



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:37 AM GMT

PDB ID : 3BG1
Title : Architecture of a Coat for the Nuclear Pore Membrane
Authors : Hoelz, A.
Deposited on : 2007-11-23
Resolution : 3.00 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

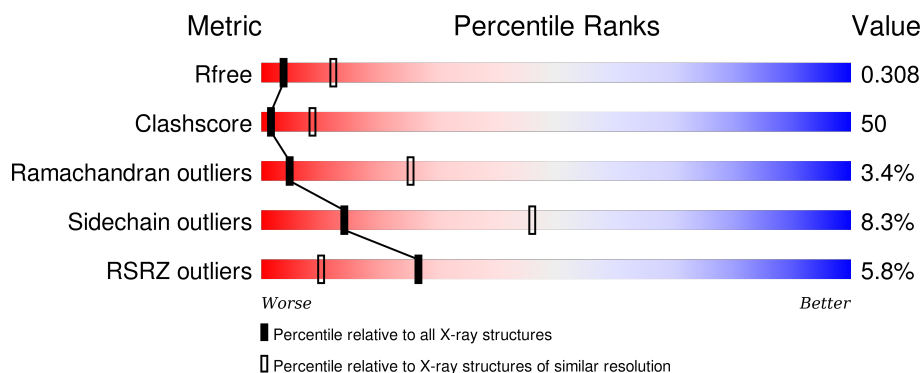
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

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	316	<div> <div>3%</div> <div>34% 50% 6% 10%</div> </div>
1	D	316	<div> <div>17%</div> <div>34% 49% 7% 10%</div> </div>
1	E	316	<div> <div>5%</div> <div>34% 50% 6% 10%</div> </div>
1	H	316	<div> <div>9%</div> <div>32% 51% 7% 10%</div> </div>
2	B	442	<div> <div>2%</div> <div>31% 56% 8% .</div> </div>

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Mol	Chain	Length	Quality of chain
2	C	442	<div> <div>4%</div> <div> <div></div> <div>33%</div> <div>55%</div> <div>7%</div> <div>5%</div> </div> </div>
2	F	442	<div> <div>4%</div> <div> <div></div> <div>33%</div> <div>53%</div> <div>8%</div> <div>.</div> </div> </div>
2	G	442	<div> <div>3%</div> <div> <div></div> <div>36%</div> <div>52%</div> <div>7%</div> <div>5%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 22614 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 Protein SEC13 homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	285	Total	C	N	O	S	0	0	0
			2233	1407	389	425	12			
1	D	283	Total	C	N	O	S	0	0	0
			2218	1398	386	422	12			
1	E	285	Total	C	N	O	S	0	0	0
			2233	1407	389	425	12			
1	H	283	Total	C	N	O	S	0	0	0
			2218	1398	386	422	12			

- Molecule 2 is a protein called Nucleoporin NUP145.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	423	Total	C	N	O	S	0	0	0
			3438	2201	570	656	11			
2	C	420	Total	C	N	O	S	0	0	0
			3418	2188	566	653	11			
2	F	423	Total	C	N	O	S	0	0	0
			3438	2201	570	656	11			
2	G	420	Total	C	N	O	S	0	0	0
			3418	2188	566	653	11			

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	111	MET	-	EXPRESSION TAG	UNP P49687
B	112	GLY	-	EXPRESSION TAG	UNP P49687
B	113	SER	-	EXPRESSION TAG	UNP P49687
B	114	SER	-	EXPRESSION TAG	UNP P49687
B	115	HIS	-	EXPRESSION TAG	UNP P49687
B	116	HIS	-	EXPRESSION TAG	UNP P49687
B	117	HIS	-	EXPRESSION TAG	UNP P49687
B	118	HIS	-	EXPRESSION TAG	UNP P49687

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Chain	Residue	Modelled	Actual	Comment	Reference
B	119	HIS	-	EXPRESSION TAG	UNP P49687
B	120	HIS	-	EXPRESSION TAG	UNP P49687
B	121	SER	-	EXPRESSION TAG	UNP P49687
B	122	GLY	-	EXPRESSION TAG	UNP P49687
B	123	ASP	-	EXPRESSION TAG	UNP P49687
B	124	PRO	-	EXPRESSION TAG	UNP P49687
C	111	MET	-	EXPRESSION TAG	UNP P49687
C	112	GLY	-	EXPRESSION TAG	UNP P49687
C	113	SER	-	EXPRESSION TAG	UNP P49687
C	114	SER	-	EXPRESSION TAG	UNP P49687
C	115	HIS	-	EXPRESSION TAG	UNP P49687
C	116	HIS	-	EXPRESSION TAG	UNP P49687
C	117	HIS	-	EXPRESSION TAG	UNP P49687
C	118	HIS	-	EXPRESSION TAG	UNP P49687
C	119	HIS	-	EXPRESSION TAG	UNP P49687
C	120	HIS	-	EXPRESSION TAG	UNP P49687
C	121	SER	-	EXPRESSION TAG	UNP P49687
C	122	GLY	-	EXPRESSION TAG	UNP P49687
C	123	ASP	-	EXPRESSION TAG	UNP P49687
C	124	PRO	-	EXPRESSION TAG	UNP P49687
F	111	MET	-	EXPRESSION TAG	UNP P49687
F	112	GLY	-	EXPRESSION TAG	UNP P49687
F	113	SER	-	EXPRESSION TAG	UNP P49687
F	114	SER	-	EXPRESSION TAG	UNP P49687
F	115	HIS	-	EXPRESSION TAG	UNP P49687
F	116	HIS	-	EXPRESSION TAG	UNP P49687
F	117	HIS	-	EXPRESSION TAG	UNP P49687
F	118	HIS	-	EXPRESSION TAG	UNP P49687
F	119	HIS	-	EXPRESSION TAG	UNP P49687
F	120	HIS	-	EXPRESSION TAG	UNP P49687
F	121	SER	-	EXPRESSION TAG	UNP P49687
F	122	GLY	-	EXPRESSION TAG	UNP P49687
F	123	ASP	-	EXPRESSION TAG	UNP P49687
F	124	PRO	-	EXPRESSION TAG	UNP P49687
G	111	MET	-	EXPRESSION TAG	UNP P49687
G	112	GLY	-	EXPRESSION TAG	UNP P49687
G	113	SER	-	EXPRESSION TAG	UNP P49687
G	114	SER	-	EXPRESSION TAG	UNP P49687
G	115	HIS	-	EXPRESSION TAG	UNP P49687
G	116	HIS	-	EXPRESSION TAG	UNP P49687
G	117	HIS	-	EXPRESSION TAG	UNP P49687
G	118	HIS	-	EXPRESSION TAG	UNP P49687

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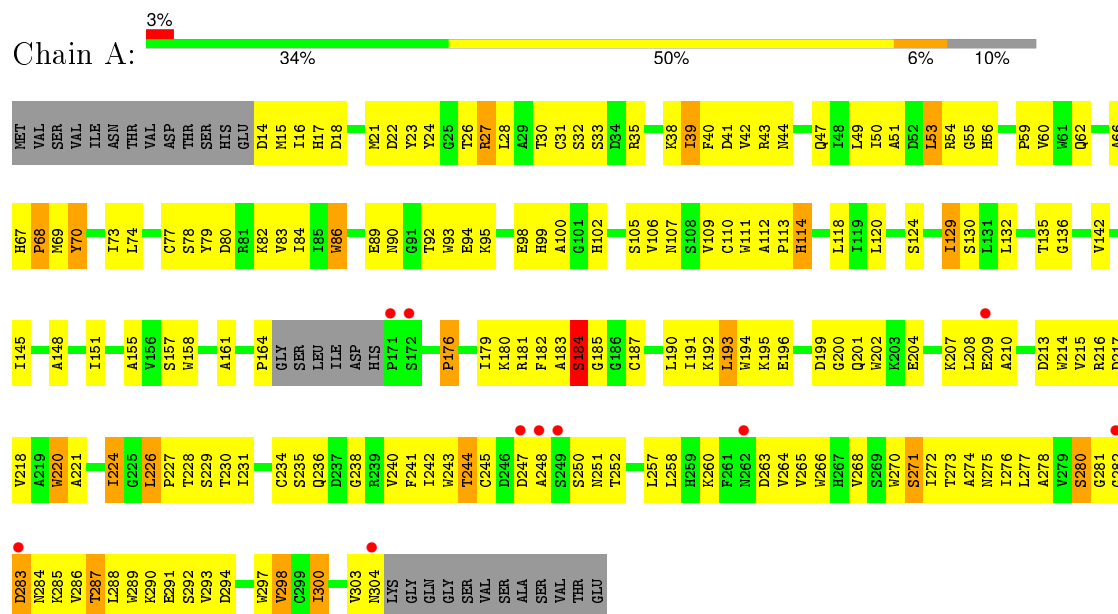
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Chain	Residue	Modelled	Actual	Comment	Reference
G	119	HIS	-	EXPRESSION TAG	UNP P49687
G	120	HIS	-	EXPRESSION TAG	UNP P49687
G	121	SER	-	EXPRESSION TAG	UNP P49687
G	122	GLY	-	EXPRESSION TAG	UNP P49687
G	123	ASP	-	EXPRESSION TAG	UNP P49687
G	124	PRO	-	EXPRESSION TAG	UNP P49687

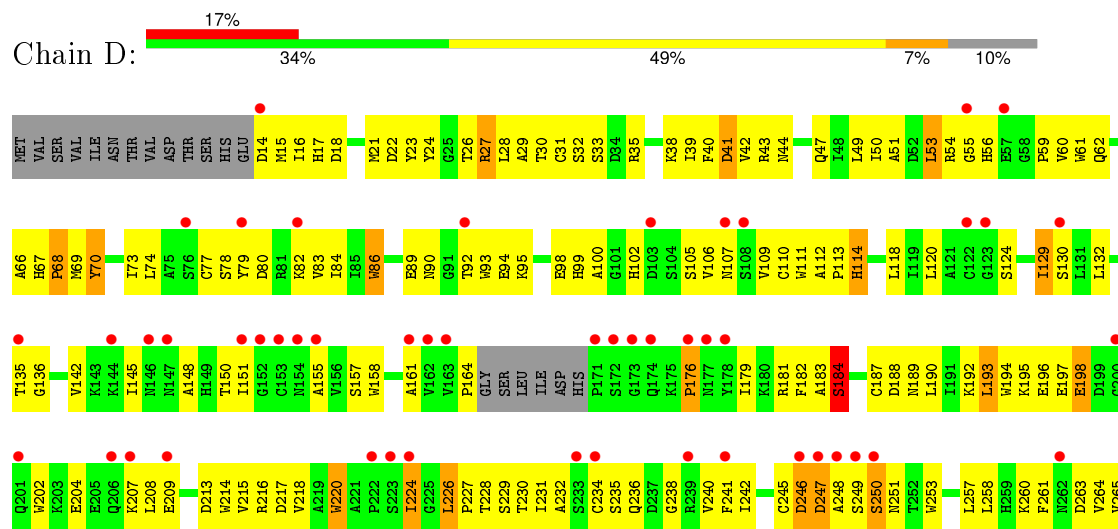
3 Residue-property plots

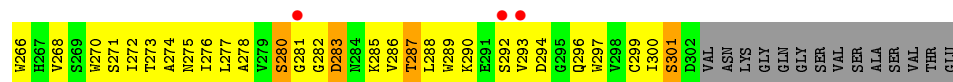
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: Protein SEC13 homolog

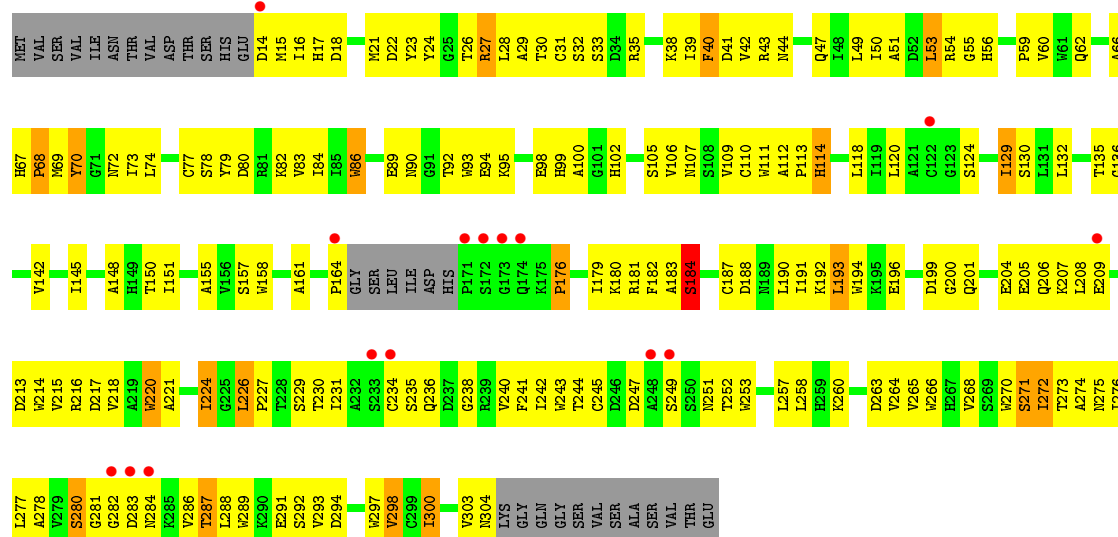


• Molecule 1: Protein SEC13 homolog

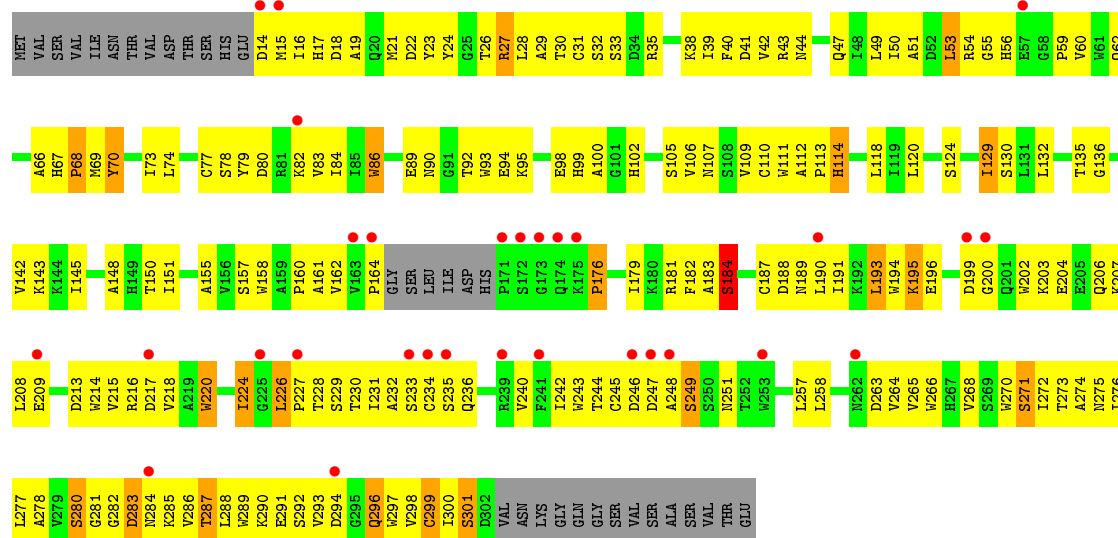
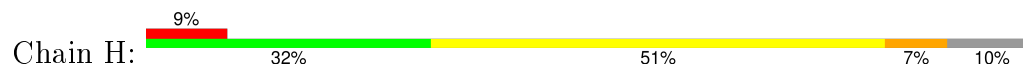




• Molecule 1: Protein SEC13 homolog

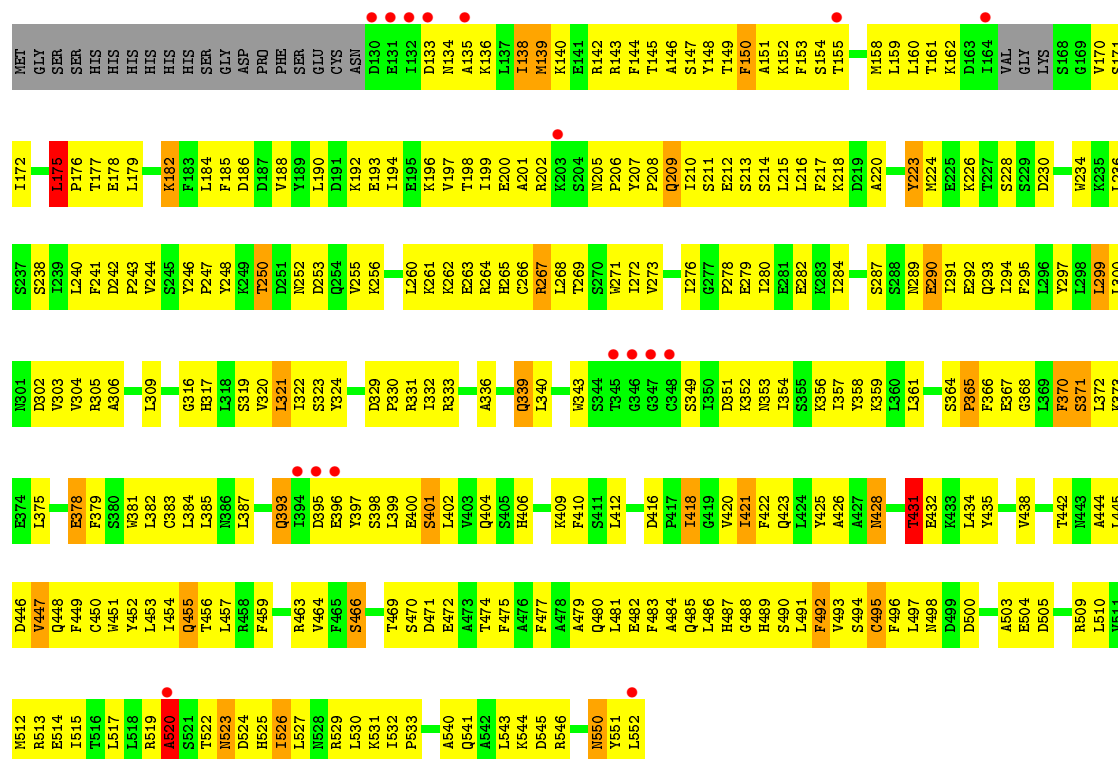
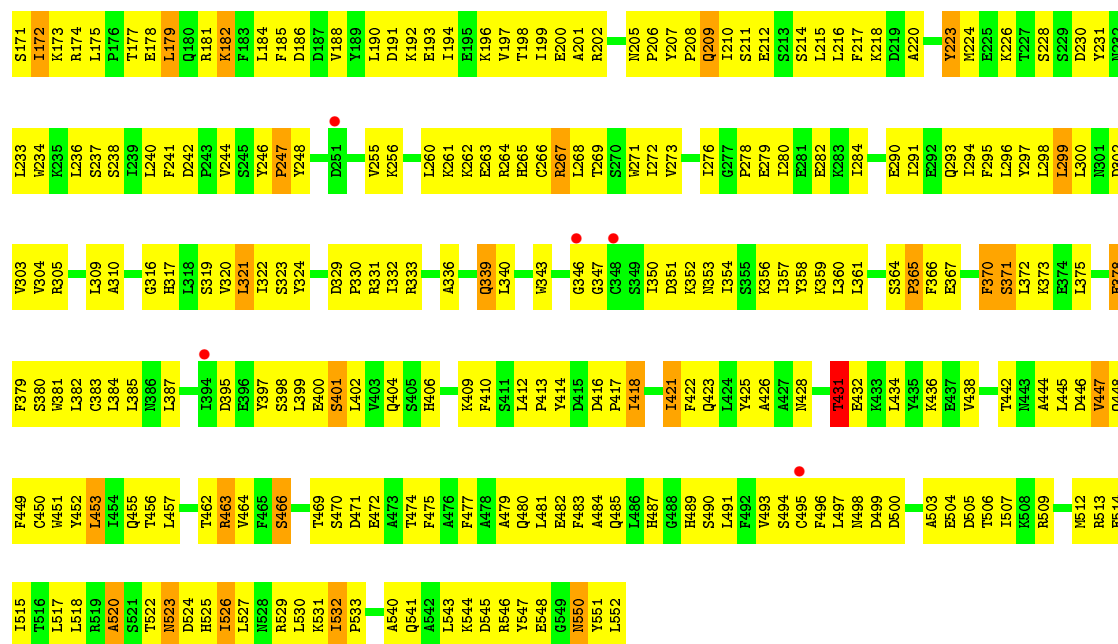


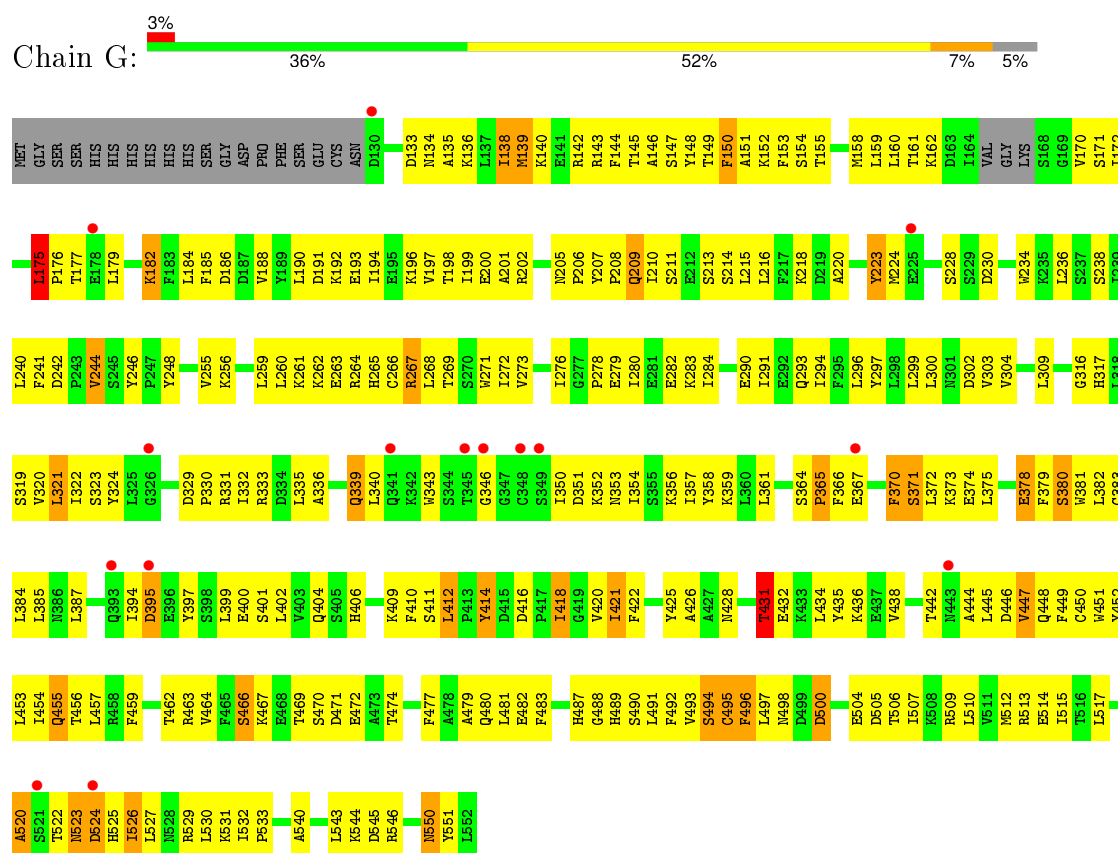
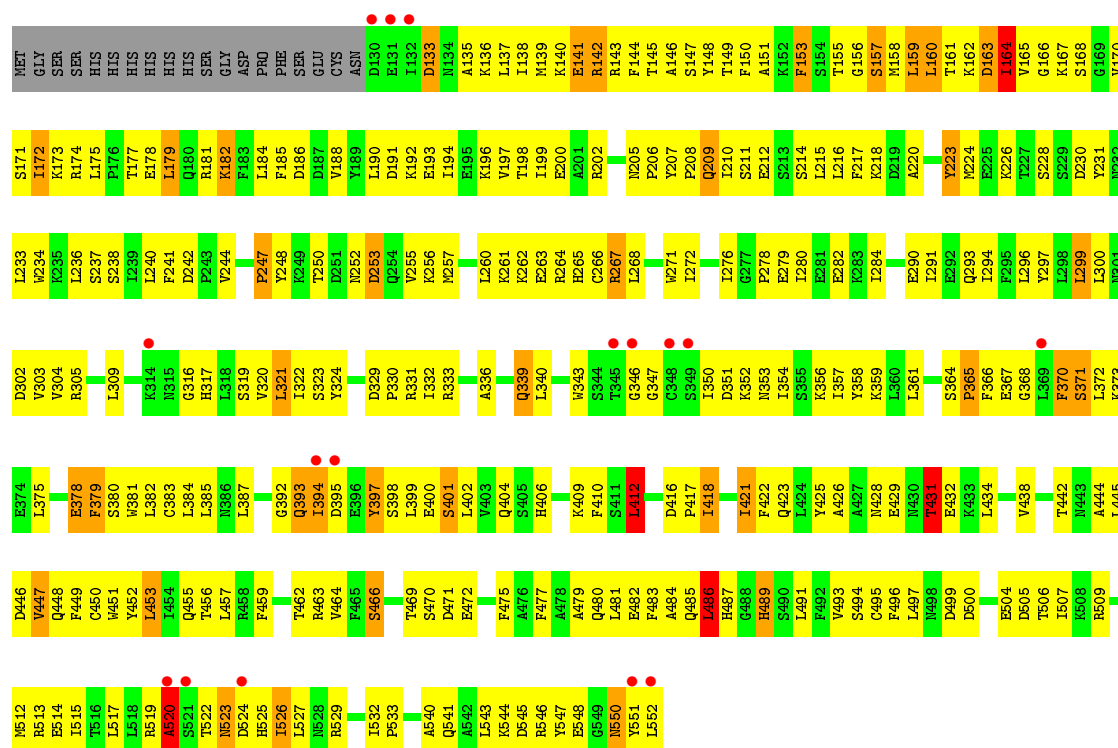
• Molecule 1: Protein SEC13 homolog



• Molecule 2: Nucleoporin NUP145







4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	181.37Å 216.79Å 192.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00 20.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	97.3 (20.00-3.00) 84.6 (20.00-3.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.38 (at 2.98Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.249 , 0.294 0.263 , 0.308	Depositor DCC
R_{free} test set	5198 reflections (8.10%)	DCC
Wilson B-factor (Å ²)	87.9	Xtriage
Anisotropy	0.769	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 78.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	5 of 71309 reflections (0.007%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	22614	wwPDB-VP
Average B, all atoms (Å ²)	149.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 24.84 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 3.5507e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.48	0/2297	0.74	1/3131 (0.0%)
1	D	0.45	0/2282	0.76	1/3110 (0.0%)
1	E	0.47	0/2297	0.74	2/3131 (0.1%)
1	H	0.43	0/2282	0.72	1/3110 (0.0%)
2	B	0.52	1/3504 (0.0%)	0.76	1/4728 (0.0%)
2	C	0.49	0/3483	0.76	3/4699 (0.1%)
2	F	0.52	1/3504 (0.0%)	0.77	2/4728 (0.0%)
2	G	0.48	0/3483	0.75	2/4699 (0.0%)
All	All	0.49	2/23132 (0.0%)	0.75	13/31336 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	153	PHE	CE2-CZ	5.19	1.47	1.37
2	B	153	PHE	CE2-CZ	5.05	1.47	1.37

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	175	LEU	CA-CB-CG	5.86	128.77	115.30
2	G	175	LEU	CA-CB-CG	5.85	128.75	115.30
2	C	397	TYR	N-CA-C	5.74	126.49	111.00
1	H	272	ILE	N-CA-C	5.58	126.06	111.00
1	D	272	ILE	N-CA-C	5.51	125.89	111.00
1	E	272	ILE	N-CA-C	5.48	125.80	111.00
1	A	272	ILE	N-CA-C	5.46	125.74	111.00
2	C	520	ALA	N-CA-C	5.23	125.12	111.00
2	B	520	ALA	N-CA-C	5.22	125.09	111.00
2	F	520	ALA	N-CA-C	5.19	125.02	111.00
2	G	520	ALA	N-CA-C	5.19	125.02	111.00
2	F	412	LEU	CA-CB-CG	-5.18	103.38	115.30
1	E	40	PHE	CB-CA-C	-5.06	100.28	110.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2233	0	2109	240	0
1	D	2218	0	2094	244	0
1	E	2233	0	2109	255	0
1	H	2218	0	2094	238	0
2	B	3438	0	3452	370	0
2	C	3418	0	3426	341	0
2	F	3438	0	3452	375	0
2	G	3418	0	3426	334	0
All	All	22614	0	22162	2245	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 50.

