



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 01:53 PM BST

PDB ID : 3J7W
EMDB ID: : EMD-6035
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 : 3.50 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

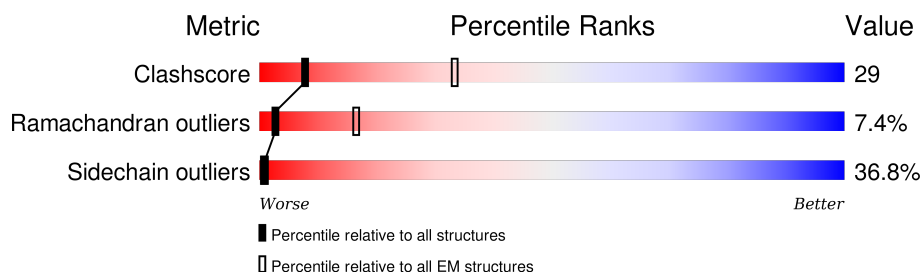
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	345	
1	B	345	
1	C	345	
1	D	345	
1	E	345	
1	F	345	
1	G	345	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 17829 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.

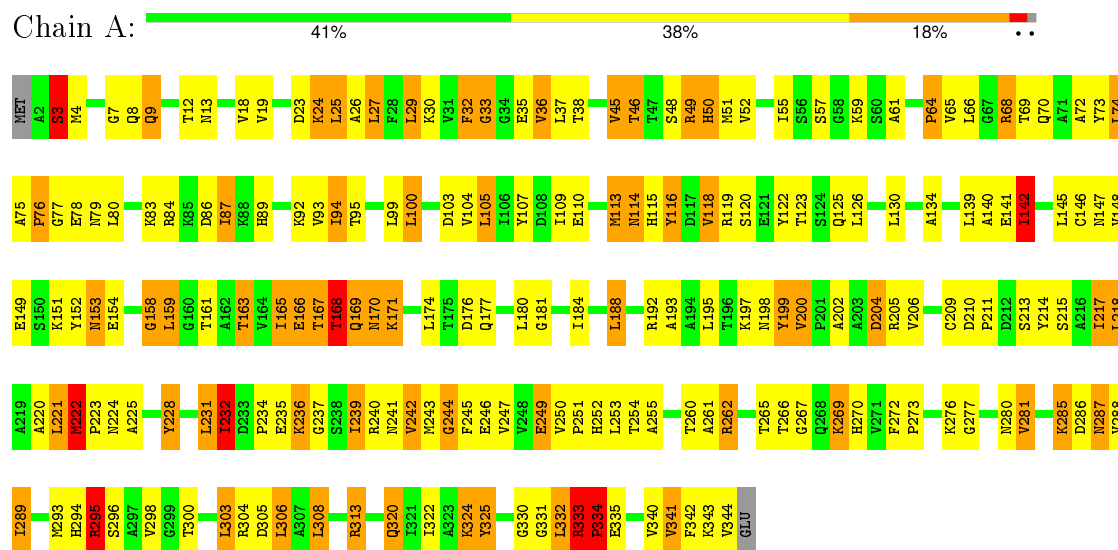
- Molecule 1 is a protein called Major capsid protein 10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	343	Total	C	N	O	S	0	0
			2547	1593	452	491	11		
1	B	343	Total	C	N	O	S	0	0
			2547	1593	452	491	11		
1	C	343	Total	C	N	O	S	0	0
			2547	1593	452	491	11		
1	D	343	Total	C	N	O	S	0	0
			2547	1593	452	491	11		
1	E	343	Total	C	N	O	S	0	0
			2547	1593	452	491	11		
1	F	343	Total	C	N	O	S	0	0
			2547	1593	452	491	11		
1	G	343	Total	C	N	O	S	0	0
			2547	1593	452	491	11		

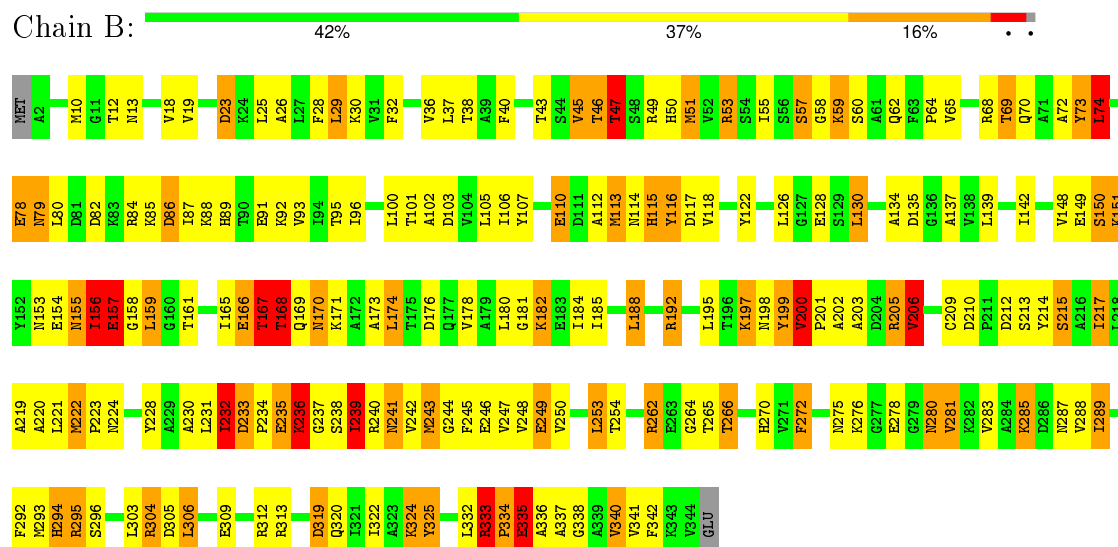
3 Residue-property plots

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

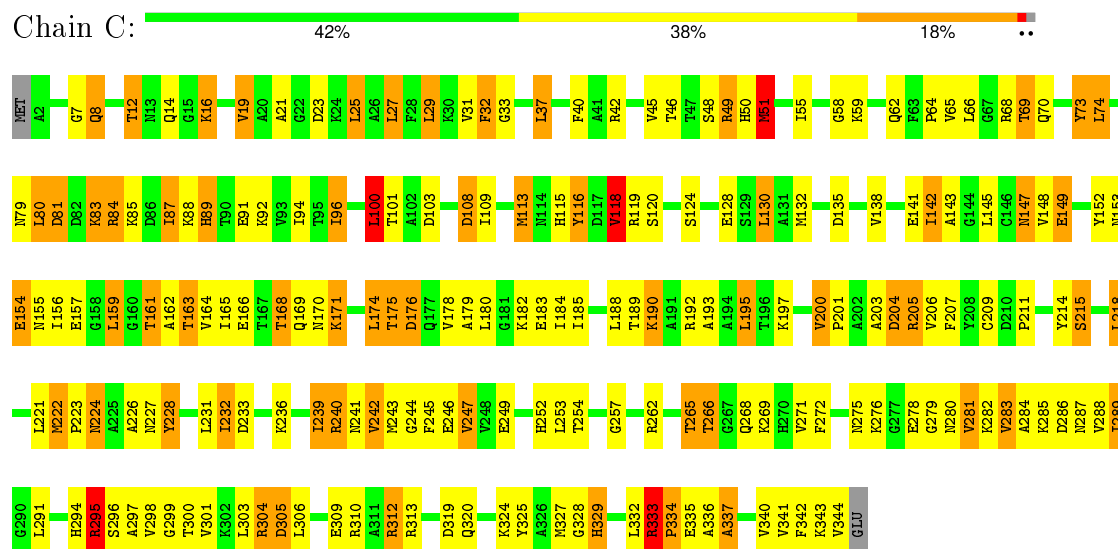
• Molecule 1: Major capsid protein 10A



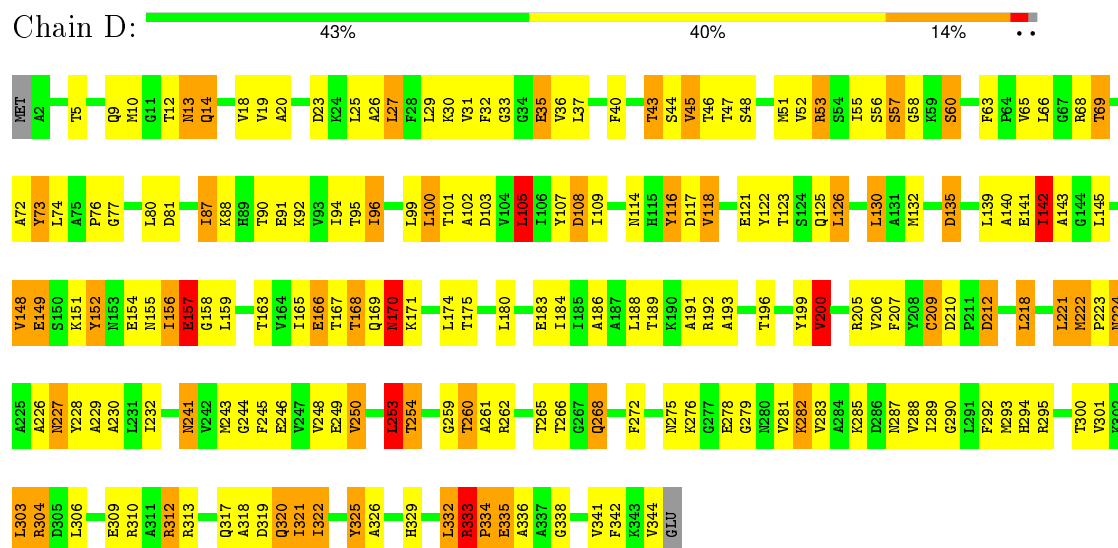
• Molecule 1: Major capsid protein 10A



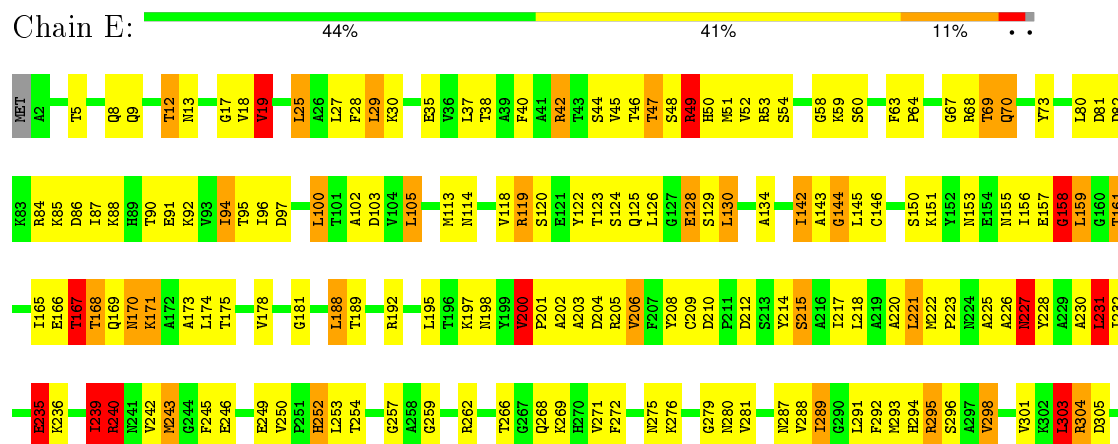
• Molecule 1: Major capsid protein 10A



• Molecule 1: Major capsid protein 10A



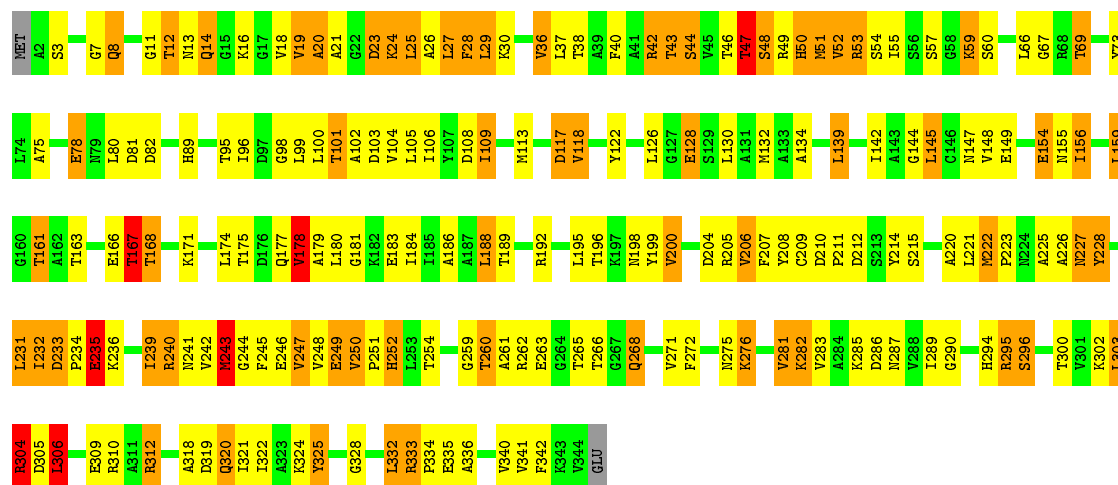
• Molecule 1: Major capsid protein 10A





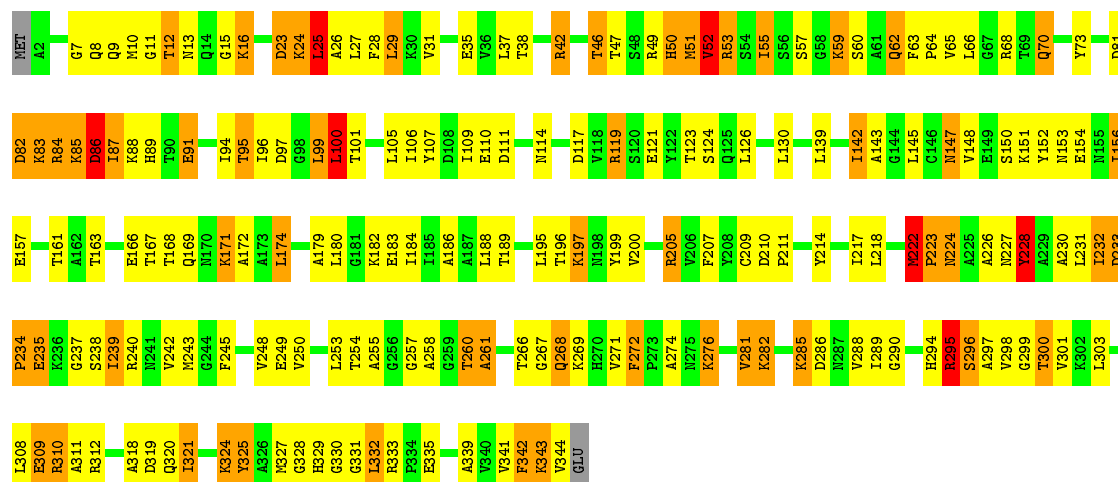
• Molecule 1: Major capsid protein 10A

Chain F: 43% 36% 18% ..



• Molecule 1: Major capsid protein 10A

Chain G: 44% 37% 16% ..



