



Full wwPDB EM Validation Report ⓘ

Aug 14, 2025 – 12:14 PM JST

PDB ID : 9IRC / pdb_00009irc
EMDB ID : EMD-60809
Title : CryoEM structure of hSLC15A4+TASL+Fab235
Authors : Zhu, Y.L.; Zhang, Q.X.; Gao, P.
Deposited on : 2024-07-15
Resolution : 2.82 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.dev126
MolProbity : 4-5-2 with Phenix2.0rc1
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) : 2.45.1

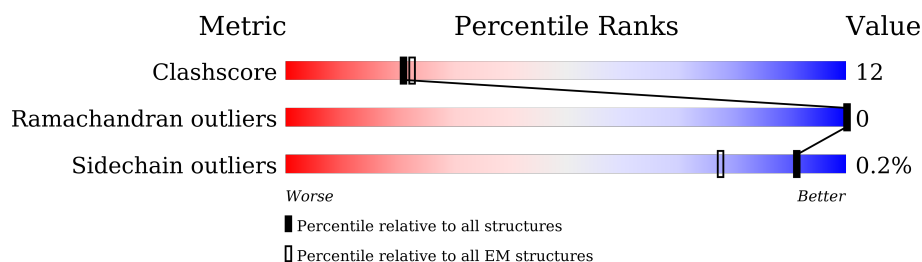
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.82 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	A	602	
2	B	170	
3	H	120	
4	L	108	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5589 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 Solute carrier family 15 member 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	479	Total	C	N	O	S	0	0
			3675	2437	588	629	21		

There are 25 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	578	LYS	-	expression tag	UNP Q8N697
A	579	LEU	-	expression tag	UNP Q8N697
A	580	GLY	-	expression tag	UNP Q8N697
A	581	SER	-	expression tag	UNP Q8N697
A	582	GLU	-	expression tag	UNP Q8N697
A	583	ASN	-	expression tag	UNP Q8N697
A	584	LEU	-	expression tag	UNP Q8N697
A	585	TYR	-	expression tag	UNP Q8N697
A	586	PHE	-	expression tag	UNP Q8N697
A	587	GLN	-	expression tag	UNP Q8N697
A	588	GLY	-	expression tag	UNP Q8N697
A	589	GLY	-	expression tag	UNP Q8N697
A	590	SER	-	expression tag	UNP Q8N697
A	591	GLY	-	expression tag	UNP Q8N697
A	592	GLY	-	expression tag	UNP Q8N697
A	593	SER	-	expression tag	UNP Q8N697
A	594	GLY	-	expression tag	UNP Q8N697
A	595	HIS	-	expression tag	UNP Q8N697
A	596	HIS	-	expression tag	UNP Q8N697
A	597	HIS	-	expression tag	UNP Q8N697
A	598	HIS	-	expression tag	UNP Q8N697
A	599	HIS	-	expression tag	UNP Q8N697
A	600	HIS	-	expression tag	UNP Q8N697
A	601	HIS	-	expression tag	UNP Q8N697
A	602	HIS	-	expression tag	UNP Q8N697

- Molecule 2 is a protein called TLR adapter interacting with SLC15A4 on the lysosome.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	19	Total 164	C 107	N 25	O 31	S 1	0	0

There are 75 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	initiating methionine	UNP Q9D3J9
B	2	LEU	-	expression tag	UNP Q9D3J9
B	3	SER	-	expression tag	UNP Q9D3J9
B	4	GLU	-	expression tag	UNP Q9D3J9
B	5	GLY	-	expression tag	UNP Q9D3J9
B	6	TYR	-	expression tag	UNP Q9D3J9
B	7	LEU	-	expression tag	UNP Q9D3J9
B	8	SER	-	expression tag	UNP Q9D3J9
B	9	GLY	-	expression tag	UNP Q9D3J9
B	10	LEU	-	expression tag	UNP Q9D3J9
B	11	GLU	-	expression tag	UNP Q9D3J9
B	12	TYR	-	expression tag	UNP Q9D3J9
B	13	TRP	-	expression tag	UNP Q9D3J9
B	14	ASN	-	expression tag	UNP Q9D3J9
B	15	ASP	-	expression tag	UNP Q9D3J9
B	16	ILE	-	expression tag	UNP Q9D3J9
B	17	HIS	-	expression tag	UNP Q9D3J9
B	18	TRP	-	expression tag	UNP Q9D3J9
B	19	ASN	-	expression tag	UNP Q9D3J9
B	20	CYS	-	expression tag	UNP Q9D3J9
B	21	ALA	-	expression tag	UNP Q9D3J9
B	22	SER	-	expression tag	UNP Q9D3J9
B	23	TYR	-	expression tag	UNP Q9D3J9
B	24	ASN	-	expression tag	UNP Q9D3J9
B	25	GLU	-	expression tag	UNP Q9D3J9
B	26	PRO	-	expression tag	UNP Q9D3J9
B	27	VAL	-	expression tag	UNP Q9D3J9
B	28	ALA	-	expression tag	UNP Q9D3J9
B	29	GLY	-	expression tag	UNP Q9D3J9
B	30	ASP	-	expression tag	UNP Q9D3J9
B	31	GLN	-	expression tag	UNP Q9D3J9
B	32	GLY	-	expression tag	UNP Q9D3J9
B	33	LYS	-	expression tag	UNP Q9D3J9
B	34	GLU	-	expression tag	UNP Q9D3J9
B	130	LYS	-	expression tag	UNP Q9D3J9
B	131	LEU	-	expression tag	UNP Q9D3J9
B	132	GLY	-	expression tag	UNP Q9D3J9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	133	SER	-	expression tag	UNP Q9D3J9
B	134	GLU	-	expression tag	UNP Q9D3J9
B	135	ASN	-	expression tag	UNP Q9D3J9
B	136	LEU	-	expression tag	UNP Q9D3J9
B	137	TYR	-	expression tag	UNP Q9D3J9
B	138	PHE	-	expression tag	UNP Q9D3J9
B	139	GLN	-	expression tag	UNP Q9D3J9
B	140	GLY	-	expression tag	UNP Q9D3J9
B	141	GLY	-	expression tag	UNP Q9D3J9
B	142	SER	-	expression tag	UNP Q9D3J9
B	143	GLY	-	expression tag	UNP Q9D3J9
B	144	GLY	-	expression tag	UNP Q9D3J9
B	145	SER	-	expression tag	UNP Q9D3J9
B	146	GLY	-	expression tag	UNP Q9D3J9
B	147	HIS	-	expression tag	UNP Q9D3J9
B	148	HIS	-	expression tag	UNP Q9D3J9
B	149	HIS	-	expression tag	UNP Q9D3J9
B	150	HIS	-	expression tag	UNP Q9D3J9
B	151	HIS	-	expression tag	UNP Q9D3J9
B	152	HIS	-	expression tag	UNP Q9D3J9
B	153	HIS	-	expression tag	UNP Q9D3J9
B	154	HIS	-	expression tag	UNP Q9D3J9
B	155	TRP	-	expression tag	UNP Q9D3J9
B	156	SER	-	expression tag	UNP Q9D3J9
B	157	HIS	-	expression tag	UNP Q9D3J9
B	158	PRO	-	expression tag	UNP Q9D3J9
B	159	GLN	-	expression tag	UNP Q9D3J9
B	160	PHE	-	expression tag	UNP Q9D3J9
B	161	GLU	-	expression tag	UNP Q9D3J9
B	162	LYS	-	expression tag	UNP Q9D3J9
B	163	TRP	-	expression tag	UNP Q9D3J9
B	164	SER	-	expression tag	UNP Q9D3J9
B	165	HIS	-	expression tag	UNP Q9D3J9
B	166	PRO	-	expression tag	UNP Q9D3J9
B	167	GLN	-	expression tag	UNP Q9D3J9
B	168	PHE	-	expression tag	UNP Q9D3J9
B	169	GLU	-	expression tag	UNP Q9D3J9
B	170	LYS	-	expression tag	UNP Q9D3J9

- Molecule 3 is a protein called Fab235 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	120	Total	C	N	O	S	0	0
			935	591	161	178	5		

