Full wwPDB EM Validation Report ⓘ

Sep 24, 2026 – 10:19 AM JST

PDB ID	:	9LLZ / pdb_00009llz
EMDB ID	:	EMD-63210
Title	:	Cryo-EM structure of a class C GPCR (Global, without symmetry)
Authors	:	Lee, S.Y.; Yun, Y.; Ji, J.S.; Jeong, H.; Lee, H.H.
Deposited on	:	2025-01-18
Resolution	:	3.20 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:

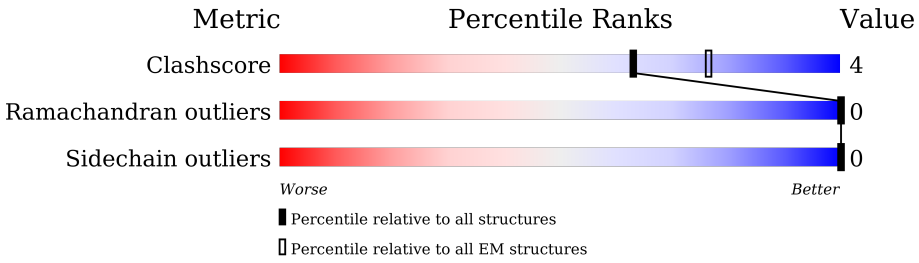
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using 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)	:	2.50

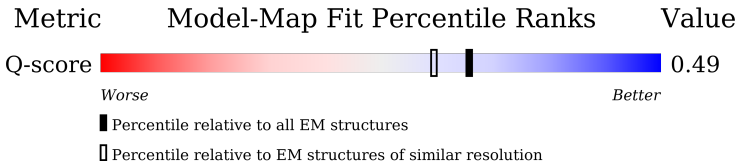
1 Overall quality at a glance

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

The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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 <=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	877	7% 79% 10% 11%
1	B	877	7% 79% 10% 11%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 11980 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 Metabotropic glutamate receptor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	779	Total	C	N	O	S	0	0
			5977	3802	1029	1108	38		
1	A	779	Total	C	N	O	S	0	0
			5981	3809	1029	1105	38		

There are 48 discrepancies between the modelled and reference sequences:

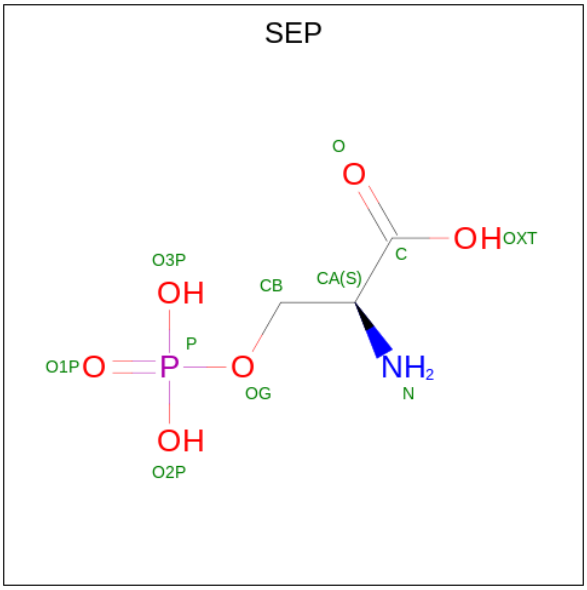
Chain	Residue	Modelled	Actual	Comment	Reference
B	878	PHE	-	expression tag	UNP O15303
B	879	GLU	-	expression tag	UNP O15303
B	880	SER	-	expression tag	UNP O15303
B	881	ARG	-	expression tag	UNP O15303
B	882	ALA	-	expression tag	UNP O15303
B	883	SER	-	expression tag	UNP O15303
B	884	THR	-	expression tag	UNP O15303
B	885	VAL	-	expression tag	UNP O15303
B	886	PRO	-	expression tag	UNP O15303
B	887	ARG	-	expression tag	UNP O15303
B	888	ALA	-	expression tag	UNP O15303
B	889	ARG	-	expression tag	UNP O15303
B	890	ASP	-	expression tag	UNP O15303
B	891	PRO	-	expression tag	UNP O15303
B	892	PRO	-	expression tag	UNP O15303
B	893	VAL	-	expression tag	UNP O15303
B	894	ALA	-	expression tag	UNP O15303
B	895	THR	-	expression tag	UNP O15303
B	896	LEU	-	expression tag	UNP O15303
B	897	GLU	-	expression tag	UNP O15303
B	898	VAL	-	expression tag	UNP O15303
B	899	LEU	-	expression tag	UNP O15303
B	900	PHE	-	expression tag	UNP O15303
B	901	GLN	-	expression tag	UNP O15303
A	878	PHE	-	expression tag	UNP O15303
A	879	GLU	-	expression tag	UNP O15303

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Chain	Residue	Modelled	Actual	Comment	Reference
A	880	SER	-	expression tag	UNP O15303
A	881	ARG	-	expression tag	UNP O15303
A	882	ALA	-	expression tag	UNP O15303
A	883	SER	-	expression tag	UNP O15303
A	884	THR	-	expression tag	UNP O15303
A	885	VAL	-	expression tag	UNP O15303
A	886	PRO	-	expression tag	UNP O15303
A	887	ARG	-	expression tag	UNP O15303
A	888	ALA	-	expression tag	UNP O15303
A	889	ARG	-	expression tag	UNP O15303
A	890	ASP	-	expression tag	UNP O15303
A	891	PRO	-	expression tag	UNP O15303
A	892	PRO	-	expression tag	UNP O15303
A	893	VAL	-	expression tag	UNP O15303
A	894	ALA	-	expression tag	UNP O15303
A	895	THR	-	expression tag	UNP O15303
A	896	LEU	-	expression tag	UNP O15303
A	897	GLU	-	expression tag	UNP O15303
A	898	VAL	-	expression tag	UNP O15303
A	899	LEU	-	expression tag	UNP O15303
A	900	PHE	-	expression tag	UNP O15303
A	901	GLN	-	expression tag	UNP O15303

- Molecule 2 is PHOSPHOSERINE (CCD ID: SEP) (formula: $C_3H_8NO_6P$) (labeled as "Ligand of Interest" by depositor).



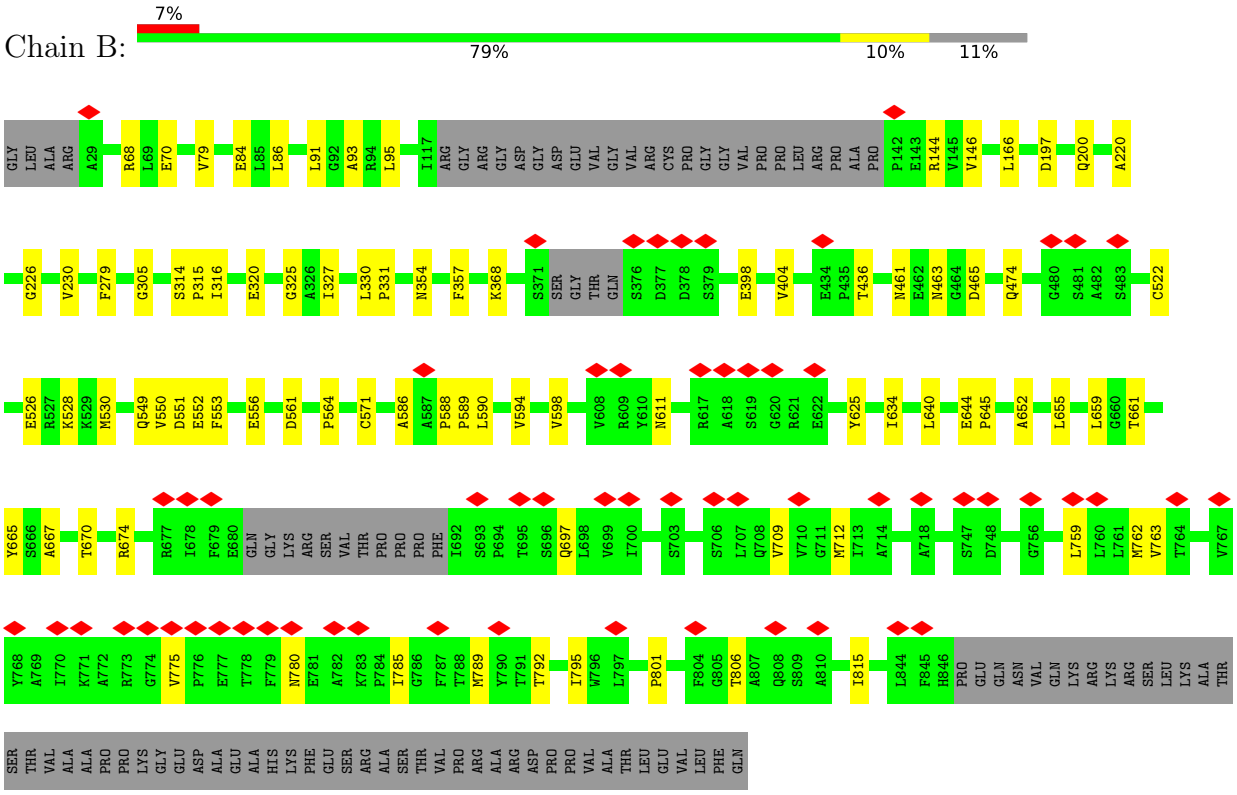
Mol	Chain	Residues	Atoms					AltConf
2	B	1	Total	C	N	O	P	0
			11	3	1	6	1	
2	A	1	Total	C	N	O	P	0
			11	3	1	6	1	

