



Full wwPDB EM Validation Report ⓘ

Apr 1, 2025 – 09:21 pm BST

PDB ID : 6ZIQ / pdb_00006ziq
EMDB ID : EMD-11228
Title : bovine ATP synthase stator domain, state 1
Authors : Spikes, T.E.; Montgomery, M.G.; Walker, J.E.
Deposited on : 2020-06-26
Resolution : 4.33 Å (reported)
Based on initial models : 2V7Q, 2CLY, 2WSS

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.dev117
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

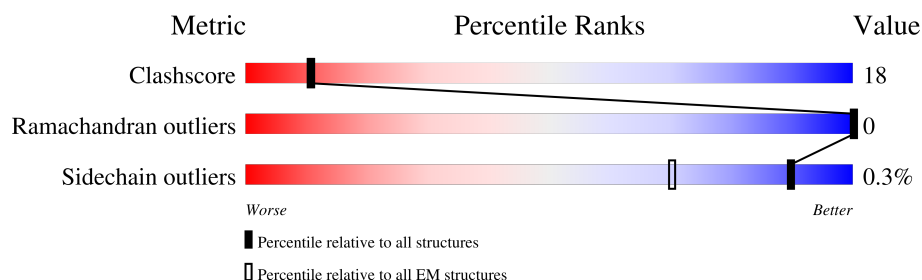
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.33 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	8	66	<div> <div>14%</div> <div>45%</div> <div>17%</div> <div>38%</div> </div>
2	a	226	<div> <div>21%</div> <div>100%</div> </div>
3	d	160	<div> <div>19%</div> <div>96%</div> <div>..</div> </div>
4	e	70	<div> <div>30%</div> <div>57%</div> <div>41%</div> </div>
5	f	87	<div> <div>25%</div> <div>95%</div> <div>5%</div> </div>
6	g	102	<div> <div>40%</div> <div>77%</div> <div>23%</div> </div>
7	j	60	<div> <div>53%</div> <div>80%</div> <div>20%</div> </div>
8	k	57	<div> <div>58%</div> <div>63%</div> <div>37%</div> </div>

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Mol	Chain	Length	Quality of chain
9	M	75	<div><div>52%</div><div><div></div><div></div><div></div><div></div></div><div>60%</div><div>31%</div><div>9%</div></div>
9	N	75	<div><div>51%</div><div><div></div><div></div><div></div><div></div></div><div>60%</div><div>39%</div><div>.</div></div>
9	O	75	<div><div>51%</div><div><div></div><div></div><div></div><div></div></div><div>36%</div><div>20%</div><div>.</div><div>41%</div></div>
10	b	214	<div><div>6%</div><div><div></div><div></div><div></div><div></div></div><div>97%</div><div>.</div></div>
11	h	76	<div><div>21%</div><div><div></div><div></div><div></div><div></div></div><div>82%</div><div>18%</div></div>
12	S	190	<div><div>21%</div><div><div></div><div></div><div></div><div></div></div><div>40%</div><div>28%</div><div>32%</div></div>
13	C	510	<div><div>6%</div><div><div></div><div></div><div></div><div></div></div><div>10%</div><div>7%</div><div>83%</div></div>

2 Entry composition [i](#)

There are 13 unique types of molecules in this entry. The entry contains 22312 atoms, of which 11373 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 protein 8.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	8	41	Total	C	H	N	O	S	0	0
			696	231	352	52	58	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
2	a	226	Total	C	H	N	O	S	0	0
			3611	1155	1870	276	298	12		

- Molecule 3 is a protein called ATP synthase subunit d, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	d	155	Total	C	H	N	O	S	0	0
			2549	821	1276	207	242	3		

- Molecule 4 is a protein called ATP synthase subunit e, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	e	41	Total	C	H	N	O	S	0	0
			687	218	352	61	55	1		

- Molecule 5 is a protein called ATP synthase subunit f, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	f	83	Total	C	H	N	O	S	0	0
			1411	456	718	120	114	3		

- Molecule 6 is a protein called ATP synthase subunit g, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	g	79	Total	C	H	N	O	S	0	0
			1291	420	662	100	108	1		

- Molecule 7 is a protein called ATP synthase subunit ATP5MPL, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	j	48	Total	C	H	N	O	S	0	0
			828	267	428	66	65	2		

- Molecule 8 is a protein called ATP synthase membrane subunit DAPIT, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	k	36	Total	C	H	N	O	S	0	0
			596	192	307	47	48	2		

- Molecule 9 is a protein called ATP synthase F(0) complex subunit C1, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	M	68	Total	C	H	N	O	S	0	0
			994	326	507	75	82	4		
9	N	75	Total	C	H	N	O	S	0	0
			1096	356	559	83	94	4		
9	O	44	Total	C	H	N	O	S	0	0
			707	234	364	51	55	3		

- Molecule 10 is a protein called ATP synthase F(0) complex subunit B1, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	b	209	Total	C	H	N	O	S	0	0
			3456	1095	1755	292	308	6		

- Molecule 11 is a protein called ATP synthase-coupling factor 6, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	h	62	Total	C	H	N	O	S	0	0
			1009	326	495	87	99	2		

- Molecule 12 is a protein called ATP synthase subunit O, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	S	129	Total	C	H	N	O	S	0	0
			2048	627	1057	171	186	7		

- Molecule 13 is a protein called ATP synthase subunit alpha, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	C	89	Total	C	H	N	O	S	0	0
			1333	409	671	115	136	2		

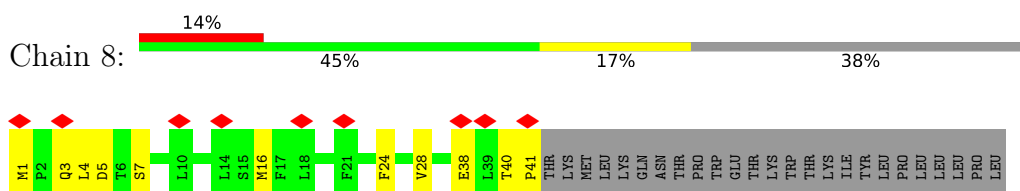
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1	GLU	GLN	microheterogeneity	UNP P19483

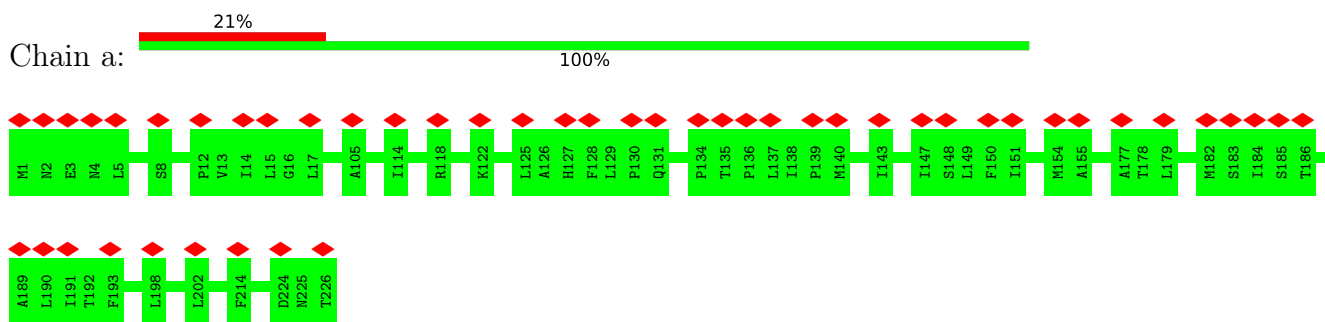
3 Residue-property plots [i](#)

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

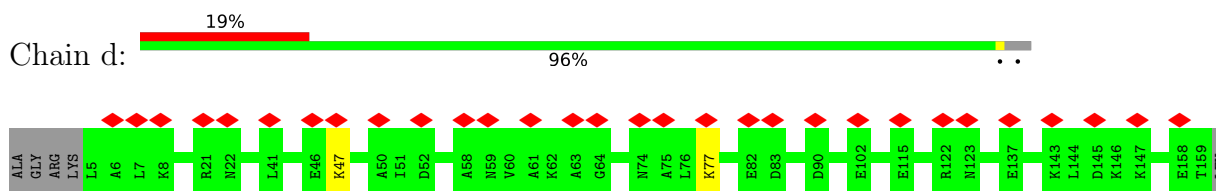
- Molecule 1: ATP synthase protein 8



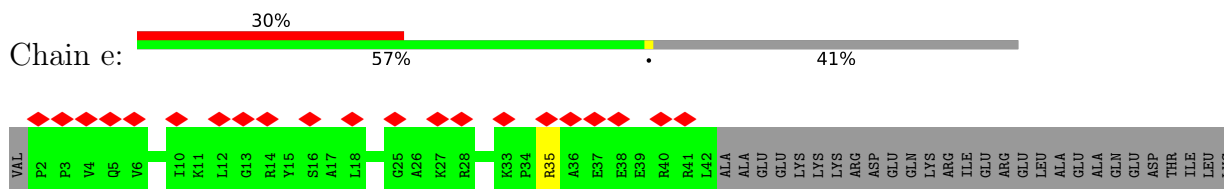
- Molecule 2: ATP synthase subunit a



- Molecule 3: ATP synthase subunit d, mitochondrial

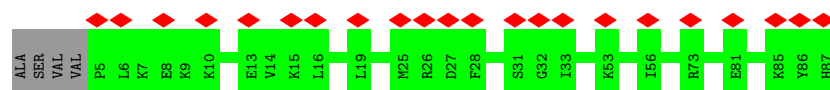


- Molecule 4: ATP synthase subunit e, mitochondrial

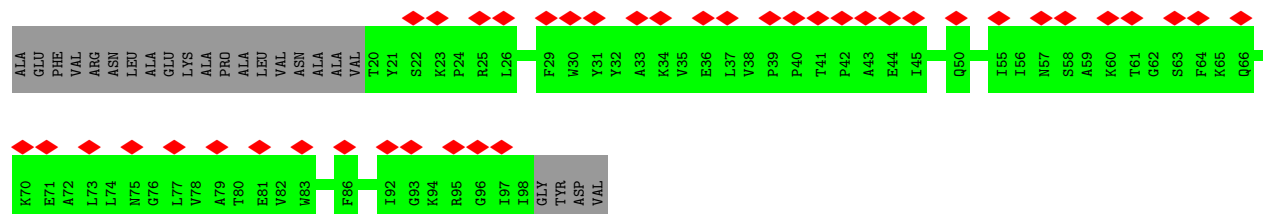
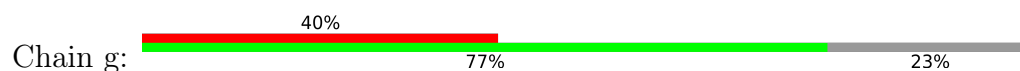


