



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:42 PM GMT

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
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

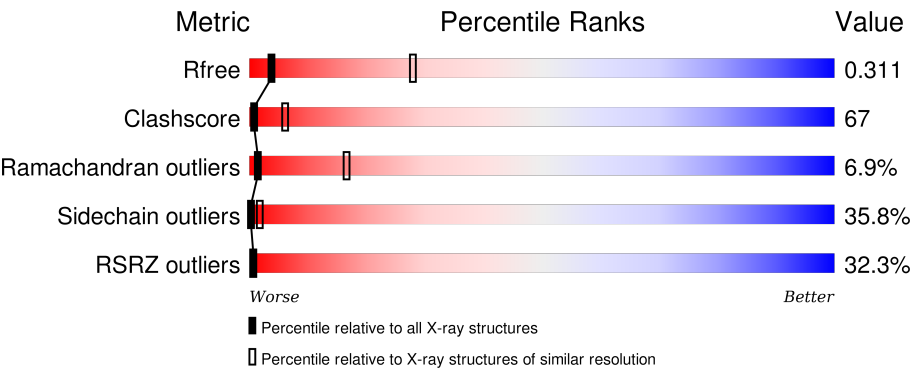
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.45 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}	91344	1000 (3.56-3.36)
Clashscore	102246	1090 (3.56-3.36)
Ramachandran outliers	100387	1057 (3.56-3.36)
Sidechain outliers	100360	1058 (3.56-3.36)
RSRZ outliers	91569	1005 (3.56-3.36)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	<div><div>20%</div><div><div>23%</div><div>47%</div><div>23%</div><div>.</div><div>.</div></div></div>
1	B	503	<div><div>33%</div><div><div>23%</div><div>49%</div><div>20%</div><div>.</div><div>.</div></div></div>
1	C	503	<div><div>32%</div><div><div>23%</div><div>47%</div><div>22%</div><div>.</div><div>.</div></div></div>
1	D	503	<div><div>33%</div><div><div>22%</div><div>47%</div><div>24%</div><div>.</div><div>.</div></div></div>
1	E	503	<div><div>39%</div><div><div>23%</div><div>46%</div><div>24%</div><div>.</div><div>.</div></div></div>

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Mol	Chain	Length	Quality of chain
1	F	503	<p>25% 23% 46% 22% 5%</p>
1	G	503	<p>35% 23% 48% 22%</p>

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
1	A	483	Total	C	N	O	S	0	0	0
			3744	2341	657	721	25			
1	B	483	Total	C	N	O	S	0	0	0
			3744	2341	657	721	25			
1	C	483	Total	C	N	O	S	0	0	0
			3744	2341	657	721	25			
1	D	483	Total	C	N	O	S	0	0	0
			3744	2341	657	721	25			
1	E	483	Total	C	N	O	S	0	0	0
			3744	2341	657	721	25			
1	F	483	Total	C	N	O	S	0	0	0
			3744	2341	657	721	25			
1	G	483	Total	C	N	O	S	0	0	0
			3744	2341	657	721	25			

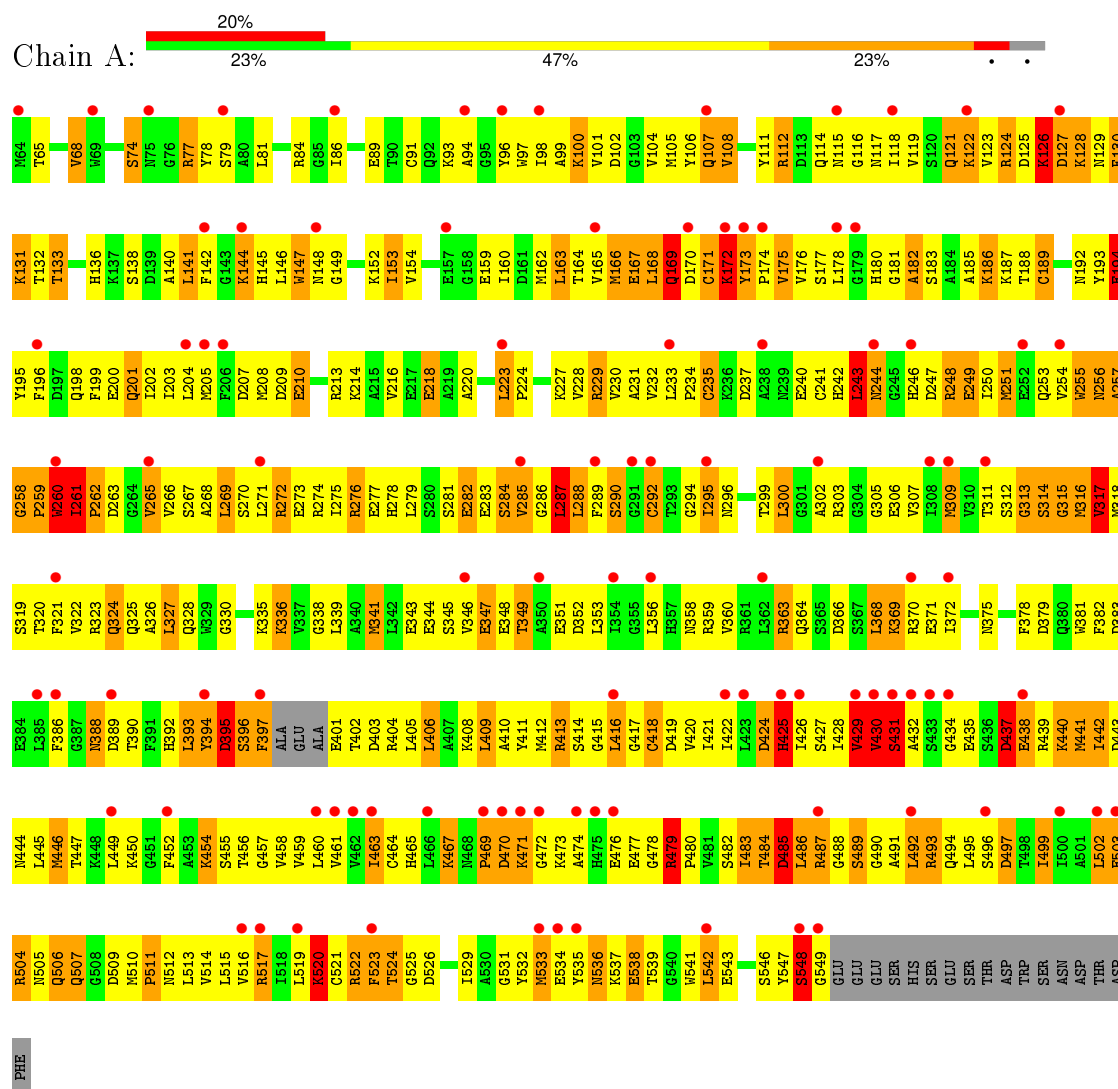
There are 14 discrepancies between the modelled and reference sequences:

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

3 Residue-property plots

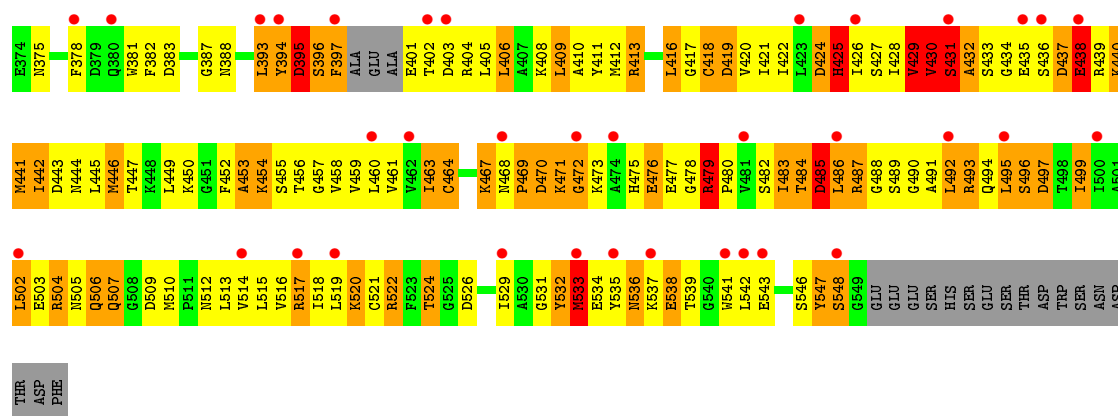
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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

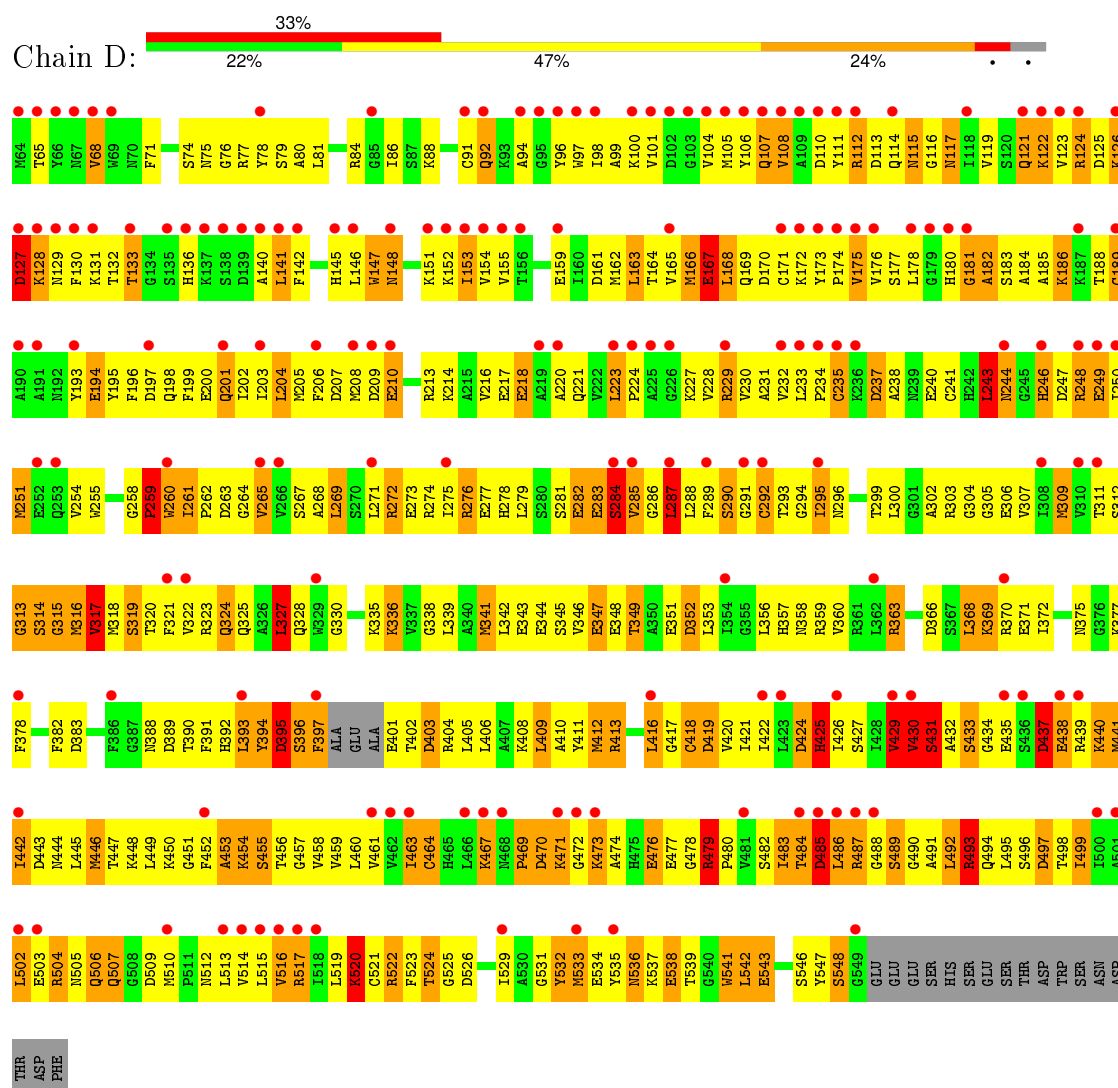


• Molecule 1: DNA primase/helicase

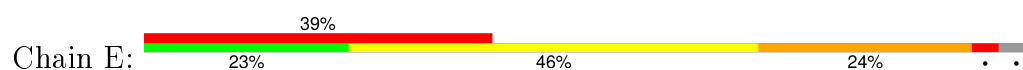


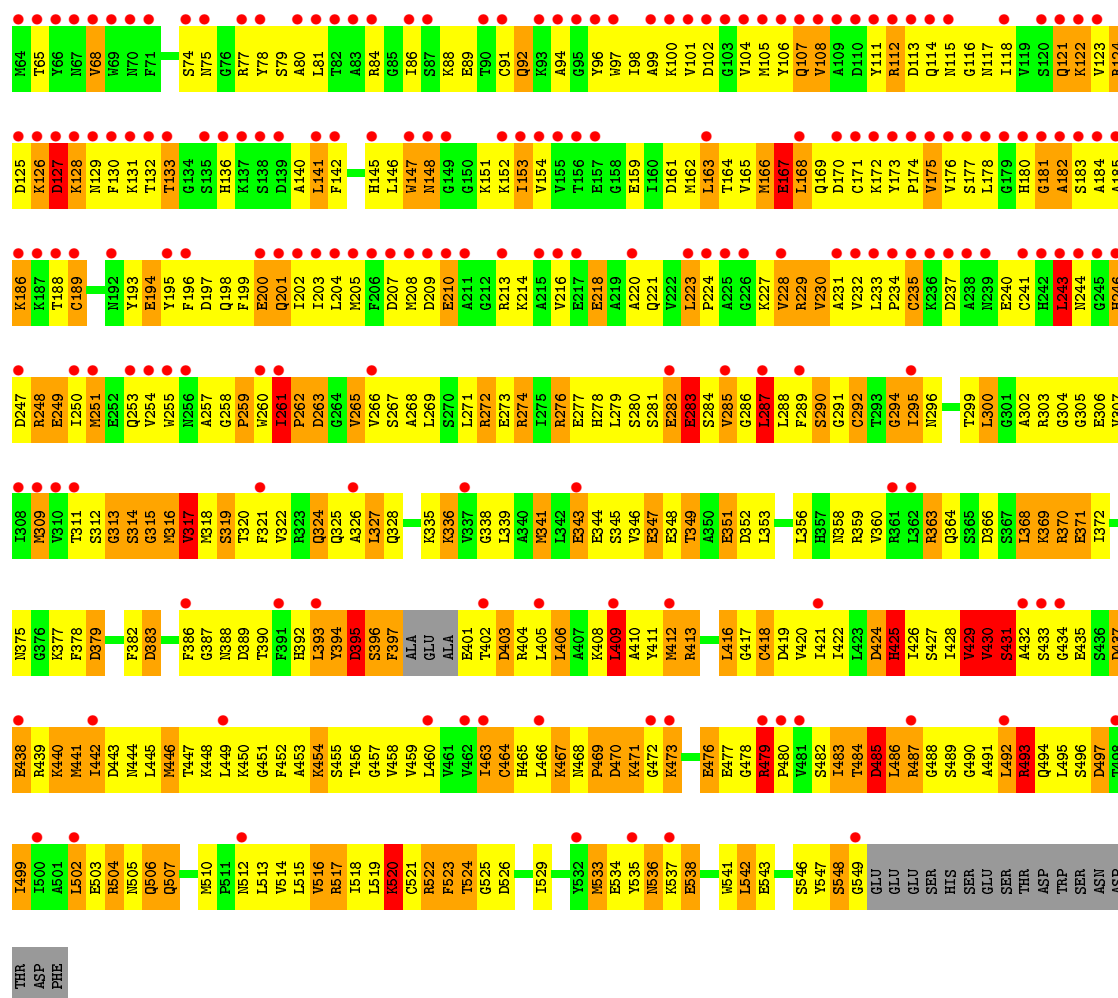


• Molecule 1: DNA primase/helicase

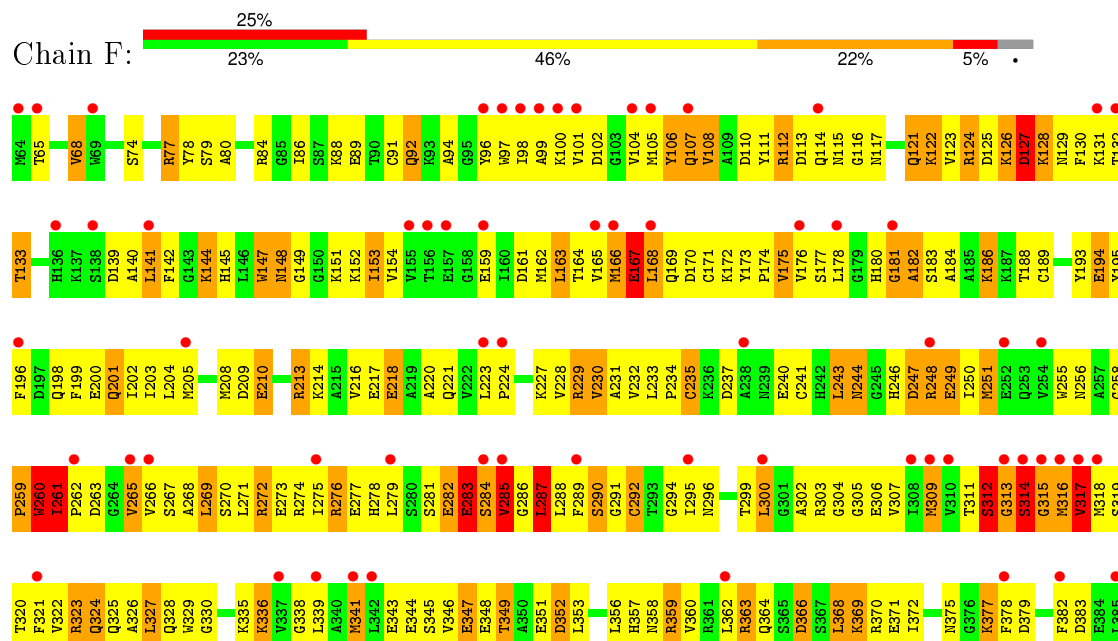


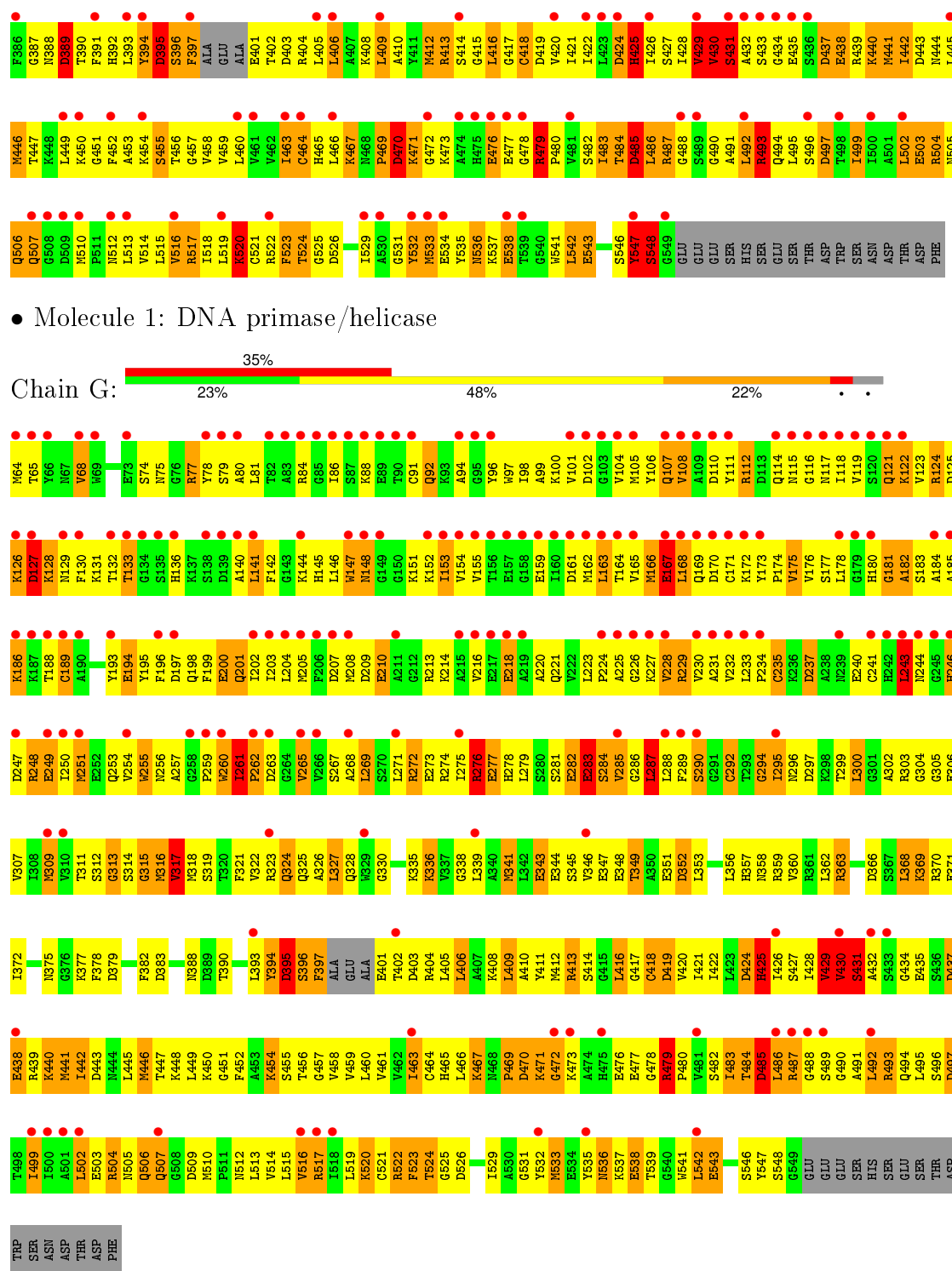
• Molecule 1: DNA primase/helicase





• Molecule 1: DNA primase/helicase





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)	Xtriage
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 (5.34%)	DCC
Wilson B-factor (Å ²)	127.0	Xtriage
Anisotropy	0.322	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 197.2	EDS
Estimated twinning fraction	0.001 for l,-k,h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 60583 reflections	Xtriage
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

Xtriage'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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.96	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

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:CB	1:G:276:ARG:HH11	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:HB3	1:B:248:ARG:NH1	1.38	1.33
1:B:244:ASN:C	1:B:244:ASN:HD22	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:HD12	1:B:483:ILE:H	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:G:483:ILE:O	1:G:486:LEU:HB2	1.45	1.15
1:D:290:SER:H	1:D:325:GLN:NE2	1.43	1.15
1:G:483:ILE:HD12	1:G:483:ILE:H	1.07	1.15
1:E:440:LYS:NZ	1:E:441:MET:HA	1.63	1.14
1:C:208:MET:HE1	1:C:232:VAL:HA	1.25	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:E:483:ILE:O	1:E:486:LEU:HB2	1.46	1.14
1:A:208:MET:HE1	1:A:232:VAL:HA	1.30	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:F:440:LYS:HZ3	1:F:441:MET:HA	0.97	1.13
1:B:127:ASP:O	1:B:128:LYS:HB2	1.43	1.13
1:F:483:ILE:H	1:F:483:ILE:HD12	1.13	1.12
1:B:208:MET:HE1	1:B:232:VAL:HA	1.31	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:290:SER:H	1:A:325:GLN:NE2	1.46	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:G:220:ALA:HB3	1:G:261:ILE:HG21	1.12	1.10
1:E:220:ALA:HB3	1:E:261:ILE:HG21	1.22	1.10
1:G:504:ARG:HD3	1:G:506:GLN:HG2	1.23	1.09
1:B:244:ASN:ND2	1:B:244:ASN:O	1.83	1.09
1:D:483:ILE:H	1:D:483:ILE:HD12	1.15	1.09
1:C:441:MET:HE2	1:C:441:MET:O	1.48	1.09
1:B:283:GLU:HG3	1:B:286:GLY:HA2	1.24	1.09
1:A:260:TRP:O	1:A:261:ILE:CG2	2.00	1.09
1:D:261:ILE:N	1:D:262:PRO:CD	2.12	1.09
1:B:504:ARG:HD3	1:B:506:GLN:HG2	1.32	1.09
1:B:283:GLU:HG3	1:B:286:GLY:CA	1.83	1.09
1:G:290:SER:H	1:G:325:GLN:NE2	1.48	1.09
1:E:127:ASP:O	1:E:128:LYS:HB2	1.32	1.09
1:C:483:ILE:HD12	1:C:483:ILE:H	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:NH1	1:B:248:ARG:CB	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:N	1:B:483:ILE:HD12	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:F:440:LYS:NZ	1:F:441:MET:HA	1.69	1.07
1:E:253:GLN:HA	1:E:257:ALA:HB2	1.37	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:F:290:SER:H	1:F:325:GLN:NE2	1.52	1.05
1:E:412:MET:HA	1:E:416:LEU:HD12	1.35	1.05
1:C:504:ARG:HD3	1:C:506:GLN:HG2	1.35	1.05
1:E:483:ILE:HD12	1:E:483:ILE:H	1.19	1.04
1:G:358:ASN:O	1:G:360:VAL:HG13	1.57	1.04
1:G:483:ILE:HD12	1:G:483:ILE:N	1.72	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:D:440:LYS:NZ	1:D:441:MET:HA	1.71	1.04
1:B:412:MET:HA	1:B:416:LEU:HD12	1.37	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: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:A:339:LEU:HB3	1:A:341:MET:CE	1.86	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:G:440:LYS:NZ	1:G:441:MET:HA	1.74	1.03
1:C:450:LYS:CE	1:C:454:LYS:HD3	1.88	1.03
1:C:450:LYS:HE2	1:C:454:LYS:HD3	1.38	1.02
1:C:312:SER:HB2	1:C:502:LEU:O	1.60	1.02
1:B:483:ILE:CD1	1:B:483:ILE:H	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:H	1:A:483:ILE:HD12	1.18	1.02
1:E:450:LYS:HE2	1:E:454:LYS:HD3	1.40	1.02
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:B:440:LYS:HZ3	1:B:441:MET:HA	1.23	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:B:450:LYS:CE	1:B:454:LYS:HD3	1.91	1.00
1:A:450:LYS:HE2	1:A:454:LYS:HD3	1.43	1.00
1:B:450:LYS:HE2	1:B:454:LYS:HD3	1.43	1.00
1:E:450:LYS:CE	1:E:454:LYS:HD3	1.91	1.00
1:A:172:LYS:CG	1:A:172:LYS:O	2.06	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:D:260:TRP:HB2	1:D:262:PRO:CG	1.92	0.99
1:C:447:THR:HG22	1:C:495:LEU:HD21	1.44	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:E:483:ILE:N	1:E:483:ILE:HD12	1.77	0.98
1:A:450:LYS:CE	1:A:454:LYS:HD3	1.92	0.98
1:A:259:PRO:O	1:A:260:TRP:HB3	1.64	0.98
1:F:483:ILE:N	1:F:483:ILE:HD12	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:CD1	1:G:483:ILE:H	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:CD1	1:C:483:ILE:H	1.78	0.97
1:C:260:TRP:O	1:C:261:ILE:HG23	1.63	0.96
1:A:311:THR:HA	1:A:318:MET:HE1	1.46	0.96
1:G:492:LEU:HD12	1:G:492:LEU:H	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:HG3	1:A:172:LYS:O	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:H	1:D:492:LEU:HD12	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:G:276:ARG:CB	1:G:276:ARG:NH1	2.02	0.94
1:C:412:MET:HA	1:C:416:LEU:CD1	1.97	0.94
1:F:248:ARG:HH11	1:F:248:ARG:HB3	1.29	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:366:ASP:HB2	1:E:284:SER:CB	1.97	0.94
1:D:186:LYS:HD3	1:D:218:GLU:HG3	1.49	0.94
1:F:483:ILE:H	1:F:483:ILE:CD1	1.81	0.94
1:B:339:LEU:HB3	1:B:341:MET:HE1	1.49	0.94
1:B:229:ARG:HB3	1:B:259:PRO:HA	1.49	0.94
1:F:412:MET:HA	1:F:416:LEU:CD1	1.96	0.94
1:G:316:MET:HE1	1:G:535:TYR:CZ	2.03	0.94
1:F:499:ILE:HG22	1:F:519:LEU:HB2	1.45	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:G:276:ARG:CG	1:G:276:ARG:HH11	1.82	0.93
1:F:309:MET:HB3	1:F:499:ILE:HD12	1.48	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:D:260:TRP:C	1:D:262:PRO:HD2	1.89	0.93
1:C:186:LYS:HD3	1:C:218:GLU:HG3	1.50	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:HB3	1:D:248:ARG:HH11	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:E:483:ILE:CD1	1:E:483:ILE:H	1.83	0.91
1:B:344:GLU:HG3	1:B:349:THR:HG22	1.51	0.91
1:E:499:ILE:HG22	1:E:519:LEU:HB2	1.53	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:510:MET:CE	1:B:547:TYR:HE1	1.84	0.90
1:B:282:GLU:HA	1:B:282:GLU:OE2	1.69	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:D:152:LYS:HD3	1:D:203:ILE:HD11	1.53	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:F:344:GLU:HG3	1:F:349:THR:HG22	1.51	0.90
1:E:469:PRO:O	1:E:470:ASP:HB2	1.71	0.90
1:G:312:SER:HB2	1:G:502:LEU:O	1.72	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:A:510:MET:CE	1:A:547:TYR:CE1	2.55	0.90
1:D:260:TRP:HB2	1:D:262:PRO:HG3	1.49	0.90
1:A:499:ILE:HG22	1:A:519:LEU:HB2	1.53	0.89
1:A:186:LYS:HD3	1:A:218:GLU:HG3	1.52	0.89
1:E:97:TRP:CZ3	1:E:99:ALA:HB2	2.08	0.89
1:E:127:ASP:O	1:E:128:LYS:CB	2.19	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:409:LEU:HD23	1:B:421:ILE:HG21	1.53	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:B:441:MET:CE	1:B:441:MET:O	2.21	0.89
1:A:97:TRP:CZ3	1:A:99:ALA:HB2	2.07	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:F:546:SER:O	1:F:547:TYR:HB2	1.70	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:G:510:MET:CE	1:G:547:TYR:HE1	1.86	0.89
1:C:344:GLU:HG3	1:C:349:THR:HG22	1.53	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:E:107:GLN:HB2	1:E:124:ARG:HG3	1.56	0.88
1:A:248:ARG:HB3	1:A:248:ARG:HH11	1.38	0.88
1:F:217:GLU:OE2	1:F:261:ILE:HG22	1.72	0.88
1:A:412:MET:HA	1:A:416:LEU:CD1	2.03	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:D:339:LEU:HB3	1:D:341:MET:HE1	1.55	0.86
1:A:510:MET:CE	1:A:547:TYR:HE1	1.88	0.86
1:G:168:LEU:HD21	1:G:247:ASP:OD2	1.74	0.86
1:G:276:ARG:HB3	1:G:276:ARG:HH11	0.69	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:283:GLU:HG2	1:E:284:SER:N	1.89	0.86
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:A:366:ASP:HB2	1:C:285:VAL:CG2	2.05	0.86
1:F:107:GLN:CB	1:F:124:ARG:HG3	2.06	0.86
1:D:450:LYS:HE2	1:D:454:LYS:HD3	1.58	0.86
1:C:316:MET:HE1	1:C:535:TYR:CZ	2.09	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: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:107:GLN:HB2	1:D:124:ARG:HG3	1.56	0.86
1:G:504:ARG:CD	1:G:506:GLN:HG2	2.06	0.85
1:G:107:GLN:HB2	1:G:124:ARG:HG3	1.56	0.85
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: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:E:482:SER:H	1:E:485:ASP:HB2	1.41	0.85
1:C:108:VAL:HG13	1:C:123:VAL:HG22	1.59	0.85
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:108:VAL:HG13	1:B:123:VAL:HG22	1.56	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:F:425:HIS:CE1	1:F:427:SER:HB2	2.13	0.84
1:D:168:LEU:HD21	1:D:247:ASP:OD2	1.75	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: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
1:C:369:LYS:HG2	1:D:279:LEU:HD23	1.58	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:442:ILE:HD11	1:D:492:LEU:HD21	1.60	0.84
1:B:289:PHE:H	1:B:296:ASN:HD21	1.25	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:482:SER:H	1:G:485:ASP:HB2	1.44	0.83
1:G:166:MET:HE2	1:G:171:CYS:SG	2.19	0.83
1:A:492:LEU:HD12	1:A:492:LEU:H	1.41	0.83
1:E:492:LEU:HD12	1:E:492:LEU:H	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:F:290:SER:H	1:F:325:GLN:HE21	1.22	0.83
1:B:309:MET:HB3	1:B:499:ILE:HD12	1.59	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:D:490:GLY:HA2	1:D:493:ARG:HG3	1.59	0.82
1:D:338:GLY:HA3	1:D:412:MET:CE	2.10	0.82
1:B:441:MET:O	1:B:441:MET:HE1	1.78	0.82
1:B:253:GLN:HA	1:B:257:ALA:HB2	1.62	0.82
1:C:178:LEU:CB	1:C:181:GLY:HA2	2.09	0.82
1:G:178:LEU:CB	1:G:181:GLY:HA2	2.09	0.82
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:A:178:LEU:CB	1:A:181:GLY:HA2	2.09	0.81
1:C:405:LEU:HG	1:C:409:LEU:HD12	1.62	0.81
1:G:315:GLY:HA2	1:G:317:VAL:HG23	1.62	0.81
1:F:469:PRO:O	1:F:470:ASP:HB2	1.80	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
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

