



wwPDB EM Validation Summary Report ⓘ

Jul 27, 2024 – 01:23 PM EDT

PDB ID : 9BRU
EMDB ID : EMD-44844
Title : Intact V-ATPase State 1 in synaptophysin knock-out isolated synaptic vesicles
Authors : Wang, C.; Jiang, W.; Yang, K.; Wang, X.; Guo, Q.; Brunger, A.T.
Deposited on : 2024-05-11
Resolution : 4.40 Å(reported)

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
MolProbity : 4.02b-467
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) : 2.37.1

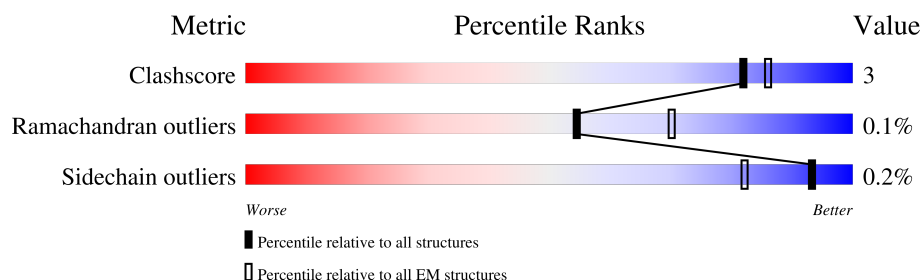
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.40 Å.

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



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

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	7	247	<div> <div>21%</div> <div>80%</div> <div>16%</div> <div>.</div> </div>
2	8	226	<div> <div>10%</div> <div>93%</div> <div>6%</div> </div>
2	9	226	<div> <div>6%</div> <div>96%</div> <div>.</div> </div>
2	Q	226	<div> <div>9%</div> <div>97%</div> <div>.</div> </div>
3	R	118	<div> <div>10%</div> <div>86%</div> <div>10%</div> <div>.</div> </div>
3	T	118	<div> <div>11%</div> <div>97%</div> <div>.</div> </div>
3	V	118	<div> <div>13%</div> <div>93%</div> <div>.</div> <div>.</div> </div>
4	6	382	<div> <div>36%</div> <div>92%</div> <div>.</div> <div>5%</div> </div>

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Mol	Chain	Length	Quality of chain
5	U	483	
6	a	838	
7	e	81	
8	f	98	
9	b	205	
10	g	155	
10	h	155	
10	i	155	
10	j	155	
10	k	155	
10	l	155	
10	m	155	
10	n	155	
10	o	155	
11	X	119	
12	d	351	
13	c	463	
14	p	350	
15	0	617	
15	1	617	
15	2	617	
16	3	511	
16	4	511	
16	5	511	

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 65548 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 D.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	7	208	Total	C	N	O	S	0	0
			1676	1064	303	304	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	8	225	Total	C	N	O	S	0	0
			1823	1146	322	345	10		
2	9	225	Total	C	N	O	S	0	0
			1823	1146	322	345	10		
2	Q	225	Total	C	N	O	S	0	0
			1823	1146	322	345	10		

- Molecule 3 is a protein called V-type proton ATPase subunit G 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	R	114	Total	C	N	O	S	0	0
			925	552	192	176	5		
3	T	114	Total	C	N	O	S	0	0
			925	552	192	176	5		
3	V	114	Total	C	N	O	S	0	0
			925	552	192	176	5		

- Molecule 4 is a protein called V-type proton ATPase subunit C 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	6	361	Total	C	N	O	S	0	0
			2931	1877	495	550	9		

- Molecule 5 is a protein called V-type proton ATPase subunit H.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	U	426	Total	C	N	O	S	0	0
			3501	2224	604	648	25		

- Molecule 6 is a protein called V-type proton ATPase 116 kDa subunit a 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	a	752	Total	C	N	O	S	0	0
			6117	3991	1027	1058	41		

- Molecule 7 is a protein called V-type proton ATPase subunit e 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	e	77	Total	C	N	O	S	0	0
			623	431	97	92	3		

- Molecule 8 is a protein called Ribonuclease kappa.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	f	85	Total	C	N	O	S	0	0
			658	434	102	115	7		

- Molecule 9 is a protein called V-type proton ATPase 21 kDa proteolipid subunit c”.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	b	200	Total	C	N	O	S	0	0
			1484	983	234	256	11		

- Molecule 10 is a protein called V-type proton ATPase 16 kDa proteolipid subunit c.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	g	150	Total	C	N	O	S	0	0
			1069	699	171	191	8		
10	h	150	Total	C	N	O	S	0	0
			1069	699	171	191	8		
10	i	150	Total	C	N	O	S	0	0
			1069	699	171	191	8		
10	j	150	Total	C	N	O	S	0	0
			1069	699	171	191	8		
10	k	150	Total	C	N	O	S	0	0
			1069	699	171	191	8		
10	l	150	Total	C	N	O	S	0	0
			1069	699	171	191	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	m	150	Total	C	N	O	S	0	0
			1069	699	171	191	8		
10	n	150	Total	C	N	O	S	0	0
			1069	699	171	191	8		
10	o	150	Total	C	N	O	S	0	0
			1069	699	171	191	8		

- Molecule 11 is a protein called V-type proton ATPase subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	X	110	Total	C	N	O	S	0	0
			875	553	157	163	2		

- Molecule 12 is a protein called V-type proton ATPase subunit d 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	d	351	Total	C	N	O	S	0	0
			2842	1834	461	532	15		

- Molecule 13 is a protein called V-type proton ATPase subunit S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	c	203	Total	C	N	O	S	0	0
			1642	1079	259	295	9		

- Molecule 14 is a protein called Renin receptor cytoplasmic fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	p	49	Total	C	N	O	S	0	0
			407	277	57	71	2		

- Molecule 15 is a protein called V-type proton ATPase catalytic subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	1	600	Total	C	N	O	S	0	0
			4656	2953	787	889	27		
15	0	602	Total	C	N	O	S	0	0
			4671	2961	789	894	27		
15	2	600	Total	C	N	O	S	0	0
			4656	2953	787	889	27		

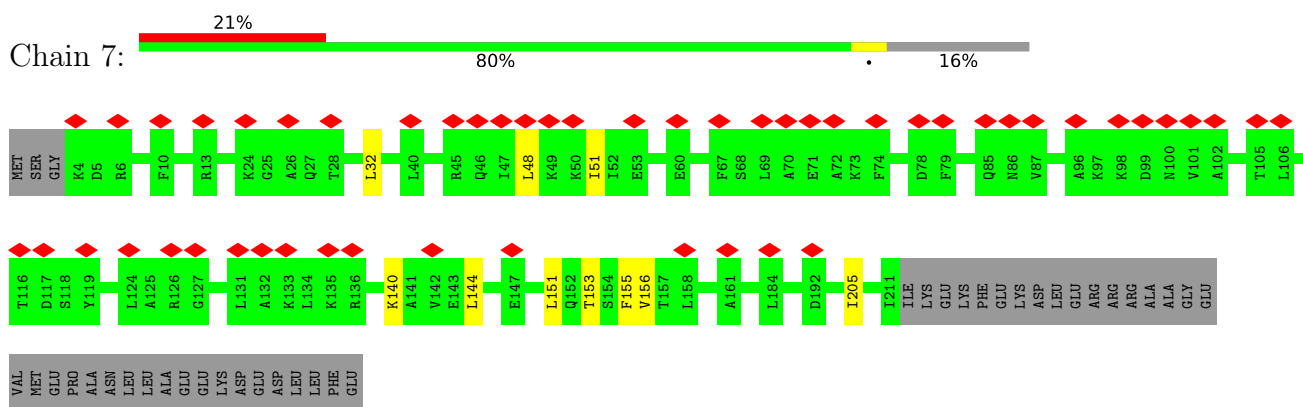
- Molecule 16 is a protein called V-type proton ATPase subunit B, brain isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	3	461	Total	C	N	O	S	0	0
			3610	2290	615	685	20		
16	4	468	Total	C	N	O	S	0	0
			3667	2326	623	698	20		
16	5	468	Total	C	N	O	S	0	0
			3667	2326	623	698	20		

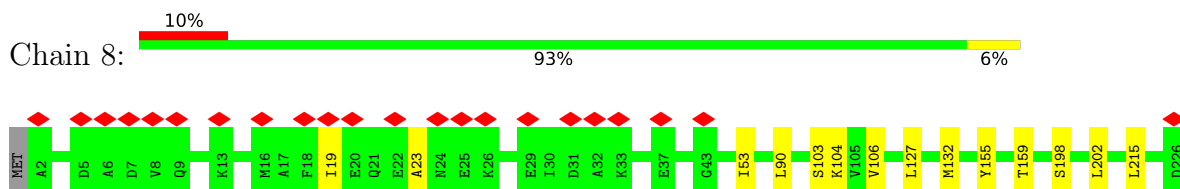
3 Residue-property plots

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.

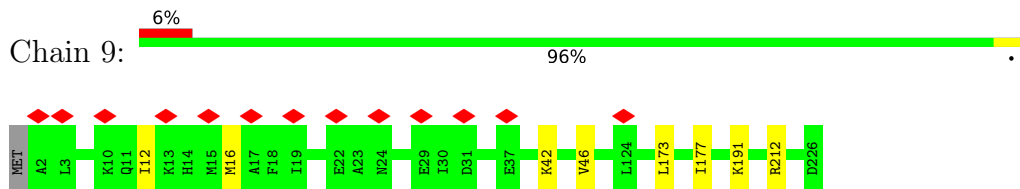
- Molecule 1: V-type proton ATPase subunit D



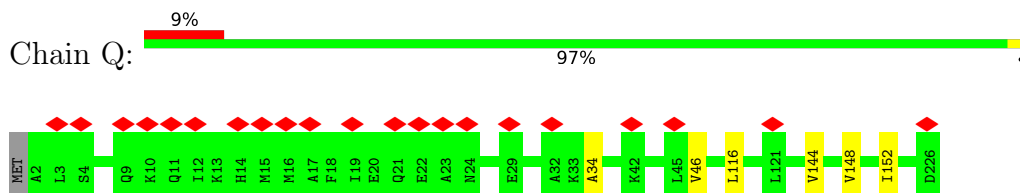
- Molecule 2: V-type proton ATPase subunit E 1



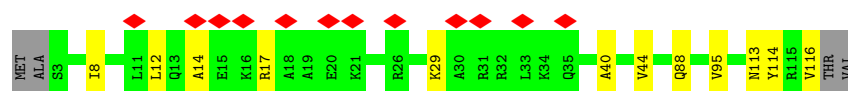
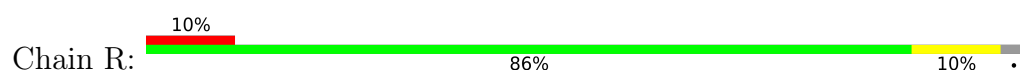
- Molecule 2: V-type proton ATPase subunit E 1



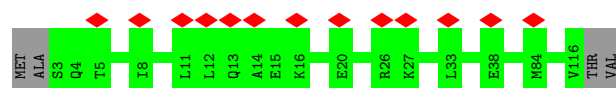
- Molecule 2: V-type proton ATPase subunit E 1



