



wwPDB EM Validation Summary Report ⓘ

Apr 17, 2024 – 11:24 am BST

PDB ID : 7PO1
EMDB ID : EMD-13559
Title : Initiation complex of human mitochondrial ribosome small subunit with IF3
Authors : Itoh, Y.; Khawaja, A.; Rorbach, J.; Amunts, A.
Deposited on : 2021-09-08
Resolution : 2.92 Å (reported)
Based on initial model : 6RW4

This is a wwPDB EM Validation Summary 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.dev92
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

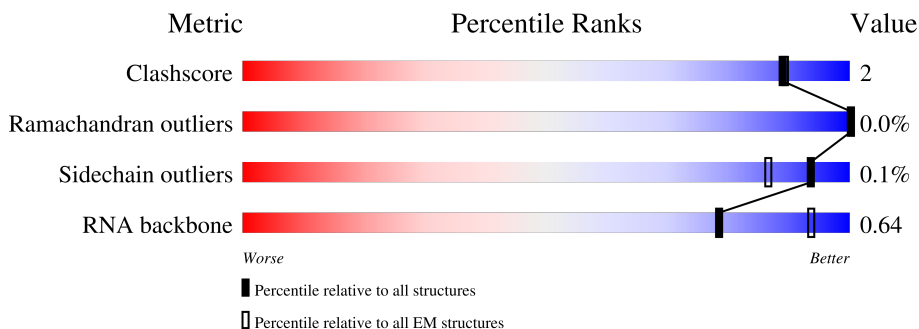
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.92 Å.

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






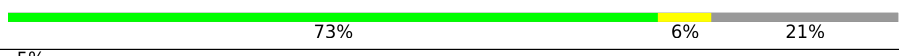



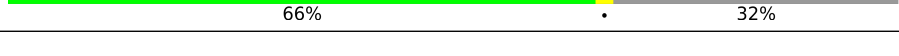
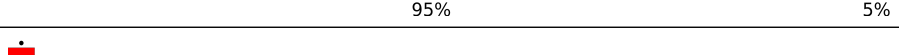
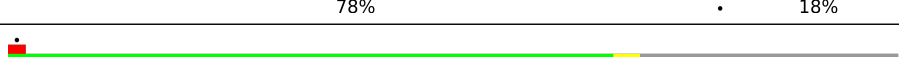
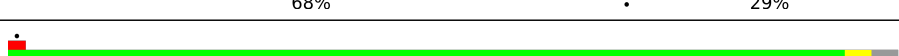
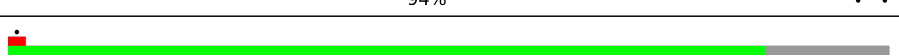
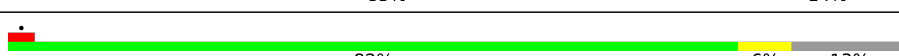
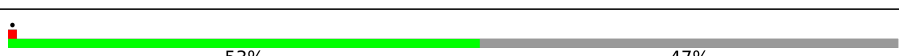
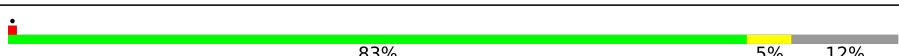
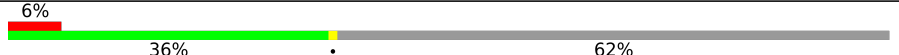
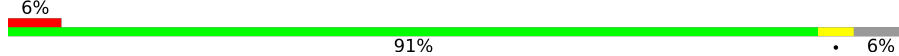
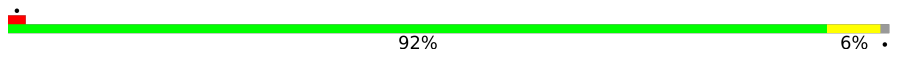

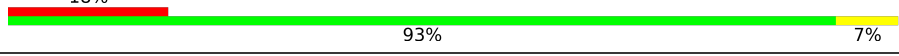



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	A	955	79% 19%
2	B	296	72% 24%
3	C	167	74% 5% 21%
4	D	430	77% 20%
5	E	125	96%
6	F	242	81% 5% 14%
7	G	396	5% 79% 18%

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Mol	Chain	Length	Quality of chain
8	H	201	
9	I	194	
10	J	138	
11	K	128	
12	L	257	
13	M	137	
14	N	130	
15	O	258	
16	P	142	
17	Q	86	
18	R	360	
19	S	190	
20	T	173	
21	U	205	
22	V	414	
23	W	187	
24	X	398	
25	Y	395	
26	Z	106	
27	0	218	
28	1	323	
29	2	117	
30	3	199	
31	4	689	
32	8	278	

2 Entry composition [i](#)

There are 39 unique types of molecules in this entry. The entry contains 129179 atoms, of which 59303 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 RNA chain called 12S mitochondrial rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
1	A	955	30595	9098	10313	3652	6577	955	0	0

- Molecule 2 is a protein called 28S ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
2	B	225	3644	1164	1816	331	323	10	0	0

- Molecule 3 is a protein called 28S ribosomal protein S24, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	C	132	2172	699	1089	195	185	4	0	0

- Molecule 4 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	D	343	5536	1713	2805	518	487	13	0	0

- Molecule 5 is a protein called 28S ribosomal protein S6, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	E	122	1973	614	1001	177	177	4	0	0

- Molecule 6 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
6	F	208	3495	1104	1770	312	298	11	0	0

- Molecule 7 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
7	G	325	5348	1698	2676	475	485	14	0	0

- Molecule 8 is a protein called 28S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
8	H	140	2336	745	1184	194	210	3	0	0

- Molecule 9 is a protein called 28S ribosomal protein S11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
9	I	137	2081	642	1061	192	182	4	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	184	5F0	ASN	conflict	UNP P82912

- Molecule 10 is a protein called 28S ribosomal protein S12, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
10	J	108	1727	521	888	169	143	6	0	0

- Molecule 11 is a protein called 28S ribosomal protein S14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
11	K	101	1748	537	886	179	141	5	0	0

- Molecule 12 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
12	L	174	2994	925	1541	270	251	7	0	0

- Molecule 13 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
13	M	119	1908	594	966	185	157	6	0	0

- Molecule 14 is a protein called 28S ribosomal protein S17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
14	N	110	1797	562	929	156	147	3	0	0

- Molecule 15 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
15	O	193	3149	1014	1557	294	277	7	0	0

- Molecule 16 is a protein called 28S ribosomal protein S18c, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
16	P	97	1588	501	807	134	138	8	0	0

- Molecule 17 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
17	Q	86	1502	460	758	150	126	8	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	50	ARG	CYS	variant	UNP P82921

- Molecule 18 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
18	R	295	4838	1533	2429	413	455	8	0	0

- Molecule 19 is a protein called 28S ribosomal protein S23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
19	S	135	2227	716	1116	198	196	1	0	0

- Molecule 20 is a protein called 28S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
20	T	168	2765	877	1394	239	244	11	0	0

- Molecule 21 is a protein called 28S ribosomal protein S26, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
21	U	176	2988	916	1500	301	267	4	0	0

- Molecule 22 is a protein called 28S ribosomal protein S27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
22	V	362	5933	1904	2964	495	558	12	0	0

- Molecule 23 is a protein called 28S ribosomal protein S28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
23	W	100	1592	498	803	141	146	4	0	0

- Molecule 24 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
24	X	352	5694	1822	2845	499	517	11	0	0

- Molecule 25 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
25	Y	149	2444	801	1198	207	234	4	0	0

- Molecule 26 is a protein called 28S ribosomal protein S33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
26	Z	100	1699	534	860	153	148	4	0	0

- Molecule 27 is a protein called 28S ribosomal protein S34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
27	0	215	3584	1130	1797	339	313	5	0	0

- Molecule 28 is a protein called 28S ribosomal protein S35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
28	1	276	4507	1419	2269	381	427	11	0	0

- Molecule 29 is a protein called Coiled-coil-helix-coiled-coil-helix domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
29	2	117	1904	579	969	182	166	8	0	0

- Molecule 30 is a protein called Aurora kinase A-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
30	3	71	1331	403	702	135	90	1	0	0

- Molecule 31 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
31	4	592	9593	3070	4798	812	885	28	0	0

- Molecule 32 is a protein called Mitochondrial translational initiation factor 3, isoform CRA_a.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
32	8	191	3131	953	1588	289	293	8	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
8	68	ILE	THR	variant	UNP A0A024RDQ7

- Molecule 33 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
33	A	68	Total 68	Mg 68	0
33	B	1	Total 1	Mg 1	0
33	X	1	Total 1	Mg 1	0
33	3	1	Total 1	Mg 1	0

- Molecule 34 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
34	A	20	Total 20	K 20	0

- Molecule 35 is ZINC ION (three-letter code: ZN) (formula: Zn).

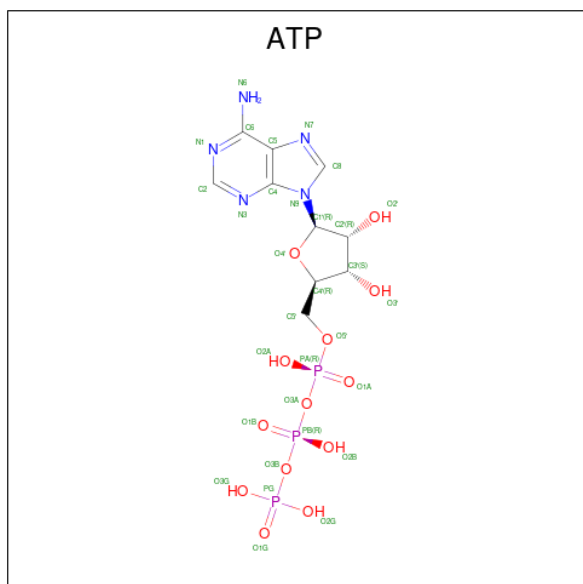
Mol	Chain	Residues	Atoms		AltConf
35	O	1	Total 1	Zn 1	0

- Molecule 36 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂) (labeled as "Ligand of Interest" by depositor).



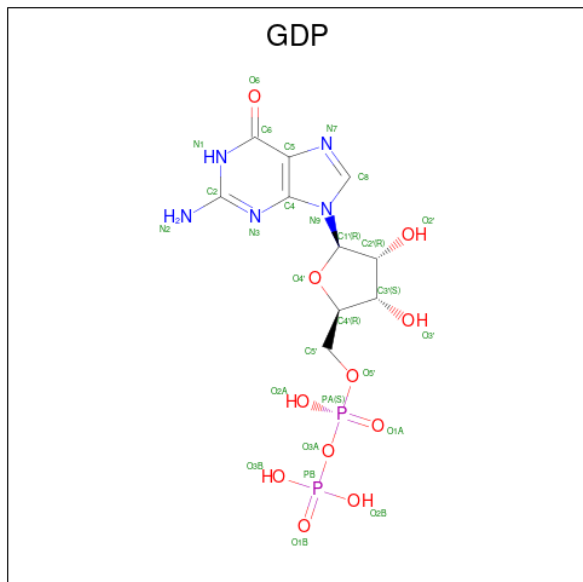
Mol	Chain	Residues	Atoms			AltConf
36	P	1	Total	Fe	S	0
			4	2	2	
36	T	1	Total	Fe	S	0
			4	2	2	

- Molecule 37 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf	
37	X	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	

- Molecule 38 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					AltConf	
			Total	C	H	N	O		P
38	X	1	40	10	12	5	11	2	0

- Molecule 39 is water.