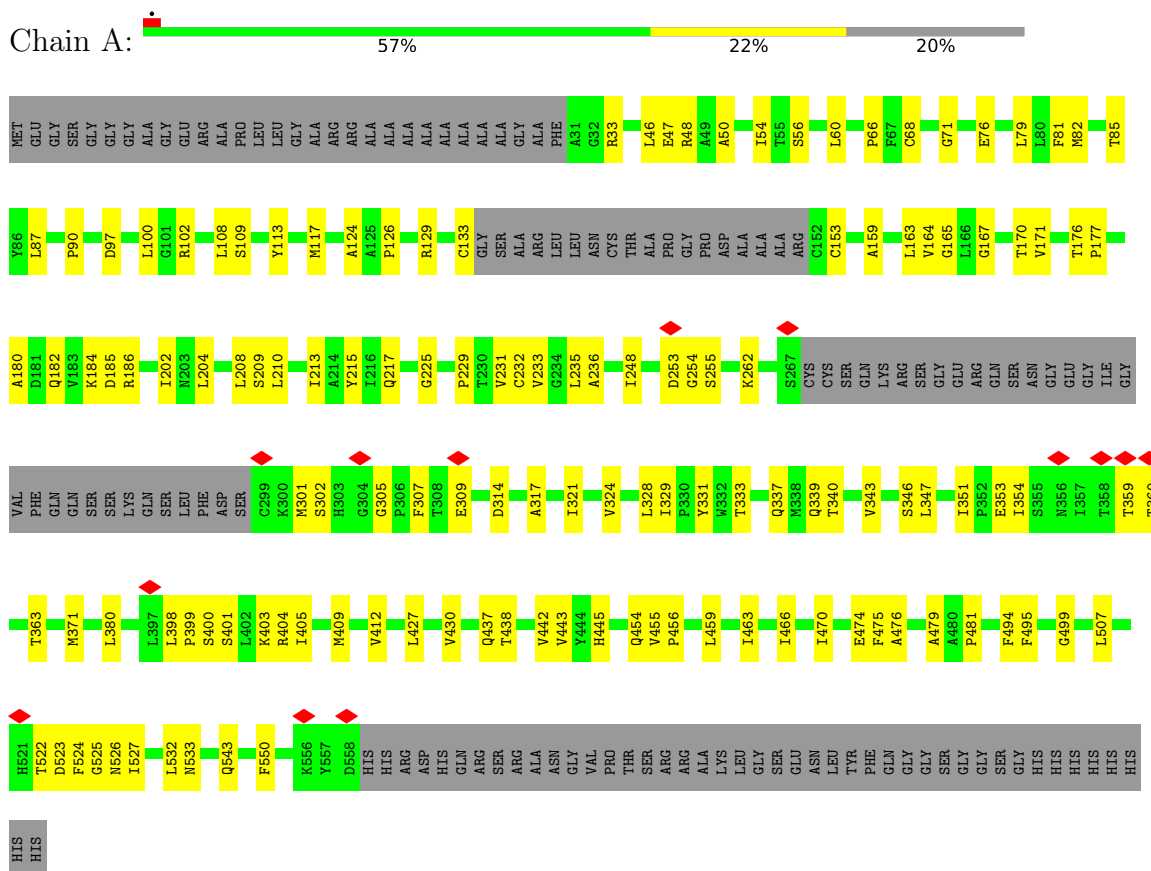
- Molecule 4 is a protein called Fab235 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	108	Total	C	N	O	S	0	0
			815	511	138	161	5		

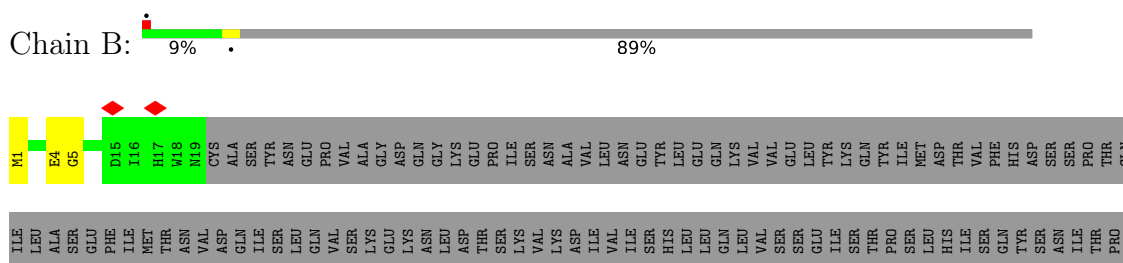
3 Residue-property plots

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: Solute carrier family 15 member 4



- Molecule 2: TLR adapter interacting with SLC15A4 on the lysosome



- Molecule 3: Fab235 heavy chain

I103	R104	A105	F106	F107	D108	Y109	G113	T117	S120	D1	V2	Q3	L4	V5	A24	F27	S30	R31	F32	G33	V37	R38	Q39	A40	P41	E42	K43	G44	L45	E46	V47	V48	A49	Y50	S52	S53	S56	N57	I58	Y59	V64	R67	R72	M83	L86	R87	S88	E89	D90	T91	Y94	R98	S99	T100	T101
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- Molecule 4: Fab235 light chain

Q1	V19	V29	S30	V33	L34	H35	Q38	Q39	K40	R46	L47	Y50	R62	F63	S66	G67	Y72	S73	I76	D83	A84	A85	T86	Y87	Y92	K108
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	226165	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	2.228	Depositor
Minimum map value	-0.948	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.043	Depositor
Recommended contour level	0.471	Depositor
Map size (Å)	320.0, 320.0, 320.0	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	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	A	0.13	0/3769	0.32	0/5129
2	B	0.25	0/170	0.48	0/231
3	H	0.12	0/957	0.34	0/1294
4	L	0.29	0/837	0.45	0/1137
All	All	0.17	0/5733	0.35	0/7791

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	L	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	L	46	ARG	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3675	0	3772	92	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	164	0	144	2	0
3	H	935	0	904	32	0
4	L	815	0	780	15	0
All	All	5589	0	5600	131	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 12.

