



Full wwPDB EM Validation Report ⓘ

Mar 23, 2026 – 04:19 AM UTC

PDB ID : 9B8Q / pdb_00009b8q
EMDB ID : EMD-44352
Title : Synaptic Vesicle V-ATPase with synaptophysin and SidK, State 3, peripheral stalks
Authors : Coupland, C.E.; Rubinstein, J.L.
Deposited on : 2024-03-31
Resolution : 3.80 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

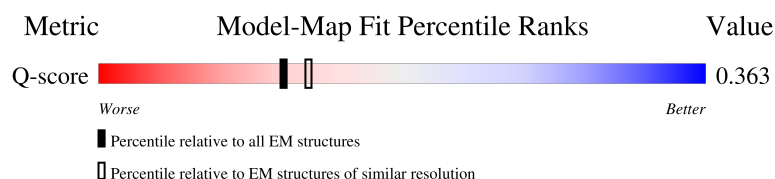
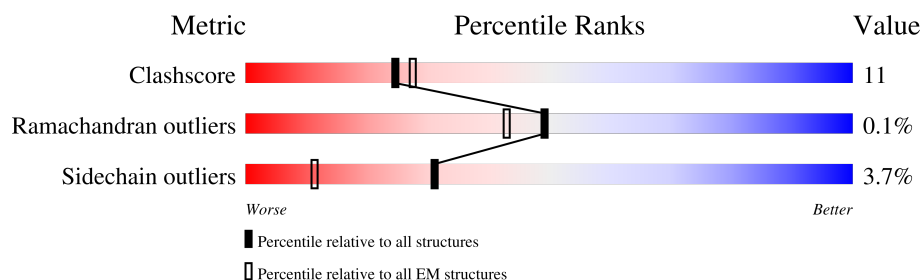
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	G	382	
2	I	226	
2	J	226	
2	K	226	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	M	118	9% 71% 15% 14%
3	N	118	73% 15% 10%
3	O	118	29% 76% 11% 13%
4	T	483	25% 88% 11%
5	a	838	27% 13% 60%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12348 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called V-type proton ATPase subunit C 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	G	375	Total	C	N	O	0	0
			2155	1347	400	408		

- Molecule 2 is a protein called V-type proton ATPase subunit E 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	148	Total	C	N	O	S	0	0
			1087	668	200	214	5		
2	J	149	Total	C	N	O	S	0	0
			1171	728	212	224	7		
2	K	137	Total	C	N	O	S	0	0
			914	561	171	177	5		

- Molecule 3 is a protein called V-type proton ATPase subunit G.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	M	102	Total	C	N	O	S	0	0
			740	440	156	140	4		
3	N	106	Total	C	N	O	S	0	0
			825	492	173	156	4		
3	O	103	Total	C	N	O	S	0	0
			625	370	127	125	3		

- Molecule 4 is a protein called V-type proton ATPase subunit H.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	T	430	Total	C	N	O	0	0
			2136	1276	430	430		

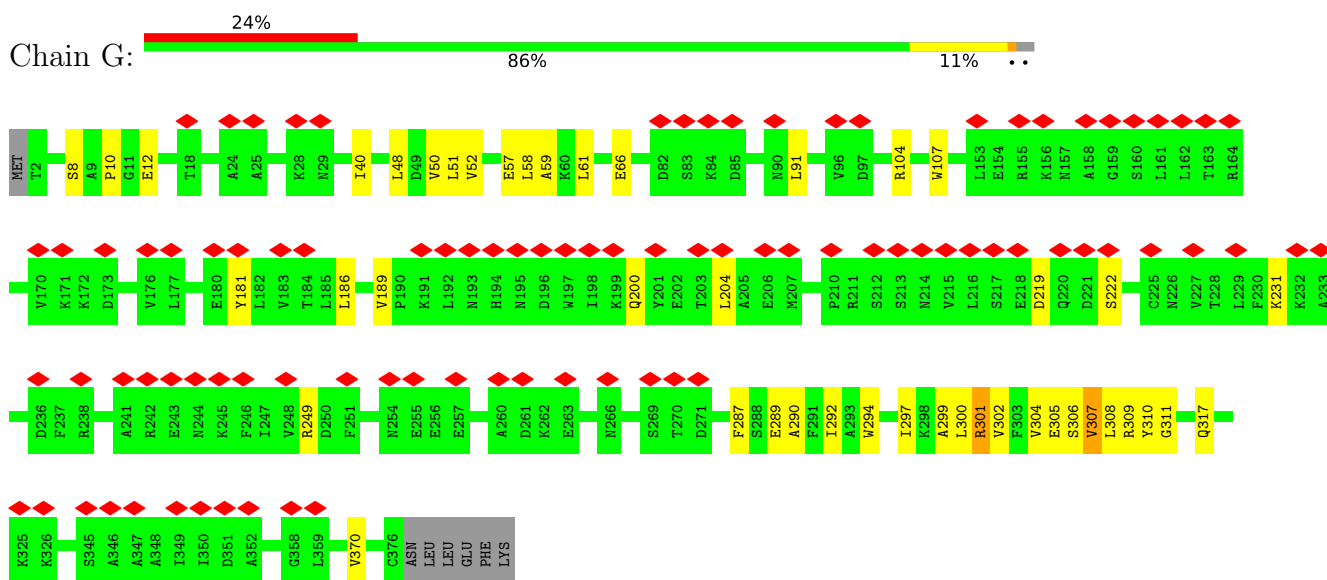
- Molecule 5 is a protein called V-type proton ATPase 116 kDa subunit a isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	a	336	Total	C	N	O	S	0	0
			2695	1697	487	494	17		

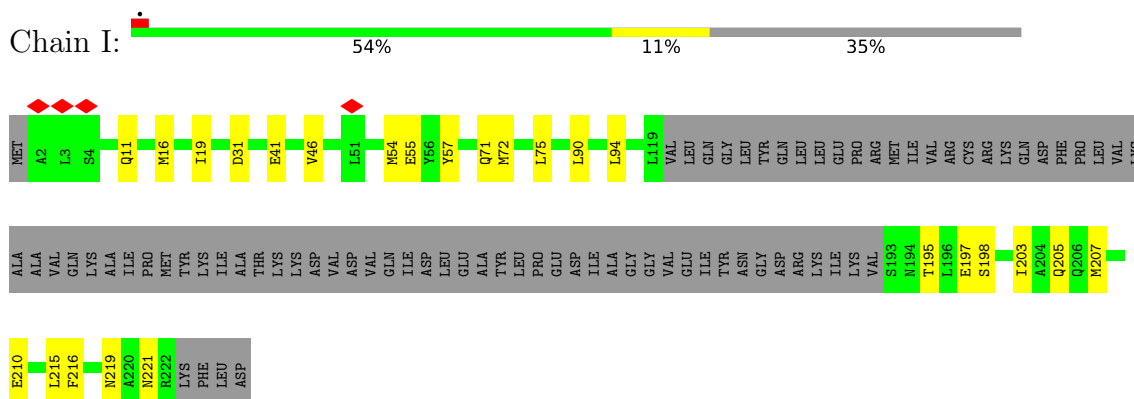
3 Residue-property plots

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: V-type proton ATPase subunit C 1

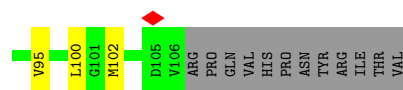


• Molecule 2: V-type proton ATPase subunit E 1

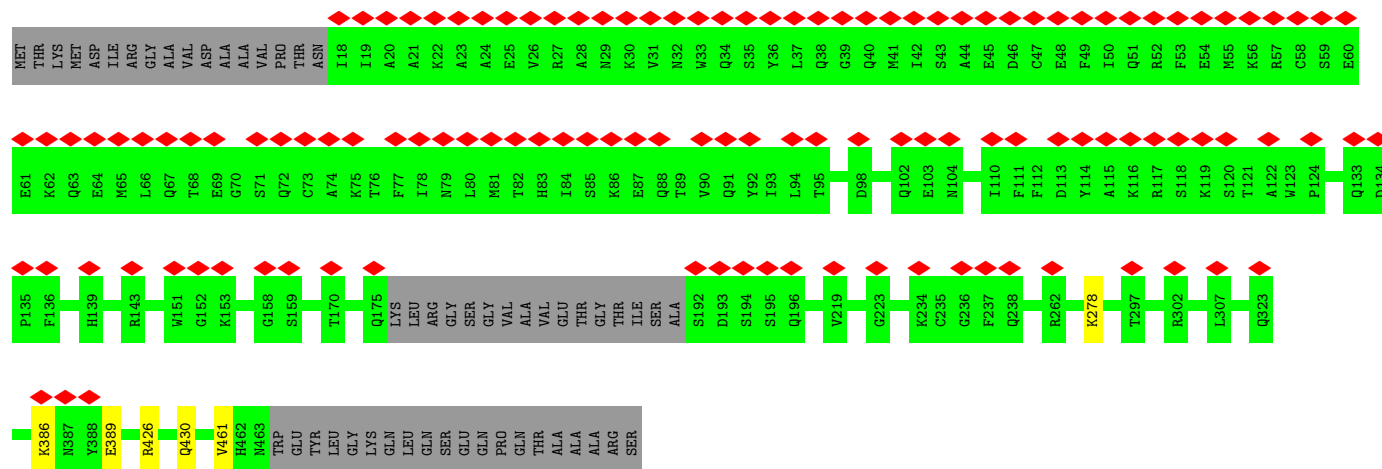
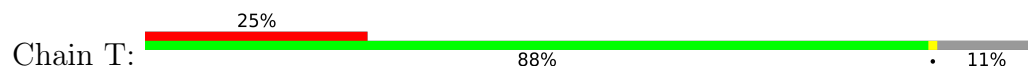