- Molecule 5: ATP synthase subunit f, mitochondrial

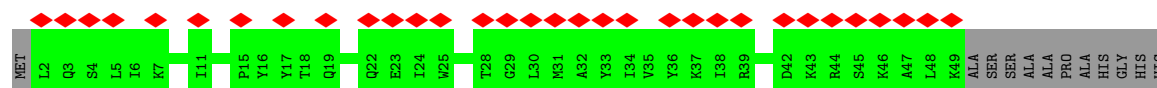
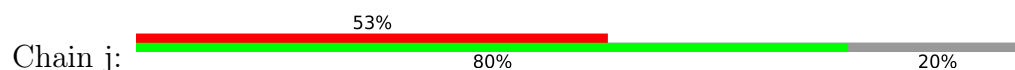




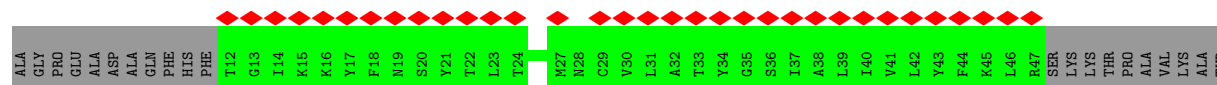
- Molecule 6: ATP synthase subunit g, mitochondrial



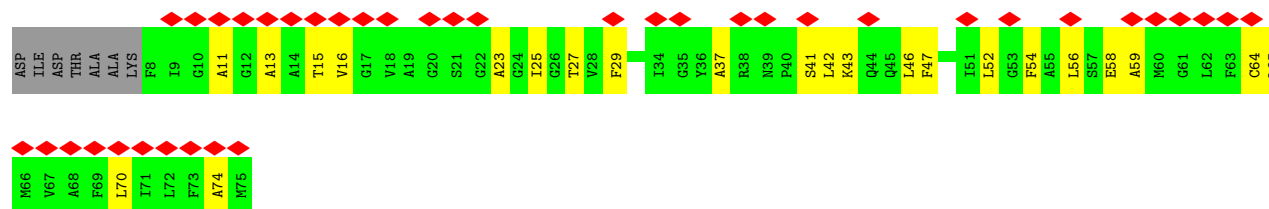
- Molecule 7: ATP synthase subunit ATP5MPL, mitochondrial



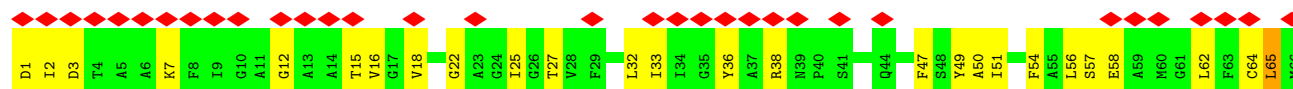
- Molecule 8: ATP synthase membrane subunit DAPIT, mitochondrial

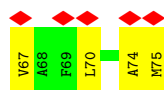


- Molecule 9: ATP synthase F(0) complex subunit C1, mitochondrial

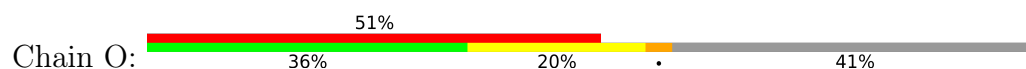


- Molecule 9: ATP synthase F(0) complex subunit C1, mitochondrial

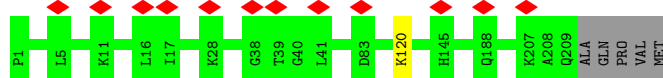




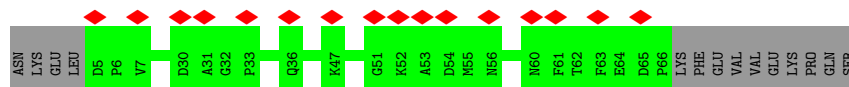
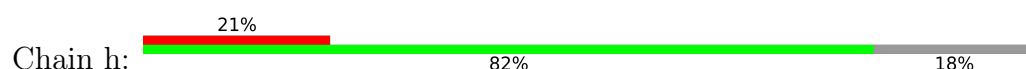
- Molecule 9: ATP synthase F(0) complex subunit C1, mitochondrial



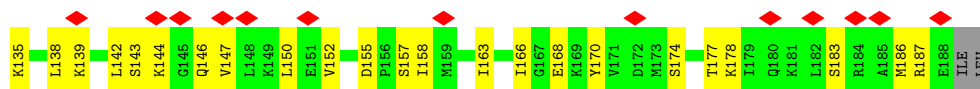
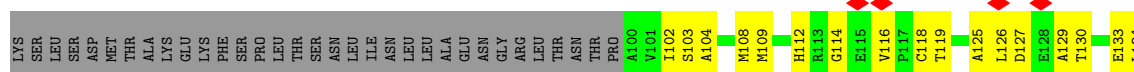
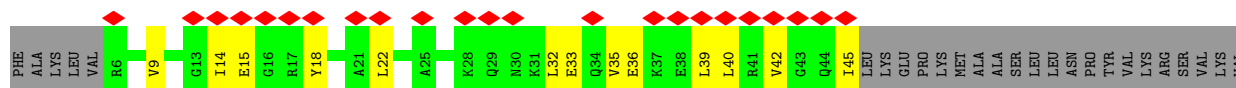
- Molecule 10: ATP synthase F(0) complex subunit B1, mitochondrial



- Molecule 11: ATP synthase-coupling factor 6, mitochondrial



- Molecule 12: ATP synthase subunit O, mitochondrial



- Molecule 13: ATP synthase subunit alpha, mitochondrial



GLU	LYS	THR	GLY	THR	A6	E7	V8	S9	S10	I11	L12	E13	E14	R15	I16	L17	D20	T21	S22	V23	D24	L25	E26	E27	T28	V31	S33	I34	G35	D36	G37	I38	A39	R40	V41	H42	C43	L44	R45	H46	V47	Q48	A49	E50	E51	E54	F55	L59	S63	L64	N65	L66	E67
P68	D69	N70	V71	G72	V75	N78	D79	K80	L81	I82	G85	K89	R90	T91	G92	A93	I94	VAL	ASP	VAL	ASP	VAL	PRO	VAL	ILE	GLY	VAL	GLY	ARG	GLY	GLY	GLN	GLU	LEU	LEU	ASP	ASP	ILE	GLY	LYS	GLY	PRO	ILE	GLY	SER	LYS	ALA	ARG	ARG	VAL	GLY	LEU	LYS
ALA	PRO	GLY	ILE	PRO	ARG	ILE	VAL	ARG	GLU	PRO	MET	GLN	THR	GLY	ILE	LYS	ALA	VAL	VAL	LEU	VAL	PRO	ILE	GLY	ARG	GLY	GLN	ARG	GLY	GLY	GLN	THR	LYS	THR	THR	SER	ILE	ALA	ILE	ASP	PRO	THR	ILE	GLY	ASN	GLN	LYS	ARG	PHE	ASN	VAL	ASP	GLY
THR	ASP	GLU	LYS	LYS	LEU	TYR	CYS	THR	VAL	ILE	GLY	LYS	ARG	SER	THR	VAL	ALA	GLN	LEU	VAL	VAL	LYS	ARG	LEU	THR	ALA	ASP	ILE	ALA	VAL	VAL	SER	THR	THR	ALA	ASP	ASP	ILE	ALA	ILE	ASP	PRO	THR	ILE	GLN	TYR	LEU	ALA	PRO	TYR	SER		
MET	GLY	GLU	TYR	PHE	ASP	GLY	HIS	ALA	LEU	ILE	ILE	TYR	ASP	ASP	LEU	SER	LYS	GLN	ALA	VAL	ALA	TYR	ARG	GLN	MET	SER	LEU	LEU	PRO	GLY	ILE	ARG	GLU	ALA	THR	VAL	PHE	TYR	ALA	ALA	LEU	HIS	SER	ARG	ALA	ALA	GLY	MET					
ASN	ASP	ALA	PHE	GLY	GLY	SER	THR	LEU	ALA	PRO	VAL	ILE	GLY	THR	GLN	ALA	GLY	ILE	THR	TYR	ILE	PRO	THR	ASN	VAL	ILE	LEU	SER	ILE	GLY	GLY	THR	THR	GLU	GLY	THR	TYR	LYS	GLY	ILE	ARG	PRO	ALA	ILE	ASN	VAL	GLY	SER					
ARG	VAL	GLY	SER	ALA	ALA	GLN	ARG	MET	ALA	LYS	GLY	THR	MET	THR	LYS	LYS	LEU	GLY	VAL	ARG	GLU	VAL	GLU	ALA	ALA	THR	ALA	THR	GLN	GLN	LEU	LEU	LEU	LEU	THR	VAL	SER	ARG	GLY	ILE	ARG	VAL	GLY	THR	THR	GLY	GLU	LEU	GLN				
TYR	SER	PRO	MET	ILE	GLU	GLU	GLN	VAL	ALA	TYR	ALA	GLY	VAL	ARG	GLY	TYR	LEU	ASP	LYS	LEU	PRO	SER	LYS	ILE	THR	PHE	GLU	ASN	ALA	PHE	GLU	ASN	ALA	GLY	THR	THR	LEU	SER	GLY	VAL	ARG	LEU	THR	THR	GLY	GLU	LYS	GLN					
SER	ASP	ALA	LYS	LEU	LYS	GLU	ILE	VAL	THR	ASN	PHE	LEU	ALA	PHE	GLY	GLU	ALA	TYR	LEU	GLU	LEU	GLY	ASP	LEU	LEU	VAL	VAL	ILE	SER	SER	GLN	GLN	HIS	GLN	GLY	THR	ALA	LEU	SER	GLY	VAL	ARG	LEU	THR	THR	GLY	GLU	GLU					