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of images	43417	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3300	Depositor
Magnification	59000	Depositor
Image detector	KODAK SO-163 FILM	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
1	A	0.33	1/2582 (0.0%)	0.69	5/3491 (0.1%)
1	B	0.34	1/2582 (0.0%)	0.66	2/3491 (0.1%)
1	C	0.33	1/2582 (0.0%)	0.66	3/3491 (0.1%)
1	D	0.34	0/2582	0.65	4/3491 (0.1%)
1	E	0.32	0/2582	0.62	3/3491 (0.1%)
1	F	0.31	0/2582	0.65	2/3491 (0.1%)
1	G	0.33	1/2582 (0.0%)	0.68	4/3491 (0.1%)
All	All	0.33	4/18074 (0.0%)	0.66	23/24437 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	334	PRO	N-CD	5.34	1.55	1.47
1	A	334	PRO	N-CD	5.30	1.55	1.47
1	B	334	PRO	N-CD	5.16	1.55	1.47
1	G	223	PRO	N-CD	5.00	1.54	1.47

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	74	LEU	CA-CB-CG	6.88	131.12	115.30
1	D	27	LEU	CA-CB-CG	6.70	130.71	115.30
1	G	333	ARG	NE-CZ-NH1	6.52	123.56	120.30
1	G	100	LEU	CA-CB-CG	6.33	129.87	115.30
1	G	222	MET	C-N-CD	5.95	140.89	128.40
1	F	304	ARG	NE-CZ-NH1	5.90	123.25	120.30
1	D	222	MET	C-N-CD	5.88	140.74	128.40
1	D	253	LEU	CA-CB-CG	5.86	128.77	115.30
1	D	105	LEU	CA-CB-CG	5.79	128.63	115.30
1	A	333	ARG	C-N-CD	5.74	140.46	128.40
1	C	333	ARG	C-N-CD	5.68	140.34	128.40
1	E	303	LEU	CA-CB-CG	5.68	128.37	115.30
1	B	333	ARG	C-N-CD	5.68	140.32	128.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	306	LEU	CA-CB-CG	5.44	127.82	115.30
1	A	303	LEU	CA-CB-CG	5.36	127.62	115.30
1	A	308	LEU	CA-CB-CG	5.32	127.54	115.30
1	C	100	LEU	CA-CB-CG	5.30	127.50	115.30
1	G	25	LEU	CA-CB-CG	5.28	127.45	115.30
1	E	158	GLY	C-N-CA	5.27	134.87	121.70
1	A	27	LEU	CA-CB-CG	5.16	127.17	115.30
1	E	231	LEU	CA-CB-CG	5.15	127.15	115.30
1	C	27	LEU	CA-CB-CG	5.10	127.04	115.30
1	A	158	GLY	N-CA-C	-5.04	100.49	113.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2547	0	2571	189	0
1	B	2547	0	2573	180	0
1	C	2547	0	2573	177	0
1	D	2547	0	2573	134	0
1	E	2547	0	2573	124	0
1	F	2547	0	2573	171	0
1	G	2547	0	2573	183	0
All	All	17829	0	18009	1051	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 29.