• Molecule 2: V-type proton ATPase subunit E 1

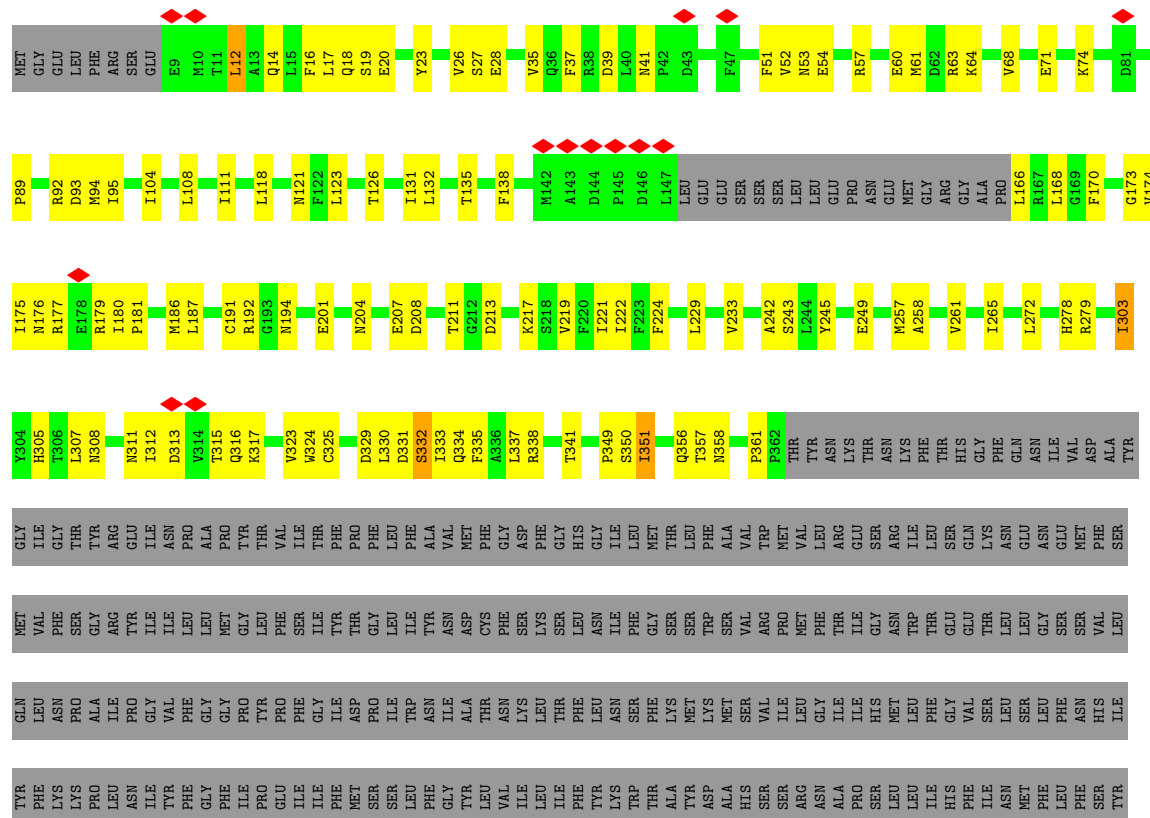




• Molecule 4: V-type proton ATPase subunit H



• Molecule 5: V-type proton ATPase 116 kDa subunit a isoform 1



HIS ALA LEU LEU ARG LEU LEU HIS TRP VAL PHE PHE GLN ASN LYS PHE TYR THR GLY THR GLY PHE LYS PHE GLU HIS ILE ARG GLU GLY LYS PHE ASP GLU	PRO	GLU	TRP	THR	PRO	THR	GLY	GLY	ASN	ALA	MET	LEU	LEU	TYR	SER	GLN	GLY	LYS	ILE	GLY	CYS	PHE	LEU	ILE	VAL	ALA	MET	LEU	CYS	VAL	PRO	TRP	MET	LEU	PHE	LEU	LYS	ARG	HIS	GLN	TYR	LEU	LYS	HIS	LEU	GLY	THR	CYS	ASN	PHE	GLY	ILE	ARG	VAL	GLY	ASN	PRO
	GLY	THR	PRO	GLU	GLU	ASP	ALA	GLU	GLN	ASP	HIS	THR	SER	ILE	GLU	ASP	GLY	PRO	THR	GLU	VAL	PHE	ASP	THR	MET	ILE	VAL	HIS	GLN	ALA	ILE	HIS	THR	GLU	CYS	LEU	GLY	THR	CYS	ILE	ASN	SER	THR	TYR	VAL	GLY	ASN	LEU	ARG								
	LEU	TRP	ALA	LEU	SER	LEU	ALA	HIS	LEU	SER	GLU	VAL	LEU	TRP	THR	MET	VAL	HIS	VAL	LEU	GLY	LEU	HIS	VAL	ARG	SER	LEU	ALA	GLY	GLY	LEU	PHE	PHE	ILE	ALA	PHE	ALA	THR	LEU	VAL	ALA	ILE	LEU	MET	GLU	GLY	SER	ALA	PHE	THR							

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	198533	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	37.5	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1900	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	1.027	Depositor
Minimum map value	-0.944	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.099	Depositor
Map size (Å)	309.0, 309.0, 309.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.03, 1.03, 1.03	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	G	0.24	0/2177	0.42	0/3017
2	I	0.27	0/1091	0.43	0/1465
2	J	0.25	0/1177	0.39	0/1573
2	K	0.26	0/915	0.40	0/1237
3	M	0.22	0/741	0.40	0/990
3	N	0.19	0/827	0.32	0/1100
3	O	0.71	1/624 (0.2%)	0.40	0/852
4	T	0.15	0/2134	0.30	0/2976
5	a	0.29	0/2737	0.44	0/3690
All	All	0.28	1/12423 (0.0%)	0.39	0/16900

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	O	17	ARG	C-N	17.07	1.56	1.33

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	G	2155	0	1372	37	0
2	I	1087	0	1000	23	0
2	J	1171	0	1169	34	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	K	914	0	782	18	0
3	M	740	0	677	18	0
3	N	825	0	811	20	0
3	O	625	0	472	15	0
4	T	2136	0	948	4	0
5	a	2695	0	2656	96	0
All	All	12348	0	9887	235	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 11.