3 Residue-property plots (i)

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

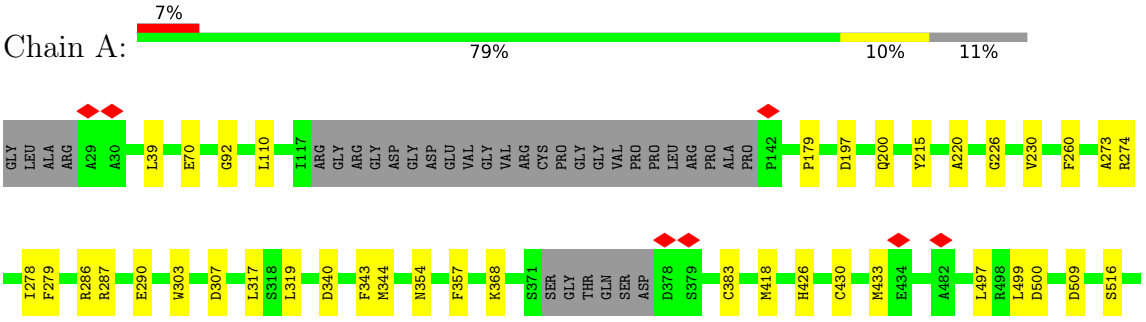
• Molecule 1: Metabotropic glutamate receptor 6

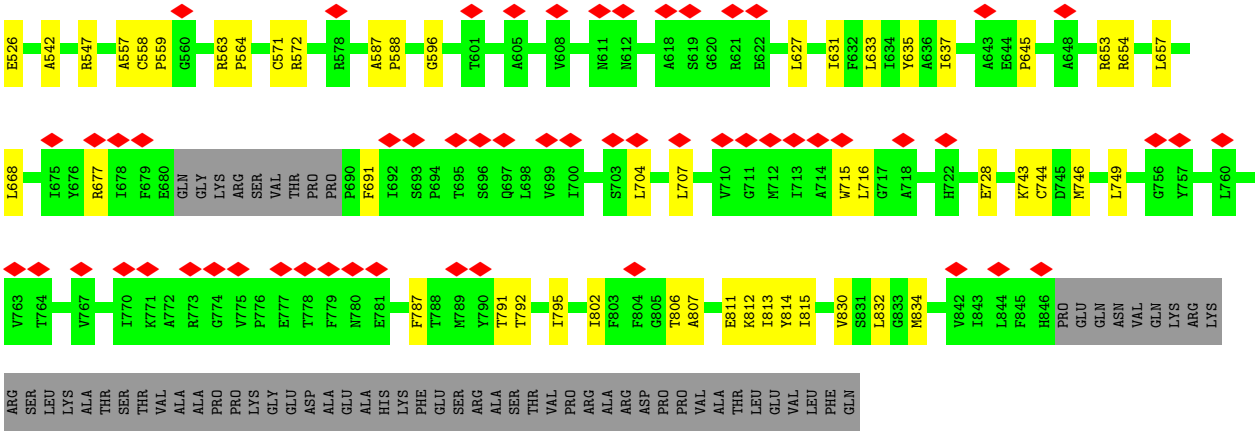
Chain B:



• Molecule 1: Metabotropic glutamate receptor 6

Chain A:




E526 A542 R547 A557 C558 P559 G560 R563 P564 C571 R572 R578 A587 P588 G596 T601 A605 V608 N611 N612 A618 S619 G620 R621 E622 L627 I631 F632 L633 I634 Y635 A636 I637 A643 E644 P645 A648 R653 R654 L657
L668 I675 Y676 R677 I678 F679 E680 GLN GLY LYS ARG SER VAL THR PRO PRO P690 F691 I692 S693 P694 T695 S696 Q697 L698 V699 I700 S703 L704 L707 V710 G711 M712 I713 A714 W715 L716 G717 A718 H722 E728 K743 C744 D745 M746 L749 G756 Y757 L760
V763 T764 V767 I770 K771 A772 R773 G774 V775 P776 E777 T778 F779 N780 E781 F787 T788 M789 Y790 T791 T792 I795 I802 P803 F804 G805 T806 A807 E811 K812 I813 Y814 I815 V830 S831 L832 G833 M834 V842 I843 L844 P845 H846 PRO GLU GLN ASN VAL GLN LYS ARG LYS
ARG SER LEU LYS ALA THR SER THR VAL ALA ALA ALA PRO PRO LYS GLY GLU ASP ALA GLU ALA HIS LYS PHE GLU SER ARG ALA ALA SER THR VAL PRO ARG ALA ALA ARG ASP PRO PRO VAL ALA THR LEU GLU VAL LEU PHE GLN

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	244484	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	67.8	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	3.201	Depositor
Minimum map value	-1.989	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.043	Depositor
Recommended contour level	0.23	Depositor
Map size (Å)	366.336, 366.336, 366.336	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.848, 0.848, 0.848	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.10	0/6116	0.27	0/8319
1	B	0.11	0/6110	0.28	0/8311
All	All	0.10	0/12226	0.27	0/16630

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	A	5981	0	5948	52	0
1	B	5977	0	5942	51	0
2	A	11	0	5	0	0
2	B	11	0	5	0	0
All	All	11980	0	11900	101	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 4.