Mol	Chain	Residues	Atoms		AltConf
39	A	762	Total	O	0
			762	762	
39	B	39	Total	O	0
			39	39	
39	C	29	Total	O	0
			29	29	
39	D	29	Total	O	0
			29	29	
39	E	8	Total	O	0
			8	8	
39	F	6	Total	O	0
			6	6	
39	G	29	Total	O	0
			29	29	
39	H	25	Total	O	0
			25	25	
39	I	12	Total	O	0
			12	12	

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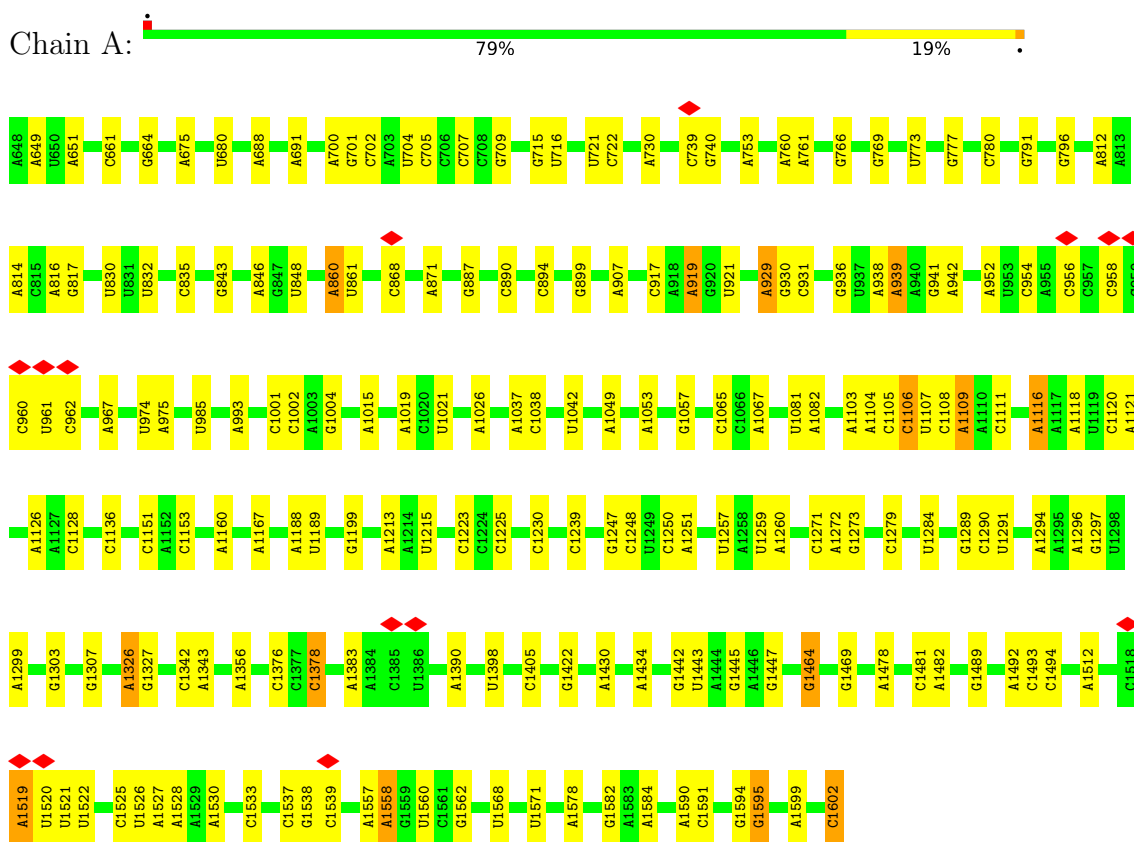
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Mol	Chain	Residues	Atoms		AltConf
39	J	6	Total 6	O 6	0
39	K	27	Total 27	O 27	0
39	L	7	Total 7	O 7	0
39	M	23	Total 23	O 23	0
39	N	10	Total 10	O 10	0
39	O	16	Total 16	O 16	0
39	P	11	Total 11	O 11	0
39	Q	15	Total 15	O 15	0
39	R	8	Total 8	O 8	0
39	S	11	Total 11	O 11	0
39	T	9	Total 9	O 9	0
39	U	3	Total 3	O 3	0
39	W	8	Total 8	O 8	0
39	X	5	Total 5	O 5	0
39	Y	5	Total 5	O 5	0
39	Z	14	Total 14	O 14	0
39	0	18	Total 18	O 18	0
39	1	14	Total 14	O 14	0
39	2	10	Total 10	O 10	0
39	3	11	Total 11	O 11	0
39	4	3	Total 3	O 3	0

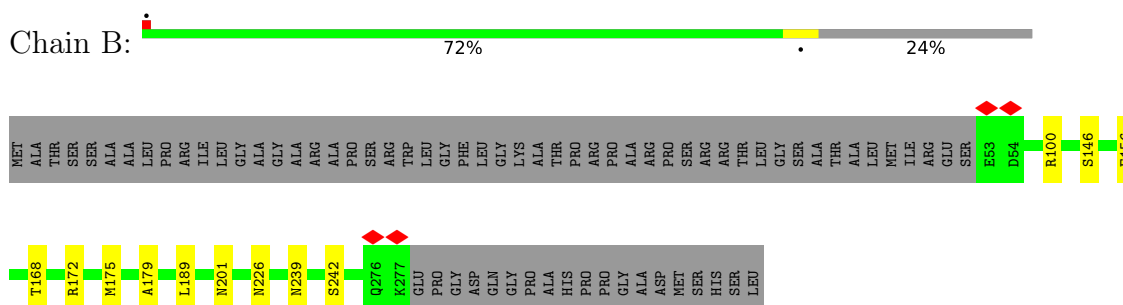
3 Residue-property plots

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.

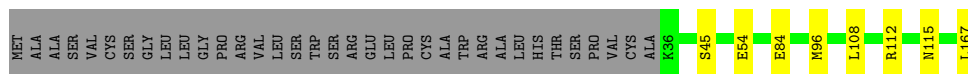
- Molecule 1: 12S mitochondrial rRNA



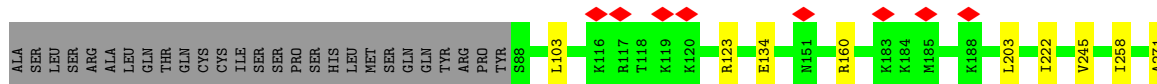
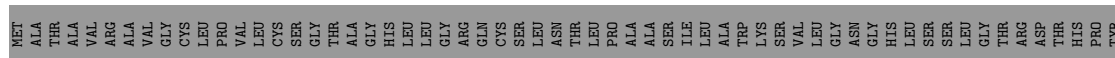
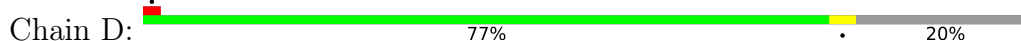
- Molecule 2: 28S ribosomal protein S2, mitochondrial



• Molecule 3: 28S ribosomal protein S24, mitochondrial



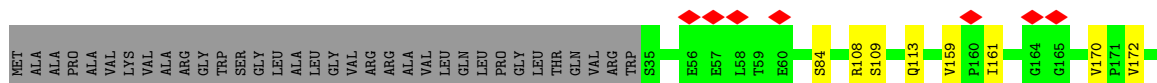
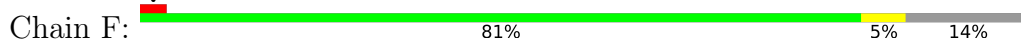
• Molecule 4: 28S ribosomal protein S5, mitochondrial



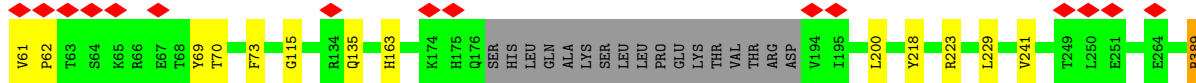
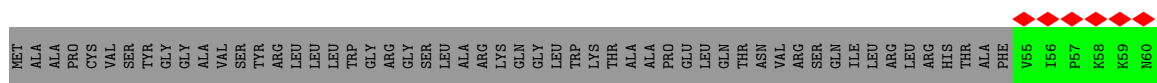
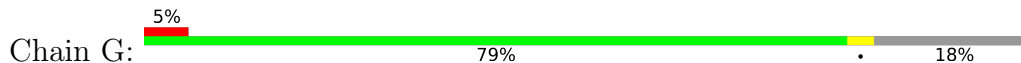
• Molecule 5: 28S ribosomal protein S6, mitochondrial



• Molecule 6: 28S ribosomal protein S7, mitochondrial

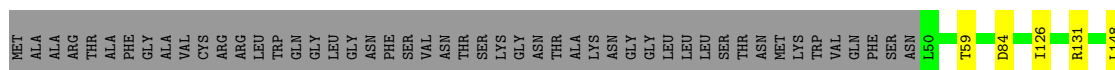


• Molecule 7: 28S ribosomal protein S9, mitochondrial

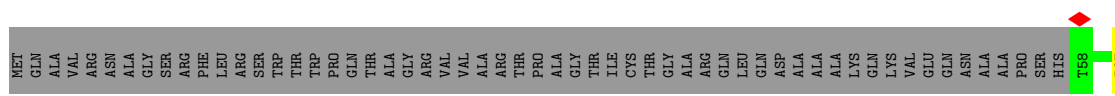




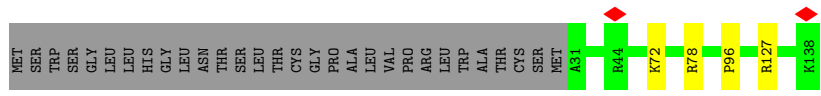
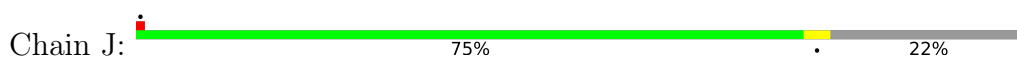
- Molecule 8: 28S ribosomal protein S10, mitochondrial



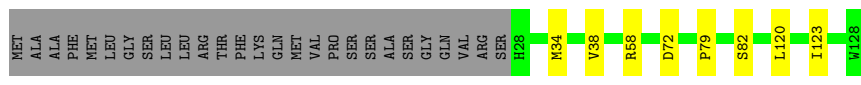
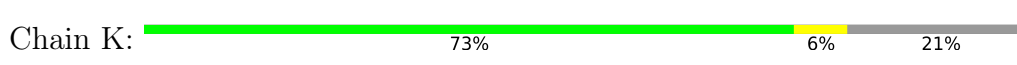
- Molecule 9: 28S ribosomal protein S11, mitochondrial



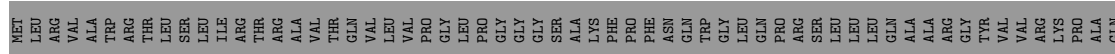
- Molecule 10: 28S ribosomal protein S12, mitochondrial



- Molecule 11: 28S ribosomal protein S14, mitochondrial

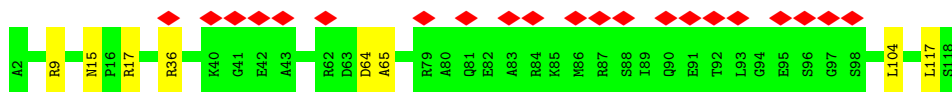
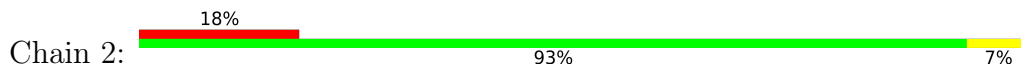