All (2245) 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:E:278:ALA:HB2	2:F:153:PHE:CE1	1.79	1.18
2:G:481:LEU:HD13	2:G:489:HIS:HB3	1.23	1.17
2:C:479:ALA:CB	1:D:273:THR:HG21	1.76	1.14
1:E:107:ASN:HD21	2:F:142:ARG:NH2	1.47	1.12
1:E:278:ALA:HB2	2:F:153:PHE:HE1	0.98	1.10
2:C:479:ALA:HB1	1:D:273:THR:HG21	1.34	1.09
1:A:278:ALA:HB2	2:B:153:PHE:HE1	1.07	1.08
1:E:69:MET:HE3	1:E:70:TYR:HE1	1.19	1.08
1:A:278:ALA:HB2	2:B:153:PHE:CE1	1.89	1.07
1:A:69:MET:HE3	1:A:70:TYR:HE1	1.19	1.07
1:D:135:THR:HG22	1:D:136:GLY:H	1.17	1.05
1:A:135:THR:HG22	1:A:136:GLY:H	1.17	1.05
2:B:432:GLU:OE2	2:B:466:SER:HB3	1.56	1.05
2:B:350:ILE:HG23	2:B:354:ILE:HD12	1.39	1.04
2:G:479:ALA:CB	1:H:273:THR:HG21	1.87	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:41:ASP:HB2	1:A:50:ILE:HD11	1.38	1.04
2:C:481:LEU:HD13	2:C:489:HIS:HB3	1.39	1.04
2:G:432:GLU:OE2	2:G:466:SER:HB3	1.56	1.03
1:E:135:THR:HG22	1:E:136:GLY:H	1.17	1.03
2:B:404:GLN:HG2	2:B:426:ALA:HB1	1.39	1.03
1:D:69:MET:HE3	1:D:70:TYR:HE1	1.19	1.03
1:H:69:MET:HE3	1:H:70:TYR:HE1	1.19	1.02
1:H:135:THR:HG22	1:H:136:GLY:H	1.17	1.02
2:G:479:ALA:HB1	1:H:273:THR:CG2	1.90	1.01
2:G:155:THR:HG22	2:G:513:ARG:HD2	1.42	1.01
2:F:484:ALA:HB3	2:F:486:LEU:CD1	1.90	1.01
2:C:479:ALA:HB1	1:D:273:THR:CG2	1.90	1.00
1:A:107:ASN:HD21	2:B:142:ARG:NH2	1.57	1.00
2:F:202:ARG:HG3	2:F:500:ASP:OD1	1.61	0.98
1:E:70:TYR:CE2	1:E:118:LEU:HB2	1.98	0.98
2:F:432:GLU:OE2	2:F:466:SER:HB3	1.63	0.98
2:C:442:THR:HG22	2:C:444:ALA:H	1.28	0.98
1:A:70:TYR:CE2	1:A:118:LEU:HB2	1.98	0.98
1:D:70:TYR:CE2	1:D:118:LEU:HB2	1.99	0.98
1:E:102:HIS:ND1	1:E:124:SER:HB3	1.79	0.98
1:H:102:HIS:ND1	1:H:124:SER:HB3	1.79	0.98
1:E:206:GLN:OE1	1:E:251:ASN:HB3	1.62	0.98
1:A:102:HIS:ND1	1:A:124:SER:HB3	1.79	0.97
2:C:479:ALA:CB	1:D:273:THR:CG2	2.41	0.97
2:B:276:ILE:HD13	2:B:383:CYS:HA	1.44	0.97
2:C:162:LYS:HZ3	1:D:15:MET:CE	1.76	0.97
1:H:70:TYR:CE2	1:H:118:LEU:HB2	1.99	0.97
2:F:442:THR:HG22	2:F:444:ALA:H	1.29	0.97
2:G:479:ALA:CB	1:H:273:THR:CG2	2.41	0.96
1:D:102:HIS:ND1	1:D:124:SER:HB3	1.79	0.96
2:B:487:HIS:HD2	2:B:517:LEU:HD23	1.31	0.95
2:G:479:ALA:HB1	1:H:273:THR:HG21	1.46	0.95
2:G:291:ILE:HG22	2:G:353:ASN:HB2	1.47	0.94
2:G:177:THR:HG22	2:G:179:LEU:H	1.29	0.94
2:G:276:ILE:HD13	2:G:383:CYS:HA	1.47	0.94
2:G:442:THR:HG22	2:G:444:ALA:H	1.30	0.94
2:C:291:ILE:HG22	2:C:353:ASN:HB2	1.49	0.93
2:B:149:THR:HG22	2:B:150:PHE:H	1.32	0.93
2:B:201:ALA:H	2:B:531:LYS:HZ2	1.12	0.93
2:F:149:THR:HG22	2:F:150:PHE:H	1.33	0.93
2:C:177:THR:HG22	2:C:179:LEU:H	1.29	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:162:LYS:HZ3	1:D:15:MET:HE2	1.33	0.92
1:E:242:ILE:HD13	1:E:297:TRP:NE1	1.84	0.92
2:G:159:LEU:HD12	2:G:160:LEU:H	1.35	0.91
2:G:462:THR:O	2:G:463:ARG:HD3	1.71	0.91
2:B:522:THR:O	2:B:523:ASN:CG	2.09	0.91
2:C:159:LEU:HD12	2:C:160:LEU:H	1.35	0.91
1:E:107:ASN:ND2	2:F:142:ARG:HH22	1.67	0.91
1:A:28:LEU:HD21	2:B:170:VAL:HG11	1.54	0.90
2:B:184:LEU:HD21	2:B:448:GLN:HE22	1.34	0.90
2:F:207:TYR:CD2	2:F:504:GLU:HA	2.05	0.90
2:G:267:ARG:HG3	2:G:267:ARG:HH11	1.37	0.90
1:H:288:LEU:H	1:H:301:SER:HB3	1.37	0.89
1:E:41:ASP:HB2	1:E:50:ILE:HD11	1.51	0.89
1:A:40:PHE:CZ	2:B:168:SER:HB2	2.07	0.89
1:E:107:ASN:HD21	2:F:142:ARG:HH22	1.10	0.89
2:G:294:ILE:HG12	2:G:309:LEU:HD23	1.54	0.89
2:F:238:SER:HA	2:F:242:ASP:OD2	1.73	0.89
1:A:214:TRP:O	1:A:235:SER:HB2	1.74	0.88
1:E:214:TRP:O	1:E:235:SER:HB2	1.73	0.88
1:D:195:LYS:HG2	1:D:196:GLU:H	1.36	0.88
2:F:484:ALA:HB3	2:F:486:LEU:HD12	1.52	0.88
1:A:107:ASN:HD21	2:B:142:ARG:HH22	1.14	0.88
2:F:522:THR:O	2:F:523:ASN:CG	2.12	0.88
2:F:267:ARG:HG3	2:F:267:ARG:HH11	1.38	0.88
1:H:82:LYS:HG2	1:H:100:ALA:HB2	1.56	0.88
1:D:82:LYS:HG2	1:D:100:ALA:HB2	1.56	0.88
2:B:163:ASP:HB2	2:B:171:SER:OG	1.73	0.88
2:F:404:GLN:HG2	2:F:426:ALA:HB1	1.54	0.88
1:E:69:MET:HE3	1:E:70:TYR:CE1	2.09	0.87
1:E:135:THR:HG22	1:E:136:GLY:N	1.90	0.87
2:F:163:ASP:HB2	2:F:171:SER:OG	1.73	0.87
1:D:214:TRP:O	1:D:235:SER:HB2	1.74	0.87
2:B:442:THR:HG22	2:B:444:ALA:H	1.39	0.87
2:G:551:TYR:HD1	1:H:27:ARG:HE	1.23	0.87
1:A:82:LYS:HG2	1:A:100:ALA:HB2	1.56	0.87
2:B:267:ARG:HG3	2:B:267:ARG:HH11	1.38	0.87
1:D:69:MET:HE3	1:D:70:TYR:CE1	2.10	0.87
1:H:135:THR:HG22	1:H:136:GLY:N	1.90	0.87
1:D:135:THR:HG22	1:D:136:GLY:N	1.90	0.87
1:A:69:MET:HE3	1:A:70:TYR:CE1	2.09	0.87
2:B:202:ARG:HG3	2:B:500:ASP:OD1	1.75	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:107:ASN:ND2	2:F:142:ARG:NH2	2.20	0.86
1:D:249:SER:O	1:D:250:SER:HB2	1.73	0.86
1:A:49:LEU:HD12	1:A:50:ILE:H	1.40	0.86
1:H:151:ILE:HB	1:H:187:CYS:HB2	1.55	0.86
1:A:135:THR:HG22	1:A:136:GLY:N	1.90	0.86
1:H:69:MET:HE3	1:H:70:TYR:CE1	2.10	0.86
2:B:515:ILE:HD11	2:B:540:ALA:HB3	1.54	0.86
2:C:267:ARG:HG3	2:C:267:ARG:HH11	1.37	0.86
1:E:82:LYS:HG2	1:E:100:ALA:HB2	1.56	0.86
2:B:487:HIS:CD2	2:B:517:LEU:HD23	2.08	0.86
1:A:107:ASN:ND2	2:B:142:ARG:HH22	1.73	0.86
2:G:291:ILE:HG22	2:G:353:ASN:CB	2.04	0.86
1:E:49:LEU:HD12	1:E:50:ILE:H	1.40	0.86
1:H:41:ASP:HB2	1:H:50:ILE:HD11	1.58	0.86
1:H:49:LEU:HD12	1:H:50:ILE:H	1.40	0.85
2:B:365:PRO:HB2	2:B:372:LEU:HD12	1.58	0.85
2:F:276:ILE:HD13	2:F:383:CYS:HA	1.56	0.85
1:H:214:TRP:O	1:H:235:SER:HB2	1.74	0.85
1:E:40:PHE:CZ	2:F:168:SER:HB2	2.12	0.85
2:G:218:LYS:HG2	2:G:238:SER:OG	1.76	0.85
2:F:365:PRO:HB2	2:F:372:LEU:HD12	1.59	0.85
2:F:218:LYS:HG2	2:F:238:SER:OG	1.76	0.85
2:C:365:PRO:HB2	2:C:372:LEU:HD12	1.59	0.85
2:B:149:THR:HG22	2:B:150:PHE:N	1.92	0.84
2:C:280:ILE:HG13	2:C:300:LEU:HD21	1.58	0.84
2:C:218:LYS:HG2	2:C:238:SER:OG	1.76	0.84
2:F:481:LEU:HD13	2:F:489:HIS:HB3	1.58	0.84
2:B:184:LEU:HD21	2:B:448:GLN:NE2	1.93	0.84
1:D:155:ALA:HB2	1:D:217:ASP:HA	1.60	0.84
2:F:149:THR:HG22	2:F:150:PHE:N	1.92	0.84
1:D:49:LEU:HD12	1:D:50:ILE:H	1.41	0.84
2:B:218:LYS:HG2	2:B:238:SER:OG	1.76	0.84
2:G:343:TRP:CZ3	2:G:350:ILE:HG13	2.12	0.84
1:A:28:LEU:HD11	2:B:160:LEU:HD13	1.60	0.83
2:C:416:ASP:OD1	2:C:418:ILE:HG13	1.78	0.83
2:B:151:ALA:HB1	2:B:159:LEU:HD11	1.60	0.83
2:B:416:ASP:OD1	2:B:418:ILE:HG13	1.78	0.83
2:C:276:ILE:HD13	2:C:383:CYS:HA	1.59	0.83
2:F:151:ALA:HB1	2:F:159:LEU:HD11	1.60	0.83
2:G:365:PRO:HB2	2:G:372:LEU:HD12	1.58	0.83
2:G:416:ASP:OD1	2:G:418:ILE:HG13	1.78	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:175:LEU:HD13	2:G:176:PRO:HD2	1.60	0.82
2:G:494:SER:O	2:G:497:LEU:HG	1.79	0.82
2:F:416:ASP:OD1	2:F:418:ILE:HG13	1.78	0.82
2:F:484:ALA:HB3	2:F:486:LEU:HD11	1.60	0.82
2:C:175:LEU:HD13	2:C:176:PRO:HD2	1.60	0.82
2:B:350:ILE:CG2	2:B:354:ILE:HD12	2.09	0.82
2:F:216:LEU:HB3	2:F:242:ASP:OD1	1.78	0.82
2:B:218:LYS:HG3	2:B:242:ASP:OD2	1.80	0.82
1:H:155:ALA:HB2	1:H:217:ASP:HA	1.59	0.82
2:F:515:ILE:HD11	2:F:540:ALA:HB3	1.62	0.81
2:C:142:ARG:O	2:C:143:ARG:HB2	1.79	0.81
2:B:497:LEU:HD12	2:B:503:ALA:HA	1.62	0.81
2:C:276:ILE:CD1	2:C:383:CYS:HA	2.10	0.81
2:F:320:VAL:O	2:F:323:SER:HB3	1.81	0.81
2:C:291:ILE:HG22	2:C:353:ASN:CB	2.10	0.80
2:G:145:THR:HG22	2:G:147:SER:H	1.46	0.80
2:C:145:THR:HG22	2:C:147:SER:H	1.46	0.80
2:C:515:ILE:HD11	2:C:540:ALA:HB3	1.62	0.80
2:G:471:ASP:OD1	2:G:497:LEU:HD22	1.82	0.80
2:C:155:THR:HG22	2:C:513:ARG:HD2	1.63	0.80
1:E:245:CYS:HB2	1:E:253:TRP:CE3	2.17	0.80
2:B:320:VAL:O	2:B:323:SER:HB3	1.82	0.80
2:B:159:LEU:HD12	2:B:160:LEU:N	1.97	0.80
2:F:159:LEU:HD12	2:F:160:LEU:N	1.96	0.80
2:G:320:VAL:O	2:G:323:SER:HB3	1.82	0.80
1:H:220:TRP:CE2	1:H:231:ILE:HD11	2.17	0.80
2:F:431:THR:HG22	2:F:432:GLU:N	1.97	0.79
2:B:190:LEU:HD13	2:B:489:HIS:ND1	1.97	0.79
2:B:431:THR:HG22	2:B:432:GLU:N	1.96	0.79
1:E:208:LEU:HB3	1:E:243:TRP:CZ3	2.18	0.79
2:G:479:ALA:CA	1:H:273:THR:HG21	2.11	0.79
2:C:149:THR:HG23	2:C:162:LYS:HG2	1.64	0.79
1:A:220:TRP:CE2	1:A:231:ILE:HD11	2.18	0.79
2:C:320:VAL:O	2:C:323:SER:HB3	1.82	0.79
2:G:149:THR:HG23	2:G:162:LYS:HG2	1.64	0.79
2:C:431:THR:HG22	2:C:432:GLU:N	1.97	0.79
2:B:207:TYR:CD2	2:B:504:GLU:HA	2.18	0.79
2:F:238:SER:O	2:F:242:ASP:HB2	1.81	0.79
2:G:431:THR:HG22	2:G:432:GLU:N	1.97	0.79
1:E:28:LEU:HD21	2:F:170:VAL:HG11	1.65	0.79
1:A:107:ASN:ND2	2:B:142:ARG:NH2	2.30	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:494:SER:O	2:C:497:LEU:HG	1.82	0.79
1:E:220:TRP:CE2	1:E:231:ILE:HD11	2.17	0.79
2:F:445:LEU:HD22	2:F:449:PHE:CD2	2.18	0.78
2:G:142:ARG:O	2:G:143:ARG:HB2	1.79	0.78
2:B:276:ILE:CD1	2:B:383:CYS:HA	2.13	0.78
1:D:220:TRP:CE2	1:D:231:ILE:HD11	2.18	0.78
2:B:172:ILE:HG22	2:B:172:ILE:O	1.83	0.78
2:G:479:ALA:HB1	1:H:273:THR:HG22	1.65	0.78
1:E:180:LYS:HD2	1:E:196:GLU:OE1	1.82	0.78
1:H:244:THR:HG22	1:H:245:CYS:H	1.48	0.78
1:A:41:ASP:HB2	1:A:50:ILE:CD1	2.13	0.78
2:B:398:SER:OG	2:B:401:SER:HB3	1.83	0.78
2:G:512:MET:SD	2:G:540:ALA:HB2	2.24	0.77
1:E:273:THR:HG21	2:F:479:ALA:CB	2.14	0.77
2:F:177:THR:HG21	2:F:179:LEU:HD23	1.67	0.77
2:B:177:THR:HG21	2:B:179:LEU:HD23	1.67	0.77
2:C:442:THR:CG2	2:C:444:ALA:H	1.96	0.77
2:C:432:GLU:OE2	2:C:466:SER:HB3	1.85	0.77
1:E:135:THR:CG2	1:E:136:GLY:H	1.98	0.77
2:F:442:THR:CG2	2:F:444:ALA:H	1.97	0.77
2:F:172:ILE:O	2:F:172:ILE:HG22	1.84	0.76
2:C:487:HIS:HD2	2:C:517:LEU:HD23	1.49	0.76
2:F:250:THR:HG21	2:G:335:LEU:HD13	1.67	0.76
2:C:134:ASN:O	2:C:138:ILE:HB	1.85	0.76
2:G:134:ASN:O	2:G:138:ILE:HB	1.85	0.76
2:G:352:LYS:CE	2:G:374:GLU:OE2	2.33	0.76
2:C:522:THR:O	2:C:523:ASN:CG	2.23	0.76
2:G:291:ILE:CG2	2:G:353:ASN:HB2	2.16	0.76
1:H:226:LEU:HD13	1:H:227:PRO:HD2	1.67	0.76
2:B:210:ILE:HD11	2:B:495:CYS:HB2	1.65	0.76
1:A:220:TRP:CZ3	1:A:229:SER:HB2	2.21	0.76
2:F:343:TRP:CZ3	2:F:350:ILE:HG21	2.21	0.76
2:G:359:LYS:HD2	2:G:365:PRO:HA	1.68	0.76
1:H:220:TRP:CZ3	1:H:229:SER:HB2	2.21	0.76
1:E:220:TRP:CZ3	1:E:229:SER:HB2	2.21	0.76
1:D:220:TRP:CZ3	1:D:229:SER:HB2	2.21	0.76
2:B:177:THR:CG2	2:B:179:LEU:HD23	2.16	0.75
2:F:159:LEU:C	2:F:160:LEU:HD23	2.06	0.75
1:D:226:LEU:HD13	1:D:227:PRO:HD2	1.68	0.75
2:C:284:ILE:HD13	2:C:297:TYR:CE1	2.22	0.75
1:A:102:HIS:HE2	1:A:130:SER:HB3	1.52	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:79:TYR:HA	1:H:105:SER:HB2	1.68	0.75
2:F:364:SER:HB3	2:F:394:ILE:HG12	1.69	0.75
2:B:359:LYS:HD2	2:B:365:PRO:HA	1.68	0.75
2:B:321:LEU:HB3	2:B:361:LEU:HD11	1.67	0.75
2:G:276:ILE:CD1	2:G:383:CYS:HA	2.15	0.75
1:H:102:HIS:HE2	1:H:130:SER:HB3	1.52	0.75
2:G:216:LEU:HB3	2:G:242:ASP:OD1	1.86	0.75
2:F:484:ALA:CB	2:F:486:LEU:HD11	2.17	0.74
1:D:102:HIS:HE2	1:D:130:SER:HB3	1.52	0.74
2:F:359:LYS:HD2	2:F:365:PRO:HA	1.68	0.74
1:A:226:LEU:HD13	1:A:227:PRO:HD2	1.67	0.74
1:E:79:TYR:HA	1:E:105:SER:HB2	1.69	0.74
1:D:195:LYS:HG2	1:D:196:GLU:N	2.01	0.74
2:C:359:LYS:HD2	2:C:365:PRO:HA	1.68	0.74
1:A:242:ILE:HD11	1:A:258:LEU:HD22	1.69	0.74
1:E:226:LEU:HD13	1:E:227:PRO:HD2	1.68	0.74
1:A:135:THR:CG2	1:A:136:GLY:H	1.98	0.74
2:G:151:ALA:HA	2:G:160:LEU:O	1.87	0.74
2:C:151:ALA:HA	2:C:160:LEU:O	1.87	0.74
2:B:159:LEU:C	2:B:160:LEU:HD23	2.07	0.74
2:C:294:ILE:HG12	2:C:309:LEU:HD23	1.67	0.74
1:A:41:ASP:CB	1:A:50:ILE:HD11	2.17	0.74
2:F:177:THR:CG2	2:F:179:LEU:HD23	2.16	0.74
1:A:79:TYR:HA	1:A:105:SER:HB2	1.68	0.74
2:G:284:ILE:HD13	2:G:297:TYR:CE1	2.23	0.74
1:D:151:ILE:HB	1:D:187:CYS:HB2	1.70	0.74
2:F:179:LEU:O	2:F:179:LEU:HG	1.88	0.74
1:D:135:THR:CG2	1:D:136:GLY:H	1.98	0.74
1:D:79:TYR:HA	1:D:105:SER:HB2	1.68	0.74
1:D:29:ALA:HB2	1:D:39:ILE:CD1	2.18	0.74
1:E:107:ASN:OD1	2:F:142:ARG:NH1	2.21	0.74
2:G:280:ILE:HB	2:G:300:LEU:HD21	1.68	0.74
2:B:177:THR:HG22	2:B:179:LEU:HB3	1.70	0.73
1:E:17:HIS:CE1	2:F:148:TYR:CE2	2.76	0.73
2:G:240:LEU:HD21	2:G:268:LEU:CD1	2.17	0.73
1:D:290:LYS:HB3	1:D:300:ILE:HD11	1.70	0.73
1:D:249:SER:O	1:D:250:SER:CB	2.34	0.73
1:E:102:HIS:HE2	1:E:130:SER:HB3	1.52	0.73
2:C:483:PHE:O	2:C:485:GLN:HG2	1.88	0.73
2:C:197:VAL:HG12	2:C:198:THR:N	2.04	0.73
2:B:244:VAL:HG23	2:B:264:ARG:HH21	1.54	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:216:LEU:HB3	2:B:242:ASP:OD2	1.88	0.73
2:C:421:ILE:HD11	2:C:449:PHE:HZ	1.54	0.73
2:B:197:VAL:HG12	2:B:198:THR:N	2.03	0.73
1:H:95:LYS:HE3	1:H:98:GLU:HB2	1.71	0.73
2:G:197:VAL:HG12	2:G:198:THR:N	2.03	0.73
2:G:412:LEU:N	2:G:412:LEU:HD12	2.04	0.73
2:F:336:ALA:O	2:F:340:LEU:HD23	1.89	0.73
1:D:95:LYS:HE3	1:D:98:GLU:HB2	1.71	0.73
2:C:199:ILE:CD1	2:C:530:LEU:HA	2.19	0.72
2:F:179:LEU:HD11	2:F:184:LEU:CD1	2.19	0.72
2:G:442:THR:CG2	2:G:444:ALA:H	2.01	0.72
1:H:195:LYS:HE2	1:H:203:LYS:HB2	1.71	0.72
1:E:41:ASP:CB	1:E:50:ILE:HD11	2.18	0.72
1:D:41:ASP:CB	1:D:50:ILE:HD11	2.19	0.72
2:C:428:ASN:HA	2:C:463:ARG:NH1	2.04	0.72
2:C:471:ASP:OD1	2:C:497:LEU:HA	1.89	0.72
1:E:230:THR:HG22	1:E:231:ILE:H	1.55	0.72
2:F:197:VAL:HG12	2:F:198:THR:N	2.04	0.72
2:B:336:ALA:O	2:B:340:LEU:HD23	1.89	0.72
1:A:95:LYS:HE3	1:A:98:GLU:HB2	1.71	0.72
2:C:421:ILE:HD11	2:C:449:PHE:CZ	2.24	0.72
2:C:336:ALA:O	2:C:340:LEU:HD23	1.90	0.72
2:F:177:THR:HG22	2:F:179:LEU:HB3	1.70	0.72
1:H:69:MET:CE	1:H:114:HIS:HB2	2.20	0.72
2:G:336:ALA:O	2:G:340:LEU:HD23	1.89	0.72
2:F:184:LEU:HD21	2:F:448:GLN:HE22	1.52	0.72
2:C:162:LYS:NZ	1:D:15:MET:CE	2.52	0.72
2:B:179:LEU:O	2:B:179:LEU:HG	1.87	0.72
2:G:175:LEU:CD1	2:G:176:PRO:HD2	2.18	0.72
2:C:175:LEU:CD1	2:C:176:PRO:HD2	2.18	0.71
2:G:149:THR:HG22	2:G:150:PHE:H	1.55	0.71
1:D:69:MET:CE	1:D:114:HIS:HB2	2.20	0.71
2:C:223:TYR:CD1	2:C:223:TYR:N	2.58	0.71
2:F:343:TRP:CE3	2:F:350:ILE:HD13	2.25	0.71
1:D:234:CYS:SG	1:D:268:VAL:HG23	2.30	0.71
2:B:223:TYR:CD1	2:B:223:TYR:N	2.58	0.71
1:E:69:MET:CE	1:E:114:HIS:HB2	2.20	0.71
1:A:69:MET:CE	1:A:114:HIS:HB2	2.20	0.71
1:A:230:THR:HG22	1:A:231:ILE:H	1.55	0.71
2:G:280:ILE:CB	2:G:300:LEU:HD21	2.19	0.71
2:G:148:TYR:HB2	1:H:266:TRP:CG	2.24	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:512:MET:SD	2:C:540:ALA:HB2	2.30	0.71
2:C:194:ILE:HG12	2:C:492:PHE:CE2	2.26	0.71
2:C:149:THR:HG22	2:C:150:PHE:H	1.55	0.71
2:F:276:ILE:CD1	2:F:383:CYS:HA	2.21	0.71
1:D:29:ALA:CB	1:D:39:ILE:CD1	2.69	0.71
2:F:385:LEU:HA	2:F:406:HIS:CE1	2.26	0.71
1:E:95:LYS:HE3	1:E:98:GLU:HB2	1.72	0.71
2:F:247:PRO:HG2	2:F:248:TYR:CE1	2.26	0.71
2:F:343:TRP:HZ3	2:F:350:ILE:CG2	2.04	0.70
2:C:216:LEU:HB3	2:C:242:ASP:OD1	1.92	0.70
1:H:230:THR:HG22	1:H:231:ILE:H	1.56	0.70
2:C:149:THR:HG22	2:C:150:PHE:N	2.06	0.70
2:F:223:TYR:N	2:F:223:TYR:CD1	2.58	0.70
2:F:445:LEU:HD22	2:F:449:PHE:HD2	1.56	0.70
1:A:22:ASP:OD1	1:A:23:TYR:N	2.24	0.70
1:H:22:ASP:OD1	1:H:23:TYR:N	2.25	0.70
1:D:230:THR:HG22	1:D:231:ILE:H	1.56	0.70
2:F:524:ASP:O	2:F:524:ASP:OD1	2.10	0.70
2:F:480:GLN:OE1	2:F:480:GLN:HA	1.91	0.70
1:E:145:ILE:HD13	1:E:194:TRP:CZ3	2.26	0.70
2:C:480:GLN:HA	2:C:480:GLN:OE1	1.92	0.70
1:A:107:ASN:OD1	2:B:142:ARG:NH1	2.24	0.70
1:E:22:ASP:OD1	1:E:23:TYR:N	2.24	0.70
2:C:291:ILE:CG2	2:C:353:ASN:HB2	2.21	0.70
1:A:242:ILE:HD12	1:A:297:TRP:CE2	2.27	0.70
2:G:149:THR:HG22	2:G:150:PHE:N	2.06	0.70
2:F:294:ILE:HG12	2:F:309:LEU:HD23	1.72	0.70
2:G:223:TYR:N	2:G:223:TYR:CD1	2.58	0.70
1:D:22:ASP:OD1	1:D:23:TYR:N	2.25	0.70
2:F:431:THR:HG22	2:F:432:GLU:H	1.56	0.69
2:F:244:VAL:HG23	2:F:264:ARG:HH21	1.56	0.69
1:D:190:LEU:CD2	1:D:209:GLU:HB3	2.22	0.69
2:F:395:ASP:HB2	2:F:397:TYR:CE2	2.27	0.69
1:E:179:ILE:HG21	1:E:181:ARG:HE	1.57	0.69
2:G:215:LEU:O	2:G:456:THR:HG23	1.92	0.69
1:H:135:THR:CG2	1:H:136:GLY:H	1.98	0.69
1:D:179:ILE:HG21	1:D:181:ARG:HE	1.57	0.69
1:E:26:THR:HB	2:F:547:TYR:OH	1.92	0.69
2:F:343:TRP:HZ3	2:F:350:ILE:HG21	1.56	0.69
2:C:479:ALA:HB2	1:D:273:THR:CG2	2.21	0.69
2:F:475:PHE:HE2	2:F:497:LEU:HD21	1.56	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:162:LYS:HZ3	1:D:15:MET:HE1	1.56	0.69
2:C:170:VAL:HG12	2:C:171:SER:N	2.07	0.69
2:B:480:GLN:HA	2:B:480:GLN:OE1	1.92	0.69
2:G:353:ASN:O	2:G:357:ILE:HG13	1.92	0.69
1:D:41:ASP:HB3	1:D:50:ILE:HD11	1.75	0.69
2:C:431:THR:HG22	2:C:432:GLU:H	1.57	0.69
2:B:385:LEU:HA	2:B:406:HIS:CE1	2.28	0.69
2:G:480:GLN:OE1	2:G:480:GLN:HA	1.92	0.69
2:B:524:ASP:OD1	2:B:524:ASP:O	2.10	0.69
2:C:479:ALA:CA	1:D:273:THR:HG21	2.23	0.69
2:F:353:ASN:O	2:F:357:ILE:HG13	1.93	0.69
1:H:29:ALA:HB2	1:H:39:ILE:CD1	2.23	0.69
2:B:404:GLN:CG	2:B:426:ALA:HB1	2.21	0.69
1:A:179:ILE:CG2	1:A:181:ARG:HE	2.06	0.69
1:H:179:ILE:HG21	1:H:181:ARG:HE	1.57	0.69
2:B:304:VAL:HG21	2:C:302:ASP:HA	1.75	0.68
2:F:224:MET:CE	2:F:230:ASP:HB3	2.24	0.68
1:E:29:ALA:HB2	1:E:39:ILE:CD1	2.23	0.68
2:G:479:ALA:HA	1:H:273:THR:HG21	1.74	0.68
2:C:224:MET:CE	2:C:230:ASP:HB3	2.23	0.68
2:G:291:ILE:HD12	2:G:351:ASP:OD2	1.93	0.68
1:H:53:LEU:N	1:H:53:LEU:HD23	2.09	0.68
2:F:432:GLU:CD	2:F:466:SER:HB3	2.13	0.68
2:C:353:ASN:O	2:C:357:ILE:HG13	1.93	0.68
1:A:28:LEU:HD11	2:B:160:LEU:CD1	2.23	0.68
1:H:288:LEU:N	1:H:301:SER:HB3	2.06	0.68
1:E:39:ILE:HD11	1:E:74:LEU:HD22	1.75	0.68
2:G:202:ARG:HG2	2:G:209:GLN:OE1	1.94	0.68
2:B:491:LEU:O	2:B:494:SER:HB2	1.93	0.68
2:G:170:VAL:HG12	2:G:171:SER:N	2.08	0.68
1:H:220:TRP:HZ3	1:H:229:SER:HB2	1.58	0.68
2:G:284:ILE:HG12	2:G:296:LEU:HD12	1.76	0.68
2:B:353:ASN:O	2:B:357:ILE:HG13	1.92	0.68
2:B:202:ARG:HG2	2:B:209:GLN:OE1	1.94	0.68
2:G:352:LYS:HG2	2:G:356:LYS:HE3	1.73	0.68
2:B:223:TYR:HD1	2:B:223:TYR:H	1.42	0.68
2:C:215:LEU:O	2:C:456:THR:HG23	1.93	0.68
2:G:400:GLU:HG3	2:G:425:TYR:CZ	2.28	0.68
2:G:404:GLN:HG2	2:G:426:ALA:HB1	1.74	0.68
2:G:431:THR:HG22	2:G:432:GLU:H	1.56	0.68
1:E:107:ASN:OD1	2:F:142:ARG:CZ	2.42	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:202:ARG:HG2	2:F:209:GLN:OE1	1.94	0.68
2:C:238:SER:O	2:C:242:ASP:HB2	1.93	0.68
2:F:280:ILE:HG13	2:F:300:LEU:HD21	1.75	0.68
2:C:378:GLU:N	2:C:378:GLU:OE1	2.27	0.68
2:F:184:LEU:HD21	2:F:448:GLN:NE2	2.08	0.68
2:C:159:LEU:HD12	2:C:160:LEU:N	2.09	0.68
2:B:156:GLY:O	2:B:157:SER:HB2	1.94	0.68
1:A:53:LEU:HD23	1:A:53:LEU:N	2.09	0.68
2:B:431:THR:HG22	2:B:432:GLU:H	1.56	0.67
1:H:179:ILE:CG2	1:H:181:ARG:HE	2.06	0.67
2:G:210:ILE:CD1	2:G:495:CYS:HB3	2.24	0.67
1:E:53:LEU:N	1:E:53:LEU:HD23	2.08	0.67
2:F:378:GLU:OE1	2:F:378:GLU:N	2.27	0.67
1:A:42:VAL:HG12	1:A:42:VAL:O	1.94	0.67
2:G:224:MET:CE	2:G:230:ASP:HB3	2.23	0.67
1:A:268:VAL:CG1	1:A:277:LEU:HD11	2.25	0.67
2:C:202:ARG:HG2	2:C:209:GLN:OE1	1.94	0.67
1:E:271:SER:HB2	2:F:153:PHE:CD2	2.29	0.67
2:C:280:ILE:CG1	2:C:300:LEU:HD21	2.24	0.67
2:G:352:LYS:HE2	2:G:374:GLU:OE2	1.94	0.67
1:D:179:ILE:CG2	1:D:181:ARG:HE	2.06	0.67
2:B:224:MET:CE	2:B:230:ASP:HB3	2.23	0.67
1:D:288:LEU:H	1:D:301:SER:HB3	1.59	0.67
2:C:364:SER:HB2	2:C:367:GLU:HG2	1.76	0.67
2:B:487:HIS:CE1	2:B:514:GLU:HG3	2.30	0.67
1:D:53:LEU:HD23	1:D:53:LEU:N	2.08	0.67
1:A:179:ILE:HG21	1:A:181:ARG:HE	1.57	0.67
2:B:378:GLU:OE1	2:B:378:GLU:N	2.27	0.67
1:H:268:VAL:CG1	1:H:277:LEU:HD11	2.25	0.67
2:G:202:ARG:CZ	2:G:209:GLN:HB3	2.25	0.67
1:H:23:TYR:HD2	1:H:24:TYR:CD1	2.12	0.67
1:D:232:ALA:HB2	1:D:270:TRP:CZ2	2.29	0.67
2:F:202:ARG:CZ	2:F:209:GLN:HB3	2.25	0.67
1:E:28:LEU:HD11	2:F:160:LEU:HD13	1.76	0.67
2:F:156:GLY:O	2:F:157:SER:HB2	1.94	0.67
2:G:138:ILE:HG22	2:G:139:MET:HG2	1.77	0.67
2:F:421:ILE:HD11	2:F:449:PHE:HZ	1.59	0.67
1:H:230:THR:CG2	1:H:242:ILE:HG23	2.25	0.67
1:E:179:ILE:CG2	1:E:181:ARG:HE	2.06	0.67
1:E:23:TYR:HD2	1:E:24:TYR:CD1	2.13	0.66
1:A:273:THR:HG21	2:B:479:ALA:CB	2.25	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:202:ARG:CZ	2:C:209:GLN:HB3	2.25	0.66
2:F:167:LYS:HD3	2:F:167:LYS:O	1.95	0.66
2:B:284:ILE:HG12	2:B:296:LEU:HD12	1.76	0.66
2:B:167:LYS:O	2:B:167:LYS:HD3	1.95	0.66
1:A:17:HIS:CE1	2:B:148:TYR:CE2	2.83	0.66
2:C:223:TYR:HD1	2:C:223:TYR:H	1.42	0.66
2:G:240:LEU:HD21	2:G:268:LEU:HD12	1.75	0.66
1:E:208:LEU:HD13	1:E:243:TRP:CE3	2.30	0.66
1:D:268:VAL:CG1	1:D:277:LEU:HD11	2.24	0.66
2:B:491:LEU:HD21	2:B:532:ILE:HD11	1.78	0.66
1:E:242:ILE:HD13	1:E:297:TRP:CE2	2.30	0.66
2:B:522:THR:CG2	2:B:526:ILE:HD11	2.25	0.66
1:E:220:TRP:HZ3	1:E:229:SER:HB2	1.58	0.66
1:D:274:ALA:HB1	1:D:290:LYS:HE3	1.78	0.66
2:B:364:SER:HB2	2:B:367:GLU:HG2	1.77	0.66
2:G:223:TYR:HD1	2:G:223:TYR:H	1.42	0.66
1:H:39:ILE:HD11	1:H:74:LEU:HD22	1.75	0.66
2:G:479:ALA:CB	1:H:273:THR:HG22	2.24	0.66
2:C:487:HIS:CD2	2:C:517:LEU:HD23	2.31	0.66
2:F:223:TYR:HD1	2:F:223:TYR:H	1.42	0.66
1:A:23:TYR:HD2	1:A:24:TYR:CD1	2.13	0.66
1:D:23:TYR:HD2	1:D:24:TYR:CD1	2.12	0.66
2:C:240:LEU:HD21	2:C:268:LEU:CD1	2.26	0.66
1:A:26:THR:HB	2:B:547:TYR:OH	1.96	0.66
2:C:177:THR:HG22	2:C:179:LEU:N	2.08	0.66
2:B:202:ARG:CZ	2:B:209:GLN:HB3	2.25	0.66
1:E:26:THR:HG22	1:E:27:ARG:HD2	1.78	0.66
2:C:321:LEU:HB3	2:C:361:LEU:HD11	1.76	0.66
2:G:364:SER:HB2	2:G:367:GLU:HG2	1.77	0.66
1:A:220:TRP:HZ3	1:A:229:SER:HB2	1.58	0.66
2:B:246:TYR:CD1	2:B:247:PRO:HD2	2.31	0.66
2:G:202:ARG:HG3	2:G:500:ASP:OD1	1.97	0.65
2:F:364:SER:HB2	2:F:367:GLU:HG2	1.77	0.65
1:D:39:ILE:HD11	1:D:74:LEU:HD22	1.77	0.65
1:E:288:LEU:HB2	1:E:300:ILE:HG13	1.78	0.65
2:G:378:GLU:OE1	2:G:378:GLU:N	2.27	0.65
1:E:268:VAL:CG1	1:E:277:LEU:HD11	2.25	0.65
1:A:26:THR:HG22	1:A:27:ARG:HD2	1.78	0.65
1:D:220:TRP:HZ3	1:D:229:SER:HB2	1.58	0.65
2:C:138:ILE:HG22	2:C:139:MET:HG2	1.77	0.65
2:C:223:TYR:HD1	2:C:223:TYR:N	1.94	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:ASN:OD1	2:B:142:ARG:CZ	2.45	0.65
1:H:26:THR:HG22	1:H:27:ARG:HD2	1.78	0.65
2:G:421:ILE:HD11	2:G:449:PHE:HZ	1.62	0.65
1:H:244:THR:HG22	1:H:245:CYS:N	2.11	0.65
2:C:487:HIS:O	2:C:488:GLY:C	2.35	0.65
1:H:29:ALA:CB	1:H:39:ILE:CD1	2.75	0.65
1:A:15:MET:HG3	2:B:162:LYS:NZ	2.12	0.65
2:F:484:ALA:CB	2:F:486:LEU:CD1	2.70	0.65
2:C:291:ILE:HD12	2:C:351:ASP:OD2	1.96	0.65
2:C:491:LEU:O	2:C:494:SER:HB3	1.97	0.65
2:F:149:THR:CG2	2:F:150:PHE:H	2.06	0.65
2:B:280:ILE:CB	2:B:300:LEU:HD21	2.27	0.65
2:G:421:ILE:HD11	2:G:449:PHE:CZ	2.31	0.65
2:G:280:ILE:HG13	2:G:300:LEU:HD21	1.78	0.65
2:F:223:TYR:HD1	2:F:223:TYR:N	1.94	0.65
1:D:26:THR:HG22	1:D:27:ARG:HD2	1.78	0.65
1:E:29:ALA:CB	1:E:39:ILE:CD1	2.75	0.65
2:B:431:THR:CG2	2:B:432:GLU:N	2.60	0.65
2:G:431:THR:CG2	2:G:432:GLU:N	2.60	0.65
2:G:159:LEU:HD12	2:G:160:LEU:N	2.09	0.65
2:B:522:THR:O	2:B:523:ASN:ND2	2.29	0.65
1:D:209:GLU:O	1:D:209:GLU:HG3	1.97	0.65
1:E:288:LEU:CB	1:E:300:ILE:HG13	2.27	0.65
2:C:435:TYR:CE2	2:C:454:ILE:HD11	2.32	0.65
2:B:149:THR:CG2	2:B:150:PHE:H	2.06	0.64
1:H:16:ILE:HD12	1:H:30:THR:HG21	1.79	0.64
2:C:210:ILE:HG22	2:C:459:PHE:HE2	1.61	0.64
1:A:190:LEU:CD2	1:A:209:GLU:HB3	2.27	0.64
1:E:16:ILE:HD12	1:E:30:THR:HG21	1.79	0.64
2:F:252:ASN:HB3	2:F:255:VAL:HB	1.79	0.64
1:A:151:ILE:HB	1:A:187:CYS:HB2	1.80	0.64
1:A:113:PRO:CB	1:A:161:ALA:HB2	2.27	0.64
1:H:209:GLU:O	1:H:209:GLU:HG3	1.97	0.64
2:G:210:ILE:HD12	2:G:495:CYS:HB3	1.77	0.64
2:C:479:ALA:HB1	1:D:273:THR:HG22	1.79	0.64
2:B:280:ILE:HB	2:B:300:LEU:HD21	1.79	0.64
1:A:16:ILE:HD12	1:A:30:THR:HG21	1.79	0.64
1:A:182:PHE:O	1:A:182:PHE:CD1	2.51	0.64
1:E:278:ALA:CB	2:F:153:PHE:HE1	1.93	0.64
1:D:29:ALA:HB2	1:D:39:ILE:HD12	1.80	0.64
2:B:197:VAL:CG1	2:B:198:THR:N	2.61	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:182:PHE:O	1:E:182:PHE:CD1	2.50	0.64
2:C:524:ASP:O	2:C:524:ASP:OD1	2.15	0.64
2:G:223:TYR:N	2:G:223:TYR:HD1	1.94	0.64
1:A:155:ALA:HB2	1:A:217:ASP:HA	1.79	0.64
2:G:246:TYR:HE2	2:G:248:TYR:HB2	1.63	0.64
2:F:431:THR:CG2	2:F:432:GLU:N	2.60	0.64
1:D:274:ALA:O	1:D:275:ASN:HB2	1.97	0.64
1:E:15:MET:HG3	2:F:162:LYS:NZ	2.12	0.64
2:B:179:LEU:HD11	2:B:184:LEU:CD1	2.28	0.64
2:B:384:LEU:O	2:B:387:LEU:HB2	1.98	0.64
2:F:197:VAL:CG1	2:F:198:THR:N	2.61	0.64
2:F:284:ILE:HG12	2:F:296:LEU:HD12	1.80	0.64
2:G:481:LEU:CD1	2:G:489:HIS:HB3	2.15	0.64
2:C:170:VAL:HG12	2:C:171:SER:H	1.63	0.64
2:C:384:LEU:O	2:C:387:LEU:HB2	1.98	0.64
1:A:274:ALA:HB3	1:A:276:ILE:HG13	1.80	0.64
2:C:420:VAL:HG11	2:C:445:LEU:HD11	1.80	0.64
2:B:404:GLN:HG2	2:B:426:ALA:CB	2.23	0.63
1:H:151:ILE:HB	1:H:187:CYS:CB	2.28	0.63
2:C:152:LYS:NZ	1:D:62:GLN:HE21	1.96	0.63
1:D:182:PHE:CD1	1:D:182:PHE:O	2.51	0.63
2:C:280:ILE:CB	2:C:300:LEU:HD21	2.29	0.63
2:C:381:TRP:CZ3	2:C:382:LEU:HD13	2.33	0.63
2:B:485:GLN:HE21	2:B:517:LEU:HD22	1.63	0.63
2:C:162:LYS:NZ	1:D:15:MET:HE2	2.11	0.63
1:E:274:ALA:O	1:E:275:ASN:HB2	1.98	0.63
1:A:209:GLU:O	1:A:209:GLU:HG3	1.97	0.63
2:F:321:LEU:HB3	2:F:361:LEU:HD11	1.78	0.63
1:A:193:LEU:C	1:A:194:TRP:CD1	2.72	0.63
1:D:193:LEU:C	1:D:194:TRP:CD1	2.72	0.63
2:G:384:LEU:O	2:G:387:LEU:HB2	1.98	0.63
2:C:431:THR:CG2	2:C:432:GLU:N	2.61	0.63
1:E:193:LEU:C	1:E:194:TRP:CD1	2.72	0.63
2:G:512:MET:HA	2:G:540:ALA:HB1	1.81	0.63
2:B:223:TYR:HD1	2:B:223:TYR:N	1.94	0.63
1:D:79:TYR:CD1	1:D:105:SER:HB3	2.34	0.63
2:C:197:VAL:CG1	2:C:198:THR:N	2.61	0.63
1:E:209:GLU:O	1:E:209:GLU:HG3	1.98	0.63
2:G:197:VAL:CG1	2:G:198:THR:N	2.61	0.63
2:G:201:ALA:HB2	2:G:531:LYS:NZ	2.14	0.63
1:H:274:ALA:HB3	1:H:276:ILE:HG13	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:155:THR:HG22	2:G:513:ARG:CD	2.25	0.63
1:D:16:ILE:HD12	1:D:30:THR:HG21	1.79	0.63
2:B:494:SER:O	2:B:497:LEU:HG	1.99	0.63
2:B:164:ILE:HG23	2:B:164:ILE:O	1.98	0.63
1:H:226:LEU:HD13	1:H:227:PRO:CD	2.29	0.63
1:A:274:ALA:O	1:A:275:ASN:HB2	1.98	0.63
1:A:79:TYR:CD1	1:A:105:SER:HB3	2.34	0.63
2:C:381:TRP:CE3	2:C:412:LEU:CD2	2.82	0.63
1:H:190:LEU:CD2	1:H:209:GLU:HB3	2.29	0.63