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	90850	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 ($e^-/\text{\AA}^2$)	4.6	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.060	Depositor
Minimum map value	-0.031	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0187	Depositor
Map size (Å)	524.0, 524.0, 524.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.048, 1.048, 1.048	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: M3L

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	8	0.33	0/355	0.42	0/483
2	a	0.32	0/1779	0.50	0/2433
3	d	0.29	0/1304	0.42	0/1768
4	e	0.29	0/343	0.46	0/460
5	f	0.32	0/711	0.42	0/952
6	g	0.27	0/646	0.47	0/879
7	j	0.30	0/410	0.49	0/552
8	k	0.26	0/294	0.43	0/395
9	M	0.32	0/484	0.47	0/653
9	N	0.36	0/534	0.56	1/721 (0.1%)
9	O	0.36	0/338	0.81	6/456 (1.3%)
10	b	0.32	0/1733	0.44	0/2334
11	h	0.32	0/526	0.52	0/707
12	S	0.29	0/1000	0.46	0/1341
13	C	0.28	0/665	0.49	0/894
All	All	0.31	0/11122	0.48	7/15028 (0.0%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	O	70	LEU	CB-CG-CD2	5.99	121.18	111.00
9	O	52	LEU	CB-CG-CD2	5.76	120.80	111.00
9	O	65	LEU	CB-CG-CD1	5.69	120.67	111.00
9	O	65	LEU	CB-CG-CD2	5.69	120.67	111.00
9	N	65	LEU	CB-CG-CD1	-5.44	101.75	111.00
9	O	52	LEU	CB-CG-CD1	5.40	120.18	111.00
9	O	70	LEU	CB-CG-CD1	5.33	120.06	111.00

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	8	344	352	352	9	0
2	a	1741	1870	1870	0	0
3	d	1273	1276	1275	0	0
4	e	335	352	352	0	0
5	f	693	718	718	0	0
6	g	629	662	662	0	0
7	j	400	428	428	0	0
8	k	289	307	307	0	0
9	M	487	507	506	21	0
9	N	537	559	558	35	0
9	O	343	364	363	22	0
10	b	1701	1755	1755	0	0
11	h	514	495	495	0	0
12	S	991	1057	1055	46	0
13	C	662	671	671	31	0
All	All	10939	11373	11367	137	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 18.

All (137) 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)
9:N:70:LEU:O	9:N:74:ALA:N	2.09	0.86
9:N:15:THR:HG1	9:O:64:CYS:HG	1.15	0.85
13:C:78:ASN:OD1	13:C:79:ASP:N	2.11	0.83
9:M:37:ALA:O	9:N:38:ARG:NH2	2.11	0.82
13:C:54:GLU:OE1	13:C:91:THR:HG23	1.82	0.80
9:M:11:ALA:O	9:M:15:THR:HG23	1.85	0.77
12:S:183:SER:O	12:S:187:ARG:NH1	2.17	0.77
12:S:33:GLU:N	12:S:33:GLU:OE1	2.17	0.76
12:S:127:ASP:O	12:S:130:THR:OG1	2.03	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:S:139:LYS:NZ	12:S:146:GLN:O	2.14	0.75
9:M:54:PHE:CZ	9:N:56:LEU:HD13	2.22	0.75
9:O:62:LEU:HD13	9:O:65:LEU:HD12	1.71	0.71
9:M:43:M3L:O	9:M:46:LEU:N	2.23	0.70
13:C:59:LEU:HD21	13:C:78:ASN:O	1.91	0.70
9:N:36:TYR:CD2	9:O:42:LEU:HD21	2.28	0.68
13:C:67:GLU:OE1	13:C:69:ASP:N	2.26	0.67
13:C:48:GLN:N	13:C:51:GLU:OE1	2.28	0.67
13:C:32:LEU:HD21	13:C:42:HIS:HB3	1.78	0.66
13:C:78:ASN:OD1	13:C:80:LYS:N	2.28	0.66
1:8:24:PHE:O	1:8:28:VAL:HG22	1.97	0.65
9:N:54:PHE:CE1	9:O:56:LEU:HD13	2.36	0.61
9:M:13:ALA:O	9:M:16:VAL:HG22	2.00	0.61
9:M:25:ILE:HD11	9:N:57:SER:HA	1.82	0.61
9:N:1:ASP:OD1	9:N:2:ILE:N	2.35	0.60
9:N:65:LEU:HD21	9:O:63:PHE:CZ	2.37	0.59
9:N:7:LYS:NZ	9:N:75:MET:SD	2.78	0.57
13:C:32:LEU:HD21	13:C:42:HIS:CB	2.34	0.57
12:S:186:MET:SD	12:S:187:ARG:NH2	2.74	0.57
13:C:79:ASP:O	13:C:82:ILE:N	2.37	0.56
13:C:10:SER:O	13:C:13:GLU:N	2.38	0.56
12:S:116:VAL:HG21	12:S:142:LEU:HD22	1.88	0.56
12:S:155:ASP:OD2	12:S:157:SER:N	2.37	0.56
9:O:66:MET:SD	9:O:67:VAL:N	2.79	0.55
12:S:125:ALA:C	12:S:126:LEU:HD22	2.27	0.55
9:O:58:GLU:O	9:O:62:LEU:HD23	2.07	0.55
1:8:1:MET:HG2	1:8:4:LEU:HD23	1.89	0.54
9:N:65:LEU:HD11	9:O:63:PHE:CE2	2.43	0.54
9:M:41:SER:C	9:M:42:LEU:HD22	2.28	0.54
12:S:36:GLU:O	12:S:40:LEU:HD23	2.08	0.53
13:C:10:SER:O	13:C:14:GLU:OE1	2.25	0.53
12:S:9:VAL:HG13	12:S:9:VAL:O	2.09	0.52
9:N:15:THR:OG1	9:O:64:CYS:SG	2.40	0.52
13:C:47:VAL:HG13	13:C:47:VAL:O	2.10	0.52
9:N:47:PHE:O	9:N:51:ILE:HD12	2.11	0.51
13:C:28:THR:HG22	13:C:89:LYS:HG3	1.92	0.51
9:M:54:PHE:CZ	9:N:56:LEU:HD22	2.45	0.51
12:S:158:ILE:HD13	12:S:163:ILE:CD1	2.41	0.51
12:S:158:ILE:HD13	12:S:163:ILE:HD13	1.92	0.51
13:C:26:GLU:O	13:C:28:THR:HG23	2.11	0.50
9:N:33:ILE:HG23	9:O:46:LEU:HD22	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:S:116:VAL:HG23	12:S:116:VAL:O	2.11	0.50
13:C:59:LEU:HD22	13:C:81:LEU:HD21	1.92	0.50
13:C:27:GLU:OE2	13:C:45:ARG:N	2.45	0.50
9:N:65:LEU:HD11	9:O:63:PHE:CZ	2.46	0.50
9:M:52:LEU:O	9:M:56:LEU:HD23	2.11	0.50
9:N:64:CYS:O	9:N:67:VAL:HG12	2.11	0.50
12:S:170:TYR:CB	13:C:28:THR:HG21	2.42	0.50
9:O:66:MET:SD	9:O:67:VAL:HG23	2.52	0.49
12:S:114:GLY:O	12:S:147:VAL:N	2.43	0.49
9:O:70:LEU:O	9:O:74:ALA:N	2.40	0.49
9:N:47:PHE:HZ	9:O:49:TYR:CE1	2.31	0.49
12:S:150:LEU:HD13	12:S:152:VAL:HG23	1.95	0.49
12:S:14:ILE:HG13	12:S:15:GLU:N	2.29	0.48
13:C:31:VAL:O	13:C:85:GLY:N	2.43	0.48
1:8:5:ASP:O	1:8:7:SER:N	2.46	0.48
1:8:1:MET:SD	9:N:70:LEU:HD22	2.54	0.48
12:S:129:ALA:O	12:S:133:GLU:OE1	2.31	0.48
9:M:54:PHE:HZ	9:N:56:LEU:HD22	1.79	0.48
9:M:41:SER:O	9:M:42:LEU:HD22	2.14	0.48
12:S:178:LYS:NZ	13:C:23:VAL:HG11	2.28	0.48
12:S:118:CYS:SG	12:S:119:THR:N	2.87	0.48
9:O:62:LEU:HA	9:O:65:LEU:HG	1.96	0.47
12:S:39:LEU:HD23	12:S:102:ILE:HA	1.96	0.47
9:M:70:LEU:O	9:M:74:ALA:N	2.47	0.47
13:C:12:LEU:HD23	13:C:15:ARG:HH21	1.80	0.47
9:M:27:THR:HA	9:N:27:THR:HG21	1.96	0.47
12:S:35:VAL:O	12:S:39:LEU:CD1	2.63	0.47
12:S:143:SER:OG	12:S:144:LYS:N	2.48	0.46
13:C:44:LEU:O	13:C:47:VAL:HG12	2.15	0.46
9:N:18:VAL:HG11	9:N:65:LEU:HD12	1.98	0.46
12:S:35:VAL:O	12:S:39:LEU:HD12	2.16	0.46
12:S:18:TYR:O	12:S:22:LEU:HD23	2.16	0.46
13:C:55:PHE:CE1	13:C:75:VAL:HG22	2.52	0.45
13:C:8:VAL:O	13:C:11:ILE:HG22	2.15	0.45
9:M:47:PHE:HE1	9:N:49:TYR:CZ	2.34	0.45
12:S:104:ALA:O	12:S:108:MET:HG3	2.16	0.45
12:S:118:CYS:SG	12:S:166:ILE:HD13	2.56	0.45
9:N:58:GLU:OE2	9:N:62:LEU:HD21	2.17	0.45
9:M:47:PHE:CE1	9:N:49:TYR:CZ	3.05	0.45
1:8:38:GLU:OE1	1:8:40:THR:N	2.50	0.45
12:S:102:ILE:HG13	12:S:103:SER:N	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:N:58:GLU:O	9:N:62:LEU:HD23	2.17	0.44
12:S:109:MET:SD	12:S:112:HIS:ND1	2.85	0.44
12:S:130:THR:O	12:S:134:LEU:HG	2.17	0.44
12:S:150:LEU:CD1	12:S:152:VAL:HG23	2.47	0.44
12:S:170:TYR:HB3	13:C:28:THR:HG21	2.00	0.44
12:S:187:ARG:HA	12:S:187:ARG:NE	2.33	0.44
9:N:2:ILE:HG23	9:N:3:ASP:N	2.33	0.44
9:O:63:PHE:C	9:O:63:PHE:CD2	2.91	0.44
9:M:54:PHE:CE2	9:N:56:LEU:HD13	2.52	0.43
12:S:135:LYS:O	12:S:139:LYS:HG2	2.18	0.43
12:S:138:LEU:HD22	12:S:166:ILE:HD11	2.00	0.43
9:O:42:LEU:O	9:O:46:LEU:HD12	2.18	0.43
12:S:42:VAL:HA	12:S:45:ILE:HD12	2.00	0.43
1:8:40:THR:HB	1:8:41:PRO:HD2	2.00	0.43
12:S:32:LEU:HA	12:S:35:VAL:HG12	2.01	0.43
9:M:64:CYS:SG	9:M:65:LEU:N	2.91	0.43
12:S:186:MET:HA	13:C:15:ARG:HD2	1.99	0.43
12:S:186:MET:HG3	13:C:16:ILE:HD11	1.99	0.43
9:M:23:ALA:O	9:M:27:THR:HG23	2.19	0.43
12:S:174:SER:OG	12:S:177:THR:HG22	2.18	0.43
9:N:32:LEU:HD12	9:N:50:ALA:CB	2.49	0.43
1:8:38:GLU:OE1	1:8:40:THR:OG1	2.30	0.42
9:O:63:PHE:CE2	9:O:67:VAL:HG21	2.53	0.42
13:C:8:VAL:HG23	13:C:9:SER:N	2.33	0.42
12:S:39:LEU:HA	12:S:42:VAL:HG22	2.01	0.42
9:M:58:GLU:O	9:M:59:ALA:C	2.58	0.42
9:N:16:VAL:O	9:N:18:VAL:N	2.52	0.42
9:N:47:PHE:O	9:N:51:ILE:CD1	2.67	0.42
13:C:27:GLU:HG2	13:C:44:LEU:HD23	2.02	0.42
9:N:12:GLY:O	9:N:15:THR:HG22	2.20	0.42
12:S:109:MET:O	12:S:112:HIS:HB3	2.20	0.42
9:O:60:MET:HA	9:O:60:MET:CE	2.50	0.41
12:S:158:ILE:HG21	12:S:163:ILE:CD1	2.49	0.41
9:M:29:PHE:CE2	9:N:56:LEU:HD12	2.56	0.41
12:S:168:GLU:O	13:C:28:THR:N	2.53	0.41
12:S:163:ILE:CG2	12:S:170:TYR:HE1	2.33	0.41
13:C:32:LEU:HD11	13:C:42:HIS:HB2	2.03	0.41
1:8:3:GLN:C	1:8:4:LEU:HD22	2.41	0.41
9:O:71:ILE:HG13	9:O:72:LEU:N	2.36	0.41
12:S:150:LEU:HD12	12:S:150:LEU:C	2.42	0.40
9:M:43:M3L:O	9:M:46:LEU:HB2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:N:36:TYR:CE2	9:O:42:LEU:HD21	2.56	0.40
13:C:67:GLU:HB3	13:C:70:ASN:O	2.22	0.40
9:O:63:PHE:O	9:O:66:MET:HG3	2.21	0.40
1:8:16:MET:SD	1:8:16:MET:C	3.00	0.40
9:N:22:GLY:HA2	9:N:25:ILE:HG12	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	8	39/66 (59%)	29 (74%)	10 (26%)	0	100	100
2	a	224/226 (99%)	210 (94%)	14 (6%)	0	100	100
3	d	153/160 (96%)	134 (88%)	19 (12%)	0	100	100
4	e	39/70 (56%)	39 (100%)	0	0	100	100
5	f	81/87 (93%)	74 (91%)	7 (9%)	0	100	100
6	g	77/102 (76%)	71 (92%)	6 (8%)	0	100	100
7	j	46/60 (77%)	43 (94%)	3 (6%)	0	100	100
8	k	34/57 (60%)	32 (94%)	2 (6%)	0	100	100
9	M	65/75 (87%)	62 (95%)	3 (5%)	0	100	100
9	N	72/75 (96%)	64 (89%)	8 (11%)	0	100	100
9	O	41/75 (55%)	38 (93%)	3 (7%)	0	100	100
10	b	207/214 (97%)	196 (95%)	11 (5%)	0	100	100
11	h	60/76 (79%)	49 (82%)	11 (18%)	0	100	100
12	S	125/190 (66%)	114 (91%)	11 (9%)	0	100	100
13	C	87/510 (17%)	78 (90%)	9 (10%)	0	100	100
All	All	1350/2043 (66%)	1233 (91%)	117 (9%)	0	100	100