All (101) 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:654:ARG:HH22	1:A:715:TRP:CD1	2.08	0.71
1:A:627:LEU:HD11	1:A:668:LEU:HG	1.74	0.69
1:A:811:GLU:HB2	1:A:814:TYR:HB2	1.76	0.66
1:A:746:MET:HE3	1:A:749:LEU:H	1.59	0.66
1:A:274:ARG:NH2	1:A:509:ASP:OD1	2.23	0.65
1:A:728:GLU:N	1:A:728:GLU:OE2	2.29	0.65
1:B:775:VAL:HG11	1:B:780:ASN:HD21	1.63	0.64
1:B:806:THR:HG21	1:B:815:ILE:HG21	1.81	0.63
1:A:220:ALA:HB2	1:A:230:VAL:HG21	1.81	0.62
1:B:68:ARG:NH2	1:B:398:GLU:OE2	2.32	0.61
1:B:785:ILE:HG23	1:B:789:MET:HE2	1.81	0.61
1:B:84:GLU:N	1:B:84:GLU:OE2	2.34	0.61
1:A:564:PRO:HA	1:A:571:CYS:HA	1.83	0.59
1:A:637:ILE:HG21	1:A:657:LEU:HD23	1.84	0.59
1:A:563:ARG:O	1:A:572:ARG:N	2.34	0.58
1:A:286:ARG:HH21	1:A:317:LEU:HB3	1.68	0.58
1:B:220:ALA:HB2	1:B:230:VAL:HG21	1.86	0.57
1:B:665:TYR:HB3	1:B:762:MET:HE3	1.87	0.57
1:B:68:ARG:HB2	1:B:404:VAL:HG21	1.88	0.55
1:B:526:GLU:O	1:B:549:GLN:NE2	2.40	0.55
1:B:461:ASN:ND2	1:B:465:ASP:OD2	2.38	0.54
1:B:588:PRO:HG2	1:B:589:PRO:HD3	1.89	0.54
1:A:215:TYR:O	1:A:516:SER:OG	2.25	0.54
1:B:70:GLU:OE2	1:B:354:ASN:ND2	2.41	0.53
1:A:497:LEU:HG	1:A:499:LEU:H	1.75	0.52
1:A:631:ILE:HG21	1:A:832:LEU:HD12	1.93	0.51
1:A:633:LEU:O	1:A:637:ILE:HG13	2.10	0.50
1:B:785:ILE:O	1:B:789:MET:HG2	2.11	0.50
1:A:787:PHE:HB2	1:A:834:MET:HE1	1.93	0.50
1:A:226:GLY:HA2	1:A:279:PHE:HB3	1.94	0.49
1:B:226:GLY:HA2	1:B:279:PHE:HB3	1.94	0.49
1:B:674:ARG:HE	1:B:697:GLN:HE22	1.60	0.49
1:A:354:ASN:HB3	1:A:357:PHE:HB2	1.94	0.49
1:A:791:THR:HG21	1:A:830:VAL:HG21	1.93	0.49
1:A:807:ALA:HA	1:A:812:LYS:HE2	1.94	0.49
1:B:586:ALA:O	1:B:590:LEU:HD23	2.13	0.49
1:A:653:ARG:NH2	1:A:744:CYS:SG	2.70	0.49
1:B:314:SER:HB2	1:B:315:PRO:HD3	1.95	0.49
1:B:655:LEU:O	1:B:659:LEU:HD23	2.13	0.49
1:B:550:VAL:HB	1:B:556:GLU:HG2	1.94	0.48
1:A:806:THR:HG21	1:A:815:ILE:HG21	1.95	0.48
1:A:70:GLU:HG3	1:A:343:PHE:HE1	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:PHE:CE2	1:A:287:ARG:HD2	2.49	0.47
1:B:146:VAL:HG12	1:B:436:THR:HG21	1.97	0.47
1:B:634:ILE:HD11	1:B:661:THR:HA	1.96	0.47
1:B:330:LEU:HD12	1:B:331:PRO:HD2	1.97	0.47
1:A:368:LYS:H	1:A:383:CYS:HB2	1.79	0.47
1:A:677:ARG:HH21	1:A:691:PHE:HB2	1.80	0.47
1:B:461:ASN:OD1	1:B:463:ASN:N	2.46	0.47
1:B:801:PRO:HG2	1:A:802:ILE:HG12	1.97	0.47
1:A:631:ILE:HD13	1:A:832:LEU:HB2	1.96	0.46
1:B:325:GLY:HA2	1:B:474:GLN:HE21	1.81	0.46
1:B:659:LEU:HD21	1:B:709:VAL:HG22	1.98	0.46
1:B:368:LYS:HA	1:B:368:LYS:HD2	1.65	0.45
1:A:558:CYS:SG	1:A:559:PRO:HD2	2.56	0.45
1:B:79:VAL:HG11	1:B:91:LEU:HD12	1.98	0.45
1:B:551:ASP:OD1	1:B:552:GLU:N	2.43	0.45
1:A:500:ASP:OD1	1:A:500:ASP:N	2.47	0.45
1:A:426:HIS:CD2	1:A:430:CYS:HB3	2.52	0.44
1:B:530:MET:HE3	1:B:553:PHE:HE1	1.83	0.44
1:B:354:ASN:HB3	1:B:357:PHE:HB2	2.00	0.43
1:A:286:ARG:NH2	1:A:317:LEU:O	2.51	0.43
1:B:792:THR:HA	1:B:795:ILE:HG12	1.98	0.43
1:A:39:LEU:O	1:A:92:GLY:N	2.30	0.43
1:B:655:LEU:HA	1:B:712:MET:CE	2.49	0.43
1:A:654:ARG:HD3	1:A:716:LEU:HD13	2.01	0.43
1:B:166:LEU:HD13	1:A:110:LEU:HD22	1.99	0.42
1:A:704:LEU:HD13	1:A:707:LEU:HD21	2.01	0.42
1:A:526:GLU:HG2	1:A:542:ALA:HA	2.00	0.42
1:A:215:TYR:CD2	1:A:273:ALA:HB2	2.54	0.42
1:B:611:ASN:OD1	1:B:625:TYR:OH	2.33	0.42
1:B:655:LEU:HA	1:B:712:MET:HE3	2.02	0.42
1:A:278:ILE:HD11	1:A:303:TRP:CE3	2.55	0.42
1:A:340:ASP:HB3	1:A:344:MET:HE2	2.01	0.42
1:A:179:PRO:HD3	1:A:197:ASP:HB2	2.00	0.42
1:A:813:ILE:HG23	1:A:814:TYR:HD1	1.85	0.42
1:A:290:GLU:HG3	1:A:319:LEU:HD11	2.02	0.42
1:B:86:LEU:HD23	1:B:86:LEU:HA	1.89	0.42
1:B:667:ALA:O	1:B:670:THR:HG22	2.20	0.41
1:A:418:MET:HG2	1:A:433:MET:HE2	2.02	0.41
1:B:640:LEU:HD21	1:B:652:ALA:C	2.45	0.41
1:B:197:ASP:OD1	1:B:200:GLN:NE2	2.54	0.41
1:B:93:ALA:HB1	1:B:95:LEU:HD13	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:561:ASP:OD1	1:B:561:ASP:N	2.51	0.41
1:A:200:GLN:HE22	1:A:307:ASP:HB3	1.85	0.41
1:A:792:THR:HA	1:A:795:ILE:HG22	2.02	0.41
1:B:305:GLY:N	1:B:327:ILE:O	2.48	0.41
1:B:759:LEU:O	1:B:763:VAL:HG23	2.20	0.41
1:B:644:GLU:HA	1:B:645:PRO:HD3	1.96	0.41
1:A:286:ARG:NH2	1:A:317:LEU:HB3	2.34	0.41
1:B:316:ILE:HG22	1:B:320:GLU:HG3	2.02	0.41
1:B:522:CYS:SG	1:B:528:LYS:HG2	2.61	0.40
1:A:547:ARG:HA	1:A:557:ALA:HA	2.03	0.40
1:A:596:GLY:HA3	1:A:635:TYR:CE1	2.56	0.40
1:B:564:PRO:HA	1:B:571:CYS:HA	2.03	0.40
1:A:587:ALA:HB3	1:A:588:PRO:HD3	2.03	0.40
1:B:144:ARG:HE	1:B:144:ARG:HB2	1.67	0.40
1:B:588:PRO:CG	1:B:589:PRO:HD3	2.50	0.40
1:B:594:VAL:O	1:B:598:VAL:HG13	2.22	0.40
1:A:317:LEU:HD12	1:A:317:LEU:HA	1.97	0.40
1:A:645:PRO:HG3	1:A:743:LYS:HA	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	771/877 (88%)	750 (97%)	21 (3%)	0	100	100
1	B	771/877 (88%)	742 (96%)	29 (4%)	0	100	100
All	All	1542/1754 (88%)	1492 (97%)	50 (3%)	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	641/719 (89%)	641 (100%)	0	100	100
1	B	641/719 (89%)	641 (100%)	0	100	100
All	All	1282/1438 (89%)	1282 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	B	114	GLN
1	B	426	HIS
1	B	474	GLN
1	A	64	GLN
1	A	200	GLN
1	A	300	HIS
1	A	413	HIS

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)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	SEP	B	1001	-	9,10,10	1.02	0	12,14,14	0.97	1 (8%)
2	SEP	A	1001	-	9,10,10	1.01	0	12,14,14	0.92	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SEP	B	1001	-	-	0/10/10/10	-
2	SEP	A	1001	-	-	0/10/10/10	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1001	SEP	OXT-C-CA	2.02	120.25	113.38

There are no chirality outliers.

There are no torsion outliers.

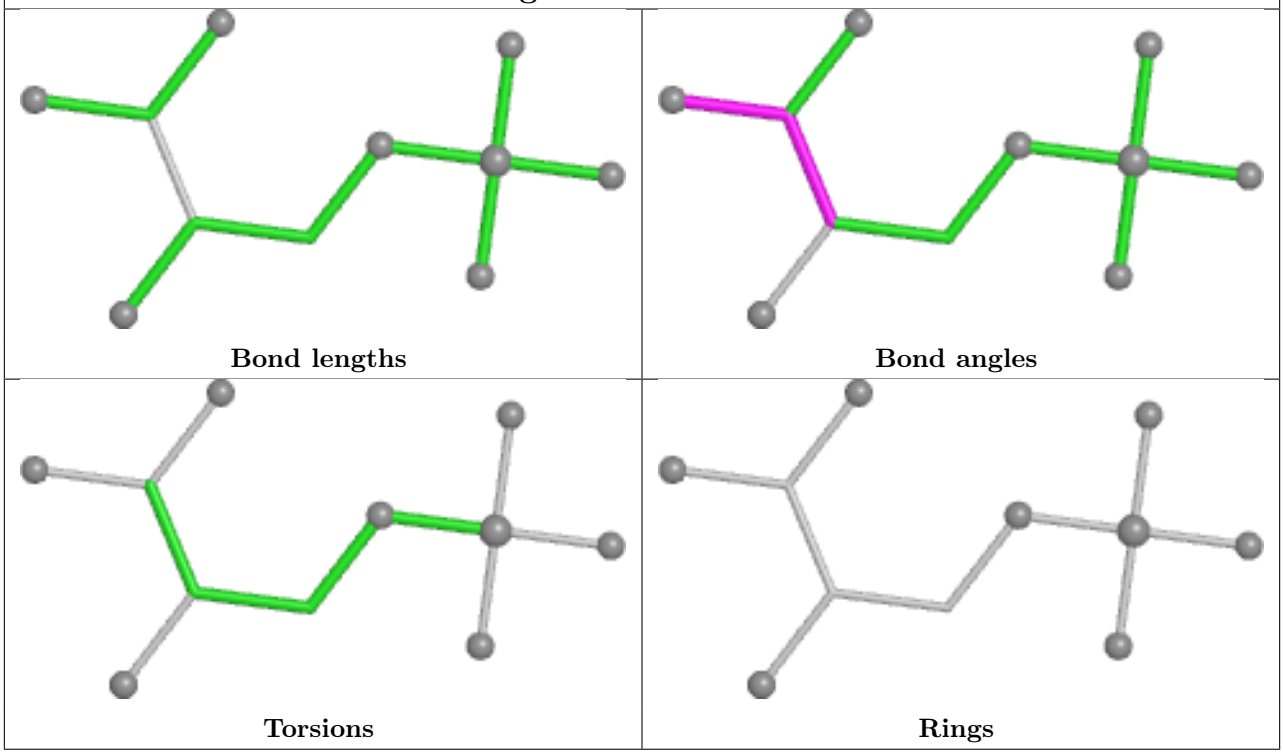
There are no ring outliers.