- Molecule 12: 28S ribosomal protein S15, mitochondrial

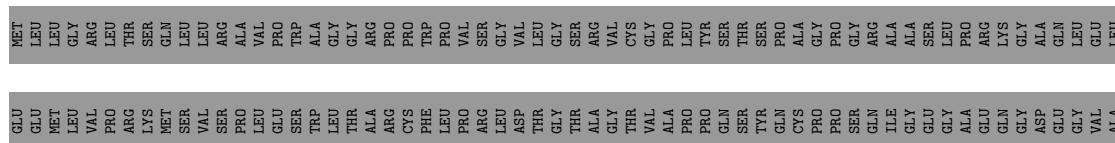


- Molecule 13: 28S ribosomal protein S16, mitochondrial

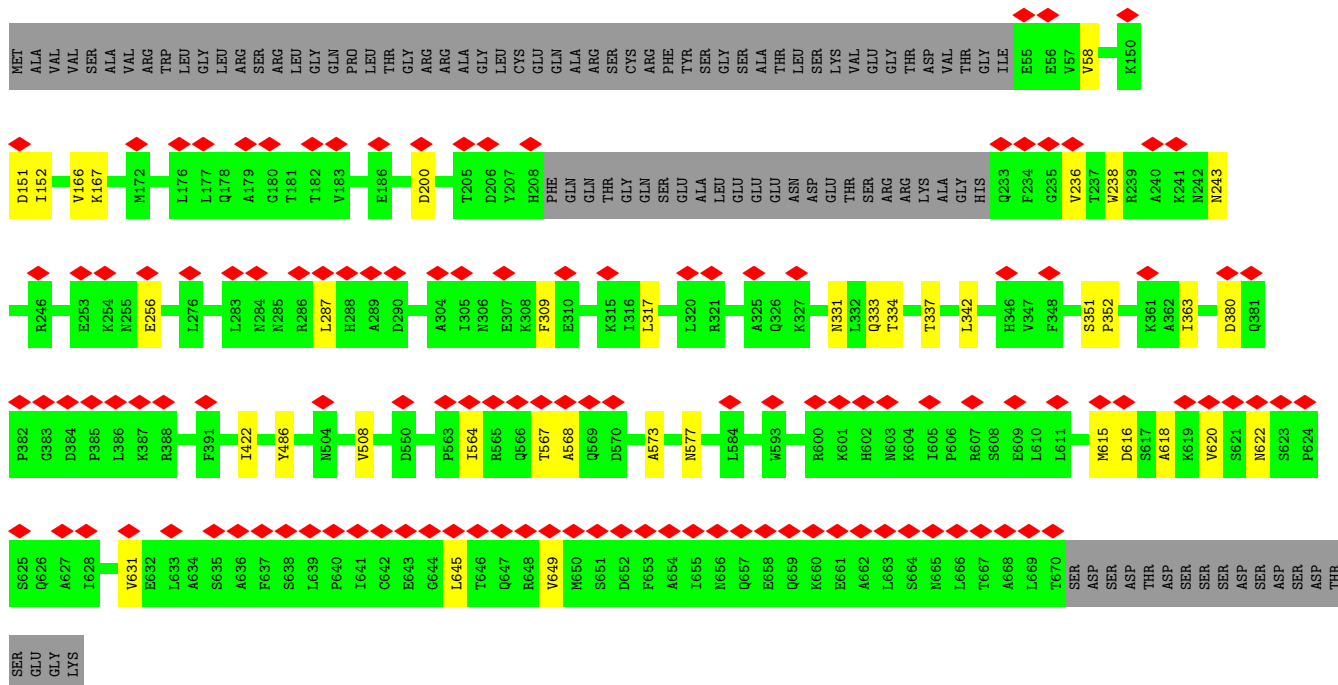
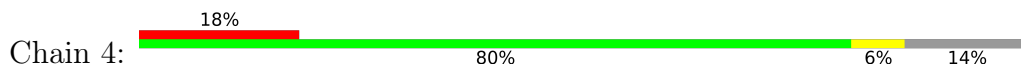
- Molecule 29: Coiled-coil-helix-coiled-coil-helix domain-containing protein 1



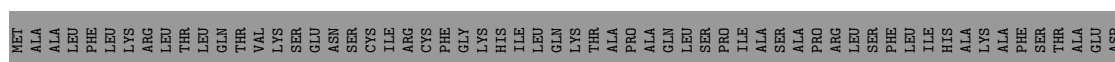
- Molecule 30: Aurora kinase A-interacting protein

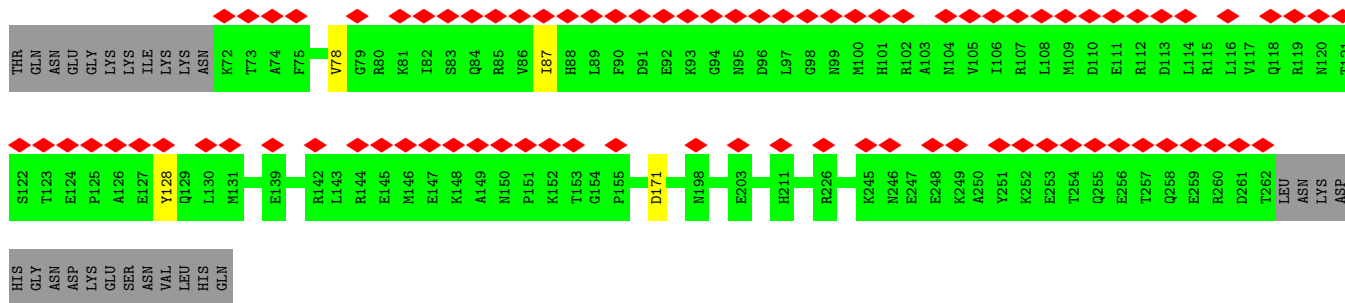


- Molecule 31: Pentatricopeptide repeat domain-containing protein 3, mitochondrial



- Molecule 32: Mitochondrial translational initiation factor 3, isoform CRA_a





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	45435	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	31	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	165000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.797	Depositor
Minimum map value	-0.770	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.033	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	388.8, 388.8, 388.8	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.648, 0.648, 0.648	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, B8T, 5MC, 5F0, 5MU, K, GDP, FES, MA6, ATP, AYA

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	0.26	0/22562	0.67	0/35124
2	B	0.25	0/1871	0.41	0/2531
3	C	0.26	0/1113	0.41	0/1505
4	D	0.25	0/2783	0.42	0/3724
5	E	0.25	0/989	0.42	0/1335
6	F	0.24	0/1767	0.36	0/2373
7	G	0.25	0/2729	0.39	0/3658
8	H	0.25	0/1178	0.42	0/1598
9	I	0.26	0/1030	0.43	0/1386
10	J	0.26	0/855	0.46	0/1148
11	K	0.23	0/880	0.41	0/1182
12	L	0.24	0/1477	0.36	0/1974
13	M	0.25	0/963	0.42	0/1295
14	N	0.25	0/886	0.45	0/1199
15	O	0.25	0/1648	0.40	0/2243
16	P	0.26	0/798	0.41	0/1070
17	Q	0.24	0/748	0.39	0/994
18	R	0.25	0/2456	0.38	0/3317
19	S	0.26	0/1138	0.39	0/1533
20	T	0.25	0/1402	0.40	0/1883
21	U	0.23	0/1510	0.37	0/2025
22	V	0.23	0/3030	0.35	0/4093
23	W	0.26	0/801	0.42	0/1079
24	X	0.24	0/2921	0.38	0/3954
25	Y	0.24	0/1280	0.37	0/1725
26	Z	0.25	0/857	0.39	0/1141
27	0	0.25	0/1834	0.41	0/2484
28	1	0.24	0/2285	0.38	0/3090
29	2	0.23	0/941	0.38	0/1257
30	3	0.24	0/640	0.38	0/844
31	4	0.24	0/4904	0.36	0/6636
32	8	0.23	0/1560	0.39	0/2089

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.25	0/71836	0.51	0/101489

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
9	I	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	I	184	5F0	Mainchain

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	20282	10313	10297	67	0
2	B	1828	1816	1815	8	0
3	C	1083	1089	1088	6	0
4	D	2731	2805	2804	9	0
5	E	972	1001	1000	2	0
6	F	1725	1770	1769	12	0
7	G	2672	2676	2673	9	0
8	H	1152	1184	1183	8	0
9	I	1020	1061	1053	5	0
10	J	839	888	887	3	0
11	K	862	886	885	4	0
12	L	1453	1541	1540	7	0
13	M	942	966	965	0	0
14	N	868	929	928	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	O	1592	1557	1557	4	0
16	P	781	807	806	2	0
17	Q	744	758	758	5	0
18	R	2409	2429	2428	10	0
19	S	1111	1116	1115	4	0
20	T	1371	1394	1393	4	0
21	U	1488	1500	1499	1	0
22	V	2969	2964	2961	15	0
23	W	789	803	802	0	0
24	X	2849	2845	2843	13	0
25	Y	1246	1198	1197	4	0
26	Z	839	860	858	3	0
27	0	1787	1797	1796	10	0
28	1	2238	2269	2269	6	0
29	2	935	969	971	8	0
30	3	629	702	702	2	0
31	4	4795	4798	4796	24	0
32	8	1543	1588	1587	4	0
33	3	1	0	0	0	0
33	A	68	0	0	0	0
33	B	1	0	0	0	0
33	X	1	0	0	0	0
34	A	20	0	0	0	0
35	O	1	0	0	0	0
36	P	4	0	0	0	0
36	T	4	0	0	0	0
37	X	31	12	12	0	0
38	X	28	12	12	0	0
39	0	18	0	0	1	0
39	1	14	0	0	1	0
39	2	10	0	0	0	0
39	3	11	0	0	0	0
39	4	3	0	0	0	0
39	A	762	0	0	12	0
39	B	39	0	0	1	0
39	C	29	0	0	2	0
39	D	29	0	0	0	0
39	E	8	0	0	0	0
39	F	6	0	0	1	0
39	G	29	0	0	1	0
39	H	25	0	0	1	0
39	I	12	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
39	J	6	0	0	0	0
39	K	27	0	0	0	0
39	L	7	0	0	0	0
39	M	23	0	0	0	0
39	N	10	0	0	0	0
39	O	16	0	0	0	0
39	P	11	0	0	0	0
39	Q	15	0	0	0	0
39	R	8	0	0	0	0
39	S	11	0	0	0	0
39	T	9	0	0	0	0
39	U	3	0	0	0	0
39	W	8	0	0	0	0
39	X	5	0	0	0	0
39	Y	5	0	0	0	0
39	Z	14	0	0	0	0
All	All	69876	59303	59249	216	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 2.

The worst 5 of 216 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1294:A:OP1	2:B:201:ASN:ND2	2.13	0.82
1:A:1342:C:OP2	26:Z:96:LYS:NZ	2.23	0.71
1:A:1021:U:OP2	29:2:9:ARG:NH2	2.23	0.70
15:O:54:GLU:OE1	15:O:57:LYS:NZ	2.24	0.69
22:V:39:LYS:NZ	22:V:376:GLU:OE2	2.25	0.69

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	223/296 (75%)	222 (100%)	1 (0%)	0	100	100
3	C	130/167 (78%)	127 (98%)	3 (2%)	0	100	100
4	D	341/430 (79%)	334 (98%)	7 (2%)	0	100	100
5	E	120/125 (96%)	120 (100%)	0	0	100	100
6	F	206/242 (85%)	204 (99%)	2 (1%)	0	100	100
7	G	321/396 (81%)	316 (98%)	5 (2%)	0	100	100
8	H	138/201 (69%)	136 (99%)	1 (1%)	1 (1%)	22	53
9	I	134/194 (69%)	132 (98%)	2 (2%)	0	100	100
10	J	106/138 (77%)	104 (98%)	2 (2%)	0	100	100
11	K	99/128 (77%)	98 (99%)	1 (1%)	0	100	100
12	L	172/257 (67%)	172 (100%)	0	0	100	100
13	M	117/137 (85%)	117 (100%)	0	0	100	100
14	N	108/130 (83%)	108 (100%)	0	0	100	100
15	O	191/258 (74%)	189 (99%)	2 (1%)	0	100	100
16	P	95/142 (67%)	94 (99%)	1 (1%)	0	100	100
17	Q	84/86 (98%)	84 (100%)	0	0	100	100
18	R	293/360 (81%)	286 (98%)	7 (2%)	0	100	100
19	S	133/190 (70%)	132 (99%)	1 (1%)	0	100	100
20	T	166/173 (96%)	164 (99%)	2 (1%)	0	100	100
21	U	174/205 (85%)	174 (100%)	0	0	100	100
22	V	358/414 (86%)	355 (99%)	3 (1%)	0	100	100
23	W	98/187 (52%)	97 (99%)	1 (1%)	0	100	100
24	X	350/398 (88%)	346 (99%)	4 (1%)	0	100	100
25	Y	147/395 (37%)	146 (99%)	1 (1%)	0	100	100
26	Z	98/106 (92%)	97 (99%)	1 (1%)	0	100	100
27	0	213/218 (98%)	212 (100%)	1 (0%)	0	100	100
28	1	274/323 (85%)	271 (99%)	3 (1%)	0	100	100
29	2	115/117 (98%)	115 (100%)	0	0	100	100
30	3	69/199 (35%)	68 (99%)	1 (1%)	0	100	100
31	4	588/689 (85%)	581 (99%)	7 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	8	189/278 (68%)	186 (98%)	3 (2%)	0	100	100
All	All	5850/7579 (77%)	5787 (99%)	62 (1%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	H	126	ILE

