



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 08:04 PM UTC

PDB ID : 9B0X / pdb_00009b0x
EMDB ID : EMD-44061
Title : Artemia franciscana ATP synthase state 2 (composite structure), pH 7.0
Authors : Mnatsakanyan, N.; Mello, J.F.R.
Deposited on : 2024-03-12
Resolution : 2.60 Å(reported)
Based on initial model : .

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMD archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

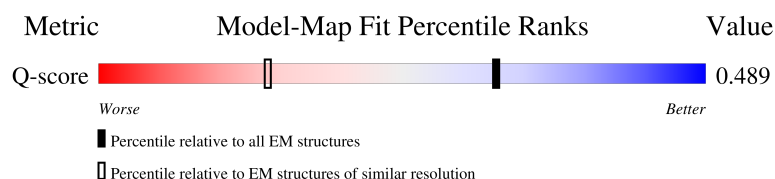
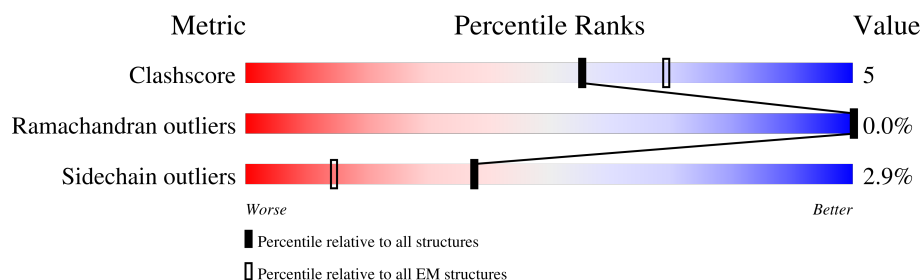
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.60 Å.

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



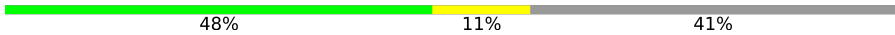
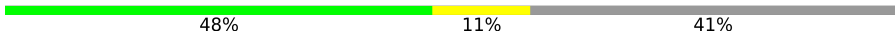
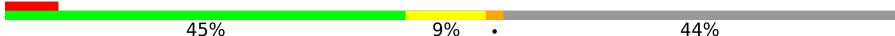
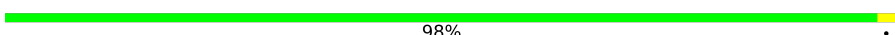
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	8728 (2.10 - 3.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	1	128	
1	2	128	
1	3	128	
1	4	128	

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Mol	Chain	Length	Quality of chain
1	5	128	
1	6	128	
1	7	128	
1	8	128	
2	A	551	
2	B	551	
2	C	551	
3	D	524	
3	E	524	
3	F	524	
4	G	290	
5	H	169	
6	I	66	
7	J	105	
8	K	265	
9	L	99	
10	M	219	
11	N	219	
12	O	207	
13	P	44	
14	Q	53	
15	R	119	
16	S	103	
17	T	84	

2 Entry composition [i](#)

There are 21 unique types of molecules in this entry. The entry contains 39830 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 ATP synthase subunit c.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	75	Total	C	N	O	S	0	0
			537	355	83	95	4		
1	2	75	Total	C	N	O	S	0	0
			537	355	83	95	4		
1	3	75	Total	C	N	O	S	0	0
			537	355	83	95	4		
1	4	75	Total	C	N	O	S	0	0
			537	355	83	95	4		
1	5	75	Total	C	N	O	S	0	0
			537	355	83	95	4		
1	6	75	Total	C	N	O	S	0	0
			537	355	83	95	4		
1	7	75	Total	C	N	O	S	0	0
			537	355	83	95	4		
1	8	75	Total	C	N	O	S	0	0
			537	355	83	95	4		

- Molecule 2 is a protein called ATP synthase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	504	Total	C	N	O	S	0	0
			3844	2419	677	734	14		
2	B	503	Total	C	N	O	S	0	0
			3842	2419	676	733	14		
2	C	501	Total	C	N	O	S	0	0
			3828	2411	674	729	14		

- Molecule 3 is a protein called ATP synthase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	465	Total	C	N	O	S	0	0
			3525	2239	597	678	11		
3	E	469	Total	C	N	O	S	0	0
			3554	2255	602	686	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	469	Total	C	N	O	S	0	0
			3554	2255	602	686	11		

- Molecule 4 is a protein called ATP synthase subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	261	Total	C	N	O	S	0	0
			2013	1258	352	389	14		

- Molecule 5 is a protein called ATP synthase subunit delta.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	134	Total	C	N	O	S	0	0
			984	620	161	201	2		

- Molecule 6 is a protein called ATP synthase subunit epsilon.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	37	Total	C	N	O	S	0	0
			304	185	65	52	2		

- Molecule 7 is a protein called ATP synthase inhibitory factor 1, IF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	42	Total	C	N	O	S	0	0
			292	174	58	60			

- Molecule 8 is a protein called ATP synthase subunit b.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	K	208	Total	C	N	O	S	0	0
			1686	1081	292	306	7		

- Molecule 9 is a protein called ATP synthase coupling factor 6, F6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L	75	Total	C	N	O	S	0	0
			594	380	95	117	2		

- Molecule 10 is a protein called ATP synthase subunit d.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	M	161	Total	C	N	O	S	0	0
			1309	836	222	246	5		

- Molecule 11 is a protein called ATP synthase subunit a.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	N	219	Total	C	N	O	S	0	0
			1716	1157	256	287	16		

- Molecule 12 is a protein called ATP synthase subunit OSCP.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	O	189	Total	C	N	O	S	0	0
			1451	928	252	266	5		

- Molecule 13 is a protein called ATP synthase subunit 6.8PL.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	P	44	Total	C	N	O	0	0
			220	132	44	44		

- Molecule 14 is a protein called ATP synthase protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Q	46	Total	C	N	O	S	0	0
			390	266	60	60	4		

- Molecule 15 is a protein called ATP synthase subunit f.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	R	104	Total	C	N	O	S	0	0
			851	555	158	136	2		

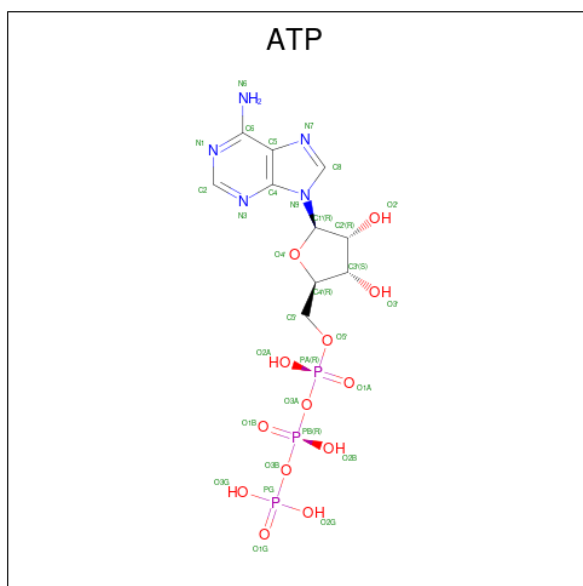
- Molecule 16 is a protein called ATP synthase subunit g.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	S	76	Total	C	N	O	S	0	0
			596	392	99	103	2		

- Molecule 17 is a protein called ATP synthase subunit e.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	T	82	Total	C	N	O	S	0	0
			658	418	122	117	1		

- Molecule 18 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
18	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
18	B	1	Total	C	N	O	P	0
			31	10	5	13	3	
18	C	1	Total	C	N	O	P	0
			31	10	5	13	3	
18	D	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 19 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

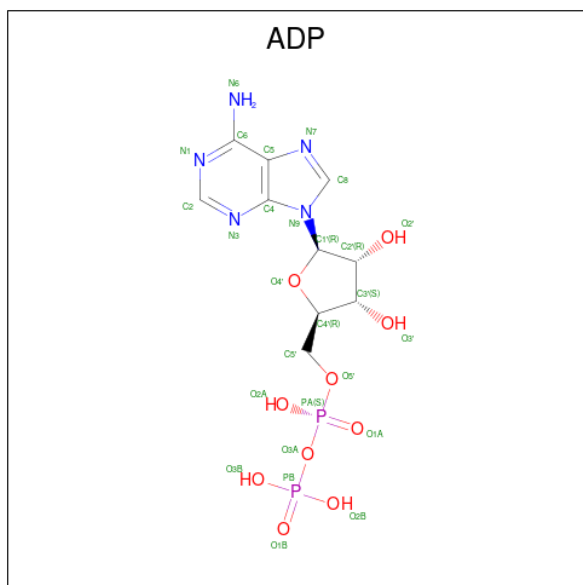
Mol	Chain	Residues	Atoms		AltConf
19	A	1	Total	Mg	0
			1	1	
19	B	1	Total	Mg	0
			1	1	
19	C	1	Total	Mg	0
			1	1	
19	D	1	Total	Mg	0
			1	1	

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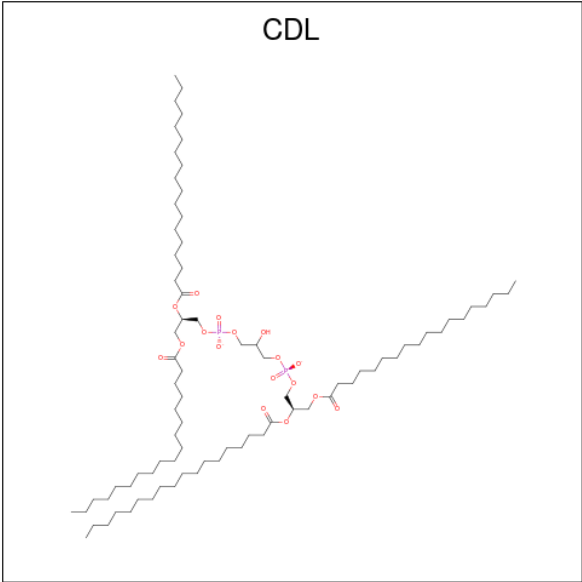
Mol	Chain	Residues	Atoms		AltConf
19	E	1	Total	Mg	0
			1	1	

- Molecule 20 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
20	E	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 21 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$) (labeled as "Ligand of Interest" by depositor).

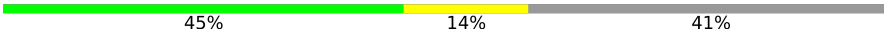


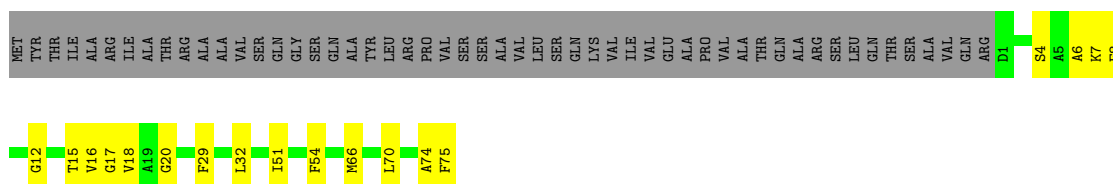
Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
21	K	1	90	71	17	2	0
21	K	1	77	58	17	2	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

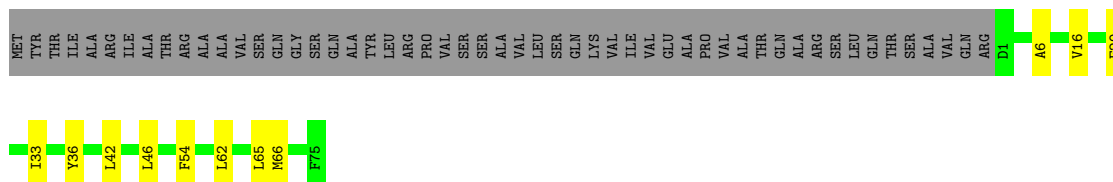
- Molecule 1: ATP synthase subunit c

Chain 1: 



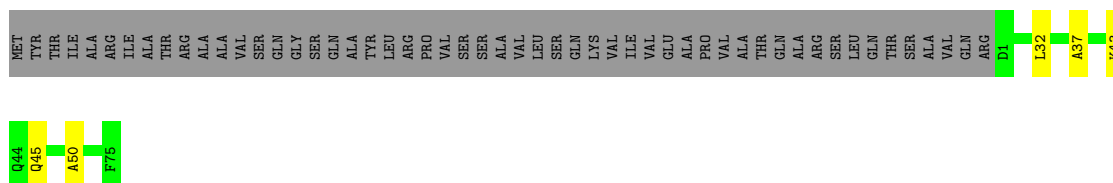
- Molecule 1: ATP synthase subunit c

Chain 2: 



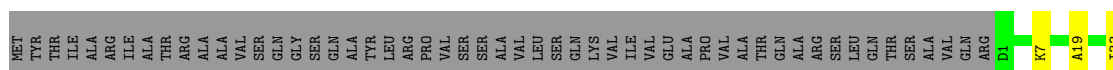
- Molecule 1: ATP synthase subunit c

Chain 3: 



- Molecule 1: ATP synthase subunit c

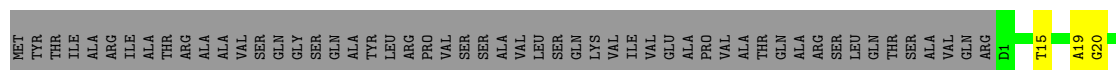
Chain 4: 





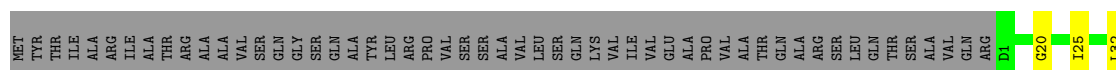
- Molecule 1: ATP synthase subunit c

Chain 5: 55% 41%



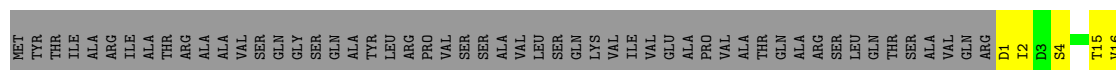
- Molecule 1: ATP synthase subunit c

Chain 6: 52% 41% 6%



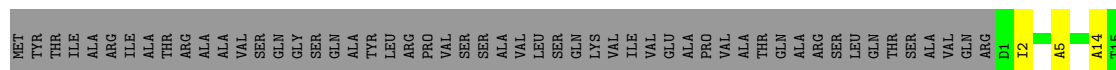
- Molecule 1: ATP synthase subunit c

Chain 7: 48% 41% 11%



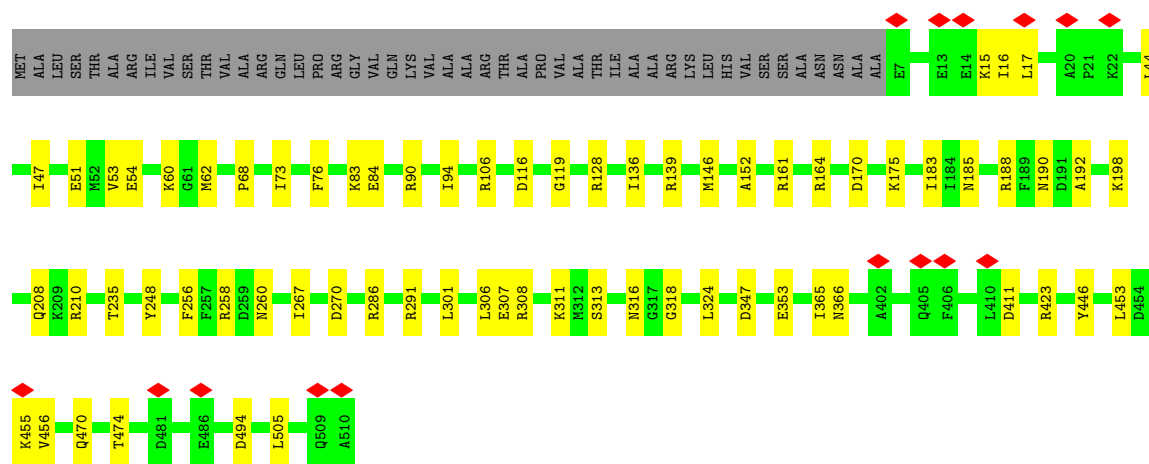
- Molecule 1: ATP synthase subunit c

Chain 8: 48% 41% 11%

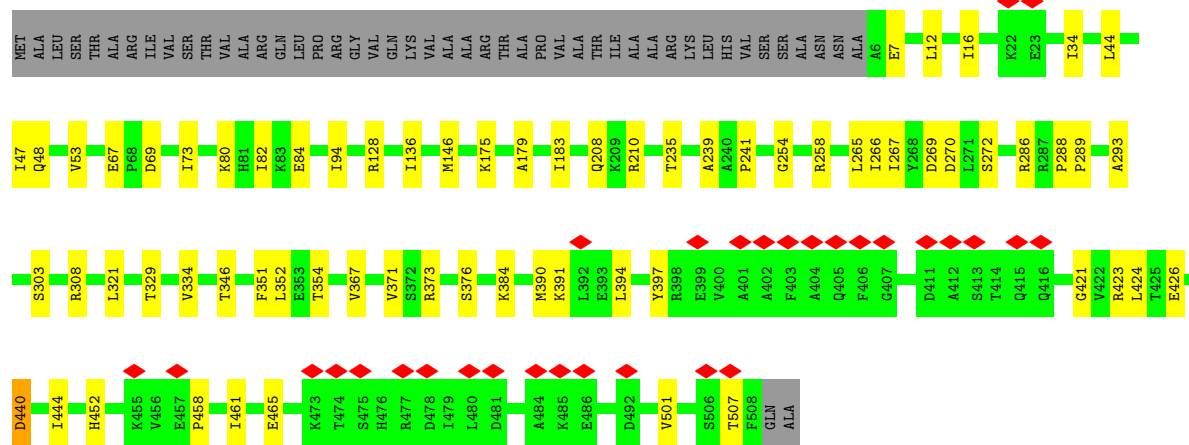
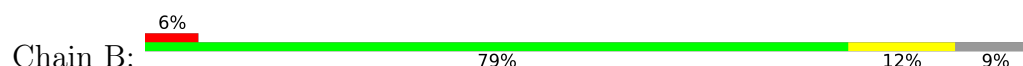