No monomer is involved in short contacts.

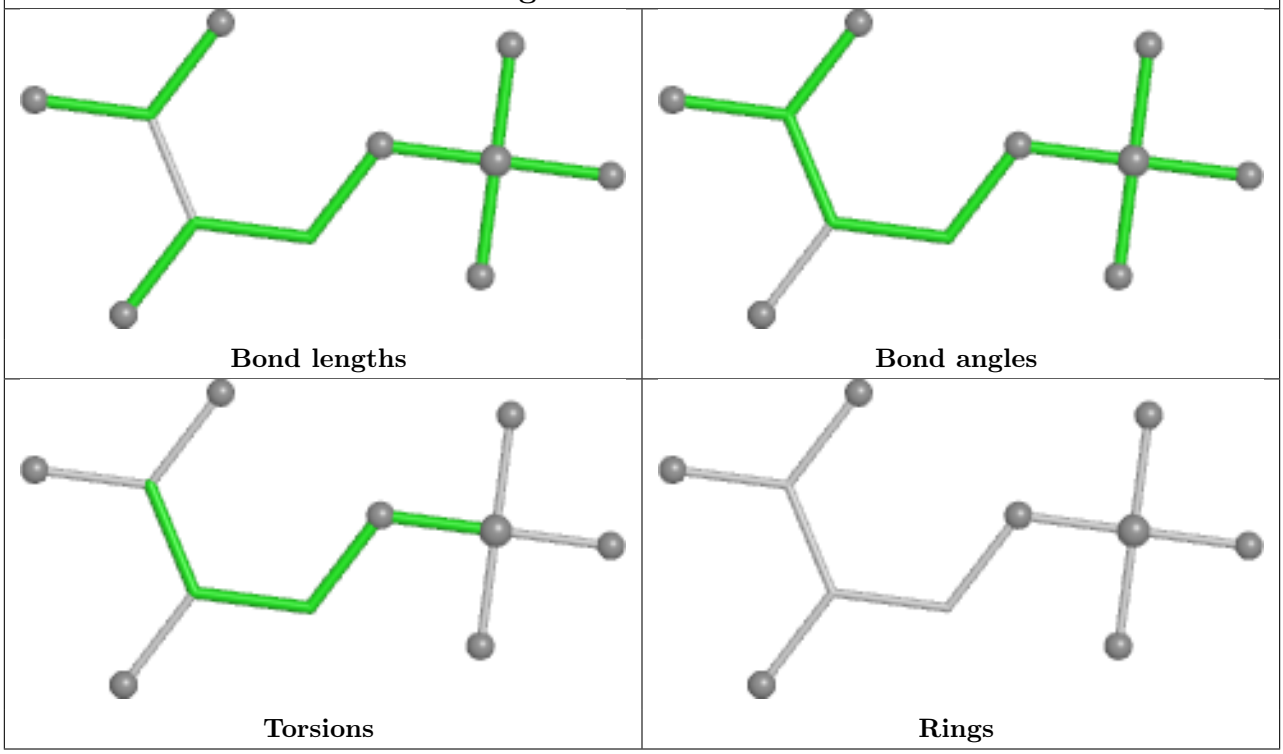
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring

in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand SEP B 1001



Ligand SEP A 1001



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.

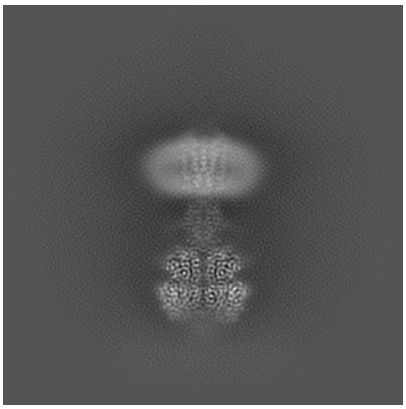
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-63210. These allow visual inspection of the internal detail of the map and identification of artifacts.

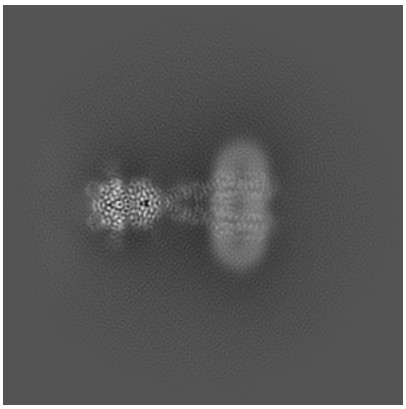
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

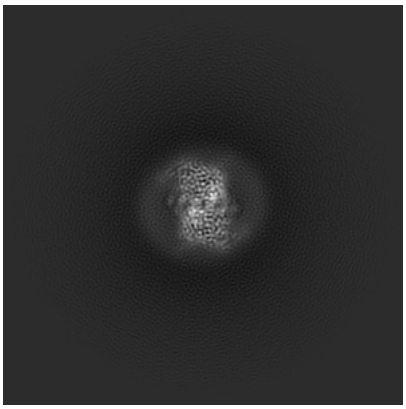
6.1.1 Primary map



X

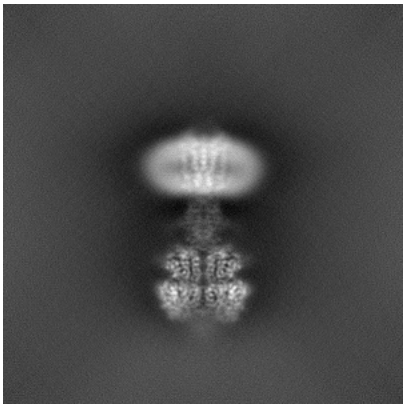


Y

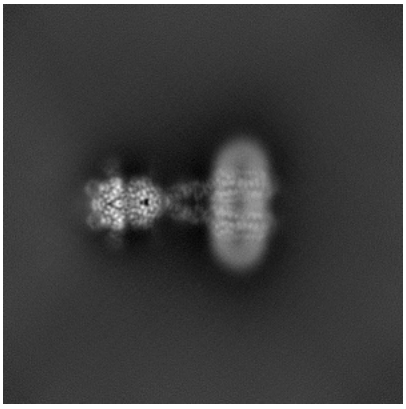


Z

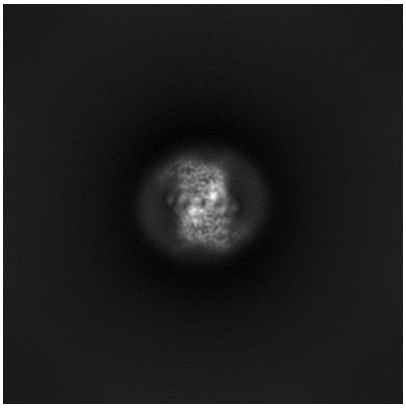
6.1.2 Raw map



X



Y

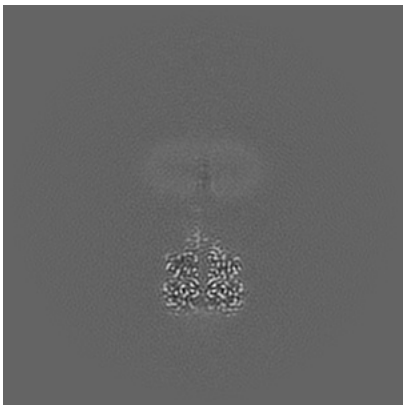


Z

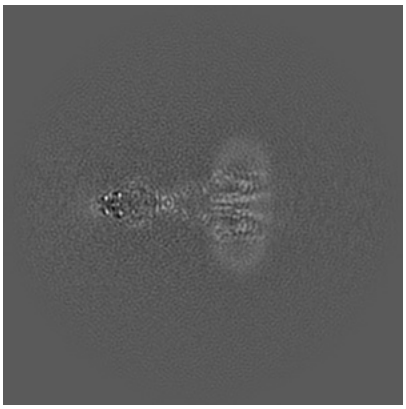
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