1:H:274:ALA:O	1:H:275:ASN:HB2	1.98	0.63
1:E:17:HIS:ND1	2:F:148:TYR:HE2	1.96	0.62
2:C:240:LEU:HD21	2:C:268:LEU:HD12	1.81	0.62
1:D:224:ILE:C	1:D:226:LEU:H	2.03	0.62
1:A:224:ILE:C	1:A:226:LEU:H	2.03	0.62
2:C:151:ALA:HB2	1:D:286:VAL:HG21	1.81	0.62
2:G:138:ILE:HG22	2:G:139:MET:H	1.64	0.62
2:B:238:SER:O	2:B:242:ASP:HB3	1.99	0.62
2:C:267:ARG:CG	2:C:267:ARG:HH11	2.10	0.62
1:E:230:THR:HG22	1:E:231:ILE:N	2.14	0.62
1:A:226:LEU:HD13	1:A:227:PRO:CD	2.29	0.62
1:E:274:ALA:HB3	1:E:276:ILE:HG13	1.80	0.62
1:H:182:PHE:O	1:H:182:PHE:CD1	2.51	0.62
2:C:136:LYS:O	2:C:140:LYS:HB2	1.99	0.62
1:E:30:THR:HG22	1:E:31:CYS:N	2.14	0.62
2:F:149:THR:CG2	2:F:150:PHE:N	2.63	0.62
1:H:42:VAL:HG12	1:H:42:VAL:O	1.98	0.62
1:H:79:TYR:CD1	1:H:105:SER:HB3	2.34	0.62
2:F:164:ILE:O	2:F:164:ILE:HG23	1.99	0.62
2:F:240:LEU:HD21	2:F:268:LEU:HD12	1.80	0.62
1:D:274:ALA:HB3	1:D:276:ILE:HG13	1.80	0.62
2:F:177:THR:C	2:F:179:LEU:H	2.03	0.62
2:F:237:SER:OG	2:F:421:ILE:CD1	2.48	0.62
2:G:515:ILE:HD11	2:G:540:ALA:HB3	1.82	0.62
1:D:226:LEU:HD13	1:D:227:PRO:CD	2.29	0.62
1:E:226:LEU:HD13	1:E:227:PRO:CD	2.29	0.62
1:H:30:THR:HG22	1:H:31:CYS:N	2.15	0.62
1:H:193:LEU:C	1:H:194:TRP:CD1	2.72	0.62
1:E:79:TYR:CD1	1:E:105:SER:HB3	2.35	0.62
2:B:177:THR:C	2:B:179:LEU:H	2.02	0.62
2:G:432:GLU:CD	2:G:466:SER:HB3	2.18	0.62
2:F:384:LEU:O	2:F:387:LEU:HB2	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:148:TYR:HB2	1:D:266:TRP:CG	2.35	0.62
1:H:39:ILE:HD11	1:H:74:LEU:CD2	2.29	0.62
2:F:155:THR:HG22	2:F:513:ARG:CD	2.30	0.62
2:G:194:ILE:HG12	2:G:492:PHE:CE2	2.35	0.62
2:B:276:ILE:HD13	2:B:383:CYS:CA	2.27	0.62
2:F:522:THR:O	2:F:523:ASN:ND2	2.32	0.62
2:G:136:LYS:O	2:G:140:LYS:HB2	1.99	0.62
2:G:162:LYS:NZ	1:H:15:MET:HE2	2.15	0.62
1:H:208:LEU:HB3	1:H:243:TRP:CZ3	2.35	0.62
2:F:155:THR:HG22	2:F:513:ARG:HD2	1.82	0.62
1:A:238:GLY:O	1:A:260:LYS:HA	2.00	0.62
1:E:221:ALA:HB2	1:E:270:TRP:CE2	2.34	0.62
2:F:210:ILE:HD11	2:F:495:CYS:HB2	1.81	0.61
2:B:267:ARG:CG	2:B:267:ARG:HH11	2.11	0.61
2:B:421:ILE:HD11	2:B:449:PHE:HZ	1.63	0.61
2:C:138:ILE:HG22	2:C:139:MET:H	1.64	0.61
2:B:240:LEU:HD21	2:B:268:LEU:CD1	2.30	0.61
2:G:524:ASP:O	2:G:524:ASP:OD1	2.18	0.61
1:A:30:THR:HG22	1:A:31:CYS:N	2.15	0.61
2:G:343:TRP:HZ3	2:G:350:ILE:HG21	1.65	0.61
1:E:190:LEU:HD13	1:E:207:LYS:HD3	1.80	0.61
1:E:27:ARG:HE	2:F:551:TYR:HD1	1.46	0.61
1:D:30:THR:HG22	1:D:31:CYS:N	2.15	0.61
2:F:280:ILE:CB	2:F:300:LEU:HD21	2.30	0.61
1:E:70:TYR:CD2	1:E:118:LEU:HB2	2.35	0.61
1:D:263:ASP:OD1	1:D:264:VAL:N	2.34	0.61
1:A:180:LYS:HD2	1:A:196:GLU:OE1	2.00	0.61
1:A:271:SER:HB2	2:B:153:PHE:CD2	2.35	0.61
2:C:160:LEU:HA	2:C:171:SER:O	2.00	0.61
2:G:175:LEU:HG	2:G:483:PHE:CD2	2.35	0.61
2:C:512:MET:HA	2:C:540:ALA:HB1	1.81	0.61
1:D:230:THR:HG22	1:D:231:ILE:N	2.16	0.61
1:A:70:TYR:CD2	1:A:118:LEU:HB2	2.35	0.61
2:G:479:ALA:HB2	1:H:273:THR:CG2	2.29	0.61
1:A:263:ASP:OD1	1:A:264:VAL:N	2.33	0.61
2:G:160:LEU:HA	2:G:171:SER:O	2.00	0.61
2:F:512:MET:SD	2:F:540:ALA:HB2	2.41	0.61
2:F:263:GLU:HA	2:G:320:VAL:HG22	1.83	0.61
1:E:224:ILE:C	1:E:226:LEU:H	2.02	0.61
1:E:263:ASP:OD1	1:E:264:VAL:N	2.33	0.61
1:D:145:ILE:HD11	1:D:202:TRP:CB	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:70:TYR:CD2	1:D:118:LEU:HB2	2.35	0.61
1:H:70:TYR:CD2	1:H:118:LEU:HB2	2.36	0.61
2:B:138:ILE:O	2:B:142:ARG:HB2	2.00	0.61
2:F:491:LEU:HD21	2:F:532:ILE:CD1	2.30	0.61
1:H:224:ILE:C	1:H:226:LEU:H	2.03	0.61
1:D:39:ILE:HD11	1:D:74:LEU:CD2	2.30	0.61
1:H:263:ASP:OD1	1:H:264:VAL:N	2.33	0.61
1:E:39:ILE:HD11	1:E:74:LEU:CD2	2.30	0.61
2:F:145:THR:HG22	2:F:147:SER:H	1.66	0.61
1:D:248:ALA:O	1:D:249:SER:OG	2.16	0.61
2:G:238:SER:HA	2:G:242:ASP:OD2	2.01	0.61
2:B:284:ILE:HG12	2:B:296:LEU:CD1	2.30	0.61
2:G:236:LEU:HD22	2:G:418:ILE:HG22	1.83	0.61
2:C:138:ILE:CG2	2:C:139:MET:N	2.64	0.61
1:H:208:LEU:HB3	1:H:243:TRP:CH2	2.36	0.61
1:D:70:TYR:HE2	1:D:118:LEU:HB2	1.64	0.61
1:A:230:THR:HG22	1:A:231:ILE:N	2.15	0.61
1:D:238:GLY:O	1:D:260:LYS:HA	2.01	0.61
2:F:487:HIS:CD2	2:F:517:LEU:HD23	2.36	0.60
2:F:138:ILE:O	2:F:142:ARG:HB2	2.01	0.60
2:G:177:THR:HG22	2:G:179:LEU:N	2.08	0.60
2:G:162:LYS:HZ2	1:H:15:MET:HE2	1.66	0.60
1:H:208:LEU:HD13	1:H:243:TRP:CE3	2.36	0.60
2:G:205:ASN:HB2	2:G:206:PRO:HD2	1.83	0.60
2:F:399:LEU:HD23	2:F:425:TYR:OH	2.01	0.60
2:F:142:ARG:HB3	2:F:144:PHE:CD1	2.36	0.60
2:B:375:LEU:HB2	2:B:384:LEU:HD21	1.82	0.60
1:H:230:THR:HG22	1:H:231:ILE:N	2.15	0.60
2:B:240:LEU:HD21	2:B:268:LEU:HD12	1.82	0.60
2:G:142:ARG:NH2	1:H:107:ASN:OD1	2.35	0.60
2:B:205:ASN:HB2	2:B:206:PRO:HD2	1.84	0.60
2:G:210:ILE:HG22	2:G:459:PHE:HE2	1.66	0.60
2:B:442:THR:HG22	2:B:444:ALA:N	2.15	0.60
2:F:412:LEU:H	2:F:412:LEU:CD1	2.10	0.60
1:H:287:THR:CG2	1:H:299:CYS:SG	2.89	0.60
2:B:237:SER:OG	2:B:421:ILE:CD1	2.49	0.60
2:C:224:MET:HE2	2:C:230:ASP:HB3	1.83	0.60
1:E:183:ALA:O	1:E:184:SER:HB3	2.00	0.60
1:A:70:TYR:HE2	1:A:118:LEU:HB2	1.64	0.60
2:G:170:VAL:HG12	2:G:171:SER:H	1.64	0.60
2:F:240:LEU:HD21	2:F:268:LEU:CD1	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:224:MET:HE1	2:F:230:ASP:HB3	1.82	0.60
2:G:283:LYS:NZ	2:G:378:GLU:HB2	2.16	0.60
2:G:138:ILE:CG2	2:G:139:MET:N	2.64	0.60
2:B:149:THR:CG2	2:B:150:PHE:N	2.63	0.60
2:F:446:ASP:O	2:F:449:PHE:N	2.35	0.60
2:F:485:GLN:O	2:F:487:HIS:N	2.35	0.60
2:B:446:ASP:O	2:B:449:PHE:N	2.35	0.60
2:B:294:ILE:HG12	2:B:309:LEU:HD23	1.83	0.60
1:H:113:PRO:HB2	1:H:161:ALA:HB2	1.84	0.60
2:G:451:TRP:CZ2	2:G:493:VAL:HG13	2.36	0.60
1:E:151:ILE:HB	1:E:187:CYS:HB2	1.83	0.60
2:B:142:ARG:HB3	2:B:144:PHE:CD1	2.37	0.59
2:F:532:ILE:HG23	2:F:533:PRO:HD2	1.84	0.59
2:B:522:THR:HG22	2:B:526:ILE:HD11	1.83	0.59
1:D:195:LYS:CG	1:D:196:GLU:H	2.11	0.59
1:E:190:LEU:CD2	1:E:209:GLU:HB3	2.32	0.59
2:C:205:ASN:HB2	2:C:206:PRO:HD2	1.83	0.59
2:F:205:ASN:HB2	2:F:206:PRO:HD2	1.83	0.59
1:H:287:THR:HA	1:H:301:SER:CB	2.32	0.59
1:D:213:ASP:HB3	1:D:236:GLN:HB2	1.84	0.59
1:D:145:ILE:HD11	1:D:202:TRP:HB2	1.83	0.59
1:E:238:GLY:O	1:E:260:LYS:HA	2.01	0.59
1:D:183:ALA:O	1:D:184:SER:HB3	2.01	0.59
1:A:221:ALA:HB2	1:A:270:TRP:CE2	2.38	0.59
2:B:162:LYS:O	2:B:162:LYS:HG3	2.02	0.59
2:B:332:ILE:HD12	2:B:332:ILE:H	1.67	0.59
1:A:89:GLU:O	1:A:90:ASN:HB2	2.02	0.59
1:D:77:CYS:HB3	1:D:109:VAL:CG2	2.32	0.59
1:E:192:LYS:HD3	1:E:204:GLU:OE1	2.02	0.59
2:F:198:THR:HG22	2:F:211:SER:HB3	1.84	0.59
2:F:162:LYS:O	2:F:162:LYS:HG3	2.02	0.59
2:F:332:ILE:HD12	2:F:332:ILE:H	1.67	0.59
2:B:497:LEU:CD1	2:B:503:ALA:HA	2.31	0.59
1:E:258:LEU:HD13	1:E:297:TRP:CB	2.32	0.59
2:C:202:ARG:HG3	2:C:500:ASP:OD1	2.02	0.59
1:E:155:ALA:HB2	1:E:217:ASP:HA	1.84	0.59
2:B:145:THR:HG22	2:B:147:SER:H	1.66	0.59
1:H:183:ALA:O	1:H:184:SER:HB3	2.01	0.59
2:C:451:TRP:CD1	2:C:474:THR:HA	2.37	0.59
1:E:49:LEU:HD12	1:E:50:ILE:N	2.16	0.59
1:H:190:LEU:HD22	1:H:209:GLU:HB3	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:423:GLN:HB3	2:F:434:LEU:HD21	1.84	0.59
1:E:213:ASP:HB3	1:E:236:GLN:HB2	1.84	0.59
1:D:29:ALA:HA	1:D:39:ILE:HD13	1.85	0.59
2:B:464:VAL:O	2:B:464:VAL:HG23	2.03	0.59
1:A:213:ASP:HB3	1:A:236:GLN:HB2	1.84	0.59
2:C:446:ASP:O	2:C:449:PHE:N	2.36	0.59
1:A:183:ALA:O	1:A:184:SER:HB3	2.01	0.59
2:G:321:LEU:HB3	2:G:361:LEU:HD11	1.84	0.59
1:A:77:CYS:HB3	1:A:109:VAL:CG2	2.33	0.59
2:C:160:LEU:CD2	2:C:172:ILE:HG12	2.33	0.59
2:B:198:THR:HG22	2:B:211:SER:HB3	1.84	0.59
2:F:384:LEU:HD13	2:F:410:PHE:CE1	2.38	0.58
1:D:41:ASP:HB2	1:D:50:ILE:HD11	1.85	0.58
1:H:89:GLU:O	1:H:90:ASN:HB2	2.02	0.58
2:C:332:ILE:H	2:C:332:ILE:HD12	1.67	0.58
1:D:242:ILE:HG12	1:D:297:TRP:CE2	2.38	0.58
2:B:491:LEU:HD21	2:B:532:ILE:CD1	2.33	0.58
1:H:77:CYS:HB3	1:H:109:VAL:CG2	2.33	0.58
2:G:491:LEU:HD13	2:G:510:LEU:HD23	1.85	0.58
2:G:199:ILE:CD1	2:G:530:LEU:HA	2.32	0.58
2:G:464:VAL:HG23	2:G:464:VAL:O	2.04	0.58
2:C:218:LYS:HG3	2:C:242:ASP:OD2	2.03	0.58
2:C:152:LYS:HZ1	1:D:62:GLN:NE2	2.00	0.58
2:G:332:ILE:H	2:G:332:ILE:HD12	1.67	0.58
2:F:233:LEU:HD13	2:F:417:PRO:HB2	1.85	0.58
2:G:160:LEU:CD2	2:G:172:ILE:HG12	2.33	0.58
2:F:267:ARG:CG	2:F:267:ARG:HH11	2.11	0.58
1:H:213:ASP:HB3	1:H:236:GLN:HB2	1.84	0.58
1:E:89:GLU:O	1:E:90:ASN:HB2	2.02	0.58
1:E:70:TYR:CD1	1:E:70:TYR:N	2.72	0.58
2:C:351:ASP:HB2	2:C:354:ILE:HG13	1.86	0.58
2:G:238:SER:O	2:G:242:ASP:HB2	2.04	0.58
2:G:198:THR:HG22	2:G:211:SER:HB3	1.84	0.58
2:F:247:PRO:HG2	2:F:248:TYR:CD1	2.38	0.58
1:D:89:GLU:O	1:D:90:ASN:HB2	2.02	0.58
1:H:70:TYR:CD1	1:H:70:TYR:N	2.72	0.58
1:A:208:LEU:HB3	1:A:243:TRP:CZ3	2.39	0.58
2:C:152:LYS:NZ	1:D:62:GLN:NE2	2.51	0.58
2:B:210:ILE:CD1	2:B:495:CYS:HB2	2.33	0.58
2:C:262:LYS:O	2:C:265:HIS:N	2.36	0.58
2:F:340:LEU:HD21	2:F:358:TYR:HB3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:23:TYR:CD2	1:E:68:PRO:HG3	2.39	0.58
1:E:29:ALA:HB2	1:E:39:ILE:HD12	1.85	0.58
1:A:193:LEU:N	1:A:193:LEU:CD2	2.67	0.58
1:H:191:ILE:HG23	1:H:218:VAL:HG21	1.86	0.58
1:E:77:CYS:HB3	1:E:109:VAL:CG2	2.33	0.58
2:B:210:ILE:CD1	2:B:495:CYS:CB	2.82	0.58
2:B:160:LEU:N	2:B:160:LEU:HD23	2.18	0.58
2:F:381:TRP:CG	2:F:382:LEU:N	2.71	0.58
2:F:421:ILE:HD11	2:F:449:PHE:CZ	2.39	0.58
1:A:190:LEU:HD22	1:A:209:GLU:HB3	1.86	0.58
1:H:132:LEU:HD23	1:H:142:VAL:HG13	1.86	0.58
2:G:487:HIS:HD2	2:G:517:LEU:HD23	1.69	0.58
1:E:109:VAL:HG12	1:E:120:LEU:HD11	1.86	0.58
1:H:287:THR:HA	1:H:301:SER:HB3	1.86	0.58
2:G:175:LEU:HG	2:G:483:PHE:HD2	1.69	0.58
1:H:291:GLU:HG3	1:H:291:GLU:O	2.01	0.58
2:C:400:GLU:HG3	2:C:425:TYR:CZ	2.39	0.58
1:D:132:LEU:HD23	1:D:142:VAL:HG13	1.86	0.58
1:A:16:ILE:HG22	1:A:17:HIS:N	2.19	0.57
1:D:16:ILE:HG22	1:D:17:HIS:N	2.19	0.57
2:G:351:ASP:HB2	2:G:354:ILE:HG13	1.86	0.57
2:F:262:LYS:O	2:F:265:HIS:N	2.36	0.57
1:E:208:LEU:HB3	1:E:243:TRP:CH2	2.38	0.57
2:C:492:PHE:CD1	2:C:492:PHE:C	2.77	0.57
2:G:291:ILE:HG22	2:G:353:ASN:HB3	1.86	0.57
2:G:551:TYR:HD1	1:H:27:ARG:NE	1.99	0.57
1:H:23:TYR:CD2	1:H:68:PRO:HG3	2.39	0.57
1:D:193:LEU:N	1:D:193:LEU:CD2	2.68	0.57
2:G:207:TYR:CD2	2:G:504:GLU:HA	2.39	0.57
1:E:286:VAL:O	1:E:303:VAL:HG23	2.05	0.57
2:B:532:ILE:HG23	2:B:533:PRO:HD2	1.84	0.57
2:F:464:VAL:HG23	2:F:464:VAL:O	2.04	0.57
2:G:202:ARG:NH2	2:G:209:GLN:HB3	2.20	0.57
1:E:16:ILE:HG22	1:E:17:HIS:N	2.18	0.57
1:A:17:HIS:ND1	2:B:148:TYR:HE2	2.03	0.57
1:D:42:VAL:HG12	1:D:42:VAL:O	2.05	0.57
2:G:294:ILE:CG1	2:G:309:LEU:HD23	2.31	0.57
2:F:215:LEU:O	2:F:456:THR:HG23	2.04	0.57
1:H:16:ILE:HG22	1:H:17:HIS:N	2.19	0.57
1:A:208:LEU:HB3	1:A:243:TRP:CH2	2.39	0.57
2:F:177:THR:OG1	2:F:483:PHE:HB2	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:210:ILE:HD13	2:G:496:PHE:CD1	2.39	0.57
1:E:109:VAL:CG1	1:E:120:LEU:HD11	2.35	0.57
2:B:280:ILE:HG13	2:B:300:LEU:HD21	1.87	0.57
2:C:289:ASN:O	2:C:292:GLU:N	2.37	0.57
2:F:339:GLN:O	2:F:343:TRP:HD1	1.87	0.57
1:D:23:TYR:CD2	1:D:68:PRO:HG3	2.39	0.57
2:C:149:THR:CG2	2:C:162:LYS:HG2	2.35	0.57
2:G:446:ASP:O	2:G:449:PHE:N	2.36	0.57
2:F:351:ASP:HB2	2:F:354:ILE:HG13	1.86	0.57
1:A:70:TYR:CD1	1:A:70:TYR:N	2.72	0.57
2:F:267:ARG:NH1	2:F:267:ARG:HG3	2.15	0.57
2:B:262:LYS:O	2:B:265:HIS:N	2.36	0.57
1:E:193:LEU:N	1:E:193:LEU:CD2	2.67	0.57
2:B:246:TYR:CG	2:B:247:PRO:HD2	2.40	0.57
1:E:132:LEU:HD23	1:E:142:VAL:HG13	1.86	0.57
2:C:371:SER:OG	2:C:373:LYS:HG3	2.05	0.57
2:C:198:THR:HG22	2:C:211:SER:HB3	1.84	0.57
1:A:132:LEU:HD23	1:A:142:VAL:HG13	1.86	0.57
1:E:41:ASP:OD1	1:E:41:ASP:C	2.43	0.57
1:A:258:LEU:HD13	1:A:297:TRP:CB	2.35	0.57
1:H:29:ALA:HB2	1:H:39:ILE:HD12	1.85	0.57
1:H:292:SER:C	1:H:294:ASP:H	2.08	0.57
1:D:109:VAL:CG1	1:D:120:LEU:HD11	2.35	0.57
2:G:149:THR:CG2	2:G:150:PHE:H	2.18	0.57
2:C:201:ALA:HB2	2:C:531:LYS:HE2	1.87	0.57
1:A:113:PRO:HB2	1:A:161:ALA:HB2	1.86	0.57
2:C:464:VAL:HG23	2:C:464:VAL:O	2.04	0.57
2:C:190:LEU:O	2:C:194:ILE:HG13	2.05	0.56
2:C:149:THR:CG2	2:C:150:PHE:H	2.18	0.56
2:F:371:SER:OG	2:F:373:LYS:HG3	2.05	0.56
2:G:371:SER:OG	2:G:373:LYS:HG3	2.05	0.56
2:B:190:LEU:O	2:B:194:ILE:HG13	2.05	0.56
1:A:23:TYR:CD2	1:A:68:PRO:HG3	2.39	0.56
1:H:193:LEU:CD2	1:H:193:LEU:N	2.68	0.56
2:C:451:TRP:CZ2	2:C:493:VAL:HG13	2.39	0.56
2:B:351:ASP:HB2	2:B:354:ILE:HG13	1.86	0.56
2:C:194:ILE:HG12	2:C:492:PHE:HE2	1.69	0.56
2:G:280:ILE:CG1	2:G:300:LEU:HD21	2.35	0.56
1:H:109:VAL:HG12	1:H:120:LEU:HD11	1.88	0.56
2:F:284:ILE:HD13	2:F:297:TYR:CE1	2.40	0.56
2:G:332:ILE:N	2:G:332:ILE:HD12	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:150:THR:HB	1:H:188:ASP:HB3	1.86	0.56
2:G:532:ILE:HG23	2:G:533:PRO:HD2	1.87	0.56
1:D:70:TYR:CD1	1:D:70:TYR:N	2.72	0.56
2:G:339:GLN:O	2:G:343:TRP:HD1	1.87	0.56
1:D:80:ASP:OD2	1:D:82:LYS:HB2	2.05	0.56
2:F:352:LYS:O	2:F:356:LYS:HG3	2.05	0.56
2:C:381:TRP:CE3	2:C:412:LEU:HD21	2.40	0.56
2:F:151:ALA:HB1	2:F:159:LEU:CD1	2.33	0.56
1:H:234:CYS:SG	1:H:268:VAL:HG23	2.45	0.56
1:E:151:ILE:O	1:E:151:ILE:HG22	2.06	0.56
2:B:233:LEU:HD13	2:B:417:PRO:HB2	1.87	0.56
1:E:35:ARG:HD3	1:E:56:HIS:O	2.05	0.56
2:C:339:GLN:O	2:C:343:TRP:HD1	1.87	0.56
1:A:35:ARG:HD3	1:A:56:HIS:O	2.05	0.56
1:H:80:ASP:OD2	1:H:82:LYS:HB2	2.06	0.56
1:A:80:ASP:OD2	1:A:82:LYS:HB2	2.05	0.56
2:G:262:LYS:O	2:G:265:HIS:N	2.37	0.56
2:C:284:ILE:HD13	2:C:297:TYR:HE1	1.68	0.56
2:F:392:GLY:C	2:F:394:ILE:H	2.08	0.56
2:F:280:ILE:HB	2:F:300:LEU:HD21	1.85	0.56
2:F:332:ILE:N	2:F:332:ILE:HD12	2.21	0.56
1:H:35:ARG:HD3	1:H:56:HIS:O	2.05	0.56
1:D:35:ARG:HD3	1:D:56:HIS:O	2.05	0.56
1:D:151:ILE:HG22	1:D:151:ILE:O	2.06	0.56
2:B:177:THR:OG1	2:B:483:PHE:HB3	2.06	0.56
2:B:431:THR:OG1	2:B:463:ARG:HG2	2.06	0.56
2:C:162:LYS:NZ	1:D:15:MET:HE1	2.18	0.56
2:C:267:ARG:HG3	2:C:267:ARG:NH1	2.14	0.56
2:B:321:LEU:HD23	2:B:321:LEU:N	2.20	0.56
1:H:232:ALA:HB2	1:H:270:TRP:CZ2	2.41	0.56
1:D:112:ALA:HB2	1:D:158:TRP:CZ2	2.41	0.56
2:F:181:ARG:HD2	2:F:448:GLN:OE1	2.05	0.56
2:F:160:LEU:N	2:F:160:LEU:HD23	2.18	0.56
2:G:352:LYS:O	2:G:356:LYS:HG3	2.06	0.56
2:C:202:ARG:NH2	2:C:209:GLN:HB3	2.20	0.56
1:H:109:VAL:CG1	1:H:120:LEU:HD11	2.36	0.56
2:B:339:GLN:O	2:B:343:TRP:HD1	1.87	0.56
2:G:495:CYS:O	2:G:497:LEU:N	2.38	0.56
1:E:80:ASP:OD2	1:E:82:LYS:HB2	2.05	0.56
2:G:162:LYS:NZ	1:H:15:MET:CE	2.68	0.56
2:B:448:GLN:HB2	2:B:477:PHE:CE1	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:70:TYR:HE2	1:H:118:LEU:HB2	1.64	0.56
1:A:304:ASN:OD1	2:B:161:THR:HG21	2.06	0.56
2:C:352:LYS:O	2:C:356:LYS:HG3	2.05	0.56
2:G:224:MET:HE2	2:G:230:ASP:HB3	1.88	0.56
2:G:321:LEU:HD23	2:G:321:LEU:N	2.20	0.56
1:E:112:ALA:HB2	1:E:158:TRP:CZ2	2.41	0.56
2:G:190:LEU:O	2:G:194:ILE:HG13	2.05	0.56
2:B:179:LEU:HD11	2:B:184:LEU:HD13	1.87	0.56
2:F:202:ARG:NH2	2:F:209:GLN:HB3	2.20	0.56
1:E:31:CYS:HB2	1:E:60:VAL:HB	1.88	0.56
2:B:371:SER:OG	2:B:373:LYS:HG3	2.05	0.56
2:B:197:VAL:CG1	2:B:198:THR:H	2.19	0.56
2:F:156:GLY:O	2:F:157:SER:CB	2.54	0.56
1:A:190:LEU:HD13	1:A:207:LYS:HD3	1.88	0.56
1:H:290:LYS:HB3	1:H:300:ILE:HD11	1.87	0.56
2:F:190:LEU:O	2:F:194:ILE:HG13	2.05	0.55
2:C:321:LEU:N	2:C:321:LEU:HD23	2.20	0.55
2:G:451:TRP:CD1	2:G:474:THR:HA	2.41	0.55
2:B:210:ILE:HD12	2:B:495:CYS:HB3	1.89	0.55
2:B:202:ARG:NH2	2:B:209:GLN:HB3	2.20	0.55
1:H:151:ILE:O	1:H:151:ILE:HG22	2.06	0.55
2:F:343:TRP:HE3	2:F:350:ILE:HD13	1.69	0.55
2:F:321:LEU:HD23	2:F:321:LEU:N	2.21	0.55
2:B:332:ILE:HD12	2:B:332:ILE:N	2.20	0.55
1:A:112:ALA:HB2	1:A:158:TRP:CZ2	2.41	0.55
1:A:109:VAL:CG1	1:A:120:LEU:HD11	2.35	0.55
1:A:31:CYS:HB2	1:A:60:VAL:HB	1.89	0.55
1:E:42:VAL:HG12	1:E:42:VAL:O	2.05	0.55
2:B:352:LYS:O	2:B:356:LYS:HG3	2.05	0.55
1:D:49:LEU:HD12	1:D:50:ILE:N	2.17	0.55
1:A:273:THR:HG21	2:B:479:ALA:HB2	1.87	0.55
1:A:151:ILE:HG22	1:A:151:ILE:O	2.06	0.55
1:H:112:ALA:HB2	1:H:158:TRP:CZ2	2.41	0.55
1:D:31:CYS:HB2	1:D:60:VAL:HB	1.88	0.55
2:G:224:MET:HE1	2:G:230:ASP:HB3	1.88	0.55
2:G:190:LEU:HB2	2:G:489:HIS:CE1	2.42	0.55
1:A:304:ASN:HA	2:B:173:LYS:NZ	2.22	0.55
2:C:512:MET:HA	2:C:540:ALA:CB	2.37	0.55
2:G:149:THR:CG2	2:G:162:LYS:HG2	2.34	0.55
1:D:29:ALA:CB	1:D:39:ILE:HD13	2.36	0.55
1:E:289:TRP:HA	1:E:298:VAL:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:268:LEU:HD21	2:F:272:ILE:HD11	1.88	0.55
2:F:197:VAL:CG1	2:F:198:THR:H	2.19	0.55
2:F:491:LEU:HD21	2:F:532:ILE:HD11	1.88	0.55
1:D:109:VAL:HG12	1:D:120:LEU:HD11	1.87	0.55
1:E:207:LYS:O	1:E:208:LEU:HD23	2.07	0.55
2:B:224:MET:HE1	2:B:230:ASP:HB3	1.86	0.55
1:E:113:PRO:CB	1:E:161:ALA:HB2	2.36	0.55
1:A:109:VAL:HG12	1:A:120:LEU:HD11	1.87	0.55
2:C:154:SER:HB2	1:D:21:MET:HB3	1.88	0.55
2:G:512:MET:SD	2:G:540:ALA:CB	2.95	0.55
2:F:462:THR:O	2:F:463:ARG:HD3	2.07	0.55
1:H:242:ILE:HD11	1:H:258:LEU:HD22	1.89	0.55
2:G:197:VAL:CG1	2:G:198:THR:H	2.19	0.55
2:C:210:ILE:HG22	2:C:459:PHE:CE2	2.41	0.55
2:C:332:ILE:N	2:C:332:ILE:HD12	2.21	0.55
2:B:151:ALA:HB1	2:B:159:LEU:CD1	2.33	0.55
2:F:381:TRP:CZ2	2:F:382:LEU:HD13	2.42	0.55
2:C:375:LEU:HB3	2:C:379:PHE:HD2	1.71	0.55
2:C:375:LEU:HB2	2:C:384:LEU:HD21	1.88	0.55
2:C:268:LEU:HD21	2:C:272:ILE:HD11	1.89	0.55
1:D:207:LYS:O	1:D:208:LEU:HD23	2.07	0.55
2:B:268:LEU:HD21	2:B:272:ILE:HD11	1.89	0.55
1:A:250:SER:O	1:A:252:THR:N	2.35	0.55
2:G:267:ARG:HH11	2:G:267:ARG:CG	2.10	0.54
2:B:512:MET:SD	2:B:540:ALA:HB2	2.46	0.54
2:G:268:LEU:HD21	2:G:272:ILE:HD11	1.89	0.54
1:E:145:ILE:HD13	1:E:194:TRP:CE3	2.43	0.54
1:D:190:LEU:HD13	1:D:207:LYS:HD3	1.89	0.54
2:C:207:TYR:CD2	2:C:504:GLU:HA	2.43	0.54
2:G:343:TRP:CZ3	2:G:350:ILE:HG21	2.42	0.54
1:D:79:TYR:HD1	1:D:105:SER:HB3	1.72	0.54
1:A:265:VAL:HA	1:A:281:GLY:HA3	1.89	0.54
1:E:242:ILE:HD13	1:E:297:TRP:CD1	2.43	0.54
1:D:190:LEU:HD22	1:D:209:GLU:HB3	1.90	0.54
2:B:156:GLY:O	2:B:157:SER:CB	2.55	0.54
2:B:484:ALA:O	2:B:485:GLN:HB3	2.07	0.54
2:F:491:LEU:O	2:F:494:SER:HB2	2.08	0.54
2:G:242:ASP:O	2:G:264:ARG:NH2	2.40	0.54
2:F:280:ILE:CG1	2:F:300:LEU:HD21	2.37	0.54
1:A:207:LYS:O	1:A:208:LEU:HD23	2.07	0.54
2:G:210:ILE:HD13	2:G:496:PHE:CG	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:477:PHE:CE2	2:B:493:VAL:HG21	2.43	0.54
2:C:194:ILE:HG12	2:C:492:PHE:CD2	2.42	0.54
1:D:60:VAL:HG13	1:D:77:CYS:O	2.08	0.54
1:H:265:VAL:HA	1:H:281:GLY:HA3	1.89	0.54
1:H:31:CYS:HB2	1:H:60:VAL:HB	1.88	0.54
2:C:451:TRP:HE1	2:C:474:THR:HG23	1.73	0.54
1:E:304:ASN:OD1	2:F:161:THR:HG21	2.08	0.54
1:E:60:VAL:HG13	1:E:77:CYS:O	2.08	0.54
1:D:41:ASP:OD1	1:D:41:ASP:C	2.46	0.54
2:G:382:LEU:HD12	2:G:385:LEU:HD23	1.90	0.54
1:H:291:GLU:HB3	1:H:297:TRP:CD2	2.42	0.54
2:C:138:ILE:HG22	2:C:139:MET:N	2.23	0.54
2:G:170:VAL:H	1:H:47:GLN:HE22	1.55	0.54
2:C:267:ARG:NH1	2:C:267:ARG:CG	2.71	0.54
2:F:512:MET:HA	2:F:540:ALA:HB1	1.90	0.54
2:G:284:ILE:HG12	2:G:296:LEU:CD1	2.37	0.54
2:G:367:GLU:O	2:G:367:GLU:HG3	2.08	0.54
2:C:482:GLU:CD	2:C:509:ARG:HH22	2.11	0.54
1:E:70:TYR:HE2	1:E:118:LEU:HB2	1.64	0.54
1:E:67:HIS:ND1	1:E:69:MET:HB3	2.23	0.54
1:D:67:HIS:ND1	1:D:69:MET:HB3	2.23	0.54
1:D:82:LYS:HG2	1:D:100:ALA:CB	2.35	0.54
2:F:375:LEU:HB2	2:F:384:LEU:HD21	1.90	0.54
1:D:265:VAL:HA	1:D:281:GLY:HA3	1.89	0.54
1:H:60:VAL:HG13	1:H:77:CYS:O	2.07	0.54
2:F:145:THR:HG22	2:F:146:ALA:N	2.23	0.54
2:B:145:THR:HG22	2:B:146:ALA:N	2.23	0.54
1:A:56:HIS:NE2	1:A:84:ILE:HD12	2.22	0.54
2:F:379:PHE:CD1	2:F:379:PHE:N	2.75	0.54
1:A:67:HIS:ND1	1:A:69:MET:HB3	2.23	0.54
1:H:79:TYR:HD1	1:H:105:SER:HB3	1.72	0.54
2:F:236:LEU:HD21	2:F:422:PHE:CE1	2.43	0.54
2:B:382:LEU:HD12	2:B:385:LEU:HD23	1.90	0.54
2:B:177:THR:OG1	2:B:483:PHE:CB	2.56	0.54
1:A:102:HIS:HE2	1:A:130:SER:CB	2.21	0.54
2:B:201:ALA:H	2:B:531:LYS:NZ	1.96	0.54
2:C:366:PHE:CZ	2:C:384:LEU:HD22	2.42	0.54
2:C:236:LEU:HD21	2:C:422:PHE:CE1	2.42	0.54
2:G:244:VAL:HG12	2:G:263:GLU:OE2	2.08	0.54
2:C:428:ASN:HA	2:C:463:ARG:HH12	1.73	0.54
2:C:197:VAL:CG1	2:C:198:THR:H	2.19	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:LYS:HG2	1:A:100:ALA:CB	2.34	0.53
1:A:179:ILE:HG21	1:A:181:ARG:NE	2.23	0.53
1:A:60:VAL:HG13	1:A:77:CYS:O	2.07	0.53
1:H:113:PRO:CB	1:H:161:ALA:HB2	2.38	0.53
2:G:241:PHE:CD2	2:G:457:LEU:HD21	2.43	0.53
2:G:495:CYS:C	2:G:497:LEU:H	2.11	0.53
1:A:49:LEU:HD12	1:A:50:ILE:N	2.16	0.53
1:E:205:GLU:HG2	1:E:251:ASN:ND2	2.22	0.53
2:B:159:LEU:HD12	2:B:160:LEU:H	1.74	0.53
2:C:142:ARG:HG3	1:D:61:TRP:CZ2	2.44	0.53
1:H:207:LYS:O	1:H:208:LEU:HD23	2.07	0.53
2:G:487:HIS:HA	2:G:490:SER:HB2	1.91	0.53
1:H:56:HIS:NE2	1:H:84:ILE:HD12	2.23	0.53
2:F:174:ARG:HG2	2:F:175:LEU:H	1.74	0.53
1:A:145:ILE:HD13	1:A:194:TRP:CZ3	2.43	0.53
2:F:272:ILE:HG23	2:F:382:LEU:HG	1.90	0.53
1:A:291:GLU:N	1:A:297:TRP:CE3	2.77	0.53
1:E:273:THR:HG21	2:F:479:ALA:HB2	1.89	0.53
2:B:291:ILE:HG22	2:B:353:ASN:HB2	1.90	0.53
1:D:245:CYS:SG	1:D:251:ASN:HB2	2.48	0.53
2:G:138:ILE:HG22	2:G:139:MET:N	2.22	0.53
1:H:78:SER:HB3	1:H:80:ASP:OD1	2.09	0.53
2:B:236:LEU:HD21	2:B:422:PHE:CE1	2.44	0.53
2:C:515:ILE:HD12	2:C:541:GLN:N	2.24	0.53
1:A:145:ILE:O	1:A:145:ILE:HG22	2.08	0.53
1:D:242:ILE:HD11	1:D:258:LEU:HB2	1.89	0.53
1:D:38:LYS:HB2	1:D:40:PHE:HE1	1.73	0.53
2:B:175:LEU:HD23	2:B:483:PHE:CE2	2.44	0.53
1:H:82:LYS:HG2	1:H:100:ALA:CB	2.34	0.53
2:F:382:LEU:HD12	2:F:385:LEU:HD23	1.90	0.53
2:C:208:PRO:HG3	2:C:530:LEU:O	2.08	0.53
1:D:263:ASP:HB3	1:D:282:GLY:HA2	1.91	0.53
1:H:67:HIS:ND1	1:H:69:MET:HB3	2.23	0.53
1:E:29:ALA:CB	1:E:39:ILE:HD13	2.39	0.53
2:B:291:ILE:HG22	2:B:353:ASN:CB	2.39	0.53
1:E:56:HIS:NE2	1:E:84:ILE:HD12	2.23	0.53
1:H:145:ILE:HG22	1:H:145:ILE:O	2.08	0.53
2:C:404:GLN:HG2	2:C:426:ALA:HB1	1.90	0.53
1:E:67:HIS:O	1:E:69:MET:N	2.42	0.52
2:C:149:THR:CG2	2:C:150:PHE:N	2.72	0.52
2:B:210:ILE:HD12	2:B:495:CYS:CB	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:49:LEU:HD12	1:H:50:ILE:N	2.16	0.52
1:E:38:LYS:HB2	1:E:40:PHE:HE1	1.73	0.52
2:C:280:ILE:HB	2:C:300:LEU:HD21	1.91	0.52
2:C:236:LEU:HD22	2:C:418:ILE:HG22	1.89	0.52
2:C:382:LEU:HD12	2:C:385:LEU:HD23	1.90	0.52
1:E:243:TRP:CD1	1:E:243:TRP:N	2.76	0.52
1:E:145:ILE:HG22	1:E:145:ILE:O	2.08	0.52
1:E:276:ILE:CG2	1:E:300:ILE:HD11	2.38	0.52
2:F:155:THR:O	2:F:513:ARG:NH1	2.39	0.52
2:B:331:ARG:HB2	2:B:332:ILE:HD12	1.91	0.52
1:D:56:HIS:NE2	1:D:84:ILE:HD12	2.24	0.52
1:H:102:HIS:HE2	1:H:130:SER:CB	2.21	0.52
1:A:78:SER:HB3	1:A:80:ASP:OD1	2.09	0.52
2:F:272:ILE:CG2	2:F:382:LEU:HG	2.39	0.52
2:F:284:ILE:HG12	2:F:296:LEU:CD1	2.38	0.52
1:H:292:SER:C	1:H:294:ASP:N	2.62	0.52
1:E:79:TYR:HD1	1:E:105:SER:HB3	1.73	0.52
2:B:359:LYS:HZ1	2:B:370:PHE:H	1.57	0.52
2:G:162:LYS:HZ3	1:H:15:MET:CE	2.22	0.52
2:B:224:MET:HE2	2:B:230:ASP:HB3	1.90	0.52
1:E:263:ASP:HB3	1:E:282:GLY:HA2	1.91	0.52
2:F:302:ASP:HA	2:G:304:VAL:HG21	1.92	0.52
1:D:197:GLU:O	1:D:198:GLU:HB2	2.08	0.52
1:D:290:LYS:CB	1:D:300:ILE:HD11	2.36	0.52
2:C:367:GLU:O	2:C:367:GLU:HG3	2.08	0.52
1:E:265:VAL:HA	1:E:281:GLY:HA3	1.90	0.52
1:D:67:HIS:O	1:D:69:MET:N	2.43	0.52
2:C:170:VAL:H	1:D:47:GLN:HE22	1.58	0.52
1:A:79:TYR:HD1	1:A:105:SER:HB3	1.72	0.52
1:H:29:ALA:HA	1:H:39:ILE:HD13	1.91	0.52
1:A:39:ILE:HD11	1:A:74:LEU:HD22	1.90	0.52
1:E:264:VAL:HG12	1:E:265:VAL:N	2.25	0.52
2:F:302:ASP:OD1	2:F:305:ARG:HB2	2.10	0.52
1:H:38:LYS:HB2	1:H:40:PHE:HE1	1.73	0.52
2:B:174:ARG:HG2	2:B:175:LEU:H	1.74	0.52
1:A:234:CYS:HB2	1:A:265:VAL:HB	1.91	0.52
2:F:367:GLU:HG3	2:F:367:GLU:O	2.08	0.52
1:H:263:ASP:HB3	1:H:282:GLY:HA2	1.91	0.52
1:E:292:SER:C	1:E:294:ASP:H	2.13	0.52
2:F:175:LEU:HD23	2:F:483:PHE:CE2	2.44	0.52
2:B:181:ARG:HD2	2:B:448:GLN:OE1	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:258:LEU:CD1	1:H:297:TRP:HB2	2.40	0.52
1:A:220:TRP:CH2	1:A:229:SER:HB2	2.45	0.52
1:H:29:ALA:CB	1:H:39:ILE:HD13	2.39	0.52
1:D:145:ILE:O	1:D:145:ILE:HG22	2.09	0.52
1:E:78:SER:HB3	1:E:80:ASP:OD1	2.09	0.52
2:B:471:ASP:OD1	2:B:497:LEU:HA	2.10	0.52
1:A:28:LEU:HD13	2:B:172:ILE:HD11	1.92	0.52
2:C:375:LEU:HB3	2:C:379:PHE:CD2	2.44	0.52
1:E:220:TRP:CH2	1:E:229:SER:HB2	2.45	0.52
1:H:109:VAL:HG12	1:H:110:CYS:N	2.25	0.52
2:F:304:VAL:HG21	2:G:302:ASP:HA	1.92	0.52
2:G:372:LEU:O	2:G:375:LEU:HG	2.10	0.52
1:E:273:THR:CG2	2:F:479:ALA:CB	2.85	0.52
1:E:273:THR:CG2	2:F:479:ALA:HB2	2.40	0.52
2:B:367:GLU:HG3	2:B:367:GLU:O	2.08	0.52
1:A:67:HIS:O	1:A:69:MET:N	2.43	0.52
1:H:67:HIS:O	1:H:69:MET:N	2.43	0.52
2:B:372:LEU:O	2:B:375:LEU:HG	2.10	0.52
2:F:372:LEU:O	2:F:375:LEU:HG	2.10	0.52
2:B:421:ILE:HD11	2:B:449:PHE:CZ	2.44	0.52
2:G:175:LEU:HD12	2:G:176:PRO:N	2.24	0.52
2:F:236:LEU:HD23	2:F:421:ILE:HG21	1.92	0.52
1:D:220:TRP:CH2	1:D:229:SER:HB2	2.45	0.52
2:G:412:LEU:N	2:G:412:LEU:CD1	2.71	0.52
2:G:148:TYR:HB2	1:H:266:TRP:CD2	2.44	0.52
1:E:29:ALA:HA	1:E:39:ILE:HD13	1.91	0.52
2:F:412:LEU:HD12	2:F:412:LEU:H	1.75	0.52
2:G:420:VAL:HG11	2:G:445:LEU:HD11	1.92	0.52
1:D:292:SER:C	1:D:294:ASP:H	2.13	0.52
2:G:138:ILE:HD11	1:H:79:TYR:CD2	2.45	0.51
1:D:78:SER:HB3	1:D:80:ASP:OD1	2.09	0.51
2:C:242:ASP:O	2:C:264:ARG:NH2	2.42	0.51
1:E:28:LEU:HD13	2:F:172:ILE:HD11	1.92	0.51
2:C:175:LEU:HD12	2:C:176:PRO:N	2.24	0.51
1:D:151:ILE:HB	1:D:187:CYS:CB	2.38	0.51
2:C:340:LEU:HD21	2:C:358:TYR:HB3	1.92	0.51
1:H:23:TYR:CD2	1:H:24:TYR:CD1	2.97	0.51
2:G:210:ILE:HG22	2:G:459:PHE:CE2	2.45	0.51
1:A:264:VAL:HG12	1:A:265:VAL:N	2.25	0.51
1:A:263:ASP:HB3	1:A:282:GLY:HA2	1.91	0.51