All (131) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:523:ASP:OD2	3:H:31:ARG:HG3	1.61	1.01
4:L:47:LEU:HD11	4:L:50:TYR:HB3	1.54	0.88
1:A:33:ARG:HH12	1:A:185:ASP:HB2	1.43	0.82
1:A:47:GLU:OE2	1:A:48:ARG:NH1	2.14	0.80
1:A:443:VAL:HG21	3:H:105:ALA:HB2	1.66	0.78
1:A:523:ASP:OD2	1:A:524:PHE:CE2	2.42	0.73
1:A:526:ASN:ND2	3:H:56:SER:OG	2.20	0.73
1:A:405:ILE:HG22	1:A:409:MET:HE2	1.78	0.66
1:A:301:MET:SD	1:A:302:SER:N	2.69	0.65
1:A:380:LEU:HD13	1:A:466:ILE:HD13	1.79	0.65
1:A:113:TYR:HE1	1:A:164:VAL:HG13	1.62	0.64
1:A:76:GLU:HG3	1:A:507:LEU:HD23	1.78	0.64
1:A:523:ASP:CG	1:A:524:PHE:CD2	2.76	0.63
1:A:117:MET:HG3	1:A:233:VAL:HG21	1.78	0.63
1:A:351:ILE:N	1:A:437:GLN:OE1	2.31	0.63
1:A:90:PRO:HG2	1:A:494:PHE:HB2	1.81	0.62
1:A:398:LEU:HD12	1:A:399:PRO:HD2	1.81	0.61
1:A:97:ASP:OD1	1:A:102:ARG:NH2	2.33	0.60
1:A:438:THR:N	4:L:33:TYR:OH	2.33	0.60
3:H:98:ARG:NH2	3:H:108:ASP:OD2	2.27	0.59
1:A:321:ILE:HD12	1:A:476:ALA:HA	1.85	0.59
3:H:48:VAL:HG13	3:H:64:VAL:HG21	1.84	0.59
3:H:39:GLN:HB2	3:H:45:LEU:HD23	1.85	0.58
1:A:445:HIS:NE2	3:H:50:TYR:OH	2.33	0.58
3:H:100:THR:OG1	3:H:104:ARG:O	2.22	0.58
1:A:85:THR:HG22	1:A:165:GLY:HA2	1.86	0.57
1:A:71:GLY:N	1:A:525:GLY:HA2	2.20	0.57
4:L:29:VAL:O	4:L:72:TYR:OH	2.23	0.57
1:A:113:TYR:CE1	1:A:164:VAL:HG13	2.38	0.56
1:A:97:ASP:HB2	1:A:255:SER:HB3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:52:SER:HB2	3:H:57:ASN:HB2	1.86	0.56
3:H:83:MET:SD	3:H:86:LEU:HD21	2.46	0.55
4:L:30:SER:HB3	4:L:33:TYR:HD2	1.71	0.54
1:A:523:ASP:CG	1:A:524:PHE:CE2	2.86	0.54
1:A:302:SER:OG	1:A:309:GLU:OE1	2.25	0.54
1:A:527:ILE:HD12	1:A:532:LEU:HD12	1.90	0.54
3:H:57:ASN:ND2	3:H:59:TYR:OH	2.40	0.54
1:A:314:ASP:OD1	1:A:481:PRO:HG3	2.08	0.54
1:A:66:PRO:HG3	1:A:129:ARG:CZ	2.38	0.54
3:H:94:TYR:O	3:H:113:GLY:HA2	2.07	0.54
1:A:331:TYR:HD1	1:A:412:VAL:HG11	1.73	0.53
1:A:346:SER:OG	1:A:454:GLN:OE1	2.16	0.53
3:H:108:ASP:OD1	3:H:109:TYR:N	2.41	0.53
1:A:253:ASP:OD1	1:A:254:GLY:N	2.42	0.53
3:H:33:GLY:HA2	3:H:72:ARG:HH12	1.73	0.52
3:H:102:ILE:HG13	3:H:103:ILE:H	1.74	0.52
1:A:60:LEU:HD11	1:A:347:LEU:HD21	1.90	0.52
3:H:67:ARG:NH1	3:H:90:ASP:OD2	2.38	0.52
3:H:91:THR:HG23	3:H:117:THR:HA	1.92	0.51
4:L:19:VAL:HB	4:L:76:ILE:HB	1.92	0.51
1:A:124:ALA:O	1:A:129:ARG:NH2	2.38	0.51
1:A:404:ARG:NH2	1:A:474:GLU:OE2	2.44	0.51
3:H:30:SER:O	3:H:53:SER:OG	2.24	0.51
1:A:50:ALA:HB2	1:A:232:CYS:SG	2.51	0.51
1:A:113:TYR:O	1:A:117:MET:HG2	2.12	0.49
1:A:56:SER:HB3	1:A:210:LEU:HD23	1.94	0.49
1:A:90:PRO:CG	1:A:494:PHE:HB2	2.43	0.49
1:A:231:VAL:O	1:A:235:LEU:HG	2.12	0.49
1:A:204:LEU:O	1:A:208:LEU:HG	2.13	0.48
1:A:262:LYS:HB3	1:A:307:PHE:HZ	1.78	0.48
1:A:46:LEU:HD22	1:A:232:CYS:HB2	1.95	0.48
1:A:333:THR:O	1:A:337:GLN:HG2	2.13	0.48
3:H:87:ARG:HG3	3:H:89:GLU:HG3	1.95	0.48
4:L:62:ARG:NE	4:L:83:ASP:OD2	2.46	0.48
4:L:34:LEU:HD22	4:L:72:TYR:CG	2.48	0.48
1:A:409:MET:HA	1:A:412:VAL:HG12	1.95	0.48
1:A:522:THR:HG21	3:H:56:SER:HB3	1.96	0.47
1:A:100:LEU:HD11	1:A:108:LEU:HD12	1.97	0.47
1:A:229:PRO:O	1:A:233:VAL:HG23	2.14	0.47
3:H:37:VAL:HG22	3:H:47:TRP:HA	1.95	0.47
3:H:40:ALA:HB3	3:H:43:LYS:HB2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:400:SER:H	1:A:403:LYS:HE3	1.79	0.47
1:A:215:TYR:HE2	1:A:354:ILE:HD11	1.81	0.46
3:H:32:PHE:HB3	3:H:98:ARG:HG2	1.98	0.46
1:A:33:ARG:HH11	1:A:186:ARG:HG3	1.81	0.46
1:A:329:ILE:HD11	1:A:495:PHE:HD1	1.80	0.46
1:A:523:ASP:OD2	1:A:524:PHE:HE2	1.93	0.46
4:L:67:GLY:HA3	4:L:72:TYR:HA	1.97	0.46
1:A:210:LEU:HB3	1:A:371:MET:HB2	1.98	0.46
1:A:82:MET:HE1	1:A:339:GLN:HB3	1.97	0.46
4:L:35:HIS:HB3	4:L:47:LEU:HD21	1.98	0.45
1:A:54:ILE:HD11	1:A:117:MET:HE1	1.98	0.45
1:A:133:CYS:HB2	1:A:153:CYS:HB3	1.67	0.45
1:A:180:ALA:O	1:A:184:LYS:N	2.50	0.45
1:A:466:ILE:HA	1:A:470:ILE:HD13	1.97	0.45
1:A:321:ILE:HD11	1:A:479:ALA:HB3	1.99	0.45
3:H:52:SER:O	3:H:72:ARG:NH1	2.49	0.45
1:A:46:LEU:HB2	1:A:236:ALA:HB2	1.99	0.45
1:A:470:ILE:H	1:A:470:ILE:HD12	1.80	0.45
1:A:202:ILE:HD12	2:B:5:GLY:HA2	1.99	0.45
3:H:24:ALA:HB1	3:H:27:PHE:CE1	2.51	0.45
3:H:2:VAL:HG23	3:H:27:PHE:CD1	2.52	0.44
1:A:87:LEU:O	1:A:90:PRO:HD2	2.17	0.44
1:A:217:GLN:HG3	1:A:225:GLY:HA3	1.99	0.44
1:A:409:MET:HB3	1:A:543:GLN:NE2	2.32	0.44
1:A:317:ALA:O	1:A:321:ILE:HG12	2.17	0.44
2:B:1:MET:CG	2:B:4:GLU:HG3	2.48	0.44
3:H:105:ALA:O	4:L:35:HIS:NE2	2.51	0.43
4:L:63:PHE:CE2	4:L:76:ILE:HG12	2.53	0.43
1:A:126:PRO:HA	1:A:129:ARG:NE	2.33	0.43
3:H:106:PHE:CE1	3:H:108:ASP:HB3	2.54	0.43
4:L:38:GLN:HG3	4:L:87:TYR:CE2	2.54	0.43
1:A:113:TYR:HB2	1:A:167:GLY:HA3	1.99	0.43
1:A:182:GLN:NE2	1:A:248:ILE:O	2.43	0.43
1:A:401:SER:HB3	1:A:475:PHE:HB2	1.99	0.43
4:L:66:SER:OG	4:L:73:SER:OG	2.36	0.43
1:A:79:LEU:HG	1:A:340:THR:HG21	2.00	0.43
3:H:3:GLN:OE1	3:H:5:VAL:HG13	2.19	0.42
1:A:109:SER:OG	1:A:171:VAL:HG23	2.19	0.42
1:A:343:VAL:O	1:A:347:LEU:HG	2.19	0.42
1:A:427:LEU:HA	1:A:430:VAL:HG12	2.01	0.42
3:H:105:ALA:HB1	4:L:92:TYR:CE2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:353:GLU:HG2	1:A:363:THR:HG22	2.02	0.42
1:A:324:VAL:HG21	1:A:475:PHE:CE2	2.55	0.42
1:A:329:ILE:HG23	1:A:499:GLY:HA2	2.02	0.42
1:A:455:VAL:N	1:A:456:PRO:HD2	2.34	0.42
3:H:101:THR:HG22	3:H:101:THR:O	2.20	0.41
1:A:176:THR:HB	1:A:177:PRO:HD3	2.03	0.41
1:A:109:SER:OG	1:A:170:THR:HB	2.20	0.41
1:A:459:LEU:O	1:A:463:ILE:HG12	2.21	0.41
1:A:328:LEU:HD23	1:A:328:LEU:HA	1.91	0.41
1:A:81:PHE:O	1:A:85:THR:HG23	2.20	0.41
1:A:159:ALA:O	1:A:163:LEU:HD23	2.21	0.41
1:A:409:MET:HE1	1:A:550:PHE:CG	2.56	0.41
1:A:533:ASN:OD1	1:A:533:ASN:N	2.54	0.40
1:A:68:CYS:HB2	3:H:31:ARG:NH2	2.36	0.40
1:A:359:THR:HG23	1:A:360:THR:HG22	2.02	0.40
1:A:442:VAL:HG21	1:A:524:PHE:HB3	2.01	0.40
4:L:40:LYS:HD3	4:L:85:ALA:HB2	2.04	0.40
1:A:209:SER:HA	1:A:213:ILE:HG12	2.04	0.40
1:A:301:MET:HE1	1:A:305:GLY:HA3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	473/602 (79%)	447 (94%)	26 (6%)	0	100	100
2	B	17/170 (10%)	16 (94%)	1 (6%)	0	100	100
3	H	118/120 (98%)	111 (94%)	7 (6%)	0	100	100
4	L	106/108 (98%)	104 (98%)	2 (2%)	0	100	100
All	All	714/1000 (71%)	678 (95%)	36 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	385/469 (82%)	385 (100%)	0	100	100
2	B	17/156 (11%)	17 (100%)	0	100	100
3	H	100/100 (100%)	100 (100%)	0	100	100
4	L	89/89 (100%)	88 (99%)	1 (1%)	70	90
All	All	591/814 (73%)	590 (100%)	1 (0%)	91	97

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	L	47	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	174	ASN
1	A	526	ASN
1	A	543	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

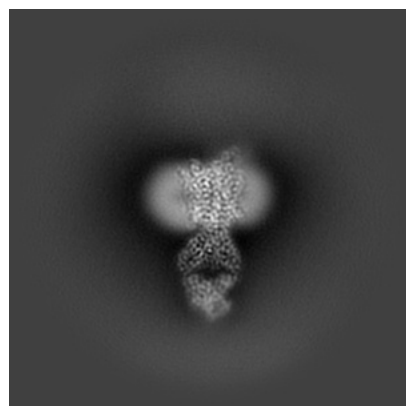
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60809. These allow visual inspection of the internal detail of the map and identification of artifacts.