- Molecule 3: V-type proton ATPase subunit G 2



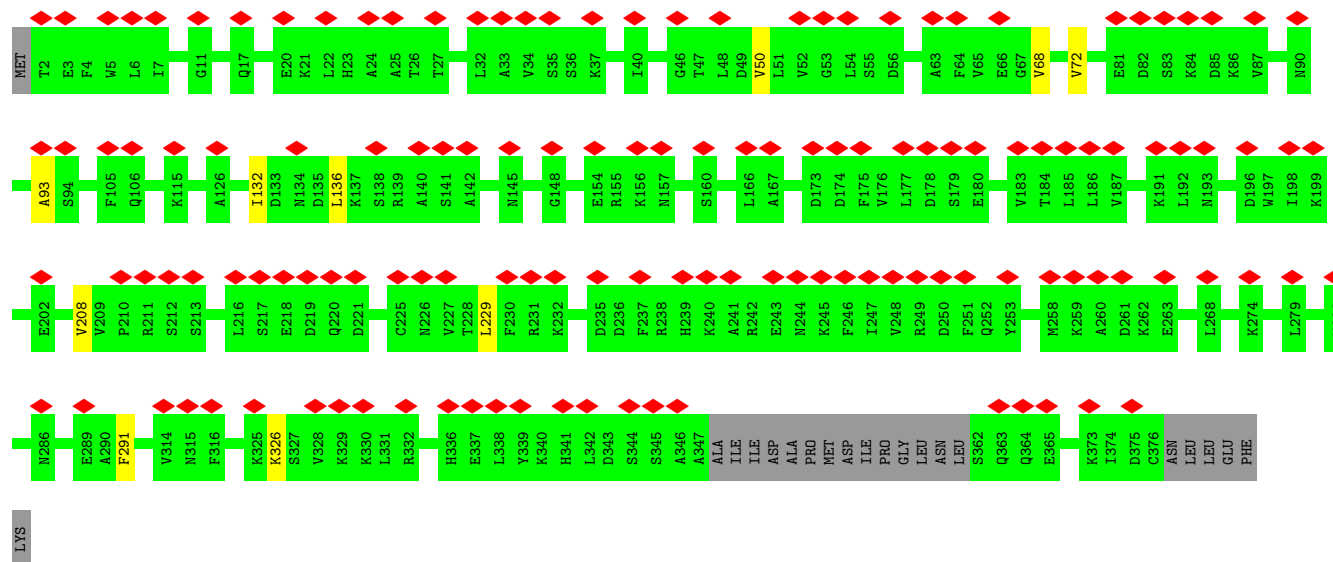
• Molecule 3: V-type proton ATPase subunit G 2



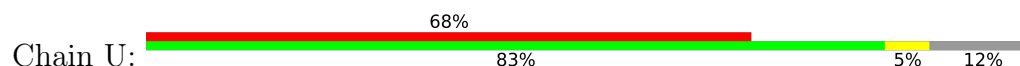
• Molecule 3: V-type proton ATPase subunit G 2

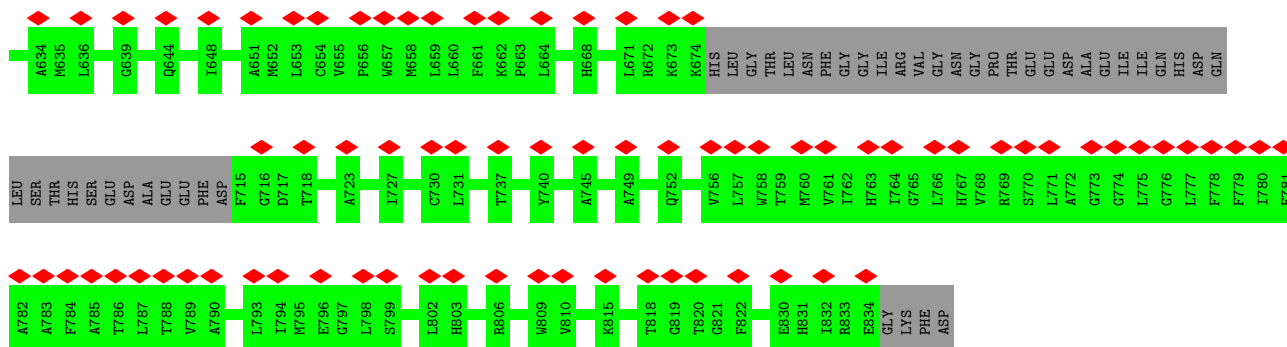


• Molecule 4: V-type proton ATPase subunit C 1



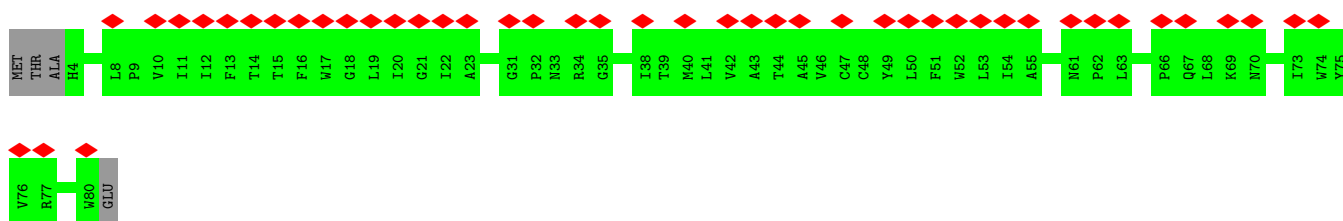
• Molecule 5: V-type proton ATPase subunit H





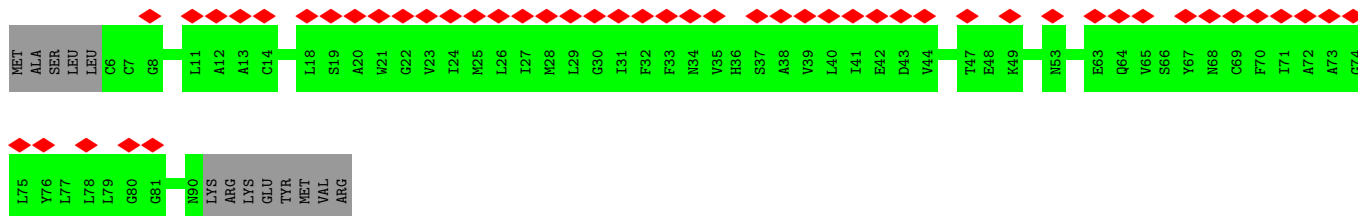
• Molecule 7: V-type proton ATPase subunit e 2

Chain e:



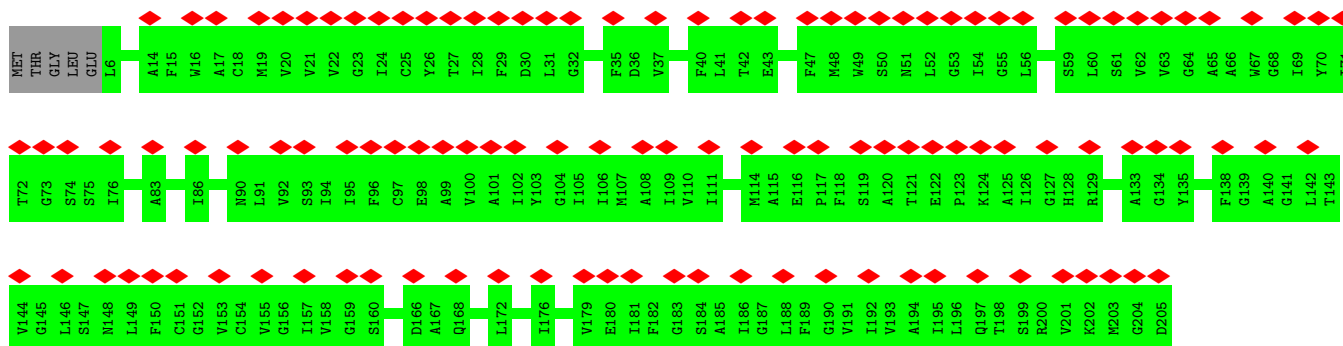
• Molecule 8: Ribonuclease kappa

Chain f:

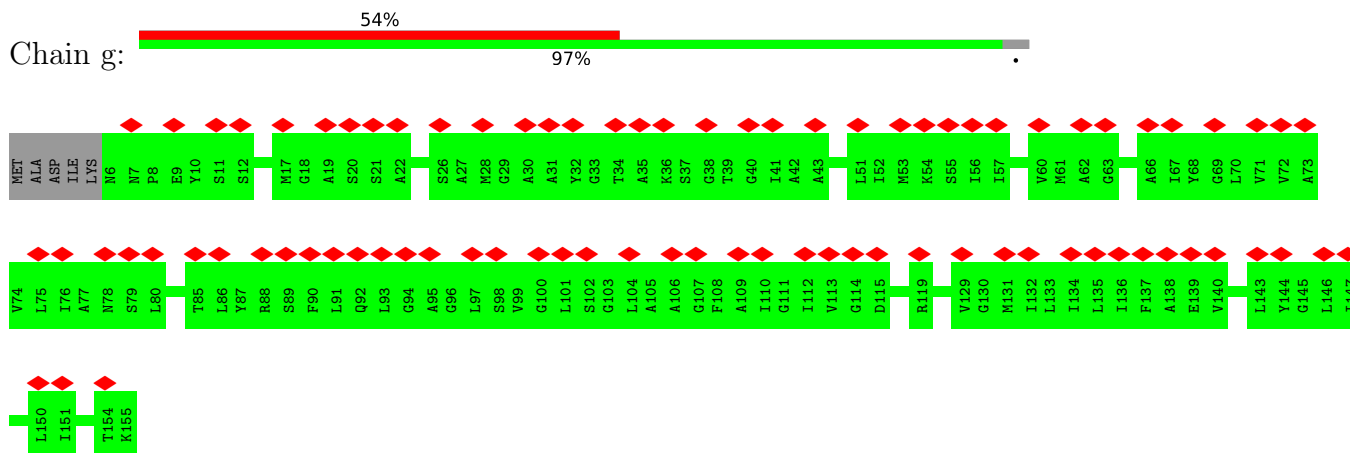


• Molecule 9: V-type proton ATPase 21 kDa proteolipid subunit c''

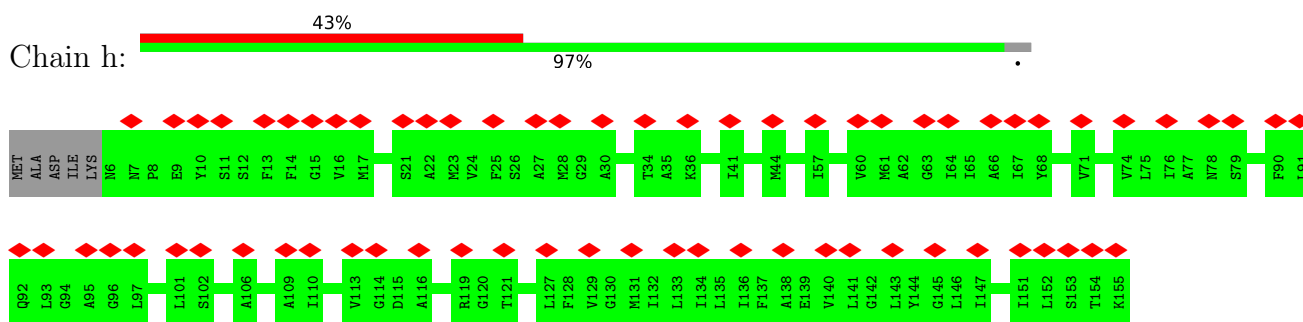
Chain b:



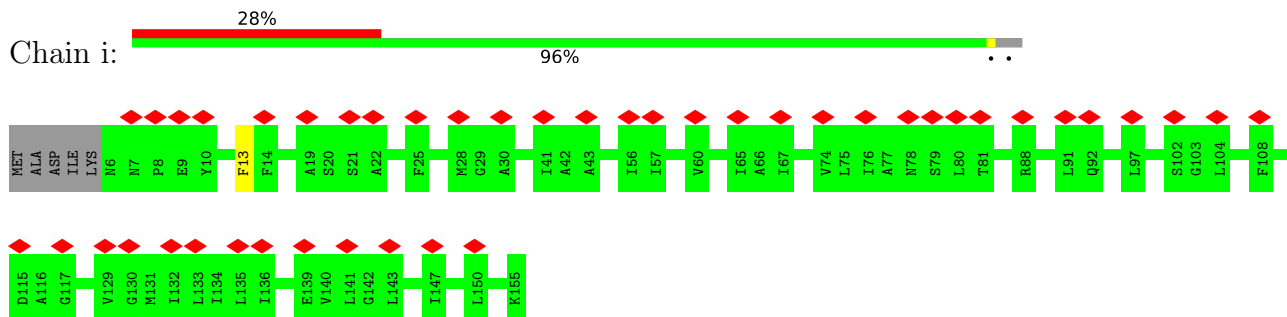
• Molecule 10: V-type proton ATPase 16 kDa proteolipid subunit c



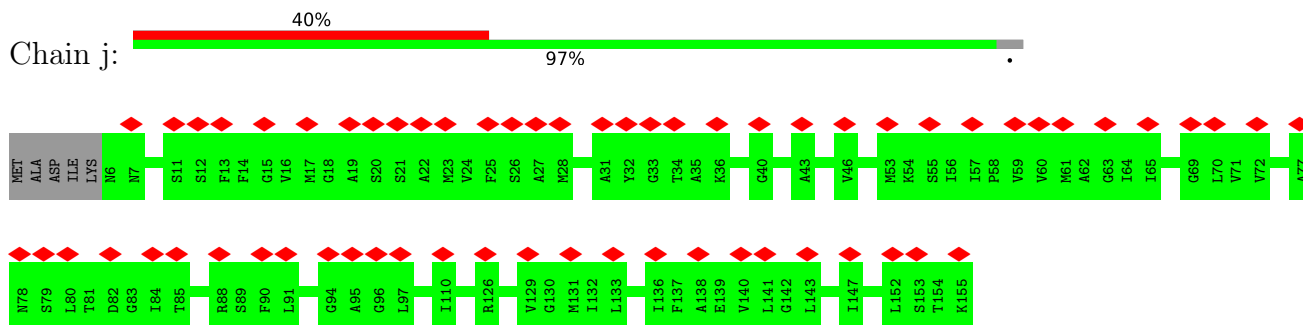
- Molecule 10: V-type proton ATPase 16 kDa proteolipid subunit c



- Molecule 10: V-type proton ATPase 16 kDa proteolipid subunit c

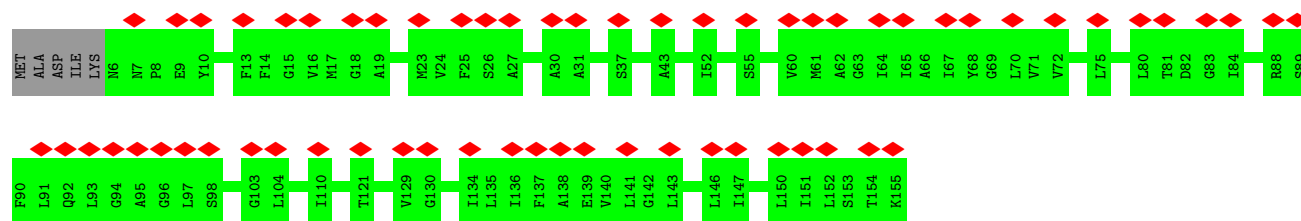


- Molecule 10: V-type proton ATPase 16 kDa proteolipid subunit c



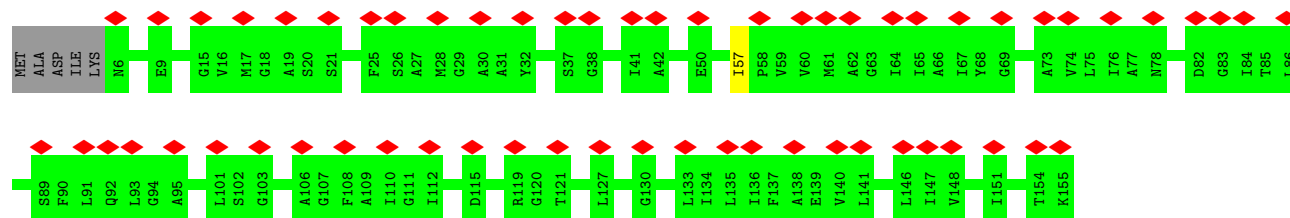
- Molecule 10: V-type proton ATPase 16 kDa proteolipid subunit c





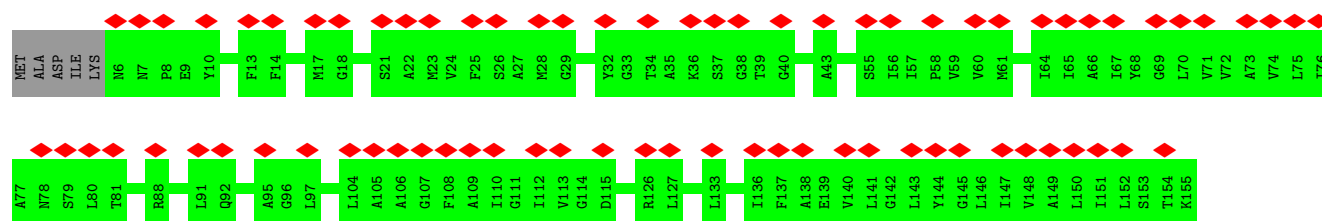
- Molecule 10: V-type proton ATPase 16 kDa proteolipid subunit c

Chain l:



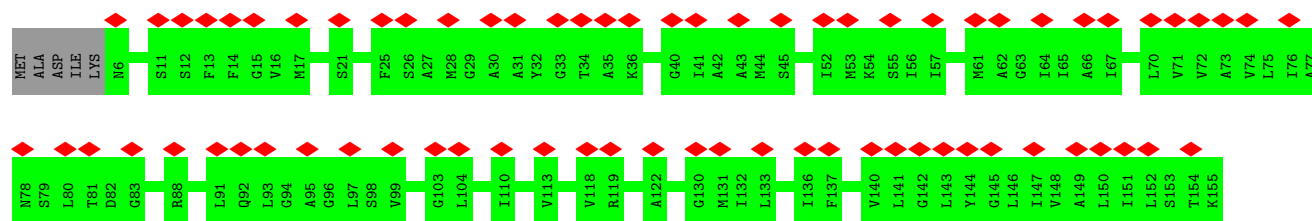
- Molecule 10: V-type proton ATPase 16 kDa proteolipid subunit c

Chain m:



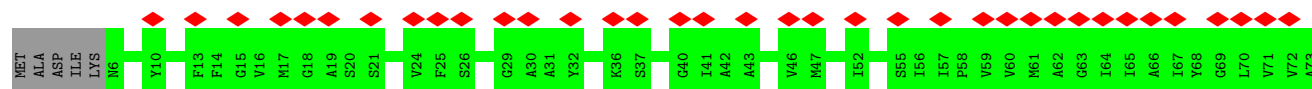
- Molecule 10: V-type proton ATPase 16 kDa proteolipid subunit c

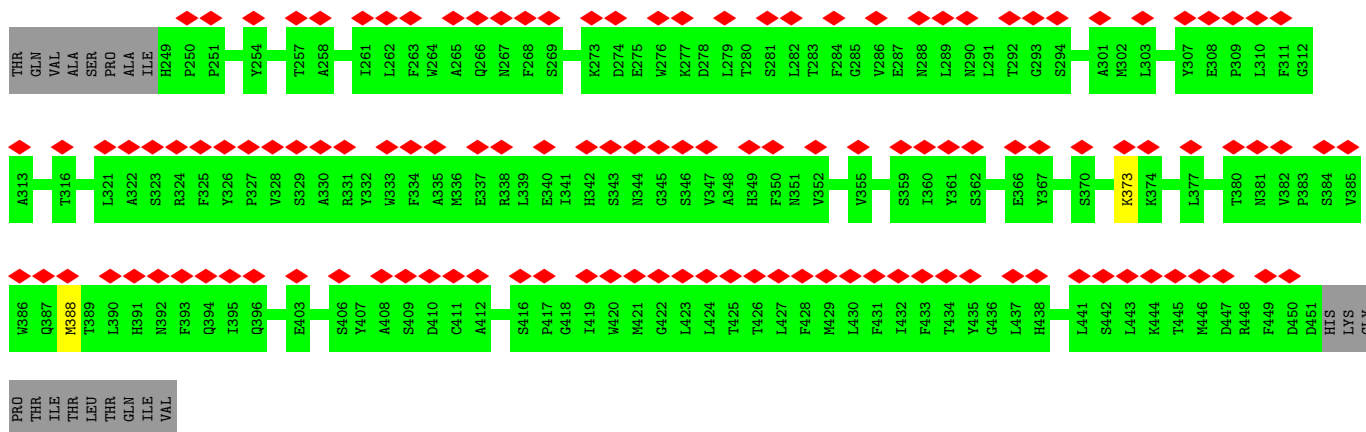
Chain n:



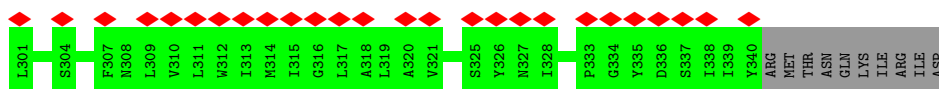
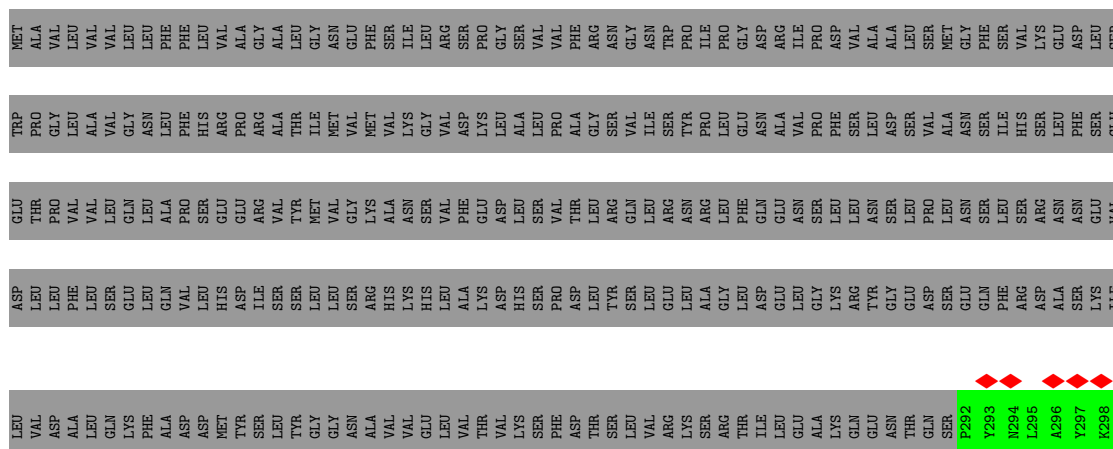
- Molecule 10: V-type proton ATPase 16 kDa proteolipid subunit c

Chain o:

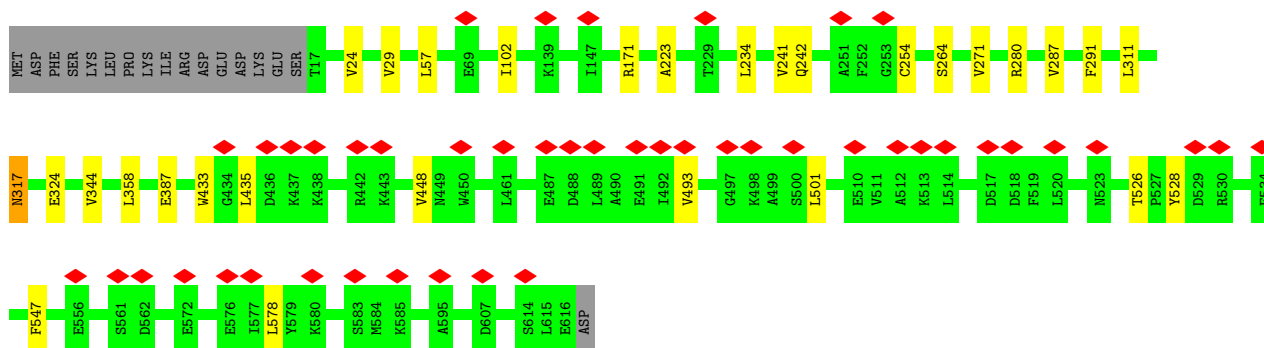
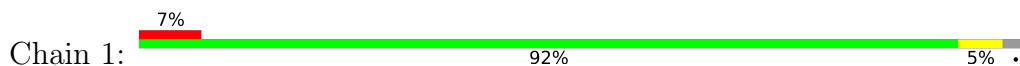




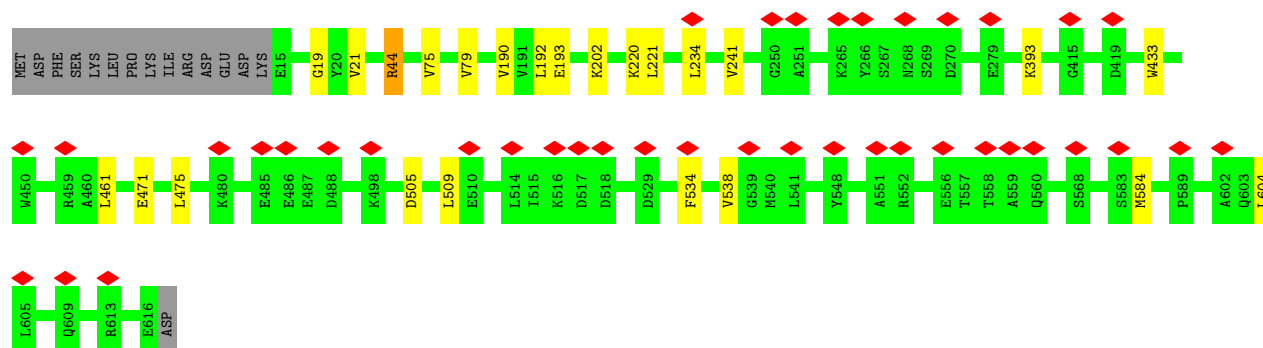
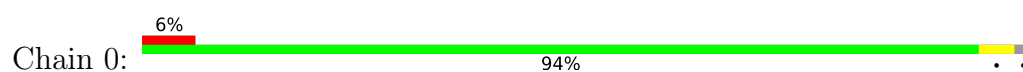
- Molecule 14: Renin receptor cytoplasmic fragment



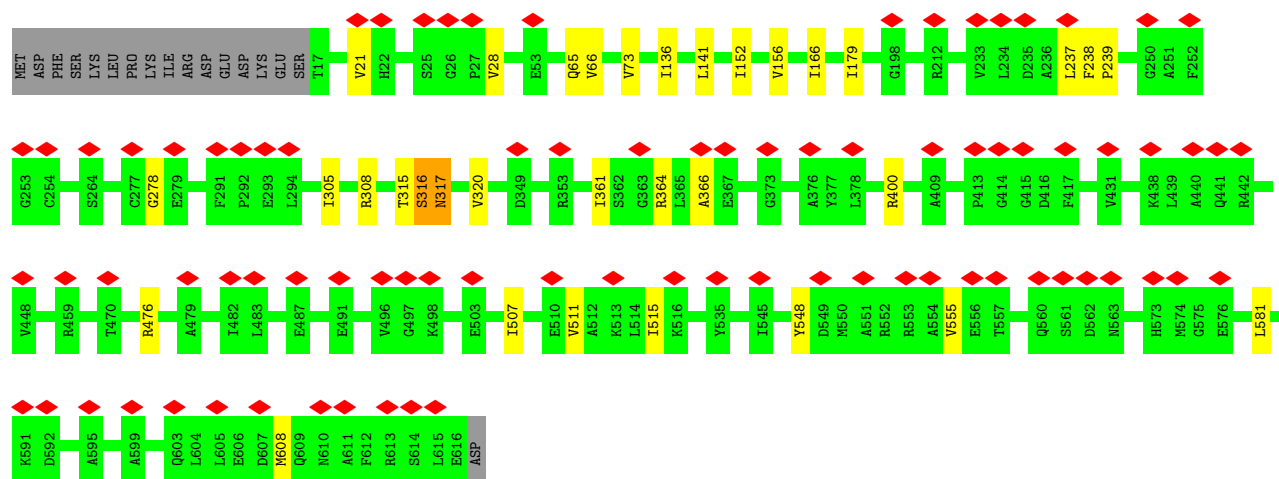
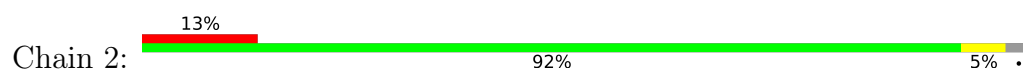
- Molecule 15: V-type proton ATPase catalytic subunit A



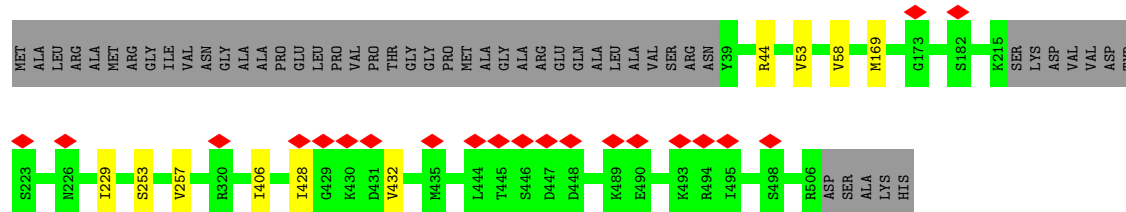
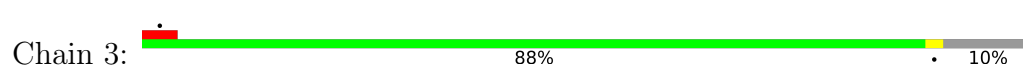
- Molecule 15: V-type proton ATPase catalytic subunit A



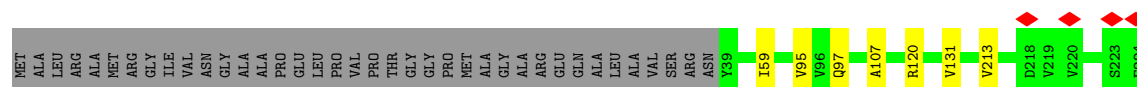
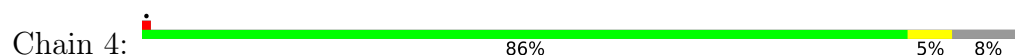
• Molecule 15: V-type proton ATPase catalytic subunit A



• Molecule 16: V-type proton ATPase subunit B, brain isoform

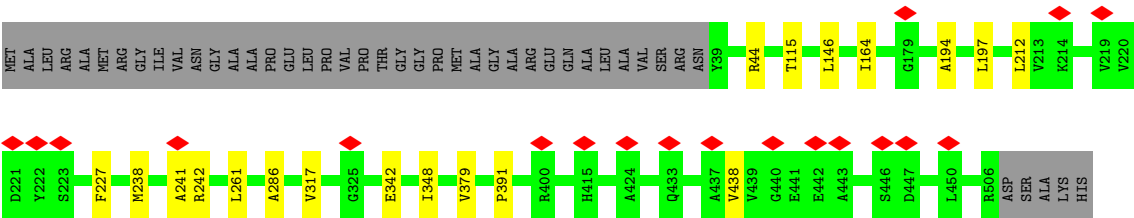
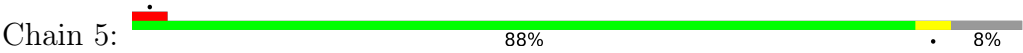


• Molecule 16: V-type proton ATPase subunit B, brain isoform





• Molecule 16: V-type proton ATPase subunit B, brain isoform



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	32181	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.031	Depositor
Minimum map value	-0.022	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0035	Depositor
Map size (Å)	495.6672, 495.6672, 495.6672	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1064, 1.1064, 1.1064	Depositor

5 Model quality

5.1 Standard geometry

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	7	0.29	0/1694	0.60	0/2267
2	8	0.30	0/1840	0.60	0/2462
2	9	0.29	0/1840	0.58	0/2462
2	Q	0.29	0/1840	0.59	0/2462
3	R	0.30	0/930	0.60	0/1237
3	T	0.28	0/930	0.63	0/1237
3	V	0.30	0/930	0.63	0/1237
4	6	0.28	0/2985	0.53	0/4032
5	U	0.28	0/3568	0.55	0/4806
6	a	0.29	0/6274	0.57	0/8486
7	e	0.31	0/648	0.49	0/891
8	f	0.29	0/674	0.46	0/915
9	b	0.30	0/1518	0.53	0/2061
10	g	0.30	0/1084	0.54	0/1466
10	h	0.29	0/1084	0.53	0/1466
10	i	0.37	0/1084	0.64	0/1466
10	j	0.28	0/1084	0.53	0/1466
10	k	0.29	0/1084	0.59	0/1466
10	l	0.33	0/1084	0.57	0/1466
10	m	0.31	0/1084	0.59	0/1466
10	n	0.30	0/1084	0.57	0/1466
10	o	0.30	0/1084	0.58	0/1466
11	X	0.26	0/889	0.56	0/1199
12	d	0.29	0/2908	0.51	0/3937
13	c	0.31	0/1697	0.60	0/2311
14	p	0.26	0/420	0.43	0/576
15	0	0.27	0/4767	0.55	0/6453
15	1	0.28	0/4752	0.56	0/6433
15	2	0.28	0/4752	0.56	0/6433
16	3	0.29	0/3681	0.56	0/4987
16	4	0.29	0/3740	0.58	0/5069
16	5	0.27	0/3740	0.56	0/5069
All	All	0.29	0/66773	0.56	0/90216

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	7	1676	0	1781	7	0
2	8	1823	0	1895	11	0
2	9	1823	0	1895	5	0
2	Q	1823	0	1895	6	0
3	R	925	0	935	10	0
3	T	925	0	935	0	0
3	V	925	0	935	4	0
4	6	2931	0	2969	7	0
5	U	3501	0	3481	14	0
6	a	6117	0	6154	0	0
7	e	623	0	641	0	0
8	f	658	0	652	0	0
9	b	1484	0	1528	0	0
10	g	1069	0	1136	0	0
10	h	1069	0	1136	0	0
10	i	1069	0	1136	0	0
10	j	1069	0	1136	0	0
10	k	1069	0	1136	0	0
10	l	1069	0	1136	0	0
10	m	1069	0	1136	0	0
10	n	1069	0	1136	0	0
10	o	1069	0	1136	0	0
11	X	875	0	883	3	0
12	d	2842	0	2782	0	0
13	c	1642	0	1568	0	0
14	p	407	0	403	0	0
15	0	4671	0	4654	16	0
15	1	4656	0	4643	22	0
15	2	4656	0	4643	37	0
16	3	3610	0	3613	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	4	3667	0	3667	19	0
16	5	3667	0	3667	17	0
All	All	65548	0	66443	164	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 3.