There are no Ramachandran outliers to report.

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	8	41/66 (62%)	41 (100%)	0	100	100
2	a	200/200 (100%)	200 (100%)	0	100	100
3	d	139/142 (98%)	137 (99%)	2 (1%)	62	76
4	e	34/59 (58%)	33 (97%)	1 (3%)	37	58
5	f	72/75 (96%)	72 (100%)	0	100	100
6	g	67/83 (81%)	67 (100%)	0	100	100
7	j	42/49 (86%)	42 (100%)	0	100	100
8	k	31/46 (67%)	31 (100%)	0	100	100
9	M	45/50 (90%)	45 (100%)	0	100	100
9	N	50/50 (100%)	50 (100%)	0	100	100
9	O	34/50 (68%)	34 (100%)	0	100	100
10	b	186/190 (98%)	185 (100%)	1 (0%)	86	90
11	h	56/70 (80%)	56 (100%)	0	100	100
12	S	110/165 (67%)	110 (100%)	0	100	100
13	C	73/413 (18%)	73 (100%)	0	100	100
All	All	1180/1708 (69%)	1176 (100%)	4 (0%)	90	92

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	d	47	LYS
3	d	77	LYS
4	e	35	ARG
10	b	120	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	8	32	ASN
1	8	36	ASN
2	a	101	ASN
2	a	119	ASN
2	a	168	HIS
6	g	57	ASN
9	N	45	GLN
10	b	122	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

3 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	$\# Z > 2$
9	M3L	N	43	9	10,11,12	0.51	0	9,14,16	0.65	0
9	M3L	O	43	9	10,11,12	0.55	0	9,14,16	0.54	0
9	M3L	M	43	9	10,11,12	0.42	0	9,14,16	0.40	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
9	M3L	N	43	9	-	6/9/10/12	-
9	M3L	O	43	9	-	1/9/10/12	-
9	M3L	M	43	9	-	2/9/10/12	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	M	43	M3L	N-CA-CB-CG
9	M	43	M3L	C-CA-CB-CG
9	N	43	M3L	N-CA-CB-CG
9	N	43	M3L	C-CA-CB-CG
9	O	43	M3L	CG-CD-CE-NZ
9	N	43	M3L	CD-CE-NZ-CM2
9	N	43	M3L	CD-CE-NZ-CM3
9	N	43	M3L	CD-CE-NZ-CM1
9	N	43	M3L	CE-CD-CG-CB

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	M	43	M3L	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

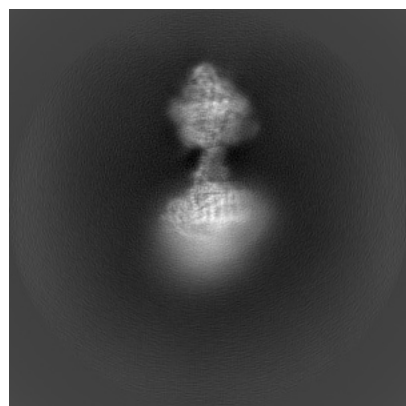
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11228. These allow visual inspection of the internal detail of the map and identification of artifacts.