5.3.2 Protein sidechains [i](#)

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

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	198/249 (80%)	198 (100%)	0	100	100
3	C	115/143 (80%)	115 (100%)	0	100	100
4	D	286/357 (80%)	286 (100%)	0	100	100
5	E	104/107 (97%)	104 (100%)	0	100	100
6	F	185/209 (88%)	185 (100%)	0	100	100
7	G	284/342 (83%)	283 (100%)	1 (0%)	91	97
8	H	130/180 (72%)	130 (100%)	0	100	100
9	I	104/146 (71%)	104 (100%)	0	100	100
10	J	93/118 (79%)	93 (100%)	0	100	100
11	K	91/113 (80%)	91 (100%)	0	100	100
12	L	158/226 (70%)	158 (100%)	0	100	100
13	M	97/113 (86%)	97 (100%)	0	100	100
14	N	96/115 (84%)	96 (100%)	0	100	100
15	O	174/230 (76%)	174 (100%)	0	100	100
16	P	88/123 (72%)	88 (100%)	0	100	100
17	Q	78/78 (100%)	78 (100%)	0	100	100
18	R	264/318 (83%)	264 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	S	116/164 (71%)	116 (100%)	0	100	100
20	T	153/157 (98%)	153 (100%)	0	100	100
21	U	152/174 (87%)	152 (100%)	0	100	100
22	V	325/364 (89%)	324 (100%)	1 (0%)	92	98
23	W	87/158 (55%)	87 (100%)	0	100	100
24	X	311/351 (89%)	309 (99%)	2 (1%)	86	95
25	Y	137/357 (38%)	137 (100%)	0	100	100
26	Z	90/95 (95%)	90 (100%)	0	100	100
27	0	188/190 (99%)	188 (100%)	0	100	100
28	1	254/291 (87%)	253 (100%)	1 (0%)	91	97
29	2	100/100 (100%)	100 (100%)	0	100	100
30	3	65/166 (39%)	65 (100%)	0	100	100
31	4	529/609 (87%)	528 (100%)	1 (0%)	93	98
32	8	172/247 (70%)	172 (100%)	0	100	100
All	All	5224/6590 (79%)	5218 (100%)	6 (0%)	93	98

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	X	394	HIS
28	1	305	ASN
31	4	486	TYR
22	V	226	TYR
7	G	389	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
24	X	385	ASN
25	Y	290	ASN
32	8	118	GLN
31	4	257	HIS
31	4	295	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	951/955 (99%)	118 (12%)	0

5 of 118 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	649	A
1	A	651	A
1	A	680	U
1	A	688	A
1	A	704	U

There are no RNA pucker outliers to report.

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

8 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\# Z > 2$
17	AYA	Q	2	17	6,7,8	0.76	0	5,8,10	0.52	0
1	5MU	A	1076	1	19,22,23	0.30	0	28,32,35	0.29	0
1	MA6	A	1583	1	18,26,27	0.75	0	19,38,41	0.60	0
1	MA6	A	1584	1	18,26,27	0.76	0	19,38,41	0.57	0
29	AYA	2	2	29	6,7,8	0.79	0	5,8,10	0.57	0
9	5F0	I	184	9	8,8,9	0.60	0	7,9,11	1.10	1 (14%)
1	5MC	A	1488	1	18,22,23	0.33	0	26,32,35	0.45	0
1	B8T	A	1486	1	19,22,23	0.32	0	26,31,34	0.33	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
17	AYA	Q	2	17	-	0/4/6/8	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	5MU	A	1076	1	-	0/7/25/26	0/2/2/2
1	MA6	A	1583	1	-	0/7/29/30	0/3/3/3
1	MA6	A	1584	1	-	2/7/29/30	0/3/3/3
29	AYA	2	2	29	-	0/4/6/8	-
9	5F0	I	184	9	-	0/9/9/10	-
1	5MC	A	1488	1	-	0/7/25/26	0/2/2/2
1	B8T	A	1486	1	-	0/7/27/28	0/2/2/2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	I	184	5F0	O-C-CB	-2.37	118.53	125.43

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1584	MA6	C5-C6-N6-C9
1	A	1584	MA6	C4'-C5'-O5'-P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1584	MA6	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 96 ligands modelled in this entry, 92 are monoatomic - leaving 4 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
36	FES	T	201	20,13	0,4,4	-	-	-		
38	GDP	X	502	-	24,30,30	0.87	1 (4%)	30,47,47	0.63	0
36	FES	P	201	16,5	0,4,4	-	-	-		
37	ATP	X	501	33	26,33,33	0.76	0	31,52,52	0.63	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
36	FES	T	201	20,13	-	-	0/1/1/1
38	GDP	X	502	-	-	0/12/32/32	0/3/3/3
36	FES	P	201	16,5	-	-	0/1/1/1
37	ATP	X	501	33	-	0/18/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	X	502	GDP	C5-C6	-2.09	1.43	1.47

There are no bond angle outliers.

There are no chirality outliers.

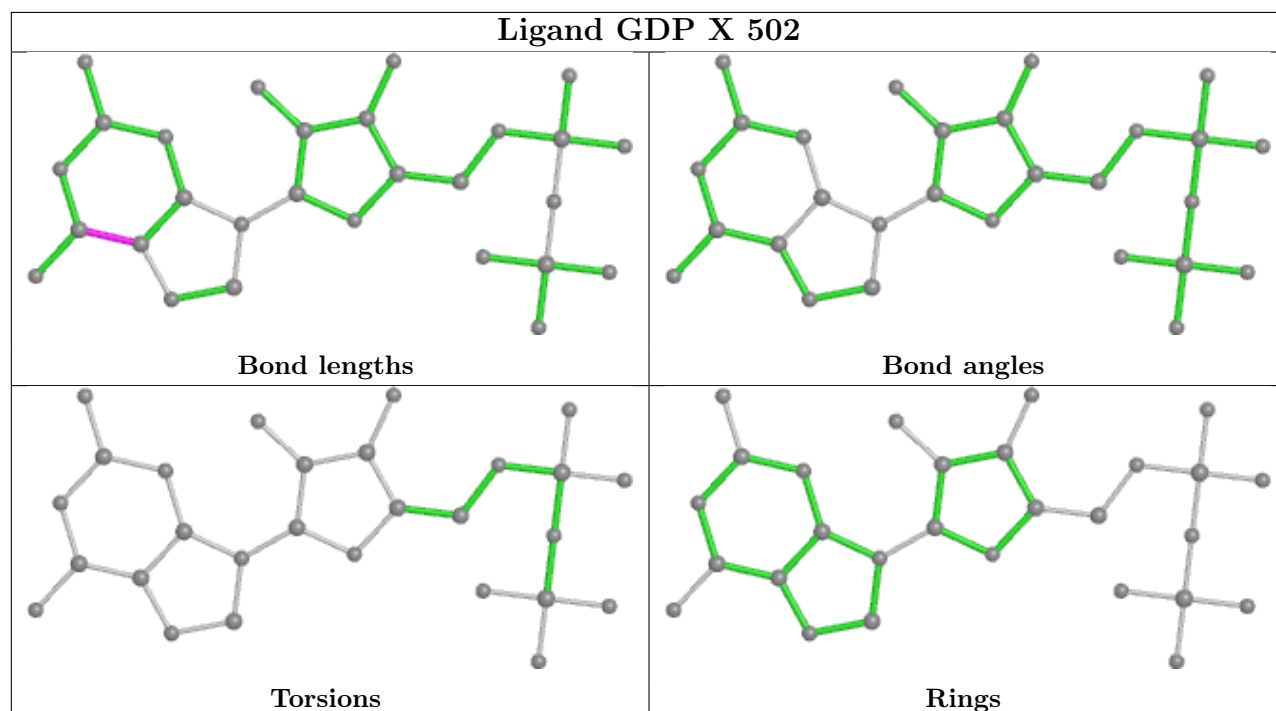
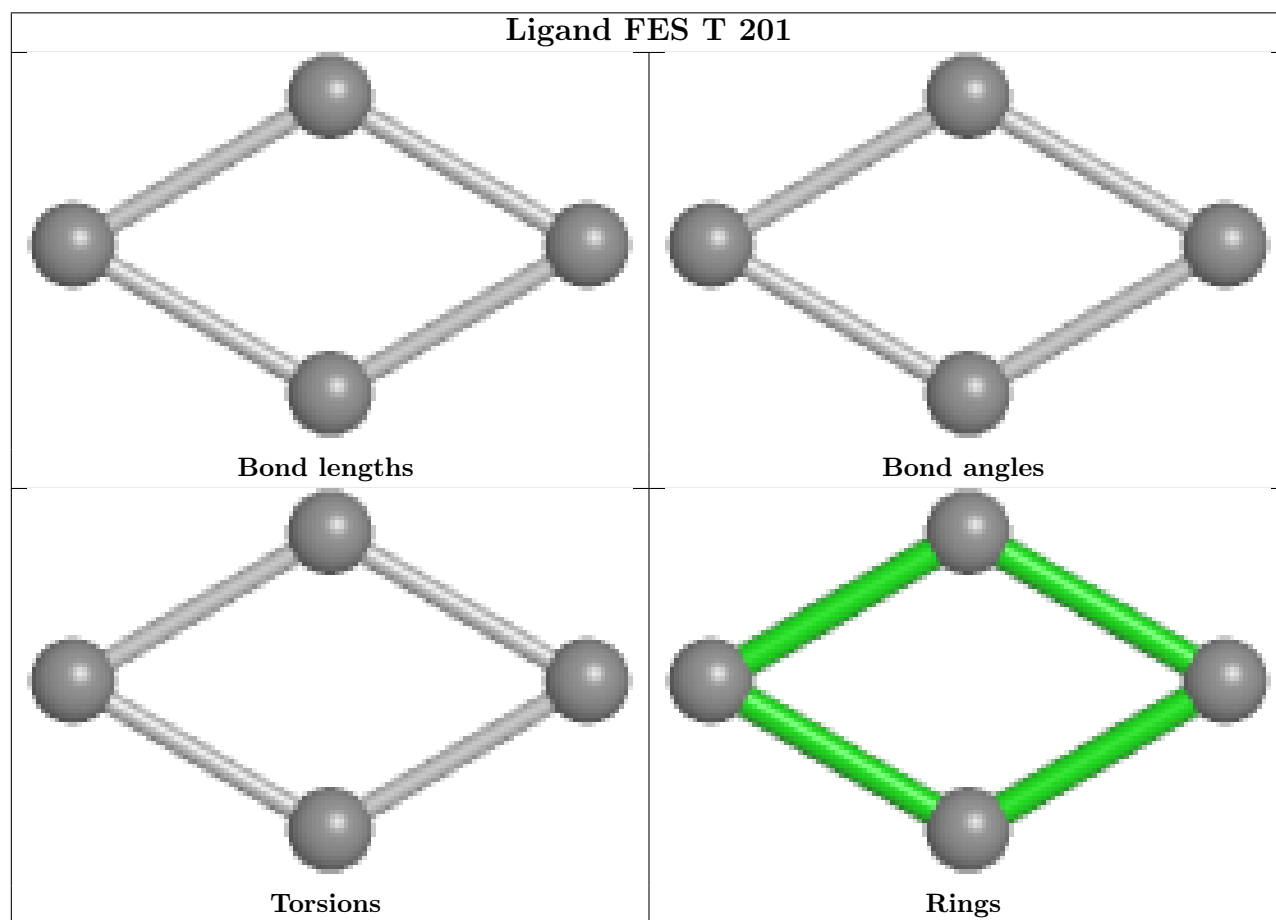
There are no torsion outliers.