All (235) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:a:57:ARG:NH2	5:a:94:MET:SD	2.53	0.81
2:J:211:VAL:HG23	3:N:95:VAL:HG11	1.61	0.81
5:a:187:LEU:HD11	5:a:222:ILE:HD11	1.61	0.81
5:a:356:GLN:N	5:a:356:GLN:OE1	2.16	0.79
5:a:176:ASN:OD1	5:a:217:LYS:NZ	2.16	0.78
5:a:316:GLN:OE1	5:a:317:LYS:N	2.15	0.78
1:G:181:TYR:O	1:G:231:LYS:N	2.16	0.78
2:J:215:LEU:O	3:N:87:SER:OG	2.03	0.76
2:J:195:THR:O	2:J:198:SER:OG	2.04	0.76
2:I:197:GLU:N	2:I:197:GLU:OE1	2.19	0.76
5:a:111:ILE:HD11	5:a:278:HIS:ND1	2.02	0.75
1:G:317:GLN:OE1	1:G:317:GLN:N	2.18	0.75
2:K:57:TYR:OH	3:O:48:ARG:O	2.05	0.74
3:N:11:LEU:HD12	5:a:168:LEU:HD11	1.68	0.74
1:G:200:GLN:O	1:G:204:LEU:N	2.22	0.73
2:K:219:ASN:OD1	2:K:221:ASN:N	2.22	0.72
5:a:175:ILE:HD13	5:a:242:ALA:HB2	1.73	0.70
3:M:73:VAL:O	3:M:77:THR:HG23	1.90	0.70
3:M:3:SER:O	3:M:7:GLY:N	2.23	0.70
3:N:42:MET:N	3:N:42:MET:HE2	2.06	0.69
5:a:311:ASN:OD1	5:a:312:ILE:N	2.25	0.69
2:I:75:LEU:HD11	3:M:73:VAL:HG11	1.73	0.69
3:O:74:GLU:OE1	3:O:75:GLN:N	2.26	0.69
1:G:289:GLU:OE1	1:G:290:ALA:N	2.26	0.67
5:a:187:LEU:HD11	5:a:222:ILE:CD1	2.25	0.67
5:a:138:PHE:HD2	5:a:221:ILE:HD12	1.61	0.65
5:a:175:ILE:CD1	5:a:242:ALA:HB2	2.28	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:215:LEU:HD21	3:O:95:VAL:HG11	1.81	0.62
5:a:338:ARG:O	5:a:341:THR:OG1	2.16	0.62
5:a:39:ASP:OD1	5:a:41:ASN:N	2.33	0.62
5:a:27:SER:HA	5:a:303:ILE:HD11	1.81	0.61
5:a:211:THR:HG22	5:a:213:ASP:OD1	2.01	0.61
5:a:132:LEU:HD11	5:a:257:MET:SD	2.41	0.61
5:a:135:THR:OG1	5:a:221:ILE:HD11	2.00	0.61
5:a:329:ASP:O	5:a:332:SER:OG	2.15	0.60
1:G:40:ILE:CD1	1:G:299:ALA:HB1	2.32	0.60
1:G:40:ILE:HD11	1:G:299:ALA:HB1	1.84	0.60
5:a:249:GLU:N	5:a:249:GLU:OE1	2.35	0.60
3:N:52:GLU:O	3:N:56:GLN:NE2	2.35	0.59
5:a:35:VAL:HG22	5:a:325:CYS:SG	2.42	0.59
2:J:36:GLU:O	2:J:40:ILE:HG22	2.03	0.58
2:I:203:ILE:HD11	3:M:102:MET:HG2	1.85	0.58
2:J:55:GLU:OE1	2:J:56:TYR:N	2.37	0.58
1:G:48:LEU:HD13	2:J:18:PHE:CG	2.38	0.58
2:I:90:LEU:HD22	3:M:88:GLN:HG3	1.85	0.58
3:O:73:VAL:O	3:O:77:THR:HG23	2.04	0.57
3:M:45:GLU:OE2	3:M:46:GLN:N	2.37	0.57
2:I:94:LEU:CD1	2:I:215:LEU:HD11	2.35	0.57
2:J:115:LEU:CD2	2:J:119:LEU:HD11	2.35	0.56
1:G:305:GLU:CG	1:G:370:VAL:HG13	2.36	0.56
1:G:61:LEU:HB3	1:G:297:ILE:HD13	1.88	0.55
5:a:26:VAL:HG11	5:a:307:LEU:HD21	1.89	0.55
2:J:115:LEU:HD22	2:J:119:LEU:HD11	1.89	0.55
1:G:104:ARG:NH1	1:G:104:ARG:HA	2.21	0.54
5:a:126:THR:HA	5:a:265:ILE:HD11	1.89	0.54
2:J:87:ARG:CD	3:N:84:MET:HE1	2.37	0.54
5:a:331:ASP:OD1	5:a:331:ASP:N	2.41	0.54
5:a:57:ARG:HB2	5:a:94:MET:HE1	1.89	0.54
3:N:42:MET:HE2	3:N:42:MET:CA	2.37	0.54
1:G:57:GLU:OE1	1:G:57:GLU:HA	2.09	0.53
2:J:92:THR:O	2:J:96:ASN:OD1	2.26	0.53
2:K:207:MET:O	2:K:208:MET:C	2.51	0.53
1:G:58:LEU:O	1:G:301:ARG:NE	2.35	0.53
2:I:31:ASP:C	2:I:31:ASP:OD1	2.51	0.53
5:a:51:PHE:HB2	5:a:308:ASN:OD1	2.09	0.52
5:a:60:GLU:OE1	5:a:61:MET:N	2.42	0.52
3:M:41:GLN:OE1	3:M:41:GLN:HA	2.08	0.52
2:K:79:ALA:HB1	3:O:77:THR:HG22	1.91	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:a:222:ILE:HG21	5:a:233:VAL:HG11	1.91	0.52
5:a:104:ILE:O	5:a:104:ILE:HG22	2.09	0.52
1:G:305:GLU:OE2	1:G:309:ARG:NH2	2.43	0.51
2:J:11:GLN:O	2:J:15:MET:SD	2.68	0.51
5:a:313:ASP:OD1	5:a:317:LYS:HA	2.10	0.51
5:a:138:PHE:CD2	5:a:221:ILE:HD12	2.44	0.51
2:I:71:GLN:C	2:I:71:GLN:CD	2.79	0.51
3:N:53:GLN:OE1	3:N:53:GLN:O	2.29	0.51
5:a:187:LEU:HD21	5:a:233:VAL:HG22	1.93	0.51
2:I:207:MET:HE3	3:M:102:MET:HE1	1.93	0.51
5:a:135:THR:HA	5:a:221:ILE:HD11	1.92	0.51
2:J:38:PHE:CD2	3:N:36:ALA:HB2	2.47	0.50
5:a:16:PHE:HD2	5:a:351:ILE:HG23	1.77	0.50
5:a:123:LEU:HD11	5:a:207:GLU:CG	2.41	0.50
2:J:102:LEU:HD11	2:J:200:LEU:HD13	1.93	0.50
5:a:186:MET:HA	5:a:186:MET:HE2	1.94	0.50
5:a:335:PHE:CD1	5:a:335:PHE:C	2.89	0.50
5:a:334:GLN:OE1	5:a:335:PHE:N	2.44	0.50
3:M:78:ARG:NE	3:M:78:ARG:HA	2.27	0.50
1:G:305:GLU:HG3	1:G:370:VAL:HG13	1.93	0.50
2:I:219:ASN:OD1	2:I:219:ASN:C	2.54	0.50
2:K:200:LEU:O	2:K:200:LEU:HD23	2.12	0.49
5:a:118:LEU:CB	5:a:272:LEU:HD21	2.42	0.49
2:I:41:GLU:HA	2:I:41:GLU:OE1	2.13	0.49
2:J:87:ARG:HG3	3:N:84:MET:HE1	1.94	0.49
2:K:200:LEU:HD23	2:K:200:LEU:C	2.37	0.49
2:I:57:TYR:OH	3:M:52:GLU:OE2	2.21	0.49
2:J:102:LEU:HA	2:J:105:VAL:HG12	1.95	0.49
2:I:71:GLN:OE1	2:I:72:MET:N	2.45	0.49
2:J:80:ARG:O	2:J:83:VAL:HG12	2.13	0.49
5:a:175:ILE:HG22	5:a:176:ASN:N	2.28	0.49
5:a:194:ASN:OD1	5:a:229:LEU:HD13	2.13	0.49
5:a:204:ASN:OD1	5:a:204:ASN:O	2.31	0.49
2:K:180:GLY:O	2:K:181:VAL:HG23	2.12	0.48
2:K:80:ARG:O	2:K:83:VAL:HG12	2.13	0.48
5:a:131:ILE:HD11	5:a:173:GLY:HA2	1.95	0.48
2:J:208:MET:O	2:J:211:VAL:HG12	2.14	0.48
1:G:305:GLU:OE2	5:a:192:ARG:HD3	2.14	0.48
2:K:79:ALA:HB1	3:O:77:THR:CG2	2.44	0.48
3:N:15:GLU:OE2	5:a:166:LEU:N	2.47	0.48
2:K:219:ASN:OD1	2:K:219:ASN:C	2.57	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:a:26:VAL:HG11	5:a:307:LEU:CD2	2.44	0.47
2:J:4:SER:O	2:J:7:ASP:N	2.47	0.47
4:T:278:LYS:N	5:a:20:GLU:OE2	2.47	0.47
3:N:41:GLN:C	3:N:42:MET:HE2	2.38	0.47
3:O:100:LEU:O	3:O:100:LEU:HD23	2.14	0.47
5:a:23:TYR:CD1	5:a:23:TYR:C	2.92	0.47
5:a:224:PHE:CD1	5:a:224:PHE:N	2.83	0.47
4:T:426:ARG:O	4:T:430:GLN:N	2.39	0.47
2:I:94:LEU:HD12	2:I:215:LEU:HD11	1.95	0.47
2:I:219:ASN:OD1	2:I:221:ASN:N	2.42	0.47
3:M:99:LEU:HD23	3:M:99:LEU:O	2.15	0.47
3:O:72:GLU:HA	3:O:72:GLU:OE1	2.14	0.47
5:a:191:CYS:SG	5:a:229:LEU:HD23	2.54	0.47
5:a:191:CYS:O	5:a:194:ASN:ND2	2.48	0.47
2:I:94:LEU:HD23	2:I:94:LEU:O	2.16	0.46
3:N:42:MET:HE2	3:N:42:MET:HA	1.96	0.46
5:a:92:ARG:O	5:a:95:ILE:HD12	2.14	0.46
1:G:51:LEU:CD1	1:G:304:VAL:HG22	2.46	0.46
2:K:208:MET:O	2:K:209:PRO:C	2.58	0.46
3:O:100:LEU:HD23	3:O:100:LEU:C	2.40	0.46
2:J:102:LEU:HD12	2:J:200:LEU:HD22	1.98	0.46
2:K:207:MET:HE2	3:O:102:MET:HE3	1.98	0.46
2:J:196:LEU:H	2:J:196:LEU:HD12	1.80	0.45
1:G:186:LEU:O	1:G:249:ARG:CB	2.64	0.45
2:J:100:GLN:OE1	2:J:101:ARG:N	2.49	0.45
5:a:208:ASP:OD2	5:a:213:ASP:N	2.46	0.45
2:J:208:MET:HA	2:J:211:VAL:HG12	1.97	0.45
5:a:12:LEU:HD23	5:a:324:TRP:CE3	2.52	0.45
5:a:27:SER:OG	5:a:28:GLU:OE2	2.35	0.45
5:a:111:ILE:HG21	5:a:279:ARG:HG3	1.98	0.45
1:G:8:SER:CB	1:G:370:VAL:HB	2.47	0.45
3:M:79:ARG:HE	3:M:79:ARG:C	2.24	0.45
1:G:52:VAL:HG21	5:a:229:LEU:HD21	1.98	0.45
3:M:41:GLN:HA	3:M:44:VAL:HG22	1.98	0.45
5:a:17:LEU:HD23	5:a:17:LEU:N	2.32	0.45
1:G:48:LEU:HD13	2:J:18:PHE:CD1	2.52	0.45
3:O:74:GLU:O	3:O:77:THR:OG1	2.29	0.45
5:a:334:GLN:HA	5:a:337:LEU:HD12	1.98	0.45
5:a:357:THR:HG22	5:a:358:ASN:H	1.82	0.45
1:G:91:LEU:O	1:G:287:PHE:CD1	2.70	0.44
1:G:104:ARG:HA	1:G:104:ARG:HH11	1.82	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:58:LEU:HD13	1:G:300:LEU:HB3	1.98	0.44
2:J:23:ALA:HB2	3:N:18:ALA:HB1	1.99	0.44
3:N:85:GLN:C	3:N:85:GLN:CD	2.85	0.44
2:J:207:MET:O	2:J:208:MET:C	2.59	0.44
2:K:75:LEU:C	2:K:75:LEU:HD23	2.43	0.44
3:N:88:GLN:OE1	3:N:89:GLN:N	2.49	0.44
1:G:51:LEU:HD11	1:G:304:VAL:HG22	1.99	0.44
5:a:324:TRP:CZ2	5:a:361:PRO:HA	2.52	0.44
1:G:219:ASP:N	1:G:222:SER:O	2.49	0.44
2:K:57:TYR:OH	3:O:52:GLU:CB	2.66	0.44
5:a:54:GLU:OE1	5:a:54:GLU:HA	2.17	0.44
2:I:71:GLN:C	2:I:71:GLN:OE1	2.61	0.44
5:a:330:LEU:HA	5:a:333:ILE:HD12	2.00	0.44
1:G:59:ALA:HA	1:G:301:ARG:NH2	2.32	0.44
3:M:38:GLU:C	3:M:38:GLU:OE1	2.61	0.44
5:a:123:LEU:HD11	5:a:207:GLU:HG3	1.98	0.44
2:I:215:LEU:C	2:I:216:PHE:CD1	2.96	0.43
4:T:386:LYS:CB	4:T:389:GLU:CB	2.96	0.43
2:I:94:LEU:HD23	2:I:94:LEU:C	2.43	0.43
5:a:18:GLN:OE1	5:a:19:SER:N	2.50	0.43
5:a:35:VAL:HG11	5:a:37:PHE:HE1	1.83	0.43
3:N:106:VAL:HG23	3:N:107:ARG:N	2.32	0.43
5:a:170:PHE:CE2	5:a:221:ILE:HG23	2.53	0.43
5:a:180:ILE:N	5:a:181:PRO:HD2	2.34	0.43
2:I:16:MET:O	2:I:19:ILE:HG22	2.18	0.43
3:O:75:GLN:OE1	3:O:75:GLN:HA	2.18	0.43
5:a:52:VAL:O	5:a:53:ASN:C	2.59	0.43
1:G:305:GLU:HG2	1:G:370:VAL:HG13	2.00	0.43
1:G:307:VAL:O	1:G:308:LEU:C	2.60	0.43
1:G:10:PRO:CB	1:G:310:TYR:CZ	3.02	0.43
2:K:179:GLY:C	2:K:196:LEU:HG	2.44	0.43
1:G:58:LEU:CD1	1:G:300:LEU:HB3	2.49	0.43
5:a:71:GLU:OE1	5:a:74:LYS:NZ	2.45	0.43
5:a:341:THR:HG21	5:a:349:PRO:HA	2.00	0.43
1:G:107:TRP:C	1:G:107:TRP:CD1	2.97	0.42
3:M:43:GLU:OE1	3:M:43:GLU:HA	2.19	0.42
5:a:35:VAL:HG22	5:a:325:CYS:HG	1.84	0.42
5:a:118:LEU:HB3	5:a:272:LEU:HD21	2.01	0.42
1:G:302:VAL:O	1:G:306:SER:HB3	2.19	0.42
3:N:107:ARG:NH1	3:N:107:ARG:HB2	2.34	0.42
5:a:35:VAL:HG13	5:a:323:VAL:CG1	2.49	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:a:177:ARG:HG3	5:a:177:ARG:HH11	1.83	0.42
2:J:100:GLN:CD	2:J:100:GLN:C	2.88	0.42
5:a:131:ILE:HG12	5:a:219:VAL:HG23	2.01	0.42
5:a:175:ILE:HD13	5:a:242:ALA:CB	2.46	0.42
3:N:100:LEU:C	3:N:100:LEU:HD23	2.44	0.42
5:a:68:VAL:HG21	5:a:104:ILE:HG22	2.01	0.42
2:K:203:ILE:HD13	3:O:102:MET:SD	2.60	0.42
5:a:89:PRO:CB	5:a:93:ASP:OD2	2.68	0.42
2:J:16:MET:O	2:J:19:ILE:HG22	2.20	0.42
3:N:106:VAL:CG2	3:N:107:ARG:N	2.83	0.42
5:a:177:ARG:NH1	5:a:201:GLU:OE2	2.53	0.42
2:J:15:MET:HE2	2:J:15:MET:HB2	1.91	0.42
5:a:243:SER:HB3	5:a:245:TYR:CZ	2.54	0.42
1:G:10:PRO:O	1:G:12:GLU:N	2.47	0.42
1:G:311:GLY:HA2	2:J:18:PHE:CZ	2.55	0.42
2:J:75:LEU:HD23	2:J:75:LEU:HA	1.88	0.42
3:M:33:LEU:O	3:M:33:LEU:HD23	2.20	0.42
5:a:132:LEU:HD12	5:a:258:ALA:HA	2.01	0.42
2:J:63:GLN:CD	2:J:63:GLN:C	2.87	0.42
5:a:329:ASP:OD1	5:a:329:ASP:N	2.53	0.41
5:a:357:THR:HG22	5:a:358:ASN:N	2.35	0.41
2:I:195:THR:O	2:I:198:SER:N	2.52	0.41
5:a:63:ARG:O	5:a:64:LYS:C	2.62	0.41
5:a:104:ILE:O	5:a:104:ILE:CG2	2.68	0.41
1:G:61:LEU:HD13	1:G:297:ILE:HD11	2.03	0.41
2:I:11:GLN:CB	5:a:351:ILE:HD13	2.50	0.41
5:a:311:ASN:HD21	5:a:315:THR:HG21	1.85	0.41
2:K:215:LEU:HD23	3:O:91:ASN:HB2	2.03	0.41
2:J:84:LEU:CD2	2:J:87:ARG:NH2	2.84	0.41
5:a:187:LEU:CD1	5:a:222:ILE:HD11	2.43	0.41
1:G:66:GLU:OE1	1:G:294:TRP:CZ2	2.74	0.41
2:I:54:MET:HE3	2:I:54:MET:HA	2.02	0.41
2:J:50:ARG:HG2	2:J:54:MET:HE3	2.01	0.41
4:T:461:VAL:O	5:a:121:ASN:ND2	2.54	0.41
5:a:131:ILE:HA	5:a:219:VAL:HG21	2.03	0.40
5:a:118:LEU:HB2	5:a:272:LEU:HD21	2.02	0.40
2:I:203:ILE:HD11	3:M:102:MET:CG	2.49	0.40
5:a:174:VAL:HG22	5:a:217:LYS:HE3	2.03	0.40
5:a:177:ARG:C	5:a:179:ARG:H	2.30	0.40
1:G:200:GLN:O	1:G:204:LEU:CA	2.69	0.40
2:J:100:GLN:OE1	2:J:100:GLN:C	2.65	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:a:337:LEU:HD22	5:a:350:SER:OG	2.21	0.40
3:M:45:GLU:CD	3:M:45:GLU:C	2.90	0.40
5:a:191:CYS:SG	5:a:229:LEU:CD2	3.09	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	G	373/382 (98%)	345 (92%)	27 (7%)	1 (0%)	36	67
2	I	144/226 (64%)	139 (96%)	5 (4%)	0	100	100
2	J	145/226 (64%)	142 (98%)	3 (2%)	0	100	100
2	K	131/226 (58%)	127 (97%)	4 (3%)	0	100	100
3	M	100/118 (85%)	100 (100%)	0	0	100	100
3	N	104/118 (88%)	103 (99%)	1 (1%)	0	100	100
3	O	101/118 (86%)	100 (99%)	1 (1%)	0	100	100
4	T	426/483 (88%)	416 (98%)	10 (2%)	0	100	100
5	a	332/838 (40%)	304 (92%)	28 (8%)	0	100	100
All	All	1856/2735 (68%)	1776 (96%)	79 (4%)	1 (0%)	49	79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	189	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	77/344 (22%)	73 (95%)	4 (5%)	21	46
2	I	96/198 (48%)	92 (96%)	4 (4%)	26	50
2	J	119/198 (60%)	114 (96%)	5 (4%)	26	50
2	K	67/198 (34%)	64 (96%)	3 (4%)	24	48
3	M	60/100 (60%)	59 (98%)	1 (2%)	53	67
3	N	78/100 (78%)	74 (95%)	4 (5%)	21	46
3	O	35/100 (35%)	34 (97%)	1 (3%)	37	58
5	a	288/743 (39%)	280 (97%)	8 (3%)	38	58
All	All	820/1981 (41%)	790 (96%)	30 (4%)	31	54