- Molecule 2: ATP synthase subunit alpha

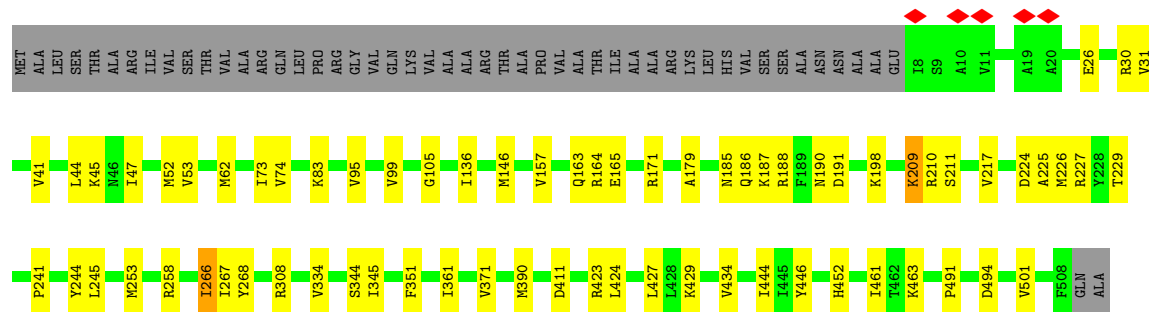
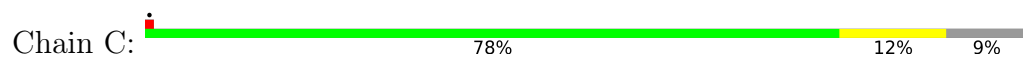
Chain A: 79% 13% 9%



• Molecule 2: ATP synthase subunit alpha



• Molecule 2: ATP synthase subunit alpha



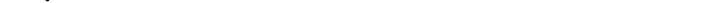
• Molecule 3: ATP synthase subunit beta



- Molecule 3: ATP synthase subunit beta

Chain E: 76% 13% 10%

- Molecule 3: ATP synthase subunit beta

Chain F:  77% 12% 10%

- Molecule 4: ATP synthase subunit gamma

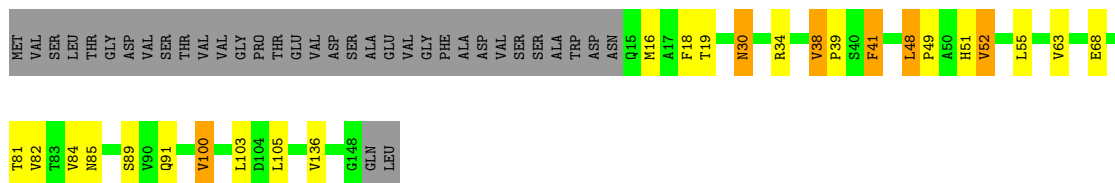
Chain G: 78% 12% 10%





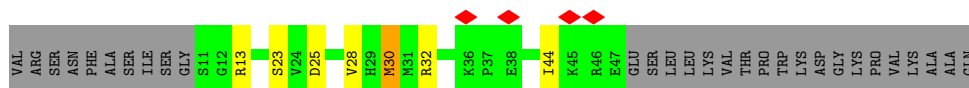
• Molecule 5: ATP synthase subunit delta

Chain H: 64% 11% 21%



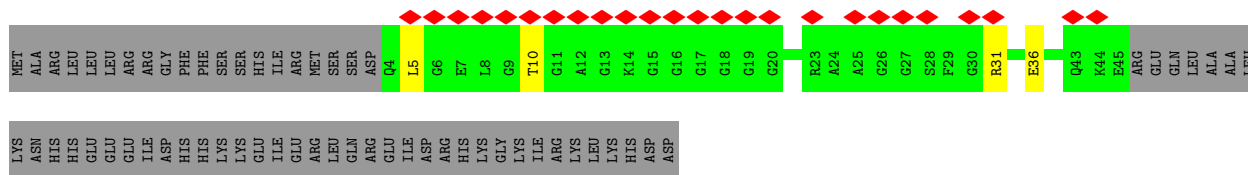
• Molecule 6: ATP synthase subunit epsilon

Chain I: 6% 45% 9% 44%



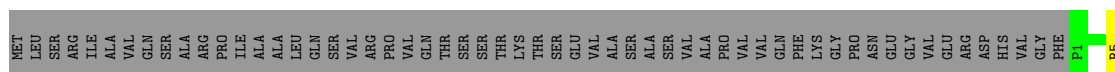
• Molecule 7: ATP synthase inhibitory factor 1, IF1

Chain J: 24% 36% 60%



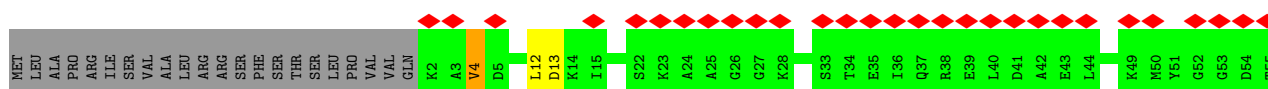
• Molecule 8: ATP synthase subunit b

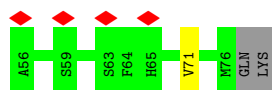
Chain K: 69% 9% 22%



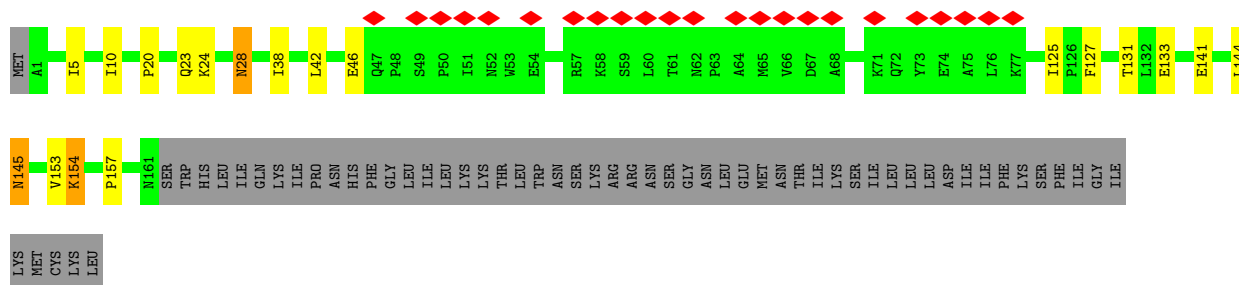
• Molecule 9: ATP synthase coupling factor 6, F6

Chain L: 33% 72% 24%

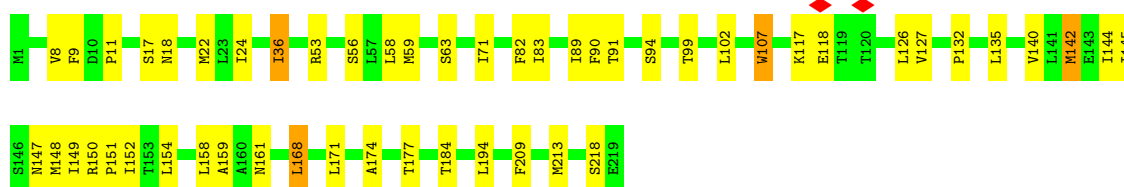
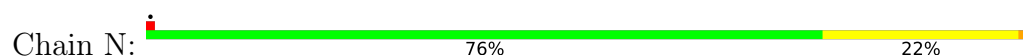




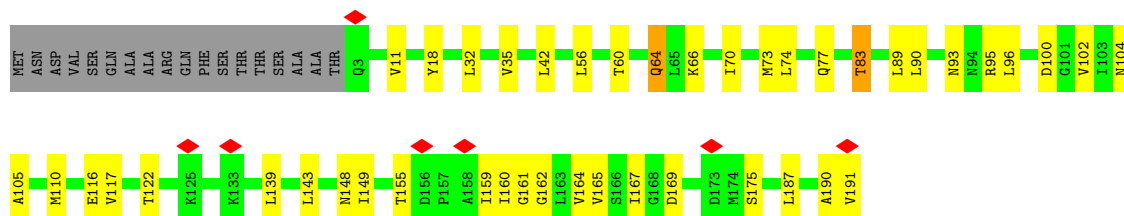
- Molecule 10: ATP synthase subunit d



- Molecule 11: ATP synthase subunit a



- Molecule 12: ATP synthase subunit OSCP



- Molecule 13: ATP synthase subunit 6.8PL

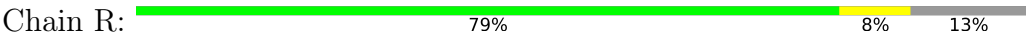


- Molecule 14: ATP synthase protein 8





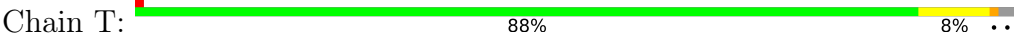
● Molecule 15: ATP synthase subunit f



● Molecule 16: ATP synthase subunit g



● Molecule 17: ATP synthase subunit e



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	232736	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 ($e^-/\text{\AA}^2$)	15.8	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	75.979	Depositor
Minimum map value	-49.967	Depositor
Average map value	-0.010	Depositor
Map value standard deviation	1.010	Depositor
Recommended contour level	4.51	Depositor
Map size (Å)	546.816, 546.816, 546.816	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.068, 1.068, 1.068	Depositor

5 Model quality

5.1 Standard geometry

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

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	1	0.13	0/547	0.29	0/734
1	2	0.13	0/547	0.28	0/734
1	3	0.14	0/547	0.30	0/734
1	4	0.14	0/547	0.31	0/734
1	5	0.16	0/547	0.30	0/734
1	6	0.15	0/547	0.32	0/734
1	7	0.14	0/547	0.30	0/734
1	8	0.14	0/547	0.29	0/734
2	A	0.15	0/3898	0.30	0/5260
2	B	0.14	0/3896	0.30	0/5257
2	C	0.16	0/3882	0.30	0/5238
3	D	0.15	0/3582	0.32	0/4862
3	E	0.15	0/3611	0.32	0/4901
3	F	0.16	0/3611	0.32	0/4901
4	G	0.13	0/2035	0.28	0/2735
5	H	0.15	0/998	0.30	0/1359
6	I	0.18	0/308	0.38	0/407
7	J	0.08	0/294	0.24	0/386
8	K	0.10	0/1720	0.23	0/2311
9	L	0.07	0/604	0.20	0/809
10	M	0.12	0/1343	0.33	0/1808
11	N	0.16	0/1761	0.32	0/2402
12	O	0.10	0/1466	0.27	0/1969
14	Q	0.14	0/405	0.22	0/549
15	R	0.17	0/882	0.37	0/1196
16	S	0.12	0/611	0.31	0/829
17	T	0.09	0/670	0.25	0/902
All	All	0.14	0/39953	0.30	0/53953

There are no bond length outliers.

There are no bond angle outliers.

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	1	537	0	549	15	0
1	2	537	0	549	9	0
1	3	537	0	549	4	0
1	4	537	0	549	6	0
1	5	537	0	549	6	0
1	6	537	0	549	7	0
1	7	537	0	549	12	0
1	8	537	0	549	16	0
2	A	3844	0	3938	46	0
2	B	3842	0	3945	45	0
2	C	3828	0	3934	42	0
3	D	3525	0	3593	41	0
3	E	3554	0	3617	41	0
3	F	3554	0	3618	40	0
4	G	2013	0	2062	19	0
5	H	984	0	974	12	0
6	I	304	0	305	5	0
7	J	292	0	270	5	0
8	K	1686	0	1709	17	0
9	L	594	0	599	2	0
10	M	1309	0	1304	12	0
11	N	1716	0	1811	24	0
12	O	1451	0	1566	25	0
13	P	220	0	46	1	0
14	Q	390	0	393	4	0
15	R	851	0	840	7	0
16	S	596	0	617	10	0
17	T	658	0	672	6	0
18	A	31	0	12	0	0
18	B	31	0	12	0	0
18	C	31	0	12	0	0
18	D	31	0	12	0	0
19	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	B	1	0	0	0	0
19	C	1	0	0	0	0
19	D	1	0	0	0	0
19	E	1	0	0	0	0
20	E	27	0	12	1	0
21	K	167	0	231	5	0
All	All	39830	0	40496	400	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 5.