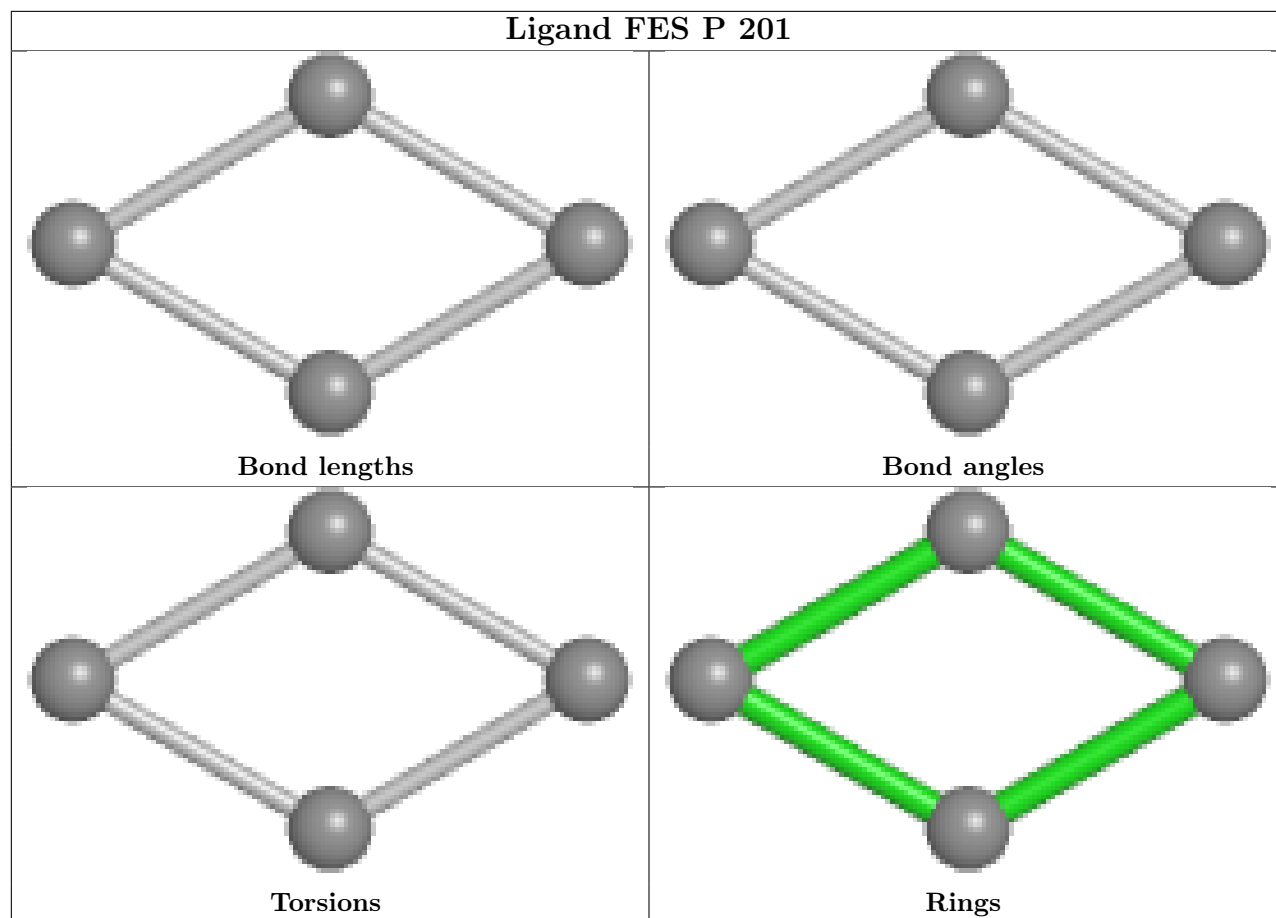
There are no ring outliers.

No monomer is involved in short contacts.

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.

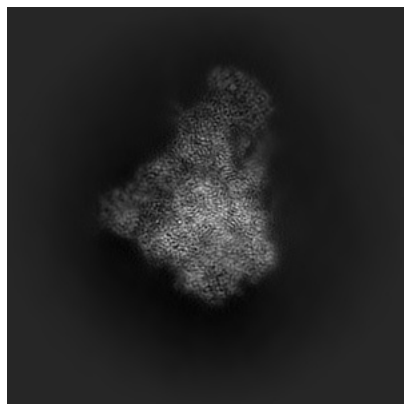
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13559. These allow visual inspection of the internal detail of the map and identification of artifacts.

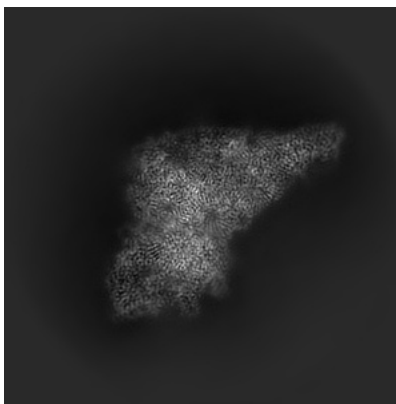
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

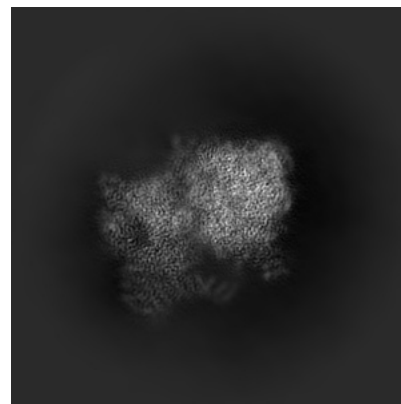
6.1.1 Primary map



X

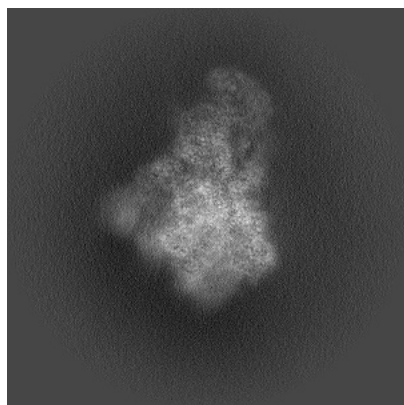


Y

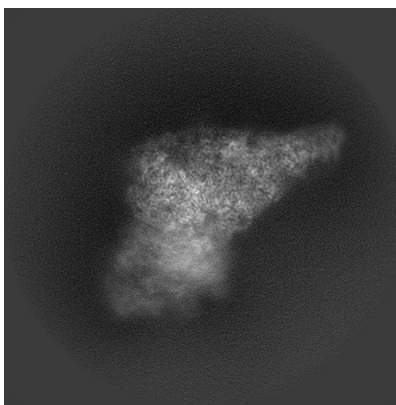


Z

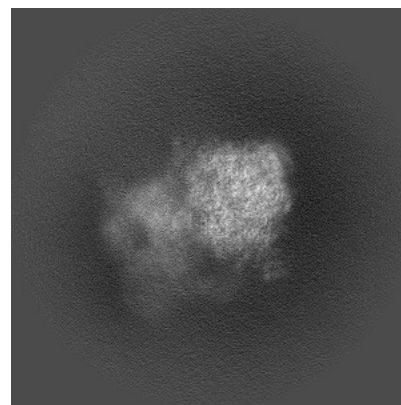
6.1.2 Raw map



X



Y

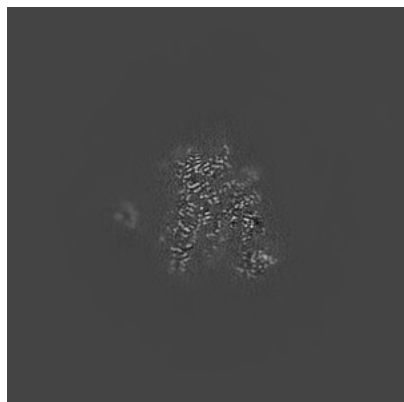


Z

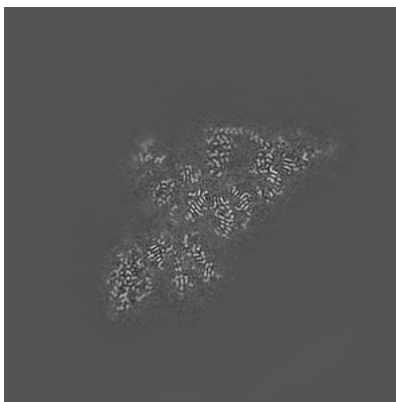
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

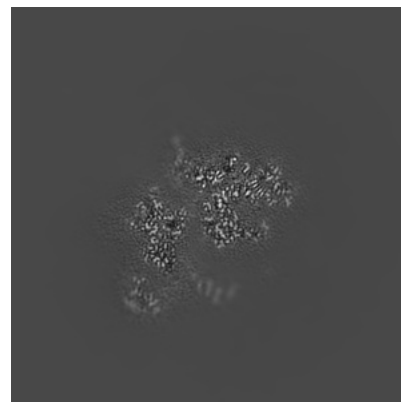
6.2.1 Primary map



X Index: 300

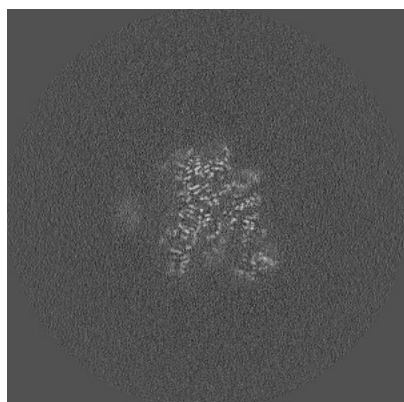


Y Index: 300

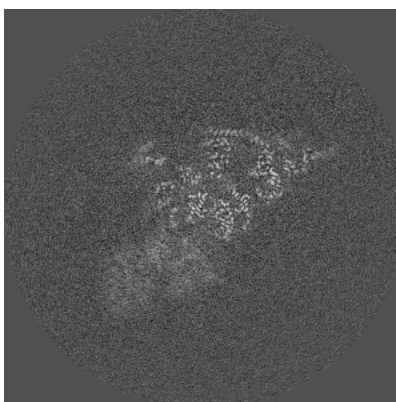


Z Index: 300

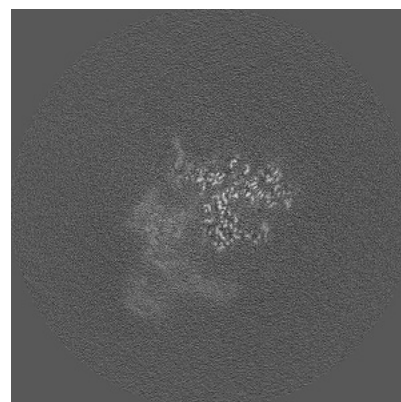
6.2.2 Raw map



X Index: 240



Y Index: 240

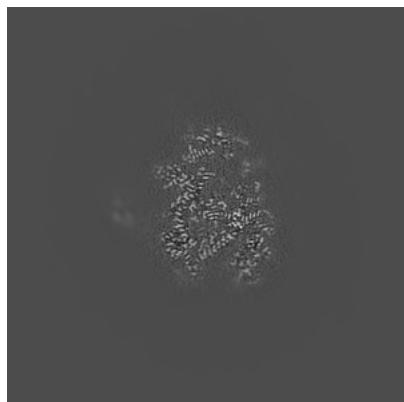


Z Index: 240

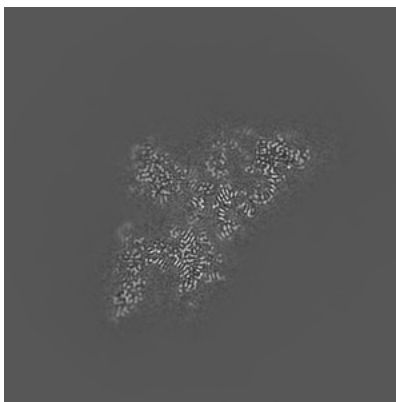
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

