



## Full wwPDB EM Validation Report ⓘ

Jun 23, 2025 – 03:27 PM EDT

PDB ID : 9MOI / pdb\_00009moi  
EMDB ID : EMD-48467  
Title : Structure of native murine cardiac thin filament at pCa=5.8 in Ca<sup>2+</sup>-free  
rotated state (lower strand)  
Authors : Galkin, V.E.; Risi, C.M.  
Deposited on : 2024-12-26  
Resolution : 5.40 Å (reported)  
Based on initial models : 8DD0, 8UZ5, 7KO4, 7UTL

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev118  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0rc1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.44

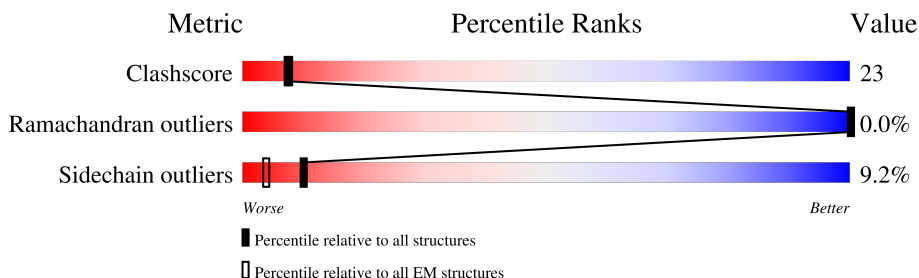
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 5.40 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.





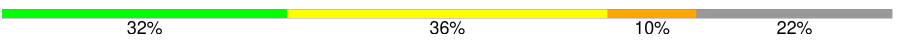
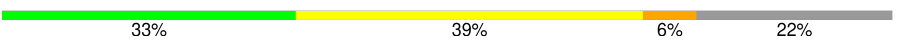


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	377	
1	B	377	
1	C	377	
1	D	377	
1	E	377	
1	F	377	
2	G	161	
3	H	211	

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Mol	Chain	Length	Quality of chain
4	I	291	 17% 5% 78%
4	J	291	 16% 9% 75%
5	K	284	 32% 36% 10% 22%
5	L	284	 33% 39% 6% 22%
5	M	284	 12% 7% 81%
5	N	284	 12% 7% 81%

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 25967 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 Actin, alpha cardiac muscle 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	371	Total	C	N	O	S	0	0
			2898	1836	489	553	20		
1	B	371	Total	C	N	O	S	0	0
			2898	1836	489	553	20		
1	C	371	Total	C	N	O	S	0	0
			2898	1836	489	553	20		
1	D	371	Total	C	N	O	S	0	0
			2898	1836	489	553	20		
1	E	371	Total	C	N	O	S	0	0
			2898	1836	489	553	20		
1	F	371	Total	C	N	O	S	0	0
			2898	1836	489	553	20		

- Molecule 2 is a protein called Troponin C, slow skeletal and cardiac muscles.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	160	Total	C	N	O	S	0	0
			1273	787	195	278	13		

- Molecule 3 is a protein called Troponin I, cardiac muscle.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	170	Total	C	N	O	S	0	0
			1389	855	266	261	7		

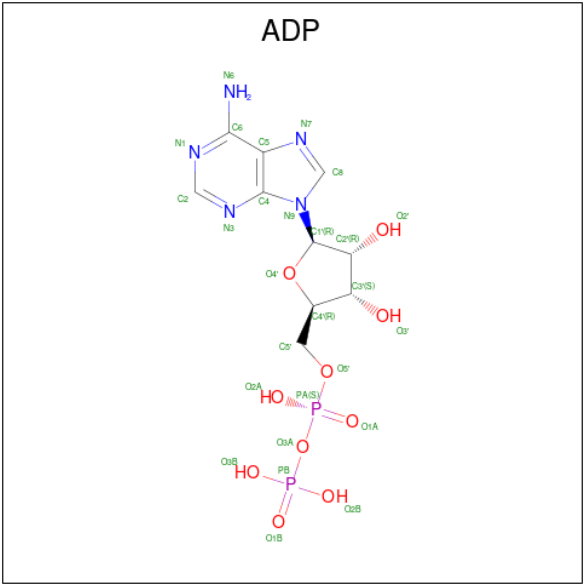
- Molecule 4 is a protein called Isoform A2 of Troponin T, cardiac muscle.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	I	74	Total	C	N	O		0	0
			639	396	125	118			
4	J	77	Total	C	N	O		0	0
			670	405	136	129			

- Molecule 5 is a protein called Tropomyosin alpha-1 chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	K	221	Total	C	N	O	S	0	0
			1783	1091	302	386	4		
5	L	221	Total	C	N	O	S	0	0
			1783	1091	302	386	4		
5	M	55	Total	C	N	O	S	0	0
			437	266	77	91	3		
5	N	55	Total	C	N	O	S	0	0
			437	266	77	91	3		

- Molecule 6 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>).



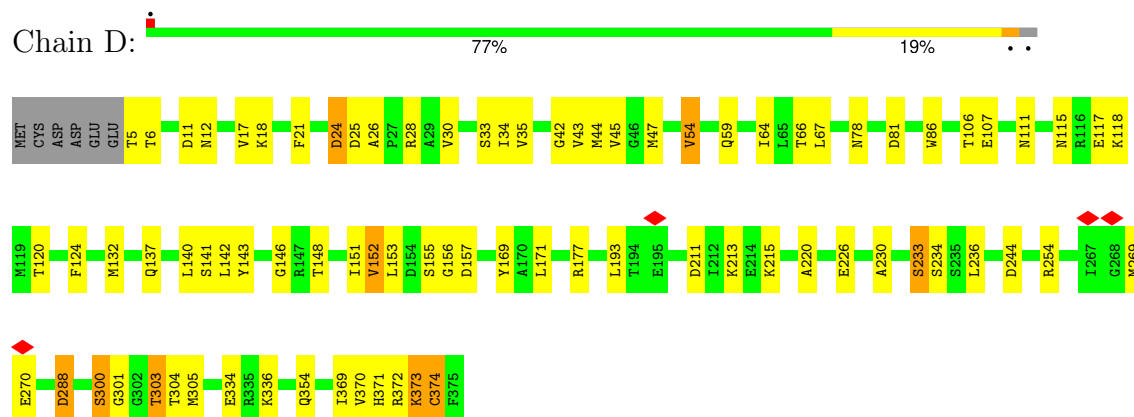
Mol	Chain	Residues	Atoms					AltConf
6	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
6	B	1	Total	C	N	O	P	0
			27	10	5	10	2	
6	C	1	Total	C	N	O	P	0
			27	10	5	10	2	
6	D	1	Total	C	N	O	P	0
			27	10	5	10	2	
6	E	1	Total	C	N	O	P	0
			27	10	5	10	2	
6	F	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 7 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

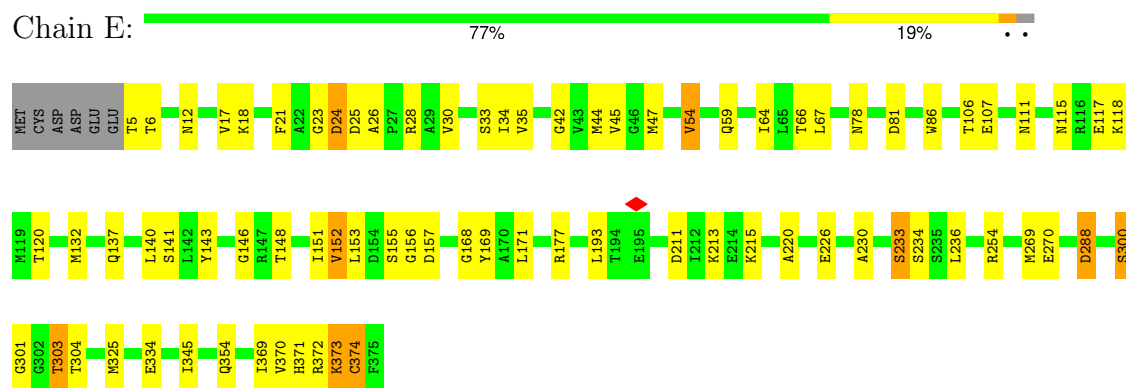
Mol	Chain	Residues	Atoms		AltConf
7	A	1	Total 1	Mg 1	0
7	B	1	Total 1	Mg 1	0
7	C	1	Total 1	Mg 1	0
7	D	1	Total 1	Mg 1	0
7	E	1	Total 1	Mg 1	0
7	F	1	Total 1	Mg 1	0



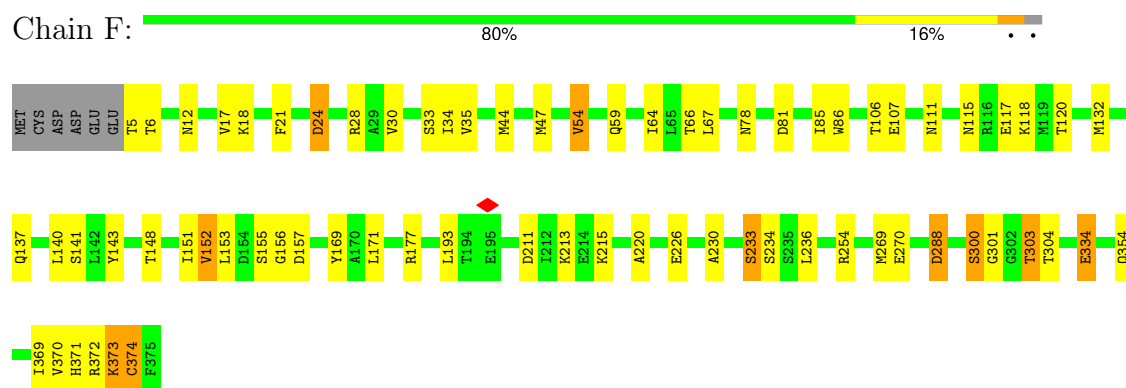
- Molecule 1: Actin, alpha cardiac muscle 1



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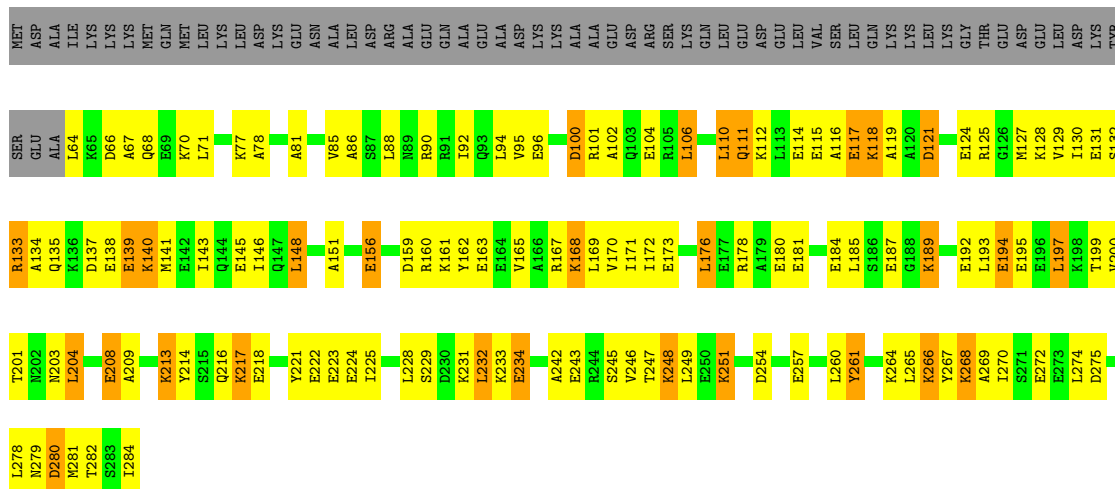


- Molecule 2: Troponin C, slow skeletal and cardiac muscles

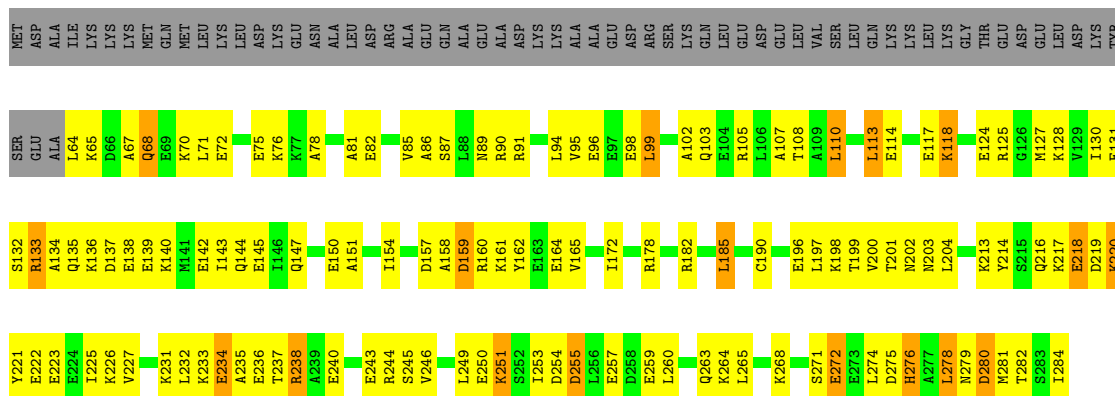








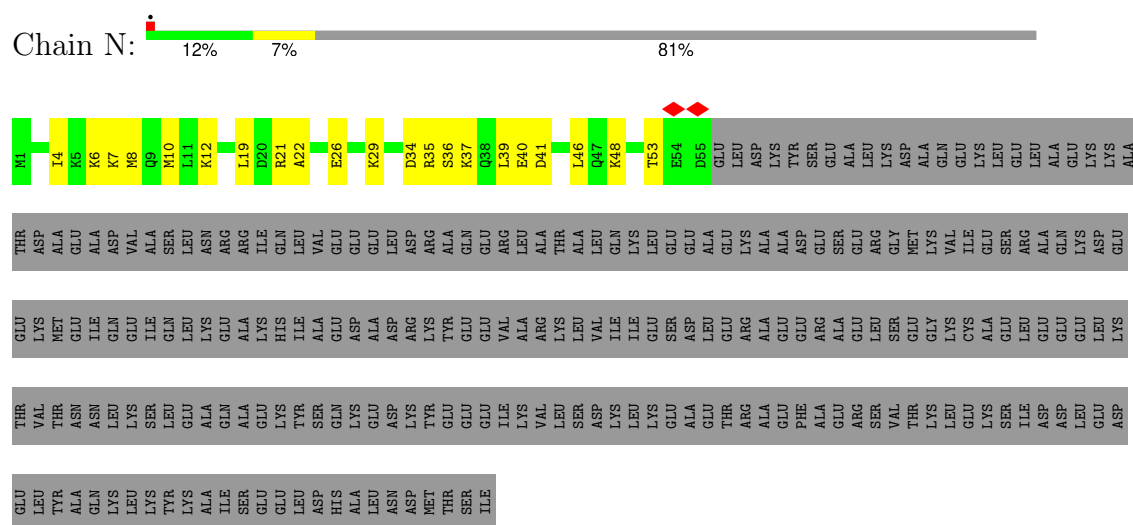
- Molecule 5: Tropomyosin alpha-1 chain



- Molecule 5: Tropomyosin alpha-1 chain



- Molecule 5: Tropomyosin alpha-1 chain



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	70248	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	34	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	9.413	Depositor
Minimum map value	-3.067	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.270	Depositor
Recommended contour level	0.515	Depositor
Map size (Å)	439.344, 439.344, 439.344	wwPDB
Map dimensions	324, 324, 324	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.356, 1.356, 1.356	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ADP, MG

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	0.38	0/2961	0.45	0/4011
1	B	0.38	0/2961	0.45	0/4011
1	C	0.38	0/2961	0.46	0/4011
1	D	0.38	0/2961	0.46	0/4011
1	E	0.38	0/2961	0.46	0/4011
1	F	0.38	0/2961	0.45	0/4011
2	G	0.13	0/1286	0.28	0/1718
3	H	0.17	0/1399	0.32	0/1858
4	I	0.17	0/645	0.33	0/855
4	J	0.38	1/676 (0.1%)	0.68	2/898 (0.2%)
5	K	0.25	0/1790	0.39	0/2388
5	L	0.26	0/1790	0.41	0/2388
5	M	0.23	0/436	0.40	0/574
5	N	0.21	0/436	0.36	0/574
All	All	0.34	1/26224 (0.0%)	0.44	2/35319 (0.0%)

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
4	I	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	J	83	PRO	N-CD	5.44	1.55	1.47

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	J	87	ARG	CA-C-N	8.60	137.18	121.70
4	J	87	ARG	C-N-CA	8.60	137.18	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	I	203	LYS	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	2898	0	2871	64	0
1	B	2898	0	2871	80	0
1	C	2898	0	2871	106	0
1	D	2898	0	2871	90	0
1	E	2898	0	2871	102	0
1	F	2898	0	2871	59	0
2	G	1273	0	1199	103	0
3	H	1389	0	1446	181	0
4	I	639	0	657	110	0
4	J	670	0	673	99	0
5	K	1783	0	1779	206	0
5	L	1783	0	1779	287	0
5	M	437	0	458	49	0
5	N	437	0	458	67	0
6	A	27	0	12	2	0
6	B	27	0	12	2	0
6	C	27	0	12	2	0
6	D	27	0	12	2	0
6	E	27	0	12	2	0
6	F	27	0	12	2	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
7	E	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	F	1	0	0	0	0
All	All	25967	0	25747	1177	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 23.