All (400) 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)
1:5:33:ILE:HG21	1:6:32:LEU:HA	1.71	0.72
1:1:16:VAL:HG13	1:2:16:VAL:HG11	1.76	0.66
8:K:6:PRO:HG2	15:R:70:PRO:HG3	1.77	0.66
1:7:16:VAL:HG13	1:8:16:VAL:HG11	1.77	0.66
3:F:44:ARG:HH12	3:F:71:GLY:H	1.45	0.65
2:C:53:VAL:HG21	2:C:73:ILE:HD13	1.80	0.64
5:H:100:VAL:HA	5:H:103:LEU:HD12	1.81	0.63
11:N:99:THR:HG21	11:N:159:ALA:HB2	1.82	0.61
3:F:299:ILE:HG21	3:F:309:SER:HB2	1.83	0.61
3:D:191:GLU:OE2	3:D:260:ASN:ND2	2.33	0.61
1:7:28:VAL:HG21	1:7:53:GLY:HA3	1.81	0.61
11:N:168:LEU:HB3	11:N:194:LEU:HD21	1.82	0.60
10:M:133:GLU:OE2	13:P:1:UNK:N	2.34	0.60
3:D:141:LYS:HD2	3:D:435:VAL:HG21	1.82	0.60
2:A:185:ASN:OD1	2:A:188:ARG:NH1	2.35	0.60
4:G:104:VAL:HA	4:G:124:CYS:HB2	1.84	0.60
10:M:28:ASN:N	10:M:28:ASN:OD1	2.34	0.59
15:R:34:LYS:HA	16:S:68:SER:HA	1.84	0.59
1:1:32:LEU:HA	1:8:33:ILE:HG21	1.83	0.59
3:E:240:LEU:HD13	3:E:299:ILE:HG12	1.83	0.59
2:A:286:ARG:NH2	3:F:276:GLY:O	2.36	0.59
2:C:52:MET:HG3	2:C:95:VAL:HG22	1.84	0.59
4:G:132:PRO:O	4:G:214:LYS:NZ	2.35	0.59
3:E:141:LYS:HD2	3:E:435:VAL:HG21	1.84	0.59
2:B:334:VAL:HG11	2:B:351:PHE:HE2	1.67	0.59
12:O:122:THR:HB	12:O:164:VAL:HB	1.84	0.58
3:F:97:ILE:HG12	3:F:220:LEU:HD12	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:H:89:SER:HB2	5:H:91:GLN:HE22	1.68	0.58
3:E:140:ILE:HA	3:E:419:GLN:HE22	1.69	0.58
2:A:258:ARG:NH1	2:A:308:ARG:O	2.37	0.58
1:6:33:ILE:HG21	1:7:32:LEU:HA	1.86	0.58
2:A:53:VAL:HG21	2:A:73:ILE:HD13	1.86	0.58
3:D:347:ILE:HG23	3:D:418:SER:HB3	1.86	0.58
2:C:185:ASN:OD1	2:C:188:ARG:NH1	2.37	0.57
3:F:51:GLU:OE2	3:F:120:HIS:NE2	2.34	0.57
2:A:267:ILE:HG13	2:A:324:LEU:HB2	1.87	0.57
4:G:183:ALA:HB3	4:G:186:ILE:HB	1.86	0.57
5:H:38:VAL:HG21	5:H:82:VAL:HG21	1.86	0.57
2:C:83:LYS:HE3	3:E:34:PRO:HG3	1.84	0.57
2:C:95:VAL:HG11	2:C:245:LEU:HD21	1.86	0.57
3:E:258:ILE:HG21	3:E:261:ILE:HD13	1.85	0.57
3:F:278:ILE:HG23	4:G:262:ILE:HD13	1.87	0.57
2:A:68:PRO:HG3	3:D:17:THR:HG22	1.87	0.57
2:B:175:LYS:HG3	2:B:352:LEU:HD12	1.85	0.57
6:I:13:ARG:NH1	6:I:23:SER:OG	2.37	0.56
16:S:35:VAL:HG12	16:S:36:GLU:HG3	1.87	0.56
2:B:288:PRO:HG2	3:E:273:ALA:HB1	1.86	0.56
1:1:8:PHE:HB2	1:2:6:ALA:HB1	1.86	0.56
2:B:373:ARG:HG2	20:E:601:ADP:H5'1	1.87	0.56
2:C:163:GLN:NE2	2:C:165:GLU:OE1	2.39	0.56
3:E:209:ILE:HD11	3:E:220:LEU:HD11	1.87	0.56
2:B:303:SER:HB2	3:E:225:MET:HB3	1.86	0.56
2:C:171:ARG:NH2	3:E:355:ASP:OD1	2.38	0.56
8:K:5:ARG:NH1	11:N:36:ILE:O	2.33	0.56
1:2:36:TYR:OH	1:3:45:GLN:OE1	2.23	0.56
10:M:20:PRO:HB2	10:M:23:GLN:HB3	1.88	0.56
11:N:142:MET:SD	11:N:142:MET:N	2.79	0.56
3:F:301:THR:HG23	3:F:306:SER:HB3	1.88	0.55
3:E:161:ALA:O	3:E:340:ARG:NH2	2.39	0.55
2:B:84:GLU:H	3:D:55:HIS:HD2	1.53	0.55
3:F:12:SER:HB2	3:F:31:GLN:HE21	1.70	0.55
2:B:53:VAL:HG21	2:B:73:ILE:HD13	1.90	0.54
10:M:145:ASN:OD1	10:M:145:ASN:N	2.38	0.54
3:F:465:PRO:HD2	3:F:468:GLU:HG3	1.89	0.54
2:A:17:LEU:HD21	9:L:12:LEU:HD11	1.89	0.54
2:A:44:LEU:O	3:D:74:ARG:NH2	2.40	0.54
3:D:199:LEU:HD11	3:D:203:MET:HE2	1.88	0.54
1:4:33:ILE:HG21	1:5:32:LEU:HA	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:396:MET:H	7:J:36:GLU:HG2	1.73	0.54
8:K:170:GLN:NE2	12:O:191:VAL:O	2.40	0.54
1:1:12:GLY:O	1:1:15:THR:OG1	2.25	0.54
1:7:15:THR:HB	1:8:14:ALA:HA	1.90	0.54
4:G:127:PHE:HA	4:G:130:ARG:HE	1.73	0.54
8:K:71:VAL:HG22	21:K:301:CDL:H521	1.90	0.54
4:G:68:ILE:HB	4:G:101:VAL:HG22	1.90	0.54
1:6:25:ILE:HD11	1:6:58:GLU:HB2	1.90	0.54
2:C:26:GLU:HA	2:C:45:LYS:HB3	1.89	0.54
3:F:347:ILE:HG23	3:F:418:SER:HB3	1.90	0.54
8:K:21:TRP:HE1	21:K:302:CDL:HA62	1.73	0.53
2:A:139:ARG:NH2	2:A:307:GLU:O	2.41	0.53
3:D:258:ILE:HG21	3:D:261:ILE:HD13	1.90	0.53
1:1:4:SER:HA	1:1:7:LYS:HD2	1.90	0.53
2:C:423:ARG:HD2	2:C:461:ILE:HD11	1.91	0.53
8:K:93:PHE:HB3	10:M:127:PHE:HD2	1.73	0.53
16:S:91:CYS:HA	16:S:94:LYS:HE2	1.90	0.53
3:F:334:ALA:HA	3:F:358:SER:HA	1.90	0.53
12:O:100:ASP:OD1	12:O:104:ASN:ND2	2.42	0.53
1:2:42:LEU:HB3	1:2:46:LEU:HD13	1.90	0.53
11:N:89:ILE:HG12	15:R:89:PHE:HD2	1.73	0.53
3:F:240:LEU:HD21	3:F:298:ARG:HB2	1.91	0.52
2:C:62:MET:HE2	2:C:95:VAL:HG21	1.91	0.52
5:H:51:HIS:HB3	5:H:84:VAL:HG11	1.89	0.52
2:B:48:GLN:HB3	3:E:71:GLY:HA2	1.91	0.52
12:O:18:TYR:OH	12:O:93:ASN:ND2	2.41	0.52
2:A:106:ARG:NH2	2:A:119:GLY:O	2.41	0.52
2:B:69:ASP:OD1	2:B:69:ASP:N	2.39	0.52
3:E:199:LEU:HD11	3:E:203:MET:HE2	1.91	0.52
11:N:149:ILE:HG23	11:N:152:ILE:HD12	1.91	0.52
2:A:94:ILE:HB	2:A:128:ARG:HD3	1.91	0.52
8:K:110:LEU:HD13	14:Q:46:THR:HG22	1.92	0.52
3:F:319:ASP:OD2	4:G:251:GLN:NE2	2.41	0.52
4:G:100:MET:HB3	4:G:121:ALA:HB2	1.92	0.52
3:D:255:LEU:HD23	3:D:308:THR:HB	1.92	0.52
2:B:44:LEU:HD13	2:B:47:ILE:HD12	1.91	0.52
2:C:187:LYS:NZ	2:C:191:ASP:OD2	2.42	0.52
2:A:164:ARG:NH2	2:A:347:ASP:OD1	2.43	0.51
2:B:423:ARG:HG3	2:B:461:ILE:HD11	1.90	0.51
3:E:87:ILE:HG21	3:E:238:THR:HG23	1.91	0.51
4:G:164:VAL:O	4:G:222:SER:OG	2.29	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:K:162:GLU:OE2	8:K:166:ARG:NH2	2.40	0.51
2:C:411:ASP:OD1	2:C:411:ASP:N	2.42	0.51
3:F:247:ARG:HD3	3:F:307:ILE:HG13	1.92	0.51
3:E:347:ILE:HG23	3:E:418:SER:HB3	1.92	0.51
2:A:44:LEU:HD13	2:A:47:ILE:HD12	1.93	0.51
1:8:42:LEU:HB3	1:8:46:LEU:HD13	1.93	0.51
1:7:2:ILE:HD12	17:T:76:THR:HA	1.92	0.51
2:A:170:ASP:O	2:A:175:LYS:NZ	2.42	0.51
2:B:179:ALA:HB1	2:B:267:ILE:HG12	1.92	0.51
2:B:394:LEU:HD22	7:J:5:LEU:HD11	1.93	0.51
3:D:419:GLN:NE2	3:D:433:LYS:O	2.41	0.51
1:1:6:ALA:HB3	1:8:5:ALA:HB1	1.93	0.51
1:1:70:LEU:HA	1:1:74:ALA:HB3	1.93	0.51
3:E:12:SER:OG	3:E:13:ASN:N	2.44	0.51
2:A:423:ARG:NH1	2:A:456:VAL:O	2.45	0.50
3:D:154:LYS:HZ3	3:D:299:ILE:HB	1.75	0.50
1:2:29:PHE:HE1	1:2:54:PHE:HB2	1.76	0.50
2:A:84:GLU:H	3:F:55:HIS:HD2	1.59	0.50
2:A:423:ARG:NH1	2:A:453:LEU:O	2.39	0.50
3:D:411:ARG:HH21	3:D:415:ARG:HH22	1.59	0.50
10:M:154:LYS:H	10:M:157:PRO:HG3	1.75	0.50
2:B:367:VAL:HB	7:J:5:LEU:HA	1.93	0.50
2:B:390:MET:HE3	2:B:424:LEU:HD22	1.94	0.50
2:C:258:ARG:NH1	2:C:308:ARG:O	2.44	0.50
3:F:140:ILE:HA	3:F:419:GLN:HE22	1.77	0.50
6:I:30:MET:SD	6:I:30:MET:N	2.84	0.50
2:B:376:SER:HB2	2:B:384:LYS:HG3	1.94	0.50
11:N:154:LEU:HB3	11:N:209:PHE:HE1	1.77	0.50
2:A:136:ILE:O	3:D:197:ASN:ND2	2.45	0.50
12:O:35:VAL:HG23	12:O:83:THR:HG22	1.93	0.50
16:S:58:SER:HB3	16:S:63:LYS:HB2	1.94	0.50
2:C:446:TYR:OH	2:C:494:ASP:OD1	2.29	0.50
3:D:47:ARG:NH2	3:D:103:GLU:OE2	2.45	0.49
3:E:170:MET:HB3	3:E:423:VAL:HG21	1.94	0.49
3:F:145:LEU:HD11	3:F:373:ILE:HG22	1.94	0.49
5:H:39:PRO:HD2	5:H:63:VAL:HG22	1.93	0.49
2:B:346:THR:O	3:E:192:ARG:NH2	2.45	0.49
3:E:129:MET:O	3:E:303:LYS:NZ	2.42	0.49
2:A:313:SER:OG	2:A:316:ASN:ND2	2.45	0.49
3:D:161:ALA:O	3:D:340:ARG:NH2	2.45	0.49
1:8:38:ARG:HA	5:H:52:VAL:HB	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:H:18:PHE:O	5:H:30:ASN:N	2.42	0.49
1:4:7:LYS:HZ1	1:4:75:PHE:HB2	1.78	0.49
2:A:446:TYR:OH	2:A:494:ASP:OD1	2.30	0.49
3:F:154:LYS:HG3	3:F:309:SER:HB3	1.93	0.49
17:T:9:VAL:HB	17:T:14:ARG:HE	1.77	0.49
1:1:20:GLY:H	1:8:19:ALA:HB1	1.77	0.49
2:B:258:ARG:NH2	2:B:308:ARG:O	2.35	0.49
8:K:26:TYR:OH	17:T:5:PRO:O	2.25	0.49
1:3:43:LYS:NZ	1:4:45:GLN:OE1	2.45	0.49
3:D:156:GLY:HA3	3:D:332:LEU:HD13	1.94	0.48
3:D:160:GLY:O	3:D:165:LYS:NZ	2.46	0.48
17:T:9:VAL:H	17:T:14:ARG:HH21	1.60	0.48
3:E:52:VAL:HA	3:E:63:THR:HG22	1.94	0.48
2:A:256:PHE:O	2:A:260:ASN:ND2	2.37	0.48
2:C:105:GLY:HA2	2:C:226:MET:HG3	1.95	0.48
2:C:179:ALA:HB1	2:C:267:ILE:HG12	1.94	0.48
2:C:361:ILE:HD13	2:C:429:LYS:HE2	1.95	0.48
3:D:147:ALA:HA	3:D:358:SER:HB3	1.94	0.48
5:H:85:ASN:ND2	5:H:91:GLN:OE1	2.46	0.48
1:8:66:MET:HE2	11:N:145:ILE:HG21	1.93	0.48
3:F:258:ILE:HB	3:F:311:GLN:HG2	1.95	0.48
10:M:38:ILE:O	10:M:42:LEU:N	2.47	0.48
11:N:102:LEU:HD13	11:N:158:LEU:HD13	1.94	0.48
15:R:46:ASN:ND2	15:R:48:ASN:OD1	2.42	0.48
2:C:74:VAL:HB	2:C:241:PRO:HG3	1.96	0.48
3:E:156:GLY:HA3	3:E:332:LEU:HD13	1.95	0.48
2:C:217:VAL:HG13	2:C:226:MET:HE3	1.95	0.48
3:E:16:ILE:HA	3:E:26:VAL:HG12	1.96	0.48
5:H:34:ARG:HG3	5:H:68:GLU:HA	1.95	0.48
2:C:44:LEU:HD13	2:C:47:ILE:HD12	1.96	0.48
12:O:162:GLY:HA3	12:O:175:SER:HA	1.96	0.48
2:B:94:ILE:HD11	2:B:128:ARG:HD2	1.96	0.48
2:C:266:ILE:HG12	2:C:268:TYR:CZ	2.49	0.48
3:D:301:THR:HG22	3:D:307:ILE:H	1.78	0.48
11:N:147:ASN:OD1	11:N:150:ARG:NH2	2.47	0.48
2:C:224:ASP:OD1	2:C:227:ARG:NH1	2.45	0.47
11:N:58:LEU:O	11:N:218:SER:OG	2.27	0.47
2:B:67:GLU:O	3:E:74:ARG:NH1	2.40	0.47
2:B:210:ARG:HG2	2:B:235:THR:HG21	1.94	0.47
3:E:240:LEU:HD21	3:E:298:ARG:HB2	1.95	0.47
2:C:136:ILE:O	3:F:197:ASN:ND2	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:80:LYS:HA	3:D:35:ILE:HB	1.96	0.47
2:B:286:ARG:NH2	3:D:276:GLY:O	2.47	0.47
11:N:127:VAL:HG22	11:N:140:VAL:HG22	1.96	0.47
1:5:33:ILE:HG22	1:6:35:GLY:HA3	1.96	0.47
2:B:136:ILE:O	3:E:197:ASN:ND2	2.46	0.47
2:C:209:LYS:HD3	2:C:211:SER:H	1.78	0.47
8:K:141:ARG:NH1	10:M:46:GLU:OE2	2.48	0.47
15:R:105:TYR:O	15:R:106:HIS:ND1	2.47	0.47
3:E:140:ILE:HB	3:E:143:VAL:HB	1.97	0.47
3:E:237:LEU:O	3:E:241:THR:OG1	2.28	0.47
8:K:13:ARG:NH2	8:K:19:GLU:OE2	2.48	0.47
1:3:37:ALA:HB2	1:4:46:LEU:HD21	1.97	0.47
2:A:15:LYS:NZ	12:O:190:ALA:O	2.48	0.47
2:A:291:ARG:NH1	3:D:322:ASP:OD2	2.38	0.47
2:C:186:GLN:O	2:C:190:ASN:ND2	2.37	0.47
3:E:391:ILE:HG12	3:E:399:LEU:HD11	1.96	0.47
11:N:117:LYS:HG2	11:N:118:GLU:HG3	1.97	0.47
3:F:168:LEU:HD22	3:F:338:LEU:HD21	1.96	0.46
2:A:353:GLU:OE2	2:A:366:ASN:ND2	2.47	0.46
21:K:302:CDL:H711	21:K:302:CDL:HB61	1.70	0.46
2:C:390:MET:HE3	2:C:424:LEU:HD22	1.97	0.46
3:D:172:LEU:HD13	3:D:310:VAL:HG11	1.96	0.46
3:D:324:ALA:O	3:D:328:THR:OG1	2.32	0.46
8:K:24:PHE:HE1	16:S:70:ARG:HE	1.63	0.46
11:N:11:PRO:O	11:N:17:SER:OG	2.30	0.46
3:D:201:HIS:HA	3:D:204:ILE:HG12	1.98	0.46
3:F:187:ALA:HA	3:F:221:VAL:HG22	1.96	0.46
4:G:145:LEU:HD11	4:G:202:GLU:HB2	1.97	0.46
1:6:38:ARG:HG2	1:7:38:ARG:HH11	1.80	0.46
2:A:62:MET:HE3	2:A:76:PHE:HZ	1.81	0.46
5:H:16:MET:HB2	5:H:49:PRO:HG3	1.97	0.46
11:N:53:ARG:O	11:N:56:SER:OG	2.32	0.46
2:A:311:LYS:NZ	2:A:318:GLY:O	2.48	0.46
3:E:193:THR:HA	3:E:224:GLN:HE21	1.80	0.46
11:N:177:THR:O	11:N:184:THR:OG1	2.32	0.46
2:B:426:GLU:HG3	2:B:458:PRO:HB3	1.97	0.46
3:F:141:LYS:H	3:F:419:GLN:HE22	1.62	0.46
4:G:198:GLN:NE2	4:G:202:GLU:OE2	2.48	0.46
11:N:59:MET:O	11:N:63:SER:OG	2.34	0.46
1:5:15:THR:HG21	1:6:67:MET:HG2	1.97	0.45
2:A:16:ILE:HD11	12:O:187:LEU:HD21	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:255:LEU:HD23	3:E:308:THR:HB	1.98	0.45
11:N:11:PRO:HA	11:N:18:ASN:HB2	1.98	0.45
1:7:30:GLY:O	1:8:31:SER:OG	2.25	0.45
2:C:187:LYS:HE2	2:C:224:ASP:HB3	1.98	0.45
3:E:51:GLU:OE2	3:E:120:HIS:NE2	2.46	0.45
3:F:18:ALA:HB3	3:F:25:ASP:HB2	1.98	0.45
5:H:48:LEU:H	5:H:51:HIS:CD2	2.34	0.45
11:N:107:TRP:CG	11:N:151:PRO:HG3	2.51	0.45
2:A:208:GLN:O	2:A:235:THR:OG1	2.30	0.45
2:C:31:VAL:HA	2:C:41:VAL:HG12	1.99	0.45
12:O:66:LYS:HD3	12:O:96:LEU:HD11	1.96	0.45
3:E:87:ILE:HD11	3:E:241:THR:HB	1.97	0.45
3:D:39:LEU:HB2	3:D:50:LEU:HB2	1.99	0.45
17:T:31:ARG:HG2	17:T:35:LEU:HD23	1.99	0.45
2:A:83:LYS:HD3	3:F:34:PRO:HG3	1.97	0.45
4:G:14:LYS:HA	4:G:239:ILE:HD11	1.98	0.45
2:B:7:GLU:OE2	12:O:95:ARG:NH2	2.50	0.45
2:B:270:ASP:OD2	2:B:272:SER:OG	2.34	0.45
2:C:210:ARG:NH1	3:E:124:PRO:O	2.48	0.45
1:1:16:VAL:HG22	1:2:16:VAL:HG21	1.99	0.45
2:A:192:ALA:O	2:A:198:LYS:NZ	2.43	0.45
12:O:56:LEU:HD11	12:O:73:MET:HE1	1.98	0.45
2:B:12:LEU:HD22	12:O:89:LEU:HD21	1.98	0.45
2:B:254:GLY:HA3	2:B:266:ILE:HD11	1.98	0.45
4:G:109:ARG:HB2	4:G:123:VAL:HG11	1.98	0.45
16:S:85:TRP:CD1	17:T:17:ARG:HG3	2.52	0.45
8:K:55:HIS:HB3	11:N:174:ALA:N	2.32	0.44
3:F:31:GLN:HE21	3:F:31:GLN:HB2	1.62	0.44
12:O:90:LEU:HD21	12:O:102:VAL:HG21	1.99	0.44
2:B:440:ASP:N	2:B:440:ASP:OD1	2.50	0.44
3:D:52:VAL:HA	3:D:63:THR:HG22	2.00	0.44
3:E:144:ASP:HB3	3:E:437:ILE:HD13	1.99	0.44
3:F:44:ARG:NH2	3:F:68:GLY:O	2.50	0.44
12:O:74:LEU:HD12	12:O:77:GLN:HG3	1.99	0.44
2:C:427:LEU:HD11	2:C:444:ILE:HG13	1.99	0.44
3:F:387:LEU:HD23	3:F:390:ILE:HD12	1.98	0.44
12:O:159:ILE:O	12:O:161:GLY:N	2.50	0.44
16:S:57:HIS:O	16:S:61:THR:OG1	2.34	0.44
1:4:19:ALA:HA	1:5:20:GLY:HA3	1.99	0.44
3:F:259:ASP:HA	3:F:260:ASN:HA	1.67	0.44
1:2:66:MET:HE2	11:N:168:LEU:HD21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:190:ASN:HA	2:C:198:LYS:HG2	2.00	0.44
2:B:270:ASP:OD1	2:B:270:ASP:N	2.51	0.44
1:2:33:ILE:HD13	1:2:33:ILE:HA	1.86	0.43
2:B:34:ILE:HG12	2:B:82:ILE:HB	2.00	0.43
11:N:132:PRO:HD2	11:N:135:LEU:HD12	2.00	0.43
12:O:100:ASP:O	12:O:104:ASN:ND2	2.38	0.43
2:B:183:ILE:HD11	2:B:267:ILE:HD13	2.00	0.43
3:D:397:ASP:OD1	3:D:397:ASP:N	2.50	0.43
3:E:259:ASP:HA	3:E:260:ASN:HA	1.66	0.43
10:M:24:LYS:HA	10:M:24:LYS:HD3	1.80	0.43
12:O:116:GLU:HG2	12:O:148:ASN:HB2	2.00	0.43
3:D:56:LEU:HD11	3:D:62:ARG:HB2	2.00	0.43
2:B:208:GLN:NE2	2:B:269:ASP:O	2.45	0.43
3:D:28:PHE:HB2	3:D:32:LEU:HD23	1.99	0.43
8:K:196:LYS:NZ	9:L:4:VAL:O	2.51	0.43
1:1:29:PHE:HE1	1:1:54:PHE:HB2	1.83	0.43
2:A:164:ARG:HD2	2:A:306:LEU:HB3	2.00	0.43
2:A:270:ASP:OD1	2:A:270:ASP:N	2.51	0.43
2:C:491:PRO:HA	2:C:494:ASP:HB3	2.00	0.43
3:E:142:VAL:HG23	3:E:146:LEU:HD12	2.00	0.43
12:O:32:LEU:HD22	12:O:110:MET:HE1	2.00	0.43
1:7:19:ALA:HB2	1:8:17:GLY:HA2	2.00	0.43
1:7:36:TYR:HE2	1:8:45:GLN:HG3	1.84	0.43
3:E:322:ASP:HB3	3:E:325:PRO:HD2	2.00	0.43
1:3:32:LEU:HD13	1:3:50:ALA:HB2	2.01	0.43
2:B:266:ILE:HD11	2:B:321:LEU:HD11	2.01	0.43
12:O:143:LEU:HD11	12:O:149:ILE:HG13	2.00	0.43
2:A:44:LEU:HD22	2:A:90:ARG:HG3	2.01	0.43
2:A:190:ASN:HA	2:A:198:LYS:HG2	2.00	0.43
2:C:334:VAL:HG11	2:C:351:PHE:HE2	1.84	0.43
3:D:280:SER:OG	3:D:281:ALA:N	2.52	0.43
12:O:42:LEU:HD11	12:O:73:MET:HE3	2.01	0.43
16:S:58:SER:O	16:S:62:GLY:N	2.45	0.43
1:1:17:GLY:HA2	1:8:19:ALA:HB2	2.01	0.42
1:1:51:ILE:HD13	1:1:51:ILE:HA	1.83	0.42
12:O:64:GLN:HE21	12:O:64:GLN:HB3	1.64	0.42
2:B:391:LYS:HE3	2:B:391:LYS:HB2	1.85	0.42
4:G:78:CYS:HB3	4:G:224:ARG:HE	1.83	0.42
1:1:66:MET:HE2	1:1:66:MET:HB3	1.95	0.42
3:E:99:ASN:OD1	3:E:103:GLU:N	2.51	0.42
3:E:324:ALA:O	3:E:328:THR:OG1	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:32:LEU:HD11	3:F:59:ASN:HA	2.02	0.42
1:1:70:LEU:O	1:1:75:PHE:N	2.52	0.42
2:A:51:GLU:HA	2:A:94:ILE:HA	2.00	0.42
2:A:84:GLU:H	3:F:55:HIS:CD2	2.36	0.42
3:D:253:ASP:OD1	3:D:253:ASP:N	2.40	0.42
2:B:452:HIS:HB3	2:B:501:VAL:HG11	2.01	0.42
2:C:99:VAL:HG12	2:C:253:MET:HA	2.02	0.42
3:E:165:LYS:HE3	3:E:165:LYS:HB2	1.77	0.42
8:K:16:PHE:HE2	21:K:301:CDL:H161	1.84	0.42
1:1:16:VAL:HB	1:8:16:VAL:HG22	2.02	0.42
3:F:204:ILE:HD13	3:F:211:LEU:HD11	2.01	0.42
2:B:394:LEU:HD13	7:J:5:LEU:HD21	2.02	0.42
3:D:157:LEU:HB2	3:D:312:ALA:HA	2.00	0.42
2:C:30:ARG:HG3	12:O:60:THR:HG21	2.01	0.42
3:D:170:MET:HB3	3:D:423:VAL:HG21	2.02	0.42
10:M:144:LEU:HD12	10:M:144:LEU:HA	1.96	0.42
11:N:91:THR:O	11:N:94:SER:OG	2.29	0.42
1:2:62:LEU:HA	1:2:65:LEU:HB2	2.01	0.42
1:8:51:ILE:HD13	1:8:51:ILE:HA	1.92	0.42
2:C:52:MET:HE3	2:C:95:VAL:HG13	2.00	0.42
2:C:452:HIS:HB3	2:C:501:VAL:HG11	2.02	0.42
3:D:51:GLU:OE2	3:D:120:HIS:NE2	2.39	0.42
1:4:56:LEU:HD23	1:4:56:LEU:HA	1.91	0.42
3:F:322:ASP:HB3	3:F:325:PRO:HD2	2.02	0.42
2:A:106:ARG:NH1	2:A:116:ASP:OD1	2.53	0.41
2:A:183:ILE:HD11	2:A:267:ILE:HD13	2.02	0.41
3:E:170:MET:SD	3:E:199:LEU:HD13	2.60	0.41
3:F:141:LYS:H	3:F:419:GLN:NE2	2.18	0.41
12:O:70:ILE:HA	12:O:73:MET:HE2	2.01	0.41
12:O:139:LEU:HB3	12:O:149:ILE:HD13	2.01	0.41
1:7:1:ASP:O	1:7:4:SER:OG	2.28	0.41
1:7:38:ARG:HE	1:8:38:ARG:CZ	2.33	0.41
2:C:225:ALA:O	2:C:229:THR:OG1	2.28	0.41
3:D:12:SER:OG	3:D:13:ASN:N	2.42	0.41
3:F:52:VAL:HA	3:F:63:THR:HG22	2.02	0.41
4:G:36:ARG:HG3	4:G:39:ARG:HH22	1.84	0.41
5:H:41:PHE:HD1	5:H:41:PHE:HA	1.73	0.41
6:I:32:ARG:HB3	6:I:44:ILE:HD11	2.02	0.41
2:A:411:ASP:OD1	2:A:411:ASP:N	2.52	0.41
3:F:199:LEU:HD11	3:F:203:MET:HE3	2.02	0.41
7:J:10:THR:HG22	7:J:31:ARG:HE	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:K:63:ILE:HG22	21:K:301:CDL:H361	2.02	0.41
10:M:125:ILE:H	10:M:125:ILE:HG12	1.70	0.41
10:M:133:GLU:OE2	15:R:5:TYR:OH	2.36	0.41
3:D:170:MET:SD	3:D:199:LEU:HD13	2.61	0.41
1:7:70:LEU:HA	1:7:74:ALA:HB3	2.03	0.41
2:A:210:ARG:HE	2:A:235:THR:HG21	1.85	0.41
2:A:455:LYS:HD2	2:A:505:LEU:HD22	2.03	0.41
2:B:444:ILE:HG13	2:B:465:GLU:HG3	2.01	0.41
6:I:25:ASP:HA	6:I:28:VAL:HG12	2.02	0.41
11:N:126:LEU:HD22	11:N:144:ILE:HA	2.03	0.41
12:O:11:VAL:HG11	12:O:105:ALA:HB1	2.03	0.41
14:Q:40:LYS:O	14:Q:43:SER:OG	2.36	0.41
2:A:146:MET:HE2	2:A:161:ARG:HG2	2.03	0.41
2:C:164:ARG:NH2	2:C:345:ILE:O	2.54	0.41
16:S:77:LEU:HD12	16:S:77:LEU:HA	1.83	0.41
2:A:54:GLU:HG2	2:A:60:LYS:HE2	2.03	0.41
2:B:239:ALA:HB1	2:B:241:PRO:HD2	2.03	0.41
2:C:463:LYS:HE2	2:C:463:LYS:HB3	1.91	0.41
3:D:261:ILE:HD12	3:D:261:ILE:HA	1.92	0.41
6:I:32:ARG:HD3	6:I:44:ILE:HG12	2.03	0.41
2:A:152:ALA:HB3	2:A:365:ILE:HD12	2.02	0.41
14:Q:46:THR:O	14:Q:46:THR:OG1	2.36	0.41
1:5:19:ALA:O	1:6:20:GLY:HA3	2.20	0.41
3:F:319:ASP:OD2	4:G:250:ARG:NH2	2.54	0.41
2:B:12:LEU:O	2:B:16:ILE:HG12	2.21	0.41
15:R:34:LYS:NZ	16:S:65:LYS:O	2.54	0.41
1:8:2:ILE:HA	1:8:5:ALA:HB3	2.03	0.40
2:A:248:TYR:OH	2:A:301:LEU:O	2.36	0.40
2:A:470:GLN:OE1	2:A:474:THR:OG1	2.38	0.40
2:B:289:PRO:HB2	2:B:293:ALA:HA	2.04	0.40
2:B:397:TYR:CG	2:B:421:GLY:HA3	2.56	0.40
3:D:210:SER:OG	3:D:213:ASP:OD1	2.27	0.40
3:F:255:LEU:HD23	3:F:255:LEU:HA	1.94	0.40
4:G:67:LEU:HD11	4:G:102:ILE:HG13	2.03	0.40
8:K:121:GLN:HE21	8:K:121:GLN:HB2	1.63	0.40
2:B:329:THR:HG21	2:B:334:VAL:HG12	2.03	0.40
3:D:295:MET:HE3	3:D:295:MET:HB3	1.86	0.40
3:D:380:ILE:HG22	3:D:410:ALA:HB2	2.03	0.40
3:F:87:ILE:HD11	3:F:241:THR:HB	2.02	0.40
2:C:62:MET:HE1	2:C:245:LEU:HD13	2.04	0.40
2:C:344:SER:O	3:F:192:ARG:NH2	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:160:ALA:N	4:G:168:ARG:O	2.46	0.40
4:G:186:ILE:HD12	4:G:186:ILE:HA	1.87	0.40
2:B:146:MET:HE3	2:B:265:LEU:HD22	2.04	0.40
14:Q:32:GLN:NE2	14:Q:33:PRO:O	2.48	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	1	73/128 (57%)	68 (93%)	5 (7%)	0	100	100
1	2	73/128 (57%)	70 (96%)	3 (4%)	0	100	100
1	3	73/128 (57%)	71 (97%)	2 (3%)	0	100	100
1	4	73/128 (57%)	73 (100%)	0	0	100	100
1	5	73/128 (57%)	71 (97%)	2 (3%)	0	100	100
1	6	73/128 (57%)	71 (97%)	2 (3%)	0	100	100
1	7	73/128 (57%)	72 (99%)	1 (1%)	0	100	100
1	8	73/128 (57%)	68 (93%)	5 (7%)	0	100	100
2	A	502/551 (91%)	497 (99%)	5 (1%)	0	100	100
2	B	501/551 (91%)	495 (99%)	6 (1%)	0	100	100
2	C	240/551 (44%)	237 (99%)	3 (1%)	0	100	100
3	D	366/524 (70%)	352 (96%)	14 (4%)	0	100	100
3	E	467/524 (89%)	447 (96%)	20 (4%)	0	100	100
3	F	467/524 (89%)	449 (96%)	18 (4%)	0	100	100
4	G	257/290 (89%)	253 (98%)	4 (2%)	0	100	100
5	H	132/169 (78%)	128 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	I	35/66 (53%)	31 (89%)	4 (11%)	0	100	100
7	J	40/105 (38%)	36 (90%)	4 (10%)	0	100	100
8	K	206/265 (78%)	202 (98%)	4 (2%)	0	100	100
9	L	73/99 (74%)	73 (100%)	0	0	100	100
10	M	159/219 (73%)	138 (87%)	21 (13%)	0	100	100
11	N	217/219 (99%)	205 (94%)	12 (6%)	0	100	100
12	O	187/207 (90%)	176 (94%)	10 (5%)	1 (0%)	24	46
14	Q	44/53 (83%)	42 (96%)	2 (4%)	0	100	100
15	R	102/119 (86%)	93 (91%)	9 (9%)	0	100	100
16	S	74/103 (72%)	72 (97%)	2 (3%)	0	100	100
17	T	80/84 (95%)	77 (96%)	3 (4%)	0	100	100
All	All	4733/6247 (76%)	4567 (96%)	165 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	O	160	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	1	18/93 (19%)	17 (94%)	1 (6%)	19	40
1	3	16/93 (17%)	16 (100%)	0	100	100
2	A	92/446 (21%)	92 (100%)	0	100	100
2	B	345/446 (77%)	341 (99%)	4 (1%)	63	83
2	C	287/446 (64%)	280 (98%)	7 (2%)	43	70
3	D	327/418 (78%)	322 (98%)	5 (2%)	57	80
3	E	382/418 (91%)	377 (99%)	5 (1%)	61	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	F	382/418 (91%)	376 (98%)	6 (2%)	55	79
4	G	220/244 (90%)	218 (99%)	2 (1%)	70	87
5	H	106/135 (78%)	95 (90%)	11 (10%)	7	14
6	I	31/55 (56%)	30 (97%)	1 (3%)	34	62
7	J	23/82 (28%)	23 (100%)	0	100	100
8	K	178/225 (79%)	171 (96%)	7 (4%)	28	55
9	L	65/87 (75%)	62 (95%)	3 (5%)	24	49
10	M	142/197 (72%)	134 (94%)	8 (6%)	19	40
11	N	194/194 (100%)	178 (92%)	16 (8%)	10	24
12	O	157/171 (92%)	150 (96%)	7 (4%)	24	50
14	Q	42/49 (86%)	40 (95%)	2 (5%)	23	47
15	R	83/97 (86%)	81 (98%)	2 (2%)	43	70
16	S	63/85 (74%)	60 (95%)	3 (5%)	23	47
17	T	67/69 (97%)	65 (97%)	2 (3%)	36	64
All	All	3220/4468 (72%)	3128 (97%)	92 (3%)	38	65

