



# Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 04:48 am BST

PDB ID : 3BG0  
Title : Architecture of a Coat for the Nuclear Pore Membrane  
Authors : Hoelz, A.  
Deposited on : 2007-11-23  
Resolution : 3.15 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

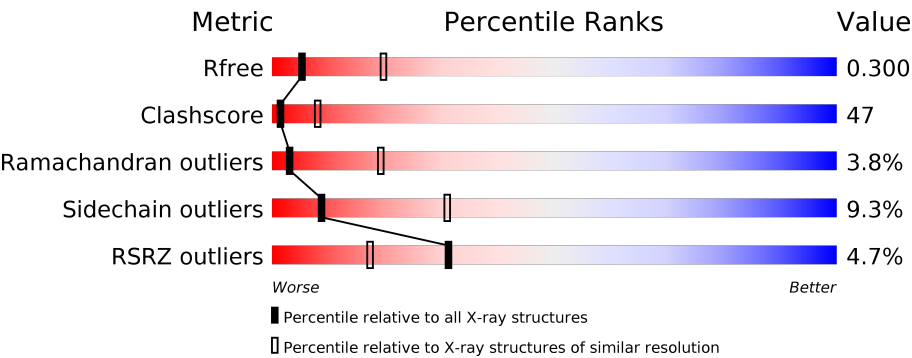
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.15 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1665 (3.20-3.12)
Clashscore	141614	1804 (3.20-3.12)
Ramachandran outliers	138981	1770 (3.20-3.12)
Sidechain outliers	138945	1769 (3.20-3.12)
RSRZ outliers	127900	1616 (3.20-3.12)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	316	<div><div>3%</div><div><div></div><div>31%</div><div>49%</div><div>9%</div><div>10%</div></div></div>
1	D	316	<div><div>11%</div><div><div></div><div>32%</div><div>49%</div><div>8%</div><div>11%</div></div></div>
1	E	316	<div><div>2%</div><div><div></div><div>31%</div><div>49%</div><div>9%</div><div>10%</div></div></div>
1	H	316	<div><div>10%</div><div><div></div><div>30%</div><div>51%</div><div>8%</div><div>11%</div></div></div>
2	B	442	<div><div>2%</div><div><div></div><div>42%</div><div>46%</div><div>8%</div><div>•</div></div></div>
2	C	442	<div><div>2%</div><div><div></div><div>39%</div><div>47%</div><div>8%</div><div>5%</div></div></div>

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Mol	Chain	Length	Quality of chain
2	F	442	
2	G	442	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 22562 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	283	Total	C	N	O	S	0	0	0
			2220	1399	387	422	12			
1	D	281	Total	C	N	O	S	0	0	0
			2205	1390	384	419	12			
1	E	283	Total	C	N	O	S	0	0	0
			2220	1399	387	422	12			
1	H	281	Total	C	N	O	S	0	0	0
			2205	1390	384	419	12			

- Molecule 2 is a protein called Nucleoporin NUP145.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	423	Total	C	N	O	S	19	0	0
			3438	2201	570	656	11			
2	C	420	Total	C	N	O	S	19	0	0
			3418	2188	566	653	11			
2	F	423	Total	C	N	O	S	19	0	0
			3438	2201	570	656	11			
2	G	420	Total	C	N	O	S	19	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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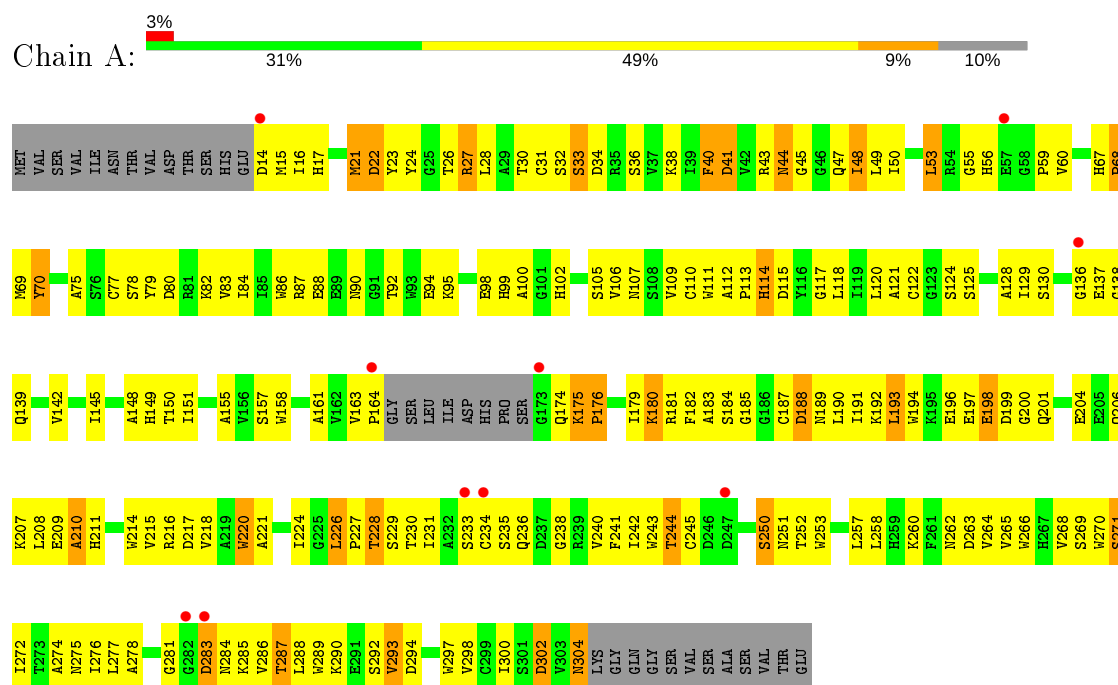
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Chain	Residue	Modelled	Actual	Comment	Reference
G	119	HIS	-	EXPRESSION TAG	UNP P49687
G	120	HIS	-	EXPRESSION TAG	UNP P49687
G	121	SER	-	EXPRESSION TAG	UNP P49687
G	122	GLY	-	EXPRESSION TAG	UNP P49687
G	123	ASP	-	EXPRESSION TAG	UNP P49687
G	124	PRO	-	EXPRESSION TAG	UNP P49687

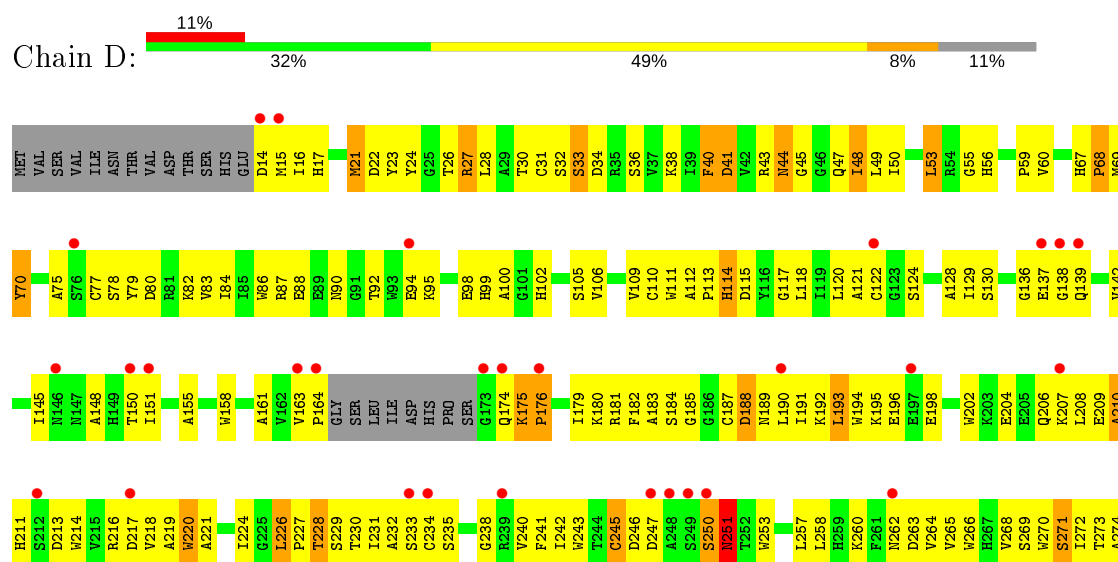
### 3 Residue-property plots

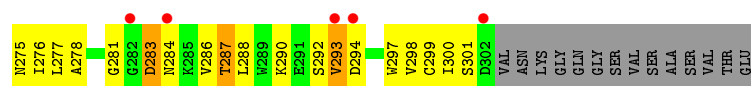
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: Protein SEC13 homolog

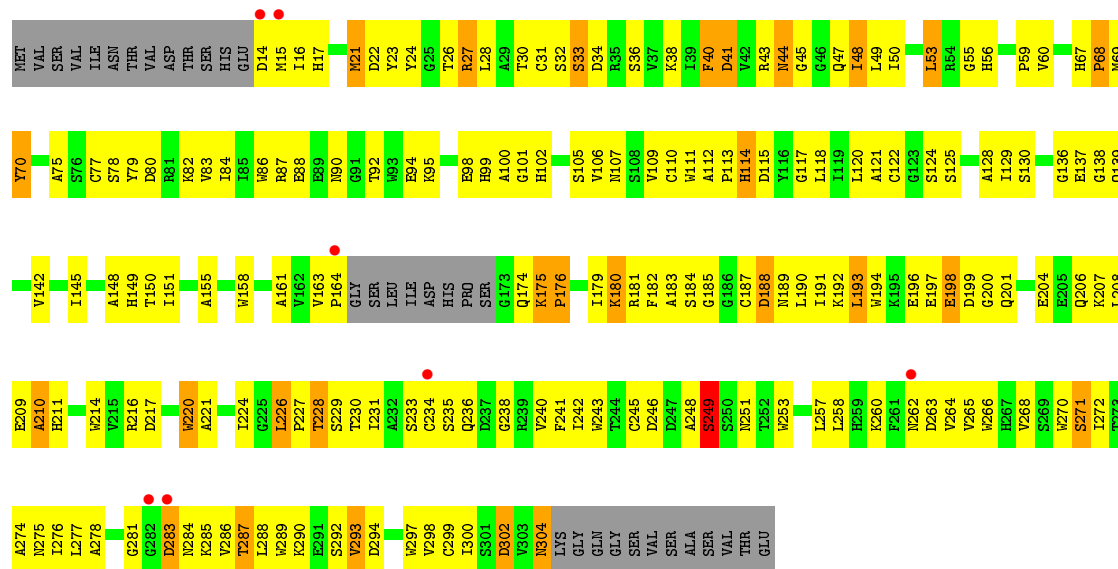


#### • Molecule 1: Protein SEC13 homolog

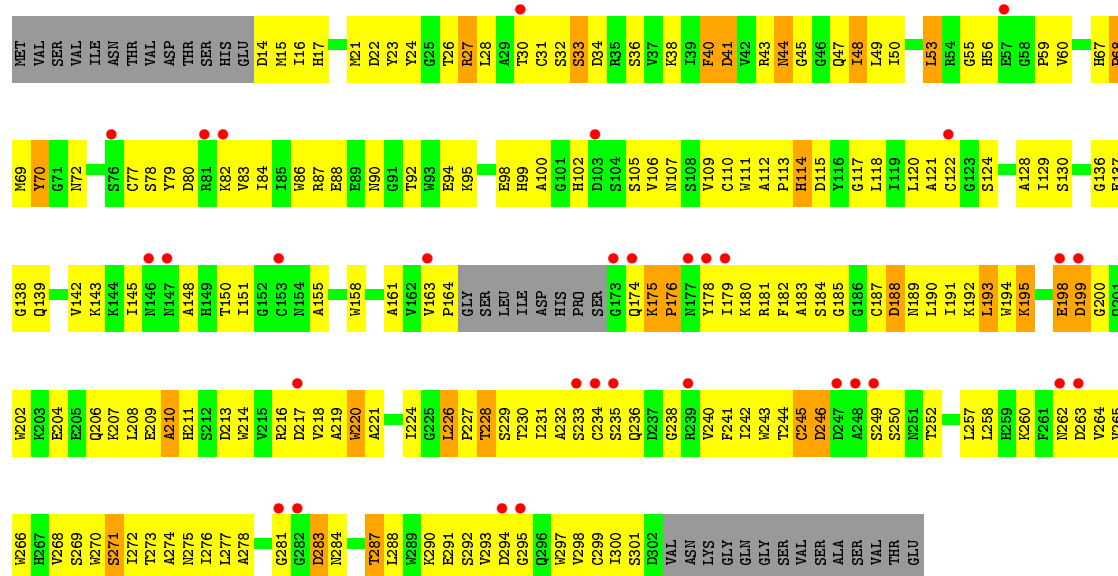




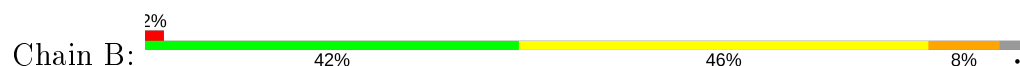
• Molecule 1: Protein SEC13 homolog



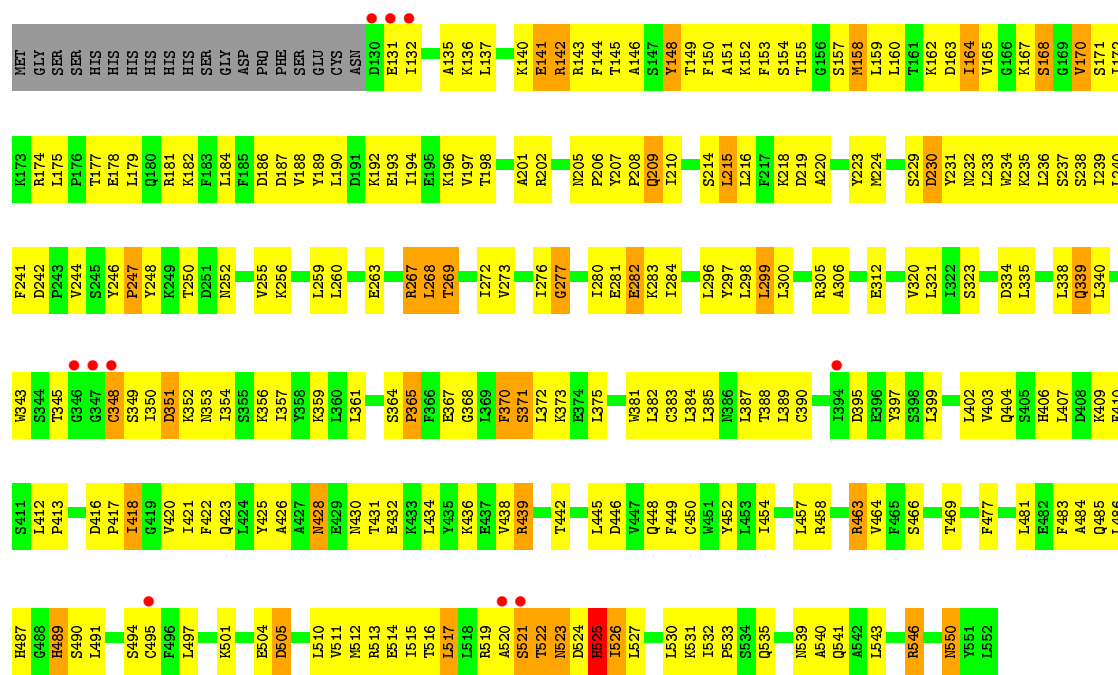
• Molecule 1: Protein SEC13 homolog



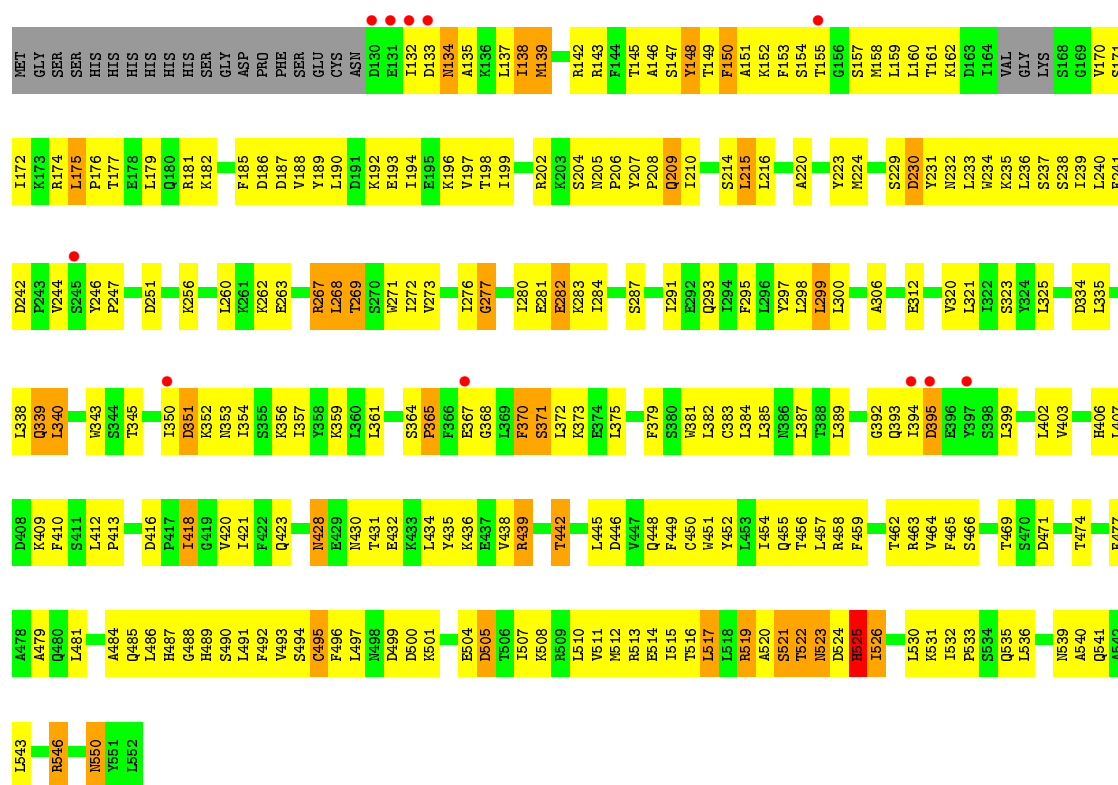
• Molecule 2: Nucleoporin NUP145





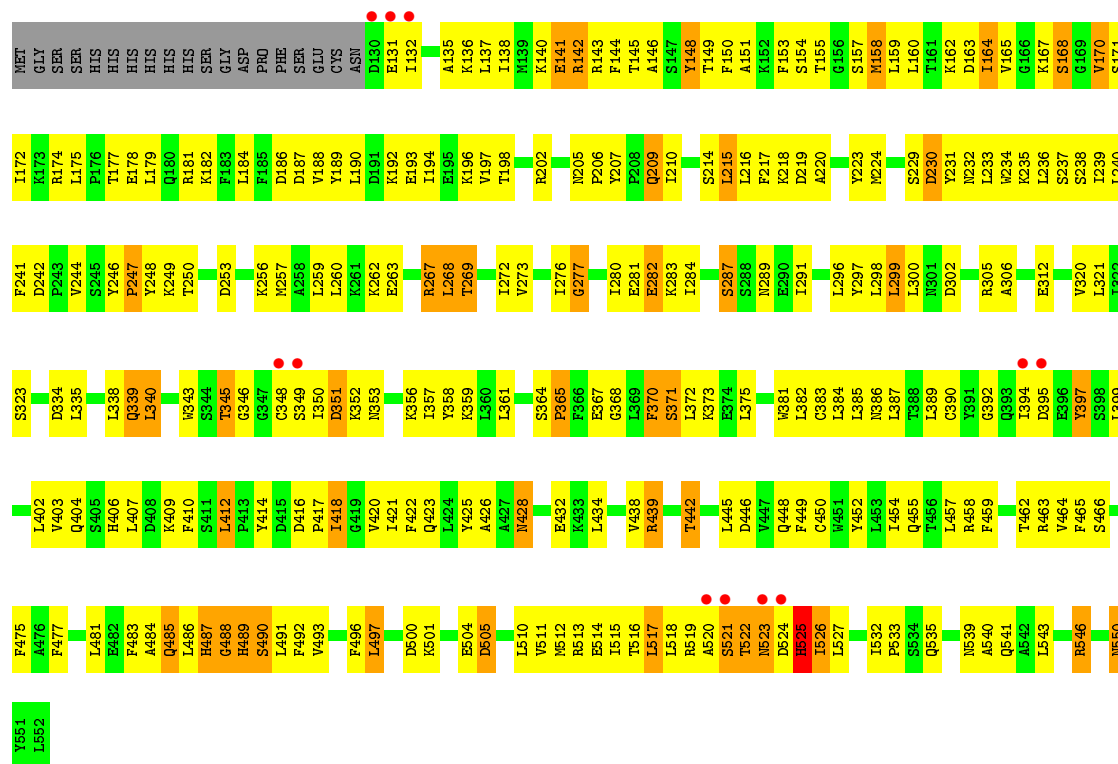


### • Molecule 2: Nucleoporin NUP145

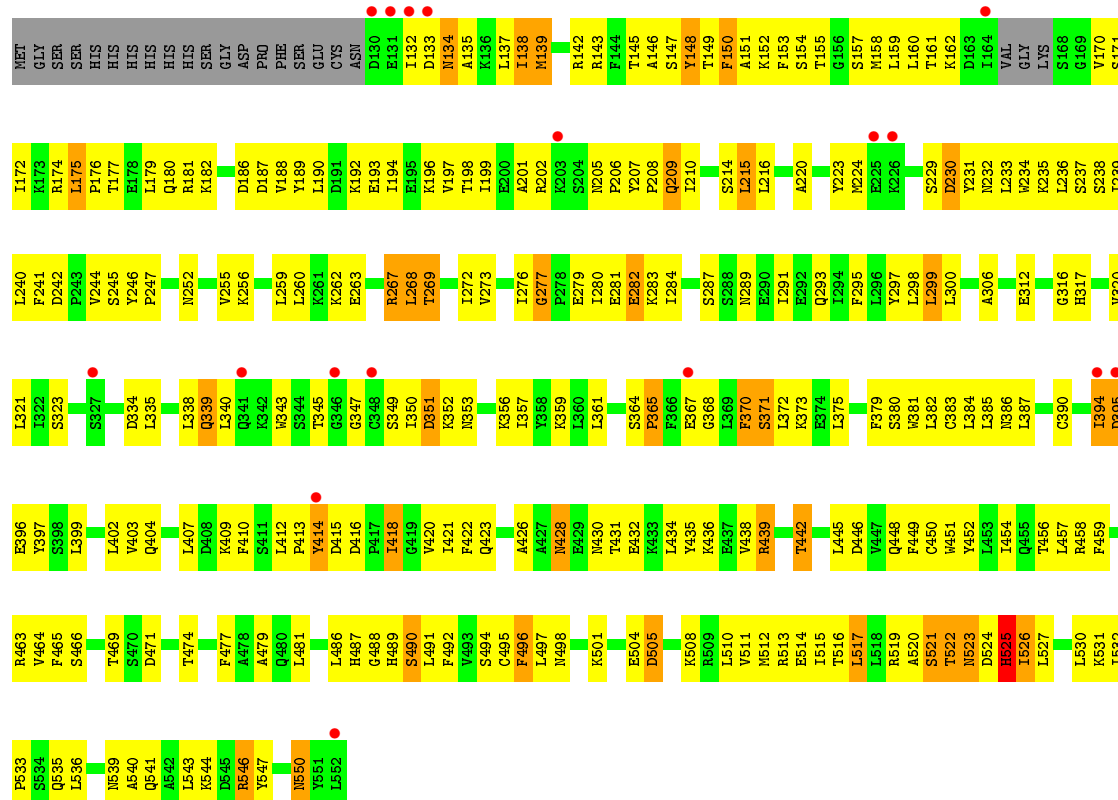


### • Molecule 2: Nucleoporin NUP145





• Molecule 2: Nucleoporin NUP145



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	181.82Å 216.57Å 100.96Å 90.00° 108.11° 90.00°	Depositor
Resolution (Å)	20.00 – 3.15 19.92 – 3.12	Depositor EDS
% Data completeness (in resolution range)	95.7 (20.00-3.15) 85.8 (19.92-3.12)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.80 (at 3.09Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.252 , 0.294 0.264 , 0.300	Depositor DCC
$R_{free}$ test set	3096 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	99.0	Xtriage
Anisotropy	0.682	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.25 , 88.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	22562	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	153.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.75% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality

### 5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z  > 5$	RMSZ	# $ Z  > 5$
1	A	0.50	0/2283	0.74	0/3112
1	D	0.49	0/2268	0.73	2/3091 (0.1%)
1	E	0.52	0/2283	0.74	0/3112
1	H	0.49	0/2268	0.72	1/3091 (0.0%)
2	B	0.51	0/3504	0.76	1/4728 (0.0%)
2	C	0.50	0/3483	0.75	1/4699 (0.0%)
2	F	0.52	0/3504	0.78	3/4728 (0.1%)
2	G	0.49	0/3483	0.76	3/4699 (0.1%)
All	All	0.50	0/23076	0.75	11/31260 (0.0%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	488	GLY	N-CA-C	-5.68	98.89	113.10
2	G	394	ILE	N-CA-C	-5.62	95.84	111.00
2	F	287	SER	N-CA-C	5.60	126.11	111.00
1	D	251	ASN	N-CA-C	5.58	126.08	111.00
1	D	41	ASP	CB-CA-C	5.36	121.13	110.40
1	H	41	ASP	CB-CA-C	5.35	121.10	110.40
2	C	182	LYS	N-CA-C	5.10	124.76	111.00
2	F	182	LYS	N-CA-C	5.08	124.72	111.00
2	G	182	LYS	N-CA-C	5.08	124.72	111.00
2	B	182	LYS	N-CA-C	5.05	124.64	111.00
2	G	486	LEU	N-CA-C	-5.03	97.42	111.00

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	2220	0	2096	243	0
1	D	2205	0	2081	217	0
1	E	2220	0	2096	241	0
1	H	2205	0	2081	229	0
2	B	3438	0	3452	311	0
2	C	3418	0	3426	299	0
2	F	3438	0	3452	342	0
2	G	3418	0	3426	339	0
All	All	22562	0	22110	2072	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 47.