All (1177) 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)
5:K:281:MET:SD	5:M:3:ALA:HB1	1.40	1.59
5:L:284:ILE:HG21	5:N:7:LYS:CE	1.40	1.50
4:J:124:ILE:CD1	5:L:268:LYS:CD	1.93	1.45
4:J:124:ILE:CD1	5:L:268:LYS:HD3	0.98	1.44
1:E:146:GLY:O	3:H:174:LEU:CD1	1.68	1.42
1:D:25:ASP:HB3	3:H:148:VAL:CB	1.48	1.41
5:L:280:ASP:HB3	5:M:5:LYS:NZ	1.23	1.41
5:K:284:ILE:HG13	5:N:8:MET:CE	1.51	1.40
5:L:284:ILE:CG2	5:N:7:LYS:HE2	1.51	1.39
4:J:109:ILE:HD11	5:L:281:MET:CE	1.53	1.36
4:J:112:HIS:NE2	5:L:278:LEU:HD22	1.41	1.33
4:J:116:ARG:NE	5:L:275:ASP:OD2	1.57	1.33
3:H:200:SER:HB2	5:L:99:LEU:CD1	1.58	1.33
1:C:83:GLU:CD	4:I:204:ARG:HG3	1.53	1.30
4:J:109:ILE:CG1	5:L:281:MET:HE1	1.63	1.29
5:N:6:LYS:CG	5:N:10:MET:HE1	1.62	1.28
4:J:112:HIS:NE2	5:L:278:LEU:CD2	1.97	1.28
4:J:112:HIS:CD2	5:L:278:LEU:HD22	1.71	1.25
5:L:280:ASP:CB	5:M:5:LYS:NZ	2.00	1.24
1:D:25:ASP:CB	3:H:148:VAL:HB	1.67	1.23
5:L:280:ASP:CB	5:M:5:LYS:HZ3	1.49	1.22
5:L:284:ILE:HD13	5:N:7:LYS:CG	1.69	1.21
1:C:83:GLU:OE1	4:I:204:ARG:HG3	1.39	1.21
4:J:124:ILE:HD12	5:L:268:LYS:CD	1.59	1.20
5:L:284:ILE:HD13	5:N:7:LYS:CD	1.71	1.19
4:J:109:ILE:CD1	5:L:281:MET:HE1	1.73	1.18
1:E:23:GLY:C	3:H:185:GLU:HB2	1.67	1.18
5:L:196:GLU:O	5:L:199:THR:HG22	1.43	1.18
1:C:83:GLU:OE1	4:I:204:ARG:CG	1.93	1.16
1:B:47:MET:HE2	1:C:148:THR:OG1	1.46	1.16
4:J:109:ILE:CD1	5:L:281:MET:CE	2.22	1.16
1:E:23:GLY:O	3:H:185:GLU:HB2	1.46	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:120:GLU:OE1	5:L:268:LYS:HA	1.41	1.15
3:H:160:LEU:HD22	5:L:147:GLN:CD	1.71	1.15
3:H:197:ASP:O	5:L:103:GLN:OE1	1.65	1.15
4:J:96:LYS:HD2	4:J:96:LYS:O	1.46	1.15
1:C:83:GLU:OE1	4:I:204:ARG:CB	1.95	1.15
5:L:284:ILE:CD1	5:N:7:LYS:CD	2.24	1.15
5:K:281:MET:SD	5:M:3:ALA:CB	2.35	1.14
4:J:130:ILE:CG2	5:L:257:GLU:OE2	1.96	1.13
5:M:7:LYS:CE	5:N:8:MET:HE3	1.76	1.13
4:J:137:ARG:NH2	5:L:254:ASP:OD1	1.79	1.13
5:L:284:ILE:HD12	5:N:7:LYS:HD3	1.30	1.13
1:C:126:THR:HG23	4:I:211:LYS:HZ1	1.14	1.12
1:D:25:ASP:HB3	3:H:148:VAL:CG1	1.78	1.12
1:C:126:THR:HG23	4:I:211:LYS:NZ	1.65	1.12
4:J:109:ILE:HG13	5:L:281:MET:HE1	1.23	1.11
3:H:205:ARG:HD2	5:K:94:LEU:HD11	1.29	1.11
5:L:284:ILE:HD13	5:N:7:LYS:HG2	1.22	1.11
4:J:124:ILE:CG1	5:L:268:LYS:HD3	1.80	1.09
3:H:200:SER:CB	5:L:99:LEU:CD1	2.31	1.08
1:B:326:LYS:NZ	5:K:257:GLU:HG2	1.68	1.07
5:L:284:ILE:CD1	5:N:7:LYS:HD3	1.83	1.07
5:M:7:LYS:HE3	5:N:8:MET:HE3	1.33	1.07
1:C:80:ASP:N	4:I:202:GLY:O	1.88	1.07
1:A:47:MET:HE2	1:B:148:THR:OG1	1.55	1.06
1:C:47:MET:HE2	1:D:148:THR:OG1	1.55	1.06
3:H:200:SER:CB	5:L:99:LEU:HD12	1.84	1.06
1:D:24:ASP:OD1	3:H:147:ARG:NH2	1.87	1.06
3:H:193:ARG:NH1	5:L:114:GLU:OE2	1.87	1.06
1:C:83:GLU:OE2	4:I:207:GLU:OE1	1.75	1.05
1:E:24:ASP:HA	3:H:185:GLU:O	1.56	1.05
3:H:197:ASP:O	5:L:103:GLN:CD	1.99	1.05
5:N:6:LYS:HG3	5:N:10:MET:HE1	1.07	1.05
4:J:109:ILE:HD11	5:L:281:MET:HE3	1.37	1.03
1:D:47:MET:HE2	1:E:148:THR:OG1	1.59	1.03
1:E:24:ASP:HA	3:H:185:GLU:CB	1.89	1.03
5:M:21:ARG:HD2	5:N:26:GLU:OE2	1.56	1.03
5:K:284:ILE:CG1	5:N:8:MET:CE	2.36	1.02
4:J:124:ILE:HD12	5:L:268:LYS:CE	1.86	1.02
1:C:83:GLU:OE1	4:I:204:ARG:HB2	1.56	1.01
5:L:279:ASN:O	5:L:282:THR:OG1	1.78	1.01
1:C:79:TRP:C	4:I:202:GLY:O	2.04	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:284:ILE:HG13	5:N:8:MET:HE1	1.02	1.01
2:G:46:ARG:HG2	5:K:160:ARG:NH2	1.76	1.01
1:A:373:LYS:HD2	1:A:373:LYS:N	1.76	1.00
3:H:200:SER:C	5:L:99:LEU:CD1	2.34	1.00
1:B:373:LYS:N	1:B:373:LYS:HD2	1.76	1.00
2:G:46:ARG:C	5:K:160:ARG:HH21	1.67	1.00
1:E:146:GLY:O	3:H:174:LEU:HD13	0.83	0.99
1:F:373:LYS:HD2	1:F:373:LYS:N	1.76	0.99
3:H:197:ASP:O	5:L:103:GLN:NE2	1.95	0.99
5:L:284:ILE:CD1	5:N:7:LYS:HG2	1.92	0.99
1:C:373:LYS:HD2	1:C:373:LYS:N	1.76	0.98
1:E:373:LYS:HD2	1:E:373:LYS:N	1.76	0.98
3:H:200:SER:CA	5:L:99:LEU:HD13	1.93	0.98
5:L:284:ILE:CD1	5:N:7:LYS:CG	2.42	0.98
4:J:124:ILE:HD12	5:L:268:LYS:HD3	0.99	0.97
1:B:42:GLY:HA2	1:C:169:TYR:HA	1.46	0.97
1:E:146:GLY:C	3:H:174:LEU:HD13	1.88	0.97
4:J:124:ILE:HD11	5:L:268:LYS:HD3	1.01	0.97
5:K:284:ILE:CG1	5:N:8:MET:HE1	1.93	0.97
5:N:6:LYS:HG3	5:N:10:MET:CE	1.92	0.97
5:M:7:LYS:NZ	5:N:8:MET:HE3	1.79	0.97
1:D:373:LYS:HD2	1:D:373:LYS:N	1.76	0.97
1:E:47:MET:HE2	1:F:148:THR:OG1	1.64	0.97
1:A:373:LYS:H	1:A:373:LYS:NZ	1.63	0.96
1:A:373:LYS:N	1:A:373:LYS:HZ3	1.63	0.96
1:D:373:LYS:N	1:D:373:LYS:HZ3	1.62	0.96
1:B:373:LYS:N	1:B:373:LYS:HZ3	1.62	0.96
1:D:373:LYS:H	1:D:373:LYS:NZ	1.63	0.96
5:L:284:ILE:HD13	5:N:7:LYS:CE	1.96	0.95
1:B:373:LYS:H	1:B:373:LYS:NZ	1.63	0.95
1:E:373:LYS:N	1:E:373:LYS:HZ2	1.62	0.95
1:E:373:LYS:H	1:E:373:LYS:NZ	1.63	0.95
1:C:373:LYS:H	1:C:373:LYS:NZ	1.63	0.95
4:J:105:LEU:HD21	5:L:284:ILE:HD12	1.49	0.94
5:L:280:ASP:CG	5:M:5:LYS:HZ1	1.75	0.94
1:F:373:LYS:N	1:F:373:LYS:HZ3	1.62	0.94
1:C:373:LYS:N	1:C:373:LYS:HZ2	1.63	0.94
1:F:373:LYS:H	1:F:373:LYS:NZ	1.63	0.94
1:D:42:GLY:HA2	1:E:169:TYR:HA	1.49	0.94
3:H:200:SER:C	5:L:99:LEU:HD11	1.94	0.93
1:C:83:GLU:CD	4:I:204:ARG:CG	2.39	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:24:ASP:HA	3:H:185:GLU:HB2	1.52	0.92
1:E:24:ASP:CA	3:H:185:GLU:HB2	1.99	0.92
5:M:7:LYS:HE3	5:N:8:MET:CE	1.98	0.92
5:K:135:GLN:OE1	5:L:133:ARG:NH2	2.03	0.92
1:B:326:LYS:HB2	5:K:261:TYR:HE2	1.36	0.91
3:H:200:SER:O	5:L:99:LEU:CD1	2.19	0.91
3:H:205:ARG:CD	5:K:94:LEU:HD11	2.00	0.91
4:J:127:LYS:HZ3	5:L:264:LYS:HE2	1.34	0.90
3:H:200:SER:CA	5:L:99:LEU:CD1	2.50	0.90
4:J:112:HIS:NE2	5:L:278:LEU:HD23	1.83	0.90
4:J:81:LYS:HA	4:J:81:LYS:NZ	1.87	0.90
2:G:47:MET:HA	5:K:160:ARG:HH22	1.35	0.90
4:I:255:GLU:HG2	4:I:259:GLN:HE22	1.37	0.89
5:L:217:LYS:O	5:L:220:LYS:NZ	2.05	0.89
5:N:6:LYS:HG2	5:N:10:MET:HE1	1.55	0.89
1:C:42:GLY:HA2	1:D:169:TYR:HA	1.54	0.88
1:D:25:ASP:HB3	3:H:148:VAL:HB	0.90	0.88
1:E:24:ASP:N	3:H:185:GLU:HB2	1.88	0.88
3:H:193:ARG:HH22	5:L:114:GLU:CD	1.81	0.88
3:H:200:SER:C	5:L:99:LEU:HD13	1.99	0.88
4:J:127:LYS:HE2	5:L:264:LYS:HD2	1.55	0.88
4:J:130:ILE:HG22	5:L:257:GLU:OE2	1.73	0.88
1:E:23:GLY:O	3:H:185:GLU:CB	2.21	0.87
5:L:280:ASP:CG	5:M:5:LYS:NZ	2.31	0.87
5:K:216:GLN:OE1	5:K:217:LYS:NZ	2.07	0.87
1:A:42:GLY:HA2	1:B:169:TYR:HA	1.53	0.87
4:J:120:GLU:OE1	5:L:268:LYS:CA	2.21	0.87
3:H:200:SER:HB2	5:L:99:LEU:HD12	0.89	0.87
5:K:284:ILE:CD1	5:N:8:MET:HE2	2.04	0.87
3:H:112:ARG:HH21	4:I:247:GLU:HG2	1.39	0.87
5:K:101:ARG:O	5:K:104:GLU:HG3	1.75	0.87
5:L:284:ILE:CB	5:N:7:LYS:HE2	2.05	0.87
5:L:280:ASP:CB	5:M:5:LYS:HZ1	1.84	0.86
4:J:127:LYS:NZ	5:L:264:LYS:HE2	1.91	0.86
5:L:124:GLU:OE1	5:L:125:ARG:NE	2.09	0.86
1:E:24:ASP:CA	3:H:185:GLU:CB	2.55	0.85
1:E:345:ILE:HG12	3:H:181:ASP:CG	2.00	0.85
3:H:160:LEU:HD13	5:L:147:GLN:HE21	1.41	0.85
5:L:139:GLU:O	5:L:142:GLU:HG2	1.77	0.85
5:L:220:LYS:HZ2	5:L:220:LYS:HB3	1.42	0.84
1:C:373:LYS:H	1:C:373:LYS:HZ2	0.84	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:104:GLU:OE2	5:N:6:LYS:NZ	2.09	0.83
2:G:46:ARG:HG2	5:K:160:ARG:CZ	2.08	0.83
5:L:284:ILE:HG21	5:N:7:LYS:HE3	1.57	0.83
2:G:46:ARG:O	5:K:160:ARG:NH2	2.11	0.83
1:E:24:ASP:OD1	3:H:185:GLU:CB	2.27	0.83
4:J:124:ILE:HD11	5:L:268:LYS:CD	1.77	0.83
5:M:7:LYS:HZ1	5:N:8:MET:HE3	1.44	0.82
5:L:284:ILE:CD1	5:N:7:LYS:HE2	2.09	0.82
5:K:281:MET:HE1	5:M:3:ALA:HA	1.62	0.82
5:L:275:ASP:O	5:L:279:ASN:ND2	2.12	0.82
1:F:373:LYS:HZ3	1:F:373:LYS:H	0.83	0.82
3:H:160:LEU:HD11	5:L:143:ILE:HG23	1.61	0.81
1:E:24:ASP:CA	3:H:185:GLU:O	2.26	0.81
1:A:373:LYS:H	1:A:373:LYS:HZ3	0.84	0.81
5:K:199:THR:O	5:K:203:ASN:ND2	2.14	0.81
3:H:200:SER:O	5:L:99:LEU:HD13	1.81	0.81
4:J:109:ILE:HD11	5:L:281:MET:SD	2.20	0.81
5:K:232:LEU:HD23	5:K:233:LYS:HD2	1.63	0.81
5:L:284:ILE:HD13	5:N:7:LYS:HE2	1.59	0.81
1:B:326:LYS:HB2	5:K:261:TYR:CE2	2.14	0.81
1:D:373:LYS:HZ3	1:D:373:LYS:H	0.82	0.80
1:E:373:LYS:H	1:E:373:LYS:HZ2	0.82	0.80
5:K:231:LYS:NZ	5:K:234:GLU:OE2	2.13	0.80
1:C:126:THR:HA	4:I:211:LYS:NZ	1.97	0.80
5:K:141:MET:CE	5:L:140:LYS:HB3	2.12	0.80
5:L:284:ILE:CD1	5:N:7:LYS:CE	2.57	0.80
4:J:116:ARG:CD	5:L:275:ASP:OD2	2.29	0.79
5:M:7:LYS:HZ2	5:N:8:MET:HG3	1.47	0.79
3:H:160:LEU:HD13	5:L:147:GLN:NE2	1.96	0.79
5:K:141:MET:HE2	5:L:140:LYS:HB3	1.64	0.79
4:J:116:ARG:CZ	5:L:275:ASP:OD2	2.30	0.79
1:C:91:TYR:CE1	3:H:121:LYS:NZ	2.50	0.78
4:J:109:ILE:CG1	5:L:281:MET:CE	2.52	0.78
5:L:86:ALA:O	5:L:90:ARG:HD3	1.84	0.78
5:L:91:ARG:HE	5:L:94:LEU:HD21	1.49	0.78
1:B:373:LYS:HZ3	1:B:373:LYS:H	0.82	0.78
1:E:24:ASP:OD1	3:H:185:GLU:HG3	1.84	0.78
1:D:25:ASP:CB	3:H:148:VAL:CG1	2.60	0.78
4:I:255:GLU:HA	4:I:258:LYS:HD3	1.64	0.78
4:J:113:PHE:CE1	5:L:278:LEU:HD11	2.19	0.78
1:B:326:LYS:HZ1	5:K:257:GLU:HG2	1.49	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:232:LEU:CD2	5:K:233:LYS:HD2	2.14	0.77
4:I:213:LYS:HB3	4:I:218:ARG:HG2	1.66	0.77
5:L:198:LYS:O	5:L:202:ASN:ND2	2.17	0.77
1:C:47:MET:CE	1:D:148:THR:OG1	2.33	0.77
5:K:243:GLU:OE2	5:L:238:ARG:NH1	2.17	0.77
2:G:46:ARG:C	5:K:160:ARG:NH2	2.42	0.77
2:G:158:LYS:HE2	2:G:158:LYS:H	1.49	0.77
3:H:144:THR:HA	3:H:146:ARG:HH21	1.50	0.77
5:K:247:THR:OG1	5:K:248:LYS:NZ	2.18	0.77
5:K:284:ILE:CG1	5:N:8:MET:HE2	2.14	0.77
4:J:130:ILE:HG21	5:L:257:GLU:OE2	1.82	0.76
1:E:42:GLY:HA2	1:F:169:TYR:HA	1.68	0.76
4:J:96:LYS:HD2	4:J:96:LYS:C	2.10	0.76
1:C:91:TYR:HE1	3:H:121:LYS:HZ2	1.32	0.76
5:K:194:GLU:OE1	5:K:195:GLU:N	2.18	0.76
5:K:170:VAL:O	5:K:173:GLU:HG3	1.86	0.76
1:B:47:MET:CE	1:C:148:THR:OG1	2.30	0.76
1:D:146:GLY:HA2	3:H:143:PRO:HG2	1.66	0.76
1:B:326:LYS:CE	5:K:257:GLU:HG2	2.15	0.75
4:J:96:LYS:O	4:J:96:LYS:CD	2.32	0.75
5:M:6:LYS:HD2	5:M:6:LYS:C	2.11	0.75
4:J:118:LYS:HD2	4:J:118:LYS:C	2.11	0.75
1:F:211:ASP:OD1	1:F:215:LYS:HE2	1.87	0.75
1:C:373:LYS:N	1:C:373:LYS:CD	2.50	0.75
1:A:211:ASP:OD1	1:A:215:LYS:HE2	1.87	0.75
1:B:211:ASP:OD1	1:B:215:LYS:HE2	1.87	0.74
5:K:268:LYS:O	5:K:272:GLU:HG2	1.87	0.74
1:B:373:LYS:N	1:B:373:LYS:CD	2.50	0.74
2:G:47:MET:HA	5:K:160:ARG:NH2	2.02	0.74
2:G:46:ARG:HG2	5:K:160:ARG:HH21	1.53	0.74
5:L:259:GLU:O	5:L:263:GLN:HG2	1.87	0.74
5:L:280:ASP:OD2	5:M:5:LYS:HE2	1.87	0.74
1:C:211:ASP:OD1	1:C:215:LYS:HE2	1.87	0.74
1:D:373:LYS:N	1:D:373:LYS:CD	2.50	0.74
1:F:373:LYS:N	1:F:373:LYS:CD	2.50	0.74
5:L:222:GLU:O	5:L:226:LYS:HG3	1.87	0.74
1:A:373:LYS:N	1:A:373:LYS:CD	2.50	0.74
5:K:189:LYS:HA	5:K:189:LYS:HZ3	1.53	0.74
1:C:80:ASP:HB2	4:I:203:LYS:HB3	1.69	0.73
1:C:126:THR:CG2	4:I:211:LYS:NZ	2.47	0.73
1:D:211:ASP:OD1	1:D:215:LYS:HE2	1.87	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:373:LYS:O	4:J:80:PRO:HB3	1.89	0.73
1:E:211:ASP:OD1	1:E:215:LYS:HE2	1.87	0.73
2:G:43:LYS:HD2	2:G:46:ARG:HH22	1.53	0.73
5:K:242:ALA:O	5:K:246:VAL:HG23	1.89	0.73
4:I:205:GLN:O	4:I:209:GLU:HB3	1.88	0.73
2:G:13:THR:H	2:G:16:GLN:HE21	1.33	0.73
5:L:196:GLU:O	5:L:199:THR:CG2	2.29	0.73
1:C:126:THR:HA	4:I:211:LYS:HZ3	1.53	0.73
1:E:24:ASP:HA	3:H:185:GLU:C	2.13	0.73
5:K:78:ALA:HA	5:L:78:ALA:HB2	1.71	0.73
1:E:373:LYS:N	1:E:373:LYS:CD	2.50	0.72
4:J:124:ILE:HD11	5:L:268:LYS:CG	2.18	0.72
1:B:326:LYS:HZ2	5:K:257:GLU:HG2	1.53	0.72
4:J:109:ILE:CD1	5:L:281:MET:SD	2.78	0.72
1:A:107:GLU:OE2	1:A:115:ASN:ND2	2.23	0.72
1:B:107:GLU:OE2	1:B:115:ASN:ND2	2.23	0.72
1:F:107:GLU:OE2	1:F:115:ASN:ND2	2.23	0.72
4:J:119:GLU:CD	4:J:123:LEU:HD11	2.15	0.72
1:C:107:GLU:OE2	1:C:115:ASN:ND2	2.23	0.72
5:K:151:ALA:HB1	5:L:151:ALA:CB	2.20	0.72
1:D:107:GLU:OE2	1:D:115:ASN:ND2	2.23	0.72
1:E:107:GLU:OE2	1:E:115:ASN:ND2	2.23	0.72
4:J:119:GLU:OE2	4:J:123:LEU:HD11	1.90	0.71
5:K:178:ARG:O	5:K:181:GLU:HG3	1.89	0.71
3:H:193:ARG:NH2	5:L:114:GLU:CD	2.48	0.71
3:H:135:ASP:O	3:H:139:LYS:NZ	2.23	0.71
5:K:284:ILE:HD12	5:N:8:MET:HE2	1.70	0.71
3:H:200:SER:HA	5:L:99:LEU:HD13	1.69	0.71
5:L:81:ALA:O	5:L:85:VAL:HG23	1.91	0.71
1:C:288:ASP:OD1	1:C:288:ASP:N	2.24	0.71
4:I:213:LYS:O	4:I:218:ARG:N	2.22	0.71
1:C:95:ARG:NE	4:I:268:ARG:NH1	2.39	0.71
5:L:284:ILE:HG21	5:N:7:LYS:HE2	0.75	0.71
5:L:284:ILE:CG2	5:N:7:LYS:CE	2.32	0.71
1:C:95:ARG:NE	4:I:268:ARG:HH12	1.89	0.71
5:L:91:ARG:O	5:L:95:VAL:HG23	1.91	0.71
1:B:288:ASP:N	1:B:288:ASP:OD1	2.24	0.70
1:C:95:ARG:CD	4:I:268:ARG:HH12	2.05	0.70
1:E:24:ASP:OD1	3:H:185:GLU:CG	2.40	0.70
1:A:288:ASP:OD1	1:A:288:ASP:N	2.24	0.70
2:G:93:SER:HB2	2:G:96:GLU:HB3	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:163:GLU:O	5:K:167:ARG:HG2	1.92	0.70
4:J:124:ILE:HG13	5:L:268:LYS:CD	2.21	0.70
5:K:140:LYS:HE3	5:K:140:LYS:HA	1.72	0.70
1:F:288:ASP:OD1	1:F:288:ASP:N	2.24	0.70
3:H:200:SER:HB3	5:L:103:GLN:HB2	1.73	0.70
2:G:43:LYS:HZ2	2:G:47:MET:HB2	1.56	0.70
1:E:24:ASP:OD1	3:H:185:GLU:HB3	1.92	0.69
3:H:115:VAL:HG23	4:I:253:LEU:HD12	1.71	0.69
5:K:151:ALA:HB1	5:L:151:ALA:HB1	1.73	0.69
5:K:140:LYS:HA	5:K:140:LYS:CE	2.21	0.69
1:E:288:ASP:OD1	1:E:288:ASP:N	2.24	0.69
3:H:65:GLU:OE1	3:H:69:ARG:NH1	2.26	0.69
4:J:81:LYS:HA	4:J:81:LYS:HZ2	1.57	0.69
5:K:221:TYR:HB3	5:L:221:TYR:CD1	2.28	0.69
1:C:95:ARG:HD3	4:I:268:ARG:NH1	2.07	0.69
5:K:115:GLU:O	5:K:118:LYS:HG3	1.94	0.68
5:M:7:LYS:HZ3	5:M:11:LEU:HD11	1.56	0.68
2:G:124:THR:HB	3:H:53:LEU:HB3	1.76	0.68
3:H:197:ASP:C	5:L:103:GLN:HE22	2.01	0.68
5:K:189:LYS:HA	5:K:189:LYS:NZ	2.08	0.68
1:D:24:ASP:CG	3:H:147:ARG:HH22	2.02	0.68
4:J:124:ILE:CG1	5:L:268:LYS:CD	2.53	0.68
5:K:279:ASN:O	5:K:282:THR:OG1	2.11	0.68
1:E:345:ILE:CG1	3:H:181:ASP:CG	2.66	0.68
4:J:127:LYS:HE3	5:L:260:LEU:HD22	1.76	0.68
2:G:127:THR:HG23	3:H:46:ARG:HD2	1.74	0.68
3:H:160:LEU:HD22	5:L:147:GLN:NE2	2.08	0.68
5:M:35:ARG:NH2	5:N:40:GLU:OE1	2.27	0.68
5:K:138:GLU:OE2	5:L:133:ARG:NH2	2.26	0.67
1:D:288:ASP:N	1:D:288:ASP:OD1	2.24	0.67
5:K:218:GLU:HB2	5:L:217:LYS:HE3	1.76	0.67
3:H:193:ARG:CZ	5:L:114:GLU:OE2	2.42	0.67
5:L:130:ILE:HD12	5:L:133:ARG:HD2	1.75	0.67
1:A:373:LYS:CD	1:A:374:CYS:H	2.08	0.67
5:L:240:GLU:O	5:L:244:ARG:HG2	1.93	0.67
1:A:47:MET:CE	1:B:148:THR:OG1	2.40	0.67
1:C:373:LYS:CD	1:C:374:CYS:H	2.08	0.67
1:E:300:SER:OG	1:E:301:GLY:N	2.28	0.67
5:K:131:GLU:O	5:K:135:GLN:NE2	2.27	0.67
5:K:275:ASP:O	5:K:279:ASN:ND2	2.27	0.67
1:E:373:LYS:CD	1:E:374:CYS:H	2.08	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:184:LYS:HG3	3:H:185:GLU:HG2	1.77	0.67
1:F:373:LYS:CD	1:F:374:CYS:H	2.08	0.66
3:H:205:ARG:HD2	5:K:94:LEU:CD1	2.17	0.66
1:B:373:LYS:CD	1:B:374:CYS:H	2.08	0.66
1:D:300:SER:OG	1:D:301:GLY:N	2.28	0.66
3:H:200:SER:O	5:L:99:LEU:HD11	1.90	0.66
4:J:81:LYS:HA	4:J:81:LYS:HZ3	1.60	0.66
1:D:373:LYS:CD	1:D:374:CYS:H	2.08	0.66
1:E:345:ILE:HG12	3:H:181:ASP:CB	2.24	0.66
5:K:118:LYS:HZ2	5:K:118:LYS:C	2.04	0.66
4:J:127:LYS:NZ	5:L:264:LYS:CE	2.59	0.66
1:A:300:SER:OG	1:A:301:GLY:N	2.28	0.65
2:G:104:PHE:HA	2:G:120:MET:HE3	1.78	0.65
4:I:219:ARG:NH2	4:I:220:LYS:O	2.29	0.65
5:K:242:ALA:O	5:K:245:SER:OG	2.13	0.65
3:H:112:ARG:HG2	4:I:250:LYS:HE3	1.79	0.65
2:G:121:LEU:O	2:G:124:THR:OG1	2.13	0.65
4:I:214:ILE:HA	4:I:218:ARG:HB2	1.78	0.65
1:F:300:SER:OG	1:F:301:GLY:N	2.28	0.65
3:H:110:GLU:HG2	4:I:215:LEU:HB2	1.79	0.65
1:E:24:ASP:C	3:H:185:GLU:O	2.40	0.65
2:G:46:ARG:HG3	5:K:160:ARG:HE	1.60	0.65
4:J:127:LYS:HZ3	5:L:264:LYS:CE	2.08	0.65
5:L:220:LYS:NZ	5:L:220:LYS:HB3	2.08	0.65
1:B:45:VAL:HG12	1:C:143:TYR:OH	1.97	0.64
5:L:199:THR:HG23	5:L:200:VAL:N	2.11	0.64
5:K:117:GLU:N	5:K:117:GLU:OE1	2.30	0.64
5:L:233:LYS:HD3	5:L:234:GLU:N	2.12	0.64
1:D:25:ASP:OD1	1:D:26:ALA:N	2.31	0.64
3:H:112:ARG:HA	3:H:115:VAL:HG22	1.80	0.64
5:K:197:LEU:HD22	5:K:201:THR:HG23	1.79	0.64
5:L:159:ASP:OD1	5:L:160:ARG:N	2.31	0.64
1:E:25:ASP:OD1	1:E:26:ALA:N	2.30	0.64
5:L:284:ILE:HD12	5:N:7:LYS:CD	2.04	0.63
1:B:300:SER:OG	1:B:301:GLY:N	2.28	0.63
1:C:300:SER:OG	1:C:301:GLY:N	2.28	0.63
1:A:373:LYS:HD2	1:A:373:LYS:H	1.63	0.63
5:M:21:ARG:CD	5:N:26:GLU:OE2	2.39	0.63
4:J:124:ILE:HG13	5:L:268:LYS:HD2	1.79	0.63
5:L:233:LYS:HE3	5:L:237:THR:HG21	1.81	0.63
5:K:88:LEU:HD21	5:L:89:ASN:OD1	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:111:GLN:HA	5:K:114:GLU:OE2	1.99	0.63
5:K:134:ALA:HB2	5:L:134:ALA:HB2	1.79	0.63
5:K:180:GLU:O	5:K:184:GLU:HG2	1.98	0.63
5:K:169:LEU:HD12	5:K:172:ILE:HD11	1.81	0.63
1:E:24:ASP:CG	3:H:185:GLU:HB3	2.24	0.63
1:B:213:LYS:NZ	6:B:401:ADP:O2'	2.27	0.62
1:E:47:MET:CE	1:F:148:THR:OG1	2.45	0.62
3:H:196:ILE:HG13	3:H:198:ALA:H	1.64	0.62
4:J:127:LYS:CE	5:L:264:LYS:HD2	2.28	0.62
5:K:278:LEU:O	5:K:282:THR:HG23	1.99	0.62
1:C:87:HIS:HE1	3:H:121:LYS:HD2	1.63	0.62
1:C:95:ARG:CD	4:I:268:ARG:NH1	2.62	0.62
5:K:132:SER:CB	5:K:133:ARG:HH21	2.13	0.62
5:K:218:GLU:OE1	5:L:217:LYS:HE2	2.00	0.62
5:K:284:ILE:CD1	5:N:8:MET:CE	2.74	0.62
1:C:87:HIS:HE1	3:H:121:LYS:CD	2.12	0.62
1:E:23:GLY:O	3:H:185:GLU:N	2.32	0.62
1:E:24:ASP:HA	3:H:185:GLU:HB3	1.81	0.62
3:H:135:ASP:HA	3:H:139:LYS:HB2	1.79	0.62
5:M:26:GLU:OE2	5:N:21:ARG:NH2	2.32	0.62
1:D:25:ASP:CA	3:H:148:VAL:HG12	2.28	0.62
5:K:222:GLU:CD	5:L:221:TYR:HH	2.05	0.62
1:B:326:LYS:CB	5:K:261:TYR:HE2	2.12	0.62
2:G:46:ARG:CG	5:K:160:ARG:NE	2.62	0.62
2:G:102:ARG:NH2	4:I:263:GLU:OE2	2.33	0.62
4:I:220:LYS:HG2	4:I:222:LEU:HD23	1.81	0.61
5:L:217:LYS:HG2	5:L:221:TYR:CE2	2.34	0.61
1:C:95:ARG:HE	4:I:268:ARG:HH12	1.48	0.61
4:I:257:PHE:HA	4:I:260:GLN:HE21	1.65	0.61
2:G:24:PHE:O	2:G:28:VAL:N	2.30	0.61
5:L:278:LEU:C	5:L:278:LEU:HD12	2.26	0.61
1:E:23:GLY:C	3:H:185:GLU:CB	2.61	0.61
1:F:233:SER:OG	1:F:234:SER:N	2.33	0.61
5:K:156:GLU:OE1	5:K:156:GLU:N	2.34	0.61
4:J:90:PHE:O	4:J:90:PHE:CD1	2.53	0.61
5:K:141:MET:SD	5:L:140:LYS:HB3	2.41	0.61
5:L:217:LYS:NZ	5:L:221:TYR:OH	2.33	0.61
4:I:223:ALA:O	4:I:226:HIS:NE2	2.34	0.61