The worst 5 of 164 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)
15:0:220:LYS:HG2	16:5:242:ARG:NH1	1.80	0.97
15:0:220:LYS:HG2	16:5:242:ARG:HH12	1.36	0.88
15:2:239:PRO:HD2	15:2:476:ARG:HH22	1.41	0.82
15:2:239:PRO:CD	15:2:476:ARG:NH2	2.51	0.73
2:Q:148:VAL:O	2:Q:152:ILE:HD12	1.90	0.72

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	7	206/247 (83%)	197 (96%)	9 (4%)	0	100	100
2	8	223/226 (99%)	219 (98%)	4 (2%)	0	100	100
2	9	223/226 (99%)	220 (99%)	3 (1%)	0	100	100
2	Q	223/226 (99%)	218 (98%)	5 (2%)	0	100	100
3	R	112/118 (95%)	107 (96%)	5 (4%)	0	100	100
3	T	112/118 (95%)	112 (100%)	0	0	100	100
3	V	112/118 (95%)	108 (96%)	4 (4%)	0	100	100
4	6	357/382 (94%)	339 (95%)	18 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	U	422/483 (87%)	394 (93%)	26 (6%)	2 (0%)	29	68
6	a	746/838 (89%)	697 (93%)	49 (7%)	0	100	100
7	e	75/81 (93%)	71 (95%)	4 (5%)	0	100	100
8	f	83/98 (85%)	79 (95%)	4 (5%)	0	100	100
9	b	198/205 (97%)	192 (97%)	6 (3%)	0	100	100
10	g	148/155 (96%)	142 (96%)	6 (4%)	0	100	100
10	h	148/155 (96%)	144 (97%)	4 (3%)	0	100	100
10	i	148/155 (96%)	144 (97%)	4 (3%)	0	100	100
10	j	148/155 (96%)	143 (97%)	5 (3%)	0	100	100
10	k	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
10	l	148/155 (96%)	143 (97%)	4 (3%)	1 (1%)	22	62
10	m	148/155 (96%)	136 (92%)	12 (8%)	0	100	100
10	n	148/155 (96%)	142 (96%)	6 (4%)	0	100	100
10	o	148/155 (96%)	142 (96%)	6 (4%)	0	100	100
11	X	108/119 (91%)	103 (95%)	5 (5%)	0	100	100
12	d	349/351 (99%)	330 (95%)	19 (5%)	0	100	100
13	c	201/463 (43%)	166 (83%)	33 (16%)	2 (1%)	15	54
14	p	47/350 (13%)	43 (92%)	4 (8%)	0	100	100
15	0	600/617 (97%)	563 (94%)	37 (6%)	0	100	100
15	1	598/617 (97%)	564 (94%)	34 (6%)	0	100	100
15	2	598/617 (97%)	552 (92%)	44 (7%)	2 (0%)	41	76
16	3	457/511 (89%)	429 (94%)	28 (6%)	0	100	100
16	4	466/511 (91%)	442 (95%)	24 (5%)	0	100	100
16	5	466/511 (91%)	451 (97%)	15 (3%)	0	100	100
All	All	8314/9428 (88%)	7877 (95%)	430 (5%)	7 (0%)	54	85

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	U	134	ASP
13	c	388	MET
15	2	316	SER
15	2	317	ASN
10	l	57	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	7	179/212 (84%)	179 (100%)	0	100	100
2	8	197/198 (100%)	196 (100%)	1 (0%)	88	93
2	9	197/198 (100%)	196 (100%)	1 (0%)	88	93
2	Q	197/198 (100%)	197 (100%)	0	100	100
3	R	96/99 (97%)	95 (99%)	1 (1%)	76	86
3	T	96/99 (97%)	96 (100%)	0	100	100
3	V	96/99 (97%)	96 (100%)	0	100	100
4	6	326/344 (95%)	325 (100%)	1 (0%)	92	95
5	U	384/429 (90%)	384 (100%)	0	100	100
6	a	669/741 (90%)	669 (100%)	0	100	100
7	e	65/68 (96%)	65 (100%)	0	100	100
8	f	71/83 (86%)	71 (100%)	0	100	100
9	b	154/158 (98%)	154 (100%)	0	100	100
10	g	109/113 (96%)	109 (100%)	0	100	100
10	h	109/113 (96%)	109 (100%)	0	100	100
10	i	109/113 (96%)	108 (99%)	1 (1%)	78	88
10	j	109/113 (96%)	109 (100%)	0	100	100
10	k	109/113 (96%)	109 (100%)	0	100	100
10	l	109/113 (96%)	109 (100%)	0	100	100
10	m	109/113 (96%)	109 (100%)	0	100	100
10	n	109/113 (96%)	109 (100%)	0	100	100
10	o	109/113 (96%)	109 (100%)	0	100	100
11	X	94/100 (94%)	94 (100%)	0	100	100
12	d	306/306 (100%)	306 (100%)	0	100	100
13	c	180/395 (46%)	180 (100%)	0	100	100
14	p	44/309 (14%)	44 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	0	509/524 (97%)	508 (100%)	1 (0%)	93	96
15	1	507/524 (97%)	504 (99%)	3 (1%)	86	92
15	2	507/524 (97%)	507 (100%)	0	100	100
16	3	395/431 (92%)	394 (100%)	1 (0%)	92	95
16	4	402/431 (93%)	401 (100%)	1 (0%)	93	96
16	5	402/431 (93%)	402 (100%)	0	100	100
All	All	7054/7918 (89%)	7043 (100%)	11 (0%)	93	96

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	1	317	ASN
15	0	44	ARG
16	4	120	ARG
16	3	44	ARG
10	i	13	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
5	U	440	HIS
12	d	84	HIS
15	1	317	ASN
16	4	415	HIS
16	5	384	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides 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.

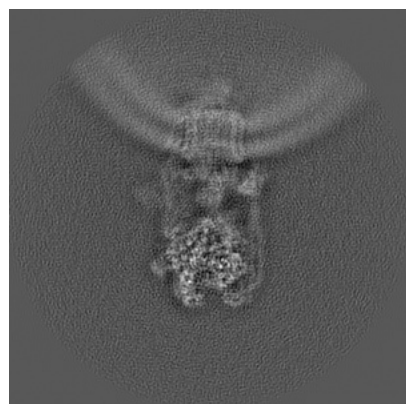
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44844. These allow visual inspection of the internal detail of the map and identification of artifacts.

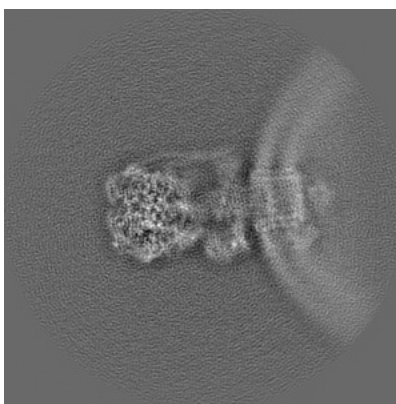
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

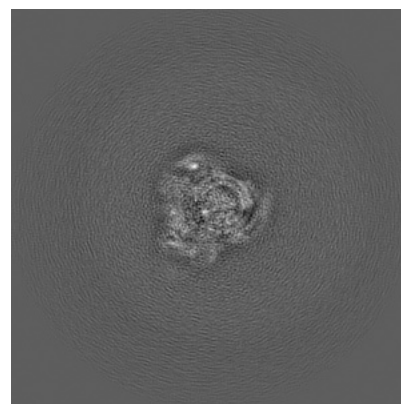
6.1.1 Primary map



X

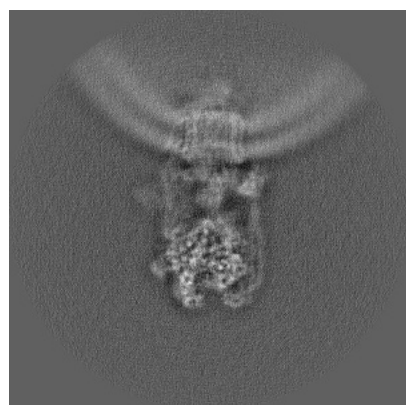


Y

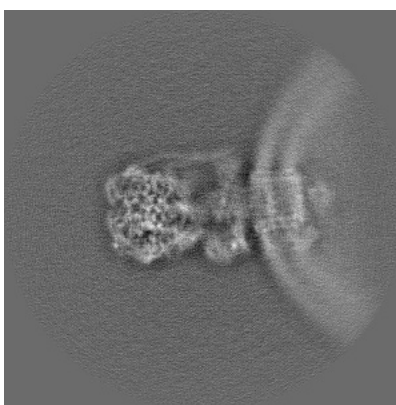


Z

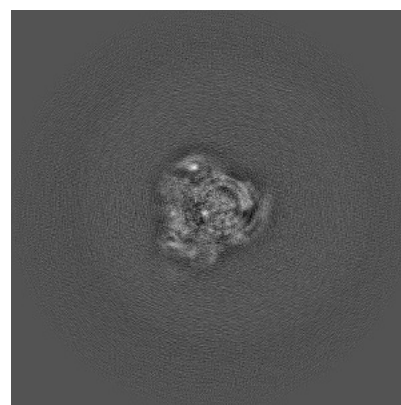
6.1.2 Raw map



X



Y

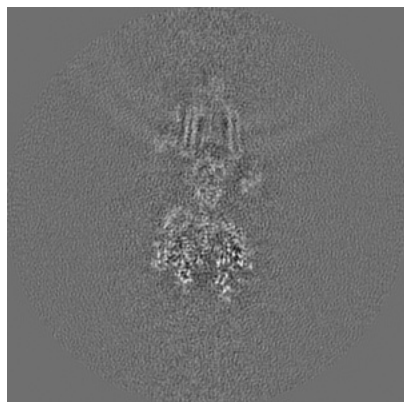


Z

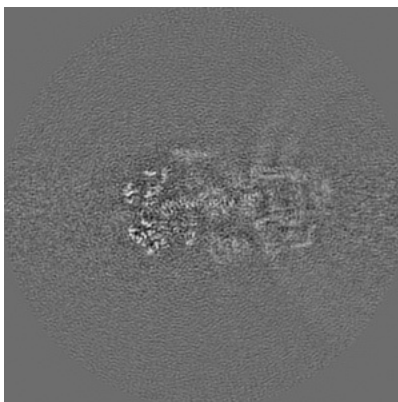
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

