Full wwPDB EM Validation Report (i)

Feb 12, 2024 – 07:37 PM EST

PDB ID	:	3J7V
EMDB ID	:	EMD-6034
Title	:	Capsid Expansion Mechanism Of Bacteriophage T7 Revealed By Multi-State Atomic Models Derived From Cryo-EM Reconstructions
Authors	:	Guo, F.; Liu, Z.; Fang, P.A.; Zhang, Q.; Wright, E.T.; Wu, W.; Zhang, C.; Vago, F.; Ren, Y.; Jakata, J.; Chiu, W.; Serwer, P.; Jiang, W.
Deposited on	:	2014-08-12
Resolution	:	4.60 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

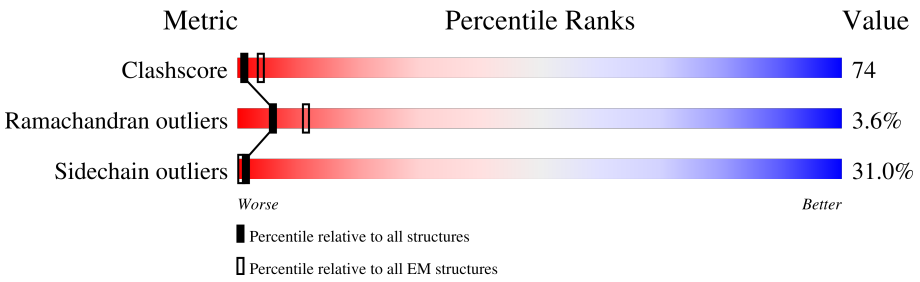
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.60 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)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	345	12% 30% 42% 13% • 13%
1	B	345	18% 29% 40% 19% • 10%
1	C	345	8% 23% 40% 21% • 14%
1	D	345	9% 31% 37% 17% • 14%
1	E	345	12% 28% 39% 16% • 15%
1	F	345	9% 32% 39% 14% • 13%
1	G	345	38% 31% 43% 17% • 8%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 15873 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Major capsid protein 10A.

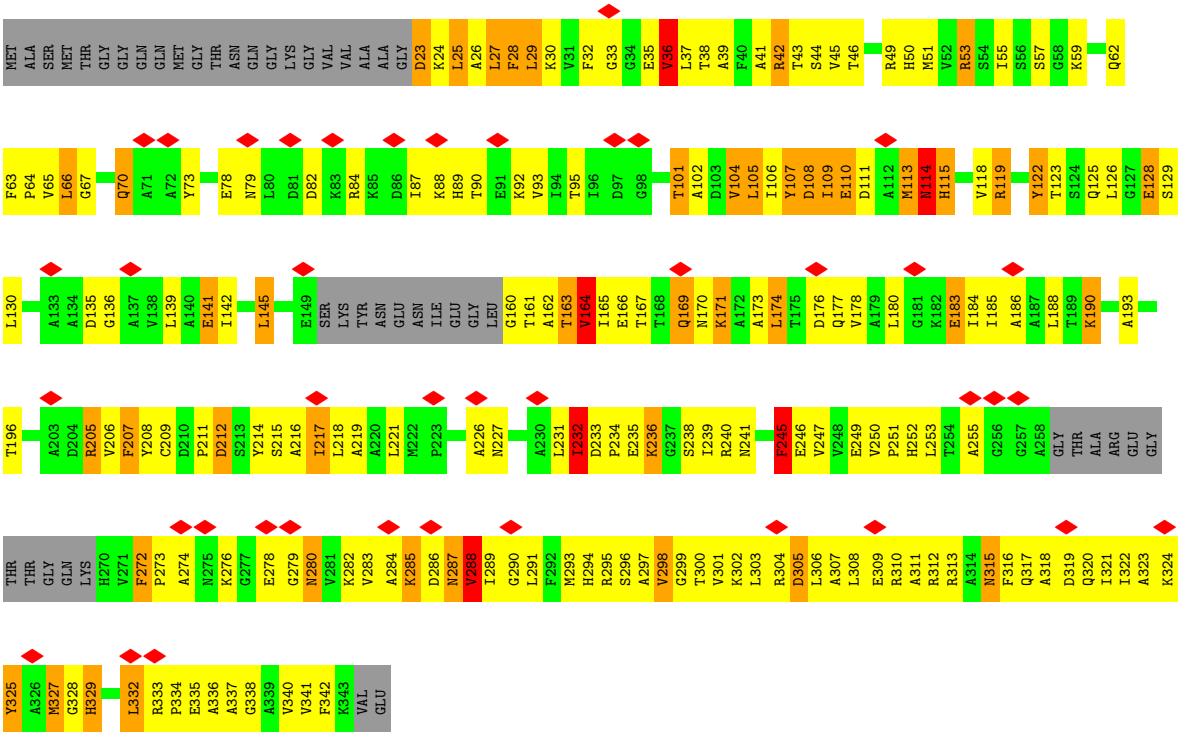
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	300	2250	1418	396	427	9	0	0
1	B	309	2321	1462	406	444	9	0	0
1	C	296	2234	1411	393	421	9	0	0
1	D	298	2241	1413	394	425	9	0	0
1	E	293	2208	1393	387	419	9	0	0
1	F	299	2245	1415	395	426	9	0	0
1	G	317	2374	1492	419	454	9	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

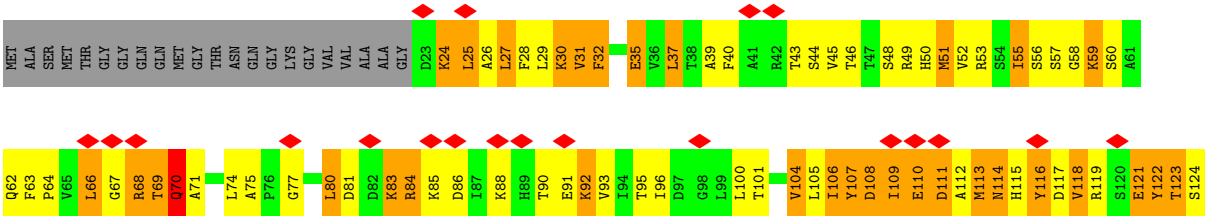
• Molecule 1: Major capsid protein 10A

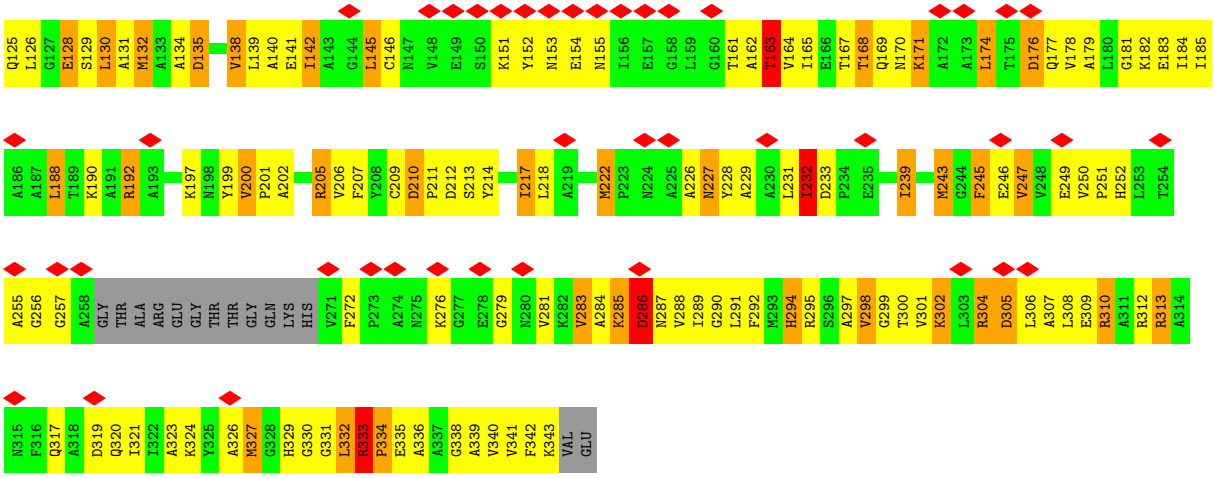
Chain A: 12% 30% 42% 13% • 13%



• Molecule 1: Major capsid protein 10A

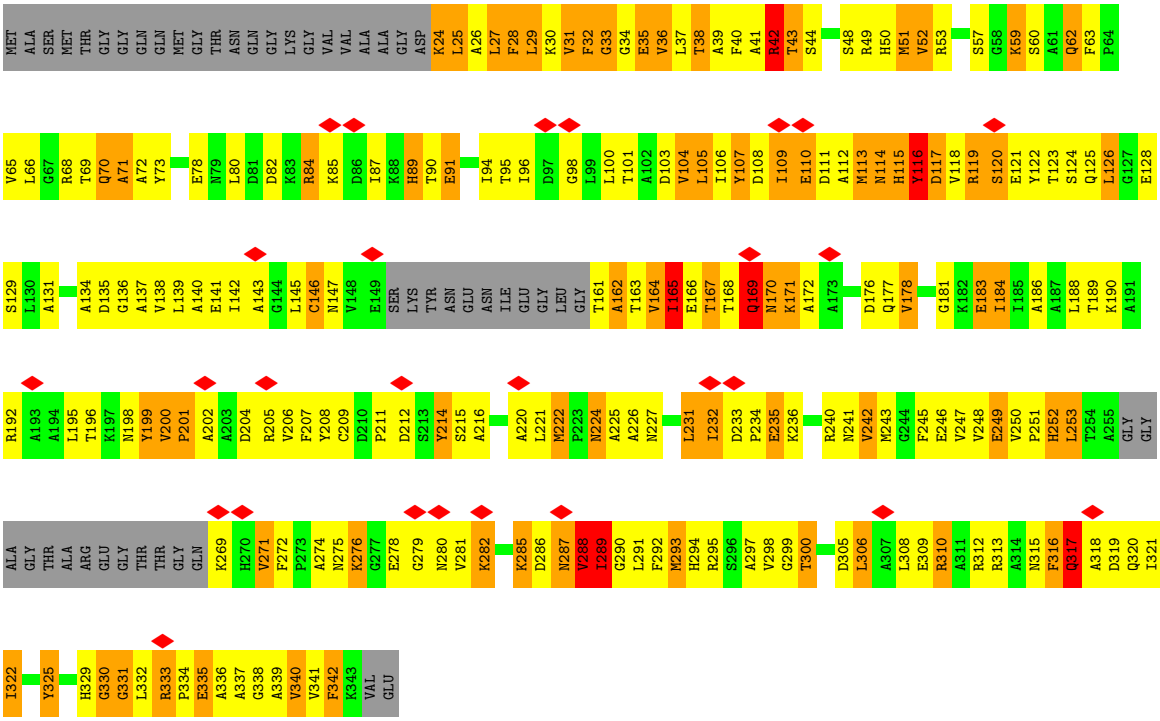
Chain B: 18% 29% 40% 19% • 10%





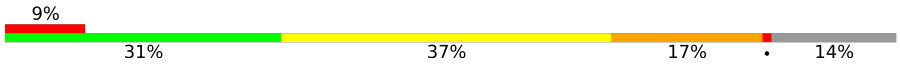
- Molecule 1: Major capsid protein 10A

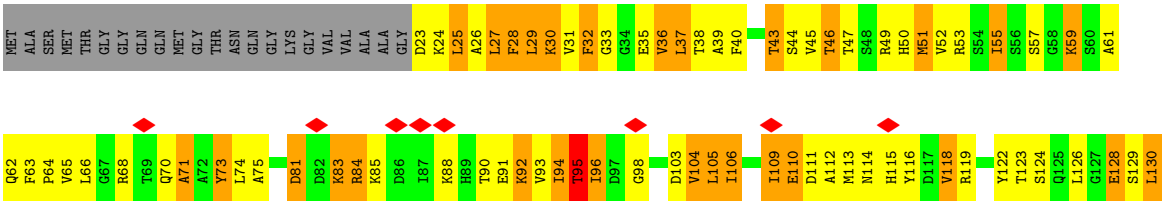
Chain C:

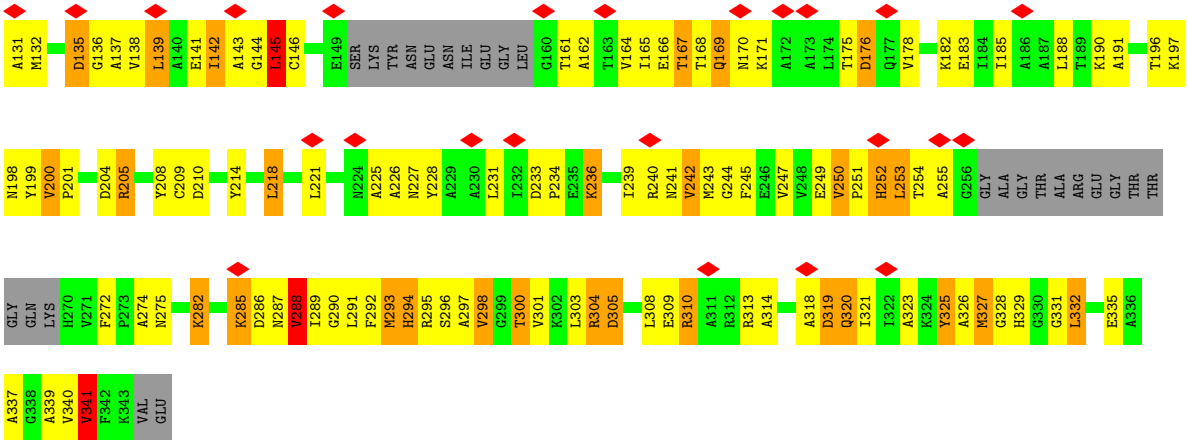


- Molecule 1: Major capsid protein 10A

Chain D:

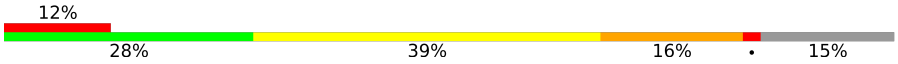


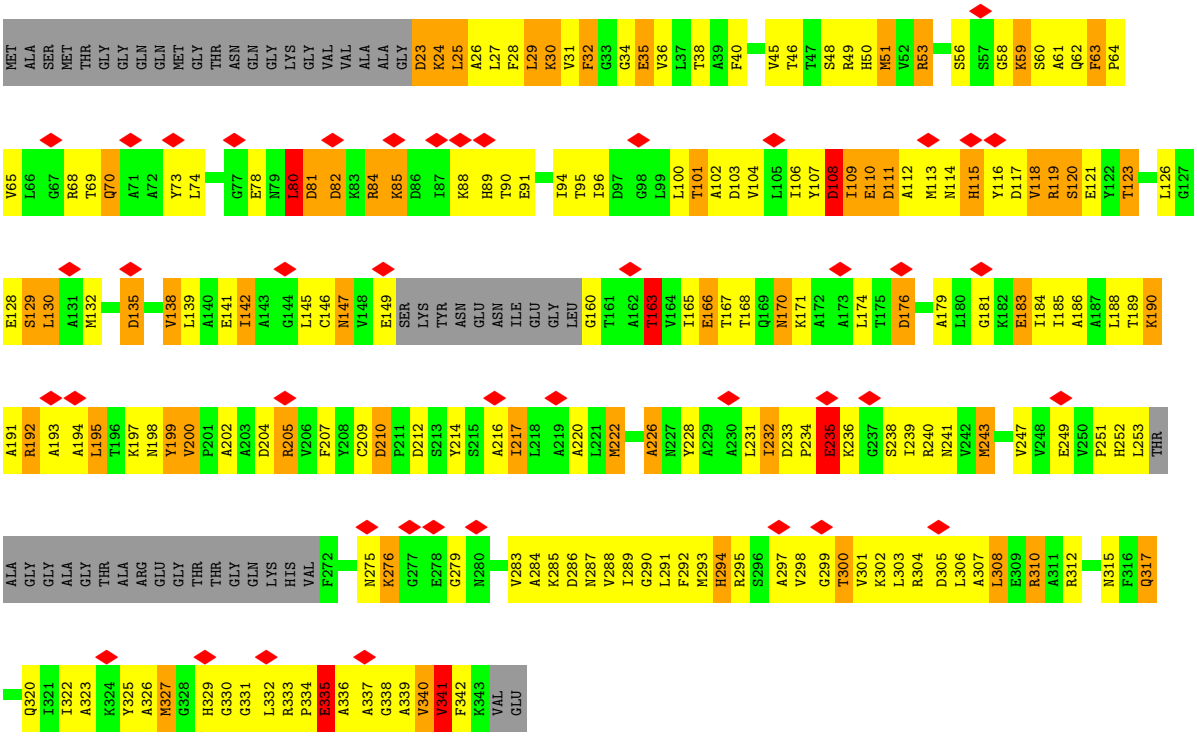




• Molecule 1: Major capsid protein 10A

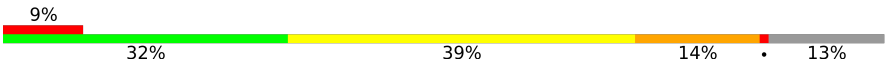
Chain E:

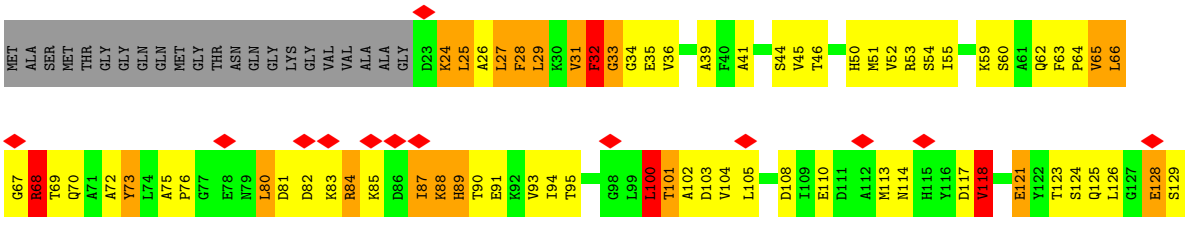


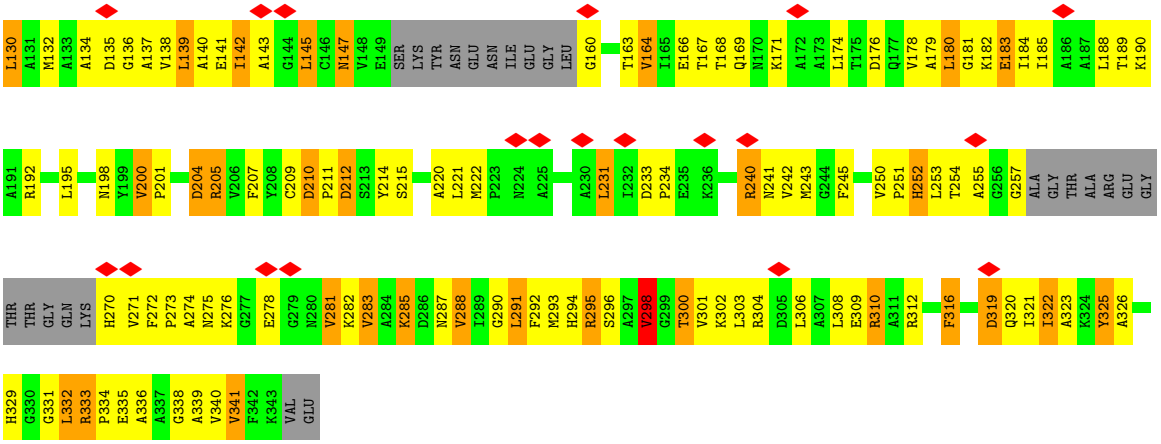


• Molecule 1: Major capsid protein 10A

Chain F:

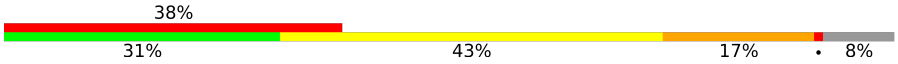


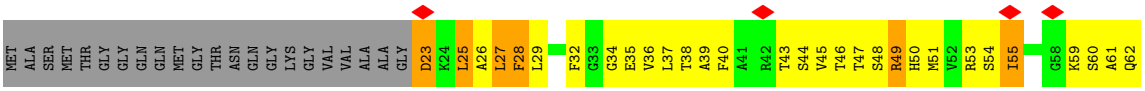


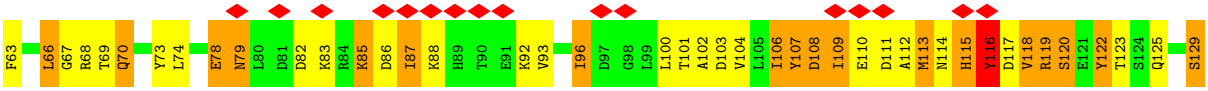


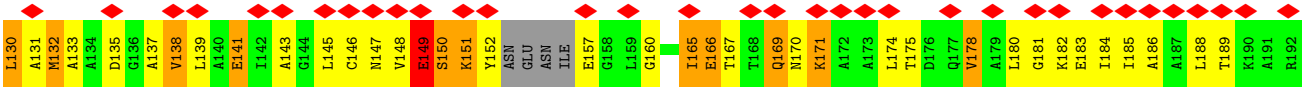
- Molecule 1: Major capsid protein 10A

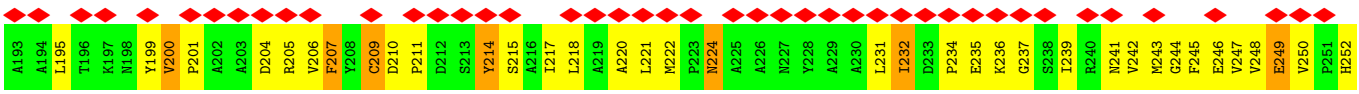
Chain G:

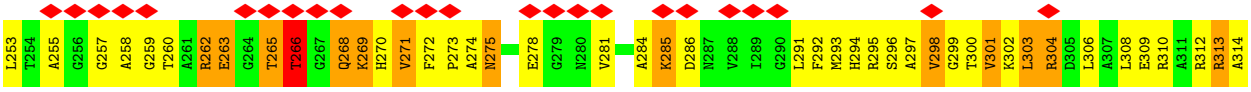


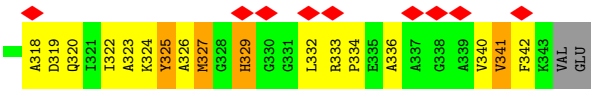












4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	27520	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	25	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	57727	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	25.766	Depositor
Minimum map value	-13.498	Depositor
Average map value	0.111	Depositor
Map value standard deviation	1.331	Depositor
Recommended contour level	4.55	Depositor
Map size (Å)	792.0, 792.0, 792.0	wwPDB
Map dimensions	720, 720, 720	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	A	0.35	0/2282	0.69	1/3087 (0.0%)
1	B	0.40	0/2354	0.82	3/3185 (0.1%)
1	C	0.45	0/2266	0.82	2/3065 (0.1%)
1	D	0.38	0/2273	0.74	2/3075 (0.1%)
1	E	0.38	0/2239	0.70	2/3028 (0.1%)
1	F	0.37	0/2277	0.70	2/3080 (0.1%)
1	G	0.30	0/2408	0.65	1/3256 (0.0%)
All	All	0.38	0/16099	0.73	13/21776 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
1	B	0	3
1	C	0	6
1	D	0	5
1	E	0	7
1	F	0	3
1	G	0	1
All	All	0	30

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	333	ARG	C-N-CD	-20.55	75.40	120.60
1	B	70	GLN	CB-CA-C	-7.36	95.67	110.40
1	C	200	VAL	C-N-CD	6.03	141.06	128.40
1	E	80	LEU	CA-CB-CG	5.80	128.65	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	331	GLY	N-CA-C	5.50	126.84	113.10
1	B	70	GLN	C-N-CA	5.49	135.41	121.70
1	F	69	THR	N-CA-C	-5.43	96.33	111.00
1	G	23	ASP	CB-CG-OD2	5.24	123.02	118.30
1	D	23	ASP	CB-CG-OD2	5.21	122.99	118.30
1	E	23	ASP	CB-CG-OD2	5.17	122.96	118.30
1	A	305	ASP	CB-CG-OD2	5.16	122.94	118.30
1	D	288	VAL	CB-CA-C	-5.09	101.73	111.40
1	F	100	LEU	CA-CB-CG	5.02	126.84	115.30

There are no chirality outliers.

All (30) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	108	ASP	Peptide
1	A	114	ASN	Peptide
1	A	316	PHE	Peptide
1	A	329	HIS	Peptide
1	A	332	LEU	Peptide
1	B	106	ILE	Peptide
1	B	163	THR	Peptide
1	B	70	GLN	Peptide
1	C	164	VAL	Peptide
1	C	233	ASP	Peptide
1	C	287	ASN	Peptide
1	C	317	GLN	Peptide
1	C	330	GLY	Peptide
1	C	71	ALA	Peptide
1	D	250	VAL	Peptide
1	D	292	PHE	Peptide
1	D	331	GLY	Peptide
1	D	95	THR	Peptide
1	D	98	GLY	Peptide
1	E	107	TYR	Peptide
1	E	108	ASP	Peptide
1	E	146	CYS	Peptide
1	E	163	THR	Peptide
1	E	231	LEU	Peptide
1	E	232	ILE	Peptide
1	E	317	GLN	Peptide
1	F	316	PHE	Peptide
1	F	66	LEU	Peptide

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Mol	Chain	Res	Type	Group
1	F	68	ARG	Peptide
1	G	292	PHE	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2250	0	2279	343	0
1	B	2321	0	2348	415	0
1	C	2234	0	2271	465	0
1	D	2241	0	2272	281	0
1	E	2208	0	2240	372	0
1	F	2245	0	2275	229	0
1	G	2374	0	2403	333	0
All	All	15873	0	16088	2351	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 74.