All (1051) 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:A:159:LEU:CB	1:A:335:GLU:HG2	1.27	1.63
1:B:74:LEU:HD22	1:B:80:LEU:CD2	1.35	1.53
1:C:159:LEU:CD1	1:C:335:GLU:HA	1.41	1.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:LEU:HB2	1:A:335:GLU:CD	1.33	1.47
1:A:159:LEU:CB	1:A:335:GLU:CG	1.94	1.44
1:A:159:LEU:CD2	1:A:335:GLU:HB3	1.47	1.41
1:C:159:LEU:HD13	1:C:335:GLU:CA	1.52	1.39
1:D:117:ASP:HA	1:D:118:VAL:CB	1.39	1.37
1:D:117:ASP:HA	1:D:118:VAL:CG1	1.57	1.35
1:C:296:SER:N	1:C:297:ALA:HB3	1.37	1.34
1:F:27:LEU:HD12	1:F:28:PHE:N	1.42	1.34
1:B:236:LYS:HA	1:C:243:MET:O	1.25	1.33
1:B:334:PRO:HA	1:B:335:GLU:O	1.27	1.32
1:B:74:LEU:CD2	1:B:80:LEU:HD21	1.62	1.29
1:B:236:LYS:CA	1:C:243:MET:O	1.81	1.29
1:D:117:ASP:CB	1:D:118:VAL:HG12	1.63	1.28
1:F:27:LEU:C	1:F:27:LEU:HD12	1.52	1.28
1:A:159:LEU:HD22	1:A:335:GLU:CB	1.63	1.26
1:G:85:LYS:HA	1:G:85:LYS:CE	1.50	1.25
1:A:159:LEU:HB2	1:A:335:GLU:CG	1.56	1.24
1:B:74:LEU:CD2	1:B:80:LEU:CD2	2.19	1.19
1:F:25:LEU:N	1:F:26:ALA:HB3	1.57	1.17
1:A:159:LEU:HB3	1:A:335:GLU:CG	1.63	1.17
1:C:295:ARG:C	1:C:297:ALA:HB3	1.63	1.17
1:B:40:PHE:CE1	1:C:333:ARG:NH2	2.14	1.14
1:G:85:LYS:HE2	1:G:85:LYS:HA	1.28	1.13
1:A:159:LEU:HB2	1:A:335:GLU:OE2	1.46	1.12
1:B:40:PHE:CZ	1:C:333:ARG:NH2	2.17	1.12
1:D:117:ASP:CA	1:D:118:VAL:HG12	1.79	1.12
1:D:117:ASP:HB2	1:D:118:VAL:HG12	1.31	1.12
1:G:51:MET:O	1:G:52:VAL:HG13	1.49	1.11
1:G:85:LYS:HA	1:G:85:LYS:HE3	1.22	1.11
1:G:298:VAL:HG13	1:G:331:GLY:HA2	1.25	1.10
1:B:74:LEU:HD22	1:B:80:LEU:HD23	1.23	1.10
1:G:51:MET:HG3	1:G:299:GLY:HA3	1.31	1.10
1:G:53:ARG:CG	1:G:53:ARG:HH11	1.64	1.10
1:D:117:ASP:CA	1:D:118:VAL:CB	2.30	1.10
1:G:300:THR:CG2	1:G:329:HIS:ND1	2.14	1.09
1:D:117:ASP:CA	1:D:118:VAL:HB	1.82	1.09
1:G:29:LEU:HD22	1:G:29:LEU:H	0.94	1.09
1:D:117:ASP:CA	1:D:118:VAL:CG1	2.30	1.09
1:D:222:MET:HG3	1:D:223:PRO:HD2	1.24	1.09
1:G:222:MET:HB3	1:G:223:PRO:HD2	1.33	1.08
1:B:45:VAL:HG12	1:B:46:THR:H	1.19	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:27:LEU:CD1	1:F:28:PHE:N	2.17	1.06
1:B:114:ASN:C	1:B:115:HIS:CD2	2.30	1.04
1:G:85:LYS:HE2	1:G:85:LYS:CA	1.86	1.04
1:G:85:LYS:CA	1:G:85:LYS:CE	2.30	1.03
1:A:332:LEU:O	1:A:332:LEU:HD22	1.60	1.02
1:B:45:VAL:HG12	1:B:46:THR:N	1.74	1.01
1:G:168:THR:HG22	1:G:168:THR:O	1.59	1.01
1:D:117:ASP:HA	1:D:118:VAL:HB	1.04	1.00
1:G:29:LEU:CD2	1:G:29:LEU:H	1.74	1.00
1:G:295:ARG:O	1:G:296:SER:OG	1.76	1.00
1:F:24:LYS:HZ3	1:F:24:LYS:HB3	1.27	0.99
1:G:300:THR:HG21	1:G:329:HIS:CE1	1.96	0.99
1:B:74:LEU:HD22	1:B:80:LEU:HD21	1.00	0.98
1:G:51:MET:C	1:G:52:VAL:HG13	1.83	0.98
1:G:222:MET:HB3	1:G:223:PRO:CD	1.93	0.97
1:A:168:THR:HG23	1:A:169:GLN:N	1.79	0.97
1:F:25:LEU:HD13	1:F:25:LEU:O	1.63	0.97
1:F:27:LEU:C	1:F:27:LEU:CD1	2.30	0.97
1:C:296:SER:HA	1:C:298:VAL:H	1.30	0.96
1:A:159:LEU:CB	1:A:335:GLU:CD	2.18	0.96
1:F:25:LEU:HD22	1:F:25:LEU:O	1.63	0.96
1:G:169:GLN:NE2	1:G:174:LEU:HD21	1.79	0.96
1:B:236:LYS:N	1:C:243:MET:O	1.98	0.95
1:G:29:LEU:N	1:G:29:LEU:HD22	1.76	0.95
1:C:296:SER:N	1:C:297:ALA:CB	2.30	0.95
1:F:25:LEU:N	1:F:26:ALA:CB	2.30	0.94
1:F:25:LEU:H	1:F:26:ALA:HB3	1.24	0.94
1:D:229:ALA:HB2	1:E:228:TYR:CZ	2.03	0.93
1:C:295:ARG:C	1:C:297:ALA:CB	2.36	0.93
1:A:146:CYS:SG	1:A:334:PRO:HB3	2.09	0.92
1:G:53:ARG:HG3	1:G:53:ARG:HH11	1.32	0.92
1:B:116:TYR:HD2	1:B:116:TYR:N	1.68	0.92
1:C:159:LEU:HD12	1:C:335:GLU:HA	1.50	0.92
1:C:159:LEU:HD13	1:C:335:GLU:HA	0.91	0.91
1:C:161:THR:HG22	1:C:334:PRO:O	1.70	0.91
1:A:332:LEU:HD13	1:A:332:LEU:H	1.35	0.90
1:B:37:LEU:HB2	1:C:65:VAL:HG12	1.54	0.90
1:A:159:LEU:HD13	1:A:335:GLU:OE1	1.73	0.89
1:A:250:VAL:HG23	1:A:253:LEU:HG	1.53	0.89
1:G:300:THR:HG21	1:G:329:HIS:ND1	1.86	0.89
1:F:249:GLU:HG2	1:F:249:GLU:O	1.69	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:29:LEU:O	1:G:29:LEU:HD23	1.73	0.88
1:D:116:TYR:O	1:D:118:VAL:HB	1.71	0.88
1:G:85:LYS:HE2	1:G:85:LYS:O	1.73	0.88
1:G:51:MET:CG	1:G:299:GLY:HA3	2.03	0.88
1:D:117:ASP:CB	1:D:118:VAL:CG1	2.50	0.87
1:A:254:THR:HG22	1:A:255:ALA:H	1.39	0.86
1:G:298:VAL:CG1	1:G:330:GLY:O	2.23	0.86
1:D:227:ASN:O	1:D:228:TYR:CG	2.30	0.85
1:D:222:MET:HG3	1:D:223:PRO:CD	2.08	0.84
1:D:227:ASN:O	1:D:228:TYR:CD2	2.30	0.84
1:G:297:ALA:O	1:G:332:LEU:O	1.95	0.84
1:B:114:ASN:O	1:B:115:HIS:CG	2.30	0.83
1:B:334:PRO:CA	1:B:335:GLU:O	2.20	0.83
1:B:114:ASN:O	1:B:116:TYR:CE2	2.30	0.83
1:A:159:LEU:CD2	1:A:335:GLU:CB	2.36	0.83
1:F:27:LEU:HD12	1:F:28:PHE:CA	2.06	0.83
1:C:159:LEU:HD13	1:C:335:GLU:CB	2.07	0.83
1:F:24:LYS:NZ	1:F:24:LYS:HB3	1.92	0.83
1:G:298:VAL:HG12	1:G:330:GLY:O	1.80	0.82
1:G:53:ARG:HG2	1:G:53:ARG:HH11	1.42	0.82
1:G:294:HIS:CE1	1:G:296:SER:OG	2.32	0.82
1:G:25:LEU:HB2	1:G:26:ALA:HB2	1.62	0.82
1:G:85:LYS:HE2	1:G:85:LYS:C	1.99	0.82
1:B:206:VAL:HG23	1:B:246:GLU:HB3	1.61	0.81
1:C:159:LEU:CD1	1:C:335:GLU:CA	2.29	0.81
1:A:273:PRO:HG2	1:A:281:VAL:HG11	1.63	0.81
1:B:114:ASN:O	1:B:115:HIS:CD2	2.34	0.80
1:F:249:GLU:O	1:F:249:GLU:CG	2.30	0.80
1:A:332:LEU:HD23	1:A:333:ARG:HG2	1.64	0.80
1:G:168:THR:O	1:G:168:THR:CG2	2.30	0.80
1:B:116:TYR:CD2	1:B:116:TYR:N	2.42	0.79
1:G:230:ALA:HB1	1:G:231:LEU:HD23	1.63	0.79
1:F:24:LYS:O	1:F:25:LEU:CD1	2.30	0.79
1:F:25:LEU:CD1	1:F:25:LEU:O	2.30	0.79
1:F:25:LEU:O	1:F:25:LEU:CD2	2.30	0.79
1:F:208:TYR:CD2	1:F:248:VAL:HG21	2.17	0.79
1:G:51:MET:O	1:G:52:VAL:CG1	2.30	0.79
1:F:25:LEU:CA	1:F:26:ALA:HB3	2.14	0.78
1:G:51:MET:HG3	1:G:299:GLY:CA	2.14	0.78
1:G:171:LYS:HD3	1:G:172:ALA:H	1.48	0.78
1:A:332:LEU:CD2	1:A:333:ARG:HG2	2.14	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:297:ALA:O	1:G:332:LEU:HD22	1.84	0.77
1:A:168:THR:CG2	1:A:169:GLN:N	2.48	0.77
1:G:300:THR:CG2	1:G:329:HIS:CE1	2.63	0.77
1:A:332:LEU:O	1:A:333:ARG:HG3	1.86	0.76
1:B:114:ASN:O	1:B:116:TYR:HE2	1.65	0.76
1:G:51:MET:CG	1:G:299:GLY:CA	2.62	0.76
1:A:159:LEU:HD21	1:A:198:ASN:HB3	1.66	0.76
1:B:45:VAL:HG12	1:B:46:THR:HG22	1.66	0.76
1:G:298:VAL:HG13	1:G:331:GLY:CA	2.13	0.75
1:A:168:THR:HG23	1:A:169:GLN:H	1.46	0.75
1:C:203:ALA:HA	1:C:205:ARG:HD2	1.69	0.75
1:C:159:LEU:HB2	1:C:335:GLU:HG3	1.67	0.75
1:G:294:HIS:ND1	1:G:296:SER:OG	2.19	0.75
1:F:159:LEU:HB3	1:F:335:GLU:HB2	1.68	0.75
1:B:74:LEU:HD11	1:B:78:GLU:O	1.87	0.75
1:B:294:HIS:H	1:B:336:ALA:HB1	1.51	0.75
1:A:221:LEU:O	1:A:222:MET:HB2	1.86	0.75
1:B:159:LEU:HD11	1:B:335:GLU:H	1.51	0.74
1:D:218:LEU:HD23	1:D:232:ILE:HD11	1.67	0.74
1:D:36:VAL:HG12	1:E:64:PRO:HG2	1.68	0.74
1:A:159:LEU:HB3	1:A:335:GLU:HG2	0.74	0.74
1:A:332:LEU:HD13	1:A:332:LEU:N	2.02	0.74
1:G:295:ARG:C	1:G:296:SER:OG	2.24	0.74
1:G:294:HIS:ND1	1:G:295:ARG:O	2.20	0.73
1:G:51:MET:C	1:G:52:VAL:CG1	2.55	0.73
1:A:142:ILE:HB	1:A:298:VAL:HG21	1.70	0.73
1:A:159:LEU:HD13	1:A:335:GLU:CD	2.09	0.73
1:B:46:THR:O	1:B:47:THR:HB	1.88	0.73
1:G:51:MET:CB	1:G:299:GLY:HA2	2.19	0.73
1:D:287:ASN:HB3	1:D:341:VAL:HG13	1.69	0.73
1:C:154:GLU:HB3	1:C:334:PRO:CD	2.18	0.72
1:C:37:LEU:HD21	1:D:332:LEU:HD23	1.71	0.72
1:B:74:LEU:CD2	1:B:80:LEU:HD23	2.07	0.72
1:B:45:VAL:CG1	1:B:46:THR:H	1.93	0.72
1:F:103:ASP:OD1	1:F:262:ARG:NH2	2.23	0.71
1:C:332:LEU:O	1:C:333:ARG:HB3	1.90	0.71
1:A:159:LEU:HD22	1:A:335:GLU:HB3	0.73	0.71
1:B:114:ASN:C	1:B:115:HIS:CG	2.64	0.71
1:F:24:LYS:O	1:F:25:LEU:HD13	1.91	0.71
1:B:45:VAL:HG12	1:B:46:THR:CG2	2.21	0.70
1:C:336:ALA:O	1:C:337:ALA:CB	2.38	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:ILE:HD11	1:A:247:VAL:HB	1.73	0.70
1:G:85:LYS:O	1:G:86:ASP:CG	2.30	0.70
1:D:312:ARG:HG2	1:D:319:ASP:HB3	1.73	0.70
1:A:215:SER:OG	1:B:192:ARG:NH1	2.25	0.70
1:C:184:ILE:HD12	1:C:289:ILE:HG21	1.73	0.70
1:A:73:TYR:HD1	1:F:259:GLY:HA2	1.56	0.69
1:A:146:CYS:SG	1:A:334:PRO:CB	2.81	0.69
1:C:332:LEU:O	1:C:333:ARG:CB	2.41	0.69
1:G:29:LEU:CD2	1:G:29:LEU:N	2.42	0.69
1:F:248:VAL:O	1:F:249:GLU:CD	2.30	0.69
1:G:254:THR:HG23	1:G:272:PHE:HD2	1.55	0.69
1:D:223:PRO:HG3	1:E:230:ALA:CB	2.23	0.69
1:D:159:LEU:HD22	1:D:335:GLU:HG2	1.75	0.69
1:F:42:ARG:NH1	1:F:128:GLU:OE1	2.24	0.69
1:F:47:THR:OG1	1:F:48:SER:N	2.25	0.69
1:C:174:LEU:O	1:C:176:ASP:N	2.26	0.69
1:E:333:ARG:NH1	1:E:335:GLU:OE1	2.25	0.68
1:D:96:ILE:HD13	1:D:303:LEU:HD11	1.76	0.68
1:F:27:LEU:O	1:F:28:PHE:CG	2.46	0.68
1:B:51:MET:HE1	1:B:53:ARG:HD2	1.75	0.68
1:F:24:LYS:O	1:F:25:LEU:HD12	1.93	0.68
1:F:25:LEU:CG	1:F:25:LEU:O	2.42	0.68
1:E:96:ILE:HD11	1:E:303:LEU:HB3	1.75	0.68
1:E:242:VAL:HG12	1:E:243:MET:HG2	1.75	0.68
1:A:204:ASP:OD1	1:A:294:HIS:CD2	2.47	0.67
1:F:312:ARG:HG2	1:F:319:ASP:HB3	1.76	0.67
1:E:17:GLY:O	1:E:19:VAL:N	2.26	0.67
1:B:45:VAL:CG1	1:B:46:THR:N	2.48	0.67
1:A:332:LEU:O	1:A:333:ARG:CG	2.42	0.67
1:C:154:GLU:HB3	1:C:334:PRO:HD3	1.76	0.67
1:A:250:VAL:CG2	1:A:253:LEU:HG	2.23	0.67
1:G:26:ALA:HB1	1:G:28:PHE:H	1.59	0.67
1:E:150:SER:OG	1:E:280:ASN:ND2	2.27	0.67
1:D:226:ALA:C	1:D:227:ASN:OD1	2.33	0.67
1:B:289:ILE:HG12	1:B:340:VAL:O	1.95	0.67
1:E:202:ALA:HA	1:E:205:ARG:HH12	1.60	0.67
1:C:157:GLU:HB2	1:C:159:LEU:HB3	1.77	0.67
1:G:86:ASP:OD2	1:G:86:ASP:C	2.32	0.66
1:G:254:THR:HG22	1:G:255:ALA:H	1.61	0.66
1:D:241:ASN:OD1	1:D:241:ASN:N	2.25	0.66
1:D:51:MET:SD	1:D:53:ARG:NH1	2.68	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:259:GLY:HA2	1:F:73:TYR:HD1	1.59	0.66
1:E:25:LEU:HD22	1:F:59:LYS:HE3	1.77	0.66
1:G:171:LYS:HD3	1:G:172:ALA:N	2.11	0.66
1:C:48:SER:O	1:C:49:ARG:HD2	1.96	0.66
1:E:227:ASN:H	1:F:227:ASN:HD22	1.41	0.66
1:F:59:LYS:HD2	1:F:60:SER:HB2	1.78	0.66
1:B:36:VAL:HG22	1:C:64:PRO:HG2	1.76	0.66
1:B:137:ALA:HB1	1:B:270:HIS:HD2	1.61	0.66
1:A:30:LYS:HG2	1:B:60:SER:HB3	1.77	0.65
1:G:111:ASP:OD1	1:G:119:ARG:NH1	2.28	0.65
1:A:92:LYS:NZ	1:A:333:ARG:H	1.95	0.65
1:A:159:LEU:HD23	1:A:335:GLU:HB3	1.68	0.65
1:G:53:ARG:HG2	1:G:53:ARG:NH1	2.05	0.65
1:G:52:VAL:HG23	1:G:52:VAL:O	1.95	0.65
1:F:50:HIS:HB3	1:F:52:VAL:HG12	1.79	0.65
1:B:115:HIS:CD2	1:B:115:HIS:N	2.64	0.65
1:D:209:CYS:SG	1:D:210:ASP:N	2.69	0.65
1:E:97:ASP:OD2	1:E:269:LYS:NZ	2.28	0.65
1:B:222:MET:CE	1:C:243:MET:CE	2.75	0.65
1:A:35:GLU:OE2	1:B:53:ARG:NH1	2.30	0.65
1:A:87:ILE:HD11	1:F:104:VAL:HG12	1.79	0.65
1:G:166:GLU:OE1	1:G:342:PHE:HB3	1.97	0.64
1:F:276:LYS:HG3	1:F:282:LYS:HA	1.77	0.64
1:F:43:THR:OG1	1:F:44:SER:N	2.30	0.64
1:A:197:LYS:O	1:A:198:ASN:HB2	1.98	0.64
1:F:199:TYR:O	1:F:200:VAL:HB	1.97	0.64
1:B:107:TYR:HB2	1:B:110:GLU:HG2	1.78	0.64
1:D:140:ALA:HA	1:D:272:PHE:HE1	1.63	0.64
1:B:116:TYR:HD2	1:B:116:TYR:H	1.45	0.63
1:E:257:GLY:HA3	1:E:268:GLN:HG2	1.78	0.63
1:E:49:ARG:NH1	1:E:246:GLU:OE2	2.31	0.63
1:B:222:MET:CE	1:C:243:MET:HE2	2.29	0.63
1:G:42:ARG:HD3	1:G:42:ARG:H	1.62	0.63
1:G:169:GLN:HE21	1:G:174:LEU:HD21	1.60	0.63
1:D:310:ARG:HH21	1:D:321:ILE:HD11	1.64	0.63
1:E:259:GLY:HA2	1:F:73:TYR:CD1	2.34	0.63
1:F:304:ARG:HH11	1:F:304:ARG:HG2	1.64	0.63
1:C:161:THR:OG1	1:C:162:ALA:N	2.27	0.62
1:C:296:SER:H	1:C:297:ALA:HB3	1.51	0.62
1:C:286:ASP:OD2	1:C:287:ASN:N	2.32	0.62
1:F:25:LEU:HD13	1:F:25:LEU:C	2.19	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:66:LEU:HB3	1:C:89:HIS:HB3	1.82	0.62
1:D:262:ARG:O	1:E:70:GLN:NE2	2.31	0.62
1:F:53:ARG:HH11	1:F:53:ARG:HB3	1.63	0.62
1:C:232:ILE:HG22	1:C:233:ASP:H	1.64	0.62
1:G:70:GLN:HA	1:G:70:GLN:HE21	1.64	0.62
1:C:296:SER:CA	1:C:298:VAL:H	2.09	0.62
1:A:140:ALA:HA	1:A:272:PHE:HE1	1.65	0.62
1:F:184:ILE:HD12	1:F:289:ILE:HG21	1.82	0.62
1:A:214:TYR:HE1	1:A:239:ILE:HD12	1.65	0.62
1:B:69:THR:OG1	1:B:70:GLN:N	2.31	0.62
1:C:147:ASN:HD21	1:C:163:THR:HG21	1.65	0.62
1:F:161:THR:HG22	1:F:334:PRO:HB2	1.82	0.62
1:A:3:SER:OG	1:A:4:MET:N	2.29	0.61
1:B:334:PRO:HA	1:B:335:GLU:C	2.10	0.61
1:B:59:LYS:HE3	1:B:60:SER:H	1.65	0.61
1:F:243:MET:N	1:F:243:MET:SD	2.73	0.61
1:F:102:ALA:HB1	1:F:126:LEU:HD22	1.81	0.61
1:A:55:ILE:HD13	1:A:61:ALA:HB2	1.82	0.61
1:F:166:GLU:HG3	1:F:167:THR:O	2.01	0.61
1:C:295:ARG:CA	1:C:297:ALA:HB3	2.30	0.61
1:B:156:ILE:HG23	1:B:157:GLU:H	1.66	0.61
1:G:300:THR:HG22	1:G:329:HIS:ND1	2.12	0.61
1:E:69:THR:OG1	1:E:70:GLN:N	2.31	0.61
1:G:166:GLU:OE2	1:G:183:GLU:HB3	2.01	0.61
1:F:105:LEU:HA	1:F:320:GLN:HB2	1.83	0.61
1:E:53:ARG:O	1:E:301:VAL:HA	2.01	0.61
1:A:161:THR:HB	1:A:334:PRO:O	2.01	0.60
1:G:254:THR:HG23	1:G:272:PHE:CD2	2.35	0.60
1:A:204:ASP:OD2	1:A:295:ARG:HG2	2.02	0.60
1:F:287:ASN:HB3	1:F:341:VAL:HG13	1.82	0.60
1:B:37:LEU:HD12	1:C:333:ARG:HH12	1.66	0.60
1:A:107:TYR:HB2	1:A:110:GLU:HG2	1.82	0.60
1:D:169:GLN:O	1:D:170:ASN:ND2	2.21	0.60
1:G:207:PHE:CZ	1:G:290:GLY:HA3	2.37	0.60
1:G:312:ARG:HG2	1:G:319:ASP:HB3	1.84	0.60
1:E:231:LEU:HD23	1:E:232:ILE:HG23	1.82	0.60
1:A:221:LEU:HB3	1:A:232:ILE:HG21	1.84	0.60
1:D:142:ILE:HG23	1:D:143:ALA:H	1.66	0.60
1:G:257:GLY:HA3	1:G:268:GLN:HB3	1.84	0.60
1:C:296:SER:HA	1:C:298:VAL:N	2.09	0.60
1:G:51:MET:HB2	1:G:299:GLY:HA2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:178:VAL:HG12	1:B:182:LYS:HE2	1.84	0.60
1:B:102:ALA:HB1	1:B:126:LEU:HD22	1.83	0.60
1:C:50:HIS:HE1	1:C:298:VAL:C	2.05	0.60
1:E:304:ARG:HA	1:E:304:ARG:HH11	1.66	0.60
1:B:37:LEU:HD12	1:C:333:ARG:NH1	2.16	0.59
1:D:333:ARG:HG3	1:D:335:GLU:HB2	1.83	0.59
1:E:232:ILE:HG21	1:E:239:ILE:HA	1.84	0.59
1:B:232:ILE:HB	1:B:239:ILE:HA	1.84	0.59
1:C:40:PHE:HE2	1:D:335:GLU:HG3	1.67	0.59
1:G:169:GLN:NE2	1:G:174:LEU:CD2	2.62	0.59
1:D:157:GLU:OE2	1:D:158:GLY:N	2.35	0.59
1:C:50:HIS:HE1	1:C:298:VAL:O	1.85	0.59
1:G:51:MET:O	1:G:52:VAL:HG22	2.01	0.59
1:A:294:HIS:O	1:A:295:ARG:HB3	2.01	0.59
1:F:305:ASP:O	1:F:325:TYR:HB2	2.03	0.59
1:D:100:LEU:HB3	1:D:130:LEU:HD11	1.84	0.59
1:E:166:GLU:HB3	1:E:342:PHE:HA	1.84	0.59
1:C:116:TYR:HD1	1:C:118:VAL:HG22	1.67	0.59
1:B:289:ILE:HD12	1:B:342:PHE:CE1	2.38	0.59
1:G:142:ILE:HB	1:G:298:VAL:HG21	1.85	0.59
1:F:208:TYR:CE2	1:F:248:VAL:HG21	2.38	0.59
1:B:167:THR:OG1	1:B:168:THR:N	2.35	0.59
1:A:99:LEU:HD11	1:A:324:LYS:HB2	1.84	0.59
1:D:142:ILE:HD11	1:D:293:MET:HB3	1.83	0.59
1:G:184:ILE:HD12	1:G:289:ILE:HG21	1.84	0.58
1:D:116:TYR:O	1:D:118:VAL:CB	2.49	0.58
1:B:46:THR:HG21	1:B:139:LEU:HG	1.85	0.58
1:A:167:THR:O	1:A:168:THR:HB	2.03	0.58
1:C:143:ALA:HB2	1:C:291:LEU:HD13	1.84	0.58
1:A:159:LEU:CD1	1:A:335:GLU:CD	2.71	0.58
1:C:166:GLU:HB3	1:C:342:PHE:HA	1.85	0.58
1:G:205:ARG:HB2	1:G:245:PHE:CD2	2.39	0.58
1:A:243:MET:O	1:A:245:PHE:N	2.36	0.58
1:G:49:ARG:O	1:G:295:ARG:NH1	2.37	0.58
1:A:241:ASN:ND2	1:A:245:PHE:O	2.37	0.58
1:E:235:GLU:HG2	1:F:241:ASN:HB2	1.85	0.58
1:F:186:ALA:O	1:F:189:THR:OG1	2.20	0.58
1:A:134:ALA:HB2	1:A:325:TYR:OH	2.04	0.58
1:B:114:ASN:O	1:B:116:TYR:CD2	2.56	0.58
1:G:11:GLY:O	1:G:24:LYS:HB2	2.04	0.58
1:B:222:MET:HE1	1:C:243:MET:HE2	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:202:ALA:HB2	1:B:205:ARG:HH11	1.68	0.58
1:G:230:ALA:HB1	1:G:231:LEU:HA	1.85	0.58
1:D:45:VAL:N	1:D:135:ASP:OD2	2.37	0.58
1:F:289:ILE:HD11	1:F:342:PHE:HD2	1.69	0.57
1:F:148:VAL:HG22	1:F:281:VAL:HB	1.85	0.57
1:C:155:ASN:OD1	1:C:156:ILE:N	2.33	0.57
1:B:262:ARG:HD2	1:C:84:ARG:HA	1.85	0.57
1:C:168:THR:OG1	1:C:169:GLN:N	2.37	0.57
1:D:260:THR:H	1:E:73:TYR:HB2	1.67	0.57
1:A:104:VAL:HG23	1:A:126:LEU:HD21	1.86	0.57
1:B:23:ASP:OD2	1:B:23:ASP:N	2.37	0.57
1:G:300:THR:HG23	1:G:329:HIS:ND1	2.13	0.57
1:A:167:THR:O	1:A:168:THR:CB	2.52	0.57
1:D:332:LEU:O	1:D:333:ARG:HB2	2.03	0.57
1:E:231:LEU:HD22	1:E:231:LEU:H	1.69	0.57
1:F:232:ILE:HG12	1:F:233:ASP:N	2.19	0.57
1:F:47:THR:O	1:F:49:ARG:N	2.38	0.57
1:F:207:PHE:HB2	1:F:245:PHE:HD1	1.69	0.57
1:A:23:ASP:HA	1:A:24:LYS:HG2	1.85	0.57
1:C:142:ILE:HB	1:C:298:VAL:HG21	1.87	0.57
1:C:51:MET:HG2	1:C:296:SER:HB2	1.87	0.57
1:G:53:ARG:HG3	1:G:53:ARG:NH1	2.09	0.57