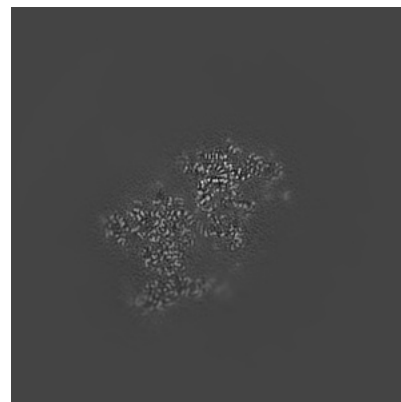
6.3.1 Primary map



X Index: 323

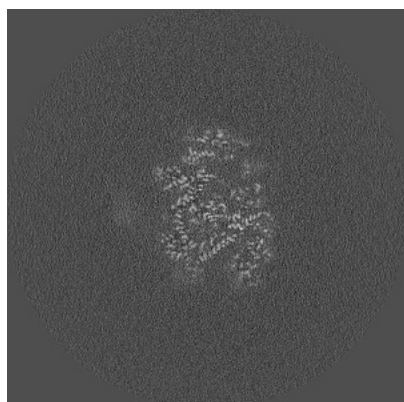


Y Index: 291

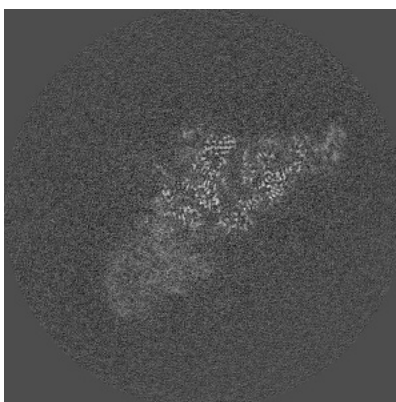


Z Index: 276

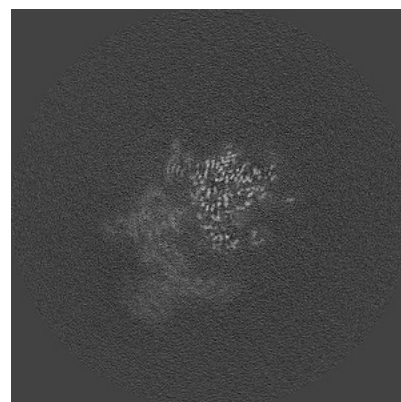
6.3.2 Raw map



X Index: 258



Y Index: 254

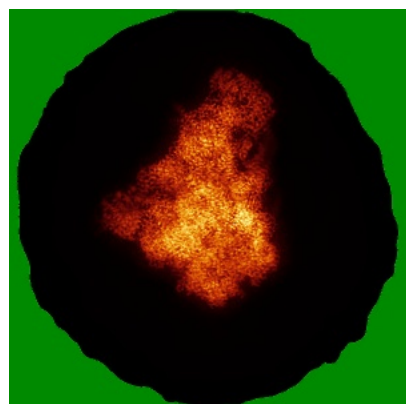


Z Index: 231

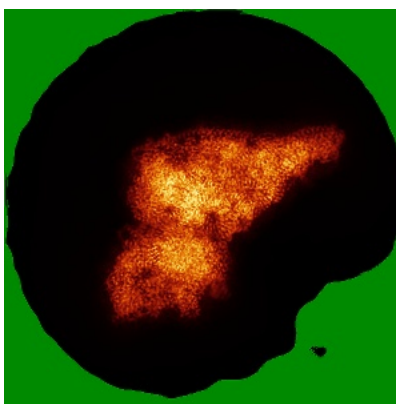
The images above show the largest variance slices of the map in three orthogonal directions.

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

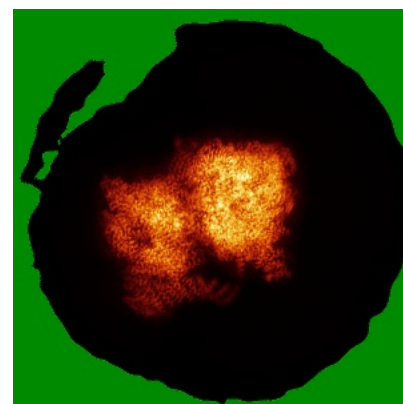
6.4.1 Primary map



X

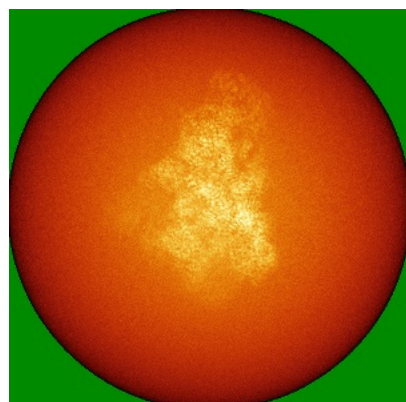


Y

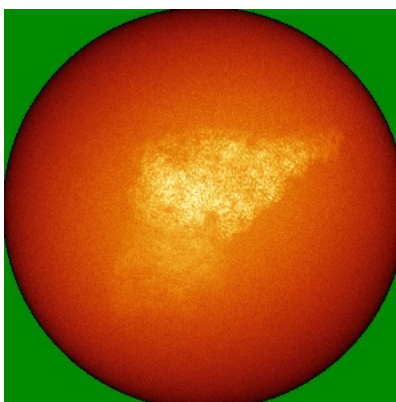


Z

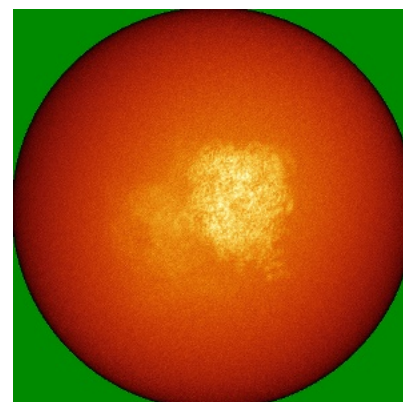
6.4.2 Raw map



X



Y

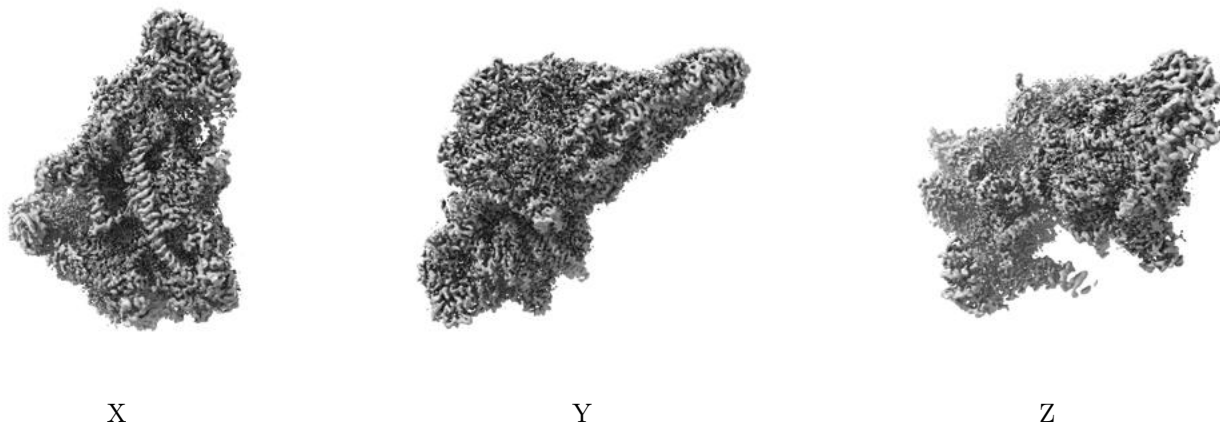


Z

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.

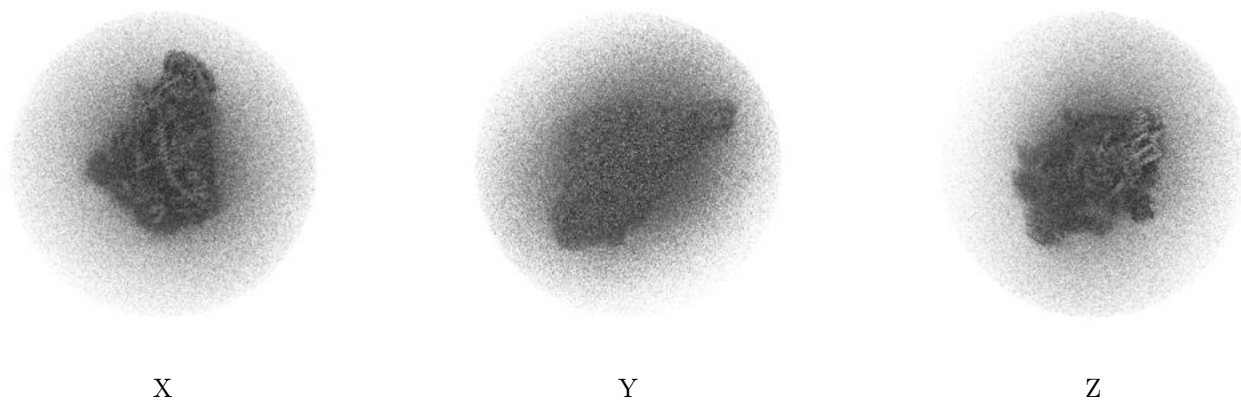
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.12. 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.

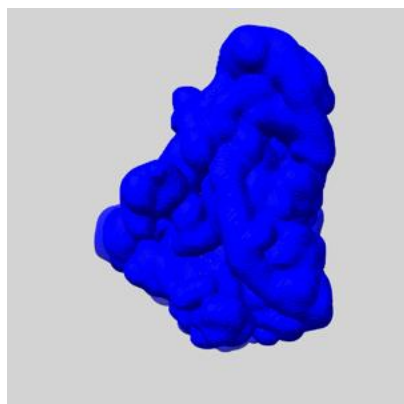
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

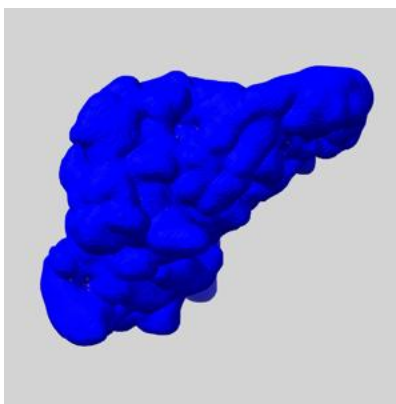
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

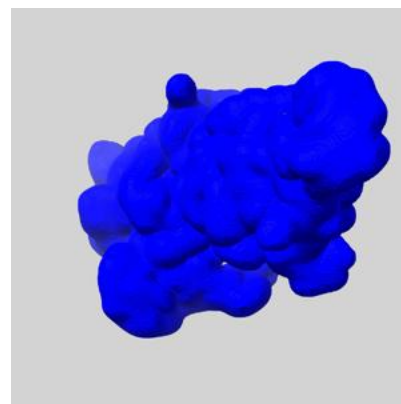
6.6.1 emd_13559_msk_1.map [i](#)