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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:C:166:MET:HE1	1:C:171:CYS:HB3	1.63	0.79
1:A:141:LEU:HD13	1:A:176:VAL:HG21	1.63	0.79
1:D:141:LEU:HD11	1:D:196:PHE:CZ	2.16	0.79
1:A:427:SER:HB3	1:A:487:ARG:HH12	1.48	0.79
1:C:492:LEU:HD12	1:C:492:LEU:H	1.46	0.79
1:G:510:MET:HE3	1:G:547:TYR:HE1	1.45	0.79
1:C:141:LEU:HD11	1:C:196:PHE:CZ	2.18	0.79
1:A:261:ILE:HG12	1:A:261:ILE:O	1.83	0.79
1:A:121:GLN:HB2	1:A:133:THR:OG1	1.82	0.79
1:E:178:LEU:CB	1:E:181:GLY:HA2	2.13	0.79
1:E:411:TYR:HE1	1:F:265:VAL:HG11	1.47	0.79
1:A:413:ARG:HE	1:A:458:VAL:HB	1.48	0.79
1:A:199:PHE:O	1:A:227:LYS:HE2	1.83	0.79
1:F:166:MET:CE	1:F:171:CYS:SG	2.71	0.79
1:D:515:LEU:HD21	1:D:529:ILE:CD1	2.13	0.79
1:A:152:LYS:HG3	1:A:201:GLN:HG2	1.65	0.79
1:C:168:LEU:CD2	1:C:247:ASP:OD2	2.31	0.79
1:G:405:LEU:HG	1:G:409:LEU:HD12	1.65	0.79
1:E:168:LEU:CD2	1:E:247:ASP:OD2	2.30	0.79
1:E:108:VAL:CG1	1:E:121:GLN:HG2	2.13	0.79
1:F:473:LYS:HE2	1:F:479:ARG:HA	1.64	0.79
1:A:473:LYS:HG3	1:A:479:ARG:HB2	1.65	0.79
1:D:483:ILE:O	1:D:486:LEU:CB	2.25	0.78
1:A:220:ALA:HB1	1:A:261:ILE:HD12	1.65	0.78
1:F:292:CYS:O	1:F:295:ILE:HG12	1.82	0.78
1:G:425:HIS:CE1	1:G:427:SER:OG	2.35	0.78
1:C:488:GLY:HA3	1:C:492:LEU:HD11	1.66	0.78
1:C:107:GLN:HB2	1:C:124:ARG:CG	2.13	0.78
1:E:442:ILE:HD11	1:E:492:LEU:HD21	1.63	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:G:425:HIS:HE1	1:G:427:SER:OG	1.65	0.78
1:E:216:VAL:HG11	1:E:230: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:A:395:ASP:HB3	1:C:266:VAL:HG21	1.64	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:C:339:LEU:HB3	1:C:341:MET:HE1	1.66	0.78
1:A:178:LEU:HB3	1:A:181:GLY:HA2	1.64	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:F:168:LEU:CD2	1:F:247:ASP:OD2	2.32	0.78
1:C:368:LEU:O	1:C:368:LEU:HD22	1.84	0.78
1:F:378:PHE:CE2	1:G:276:ARG:HD3	2.19	0.78
1:D:153:ILE:HG13	1:D:174:PRO:HB2	1.66	0.78
1:A:154:VAL:HB	1:A:175:VAL:HG13	1.65	0.78
1:E:473:LYS:HG3	1:E:479:ARG:HB2	1.66	0.78
1:G:168:LEU:CD2	1:G:247:ASP:OD2	2.32	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:D:321:PHE:HD2	1:D:533:MET:HE1	1.47	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:414:SER:HB3	1:C:226:GLY:H	1.50	0.77
1:A:401:GLU:HG2	1:A:402:THR:N	1.99	0.77
1:A:405:LEU:HG	1:A:409:LEU:HD12	1.65	0.77
1:A:126:LYS:CG	1:A:127:ASP:N	2.44	0.77
1:F:504:ARG:HH21	1:F:506:GLN:HB3	1.47	0.77
1:E:290:SER:N	1:E:325:GLN:NE2	2.32	0.77
1:G:108:VAL:HG12	1:G:121:GLN:HG2	1.65	0.77
1:F:121:GLN:HB3	1:F:133:THR:HG23	1.65	0.77
1:F:220:ALA:CB	1:F:261:ILE:HG12	2.15	0.77
1:D:259:PRO:O	1:D:260:TRP:CB	2.33	0.77
1:B:168:LEU:CD2	1:B:247:ASP:OD2	2.32	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:C:409:LEU:CD2	1:C:421:ILE:HG21	2.15	0.77
1:B:290:SER:H	1:B:325:GLN:HE21	1.32	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:G:141:LEU:HD11	1:G:196:PHE:CZ	2.20	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: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:D:482:SER:H	1:D:485:ASP:HB2	1.48	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:A:442:ILE:HD11	1:A:492:LEU:HD21	1.66	0.77
1:D:127:ASP:O	1:D:128:LYS:CB	2.23	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:CE	1:F:251:MET:HA	2.16	0.76
1:F:409:LEU:CD2	1:F:421:ILE:HG21	2.15	0.76
1:D:499:ILE:CG2	1:D:519:LEU:HB2	2.16	0.76
1:B:321:PHE:HD2	1:B:533:MET:HE3	1.50	0.76
1:B:178:LEU:CB	1:B:181:GLY:HA2	2.14	0.76
1:B:248:ARG:HH11	1:B:248:ARG:HB3	0.59	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: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:B:292:CYS:O	1:B:295:ILE:HG12	1.85	0.76
1:B:290:SER:N	1:B:325:GLN:NE2	2.33	0.76
1:F:112:ARG:HG3	1:F:145:HIS:CD2	2.20	0.76
1:B:473:LYS:HE2	1:B:479:ARG:HA	1.68	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:F:315:GLY:HA2	1:F:317:VAL:HG23	1.66	0.76
1:B:107:GLN:CB	1:B:124:ARG:HG3	2.14	0.76
1:F:217:GLU:OE2	1:F:261:ILE:CG2	2.33	0.76
1:E:482:SER:OG	1:E:484:THR:HG23	1.85	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:483:ILE:O	1:B:486:LEU:CB	2.29	0.75
1:G:490:GLY:HA2	1:G:493:ARG:HG3	1.67	0.75
1:B:316:MET:HE1	1:B:535:TYR:CE2	2.21	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: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:E:261:ILE:H	1:E:262:PRO:HD2	1.47	0.75
1:B:283:GLU:OE2	1:B:286:GLY:HA2	1.86	0.75
1:G:504:ARG:HH21	1:G:506:GLN:HB3	1.52	0.75
1:C:482:SER:OG	1:C:484:THR:HG23	1.87	0.75
1:F:473:LYS:HG3	1:F:479:ARG:HB2	1.66	0.75
1:B:358:ASN:O	1:B:360:VAL:HG13	1.85	0.75
1:G:482:SER:OG	1:G:484:THR:HG23	1.87	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:442:ILE:CD1	1:G:492:LEU:HD11	2.17	0.75
1:F:415:GLY:HA2	1:G:226:GLY:N	2.01	0.75
1:E:358:ASN:O	1:E:360:VAL:HG13	1.87	0.75
1:F:425:HIS:HE1	1:F:427:SER:OG	1.66	0.75
1:E:229:ARG:NH2	1:E:259:PRO:HG3	2.02	0.75
1:G:205:MET:HA	1:G:231:ALA:HB3	1.68	0.75
1:C:442:ILE:CD1	1:C:492:LEU:HD11	2.15	0.75
1:B:121:GLN:HB2	1:B:133:THR:OG1	1.86	0.75
1:A:369:LYS:HG2	1:C:279:LEU:HD23	1.66	0.75
1:C:295:ILE:O	1:C:299:THR:HG23	1.87	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:D:303:ARG:O	1:D:306:GLU:HG3	1.86	0.75
1:F:368:LEU:HD22	1:F:368:LEU:O	1.87	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: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:482:SER:OG	1:B:484:THR:HG23	1.86	0.74
1:B:127:ASP:O	1:B:128:LYS:CB	2.30	0.74
1:C:442:ILE:HD12	1:C:488:GLY:HA2	1.69	0.74
1:G:121:GLN:HB2	1:G:133:THR:OG1	1.87	0.74
1:E:246:HIS:HB2	1:E:249:GLU:HB2	1.69	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:A:126:LYS:HZ2	1:A:127:ASP:N	1.85	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:G:260:TRP:O	1:G:262:PRO:HD2	1.87	0.74
1:F:405:LEU:HG	1:F:409:LEU:HD12	1.68	0.74
1:G:412:MET:HE2	1:G:421:ILE:CD1	2.18	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:A:261:ILE:CG1	1:A:261:ILE:O	2.34	0.74
1:G:107:GLN:CB	1:G:124:ARG:HG3	2.18	0.74
1:B:108:VAL:CG1	1:B:121:GLN:HG2	2.18	0.74
1:E:473:LYS:HE2	1:E:479:ARG:HA	1.70	0.74
1:D:205:MET:HA	1:D:231:ALA:HB3	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:368:LEU:O	1:B:368:LEU:HD22	1.88	0.74
1:F:372:ILE:HA	1:F:375:ASN:OD1	1.87	0.74
1:E:107:GLN:CB	1:E:124:ARG:HG3	2.17	0.74
1:F:499:ILE:CG2	1:F:519:LEU:HB2	2.18	0.74
1:D:178:LEU:HB3	1:D:181:GLY:HA2	1.70	0.74
1:D:141:LEU:HD13	1:D:176:VAL:HG21	1.69	0.74
1:C:446:MET:HE3	1:C:492:LEU:HA	1.70	0.73
1:A:510:MET:HE2	1:A:513:LEU:HD22	1.68	0.73
1:E:420:VAL:HG22	1:E:459:VAL:HB	1.68	0.73
1:E:411:TYR:CE1	1:F:262:PRO:HB3	2.23	0.73
1:B:450:LYS:CE	1:B:454:LYS:CD	2.66	0.73
1:B:289:PHE:N	1:B:296:ASN:HD21	1.86	0.73
1:B:166:MET:HE1	1:B:171:CYS:HB3	1.70	0.73
1:E:322:VAL:HG21	1:E:463:ILE:HD11	1.70	0.73
1:C:413:ARG:HE	1:C:458:VAL:HB	1.53	0.73
1:C:251:MET:HE2	1:C:251:MET:HA	1.68	0.73
1:E:261:ILE:N	1:E:262:PRO:HD2	2.02	0.73
1:D:311:THR:O	1:D:312:SER:HB3	1.88	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:F:366:ASP:HB2	1:G:284:SER:CB	2.17	0.73
1:C:229:ARG:CZ	1:C:259:PRO:HB3	2.18	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: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:E:409:LEU:CD2	1:E:421:ILE:HG21	2.17	0.73
1:B:186:LYS:HD3	1:B:218:GLU:CG	2.19	0.73
1:C:369:LYS:HG2	1:D:279:LEU:CD2	2.17	0.73
1:C:152:LYS:HG3	1:C:201:GLN:HG2	1.71	0.73
1:E:199:PHE:O	1:E:227:LYS:HE2	1.89	0.73
1:A:368:LEU:O	1:A:368:LEU:HD22	1.88	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:D:108:VAL:HG12	1:D:121:GLN:HG2	1.68	0.73
1:C:515:LEU:HD21	1:C:529:ILE:CD1	2.19	0.73
1:F:515:LEU:HD21	1:F:529:ILE:CD1	2.18	0.73
1:G:427:SER:HB3	1:G:487:ARG:HH12	1.53	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:F:321:PHE:HD2	1:F:533:MET:HE3	1.54	0.73
1:A:112:ARG:HG3	1:A:145:HIS:CD2	2.23	0.73
1:F:248:ARG:NH1	1:F:248:ARG:HB3	2.04	0.73
1:E:121:GLN:HB2	1:E:133:THR:OG1	1.88	0.73
1:G:413:ARG:HE	1:G:458:VAL:HB	1.53	0.73
1:D:217:GLU:OE2	1:D:261:ILE:HA	1.89	0.72
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:A:488:GLY:HA3	1:A:492:LEU:HD11	1.71	0.72
1:F:290:SER:N	1:F:325:GLN:NE2	2.32	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:E:442:ILE:CD1	1:E:492:LEU:HD11	2.19	0.72
1:C:248:ARG:NH1	1:C:248:ARG:HB3	2.04	0.72
1:B:248:ARG:HH11	1:B:248:ARG:HB2	1.45	0.72
1:A:446:MET:HE2	1:A:492:LEU:HB3	1.71	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: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:C:246:HIS:HB2	1:C:249:GLU:HB2	1.71	0.72
1:A:253:GLN:O	1:A:257:ALA:HB2	1.90	0.72
1:C:261:ILE:N	1:C:262:PRO:CD	2.35	0.72
1:C:490:GLY:HA2	1:C:493:ARG:HG3	1.70	0.72
1:E:488:GLY:HA3	1:E:492:LEU:HD11	1.72	0.72
1:C:94:ALA:HB1	1:C:162:MET:HE3	1.72	0.72
1:E:321:PHE:HD2	1:E:533:MET:HE3	1.53	0.72
1:C:268:ALA:HA	1:C:271:LEU:CD1	2.19	0.72
1:B:467:LYS:HE3	1:B:486:LEU:O	1.90	0.72
1:A:409:LEU:CD2	1:A:421:ILE:HG21	2.20	0.72
1:E:425:HIS:CE1	1:E:427:SER:OG	2.43	0.72
1:F:316:MET:HE1	1:F:535:TYR:CE2	2.24	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: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:C:290:SER:H	1:C:325:GLN:HE22	1.33	0.72
1:A:467:LYS:HE3	1:A:486:LEU:O	1.89	0.72
1:B:454:LYS:HZ2	1:G:344:GLU:HA	1.53	0.72
1:B:447:THR:HG22	1:B:495:LEU:CD2	2.18	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:260:TRP:O	1:B:261:ILE:HG12	1.90	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: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:F:483:ILE:O	1:F:486:LEU:CB	2.32	0.71
1:F:442:ILE:HD11	1:F:492:LEU:HD21	1.71	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:B:112:ARG:HG3	1:B:145:HIS:CD2	2.25	0.71
1:A:412:MET:CE	1:A:421:ILE:CD1	2.67	0.71
1:F:339:LEU:HB3	1:F:341:MET:HE1	1.73	0.71
1:A:366:ASP:HB2	1:C:285:VAL:HG23	1.72	0.71
1:C:521:CYS:SG	1:C:524:THR:HG23	2.30	0.71
1:C:178:LEU:HB3	1:C:181:GLY:HA2	1.71	0.71
1:F:104:VAL:HG12	1:F:106:TYR:CE1	2.24	0.71
1:A:442:ILE:HD12	1:A:488:GLY:HA2	1.72	0.71
1:G:292:CYS:O	1:G:295:ILE:HG12	1.91	0.71
1:G:104:VAL:HG12	1:G:106:TYR:CE1	2.24	0.71
1:F:251:MET:HE2	1:F:251:MET:HA	1.73	0.71
1:G:504:ARG:NH2	1:G:506:GLN:HB3	2.03	0.71
1:C:504:ARG:CD	1:C:506:GLN:HG2	2.18	0.71
1:A:372:ILE:HA	1:A:375:ASN:OD1	1.90	0.71
1:D:246:HIS:HB2	1:D:249:GLU:HB2	1.73	0.71
1:F:482:SER:OG	1:F:484:THR:HG23	1.91	0.71
1:A:251:MET:CE	1:A:251:MET:HA	2.20	0.71
1:F:229:ARG:HB2	1:F:258:GLY:O	1.90	0.71
1:E:504:ARG:CD	1:E:506:GLN:HG2	2.12	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: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:B:246:HIS:HB2	1:B:249:GLU:HB2	1.71	0.71
1:E:467:LYS:HE3	1:E:486:LEU:O	1.89	0.71
1:C:441:MET:CE	1:C:444:ASN:HB3	2.20	0.71
1:F:289:PHE:H	1:F:296:ASN:HD21	1.39	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:A:86:ILE:HG21	1:A:163:LEU:HD12	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:C:186:LYS:HD3	1:C:218:GLU:CG	2.20	0.71
1:D:369:LYS:HG2	1:E:279:LEU:CD2	2.21	0.71
1:D:292:CYS:O	1:D:295:ILE:HG12	1.91	0.71
1:G:228:VAL:HB	1:G:261:ILE:CD1	2.21	0.70
1:G:154:VAL:HB	1:G:175:VAL:HG13	1.73	0.70
1:A:246:HIS:HB2	1:A:249:GLU:HB2	1.73	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:B:442:ILE:HD12	1:B:488:GLY:CA	2.21	0.70
1:G:220:ALA:CB	1:G:261:ILE:CG2	2.58	0.70
1:E:490:GLY:CA	1:E:493:ARG:HG3	2.21	0.70
1:B:499:ILE:CG2	1:B:519:LEU:HB2	2.21	0.70
1:C:289:PHE:N	1:C:296:ASN:HD21	1.86	0.70
1:D:121:GLN:HB3	1:D:133:THR:HG23	1.73	0.70
1:D:107:GLN:CB	1:D:124:ARG:HG3	2.20	0.70
1:C:111:TYR:CE2	1:C:142:PHE:HB2	2.26	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:F:424:ASP:OD2	1:F:425:HIS:HB2	1.90	0.70
1:A:424:ASP:OD2	1:A:425:HIS:HB2	1.92	0.70
1:D:216:VAL:HG11	1:D:230:VAL:HG21	1.72	0.70
1:C:112:ARG:HG3	1:C:145:HIS:CD2	2.25	0.70
1:B:154:VAL:HB	1:B:175:VAL:HG13	1.73	0.70
1:G:368:LEU:O	1:G:368:LEU:HD22	1.92	0.70
1:F:259:PRO:O	1:F:260:TRP:HB3	1.89	0.70
1:D:504:ARG:NH2	1:D:506:GLN:HB3	2.06	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:D:79:SER:H	1:D:98:ILE:HD13	1.56	0.70
1:C:420:VAL:HG22	1:C:459:VAL:HB	1.74	0.70
1:G:467:LYS:HE3	1:G:486:LEU:O	1.91	0.70
1:D:111:TYR:CE2	1:D:142:PHE:HB2	2.26	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: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:D:490:GLY:CA	1:D:493:ARG:HG3	2.22	0.70
1:E:413:ARG:O	1:E:417:GLY:HA2	1.91	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:B:278:HIS:CD2	1:G:351:GLU:OE1	2.45	0.70
1:F:378:PHE:CD2	1:G:276:ARG:CD	2.75	0.69
1:A:312:SER:N	1:A:318:MET:CE	2.54	0.69
1:E:107:GLN:HB2	1:E:124:ARG:CG	2.21	0.69
1:A:515:LEU:HD21	1:A:529:ILE:CD1	2.22	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:D:194:GLU:CD	1:D:194:GLU:H	1.92	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:B:441:MET:HE2	1:B:444:ASN:HB3	1.73	0.69
1:A:268:ALA:HA	1:A:271:LEU:CD1	2.22	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:B:338:GLY:HA3	1:B:412:MET:CE	2.23	0.69
1:E:499:ILE:CG2	1:E:519:LEU:HB2	2.21	0.69
1:A:499:ILE:CG2	1:A:519:LEU:HB2	2.23	0.69
1:A:473:LYS:HE2	1:A:479:ARG:HA	1.73	0.69
1:D:321:PHE:CD2	1:D:533:MET:HE1	2.26	0.69
1:G:112:ARG:HG3	1:G:145:HIS:CD2	2.27	0.69
1:G:424:ASP:OD2	1:G:425:HIS:HB2	1.92	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:E:427:SER:HB3	1:E:487:ARG:HH12	1.56	0.69
1:B:394:TYR:HE1	1:B:396:SER:HB2	1.57	0.69
1:F:108:VAL:CG1	1:F:121:GLN:HG2	2.22	0.69
1:D:347:GLU:OE1	1:E:274:ARG:HD2	1.93	0.69
1:F:220:ALA:HB1	1:F:261:ILE:HG12	1.73	0.69
1:C:412:MET:CA	1:C:416:LEU:HD12	2.18	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:E:141:LEU:HD13	1:E:176:VAL:CG2	2.22	0.69
1:C:288:LEU:N	1:C:288:LEU:HD12	2.08	0.69
1:B:490:GLY:CA	1:B:493:ARG:HG3	2.23	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:305:GLY:O	1:C:454:LYS:HD2	1.93	0.69
1:B:86:ILE:HG21	1:B:163:LEU:HD12	1.73	0.69
1:A:316:MET:HE3	1:A:535:TYR:CZ	2.28	0.69
1:A:311:THR:O	1:A:312:SER:HB3	1.92	0.69
1:C:425:HIS:CE1	1:C:427:SER:OG	2.46	0.69
1:A:450:LYS:CE	1:A:454:LYS:CD	2.71	0.69
1:E:248:ARG:NH1	1:E:248:ARG:HB3	2.07	0.69
1:A:309:MET:HB3	1:A:499:ILE:HD12	1.75	0.69
1:C:104:VAL:HG12	1:C:106:TYR:CE1	2.28	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:A:111:TYR:CE2	1:A:142:PHE:HB2	2.28	0.69
1:F:86:ILE:HG21	1:F:163:LEU:HD12	1.75	0.69
1:A:205:MET:HA	1:A:231:ALA:HB3	1.73	0.69
1:B:79:SER:H	1:B:98:ILE:HD13	1.58	0.69
1:B:504:ARG:HH21	1:B:506:GLN:HB3	1.58	0.68
1:G:295:ILE:O	1:G:299:THR:HG23	1.92	0.68
1:E:186:LYS:HD3	1:E:218:GLU:CG	2.22	0.68
1:F:309:MET:HB3	1:F:499:ILE:CD1	2.21	0.68
1:D:108:VAL:CG1	1:D:121:GLN:HG2	2.22	0.68
1:B:504:ARG:NH2	1:B:506:GLN:HB3	2.08	0.68
1:G:311:THR:O	1:G:312:SER:HB3	1.92	0.68
1:C:141:LEU:HD13	1:C:176:VAL:CG2	2.23	0.68
1:B:413:ARG:HE	1:B:458:VAL:HB	1.58	0.68
1:A:124:ARG:CZ	1:A:126:LYS:HA	2.23	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:108:VAL:HG13	1:A:123:VAL:HG22	1.76	0.68
1:A:275:ILE:HD12	1:B:382:PHE:HE1	1.57	0.68
1:C:290:SER:N	1:C:325:GLN:HE21	1.87	0.68
1:B:283:GLU:CG	1:B:286:GLY:CA	2.56	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:A:186:LYS:HD3	1:A:218:GLU:CG	2.22	0.68
1:E:351:GLU:OE1	1:F:278:HIS:CD2	2.46	0.68
1:B:372:ILE:HA	1:B:375:ASN:OD1	1.94	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:F:427:SER:HB3	1:F:487:ARG:HH12	1.58	0.68
1:E:339:LEU:HB3	1:E:341:MET:HE2	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:504:ARG:CD	1:B:506:GLN:HG2	2.16	0.68
1:C:424:ASP:OD2	1:C:425:HIS:HB2	1.94	0.68
1:G:141:LEU:HD13	1:G:176:VAL:CG2	2.24	0.68
1:C:368:LEU:HD22	1:C:372:ILE:HG23	1.76	0.68
1:G:78:TYR:CD2	1:G:92:GLN:HG2	2.28	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:F:260:TRP:HB2	1:F:262:PRO:HD2	0.71	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:D:504:ARG:HH21	1:D:506:GLN:HB3	1.56	0.68
1:G:488:GLY:HA3	1:G:492:LEU:HD11	1.76	0.68
1:C:510:MET:HE3	1:C:547:TYR:HE1	1.56	0.68
1:A:74:SER:HB2	1:A:99:ALA:HB1	1.76	0.68
1:D:104:VAL:HG12	1:D:106:TYR:CE1	2.29	0.68
1:C:166:MET:CE	1:C:171:CYS:CB	2.72	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:C:167:GLU:C	1:C:169:GLN:N	2.48	0.68
1:F:260:TRP:CG	1:F:262:PRO:HD2	2.27	0.68
1:G:312:SER:O	1:G:313:GLY:O	2.12	0.68
1:C:292:CYS:O	1:C:295:ILE:HG12	1.93	0.68
1:A:169:GLN:HE22	1:A:254:VAL:HG11	1.58	0.68
1:F:413:ARG:HE	1:F:458:VAL:HB	1.58	0.68
1:E:202:ILE:HD13	1:E:223:LEU:HD22	1.76	0.68
1:E:412:MET:CA	1:E:416:LEU:HD12	2.19	0.67
1:A:504:ARG:CD	1:A:506:GLN:HG2	2.22	0.67
1:F:307:VAL:O	1:F:307:VAL:HG12	1.95	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:F:167:GLU:C	1:F:169:GLN:N	2.46	0.67
1:E:167:GLU:C	1:E:169:GLN:N	2.47	0.67
1:F:153:ILE:HG13	1:F:174:PRO:HB2	1.77	0.67
1:B:251:MET:HE2	1:B:251:MET:HA	1.76	0.67
1:D:368:LEU:HD22	1:D:368:LEU:O	1.94	0.67
1:F:490:GLY:HA2	1:F:493:ARG:HG3	1.76	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:B:260:TRP:C	1:B:261:ILE:HG12	2.14	0.67
1:A:108:VAL:HG12	1:A:121:GLN:HG2	1.74	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:F:127:ASP:O	1:F:128:LYS:CB	2.26	0.67
1:C:96:TYR:HE2	1:C:107:GLN:HE21	1.43	0.67
1:G:121:GLN:HB3	1:G:133:THR:HG23	1.74	0.67
1:A:261:ILE:O	1:A:261:ILE:CD1	2.43	0.67
1:D:230:VAL:HG11	1:D:260:TRP:HE1	1.59	0.67
1:A:126:LYS:NZ	1:A:127:ASP:CA	2.40	0.67
1:G:68:VAL:HG12	1:G:121:GLN:OE1	1.95	0.67
1:E:311:THR:O	1:E:312:SER:HB3	1.94	0.67
1:B:94:ALA:HB1	1:B:162:MET:HE3	1.76	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:F:389:ASP:H	1:G:269:LEU:HD21	1.59	0.67
1:G:86:ILE:HG21	1:G:163:LEU:HD12	1.75	0.67
1:C:194:GLU:CD	1:C:194:GLU:H	1.95	0.67
1:G:420:VAL:HG22	1:G:459:VAL:HB	1.77	0.67
1:G:287:LEU:HD11	1:G:335:LYS:HG3	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: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: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:294:GLY:O	1:C:295:ILE:C	2.29	0.67
1:E:121:GLN:HB3	1:E:133:THR:HG23	1.75	0.67
1:D:107:GLN:HB2	1:D:124:ARG:CG	2.25	0.67
1:E:276:ARG:HG2	1:E:276:ARG:HH11	1.58	0.67
1:B:167:GLU:C	1:B:169:GLN:N	2.46	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:394:TYR:CE2	1:F:405:LEU:HD12	2.29	0.67
1:F:199:PHE:O	1:F:227:LYS:HE2	1.95	0.67
1:C:338:GLY:HA3	1:C:412:MET:CE	2.24	0.67
1:E:338:GLY:HA3	1:E:412:MET:CE	2.25	0.67
1:D:78:TYR:CD2	1:D:92:GLN:HG2	2.30	0.67
1:A:169:GLN:O	1:A:170:ASP:HB2	1.94	0.67
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:A:94:ALA:HB1	1:A:162:MET:HE3	1.77	0.66
1:E:205:MET:HA	1:E:231:ALA:HB3	1.77	0.66
1:E:412:MET:CE	1:E:421:ILE:CD1	2.73	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:305:GLY:O	1:G:454:LYS:HD2	1.95	0.66
1:B:439:ARG:O	1:B:442:ILE:HG22	1.94	0.66
1:F:246:HIS:HB2	1:F:249:GLU:HB2	1.76	0.66
1:A:260:TRP:O	1:A:261:ILE:HG23	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: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:E:425:HIS:HE1	1:E:427:SER:OG	1.76	0.66
1:B:283:GLU:HG3	1:B:286:GLY:N	2.11	0.66
1:G:515:LEU:HD21	1:G:529:ILE:HD11	1.78	0.66
1:B:78:TYR:CE1	1:B:97:TRP:HB3	2.31	0.66
1:A:261:ILE:HD13	1:A:261:ILE:O	1.95	0.66
1:E:339:LEU:HB3	1:E:341:MET:HE1	1.76	0.66
1:G:504:ARG:HD3	1:G:506:GLN:CG	2.15	0.66
1:G:289:PHE:N	1:G:296:ASN:HD21	1.92	0.66
1:C:467:LYS:HE3	1:C:486:LEU:O	1.95	0.66
1:F:338:GLY:HA3	1:F:412:MET:CE	2.25	0.66
1:D:268:ALA:HA	1:D:271:LEU:CD1	2.24	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:E:295:ILE:O	1:E:299:THR:HG23	1.95	0.66
1:D:307:VAL:O	1:D:307:VAL:HG12	1.95	0.66
1:E:411:TYR:CE1	1:F:265:VAL:HG11	2.29	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:C:311:THR:O	1:C:312:SER:HB3	1.94	0.66
1:E:305:GLY:O	1:E:454:LYS:HD2	1.95	0.66
1:A:79:SER:H	1:A:98:ILE:HD13	1.61	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:194:GLU:H	1:B:194:GLU:CD	1.97	0.66
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:CD	1:F:476:GLU:H	2.00	0.65
1:B:409:LEU:CD2	1:B:421:ILE:HG21	2.23	0.65
1:G:394:TYR:HE1	1:G:396:SER:HB2	1.60	0.65
1:D:147:TRP:CG	1:D:174:PRO:HB3	2.31	0.65
1:B:427:SER:HB3	1:B:487:ARG:NH1	2.10	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:442:ILE:HD12	1:C:488:GLY:CA	2.27	0.65
1:A:496:SER:HB2	1:A:499:ILE:HD11	1.78	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:B:420:VAL:HG22	1:B:459:VAL:HB	1.78	0.65
1:A:289:PHE:N	1:A:296:ASN:HD21	1.94	0.65
1:A:124:ARG:HD3	1:A:125:ASP:C	2.16	0.65
1:D:78:TYR:CE1	1:D:97:TRP:HB3	2.32	0.65
1:D:248:ARG:NH1	1:D:248:ARG:HB3	2.08	0.65
1:E:322:VAL:CG2	1:E:463:ILE:HD11	2.27	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:424:ASP:OD2	1:B:425:HIS:HB2	1.96	0.65
1:D:424:ASP:OD2	1:D:425:HIS:HB2	1.96	0.65
1:F:107:GLN:CB	1:F:124:ARG:CG	2.71	0.65
1:C:476:GLU:H	1:C:476:GLU:CD	1.98	0.65
1:B:441:MET:O	1:B:441:MET:HE2	1.95	0.65
1:E:111:TYR:CE2	1:E:142:PHE:HB2	2.31	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: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:C:358:ASN:O	1:C:360:VAL:HG13	1.96	0.65
1:F:260:TRP:HB2	1:F:262:PRO:HD3	1.69	0.65
1:B:441:MET:HE1	1:B:445:LEU:H	1.61	0.65
1:F:321:PHE:CD2	1:F:533:MET:HE3	2.31	0.65
1:E:389:ASP:HA	1:F:269:LEU:HD23	1.77	0.65
1:E:86:ILE:HG21	1:E:163:LEU:HD12	1.77	0.65
1:G:96:TYR:HE2	1:G:107:GLN:HE21	1.43	0.65
1:D:517:ARG:HB3	1:D:519:LEU:CD1	2.27	0.65
1:G:442:ILE:HD11	1:G:492:LEU:HD21	1.78	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:394:TYR:HE1	1:D:396:SER:HB2	1.61	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
1:D:166:MET:CE	1:D:171:CYS:CB	2.75	0.65
1:A:108:VAL:CG1	1:A:121:GLN:HG2	2.26	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:476:GLU:HB3	1:F:506:GLN:OE1	1.97	0.64
1:C:425:HIS:CE1	1:C:427:SER:HB2	2.32	0.64
1:C:78:TYR:CD2	1:C:92:GLN:HG2	2.31	0.64
1:A:414:SER:CB	1:C:226:GLY:H	2.10	0.64
1:B:248:ARG:NH1	1:B:248:ARG:HB2	2.04	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: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:B:68:VAL:HG12	1:B:121:GLN:OE1	1.97	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:G:490:GLY:CA	1:G:493:ARG:HG3	2.27	0.64
1:C:412:MET:HE2	1:C:421:ILE:HD13	1.80	0.64
1:A:107:GLN:HB2	1:A:124:ARG:CG	2.28	0.64
1:C:427:SER:HB3	1:C:487:ARG:HH12	1.62	0.64
1:B:262:PRO:HB2	1:B:265:VAL:HG12	1.77	0.64
1:A:414:SER:HB3	1:C:226:GLY:N	2.11	0.64
1:E:504:ARG:HH21	1:E:506:GLN:HB3	1.63	0.64
1:D:312:SER:CB	1:D:502:LEU:O	2.44	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:339:LEU:HB3	1:D:341:MET:HE3	1.76	0.64
1:E:439:ARG:O	1:E:442:ILE:HG22	1.97	0.64
1:F:496:SER:O	1:F:520:LYS:HE2	1.98	0.64
1:F:121:GLN:CB	1:F:133:THR:HG23	2.27	0.64
1:F:121:GLN:HB2	1:F:133:THR:OG1	1.96	0.64
1:D:452:PHE:O	1:D:456:THR:HG23	1.97	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:78:TYR:CE1	1:A:97:TRP:HB3	2.33	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: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:D:74:SER:HB2	1:D:99:ALA:HB1	1.80	0.64
1:C:154:VAL:HB	1:C:175:VAL:HG13	1.79	0.64
1:A:278:HIS:CD2	1:B:351:GLU:OE1	2.51	0.64
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:A:480:PRO:HA	1:A:503:GLU:CD	2.18	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:303:ARG:O	1:F:306:GLU:HG3	1.97	0.64
1:A:536:ASN:HD22	1:A:538:GLU:H	1.45	0.64
1:A:194:GLU:H	1:A:194:GLU:CD	1.99	0.64
1:A:145:HIS:CE1	1:A:146:LEU:HD23	2.33	0.64
1:A:490:GLY:CA	1:A:493:ARG:HG3	2.27	0.64
1:F:208:MET:HE1	1:F:232:VAL:CA	2.22	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:G:510:MET:HE3	1:G:547:TYR:CE1	2.27	0.64
1:A:248:ARG:HB3	1:A:248:ARG:NH1	2.10	0.64
1:A:130:PHE:O	1:A:131:LYS:HG3	1.98	0.64
1:G:356:LEU:HD12	1:G:541:TRP:NE1	2.13	0.64
1:E:504:ARG:NH2	1:E:506:GLN:HB3	2.13	0.64
1:C:504:ARG:HH21	1:C:506:GLN:HB3	1.63	0.64
1:E:389:ASP:H	1:F:269:LEU:HD21	1.63	0.64
1:F:79:SER:H	1:F:98:ILE:HD13	1.63	0.64
1:E:84:ARG:HA	1:E:243:LEU:HD21	1.80	0.64
1:F:84:ARG:HA	1:F:243:LEU:HD21	1.80	0.64
1:F:261:ILE:H	1:F:262:PRO:CD	2.11	0.63
1:F:446:MET:HE2	1:F:492:LEU:HB3	1.80	0.63
1:F:283:GLU:CD	1:F:286:GLY:HA2	2.18	0.63
1:G:316:MET:HE1	1:G:535:TYR:CE2	2.33	0.63
1:A:517:ARG:HB3	1:A:519:LEU:CD1	2.28	0.63
1:A:446:MET:HE3	1:A:492:LEU:HA	1.79	0.63
1:E:424:ASP:OD2	1:E:425:HIS:HB2	1.98	0.63
1:B:480:PRO:HA	1:B:503:GLU:OE1	1.99	0.63
1:G:152:LYS:HD3	1:G:203:ILE:CD1	2.28	0.63
1:D:321:PHE:CD2	1:D:533:MET:CE	2.81	0.63
1:C:287:LEU:HD11	1:C:335:LYS:HG3	1.79	0.63
1:B:356:LEU:HD12	1:B:541:TRP:NE1	2.13	0.63
1:D:84:ARG:HA	1:D:243:LEU:HD21	1.80	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: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:B:346:VAL:HB	1:B:395:ASP:HB2	1.80	0.63
1:E:441:MET:HE2	1:E:444:ASN:HB3	1.81	0.63
1:A:504:ARG:HH21	1:A:506:GLN:HG2	1.64	0.63
1:G:152:LYS:HG3	1:G:201:GLN:CG	2.29	0.63
1:F:216:VAL:HG11	1:F:230:VAL:HG21	1.80	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:C:411:TYR:OH	1:D:260:TRP:CB	2.46	0.63
1:G:290:SER:N	1:G:325:GLN:HE21	1.91	0.63
1:F:94:ALA:HB1	1:F:162:MET:HE3	1.80	0.63
1:B:285:VAL:HG22	1:B:300:LEU:HD11	1.81	0.63
1:C:510:MET:HE2	1:C:547:TYR:HE1	1.60	0.63
1:F:446:MET:HE3	1:F:492:LEU:HA	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:A:269:LEU:HD11	1:B:387:GLY:HA2	1.80	0.63
1:A:253:GLN:O	1:A:257:ALA:CB	2.47	0.62
1:F:486:LEU:HB3	1:F:493:ARG:HD2	1.80	0.62
1:C:446:MET:HE2	1:C:492:LEU:HB3	1.81	0.62
1:B:454:LYS:HZ1	1:G:344:GLU:HA	1.60	0.62
1:E:229:ARG:HB3	1:E:259:PRO:HB3	1.80	0.62
1:G:283:GLU:O	1:G:303:ARG:HG2	1.98	0.62
1:A:220:ALA:HB3	1:A:261:ILE:HG21	1.80	0.62
1:C:259:PRO:O	1:C:260:TRP:HB3	1.99	0.62
1:B:412:MET:HE2	1:B:421:ILE:CD1	2.29	0.62
1:F:517:ARG:HB3	1:F:519:LEU:CD1	2.29	0.62
1:A:141:LEU:HD11	1:A:196:PHE:HZ	1.64	0.62
1:D:486:LEU:HB3	1:D:493:ARG:HD2	1.81	0.62
1:F:504:ARG:HH21	1:F:506:GLN:CB	2.13	0.62
1:E:166:MET:CE	1:E:171:CYS:CB	2.77	0.62
1:B:352:ASP:CG	1:B:363:ARG:HD3	2.20	0.62
1:E:411:TYR:OH	1:F:262:PRO:HG3	1.99	0.62
1:A:290:SER:N	1:A:325:GLN:HE21	1.92	0.62
1:C:441:MET:CE	1:C:441:MET:O	2.36	0.62
1:F:290:SER:N	1:F:325:GLN:HE21	1.96	0.62
1:D:152:LYS:HG3	1:D:201:GLN:CG	2.28	0.62
1:A:521:CYS:SG	1:A:524:THR:HG23	2.39	0.62
1:C:152:LYS:HG3	1:C:201:GLN:CG	2.29	0.62
1:D:316:MET:HE1	1:D:535:TYR:CE2	2.34	0.62
1:C:111:TYR:CZ	1:C:142:PHE:HB2	2.35	0.62
1:B:312:SER:HB2	1:B:502:LEU:O	1.99	0.62
1:F:346:VAL:HB	1:F:395:ASP:HB2	1.80	0.62
1:F:194:GLU:H	1:F:194:GLU:CD	2.01	0.62
1:D:339:LEU:HB3	1:D:341:MET:HE2	1.78	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:344:GLU:CG	1:G:349:THR:HG22	2.28	0.62