All (2351) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:28:PHE:CE1	1:B:112:ALA:HA	1.24	1.71
1:B:251:PRO:HB2	1:C:199:TYR:CZ	1.09	1.60
1:E:298:VAL:C	1:E:333:ARG:HH12	1.06	1.57
1:E:25:LEU:HD21	1:E:310:ARG:CZ	1.08	1.55
1:E:189:THR:HG22	1:E:243:MET:SD	1.45	1.55
1:A:207:PHE:CZ	1:A:209:CYS:HB2	1.36	1.54
1:A:309:GLU:CB	1:A:322:ILE:HG13	1.38	1.53
1:D:142:ILE:CA	1:D:145:LEU:HD23	1.31	1.53
1:B:251:PRO:CB	1:C:199:TYR:CE1	1.93	1.52
1:B:251:PRO:CG	1:C:199:TYR:CE1	1.92	1.52
1:E:25:LEU:CD2	1:E:310:ARG:NH2	1.70	1.51
1:B:28:PHE:CZ	1:B:112:ALA:HA	1.44	1.51
1:E:25:LEU:CD2	1:E:310:ARG:CZ	1.89	1.50
1:B:251:PRO:CB	1:C:199:TYR:CZ	1.93	1.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:142:ILE:HA	1:D:145:LEU:CD2	1.40	1.49
1:E:189:THR:CG2	1:E:243:MET:CE	1.91	1.49
1:G:110:GLU:HA	1:G:114:ASN:CG	1.35	1.48
1:E:189:THR:CG2	1:E:243:MET:SD	2.04	1.45
1:C:195:LEU:CD2	1:C:205:ARG:NH2	1.78	1.44
1:B:141:GLU:OE1	1:B:330:GLY:CA	1.65	1.43
1:E:145:LEU:CB	1:E:332:LEU:HD23	1.45	1.43
1:C:161:THR:OG1	1:C:336:ALA:CB	1.64	1.42
1:D:138:VAL:HG23	1:D:139:LEU:CD1	1.51	1.40
1:E:25:LEU:HD21	1:E:310:ARG:NH2	1.10	1.38
1:E:192:ARG:HA	1:E:195:LEU:CD1	1.53	1.38
1:D:130:LEU:HD12	1:D:131:ALA:N	1.38	1.36
1:B:145:LEU:HD21	1:B:332:LEU:CD1	1.53	1.36
1:C:195:LEU:CD2	1:C:202:ALA:HB1	1.54	1.36
1:F:25:LEU:HA	1:F:28:PHE:CD2	1.61	1.36
1:B:145:LEU:CD2	1:B:332:LEU:HG	1.55	1.35
1:E:192:ARG:CA	1:E:195:LEU:HD11	1.53	1.35
1:D:29:LEU:HD13	1:D:30:LYS:N	1.36	1.34
1:C:25:LEU:HD23	1:C:26:ALA:N	1.41	1.33
1:A:289:ILE:HG13	1:A:340:VAL:CG2	1.57	1.33
1:B:109:ILE:HD13	1:B:110:GLU:N	1.37	1.33
1:E:25:LEU:CG	1:E:310:ARG:NH2	1.89	1.33
1:B:40:PHE:HE1	1:B:130:LEU:CD1	1.11	1.33
1:B:40:PHE:CE1	1:B:130:LEU:HD11	1.41	1.33
1:A:27:LEU:HD12	1:A:28:PHE:N	1.41	1.32
1:B:113:MET:HA	1:B:115:HIS:NE2	1.42	1.32
1:A:309:GLU:CB	1:A:322:ILE:CG1	2.07	1.31
1:E:145:LEU:HD22	1:E:332:LEU:CD2	1.58	1.31
1:E:40:PHE:HA	1:E:130:LEU:CD2	1.35	1.31
1:E:181:GLY:O	1:E:185:ILE:CD1	1.75	1.31
1:B:28:PHE:CE1	1:B:112:ALA:CA	2.14	1.30
1:E:25:LEU:CD2	1:E:310:ARG:NH1	1.91	1.29
1:C:195:LEU:HD23	1:C:205:ARG:CZ	1.60	1.29
1:A:309:GLU:CA	1:A:322:ILE:HG13	1.59	1.29
1:A:119:ARG:HH11	1:A:119:ARG:CB	1.46	1.28
1:B:251:PRO:HG3	1:C:199:TYR:CE1	1.59	1.28
1:C:188:LEU:HD22	1:C:207:PHE:CE1	1.69	1.28
1:G:149:GLU:CG	1:G:150:SER:H	1.45	1.27
1:C:26:ALA:CA	1:C:29:LEU:HD13	1.62	1.27
1:C:195:LEU:HD21	1:C:202:ALA:CB	1.63	1.27
1:C:206:VAL:HA	1:C:246:GLU:O	1.20	1.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:106:ILE:C	1:G:106:ILE:HD13	1.54	1.27
1:E:189:THR:HG22	1:E:243:MET:CE	1.54	1.26
1:A:26:ALA:O	1:A:29:LEU:HD12	1.36	1.26
1:E:145:LEU:HD22	1:E:332:LEU:CG	1.66	1.26
1:E:145:LEU:HB2	1:E:332:LEU:CD2	1.65	1.26
1:A:309:GLU:HB3	1:A:322:ILE:CD1	1.66	1.26
1:A:309:GLU:O	1:A:322:ILE:HG12	1.26	1.26
1:C:26:ALA:HA	1:C:29:LEU:CD1	1.65	1.25
1:C:27:LEU:HD23	1:C:27:LEU:C	1.53	1.25
1:E:25:LEU:HD22	1:E:310:ARG:NH1	1.45	1.25
1:B:113:MET:SD	1:B:115:HIS:CE1	2.30	1.25
1:E:298:VAL:C	1:E:333:ARG:NH1	1.86	1.25
1:D:36:VAL:O	1:D:39:ALA:N	1.69	1.25
1:A:289:ILE:CG1	1:A:340:VAL:HG22	1.64	1.24
1:E:181:GLY:O	1:E:185:ILE:HD12	1.10	1.24
1:C:109:ILE:HD13	1:C:109:ILE:C	1.54	1.24
1:A:207:PHE:CZ	1:A:209:CYS:CB	2.21	1.23
1:B:130:LEU:C	1:B:130:LEU:HD12	1.53	1.23
1:G:25:LEU:O	1:G:29:LEU:HG	1.39	1.23
1:C:195:LEU:HD23	1:C:205:ARG:NH2	0.90	1.23
1:C:207:PHE:CD2	1:C:247:VAL:HG22	1.72	1.23
1:G:110:GLU:HA	1:G:114:ASN:CB	1.68	1.23
1:D:144:GLY:O	1:D:146:CYS:N	1.69	1.22
1:B:139:LEU:O	1:B:142:ILE:HG23	1.34	1.22
1:D:142:ILE:O	1:D:145:LEU:HB2	1.36	1.22
1:G:146:CYS:CB	1:G:336:ALA:HB3	1.69	1.22
1:B:31:VAL:CG1	1:B:35:GLU:OE2	1.87	1.21
1:B:145:LEU:CD2	1:B:332:LEU:CD1	2.17	1.21
1:E:40:PHE:CA	1:E:130:LEU:HD22	1.52	1.21
1:E:142:ILE:C	1:E:142:ILE:HD12	1.59	1.21
1:C:116:TYR:O	1:C:118:VAL:N	1.73	1.21
1:E:142:ILE:HD12	1:E:142:ILE:O	1.37	1.21
1:G:25:LEU:HA	1:G:28:PHE:CD2	1.77	1.20
1:A:27:LEU:HD12	1:A:27:LEU:C	1.58	1.20
1:A:309:GLU:O	1:A:322:ILE:CG1	1.90	1.20
1:G:109:ILE:H	1:G:109:ILE:CD1	1.51	1.20
1:G:130:LEU:C	1:G:130:LEU:HD23	1.59	1.20
1:B:145:LEU:CD2	1:B:332:LEU:CG	2.19	1.19
1:G:110:GLU:OE2	1:G:118:VAL:CG1	1.90	1.19
1:B:132:MET:HE2	1:B:132:MET:HA	1.21	1.19
1:B:40:PHE:CE1	1:B:130:LEU:CD1	1.86	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:113:MET:HA	1:B:115:HIS:CD2	1.78	1.19
1:G:113:MET:CA	1:G:113:MET:HE3	1.72	1.19
1:A:119:ARG:HH11	1:A:119:ARG:HB2	1.07	1.18
1:A:114:ASN:N	1:A:115:HIS:CD2	2.09	1.18
1:C:25:LEU:CD2	1:C:26:ALA:H	1.58	1.17
1:B:132:MET:HA	1:B:132:MET:CE	1.64	1.17
1:D:46:THR:HG23	1:D:135:ASP:OD1	1.41	1.17
1:E:25:LEU:C	1:E:25:LEU:HD12	1.54	1.17
1:A:25:LEU:O	1:A:25:LEU:HD13	1.39	1.16
1:E:145:LEU:CD2	1:E:332:LEU:CD2	2.24	1.16
1:F:25:LEU:HA	1:F:28:PHE:CE2	1.80	1.16
1:G:28:PHE:CE1	1:G:111:ASP:OD2	1.99	1.16
1:G:106:ILE:HD13	1:G:107:TYR:N	1.59	1.16
1:G:110:GLU:O	1:G:114:ASN:HB3	1.41	1.16
1:A:289:ILE:HG12	1:A:340:VAL:O	1.42	1.16
1:A:309:GLU:CB	1:A:322:ILE:CD1	2.23	1.16
1:A:309:GLU:O	1:A:322:ILE:N	1.78	1.16
1:E:63:PHE:CE2	1:E:333:ARG:NH2	2.13	1.16
1:B:24:LYS:HD2	1:B:24:LYS:C	1.64	1.15
1:C:26:ALA:C	1:C:29:LEU:HD13	1.65	1.15
1:A:294:HIS:CD2	1:A:337:ALA:HA	1.81	1.15
1:B:138:VAL:O	1:B:142:ILE:HG22	1.43	1.15
1:C:26:ALA:HA	1:C:29:LEU:HD13	1.15	1.15
1:E:24:LYS:HZ1	1:E:112:ALA:HB1	1.01	1.15
1:E:40:PHE:CA	1:E:130:LEU:CD2	2.03	1.15
1:A:109:ILE:HD13	1:A:109:ILE:N	1.55	1.14
1:D:130:LEU:HD12	1:D:130:LEU:C	1.60	1.14
1:C:25:LEU:HD22	1:C:25:LEU:N	1.58	1.14
1:C:116:TYR:CD2	1:C:117:ASP:N	2.15	1.14
1:E:298:VAL:CA	1:E:333:ARG:HH12	1.59	1.14
1:F:25:LEU:CA	1:F:28:PHE:CE2	2.30	1.14
1:A:309:GLU:HB2	1:A:322:ILE:CG1	1.72	1.14
1:E:25:LEU:CD1	1:E:310:ARG:NH2	2.10	1.14
1:G:270:HIS:O	1:G:272:PHE:N	1.78	1.14
1:E:119:ARG:HH11	1:E:119:ARG:HG2	1.03	1.14
1:E:145:LEU:HD22	1:E:332:LEU:HG	1.30	1.14
1:A:110:GLU:OE1	1:A:118:VAL:HG11	1.46	1.14
1:B:251:PRO:HB2	1:C:199:TYR:CE2	1.83	1.14
1:F:29:LEU:O	1:F:29:LEU:HD23	1.45	1.13
1:A:119:ARG:O	1:A:123:THR:HG23	1.46	1.13
1:E:40:PHE:CZ	1:E:130:LEU:CD1	2.24	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:128:GLU:OE2	1:F:201:PRO:HG3	1.45	1.13
1:F:27:LEU:O	1:F:27:LEU:HD13	1.45	1.13
1:B:334:PRO:HA	1:B:335:GLU:HB2	1.23	1.13
1:C:205:ARG:O	1:C:246:GLU:HB3	1.49	1.12
1:A:308:LEU:HA	1:A:323:ALA:HA	1.15	1.12
1:D:27:LEU:HD12	1:D:27:LEU:C	1.69	1.12
1:E:109:ILE:N	1:E:109:ILE:HD12	1.55	1.12
1:F:25:LEU:HD12	1:F:26:ALA:H	1.00	1.12
1:G:110:GLU:HA	1:G:114:ASN:ND2	1.62	1.12
1:E:119:ARG:HH11	1:E:119:ARG:CG	1.63	1.12
1:A:309:GLU:HB2	1:A:322:ILE:HG13	1.16	1.12
1:C:207:PHE:CZ	1:C:245:PHE:CD2	2.37	1.12
1:E:189:THR:HG21	1:E:243:MET:CE	1.67	1.12
1:G:257:GLY:HA3	1:G:268:GLN:OE1	1.47	1.12
1:B:113:MET:SD	1:B:115:HIS:NE2	2.22	1.11
1:C:208:TYR:HB2	1:C:291:LEU:HG	1.31	1.11
1:D:25:LEU:C	1:D:25:LEU:HD12	1.70	1.11
1:B:141:GLU:OE1	1:B:330:GLY:HA2	0.95	1.10
1:A:205:ARG:NH1	1:A:293:MET:SD	2.24	1.10
1:C:161:THR:OG1	1:C:336:ALA:HB2	1.38	1.10
1:G:25:LEU:N	1:G:25:LEU:HD23	1.56	1.10
1:C:208:TYR:HB3	1:C:291:LEU:HD11	1.27	1.10
1:G:113:MET:CA	1:G:113:MET:CE	2.30	1.10
1:G:132:MET:SD	1:G:132:MET:C	2.30	1.10
1:B:132:MET:CE	1:B:132:MET:CA	2.30	1.10
1:C:204:ASP:O	1:C:205:ARG:HG3	1.50	1.10
1:C:206:VAL:HG21	1:C:248:VAL:HG23	1.28	1.10
1:D:110:GLU:HB2	1:D:114:ASN:HB2	1.25	1.10
1:D:138:VAL:HG23	1:D:139:LEU:HD13	1.20	1.10
1:E:110:GLU:CG	1:E:118:VAL:HG21	1.78	1.10
1:B:132:MET:HA	1:B:135:ASP:OD2	1.52	1.09
1:C:201:PRO:HA	1:C:202:ALA:HB3	1.34	1.09
1:E:145:LEU:CD2	1:E:332:LEU:HD21	1.82	1.09
1:G:109:ILE:HD13	1:G:109:ILE:N	1.54	1.09
1:A:302:LYS:HE2	1:A:327:MET:HG2	1.34	1.09
1:E:109:ILE:H	1:E:109:ILE:CD1	1.51	1.09
1:C:33:GLY:HA2	1:C:36:VAL:CG2	1.82	1.09
1:E:110:GLU:HG3	1:E:118:VAL:CG1	1.83	1.09
1:B:251:PRO:HB2	1:C:199:TYR:CE1	1.72	1.08
1:C:207:PHE:HD2	1:C:247:VAL:CG2	1.65	1.08
1:E:110:GLU:HG2	1:E:118:VAL:HG21	1.34	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:145:LEU:CB	1:E:332:LEU:CD2	2.28	1.08
1:G:110:GLU:CD	1:G:118:VAL:HB	1.74	1.08
1:G:115:HIS:CD2	1:G:119:ARG:HH22	1.70	1.08
1:A:287:ASN:HD22	1:A:288:VAL:N	1.50	1.08
1:A:309:GLU:HB3	1:A:322:ILE:HD11	1.20	1.08
1:B:29:LEU:HD11	1:B:310:ARG:HD3	1.09	1.08
1:E:25:LEU:HD11	1:E:310:ARG:NH2	1.64	1.08
1:A:208:TYR:HE2	1:A:293:MET:HE3	1.17	1.08
1:C:27:LEU:HD23	1:C:28:PHE:N	1.66	1.08
1:D:142:ILE:HD13	1:D:145:LEU:CD2	1.82	1.08
1:B:128:GLU:OE1	1:C:68:ARG:HD3	1.54	1.08
1:C:119:ARG:HG3	1:C:119:ARG:HH11	1.19	1.08
1:B:114:ASN:OD1	1:C:53:ARG:NH2	1.86	1.07
1:C:29:LEU:H	1:C:29:LEU:HD12	0.96	1.07
1:A:55:ILE:CG2	1:A:301:VAL:HG23	1.83	1.07
1:A:109:ILE:HD13	1:A:109:ILE:H	1.09	1.07
1:B:114:ASN:H	1:B:115:HIS:CD2	1.72	1.07
1:G:34:GLY:O	1:G:38:THR:HG23	1.51	1.07
1:G:113:MET:CE	1:G:113:MET:HA	1.81	1.07
1:G:113:MET:HE3	1:G:113:MET:HA	1.09	1.07
1:B:28:PHE:CZ	1:B:112:ALA:CA	2.31	1.06
1:B:114:ASN:N	1:B:115:HIS:HD2	1.54	1.06
1:A:287:ASN:ND2	1:A:288:VAL:H	1.51	1.06
1:B:31:VAL:HG13	1:B:35:GLU:OE2	1.54	1.06
1:B:145:LEU:HD22	1:B:332:LEU:CG	1.82	1.06
1:C:110:GLU:OE2	1:C:118:VAL:HG21	1.52	1.06
1:E:303:LEU:HB2	1:E:327:MET:HG2	1.32	1.06
1:A:302:LYS:HG2	1:A:327:MET:CB	1.84	1.05
1:B:130:LEU:HD12	1:B:130:LEU:O	1.54	1.05
1:G:25:LEU:HD23	1:G:25:LEU:H	0.90	1.05
1:G:119:ARG:HH11	1:G:119:ARG:CG	1.69	1.05
1:B:24:LYS:NZ	1:B:24:LYS:HB3	1.69	1.05
1:G:132:MET:HE3	1:G:252:HIS:NE2	1.71	1.05
1:B:29:LEU:CD1	1:B:310:ARG:HD3	1.85	1.05
1:C:161:THR:OG1	1:C:336:ALA:HB1	1.30	1.05
1:G:132:MET:SD	1:G:133:ALA:N	2.30	1.05
1:G:149:GLU:HG2	1:G:150:SER:N	1.70	1.05
1:C:28:PHE:C	1:C:28:PHE:CD2	2.30	1.04
1:G:25:LEU:HA	1:G:28:PHE:CE2	1.92	1.04
1:G:113:MET:HE1	1:G:115:HIS:HB2	1.36	1.04
1:C:33:GLY:CA	1:C:36:VAL:HG23	1.88	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:146:CYS:SG	1:G:336:ALA:N	2.30	1.04
1:A:208:TYR:CE2	1:A:293:MET:HE3	1.92	1.04
1:B:35:GLU:HB2	1:B:123:THR:HG23	1.36	1.04
1:E:25:LEU:HD12	1:E:25:LEU:O	1.58	1.04
1:E:298:VAL:CA	1:E:333:ARG:NH1	2.17	1.04
1:G:113:MET:C	1:G:113:MET:HE2	1.78	1.04
1:D:141:GLU:O	1:D:145:LEU:HD22	1.56	1.04
1:B:40:PHE:CE1	1:B:130:LEU:HD13	1.92	1.04
1:B:108:ASP:HA	1:B:111:ASP:OD2	1.57	1.04
1:D:139:LEU:HD13	1:D:139:LEU:N	1.73	1.03
1:B:30:LYS:C	1:B:30:LYS:HD3	1.76	1.03
1:B:132:MET:HE2	1:B:132:MET:CA	1.84	1.03
1:G:146:CYS:CB	1:G:336:ALA:CB	2.35	1.03
1:D:26:ALA:O	1:D:29:LEU:HD12	1.56	1.03
1:D:142:ILE:HD13	1:D:145:LEU:HD21	1.35	1.03
1:E:110:GLU:OE2	1:E:111:ASP:HA	1.56	1.03
1:E:299:GLY:N	1:E:331:GLY:O	1.91	1.03
1:A:36:VAL:O	1:A:39:ALA:N	1.91	1.02
1:A:302:LYS:HG2	1:A:327:MET:HB3	1.39	1.02
1:G:110:GLU:OE2	1:G:118:VAL:HG12	1.59	1.02
1:G:119:ARG:HH11	1:G:119:ARG:HG3	0.86	1.02
1:D:139:LEU:HD13	1:D:139:LEU:H	1.23	1.02
1:A:207:PHE:HE1	1:A:290:GLY:HA3	1.23	1.02
1:C:33:GLY:HA2	1:C:36:VAL:HG23	1.40	1.01
1:A:309:GLU:C	1:A:322:ILE:HG12	1.81	1.01
1:E:189:THR:HG21	1:E:243:MET:HE3	1.02	1.01
1:F:25:LEU:CA	1:F:28:PHE:CD2	2.41	1.01
1:G:141:GLU:N	1:G:270:HIS:ND1	2.06	1.01
1:B:116:TYR:HD1	1:B:116:TYR:H	1.07	1.01
1:F:25:LEU:HD12	1:F:26:ALA:N	1.76	1.01
1:A:309:GLU:C	1:A:322:ILE:CG1	2.27	1.01
1:G:141:GLU:N	1:G:270:HIS:CE1	2.29	1.01
1:E:110:GLU:HG3	1:E:118:VAL:HG11	1.04	1.00
1:G:26:ALA:HA	1:G:29:LEU:HD12	1.37	1.00
1:G:113:MET:CE	1:G:115:HIS:HB2	1.91	1.00
1:B:27:LEU:HD23	1:B:30:LYS:HB3	1.40	1.00
1:G:110:GLU:CA	1:G:114:ASN:CG	2.30	1.00
1:B:141:GLU:CD	1:B:330:GLY:HA2	1.82	1.00
1:D:25:LEU:HD12	1:D:25:LEU:O	1.62	1.00
1:G:149:GLU:HG2	1:G:150:SER:H	0.87	1.00
1:A:27:LEU:C	1:A:27:LEU:CD1	2.30	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:24:LYS:NZ	1:E:112:ALA:HB1	1.76	1.00
1:F:27:LEU:CD1	1:F:27:LEU:C	2.30	1.00
1:A:302:LYS:HG2	1:A:327:MET:CG	1.90	0.99
1:C:26:ALA:O	1:C:29:LEU:HD13	1.60	0.99
1:E:189:THR:HG23	1:E:243:MET:SD	1.96	0.99
1:C:29:LEU:O	1:C:32:PHE:HB3	1.61	0.99
1:E:115:HIS:CE1	1:E:119:ARG:NH2	2.30	0.99
1:G:25:LEU:H	1:G:25:LEU:CD2	1.71	0.99
1:B:141:GLU:OE2	1:B:331:GLY:N	1.94	0.99
1:F:28:PHE:CD1	1:F:29:LEU:N	2.30	0.99
1:G:113:MET:CE	1:G:113:MET:C	2.30	0.99
1:B:116:TYR:HD1	1:B:116:TYR:N	1.60	0.99
1:C:29:LEU:CD1	1:C:29:LEU:H	1.76	0.99
1:D:45:VAL:HG23	1:D:135:ASP:OD2	1.62	0.99
1:D:130:LEU:HD12	1:D:131:ALA:CA	1.93	0.99
1:F:25:LEU:CD1	1:F:26:ALA:H	1.75	0.99
1:G:106:ILE:C	1:G:106:ILE:CD1	2.30	0.99
1:A:25:LEU:HD13	1:A:25:LEU:C	1.84	0.99
1:C:26:ALA:CA	1:C:29:LEU:CD1	2.30	0.99
1:E:25:LEU:C	1:E:25:LEU:CD1	2.30	0.99
1:A:287:ASN:OD1	1:A:341:VAL:HB	1.63	0.98
1:E:115:HIS:CE1	1:E:119:ARG:HH22	1.81	0.98
1:G:130:LEU:C	1:G:130:LEU:CD2	2.30	0.98
1:C:27:LEU:C	1:C:27:LEU:CD2	2.30	0.98
1:F:27:LEU:HD13	1:F:27:LEU:C	1.79	0.98
1:C:28:PHE:HD2	1:C:29:LEU:N	1.61	0.98
1:D:138:VAL:CG2	1:D:139:LEU:CD1	2.41	0.98
1:G:148:VAL:O	1:G:148:VAL:HG23	1.59	0.98
1:B:107:TYR:HD2	1:B:107:TYR:N	1.61	0.98
1:G:147:ASN:ND2	1:G:273:PRO:HG3	1.78	0.98
1:G:149:GLU:OE1	1:G:150:SER:N	1.96	0.98
1:C:113:MET:HE1	1:C:119:ARG:NH2	1.79	0.97
1:E:114:ASN:O	1:E:115:HIS:HB2	1.62	0.97
1:G:27:LEU:C	1:G:27:LEU:HD12	1.84	0.97
1:G:146:CYS:HB2	1:G:336:ALA:CB	1.94	0.97
1:C:207:PHE:HD2	1:C:247:VAL:HG22	0.82	0.97
1:G:146:CYS:SG	1:G:336:ALA:HB3	2.04	0.97
1:C:109:ILE:HD13	1:C:109:ILE:O	1.65	0.97
1:D:32:PHE:CD1	1:D:32:PHE:C	2.37	0.97
1:D:130:LEU:C	1:D:130:LEU:CD1	2.30	0.97
1:D:138:VAL:CG2	1:D:139:LEU:HD13	1.95	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:110:GLU:OE2	1:G:118:VAL:HG11	1.63	0.97
1:B:24:LYS:C	1:B:24:LYS:CD	2.30	0.97
1:B:145:LEU:HD21	1:B:332:LEU:HD12	1.00	0.97
1:C:109:ILE:C	1:C:109:ILE:CD1	2.30	0.97
1:C:28:PHE:C	1:C:28:PHE:HD2	1.67	0.96
1:B:31:VAL:HG12	1:B:35:GLU:OE2	1.65	0.96
1:G:146:CYS:SG	1:G:336:ALA:CB	2.53	0.96
1:B:69:THR:HG22	1:B:70:GLN:H	1.30	0.96
1:C:107:TYR:CD2	1:C:107:TYR:N	2.30	0.96
1:C:119:ARG:HH11	1:C:119:ARG:CG	1.77	0.96
1:B:24:LYS:HD2	1:B:24:LYS:O	1.63	0.96
1:C:207:PHE:HZ	1:C:245:PHE:CD2	1.83	0.96
1:A:55:ILE:CG2	1:A:301:VAL:CG2	2.44	0.96
1:C:117:ASP:OD2	1:D:51:MET:CE	2.13	0.96
1:G:110:GLU:HG2	1:G:118:VAL:HG21	1.43	0.96
1:A:302:LYS:CE	1:A:327:MET:HG2	1.96	0.95
1:B:30:LYS:HE2	1:B:30:LYS:O	1.66	0.95
1:B:35:GLU:HB2	1:B:123:THR:CG2	1.95	0.95
1:B:130:LEU:CD1	1:B:130:LEU:C	2.30	0.95
1:E:189:THR:CG2	1:E:243:MET:HE3	1.67	0.95
1:A:119:ARG:CB	1:A:119:ARG:NH1	2.30	0.95
1:B:24:LYS:CE	1:B:25:LEU:N	2.30	0.95
1:G:110:GLU:CA	1:G:114:ASN:ND2	2.30	0.95
1:C:40:PHE:HE1	1:C:131:ALA:HA	1.32	0.95
1:D:28:PHE:CD2	1:D:29:LEU:N	2.34	0.95
1:D:139:LEU:CD1	1:D:139:LEU:N	2.30	0.95
1:C:29:LEU:HD12	1:C:29:LEU:N	1.78	0.95
1:C:188:LEU:CD2	1:C:207:PHE:CE1	2.49	0.95
1:B:29:LEU:HD11	1:B:310:ARG:CD	1.98	0.94
1:D:29:LEU:CD1	1:D:30:LYS:N	2.30	0.94
1:G:141:GLU:OE1	1:G:141:GLU:HA	1.63	0.94
1:A:109:ILE:N	1:A:109:ILE:CD1	2.30	0.94
1:C:207:PHE:CD2	1:C:247:VAL:CG2	2.45	0.94
1:G:109:ILE:O	1:G:114:ASN:HB2	1.67	0.94
1:A:119:ARG:HB2	1:A:119:ARG:NH1	1.81	0.94
1:B:24:LYS:HB3	1:B:24:LYS:HZ2	1.28	0.94
1:C:195:LEU:HD21	1:C:202:ALA:HB1	0.95	0.94
1:F:29:LEU:C	1:F:29:LEU:CD2	2.33	0.94
1:G:110:GLU:CA	1:G:114:ASN:CB	2.45	0.94
1:G:149:GLU:CG	1:G:150:SER:N	2.17	0.94
1:E:40:PHE:HA	1:E:130:LEU:HD22	1.07	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:130:LEU:CD2	1:G:131:ALA:N	2.30	0.94
1:D:46:THR:CG2	1:D:135:ASP:OD1	2.16	0.94
1:A:205:ARG:HE	1:A:295:ARG:HA	1.31	0.93
1:C:27:LEU:CD2	1:C:28:PHE:N	2.30	0.93
1:G:106:ILE:CD1	1:G:107:TYR:N	2.30	0.93
1:B:24:LYS:NZ	1:B:24:LYS:CB	2.30	0.93
1:B:30:LYS:HD3	1:B:30:LYS:O	1.67	0.93
1:B:114:ASN:H	1:B:115:HIS:HD2	0.97	0.93
1:C:41:ALA:O	1:C:42:ARG:HB2	1.64	0.93
1:B:132:MET:HE2	1:B:135:ASP:OD2	1.67	0.93
1:F:29:LEU:HD23	1:F:29:LEU:C	1.84	0.93
1:A:107:TYR:OH	1:B:90:THR:HG21	1.68	0.93
1:B:28:PHE:HZ	1:B:111:ASP:O	1.50	0.93
1:D:142:ILE:CD1	1:D:145:LEU:CD2	2.46	0.93
1:F:25:LEU:HA	1:F:28:PHE:HD2	1.32	0.93
1:C:25:LEU:CD2	1:C:25:LEU:N	2.30	0.93
1:A:57:SER:H	1:A:303:LEU:HD13	1.30	0.93
1:A:115:HIS:CD2	1:A:115:HIS:H	1.83	0.93
1:B:113:MET:CA	1:B:115:HIS:NE2	2.30	0.93
1:C:25:LEU:HD22	1:C:25:LEU:H	1.16	0.93
1:E:25:LEU:HD22	1:E:310:ARG:HH12	0.99	0.93
1:C:188:LEU:HD22	1:C:207:PHE:CZ	2.03	0.92
1:G:113:MET:HE1	1:G:115:HIS:CB	2.00	0.92
1:E:186:ALA:O	1:E:190:LYS:HD3	1.70	0.92
1:D:252:HIS:HE1	1:E:192:ARG:HH21	1.16	0.92
1:E:63:PHE:HE2	1:E:333:ARG:NH2	1.59	0.92
1:D:40:PHE:CE1	1:D:131:ALA:HA	2.03	0.92
1:G:119:ARG:HG3	1:G:119:ARG:NH1	1.69	0.92
1:A:27:LEU:CD1	1:A:28:PHE:N	2.33	0.92
1:C:162:ALA:HB3	1:C:337:ALA:O	1.70	0.92
1:E:40:PHE:HA	1:E:130:LEU:HD23	1.50	0.92
1:A:119:ARG:HH11	1:A:119:ARG:CG	1.81	0.92
1:G:130:LEU:HD23	1:G:131:ALA:N	1.85	0.92
1:E:24:LYS:HZ1	1:E:112:ALA:CB	1.81	0.92
1:A:302:LYS:HG2	1:A:327:MET:HG2	1.48	0.92
1:D:141:GLU:C	1:D:145:LEU:HD22	1.90	0.92
1:E:145:LEU:CG	1:E:332:LEU:HD23	1.99	0.92
1:B:109:ILE:CD1	1:B:110:GLU:N	2.30	0.91
1:A:207:PHE:HZ	1:A:209:CYS:HB2	1.16	0.91
1:C:113:MET:CE	1:C:119:ARG:CZ	2.48	0.91
1:G:113:MET:HE2	1:G:114:ASN:N	1.83	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:109:ILE:HD12	1:E:109:ILE:H	0.75	0.91
1:C:107:TYR:N	1:C:107:TYR:HD2	1.67	0.91
1:C:208:TYR:HB3	1:C:291:LEU:CD1	2.00	0.91
1:D:135:ASP:O	1:D:139:LEU:HD22	1.70	0.91
1:A:106:ILE:C	1:A:107:TYR:HD2	1.72	0.91
1:D:92:LYS:HD2	1:D:332:LEU:H	1.36	0.91
1:E:28:PHE:CE1	1:E:111:ASP:O	2.24	0.91
1:E:142:ILE:HA	1:E:332:LEU:HD22	1.52	0.91
1:D:33:GLY:O	1:D:36:VAL:HG12	1.70	0.91
1:A:106:ILE:HG22	1:A:122:TYR:CE2	2.06	0.91
1:B:24:LYS:HZ3	1:B:24:LYS:CA	1.83	0.91
1:D:32:PHE:O	1:D:32:PHE:HD1	1.53	0.90
1:D:130:LEU:CD1	1:D:131:ALA:N	2.30	0.90
1:E:299:GLY:CA	1:E:333:ARG:HH22	1.84	0.90
1:A:107:TYR:HD2	1:A:107:TYR:N	1.69	0.90
1:C:117:ASP:OD2	1:D:51:MET:HE3	1.69	0.90
1:C:208:TYR:HB2	1:C:291:LEU:CG	2.01	0.90
1:E:141:GLU:HG3	1:E:330:GLY:C	1.91	0.90
1:G:114:ASN:O	1:G:116:TYR:N	2.04	0.90
1:F:25:LEU:CB	1:F:28:PHE:CE2	2.54	0.90
1:G:110:GLU:CD	1:G:118:VAL:CB	2.40	0.90
1:D:135:ASP:O	1:D:139:LEU:HD13	1.72	0.90
1:E:142:ILE:C	1:E:142:ILE:CD1	2.34	0.90
1:B:251:PRO:HB2	1:C:199:TYR:OH	1.72	0.90
1:B:251:PRO:HG3	1:C:199:TYR:HE1	1.02	0.90
1:C:206:VAL:CG2	1:C:246:GLU:OE1	2.20	0.90
1:B:63:PHE:O	1:B:333:ARG:NH2	2.04	0.90
1:C:206:VAL:CA	1:C:246:GLU:O	2.16	0.90
1:E:303:LEU:CB	1:E:327:MET:HG2	2.02	0.90
1:B:145:LEU:HD22	1:B:332:LEU:HG	0.90	0.90
1:D:110:GLU:CB	1:D:114:ASN:HB2	2.01	0.90
1:D:201:PRO:O	1:D:205:ARG:NH2	2.05	0.90
1:E:192:ARG:O	1:E:195:LEU:HD12	1.72	0.90
1:A:27:LEU:HD12	1:A:28:PHE:CA	2.02	0.89
1:B:28:PHE:HE1	1:B:112:ALA:HA	1.17	0.89
1:C:113:MET:HE2	1:C:119:ARG:CZ	2.02	0.89
1:E:192:ARG:HA	1:E:195:LEU:CG	2.02	0.89
1:B:107:TYR:N	1:B:107:TYR:CD2	2.37	0.89
1:E:119:ARG:HG2	1:E:119:ARG:NH1	1.84	0.89
1:C:32:PHE:CE2	1:C:123:THR:HG22	2.07	0.89
1:C:42:ARG:HH11	1:C:42:ARG:HG3	1.35	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:297:ALA:O	1:E:333:ARG:N	2.06	0.89
1:E:110:GLU:C	1:E:110:GLU:CD	2.30	0.89
1:F:25:LEU:CB	1:F:28:PHE:HE2	1.84	0.89
1:E:145:LEU:HD22	1:E:332:LEU:HD21	1.42	0.89
1:E:25:LEU:CD2	1:E:310:ARG:HH12	1.69	0.88
1:C:119:ARG:O	1:C:123:THR:HG23	1.74	0.88
1:D:128:GLU:C	1:D:128:GLU:CD	2.30	0.88
1:F:25:LEU:CD1	1:F:26:ALA:N	2.35	0.88
1:A:114:ASN:N	1:A:115:HIS:HD2	1.69	0.88
1:C:35:GLU:HA	1:C:38:THR:OG1	1.72	0.88
1:F:143:ALA:O	1:F:147:ASN:CG	2.11	0.88
1:D:132:MET:HE1	1:D:251:PRO:CG	2.03	0.88
1:G:146:CYS:HB3	1:G:336:ALA:HB3	1.52	0.88
1:A:308:LEU:HA	1:A:323:ALA:CA	2.03	0.88
1:E:110:GLU:CG	1:E:118:VAL:HG11	2.00	0.88
1:B:116:TYR:N	1:B:116:TYR:CD1	2.35	0.88
1:C:206:VAL:HB	1:C:246:GLU:OE1	1.74	0.88
1:E:192:ARG:CA	1:E:195:LEU:CD1	2.30	0.88
1:A:49:ARG:HD3	1:A:206:VAL:HG21	1.55	0.88
1:B:251:PRO:CG	1:C:199:TYR:HE1	1.52	0.88
1:A:294:HIS:HD2	1:A:337:ALA:HA	1.37	0.87
1:B:251:PRO:HB3	1:C:199:TYR:CE1	2.06	0.87
1:C:33:GLY:C	1:C:36:VAL:HG23	1.94	0.87
1:G:110:GLU:CD	1:G:118:VAL:CG1	2.41	0.87
1:B:145:LEU:HD12	1:B:145:LEU:O	1.72	0.87
1:B:332:LEU:HD12	1:B:334:PRO:HD2	1.54	0.87
1:A:207:PHE:CE2	1:A:247:VAL:HG23	2.09	0.87
1:C:207:PHE:HE2	1:C:242:VAL:HG21	1.39	0.87
1:E:110:GLU:CD	1:E:111:ASP:HA	1.93	0.87
1:C:26:ALA:HA	1:C:29:LEU:HD11	1.56	0.87
1:G:109:ILE:H	1:G:109:ILE:HD13	0.71	0.87
1:A:302:LYS:HE2	1:A:327:MET:CE	2.05	0.87
1:C:161:THR:O	1:C:336:ALA:HB1	1.73	0.87
1:G:25:LEU:N	1:G:25:LEU:CD2	2.30	0.87
1:D:132:MET:HE1	1:D:251:PRO:CB	2.04	0.87
1:G:135:ASP:O	1:G:138:VAL:HG23	1.74	0.87
1:A:115:HIS:CD2	1:A:115:HIS:N	2.42	0.87
1:A:115:HIS:H	1:A:115:HIS:HD2	1.22	0.87
1:C:207:PHE:CZ	1:C:245:PHE:HD2	1.88	0.87
1:G:165:ILE:HD13	1:G:166:GLU:N	1.90	0.87
1:B:117:ASP:OD2	1:C:51:MET:CE	2.23	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:289:ILE:CG1	1:A:340:VAL:O	2.23	0.86
1:C:26:ALA:C	1:C:29:LEU:CD1	2.42	0.86
1:B:24:LYS:HE2	1:B:25:LEU:CA	2.04	0.86
1:C:204:ASP:O	1:C:205:ARG:CG	2.23	0.86
1:D:40:PHE:HE1	1:D:131:ALA:HA	1.36	0.86
1:G:115:HIS:O	1:G:119:ARG:HB3	1.74	0.86
1:A:207:PHE:HZ	1:A:209:CYS:CB	1.75	0.86
1:A:55:ILE:HG22	1:A:301:VAL:HG23	1.57	0.86
1:A:207:PHE:CE1	1:A:209:CYS:HB2	2.08	0.86
1:C:114:ASN:O	1:C:115:HIS:CG	2.29	0.86
1:G:28:PHE:CZ	1:G:111:ASP:OD1	2.27	0.86
1:C:146:CYS:HG	1:C:161:THR:N	1.73	0.86
1:C:195:LEU:CD2	1:C:202:ALA:CB	2.36	0.86
1:G:150:SER:O	1:G:151:LYS:O	1.93	0.86
1:D:128:GLU:OE2	1:D:129:SER:HA	1.76	0.86
1:C:195:LEU:HD23	1:C:205:ARG:HH22	1.03	0.85
1:C:206:VAL:CG2	1:C:248:VAL:N	2.39	0.85
1:E:128:GLU:OE2	1:F:201:PRO:CG	2.23	0.85
1:E:189:THR:HG22	1:E:243:MET:HE1	1.55	0.85
1:G:149:GLU:CD	1:G:150:SER:N	2.29	0.85
1:G:27:LEU:HD12	1:G:27:LEU:O	1.76	0.85
1:B:106:ILE:HG22	1:B:122:TYR:OH	1.76	0.85
1:D:28:PHE:HD2	1:D:29:LEU:N	1.73	0.85
1:D:29:LEU:HD13	1:D:30:LYS:H	1.39	0.85
1:E:121:GLU:OE1	1:F:51:MET:SD	2.34	0.85
1:B:131:ALA:C	1:B:132:MET:HE2	1.96	0.85
1:B:132:MET:HE2	1:B:132:MET:N	1.92	0.85
1:D:142:ILE:N	1:D:145:LEU:HD23	1.90	0.85
1:E:31:VAL:HG12	1:E:35:GLU:OE2	1.77	0.85
1:E:191:ALA:O	1:E:195:LEU:HG	1.76	0.85
1:B:109:ILE:HD13	1:B:110:GLU:H	1.42	0.85
1:F:25:LEU:O	1:F:28:PHE:CD2	2.30	0.85
1:G:132:MET:CE	1:G:252:HIS:NE2	2.38	0.85
1:C:208:TYR:CB	1:C:291:LEU:CG	2.55	0.85
1:E:189:THR:CG2	1:E:243:MET:HE1	2.07	0.85
1:B:28:PHE:CZ	1:B:111:ASP:O	2.30	0.84
1:B:29:LEU:HD21	1:B:310:ARG:HG2	1.57	0.84
1:B:206:VAL:HG13	1:B:246:GLU:HB3	1.59	0.84
1:E:24:LYS:NZ	1:E:112:ALA:CB	2.38	0.84
1:E:298:VAL:O	1:E:333:ARG:NH1	2.08	0.84
1:D:128:GLU:CD	1:D:129:SER:N	2.30	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:174:LEU:HB2	1:B:179:ALA:HB1	1.58	0.84
1:G:147:ASN:HD21	1:G:273:PRO:HG3	1.41	0.84
1:G:132:MET:O	1:G:132:MET:HE2	1.78	0.84
1:A:302:LYS:CG	1:A:327:MET:HG2	2.07	0.84
1:B:334:PRO:HA	1:B:335:GLU:CB	2.08	0.84
1:C:116:TYR:O	1:C:118:VAL:HG12	1.76	0.84
1:A:207:PHE:HE1	1:A:290:GLY:CA	1.90	0.84
1:B:24:LYS:CB	1:B:24:LYS:HZ3	1.88	0.84
1:C:25:LEU:HD23	1:C:26:ALA:H	0.71	0.84
1:C:114:ASN:O	1:C:115:HIS:CD2	2.30	0.84
1:A:288:VAL:O	1:A:289:ILE:HD13	1.78	0.84
1:E:298:VAL:CG1	1:E:332:LEU:CD1	2.55	0.84
1:A:302:LYS:HE2	1:A:327:MET:CG	2.08	0.84
1:C:33:GLY:HA2	1:C:36:VAL:HG21	1.58	0.84
1:B:132:MET:CE	1:B:132:MET:N	2.41	0.83
1:E:96:ILE:HD11	1:E:327:MET:O	1.78	0.83
1:C:42:ARG:HG3	1:C:42:ARG:NH1	1.90	0.83
1:C:110:GLU:OE1	1:C:122:TYR:CD2	2.31	0.83
1:A:107:TYR:N	1:A:107:TYR:CD2	2.44	0.83
1:A:309:GLU:HB2	1:A:322:ILE:CD1	1.99	0.83
1:B:128:GLU:OE1	1:C:68:ARG:CD	2.26	0.83
1:C:40:PHE:HE1	1:C:131:ALA:CA	1.91	0.83
1:E:115:HIS:HE1	1:E:119:ARG:HH22	1.25	0.83
1:D:45:VAL:CG2	1:D:135:ASP:OD2	2.26	0.83
1:D:110:GLU:O	1:D:113:MET:HG3	1.76	0.83
1:A:108:ASP:HB2	1:A:111:ASP:HB2	1.61	0.83
1:B:139:LEU:C	1:B:142:ILE:HG23	1.98	0.83
1:D:40:PHE:HE1	1:D:131:ALA:CA	1.92	0.83
1:B:114:ASN:N	1:B:115:HIS:CD2	2.39	0.83
1:D:29:LEU:HD13	1:D:29:LEU:C	1.98	0.83
1:A:286:ASP:N	1:A:287:ASN:O	2.12	0.83
1:B:117:ASP:OD1	1:C:53:ARG:HA	1.77	0.83
1:E:114:ASN:O	1:E:115:HIS:CB	2.26	0.83
1:E:333:ARG:HH11	1:E:333:ARG:HG3	1.43	0.83
1:C:188:LEU:HD22	1:C:207:PHE:HE1	1.37	0.83
1:G:146:CYS:HB2	1:G:336:ALA:HB2	1.60	0.83
1:C:109:ILE:HD13	1:C:110:GLU:N	1.93	0.82
1:C:202:ALA:HB1	1:C:205:ARG:NH2	1.94	0.82
1:E:25:LEU:HG	1:E:310:ARG:NH2	1.94	0.82
1:B:192:ARG:NE	1:B:243:MET:SD	2.52	0.82
1:G:110:GLU:C	1:G:114:ASN:HB3	1.99	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:107:TYR:N	1:G:107:TYR:HD2	1.75	0.82
1:A:308:LEU:CA	1:A:323:ALA:HA	2.06	0.82
1:B:239:ILE:HB	1:B:247:VAL:HG23	1.60	0.82
1:D:142:ILE:HD12	1:D:145:LEU:HG	1.62	0.82
1:A:110:GLU:OE1	1:A:118:VAL:CG1	2.25	0.82
1:E:119:ARG:CG	1:E:119:ARG:NH1	2.34	0.82
1:A:287:ASN:ND2	1:A:288:VAL:N	2.16	0.82
1:A:309:GLU:C	1:A:322:ILE:HG13	1.92	0.82
1:B:106:ILE:C	1:B:107:TYR:HD2	1.81	0.82
1:G:40:PHE:HD1	1:G:131:ALA:HB2	1.44	0.82
1:C:206:VAL:CG2	1:C:248:VAL:H	1.92	0.82
1:D:313:ARG:HB2	1:D:318:ALA:HB3	1.60	0.82
1:E:24:LYS:CD	1:E:24:LYS:C	2.46	0.82
1:G:107:TYR:N	1:G:107:TYR:CD2	2.45	0.82
1:C:110:GLU:OE2	1:C:118:VAL:CG2	2.26	0.82
1:D:36:VAL:CG1	1:D:37:LEU:N	2.43	0.82
1:G:110:GLU:HG2	1:G:118:VAL:CG2	2.09	0.82
1:G:110:GLU:CG	1:G:118:VAL:HB	2.10	0.82
1:C:110:GLU:OE1	1:C:122:TYR:CE2	2.33	0.81
1:G:28:PHE:CE2	1:G:111:ASP:OD1	2.32	0.81
1:B:92:LYS:HZ1	1:B:333:ARG:HE	1.28	0.81
1:B:332:LEU:HD12	1:B:334:PRO:CD	2.10	0.81
1:C:43:THR:HG21	1:C:128:GLU:HG3	1.62	0.81
1:C:106:ILE:C	1:C:107:TYR:CD2	2.54	0.81
1:C:119:ARG:NH1	1:C:119:ARG:HB2	1.95	0.81
1:D:49:ARG:O	1:D:50:HIS:ND1	2.14	0.81
1:D:27:LEU:HD12	1:D:28:PHE:N	1.95	0.81
1:G:79:ASN:HB2	1:G:82:ASP:HB2	1.62	0.81
1:G:113:MET:HG3	1:G:114:ASN:H	1.46	0.81
1:A:108:ASP:CB	1:A:111:ASP:HB2	2.11	0.81
1:C:110:GLU:CD	1:C:118:VAL:CG2	2.48	0.81
1:G:222:MET:SD	1:G:224:ASN:ND2	2.53	0.81
1:A:26:ALA:HA	1:A:29:LEU:HD11	1.60	0.81
1:B:141:GLU:OE1	1:B:330:GLY:C	2.17	0.81
1:D:205:ARG:HG2	1:D:245:PHE:HA	1.62	0.81
1:E:53:ARG:HH12	1:E:62:GLN:H	1.29	0.81
1:A:302:LYS:CD	1:A:327:MET:HG2	2.09	0.81
1:B:109:ILE:HD13	1:B:109:ILE:C	2.01	0.81