1:F:231:LEU:HD23	1:F:232:ILE:HG22	1.86	0.57
1:F:294:HIS:HB3	1:F:336:ALA:HB1	1.87	0.57
1:D:300:THR:HG22	1:D:329:HIS:ND1	2.19	0.57
1:D:243:MET:O	1:D:245:PHE:N	2.38	0.57
1:G:7:GLY:O	1:G:9:GLN:N	2.35	0.57
1:G:209:CYS:SG	1:G:210:ASP:N	2.77	0.57
1:D:212:ASP:OD1	1:D:212:ASP:N	2.36	0.56
1:B:232:ILE:HG12	1:B:233:ASP:N	2.20	0.56
1:D:223:PRO:HG3	1:E:230:ALA:HB2	1.88	0.56
1:E:49:ARG:HE	1:E:206:VAL:HG21	1.70	0.56
1:C:242:VAL:HG12	1:C:243:MET:CE	2.35	0.56
1:B:235:GLU:O	1:B:236:LYS:HB3	2.06	0.56
1:B:254:THR:HG21	1:B:285:LYS:HE3	1.86	0.56
1:D:166:GLU:HB2	1:D:342:PHE:HA	1.88	0.56
1:A:181:GLY:HA3	1:A:220:ALA:HB2	1.88	0.56
1:A:139:LEU:CD2	1:A:253:LEU:CD2	2.83	0.56
1:E:181:GLY:HA3	1:E:220:ALA:HB2	1.86	0.56
1:A:159:LEU:CG	1:A:335:GLU:CD	2.74	0.56
1:D:102:ALA:HB1	1:D:126:LEU:HD12	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:332:LEU:CD1	1:A:332:LEU:N	2.69	0.55
1:A:231:LEU:HD23	1:A:232:ILE:H	1.70	0.55
1:A:204:ASP:O	1:A:204:ASP:CG	2.44	0.55
1:D:148:VAL:HG13	1:D:281:VAL:HB	1.87	0.55
1:D:227:ASN:OD1	1:D:227:ASN:N	2.35	0.55
1:F:117:ASP:N	1:F:117:ASP:OD1	2.34	0.55
1:E:159:LEU:HD23	1:E:335:GLU:HG2	1.88	0.55
1:F:305:ASP:CG	1:F:306:LEU:H	2.09	0.55
1:B:134:ALA:HB2	1:B:325:TYR:OH	2.05	0.55
1:C:257:GLY:HA3	1:C:268:GLN:HB2	1.89	0.55
1:F:96:ILE:HA	1:F:328:GLY:HA3	1.89	0.55
1:G:169:GLN:HG3	1:G:174:LEU:HD11	1.88	0.55
1:A:254:THR:HG23	1:A:272:PHE:HB2	1.89	0.55
1:A:214:TYR:CE1	1:A:239:ILE:HD12	2.42	0.55
1:A:103:ASP:H	1:A:262:ARG:HH22	1.55	0.55
1:F:75:ALA:HB3	1:F:78:GLU:HG3	1.89	0.55
1:D:229:ALA:HB2	1:E:228:TYR:CE1	2.41	0.55
1:A:163:THR:O	1:A:163:THR:OG1	2.25	0.55
1:F:19:VAL:O	1:F:21:ALA:N	2.37	0.55
1:E:294:HIS:ND1	1:E:295:ARG:O	2.39	0.55
1:E:102:ALA:HB1	1:E:126:LEU:HD22	1.87	0.55
1:A:75:ALA:HB1	1:A:76:PRO:HD2	1.89	0.55
1:F:205:ARG:HB2	1:F:244:GLY:O	2.07	0.55
1:E:120:SER:O	1:E:123:THR:OG1	2.22	0.55
1:A:29:LEU:H	1:A:29:LEU:HD13	1.72	0.55
1:F:333:ARG:HH11	1:F:333:ARG:HB2	1.72	0.55
1:D:293:MET:HA	1:D:336:ALA:O	2.07	0.55
1:D:259:GLY:HA2	1:E:73:TYR:HD1	1.71	0.55
1:F:294:HIS:O	1:F:295:ARG:HB3	2.07	0.55
1:E:113:MET:O	1:E:114:ASN:ND2	2.40	0.55
1:A:166:GLU:OE1	1:A:167:THR:O	2.25	0.54
1:F:179:ALA:O	1:F:183:GLU:HG2	2.06	0.54
1:B:313:ARG:NH2	1:C:81:ASP:OD2	2.41	0.54
1:C:265:THR:HG22	1:C:266:THR:H	1.72	0.54
1:A:73:TYR:CD1	1:F:259:GLY:HA2	2.40	0.54
1:B:150:SER:O	1:B:151:LYS:HG2	2.08	0.54
1:E:289:ILE:HD11	1:E:342:PHE:CE2	2.42	0.54
1:A:262:ARG:O	1:B:70:GLN:NE2	2.41	0.54
1:B:181:GLY:HA3	1:B:220:ALA:HB2	1.89	0.54
1:D:14:GLN:HE21	1:D:14:GLN:HA	1.71	0.54
1:B:65:VAL:HG13	1:B:91:GLU:HA	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:224:ASN:HB3	1:C:182:LYS:HE2	1.90	0.54
1:C:298:VAL:HG12	1:C:299:GLY:N	2.23	0.54
1:G:50:HIS:HA	1:G:295:ARG:HH11	1.73	0.54
1:B:214:TYR:OH	1:B:237:GLY:O	2.22	0.54
1:G:85:LYS:CA	1:G:85:LYS:HE3	2.15	0.54
1:D:159:LEU:HB3	1:D:335:GLU:HA	1.89	0.54
1:G:148:VAL:HG22	1:G:282:LYS:H	1.73	0.54
1:C:242:VAL:HG12	1:C:243:MET:HE2	1.90	0.54
1:E:236:LYS:H	1:F:243:MET:HA	1.72	0.54
1:D:184:ILE:HD12	1:D:289:ILE:HG21	1.89	0.54
1:D:306:LEU:HD23	1:D:325:TYR:HB3	1.90	0.54
1:D:26:ALA:O	1:D:27:LEU:HB3	2.08	0.54
1:G:169:GLN:HE21	1:G:174:LEU:CG	2.20	0.54
1:F:304:ARG:HH11	1:F:304:ARG:CG	2.21	0.54
1:F:231:LEU:HD23	1:F:232:ILE:H	1.73	0.54
1:B:122:TYR:CD1	1:C:87:ILE:HD12	2.43	0.54
1:B:234:PRO:HB2	1:C:231:LEU:HD21	1.90	0.53
1:G:169:GLN:HE21	1:G:174:LEU:CD2	2.20	0.53
1:G:166:GLU:OE2	1:G:183:GLU:CB	2.56	0.53
1:A:197:LYS:HB3	1:F:211:PRO:HG3	1.88	0.53
1:A:254:THR:HG22	1:A:255:ALA:N	2.17	0.53
1:G:224:ASN:N	1:G:224:ASN:HD22	2.07	0.53
1:A:32:PHE:CG	1:A:33:GLY:N	2.76	0.53
1:A:252:HIS:H	1:A:252:HIS:CD2	2.26	0.53
1:C:138:VAL:O	1:C:141:GLU:HG2	2.08	0.53
1:F:214:TYR:HB2	1:F:249:GLU:HB2	1.89	0.53
1:A:72:ALA:O	1:F:100:LEU:HD23	2.09	0.53
1:E:206:VAL:HG23	1:E:246:GLU:HB3	1.90	0.53
1:G:274:ALA:HA	1:G:285:LYS:HG2	1.91	0.53
1:G:51:MET:CB	1:G:299:GLY:CA	2.86	0.53
1:E:228:TYR:HD1	1:E:230:ALA:H	1.57	0.53
1:A:193:ALA:HB2	1:F:215:SER:HB2	1.91	0.53
1:D:116:TYR:C	1:D:118:VAL:HB	2.29	0.53
1:F:149:GLU:CD	1:F:149:GLU:H	2.11	0.53
1:C:108:ASP:N	1:C:108:ASP:OD1	2.41	0.53
1:C:159:LEU:HD13	1:C:335:GLU:N	2.16	0.53
1:F:24:LYS:HD2	1:F:24:LYS:O	2.09	0.53
1:E:202:ALA:HA	1:E:205:ARG:NH1	2.22	0.53
1:F:19:VAL:HG22	1:F:20:ALA:H	1.73	0.53
1:C:148:VAL:HG12	1:C:283:VAL:HG13	1.91	0.53
1:B:222:MET:SD	1:C:243:MET:HE1	2.49	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:336:ALA:O	1:C:337:ALA:HB2	2.08	0.53
1:F:23:ASP:OD2	1:F:26:ALA:HB2	2.09	0.52
1:F:208:TYR:CD2	1:F:248:VAL:CG2	2.90	0.52
1:E:276:LYS:HA	1:E:281:VAL:HG13	1.91	0.52
1:A:113:MET:O	1:A:114:ASN:ND2	2.32	0.52
1:E:252:HIS:H	1:E:252:HIS:CD2	2.28	0.52
1:B:170:ASN:OD1	1:B:170:ASN:N	2.42	0.52
1:A:159:LEU:HB3	1:A:335:GLU:CB	2.36	0.52
1:B:45:VAL:HB	1:B:135:ASP:OD1	2.10	0.52
1:C:33:GLY:HA3	1:D:63:PHE:CE1	2.43	0.52
1:A:158:GLY:O	1:A:159:LEU:HD12	2.08	0.52
1:F:27:LEU:HD12	1:F:28:PHE:HA	1.91	0.52
1:A:305:ASP:CG	1:A:306:LEU:H	2.12	0.52
1:B:205:ARG:HA	1:B:294:HIS:HA	1.91	0.52
1:A:221:LEU:HD23	1:A:232:ILE:HB	1.91	0.52
1:C:103:ASP:H	1:C:262:ARG:NH2	2.06	0.52
1:D:60:SER:HB3	1:D:95:THR:HG22	1.91	0.52
1:F:132:MET:HG3	1:F:252:HIS:CE1	2.44	0.52
1:A:50:HIS:CE1	1:A:300:THR:HG23	2.45	0.52
1:B:305:ASP:O	1:B:325:TYR:HB2	2.09	0.52
1:E:155:ASN:OD1	1:E:156:ILE:N	2.40	0.52
1:B:79:ASN:N	1:B:79:ASN:HD22	2.07	0.52
1:F:207:PHE:O	1:F:248:VAL:HG22	2.10	0.52
1:C:224:ASN:N	1:C:224:ASN:HD22	2.08	0.52
1:A:167:THR:CG2	1:A:168:THR:N	2.73	0.51
1:B:166:GLU:HB2	1:B:341:VAL:O	2.10	0.51
1:E:42:ARG:HB3	1:F:199:TYR:CE1	2.45	0.51
1:G:156:ILE:HG13	1:G:157:GLU:H	1.75	0.51
1:D:265:THR:OG1	1:D:268:GLN:OE1	2.27	0.51
1:E:105:LEU:HA	1:E:320:GLN:HB2	1.91	0.51
1:E:343:LYS:HD3	1:E:344:VAL:HG23	1.92	0.51
1:C:159:LEU:HB2	1:C:335:GLU:CG	2.36	0.51
1:F:27:LEU:HD22	1:G:91:GLU:HB3	1.93	0.51
1:D:223:PRO:HB3	1:E:228:TYR:CE1	2.44	0.51
1:C:169:GLN:HB3	1:C:343:LYS:HE2	1.92	0.51
1:B:224:ASN:HA	1:C:226:ALA:HA	1.92	0.51
1:D:30:LYS:HB3	1:E:60:SER:HB3	1.91	0.51
1:B:222:MET:HE3	1:C:243:MET:CE	2.39	0.51
1:E:239:ILE:HG22	1:E:240:ARG:N	2.25	0.51
1:F:24:LYS:NZ	1:F:24:LYS:CB	2.63	0.51
1:G:85:LYS:O	1:G:86:ASP:CB	2.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:222:MET:HG3	1:A:223:PRO:HD2	1.92	0.51
1:B:319:ASP:OD2	1:B:319:ASP:N	2.44	0.51
1:C:244:GLY:O	1:C:245:PHE:CD1	2.63	0.51
1:E:253:LEU:HD23	1:E:254:THR:N	2.26	0.51
1:C:91:GLU:OE1	1:C:91:GLU:N	2.44	0.51
1:A:210:ASP:HB2	1:A:211:PRO:HD2	1.92	0.51
1:B:46:THR:HG21	1:B:139:LEU:CG	2.40	0.51
1:G:180:LEU:O	1:G:184:ILE:HG12	2.10	0.51
1:G:151:LYS:O	1:G:153:ASN:N	2.43	0.51
1:A:171:LYS:HB3	1:A:342:PHE:HE2	1.74	0.51
1:F:207:PHE:HE2	1:F:209:CYS:HB3	1.75	0.51
1:F:174:LEU:HD11	1:F:180:LEU:HD13	1.92	0.51
1:A:205:ARG:HB2	1:A:244:GLY:O	2.11	0.51
1:B:46:THR:O	1:B:47:THR:CB	2.58	0.51
1:E:102:ALA:HA	1:E:262:ARG:HH22	1.76	0.51
1:E:214:TYR:CZ	1:E:239:ILE:HG13	2.45	0.51
1:A:209:CYS:SG	1:A:213:SER:HB2	2.50	0.51
1:C:179:ALA:O	1:C:183:GLU:HG2	2.11	0.51
1:B:29:LEU:H	1:B:29:LEU:HD13	1.76	0.51
1:G:26:ALA:HB1	1:G:28:PHE:HB2	1.92	0.50
1:A:35:GLU:OE2	1:B:53:ARG:HD3	2.10	0.50
1:B:171:LYS:HB3	1:B:342:PHE:CD1	2.46	0.50
1:D:169:GLN:C	1:D:170:ASN:HD22	2.10	0.50
1:G:147:ASN:HD21	1:G:339:ALA:HB3	1.76	0.50
1:C:306:LEU:HA	1:C:325:TYR:HB3	1.92	0.50
1:D:294:HIS:O	1:D:294:HIS:ND1	2.44	0.50
1:B:45:VAL:HG21	1:B:250:VAL:HG23	1.93	0.50
1:E:289:ILE:HD11	1:E:342:PHE:CD2	2.46	0.50
1:F:227:ASN:N	1:F:227:ASN:OD1	2.45	0.50
1:C:74:LEU:HG	1:C:80:LEU:HB2	1.93	0.50
1:D:155:ASN:CG	1:D:156:ILE:H	2.14	0.50
1:E:312:ARG:CZ	1:E:312:ARG:HB2	2.39	0.50
1:G:207:PHE:HE2	1:G:209:CYS:HB2	1.75	0.50
1:E:128:GLU:HG3	1:E:129:SER:N	2.26	0.50
1:F:181:GLY:HA3	1:F:220:ALA:HB2	1.92	0.50
1:F:248:VAL:O	1:F:249:GLU:OE2	2.30	0.50
1:G:171:LYS:HB3	1:G:342:PHE:CZ	2.46	0.50
1:G:224:ASN:HD22	1:G:224:ASN:H	1.59	0.50
1:C:148:VAL:HB	1:C:281:VAL:HG22	1.93	0.50
1:C:96:ILE:HA	1:C:328:GLY:HA3	1.93	0.50
1:B:214:TYR:CG	1:B:249:GLU:HG2	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:49:ARG:NH2	1:B:248:VAL:HG11	2.26	0.50
1:C:138:VAL:O	1:C:142:ILE:HG22	2.12	0.50
1:G:51:MET:CG	1:G:299:GLY:HA2	2.39	0.50
1:F:134:ALA:HB2	1:F:325:TYR:OH	2.11	0.50
1:A:100:LEU:HD21	1:A:325:TYR:HE2	1.76	0.50
1:B:241:ASN:OD1	1:B:241:ASN:N	2.22	0.50
1:B:155:ASN:HD22	1:B:156:ILE:N	2.10	0.49
1:B:159:LEU:HD11	1:B:335:GLU:N	2.24	0.49
1:A:332:LEU:C	1:A:332:LEU:HD22	2.31	0.49
1:F:207:PHE:CD2	1:F:247:VAL:HG12	2.47	0.49
1:D:200:VAL:HG11	1:D:335:GLU:OE2	2.11	0.49
1:D:45:VAL:HG13	1:D:46:THR:HG23	1.92	0.49
1:B:122:TYR:HD1	1:C:87:ILE:HD12	1.76	0.49
1:A:94:ILE:HD13	1:A:95:THR:H	1.76	0.49
1:C:295:ARG:CA	1:C:297:ALA:CB	2.87	0.49
1:G:294:HIS:O	1:G:295:ARG:HB3	2.11	0.49
1:G:171:LYS:CD	1:G:171:LYS:H	2.25	0.49
1:D:180:LEU:O	1:D:184:ILE:HG12	2.12	0.49
1:A:313:ARG:HG2	1:A:313:ARG:HH11	1.78	0.49
1:F:249:GLU:O	1:F:249:GLU:OE2	2.30	0.49
1:B:294:HIS:HB3	1:B:336:ALA:CB	2.42	0.49
1:F:159:LEU:HB3	1:F:335:GLU:CB	2.40	0.49
1:E:171:LYS:HE2	1:E:342:PHE:CZ	2.47	0.49
1:E:170:ASN:HD21	1:E:173:ALA:HB3	1.77	0.49
1:G:186:ALA:O	1:G:189:THR:OG1	2.23	0.49
1:C:12:THR:HG23	1:C:14:GLN:HG2	1.94	0.49
1:B:57:SER:OG	1:B:58:GLY:N	2.45	0.49
1:B:333:ARG:CG	1:B:333:ARG:HH11	2.26	0.49
1:G:298:VAL:HG13	1:G:330:GLY:O	2.07	0.49
1:G:168:THR:O	1:G:169:GLN:OE1	2.30	0.49
1:A:45:VAL:HG22	1:A:49:ARG:HH12	1.77	0.49
1:D:87:ILE:HD13	1:D:87:ILE:H	1.77	0.49
1:D:292:PHE:CZ	1:D:338:GLY:HA3	2.46	0.49
1:C:45:VAL:O	1:C:135:ASP:OD2	2.30	0.49
1:D:223:PRO:HG3	1:E:230:ALA:HB1	1.93	0.49
1:C:343:LYS:HG2	1:C:344:VAL:H	1.77	0.49
1:F:295:ARG:HG3	1:F:296:SER:N	2.26	0.49
1:B:254:THR:HG22	1:B:272:PHE:CD2	2.47	0.49
1:E:218:LEU:O	1:E:222:MET:HG2	2.13	0.49
1:B:199:TYR:O	1:B:200:VAL:HG13	2.12	0.49
1:E:313:ARG:NH2	1:F:81:ASP:OD1	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:276:LYS:HB2	1:C:284:ALA:HB2	1.94	0.49
1:G:23:ASP:OD2	1:G:23:ASP:N	2.44	0.49
1:G:167:THR:O	1:G:169:GLN:OE1	2.30	0.49
1:A:214:TYR:CD2	1:A:249:GLU:HG2	2.48	0.49
1:C:289:ILE:HG12	1:C:342:PHE:CE2	2.48	0.49
1:C:189:THR:OG1	1:C:190:LYS:N	2.45	0.49
1:G:25:LEU:H	1:G:25:LEU:HD13	1.76	0.49
1:F:46:THR:HB	1:F:47:THR:HA	1.94	0.49
1:A:49:ARG:O	1:A:295:ARG:HD3	2.12	0.49
1:G:55:ILE:HG23	1:G:301:VAL:HG13	1.95	0.49
1:C:222:MET:C	1:D:228:TYR:HH	2.16	0.48
1:F:154:GLU:HG3	1:F:159:LEU:HD21	1.95	0.48
1:D:13:ASN:HA	1:D:27:LEU:HD22	1.94	0.48
1:C:294:HIS:HD2	1:C:295:ARG:O	1.96	0.48
1:G:227:ASN:O	1:G:228:TYR:HB2	2.13	0.48
1:A:36:VAL:HG13	1:B:64:PRO:HG2	1.94	0.48
1:G:214:TYR:CE1	1:G:239:ILE:HD11	2.47	0.48
1:F:207:PHE:CZ	1:F:290:GLY:HA3	2.48	0.48
1:F:154:GLU:HG3	1:F:159:LEU:HD11	1.95	0.48
1:F:304:ARG:NH1	1:F:304:ARG:HG2	2.26	0.48
1:C:66:LEU:CB	1:C:89:HIS:HB3	2.43	0.48
1:B:292:PHE:CZ	1:B:338:GLY:HA3	2.49	0.48
1:F:8:GLN:OE1	1:G:87:ILE:HB	2.13	0.48
1:A:72:ALA:HB2	1:F:262:ARG:CZ	2.43	0.48
1:E:144:GLY:O	1:E:146:CYS:N	2.47	0.48
1:G:169:GLN:HE22	1:G:174:LEU:HD21	1.71	0.48
1:A:228:TYR:CE1	1:F:223:PRO:HA	2.49	0.48
1:A:228:TYR:HE1	1:F:223:PRO:HA	1.79	0.48
1:D:122:TYR:HE1	1:E:87:ILE:HG13	1.78	0.48
1:B:180:LEU:O	1:B:184:ILE:HG12	2.13	0.48
1:E:100:LEU:HB3	1:E:130:LEU:HD11	1.95	0.48
1:E:305:ASP:O	1:E:325:TYR:HB2	2.13	0.48
1:G:143:ALA:HB3	1:G:272:PHE:CZ	2.49	0.48
1:G:148:VAL:HG13	1:G:281:VAL:HA	1.94	0.48
1:C:19:VAL:O	1:C:21:ALA:N	2.47	0.48
1:B:231:LEU:H	1:B:231:LEU:HD23	1.78	0.48
1:D:186:ALA:O	1:D:189:THR:OG1	2.26	0.48
1:A:269:LYS:HB3	1:A:270:HIS:CD2	2.49	0.48
1:D:243:MET:HB2	1:D:245:PHE:CD1	2.48	0.48
1:B:333:ARG:HG2	1:B:333:ARG:HH11	1.77	0.48
1:E:315:ASN:HD22	1:E:315:ASN:N	2.10	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:117:ASP:OD2	1:D:117:ASP:O	2.30	0.48
1:A:46:THR:H	1:A:49:ARG:HH11	1.62	0.48
1:B:289:ILE:N	1:B:289:ILE:HD13	2.29	0.48
1:F:180:LEU:O	1:F:184:ILE:HG12	2.13	0.48
1:G:300:THR:CG2	1:G:329:HIS:CG	2.95	0.47
1:B:243:MET:O	1:B:245:PHE:N	2.47	0.47
1:A:50:HIS:HE1	1:A:300:THR:HG23	1.78	0.47
1:D:207:PHE:CZ	1:D:290:GLY:HA3	2.49	0.47
1:A:241:ASN:HB2	1:F:235:GLU:HG3	1.95	0.47
1:A:217:ILE:HD13	1:A:217:ILE:HA	1.75	0.47
1:A:159:LEU:CG	1:A:335:GLU:CG	2.83	0.47
1:C:103:ASP:OD1	1:C:262:ARG:NH2	2.48	0.47
1:C:164:VAL:HG12	1:C:340:VAL:HG12	1.96	0.47
1:B:222:MET:CE	1:C:243:MET:HE1	2.43	0.47
1:A:165:ILE:HD13	1:A:166:GLU:H	1.78	0.47
1:C:116:TYR:CD1	1:C:118:VAL:HG22	2.48	0.47
1:A:202:ALA:HA	1:A:205:ARG:HH12	1.80	0.47
1:G:51:MET:O	1:G:52:VAL:CB	2.62	0.47
1:A:139:LEU:HD21	1:A:253:LEU:CD2	2.44	0.47
1:C:180:LEU:O	1:C:184:ILE:HG12	2.13	0.47
1:F:167:THR:HG22	1:F:168:THR:H	1.80	0.47
1:A:7:GLY:C	1:A:9:GLN:H	2.17	0.47
1:A:170:ASN:N	1:A:170:ASN:OD1	2.45	0.47
1:B:197:LYS:HE3	1:B:197:LYS:HB2	1.79	0.47
1:C:294:HIS:HD2	1:C:295:ARG:HG3	1.80	0.47
1:C:297:ALA:O	1:C:298:VAL:CG2	2.62	0.47
1:F:171:LYS:O	1:F:174:LEU:HG	2.14	0.47
1:E:289:ILE:CD1	1:E:289:ILE:N	2.78	0.47
1:A:242:VAL:O	1:F:235:GLU:HA	2.13	0.47
1:D:99:LEU:HD12	1:D:326:ALA:HB2	1.96	0.47
1:A:105:LEU:HA	1:A:320:GLN:HB2	1.95	0.47
1:B:253:LEU:HA	1:B:253:LEU:HD13	1.71	0.47
1:B:209:CYS:SG	1:B:213:SER:HB2	2.54	0.47
1:A:159:LEU:HD11	1:A:198:ASN:HB3	1.95	0.47
1:C:195:LEU:O	1:C:200:VAL:HG13	2.14	0.47
1:A:231:LEU:HD22	1:A:231:LEU:H	1.80	0.47
1:G:161:THR:HA	1:G:335:GLU:HA	1.97	0.47
1:A:218:LEU:HD21	1:A:237:GLY:O	2.14	0.47
1:A:159:LEU:CD2	1:A:335:GLU:CG	2.88	0.47
1:D:229:ALA:HB2	1:E:228:TYR:CE2	2.49	0.47
1:F:207:PHE:HB2	1:F:245:PHE:CD1	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:37:LEU:HB2	1:D:65:VAL:HG12	1.95	0.47
1:E:243:MET:HE3	1:E:243:MET:HA	1.96	0.47
1:F:178:VAL:O	1:F:180:LEU:N	2.42	0.47
1:B:64:PRO:HA	1:B:91:GLU:HB2	1.97	0.47
1:E:279:GLY:O	1:E:281:VAL:HG12	2.14	0.47
1:E:252:HIS:H	1:E:252:HIS:HD2	1.61	0.47
1:E:170:ASN:HB3	1:E:344:VAL:HB	1.96	0.47
1:A:195:LEU:HD22	1:A:205:ARG:HE	1.80	0.47
1:G:83:LYS:H	1:G:83:LYS:HD3	1.79	0.47
1:A:287:ASN:HD22	1:A:287:ASN:H	1.61	0.47
1:D:68:ARG:O	1:D:69:THR:OG1	2.27	0.47
1:B:304:ARG:HH11	1:B:304:ARG:HA	1.80	0.47
1:G:50:HIS:O	1:G:50:HIS:ND1	2.48	0.47
1:C:118:VAL:O	1:C:120:SER:N	2.42	0.47
1:E:94:ILE:HB	1:E:330:GLY:HA3	1.97	0.47
1:B:215:SER:HB2	1:C:193:ALA:HB2	1.97	0.47
1:A:139:LEU:HD22	1:A:253:LEU:CD2	2.45	0.47
1:B:59:LYS:HE2	1:B:59:LYS:HB3	1.45	0.47
1:E:169:GLN:HG3	1:E:170:ASN:ND2	2.30	0.47
1:E:47:THR:HA	1:E:48:SER:HA	1.59	0.47
1:G:59:LYS:HD2	1:G:60:SER:OG	2.15	0.47
1:D:43:THR:HB	1:D:44:SER:H	1.41	0.47
1:A:72:ALA:O	1:F:100:LEU:HA	2.15	0.47
1:B:64:PRO:HA	1:B:91:GLU:CB	2.45	0.47
1:C:244:GLY:O	1:C:245:PHE:CG	2.68	0.47
1:F:268:GLN:HE21	1:F:268:GLN:HB2	1.50	0.47
1:F:51:MET:HG3	1:F:296:SER:HA	1.97	0.46
1:E:126:LEU:HD23	1:F:69:THR:HG21	1.96	0.46
1:C:239:ILE:O	1:C:240:ARG:HB2	2.15	0.46
1:F:147:ASN:HB2	1:F:283:VAL:HG11	1.98	0.46
1:G:325:TYR:CD2	1:G:327:MET:HG3	2.50	0.46
1:A:159:LEU:CB	1:A:335:GLU:OE2	2.39	0.46
1:C:200:VAL:HG23	1:C:294:HIS:ND1	2.30	0.46
1:G:300:THR:HG22	1:G:329:HIS:CG	2.49	0.46
1:G:289:ILE:HD11	1:G:342:PHE:CG	2.50	0.46
1:A:209:CYS:SG	1:A:210:ASP:N	2.87	0.46
1:D:40:PHE:CZ	1:E:200:VAL:HG23	2.51	0.46
1:B:169:GLN:HB2	1:B:173:ALA:HB3	1.97	0.46
1:C:152:TYR:O	1:C:153:ASN:ND2	2.48	0.46
1:C:294:HIS:CD2	1:C:295:ARG:HG3	2.50	0.46
1:G:64:PRO:HA	1:G:91:GLU:HA	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:298:VAL:HG22	1:A:331:GLY:HA2	1.97	0.46
1:A:325:TYR:CD2	1:A:325:TYR:C	2.89	0.46
1:E:292:PHE:CZ	1:E:338:GLY:HA3	2.51	0.46
1:F:27:LEU:CD1	1:F:28:PHE:CA	2.81	0.46
1:B:205:ARG:HG2	1:B:245:PHE:CE1	2.51	0.46
1:C:336:ALA:O	1:C:337:ALA:HB3	2.13	0.46
1:A:295:ARG:HD2	1:A:296:SER:H	1.81	0.46
