIS
1	B	472	GLY

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Mol	Chain	Res	Type
1	B	485	ASP
1	C	168	LEU
1	C	210	GLU
1	C	243	LEU
1	C	313	GLY
1	C	425	HIS
1	C	472	GLY
1	D	168	LEU
1	D	210	GLU
1	D	243	LEU
1	D	260	TRP
1	D	287	LEU
1	D	313	GLY
1	D	315	GLY
1	D	425	HIS
1	D	429	VAL
1	D	472	GLY
1	E	168	LEU
1	E	210	GLU
1	E	243	LEU
1	E	292	CYS
1	E	313	GLY
1	E	314	SER
1	E	315	GLY
1	E	429	VAL
1	E	472	GLY
1	F	168	LEU
1	F	181	GLY
1	F	210	GLU
1	F	287	LEU
1	F	313	GLY
1	F	315	GLY
1	F	472	GLY
1	F	548	SER
1	G	168	LEU
1	G	210	GLU
1	G	243	LEU
1	G	315	GLY
1	G	425	HIS
1	G	472	GLY
1	A	243	LEU
1	A	256	ASN

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Mol	Chain	Res	Type
1	A	259	PRO
1	A	284	SER
1	A	523	PHE
1	B	292	CYS
1	B	317	VAL
1	C	181	GLY
1	C	287	LEU
1	C	292	CYS
1	D	292	CYS
1	D	314	SER
1	D	485	ASP
1	E	259	PRO
1	E	287	LEU
1	E	485	ASP
1	E	523	PHE
1	F	243	LEU
1	F	292	CYS
1	F	314	SER
1	F	453	ALA
1	F	485	ASP
1	F	493	ARG
1	G	287	LEU
1	G	317	VAL
1	G	485	ASP
1	B	181	GLY
1	B	469	PRO
1	B	487	ARG
1	B	520	LYS
1	C	260	TRP
1	C	431	SER
1	C	469	PRO
1	C	479	ARG
1	C	485	ASP
1	C	547	TYR
1	D	75	ASN
1	D	453	ALA
1	D	469	PRO
1	E	181	GLY
1	E	317	VAL
1	E	469	PRO
1	E	493	ARG
1	F	469	PRO

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Mol	Chain	Res	Type
1	F	520	LYS
1	F	547	TYR
1	G	181	GLY
1	G	292	CYS
1	G	523	PHE
1	A	430	VAL
1	A	431	SER
1	A	469	PRO
1	A	474	ALA
1	A	485	ASP
1	A	520	LYS
1	A	548	SER
1	B	430	VAL
1	B	431	SER
1	B	479	ARG
1	B	493	ARG
1	B	495	LEU
1	C	75	ASN
1	C	259	PRO
1	C	262	PRO
1	C	295	ILE
1	C	430	VAL
1	C	453	ALA
1	C	548	SER
1	D	430	VAL
1	D	431	SER
1	D	520	LYS
1	E	364	GLN
1	E	430	VAL
1	E	431	SER
1	E	520	LYS
1	F	312	SER
1	F	389	ASP
1	F	430	VAL
1	F	431	SER
1	F	479	ARG
1	F	523	PHE
1	G	75	ASN
1	G	430	VAL
1	G	431	SER
1	G	469	PRO
1	G	479	ARG

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Mol	Chain	Res	Type
1	A	434	GLY
1	A	479	ARG
1	C	436	SER
1	D	181	GLY
1	D	327	LEU
1	D	474	ALA
1	D	479	ARG
1	D	493	ARG
1	D	548	SER
1	E	75	ASN
1	E	453	ALA
1	F	317	VAL
1	F	364	GLN
1	G	295	ILE
1	B	286	GLY
1	C	317	VAL
1	C	354	ILE
1	D	317	VAL
1	F	434	GLY
1	B	354	ILE
1	B	434	GLY
1	C	434	GLY
1	D	434	GLY
1	E	434	GLY
1	G	434	GLY
1	B	295	ILE
1	D	285	VAL
1	E	285	VAL
1	E	479	ARG
1	A	285	VAL
1	C	266	VAL
1	C	285	VAL
1	D	259	PRO
1	D	264	GLY
1	D	295	ILE
1	E	262	PRO
1	F	285	VAL
1	B	285	VAL

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	401/421 (95%)	254 (63%)	147 (37%)	0	1
1	B	401/421 (95%)	264 (66%)	137 (34%)	0	1
1	C	401/421 (95%)	257 (64%)	144 (36%)	0	1
1	D	401/421 (95%)	254 (63%)	147 (37%)	0	1
1	E	401/421 (95%)	257 (64%)	144 (36%)	0	1
1	F	401/421 (95%)	254 (63%)	147 (37%)	0	1
1	G	401/421 (95%)	261 (65%)	140 (35%)	0	1
All	All	2807/2947 (95%)	1801 (64%)	1006 (36%)	0	1

All (1006) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	THR
1	A	68	VAL
1	A	74	SER
1	A	77	ARG
1	A	89	GLU
1	A	93	LYS
1	A	100	LYS
1	A	107	GLN
1	A	108	VAL
1	A	112	ARG
1	A	115	ASN
1	A	117	ASN
1	A	119	VAL
1	A	121	GLN
1	A	122	LYS
1	A	124	ARG
1	A	126	LYS
1	A	127	ASP
1	A	131	LYS
1	A	132	THR

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Mol	Chain	Res	Type
1	A	133	THR
1	A	141	LEU
1	A	144	LYS
1	A	147	TRP
1	A	148	ASN
1	A	153	ILE
1	A	163	LEU
1	A	166	MET
1	A	167	GLU
1	A	168	LEU
1	A	169	GLN
1	A	172	LYS
1	A	175	VAL
1	A	177	SER
1	A	183	SER
1	A	186	LYS
1	A	188	THR
1	A	189	CYS
1	A	194	GLU
1	A	200	GLU
1	A	201	GLN
1	A	204	LEU
1	A	210	GLU
1	A	213	ARG
1	A	214	LYS
1	A	218	GLU
1	A	223	LEU
1	A	228	VAL
1	A	229	ARG
1	A	235	CYS
1	A	237	ASP
1	A	243	LEU
1	A	248	ARG
1	A	249	GLU
1	A	251	MET
1	A	255	TRP
1	A	261	ILE
1	A	265	VAL
1	A	269	LEU
1	A	272	ARG
1	A	274	ARG
1	A	276	ARG

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Mol	Chain	Res	Type
1	A	277	GLU
1	A	281	SER
1	A	282	GLU
1	A	283	GLU
1	A	284	SER
1	A	285	VAL
1	A	287	LEU
1	A	290	SER
1	A	295	ILE
1	A	300	LEU
1	A	309	MET
1	A	316	MET
1	A	317	VAL
1	A	319	SER
1	A	323	ARG
1	A	324	GLN
1	A	327	LEU
1	A	328	GLN
1	A	336	LYS
1	A	341	MET
1	A	347	GLU
1	A	349	THR
1	A	363	ARG
1	A	368	LEU
1	A	369	LYS
1	A	370	ARG
1	A	371	GLU
1	A	388	ASN
1	A	390	THR
1	A	393	LEU
1	A	394	TYR
1	A	395	ASP
1	A	397	PHE
1	A	406	LEU
1	A	409	LEU
1	A	413	ARG
1	A	416	LEU
1	A	418	CYS
1	A	419	ASP
1	A	426	ILE
1	A	430	VAL
1	A	431	SER

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Mol	Chain	Res	Type
1	A	435	GLU
1	A	437	ASP
1	A	438	GLU
1	A	440	LYS
1	A	441	MET
1	A	442	ILE
1	A	446	MET
1	A	454	LYS
1	A	455	SER
1	A	461	VAL
1	A	463	ILE
1	A	464	CYS
1	A	467	LYS
1	A	470	ASP
1	A	471	LYS
1	A	479	ARG
1	A	483	ILE
1	A	484	THR
1	A	485	ASP
1	A	486	LEU
1	A	487	ARG
1	A	489	SER
1	A	492	LEU
1	A	493	ARG
1	A	499	ILE
1	A	502	LEU
1	A	503	GLU
1	A	504	ARG
1	A	506	GLN
1	A	507	GLN
1	A	511	PRO
1	A	514	VAL
1	A	516	VAL
1	A	517	ARG
1	A	520	LYS
1	A	522	ARG
1	A	524	THR
1	A	533	MET
1	A	534	GLU
1	A	536	ASN
1	A	538	GLU
1	A	542	LEU