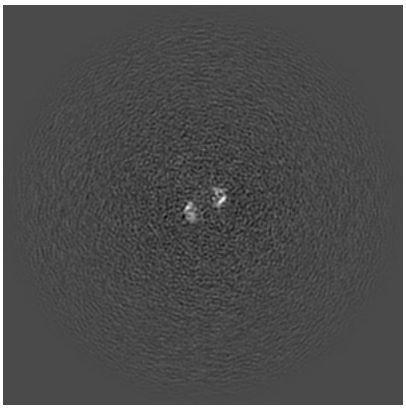
6.2.1 Primary map



X Index: 216

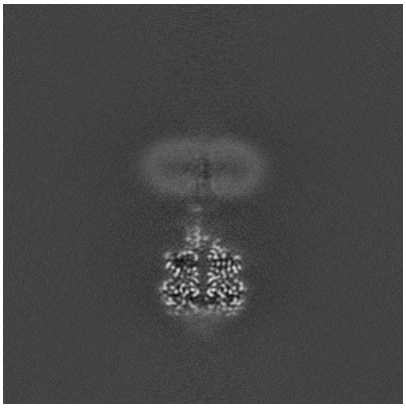


Y Index: 216

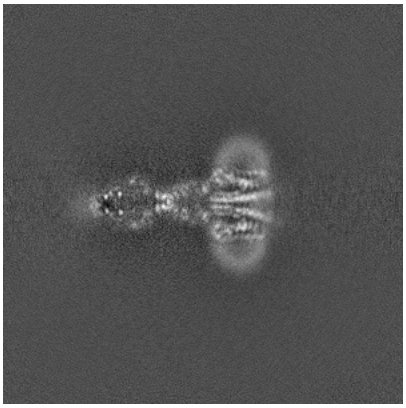


Z Index: 216

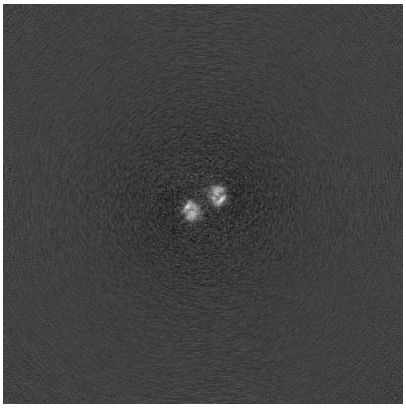
6.2.2 Raw map



X Index: 216



Y Index: 216

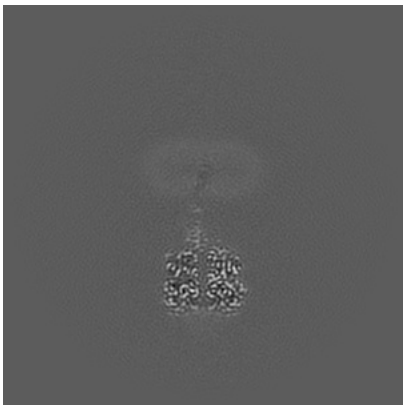


Z Index: 216

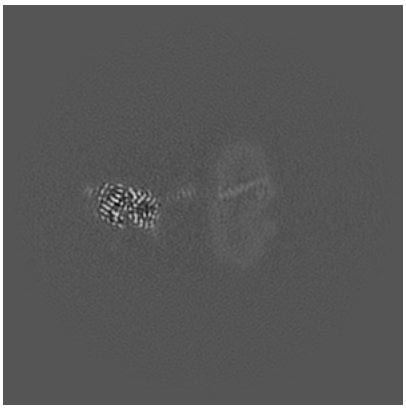
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

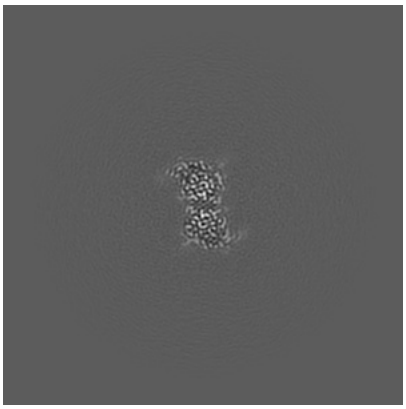
6.3.1 Primary map



X Index: 215

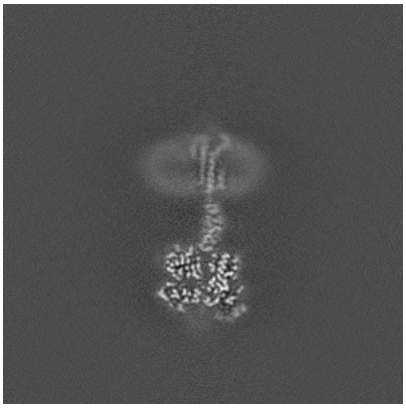


Y Index: 236

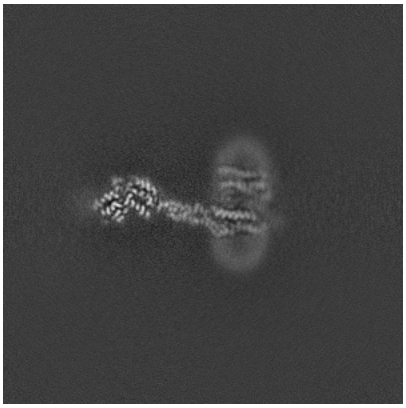


Z Index: 123

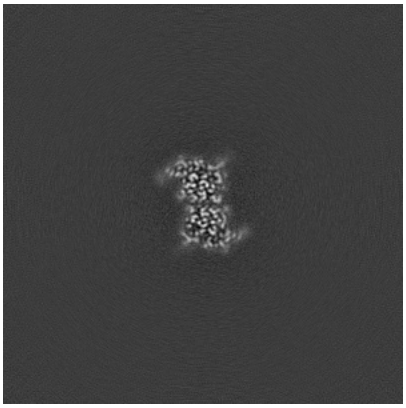
6.3.2 Raw map



X Index: 225



Y Index: 209

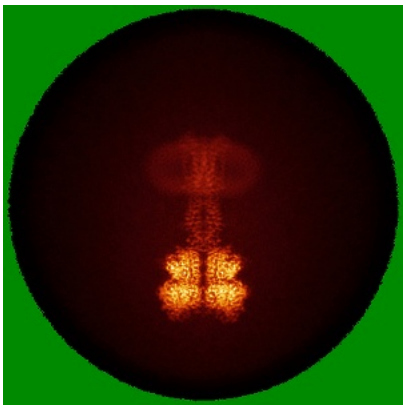


Z Index: 122

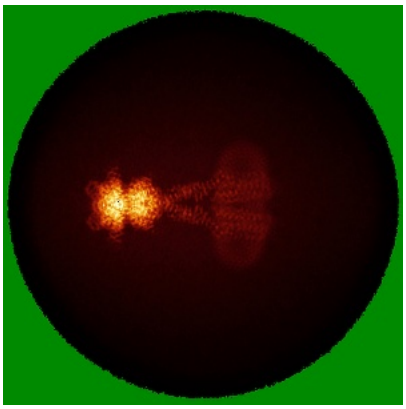
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

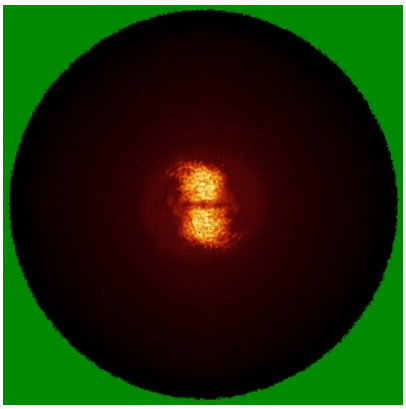
6.4.1 Primary map



X

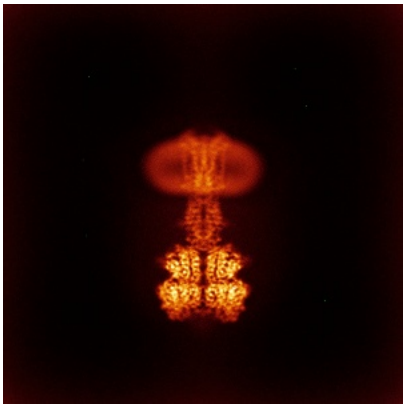


Y

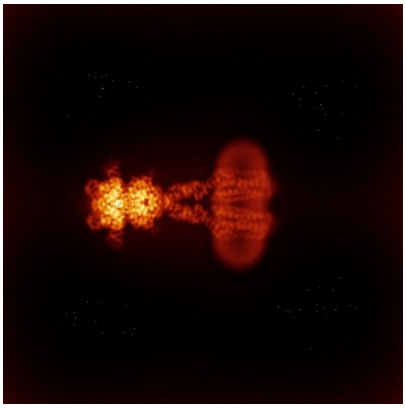


Z

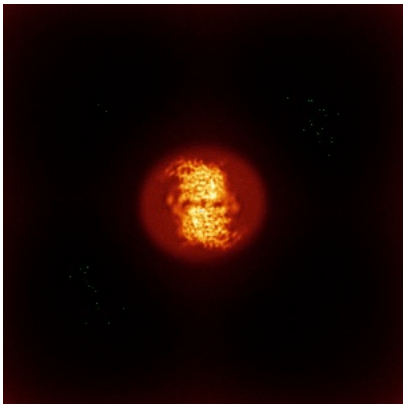
6.4.2 Raw map



X



Y

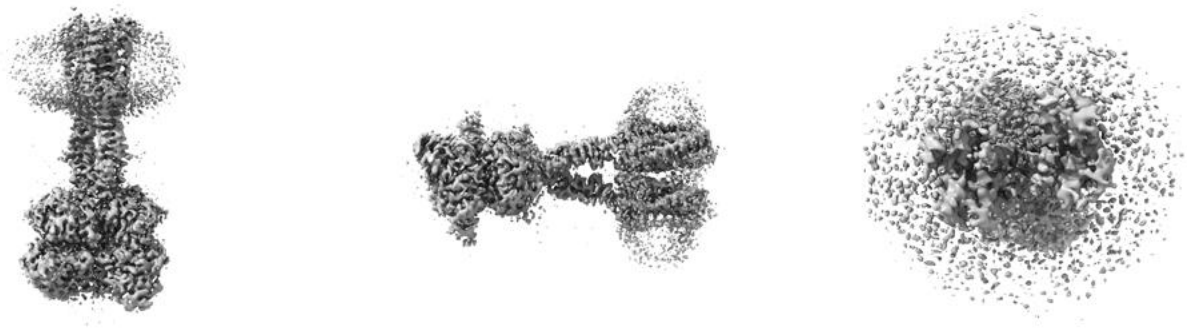


Z

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)