1:B:134:ALA:O	1:B:138:VAL:HG22	1.81	0.81
1:E:116:TYR:O	1:E:120:SER:HB3	1.80	0.81
1:B:24:LYS:NZ	1:B:25:LEU:N	2.30	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:GLN:HG3	1:C:66:LEU:HD13	1.62	0.80
1:E:298:VAL:CG1	1:E:332:LEU:HD13	2.12	0.80
1:B:30:LYS:O	1:B:30:LYS:CE	2.30	0.80
1:D:27:LEU:O	1:D:31:VAL:HG23	1.81	0.80
1:B:332:LEU:CD1	1:B:334:PRO:HG2	2.11	0.80
1:C:108:ASP:OD2	1:C:111:ASP:CB	2.30	0.80
1:A:306:LEU:HD12	1:A:306:LEU:O	1.81	0.80
1:E:24:LYS:CD	1:E:24:LYS:O	2.30	0.80
1:B:28:PHE:HE1	1:B:112:ALA:CA	1.73	0.80
1:E:110:GLU:CD	1:E:111:ASP:N	2.35	0.80
1:D:141:GLU:C	1:D:145:LEU:CD2	2.49	0.80
1:E:194:ALA:O	1:E:197:LYS:HB3	1.81	0.80
1:A:289:ILE:HG13	1:A:340:VAL:HG22	0.81	0.80
1:D:135:ASP:O	1:D:139:LEU:CD2	2.30	0.80
1:D:252:HIS:CE1	1:E:192:ARG:NH2	2.49	0.80
1:E:300:THR:OG1	1:E:301:VAL:N	2.13	0.80
1:E:25:LEU:CD1	1:E:25:LEU:O	2.30	0.80
1:E:135:ASP:OD1	1:E:252:HIS:CE1	2.34	0.80
1:E:119:ARG:O	1:E:123:THR:HG22	1.83	0.79
1:A:26:ALA:O	1:A:29:LEU:CD1	2.25	0.79
1:D:141:GLU:O	1:D:145:LEU:CD2	2.30	0.79
1:E:138:VAL:O	1:E:142:ILE:HG22	1.81	0.79
1:G:132:MET:CE	1:G:132:MET:O	2.30	0.79
1:G:148:VAL:O	1:G:148:VAL:CG2	2.30	0.79
1:A:92:LYS:NZ	1:A:93:VAL:O	2.15	0.79
1:B:132:MET:CE	1:B:135:ASP:OD2	2.30	0.79
1:G:137:ALA:O	1:G:270:HIS:CE1	2.35	0.79
1:A:185:ILE:HD13	1:A:188:LEU:HD12	1.64	0.79
1:A:207:PHE:CE1	1:A:209:CYS:CB	2.65	0.79
1:A:274:ALA:HA	1:A:285:LYS:O	1.82	0.79
1:B:40:PHE:HE1	1:B:130:LEU:HD11	0.64	0.79
1:C:25:LEU:O	1:C:29:LEU:CD1	2.30	0.79
1:G:148:VAL:O	1:G:149:GLU:HB3	1.79	0.79
1:C:26:ALA:O	1:C:29:LEU:CD1	2.30	0.79
1:D:25:LEU:C	1:D:25:LEU:CD1	2.47	0.79
1:D:135:ASP:O	1:D:139:LEU:CD1	2.30	0.79
1:G:115:HIS:O	1:G:119:ARG:CB	2.30	0.79
1:G:141:GLU:OE1	1:G:141:GLU:CA	2.30	0.79
1:C:116:TYR:CG	1:C:117:ASP:N	2.42	0.79
1:D:32:PHE:C	1:D:32:PHE:HD1	1.85	0.79
1:E:40:PHE:CZ	1:E:130:LEU:HD12	2.18	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:141:GLU:CD	1:E:330:GLY:O	2.20	0.79
1:B:30:LYS:O	1:B:30:LYS:CD	2.30	0.79
1:C:206:VAL:CB	1:C:246:GLU:OE1	2.31	0.79
1:A:119:ARG:O	1:A:123:THR:CG2	2.30	0.79
1:C:116:TYR:CD2	1:C:116:TYR:C	2.55	0.79
1:E:60:SER:HA	1:E:95:THR:HA	1.65	0.79
1:B:125:GLN:HG3	1:C:66:LEU:CD1	2.12	0.79
1:A:205:ARG:NH1	1:A:293:MET:HG2	1.98	0.78
1:B:26:ALA:O	1:B:29:LEU:HB2	1.82	0.78
1:B:132:MET:CA	1:B:135:ASP:OD2	2.30	0.78
1:E:192:ARG:O	1:E:195:LEU:CD1	2.30	0.78
1:B:113:MET:CA	1:B:115:HIS:CD2	2.63	0.78
1:B:125:GLN:CG	1:C:66:LEU:CD1	2.62	0.78
1:B:109:ILE:HD13	1:B:110:GLU:CA	2.12	0.78
1:C:299:GLY:O	1:C:330:GLY:HA2	1.82	0.78
1:E:298:VAL:HG12	1:E:332:LEU:CD1	2.14	0.78
1:G:87:ILE:HG22	1:G:88:LYS:HG2	1.65	0.78
1:A:308:LEU:HD12	1:A:308:LEU:O	1.84	0.78
1:C:112:ALA:HB3	1:C:115:HIS:CE1	2.18	0.78
1:D:252:HIS:CE1	1:E:192:ARG:HH21	1.99	0.78
1:A:208:TYR:OH	1:A:293:MET:CE	2.31	0.78
1:C:206:VAL:HG22	1:C:248:VAL:H	1.47	0.78
1:C:208:TYR:CB	1:C:291:LEU:HD11	2.09	0.78
1:G:130:LEU:HD23	1:G:130:LEU:O	1.84	0.78
1:A:55:ILE:HG21	1:A:301:VAL:CG2	2.12	0.78
1:B:138:VAL:O	1:B:142:ILE:CG2	2.30	0.78
1:C:205:ARG:O	1:C:246:GLU:CB	2.30	0.78
1:E:191:ALA:O	1:E:195:LEU:CD2	2.31	0.78
1:D:36:VAL:O	1:D:37:LEU:C	2.22	0.77
1:C:25:LEU:CD2	1:C:26:ALA:N	2.30	0.77
1:C:25:LEU:O	1:C:29:LEU:HD11	1.83	0.77
1:D:36:VAL:HG13	1:D:37:LEU:N	1.98	0.77
1:E:110:GLU:OE2	1:E:111:ASP:CA	2.30	0.77
1:G:106:ILE:HD13	1:G:107:TYR:CA	2.13	0.77
1:B:30:LYS:C	1:B:30:LYS:CD	2.52	0.77
1:E:145:LEU:HB2	1:E:332:LEU:HD23	0.78	0.77
1:B:68:ARG:O	1:B:69:THR:OG1	2.02	0.77
1:C:205:ARG:HE	1:C:294:HIS:HB3	1.50	0.77
1:B:251:PRO:CB	1:C:199:TYR:CD1	2.65	0.77
1:C:288:VAL:HG12	1:C:341:VAL:HA	1.66	0.77
1:B:125:GLN:HG2	1:C:66:LEU:HD12	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:142:ILE:HG21	1:D:293:MET:HE3	1.67	0.77
1:C:53:ARG:NH1	1:C:62:GLN:O	2.17	0.77
1:D:138:VAL:HG23	1:D:139:LEU:HD12	1.64	0.77
1:D:142:ILE:O	1:D:145:LEU:CB	2.28	0.77
1:E:192:ARG:HA	1:E:195:LEU:HD11	0.79	0.77
1:C:208:TYR:CB	1:C:291:LEU:HG	2.13	0.77
1:A:25:LEU:O	1:A:25:LEU:CD1	2.30	0.77
1:E:65:VAL:HG12	1:E:333:ARG:HD3	1.67	0.77
1:E:327:MET:N	1:E:327:MET:SD	2.57	0.76
1:F:300:THR:OG1	1:F:301:VAL:N	2.16	0.76
1:A:205:ARG:NH1	1:A:293:MET:CG	2.48	0.76
1:F:29:LEU:O	1:F:29:LEU:CD2	2.30	0.76
1:F:24:LYS:H	1:F:24:LYS:HD2	1.49	0.76
1:C:36:VAL:HG11	1:C:126:LEU:HD21	1.66	0.76
1:D:142:ILE:C	1:D:145:LEU:HB2	2.05	0.76
1:F:141:GLU:HG2	1:F:329:HIS:NE2	2.01	0.76
1:A:207:PHE:CE1	1:A:290:GLY:HA3	2.15	0.76
1:B:68:ARG:N	1:B:68:ARG:HD2	2.00	0.76
1:C:195:LEU:HD23	1:C:202:ALA:HB1	1.63	0.76
1:D:27:LEU:C	1:D:27:LEU:CD1	2.46	0.76
1:D:36:VAL:O	1:D:38:THR:N	2.18	0.76
1:F:141:GLU:HG2	1:F:329:HIS:CD2	2.20	0.76
1:C:195:LEU:HD23	1:C:205:ARG:HH21	1.43	0.76
1:D:53:ARG:HB3	1:D:301:VAL:HG12	1.67	0.76
1:E:119:ARG:O	1:E:123:THR:CG2	2.33	0.76
1:E:145:LEU:HD23	1:E:332:LEU:HD21	1.68	0.76
1:A:207:PHE:HZ	1:A:209:CYS:SG	2.08	0.76
1:E:119:ARG:NH1	1:E:119:ARG:CB	2.49	0.76
1:C:225:ALA:HA	1:C:226:ALA:HB3	1.66	0.76
1:E:298:VAL:O	1:E:333:ARG:CZ	2.33	0.76
1:C:288:VAL:HG22	1:C:289:ILE:HG13	1.66	0.75
1:F:25:LEU:O	1:F:28:PHE:CE2	2.38	0.75
1:F:136:GLY:O	1:F:140:ALA:N	2.18	0.75
1:D:40:PHE:CE1	1:D:131:ALA:CA	2.67	0.75
1:E:68:ARG:HE	1:E:70:GLN:HE22	1.34	0.75
1:E:192:ARG:CB	1:E:195:LEU:HD11	2.16	0.75
1:G:25:LEU:O	1:G:29:LEU:CG	2.29	0.75
1:G:110:GLU:CG	1:G:118:VAL:CB	2.64	0.75
1:A:106:ILE:C	1:A:107:TYR:CD2	2.58	0.75
1:B:145:LEU:HD21	1:B:332:LEU:CG	1.98	0.75
1:B:334:PRO:CA	1:B:335:GLU:HB2	2.12	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:42:ARG:O	1:C:44:SER:OG	2.01	0.75
1:C:110:GLU:CD	1:C:118:VAL:HG21	2.07	0.75
1:D:138:VAL:HG23	1:D:139:LEU:HD11	1.67	0.75
1:A:29:LEU:CD2	1:A:310:ARG:HD3	2.17	0.75
1:D:252:HIS:HE1	1:E:192:ARG:NH2	1.84	0.75
1:A:309:GLU:HB3	1:A:322:ILE:CG1	1.93	0.75
1:E:135:ASP:OD1	1:E:252:HIS:NE2	2.19	0.75
1:E:24:LYS:O	1:E:24:LYS:HD2	1.87	0.75
1:E:29:LEU:O	1:E:32:PHE:N	2.20	0.75
1:E:110:GLU:CG	1:E:118:VAL:CG2	2.62	0.75
1:E:298:VAL:CG1	1:E:332:LEU:HD12	2.17	0.75
1:C:43:THR:HG21	1:C:128:GLU:CG	2.17	0.74
1:B:132:MET:SD	1:C:199:TYR:CE1	2.80	0.74
1:B:251:PRO:HB3	1:C:199:TYR:CD1	2.21	0.74
1:B:251:PRO:HG2	1:C:199:TYR:CE1	2.18	0.74
1:D:29:LEU:HD13	1:D:30:LYS:CA	2.16	0.74
1:E:135:ASP:CG	1:E:252:HIS:CE1	2.61	0.74
1:G:130:LEU:HD22	1:G:131:ALA:N	2.00	0.74
1:E:96:ILE:CD1	1:E:327:MET:O	2.35	0.74
1:E:145:LEU:CD2	1:E:332:LEU:HG	2.15	0.74
1:G:110:GLU:O	1:G:114:ASN:CB	2.30	0.74
1:C:40:PHE:CE1	1:C:131:ALA:HA	2.18	0.74
1:E:141:GLU:HG3	1:E:330:GLY:CA	2.18	0.74
1:G:25:LEU:CA	1:G:28:PHE:CE2	2.69	0.74
1:B:101:THR:HG21	1:B:323:ALA:H	1.53	0.74
1:C:33:GLY:O	1:C:36:VAL:HG23	1.87	0.74
1:E:186:ALA:HB1	1:E:190:LYS:HZ2	1.52	0.74
1:A:205:ARG:HH21	1:A:296:SER:H	1.33	0.74
1:D:227:ASN:O	1:D:231:LEU:N	2.19	0.73
1:F:24:LYS:HD2	1:F:24:LYS:N	2.02	0.73
1:F:143:ALA:O	1:F:147:ASN:ND2	2.21	0.73
1:A:32:PHE:O	1:A:36:VAL:HG23	1.87	0.73
1:B:69:THR:HG22	1:B:70:GLN:N	2.02	0.73
1:B:288:VAL:HA	1:B:341:VAL:HG12	1.69	0.73
1:D:142:ILE:CD1	1:D:145:LEU:HD23	2.16	0.73
1:A:32:PHE:O	1:A:36:VAL:CG2	2.35	0.73
1:C:89:HIS:ND1	1:C:89:HIS:O	2.21	0.73
1:C:206:VAL:HG23	1:C:247:VAL:CA	2.18	0.73
1:E:32:PHE:O	1:E:32:PHE:HD1	1.71	0.73
1:G:165:ILE:HG12	1:G:341:VAL:HG12	1.70	0.73
1:E:50:HIS:CE1	1:E:300:THR:HG22	2.23	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:214:TYR:HA	1:E:217:ILE:HG23	1.70	0.73
1:C:104:VAL:O	1:C:320:GLN:NE2	2.21	0.73
1:E:110:GLU:CD	1:E:111:ASP:CA	2.56	0.73
1:A:160:GLY:N	1:A:334:PRO:O	2.21	0.73
1:C:117:ASP:OD2	1:D:51:MET:HE1	1.86	0.73
1:E:117:ASP:HB3	1:F:53:ARG:HD2	1.68	0.73
1:G:28:PHE:CZ	1:G:111:ASP:CG	2.62	0.73
1:C:35:GLU:CA	1:C:38:THR:OG1	2.37	0.73
1:E:298:VAL:O	1:E:333:ARG:NH2	2.22	0.73
1:B:24:LYS:HZ3	1:B:25:LEU:N	1.86	0.73
1:B:332:LEU:CD1	1:B:334:PRO:CD	2.66	0.73
1:F:145:LEU:HD21	1:F:334:PRO:HB3	1.69	0.73
1:F:308:LEU:HB3	1:F:323:ALA:HA	1.69	0.73
1:B:70:GLN:NE2	1:B:70:GLN:HA	2.02	0.73
1:C:28:PHE:CD2	1:C:29:LEU:N	2.51	0.73
1:C:142:ILE:HA	1:C:145:LEU:HD23	1.70	0.73
1:A:306:LEU:HB3	1:A:325:TYR:CZ	2.24	0.72
1:B:24:LYS:HE2	1:B:25:LEU:N	2.01	0.72
1:B:209:CYS:SG	1:B:210:ASP:N	2.61	0.72
1:C:119:ARG:O	1:C:123:THR:CG2	2.37	0.72
1:E:145:LEU:CG	1:E:332:LEU:CD2	2.64	0.72
1:D:28:PHE:CD2	1:D:28:PHE:C	2.63	0.72
1:E:235:GLU:HG2	1:E:236:LYS:HG2	1.70	0.72
1:A:209:CYS:HA	1:A:290:GLY:CA	2.19	0.72
1:B:115:HIS:CD2	1:B:115:HIS:N	2.55	0.72
1:G:115:HIS:CD2	1:G:119:ARG:NH2	2.53	0.72
1:B:60:SER:HA	1:B:95:THR:HA	1.70	0.72
1:E:147:ASN:OD1	1:E:147:ASN:N	2.19	0.72
1:A:114:ASN:H	1:A:115:HIS:CD2	2.08	0.72
1:C:42:ARG:HH11	1:C:42:ARG:CG	2.02	0.72
1:D:293:MET:N	1:D:293:MET:SD	2.60	0.72
1:G:302:LYS:HA	1:G:327:MET:HA	1.71	0.72
1:A:207:PHE:HE2	1:A:247:VAL:HG23	1.51	0.72
1:D:26:ALA:O	1:D:29:LEU:CD1	2.36	0.72
1:A:309:GLU:CA	1:A:322:ILE:CG1	2.46	0.72
1:C:208:TYR:CB	1:C:291:LEU:CD1	2.68	0.72
1:D:113:MET:SD	1:D:114:ASN:ND2	2.63	0.72
1:E:25:LEU:HD12	1:E:26:ALA:N	2.05	0.72
1:E:333:ARG:NH1	1:E:333:ARG:HG3	2.03	0.72
1:C:207:PHE:HZ	1:C:245:PHE:CE2	2.07	0.71
1:G:115:HIS:NE2	1:G:119:ARG:NH2	2.38	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:28:PHE:CG	1:E:111:ASP:OD1	2.27	0.71
1:E:119:ARG:HH11	1:E:119:ARG:CB	2.03	0.71
1:A:289:ILE:HG22	1:A:290:GLY:N	2.06	0.71
1:B:27:LEU:CD2	1:B:30:LYS:HB3	2.18	0.71
1:F:25:LEU:C	1:F:28:PHE:CE2	2.63	0.71
1:G:32:PHE:O	1:G:36:VAL:HG23	1.90	0.71
1:B:300:THR:OG1	1:B:301:VAL:N	2.24	0.71
1:C:310:ARG:NH2	1:C:319:ASP:OD2	2.23	0.71
1:F:205:ARG:HG2	1:F:245:PHE:HA	1.73	0.71
1:G:120:SER:O	1:G:123:THR:OG1	2.06	0.71
1:A:287:ASN:HD21	1:A:341:VAL:CG1	2.04	0.71
1:B:49:ARG:NH2	1:B:246:GLU:OE2	2.23	0.71
1:B:108:ASP:CA	1:B:111:ASP:OD2	2.37	0.71
1:B:113:MET:SD	1:B:115:HIS:HE1	2.09	0.71
1:D:27:LEU:HD12	1:D:27:LEU:O	1.91	0.71
1:D:132:MET:HE1	1:D:251:PRO:HB2	1.72	0.71
1:G:40:PHE:CD1	1:G:131:ALA:HB2	2.26	0.71
1:B:96:ILE:HG22	1:B:327:MET:HB3	1.73	0.71
1:C:207:PHE:CZ	1:C:245:PHE:CE2	2.78	0.71
1:E:115:HIS:ND1	1:E:119:ARG:NH2	2.38	0.71
1:E:117:ASP:HB3	1:F:53:ARG:CD	2.20	0.71
1:E:147:ASN:HB3	1:E:283:VAL:H	1.55	0.71
1:E:335:GLU:O	1:E:336:ALA:C	2.28	0.71
1:A:109:ILE:H	1:A:109:ILE:CD1	1.79	0.71
1:C:36:VAL:CG1	1:C:126:LEU:HG	2.20	0.71
1:E:170:ASN:HA	1:E:342:PHE:HB3	1.72	0.71
1:A:240:ARG:NH1	1:A:246:GLU:OE2	2.24	0.71
1:C:38:THR:O	1:C:41:ALA:HB3	1.90	0.71
1:E:80:LEU:HD13	1:E:81:ASP:H	1.54	0.71
1:D:32:PHE:CD1	1:D:32:PHE:O	2.37	0.70
1:B:111:ASP:OD1	1:B:112:ALA:N	2.23	0.70
1:E:202:ALA:HB1	1:E:205:ARG:CZ	2.20	0.70
1:B:110:GLU:C	1:B:110:GLU:OE1	2.30	0.70
1:C:29:LEU:O	1:C:32:PHE:CB	2.39	0.70
1:C:42:ARG:N	1:C:44:SER:OG	2.24	0.70
1:E:108:ASP:C	1:E:108:ASP:OD1	2.30	0.70
1:G:150:SER:OG	1:G:334:PRO:O	2.09	0.70
1:B:57:SER:O	1:B:59:LYS:NZ	2.23	0.70
1:C:27:LEU:HD23	1:C:27:LEU:O	1.91	0.70
1:D:45:VAL:CB	1:D:135:ASP:OD2	2.40	0.70
1:D:142:ILE:N	1:D:145:LEU:CD2	2.53	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:106:ILE:CG1	1:G:107:TYR:N	2.54	0.70
1:A:110:GLU:OE2	1:A:110:GLU:C	2.30	0.70
1:B:130:LEU:HD12	1:B:131:ALA:N	2.05	0.70
1:C:119:ARG:CG	1:C:119:ARG:NH1	2.46	0.70
1:G:28:PHE:CZ	1:G:111:ASP:OD2	2.45	0.70
1:B:113:MET:O	1:B:114:ASN:CG	2.30	0.70
1:D:144:GLY:C	1:D:146:CYS:H	1.92	0.70
1:D:294:HIS:HD2	1:D:297:ALA:HB2	1.56	0.70
1:D:300:THR:OG1	1:D:301:VAL:N	2.18	0.70
1:D:313:ARG:N	1:D:318:ALA:O	2.24	0.70
1:G:108:ASP:OD2	1:G:108:ASP:C	2.30	0.70
1:G:149:GLU:OE1	1:G:149:GLU:C	2.30	0.70
1:B:181:GLY:HA2	1:B:184:ILE:HB	1.72	0.70
1:C:195:LEU:HD21	1:C:202:ALA:HB3	1.72	0.70
1:E:40:PHE:CA	1:E:130:LEU:HD21	1.92	0.70
1:E:121:GLU:OE1	1:F:51:MET:HG2	1.92	0.70
1:A:55:ILE:HG21	1:A:301:VAL:HG21	1.72	0.70
1:F:143:ALA:O	1:F:147:ASN:OD1	2.09	0.70
1:A:205:ARG:NE	1:A:295:ARG:HA	2.04	0.70
1:B:125:GLN:CG	1:C:66:LEU:HD12	2.22	0.70
1:E:111:ASP:OD1	1:E:111:ASP:C	2.30	0.69
1:E:299:GLY:HA2	1:E:333:ARG:HH22	1.56	0.69
1:C:201:PRO:CA	1:C:202:ALA:HB3	2.16	0.69
1:A:240:ARG:HG3	1:A:241:ASN:H	1.56	0.69
1:C:37:LEU:HD13	1:C:306:LEU:HD11	1.73	0.69
1:D:132:MET:CE	1:D:251:PRO:CG	2.71	0.69
1:D:142:ILE:CA	1:D:145:LEU:CD2	2.26	0.69
1:G:132:MET:C	1:G:132:MET:CE	2.61	0.69
1:A:23:ASP:C	1:A:23:ASP:OD1	2.30	0.69
1:C:117:ASP:CG	1:D:51:MET:HE1	2.13	0.69
1:C:195:LEU:CD2	1:C:205:ARG:CZ	2.49	0.69
1:C:206:VAL:HG23	1:C:246:GLU:OE1	1.91	0.69
1:F:32:PHE:O	1:F:35:GLU:N	2.25	0.69
1:G:106:ILE:HD13	1:G:106:ILE:O	1.91	0.69
1:B:114:ASN:O	1:B:118:VAL:HB	1.93	0.69
1:B:141:GLU:OE1	1:B:329:HIS:O	2.09	0.69
1:B:132:MET:SD	1:B:135:ASP:OD2	2.51	0.69
1:C:108:ASP:OD1	1:C:111:ASP:CG	2.30	0.69
1:C:162:ALA:CB	1:C:337:ALA:O	2.41	0.69
1:D:165:ILE:HD11	1:D:190:LYS:HD2	1.73	0.69
1:E:141:GLU:HG3	1:E:330:GLY:HA3	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:191:ALA:O	1:E:195:LEU:CG	2.39	0.69
1:A:59:LYS:O	1:A:95:THR:OG1	2.10	0.69
1:A:302:LYS:CG	1:A:327:MET:HB3	2.22	0.69
1:A:311:ALA:O	1:A:319:ASP:OD1	2.11	0.69
1:B:110:GLU:OE1	1:B:111:ASP:HA	1.92	0.69
1:F:25:LEU:O	1:F:28:PHE:CG	2.46	0.69
1:A:29:LEU:HD22	1:A:310:ARG:HD3	1.75	0.69
1:C:27:LEU:HD23	1:C:28:PHE:CA	2.23	0.69
1:C:40:PHE:O	1:C:44:SER:HB3	1.93	0.69
1:B:28:PHE:CE1	1:B:112:ALA:CB	2.76	0.69
1:A:208:TYR:CE2	1:A:293:MET:CE	2.75	0.68
1:C:168:THR:O	1:C:169:GLN:NE2	2.26	0.68
1:D:142:ILE:HG21	1:D:293:MET:CE	2.23	0.68
1:G:314:ALA:HA	1:G:318:ALA:H	1.57	0.68
1:B:24:LYS:NZ	1:B:25:LEU:H	1.91	0.68
1:C:207:PHE:CE2	1:C:242:VAL:HG21	2.27	0.68
1:G:129:SER:O	1:G:132:MET:HG3	1.93	0.68
1:C:208:TYR:CB	1:C:291:LEU:HD21	2.16	0.68
1:G:25:LEU:HA	1:G:28:PHE:HD2	1.56	0.68
1:G:113:MET:CE	1:G:115:HIS:CB	2.66	0.68
1:B:145:LEU:CD2	1:B:332:LEU:HD12	1.91	0.68
1:C:200:VAL:O	1:C:202:ALA:HB3	1.93	0.68
1:G:106:ILE:C	1:G:107:TYR:CD2	2.67	0.68
1:A:101:THR:C	1:B:71:ALA:HB1	2.14	0.68
1:B:312:ARG:NH1	1:B:317:GLN:O	2.17	0.68
1:B:332:LEU:CD1	1:B:334:PRO:CG	2.72	0.68
1:C:108:ASP:O	1:C:111:ASP:HB3	1.93	0.68
1:F:68:ARG:O	1:F:68:ARG:NH1	2.23	0.68
1:C:195:LEU:CD2	1:C:205:ARG:HH22	1.71	0.68
1:C:206:VAL:CG2	1:C:248:VAL:HG23	2.16	0.68
1:D:209:CYS:HB2	1:D:249:GLU:HG2	1.75	0.68
1:E:135:ASP:OD1	1:E:135:ASP:C	2.30	0.68
1:A:289:ILE:CB	1:A:340:VAL:HG22	2.23	0.68
1:C:113:MET:SD	1:C:113:MET:O	2.51	0.68
1:B:281:VAL:HB	1:B:283:VAL:HG23	1.76	0.68
1:D:36:VAL:CG1	1:D:37:LEU:H	2.05	0.68
1:E:103:ASP:HB2	1:E:322:ILE:HA	1.76	0.68
1:F:163:THR:OG1	1:F:164:VAL:N	2.26	0.68
1:B:214:TYR:HA	1:B:217:ILE:HG23	1.76	0.67
1:A:309:GLU:O	1:A:322:ILE:CA	2.41	0.67
1:C:37:LEU:CD1	1:C:306:LEU:HD21	2.23	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:186:ALA:O	1:C:189:THR:OG1	2.12	0.67
1:D:214:TYR:HD1	1:D:249:GLU:HB2	1.59	0.67
1:F:59:LYS:O	1:F:95:THR:OG1	2.09	0.67
1:G:149:GLU:CD	1:G:150:SER:H	1.91	0.67
1:B:112:ALA:O	1:B:113:MET:SD	2.52	0.67
1:C:124:SER:OG	1:C:125:GLN:N	2.24	0.67
1:C:171:LYS:HE3	1:C:171:LYS:H	1.59	0.67
1:E:50:HIS:CD2	1:E:51:MET:H	2.12	0.67
1:E:298:VAL:HA	1:E:332:LEU:HA	1.77	0.67
1:G:110:GLU:HG2	1:G:118:VAL:CB	2.24	0.67
1:C:32:PHE:O	1:C:35:GLU:N	2.27	0.67
1:G:132:MET:SD	1:G:133:ALA:CA	2.83	0.67
1:G:132:MET:C	1:G:132:MET:HE2	2.15	0.67
1:G:271:VAL:O	1:G:271:VAL:HG22	1.93	0.67
1:B:327:MET:N	1:B:327:MET:SD	2.68	0.67
1:D:136:GLY:HA2	1:D:139:LEU:HD22	1.76	0.67
1:E:192:ARG:C	1:E:195:LEU:CD1	2.62	0.67
1:A:25:LEU:C	1:A:25:LEU:CD1	2.57	0.67
1:A:211:PRO:HG3	1:A:251:PRO:HA	1.75	0.67
1:A:306:LEU:HB3	1:A:325:TYR:CE1	2.30	0.67
1:D:29:LEU:O	1:D:29:LEU:HD22	1.94	0.67
1:D:95:THR:HA	1:D:96:ILE:HG23	1.77	0.67
1:E:110:GLU:OE1	1:E:111:ASP:CA	2.42	0.67
1:A:287:ASN:ND2	1:A:341:VAL:HG12	2.10	0.67
1:B:251:PRO:HG3	1:C:199:TYR:CD1	2.27	0.67
1:C:109:ILE:CD1	1:C:110:GLU:N	2.56	0.67
1:E:110:GLU:OE1	1:E:111:ASP:HA	1.94	0.67
1:A:205:ARG:HG3	1:A:293:MET:O	1.95	0.66
1:B:66:LEU:HD23	1:B:201:PRO:HD2	1.77	0.66
1:E:119:ARG:NH1	1:E:119:ARG:HB3	2.08	0.66
1:A:207:PHE:CZ	1:A:209:CYS:SG	2.87	0.66
1:B:66:LEU:CD2	1:B:200:VAL:HB	2.26	0.66
1:E:24:LYS:C	1:E:24:LYS:HD2	2.16	0.66
1:E:298:VAL:N	1:E:333:ARG:NH1	2.41	0.66
1:G:300:THR:OG1	1:G:301:VAL:N	2.27	0.66
1:B:24:LYS:HE2	1:B:25:LEU:HA	1.77	0.66
1:B:88:LYS:NZ	1:B:154:GLU:OE2	2.28	0.66
1:C:100:LEU:O	1:C:101:THR:OG1	2.12	0.66
1:C:290:GLY:HA3	1:C:340:VAL:H	1.61	0.66
1:E:121:GLU:OE1	1:F:51:MET:CG	2.43	0.66
1:F:25:LEU:C	1:F:28:PHE:CD2	2.68	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:PHE:HB2	1:A:291:LEU:O	1.94	0.66
1:B:115:HIS:CD2	1:B:115:HIS:H	2.14	0.66
1:C:119:ARG:NH1	1:C:119:ARG:CB	2.57	0.66
1:C:181:GLY:HA2	1:C:216:ALA:HB1	1.78	0.66
1:B:145:LEU:CD2	1:B:332:LEU:HD11	2.21	0.66
1:C:208:TYR:CB	1:C:291:LEU:CD2	2.73	0.66
1:D:218:LEU:HD22	1:D:221:LEU:HD23	1.76	0.66
1:G:110:GLU:CA	1:G:114:ASN:HB3	2.22	0.66
1:G:217:ILE:HG12	1:G:221:LEU:HB2	1.76	0.66
1:A:284:ALA:O	1:A:288:VAL:HB	1.94	0.66
1:C:110:GLU:OE2	1:C:110:GLU:C	2.34	0.66
1:E:299:GLY:N	1:E:333:ARG:HH12	1.86	0.66
1:G:28:PHE:CD1	1:G:111:ASP:OD2	2.48	0.66
1:A:36:VAL:CG1	1:A:126:LEU:HD11	2.26	0.66
1:A:205:ARG:HH21	1:A:296:SER:N	1.94	0.66
1:B:28:PHE:CZ	1:B:111:ASP:C	2.69	0.66
1:C:107:TYR:HA	1:C:318:ALA:HB3	1.78	0.66
1:E:24:LYS:O	1:E:24:LYS:HD3	1.95	0.66
1:E:34:GLY:O	1:E:38:THR:HG23	1.96	0.66
1:E:298:VAL:C	1:E:333:ARG:CZ	2.63	0.66
1:F:28:PHE:CD1	1:F:28:PHE:C	2.69	0.66
1:F:254:THR:OG1	1:F:285:LYS:NZ	2.29	0.66
1:B:66:LEU:CD1	1:B:66:LEU:H	2.08	0.66
1:B:106:ILE:CG2	1:B:122:TYR:OH	2.44	0.66
1:G:241:ASN:ND2	1:G:245:PHE:O	2.28	0.66
1:F:113:MET:SD	1:F:114:ASN:ND2	2.57	0.66
1:E:298:VAL:HG13	1:E:332:LEU:HD12	1.78	0.65
1:C:113:MET:CE	1:C:119:ARG:NH2	2.49	0.65
1:C:195:LEU:CD2	1:C:205:ARG:HH21	2.03	0.65
1:C:205:ARG:NE	1:C:294:HIS:HB3	2.10	0.65
1:D:40:PHE:O	1:D:43:THR:OG1	2.13	0.65
1:B:27:LEU:O	1:B:27:LEU:HD22	1.96	0.65
1:C:108:ASP:O	1:C:111:ASP:CB	2.45	0.65
1:E:142:ILE:O	1:E:142:ILE:CD1	2.30	0.65
1:F:250:VAL:HG21	1:F:253:LEU:HG	1.77	0.65
1:G:262:ARG:NH2	1:G:263:GLU:OE2	2.29	0.65
1:B:113:MET:O	1:B:114:ASN:ND2	2.30	0.65
1:D:36:VAL:HG12	1:D:37:LEU:H	1.61	0.65
1:E:186:ALA:HB1	1:E:190:LYS:NZ	2.12	0.65
1:E:195:LEU:O	1:E:199:TYR:N	2.30	0.65
1:D:132:MET:HE1	1:D:251:PRO:HG2	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:45:VAL:HG13	1:E:46:THR:HG23	1.78	0.65
1:E:110:GLU:OE1	1:E:111:ASP:N	2.30	0.65
1:A:41:ALA:HA	1:A:44:SER:HB3	1.78	0.65
1:A:309:GLU:N	1:A:322:ILE:HG13	2.12	0.65
1:B:45:VAL:HG13	1:B:46:THR:HG23	1.77	0.65
1:B:64:PRO:O	1:B:333:ARG:NH1	2.26	0.65
1:E:298:VAL:HG13	1:E:332:LEU:CD1	2.25	0.65
1:G:106:ILE:C	1:G:107:TYR:HD2	2.00	0.65
1:A:297:ALA:HB1	1:A:334:PRO:HB3	1.79	0.65
1:C:211:PRO:HG3	1:C:251:PRO:HA	1.79	0.65
1:C:297:ALA:O	1:C:298:VAL:HG13	1.97	0.65
1:D:288:VAL:HG11	1:D:340:VAL:HG13	1.79	0.65
1:A:208:TYR:OH	1:A:293:MET:HE1	1.97	0.65
1:E:291:LEU:HD13	1:E:339:ALA:HB2	1.79	0.65
1:G:141:GLU:HB2	1:G:270:HIS:HE1	1.62	0.65
1:A:53:ARG:NH2	1:F:114:ASN:OD1	2.30	0.65
1:A:285:LYS:HG2	1:A:286:ASP:N	2.11	0.65
1:B:110:GLU:OE1	1:B:111:ASP:N	2.30	0.65
1:B:125:GLN:NE2	1:C:66:LEU:O	2.26	0.65
1:F:25:LEU:HB2	1:F:28:PHE:CE2	2.30	0.65
1:A:57:SER:N	1:A:303:LEU:HD13	2.09	0.64
1:C:329:HIS:CD2	1:C:331:GLY:H	2.15	0.64
1:E:195:LEU:O	1:E:199:TYR:O	2.15	0.64
1:G:53:ARG:NH1	1:G:62:GLN:O	2.30	0.64
1:G:115:HIS:CE1	1:G:119:ARG:NH2	2.65	0.64
1:G:141:GLU:H	1:G:270:HIS:CE1	2.14	0.64
1:A:70:GLN:NE2	1:F:129:SER:OG	2.30	0.64
1:F:295:ARG:NH2	1:F:296:SER:OG	2.28	0.64
1:B:24:LYS:HD2	1:B:25:LEU:N	2.11	0.64
1:B:24:LYS:HZ3	1:B:24:LYS:N	1.94	0.64
1:B:55:ILE:O	1:B:304:ARG:NH2	2.31	0.64
1:C:35:GLU:O	1:C:39:ALA:N	2.30	0.64
1:G:49:ARG:HH22	1:G:248:VAL:HG21	1.63	0.64
1:C:248:VAL:HG12	1:C:249:GLU:H	1.63	0.64
1:A:287:ASN:CG	1:A:341:VAL:HB	2.18	0.64
1:C:43:THR:CG2	1:C:128:GLU:HG3	2.27	0.64
1:C:110:GLU:OE1	1:C:122:TYR:HD2	1.81	0.64
1:C:110:GLU:HG2	1:C:122:TYR:HE2	1.62	0.64
1:D:200:VAL:HG22	1:D:201:PRO:HD2	1.79	0.64
1:G:25:LEU:HB3	1:G:28:PHE:CE2	2.33	0.64
1:G:28:PHE:CD1	1:G:28:PHE:C	2.70	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:50:HIS:NE2	1:B:298:VAL:HB	2.12	0.64
1:G:110:GLU:N	1:G:114:ASN:ND2	2.45	0.64
1:A:45:VAL:HG22	1:A:250:VAL:HG11	1.80	0.64
1:A:300:THR:OG1	1:A:301:VAL:N	2.28	0.64
1:B:106:ILE:C	1:B:107:TYR:CD2	2.67	0.64
1:B:139:LEU:HA	1:B:142:ILE:CG2	2.28	0.64
1:E:106:ILE:HD12	1:E:108:ASP:HA	1.80	0.64
1:E:139:LEU:O	1:E:142:ILE:HG23	1.98	0.64
1:F:332:LEU:HD13	1:F:333:ARG:H	1.62	0.64
1:G:109:ILE:C	1:G:114:ASN:HD22	2.01	0.64
1:A:302:LYS:CE	1:A:327:MET:CE	2.76	0.64
1:G:303:LEU:HD22	1:G:304:ARG:HG3	1.80	0.64
1:A:161:THR:H	1:A:336:ALA:HA	1.62	0.63
1:A:327:MET:SD	1:A:328:GLY:N	2.66	0.63
1:B:24:LYS:CD	1:B:25:LEU:N	2.59	0.63
1:B:113:MET:CG	1:B:115:HIS:NE2	2.61	0.63
1:C:129:SER:OG	1:D:70:GLN:O	2.15	0.63
1:C:114:ASN:OD1	1:C:114:ASN:N	2.30	0.63
1:A:294:HIS:NE2	1:A:337:ALA:HA	2.11	0.63
1:C:49:ARG:NH2	1:C:246:GLU:OE2	2.30	0.63
1:G:78:GLU:OE2	1:G:79:ASN:N	2.31	0.63
1:B:27:LEU:HD23	1:B:30:LYS:CB	2.22	0.63
1:B:53:ARG:NH1	1:B:62:GLN:O	2.23	0.63
1:D:29:LEU:C	1:D:29:LEU:HD22	2.19	0.63
1:G:25:LEU:CA	1:G:28:PHE:CD2	2.70	0.63
1:B:92:LYS:HZ1	1:B:333:ARG:NE	1.96	0.63
1:F:276:LYS:HZ2	1:F:278:GLU:H	1.46	0.63
1:G:54:SER:OG	1:G:302:LYS:N	2.31	0.63
1:A:208:TYR:OH	1:A:293:MET:SD	2.57	0.63
1:C:43:THR:CB	1:C:128:GLU:HG3	2.29	0.63
1:C:205:ARG:HG2	1:C:294:HIS:HB3	1.80	0.63
1:D:128:GLU:OE1	1:D:129:SER:N	2.30	0.63
1:C:36:VAL:CG1	1:C:126:LEU:HD21	2.28	0.63
1:C:162:ALA:O	1:C:164:VAL:N	2.31	0.63
1:F:167:THR:OG1	1:F:168:THR:N	2.32	0.63
1:G:119:ARG:CG	1:G:119:ARG:NH1	2.39	0.63
1:B:113:MET:O	1:B:114:ASN:CB	2.47	0.63
1:B:161:THR:OG1	1:B:162:ALA:N	2.32	0.63
1:G:165:ILE:HG12	1:G:341:VAL:CG1	2.28	0.63
1:B:145:LEU:HD23	1:B:332:LEU:CD1	2.24	0.63
1:E:138:VAL:O	1:E:142:ILE:CG2	2.45	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:36:VAL:HG13	1:C:126:LEU:HG	1.80	0.62
1:E:50:HIS:CD2	1:E:298:VAL:HG23	2.34	0.62
1:A:309:GLU:HB2	1:A:322:ILE:HD12	1.81	0.62
1:B:332:LEU:HD12	1:B:334:PRO:HG2	1.80	0.62
1:F:36:VAL:HG21	1:F:126:LEU:HD11	1.81	0.62
1:F:145:LEU:CD2	1:F:334:PRO:HB3	2.29	0.62
1:D:59:LYS:O	1:D:96:ILE:HG21	1.98	0.62
1:D:110:GLU:OE1	1:D:111:ASP:N	2.30	0.62
1:D:142:ILE:HA	1:D:145:LEU:CG	2.25	0.62
1:A:57:SER:H	1:A:303:LEU:CD1	2.07	0.62
1:A:207:PHE:CE1	1:A:209:CYS:CA	2.83	0.62
1:B:128:GLU:OE1	1:C:68:ARG:CG	2.47	0.62
1:C:40:PHE:CE1	1:C:131:ALA:CA	2.78	0.62
1:C:170:ASN:HB3	1:C:172:ALA:H	1.64	0.62
1:G:110:GLU:C	1:G:114:ASN:CB	2.65	0.62
1:D:142:ILE:CD1	1:D:145:LEU:HD21	2.20	0.62
1:G:27:LEU:C	1:G:27:LEU:CD1	2.58	0.62
1:A:207:PHE:HE2	1:A:247:VAL:CG2	2.13	0.62
1:A:209:CYS:HA	1:A:290:GLY:HA3	1.82	0.62
1:D:128:GLU:OE2	1:D:129:SER:CA	2.47	0.62
1:E:135:ASP:OD2	1:E:252:HIS:CE1	2.52	0.62
1:E:192:ARG:CA	1:E:195:LEU:CG	2.74	0.62
1:F:171:LYS:HD2	1:F:174:LEU:HD12	1.82	0.62
1:G:209:CYS:SG	1:G:210:ASP:N	2.73	0.62
1:A:110:GLU:HB2	1:A:114:ASN:ND2	2.15	0.62
1:D:110:GLU:HG2	1:D:113:MET:O	2.00	0.62
1:F:51:MET:SD	1:F:295:ARG:NH2	2.72	0.62
1:F:135:ASP:OD1	1:F:252:HIS:NE2	2.31	0.62
1:B:59:LYS:HB2	1:B:96:ILE:HD13	1.81	0.62
1:D:142:ILE:HD12	1:D:145:LEU:CG	2.29	0.62
1:A:27:LEU:HD12	1:A:28:PHE:HA	1.81	0.62
1:A:315:ASN:OD1	1:A:315:ASN:N	2.31	0.62
1:B:117:ASP:OD2	1:C:51:MET:HE1	1.98	0.62
1:C:24:LYS:CG	1:C:25:LEU:N	2.63	0.62
1:B:251:PRO:CG	1:C:199:TYR:CZ	2.53	0.62
1:C:98:GLY:HA2	1:D:75:ALA:HB2	1.82	0.62
1:E:192:ARG:HG2	1:E:193:ALA:N	2.14	0.62
1:A:209:CYS:HA	1:A:290:GLY:HA2	1.82	0.61
1:B:28:PHE:HZ	1:B:112:ALA:CA	2.07	0.61
1:E:59:LYS:O	1:E:95:THR:OG1	2.12	0.61
1:B:132:MET:N	1:B:132:MET:HE3	2.14	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:36:VAL:CG1	1:C:126:LEU:CG	2.78	0.61
1:A:294:HIS:HD2	1:A:337:ALA:CA	2.11	0.61
1:G:26:ALA:CA	1:G:29:LEU:HD12	2.23	0.61
1:B:50:HIS:CD2	1:B:51:MET:H	2.18	0.61
1:C:142:ILE:O	1:C:145:LEU:HB2	2.01	0.61
1:F:288:VAL:HG21	1:F:340:VAL:O	1.99	0.61
1:G:206:VAL:HA	1:G:246:GLU:HG2	1.81	0.61
1:B:276:LYS:HD2	1:B:279:GLY:HA3	1.82	0.61
1:C:33:GLY:O	1:C:37:LEU:N	2.31	0.61
1:C:108:ASP:CG	1:C:111:ASP:CG	2.59	0.61
1:D:104:VAL:HG22	1:D:321:ILE:HD11	1.81	0.61
1:C:115:HIS:CD2	1:C:115:HIS:O	2.53	0.61
1:E:299:GLY:HA3	1:E:333:ARG:HH22	1.65	0.61
1:F:201:PRO:O	1:F:205:ARG:NH2	2.33	0.61
1:A:287:ASN:O	1:A:288:VAL:HG12	2.00	0.61
1:A:303:LEU:O	1:A:304:ARG:HB2	1.99	0.61
1:B:110:GLU:OE1	1:B:111:ASP:CA	2.49	0.61
1:C:294:HIS:CE1	1:C:335:GLU:HB2	2.35	0.61
1:G:275:ASN:OD1	1:G:275:ASN:N	2.33	0.61
1:B:109:ILE:CD1	1:B:109:ILE:C	2.66	0.61
1:D:135:ASP:C	1:D:139:LEU:HD22	2.20	0.61
1:G:178:VAL:O	1:G:182:LYS:NZ	2.28	0.61
1:A:119:ARG:NH1	1:A:119:ARG:CG	2.47	0.61
1:A:128:GLU:OE2	1:A:129:SER:N	2.34	0.61
1:C:36:VAL:CG1	1:C:126:LEU:CD2	2.79	0.61
1:A:102:ALA:HB2	1:B:71:ALA:HA	1.83	0.60
1:B:125:GLN:HG2	1:C:66:LEU:CD1	2.28	0.60
1:C:125:GLN:HG2	1:D:66:LEU:HB3	1.83	0.60
1:C:298:VAL:HG12	1:C:331:GLY:C	2.20	0.60
1:B:214:TYR:O	1:B:217:ILE:HG12	2.01	0.60
1:F:166:GLU:HA	1:F:341:VAL:HG13	1.83	0.60
1:B:118:VAL:CG1	1:B:119:ARG:N	2.64	0.60
1:C:208:TYR:HB3	1:C:291:LEU:CG	2.25	0.60
1:D:196:THR:O	1:D:199:TYR:N	2.34	0.60
1:F:293:MET:HA	1:F:336:ALA:O	2.01	0.60
1:G:180:LEU:O	1:G:184:ILE:N	2.35	0.60
1:B:67:GLY:HA3	1:B:68:ARG:NH1	2.16	0.60
1:E:299:GLY:O	1:E:331:GLY:N	2.33	0.60
1:A:288:VAL:O	1:A:289:ILE:CD1	2.50	0.60
1:B:131:ALA:O	1:B:135:ASP:CG	2.40	0.60
1:B:139:LEU:HA	1:B:142:ILE:HG21	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:286:ASP:OD2	1:B:286:ASP:N	2.33	0.60
1:C:206:VAL:HG23	1:C:247:VAL:C	2.21	0.60
1:G:167:THR:C	1:G:169:GLN:H	2.04	0.60
1:B:108:ASP:O	1:B:111:ASP:CG	2.40	0.60
1:D:45:VAL:HB	1:D:135:ASP:OD2	2.02	0.60
1:F:303:LEU:HB2	1:F:326:ALA:HB2	1.82	0.60
1:B:114:ASN:CB	1:B:118:VAL:HB	2.32	0.60
1:F:253:LEU:O	1:F:285:LYS:NZ	2.27	0.60
1:G:234:PRO:HD2	1:G:236:LYS:HE3	1.82	0.60
1:B:332:LEU:HD12	1:B:334:PRO:CG	2.30	0.60
1:G:167:THR:HG23	1:G:341:VAL:O	2.01	0.60
1:A:29:LEU:HD21	1:A:310:ARG:HD3	1.84	0.60
1:B:92:LYS:NZ	1:B:333:ARG:HE	1.98	0.60