1:G:216:VAL:HG11	1:G:230:VAL:HG21	1.79	0.62
1:E:262:PRO:HB2	1:E:265:VAL:HG12	1.81	0.62
1:A:482:SER:OG	1:A:484:THR:HG23	2.00	0.62
1:D:68:VAL:HG12	1:D:121:GLN:OE1	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:F:401:GLU:HG3	1:F:431:SER:O	1.99	0.62
1:D:504:ARG:CD	1:D:506:GLN:HG2	2.26	0.62
1:G:496:SER:HB2	1:G:499:ILE:HD11	1.79	0.62
1:F:68:VAL:HG12	1:F:121:GLN:OE1	1.99	0.62
1:D:346:VAL:HB	1:D:395:ASP:HB2	1.82	0.62
1:E:251:MET:HA	1:E:251:MET:HE2	1.82	0.62
1:E:307:VAL:HG12	1:E:307:VAL:O	1.99	0.62
1:A:318:MET:SD	1:A:463:ILE:CD1	2.88	0.62
1:E:96:TYR:HE2	1:E:107:GLN:HE21	1.47	0.62
1:C:345:SER:O	1:C:349:THR:CG2	2.48	0.62
1:G:178:LEU:HB2	1:G:181:GLY:HA2	1.80	0.62
1:E:478:GLY:CA	1:E:505:ASN:HB2	2.30	0.62
1:C:251:MET:CE	1:C:251:MET:HA	2.29	0.62
1:G:322:VAL:HG21	1:G:463:ILE:HD11	1.80	0.62
1:D:112:ARG:HG3	1:D:145:HIS:CD2	2.34	0.62
1:E:194:GLU:H	1:E:194:GLU:CD	2.02	0.62
1:C:312:SER:CB	1:C:502:LEU:O	2.42	0.62
1:B:309:MET:HB3	1:B:499:ILE:CD1	2.30	0.62
1:D:482:SER:OG	1:D:484:THR:HG23	1.99	0.61
1:B:471:LYS:HB3	1:B:479:ARG:NH1	2.15	0.61
1:B:253:GLN:CA	1:B:257:ALA:HB2	2.30	0.61
1:B:78:TYR:CD2	1:B:92:GLN:HG2	2.34	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:G:504:ARG:HH21	1:G:506:GLN:CB	2.12	0.61
1:D:447:THR:HA	1:D:495:LEU:HD23	1.82	0.61
1:A:504:ARG:NH2	1:A:506:GLN:HB3	2.15	0.61
1:D:476:GLU:CD	1:D:476:GLU:H	2.03	0.61
1:B:368:LEU:HD22	1:B:372:ILE:HG23	1.82	0.61
1:B:322:VAL:HG21	1:B:463:ILE:HD11	1.80	0.61
1:E:79:SER:H	1:E:98:ILE:HD13	1.64	0.61
1:B:303:ARG:O	1:B:306:GLU:HG3	1.99	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:D:217:GLU:HA	1:D:261:ILE:HG22	1.82	0.61
1:E:440:LYS:HE2	1:E:440:LYS:O	1.99	0.61
1:D:412:MET:CA	1:D:416:LEU:HD12	2.21	0.61
1:B:186:LYS:CD	1:B:218:GLU:HG3	2.27	0.61
1:C:344:GLU:HB2	1:C:348:GLU:OE2	2.00	0.61
1:G:401:GLU:HG2	1:G:402:THR:H	1.64	0.61
1:C:309:MET:HB3	1:C:499:ILE:CD1	2.30	0.61
1:A:394:TYR:C	1:A:394:TYR:CD1	2.74	0.61
1:D:372:ILE:HA	1:D:375:ASN:OD1	1.99	0.61
1:A:256:ASN:C	1:A:256:ASN:OD1	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:F:406:LEU:HD21	1:F:449:LEU:HD23	1.81	0.61
1:C:442:ILE:HD11	1:C:492:LEU:HD11	1.82	0.61
1:E:442:ILE:HD12	1:E:488:GLY:CA	2.31	0.61
1:C:450:LYS:CE	1:C:454:LYS:CD	2.73	0.61
1:E:450:LYS:CE	1:E:454:LYS:CD	2.72	0.61
1:G:127:ASP:O	1:G:128:LYS:CB	2.39	0.61
1:E:78:TYR:CE1	1:E:97:TRP:HB3	2.36	0.61
1:D:305:GLY:O	1:D:454:LYS:HD2	2.01	0.61
1:A:84:ARG:HA	1:A:243:LEU:HD21	1.81	0.61
1:G:406:LEU:HD21	1:G:449:LEU:HD23	1.82	0.61
1:C:84:ARG:HA	1:C:243:LEU:HD21	1.83	0.61
1:E:258:GLY:HA3	1:E:260:TRP:CZ3	2.35	0.61
1:B:394:TYR:CE2	1:B:405:LEU:HD12	2.35	0.61
1:A:305:GLY:O	1:A:454:LYS:HD2	2.00	0.61
1:E:521:CYS:SG	1:E:524:THR:HG23	2.40	0.61
1:E:147:TRP:CG	1:E:174:PRO:HB3	2.36	0.61
1:E:345:SER:O	1:E:349:THR:CG2	2.49	0.61
1:B:202:ILE:HD13	1:B:223:LEU:HD22	1.81	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:E:287:LEU:HD11	1:E:335:LYS:HG3	1.82	0.61
1:F:442:ILE:HD12	1:F:488:GLY:HA2	1.80	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:G:78:TYR:CE1	1:G:97:TRP:HB3	2.34	0.61
1:E:153:ILE:HG13	1:E:174:PRO:HB2	1.81	0.61
1:G:478:GLY:HA3	1:G:505:ASN:HB2	1.81	0.61
1:B:372:ILE:HG13	1:B:378:PHE:HB2	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:251:MET:HA	1:G:251:MET:HE2	1.83	0.61
1:B:195:TYR:O	1:B:198:GLN:HB2	2.01	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:D:202:ILE:HD13	1:D:223:LEU:HD22	1.82	0.61
1:F:229:ARG:HB3	1:F:259:PRO:HA	1.82	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:B:216:VAL:HG11	1:B:230:VAL:HG21	1.81	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:F:378:PHE:CE2	1:G:276:ARG:CD	2.83	0.60
1:D:96:TYR:HE2	1:D:107:GLN:HE21	1.46	0.60
1:C:166:MET:CE	1:C:171:CYS:HB3	2.31	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:401:GLU:CG	1:C:402:THR:H	2.14	0.60
1:G:261:ILE:CG2	1:G:261:ILE:O	2.46	0.60
1:A:220:ALA:CB	1:A:261:ILE:CG2	2.77	0.60
1:D:338:GLY:HA3	1:D:412:MET:HE1	1.82	0.60
1:C:531:GLY:C	1:C:532:TYR:CD1	2.74	0.60
1:C:413:ARG:O	1:C:417:GLY:HA2	2.01	0.60
1:C:536:ASN:HD21	1:C:538:GLU:CB	2.14	0.60
1:C:437:ASP:OD1	1:C:439:ARG:HB2	2.01	0.60
1:C:124:ARG:HD3	1:C:125:ASP:C	2.22	0.60
1:D:520:LYS:HG3	1:D:521:CYS:N	2.16	0.60
1:G:517:ARG:HB3	1:G:519:LEU:CD1	2.32	0.60
1:A:344:GLU:HB2	1:A:348:GLU:OE2	2.02	0.60
1:D:121:GLN:CB	1:D:133:THR:HG23	2.31	0.60
1:G:166:MET:CE	1:G:171:CYS:HB3	2.27	0.60
1:C:478:GLY:HA3	1:C:505:ASN:HB2	1.81	0.60
1:D:413:ARG:NE	1:D:458:VAL:HB	2.16	0.60
1:F:276:ARG:HG2	1:F:276:ARG:HH11	1.66	0.60
1:A:311:THR:CA	1:A:318:MET:HE1	2.28	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:141:LEU:HD11	1:B:196:PHE:HZ	1.65	0.60
1:C:504:ARG:NH2	1:C:506:GLN:HB3	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:121:GLN:CB	1:B:133:THR:HG23	2.31	0.60
1:E:486:LEU:HB3	1:E:493:ARG:HD2	1.84	0.60
1:G:208:MET:HE1	1:G:232:VAL:CA	2.20	0.60
1:D:442:ILE:CD1	1:D:492:LEU:HD11	2.31	0.60
1:E:502:LEU:N	1:E:502:LEU:HD12	2.16	0.60
1:D:145:HIS:CE1	1:D:146:LEU:HD23	2.37	0.60
1:B:477:GLU:HG3	1:B:507:GLN:NE2	2.15	0.60
1:F:486:LEU:HD12	1:F:493:ARG:CD	2.32	0.60
1:E:446:MET:HE2	1:E:492:LEU:HB3	1.82	0.60
1:D:338:GLY:HA3	1:D:412:MET:HE3	1.84	0.60
1:G:268:ALA:HA	1:G:271:LEU:HD13	1.82	0.60
1:G:111:TYR:CZ	1:G:142:PHE:HB2	2.36	0.60
1:F:260:TRP:C	1:F:261:ILE:HG13	2.23	0.60
1:B:478:GLY:HA3	1:B:505:ASN:HB2	1.83	0.60
1:G:94:ALA:HB1	1:G:162:MET:HE3	1.83	0.60
1:F:223:LEU:HD23	1:F:224:PRO:HD2	1.83	0.60
1:C:477:GLU:HG3	1:C:507:GLN:NE2	2.17	0.60
1:C:208:MET:HE1	1:C:232:VAL:CA	2.16	0.60
1:A:294:GLY:O	1:A:295:ILE:C	2.39	0.60
1:G:307:VAL:O	1:G:307:VAL:HG12	2.01	0.60
1:G:194:GLU:CD	1:G:194:GLU:H	2.04	0.60
1:A:229:ARG:HB3	1:A:258:GLY:O	2.01	0.59
1:A:482:SER:H	1:A:485:ASP:CB	2.14	0.59
1:E:510:MET:HE2	1:E:547:TYR:HE1	1.67	0.59
1:A:141:LEU:HD13	1:A:176:VAL:CG2	2.32	0.59
1:D:478:GLY:HA3	1:D:505:ASN:HB2	1.85	0.59
1:A:480:PRO:HA	1:A:503:GLU:OE1	2.01	0.59
1:G:303:ARG:CZ	1:G:523:PHE:CD1	2.85	0.59
1:G:372:ILE:HA	1:G:375:ASN:OD1	2.01	0.59
1:A:306:GLU:HA	1:A:497:ASP:OD2	2.02	0.59
1:G:326:ALA:HB2	1:G:422:ILE:HD12	1.84	0.59
1:A:287:LEU:HD11	1:A:335:LYS:HG3	1.83	0.59
1:D:287:LEU:HD11	1:D:335:LYS:HG3	1.84	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:F:368:LEU:HD22	1:F:372:ILE:HG23	1.85	0.59
1:B:484:THR:O	1:B:486:LEU:N	2.35	0.59
1:A:96:TYR:HE2	1:A:107:GLN:HE21	1.49	0.59
1:C:441:MET:HE2	1:C:444:ASN:HB3	1.83	0.59
1:B:152:LYS:HD3	1:B:203:ILE:CD1	2.30	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:A:410:ALA:HA	1:A:452:PHE:CE1	2.38	0.59
1:E:441:MET:CE	1:E:444:ASN:HB3	2.32	0.59
1:C:107:GLN:CB	1:C:124:ARG:CG	2.78	0.59
1:D:521:CYS:O	1:D:525:GLY:N	2.33	0.59
1:B:442:ILE:HD11	1:B:492:LEU:HD11	1.83	0.59
1:C:162:MET:SD	1:C:166:MET:HG3	2.42	0.59
1:C:473:LYS:CG	1:C:479:ARG:HB2	2.32	0.59
1:C:473:LYS:HE2	1:C:479:ARG:CA	2.31	0.59
1:D:424:ASP:O	1:D:425:HIS:HB3	2.01	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:F:546:SER:O	1:F:547:TYR:CB	2.42	0.59
1:C:366:ASP:HB2	1:D:284:SER:OG	2.03	0.59
1:F:366:ASP:CB	1:G:284:SER:OG	2.50	0.59
1:E:251:MET:HA	1:E:251:MET:CE	2.33	0.59
1:D:290:SER:H	1:D:325:GLN:HE22	1.44	0.59
1:B:440:LYS:O	1:B:440:LYS:HE2	2.02	0.59
1:C:316:MET:HE1	1:C:535:TYR:CE2	2.37	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:288:LEU:HD12	1:A:288:LEU:N	2.18	0.59
1:A:476:GLU:CD	1:A:476:GLU:H	2.06	0.59
1:D:366:ASP:CB	1:E:284:SER:OG	2.31	0.59
1:C:440:LYS:O	1:C:440:LYS:HE2	2.02	0.59
1:F:382:PHE:CE1	1:G:272:ARG:HA	2.38	0.59
1:E:186:LYS:CD	1:E:218:GLU:HG3	2.28	0.59
1:C:74:SER:HB2	1:C:99:ALA:HB1	1.83	0.59
1:A:344:GLU:CG	1:A:349:THR:HG22	2.30	0.59
1:A:168:LEU:HD22	1:A:247:ASP:OD2	2.03	0.59
1:C:152:LYS:HD3	1:C:203:ILE:CD1	2.30	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:A:216:VAL:HG11	1:A:230:VAL:HG21	1.83	0.59
1:G:220:ALA:CB	1:G:261:ILE:HD13	2.32	0.59
1:E:124:ARG:HD3	1:E:125:ASP:C	2.23	0.59
1:D:442:ILE:HD11	1:D:492:LEU:CD2	2.31	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:E:229:ARG:CZ	1:E:259:PRO:HB3	2.32	0.59
1:B:288:LEU:HD12	1:B:288:LEU:N	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:84:ARG:HA	1:B:243:LEU:HD21	1.84	0.59
1:D:480:PRO:HA	1:D:503:GLU:OE1	2.03	0.59
1:B:484:THR:C	1:B:486:LEU:N	2.56	0.59
1:E:394:TYR:CE2	1:E:405:LEU:HD12	2.38	0.59
1:B:471:LYS:HB3	1:B:479:ARG:HH11	1.68	0.59
1:B:285:VAL:HG12	1:B:285:VAL:O	2.03	0.59
1:C:223:LEU:HD23	1:C:224:PRO:HD2	1.84	0.59
1:F:450:LYS:CE	1:F:454:LYS:CD	2.79	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: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: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:G:141:LEU:HD11	1:G:196:PHE:HZ	1.68	0.58
1:B:178:LEU:HB2	1:B:181:GLY:HA2	1.83	0.58
1:C:536:ASN:C	1:C:536:ASN:HD22	2.06	0.58
1:D:251:MET:HA	1:D:251:MET:CE	2.33	0.58
1:C:229:ARG:HA	1:C:259:PRO:HA	1.84	0.58
1:F:124:ARG:HD3	1:F:125:ASP:C	2.23	0.58
1:D:394:TYR:C	1:D:394:TYR:CD1	2.76	0.58
1:G:442:ILE:HD12	1:G:488:GLY:CA	2.32	0.58
1:C:517:ARG:HB3	1:C:519:LEU:CD1	2.33	0.58
1:D:515:LEU:HD21	1:D:529:ILE:HD11	1.85	0.58
1:A:480:PRO:HA	1:A:503:GLU:OE2	2.03	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:C:86:ILE:HG21	1:C:163:LEU:HD12	1.83	0.58
1:D:467:LYS:HE3	1:D:486:LEU:O	2.03	0.58
1:A:253:GLN:C	1:A:257:ALA:HB2	2.23	0.58
1:E:425:HIS:CE1	1:E:427:SER:CB	2.86	0.58
1:D:440:LYS:CE	1:D:441:MET:HA	2.33	0.58
1:D:186:LYS:CD	1:D:218:GLU:HG3	2.29	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:F:413:ARG:O	1:F:417:GLY:HA2	2.02	0.58
1:F:356:LEU:HD12	1:F:541:TRP:NE1	2.18	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
1:G:121:GLN:CB	1:G:133:THR:HG23	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:181:GLY:O	1:A:182:ALA:C	2.40	0.58
1:F:261:ILE:O	1:F:263:ASP:N	2.36	0.58
1:G:262:PRO:HB2	1:G:265:VAL:HG12	1.85	0.58
1:C:230:VAL:N	1:C:258:GLY:O	2.35	0.58
1:F:124:ARG:CZ	1:F:126:LYS:HA	2.34	0.58
1:F:344:GLU:CG	1:F:349:THR:HG22	2.28	0.58
1:E:152:LYS:HD3	1:E:203:ILE:CD1	2.31	0.58
1:C:480:PRO:HA	1:C:503:GLU:OE1	2.03	0.58
1:A:369:LYS:HG2	1:C:279:LEU:HD22	1.85	0.58
1:A:121:GLN:HB3	1:A:133:THR:HG23	1.85	0.58
1:E:471:LYS:HB3	1:E:479:ARG:NH1	2.18	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:E:227:LYS:O	1:E:229:ARG:HD2	2.03	0.58
1:C:536:ASN:ND2	1:C:538:GLU:H	2.01	0.58
1:F:322:VAL:CG1	1:F:422:ILE:HG21	2.33	0.58
1:E:496:SER:O	1:E:520:LYS:HE2	2.04	0.58
1:G:321:PHE:HD2	1:G:533:MET:HE1	1.68	0.58
1:F:141:LEU:HD11	1:F:196:PHE:HZ	1.69	0.58
1:D:484:THR:C	1:D:486:LEU:H	2.07	0.58
1:A:412:MET:HE2	1:A:421:ILE:HD12	1.81	0.58
1:C:492:LEU:CD1	1:C:492:LEU:H	2.17	0.58
1:F:394:TYR:C	1:F:394:TYR:CD1	2.77	0.58
1:C:520:LYS:HG3	1:C:521:CYS:N	2.14	0.58
1:F:478:GLY:HA3	1:F:505:ASN:HB2	1.85	0.58
1:B:166:MET:HG2	1:B:175:VAL:HG23	1.85	0.58
1:C:536:ASN:ND2	1:C:538:GLU:CB	2.67	0.58
1:F:86:ILE:HD12	1:F:163:LEU:HB3	1.85	0.58
1:A:452:PHE:O	1:A:456:THR:HG23	2.04	0.58
1:C:202:ILE:HD13	1:C:223:LEU:HD22	1.84	0.58
1:F:452:PHE:O	1:F:456:THR:HG23	2.03	0.58
1:D:322:VAL:CG2	1:D:463:ILE:HD11	2.34	0.58
1:A:195:TYR:O	1:A:198:GLN:HB2	2.03	0.58
1:F:490:GLY:CA	1:F:493:ARG:HG3	2.34	0.58
1:D:499:ILE:CG2	1:D:519:LEU:CB	2.82	0.58
1:B:494:GLN:HE21	1:G:428:ILE:HG13	1.69	0.58
1:E:152:LYS:HG3	1:E:201:GLN:CG	2.34	0.58
1:D:413:ARG:HH21	1:D:458:VAL:N	2.01	0.58
1:E:382:PHE:HE1	1:F:275:ILE:HD12	1.69	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:145:HIS:CE1	1:D:146:LEU:CD2	2.87	0.58
1:F:378:PHE:HE2	1:G:276:ARG:HD3	1.66	0.58
1:A:145:HIS:CE1	1:A:146:LEU:CD2	2.86	0.58
1:E:425:HIS:CE1	1:E:427:SER:HB2	2.38	0.58
1:D:492:LEU:HD12	1:D:492:LEU:N	2.12	0.58
1:E:442:ILE:HD11	1:E:492:LEU:CD2	2.34	0.58
1:B:494:GLN:NE2	1:G:428:ILE:HG13	2.19	0.58
1:G:510:MET:HE2	1:G:513:LEU:HD22	1.85	0.58
1:D:368:LEU:HD22	1:D:372:ILE:HG23	1.85	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:268:ALA:HA	1:B:271:LEU:CD1	2.34	0.58
1:F:467:LYS:HE3	1:F:486:LEU:O	2.04	0.58
1:C:405:LEU:HG	1:C:409:LEU:CD1	2.32	0.58
1:A:91:CYS:HB3	1:A:96:TYR:O	2.04	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: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:510:MET:HB3	1:A:513:LEU:HB2	1.86	0.57
1:B:427:SER:CB	1:B:487:ARG:HH12	2.15	0.57
1:E:394:TYR:CD1	1:E:394:TYR:C	2.77	0.57
1:A:504:ARG:HH21	1:A:506:GLN:HB3	1.69	0.57
1:F:166:MET:HG2	1:F:175:VAL:CG2	2.34	0.57
1:A:279:LEU:HD23	1:B:369:LYS:HG2	1.87	0.57
1:C:344:GLU:CG	1:C:349:THR:HG22	2.30	0.57
1:B:153:ILE:HG13	1:B:174:PRO:HB2	1.86	0.57
1:A:413:ARG:NE	1:A:458:VAL:HB	2.18	0.57
1:A:346:VAL:CG2	1:C:271:LEU:HD21	2.34	0.57
1:B:321:PHE:CD2	1:B:533:MET:CE	2.86	0.57
1:A:368:LEU:HD22	1:A:372:ILE:HG23	1.86	0.57
1:G:322:VAL:CG2	1:G:463:ILE:HD11	2.33	0.57
1:F:195:TYR:O	1:F:198:GLN:HB2	2.04	0.57
1:A:290:SER:H	1:A:325:GLN:HE22	1.46	0.57
1:D:440:LYS:O	1:D:440:LYS:HE2	2.04	0.57
1:F:499:ILE:CG2	1:F:519:LEU:CB	2.81	0.57
1:E:510:MET:HE3	1:E:547:TYR:HE1	1.68	0.57
1:E:166:MET:CE	1:E:171:CYS:HB3	2.35	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:339:LEU:CB	1:G:341:MET:HE1	2.28	0.57
1:G:124:ARG:HD3	1:G:125:ASP:C	2.24	0.57
1:C:186:LYS:CD	1:C:218:GLU:HG3	2.29	0.57
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:E:283:GLU:CG	1:E:284:SER:N	2.64	0.57
1:A:312:SER:CB	1:A:502:LEU:O	2.47	0.57
1:E:437:ASP:OD1	1:E:439:ARG:HB2	2.04	0.57
1:D:421:ILE:HB	1:D:460:LEU:HD12	1.87	0.57
1:G:312:SER:CB	1:G:502:LEU:O	2.50	0.57
1:B:480:PRO:HA	1:B:503:GLU:CD	2.24	0.57
1:D:480:PRO:HA	1:D:503:GLU:CD	2.24	0.57
1:D:322:VAL:HG21	1:D:463:ILE:HD11	1.86	0.57
1:D:477:GLU:HG3	1:D:507:GLN:NE2	2.18	0.57
1:C:229:ARG:NH2	1:C:259:PRO:CB	2.68	0.57
1:E:401:GLU:CG	1:E:402:THR:N	2.66	0.57
1:E:338:GLY:HA3	1:E:412:MET:HE3	1.87	0.57
1:G:446:MET:HE2	1:G:492:LEU:HB3	1.85	0.57
1:G:153:ILE:HG13	1:G:174:PRO:HB2	1.86	0.57
1:C:289:PHE:H	1:C:296:ASN:ND2	1.99	0.57
1:G:216:VAL:CG1	1:G:230:VAL:CG2	2.82	0.57
1:E:413:ARG:NE	1:E:458:VAL:HB	2.15	0.57
1:E:141:LEU:CD1	1:E:176:VAL:HG21	2.34	0.57
1:E:94:ALA:HB1	1:E:162:MET:HE3	1.87	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:D:347:GLU:CD	1:E:274:ARG:HD2	2.24	0.57
1:A:122:LYS:HE2	1:A:159:GLU:OE1	2.04	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: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:480:PRO:HA	1:E:503:GLU:OE1	2.05	0.57
1:E:386:PHE:O	1:F:269:LEU:HD21	2.04	0.57
1:A:510:MET:CE	1:A:513:LEU:HD22	2.34	0.57
1:G:401:GLU:CG	1:G:431:SER:O	2.50	0.57
1:G:74:SER:HB2	1:G:99:ALA:HB1	1.87	0.57
1:E:141:LEU:HD11	1:E:196:PHE:HZ	1.69	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:A:478:GLY:HA3	1:A:505:ASN:HB2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:536:ASN:HD22	1:F:538:GLU:H	1.53	0.57
1:D:427:SER:HB3	1:D:487:ARG:NH1	2.19	0.57
1:C:441:MET:HE3	1:C:444:ASN:HB3	1.87	0.57
1:B:241:CYS:HB2	1:B:250:ILE:HD11	1.85	0.57
1:B:74:SER:HB3	1:B:101:VAL:HG22	1.87	0.57
1:A:346:VAL:HB	1:A:395:ASP:HB2	1.87	0.57
1:G:251:MET:HA	1:G:251:MET:CE	2.35	0.57
1:F:486:LEU:HD12	1:F:493:ARG:CG	2.35	0.56
1:A:413:ARG:O	1:A:417:GLY:HA2	2.05	0.56
1:E:471:LYS:HB3	1:E:479:ARG:HH11	1.69	0.56
1:A:402:THR:HG23	1:A:403:ASP:H	1.70	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: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:G:484:THR:C	1:G:486:LEU:N	2.58	0.56
1:E:424:ASP:O	1:E:425:HIS:HB3	2.05	0.56
1:E:486:LEU:HD13	1:E:487:ARG:O	2.05	0.56
1:G:438:GLU:O	1:G:442:ILE:HG22	2.05	0.56
1:C:532:TYR:N	1:C:532:TYR:CD1	2.73	0.56
1:F:186:LYS:HD3	1:F:218:GLU:CG	2.30	0.56
1:G:186:LYS:CD	1:G:218:GLU:HG3	2.30	0.56
1:B:438:GLU:O	1:B:442:ILE:HG22	2.05	0.56
1:G:74:SER:HB3	1:G:101:VAL:HG22	1.87	0.56
1:E:480:PRO:HA	1:E:503:GLU:CD	2.26	0.56
1:F:369:LYS:HG2	1:G:279:LEU:HD23	1.88	0.56
1:E:122:LYS:HE2	1:E:159:GLU:OE1	2.05	0.56
1:F:482:SER:N	1:F:485:ASP:HB2	2.19	0.56
1:A:313:GLY:O	1:A:315:GLY:N	2.38	0.56
1:E:483:ILE:O	1:E:486:LEU:CB	2.38	0.56
1:C:424:ASP:O	1:C:425:HIS:HB3	2.06	0.56
1:E:368:LEU:O	1:E:368:LEU:HD22	2.05	0.56
1:G:447:THR:HA	1:G:495:LEU:HD23	1.87	0.56
1:G:499:ILE:CG2	1:G:519:LEU:CB	2.83	0.56
1:E:216:VAL:HG11	1:E:230:VAL:HG22	1.83	0.56
1:E:515:LEU:HD21	1:E:529:ILE:HD11	1.86	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:473:LYS:CE	1:C:479:ARG:HA	2.34	0.56
1:A:477:GLU:HG3	1:A:507:GLN:NE2	2.21	0.56
1:C:322:VAL:CG1	1:C:422:ILE:HG21	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:477:GLU:HG3	1:G:507:GLN:NE2	2.19	0.56
1:G:151:LYS:HG2	1:G:200:GLU:OE2	2.05	0.56
1:A:307:VAL:O	1:A:307:VAL:HG12	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: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:A:345:SER:O	1:A:349:THR:HG23	2.05	0.56
1:E:233:LEU:HD22	1:E:241:CYS:SG	2.45	0.56
1:E:121:GLN:CB	1:E:133:THR:HG23	2.36	0.56
1:A:166:MET:HG2	1:A:175:VAL:HG23	1.88	0.56
1:F:473:LYS:CG	1:F:479:ARG:HB2	2.33	0.56
1:E:276:ARG:HH11	1:E:276:ARG:CG	2.18	0.56
1:A:486:LEU:HB3	1:A:493:ARG:HD2	1.86	0.56
1:C:394:TYR:C	1:C:394:TYR:CD1	2.78	0.56
1:G:446:MET:HE3	1:G:492:LEU:HA	1.87	0.56
1:F:181:GLY:O	1:F:182:ALA:C	2.43	0.56
1:C:154:VAL:HG21	1:C:254:VAL:HG22	1.87	0.56
1:B:216:VAL:HG11	1:B:230:VAL:HG22	1.85	0.56
1:E:229:ARG:NH2	1:E:259:PRO:CG	2.68	0.56
1:C:364:GLN:HA	1:D:523:PHE:CZ	2.40	0.56
1:C:229:ARG:NE	1:C:259:PRO:HB3	2.20	0.56
1:D:262:PRO:HB2	1:D:265:VAL:HG12	1.86	0.56
1:G:486:LEU:HB3	1:G:493:ARG:HD2	1.87	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:A:369:LYS:CG	1:C:279:LEU:CD2	2.83	0.56
1:E:322:VAL:HG21	1:E:463:ILE:CD1	2.35	0.56
1:C:328:GLN:HA	1:C:331:THR:OG1	2.05	0.56
1:E:336:LYS:HB3	1:E:418:CYS:HB3	1.88	0.56
1:C:546:SER:O	1:C:547:TYR:HB2	2.05	0.56
1:F:178:LEU:HB2	1:F:181:GLY:HA2	1.87	0.56
1:D:205:MET:HG3	1:D:231:ALA:CB	2.35	0.56
1:F:268:ALA:HA	1:F:271:LEU:HD12	1.88	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:F:152:LYS:HD3	1:F:203:ILE:CD1	2.33	0.56
1:G:473:LYS:CG	1:G:479:ARG:HB2	2.34	0.56
1:F:515:LEU:HD21	1:F:529:ILE:HD11	1.87	0.56
1:E:359:ARG:HD3	1:E:541:TRP:NE1	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:151:LYS:HG2	1:C:200:GLU:OE2	2.05	0.56
1:B:343:GLU:HA	1:B:343:GLU:OE1	2.06	0.56
1:G:336:LYS:HB3	1:G:418:CYS:HA	1.87	0.56
1:A:499:ILE:CG2	1:A:519:LEU:CB	2.84	0.56
1:E:74:SER:HB2	1:E:99:ALA:HB1	1.88	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:F:471:LYS:HB3	1:F:479:ARG:NH1	2.21	0.56
1:A:473:LYS:CG	1:A:479:ARG:HB2	2.35	0.56
1:D:347:GLU:OE2	1:E:274:ARG:HD2	2.06	0.56
1:B:424:ASP:O	1:B:425:HIS:HB3	2.06	0.56
1:E:477:GLU:HG3	1:E:507:GLN:NE2	2.20	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:413:ARG:HH21	1:C:458:VAL:N	2.03	0.56
1:C:382:PHE:HE1	1:D:275:ILE:HD12	1.71	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:E:394:TYR:HE1	1:E:396:SER:CB	2.19	0.55
1:G:515:LEU:HD21	1:G:529:ILE:HD12	1.89	0.55
1:F:152:LYS:HG3	1:F:201:GLN:CG	2.34	0.55
1:D:369:LYS:CG	1:E:279:LEU:HD22	2.35	0.55
1:D:195:TYR:O	1:D:198:GLN:HB2	2.05	0.55
1:C:439:ARG:O	1:C:442:ILE:HG22	2.06	0.55
1:E:504:ARG:HH21	1:E:506:GLN:CB	2.19	0.55
1:E:312:SER:CB	1:E:502:LEU:O	2.53	0.55
1:A:351:GLU:HB2	1:A:363:ARG:HD2	1.88	0.55
1:E:473:LYS:CG	1:E:479:ARG:HB2	2.35	0.55
1:F:389:ASP:CA	1:G:269:LEU:HD23	2.36	0.55
1:F:74:SER:HB3	1:F:101:VAL:HG22	1.88	0.55
1:A:268:ALA:HA	1:A:271:LEU:HD13	1.87	0.55
1:D:276:ARG:HG2	1:D:276:ARG:HH11	1.69	0.55
1:A:229:ARG:HB3	1:A:259:PRO:HA	1.88	0.55
1:G:482:SER:N	1:G:485:ASP:HB2	2.19	0.55
1:C:438:GLU:O	1:C:442:ILE:HG22	2.06	0.55
1:A:521:CYS:O	1:A:525:GLY:N	2.34	0.55
1:C:471:LYS:HB3	1:C:479:ARG:NH1	2.21	0.55
1:A:429:VAL:HG23	1:A:430:VAL:H	1.71	0.55
1:F:141:LEU:HD13	1:F:176:VAL:CG2	2.35	0.55
1:C:322:VAL:CG2	1:C:463:ILE:HD11	2.37	0.55
1:D:429:VAL:HG23	1:D:430:VAL:H	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:262:PRO:HB2	1:F:265:VAL:HG12	1.88	0.55
1:A:318:MET:SD	1:A:463:ILE:HD12	2.46	0.55
1:F:480:PRO:HA	1:F:503:GLU:OE1	2.05	0.55
1:B:345:SER:O	1:B:349:THR:HG23	2.06	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:B:351:GLU:HB2	1:B:363:ARG:HD2	1.89	0.55
1:E:195:TYR:O	1:E:198:GLN:HB2	2.06	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:E:499:ILE:CG2	1:E:519:LEU:CB	2.84	0.55
1:C:166:MET:HE1	1:C:171:CYS:CB	2.32	0.55
1:F:478:GLY:CA	1:F:505:ASN:HB2	2.37	0.55
1:D:536:ASN:ND2	1:D:538:GLU:H	2.04	0.55
1:A:405:LEU:HG	1:A:409:LEU:CD1	2.34	0.55
1:C:216:VAL:CG1	1:C:230:VAL:CG2	2.84	0.55
1:E:290:SER:N	1:E:325:GLN:HE21	1.97	0.55
1:G:442:ILE:HD11	1:G:492:LEU:HD11	1.89	0.55
1:G:147:TRP:CG	1:G:174:PRO:HB3	2.42	0.55
1:F:321:PHE:CD2	1:F:533:MET:CE	2.88	0.55
1:E:205:MET:HG3	1:E:231:ALA:CB	2.36	0.55
1:B:111:TYR:CZ	1:B:142:PHE:HB2	2.42	0.55
1:A:359:ARG:HD3	1:A:541:TRP:NE1	2.22	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:B:412:MET:CA	1:B:416:LEU:HD12	2.24	0.55
1:F:392:HIS:ND1	1:G:267:SER:HB2	2.21	0.55
1:A:454:LYS:HE3	1:A:522:ARG:HH22	1.72	0.55
1:G:405:LEU:HG	1:G:409:LEU:CD1	2.36	0.55
1:D:496:SER:HB2	1:D:499:ILE:HD11	1.87	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:G:229:ARG:NH2	1:G:259:PRO:HG3	2.21	0.55
1:E:154:VAL:HG21	1:E:254:VAL:HG22	1.88	0.55
1:C:515:LEU:HD21	1:C:529:ILE:HD11	1.89	0.55
1:D:352:ASP:CG	1:D:363:ARG:HD3	2.26	0.55
1:B:312:SER:CB	1:B:502:LEU:O	2.55	0.55
1:A:243:LEU:O	1:A:244:ASN:O	2.25	0.55
1:G:122:LYS:HE2	1:G:159:GLU:OE1	2.06	0.55
1:B:122:LYS:HE2	1:B:159:GLU:OE1	2.07	0.55
1:E:484:THR:C	1:E:486:LEU:H	2.10	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:401:GLU:CG	1:E:402:THR:H	2.19	0.55
1:G:447:THR:HG22	1:G:495:LEU:CD2	2.26	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:B:205:MET:HG3	1:B:231:ALA:CB	2.36	0.55
1:D:360:VAL:O	1:D:360:VAL:HG23	2.07	0.55
1:G:352:ASP:CG	1:G:363:ARG:HD3	2.27	0.55
1:F:202:ILE:HD13	1:F:223:LEU:HD22	1.89	0.55
1:C:322:VAL:HG21	1:C:463:ILE:HD11	1.89	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:162:MET:SD	1:A:166:MET:HG3	2.46	0.55
1:A:162:MET:HG2	1:A:175:VAL:HB	1.89	0.55
1:E:369:LYS:HG2	1:F:279:LEU:CD2	2.37	0.55
1:F:260:TRP:CB	1:F:262:PRO:CD	2.44	0.55
1:A:126:LYS:NZ	1:A:127:ASP:OD1	2.40	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:C:121:GLN:HB2	1:C:133:THR:HG1	1.71	0.55
1:F:471:LYS:HB3	1:F:479:ARG:HH11	1.72	0.55
1:F:336:LYS:HB3	1:F:418:CYS:HA	1.89	0.55
1:A:276:ARG:HH11	1:A:276:ARG:HG2	1.71	0.55
1:E:476:GLU:H	1:E:476:GLU:CD	2.09	0.55
1:A:322:VAL:CG2	1:A:463:ILE:HD11	2.37	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:E:440:LYS:CE	1:E:441:MET:HA	2.36	0.54
1:E:126:LYS:HG2	1:E:127:ASP:H	1.72	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:D:91:CYS:HB3	1:D:96:TYR:O	2.07	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:C:512:ASN:HD21	1:C:537:LYS:HE3	1.71	0.54
1:D:126:LYS:HG2	1:D:127:ASP:H	1.73	0.54
1:C:338:GLY:HA3	1:C:412:MET:HE3	1.88	0.54
1:B:504:ARG:HH21	1:B:506:GLN:CB	2.20	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:E:303:ARG:CZ	1:E:523:PHE:CD1	2.90	0.54
1:A:402:THR:HG23	1:A:403:ASP:N	2.22	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:A:79:SER:H	1:A:98:ILE:CD1	2.20	0.54
1:F:521:CYS:SG	1:F:524:THR:HG23	2.47	0.54
1:A:420:VAL:HG22	1:A:459:VAL:HB	1.88	0.54
1:D:359:ARG:HD3	1:D:541:TRP:NE1	2.20	0.54
1:A:259:PRO:O	1:A:259:PRO:HD2	2.08	0.54
1:C:260:TRP:C	1:C:261:ILE:HD13	2.27	0.54
1:F:91:CYS:HB3	1:F:96:TYR:O	2.07	0.54
1:D:142:PHE:CE2	1:D:162:MET:HE3	2.42	0.54
1:B:303:ARG:CZ	1:B:523:PHE:CD1	2.90	0.54
1:C:283:GLU:CD	1:C:286:GLY:HA2	2.27	0.54
1:B:275:ILE:HD12	1:G:382:PHE:HE1	1.72	0.54
1:D:288:LEU:N	1:D:288:LEU:HD12	2.21	0.54
1:D:484:THR:C	1:D:486:LEU:N	2.59	0.54
1:F:286:GLY:O	1:F:302:ALA:N	2.41	0.54
1:D:521:CYS:SG	1:D:524:THR:HG23	2.48	0.54
1:G:429:VAL:HG23	1:G:430:VAL:H	1.72	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:E:321:PHE:CD2	1:E:533:MET:CE	2.90	0.54
1:C:352:ASP:CG	1:C:363:ARG:HD3	2.27	0.54
1:A:318:MET:SD	1:A:463:ILE:HD13	2.47	0.54
1:A:232:VAL:HG12	1:A:232:VAL:O	2.06	0.54
1:F:440:LYS:O	1:F:440:LYS:HE2	2.07	0.54
1:C:486:LEU:HB3	1:C:493:ARG:HD2	1.90	0.54
1:G:521:CYS:SG	1:G:524:THR:HG23	2.48	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:B:141:LEU:CD1	1:B:176:VAL:HG21	2.34	0.54
1:E:546:SER:O	1:E:547:TYR:HB2	2.07	0.54
1:C:268:ALA:HA	1:C:271:LEU:HD12	1.90	0.54
1:F:74:SER:HB2	1:F:99:ALA:HB1	1.90	0.54
1:E:346:VAL:HB	1:E:395:ASP:HB2	1.88	0.54
1:G:480:PRO:HA	1:G:503:GLU:CD	2.28	0.54
1:B:397:PHE:C	1:B:397:PHE:CD1	2.80	0.54
1:A:112:ARG:NH2	1:A:118:ILE:HD11	2.23	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
1:C:536:ASN:HD21	1:C:538:GLU:HB2	1.71	0.54
1:E:318:MET:CE	1:E:465:HIS:CD2	2.91	0.54
1:E:151:LYS:HG2	1:E:200:GLU:OE2	2.08	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:C:484:THR:C	1:C:486:LEU:H	2.09	0.54
1:C:317:VAL:HG21	1:C:504:ARG:HD2	1.90	0.54
1:B:421:ILE:HB	1:B:460:LEU:HD12	1.90	0.54
1:B:265:VAL:HG11	1:G:411:TYR:HE1	1.73	0.54
1:E:521:CYS:O	1:E:525:GLY:N	2.34	0.54
1:F:241:CYS:HB2	1:F:250:ILE:HD11	1.90	0.54
1:F:233:LEU:HD22	1:F:241:CYS:SG	2.48	0.54
1:D:536:ASN:ND2	1:D:538:GLU:CB	2.71	0.54
1:D:223:LEU:HD23	1:D:224:PRO:HD2	1.90	0.54
1:F:320:THR:HG22	1:F:324:GLN:NE2	2.23	0.54
1:C:122:LYS:HE3	1:C:130:PHE:CE2	2.43	0.54
1:E:343:GLU:HA	1:E:343:GLU:OE1	2.07	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:B:447:THR:HA	1:B:495:LEU:HD23	1.90	0.54
1:F:186:LYS:CD	1:F:218:GLU:HG3	2.32	0.54
1:E:241:CYS:HB2	1:E:250:ILE:HD11	1.89	0.54
1:F:294:GLY:O	1:F:295:ILE:C	2.42	0.54
1:E:392:HIS:ND1	1:F:267:SER:HB2	2.23	0.54
1:E:382:PHE:CE1	1:F:272:ARG:HA	2.43	0.54
1:C:351:GLU:HB2	1:C:363:ARG:HD2	1.90	0.54
1:F:369:LYS:HG2	1:G:279:LEU:CD2	2.37	0.54
1:E:536:ASN:HD22	1:E:538:GLU:H	1.56	0.54
1:D:487:ARG:O	1:D:493:ARG:HD3	2.08	0.54
1:F:446:MET:CE	1:F:492:LEU:HA	2.38	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:C:153:ILE:HG13	1:C:174:PRO:HB2	1.89	0.54
1:D:471:LYS:HB3	1:D:479:ARG:HH11	1.72	0.54
1:F:111:TYR:CZ	1:F:142:PHE:HB2	2.43	0.54
1:E:512:ASN:HD21	1:E:537:LYS:HE3	1.73	0.54
1:C:411:TYR:CZ	1:D:262:PRO:HD3	2.42	0.54
1:C:208:MET:CE	1:C:232:VAL:HA	2.18	0.54
1:E:401:GLU:HG2	1:E:402:THR:H	1.71	0.54
1:C:166:MET:HG2	1:C:175:VAL:HG23	1.90	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
1:C:145:HIS:CE1	1:C:146:LEU:CD2	2.91	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