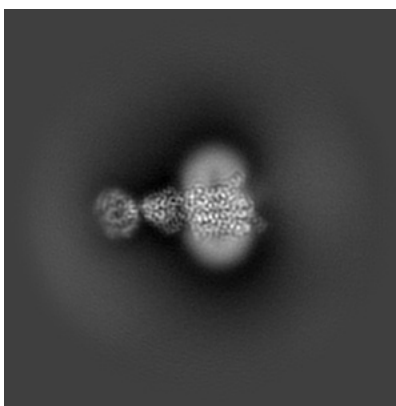
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

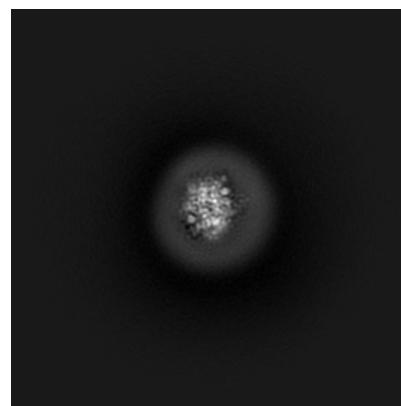
6.1.1 Primary map



X

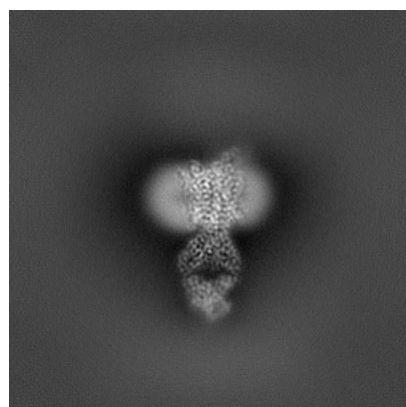


Y

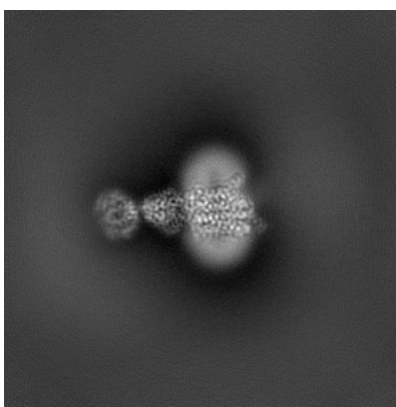


Z

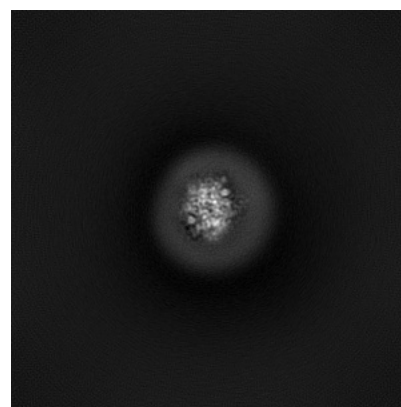
6.1.2 Raw map



X



Y

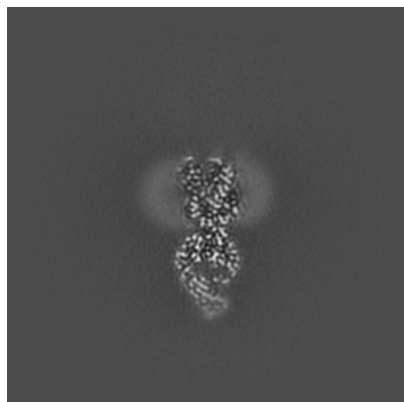


Z

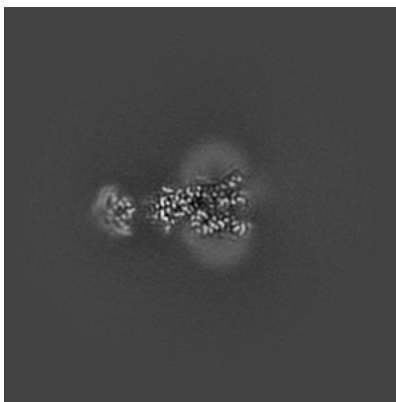
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

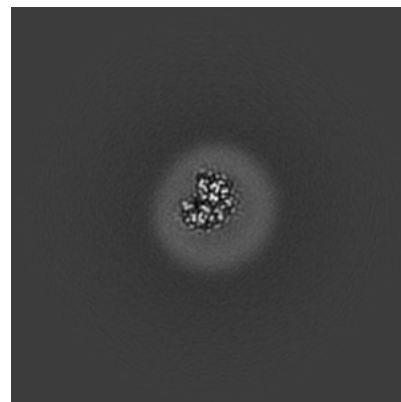
6.2.1 Primary map



X Index: 160

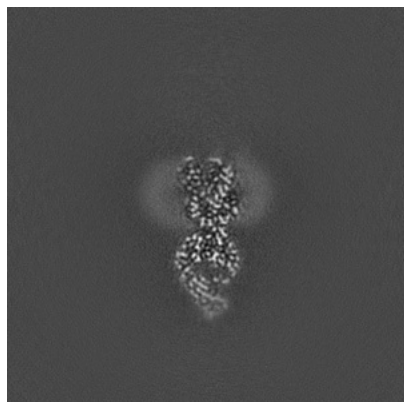


Y Index: 160

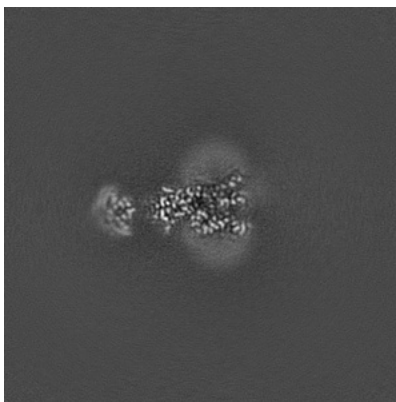


Z Index: 160

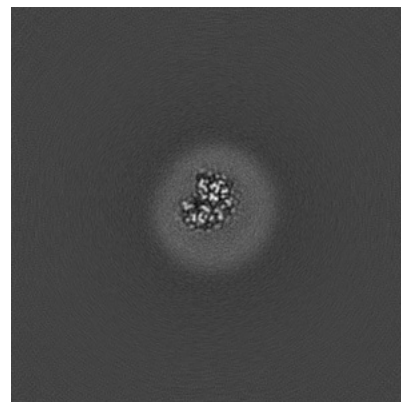
6.2.2 Raw map



X Index: 160



Y Index: 160

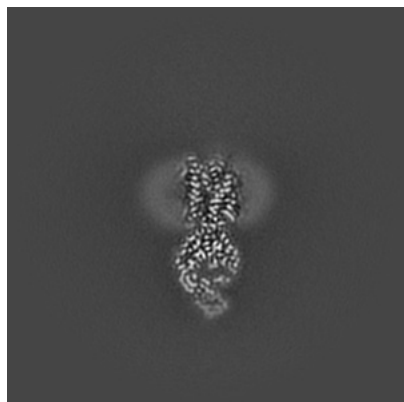


Z Index: 160

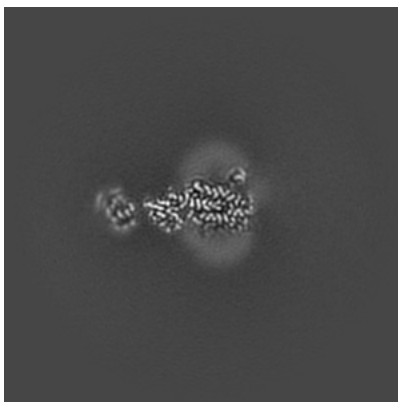
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