2:G:131:ASP:OD1	2:G:131:ASP:N	2.26	0.61
3:H:94:LEU:HD21	4:I:232:LEU:HB3	1.83	0.61
5:M:24:GLN:OE1	5:N:29:LYS:NZ	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:118:LYS:HD2	4:J:118:LYS:O	2.00	0.60
5:K:265:LEU:HA	5:K:268:LYS:HG2	1.83	0.60
1:C:95:ARG:HE	4:I:268:ARG:NH1	1.99	0.60
2:G:35:CYS:SG	2:G:36:ILE:N	2.70	0.60
3:H:56:GLN:O	3:H:59:LYS:NZ	2.34	0.60
5:L:72:GLU:O	5:L:75:GLU:HG3	2.01	0.60
2:G:43:LYS:NZ	2:G:43:LYS:O	2.34	0.60
1:B:373:LYS:HD2	1:B:374:CYS:H	1.67	0.60
4:J:137:ARG:HD2	4:J:137:ARG:C	2.26	0.60
1:D:233:SER:OG	1:D:234:SER:N	2.33	0.60
1:D:45:VAL:HG12	1:E:143:TYR:OH	2.01	0.60
3:H:134:TYR:O	3:H:138:GLY:N	2.34	0.60
1:C:233:SER:OG	1:C:234:SER:N	2.33	0.60
1:E:233:SER:OG	1:E:234:SER:N	2.33	0.60
1:E:373:LYS:HD2	1:E:373:LYS:H	1.63	0.60
5:L:117:GLU:OE1	5:L:118:LYS:NZ	2.26	0.60
1:A:213:LYS:NZ	6:A:401:ADP:O2'	2.27	0.59
4:I:238:GLU:O	4:I:241:GLN:NE2	2.34	0.59
5:K:66:ASP:OD1	5:K:67:ALA:N	2.34	0.59
5:L:135:GLN:HG3	5:L:136:LYS:HD2	1.83	0.59
1:A:157:ASP:HB2	6:A:401:ADP:H4'	1.84	0.59
1:A:373:LYS:HD2	1:A:374:CYS:H	1.67	0.59
1:E:373:LYS:HD2	1:E:374:CYS:H	1.66	0.59
1:D:25:ASP:HB3	3:H:148:VAL:HG12	1.78	0.59
1:E:157:ASP:HB2	6:E:401:ADP:H4'	1.84	0.59
1:C:45:VAL:HG12	1:D:143:TYR:OH	2.02	0.59
1:A:45:VAL:HG12	1:B:143:TYR:OH	2.02	0.59
1:C:373:LYS:HD2	1:C:374:CYS:H	1.67	0.59
1:D:117:GLU:OE2	1:D:371:HIS:NE2	2.35	0.59
3:H:160:LEU:CD2	5:L:147:GLN:CD	2.63	0.59
4:J:127:LYS:HE3	5:L:260:LEU:CD2	2.33	0.59
1:C:126:THR:CA	4:I:211:LYS:NZ	2.66	0.59
1:D:157:ASP:HB2	6:D:401:ADP:H4'	1.84	0.59
2:G:74:PHE:HA	2:G:77:PHE:HD2	1.67	0.59
3:H:126:ILE:HG13	4:I:260:GLN:HG2	1.83	0.59
5:K:187:GLU:OE2	5:L:182:ARG:NH1	2.35	0.59
5:L:222:GLU:HA	5:L:225:ILE:HD12	1.83	0.59
1:F:220:ALA:HB1	1:F:226:GLU:HG3	1.85	0.59
1:B:233:SER:OG	1:B:234:SER:N	2.33	0.59
1:E:213:LYS:NZ	6:E:401:ADP:O2'	2.27	0.59
1:F:157:ASP:HB2	6:F:401:ADP:H4'	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:157:ASP:HB2	6:C:401:ADP:H4'	1.84	0.58
1:C:300:SER:O	1:C:304:THR:OG1	2.20	0.58
1:D:25:ASP:N	3:H:148:VAL:HG12	2.18	0.58
3:H:167:SER:O	3:H:171:ARG:HG2	2.03	0.58
4:J:124:ILE:HG12	5:L:265:LEU:HD12	1.85	0.58
5:K:251:LYS:NZ	5:K:254:ASP:OD2	2.36	0.58
1:B:157:ASP:HB2	6:B:401:ADP:H4'	1.84	0.58
1:E:220:ALA:HB1	1:E:226:GLU:HG3	1.85	0.58
5:L:281:MET:O	5:L:284:ILE:N	2.30	0.58
1:C:220:ALA:HB1	1:C:226:GLU:HG3	1.85	0.58
1:D:373:LYS:HD2	1:D:374:CYS:H	1.67	0.58
3:H:160:LEU:HD22	5:L:147:GLN:CG	2.34	0.58
3:H:197:ASP:HB3	5:L:103:GLN:NE2	2.17	0.58
5:L:204:LEU:HD23	5:L:204:LEU:O	2.04	0.58
1:D:213:LYS:NZ	6:D:401:ADP:O2'	2.27	0.58
1:E:24:ASP:CA	3:H:185:GLU:HB3	2.32	0.58
5:K:200:VAL:HG23	5:L:200:VAL:HG11	1.84	0.58
1:C:117:GLU:OE2	1:C:371:HIS:NE2	2.36	0.58
5:M:7:LYS:NZ	5:N:8:MET:HG3	2.18	0.58
1:D:25:ASP:CG	3:H:148:VAL:HB	2.29	0.58
1:E:24:ASP:CB	3:H:185:GLU:HB3	2.33	0.58
5:K:112:LYS:NZ	5:K:115:GLU:OE2	2.28	0.58
1:D:373:LYS:H	1:D:373:LYS:CD	2.15	0.58
2:G:101:PHE:O	2:G:105:ASP:N	2.34	0.58
5:K:257:GLU:HA	5:K:260:LEU:CD2	2.34	0.58
5:K:267:TYR:HD2	5:K:267:TYR:O	1.86	0.58
1:B:117:GLU:OE2	1:B:371:HIS:NE2	2.36	0.58
1:C:373:LYS:H	1:C:373:LYS:CD	2.15	0.58
1:D:300:SER:O	1:D:304:THR:OG1	2.20	0.58
1:A:373:LYS:H	1:A:373:LYS:CD	2.15	0.58
1:B:326:LYS:NZ	5:K:257:GLU:CG	2.55	0.58
2:G:67:ASP:OD2	2:G:69:SER:OG	2.17	0.58
5:L:280:ASP:CG	5:M:5:LYS:CE	2.77	0.58
1:C:91:TYR:HE1	3:H:121:LYS:NZ	1.97	0.57
1:B:373:LYS:H	1:B:373:LYS:CD	2.15	0.57
1:D:220:ALA:HB1	1:D:226:GLU:HG3	1.85	0.57
1:E:373:LYS:H	1:E:373:LYS:CD	2.15	0.57
2:G:132:ASP:OD1	3:H:46:ARG:NH2	2.37	0.57
5:L:233:LYS:HD3	5:L:233:LYS:C	2.30	0.57
1:A:233:SER:OG	1:A:234:SER:N	2.34	0.57
3:H:119:VAL:HG11	4:I:253:LEU:HD22	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:208:LYS:HE3	3:H:210:GLU:HB2	1.86	0.57
4:I:251:PHE:HD1	4:I:254:GLN:HE22	1.53	0.57
4:I:252:ASP:O	4:I:256:LYS:NZ	2.36	0.57
1:A:220:ALA:HB1	1:A:226:GLU:HG3	1.85	0.57
5:K:249:LEU:CD1	5:L:246:VAL:HG23	2.35	0.57
5:M:32:ALA:O	5:M:36:SER:OG	2.23	0.57
3:H:187:ARG:HH22	5:L:125:ARG:HH12	1.52	0.57
5:L:246:VAL:O	5:L:250:GLU:HG2	2.03	0.57
1:F:373:LYS:HD2	1:F:374:CYS:H	1.67	0.57
2:G:96:GLU:O	2:G:100:LEU:HG	2.04	0.57
2:G:100:LEU:HB3	3:H:58:ALA:HB1	1.87	0.57
4:J:120:GLU:OE1	5:L:268:LYS:CB	2.52	0.57
5:K:140:LYS:HA	5:K:140:LYS:HZ1	1.70	0.57
5:L:132:SER:O	5:L:136:LYS:HD3	2.05	0.57
1:B:220:ALA:HB1	1:B:226:GLU:HG3	1.85	0.57
5:K:111:GLN:NE2	5:K:112:LYS:HD2	2.18	0.57
1:D:47:MET:CE	1:E:148:THR:OG1	2.45	0.57
3:H:44:ALA:HA	3:H:47:LYS:HE2	1.86	0.57
1:F:213:LYS:NZ	6:F:401:ADP:O2'	2.27	0.57
2:G:5:TYR:HB3	2:G:83:ARG:HH21	1.69	0.57
5:K:102:ALA:HB1	5:L:102:ALA:HB1	1.87	0.57
1:F:373:LYS:H	1:F:373:LYS:CD	2.14	0.57
1:C:213:LYS:NZ	6:C:401:ADP:O2'	2.27	0.56
1:D:111:ASN:OD1	1:D:177:ARG:NH1	2.38	0.56
3:H:60:GLN:NE2	3:H:63:GLU:OE2	2.38	0.56
4:J:87:ARG:HB3	4:J:88:VAL:HG22	1.87	0.56
1:A:111:ASN:OD1	1:A:177:ARG:NH1	2.38	0.56
1:C:372:ARG:HB3	1:C:373:LYS:NZ	2.20	0.56
1:D:372:ARG:HB3	1:D:373:LYS:NZ	2.20	0.56
4:J:130:ILE:HG22	5:L:257:GLU:CD	2.30	0.56
1:E:111:ASN:OD1	1:E:177:ARG:NH1	2.38	0.56
5:K:281:MET:HE1	5:M:3:ALA:CA	2.35	0.56
5:N:34:ASP:HA	5:N:37:LYS:HE2	1.88	0.56
1:B:372:ARG:HB3	1:B:373:LYS:NZ	2.20	0.56
1:C:111:ASN:OD1	1:C:177:ARG:NH1	2.38	0.56
1:F:117:GLU:OE2	1:F:371:HIS:NE2	2.35	0.56
4:I:259:GLN:HA	4:I:262:TYR:CD2	2.41	0.56
1:A:372:ARG:HB3	1:A:373:LYS:NZ	2.20	0.56
1:E:372:ARG:HB3	1:E:373:LYS:NZ	2.20	0.56
3:H:160:LEU:HD11	5:L:143:ILE:CG2	2.33	0.56
5:K:141:MET:HE1	5:L:144:GLN:CD	2.31	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:M:7:LYS:NZ	5:M:11:LEU:HD11	2.20	0.56
1:E:5:THR:OG1	1:E:6:THR:N	2.39	0.56
1:E:117:GLU:OE2	1:E:371:HIS:NE2	2.35	0.56
5:L:197:LEU:O	5:L:201:THR:HG23	2.06	0.56
1:A:156:GLY:O	1:A:303:THR:OG1	2.24	0.56
4:I:205:GLN:HA	4:I:208:ARG:HE	1.71	0.56
5:K:284:ILE:HD12	5:N:12:LYS:HD2	1.88	0.56
1:B:5:THR:OG1	1:B:6:THR:N	2.39	0.56
2:G:149:ASP:O	2:G:153:PHE:N	2.35	0.56
3:H:67:GLU:HA	3:H:70:ARG:HD3	1.88	0.56
5:K:213:LYS:HA	5:K:213:LYS:HZ3	1.71	0.56
1:B:326:LYS:HE3	5:K:257:GLU:HG2	1.87	0.55
1:C:373:LYS:HD2	1:C:373:LYS:H	1.63	0.55
2:G:99:ASP:HA	2:G:102:ARG:HG2	1.86	0.55
5:K:162:TYR:OH	5:L:161:LYS:HD2	2.06	0.55
5:K:208:GLU:OE1	5:K:209:ALA:N	2.39	0.55
1:F:372:ARG:HB3	1:F:373:LYS:NZ	2.20	0.55
5:K:197:LEU:C	5:K:197:LEU:HD13	2.31	0.55
1:C:5:THR:OG1	1:C:6:THR:N	2.39	0.55
2:G:46:ARG:CG	5:K:160:ARG:HE	2.18	0.55
5:K:115:GLU:O	5:K:118:LYS:HE3	2.06	0.55
1:A:5:THR:OG1	1:A:6:THR:N	2.39	0.55
5:K:192:GLU:HA	5:K:192:GLU:OE1	2.07	0.55
4:J:116:ARG:HD2	5:L:272:GLU:OE1	2.06	0.55
5:K:251:LYS:NZ	5:K:251:LYS:HA	2.22	0.55
1:C:156:GLY:O	1:C:303:THR:OG1	2.24	0.55
3:H:70:ARG:HA	3:H:73:LYS:HE3	1.89	0.55
4:I:254:GLN:HA	4:I:257:PHE:CD2	2.41	0.55
2:G:131:ASP:HB3	3:H:42:ILE:HG23	1.88	0.55
5:K:92:ILE:O	5:K:96:GLU:HG3	2.06	0.55
1:A:21:PHE:HD2	1:A:28:ARG:HH21	1.55	0.54
1:D:5:THR:OG1	1:D:6:THR:N	2.39	0.54
1:E:156:GLY:O	1:E:303:THR:OG1	2.24	0.54
5:K:185:LEU:O	5:K:189:LYS:HG2	2.07	0.54
1:A:117:GLU:OE2	1:A:371:HIS:NE2	2.36	0.54
2:G:107:ASN:OD1	2:G:108:ALA:N	2.40	0.54
4:J:120:GLU:HB3	5:L:268:LYS:HG3	1.88	0.54
5:K:267:TYR:HA	5:K:270:ILE:HG22	1.89	0.54
1:B:21:PHE:HD2	1:B:28:ARG:HH21	1.55	0.54
5:K:232:LEU:HD23	5:K:233:LYS:N	2.22	0.54
5:L:91:ARG:HE	5:L:94:LEU:CD2	2.19	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:185:LEU:C	5:L:185:LEU:HD13	2.33	0.54
5:L:274:LEU:HD13	5:L:274:LEU:C	2.32	0.54
5:K:224:GLU:HA	5:K:224:GLU:OE1	2.06	0.54
5:L:232:LEU:HD12	5:L:233:LYS:N	2.23	0.54
1:F:111:ASN:OD1	1:F:177:ARG:NH1	2.38	0.54
1:F:156:GLY:O	1:F:303:THR:OG1	2.24	0.54
5:M:6:LYS:HD2	5:M:6:LYS:O	2.08	0.54
1:B:111:ASN:OD1	1:B:177:ARG:NH1	2.38	0.54
1:B:373:LYS:HD2	1:B:373:LYS:H	1.63	0.54
2:G:92:LYS:NZ	2:G:161:GLU:OXT	2.40	0.54
5:K:213:LYS:HA	5:K:213:LYS:NZ	2.22	0.54
5:M:21:ARG:HE	5:N:22:ALA:HB1	1.73	0.54
1:E:24:ASP:HA	3:H:185:GLU:CA	2.36	0.54
4:J:124:ILE:HD12	5:L:268:LYS:NZ	2.23	0.54
5:K:223:GLU:OE1	5:K:224:GLU:N	2.41	0.54
5:L:64:LEU:HB2	5:L:67:ALA:HB3	1.90	0.54
5:L:213:LYS:HA	5:L:216:GLN:HG2	1.89	0.54
1:A:300:SER:O	1:A:304:THR:OG1	2.20	0.54
1:D:156:GLY:O	1:D:303:THR:OG1	2.24	0.53
3:H:112:ARG:NH2	4:I:247:GLU:HG2	2.17	0.53
1:D:21:PHE:HD2	1:D:28:ARG:HH21	1.55	0.53
1:F:21:PHE:HD2	1:F:28:ARG:HH21	1.55	0.53
5:M:22:ALA:HB2	5:N:22:ALA:HA	1.90	0.53
1:E:21:PHE:HD2	1:E:28:ARG:HH21	1.55	0.53
3:H:112:ARG:CD	4:I:246:LEU:HB3	2.38	0.53
5:K:165:VAL:HG11	5:L:165:VAL:HG21	1.91	0.53
5:L:113:LEU:HD23	5:L:114:GLU:N	2.23	0.53
1:C:21:PHE:HD2	1:C:28:ARG:HH21	1.55	0.53
1:F:373:LYS:HD2	1:F:373:LYS:H	1.63	0.53
4:I:212:LYS:HD3	4:I:215:LEU:HD21	1.90	0.53
5:K:143:ILE:O	5:K:146:ILE:HG13	2.09	0.53
1:D:148:THR:HG21	3:H:139:LYS:HE3	1.90	0.53
2:G:42:GLY:HA2	2:G:57:LEU:HD22	1.91	0.53
2:G:130:GLU:OE1	3:H:42:ILE:N	2.41	0.53
3:H:138:GLY:HA2	3:H:141:LYS:HD3	1.90	0.53
5:K:140:LYS:HA	5:K:140:LYS:NZ	2.23	0.53
5:M:7:LYS:HZ3	5:M:11:LEU:CD1	2.22	0.53
1:E:25:ASP:N	3:H:185:GLU:O	2.42	0.53
4:I:255:GLU:HB3	4:I:256:LYS:HZ2	1.74	0.53
4:J:120:GLU:HB3	5:L:268:LYS:HE2	1.90	0.53
5:K:162:TYR:CE2	5:L:161:LYS:HE3	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:126:THR:HA	4:I:211:LYS:HZ2	1.73	0.53
4:J:80:PRO:O	4:J:81:LYS:NZ	2.29	0.53
1:C:372:ARG:HB3	1:C:373:LYS:CE	2.40	0.52
3:H:104:ARG:O	3:H:108:VAL:HG22	2.09	0.52
5:K:275:ASP:HA	5:K:278:LEU:HG	1.91	0.52
5:L:284:ILE:CG1	5:N:7:LYS:HE2	2.39	0.52
1:B:156:GLY:O	1:B:303:THR:OG1	2.24	0.52
3:H:48:LEU:HD22	3:H:48:LEU:H	1.75	0.52
5:L:199:THR:CG2	5:L:200:VAL:N	2.72	0.52
4:I:217:GLU:HG2	4:I:218:ARG:HH11	1.74	0.52
4:I:235:LYS:NZ	4:I:238:GLU:OE1	2.43	0.52
4:J:104:GLU:OE2	5:N:6:LYS:CE	2.57	0.52
4:J:120:GLU:O	5:L:268:LYS:HD2	2.09	0.52
1:F:5:THR:OG1	1:F:6:THR:N	2.39	0.52
4:J:120:GLU:OE1	5:L:268:LYS:HG3	2.10	0.52
1:D:24:ASP:CG	3:H:147:ARG:NH2	2.62	0.52
5:L:99:LEU:HD12	5:L:99:LEU:C	2.35	0.52
1:A:372:ARG:HB3	1:A:373:LYS:CE	2.40	0.52
1:B:372:ARG:HB3	1:B:373:LYS:CE	2.40	0.52
2:G:147:ARG:NH1	2:G:149:ASP:OD2	2.43	0.52
2:G:149:ASP:OD1	2:G:149:ASP:N	2.41	0.52
1:B:326:LYS:HD2	5:K:261:TYR:CE2	2.45	0.52
1:D:244:ASP:C	1:E:325:MET:HE3	2.35	0.52
5:L:245:SER:O	5:L:249:LEU:HG	2.10	0.52
1:D:372:ARG:HB3	1:D:373:LYS:CE	2.40	0.51
5:K:216:GLN:O	5:K:216:GLN:NE2	2.43	0.51
2:G:60:MET:HG2	2:G:80:MET:HG2	1.92	0.51
2:G:156:PHE:CD2	2:G:157:MET:HB2	2.46	0.51
3:H:108:VAL:O	3:H:112:ARG:HG3	2.10	0.51
4:I:214:ILE:HD13	4:I:218:ARG:HB2	1.93	0.51
4:J:127:LYS:HG3	5:L:264:LYS:HD2	1.91	0.51
1:F:372:ARG:HB3	1:F:373:LYS:CE	2.40	0.51
4:J:123:LEU:HD22	5:L:264:LYS:HE3	1.92	0.51
5:K:71:LEU:HD21	5:L:67:ALA:HB1	1.91	0.51
5:K:112:LYS:HA	5:K:115:GLU:OE1	2.10	0.51
5:K:229:SER:O	5:K:233:LYS:HG2	2.11	0.51
1:E:372:ARG:HB3	1:E:373:LYS:CE	2.40	0.51
4:I:255:GLU:O	4:I:259:GLN:NE2	2.44	0.51
5:K:260:LEU:C	5:K:260:LEU:HD12	2.35	0.51
1:F:17:VAL:HG23	1:F:33:SER:HB3	1.93	0.51
1:C:126:THR:CA	4:I:211:LYS:HZ3	2.19	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:123:LEU:HD22	5:L:264:LYS:CE	2.40	0.51
3:H:70:ARG:HG2	3:H:71:GLY:N	2.26	0.51
5:K:106:LEU:HD12	5:K:106:LEU:C	2.36	0.51
5:K:281:MET:HG3	5:M:7:LYS:HD2	1.93	0.51
5:L:130:ILE:CD1	5:L:133:ARG:HD2	2.41	0.51
4:J:119:GLU:O	4:J:123:LEU:HG	2.11	0.51
5:K:257:GLU:O	5:K:260:LEU:HG	2.10	0.51
1:A:354:GLN:N	1:A:354:GLN:OE1	2.44	0.51
1:B:326:LYS:HZ2	5:K:257:GLU:CG	2.18	0.51
1:D:35:VAL:HG13	1:D:54:VAL:HG12	1.93	0.51
1:F:354:GLN:N	1:F:354:GLN:OE1	2.44	0.51
2:G:117:LEU:HB3	2:G:118:LYS:HZ3	1.75	0.51
2:G:91:GLY:HA3	2:G:159:GLY:HA2	1.93	0.50
5:L:275:ASP:OD1	5:L:279:ASN:ND2	2.42	0.50
5:L:278:LEU:HD12	5:L:278:LEU:O	2.11	0.50
1:A:17:VAL:HG23	1:A:33:SER:HB3	1.93	0.50
1:C:373:LYS:H	1:C:373:LYS:CE	2.24	0.50
1:D:373:LYS:H	1:D:373:LYS:CE	2.24	0.50
2:G:60:MET:O	2:G:64:VAL:N	2.27	0.50
1:A:35:VAL:HG13	1:A:54:VAL:HG12	1.93	0.50
1:D:373:LYS:CG	1:D:374:CYS:N	2.74	0.50
2:G:92:LYS:NZ	2:G:161:GLU:OE2	2.43	0.50
5:K:249:LEU:HD13	5:L:246:VAL:HG23	1.93	0.50
1:B:300:SER:O	1:B:304:THR:OG1	2.20	0.50
1:D:17:VAL:HG23	1:D:33:SER:HB3	1.93	0.50
1:E:17:VAL:HG23	1:E:33:SER:HB3	1.93	0.50
1:E:373:LYS:H	1:E:373:LYS:CE	2.24	0.50
4:I:208:ARG:HA	4:I:211:LYS:HD2	1.94	0.50
5:L:260:LEU:HD23	5:L:260:LEU:C	2.36	0.50
5:L:280:ASP:HB3	5:M:5:LYS:HZ3	0.55	0.50
1:B:47:MET:CE	1:C:148:THR:CB	2.89	0.50
1:B:354:GLN:N	1:B:354:GLN:OE1	2.44	0.50
1:C:17:VAL:HG23	1:C:33:SER:HB3	1.92	0.50
1:E:35:VAL:HG13	1:E:54:VAL:HG12	1.94	0.50
1:F:35:VAL:HG13	1:F:54:VAL:HG12	1.94	0.50
1:F:300:SER:O	1:F:304:THR:OG1	2.20	0.50
3:H:147:ARG:NH1	3:H:150:ILE:HG21	2.26	0.50
5:K:213:LYS:HA	5:K:213:LYS:CE	2.42	0.50
1:B:17:VAL:HG23	1:B:33:SER:HB3	1.93	0.50
1:C:35:VAL:HG13	1:C:54:VAL:HG12	1.94	0.50
1:D:25:ASP:CB	3:H:148:VAL:HG12	2.37	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:95:GLU:OE1	2:G:96:GLU:N	2.44	0.50
1:B:373:LYS:H	1:B:373:LYS:CE	2.24	0.50
5:L:223:GLU:O	5:L:227:VAL:HG23	2.12	0.50
1:C:373:LYS:CG	1:C:374:CYS:N	2.75	0.50
2:G:17:LYS:HG2	2:G:21:LYS:HE2	1.93	0.50
1:A:44:MET:HB3	1:A:47:MET:CG	2.42	0.50
1:A:373:LYS:CG	1:A:374:CYS:N	2.75	0.50
1:B:35:VAL:HG13	1:B:54:VAL:HG12	1.94	0.50
1:C:44:MET:HB3	1:C:47:MET:CG	2.42	0.49
1:C:80:ASP:CB	4:I:203:LYS:HB3	2.40	0.49
4:J:119:GLU:HG3	4:J:123:LEU:HD12	1.93	0.49
1:A:230:ALA:HB2	1:A:236:LEU:HD12	1.95	0.49
1:C:354:GLN:N	1:C:354:GLN:OE1	2.44	0.49
1:F:373:LYS:H	1:F:373:LYS:CE	2.24	0.49
5:K:162:TYR:OH	5:L:161:LYS:HB3	2.12	0.49
5:L:196:GLU:C	5:L:199:THR:HG22	2.32	0.49
5:L:281:MET:O	5:L:284:ILE:HG12	2.12	0.49
2:G:5:TYR:OH	3:H:45:SER:HA	2.13	0.49
5:K:64:LEU:O	5:K:68:GLN:N	2.36	0.49
5:L:128:LYS:HA	5:L:131:GLU:HG2	1.94	0.49
5:L:281:MET:HG2	5:L:284:ILE:HG12	1.94	0.49
1:E:230:ALA:HB2	1:E:236:LEU:HD12	1.95	0.49
1:E:373:LYS:CG	1:E:374:CYS:N	2.75	0.49
2:G:75:ASP:OD1	2:G:76:GLU:N	2.42	0.49
2:G:157:MET:HE3	2:G:157:MET:HA	1.94	0.49
5:L:91:ARG:HH21	5:L:94:LEU:CD2	2.25	0.49
1:B:230:ALA:HB2	1:B:236:LEU:HD12	1.95	0.49
1:B:373:LYS:CG	1:B:374:CYS:N	2.75	0.49
1:D:230:ALA:HB2	1:D:236:LEU:HD12	1.95	0.49
1:E:44:MET:HB3	1:E:47:MET:CG	2.42	0.49
2:G:43:LYS:NZ	2:G:47:MET:HB2	2.24	0.49
5:K:257:GLU:HA	5:K:260:LEU:HD23	1.95	0.49
5:L:105:ARG:HA	5:L:108:THR:HG22	1.94	0.49
1:B:373:LYS:HG2	1:B:374:CYS:N	2.28	0.49
4:J:134:ARG:HD3	5:L:257:GLU:OE1	2.13	0.49
1:C:155:SER:HB3	1:C:304:THR:HG23	1.95	0.49
4:I:204:ARG:NH1	4:I:207:GLU:HB2	2.28	0.49
4:I:209:GLU:OE2	4:I:213:LYS:NZ	2.45	0.49
5:K:118:LYS:HZ2	5:K:119:ALA:N	2.10	0.49
5:M:7:LYS:NZ	5:N:8:MET:CE	2.66	0.49
1:B:44:MET:HB3	1:B:47:MET:CG	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:230:ALA:HB2	1:C:236:LEU:HD12	1.95	0.49
1:D:44:MET:HB3	1:D:47:MET:CG	2.43	0.49
5:K:281:MET:SD	5:M:3:ALA:CA	2.99	0.49
1:D:155:SER:HB3	1:D:304:THR:HG23	1.95	0.49
1:E:300:SER:O	1:E:304:THR:OG1	2.20	0.49
1:F:373:LYS:HG2	1:F:374:CYS:N	2.28	0.49
2:G:101:PHE:CE2	2:G:112:ILE:HD13	2.48	0.49
2:G:119:MET:O	2:G:122:GLN:HG2	2.12	0.49
3:H:133:ILE:HD12	3:H:137:ARG:HH22	1.77	0.49
1:B:155:SER:HB3	1:B:304:THR:HG23	1.95	0.48
4:J:105:LEU:HD21	5:L:284:ILE:CD1	2.34	0.48
1:A:373:LYS:HG2	1:A:374:CYS:N	2.28	0.48
1:D:354:GLN:N	1:D:354:GLN:OE1	2.44	0.48
1:F:230:ALA:HB2	1:F:236:LEU:HD12	1.95	0.48
2:G:160:VAL:HG13	3:H:51:LYS:HB2	1.93	0.48
1:A:373:LYS:H	1:A:373:LYS:CE	2.25	0.48
1:F:373:LYS:CG	1:F:374:CYS:N	2.75	0.48
2:G:139:ASP:HB3	2:G:156:PHE:HD1	1.76	0.48
3:H:102:HIS:NE2	4:I:222:LEU:O	2.46	0.48
5:K:110:LEU:HG	5:K:111:GLN:N	2.28	0.48
5:K:132:SER:OG	5:K:133:ARG:NH2	2.45	0.48
5:K:204:LEU:HD11	5:L:203:ASN:HB2	1.96	0.48
1:E:354:GLN:OE1	1:E:354:GLN:N	2.44	0.48
5:K:284:ILE:HG21	5:N:12:LYS:HE2	1.94	0.48
1:A:24:ASP:OD1	1:A:24:ASP:N	2.47	0.48
1:E:155:SER:HB3	1:E:304:THR:HG23	1.95	0.48
1:F:155:SER:HB3	1:F:304:THR:HG23	1.95	0.48
4:J:127:LYS:HE2	5:L:264:LYS:CD	2.37	0.48
5:L:243:GLU:O	5:L:246:VAL:HG12	2.13	0.48
5:L:263:GLN:HA	5:L:263:GLN:OE1	2.14	0.48
5:L:274:LEU:HD13	5:L:274:LEU:O	2.13	0.48
1:E:373:LYS:HG2	1:E:374:CYS:N	2.28	0.48
2:G:88:ASP:OD2	2:G:91:GLY:N	2.46	0.48
1:C:373:LYS:HG2	1:C:374:CYS:N	2.28	0.48
1:D:373:LYS:HG2	1:D:374:CYS:N	2.28	0.48
1:E:45:VAL:HG12	1:F:143:TYR:OH	2.13	0.48
2:G:114:LEU:HB2	2:G:118:LYS:HE2	1.95	0.48
5:K:92:ILE:HA	5:K:95:VAL:HG22	1.94	0.48
5:K:132:SER:HB2	5:K:133:ARG:HH21	1.77	0.48
5:K:137:ASP:OD2	5:L:138:GLU:N	2.46	0.48
5:K:197:LEU:O	5:K:201:THR:HG23	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:44:MET:HB3	1:F:47:MET:CG	2.43	0.48
2:G:46:ARG:HG3	5:K:160:ARG:NE	2.27	0.48
2:G:64:VAL:HG12	2:G:65:ASP:H	1.78	0.48
4:J:112:HIS:CE1	5:L:274:LEU:CD1	2.96	0.48
5:K:127:MET:O	5:K:131:GLU:HG2	2.14	0.48
1:A:155:SER:HB3	1:A:304:THR:HG23	1.95	0.48
2:G:44:VAL:HA	2:G:47:MET:HB3	1.96	0.48
2:G:161:GLU:H	3:H:51:LYS:HE2	1.79	0.48
1:B:24:ASP:OD1	1:B:24:ASP:N	2.47	0.47
3:H:112:ARG:HD2	4:I:246:LEU:HB3	1.94	0.47
3:H:115:VAL:HG21	4:I:250:LYS:HD3	1.96	0.47
5:K:214:TYR:OH	5:L:218:GLU:N	2.47	0.47
5:K:232:LEU:HD23	5:K:232:LEU:C	2.39	0.47
5:K:165:VAL:HG23	5:K:168:LYS:NZ	2.29	0.47
2:G:100:LEU:HD22	3:H:58:ALA:HB1	1.96	0.47
4:I:261:LYS:HD2	4:I:262:TYR:CD1	2.50	0.47
1:B:43:VAL:N	1:C:168:GLY:O	2.45	0.47
2:G:51:ASN:ND2	2:G:85:MET:SD	2.87	0.47
2:G:131:ASP:OD2	3:H:46:ARG:NH1	2.46	0.47
4:I:204:ARG:HA	4:I:204:ARG:NE	2.30	0.47
5:K:141:MET:HE1	5:L:144:GLN:NE2	2.30	0.47
5:L:68:GLN:O	5:L:71:LEU:HG	2.14	0.47
5:L:78:ALA:O	5:L:82:GLU:HG2	2.14	0.47
5:L:260:LEU:HD23	5:L:260:LEU:O	2.14	0.47
5:M:35:ARG:HH12	5:N:36:SER:HB3	1.80	0.47
3:H:101:LEU:HG	4:I:239:LEU:HB3	1.95	0.47
5:L:87:SER:O	5:L:91:ARG:HG2	2.14	0.47