All (92) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	18	VAL
2	B	354	THR
2	B	371	VAL
2	B	440	ASP
2	B	507	THR
2	C	146	MET
2	C	157	VAL
2	C	209	LYS
2	C	244	TYR
2	C	266	ILE
2	C	371	VAL
2	C	434	VAL
3	D	87	ILE
3	D	282	VAL
3	D	397	ASP
3	D	398	GLU
3	D	463	VAL
3	E	265	THR

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Mol	Chain	Res	Type
3	E	302	THR
3	E	328	THR
3	E	433	LYS
3	E	463	VAL
3	F	31	GLN
3	F	79	LEU
3	F	131	VAL
3	F	282	VAL
3	F	397	ASP
3	F	463	VAL
4	G	107	LYS
4	G	258	LEU
5	H	19	THR
5	H	30	ASN
5	H	38	VAL
5	H	41	PHE
5	H	48	LEU
5	H	52	VAL
5	H	55	LEU
5	H	81	THR
5	H	100	VAL
5	H	105	LEU
5	H	136	VAL
6	I	30	MET
8	K	12	VAL
8	K	14	VAL
8	K	32	THR
8	K	55	HIS
8	K	124	LEU
8	K	134	PHE
8	K	137	GLU
9	L	4	VAL
9	L	13	ASP
9	L	71	VAL
10	M	5	ILE
10	M	10	ILE
10	M	28	ASN
10	M	131	THR
10	M	141	GLU
10	M	145	ASN
10	M	153	VAL
10	M	154	LYS

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Mol	Chain	Res	Type
11	N	8	VAL
11	N	9	PHE
11	N	22	MET
11	N	24	ILE
11	N	36	ILE
11	N	71	ILE
11	N	82	PHE
11	N	83	ILE
11	N	90	PHE
11	N	107	TRP
11	N	142	MET
11	N	148	MET
11	N	161	ASN
11	N	168	LEU
11	N	171	LEU
11	N	213	MET
12	O	64	GLN
12	O	83	THR
12	O	117	VAL
12	O	155	THR
12	O	165	VAL
12	O	167	ILE
12	O	169	ASP
14	Q	20	LEU
14	Q	26	MET
15	R	35	LEU
15	R	65	HIS
16	S	31	LYS
16	S	77	LEU
16	S	84	MET
17	T	9	VAL
17	T	80	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (54) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	330	GLN
2	B	316	ASN
2	B	405	GLN
2	B	470	GLN
2	C	46	ASN
2	C	186	GLN

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Mol	Chain	Res	Type
3	D	13	ASN
3	D	15	GLN
3	D	31	GLN
3	D	76	GLN
3	D	133	GLN
3	D	180	HIS
3	D	331	HIS
3	D	372	ASN
3	D	422	GLN
3	E	27	GLN
3	E	59	ASN
3	E	132	GLN
3	E	174	ASN
3	E	175	ASN
3	E	180	HIS
3	E	224	GLN
3	E	249	GLN
3	E	331	HIS
3	E	382	GLN
3	E	419	GLN
3	F	15	GLN
3	F	27	GLN
3	F	31	GLN
3	F	55	HIS
3	F	133	GLN
3	F	174	ASN
3	F	201	HIS
3	F	249	GLN
3	F	266	GLN
3	F	311	GLN
3	F	372	ASN
3	F	388	GLN
3	F	414	GLN
3	F	419	GLN
3	F	480	GLN
4	G	153	ASN
5	H	85	ASN
5	H	91	GLN
5	H	102	ASN
7	J	4	GLN
8	K	115	GLN
10	M	29	GLN

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Mol	Chain	Res	Type
10	M	52	ASN
10	M	113	ASN
10	M	152	ASN
11	N	161	ASN
12	O	41	GLN
12	O	147	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 5 are monoatomic - leaving 7 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	$\# Z > 2$
20	ADP	E	601	19	28,29,29	1.38	4 (14%)	43,45,45	1.89	8 (18%)
21	CDL	K	301	-	89,89,99	0.33	0	95,101,111	0.23	0
18	ATP	A	601	19	32,33,33	0.65	0	48,52,52	0.60	0
18	ATP	D	601	19	32,33,33	0.63	0	48,52,52	0.59	0
21	CDL	K	302	-	76,76,99	0.35	0	82,88,111	0.22	0
18	ATP	B	601	19	32,33,33	0.64	0	48,52,52	0.57	0
18	ATP	C	601	19	32,33,33	0.64	0	48,52,52	0.55	0

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
20	ADP	E	601	19	-	4/16/32/32	0/3/3/3
21	CDL	K	301	-	-	35/100/100/110	-
18	ATP	A	601	19	-	2/22/38/38	0/3/3/3
18	ATP	D	601	19	-	11/22/38/38	0/3/3/3
21	CDL	K	302	-	-	29/87/87/110	-
18	ATP	B	601	19	-	0/22/38/38	0/3/3/3
18	ATP	C	601	19	-	1/22/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	E	601	ADP	C5-C4	4.58	1.47	1.39
20	E	601	ADP	C5-C6	2.58	1.48	1.41
20	E	601	ADP	C5-N7	-2.45	1.34	1.39
20	E	601	ADP	C8-N7	2.11	1.35	1.31

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	E	601	ADP	C5-C4-N3	-6.08	118.34	126.72
20	E	601	ADP	N3-C4-N9	4.93	135.56	127.17
20	E	601	ADP	C2-N3-C4	3.79	121.09	111.83
20	E	601	ADP	C4-C5-N7	-3.30	106.81	110.58
20	E	601	ADP	N3-C2-N1	-3.27	123.64	128.58
20	E	601	ADP	C3'-C2'-C1'	2.85	106.86	101.46
20	E	601	ADP	C4-N9-C8	2.53	108.40	105.74
20	E	601	ADP	C5-N7-C8	2.48	107.35	103.45

There are no chirality outliers.