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Mol	Chain	Res	Type
1	A	548	SER
1	B	65	THR
1	B	68	VAL
1	B	77	ARG
1	B	92	GLN
1	B	100	LYS
1	B	105	MET
1	B	107	GLN
1	B	108	VAL
1	B	112	ARG
1	B	115	ASN
1	B	117	ASN
1	B	119	VAL
1	B	121	GLN
1	B	122	LYS
1	B	124	ARG
1	B	126	LYS
1	B	127	ASP
1	B	131	LYS
1	B	132	THR
1	B	133	THR
1	B	141	LEU
1	B	147	TRP
1	B	148	ASN
1	B	153	ILE
1	B	163	LEU
1	B	166	MET
1	B	167	GLU
1	B	175	VAL
1	B	177	SER
1	B	183	SER
1	B	186	LYS
1	B	188	THR
1	B	189	CYS
1	B	194	GLU
1	B	201	GLN
1	B	210	GLU
1	B	213	ARG
1	B	214	LYS
1	B	218	GLU
1	B	221	GLN
1	B	228	VAL

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Mol	Chain	Res	Type
1	B	229	ARG
1	B	235	CYS
1	B	237	ASP
1	B	243	LEU
1	B	244	ASN
1	B	246	HIS
1	B	248	ARG
1	B	249	GLU
1	B	251	MET
1	B	255	TRP
1	B	256	ASN
1	B	261	ILE
1	B	265	VAL
1	B	269	LEU
1	B	272	ARG
1	B	274	ARG
1	B	276	ARG
1	B	277	GLU
1	B	280	SER
1	B	281	SER
1	B	282	GLU
1	B	287	LEU
1	B	290	SER
1	B	300	LEU
1	B	309	MET
1	B	316	MET
1	B	317	VAL
1	B	319	SER
1	B	324	GLN
1	B	325	GLN
1	B	327	LEU
1	B	328	GLN
1	B	341	MET
1	B	343	GLU
1	B	347	GLU
1	B	349	THR
1	B	363	ARG
1	B	368	LEU
1	B	369	LYS
1	B	370	ARG
1	B	371	GLU
1	B	377	LYS

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Mol	Chain	Res	Type
1	B	388	ASN
1	B	390	THR
1	B	395	ASP
1	B	397	PHE
1	B	406	LEU
1	B	409	LEU
1	B	412	MET
1	B	413	ARG
1	B	416	LEU
1	B	418	CYS
1	B	419	ASP
1	B	426	ILE
1	B	430	VAL
1	B	431	SER
1	B	435	GLU
1	B	437	ASP
1	B	440	LYS
1	B	441	MET
1	B	442	ILE
1	B	446	MET
1	B	450	LYS
1	B	454	LYS
1	B	455	SER
1	B	463	ILE
1	B	464	CYS
1	B	467	LYS
1	B	470	ASP
1	B	471	LYS
1	B	479	ARG
1	B	483	ILE
1	B	484	THR
1	B	485	ASP
1	B	486	LEU
1	B	487	ARG
1	B	492	LEU
1	B	493	ARG
1	B	499	ILE
1	B	502	LEU
1	B	504	ARG
1	B	506	GLN
1	B	507	GLN
1	B	514	VAL

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Mol	Chain	Res	Type
1	B	515	LEU
1	B	516	VAL
1	B	517	ARG
1	B	520	LYS
1	B	522	ARG
1	B	524	THR
1	B	533	MET
1	B	534	GLU
1	B	536	ASN
1	B	542	LEU
1	B	543	GLU
1	B	548	SER
1	C	65	THR
1	C	68	VAL
1	C	77	ARG
1	C	92	GLN
1	C	100	LYS
1	C	105	MET
1	C	107	GLN
1	C	108	VAL
1	C	112	ARG
1	C	115	ASN
1	C	117	ASN
1	C	121	GLN
1	C	122	LYS
1	C	124	ARG
1	C	126	LYS
1	C	127	ASP
1	C	131	LYS
1	C	132	THR
1	C	133	THR
1	C	141	LEU
1	C	147	TRP
1	C	148	ASN
1	C	153	ILE
1	C	163	LEU
1	C	166	MET
1	C	167	GLU
1	C	175	VAL
1	C	177	SER
1	C	183	SER
1	C	186	LYS

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Mol	Chain	Res	Type
1	C	188	THR
1	C	189	CYS
1	C	194	GLU
1	C	201	GLN
1	C	204	LEU
1	C	210	GLU
1	C	213	ARG
1	C	214	LYS
1	C	218	GLU
1	C	221	GLN
1	C	228	VAL
1	C	229	ARG
1	C	235	CYS
1	C	237	ASP
1	C	243	LEU
1	C	246	HIS
1	C	248	ARG
1	C	249	GLU
1	C	251	MET
1	C	255	TRP
1	C	260	TRP
1	C	261	ILE
1	C	265	VAL
1	C	269	LEU
1	C	272	ARG
1	C	274	ARG
1	C	276	ARG
1	C	277	GLU
1	C	281	SER
1	C	282	GLU
1	C	283	GLU
1	C	284	SER
1	C	285	VAL
1	C	287	LEU
1	C	290	SER
1	C	295	ILE
1	C	300	LEU
1	C	309	MET
1	C	316	MET
1	C	319	SER
1	C	323	ARG
1	C	324	GLN

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Mol	Chain	Res	Type
1	C	327	LEU
1	C	336	LYS
1	C	341	MET
1	C	343	GLU
1	C	347	GLU
1	C	349	THR
1	C	363	ARG
1	C	368	LEU
1	C	369	LYS
1	C	370	ARG
1	C	371	GLU
1	C	388	ASN
1	C	393	LEU
1	C	394	TYR
1	C	395	ASP
1	C	397	PHE
1	C	406	LEU
1	C	409	LEU
1	C	413	ARG
1	C	416	LEU
1	C	418	CYS
1	C	419	ASP
1	C	426	ILE
1	C	430	VAL
1	C	431	SER
1	C	435	GLU
1	C	437	ASP
1	C	438	GLU
1	C	440	LYS
1	C	441	MET
1	C	442	ILE
1	C	446	MET
1	C	454	LYS
1	C	455	SER
1	C	461	VAL
1	C	463	ILE
1	C	464	CYS
1	C	467	LYS
1	C	468	ASN
1	C	470	ASP
1	C	471	LYS
1	C	476	GLU

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Mol	Chain	Res	Type
1	C	479	ARG
1	C	483	ILE
1	C	484	THR
1	C	485	ASP
1	C	486	LEU
1	C	487	ARG
1	C	489	SER
1	C	492	LEU
1	C	493	ARG
1	C	495	LEU
1	C	496	SER
1	C	499	ILE
1	C	502	LEU
1	C	504	ARG
1	C	506	GLN
1	C	507	GLN
1	C	514	VAL
1	C	516	VAL
1	C	517	ARG
1	C	520	LYS
1	C	522	ARG
1	C	524	THR
1	C	532	TYR
1	C	533	MET
1	C	534	GLU
1	C	536	ASN
1	C	538	GLU
1	C	542	LEU
1	C	543	GLU
1	C	548	SER
1	D	65	THR
1	D	68	VAL
1	D	71	PHE
1	D	77	ARG
1	D	92	GLN
1	D	100	LYS
1	D	105	MET
1	D	107	GLN
1	D	108	VAL
1	D	112	ARG
1	D	115	ASN
1	D	117	ASN

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Mol	Chain	Res	Type
1	D	119	VAL
1	D	121	GLN
1	D	122	LYS
1	D	124	ARG
1	D	126	LYS
1	D	127	ASP
1	D	131	LYS
1	D	132	THR
1	D	133	THR
1	D	141	LEU
1	D	147	TRP
1	D	148	ASN
1	D	153	ILE
1	D	163	LEU
1	D	166	MET
1	D	167	GLU
1	D	175	VAL
1	D	177	SER
1	D	183	SER
1	D	186	LYS
1	D	188	THR
1	D	189	CYS
1	D	194	GLU
1	D	201	GLN
1	D	204	LEU
1	D	210	GLU
1	D	213	ARG
1	D	214	LYS
1	D	218	GLU
1	D	221	GLN
1	D	223	LEU
1	D	228	VAL
1	D	229	ARG
1	D	235	CYS
1	D	237	ASP
1	D	243	LEU
1	D	246	HIS
1	D	248	ARG
1	D	249	GLU
1	D	251	MET
1	D	255	TRP
1	D	261	ILE

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Mol	Chain	Res	Type
1	D	265	VAL
1	D	269	LEU
1	D	272	ARG
1	D	274	ARG
1	D	276	ARG
1	D	277	GLU
1	D	281	SER
1	D	282	GLU
1	D	283	GLU
1	D	284	SER
1	D	285	VAL
1	D	287	LEU
1	D	290	SER
1	D	300	LEU
1	D	309	MET
1	D	316	MET
1	D	317	VAL
1	D	319	SER
1	D	324	GLN
1	D	327	LEU
1	D	328	GLN
1	D	336	LYS
1	D	341	MET
1	D	347	GLU
1	D	349	THR
1	D	363	ARG
1	D	368	LEU
1	D	369	LYS
1	D	370	ARG
1	D	371	GLU
1	D	377	LYS
1	D	388	ASN
1	D	390	THR
1	D	393	LEU
1	D	394	TYR
1	D	395	ASP
1	D	397	PHE
1	D	406	LEU
1	D	409	LEU
1	D	412	MET
1	D	413	ARG
1	D	416	LEU