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	50	VAL
1	G	292	ILE
1	G	301	ARG
1	G	307	VAL
2	I	46	VAL
2	I	55	GLU
2	I	205	GLN
2	I	210	GLU
2	J	31	ASP
2	J	42	LYS
2	J	55	GLU
2	J	75	LEU
2	J	201	ASP
2	K	92	THR
2	K	198	SER
2	K	203	ILE
3	M	103	VAL
3	N	44	VAL
3	N	52	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	N	88	GLN
3	N	103	VAL
3	O	84	MET
5	a	12	LEU
5	a	14	GLN
5	a	108	LEU
5	a	261	VAL
5	a	303	ILE
5	a	305	HIS
5	a	332	SER
5	a	351	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	286	ASN
2	I	205	GLN
2	J	14	HIS
2	J	63	GLN
2	K	77	ASN
3	M	35	GLN
3	O	89	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

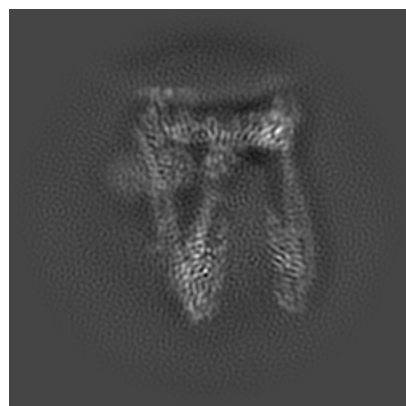
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44352. These allow visual inspection of the internal detail of the map and identification of artifacts.