5:L:220:LYS:C	5:L:220:LYS:HD2	2.39	0.47
4:J:123:LEU:HB3	5:L:264:LYS:HD3	1.96	0.47
5:K:86:ALA:O	5:K:90:ARG:NH1	2.48	0.47
5:K:193:LEU:HD12	5:L:190:CYS:SG	2.55	0.47
5:L:233:LYS:O	5:L:236:GLU:HG3	2.13	0.47
1:F:12:ASN:OD1	1:F:86:TRP:NE1	2.42	0.47
3:H:134:TYR:HE2	3:H:142:ARG:HG2	1.80	0.47
3:H:134:TYR:CE2	3:H:142:ARG:HG2	2.49	0.47
3:H:197:ASP:CA	5:L:103:GLN:HE22	2.28	0.47
4:I:207:GLU:HG2	4:I:211:LYS:HE3	1.96	0.47
4:I:210:LYS:O	4:I:214:ILE:HG12	2.15	0.47
1:E:44:MET:HB2	1:E:47:MET:HG3	1.97	0.47
2:G:2:ASP:HB3	3:H:45:SER:HB2	1.96	0.47
3:H:146:ARG:HB2	3:H:148:VAL:HG13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:105:ARG:HB3	5:L:105:ARG:CZ	2.44	0.47
5:M:7:LYS:HZ1	5:N:8:MET:CE	2.20	0.47
1:B:44:MET:HB2	1:B:47:MET:HG3	1.97	0.47
1:E:23:GLY:O	3:H:185:GLU:CA	2.63	0.47
1:A:44:MET:HB2	1:A:47:MET:HG3	1.97	0.47
1:D:44:MET:HB2	1:D:47:MET:HG3	1.97	0.47
5:N:35:ARG:HE	5:N:39:LEU:HD11	1.79	0.47
1:B:33:SER:O	1:B:33:SER:OG	2.33	0.46
1:F:44:MET:HB2	1:F:47:MET:HG3	1.97	0.46
2:G:136:LEU:H	2:G:136:LEU:HD12	1.80	0.46
5:K:280:ASP:OD1	5:N:8:MET:SD	2.73	0.46
1:C:44:MET:HB2	1:C:47:MET:HG3	1.97	0.46
1:D:34:ILE:HD11	1:D:59:GLN:HG2	1.97	0.46
5:K:268:LYS:HG3	5:K:269:ALA:N	2.30	0.46
5:M:5:LYS:O	5:M:9:GLN:HG2	2.15	0.46
1:F:24:ASP:OD1	1:F:24:ASP:N	2.47	0.46
5:K:221:TYR:HB3	5:L:221:TYR:CE1	2.50	0.46
5:K:267:TYR:C	5:K:267:TYR:CD2	2.93	0.46
5:K:280:ASP:OD1	5:N:8:MET:HE1	2.15	0.46
5:L:220:LYS:HZ2	5:L:220:LYS:CB	2.21	0.46
3:H:210:GLU:H	3:H:210:GLU:CD	2.23	0.46
5:K:274:LEU:O	5:K:278:LEU:HG	2.15	0.46
1:C:34:ILE:HD11	1:C:59:GLN:HG2	1.97	0.46
4:I:255:GLU:HB3	4:I:256:LYS:NZ	2.31	0.46
5:L:251:LYS:NZ	5:L:255:ASP:HB3	2.31	0.46
1:C:24:ASP:OD1	1:C:24:ASP:N	2.47	0.46
4:I:228:ASN:ND2	4:I:230:ASP:OD1	2.48	0.46
1:D:24:ASP:OD1	1:D:24:ASP:N	2.47	0.46
1:D:34:ILE:HD12	1:D:67:LEU:HD13	1.98	0.46
1:E:34:ILE:HD11	1:E:59:GLN:HG2	1.98	0.46
3:H:205:ARG:HH11	5:K:94:LEU:HG	1.80	0.46
1:C:78:ASN:ND2	1:C:81:ASP:OD2	2.49	0.46
1:D:25:ASP:CG	3:H:149:ARG:H	2.23	0.46
3:H:80:ARG:NH2	4:I:247:GLU:HB3	2.30	0.46
3:H:160:LEU:CD2	5:L:147:GLN:CG	2.94	0.46
4:I:249:GLU:O	4:I:253:LEU:HG	2.14	0.46
1:B:34:ILE:HD11	1:B:59:GLN:HG2	1.97	0.46
2:G:141:ASP:HB3	2:G:144:ASN:ND2	2.31	0.46
3:H:153:ASP:OD1	3:H:153:ASP:N	2.48	0.46
4:I:252:ASP:O	4:I:256:LYS:HG2	2.16	0.46
4:J:127:LYS:CE	5:L:260:LEU:CD2	2.93	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:120:THR:OG1	1:B:132:MET:SD	2.67	0.46
1:C:120:THR:OG1	1:C:132:MET:SD	2.67	0.46
1:D:78:ASN:ND2	1:D:81:ASP:OD2	2.49	0.46
1:E:24:ASP:N	1:E:24:ASP:OD1	2.47	0.46
3:H:160:LEU:CD2	5:L:147:GLN:HG3	2.46	0.46
4:I:219:ARG:O	4:I:221:ALA:N	2.47	0.46
5:K:111:GLN:HE22	5:K:112:LYS:HD2	1.80	0.46
5:K:115:GLU:HG2	5:K:116:ALA:N	2.31	0.46
5:K:284:ILE:HG21	5:N:12:LYS:CE	2.46	0.46
5:L:280:ASP:CG	5:M:5:LYS:HE2	2.40	0.46
2:G:47:MET:CA	5:K:160:ARG:NH2	2.76	0.45
5:K:213:LYS:HA	5:K:213:LYS:HE2	1.98	0.45
5:L:91:ARG:HH21	5:L:94:LEU:HD23	1.81	0.45
1:F:34:ILE:HD11	1:F:59:GLN:HG2	1.97	0.45
4:I:204:ARG:HA	4:I:204:ARG:HE	1.81	0.45
5:K:261:TYR:HD1	5:K:261:TYR:HA	1.71	0.45
5:L:280:ASP:OD2	5:M:5:LYS:CE	2.61	0.45
1:A:34:ILE:HD11	1:A:59:GLN:HG2	1.97	0.45
1:A:78:ASN:ND2	1:A:81:ASP:OD2	2.49	0.45
1:B:34:ILE:HD12	1:B:67:LEU:HD13	1.98	0.45
3:H:76:VAL:HA	3:H:79:THR:HG22	1.99	0.45
4:J:90:PHE:O	4:J:90:PHE:CG	2.69	0.45
5:L:219:ASP:O	5:L:222:GLU:HG3	2.15	0.45
1:C:95:ARG:HD3	4:I:268:ARG:HH12	1.67	0.45
1:D:120:THR:OG1	1:D:132:MET:SD	2.67	0.45
1:E:373:LYS:HD2	1:E:374:CYS:N	2.31	0.45
2:G:2:ASP:N	3:H:45:SER:O	2.50	0.45
2:G:41:LEU:HD11	2:G:77:PHE:HD1	1.79	0.45
3:H:59:LYS:HB3	3:H:59:LYS:HZ2	1.80	0.45
4:J:109:ILE:HD12	5:L:281:MET:SD	2.54	0.45
5:K:88:LEU:HD21	5:L:89:ASN:CG	2.41	0.45
1:A:12:ASN:OD1	1:A:86:TRP:NE1	2.42	0.45
1:A:33:SER:O	1:A:33:SER:OG	2.33	0.45
1:F:373:LYS:HD2	1:F:374:CYS:N	2.32	0.45
2:G:132:ASP:O	2:G:134:GLU:N	2.49	0.45
3:H:160:LEU:HD21	5:L:147:GLN:HG3	1.99	0.45
4:I:257:PHE:HA	4:I:260:GLN:NE2	2.31	0.45
1:C:126:THR:CB	4:I:211:LYS:NZ	2.79	0.45
1:D:25:ASP:CA	3:H:148:VAL:CG1	2.93	0.45
1:D:43:VAL:N	1:E:168:GLY:O	2.47	0.45
1:F:78:ASN:ND2	1:F:81:ASP:OD2	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:127:LYS:CE	5:L:260:LEU:HD22	2.44	0.45
5:K:214:TYR:CD2	5:L:214:TYR:CG	3.04	0.45
5:M:54:GLU:HG3	5:N:53:THR:HG21	1.98	0.45
5:N:35:ARG:NE	5:N:39:LEU:HD11	2.31	0.45
1:A:34:ILE:HD12	1:A:67:LEU:HD13	1.98	0.45
1:B:373:LYS:NZ	1:B:373:LYS:HB3	2.31	0.45
1:C:373:LYS:NZ	1:C:373:LYS:HB3	2.31	0.45
1:E:373:LYS:NZ	1:E:373:LYS:HB3	2.31	0.45
1:F:34:ILE:HD12	1:F:67:LEU:HD13	1.98	0.45
1:F:373:LYS:NZ	1:F:373:LYS:HB3	2.31	0.45
4:I:218:ARG:NH1	4:I:218:ARG:HA	2.32	0.45
4:J:120:GLU:OE1	5:L:271:SER:HB3	2.16	0.45
5:K:106:LEU:HD12	5:K:106:LEU:O	2.16	0.45
5:L:145:GLU:OE1	5:L:145:GLU:HA	2.16	0.45
5:L:234:GLU:OE1	5:L:235:ALA:N	2.50	0.45
5:N:48:LYS:HE2	5:N:48:LYS:HB3	1.85	0.45
1:A:373:LYS:NZ	1:A:373:LYS:HB3	2.31	0.45
1:E:12:ASN:OD1	1:E:86:TRP:NE1	2.42	0.45
1:E:78:ASN:ND2	1:E:81:ASP:OD2	2.49	0.45
2:G:15:GLU:H	2:G:15:GLU:HG3	1.40	0.45
2:G:35:CYS:O	2:G:72:VAL:N	2.45	0.45
4:I:228:ASN:OD1	4:I:229:GLU:N	2.50	0.45
5:K:100:ASP:OD1	5:K:100:ASP:N	2.50	0.45
5:K:132:SER:OG	5:K:133:ARG:NE	2.46	0.45
5:L:85:VAL:O	5:L:89:ASN:ND2	2.50	0.45
1:B:78:ASN:ND2	1:B:81:ASP:OD2	2.49	0.45
1:C:373:LYS:HD2	1:C:374:CYS:N	2.32	0.45
1:D:373:LYS:HD2	1:D:374:CYS:N	2.32	0.45
1:D:373:LYS:NZ	1:D:373:LYS:HB3	2.31	0.45
1:E:44:MET:CB	1:E:47:MET:HG3	2.47	0.45
1:E:345:ILE:HG13	3:H:181:ASP:OD2	2.16	0.45
4:I:208:ARG:O	4:I:212:LYS:HE2	2.17	0.45
5:K:128:LYS:HD2	5:K:128:LYS:N	2.30	0.45
5:L:196:GLU:O	5:L:200:VAL:HG23	2.16	0.45
1:C:34:ILE:HD12	1:C:67:LEU:HD13	1.99	0.45
3:H:76:VAL:HG12	3:H:80:ARG:NE	2.32	0.45
3:H:193:ARG:NH2	5:L:114:GLU:OE2	2.50	0.45
5:K:148:LEU:HD12	5:K:148:LEU:C	2.42	0.45
4:J:100:LYS:O	4:J:104:GLU:HB3	2.17	0.44
1:A:373:LYS:HD3	1:A:374:CYS:SG	2.58	0.44
1:B:47:MET:HE1	1:C:148:THR:HB	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:373:LYS:HD3	1:E:374:CYS:SG	2.58	0.44
1:F:44:MET:CB	1:F:47:MET:HG3	2.48	0.44
2:G:51:ASN:OD1	2:G:51:ASN:N	2.51	0.44
2:G:149:ASP:N	2:G:152:GLU:HB2	2.32	0.44
3:H:139:LYS:HA	3:H:142:ARG:HH11	1.83	0.44
5:L:140:LYS:O	5:L:144:GLN:HG2	2.17	0.44
5:L:157:ASP:OD1	5:L:158:ALA:N	2.50	0.44
1:B:373:LYS:HD3	1:B:374:CYS:SG	2.58	0.44
1:E:345:ILE:CG1	3:H:181:ASP:OD2	2.65	0.44
1:F:120:THR:OG1	1:F:132:MET:SD	2.67	0.44
1:F:373:LYS:HD3	1:F:374:CYS:SG	2.58	0.44
3:H:77:LEU:HD21	4:I:247:GLU:HB2	1.99	0.44
4:I:240:TRP:NE1	4:I:244:HIS:HE2	2.15	0.44
4:I:246:LEU:HA	4:I:249:GLU:CD	2.41	0.44
5:L:217:LYS:HE3	5:L:221:TYR:CE2	2.53	0.44
1:A:47:MET:CE	1:B:148:THR:CB	2.96	0.44
1:E:34:ILE:HD12	1:E:67:LEU:HD13	1.98	0.44
2:G:12:LEU:H	2:G:12:LEU:HG	1.57	0.44
5:K:111:GLN:OE1	5:K:112:LYS:HG2	2.17	0.44
5:K:260:LEU:HD12	5:K:261:TYR:N	2.32	0.44
1:C:373:LYS:HD3	1:C:374:CYS:SG	2.58	0.44
2:G:5:TYR:HD2	2:G:83:ARG:NE	2.16	0.44
2:G:55:GLU:H	2:G:55:GLU:CD	2.26	0.44
3:H:48:LEU:O	3:H:51:LYS:HG2	2.18	0.44
1:A:120:THR:OG1	1:A:132:MET:SD	2.67	0.44
1:C:83:GLU:CG	4:I:204:ARG:HG3	2.39	0.44
3:H:81:CYS:SG	3:H:104:ARG:NH2	2.91	0.44
3:H:110:GLU:HA	3:H:113:TYR:HD2	1.82	0.44
4:J:120:GLU:HG3	5:L:271:SER:OG	2.18	0.44
5:K:121:ASP:O	5:K:124:GLU:HG2	2.18	0.44
5:K:129:VAL:O	5:K:133:ARG:HD2	2.18	0.44
1:D:47:MET:HE2	1:E:148:THR:CB	2.46	0.44
1:D:373:LYS:HD3	1:D:374:CYS:SG	2.58	0.44
2:G:13:THR:O	2:G:17:LYS:HB2	2.17	0.44
4:I:275:GLN:HE21	4:I:275:GLN:HB3	1.59	0.44
3:H:84:LEU:HB2	4:I:240:TRP:CE2	2.53	0.44
4:I:270:ARG:HH11	4:I:270:ARG:HB3	1.82	0.44
4:I:270:ARG:NH1	4:I:274:ASN:HD21	2.15	0.44
5:K:112:LYS:HB3	5:L:113:LEU:HD12	1.98	0.44
1:B:44:MET:CB	1:B:47:MET:HG3	2.48	0.44
1:B:193:LEU:HD23	1:B:193:LEU:HA	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:95:ARG:HD3	4:I:268:ARG:CZ	2.48	0.44
1:C:193:LEU:HD23	1:C:193:LEU:HA	1.82	0.44
2:G:134:GLU:HA	2:G:137:MET:HB3	2.00	0.44
3:H:204:GLY:O	3:H:206:LYS:NZ	2.44	0.44
4:J:105:LEU:CD2	5:L:284:ILE:HD12	2.34	0.44
5:K:156:GLU:HB3	5:K:160:ARG:NH1	2.33	0.44
5:K:161:LYS:HB3	5:L:162:TYR:CE1	2.53	0.44
1:A:44:MET:CB	1:A:47:MET:HG3	2.48	0.43
1:B:373:LYS:CD	1:B:374:CYS:N	2.80	0.43
4:I:264:ILE:O	4:I:268:ARG:HG2	2.18	0.43
5:K:111:GLN:CD	5:K:112:LYS:HD2	2.43	0.43
5:L:204:LEU:HD23	5:L:204:LEU:C	2.42	0.43
5:L:217:LYS:HZ1	5:L:221:TYR:HH	1.64	0.43
1:D:44:MET:CB	1:D:47:MET:HG3	2.48	0.43
2:G:101:PHE:HA	2:G:104:PHE:HB2	2.00	0.43
2:G:131:ASP:CG	3:H:43:SER:H	2.26	0.43
1:D:12:ASN:OD1	1:D:86:TRP:NE1	2.42	0.43
1:D:33:SER:O	1:D:33:SER:OG	2.32	0.43
1:D:373:LYS:HD2	1:D:373:LYS:H	1.64	0.43
5:L:164:GLU:HA	5:L:164:GLU:OE1	2.17	0.43
1:A:193:LEU:HD23	1:A:193:LEU:HA	1.83	0.43
1:C:44:MET:CB	1:C:47:MET:HG3	2.48	0.43
1:D:18:LYS:HG2	1:D:30:VAL:HG22	2.01	0.43
3:H:160:LEU:HD22	5:L:147:GLN:OE1	2.14	0.43
4:J:124:ILE:HD12	5:L:268:LYS:HE3	1.91	0.43
1:A:18:LYS:HG2	1:A:30:VAL:HG22	2.01	0.43
1:C:33:SER:O	1:C:33:SER:OG	2.33	0.43
4:J:137:ARG:HD2	4:J:137:ARG:O	2.18	0.43
5:K:204:LEU:HD11	5:L:203:ASN:CB	2.48	0.43
1:A:373:LYS:HD2	1:A:374:CYS:N	2.31	0.43
1:B:18:LYS:HG2	1:B:30:VAL:HG22	2.01	0.43
2:G:110:GLY:HA3	4:I:269:ASN:HB2	2.00	0.43
1:D:305:MET:HE3	1:D:305:MET:HB3	1.93	0.43
4:J:104:GLU:OE2	5:N:6:LYS:HE3	2.19	0.43
5:L:154:ILE:HA	5:L:157:ASP:OD2	2.18	0.43
5:M:51:LYS:HB3	5:M:51:LYS:HE3	1.77	0.43
5:N:10:MET:SD	5:N:10:MET:N	2.92	0.43
1:C:73:HIS:O	1:C:75:ILE:N	2.49	0.43
4:J:124:ILE:HD11	5:L:268:LYS:CB	2.48	0.43
4:J:137:ARG:HH21	5:L:254:ASP:CG	2.08	0.43
5:K:124:GLU:HG3	5:K:125:ARG:N	2.30	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:107:ALA:O	5:L:110:LEU:HG	2.19	0.43
5:M:35:ARG:NH1	5:N:36:SER:HB3	2.34	0.43
1:E:120:THR:OG1	1:E:132:MET:SD	2.67	0.43
4:I:237:LYS:HB2	4:I:237:LYS:HE2	1.86	0.43
4:I:256:LYS:HA	4:I:256:LYS:HD3	1.72	0.43
4:J:144:ARG:HD3	4:J:147:ARG:HD3	1.99	0.43
5:L:96:GLU:HA	5:L:99:LEU:HD23	2.01	0.43
1:B:373:LYS:HD2	1:B:374:CYS:N	2.31	0.43
1:C:80:ASP:HB2	4:I:203:LYS:CB	2.42	0.43
1:D:336:LYS:HB3	1:D:336:LYS:HE2	1.81	0.43
5:L:238:ARG:NH1	5:L:238:ARG:HB2	2.34	0.43
3:H:67:GLU:HG3	3:H:70:ARG:CZ	2.49	0.42
3:H:77:LEU:HD11	4:I:248:ALA:HB2	2.01	0.42
5:K:145:GLU:HA	5:K:148:LEU:HD23	1.99	0.42
5:L:281:MET:HE2	5:L:284:ILE:HG13	2.00	0.42
1:A:11:ASP:OD1	1:A:106:THR:OG1	2.36	0.42
2:G:133:ILE:HG22	2:G:134:GLU:HG2	2.01	0.42
1:C:87:HIS:CE1	3:H:121:LYS:HD2	2.50	0.42
1:D:142:LEU:HD12	1:D:142:LEU:HA	1.84	0.42
1:E:18:LYS:HG2	1:E:30:VAL:HG22	2.01	0.42
2:G:46:ARG:HG2	5:K:160:ARG:NE	2.23	0.42
2:G:102:ARG:HH11	4:I:259:GLN:HG3	1.84	0.42
3:H:73:LYS:HB2	4:I:251:PHE:CD2	2.54	0.42
4:I:212:LYS:HA	4:I:215:LEU:HG	2.01	0.42
1:A:73:HIS:O	1:A:75:ILE:N	2.50	0.42
2:G:6:LYS:NZ	2:G:79:VAL:HG21	2.34	0.42
2:G:111:TYR:CG	2:G:147:ARG:HD2	2.55	0.42
3:H:171:ARG:O	3:H:174:LEU:HG	2.19	0.42
3:H:187:ARG:HH22	5:L:125:ARG:NH1	2.15	0.42
4:J:118:LYS:C	4:J:118:LYS:CD	2.86	0.42
5:K:167:ARG:O	5:K:171:ILE:HG12	2.20	0.42
5:K:171:ILE:N	5:K:171:ILE:HD13	2.33	0.42
5:K:267:TYR:O	5:K:270:ILE:HG22	2.19	0.42
1:C:336:LYS:HE2	1:C:336:LYS:HB3	1.81	0.42
2:G:12:LEU:HB2	2:G:17:LYS:HE2	2.00	0.42
2:G:129:THR:HG22	2:G:130:GLU:H	1.85	0.42
5:L:82:GLU:O	5:L:85:VAL:HB	2.20	0.42
5:L:178:ARG:CZ	5:L:178:ARG:HB3	2.50	0.42
1:A:369:ILE:HD12	1:A:372:ARG:HD3	2.01	0.42
1:C:18:LYS:HG2	1:C:30:VAL:HG22	2.01	0.42
2:G:43:LYS:HD2	2:G:46:ARG:NH2	2.29	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:54:PRO:O	2:G:58:GLN:HG2	2.19	0.42
3:H:200:SER:CB	5:L:103:GLN:HB2	2.44	0.42
5:K:111:GLN:NE2	5:K:115:GLU:OE1	2.52	0.42
1:D:193:LEU:HD23	1:D:193:LEU:HA	1.83	0.42
1:F:106:THR:HB	1:F:137:GLN:HG2	2.02	0.42
2:G:2:ASP:N	2:G:2:ASP:OD1	2.53	0.42
2:G:120:MET:O	2:G:124:THR:HG23	2.20	0.42
1:C:373:LYS:CD	1:C:374:CYS:N	2.80	0.42
4:J:93:ILE:O	4:J:97:ARG:HB3	2.20	0.42
4:J:121:GLU:OE1	4:J:121:GLU:N	2.53	0.42
5:K:139:GLU:HG2	5:K:140:LYS:N	2.35	0.42
1:A:336:LYS:HE2	1:A:336:LYS:HB3	1.81	0.42
1:E:118:LYS:HE3	1:E:118:LYS:HB3	1.83	0.42
1:F:18:LYS:HG2	1:F:30:VAL:HG22	2.00	0.42
4:I:224:ILE:HG22	4:I:235:LYS:HD3	2.02	0.42
1:A:106:THR:HB	1:A:137:GLN:HG2	2.02	0.41
1:A:354:GLN:HE21	4:J:83:PRO:CG	2.32	0.41
1:B:44:MET:CG	1:C:168:GLY:HA2	2.50	0.41
1:E:193:LEU:HD23	1:E:193:LEU:HA	1.82	0.41
2:G:93:SER:HB3	2:G:95:GLU:OE2	2.20	0.41
3:H:104:ARG:HA	3:H:107:LYS:HE3	2.01	0.41
1:D:11:ASP:OD1	1:D:106:THR:OG1	2.36	0.41
1:E:106:THR:HB	1:E:137:GLN:HG2	2.02	0.41
1:F:369:ILE:HD12	1:F:372:ARG:HD3	2.01	0.41
3:H:112:ARG:HD3	4:I:246:LEU:O	2.20	0.41
3:H:113:TYR:CE2	4:I:215:LEU:HB3	2.55	0.41
5:K:274:LEU:CD1	5:K:278:LEU:HD21	2.50	0.41
1:A:375:PHE:HB2	4:J:80:PRO:HG3	2.02	0.41
2:G:102:ARG:HH22	4:I:263:GLU:HG2	1.85	0.41
3:H:116:GLU:O	3:H:119:VAL:HG12	2.20	0.41
5:K:117:GLU:OE1	5:K:117:GLU:CA	2.69	0.41
5:K:134:ALA:HB1	5:L:133:ARG:HD3	2.02	0.41
5:K:137:ASP:OD2	5:L:137:ASP:C	2.64	0.41
5:L:68:GLN:HA	5:L:71:LEU:HD23	2.02	0.41
5:L:250:GLU:HA	5:L:253:ILE:HD12	2.02	0.41
5:L:251:LYS:NZ	5:L:255:ASP:OD2	2.52	0.41
1:A:47:MET:HE2	1:B:148:THR:CB	2.46	0.41
1:C:305:MET:HE3	1:C:305:MET:HB3	1.93	0.41
1:C:369:ILE:HD12	1:C:372:ARG:HD3	2.01	0.41
1:D:42:GLY:HA2	1:E:168:GLY:O	2.19	0.41
1:E:345:ILE:HG12	3:H:181:ASP:HB2	2.00	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:133:ILE:HD13	3:H:133:ILE:HA	1.93	0.41
3:H:193:ARG:HH22	5:L:114:GLU:CG	2.33	0.41
5:L:234:GLU:CD	5:L:234:GLU:C	2.88	0.41
5:M:20:ASP:OD1	5:M:21:ARG:N	2.54	0.41
5:M:36:SER:OG	5:N:36:SER:OG	2.17	0.41
1:D:148:THR:CG2	3:H:139:LYS:HE3	2.50	0.41
1:E:369:ILE:HD12	1:E:372:ARG:HD3	2.01	0.41
1:F:141:SER:OG	1:F:152:VAL:HG21	2.21	0.41
1:F:334:GLU:OE2	5:K:90:ARG:NH2	2.53	0.41
5:K:92:ILE:HD11	5:L:91:ARG:CB	2.50	0.41
5:K:176:LEU:HD13	5:K:176:LEU:O	2.21	0.41
5:L:64:LEU:O	5:L:68:GLN:N	2.48	0.41
1:C:12:ASN:OD1	1:C:86:TRP:NE1	2.42	0.41
1:D:106:THR:HB	1:D:137:GLN:HG2	2.02	0.41
1:E:33:SER:O	1:E:33:SER:OG	2.32	0.41
1:E:141:SER:OG	1:E:152:VAL:HG21	2.21	0.41
2:G:119:MET:HA	2:G:122:GLN:NE2	2.36	0.41
3:H:99:ARG:HB2	4:I:225:ASP:OD2	2.21	0.41
5:K:81:ALA:O	5:K:85:VAL:HG12	2.20	0.41
5:K:111:GLN:O	5:K:114:GLU:HG2	2.21	0.41
5:L:276:HIS:HA	5:L:279:ASN:HD22	1.86	0.41
1:A:85:ILE:HD13	1:A:85:ILE:HA	1.96	0.41
1:A:141:SER:OG	1:A:152:VAL:HG21	2.21	0.41
1:B:141:SER:OG	1:B:152:VAL:HG21	2.21	0.41
1:B:369:ILE:HD12	1:B:372:ARG:HD3	2.01	0.41
4:I:238:GLU:OE1	4:I:239:LEU:HD12	2.20	0.41
5:K:197:LEU:HD22	5:K:201:THR:CG2	2.48	0.41
5:K:278:LEU:HD23	5:K:278:LEU:N	2.36	0.41
1:C:106:THR:HB	1:C:137:GLN:HG2	2.02	0.41
1:D:47:MET:CE	1:E:148:THR:CB	2.98	0.41
1:D:118:LYS:HE3	1:D:118:LYS:HB3	1.83	0.41
1:D:369:ILE:HD12	1:D:372:ARG:HD3	2.01	0.41
5:K:162:TYR:CE2	5:L:161:LYS:CB	3.04	0.41
5:K:162:TYR:CE2	5:L:161:LYS:HB2	2.55	0.41
5:K:217:LYS:HE3	5:K:217:LYS:HA	2.03	0.41
5:K:266:LYS:HZ3	5:K:266:LYS:C	2.28	0.41
5:L:161:LYS:HE3	5:L:161:LYS:HB2	1.73	0.41
5:M:50:LEU:HD22	5:N:46:LEU:HD11	2.02	0.41
1:B:47:MET:HE1	1:C:148:THR:CB	2.51	0.41
1:B:305:MET:HE3	1:B:305:MET:HB3	1.93	0.41
1:C:126:THR:CB	4:I:211:LYS:HZ2	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:372:ARG:HE	1:E:373:LYS:HE2	1.86	0.41
1:F:193:LEU:HD23	1:F:193:LEU:HA	1.83	0.41
3:H:97:LEU:HA	3:H:100:GLN:NE2	2.36	0.41
3:H:107:LYS:O	3:H:111:GLU:HG3	2.19	0.41
3:H:205:ARG:HE	3:H:206:LYS:H	1.69	0.41
4:I:206:THR:HA	4:I:209:GLU:OE1	2.21	0.41
5:K:71:LEU:HD23	5:L:71:LEU:HB3	2.01	0.41
5:K:127:MET:O	5:K:130:ILE:HG22	2.21	0.41
5:L:127:MET:O	5:L:130:ILE:HG22	2.21	0.41
5:N:35:ARG:O	5:N:39:LEU:HG	2.21	0.41
1:D:141:SER:OG	1:D:152:VAL:HG21	2.21	0.41
1:F:373:LYS:CD	1:F:374:CYS:N	2.80	0.41
5:K:214:TYR:CZ	5:L:214:TYR:O	2.74	0.41
1:B:372:ARG:HE	1:B:373:LYS:HE2	1.87	0.40
1:F:118:LYS:HE3	1:F:118:LYS:HB3	1.83	0.40
1:F:372:ARG:HE	1:F:373:LYS:HE2	1.86	0.40
1:D:373:LYS:CD	1:D:374:CYS:N	2.80	0.40
2:G:43:LYS:HA	2:G:46:ARG:NH2	2.37	0.40
4:I:271:ILE:HD13	4:I:271:ILE:HA	1.97	0.40
5:L:91:ARG:NE	5:L:91:ARG:HA	2.36	0.40
5:L:124:GLU:C	5:L:124:GLU:CD	2.90	0.40
5:M:36:SER:O	5:M:40:GLU:HG3	2.20	0.40
1:C:372:ARG:HE	1:C:373:LYS:HE2	1.86	0.40
5:K:234:GLU:C	5:K:234:GLU:CD	2.88	0.40
5:K:267:TYR:HD2	5:K:267:TYR:C	2.30	0.40
5:M:19:LEU:HD23	5:M:19:LEU:HA	1.92	0.40
1:B:85:ILE:HD13	1:B:85:ILE:HA	1.96	0.40
1:E:373:LYS:CD	1:E:374:CYS:N	2.80	0.40
2:G:38:THR:HG21	2:G:61:ILE:HA	2.03	0.40
5:K:162:TYR:HE2	5:L:161:LYS:CB	2.35	0.40
5:L:150:GLU:O	5:L:154:ILE:HG12	2.21	0.40
1:B:11:ASP:OD1	1:B:106:THR:OG1	2.36	0.40
1:D:124:PHE:HD1	1:D:124:PHE:HA	1.77	0.40
1:F:85:ILE:HD13	1:F:85:ILE:HA	1.96	0.40
2:G:83:ARG:NH1	2:G:87:ASP:HB2	2.36	0.40
2:G:147:ARG:NH2	4:I:273:ASP:OD1	2.55	0.40
5:K:88:LEU:HD22	5:L:85:VAL:HA	2.04	0.40
5:L:251:LYS:HZ3	5:L:255:ASP:HB3	1.87	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	369/377 (98%)	352 (95%)	17 (5%)	0	100	100
1	B	369/377 (98%)	351 (95%)	18 (5%)	0	100	100
1	C	369/377 (98%)	353 (96%)	16 (4%)	0	100	100
1	D	369/377 (98%)	353 (96%)	16 (4%)	0	100	100
1	E	369/377 (98%)	351 (95%)	18 (5%)	0	100	100
1	F	369/377 (98%)	351 (95%)	18 (5%)	0	100	100
2	G	158/161 (98%)	142 (90%)	15 (10%)	1 (1%)	22	60
3	H	168/211 (80%)	162 (96%)	6 (4%)	0	100	100
4	I	72/291 (25%)	66 (92%)	6 (8%)	0	100	100
4	J	75/291 (26%)	71 (95%)	4 (5%)	0	100	100
5	K	219/284 (77%)	219 (100%)	0	0	100	100
5	L	219/284 (77%)	218 (100%)	1 (0%)	0	100	100
5	M	53/284 (19%)	52 (98%)	1 (2%)	0	100	100
5	N	53/284 (19%)	52 (98%)	1 (2%)	0	100	100
All	All	3231/4352 (74%)	3093 (96%)	137 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	G	36	ILE