1:D:45:VAL:HG11	1:D:250:VAL:HG11	1.97	0.46
1:D:102:ALA:O	1:D:322:ILE:HG12	2.16	0.46
1:A:184:ILE:O	1:A:188:LEU:HB2	2.16	0.46
1:B:157:GLU:OE2	1:B:159:LEU:HB2	2.15	0.46
1:B:159:LEU:CD1	1:B:335:GLU:H	2.22	0.46
1:F:7:GLY:O	1:F:8:GLN:HB3	2.15	0.46
1:D:191:ALA:HB1	1:D:292:PHE:CZ	2.51	0.46
1:G:214:TYR:HE1	1:G:239:ILE:HD11	1.80	0.46
1:F:239:ILE:O	1:F:240:ARG:HB2	2.15	0.46
1:B:74:LEU:CD1	1:B:78:GLU:O	2.59	0.46
1:E:157:GLU:O	1:E:159:LEU:HD12	2.15	0.46
1:G:12:THR:OG1	1:G:13:ASN:N	2.49	0.46
1:A:200:VAL:HG22	1:F:40:PHE:CE1	2.51	0.46
1:F:171:LYS:HB2	1:F:342:PHE:CE1	2.51	0.46
1:A:153:ASN:OD1	1:A:153:ASN:N	2.47	0.46
1:B:234:PRO:O	1:C:231:LEU:HD21	2.14	0.46
1:G:86:ASP:O	1:G:87:ILE:HD13	2.16	0.46
1:G:53:ARG:CG	1:G:53:ARG:NH1	2.36	0.46
1:A:171:LYS:HG2	1:A:171:LYS:H	1.55	0.46
1:G:228:TYR:CD2	1:G:230:ALA:HB3	2.51	0.46
1:D:260:THR:HB	1:D:261:ALA:H	1.52	0.46
1:D:206:VAL:HG23	1:D:246:GLU:HB2	1.98	0.46
1:F:225:ALA:HA	1:F:226:ALA:HA	1.51	0.46
1:E:42:ARG:NE	1:E:128:GLU:OE1	2.38	0.45
1:E:239:ILE:HG22	1:E:240:ARG:H	1.80	0.45
1:E:304:ARG:HA	1:E:304:ARG:HD3	1.63	0.45
1:G:205:ARG:O	1:G:245:PHE:HA	2.17	0.45
1:E:167:THR:O	1:E:168:THR:HG22	2.17	0.45
1:G:166:GLU:HB3	1:G:342:PHE:HB3	1.99	0.45
1:B:265:THR:HG22	1:B:266:THR:H	1.82	0.45
1:F:109:ILE:HG12	1:G:99:LEU:HD23	1.99	0.45
1:A:166:GLU:HB2	1:A:341:VAL:O	2.17	0.45
1:A:254:THR:HG21	1:A:285:LYS:HE2	1.98	0.45
1:C:289:ILE:HD12	1:C:289:ILE:HA	1.68	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:325:TYR:HD2	1:A:325:TYR:C	2.20	0.45
1:D:45:VAL:HG22	1:D:46:THR:H	1.81	0.45
1:G:27:LEU:O	1:G:27:LEU:HG	2.16	0.45
1:C:252:HIS:ND1	1:C:252:HIS:O	2.49	0.45
1:D:253:LEU:O	1:D:254:THR:HB	2.16	0.45
1:D:46:THR:OG1	1:D:47:THR:N	2.49	0.45
1:F:144:GLY:O	1:F:148:VAL:HB	2.16	0.45
1:E:103:ASP:OD1	1:E:262:ARG:NH1	2.49	0.45
1:B:322:ILE:HD11	1:C:80:LEU:HD11	1.98	0.45
1:D:254:THR:HG21	1:D:285:LYS:HD3	1.97	0.45
1:G:195:LEU:HD23	1:G:205:ARG:HE	1.81	0.45
1:E:171:LYS:HE2	1:E:342:PHE:CE1	2.52	0.45
1:G:276:LYS:HE2	1:G:343:LYS:HG2	1.97	0.45
1:E:298:VAL:HG12	1:E:331:GLY:HA2	1.98	0.45
1:D:76:PRO:HA	1:D:77:GLY:HA2	1.55	0.45
1:G:81:ASP:OD2	1:G:84:ARG:NH1	2.34	0.45
1:F:14:GLN:HB3	1:G:88:LYS:HE2	1.99	0.45
1:E:29:LEU:HD22	1:E:29:LEU:H	1.82	0.45
1:C:221:LEU:HA	1:C:221:LEU:HD13	1.71	0.45
1:G:106:ILE:O	1:G:318:ALA:HB1	2.16	0.45
1:F:155:ASN:CG	1:F:156:ILE:H	2.18	0.45
1:C:297:ALA:C	1:C:298:VAL:HG23	2.37	0.45
1:G:171:LYS:CD	1:G:171:LYS:N	2.78	0.45
1:E:158:GLY:N	1:E:159:LEU:HB2	2.32	0.45
1:A:105:LEU:HD13	1:A:320:GLN:HB2	1.99	0.45
1:A:141:GLU:OE2	1:A:330:GLY:HA2	2.17	0.45
1:C:69:THR:OG1	1:C:70:GLN:N	2.49	0.45
1:A:332:LEU:CD2	1:A:332:LEU:O	2.48	0.45
1:A:86:ASP:OD2	1:A:86:ASP:N	2.45	0.45
1:D:103:ASP:N	1:D:103:ASP:OD2	2.50	0.45
1:F:98:GLY:HA2	1:F:99:LEU:HA	1.63	0.45
1:G:234:PRO:O	1:G:235:GLU:HB3	2.16	0.45
1:E:236:LYS:N	1:F:243:MET:HA	2.32	0.45
1:G:147:ASN:ND2	1:G:339:ALA:HB3	2.32	0.45
1:A:287:ASN:HD22	1:A:287:ASN:N	2.13	0.45
1:E:215:SER:HB2	1:F:192:ARG:HH12	1.82	0.45
1:A:119:ARG:O	1:A:122:TYR:HB2	2.16	0.45
1:D:105:LEU:HA	1:D:320:GLN:HB2	1.97	0.45
1:A:240:ARG:HG2	1:A:240:ARG:H	1.55	0.45
1:B:157:GLU:HB2	1:B:158:GLY:H	1.56	0.45
1:B:45:VAL:CG1	1:B:46:THR:HG22	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:LEU:HD11	1:A:253:LEU:HD21	1.99	0.45
1:D:35:GLU:CD	1:E:53:ARG:HE	2.20	0.45
1:D:289:ILE:HD11	1:D:342:PHE:CD2	2.52	0.45
1:A:184:ILE:HD11	1:A:289:ILE:HG21	1.98	0.45
1:B:280:ASN:N	1:B:280:ASN:HD22	2.15	0.45
1:C:215:SER:OG	1:D:193:ALA:HB2	2.16	0.45
1:B:46:THR:HG21	1:B:139:LEU:CD2	2.47	0.44
1:E:49:ARG:HD3	1:E:208:TYR:OH	2.16	0.44
1:C:96:ILE:HG12	1:C:328:GLY:N	2.32	0.44
1:E:9:GLN:O	1:E:12:THR:HG22	2.17	0.44
1:B:287:ASN:O	1:B:287:ASN:ND2	2.49	0.44
1:C:222:MET:C	1:D:228:TYR:OH	2.56	0.44
1:A:223:PRO:HG3	1:B:230:ALA:HB2	1.99	0.44
1:A:139:LEU:HD22	1:A:253:LEU:HD22	1.98	0.44
1:B:13:ASN:HB3	1:B:18:VAL:HG11	2.00	0.44
1:C:89:HIS:N	1:C:89:HIS:CD2	2.85	0.44
1:E:325:TYR:C	1:E:325:TYR:HD2	2.21	0.44
1:A:7:GLY:HA3	1:A:9:GLN:HE21	1.83	0.44
1:D:68:ARG:HD3	1:D:68:ARG:HA	1.67	0.44
1:E:143:ALA:HB2	1:E:291:LEU:HD13	2.00	0.44
1:F:106:ILE:O	1:F:318:ALA:HB1	2.17	0.44
1:C:207:PHE:CE2	1:C:209:CYS:HB2	2.52	0.44
1:C:159:LEU:HD13	1:C:335:GLU:HB2	1.97	0.44
1:G:51:MET:O	1:G:52:VAL:CG2	2.66	0.44
1:C:185:ILE:O	1:C:189:THR:HG23	2.18	0.44
1:G:82:ASP:OD1	1:G:83:LYS:HG3	2.18	0.44
1:G:15:GLY:O	1:G:16:LYS:HD2	2.18	0.44
1:B:46:THR:HG21	1:B:139:LEU:HD21	2.00	0.44
1:A:92:LYS:HZ1	1:A:333:ARG:H	1.65	0.44
1:B:293:MET:HA	1:B:336:ALA:O	2.17	0.44
1:E:197:LYS:HB2	1:E:197:LYS:HE3	1.71	0.44
1:G:295:ARG:C	1:G:297:ALA:H	2.21	0.44
1:E:295:ARG:O	1:E:296:SER:OG	2.35	0.44
1:G:260:THR:HG23	1:G:261:ALA:N	2.33	0.44
1:G:96:ILE:HG22	1:G:328:GLY:HA3	1.98	0.44
1:G:309:GLU:OE1	1:G:311:ALA:HB2	2.18	0.44
1:A:139:LEU:CD2	1:A:253:LEU:HD22	2.48	0.44
1:A:313:ARG:CG	1:A:313:ARG:HH11	2.30	0.44
1:F:222:MET:SD	1:F:223:PRO:HD2	2.58	0.44
1:D:57:SER:OG	1:D:58:GLY:N	2.49	0.44
1:D:107:TYR:HD1	1:D:318:ALA:HB2	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:188:LEU:HD13	1:C:242:VAL:HG21	1.99	0.44
1:D:279:GLY:C	1:D:281:VAL:H	2.21	0.44
1:D:325:TYR:C	1:D:325:TYR:CD2	2.91	0.44
1:F:252:HIS:CD2	1:F:252:HIS:H	2.36	0.44
1:C:239:ILE:HB	1:C:240:ARG:H	1.56	0.44
1:B:101:THR:HG22	1:B:324:LYS:HB3	1.99	0.44
1:B:236:LYS:HA	1:C:243:MET:C	2.22	0.43
1:G:276:LYS:HB3	1:G:276:LYS:HE3	1.62	0.43
1:C:254:THR:HG23	1:C:272:PHE:CD2	2.53	0.43
1:F:145:LEU:HA	1:F:145:LEU:HD22	1.84	0.43
1:F:250:VAL:HA	1:F:251:PRO:HD3	1.77	0.43
1:C:204:ASP:OD2	1:C:295:ARG:HG2	2.18	0.43
1:F:198:ASN:HB3	1:F:335:GLU:HG2	2.01	0.43
1:G:285:LYS:HE2	1:G:285:LYS:HB3	1.91	0.43
1:G:156:ILE:HD12	1:G:156:ILE:HA	1.84	0.43
1:E:161:THR:HB	1:E:334:PRO:O	2.18	0.43
1:F:282:LYS:HE2	1:F:282:LYS:HB3	1.79	0.43
1:C:33:GLY:HA3	1:D:63:PHE:HE1	1.82	0.43
1:B:161:THR:HB	1:B:337:ALA:O	2.18	0.43
1:G:46:THR:CB	1:G:47:THR:HA	2.47	0.43
1:A:74:LEU:HG	1:F:101:THR:HG21	2.01	0.43
1:G:197:LYS:HE3	1:G:197:LYS:HB2	1.64	0.43
1:G:86:ASP:OD2	1:G:87:ILE:N	2.51	0.43
1:C:223:PRO:HG2	1:D:221:LEU:HD11	2.00	0.43
1:G:26:ALA:HB1	1:G:28:PHE:N	2.31	0.43
1:B:205:ARG:HB3	1:B:206:VAL:H	1.54	0.43
1:A:70:GLN:NE2	1:F:262:ARG:O	2.51	0.43
1:B:289:ILE:HD11	1:B:341:VAL:C	2.39	0.43
1:B:305:ASP:CG	1:B:306:LEU:H	2.20	0.43
1:F:96:ILE:HD12	1:F:303:LEU:HD11	1.99	0.43
1:E:325:TYR:C	1:E:325:TYR:CD2	2.92	0.43
1:F:260:THR:HB	1:F:261:ALA:H	1.55	0.43
1:E:217:ILE:O	1:E:221:LEU:HD22	2.18	0.43
1:A:65:VAL:HG22	1:F:37:LEU:HB3	2.01	0.43
1:B:214:TYR:CE1	1:B:239:ILE:HD12	2.53	0.43
1:B:159:LEU:HA	1:B:159:LEU:HD13	1.72	0.43
1:E:70:GLN:HE21	1:E:70:GLN:HB3	1.66	0.43
1:E:100:LEU:O	1:E:324:LYS:HA	2.19	0.43
1:B:25:LEU:HA	1:B:26:ALA:HA	1.58	0.43
1:C:29:LEU:HD22	1:C:29:LEU:H	1.83	0.43
1:B:249:GLU:HG3	1:B:249:GLU:H	1.57	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:206:VAL:HG22	1:A:246:GLU:HB3	2.01	0.43
1:G:60:SER:OG	1:G:95:THR:HA	2.19	0.43
1:B:148:VAL:HG13	1:B:281:VAL:HA	2.00	0.43
1:F:27:LEU:CD1	1:F:28:PHE:HA	2.49	0.43
1:E:228:TYR:HA	1:F:228:TYR:CG	2.53	0.43
1:A:100:LEU:HB3	1:B:73:TYR:CD2	2.53	0.43
1:A:25:LEU:HA	1:A:26:ALA:HA	1.72	0.43
1:D:294:HIS:CG	1:D:294:HIS:O	2.72	0.43
1:B:174:LEU:HD21	1:B:180:LEU:HD13	2.00	0.43
1:C:254:THR:HG21	1:C:285:LYS:HZ3	1.83	0.43
1:C:42:ARG:NE	1:C:128:GLU:OE1	2.31	0.43
1:B:232:ILE:HG21	1:B:239:ILE:HG12	2.00	0.43
1:A:46:THR:O	1:A:50:HIS:HD2	2.02	0.43
1:F:178:VAL:HG13	1:F:179:ALA:N	2.34	0.43
1:A:243:MET:N	1:A:243:MET:SD	2.91	0.43
1:A:23:ASP:H	1:A:24:LYS:HZ2	1.65	0.43
1:A:199:TYR:O	1:A:200:VAL:HB	2.19	0.43
1:G:232:ILE:HG22	1:G:233:ASP:H	1.84	0.43
1:G:253:LEU:HD23	1:G:254:THR:H	1.84	0.43
1:E:37:LEU:HD11	1:F:333:ARG:NH1	2.34	0.43
1:E:134:ALA:HB2	1:E:325:TYR:OH	2.19	0.43
1:C:239:ILE:HG13	1:C:247:VAL:HG21	2.01	0.43
1:B:100:LEU:HG	1:C:73:TYR:CD2	2.53	0.43
1:E:293:MET:HG3	1:E:295:ARG:H	1.84	0.43
1:B:312:ARG:HA	1:B:319:ASP:HB3	2.01	0.43
1:D:241:ASN:HB3	1:D:245:PHE:O	2.18	0.42
1:G:210:ASP:HB2	1:G:211:PRO:HD2	2.01	0.42
1:G:235:GLU:O	1:G:235:GLU:HG2	2.18	0.42
1:G:260:THR:HG21	1:G:266:THR:OG1	2.18	0.42
1:F:254:THR:HA	1:F:272:PHE:CD1	2.54	0.42
1:D:168:THR:HG21	1:D:174:LEU:HD23	2.00	0.42
1:F:139:LEU:HA	1:F:139:LEU:HD13	1.87	0.42
1:G:179:ALA:O	1:G:183:GLU:HG2	2.19	0.42
1:G:59:LYS:HE2	1:G:59:LYS:HB3	1.27	0.42
1:C:145:LEU:O	1:C:149:GLU:HG3	2.19	0.42
1:D:304:ARG:HA	1:D:304:ARG:HH11	1.83	0.42
1:A:224:ASN:HA	1:A:225:ALA:HA	1.66	0.42
1:C:222:MET:HB3	1:C:223:PRO:CD	2.50	0.42
1:C:147:ASN:ND2	1:C:163:THR:HG21	2.33	0.42
1:B:333:ARG:NH1	1:B:333:ARG:CG	2.82	0.42
1:C:31:VAL:O	1:C:32:PHE:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:222:MET:HE3	1:C:243:MET:HE2	2.00	0.42
1:A:45:VAL:HG22	1:A:49:ARG:NH1	2.34	0.42
1:A:262:ARG:HD3	1:B:72:ALA:HB2	2.01	0.42
1:G:99:LEU:HB3	1:G:100:LEU:H	1.41	0.42
1:C:42:ARG:HG3	1:D:199:TYR:CE1	2.55	0.42
1:D:282:LYS:HG2	1:D:282:LYS:H	1.60	0.42
1:B:236:LYS:HE2	1:B:238:SER:HB3	2.01	0.42
1:F:148:VAL:HG13	1:F:281:VAL:HB	2.02	0.42
1:C:84:ARG:C	1:C:85:LYS:HD3	2.40	0.42
1:C:68:ARG:HA	1:C:68:ARG:HD3	1.76	0.42
1:C:188:LEU:HD23	1:C:188:LEU:HA	1.84	0.42
1:E:64:PRO:HA	1:E:91:GLU:CB	2.48	0.42
1:C:40:PHE:CE2	1:D:335:GLU:HG3	2.51	0.42
1:A:24:LYS:HD3	1:A:25:LEU:H	1.84	0.42
1:G:46:THR:HB	1:G:47:THR:HA	2.01	0.42
1:D:151:LYS:HG3	1:D:152:TYR:CD2	2.54	0.42
1:C:50:HIS:O	1:C:51:MET:C	2.58	0.42
1:A:49:ARG:NH2	1:A:246:GLU:OE1	2.28	0.42
1:B:171:LYS:HE2	1:B:171:LYS:HB2	1.90	0.42
1:F:53:ARG:NH1	1:F:53:ARG:HB3	2.30	0.42
1:G:205:ARG:HB2	1:G:245:PHE:HD2	1.84	0.42
1:A:75:ALA:O	1:A:77:GLY:N	2.52	0.42
1:E:130:LEU:HD13	1:E:130:LEU:HA	1.78	0.42
1:G:100:LEU:HD21	1:G:258:ALA:O	2.20	0.42
1:A:64:PRO:HG2	1:F:36:VAL:HG22	2.01	0.42
1:F:206:VAL:HG23	1:F:246:GLU:HB2	2.00	0.42
1:C:100:LEU:HB3	1:D:73:TYR:CD2	2.55	0.42
1:B:46:THR:HG23	1:B:135:ASP:OD2	2.19	0.42
1:A:139:LEU:HD21	1:A:253:LEU:HD21	2.01	0.42
1:B:51:MET:HE3	1:B:51:MET:HB2	1.88	0.42
1:A:313:ARG:HG2	1:A:313:ARG:NH1	2.35	0.42
1:B:185:ILE:HD13	1:B:185:ILE:HA	1.93	0.42
1:C:7:GLY:O	1:C:8:GLN:HB2	2.19	0.42
1:A:197:LYS:O	1:A:198:ASN:CB	2.67	0.42
1:B:202:ALA:HB2	1:B:205:ARG:NH1	2.33	0.42
1:D:333:ARG:C	1:D:335:GLU:H	2.23	0.42
1:E:158:GLY:CA	1:E:159:LEU:HB2	2.50	0.42
1:D:310:ARG:NH2	1:D:321:ILE:HD11	2.31	0.42
1:G:150:SER:O	1:G:151:LYS:HB3	2.20	0.42
1:G:107:TYR:HA	1:G:318:ALA:HB1	2.01	0.42
1:D:56:SER:OG	1:D:57:SER:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:25:LEU:HD23	1:C:25:LEU:HA	1.80	0.42
1:B:222:MET:HE2	1:B:234:PRO:HB3	2.01	0.42
1:E:37:LEU:HD21	1:F:332:LEU:HD23	2.02	0.42
1:C:262:ARG:NH1	1:D:72:ALA:HB2	2.35	0.42
1:A:7:GLY:O	1:A:8:GLN:HB3	2.19	0.42
1:B:215:SER:CB	1:C:193:ALA:HB2	2.49	0.42
1:C:227:ASN:HB3	1:C:228:TYR:H	1.57	0.42
1:B:113:MET:HG2	1:B:113:MET:O	2.20	0.42
1:B:156:ILE:HG23	1:B:157:GLU:N	2.34	0.41
1:D:224:ASN:C	1:D:226:ALA:H	2.22	0.41
1:B:294:HIS:HB3	1:B:336:ALA:HB2	2.01	0.41
1:A:94:ILE:HD13	1:A:95:THR:N	2.35	0.41
1:B:304:ARG:CA	1:B:304:ARG:HH11	2.33	0.41
1:B:185:ILE:HG12	1:B:217:ILE:HD11	2.01	0.41
1:B:217:ILE:HA	1:B:217:ILE:HD13	1.69	0.41
1:E:225:ALA:HA	1:E:226:ALA:HA	1.78	0.41
1:G:310:ARG:HB3	1:G:321:ILE:HG13	2.01	0.41
1:A:250:VAL:HA	1:A:251:PRO:HD2	1.88	0.41
1:D:333:ARG:C	1:D:335:GLU:N	2.74	0.41
1:B:219:ALA:HB2	1:C:189:THR:HG21	2.02	0.41
1:G:99:LEU:HD22	1:G:99:LEU:HA	1.74	0.41
1:E:50:HIS:CG	1:E:51:MET:N	2.88	0.41
1:C:312:ARG:HG2	1:C:319:ASP:HB3	2.02	0.41
1:A:176:ASP:O	1:A:177:GLN:HB3	2.21	0.41
1:F:25:LEU:CA	1:F:26:ALA:CB	2.84	0.41
1:D:92:LYS:HD3	1:D:332:LEU:HA	2.02	0.41
1:G:143:ALA:HB3	1:G:272:PHE:HZ	1.85	0.41
1:G:207:PHE:N	1:G:245:PHE:HB3	2.35	0.41
1:B:285:LYS:O	1:B:285:LYS:HE2	2.20	0.41
1:D:14:GLN:O	1:D:14:GLN:HG3	2.19	0.41
1:C:211:PRO:O	1:C:214:TYR:HB3	2.20	0.41
1:G:286:ASP:N	1:G:286:ASP:OD1	2.53	0.41
1:D:108:ASP:HB2	1:D:317:GLN:O	2.19	0.41
1:C:304:ARG:HD3	1:C:304:ARG:HA	1.60	0.41
1:F:27:LEU:HD12	1:F:27:LEU:O	2.09	0.41
1:A:100:LEU:HD22	1:B:73:TYR:CE2	2.56	0.41
1:E:200:VAL:HG22	1:E:201:PRO:HD2	2.02	0.41
1:A:13:ASN:OD1	1:A:18:VAL:HG11	2.20	0.41
1:E:67:GLY:O	1:E:68:ARG:HB3	2.20	0.41
1:E:37:LEU:HA	1:E:37:LEU:HD12	1.77	0.41
1:A:242:VAL:HG12	1:A:243:MET:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:170:ASN:C	1:E:170:ASN:HD22	2.23	0.41
1:G:101:THR:HG23	1:G:324:LYS:HB3	2.02	0.41
1:E:188:LEU:HD13	1:E:188:LEU:HA	1.72	0.41
1:A:165:ILE:HD13	1:A:166:GLU:N	2.36	0.41
1:G:211:PRO:HA	1:G:249:GLU:OE1	2.21	0.41
1:B:65:VAL:O	1:B:89:HIS:HB2	2.21	0.41
1:C:241:ASN:ND2	1:C:246:GLU:OE2	2.53	0.41
1:C:141:GLU:OE2	1:C:329:HIS:HB2	2.21	0.41
1:F:25:LEU:HD23	1:F:28:PHE:CE1	2.56	0.41
1:C:231:LEU:HD23	1:C:231:LEU:HA	1.88	0.41
1:E:195:LEU:HD21	1:E:205:ARG:HD3	2.03	0.41
1:D:207:PHE:HE2	1:D:209:CYS:HB2	1.86	0.41
1:A:87:ILE:HG13	1:F:122:TYR:CE1	2.56	0.41
1:F:177:GLN:O	1:F:178:VAL:HG12	2.21	0.41
1:A:75:ALA:HB3	1:A:78:GLU:OE2	2.20	0.41
1:E:253:LEU:O	1:E:254:THR:HB	2.21	0.41
1:E:142:ILE:HB	1:E:298:VAL:HG11	2.02	0.41
1:G:310:ARG:HE	1:G:321:ILE:HD11	1.85	0.41
1:C:130:LEU:HD12	1:C:130:LEU:HA	1.90	0.41
1:F:11:GLY:O	1:F:12:THR:HB	2.21	0.41
1:F:27:LEU:HD13	1:F:28:PHE:N	2.21	0.41
1:C:192:ARG:HD2	1:C:243:MET:HB3	2.02	0.41
1:C:218:LEU:HD22	1:C:232:ILE:HG21	2.03	0.41
1:D:121:GLU:O	1:D:125:GLN:HG2	2.20	0.41
1:B:295:ARG:HD2	1:B:296:SER:H	1.85	0.41
1:C:113:MET:N	1:C:113:MET:SD	2.90	0.41
1:C:83:LYS:HD3	1:C:83:LYS:N	2.36	0.41
1:B:201:PRO:HB2	1:B:203:ALA:HB3	2.03	0.41
1:C:50:HIS:ND1	1:C:51:MET:N	2.69	0.40
1:A:24:LYS:HZ2	1:A:24:LYS:HG2	1.81	0.40
1:A:116:TYR:HE2	1:A:118:VAL:HG23	1.85	0.40
1:B:188:LEU:HA	1:B:188:LEU:HD13	1.91	0.40
1:D:33:GLY:HA3	1:E:63:PHE:HE1	1.85	0.40
1:C:295:ARG:C	1:C:297:ALA:HB2	2.34	0.40
1:F:28:PHE:HB3	1:F:29:LEU:H	1.71	0.40
1:B:233:ASP:HA	1:B:234:PRO:HD3	1.77	0.40
1:D:333:ARG:N	1:D:334:PRO:HD2	2.36	0.40
1:F:147:ASN:HB2	1:F:283:VAL:CG1	2.51	0.40
1:B:112:ALA:O	1:B:113:MET:HG2	2.21	0.40
1:E:85:LYS:HA	1:E:85:LYS:HD3	1.77	0.40
1:F:188:LEU:HB3	1:F:242:VAL:HG11	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:VAL:HG13	1:A:281:VAL:HA	2.04	0.40
1:F:234:PRO:O	1:F:235:GLU:HB3	2.21	0.40
1:G:343:LYS:HD3	1:G:344:VAL:O	2.20	0.40
1:D:145:LEU:HD12	1:D:145:LEU:HA	1.92	0.40
1:G:109:ILE:HA	1:G:109:ILE:HD12	1.94	0.40
1:C:171:LYS:HG3	1:C:171:LYS:H	1.51	0.40
1:C:159:LEU:HD12	1:C:161:THR:H	1.87	0.40
1:G:62:GLN:OE1	1:G:91:GLU:HG3	2.20	0.40
1:D:228:TYR:HE1	1:D:230:ALA:HB3	1.86	0.40
1:E:227:ASN:OD1	1:E:227:ASN:N	2.55	0.40
1:C:305:ASP:CG	1:C:306:LEU:N	2.74	0.40
1:F:254:THR:HG21	1:F:285:LYS:HE3	2.02	0.40
1:B:295:ARG:HD2	1:B:296:SER:N	2.37	0.40
1:A:147:ASN:N	1:A:147:ASN:HD22	2.19	0.40
1:F:25:LEU:HA	1:F:26:ALA:HB3	2.00	0.40
1:C:332:LEU:O	1:C:332:LEU:HD12	2.21	0.40
1:D:223:PRO:O	1:D:224:ASN:CB	2.70	0.40
1:G:25:LEU:HB2	1:G:26:ALA:CB	2.44	0.40
1:G:231:LEU:HB3	1:G:233:ASP:HB2	2.03	0.40
1:A:223:PRO:HG3	1:B:230:ALA:CB	2.52	0.40
1:E:125:GLN:NE2	1:F:67:GLY:O	2.55	0.40
1:B:130:LEU:HD12	1:B:130:LEU:HA	1.84	0.40
1:C:16:LYS:HE3	1:C:16:LYS:HB3	1.44	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	341/345 (99%)	262 (77%)	51 (15%)	28 (8%)	1	13
1	B	341/345 (99%)	275 (81%)	40 (12%)	26 (8%)	1	15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	341/345 (99%)	267 (78%)	48 (14%)	26 (8%)	1	15
1	D	341/345 (99%)	271 (80%)	46 (14%)	24 (7%)	1	18
1	E	341/345 (99%)	266 (78%)	50 (15%)	25 (7%)	1	16
1	F	341/345 (99%)	280 (82%)	38 (11%)	23 (7%)	1	19
1	G	341/345 (99%)	281 (82%)	36 (11%)	24 (7%)	1	18
All	All	2387/2415 (99%)	1902 (80%)	309 (13%)	176 (7%)	3	16