1:C:31:VAL:CG1	1:C:32:PHE:N	2.65	0.60
1:E:50:HIS:CD2	1:E:51:MET:N	2.70	0.60
1:E:109:ILE:N	1:E:109:ILE:CD1	2.30	0.60
1:A:163:THR:HB	1:A:338:GLY:HA3	1.83	0.60
1:A:287:ASN:ND2	1:A:341:VAL:CG1	2.64	0.60
1:D:290:GLY:O	1:D:339:ALA:HA	2.02	0.60
1:D:293:MET:HB3	1:D:337:ALA:HB2	1.82	0.60
1:G:232:ILE:HG22	1:G:234:PRO:HD3	1.84	0.60
1:B:24:LYS:C	1:B:24:LYS:HZ3	2.04	0.59
1:D:81:ASP:N	1:D:81:ASP:OD1	2.33	0.59
1:E:141:GLU:HG3	1:E:330:GLY:O	2.02	0.59
1:F:174:LEU:HD22	1:F:180:LEU:HD21	1.84	0.59
1:B:92:LYS:HZ1	1:B:333:ARG:HH21	1.49	0.59
1:B:114:ASN:O	1:B:118:VAL:N	2.31	0.59
1:C:202:ALA:HB1	1:C:205:ARG:HH21	1.63	0.59
1:E:298:VAL:HG12	1:E:332:LEU:HD12	1.82	0.59
1:G:119:ARG:O	1:G:123:THR:HG23	2.01	0.59
1:C:275:ASN:HA	1:C:285:LYS:HE2	1.85	0.59
1:D:310:ARG:HG2	1:D:321:ILE:HG22	1.85	0.59
1:B:131:ALA:O	1:B:132:MET:HE2	2.02	0.59
1:B:332:LEU:CD1	1:B:334:PRO:HD2	2.29	0.59
1:E:61:ALA:N	1:E:94:ILE:O	2.33	0.59
1:G:270:HIS:HE2	1:G:329:HIS:HE1	1.49	0.59
1:A:294:HIS:CD2	1:A:337:ALA:CA	2.73	0.59
1:B:62:GLN:HB3	1:B:93:VAL:HG12	1.84	0.59
1:C:24:LYS:HG3	1:C:25:LEU:N	2.18	0.59
1:F:27:LEU:C	1:F:27:LEU:HD12	2.20	0.59
1:G:113:MET:HE3	1:G:113:MET:C	2.08	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:25:LEU:HD11	1:E:310:ARG:CZ	2.30	0.59
1:E:209:CYS:SG	1:E:210:ASP:N	2.75	0.59
1:G:28:PHE:CE1	1:G:29:LEU:HD23	2.37	0.59
1:B:227:ASN:O	1:B:227:ASN:ND2	2.26	0.59
1:E:239:ILE:HB	1:E:247:VAL:HB	1.84	0.59
1:E:298:VAL:HA	1:E:333:ARG:NH1	2.11	0.59
1:C:108:ASP:CG	1:C:111:ASP:HB3	2.23	0.59
1:C:35:GLU:OE1	1:C:119:ARG:O	2.21	0.59
1:E:56:SER:OG	1:E:304:ARG:NH2	2.29	0.59
1:G:25:LEU:HB3	1:G:28:PHE:HE2	1.68	0.59
1:B:307:ALA:HB3	1:B:324:LYS:HB3	1.85	0.59
1:C:235:GLU:OE1	1:C:236:LYS:N	2.26	0.59
1:E:110:GLU:HG3	1:E:118:VAL:CB	2.33	0.59
1:E:284:ALA:H	1:E:288:VAL:HG21	1.68	0.59
1:B:131:ALA:C	1:B:132:MET:CE	2.71	0.58
1:C:201:PRO:HA	1:C:202:ALA:CB	2.13	0.58
1:G:110:GLU:N	1:G:114:ASN:HD22	2.01	0.58
1:B:66:LEU:O	1:B:66:LEU:HD22	2.02	0.58
1:B:134:ALA:O	1:B:138:VAL:CG2	2.50	0.58
1:C:188:LEU:HB3	1:C:245:PHE:HE2	1.67	0.58
1:C:294:HIS:NE2	1:C:335:GLU:OE2	2.35	0.58
1:D:142:ILE:HD12	1:D:145:LEU:CD2	2.32	0.58
1:F:28:PHE:HD1	1:F:29:LEU:N	1.95	0.58
1:C:32:PHE:CE1	1:C:36:VAL:CG2	2.87	0.58
1:C:135:ASP:OD1	1:C:135:ASP:N	2.34	0.58
1:C:208:TYR:HB3	1:C:291:LEU:HD21	1.82	0.58
1:B:298:VAL:HA	1:B:332:LEU:HD22	1.86	0.58
1:C:32:PHE:CZ	1:C:126:LEU:HD23	2.39	0.58
1:D:161:THR:OG1	1:D:162:ALA:N	2.35	0.58
1:G:113:MET:CG	1:G:114:ASN:H	2.09	0.58
1:G:165:ILE:HD13	1:G:166:GLU:CA	2.32	0.58
1:A:41:ALA:C	1:A:43:THR:H	2.07	0.58
1:A:279:GLY:O	1:A:280:ASN:ND2	2.37	0.58
1:B:63:PHE:CZ	1:B:299:GLY:HA3	2.38	0.58
1:B:117:ASP:OD2	1:C:51:MET:HE3	2.02	0.58
1:G:132:MET:SD	1:G:133:ALA:HA	2.43	0.58
1:A:26:ALA:HA	1:A:29:LEU:CD1	2.31	0.58
1:A:250:VAL:HB	1:A:251:PRO:HD2	1.86	0.58
1:B:161:THR:HG22	1:B:335:GLU:N	2.18	0.58
1:C:214:TYR:CD1	1:C:249:GLU:HG2	2.39	0.58
1:D:57:SER:O	1:D:59:LYS:NZ	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:28:PHE:CD2	1:E:111:ASP:OD2	2.56	0.58
1:E:100:LEU:HA	1:F:72:ALA:O	2.03	0.58
1:G:101:THR:O	1:G:262:ARG:NH1	2.34	0.58
1:G:146:CYS:SG	1:G:336:ALA:CA	2.92	0.58
1:B:214:TYR:OH	1:C:192:ARG:NE	2.36	0.57
1:C:116:TYR:C	1:C:116:TYR:HD2	2.03	0.57
1:C:240:ARG:HG3	1:C:241:ASN:H	1.69	0.57
1:D:295:ARG:NE	1:D:296:SER:OG	2.38	0.57
1:F:310:ARG:HB3	1:F:321:ILE:HG22	1.86	0.57
1:G:143:ALA:HB1	1:G:272:PHE:CB	2.34	0.57
1:A:139:LEU:HD21	1:A:291:LEU:HD11	1.85	0.57
1:C:32:PHE:CE1	1:C:36:VAL:HG22	2.39	0.57
1:F:141:GLU:CG	1:F:329:HIS:CD2	2.87	0.57
1:F:212:ASP:O	1:F:215:SER:OG	2.22	0.57
1:G:45:VAL:HG22	1:G:46:THR:HG23	1.86	0.57
1:C:71:ALA:HB1	1:C:72:ALA:HA	1.85	0.57
1:C:206:VAL:HA	1:C:246:GLU:C	2.17	0.57
1:C:271:VAL:H	1:C:274:ALA:HB2	1.69	0.57
1:E:293:MET:HA	1:E:337:ALA:H	1.69	0.57
1:A:141:GLU:OE1	1:A:142:ILE:HG12	2.05	0.57
1:A:302:LYS:HE2	1:A:327:MET:SD	2.45	0.57
1:B:285:LYS:O	1:B:288:VAL:N	2.32	0.57
1:C:171:LYS:HB3	1:C:342:PHE:CZ	2.39	0.57
1:E:189:THR:HG23	1:E:243:MET:CG	2.35	0.57
1:F:147:ASN:OD1	1:F:147:ASN:N	2.36	0.57
1:A:287:ASN:HD22	1:A:287:ASN:C	2.04	0.57
1:B:115:HIS:HD2	1:B:115:HIS:N	2.01	0.57
1:C:108:ASP:CG	1:C:111:ASP:CB	2.73	0.57
1:C:110:GLU:OE1	1:C:122:TYR:HE2	1.85	0.57
1:B:28:PHE:HE1	1:B:112:ALA:CB	2.17	0.57
1:E:29:LEU:O	1:E:30:LYS:C	2.42	0.57
1:F:183:GLU:OE1	1:F:184:ILE:N	2.38	0.57
1:G:171:LYS:H	1:G:342:PHE:HE2	1.50	0.57
1:E:29:LEU:O	1:E:31:VAL:N	2.37	0.57
1:G:115:HIS:HA	1:G:119:ARG:NH1	2.20	0.57
1:B:24:LYS:HB3	1:B:24:LYS:HZ3	1.52	0.57
1:C:188:LEU:HD13	1:C:207:PHE:CZ	2.40	0.57
1:C:312:ARG:NH1	1:C:318:ALA:O	2.37	0.57
1:D:290:GLY:HA3	1:D:340:VAL:H	1.70	0.57
1:A:55:ILE:HG23	1:A:301:VAL:CG2	2.35	0.57
1:A:108:ASP:HB3	1:A:111:ASP:HB2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:PHE:CE1	1:A:290:GLY:CA	2.81	0.57
1:B:141:GLU:CD	1:B:330:GLY:CA	2.58	0.57
1:B:206:VAL:HA	1:B:246:GLU:H	1.70	0.57
1:C:119:ARG:HH11	1:C:119:ARG:CB	2.15	0.57
1:B:139:LEU:C	1:B:142:ILE:CG2	2.71	0.56
1:C:41:ALA:O	1:C:42:ARG:CB	2.41	0.56
1:C:119:ARG:HG3	1:C:119:ARG:NH1	2.01	0.56
1:D:28:PHE:HD2	1:D:29:LEU:H	1.49	0.56
1:E:110:GLU:CD	1:E:118:VAL:HG21	2.25	0.56
1:F:242:VAL:HG22	1:F:243:MET:H	1.70	0.56
1:B:319:ASP:OD2	1:B:320:GLN:N	2.38	0.56
1:E:25:LEU:CD1	1:E:310:ARG:CZ	2.79	0.56
1:E:294:HIS:NE2	1:E:295:ARG:O	2.37	0.56
1:F:141:GLU:CG	1:F:329:HIS:NE2	2.69	0.56
1:F:143:ALA:CB	1:F:272:PHE:CD2	2.89	0.56
1:F:181:GLY:HA3	1:F:220:ALA:HB2	1.87	0.56
1:F:272:PHE:O	1:F:274:ALA:N	2.37	0.56
1:A:212:ASP:OD2	1:A:212:ASP:N	2.30	0.56
1:A:289:ILE:HG13	1:A:340:VAL:HG23	1.77	0.56
1:A:309:GLU:CB	1:A:322:ILE:HD12	2.27	0.56
1:B:121:GLU:OE1	1:B:121:GLU:HA	2.05	0.56
1:B:139:LEU:CA	1:B:142:ILE:CG2	2.84	0.56
1:C:137:ALA:O	1:C:140:ALA:N	2.37	0.56
1:C:207:PHE:O	1:C:248:VAL:O	2.23	0.56
1:C:271:VAL:HG23	1:C:274:ALA:HA	1.86	0.56
1:E:141:GLU:CG	1:E:330:GLY:O	2.52	0.56
1:E:234:PRO:O	1:E:236:LYS:N	2.38	0.56
1:F:32:PHE:O	1:F:34:GLY:N	2.38	0.56
1:F:308:LEU:CB	1:F:323:ALA:HA	2.34	0.56
1:A:276:LYS:HZ2	1:A:278:GLU:H	1.52	0.56
1:G:44:SER:OG	1:G:135:ASP:HB2	2.05	0.56
1:A:114:ASN:CG	1:A:114:ASN:O	2.43	0.56
1:A:307:ALA:O	1:A:324:LYS:N	2.38	0.56
1:B:210:ASP:OD2	1:B:213:SER:OG	2.23	0.56
1:C:188:LEU:CD2	1:C:207:PHE:CZ	2.85	0.56
1:D:164:VAL:HA	1:D:339:ALA:H	1.70	0.56
1:D:205:ARG:HB3	1:D:205:ARG:CZ	2.35	0.56
1:F:29:LEU:O	1:F:32:PHE:HB3	2.05	0.56
1:G:110:GLU:OE1	1:G:118:VAL:HB	2.05	0.56
1:A:73:TYR:HE1	1:F:102:ALA:HB2	1.70	0.56
1:A:320:GLN:NE2	1:A:321:ILE:O	2.32	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:115:HIS:O	1:B:119:ARG:HB2	2.05	0.56
1:B:121:GLU:O	1:B:121:GLU:CD	2.44	0.56
1:E:299:GLY:CA	1:E:333:ARG:NH2	2.63	0.56
1:D:136:GLY:CA	1:D:139:LEU:HD22	2.35	0.56
1:E:233:ASP:OD2	1:E:238:SER:N	2.37	0.56
1:F:130:LEU:HD11	1:F:325:TYR:HD2	1.71	0.56
1:B:25:LEU:HD13	1:B:25:LEU:C	2.26	0.56
1:G:113:MET:O	1:G:115:HIS:N	2.39	0.56
1:B:28:PHE:CZ	1:B:112:ALA:N	2.74	0.56
1:C:48:SER:OG	1:C:49:ARG:N	2.36	0.56
1:C:202:ALA:CB	1:C:205:ARG:HH21	2.19	0.56
1:E:53:ARG:HD3	1:E:63:PHE:CD1	2.41	0.56
1:G:106:ILE:HD11	1:G:107:TYR:O	2.05	0.56
1:A:66:LEU:HD23	1:A:89:HIS:HE1	1.69	0.56
1:B:132:MET:HE2	1:B:135:ASP:CG	2.25	0.56
1:C:290:GLY:HA2	1:C:340:VAL:HG22	1.87	0.56
1:D:225:ALA:HB1	1:D:226:ALA:C	2.25	0.56
1:F:147:ASN:HA	1:F:283:VAL:HG21	1.87	0.56
1:G:110:GLU:CD	1:G:118:VAL:HG11	2.18	0.56
1:G:130:LEU:HD23	1:G:131:ALA:CA	2.36	0.56
1:C:29:LEU:O	1:C:32:PHE:N	2.39	0.55
1:D:36:VAL:HG22	1:D:39:ALA:HB3	1.87	0.55
1:E:50:HIS:HE2	1:E:299:GLY:HA2	1.71	0.55
1:E:297:ALA:O	1:E:332:LEU:HD12	2.06	0.55
1:C:162:ALA:C	1:C:164:VAL:H	2.09	0.55
1:C:183:GLU:OE1	1:C:183:GLU:N	2.39	0.55
1:E:167:THR:OG1	1:E:168:THR:N	2.39	0.55
1:F:32:PHE:O	1:F:33:GLY:C	2.43	0.55
1:C:49:ARG:HH12	1:C:248:VAL:HG21	1.69	0.55
1:C:299:GLY:H	1:C:330:GLY:C	2.09	0.55
1:E:28:PHE:HE1	1:E:111:ASP:O	1.85	0.55
1:E:110:GLU:OE2	1:E:110:GLU:C	2.43	0.55
1:E:232:ILE:HG22	1:E:240:ARG:HB2	1.88	0.55
1:A:312:ARG:NH1	1:A:318:ALA:O	2.40	0.55
1:F:164:VAL:HG12	1:F:339:ALA:H	1.72	0.55
1:A:125:GLN:O	1:A:129:SER:OG	2.25	0.55
1:B:66:LEU:H	1:B:66:LEU:HD12	1.72	0.55
1:C:108:ASP:OD2	1:C:111:ASP:HB3	2.06	0.55
1:C:108:ASP:O	1:C:111:ASP:CG	2.45	0.55
1:D:46:THR:CB	1:D:135:ASP:OD1	2.54	0.55
1:D:128:GLU:C	1:D:128:GLU:OE2	2.44	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:272:PHE:HE1	1:F:285:LYS:HB2	1.71	0.55
1:D:300:THR:HG21	1:D:329:HIS:N	2.21	0.55
1:E:226:ALA:O	1:E:228:TYR:N	2.40	0.55
1:E:325:TYR:CG	1:E:326:ALA:N	2.75	0.55
1:F:25:LEU:HD13	1:F:26:ALA:N	2.20	0.55
1:E:298:VAL:HG12	1:E:332:LEU:HA	1.87	0.55
1:F:32:PHE:CE1	1:F:123:THR:HG22	2.41	0.55
1:G:102:ALA:HB2	1:G:262:ARG:CZ	2.37	0.55
1:B:39:ALA:O	1:B:43:THR:OG1	2.21	0.55
1:B:181:GLY:O	1:B:185:ILE:HG13	2.06	0.55
1:C:103:ASP:HB3	1:C:321:ILE:HD12	1.87	0.55
1:F:29:LEU:C	1:F:29:LEU:HD22	2.21	0.55
1:F:36:VAL:HA	1:F:39:ALA:HB3	1.89	0.55
1:F:124:SER:OG	1:F:125:GLN:N	2.39	0.55
1:F:200:VAL:HG22	1:F:201:PRO:HD2	1.87	0.55
1:G:92:LYS:HD3	1:G:332:LEU:N	2.22	0.55
1:A:287:ASN:HD21	1:A:341:VAL:HG12	1.70	0.55
1:C:206:VAL:HG23	1:C:248:VAL:N	2.19	0.55
1:B:63:PHE:HZ	1:B:299:GLY:HA3	1.72	0.55
1:B:141:GLU:CD	1:B:331:GLY:N	2.59	0.55
1:D:254:THR:HG22	1:D:255:ALA:H	1.72	0.55
1:F:291:LEU:H	1:F:291:LEU:HD13	1.71	0.55
1:G:268:GLN:O	1:G:271:VAL:HG12	2.06	0.55
1:A:36:VAL:O	1:A:37:LEU:C	2.45	0.54
1:A:119:ARG:NH1	1:A:119:ARG:HG3	2.22	0.54
1:A:289:ILE:CG2	1:A:290:GLY:N	2.70	0.54
1:C:108:ASP:O	1:C:108:ASP:CG	2.45	0.54
1:C:285:LYS:NZ	1:C:286:ASP:OD2	2.27	0.54
1:A:90:THR:HG21	1:A:333:ARG:HH22	1.72	0.54
1:A:113:MET:O	1:A:114:ASN:HB3	2.06	0.54
1:A:285:LYS:HA	1:A:287:ASN:O	2.08	0.54
1:A:303:LEU:HG	1:A:304:ARG:HG3	1.89	0.54
1:B:32:PHE:O	1:B:35:GLU:HG2	2.07	0.54
1:C:204:ASP:C	1:C:205:ARG:HG3	2.24	0.54
1:D:112:ALA:O	1:D:115:HIS:NE2	2.40	0.54
1:D:113:MET:HA	1:D:115:HIS:CE1	2.42	0.54
1:F:24:LYS:H	1:F:24:LYS:CD	2.16	0.54
1:G:171:LYS:HA	1:G:174:LEU:HB2	1.89	0.54
1:A:28:PHE:C	1:A:28:PHE:CD2	2.81	0.54
1:A:289:ILE:HG22	1:A:290:GLY:H	1.73	0.54
1:B:309:GLU:OE1	1:B:310:ARG:NE	2.35	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:235:GLU:HG2	1:C:236:LYS:HG3	1.89	0.54
1:D:138:VAL:CG2	1:D:139:LEU:HD11	2.33	0.54
1:A:235:GLU:O	1:A:236:LYS:NZ	2.32	0.54
1:B:25:LEU:O	1:B:25:LEU:HD22	2.08	0.54
1:B:81:ASP:HA	1:B:84:ARG:HB2	1.88	0.54
1:B:118:VAL:HG12	1:B:119:ARG:N	2.21	0.54
1:E:216:ALA:O	1:E:220:ALA:N	2.33	0.54
1:G:137:ALA:HB2	1:G:258:ALA:HB2	1.88	0.54
1:A:207:PHE:CB	1:A:291:LEU:O	2.55	0.54
1:A:328:GLY:O	1:A:329:HIS:HB3	2.08	0.54
1:B:232:ILE:HA	1:B:239:ILE:HA	1.89	0.54
1:C:25:LEU:O	1:C:29:LEU:HD12	2.07	0.54
1:D:132:MET:CE	1:D:251:PRO:HG2	2.35	0.54
1:E:24:LYS:NZ	1:E:112:ALA:HB2	2.22	0.54
1:C:36:VAL:HG13	1:C:126:LEU:CD2	2.38	0.54
1:E:307:ALA:H	1:E:325:TYR:HB2	1.73	0.54
1:F:298:VAL:HA	1:F:332:LEU:HB2	1.89	0.54
1:G:141:GLU:HG2	1:G:329:HIS:ND1	2.22	0.54
1:B:28:PHE:CZ	1:B:111:ASP:OD1	2.60	0.54
1:B:40:PHE:HE1	1:B:130:LEU:HD13	1.32	0.54
1:D:298:VAL:HG12	1:D:332:LEU:HB2	1.89	0.54
1:A:302:LYS:HE2	1:A:327:MET:HE2	1.86	0.54
1:B:35:GLU:CB	1:B:123:THR:CG2	2.80	0.54
1:C:110:GLU:CD	1:C:118:VAL:HG23	2.29	0.54
1:C:206:VAL:HG23	1:C:247:VAL:HA	1.87	0.54
1:D:196:THR:OG1	1:D:197:LYS:N	2.40	0.54
1:C:28:PHE:CD2	1:C:28:PHE:O	2.61	0.54
1:E:24:LYS:HZ3	1:E:112:ALA:HB2	1.71	0.54
1:E:50:HIS:HE1	1:E:300:THR:HG22	1.73	0.54
1:E:306:LEU:HA	1:E:325:TYR:CD1	2.43	0.54
1:B:145:LEU:HD23	1:B:332:LEU:HD11	1.85	0.54
1:C:113:MET:HE2	1:C:119:ARG:NE	2.23	0.54
1:E:50:HIS:HD2	1:E:51:MET:H	1.56	0.54
1:E:104:VAL:HG21	1:F:66:LEU:HD21	1.90	0.54
1:G:303:LEU:HB2	1:G:326:ALA:HB3	1.89	0.54
1:A:186:ALA:O	1:A:190:LYS:NZ	2.41	0.53
1:A:208:TYR:CZ	1:A:293:MET:CE	2.91	0.53
1:B:167:THR:OG1	1:B:168:THR:N	2.38	0.53
1:C:162:ALA:HB3	1:C:338:GLY:HA3	1.90	0.53
1:C:205:ARG:CG	1:C:294:HIS:HB3	2.37	0.53
1:D:50:HIS:CD2	1:D:298:VAL:HG23	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:VAL:O	1:A:320:GLN:NE2	2.41	0.53
1:C:110:GLU:O	1:C:118:VAL:HG21	2.08	0.53
1:D:110:GLU:CG	1:D:113:MET:O	2.57	0.53
1:E:81:ASP:OD2	1:E:81:ASP:N	2.40	0.53
1:E:298:VAL:CA	1:E:331:GLY:O	2.56	0.53
1:E:299:GLY:HA3	1:E:333:ARG:NH2	2.22	0.53
1:F:300:THR:HG1	1:F:301:VAL:H	1.52	0.53
1:G:44:SER:HB2	1:G:131:ALA:HB1	1.90	0.53
1:G:130:LEU:CD2	1:G:131:ALA:CA	2.86	0.53
1:E:112:ALA:O	1:E:113:MET:HB2	2.09	0.53
1:B:24:LYS:CE	1:B:25:LEU:CA	2.78	0.53
1:B:209:CYS:O	1:B:250:VAL:HG22	2.08	0.53
1:C:31:VAL:HG12	1:C:32:PHE:N	2.23	0.53
1:F:25:LEU:O	1:F:28:PHE:CZ	2.61	0.53
1:G:92:LYS:HD3	1:G:332:LEU:H	1.74	0.53
1:C:32:PHE:CD1	1:C:33:GLY:N	2.77	0.53
1:E:115:HIS:HE1	1:E:119:ARG:NH2	1.90	0.53
1:D:116:TYR:O	1:D:119:ARG:HB3	2.09	0.53
1:A:66:LEU:HD23	1:A:89:HIS:CE1	2.44	0.53
1:B:58:GLY:O	1:B:59:LYS:HG2	2.08	0.53
1:C:32:PHE:HZ	1:C:126:LEU:HD23	1.74	0.53
1:E:192:ARG:C	1:E:195:LEU:HG	2.29	0.53
1:F:211:PRO:HD3	1:F:250:VAL:O	2.08	0.53
1:F:312:ARG:NH1	1:F:319:ASP:OD2	2.41	0.53
1:B:165:ILE:H	1:B:340:VAL:HG12	1.74	0.53
1:C:37:LEU:HD13	1:C:306:LEU:HD21	1.89	0.53
1:D:242:VAL:HG22	1:D:243:MET:H	1.72	0.53
1:A:207:PHE:CE1	1:A:290:GLY:C	2.83	0.53
1:B:50:HIS:CD2	1:B:51:MET:N	2.77	0.53
1:D:167:THR:O	1:D:168:THR:OG1	2.27	0.53
1:F:250:VAL:HG21	1:F:253:LEU:CG	2.39	0.53
1:G:106:ILE:HD11	1:G:107:TYR:C	2.29	0.53
1:A:73:TYR:CE1	1:F:102:ALA:HB2	2.44	0.53
1:E:298:VAL:HG12	1:E:332:LEU:HD13	1.85	0.53
1:A:115:HIS:HB2	1:A:119:ARG:CG	2.39	0.52
1:D:53:ARG:HH12	1:D:61:ALA:HB1	1.73	0.52
1:D:253:LEU:O	1:D:254:THR:OG1	2.26	0.52
1:G:260:THR:CG2	1:G:269:LYS:NZ	2.73	0.52
1:G:306:LEU:HD13	1:G:325:TYR:CE1	2.44	0.52
1:A:110:GLU:OE1	1:A:118:VAL:CB	2.57	0.52
1:B:151:LYS:HG2	1:B:152:TYR:H	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:84:ARG:HD2	1:F:84:ARG:O	2.08	0.52
1:A:305:ASP:C	1:A:325:TYR:HE1	2.12	0.52
1:E:65:VAL:CG1	1:E:333:ARG:HD3	2.37	0.52
1:G:341:VAL:HG22	1:G:342:PHE:H	1.75	0.52
1:C:141:GLU:HG3	1:C:329:HIS:HE1	1.74	0.52
1:C:184:ILE:HD11	1:C:289:ILE:HD13	1.92	0.52
1:D:166:GLU:HA	1:D:341:VAL:HG23	1.91	0.52
1:D:272:PHE:HE1	1:D:285:LYS:HB2	1.74	0.52
1:E:24:LYS:C	1:E:24:LYS:HD3	2.28	0.52
1:F:204:ASP:N	1:F:205:ARG:HH21	2.07	0.52
1:G:146:CYS:SG	1:G:336:ALA:HB2	2.49	0.52
1:G:149:GLU:OE1	1:G:150:SER:CA	2.57	0.52
1:G:304:ARG:O	1:G:304:ARG:NE	2.39	0.52
1:A:273:PRO:HD2	1:A:284:ALA:HB2	1.92	0.52
1:B:27:LEU:CD2	1:B:27:LEU:O	2.56	0.52
1:C:134:ALA:O	1:C:138:VAL:HG13	2.09	0.52
1:D:272:PHE:CE1	1:D:285:LYS:HB2	2.44	0.52
1:F:28:PHE:CE1	1:F:29:LEU:HB2	2.44	0.52
1:F:241:ASN:N	1:F:241:ASN:OD1	2.43	0.52
1:G:100:LEU:O	1:G:325:TYR:N	2.39	0.52
1:G:115:HIS:O	1:G:119:ARG:HB2	2.10	0.52
1:F:143:ALA:CB	1:F:272:PHE:CE2	2.92	0.52
1:G:270:HIS:HE2	1:G:329:HIS:CE1	2.27	0.52
1:A:51:MET:HB2	1:A:299:GLY:HA3	1.92	0.52
1:B:24:LYS:HZ3	1:B:25:LEU:H	1.55	0.52
1:C:34:GLY:O	1:C:38:THR:N	2.30	0.52
1:D:142:ILE:CD1	1:D:145:LEU:HG	2.38	0.52
1:A:313:ARG:HH11	1:A:320:GLN:HG2	1.74	0.52
1:B:53:ARG:HH11	1:B:63:PHE:HB3	1.73	0.52
1:B:113:MET:CB	1:B:115:HIS:NE2	2.73	0.52
1:C:208:TYR:HB3	1:C:291:LEU:CD2	2.39	0.52
1:E:36:VAL:HG22	1:E:126:LEU:HD12	1.91	0.52
1:E:102:ALA:O	1:F:70:GLN:NE2	2.43	0.52
1:B:163:THR:HG23	1:B:164:VAL:HG12	1.92	0.52
1:B:309:GLU:OE1	1:B:310:ARG:N	2.41	0.52
1:C:32:PHE:O	1:C:34:GLY:N	2.43	0.52
1:C:299:GLY:O	1:C:300:THR:HB	2.10	0.52
1:F:31:VAL:HG12	1:F:32:PHE:N	2.24	0.52
1:G:46:THR:HG23	1:G:135:ASP:OD1	2.10	0.52
1:G:242:VAL:HG22	1:G:243:MET:H	1.75	0.52
1:A:62:GLN:OE1	1:A:62:GLN:N	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:GLU:OE2	1:A:129:SER:OG	2.27	0.52
1:B:92:LYS:NZ	1:B:333:ARG:HH21	2.08	0.52
1:C:91:GLU:OE1	1:C:91:GLU:N	2.42	0.52
1:C:117:ASP:CG	1:D:51:MET:CE	2.73	0.52
1:E:181:GLY:N	1:E:183:GLU:OE1	2.43	0.52
1:G:143:ALA:CB	1:G:272:PHE:HB3	2.39	0.52
1:A:170:ASN:OD1	1:A:171:LYS:NZ	2.43	0.51
1:C:27:LEU:HD22	1:C:28:PHE:N	2.20	0.51
1:E:192:ARG:HA	1:E:195:LEU:CD2	2.40	0.51
1:F:195:LEU:HD21	1:F:205:ARG:NH1	2.26	0.51
1:F:294:HIS:CG	1:F:295:ARG:N	2.78	0.51
1:B:68:ARG:N	1:B:68:ARG:CD	2.73	0.51
1:C:178:VAL:HG13	1:C:220:ALA:HA	1.92	0.51
1:C:192:ARG:O	1:C:195:LEU:HB3	2.10	0.51
1:D:46:THR:HG23	1:D:135:ASP:CG	2.25	0.51
1:E:40:PHE:C	1:E:130:LEU:HD21	2.29	0.51
1:A:302:LYS:CE	1:A:327:MET:HE2	2.40	0.51
1:B:139:LEU:HD21	1:B:255:ALA:HA	1.91	0.51
1:C:32:PHE:HD1	1:C:33:GLY:N	2.08	0.51
1:C:162:ALA:C	1:C:164:VAL:N	2.63	0.51
1:D:62:GLN:HB2	1:D:93:VAL:HG12	1.92	0.51
1:D:204:ASP:N	1:D:205:ARG:HH21	2.08	0.51
1:G:100:LEU:HD13	1:G:259:GLY:N	2.25	0.51
1:A:32:PHE:O	1:A:36:VAL:HG22	2.10	0.51
1:A:142:ILE:HA	1:A:145:LEU:HD22	1.92	0.51
1:D:130:LEU:HD12	1:D:131:ALA:HA	1.76	0.51
1:F:25:LEU:HB3	1:F:28:PHE:HE2	1.70	0.51
1:F:254:THR:HA	1:F:270:HIS:NE2	2.25	0.51
1:A:211:PRO:HA	1:A:214:TYR:HB2	1.93	0.51
1:B:59:LYS:O	1:B:95:THR:OG1	2.27	0.51
1:B:135:ASP:O	1:B:138:VAL:HG23	2.11	0.51
1:G:181:GLY:HA3	1:G:220:ALA:HB2	1.92	0.51
1:A:166:GLU:OE1	1:A:166:GLU:N	2.43	0.51
1:C:103:ASP:CG	1:C:322:ILE:HA	2.31	0.51
1:C:108:ASP:OD2	1:C:111:ASP:CG	2.48	0.51
1:D:51:MET:HB2	1:D:298:VAL:O	2.10	0.51
1:E:333:ARG:HH11	1:E:333:ARG:CG	2.19	0.51
1:G:50:HIS:HD2	1:G:298:VAL:HG23	1.76	0.51
1:B:64:PRO:HA	1:B:91:GLU:HB3	1.93	0.51
1:B:171:LYS:HG3	1:B:342:PHE:CZ	2.45	0.51
1:C:162:ALA:HB3	1:C:337:ALA:C	2.29	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:285:LYS:NZ	1:C:285:LYS:O	2.40	0.51
1:F:64:PRO:N	1:F:91:GLU:HG3	2.25	0.51
1:F:295:ARG:HE	1:F:296:SER:N	2.09	0.51
1:F:306:LEU:HB2	1:F:325:TYR:CZ	2.45	0.51
1:G:106:ILE:HG12	1:G:107:TYR:N	2.26	0.51
1:A:135:ASP:OD1	1:A:135:ASP:N	2.43	0.51
1:B:121:GLU:CD	1:B:121:GLU:C	2.70	0.51
1:B:132:MET:CA	1:B:132:MET:HE3	2.36	0.51
1:B:294:HIS:CG	1:B:295:ARG:N	2.79	0.51
1:D:83:LYS:HZ2	1:D:83:LYS:H	1.58	0.51
1:E:181:GLY:O	1:E:185:ILE:HD11	1.93	0.51
1:F:134:ALA:O	1:F:137:ALA:HB3	2.11	0.51
1:A:207:PHE:HD1	1:A:291:LEU:O	1.93	0.51
1:B:81:ASP:H	1:B:83:LYS:CE	2.24	0.51
1:B:132:MET:SD	1:C:199:TYR:HE1	2.32	0.51
1:B:298:VAL:HG12	1:B:299:GLY:H	1.76	0.51
1:F:251:PRO:HD2	1:F:252:HIS:CE1	2.46	0.51
1:F:270:HIS:N	1:F:272:PHE:O	2.44	0.51
1:G:200:VAL:HG22	1:G:201:PRO:HD2	1.92	0.51
1:A:26:ALA:C	1:A:29:LEU:HD12	2.24	0.51
1:B:70:GLN:NE2	1:B:70:GLN:CA	2.72	0.51
1:B:130:LEU:CD1	1:B:130:LEU:O	2.41	0.51
1:B:312:ARG:NH2	1:B:317:GLN:OE1	2.44	0.51
1:F:103:ASP:CG	1:F:322:ILE:HA	2.31	0.51
1:A:78:GLU:OE1	1:A:79:ASN:N	2.44	0.50
1:B:92:LYS:HZ1	1:B:333:ARG:NH2	2.09	0.50
1:B:100:LEU:HB3	1:B:326:ALA:HB3	1.92	0.50
1:B:292:PHE:N	1:B:338:GLY:O	2.31	0.50
1:C:36:VAL:HG11	1:C:126:LEU:CD2	2.37	0.50
1:C:192:ARG:HH21	1:C:243:MET:HG3	1.75	0.50
1:C:207:PHE:CE2	1:C:245:PHE:HD2	2.28	0.50
1:D:142:ILE:CD1	1:D:145:LEU:CG	2.89	0.50
1:D:214:TYR:N	1:D:249:GLU:OE1	2.45	0.50
1:D:305:ASP:OD2	1:D:305:ASP:N	2.44	0.50
1:F:63:PHE:C	1:F:91:GLU:HG3	2.31	0.50
1:G:106:ILE:CD1	1:G:107:TYR:CA	2.87	0.50
1:B:332:LEU:HD13	1:B:334:PRO:CD	2.41	0.50
1:D:135:ASP:O	1:D:138:VAL:HG22	2.11	0.50
1:D:204:ASP:O	1:D:295:ARG:HB3	2.11	0.50
1:D:310:ARG:HG2	1:D:321:ILE:HA	1.93	0.50
1:F:138:VAL:HG12	1:F:329:HIS:HE1	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:312:ARG:HA	1:F:319:ASP:HA	1.92	0.50
1:G:239:ILE:HB	1:G:247:VAL:HB	1.93	0.50
1:B:28:PHE:HZ	1:B:111:ASP:C	2.09	0.50
1:B:112:ALA:C	1:B:113:MET:SD	2.89	0.50
1:E:119:ARG:O	1:E:123:THR:HG23	2.11	0.50
1:F:135:ASP:HB3	1:F:252:HIS:CE1	2.46	0.50
1:G:110:GLU:CG	1:G:118:VAL:CG2	2.84	0.50
1:A:114:ASN:O	1:A:114:ASN:OD1	2.30	0.50
1:A:226:ALA:HB3	1:C:232:ILE:HB	1.92	0.50
1:A:302:LYS:HE2	1:A:327:MET:HE3	1.90	0.50
1:E:110:GLU:OE2	1:E:110:GLU:O	2.30	0.50
1:G:110:GLU:CG	1:G:118:VAL:HG11	2.42	0.50
1:G:115:HIS:O	1:G:116:TYR:O	2.30	0.50
1:G:205:ARG:HE	1:G:294:HIS:HB2	1.76	0.50
1:A:115:HIS:O	1:A:119:ARG:HG3	2.11	0.50
1:A:232:ILE:HB	1:A:240:ARG:HB2	1.93	0.50
1:A:233:ASP:HA	1:A:236:LYS:HZ1	1.76	0.50
1:B:132:MET:O	1:B:135:ASP:OD2	2.30	0.50
1:C:63:PHE:HE1	1:C:94:ILE:HD11	1.76	0.50
1:C:108:ASP:OD1	1:C:108:ASP:O	2.30	0.50
1:C:121:GLU:O	1:C:124:SER:OG	2.25	0.50
1:D:253:LEU:O	1:D:285:LYS:NZ	2.44	0.50
1:A:183:GLU:OE1	1:A:184:ILE:N	2.34	0.50
1:C:57:SER:O	1:C:59:LYS:NZ	2.43	0.50
1:C:108:ASP:OD2	1:C:111:ASP:OD1	2.30	0.50
1:C:147:ASN:HB3	1:C:281:VAL:HG11	1.93	0.50
1:D:24:LYS:O	1:D:27:LEU:HG	2.11	0.50
1:D:123:THR:OG1	1:D:124:SER:N	2.45	0.50
1:D:240:ARG:NE	1:D:241:ASN:H	2.10	0.50
1:F:41:ALA:O	1:F:44:SER:OG	2.26	0.50
1:F:174:LEU:HD13	1:F:180:LEU:HD11	1.94	0.50
1:G:265:THR:C	1:G:266:THR:OG1	2.49	0.50
1:C:143:ALA:HB3	1:C:271:VAL:HG13	1.94	0.50
1:D:176:ASP:OD2	1:D:178:VAL:N	2.34	0.50
1:F:143:ALA:HB3	1:F:272:PHE:CD2	2.47	0.50
1:G:109:ILE:O	1:G:112:ALA:O	2.30	0.50
1:G:291:LEU:H	1:G:291:LEU:HD12	1.77	0.50
1:B:170:ASN:O	1:B:171:LYS:NZ	2.36	0.50
1:E:110:GLU:HG3	1:E:118:VAL:CG2	2.37	0.50
1:B:66:LEU:HD21	1:B:200:VAL:HB	1.93	0.50
1:B:108:ASP:O	1:B:111:ASP:OD2	2.30	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:300:THR:HB	1:B:329:HIS:HA	1.94	0.50
1:F:129:SER:HA	1:F:132:MET:HB2	1.93	0.50
1:F:253:LEU:O	1:F:270:HIS:NE2	2.42	0.50
1:G:106:ILE:CD1	1:G:107:TYR:C	2.80	0.50
1:G:141:GLU:OE1	1:G:141:GLU:O	2.30	0.50
1:G:295:ARG:CZ	1:G:296:SER:HB2	2.41	0.50
1:A:64:PRO:HG2	1:F:121:GLU:HG2	1.94	0.49
1:F:50:HIS:CD2	1:F:51:MET:H	2.30	0.49
1:G:104:VAL:HG21	1:G:122:TYR:HE1	1.77	0.49
1:A:171:LYS:HE3	1:A:342:PHE:HD2	1.76	0.49
1:B:332:LEU:HD11	1:B:334:PRO:HG2	1.94	0.49
1:C:35:GLU:O	1:C:38:THR:OG1	2.30	0.49
1:C:82:ASP:HA	1:C:85:LYS:HB3	1.93	0.49
1:C:166:GLU:HA	1:C:341:VAL:O	2.12	0.49
1:E:212:ASP:C	1:E:214:TYR:H	2.16	0.49
1:F:251:PRO:HB2	1:F:252:HIS:CD2	2.47	0.49
1:G:110:GLU:O	1:G:113:MET:O	2.30	0.49
1:A:55:ILE:HG21	1:A:301:VAL:HG23	1.77	0.49
1:B:46:THR:C	1:B:48:SER:H	2.14	0.49
1:B:111:ASP:OD1	1:B:111:ASP:C	2.50	0.49
1:B:255:ALA:HB3	1:B:272:PHE:CZ	2.47	0.49
1:B:285:LYS:O	1:B:287:ASN:N	2.45	0.49
1:F:221:LEU:HG	1:F:222:MET:HG3	1.94	0.49
1:G:113:MET:CG	1:G:114:ASN:N	2.74	0.49
1:G:114:ASN:O	1:G:116:TYR:HB2	2.11	0.49
1:A:207:PHE:CE1	1:A:209:CYS:HA	2.47	0.49
1:A:236:LYS:HE2	1:A:238:SER:HB2	1.94	0.49
1:B:252:HIS:N	1:C:199:TYR:OH	2.45	0.49
1:C:292:PHE:O	1:C:337:ALA:HB1	2.11	0.49
1:D:45:VAL:N	1:D:135:ASP:OD2	2.45	0.49
1:D:128:GLU:OE2	1:D:128:GLU:O	2.30	0.49
1:D:303:LEU:H	1:D:326:ALA:HB3	1.76	0.49
1:G:116:TYR:O	1:G:120:SER:OG	2.30	0.49
1:A:105:LEU:O	1:A:107:TYR:HE2	1.95	0.49
1:B:119:ARG:O	1:B:123:THR:OG1	2.30	0.49
1:B:131:ALA:O	1:B:135:ASP:OD2	2.30	0.49
1:D:83:LYS:H	1:D:83:LYS:CE	2.25	0.49
1:D:340:VAL:HG22	1:D:341:VAL:H	1.77	0.49
1:F:301:VAL:HG12	1:F:302:LYS:H	1.76	0.49
1:G:25:LEU:CB	1:G:28:PHE:CE2	2.94	0.49
1:G:137:ALA:HB2	1:G:258:ALA:CB	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:108:ASP:HB3	1:A:111:ASP:N	2.27	0.49
1:E:294:HIS:CG	1:E:295:ARG:N	2.80	0.49
1:F:205:ARG:HE	1:F:205:ARG:N	2.09	0.49
1:G:45:VAL:HG22	1:G:135:ASP:CG	2.32	0.49
1:B:114:ASN:HB3	1:B:118:VAL:HB	1.93	0.49
1:C:116:TYR:O	1:C:118:VAL:CG1	2.56	0.49
1:E:192:ARG:O	1:E:195:LEU:CG	2.60	0.49
1:B:131:ALA:O	1:B:135:ASP:OD1	2.30	0.49
1:C:195:LEU:HB2	1:C:205:ARG:HH12	1.77	0.49
1:D:228:TYR:HA	1:D:231:LEU:HB3	1.94	0.49
1:F:27:LEU:O	1:F:27:LEU:CD1	2.32	0.49
1:F:62:GLN:HB2	1:F:91:GLU:HB3	1.93	0.49
1:F:83:LYS:O	1:F:83:LYS:NZ	2.34	0.49
1:G:143:ALA:HB1	1:G:272:PHE:HB3	1.94	0.49
1:A:62:GLN:HA	1:A:93:VAL:HA	1.94	0.49
1:B:308:LEU:HA	1:B:323:ALA:HA	1.94	0.49
1:C:110:GLU:OE2	1:C:110:GLU:O	2.30	0.49
1:D:327:MET:SD	1:D:328:GLY:N	2.86	0.49
1:E:32:PHE:HD1	1:E:32:PHE:C	2.16	0.49
1:G:108:ASP:OD2	1:G:109:ILE:N	2.45	0.49
1:A:306:LEU:HD12	1:A:306:LEU:C	2.34	0.49
1:C:165:ILE:CG2	1:C:340:VAL:HB	2.43	0.49
1:C:192:ARG:NH2	1:C:243:MET:HG3	2.28	0.49
1:C:294:HIS:HE1	1:C:335:GLU:HB2	1.74	0.49
1:D:94:ILE:H	1:D:94:ILE:HD13	1.78	0.49
1:D:204:ASP:H	1:D:205:ARG:HH21	1.60	0.49
1:E:101:THR:OG1	1:E:323:ALA:O	2.28	0.49
1:E:240:ARG:HG3	1:E:241:ASN:ND2	2.28	0.49
1:E:285:LYS:O	1:E:287:ASN:N	2.46	0.49
1:F:278:GLU:OE2	1:F:287:ASN:ND2	2.46	0.49
1:C:108:ASP:OD1	1:C:111:ASP:OD1	2.30	0.48
1:D:272:PHE:O	1:D:274:ALA:N	2.46	0.48
1:F:189:THR:OG1	1:F:190:LYS:N	2.45	0.48
1:F:209:CYS:O	1:F:250:VAL:HG22	2.13	0.48
1:G:132:MET:SD	1:G:132:MET:O	2.66	0.48
1:G:204:ASP:O	1:G:205:ARG:NH1	2.36	0.48
1:A:33:GLY:HA2	1:A:36:VAL:HG23	1.95	0.48
1:A:234:PRO:HD2	1:A:236:LYS:HE3	1.95	0.48
1:B:140:ALA:HB2	1:B:256:GLY:HA3	1.95	0.48
1:C:108:ASP:O	1:C:111:ASP:OD2	2.30	0.48
1:E:106:ILE:CD1	1:E:108:ASP:HA	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:145:LEU:HD21	1:E:334:PRO:HA	1.95	0.48
1:G:53:ARG:O	1:G:301:VAL:HA	2.13	0.48
1:B:104:VAL:HG23	1:B:321:ILE:HD11	1.94	0.48
1:C:32:PHE:CD1	1:C:36:VAL:CG2	2.97	0.48
1:C:298:VAL:HB	1:C:330:GLY:HA3	1.94	0.48
1:D:241:ASN:ND2	1:D:242:VAL:O	2.46	0.48
1:E:65:VAL:HG12	1:E:333:ARG:CD	2.40	0.48
1:E:160:GLY:N	1:E:336:ALA:O	2.46	0.48
1:E:276:LYS:HD2	1:E:279:GLY:HA3	1.95	0.48
1:C:108:ASP:OD2	1:C:111:ASP:HB2	2.12	0.48
1:E:183:GLU:OE1	1:E:183:GLU:N	2.47	0.48
1:B:29:LEU:HD21	1:B:310:ARG:CG	2.35	0.48
1:B:284:ALA:O	1:B:288:VAL:HB	2.12	0.48
1:C:299:GLY:O	1:C:330:GLY:CA	2.59	0.48
1:C:334:PRO:C	1:C:336:ALA:H	2.16	0.48
1:F:28:PHE:CD1	1:F:29:LEU:CA	2.96	0.48
1:F:55:ILE:HD13	1:F:301:VAL:HG11	1.95	0.48
1:F:207:PHE:HE2	1:F:209:CYS:HB3	1.77	0.48
1:G:115:HIS:CG	1:G:119:ARG:HH22	2.25	0.48
1:A:29:LEU:HD21	1:A:310:ARG:CD	2.43	0.48
1:C:282:LYS:H	1:C:282:LYS:HE2	1.78	0.48
1:D:319:ASP:OD1	1:D:319:ASP:N	2.47	0.48
1:F:145:LEU:HD21	1:F:334:PRO:CB	2.42	0.48
1:G:37:LEU:HD12	1:G:40:PHE:HD2	1.78	0.48
1:G:110:GLU:CG	1:G:114:ASN:ND2	2.76	0.48
1:G:146:CYS:CB	1:G:336:ALA:HB2	2.25	0.48
1:G:201:PRO:HG2	1:G:205:ARG:HH22	1.78	0.48
1:G:265:THR:O	1:G:266:THR:OG1	2.30	0.48
1:A:29:LEU:CD2	1:A:310:ARG:CD	2.88	0.48
1:A:308:LEU:HD12	1:A:308:LEU:C	2.33	0.48
1:B:121:GLU:OE1	1:B:121:GLU:CA	2.61	0.48