1:D:110:CYS:O	1:D:120:LEU:HD12	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:522:THR:HG21	2:C:526:ILE:CD1	2.41	0.51
1:H:268:VAL:HG13	1:H:277:LEU:HD11	1.93	0.51
2:G:487:HIS:O	2:G:488:GLY:C	2.47	0.51
1:E:110:CYS:O	1:E:120:LEU:HD12	2.10	0.51
1:D:290:LYS:HB2	1:D:300:ILE:HD12	1.93	0.51
1:H:264:VAL:HG12	1:H:265:VAL:N	2.25	0.51
1:D:102:HIS:HE2	1:D:130:SER:CB	2.22	0.51
1:D:109:VAL:HG12	1:D:110:CYS:N	2.25	0.51
2:G:385:LEU:HD21	2:G:422:PHE:CE2	2.45	0.51
1:A:258:LEU:CD1	1:A:297:TRP:CB	2.89	0.51
1:E:234:CYS:HB2	1:E:265:VAL:HB	1.93	0.51
2:C:551:TYR:HD1	1:D:27:ARG:HE	1.57	0.51
1:H:157:SER:HB2	1:H:218:VAL:O	2.11	0.51
2:F:548:GLU:O	2:F:552:LEU:HG	2.10	0.51
2:B:400:GLU:HG3	2:B:425:TYR:CZ	2.46	0.51
2:F:210:ILE:CD1	2:F:495:CYS:HB2	2.40	0.51
2:C:449:PHE:O	2:C:450:CYS:C	2.49	0.51
2:G:366:PHE:CZ	2:G:387:LEU:HD12	2.46	0.51
2:G:236:LEU:HD21	2:G:422:PHE:CE1	2.46	0.51
2:G:175:LEU:CD1	2:G:176:PRO:CD	2.88	0.51
2:F:320:VAL:HG22	2:G:263:GLU:HA	1.92	0.51
2:B:475:PHE:CE2	2:B:497:LEU:HD21	2.46	0.51
2:C:170:VAL:CG1	2:C:171:SER:N	2.74	0.51
1:E:41:ASP:HB2	1:E:50:ILE:CD1	2.33	0.51
2:C:475:PHE:HE2	2:C:497:LEU:HD11	1.74	0.51
1:A:292:SER:C	1:A:294:ASP:H	2.13	0.51
1:E:109:VAL:HG12	1:E:110:CYS:N	2.26	0.51
1:E:17:HIS:ND1	2:F:148:TYR:CE2	2.76	0.51
2:C:175:LEU:CD1	2:C:176:PRO:CD	2.88	0.51
1:H:220:TRP:CH2	1:H:229:SER:HB2	2.45	0.51
1:D:23:TYR:CD2	1:D:24:TYR:CD1	2.98	0.51
1:D:179:ILE:HG21	1:D:181:ARG:NE	2.23	0.51
2:F:331:ARG:HB2	2:F:332:ILE:HD12	1.91	0.51
2:F:179:LEU:HD11	2:F:184:LEU:HD13	1.91	0.51
2:G:462:THR:O	2:G:463:ARG:CD	2.53	0.51
2:C:216:LEU:HD13	2:C:243:PRO:HD2	1.93	0.51
2:C:385:LEU:HA	2:C:406:HIS:CE1	2.46	0.51
1:H:179:ILE:HG21	1:H:181:ARG:NE	2.23	0.51
2:G:331:ARG:HB2	2:G:332:ILE:HD12	1.92	0.51
2:F:196:LYS:HD2	2:F:214:SER:O	2.11	0.51
2:C:479:ALA:CB	1:D:273:THR:HG22	2.35	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:VAL:HG12	1:A:110:CYS:N	2.25	0.51
1:D:111:TRP:CD2	1:D:120:LEU:HD13	2.47	0.51
2:G:267:ARG:NH1	2:G:267:ARG:CG	2.71	0.51
1:A:38:LYS:HB2	1:A:40:PHE:HE1	1.74	0.51
2:C:366:PHE:CE2	2:C:384:LEU:HD22	2.46	0.51
2:C:199:ILE:HD12	2:C:530:LEU:HA	1.92	0.51
1:A:98:GLU:HG2	1:A:99:HIS:N	2.26	0.51
2:C:210:ILE:HD13	2:C:496:PHE:CG	2.46	0.51
2:F:398:SER:OG	2:F:401:SER:HB3	2.11	0.51
1:A:268:VAL:HG13	1:A:277:LEU:HD11	1.93	0.50
1:A:110:CYS:O	1:A:120:LEU:HD12	2.10	0.50
2:G:170:VAL:CG1	2:G:171:SER:N	2.74	0.50
1:A:28:LEU:CD2	2:B:170:VAL:HG11	2.35	0.50
1:A:185:GLY:HA3	1:A:215:VAL:HG11	1.91	0.50
2:C:457:LEU:HD13	2:C:463:ARG:HG3	1.93	0.50
1:D:264:VAL:HG12	1:D:265:VAL:N	2.25	0.50
2:F:434:LEU:O	2:F:438:VAL:HG23	2.11	0.50
2:G:191:ASP:OD1	2:G:529:ARG:NH1	2.44	0.50
2:F:482:GLU:CD	2:F:509:ARG:HH22	2.14	0.50
2:B:196:LYS:HD2	2:B:214:SER:O	2.11	0.50
1:E:111:TRP:CD2	1:E:120:LEU:HD13	2.46	0.50
2:B:208:PRO:HB3	2:B:531:LYS:HB3	1.93	0.50
2:C:153:PHE:CE2	1:D:278:ALA:HB2	2.46	0.50
1:A:230:THR:CG2	1:A:242:ILE:HG22	2.42	0.50
2:C:431:THR:HG21	2:C:463:ARG:HB3	1.93	0.50
2:C:471:ASP:OD2	2:C:498:ASN:ND2	2.44	0.50
2:F:347:GLY:O	2:F:350:ILE:HD12	2.12	0.50
1:H:16:ILE:HD12	1:H:30:THR:CG2	2.41	0.50
1:E:92:THR:HG22	1:E:94:GLU:HG3	1.93	0.50
2:F:486:LEU:H	2:F:486:LEU:HD12	1.76	0.50
1:A:111:TRP:CD2	1:A:120:LEU:HD13	2.46	0.50
2:C:372:LEU:O	2:C:375:LEU:HG	2.10	0.50
2:C:276:ILE:HD13	2:C:383:CYS:CA	2.38	0.50
1:E:98:GLU:HG2	1:E:99:HIS:N	2.26	0.50
2:G:184:LEU:HD21	2:G:448:GLN:HE22	1.76	0.50
2:B:174:ARG:HG2	2:B:175:LEU:N	2.27	0.50
2:B:477:PHE:HD2	2:B:493:VAL:HG11	1.75	0.50
1:A:40:PHE:CZ	2:B:168:SER:CB	2.89	0.50
2:B:241:PHE:O	2:B:242:ASP:C	2.49	0.50
2:B:215:LEU:O	2:B:456:THR:HG23	2.11	0.50
2:B:236:LEU:HD23	2:B:421:ILE:HG21	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:359:LYS:HZ1	2:G:370:PHE:H	1.58	0.50
2:C:142:ARG:NH2	1:D:107:ASN:OD1	2.44	0.50
1:H:98:GLU:HG2	1:H:99:HIS:N	2.27	0.50
2:G:196:LYS:HD2	2:G:214:SER:O	2.12	0.50
1:E:102:HIS:HE2	1:E:130:SER:CB	2.21	0.50
2:F:159:LEU:HD12	2:F:160:LEU:H	1.74	0.50
2:G:409:LYS:C	2:G:410:PHE:CD2	2.85	0.50
1:H:111:TRP:CD2	1:H:120:LEU:HD13	2.46	0.50
2:G:474:THR:CG2	2:G:493:VAL:HG12	2.42	0.50
2:G:474:THR:HG23	2:G:493:VAL:HG12	1.93	0.50
2:C:331:ARG:HB2	2:C:332:ILE:HD12	1.91	0.50
2:B:255:VAL:HG12	2:B:256:LYS:N	2.27	0.50
2:F:451:TRP:HZ2	2:F:496:PHE:CD1	2.30	0.50
1:A:16:ILE:HD12	1:A:30:THR:CG2	2.41	0.50
1:H:43:ARG:O	1:H:44:ASN:HB2	2.11	0.50
1:E:179:ILE:HG21	1:E:181:ARG:NE	2.23	0.50
1:H:110:CYS:O	1:H:120:LEU:HD12	2.11	0.50
2:C:448:GLN:HB2	2:C:477:PHE:CE1	2.46	0.50
1:D:245:CYS:HB2	1:D:253:TRP:CE3	2.46	0.50
1:H:92:THR:HG22	1:H:94:GLU:HG3	1.93	0.50
1:A:43:ARG:O	1:A:44:ASN:HB2	2.11	0.50
1:A:49:LEU:CD1	1:A:50:ILE:H	2.20	0.50
1:E:258:LEU:HD13	1:E:297:TRP:HB2	1.92	0.50
2:B:215:LEU:HD22	2:B:452:TYR:OH	2.11	0.50
1:E:43:ARG:O	1:E:44:ASN:HB2	2.11	0.50
2:C:434:LEU:O	2:C:438:VAL:HG23	2.12	0.50
1:E:205:GLU:HG2	1:E:251:ASN:HD21	1.77	0.50
2:B:449:PHE:O	2:B:450:CYS:C	2.49	0.50
1:H:230:THR:HG21	1:H:242:ILE:HG23	1.92	0.50
2:F:332:ILE:H	2:F:332:ILE:CD1	2.25	0.50
2:G:380:SER:OG	2:G:382:LEU:N	2.45	0.50
2:G:175:LEU:HD12	2:G:176:PRO:CD	2.42	0.50
2:F:255:VAL:HG12	2:F:256:LYS:N	2.27	0.50
1:D:98:GLU:HG2	1:D:99:HIS:N	2.26	0.50
1:E:23:TYR:CD2	1:E:24:TYR:CD1	2.98	0.50
2:C:184:LEU:O	2:C:486:LEU:HD13	2.12	0.50
2:G:436:LYS:HE3	2:G:469:THR:OG1	2.12	0.50
2:C:409:LYS:C	2:C:410:PHE:CD2	2.85	0.50
2:G:255:VAL:HG12	2:G:256:LYS:N	2.27	0.50
2:B:434:LEU:O	2:B:438:VAL:HG23	2.11	0.50
2:C:479:ALA:HA	1:D:273:THR:HG21	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:267:ARG:CG	2:B:267:ARG:NH1	2.71	0.49
2:F:372:LEU:HD22	2:F:375:LEU:HD11	1.94	0.49
2:F:224:MET:HE2	2:F:230:ASP:HB3	1.94	0.49
2:C:477:PHE:CD2	2:C:493:VAL:HG21	2.47	0.49
2:C:196:LYS:HD2	2:C:214:SER:O	2.12	0.49
2:F:174:ARG:HG2	2:F:175:LEU:N	2.27	0.49
1:E:16:ILE:HD12	1:E:30:THR:CG2	2.41	0.49
1:A:30:THR:CG2	1:A:31:CYS:N	2.75	0.49
2:F:385:LEU:CA	2:F:406:HIS:CE1	2.95	0.49
2:F:449:PHE:O	2:F:450:CYS:C	2.49	0.49
1:A:27:ARG:HE	2:B:551:TYR:HD1	1.60	0.49
1:E:268:VAL:HG13	1:E:277:LEU:HD11	1.93	0.49
1:D:92:THR:HG22	1:D:94:GLU:HG3	1.93	0.49
2:G:449:PHE:O	2:G:450:CYS:C	2.49	0.49
2:B:244:VAL:HG23	2:B:264:ARG:NH2	2.24	0.49
2:C:332:ILE:H	2:C:332:ILE:CD1	2.25	0.49
1:D:241:PHE:CD2	1:D:257:LEU:HA	2.48	0.49
2:B:409:LYS:C	2:B:410:PHE:CD2	2.86	0.49
2:C:255:VAL:HG12	2:C:256:LYS:N	2.27	0.49
2:G:290:GLU:O	2:G:293:GLN:HB2	2.12	0.49
1:A:111:TRP:CE2	1:A:120:LEU:HD13	2.48	0.49
1:E:242:ILE:HD11	1:E:258:LEU:HD22	1.94	0.49
1:H:287:THR:HG22	1:H:299:CYS:SG	2.52	0.49
2:F:404:GLN:CG	2:F:426:ALA:HB1	2.34	0.49
2:F:409:LYS:C	2:F:410:PHE:CD2	2.86	0.49
2:C:175:LEU:HD12	2:C:176:PRO:CD	2.42	0.49
2:B:525:HIS:O	2:B:527:LEU:N	2.45	0.49
1:E:82:LYS:HG2	1:E:100:ALA:CB	2.34	0.49
2:F:475:PHE:CE2	2:F:497:LEU:HD21	2.44	0.49
2:G:170:VAL:CG1	2:G:171:SER:H	2.25	0.49
2:C:372:LEU:HD22	2:C:375:LEU:HD11	1.94	0.49
2:G:356:LYS:O	2:G:359:LYS:HB3	2.12	0.49
2:F:217:PHE:HE2	2:F:449:PHE:CE1	2.31	0.49
1:E:190:LEU:HD22	1:E:209:GLU:HB3	1.94	0.49
2:B:340:LEU:HD21	2:B:358:TYR:HB3	1.94	0.49
2:B:332:ILE:H	2:B:332:ILE:CD1	2.25	0.49
1:D:240:VAL:O	1:D:258:LEU:HB3	2.11	0.49
1:D:43:ARG:O	1:D:44:ASN:HB2	2.11	0.49
2:F:210:ILE:HG22	2:F:459:PHE:HE2	1.78	0.49
1:H:106:VAL:HA	1:H:124:SER:HA	1.94	0.49
2:C:170:VAL:CG1	2:C:171:SER:H	2.25	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:409:LYS:C	2:G:410:PHE:HD2	2.16	0.49
2:F:145:THR:C	2:F:147:SER:H	2.15	0.49
2:F:191:ASP:OD1	2:F:529:ARG:NH1	2.45	0.49
1:D:157:SER:HB2	1:D:218:VAL:O	2.13	0.49
2:C:252:ASN:OD1	2:C:253:ASP:N	2.46	0.49
2:B:548:GLU:O	2:B:552:LEU:HG	2.13	0.49
1:A:192:LYS:HD3	1:A:204:GLU:OE1	2.13	0.49
2:B:290:GLU:O	2:B:293:GLN:HB2	2.13	0.49
1:A:92:THR:HG22	1:A:94:GLU:HG3	1.93	0.49
1:D:16:ILE:HD12	1:D:30:THR:CG2	2.41	0.49
2:B:515:ILE:HD12	2:B:541:GLN:N	2.26	0.49
2:C:356:LYS:O	2:C:359:LYS:HB3	2.13	0.49
2:C:280:ILE:HG13	2:C:300:LEU:CD2	2.37	0.49
1:D:242:ILE:HG12	1:D:297:TRP:NE1	2.28	0.49
1:H:112:ALA:HA	1:H:158:TRP:CD2	2.48	0.49
2:F:525:HIS:O	2:F:527:LEU:N	2.46	0.49
2:G:152:LYS:NZ	1:H:62:GLN:HE21	2.11	0.49
2:F:290:GLU:O	2:F:293:GLN:HB2	2.13	0.49
1:D:70:TYR:HD1	1:D:70:TYR:N	2.11	0.49
2:B:280:ILE:HD11	2:B:383:CYS:SG	2.53	0.49
2:B:170:VAL:O	2:B:170:VAL:HG12	2.12	0.49
2:F:356:LYS:O	2:F:359:LYS:HB3	2.13	0.49
1:D:49:LEU:CD1	1:D:50:ILE:H	2.21	0.49
2:C:224:MET:HE1	2:C:230:ASP:HB3	1.93	0.49
1:H:111:TRP:CE2	1:H:120:LEU:HD13	2.48	0.49
1:A:56:HIS:CE1	1:A:84:ILE:HD12	2.48	0.49
2:F:182:LYS:O	2:F:185:PHE:HD1	1.96	0.49
1:A:157:SER:HB2	1:A:218:VAL:O	2.12	0.49
2:F:135:ALA:O	2:F:139:MET:HB3	2.12	0.49
1:A:70:TYR:HD1	1:A:70:TYR:N	2.10	0.49
1:E:291:GLU:N	1:E:297:TRP:CE3	2.80	0.49
2:G:267:ARG:NH1	2:G:267:ARG:HG3	2.14	0.49
1:D:268:VAL:HG13	1:D:277:LEU:HD11	1.92	0.49
2:B:145:THR:C	2:B:147:SER:H	2.15	0.49
2:B:140:LYS:C	2:B:142:ARG:H	2.16	0.49
2:C:290:GLU:O	2:C:293:GLN:HB2	2.13	0.49
2:C:385:LEU:HD21	2:C:422:PHE:CE2	2.48	0.49
2:B:236:LEU:HD22	2:B:418:ILE:HG22	1.95	0.49
2:G:372:LEU:HD22	2:G:375:LEU:HD11	1.95	0.49
2:C:145:THR:HG22	2:C:146:ALA:N	2.28	0.49
2:C:491:LEU:HD13	2:C:510:LEU:HD23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:208:PRO:HG3	2:G:530:LEU:O	2.12	0.49
2:C:246:TYR:CD1	2:C:247:PRO:HD2	2.48	0.49
1:D:164:PRO:CD	1:D:176:PRO:HB2	2.43	0.49
1:H:70:TYR:HD1	1:H:70:TYR:N	2.11	0.48
1:H:49:LEU:CD1	1:H:50:ILE:H	2.20	0.48
1:E:28:LEU:HD11	2:F:160:LEU:CD1	2.40	0.48
2:G:145:THR:HG22	2:G:146:ALA:N	2.28	0.48
1:E:208:LEU:HD22	1:E:243:TRP:CZ3	2.48	0.48
1:H:244:THR:CG2	1:H:245:CYS:H	2.23	0.48
2:C:199:ILE:HG22	2:C:200:GLU:N	2.27	0.48
2:G:434:LEU:O	2:G:438:VAL:HG23	2.12	0.48
2:B:135:ALA:O	2:B:139:MET:HB3	2.13	0.48
2:F:207:TYR:CZ	2:F:504:GLU:HG3	2.49	0.48
2:B:238:SER:O	2:B:242:ASP:CB	2.60	0.48
1:H:30:THR:CG2	1:H:31:CYS:N	2.75	0.48
2:C:182:LYS:O	2:C:185:PHE:HD1	1.96	0.48
1:E:113:PRO:HB2	1:E:161:ALA:HB2	1.95	0.48
2:B:409:LYS:C	2:B:410:PHE:HD2	2.16	0.48
2:B:436:LYS:HE3	2:B:469:THR:OG1	2.13	0.48
2:F:487:HIS:HD2	2:F:517:LEU:HD23	1.77	0.48
2:C:492:PHE:HD1	2:C:492:PHE:C	2.16	0.48
1:E:30:THR:CG2	1:E:31:CYS:N	2.75	0.48
1:D:30:THR:CG2	1:D:31:CYS:N	2.75	0.48
1:E:240:VAL:HB	1:E:258:LEU:HB3	1.96	0.48
1:D:74:LEU:O	1:D:86:TRP:HD1	1.96	0.48
1:D:182:PHE:HE2	1:D:202:TRP:CD1	2.31	0.48
1:D:112:ALA:HA	1:D:158:TRP:CD2	2.48	0.48
2:C:398:SER:HB3	2:C:401:SER:HB3	1.96	0.48
2:F:142:ARG:HG3	2:F:142:ARG:HH11	1.79	0.48
2:B:485:GLN:O	2:B:485:GLN:HG3	2.13	0.48
2:B:372:LEU:HD22	2:B:375:LEU:HD11	1.95	0.48
2:F:215:LEU:HD13	2:F:452:TYR:HE1	1.78	0.48
2:F:515:ILE:HD12	2:F:541:GLN:N	2.28	0.48
1:H:220:TRP:NE1	1:H:231:ILE:HD11	2.28	0.48
2:C:525:HIS:O	2:C:527:LEU:N	2.46	0.48
2:G:332:ILE:H	2:G:332:ILE:CD1	2.25	0.48
1:E:112:ALA:HA	1:E:158:TRP:CD2	2.48	0.48
2:C:423:GLN:HB3	2:C:434:LEU:HD21	1.94	0.48
1:A:164:PRO:CD	1:A:176:PRO:HB2	2.44	0.48
1:A:288:LEU:HB2	1:A:300:ILE:HG13	1.95	0.48
2:B:356:LYS:O	2:B:359:LYS:HB3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:237:SER:OG	2:F:421:ILE:HD13	2.13	0.48
1:A:220:TRP:NE1	1:A:231:ILE:HD11	2.28	0.48
1:E:47:GLN:OE1	2:F:167:LYS:N	2.46	0.48
2:B:294:ILE:HD11	2:B:310:ALA:HA	1.95	0.48
2:G:332:ILE:O	2:G:333:ARG:C	2.52	0.48
1:D:106:VAL:HA	1:D:124:SER:HA	1.94	0.48
1:D:111:TRP:CE2	1:D:120:LEU:HD13	2.48	0.48
2:F:207:TYR:CE2	2:F:504:GLU:HA	2.45	0.48
2:F:267:ARG:NH1	2:F:267:ARG:CG	2.71	0.48
1:E:40:PHE:CZ	2:F:168:SER:CB	2.93	0.48
2:F:409:LYS:C	2:F:410:PHE:HD2	2.16	0.48
1:A:73:ILE:HG22	1:A:74:LEU:N	2.28	0.48
1:A:74:LEU:O	1:A:86:TRP:HD1	1.97	0.48
1:D:242:ILE:HG12	1:D:297:TRP:CZ2	2.48	0.48
2:C:409:LYS:C	2:C:410:PHE:HD2	2.16	0.48
2:C:409:LYS:O	2:C:410:PHE:HD2	1.97	0.48
2:F:241:PHE:CD2	2:F:457:LEU:HD21	2.48	0.48
2:G:394:ILE:O	2:G:397:TYR:CE1	2.66	0.48
2:G:210:ILE:HD11	2:G:495:CYS:HB3	1.93	0.48
2:B:485:GLN:HE21	2:B:517:LEU:CD2	2.26	0.48
2:F:170:VAL:HG12	2:F:170:VAL:O	2.13	0.48
1:D:274:ALA:O	1:D:275:ASN:CB	2.61	0.48
1:A:23:TYR:CD2	1:A:24:TYR:CD1	2.98	0.48
2:C:524:ASP:O	2:C:524:ASP:CG	2.51	0.48
1:A:112:ALA:HA	1:A:158:TRP:CD2	2.48	0.48
2:F:525:HIS:CD2	2:F:529:ARG:HG3	2.49	0.48
2:G:492:PHE:O	2:G:495:CYS:HB2	2.14	0.48
1:E:70:TYR:N	1:E:70:TYR:HD1	2.10	0.48
2:C:525:HIS:CD2	2:C:529:ARG:HG3	2.49	0.48
1:H:16:ILE:HA	1:H:32:SER:HB3	1.96	0.48
1:A:112:ALA:HB2	1:A:158:TRP:CH2	2.49	0.48
1:H:112:ALA:HB2	1:H:158:TRP:CH2	2.49	0.48
2:B:182:LYS:O	2:B:185:PHE:HD1	1.96	0.48
2:F:448:GLN:HB2	2:F:477:PHE:CE1	2.48	0.48
2:F:485:GLN:O	2:F:487:HIS:CG	2.67	0.48
1:E:106:VAL:HA	1:E:124:SER:HA	1.94	0.48
1:E:111:TRP:CE2	1:E:120:LEU:HD13	2.48	0.48
1:A:284:ASN:HA	2:B:149:THR:OG1	2.12	0.48
2:B:199:ILE:HG22	2:B:200:GLU:N	2.27	0.48
2:B:471:ASP:OD2	2:B:498:ASN:ND2	2.37	0.48
1:E:215:VAL:HA	1:E:235:SER:HB3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:213:ASP:OD1	1:D:214:TRP:N	2.38	0.48
2:C:135:ALA:O	2:C:139:MET:HG3	2.14	0.48
2:C:297:TYR:CE2	2:C:305:ARG:HB3	2.48	0.48
2:F:364:SER:CB	2:F:394:ILE:HG12	2.42	0.48
2:G:199:ILE:HG22	2:G:200:GLU:N	2.27	0.48
1:D:112:ALA:HB2	1:D:158:TRP:CH2	2.49	0.48
2:G:210:ILE:CD1	2:G:496:PHE:CD1	2.97	0.48
1:A:106:VAL:HA	1:A:124:SER:HA	1.95	0.48
2:B:299:LEU:HD13	2:B:379:PHE:HE2	1.79	0.48
1:D:16:ILE:HA	1:D:32:SER:HB3	1.96	0.48
2:G:276:ILE:O	2:G:276:ILE:HG22	2.14	0.48
2:C:291:ILE:HG22	2:C:353:ASN:HB3	1.95	0.48
2:G:284:ILE:HD13	2:G:297:TYR:HE1	1.78	0.48
2:B:332:ILE:O	2:B:333:ARG:C	2.52	0.48
2:C:451:TRP:CE2	2:C:493:VAL:HG13	2.49	0.48
2:B:409:LYS:O	2:B:410:PHE:HD2	1.97	0.48
1:E:164:PRO:CD	1:E:176:PRO:HB2	2.44	0.48
2:B:487:HIS:CD2	2:B:517:LEU:CD2	2.91	0.47
1:A:234:CYS:SG	1:A:268:VAL:HG23	2.54	0.47
2:B:142:ARG:HH11	2:B:142:ARG:HG3	1.79	0.47
1:A:17:HIS:ND1	2:B:148:TYR:CE2	2.82	0.47
2:B:532:ILE:CG2	2:B:533:PRO:HD2	2.44	0.47
2:F:199:ILE:HG22	2:F:200:GLU:N	2.27	0.47
2:B:217:PHE:HZ	2:B:453:LEU:HD23	1.77	0.47
2:G:409:LYS:O	2:G:410:PHE:HD2	1.97	0.47
2:F:215:LEU:HD22	2:F:452:TYR:OH	2.14	0.47
1:A:258:LEU:CD1	1:A:297:TRP:HB2	2.43	0.47
2:C:495:CYS:C	2:C:497:LEU:H	2.17	0.47
2:G:283:LYS:HZ3	2:G:378:GLU:HB2	1.77	0.47
1:A:18:ASP:OD2	2:B:152:LYS:NZ	2.43	0.47
2:F:409:LYS:O	2:F:410:PHE:HD2	1.97	0.47
2:F:190:LEU:HD13	2:F:489:HIS:ND1	2.29	0.47
1:E:276:ILE:HG21	1:E:300:ILE:HD11	1.96	0.47
1:E:112:ALA:HB2	1:E:158:TRP:CH2	2.49	0.47
2:B:174:ARG:NH2	2:B:485:GLN:OE1	2.47	0.47
2:C:190:LEU:HB2	2:C:489:HIS:CE1	2.48	0.47
2:F:471:ASP:OD1	2:F:497:LEU:HA	2.14	0.47
1:H:189:ASN:OD1	1:H:213:ASP:C	2.52	0.47
2:C:299:LEU:HD22	2:C:383:CYS:SG	2.54	0.47
2:C:471:ASP:OD1	2:C:497:LEU:CA	2.59	0.47
2:G:284:ILE:HD13	2:G:297:TYR:CD1	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:215:LEU:HD22	2:G:452:TYR:OH	2.15	0.47
1:H:274:ALA:O	1:H:275:ASN:CB	2.62	0.47
1:D:56:HIS:CE1	1:D:84:ILE:HD12	2.49	0.47
2:G:525:HIS:O	2:G:527:LEU:N	2.47	0.47
2:F:543:LEU:O	2:F:546:ARG:HB3	2.14	0.47
1:H:215:VAL:HA	1:H:235:SER:HB3	1.96	0.47
2:F:370:PHE:O	2:F:371:SER:O	2.32	0.47
2:C:370:PHE:O	2:C:371:SER:O	2.33	0.47
1:D:220:TRP:NE1	1:D:231:ILE:HD11	2.29	0.47
1:E:74:LEU:O	1:E:86:TRP:HD1	1.96	0.47
1:H:56:HIS:CE1	1:H:84:ILE:HD12	2.49	0.47
1:D:251:ASN:ND2	1:D:253:TRP:HE1	2.13	0.47
2:G:525:HIS:CD2	2:G:529:ARG:HG3	2.49	0.47
2:B:149:THR:O	2:B:150:PHE:HB3	2.15	0.47
2:G:135:ALA:O	2:G:139:MET:HG3	2.14	0.47
2:F:359:LYS:HZ1	2:F:370:PHE:H	1.62	0.47
2:C:217:PHE:HE2	2:C:449:PHE:CE1	2.32	0.47
2:B:215:LEU:HD13	2:B:452:TYR:HE1	1.78	0.47
2:C:276:ILE:O	2:C:276:ILE:HG22	2.14	0.47
2:G:370:PHE:O	2:G:371:SER:O	2.33	0.47
2:C:522:THR:O	2:C:523:ASN:OD1	2.31	0.47
1:H:74:LEU:O	1:H:86:TRP:HD1	1.97	0.47
1:E:182:PHE:CG	1:E:182:PHE:O	2.68	0.47
2:F:332:ILE:O	2:F:333:ARG:C	2.52	0.47
2:C:332:ILE:O	2:C:333:ARG:C	2.52	0.47
2:B:525:HIS:CD2	2:B:529:ARG:HG3	2.49	0.47
1:H:129:ILE:HG22	1:H:129:ILE:O	2.15	0.47
2:F:140:LYS:C	2:F:142:ARG:H	2.16	0.47
2:B:425:TYR:O	2:B:463:ARG:NH2	2.47	0.47
1:H:79:TYR:HD1	1:H:105:SER:CB	2.28	0.47
2:B:237:SER:OG	2:B:421:ILE:HD13	2.15	0.47
2:C:497:LEU:HD12	2:C:503:ALA:HA	1.97	0.47
1:H:73:ILE:HG22	1:H:74:LEU:N	2.30	0.47
2:C:152:LYS:HZ2	1:D:62:GLN:HE21	1.62	0.47
2:B:145:THR:HG22	2:B:147:SER:N	2.29	0.47
1:A:16:ILE:HA	1:A:32:SER:HB3	1.96	0.47
2:B:280:ILE:CG1	2:B:300:LEU:HD21	2.45	0.47
1:E:291:GLU:HA	1:E:297:TRP:HA	1.96	0.47
1:H:280:SER:HA	1:H:286:VAL:HG22	1.96	0.47
2:G:172:ILE:CD1	1:H:42:VAL:HG21	2.44	0.47
1:D:79:TYR:HD1	1:D:105:SER:CB	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:164:ILE:CG2	2:B:164:ILE:O	2.63	0.47
2:B:515:ILE:HD11	2:B:540:ALA:CB	2.35	0.47
2:C:276:ILE:HG21	2:C:383:CYS:SG	2.55	0.47
2:G:271:TRP:HE3	2:G:272:ILE:HG12	1.80	0.47
2:F:217:PHE:HA	2:F:452:TYR:HE2	1.78	0.47
2:B:323:SER:OG	2:C:262:LYS:HE2	2.14	0.47
1:A:240:VAL:HB	1:A:258:LEU:HB3	1.97	0.47
1:E:220:TRP:NE1	1:E:231:ILE:HD11	2.28	0.47
1:E:27:ARG:HH12	1:E:93:TRP:HZ2	1.62	0.47
1:A:27:ARG:HH12	1:A:93:TRP:HZ2	1.62	0.47
2:G:474:THR:HG23	2:G:493:VAL:CG1	2.45	0.47
1:E:56:HIS:CE1	1:E:84:ILE:HD12	2.49	0.47
2:G:182:LYS:O	2:G:185:PHE:HD1	1.96	0.47
2:F:177:THR:CG2	2:F:179:LEU:HB3	2.43	0.47
1:E:16:ILE:HA	1:E:32:SER:HB3	1.96	0.47
1:A:241:PHE:HD2	1:A:257:LEU:HA	1.80	0.47
2:C:199:ILE:HD13	2:C:530:LEU:HA	1.95	0.47
1:H:145:ILE:HD11	1:H:202:TRP:HB2	1.97	0.47
1:H:27:ARG:HH12	1:H:93:TRP:HZ2	1.63	0.47
2:G:162:LYS:HZ3	1:H:15:MET:HE1	1.78	0.47
2:F:207:TYR:CE1	2:F:504:GLU:HG3	2.50	0.47
2:C:209:GLN:HG2	2:C:497:LEU:O	2.15	0.47
1:D:73:ILE:HG22	1:D:74:LEU:N	2.30	0.47
2:F:291:ILE:HG22	2:F:353:ASN:HB2	1.97	0.47
1:H:53:LEU:H	1:H:53:LEU:HD23	1.80	0.47
1:A:244:THR:HG22	1:A:245:CYS:N	2.30	0.47
2:G:543:LEU:O	2:G:546:ARG:HB3	2.15	0.47
1:A:79:TYR:HD1	1:A:105:SER:CB	2.28	0.46
2:B:370:PHE:O	2:B:371:SER:O	2.33	0.46
2:F:299:LEU:HD22	2:F:383:CYS:SG	2.55	0.46
2:F:515:ILE:HD11	2:F:540:ALA:CB	2.40	0.46
1:E:43:ARG:NH2	2:F:551:TYR:CE2	2.83	0.46
1:D:292:SER:C	1:D:294:ASP:N	2.69	0.46
2:G:394:ILE:O	2:G:395:ASP:HB2	2.15	0.46
1:H:164:PRO:CD	1:H:176:PRO:HB2	2.43	0.46
2:G:194:ILE:HG12	2:G:492:PHE:CD2	2.50	0.46
2:B:276:ILE:HG22	2:B:276:ILE:O	2.15	0.46
1:E:242:ILE:CD1	1:E:297:TRP:CD1	2.99	0.46
1:E:273:THR:HG21	2:F:479:ALA:HB1	1.94	0.46
2:F:343:TRP:CE3	2:F:350:ILE:HG21	2.51	0.46
1:D:290:LYS:CB	1:D:300:ILE:CD1	2.93	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:276:ILE:HG23	1:E:289:TRP:O	2.15	0.46
2:G:445:LEU:HD23	2:G:445:LEU:HA	1.74	0.46
2:B:423:GLN:HB3	2:B:434:LEU:HD21	1.97	0.46
2:B:142:ARG:HA	2:B:142:ARG:HD3	1.52	0.46
2:F:149:THR:O	2:F:150:PHE:HB3	2.14	0.46
1:E:49:LEU:CD1	1:E:50:ILE:H	2.20	0.46
1:H:214:TRP:O	1:H:235:SER:CB	2.56	0.46
2:B:543:LEU:O	2:B:546:ARG:HB3	2.15	0.46
2:C:543:LEU:O	2:C:546:ARG:HB3	2.15	0.46
2:F:153:PHE:HE2	2:F:175:LEU:HD22	1.81	0.46
1:A:215:VAL:HA	1:A:235:SER:HB3	1.96	0.46
2:B:241:PHE:CD2	2:B:457:LEU:HD21	2.51	0.46
2:G:153:PHE:CE2	1:H:278:ALA:HB2	2.51	0.46
2:F:255:VAL:HG11	2:G:335:LEU:HD22	1.97	0.46
2:B:177:THR:CG2	2:B:179:LEU:HB3	2.43	0.46
1:A:50:ILE:O	1:A:50:ILE:HG22	2.16	0.46
2:F:202:ARG:HA	2:F:202:ARG:HD3	1.55	0.46
2:G:161:THR:O	2:G:170:VAL:HG13	2.15	0.46
1:H:224:ILE:HG13	1:H:226:LEU:HB2	1.98	0.46
1:E:234:CYS:SG	1:E:268:VAL:HG23	2.56	0.46
1:D:27:ARG:HH12	1:D:93:TRP:HZ2	1.62	0.46
1:H:16:ILE:HG22	1:H:17:HIS:H	1.80	0.46
2:B:136:LYS:O	2:B:140:LYS:HB2	2.15	0.46
1:E:280:SER:HA	1:E:286:VAL:HG22	1.96	0.46
1:D:16:ILE:HG22	1:D:17:HIS:H	1.81	0.46
2:G:151:ALA:HB2	1:H:286:VAL:HG21	1.97	0.46
2:C:161:THR:O	2:C:170:VAL:HG13	2.15	0.46
1:D:280:SER:HA	1:D:286:VAL:HG22	1.96	0.46
2:B:163:ASP:O	2:B:164:ILE:HB	2.16	0.46
1:D:215:VAL:HA	1:D:235:SER:HB3	1.96	0.46
2:F:276:ILE:O	2:F:276:ILE:HG22	2.15	0.46
1:D:190:LEU:HD21	1:D:209:GLU:HB3	1.97	0.46
1:E:53:LEU:N	1:E:53:LEU:CD2	2.77	0.46
1:E:289:TRP:CE3	1:E:298:VAL:C	2.89	0.46
1:H:296:GLN:O	1:H:296:GLN:NE2	2.48	0.46
2:F:165:VAL:O	2:F:165:VAL:HG12	2.14	0.46
2:G:303:VAL:HG13	2:G:322:ILE:CG2	2.46	0.46
1:A:16:ILE:HG22	1:A:17:HIS:H	1.80	0.46
1:A:280:SER:HA	1:A:286:VAL:HG22	1.96	0.46
2:F:343:TRP:CZ3	2:F:350:ILE:CG2	2.88	0.46
2:B:271:TRP:HE3	2:B:272:ILE:HG12	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:272:ILE:HG23	2:B:382:LEU:HG	1.98	0.46
1:E:272:ILE:HD11	2:F:155:THR:HA	1.97	0.46
2:F:429:GLU:O	2:F:464:VAL:HG21	2.16	0.46
1:H:296:GLN:HE21	1:H:298:VAL:HG23	1.80	0.46
1:H:143:LYS:HD2	1:H:200:GLY:O	2.15	0.46
2:F:177:THR:HG22	2:F:179:LEU:HD23	1.97	0.46
2:G:471:ASP:OD1	2:G:497:LEU:CD2	2.58	0.46
2:F:136:LYS:O	2:F:140:LYS:HB2	2.15	0.46
1:E:304:ASN:HA	2:F:173:LYS:NZ	2.30	0.46
1:H:216:ARG:HD3	1:H:216:ARG:HA	1.67	0.46
2:B:284:ILE:HD13	2:B:297:TYR:CE1	2.51	0.46
1:D:145:ILE:HG22	1:D:148:ALA:HB2	1.98	0.46
1:E:292:SER:C	1:E:294:ASP:N	2.69	0.46
1:E:50:ILE:HG22	1:E:50:ILE:O	2.16	0.46
2:F:271:TRP:HE3	2:F:272:ILE:HG12	1.81	0.46
1:H:145:ILE:HG22	1:H:148:ALA:HB2	1.98	0.46
1:A:292:SER:C	1:A:294:ASP:N	2.69	0.46
2:F:137:LEU:O	2:F:141:GLU:HB3	2.16	0.46
2:F:532:ILE:HG23	2:F:533:PRO:CD	2.45	0.46
1:D:77:CYS:HB3	1:D:109:VAL:HG23	1.98	0.46
1:D:50:ILE:O	1:D:50:ILE:HG22	2.16	0.46
2:F:217:PHE:HZ	2:F:453:LEU:HD23	1.80	0.46
1:E:192:LYS:HE2	1:E:207:LYS:HE2	1.98	0.46
1:D:53:LEU:CD2	1:D:53:LEU:N	2.77	0.46
1:E:73:ILE:HG22	1:E:74:LEU:N	2.30	0.46
1:A:53:LEU:N	1:A:53:LEU:CD2	2.78	0.46
2:B:256:LYS:O	2:B:260:LEU:HG	2.16	0.46
1:D:129:ILE:O	1:D:129:ILE:HG22	2.15	0.46
1:A:77:CYS:HB3	1:A:109:VAL:HG23	1.98	0.45
1:H:50:ILE:O	1:H:50:ILE:HG22	2.16	0.45
2:F:244:VAL:HG11	2:F:263:GLU:HB3	1.98	0.45
1:A:224:ILE:HG13	1:A:226:LEU:HB2	1.98	0.45
1:A:15:MET:HG3	2:B:162:LYS:HZ2	1.81	0.45
2:C:213:SER:HB3	2:C:459:PHE:CD2	2.52	0.45
1:A:182:PHE:O	1:A:182:PHE:CG	2.68	0.45
2:B:137:LEU:O	2:B:141:GLU:N	2.32	0.45
2:B:295:PHE:CE1	2:B:360:LEU:HD11	2.52	0.45
2:F:550:ASN:OD1	2:F:550:ASN:N	2.50	0.45
2:F:475:PHE:CE2	2:F:497:LEU:HD11	2.50	0.45
2:G:350:ILE:HG22	2:G:351:ASP:N	2.30	0.45
2:C:271:TRP:HE3	2:C:272:ILE:HG12	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:191:ILE:HB	1:E:208:LEU:HB2	1.98	0.45
1:E:53:LEU:HD12	1:E:86:TRP:CD2	2.52	0.45
1:D:182:PHE:CG	1:D:182:PHE:O	2.69	0.45
2:G:394:ILE:O	2:G:397:TYR:CD1	2.70	0.45
2:C:303:VAL:HG13	2:C:322:ILE:CG2	2.46	0.45
2:F:303:VAL:HG13	2:F:322:ILE:CG2	2.47	0.45
2:B:165:VAL:O	2:B:165:VAL:HG12	2.15	0.45
2:G:550:ASN:N	2:G:550:ASN:OD1	2.49	0.45
1:E:79:TYR:HD1	1:E:105:SER:CB	2.29	0.45
2:B:487:HIS:HE1	2:B:513:ARG:HH21	1.65	0.45
1:A:28:LEU:HD13	2:B:172:ILE:CD1	2.46	0.45
2:C:359:LYS:HZ1	2:C:370:PHE:H	1.65	0.45
2:G:375:LEU:HB2	2:G:384:LEU:HD21	1.98	0.45
1:E:145:ILE:HG22	1:E:148:ALA:HB2	1.98	0.45
1:E:294:ASP:O	1:E:294:ASP:OD1	2.34	0.45
1:E:150:THR:HB	1:E:188:ASP:HB3	1.99	0.45
1:A:129:ILE:HG22	1:A:129:ILE:O	2.14	0.45
1:H:276:ILE:HG23	1:H:289:TRP:O	2.16	0.45
1:D:242:ILE:CD1	1:D:258:LEU:HB2	2.46	0.45
2:B:137:LEU:O	2:B:141:GLU:HB3	2.15	0.45
1:H:248:ALA:O	1:H:249:SER:HB3	2.16	0.45
2:B:153:PHE:HE2	2:B:175:LEU:HD22	1.81	0.45
2:B:484:ALA:O	2:B:485:GLN:CB	2.65	0.45
2:G:155:THR:CG2	2:G:513:ARG:HD2	2.30	0.45
2:F:164:ILE:O	2:F:164:ILE:CG2	2.63	0.45
1:D:189:ASN:HA	1:D:215:VAL:HG23	1.98	0.45
2:B:512:MET:HA	2:B:540:ALA:HB1	1.98	0.45
1:H:266:TRP:HD1	1:H:281:GLY:HA2	1.82	0.45
1:A:53:LEU:HD12	1:A:86:TRP:CD2	2.52	0.45
1:D:232:ALA:HB2	1:D:270:TRP:HZ2	1.77	0.45
1:E:266:TRP:HD1	1:E:281:GLY:HA2	1.81	0.45
1:A:276:ILE:HG23	1:A:289:TRP:O	2.16	0.45
1:H:145:ILE:HD11	1:H:202:TRP:CB	2.47	0.45
2:B:409:LYS:H	2:B:409:LYS:HG2	1.56	0.45
2:B:482:GLU:CD	2:B:509:ARG:HH22	2.20	0.45
2:G:209:GLN:HG3	2:G:495:CYS:O	2.17	0.45
1:E:70:TYR:CD2	1:E:118:LEU:HD13	2.52	0.45
1:E:77:CYS:SG	1:E:106:VAL:O	2.67	0.45
2:B:199:ILE:HG21	2:B:208:PRO:HB2	1.99	0.45
1:E:258:LEU:CD1	1:E:297:TRP:CB	2.94	0.45
1:D:214:TRP:O	1:D:235:SER:CB	2.56	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:224:ILE:HG13	1:E:226:LEU:HB2	1.98	0.45
1:A:193:LEU:N	1:A:193:LEU:HD23	2.32	0.45
2:G:256:LYS:O	2:G:260:LEU:HG	2.16	0.45
2:C:519:ARG:HB3	2:C:520:ALA:H	1.48	0.45
1:E:129:ILE:HG22	1:E:129:ILE:O	2.14	0.45
2:B:299:LEU:HD13	2:B:379:PHE:CE2	2.52	0.45
2:G:266:CYS:O	2:G:267:ARG:C	2.55	0.45
1:A:213:ASP:OD1	1:A:214:TRP:N	2.38	0.45
2:F:163:ASP:O	2:F:164:ILE:HB	2.16	0.45
2:G:385:LEU:HA	2:G:406:HIS:CE1	2.52	0.45
2:C:522:THR:CG2	2:C:526:ILE:HG13	2.47	0.45
2:G:201:ALA:HB2	2:G:531:LYS:HZ2	1.80	0.45
2:F:513:ARG:HE	2:F:514:GLU:HG2	1.82	0.45
1:D:294:ASP:O	1:D:294:ASP:OD1	2.34	0.45
1:D:150:THR:HB	1:D:188:ASP:HB3	1.98	0.45
1:A:216:ARG:HA	1:A:216:ARG:HD3	1.66	0.45
2:B:177:THR:O	2:B:179:LEU:N	2.49	0.45
2:B:513:ARG:HE	2:B:514:GLU:HG2	1.81	0.45
1:E:284:ASN:HA	2:F:149:THR:OG1	2.16	0.45
1:E:213:ASP:OD1	1:E:214:TRP:N	2.38	0.45
2:G:373:LYS:HE2	2:G:410:PHE:HE2	1.81	0.45
1:D:290:LYS:HB2	1:D:300:ILE:CD1	2.46	0.45
2:B:272:ILE:CG2	2:B:382:LEU:HG	2.47	0.45
2:C:215:LEU:HD22	2:C:452:TYR:OH	2.17	0.45
2:C:486:LEU:HA	2:C:486:LEU:HD23	1.83	0.45
2:C:256:LYS:O	2:C:260:LEU:HG	2.17	0.45
2:B:469:THR:O	2:B:472:GLU:HB3	2.17	0.45
2:F:469:THR:O	2:F:472:GLU:HB3	2.17	0.45
2:C:469:THR:O	2:C:472:GLU:HB3	2.17	0.45
2:G:202:ARG:HA	2:G:202:ARG:HD3	1.55	0.45
1:E:258:LEU:CD1	1:E:297:TRP:HB2	2.47	0.45
1:E:41:ASP:OD1	1:E:42:VAL:N	2.49	0.45