All (176) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	9	GLN
1	A	19	VAL
1	A	76	PRO
1	A	222	MET
1	A	236	LYS
1	A	244	GLY
1	A	277	GLY
1	A	288	VAL
1	A	295	ARG
1	B	47	THR
1	B	118	VAL
1	B	156	ILE
1	B	157	GLU
1	B	200	VAL
1	B	206	VAL
1	B	232	ILE
1	B	236	LYS
1	B	239	ILE
1	B	333	ARG
1	B	335	GLU
1	C	8	GLN
1	C	12	THR
1	C	51	MET
1	C	116	TYR
1	C	170	ASN
1	C	175	THR
1	C	240	ARG
1	C	288	VAL
1	C	295	ARG
1	C	337	ALA

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Mol	Chain	Res	Type
1	D	69	THR
1	D	118	VAL
1	D	142	ILE
1	D	148	VAL
1	D	333	ARG
1	D	334	PRO
1	E	18	VAL
1	E	19	VAL
1	E	49	ARG
1	E	159	LEU
1	E	239	ILE
1	E	288	VAL
1	F	8	GLN
1	F	12	THR
1	F	28	PHE
1	F	48	SER
1	F	118	VAL
1	F	178	VAL
1	F	240	ARG
1	F	266	THR
1	G	12	THR
1	G	52	VAL
1	G	100	LEU
1	G	117	ASP
1	G	156	ILE
1	G	222	MET
1	G	234	PRO
1	A	116	TYR
1	B	57	SER
1	B	228	TYR
1	B	235	GLU
1	B	244	GLY
1	B	288	VAL
1	C	58	GLY
1	C	118	VAL
1	C	201	PRO
1	C	266	THR
1	C	278	GLU
1	D	20	ALA
1	D	48	SER
1	D	149	GLU
1	D	244	GLY