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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: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:G:450:LYS:CE	1:G:454:LYS:CD	2.81	0.53
1:G:492:LEU:HD12	1:G:492:LEU:N	2.12	0.53
1:F:499:ILE:HG22	1:F:519:LEU:CB	2.27	0.53
1:D:111:TYR:CZ	1:D:142:PHE:HB2	2.43	0.53
1:E:515:LEU:HD21	1:E:529:ILE:HD12	1.91	0.53
1:G:311:THR:OG1	1:G:466:LEU:HD21	2.07	0.53
1:G:241:CYS:HB2	1:G:250:ILE:HD11	1.89	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:G:471:LYS:HB3	1:G:479:ARG:NH1	2.23	0.53
1:D:294:GLY:O	1:D:295:ILE:C	2.44	0.53
1:C:195:TYR:O	1:C:198:GLN:HB2	2.08	0.53
1:E:320:THR:HG22	1:E:324:GLN:NE2	2.23	0.53
1:F:372:ILE:HG13	1:F:378:PHE:HB2	1.90	0.53
1:D:401:GLU:HG2	1:D:402:THR:H	1.73	0.53
1:B:429:VAL:HG23	1:B:430:VAL:H	1.73	0.53
1:G:510:MET:HB3	1:G:513:LEU:HB2	1.90	0.53
1:C:147:TRP:CG	1:C:174:PRO:HB3	2.42	0.53
1:D:372:ILE:HG13	1:D:378:PHE:HB2	1.89	0.53
1:C:356:LEU:HD12	1:C:541:TRP:NE1	2.23	0.53
1:C:347:GLU:O	1:C:351:GLU:HG3	2.09	0.53
1:B:397:PHE:C	1:B:397:PHE:HD1	2.11	0.53
1:D:230:VAL:HB	1:D:260:TRP:NE1	2.22	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:C:486:LEU:HD12	1:C:493:ARG:CD	2.38	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:166:MET:CE	1:D:171:CYS:HB3	2.37	0.53
1:D:536:ASN:HD21	1:D:538:GLU:CB	2.20	0.53
1:B:413:ARG:O	1:B:417:GLY:HA2	2.08	0.53
1:D:217:GLU:OE2	1:D:261:ILE:CA	2.54	0.53
1:B:441:MET:CE	1:B:445:LEU:H	2.21	0.53
1:G:394:TYR:C	1:G:394:TYR:CD1	2.82	0.53
1:G:338:GLY:HA3	1:G:412:MET:HE1	1.90	0.53
1:B:86:ILE:HG21	1:B:163:LEU:CD1	2.38	0.53
1:C:471:LYS:HB3	1:C:479:ARG:HH11	1.72	0.53
1:C:268:ALA:HA	1:C:271:LEU:HD13	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:141:LEU:CD1	1:G:176:VAL:HG21	2.36	0.53
1:D:306:GLU:HA	1:D:497:ASP:OD2	2.08	0.53
1:D:318:MET:SD	1:D:463:ILE:HG23	2.48	0.53
1:B:235:CYS:CB	1:B:240:GLU:HG2	2.39	0.53
1:B:246:HIS:HB3	1:B:249:GLU:OE1	2.09	0.53
1:G:412:MET:CA	1:G:416:LEU:HD12	2.28	0.53
1:F:496:SER:CB	1:F:499:ILE:HD11	2.39	0.53
1:F:305:GLY:O	1:F:454:LYS:HD2	2.09	0.53
1:E:517:ARG:HB3	1:E:519:LEU:CD1	2.38	0.53
1:D:345:SER:O	1:D:349:THR:HG23	2.08	0.53
1:D:345:SER:O	1:D:349:THR:CG2	2.56	0.53
1:F:78:TYR:CD2	1:F:92:GLN:HG2	2.43	0.53
1:A:356:LEU:HD12	1:A:541:TRP:NE1	2.24	0.53
1:D:512:ASN:HD21	1:D:537:LYS:HE3	1.73	0.53
1:F:447:THR:HA	1:F:495:LEU:HD23	1.90	0.53
1:E:447:THR:HA	1:E:495:LEU:HD23	1.90	0.53
1:B:439:ARG:HG2	1:B:489:SER:OG	2.09	0.53
1:B:345:SER:O	1:B:349:THR:CG2	2.56	0.53
1:B:546:SER:O	1:B:547:TYR:HB2	2.08	0.53
1:B:322:VAL:HG21	1:B:463:ILE:CG1	2.38	0.53
1:G:256:ASN:ND2	1:G:256:ASN:O	2.42	0.53
1:B:307:VAL:O	1:B:307:VAL:HG12	2.07	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:C:440:LYS:C	1:C:440:LYS:HE2	2.28	0.53
1:B:445:LEU:HD12	1:B:445:LEU:O	2.09	0.53
1:A:166:MET:O	1:A:171:CYS:HB3	2.08	0.53
1:C:121:GLN:CB	1:C:133:THR:HG23	2.39	0.53
1:E:152:LYS:O	1:E:174:PRO:HD2	2.08	0.53
1:E:166:MET:HG2	1:E:175:VAL:HG23	1.91	0.53
1:B:154:VAL:HG21	1:B:254:VAL:HG22	1.90	0.53
1:E:164:THR:O	1:E:167:GLU:HB2	2.09	0.53
1:G:86:ILE:HG21	1:G:163:LEU:CD1	2.38	0.53
1:C:401:GLU:CG	1:C:402:THR:N	2.71	0.53
1:A:235:CYS:CB	1:A:240:GLU:HG2	2.39	0.53
1:G:343:GLU:HA	1:G:343:GLU:OE1	2.09	0.53
1:D:486:LEU:HD12	1:D:493:ARG:CD	2.38	0.53
1:F:286:GLY:O	1:F:287:LEU:O	2.27	0.53
1:A:504:ARG:HH21	1:A:506:GLN:CG	2.21	0.53
1:D:504:ARG:HH21	1:D:506:GLN:CB	2.21	0.53
1:A:510:MET:HB2	1:A:513:LEU:HB3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:91:CYS:HB3	1:B:96:TYR:O	2.09	0.53
1:E:312:SER:O	1:E:313:GLY:O	2.26	0.53
1:D:241:CYS:HB2	1:D:250:ILE:HD11	1.91	0.53
1:C:382:PHE:CE1	1:D:272:ARG:HA	2.44	0.53
1:A:321:PHE:HD2	1:A:533:MET:HE3	1.74	0.53
1:C:406:LEU:HD21	1:C:449:LEU:HD23	1.89	0.53
1:C:314:SER:O	1:C:315:GLY:C	2.47	0.53
1:D:394:TYR:CE2	1:D:405:LEU:HD12	2.44	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:B:536:ASN:ND2	1:B:538:GLU:H	2.07	0.53
1:E:86:ILE:HG21	1:E:163:LEU:CD1	2.39	0.53
1:D:322:VAL:HG21	1:D:463:ILE:CG1	2.39	0.53
1:A:324:GLN:OE1	1:A:541:TRP:CE3	2.61	0.53
1:D:180:HIS:HB2	1:D:184:ALA:HB3	1.91	0.53
1:A:343:GLU:OE1	1:A:343:GLU:HA	2.09	0.53
1:G:476:GLU:H	1:G:476:GLU:CD	2.11	0.53
1:F:125:ASP:OD1	1:F:129:ASN:HB2	2.08	0.53
1:D:232:VAL:O	1:D:232:VAL:HG12	2.07	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:E:114:GLN:NE2	1:E:195:TYR:HD1	2.07	0.53
1:A:164:THR:O	1:A:167:GLU:HB2	2.09	0.53
1:A:259:PRO:O	1:A:260:TRP:CB	2.46	0.52
1:C:411:TYR:OH	1:D:260:TRP:HA	2.09	0.52
1:A:262:PRO:HB2	1:A:265:VAL:HG12	1.90	0.52
1:G:412:MET:CE	1:G:421:ILE:CD1	2.87	0.52
1:B:152:LYS:O	1:B:174:PRO:HD2	2.09	0.52
1:E:510:MET:HE2	1:E:547:TYR:CE1	2.43	0.52
1:B:216:VAL:CG1	1:B:230:VAL:CG2	2.85	0.52
1:D:515:LEU:HD21	1:D:529:ILE:HD12	1.90	0.52
1:G:471:LYS:HB3	1:G:479:ARG:HH11	1.74	0.52
1:G:145:HIS:CE1	1:G:146:LEU:CD2	2.92	0.52
1:E:386:PHE:O	1:F:269:LEU:CD2	2.58	0.52
1:B:114:GLN:NE2	1:B:195:TYR:HD1	2.07	0.52
1:F:343:GLU:OE1	1:F:343:GLU:HA	2.09	0.52
1:G:487:ARG:O	1:G:493:ARG:HD3	2.09	0.52
1:E:484:THR:C	1:E:486:LEU:N	2.62	0.52
1:B:126:LYS:HG2	1:B:127:ASP:H	1.74	0.52
1:C:445:LEU:HD12	1:C:445:LEU:O	2.09	0.52
1:F:338:GLY:HA3	1:F:412:MET:HE3	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:106:TYR:HB3	1:C:123:VAL:HG12	1.91	0.52
1:G:166:MET:HE3	1:G:171:CYS:HA	1.91	0.52
1:A:347:GLU:CD	1:C:274:ARG:HG2	2.30	0.52
1:F:268:ALA:HA	1:F:271:LEU:HD13	1.91	0.52
1:G:145:HIS:CE1	1:G:146:LEU:HD23	2.44	0.52
1:F:86:ILE:HG21	1:F:163:LEU:CD1	2.39	0.52
1:B:359:ARG:HD3	1:B:541:TRP:NE1	2.23	0.52
1:D:230:VAL:HG11	1:D:260:TRP:NE1	2.24	0.52
1:E:232:VAL:O	1:E:232:VAL:HG12	2.08	0.52
1:G:492:LEU:H	1:G:492:LEU:CD1	2.05	0.52
1:A:344:GLU:OE1	1:A:349:THR:HB	2.10	0.52
1:A:74:SER:HB3	1:A:101:VAL:HG22	1.90	0.52
1:C:145:HIS:CE1	1:C:146:LEU:HD23	2.45	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:B:536:ASN:ND2	1:B:538:GLU:CB	2.72	0.52
1:A:536:ASN:ND2	1:A:538:GLU:H	2.08	0.52
1:D:122:LYS:HE3	1:D:130:PHE:CE2	2.45	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: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: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:74:SER:HB3	1:A:101:VAL:CG2	2.40	0.52
1:B:478:GLY:CA	1:B:505:ASN:HB2	2.39	0.52
1:D:344:GLU:OE1	1:D:349:THR:HB	2.10	0.52
1:G:166:MET:HG2	1:G:175:VAL:CG2	2.39	0.52
1:C:141:LEU:CD1	1:C:176:VAL:HG21	2.35	0.52
1:F:359:ARG:HD3	1:F:541:TRP:NE1	2.25	0.52
1:C:273:GLU:OE2	1:C:276:ARG:NH1	2.42	0.52
1:A:147:TRP:CG	1:A:174:PRO:HB3	2.45	0.52
1:F:445:LEU:CD1	1:F:449:LEU:HG	2.39	0.52
1:B:229:ARG:CB	1:B:258:GLY:O	2.58	0.52
1:G:205:MET:HG3	1:G:231:ALA:CB	2.39	0.52
1:F:401:GLU:CG	1:F:431:SER:O	2.57	0.52
1:F:347:GLU:O	1:F:351:GLU:HG3	2.09	0.52
1:B:487:ARG:O	1:B:493:ARG:HD3	2.10	0.52
1:F:440:LYS:CE	1:F:441:MET:HA	2.39	0.52
1:C:447:THR:HA	1:C:495:LEU:HD23	1.91	0.52
1:B:290:SER:N	1:B:325:GLN:HE21	2.02	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:A:478:GLY:CA	1:A:505:ASN:HB2	2.40	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:205:MET:HG3	1:A:231:ALA:CB	2.40	0.52
1:D:318:MET:SD	1:D:463:ILE:CD1	2.98	0.52
1:D:341:MET:SD	1:D:424:ASP:HB2	2.50	0.52
1:E:486:LEU:HD12	1:E:493:ARG:CD	2.39	0.52
1:B:338:GLY:HA3	1:B:412:MET:HE1	1.91	0.52
1:B:140:ALA:O	1:B:141:LEU:HD23	2.10	0.52
1:C:140:ALA:O	1:C:141:LEU:HD23	2.10	0.52
1:B:162:MET:SD	1:B:166:MET:HG3	2.49	0.52
1:A:536:ASN:HD21	1:A:538:GLU:CB	2.23	0.52
1:D:359:ARG:HD3	1:D:541:TRP:HE1	1.75	0.52
1:C:122:LYS:HE2	1:C:159:GLU:OE1	2.10	0.52
1:G:114:GLN:NE2	1:G:195:TYR:HD1	2.07	0.52
1:A:428:ILE:H	1:A:428:ILE:HD12	1.75	0.52
1:B:362:LEU:O	1:B:362:LEU:HD12	2.10	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:G:447:THR:CG2	1:G:495:LEU:HD21	2.27	0.52
1:G:440:LYS:O	1:G:440:LYS:HE2	2.10	0.52
1:B:440:LYS:HE2	1:B:440:LYS:C	2.30	0.52
1:B:439:ARG:O	1:B:442:ILE:CG2	2.57	0.52
1:D:164:THR:O	1:D:167:GLU:HB2	2.09	0.52
1:B:352:ASP:OD2	1:B:363:ARG:NH1	2.43	0.52
1:D:318:MET:SD	1:D:463:ILE:HD13	2.50	0.52
1:C:322:VAL:HG21	1:C:463:ILE:CG1	2.40	0.52
1:F:324:GLN:HE22	1:F:542:LEU:H	1.58	0.52
1:A:233:LEU:HD22	1:A:241:CYS:SG	2.50	0.52
1:B:305:GLY:O	1:B:454:LYS:HD2	2.10	0.52
1:C:504:ARG:HH21	1:C:506:GLN:HG2	1.73	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: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
1:B:304:GLY:HA2	1:B:459:VAL:HG22	1.92	0.52
1:B:311:THR:O	1:B:312:SER:HB3	2.10	0.52
1:A:321:PHE:CD2	1:A:533:MET:CE	2.93	0.52
1:G:536:ASN:HD22	1:G:538:GLU:H	1.56	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:410:ALA:HA	1:C:452:PHE:CE1	2.45	0.52
1:G:288:LEU:HD12	1:G:288:LEU:N	2.25	0.52
1:F:378:PHE:CD2	1:G:276:ARG:HD3	2.40	0.52
1:C:229:ARG:HB3	1:C:259:PRO:HA	1.91	0.52
1:C:126:LYS:HG2	1:C:127:ASP:H	1.73	0.52
1:G:496:SER:O	1:G:520:LYS:HE2	2.09	0.52
1:F:517:ARG:HB3	1:F:519:LEU:HD13	1.92	0.52
1:B:488:GLY:HA3	1:B:492:LEU:CD1	2.38	0.52
1:A:345:SER:O	1:A:349:THR:CG2	2.58	0.52
1:B:499:ILE:CG2	1:B:519:LEU:CB	2.87	0.52
1:A:413:ARG:HH21	1:A:458:VAL:N	2.08	0.52
1:G:372:ILE:HG13	1:G:378:PHE:HB2	1.91	0.52
1:B:536:ASN:HD21	1:B:538:GLU:CB	2.22	0.52
1:F:413:ARG:NE	1:F:458:VAL:HB	2.24	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:A:324:GLN:HE22	1:A:542:LEU:H	1.58	0.52
1:C:276:ARG:HH11	1:C:276:ARG:HG2	1.75	0.52
1:F:378:PHE:CD2	1:G:276:ARG:HD2	2.44	0.51
1:A:338:GLY:HA3	1:A:412:MET:HE3	1.92	0.51
1:C:446:MET:O	1:C:449:LEU:HB2	2.10	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: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:B:486:LEU:HD12	1:B:493:ARG:CD	2.40	0.51
1:C:227:LYS:O	1:C:229:ARG:HD2	2.10	0.51
1:F:484:THR:C	1:F:486:LEU:H	2.13	0.51
1:A:406:LEU:HD21	1:A:449:LEU:HD23	1.93	0.51
1:C:125:ASP:OD1	1:C:129:ASN:HB2	2.10	0.51
1:F:232:VAL:HG12	1:F:232:VAL:O	2.09	0.51
1:B:394:TYR:C	1:B:394:TYR:CD1	2.83	0.51
1:G:421:ILE:HB	1:G:460:LEU:HD12	1.92	0.51
1:C:510:MET:HB2	1:C:513:LEU:CB	2.39	0.51
1:E:289:PHE:H	1:E:296:ASN:ND2	1.96	0.51
1:B:496:SER:O	1:B:520:LYS:HE2	2.10	0.51
1:E:322:VAL:HG21	1:E:463:ILE:CG1	2.40	0.51
1:F:322:VAL:HG21	1:F:463:ILE:HD11	1.92	0.51
1:E:148:ASN:HD22	1:E:198:GLN:HE22	1.58	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:F:482:SER:H	1:F:485:ASP:CB	2.20	0.51
1:D:260:TRP:HB2	1:D:262:PRO:HD2	1.87	0.51
1:F:429:VAL:HG23	1:F:430:VAL:H	1.75	0.51
1:G:504:ARG:HH21	1:G:506:GLN:HG2	1.74	0.51
1:C:504:ARG:HH21	1:C:506:GLN:CB	2.24	0.51
1:B:440:LYS:CE	1:B:441:MET:HA	2.41	0.51
1:E:309:MET:HB3	1:E:499:ILE:CD1	2.40	0.51
1:C:166:MET:HG2	1:C:175:VAL:CG2	2.41	0.51
1:F:162:MET:HG2	1:F:175:VAL:HB	1.92	0.51
1:A:471:LYS:HB3	1:A:479:ARG:HH11	1.75	0.51
1:E:111:TYR:CZ	1:E:142:PHE:HB2	2.44	0.51
1:F:401:GLU:HB3	1:F:404:ARG:HB3	1.92	0.51
1:G:195:TYR:O	1:G:198:GLN:HB2	2.09	0.51
1:G:180:HIS:HB2	1:G:184:ALA:HB3	1.92	0.51
1:F:362:LEU:HD12	1:F:362:LEU:O	2.11	0.51
1:F:447:THR:CG2	1:F:495:LEU:HD21	2.25	0.51
1:F:412:MET:CE	1:F:421:ILE:CD1	2.87	0.51
1:D:517:ARG:HB3	1:D:519:LEU:HD13	1.92	0.51
1:G:309:MET:HB3	1:G:499:ILE:CD1	2.39	0.51
1:A:520:LYS:HG3	1:A:521:CYS:N	2.24	0.51
1:E:533:MET:HB3	1:E:543:GLU:O	2.11	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:C:428:ILE:H	1:C:428:ILE:HD12	1.75	0.51
1:C:387:GLY:HA2	1:D:269:LEU:HD11	1.91	0.51
1:C:484:THR:C	1:C:486:LEU:N	2.64	0.51
1:E:402:THR:HG23	1:E:403:ASP:N	2.25	0.51
1:A:265:VAL:HG11	1:B:411:TYR:HE1	1.76	0.51
1:G:437:ASP:OD1	1:G:439:ARG:HB2	2.09	0.51
1:E:162:MET:SD	1:E:166:MET:HG3	2.50	0.51
1:D:336:LYS:HB3	1:D:418:CYS:HA	1.92	0.51
1:E:482:SER:N	1:E:485:ASP:HB2	2.19	0.51
1:A:339:LEU:HB3	1:A:341:MET:HE2	1.84	0.51
1:B:401:GLU:HG2	1:B:402:THR:N	2.26	0.51
1:G:78:TYR:CG	1:G:92:GLN:HG2	2.45	0.51
1:B:106:TYR:HB3	1:B:123:VAL:HG12	1.93	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:D:510:MET:HE2	1:D:547:TYR:CE1	2.44	0.51
1:D:80:ALA:HB2	1:D:88:LYS:HB2	1.92	0.51
1:B:401:GLU:HG3	1:B:431:SER:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:547:TYR:CD2	1:F:548:SER:N	2.79	0.51
1:C:166:MET:HE3	1:C:171:CYS:HA	1.91	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
1:G:306:GLU:HA	1:G:497:ASP:OD2	2.10	0.51
1:A:234:PRO:CG	1:A:249:GLU:HG2	2.40	0.51
1:C:164:THR:O	1:C:167:GLU:HB2	2.11	0.51
1:F:402:THR:HG23	1:F:403:ASP:N	2.26	0.51
1:A:445:LEU:CD1	1:A:449:LEU:HG	2.41	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:E:421:ILE:HB	1:E:460:LEU:HD12	1.92	0.51
1:G:91:CYS:HB3	1:G:96:TYR:O	2.11	0.51
1:C:74:SER:HB3	1:C:101:VAL:HG22	1.92	0.51
1:D:166:MET:HE3	1:D:171:CYS:HA	1.93	0.51
1:B:492:LEU:H	1:B:492:LEU:CD1	2.05	0.51
1:F:313:GLY:O	1:F:315:GLY:N	2.44	0.51
1:G:402:THR:HG23	1:G:403:ASP:N	2.26	0.51
1:F:306:GLU:HA	1:F:497:ASP:OD2	2.11	0.51
1:C:286:GLY:O	1:C:302:ALA:N	2.44	0.51
1:C:235:CYS:CB	1:C:240:GLU:HG2	2.40	0.51
1:C:411:TYR:OH	1:D:260:TRP:HB3	2.11	0.51
1:C:91:CYS:HB3	1:C:96:TYR:O	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:107:GLN:CB	1:B:124:ARG:CG	2.84	0.51
1:A:346:VAL:HG22	1:C:271:LEU:HD21	1.91	0.51
1:G:276:ARG:CG	1:G:276:ARG:NH1	2.48	0.51
1:F:424:ASP:O	1:F:425:HIS:HB3	2.10	0.51
1:B:450:LYS:NZ	1:B:454:LYS:HD3	2.25	0.51
1:E:446:MET:HE3	1:E:492:LEU:HA	1.93	0.51
1:D:394:TYR:HE1	1:D:396:SER:CB	2.22	0.51
1:D:165:VAL:HB	1:D:175:VAL:HG11	1.91	0.51
1:G:321:PHE:CD2	1:G:533:MET:HE1	2.46	0.51
1:G:165:VAL:HB	1:G:175:VAL:HG11	1.92	0.51
1:G:413:ARG:NE	1:G:458:VAL:HB	2.24	0.51
1:G:351:GLU:HB2	1:G:363:ARG:HD2	1.92	0.51
1:D:268:ALA:HA	1:D:271:LEU:HD12	1.91	0.51
1:D:112:ARG:HD3	1:D:116:GLY:O	2.11	0.51
1:D:251:MET:HE2	1:D:251:MET:HA	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:122:LYS:HE2	1:D:159:GLU:OE1	2.11	0.51
1:B:208:MET:HE1	1:B:232:VAL:CA	2.22	0.50
1:E:125:ASP:OD1	1:E:129:ASN:HB2	2.11	0.50
1:D:401:GLU:HB3	1:D:404:ARG:HB3	1.92	0.50
1:B:233:LEU:HD22	1:B:241:CYS:SG	2.51	0.50
1:D:478:GLY:CA	1:D:505:ASN:HB2	2.40	0.50
1:F:389:ASP:CA	1:G:269:LEU:CD2	2.87	0.50
1:C:536:ASN:ND2	1:C:538:GLU:HB2	2.26	0.50
1:F:304:GLY:HA2	1:F:459:VAL:HG22	1.92	0.50
1:E:379:ASP:OD1	1:F:276:ARG:NH2	2.42	0.50
1:C:463:ILE:CG2	1:C:464:CYS:N	2.74	0.50
1:F:180:HIS:HB2	1:F:184:ALA:HB3	1.93	0.50
1:D:425:HIS:CE1	1:D:427:SER:OG	2.64	0.50
1:G:425:HIS:CE1	1:G:427:SER:CB	2.94	0.50
1:G:321:PHE:CD2	1:G:533:MET:CE	2.94	0.50
1:F:168:LEU:HD11	1:F:250:ILE:HD12	1.92	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:C:536:ASN:C	1:C:538:GLU:H	2.13	0.50
1:C:330:GLY:HA2	1:C:335:LYS:O	2.12	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:B:279:LEU:HD23	1:G:369:LYS:HG2	1.94	0.50
1:A:286:GLY:O	1:A:302:ALA:N	2.44	0.50
1:G:220:ALA:HB2	1:G:261:ILE:HD13	1.94	0.50
1:D:482:SER:H	1:D:485:ASP:CB	2.23	0.50
1:B:482:SER:N	1:B:485:ASP:HB2	2.22	0.50
1:A:326:ALA:HB2	1:A:422:ILE:HD12	1.92	0.50
1:C:168:LEU:HD11	1:C:250:ILE:HD12	1.92	0.50
1:D:412:MET:CE	1:D:421:ILE:CD1	2.86	0.50
1:B:402:THR:HG23	1:B:403:ASP:N	2.26	0.50
1:E:311:THR:OG1	1:E:466:LEU:HD21	2.11	0.50
1:D:168:LEU:HD11	1:D:250:ILE:HD12	1.93	0.50
1:B:166:MET:HE3	1:B:171:CYS:HA	1.94	0.50
1:C:401:GLU:N	1:C:404:ARG:HD2	2.26	0.50
1:G:322:VAL:HG21	1:G:463:ILE:CG1	2.41	0.50
1:D:463:ILE:CG2	1:D:464:CYS:N	2.74	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:B:427:SER:CB	1:B:487:ARG:NH1	2.74	0.50
1:F:487:ARG:O	1:F:493:ARG:HD3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:318:MET:SD	1:A:463:ILE:HG23	2.52	0.50
1:F:439:ARG:O	1:F:442:ILE:CG2	2.59	0.50
1:C:443:ASP:HA	1:C:491:ALA:CB	2.42	0.50
1:G:504:ARG:HH21	1:G:506:GLN:CG	2.25	0.50
1:G:502:LEU:N	1:G:502:LEU:HD12	2.27	0.50
1:F:387:GLY:HA2	1:G:269:LEU:HD11	1.92	0.50
1:B:112:ARG:HD2	1:B:145:HIS:CE1	2.46	0.50
1:G:148:ASN:HD22	1:G:198:GLN:HE22	1.58	0.50
1:B:80:ALA:HB2	1:B:88:LYS:HB2	1.94	0.50
1:E:180:HIS:HB2	1:E:184:ALA:HB3	1.93	0.50
1:G:260:TRP:C	1:G:262:PRO:HD2	2.32	0.50
1:D:484:THR:O	1:D:486:LEU:N	2.45	0.50
1:G:358:ASN:O	1:G:360:VAL:CG1	2.47	0.50
1:F:311:THR:O	1:F:502:LEU:HD12	2.11	0.50
1:E:74:SER:HB3	1:E:101:VAL:CG2	2.42	0.50
1:G:168:LEU:HD11	1:G:250:ILE:HD12	1.93	0.50
1:F:473:LYS:CE	1:F:479:ARG:HA	2.36	0.50
1:D:351:GLU:HB2	1:D:363:ARG:HD2	1.93	0.50
1:B:79:SER:H	1:B:98:ILE:CD1	2.23	0.50
1:G:202:ILE:HD13	1:G:223:LEU:CD2	2.41	0.50
1:G:480:PRO:HA	1:G:503:GLU:OE2	2.11	0.50
1:A:502:LEU:HD12	1:A:502:LEU:N	2.27	0.50
1:A:447:THR:HA	1:A:495:LEU:HD23	1.93	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:345:SER:O	1:F:349:THR:HG23	2.11	0.50
1:A:186:LYS:CD	1:A:218:GLU:HG3	2.32	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:F:322:VAL:CG2	1:F:463:ILE:HD11	2.42	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:B:234:PRO:HG2	1:B:249:GLU:HG2	1.94	0.50
1:A:425:HIS:HE1	1:A:427:SER:OG	1.90	0.50
1:D:441:MET:CE	1:D:444:ASN:HB3	2.41	0.50
1:F:480:PRO:HA	1:F:503:GLU:OE2	2.11	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:442:ILE:HD11	1:F:492:LEU:CD2	2.41	0.50
1:F:441:MET:HE1	1:F:444:ASN:HB3	1.93	0.50
1:E:81:LEU:HG	1:E:91:CYS:SG	2.52	0.50
1:A:504:ARG:HH21	1:A:506:GLN:CB	2.23	0.50
1:F:316:MET:CE	1:F:535:TYR:CE2	2.94	0.50
1:C:162:MET:HG2	1:C:175:VAL:HB	1.92	0.50
1:G:74:SER:HB3	1:G:101:VAL:CG2	2.42	0.50
1:E:112:ARG:HD2	1:E:145:HIS:CE1	2.47	0.50
1:G:86:ILE:HD12	1:G:163:LEU:HB3	1.93	0.50
1:F:443:ASP:HA	1:F:491:ALA:CB	2.41	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: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:F:486:LEU:HD22	1:F:487:ARG:H	1.77	0.49
1:G:486:LEU:HD12	1:G:493:ARG:CD	2.42	0.49
1:G:232:VAL:O	1:G:232:VAL:HG12	2.12	0.49
1:G:295:ILE:HD12	1:G:516:VAL:HG11	1.94	0.49
1:B:227:LYS:O	1:B:229:ARG:HD2	2.11	0.49
1:E:246:HIS:HB3	1:E:249:GLU:OE1	2.12	0.49
1:C:515:LEU:HD21	1:C:529:ILE:HD12	1.93	0.49
1:D:480:PRO:HA	1:D:503:GLU:OE2	2.12	0.49
1:D:114:GLN:NE2	1:D:195:TYR:HD1	2.10	0.49
1:G:288:LEU:HD12	1:G:288:LEU:H	1.77	0.49
1:G:344:GLU:HB2	1:G:348:GLU:OE2	2.11	0.49
1:D:499:ILE:HG22	1:D:519:LEU:CB	2.31	0.49
1:B:510:MET:HE2	1:B:547:TYR:CE1	2.47	0.49
1:G:510:MET:CB	1:G:513:LEU:HB2	2.42	0.49
1:D:286:GLY:O	1:D:302:ALA:N	2.45	0.49
1:G:413:ARG:HH21	1:G:458:VAL:N	2.10	0.49
1:A:536:ASN:ND2	1:A:538:GLU:CB	2.75	0.49
1:F:401:GLU:HG2	1:F:402:THR:N	2.26	0.49
1:B:122:LYS:HE3	1:B:130:PHE:CE2	2.47	0.49
1:A:321:PHE:CD2	1:A:533:MET:HE3	2.48	0.49
1:E:235:CYS:CB	1:E:240:GLU:HG2	2.41	0.49
1:B:234:PRO:CG	1:B:249:GLU:HG2	2.42	0.49
1:D:482:SER:N	1:D:485:ASP:HB2	2.22	0.49
1:C:412:MET:CE	1:C:421:ILE:CD1	2.81	0.49
1:F:440:LYS:C	1:F:440:LYS:HE2	2.32	0.49
1:F:330:GLY:HA2	1:F:335:LYS:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:492:LEU:C	1:G:494:GLN:N	2.66	0.49
1:D:78:TYR:CG	1:D:92:GLN:HG2	2.47	0.49
1:A:515:LEU:HD21	1:A:529:ILE:HD11	1.94	0.49
1:E:166:MET:HG2	1:E:175:VAL:CG2	2.41	0.49
1:E:392:HIS:ND1	1:F:267:SER:HB3	2.27	0.49
1:D:79:SER:H	1:D:98:ILE:CD1	2.24	0.49
1:C:304:GLY:HA2	1:C:459:VAL:HG22	1.94	0.49
1:E:389:ASP:CA	1:F:269:LEU:HD23	2.43	0.49
1:E:122:LYS:HE3	1:E:130:PHE:CE2	2.47	0.49
1:G:480:PRO:HA	1:G:503:GLU:OE1	2.12	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: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:E:86:ILE:HD12	1:E:163:LEU:HB3	1.94	0.49
1:D:397:PHE:C	1:D:397:PHE:CD1	2.86	0.49
1:A:492:LEU:C	1:A:494:GLN:N	2.65	0.49
1:C:487:ARG:O	1:C:493:ARG:HD3	2.13	0.49
1:G:345:SER:O	1:G:349:THR:HG23	2.13	0.49
1:B:445:LEU:CD1	1:B:449:LEU:HG	2.42	0.49
1:F:344:GLU:HB2	1:F:348:GLU:OE2	2.13	0.49
1:C:165:VAL:HB	1:C:175:VAL:HG11	1.93	0.49
1:E:112:ARG:HD3	1:E:116:GLY:O	2.12	0.49
1:A:346:VAL:HG23	1:A:393:LEU:HB2	1.94	0.49
1:C:372:ILE:HG13	1:C:378:PHE:HB2	1.94	0.49
1:C:205:MET:HG3	1:C:231:ALA:CB	2.42	0.49
1:F:510:MET:HE2	1:F:513:LEU:HD22	1.93	0.49
1:A:272:ARG:HA	1:B:382:PHE:CE1	2.48	0.49
1:G:397:PHE:C	1:G:397:PHE:CD1	2.86	0.49
1:F:425:HIS:CD2	1:F:465:HIS:CE1	3.01	0.49
1:B:74:SER:HB3	1:B:101:VAL:CG2	2.42	0.49
1:D:205:MET:HG3	1:D:231:ALA:HB1	1.94	0.49
1:C:413:ARG:NE	1:C:458:VAL:HB	2.24	0.49
1:A:358:ASN:ND2	1:A:381:TRP:CE2	2.81	0.49
1:D:536:ASN:HD21	1:D:538:GLU:HB2	1.77	0.49
1:A:330:GLY:HA2	1:A:335:LYS:O	2.13	0.49
1:F:318:MET:SD	1:F:463:ILE:HG23	2.52	0.49
1:A:512:ASN:HD21	1:A:537:LYS:HE3	1.77	0.49
1:D:425:HIS:CE1	1:D:427:SER:HB2	2.48	0.49
1:C:260:TRP:HE3	1:C:260:TRP:N	2.10	0.49
1:B:504:ARG:HH21	1:B:506:GLN:HG2	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:A:397:PHE:C	1:A:397:PHE:CD1	2.86	0.49
1:A:312:SER:O	1:A:313:GLY:O	2.31	0.49
1:E:439:ARG:O	1:E:442:ILE:CG2	2.61	0.49
1:D:401:GLU:CG	1:D:431:SER:O	2.44	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:A:440:LYS:HE2	1:A:440:LYS:O	2.13	0.49
1:G:427:SER:HB3	1:G:487:ARG:NH1	2.25	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:B:437:ASP:OD1	1:B:439:ARG:HB2	2.13	0.49
1:E:168:LEU:HD11	1:E:250:ILE:HD12	1.94	0.49
1:C:112:ARG:HD3	1:C:116:GLY:O	2.12	0.49
1:G:473:LYS:CE	1:G:479:ARG:HA	2.42	0.49
1:D:360:VAL:CG2	1:D:360:VAL:O	2.59	0.49
1:C:382:PHE:C	1:C:382:PHE:CD2	2.86	0.49
1:E:389:ASP:HA	1:F:269:LEU:CD2	2.43	0.49
1:B:322:VAL:CG1	1:B:422:ILE:HG21	2.43	0.49
1:B:202:ILE:HD13	1:B:223:LEU:CD2	2.42	0.49
1:E:80:ALA:HB2	1:E:88:LYS:HB2	1.93	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: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:F:392:HIS:ND1	1:G:267:SER:CB	2.75	0.49
1:D:229:ARG:HB2	1:D:258:GLY:O	2.13	0.49
1:G:229:ARG:HH21	1:G:259:PRO:HG3	1.78	0.49
1:D:271:LEU:O	1:D:272:ARG:C	2.51	0.49
1:B:279:LEU:CD2	1:G:369:LYS:HG2	2.42	0.49
1:F:443:ASP:HA	1:F:491:ALA:HB3	1.95	0.48
1:C:510:MET:HE2	1:C:513:LEU:HD22	1.94	0.48
1:B:401:GLU:CG	1:B:402:THR:N	2.75	0.48
1:A:346:VAL:HG22	1:C:271:LEU:CD2	2.42	0.48
1:E:234:PRO:HG2	1:E:249:GLU:HG2	1.95	0.48
1:F:140:ALA:O	1:F:141:LEU:HD23	2.12	0.48
1:E:397:PHE:C	1:E:397:PHE:CD1	2.87	0.48
1:F:220:ALA:HB3	1:F:261:ILE:HG12	1.92	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:486:LEU:HD12	1:D:493:ARG:CG	2.43	0.48
1:C:482:SER:N	1:C:485:ASP:HB2	2.22	0.48
1:E:370:ARG:C	1:E:370:ARG:CD	2.81	0.48
1:B:405:LEU:HG	1:B:409:LEU:CD1	2.42	0.48
1:D:496:SER:CB	1:D:499:ILE:HD11	2.43	0.48
1:B:401:GLU:HB3	1:B:404:ARG:HB3	1.94	0.48
1:B:228:VAL:CB	1:B:261:ILE:HD11	2.36	0.48
1:G:168:LEU:HD22	1:G:247:ASP:OD2	2.13	0.48
1:E:326:ALA:HB2	1:E:422:ILE:HD12	1.95	0.48
1:D:167:GLU:C	1:D:169:GLN:H	2.13	0.48
1:E:204:LEU:HD23	1:E:204:LEU:N	2.27	0.48
1:C:262:PRO:HB2	1:C:265:VAL:HG12	1.94	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:E:439:ARG:HG2	1:E:489:SER:OG	2.13	0.48
1:G:267:SER:O	1:G:271:LEU:HD12	2.14	0.48
1:E:454:LYS:HE3	1:E:522:ARG:HH22	1.78	0.48
1:C:531:GLY:C	1:C:532:TYR:HD1	2.16	0.48
1:D:510:MET:HE2	1:D:547:TYR:HE1	1.67	0.48
1:B:510:MET:HE2	1:B:547:TYR:HE1	1.74	0.48
1:C:345:SER:O	1:C:349:THR:HG22	2.13	0.48
1:A:469:PRO:O	1:A:470:ASP:CB	2.54	0.48
1:F:153:ILE:HG13	1:F:174:PRO:CB	2.43	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:185:ALA:O	1:A:189:CYS:HB2	2.12	0.48
1:C:229:ARG:NH2	1:C:259:PRO:HG3	2.27	0.48
1:B:536:ASN:HD21	1:B:538:GLU:HB3	1.78	0.48
1:A:279:LEU:CD2	1:B:369:LYS:HG2	2.43	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:F:441:MET:HE1	1:F:445:LEU:N	2.29	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:B:289:PHE:HA	1:B:325:GLN:HE21	1.77	0.48
1:F:405:LEU:HG	1:F:409:LEU:CD1	2.41	0.48
1:G:402:THR:HG23	1:G:403:ASP:H	1.79	0.48
1:G:162:MET:HG2	1:G:175:VAL:HB	1.96	0.48
1:A:121:GLN:HB2	1:A:133:THR:HG1	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:294:GLY:O	1:E:295:ILE:C	2.49	0.48
1:G:235:CYS:CB	1:G:240:GLU:HG2	2.43	0.48
1:D:185:ALA:O	1:D:189:CYS:HB2	2.13	0.48
1:A:126:LYS:HZ2	1:A:127:ASP:CB	2.22	0.48
1:F:289:PHE:HA	1:F:325:GLN:HE21	1.78	0.48
1:E:492:LEU:C	1:E:494:GLN:N	2.65	0.48
1:G:394:TYR:CE2	1:G:405:LEU:HD12	2.49	0.48
1:D:312:SER:O	1:D:313:GLY:O	2.30	0.48
1:G:499:ILE:HG22	1:G:519:LEU:CB	2.31	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:A:216:VAL:CG1	1:A:230:VAL:CG2	2.90	0.48
1:G:330:GLY:HA2	1:G:335:LYS:O	2.14	0.48
1:A:122:LYS:HE3	1:A:130:PHE:CE2	2.48	0.48
1:F:351:GLU:OE1	1:G:278:HIS:CD2	2.66	0.48
1:E:443:ASP:HA	1:E:491:ALA:CB	2.44	0.48
1:D:404:ARG:O	1:D:408:LYS:HG2	2.14	0.48
1:A:510:MET:CB	1:A:513:LEU:HB2	2.43	0.48
1:E:121:GLN:HB2	1:E:133:THR:HG1	1.77	0.48