### 5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	314/320 (98%)	294 (94%)	20 (6%)	14	36
1	B	314/320 (98%)	294 (94%)	20 (6%)	14	36
1	C	314/320 (98%)	294 (94%)	20 (6%)	14	36
1	D	314/320 (98%)	294 (94%)	20 (6%)	14	36
1	E	314/320 (98%)	294 (94%)	20 (6%)	14	36
1	F	314/320 (98%)	294 (94%)	20 (6%)	14	36
2	G	141/142 (99%)	117 (83%)	24 (17%)	1	9
3	H	148/179 (83%)	124 (84%)	24 (16%)	2	10
4	I	68/257 (26%)	50 (74%)	18 (26%)	0	3
4	J	73/257 (28%)	67 (92%)	6 (8%)	9	28
5	K	191/245 (78%)	156 (82%)	35 (18%)	1	8
5	L	191/245 (78%)	167 (87%)	24 (13%)	3	15
5	M	47/245 (19%)	44 (94%)	3 (6%)	14	36
5	N	47/245 (19%)	44 (94%)	3 (6%)	14	36
All	All	2790/3735 (75%)	2533 (91%)	257 (9%)	10	24

All (257) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	ASP
1	A	54	VAL
1	A	64	ILE
1	A	66	THR
1	A	140	LEU
1	A	151	ILE
1	A	152	VAL
1	A	153	LEU
1	A	171	LEU
1	A	233	SER
1	A	254	ARG
1	A	269	MET
1	A	270	GLU
1	A	288	ASP
1	A	300	SER
1	A	303	THR
1	A	334	GLU