1:C:32:PHE:CE1	1:C:36:VAL:HG21	2.49	0.48
1:C:36:VAL:HG13	1:C:126:LEU:CG	2.43	0.48
1:C:240:ARG:HG3	1:C:240:ARG:HH21	1.79	0.48
1:D:65:VAL:HG11	1:D:90:THR:HG23	1.95	0.48
1:D:122:TYR:CE1	1:E:64:PRO:HG3	2.49	0.48
1:F:89:HIS:O	1:F:89:HIS:CG	2.67	0.48
1:G:25:LEU:C	1:G:29:LEU:HG	2.27	0.48
1:A:110:GLU:OE2	1:A:110:GLU:O	2.30	0.48
1:A:110:GLU:HB2	1:A:114:ASN:HD22	1.78	0.48
1:A:113:MET:HG2	1:A:114:ASN:H	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:211:PRO:HA	1:B:249:GLU:HB3	1.95	0.48
1:D:53:ARG:HD3	1:D:63:PHE:CZ	2.49	0.48
1:D:106:ILE:HG13	1:D:122:TYR:CZ	2.49	0.48
1:E:28:PHE:CE1	1:E:111:ASP:C	2.87	0.48
1:E:68:ARG:HG2	1:E:69:THR:H	1.78	0.48
1:F:204:ASP:C	1:F:205:ARG:HE	2.17	0.48
1:G:215:SER:HA	1:G:218:LEU:HD23	1.96	0.48
1:C:207:PHE:CE2	1:C:247:VAL:CG2	2.95	0.48
1:C:287:ASN:O	1:C:288:VAL:HB	2.14	0.48
1:E:117:ASP:OD1	1:F:52:VAL:O	2.31	0.48
1:E:191:ALA:C	1:E:195:LEU:HD21	2.34	0.48
1:E:234:PRO:C	1:E:236:LYS:H	2.17	0.48
1:E:289:ILE:O	1:E:339:ALA:HB1	2.14	0.48
1:E:289:ILE:HG22	1:E:290:GLY:H	1.79	0.48
1:G:122:TYR:O	1:G:125:GLN:HB3	2.13	0.48
1:G:260:THR:CG2	1:G:269:LYS:HZ1	2.27	0.48
1:C:269:LYS:HD2	1:C:289:ILE:N	2.29	0.48
1:D:287:ASN:HB3	1:D:341:VAL:HG12	1.96	0.48
1:G:49:ARG:O	1:G:50:HIS:ND1	2.47	0.48
1:G:151:LYS:NZ	1:G:160:GLY:O	2.35	0.48
1:B:67:GLY:HA3	1:B:68:ARG:CZ	2.44	0.47
1:C:329:HIS:CG	1:C:330:GLY:N	2.83	0.47
1:D:40:PHE:CD1	1:D:131:ALA:HB2	2.49	0.47
1:E:32:PHE:C	1:E:32:PHE:CD1	2.87	0.47
1:E:80:LEU:HD22	1:E:82:ASP:H	1.79	0.47
1:A:73:TYR:HB2	1:F:100:LEU:HD22	1.95	0.47
1:C:100:LEU:HA	1:D:73:TYR:HB3	1.95	0.47
1:D:84:ARG:NH1	1:D:84:ARG:HB3	2.29	0.47
1:D:106:ILE:HG13	1:D:122:TYR:CE2	2.49	0.47
1:D:128:GLU:CD	1:D:129:SER:CA	2.81	0.47
1:E:60:SER:HA	1:E:95:THR:CA	2.40	0.47
1:E:284:ALA:N	1:E:288:VAL:HG21	2.29	0.47
1:F:25:LEU:O	1:F:28:PHE:CD1	2.67	0.47
1:G:38:THR:OG1	1:G:39:ALA:N	2.47	0.47
1:E:46:THR:C	1:E:48:SER:H	2.17	0.47
1:E:222:MET:SD	1:E:222:MET:N	2.87	0.47
1:F:27:LEU:HD12	1:F:28:PHE:N	2.28	0.47
1:F:290:GLY:HA3	1:F:340:VAL:H	1.79	0.47
1:A:162:ALA:O	1:A:163:THR:OG1	2.32	0.47
1:E:96:ILE:HD13	1:E:327:MET:O	2.14	0.47
1:E:189:THR:HG23	1:E:243:MET:HG3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:291:LEU:HA	1:F:338:GLY:O	2.14	0.47
1:B:66:LEU:CD1	1:B:66:LEU:N	2.73	0.47
1:B:67:GLY:C	1:B:68:ARG:HD2	2.35	0.47
1:B:251:PRO:HG2	1:C:199:TYR:HE1	1.61	0.47
1:C:165:ILE:HA	1:C:165:ILE:HD12	1.60	0.47
1:D:55:ILE:HG23	1:D:303:LEU:HD23	1.96	0.47
1:D:288:VAL:HG21	1:D:340:VAL:O	2.15	0.47
1:A:65:VAL:HB	1:A:90:THR:HB	1.95	0.47
1:A:309:GLU:O	1:A:322:ILE:CB	2.59	0.47
1:A:310:ARG:HA	1:A:321:ILE:HA	1.97	0.47
1:C:32:PHE:O	1:C:33:GLY:C	2.51	0.47
1:C:251:PRO:O	1:C:252:HIS:ND1	2.48	0.47
1:D:103:ASP:CG	1:D:323:ALA:H	2.18	0.47
1:E:53:ARG:HD3	1:E:63:PHE:CE1	2.50	0.47
1:E:101:THR:N	1:F:72:ALA:HB1	2.29	0.47
1:E:288:VAL:HA	1:E:341:VAL:HG12	1.96	0.47
1:B:24:LYS:HE2	1:B:25:LEU:CB	2.44	0.47
1:B:207:PHE:HE1	1:B:290:GLY:HA2	1.79	0.47
1:B:251:PRO:CB	1:C:199:TYR:CE2	2.66	0.47
1:C:25:LEU:C	1:C:29:LEU:HD11	2.35	0.47
1:C:26:ALA:CA	1:C:29:LEU:HD11	2.25	0.47
1:C:27:LEU:HA	1:C:30:LYS:HD2	1.96	0.47
1:E:204:ASP:OD2	1:E:204:ASP:N	2.48	0.47
1:F:129:SER:O	1:F:132:MET:N	2.48	0.47
1:G:188:LEU:HD23	1:G:245:PHE:CD1	2.50	0.47
1:A:23:ASP:O	1:A:26:ALA:HB3	2.14	0.47
1:B:70:GLN:HA	1:B:70:GLN:HE21	1.78	0.47
1:B:117:ASP:OD1	1:C:53:ARG:CA	2.56	0.47
1:B:176:ASP:OD1	1:B:178:VAL:N	2.47	0.47
1:C:141:GLU:HG3	1:C:329:HIS:CE1	2.49	0.47
1:E:110:GLU:HG3	1:E:118:VAL:HG21	1.83	0.47
1:E:325:TYR:HA	1:E:327:MET:CE	2.45	0.47
1:F:128:GLU:OE2	1:F:129:SER:N	2.47	0.47
1:F:136:GLY:HA2	1:F:139:LEU:HB2	1.97	0.47
1:G:113:MET:HE1	1:G:115:HIS:HB3	1.93	0.47
1:A:174:LEU:HD13	1:A:183:GLU:HG2	1.97	0.47
1:A:289:ILE:CG2	1:A:290:GLY:H	2.28	0.47
1:B:297:ALA:O	1:B:332:LEU:HD13	2.15	0.47
1:D:165:ILE:HD12	1:D:165:ILE:HA	1.77	0.47
1:A:205:ARG:CZ	1:A:293:MET:HG2	2.45	0.47
1:B:332:LEU:HD13	1:B:333:ARG:H	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:218:LEU:HA	1:D:221:LEU:HB3	1.97	0.47
1:E:117:ASP:CG	1:F:53:ARG:HA	2.23	0.47
1:E:207:PHE:CZ	1:E:209:CYS:HB2	2.49	0.47
1:G:205:ARG:HD2	1:G:294:HIS:HA	1.97	0.47
1:A:33:GLY:CA	1:A:36:VAL:HG23	2.45	0.46
1:A:207:PHE:CD1	1:A:291:LEU:O	2.68	0.46
1:B:37:LEU:O	1:B:40:PHE:HB3	2.16	0.46
1:B:59:LYS:O	1:B:96:ILE:HG12	2.15	0.46
1:C:34:GLY:O	1:C:38:THR:OG1	2.30	0.46
1:D:25:LEU:O	1:D:28:PHE:HD2	1.98	0.46
1:D:288:VAL:HG23	1:D:290:GLY:H	1.80	0.46
1:E:35:GLU:H	1:E:35:GLU:HG2	1.39	0.46
1:F:65:VAL:HG23	1:F:333:ARG:NH1	2.30	0.46
1:A:136:GLY:HA3	1:A:255:ALA:HB3	1.97	0.46
1:B:212:ASP:C	1:B:214:TYR:H	2.19	0.46
1:C:177:GLN:HE21	1:C:215:SER:HG	1.57	0.46
1:D:314:ALA:HA	1:D:318:ALA:H	1.80	0.46
1:F:160:GLY:HA2	1:F:198:ASN:HD21	1.80	0.46
1:G:28:PHE:CD1	1:G:29:LEU:N	2.83	0.46
1:A:115:HIS:HD2	1:A:115:HIS:N	1.93	0.46
1:A:142:ILE:O	1:A:145:LEU:HB2	2.15	0.46
1:C:27:LEU:HD23	1:C:28:PHE:HA	1.97	0.46
1:D:27:LEU:CD1	1:D:28:PHE:N	2.74	0.46
1:D:208:TYR:HD1	1:D:293:MET:HE2	1.80	0.46
1:D:214:TYR:OH	1:D:239:ILE:HG12	2.15	0.46
1:D:294:HIS:CE1	1:D:295:ARG:O	2.68	0.46
1:E:240:ARG:HH11	1:E:240:ARG:HA	1.80	0.46
1:G:66:LEU:HB2	1:G:67:GLY:H	1.52	0.46
1:G:104:VAL:HG21	1:G:122:TYR:CE1	2.50	0.46
1:G:211:PRO:O	1:G:214:TYR:HB2	2.15	0.46
1:G:248:VAL:HG12	1:G:249:GLU:H	1.81	0.46
1:G:272:PHE:O	1:G:274:ALA:N	2.44	0.46
1:G:294:HIS:CE1	1:G:297:ALA:HB2	2.50	0.46
1:A:136:GLY:HA2	1:A:139:LEU:HB3	1.97	0.46
1:B:50:HIS:CE1	1:B:298:VAL:HB	2.51	0.46
1:B:62:GLN:OE1	1:B:62:GLN:N	2.48	0.46
1:C:111:ASP:OD2	1:C:112:ALA:N	2.48	0.46
1:D:314:ALA:H	1:D:318:ALA:H	1.62	0.46
1:G:109:ILE:CD1	1:G:109:ILE:N	2.30	0.46
1:G:110:GLU:HG2	1:G:118:VAL:HG11	1.95	0.46
1:A:209:CYS:SG	1:A:290:GLY:HA3	2.56	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:136:GLY:O	1:C:139:LEU:HB3	2.15	0.46
1:E:232:ILE:HG12	1:E:233:ASP:N	2.31	0.46
1:G:108:ASP:OD2	1:G:109:ILE:HA	2.15	0.46
1:G:141:GLU:CA	1:G:270:HIS:CE1	2.96	0.46
1:B:81:ASP:H	1:B:83:LYS:HE2	1.78	0.46
1:B:114:ASN:O	1:B:118:VAL:CB	2.61	0.46
1:B:165:ILE:HG21	1:B:190:LYS:HD3	1.98	0.46
1:B:301:VAL:HG22	1:B:302:LYS:H	1.79	0.46
1:C:278:GLU:OE1	1:C:287:ASN:ND2	2.41	0.46
1:F:121:GLU:O	1:F:124:SER:OG	2.26	0.46
1:G:106:ILE:HG12	1:G:107:TYR:H	1.81	0.46
1:B:132:MET:C	1:B:135:ASP:OD2	2.53	0.46
1:D:46:THR:H	1:D:135:ASP:CG	2.19	0.46
1:E:28:PHE:CE2	1:E:111:ASP:OD2	2.40	0.46
1:F:210:ASP:HA	1:F:250:VAL:HG22	1.98	0.46
1:A:207:PHE:CE2	1:A:247:VAL:CG2	2.88	0.46
1:E:192:ARG:O	1:E:195:LEU:HG	2.15	0.46
1:E:232:ILE:O	1:E:233:ASP:HB2	2.16	0.46
1:G:96:ILE:H	1:G:96:ILE:HG13	1.47	0.46
1:B:141:GLU:CD	1:B:330:GLY:C	2.72	0.46
1:B:291:LEU:H	1:B:339:ALA:HA	1.81	0.46
1:D:109:ILE:HG13	1:D:110:GLU:H	1.80	0.46
1:E:298:VAL:HA	1:E:331:GLY:O	2.15	0.46
1:C:109:ILE:HD13	1:C:110:GLU:CA	2.46	0.46
1:D:36:VAL:C	1:D:38:THR:N	2.67	0.46
1:D:209:CYS:O	1:D:249:GLU:HA	2.15	0.46
1:A:36:VAL:HG13	1:A:126:LEU:HD11	1.98	0.45
1:B:141:GLU:OE1	1:B:329:HIS:C	2.54	0.45
1:B:294:HIS:NE2	1:B:295:ARG:O	2.49	0.45
1:C:40:PHE:CE1	1:C:131:ALA:HB2	2.51	0.45
1:E:176:ASP:OD2	1:E:179:ALA:N	2.47	0.45
1:F:91:GLU:OE1	1:F:91:GLU:N	2.49	0.45
1:F:209:CYS:O	1:F:250:VAL:N	2.28	0.45
1:G:235:GLU:HG2	1:G:237:GLY:H	1.81	0.45
1:A:302:LYS:CE	1:A:327:MET:HE3	2.45	0.45
1:C:105:LEU:HD21	1:D:84:ARG:CZ	2.47	0.45
1:D:137:ALA:O	1:D:141:GLU:HG2	2.16	0.45
1:E:31:VAL:O	1:E:35:GLU:CD	2.55	0.45
1:E:308:LEU:HB3	1:E:323:ALA:HA	1.97	0.45
1:F:83:LYS:HA	1:F:83:LYS:HD2	1.76	0.45
1:G:285:LYS:HD2	1:G:286:ASP:N	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:29:LEU:CD1	1:D:30:LYS:H	2.17	0.45
1:D:239:ILE:HB	1:D:247:VAL:HB	1.98	0.45
1:D:250:VAL:HB	1:D:251:PRO:HD3	1.98	0.45
1:E:192:ARG:HB2	1:E:195:LEU:HD11	1.95	0.45
1:F:66:LEU:HB3	1:F:67:GLY:H	1.49	0.45
1:B:132:MET:CE	1:B:135:ASP:CG	2.84	0.45
1:B:341:VAL:HG23	1:B:342:PHE:H	1.81	0.45
1:C:107:TYR:HA	1:C:318:ALA:CB	2.43	0.45
1:D:138:VAL:HG23	1:D:139:LEU:N	2.32	0.45
1:F:231:LEU:HB3	1:F:233:ASP:OD2	2.17	0.45
1:G:53:ARG:NH1	1:G:62:GLN:H	2.14	0.45
1:G:141:GLU:CB	1:G:270:HIS:HE1	2.27	0.45
1:G:272:PHE:HE1	1:G:285:LYS:HB2	1.81	0.45
1:A:27:LEU:CD1	1:A:28:PHE:HA	2.47	0.45
1:A:231:LEU:HD13	1:A:231:LEU:HA	1.84	0.45
1:B:255:ALA:HB3	1:B:272:PHE:CE2	2.51	0.45
1:D:169:GLN:NE2	1:D:170:ASN:O	2.50	0.45
1:G:32:PHE:HA	1:G:35:GLU:OE2	2.15	0.45
1:B:250:VAL:HG23	1:B:251:PRO:O	2.16	0.45
1:C:29:LEU:C	1:C:32:PHE:HB3	2.33	0.45
1:C:70:GLN:OE1	1:C:71:ALA:N	2.49	0.45
1:E:28:PHE:CD2	1:E:111:ASP:CG	2.49	0.45
1:F:25:LEU:HD12	1:F:25:LEU:N	2.31	0.45
1:F:240:ARG:NE	1:F:241:ASN:OD1	2.46	0.45
1:A:113:MET:O	1:A:114:ASN:CB	2.65	0.45
1:A:142:ILE:O	1:A:145:LEU:N	2.50	0.45
1:C:35:GLU:C	1:C:38:THR:OG1	2.55	0.45
1:C:293:MET:SD	1:C:294:HIS:N	2.90	0.45
1:E:88:LYS:HB2	1:E:88:LYS:HE3	1.75	0.45
1:B:59:LYS:HE3	1:B:59:LYS:HB3	1.82	0.45
1:B:66:LEU:H	1:B:66:LEU:HD13	1.81	0.45
1:C:290:GLY:O	1:C:339:ALA:HA	2.16	0.45
1:D:288:VAL:HB	1:D:289:ILE:H	1.61	0.45
1:E:82:ASP:O	1:E:85:LYS:N	2.43	0.45
1:G:62:GLN:HB3	1:G:93:VAL:HG13	1.99	0.45
1:G:217:ILE:O	1:G:221:LEU:N	2.26	0.45
1:G:270:HIS:NE2	1:G:329:HIS:HE1	2.15	0.45
1:G:301:VAL:HG12	1:G:302:LYS:H	1.82	0.45
1:B:313:ARG:O	1:B:317:GLN:N	2.50	0.45
1:C:252:HIS:HB2	1:C:253:LEU:H	1.55	0.45
1:D:40:PHE:CE1	1:D:131:ALA:CB	2.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:50:HIS:NE2	1:E:298:VAL:O	2.48	0.45
1:A:35:GLU:O	1:A:38:THR:OG1	2.32	0.45
1:A:251:PRO:HB2	1:A:252:HIS:CD2	2.52	0.45
1:B:117:ASP:OD2	1:C:51:MET:SD	2.74	0.45
1:C:222:MET:HA	1:C:224:ASN:HD21	1.82	0.45
1:D:126:LEU:O	1:D:129:SER:OG	2.28	0.45
1:E:32:PHE:O	1:E:32:PHE:CD1	2.62	0.45
1:E:108:ASP:OD1	1:E:109:ILE:HA	2.17	0.45
1:A:227:ASN:OD1	1:A:227:ASN:N	2.48	0.44
1:B:257:GLY:N	1:B:272:PHE:HB3	2.32	0.44
1:B:285:LYS:HE3	1:B:286:ASP:H	1.82	0.44
1:C:62:GLN:HB2	1:C:91:GLU:HB2	1.99	0.44
1:D:233:ASP:OD1	1:D:240:ARG:N	2.49	0.44
1:F:45:VAL:HG23	1:F:46:THR:HG22	1.97	0.44
1:F:167:THR:HB	1:F:169:GLN:O	2.17	0.44
1:B:27:LEU:O	1:B:30:LYS:N	2.49	0.44
1:B:56:SER:OG	1:B:304:ARG:NH2	2.49	0.44
1:B:86:ASP:O	1:B:155:ASN:ND2	2.48	0.44
1:B:199:TYR:O	1:B:200:VAL:HG22	2.18	0.44
1:D:196:THR:O	1:D:198:ASN:N	2.51	0.44
1:E:103:ASP:CG	1:E:323:ALA:H	2.17	0.44
1:E:305:ASP:OD2	1:E:306:LEU:N	2.44	0.44
1:F:294:HIS:NE2	1:F:295:ARG:O	2.50	0.44
1:C:110:GLU:CG	1:C:122:TYR:HE2	2.29	0.44
1:C:117:ASP:O	1:C:117:ASP:OD1	2.36	0.44
1:D:40:PHE:CE1	1:D:131:ALA:HB2	2.52	0.44
1:E:31:VAL:O	1:E:35:GLU:OE2	2.36	0.44
1:G:60:SER:OG	1:G:61:ALA:N	2.51	0.44
1:A:36:VAL:HG11	1:A:126:LEU:HD11	1.98	0.44
1:B:44:SER:OG	1:B:46:THR:N	2.36	0.44
1:C:231:LEU:HB2	1:C:234:PRO:CG	2.47	0.44
1:C:306:LEU:HB3	1:C:325:TYR:CZ	2.52	0.44
1:E:119:ARG:CB	1:E:119:ARG:CZ	2.95	0.44
1:E:198:ASN:O	1:E:198:ASN:ND2	2.51	0.44
1:F:84:ARG:HH11	1:F:84:ARG:C	2.20	0.44
1:F:128:GLU:O	1:F:132:MET:HB2	2.17	0.44
1:G:151:LYS:HG2	1:G:152:TYR:H	1.82	0.44
1:G:170:ASN:OD1	1:G:171:LYS:N	2.51	0.44
1:G:241:ASN:ND2	1:G:244:GLY:O	2.47	0.44
1:B:305:ASP:OD2	1:B:305:ASP:N	2.49	0.44
1:C:288:VAL:N	1:C:341:VAL:HG12	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:84:ARG:HB3	1:E:84:ARG:NH1	2.33	0.44
1:E:207:PHE:HB2	1:E:292:PHE:HB3	1.99	0.44
1:G:49:ARG:NH2	1:G:248:VAL:HG21	2.31	0.44
1:C:24:LYS:HB2	1:C:24:LYS:HE3	1.46	0.44
1:E:108:ASP:OD1	1:E:108:ASP:O	2.35	0.44
1:G:274:ALA:HA	1:G:284:ALA:HB1	2.00	0.44
1:A:102:ALA:HB2	1:B:71:ALA:CA	2.46	0.44
1:B:95:THR:OG1	1:B:96:ILE:N	2.51	0.44
1:C:251:PRO:C	1:C:252:HIS:CG	2.91	0.44
1:D:25:LEU:O	1:D:28:PHE:CD2	2.70	0.44
1:D:46:THR:O	1:D:46:THR:OG1	2.35	0.44
1:A:66:LEU:HD22	1:F:125:GLN:HG2	2.00	0.44
1:A:160:GLY:N	1:A:334:PRO:HG2	2.33	0.44
1:B:171:LYS:HE3	1:B:171:LYS:HB3	1.79	0.44
1:B:188:LEU:H	1:B:188:LEU:HG	1.38	0.44
1:C:120:SER:O	1:C:124:SER:HB3	2.18	0.44
1:E:100:LEU:HD21	1:F:73:TYR:CE1	2.53	0.44
1:F:136:GLY:HA3	1:F:255:ALA:HB3	1.99	0.44
1:G:265:THR:O	1:G:266:THR:HG23	2.18	0.44
1:B:176:ASP:OD2	1:B:179:ALA:HB2	2.18	0.44
1:E:239:ILE:HG22	1:E:240:ARG:N	2.33	0.44
1:G:110:GLU:CA	1:G:114:ASN:HB2	2.44	0.44
1:G:116:TYR:HB3	1:G:117:ASP:H	1.29	0.44
1:G:132:MET:CG	1:G:133:ALA:N	2.81	0.44
1:A:45:VAL:HG12	1:A:46:THR:HG23	2.00	0.43
1:D:239:ILE:HD13	1:D:239:ILE:HA	1.85	0.43
1:F:31:VAL:O	1:F:32:PHE:C	2.55	0.43
1:F:101:THR:OG1	1:F:325:TYR:N	2.38	0.43
1:A:67:GLY:O	1:F:125:GLN:NE2	2.51	0.43
1:B:145:LEU:HD13	1:B:145:LEU:HA	1.76	0.43
1:C:68:ARG:H	1:C:68:ARG:HG3	1.65	0.43
1:C:110:GLU:HB2	1:C:118:VAL:CG2	2.49	0.43
1:C:115:HIS:O	1:C:115:HIS:HD2	2.00	0.43
1:C:125:GLN:HE22	1:D:68:ARG:HG3	1.82	0.43
1:D:25:LEU:O	1:D:25:LEU:CD1	2.49	0.43
1:D:290:GLY:CA	1:D:340:VAL:HG12	2.47	0.43
1:G:47:THR:OG1	1:G:48:SER:N	2.51	0.43
1:A:193:ALA:O	1:A:196:THR:OG1	2.30	0.43
1:B:24:LYS:HE2	1:B:25:LEU:HB2	2.00	0.43
1:C:40:PHE:CD1	1:C:131:ALA:HB2	2.52	0.43
1:C:113:MET:SD	1:C:113:MET:C	2.95	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:119:ARG:CZ	1:C:119:ARG:HB2	2.49	0.43
1:F:142:ILE:HD12	1:F:142:ILE:HA	1.73	0.43
1:F:240:ARG:NH1	1:F:240:ARG:HA	2.33	0.43
1:A:167:THR:HG21	1:A:183:GLU:HB3	2.01	0.43
1:A:245:PHE:HB2	1:A:246:GLU:H	1.52	0.43
1:B:50:HIS:CG	1:B:51:MET:N	2.86	0.43
1:C:119:ARG:CZ	1:C:119:ARG:CB	2.96	0.43
1:C:162:ALA:CB	1:C:337:ALA:C	2.86	0.43
1:C:202:ALA:HB1	1:C:205:ARG:CZ	2.46	0.43
1:D:122:TYR:HE1	1:E:64:PRO:HG3	1.84	0.43
1:E:329:HIS:HE1	1:F:73:TYR:OH	2.01	0.43
1:A:160:GLY:HA2	1:A:336:ALA:HA	2.01	0.43
1:B:153:ASN:OD1	1:B:153:ASN:N	2.51	0.43
1:B:183:GLU:H	1:B:183:GLU:CD	2.21	0.43
1:D:63:PHE:HA	1:D:64:PRO:HD2	1.76	0.43
1:E:181:GLY:H	1:E:184:ILE:HG12	1.83	0.43
1:E:212:ASP:O	1:E:214:TYR:N	2.50	0.43
1:F:132:MET:HA	1:F:135:ASP:OD1	2.19	0.43
1:A:276:LYS:NZ	1:A:278:GLU:H	2.16	0.43
1:B:130:LEU:HD12	1:B:131:ALA:CA	2.48	0.43
1:C:135:ASP:OD1	1:C:136:GLY:N	2.50	0.43
1:C:206:VAL:HG21	1:C:248:VAL:CG2	2.21	0.43
1:C:297:ALA:O	1:C:298:VAL:CG1	2.66	0.43
1:D:325:TYR:HD1	1:D:325:TYR:HA	1.69	0.43
1:E:31:VAL:O	1:E:35:GLU:HG2	2.18	0.43
1:F:28:PHE:CG	1:F:29:LEU:N	2.84	0.43
1:F:143:ALA:HB3	1:F:272:PHE:CE2	2.52	0.43
1:F:179:ALA:HA	1:F:182:LYS:HZ1	1.83	0.43
1:G:110:GLU:HG2	1:G:118:VAL:CG1	2.48	0.43
1:G:167:THR:C	1:G:169:GLN:N	2.71	0.43
1:A:107:TYR:HA	1:A:318:ALA:HB1	2.01	0.43
1:A:302:LYS:CG	1:A:327:MET:CB	2.76	0.43
1:B:57:SER:O	1:B:57:SER:OG	2.35	0.43
1:B:335:GLU:O	1:B:336:ALA:C	2.57	0.43
1:C:313:ARG:O	1:C:317:GLN:HB3	2.18	0.43
1:D:241:ASN:HB2	1:D:244:GLY:O	2.19	0.43
1:F:32:PHE:HB3	1:F:33:GLY:H	1.69	0.43
1:G:270:HIS:O	1:G:271:VAL:C	2.48	0.43
1:A:185:ILE:O	1:A:188:LEU:N	2.51	0.43
1:B:40:PHE:HB2	1:B:130:LEU:HD23	1.63	0.43
1:C:28:PHE:HD2	1:C:29:LEU:CA	2.30	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:321:ILE:H	1:C:321:ILE:HG13	1.59	0.43
1:C:329:HIS:CG	1:C:330:GLY:H	2.36	0.43
1:D:104:VAL:H	1:D:321:ILE:HD12	1.83	0.43
1:E:301:VAL:HG22	1:E:302:LYS:H	1.84	0.43
1:G:250:VAL:HG22	1:G:252:HIS:O	2.18	0.43
1:A:55:ILE:CG2	1:A:301:VAL:HG21	2.31	0.43
1:C:288:VAL:H	1:C:341:VAL:HG12	1.84	0.43
1:D:185:ILE:O	1:D:188:LEU:N	2.51	0.43
1:E:192:ARG:CA	1:E:195:LEU:HG	2.47	0.43
1:F:28:PHE:C	1:F:28:PHE:HD1	2.16	0.43
1:F:211:PRO:HA	1:F:214:TYR:HB3	2.00	0.43
1:G:252:HIS:CE1	1:G:255:ALA:HB3	2.54	0.43
1:C:107:TYR:HD2	1:C:107:TYR:H	1.58	0.43
1:E:253:LEU:O	1:E:285:LYS:NZ	2.41	0.43
1:F:298:VAL:HG12	1:F:331:GLY:HA2	2.01	0.43
1:G:132:MET:HE2	1:G:132:MET:CA	2.49	0.43
1:A:305:ASP:C	1:A:325:TYR:CE1	2.91	0.42
1:B:110:GLU:HG2	1:C:53:ARG:HH22	1.84	0.42
1:B:176:ASP:OD1	1:B:177:GLN:N	2.52	0.42
1:C:227:ASN:OD1	1:C:227:ASN:N	2.46	0.42
1:E:145:LEU:HB3	1:E:332:LEU:CD2	2.40	0.42
1:F:62:GLN:HB3	1:F:93:VAL:HG12	2.01	0.42
1:G:23:ASP:HB3	1:G:26:ALA:HB3	2.01	0.42
1:G:185:ILE:O	1:G:189:THR:HG23	2.18	0.42
1:G:195:LEU:HD11	1:G:205:ARG:HG3	2.01	0.42
1:D:83:LYS:H	1:D:83:LYS:NZ	2.17	0.42
1:E:192:ARG:HA	1:E:195:LEU:HD21	2.01	0.42
1:F:183:GLU:OE1	1:F:184:ILE:HG13	2.19	0.42
1:G:207:PHE:CE2	1:G:247:VAL:HG22	2.54	0.42
1:B:80:LEU:H	1:B:80:LEU:HD12	1.84	0.42
1:B:334:PRO:HB3	1:B:335:GLU:O	2.19	0.42
1:E:126:LEU:O	1:E:129:SER:OG	2.31	0.42
1:F:55:ILE:HD12	1:F:55:ILE:HA	1.77	0.42
1:G:115:HIS:HA	1:G:119:ARG:HH12	1.85	0.42
1:G:270:HIS:NE2	1:G:329:HIS:CE1	2.87	0.42
1:G:294:HIS:NE2	1:G:297:ALA:HB2	2.34	0.42
1:A:92:LYS:HA	1:A:92:LYS:HD2	1.68	0.42
1:A:101:THR:HG21	1:A:323:ALA:O	2.20	0.42
1:A:115:HIS:HB2	1:A:119:ARG:HG3	2.01	0.42
1:B:114:ASN:HB2	1:B:118:VAL:HB	1.99	0.42
1:E:103:ASP:CB	1:E:322:ILE:HA	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:163:THR:HB	1:E:338:GLY:HA2	2.01	0.42
1:E:166:GLU:HA	1:E:340:VAL:HG23	2.02	0.42
1:E:207:PHE:HA	1:E:292:PHE:HA	2.00	0.42
1:E:239:ILE:HG22	1:E:240:ARG:H	1.83	0.42
1:G:147:ASN:ND2	1:G:273:PRO:CG	2.66	0.42
1:A:287:ASN:CG	1:A:288:VAL:H	2.08	0.42
1:B:202:ALA:HB1	1:B:205:ARG:CZ	2.49	0.42
1:C:27:LEU:CD2	1:C:28:PHE:CA	2.92	0.42
1:E:320:GLN:HE21	1:E:322:ILE:HG23	1.83	0.42
1:F:94:ILE:HA	1:F:94:ILE:HD12	1.67	0.42
1:F:233:ASP:N	1:F:234:PRO:HD3	2.34	0.42
1:G:186:ALA:O	1:G:189:THR:OG1	2.33	0.42
1:G:217:ILE:HA	1:G:220:ALA:HB3	2.02	0.42
1:A:106:ILE:HG22	1:A:122:TYR:HE2	1.73	0.42
1:A:274:ALA:CB	1:A:285:LYS:HD2	2.49	0.42
1:B:218:LEU:HD23	1:B:228:TYR:CD1	2.54	0.42
1:B:222:MET:H	1:B:222:MET:HG3	1.76	0.42
1:C:29:LEU:O	1:C:32:PHE:CA	2.67	0.42
1:C:167:THR:OG1	1:C:168:THR:N	2.52	0.42
1:C:332:LEU:HB3	1:C:333:ARG:H	1.42	0.42
1:D:166:GLU:HB3	1:D:167:THR:HG22	2.01	0.42
1:G:130:LEU:HD23	1:G:131:ALA:HA	2.01	0.42
1:B:139:LEU:CA	1:B:142:ILE:HG23	2.49	0.42
1:C:32:PHE:CZ	1:C:126:LEU:CD2	3.02	0.42
1:D:27:LEU:HD12	1:D:28:PHE:CA	2.49	0.42
1:E:58:GLY:C	1:E:59:LYS:HD2	2.40	0.42
1:E:202:ALA:HB1	1:E:205:ARG:NH1	2.34	0.42
1:G:130:LEU:CD2	1:G:131:ALA:HA	2.50	0.42
1:C:280:ASN:O	1:C:280:ASN:ND2	2.52	0.42
1:C:299:GLY:C	1:C:330:GLY:HA2	2.40	0.42
1:D:43:THR:HG21	1:D:128:GLU:HA	2.02	0.42
1:E:48:SER:OG	1:E:49:ARG:N	2.52	0.42
1:F:29:LEU:O	1:F:32:PHE:CB	2.67	0.42
1:F:80:LEU:H	1:F:80:LEU:HG	1.46	0.42
1:F:275:ASN:OD1	1:F:275:ASN:N	2.52	0.42
1:A:161:THR:N	1:A:336:ALA:HA	2.31	0.42
1:A:206:VAL:HG12	1:A:246:GLU:HB3	2.02	0.42
1:C:115:HIS:O	1:C:118:VAL:HG12	2.20	0.42
1:C:171:LYS:H	1:C:171:LYS:CE	2.31	0.42
1:D:46:THR:OG1	1:D:135:ASP:OD1	2.36	0.42
1:D:171:LYS:HE3	1:D:171:LYS:HB2	1.90	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:285:LYS:HD3	1:D:286:ASP:H	1.85	0.42
1:E:53:ARG:HD3	1:E:63:PHE:HD1	1.83	0.42
1:E:298:VAL:HG12	1:E:332:LEU:CB	2.50	0.42
1:C:37:LEU:HD12	1:C:37:LEU:HA	1.77	0.42
1:D:95:THR:OG1	1:D:96:ILE:HG12	2.20	0.42
1:D:142:ILE:HG22	1:D:143:ALA:N	2.35	0.42
1:E:298:VAL:C	1:E:333:ARG:NH2	2.72	0.42
1:F:276:LYS:NZ	1:F:278:GLU:H	2.17	0.42
1:G:32:PHE:CE1	1:G:36:VAL:HG21	2.55	0.42
1:G:106:ILE:CD1	1:G:107:TYR:O	2.67	0.42
1:G:313:ARG:N	1:G:318:ALA:O	2.42	0.42
1:B:125:GLN:HG2	1:C:66:LEU:HB2	1.56	0.41
1:C:49:ARG:O	1:C:50:HIS:HB3	2.20	0.41
1:D:135:ASP:C	1:D:139:LEU:CD2	2.86	0.41
1:E:168:THR:HG22	1:E:183:GLU:HB2	2.02	0.41
1:F:233:ASP:OD2	1:F:233:ASP:N	2.49	0.41
1:F:257:GLY:HA3	1:F:271:VAL:HB	2.01	0.41
1:A:122:TYR:HD1	1:A:122:TYR:HA	1.65	0.41
1:A:272:PHE:O	1:A:274:ALA:N	2.53	0.41
1:C:177:GLN:NE2	1:C:215:SER:OG	2.27	0.41
1:D:142:ILE:HD13	1:D:145:LEU:HD23	1.71	0.41
1:D:282:LYS:H	1:D:282:LYS:NZ	2.18	0.41
1:E:292:PHE:O	1:E:337:ALA:N	2.53	0.41
1:F:81:ASP:OD2	1:F:81:ASP:N	2.51	0.41
1:F:82:ASP:HA	1:F:85:LYS:HB2	2.01	0.41
1:F:123:THR:OG1	1:F:124:SER:N	2.53	0.41
1:F:240:ARG:NE	1:F:241:ASN:H	2.19	0.41
1:A:42:ARG:HB3	1:A:42:ARG:NH2	2.35	0.41
1:A:108:ASP:HB3	1:A:111:ASP:H	1.85	0.41
1:A:215:SER:OG	1:A:218:LEU:HD13	2.20	0.41
1:A:218:LEU:HD12	1:A:221:LEU:HD12	2.02	0.41
1:B:125:GLN:OE1	1:B:125:GLN:HA	2.20	0.41
1:B:161:THR:CG2	1:B:335:GLU:H	2.32	0.41
1:C:161:THR:OG1	1:C:161:THR:O	2.37	0.41
1:D:105:LEU:HA	1:D:320:GLN:CB	2.50	0.41
1:D:128:GLU:OE2	1:D:129:SER:N	2.52	0.41
1:D:175:THR:OG1	1:D:176:ASP:N	2.52	0.41
1:D:188:LEU:HA	1:D:191:ALA:HB3	2.02	0.41
1:F:88:LYS:HG3	1:F:90:THR:H	1.84	0.41
1:F:182:LYS:O	1:F:185:ILE:N	2.53	0.41
1:F:205:ARG:CG	1:F:245:PHE:HA	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:287:ASN:HB3	1:F:288:VAL:HG22	2.01	0.41
1:G:51:MET:N	1:G:299:GLY:HA3	2.36	0.41
1:G:188:LEU:HB3	1:G:245:PHE:CE1	2.55	0.41
1:A:63:PHE:N	1:A:92:LYS:O	2.49	0.41
1:B:228:TYR:O	1:B:232:ILE:HG12	2.19	0.41
1:C:33:GLY:O	1:C:36:VAL:CG2	2.64	0.41
1:C:60:SER:OG	1:C:94:ILE:O	2.27	0.41
1:C:242:VAL:HG23	1:C:243:MET:O	2.21	0.41
1:C:308:LEU:HD23	1:C:308:LEU:H	1.85	0.41
1:D:53:ARG:HD3	1:D:63:PHE:HZ	1.84	0.41
1:F:128:GLU:OE2	1:F:128:GLU:N	2.53	0.41
1:F:273:PRO:HG3	1:F:281:VAL:HG21	2.01	0.41
1:G:115:HIS:CG	1:G:119:ARG:NH2	2.86	0.41
1:A:36:VAL:O	1:A:38:THR:N	2.54	0.41
1:A:126:LEU:O	1:A:130:LEU:HG	2.20	0.41
1:A:207:PHE:HD1	1:A:291:LEU:N	2.18	0.41
1:B:92:LYS:HZ1	1:B:333:ARG:CZ	2.33	0.41
1:B:181:GLY:O	1:B:185:ILE:N	2.48	0.41
1:C:104:VAL:H	1:C:321:ILE:HD11	1.86	0.41
1:C:209:CYS:HB3	1:C:249:GLU:HB3	2.01	0.41
1:E:301:VAL:HG22	1:E:302:LYS:N	2.36	0.41
1:G:265:THR:O	1:G:266:THR:CB	2.69	0.41
1:B:28:PHE:CE2	1:B:111:ASP:OD1	2.73	0.41
1:B:130:LEU:CD1	1:B:131:ALA:N	2.75	0.41
1:B:130:LEU:CG	1:B:131:ALA:N	2.81	0.41
1:B:141:GLU:OE1	1:B:330:GLY:N	2.41	0.41
1:E:53:ARG:NH1	1:E:62:GLN:H	2.09	0.41
1:E:110:GLU:CG	1:E:118:VAL:CB	2.96	0.41
1:F:117:ASP:O	1:F:118:VAL:HG12	2.21	0.41
1:G:110:GLU:HG2	1:G:114:ASN:ND2	2.35	0.41
1:G:137:ALA:CB	1:G:258:ALA:HB3	2.50	0.41
1:G:312:ARG:HD3	1:G:319:ASP:OD1	2.20	0.41
1:A:30:LYS:HE3	1:A:30:LYS:HB3	1.84	0.41
1:A:41:ALA:C	1:A:43:THR:N	2.72	0.41
1:A:115:HIS:O	1:A:119:ARG:CG	2.69	0.41
1:A:239:ILE:HB	1:A:247:VAL:O	2.21	0.41
1:B:178:VAL:O	1:B:182:LYS:HB2	2.20	0.41
1:C:95:THR:OG1	1:C:96:ILE:N	2.53	0.41
1:D:29:LEU:C	1:D:29:LEU:CD2	2.85	0.41
1:D:231:LEU:O	1:D:234:PRO:HD3	2.21	0.41
1:D:236:LYS:HD3	1:D:236:LYS:HA	1.96	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:286:ASP:OD2	1:D:286:ASP:N	2.54	0.41
1:F:63:PHE:HA	1:F:64:PRO:HD2	1.85	0.41
1:F:143:ALA:HB1	1:F:272:PHE:CD2	2.56	0.41
1:F:310:ARG:HB3	1:F:321:ILE:HA	2.02	0.41
1:A:207:PHE:CD1	1:A:290:GLY:C	2.93	0.41
1:A:215:SER:O	1:A:216:ALA:HB3	2.21	0.41
1:A:232:ILE:HB	1:A:240:ARG:CB	2.51	0.41
1:B:205:ARG:O	1:B:245:PHE:HA	2.20	0.41
1:E:199:TYR:HB3	1:E:200:VAL:H	1.37	0.41
1:G:101:THR:HG23	1:G:323:ALA:O	2.21	0.41
1:G:298:VAL:HB	1:G:299:GLY:H	1.71	0.41
1:A:110:GLU:OE2	1:A:111:ASP:HA	2.19	0.41
1:A:163:THR:O	1:A:164:VAL:HG13	2.21	0.41
1:A:217:ILE:O	1:A:219:ALA:N	2.54	0.41
1:B:75:ALA:C	1:B:77:GLY:H	2.24	0.41
1:B:145:LEU:HD12	1:B:145:LEU:C	2.32	0.41
1:B:227:ASN:O	1:B:229:ALA:N	2.54	0.41
1:C:236:LYS:HB2	1:C:236:LYS:NZ	2.36	0.41
1:C:325:TYR:HD1	1:C:325:TYR:HA	1.75	0.41
1:D:73:TYR:CD2	1:D:73:TYR:N	2.88	0.41
1:D:113:MET:SD	1:D:114:ASN:N	2.94	0.41
1:D:164:VAL:HG12	1:D:339:ALA:N	2.36	0.41
1:E:100:LEU:HG	1:F:72:ALA:O	2.21	0.41
1:E:195:LEU:HG	1:E:195:LEU:H	1.42	0.41
1:E:288:VAL:HG22	1:E:341:VAL:CG1	2.50	0.41
1:E:315:ASN:H	1:E:315:ASN:ND2	2.19	0.41
1:F:25:LEU:O	1:F:28:PHE:CE1	2.74	0.41
1:G:37:LEU:HD12	1:G:40:PHE:CD2	2.56	0.41
1:G:39:ALA:O	1:G:43:THR:OG1	2.38	0.41
1:G:69:THR:H	1:G:70:GLN:NE2	2.19	0.41
1:G:113:MET:CE	1:G:114:ASN:N	2.65	0.41
1:A:29:LEU:H	1:A:29:LEU:HG	1.72	0.41
1:C:43:THR:HG21	1:C:128:GLU:OE2	2.21	0.41
1:C:141:GLU:OE1	1:C:141:GLU:N	2.53	0.41
1:C:146:CYS:SG	1:C:161:THR:N	2.87	0.41
1:C:196:THR:C	1:C:198:ASN:H	2.24	0.41
1:C:299:GLY:N	1:C:330:GLY:O	2.44	0.41
1:D:303:LEU:HB3	1:D:304:ARG:HD3	2.03	0.41
1:E:23:ASP:O	1:E:26:ALA:HB3	2.20	0.41
1:E:73:TYR:O	1:E:74:LEU:HD23	2.21	0.41
1:F:54:SER:OG	1:F:302:LYS:NZ	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:178:VAL:O	1:F:182:LYS:HG3	2.20	0.41
1:G:285:LYS:HD2	1:G:286:ASP:H	1.86	0.41
1:B:27:LEU:CD2	1:B:27:LEU:C	2.90	0.40
1:C:40:PHE:CE1	1:C:131:ALA:CB	3.04	0.40
1:D:209:CYS:CB	1:D:249:GLU:HG2	2.48	0.40
1:G:210:ASP:OD1	1:G:253:LEU:HD11	2.21	0.40
1:A:233:ASP:O	1:A:235:GLU:N	2.55	0.40
1:A:287:ASN:HD21	1:A:341:VAL:HG11	1.83	0.40
1:B:24:LYS:C	1:B:24:LYS:CE	2.74	0.40
1:E:68:ARG:HE	1:E:70:GLN:NE2	2.09	0.40
1:E:126:LEU:HD23	1:E:126:LEU:HA	1.92	0.40
1:G:150:SER:C	1:G:151:LYS:O	2.59	0.40
1:G:205:ARG:HD3	1:G:205:ARG:HA	1.89	0.40
1:G:252:HIS:O	1:G:253:LEU:HD23	2.21	0.40
1:A:114:ASN:H	1:A:115:HIS:HD2	1.54	0.40
1:B:68:ARG:C	1:B:69:THR:OG1	2.56	0.40
1:C:292:PHE:N	1:C:338:GLY:O	2.48	0.40
1:C:315:ASN:CG	1:C:316:PHE:H	2.23	0.40
1:E:126:LEU:HA	1:E:129:SER:OG	2.22	0.40
1:E:166:GLU:CD	1:E:167:THR:H	2.25	0.40
1:F:75:ALA:HA	1:F:76:PRO:HD3	1.95	0.40
1:G:110:GLU:CG	1:G:118:VAL:HG21	2.30	0.40
1:G:271:VAL:O	1:G:271:VAL:HG13	2.21	0.40
1:A:251:PRO:O	1:A:252:HIS:ND1	2.54	0.40
1:C:84:ARG:HH12	1:C:89:HIS:CE1	2.40	0.40
1:C:141:GLU:OE2	1:C:142:ILE:HG12	2.20	0.40
1:C:231:LEU:HD22	1:C:231:LEU:HA	1.90	0.40
1:D:226:ALA:HA	1:D:228:TYR:CD2	2.57	0.40
1:E:61:ALA:O	1:E:94:ILE:N	2.45	0.40
1:E:192:ARG:C	1:E:195:LEU:CG	2.89	0.40
1:A:78:GLU:HB2	1:A:79:ASN:H	1.61	0.40
1:A:169:GLN:HE22	1:A:173:ALA:HB3	1.87	0.40
1:A:295:ARG:NE	1:A:296:SER:H	2.20	0.40
1:B:67:GLY:C	1:B:68:ARG:CD	2.90	0.40
1:C:112:ALA:O	1:C:115:HIS:NE2	2.55	0.40
1:C:276:LYS:HD3	1:C:279:GLY:HA3	2.02	0.40
1:D:70:GLN:HB2	1:D:71:ALA:H	1.70	0.40
1:E:25:LEU:HD12	1:E:26:ALA:CA	2.51	0.40
1:E:233:ASP:OD2	1:E:236:LYS:HG3	2.22	0.40
1:F:60:SER:HB3	1:F:94:ILE:O	2.22	0.40
1:F:303:LEU:H	1:F:326:ALA:HB3	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	294/345 (85%)	224 (76%)	61 (21%)	9 (3%)	4	31
1	B	305/345 (88%)	229 (75%)	67 (22%)	9 (3%)	4	31
1	C	290/345 (84%)	206 (71%)	65 (22%)	19 (7%)	1	18
1	D	292/345 (85%)	213 (73%)	70 (24%)	9 (3%)	4	31
1	E	287/345 (83%)	214 (75%)	65 (23%)	8 (3%)	5	33
1	F	293/345 (85%)	225 (77%)	61 (21%)	7 (2%)	6	36
1	G	313/345 (91%)	240 (77%)	60 (19%)	13 (4%)	3	25
All	All	2074/2415 (86%)	1551 (75%)	449 (22%)	74 (4%)	6	28