1:G:246:HIS:HB3	1:G:249:GLU:OE1	2.14	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: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:F:114:GLN:HG3	1:F:144:LYS:HE2	1.96	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: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:521:CYS:O	1:G:525:GLY:N	2.38	0.48
1:B:86:ILE:HD12	1:B:163:LEU:HB3	1.96	0.48
1:B:81:LEU:HG	1:B:91:CYS:SG	2.53	0.48
1:D:121:GLN:HB2	1:D:133:THR:HG1	1.79	0.48
1:C:368:LEU:CD2	1:C:372:ILE:HG23	2.43	0.48
1:G:164:THR:O	1:G:167:GLU:HB2	2.14	0.48
1:D:202:ILE:HD13	1:D:223:LEU:CD2	2.44	0.48
1:C:168:LEU:HD22	1:C:247:ASP:OD2	2.11	0.48
1:F:446:MET:O	1:F:449:LEU:HB2	2.14	0.48
1:C:480:PRO:HA	1:C:503:GLU:OE2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:234:PRO:CG	1:C:249:GLU:HG2	2.44	0.48
1:B:145:HIS:CE1	1:B:146:LEU:HD23	2.49	0.48
1:C:359:ARG:HD3	1:C:541:TRP:HE1	1.79	0.48
1:G:445:LEU:CD1	1:G:449:LEU:HG	2.43	0.48
1:E:336:LYS:HB3	1:E:418:CYS:HA	1.95	0.48
1:D:420:VAL:HG22	1:D:459:VAL:HB	1.96	0.48
1:C:353:LEU:HD23	1:C:353:LEU:HA	1.72	0.48
1:F:492:LEU:C	1:F:494:GLN:N	2.67	0.48
1:C:446:MET:CE	1:C:492:LEU:HA	2.40	0.48
1:C:510:MET:HB2	1:C:513:LEU:HB2	1.95	0.48
1:A:517:ARG:HB3	1:A:519:LEU:HD13	1.95	0.48
1:C:479:ARG:HA	1:C:480:PRO:HD3	1.76	0.48
1:E:291:GLY:O	1:E:292:CYS:HB2	2.13	0.48
1:B:162:MET:HG2	1:B:175:VAL:HB	1.93	0.48
1:A:303:ARG:CZ	1:A:523:PHE:CD1	2.97	0.48
1:G:536:ASN:C	1:G:536:ASN:HD22	2.17	0.48
1:G:452:PHE:O	1:G:456:THR:HG23	2.14	0.48
1:A:322:VAL:CG1	1:A:422:ILE:HG21	2.43	0.47
1:E:504:ARG:HH21	1:E:506:GLN:CG	2.26	0.47
1:D:492:LEU:H	1:D:492:LEU:CD1	2.06	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:B:344:GLU:HB2	1:B:348:GLU:OE2	2.14	0.47
1:G:162:MET:SD	1:G:166:MET:HG3	2.54	0.47
1:F:166:MET:HG2	1:F:175:VAL:HG23	1.94	0.47
1:E:300:LEU:HB3	1:E:303:ARG:HH12	1.79	0.47
1:B:306:GLU:HA	1:B:497:ASP:OD2	2.13	0.47
1:A:114:GLN:NE2	1:A:195:TYR:HD1	2.11	0.47
1:C:452:PHE:O	1:C:456:THR:HG23	2.14	0.47
1:B:327:LEU:HD11	1:B:357:HIS:HA	1.96	0.47
1:G:512:ASN:HD21	1:G:537:LYS:HE3	1.78	0.47
1:F:486:LEU:HB3	1:F:493:ARG:CD	2.44	0.47
1:D:411:TYR:HE1	1:E:265:VAL:HG11	1.78	0.47
1:A:467:LYS:H	1:A:467:LYS:HG3	1.53	0.47
1:E:486:LEU:HD12	1:E:493:ARG:CG	2.44	0.47
1:C:486:LEU:HD13	1:C:487:ARG:O	2.14	0.47
1:C:248:ARG:O	1:C:248:ARG:HG2	2.14	0.47
1:D:154:VAL:HG21	1:D:254:VAL:HG22	1.96	0.47
1:F:312:SER:O	1:F:313:GLY:O	2.32	0.47
1:B:478:GLY:O	1:B:479:ARG:C	2.51	0.47
1:B:125:ASP:OD1	1:B:129:ASN:HB2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:344:GLU:HB2	1:E:348:GLU:OE2	2.14	0.47
1:F:106:TYR:HB3	1:F:123:VAL:HG12	1.96	0.47
1:G:234:PRO:CG	1:G:249:GLU:HG2	2.44	0.47
1:D:86:ILE:HD12	1:D:163:LEU:HB3	1.96	0.47
1:B:288:LEU:HD12	1:B:288:LEU:H	1.79	0.47
1:F:77:ARG:HE	1:F:77:ARG:HB2	1.49	0.47
1:F:265:VAL:O	1:F:265:VAL:HG12	2.14	0.47
1:G:439:ARG:O	1:G:442:ILE:CG2	2.62	0.47
1:B:402:THR:HG23	1:B:403:ASP:H	1.79	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:B:496:SER:HB2	1:B:499:ILE:HD11	1.96	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:A:111:TYR:CZ	1:A:142:PHE:HB2	2.48	0.47
1:B:148:ASN:HD22	1:B:198:GLN:HE22	1.62	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:A:180:HIS:CD2	1:A:180:HIS:N	2.81	0.47
1:D:419:ASP:OD2	1:D:419:ASP:N	2.47	0.47
1:F:445:LEU:HD12	1:F:445:LEU:O	2.13	0.47
1:A:126:LYS:NZ	1:A:127:ASP:CB	2.76	0.47
1:B:287:LEU:HD23	1:B:329:TRP:CE2	2.49	0.47
1:B:440:LYS:O	1:B:443:ASP:HB2	2.15	0.47
1:E:78:TYR:CG	1:E:92:GLN:HG2	2.50	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:E:510:MET:HB3	1:E:513:LEU:HB2	1.96	0.47
1:A:140:ALA:O	1:A:141:LEU:HD23	2.15	0.47
1:E:146:LEU:HB2	1:E:147:TRP:CE2	2.50	0.47
1:D:268:ALA:HA	1:D:271:LEU:HD13	1.95	0.47
1:B:347:GLU:O	1:B:351:GLU:HG3	2.13	0.47
1:A:336:LYS:HB3	1:A:418:CYS:HA	1.96	0.47
1:F:428:ILE:H	1:F:428:ILE:HD12	1.80	0.47
1:G:353:LEU:HD23	1:G:353:LEU:HA	1.71	0.47
1:G:220:ALA:HB1	1:G:261:ILE:CG2	2.37	0.47
1:A:442:ILE:HD11	1:A:492:LEU:CG	2.44	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:F:492:LEU:HD12	1:F:492:LEU:N	2.21	0.47
1:A:499:ILE:HG22	1:A:499:ILE:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:480:PRO:HA	1:B:503:GLU:OE2	2.15	0.47
1:A:168:LEU:HB2	1:A:251:MET:HE1	1.97	0.47
1:D:344:GLU:HB2	1:D:348:GLU:OE2	2.14	0.47
1:G:112:ARG:HD3	1:G:116:GLY:O	2.14	0.47
1:F:401:GLU:CG	1:F:402:THR:N	2.77	0.47
1:A:412:MET:CE	1:A:421:ILE:HD12	2.40	0.47
1:E:228:VAL:CG2	1:E:261:ILE:HD11	2.45	0.47
1:A:482:SER:O	1:A:485:ASP:CB	2.62	0.47
1:B:283:GLU:O	1:B:283:GLU:CG	2.62	0.47
1:C:81:LEU:HG	1:C:91:CYS:SG	2.54	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:D:168:LEU:HD22	1:D:247:ASP:OD2	2.15	0.47
1:B:205:MET:HG3	1:B:231:ALA:HB1	1.95	0.47
1:D:536:ASN:HD22	1:D:536:ASN:C	2.16	0.47
1:F:413:ARG:HH21	1:F:457:GLY:C	2.18	0.47
1:F:167:GLU:C	1:F:169:GLN:H	2.15	0.47
1:A:223:LEU:HD23	1:A:224:PRO:HD2	1.96	0.47
1:F:368:LEU:HD22	1:F:368:LEU:C	2.35	0.47
1:A:152:LYS:NZ	1:A:256:ASN:H	2.13	0.47
1:E:260:TRP:O	1:E:261:ILE:CG1	2.63	0.47
1:A:487:ARG:O	1:A:493:ARG:HD3	2.14	0.47
1:B:476:GLU:H	1:B:476:GLU:CD	2.18	0.47
1:D:446:MET:HE2	1:D:492:LEU:HB3	1.96	0.47
1:G:125:ASP:OD1	1:G:129:ASN:HB2	2.15	0.47
1:D:510:MET:CE	1:D:513:LEU:HD22	2.44	0.47
1:D:74:SER:HB3	1:D:101:VAL:CG2	2.45	0.47
1:B:492:LEU:C	1:B:494:GLN:N	2.68	0.47
1:A:248:ARG:O	1:A:248:ARG:HG2	2.14	0.47
1:E:315:GLY:HA2	1:E:317:VAL:CG2	2.39	0.47
1:C:499:ILE:CG2	1:C:519:LEU:CB	2.93	0.47
1:D:233:LEU:HD22	1:D:241:CYS:SG	2.54	0.47
1:C:153:ILE:HG23	1:C:153:ILE:O	2.14	0.47
1:F:163:LEU:N	1:F:163:LEU:HD23	2.30	0.47
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:F:273:GLU:OE2	1:F:276:ARG:NH1	2.48	0.47
1:C:202:ILE:HD13	1:C:223:LEU:CD2	2.44	0.47
1:F:463:ILE:CG2	1:F:464:CYS:N	2.78	0.47
1:E:324:GLN:HE22	1:E:542:LEU:H	1.63	0.47
1:A:235:CYS:HB2	1:A:240:GLU:HG2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:382:PHE:CZ	1:E:272:ARG:HB2	2.50	0.47
1:C:419:ASP:OD2	1:C:419:ASP:N	2.47	0.47
1:F:486:LEU:HD12	1:F:493:ARG:HG2	1.97	0.47
1:F:484:THR:C	1:F:486:LEU:N	2.67	0.47
1:A:484:THR:C	1:A:486:LEU:H	2.18	0.47
1:C:476:GLU:CD	1:C:476:GLU:N	2.68	0.47
1:A:169:GLN:HE22	1:A:254:VAL:CG1	2.27	0.47
1:B:78:TYR:CG	1:B:92:GLN:HG2	2.49	0.47
1:D:536:ASN:ND2	1:D:538:GLU:HB2	2.30	0.47
1:B:413:ARG:NE	1:B:458:VAL:HB	2.28	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:D:230:VAL:CB	1:D:260:TRP:NE1	2.78	0.47
1:G:493:ARG:H	1:G:493:ARG:HG2	1.47	0.47
1:C:486:LEU:HD12	1:C:493:ARG:CG	2.45	0.47
1:F:311:THR:OG1	1:F:466:LEU:HD21	2.15	0.47
1:F:166:MET:HG2	1:F:175:VAL:HG21	1.97	0.47
1:C:205:MET:HG3	1:C:231:ALA:HB1	1.97	0.47
1:F:216:VAL:CG1	1:F:230:VAL:CG2	2.93	0.47
1:C:194:GLU:CD	1:C:194:GLU:N	2.67	0.47
1:F:322:VAL:HG11	1:F:422:ILE:HG21	1.97	0.47
1:A:542:LEU:HD12	1:A:542:LEU:HA	1.60	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:B:353:LEU:HD23	1:B:353:LEU:HA	1.69	0.47
1:A:322:VAL:HG21	1:A:463:ILE:CG1	2.44	0.47
1:A:486:LEU:HD12	1:A:493:ARG:CD	2.45	0.47
1:A:440:LYS:CE	1:A:441:MET:HA	2.42	0.47
1:F:441:MET:HE1	1:F:445:LEU:H	1.80	0.47
1:C:339:LEU:CB	1:C:341:MET:HE1	2.42	0.47
1:E:372:ILE:HG13	1:E:378:PHE:HB2	1.95	0.47
1:G:81:LEU:HG	1:G:91:CYS:SG	2.54	0.47
1:B:220:ALA:HB1	1:B:261:ILE:CD1	2.41	0.47
1:B:168:LEU:HD11	1:B:250:ILE:HD12	1.96	0.47
1:C:369:LYS:HZ2	1:D:284:SER:H	1.62	0.47
1:F:292:CYS:HB3	1:F:295:ILE:CG1	2.45	0.47
1:E:162:MET:HG2	1:E:175:VAL:HB	1.96	0.47
1:D:283:GLU:OE2	1:D:286:GLY:CA	2.60	0.47
1:B:145:HIS:CE1	1:B:146:LEU:CD2	2.97	0.47
1:C:288:LEU:HD12	1:C:288:LEU:H	1.77	0.47
1:E:268:ALA:HA	1:E:271:LEU:HD13	1.96	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:F:151:LYS:HG2	1:F:200:GLU:OE2	2.14	0.47
1:F:124:ARG:HD3	1:F:125:ASP:CA	2.45	0.46
1:D:314:SER:O	1:D:315:GLY:C	2.53	0.46
1:C:78:TYR:CG	1:C:92:GLN:HG2	2.49	0.46
1:F:345:SER:O	1:F:349:THR:CG2	2.63	0.46
1:G:510:MET:HE2	1:G:547:TYR:CE1	2.50	0.46
1:E:326:ALA:HB2	1:E:422:ILE:CD1	2.45	0.46
1:A:246:HIS:HB3	1:A:249:GLU:OE1	2.14	0.46
1:C:79:SER:H	1:C:98:ILE:CD1	2.28	0.46
1:A:288:LEU:HD12	1:A:288:LEU:H	1.80	0.46
1:E:369:LYS:HG2	1:F:279:LEU:HD22	1.97	0.46
1:G:397:PHE:HD1	1:G:397:PHE:C	2.18	0.46
1:E:327:LEU:HD23	1:E:327:LEU:HA	1.44	0.46
1:A:394:TYR:C	1:A:394:TYR:HD1	2.18	0.46
1:A:126:LYS:NZ	1:A:127:ASP:CG	2.68	0.46
1:G:496:SER:CB	1:G:499:ILE:HD11	2.45	0.46
1:F:312:SER:CB	1:F:502:LEU:O	2.54	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:A:414:SER:CB	1:C:226:GLY:N	2.76	0.46
1:C:251:MET:CE	1:C:251:MET:CA	2.92	0.46
1:F:510:MET:HB3	1:F:513:LEU:HB2	1.97	0.46
1:C:246:HIS:HB3	1:C:249:GLU:OE1	2.14	0.46
1:G:322:VAL:HG21	1:G:463:ILE:CD1	2.43	0.46
1:G:253:GLN:O	1:G:257:ALA:HB2	2.16	0.46
1:F:353:LEU:HD23	1:F:353:LEU:HA	1.65	0.46
1:C:307:VAL:O	1:C:307:VAL:HG12	2.14	0.46
1:F:229:ARG:HB3	1:F:258:GLY:O	2.14	0.46
1:G:220:ALA:HB1	1:G:261:ILE:HD13	1.96	0.46
1:A:486:LEU:HD13	1:A:487:ARG:O	2.15	0.46
1:G:482:SER:H	1:G:485:ASP:CB	2.19	0.46
1:B:443:ASP:HA	1:B:491:ALA:HB3	1.97	0.46
1:G:429:VAL:HG13	1:G:438:GLU:OE1	2.15	0.46
1:F:344:GLU:OE1	1:F:349:THR:HB	2.15	0.46
1:E:168:LEU:HD22	1:E:247:ASP:OD2	2.12	0.46
1:C:166:MET:O	1:C:171:CYS:SG	2.69	0.46
1:E:413:ARG:HH21	1:E:458:VAL:N	2.13	0.46
1:G:300:LEU:HB3	1:G:303:ARG:NH1	2.29	0.46
1:F:205:MET:HG3	1:F:231:ALA:HB1	1.97	0.46
1:B:114:GLN:HG3	1:B:144:LYS:HE2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:86:ILE:HG21	1:C:163:LEU:CD1	2.45	0.46
1:F:326:ALA:HB2	1:F:422:ILE:HD12	1.97	0.46
1:G:531:GLY:C	1:G:532:TYR:CD1	2.88	0.46
1:B:267:SER:O	1:B:270:SER:OG	2.31	0.46
1:E:411:TYR:C	1:E:411:TYR:CD1	2.89	0.46
1:F:427:SER:HB3	1:F:487:ARG:NH1	2.29	0.46
1:E:492:LEU:C	1:E:494:GLN:H	2.18	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:G:304:GLY:HA2	1:G:459:VAL:HG22	1.96	0.46
1:A:536:ASN:OD1	1:A:539:THR:HG23	2.15	0.46
1:G:136:HIS:CD2	1:G:180:HIS:CE1	3.03	0.46
1:A:382:PHE:CD2	1:A:382:PHE:C	2.88	0.46
1:F:486:LEU:HD13	1:F:487:ARG:O	2.15	0.46
1:E:406:LEU:HD21	1:E:449:LEU:HD23	1.98	0.46
1:B:394:TYR:HE1	1:B:396:SER:CB	2.26	0.46
1:F:311:THR:O	1:F:312:SER:CB	2.59	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:E:295:ILE:HD12	1:E:516:VAL:HG11	1.98	0.46
1:A:160:ILE:O	1:A:163:LEU:HB2	2.16	0.46
1:E:353:LEU:HD23	1:E:353:LEU:HA	1.65	0.46
1:A:322:VAL:HG21	1:A:463:ILE:CD1	2.46	0.46
1:G:486:LEU:HD13	1:G:487:ARG:O	2.15	0.46
1:C:412:MET:HE2	1:C:421:ILE:HD12	1.90	0.46
1:G:271:LEU:O	1:G:272:ARG:C	2.53	0.46
1:D:401:GLU:N	1:D:404:ARG:HD2	2.31	0.46
1:D:162:MET:HG2	1:D:175:VAL:HB	1.98	0.46
1:C:473:LYS:CD	1:C:479:ARG:HB2	2.46	0.46
1:G:234:PRO:HG2	1:G:249:GLU:HG2	1.98	0.46
1:D:205:MET:SD	1:D:238:ALA:HB2	2.56	0.46
1:F:79:SER:H	1:F:98:ILE:CD1	2.27	0.46
1:B:300:LEU:O	1:B:300:LEU:CD1	2.64	0.46
1:G:114:GLN:HG3	1:G:144:LYS:HE2	1.98	0.46
1:A:241:CYS:HB2	1:A:250:ILE:HD11	1.97	0.46
1:A:443:ASP:HA	1:A:491:ALA:HB3	1.97	0.46
1:E:487:ARG:O	1:E:493:ARG:HD3	2.15	0.46
1:D:442:ILE:HD11	1:D:492:LEU:CG	2.46	0.46
1:E:402:THR:HG23	1:E:403:ASP:H	1.80	0.46
1:G:339:LEU:HD22	1:G:341:MET:HE1	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:311:THR:O	1:G:502:LEU:HD12	2.16	0.46
1:D:125:ASP:OD1	1:D:129:ASN:HB2	2.15	0.46
1:E:142:PHE:CE2	1:E:162:MET:HE3	2.51	0.46
1:E:322:VAL:CG1	1:E:422:ILE:HG21	2.45	0.46
1:G:167:GLU:C	1:G:169:GLN:H	2.15	0.46
1:E:205:MET:HG3	1:E:231:ALA:HB1	1.97	0.46
1:A:243:LEU:O	1:A:244:ASN:C	2.53	0.46
1:D:276:ARG:CG	1:D:276:ARG:HH11	2.29	0.46
1:F:170:ASP:O	1:F:172:LYS:HG3	2.16	0.46
1:G:327:LEU:HA	1:G:327:LEU:HD23	1.55	0.46
1:A:152:LYS:O	1:A:174:PRO:HD2	2.16	0.46
1:F:467:LYS:HG3	1:F:467:LYS:H	1.50	0.46
1:B:504:ARG:HH21	1:B:506:GLN:CG	2.29	0.46
1:C:425:HIS:HE1	1:C:427:SER:CB	2.27	0.46
1:B:289:PHE:H	1:B:296:ASN:ND2	2.04	0.46
1:A:154:VAL:HB	1:A:175:VAL:CG1	2.43	0.46
1:E:413:ARG:HH21	1:E:457:GLY:C	2.19	0.46
1:E:351:GLU:HB2	1:E:363:ARG:HD2	1.98	0.46
1:D:140:ALA:O	1:D:141:LEU:HD23	2.15	0.46
1:C:368:LEU:HD22	1:C:368:LEU:C	2.36	0.46
1:G:205:MET:HG3	1:G:231:ALA:HB1	1.98	0.46
1:E:167:GLU:C	1:E:169:GLN:H	2.16	0.46
1:C:327:LEU:HD11	1:C:357:HIS:HA	1.98	0.46
1:F:451:GLY:O	1:F:455:SER:HB3	2.16	0.46
1:F:213:ARG:HA	1:F:213:ARG:NE	2.30	0.46
1:G:228:VAL:HB	1:G:261:ILE:HD13	1.97	0.46
1:A:488:GLY:HA3	1:A:492:LEU:CD1	2.42	0.46
1:C:312:SER:O	1:C:313:GLY:O	2.34	0.46
1:E:450:LYS:HA	1:E:450:LYS:HD2	1.68	0.46
1:B:442:ILE:HD11	1:B:492:LEU:CD2	2.45	0.46
1:D:283:GLU:CD	1:D:286:GLY:HA2	2.36	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:D:324:GLN:HE22	1:D:542:LEU:H	1.63	0.46
1:F:80:ALA:HB2	1:F:88:LYS:HB2	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:C:241:CYS:HB2	1:C:250:ILE:HD11	1.98	0.46
1:D:446:MET:CE	1:D:492:LEU:HA	2.45	0.46
1:G:440:LYS:CE	1:G:441:MET:HA	2.43	0.46
1:G:81:LEU:HD11	1:G:96:TYR:CD2	2.51	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:G:446:MET:CE	1:G:492:LEU:HA	2.46	0.46
1:F:248:ARG:HG2	1:F:248:ARG:O	2.15	0.46
1:B:510:MET:HB2	1:B:513:LEU:CB	2.46	0.46
1:F:510:MET:CB	1:F:513:LEU:HB2	2.45	0.46
1:F:194:GLU:N	1:F:194:GLU:CD	2.66	0.46
1:D:391:PHE:C	1:D:392:HIS:CD2	2.89	0.46
1:A:314:SER:O	1:A:315:GLY:C	2.54	0.45
1:D:216:VAL:CG1	1:D:230:VAL:HG22	2.45	0.45
1:C:476:GLU:HB3	1:C:506:GLN:OE1	2.16	0.45
1:B:406:LEU:HD21	1:B:449:LEU:HD23	1.97	0.45
1:B:401:GLU:CG	1:B:402:THR:H	2.29	0.45
1:D:471:LYS:HA	1:D:471:LYS:HD2	1.60	0.45
1:A:360:VAL:O	1:A:360:VAL:HG23	2.16	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:C:223:LEU:CD2	1:C:224:PRO:HD2	2.46	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:454:LYS:HE3	1:C:522:ARG:HH22	1.82	0.45
1:B:517:ARG:CZ	1:B:529:ILE:HD11	2.46	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:C:234:PRO:HG2	1:C:249:GLU:HG2	1.98	0.45
1:D:148:ASN:HD22	1:D:198:GLN:HE22	1.63	0.45
1:F:327:LEU:HA	1:F:327:LEU:HD23	1.55	0.45
1:F:397:PHE:C	1:F:397:PHE:CD1	2.90	0.45
1:D:427:SER:CB	1:D:487:ARG:HH12	2.22	0.45
1:F:124:ARG:HD3	1:F:125:ASP:N	2.31	0.45
1:G:506:GLN:HG3	1:G:506:GLN:H	1.56	0.45
1:D:443:ASP:HA	1:D:491:ALA:CB	2.47	0.45
1:G:517:ARG:HB3	1:G:519:LEU:HD13	1.96	0.45
1:B:401:GLU:CG	1:B:431:SER:O	2.64	0.45
1:G:181:GLY:O	1:G:182:ALA:C	2.54	0.45
1:D:181:GLY:O	1:D:182:ALA:C	2.55	0.45
1:B:112:ARG:NH2	1:B:118:ILE:HD11	2.31	0.45
1:C:402:THR:HG23	1:C:403:ASP:N	2.31	0.45
1:D:346:VAL:HG13	1:E:271:LEU:CD2	2.47	0.45
1:D:193:TYR:CE1	1:D:224:PRO:HA	2.52	0.45
1:C:327:LEU:HA	1:C:327:LEU:HD23	1.59	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:TYR:CE1	1:A:224:PRO:HA	2.51	0.45
1:A:153:ILE:O	1:A:153:ILE:HG23	2.16	0.45
1:B:486:LEU:HD12	1:B:493:ARG:CG	2.47	0.45
1:A:439:ARG:O	1:A:442:ILE:CG2	2.62	0.45
1:A:491:ALA:O	1:A:495:LEU:N	2.46	0.45
1:F:440:LYS:NZ	1:F:441:MET:CA	2.60	0.45
1:B:232:VAL:O	1:B:232:VAL:HG12	2.14	0.45
1:G:314:SER:O	1:G:315:GLY:C	2.55	0.45
1:A:450:LYS:HD2	1:A:450:LYS:HA	1.61	0.45
1:C:532:TYR:N	1:C:532:TYR:HD1	2.14	0.45
1:E:314:SER:O	1:E:315:GLY:C	2.54	0.45
1:G:112:ARG:HD2	1:G:145:HIS:CE1	2.51	0.45
1:B:413:ARG:HH21	1:B:457:GLY:C	2.18	0.45
1:E:193:TYR:CE1	1:E:224:PRO:HA	2.52	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:F:243:LEU:O	1:F:244:ASN:C	2.55	0.45
1:C:397:PHE:CD1	1:C:397:PHE:C	2.89	0.45
1:E:220:ALA:HB1	1:E:261:ILE:HG21	1.87	0.45
1:A:441:MET:HE3	1:A:444:ASN:HB3	1.98	0.45
1:E:482:SER:CB	1:E:484:THR:HG23	2.46	0.45
1:C:124:ARG:HD3	1:C:125:ASP:N	2.32	0.45
1:F:504:ARG:HH21	1:F:506:GLN:HG2	1.82	0.45
1:D:502:LEU:HD12	1:D:502:LEU:N	2.31	0.45
1:E:248:ARG:HG2	1:E:248:ARG:O	2.16	0.45
1:B:492:LEU:HD12	1:B:492:LEU:N	2.16	0.45
1:B:265:VAL:HG11	1:G:411:TYR:CE1	2.52	0.45
1:G:121:GLN:HB2	1:G:133:THR:HG1	1.81	0.45
1:C:496:SER:O	1:C:520:LYS:CE	2.63	0.45
1:A:168:LEU:HD12	1:A:251:MET:CE	2.46	0.45
1:E:345:SER:O	1:E:349:THR:HG22	2.16	0.45
1:F:389:ASP:H	1:G:269:LEU:CD2	2.29	0.45
1:F:267:SER:O	1:F:271:LEU:HD12	2.16	0.45
1:D:536:ASN:OD1	1:D:539:THR:HG23	2.17	0.45
1:C:167:GLU:C	1:C:169:GLN:H	2.17	0.45
1:B:311:THR:OG1	1:B:466:LEU:HD21	2.16	0.45
1:E:356:LEU:HD12	1:E:541:TRP:NE1	2.32	0.45
1:A:359:ARG:HD3	1:A:541:TRP:HE1	1.80	0.45
1:G:122:LYS:HE3	1:G:130:PHE:CE2	2.52	0.45
1:G:261:ILE:N	1:G:262:PRO:HD2	2.30	0.45
1:A:289:PHE:HA	1:A:325:GLN:HE21	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:467:LYS:HG3	1:C:467:LYS:H	1.36	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:C:450:LYS:O	1:C:453:ALA:HB3	2.16	0.45
1:C:321:PHE:CD2	1:C:533:MET:CE	3.00	0.45
1:F:515:LEU:HD21	1:F:529:ILE:HD12	1.95	0.45
1:F:303:ARG:HB2	1:F:306:GLU:CD	2.37	0.45
1:E:288:LEU:N	1:E:288:LEU:HD12	2.31	0.45
1:A:483:ILE:O	1:A:486:LEU:CB	2.41	0.45
1:G:486:LEU:HD12	1:G:493:ARG:CG	2.47	0.45
1:C:124:ARG:CD	1:C:124:ARG:C	2.84	0.45
1:F:112:ARG:HB3	1:F:117:ASN:C	2.34	0.45
1:G:248:ARG:O	1:G:248:ARG:HG2	2.15	0.45
1:D:142:PHE:CE2	1:D:162:MET:CE	2.99	0.45
1:C:294:GLY:O	1:C:296:ASN:N	2.49	0.45
1:E:344:GLU:OE1	1:E:349:THR:HB	2.16	0.45
1:C:473:LYS:HE2	1:C:479:ARG:CB	2.46	0.45
1:E:300:LEU:HB3	1:E:303:ARG:NH1	2.32	0.45
1:D:246:HIS:HB3	1:D:249:GLU:OE1	2.17	0.45
1:A:267:SER:CB	1:B:392:HIS:ND1	2.80	0.45
1:D:410:ALA:HA	1:D:452:PHE:CE1	2.51	0.45
1:B:359:ARG:HD3	1:B:541:TRP:HE1	1.81	0.45
1:G:324:GLN:NE2	1:G:542:LEU:H	2.14	0.45
1:E:320:THR:HG22	1:E:324:GLN:HE21	1.82	0.45
1:C:518:ILE:HA	1:C:518:ILE:HD13	1.76	0.45
1:A:446:MET:HB3	1:A:491:ALA:HB1	1.99	0.45
1:F:504:ARG:HH21	1:F:506:GLN:CG	2.30	0.45
1:B:450:LYS:HE3	1:B:454:LYS:CD	2.45	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:C:316:MET:CE	1:C:535:TYR:CE2	3.00	0.45
1:D:321:PHE:CE2	1:D:533:MET:HE2	2.52	0.45
1:F:251:MET:CE	1:F:251:MET:CA	2.92	0.45
1:E:229:ARG:HB3	1:E:259:PRO:CB	2.46	0.45
1:D:234:PRO:CG	1:D:249:GLU:HG2	2.47	0.45
1:F:276:ARG:CG	1:F:276:ARG:HH11	2.28	0.45
1:E:548:SER:HB3	1:E:549:GLY:H	1.61	0.45
1:C:258:GLY:HA2	1:C:259:PRO:HD3	1.78	0.45
1:A:492:LEU:HD12	1:A:492:LEU:N	2.21	0.45
1:D:230:VAL:CG1	1:D:260:TRP:NE1	2.80	0.45
1:B:510:MET:HE2	1:B:513:LEU:HD22	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:145:HIS:CE1	1:E:146:LEU:HD23	2.52	0.45
1:A:413:ARG:O	1:A:413:ARG:HD2	2.17	0.45
1:G:473:LYS:HE2	1:G:479:ARG:CA	2.46	0.45
1:C:401:GLU:OE2	1:C:432:ALA:HB2	2.17	0.45
1:F:243:LEU:O	1:F:244:ASN:O	2.34	0.45
1:C:243:LEU:O	1:C:244:ASN:O	2.35	0.45
1:B:531:GLY:C	1:B:532:TYR:CD1	2.90	0.45
1:F:288:LEU:HD12	1:F:288:LEU:N	2.32	0.45
1:G:286:GLY:O	1:G:302:ALA:N	2.49	0.45
1:D:493:ARG:H	1:D:493:ARG:HG2	1.40	0.45
1:G:427:SER:CB	1:G:487:ARG:HH12	2.26	0.45
1:E:493:ARG:HG2	1:E:493:ARG:H	1.41	0.45
1:A:292:CYS:HB3	1:A:295:ILE:CG1	2.47	0.45
1:F:382:PHE:CD2	1:F:382:PHE:C	2.91	0.45
1:A:450:LYS:HE2	1:A:454:LYS:CD	2.30	0.45
1:E:447:THR:CG2	1:E:495:LEU:HD21	2.31	0.45
1:D:166:MET:HG2	1:D:175:VAL:HG23	1.99	0.45
1:E:510:MET:HB2	1:E:513:LEU:HB3	1.98	0.45
1:A:479:ARG:HA	1:A:480:PRO:HD3	1.85	0.45
1:C:364:GLN:HG3	1:D:523:PHE:CZ	2.52	0.45
1:B:368:LEU:C	1:B:368:LEU:HD22	2.38	0.45
1:D:194:GLU:N	1:D:194:GLU:CD	2.64	0.45
1:B:312:SER:N	1:B:318:MET:HE2	2.32	0.45
1:C:114:GLN:HG3	1:C:144:LYS:HE2	1.99	0.45
1:E:542:LEU:HD12	1:E:542:LEU:HA	1.56	0.45
1:A:412:MET:CE	1:A:421:ILE:HD13	2.44	0.44
1:F:425:HIS:HE1	1:F:427:SER:HB2	1.60	0.44
1:A:486:LEU:HD22	1:A:487:ARG:H	1.83	0.44
1:A:441:MET:HE2	1:A:445:LEU:N	2.32	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:B:510:MET:CB	1:B:513:LEU:HB2	2.46	0.44
1:A:106:TYR:HB3	1:A:123:VAL:HG12	1.99	0.44
1:A:515:LEU:HD21	1:A:529:ILE:HD12	1.99	0.44
1:F:533:MET:HB3	1:F:543:GLU:O	2.17	0.44
1:B:194:GLU:N	1:B:194:GLU:CD	2.70	0.44
1:A:130:PHE:O	1:A:131:LYS:CG	2.64	0.44
1:G:223:LEU:CD2	1:G:224:PRO:HD2	2.47	0.44
1:C:346:VAL:HG23	1:C:393:LEU:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:536:ASN:ND2	1:F:538:GLU:CB	2.80	0.44
1:E:484:THR:O	1:E:486:LEU:N	2.50	0.44
1:F:491:ALA:O	1:F:495:LEU:N	2.48	0.44
1:C:427:SER:CB	1:C:487:ARG:HH12	2.30	0.44
1:D:496:SER:O	1:D:520:LYS:CE	2.65	0.44
1:G:439:ARG:HG2	1:G:489:SER:OG	2.16	0.44
1:F:496:SER:O	1:F:520:LYS:CE	2.65	0.44
1:B:496:SER:CB	1:B:499:ILE:HD11	2.47	0.44
1:D:303:ARG:CZ	1:D:523:PHE:CD1	3.00	0.44
1:E:276:ARG:NH1	1:E:276:ARG:CG	2.76	0.44
1:E:185:ALA:O	1:E:189:CYS:HB2	2.17	0.44
1:F:235:CYS:CB	1:F:240:GLU:HG2	2.46	0.44
1:A:138:SER:HB3	1:A:187:LYS:HD3	1.99	0.44
1:E:260:TRP:C	1:E:261:ILE:HG13	2.37	0.44
1:F:492:LEU:C	1:F:494:GLN:H	2.21	0.44
1:C:482:SER:CB	1:C:484:THR:HG23	2.47	0.44
1:D:401:GLU:HB2	1:D:404:ARG:NH2	2.32	0.44
1:F:516:VAL:HG23	1:F:531:GLY:O	2.17	0.44
1:D:321:PHE:CD2	1:D:533:MET:HE2	2.52	0.44
1:F:510:MET:HB2	1:F:513:LEU:HB3	1.98	0.44
1:F:74:SER:HB3	1:F:101:VAL:CG2	2.47	0.44
1:A:320:THR:HG22	1:A:324:GLN:NE2	2.32	0.44
1:G:443:ASP:HA	1:G:491:ALA:HB3	1.99	0.44
1:A:392:HIS:ND1	1:C:267:SER:HB2	2.32	0.44
1:A:77:ARG:HE	1:A:77:ARG:HB2	1.60	0.44
1:F:259:PRO:O	1:F:259:PRO:CG	2.64	0.44
1:A:220:ALA:HB1	1:A:261:ILE:CG2	2.47	0.44
1:F:107:GLN:H	1:F:124:ARG:HG3	1.82	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:A:510:MET:HB2	1:A:513:LEU:CB	2.47	0.44
1:F:106:TYR:N	1:F:106:TYR:CD1	2.85	0.44
1:A:121:GLN:CB	1:A:133:THR:HG23	2.48	0.44
1:F:532:TYR:CD1	1:F:532:TYR:N	2.85	0.44
1:D:368:LEU:HD22	1:D:368:LEU:C	2.36	0.44
1:F:234:PRO:CG	1:F:249:GLU:HG2	2.48	0.44
1:F:404:ARG:O	1:F:408:LYS:HG2	2.16	0.44
1:E:318:MET:HE3	1:E:465:HIS:CD2	2.52	0.44
1:C:362:LEU:HD12	1:C:362:LEU:O	2.17	0.44
1:B:493:ARG:HG2	1:B:493:ARG:H	1.43	0.44
1:C:220:ALA:HB3	1:C:261:ILE:HG21	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:440:LYS:HE2	1:A:440:LYS:C	2.38	0.44
1:C:440:LYS:HZ2	1:C:441:MET:HA	1.70	0.44
1:E:408:LYS:O	1:E:412:MET:HG3	2.18	0.44
1:D:78:TYR:O	1:D:88:LYS:HG3	2.17	0.44
1:B:510:MET:HB2	1:B:513:LEU:HB3	2.00	0.44
1:G:401:GLU:HB3	1:G:404:ARG:HB3	2.00	0.44
1:C:271:LEU:O	1:C:272:ARG:C	2.54	0.44
1:F:510:MET:HB2	1:F:513:LEU:CB	2.47	0.44
1:B:136:HIS:CD2	1:B:180:HIS:CE1	3.06	0.44
1:G:185:ALA:O	1:G:189:CYS:HB2	2.18	0.44
1:A:440:LYS:O	1:A:443:ASP:HB2	2.17	0.44
1:G:315:GLY:HA2	1:G:317:VAL:CG2	2.42	0.44
1:E:488:GLY:HA3	1:E:492:LEU:CD1	2.44	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:A:546:SER:O	1:A:547:TYR:HB2	2.17	0.44
1:G:152:LYS:O	1:G:174:PRO:HD2	2.17	0.44
1:C:517:ARG:HB3	1:C:519:LEU:HD13	1.99	0.44
1:E:463:ILE:CG2	1:E:464:CYS:N	2.79	0.44
1:B:536:ASN:ND2	1:B:538:GLU:HB3	2.32	0.44
1:A:536:ASN:C	1:A:538:GLU:H	2.21	0.44
1:E:79:SER:H	1:E:98:ILE:CD1	2.29	0.44
1:A:202:ILE:HD13	1:A:223:LEU:HD22	2.00	0.44
1:B:180:HIS:N	1:B:180:HIS:CD2	2.85	0.44
1:D:204:LEU:HD13	1:D:206:PHE:CZ	2.53	0.44
1:A:100:LYS:HD3	1:A:105:MET:HB2	1.99	0.44
1:D:486:LEU:HB3	1:D:493:ARG:CD	2.45	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:D:227:LYS:O	1:D:229:ARG:HD2	2.18	0.44
1:E:352:ASP:CG	1:E:363:ARG:HD3	2.38	0.44
1:E:304:GLY:HA2	1:E:459:VAL:HG22	1.98	0.44
1:D:295:ILE:HD12	1:D:516:VAL:HG11	1.97	0.44
1:D:395:ASP:HB3	1:E:266:VAL:HG21	2.00	0.44
1:G:193:TYR:CE1	1:G:224:PRO:HA	2.53	0.44
1:D:304:GLY:HA2	1:D:459:VAL:HG22	1.98	0.44
1:A:336:LYS:HB3	1:A:418:CYS:HB3	1.98	0.44
1:G:362:LEU:O	1:G:362:LEU:HD12	2.17	0.44
1:C:409:LEU:HD23	1:C:421:ILE:CG2	2.33	0.44
1:C:406:LEU:HD13	1:C:406:LEU:HA	1.80	0.44
1:D:447:THR:O	1:D:448:LYS:C	2.56	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:492:LEU:O	1:E:494:GLN:N	2.51	0.44
1:G:339:LEU:HD13	1:G:341:MET:CE	2.48	0.44
1:G:338:GLY:HA3	1:G:412:MET:HE3	2.00	0.44
1:D:498:THR:C	1:D:499:ILE:HD13	2.37	0.44
1:G:488:GLY:HA3	1:G:492:LEU:CD1	2.46	0.44
1:A:510:MET:CE	1:A:513:LEU:CD2	2.95	0.44
1:D:96:TYR:CE2	1:D:107:GLN:HG2	2.53	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:C:327:LEU:HB3	1:C:328:GLN:H	1.70	0.44
1:A:321:PHE:CE2	1:A:533:MET:HE1	2.53	0.44
1:E:286:GLY:O	1:E:302:ALA:N	2.51	0.44
1:G:228:VAL:HB	1:G:261:ILE:HD12	1.99	0.44
1:A:425:HIS:CE1	1:A:465:HIS:HB2	2.50	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:C:124:ARG:HD3	1:C:125:ASP:CA	2.47	0.44
1:E:370:ARG:HH12	1:E:371:GLU:HG2	1.71	0.44
1:D:405:LEU:HG	1:D:409:LEU:CD1	2.42	0.44
1:F:412:MET:HB3	1:F:412:MET:HE2	1.53	0.44
1:G:450:LYS:HA	1:G:450:LYS:HD2	1.67	0.44
1:G:510:MET:HB2	1:G:513:LEU:HB3	2.00	0.44
1:A:251:MET:CE	1:A:251:MET:CA	2.92	0.44
1:A:473:LYS:CE	1:A:479:ARG:HA	2.44	0.44
1:A:401:GLU:CG	1:A:402:THR:N	2.76	0.44
1:D:347:GLU:OE2	1:E:274:ARG:CD	2.66	0.44
1:A:316:MET:CE	1:A:535:TYR:CZ	3.00	0.44
1:B:320:THR:HG22	1:B:324:GLN:NE2	2.33	0.44
1:F:401:GLU:CG	1:F:402:THR:H	2.30	0.44
1:D:322:VAL:HG21	1:D:463:ILE:CD1	2.47	0.44
1:A:136:HIS:CD2	1:A:180:HIS:CE1	3.05	0.44