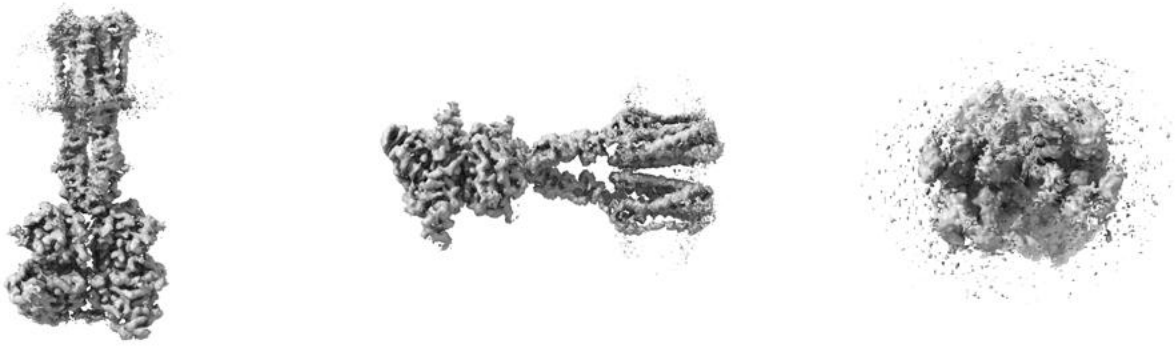
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.23. 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



X Y Z

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.

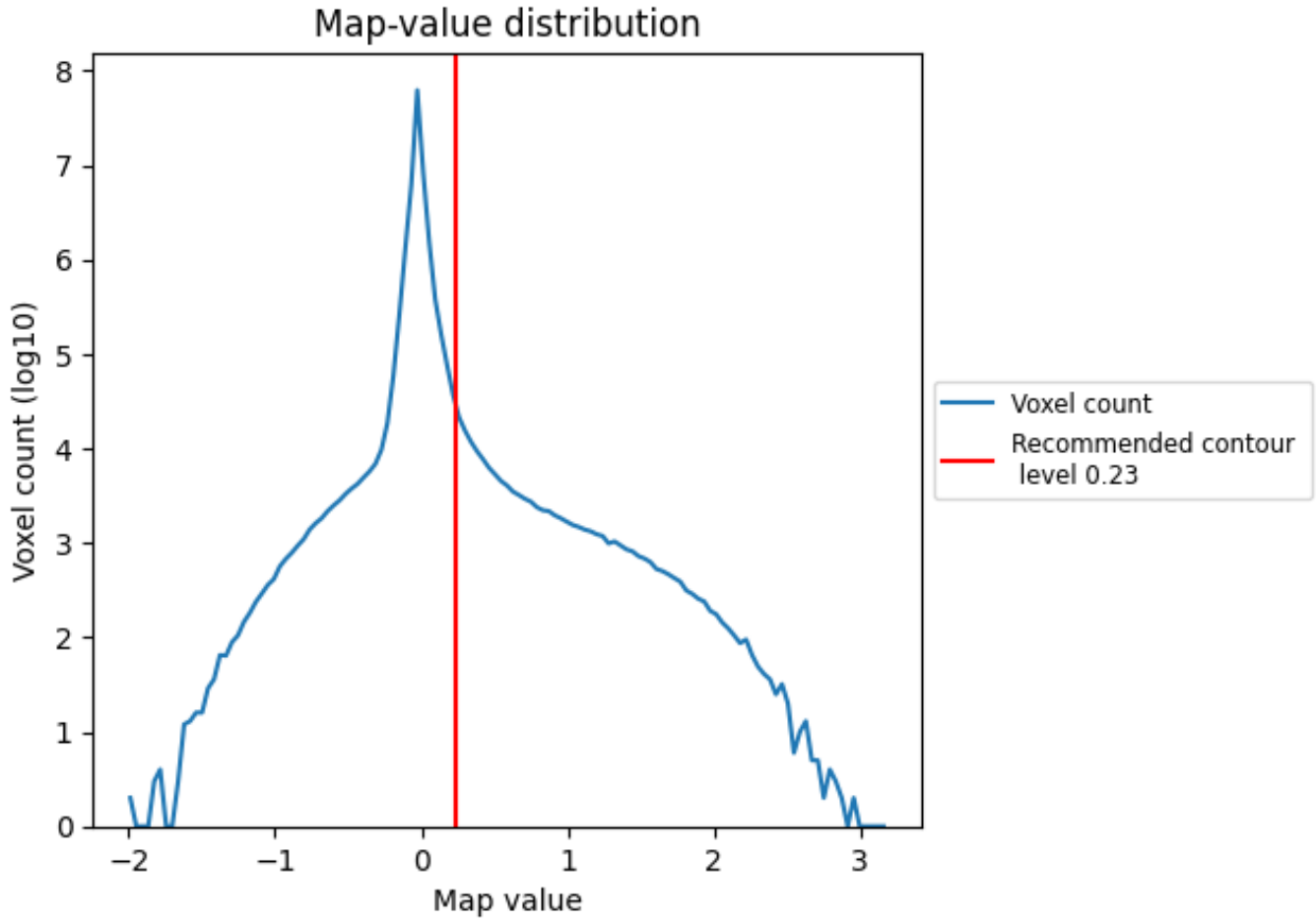
6.6 Mask visualisation (i)

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

7 Map analysis

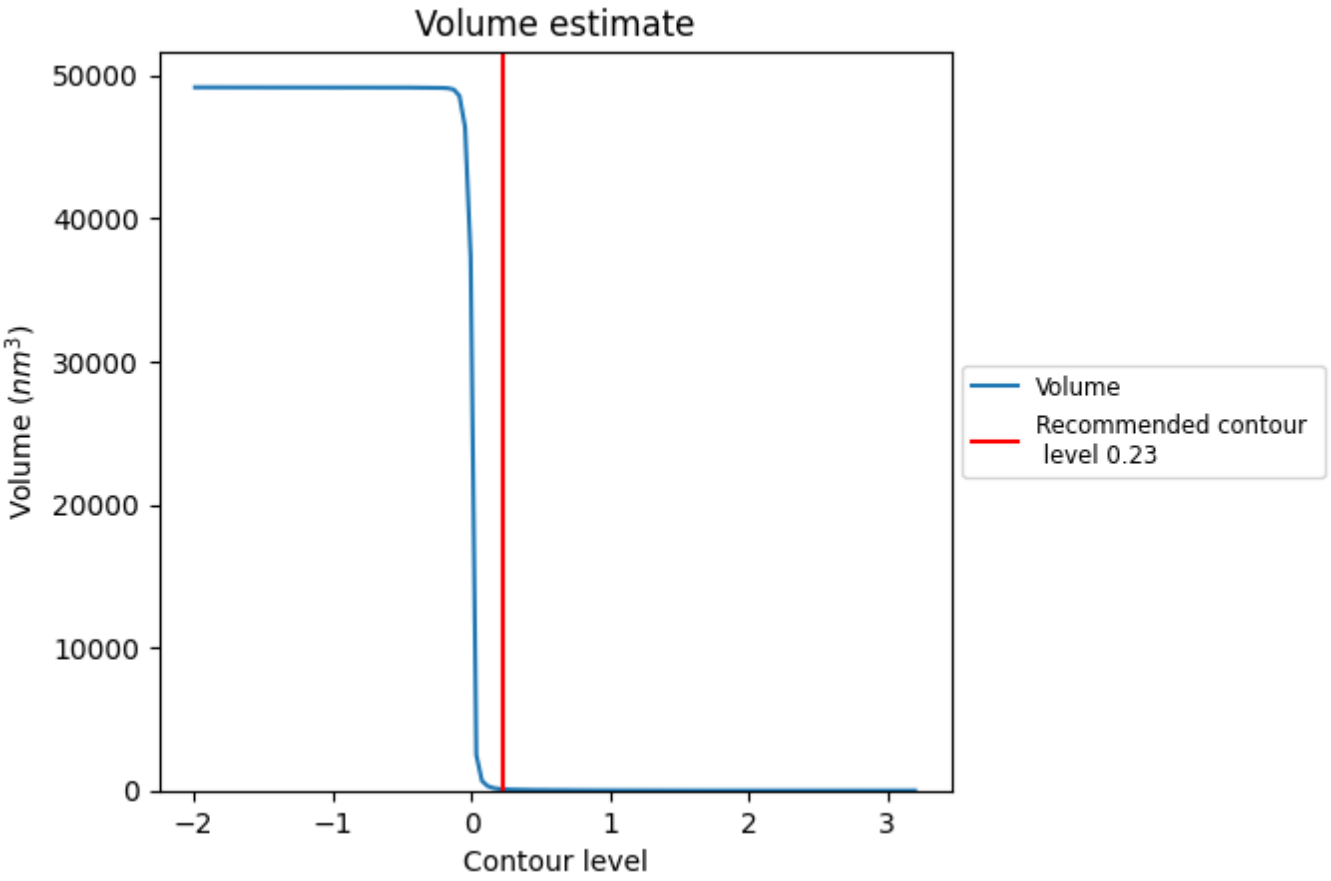
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