All (82) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
18	A	601	ATP	PB-O3B-PG-O2G
18	D	601	ATP	PB-O3B-PG-O2G
18	D	601	ATP	PB-O3B-PG-O3G
18	D	601	ATP	C5'-O5'-PA-O2A

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Mol	Chain	Res	Type	Atoms
20	E	601	ADP	C5'-O5'-PA-O1A
20	E	601	ADP	C5'-O5'-PA-O3A
21	K	301	CDL	CA2-OA2-PA1-OA3
21	K	301	CDL	CA2-OA2-PA1-OA5
21	K	301	CDL	CA3-OA5-PA1-OA2
21	K	301	CDL	C51-CB5-OB6-CB4
21	K	302	CDL	CA2-OA2-PA1-OA3
21	K	302	CDL	CA2-OA2-PA1-OA4
21	K	302	CDL	CA2-OA2-PA1-OA5
21	K	302	CDL	CA3-OA5-PA1-OA2
21	K	302	CDL	CA3-OA5-PA1-OA3
21	K	302	CDL	CB3-OB5-PB2-OB2
21	K	302	CDL	CB3-OB5-PB2-OB3
21	K	302	CDL	OB9-CB7-OB8-CB6
21	K	301	CDL	OB7-CB5-OB6-CB4
21	K	302	CDL	C31-CA7-OA8-CA6
21	K	302	CDL	C71-CB7-OB8-CB6
21	K	302	CDL	OA9-CA7-OA8-CA6
21	K	301	CDL	C11-CA5-OA6-CA4
21	K	301	CDL	OA7-CA5-OA6-CA4
21	K	302	CDL	C51-CB5-OB6-CB4
21	K	302	CDL	OB7-CB5-OB6-CB4
21	K	301	CDL	C71-CB7-OB8-CB6
21	K	301	CDL	C13-C14-C15-C16
21	K	301	CDL	C40-C41-C42-C43
21	K	302	CDL	C11-CA5-OA6-CA4
21	K	301	CDL	OB9-CB7-OB8-CB6
21	K	301	CDL	C32-C33-C34-C35
21	K	302	CDL	CB7-C71-C72-C73
18	D	601	ATP	O4'-C4'-C5'-O5'
21	K	301	CDL	C74-C75-C76-C77
21	K	301	CDL	OA6-CA4-CA6-OA8
21	K	302	CDL	C32-C33-C34-C35
18	D	601	ATP	C3'-C4'-C5'-O5'
21	K	301	CDL	C19-C20-C21-C22
21	K	302	CDL	OA7-CA5-OA6-CA4
21	K	301	CDL	C34-C35-C36-C37
21	K	301	CDL	C11-C12-C13-C14
18	C	601	ATP	PB-O3B-PG-O1G
21	K	301	CDL	CA5-C11-C12-C13
21	K	302	CDL	C14-C15-C16-C17
21	K	302	CDL	CA4-CA3-OA5-PA1

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Mol	Chain	Res	Type	Atoms
21	K	301	CDL	OB5-CB3-CB4-CB6
21	K	302	CDL	OA5-CA3-CA4-CA6
21	K	302	CDL	C72-C73-C74-C75
21	K	301	CDL	CA3-CA4-CA6-OA8
21	K	301	CDL	CB3-CB4-CB6-OB8
21	K	302	CDL	OA5-CA3-CA4-OA6
21	K	301	CDL	C39-C40-C41-C42
21	K	301	CDL	CA3-CA4-OA6-CA5
21	K	301	CDL	OB6-CB4-CB6-OB8
21	K	301	CDL	OB5-CB3-CB4-OB6
18	D	601	ATP	C5'-O5'-PA-O1A
18	D	601	ATP	C5'-O5'-PA-O3A
21	K	301	CDL	CA3-OA5-PA1-OA3
21	K	302	CDL	CB3-OB5-PB2-OB4
21	K	301	CDL	C52-C53-C54-C55
21	K	301	CDL	C1-CA2-OA2-PA1
21	K	301	CDL	C79-C80-C81-C82
18	D	601	ATP	PA-O3A-PB-O1B
18	D	601	ATP	PA-O3A-PB-O2B
21	K	302	CDL	C37-C38-C39-C40
21	K	301	CDL	C33-C34-C35-C36
21	K	302	CDL	C13-C14-C15-C16
18	D	601	ATP	PG-O3B-PB-O1B
21	K	301	CDL	CB2-C1-CA2-OA2
20	E	601	ADP	C3'-C4'-C5'-O5'
18	A	601	ATP	PB-O3B-PG-O1G
21	K	302	CDL	CA3-CA4-CA6-OA8
18	D	601	ATP	PG-O3B-PB-O2B
21	K	302	CDL	C12-C11-CA5-OA6
21	K	301	CDL	C20-C21-C22-C23
21	K	301	CDL	C80-C81-C82-C83
21	K	301	CDL	C32-C31-CA7-OA8
20	E	601	ADP	O4'-C4'-C5'-O5'
21	K	302	CDL	C53-C54-C55-C56
21	K	302	CDL	C12-C11-CA5-OA7
21	K	301	CDL	C41-C42-C43-C44

There are no ring outliers.

3 monomers are involved in 6 short contacts:

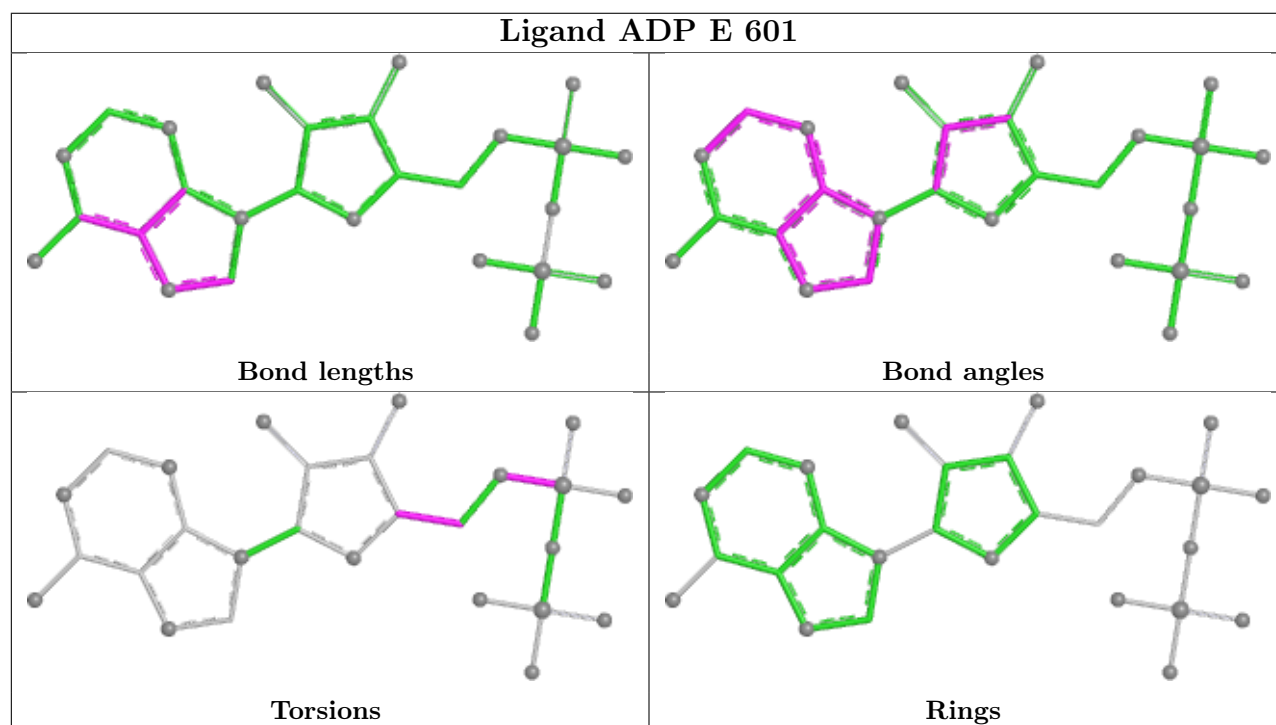
Mol	Chain	Res	Type	Clashes	Symm-Clashes
20	E	601	ADP	1	0

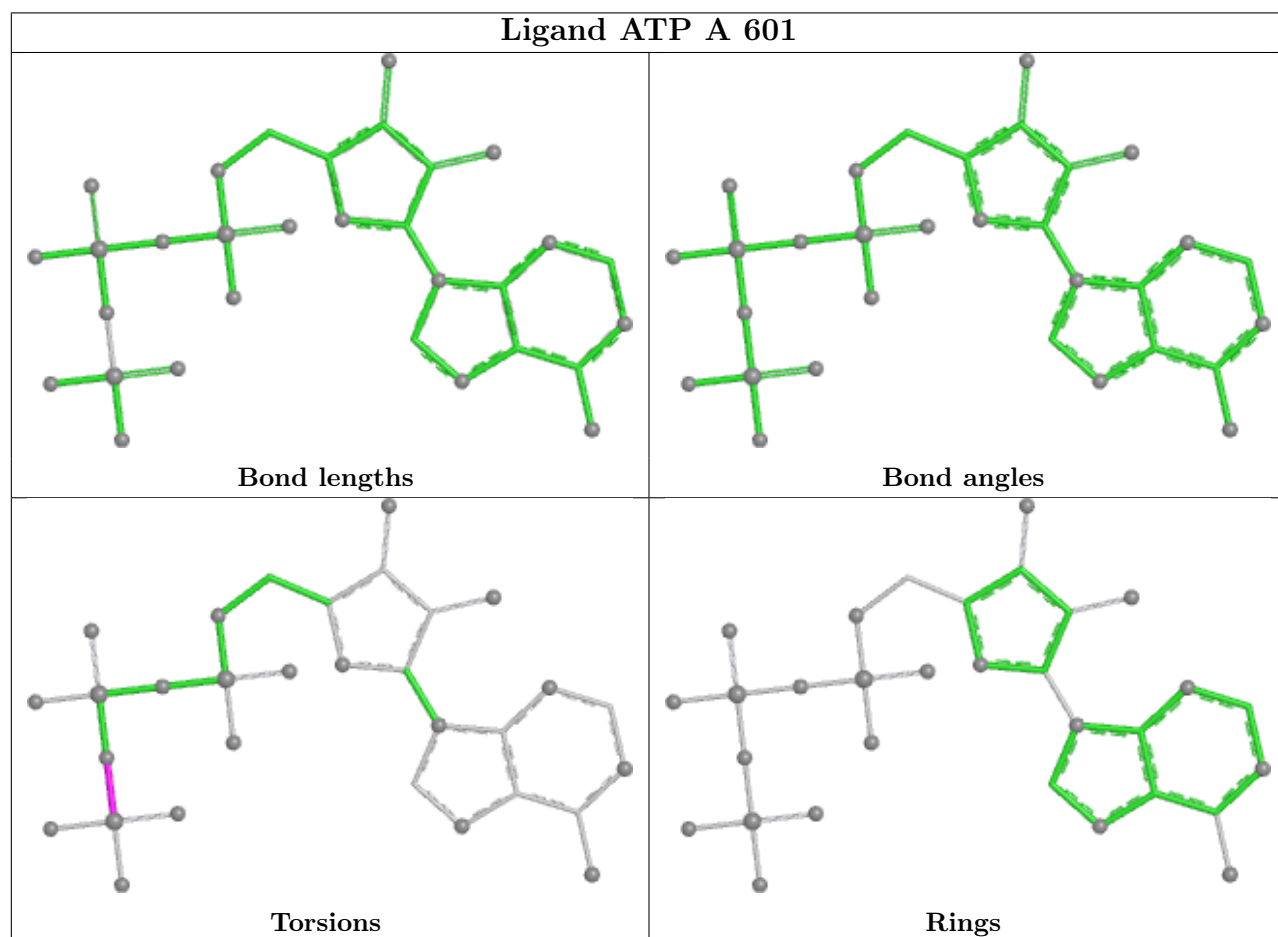
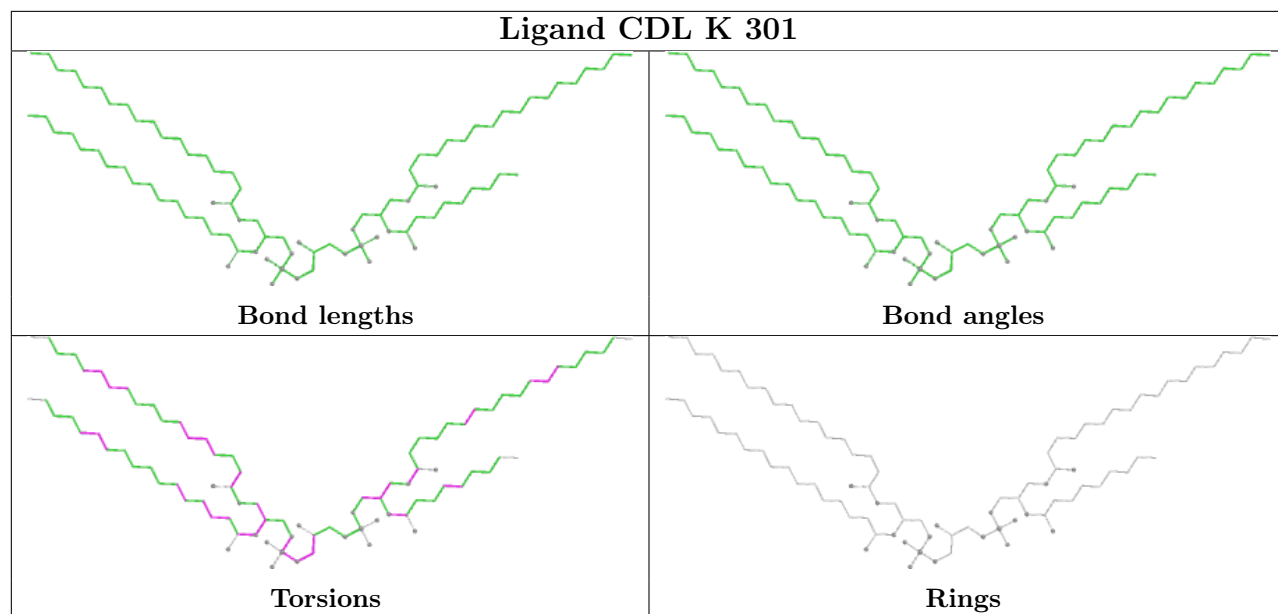
Continued on next page...