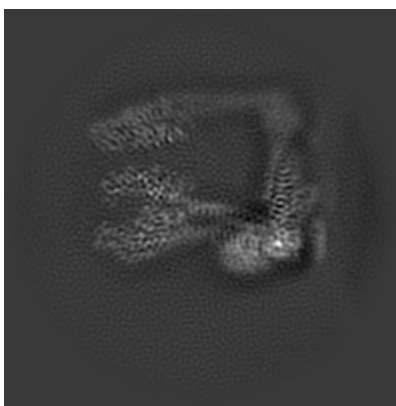
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

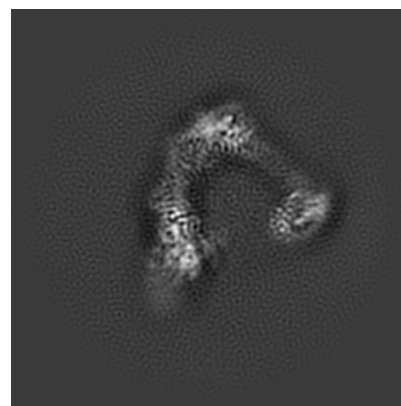
6.1.1 Primary map



X

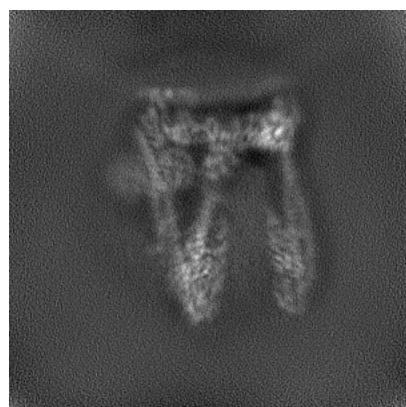


Y

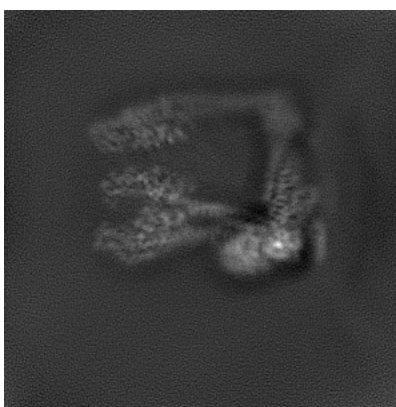


Z

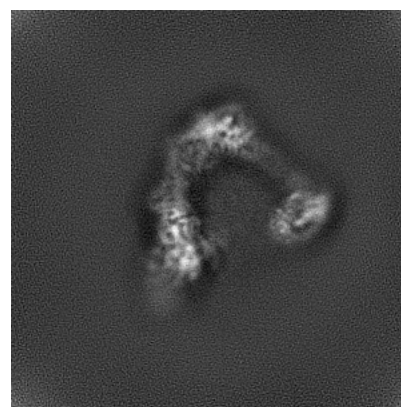
6.1.2 Raw map



X



Y

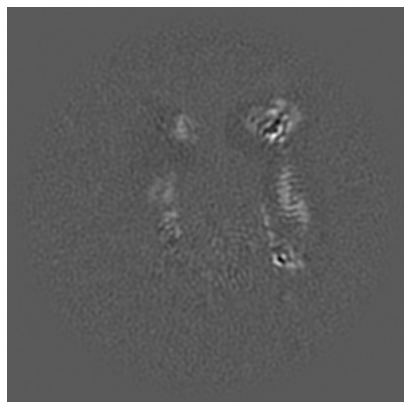


Z

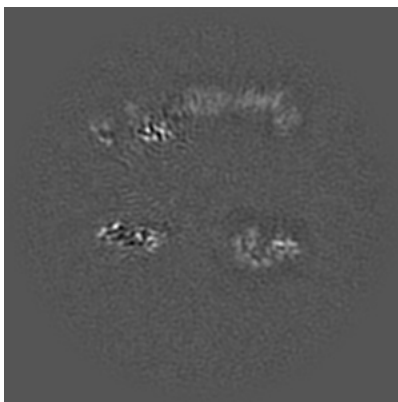
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

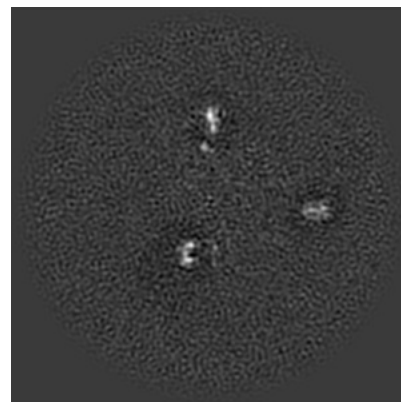
6.2.1 Primary map



X Index: 150



Y Index: 150

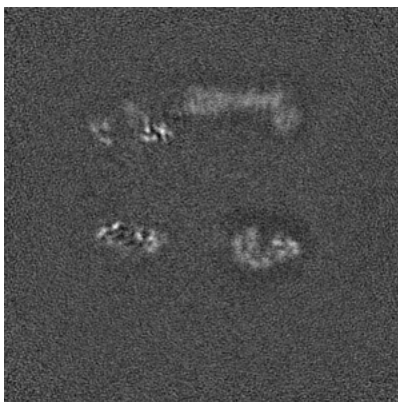


Z Index: 150

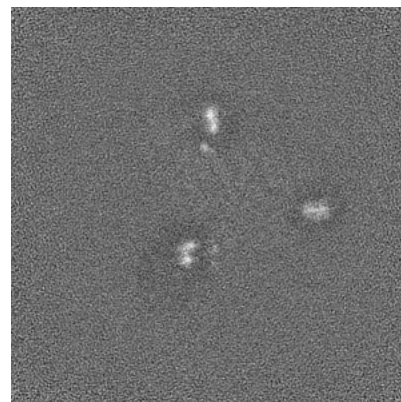
6.2.2 Raw map



X Index: 150



Y Index: 150

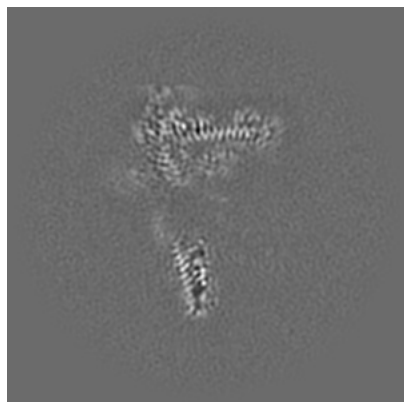


Z Index: 150

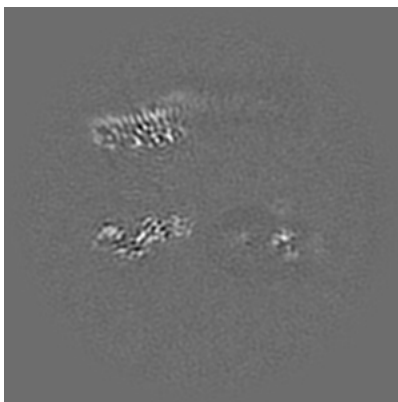
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

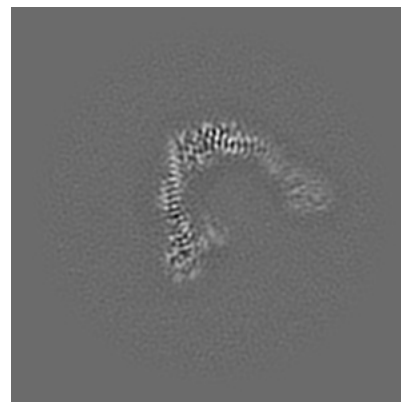
6.3.1 Primary map



X Index: 124

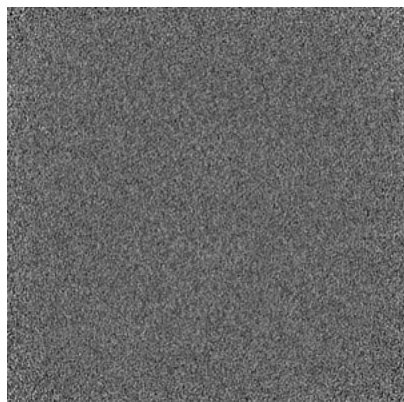


Y Index: 141

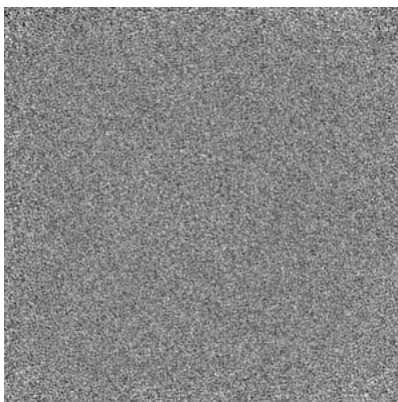


Z Index: 207

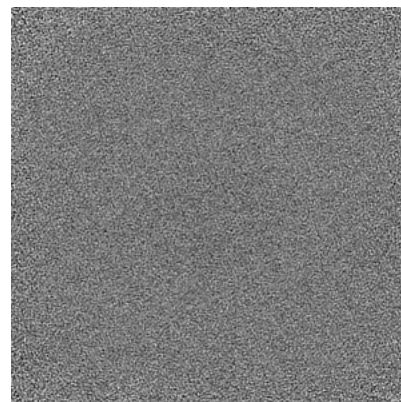
6.3.2 Raw map



X Index: 0



Y Index: 0

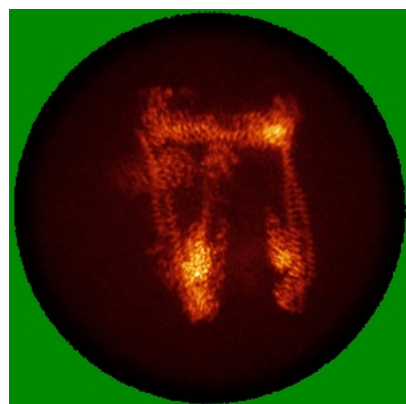


Z Index: 0

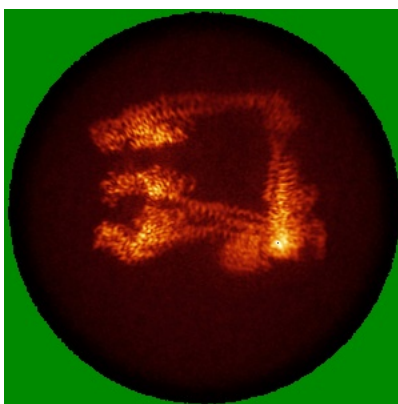
The images above show the largest variance slices of the map in three orthogonal directions.