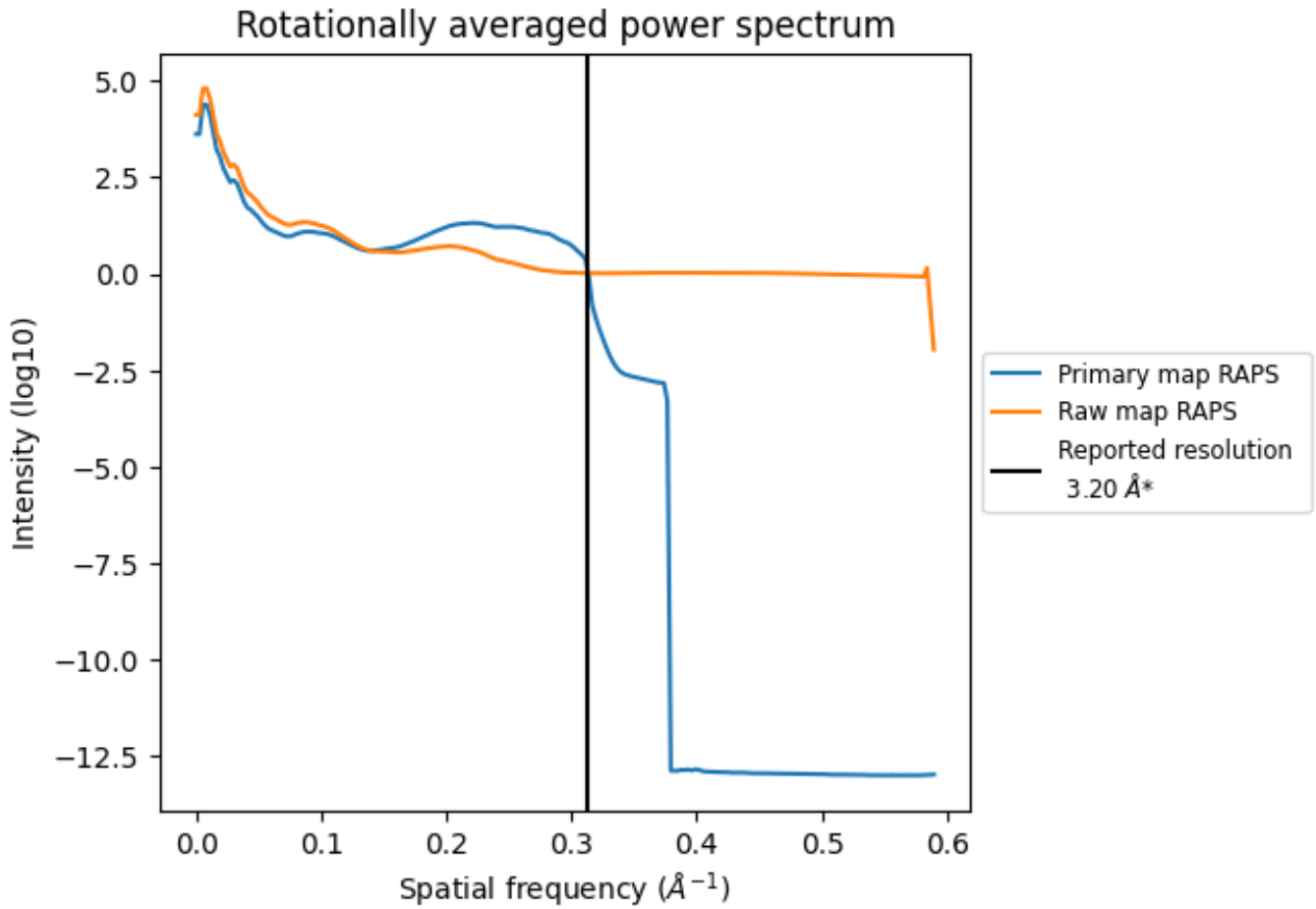
7.2 Volume estimate



The volume at the recommended contour level is 95 nm^3; this corresponds to an approximate mass of 86 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 (i)

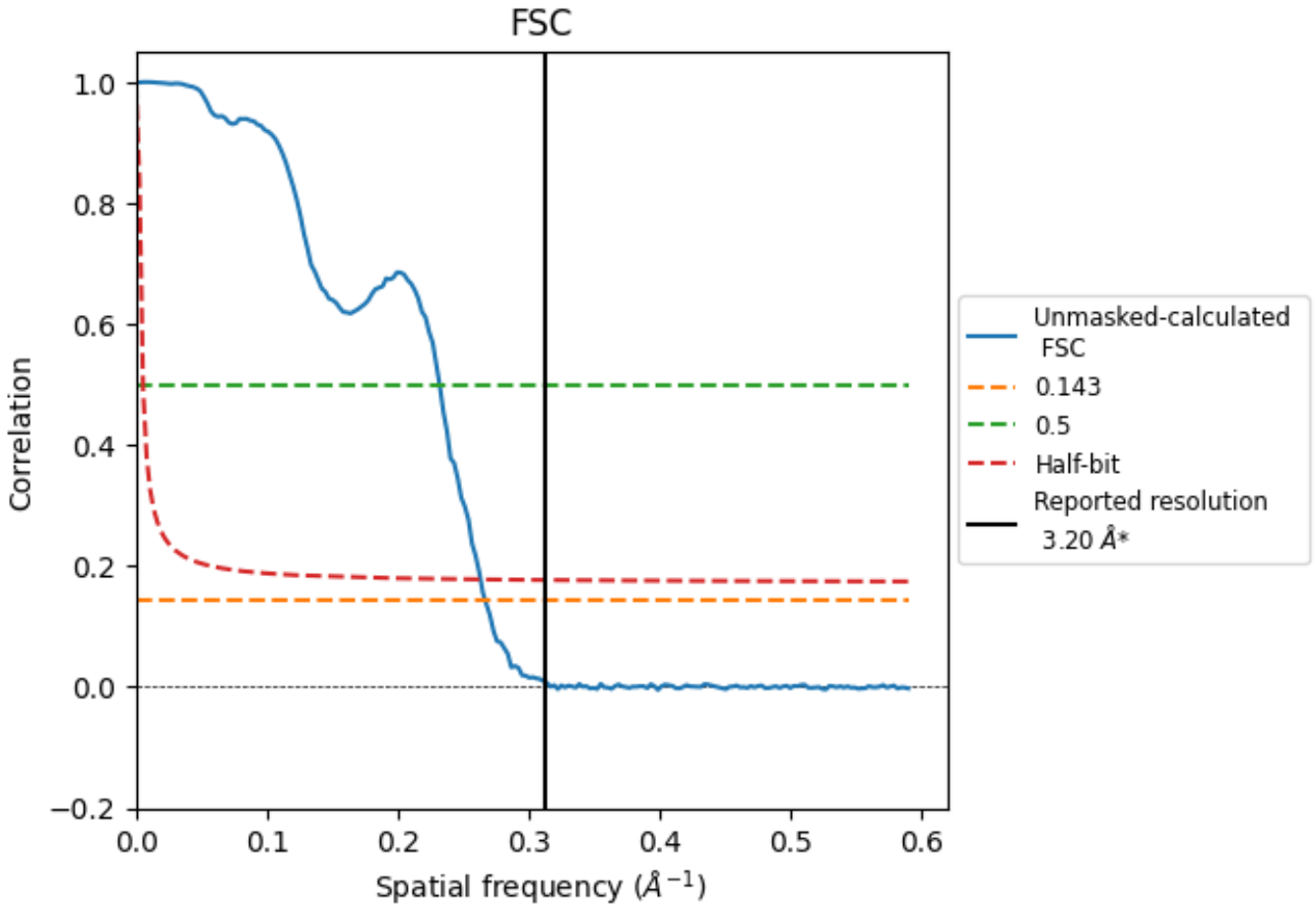


*Reported resolution corresponds to spatial frequency of 0.312 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.312 Å^{-1}

8.2 Resolution estimates (i)

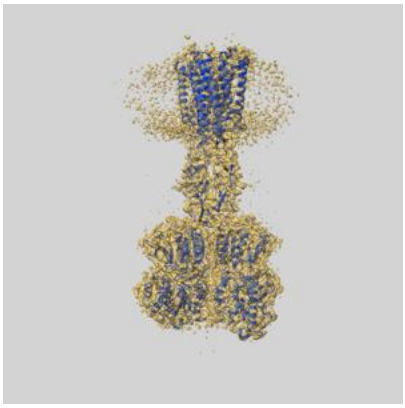
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.75	4.31	3.80

*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 3.75 differs from the reported value 3.2 by more than 10 %

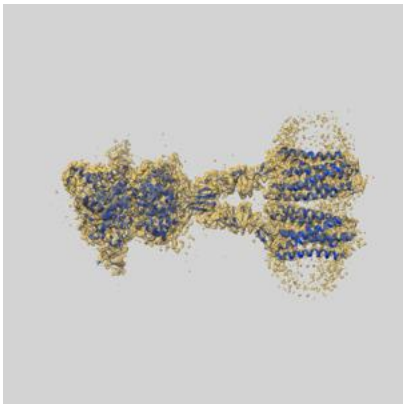
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-63210 and PDB model 9LLZ. Per-residue inclusion information can be found in section 3 on page 6.