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Mol	Chain	Res	Type
1	D	418	CYS
1	D	419	ASP
1	D	426	ILE
1	D	430	VAL
1	D	431	SER
1	D	433	SER
1	D	435	GLU
1	D	437	ASP
1	D	438	GLU
1	D	440	LYS
1	D	441	MET
1	D	442	ILE
1	D	446	MET
1	D	454	LYS
1	D	455	SER
1	D	461	VAL
1	D	463	ILE
1	D	464	CYS
1	D	467	LYS
1	D	470	ASP
1	D	471	LYS
1	D	473	LYS
1	D	476	GLU
1	D	479	ARG
1	D	483	ILE
1	D	484	THR
1	D	485	ASP
1	D	486	LEU
1	D	487	ARG
1	D	489	SER
1	D	492	LEU
1	D	493	ARG
1	D	499	ILE
1	D	502	LEU
1	D	504	ARG
1	D	506	GLN
1	D	507	GLN
1	D	514	VAL
1	D	516	VAL
1	D	517	ARG
1	D	520	LYS
1	D	522	ARG

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Mol	Chain	Res	Type
1	D	524	THR
1	D	532	TYR
1	D	533	MET
1	D	534	GLU
1	D	536	ASN
1	D	538	GLU
1	D	542	LEU
1	D	543	GLU
1	D	548	SER
1	E	65	THR
1	E	68	VAL
1	E	77	ARG
1	E	92	GLN
1	E	100	LYS
1	E	105	MET
1	E	107	GLN
1	E	108	VAL
1	E	112	ARG
1	E	115	ASN
1	E	117	ASN
1	E	121	GLN
1	E	122	LYS
1	E	124	ARG
1	E	126	LYS
1	E	127	ASP
1	E	131	LYS
1	E	132	THR
1	E	133	THR
1	E	141	LEU
1	E	147	TRP
1	E	148	ASN
1	E	153	ILE
1	E	163	LEU
1	E	166	MET
1	E	167	GLU
1	E	175	VAL
1	E	177	SER
1	E	183	SER
1	E	186	LYS
1	E	188	THR
1	E	189	CYS
1	E	194	GLU

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Mol	Chain	Res	Type
1	E	200	GLU
1	E	201	GLN
1	E	210	GLU
1	E	213	ARG
1	E	214	LYS
1	E	218	GLU
1	E	221	GLN
1	E	223	LEU
1	E	228	VAL
1	E	229	ARG
1	E	230	VAL
1	E	235	CYS
1	E	237	ASP
1	E	243	LEU
1	E	246	HIS
1	E	248	ARG
1	E	249	GLU
1	E	251	MET
1	E	255	TRP
1	E	261	ILE
1	E	265	VAL
1	E	269	LEU
1	E	272	ARG
1	E	274	ARG
1	E	276	ARG
1	E	277	GLU
1	E	280	SER
1	E	281	SER
1	E	282	GLU
1	E	283	GLU
1	E	285	VAL
1	E	287	LEU
1	E	290	SER
1	E	295	ILE
1	E	300	LEU
1	E	309	MET
1	E	316	MET
1	E	317	VAL
1	E	319	SER
1	E	324	GLN
1	E	327	LEU
1	E	328	GLN

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Mol	Chain	Res	Type
1	E	336	LYS
1	E	341	MET
1	E	343	GLU
1	E	347	GLU
1	E	349	THR
1	E	363	ARG
1	E	368	LEU
1	E	369	LYS
1	E	370	ARG
1	E	371	GLU
1	E	377	LYS
1	E	388	ASN
1	E	390	THR
1	E	393	LEU
1	E	394	TYR
1	E	395	ASP
1	E	397	PHE
1	E	406	LEU
1	E	409	LEU
1	E	412	MET
1	E	413	ARG
1	E	416	LEU
1	E	418	CYS
1	E	419	ASP
1	E	426	ILE
1	E	430	VAL
1	E	431	SER
1	E	435	GLU
1	E	437	ASP
1	E	438	GLU
1	E	440	LYS
1	E	441	MET
1	E	442	ILE
1	E	446	MET
1	E	454	LYS
1	E	455	SER
1	E	463	ILE
1	E	464	CYS
1	E	467	LYS
1	E	468	ASN
1	E	470	ASP
1	E	471	LYS

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Mol	Chain	Res	Type
1	E	473	LYS
1	E	476	GLU
1	E	479	ARG
1	E	483	ILE
1	E	484	THR
1	E	485	ASP
1	E	486	LEU
1	E	487	ARG
1	E	492	LEU
1	E	493	ARG
1	E	499	ILE
1	E	502	LEU
1	E	504	ARG
1	E	506	GLN
1	E	507	GLN
1	E	514	VAL
1	E	516	VAL
1	E	517	ARG
1	E	520	LYS
1	E	522	ARG
1	E	524	THR
1	E	533	MET
1	E	534	GLU
1	E	536	ASN
1	E	538	GLU
1	E	542	LEU
1	E	548	SER
1	F	65	THR
1	F	68	VAL
1	F	77	ARG
1	F	89	GLU
1	F	92	GLN
1	F	100	LYS
1	F	105	MET
1	F	106	TYR
1	F	107	GLN
1	F	108	VAL
1	F	112	ARG
1	F	115	ASN
1	F	121	GLN
1	F	122	LYS
1	F	124	ARG

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Mol	Chain	Res	Type
1	F	126	LYS
1	F	127	ASP
1	F	131	LYS
1	F	132	THR
1	F	133	THR
1	F	141	LEU
1	F	144	LYS
1	F	147	TRP
1	F	148	ASN
1	F	153	ILE
1	F	163	LEU
1	F	166	MET
1	F	167	GLU
1	F	175	VAL
1	F	177	SER
1	F	183	SER
1	F	186	LYS
1	F	188	THR
1	F	189	CYS
1	F	194	GLU
1	F	201	GLN
1	F	210	GLU
1	F	213	ARG
1	F	214	LYS
1	F	218	GLU
1	F	221	GLN
1	F	228	VAL
1	F	229	ARG
1	F	230	VAL
1	F	235	CYS
1	F	237	ASP
1	F	248	ARG
1	F	249	GLU
1	F	251	MET
1	F	255	TRP
1	F	260	TRP
1	F	261	ILE
1	F	265	VAL
1	F	269	LEU
1	F	272	ARG
1	F	274	ARG
1	F	276	ARG

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Mol	Chain	Res	Type
1	F	277	GLU
1	F	281	SER
1	F	282	GLU
1	F	283	GLU
1	F	284	SER
1	F	285	VAL
1	F	287	LEU
1	F	290	SER
1	F	300	LEU
1	F	309	MET
1	F	312	SER
1	F	314	SER
1	F	316	MET
1	F	317	VAL
1	F	319	SER
1	F	323	ARG
1	F	324	GLN
1	F	327	LEU
1	F	328	GLN
1	F	336	LYS
1	F	341	MET
1	F	347	GLU
1	F	349	THR
1	F	359	ARG
1	F	363	ARG
1	F	368	LEU
1	F	369	LYS
1	F	370	ARG
1	F	371	GLU
1	F	377	LYS
1	F	388	ASN
1	F	390	THR
1	F	393	LEU
1	F	394	TYR
1	F	395	ASP
1	F	397	PHE
1	F	406	LEU
1	F	409	LEU
1	F	412	MET
1	F	413	ARG
1	F	416	LEU
1	F	418	CYS

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Mol	Chain	Res	Type
1	F	419	ASP
1	F	425	HIS
1	F	426	ILE
1	F	430	VAL
1	F	431	SER
1	F	435	GLU
1	F	437	ASP
1	F	438	GLU
1	F	440	LYS
1	F	441	MET
1	F	442	ILE
1	F	446	MET
1	F	455	SER
1	F	463	ILE
1	F	464	CYS
1	F	467	LYS
1	F	470	ASP
1	F	471	LYS
1	F	476	GLU
1	F	479	ARG
1	F	483	ILE
1	F	484	THR
1	F	485	ASP
1	F	486	LEU
1	F	487	ARG
1	F	492	LEU
1	F	493	ARG
1	F	499	ILE
1	F	502	LEU
1	F	503	GLU
1	F	504	ARG
1	F	506	GLN
1	F	507	GLN
1	F	514	VAL
1	F	516	VAL
1	F	517	ARG
1	F	520	LYS
1	F	522	ARG
1	F	524	THR
1	F	532	TYR
1	F	533	MET
1	F	534	GLU