All (2072) 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)
2:F:174:ARG:HH22	2:F:485:GLN:HB2	0.96	1.12
2:C:481:LEU:HD13	2:C:489:HIS:HB3	1.31	1.11
2:B:174:ARG:HH22	2:B:485:GLN:HG2	0.96	1.11
2:F:481:LEU:HD13	2:F:489:HIS:HB3	1.16	1.11
2:B:174:ARG:HH22	2:B:485:GLN:CG	1.64	1.09
2:C:364:SER:HB3	2:C:394:ILE:HG13	1.32	1.09
2:G:481:LEU:HD13	2:G:489:HIS:HB3	1.24	1.08
2:F:343:TRP:HZ3	2:F:350:ILE:HG21	1.17	1.06
2:B:177:THR:CG2	2:B:179:LEU:HB3	1.85	1.06
2:F:177:THR:CG2	2:F:179:LEU:HB3	1.85	1.05
2:B:174:ARG:NH2	2:B:485:GLN:HG2	1.72	1.03
2:B:250:THR:HG22	2:B:252:ASN:H	1.24	1.02
2:F:233:LEU:HD13	2:F:417:PRO:HB2	1.41	1.01
2:G:532:ILE:HG23	2:G:533:PRO:HD2	1.43	1.01
1:A:28:LEU:CD1	2:B:172:ILE:HD11	1.90	1.01
2:F:343:TRP:CZ3	2:F:350:ILE:HG21	1.97	1.00
2:G:134:ASN:O	2:G:138:ILE:HB	1.62	0.99
2:C:134:ASN:O	2:C:138:ILE:HB	1.61	0.98
2:G:238:SER:HA	2:G:242:ASP:OD2	1.63	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:79:TYR:HD1	1:H:105:SER:HB2	1.30	0.97
1:A:79:TYR:HD1	1:A:105:SER:HB2	1.30	0.97
1:D:79:TYR:HD1	1:D:105:SER:HB2	1.30	0.97
1:E:79:TYR:HD1	1:E:105:SER:HB2	1.30	0.96
2:C:375:LEU:HB3	2:C:379:PHE:HD2	1.28	0.96
1:E:28:LEU:CD1	2:F:172:ILE:HD11	1.95	0.95
2:F:174:ARG:NH2	2:F:485:GLN:HB2	1.81	0.95
2:G:380:SER:HB3	2:G:383:CYS:HB2	1.47	0.95
1:D:151:ILE:HB	1:D:187:CYS:HB2	1.49	0.94
2:G:442:THR:HG23	2:G:445:LEU:HB2	1.49	0.93
2:G:155:THR:HG22	2:G:513:ARG:HD2	1.47	0.92
1:E:278:ALA:HB2	2:F:153:PHE:HE1	1.32	0.92
2:B:404:GLN:HG2	2:B:426:ALA:HB1	1.51	0.92
1:E:226:LEU:HD13	1:E:227:PRO:HD2	1.51	0.92
1:A:226:LEU:HD13	1:A:227:PRO:HD2	1.51	0.91
1:H:226:LEU:HD13	1:H:227:PRO:HD2	1.51	0.91
1:A:278:ALA:HB2	2:B:153:PHE:HE1	1.35	0.91
1:D:226:LEU:HD13	1:D:227:PRO:HD2	1.51	0.91
2:G:442:THR:HG22	2:G:442:THR:O	1.71	0.90
2:B:442:THR:HG22	2:B:442:THR:O	1.71	0.90
2:B:491:LEU:HD21	2:B:532:ILE:HD11	1.51	0.90
2:G:155:THR:CG2	2:G:513:ARG:HD2	2.01	0.90
2:G:532:ILE:CG2	2:G:533:PRO:HD2	2.01	0.90
2:F:343:TRP:HZ3	2:F:350:ILE:CG2	1.85	0.89
2:C:442:THR:O	2:C:442:THR:HG22	1.71	0.89
2:B:359:LYS:HD2	2:B:365:PRO:HA	1.55	0.89
2:F:359:LYS:HD2	2:F:365:PRO:HA	1.55	0.89
2:B:515:ILE:HD11	2:B:540:ALA:HB1	1.55	0.88
1:E:40:PHE:CE2	2:F:168:SER:HB2	2.09	0.88
2:G:359:LYS:HD2	2:G:365:PRO:HA	1.55	0.88
2:F:442:THR:HG22	2:F:442:THR:O	1.71	0.88
2:C:359:LYS:HD2	2:C:365:PRO:HA	1.55	0.87
2:B:172:ILE:HG22	2:B:172:ILE:O	1.75	0.86
2:F:439:ARG:HA	2:F:442:THR:OG1	1.74	0.86
2:C:439:ARG:HG2	2:C:439:ARG:HH11	1.41	0.86
2:B:177:THR:HG22	2:B:179:LEU:H	1.41	0.86
2:B:439:ARG:HA	2:B:442:THR:OG1	1.74	0.86
2:G:439:ARG:HA	2:G:442:THR:OG1	1.74	0.86
1:E:278:ALA:HB2	2:F:153:PHE:CE1	2.11	0.86
1:D:95:LYS:HE3	1:D:98:GLU:HB2	1.58	0.85
2:B:439:ARG:HG2	2:B:439:ARG:HH11	1.41	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:439:ARG:HA	2:C:442:THR:OG1	1.74	0.85
1:A:220:TRP:CZ3	1:A:229:SER:HB2	2.12	0.85
2:C:532:ILE:HG23	2:C:533:PRO:HD2	1.56	0.85
1:D:220:TRP:CZ3	1:D:229:SER:HB2	2.11	0.85
2:B:490:SER:OG	2:B:510:LEU:HD21	1.76	0.85
1:E:220:TRP:CZ3	1:E:229:SER:HB2	2.11	0.85
2:G:439:ARG:HH11	2:G:439:ARG:HG2	1.41	0.85
2:C:210:ILE:CD1	2:C:495:CYS:HB2	2.05	0.85
2:F:484:ALA:O	2:F:486:LEU:HG	1.76	0.85
1:A:40:PHE:CZ	2:B:168:SER:HB2	2.12	0.85
2:C:151:ALA:HA	2:C:160:LEU:O	1.77	0.85
1:E:95:LYS:HE3	1:E:98:GLU:HB2	1.59	0.85
2:G:490:SER:HB3	2:G:510:LEU:HD21	1.55	0.85
1:H:95:LYS:HE3	1:H:98:GLU:HB2	1.58	0.85
1:H:220:TRP:CZ3	1:H:229:SER:HB2	2.11	0.84
2:G:291:ILE:HG22	2:G:353:ASN:HB2	1.58	0.84
2:G:522:THR:HG22	2:G:526:ILE:HD11	1.59	0.84
2:B:159:LEU:C	2:B:160:LEU:HD23	1.98	0.84
2:F:172:ILE:O	2:F:172:ILE:HG22	1.75	0.84
2:F:439:ARG:HH11	2:F:439:ARG:HG2	1.41	0.84
2:C:522:THR:HG22	2:C:526:ILE:HD11	1.59	0.84
1:A:278:ALA:HB2	2:B:153:PHE:CE1	2.13	0.84
2:C:365:PRO:HB2	2:C:372:LEU:HD12	1.59	0.84
2:F:522:THR:HG22	2:F:526:ILE:HD11	1.59	0.84
2:B:321:LEU:HB3	2:B:361:LEU:HD11	1.60	0.84
2:B:365:PRO:HB2	2:B:372:LEU:HD12	1.59	0.84
1:E:221:ALA:HB2	1:E:270:TRP:CE2	2.12	0.84
2:G:151:ALA:HA	2:G:160:LEU:O	1.77	0.83
2:G:365:PRO:HB2	2:G:372:LEU:HD12	1.59	0.83
2:F:442:THR:O	2:F:442:THR:CG2	2.26	0.83
2:F:159:LEU:C	2:F:160:LEU:HD23	1.98	0.83
2:F:177:THR:HG22	2:F:179:LEU:H	1.41	0.83
1:A:40:PHE:CE2	2:B:168:SER:HB2	2.14	0.83
1:E:40:PHE:CZ	2:F:168:SER:HB2	2.13	0.83
2:B:151:ALA:HB1	2:B:159:LEU:HD11	1.61	0.83
2:C:149:THR:HG22	2:C:150:PHE:H	1.44	0.83
1:A:82:LYS:HG2	1:A:100:ALA:HB2	1.60	0.83
1:A:95:LYS:HE3	1:A:98:GLU:HB2	1.59	0.83
2:B:522:THR:HG22	2:B:526:ILE:HD11	1.59	0.82
2:F:365:PRO:HB2	2:F:372:LEU:HD12	1.59	0.82
2:B:487:HIS:CD2	2:B:487:HIS:H	1.95	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:515:ILE:HD11	2:C:540:ALA:HB1	1.59	0.82
2:G:481:LEU:HD13	2:G:489:HIS:CB	2.09	0.82
1:H:82:LYS:HG2	1:H:100:ALA:HB2	1.60	0.82
1:D:82:LYS:HG2	1:D:100:ALA:HB2	1.60	0.82
1:H:79:TYR:CD1	1:H:105:SER:HB2	2.14	0.82
2:B:442:THR:CG2	2:B:442:THR:O	2.27	0.82
2:C:238:SER:HA	2:C:242:ASP:OD2	1.79	0.82
2:G:442:THR:O	2:G:442:THR:CG2	2.26	0.82
1:D:79:TYR:CD1	1:D:105:SER:HB2	2.13	0.82
1:E:82:LYS:HG2	1:E:100:ALA:HB2	1.60	0.81
2:G:284:ILE:HD13	2:G:297:TYR:CE1	2.15	0.81
1:A:79:TYR:CD1	1:A:105:SER:HB2	2.13	0.81
1:A:190:LEU:HD13	1:A:207:LYS:HD3	1.61	0.81
2:C:515:ILE:HD11	2:C:540:ALA:CB	2.10	0.81
1:D:290:LYS:HB2	1:D:300:ILE:CD1	2.09	0.81
2:B:343:TRP:HZ3	2:B:350:ILE:HG21	1.45	0.81
2:G:158:MET:HE2	2:G:174:ARG:HA	1.61	0.81
1:E:16:ILE:HA	1:E:32:SER:HB3	1.63	0.81
1:D:16:ILE:HA	1:D:32:SER:HB3	1.63	0.81
1:E:151:ILE:HB	1:E:187:CYS:HB2	1.62	0.81
2:F:151:ALA:HB1	2:F:159:LEU:HD11	1.61	0.81
1:E:79:TYR:CD1	1:E:105:SER:HB2	2.14	0.80
1:E:190:LEU:HD13	1:E:207:LYS:HD3	1.63	0.80
2:F:455:GLN:HG2	2:F:496:PHE:CE2	2.16	0.80
2:C:532:ILE:CG2	2:C:533:PRO:HD2	2.11	0.80
2:G:149:THR:HG22	2:G:150:PHE:H	1.44	0.80
2:C:284:ILE:HD13	2:C:297:TYR:CE1	2.16	0.80
1:E:180:LYS:HD2	1:E:196:GLU:OE1	1.82	0.80
1:E:263:ASP:OD1	1:E:264:VAL:N	2.15	0.80
1:D:263:ASP:OD1	1:D:264:VAL:N	2.15	0.79
2:B:515:ILE:HD11	2:B:540:ALA:CB	2.12	0.79
2:B:481:LEU:HD13	2:B:489:HIS:HB3	1.65	0.79
1:A:16:ILE:HA	1:A:32:SER:HB3	1.63	0.79
2:F:491:LEU:CD1	2:F:510:LEU:HD23	2.13	0.79
2:C:442:THR:O	2:C:442:THR:CG2	2.26	0.79
1:H:151:ILE:HB	1:H:187:CYS:HB2	1.64	0.79
2:F:490:SER:HB3	2:F:510:LEU:HD21	1.62	0.79
2:B:233:LEU:HD13	2:B:417:PRO:HB2	1.64	0.79
1:H:263:ASP:OD1	1:H:264:VAL:N	2.15	0.79
1:H:16:ILE:HA	1:H:32:SER:HB3	1.63	0.79
2:C:155:THR:HG22	2:C:513:ARG:HD2	1.65	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:375:LEU:HB3	2:C:379:PHE:CD2	2.17	0.79
2:G:432:GLU:OE2	2:G:466:SER:HB2	1.83	0.79
1:A:263:ASP:OD1	1:A:264:VAL:N	2.15	0.79
2:F:491:LEU:HD12	2:F:510:LEU:HD23	1.65	0.79
2:F:162:LYS:O	2:F:162:LYS:HG3	1.81	0.78
2:G:343:TRP:CZ3	2:G:350:ILE:HD12	2.18	0.78
1:A:70:TYR:CE2	1:A:118:LEU:HB2	2.18	0.78
1:D:70:TYR:CE2	1:D:118:LEU:HB2	2.19	0.78
1:E:226:LEU:HD12	1:E:228:THR:OG1	1.84	0.78
1:A:102:HIS:HD1	1:A:124:SER:HB3	1.48	0.78
2:C:181:ARG:HH12	2:C:234:TRP:HE1	1.32	0.78
2:C:246:TYR:CD1	2:C:247:PRO:HD2	2.18	0.78
2:F:248:TYR:CE2	2:G:343:TRP:CZ2	2.71	0.78
2:B:162:LYS:O	2:B:162:LYS:HG3	1.81	0.78
2:C:177:THR:HG22	2:C:179:LEU:H	1.49	0.78
1:E:70:TYR:CE2	1:E:118:LEU:HB2	2.18	0.78
1:H:70:TYR:CE2	1:H:118:LEU:HB2	2.18	0.78
1:D:190:LEU:HD13	1:D:207:LYS:HD3	1.64	0.78
1:D:226:LEU:HD12	1:D:228:THR:OG1	1.84	0.78
1:E:102:HIS:HD1	1:E:124:SER:HB3	1.48	0.78
2:F:339:GLN:O	2:F:343:TRP:HD1	1.68	0.77
2:C:287:SER:HB3	2:C:293:GLN:NE2	1.99	0.77
2:C:339:GLN:O	2:C:343:TRP:HD1	1.68	0.77
1:D:102:HIS:HD1	1:D:124:SER:HB3	1.48	0.77
1:A:145:ILE:HG22	1:A:148:ALA:HB2	1.67	0.77
2:G:339:GLN:O	2:G:343:TRP:HD1	1.68	0.77
1:A:226:LEU:HD12	1:A:228:THR:OG1	1.84	0.77
2:G:531:LYS:O	2:G:531:LYS:HG3	1.83	0.77
1:E:107:ASN:CG	2:F:142:ARG:HH12	1.88	0.77
2:B:339:GLN:O	2:B:343:TRP:HD1	1.68	0.77
1:D:145:ILE:HG22	1:D:148:ALA:HB2	1.67	0.77
2:F:159:LEU:O	2:F:160:LEU:HD23	1.85	0.77
2:G:215:LEU:HD12	2:G:452:TYR:OH	1.84	0.77
1:H:226:LEU:HD12	1:H:228:THR:OG1	1.85	0.77
2:F:404:GLN:HG2	2:F:426:ALA:HB1	1.65	0.76
2:G:177:THR:HG22	2:G:179:LEU:H	1.49	0.76
2:F:177:THR:HG21	2:F:179:LEU:HB3	1.67	0.76
2:B:238:SER:HA	2:B:242:ASP:OD2	1.85	0.76
2:B:177:THR:HG21	2:B:179:LEU:HB3	1.68	0.76
2:G:527:LEU:HA	2:G:532:ILE:HD12	1.66	0.76
1:H:102:HIS:HD1	1:H:124:SER:HB3	1.48	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:248:ALA:O	1:E:249:SER:HB2	1.85	0.76
2:F:276:ILE:CD1	2:F:383:CYS:HA	2.14	0.76
1:E:220:TRP:HZ3	1:E:229:SER:HB2	1.51	0.76
1:H:145:ILE:HG22	1:H:148:ALA:HB2	1.67	0.76
1:A:40:PHE:N	1:A:40:PHE:HD1	1.84	0.75
2:B:276:ILE:CD1	2:B:383:CYS:HA	2.15	0.75
1:E:294:ASP:O	1:E:294:ASP:OD1	2.04	0.75
2:B:197:VAL:HG12	2:B:198:THR:N	2.02	0.75
1:E:145:ILE:HG22	1:E:148:ALA:HB2	1.66	0.75
1:E:40:PHE:HD1	1:E:40:PHE:N	1.84	0.75
2:F:276:ILE:HD13	2:F:383:CYS:HA	1.67	0.75
2:G:267:ARG:HG3	2:G:267:ARG:HH11	1.52	0.75
2:C:197:VAL:HG12	2:C:198:THR:N	2.02	0.75
1:E:245:CYS:HB2	1:E:253:TRP:CE3	2.22	0.75
2:G:320:VAL:O	2:G:323:SER:HB3	1.86	0.75
2:B:159:LEU:O	2:B:160:LEU:HD23	1.84	0.75
1:D:155:ALA:HB2	1:D:217:ASP:HA	1.68	0.75
1:D:257:LEU:HD12	1:D:258:LEU:N	2.01	0.75
1:H:257:LEU:HD12	1:H:258:LEU:N	2.01	0.75
1:E:257:LEU:HD12	1:E:258:LEU:N	2.01	0.75
1:D:220:TRP:HZ3	1:D:229:SER:HB2	1.51	0.75
1:E:16:ILE:HD11	2:F:168:SER:O	1.87	0.75
2:G:531:LYS:CG	2:G:531:LYS:O	2.34	0.74
2:G:197:VAL:HG12	2:G:198:THR:N	2.02	0.74
1:A:257:LEU:HD12	1:A:258:LEU:N	2.00	0.74
2:B:159:LEU:HD12	2:B:160:LEU:H	1.53	0.74
1:H:143:LYS:HD2	1:H:200:GLY:O	1.87	0.74
1:A:221:ALA:HB2	1:A:270:TRP:CE2	2.22	0.74
1:E:230:THR:HG22	1:E:231:ILE:N	2.02	0.74
2:G:256:LYS:O	2:G:260:LEU:HG	1.87	0.74
1:H:220:TRP:HZ3	1:H:229:SER:HB2	1.51	0.74
1:A:294:ASP:O	1:A:294:ASP:OD1	2.04	0.74
2:B:527:LEU:HD22	2:B:532:ILE:HD12	1.69	0.74
2:B:320:VAL:O	2:B:323:SER:HB3	1.86	0.74
1:E:150:THR:HB	1:E:188:ASP:HB3	1.69	0.74
2:F:159:LEU:HD12	2:F:160:LEU:H	1.53	0.74
1:A:230:THR:HG22	1:A:231:ILE:N	2.03	0.74
2:C:267:ARG:HG3	2:C:267:ARG:HH11	1.52	0.74
2:C:320:VAL:O	2:C:323:SER:HB3	1.87	0.74
2:F:174:ARG:HH22	2:F:485:GLN:CB	1.90	0.74
2:G:276:ILE:CD1	2:G:383:CYS:HA	2.18	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:294:ASP:O	1:D:294:ASP:OD1	2.04	0.74
2:B:267:ARG:HH11	2:B:267:ARG:HG3	1.52	0.74
2:G:280:ILE:HB	2:G:300:LEU:HD21	1.69	0.74
1:H:230:THR:HG22	1:H:231:ILE:N	2.03	0.74
1:H:40:PHE:N	1:H:40:PHE:HD1	1.85	0.74
2:F:320:VAL:O	2:F:323:SER:HB3	1.86	0.74
2:G:436:LYS:HE3	2:G:469:THR:OG1	1.88	0.74
1:A:220:TRP:HZ3	1:A:229:SER:HB2	1.51	0.73
2:B:256:LYS:O	2:B:260:LEU:HG	1.87	0.73
2:F:256:LYS:O	2:F:260:LEU:HG	1.87	0.73
2:B:484:ALA:HB3	2:B:486:LEU:HD12	1.69	0.73
2:G:527:LEU:CA	2:G:532:ILE:HD12	2.18	0.73
2:G:289:ASN:OD1	2:G:291:ILE:HB	1.89	0.73
2:G:421:ILE:HD11	2:G:449:PHE:HE2	1.54	0.73
2:B:381:TRP:CE3	2:B:412:LEU:HD22	2.24	0.73
1:D:40:PHE:HD1	1:D:40:PHE:N	1.85	0.73
1:E:40:PHE:CD1	1:E:40:PHE:N	2.56	0.73
2:F:197:VAL:HG12	2:F:198:THR:N	2.02	0.73
2:C:321:LEU:HB3	2:C:361:LEU:HD11	1.71	0.73
2:C:215:LEU:HD12	2:C:452:TYR:OH	1.89	0.73
1:A:40:PHE:N	1:A:40:PHE:CD1	2.56	0.73
2:C:256:LYS:O	2:C:260:LEU:HG	1.88	0.72
2:F:267:ARG:HG3	2:F:267:ARG:HH11	1.52	0.72
2:F:481:LEU:HD13	2:F:489:HIS:CB	2.08	0.72
2:G:145:THR:HG22	2:G:147:SER:H	1.55	0.72
2:B:276:ILE:HD13	2:B:383:CYS:HA	1.71	0.72
1:H:95:LYS:CE	1:H:98:GLU:HB2	2.19	0.72
1:E:245:CYS:HB2	1:E:253:TRP:CD2	2.25	0.72
2:F:462:THR:O	2:F:463:ARG:HD3	1.87	0.72
2:G:190:LEU:HB2	2:G:489:HIS:CE1	2.24	0.72
2:F:321:LEU:HB3	2:F:361:LEU:HD11	1.69	0.72
2:C:394:ILE:O	2:C:395:ASP:HB2	1.89	0.72
1:D:95:LYS:CE	1:D:98:GLU:HB2	2.19	0.72
2:G:279:GLU:OE2	2:G:380:SER:HB2	1.89	0.72
2:G:284:ILE:HD13	2:G:297:TYR:CD1	2.24	0.72
1:D:150:THR:HB	1:D:188:ASP:HB3	1.72	0.72
2:F:359:LYS:NZ	2:F:368:GLY:HA3	2.05	0.72
2:G:149:THR:HG22	2:G:150:PHE:N	2.04	0.72
1:D:230:THR:HG22	1:D:231:ILE:N	2.03	0.71
1:H:26:THR:HG22	1:H:27:ARG:HD2	1.72	0.71
1:A:107:ASN:ND2	2:B:142:ARG:HH22	1.89	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:491:LEU:CD2	2:B:532:ILE:HD11	2.20	0.71
2:C:149:THR:HG22	2:C:150:PHE:N	2.04	0.71
2:C:145:THR:HG22	2:C:147:SER:H	1.55	0.71
1:A:155:ALA:HB2	1:A:217:ASP:HA	1.71	0.71
2:B:494:SER:O	2:B:497:LEU:HD13	1.90	0.71
1:D:26:THR:HG22	1:D:27:ARG:HD2	1.72	0.71
1:E:28:LEU:HD12	2:F:172:ILE:HD11	1.72	0.71
2:B:359:LYS:NZ	2:B:368:GLY:HA3	2.06	0.71
2:B:215:LEU:HD12	2:B:452:TYR:OH	1.91	0.71
1:E:107:ASN:OD1	2:F:142:ARG:NH1	2.24	0.71
1:E:95:LYS:CE	1:E:98:GLU:HB2	2.20	0.71
2:G:359:LYS:NZ	2:G:368:GLY:HA3	2.05	0.71
1:E:56:HIS:CE1	1:E:84:ILE:HD12	2.26	0.71
1:A:26:THR:HG22	1:A:27:ARG:HD2	1.72	0.71
2:F:233:LEU:CD1	2:F:417:PRO:HB2	2.20	0.71
1:H:190:LEU:HD13	1:H:207:LYS:HD3	1.71	0.71
1:A:95:LYS:CE	1:A:98:GLU:HB2	2.20	0.70
2:F:177:THR:HG22	2:F:179:LEU:N	2.06	0.70
1:D:102:HIS:NE2	1:D:130:SER:HB3	2.06	0.70
1:D:40:PHE:CD1	1:D:40:PHE:N	2.57	0.70
1:E:107:ASN:ND2	2:F:142:ARG:HH22	1.88	0.70
2:C:170:VAL:HG12	2:C:171:SER:N	2.06	0.70
1:E:26:THR:HG22	1:E:27:ARG:HD2	1.72	0.70
1:H:56:HIS:CE1	1:H:84:ILE:HD12	2.27	0.70
2:C:448:GLN:HG3	2:C:477:PHE:CE1	2.26	0.70
1:H:102:HIS:NE2	1:H:130:SER:HB3	2.06	0.70
1:A:16:ILE:HD11	2:B:168:SER:O	1.92	0.70
1:D:290:LYS:HB2	1:D:300:ILE:HD11	1.72	0.70
1:E:208:LEU:HB3	1:E:243:TRP:CZ3	2.26	0.70
2:B:384:LEU:HD13	2:B:410:PHE:CE1	2.27	0.70
1:E:125:SER:HB2	2:F:142:ARG:NH2	2.07	0.70
2:C:481:LEU:HD13	2:C:489:HIS:CB	2.17	0.70
2:B:177:THR:HG22	2:B:179:LEU:N	2.06	0.70
2:C:210:ILE:HD12	2:C:495:CYS:HB2	1.73	0.69
2:G:170:VAL:HG12	2:G:171:SER:N	2.06	0.69
1:E:102:HIS:NE2	1:E:130:SER:HB3	2.07	0.69
1:E:214:TRP:O	1:E:235:SER:HB2	1.92	0.69
1:A:56:HIS:CE1	1:A:84:ILE:HD12	2.26	0.69
1:D:30:THR:HG22	1:D:31:CYS:N	2.08	0.69
1:E:137:GLU:O	1:E:139:GLN:N	2.24	0.69
2:G:515:ILE:HD11	2:G:540:ALA:CB	2.22	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:137:GLU:O	1:H:139:GLN:N	2.25	0.69
1:A:102:HIS:NE2	1:A:130:SER:HB3	2.06	0.69
1:D:56:HIS:CE1	1:D:84:ILE:HD12	2.27	0.69
2:G:150:PHE:HD2	2:G:150:PHE:H	1.40	0.69
2:G:421:ILE:HD11	2:G:449:PHE:CE2	2.27	0.69
1:H:288:LEU:N	1:H:301:SER:HB3	2.08	0.69
2:F:428:ASN:C	2:F:428:ASN:OD1	2.31	0.69
2:C:359:LYS:NZ	2:C:368:GLY:HA3	2.05	0.69
1:E:230:THR:HG22	1:E:231:ILE:H	1.57	0.69
1:A:230:THR:HG22	1:A:231:ILE:H	1.57	0.69
1:D:137:GLU:O	1:D:139:GLN:N	2.25	0.69
1:E:17:HIS:ND1	2:F:148:TYR:HE2	1.91	0.69
1:D:214:TRP:O	1:D:235:SER:HB2	1.93	0.69
1:H:40:PHE:N	1:H:40:PHE:CD1	2.57	0.69
2:C:481:LEU:CD1	2:C:489:HIS:HB3	2.18	0.68
1:E:30:THR:HG22	1:E:31:CYS:N	2.07	0.68
2:F:515:ILE:HD11	2:F:540:ALA:HB1	1.75	0.68
2:G:428:ASN:C	2:G:428:ASN:OD1	2.31	0.68
1:A:137:GLU:O	1:A:139:GLN:N	2.25	0.68
1:A:30:THR:HG22	1:A:31:CYS:N	2.07	0.68
2:G:181:ARG:HH12	2:G:234:TRP:HE1	1.39	0.68
2:C:150:PHE:H	2:C:150:PHE:HD2	1.40	0.68
1:A:214:TRP:O	1:A:235:SER:HB2	1.93	0.68
1:A:28:LEU:HD12	2:B:172:ILE:HD11	1.72	0.68
2:F:170:VAL:O	2:F:172:ILE:HG13	1.93	0.68
1:E:216:ARG:NH2	2:F:142:ARG:O	2.26	0.68
2:G:527:LEU:HD22	2:G:532:ILE:CD1	2.24	0.68
2:G:515:ILE:HD11	2:G:540:ALA:HB1	1.74	0.68
1:H:30:THR:HG22	1:H:31:CYS:N	2.08	0.68
1:H:150:THR:HB	1:H:188:ASP:HB3	1.76	0.68
1:A:107:ASN:HD21	2:B:142:ARG:HH22	1.37	0.68
2:C:439:ARG:HD2	2:C:442:THR:HG21	1.76	0.68
2:B:210:ILE:CD1	2:B:495:CYS:HB2	2.23	0.68
2:B:210:ILE:HD11	2:B:495:CYS:HB2	1.76	0.68
2:B:428:ASN:OD1	2:B:428:ASN:C	2.32	0.68
1:D:290:LYS:CB	1:D:300:ILE:HD11	2.24	0.68
2:B:197:VAL:HG12	2:B:198:THR:H	1.59	0.67
2:G:515:ILE:HD13	2:G:541:GLN:HA	1.76	0.67
2:B:439:ARG:HD2	2:B:442:THR:HG21	1.76	0.67
2:G:291:ILE:HG22	2:G:353:ASN:CB	2.24	0.67
2:G:527:LEU:CB	2:G:532:ILE:HD12	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:ILE:HB	1:A:187:CYS:HB2	1.76	0.67
2:C:135:ALA:O	2:C:139:MET:HG3	1.94	0.67
1:H:288:LEU:H	1:H:301:SER:HB3	1.59	0.67
2:C:428:ASN:OD1	2:C:428:ASN:C	2.32	0.67
1:D:195:LYS:CG	1:D:196:GLU:N	2.57	0.67
2:G:205:ASN:HB2	2:G:206:PRO:HD2	1.77	0.67
1:H:214:TRP:O	1:H:235:SER:HB2	1.93	0.67
1:A:163:VAL:HG13	1:A:164:PRO:HD2	1.77	0.67
1:H:230:THR:HG22	1:H:231:ILE:H	1.58	0.67
2:C:277:GLY:O	2:C:281:GLU:HB2	1.95	0.67
1:E:163:VAL:HG13	1:E:164:PRO:HD2	1.77	0.67
1:H:287:THR:HG22	1:H:301:SER:OG	1.95	0.67
2:F:197:VAL:HG12	2:F:198:THR:H	1.60	0.67
2:G:135:ALA:O	2:G:139:MET:HG3	1.94	0.67
1:A:180:LYS:HD2	1:A:196:GLU:OE1	1.94	0.67
2:C:205:ASN:HB2	2:C:206:PRO:HD2	1.77	0.67
2:F:277:GLY:O	2:F:281:GLU:HB2	1.95	0.67
2:G:481:LEU:CD1	2:G:489:HIS:HB3	2.14	0.67
2:G:142:ARG:NH2	1:H:107:ASN:HD21	1.93	0.67
2:B:170:VAL:O	2:B:172:ILE:HG13	1.95	0.67
1:D:230:THR:HG22	1:D:231:ILE:H	1.58	0.67
2:C:381:TRP:CE3	2:C:412:LEU:HD21	2.30	0.66
1:E:257:LEU:HD12	1:E:258:LEU:H	1.60	0.66
2:G:277:GLY:O	2:G:281:GLU:HB2	1.95	0.66
2:F:205:ASN:HB2	2:F:206:PRO:HD2	1.77	0.66
2:B:165:VAL:O	2:B:165:VAL:HG12	1.96	0.66
2:F:238:SER:O	2:F:242:ASP:HB2	1.96	0.66
2:G:159:LEU:O	2:G:160:LEU:HD23	1.95	0.66
2:G:161:THR:O	2:G:170:VAL:HG13	1.95	0.66
1:H:163:VAL:HG13	1:H:164:PRO:HD2	1.77	0.66
1:H:234:CYS:SG	1:H:268:VAL:HG23	2.36	0.66
1:H:290:LYS:HB3	1:H:300:ILE:HD11	1.77	0.66
1:D:287:THR:HG22	1:D:301:SER:OG	1.96	0.66
2:F:487:HIS:HB2	2:F:518:LEU:HD21	1.75	0.66
2:C:159:LEU:O	2:C:160:LEU:HD23	1.96	0.66
1:E:145:ILE:HG22	1:E:145:ILE:O	1.95	0.66
2:G:439:ARG:HD2	2:G:442:THR:HG21	1.76	0.66
2:B:205:ASN:HB2	2:B:206:PRO:HD2	1.77	0.66
1:D:163:VAL:HG13	1:D:164:PRO:HD2	1.77	0.66
2:F:246:TYR:HD1	2:F:248:TYR:O	1.79	0.66
2:B:136:LYS:O	2:B:140:LYS:HB2	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:276:ILE:CD1	2:C:383:CYS:HA	2.26	0.66
2:C:494:SER:O	2:C:497:LEU:HG	1.96	0.66
2:F:532:ILE:HG23	2:F:533:PRO:HD2	1.76	0.66
1:H:257:LEU:HD12	1:H:258:LEU:H	1.60	0.66
1:D:221:ALA:HB2	1:D:270:TRP:CE2	2.30	0.66
1:D:257:LEU:HD12	1:D:258:LEU:H	1.60	0.66
1:D:290:LYS:HB2	1:D:300:ILE:HD12	1.76	0.66
2:G:246:TYR:CE1	2:G:259:LEU:HD13	2.30	0.66
2:C:197:VAL:HG12	2:C:198:THR:H	1.60	0.65
2:G:152:LYS:O	2:G:159:LEU:HD12	1.96	0.65
2:B:277:GLY:O	2:B:281:GLU:HB2	1.95	0.65
2:C:161:THR:O	2:C:170:VAL:HG13	1.95	0.65
2:F:439:ARG:HD2	2:F:442:THR:HG21	1.76	0.65
2:F:172:ILE:O	2:F:172:ILE:CG2	2.45	0.65
1:A:145:ILE:O	1:A:145:ILE:HG22	1.95	0.65
1:D:151:ILE:HB	1:D:187:CYS:CB	2.23	0.65
1:D:195:LYS:HG2	1:D:196:GLU:N	2.11	0.65
2:G:197:VAL:HG12	2:G:198:THR:H	1.60	0.65
1:A:109:VAL:CG1	1:A:120:LEU:HD11	2.26	0.65
2:F:177:THR:HG22	2:F:179:LEU:HB3	1.77	0.65
2:F:249:LYS:O	2:F:249:LYS:HG3	1.95	0.65
2:F:490:SER:CB	2:F:510:LEU:HD21	2.27	0.65
2:G:142:ARG:HH22	1:H:107:ASN:HD21	1.44	0.65