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

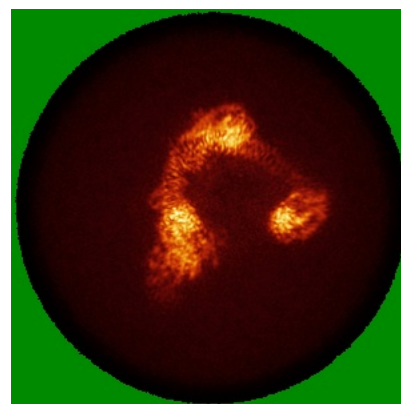
6.4.1 Primary map



X

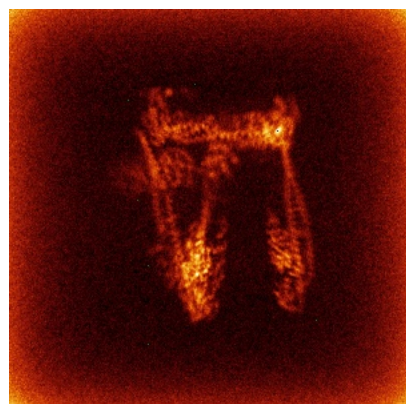


Y

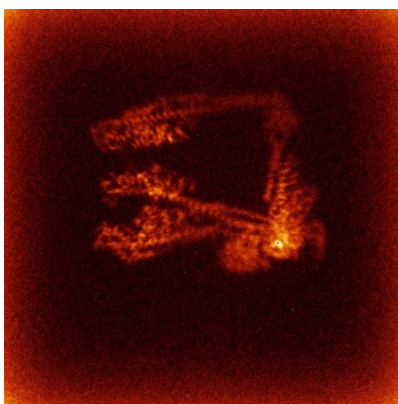


Z

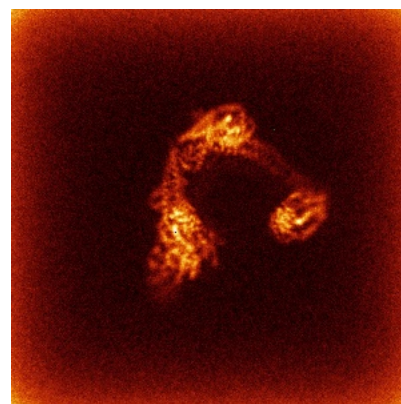
6.4.2 Raw map



X



Y

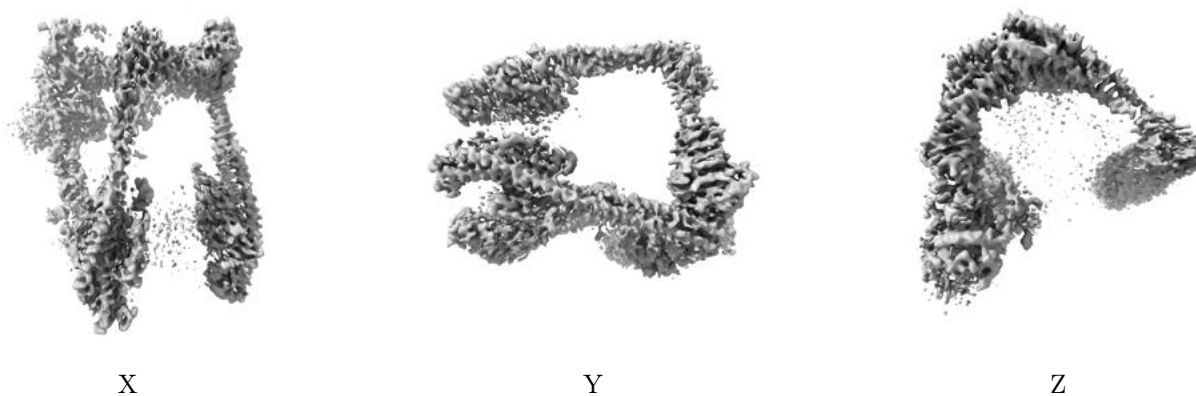


Z

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.

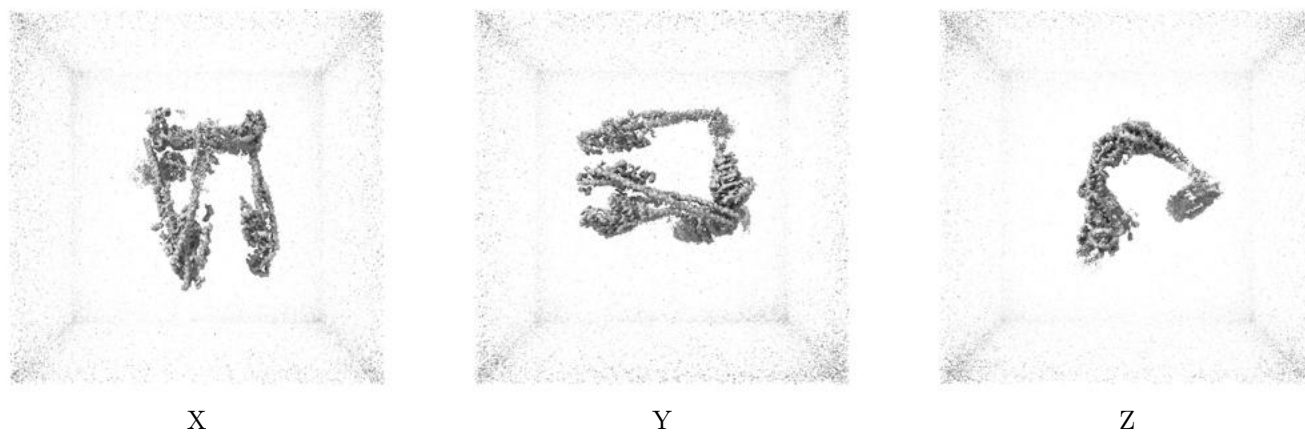
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.099. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

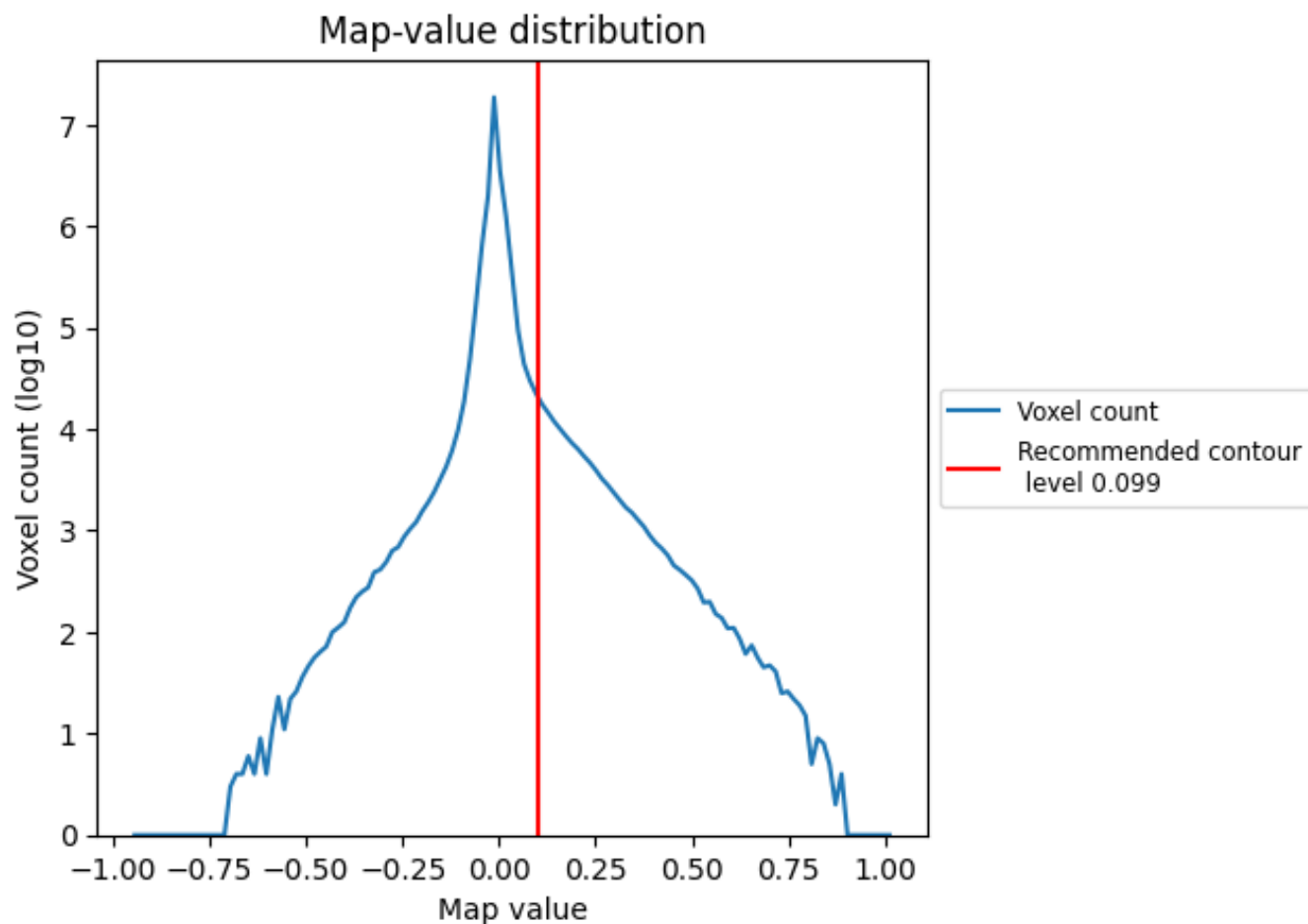
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