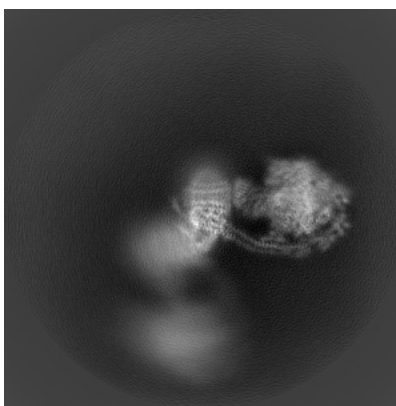
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

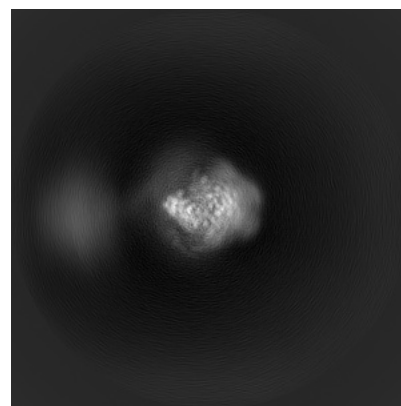
6.1.1 Primary map



X

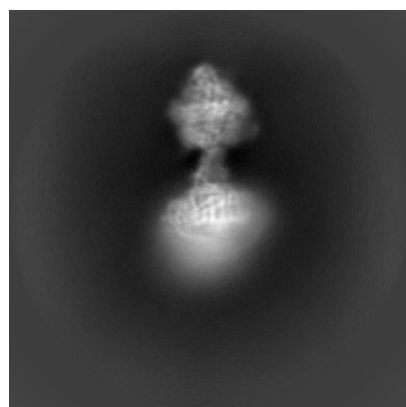


Y

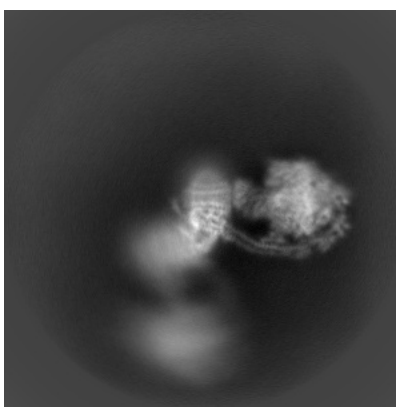


Z

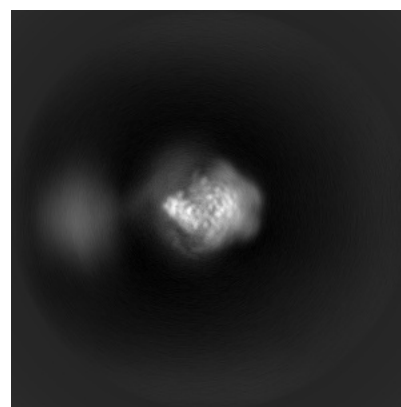
6.1.2 Raw map



X



Y

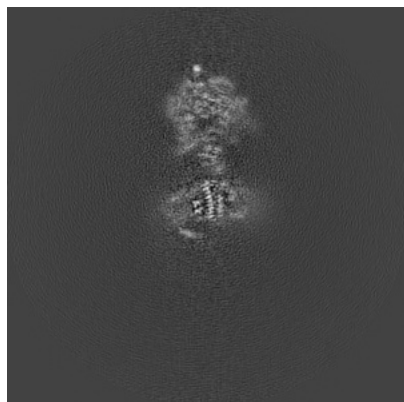


Z

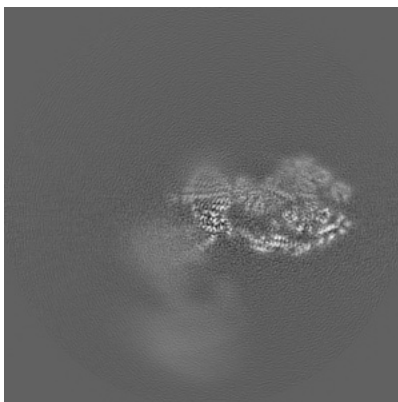
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

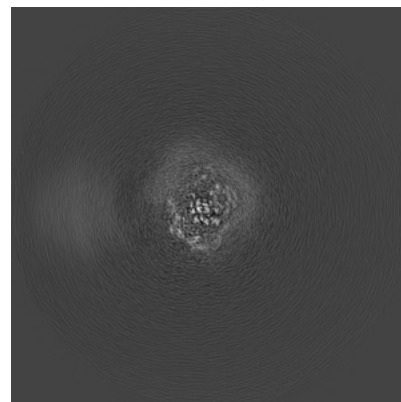
6.2.1 Primary map



X Index: 250

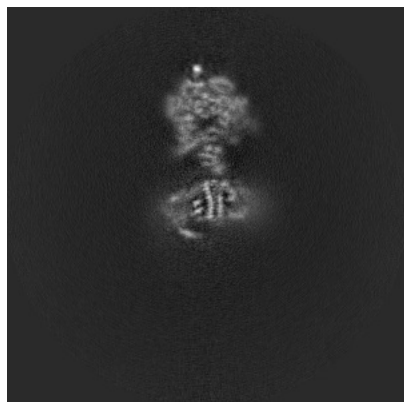


Y Index: 250

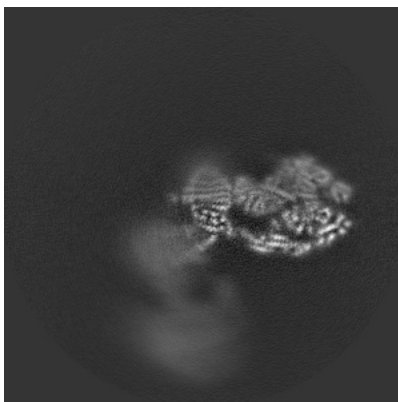


Z Index: 250

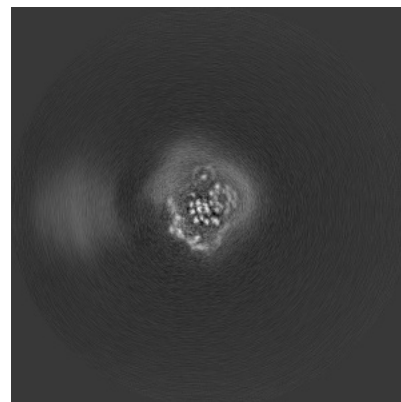
6.2.2 Raw map



X Index: 250



Y Index: 250

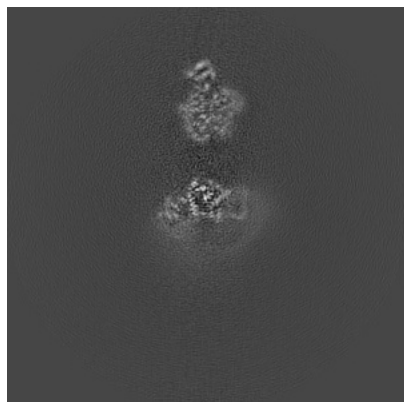


Z Index: 250

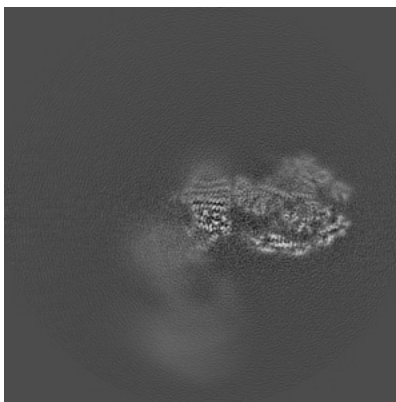
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

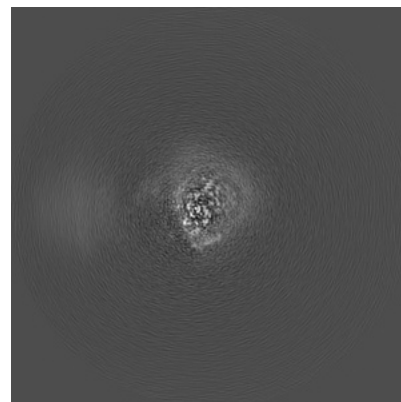
6.3.1 Primary map



X Index: 231

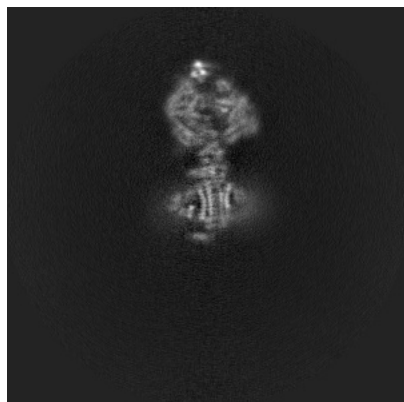


Y Index: 252

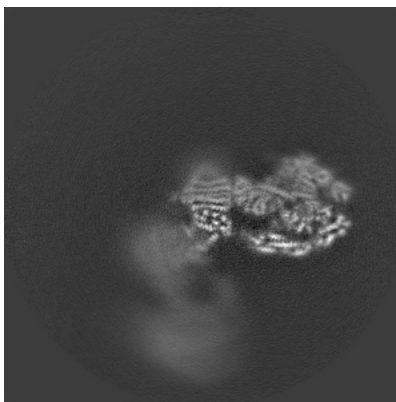


Z Index: 259

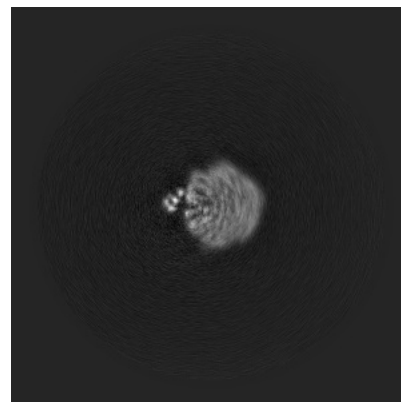
6.3.2 Raw map



X Index: 258



Y Index: 252

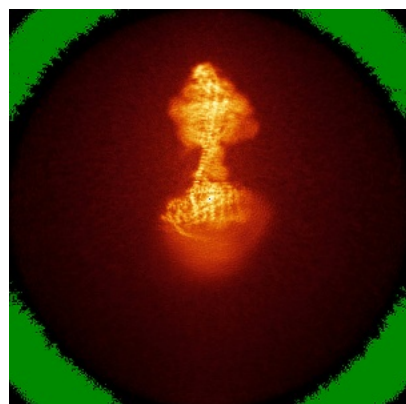


Z Index: 377

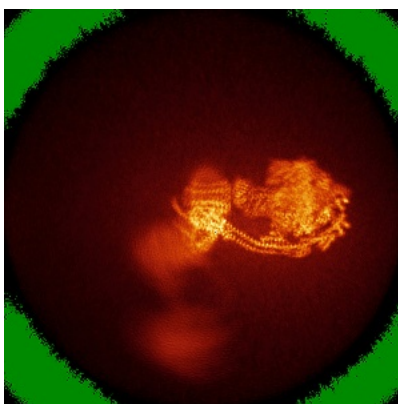
The images above show the largest variance slices of the map in three orthogonal directions.