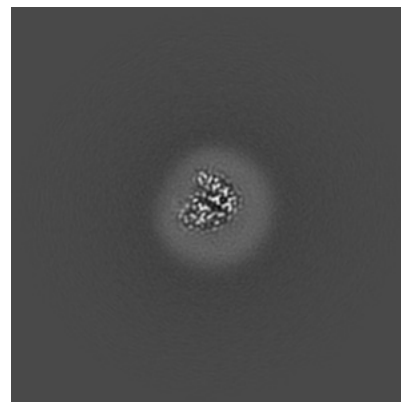
6.3.1 Primary map



X Index: 162

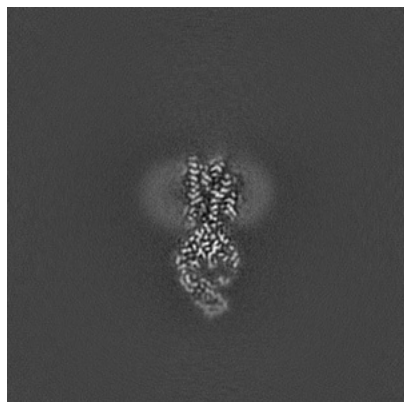


Y Index: 166

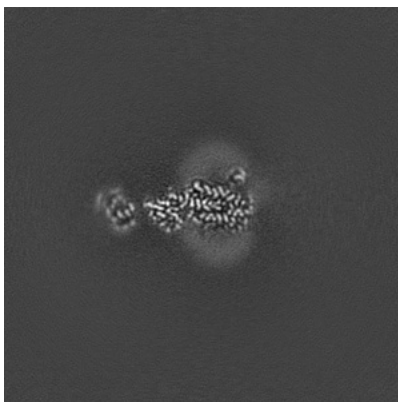


Z Index: 155

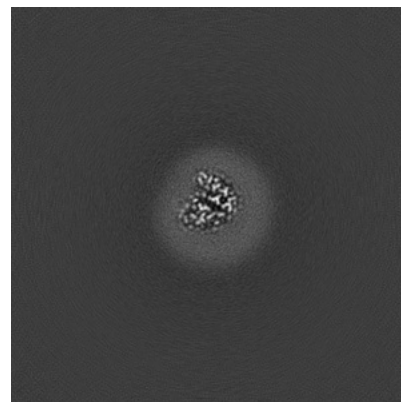
6.3.2 Raw map



X Index: 163



Y Index: 166

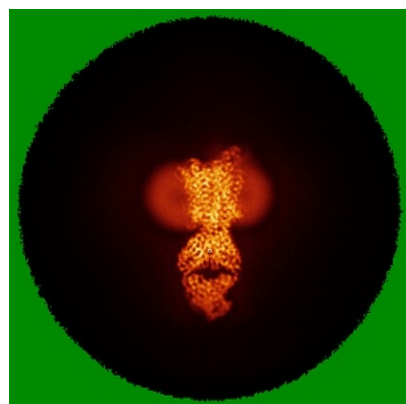


Z Index: 155

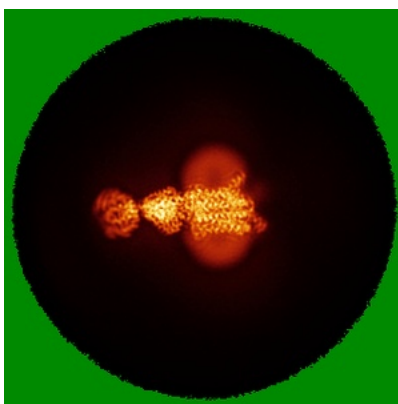
The images above show the largest variance slices of the map in three orthogonal directions.

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

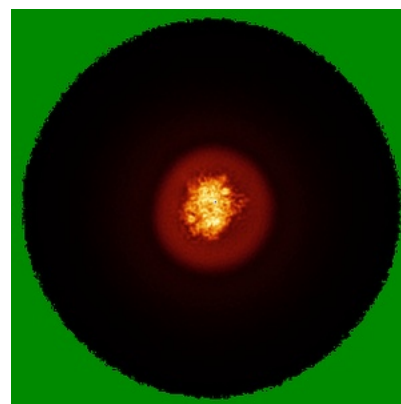
6.4.1 Primary map



X

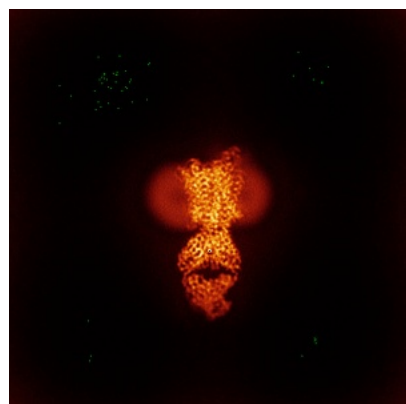


Y

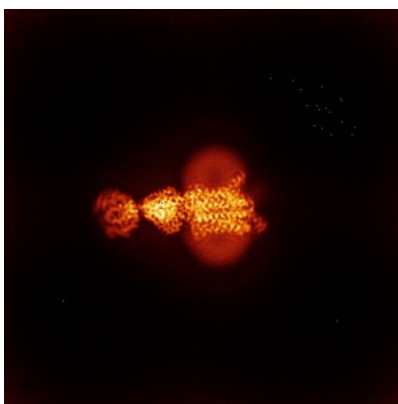


Z

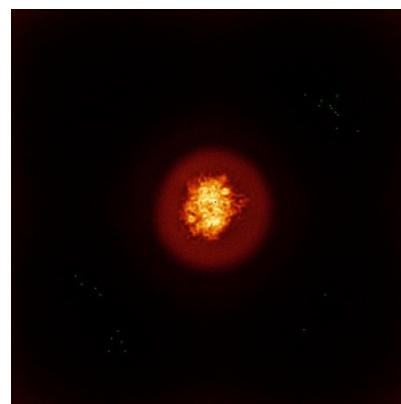
6.4.2 Raw map



X



Y

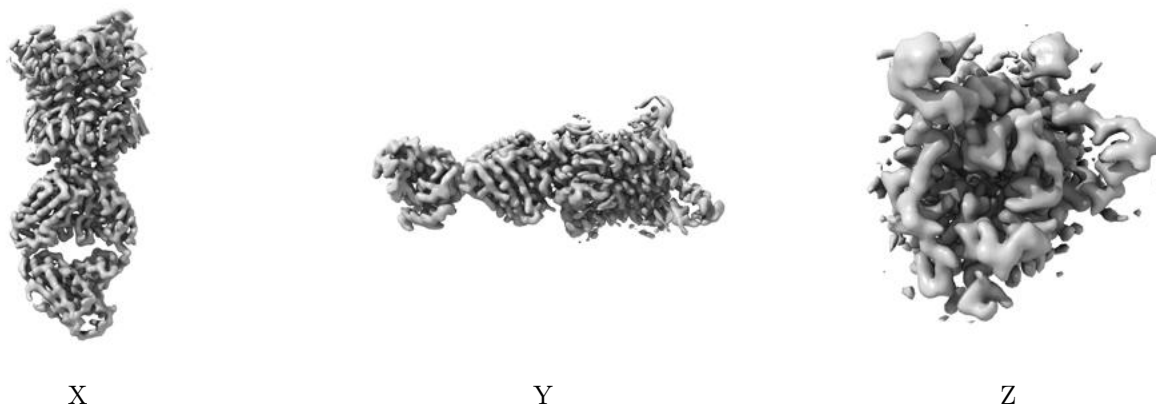


Z

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.

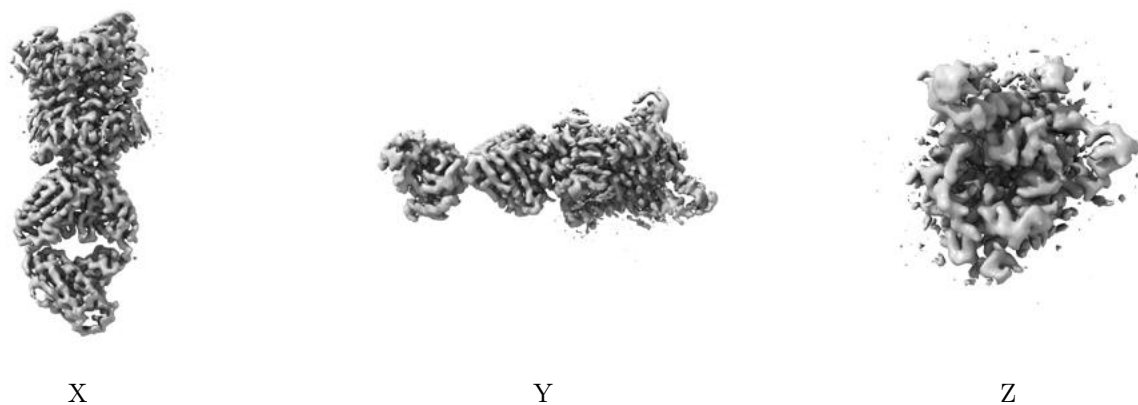
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.471. 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.