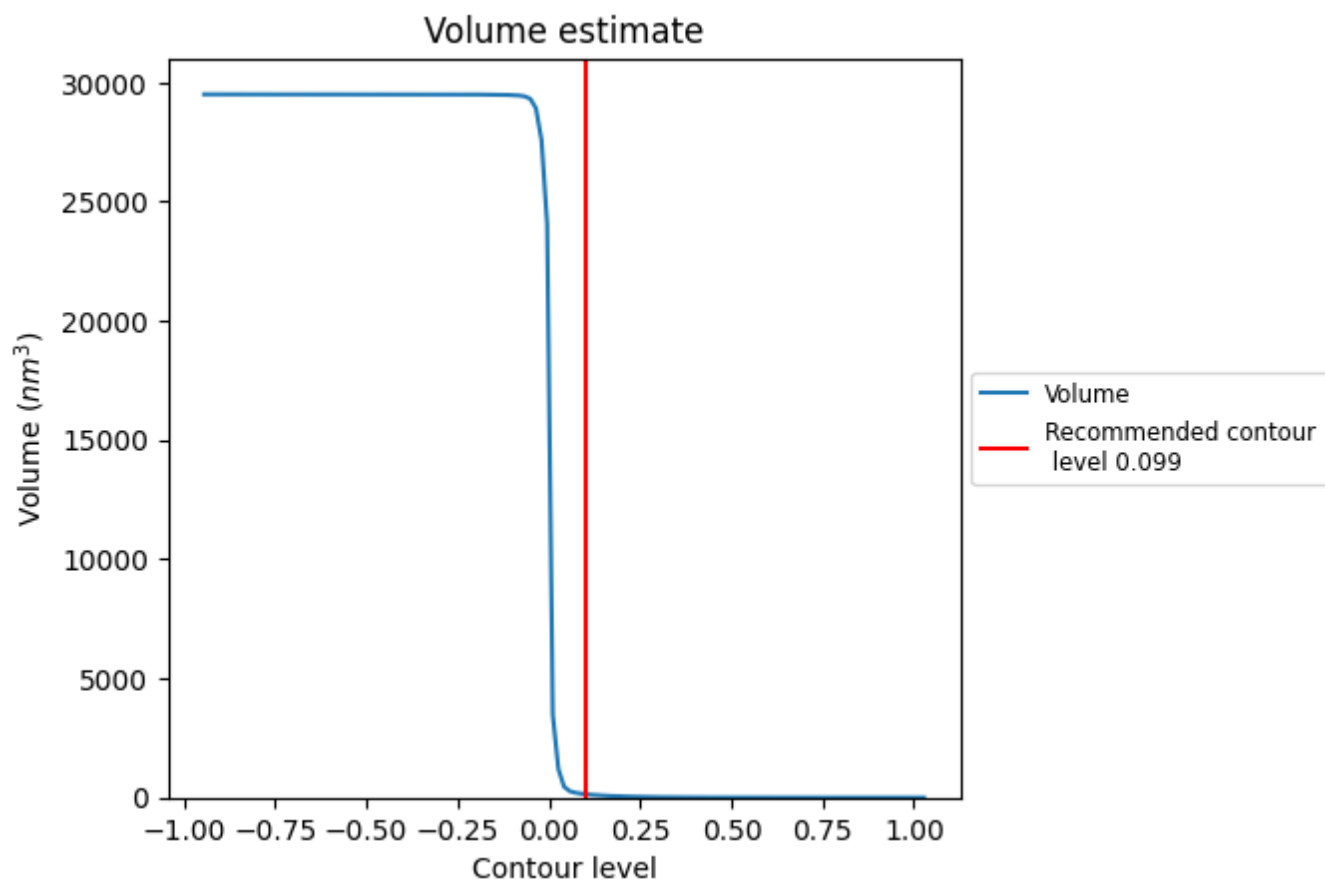
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

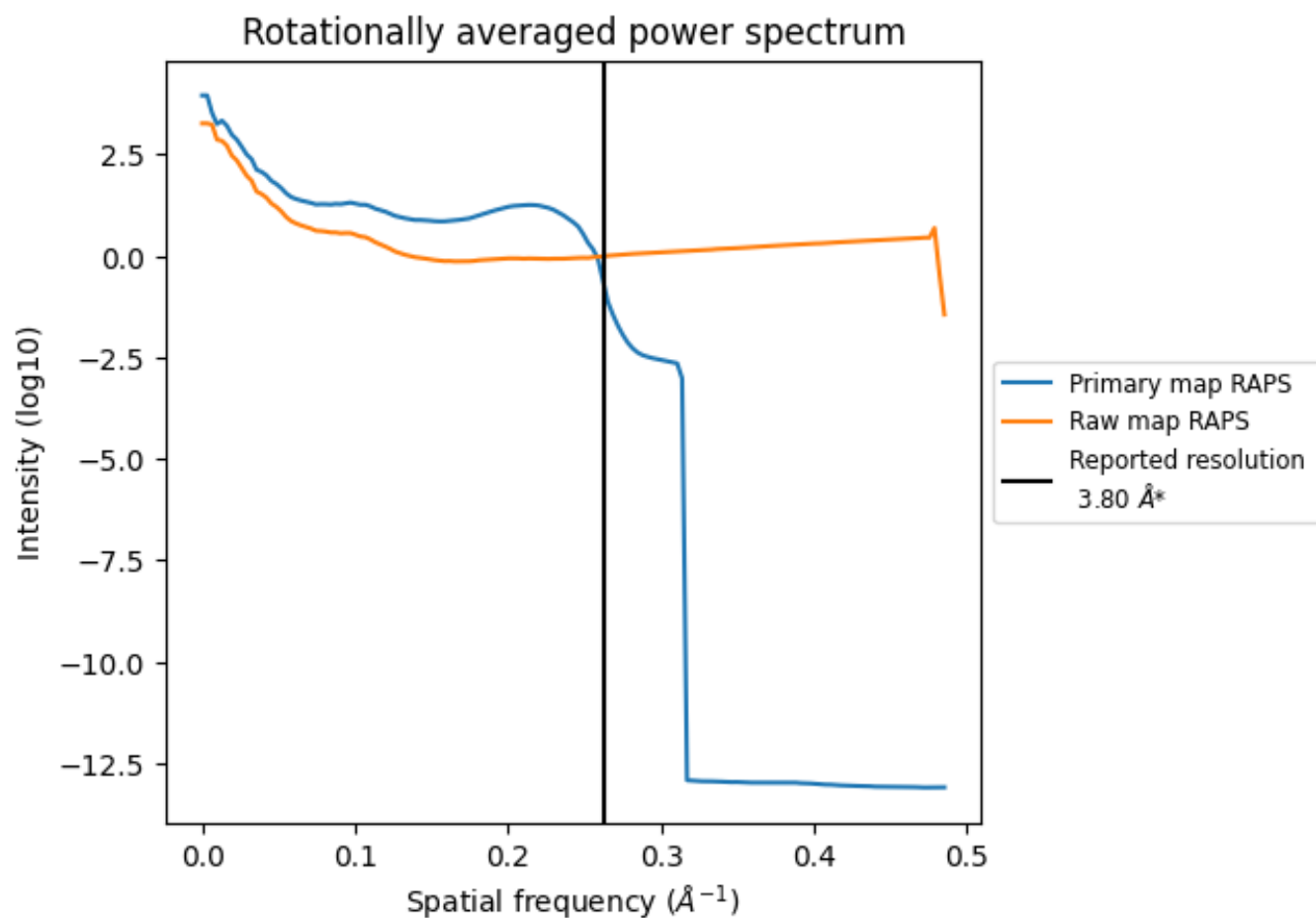
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 143 nm³; this corresponds to an approximate mass of 130 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 ⓘ