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

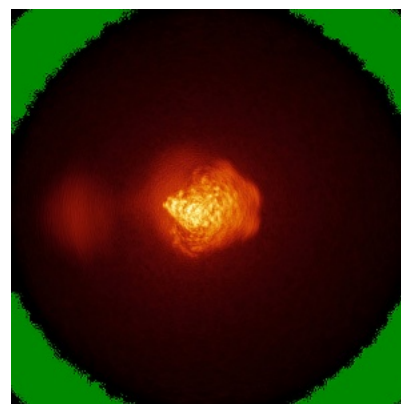
6.4.1 Primary map



X



Y



Z

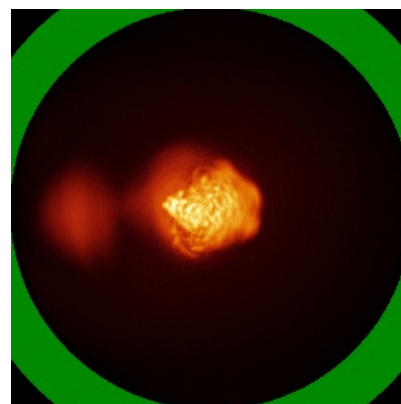
6.4.2 Raw map



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 0.0187. 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.

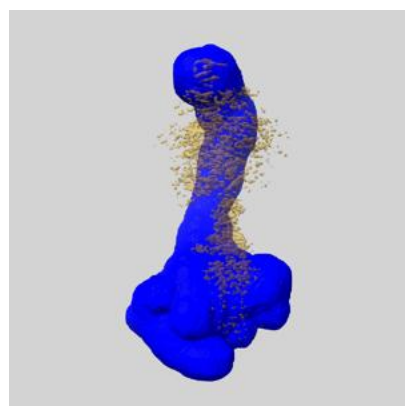
6.6 Mask visualisation [i](#)

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

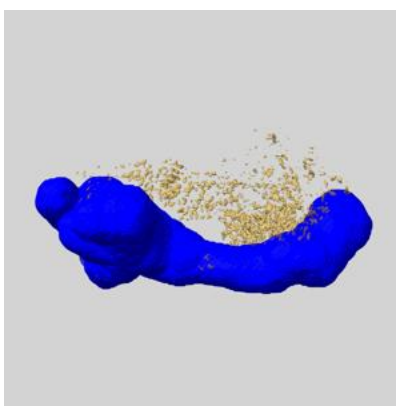
A mask typically either:

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

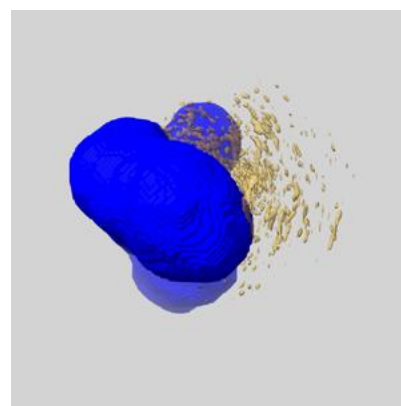
6.6.1 emd_11228_msk_1.map [i](#)



X



Y

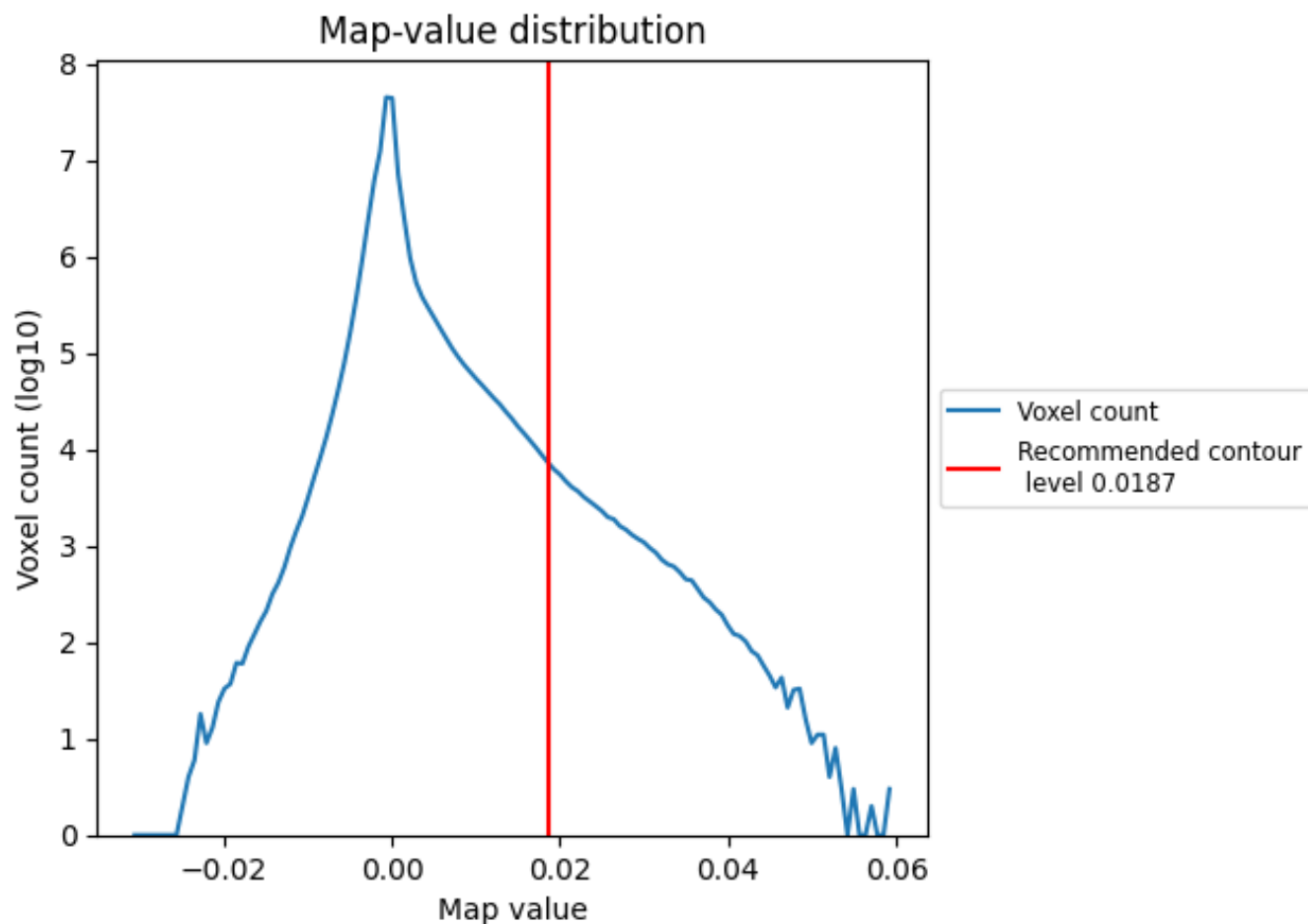


Z

7 Map analysis [i](#)

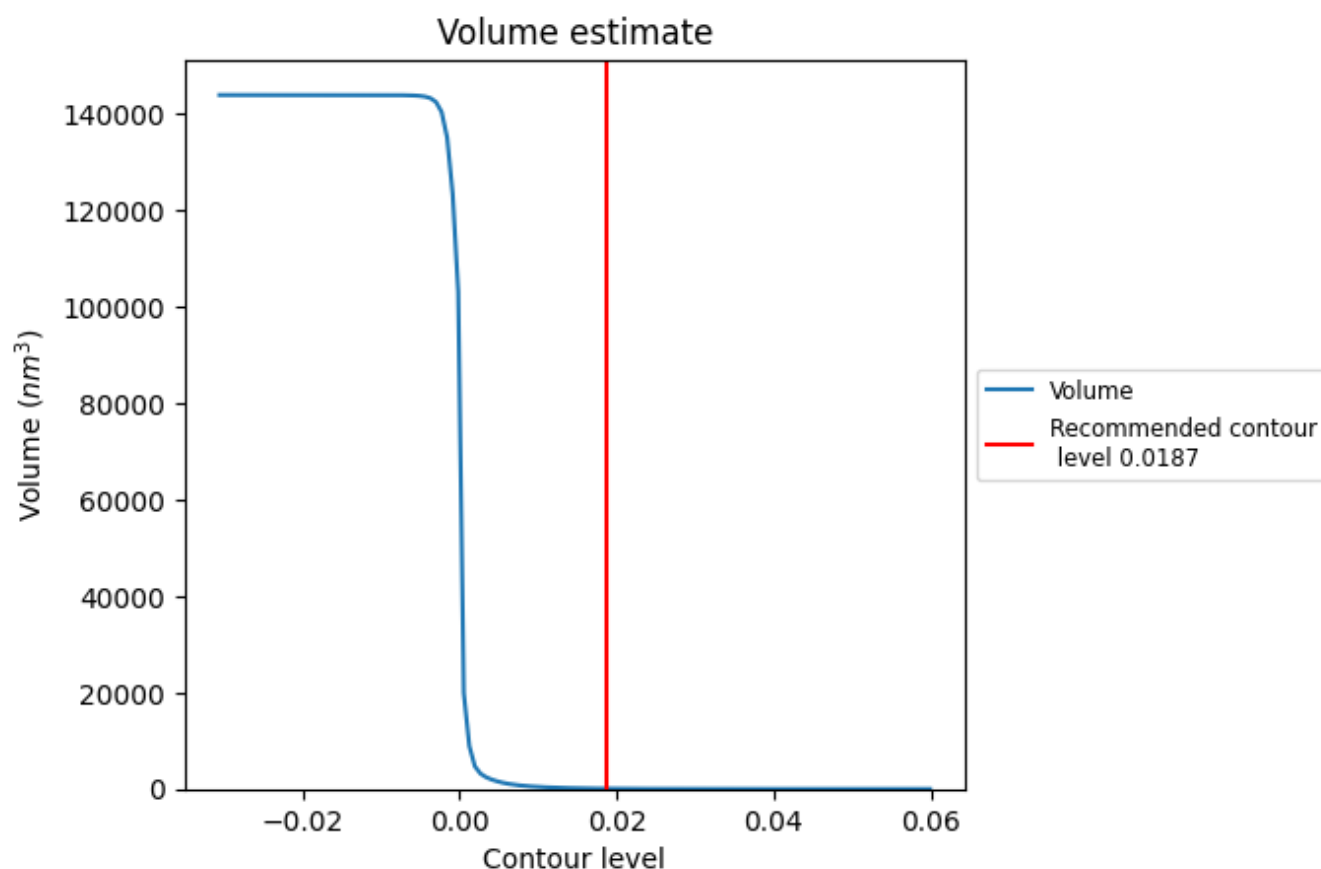
This section contains the results of statistical analysis of the map.