1:D:145:ILE:O	1:D:145:ILE:HG22	1.96	0.65
2:F:165:VAL:O	2:F:165:VAL:HG12	1.95	0.65
2:B:174:ARG:HH22	2:B:485:GLN:CD	2.00	0.65
2:C:238:SER:O	2:C:242:ASP:HB2	1.95	0.65
1:D:109:VAL:CG1	1:D:120:LEU:HD11	2.26	0.65
2:F:136:LYS:O	2:F:140:LYS:HB2	1.96	0.65
2:G:448:GLN:HG3	2:G:477:PHE:CE1	2.31	0.65
2:G:152:LYS:HG2	1:H:269:SER:HB2	1.77	0.65
2:C:133:ASP:O	2:C:137:LEU:HG	1.97	0.65
2:C:241:PHE:CD2	2:C:457:LEU:HD21	2.31	0.65
1:E:109:VAL:CG1	1:E:120:LEU:HD11	2.27	0.65
1:H:145:ILE:HG22	1:H:145:ILE:O	1.96	0.65
2:B:241:PHE:CD2	2:B:457:LEU:HD21	2.32	0.65
1:E:107:ASN:HD21	2:F:142:ARG:NH2	1.94	0.65
1:E:274:ALA:HB1	1:E:290:LYS:HE3	1.79	0.65
2:F:353:ASN:O	2:F:357:ILE:HG13	1.97	0.65
2:G:353:ASN:O	2:G:357:ILE:HG13	1.97	0.65
2:G:142:ARG:O	1:H:216:ARG:NH2	2.28	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:291:GLU:HB3	1:H:297:TRP:CE3	2.32	0.65
1:A:257:LEU:HD12	1:A:258:LEU:H	1.60	0.64
2:C:158:MET:HE1	2:C:174:ARG:HG3	1.79	0.64
1:E:155:ALA:HB2	1:E:217:ASP:HA	1.79	0.64
2:B:172:ILE:O	2:B:172:ILE:CG2	2.45	0.64
1:E:47:GLN:OE1	2:F:167:LYS:N	2.29	0.64
1:E:107:ASN:HD21	2:F:142:ARG:HH22	1.45	0.64
2:G:133:ASP:O	2:G:137:LEU:HG	1.97	0.64
2:G:547:TYR:HE1	1:H:72:ASN:HD21	1.45	0.64
2:G:287:SER:HB3	2:G:293:GLN:NE2	2.12	0.64
2:C:392:GLY:O	2:C:394:ILE:N	2.31	0.64
2:C:421:ILE:HD11	2:C:449:PHE:HE2	1.62	0.64
2:F:399:LEU:HD23	2:F:425:TYR:OH	1.98	0.64
2:C:280:ILE:HB	2:C:300:LEU:HD21	1.80	0.64
2:F:207:TYR:CD2	2:F:504:GLU:HA	2.33	0.64
1:H:206:GLN:HG3	1:H:207:LYS:N	2.12	0.64
1:A:206:GLN:HG3	1:A:207:LYS:N	2.13	0.64
1:E:17:HIS:CE1	2:F:148:TYR:CE2	2.86	0.64
2:F:455:GLN:HG2	2:F:496:PHE:HE2	1.63	0.64
2:G:241:PHE:CD2	2:G:457:LEU:HD21	2.33	0.64
2:G:521:SER:C	2:G:523:ASN:H	2.01	0.64
1:H:109:VAL:CG1	1:H:120:LEU:HD11	2.27	0.64
1:A:268:VAL:CG1	1:A:277:LEU:HD11	2.28	0.64
1:E:268:VAL:CG1	1:E:277:LEU:HD11	2.28	0.64
1:E:49:LEU:HD12	1:E:50:ILE:N	2.13	0.64
1:H:268:VAL:CG1	1:H:277:LEU:HD11	2.28	0.64
1:A:107:ASN:HD21	2:B:142:ARG:NH2	1.96	0.64
1:D:193:LEU:HD21	1:D:208:LEU:HD11	1.80	0.64
1:D:206:GLN:HG3	1:D:207:LYS:N	2.13	0.64
1:D:268:VAL:CG1	1:D:277:LEU:HD11	2.28	0.64
1:E:238:GLY:O	1:E:260:LYS:HA	1.97	0.64
1:A:49:LEU:HD12	1:A:50:ILE:N	2.13	0.63
2:C:276:ILE:HG22	2:C:280:ILE:HG13	1.80	0.63
2:B:353:ASN:O	2:B:357:ILE:HG13	1.97	0.63
1:A:174:GLN:O	1:A:175:LYS:HB2	1.99	0.63
2:C:353:ASN:O	2:C:357:ILE:HG13	1.97	0.63
2:F:455:GLN:HG2	2:F:496:PHE:CD2	2.32	0.63
1:H:221:ALA:HB2	1:H:270:TRP:CE2	2.34	0.63
1:H:226:LEU:HD13	1:H:227:PRO:CD	2.28	0.63
2:C:224:MET:HE2	2:C:230:ASP:HB3	1.81	0.63
1:E:283:ASP:O	1:E:284:ASN:HB2	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:152:LYS:O	2:C:159:LEU:HD12	1.96	0.63
2:C:487:HIS:HA	2:C:490:SER:CB	2.28	0.63
2:C:190:LEU:HD21	2:C:488:GLY:HA3	1.81	0.63
2:G:512:MET:SD	2:G:540:ALA:HB2	2.38	0.63
1:E:206:GLN:HG3	1:E:207:LYS:N	2.13	0.63
2:F:246:TYR:CD1	2:F:248:TYR:O	2.52	0.63
2:G:439:ARG:NH1	2:G:439:ARG:HG2	2.12	0.63
1:E:174:GLN:O	1:E:175:LYS:HB2	1.99	0.63
1:E:49:LEU:HD12	1:E:50:ILE:H	1.64	0.63
2:F:439:ARG:NH1	2:F:439:ARG:HG2	2.12	0.63
2:F:521:SER:C	2:F:523:ASN:H	2.01	0.63
2:G:276:ILE:HD13	2:G:383:CYS:HA	1.79	0.63
1:A:49:LEU:HD12	1:A:50:ILE:H	1.64	0.63
2:C:521:SER:C	2:C:523:ASN:H	2.01	0.63
1:D:242:ILE:N	1:D:242:ILE:HD12	2.14	0.63
1:H:155:ALA:HB2	1:H:217:ASP:HA	1.81	0.63
1:D:208:LEU:HD22	1:D:243:TRP:CE3	2.34	0.62
1:D:49:LEU:HD12	1:D:50:ILE:N	2.14	0.62
2:F:276:ILE:HG22	2:F:280:ILE:HG13	1.81	0.62
1:H:49:LEU:HD12	1:H:50:ILE:N	2.14	0.62
1:A:283:ASP:O	1:A:284:ASN:HB2	1.98	0.62
1:H:246:ASP:HB2	1:H:252:THR:O	1.99	0.62
2:C:181:ARG:NH1	2:C:234:TRP:HE1	1.98	0.62
2:C:515:ILE:HD13	2:C:541:GLN:HA	1.81	0.62
1:H:82:LYS:HG2	1:H:100:ALA:CB	2.28	0.62
2:B:188:VAL:O	2:B:192:LYS:HB2	2.00	0.62
2:C:188:VAL:O	2:C:192:LYS:HB2	2.00	0.62
2:C:487:HIS:HA	2:C:490:SER:HB2	1.81	0.62
1:D:82:LYS:HG2	1:D:100:ALA:CB	2.29	0.62
1:D:174:GLN:O	1:D:175:LYS:HB2	1.99	0.62
2:F:392:GLY:O	2:F:394:ILE:HG13	1.99	0.62
1:A:285:LYS:HG2	1:A:304:ASN:HD21	1.65	0.62
2:C:359:LYS:HZ2	2:C:368:GLY:HA3	1.63	0.62
2:F:432:GLU:OE2	2:F:466:SER:HB2	2.00	0.62
2:F:515:ILE:HD11	2:F:540:ALA:CB	2.28	0.62
2:G:276:ILE:HG22	2:G:280:ILE:HG13	1.80	0.62
2:B:521:SER:C	2:B:523:ASN:H	2.01	0.62
1:E:38:LYS:HB3	1:E:40:PHE:HE1	1.65	0.62
1:H:174:GLN:O	1:H:175:LYS:HB2	1.99	0.62
1:H:49:LEU:HD12	1:H:50:ILE:H	1.65	0.62
2:C:339:GLN:O	2:C:343:TRP:CD1	2.52	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:226:LEU:HD13	1:E:227:PRO:CD	2.28	0.62
1:D:60:VAL:HG13	1:D:77:CYS:O	2.00	0.62
2:F:188:VAL:O	2:F:192:LYS:HB2	2.00	0.62
2:G:172:ILE:O	2:G:172:ILE:HG22	2.00	0.62
2:G:188:VAL:O	2:G:192:LYS:HB2	2.00	0.62
1:A:82:LYS:HG2	1:A:100:ALA:CB	2.29	0.61
1:A:226:LEU:HD13	1:A:227:PRO:CD	2.27	0.61
2:B:276:ILE:HG22	2:B:280:ILE:HG13	1.80	0.61
2:B:339:GLN:O	2:B:343:TRP:CD1	2.52	0.61
2:C:155:THR:HG21	1:D:23:TYR:O	2.00	0.61
2:C:515:ILE:HD13	2:C:541:GLN:N	2.15	0.61
2:F:339:GLN:O	2:F:343:TRP:CD1	2.52	0.61
2:B:432:GLU:OE2	2:B:466:SER:HB2	1.99	0.61
2:C:287:SER:CB	2:C:293:GLN:NE2	2.63	0.61
1:A:60:VAL:HG13	1:A:77:CYS:O	2.00	0.61
2:C:524:ASP:O	2:C:525:HIS:HB3	2.01	0.61
1:D:234:CYS:SG	1:D:268:VAL:HG23	2.41	0.61
1:E:145:ILE:CG2	1:E:148:ALA:HB2	2.30	0.61
1:D:220:TRP:CH2	1:D:229:SER:HB2	2.36	0.61
1:E:38:LYS:CB	1:E:40:PHE:HE1	2.14	0.61
1:H:69:MET:HE2	1:H:70:TYR:HE1	1.65	0.61
1:A:38:LYS:CB	1:A:40:PHE:HE1	2.14	0.61
2:C:299:LEU:HD22	2:C:383:CYS:SG	2.40	0.61
1:D:49:LEU:HD12	1:D:50:ILE:H	1.65	0.61
1:H:145:ILE:CG2	1:H:148:ALA:HB2	2.31	0.61
2:C:162:LYS:HG3	2:C:162:LYS:O	2.00	0.61
2:C:172:ILE:HG22	2:C:172:ILE:O	2.00	0.61
2:C:210:ILE:HG22	2:C:459:PHE:CE2	2.35	0.61
2:F:421:ILE:HD11	2:F:449:PHE:CE2	2.36	0.61
2:G:210:ILE:HG22	2:G:459:PHE:CE2	2.36	0.61
1:A:145:ILE:CG2	1:A:148:ALA:HB2	2.30	0.61
1:A:238:GLY:O	1:A:260:LYS:HA	2.01	0.61
2:B:524:ASP:O	2:B:525:HIS:HB3	2.01	0.61
2:G:162:LYS:O	2:G:162:LYS:HG3	2.01	0.61
1:A:150:THR:HB	1:A:188:ASP:HB3	1.83	0.61
1:A:220:TRP:CH2	1:A:229:SER:HB2	2.36	0.61
1:A:48:ILE:O	1:A:48:ILE:HG22	2.00	0.61
2:B:177:THR:HG22	2:B:179:LEU:HB3	1.77	0.61
1:D:226:LEU:HD13	1:D:227:PRO:CD	2.28	0.61
2:G:527:LEU:CD2	2:G:532:ILE:CD1	2.79	0.61
1:D:38:LYS:CB	1:D:40:PHE:HE1	2.14	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:78:SER:HB3	1:E:80:ASP:OD1	2.01	0.61
2:G:149:THR:CG2	2:G:150:PHE:H	2.13	0.61
2:G:246:TYR:HB2	2:G:260:LEU:HD21	1.82	0.61
2:G:515:ILE:HD13	2:G:541:GLN:CA	2.29	0.61
1:H:38:LYS:HB3	1:H:40:PHE:HE1	1.65	0.61
2:B:421:ILE:HD11	2:B:449:PHE:CE2	2.36	0.60
2:C:151:ALA:HB2	1:D:286:VAL:HG21	1.83	0.60
2:G:524:ASP:O	2:G:525:HIS:HB3	2.01	0.60
2:C:439:ARG:NH1	2:C:439:ARG:HG2	2.12	0.60
1:E:48:ILE:O	1:E:48:ILE:HG22	2.00	0.60
2:G:435:TYR:CE2	2:G:454:ILE:HD11	2.36	0.60
2:C:523:ASN:HB3	2:C:525:HIS:CE1	2.37	0.60
1:D:78:SER:HB3	1:D:80:ASP:OD1	2.01	0.60
2:G:180:GLN:HG2	2:G:180:GLN:O	1.99	0.60
1:H:60:VAL:HG13	1:H:77:CYS:O	2.00	0.60
1:H:87:ARG:HG3	1:H:88:GLU:H	1.66	0.60
1:A:87:ARG:HG3	1:A:88:GLU:H	1.66	0.60
2:B:153:PHE:HE2	2:B:175:LEU:HD22	1.66	0.60
1:E:220:TRP:CH2	1:E:229:SER:HB2	2.36	0.60
2:C:435:TYR:CE2	2:C:454:ILE:HD11	2.36	0.60
1:E:87:ARG:HG3	1:E:88:GLU:H	1.66	0.60
2:F:532:ILE:HG23	2:F:533:PRO:CD	2.31	0.60
2:B:491:LEU:HD12	2:B:510:LEU:HD23	1.84	0.60
2:F:218:LYS:HG3	2:F:242:ASP:OD2	2.01	0.60
2:G:170:VAL:H	1:H:47:GLN:HE22	1.49	0.60
2:G:512:MET:HA	2:G:540:ALA:HB1	1.83	0.60
1:H:48:ILE:O	1:H:48:ILE:HG22	2.01	0.60
1:A:191:ILE:HD11	1:A:211:HIS:CD2	2.37	0.60
1:A:70:TYR:CD1	1:A:70:TYR:N	2.70	0.60
2:B:343:TRP:CZ3	2:B:350:ILE:HG21	2.33	0.60
2:C:515:ILE:CD1	2:C:540:ALA:C	2.70	0.60
1:H:38:LYS:CB	1:H:40:PHE:HE1	2.14	0.60
1:A:265:VAL:HA	1:A:281:GLY:HA3	1.84	0.60
2:B:439:ARG:HG2	2:B:439:ARG:NH1	2.12	0.60
1:D:87:ARG:HG3	1:D:88:GLU:H	1.67	0.60
2:F:524:ASP:O	2:F:525:HIS:HB3	2.01	0.60
2:G:216:LEU:HB3	2:G:242:ASP:OD1	2.01	0.60
2:G:527:LEU:HA	2:G:532:ILE:CD1	2.32	0.60
1:A:78:SER:HB3	1:A:80:ASP:OD1	2.01	0.60
2:B:523:ASN:HB3	2:B:525:HIS:CE1	2.37	0.60
2:B:515:ILE:CD1	2:B:540:ALA:C	2.70	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:288:LEU:HB3	1:A:300:ILE:HD11	1.83	0.60
2:C:435:TYR:CZ	2:C:454:ILE:HD11	2.36	0.60
2:C:448:GLN:HG3	2:C:477:PHE:CZ	2.36	0.60
2:C:487:HIS:HA	2:C:490:SER:OG	2.02	0.60
1:E:82:LYS:HG2	1:E:100:ALA:CB	2.29	0.60
1:E:265:VAL:HA	1:E:281:GLY:HA3	1.84	0.60
1:E:234:CYS:HB2	1:E:265:VAL:HB	1.83	0.60
2:F:269:THR:HG21	2:F:390:CYS:SG	2.42	0.60
2:G:201:ALA:HB2	2:G:531:LYS:NZ	2.16	0.60
1:H:220:TRP:CH2	1:H:229:SER:HB2	2.36	0.60
1:H:70:TYR:CD1	1:H:70:TYR:N	2.70	0.60
2:B:215:LEU:HD12	2:B:452:TYR:CZ	2.37	0.59
2:C:170:VAL:HG12	2:C:171:SER:H	1.67	0.59
2:C:276:ILE:HD13	2:C:383:CYS:HA	1.84	0.59
1:D:48:ILE:O	1:D:48:ILE:HG22	2.01	0.59
1:E:60:VAL:HG13	1:E:77:CYS:O	2.01	0.59
2:F:155:THR:HG22	2:F:513:ARG:HD2	1.84	0.59
2:B:348:CYS:O	2:B:348:CYS:SG	2.60	0.59
2:G:381:TRP:CE3	2:G:412:LEU:HD23	2.37	0.59
1:H:78:SER:HB3	1:H:80:ASP:OD1	2.01	0.59
2:B:184:LEU:HD21	2:B:448:GLN:NE2	2.17	0.59
2:F:153:PHE:HE2	2:F:175:LEU:HD22	1.66	0.59
2:C:515:ILE:HD13	2:C:541:GLN:CA	2.33	0.59
1:D:265:VAL:HA	1:D:281:GLY:HA3	1.84	0.59
1:E:243:TRP:N	1:E:243:TRP:CD1	2.70	0.59
2:F:263:GLU:HA	2:G:320:VAL:HG22	1.84	0.59
1:D:70:TYR:CD1	1:D:70:TYR:N	2.70	0.59
1:E:242:ILE:HD11	1:E:258:LEU:HD22	1.84	0.59
1:A:111:TRP:CE2	1:A:120:LEU:HD13	2.38	0.59
2:B:352:LYS:O	2:B:356:LYS:HG3	2.02	0.59
2:C:240:LEU:HD21	2:C:268:LEU:CD1	2.32	0.59
1:A:38:LYS:HB3	1:A:40:PHE:HE1	1.65	0.59
2:C:153:PHE:CE2	1:D:278:ALA:HB2	2.38	0.59
1:E:111:TRP:CE2	1:E:120:LEU:HD13	2.37	0.59
2:G:240:LEU:HD21	2:G:268:LEU:CD1	2.33	0.59
2:G:523:ASN:HB3	2:G:525:HIS:CE1	2.37	0.59
2:C:381:TRP:CE3	2:C:412:LEU:CD2	2.85	0.59
1:D:262:ASN:C	1:D:262:ASN:OD1	2.41	0.59
2:G:148:TYR:HB2	1:H:266:TRP:CD2	2.38	0.59
2:G:199:ILE:CD1	2:G:530:LEU:HA	2.32	0.59
2:G:339:GLN:O	2:G:343:TRP:CD1	2.52	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:111:TRP:CE2	1:H:120:LEU:HD13	2.38	0.59
1:A:16:ILE:HD13	1:A:30:THR:HG21	1.85	0.59
2:G:487:HIS:HA	2:G:490:SER:HB2	1.85	0.59
2:C:352:LYS:O	2:C:356:LYS:HG3	2.03	0.58
1:D:111:TRP:CE2	1:D:120:LEU:HD13	2.38	0.58
1:E:21:MET:CE	2:F:160:LEU:HD11	2.32	0.58
1:E:242:ILE:HD13	1:E:297:TRP:CE2	2.37	0.58
2:G:352:LYS:O	2:G:356:LYS:HG3	2.02	0.58
1:H:193:LEU:HD21	1:H:208:LEU:HD11	1.85	0.58
2:C:421:ILE:HD11	2:C:449:PHE:CE2	2.37	0.58
1:E:70:TYR:CD1	1:E:70:TYR:N	2.70	0.58
2:F:523:ASN:HB3	2:F:525:HIS:CE1	2.37	0.58
2:G:335:LEU:O	2:G:339:GLN:HG3	2.03	0.58
2:G:439:ARG:HA	2:G:442:THR:HG1	1.68	0.58
2:G:527:LEU:HB3	2:G:532:ILE:HD12	1.85	0.58
1:A:293:VAL:O	1:A:293:VAL:HG12	2.02	0.58
2:B:335:LEU:O	2:B:339:GLN:HG3	2.04	0.58
2:B:487:HIS:ND1	2:B:514:GLU:HG3	2.18	0.58
2:B:174:ARG:NH2	2:B:485:GLN:CG	2.46	0.58
2:C:284:ILE:HD13	2:C:297:TYR:CD1	2.38	0.58
2:C:194:ILE:HG12	2:C:492:PHE:CE2	2.39	0.58
1:A:191:ILE:HD11	1:A:211:HIS:HD2	1.69	0.58
1:D:208:LEU:HD22	1:D:243:TRP:CZ3	2.38	0.58
1:D:38:LYS:HB3	1:D:40:PHE:HE1	1.65	0.58
1:E:293:VAL:HG12	1:E:293:VAL:O	2.02	0.58
1:H:262:ASN:OD1	1:H:262:ASN:C	2.42	0.58
1:E:258:LEU:CD1	1:E:297:TRP:CB	2.81	0.58
1:A:17:HIS:ND1	2:B:148:TYR:HE2	2.01	0.58
2:B:284:ILE:HG12	2:B:296:LEU:HD12	1.86	0.58
2:B:432:GLU:OE1	2:B:466:SER:N	2.35	0.58
1:A:262:ASN:OD1	1:A:262:ASN:C	2.41	0.58
1:D:293:VAL:O	1:D:293:VAL:HG12	2.02	0.58
2:F:532:ILE:CG2	2:F:533:PRO:CD	2.82	0.58
1:H:265:VAL:HA	1:H:281:GLY:HA3	1.84	0.58
1:A:192:LYS:HE2	1:A:207:LYS:HE2	1.86	0.58
2:C:335:LEU:O	2:C:339:GLN:HG3	2.03	0.58
1:D:242:ILE:HD11	1:D:258:LEU:HB2	1.85	0.58
2:F:532:ILE:CG2	2:F:533:PRO:HD2	2.33	0.58
1:A:187:CYS:HB3	1:A:214:TRP:NE1	2.19	0.58
1:A:208:LEU:HB3	1:A:243:TRP:CZ3	2.38	0.58
2:B:269:THR:HG21	2:B:390:CYS:SG	2.44	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:145:ILE:CG2	1:D:148:ALA:HB2	2.31	0.58
2:F:299:LEU:HD22	2:F:383:CYS:SG	2.43	0.58
2:G:291:ILE:CG2	2:G:353:ASN:HB2	2.31	0.58
2:G:432:GLU:OE1	2:G:466:SER:N	2.35	0.58
2:C:499:ASP:O	2:C:501:LYS:N	2.37	0.57
1:H:271:SER:HB3	1:H:276:ILE:HB	1.86	0.57
2:B:515:ILE:HD13	2:B:541:GLN:N	2.19	0.57
1:D:28:LEU:C	1:D:28:LEU:HD23	2.25	0.57
1:E:113:PRO:HB3	1:E:161:ALA:HB2	1.85	0.57
2:F:352:LYS:O	2:F:356:LYS:HG3	2.02	0.57
2:G:196:LYS:HD2	2:G:214:SER:O	2.04	0.57
2:C:297:TYR:HB3	2:C:306:ALA:HB2	1.85	0.57
1:E:191:ILE:HD11	1:E:211:HIS:CD2	2.40	0.57
1:E:271:SER:HB3	1:E:276:ILE:HB	1.86	0.57
1:H:191:ILE:HD11	1:H:211:HIS:CD2	2.39	0.57
1:D:185:GLY:N	1:D:218:VAL:HG21	2.19	0.57
1:D:247:ASP:HA	1:D:251:ASN:HB3	1.87	0.57
2:F:543:LEU:HD12	2:F:543:LEU:O	2.04	0.57
1:A:41:ASP:O	1:A:41:ASP:OD1	2.22	0.57
2:B:142:ARG:HB3	2:B:144:PHE:CD1	2.40	0.57
1:D:179:ILE:CG2	1:D:181:ARG:HE	2.18	0.57
1:D:195:LYS:CG	1:D:196:GLU:H	2.16	0.57
2:F:142:ARG:HB3	2:F:144:PHE:CD1	2.39	0.57
2:F:335:LEU:O	2:F:339:GLN:HG3	2.04	0.57
2:F:207:TYR:CE1	2:F:504:GLU:HG3	2.40	0.57
2:G:349:SER:O	2:G:350:ILE:HG12	2.05	0.57
2:G:527:LEU:HD22	2:G:532:ILE:HD13	1.85	0.57
1:A:271:SER:HB3	1:A:276:ILE:HB	1.86	0.57
1:A:274:ALA:HB1	1:A:290:LYS:HE3	1.85	0.57
2:B:543:LEU:HD12	2:B:543:LEU:O	2.04	0.57
2:B:174:ARG:NH2	2:B:485:GLN:CD	2.58	0.57
2:B:527:LEU:CD2	2:B:532:ILE:HD12	2.33	0.57
2:C:145:THR:HG22	2:C:146:ALA:N	2.20	0.57
1:D:192:LYS:NZ	1:D:207:LYS:HE2	2.19	0.57
1:E:28:LEU:HD23	1:E:28:LEU:C	2.24	0.57
1:E:41:ASP:O	1:E:41:ASP:OD1	2.23	0.57
2:F:215:LEU:HD12	2:F:452:TYR:OH	2.05	0.57
1:A:21:MET:CE	2:B:160:LEU:HD11	2.35	0.57
1:D:16:ILE:HD13	1:D:30:THR:HG21	1.85	0.57
1:E:16:ILE:HD13	1:E:30:THR:HG21	1.86	0.57
2:G:145:THR:HG22	2:G:146:ALA:N	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:170:VAL:HG12	2:G:171:SER:H	1.67	0.57
2:G:224:MET:HE2	2:G:230:ASP:HB3	1.86	0.57
2:G:543:LEU:HD12	2:G:543:LEU:O	2.04	0.57
1:H:92:THR:HG22	1:H:94:GLU:HG3	1.87	0.57
2:C:522:THR:O	2:C:522:THR:HG22	2.05	0.57
1:E:179:ILE:CG2	1:E:181:ARG:HE	2.18	0.57
1:E:192:LYS:HE2	1:E:207:LYS:HE2	1.85	0.57
1:H:16:ILE:HD13	1:H:30:THR:HG21	1.85	0.57
1:A:92:THR:HG22	1:A:94:GLU:HG3	1.87	0.57
2:C:196:LYS:HD2	2:C:214:SER:O	2.05	0.57
2:C:210:ILE:HG22	2:C:459:PHE:HE2	1.70	0.57
1:D:181:ARG:NH2	1:D:247:ASP:OD2	2.36	0.57
2:F:434:LEU:O	2:F:438:VAL:HG23	2.05	0.57
2:F:491:LEU:HD13	2:F:510:LEU:HD23	1.87	0.57
2:C:436:LYS:HE3	2:C:469:THR:OG1	2.05	0.56
2:F:395:ASP:HB2	2:F:397:TYR:CE2	2.39	0.56
1:A:113:PRO:HB3	1:A:161:ALA:HB2	1.87	0.56
2:B:434:LEU:O	2:B:438:VAL:HG23	2.05	0.56
2:B:522:THR:O	2:B:522:THR:HG22	2.04	0.56
2:C:149:THR:CG2	2:C:150:PHE:H	2.13	0.56
1:E:206:GLN:OE1	1:E:251:ASN:HB3	2.05	0.56
2:F:240:LEU:HD21	2:F:268:LEU:CD1	2.36	0.56
2:G:522:THR:O	2:G:522:THR:HG22	2.05	0.56
2:G:515:ILE:HD13	2:G:541:GLN:N	2.20	0.56
1:E:109:VAL:HG22	1:E:122:CYS:SG	2.45	0.56
1:H:148:ALA:HB1	1:H:194:TRP:CH2	2.40	0.56
1:A:193:LEU:HD21	1:A:208:LEU:HD11	1.87	0.56
2:C:432:GLU:OE2	2:C:466:SER:HB2	2.05	0.56
2:C:434:LEU:O	2:C:438:VAL:HG23	2.05	0.56
2:C:543:LEU:O	2:C:543:LEU:HD12	2.04	0.56
2:C:148:TYR:HB2	1:D:266:TRP:CE2	2.41	0.56
1:E:107:ASN:ND2	2:F:142:ARG:HH12	2.02	0.56
2:F:196:LYS:HD2	2:F:214:SER:O	2.05	0.56
2:F:241:PHE:CD2	2:F:457:LEU:HD21	2.41	0.56
2:G:210:ILE:CD1	2:G:495:CYS:HB3	2.35	0.56
2:G:252:ASN:ND2	2:G:255:VAL:HG23	2.20	0.56
1:D:292:SER:C	1:D:294:ASP:H	2.09	0.56
1:D:92:THR:HG22	1:D:94:GLU:HG3	1.87	0.56
2:F:445:LEU:HD22	2:F:449:PHE:HD2	1.71	0.56
2:F:522:THR:HG22	2:F:522:THR:O	2.05	0.56
2:G:284:ILE:HG21	2:G:297:TYR:HE1	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:LEU:C	1:A:28:LEU:HD23	2.25	0.56
2:C:490:SER:HB3	2:C:510:LEU:HD21	1.87	0.56
1:D:271:SER:HB3	1:D:276:ILE:HB	1.86	0.56
1:A:179:ILE:CG2	1:A:181:ARG:HE	2.18	0.56
1:A:250:SER:O	1:A:252:THR:HG23	2.06	0.56
2:B:196:LYS:HD2	2:B:214:SER:O	2.05	0.56
2:C:291:ILE:HG22	2:C:353:ASN:HB2	1.88	0.56
1:D:109:VAL:HG22	1:D:122:CYS:SG	2.45	0.56
1:E:292:SER:C	1:E:294:ASP:H	2.09	0.56
2:G:434:LEU:O	2:G:438:VAL:HG23	2.05	0.56
1:A:292:SER:C	1:A:294:ASP:H	2.09	0.56
2:C:190:LEU:HB2	2:C:489:HIS:CE1	2.41	0.56
1:D:288:LEU:H	1:D:301:SER:HB3	1.71	0.56
1:E:92:THR:HG22	1:E:94:GLU:HG3	1.87	0.56
2:F:348:CYS:O	2:F:349:SER:HB2	2.05	0.56
2:F:154:SER:O	2:F:157:SER:N	2.39	0.56
2:G:190:LEU:HD22	2:G:489:HIS:ND1	2.21	0.56
2:G:436:LYS:CE	2:G:469:THR:OG1	2.53	0.56
2:G:514:GLU:OE1	2:G:517:LEU:HD23	2.06	0.56
1:H:109:VAL:HG22	1:H:122:CYS:SG	2.46	0.56
1:H:243:TRP:N	1:H:243:TRP:CD1	2.73	0.56
2:B:155:THR:HG22	2:B:513:ARG:HD2	1.88	0.56
2:B:515:ILE:HD13	2:B:541:GLN:HA	1.87	0.56
2:C:514:GLU:OE1	2:C:517:LEU:HD23	2.06	0.56
1:D:198:GLU:O	1:D:198:GLU:HG3	2.06	0.56
1:E:193:LEU:N	1:E:193:LEU:CD2	2.69	0.56
2:G:269:THR:O	2:G:273:VAL:HG23	2.06	0.56
1:H:258:LEU:CD1	1:H:297:TRP:HB2	2.36	0.56
1:A:182:PHE:CD1	1:A:182:PHE:O	2.59	0.56
2:C:210:ILE:HD11	2:C:495:CYS:HB2	1.87	0.56
1:D:232:ALA:HB2	1:D:270:TRP:CZ2	2.41	0.56
2:F:248:TYR:CE2	2:G:343:TRP:CH2	2.94	0.56
2:F:515:ILE:HD13	2:F:541:GLN:HA	1.88	0.56
2:G:190:LEU:HB2	2:G:489:HIS:HE1	1.70	0.56
1:H:28:LEU:C	1:H:28:LEU:HD23	2.25	0.56
2:F:420:VAL:HA	2:F:423:GLN:OE1	2.06	0.55
2:G:371:SER:OG	2:G:373:LYS:HG3	2.06	0.55
2:B:350:ILE:HD12	2:B:354:ILE:HD12	1.88	0.55
2:B:514:GLU:OE1	2:B:517:LEU:HD23	2.06	0.55
1:A:24:TYR:OH	2:B:543:LEU:HG	2.06	0.55
1:D:274:ALA:HB1	1:D:290:LYS:HE3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:269:THR:O	2:F:273:VAL:HG23	2.06	0.55
2:F:381:TRP:CG	2:F:382:LEU:N	2.74	0.55
2:G:276:ILE:HD11	2:G:383:CYS:HA	1.88	0.55
1:A:216:ARG:NH2	2:B:142:ARG:O	2.39	0.55
1:D:23:TYR:CD2	1:D:68:PRO:HG3	2.41	0.55
1:E:262:ASN:C	1:E:262:ASN:OD1	2.42	0.55
2:F:179:LEU:HD11	2:F:184:LEU:CD1	2.36	0.55
1:H:179:ILE:CG2	1:H:181:ARG:HE	2.18	0.55
1:A:109:VAL:HG22	1:A:122:CYS:SG	2.46	0.55
2:B:268:LEU:CD2	2:B:389:LEU:HD13	2.36	0.55
2:C:175:LEU:HD13	2:C:176:PRO:HD2	1.89	0.55
1:D:208:LEU:HB3	1:D:243:TRP:CZ3	2.41	0.55
1:E:258:LEU:HD13	1:E:297:TRP:CB	2.36	0.55
2:F:445:LEU:HD22	2:F:449:PHE:CD2	2.42	0.55
2:F:432:GLU:OE1	2:F:466:SER:N	2.39	0.55
2:B:148:TYR:CD1	2:B:148:TYR:C	2.80	0.55
2:B:267:ARG:CG	2:B:267:ARG:HH11	2.20	0.55
2:B:269:THR:O	2:B:273:VAL:HG23	2.07	0.55
2:C:269:THR:O	2:C:273:VAL:HG23	2.06	0.55
2:B:420:VAL:HA	2:B:423:GLN:OE1	2.07	0.55
2:G:280:ILE:CB	2:G:300:LEU:HD21	2.35	0.55
1:A:193:LEU:CD2	1:A:193:LEU:N	2.69	0.55
2:B:197:VAL:CG1	2:B:198:THR:N	2.69	0.55
2:C:172:ILE:HD11	1:D:28:LEU:CD1	2.37	0.55
2:C:491:LEU:O	2:C:494:SER:HB2	2.06	0.55
1:E:148:ALA:HB1	1:E:194:TRP:CH2	2.42	0.55
2:F:487:HIS:NE2	2:F:514:GLU:HG3	2.22	0.55
2:F:514:GLU:OE1	2:F:517:LEU:HD23	2.07	0.55
2:G:494:SER:O	2:G:497:LEU:HG	2.07	0.55