2:C:475:PHE:HE2	2:C:497:LEU:CD1	2.30	0.45
1:E:193:LEU:N	1:E:193:LEU:HD23	2.32	0.45
2:C:184:LEU:HD21	2:C:448:GLN:HE22	1.81	0.45
1:E:199:ASP:OD1	1:E:200:GLY:N	2.50	0.45
2:B:350:ILE:CG2	2:B:351:ASP:N	2.80	0.45
2:G:513:ARG:HE	2:G:514:GLU:HG2	1.81	0.45
2:C:155:THR:HG22	2:C:513:ARG:CD	2.42	0.45
2:F:256:LYS:O	2:F:260:LEU:HG	2.16	0.45
2:C:139:MET:HE2	2:C:144:PHE:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:208:LEU:HD13	1:A:243:TRP:CE3	2.52	0.45
1:H:182:PHE:O	1:H:182:PHE:CG	2.69	0.45
2:F:145:THR:HG22	2:F:147:SER:N	2.30	0.45
1:H:232:ALA:HB2	1:H:270:TRP:HZ2	1.79	0.45
2:G:469:THR:O	2:G:472:GLU:HB3	2.18	0.45
1:A:199:ASP:OD1	1:A:200:GLY:N	2.50	0.45
2:B:487:HIS:CE1	2:B:513:ARG:HH21	2.35	0.44
2:G:276:ILE:HD13	2:G:383:CYS:CA	2.34	0.44
2:G:366:PHE:HZ	2:G:387:LEU:HD12	1.82	0.44
2:G:149:THR:CG2	2:G:150:PHE:N	2.72	0.44
2:F:250:THR:O	2:F:256:LYS:HE3	2.17	0.44
1:D:95:LYS:HG2	1:D:95:LYS:O	2.18	0.44
1:A:145:ILE:HD13	1:A:194:TRP:CE3	2.53	0.44
1:D:38:LYS:HB2	1:D:40:PHE:CE1	2.52	0.44
1:E:157:SER:HB2	1:E:218:VAL:O	2.17	0.44
2:C:481:LEU:O	2:C:484:ALA:HB3	2.18	0.44
2:F:210:ILE:HG22	2:F:459:PHE:CE2	2.53	0.44
2:B:491:LEU:HD23	2:B:530:LEU:HD12	1.99	0.44
1:A:21:MET:HB3	2:B:154:SER:OG	2.17	0.44
2:F:218:LYS:HG2	2:F:238:SER:HG	1.79	0.44
2:C:295:PHE:CE2	2:C:356:LYS:HD3	2.53	0.44
2:B:215:LEU:HD23	2:B:215:LEU:HA	1.83	0.44
2:C:513:ARG:HE	2:C:514:GLU:HG2	1.82	0.44
1:A:258:LEU:HD13	1:A:297:TRP:HB2	1.99	0.44
2:B:321:LEU:HB3	2:B:361:LEU:CD1	2.42	0.44
1:D:53:LEU:HD12	1:D:86:TRP:CD2	2.51	0.44
1:D:266:TRP:HD1	1:D:281:GLY:HA2	1.82	0.44
1:A:191:ILE:HB	1:A:208:LEU:HB2	1.99	0.44
1:A:210:ALA:HB3	1:A:243:TRP:CZ2	2.52	0.44
2:C:474:THR:CG2	2:C:493:VAL:HG12	2.47	0.44
1:A:294:ASP:O	1:A:294:ASP:OD1	2.34	0.44
2:C:193:GLU:O	2:C:196:LYS:HB2	2.18	0.44
2:B:133:ASP:N	2:B:133:ASP:OD1	2.50	0.44
1:A:70:TYR:CD2	1:A:118:LEU:HD13	2.53	0.44
1:E:16:ILE:HG22	1:E:17:HIS:H	1.80	0.44
1:A:280:SER:HB2	2:B:150:PHE:HA	1.99	0.44
1:D:77:CYS:HB3	1:D:109:VAL:HG21	1.99	0.44
2:B:210:ILE:H	2:B:210:ILE:HD12	1.82	0.44
1:H:95:LYS:O	1:H:95:LYS:HG2	2.17	0.44
2:C:208:PRO:HD3	2:C:533:PRO:HD3	1.98	0.44
1:E:95:LYS:O	1:E:95:LYS:HG2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:43:ARG:O	1:E:44:ASN:CB	2.66	0.44
1:H:77:CYS:HB3	1:H:109:VAL:HG23	1.98	0.44
1:A:145:ILE:HG22	1:A:148:ALA:HB2	1.98	0.44
2:F:193:GLU:O	2:F:196:LYS:HB2	2.17	0.44
1:A:43:ARG:O	1:A:44:ASN:CB	2.66	0.44
1:A:300:ILE:HG12	1:A:300:ILE:H	1.59	0.44
2:F:133:ASP:N	2:F:133:ASP:OD1	2.50	0.44
2:G:551:TYR:CE2	1:H:43:ARG:NH2	2.85	0.44
1:D:224:ILE:HG13	1:D:226:LEU:HB2	1.98	0.44
1:H:53:LEU:HD12	1:H:86:TRP:CD2	2.52	0.44
1:H:199:ASP:O	1:H:199:ASP:OD1	2.36	0.44
1:A:266:TRP:HD1	1:A:281:GLY:HA2	1.82	0.44
2:B:135:ALA:O	2:B:139:MET:CB	2.65	0.44
2:F:210:ILE:H	2:F:210:ILE:HD12	1.82	0.44
1:D:78:SER:OG	1:D:79:TYR:N	2.51	0.44
2:C:284:ILE:O	2:C:287:SER:HB3	2.17	0.44
1:D:53:LEU:HD23	1:D:53:LEU:H	1.80	0.44
1:E:287:THR:O	1:E:288:LEU:HD23	2.17	0.44
1:E:264:VAL:CG1	1:E:265:VAL:N	2.81	0.44
2:C:435:TYR:CD2	2:C:454:ILE:HD11	2.53	0.44
1:D:193:LEU:N	1:D:193:LEU:HD23	2.33	0.44
2:F:145:THR:C	2:F:147:SER:N	2.70	0.44
2:C:550:ASN:N	2:C:550:ASN:OD1	2.49	0.44
2:C:396:GLU:OE1	2:C:396:GLU:HA	2.16	0.44
2:B:495:CYS:C	2:B:497:LEU:H	2.20	0.44
2:F:199:ILE:HG21	2:F:208:PRO:HB2	1.99	0.44
1:A:40:PHE:N	1:A:40:PHE:CD1	2.84	0.44
1:E:245:CYS:HB2	1:E:253:TRP:CZ3	2.51	0.44
1:D:29:ALA:CA	1:D:39:ILE:HD13	2.46	0.44
1:A:95:LYS:HG2	1:A:95:LYS:O	2.17	0.44
2:C:178:GLU:HG2	2:C:480:GLN:NE2	2.32	0.44
2:B:193:GLU:O	2:B:196:LYS:HB2	2.17	0.44
1:E:78:SER:OG	1:E:79:TYR:N	2.51	0.44
2:B:210:ILE:HD12	2:B:495:CYS:C	2.38	0.44
2:F:238:SER:CA	2:F:242:ASP:OD2	2.54	0.44
2:B:266:CYS:O	2:B:267:ARG:C	2.56	0.44
2:C:216:LEU:HB3	2:C:242:ASP:CG	2.37	0.44
2:F:323:SER:OG	2:G:262:LYS:HE2	2.18	0.44
1:D:276:ILE:HG23	1:D:289:TRP:O	2.17	0.44
1:H:77:CYS:HB3	1:H:109:VAL:HG21	2.00	0.44
2:C:185:PHE:HA	2:C:486:LEU:HD11	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:246:TYR:CE2	2:C:250:THR:OG1	2.67	0.44
2:F:137:LEU:O	2:F:141:GLU:N	2.33	0.44
2:F:177:THR:CG2	2:F:179:LEU:CD2	2.93	0.44
1:E:280:SER:HB2	2:F:150:PHE:HA	1.98	0.44
2:B:276:ILE:HG21	2:B:383:CYS:SG	2.58	0.44
1:A:38:LYS:HB2	1:A:40:PHE:CE1	2.52	0.44
2:F:266:CYS:O	2:F:267:ARG:C	2.55	0.44
2:B:412:LEU:HB3	2:B:413:PRO:HD2	1.99	0.44
2:C:272:ILE:HG23	2:C:382:LEU:HG	2.00	0.44
2:G:446:ASP:O	2:G:447:VAL:C	2.56	0.44
2:C:448:GLN:HB2	2:C:477:PHE:HE1	1.81	0.44
2:G:199:ILE:HG21	2:G:208:PRO:HB2	1.99	0.44
2:B:185:PHE:N	2:B:185:PHE:CD1	2.86	0.44
2:F:519:ARG:HB3	2:F:520:ALA:H	1.48	0.44
2:G:278:PRO:HG2	2:G:279:GLU:H	1.83	0.44
2:F:142:ARG:HA	2:F:142:ARG:HD3	1.51	0.44
2:B:485:GLN:NE2	2:B:517:LEU:HD22	2.31	0.44
1:D:70:TYR:CD2	1:D:118:LEU:HD13	2.53	0.44
1:E:303:VAL:O	1:E:304:ASN:HB2	2.17	0.44
1:A:77:CYS:HB3	1:A:109:VAL:HG21	2.00	0.44
2:C:172:ILE:CD1	1:D:42:VAL:HG21	2.47	0.44
2:G:139:MET:HE2	2:G:144:PHE:HB2	2.00	0.44
2:C:266:CYS:O	2:C:267:ARG:C	2.56	0.44
2:C:297:TYR:HB3	2:C:306:ALA:HB2	2.00	0.44
2:C:210:ILE:HD13	2:C:496:PHE:HA	2.00	0.44
1:E:183:ALA:O	1:E:184:SER:CB	2.66	0.44
2:G:152:LYS:HZ1	1:H:62:GLN:NE2	2.16	0.44
2:B:451:TRP:CD1	2:B:474:THR:HA	2.53	0.44
1:D:216:ARG:HA	1:D:216:ARG:HD3	1.67	0.44
2:B:303:VAL:HG13	2:B:322:ILE:CG2	2.46	0.44
2:F:177:THR:O	2:F:179:LEU:N	2.50	0.43
2:F:218:LYS:CG	2:F:238:SER:OG	2.59	0.43
2:G:153:PHE:HE1	2:G:175:LEU:HD22	1.82	0.43
1:E:245:CYS:HB2	1:E:253:TRP:CD2	2.53	0.43
2:C:317:HIS:O	2:C:320:VAL:HB	2.18	0.43
1:D:66:ALA:HB3	1:D:73:ILE:HB	2.00	0.43
2:C:199:ILE:HG21	2:C:208:PRO:HB2	1.99	0.43
2:G:404:GLN:CG	2:G:426:ALA:HB1	2.46	0.43
2:B:297:TYR:CE2	2:B:305:ARG:HB3	2.53	0.43
1:A:89:GLU:O	1:A:90:ASN:CB	2.66	0.43
2:G:152:LYS:NZ	1:H:62:GLN:NE2	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:188:VAL:O	2:C:192:LYS:HB2	2.18	0.43
1:E:79:TYR:CE2	2:F:138:ILE:CD1	3.01	0.43
1:E:77:CYS:HB3	1:E:109:VAL:HG23	1.98	0.43
2:B:299:LEU:HD22	2:B:383:CYS:SG	2.58	0.43
2:B:199:ILE:CD1	2:B:530:LEU:HA	2.48	0.43
2:B:522:THR:HG21	2:B:526:ILE:HD11	1.98	0.43
2:F:522:THR:CG2	2:F:526:ILE:CD1	2.96	0.43
1:A:303:VAL:O	1:A:304:ASN:HB2	2.17	0.43
2:F:380:SER:O	2:F:383:CYS:N	2.45	0.43
2:C:153:PHE:HE1	2:C:175:LEU:HD22	1.82	0.43
2:G:317:HIS:O	2:G:320:VAL:HB	2.19	0.43
1:E:288:LEU:HB3	1:E:300:ILE:HG13	2.00	0.43
2:B:330:PRO:O	2:B:331:ARG:C	2.57	0.43
2:B:145:THR:C	2:B:147:SER:N	2.71	0.43
2:F:188:VAL:O	2:F:192:LYS:HB2	2.19	0.43
1:H:160:PRO:O	1:H:162:VAL:HG23	2.18	0.43
2:G:188:VAL:O	2:G:192:LYS:HB2	2.18	0.43
2:B:550:ASN:N	2:B:550:ASN:OD1	2.50	0.43
2:B:481:LEU:HB2	2:B:490:SER:HB2	1.99	0.43
1:D:204:GLU:HG3	1:D:204:GLU:O	2.18	0.43
2:F:135:ALA:O	2:F:139:MET:CB	2.65	0.43
2:B:487:HIS:HD2	2:B:517:LEU:CD2	2.15	0.43
2:C:194:ILE:CG1	2:C:492:PHE:CE2	2.99	0.43
1:H:70:TYR:CD2	1:H:118:LEU:HD13	2.53	0.43
1:A:78:SER:OG	1:A:79:TYR:N	2.51	0.43
2:C:359:LYS:NZ	2:C:370:PHE:H	2.16	0.43
2:F:317:HIS:O	2:F:320:VAL:HB	2.19	0.43
1:H:193:LEU:HD21	1:H:208:LEU:CD1	2.48	0.43
2:G:330:PRO:O	2:G:331:ARG:C	2.57	0.43
1:A:204:GLU:HG3	1:A:204:GLU:O	2.18	0.43
2:F:253:ASP:O	2:F:257:MET:HB2	2.18	0.43
1:E:33:SER:HA	1:E:59:PRO:HB3	2.00	0.43
2:C:544:LYS:O	2:C:545:ASP:C	2.56	0.43
1:H:78:SER:OG	1:H:79:TYR:N	2.51	0.43
1:H:213:ASP:OD1	1:H:214:TRP:N	2.38	0.43
2:F:410:PHE:N	2:F:410:PHE:CD2	2.84	0.43
2:B:217:PHE:HA	2:B:452:TYR:HE2	1.82	0.43
2:G:262:LYS:O	2:G:263:GLU:C	2.56	0.43
1:D:234:CYS:HB2	1:D:265:VAL:CG1	2.47	0.43
1:H:193:LEU:HD23	1:H:193:LEU:N	2.33	0.43
1:H:89:GLU:O	1:H:90:ASN:CB	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:193:GLU:O	2:G:196:LYS:HB2	2.18	0.43
2:C:410:PHE:N	2:C:410:PHE:CD2	2.84	0.43
2:B:188:VAL:O	2:B:192:LYS:HB2	2.18	0.43
1:E:79:TYR:CD2	2:F:138:ILE:HD13	2.53	0.43
1:D:77:CYS:SG	1:D:106:VAL:O	2.66	0.43
2:C:359:LYS:HZ1	2:C:368:GLY:HA3	1.83	0.43
2:F:244:VAL:HG23	2:F:264:ARG:NH2	2.27	0.43
2:B:262:LYS:O	2:B:263:GLU:C	2.56	0.43
1:H:40:PHE:N	1:H:40:PHE:CD1	2.85	0.43
2:C:246:TYR:HA	2:C:247:PRO:HD2	1.80	0.43
1:A:287:THR:O	1:A:288:LEU:HD23	2.19	0.43
2:F:544:LYS:O	2:F:545:ASP:C	2.56	0.43
1:A:33:SER:HA	1:A:59:PRO:HB3	2.01	0.43
2:C:484:ALA:O	2:C:485:GLN:HB2	2.19	0.43
2:B:522:THR:O	2:B:522:THR:HG22	2.18	0.43
2:B:359:LYS:NZ	2:B:370:PHE:H	2.17	0.43
2:F:446:ASP:O	2:F:447:VAL:C	2.56	0.43
1:A:53:LEU:HD23	1:A:53:LEU:H	1.81	0.43
2:C:185:PHE:N	2:C:185:PHE:CD1	2.87	0.43
2:F:379:PHE:HD1	2:F:379:PHE:N	2.17	0.43
2:B:410:PHE:N	2:B:410:PHE:CD2	2.84	0.43
2:C:220:ALA:HB3	2:C:234:TRP:CE3	2.54	0.43
2:B:544:LYS:O	2:B:545:ASP:C	2.56	0.43
2:B:278:PRO:HG2	2:B:279:GLU:H	1.84	0.43
2:B:177:THR:C	2:B:179:LEU:N	2.71	0.43
1:E:77:CYS:HB3	1:E:109:VAL:HG21	2.00	0.43
2:C:289:ASN:O	2:C:290:GLU:C	2.56	0.43
1:H:43:ARG:O	1:H:44:ASN:CB	2.66	0.43
2:F:359:LYS:NZ	2:F:370:PHE:H	2.16	0.43
2:B:446:ASP:O	2:B:447:VAL:C	2.56	0.43
2:G:272:ILE:HG23	2:G:382:LEU:HG	1.99	0.43
2:F:262:LYS:HE2	2:G:323:SER:OG	2.19	0.43
2:F:262:LYS:O	2:F:263:GLU:C	2.56	0.43
1:D:264:VAL:CG1	1:D:265:VAL:N	2.82	0.43
1:E:66:ALA:HB3	1:E:73:ILE:HB	2.01	0.43
2:G:404:GLN:HG2	2:G:426:ALA:C	2.39	0.43
1:D:287:THR:O	1:D:288:LEU:HD23	2.19	0.43
2:B:294:ILE:HD13	2:B:310:ALA:HB2	1.99	0.43
2:C:339:GLN:O	2:C:343:TRP:CD1	2.71	0.43
1:D:43:ARG:O	1:D:44:ASN:CB	2.66	0.43
2:C:399:LEU:O	2:C:402:LEU:HB3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:216:ARG:HA	1:E:216:ARG:HD3	1.67	0.43
2:G:220:ALA:HB3	2:G:234:TRP:CE3	2.54	0.43
2:C:194:ILE:CG1	2:C:492:PHE:HE2	2.29	0.43
1:H:287:THR:HG21	1:H:299:CYS:SG	2.58	0.43
2:B:267:ARG:HG3	2:B:267:ARG:NH1	2.15	0.43
2:F:381:TRP:CD1	2:F:382:LEU:N	2.86	0.43
2:C:446:ASP:O	2:C:447:VAL:C	2.57	0.43
2:G:410:PHE:N	2:G:410:PHE:CD2	2.84	0.43
2:G:201:ALA:HB2	2:G:531:LYS:HZ3	1.80	0.43
1:E:89:GLU:O	1:E:90:ASN:CB	2.66	0.43
2:G:431:THR:HG21	2:G:463:ARG:HB3	2.00	0.43
1:A:264:VAL:CG1	1:A:265:VAL:N	2.81	0.43
1:A:266:TRP:CZ3	2:B:144:PHE:HD2	2.37	0.43
2:C:218:LYS:HG2	2:C:238:SER:HG	1.81	0.43
2:F:215:LEU:HA	2:F:215:LEU:HD23	1.84	0.43
1:H:292:SER:OG	1:H:294:ASP:HB2	2.19	0.43
2:B:339:GLN:O	2:B:343:TRP:CD1	2.71	0.43
1:H:164:PRO:HD2	1:H:176:PRO:HB2	2.01	0.43
2:F:278:PRO:HG2	2:F:279:GLU:H	1.83	0.43
1:H:33:SER:HA	1:H:59:PRO:HB3	2.01	0.43
2:G:399:LEU:O	2:G:402:LEU:HB3	2.19	0.43
2:B:487:HIS:HB3	2:B:518:LEU:HD21	2.01	0.43
2:F:494:SER:O	2:F:497:LEU:HB2	2.18	0.43
2:B:317:HIS:O	2:B:320:VAL:HB	2.19	0.43
1:A:224:ILE:C	1:A:226:LEU:N	2.72	0.43
1:D:183:ALA:O	1:D:184:SER:CB	2.67	0.43
2:C:330:PRO:O	2:C:331:ARG:C	2.57	0.43
1:E:164:PRO:HD2	1:E:176:PRO:HB2	2.01	0.43
2:G:544:LYS:O	2:G:545:ASP:C	2.56	0.43
2:B:493:VAL:O	2:B:493:VAL:HG12	2.19	0.42
2:B:399:LEU:O	2:B:402:LEU:HB3	2.19	0.42
1:H:49:LEU:HD11	1:H:51:ALA:O	2.19	0.42
1:E:38:LYS:HB2	1:E:40:PHE:CE1	2.53	0.42
2:G:244:VAL:CG1	2:G:263:GLU:OE2	2.66	0.42
1:H:66:ALA:HB3	1:H:73:ILE:HB	2.01	0.42
2:C:210:ILE:H	2:C:210:ILE:HD12	1.83	0.42
2:F:400:GLU:HG3	2:F:425:TYR:CZ	2.54	0.42
1:H:204:GLU:HG3	1:H:204:GLU:O	2.18	0.42
2:G:506:THR:HG22	2:G:507:ILE:N	2.35	0.42
2:F:202:ARG:HG2	2:F:209:GLN:HB2	2.02	0.42
1:A:21:MET:HA	1:A:28:LEU:HD12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:199:ILE:CG2	2:F:200:GLU:N	2.83	0.42
2:G:218:LYS:CG	2:G:238:SER:OG	2.59	0.42
2:F:384:LEU:O	2:F:387:LEU:N	2.51	0.42
2:G:409:LYS:HG2	2:G:409:LYS:H	1.56	0.42
1:E:274:ALA:O	1:E:275:ASN:CB	2.62	0.42
2:G:524:ASP:O	2:G:524:ASP:CG	2.55	0.42
1:D:89:GLU:O	1:D:90:ASN:CB	2.66	0.42
1:H:38:LYS:HB2	1:H:40:PHE:CE1	2.53	0.42
1:A:47:GLN:OE1	2:B:166:GLY:CA	2.67	0.42
2:C:393:GLN:HA	2:C:393:GLN:OE1	2.19	0.42
1:E:293:VAL:O	1:E:293:VAL:HG12	2.20	0.42
2:G:210:ILE:H	2:G:210:ILE:HD12	1.83	0.42
2:B:431:THR:HG21	2:B:463:ARG:HG2	2.01	0.42
2:B:432:GLU:CD	2:B:466:SER:H	2.23	0.42
1:E:257:LEU:HD12	1:E:258:LEU:N	2.34	0.42
2:C:218:LYS:CG	2:C:238:SER:OG	2.59	0.42
2:G:384:LEU:O	2:G:387:LEU:N	2.52	0.42
2:C:145:THR:HG21	2:C:147:SER:OG	2.19	0.42
2:C:208:PRO:HD3	2:C:531:LYS:O	2.19	0.42
1:A:274:ALA:HB1	1:A:290:LYS:HE3	2.01	0.42
1:D:240:VAL:HB	1:D:258:LEU:HB3	2.00	0.42
2:C:278:PRO:HG2	2:C:279:GLU:H	1.83	0.42
2:G:455:GLN:CG	2:G:496:PHE:CD2	3.03	0.42
2:F:207:TYR:HA	2:F:208:PRO:HD2	1.81	0.42
2:F:271:TRP:CE3	2:F:272:ILE:HG12	2.55	0.42
2:C:271:TRP:CE3	2:C:272:ILE:HG12	2.54	0.42
2:C:199:ILE:CG2	2:C:200:GLU:N	2.82	0.42
2:B:524:ASP:O	2:B:524:ASP:CG	2.58	0.42
2:C:321:LEU:O	2:C:324:TYR:N	2.53	0.42
2:F:162:LYS:O	2:F:162:LYS:CG	2.67	0.42
1:A:274:ALA:O	1:A:275:ASN:CB	2.62	0.42
2:G:448:GLN:HB2	2:G:477:PHE:CE1	2.55	0.42
2:B:506:THR:HG22	2:B:507:ILE:N	2.34	0.42
2:F:495:CYS:C	2:F:497:LEU:H	2.22	0.42
1:A:77:CYS:HA	1:A:83:VAL:HG22	2.01	0.42
2:G:359:LYS:NZ	2:G:370:PHE:H	2.16	0.42
2:G:236:LEU:HD23	2:G:421:ILE:HG21	2.01	0.42
1:H:77:CYS:HA	1:H:83:VAL:HG22	2.00	0.42
2:F:399:LEU:O	2:F:402:LEU:HB3	2.19	0.42
1:D:257:LEU:HD12	1:D:258:LEU:N	2.35	0.42
2:G:525:HIS:O	2:G:526:ILE:C	2.57	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:164:PRO:HD2	1:D:176:PRO:HB2	2.01	0.42
1:A:288:LEU:CB	1:A:300:ILE:HG13	2.50	0.42
2:B:414:TYR:CD1	2:F:143:ARG:HD3	2.54	0.42
2:F:143:ARG:HH11	2:F:143:ARG:HG3	1.84	0.42
2:F:177:THR:C	2:F:179:LEU:N	2.72	0.42
1:A:102:HIS:NE2	1:A:130:SER:HB3	2.29	0.42
2:B:320:VAL:HG22	2:C:263:GLU:HA	2.01	0.42
1:A:257:LEU:HD12	1:A:258:LEU:N	2.35	0.42
1:A:291:GLU:N	1:A:297:TRP:CZ3	2.87	0.42
1:D:224:ILE:C	1:D:226:LEU:N	2.72	0.42
2:C:455:GLN:HE21	2:C:496:PHE:HD2	1.66	0.42
1:A:289:TRP:HA	1:A:298:VAL:O	2.19	0.42
2:G:321:LEU:O	2:G:324:TYR:N	2.52	0.42
1:D:241:PHE:HD2	1:D:257:LEU:HA	1.84	0.42
2:G:487:HIS:CD2	2:G:517:LEU:HD23	2.52	0.42
2:C:343:TRP:CZ3	2:C:349:SER:CB	3.03	0.42
2:B:525:HIS:ND1	2:B:525:HIS:N	2.67	0.42
2:F:185:PHE:N	2:F:185:PHE:CD1	2.86	0.42
2:G:185:PHE:CD1	2:G:185:PHE:N	2.87	0.42
1:D:33:SER:HA	1:D:59:PRO:HB3	2.01	0.42
2:G:481:LEU:HD13	2:G:489:HIS:CB	2.17	0.42
2:B:384:LEU:O	2:B:387:LEU:N	2.51	0.42
2:F:385:LEU:N	2:F:406:HIS:CE1	2.87	0.42
2:G:154:SER:OG	2:G:158:MET:HB2	2.20	0.42
2:G:145:THR:HG21	2:G:147:SER:OG	2.19	0.42
1:E:204:GLU:O	1:E:204:GLU:HG3	2.18	0.42
2:B:263:GLU:HA	2:C:320:VAL:HG22	2.01	0.42
2:B:162:LYS:O	2:B:162:LYS:CG	2.67	0.42
2:G:246:TYR:CE1	2:G:259:LEU:HD13	2.55	0.42
1:D:40:PHE:CD1	1:D:40:PHE:N	2.88	0.42
1:A:195:LYS:O	1:A:202:TRP:HA	2.20	0.42
1:D:293:VAL:HG12	1:D:293:VAL:O	2.19	0.42
1:E:271:SER:HB2	2:F:153:PHE:CE2	2.55	0.42
2:F:148:TYR:CE1	2:F:149:THR:O	2.73	0.42
2:B:199:ILE:CG2	2:B:200:GLU:N	2.82	0.42
1:A:214:TRP:O	1:A:235:SER:CB	2.56	0.42
1:A:258:LEU:HD13	1:A:297:TRP:CG	2.53	0.42
2:C:432:GLU:CD	2:C:466:SER:HB3	2.38	0.42
1:A:66:ALA:HB3	1:A:73:ILE:HB	2.01	0.42
1:A:164:PRO:HD2	1:A:176:PRO:HB2	2.01	0.42
2:F:506:THR:HG22	2:F:507:ILE:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:283:ASP:C	1:A:285:LYS:H	2.23	0.42
1:E:40:PHE:CE2	2:F:168:SER:HB2	2.52	0.42
1:D:49:LEU:HD11	1:D:51:ALA:O	2.20	0.42
2:G:271:TRP:CE3	2:G:272:ILE:HG12	2.54	0.42
2:B:321:LEU:O	2:B:324:TYR:N	2.53	0.42
2:G:215:LEU:HD13	2:G:452:TYR:HE1	1.85	0.42
2:B:271:TRP:CE3	2:B:272:ILE:HG12	2.54	0.42
1:D:145:ILE:HD11	1:D:202:TRP:HB3	2.01	0.42
2:F:220:ALA:HB3	2:F:234:TRP:CE3	2.54	0.42
1:H:206:GLN:OE1	1:H:251:ASN:O	2.38	0.42
1:E:72:ASN:HD22	1:E:72:ASN:HA	1.71	0.42
2:B:298:LEU:HD23	2:B:298:LEU:HA	1.85	0.42
2:B:462:THR:O	2:B:463:ARG:HD2	2.19	0.42
2:G:343:TRP:HZ3	2:G:350:ILE:CG2	2.30	0.42
2:F:522:THR:HG21	2:F:526:ILE:CD1	2.50	0.42
2:G:375:LEU:HB3	2:G:379:PHE:CD1	2.54	0.42
2:C:262:LYS:O	2:C:263:GLU:C	2.56	0.42
2:F:263:GLU:HB2	2:G:320:VAL:HG21	2.02	0.42
1:H:258:LEU:HD13	1:H:297:TRP:CB	2.50	0.42
1:D:245:CYS:SG	1:D:246:ASP:N	2.92	0.42
1:D:192:LYS:HD3	1:D:204:GLU:OE1	2.19	0.42
2:G:435:TYR:CE2	2:G:454:ILE:HD11	2.55	0.42
2:B:143:ARG:HG3	2:B:143:ARG:HH11	1.84	0.42
2:B:302:ASP:HA	2:C:304:VAL:HG21	2.01	0.42
2:G:494:SER:OG	2:G:506:THR:HG21	2.20	0.41
2:B:432:GLU:OE1	2:B:466:SER:N	2.49	0.41
1:A:49:LEU:HD11	1:A:51:ALA:O	2.19	0.41
2:B:140:LYS:C	2:B:142:ARG:N	2.73	0.41
2:B:148:TYR:CE1	2:B:149:THR:O	2.73	0.41
1:D:77:CYS:HA	1:D:83:VAL:HG22	2.01	0.41
1:H:287:THR:O	1:H:288:LEU:HD23	2.19	0.41
1:E:49:LEU:HD11	1:E:51:ALA:O	2.19	0.41
1:E:214:TRP:O	1:E:235:SER:CB	2.56	0.41
2:C:236:LEU:HD23	2:C:421:ILE:HG21	2.02	0.41
1:H:257:LEU:HD12	1:H:258:LEU:N	2.35	0.41
1:H:258:LEU:HD13	1:H:297:TRP:CG	2.55	0.41
1:E:230:THR:O	1:E:231:ILE:HG13	2.20	0.41
2:B:329:ASP:HB3	2:B:332:ILE:HD13	2.02	0.41
2:G:329:ASP:HB3	2:G:332:ILE:HD13	2.02	0.41
1:A:247:ASP:OD1	1:A:248:ALA:N	2.53	0.41
2:F:451:TRP:CE2	2:F:493:VAL:HG13	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:359:LYS:HZ1	2:F:368:GLY:HA3	1.85	0.41
1:A:230:THR:O	1:A:231:ILE:HG13	2.20	0.41
1:D:234:CYS:HB3	1:D:268:VAL:HG21	2.02	0.41
1:E:47:GLN:OE1	2:F:166:GLY:CA	2.68	0.41
1:E:14:ASP:CG	1:E:15:MET:H	2.24	0.41
2:F:321:LEU:O	2:F:324:TYR:N	2.53	0.41
1:A:194:TRP:N	1:A:194:TRP:CD1	2.88	0.41
2:G:199:ILE:CG2	2:G:200:GLU:N	2.83	0.41
1:D:197:GLU:O	1:D:198:GLU:CB	2.68	0.41
2:F:525:HIS:ND1	2:F:525:HIS:N	2.67	0.41
2:G:546:ARG:HH11	2:G:546:ARG:HG3	1.86	0.41
1:E:247:ASP:C	1:E:249:SER:H	2.23	0.41
1:A:293:VAL:O	1:A:293:VAL:HG12	2.20	0.41
2:G:482:GLU:CD	2:G:509:ARG:HH22	2.24	0.41
2:F:432:GLU:OE1	2:F:466:SER:HB3	2.20	0.41
1:A:77:CYS:SG	1:A:106:VAL:O	2.67	0.41
2:B:202:ARG:HG2	2:B:209:GLN:HB2	2.02	0.41
2:B:381:TRP:HA	2:B:384:LEU:HD12	2.01	0.41
1:H:258:LEU:HD13	1:H:297:TRP:HB2	2.02	0.41
1:A:241:PHE:CD2	1:A:257:LEU:HA	2.54	0.41
1:H:224:ILE:C	1:H:226:LEU:N	2.72	0.41
2:C:148:TYR:HB2	1:D:266:TRP:CD2	2.55	0.41
1:H:264:VAL:CG1	1:H:265:VAL:N	2.82	0.41
1:A:183:ALA:O	1:A:184:SER:CB	2.67	0.41
2:C:246:TYR:CD2	2:C:248:TYR:O	2.73	0.41
2:B:451:TRP:HZ2	2:B:496:PHE:CD1	2.38	0.41
1:H:283:ASP:C	1:H:285:LYS:H	2.23	0.41
1:E:77:CYS:HA	1:E:83:VAL:HG22	2.01	0.41
2:G:375:LEU:HB3	2:G:379:PHE:HD1	1.85	0.41
2:G:143:ARG:HB2	1:H:216:ARG:NH2	2.35	0.41
2:G:340:LEU:HD21	2:G:358:TYR:HB3	2.02	0.41
2:C:480:GLN:CA	2:C:480:GLN:OE1	2.66	0.41
1:D:194:TRP:N	1:D:194:TRP:CD1	2.88	0.41
2:B:220:ALA:HB3	2:B:234:TRP:CE3	2.54	0.41
2:G:269:THR:O	2:G:273:VAL:HG23	2.20	0.41
2:F:140:LYS:C	2:F:142:ARG:N	2.73	0.41
1:A:266:TRP:CZ3	2:B:144:PHE:CD2	3.08	0.41
2:G:343:TRP:HZ3	2:G:350:ILE:CB	2.34	0.41
2:G:291:ILE:CD1	2:G:351:ASP:OD2	2.65	0.41
2:C:289:ASN:O	2:C:291:ILE:N	2.53	0.41
2:F:522:THR:HG21	2:F:526:ILE:HD12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:546:ARG:HG3	2:F:546:ARG:HH11	1.85	0.41
2:C:546:ARG:HH11	2:C:546:ARG:HG3	1.86	0.41
1:A:271:SER:HB2	2:B:153:PHE:CE2	2.56	0.41
2:C:481:LEU:HA	2:C:484:ALA:HB3	2.02	0.41
1:E:241:PHE:C	1:E:242:ILE:HG13	2.40	0.41
2:B:366:PHE:O	2:B:373:LYS:HG3	2.21	0.41
2:B:217:PHE:HE2	2:B:449:PHE:CE1	2.38	0.41
2:G:512:MET:HA	2:G:540:ALA:CB	2.50	0.41
2:C:525:HIS:O	2:C:526:ILE:C	2.58	0.41
2:B:247:PRO:HG2	2:B:248:TYR:H	1.85	0.41
2:F:329:ASP:HB3	2:F:332:ILE:HD13	2.03	0.41
1:H:196:GLU:HB3	1:H:202:TRP:CE2	2.55	0.41
2:B:445:LEU:HA	2:B:445:LEU:HD23	1.89	0.41
1:D:283:ASP:C	1:D:285:LYS:H	2.23	0.41
1:D:14:ASP:CG	1:D:15:MET:H	2.24	0.41
1:E:21:MET:HA	1:E:28:LEU:HD12	2.01	0.41
2:G:366:PHE:O	2:G:373:LYS:HG3	2.21	0.41
2:C:154:SER:OG	2:C:158:MET:HB2	2.20	0.41
2:B:230:ASP:O	2:B:231:TYR:C	2.59	0.41
2:C:551:TYR:HD2	2:C:552:LEU:HD23	1.85	0.41
2:C:474:THR:HG23	2:C:493:VAL:CG1	2.51	0.41
2:C:244:VAL:HG12	2:C:260:LEU:HD22	2.03	0.41
1:A:18:ASP:OD2	1:A:62:GLN:HG2	2.21	0.41
2:B:269:THR:O	2:B:273:VAL:HG23	2.21	0.41
2:G:213:SER:HB3	2:G:459:PHE:CD2	2.56	0.41
1:E:107:ASN:CG	2:F:142:ARG:NH2	2.73	0.41
2:B:399:LEU:HD23	2:B:425:TYR:OH	2.20	0.41
2:B:139:MET:O	2:B:144:PHE:HB2	2.21	0.41
1:D:21:MET:HA	1:D:28:LEU:HD12	2.01	0.41
1:H:240:VAL:HB	1:H:258:LEU:HB3	2.03	0.41
2:F:252:ASN:O	2:F:255:VAL:N	2.49	0.41
2:C:208:PRO:CB	2:C:530:LEU:O	2.69	0.41
2:F:291:ILE:HG22	2:F:353:ASN:CB	2.50	0.41
2:B:145:THR:CG2	2:B:146:ALA:N	2.84	0.41
2:C:343:TRP:CE3	2:C:349:SER:HB3	2.56	0.41
2:F:316:GLY:O	2:F:319:SER:N	2.54	0.41
2:F:139:MET:O	2:F:144:PHE:HB2	2.20	0.41
2:F:209:GLN:HG2	2:F:497:LEU:O	2.21	0.41
2:B:380:SER:O	2:B:383:CYS:N	2.50	0.41
2:B:532:ILE:HG23	2:B:533:PRO:CD	2.51	0.41
2:B:442:THR:CG2	2:B:444:ALA:CB	2.99	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:370:PHE:HA	2:B:370:PHE:HD2	1.75	0.41
1:E:40:PHE:CD1	1:E:40:PHE:N	2.89	0.41
2:F:381:TRP:HA	2:F:384:LEU:HD12	2.02	0.41
2:C:366:PHE:O	2:C:373:LYS:HG3	2.21	0.41
2:G:352:LYS:HE2	2:G:356:LYS:HE3	2.03	0.41
2:G:153:PHE:CE2	1:H:271:SER:HB3	2.56	0.41
2:F:236:LEU:HD22	2:F:418:ILE:HG22	2.02	0.41
2:C:153:PHE:HA	2:C:158:MET:O	2.21	0.41
1:A:241:PHE:HE2	1:A:257:LEU:HB2	1.84	0.41
1:A:226:LEU:HD12	1:A:228:THR:H	1.86	0.41
2:G:411:SER:C	2:G:412:LEU:HD12	2.41	0.41
2:F:230:ASP:O	2:F:231:TYR:C	2.59	0.41
1:A:14:ASP:CG	1:A:15:MET:H	2.24	0.41
2:C:152:LYS:NZ	1:D:18:ASP:OD2	2.50	0.41
1:D:18:ASP:OD2	1:D:62:GLN:HG2	2.21	0.41
2:F:155:THR:HG22	2:F:513:ARG:HD3	2.03	0.41
2:F:330:PRO:O	2:F:331:ARG:C	2.57	0.41
1:H:191:ILE:HD13	1:H:233:SER:HB3	2.03	0.41
2:B:316:GLY:O	2:B:319:SER:N	2.54	0.41
2:C:316:GLY:O	2:C:319:SER:N	2.54	0.41
2:C:269:THR:O	2:C:273:VAL:HG23	2.20	0.41
1:E:18:ASP:OD2	1:E:62:GLN:HG2	2.21	0.41
2:F:186:ASP:OD1	2:F:186:ASP:C	2.59	0.41
1:H:293:VAL:O	1:H:293:VAL:HG12	2.21	0.41
2:C:186:ASP:OD1	2:C:186:ASP:C	2.60	0.41
2:G:381:TRP:CH2	2:G:382:LEU:HD13	2.56	0.41
2:F:445:LEU:CD2	2:F:449:PHE:CD2	2.98	0.41
1:E:53:LEU:HD23	1:E:53:LEU:H	1.80	0.41
1:D:132:LEU:CD2	1:D:142:VAL:HG13	2.51	0.41
2:C:244:VAL:CG1	2:C:260:LEU:HD22	2.51	0.41
1:H:18:ASP:OD2	1:H:62:GLN:HG2	2.20	0.41
2:G:414:TYR:CD2	2:G:414:TYR:C	2.94	0.41
1:H:135:THR:CG2	1:H:136:GLY:N	2.62	0.40
2:F:432:GLU:OE1	2:F:466:SER:N	2.48	0.40
1:E:303:VAL:HG12	1:E:304:ASN:N	2.37	0.40
1:D:102:HIS:NE2	1:D:130:SER:HB3	2.29	0.40
2:B:202:ARG:HG2	2:B:209:GLN:CD	2.42	0.40
2:C:202:ARG:HG2	2:C:209:GLN:HB2	2.02	0.40
1:E:15:MET:HG3	2:F:162:LYS:HZ2	1.83	0.40
2:C:343:TRP:HZ3	2:C:349:SER:CB	2.33	0.40
2:B:191:ASP:OD1	2:B:529:ARG:NH1	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:467:LYS:HA	2:G:498:ASN:ND2	2.36	0.40
2:G:186:ASP:C	2:G:186:ASP:OD1	2.59	0.40
2:B:186:ASP:OD1	2:B:186:ASP:C	2.59	0.40
2:B:177:THR:HG22	2:B:179:LEU:HD23	1.98	0.40
2:C:489:HIS:O	2:C:490:SER:C	2.60	0.40
2:F:210:ILE:HD13	2:F:496:PHE:CG	2.56	0.40
2:F:366:PHE:O	2:F:373:LYS:HG3	2.21	0.40
2:G:153:PHE:HA	2:G:158:MET:O	2.21	0.40
1:H:14:ASP:CG	1:H:15:MET:H	2.24	0.40
1:D:230:THR:O	1:D:231:ILE:HG13	2.20	0.40
1:D:226:LEU:HD12	1:D:228:THR:H	1.87	0.40
2:C:530:LEU:HB2	2:C:532:ILE:HG12	2.03	0.40
1:H:194:TRP:N	1:H:194:TRP:CD1	2.88	0.40
2:C:329:ASP:HB3	2:C:332:ILE:HD13	2.03	0.40
1:D:240:VAL:O	1:D:258:LEU:CB	2.69	0.40
1:A:132:LEU:CD2	1:A:142:VAL:HG13	2.51	0.40
1:H:21:MET:HA	1:H:28:LEU:HD12	2.02	0.40
1:D:69:MET:HE1	1:D:114:HIS:HB2	2.01	0.40
2:B:199:ILE:CG2	2:B:208:PRO:HB2	2.52	0.40
2:B:371:SER:HG	2:B:373:LYS:H	1.66	0.40
2:B:217:PHE:CZ	2:B:453:LEU:HD23	2.56	0.40
2:G:261:LYS:HG3	2:G:262:LYS:N	2.36	0.40
1:H:230:THR:O	1:H:231:ILE:HG13	2.20	0.40
2:G:451:TRP:CE2	2:G:493:VAL:HG13	2.56	0.40
2:G:522:THR:O	2:G:523:ASN:CG	2.59	0.40
2:G:316:GLY:O	2:G:319:SER:N	2.54	0.40
2:B:480:GLN:OE1	2:B:483:PHE:HD1	2.05	0.40
1:A:69:MET:HE1	1:A:114:HIS:HB2	2.01	0.40
2:C:442:THR:CG2	2:C:444:ALA:CB	2.99	0.40
2:G:177:THR:C	2:G:179:LEU:H	2.25	0.40
2:C:177:THR:CG2	2:C:179:LEU:H	2.16	0.40
2:B:161:THR:O	2:B:171:SER:N	2.55	0.40
2:B:381:TRP:CD2	2:B:412:LEU:HD22	2.56	0.40
2:F:276:ILE:HD13	2:F:383:CYS:CA	2.39	0.40
2:G:272:ILE:HG13	2:G:272:ILE:H	1.67	0.40
2:C:261:LYS:HG3	2:C:262:LYS:N	2.36	0.40
2:F:261:LYS:HG3	2:F:262:LYS:N	2.36	0.40
2:C:241:PHE:CD2	2:C:457:LEU:HD21	2.57	0.40
1:H:226:LEU:HD12	1:H:228:THR:H	1.87	0.40
2:C:198:THR:HB	2:C:212:GLU:HB2	2.03	0.40
2:F:198:THR:HB	2:F:212:GLU:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:194:TRP:N	1:E:194:TRP:CD1	2.89	0.40
1:A:113:PRO:HB3	1:A:161:ALA:HB2	2.00	0.40
1:E:221:ALA:HA	1:E:270:TRP:CD1	2.56	0.40
2:F:145:THR:CG2	2:F:146:ALA:N	2.84	0.40
1:H:18:ASP:OD1	1:H:19:ALA:N	2.55	0.40
1:D:113:PRO:HB2	1:D:161:ALA:HB2	2.03	0.40
2:F:174:ARG:NH2	2:F:485:GLN:OE1	2.46	0.40
2:G:202:ARG:HG2	2:G:209:GLN:HB2	2.02	0.40
2:B:177:THR:HG21	2:B:484:ALA:HB2	2.03	0.40
1:H:102:HIS:NE2	1:H:130:SER:HB3	2.29	0.40
1:A:283:ASP:O	1:A:284:ASN:HB2	2.22	0.40
2:G:175:LEU:CD2	2:G:483:PHE:HE2	2.34	0.40
2:B:261:LYS:HG3	2:B:262:LYS:N	2.36	0.40
2:C:202:ARG:HD3	2:C:202:ARG:HA	1.55	0.40
2:B:198:THR:HB	2:B:212:GLU:HB2	2.04	0.40
1:H:283:ASP:O	1:H:284:ASN:HB2	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	281/316 (89%)	231 (82%)	42 (15%)	8 (3%)	6	30
1	D	279/316 (88%)	226 (81%)	43 (15%)	10 (4%)	4	24
1	E	281/316 (89%)	231 (82%)	43 (15%)	7 (2%)	7	34
1	H	279/316 (88%)	228 (82%)	43 (15%)	8 (3%)	6	29
2	B	421/442 (95%)	336 (80%)	68 (16%)	17 (4%)	4	21
2	C	416/442 (94%)	330 (79%)	73 (18%)	13 (3%)	5	28
2	F	421/442 (95%)	337 (80%)	65 (15%)	19 (4%)	3	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	G	416/442 (94%)	330 (79%)	73 (18%)	13 (3%)	5	28
All	All	2794/3032 (92%)	2249 (80%)	450 (16%)	95 (3%)	5	25