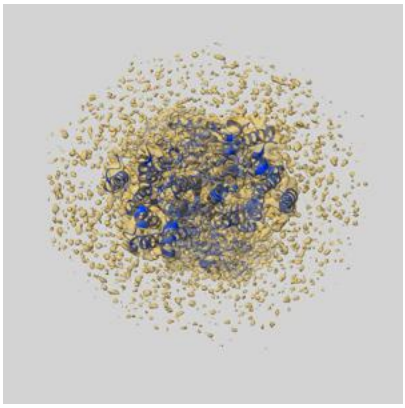
9.1 Map-model overlay



X



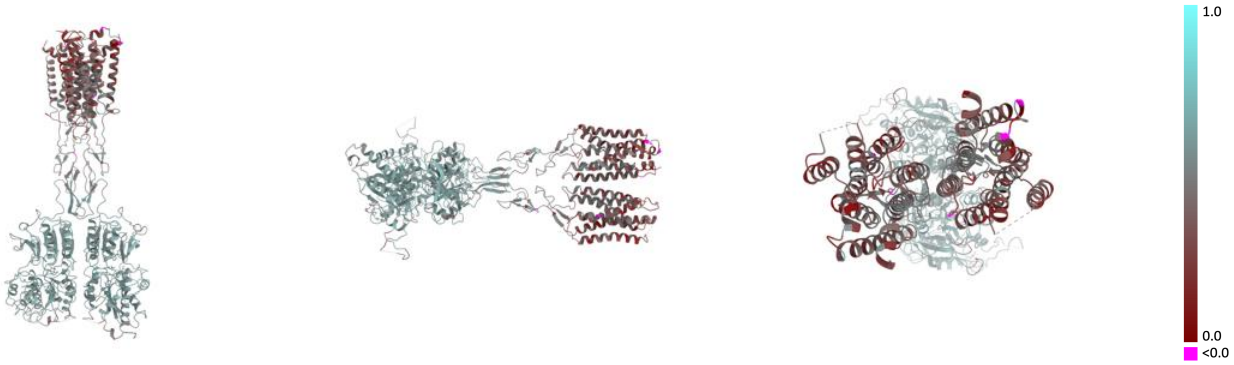
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.23 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.

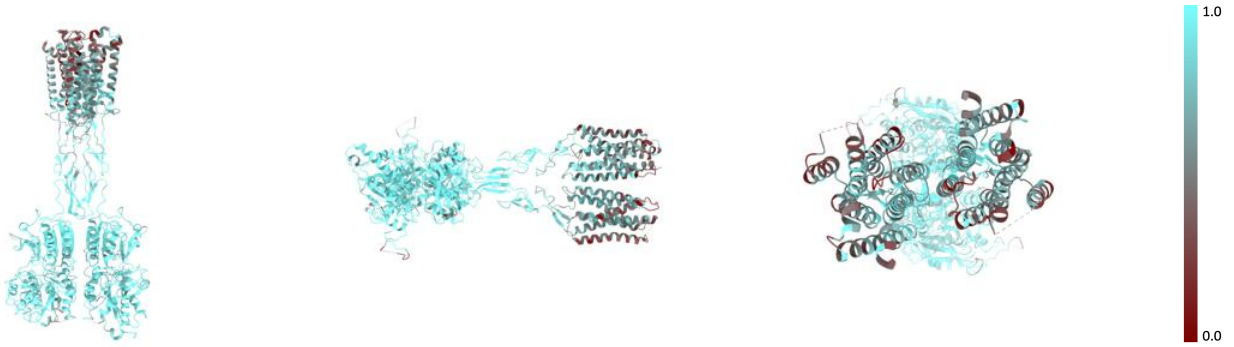
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

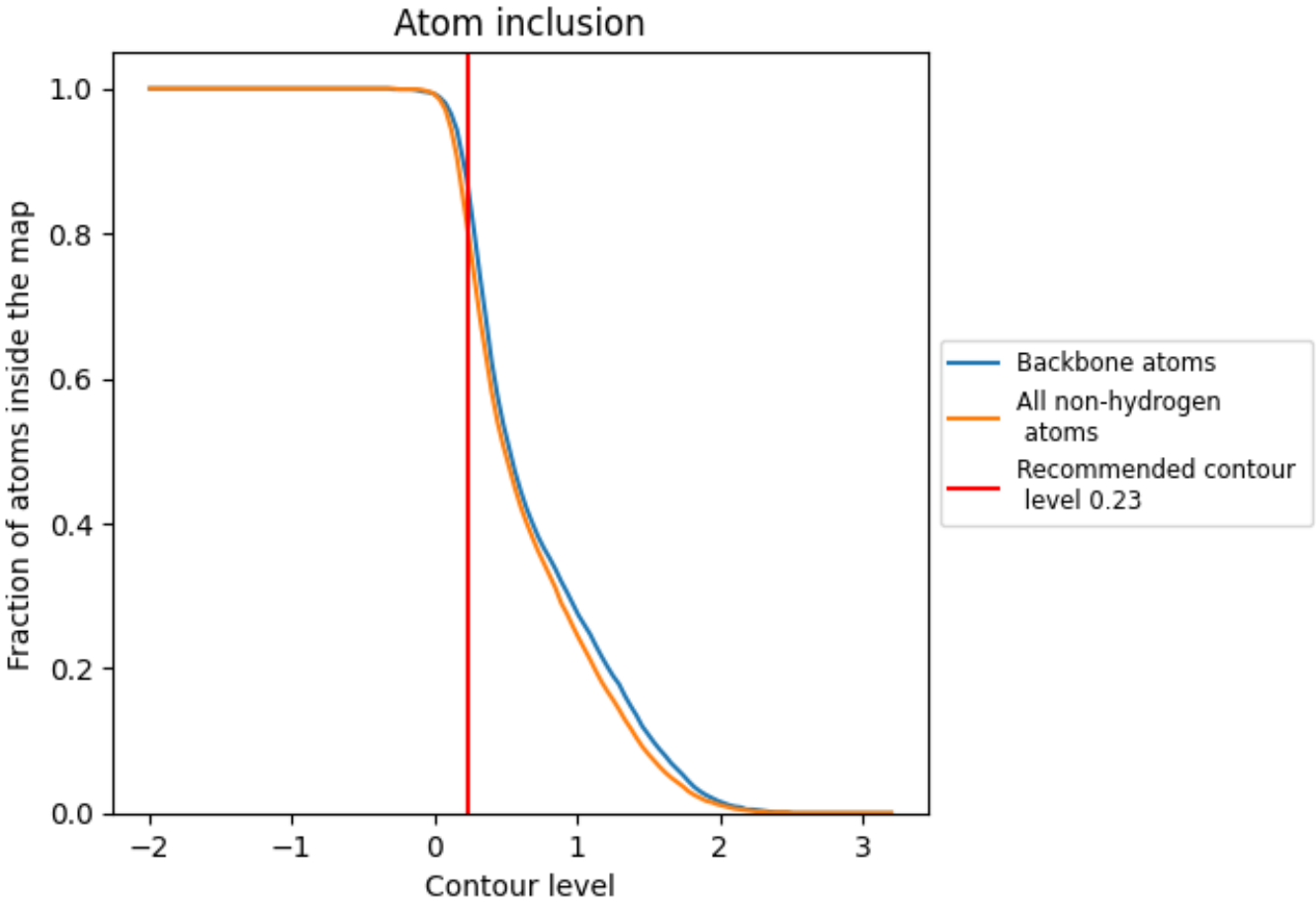
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.23).

9.4 Atom inclusion (i)



At the recommended contour level, 87% of all backbone atoms, 81% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.23) and Q-score for the entire model and for each chain.



Chain	Atom inclusion	Q-score
All	0.8130	0.4900
A	0.8120	0.4910
B	0.8140	0.4890