1:H:113:PRO:CB	1:H:161:ALA:HB2	2.37	0.55
1:A:23:TYR:CD2	1:A:68:PRO:HG3	2.42	0.55
2:C:420:VAL:HA	2:C:423:GLN:OE1	2.07	0.55
1:E:113:PRO:CB	1:E:161:ALA:HB2	2.36	0.55
1:E:43:ARG:O	1:E:44:ASN:HB2	2.07	0.55
2:F:434:LEU:O	2:F:438:VAL:N	2.39	0.55
1:A:15:MET:CE	2:B:162:LYS:HZ1	2.19	0.55
2:C:202:ARG:HG2	2:C:209:GLN:OE1	2.07	0.55
2:C:471:ASP:OD2	2:C:497:LEU:HA	2.07	0.55
1:D:193:LEU:N	1:D:193:LEU:CD2	2.70	0.55
2:G:384:LEU:HD13	2:G:410:PHE:CE1	2.41	0.55
1:H:290:LYS:CB	1:H:300:ILE:HD11	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:206:GLN:HG3	1:D:207:LYS:H	1.72	0.55
1:D:292:SER:O	1:D:294:ASP:N	2.40	0.55
1:E:30:THR:CG2	1:E:31:CYS:N	2.70	0.55
1:H:220:TRP:CE2	1:H:231:ILE:HD11	2.42	0.55
1:H:23:TYR:CD2	1:H:68:PRO:HG3	2.41	0.55
2:B:421:ILE:HD11	2:B:449:PHE:HE2	1.71	0.54
2:C:375:LEU:HD22	2:C:379:PHE:HE2	1.73	0.54
2:C:512:MET:SD	2:C:540:ALA:HB2	2.48	0.54
1:E:88:GLU:HA	1:E:92:THR:O	2.08	0.54
2:F:253:ASP:O	2:F:257:MET:HB2	2.07	0.54
2:F:280:ILE:HB	2:F:300:LEU:HD21	1.89	0.54
1:H:230:THR:CG2	1:H:242:ILE:HG23	2.37	0.54
1:A:43:ARG:O	1:A:44:ASN:HB2	2.07	0.54
2:B:487:HIS:CE1	2:B:514:GLU:HG3	2.42	0.54
2:C:412:LEU:CD2	2:C:413:PRO:HD2	2.37	0.54
2:G:150:PHE:HD2	2:G:150:PHE:N	2.06	0.54
1:A:125:SER:HB2	2:B:142:ARG:NH2	2.22	0.54
2:C:334:ASP:O	2:C:338:LEU:HB2	2.08	0.54
2:G:420:VAL:HA	2:G:423:GLN:OE1	2.07	0.54
2:G:210:ILE:HD12	2:G:495:CYS:HB3	1.89	0.54
1:H:148:ALA:HB1	1:H:194:TRP:CZ2	2.43	0.54
2:G:143:ARG:HD3	1:H:214:TRP:CZ3	2.42	0.54
1:A:234:CYS:HB2	1:A:265:VAL:HB	1.90	0.54
2:B:434:LEU:O	2:B:438:VAL:N	2.39	0.54
1:D:16:ILE:HA	1:D:32:SER:CB	2.36	0.54
1:D:30:THR:CG2	1:D:31:CYS:N	2.71	0.54
1:E:292:SER:O	1:E:294:ASP:N	2.41	0.54
2:G:380:SER:HB3	2:G:383:CYS:CB	2.31	0.54
2:G:479:ALA:HB1	1:H:273:THR:CG2	2.37	0.54
1:A:292:SER:O	1:A:294:ASP:N	2.40	0.54
1:A:107:ASN:CG	2:B:142:ARG:HH12	2.11	0.54
2:F:167:LYS:O	2:F:167:LYS:HD3	2.08	0.54
2:F:267:ARG:CG	2:F:267:ARG:HH11	2.20	0.54
2:F:287:SER:C	2:F:289:ASN:H	2.11	0.54
1:H:193:LEU:CD2	1:H:193:LEU:N	2.70	0.54
1:H:291:GLU:HB3	1:H:297:TRP:CD2	2.42	0.54
1:A:220:TRP:CE2	1:A:231:ILE:HD11	2.43	0.54
1:A:30:THR:CG2	1:A:31:CYS:N	2.70	0.54
2:B:371:SER:OG	2:B:373:LYS:HG3	2.07	0.54
2:C:371:SER:OG	2:C:373:LYS:HG3	2.07	0.54
2:C:454:ILE:O	2:C:458:ARG:HB2	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:258:LEU:CD1	1:E:297:TRP:HB3	2.38	0.54
2:G:148:TYR:HB2	1:H:266:TRP:CE2	2.43	0.54
2:G:479:ALA:CB	1:H:273:THR:CG2	2.86	0.54
1:A:199:ASP:OD1	1:A:200:GLY:N	2.40	0.54
2:B:202:ARG:HG2	2:B:209:GLN:OE1	2.07	0.54
2:C:155:THR:CG2	2:C:513:ARG:HD2	2.37	0.54
1:D:182:PHE:CD1	1:D:182:PHE:O	2.61	0.54
1:E:69:MET:HE2	1:E:70:TYR:HE1	1.71	0.54
2:F:145:THR:HG22	2:F:146:ALA:N	2.22	0.54
2:G:279:GLU:CD	2:G:380:SER:HB2	2.27	0.54
2:G:454:ILE:O	2:G:458:ARG:HB2	2.08	0.54
1:H:43:ARG:O	1:H:44:ASN:HB2	2.07	0.54
1:A:288:LEU:HB2	1:A:300:ILE:HG13	1.90	0.54
1:A:47:GLN:OE1	2:B:167:LYS:N	2.41	0.54
1:A:88:GLU:HA	1:A:92:THR:O	2.08	0.54
1:A:15:MET:CE	2:B:162:LYS:NZ	2.70	0.54
2:B:491:LEU:HD21	2:B:532:ILE:CD1	2.33	0.54
1:E:16:ILE:HA	1:E:32:SER:CB	2.36	0.54
1:E:199:ASP:OD1	1:E:200:GLY:N	2.40	0.54
2:F:137:LEU:O	2:F:141:GLU:HB3	2.08	0.54
2:G:175:LEU:HD13	2:G:176:PRO:HD2	1.89	0.54
2:G:334:ASP:O	2:G:338:LEU:HB2	2.08	0.54
1:H:238:GLY:O	1:H:260:LYS:HA	2.07	0.54
2:G:547:TYR:HE1	1:H:72:ASN:ND2	2.04	0.54
2:B:154:SER:O	2:B:157:SER:N	2.38	0.54
1:D:220:TRP:CE2	1:D:231:ILE:HD11	2.42	0.54
1:D:88:GLU:HA	1:D:92:THR:O	2.08	0.54
2:G:229:SER:O	2:G:232:ASN:HB2	2.08	0.54
1:H:30:THR:CG2	1:H:31:CYS:N	2.71	0.54
2:B:334:ASP:O	2:B:338:LEU:HB2	2.08	0.54
2:C:350:ILE:HB	2:C:354:ILE:HD12	1.90	0.54
1:E:182:PHE:O	1:E:182:PHE:CD1	2.60	0.54
1:E:23:TYR:CD2	1:E:68:PRO:HG3	2.42	0.54
2:F:202:ARG:HG2	2:F:209:GLN:OE1	2.07	0.54
2:F:268:LEU:CD2	2:F:389:LEU:HD13	2.37	0.54
2:F:371:SER:OG	2:F:373:LYS:HG3	2.07	0.54
1:A:27:ARG:HA	1:A:41:ASP:HA	1.91	0.53
2:B:145:THR:HG22	2:B:146:ALA:N	2.22	0.53
2:B:240:LEU:HD21	2:B:268:LEU:CD1	2.39	0.53
2:C:150:PHE:N	2:C:150:PHE:HD2	2.06	0.53
2:C:181:ARG:NH1	2:C:234:TRP:NE1	2.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:43:ARG:O	1:D:44:ASN:HB2	2.07	0.53
1:E:47:GLN:HE22	2:F:170:VAL:HG23	1.73	0.53
2:F:280:ILE:HD11	2:F:383:CYS:SG	2.48	0.53
2:G:170:VAL:CG1	2:G:171:SER:N	2.70	0.53
2:B:137:LEU:O	2:B:141:GLU:HB3	2.08	0.53
2:B:238:SER:O	2:B:242:ASP:HB2	2.08	0.53
1:E:206:GLN:HG3	1:E:207:LYS:H	1.72	0.53
2:F:359:LYS:HZ1	2:F:368:GLY:HA3	1.72	0.53
1:H:182:PHE:O	1:H:182:PHE:CD1	2.61	0.53
1:H:192:LYS:NZ	1:H:207:LYS:HE2	2.24	0.53
1:H:88:GLU:HA	1:H:92:THR:O	2.08	0.53
2:C:150:PHE:CD2	2:C:150:PHE:N	2.76	0.53
2:C:170:VAL:CG1	2:C:171:SER:N	2.71	0.53
2:C:208:PRO:HG3	2:C:532:ILE:HD13	1.90	0.53
2:C:229:SER:O	2:C:232:ASN:HB2	2.08	0.53
2:F:334:ASP:O	2:F:338:LEU:HB2	2.08	0.53
2:F:381:TRP:CD1	2:F:382:LEU:N	2.77	0.53
2:B:210:ILE:HD12	2:B:210:ILE:N	2.24	0.53
2:C:364:SER:HB3	2:C:394:ILE:CG1	2.22	0.53
1:E:67:HIS:O	1:E:69:MET:N	2.42	0.53
2:F:229:SER:O	2:F:232:ASN:HB2	2.08	0.53
1:H:206:GLN:HG3	1:H:207:LYS:H	1.72	0.53
2:B:454:ILE:O	2:B:458:ARG:HB2	2.09	0.53
1:E:145:ILE:HD13	1:E:194:TRP:CE3	2.44	0.53
2:G:197:VAL:CG1	2:G:198:THR:H	2.22	0.53
2:G:515:ILE:CD1	2:G:540:ALA:C	2.76	0.53
1:E:230:THR:CG2	1:E:231:ILE:H	2.21	0.53
2:G:299:LEU:HD22	2:G:383:CYS:SG	2.49	0.53
1:H:16:ILE:HA	1:H:32:SER:CB	2.36	0.53
2:B:197:VAL:CG1	2:B:198:THR:H	2.21	0.53
2:C:197:VAL:CG1	2:C:198:THR:N	2.70	0.53
2:C:546:ARG:HG3	2:C:546:ARG:HH11	1.74	0.53
1:E:148:ALA:HB1	1:E:194:TRP:CZ2	2.44	0.53
1:E:220:TRP:CE2	1:E:231:ILE:HD11	2.42	0.53
2:F:210:ILE:N	2:F:210:ILE:HD12	2.24	0.53
1:H:252:THR:O	1:H:252:THR:HG22	2.08	0.53
1:A:21:MET:HB3	2:B:154:SER:OG	2.09	0.53
2:B:167:LYS:O	2:B:167:LYS:HD3	2.08	0.53
1:D:99:HIS:CE1	1:D:142:VAL:HG11	2.44	0.53
2:F:148:TYR:C	2:F:148:TYR:CD1	2.80	0.53
2:F:202:ARG:HG2	2:F:209:GLN:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:67:HIS:O	1:A:69:MET:N	2.42	0.53
2:B:359:LYS:HZ2	2:B:368:GLY:HA3	1.73	0.53
2:C:202:ARG:HG2	2:C:209:GLN:HB2	1.91	0.53
2:C:210:ILE:HD12	2:C:210:ILE:N	2.24	0.53
1:E:193:LEU:HD21	1:E:208:LEU:HD11	1.90	0.53
1:E:27:ARG:HA	1:E:41:ASP:HA	1.90	0.53
2:G:197:VAL:CG1	2:G:198:THR:N	2.70	0.53
2:G:382:LEU:HD12	2:G:385:LEU:HD23	1.90	0.53
2:G:434:LEU:O	2:G:438:VAL:N	2.39	0.53
1:H:99:HIS:CE1	1:H:142:VAL:HG11	2.44	0.53
1:A:16:ILE:HA	1:A:32:SER:CB	2.36	0.53
1:A:230:THR:CG2	1:A:231:ILE:H	2.22	0.53
2:B:248:TYR:HB2	2:C:339:GLN:HE22	1.74	0.53
1:E:191:ILE:HD11	1:E:211:HIS:HD2	1.73	0.53
2:G:432:GLU:OE2	2:G:466:SER:CB	2.55	0.53
1:A:99:HIS:CE1	1:A:142:VAL:HG11	2.44	0.52
2:C:382:LEU:HD12	2:C:385:LEU:HD23	1.90	0.52
2:C:523:ASN:HB3	2:C:525:HIS:HE1	1.75	0.52
2:G:149:THR:CG2	2:G:150:PHE:N	2.72	0.52
2:G:202:ARG:HG2	2:G:209:GLN:OE1	2.08	0.52
2:G:202:ARG:HG2	2:G:209:GLN:HB2	1.91	0.52
2:G:343:TRP:CH2	2:G:350:ILE:HD12	2.44	0.52
2:G:384:LEU:O	2:G:387:LEU:HB2	2.10	0.52
1:A:69:MET:CE	1:A:114:HIS:HB2	2.40	0.52
1:A:17:HIS:CE1	2:B:148:TYR:CE2	2.97	0.52
2:B:174:ARG:CZ	2:B:485:GLN:HG2	2.39	0.52
2:F:181:ARG:HH12	2:F:234:TRP:HE1	1.58	0.52
2:G:394:ILE:O	2:G:397:TYR:HD1	1.91	0.52
2:G:414:TYR:HD2	2:G:415:ASP:H	1.56	0.52
1:A:230:THR:CG2	1:A:231:ILE:N	2.71	0.52
2:B:359:LYS:HZ1	2:B:368:GLY:HA3	1.74	0.52
2:C:251:ASP:O	2:C:251:ASP:OD1	2.27	0.52
1:E:287:THR:O	1:E:288:LEU:HD23	2.10	0.52
2:B:229:SER:O	2:B:232:ASN:HB2	2.08	0.52
2:B:515:ILE:HD13	2:B:541:GLN:CA	2.39	0.52
2:C:384:LEU:O	2:C:387:LEU:HB2	2.10	0.52
1:D:69:MET:CE	1:D:114:HIS:HB2	2.40	0.52
1:E:99:HIS:CE1	1:E:142:VAL:HG11	2.44	0.52
1:E:192:LYS:CE	1:E:207:LYS:HE2	2.40	0.52
2:F:382:LEU:HD12	2:F:385:LEU:HD23	1.91	0.52
2:G:150:PHE:N	2:G:150:PHE:CD2	2.76	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:210:ILE:N	2:G:210:ILE:HD12	2.24	0.52
1:H:33:SER:HA	1:H:59:PRO:HB3	1.92	0.52
1:A:33:SER:HA	1:A:59:PRO:HB3	1.92	0.52
2:B:399:LEU:O	2:B:402:LEU:HB3	2.09	0.52
2:C:399:LEU:O	2:C:402:LEU:HB3	2.10	0.52
1:D:195:LYS:HG3	1:D:196:GLU:H	1.75	0.52
1:D:221:ALA:HB2	1:D:270:TRP:CD2	2.45	0.52
1:E:125:SER:HB2	2:F:142:ARG:HH21	1.75	0.52
1:E:33:SER:HA	1:E:59:PRO:HB3	1.92	0.52
2:F:546:ARG:HG3	2:F:546:ARG:HH11	1.74	0.52
2:G:142:ARG:NH2	1:H:107:ASN:ND2	2.56	0.52
2:G:267:ARG:CG	2:G:267:ARG:HH11	2.20	0.52
2:G:546:ARG:HH11	2:G:546:ARG:HG3	1.74	0.52
2:G:544:LYS:HD2	1:H:24:TYR:CE2	2.45	0.52
2:G:172:ILE:HD11	1:H:28:LEU:CD1	2.40	0.52
1:H:67:HIS:O	1:H:69:MET:N	2.42	0.52
1:A:258:LEU:CD1	1:A:297:TRP:CB	2.88	0.52
2:B:149:THR:HG22	2:B:150:PHE:N	2.25	0.52
2:B:202:ARG:HG2	2:B:209:GLN:HB2	1.91	0.52
2:B:297:TYR:HB3	2:B:306:ALA:HB2	1.91	0.52
2:B:276:ILE:HD11	2:B:383:CYS:HA	1.91	0.52
2:B:215:LEU:CD1	2:B:452:TYR:OH	2.58	0.52
1:D:69:MET:HE2	1:D:70:TYR:HE1	1.75	0.52
2:F:399:LEU:O	2:F:402:LEU:HB3	2.09	0.52
2:F:454:ILE:O	2:F:458:ARG:HB2	2.08	0.52
2:G:149:THR:HG23	2:G:162:LYS:HG2	1.92	0.52
2:G:359:LYS:HZ2	2:G:368:GLY:HA3	1.73	0.52
1:H:244:THR:HG22	1:H:245:CYS:N	2.24	0.52
1:A:224:ILE:C	1:A:226:LEU:H	2.13	0.52
2:B:181:ARG:HH12	2:B:234:TRP:HE1	1.58	0.52
2:G:170:VAL:CG1	2:G:171:SER:H	2.23	0.52
2:G:194:ILE:HG12	2:G:492:PHE:CE2	2.45	0.52
2:G:215:LEU:CD1	2:G:452:TYR:OH	2.58	0.52
2:B:523:ASN:HB3	2:B:525:HIS:HE1	1.75	0.52
2:C:508:LYS:HA	2:C:536:LEU:HD21	1.92	0.52
1:D:287:THR:O	1:D:288:LEU:HD23	2.10	0.52
1:D:67:HIS:O	1:D:69:MET:N	2.43	0.52
1:E:230:THR:CG2	1:E:231:ILE:N	2.71	0.52
2:F:149:THR:HG22	2:F:150:PHE:N	2.24	0.52
2:F:409:LYS:C	2:F:410:PHE:HD2	2.13	0.52
2:G:399:LEU:O	2:G:402:LEU:HB3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:287:THR:O	1:H:288:LEU:HD23	2.10	0.52
1:H:69:MET:CE	1:H:114:HIS:HB2	2.40	0.52
1:H:69:MET:HE2	1:H:70:TYR:CE1	2.45	0.52
2:C:199:ILE:CD1	2:C:530:LEU:HA	2.40	0.52
1:D:33:SER:HA	1:D:59:PRO:HB3	1.92	0.52
2:F:196:LYS:HE3	2:F:219:ASP:OD1	2.10	0.52
2:G:359:LYS:HZ1	2:G:368:GLY:HA3	1.74	0.52
1:H:230:THR:CG2	1:H:231:ILE:N	2.72	0.52
1:H:293:VAL:O	1:H:293:VAL:HG12	2.09	0.52
2:F:384:LEU:O	2:F:387:LEU:HB2	2.09	0.51
2:F:523:ASN:HB3	2:F:525:HIS:HE1	1.75	0.51
2:G:435:TYR:CZ	2:G:454:ILE:HD11	2.46	0.51
1:H:288:LEU:H	1:H:301:SER:CB	2.23	0.51
2:F:177:THR:HG22	2:F:178:GLU:N	2.25	0.51
2:G:409:LYS:C	2:G:410:PHE:HD2	2.13	0.51
1:H:208:LEU:HB3	1:H:243:TRP:CZ3	2.45	0.51
2:C:512:MET:HA	2:C:540:ALA:HB1	1.92	0.51
1:E:285:LYS:HG2	1:E:304:ASN:HD21	1.75	0.51
1:E:107:ASN:OD1	2:F:142:ARG:CZ	2.58	0.51
1:E:17:HIS:CE1	2:F:148:TYR:HE2	2.28	0.51
2:F:475:PHE:CE2	2:F:497:LEU:HD11	2.45	0.51
1:H:53:LEU:N	1:H:53:LEU:HD23	2.26	0.51
1:D:113:PRO:CB	1:D:161:ALA:HB2	2.40	0.51
2:F:197:VAL:CG1	2:F:198:THR:H	2.22	0.51
1:H:102:HIS:HD1	1:H:124:SER:CB	2.22	0.51
1:A:287:THR:O	1:A:288:LEU:HD23	2.10	0.51
2:B:335:LEU:HD12	2:B:335:LEU:O	2.11	0.51
2:C:170:VAL:CG1	2:C:171:SER:H	2.23	0.51
2:C:409:LYS:C	2:C:410:PHE:HD2	2.13	0.51
1:D:155:ALA:CB	1:D:218:VAL:H	2.23	0.51
1:A:206:GLN:HG3	1:A:207:LYS:H	1.72	0.51
2:B:164:ILE:HG23	2:B:164:ILE:O	2.11	0.51
2:C:154:SER:OG	2:C:158:MET:HB2	2.11	0.51
2:C:335:LEU:HD12	2:C:335:LEU:O	2.11	0.51
1:D:230:THR:CG2	1:D:231:ILE:N	2.72	0.51
1:D:27:ARG:HA	1:D:41:ASP:HA	1.91	0.51
1:D:53:LEU:HD23	1:D:53:LEU:N	2.26	0.51
2:F:297:TYR:HB3	2:F:306:ALA:HB2	1.91	0.51
2:B:384:LEU:O	2:B:387:LEU:HB2	2.09	0.51
2:B:413:PRO:HB2	2:B:416:ASP:HB2	1.93	0.51
2:F:302:ASP:OD1	2:F:305:ARG:HB2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:250:THR:HG21	2:G:335:LEU:HD13	1.92	0.51
1:H:27:ARG:HA	1:H:41:ASP:HA	1.91	0.51
1:A:53:LEU:HD23	1:A:53:LEU:N	2.26	0.51
2:C:484:ALA:O	2:C:485:GLN:HB2	2.11	0.51
2:C:148:TYR:HD1	1:D:266:TRP:CG	2.29	0.51
1:E:69:MET:CE	1:E:114:HIS:HB2	2.40	0.51
1:E:21:MET:HE3	2:F:160:LEU:HD11	1.93	0.51
2:F:392:GLY:O	2:F:394:ILE:N	2.43	0.51
2:G:154:SER:OG	2:G:158:MET:HB2	2.10	0.51
2:G:215:LEU:HD12	2:G:452:TYR:CZ	2.45	0.51
2:B:155:THR:C	2:B:157:SER:H	2.15	0.51
2:B:280:ILE:HB	2:B:300:LEU:HD21	1.93	0.51
1:D:208:LEU:HB3	1:D:243:TRP:CH2	2.46	0.51
1:E:27:ARG:HG2	1:E:27:ARG:NH1	2.26	0.51
1:E:15:MET:HE2	2:F:162:LYS:HZ1	1.76	0.51
2:F:335:LEU:O	2:F:335:LEU:HD12	2.11	0.51
2:G:297:TYR:HB3	2:G:306:ALA:HB2	1.91	0.51
2:B:177:THR:HG22	2:B:178:GLU:N	2.25	0.51
2:B:409:LYS:C	2:B:410:PHE:HD2	2.14	0.51
2:C:175:LEU:HD13	2:C:176:PRO:CD	2.41	0.51
1:D:224:ILE:C	1:D:226:LEU:H	2.13	0.51
1:H:224:ILE:C	1:H:226:LEU:H	2.14	0.51
1:H:27:ARG:NH1	1:H:27:ARG:HG2	2.26	0.51
2:B:382:LEU:HD12	2:B:385:LEU:HD23	1.91	0.50
2:B:546:ARG:HG3	2:B:546:ARG:HH11	1.74	0.50
2:F:164:ILE:O	2:F:164:ILE:HG23	2.11	0.50
2:F:550:ASN:OD1	2:F:550:ASN:N	2.44	0.50
1:A:15:MET:O	1:A:32:SER:HB2	2.12	0.50
2:B:224:MET:HE2	2:B:230:ASP:HB3	1.93	0.50
2:C:530:LEU:HB2	2:C:532:ILE:HG12	1.92	0.50
2:G:181:ARG:NH1	2:G:234:TRP:HE1	2.07	0.50
2:G:210:ILE:HG22	2:G:459:PHE:HE2	1.76	0.50
1:H:185:GLY:N	1:H:218:VAL:HG21	2.26	0.50
1:A:109:VAL:HG12	1:A:110:CYS:N	2.27	0.50
2:B:403:VAL:O	2:B:407:LEU:HD13	2.11	0.50
2:C:149:THR:HG23	2:C:162:LYS:HG2	1.92	0.50
2:C:515:ILE:HD11	2:C:540:ALA:C	2.32	0.50
2:F:412:LEU:HD12	2:F:412:LEU:N	2.27	0.50
2:F:155:THR:HG22	2:F:513:ARG:CD	2.41	0.50
2:G:276:ILE:HD13	2:G:383:CYS:SG	2.51	0.50
2:G:523:ASN:HB3	2:G:525:HIS:HE1	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:113:PRO:CB	1:A:161:ALA:HB2	2.41	0.50
2:B:230:ASP:O	2:B:231:TYR:C	2.49	0.50
2:C:434:LEU:O	2:C:438:VAL:N	2.39	0.50
2:C:143:ARG:HD3	1:D:214:TRP:CZ3	2.47	0.50
1:E:224:ILE:C	1:E:226:LEU:H	2.13	0.50
1:E:53:LEU:N	1:E:53:LEU:HD23	2.26	0.50
2:F:197:VAL:CG1	2:F:198:THR:N	2.70	0.50
2:G:279:GLU:OE1	2:G:380:SER:HB2	2.12	0.50
1:H:109:VAL:HG12	1:H:110:CYS:N	2.27	0.50
1:H:195:LYS:HD2	1:H:195:LYS:O	2.12	0.50
1:A:145:ILE:HD13	1:A:194:TRP:CE3	2.46	0.50
1:E:40:PHE:CZ	2:F:168:SER:CB	2.91	0.50
2:G:335:LEU:O	2:G:335:LEU:HD12	2.11	0.50
1:H:15:MET:O	1:H:32:SER:HB2	2.12	0.50
1:A:15:MET:HE2	2:B:162:LYS:HZ1	1.76	0.50
2:C:197:VAL:CG1	2:C:198:THR:H	2.22	0.50
2:C:280:ILE:CB	2:C:300:LEU:HD21	2.41	0.50
2:C:451:TRP:CE2	2:C:493:VAL:HG13	2.46	0.50
1:D:15:MET:O	1:D:32:SER:HB2	2.12	0.50
1:E:149:HIS:HB3	1:E:188:ASP:OD1	2.12	0.50
1:H:290:LYS:HG2	1:H:291:GLU:N	2.27	0.50
2:C:403:VAL:O	2:C:407:LEU:HD13	2.12	0.50
1:E:107:ASN:CG	2:F:142:ARG:HH22	2.14	0.50
1:E:288:LEU:HB2	1:E:300:ILE:HG13	1.94	0.50
2:F:230:ASP:O	2:F:231:TYR:C	2.50	0.50
2:G:148:TYR:HD1	1:H:266:TRP:CG	2.30	0.50
1:A:27:ARG:NH1	1:A:27:ARG:HG2	2.26	0.50
1:A:302:ASP:C	1:A:302:ASP:OD1	2.50	0.50
2:C:216:LEU:HB3	2:C:242:ASP:OD1	2.12	0.50
2:C:384:LEU:HD13	2:C:410:PHE:CE1	2.47	0.50
1:E:109:VAL:HG12	1:E:110:CYS:N	2.26	0.50
2:F:132:ILE:HG22	2:F:135:ALA:HB3	1.94	0.50
2:F:412:LEU:HD12	2:F:412:LEU:H	1.76	0.50
2:C:185:PHE:HA	2:C:486:LEU:CD1	2.42	0.49
1:E:79:TYR:CD2	2:F:138:ILE:HD13	2.46	0.49
2:F:284:ILE:HD13	2:F:297:TYR:CE1	2.47	0.49
2:G:138:ILE:O	2:G:142:ARG:HG2	2.12	0.49
2:G:439:ARG:HA	2:G:442:THR:CB	2.42	0.49
1:A:90:ASN:C	1:A:92:THR:H	2.16	0.49
2:C:451:TRP:CZ2	2:C:493:VAL:HG13	2.46	0.49
1:E:302:ASP:C	1:E:302:ASP:OD1	2.50	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:191:ILE:HB	1:A:208:LEU:HB2	1.93	0.49
1:A:250:SER:C	1:A:252:THR:H	2.14	0.49
2:B:515:ILE:HD11	2:B:540:ALA:C	2.33	0.49
2:C:442:THR:HG23	2:C:445:LEU:HB2	1.94	0.49
1:E:236:GLN:HA	1:E:264:VAL:HG22	1.94	0.49
2:F:210:ILE:HG12	2:F:496:PHE:CE1	2.47	0.49
1:H:219:ALA:O	1:H:270:TRP:NE1	2.44	0.49
1:H:69:MET:HE1	1:H:114:HIS:HB2	1.93	0.49
1:D:191:ILE:HD11	1:D:211:HIS:CD2	2.47	0.49
1:D:230:THR:CG2	1:D:231:ILE:H	2.23	0.49
2:F:524:ASP:O	2:F:525:HIS:CB	2.60	0.49
2:G:403:VAL:O	2:G:407:LEU:HD13	2.12	0.49
2:G:479:ALA:HB1	1:H:273:THR:HG22	1.95	0.49
2:G:508:LYS:HA	2:G:536:LEU:HD21	1.94	0.49
1:A:107:ASN:OD1	2:B:142:ARG:NH1	2.45	0.49
1:A:198:GLU:O	1:A:198:GLU:HG2	2.13	0.49
1:A:204:GLU:HG3	1:A:204:GLU:O	2.13	0.49
2:B:399:LEU:HD23	2:B:425:TYR:OH	2.11	0.49
2:C:550:ASN:N	2:C:550:ASN:OD1	2.44	0.49
1:D:90:ASN:C	1:D:92:THR:H	2.16	0.49
1:E:204:GLU:O	1:E:204:GLU:HG3	2.13	0.49
2:F:155:THR:O	2:F:513:ARG:NH1	2.45	0.49
2:G:550:ASN:N	2:G:550:ASN:OD1	2.44	0.49
1:A:112:ALA:HB2	1:A:158:TRP:CZ2	2.48	0.49
1:A:47:GLN:HE22	2:B:170:VAL:HG23	1.77	0.49
1:D:109:VAL:HG12	1:D:110:CYS:N	2.27	0.49
1:E:15:MET:O	1:E:32:SER:HB2	2.12	0.49
2:F:403:VAL:O	2:F:407:LEU:HD13	2.12	0.49
2:G:175:LEU:HD13	2:G:176:PRO:CD	2.41	0.49
2:G:230:ASP:O	2:G:231:TYR:C	2.51	0.49
1:H:258:LEU:HD13	1:H:297:TRP:CB	2.43	0.49
2:B:276:ILE:CG2	2:B:280:ILE:HG13	2.42	0.49
2:B:524:ASP:O	2:B:525:HIS:CB	2.61	0.49
2:C:138:ILE:O	2:C:142:ARG:HG2	2.12	0.49
2:C:412:LEU:HD22	2:C:413:PRO:HD2	1.94	0.49
2:C:179:LEU:HD11	2:C:448:GLN:HB2	1.94	0.49
2:C:162:LYS:NZ	1:D:15:MET:CE	2.76	0.49
2:F:210:ILE:HD13	2:F:496:PHE:CD1	2.48	0.49
2:F:485:GLN:HE21	2:F:517:LEU:HD21	1.77	0.49
2:G:245:SER:O	2:G:247:PRO:HD3	2.11	0.49
1:E:102:HIS:HD1	1:E:124:SER:CB	2.22	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:359:LYS:HZ2	2:F:368:GLY:HA3	1.74	0.49
2:G:414:TYR:HD2	2:G:415:ASP:N	2.11	0.49
2:G:512:MET:SD	2:G:540:ALA:CB	3.01	0.49
1:H:230:THR:CG2	1:H:231:ILE:H	2.23	0.49
2:G:479:ALA:CB	1:H:273:THR:HG21	2.42	0.49
1:E:90:ASN:C	1:E:92:THR:H	2.16	0.49
2:F:457:LEU:HD12	2:F:465:PHE:HE1	1.78	0.49
2:G:347:GLY:C	2:G:349:SER:H	2.16	0.49
2:G:515:ILE:HD11	2:G:540:ALA:C	2.33	0.49
1:A:244:THR:O	1:A:253:TRP:HA	2.13	0.49
2:B:550:ASN:N	2:B:550:ASN:OD1	2.45	0.49
2:C:194:ILE:HG12	2:C:492:PHE:HE2	1.78	0.49
1:E:288:LEU:HB3	1:E:300:ILE:HD11	1.94	0.49
1:E:28:LEU:HD11	2:F:172:ILE:HD11	1.92	0.49
2:F:179:LEU:HD11	2:F:184:LEU:HD11	1.95	0.49
2:F:244:VAL:HG11	2:F:263:GLU:HB3	1.95	0.49
2:F:439:ARG:HA	2:F:442:THR:CB	2.42	0.49
1:A:243:TRP:CD1	1:A:243:TRP:N	2.80	0.48
2:C:230:ASP:O	2:C:231:TYR:C	2.51	0.48
1:D:204:GLU:HG3	1:D:204:GLU:O	2.13	0.48
2:F:155:THR:C	2:F:157:SER:H	2.14	0.48
2:B:223:TYR:CD1	2:B:223:TYR:N	2.81	0.48
2:C:154:SER:HB3	1:D:21:MET:HE3	1.94	0.48
2:C:267:ARG:CG	2:C:267:ARG:HH11	2.20	0.48
2:C:439:ARG:HA	2:C:442:THR:CB	2.42	0.48
1:D:113:PRO:HB3	1:D:161:ALA:HB2	1.95	0.48
1:E:15:MET:CE	2:F:162:LYS:NZ	2.76	0.48
2:F:276:ILE:CG2	2:F:280:ILE:HG13	2.43	0.48
2:F:217:PHE:HA	2:F:452:TYR:HE2	1.76	0.48
2:F:320:VAL:HG22	2:G:263:GLU:HA	1.94	0.48
2:G:269:THR:HG21	2:G:390:CYS:SG	2.52	0.48
2:G:524:ASP:O	2:G:525:HIS:CB	2.61	0.48
1:A:192:LYS:CE	1:A:207:LYS:HE2	2.43	0.48
1:A:26:THR:CG2	1:A:27:ARG:HD2	2.42	0.48
2:B:132:ILE:HG22	2:B:135:ALA:HB3	1.94	0.48
2:B:439:ARG:HA	2:B:442:THR:CB	2.42	0.48
2:B:521:SER:O	2:B:523:ASN:N	2.42	0.48
1:D:192:LYS:HE2	1:D:207:LYS:HE2	1.94	0.48
1:D:192:LYS:CE	1:D:207:LYS:HE2	2.42	0.48