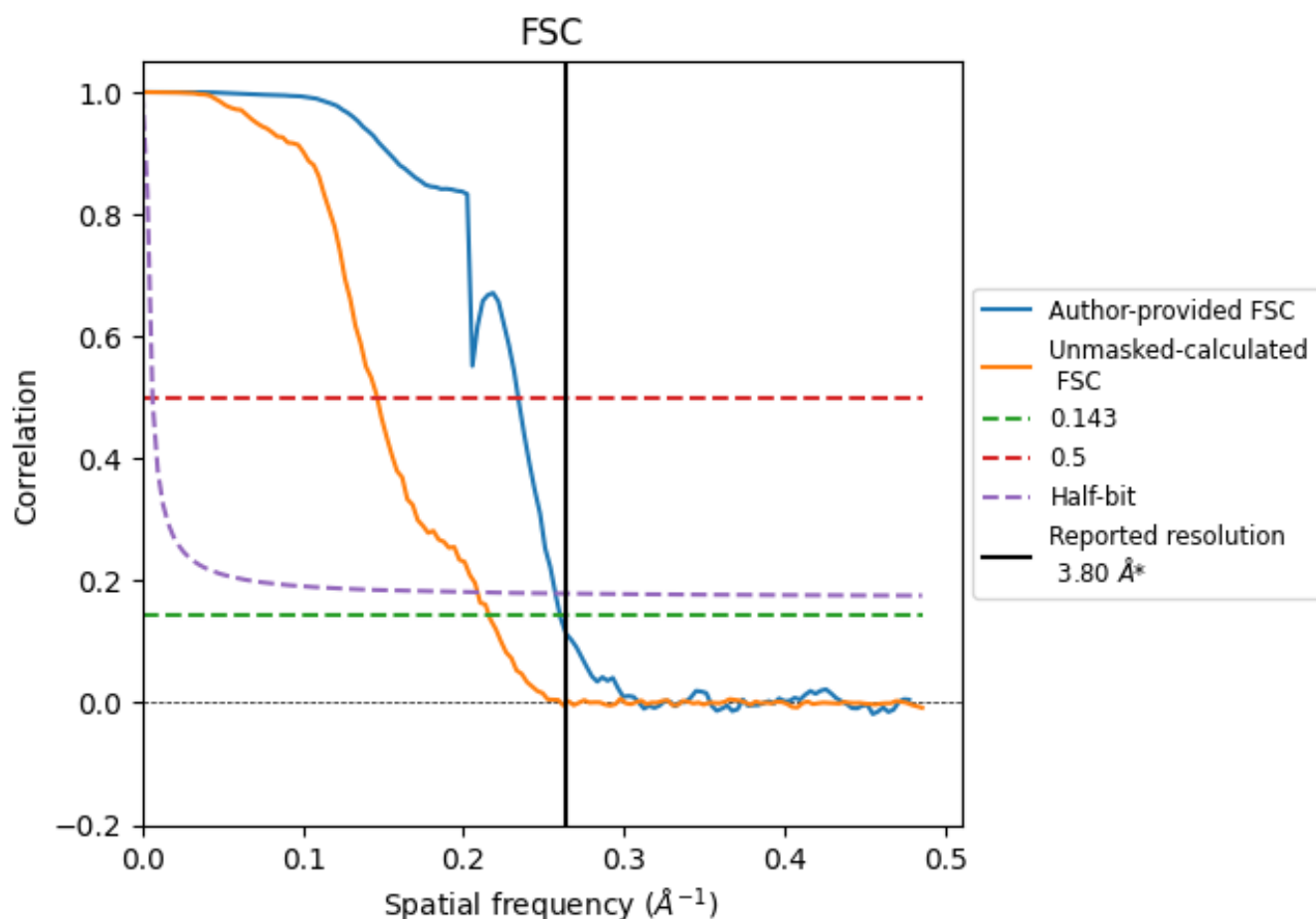


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

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 0.263 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

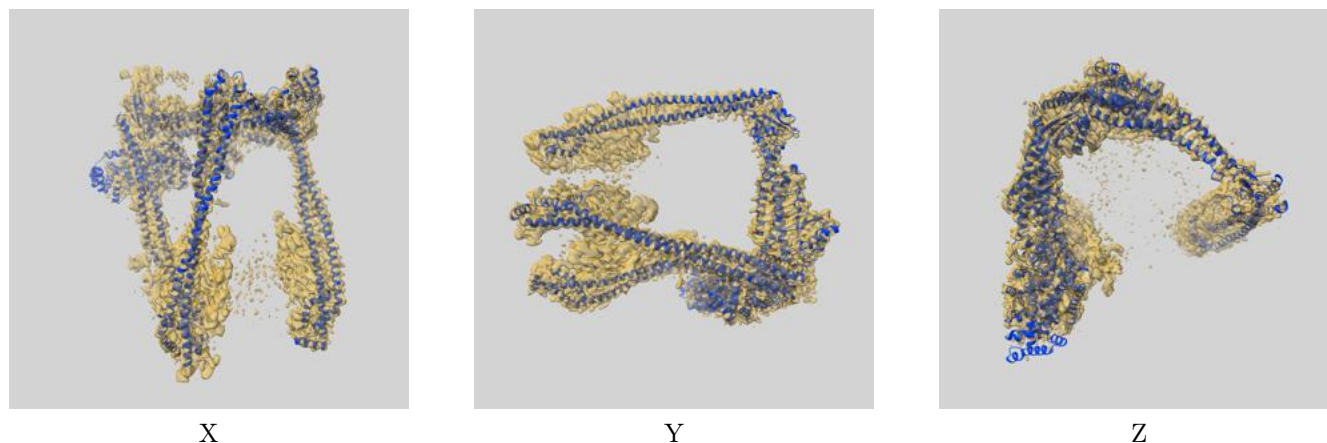
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.84	4.27	3.89
Unmasked-calculated*	4.63	6.84	4.79

*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 4.63 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-44352 and PDB model 9B8Q. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



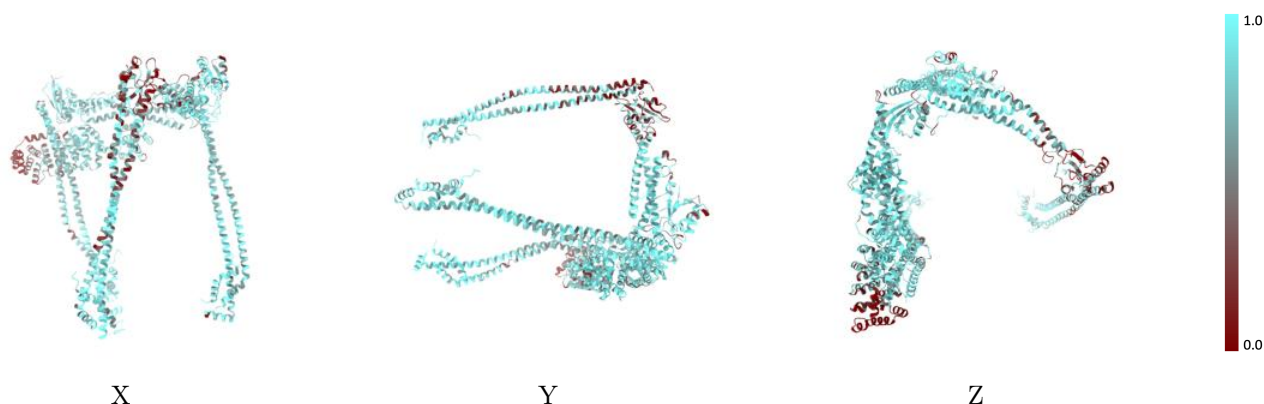
The images above show the 3D surface view of the map at the recommended contour level 0.099 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



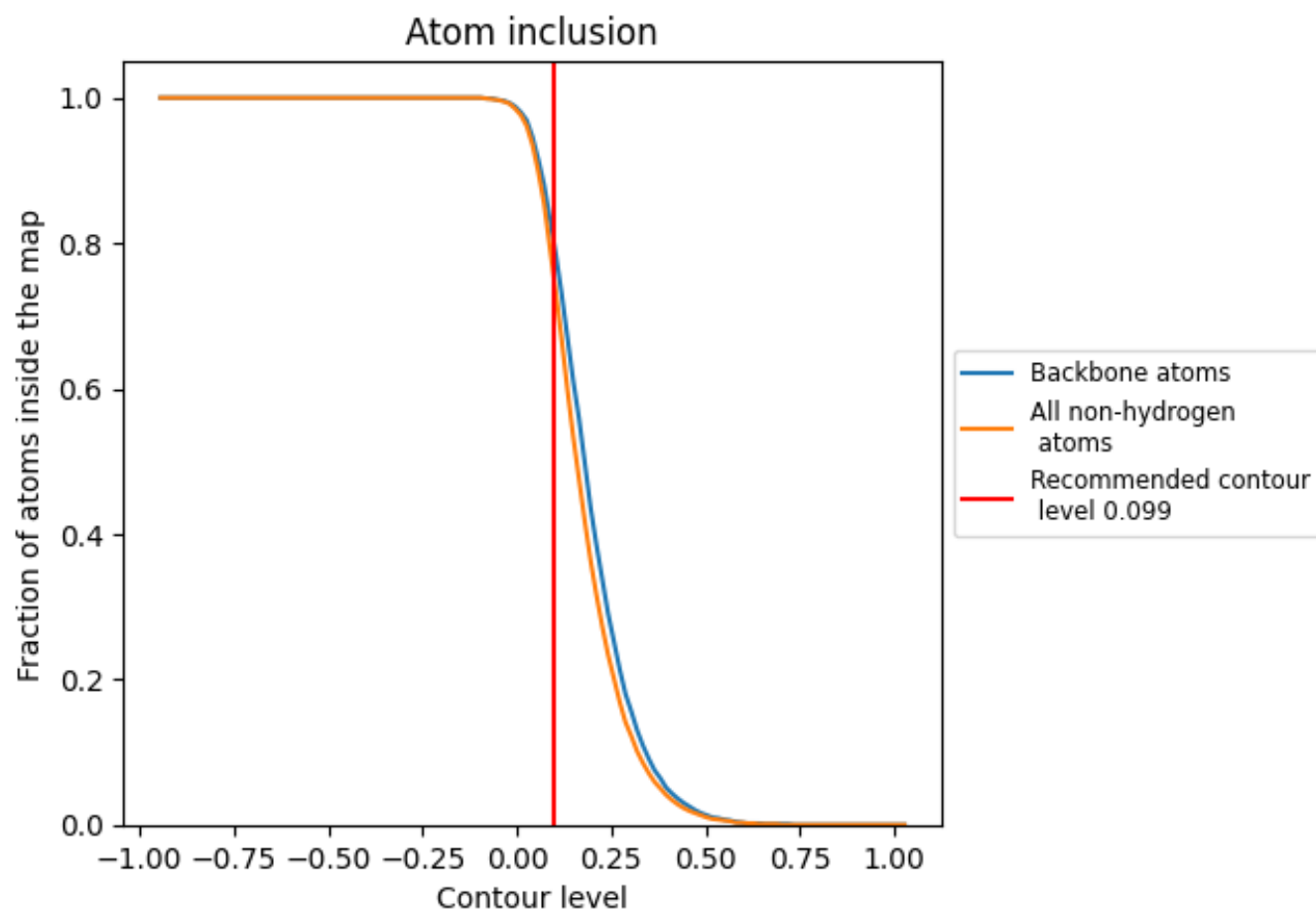
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.099).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 75% 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 (0.099) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7490	0.3630
G	0.7150	0.3360
I	0.8190	0.4040
J	0.8150	0.4150
K	0.7560	0.3480
M	0.7760	0.3840
N	0.7990	0.3950
O	0.6470	0.2480
T	0.6470	0.2900
a	0.8030	0.4190

1.0

0.0

<0.0