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Mol	Chain	Res	Type
1	F	536	ASN
1	F	538	GLU
1	F	542	LEU
1	F	543	GLU
1	F	547	TYR
1	F	548	SER
1	G	65	THR
1	G	68	VAL
1	G	77	ARG
1	G	92	GLN
1	G	100	LYS
1	G	105	MET
1	G	107	GLN
1	G	108	VAL
1	G	112	ARG
1	G	115	ASN
1	G	117	ASN
1	G	119	VAL
1	G	121	GLN
1	G	122	LYS
1	G	124	ARG
1	G	126	LYS
1	G	127	ASP
1	G	131	LYS
1	G	132	THR
1	G	133	THR
1	G	141	LEU
1	G	147	TRP
1	G	148	ASN
1	G	153	ILE
1	G	163	LEU
1	G	166	MET
1	G	167	GLU
1	G	175	VAL
1	G	177	SER
1	G	183	SER
1	G	186	LYS
1	G	188	THR
1	G	189	CYS
1	G	194	GLU
1	G	200	GLU
1	G	201	GLN

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Mol	Chain	Res	Type
1	G	210	GLU
1	G	213	ARG
1	G	214	LYS
1	G	218	GLU
1	G	221	GLN
1	G	228	VAL
1	G	229	ARG
1	G	235	CYS
1	G	237	ASP
1	G	243	LEU
1	G	246	HIS
1	G	248	ARG
1	G	249	GLU
1	G	251	MET
1	G	255	TRP
1	G	260	TRP
1	G	265	VAL
1	G	269	LEU
1	G	272	ARG
1	G	274	ARG
1	G	276	ARG
1	G	277	GLU
1	G	281	SER
1	G	282	GLU
1	G	283	GLU
1	G	284	SER
1	G	285	VAL
1	G	287	LEU
1	G	290	SER
1	G	300	LEU
1	G	309	MET
1	G	316	MET
1	G	317	VAL
1	G	319	SER
1	G	323	ARG
1	G	324	GLN
1	G	327	LEU
1	G	328	GLN
1	G	336	LYS
1	G	341	MET
1	G	343	GLU
1	G	347	GLU

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Mol	Chain	Res	Type
1	G	349	THR
1	G	363	ARG
1	G	368	LEU
1	G	369	LYS
1	G	370	ARG
1	G	371	GLU
1	G	377	LYS
1	G	388	ASN
1	G	390	THR
1	G	393	LEU
1	G	394	TYR
1	G	395	ASP
1	G	397	PHE
1	G	406	LEU
1	G	409	LEU
1	G	413	ARG
1	G	416	LEU
1	G	418	CYS
1	G	419	ASP
1	G	425	HIS
1	G	426	ILE
1	G	430	VAL
1	G	431	SER
1	G	435	GLU
1	G	437	ASP
1	G	438	GLU
1	G	440	LYS
1	G	441	MET
1	G	442	ILE
1	G	446	MET
1	G	454	LYS
1	G	455	SER
1	G	461	VAL
1	G	463	ILE
1	G	467	LYS
1	G	470	ASP
1	G	471	LYS
1	G	479	ARG
1	G	483	ILE
1	G	484	THR
1	G	485	ASP
1	G	486	LEU

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Mol	Chain	Res	Type
1	G	487	ARG
1	G	492	LEU
1	G	493	ARG
1	G	499	ILE
1	G	502	LEU
1	G	504	ARG
1	G	506	GLN
1	G	507	GLN
1	G	514	VAL
1	G	516	VAL
1	G	517	ARG
1	G	520	LYS
1	G	522	ARG
1	G	524	THR
1	G	533	MET
1	G	536	ASN
1	G	538	GLU
1	G	542	LEU
1	G	543	GLU
1	G	548	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (146) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	ASN
1	A	107	GLN
1	A	114	GLN
1	A	117	ASN
1	A	145	HIS
1	A	148	ASN
1	A	169	GLN
1	A	180	HIS
1	A	244	ASN
1	A	278	HIS
1	A	296	ASN
1	A	324	GLN
1	A	325	GLN
1	A	358	ASN
1	A	380	GLN
1	A	425	HIS
1	A	475	HIS
1	A	507	GLN

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Mol	Chain	Res	Type
1	A	536	ASN
1	B	70	ASN
1	B	92	GLN
1	B	107	GLN
1	B	114	GLN
1	B	117	ASN
1	B	145	HIS
1	B	148	ASN
1	B	180	HIS
1	B	201	GLN
1	B	244	ASN
1	B	278	HIS
1	B	296	ASN
1	B	324	GLN
1	B	325	GLN
1	B	358	ASN
1	B	380	GLN
1	B	425	HIS
1	B	475	HIS
1	B	505	ASN
1	B	507	GLN
1	B	536	ASN
1	C	70	ASN
1	C	75	ASN
1	C	92	GLN
1	C	107	GLN
1	C	114	GLN
1	C	117	ASN
1	C	145	HIS
1	C	180	HIS
1	C	198	GLN
1	C	201	GLN
1	C	244	ASN
1	C	256	ASN
1	C	278	HIS
1	C	296	ASN
1	C	324	GLN
1	C	325	GLN
1	C	358	ASN
1	C	380	GLN
1	C	425	HIS
1	C	475	HIS

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Mol	Chain	Res	Type
1	C	507	GLN
1	C	536	ASN
1	D	70	ASN
1	D	75	ASN
1	D	107	GLN
1	D	114	GLN
1	D	117	ASN
1	D	145	HIS
1	D	180	HIS
1	D	198	GLN
1	D	244	ASN
1	D	278	HIS
1	D	296	ASN
1	D	324	GLN
1	D	325	GLN
1	D	358	ASN
1	D	380	GLN
1	D	425	HIS
1	D	475	HIS
1	D	505	ASN
1	D	507	GLN
1	D	512	ASN
1	D	536	ASN
1	E	70	ASN
1	E	92	GLN
1	E	107	GLN
1	E	114	GLN
1	E	117	ASN
1	E	145	HIS
1	E	148	ASN
1	E	180	HIS
1	E	201	GLN
1	E	244	ASN
1	E	278	HIS
1	E	296	ASN
1	E	325	GLN
1	E	358	ASN
1	E	380	GLN
1	E	425	HIS
1	E	465	HIS
1	E	475	HIS
1	E	505	ASN

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Mol	Chain	Res	Type
1	E	507	GLN
1	E	536	ASN
1	F	70	ASN
1	F	75	ASN
1	F	92	GLN
1	F	107	GLN
1	F	114	GLN
1	F	145	HIS
1	F	148	ASN
1	F	180	HIS
1	F	201	GLN
1	F	244	ASN
1	F	278	HIS
1	F	296	ASN
1	F	324	GLN
1	F	325	GLN
1	F	358	ASN
1	F	380	GLN
1	F	425	HIS
1	F	475	HIS
1	F	505	ASN
1	F	507	GLN
1	F	536	ASN
1	G	70	ASN
1	G	75	ASN
1	G	92	GLN
1	G	107	GLN
1	G	114	GLN
1	G	117	ASN
1	G	145	HIS
1	G	148	ASN
1	G	180	HIS
1	G	201	GLN
1	G	244	ASN
1	G	278	HIS
1	G	296	ASN
1	G	324	GLN
1	G	325	GLN
1	G	358	ASN
1	G	380	GLN
1	G	425	HIS
1	G	475	HIS

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Mol	Chain	Res	Type
1	G	507	GLN
1	G	536	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	483/503 (96%)	1.11	99 (20%) 1 1	59, 136, 136, 136	0
1	B	483/503 (96%)	1.85	156 (32%) 0 0	94, 94, 178, 178	0
1	C	483/503 (96%)	1.58	149 (30%) 0 0	120, 120, 178, 178	0
1	D	483/503 (96%)	1.74	165 (34%) 0 0	132, 132, 178, 178	0
1	E	483/503 (96%)	2.69	190 (39%) 0 0	115, 115, 178, 178	0
1	F	483/503 (96%)	1.41	122 (25%) 0 0	103, 164, 164, 164	0
1	G	483/503 (96%)	2.13	169 (34%) 0 0	129, 129, 178, 178	0
All	All	3381/3521 (96%)	1.79	1050 (31%) 0 0	59, 132, 178, 178	0

All (1050) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	136	HIS	32.1
1	G	109	ALA	30.4
1	E	65	THR	25.2
1	G	157	GLU	22.2
1	E	181	GLY	21.0
1	E	433	SER	19.8
1	E	69	TRP	19.6
1	E	201	GLN	16.5
1	E	111	TYR	16.1
1	E	205	MET	15.0
1	G	64	MET	14.7
1	B	433	SER	14.5
1	E	174	PRO	14.4
1	F	317	VAL	14.4
1	A	432	ALA	14.1
1	E	157	GLU	13.7
1	F	432	ALA	13.6