All (74) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	178	VAL
1	A	288	VAL
1	B	70	GLN
1	B	114	ASN
1	B	232	ILE
1	B	334	PRO
1	C	42	ARG
1	C	43	THR
1	C	117	ASP
1	C	163	THR
1	C	178	VAL
1	C	300	THR
1	D	37	LEU
1	D	96	ILE
1	D	118	VAL
1	D	145	LEU

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Mol	Chain	Res	Type
1	E	115	HIS
1	E	335	GLU
1	F	32	PHE
1	F	118	VAL
1	G	116	TYR
1	G	150	SER
1	G	151	LYS
1	G	271	VAL
1	B	245	PHE
1	B	286	ASP
1	C	32	PHE
1	C	289	ILE
1	D	341	VAL
1	F	87	ILE
1	F	298	VAL
1	G	85	LYS
1	G	166	GLU
1	G	266	THR
1	B	69	THR
1	C	115	HIS
1	C	162	ALA
1	C	201	PRO
1	E	286	ASP
1	G	115	HIS
1	G	149	GLU
1	G	232	ILE
1	C	116	TYR
1	D	71	ALA
1	E	30	LYS
1	A	36	VAL
1	A	245	PHE
1	C	52	VAL
1	C	288	VAL
1	E	226	ALA
1	E	235	GLU
1	A	298	VAL
1	B	226	ALA
1	C	33	GLY
1	C	169	GLN
1	E	251	PRO
1	F	33	GLY
1	G	55	ILE