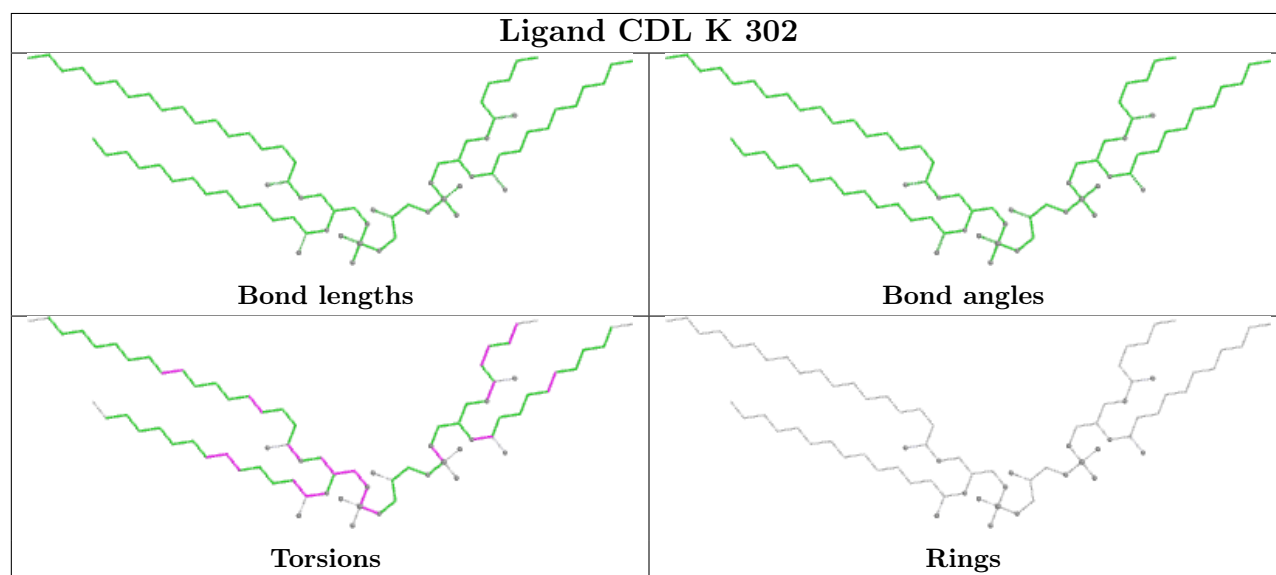
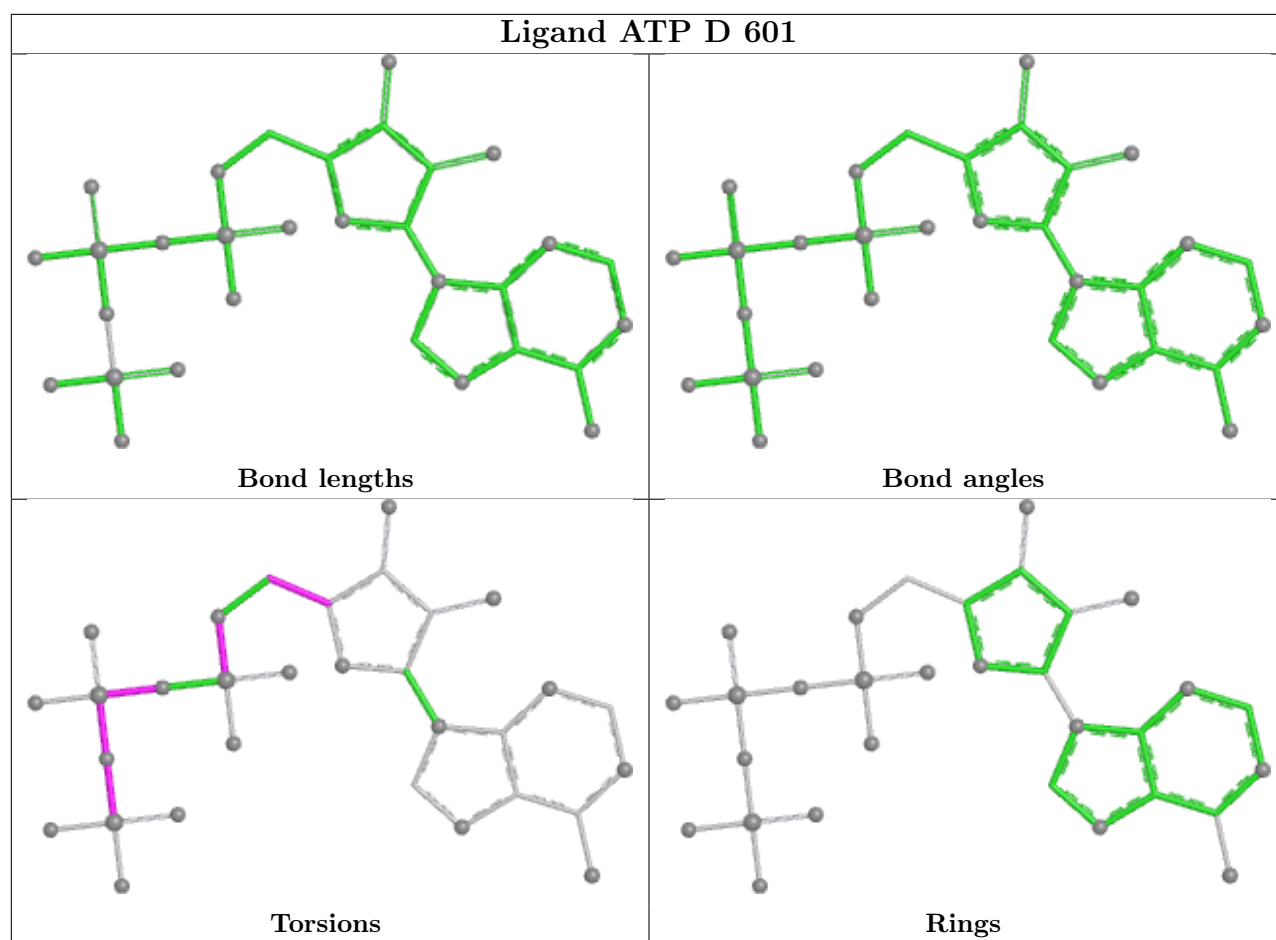
Continued from previous page...

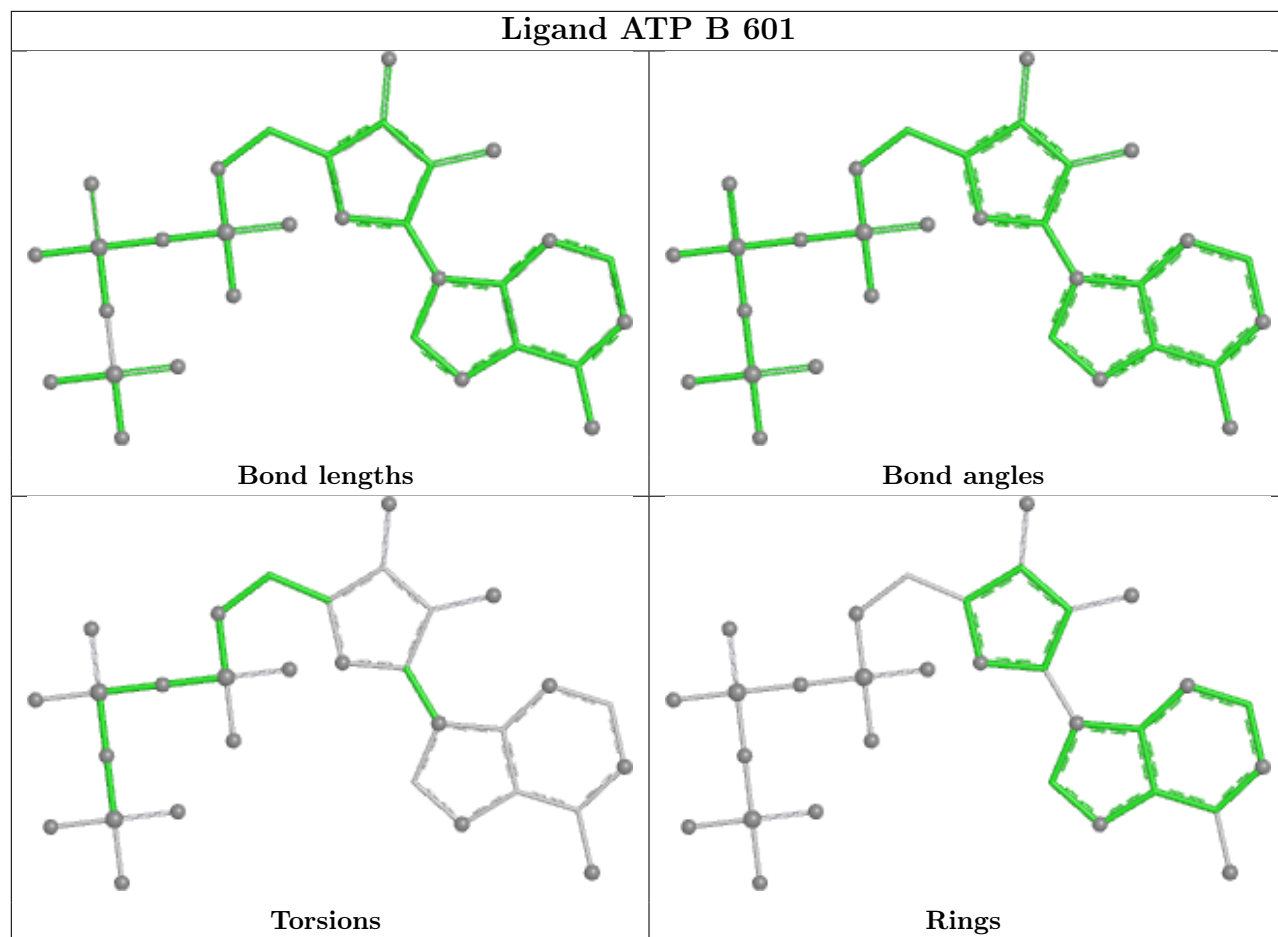
Mol	Chain	Res	Type	Clashes	Symm-Clashes
21	K	301	CDL	3	0
21	K	302	CDL	2	0

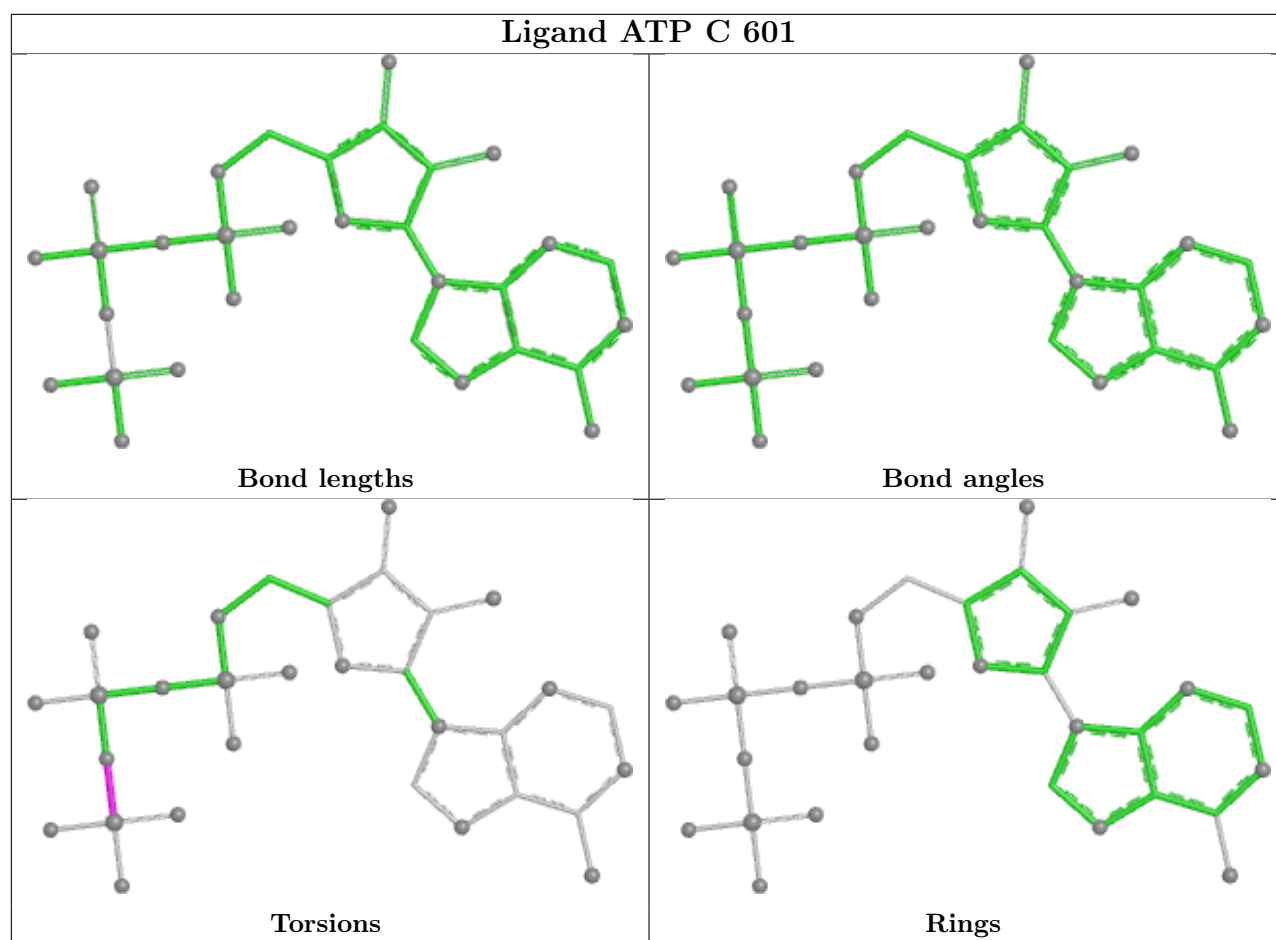
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

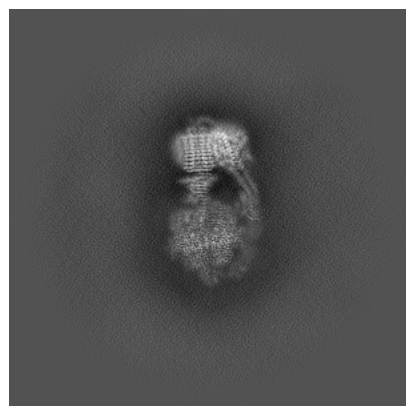
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44061. These allow visual inspection of the internal detail of the map and identification of artifacts.

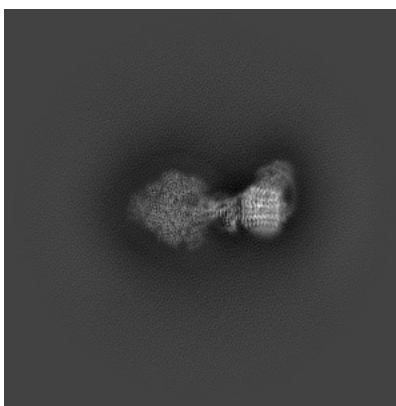
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

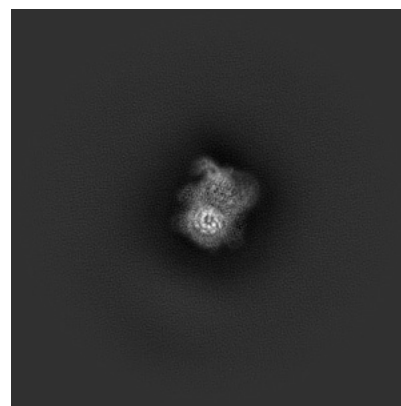
6.1.1 Primary map



X

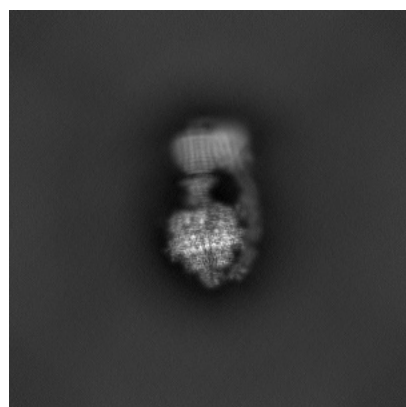


Y

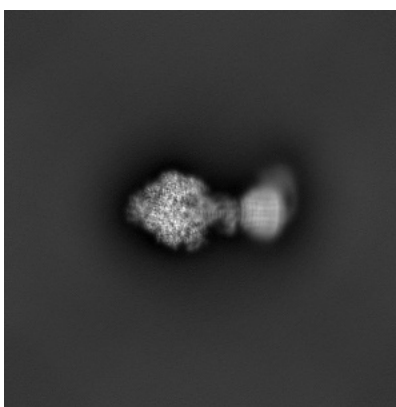


Z

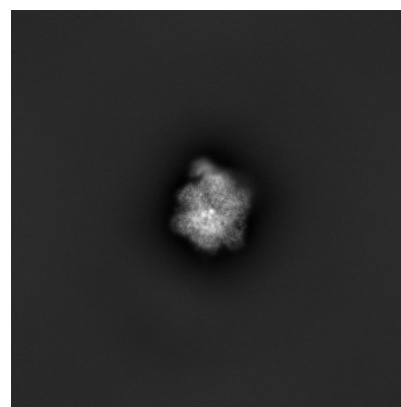
6.1.2 Raw map



X



Y

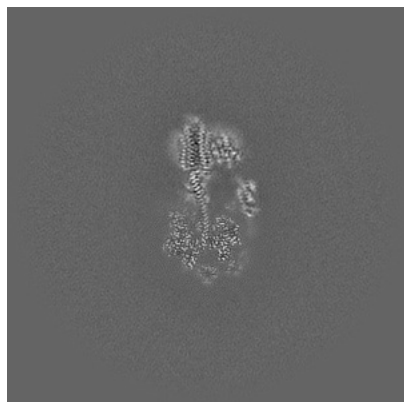


Z

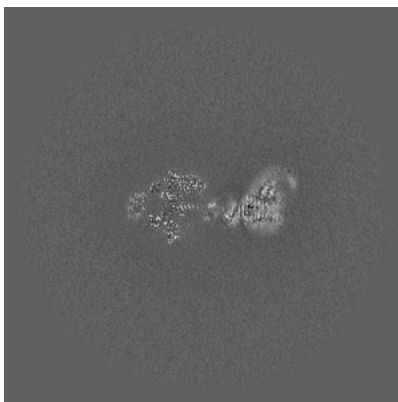
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