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Mol	Chain	Res	Type	RSRZ
1	E	244	ASN	13.4
1	F	509	ASP	12.7
1	G	188	THR	12.7
1	G	185	ALA	12.5
1	E	156	THR	12.4
1	D	153	ILE	12.3
1	A	431	SER	12.1
1	G	84	ARG	12.0
1	A	433	SER	12.0
1	G	65	THR	11.9
1	D	67	ASN	11.7
1	D	436	SER	11.6
1	E	238	ALA	11.6
1	E	171	CYS	11.4
1	E	185	ALA	11.4
1	B	130	PHE	11.4
1	D	106	TYR	11.3
1	B	202	ILE	11.2
1	E	66	TYR	11.2
1	B	250	ILE	11.1
1	E	132	THR	11.1
1	B	105	MET	11.1
1	E	189	CYS	11.1
1	E	202	ILE	11.0
1	E	207	ASP	11.0
1	G	122	LYS	10.9
1	G	96	TYR	10.8
1	E	138	SER	10.7
1	E	153	ILE	10.7
1	B	188	THR	10.7
1	E	106	TYR	10.6
1	B	164	THR	10.5
1	D	189	CYS	10.4
1	B	94	ALA	10.3
1	D	104	VAL	10.1
1	C	260	TRP	10.1
1	G	85	GLY	9.9
1	E	105	MET	9.7
1	E	209	ASP	9.6
1	E	137	LYS	9.6
1	E	142	PHE	9.6
1	E	195	TYR	9.5

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Mol	Chain	Res	Type	RSRZ
1	G	226	GLY	9.5
1	D	224	PRO	9.5
1	E	245	GLY	9.4
1	C	225	ALA	9.3
1	E	206	PHE	9.3
1	G	225	ALA	9.2
1	E	233	LEU	9.2
1	G	94	ALA	9.2
1	B	254	VAL	9.2
1	E	102	ASP	9.1
1	G	105	MET	9.1
1	B	251	MET	9.1
1	B	201	GLN	9.1
1	F	314	SER	9.0
1	E	180	HIS	9.0
1	E	64	MET	8.9
1	G	141	LEU	8.9
1	G	110	ASP	8.9
1	E	432	ALA	8.8
1	G	239	ASN	8.8
1	D	123	VAL	8.8
1	E	94	ALA	8.7
1	G	231	ALA	8.7
1	G	189	CYS	8.7
1	F	433	SER	8.7
1	G	135	SER	8.7
1	G	104	VAL	8.6
1	E	125	ASP	8.6
1	G	206	PHE	8.5
1	G	120	SER	8.5
1	E	196	PHE	8.5
1	D	223	LEU	8.4
1	E	99	ALA	8.4
1	E	129	ASN	8.4
1	E	254	VAL	8.4
1	D	131	LYS	8.4
1	C	234	PRO	8.4
1	E	109	ALA	8.3
1	B	79	SER	8.3
1	G	265	VAL	8.3
1	G	488	GLY	8.2
1	E	100	LYS	8.2

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Mol	Chain	Res	Type	RSRZ
1	E	75	ASN	8.2
1	A	434	GLY	8.2
1	B	69	TRP	8.1
1	G	232	VAL	8.1
1	E	84	ARG	8.1
1	E	217	GLU	8.1
1	G	115	ASN	8.0
1	E	231	ALA	8.0
1	F	492	LEU	7.9
1	C	196	PHE	7.9
1	B	132	THR	7.9
1	F	435	GLU	7.9
1	C	139	ASP	7.8
1	A	426	ILE	7.8
1	D	68	VAL	7.7
1	G	140	ALA	7.7
1	E	243	LEU	7.7
1	D	226	GLY	7.6
1	E	103	GLY	7.6
1	C	83	ALA	7.6
1	G	268	ALA	7.5
1	E	239	ASN	7.5
1	C	65	THR	7.5
1	B	138	SER	7.4
1	E	250	ILE	7.4
1	E	184	ALA	7.4
1	F	313	GLY	7.3
1	B	432	ALA	7.3
1	D	127	ASP	7.3
1	C	201	GLN	7.3
1	F	475	HIS	7.3
1	G	69	TRP	7.2
1	G	107	GLN	7.2
1	G	79	SER	7.2
1	D	466	LEU	7.1
1	E	126	LYS	7.1
1	G	487	ARG	7.1
1	G	91	CYS	7.1
1	D	65	THR	7.1
1	B	131	LYS	7.1
1	G	152	LYS	7.1
1	E	122	LYS	7.0

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Mol	Chain	Res	Type	RSRZ
1	D	96	TYR	7.0
1	B	203	ILE	7.0
1	D	173	TYR	7.0
1	B	64	MET	7.0
1	B	116	GLY	7.0
1	C	200	GLU	6.8
1	D	438	GLU	6.8
1	C	163	LEU	6.8
1	D	138	SER	6.8
1	B	83	ALA	6.8
1	D	145	HIS	6.7
1	E	216	VAL	6.7
1	B	86	ILE	6.7
1	G	161	ASP	6.7
1	B	152	LYS	6.7
1	C	97	TRP	6.7
1	B	165	VAL	6.6
1	B	154	VAL	6.6
1	F	512	ASN	6.6
1	B	204	LEU	6.5
1	C	153	ILE	6.5
1	D	148	ASN	6.5
1	B	153	ILE	6.5
1	G	250	ILE	6.5
1	B	115	ASN	6.5
1	E	234	PRO	6.4
1	E	173	TYR	6.4
1	F	510	MET	6.4
1	E	251	MET	6.4
1	E	108	VAL	6.4
1	D	201	GLN	6.3
1	B	84	ARG	6.2
1	E	130	PHE	6.2
1	C	169	GLN	6.2
1	C	69	TRP	6.2
1	B	65	THR	6.2
1	E	96	TYR	6.2
1	G	259	PRO	6.1
1	G	433	SER	6.1
1	B	122	LYS	6.1
1	E	110	ASP	6.1
1	B	125	ASP	6.0

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Mol	Chain	Res	Type	RSRZ
1	C	223	LEU	6.0
1	C	224	PRO	6.0
1	C	123	VAL	6.0
1	B	139	ASP	6.0
1	C	140	ALA	6.0
1	E	152	LYS	6.0
1	F	477	GLU	5.9
1	E	188	THR	5.9
1	E	186	LYS	5.9
1	G	184	ALA	5.9
1	D	101	VAL	5.9
1	C	204	LEU	5.9
1	D	114	GLN	5.9
1	C	137	LYS	5.9
1	D	174	PRO	5.8
1	D	175	VAL	5.8
1	D	488	GLY	5.8
1	F	285	VAL	5.7
1	F	513	LEU	5.7
1	B	221	GLN	5.7
1	B	189	CYS	5.7
1	G	158	GLY	5.7
1	D	151	LYS	5.7
1	G	89	GLU	5.7
1	B	136	HIS	5.7
1	F	436	SER	5.7
1	F	530	ALA	5.6
1	E	97	TRP	5.6
1	C	180	HIS	5.6
1	G	196	PHE	5.6
1	E	203	ILE	5.6
1	E	434	GLY	5.6
1	B	434	GLY	5.6
1	B	397	PHE	5.5
1	C	252	GLU	5.5
1	G	87	SER	5.5
1	D	98	ILE	5.5
1	B	244	ASN	5.5
1	C	231	ALA	5.5
1	B	255	TRP	5.5
1	F	529	ILE	5.5
1	C	135	SER	5.5

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Mol	Chain	Res	Type	RSRZ
1	E	90	THR	5.4
1	C	151	LYS	5.4
1	F	434	GLY	5.4
1	G	156	THR	5.4
1	D	435	GLU	5.4
1	C	397	PHE	5.4
1	G	119	VAL	5.4
1	G	116	GLY	5.4
1	B	88	LYS	5.3
1	E	81	LEU	5.3
1	G	136	HIS	5.3
1	E	135	SER	5.3
1	D	472	GLY	5.3
1	D	140	ALA	5.3
1	B	155	VAL	5.3
1	G	178	LEU	5.3
1	F	378	PHE	5.2
1	F	406	LEU	5.2
1	E	78	TYR	5.2
1	E	121	GLN	5.2
1	F	431	SER	5.2
1	G	108	VAL	5.2
1	E	120	SER	5.2
1	A	295	ILE	5.2
1	C	203	ILE	5.2
1	E	128	LYS	5.1
1	E	155	VAL	5.1
1	B	223	LEU	5.1
1	C	159	GLU	5.1
1	E	127	ASP	5.1
1	G	132	THR	5.1
1	B	66	TYR	5.1
1	C	108	VAL	5.1
1	D	135	SER	5.1
1	B	106	TYR	5.1
1	E	220	ALA	5.1
1	F	321	PHE	5.1
1	C	152	LYS	5.1
1	C	519	LEU	5.1
1	G	82	THR	5.0
1	D	111	TYR	5.0
1	B	121	GLN	5.0