1:D:238:GLY:O	1:D:260:LYS:HA	2.13	0.48
1:E:109:VAL:CG1	1:E:110:CYS:N	2.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:183:ALA:O	1:E:184:SER:HB3	2.13	0.48
1:E:198:GLU:O	1:E:198:GLU:HG2	2.13	0.48
1:E:107:ASN:OD1	2:F:142:ARG:NH2	2.46	0.48
2:G:223:TYR:N	2:G:223:TYR:CD1	2.81	0.48
1:H:189:ASN:ND2	1:H:213:ASP:C	2.66	0.48
1:A:102:HIS:HD1	1:A:124:SER:CB	2.22	0.48
1:A:185:GLY:HA3	1:A:215:VAL:HG11	1.96	0.48
1:A:69:MET:HE2	1:A:114:HIS:HB2	1.94	0.48
2:B:403:VAL:O	2:B:407:LEU:CD1	2.62	0.48
2:C:524:ASP:O	2:C:525:HIS:CB	2.60	0.48
2:F:512:MET:SD	2:F:540:ALA:HB2	2.53	0.48
1:H:183:ALA:O	1:H:184:SER:HB3	2.14	0.48
2:B:196:LYS:HE3	2:B:219:ASP:OD1	2.14	0.48
2:F:248:TYR:OH	2:G:343:TRP:HH2	1.96	0.48
2:F:403:VAL:O	2:F:407:LEU:CD1	2.62	0.48
2:G:395:ASP:OD1	2:G:396:GLU:HG3	2.14	0.48
1:H:113:PRO:HB3	1:H:161:ALA:HB2	1.94	0.48
1:A:148:ALA:HB1	1:A:194:TRP:CH2	2.48	0.48
2:B:207:TYR:CD2	2:B:504:GLU:HA	2.48	0.48
1:D:27:ARG:NH1	1:D:27:ARG:HG2	2.27	0.48
2:F:247:PRO:HG3	2:G:317:HIS:CD2	2.48	0.48
1:H:204:GLU:HG3	1:H:204:GLU:O	2.14	0.48
2:G:155:THR:HG21	1:H:23:TYR:O	2.13	0.48
1:H:90:ASN:C	1:H:92:THR:H	2.16	0.48
2:B:385:LEU:HA	2:B:406:HIS:CE1	2.48	0.48
1:D:241:PHE:C	1:D:242:ILE:HD12	2.33	0.48
1:D:288:LEU:N	1:D:301:SER:HB3	2.28	0.48
2:F:215:LEU:HD12	2:F:452:TYR:CZ	2.48	0.48
2:F:223:TYR:CD1	2:F:223:TYR:N	2.81	0.48
2:F:515:ILE:HD13	2:F:541:GLN:CA	2.44	0.48
2:G:521:SER:O	2:G:523:ASN:N	2.41	0.48
1:H:164:PRO:CG	1:H:176:PRO:HB2	2.44	0.48
1:H:241:PHE:C	1:H:242:ILE:HD12	2.34	0.48
1:A:185:GLY:N	1:A:218:VAL:HG21	2.28	0.48
2:C:162:LYS:NZ	1:D:15:MET:HE2	2.29	0.48
1:D:164:PRO:CG	1:D:176:PRO:HB2	2.44	0.48
2:F:522:THR:HG22	2:F:526:ILE:CD1	2.37	0.48
2:G:276:ILE:CG2	2:G:280:ILE:HG13	2.42	0.48
1:A:164:PRO:CG	1:A:176:PRO:HB2	2.44	0.48
2:B:215:LEU:HD12	2:B:452:TYR:CE1	2.49	0.48
2:C:162:LYS:HZ3	1:D:15:MET:HE2	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:403:VAL:O	2:G:407:LEU:CD1	2.62	0.48
1:H:109:VAL:CG1	1:H:110:CYS:N	2.77	0.48
1:H:112:ALA:HB2	1:H:158:TRP:CZ2	2.49	0.48
2:B:142:ARG:O	2:B:143:ARG:HB2	2.14	0.47
2:C:491:LEU:HD11	2:C:507:ILE:HG23	1.96	0.47
2:G:138:ILE:HD13	1:H:59:PRO:CD	2.43	0.47
1:A:193:LEU:HD21	1:A:208:LEU:CD1	2.45	0.47
1:A:236:GLN:NE2	1:A:264:VAL:HG21	2.29	0.47
2:C:150:PHE:HE2	2:C:162:LYS:N	2.12	0.47
1:D:112:ALA:HB2	1:D:158:TRP:CZ2	2.49	0.47
1:H:106:VAL:HA	1:H:124:SER:HA	1.96	0.47
1:H:192:LYS:CE	1:H:207:LYS:HE2	2.44	0.47
1:H:270:TRP:C	1:H:271:SER:O	2.52	0.47
1:A:109:VAL:CG1	1:A:110:CYS:N	2.77	0.47
2:C:474:THR:HG23	2:C:493:VAL:HG12	1.97	0.47
2:F:224:MET:HE1	2:F:230:ASP:OD1	2.14	0.47
2:G:385:LEU:HD21	2:G:422:PHE:CE2	2.49	0.47
1:A:183:ALA:O	1:A:184:SER:HB3	2.14	0.47
2:B:297:TYR:CE2	2:B:305:ARG:HB3	2.49	0.47
2:B:184:LEU:HD21	2:B:448:GLN:HE22	1.78	0.47
2:C:148:TYR:HB2	1:D:266:TRP:CD2	2.49	0.47
2:C:276:ILE:CG2	2:C:280:ILE:HG13	2.42	0.47
2:C:298:LEU:HD22	2:C:325:LEU:CD2	2.44	0.47
1:D:102:HIS:HD1	1:D:124:SER:CB	2.22	0.47
2:G:291:ILE:HD12	2:G:351:ASP:OD2	2.13	0.47
1:H:258:LEU:CD1	1:H:297:TRP:CB	2.92	0.47
1:A:16:ILE:HG21	1:A:30:THR:HG23	1.97	0.47
2:C:403:VAL:O	2:C:407:LEU:CD1	2.62	0.47
2:C:409:LYS:C	2:C:410:PHE:CD2	2.88	0.47
2:C:381:TRP:HE3	2:C:412:LEU:HD21	1.78	0.47
1:D:195:LYS:O	1:D:202:TRP:CD1	2.68	0.47
1:E:164:PRO:CG	1:E:176:PRO:HB2	2.44	0.47
1:E:236:GLN:NE2	1:E:264:VAL:HG21	2.30	0.47
1:E:289:TRP:HA	1:E:298:VAL:O	2.15	0.47
1:E:56:HIS:NE2	1:E:84:ILE:HD12	2.29	0.47
2:F:384:LEU:HD13	2:F:410:PHE:CE1	2.50	0.47
2:G:471:ASP:CG	2:G:498:ASN:H	2.18	0.47
2:G:547:TYR:CE1	1:H:72:ASN:ND2	2.76	0.47
1:H:26:THR:O	1:H:41:ASP:OD1	2.33	0.47
1:A:106:VAL:HA	1:A:124:SER:HA	1.97	0.47
2:B:404:GLN:CG	2:B:426:ALA:HB1	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:149:THR:CG2	2:C:150:PHE:N	2.72	0.47
1:D:183:ALA:O	1:D:184:SER:HB3	2.14	0.47
1:D:56:HIS:NE2	1:D:84:ILE:HD12	2.30	0.47
2:G:409:LYS:C	2:G:410:PHE:CD2	2.88	0.47
2:G:525:HIS:O	2:G:526:ILE:C	2.53	0.47
1:A:234:CYS:SG	1:A:268:VAL:HG23	2.54	0.47
2:B:205:ASN:HB2	2:B:206:PRO:CD	2.45	0.47
2:C:148:TYR:OH	1:D:17:HIS:CE1	2.67	0.47
2:C:223:TYR:CD1	2:C:223:TYR:N	2.82	0.47
1:D:106:VAL:HA	1:D:124:SER:HA	1.97	0.47
1:D:268:VAL:HG13	1:D:277:LEU:HD11	1.96	0.47
1:E:26:THR:CG2	1:E:27:ARG:HD2	2.42	0.47
2:C:142:ARG:O	1:D:216:ARG:NH2	2.47	0.47
2:C:175:LEU:HD22	2:C:176:PRO:HD2	1.96	0.47
1:E:220:TRP:NE1	1:E:231:ILE:HD11	2.30	0.47
1:E:268:VAL:HG13	1:E:277:LEU:HD11	1.97	0.47
2:F:175:LEU:HD23	2:F:483:PHE:CZ	2.50	0.47
2:F:525:HIS:O	2:F:526:ILE:C	2.53	0.47
2:G:150:PHE:HE2	2:G:162:LYS:N	2.13	0.47
1:H:258:LEU:HD13	1:H:297:TRP:HB2	1.97	0.47
1:A:236:GLN:HA	1:A:264:VAL:HG22	1.97	0.47
1:A:56:HIS:NE2	1:A:84:ILE:HD12	2.29	0.47
2:B:208:PRO:HB3	2:B:531:LYS:HB3	1.95	0.47
2:B:323:SER:OG	2:C:262:LYS:HE2	2.14	0.47
1:E:106:VAL:HA	1:E:124:SER:HA	1.96	0.47
1:E:270:TRP:C	1:E:271:SER:O	2.53	0.47
2:F:164:ILE:O	2:F:164:ILE:CG2	2.62	0.47
2:F:210:ILE:HG22	2:F:459:PHE:CE2	2.50	0.47
1:H:192:LYS:HE2	1:H:207:LYS:HE2	1.97	0.47
1:H:193:LEU:HD21	1:H:208:LEU:CD1	2.45	0.47
1:H:198:GLU:O	1:H:199:ASP:CB	2.63	0.47
1:A:107:ASN:CG	2:B:142:ARG:HH22	2.17	0.47
2:B:321:LEU:HD23	2:B:321:LEU:N	2.30	0.47
2:B:439:ARG:NH1	2:B:439:ARG:CG	2.78	0.47
1:D:26:THR:O	1:D:41:ASP:OD1	2.32	0.47
1:D:292:SER:C	1:D:294:ASP:N	2.68	0.47
2:G:175:LEU:HD22	2:G:176:PRO:HD2	1.97	0.47
1:A:292:SER:C	1:A:294:ASP:N	2.68	0.47
2:B:244:VAL:HG12	2:B:260:LEU:HD22	1.97	0.47
2:B:343:TRP:HZ3	2:B:350:ILE:CG2	2.23	0.47
2:B:375:LEU:HB2	2:B:384:LEU:HD21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:522:THR:HG22	2:B:526:ILE:CD1	2.37	0.47
1:D:109:VAL:CG1	1:D:110:CYS:N	2.77	0.47
1:D:16:ILE:HG21	1:D:30:THR:HG23	1.97	0.47
2:F:202:ARG:HG3	2:F:500:ASP:OD1	2.14	0.47
2:G:246:TYR:HE1	2:G:259:LEU:HD13	1.76	0.47
2:G:404:GLN:HG2	2:G:426:ALA:HB1	1.97	0.47
2:C:432:GLU:OE1	2:C:466:SER:N	2.47	0.46
1:D:179:ILE:HG21	1:D:181:ARG:HE	1.80	0.46
1:E:112:ALA:HB2	1:E:158:TRP:CZ2	2.49	0.46
1:E:179:ILE:HG21	1:E:181:ARG:HE	1.80	0.46
2:F:142:ARG:O	2:F:143:ARG:HB2	2.14	0.46
2:F:409:LYS:C	2:F:410:PHE:CD2	2.88	0.46
2:G:448:GLN:HG3	2:G:477:PHE:CZ	2.50	0.46
2:G:527:LEU:CD2	2:G:532:ILE:HD12	2.45	0.46
1:H:56:HIS:NE2	1:H:84:ILE:HD12	2.30	0.46
2:B:535:GLN:O	2:B:539:ASN:HB2	2.15	0.46
2:F:475:PHE:HE2	2:F:497:LEU:HD21	1.80	0.46
2:G:380:SER:CB	2:G:383:CYS:HB2	2.32	0.46
2:G:432:GLU:OE1	2:G:465:PHE:HA	2.15	0.46
2:B:175:LEU:HD23	2:B:483:PHE:CZ	2.51	0.46
2:C:370:PHE:O	2:C:371:SER:O	2.34	0.46
1:D:242:ILE:CD1	1:D:258:LEU:HB2	2.44	0.46
1:E:221:ALA:HB2	1:E:270:TRP:NE1	2.28	0.46
2:F:291:ILE:HG22	2:F:353:ASN:HB2	1.97	0.46
2:G:267:ARG:CG	2:G:267:ARG:NH1	2.78	0.46
2:G:479:ALA:CB	1:H:273:THR:HG22	2.45	0.46
1:A:250:SER:O	1:A:252:THR:N	2.48	0.46
2:C:525:HIS:O	2:C:526:ILE:C	2.53	0.46
1:D:188:ASP:O	1:D:189:ASN:HB2	2.15	0.46
1:E:107:ASN:ND2	2:F:142:ARG:NH2	2.56	0.46
1:E:292:SER:C	1:E:294:ASP:N	2.68	0.46
1:H:26:THR:CG2	1:H:27:ARG:HD2	2.43	0.46
1:A:258:LEU:CD1	1:A:297:TRP:HB3	2.45	0.46
2:B:381:TRP:CG	2:B:382:LEU:N	2.84	0.46
2:B:425:TYR:O	2:B:463:ARG:NH2	2.48	0.46
2:B:491:LEU:HD23	2:B:530:LEU:HD12	1.97	0.46
2:C:364:SER:HB2	2:C:367:GLU:HG2	1.98	0.46
2:C:535:GLN:O	2:C:539:ASN:HB2	2.15	0.46
1:E:16:ILE:HG21	1:E:30:THR:HG23	1.97	0.46
2:F:321:LEU:HD23	2:F:321:LEU:N	2.30	0.46
2:F:416:ASP:OD1	2:F:418:ILE:HG13	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:244:VAL:HG11	2:G:260:LEU:HA	1.97	0.46
2:G:522:THR:HG22	2:G:526:ILE:CD1	2.36	0.46
2:B:202:ARG:NE	2:B:209:GLN:HB3	2.31	0.46
2:B:232:ASN:O	2:B:233:LEU:C	2.53	0.46
2:B:501:LYS:O	2:B:505:ASP:HB2	2.16	0.46
1:D:232:ALA:HB2	1:D:270:TRP:HZ2	1.78	0.46
2:F:421:ILE:HD11	2:F:449:PHE:CZ	2.51	0.46
2:F:521:SER:O	2:F:523:ASN:N	2.42	0.46
2:G:158:MET:HE1	2:G:174:ARG:HG3	1.97	0.46
1:H:188:ASP:O	1:H:189:ASN:HB2	2.15	0.46
2:B:267:ARG:CG	2:B:267:ARG:NH1	2.78	0.46
2:B:525:HIS:O	2:B:526:ILE:C	2.53	0.46
2:C:205:ASN:HB2	2:C:206:PRO:CD	2.45	0.46
2:F:370:PHE:O	2:F:371:SER:O	2.33	0.46
1:H:290:LYS:HB2	1:H:300:ILE:HD12	1.97	0.46
1:A:14:ASP:CG	1:A:15:MET:H	2.19	0.46
1:A:179:ILE:HG21	1:A:181:ARG:HE	1.80	0.46
1:A:69:MET:HE2	1:A:70:TYR:HE1	1.79	0.46
2:B:164:ILE:O	2:B:164:ILE:CG2	2.62	0.46
1:D:220:TRP:NE1	1:D:231:ILE:HD11	2.31	0.46
1:D:270:TRP:C	1:D:271:SER:O	2.52	0.46
1:D:26:THR:CG2	1:D:27:ARG:HD2	2.43	0.46
2:F:527:LEU:HD22	2:F:532:ILE:HD12	1.98	0.46
2:G:202:ARG:NE	2:G:209:GLN:HB3	2.31	0.46
2:G:298:LEU:HD23	2:G:298:LEU:HA	1.76	0.46
2:G:409:LYS:O	2:G:410:PHE:HD2	1.99	0.46
1:H:191:ILE:HG23	1:H:218:VAL:HG21	1.97	0.46
1:H:242:ILE:HD12	1:H:242:ILE:N	2.30	0.46
1:H:290:LYS:CB	1:H:300:ILE:CD1	2.94	0.46
2:B:177:THR:CG2	2:B:178:GLU:N	2.79	0.46
2:B:409:LYS:O	2:B:410:PHE:HD2	1.99	0.46
2:B:416:ASP:OD1	2:B:418:ILE:HG13	2.16	0.46
2:C:199:ILE:HD12	2:C:530:LEU:HA	1.97	0.46
1:E:145:ILE:HG21	1:E:194:TRP:CZ3	2.51	0.46
2:F:177:THR:HG23	2:F:179:LEU:HB3	1.90	0.46
2:F:267:ARG:HH22	2:G:316:GLY:HA3	1.81	0.46
2:F:409:LYS:O	2:F:410:PHE:HD2	1.99	0.46
2:F:535:GLN:O	2:F:539:ASN:HB2	2.15	0.46
2:G:416:ASP:OD1	2:G:418:ILE:HG13	2.16	0.46
2:G:532:ILE:CG2	2:G:533:PRO:CD	2.86	0.46
2:B:409:LYS:C	2:B:410:PHE:CD2	2.88	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:501:LYS:O	2:C:505:ASP:HB2	2.16	0.46
1:D:219:ALA:O	1:D:270:TRP:NE1	2.48	0.46
1:D:245:CYS:SG	1:D:253:TRP:CE2	3.04	0.46
2:C:152:LYS:HG2	1:D:269:SER:HB2	1.98	0.46
1:E:188:ASP:O	1:E:189:ASN:HB2	2.16	0.46
1:E:67:HIS:ND1	1:E:69:MET:HB2	2.31	0.46
2:F:163:ASP:C	2:F:165:VAL:H	2.19	0.46
2:G:162:LYS:HZ3	1:H:15:MET:HE2	1.80	0.46
2:G:321:LEU:HB3	2:G:361:LEU:HD11	1.97	0.46
1:H:16:ILE:HG21	1:H:30:THR:HG23	1.97	0.46
1:A:193:LEU:C	1:A:194:TRP:CD1	2.90	0.45
1:A:157:SER:HB2	1:A:218:VAL:O	2.16	0.45
1:A:56:HIS:CE1	1:A:84:ILE:CD1	2.97	0.45
2:B:237:SER:C	2:B:239:ILE:N	2.68	0.45
2:C:321:LEU:N	2:C:321:LEU:HD23	2.30	0.45
2:C:416:ASP:OD1	2:C:418:ILE:HG13	2.16	0.45
1:D:258:LEU:CD1	1:D:297:TRP:HB2	2.46	0.45
2:F:232:ASN:O	2:F:233:LEU:C	2.54	0.45
2:F:248:TYR:CZ	2:G:343:TRP:CZ2	3.04	0.45
2:G:364:SER:HB2	2:G:367:GLU:HG2	1.98	0.45
2:G:153:PHE:CE2	1:H:278:ALA:HB2	2.50	0.45
1:H:287:THR:HA	1:H:301:SER:CB	2.46	0.45
1:H:67:HIS:ND1	1:H:69:MET:HB2	2.31	0.45
2:B:252:ASN:HB3	2:B:255:VAL:HB	1.98	0.45
2:B:370:PHE:O	2:B:371:SER:O	2.33	0.45
1:D:14:ASP:CG	1:D:15:MET:H	2.20	0.45
1:D:193:LEU:C	1:D:194:TRP:CD1	2.90	0.45
1:D:69:MET:HE2	1:D:114:HIS:HB2	1.99	0.45
1:E:182:PHE:C	1:E:182:PHE:CD1	2.90	0.45
2:F:501:LYS:O	2:F:505:ASP:HB2	2.16	0.45
1:H:268:VAL:HG13	1:H:277:LEU:HD11	1.96	0.45
1:A:193:LEU:HD23	1:A:193:LEU:N	2.32	0.45
1:A:220:TRP:NE1	1:A:231:ILE:HD11	2.30	0.45
1:D:67:HIS:ND1	1:D:69:MET:HB2	2.32	0.45
1:E:14:ASP:CG	1:E:15:MET:H	2.19	0.45
2:F:224:MET:CE	2:F:230:ASP:HB3	2.47	0.45
2:F:297:TYR:CE2	2:F:305:ARG:HB3	2.51	0.45
2:G:370:PHE:O	2:G:371:SER:O	2.34	0.45
2:G:535:GLN:O	2:G:539:ASN:HB2	2.15	0.45
1:A:87:ARG:CG	1:A:88:GLU:H	2.30	0.45
2:C:410:PHE:N	2:C:410:PHE:CD2	2.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:34:ASP:OD2	1:D:36:SER:HB2	2.17	0.45
1:E:193:LEU:C	1:E:194:TRP:CD1	2.90	0.45
1:E:34:ASP:OD2	1:E:36:SER:HB2	2.17	0.45
2:G:190:LEU:O	2:G:194:ILE:HG13	2.17	0.45
1:H:14:ASP:CG	1:H:15:MET:H	2.20	0.45
1:H:220:TRP:NE1	1:H:231:ILE:HD11	2.31	0.45
2:B:155:THR:HG22	2:B:513:ARG:CD	2.46	0.45
2:B:163:ASP:C	2:B:165:VAL:H	2.19	0.45
2:C:202:ARG:NE	2:C:209:GLN:HB3	2.31	0.45
2:F:493:VAL:O	2:F:496:PHE:HB2	2.17	0.45
2:F:525:HIS:ND1	2:F:526:ILE:N	2.65	0.45
2:G:224:MET:CE	2:G:230:ASP:HB3	2.46	0.45
2:G:321:LEU:N	2:G:321:LEU:HD23	2.31	0.45
1:H:34:ASP:OD2	1:H:36:SER:HB2	2.17	0.45
1:A:155:ALA:O	1:A:184:SER:HB2	2.17	0.45
2:F:177:THR:CG2	2:F:178:GLU:N	2.79	0.45
2:F:190:LEU:HD12	2:F:190:LEU:O	2.16	0.45
2:F:190:LEU:O	2:F:194:ILE:HG13	2.17	0.45
2:F:237:SER:C	2:F:239:ILE:N	2.69	0.45
2:G:237:SER:C	2:G:239:ILE:N	2.69	0.45
1:H:236:GLN:HA	1:H:264:VAL:HG13	1.97	0.45
1:A:182:PHE:CD1	1:A:182:PHE:C	2.89	0.45
1:A:188:ASP:O	1:A:189:ASN:HB2	2.16	0.45
1:A:197:GLU:O	1:A:199:ASP:N	2.50	0.45
2:B:190:LEU:HD12	2:B:190:LEU:O	2.17	0.45
2:B:525:HIS:ND1	2:B:526:ILE:N	2.65	0.45
2:C:190:LEU:O	2:C:194:ILE:HG13	2.17	0.45
1:A:224:ILE:O	1:A:226:LEU:N	2.46	0.45
2:B:190:LEU:O	2:B:194:ILE:HG13	2.17	0.45
2:B:224:MET:CE	2:B:230:ASP:HB3	2.46	0.45
2:C:267:ARG:NH1	2:C:267:ARG:CG	2.79	0.45
1:E:197:GLU:O	1:E:199:ASP:N	2.50	0.45
2:F:276:ILE:HD13	2:F:383:CYS:CA	2.43	0.45
2:F:343:TRP:CZ3	2:F:350:ILE:CG2	2.75	0.45
2:G:205:ASN:HB2	2:G:206:PRO:CD	2.45	0.45
2:G:215:LEU:O	2:G:456:THR:HG23	2.17	0.45
2:B:155:THR:O	2:B:513:ARG:NH1	2.50	0.45
2:B:484:ALA:CB	2:B:486:LEU:HD12	2.42	0.45
2:C:409:LYS:O	2:C:410:PHE:HD2	1.99	0.45
2:C:190:LEU:CD2	2:C:488:GLY:HA3	2.47	0.45
2:C:522:THR:HG22	2:C:526:ILE:CD1	2.36	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:242:ILE:CD1	1:D:242:ILE:N	2.79	0.45
2:F:269:THR:HG22	2:F:386:ASN:OD1	2.16	0.45
1:H:193:LEU:C	1:H:194:TRP:CD1	2.90	0.45
1:A:40:PHE:CZ	2:B:168:SER:CB	2.93	0.45
1:A:67:HIS:ND1	1:A:69:MET:HB2	2.31	0.45
2:B:527:LEU:HD22	2:B:532:ILE:CD1	2.42	0.45
1:D:283:ASP:O	1:D:284:ASN:HB3	2.17	0.45
1:D:87:ARG:CG	1:D:88:GLU:H	2.30	0.45
2:F:202:ARG:NE	2:F:209:GLN:HB3	2.31	0.45
2:G:489:HIS:O	2:G:490:SER:C	2.54	0.45
2:G:501:LYS:O	2:G:505:ASP:HB2	2.16	0.45
1:H:182:PHE:C	1:H:182:PHE:CD1	2.90	0.45
1:A:28:LEU:HD13	2:B:172:ILE:HD11	1.87	0.44
2:B:201:ALA:H	2:B:531:LYS:NZ	2.15	0.44
2:B:364:SER:HB2	2:B:367:GLU:HG2	1.99	0.44
2:B:484:ALA:O	2:B:486:LEU:HG	2.17	0.44
2:C:282:GLU:OE1	2:C:283:LYS:N	2.50	0.44
2:F:385:LEU:HA	2:F:406:HIS:CE1	2.51	0.44
2:F:385:LEU:HD21	2:F:422:PHE:CE2	2.51	0.44
2:F:420:VAL:HG11	2:F:445:LEU:HD11	1.98	0.44
2:B:410:PHE:N	2:B:410:PHE:CD2	2.84	0.44
2:C:215:LEU:HD12	2:C:452:TYR:CZ	2.52	0.44
2:C:525:HIS:ND1	2:C:526:ILE:N	2.65	0.44
1:D:189:ASN:ND2	1:D:213:ASP:C	2.70	0.44
1:D:293:VAL:O	1:D:293:VAL:CG1	2.65	0.44
2:F:284:ILE:HG12	2:F:296:LEU:HD12	1.99	0.44
1:H:56:HIS:CE1	1:H:84:ILE:CD1	2.98	0.44
1:A:268:VAL:HG13	1:A:277:LEU:HD11	1.97	0.44
2:B:282:GLU:OE1	2:B:283:LYS:N	2.50	0.44
2:B:320:VAL:HG22	2:C:263:GLU:HA	1.99	0.44
2:C:190:LEU:O	2:C:190:LEU:HD12	2.17	0.44
1:D:209:GLU:HG2	1:D:210:ALA:N	2.33	0.44
1:E:187:CYS:HB3	1:E:214:TRP:NE1	2.32	0.44
2:G:201:ALA:HB2	2:G:531:LYS:HZ1	1.79	0.44
2:G:282:GLU:OE1	2:G:283:LYS:N	2.50	0.44
1:H:195:LYS:HD2	1:H:195:LYS:C	2.37	0.44
2:C:189:TYR:CZ	2:C:193:GLU:OE1	2.70	0.44
2:C:521:SER:C	2:C:523:ASN:N	2.70	0.44
1:D:209:GLU:O	1:D:210:ALA:HB2	2.18	0.44
1:D:56:HIS:CE1	1:D:84:ILE:CD1	2.98	0.44
2:F:238:SER:HA	2:F:242:ASP:OD2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:237:SER:C	2:F:239:ILE:H	2.21	0.44
2:F:364:SER:HB2	2:F:367:GLU:HG2	1.98	0.44
2:F:515:ILE:HD13	2:F:541:GLN:N	2.32	0.44
2:G:181:ARG:NH1	2:G:234:TRP:NE1	2.66	0.44
1:A:34:ASP:OD2	1:A:36:SER:HB2	2.17	0.44
1:A:69:MET:CE	1:A:70:TYR:CE1	3.01	0.44
2:B:532:ILE:HG23	2:B:533:PRO:HD2	2.00	0.44
2:C:150:PHE:CD2	2:C:150:PHE:O	2.71	0.44
2:C:237:SER:C	2:C:239:ILE:N	2.69	0.44
2:C:287:SER:HB3	2:C:293:GLN:HE21	1.80	0.44
2:B:259:LEU:HD22	2:C:320:VAL:HG11	2.00	0.44
1:E:241:PHE:HB2	1:E:243:TRP:HE1	1.82	0.44
2:F:189:TYR:CZ	2:F:193:GLU:OE1	2.71	0.44
2:F:282:GLU:OE1	2:F:283:LYS:N	2.50	0.44
2:F:323:SER:OG	2:G:262:LYS:HE2	2.16	0.44
2:G:439:ARG:CG	2:G:439:ARG:NH1	2.78	0.44
2:G:487:HIS:O	2:G:488:GLY:C	2.55	0.44
1:A:145:ILE:HD13	1:A:194:TRP:CZ3	2.53	0.44
1:A:270:TRP:C	1:A:271:SER:O	2.52	0.44
2:B:224:MET:HE1	2:B:230:ASP:OD1	2.16	0.44
2:B:280:ILE:HD11	2:B:383:CYS:SG	2.58	0.44
2:B:299:LEU:HD22	2:B:383:CYS:SG	2.57	0.44
2:C:232:ASN:O	2:C:233:LEU:C	2.54	0.44
2:C:237:SER:C	2:C:239:ILE:H	2.21	0.44
2:C:298:LEU:HD22	2:C:325:LEU:HD21	2.00	0.44
2:C:295:PHE:CE2	2:C:356:LYS:HD3	2.53	0.44
1:D:112:ALA:HB2	1:D:158:TRP:CH2	2.53	0.44
1:D:182:PHE:CD1	1:D:182:PHE:C	2.90	0.44
1:E:258:LEU:CD1	1:E:297:TRP:HB2	2.47	0.44
1:E:87:ARG:CG	1:E:88:GLU:H	2.30	0.44
2:G:190:LEU:HD12	2:G:190:LEU:O	2.16	0.44
2:G:189:TYR:CZ	2:G:193:GLU:OE1	2.70	0.44
2:G:236:LEU:HD21	2:G:422:PHE:CE1	2.52	0.44
2:G:201:ALA:CB	2:G:531:LYS:NZ	2.81	0.44
2:G:540:ALA:O	2:G:543:LEU:HB3	2.18	0.44
1:H:179:ILE:HG21	1:H:181:ARG:HE	1.80	0.44
1:H:70:TYR:HD1	1:H:70:TYR:N	2.15	0.44
1:A:15:MET:HE2	2:B:162:LYS:NZ	2.32	0.44
2:B:312:GLU:HG3	2:B:312:GLU:O	2.18	0.44
2:B:385:LEU:HD21	2:B:422:PHE:CE2	2.53	0.44
1:D:224:ILE:O	1:D:226:LEU:N	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:112:ALA:HB2	1:E:158:TRP:CH2	2.53	0.44
1:E:27:ARG:HH11	1:E:27:ARG:HG2	1.83	0.44
2:F:259:LEU:HD11	2:G:335:LEU:HD21	1.99	0.44
2:F:268:LEU:HD23	2:F:389:LEU:HD13	1.99	0.44
1:A:209:GLU:HG2	1:A:210:ALA:N	2.33	0.44
1:A:258:LEU:HD13	1:A:297:TRP:CB	2.48	0.44
1:D:193:LEU:N	1:D:193:LEU:HD23	2.32	0.44
1:E:193:LEU:HD21	1:E:208:LEU:CD1	2.47	0.44
1:E:193:LEU:N	1:E:193:LEU:HD23	2.31	0.44
1:E:69:MET:HE2	1:E:70:TYR:CE1	2.52	0.44
2:F:284:ILE:HD13	2:F:297:TYR:CD1	2.52	0.44
2:G:312:GLU:HG3	2:G:312:GLU:O	2.18	0.44
1:H:193:LEU:N	1:H:193:LEU:HD23	2.32	0.44
1:H:242:ILE:HD11	1:H:258:LEU:HD22	2.00	0.44
2:B:189:TYR:CZ	2:B:193:GLU:OE1	2.70	0.44
2:B:486:LEU:O	2:B:489:HIS:N	2.51	0.44
2:C:267:ARG:HG3	2:C:267:ARG:NH1	2.28	0.44
2:C:148:TYR:HH	1:D:17:HIS:CE1	2.35	0.44
2:F:446:ASP:OD2	2:F:448:GLN:HB3	2.18	0.44
1:H:179:ILE:HG22	1:H:181:ARG:HE	1.83	0.44
1:H:23:TYR:HD2	1:H:24:TYR:CE1	2.36	0.44
2:B:177:THR:HG23	2:B:179:LEU:HB3	1.90	0.43
2:B:540:ALA:O	2:B:543:LEU:HB3	2.18	0.43
2:F:190:LEU:HD21	2:F:488:GLY:HA3	1.99	0.43
2:F:267:ARG:NH1	2:F:267:ARG:CG	2.79	0.43
2:F:267:ARG:NH2	2:G:316:GLY:HA3	2.33	0.43
2:G:238:SER:O	2:G:242:ASP:HB2	2.17	0.43
2:G:446:ASP:OD2	2:G:448:GLN:HB3	2.18	0.43
2:G:208:PRO:HB3	2:G:531:LYS:HG2	2.00	0.43
1:A:107:ASN:OD1	2:B:142:ARG:NH2	2.51	0.43
1:A:148:ALA:HB1	1:A:194:TRP:CZ2	2.53	0.43
1:A:179:ILE:HG22	1:A:181:ARG:HE	1.83	0.43
2:B:215:LEU:C	2:B:216:LEU:HD23	2.38	0.43
2:C:210:ILE:CG2	2:C:459:PHE:CE2	3.01	0.43
2:C:489:HIS:O	2:C:490:SER:C	2.56	0.43
1:E:69:MET:CE	1:E:70:TYR:CE1	3.01	0.43
2:F:224:MET:HE2	2:F:230:ASP:HB3	2.00	0.43
2:F:521:SER:C	2:F:523:ASN:N	2.70	0.43
2:G:232:ASN:O	2:G:233:LEU:C	2.54	0.43
1:H:112:ALA:HB2	1:H:158:TRP:CH2	2.53	0.43
1:H:209:GLU:HG2	1:H:210:ALA:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:241:PHE:HB2	1:A:243:TRP:HE1	1.82	0.43
1:A:274:ALA:O	1:A:275:ASN:C	2.57	0.43
2:B:186:ASP:OD1	2:B:187:ASP:N	2.51	0.43
2:B:446:ASP:OD2	2:B:448:GLN:HB3	2.18	0.43
2:C:215:LEU:C	2:C:216:LEU:HD23	2.39	0.43
2:C:432:GLU:OE1	2:C:465:PHE:HA	2.19	0.43