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Mol	Chain	Res	Type
1	E	8	GLN
1	E	12	THR
1	F	19	VAL
1	F	57	SER
1	F	168	THR
1	F	243	MET
1	F	247	VAL
1	G	152	TYR
1	G	199	TYR
1	G	226	ALA
1	G	267	GLY
1	G	288	VAL
1	G	295	ARG
1	A	12	THR
1	A	33	GLY
1	A	57	SER
1	A	168	THR
1	A	261	ALA
1	B	86	ASP
1	C	19	VAL
1	C	161	THR
1	C	222	MET
1	C	228	TYR
1	C	239	ILE
1	D	12	THR
1	D	23	ASP
1	D	116	TYR
1	D	152	TYR
1	D	154	GLU
1	D	157	GLU
1	D	170	ASN
1	D	254	THR
1	D	288	VAL
1	E	13	ASN
1	E	118	VAL
1	E	119	ARG
1	E	145	LEU
1	E	227	ASN
1	F	23	ASP
1	F	175	THR
1	G	8	GLN
1	G	174	LEU

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Mol	Chain	Res	Type
1	G	228	TYR
1	G	232	ILE
1	G	238	SER
1	G	261	ALA
1	A	200	VAL
1	A	234	PRO
1	A	266	THR
1	A	267	GLY
1	A	280	ASN
1	B	12	THR
1	B	45	VAL
1	B	167	THR
1	B	266	THR
1	C	23	ASP
1	C	280	ASN
1	D	57	SER
1	D	224	ASN
1	E	167	THR
1	E	175	THR
1	E	203	ALA
1	E	235	GLU
1	E	266	THR
1	F	14	GLN
1	F	20	ALA
1	F	167	THR
1	F	200	VAL
1	F	239	ILE
1	G	233	ASP
1	G	260	THR
1	A	3	SER
1	B	74	LEU
1	B	168	THR
1	C	168	THR
1	C	242	VAL
1	D	88	LYS
1	E	58	GLY
1	E	240	ARG
1	F	235	GLU
1	G	86	ASP
1	G	239	ILE
1	A	68	ARG
1	A	142	ILE

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Mol	Chain	Res	Type
1	A	152	TYR
1	A	199	TYR
1	B	223	PRO
1	C	333	ARG
1	F	47	THR
1	B	242	VAL
1	B	264	GLY
1	A	64	PRO
1	A	232	ILE
1	E	144	GLY
1	F	206	VAL
1	G	237	GLY
1	C	279	GLY
1	D	45	VAL
1	E	158	GLY
1	E	223	PRO
1	A	242	VAL
1	E	333	ARG
1	D	200	VAL
1	E	200	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	259/261 (99%)	160 (62%)	99 (38%)	0	1
1	B	259/261 (99%)	150 (58%)	109 (42%)	0	1
1	C	259/261 (99%)	171 (66%)	88 (34%)	0	2
1	D	259/261 (99%)	167 (64%)	92 (36%)	0	1
1	E	259/261 (99%)	166 (64%)	93 (36%)	0	1
1	F	259/261 (99%)	165 (64%)	94 (36%)	0	1
1	G	259/261 (99%)	166 (64%)	93 (36%)	0	1
All	All	1813/1827 (99%)	1145 (63%)	668 (37%)	1	1

All (668) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	SER
1	A	24	LYS
1	A	25	LEU
1	A	27	LEU
1	A	29	LEU
1	A	32	PHE
1	A	36	VAL
1	A	37	LEU
1	A	38	THR
1	A	45	VAL
1	A	46	THR
1	A	48	SER
1	A	49	ARG
1	A	50	HIS
1	A	51	MET
1	A	52	VAL
1	A	59	LYS
1	A	66	LEU
1	A	68	ARG
1	A	69	THR
1	A	74	LEU
1	A	79	ASN
1	A	80	LEU
1	A	83	LYS
1	A	84	ARG
1	A	87	ILE
1	A	89	HIS
1	A	93	VAL
1	A	94	ILE
1	A	100	LEU
1	A	105	LEU
1	A	109	ILE
1	A	113	MET
1	A	114	ASN
1	A	115	HIS
1	A	118	VAL
1	A	120	SER
1	A	123	THR
1	A	125	GLN
1	A	130	LEU
1	A	142	ILE
1	A	145	LEU

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Mol	Chain	Res	Type
1	A	149	GLU
1	A	151	LYS
1	A	153	ASN
1	A	154	GLU
1	A	159	LEU
1	A	163	THR
1	A	165	ILE
1	A	166	GLU
1	A	167	THR
1	A	168	THR
1	A	169	GLN
1	A	170	ASN
1	A	171	LYS
1	A	174	LEU
1	A	180	LEU
1	A	188	LEU
1	A	192	ARG
1	A	204	ASP
1	A	217	ILE
1	A	218	LEU
1	A	221	LEU
1	A	222	MET
1	A	228	TYR
1	A	231	LEU
1	A	232	ILE
1	A	235	GLU
1	A	236	LYS
1	A	239	ILE
1	A	249	GLU
1	A	260	THR
1	A	262	ARG
1	A	265	THR
1	A	269	LYS
1	A	276	LYS
1	A	281	VAL
1	A	285	LYS
1	A	286	ASP
1	A	287	ASN
1	A	289	ILE
1	A	293	MET
1	A	295	ARG
1	A	303	LEU