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Mol	Chain	Res	Type	RSRZ
1	B	190	ALA	5.0
1	B	126	LYS	5.0
1	D	112	ARG	5.0
1	G	160	ILE	5.0
1	F	478	GLY	5.0
1	A	64	MET	5.0
1	G	83	ALA	5.0
1	F	100	LYS	5.0
1	E	82	THR	5.0
1	C	189	CYS	5.0
1	G	234	PRO	5.0
1	C	244	ASN	5.0
1	A	238	ALA	5.0
1	D	154	VAL	5.0
1	E	170	ASP	5.0
1	F	300	LEU	5.0
1	G	168	LEU	5.0
1	G	202	ILE	4.9
1	G	472	GLY	4.9
1	E	114	GLN	4.9
1	B	142	PHE	4.9
1	B	112	ARG	4.9
1	F	105	MET	4.9
1	G	95	GLY	4.9
1	F	96	TYR	4.9
1	E	154	VAL	4.9
1	D	265	VAL	4.9
1	E	68	VAL	4.9
1	G	171	CYS	4.9
1	E	101	VAL	4.8
1	G	90	THR	4.8
1	E	86	ILE	4.8
1	A	205	MET	4.8
1	B	85	GLY	4.8
1	D	110	ASP	4.7
1	D	179	GLY	4.7
1	B	257	ALA	4.7
1	E	438	GLU	4.7
1	F	284	SER	4.7
1	F	426	ILE	4.7
1	G	289	PHE	4.7
1	E	215	ALA	4.7

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Mol	Chain	Res	Type	RSRZ
1	C	154	VAL	4.7
1	D	128	LYS	4.7
1	E	481	VAL	4.7
1	G	139	ASP	4.7
1	D	253	GLN	4.7
1	C	472	GLY	4.7
1	G	207	ASP	4.6
1	D	97	TRP	4.6
1	C	101	VAL	4.6
1	B	97	TRP	4.6
1	D	152	LYS	4.6
1	C	158	GLY	4.6
1	E	228	VAL	4.6
1	D	66	TYR	4.6
1	C	393	LEU	4.6
1	C	210	GLU	4.6
1	D	108	VAL	4.6
1	D	209	ASP	4.6
1	E	168	LEU	4.6
1	G	159	GLU	4.5
1	D	426	ILE	4.5
1	A	535	TYR	4.5
1	B	230	VAL	4.5
1	G	502	LEU	4.5
1	A	549	GLY	4.5
1	D	549	GLY	4.5
1	G	154	VAL	4.5
1	C	253	GLN	4.5
1	D	130	PHE	4.5
1	F	549	GLY	4.5
1	G	251	MET	4.5
1	D	64	MET	4.5
1	D	225	ALA	4.5
1	G	258	GLY	4.5
1	A	309	MET	4.5
1	A	423	LEU	4.5
1	E	241	CYS	4.5
1	D	516	VAL	4.4
1	B	104	VAL	4.4
1	C	460	LEU	4.4
1	B	171	CYS	4.4
1	D	210	GLU	4.4

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Mol	Chain	Res	Type	RSRZ
1	B	253	GLN	4.4
1	D	146	LEU	4.4
1	G	121	GLN	4.4
1	B	89	GLU	4.4
1	G	148	ASN	4.4
1	E	67	ASN	4.4
1	C	394	TYR	4.4
1	A	170	ASP	4.4
1	D	109	ALA	4.4
1	D	515	LEU	4.4
1	C	435	GLU	4.4
1	E	112	ARG	4.3
1	B	96	TYR	4.3
1	G	169	GLN	4.3
1	C	130	PHE	4.3
1	E	148	ASN	4.3
1	A	523	PHE	4.3
1	E	107	GLN	4.3
1	E	149	GLY	4.3
1	G	127	ASP	4.3
1	C	426	ILE	4.3
1	B	156	THR	4.3
1	C	235	CYS	4.3
1	B	502	LEU	4.3
1	G	475	HIS	4.3
1	C	132	THR	4.2
1	E	473	LYS	4.2
1	F	316	MET	4.2
1	G	103	GLY	4.2
1	B	124	ARG	4.2
1	D	266	VAL	4.2
1	G	170	ASP	4.2
1	B	111	TYR	4.2
1	B	123	VAL	4.2
1	A	260	TRP	4.2
1	F	394	TYR	4.2
1	A	542	LEU	4.2
1	D	208	MET	4.2
1	C	202	ILE	4.2
1	C	431	SER	4.2
1	G	426	ILE	4.2
1	C	73	GLU	4.1

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Mol	Chain	Res	Type	RSRZ
1	D	171	CYS	4.1
1	C	94	ALA	4.1
1	B	163	LEU	4.1
1	E	255	TRP	4.1
1	E	442	ILE	4.1
1	F	519	LEU	4.1
1	G	187	LYS	4.1
1	F	386	PHE	4.1
1	D	190	ALA	4.1
1	C	289	PHE	4.1
1	G	438	GLU	4.1
1	E	83	ALA	4.0
1	G	66	TYR	4.0
1	F	178	LEU	4.0
1	G	204	LEU	4.0
1	E	310	VAL	4.0
1	G	86	ILE	4.0
1	D	180	HIS	4.0
1	E	204	LEU	4.0
1	G	130	PHE	4.0
1	G	155	VAL	4.0
1	E	175	VAL	4.0
1	F	104	VAL	4.0
1	E	402	THR	4.0
1	G	489	SER	4.0
1	F	508	GLY	3.9
1	E	253	GLN	3.9
1	C	537	LYS	3.9
1	C	114	GLN	3.9
1	C	131	LYS	3.9
1	E	246	HIS	3.9
1	B	178	LEU	3.9
1	B	368	LEU	3.9
1	G	215	ALA	3.9
1	C	129	ASN	3.9
1	F	488	GLY	3.9
1	G	114	GLN	3.9
1	C	74	SER	3.9
1	E	232	VAL	3.9
1	B	205	MET	3.9
1	C	98	ILE	3.9
1	D	252	GLU	3.9

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Mol	Chain	Res	Type	RSRZ
1	B	423	LEU	3.9
1	F	409	LEU	3.9
1	G	481	VAL	3.9
1	C	438	GLU	3.8
1	C	338	GLY	3.8
1	D	100	LYS	3.8
1	E	176	VAL	3.8
1	D	284	SER	3.8
1	F	533	MET	3.8
1	A	206	PHE	3.8
1	E	247	ASP	3.8
1	E	463	ILE	3.8
1	A	165	VAL	3.8
1	A	302	ALA	3.8
1	B	211	ALA	3.8
1	C	115	ASN	3.8
1	E	208	MET	3.8
1	G	197	ASP	3.8
1	F	449	LEU	3.8
1	B	175	VAL	3.8
1	C	259	PRO	3.8
1	E	179	GLY	3.8
1	B	67	ASN	3.8
1	F	341	MET	3.8
1	G	233	LEU	3.8
1	E	210	GLU	3.8
1	C	500	ILE	3.8
1	A	291	GLY	3.7
1	E	172	LYS	3.7
1	B	191	ALA	3.7
1	F	474	ALA	3.7
1	G	271	LEU	3.7
1	E	235	CYS	3.7
1	C	243	LEU	3.7
1	C	402	THR	3.7
1	C	436	SER	3.7
1	C	329	TRP	3.7
1	E	182	ALA	3.7
1	A	289	PHE	3.7
1	G	260	TRP	3.7
1	F	318	MET	3.7
1	B	78	TYR	3.7

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Mol	Chain	Res	Type	RSRZ
1	G	203	ILE	3.7
1	E	200	GLU	3.7
1	B	236	LYS	3.7
1	A	438	GLU	3.7
1	D	467	LYS	3.7
1	G	227	LYS	3.7
1	F	275	ILE	3.7
1	F	500	ILE	3.7
1	B	486	LEU	3.7
1	C	339	LEU	3.7
1	A	394	TYR	3.7
1	C	145	HIS	3.6
1	F	342	LEU	3.6
1	F	460	LEU	3.6
1	B	109	ALA	3.6
1	B	532	TYR	3.6
1	G	144	LYS	3.6
1	G	208	MET	3.6
1	D	533	MET	3.6
1	G	134	GLY	3.6
1	D	193	TYR	3.6
1	E	287	LEU	3.6
1	C	230	VAL	3.6
1	D	232	VAL	3.6
1	D	510	MET	3.6
1	F	502	LEU	3.6
1	D	85	GLY	3.5
1	E	242	HIS	3.5
1	B	68	VAL	3.5
1	C	160	ILE	3.5
1	D	129	ASN	3.5
1	G	129	ASN	3.5
1	D	310	VAL	3.5
1	C	116	GLY	3.5
1	B	206	PHE	3.5
1	B	435	GLU	3.5
1	D	95	GLY	3.5
1	E	285	VAL	3.5
1	G	266	VAL	3.5
1	C	535	TYR	3.5
1	A	476	GLU	3.5
1	B	113	ASP	3.5