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Mol	Chain	Res	Type
1	A	370	VAL
1	A	373	LYS
1	A	374	CYS
1	B	24	ASP
1	B	54	VAL
1	B	64	ILE
1	B	66	THR
1	B	140	LEU
1	B	151	ILE
1	B	152	VAL
1	B	153	LEU
1	B	171	LEU
1	B	233	SER
1	B	254	ARG
1	B	269	MET
1	B	270	GLU
1	B	288	ASP
1	B	300	SER
1	B	303	THR
1	B	334	GLU
1	B	370	VAL
1	B	373	LYS
1	B	374	CYS
1	C	24	ASP
1	C	54	VAL
1	C	64	ILE
1	C	66	THR
1	C	140	LEU
1	C	151	ILE
1	C	152	VAL
1	C	153	LEU
1	C	171	LEU
1	C	233	SER
1	C	254	ARG
1	C	269	MET
1	C	270	GLU
1	C	288	ASP
1	C	300	SER
1	C	303	THR
1	C	334	GLU
1	C	370	VAL
1	C	373	LYS

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Mol	Chain	Res	Type
1	C	374	CYS
1	D	24	ASP
1	D	54	VAL
1	D	64	ILE
1	D	66	THR
1	D	140	LEU
1	D	151	ILE
1	D	152	VAL
1	D	153	LEU
1	D	171	LEU
1	D	233	SER
1	D	254	ARG
1	D	269	MET
1	D	270	GLU
1	D	288	ASP
1	D	300	SER
1	D	303	THR
1	D	334	GLU
1	D	370	VAL
1	D	373	LYS
1	D	374	CYS
1	E	24	ASP
1	E	54	VAL
1	E	64	ILE
1	E	66	THR
1	E	140	LEU
1	E	151	ILE
1	E	152	VAL
1	E	153	LEU
1	E	171	LEU
1	E	233	SER
1	E	254	ARG
1	E	269	MET
1	E	270	GLU
1	E	288	ASP
1	E	300	SER
1	E	303	THR
1	E	334	GLU
1	E	370	VAL
1	E	373	LYS
1	E	374	CYS
1	F	24	ASP

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Mol	Chain	Res	Type
1	F	54	VAL
1	F	64	ILE
1	F	66	THR
1	F	140	LEU
1	F	151	ILE
1	F	152	VAL
1	F	153	LEU
1	F	171	LEU
1	F	233	SER
1	F	254	ARG
1	F	269	MET
1	F	270	GLU
1	F	288	ASP
1	F	300	SER
1	F	303	THR
1	F	334	GLU
1	F	370	VAL
1	F	373	LYS
1	F	374	CYS
2	G	12	LEU
2	G	13	THR
2	G	15	GLU
2	G	26	ILE
2	G	51	ASN
2	G	59	GLU
2	G	64	VAL
2	G	77	PHE
2	G	80	MET
2	G	81	MET
2	G	86	LYS
2	G	95	GLU
2	G	97	LEU
2	G	101	PHE
2	G	112	ILE
2	G	118	LYS
2	G	121	LEU
2	G	127	THR
2	G	129	THR
2	G	131	ASP
2	G	137	MET
2	G	149	ASP
2	G	153	PHE

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Mol	Chain	Res	Type
2	G	158	LYS
3	H	48	LEU
3	H	59	LYS
3	H	60	GLN
3	H	70	ARG
3	H	86	LEU
3	H	94	LEU
3	H	95	GLN
3	H	100	GLN
3	H	107	LYS
3	H	109	ASP
3	H	113	TYR
3	H	114	ASP
3	H	133	ILE
3	H	139	LYS
3	H	140	PHE
3	H	142	ARG
3	H	150	ILE
3	H	153	ASP
3	H	157	GLN
3	H	159	LEU
3	H	188	GLU
3	H	189	VAL
3	H	205	ARG
3	H	209	PHE
4	I	203	LYS
4	I	208	ARG
4	I	209	GLU
4	I	222	LEU
4	I	224	ILE
4	I	230	ASP
4	I	232	LEU
4	I	233	ARG
4	I	235	LYS
4	I	241	GLN
4	I	250	LYS
4	I	254	GLN
4	I	258	LYS
4	I	261	LYS
4	I	265	ASN
4	I	267	LEU
4	I	270	ARG

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Mol	Chain	Res	Type
4	I	275	GLN
4	J	81	LYS
4	J	88	VAL
4	J	113	PHE
4	J	145	ASN
4	J	148	GLU
4	J	152	GLN
5	K	70	LYS
5	K	77	LYS
5	K	100	ASP
5	K	106	LEU
5	K	110	LEU
5	K	111	GLN
5	K	117	GLU
5	K	118	LYS
5	K	121	ASP
5	K	133	ARG
5	K	139	GLU
5	K	140	LYS
5	K	148	LEU
5	K	156	GLU
5	K	159	ASP
5	K	168	LYS
5	K	176	LEU
5	K	189	LYS
5	K	194	GLU
5	K	197	LEU
5	K	204	LEU
5	K	208	GLU
5	K	213	LYS
5	K	217	LYS
5	K	225	ILE
5	K	228	LEU
5	K	232	LEU
5	K	234	GLU
5	K	248	LYS
5	K	251	LYS
5	K	261	TYR
5	K	264	LYS
5	K	266	LYS
5	K	268	LYS
5	K	280	ASP

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Mol	Chain	Res	Type
5	L	65	LYS
5	L	68	GLN
5	L	70	LYS
5	L	76	LYS
5	L	98	GLU
5	L	99	LEU
5	L	110	LEU
5	L	113	LEU
5	L	118	LYS
5	L	133	ARG
5	L	159	ASP
5	L	172	ILE
5	L	185	LEU
5	L	218	GLU
5	L	220	LYS
5	L	231	LYS
5	L	234	GLU
5	L	238	ARG
5	L	251	LYS
5	L	255	ASP
5	L	272	GLU
5	L	276	HIS
5	L	278	LEU
5	L	280	ASP
5	M	4	ILE
5	M	13	LEU
5	M	36	SER
5	N	4	ILE
5	N	19	LEU
5	N	41	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	115	ASN
1	B	115	ASN
1	C	59	GLN
1	C	87	HIS
1	C	115	ASN
1	D	115	ASN
1	E	59	GLN
1	E	115	ASN

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Mol	Chain	Res	Type
1	F	115	ASN
2	G	16	GLN
2	G	143	ASN
2	G	144	ASN
3	H	60	GLN
3	H	95	GLN
3	H	100	GLN
3	H	176	GLN
3	H	186	ASN
4	I	241	GLN
4	I	254	GLN
4	I	260	GLN
4	I	269	ASN
4	I	274	ASN
4	I	275	GLN
4	J	140	GLN
4	J	145	ASN
4	J	152	GLN
4	J	153	ASN
5	K	89	ASN
5	K	93	GLN
5	L	89	ASN
5	L	103	GLN
5	L	135	GLN
5	L	144	GLN
5	L	147	GLN
5	L	202	ASN
5	M	47	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	ADP	B	401	7	24,29,29	0.84	0	29,45,45	1.16	2 (6%)
6	ADP	D	401	7	24,29,29	0.87	0	29,45,45	1.20	2 (6%)
6	ADP	C	401	7	24,29,29	0.82	0	29,45,45	1.18	2 (6%)
6	ADP	E	401	7	24,29,29	0.82	0	29,45,45	1.16	2 (6%)
6	ADP	A	401	7	24,29,29	0.84	0	29,45,45	1.19	2 (6%)
6	ADP	F	401	7	24,29,29	0.87	0	29,45,45	1.17	2 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	ADP	B	401	7	-	3/12/32/32	0/3/3/3
6	ADP	D	401	7	-	3/12/32/32	0/3/3/3
6	ADP	C	401	7	-	3/12/32/32	0/3/3/3
6	ADP	E	401	7	-	3/12/32/32	0/3/3/3
6	ADP	A	401	7	-	3/12/32/32	0/3/3/3
6	ADP	F	401	7	-	3/12/32/32	0/3/3/3

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	401	ADP	N3-C2-N1	-3.23	124.28	128.67
6	A	401	ADP	N3-C2-N1	-3.14	124.40	128.67
6	F	401	ADP	N3-C2-N1	-3.12	124.44	128.67
6	C	401	ADP	N3-C2-N1	-3.11	124.45	128.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	401	ADP	N3-C2-N1	-3.03	124.56	128.67
6	E	401	ADP	N3-C2-N1	-2.99	124.61	128.67
6	A	401	ADP	C4-C5-N7	-2.45	106.75	109.34
6	C	401	ADP	C4-C5-N7	-2.42	106.78	109.34
6	D	401	ADP	C4-C5-N7	-2.40	106.80	109.34
6	E	401	ADP	C4-C5-N7	-2.32	106.88	109.34
6	B	401	ADP	C4-C5-N7	-2.31	106.89	109.34
6	F	401	ADP	C4-C5-N7	-2.28	106.93	109.34

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	401	ADP	C5'-O5'-PA-O1A
6	A	401	ADP	C5'-O5'-PA-O2A
6	A	401	ADP	C5'-O5'-PA-O3A
6	B	401	ADP	C5'-O5'-PA-O1A
6	B	401	ADP	C5'-O5'-PA-O2A
6	B	401	ADP	C5'-O5'-PA-O3A
6	C	401	ADP	C5'-O5'-PA-O1A
6	C	401	ADP	C5'-O5'-PA-O2A
6	C	401	ADP	C5'-O5'-PA-O3A
6	D	401	ADP	C5'-O5'-PA-O1A
6	D	401	ADP	C5'-O5'-PA-O2A
6	D	401	ADP	C5'-O5'-PA-O3A
6	E	401	ADP	C5'-O5'-PA-O1A
6	E	401	ADP	C5'-O5'-PA-O2A
6	E	401	ADP	C5'-O5'-PA-O3A
6	F	401	ADP	C5'-O5'-PA-O1A
6	F	401	ADP	C5'-O5'-PA-O2A
6	F	401	ADP	C5'-O5'-PA-O3A

There are no ring outliers.

6 monomers are involved in 12 short contacts:

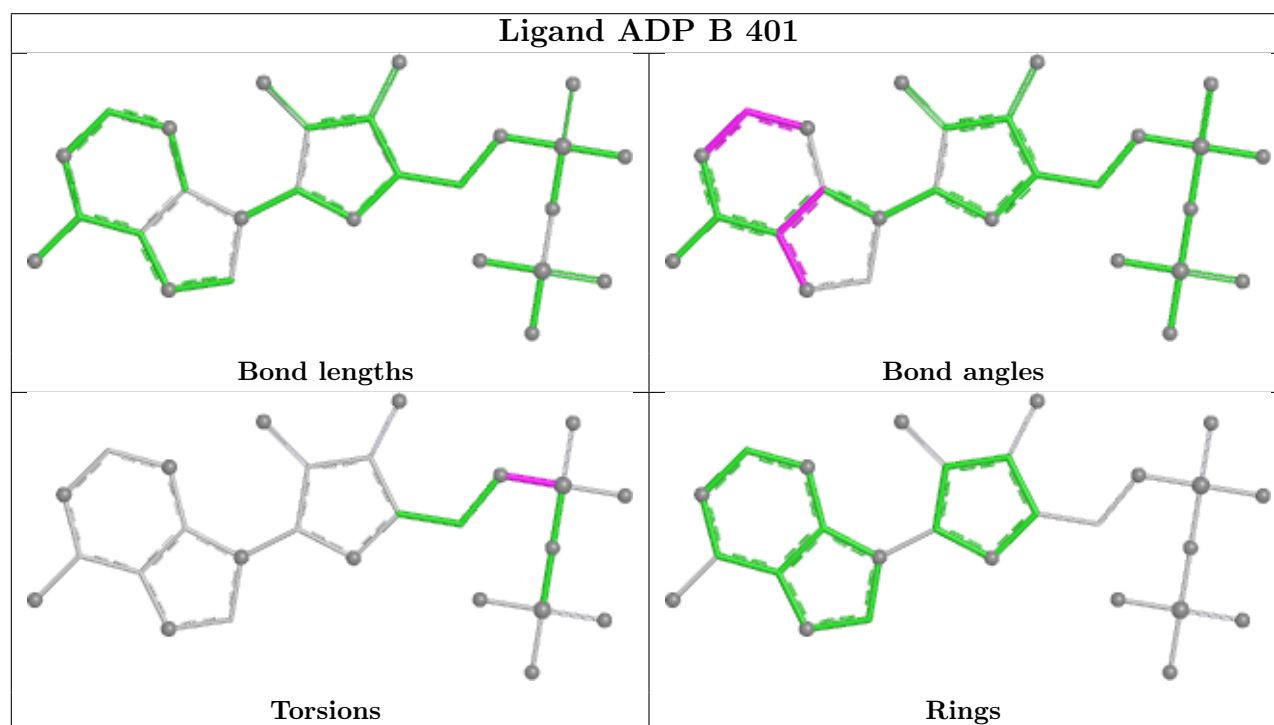
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	401	ADP	2	0
6	D	401	ADP	2	0
6	C	401	ADP	2	0
6	E	401	ADP	2	0
6	A	401	ADP	2	0

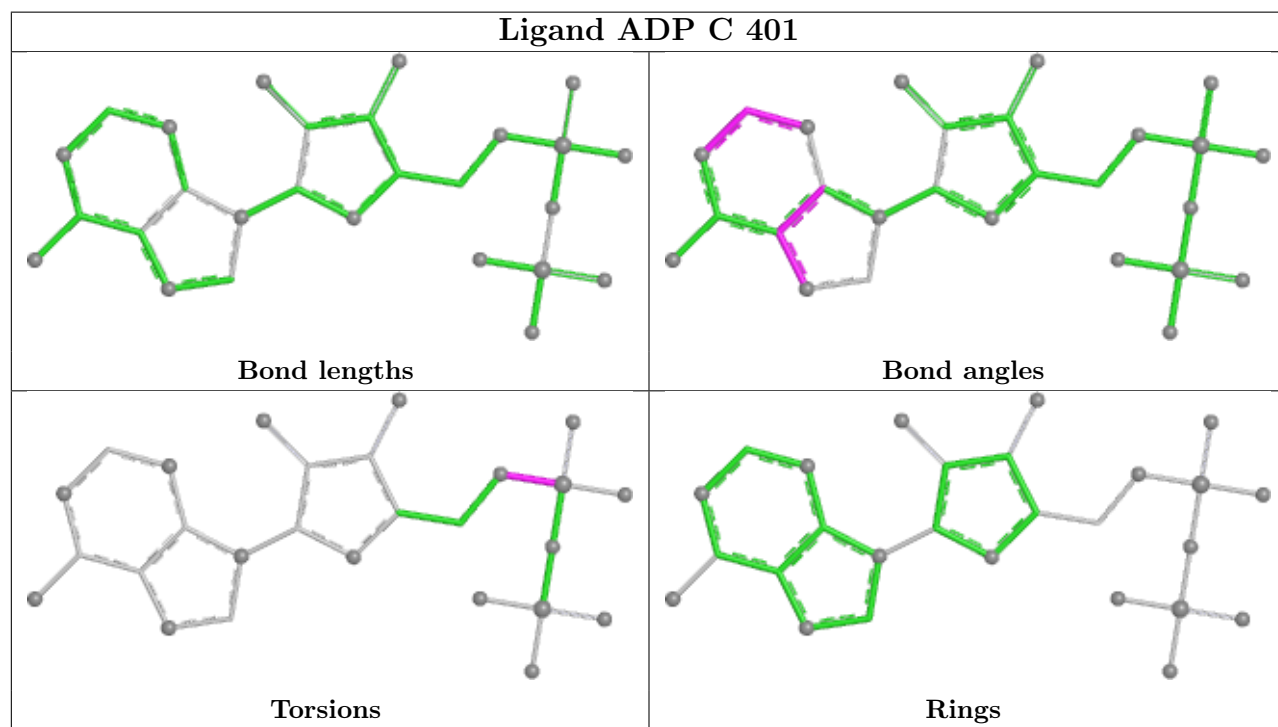
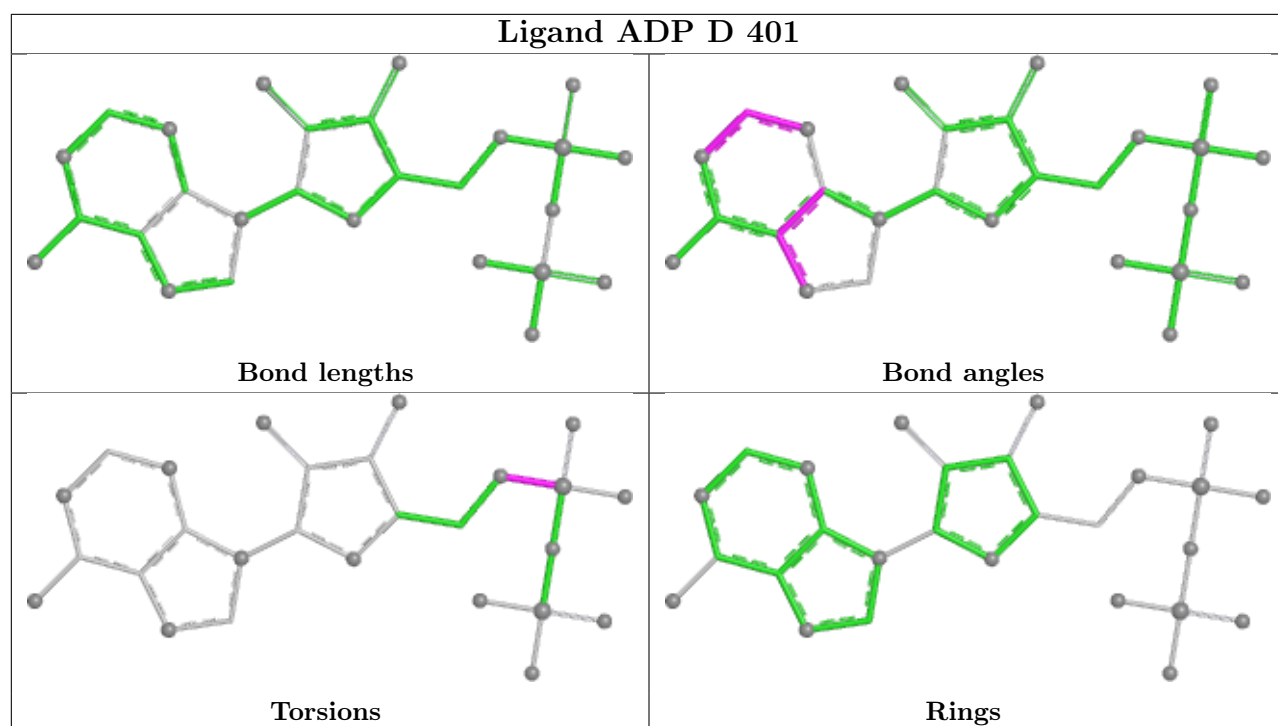
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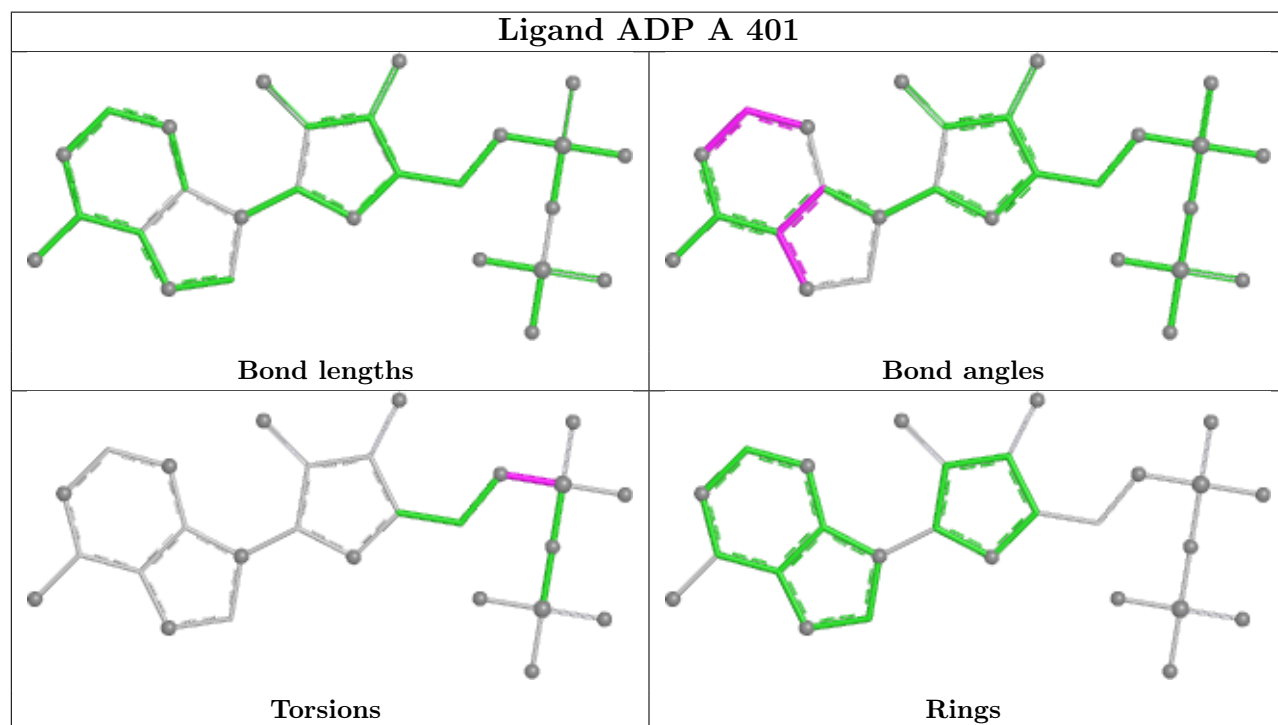
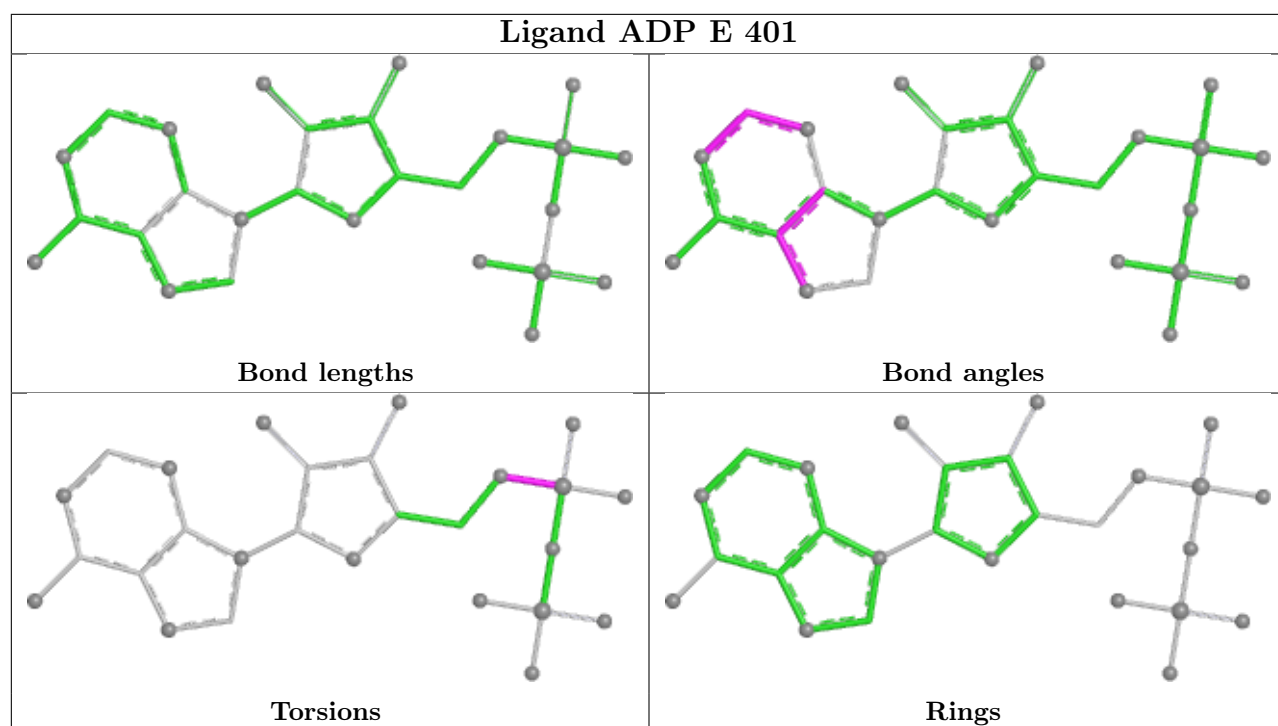
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	F	401	ADP	2	0