1:D:155:VAL:HG12	1:D:206:PHE:HE2	1.83	0.44
1:A:493:ARG:H	1:A:493:ARG:HG2	1.40	0.43
1:C:233:LEU:HD22	1:C:241:CYS:SG	2.58	0.43
1:A:125:ASP:OD1	1:A:129:ASN:HB2	2.18	0.43
1:B:450:LYS:HD2	1:B:450:LYS:HA	1.67	0.43
1:E:338:GLY:O	1:E:421:ILE:HA	2.18	0.43
1:G:492:LEU:C	1:G:494:GLN:H	2.19	0.43
1:C:513:LEU:HD11	1:C:532:TYR:HB3	2.00	0.43
1:B:401:GLU:CA	1:B:430:VAL:O	2.66	0.43
1:A:519:LEU:O	1:A:520:LYS:CB	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:GLN:O	1:A:170:ASP:CB	2.63	0.43
1:E:363:ARG:H	1:E:363:ARG:HG2	1.66	0.43
1:E:181:GLY:O	1:E:182:ALA:C	2.57	0.43
1:B:251:MET:CA	1:B:251:MET:CE	2.96	0.43
1:A:122:LYS:HE3	1:A:130:PHE:HE2	1.81	0.43
1:D:145:HIS:CE1	1:D:146:LEU:HD21	2.52	0.43
1:E:451:GLY:O	1:E:452:PHE:C	2.57	0.43
1:E:443:ASP:HA	1:E:491:ALA:HB3	2.00	0.43
1:F:492:LEU:O	1:F:494:GLN:N	2.52	0.43
1:F:287:LEU:HD23	1:F:329:TRP:CE2	2.53	0.43
1:G:546:SER:O	1:G:547:TYR:HB2	2.18	0.43
1:E:112:ARG:NH2	1:E:118:ILE:HD11	2.33	0.43
1:F:473:LYS:CD	1:F:479:ARG:HB2	2.48	0.43
1:G:471:LYS:HD2	1:G:472:GLY:N	2.33	0.43
1:E:273:GLU:OE2	1:E:276:ARG:NH1	2.50	0.43
1:D:346:VAL:HG23	1:D:393:LEU:HB2	2.00	0.43
1:G:406:LEU:HD13	1:G:406:LEU:HA	1.81	0.43
1:D:356:LEU:HD12	1:D:541:TRP:NE1	2.33	0.43
1:E:318:MET:HE1	1:E:465:HIS:CD2	2.53	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:B:428:ILE:H	1:B:428:ILE:HD12	1.83	0.43
1:D:342:LEU:HD23	1:D:342:LEU:N	2.32	0.43
1:F:368:LEU:HA	1:F:368:LEU:HD23	1.69	0.43
1:D:425:HIS:CE1	1:D:427:SER:CB	3.01	0.43
1:B:486:LEU:HA	1:B:486:LEU:HD23	1.71	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:F:391:PHE:C	1:F:392:HIS:CD2	2.91	0.43
1:A:450:LYS:NZ	1:A:454:LYS:HD3	2.31	0.43
1:F:112:ARG:HD3	1:F:116:GLY:O	2.18	0.43
1:B:446:MET:HE3	1:B:492:LEU:HA	2.00	0.43
1:B:121:GLN:HB2	1:B:133:THR:HG1	1.78	0.43
1:C:373:ILE:HD11	1:D:279:LEU:HB2	2.00	0.43
1:C:181:GLY:O	1:C:182:ALA:C	2.56	0.43
1:A:141:LEU:HG	1:A:192:ASN:ND2	2.34	0.43
1:D:352:ASP:OD2	1:D:363:ARG:HD3	2.17	0.43
1:E:536:ASN:ND2	1:E:538:GLU:H	2.17	0.43
1:G:255:TRP:O	1:G:256:ASN:C	2.57	0.43
1:G:80:ALA:HB2	1:G:88:LYS:N	2.33	0.43
1:C:336:LYS:HB3	1:C:418:CYS:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:378:PHE:HD2	1:G:276:ARG:HD2	1.83	0.43
1:F:107:GLN:HB3	1:F:124:ARG:CG	2.49	0.43
1:E:445:LEU:HD12	1:E:445:LEU:O	2.17	0.43
1:C:483:ILE:O	1:C:486:LEU:CB	2.48	0.43
1:D:402:THR:HG23	1:D:403:ASP:N	2.33	0.43
1:B:440:LYS:HZ3	1:B:444:ASN:HB3	1.82	0.43
1:G:496:SER:O	1:G:520:LYS:CE	2.66	0.43
1:F:314:SER:O	1:F:315:GLY:C	2.56	0.43
1:F:535:TYR:CE1	1:F:537:LYS:HA	2.53	0.43
1:D:473:LYS:HE2	1:D:479:ARG:CA	2.42	0.43
1:A:415:GLY:N	1:C:226:GLY:HA3	2.34	0.43
1:D:283:GLU:O	1:D:283:GLU:HG2	2.16	0.43
1:C:358:ASN:ND2	1:C:381:TRP:CE2	2.87	0.43
1:A:536:ASN:HD22	1:A:536:ASN:C	2.20	0.43
1:B:193:TYR:CE1	1:B:224:PRO:HA	2.53	0.43
1:B:180:HIS:HB2	1:B:184:ALA:HB3	1.99	0.43
1:B:319:SER:O	1:B:323:ARG:HB2	2.18	0.43
1:F:476:GLU:N	1:F:476:GLU:CD	2.69	0.43
1:G:289:PHE:HA	1:G:325:GLN:HE21	1.84	0.43
1:D:440:LYS:O	1:D:443:ASP:HB2	2.19	0.43
1:C:506:GLN:HG3	1:C:506:GLN:H	1.56	0.43
1:C:450:LYS:HE3	1:C:454:LYS:CD	2.48	0.43
1:E:447:THR:HA	1:E:495:LEU:CD2	2.48	0.43
1:D:510:MET:HB2	1:D:513:LEU:CB	2.48	0.43
1:G:321:PHE:CE2	1:G:533:MET:HE2	2.53	0.43
1:B:503:GLU:HG3	1:B:515:LEU:CD2	2.48	0.43
1:E:510:MET:CB	1:E:513:LEU:HB2	2.48	0.43
1:G:478:GLY:O	1:G:479:ARG:C	2.57	0.43
1:E:229:ARG:CA	1:E:259:PRO:HA	2.46	0.43
1:D:330:GLY:HA2	1:D:335:LYS:O	2.18	0.43
1:F:322:VAL:HG11	1:F:422:ILE:CG2	2.47	0.43
1:C:397:PHE:HD1	1:C:397:PHE:C	2.21	0.43
1:A:441:MET:HE2	1:A:445:LEU:H	1.83	0.43
1:E:486:LEU:HB3	1:E:493:ARG:CD	2.48	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: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:D:338:GLY:CA	1:D:412:MET:HE1	2.46	0.43
1:G:442:ILE:HD11	1:G:492:LEU:CD2	2.47	0.43
1:A:414:SER:C	1:C:226:GLY:HA3	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:285:VAL:HG22	1:B:300:LEU:CD1	2.47	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:C:185:ALA:O	1:C:189:CYS:HB2	2.18	0.43
1:A:492:LEU:C	1:A:494:GLN:H	2.21	0.43
1:D:220:ALA:HB1	1:D:261:ILE:HG12	2.01	0.43
1:C:440:LYS:O	1:C:443:ASP:HB2	2.19	0.43
1:B:286:GLY:O	1:B:302:ALA:O	2.35	0.43
1:D:441:MET:HE1	1:D:445:LEU:H	1.82	0.43
1:G:124:ARG:HD3	1:G:125:ASP:O	2.19	0.43
1:B:492:LEU:O	1:B:494:GLN:N	2.52	0.43
1:D:147:TRP:CD2	1:D:174:PRO:HB3	2.54	0.43
1:D:81:LEU:HG	1:D:91:CYS:SG	2.59	0.43
1:E:153:ILE:O	1:E:153:ILE:HG23	2.18	0.43
1:D:141:LEU:CD1	1:D:176:VAL:HG21	2.43	0.43
1:B:312:SER:HB3	1:B:502:LEU:H	1.83	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:C:122:LYS:HE3	1:C:130:PHE:HE2	1.81	0.43
1:E:136:HIS:CD2	1:E:180:HIS:CE1	3.06	0.43
1:E:397:PHE:C	1:E:397:PHE:HD1	2.21	0.43
1:B:204:LEU:HD13	1:B:206:PHE:CZ	2.54	0.43
1:B:248:ARG:CG	1:B:248:ARG:NH1	2.70	0.43
1:C:260:TRP:O	1:C:261:ILE:HD13	2.19	0.43
1:F:440:LYS:O	1:F:443:ASP:HB2	2.18	0.43
1:C:442:ILE:HD11	1:C:492:LEU:CD1	2.47	0.43
1:C:427:SER:HB3	1:C:487:ARG:NH1	2.33	0.43
1:E:412:MET:HE2	1:E:421:ILE:HD11	1.93	0.43
1:B:510:MET:HE1	1:B:547:TYR:CE1	2.50	0.43
1:A:401:GLU:N	1:A:404:ARG:HD2	2.34	0.43
1:F:366:ASP:CB	1:G:284:SER:CB	2.92	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:A:114:GLN:HG3	1:A:144:LYS:HE2	2.01	0.43
1:F:320:THR:HG22	1:F:324:GLN:HE21	1.84	0.43
1:A:321:PHE:CD2	1:A:533:MET:HE1	2.53	0.43
1:A:105:MET:O	1:A:105:MET:HG2	2.18	0.43
1:F:285:VAL:HG13	1:F:300:LEU:CD1	2.49	0.43
1:C:149:GLY:O	1:C:199:PHE:CE2	2.72	0.43
1:G:425:HIS:NE2	1:G:465:HIS:ND1	2.66	0.43
1:G:268:ALA:HA	1:G:271:LEU:HD12	1.98	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:450:LYS:HD2	1:F:450:LYS:HA	1.72	0.43
1:G:428:ILE:H	1:G:428:ILE:HD12	1.83	0.43
1:E:145:HIS:CE1	1:E:146:LEU:CD2	3.02	0.43
1:C:364:GLN:HA	1:D:523:PHE:HZ	1.83	0.43
1:G:413:ARG:HH21	1:G:457:GLY:C	2.22	0.43
1:C:360:VAL:CG2	1:C:360:VAL:O	2.67	0.43
1:D:322:VAL:HG11	1:D:422:ILE:HG21	2.01	0.43
1:G:536:ASN:ND2	1:G:538:GLU:H	2.16	0.43
1:A:427:SER:CB	1:A:487:ARG:NH1	2.81	0.43
1:C:208:MET:CE	1:C:233:LEU:H	2.32	0.43
1:A:208:MET:CE	1:A:232:VAL:HA	2.22	0.43
1:C:441:MET:CE	1:C:445:LEU:H	2.32	0.43
1:D:441:MET:HE1	1:D:444:ASN:HB3	2.00	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:B:344:GLU:OE1	1:B:349:THR:HB	2.19	0.43
1:E:517:ARG:CG	1:E:517:ARG:HH11	2.30	0.43
1:A:510:MET:CB	1:A:513:LEU:CB	2.97	0.43
1:A:413:ARG:HH21	1:A:457:GLY:C	2.22	0.43
1:A:216:VAL:HG11	1:A:230:VAL:HG22	1.99	0.43
1:E:251:MET:CA	1:E:251:MET:CE	2.97	0.43
1:D:251:MET:CA	1:D:251:MET:CE	2.97	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:327:LEU:HA	1:A:327:LEU:HD23	1.43	0.43
1:B:248:ARG:O	1:B:248:ARG:HG2	2.19	0.42
1:C:290:SER:N	1:C:325:GLN:HE22	2.03	0.42
1:E:449:LEU:O	1:E:452:PHE:HB3	2.18	0.42
1:G:424:ASP:O	1:G:425:HIS:HB3	2.19	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:A:265:VAL:HG21	1:B:412:MET:HG2	2.01	0.42
1:F:382:PHE:CZ	1:G:272:ARG:HA	2.54	0.42
1:A:450:LYS:HE3	1:A:454:LYS:CD	2.47	0.42
1:C:145:HIS:CE1	1:C:146:LEU:HD21	2.53	0.42
1:B:181:GLY:O	1:B:182:ALA:C	2.57	0.42
1:B:536:ASN:HD22	1:B:536:ASN:C	2.21	0.42
1:E:122:LYS:HE3	1:E:130:PHE:HE2	1.84	0.42
1:G:327:LEU:HD11	1:G:357:HIS:HA	2.00	0.42
1:E:411:TYR:CZ	1:F:262:PRO:HB3	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:145:HIS:CE1	1:A:146:LEU:HD21	2.54	0.42
1:E:445:LEU:CD1	1:E:449:LEU:HG	2.49	0.42
1:E:81:LEU:HD11	1:E:96:TYR:CD2	2.54	0.42
1:C:427:SER:HB2	1:D:494:GLN:HE22	1.84	0.42
1:D:440:LYS:NZ	1:D:441:MET:HG2	2.34	0.42
1:G:440:LYS:C	1:G:440:LYS:HE2	2.39	0.42
1:D:317:VAL:HG21	1:D:504:ARG:HD2	2.01	0.42
1:C:510:MET:CE	1:C:513:LEU:HD22	2.49	0.42
1:E:520:LYS:HG3	1:E:521:CYS:N	2.25	0.42
1:B:473:LYS:HE2	1:B:479:ARG:CA	2.44	0.42
1:E:178:LEU:HD23	1:E:178:LEU:HA	1.83	0.42
1:A:346:VAL:CG1	1:C:271:LEU:HD21	2.50	0.42
1:E:479:ARG:HA	1:E:480:PRO:HD3	1.83	0.42
1:A:401:GLU:CB	1:A:431:SER:O	2.67	0.42
1:C:86:ILE:HD12	1:C:163:LEU:HB3	2.02	0.42
1:F:180:HIS:N	1:F:180:HIS:CD2	2.87	0.42
1:F:285:VAL:HA	1:F:300:LEU:HD12	2.00	0.42
1:D:327:LEU:HD23	1:D:327:LEU:HA	1.47	0.42
1:A:313:GLY:C	1:A:315:GLY:N	2.71	0.42
1:E:441:MET:HE1	1:E:445:LEU:H	1.84	0.42
1:D:290:SER:N	1:D:325:GLN:HE22	2.08	0.42
1:F:442:ILE:HD11	1:F:492:LEU:CG	2.49	0.42
1:B:476:GLU:HB3	1:B:506:GLN:OE1	2.19	0.42
1:D:311:THR:O	1:D:502:LEU:HD12	2.18	0.42
1:C:146:LEU:HB2	1:C:147:TRP:CE2	2.54	0.42
1:D:413:ARG:HH21	1:D:457:GLY:C	2.22	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:D:542:LEU:HA	1:D:542:LEU:HD12	1.56	0.42
1:C:204:LEU:HD13	1:C:206:PHE:CZ	2.54	0.42
1:B:336:LYS:HB3	1:B:418:CYS:HA	2.00	0.42
1:B:170:ASP:O	1:B:172:LYS:HG3	2.20	0.42
1:E:518:ILE:HA	1:E:518:ILE:HD13	1.75	0.42
1:D:482:SER:O	1:D:485:ASP:CB	2.68	0.42
1:A:406:LEU:HD13	1:A:406:LEU:HA	1.74	0.42
1:D:220:ALA:CB	1:D:261:ILE:HG23	2.47	0.42
1:E:442:ILE:HD11	1:E:492:LEU:CG	2.48	0.42
1:D:412:MET:HE2	1:D:421:ILE:HD12	1.97	0.42
1:A:510:MET:HE2	1:A:547:TYR:CE1	2.51	0.42
1:A:499:ILE:HG22	1:A:519:LEU:CB	2.34	0.42
1:A:168:LEU:O	1:A:169:GLN:CB	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:267:SER:O	1:E:271:LEU:HD12	2.19	0.42
1:F:322:VAL:CG1	1:F:422:ILE:HD13	2.49	0.42
1:A:445:LEU:O	1:A:446:MET:C	2.58	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:A:339:LEU:HB3	1:A:341:MET:HE3	1.88	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:F:178:LEU:HB3	1:F:181:GLY:CA	2.40	0.42
1:A:141:LEU:CD1	1:A:176:VAL:HG21	2.43	0.42
1:F:121:GLN:HB3	1:F:133:THR:CG2	2.45	0.42
1:F:513:LEU:HD12	1:F:533:MET:O	2.18	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:F:217:GLU:OE2	1:F:261:ILE:HG23	2.18	0.42
1:D:289:PHE:HA	1:D:325:GLN:HE21	1.84	0.42
1:C:124:ARG:CZ	1:C:126:LYS:HA	2.50	0.42
1:C:339:LEU:HB3	1:C:341:MET:HE2	1.88	0.42
1:D:444:ASN:OD1	1:D:448:LYS:HE3	2.19	0.42
1:B:406:LEU:HA	1:B:406:LEU:HD13	1.59	0.42
1:D:546:SER:O	1:D:547:TYR:HB2	2.20	0.42
1:B:263:ASP:C	1:G:408:LYS:NZ	2.73	0.42
1:G:153:ILE:O	1:G:153:ILE:HG23	2.20	0.42
1:D:107:GLN:CB	1:D:124:ARG:CG	2.93	0.42
1:C:121:GLN:HB3	1:C:133:THR:CG2	2.47	0.42
1:C:141:LEU:HG	1:C:192:ASN:ND2	2.34	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:E:114:GLN:NE2	1:E:195:TYR:CD1	2.87	0.42
1:A:300:LEU:HA	1:A:300:LEU:HD22	1.78	0.42
1:F:260:TRP:CD1	1:F:262:PRO:HD2	2.55	0.42
1:D:486:LEU:HD22	1:D:487:ARG:H	1.85	0.42
1:A:229:ARG:NH2	1:A:259:PRO:HB3	2.34	0.42
1:E:341:MET:SD	1:E:424:ASP:HB2	2.59	0.42
1:E:486:LEU:HD22	1:E:487:ARG:H	1.85	0.42
1:A:124:ARG:CD	1:A:125:ASP:C	2.86	0.42
1:E:429:VAL:HG13	1:E:438:GLU:OE1	2.19	0.42
1:C:510:MET:HB2	1:C:513:LEU:HB3	2.00	0.42
1:C:74:SER:HB3	1:C:101:VAL:CG2	2.50	0.42
1:E:517:ARG:CZ	1:E:529:ILE:HD11	2.50	0.42
1:C:344:GLU:OE1	1:C:349:THR:CB	2.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:352:ASP:OD2	1:A:363:ARG:HD3	2.20	0.42
1:D:347:GLU:O	1:D:351:GLU:HG3	2.20	0.42
1:G:363:ARG:HG2	1:G:363:ARG:H	1.55	0.42
1:G:445:LEU:O	1:G:445:LEU:HD12	2.19	0.42
1:G:382:PHE:CD2	1:G:382:PHE:C	2.92	0.42
1:G:451:GLY:O	1:G:452:PHE:C	2.58	0.42
1:D:115:ASN:HB3	1:D:117:ASN:HD21	1.84	0.42
1:E:427:SER:HB3	1:E:487:ARG:NH1	2.28	0.42
1:F:415:GLY:HA2	1:G:226:GLY:H	1.82	0.42
1:F:356:LEU:HD12	1:F:541:TRP:CD1	2.54	0.42
1:E:536:ASN:C	1:E:536:ASN:HD22	2.23	0.42
1:F:362:LEU:HD12	1:F:362:LEU:C	2.40	0.42
1:C:70:ASN:HD22	1:C:70:ASN:HA	1.69	0.42
1:B:248:ARG:HD2	1:B:249:GLU:OE2	2.20	0.42
1:C:233:LEU:CD2	1:C:250:ILE:HG12	2.50	0.42
1:F:488:GLY:HA3	1:F:492:LEU:CD1	2.45	0.42
1:E:368:LEU:HD22	1:E:372:ILE:CG2	2.46	0.42
1:G:440:LYS:NZ	1:G:441:MET:HG2	2.35	0.42
1:F:307:VAL:HG12	1:F:496:SER:HA	2.01	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:F:165:VAL:HB	1:F:175:VAL:HG11	2.02	0.42
1:E:478:GLY:O	1:E:479:ARG:C	2.58	0.42
1:E:229:ARG:HB3	1:E:259:PRO:CA	2.50	0.42
1:D:347:GLU:CD	1:E:274:ARG:HG2	2.40	0.42
1:D:536:ASN:C	1:D:538:GLU:H	2.22	0.42
1:C:401:GLU:HG3	1:C:431:SER:O	2.20	0.42
1:A:269:LEU:HD21	1:B:389:ASP:H	1.84	0.42
1:D:451:GLY:O	1:D:455:SER:HB3	2.19	0.42
1:F:378:PHE:CE2	1:G:276:ARG:CG	3.03	0.42
1:B:482:SER:H	1:B:485:ASP:CB	2.23	0.42
1:A:440:LYS:NZ	1:A:441:MET:HG2	2.34	0.42
1:D:259:PRO:O	1:D:260:TRP:CE3	2.72	0.42
1:F:442:ILE:HD11	1:F:492:LEU:HD11	1.98	0.42
1:C:442:ILE:HD11	1:C:492:LEU:CD2	2.49	0.42
1:E:124:ARG:HD3	1:E:125:ASP:O	2.19	0.42
1:D:492:LEU:O	1:D:494:GLN:N	2.53	0.42
1:E:370:ARG:HD2	1:E:371:GLU:CA	2.49	0.42
1:G:307:VAL:HG22	1:G:460:LEU:HB3	2.02	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:368:LEU:C	1:A:368:LEU:HD22	2.33	0.42
1:C:536:ASN:C	1:C:538:GLU:N	2.73	0.42
1:A:242:HIS:O	1:A:244:ASN:N	2.53	0.42
1:C:204:LEU:N	1:C:204:LEU:HD23	2.35	0.42
1:G:170:ASP:O	1:G:172:LYS:HG3	2.20	0.42
1:G:77:ARG:HE	1:G:77:ARG:HB2	1.61	0.42
1:F:259:PRO:O	1:F:260:TRP:CB	2.58	0.41
1:F:482:SER:CB	1:F:484:THR:HG23	2.49	0.41
1:G:425:HIS:CE1	1:G:427:SER:HB2	2.55	0.41
1:E:208:MET:HE1	1:E:232:VAL:CA	2.23	0.41
1:C:504:ARG:HD3	1:C:506:GLN:CG	2.26	0.41
1:E:447:THR:HG22	1:E:495:LEU:CD2	2.31	0.41
1:G:517:ARG:CZ	1:G:529:ILE:HD11	2.50	0.41
1:E:496:SER:O	1:E:520:LYS:CE	2.67	0.41
1:C:366:ASP:CB	1:D:284:SER:OG	2.67	0.41
1:F:295:ILE:HD12	1:F:516:VAL:HG11	2.02	0.41
1:B:542:LEU:HA	1:B:542:LEU:HD12	1.64	0.41
1:F:536:ASN:C	1:F:536:ASN:HD22	2.22	0.41
1:C:322:VAL:HG21	1:C:463:ILE:CD1	2.49	0.41
1:B:122:LYS:HE3	1:B:130:PHE:HE2	1.85	0.41
1:G:532:TYR:CD1	1:G:532:TYR:N	2.88	0.41
1:F:397:PHE:C	1:F:397:PHE:HD1	2.22	0.41
1:C:267:SER:O	1:C:270:SER:OG	2.28	0.41
1:F:285:VAL:HA	1:F:300:LEU:CD1	2.49	0.41
1:A:173:TYR:CD1	1:A:173:TYR:N	2.88	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:A:492:LEU:CD1	1:A:492:LEU:H	2.13	0.41
1:C:440:LYS:NZ	1:C:441:MET:CA	2.58	0.41
1:D:445:LEU:HD12	1:D:445:LEU:O	2.20	0.41
1:G:272:ARG:CG	1:G:273:GLU:N	2.81	0.41
1:D:152:LYS:O	1:D:174:PRO:HD2	2.19	0.41
1:B:106:TYR:HB3	1:B:123:VAL:CG1	2.50	0.41
1:C:369:LYS:NZ	1:D:284:SER:H	2.19	0.41
1:F:366:ASP:HA	1:G:284:SER:OG	2.20	0.41
1:G:284:SER:O	1:G:300:LEU:HD12	2.19	0.41
1:F:147:TRP:CE2	1:F:174:PRO:HA	2.55	0.41
1:B:324:GLN:OE1	1:B:541:TRP:CE3	2.73	0.41
1:A:276:ARG:HH11	1:A:276:ARG:CG	2.30	0.41
1:B:185:ALA:O	1:B:189:CYS:HB2	2.19	0.41
1:F:414:SER:O	1:G:225:ALA:HB1	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:170:ASP:O	1:E:172:LYS:HG3	2.20	0.41
1:A:173:TYR:HA	1:A:174:PRO:HD3	1.94	0.41
1:F:486:LEU:HD22	1:F:487:ARG:N	2.35	0.41
1:A:424:ASP:HA	1:A:463:ILE:HB	2.01	0.41
1:C:447:THR:HG22	1:C:495:LEU:CD2	2.32	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:F:412:MET:HA	1:F:416:LEU:HD11	1.96	0.41
1:G:81:LEU:HD22	1:G:107:GLN:NE2	2.35	0.41
1:B:262:PRO:CB	1:B:265:VAL:HG12	2.49	0.41
1:B:81:LEU:HD12	1:B:86:ILE:HB	2.02	0.41
1:D:129:ASN:OD1	1:E:89:GLU:OE1	2.38	0.41
1:A:166:MET:HG2	1:A:175:VAL:HG21	2.02	0.41
1:D:533:MET:HB3	1:D:543:GLU:O	2.20	0.41
1:F:360:VAL:O	1:F:360:VAL:HG23	2.20	0.41
1:A:267:SER:O	1:A:271:LEU:HD12	2.20	0.41
1:C:402:THR:HG23	1:C:403:ASP:H	1.85	0.41
1:E:346:VAL:HG23	1:E:393:LEU:HB2	2.02	0.41
1:B:204:LEU:HD23	1:B:204:LEU:N	2.36	0.41
1:A:548:SER:HB3	1:A:549:GLY:H	1.60	0.41
1:F:375:ASN:CG	1:F:377:LYS:HG3	2.40	0.41
1:E:411:TYR:O	1:E:411:TYR:CG	2.73	0.41
1:A:227:LYS:O	1:A:229:ARG:HD2	2.21	0.41
1:C:216:VAL:CG1	1:C:230:VAL:HG22	2.47	0.41
1:C:442:ILE:HG23	1:C:443:ASP:N	2.35	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:E:450:LYS:HE3	1:E:454:LYS:CD	2.48	0.41
1:D:313:GLY:O	1:D:315:GLY:N	2.53	0.41
1:E:517:ARG:CG	1:E:517:ARG:NH1	2.82	0.41
1:C:366:ASP:HA	1:D:284:SER:OG	2.21	0.41
1:E:513:LEU:HD12	1:E:533:MET:O	2.20	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: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:C:477:GLU:HG3	1:C:507:GLN:HE22	1.86	0.41
1:C:180:HIS:CD2	1:C:180:HIS:N	2.88	0.41
1:C:170:ASP:O	1:C:172:LYS:HG3	2.20	0.41
1:G:276:ARG:O	1:G:277:GLU:C	2.58	0.41
1:D:486:LEU:HD13	1:D:487:ARG:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:439:ARG:HG2	1:A:489:SER:OG	2.20	0.41
1:A:447:THR:HA	1:A:495:LEU:CD2	2.50	0.41
1:G:442:ILE:HD11	1:G:492:LEU:CG	2.51	0.41
1:C:97:TRP:HZ3	1:C:99:ALA:HB2	1.76	0.41
1:B:492:LEU:C	1:B:494:GLN:H	2.24	0.41
1:D:147:TRP:CE2	1:D:174:PRO:HA	2.55	0.41
1:B:498:THR:C	1:B:499:ILE:HD13	2.40	0.41
1:G:233:LEU:CD2	1:G:250:ILE:HG12	2.50	0.41
1:A:165:VAL:HB	1:A:175:VAL:HG11	2.03	0.41
1:B:253:GLN:O	1:B:257:ALA:HB2	2.21	0.41
1:C:178:LEU:HA	1:C:178:LEU:HD23	1.81	0.41
1:A:529:ILE:HA	1:A:529:ILE:HD13	1.88	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: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:A:533:MET:HB3	1:A:543:GLU:O	2.20	0.41
1:F:300:LEU:HA	1:F:300:LEU:HD22	1.79	0.41
1:A:531:GLY:C	1:A:532:TYR:CD1	2.94	0.41
1:A:229:ARG:HA	1:A:259:PRO:HA	2.02	0.41
1:G:317:VAL:HG21	1:G:504:ARG:HD2	2.02	0.41
1:G:294:GLY:C	1:G:296:ASN:N	2.74	0.41
1:D:401:GLU:HB2	1:D:404:ARG:HH21	1.85	0.41
1:G:517:ARG:HG3	1:G:529:ILE:HD13	2.03	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: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:D:353:LEU:HD23	1:D:353:LEU:HA	1.56	0.41
1:F:486:LEU:HA	1:F:486:LEU:HD23	1.77	0.41
1:E:260:TRP:C	1:E:261:ILE:CG1	2.88	0.41
1:E:260:TRP:O	1:E:261:ILE:HG12	2.20	0.41
1:E:427:SER:CB	1:E:487:ARG:HH12	2.27	0.41
1:C:338:GLY:HA3	1:C:412:MET:HE1	2.02	0.41
1:C:81:LEU:HD11	1:C:96:TYR:CD2	2.55	0.41
1:C:493:ARG:HG2	1:C:493:ARG:H	1.43	0.41
1:E:370:ARG:CD	1:E:371:GLU:CA	2.99	0.41
1:E:450:LYS:NZ	1:E:454:LYS:HD3	2.35	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:155:VAL:HG22	1:B:176:VAL:CG2	2.51	0.41
1:B:147:TRP:CD2	1:B:174:PRO:HB3	2.54	0.41
1:F:471:LYS:HA	1:F:471:LYS:HD2	1.61	0.41
1:A:473:LYS:HE2	1:A:479:ARG:CA	2.47	0.41
1:A:430:VAL:HG12	1:A:430:VAL:O	2.20	0.41
1:C:529:ILE:HD13	1:C:529:ILE:HA	1.80	0.41
1:G:324:GLN:HE22	1:G:542:LEU:HB2	1.84	0.41
1:D:223:LEU:CD2	1:D:224:PRO:HD2	2.51	0.41
1:D:136:HIS:CD2	1:D:180:HIS:CE1	3.07	0.41
1:A:411:TYR:C	1:A:411:TYR:CD1	2.92	0.41
1:A:353:LEU:HA	1:A:353:LEU:HD23	1.59	0.41
1:B:115:ASN:HB3	1:B:117:ASN:HD21	1.85	0.41
1:A:486:LEU:HB3	1:A:493:ARG:CD	2.51	0.41
1:E:124:ARG:CZ	1:E:126:LYS:HA	2.51	0.41
1:D:443:ASP:HA	1:D:491:ALA:HB3	2.03	0.41
1:A:265:VAL:C	1:A:266:VAL:HG23	2.41	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:B:261:ILE:H	1:B:262:PRO:CD	2.34	0.41
1:G:510:MET:HB2	1:G:513:LEU:CB	2.50	0.41
1:B:233:LEU:CD2	1:B:250:ILE:HG12	2.50	0.41
1:G:216:VAL:CG1	1:G:230:VAL:HG22	2.49	0.41
1:C:106:TYR:HB3	1:C:123:VAL:CG1	2.50	0.41
1:A:347:GLU:OE2	1:C:274:ARG:HG2	2.21	0.41
1:D:478:GLY:O	1:D:479:ARG:C	2.59	0.41
1:F:251:MET:HA	1:F:251:MET:HE3	1.98	0.41
1:B:413:ARG:HA	1:B:413:ARG:HD3	1.92	0.41
1:B:268:ALA:HA	1:B:271:LEU:HD12	2.01	0.41
1:B:225:ALA:HB1	1:G:414:SER:CB	2.50	0.41
1:A:386:PHE:O	1:A:388:ASN:N	2.50	0.41
1:A:152:LYS:HZ2	1:A:256:ASN:H	1.68	0.41
1:C:229:ARG:HH21	1:C:259:PRO:CB	2.32	0.41
1:F:427:SER:CB	1:F:487:ARG:HH12	2.30	0.41
1:C:394:TYR:HE1	1:C:396:SER:CB	2.32	0.41
1:A:81:LEU:HD11	1:A:96:TYR:CD2	2.56	0.41
1:C:446:MET:HB3	1:C:491:ALA:HB1	2.03	0.41
1:C:445:LEU:CD1	1:C:449:LEU:HG	2.51	0.41
1:E:124:ARG:HD3	1:E:125:ASP:N	2.35	0.41
1:E:401:GLU:N	1:E:430:VAL:O	2.54	0.41
1:A:262:PRO:HB3	1:B:411:TYR:CE1	2.56	0.41
1:B:440:LYS:NZ	1:B:441:MET:CA	2.64	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:504:ARG:HH21	1:D:506:GLN:HG2	1.86	0.41
1:C:469:PRO:HD3	1:C:475:HIS:HE1	1.86	0.41
1:A:499:ILE:HD12	1:A:499:ILE:HA	1.83	0.41
1:D:454:LYS:HE3	1:D:522:ARG:HH22	1.85	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:D:200:GLU:O	1:D:227:LYS:HE3	2.21	0.41
1:B:121:GLN:CB	1:B:133:THR:CG2	2.98	0.41
1:A:503:GLU:HG3	1:A:515:LEU:CD2	2.51	0.41
1:F:291:GLY:O	1:F:292:CYS:HB2	2.21	0.41
1:E:473:LYS:HE2	1:E:479:ARG:CA	2.43	0.41
1:F:321:PHE:CE2	1:F:533:MET:HE1	2.56	0.41
1:D:243:LEU:O	1:D:244:ASN:O	2.37	0.41
1:D:112:ARG:HD2	1:D:145:HIS:CE1	2.55	0.41
1:B:223:LEU:CD2	1:B:224:PRO:HD2	2.50	0.41
1:D:273:GLU:OE2	1:D:276:ARG:NH1	2.53	0.41
1:E:235:CYS:HB2	1:E:240:GLU:HG2	2.03	0.41
1:D:327:LEU:HD11	1:D:357:HIS:HA	2.03	0.41
1:F:204:LEU:HD23	1:F:204:LEU:N	2.36	0.41
1:A:152:LYS:HD3	1:A:203:ILE:CD1	2.51	0.41
1:E:228:VAL:HG23	1:E:261:ILE:HD11	2.01	0.41
1:C:341:MET:N	1:C:341:MET:HE2	2.35	0.41
1:C:484:THR:O	1:C:486:LEU:N	2.54	0.41
1:A:265:VAL:CG2	1:B:412:MET:HG2	2.51	0.41
1:G:447:THR:O	1:G:448:LYS:C	2.60	0.41
1:E:216:VAL:CG1	1:E:230:VAL:HG22	2.49	0.41
1:E:499:ILE:HG21	1:E:519:LEU:CB	2.51	0.41
1:G:321:PHE:CD2	1:G:533:MET:HE2	2.55	0.41
1:E:303:ARG:HB2	1:E:306:GLU:CD	2.42	0.41
1:F:78:TYR:CG	1:F:92:GLN:HG2	2.55	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:G:336:LYS:HB3	1:G:418:CYS:HB3	2.03	0.41
1:E:476:GLU:N	1:E:476:GLU:CD	2.74	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:B:467:LYS:H	1:B:467:LYS:HG3	1.50	0.40
1:A:446:MET:O	1:A:449:LEU:HB2	2.20	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:F:338:GLY:HA2	1:F:392:HIS:O	2.21	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:C:478:GLY:O	1:C:479:ARG:C	2.60	0.40
1:G:155:VAL:HG22	1:G:176:VAL:CG2	2.51	0.40
1:B:295:ILE:HD12	1:B:516:VAL:HG11	2.04	0.40
1:G:285:VAL:HA	1:G:300:LEU:CD1	2.51	0.40
1:F:401:GLU:N	1:F:404:ARG:HD2	2.36	0.40
1:F:323:ARG:O	1:F:326:ALA:HB3	2.22	0.40
1:G:114:GLN:NE2	1:G:195:TYR:CD1	2.88	0.40
1:C:229:ARG:HH21	1:C:259:PRO:HB3	1.82	0.40
1:G:482:SER:CB	1:G:484:THR:HG23	2.51	0.40
1:C:492:LEU:C	1:C:494:GLN:N	2.73	0.40
1:G:504:ARG:CG	1:G:506:GLN:HG2	2.51	0.40
1:D:442:ILE:HG23	1:D:443:ASP:N	2.36	0.40
1:G:495:LEU:N	1:G:495:LEU:CD1	2.84	0.40
1:B:440:LYS:HZ2	1:B:441:MET:HA	1.76	0.40
1:F:502:LEU:HD12	1:F:502:LEU:N	2.35	0.40
1:B:168:LEU:HD22	1:B:247:ASP:OD2	2.15	0.40
1:A:478:GLY:O	1:A:479:ARG:C	2.60	0.40
1:D:292:CYS:O	1:D:293:THR:C	2.60	0.40
1:A:536:ASN:HD21	1:A:538:GLU:HB3	1.86	0.40
1:G:322:VAL:CG1	1:G:422:ILE:HG21	2.51	0.40
1:G:251:MET:CE	1:G:251:MET:CA	2.99	0.40
1:F:542:LEU:HA	1:F:542:LEU:HD12	1.63	0.40
1:B:80:ALA:HB2	1:B:88:LYS:N	2.36	0.40
1:C:232:VAL:O	1:C:232:VAL:HG12	2.20	0.40
1:C:408:LYS:O	1:C:412:MET:HG3	2.21	0.40
1:F:430:VAL:O	1:F:430:VAL:HG12	2.21	0.40
1:F:429:VAL:HG13	1:F:438:GLU:OE1	2.22	0.40
1:F:447:THR:HA	1:F:495:LEU:CD2	2.52	0.40
1:B:149:GLY:O	1:B:199:PHE:CE2	2.75	0.40
1:C:502:LEU:HD12	1:C:502:LEU:N	2.37	0.40
1:D:74:SER:O	1:D:76:GLY:N	2.54	0.40
1:D:248:ARG:HG2	1:D:248:ARG:O	2.22	0.40
1:B:81:LEU:HD22	1:B:107:GLN:NE2	2.36	0.40
1:C:152:LYS:O	1:C:174:PRO:HD2	2.21	0.40
1:F:121:GLN:CB	1:F:133:THR:CG2	2.99	0.40
1:C:471:LYS:HD2	1:C:472:GLY:N	2.36	0.40
1:A:471:LYS:HD2	1:A:471:LYS:HA	1.64	0.40
1:G:413:ARG:HD3	1:G:413:ARG:HA	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:536:ASN:HD21	1:C:538:GLU:HB3	1.83	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:G:79:SER:H	1:G:98:ILE:CD1	2.29	0.40
1:C:401:GLU:HG2	1:C:402:THR:H	1.86	0.40
1:A:536:ASN:ND2	1:A:538:GLU:HB2	2.36	0.40
1:B:300:LEU:O	1:B:300:LEU:HD13	2.21	0.40
1:D:346:VAL:CB	1:D:395:ASP:HB2	2.50	0.40
1:F:322:VAL:HG21	1:F:463:ILE:CD1	2.52	0.40
1:D:318:MET:SD	1:D:463:ILE:HD12	2.61	0.40
1:D:170:ASP:O	1:D:172:LYS:HG3	2.20	0.40
1:D:427:SER:CB	1:D:487:ARG:NH1	2.84	0.40
1:A:294:GLY:C	1:A:296:ASN:N	2.72	0.40
1:A:126:LYS:CE	1:A:127:ASP:CG	2.90	0.40
1:C:443:ASP:O	1:C:447:THR:HG23	2.22	0.40
1:D:439:ARG:HG2	1:D:489:SER:OG	2.21	0.40
1:E:405:LEU:HD21	1:E:409:LEU:HD11	2.04	0.40
1:G:339:LEU:HD22	1:G:341:MET:CE	2.51	0.40
1:G:454:LYS:HE3	1:G:522:ARG:HH22	1.87	0.40
1:C:510:MET:HE1	1:C:547:TYR:CE1	2.52	0.40
1:B:481:VAL:HG13	1:B:503:GLU:OE2	2.20	0.40
1:A:166:MET:C	1:A:171:CYS:HB3	2.42	0.40
1:E:345:SER:OG	1:E:347:GLU:HG2	2.21	0.40
1:G:112:ARG:NH2	1:G:118:ILE:HD11	2.36	0.40
1:G:445:LEU:HD11	1:G:449:LEU:HG	2.03	0.40
1:A:324:GLN:OE1	1:A:541:TRP:HE3	2.05	0.40
1:D:122:LYS:HE3	1:D:130:PHE:HE2	1.86	0.40
1:C:276:ARG:HH11	1:C:276:ARG:CG	2.34	0.40
1:E:180:HIS:N	1:E:180:HIS:CD2	2.89	0.40
1:E:80:ALA:HB2	1:E:88:LYS:N	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	479/503 (95%)	377 (79%)	68 (14%)	34 (7%)	1	16
1	B	479/503 (95%)	384 (80%)	65 (14%)	30 (6%)	2	19
1	C	479/503 (95%)	385 (80%)	57 (12%)	37 (8%)	1	14
1	D	479/503 (95%)	377 (79%)	66 (14%)	36 (8%)	1	14
1	E	479/503 (95%)	381 (80%)	65 (14%)	33 (7%)	1	16
1	F	479/503 (95%)	380 (79%)	63 (13%)	36 (8%)	1	14
1	G	479/503 (95%)	386 (81%)	67 (14%)	26 (5%)	2	23
All	All	3353/3521 (95%)	2670 (80%)	451 (14%)	232 (7%)	1	16