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Mol	Chain	Res	Type	RSRZ
1	E	213	ARG	3.5
1	B	533	MET	3.5
1	D	271	LEU	3.5
1	B	110	ASP	3.5
1	C	99	ALA	3.5
1	C	321	PHE	3.5
1	D	136	HIS	3.5
1	A	469	PRO	3.5
1	G	532	TYR	3.5
1	E	409	LEU	3.4
1	D	91	CYS	3.4
1	A	362	LEU	3.4
1	D	122	LYS	3.4
1	D	430	VAL	3.4
1	B	95	GLY	3.4
1	B	321	PHE	3.4
1	G	241	CYS	3.4
1	F	516	VAL	3.4
1	A	533	MET	3.4
1	A	172	LYS	3.4
1	C	84	ARG	3.4
1	G	190	ALA	3.4
1	A	385	LEU	3.4
1	E	80	ALA	3.4
1	E	104	VAL	3.4
1	D	378	PHE	3.4
1	B	192	ASN	3.4
1	G	217	GLU	3.4
1	C	340	ALA	3.4
1	E	549	GLY	3.4
1	C	168	LEU	3.4
1	E	289	PHE	3.4
1	F	391	PHE	3.4
1	A	265	VAL	3.4
1	A	416	LEU	3.4
1	E	141	LEU	3.4
1	F	101	VAL	3.4
1	F	405	LEU	3.3
1	C	219	ALA	3.3
1	B	127	ASP	3.3
1	G	172	LYS	3.3
1	C	104	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
1	F	382	PHE	3.3
1	E	535	TYR	3.3
1	D	487	ARG	3.3
1	F	532	TYR	3.3
1	D	139	ASP	3.3
1	F	315	GLY	3.3
1	B	471	LYS	3.3
1	D	329	TRP	3.3
1	B	82	THR	3.3
1	B	542	LEU	3.3
1	F	461	VAL	3.3
1	D	442	ILE	3.3
1	D	471	LYS	3.3
1	G	275	ILE	3.3
1	G	117	ASN	3.3
1	A	196	PHE	3.3
1	C	165	VAL	3.3
1	A	470	ASP	3.3
1	E	308	ILE	3.3
1	A	321	PHE	3.3
1	G	138	SER	3.2
1	E	362	LEU	3.2
1	A	346	VAL	3.2
1	B	285	VAL	3.2
1	B	378	PHE	3.2
1	D	285	VAL	3.2
1	E	77	ARG	3.2
1	B	120	SER	3.2
1	C	368	LEU	3.2
1	D	156	THR	3.2
1	D	121	GLN	3.2
1	D	126	LYS	3.2
1	A	69	TRP	3.2
1	A	173	TYR	3.2
1	D	500	ILE	3.2
1	E	223	LEU	3.2
1	C	209	ASP	3.2
1	F	289	PHE	3.2
1	C	195	TYR	3.2
1	D	423	LEU	3.2
1	D	529	ILE	3.2
1	B	487	ARG	3.2