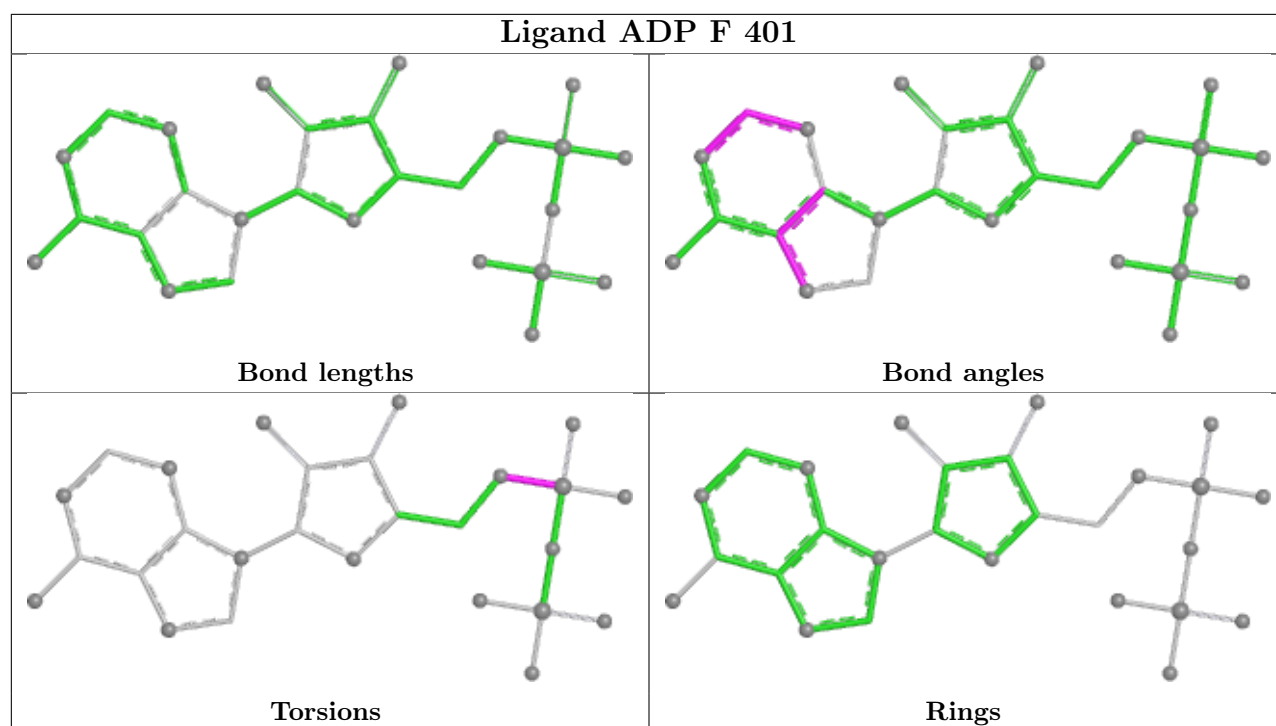
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.











## 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.

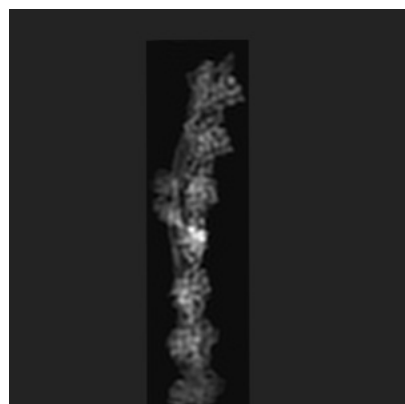
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48467. These allow visual inspection of the internal detail of the map and identification of artifacts.

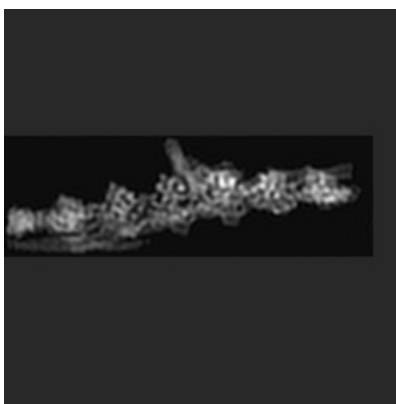
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

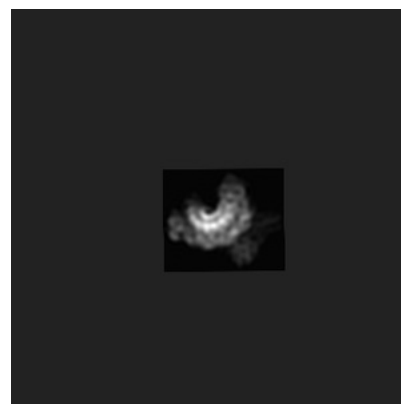
#### 6.1.1 Primary map



X

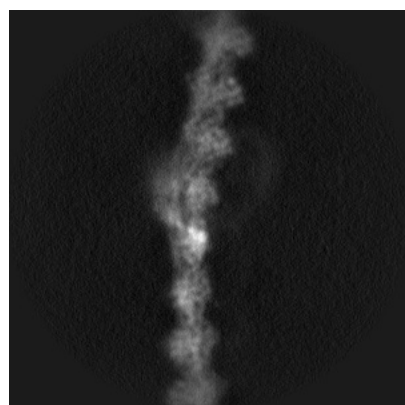


Y

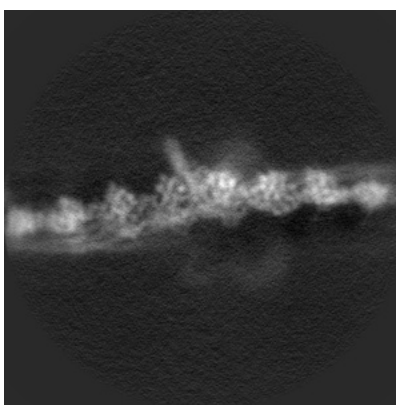


Z

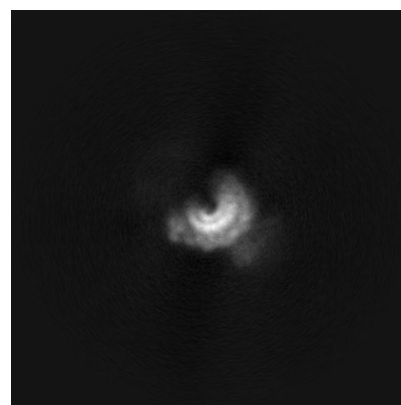
#### 6.1.2 Raw map



X



Y



Z

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

## 6.2 Central slices [i](#)

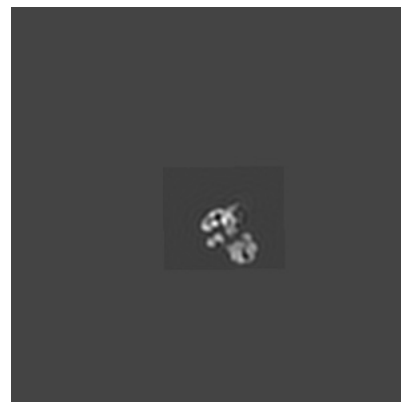
### 6.2.1 Primary map



X Index: 162



Y Index: 162

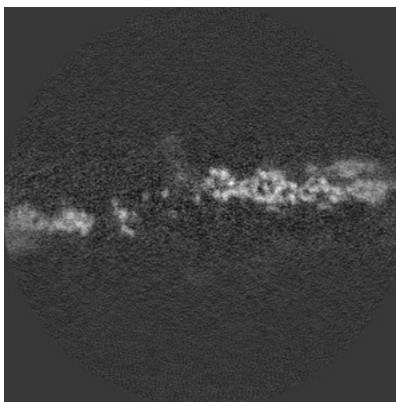


Z Index: 162

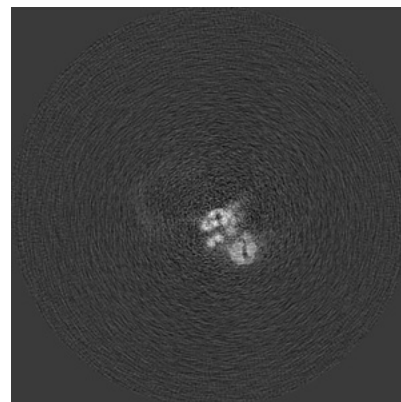
### 6.2.2 Raw map



X Index: 162



Y Index: 162



Z Index: 162

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

## 6.3 Largest variance slices [i](#)

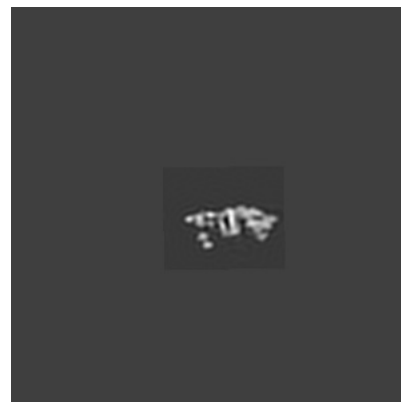
### 6.3.1 Primary map



X Index: 172

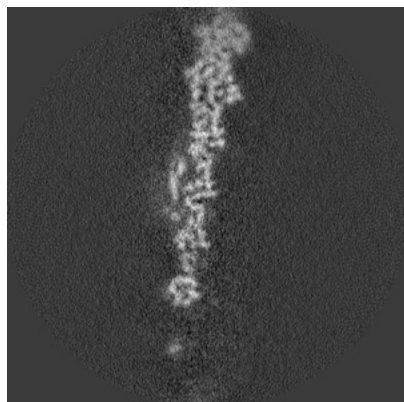


Y Index: 149

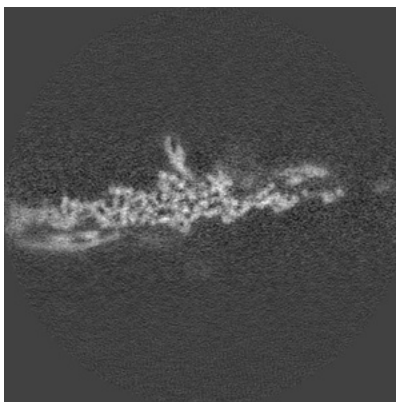


Z Index: 142

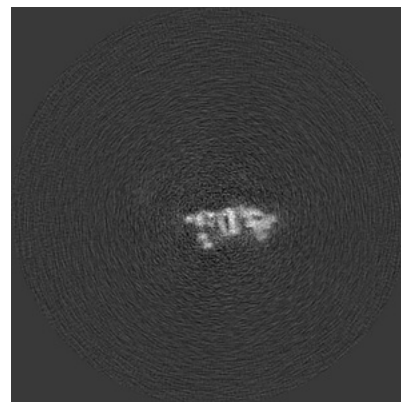
### 6.3.2 Raw map



X Index: 173



Y Index: 149

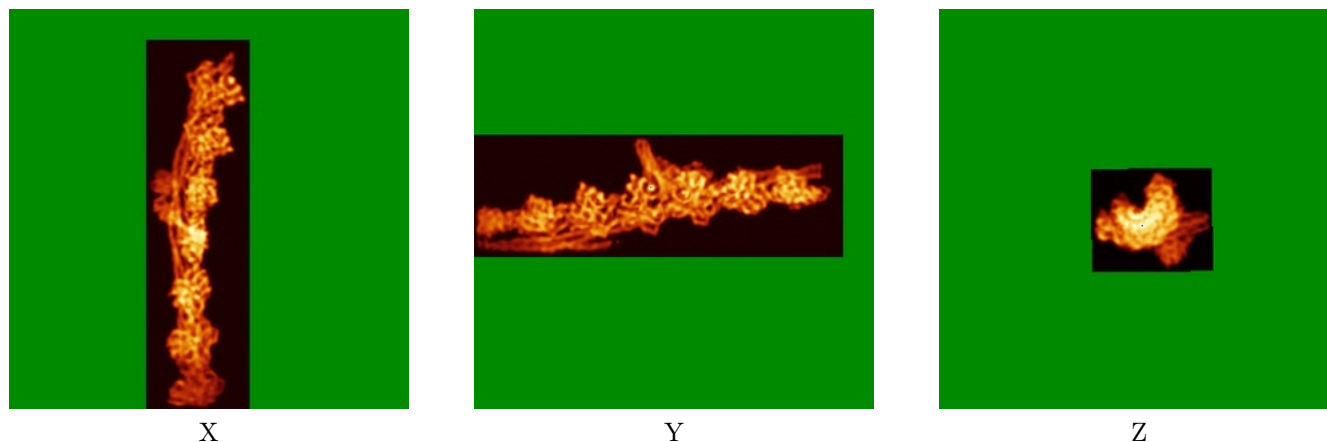


Z Index: 142

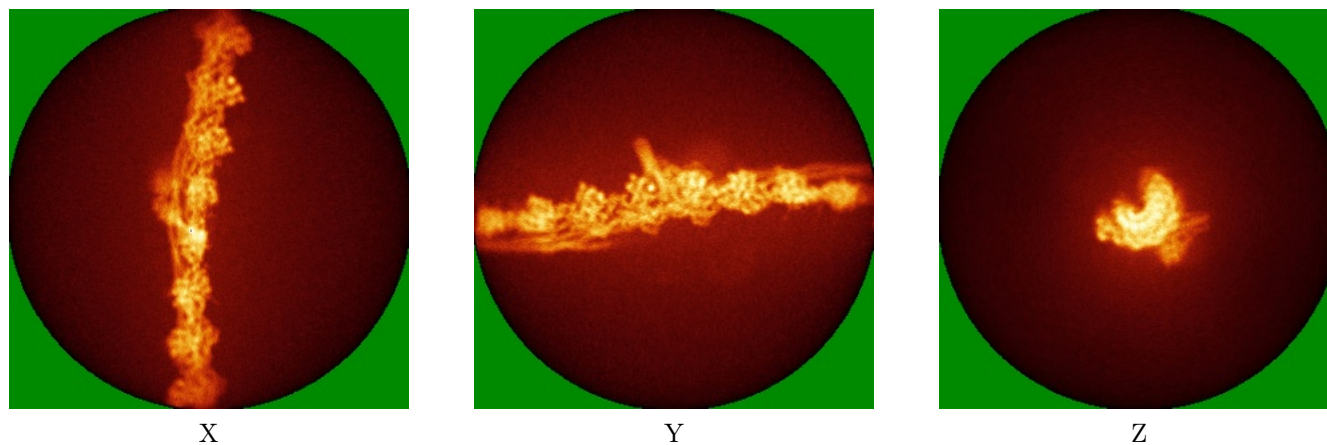
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

### 6.4.1 Primary map



### 6.4.2 Raw map



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.

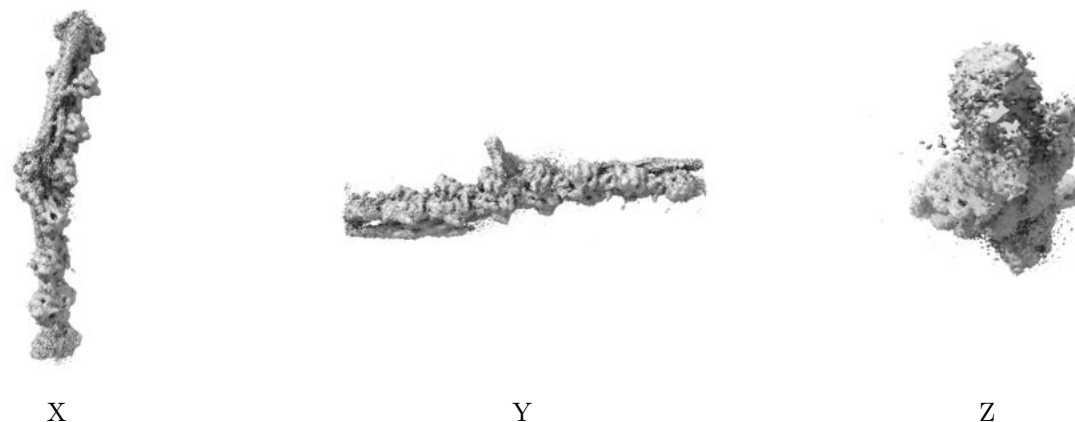
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.515. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

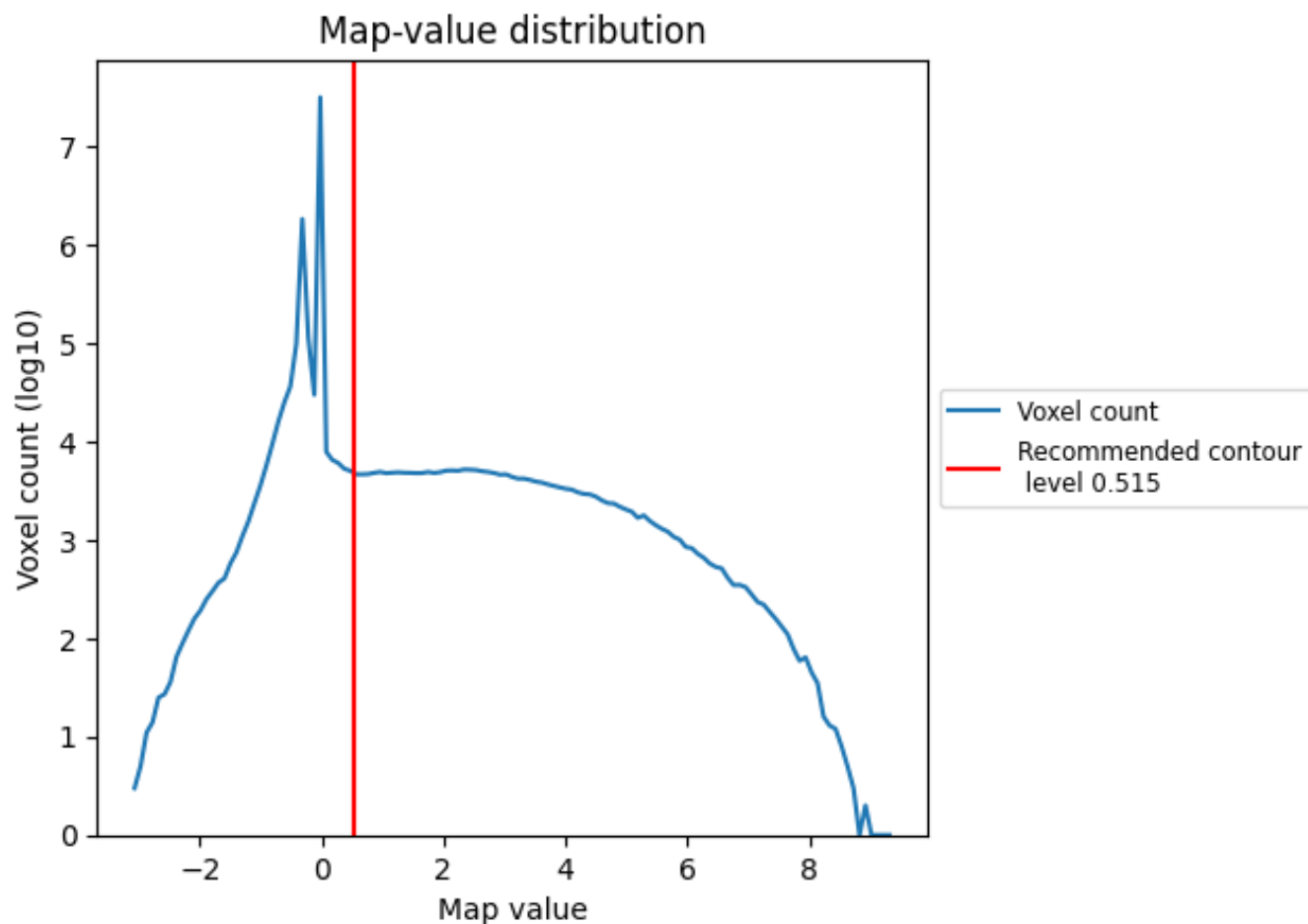
## 6.6 Mask visualisation [i](#)

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.