1:D:155:ALA:HB1	1:D:218:VAL:H	1.82	0.43
1:E:107:ASN:ND2	2:F:142:ARG:NH1	2.66	0.43
1:E:293:VAL:CG1	1:E:293:VAL:O	2.65	0.43
2:F:410:PHE:N	2:F:410:PHE:CD2	2.84	0.43
2:F:540:ALA:O	2:F:543:LEU:HB3	2.18	0.43
2:G:150:PHE:O	2:G:150:PHE:CD2	2.71	0.43
2:G:410:PHE:N	2:G:410:PHE:CD2	2.84	0.43
2:G:525:HIS:ND1	2:G:526:ILE:N	2.65	0.43
1:A:115:ASP:C	1:A:117:GLY:H	2.22	0.43
1:A:187:CYS:HB3	1:A:214:TRP:CE2	2.54	0.43
1:A:258:LEU:HD13	1:A:297:TRP:CG	2.53	0.43
2:B:181:ARG:NH1	2:B:234:TRP:HE1	2.16	0.43
2:C:224:MET:CE	2:C:230:ASP:HB3	2.46	0.43
2:C:246:TYR:CG	2:C:247:PRO:HD2	2.53	0.43
2:B:263:GLU:HA	2:C:320:VAL:HG22	2.00	0.43
2:C:276:ILE:HD11	2:C:383:CYS:HA	1.98	0.43
2:C:446:ASP:OD2	2:C:448:GLN:HB3	2.18	0.43
1:D:193:LEU:HD21	1:D:208:LEU:CD1	2.45	0.43
1:D:69:MET:CE	1:D:70:TYR:CE1	3.01	0.43
1:E:209:GLU:O	1:E:210:ALA:HB2	2.18	0.43
1:E:274:ALA:O	1:E:275:ASN:C	2.57	0.43
2:F:205:ASN:HB2	2:F:206:PRO:CD	2.46	0.43
2:G:280:ILE:CG2	2:G:300:LEU:HD21	2.49	0.43
2:G:347:GLY:C	2:G:349:SER:N	2.71	0.43
1:A:293:VAL:O	1:A:293:VAL:CG1	2.65	0.43
2:B:158:MET:HE3	2:B:174:ARG:HG3	2.01	0.43
1:A:21:MET:HE3	2:B:160:LEU:HD11	2.00	0.43
2:C:186:ASP:OD1	2:C:187:ASP:N	2.51	0.43
1:D:115:ASP:C	1:D:117:GLY:H	2.22	0.43
1:E:209:GLU:HG2	1:E:210:ALA:N	2.33	0.43
1:E:302:ASP:OD1	1:E:302:ASP:O	2.36	0.43
2:F:235:LYS:O	2:F:239:ILE:HG13	2.19	0.43
2:F:247:PRO:HG3	2:G:317:HIS:CG	2.53	0.43
1:H:230:THR:HG21	1:H:242:ILE:HG23	2.00	0.43
1:A:209:GLU:O	1:A:210:ALA:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:230:THR:CG2	1:A:242:ILE:HG23	2.48	0.43
1:A:302:ASP:O	1:A:302:ASP:OD1	2.36	0.43
1:D:23:TYR:HD2	1:D:24:TYR:CE1	2.36	0.43
1:E:115:ASP:C	1:E:117:GLY:H	2.22	0.43
2:F:298:LEU:HA	2:F:298:LEU:HD23	1.77	0.43
2:G:399:LEU:HD12	2:G:402:LEU:HD23	2.01	0.43
2:G:491:LEU:HD12	2:G:491:LEU:HA	1.85	0.43
1:H:87:ARG:CG	1:H:88:GLU:H	2.30	0.43
2:B:235:LYS:O	2:B:239:ILE:HG13	2.19	0.43
2:B:237:SER:C	2:B:239:ILE:H	2.21	0.43
2:B:431:THR:OG1	2:B:463:ARG:HG2	2.19	0.43
2:B:487:HIS:CD2	2:B:487:HIS:N	2.73	0.43
2:C:207:TYR:CD2	2:C:504:GLU:HA	2.52	0.43
1:D:274:ALA:O	1:D:275:ASN:C	2.57	0.43
1:E:286:VAL:HG21	2:F:151:ALA:HB2	1.99	0.43
1:E:288:LEU:O	1:E:299:CYS:HA	2.18	0.43
2:G:186:ASP:OD1	2:G:187:ASP:N	2.51	0.43
1:H:283:ASP:O	1:H:284:ASN:HB3	2.18	0.43
1:H:290:LYS:HB2	1:H:300:ILE:CD1	2.48	0.43
1:H:69:MET:CE	1:H:70:TYR:CE1	3.01	0.43
1:A:264:VAL:HG12	1:A:265:VAL:N	2.33	0.43
2:B:448:GLN:HG3	2:B:477:PHE:CZ	2.54	0.43
2:C:235:LYS:O	2:C:239:ILE:HG13	2.18	0.43
2:C:312:GLU:O	2:C:312:GLU:HG3	2.18	0.43
1:E:23:TYR:HD2	1:E:24:TYR:CE1	2.37	0.43
2:F:131:GLU:O	2:F:131:GLU:HG3	2.19	0.43
2:F:132:ILE:HG22	2:F:132:ILE:O	2.19	0.43
2:F:455:GLN:CG	2:F:496:PHE:CD2	3.01	0.43
2:G:237:SER:C	2:G:239:ILE:H	2.21	0.43
2:F:263:GLU:HA	2:G:320:VAL:CG2	2.47	0.43
2:G:375:LEU:HB3	2:G:379:PHE:HD1	1.83	0.43
2:B:132:ILE:HG22	2:B:132:ILE:O	2.19	0.43
2:B:420:VAL:HG11	2:B:445:LEU:HD11	2.00	0.43
1:E:16:ILE:HG22	1:E:17:HIS:N	2.33	0.43
2:F:215:LEU:HD12	2:F:452:TYR:CE1	2.54	0.43
2:F:297:TYR:HE2	2:F:305:ARG:HB3	1.84	0.43
2:F:484:ALA:O	2:F:486:LEU:N	2.52	0.43
2:G:153:PHE:CD2	1:H:271:SER:HA	2.54	0.43
1:H:16:ILE:HG22	1:H:17:HIS:N	2.34	0.43
1:H:27:ARG:HH11	1:H:27:ARG:HG2	1.83	0.43
1:A:216:ARG:HA	1:A:216:ARG:HD3	1.88	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:159:LEU:HD12	2:C:160:LEU:H	1.84	0.43
1:E:128:ALA:C	1:E:129:ILE:HG13	2.40	0.43
1:E:234:CYS:HB2	1:E:265:VAL:CG1	2.49	0.43
2:F:158:MET:HE3	2:F:174:ARG:HG3	2.00	0.43
2:F:186:ASP:OD1	2:F:187:ASP:N	2.51	0.43
2:F:312:GLU:O	2:F:312:GLU:HG3	2.18	0.43
2:F:263:GLU:HB2	2:G:320:VAL:HG21	2.00	0.43
1:H:84:ILE:HG21	1:H:86:TRP:CZ2	2.54	0.43
2:B:142:ARG:O	2:B:143:ARG:CB	2.67	0.42
1:A:271:SER:HA	2:B:153:PHE:CG	2.54	0.42
2:B:404:GLN:HG2	2:B:426:ALA:CB	2.36	0.42
2:C:161:THR:HG22	2:C:162:LYS:N	2.34	0.42
2:C:280:ILE:CG2	2:C:300:LEU:HD21	2.49	0.42
2:C:449:PHE:O	2:C:450:CYS:C	2.58	0.42
1:E:234:CYS:SG	1:E:268:VAL:HG23	2.59	0.42
2:F:215:LEU:C	2:F:216:LEU:HD23	2.39	0.42
2:G:268:LEU:O	2:G:272:ILE:HG13	2.19	0.42
1:H:145:ILE:HD11	1:H:202:TRP:CB	2.49	0.42
1:H:232:ALA:HB2	1:H:270:TRP:HZ2	1.84	0.42
1:H:274:ALA:O	1:H:275:ASN:C	2.57	0.42
1:A:70:TYR:HD1	1:A:70:TYR:N	2.15	0.42
2:B:521:SER:C	2:B:523:ASN:N	2.70	0.42
2:C:268:LEU:O	2:C:272:ILE:HG13	2.19	0.42
2:C:284:ILE:HG21	2:C:297:TYR:HE1	1.83	0.42
2:C:451:TRP:CD1	2:C:474:THR:HA	2.55	0.42
1:D:84:ILE:HG21	1:D:86:TRP:CZ2	2.54	0.42
1:E:155:ALA:O	1:E:184:SER:HB2	2.18	0.42
1:E:197:GLU:HB3	1:E:199:ASP:OD1	2.19	0.42
1:E:233:SER:O	1:E:240:VAL:HA	2.19	0.42
1:E:69:MET:HE1	1:E:114:HIS:HB2	1.99	0.42
2:F:372:LEU:HD22	2:F:375:LEU:HD11	2.01	0.42
2:G:199:ILE:HD12	2:G:530:LEU:HA	2.00	0.42
1:H:209:GLU:O	1:H:210:ALA:HB2	2.18	0.42
1:A:16:ILE:HG22	1:A:17:HIS:N	2.34	0.42
2:B:150:PHE:CE2	2:B:162:LYS:HB3	2.54	0.42
2:B:522:THR:CG2	2:B:526:ILE:HD11	2.40	0.42
2:F:150:PHE:CE2	2:F:162:LYS:HB3	2.54	0.42
2:F:449:PHE:O	2:F:450:CYS:C	2.58	0.42
2:G:372:LEU:HD22	2:G:375:LEU:HD11	2.01	0.42
2:G:172:ILE:HD11	1:H:28:LEU:HD12	2.02	0.42
1:A:112:ALA:HB2	1:A:158:TRP:CH2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:GLU:HB3	1:A:199:ASP:OD1	2.19	0.42
2:B:131:GLU:O	2:B:131:GLU:HG3	2.19	0.42
1:A:28:LEU:HD11	2:B:172:ILE:HD11	1.88	0.42
2:B:436:LYS:HE3	2:B:469:THR:OG1	2.18	0.42
2:C:170:VAL:H	1:D:47:GLN:HE22	1.67	0.42
2:C:540:ALA:O	2:C:543:LEU:HB3	2.19	0.42
1:D:179:ILE:HG22	1:D:181:ARG:HE	1.83	0.42
1:D:214:TRP:O	1:D:235:SER:CB	2.66	0.42
1:D:233:SER:O	1:D:240:VAL:HA	2.20	0.42
1:E:258:LEU:HD13	1:E:297:TRP:CG	2.54	0.42
1:E:56:HIS:CE1	1:E:84:ILE:CD1	2.98	0.42
2:F:179:LEU:HD11	2:F:184:LEU:HD12	2.01	0.42
2:F:345:THR:HG22	2:F:346:GLY:N	2.35	0.42
2:F:487:HIS:CB	2:F:518:LEU:HD21	2.46	0.42
2:G:145:THR:CG2	2:G:146:ALA:N	2.83	0.42
2:G:515:ILE:CD1	2:G:541:GLN:N	2.82	0.42
1:H:264:VAL:HG12	1:H:265:VAL:N	2.34	0.42
1:H:298:VAL:HG12	1:H:299:CYS:N	2.35	0.42
1:D:16:ILE:HG22	1:D:17:HIS:N	2.34	0.42
1:E:69:MET:HE2	1:E:114:HIS:HB2	2.02	0.42
2:F:259:LEU:HD11	2:G:335:LEU:CD2	2.50	0.42
2:F:268:LEU:O	2:F:272:ILE:HG13	2.20	0.42
2:F:399:LEU:HD12	2:F:402:LEU:HD23	2.01	0.42
2:G:158:MET:CE	2:G:174:ARG:HG3	2.50	0.42
2:F:262:LYS:HE2	2:G:323:SER:OG	2.19	0.42
1:H:224:ILE:O	1:H:226:LEU:N	2.47	0.42
1:A:128:ALA:C	1:A:129:ILE:HG13	2.40	0.42
1:A:23:TYR:HD2	1:A:24:TYR:CE1	2.37	0.42
2:B:142:ARG:HA	2:B:142:ARG:HD3	1.17	0.42
2:C:455:GLN:HG2	2:C:496:PHE:CD2	2.54	0.42
2:C:511:VAL:O	2:C:515:ILE:HG13	2.19	0.42
1:D:298:VAL:HG12	1:D:299:CYS:N	2.35	0.42
2:F:246:TYR:CD2	2:F:256:LYS:HE2	2.55	0.42
2:F:425:TYR:HA	2:F:463:ARG:HH22	1.84	0.42
2:G:492:PHE:CE1	2:G:496:PHE:CE1	3.08	0.42
2:C:215:LEU:CD1	2:C:452:TYR:OH	2.63	0.42
1:D:185:GLY:HA2	1:D:191:ILE:HA	2.02	0.42
1:E:214:TRP:O	1:E:235:SER:CB	2.65	0.42
2:G:194:ILE:HG12	2:G:492:PHE:CD2	2.54	0.42
2:G:449:PHE:O	2:G:450:CYS:C	2.57	0.42
1:H:155:ALA:O	1:H:184:SER:HB2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:ARG:HH11	1:A:27:ARG:HG2	1.84	0.42
1:A:77:CYS:HB3	1:A:109:VAL:CG2	2.50	0.42
2:B:268:LEU:O	2:B:272:ILE:HG13	2.20	0.42
1:D:264:VAL:HG12	1:D:265:VAL:N	2.34	0.42
1:E:84:ILE:HG21	1:E:86:TRP:CZ2	2.55	0.42
2:F:184:LEU:HD21	2:F:448:GLN:NE2	2.34	0.42
2:F:181:ARG:NH1	2:F:234:TRP:HE1	2.16	0.42
2:G:235:LYS:O	2:G:239:ILE:HG13	2.19	0.42
2:G:381:TRP:HE3	2:G:412:LEU:HD23	1.84	0.42
2:G:511:VAL:O	2:G:515:ILE:HG13	2.20	0.42
1:H:164:PRO:HG3	1:H:176:PRO:HB2	2.02	0.42
2:G:148:TYR:HD1	1:H:266:TRP:CB	2.32	0.42
1:A:145:ILE:HG21	1:A:194:TRP:CZ3	2.55	0.42
1:A:69:MET:HE3	1:A:70:TYR:CE1	2.55	0.42
2:B:149:THR:CG2	2:B:150:PHE:N	2.83	0.42
2:B:207:TYR:CE1	2:B:504:GLU:HG3	2.55	0.42
2:C:487:HIS:O	2:C:488:GLY:C	2.56	0.42
1:D:128:ALA:C	1:D:129:ILE:HG13	2.40	0.42
2:F:142:ARG:O	2:F:143:ARG:CB	2.67	0.42
2:F:158:MET:CE	2:F:174:ARG:HG3	2.50	0.42
2:F:477:PHE:CD2	2:F:493:VAL:HG21	2.55	0.42
2:G:224:MET:HE1	2:G:230:ASP:OD1	2.20	0.42
1:H:234:CYS:SG	1:H:268:VAL:CG2	3.07	0.42
1:H:92:THR:CG2	1:H:94:GLU:HG3	2.50	0.42
1:A:185:GLY:H	1:A:218:VAL:HG21	1.85	0.42
2:B:137:LEU:O	2:B:141:GLU:N	2.52	0.42
2:B:210:ILE:CD1	2:B:495:CYS:CB	2.96	0.42
2:B:297:TYR:HE2	2:B:305:ARG:HB3	1.84	0.42
2:B:511:VAL:O	2:B:515:ILE:HG13	2.20	0.42
2:C:220:ALA:HB3	2:C:234:TRP:CE3	2.55	0.42
2:C:499:ASP:OD2	2:C:499:ASP:C	2.58	0.42
2:C:439:ARG:O	1:D:293:VAL:HG11	2.20	0.42
1:E:107:ASN:HD21	2:F:142:ARG:CZ	2.33	0.42
1:E:128:ALA:O	1:E:129:ILE:HG13	2.20	0.42
2:F:137:LEU:O	2:F:141:GLU:N	2.52	0.42
2:F:170:VAL:O	2:F:172:ILE:N	2.53	0.42
2:G:161:THR:HG22	2:G:162:LYS:N	2.34	0.42
2:G:215:LEU:C	2:G:216:LEU:HD23	2.39	0.42
2:G:491:LEU:O	2:G:492:PHE:C	2.58	0.42
2:G:492:PHE:CE1	2:G:496:PHE:HE1	2.38	0.42
1:H:290:LYS:HG2	1:H:291:GLU:H	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:LEU:HD12	2:B:172:ILE:CD1	2.47	0.41
2:B:158:MET:CE	2:B:174:ARG:HG3	2.50	0.41
2:C:521:SER:O	2:C:523:ASN:N	2.42	0.41
1:D:77:CYS:HB3	1:D:109:VAL:CG2	2.50	0.41
1:E:208:LEU:HD22	1:E:243:TRP:CE3	2.55	0.41
1:E:264:VAL:HG12	1:E:265:VAL:N	2.34	0.41
2:F:202:ARG:NE	2:F:209:GLN:CB	2.83	0.41
2:G:159:LEU:HD12	2:G:160:LEU:H	1.84	0.41
1:H:115:ASP:C	1:H:117:GLY:H	2.22	0.41
1:H:128:ALA:C	1:H:129:ILE:HG13	2.40	0.41
1:H:77:CYS:HB3	1:H:109:VAL:CG2	2.50	0.41
1:A:16:ILE:HD11	2:B:168:SER:C	2.39	0.41
1:A:233:SER:O	1:A:240:VAL:HA	2.20	0.41
2:B:372:LEU:HD22	2:B:375:LEU:HD11	2.02	0.41
2:C:190:LEU:HD21	2:C:488:GLY:CA	2.48	0.41
2:C:399:LEU:HD12	2:C:402:LEU:HD23	2.01	0.41
2:C:490:SER:CB	2:C:510:LEU:HD21	2.48	0.41
2:C:208:PRO:HB3	2:C:531:LYS:HB3	2.02	0.41
1:D:40:PHE:HA	1:D:49:LEU:HA	2.02	0.41
1:E:111:TRP:CD2	1:E:120:LEU:HD13	2.55	0.41
2:G:162:LYS:NZ	1:H:15:MET:CE	2.83	0.41
2:G:207:TYR:CD2	2:G:504:GLU:HA	2.55	0.41
1:H:233:SER:O	1:H:240:VAL:HA	2.20	0.41
1:A:128:ALA:O	1:A:129:ILE:HG13	2.21	0.41
1:A:289:TRP:HA	1:A:298:VAL:O	2.20	0.41
1:A:38:LYS:HB3	1:A:40:PHE:CE1	2.52	0.41
2:B:145:THR:CG2	2:B:146:ALA:N	2.84	0.41
2:B:165:VAL:O	2:B:165:VAL:CG1	2.65	0.41
2:B:170:VAL:O	2:B:172:ILE:N	2.53	0.41
2:B:220:ALA:HB3	2:B:234:TRP:CE3	2.55	0.41
2:B:246:TYR:HA	2:B:247:PRO:HD2	1.75	0.41
2:C:372:LEU:HD22	2:C:375:LEU:HD11	2.02	0.41
1:D:121:ALA:CB	1:D:158:TRP:HE1	2.34	0.41
1:D:92:THR:CG2	1:D:94:GLU:HG3	2.50	0.41
2:F:149:THR:CG2	2:F:150:PHE:N	2.82	0.41
2:F:492:PHE:C	2:F:492:PHE:CD1	2.94	0.41
1:H:232:ALA:HB2	1:H:270:TRP:CZ2	2.55	0.41
1:A:271:SER:CB	1:A:276:ILE:HB	2.50	0.41
1:A:84:ILE:HG21	1:A:86:TRP:CZ2	2.55	0.41
2:B:481:LEU:HD13	2:B:489:HIS:CB	2.44	0.41
2:B:522:THR:CG2	2:B:526:ILE:CD1	2.99	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:142:ARG:O	2:C:143:ARG:HB2	2.20	0.41
2:C:340:LEU:HA	2:C:340:LEU:HD13	1.93	0.41
2:C:522:THR:CG2	2:C:526:ILE:CD1	2.98	0.41
2:C:208:PRO:CB	2:C:530:LEU:O	2.68	0.41
1:D:243:TRP:HE3	1:D:253:TRP:HB3	1.84	0.41
1:D:27:ARG:HH11	1:D:27:ARG:HG2	1.84	0.41
1:E:151:ILE:HB	1:E:187:CYS:CB	2.43	0.41
1:E:179:ILE:HG22	1:E:181:ARG:HE	1.83	0.41
1:E:21:MET:HB3	2:F:154:SER:OG	2.19	0.41
2:F:236:LEU:O	2:F:239:ILE:HB	2.20	0.41
2:F:367:GLU:OE2	2:F:394:ILE:HD13	2.20	0.41
1:A:234:CYS:HB2	1:A:265:VAL:CG1	2.49	0.41
1:A:286:VAL:HG21	2:B:151:ALA:HB2	2.03	0.41
2:B:351:ASP:C	2:B:353:ASN:N	2.74	0.41
2:B:399:LEU:HD12	2:B:402:LEU:HD23	2.01	0.41
2:B:449:PHE:O	2:B:450:CYS:C	2.58	0.41
2:C:145:THR:CG2	2:C:146:ALA:N	2.83	0.41
2:C:298:LEU:HD23	2:C:298:LEU:HA	1.76	0.41
1:E:121:ALA:CB	1:E:158:TRP:HE1	2.34	0.41
2:F:351:ASP:C	2:F:353:ASN:N	2.74	0.41
2:G:223:TYR:HD1	2:G:223:TYR:H	1.69	0.41
1:A:266:TRP:HD1	1:A:281:GLY:HA2	1.86	0.41
2:B:246:TYR:CE2	2:B:248:TYR:O	2.73	0.41
2:C:479:ALA:CB	1:D:273:THR:CG2	2.99	0.41
2:C:519:ARG:HE	2:C:541:GLN:NE2	2.18	0.41
1:E:164:PRO:HG3	1:E:176:PRO:HB2	2.02	0.41
1:E:224:ILE:O	1:E:226:LEU:N	2.46	0.41
2:F:511:VAL:O	2:F:515:ILE:HG13	2.21	0.41
2:F:522:THR:CG2	2:F:526:ILE:CD1	2.98	0.41
2:G:143:ARG:HD3	1:H:214:TRP:CH2	2.56	0.41
1:A:269:SER:HB2	2:B:152:LYS:HG2	2.03	0.41
2:C:202:ARG:NE	2:C:209:GLN:CB	2.83	0.41
1:D:121:ALA:HB3	1:D:158:TRP:HE1	1.86	0.41
1:E:145:ILE:HD13	1:E:194:TRP:CZ3	2.56	0.41
2:F:136:LYS:HA	2:F:136:LYS:HE2	2.02	0.41
2:F:439:ARG:NH1	2:F:439:ARG:CG	2.78	0.41
2:F:487:HIS:CD2	2:F:514:GLU:HG3	2.55	0.41
2:F:207:TYR:CD1	2:F:504:GLU:HG3	2.56	0.41
2:G:276:ILE:HG21	2:G:383:CYS:SG	2.61	0.41
2:G:521:SER:C	2:G:523:ASN:N	2.70	0.41
2:G:142:ARG:NH2	1:H:107:ASN:OD1	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:121:ALA:CB	1:H:158:TRP:HE1	2.34	0.41
1:H:266:TRP:HD1	1:H:281:GLY:HA2	1.86	0.41
1:A:149:HIS:HB3	1:A:188:ASP:OD1	2.20	0.41
1:A:185:GLY:HA2	1:A:191:ILE:HA	2.02	0.41
2:B:388:THR:HG22	2:B:388:THR:O	2.21	0.41
2:C:158:MET:HE1	2:C:174:ARG:CG	2.50	0.41
1:D:111:TRP:CD2	1:D:120:LEU:HD13	2.56	0.41
1:D:179:ILE:O	1:D:181:ARG:HG3	2.21	0.41
1:E:191:ILE:HB	1:E:208:LEU:HB2	2.02	0.41
1:E:75:ALA:HB2	1:E:111:TRP:HZ2	1.85	0.41
1:E:15:MET:CE	2:F:162:LYS:HZ1	2.31	0.41
2:F:220:ALA:HB3	2:F:234:TRP:CE3	2.55	0.41
1:A:151:ILE:HD13	2:F:414:TYR:OH	2.21	0.41
2:F:455:GLN:CG	2:F:496:PHE:CE2	2.99	0.41
2:G:153:PHE:HD1	2:G:158:MET:O	2.04	0.41
2:G:181:ARG:CZ	2:G:230:ASP:OD1	2.69	0.41
2:G:295:PHE:CE2	2:G:356:LYS:HD3	2.55	0.41
2:F:248:TYR:CZ	2:G:343:TRP:CH2	3.09	0.41
1:H:121:ALA:HB3	1:H:158:TRP:HE1	1.86	0.41
1:H:33:SER:HA	1:H:59:PRO:CB	2.50	0.41
1:A:230:THR:CG2	1:A:242:ILE:CG2	2.98	0.41
2:B:445:LEU:CD2	2:B:449:PHE:CD2	3.03	0.41
2:C:236:LEU:O	2:C:239:ILE:HB	2.21	0.41
2:C:351:ASP:C	2:C:353:ASN:N	2.74	0.41
2:C:359:LYS:HZ1	2:C:368:GLY:HA3	1.84	0.41
2:C:268:LEU:CD2	2:C:389:LEU:HD13	2.50	0.41
1:D:69:MET:HE1	1:D:114:HIS:HB2	2.03	0.41
2:F:155:THR:C	2:F:157:SER:N	2.74	0.41
1:H:185:GLY:HA2	1:H:191:ILE:HA	2.02	0.41
1:H:292:SER:C	1:H:294:ASP:H	2.23	0.41
1:A:111:TRP:CD2	1:A:120:LEU:HD13	2.56	0.41
1:A:164:PRO:HG3	1:A:176:PRO:HB2	2.02	0.41
1:A:40:PHE:HA	1:A:49:LEU:HA	2.03	0.41
2:B:350:ILE:HA	2:B:350:ILE:HD13	1.89	0.41
2:B:512:MET:HA	2:B:540:ALA:HB1	2.03	0.41
2:C:462:THR:C	2:C:463:ARG:HG2	2.40	0.41
1:D:67:HIS:C	1:D:69:MET:H	2.25	0.41
1:E:70:TYR:HD1	1:E:70:TYR:N	2.15	0.41
1:A:121:ALA:HB3	1:A:158:TRP:HE1	1.86	0.41
1:A:234:CYS:HB3	1:A:240:VAL:HG22	2.03	0.41
1:A:67:HIS:C	1:A:69:MET:H	2.24	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:136:LYS:HA	2:B:136:LYS:HE2	2.02	0.41
2:B:155:THR:C	2:B:157:SER:N	2.74	0.41
2:B:218:LYS:HG2	2:B:238:SER:OG	2.21	0.41
2:B:423:GLN:HB3	2:B:434:LEU:HD21	2.03	0.41
2:C:436:LYS:CE	2:C:469:THR:OG1	2.69	0.41
1:D:75:ALA:HB2	1:D:111:TRP:HZ2	1.86	0.41
1:E:16:ILE:HD11	2:F:168:SER:C	2.39	0.41
1:E:266:TRP:HD1	1:E:281:GLY:HA2	1.86	0.41
1:E:77:CYS:HB3	1:E:109:VAL:CG2	2.50	0.41
2:G:202:ARG:NE	2:G:209:GLN:CB	2.84	0.41
2:G:269:THR:HG22	2:G:386:ASN:OD1	2.20	0.41
1:H:179:ILE:O	1:H:181:ARG:HG3	2.21	0.41
2:G:148:TYR:HD1	1:H:266:TRP:HB3	1.86	0.41
1:A:121:ALA:CB	1:A:158:TRP:HE1	2.34	0.40
1:A:163:VAL:CG1	1:A:164:PRO:HD2	2.49	0.40
1:A:22:ASP:C	1:A:22:ASP:OD1	2.60	0.40
1:A:33:SER:HA	1:A:59:PRO:CB	2.51	0.40
2:B:350:ILE:CG2	2:B:351:ASP:N	2.84	0.40
2:C:284:ILE:HD13	2:C:297:TYR:HE1	1.75	0.40
2:C:457:LEU:HD23	2:C:457:LEU:HA	1.89	0.40
1:D:271:SER:CB	1:D:276:ILE:HB	2.51	0.40
1:E:185:GLY:HA2	1:E:191:ILE:HA	2.02	0.40
1:E:226:LEU:CD1	1:E:228:THR:OG1	2.63	0.40
1:E:41:ASP:OD1	1:E:41:ASP:C	2.60	0.40
1:E:40:PHE:HA	1:E:49:LEU:HA	2.03	0.40
1:E:17:HIS:O	2:F:150:PHE:CD2	2.74	0.40
2:F:223:TYR:HD1	2:F:223:TYR:H	1.69	0.40
2:F:340:LEU:HD12	2:F:370:PHE:HD1	1.86	0.40
2:F:515:ILE:CD1	2:F:540:ALA:C	2.90	0.40
2:G:220:ALA:HB3	2:G:234:TRP:CE3	2.55	0.40
2:G:283:LYS:HD2	2:G:379:PHE:HE2	1.85	0.40
2:G:430:ASN:O	2:G:431:THR:C	2.60	0.40
2:G:201:ALA:CB	2:G:531:LYS:HZ1	2.33	0.40
1:A:75:ALA:HB2	1:A:111:TRP:HZ2	1.86	0.40
2:B:236:LEU:HD21	2:B:422:PHE:CE1	2.56	0.40
2:B:298:LEU:HA	2:B:298:LEU:HD23	1.76	0.40
2:B:430:ASN:O	2:B:431:THR:C	2.60	0.40
2:B:546:ARG:NH1	2:B:546:ARG:HG3	2.36	0.40
2:C:153:PHE:HD1	2:C:158:MET:O	2.04	0.40
2:C:519:ARG:HH21	2:C:541:GLN:HE21	1.69	0.40
1:D:38:LYS:HB3	1:D:40:PHE:CE1	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:101:GLY:C	1:E:102:HIS:HD2	2.25	0.40
1:E:179:ILE:O	1:E:181:ARG:HG3	2.22	0.40
2:F:375:LEU:HB2	2:F:384:LEU:HD21	2.03	0.40
2:G:207:TYR:CE1	2:G:504:GLU:HG3	2.56	0.40
1:H:128:ALA:O	1:H:129:ILE:HG13	2.21	0.40
1:H:214:TRP:O	1:H:235:SER:CB	2.66	0.40
2:B:268:LEU:HD23	2:B:389:LEU:HD13	2.02	0.40
2:B:445:LEU:CD2	2:B:449:PHE:HD2	2.34	0.40
1:D:128:ALA:O	1:D:129:ILE:HG13	2.21	0.40
2:F:142:ARG:HD3	2:F:142:ARG:HA	1.17	0.40
2:F:532:ILE:HG22	2:F:533:PRO:N	2.37	0.40
2:G:351:ASP:C	2:G:353:ASN:N	2.74	0.40
2:G:413:PRO:HG2	2:G:413:PRO:O	2.20	0.40
2:G:533:PRO:HG2	2:G:536:LEU:HB3	2.04	0.40
1:H:163:VAL:HG22	1:H:178:TYR:HE2	1.87	0.40
1:H:67:HIS:C	1:H:69:MET:H	2.24	0.40
2:B:202:ARG:NE	2:B:209:GLN:CB	2.83	0.40
2:B:491:LEU:HD11	2:B:511:VAL:HG23	2.04	0.40
1:D:164:PRO:HG3	1:D:176:PRO:HB2	2.02	0.40
1:E:271:SER:CB	1:E:276:ILE:HB	2.50	0.40
2:F:218:LYS:HG2	2:F:238:SER:OG	2.22	0.40
2:G:210:ILE:CG2	2:G:459:PHE:CE2	3.04	0.40
2:G:457:LEU:HD13	2:G:463:ARG:HG3	2.02	0.40
2:G:451:TRP:CD1	2:G:474:THR:HA	2.56	0.40
1:H:145:ILE:HD13	1:H:194:TRP:CE3	2.57	0.40
1:A:214:TRP:O	1:A:235:SER:CB	2.66	0.40
1:A:241:PHE:HB2	1:A:243:TRP:NE1	2.37	0.40
1:A:245:CYS:HA	1:A:252:THR:O	2.21	0.40
2:C:159:LEU:HA	2:C:159:LEU:HD12	1.82	0.40
2:C:204:SER:O	2:C:205:ASN:HB3	2.22	0.40
2:C:269:THR:C	2:C:271:TRP:N	2.75	0.40
2:C:375:LEU:HD22	2:C:379:PHE:CE2	2.52	0.40
2:C:385:LEU:HA	2:C:406:HIS:CE1	2.57	0.40
2:C:430:ASN:O	2:C:431:THR:C	2.59	0.40
2:C:215:LEU:O	2:C:456:THR:HG23	2.21	0.40
1:D:206:GLN:CG	1:D:207:LYS:N	2.84	0.40
1:D:266:TRP:HD1	1:D:281:GLY:HA2	1.86	0.40
1:D:33:SER:HA	1:D:59:PRO:CB	2.51	0.40
1:D:69:MET:HE2	1:D:70:TYR:CE1	2.56	0.40
1:E:243:TRP:H	1:E:243:TRP:HD1	1.69	0.40
2:F:165:VAL:O	2:F:165:VAL:CG1	2.65	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:321:LEU:CD1	2:F:358:TYR:CE2	3.05	0.40
2:F:420:VAL:HG11	2:F:445:LEU:CD1	2.51	0.40
1:H:240:VAL:HG11	1:H:258:LEU:HD23	2.03	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	279/316 (88%)	217 (78%)	46 (16%)	16 (6%)	1	12
1	D	277/316 (88%)	216 (78%)	45 (16%)	16 (6%)	1	11
1	E	279/316 (88%)	218 (78%)	45 (16%)	16 (6%)	1	12
1	H	277/316 (88%)	215 (78%)	46 (17%)	16 (6%)	1	11
2	B	421/442 (95%)	351 (83%)	61 (14%)	9 (2%)	7	33
2	C	416/442 (94%)	353 (85%)	52 (12%)	11 (3%)	5	28
2	F	421/442 (95%)	342 (81%)	66 (16%)	13 (3%)	4	23
2	G	416/442 (94%)	344 (83%)	62 (15%)	10 (2%)	6	30
All	All	2786/3032 (92%)	2256 (81%)	423 (15%)	107 (4%)	3	19