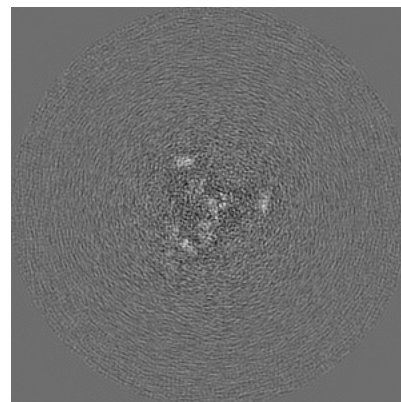
6.2.1 Primary map



X Index: 224

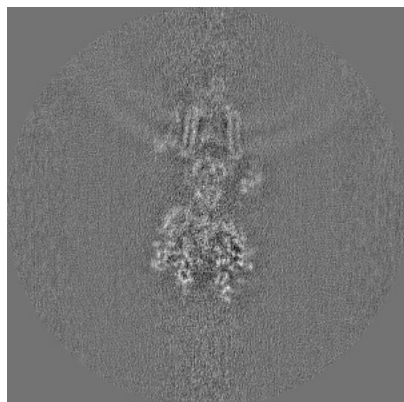


Y Index: 224

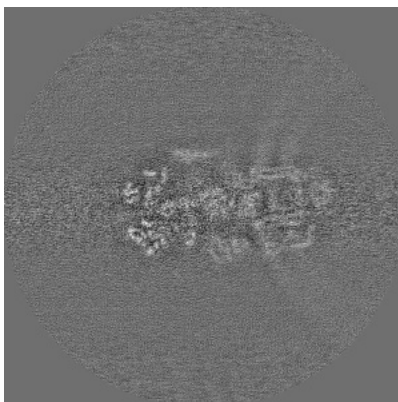


Z Index: 224

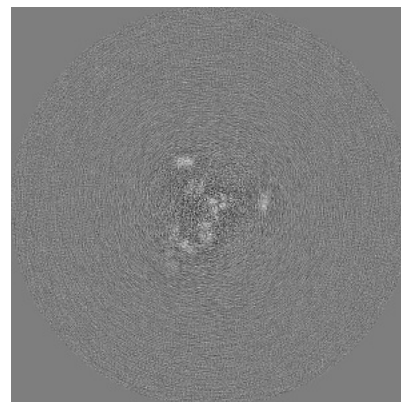
6.2.2 Raw map



X Index: 224



Y Index: 224



Z Index: 224

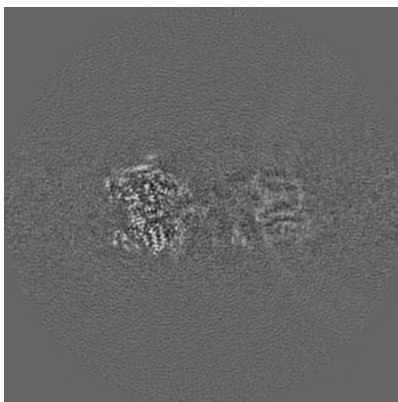
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

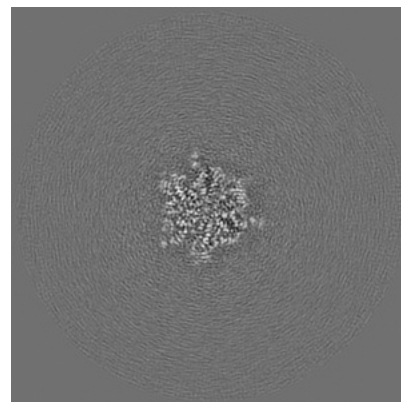
6.3.1 Primary map



X Index: 215

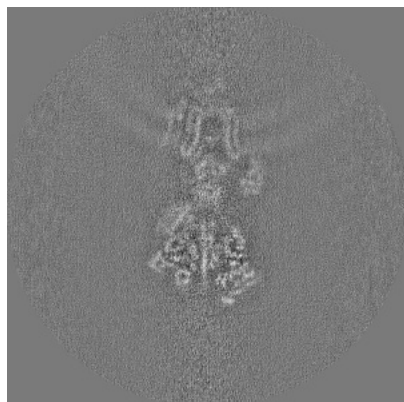


Y Index: 205



Z Index: 166

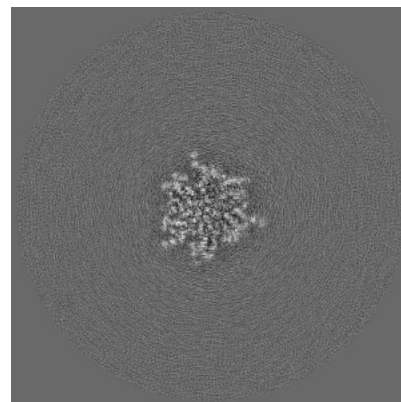
6.3.2 Raw map



X Index: 219



Y Index: 220

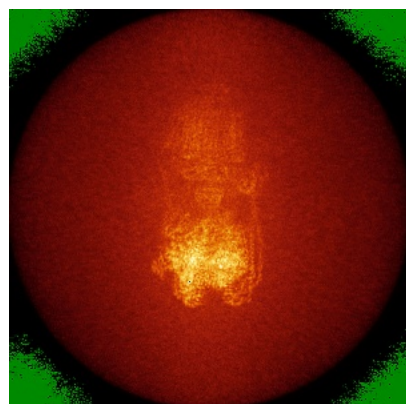


Z Index: 168

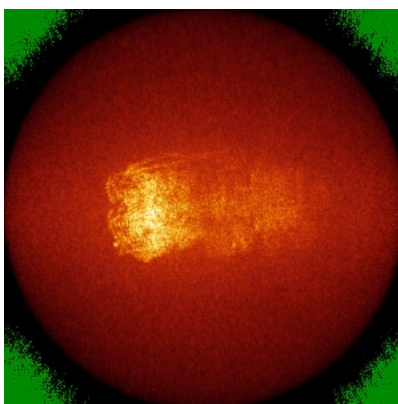
The images above show the largest variance slices of the map in three orthogonal directions.

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

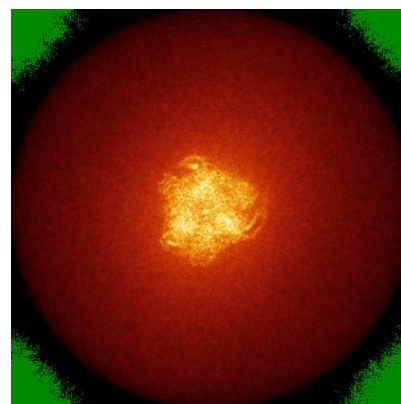
6.4.1 Primary map



X

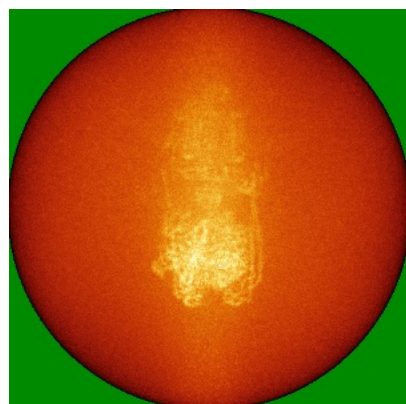


Y

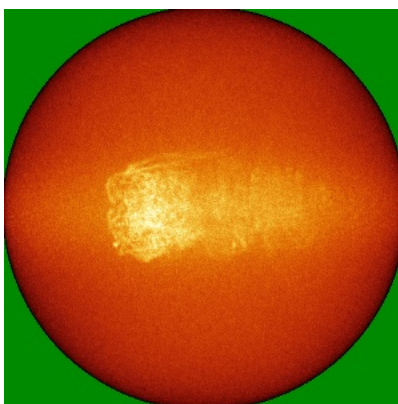


Z

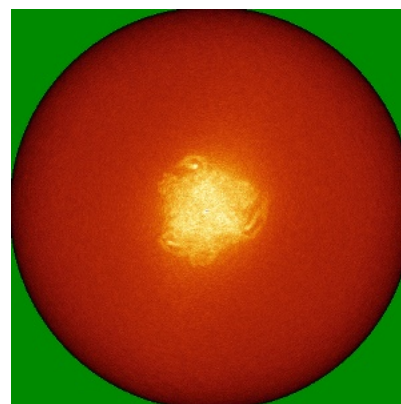
6.4.2 Raw map



X



Y

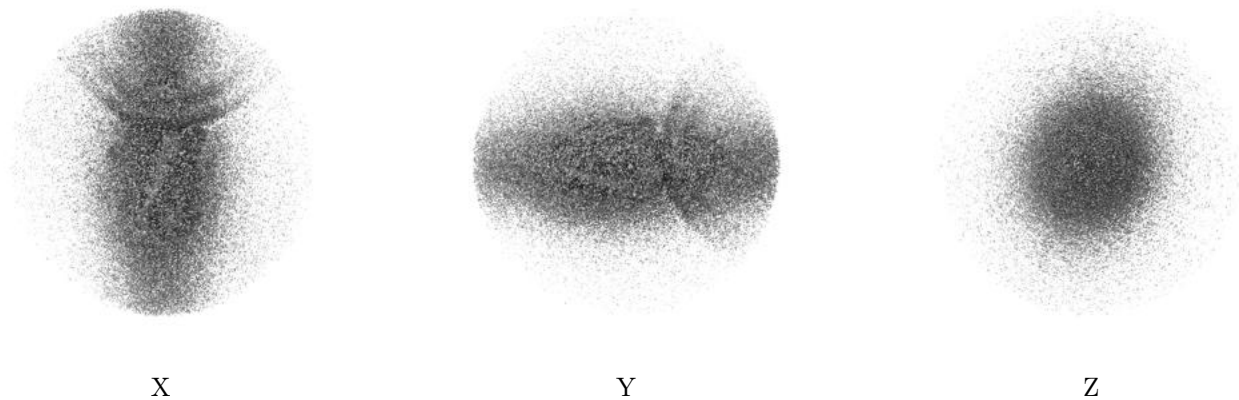


Z

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.

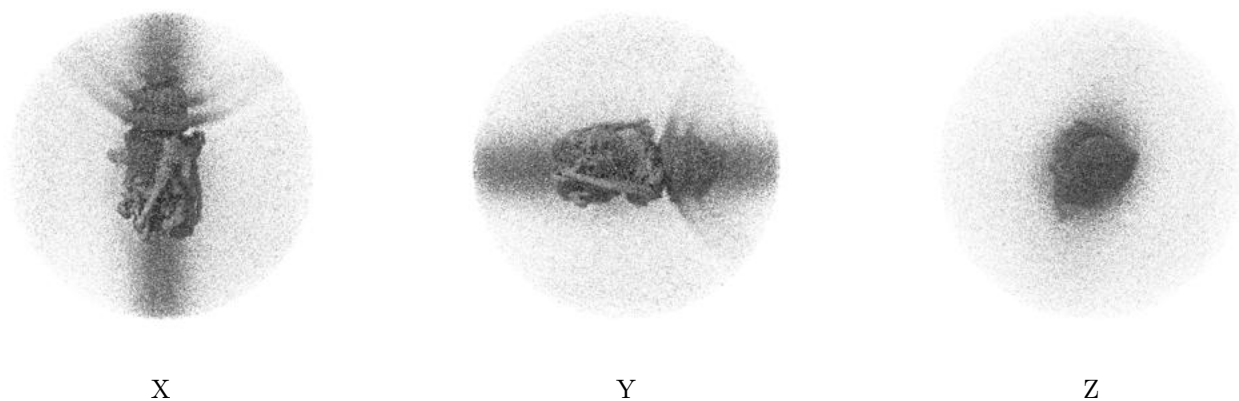
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0035. 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.