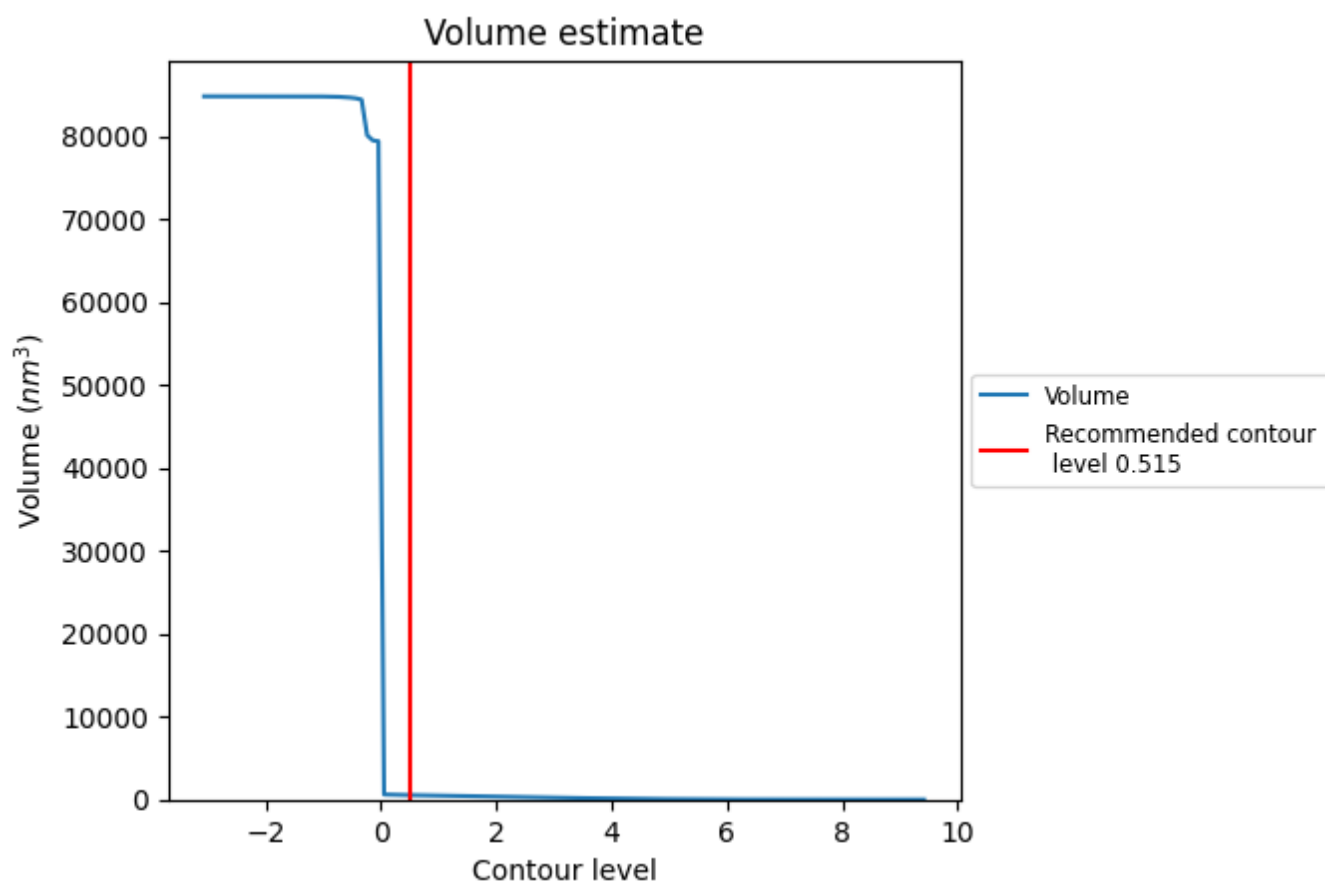
### 7.1 Map-value distribution [i](#)



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.



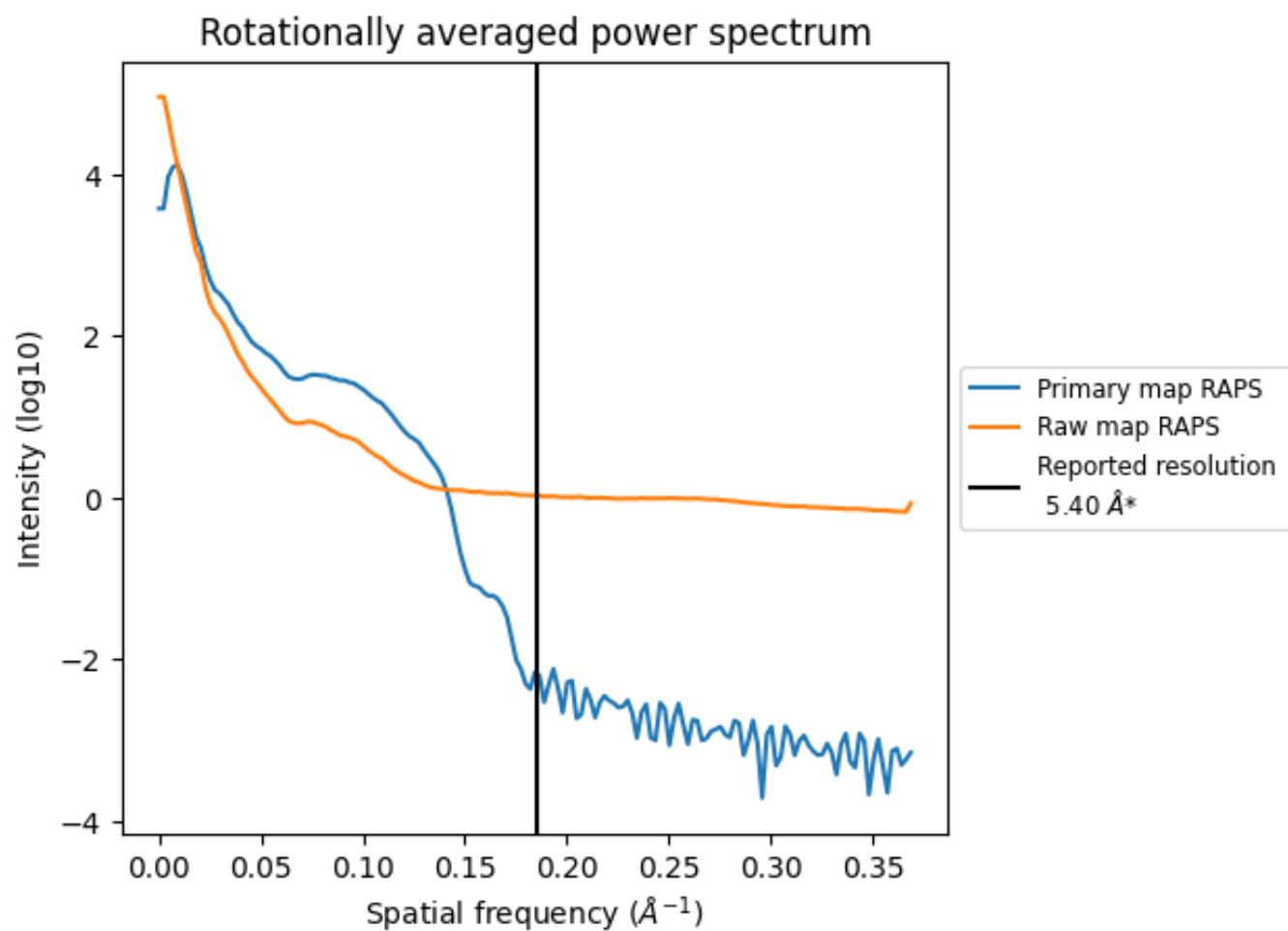
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 536  $\text{nm}^3$ ; this corresponds to an approximate mass of 484 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](#)

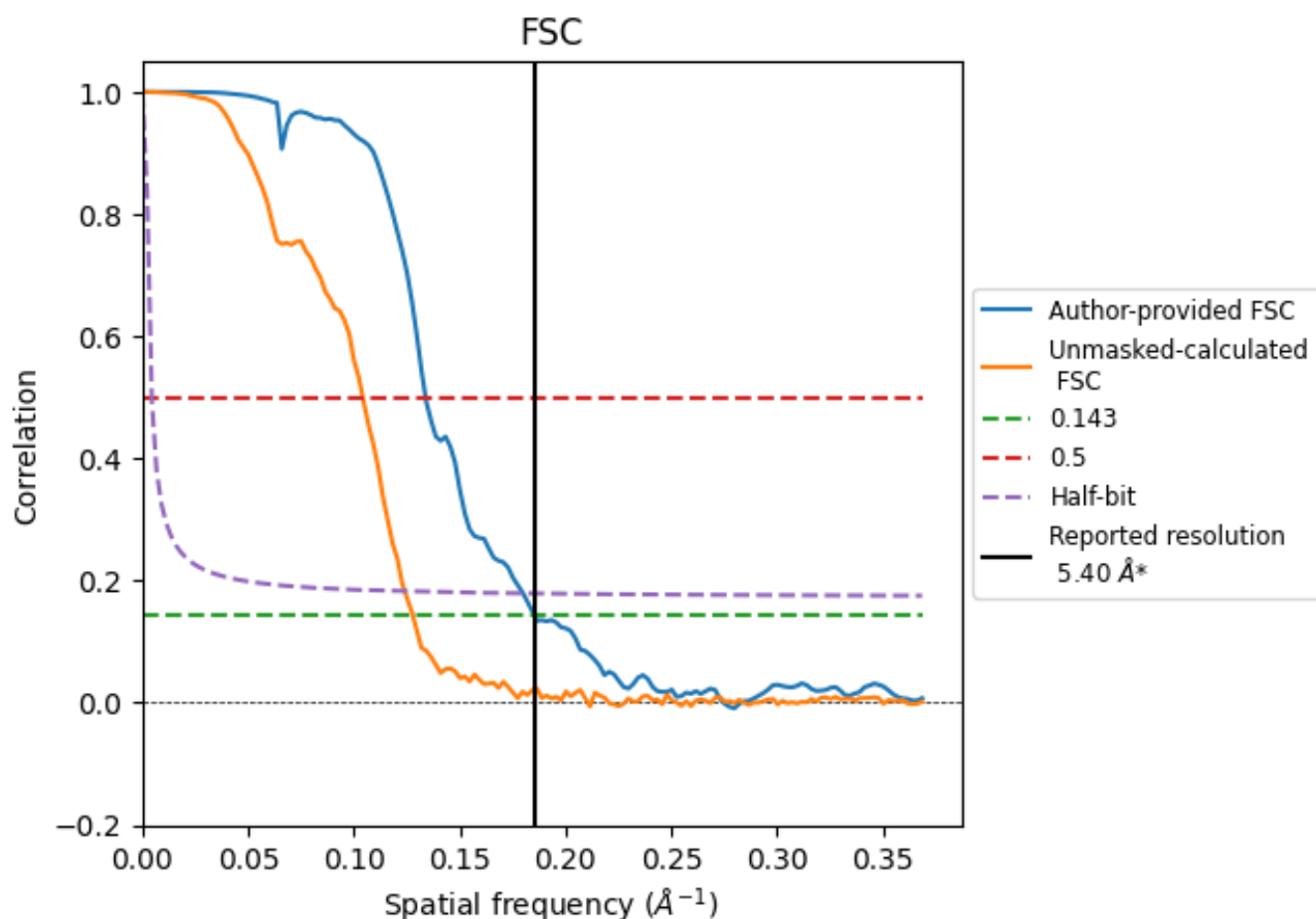


\*Reported resolution corresponds to spatial frequency of 0.185 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of  $0.185 \text{ \AA}^{-1}$

## 8.2 Resolution estimates [i](#)

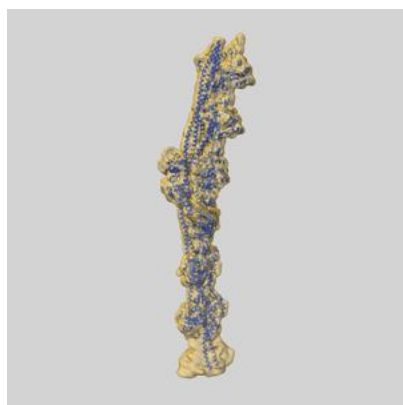
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.40	-	-
Author-provided FSC curve	5.40	7.47	5.56
Unmasked-calculated*	7.82	9.60	8.06

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.82 differs from the reported value 5.4 by more than 10 %

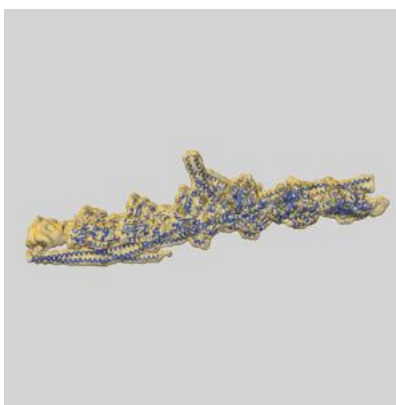
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-48467 and PDB model 9MOI. Per-residue inclusion information can be found in section [3](#) on page [7](#).

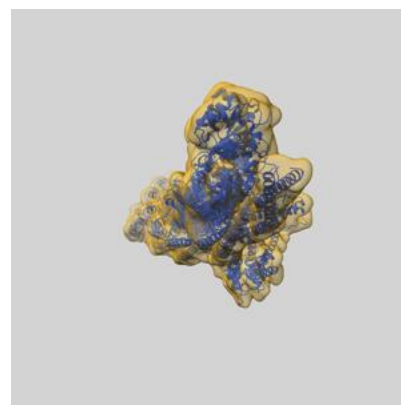
### 9.1 Map-model overlay [i](#)



X



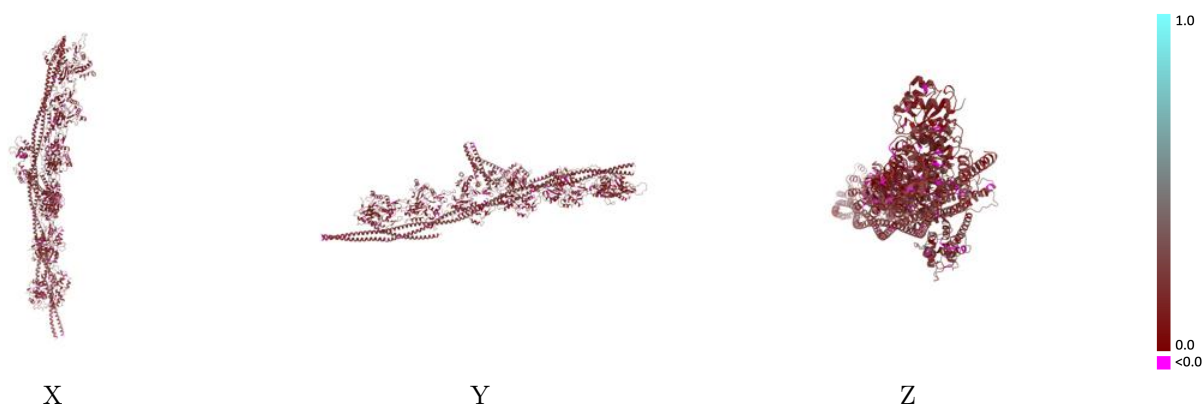
Y



Z

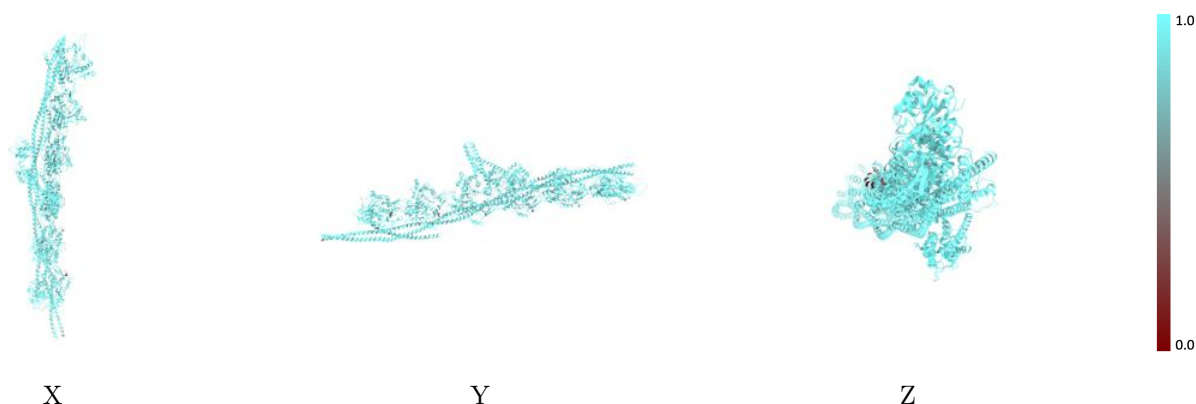
The images above show the 3D surface view of the map at the recommended contour level 0.515 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 9.2 Q-score mapped to coordinate model [i](#)



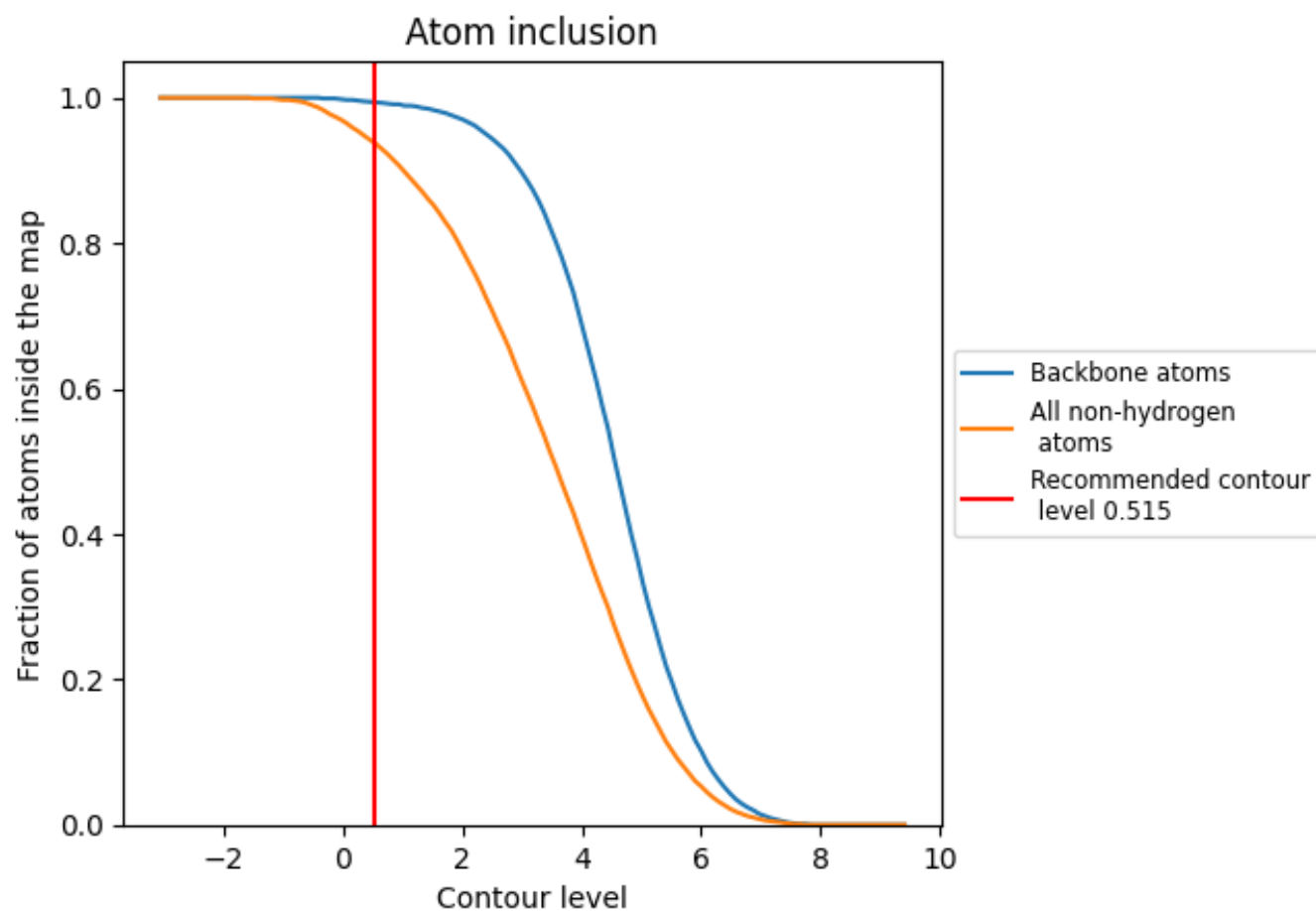
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)



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 (0.515).































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.515) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9380	 0.1790
A	 0.9470	 0.1690
B	 0.9290	 0.1700
C	 0.9180	 0.1670
D	 0.9190	 0.1650
E	 0.9310	 0.1690
F	 0.9440	 0.1720
G	 0.9910	 0.2300
H	 0.9500	 0.2060
I	 0.9780	 0.2100
J	 0.8940	 0.1610
K	 0.9580	 0.2010
L	 0.9510	 0.2010
M	 0.9330	 0.1860
N	 0.8940	 0.1740