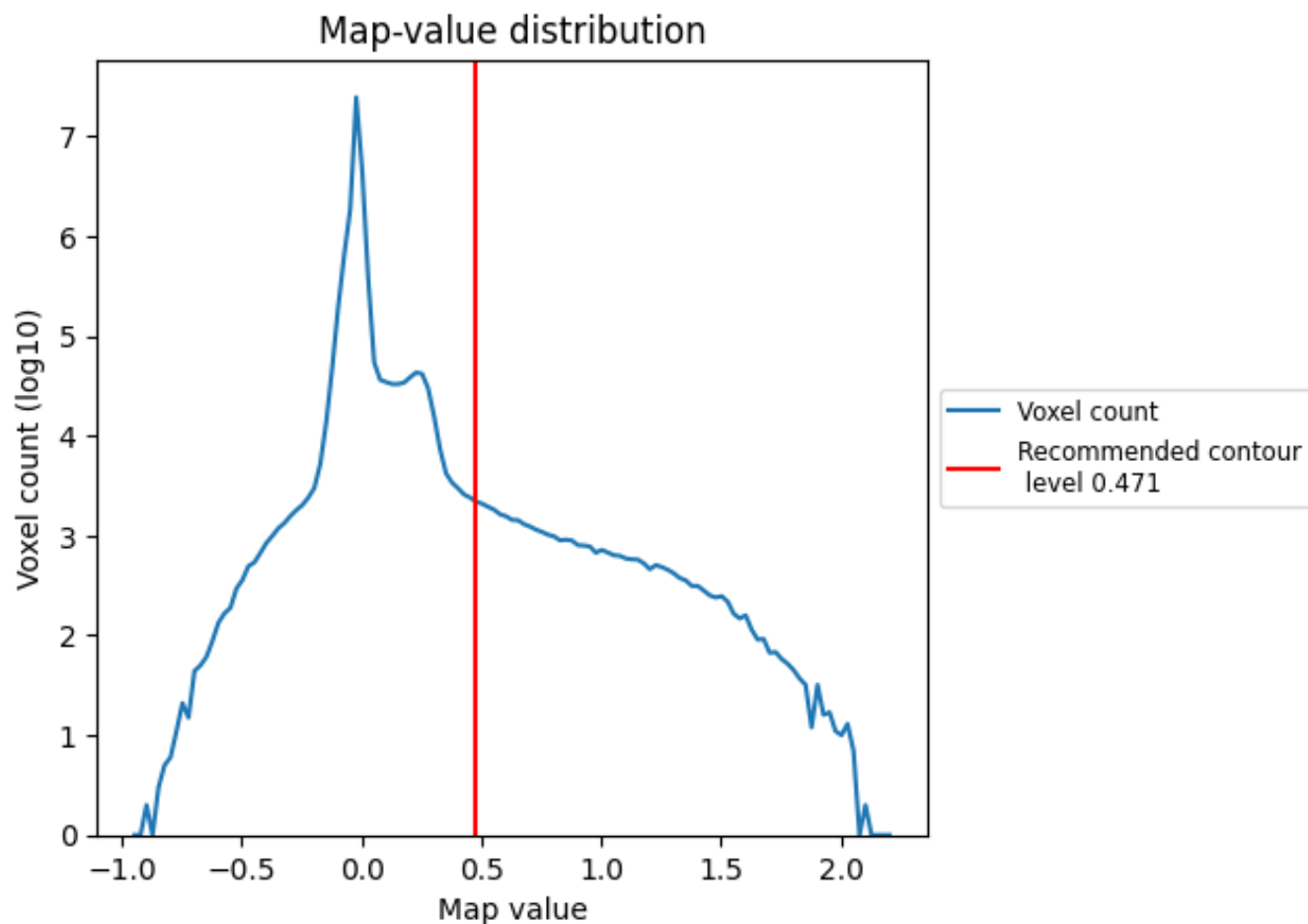
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

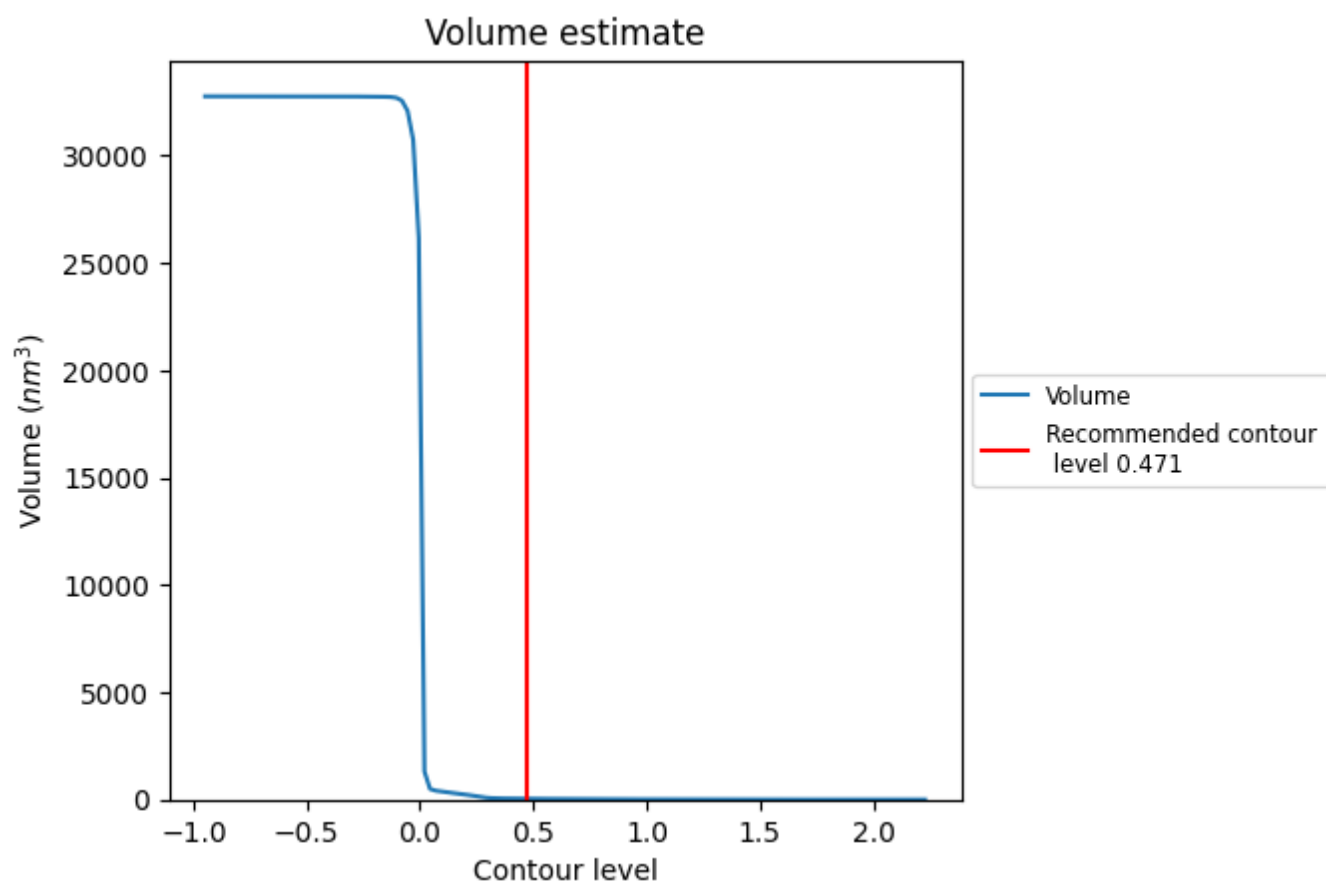
This section contains the results of statistical analysis of the map.

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.