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Mol	Chain	Res	Type
1	A	304	ARG
1	A	306	LEU
1	A	308	LEU
1	A	313	ARG
1	A	320	GLN
1	A	322	ILE
1	A	324	LYS
1	A	325	TYR
1	A	332	LEU
1	A	333	ARG
1	A	334	PRO
1	A	340	VAL
1	A	341	VAL
1	A	343	LYS
1	A	344	VAL
1	B	10	MET
1	B	19	VAL
1	B	23	ASP
1	B	28	PHE
1	B	29	LEU
1	B	30	LYS
1	B	32	PHE
1	B	38	THR
1	B	43	THR
1	B	46	THR
1	B	47	THR
1	B	50	HIS
1	B	51	MET
1	B	53	ARG
1	B	55	ILE
1	B	59	LYS
1	B	62	GLN
1	B	68	ARG
1	B	69	THR
1	B	73	TYR
1	B	78	GLU
1	B	79	ASN
1	B	82	ASP
1	B	84	ARG
1	B	85	LYS
1	B	86	ASP
1	B	87	ILE

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Mol	Chain	Res	Type
1	B	88	LYS
1	B	92	LYS
1	B	93	VAL
1	B	95	THR
1	B	96	ILE
1	B	103	ASP
1	B	105	LEU
1	B	106	ILE
1	B	110	GLU
1	B	113	MET
1	B	115	HIS
1	B	116	TYR
1	B	117	ASP
1	B	128	GLU
1	B	130	LEU
1	B	142	ILE
1	B	149	GLU
1	B	150	SER
1	B	151	LYS
1	B	153	ASN
1	B	154	GLU
1	B	155	ASN
1	B	156	ILE
1	B	157	GLU
1	B	159	LEU
1	B	165	ILE
1	B	166	GLU
1	B	167	THR
1	B	168	THR
1	B	170	ASN
1	B	174	LEU
1	B	176	ASP
1	B	182	LYS
1	B	188	LEU
1	B	192	ARG
1	B	195	LEU
1	B	197	LYS
1	B	198	ASN
1	B	199	TYR
1	B	200	VAL
1	B	205	ARG
1	B	206	VAL

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Mol	Chain	Res	Type
1	B	210	ASP
1	B	212	ASP
1	B	215	SER
1	B	217	ILE
1	B	221	LEU
1	B	222	MET
1	B	232	ILE
1	B	233	ASP
1	B	236	LYS
1	B	239	ILE
1	B	240	ARG
1	B	241	ASN
1	B	243	MET
1	B	247	VAL
1	B	249	GLU
1	B	253	LEU
1	B	262	ARG
1	B	272	PHE
1	B	275	ASN
1	B	276	LYS
1	B	278	GLU
1	B	280	ASN
1	B	281	VAL
1	B	283	VAL
1	B	285	LYS
1	B	289	ILE
1	B	294	HIS
1	B	295	ARG
1	B	303	LEU
1	B	304	ARG
1	B	306	LEU
1	B	309	GLU
1	B	319	ASP
1	B	320	GLN
1	B	324	LYS
1	B	325	TYR
1	B	332	LEU
1	B	333	ARG
1	B	335	GLU
1	B	340	VAL
1	C	16	LYS
1	C	25	LEU

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Mol	Chain	Res	Type
1	C	27	LEU
1	C	29	LEU
1	C	32	PHE
1	C	37	LEU
1	C	46	THR
1	C	49	ARG
1	C	51	MET
1	C	55	ILE
1	C	59	LYS
1	C	62	GLN
1	C	69	THR
1	C	73	TYR
1	C	74	LEU
1	C	79	ASN
1	C	80	LEU
1	C	81	ASP
1	C	83	LYS
1	C	84	ARG
1	C	87	ILE
1	C	88	LYS
1	C	89	HIS
1	C	92	LYS
1	C	94	ILE
1	C	96	ILE
1	C	100	LEU
1	C	101	THR
1	C	108	ASP
1	C	109	ILE
1	C	113	MET
1	C	115	HIS
1	C	118	VAL
1	C	119	ARG
1	C	124	SER
1	C	130	LEU
1	C	132	MET
1	C	142	ILE
1	C	147	ASN
1	C	149	GLU
1	C	154	GLU
1	C	159	LEU
1	C	163	THR
1	C	165	ILE

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Mol	Chain	Res	Type
1	C	171	LYS
1	C	174	LEU
1	C	175	THR
1	C	176	ASP
1	C	178	VAL
1	C	190	LYS
1	C	195	LEU
1	C	197	LYS
1	C	200	VAL
1	C	204	ASP
1	C	205	ARG
1	C	206	VAL
1	C	215	SER
1	C	218	LEU
1	C	224	ASN
1	C	232	ILE
1	C	236	LYS
1	C	247	VAL
1	C	249	GLU
1	C	253	LEU
1	C	265	THR
1	C	269	LYS
1	C	271	VAL
1	C	275	ASN
1	C	281	VAL
1	C	282	LYS
1	C	283	VAL
1	C	289	ILE
1	C	295	ARG
1	C	300	THR
1	C	301	VAL
1	C	303	LEU
1	C	304	ARG
1	C	305	ASP
1	C	309	GLU
1	C	310	ARG
1	C	312	ARG
1	C	313	ARG
1	C	320	GLN
1	C	324	LYS
1	C	327	MET
1	C	329	HIS

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Mol	Chain	Res	Type
1	C	333	ARG
1	C	341	VAL
1	D	5	THR
1	D	9	GLN
1	D	10	MET
1	D	13	ASN
1	D	14	GLN
1	D	18	VAL
1	D	19	VAL
1	D	25	LEU
1	D	29	LEU
1	D	31	VAL
1	D	32	PHE
1	D	35	GLU
1	D	37	LEU
1	D	43	THR
1	D	52	VAL
1	D	53	ARG
1	D	55	ILE
1	D	60	SER
1	D	66	LEU
1	D	73	TYR
1	D	74	LEU
1	D	80	LEU
1	D	81	ASP
1	D	87	ILE
1	D	90	THR
1	D	91	GLU
1	D	94	ILE
1	D	96	ILE
1	D	100	LEU
1	D	101	THR
1	D	105	LEU
1	D	108	ASP
1	D	109	ILE
1	D	114	ASN
1	D	123	THR
1	D	126	LEU
1	D	130	LEU
1	D	132	MET
1	D	135	ASP
1	D	139	LEU

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Mol	Chain	Res	Type
1	D	141	GLU
1	D	142	ILE
1	D	149	GLU
1	D	156	ILE
1	D	157	GLU
1	D	163	THR
1	D	165	ILE
1	D	166	GLU
1	D	167	THR
1	D	168	THR
1	D	170	ASN
1	D	171	LYS
1	D	175	THR
1	D	183	GLU
1	D	188	LEU
1	D	192	ARG
1	D	196	THR
1	D	200	VAL
1	D	205	ARG
1	D	209	CYS
1	D	212	ASP
1	D	218	LEU
1	D	221	LEU
1	D	227	ASN
1	D	241	ASN
1	D	248	VAL
1	D	249	GLU
1	D	250	VAL
1	D	253	LEU
1	D	260	THR
1	D	266	THR
1	D	268	GLN
1	D	275	ASN
1	D	276	LYS
1	D	278	GLU
1	D	282	LYS
1	D	283	VAL
1	D	295	ARG
1	D	301	VAL
1	D	303	LEU
1	D	304	ARG
1	D	309	GLU

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Mol	Chain	Res	Type
1	D	312	ARG
1	D	313	ARG
1	D	320	GLN
1	D	321	ILE
1	D	322	ILE
1	D	325	TYR
1	D	332	LEU
1	D	333	ARG
1	D	335	GLU
1	D	344	VAL
1	E	5	THR
1	E	19	VAL
1	E	25	LEU
1	E	27	LEU
1	E	28	PHE
1	E	29	LEU
1	E	30	LYS
1	E	35	GLU
1	E	38	THR
1	E	40	PHE
1	E	42	ARG
1	E	44	SER
1	E	45	VAL
1	E	46	THR
1	E	47	THR
1	E	49	ARG
1	E	52	VAL
1	E	54	SER
1	E	59	LYS
1	E	69	THR
1	E	70	GLN
1	E	80	LEU
1	E	81	ASP
1	E	82	ASP
1	E	84	ARG
1	E	86	ASP
1	E	88	LYS
1	E	90	THR
1	E	92	LYS
1	E	94	ILE
1	E	95	THR
1	E	100	LEU

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Mol	Chain	Res	Type
1	E	105	LEU
1	E	119	ARG
1	E	122	TYR
1	E	124	SER
1	E	128	GLU
1	E	130	LEU
1	E	142	ILE
1	E	151	LYS
1	E	153	ASN
1	E	161	THR
1	E	165	ILE
1	E	167	THR
1	E	168	THR
1	E	170	ASN
1	E	171	LYS
1	E	174	LEU
1	E	178	VAL
1	E	188	LEU
1	E	189	THR
1	E	192	ARG
1	E	198	ASN
1	E	200	VAL
1	E	204	ASP
1	E	206	VAL
1	E	209	CYS
1	E	210	ASP
1	E	212	ASP
1	E	215	SER
1	E	221	LEU
1	E	227	ASN
1	E	231	LEU
1	E	235	GLU
1	E	239	ILE
1	E	240	ARG
1	E	243	MET
1	E	245	PHE
1	E	249	GLU
1	E	250	VAL
1	E	252	HIS
1	E	271	VAL
1	E	272	PHE
1	E	275	ASN

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Mol	Chain	Res	Type
1	E	287	ASN
1	E	289	ILE
1	E	295	ARG
1	E	298	VAL
1	E	303	LEU
1	E	304	ARG
1	E	308	LEU
1	E	309	GLU
1	E	310	ARG
1	E	312	ARG
1	E	313	ARG
1	E	315	ASN
1	E	320	GLN
1	E	324	LYS
1	E	325	TYR
1	E	332	LEU
1	E	341	VAL
1	E	342	PHE
1	E	343	LYS
1	F	3	SER
1	F	13	ASN
1	F	16	LYS
1	F	18	VAL
1	F	24	LYS
1	F	25	LEU
1	F	27	LEU
1	F	29	LEU
1	F	30	LYS
1	F	36	VAL
1	F	38	THR
1	F	42	ARG
1	F	43	THR
1	F	44	SER
1	F	47	THR
1	F	50	HIS
1	F	51	MET
1	F	52	VAL
1	F	53	ARG
1	F	54	SER
1	F	55	ILE
1	F	59	LYS
1	F	66	LEU

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Mol	Chain	Res	Type
1	F	69	THR
1	F	78	GLU
1	F	80	LEU
1	F	82	ASP
1	F	89	HIS
1	F	95	THR
1	F	101	THR
1	F	108	ASP
1	F	109	ILE
1	F	113	MET
1	F	117	ASP
1	F	118	VAL
1	F	128	GLU
1	F	130	LEU
1	F	139	LEU
1	F	142	ILE
1	F	145	LEU
1	F	154	GLU
1	F	156	ILE
1	F	159	LEU
1	F	161	THR
1	F	163	THR
1	F	167	THR
1	F	178	VAL
1	F	188	LEU
1	F	195	LEU
1	F	196	THR
1	F	204	ASP
1	F	210	ASP
1	F	212	ASP
1	F	221	LEU
1	F	222	MET
1	F	227	ASN
1	F	228	TYR
1	F	231	LEU
1	F	232	ILE
1	F	233	ASP
1	F	235	GLU
1	F	236	LYS
1	F	243	MET
1	F	249	GLU
1	F	250	VAL

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Mol	Chain	Res	Type
1	F	252	HIS
1	F	260	THR
1	F	263	GLU
1	F	265	THR
1	F	268	GLN
1	F	271	VAL
1	F	275	ASN
1	F	276	LYS
1	F	281	VAL
1	F	282	LYS
1	F	286	ASP
1	F	295	ARG
1	F	296	SER
1	F	300	THR
1	F	302	LYS
1	F	303	LEU
1	F	304	ARG
1	F	306	LEU
1	F	309	GLU
1	F	310	ARG
1	F	312	ARG
1	F	320	GLN
1	F	321	ILE
1	F	322	ILE
1	F	324	LYS
1	F	325	TYR
1	F	332	LEU
1	F	333	ARG
1	F	340	VAL
1	G	10	MET
1	G	16	LYS
1	G	23	ASP
1	G	24	LYS
1	G	25	LEU
1	G	29	LEU
1	G	31	VAL
1	G	35	GLU
1	G	37	LEU
1	G	38	THR
1	G	42	ARG
1	G	46	THR
1	G	50	HIS

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Mol	Chain	Res	Type
1	G	51	MET
1	G	52	VAL
1	G	53	ARG
1	G	55	ILE
1	G	57	SER
1	G	59	LYS
1	G	62	GLN
1	G	63	PHE
1	G	65	VAL
1	G	66	LEU
1	G	68	ARG
1	G	70	GLN
1	G	73	TYR
1	G	82	ASP
1	G	83	LYS
1	G	84	ARG
1	G	85	LYS
1	G	86	ASP
1	G	87	ILE
1	G	89	HIS
1	G	91	GLU
1	G	94	ILE
1	G	95	THR
1	G	97	ASP
1	G	99	LEU
1	G	105	LEU
1	G	110	GLU
1	G	114	ASN
1	G	119	ARG
1	G	121	GLU
1	G	123	THR
1	G	124	SER
1	G	126	LEU
1	G	130	LEU
1	G	139	LEU
1	G	142	ILE
1	G	145	LEU
1	G	147	ASN
1	G	154	GLU
1	G	163	THR
1	G	171	LYS
1	G	182	LYS

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Mol	Chain	Res	Type
1	G	188	LEU
1	G	196	THR
1	G	197	LYS
1	G	200	VAL
1	G	205	ARG
1	G	217	ILE
1	G	218	LEU
1	G	224	ASN
1	G	228	TYR
1	G	235	GLU
1	G	240	ARG
1	G	242	VAL
1	G	243	MET
1	G	248	VAL
1	G	250	VAL
1	G	268	GLN
1	G	269	LYS
1	G	271	VAL
1	G	272	PHE
1	G	276	LYS
1	G	281	VAL
1	G	282	LYS
1	G	285	LYS
1	G	295	ARG
1	G	296	SER
1	G	300	THR
1	G	303	LEU
1	G	308	LEU
1	G	309	GLU
1	G	310	ARG
1	G	320	GLN
1	G	321	ILE
1	G	324	LYS
1	G	325	TYR
1	G	332	LEU
1	G	341	VAL
1	G	342	PHE
1	G	343	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (48) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	GLN
1	A	50	HIS
1	A	89	HIS
1	A	125	GLN
1	A	147	ASN
1	A	252	HIS
1	A	287	ASN
1	A	294	HIS
1	A	315	ASN
1	B	79	ASN
1	B	115	HIS
1	B	155	ASN
1	B	270	HIS
1	B	275	ASN
1	B	280	ASN
1	B	287	ASN
1	B	294	HIS
1	C	50	HIS
1	C	147	ASN
1	C	153	ASN
1	C	268	GLN
1	D	14	GLN
1	D	50	HIS
1	D	89	HIS
1	D	153	ASN
1	D	252	HIS
1	D	315	ASN
1	E	50	HIS
1	E	89	HIS
1	E	114	ASN
1	E	170	ASN
1	E	280	ASN
1	E	315	ASN
1	F	147	ASN
1	F	169	GLN
1	F	227	ASN
1	F	252	HIS
1	F	268	GLN
1	F	287	ASN
1	G	70	GLN
1	G	79	ASN
1	G	114	ASN
1	G	125	GLN

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Mol	Chain	Res	Type
1	G	147	ASN
1	G	169	GLN
1	G	224	ASN
1	G	241	ASN
1	G	315	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.