X



Y

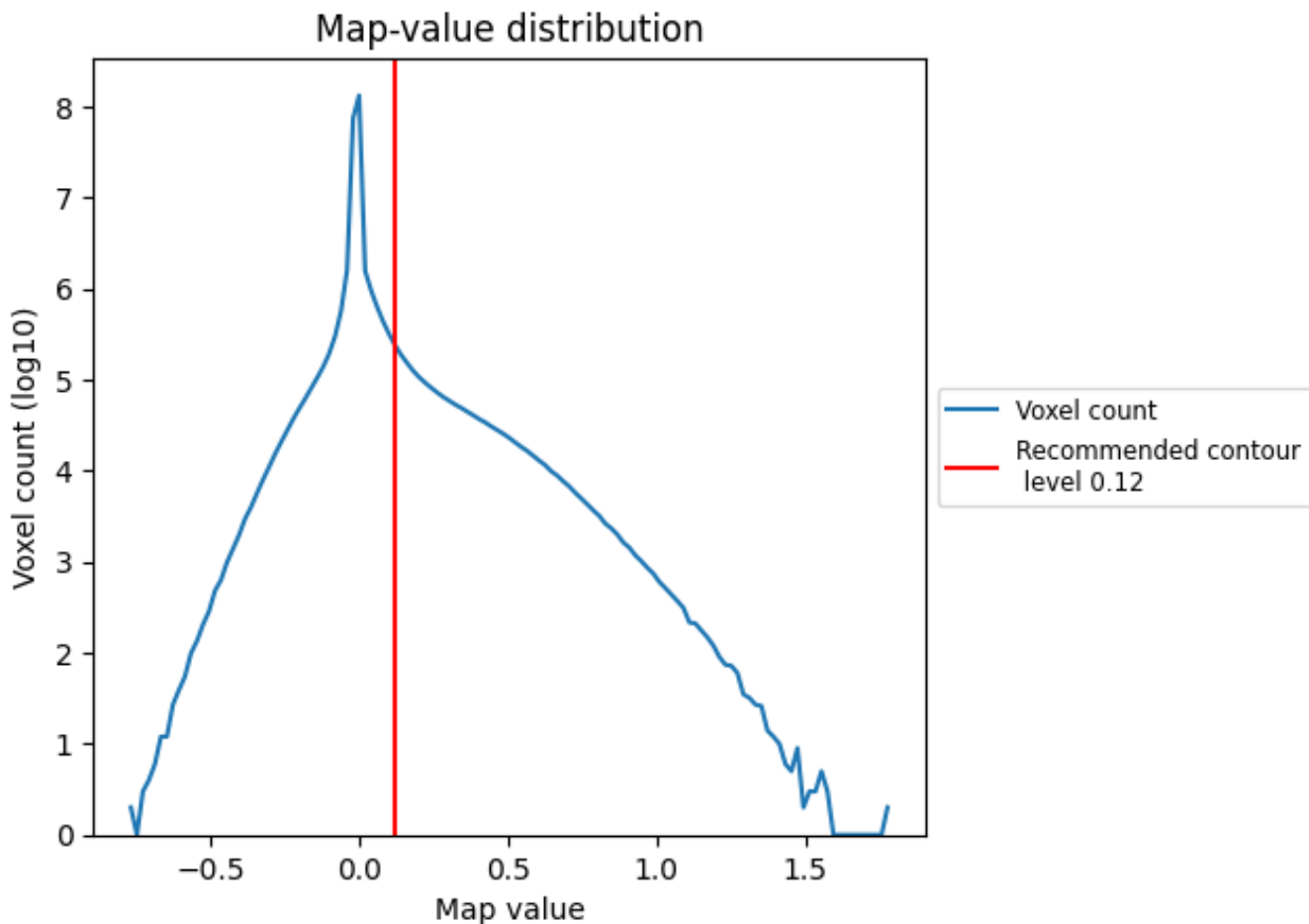


Z

7 Map analysis [i](#)

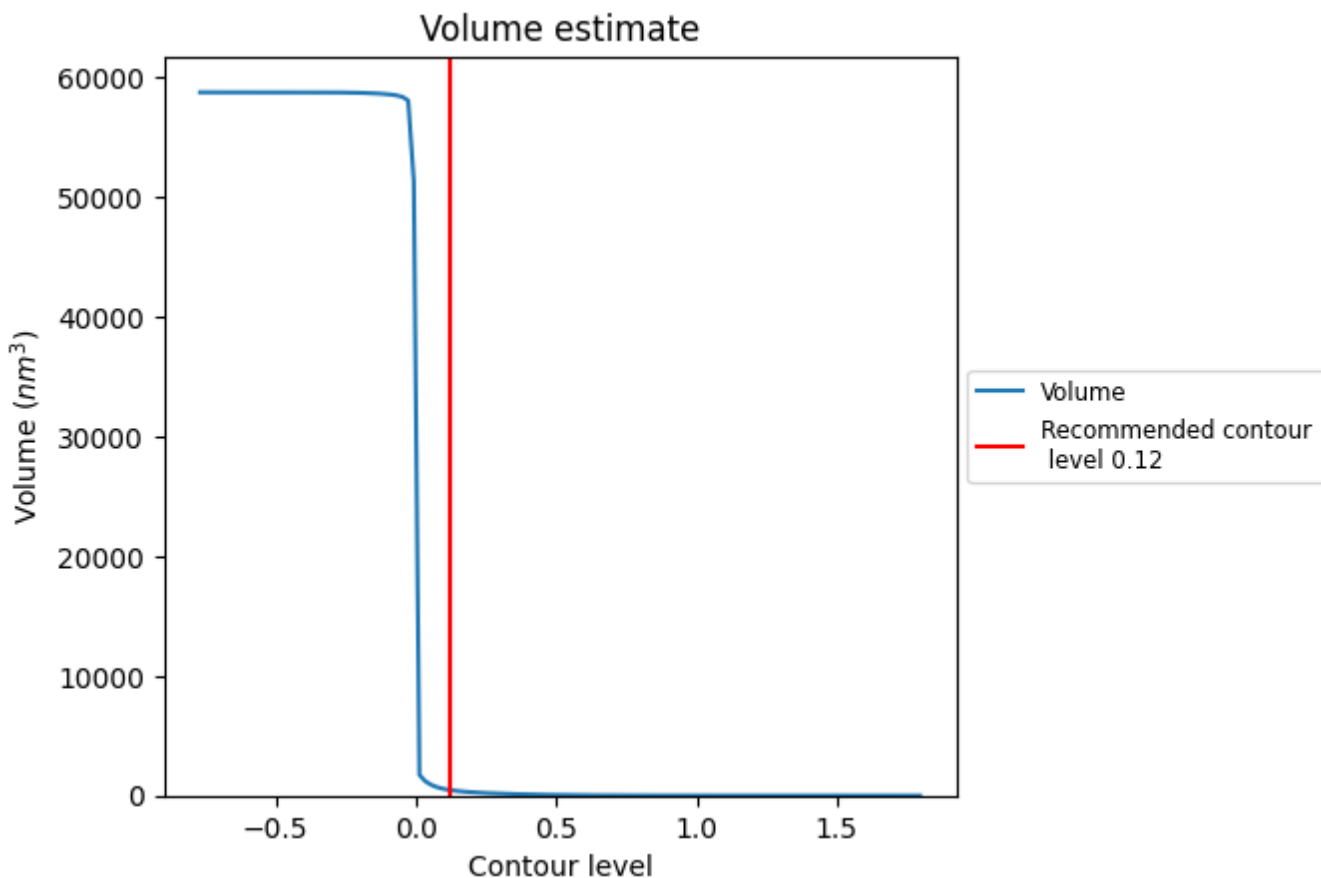
This section contains the results of statistical analysis of the map.

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.

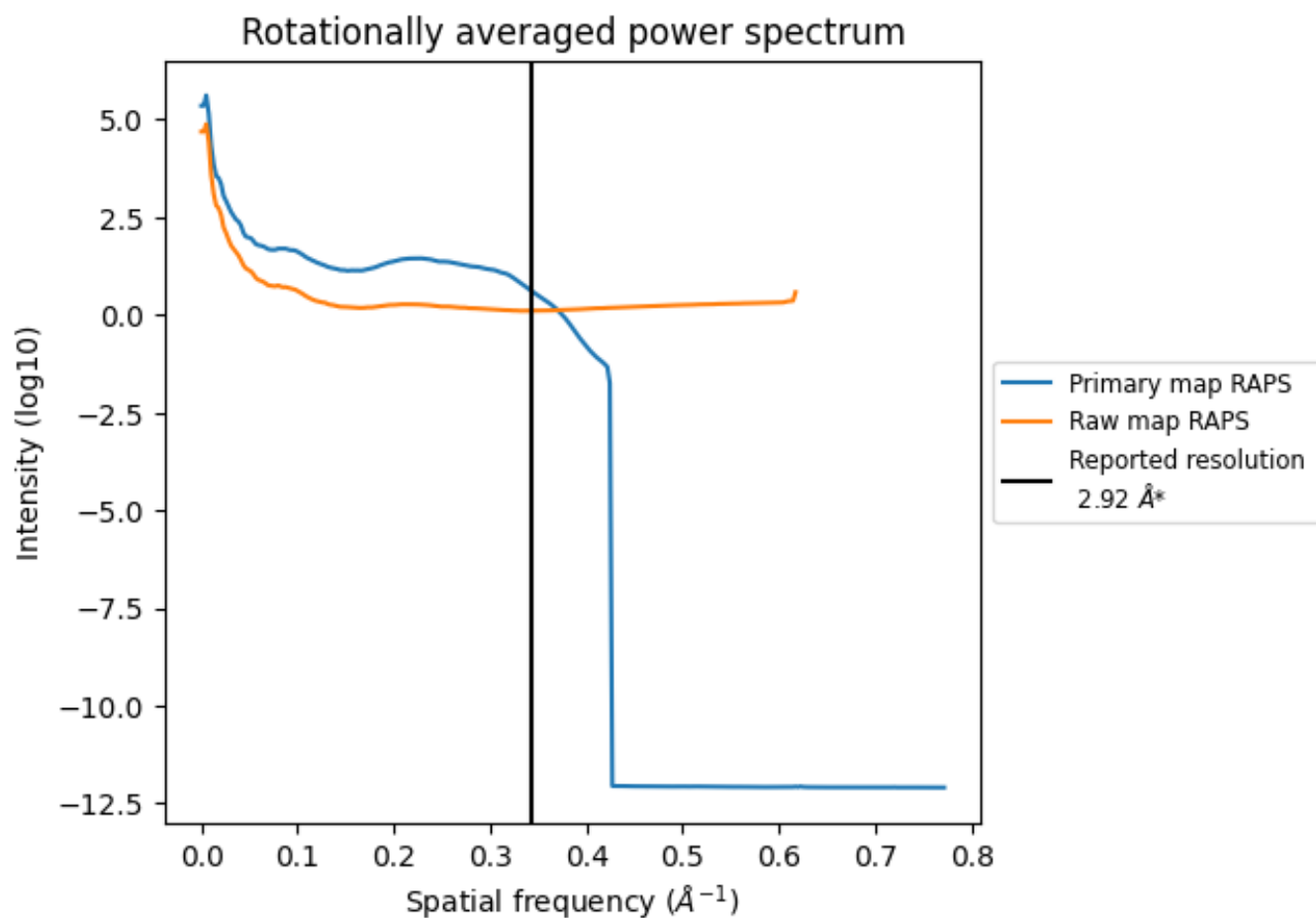
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 465 nm³; this corresponds to an approximate mass of 420 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