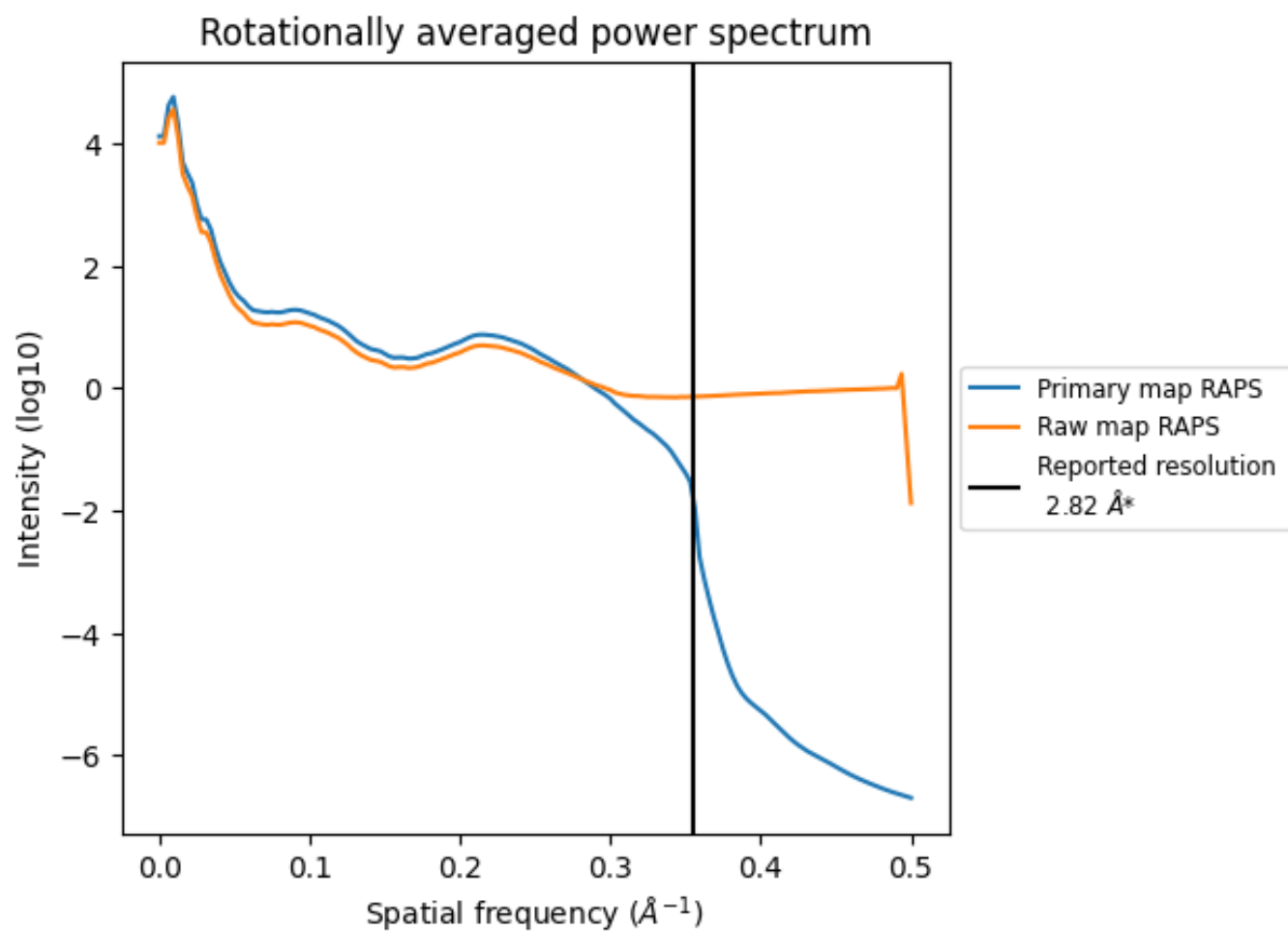
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 38 nm^3 ; this corresponds to an approximate mass of 35 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 ⓘ

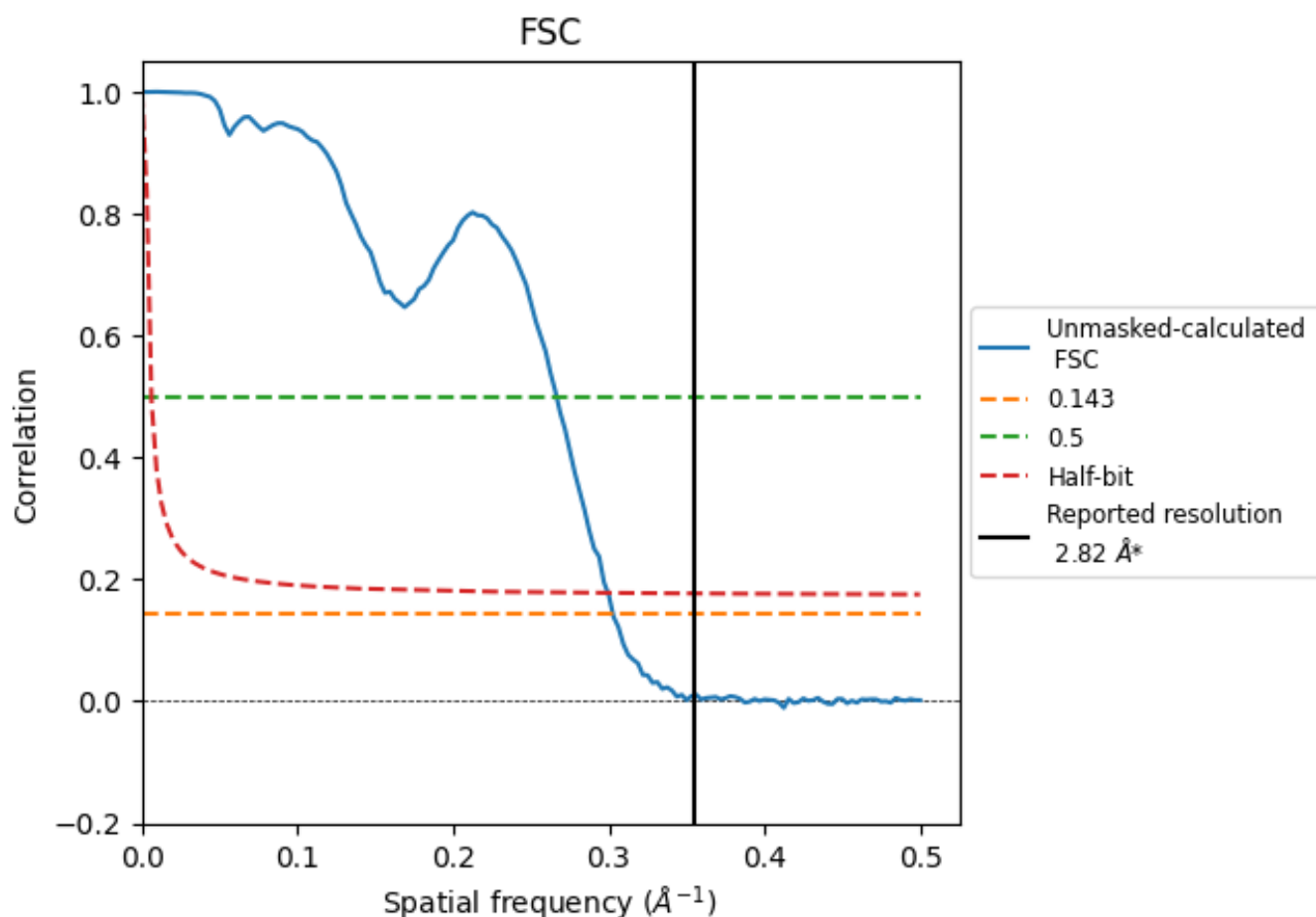


*Reported resolution corresponds to spatial frequency of 0.355 \AA^{-1}

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 0.355 Å⁻¹

8.2 Resolution estimates [i](#)

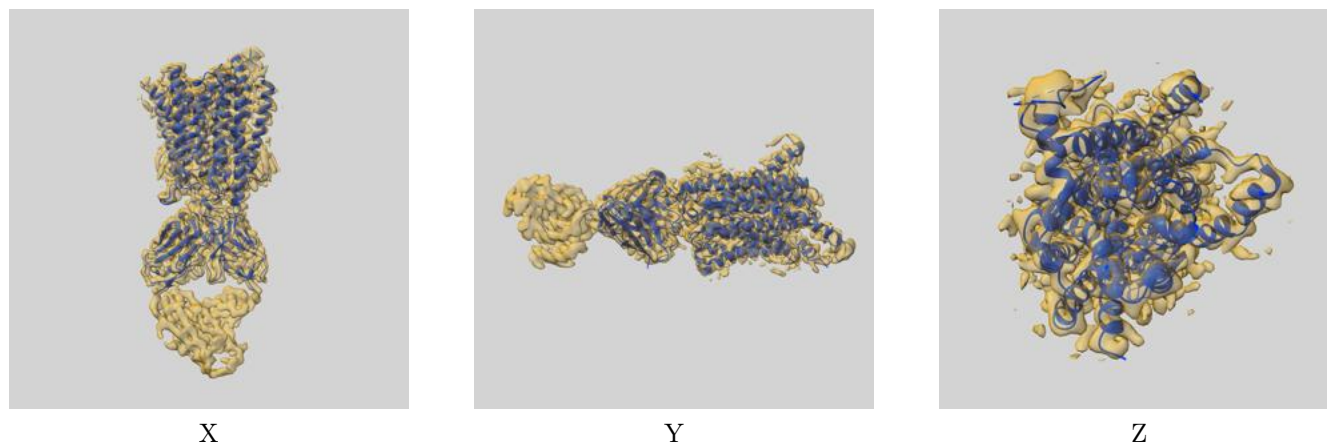
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.82	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.30	3.75	3.34