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.

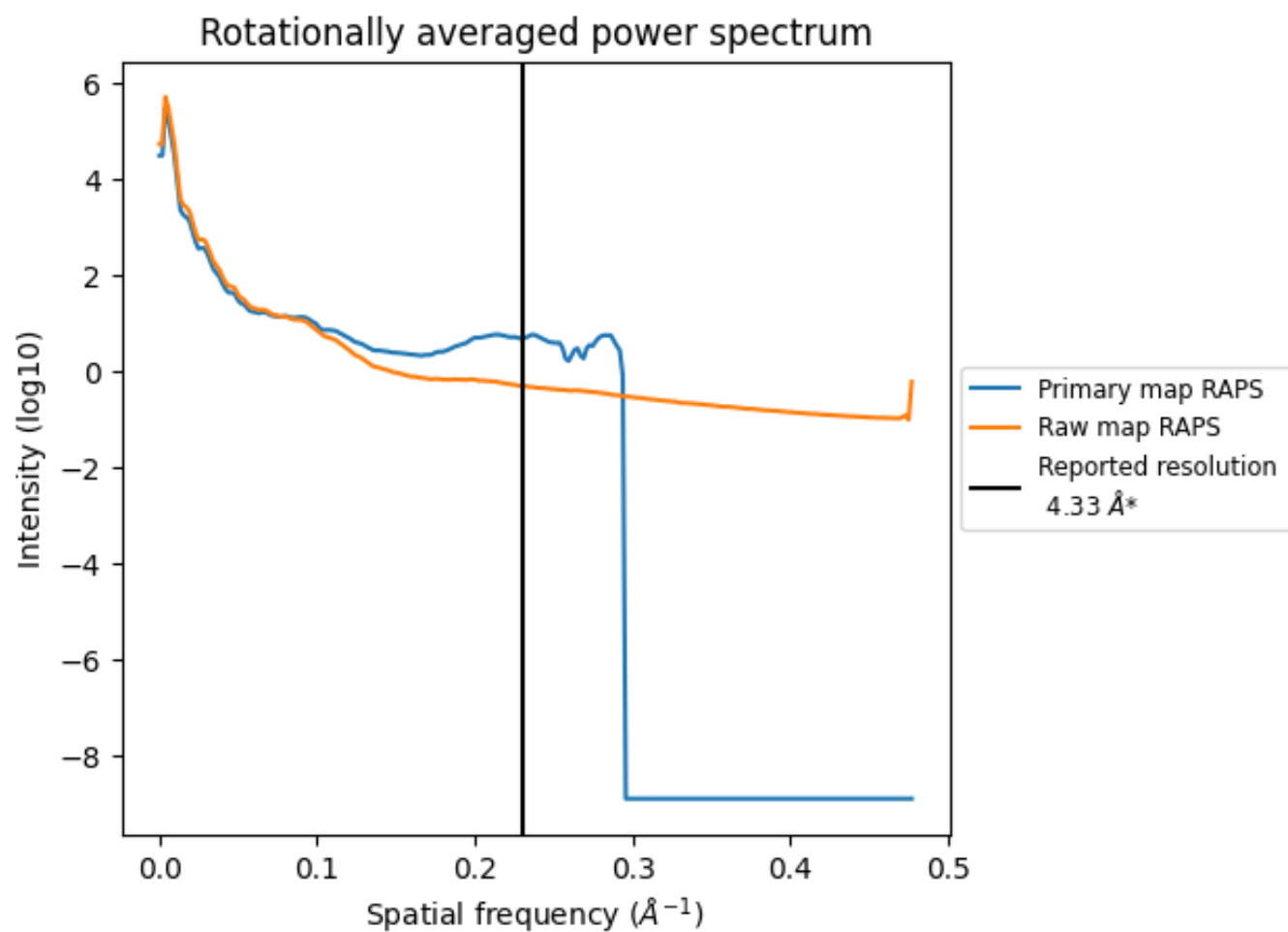
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 68 nm^3 ; this corresponds to an approximate mass of 62 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 ⓘ

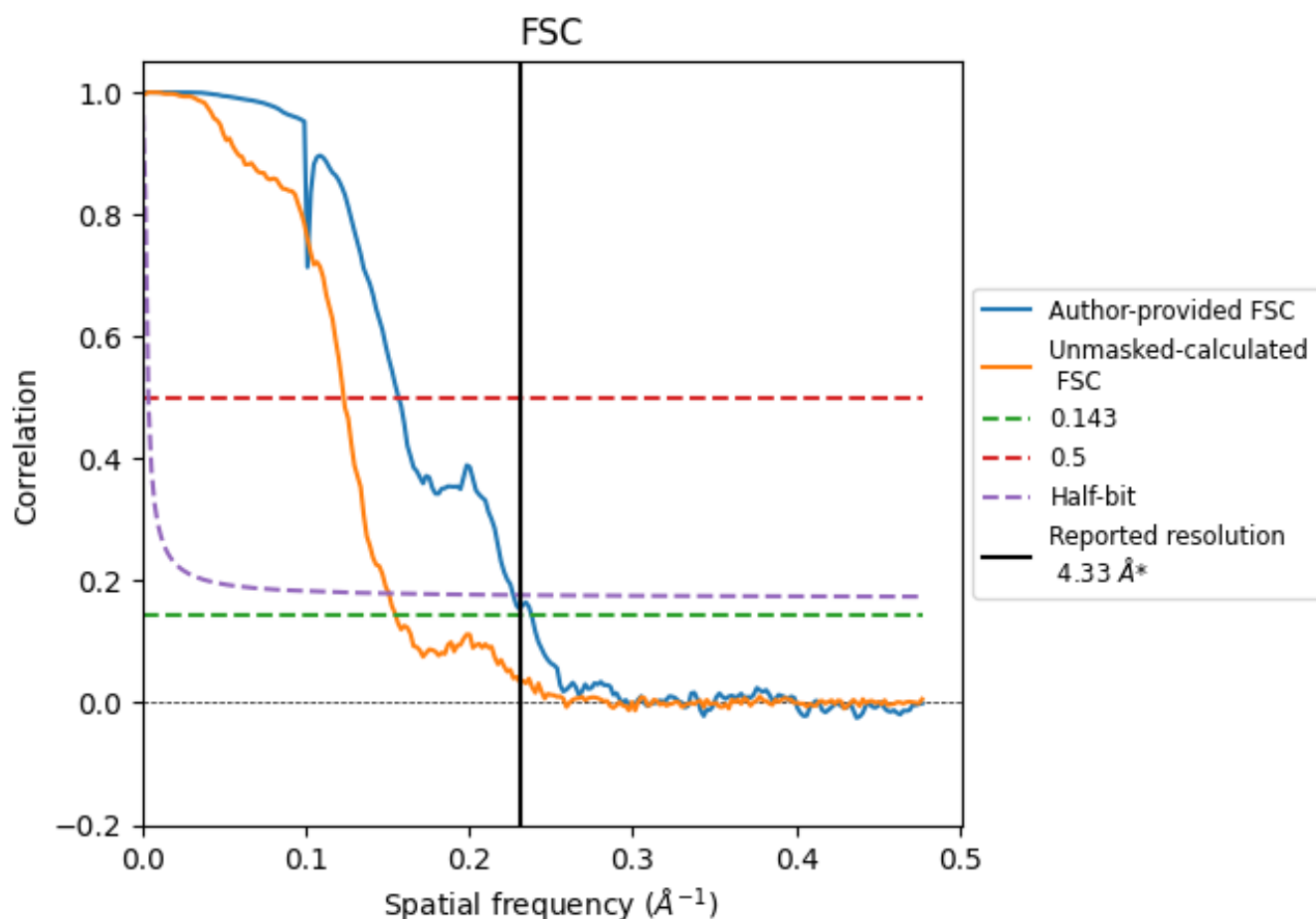


*Reported resolution corresponds to spatial frequency of 0.231 \AA^{-1}

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 0.231 \AA^{-1}

8.2 Resolution estimates [i](#)

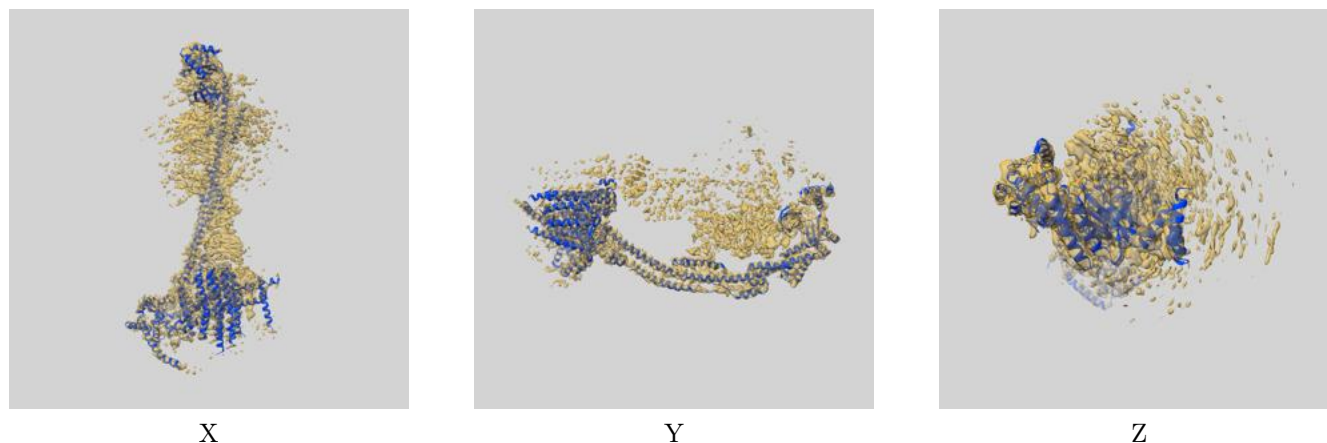
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.33	-	-
Author-provided FSC curve	4.20	6.38	4.41
Unmasked-calculated*	6.45	8.11	6.63