All (107) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	138	GLY
1	A	180	LYS
1	A	210	ALA
2	B	371	SER
2	B	520	ALA
2	B	525	HIS
2	C	371	SER

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Mol	Chain	Res	Type
2	C	393	GLN
2	C	500	ASP
2	C	520	ALA
2	C	525	HIS
1	D	138	GLY
1	D	180	LYS
1	D	210	ALA
1	E	138	GLY
1	E	180	LYS
1	E	210	ALA
2	F	371	SER
2	F	520	ALA
2	F	525	HIS
2	G	371	SER
2	G	520	ALA
2	G	525	HIS
1	H	138	GLY
1	H	180	LYS
1	H	210	ALA
1	A	136	GLY
1	A	198	GLU
1	A	293	VAL
2	B	247	PRO
2	B	345	THR
2	B	526	ILE
2	C	345	THR
2	C	395	ASP
2	C	526	ILE
1	D	136	GLY
1	D	293	VAL
1	E	136	GLY
1	E	198	GLU
1	E	249	SER
1	E	271	SER
1	E	293	VAL
2	F	345	THR
2	F	485	GLN
2	F	526	ILE
2	G	345	THR
2	G	395	ASP
2	G	526	ILE
1	H	136	GLY

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Mol	Chain	Res	Type
1	A	44	ASN
1	A	45	GLY
1	A	176	PRO
1	A	251	ASN
1	A	271	SER
1	D	44	ASN
1	D	45	GLY
1	D	176	PRO
1	D	250	SER
1	D	251	ASN
1	D	271	SER
1	E	44	ASN
1	E	45	GLY
1	E	176	PRO
1	H	44	ASN
1	H	45	GLY
1	H	176	PRO
1	H	198	GLU
1	H	271	SER
1	A	55	GLY
1	A	68	PRO
2	B	171	SER
2	B	522	THR
2	C	522	THR
1	D	55	GLY
1	D	68	PRO
1	E	55	GLY
1	E	68	PRO
2	F	171	SER
2	F	490	SER
2	F	522	THR
2	G	522	THR
1	H	55	GLY
1	H	68	PRO
1	A	114	HIS
1	A	175	LYS
1	D	114	HIS
1	D	175	LYS
1	E	114	HIS
1	E	175	LYS
2	F	487	HIS
1	H	114	HIS