*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 3.30 differs from the reported value 2.82 by more than 10 %

9 Map-model fit [i](#)

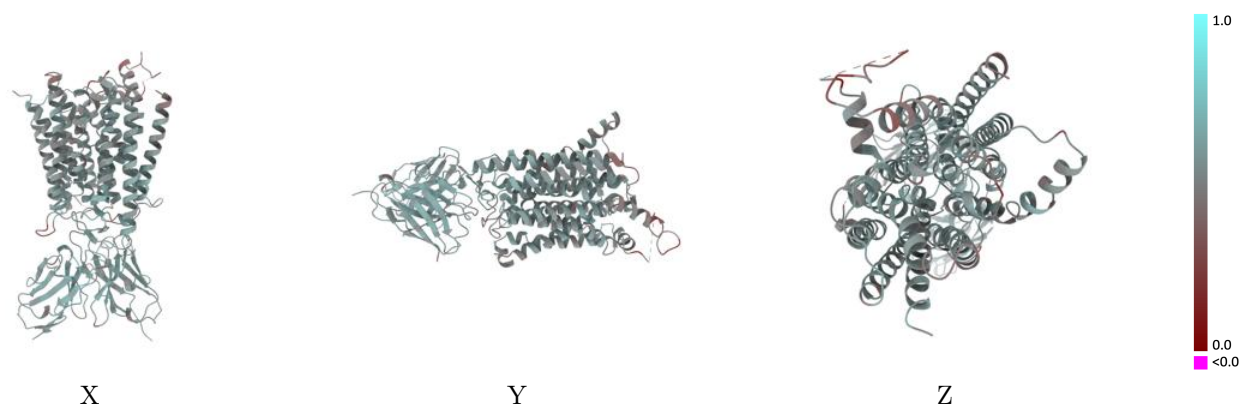
This section contains information regarding the fit between EMDB map EMD-60809 and PDB model 9IRC. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



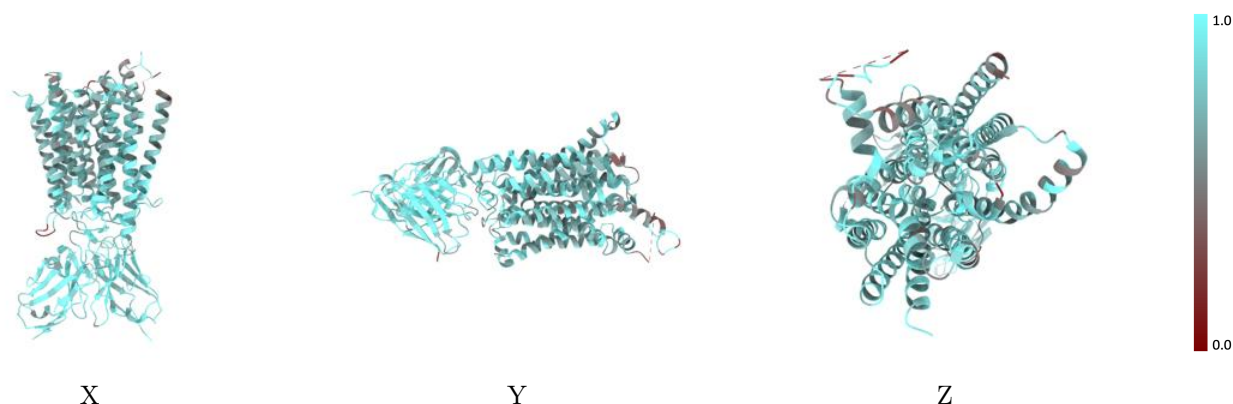
The images above show the 3D surface view of the map at the recommended contour level 0.471 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



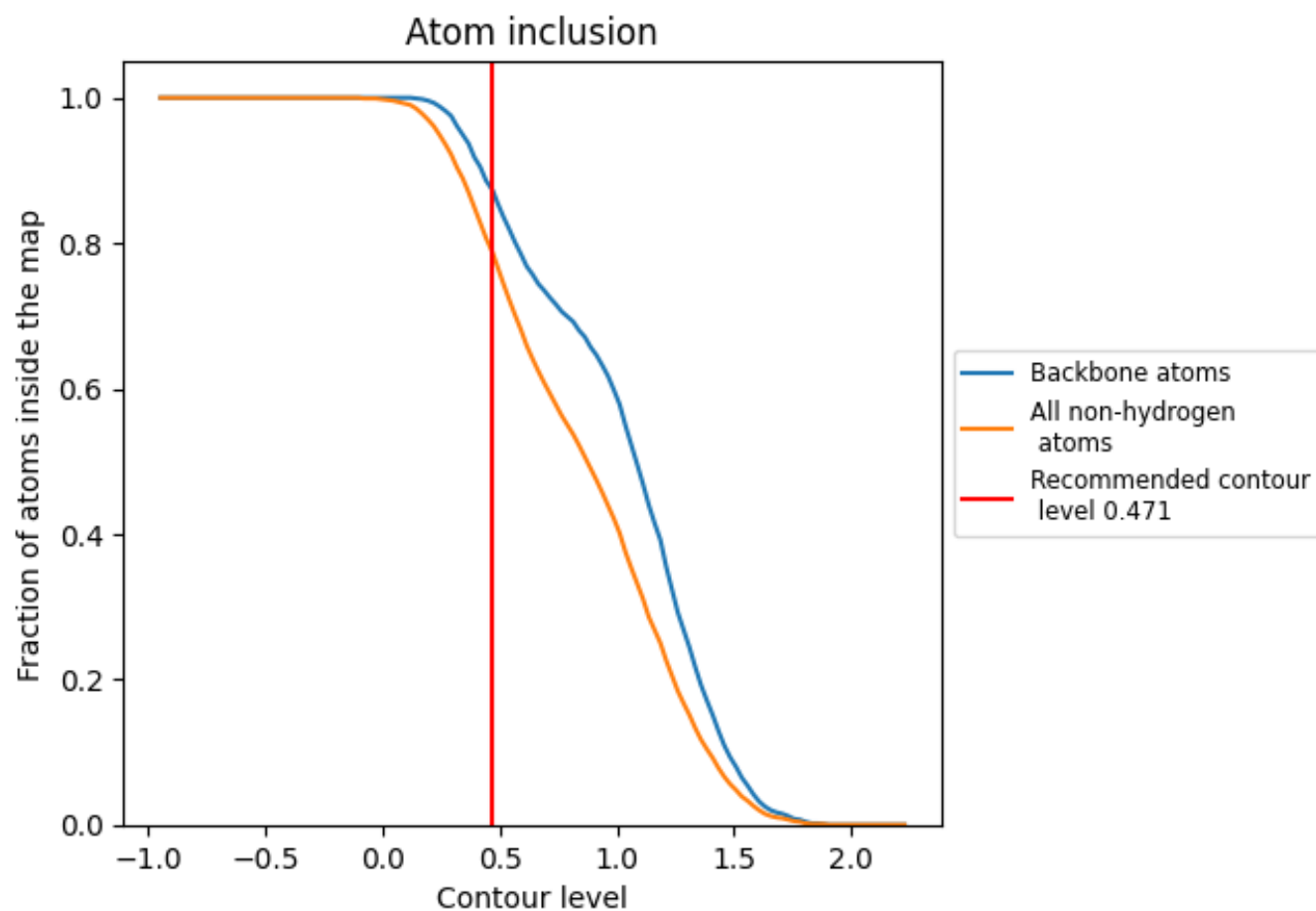
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.471).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 79% 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 (0.471) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7860	<div></div> 0.5350
A	<div></div> 0.7540	<div></div> 0.5260
B	<div></div> 0.6750	<div></div> 0.4730
H	<div></div> 0.8560	<div></div> 0.5560
L	<div></div> 0.8730	<div></div> 0.5680