*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 6.45 differs from the reported value 4.33 by more than 10 %

9 Map-model fit [i](#)

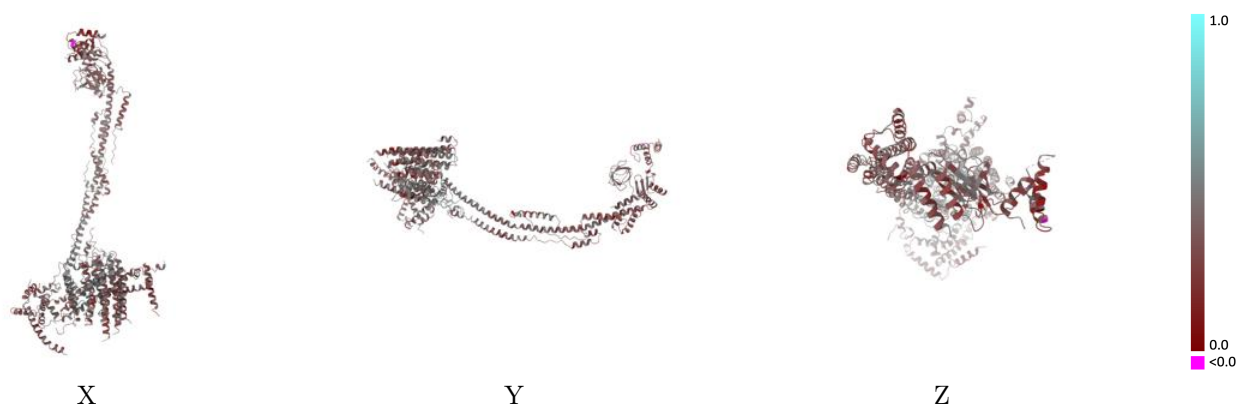
This section contains information regarding the fit between EMDB map EMD-11228 and PDB model 6ZIQ. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



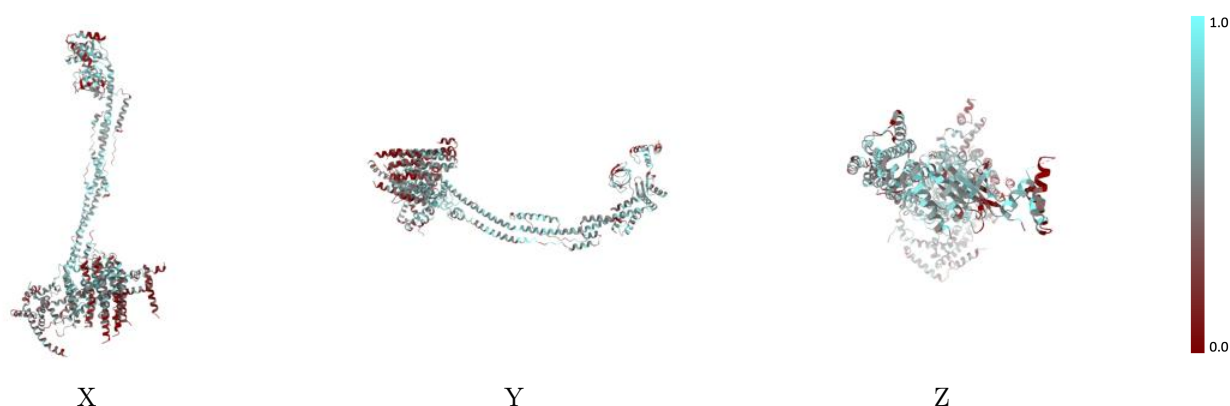
The images above show the 3D surface view of the map at the recommended contour level 0.0187 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



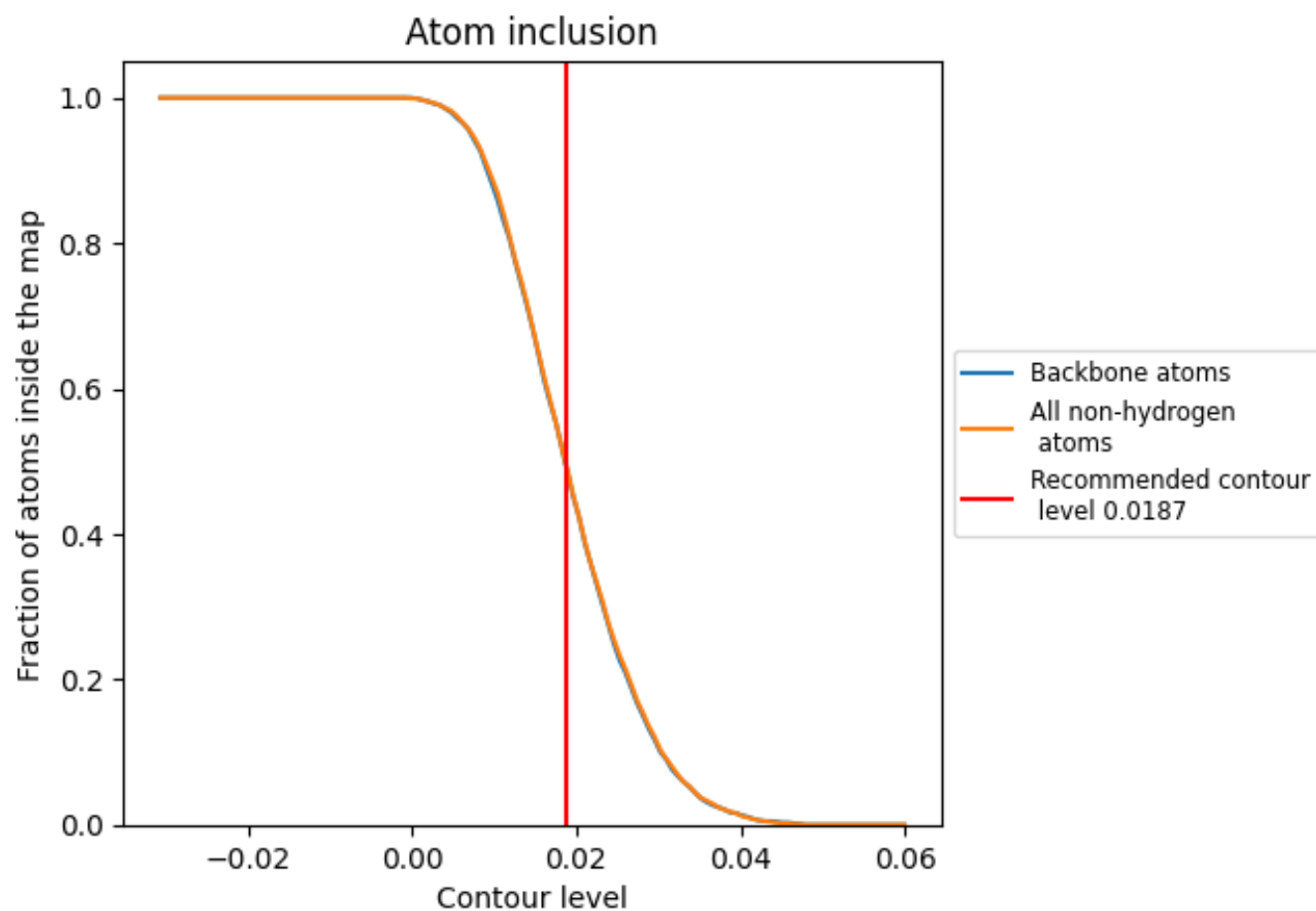
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0187).

9.4 Atom inclusion [i](#)



At the recommended contour level, 50% of all backbone atoms, 50% 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 (0.0187) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.4970	<div></div> 0.3850
8	<div></div> 0.5640	<div></div> 0.4680
C	<div></div> 0.4980	<div></div> 0.4010
M	<div></div> 0.3750	<div></div> 0.3840
N	<div></div> 0.3790	<div></div> 0.3810
O	<div></div> 0.2240	<div></div> 0.3610
S	<div></div> 0.4810	<div></div> 0.3240
a	<div></div> 0.5650	<div></div> 0.4300
b	<div></div> 0.6080	<div></div> 0.3970
d	<div></div> 0.5810	<div></div> 0.3970
e	<div></div> 0.4140	<div></div> 0.3410
f	<div></div> 0.5510	<div></div> 0.4200
g	<div></div> 0.3790	<div></div> 0.3380
h	<div></div> 0.4810	<div></div> 0.3010
j	<div></div> 0.3470	<div></div> 0.3870
k	<div></div> 0.1960	<div></div> 0.3220

1.0

0.0

<0.0