All (95) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	251	ASN
2	B	164	ILE
2	B	371	SER
2	B	428	ASN
2	B	520	ALA
2	B	523	ASN
2	C	371	SER
2	C	395	ASP
2	C	428	ASN
2	C	520	ALA
2	C	523	ASN
2	F	164	ILE
2	F	371	SER
2	F	428	ASN
2	F	520	ALA
2	F	523	ASN
2	G	371	SER
2	G	428	ASN
2	G	496	PHE
2	G	520	ALA
2	G	523	ASN
1	H	249	SER
1	A	114	HIS
2	B	178	GLU
2	B	247	PRO
2	B	346	GLY
2	B	499	ASP
2	B	526	ILE
2	C	526	ILE
1	D	114	HIS
1	D	250	SER
1	E	114	HIS
2	F	178	GLU
2	F	346	GLY
2	F	394	ILE
2	F	499	ASP

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Mol	Chain	Res	Type
2	F	526	ILE
2	G	500	ASP
2	G	526	ILE
1	H	114	HIS
1	A	184	SER
2	B	157	SER
2	B	447	VAL
2	C	393	GLN
2	C	447	VAL
1	D	184	SER
1	E	184	SER
2	F	157	SER
2	F	447	VAL
2	F	486	LEU
2	G	395	ASP
2	G	447	VAL
1	H	184	SER
1	A	55	GLY
2	B	182	LYS
2	B	431	THR
2	C	182	LYS
2	C	431	THR
1	D	55	GLY
1	D	198	GLU
1	E	55	GLY
2	F	182	LYS
2	F	431	THR
2	G	182	LYS
2	G	431	THR
1	H	55	GLY
1	A	68	PRO
2	C	250	THR
1	D	68	PRO
1	D	247	ASP
1	E	68	PRO
2	F	247	PRO
2	F	393	GLN
2	G	524	ASP
1	H	68	PRO
2	B	226	LYS
2	C	226	LYS
2	C	290	GLU