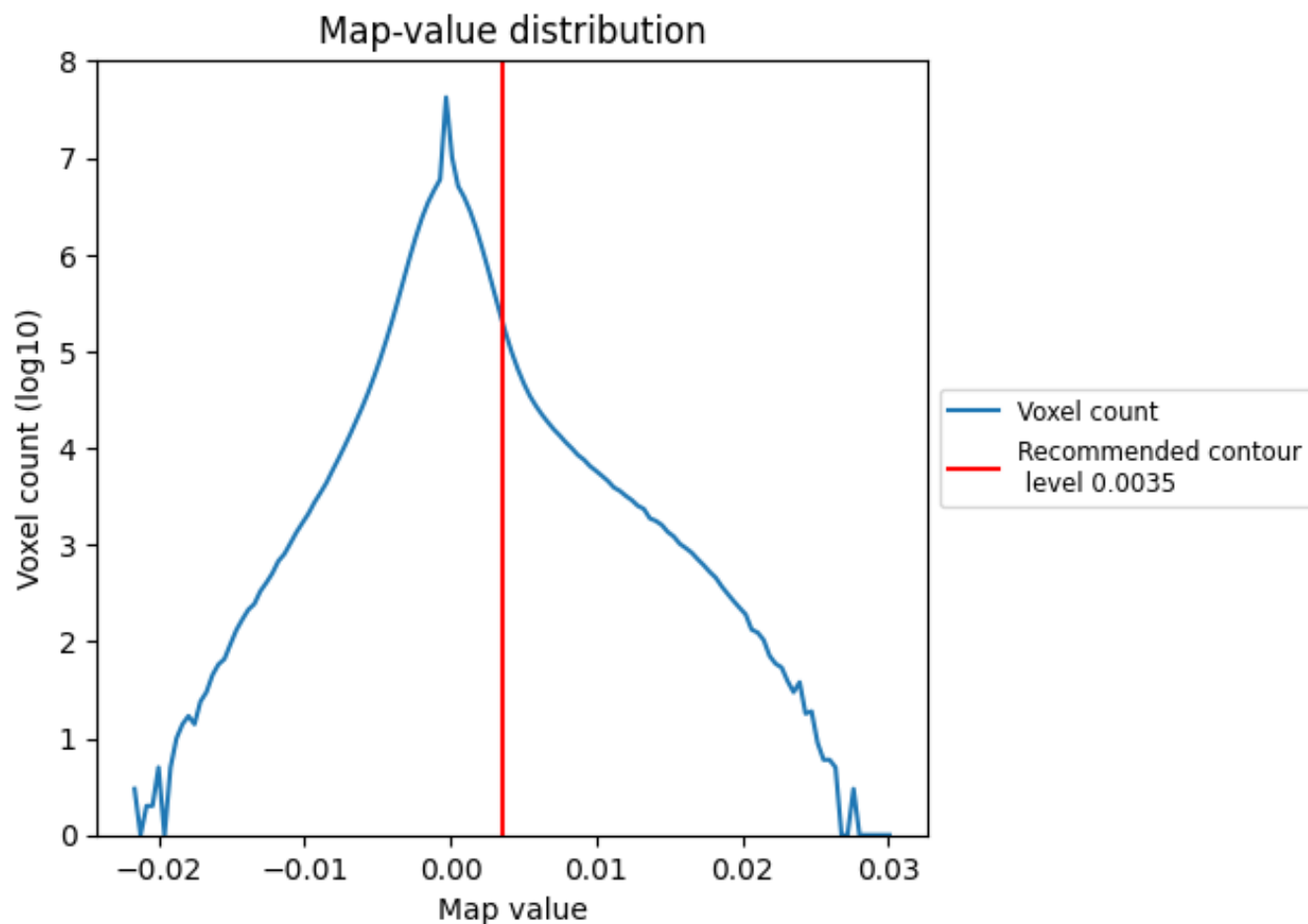
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

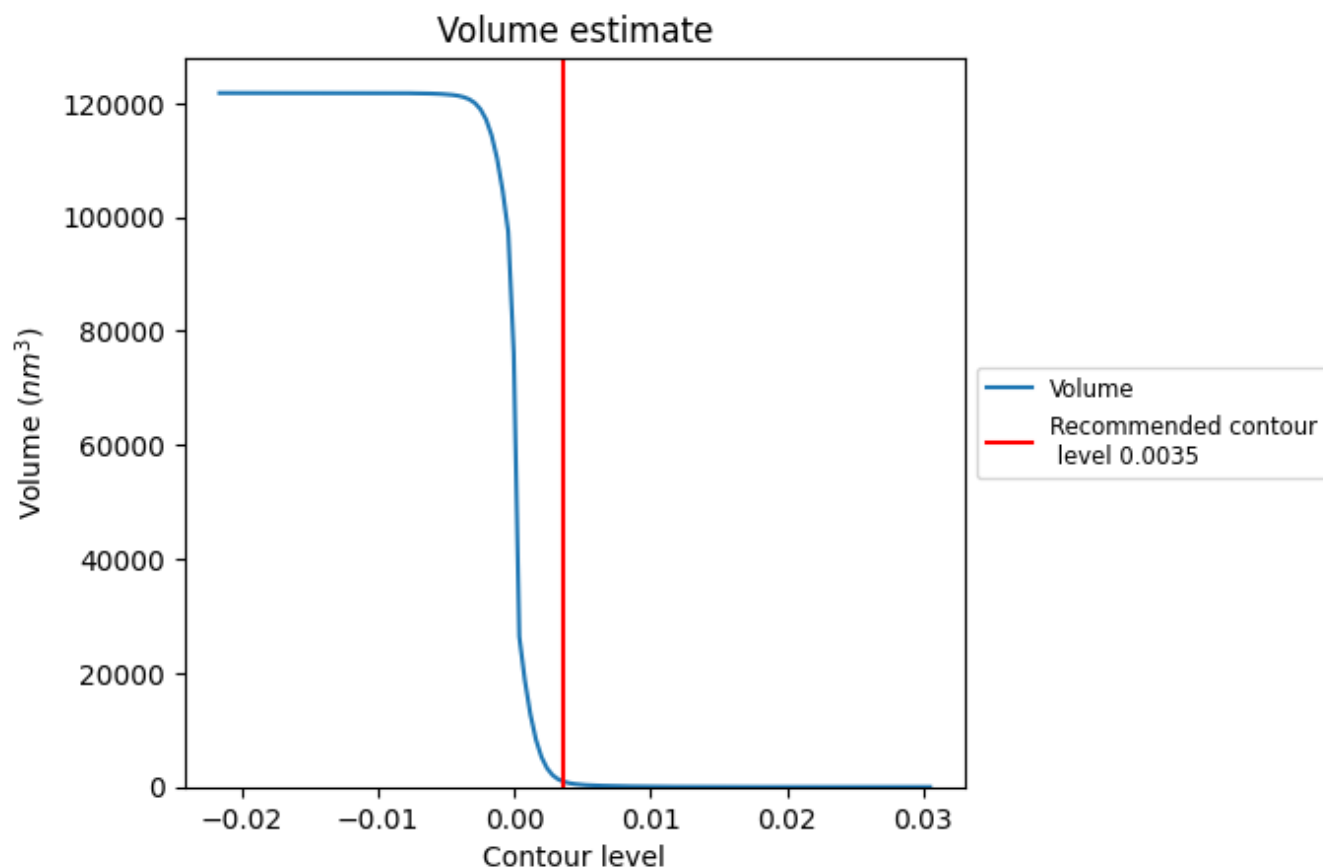
This section contains the results of statistical analysis of the map.

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.

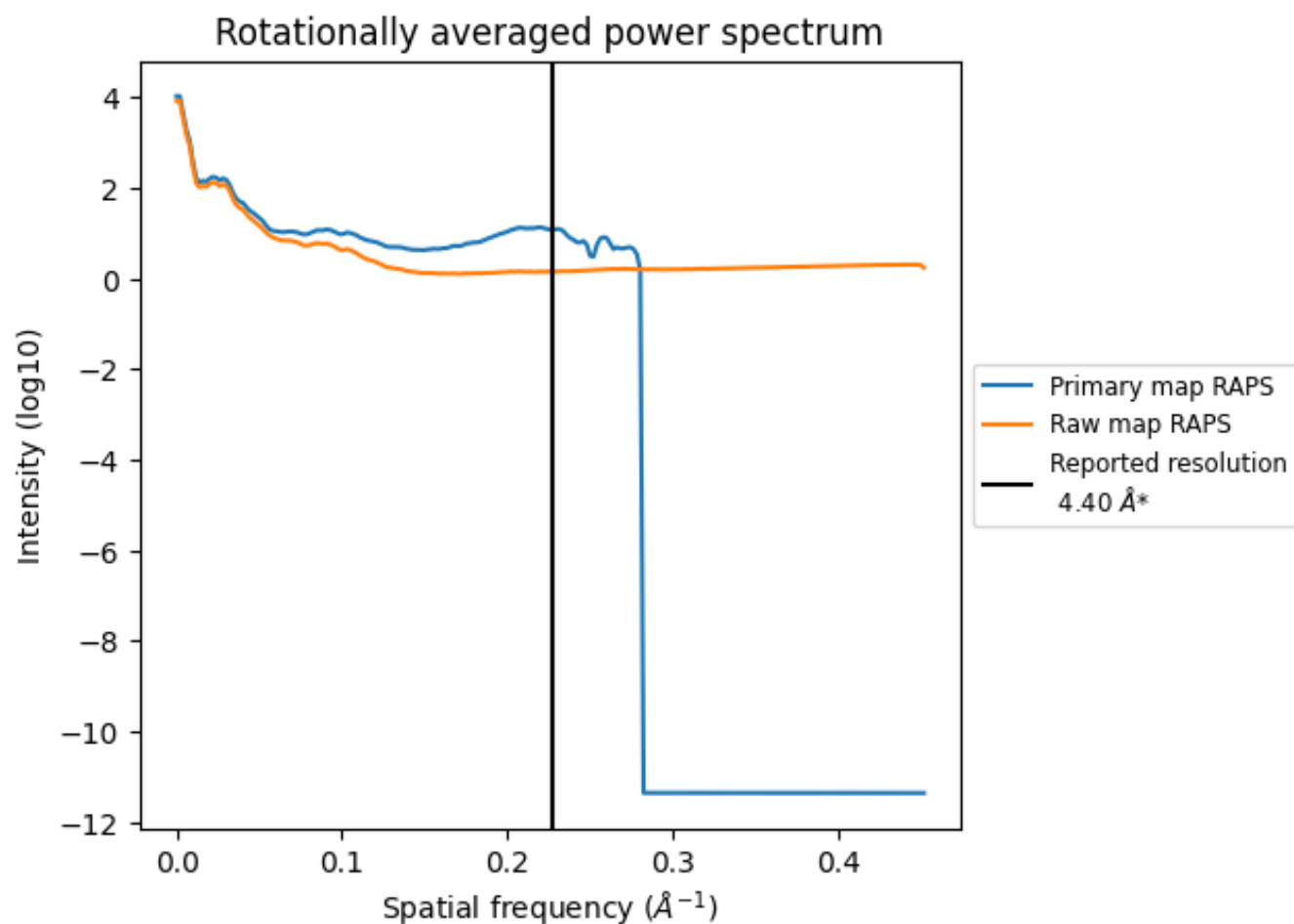
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1040 nm³; this corresponds to an approximate mass of 940 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 ⓘ