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Mol	Chain	Res	Type
1	H	175	LYS
1	H	199	ASP
1	A	48	ILE
2	C	442	THR
1	D	48	ILE
1	E	48	ILE
2	F	442	THR
2	G	442	THR
2	G	496	PHE
1	H	48	ILE
1	H	295	GLY
2	F	247	PRO
2	B	277	GLY
2	C	277	GLY
2	F	277	GLY
2	G	277	GLY

### 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	238/267 (89%)	216 (91%)	22 (9%)	9	31
1	D	236/267 (88%)	217 (92%)	19 (8%)	11	39
1	E	238/267 (89%)	216 (91%)	22 (9%)	9	31
1	H	236/267 (88%)	215 (91%)	21 (9%)	9	33
2	B	386/403 (96%)	347 (90%)	39 (10%)	7	27
2	C	384/403 (95%)	348 (91%)	36 (9%)	8	30
2	F	386/403 (96%)	349 (90%)	37 (10%)	8	29
2	G	384/403 (95%)	348 (91%)	36 (9%)	8	30
All	All	2488/2680 (93%)	2256 (91%)	232 (9%)	9	31

All (232) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	MET
1	A	22	ASP
1	A	27	ARG
1	A	33	SER
1	A	40	PHE
1	A	41	ASP
1	A	53	LEU
1	A	70	TYR
1	A	83	VAL
1	A	188	ASP
1	A	193	LEU
1	A	201	GLN
1	A	220	TRP
1	A	226	LEU
1	A	228	THR
1	A	244	THR
1	A	250	SER
1	A	272	ILE
1	A	283	ASP
1	A	287	THR
1	A	302	ASP
1	A	304	ASN
2	B	141	GLU
2	B	142	ARG
2	B	148	TYR
2	B	158	MET
2	B	164	ILE
2	B	168	SER
2	B	170	VAL
2	B	209	GLN
2	B	215	LEU
2	B	230	ASP
2	B	267	ARG
2	B	268	LEU
2	B	269	THR
2	B	282	GLU
2	B	299	LEU
2	B	339	GLN
2	B	340	LEU
2	B	348	CYS
2	B	349	SER
2	B	351	ASP
2	B	365	PRO

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Mol	Chain	Res	Type
2	B	370	PHE
2	B	395	ASP
2	B	397	TYR
2	B	418	ILE
2	B	428	ASN
2	B	439	ARG
2	B	463	ARG
2	B	464	VAL
2	B	489	HIS
2	B	505	ASP
2	B	516	THR
2	B	517	LEU
2	B	519	ARG
2	B	521	SER
2	B	523	ASN
2	B	525	HIS
2	B	546	ARG
2	B	550	ASN
2	C	132	ILE
2	C	134	ASN
2	C	138	ILE
2	C	139	MET
2	C	148	TYR
2	C	150	PHE
2	C	157	SER
2	C	175	LEU
2	C	209	GLN
2	C	215	LEU
2	C	230	ASP
2	C	244	VAL
2	C	267	ARG
2	C	268	LEU
2	C	269	THR
2	C	282	GLU
2	C	299	LEU
2	C	339	GLN
2	C	340	LEU
2	C	351	ASP
2	C	365	PRO
2	C	370	PHE
2	C	418	ILE
2	C	428	ASN

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Mol	Chain	Res	Type
2	C	439	ARG
2	C	464	VAL
2	C	495	CYS
2	C	505	ASP
2	C	516	THR
2	C	517	LEU
2	C	519	ARG
2	C	521	SER
2	C	523	ASN
2	C	525	HIS
2	C	546	ARG
2	C	550	ASN
1	D	21	MET
1	D	22	ASP
1	D	27	ARG
1	D	33	SER
1	D	40	PHE
1	D	53	LEU
1	D	70	TYR
1	D	83	VAL
1	D	188	ASP
1	D	193	LEU
1	D	220	TRP
1	D	226	LEU
1	D	228	THR
1	D	245	CYS
1	D	246	ASP
1	D	250	SER
1	D	272	ILE
1	D	283	ASP
1	D	287	THR
1	E	21	MET
1	E	22	ASP
1	E	27	ARG
1	E	33	SER
1	E	40	PHE
1	E	41	ASP
1	E	53	LEU
1	E	70	TYR
1	E	83	VAL
1	E	188	ASP
1	E	193	LEU

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Mol	Chain	Res	Type
1	E	201	GLN
1	E	220	TRP
1	E	226	LEU
1	E	228	THR
1	E	246	ASP
1	E	249	SER
1	E	272	ILE
1	E	283	ASP
1	E	287	THR
1	E	302	ASP
1	E	304	ASN
2	F	141	GLU
2	F	142	ARG
2	F	148	TYR
2	F	158	MET
2	F	164	ILE
2	F	168	SER
2	F	170	VAL
2	F	209	GLN
2	F	215	LEU
2	F	230	ASP
2	F	267	ARG
2	F	268	LEU
2	F	269	THR
2	F	282	GLU
2	F	299	LEU
2	F	339	GLN
2	F	340	LEU
2	F	351	ASP
2	F	365	PRO
2	F	370	PHE
2	F	397	TYR
2	F	412	LEU
2	F	418	ILE
2	F	428	ASN
2	F	439	ARG
2	F	464	VAL
2	F	489	HIS
2	F	497	LEU
2	F	505	ASP
2	F	516	THR
2	F	517	LEU

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Mol	Chain	Res	Type
2	F	519	ARG
2	F	521	SER
2	F	523	ASN
2	F	525	HIS
2	F	546	ARG
2	F	550	ASN
2	G	132	ILE
2	G	134	ASN
2	G	138	ILE
2	G	139	MET
2	G	148	TYR
2	G	150	PHE
2	G	157	SER
2	G	175	LEU
2	G	209	GLN
2	G	215	LEU
2	G	230	ASP
2	G	267	ARG
2	G	268	LEU
2	G	269	THR
2	G	282	GLU
2	G	299	LEU
2	G	339	GLN
2	G	340	LEU
2	G	351	ASP
2	G	365	PRO
2	G	370	PHE
2	G	414	TYR
2	G	418	ILE
2	G	428	ASN
2	G	439	ARG
2	G	464	VAL
2	G	490	SER
2	G	505	ASP
2	G	516	THR
2	G	517	LEU
2	G	519	ARG
2	G	521	SER
2	G	523	ASN
2	G	525	HIS
2	G	546	ARG
2	G	550	ASN

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Mol	Chain	Res	Type
1	H	21	MET
1	H	22	ASP
1	H	27	ARG
1	H	33	SER
1	H	40	PHE
1	H	53	LEU
1	H	70	TYR
1	H	83	VAL
1	H	188	ASP
1	H	193	LEU
1	H	195	LYS
1	H	220	TRP
1	H	226	LEU
1	H	228	THR
1	H	245	CYS
1	H	246	ASP
1	H	249	SER
1	H	250	SER
1	H	272	ILE
1	H	283	ASP
1	H	287	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	HIS
1	A	189	ASN
1	A	304	ASN
2	B	541	GLN
2	C	293	GLN
2	C	541	GLN
1	D	47	GLN
1	D	189	ASN
1	E	17	HIS
1	E	189	ASN
2	G	498	ASN
2	G	541	GLN
1	H	47	GLN
1	H	189	ASN
1	H	206	GLN
1	H	284	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	283/316 (89%)	-0.00	10 (3%) 44 27	78, 133, 192, 202	0
1	D	281/316 (88%)	0.54	34 (12%) 4 2	117, 186, 202, 202	0
1	E	283/316 (89%)	-0.04	7 (2%) 57 42	69, 127, 193, 202	0
1	H	281/316 (88%)	0.51	32 (11%) 5 3	121, 186, 202, 202	0
2	B	423/442 (95%)	-0.19	10 (2%) 59 43	74, 141, 196, 202	4 (0%)
2	C	420/442 (95%)	-0.19	11 (2%) 56 40	83, 154, 199, 202	4 (0%)
2	F	423/442 (95%)	-0.20	11 (2%) 56 40	34, 145, 194, 202	4 (0%)
2	G	420/442 (95%)	-0.16	17 (4%) 38 23	99, 161, 202, 202	4 (0%)
All	All	2814/3032 (92%)	-0.01	132 (4%) 31 17	34, 155, 202, 202	16 (0%)

All (132) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	234	CYS	6.0
1	H	234	CYS	6.0
2	F	394	ILE	6.0
1	H	233	SER	5.5
1	H	239	ARG	5.5
1	H	282	GLY	5.3
2	B	132	ILE	5.3
1	A	57	GLU	5.2
1	D	239	ARG	4.9
1	D	146	ASN	4.9
2	C	394	ILE	4.6
2	G	130	ASP	4.4
1	A	283	ASP	4.4
2	F	349	SER	4.1
1	H	248	ALA	4.1
2	G	132	ILE	4.0

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Mol	Chain	Res	Type	RSRZ
2	F	130	ASP	4.0
1	H	247	ASP	3.9
2	G	133	ASP	3.9
1	D	233	SER	3.8
1	D	249	SER	3.8
2	C	132	ILE	3.7
2	B	346	GLY	3.7
1	D	150	THR	3.6
2	B	130	ASP	3.6
2	G	395	ASP	3.6
2	G	367	GLU	3.5
2	B	348	CYS	3.5
2	F	348	CYS	3.4
2	C	350	ILE	3.4
1	H	294	ASP	3.4
2	F	395	ASP	3.4
1	D	250	SER	3.3
1	E	15	MET	3.3
1	H	249	SER	3.3
1	D	294	ASP	3.3
1	H	81	ARG	3.3
2	C	395	ASP	3.2
2	B	520	ALA	3.2
1	H	177	ASN	3.2
2	B	394	ILE	3.2
1	D	164	PRO	3.2
2	G	131	GLU	3.2
2	G	552	LEU	3.2
1	H	295	GLY	3.1
1	A	164	PRO	3.1
1	D	302	ASP	3.1
1	D	151	ILE	3.0
1	H	179	ILE	3.0
1	H	122	CYS	3.0
1	H	57	GLU	2.9
2	G	225	GLU	2.9
1	H	82	LYS	2.9
1	H	217	ASP	2.9
2	F	520	ALA	2.9
1	A	234	CYS	2.9
1	H	199	ASP	2.9
2	B	131	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	217	ASP	2.8
1	D	284	ASN	2.8
1	H	147	ASN	2.8
1	H	263	ASP	2.8
2	B	521	SER	2.8
2	B	347	GLY	2.8
1	H	178	TYR	2.8
2	G	341	GLN	2.8
1	H	235	SER	2.8
1	D	262	ASN	2.7
1	H	173	GLY	2.7
1	D	190	LEU	2.7
1	D	207	LYS	2.7
2	C	130	ASP	2.7
2	C	133	ASP	2.7
1	D	173	GLY	2.6
1	H	146	ASN	2.6
2	G	203	LYS	2.6
2	G	226	LYS	2.6
1	A	173	GLY	2.6
1	D	138	GLY	2.6
1	E	14	ASP	2.6
1	A	282	GLY	2.6
1	H	30	THR	2.6
1	H	103	ASP	2.6
2	C	397	TYR	2.5
2	G	164	ILE	2.5
2	F	521	SER	2.5
1	E	262	ASN	2.5
1	D	212	SER	2.5
1	D	293	VAL	2.5
1	D	176	PRO	2.5
1	D	174	GLN	2.4
1	H	198	GLU	2.4
1	H	76	SER	2.4
2	B	495	CYS	2.4
1	A	136	GLY	2.4
2	G	394	ILE	2.4
1	D	247	ASP	2.3
1	H	281	GLY	2.3
1	D	76	SER	2.3
2	F	523	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
2	G	414	TYR	2.3
1	D	137	GLU	2.3
1	A	247	ASP	2.3
2	C	245	SER	2.2
2	F	131	GLU	2.2
1	E	234	CYS	2.2
1	H	163	VAL	2.2
1	D	248	ALA	2.2
2	G	346	GLY	2.2
2	G	348	CYS	2.2
2	C	131	GLU	2.2
1	D	94	GLU	2.2
2	G	327	SER	2.2
2	C	367	GLU	2.2
2	F	132	ILE	2.2
1	E	283	ASP	2.1
2	F	524	ASP	2.1
1	D	122	CYS	2.1
1	H	174	GLN	2.1
1	D	197	GLU	2.1
1	E	282	GLY	2.1
1	H	153	CYS	2.1
1	D	163	VAL	2.1
1	D	14	ASP	2.0
1	D	139	GLN	2.0
1	D	15	MET	2.0
1	A	14	ASP	2.0
1	A	233	SER	2.0
1	D	282	GLY	2.0
1	E	164	PRO	2.0
1	H	262	ASN	2.0
2	C	155	THR	2.0

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

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.