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Mol	Chain	Res	Type
2	F	226	LYS
2	G	346	GLY
2	B	172	ILE
2	F	172	ILE
1	A	129	ILE
1	A	176	PRO
2	B	347	GLY
1	D	129	ILE
1	D	176	PRO
1	E	129	ILE
1	E	176	PRO
1	H	129	ILE
1	H	176	PRO
1	D	224	ILE
1	A	224	ILE
1	E	224	ILE
1	H	224	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	240/267 (90%)	222 (92%)	18 (8%)	17	51
1	D	238/267 (89%)	218 (92%)	20 (8%)	14	45
1	E	240/267 (90%)	222 (92%)	18 (8%)	17	51
1	H	238/267 (89%)	219 (92%)	19 (8%)	15	47
2	B	386/403 (96%)	352 (91%)	34 (9%)	12	42
2	C	384/403 (95%)	356 (93%)	28 (7%)	17	52
2	F	386/403 (96%)	349 (90%)	37 (10%)	10	38
2	G	384/403 (95%)	352 (92%)	32 (8%)	14	46
All	All	2496/2680 (93%)	2290 (92%)	206 (8%)	14	46

All (206) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	ARG
1	A	39	ILE
1	A	53	LEU
1	A	54	ARG
1	A	70	TYR
1	A	86	TRP
1	A	184	SER
1	A	193	LEU
1	A	201	GLN
1	A	220	TRP
1	A	226	LEU
1	A	244	THR
1	A	271	SER
1	A	280	SER
1	A	283	ASP
1	A	287	THR
1	A	298	VAL
1	A	300	ILE
2	B	133	ASP
2	B	141	GLU
2	B	142	ARG
2	B	158	MET
2	B	159	LEU
2	B	160	LEU
2	B	163	ASP
2	B	164	ILE
2	B	179	LEU
2	B	209	GLN
2	B	223	TYR
2	B	228	SER
2	B	267	ARG
2	B	282	GLU
2	B	299	LEU
2	B	321	LEU
2	B	339	GLN
2	B	365	PRO
2	B	370	PHE
2	B	378	GLU
2	B	395	ASP
2	B	397	TYR
2	B	401	SER
2	B	418	ILE
2	B	421	ILE