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Mol	Chain	Res	Type
1	G	87	ILE
1	A	217	ILE
1	C	232	ILE
1	C	242	VAL
1	D	288	VAL
1	D	298	VAL
1	F	281	VAL
1	A	232	ILE
1	B	55	ILE
1	C	165	ILE
1	D	242	VAL
1	E	341	VAL
1	F	164	VAL
1	A	164	VAL
1	A	165	ILE
1	G	281	VAL

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	230/261 (88%)	168 (73%)	62 (27%)	0 4
1	B	238/261 (91%)	157 (66%)	81 (34%)	0 1
1	C	230/261 (88%)	151 (66%)	79 (34%)	0 1
1	D	230/261 (88%)	160 (70%)	70 (30%)	0 2
1	E	227/261 (87%)	157 (69%)	70 (31%)	0 2
1	F	230/261 (88%)	167 (73%)	63 (27%)	0 3
1	G	242/261 (93%)	163 (67%)	79 (33%)	0 2
All	All	1627/1827 (89%)	1123 (69%)	504 (31%)	1 2

All (504) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	ASP

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Mol	Chain	Res	Type
1	A	24	LYS
1	A	25	LEU
1	A	27	LEU
1	A	28	PHE
1	A	29	LEU
1	A	36	VAL
1	A	42	ARG
1	A	50	HIS
1	A	53	ARG
1	A	66	LEU
1	A	70	GLN
1	A	82	ASP
1	A	84	ARG
1	A	87	ILE
1	A	88	LYS
1	A	101	THR
1	A	104	VAL
1	A	105	LEU
1	A	107	TYR
1	A	109	ILE
1	A	110	GLU
1	A	113	MET
1	A	114	ASN
1	A	115	HIS
1	A	119	ARG
1	A	122	TYR
1	A	128	GLU
1	A	141	GLU
1	A	145	LEU
1	A	163	THR
1	A	164	VAL
1	A	169	GLN
1	A	171	LYS
1	A	174	LEU
1	A	176	ASP
1	A	177	GLN
1	A	180	LEU
1	A	183	GLU
1	A	190	LYS
1	A	205	ARG
1	A	207	PHE
1	A	212	ASP

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Mol	Chain	Res	Type
1	A	232	ILE
1	A	236	LYS
1	A	245	PHE
1	A	249	GLU
1	A	253	LEU
1	A	272	PHE
1	A	280	ASN
1	A	282	LYS
1	A	283	VAL
1	A	285	LYS
1	A	287	ASN
1	A	288	VAL
1	A	298	VAL
1	A	315	ASN
1	A	317	GLN
1	A	325	TYR
1	A	327	MET
1	A	332	LEU
1	A	335	GLU
1	B	24	LYS
1	B	25	LEU
1	B	27	LEU
1	B	30	LYS
1	B	31	VAL
1	B	32	PHE
1	B	35	GLU
1	B	37	LEU
1	B	51	MET
1	B	52	VAL
1	B	59	LYS
1	B	66	LEU
1	B	68	ARG
1	B	70	GLN
1	B	74	LEU
1	B	80	LEU
1	B	83	LYS
1	B	84	ARG
1	B	85	LYS
1	B	92	LYS
1	B	104	VAL
1	B	105	LEU
1	B	107	TYR

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Mol	Chain	Res	Type
1	B	108	ASP
1	B	109	ILE
1	B	110	GLU
1	B	111	ASP
1	B	113	MET
1	B	116	TYR
1	B	118	VAL
1	B	121	GLU
1	B	122	TYR
1	B	123	THR
1	B	124	SER
1	B	126	LEU
1	B	128	GLU
1	B	129	SER
1	B	130	LEU
1	B	132	MET
1	B	135	ASP
1	B	138	VAL
1	B	142	ILE
1	B	145	LEU
1	B	146	CYS
1	B	163	THR
1	B	168	THR
1	B	169	GLN
1	B	171	LYS
1	B	174	LEU
1	B	176	ASP
1	B	188	LEU
1	B	192	ARG
1	B	197	LYS
1	B	200	VAL
1	B	205	ARG
1	B	210	ASP
1	B	217	ILE
1	B	222	MET
1	B	227	ASN
1	B	231	LEU
1	B	232	ILE
1	B	233	ASP
1	B	239	ILE
1	B	243	MET
1	B	247	VAL

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Mol	Chain	Res	Type
1	B	283	VAL
1	B	285	LYS
1	B	286	ASP
1	B	289	ILE
1	B	294	HIS
1	B	298	VAL
1	B	302	LYS
1	B	304	ARG
1	B	305	ASP
1	B	306	LEU
1	B	310	ARG
1	B	313	ARG
1	B	327	MET
1	B	332	LEU
1	B	333	ARG
1	B	343	LYS
1	C	24	LYS
1	C	25	LEU
1	C	27	LEU
1	C	28	PHE
1	C	29	LEU
1	C	31	VAL
1	C	35	GLU
1	C	36	VAL
1	C	38	THR
1	C	42	ARG
1	C	51	MET
1	C	52	VAL
1	C	59	LYS
1	C	62	GLN
1	C	65	VAL
1	C	69	THR
1	C	70	GLN
1	C	73	TYR
1	C	78	GLU
1	C	80	LEU
1	C	84	ARG
1	C	87	ILE
1	C	89	HIS
1	C	90	THR
1	C	91	GLU
1	C	104	VAL

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Mol	Chain	Res	Type
1	C	105	LEU
1	C	107	TYR
1	C	109	ILE
1	C	110	GLU
1	C	113	MET
1	C	114	ASN
1	C	116	TYR
1	C	119	ARG
1	C	120	SER
1	C	126	LEU
1	C	146	CYS
1	C	165	ILE
1	C	167	THR
1	C	169	GLN
1	C	170	ASN
1	C	171	LYS
1	C	176	ASP
1	C	183	GLU
1	C	184	ILE
1	C	190	LYS
1	C	199	TYR
1	C	212	ASP
1	C	214	TYR
1	C	221	LEU
1	C	222	MET
1	C	224	ASN
1	C	231	LEU
1	C	235	GLU
1	C	249	GLU
1	C	250	VAL
1	C	252	HIS
1	C	253	LEU
1	C	271	VAL
1	C	272	PHE
1	C	276	LYS
1	C	282	LYS
1	C	285	LYS
1	C	288	VAL
1	C	289	ILE
1	C	293	MET
1	C	295	ARG
1	C	305	ASP

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Mol	Chain	Res	Type
1	C	306	LEU
1	C	309	GLU
1	C	310	ARG
1	C	316	PHE
1	C	317	GLN
1	C	322	ILE
1	C	325	TYR
1	C	333	ARG
1	C	335	GLU
1	C	340	VAL
1	C	342	PHE
1	D	25	LEU
1	D	27	LEU
1	D	28	PHE
1	D	29	LEU
1	D	30	LYS
1	D	32	PHE
1	D	35	GLU
1	D	36	VAL
1	D	43	THR
1	D	44	SER
1	D	46	THR
1	D	47	THR
1	D	51	MET
1	D	52	VAL
1	D	55	ILE
1	D	59	LYS
1	D	73	TYR
1	D	74	LEU
1	D	81	ASP
1	D	83	LYS
1	D	84	ARG
1	D	85	LYS
1	D	88	LYS
1	D	91	GLU
1	D	92	LYS
1	D	94	ILE
1	D	95	THR
1	D	104	VAL
1	D	105	LEU
1	D	106	ILE
1	D	109	ILE

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Mol	Chain	Res	Type
1	D	110	GLU
1	D	118	VAL
1	D	128	GLU
1	D	130	LEU
1	D	135	ASP
1	D	139	LEU
1	D	142	ILE
1	D	145	LEU
1	D	167	THR
1	D	169	GLN
1	D	176	ASP
1	D	182	LYS
1	D	183	GLU
1	D	200	VAL
1	D	205	ARG
1	D	210	ASP
1	D	218	LEU
1	D	236	LYS
1	D	252	HIS
1	D	253	LEU
1	D	275	ASN
1	D	282	LYS
1	D	285	LYS
1	D	291	LEU
1	D	293	MET
1	D	294	HIS
1	D	300	THR
1	D	304	ARG
1	D	305	ASP
1	D	308	LEU
1	D	309	GLU
1	D	310	ARG
1	D	319	ASP
1	D	320	GLN
1	D	325	TYR
1	D	327	MET
1	D	332	LEU
1	D	335	GLU
1	D	341	VAL
1	E	24	LYS
1	E	25	LEU
1	E	27	LEU

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Mol	Chain	Res	Type
1	E	29	LEU
1	E	32	PHE
1	E	35	GLU
1	E	51	MET
1	E	53	ARG
1	E	59	LYS
1	E	63	PHE
1	E	70	GLN
1	E	78	GLU
1	E	80	LEU
1	E	81	ASP
1	E	82	ASP
1	E	84	ARG
1	E	85	LYS
1	E	89	HIS
1	E	90	THR
1	E	91	GLU
1	E	101	THR
1	E	108	ASP
1	E	109	ILE
1	E	110	GLU
1	E	111	ASP
1	E	118	VAL
1	E	119	ARG
1	E	120	SER
1	E	123	THR
1	E	129	SER
1	E	130	LEU
1	E	132	MET
1	E	135	ASP
1	E	138	VAL
1	E	142	ILE
1	E	147	ASN
1	E	149	GLU
1	E	163	THR
1	E	165	ILE
1	E	166	GLU
1	E	170	ASN
1	E	171	LYS
1	E	174	LEU
1	E	176	ASP
1	E	183	GLU

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Mol	Chain	Res	Type
1	E	188	LEU
1	E	190	LYS
1	E	192	ARG
1	E	195	LEU
1	E	199	TYR
1	E	200	VAL
1	E	205	ARG
1	E	210	ASP
1	E	217	ILE
1	E	222	MET
1	E	235	GLU
1	E	243	MET
1	E	249	GLU
1	E	275	ASN
1	E	276	LYS
1	E	294	HIS
1	E	300	THR
1	E	308	LEU
1	E	310	ARG
1	E	312	ARG
1	E	317	GLN
1	E	327	MET
1	E	335	GLU
1	E	340	VAL
1	E	341	VAL
1	F	24	LYS
1	F	25	LEU
1	F	27	LEU
1	F	28	PHE
1	F	29	LEU
1	F	31	VAL
1	F	32	PHE
1	F	65	VAL
1	F	68	ARG
1	F	73	TYR
1	F	80	LEU
1	F	84	ARG
1	F	87	ILE
1	F	88	LYS
1	F	89	HIS
1	F	100	LEU
1	F	101	THR

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Mol	Chain	Res	Type
1	F	104	VAL
1	F	105	LEU
1	F	108	ASP
1	F	110	GLU
1	F	118	VAL
1	F	121	GLU
1	F	128	GLU
1	F	130	LEU
1	F	139	LEU
1	F	142	ILE
1	F	145	LEU
1	F	147	ASN
1	F	176	ASP
1	F	180	LEU
1	F	183	GLU
1	F	188	LEU
1	F	192	ARG
1	F	200	VAL
1	F	204	ASP
1	F	205	ARG
1	F	210	ASP
1	F	212	ASP
1	F	231	LEU
1	F	240	ARG
1	F	252	HIS
1	F	282	LYS
1	F	283	VAL
1	F	285	LYS
1	F	288	VAL
1	F	291	LEU
1	F	292	PHE
1	F	295	ARG
1	F	298	VAL
1	F	300	THR
1	F	304	ARG
1	F	309	GLU
1	F	310	ARG
1	F	316	PHE
1	F	319	ASP
1	F	320	GLN
1	F	322	ILE
1	F	325	TYR

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Mol	Chain	Res	Type
1	F	332	LEU
1	F	333	ARG
1	F	335	GLU
1	F	341	VAL
1	G	25	LEU
1	G	27	LEU
1	G	28	PHE
1	G	49	ARG
1	G	55	ILE
1	G	59	LYS
1	G	63	PHE
1	G	66	LEU
1	G	68	ARG
1	G	70	GLN
1	G	73	TYR
1	G	74	LEU
1	G	78	GLU
1	G	79	ASN
1	G	83	LYS
1	G	85	LYS
1	G	86	ASP
1	G	96	ILE
1	G	103	ASP
1	G	106	ILE
1	G	107	TYR
1	G	108	ASP
1	G	109	ILE
1	G	113	MET
1	G	116	TYR
1	G	118	VAL
1	G	119	ARG
1	G	120	SER
1	G	122	TYR
1	G	129	SER
1	G	130	LEU
1	G	132	MET
1	G	138	VAL
1	G	139	LEU
1	G	141	GLU
1	G	145	LEU
1	G	149	GLU
1	G	157	GLU

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Mol	Chain	Res	Type
1	G	165	ILE
1	G	169	GLN
1	G	171	LYS
1	G	175	THR
1	G	178	VAL
1	G	183	GLU
1	G	199	TYR
1	G	200	VAL
1	G	207	PHE
1	G	209	CYS
1	G	214	TYR
1	G	224	ASN
1	G	231	LEU
1	G	249	GLU
1	G	262	ARG
1	G	263	GLU
1	G	265	THR
1	G	266	THR
1	G	268	GLN
1	G	269	LYS
1	G	275	ASN
1	G	278	GLU
1	G	285	LYS
1	G	293	MET
1	G	298	VAL
1	G	301	VAL
1	G	303	LEU
1	G	304	ARG
1	G	308	LEU
1	G	309	GLU
1	G	310	ARG
1	G	313	ARG
1	G	320	GLN
1	G	322	ILE
1	G	324	LYS
1	G	325	TYR
1	G	327	MET
1	G	329	HIS
1	G	333	ARG
1	G	340	VAL
1	G	341	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	GLN
1	A	89	HIS
1	A	169	GLN
1	A	287	ASN
1	B	70	GLN
1	B	115	HIS
1	B	287	ASN
1	B	315	ASN
1	C	115	HIS
1	C	169	GLN
1	C	170	ASN
1	C	280	ASN
1	C	329	HIS
1	D	125	GLN
1	D	252	HIS
1	D	294	HIS
1	D	320	GLN
1	E	70	GLN
1	E	115	HIS
1	E	177	GLN
1	E	315	ASN
1	E	320	GLN
1	E	329	HIS
1	F	79	ASN
1	F	169	GLN
1	F	198	ASN
1	F	224	ASN
1	F	317	GLN
1	G	70	GLN
1	G	79	ASN
1	G	114	ASN
1	G	115	HIS
1	G	241	ASN
1	G	329	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

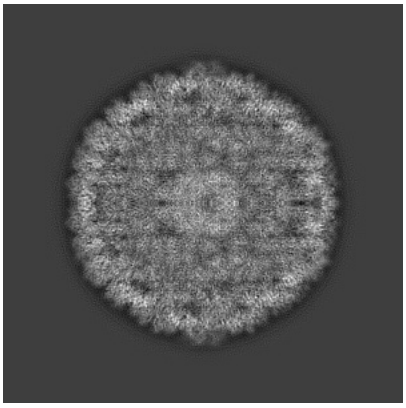
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-6034. These allow visual inspection of the internal detail of the map and identification of artifacts.