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 ⓘ

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	2
1	B	401/421 (95%)	264 (66%)	137 (34%)	0	2
1	C	401/421 (95%)	257 (64%)	144 (36%)	0	2
1	D	401/421 (95%)	254 (63%)	147 (37%)	0	2
1	E	401/421 (95%)	257 (64%)	144 (36%)	0	2
1	F	401/421 (95%)	254 (63%)	147 (37%)	0	2
1	G	401/421 (95%)	261 (65%)	140 (35%)	0	2
All	All	2807/2947 (95%)	1801 (64%)	1006 (36%)	0	2

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

Some 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 carbohydrates 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%)	1.17	102 (21%) 1 1	59, 136, 136, 136	0
1	B	483/503 (96%)	1.92	166 (34%) 0 0	94, 94, 178, 178	0
1	C	483/503 (96%)	1.65	159 (32%) 0 0	120, 120, 178, 178	0
1	D	483/503 (96%)	1.81	168 (34%) 0 0	132, 132, 178, 178	0
1	E	483/503 (96%)	2.79	194 (40%) 0 0	115, 115, 178, 178	0
1	F	483/503 (96%)	1.47	127 (26%) 1 1	103, 164, 164, 164	0
1	G	483/503 (96%)	2.22	176 (36%) 0 0	129, 129, 178, 178	0
All	All	3381/3521 (96%)	1.86	1092 (32%) 1 0	59, 132, 178, 178	0

All (1092) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	136	HIS	32.6
1	G	109	ALA	30.3
1	E	65	THR	26.0
1	G	157	GLU	23.1
1	E	181	GLY	21.7
1	E	69	TRP	20.2
1	E	433	SER	19.6
1	E	201	GLN	16.9
1	E	111	TYR	16.6
1	E	205	MET	15.3
1	G	64	MET	15.2
1	E	174	PRO	15.0
1	B	433	SER	14.9
1	F	317	VAL	14.6
1	A	432	ALA	14.5
1	E	157	GLU	14.3
1	F	432	ALA	13.9

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Mol	Chain	Res	Type	RSRZ
1	E	244	ASN	13.5
1	G	188	THR	13.0
1	E	156	THR	12.9
1	G	185	ALA	12.8
1	F	509	ASP	12.8
1	A	431	SER	12.7
1	D	153	ILE	12.7
1	G	65	THR	12.6
1	G	84	ARG	12.5
1	A	433	SER	12.3
1	D	67	ASN	12.1
1	D	436	SER	12.0
1	E	238	ALA	11.9
1	E	171	CYS	11.9
1	E	66	TYR	11.8
1	D	106	TYR	11.6
1	B	105	MET	11.6
1	B	130	PHE	11.5
1	E	185	ALA	11.5
1	E	132	THR	11.5
1	B	202	ILE	11.5
1	E	189	CYS	11.3
1	E	207	ASP	11.3
1	B	250	ILE	11.3
1	E	202	ILE	11.2
1	B	188	THR	11.1
1	E	138	SER	11.1
1	E	106	TYR	11.0
1	G	122	LYS	10.9
1	E	153	ILE	10.9
1	G	96	TYR	10.8
1	B	164	THR	10.8
1	D	189	CYS	10.6
1	C	260	TRP	10.4
1	B	94	ALA	10.4
1	G	85	GLY	10.3
1	D	104	VAL	10.1
1	E	105	MET	10.0
1	E	142	PHE	9.9
1	E	195	TYR	9.9
1	E	137	LYS	9.9
1	E	209	ASP	9.8