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Mol	Chain	Res	Type
2	B	431	THR
2	B	453	LEU
2	B	455	GLN
2	B	463	ARG
2	B	466	SER
2	B	470	SER
2	B	505	ASP
2	B	532	ILE
2	B	550	ASN
2	C	133	ASP
2	C	138	ILE
2	C	139	MET
2	C	150	PHE
2	C	175	LEU
2	C	209	GLN
2	C	223	TYR
2	C	228	SER
2	C	267	ARG
2	C	282	GLU
2	C	299	LEU
2	C	321	LEU
2	C	339	GLN
2	C	365	PRO
2	C	370	PHE
2	C	378	GLU
2	C	401	SER
2	C	418	ILE
2	C	421	ILE
2	C	431	THR
2	C	453	LEU
2	C	455	GLN
2	C	466	SER
2	C	470	SER
2	C	492	PHE
2	C	495	CYS
2	C	505	ASP
2	C	550	ASN
1	D	27	ARG
1	D	41	ASP
1	D	53	LEU
1	D	54	ARG
1	D	70	TYR

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Mol	Chain	Res	Type
1	D	86	TRP
1	D	184	SER
1	D	193	LEU
1	D	220	TRP
1	D	226	LEU
1	D	246	ASP
1	D	247	ASP
1	D	261	PHE
1	D	271	SER
1	D	280	SER
1	D	283	ASP
1	D	287	THR
1	D	296	GLN
1	D	299	CYS
1	D	301	SER
1	E	27	ARG
1	E	53	LEU
1	E	54	ARG
1	E	70	TYR
1	E	86	TRP
1	E	184	SER
1	E	193	LEU
1	E	201	GLN
1	E	220	TRP
1	E	226	LEU
1	E	244	THR
1	E	252	THR
1	E	271	SER
1	E	280	SER
1	E	283	ASP
1	E	287	THR
1	E	298	VAL
1	E	300	ILE
2	F	133	ASP
2	F	141	GLU
2	F	142	ARG
2	F	158	MET
2	F	159	LEU
2	F	160	LEU
2	F	163	ASP
2	F	164	ILE
2	F	179	LEU

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Mol	Chain	Res	Type
2	F	209	GLN
2	F	223	TYR
2	F	228	SER
2	F	253	ASP
2	F	267	ARG
2	F	282	GLU
2	F	299	LEU
2	F	321	LEU
2	F	339	GLN
2	F	365	PRO
2	F	370	PHE
2	F	378	GLU
2	F	379	PHE
2	F	393	GLN
2	F	397	TYR
2	F	401	SER
2	F	412	LEU
2	F	418	ILE
2	F	421	ILE
2	F	431	THR
2	F	453	LEU
2	F	455	GLN
2	F	466	SER
2	F	470	SER
2	F	486	LEU
2	F	489	HIS
2	F	505	ASP
2	F	550	ASN
2	G	133	ASP
2	G	138	ILE
2	G	139	MET
2	G	150	PHE
2	G	175	LEU
2	G	209	GLN
2	G	223	TYR
2	G	228	SER
2	G	244	VAL
2	G	267	ARG
2	G	282	GLU
2	G	299	LEU
2	G	321	LEU
2	G	339	GLN

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Mol	Chain	Res	Type
2	G	365	PRO
2	G	370	PHE
2	G	378	GLU
2	G	380	SER
2	G	401	SER
2	G	412	LEU
2	G	414	TYR
2	G	418	ILE
2	G	421	ILE
2	G	431	THR
2	G	453	LEU
2	G	455	GLN
2	G	466	SER
2	G	470	SER
2	G	494	SER
2	G	495	CYS
2	G	505	ASP
2	G	550	ASN
1	H	27	ARG
1	H	53	LEU
1	H	54	ARG
1	H	70	TYR
1	H	86	TRP
1	H	184	SER
1	H	193	LEU
1	H	195	LYS
1	H	220	TRP
1	H	226	LEU
1	H	246	ASP
1	H	247	ASP
1	H	271	SER
1	H	280	SER
1	H	283	ASP
1	H	287	THR
1	H	296	GLN
1	H	299	CYS
1	H	301	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	114	HIS

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Mol	Chain	Res	Type
1	A	275	ASN
1	A	296	GLN
2	B	232	ASN
2	B	341	GLN
2	B	353	ASN
2	B	448	GLN
2	B	455	GLN
2	B	487	HIS
2	C	232	ASN
2	C	275	GLN
2	C	328	ASN
2	C	341	GLN
2	C	455	GLN
2	C	487	HIS
1	D	47	GLN
1	D	62	GLN
1	D	72	ASN
1	D	114	HIS
1	E	17	HIS
1	E	107	ASN
1	E	114	HIS
1	E	251	ASN
1	E	267	HIS
1	E	275	ASN
2	F	232	ASN
2	F	275	GLN
2	F	341	GLN
2	F	455	GLN
2	G	232	ASN
2	G	275	GLN
2	G	341	GLN
2	G	353	ASN
2	G	455	GLN
2	G	487	HIS
2	G	498	ASN
1	H	47	GLN
1	H	114	HIS
1	H	206	GLN
1	H	296	GLN

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	285/316 (90%)	-0.00	10 (3%)	48	21	79, 129, 189, 200	0
1	D	283/316 (89%)	0.91	53 (18%)	2	1	119, 185, 200, 200	0
1	E	285/316 (90%)	0.05	15 (5%)	30	12	70, 128, 189, 200	0
1	H	283/316 (89%)	0.52	30 (10%)	8	3	108, 174, 200, 200	0
2	B	423/442 (95%)	-0.20	9 (2%)	67	36	70, 134, 189, 200	0
2	C	420/442 (95%)	-0.16	17 (4%)	42	17	99, 150, 195, 200	0
2	F	423/442 (95%)	-0.19	16 (3%)	44	18	70, 142, 193, 200	0
2	G	420/442 (95%)	-0.20	15 (3%)	46	20	92, 151, 197, 200	0
All	All	2822/3032 (93%)	0.04	165 (5%)	26	10	70, 149, 200, 200	0

All (165) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	248	ALA	11.1
1	H	247	ASP	8.6
1	D	155	ALA	6.1
1	E	282	GLY	6.0
1	D	122	CYS	5.9
1	H	14	ASP	5.4
1	D	233	SER	5.4
1	A	171	PRO	5.2
1	H	234	CYS	5.1
1	H	171	PRO	4.9
1	A	282	GLY	4.9
2	C	552	LEU	4.9
1	D	152	GLY	4.9
1	D	249	SER	4.9
2	F	394	ILE	4.8
1	D	57	GLU	4.8

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Mol	Chain	Res	Type	RSRZ
1	D	123	GLY	4.7
1	E	171	PRO	4.6
1	D	209	GLU	4.5
1	E	14	ASP	4.5
2	C	346	GLY	4.5
1	D	174	GLN	4.4
2	F	349	SER	4.3
1	A	283	ASP	4.2
2	F	395	ASP	4.2
1	D	207	LYS	4.1
1	E	233	SER	4.1
2	C	130	ASP	4.1
2	B	132	ILE	4.0
1	D	173	GLY	3.9
1	H	284	ASN	3.8
1	D	178	TYR	3.8
2	F	551	TYR	3.8
1	D	79	TYR	3.7
1	D	172	SER	3.7
1	H	209	GLU	3.7
1	H	174	GLN	3.7
1	E	283	ASP	3.7
1	D	146	ASN	3.6
2	B	348	CYS	3.6
1	H	173	GLY	3.6
1	D	293	VAL	3.6
1	D	151	ILE	3.6
1	D	201	GLN	3.5
1	D	239	ARG	3.5
1	A	249	SER	3.5
2	C	131	GLU	3.4
1	E	248	ALA	3.4
1	D	250	SER	3.4
2	C	203	LYS	3.4
2	B	495	CYS	3.3
2	G	395	ASP	3.3
1	E	234	CYS	3.3
1	D	206	GLN	3.3
2	B	133	ASP	3.3
1	D	177	ASN	3.2
1	H	239	ARG	3.2
2	F	131	GLU	3.2

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Mol	Chain	Res	Type	RSRZ
2	G	367	GLU	3.2
1	A	172	SER	3.2
1	E	249	SER	3.2
1	E	173	GLY	3.1
2	G	345	THR	3.0
2	G	346	GLY	3.0
2	F	520	ALA	3.0
1	E	172	SER	3.0
1	D	154	ASN	3.0
2	B	131	GLU	3.0
1	H	163	VAL	2.9
2	G	393	GLN	2.9
1	H	199	ASP	2.9
2	G	130	ASP	2.9
2	G	225	GLU	2.9
1	D	200	GLY	2.9
2	B	130	ASP	2.9
1	D	144	LYS	2.9
1	D	222	PRO	2.8
1	H	225	GLY	2.8
1	H	172	SER	2.8
1	D	241	PHE	2.8
2	G	341	GLN	2.8
1	H	227	PRO	2.8
1	D	108	SER	2.8
2	B	251	ASP	2.8
1	D	248	ALA	2.8
2	F	132	ILE	2.7
2	F	314	LYS	2.7
2	F	130	ASP	2.7
2	C	345	THR	2.7
2	C	394	ILE	2.7
2	F	369	LEU	2.7
1	D	171	PRO	2.7
1	D	176	PRO	2.6
2	G	349	SER	2.6
2	G	521	SER	2.6
1	H	241	PHE	2.6
2	G	443	ASN	2.6
2	C	135	ALA	2.6
1	D	223	SER	2.6
1	D	224	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
1	H	262	ASN	2.6
1	D	103	ASP	2.6
1	D	292	SER	2.6
1	D	14	ASP	2.6
1	D	76	SER	2.6
1	D	161	ALA	2.5
1	D	147	ASN	2.5
1	H	175	LYS	2.5
1	H	200	GLY	2.5
1	H	233	SER	2.5
1	H	253	TRP	2.5
2	G	326	GLY	2.5
1	E	209	GLU	2.5
1	E	174	GLN	2.5
2	F	521	SER	2.5
2	B	394	ILE	2.5
1	D	163	VAL	2.5
2	F	348	CYS	2.5
1	D	153	CYS	2.4
1	D	107	ASN	2.4
1	D	130	SER	2.4
1	D	281	GLY	2.4
2	C	348	CYS	2.4
2	C	132	ILE	2.4
1	H	294	ASP	2.4
2	G	348	CYS	2.4
1	H	246	ASP	2.4
1	H	217	ASP	2.3
1	D	247	ASP	2.3
1	D	55	GLY	2.3
1	E	164	PRO	2.3
2	C	164	ILE	2.3
1	D	234	CYS	2.3
2	G	178	GLU	2.3
1	D	246	ASP	2.3
2	C	133	ASP	2.3
1	H	190	LEU	2.2
2	F	346	GLY	2.2
2	G	524	ASP	2.2
2	F	345	THR	2.2
1	E	284	ASN	2.2
1	A	247	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	H	15	MET	2.2
2	C	155	THR	2.2
1	A	248	ALA	2.2
2	C	347	GLY	2.2
1	H	82	LYS	2.2
1	D	92	THR	2.2
2	B	346	GLY	2.2
1	H	164	PRO	2.1
1	D	82	LYS	2.1
1	D	135	THR	2.1
1	E	122	CYS	2.1
1	H	235	SER	2.1
1	A	209	GLU	2.1
1	D	262	ASN	2.1
2	C	396	GLU	2.1
2	F	524	ASP	2.1
1	H	57	GLU	2.1
1	A	262	ASN	2.0
1	A	304	ASN	2.0
2	C	520	ALA	2.0
2	C	395	ASP	2.0
1	D	162	VAL	2.0
2	F	552	LEU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.