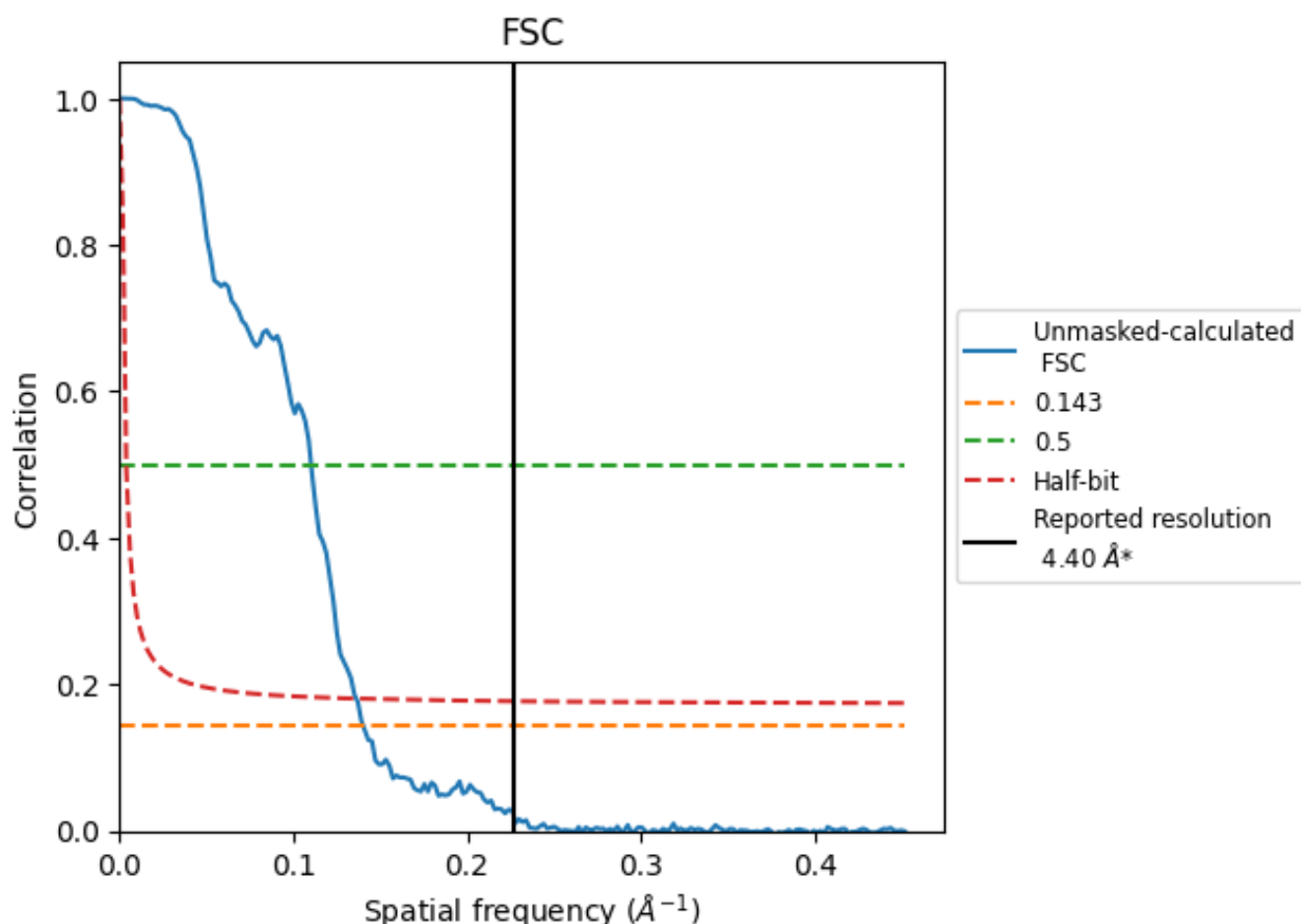


*Reported resolution corresponds to spatial frequency of 0.227 Å⁻¹

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 0.227 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.13	9.07	7.34

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.13 differs from the reported value 4.4 by more than 10 %

9 Map-model fit [i](#)

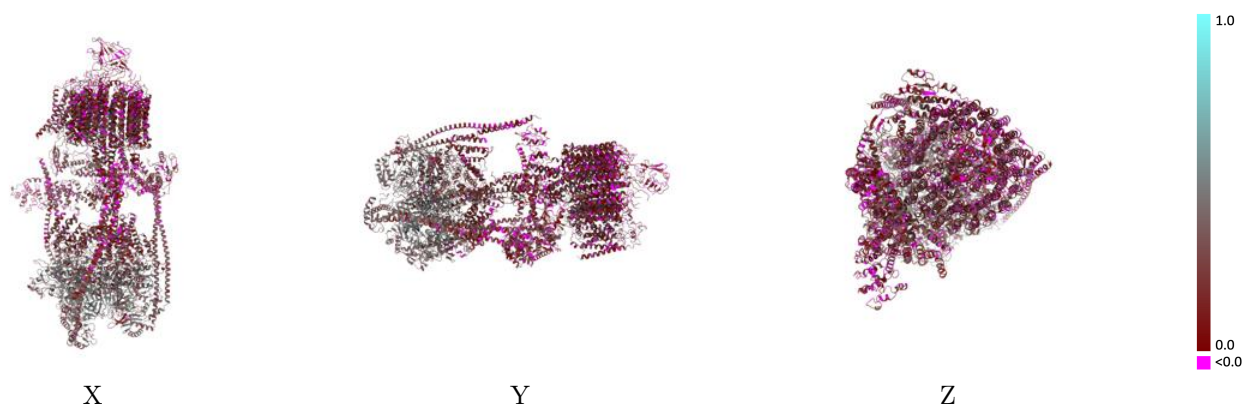
This section contains information regarding the fit between EMDB map EMD-44844 and PDB model 9BRU. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



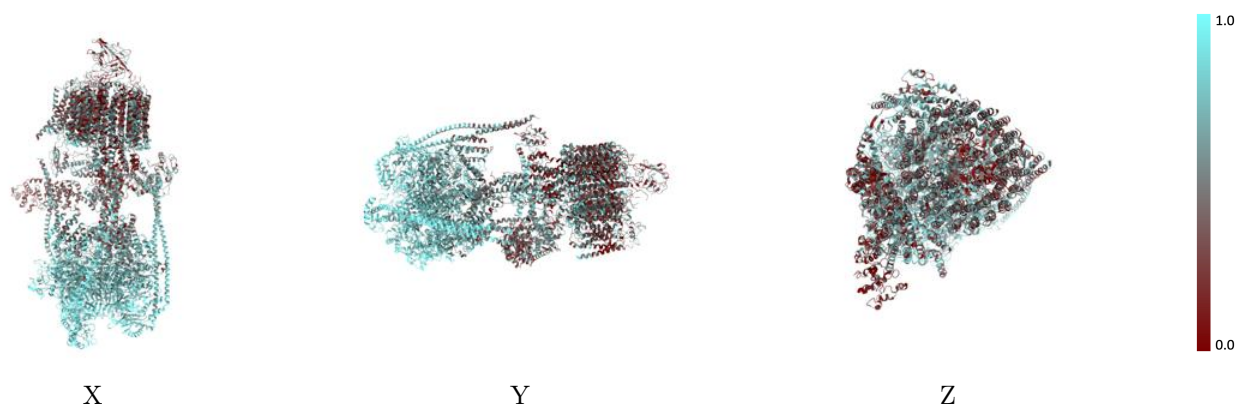
The images above show the 3D surface view of the map at the recommended contour level 0.0035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



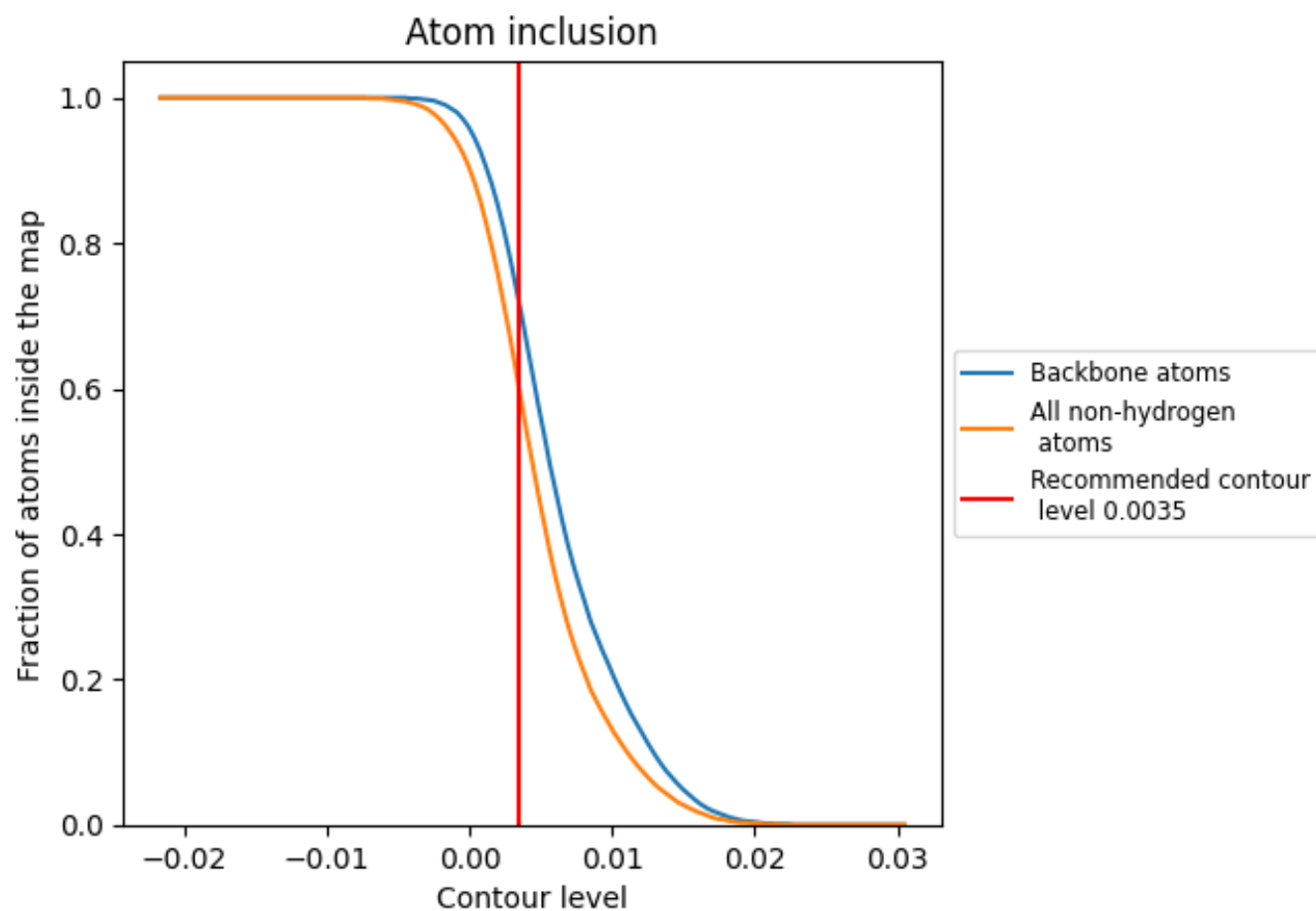
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0035).



































































9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 60% 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 (0.0035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5990	 0.2620
0	 0.7550	 0.3500
1	 0.7430	 0.3510
2	 0.6960	 0.2970
3	 0.7810	 0.3890
4	 0.7800	 0.3840
5	 0.7780	 0.3880
6	 0.5000	 0.1590
7	 0.5910	 0.2610
8	 0.7730	 0.3330
9	 0.7970	 0.3140
Q	 0.7560	 0.2960
R	 0.7270	 0.2370
T	 0.7700	 0.2550
U	 0.2680	 0.1390
V	 0.7270	 0.2120
X	 0.6140	 0.2340
a	 0.5040	 0.2070
b	 0.3850	 0.1660
c	 0.3270	 0.1450
d	 0.3670	 0.1760
e	 0.3780	 0.1540
f	 0.3620	 0.1860
g	 0.4100	 0.1740
h	 0.4610	 0.1830
i	 0.5360	 0.2170
j	 0.4850	 0.2140
k	 0.4590	 0.2050
l	 0.4780	 0.1730
m	 0.4470	 0.1810
n	 0.4390	 0.1430
o	 0.4370	 0.1890
p	 0.3440	 0.1630