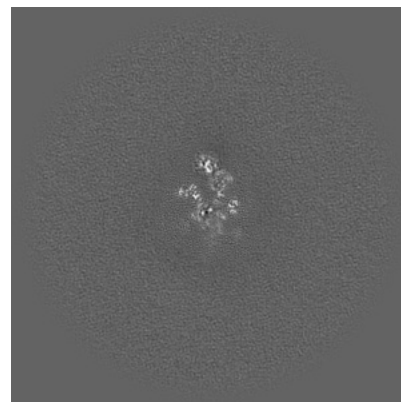
6.2.1 Primary map



X Index: 256



Y Index: 256

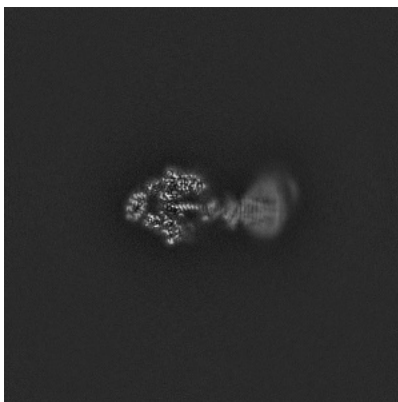


Z Index: 256

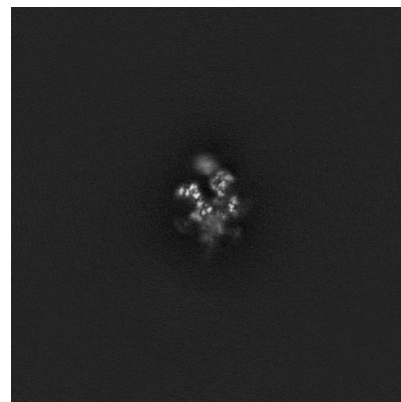
6.2.2 Raw map



X Index: 256



Y Index: 256

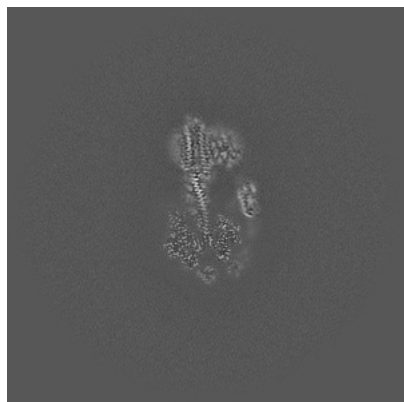


Z Index: 256

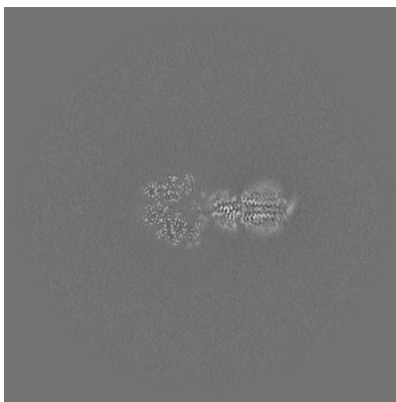
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

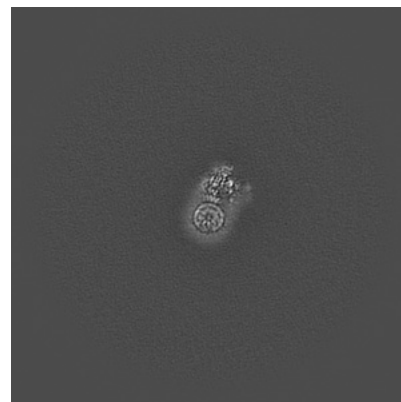
6.3.1 Primary map



X Index: 254

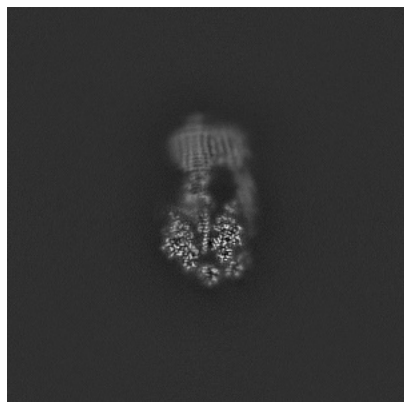


Y Index: 241

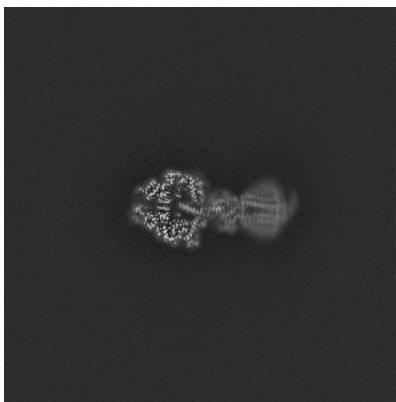


Z Index: 325

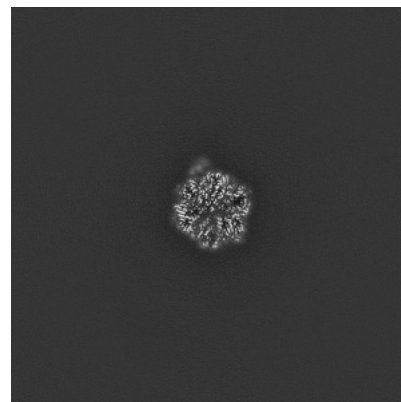
6.3.2 Raw map



X Index: 258



Y Index: 246

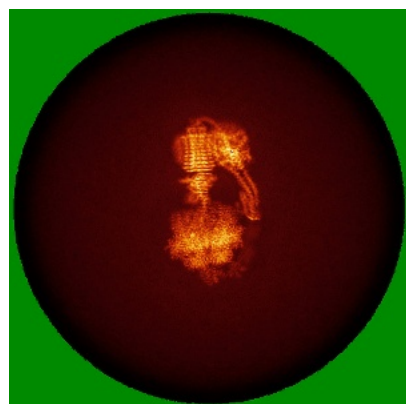


Z Index: 214

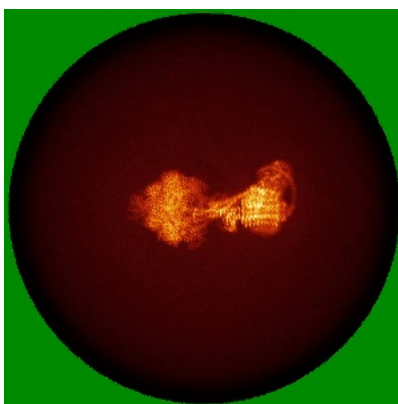
The images above show the largest variance slices of the map in three orthogonal directions.

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

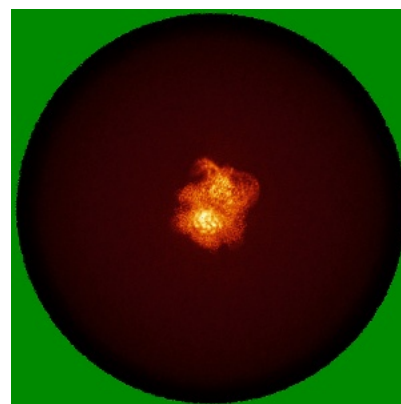
6.4.1 Primary map



X

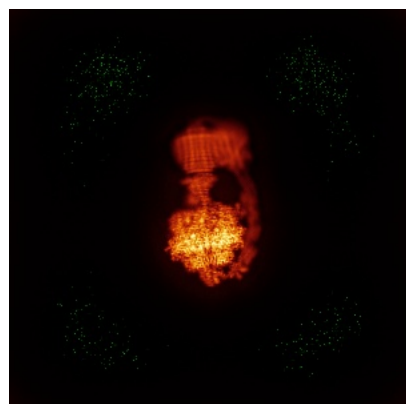


Y

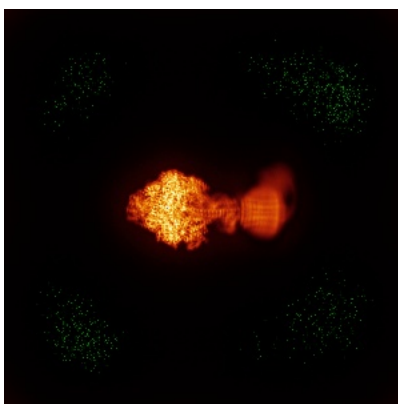


Z

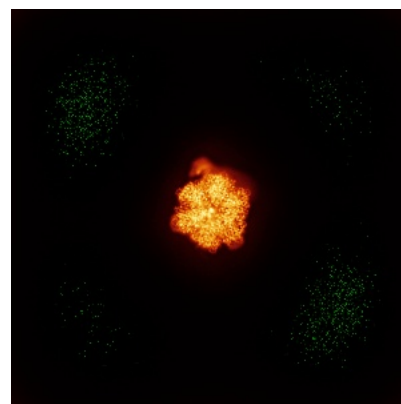
6.4.2 Raw map



X



Y

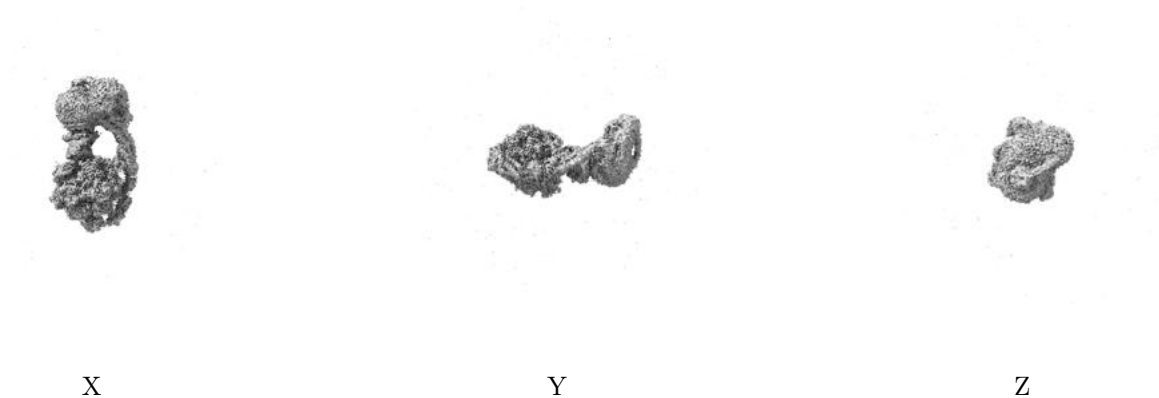


Z

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

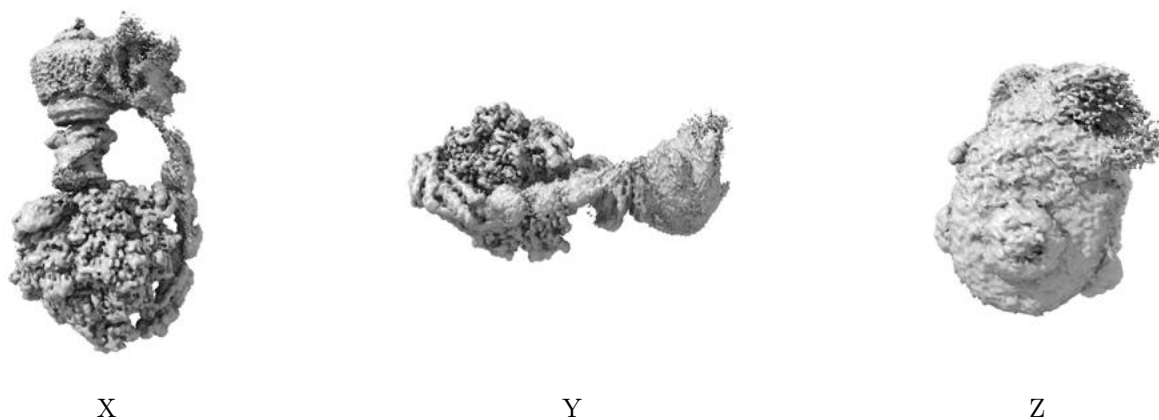
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.51. 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.

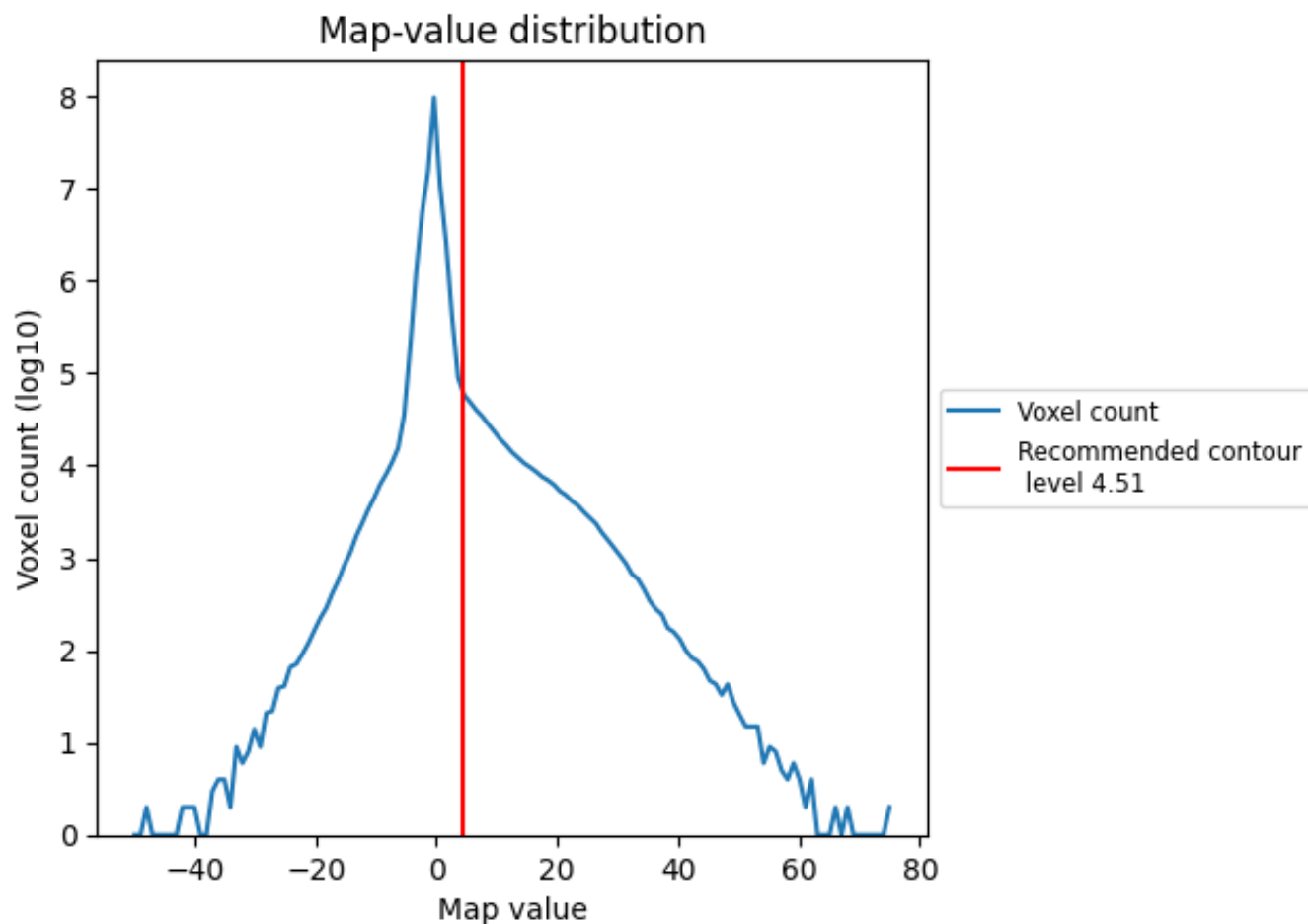
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

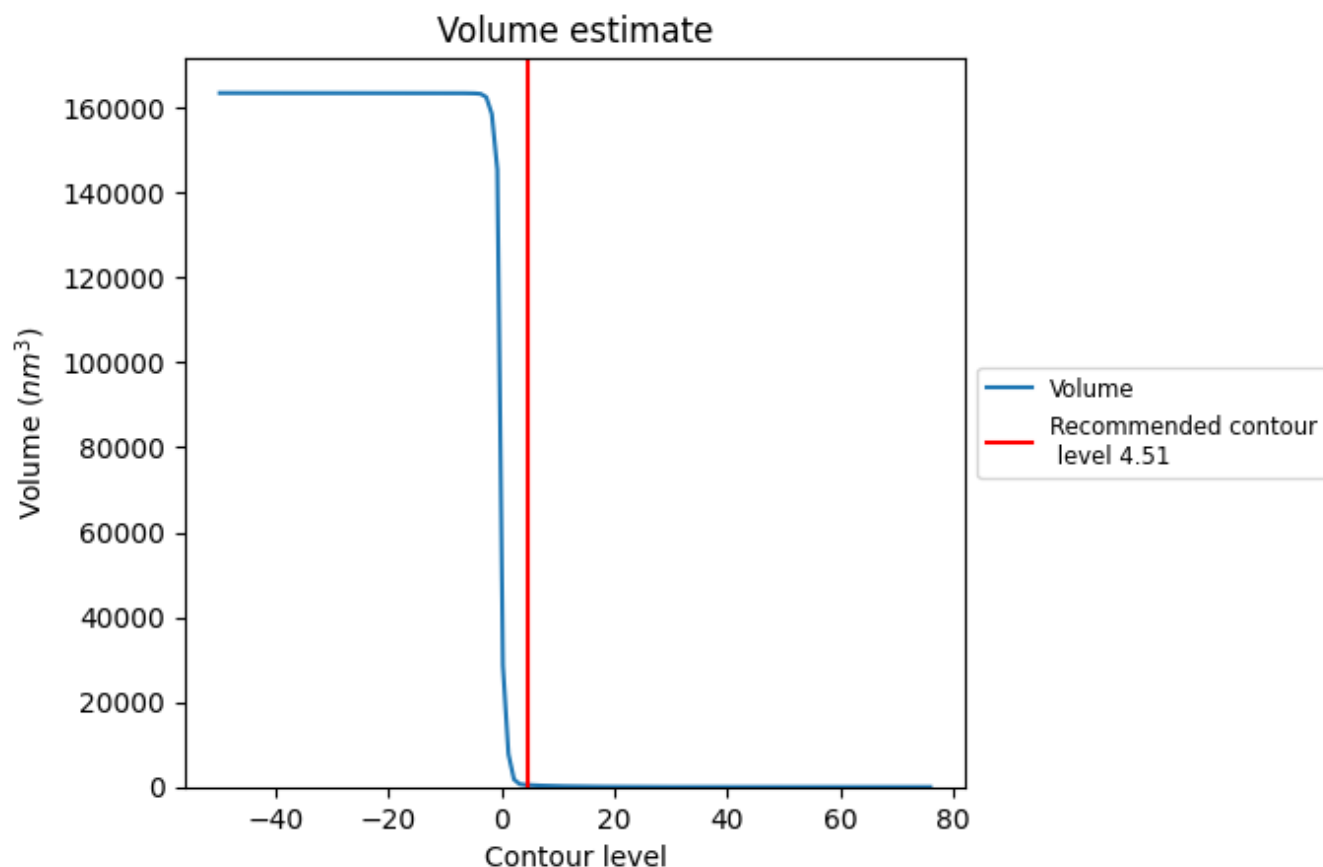
This section contains the results of statistical analysis of the map.

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.