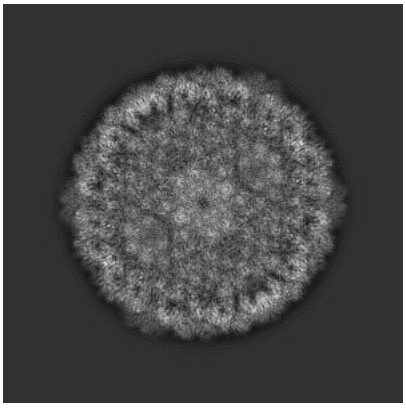
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

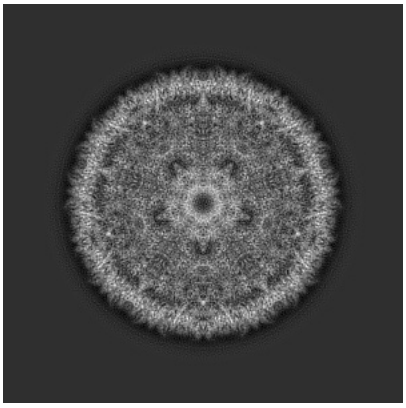
6.1.1 Primary map



X



Y

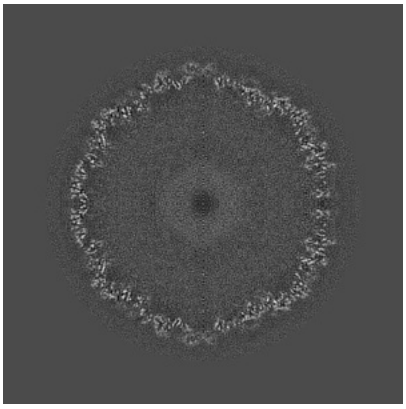


Z

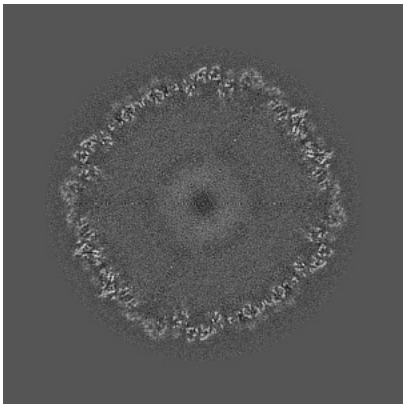
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

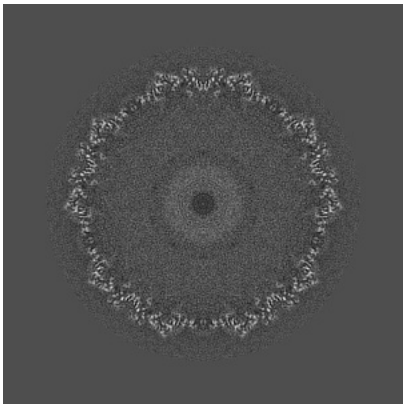
6.2.1 Primary map



X Index: 360



Y Index: 360

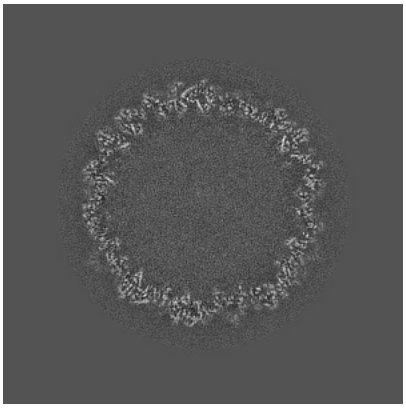


Z Index: 360

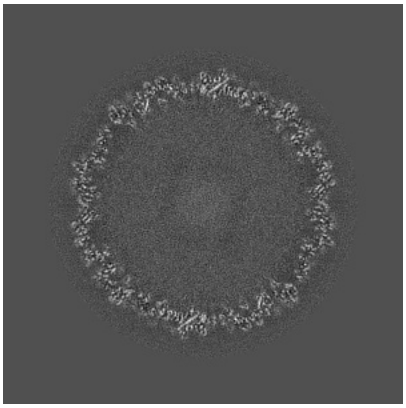
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

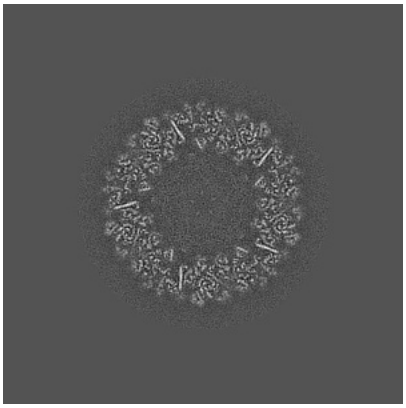
6.3.1 Primary map



X Index: 254



Y Index: 416

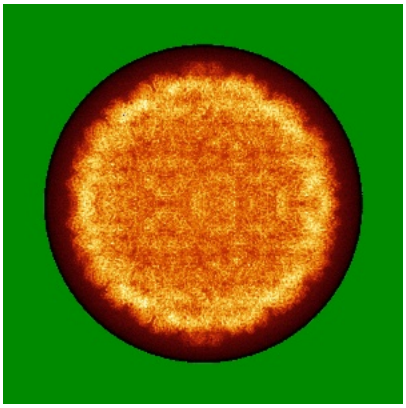


Z Index: 190

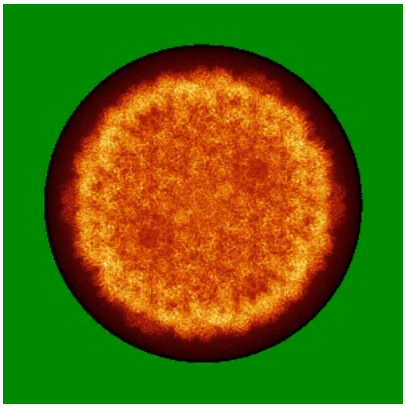
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

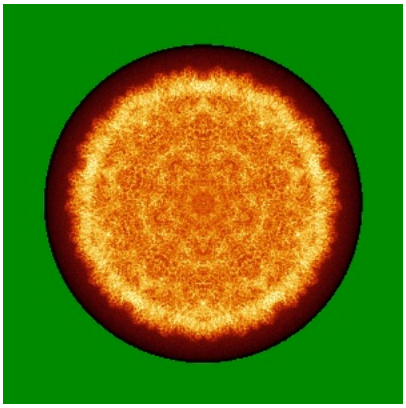
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 4.55. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

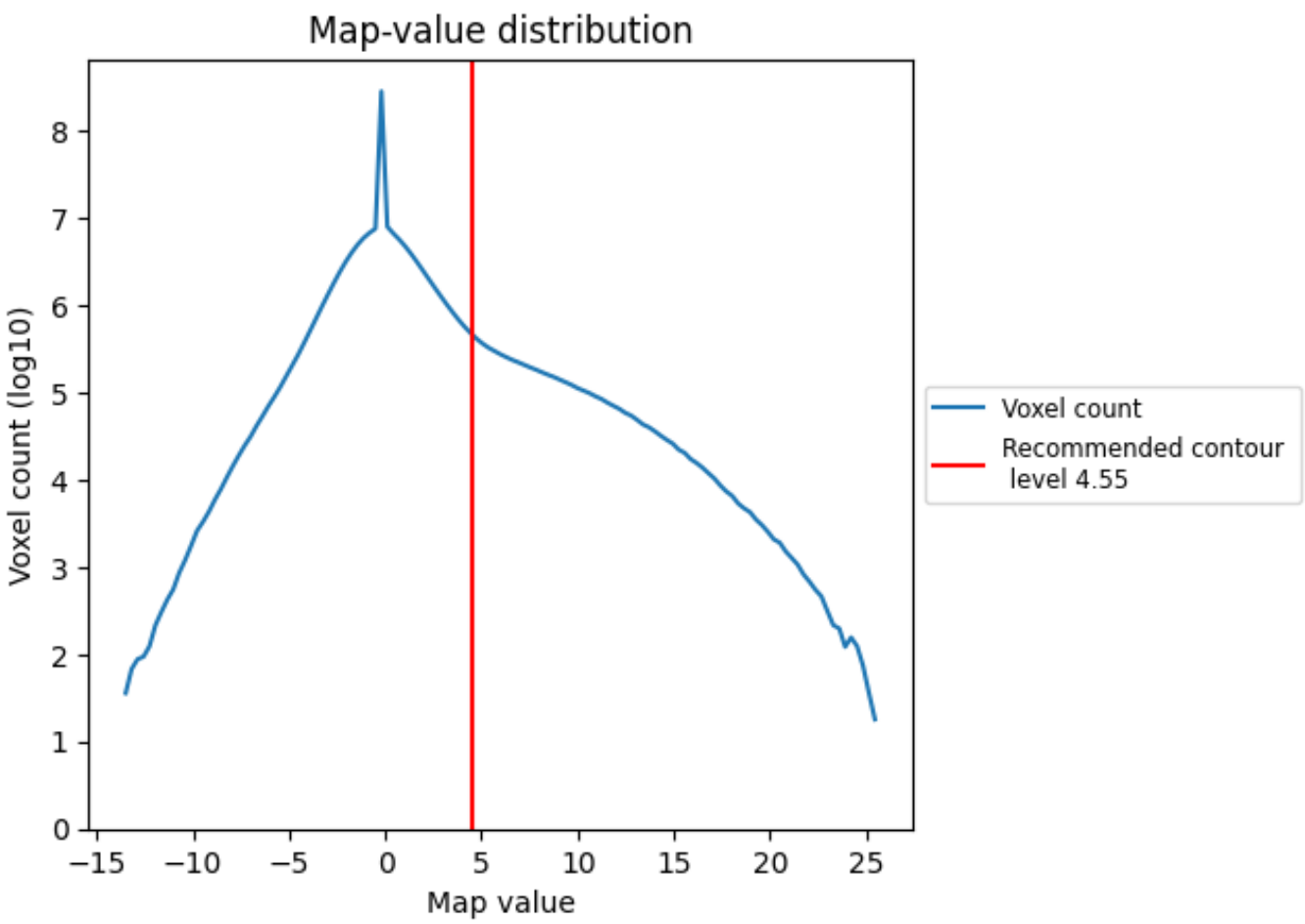
6.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis (i)

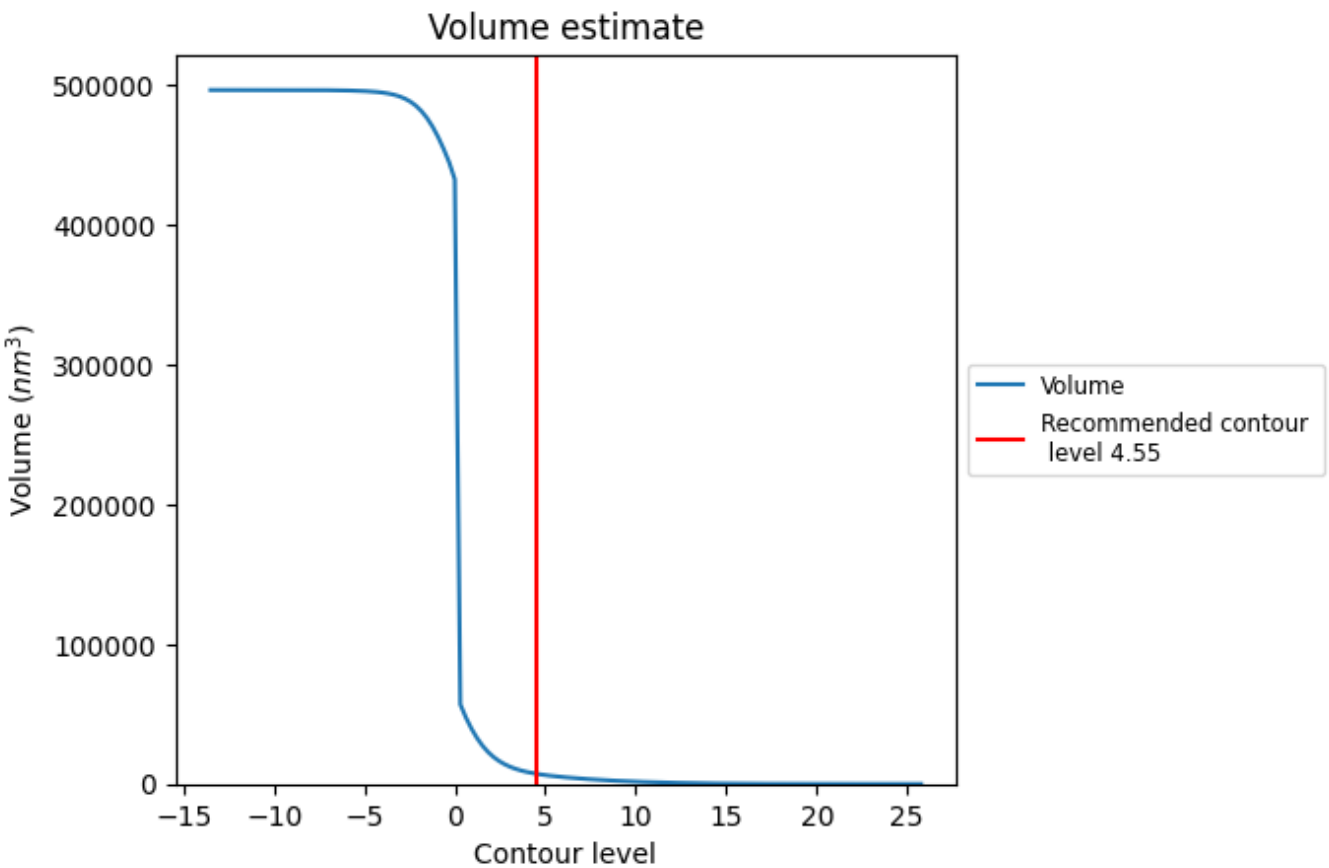
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

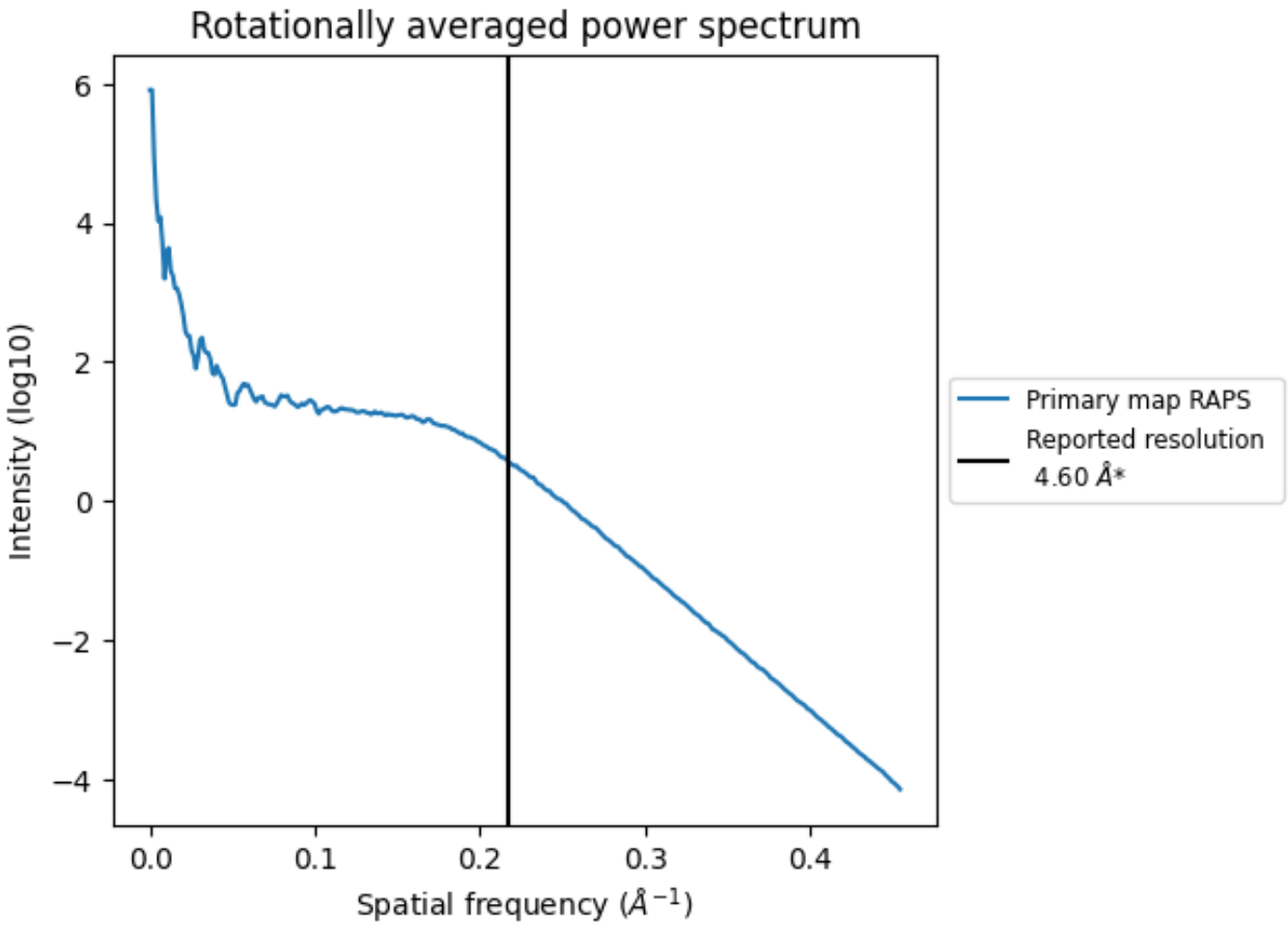
7.2 Volume estimate (i)



The volume at the recommended contour level is 7185 nm^3; this corresponds to an approximate mass of 6490 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.217 Å^{-1}

8 Fourier-Shell correlation (i)

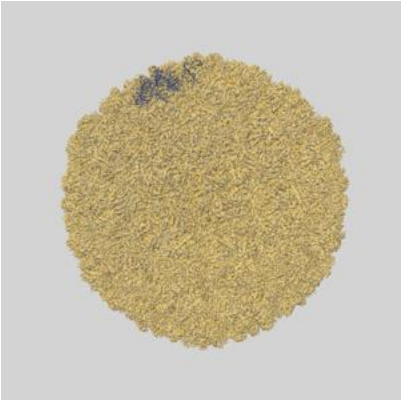
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit (i)

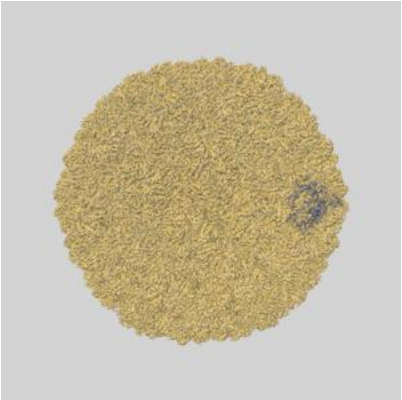
This section contains information regarding the fit between EMDB map EMD-6034 and PDB model 3J7V. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlays

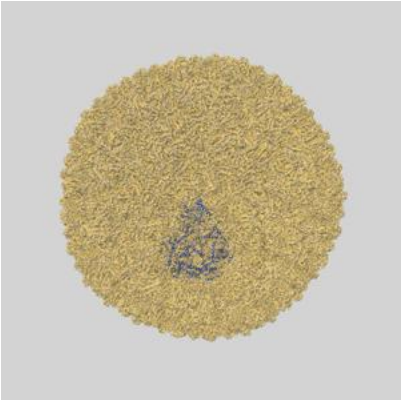
9.1.1 Map-model overlay (i)



X

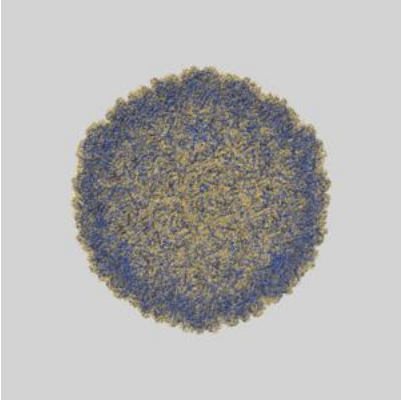


Y

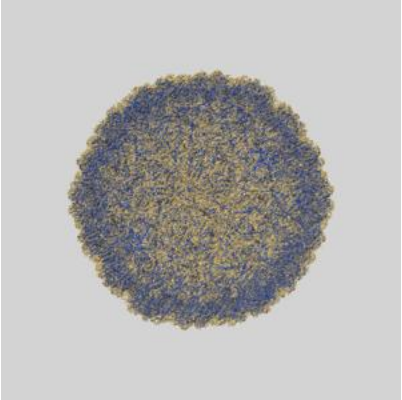


Z

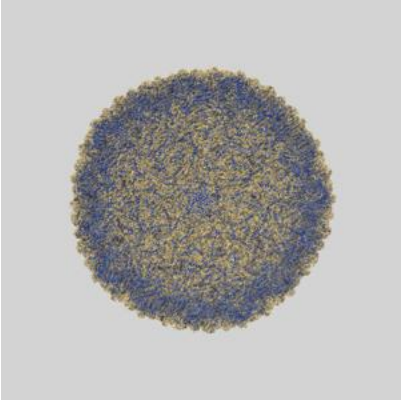
9.1.2 Map-model assembly overlay (i)



X



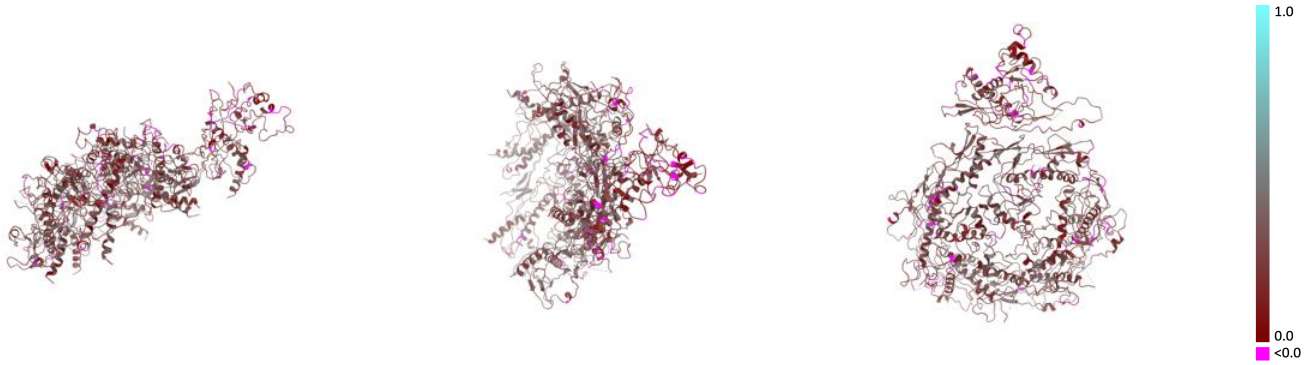
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 4.55 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

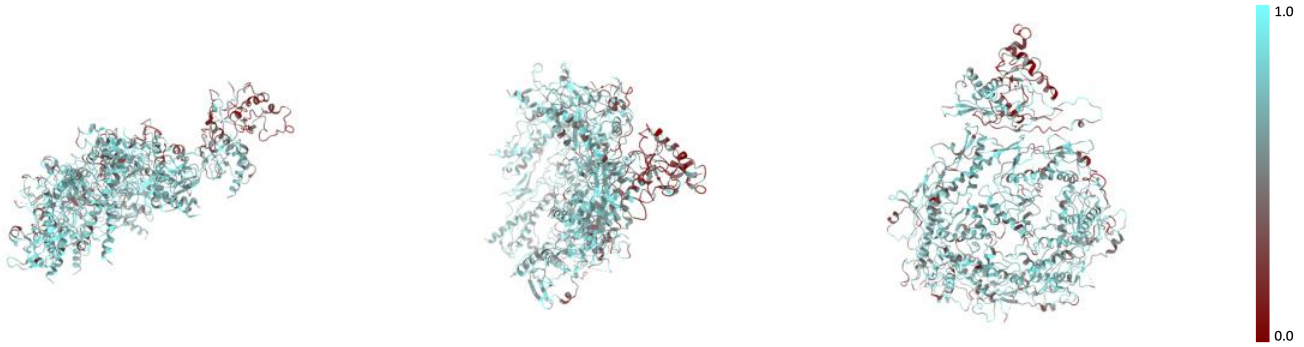
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

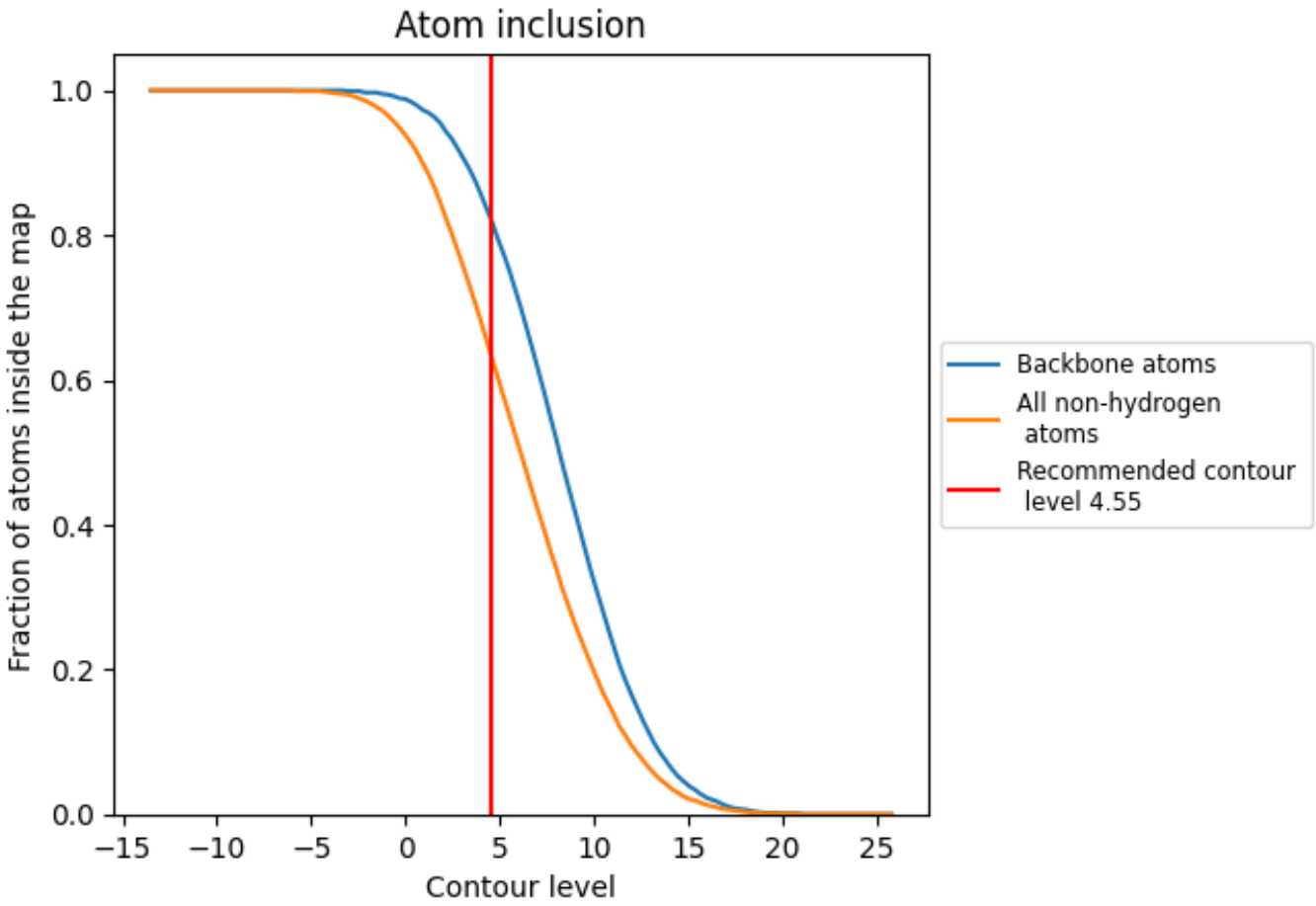
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (4.55).

9.4 Atom inclusion (i)



At the recommended contour level, 82% of all backbone atoms, 63% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (4.55) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6320	0.2740
A	0.6590	0.2830
B	0.6290	0.2740
C	0.6930	0.2960
D	0.6700	0.2970
E	0.6600	0.2910
F	0.6660	0.2880
G	0.4590	0.1960