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Mol	Chain	Res	Type	RSRZ
1	E	466	LEU	3.1
1	B	167	GLU	3.1
1	A	475	HIS	3.1
1	B	247	ASP	3.1
1	C	362	LEU	3.1
1	E	74	SER	3.1
1	D	502	LEU	3.1
1	E	237	ASP	3.1
1	D	69	TRP	3.1
1	E	192	ASN	3.1
1	C	258	GLY	3.1
1	D	103	GLY	3.1
1	B	107	GLN	3.1
1	G	500	ILE	3.1
1	C	307	VAL	3.1
1	E	113	ASP	3.1
1	F	489	SER	3.1
1	A	94	ALA	3.1
1	C	220	ALA	3.1
1	A	178	LEU	3.1
1	D	463	ILE	3.1
1	D	137	LYS	3.1
1	C	155	VAL	3.1
1	G	216	VAL	3.1
1	C	87	SER	3.1
1	D	197	ASP	3.1
1	D	468	ASN	3.1
1	G	186	LYS	3.1
1	A	127	ASP	3.0
1	E	256	ASN	3.0
1	D	517	ARG	3.0
1	D	246	HIS	3.0
1	F	157	GLU	3.0
1	G	219	ALA	3.0
1	G	501	ALA	3.0
1	B	500	ILE	3.0
1	D	518	ILE	3.0
1	F	337	VAL	3.0
1	G	165	VAL	3.0
1	G	285	VAL	3.0
1	G	167	GLU	3.0
1	G	245	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	386	PHE	3.0
1	D	78	TYR	3.0
1	G	254	VAL	3.0
1	B	284	SER	3.0
1	G	535	TYR	3.0
1	C	133	THR	3.0
1	F	454	LYS	3.0
1	D	501	ALA	3.0
1	G	211	ALA	3.0
1	D	176	VAL	3.0
1	B	239	ASN	3.0
1	E	115	ASN	3.0
1	B	146	LEU	3.0
1	F	397	PHE	3.0
1	G	402	THR	3.0
1	E	343	GLU	3.0
1	D	107	GLN	2.9
1	D	439	ARG	2.9
1	E	163	LEU	2.9
1	C	337	VAL	2.9
1	C	171	CYS	2.9
1	G	249	GLU	2.9
1	C	117	ASN	2.9
1	C	353	LEU	2.9
1	C	423	LEU	2.9
1	C	342	LEU	2.9
1	E	211	ALA	2.9
1	F	99	ALA	2.9
1	D	289	PHE	2.9
1	G	486	LEU	2.9
1	B	238	ALA	2.9
1	E	177	SER	2.9
1	D	416	LEU	2.9
1	F	339	LEU	2.9
1	G	288	LEU	2.9
1	D	484	THR	2.9
1	D	291	GLY	2.9
1	C	308	ILE	2.9
1	G	102	ASP	2.9
1	G	224	PRO	2.9
1	C	233	LEU	2.9
1	D	178	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	295	ILE	2.9
1	B	99	ALA	2.9
1	F	238	ALA	2.9
1	D	249	GLU	2.9
1	G	179	GLY	2.9
1	F	310	VAL	2.9
1	F	393	LEU	2.9
1	D	142	PHE	2.9
1	G	218	GLU	2.9
1	A	519	LEU	2.9
1	A	452	PHE	2.8
1	F	539	THR	2.8
1	D	250	ILE	2.8
1	A	252	GLU	2.8
1	E	70	ASN	2.8
1	D	513	LEU	2.8
1	F	131	LYS	2.8
1	F	156	THR	2.8
1	D	481	VAL	2.8
1	E	405	LEU	2.8
1	G	68	VAL	2.8
1	G	180	HIS	2.8
1	B	81	LEU	2.8
1	E	260	TRP	2.8
1	E	391	PHE	2.8
1	C	112	ARG	2.8
1	F	466	LEU	2.8
1	E	139	ASP	2.8
1	G	295	ILE	2.8
1	E	500	ILE	2.8
1	E	460	LEU	2.8
1	A	96	TYR	2.8
1	G	111	TYR	2.8
1	D	244	ASN	2.8
1	G	243	LEU	2.8
1	G	118	ILE	2.7
1	E	226	GLY	2.7
1	A	86	ILE	2.7
1	B	129	ASN	2.7
1	B	256	ASN	2.7
1	D	311	THR	2.7
1	B	207	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	542	LEU	2.7
1	D	141	LEU	2.7
1	D	393	LEU	2.7
1	A	179	GLY	2.7
1	B	196	PHE	2.7
1	B	220	ALA	2.7
1	D	105	MET	2.7
1	E	492	LEU	2.7
1	B	354	ILE	2.7
1	A	472	GLY	2.7
1	D	397	PHE	2.7
1	C	462	VAL	2.7
1	A	107	GLN	2.7
1	F	196	PHE	2.7
1	D	308	ILE	2.7
1	B	186	LYS	2.7
1	D	233	LEU	2.7
1	E	309	MET	2.7
1	G	88	LYS	2.7
1	G	164	THR	2.7
1	B	357	HIS	2.7
1	D	220	ALA	2.7
1	G	147	TRP	2.7
1	G	228	VAL	2.7
1	C	206	PHE	2.6
1	G	205	MET	2.6
1	B	535	TYR	2.6
1	C	184	ALA	2.6
1	A	142	PHE	2.6
1	B	512	ASN	2.6
1	E	502	LEU	2.6
1	E	131	LYS	2.6
1	E	512	ASN	2.6
1	A	308	ILE	2.6
1	F	308	ILE	2.6
1	E	480	PRO	2.6
1	F	452	PHE	2.6
1	A	503	GLU	2.6
1	F	496	SER	2.6
1	B	209	ASP	2.6
1	F	107	GLN	2.6
1	A	502	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	203	ILE	2.6
1	D	248	ARG	2.6
1	F	64	MET	2.6
1	D	287	LEU	2.6
1	D	219	ALA	2.6
1	C	514	VAL	2.6
1	D	322	VAL	2.6
1	F	279	LEU	2.6
1	B	461	VAL	2.6
1	D	514	VAL	2.6
1	D	118	ILE	2.6
1	B	140	ALA	2.6
1	D	321	PHE	2.6
1	G	73	GLU	2.6
1	F	254	VAL	2.6
1	A	311	THR	2.6
1	B	416	LEU	2.6
1	G	163	LEU	2.6
1	D	386	PHE	2.5
1	D	172	LYS	2.5
1	G	173	TYR	2.5
1	C	141	LEU	2.5
1	A	148	ASN	2.5
1	A	422	ILE	2.5
1	F	463	ILE	2.5
1	C	86	ILE	2.5
1	F	507	GLN	2.5
1	A	254	VAL	2.5
1	B	481	VAL	2.5
1	A	449	LEU	2.5
1	F	168	LEU	2.5
1	A	548	SER	2.5
1	C	529	ILE	2.5
1	E	87	SER	2.5
1	F	138	SER	2.5
1	D	234	PRO	2.5
1	F	498	THR	2.5
1	C	533	MET	2.5
1	F	424	ASP	2.5
1	A	516	VAL	2.5
1	B	145	HIS	2.5
1	G	507	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	144	LYS	2.5
1	E	236	LYS	2.5
1	G	499	ILE	2.5
1	D	94	ALA	2.5
1	G	393	LEU	2.5
1	B	463	ILE	2.5
1	F	69	TRP	2.5
1	G	244	ASN	2.5
1	G	473	LYS	2.5
1	A	474	ALA	2.5
1	F	385	LEU	2.5
1	A	354	ILE	2.5
1	C	517	ARG	2.5
1	C	403	ASP	2.5
1	E	178	LEU	2.5
1	A	534	GLU	2.5
1	D	236	LYS	2.4
1	E	123	VAL	2.4
1	D	133	THR	2.4
1	A	98	ILE	2.4
1	B	262	PRO	2.4
1	E	118	ILE	2.4
1	E	295	ILE	2.4
1	F	252	GLU	2.4
1	A	496	SER	2.4
1	A	75	ASN	2.4
1	C	250	ILE	2.4
1	C	309	MET	2.4
1	C	474	ALA	2.4
1	G	517	ARG	2.4
1	B	148	ASN	2.4
1	B	402	THR	2.4
1	C	271	LEU	2.4
1	F	423	LEU	2.4
1	G	516	VAL	2.4
1	B	133	THR	2.4
1	F	295	ILE	2.4
1	E	487	ARG	2.4
1	A	425	HIS	2.4
1	E	145	HIS	2.4
1	A	157	GLU	2.4
1	C	146	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	E	321	PHE	2.4
1	G	463	ILE	2.4
1	C	548	SER	2.4
1	D	486	LEU	2.4
1	G	133	THR	2.4
1	F	159	GLU	2.4
1	F	445	LEU	2.4
1	F	472	GLY	2.4
1	A	233	LEU	2.4
1	C	81	LEU	2.4
1	F	265	VAL	2.4
1	A	487	ARG	2.4
1	B	73	GLU	2.4
1	C	136	HIS	2.4
1	C	261	ILE	2.4
1	D	155	VAL	2.4
1	A	370	ARG	2.4
1	D	229	ARG	2.4
1	F	534	GLU	2.4
1	C	113	ASP	2.3
1	C	138	SER	2.3
1	G	339	LEU	2.3
1	G	329	TRP	2.3
1	F	309	MET	2.3
1	F	522	ARG	2.3
1	A	285	VAL	2.3
1	G	149	GLY	2.3
1	D	235	CYS	2.3
1	B	372	ILE	2.3
1	F	205	MET	2.3
1	F	65	THR	2.3
1	B	102	ASP	2.3
1	D	102	ASP	2.3
1	G	262	PRO	2.3
1	C	147	TRP	2.3
1	B	308	ILE	2.3
1	B	409	LEU	2.3
1	G	193	TYR	2.3
1	E	187	LYS	2.3
1	C	170	ASP	2.3
1	F	155	VAL	2.3
1	F	481	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	517	ARG	2.3
1	E	95	GLY	2.3
1	C	174	PRO	2.3
1	E	224	PRO	2.3
1	B	454	LYS	2.3
1	C	300	LEU	2.3
1	G	542	LEU	2.3
1	A	350	ALA	2.3
1	A	397	PHE	2.3
1	F	266	VAL	2.3
1	G	263	ASP	2.3
1	F	141	LEU	2.3
1	A	471	LYS	2.3
1	E	225	ALA	2.3
1	D	159	GLU	2.3
1	D	503	GLU	2.3
1	E	412	MET	2.3
1	C	254	VAL	2.3
1	E	71	PHE	2.3
1	F	420	VAL	2.3
1	C	543	GLU	2.2
1	E	498	THR	2.2
1	G	162	MET	2.2
1	E	261	ILE	2.2
1	B	310	VAL	2.2
1	F	476	GLU	2.2
1	E	449	LEU	2.2
1	C	468	ASN	2.2
1	C	106	TYR	2.2
1	F	547	TYR	2.2
1	G	230	VAL	2.2
1	G	242	HIS	2.2
1	A	292	CYS	2.2
1	F	224	PRO	2.2
1	D	461	VAL	2.2
1	B	80	ALA	2.2
1	B	90	THR	2.2
1	D	473	LYS	2.2
1	E	133	THR	2.2
1	B	243	LEU	2.2
1	B	87	SER	2.2
1	B	114	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	501	ALA	2.2
1	D	191	ALA	2.2
1	F	262	PRO	2.2
1	C	378	PHE	2.2
1	C	541	TRP	2.2
1	C	121	GLN	2.2
1	D	92	GLN	2.2
1	B	151	LYS	2.2
1	E	93	LYS	2.2
1	A	462	VAL	2.2
1	D	165	VAL	2.2
1	A	174	PRO	2.2
1	A	466	LEU	2.2
1	C	198	GLN	2.2
1	C	356	LEU	2.2
1	B	386	PHE	2.2
1	A	500	ILE	2.2
1	D	260	TRP	2.2
1	E	147	TRP	2.2
1	A	122	LYS	2.2
1	F	132	THR	2.2
1	F	136	HIS	2.2
1	A	79	SER	2.2
1	B	219	ALA	2.2
1	F	98	ILE	2.2
1	A	430	VAL	2.2
1	C	232	VAL	2.2
1	A	461	VAL	2.1
1	D	429	VAL	2.1
1	F	176	VAL	2.1
1	G	492	LEU	2.1
1	A	118	ILE	2.1
1	G	101	VAL	2.1
1	C	341	MET	2.1
1	D	485	ASP	2.1
1	G	247	ASP	2.1
1	A	429	VAL	2.1
1	C	354	ILE	2.1
1	F	422	ILE	2.1
1	C	156	THR	2.1
1	F	114	GLN	2.1
1	D	535	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	475	HIS	2.1
1	E	266	VAL	2.1
1	G	153	ILE	2.1
1	A	356	LEU	2.1
1	E	183	SER	2.1
1	B	77	ARG	2.1
1	C	495	LEU	2.1
1	D	452	PHE	2.1
1	B	162	MET	2.1
1	D	362	LEU	2.1
1	D	206	PHE	2.1
1	F	165	VAL	2.1
1	F	248	ARG	2.1
1	G	246	HIS	2.1
1	A	271	LEU	2.1
1	B	530	ALA	2.1
1	E	282	GLU	2.1
1	E	532	TYR	2.1
1	A	463	ILE	2.1
1	C	481	VAL	2.1
1	E	479	ARG	2.1
1	B	322	VAL	2.1
1	E	326	ALA	2.1
1	E	462	VAL	2.1
1	A	223	LEU	2.1
1	C	179	GLY	2.1
1	B	195	TYR	2.1
1	B	323	ARG	2.1
1	G	323	ARG	2.1
1	B	422	ILE	2.1
1	C	279	LEU	2.1
1	E	537	LYS	2.0
1	F	97	TRP	2.0
1	B	215	ALA	2.0
1	F	429	VAL	2.0
1	A	372	ILE	2.0
1	C	486	LEU	2.0
1	A	144	LYS	2.0
1	B	242	HIS	2.0
1	D	462	VAL	2.0
1	E	337	VAL	2.0
1	B	72	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	174	PRO	2.0
1	D	422	ILE	2.0
1	F	362	LEU	2.0
1	B	229	ARG	2.0
1	E	361	ARG	2.0
1	A	246	HIS	2.0
1	C	102	ASP	2.0
1	B	549	GLY	2.0
1	A	389	ASP	2.0
1	B	260	TRP	2.0
1	G	310	VAL	2.0
1	C	226	GLY	2.0
1	D	124	ARG	2.0
1	D	354	ILE	2.0
1	E	472	GLY	2.0
1	C	70	ASN	2.0
1	E	311	THR	2.0
1	D	187	LYS	2.0
1	F	414	SER	2.0
1	G	346	VAL	2.0
1	A	492	LEU	2.0
1	F	223	LEU	2.0
1	G	432	ALA	2.0
1	D	292	CYS	2.0
1	A	204	LEU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.