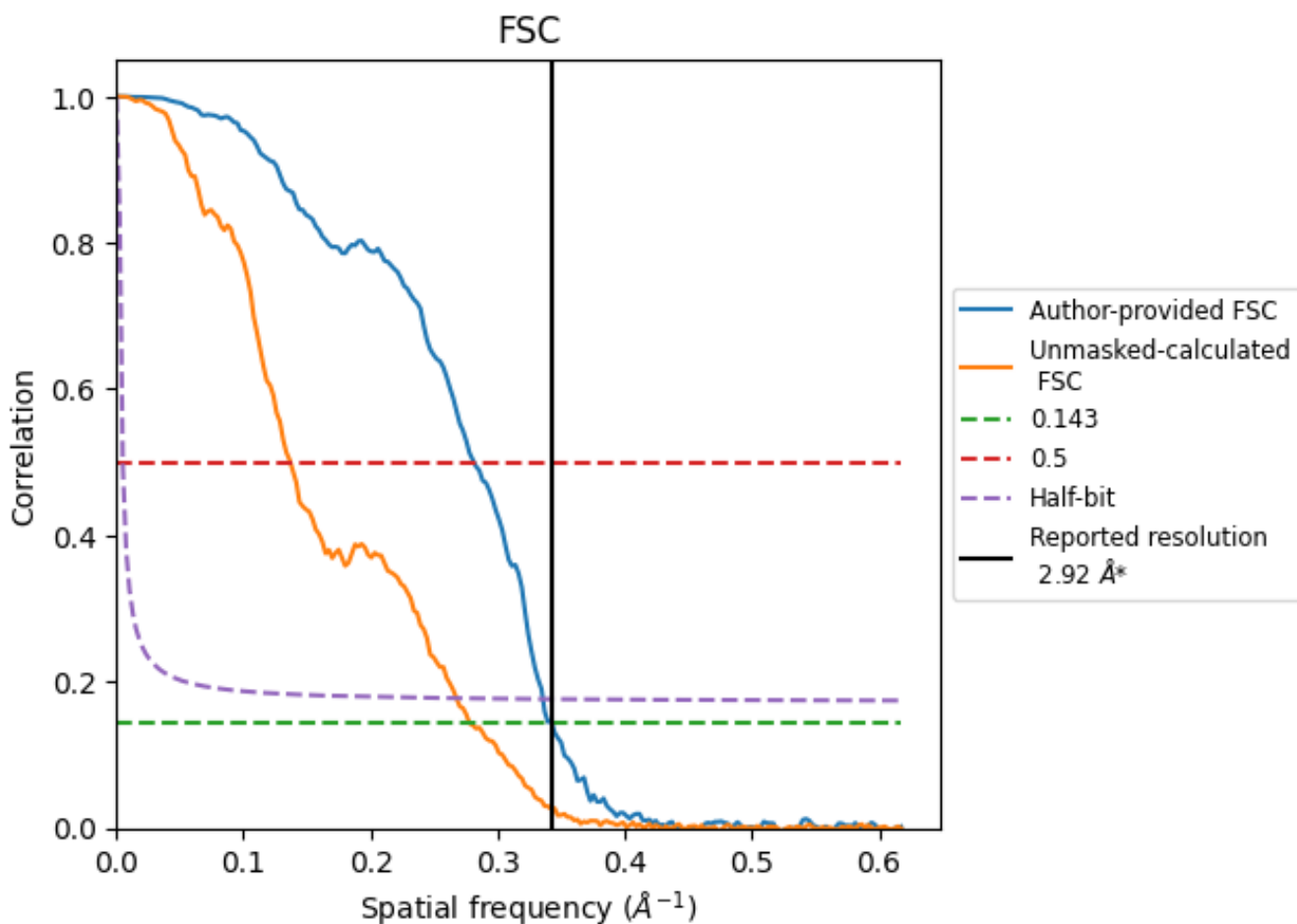


*Reported resolution corresponds to spatial frequency of 0.342 Å⁻¹

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 0.342 Å⁻¹

8.2 Resolution estimates [i](#)

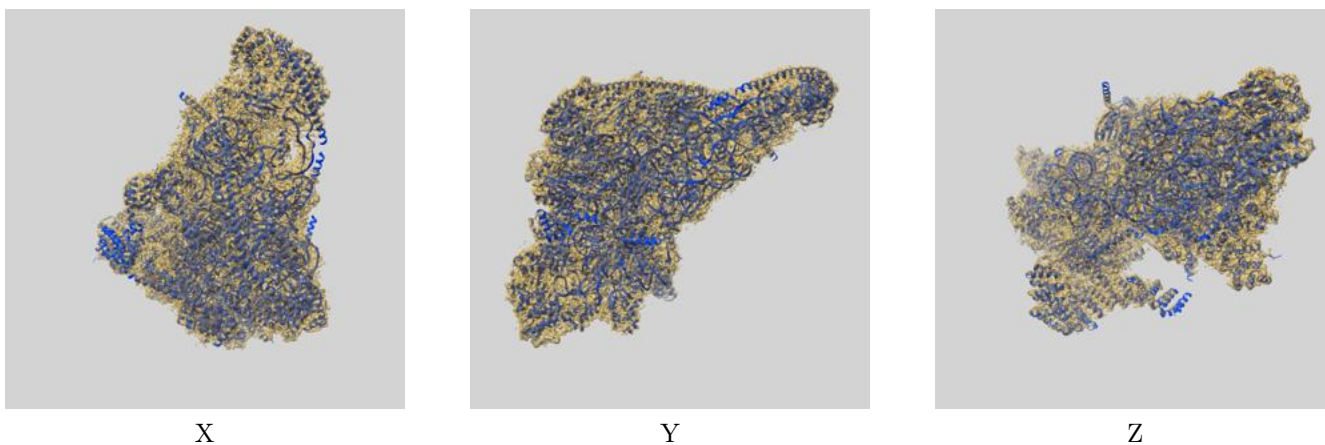
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.92	-	-
Author-provided FSC curve	2.92	3.56	2.98
Unmasked-calculated*	3.60	7.31	3.74

*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 3.60 differs from the reported value 2.92 by more than 10 %

9 Map-model fit [i](#)

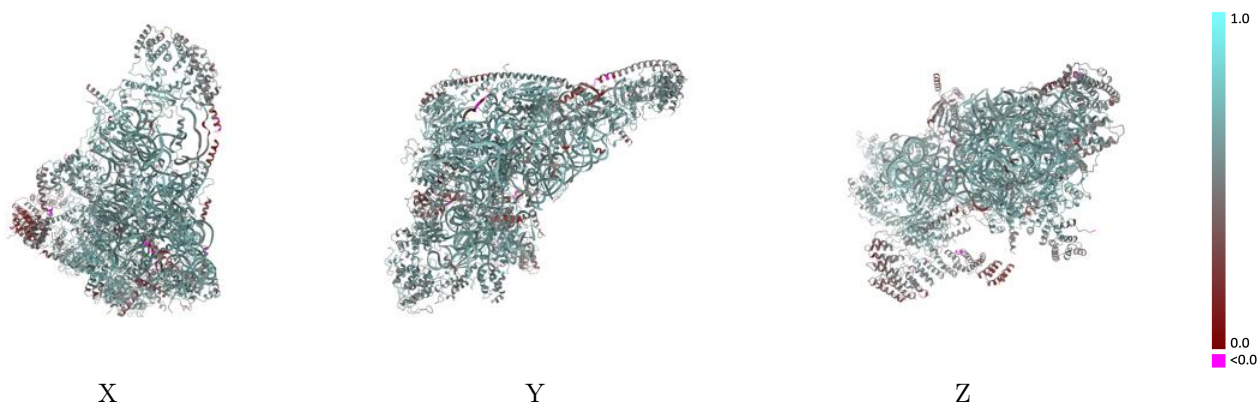
This section contains information regarding the fit between EMDB map EMD-13559 and PDB model 7PO1. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



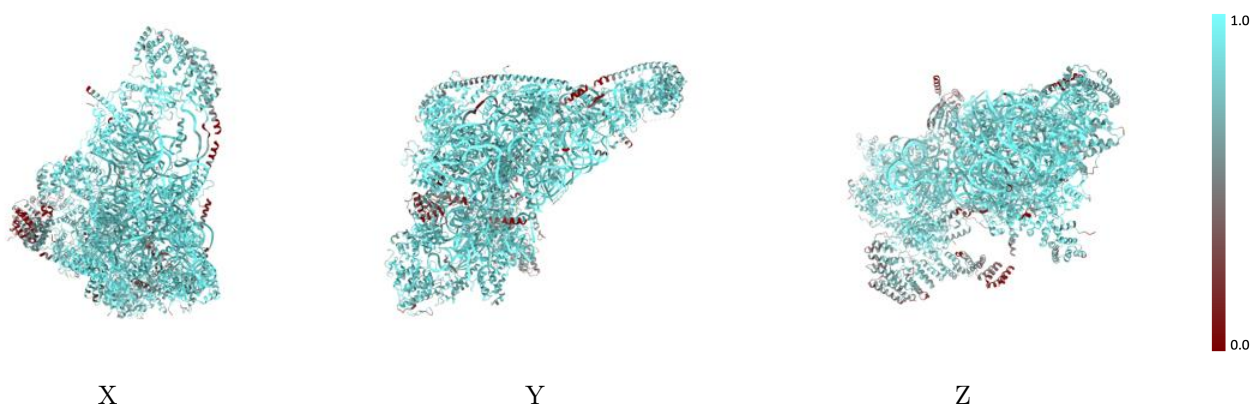
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



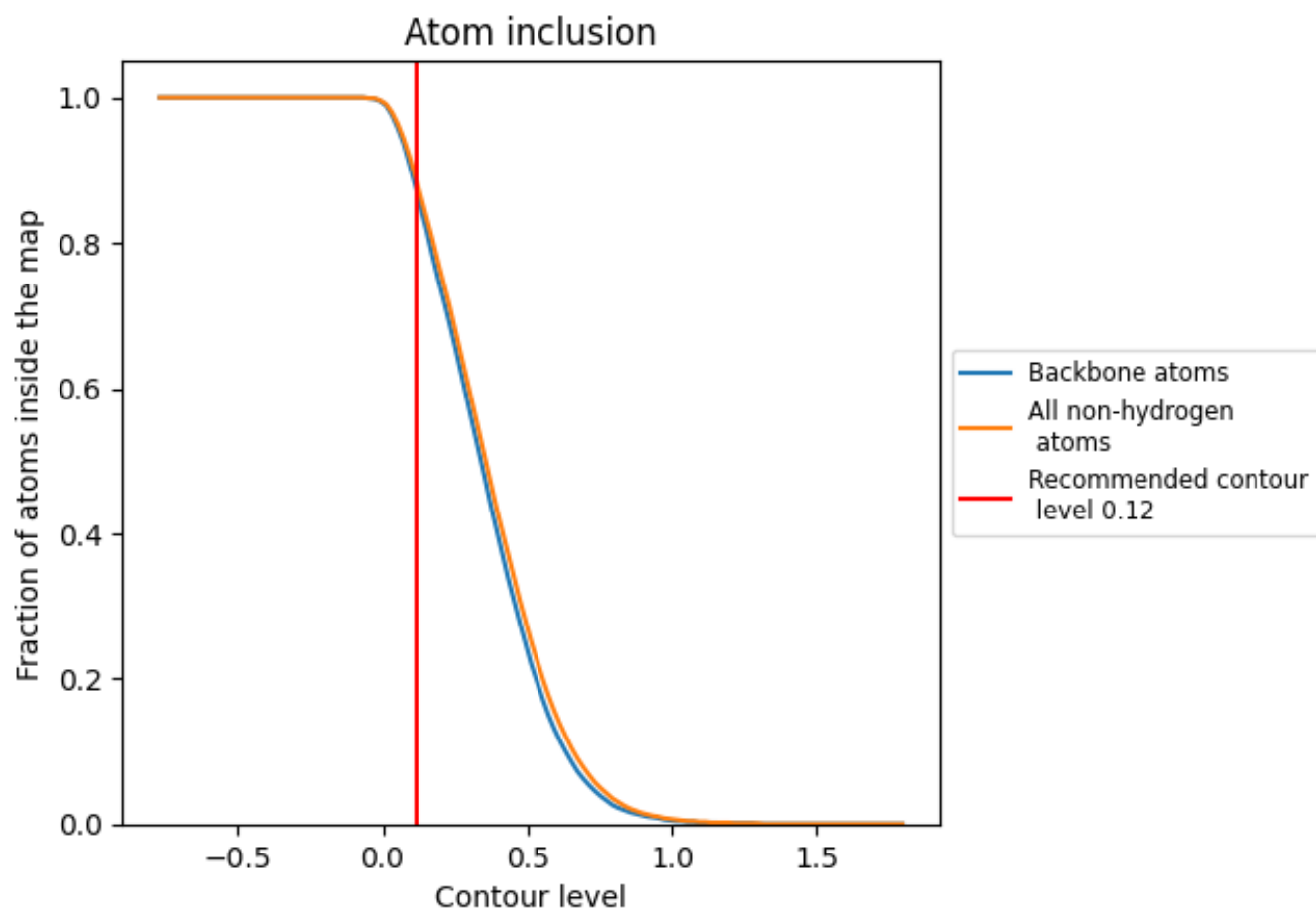
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.12).



































































9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 88% 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 (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8820	 0.5780
0	 0.9020	 0.5830
1	 0.8340	 0.5610
2	 0.7140	 0.4790
3	 0.9100	 0.5980
4	 0.6340	 0.4420
8	 0.4530	 0.4080
A	 0.9630	 0.6220
B	 0.9380	 0.6330
C	 0.9690	 0.6560
D	 0.8920	 0.5840
E	 0.9110	 0.5980
F	 0.8300	 0.5330
G	 0.8400	 0.5640
H	 0.9030	 0.6060
I	 0.9080	 0.5900
J	 0.9250	 0.5940
K	 0.9610	 0.6520
L	 0.8500	 0.5660
M	 0.9200	 0.6300
N	 0.9340	 0.6340
O	 0.9260	 0.6100
P	 0.9200	 0.6110
Q	 0.9620	 0.6410
R	 0.8620	 0.5660
S	 0.8520	 0.5540
T	 0.9130	 0.6090
U	 0.8130	 0.5350
V	 0.7930	 0.5200
W	 0.9270	 0.6110
X	 0.8700	 0.5680
Y	 0.7390	 0.5160
Z	 0.8750	 0.5690