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Mol	Chain	Res	Type	RSRZ
1	E	245	GLY	9.8
1	C	225	ALA	9.7
1	D	224	PRO	9.6
1	G	226	GLY	9.6
1	E	206	PHE	9.5
1	B	251	MET	9.5
1	B	201	GLN	9.5
1	E	102	ASP	9.4
1	E	233	LEU	9.4
1	B	254	VAL	9.3
1	G	225	ALA	9.3
1	E	125	ASP	9.2
1	G	94	ALA	9.2
1	G	141	LEU	9.2
1	G	110	ASP	9.2
1	E	64	MET	9.2
1	G	239	ASN	9.1
1	E	180	HIS	9.1
1	G	231	ALA	9.0
1	G	105	MET	9.0
1	F	433	SER	8.9
1	D	123	VAL	8.9
1	F	314	SER	8.9
1	G	189	CYS	8.9
1	E	129	ASN	8.8
1	G	206	PHE	8.8
1	E	432	ALA	8.8
1	G	135	SER	8.8
1	E	196	PHE	8.7
1	G	104	VAL	8.7
1	B	79	SER	8.7
1	G	120	SER	8.7
1	E	94	ALA	8.7
1	D	223	LEU	8.6
1	E	254	VAL	8.5
1	B	69	TRP	8.5
1	C	234	PRO	8.5
1	G	488	GLY	8.5
1	G	232	VAL	8.4
1	E	99	ALA	8.4
1	E	75	ASN	8.4
1	E	84	ARG	8.4

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Mol	Chain	Res	Type	RSRZ
1	D	131	LYS	8.3
1	E	109	ALA	8.3
1	G	265	VAL	8.3
1	E	217	GLU	8.3
1	A	434	GLY	8.3
1	G	115	ASN	8.2
1	B	132	THR	8.2
1	F	492	LEU	8.1
1	C	196	PHE	8.1
1	E	231	ALA	8.1
1	E	100	LYS	8.1
1	E	243	LEU	8.1
1	G	140	ALA	8.0
1	C	139	ASP	8.0
1	D	68	VAL	7.9
1	A	426	ILE	7.9
1	C	65	THR	7.9
1	F	435	GLU	7.9
1	E	103	GLY	7.8
1	D	226	GLY	7.8
1	E	239	ASN	7.7
1	D	127	ASP	7.7
1	G	268	ALA	7.7
1	G	79	SER	7.6
1	E	126	LYS	7.6
1	B	138	SER	7.6
1	E	250	ILE	7.6
1	C	83	ALA	7.5
1	E	184	ALA	7.5
1	G	69	TRP	7.4
1	F	313	GLY	7.4
1	G	152	LYS	7.4
1	D	173	TYR	7.4
1	B	432	ALA	7.4
1	G	91	CYS	7.3
1	D	466	LEU	7.3
1	D	96	TYR	7.3
1	F	475	HIS	7.3
1	E	122	LYS	7.3
1	C	201	GLN	7.3
1	G	107	GLN	7.3
1	D	65	THR	7.3

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Mol	Chain	Res	Type	RSRZ
1	B	64	MET	7.2
1	G	487	ARG	7.2
1	B	116	GLY	7.2
1	B	131	LYS	7.1
1	B	203	ILE	7.1
1	D	438	GLU	7.1
1	C	97	TRP	7.1
1	B	152	LYS	7.0
1	C	163	LEU	7.0
1	C	200	GLU	7.0
1	E	216	VAL	6.9
1	D	145	HIS	6.9
1	G	161	ASP	6.9
1	D	138	SER	6.9
1	B	83	ALA	6.8
1	F	512	ASN	6.8
1	B	165	VAL	6.8
1	E	173	TYR	6.8
1	B	86	ILE	6.8
1	C	153	ILE	6.7
1	E	234	PRO	6.7
1	B	154	VAL	6.7
1	D	148	ASN	6.7
1	B	204	LEU	6.7
1	B	153	ILE	6.6
1	B	115	ASN	6.6
1	E	251	MET	6.6
1	F	510	MET	6.6
1	G	250	ILE	6.6
1	E	130	PHE	6.6
1	D	201	GLN	6.5
1	B	84	ARG	6.4
1	B	65	THR	6.4
1	C	69	TRP	6.4
1	E	108	VAL	6.4
1	B	125	ASP	6.3
1	G	433	SER	6.3
1	C	169	GLN	6.3
1	E	96	TYR	6.2
1	D	174	PRO	6.2
1	B	122	LYS	6.2
1	G	259	PRO	6.2

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Mol	Chain	Res	Type	RSRZ
1	G	158	GLY	6.2
1	C	224	PRO	6.1
1	E	188	THR	6.1
1	C	223	LEU	6.1
1	E	186	LYS	6.1
1	B	139	ASP	6.1
1	B	189	CYS	6.1
1	F	477	GLU	6.0
1	C	204	LEU	6.0
1	D	101	VAL	6.0
1	D	175	VAL	6.0
1	C	140	ALA	6.0
1	G	184	ALA	6.0
1	C	137	LYS	6.0
1	G	89	GLU	6.0
1	D	114	GLN	6.0
1	F	513	LEU	6.0
1	D	488	GLY	6.0
1	C	123	VAL	6.0
1	E	152	LYS	5.9
1	E	110	ASP	5.9
1	D	151	LYS	5.9
1	B	136	HIS	5.9
1	G	87	SER	5.9
1	B	221	GLN	5.8
1	C	135	SER	5.8
1	F	436	SER	5.8
1	F	285	VAL	5.8
1	D	98	ILE	5.8
1	G	156	THR	5.7
1	G	116	GLY	5.7
1	C	180	HIS	5.7
1	C	252	GLU	5.7
1	B	244	ASN	5.7
1	C	231	ALA	5.7
1	B	88	LYS	5.7
1	G	196	PHE	5.7
1	F	530	ALA	5.7
1	E	203	ILE	5.6
1	E	97	TRP	5.6
1	B	434	GLY	5.6
1	E	434	GLY	5.6

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Mol	Chain	Res	Type	RSRZ
1	D	435	GLU	5.6
1	B	397	PHE	5.6
1	C	397	PHE	5.6
1	E	90	THR	5.6
1	E	81	LEU	5.6
1	E	78	TYR	5.6
1	F	434	GLY	5.5
1	F	529	ILE	5.5
1	B	66	TYR	5.5
1	F	431	SER	5.5
1	C	151	LYS	5.5
1	G	178	LEU	5.5
1	G	136	HIS	5.5
1	B	255	TRP	5.5
1	G	119	VAL	5.5
1	B	190	ALA	5.4
1	E	135	SER	5.4
1	F	406	LEU	5.4
1	D	111	TYR	5.4
1	F	378	PHE	5.4
1	A	64	MET	5.4
1	E	82	THR	5.4
1	G	83	ALA	5.3
1	E	127	ASP	5.3
1	E	121	GLN	5.3
1	B	106	TYR	5.3
1	E	128	LYS	5.3
1	D	472	GLY	5.3
1	G	82	THR	5.3
1	B	223	LEU	5.3
1	C	108	VAL	5.3
1	B	126	LYS	5.3
1	D	140	ALA	5.3
1	D	112	ARG	5.3
1	C	203	ILE	5.3
1	E	68	VAL	5.2
1	D	135	SER	5.2
1	E	120	SER	5.2
1	G	108	VAL	5.2
1	E	220	ALA	5.2
1	G	132	THR	5.2
1	C	159	GLU	5.2

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Mol	Chain	Res	Type	RSRZ
1	G	234	PRO	5.2
1	F	100	LYS	5.2
1	B	142	PHE	5.2
1	F	321	PHE	5.2
1	A	295	ILE	5.2
1	B	121	GLN	5.2
1	B	155	VAL	5.2
1	G	171	CYS	5.2
1	C	152	LYS	5.2
1	C	519	LEU	5.2
1	F	300	LEU	5.2
1	E	170	ASP	5.2
1	E	155	VAL	5.2
1	F	105	MET	5.2
1	C	244	ASN	5.1
1	B	112	ARG	5.1
1	G	472	GLY	5.1
1	G	90	THR	5.1
1	F	478	GLY	5.1
1	A	238	ALA	5.1
1	D	154	VAL	5.1
1	B	257	ALA	5.0
1	G	160	ILE	5.0
1	D	265	VAL	5.0
1	G	202	ILE	5.0
1	F	96	TYR	5.0
1	C	189	CYS	5.0
1	E	86	ILE	4.9
1	A	205	MET	4.9
1	C	158	GLY	4.9
1	E	154	VAL	4.9
1	G	95	GLY	4.9
1	D	253	GLN	4.9
1	D	128	LYS	4.9
1	D	152	LYS	4.9
1	D	97	TRP	4.9
1	D	110	ASP	4.9
1	D	179	GLY	4.9
1	E	228	VAL	4.9
1	E	114	GLN	4.8
1	C	154	VAL	4.8
1	E	215	ALA	4.8

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Mol	Chain	Res	Type	RSRZ
1	C	472	GLY	4.8
1	E	481	VAL	4.8
1	F	426	ILE	4.8
1	D	66	TYR	4.8
1	G	289	PHE	4.8
1	E	101	VAL	4.8
1	B	230	VAL	4.8
1	E	438	GLU	4.8
1	G	207	ASP	4.8
1	C	394	TYR	4.8
1	G	168	LEU	4.7
1	B	97	TRP	4.7
1	B	85	GLY	4.7
1	F	284	SER	4.7
1	C	393	LEU	4.7
1	C	101	VAL	4.7
1	G	139	ASP	4.7
1	D	108	VAL	4.7
1	A	549	GLY	4.7
1	B	104	VAL	4.7
1	E	241	CYS	4.7
1	E	67	ASN	4.7
1	E	168	LEU	4.7
1	G	159	GLU	4.7
1	B	171	CYS	4.7
1	D	549	GLY	4.7
1	D	209	ASP	4.7
1	G	154	VAL	4.7
1	D	64	MET	4.6
1	A	535	TYR	4.6
1	D	130	PHE	4.6
1	A	309	MET	4.6
1	C	253	GLN	4.6
1	D	225	ALA	4.6
1	F	549	GLY	4.6
1	B	89	GLU	4.6
1	G	258	GLY	4.6
1	D	426	ILE	4.6
1	C	210	GLU	4.6
1	D	146	LEU	4.6
1	G	127	ASP	4.6
1	C	435	GLU	4.6

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Mol	Chain	Res	Type	RSRZ
1	A	170	ASP	4.5
1	A	423	LEU	4.5
1	G	251	MET	4.5
1	D	210	GLU	4.5
1	C	460	LEU	4.5
1	B	253	GLN	4.5
1	D	109	ALA	4.5
1	G	502	LEU	4.5
1	B	111	TYR	4.5
1	E	112	ARG	4.5
1	G	121	GLN	4.5
1	G	170	ASP	4.5
1	D	171	CYS	4.4
1	E	473	LYS	4.4
1	D	515	LEU	4.4
1	A	523	PHE	4.4
1	G	148	ASN	4.4
1	C	130	PHE	4.4
1	C	235	CYS	4.4
1	G	66	TYR	4.4
1	D	516	VAL	4.4
1	C	426	ILE	4.4
1	B	124	ARG	4.4
1	D	266	VAL	4.4
1	B	502	LEU	4.4
1	E	107	GLN	4.4
1	G	475	HIS	4.4
1	E	255	TRP	4.3
1	E	149	GLY	4.3
1	B	163	LEU	4.3
1	C	132	THR	4.3
1	G	169	GLN	4.3
1	B	96	TYR	4.3
1	B	156	THR	4.3
1	E	402	THR	4.3
1	A	260	TRP	4.3
1	D	208	MET	4.3
1	A	542	LEU	4.3
1	C	431	SER	4.3
1	G	187	LYS	4.3
1	F	386	PHE	4.2
1	D	190	ALA	4.2

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Mol	Chain	Res	Type	RSRZ
1	C	202	ILE	4.2
1	F	316	MET	4.2
1	G	489	SER	4.2
1	G	426	ILE	4.2
1	C	129	ASN	4.2
1	E	175	VAL	4.2
1	E	442	ILE	4.2
1	B	123	VAL	4.2
1	G	103	GLY	4.2
1	F	519	LEU	4.2
1	E	310	VAL	4.2
1	C	73	GLU	4.2
1	F	394	TYR	4.2
1	C	94	ALA	4.1
1	E	83	ALA	4.1
1	F	104	VAL	4.1
1	C	289	PHE	4.1
1	E	148	ASN	4.1
1	G	438	GLU	4.1
1	F	178	LEU	4.1
1	D	252	GLU	4.1
1	G	215	ALA	4.1
1	E	176	VAL	4.1
1	C	537	LYS	4.1
1	G	86	ILE	4.1
1	E	246	HIS	4.1
1	C	115	ASN	4.1
1	G	204	LEU	4.1
1	D	284	SER	4.1
1	B	178	LEU	4.1
1	B	78	TYR	4.1
1	E	204	LEU	4.1
1	F	533	MET	4.0
1	B	368	LEU	4.0
1	C	402	THR	4.0
1	C	98	ILE	4.0
1	D	180	HIS	4.0
1	E	463	ILE	4.0
1	G	130	PHE	4.0
1	G	155	VAL	4.0
1	C	114	GLN	4.0
1	E	253	GLN	4.0

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Mol	Chain	Res	Type	RSRZ
1	B	175	VAL	4.0
1	F	409	LEU	4.0
1	B	211	ALA	4.0
1	B	67	ASN	4.0
1	G	197	ASP	4.0
1	F	508	GLY	4.0
1	G	233	LEU	4.0
1	B	191	ALA	4.0
1	G	481	VAL	4.0
1	F	341	MET	4.0
1	C	259	PRO	4.0
1	G	114	GLN	4.0
1	A	206	PHE	4.0
1	E	232	VAL	3.9
1	B	423	LEU	3.9
1	C	74	SER	3.9
1	F	449	LEU	3.9
1	E	179	GLY	3.9
1	C	438	GLU	3.9
1	D	100	LYS	3.9
1	A	165	VAL	3.9
1	E	172	LYS	3.9
1	C	243	LEU	3.9
1	E	235	CYS	3.9
1	B	205	MET	3.9
1	E	208	MET	3.9
1	F	488	GLY	3.9
1	F	318	MET	3.9
1	G	271	LEU	3.9
1	E	200	GLU	3.9
1	A	291	GLY	3.9
1	A	438	GLU	3.9
1	E	247	ASP	3.8
1	A	394	TYR	3.8
1	C	329	TRP	3.8
1	F	342	LEU	3.8
1	C	436	SER	3.8
1	C	338	GLY	3.8
1	A	302	ALA	3.8
1	D	193	TYR	3.8
1	G	260	TRP	3.8
1	G	203	ILE	3.8

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Mol	Chain	Res	Type	RSRZ
1	E	210	GLU	3.8
1	E	182	ALA	3.8
1	B	236	LYS	3.8
1	C	131	LYS	3.8
1	G	241	CYS	3.8
1	C	500	ILE	3.8
1	D	129	ASN	3.8
1	B	68	VAL	3.8
1	B	486	LEU	3.8
1	C	230	VAL	3.8
1	B	532	TYR	3.8
1	D	533	MET	3.7
1	G	227	LYS	3.7
1	G	134	GLY	3.7
1	G	208	MET	3.7
1	F	275	ILE	3.7
1	F	474	ALA	3.7
1	F	460	LEU	3.7
1	A	289	PHE	3.7
1	C	116	GLY	3.7
1	D	510	MET	3.7
1	F	502	LEU	3.7
1	G	129	ASN	3.7
1	C	145	HIS	3.7
1	D	467	LYS	3.7
1	E	80	ALA	3.7
1	A	172	LYS	3.7
1	D	85	GLY	3.7
1	G	144	LYS	3.7
1	D	271	LEU	3.7
1	E	242	HIS	3.7
1	D	232	VAL	3.6
1	E	213	ARG	3.6
1	G	190	ALA	3.6
1	E	287	LEU	3.6
1	F	500	ILE	3.6
1	G	532	TYR	3.6
1	B	206	PHE	3.6
1	C	339	LEU	3.6
1	G	217	GLU	3.6
1	C	99	ALA	3.6
1	B	533	MET	3.6

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Mol	Chain	Res	Type	RSRZ
1	C	535	TYR	3.6
1	B	113	ASP	3.6
1	D	310	VAL	3.6
1	F	101	VAL	3.6
1	F	532	TYR	3.6
1	D	430	VAL	3.6
1	B	109	ALA	3.6
1	E	285	VAL	3.6
1	C	321	PHE	3.6
1	A	476	GLU	3.6
1	A	362	LEU	3.5
1	B	321	PHE	3.5
1	B	435	GLU	3.5
1	A	533	MET	3.5
1	D	122	LYS	3.5
1	G	172	LYS	3.5
1	B	127	ASP	3.5
1	E	141	LEU	3.5
1	D	91	CYS	3.5
1	E	409	LEU	3.5
1	D	378	PHE	3.5
1	C	160	ILE	3.5
1	A	469	PRO	3.5
1	F	516	VAL	3.5
1	G	266	VAL	3.5
1	A	416	LEU	3.5
1	D	95	GLY	3.5
1	B	192	ASN	3.5
1	F	382	PHE	3.5
1	A	385	LEU	3.5
1	B	120	SER	3.5
1	D	136	HIS	3.5
1	F	391	PHE	3.5
1	D	329	TRP	3.5
1	E	104	VAL	3.5
1	E	535	TYR	3.5
1	E	549	GLY	3.4
1	C	168	LEU	3.4
1	G	117	ASN	3.4
1	C	104	VAL	3.4
1	C	87	SER	3.4
1	E	289	PHE	3.4

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Mol	Chain	Res	Type	RSRZ
1	D	487	ARG	3.4
1	B	110	ASP	3.4
1	F	405	LEU	3.4
1	A	265	VAL	3.4
1	C	84	ARG	3.4
1	A	346	VAL	3.4
1	C	258	GLY	3.4
1	C	219	ALA	3.4
1	C	340	ALA	3.4
1	B	542	LEU	3.4
1	A	173	TYR	3.4
1	G	245	GLY	3.4
1	B	471	LYS	3.4
1	A	470	ASP	3.4
1	D	139	ASP	3.4
1	A	196	PHE	3.4
1	E	77	ARG	3.3
1	A	321	PHE	3.3
1	G	275	ILE	3.3
1	B	285	VAL	3.3
1	C	195	TYR	3.3
1	D	121	GLN	3.3
1	E	362	LEU	3.3
1	D	126	LYS	3.3
1	D	442	ILE	3.3
1	F	461	VAL	3.3
1	F	489	SER	3.3
1	C	368	LEU	3.3
1	E	237	ASP	3.3
1	D	156	THR	3.3
1	B	95	GLY	3.3
1	G	138	SER	3.3
1	B	247	ASP	3.3
1	C	165	VAL	3.3
1	D	285	VAL	3.3
1	F	315	GLY	3.3
1	B	378	PHE	3.3
1	E	308	ILE	3.3
1	D	246	HIS	3.3
1	D	471	LYS	3.3
1	F	289	PHE	3.3
1	B	82	THR	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	69	TRP	3.3
1	E	223	LEU	3.3
1	G	216	VAL	3.2
1	A	178	LEU	3.2
1	G	186	LYS	3.2
1	B	167	GLU	3.2
1	D	423	LEU	3.2
1	E	74	SER	3.2
1	D	463	ILE	3.2
1	C	209	ASP	3.2
1	D	500	ILE	3.2
1	E	113	ASP	3.2
1	D	69	TRP	3.2
1	D	502	LEU	3.2
1	D	249	GLU	3.2
1	B	487	ARG	3.2
1	C	362	LEU	3.2
1	E	192	ASN	3.2
1	E	466	LEU	3.2
1	F	157	GLU	3.2
1	C	307	VAL	3.2
1	G	285	VAL	3.2
1	D	197	ASP	3.2
1	C	155	VAL	3.2
1	D	78	TYR	3.2
1	G	243	LEU	3.2
1	D	137	LYS	3.2
1	D	103	GLY	3.1
1	F	337	VAL	3.1
1	C	220	ALA	3.1
1	D	439	ARG	3.1
1	G	249	GLU	3.1
1	B	146	LEU	3.1
1	D	518	ILE	3.1
1	A	127	ASP	3.1
1	G	402	THR	3.1
1	G	219	ALA	3.1
1	B	284	SER	3.1
1	E	256	ASN	3.1
1	D	529	ILE	3.1
1	A	94	ALA	3.1
1	A	475	HIS	3.1

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Mol	Chain	Res	Type	RSRZ
1	E	177	SER	3.1
1	C	133	THR	3.1
1	D	484	THR	3.1
1	D	517	ARG	3.1
1	F	454	LYS	3.1
1	A	386	PHE	3.1
1	G	254	VAL	3.1
1	G	500	ILE	3.1
1	G	535	TYR	3.1
1	D	176	VAL	3.1
1	G	179	GLY	3.1
1	G	167	GLU	3.1
1	G	288	LEU	3.0
1	G	218	GLU	3.0
1	F	99	ALA	3.0
1	B	239	ASN	3.0
1	B	500	ILE	3.0
1	E	163	LEU	3.0
1	G	211	ALA	3.0
1	D	468	ASN	3.0
1	E	115	ASN	3.0
1	D	291	GLY	3.0
1	B	107	GLN	3.0
1	G	501	ALA	3.0
1	D	107	GLN	3.0
1	A	519	LEU	3.0
1	B	99	ALA	3.0
1	C	353	LEU	3.0
1	D	289	PHE	3.0
1	D	416	LEU	3.0
1	D	501	ALA	3.0
1	E	211	ALA	3.0
1	G	111	TYR	3.0
1	F	539	THR	3.0
1	C	423	LEU	3.0
1	C	337	VAL	3.0
1	G	165	VAL	3.0
1	C	117	ASN	3.0
1	C	171	CYS	3.0
1	G	180	HIS	3.0
1	E	260	TRP	3.0
1	G	102	ASP	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	178	LEU	3.0
1	F	397	PHE	3.0
1	G	486	LEU	3.0
1	F	310	VAL	3.0
1	A	252	GLU	3.0
1	F	339	LEU	3.0
1	G	118	ILE	2.9
1	D	142	PHE	2.9
1	F	156	THR	2.9
1	D	295	ILE	2.9
1	F	238	ALA	2.9
1	A	452	PHE	2.9
1	D	513	LEU	2.9
1	D	481	VAL	2.9
1	C	342	LEU	2.9
1	C	112	ARG	2.9
1	E	139	ASP	2.9
1	E	70	ASN	2.9
1	E	405	LEU	2.9
1	G	88	LYS	2.9
1	B	207	ASP	2.9
1	C	233	LEU	2.9
1	F	466	LEU	2.9
1	E	343	GLU	2.9
1	B	238	ALA	2.9
1	C	308	ILE	2.9
1	B	129	ASN	2.9
1	G	224	PRO	2.9
1	D	248	ARG	2.9
1	E	391	PHE	2.9
1	B	186	LYS	2.9
1	D	250	ILE	2.9
1	A	96	TYR	2.9
1	F	64	MET	2.8
1	G	147	TRP	2.8
1	D	397	PHE	2.8
1	A	179	GLY	2.8
1	F	393	LEU	2.8
1	E	500	ILE	2.8
1	C	542	LEU	2.8
1	B	220	ALA	2.8
1	D	311	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	G	295	ILE	2.8
1	B	209	ASP	2.8
1	G	68	VAL	2.8
1	B	196	PHE	2.8
1	E	460	LEU	2.8
1	E	492	LEU	2.8
1	C	462	VAL	2.8
1	F	131	LYS	2.8
1	B	535	TYR	2.8
1	D	393	LEU	2.8
1	F	196	PHE	2.8
1	G	244	ASN	2.8
1	A	86	ILE	2.8
1	A	503	GLU	2.8
1	D	220	ALA	2.8
1	E	131	LYS	2.8
1	A	107	GLN	2.8
1	A	142	PHE	2.7
1	A	472	GLY	2.7
1	B	354	ILE	2.7
1	C	206	PHE	2.7
1	E	309	MET	2.7
1	G	205	MET	2.7
1	E	502	LEU	2.7
1	F	452	PHE	2.7
1	F	424	ASP	2.7
1	C	184	ALA	2.7
1	E	480	PRO	2.7
1	F	496	SER	2.7
1	B	512	ASN	2.7
1	B	81	LEU	2.7
1	D	233	LEU	2.7
1	D	308	ILE	2.7
1	E	512	ASN	2.7
1	C	403	ASP	2.7
1	B	357	HIS	2.7
1	B	256	ASN	2.7
1	D	118	ILE	2.7
1	D	141	LEU	2.7
1	F	463	ILE	2.7
1	G	173	TYR	2.7
1	A	308	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	322	VAL	2.7
1	A	502	LEU	2.7
1	D	203	ILE	2.7
1	D	234	PRO	2.7
1	C	514	VAL	2.7
1	D	219	ALA	2.7
1	G	507	GLN	2.7
1	D	514	VAL	2.7
1	G	228	VAL	2.7
1	B	140	ALA	2.6
1	F	308	ILE	2.6
1	D	105	MET	2.6
1	D	244	ASN	2.6
1	B	461	VAL	2.6
1	F	107	GLN	2.6
1	D	287	LEU	2.6
1	E	226	GLY	2.6
1	F	279	LEU	2.6
1	F	138	SER	2.6
1	F	507	GLN	2.6
1	G	473	LYS	2.6
1	D	321	PHE	2.6
1	A	311	THR	2.6
1	C	86	ILE	2.6
1	E	87	SER	2.6
1	D	236	LYS	2.6
1	D	386	PHE	2.6
1	B	133	THR	2.6
1	B	145	HIS	2.6
1	F	254	VAL	2.6
1	G	73	GLU	2.6
1	G	499	ILE	2.6
1	C	533	MET	2.6
1	F	498	THR	2.6
1	A	548	SER	2.6
1	B	416	LEU	2.6
1	A	422	ILE	2.6
1	B	463	ILE	2.6
1	D	172	LYS	2.6
1	E	236	LYS	2.6
1	F	69	TRP	2.6
1	G	164	THR	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	75	ASN	2.6
1	E	123	VAL	2.6
1	F	385	LEU	2.6
1	C	529	ILE	2.6
1	B	481	VAL	2.6
1	A	449	LEU	2.6
1	F	168	LEU	2.6
1	C	141	LEU	2.6
1	F	65	THR	2.6
1	C	144	LYS	2.6
1	A	148	ASN	2.6
1	G	163	LEU	2.6
1	A	254	VAL	2.6
1	C	271	LEU	2.5
1	F	252	GLU	2.6
1	C	517	ARG	2.5
1	A	496	SER	2.5
1	G	393	LEU	2.5
1	G	517	ARG	2.5
1	D	133	THR	2.5
1	E	178	LEU	2.5
1	E	118	ILE	2.5
1	G	463	ILE	2.5
1	E	145	HIS	2.5
1	A	474	ALA	2.5
1	A	516	VAL	2.5
1	B	262	PRO	2.5
1	B	402	THR	2.5
1	D	235	CYS	2.5
1	A	98	ILE	2.5
1	A	354	ILE	2.5
1	G	193	TYR	2.5
1	A	487	ARG	2.5
1	A	425	HIS	2.5
1	B	148	ASN	2.5
1	D	229	ARG	2.5
1	F	472	GLY	2.5
1	A	534	GLU	2.5
1	E	321	PHE	2.5
1	C	309	MET	2.5
1	E	295	ILE	2.5
1	A	157	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	146	LEU	2.5
1	G	516	VAL	2.5
1	C	136	HIS	2.5
1	A	370	ARG	2.5
1	F	445	LEU	2.5
1	G	162	MET	2.5
1	F	295	ILE	2.4
1	F	265	VAL	2.4
1	F	423	LEU	2.4
1	C	261	ILE	2.4
1	G	329	TRP	2.4
1	A	233	LEU	2.4
1	D	486	LEU	2.4
1	F	481	VAL	2.4
1	C	250	ILE	2.4
1	F	534	GLU	2.4
1	G	133	THR	2.4
1	D	94	ALA	2.4
1	F	159	GLU	2.4
1	C	147	TRP	2.4
1	F	309	MET	2.4
1	E	487	ARG	2.4
1	F	522	ARG	2.4
1	C	174	PRO	2.4
1	G	339	LEU	2.4
1	C	138	SER	2.4
1	F	547	TYR	2.4
1	E	71	PHE	2.4
1	G	262	PRO	2.4
1	A	517	ARG	2.4
1	E	187	LYS	2.4
1	G	242	HIS	2.4
1	B	102	ASP	2.4
1	C	113	ASP	2.4
1	C	474	ALA	2.4
1	B	73	GLU	2.4
1	C	106	TYR	2.4
1	A	285	VAL	2.4
1	B	243	LEU	2.4
1	D	102	ASP	2.4
1	G	149	GLY	2.4
1	C	81	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	155	VAL	2.4
1	A	174	PRO	2.4
1	F	205	MET	2.4
1	E	147	TRP	2.4
1	C	300	LEU	2.4
1	C	548	SER	2.4
1	D	159	GLU	2.4
1	B	372	ILE	2.4
1	B	409	LEU	2.4
1	E	412	MET	2.3
1	F	224	PRO	2.3
1	A	397	PHE	2.3
1	A	471	LYS	2.3
1	B	151	LYS	2.3
1	B	454	LYS	2.3
1	C	170	ASP	2.3
1	D	503	GLU	2.3
1	E	261	ILE	2.3
1	F	266	VAL	2.3
1	C	121	GLN	2.3
1	E	133	THR	2.3
1	E	498	THR	2.3
1	B	310	VAL	2.3
1	D	260	TRP	2.3
1	G	263	ASP	2.3
1	E	449	LEU	2.3
1	F	155	VAL	2.3
1	F	420	VAL	2.3
1	A	292	CYS	2.3
1	B	308	ILE	2.3
1	D	191	ALA	2.3
1	E	224	PRO	2.3
1	B	90	THR	2.3
1	A	350	ALA	2.3
1	C	356	LEU	2.3
1	F	141	LEU	2.3
1	G	542	LEU	2.3
1	A	430	VAL	2.3
1	F	262	PRO	2.3
1	C	156	THR	2.3
1	C	541	TRP	2.3
1	B	162	MET	2.3

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Mol	Chain	Res	Type	RSRZ
1	G	230	VAL	2.3
1	F	476	GLU	2.3
1	B	77	ARG	2.3
1	B	114	GLN	2.3
1	C	198	GLN	2.3
1	B	80	ALA	2.3
1	A	79	SER	2.3
1	B	87	SER	2.3
1	B	386	PHE	2.3
1	F	132	THR	2.3
1	A	462	VAL	2.3
1	B	219	ALA	2.3
1	B	501	ALA	2.3
1	E	93	LYS	2.3
1	G	101	VAL	2.3
1	C	543	GLU	2.3
1	D	485	ASP	2.3
1	C	378	PHE	2.3
1	F	136	HIS	2.3
1	G	246	HIS	2.3
1	C	254	VAL	2.3
1	D	461	VAL	2.3
1	A	118	ILE	2.2
1	G	492	LEU	2.2
1	A	429	VAL	2.2
1	A	461	VAL	2.2
1	A	466	LEU	2.2
1	C	232	VAL	2.2
1	F	176	VAL	2.2
1	C	468	ASN	2.2
1	B	174	PRO	2.2
1	D	473	LYS	2.2
1	A	356	LEU	2.2
1	B	229	ARG	2.2
1	D	429	VAL	2.2
1	D	92	GLN	2.2
1	G	247	ASP	2.2
1	E	361	ARG	2.2
1	E	183	SER	2.2
1	A	463	ILE	2.2
1	G	153	ILE	2.2
1	A	271	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	E	95	GLY	2.2
1	D	165	VAL	2.2
1	E	532	TYR	2.2
1	F	98	ILE	2.2
1	C	341	MET	2.2
1	C	495	LEU	2.2
1	D	452	PHE	2.2
1	A	122	LYS	2.2
1	F	114	GLN	2.2
1	F	248	ARG	2.2
1	A	500	ILE	2.2
1	D	535	TYR	2.2
1	F	97	TRP	2.2
1	E	479	ARG	2.2
1	D	206	PHE	2.2
1	C	226	GLY	2.2
1	F	165	VAL	2.2
1	B	215	ALA	2.2
1	B	241	CYS	2.2
1	C	179	GLY	2.2
1	B	242	HIS	2.2
1	G	323	ARG	2.2
1	E	537	LYS	2.1
1	E	326	ALA	2.1
1	B	322	VAL	2.1
1	E	266	VAL	2.1
1	E	462	VAL	2.1
1	F	422	ILE	2.1
1	B	323	ARG	2.1
1	B	530	ALA	2.1
1	D	362	LEU	2.1
1	E	225	ALA	2.1
1	B	195	TYR	2.1
1	B	72	GLY	2.1
1	A	372	ILE	2.1
1	C	481	VAL	2.1
1	D	187	LYS	2.1
1	E	337	VAL	2.1
1	C	279	LEU	2.1
1	B	549	GLY	2.1
1	E	282	GLU	2.1
1	A	223	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	389	ASP	2.1
1	F	362	LEU	2.1
1	B	212	GLY	2.1
1	D	292	CYS	2.1
1	D	124	ARG	2.1
1	D	370	ARG	2.1
1	C	142	PHE	2.1
1	C	486	LEU	2.1
1	G	78	TYR	2.1
1	G	346	VAL	2.1
1	C	183	SER	2.1
1	F	414	SER	2.1
1	C	70	ASN	2.1
1	E	311	THR	2.1
1	G	432	ALA	2.1
1	B	422	ILE	2.1
1	C	229	ARG	2.1
1	C	354	ILE	2.1
1	A	144	LYS	2.1
1	F	464	CYS	2.1
1	C	237	ASP	2.1
1	B	260	TRP	2.1
1	D	422	ILE	2.1
1	A	492	LEU	2.1
1	F	450	LYS	2.1
1	G	126	LYS	2.1
1	G	430	VAL	2.1
1	C	102	ASP	2.1
1	D	354	ILE	2.1
1	A	204	LEU	2.1
1	F	223	LEU	2.1
1	D	181	GLY	2.1
1	F	538	GLU	2.1
1	F	429	VAL	2.1
1	G	290	SER	2.1
1	A	246	HIS	2.0
1	B	465	HIS	2.0
1	G	310	VAL	2.1
1	C	380	GLN	2.0
1	D	275	ILE	2.0
1	G	518	ILE	2.0
1	C	502	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	187	LYS	2.0
1	B	314	SER	2.0
1	A	115	ASN	2.0
1	D	462	VAL	2.0
1	G	309	MET	2.0
1	B	426	ILE	2.0
1	E	421	ILE	2.0
1	C	72	GLY	2.0
1	E	91	CYS	2.0
1	F	181	GLY	2.0
1	B	228	VAL	2.0
1	C	295	ILE	2.0
1	E	386	PHE	2.0
1	E	393	LEU	2.0
1	B	252	GLU	2.0
1	E	472	GLY	2.0
1	A	244	ASN	2.0
1	C	172	LYS	2.0
1	C	211	ALA	2.0
1	F	166	MET	2.0
1	G	80	ALA	2.0
1	B	168	LEU	2.0
1	B	329	TRP	2.0
1	A	460	LEU	2.0
1	C	492	LEU	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.