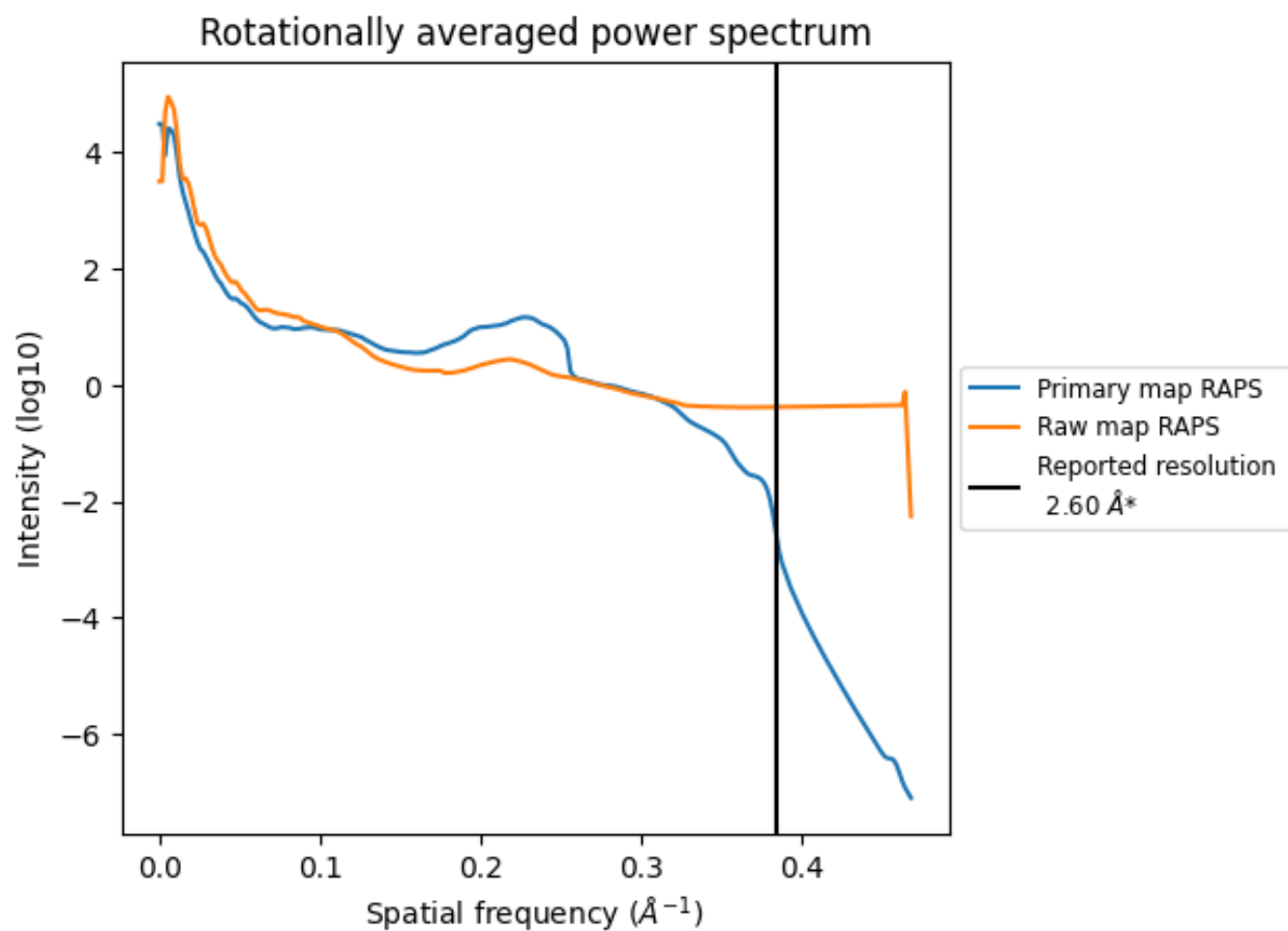
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 474 nm³; this corresponds to an approximate mass of 428 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 ⓘ

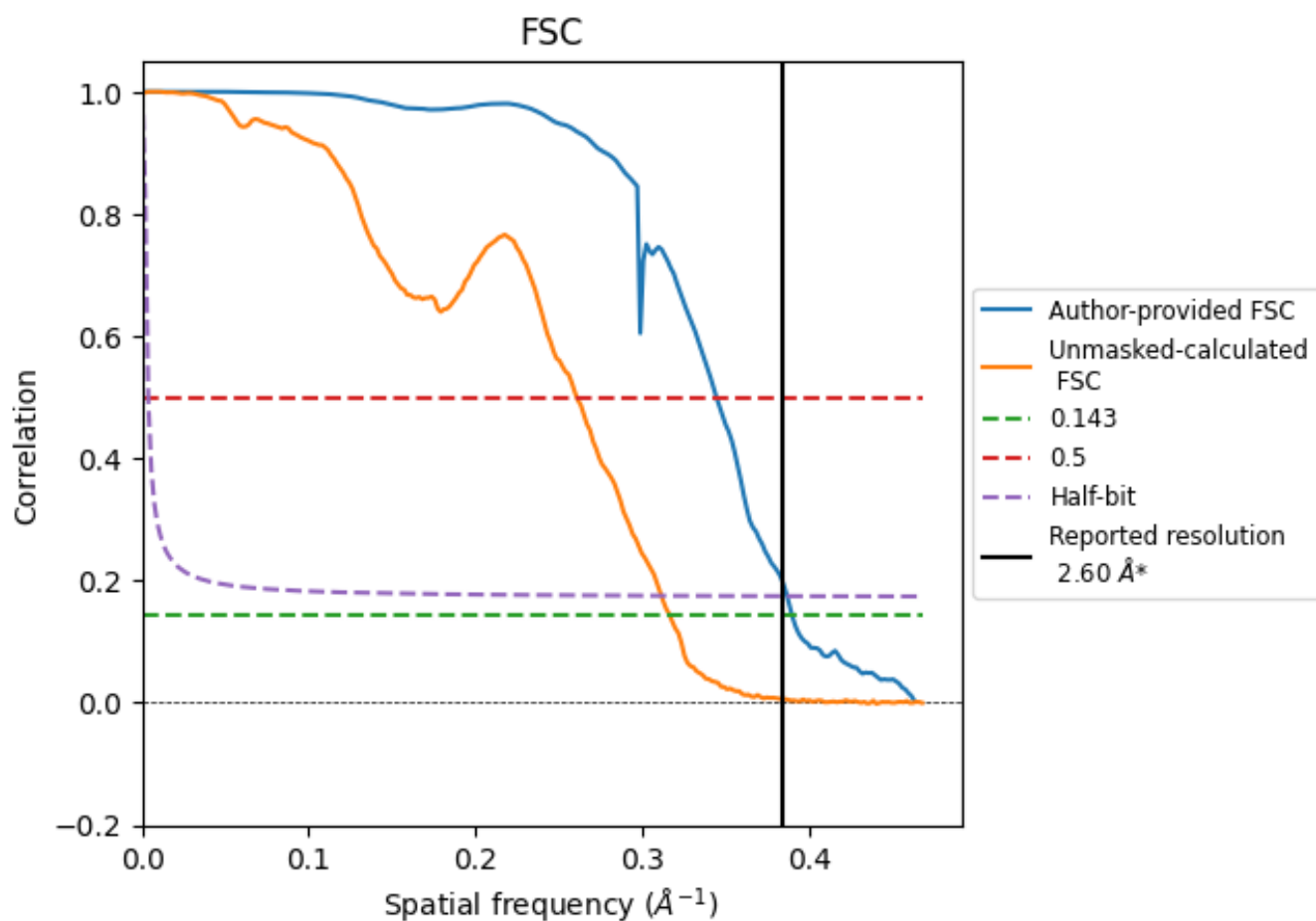


*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

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 0.385 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

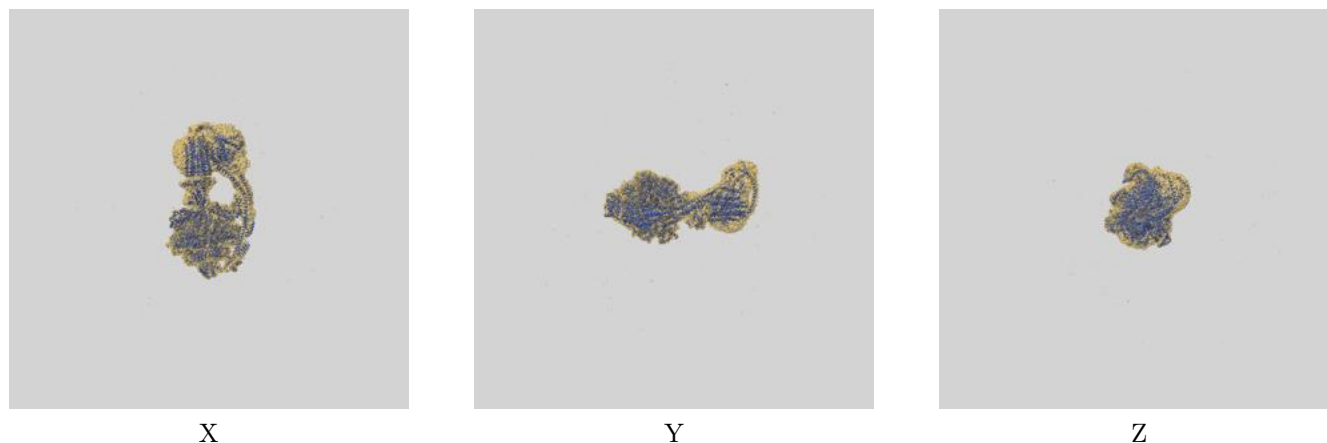
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.56	2.90	2.58
Unmasked-calculated*	3.16	3.83	3.21

*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 3.16 differs from the reported value 2.6 by more than 10 %

9 Map-model fit [i](#)

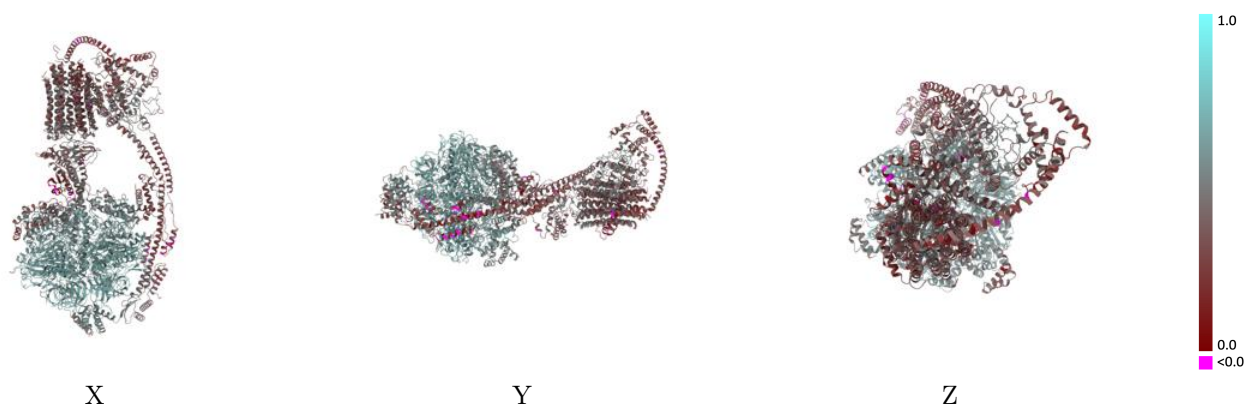
This section contains information regarding the fit between EMDB map EMD-44061 and PDB model 9B0X. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



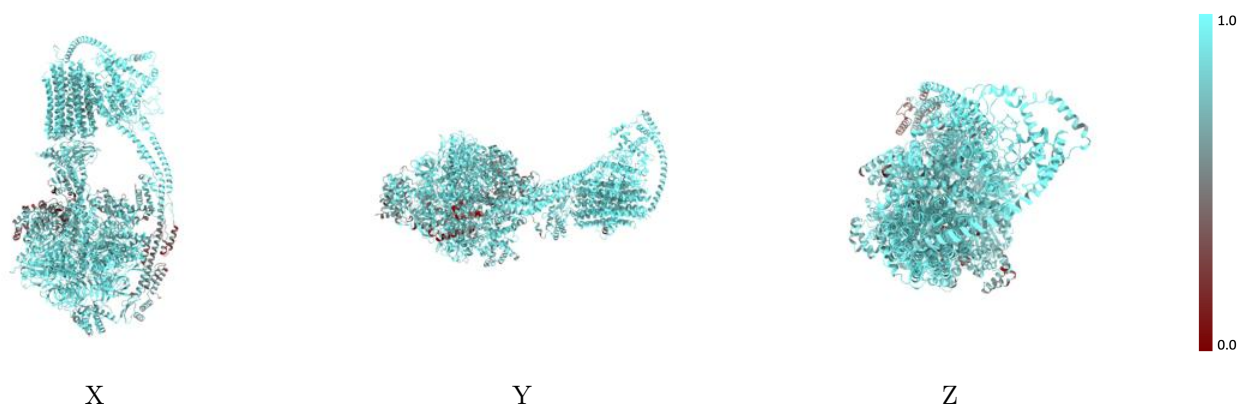
The images above show the 3D surface view of the map at the recommended contour level 4.51 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



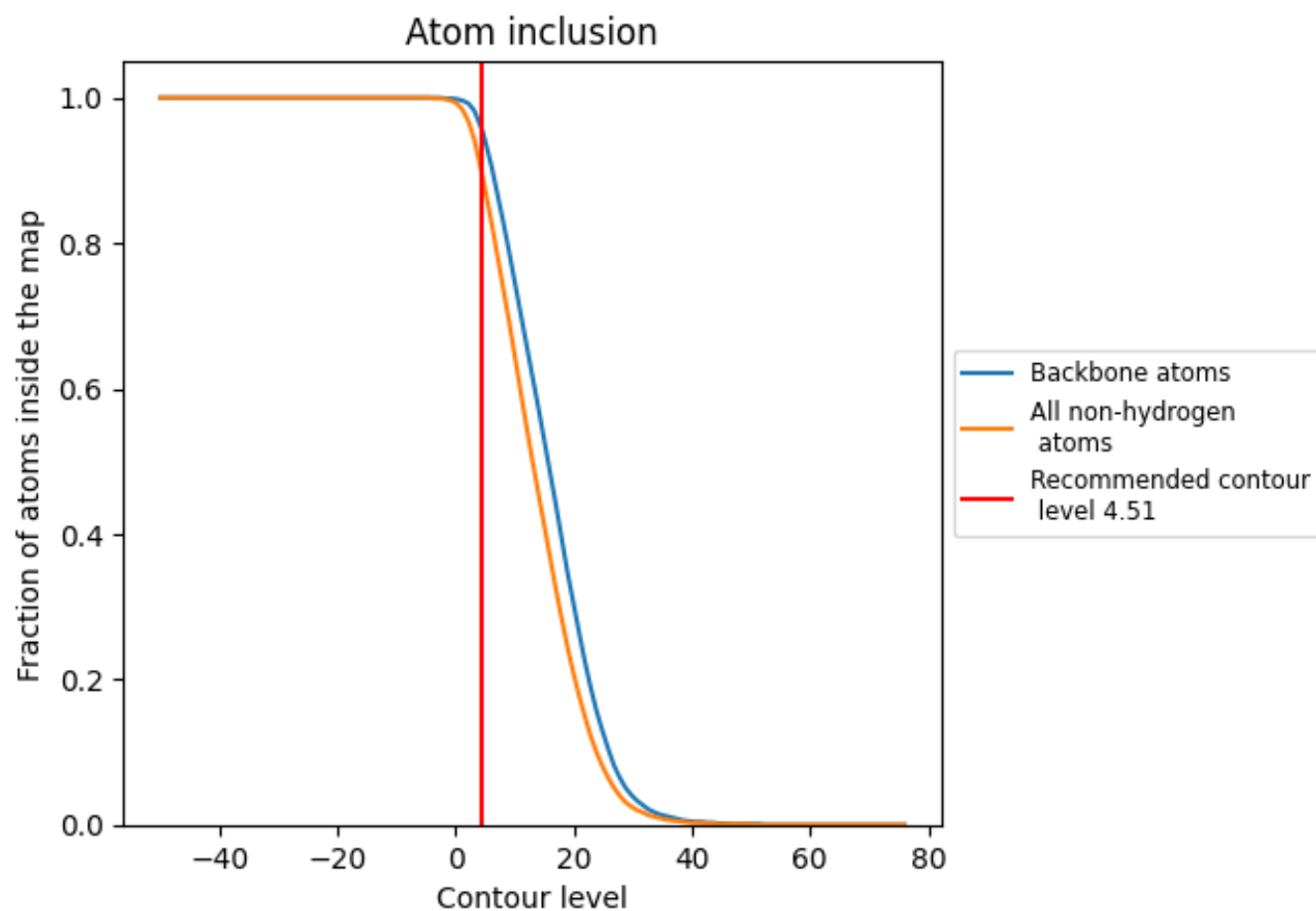
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4.51).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 89% 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 (4.51) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8930	 0.4890
1	 0.9140	 0.3160
2	 0.9360	 0.3480
3	 0.9320	 0.3890
4	 0.9510	 0.3820
5	 0.9550	 0.3860
6	 0.9400	 0.3880
7	 0.9420	 0.3540
8	 0.9230	 0.3090
A	 0.8860	 0.5710
B	 0.8630	 0.5570
C	 0.9190	 0.5910
D	 0.9470	 0.6120
E	 0.9350	 0.6070
F	 0.9320	 0.6070
G	 0.8560	 0.3800
H	 0.9320	 0.3560
I	 0.8000	 0.3160
J	 0.4130	 0.4540
K	 0.8530	 0.3610
L	 0.4930	 0.2710
M	 0.7930	 0.2940
N	 0.9360	 0.3450
O	 0.7760	 0.4840
P	 1.0000	 0.3620
Q	 0.9420	 0.3640
R	 0.9650	 0.4070
S	 0.9200	 0.3040
T	 0.8990	 0.2760

