wwPDB EM Validation Summary Report (i)

Jan 13, 2024 – 12:44 PM EST

PDB ID	:	8U26
EMDB ID	:	EMD-41840
Title	:	Gaussian Mixture Models based single particle refinement - GPCR (Substance P bound to active human neurokinin 1 receptor in complex with miniGs399 from EMPIAR-10786)
Authors	:	Chen, M.; Pintilie, G.
Deposited on	:	2023-09-05
Resolution	:	2.50 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 (i) 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 (i)) were used in the production of this report:

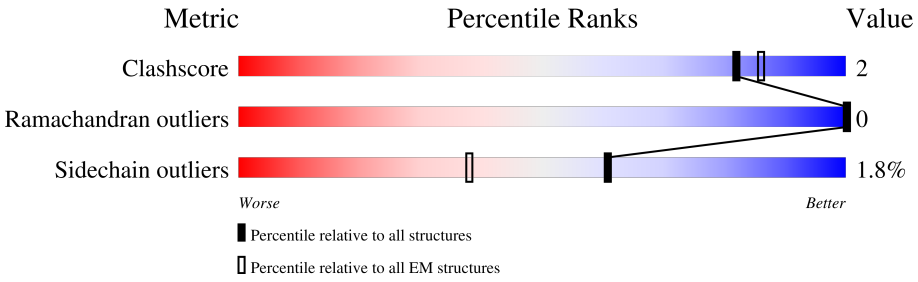
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.50 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 <=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	248	82% 5% 13%
2	B	370	83% • 13%
3	G	68	49% 7% 44%
4	N	142	77% • 19%
5	R	418	60% 7% 32%
6	S	11	91% 9%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 14468 atoms, of which 7032 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 Guanine nucleotide-binding protein G(s) subunit alpha isoforms short.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A	216	3217	1071	1552	305	282	7	0	0

There are 81 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	6	ASN	-	expression tag	UNP P63092
A	7	SER	-	expression tag	UNP P63092
A	8	LYS	-	expression tag	UNP P63092
A	9	THR	-	expression tag	UNP P63092
A	10	GLU	-	expression tag	UNP P63092
A	11	ASP	-	expression tag	UNP P63092
A	12	GLN	-	expression tag	UNP P63092
A	13	ARG	-	expression tag	UNP P63092
A	14	ASN	-	expression tag	UNP P63092
A	15	GLU	-	expression tag	UNP P63092
A	16	GLU	-	expression tag	UNP P63092
A	17	LYS	-	expression tag	UNP P63092
A	18	ALA	-	expression tag	UNP P63092
A	19	GLN	-	expression tag	UNP P63092
A	20	ARG	-	expression tag	UNP P63092
A	21	GLU	-	expression tag	UNP P63092
A	22	ALA	-	expression tag	UNP P63092
A	23	ASN	-	expression tag	UNP P63092
A	24	LYS	-	expression tag	UNP P63092
A	25	LYS	-	expression tag	UNP P63092
A	26	ILE	-	expression tag	UNP P63092
A	27	GLU	-	expression tag	UNP P63092
A	28	LYS	-	expression tag	UNP P63092
A	29	GLN	-	expression tag	UNP P63092
A	30	LEU	-	expression tag	UNP P63092
A	31	GLN	-	expression tag	UNP P63092
A	32	LYS	-	expression tag	UNP P63092

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Chain	Residue	Modelled	Actual	Comment	Reference
A	33	ASP	-	expression tag	UNP P63092
A	34	LYS	-	expression tag	UNP P63092
A	35	GLN	-	expression tag	UNP P63092
A	36	VAL	-	expression tag	UNP P63092
A	37	TYR	-	expression tag	UNP P63092
A	38	ARG	-	expression tag	UNP P63092
A	39	ALA	-	expression tag	UNP P63092
A	40	THR	-	expression tag	UNP P63092
A	41	HIS	-	expression tag	UNP P63092
A	42	ARG	-	expression tag	UNP P63092
A	43	LEU	-	expression tag	UNP P63092
A	44	LEU	-	expression tag	UNP P63092
A	45	LEU	-	expression tag	UNP P63092
A	46	LEU	-	expression tag	UNP P63092
A	47	GLY	-	expression tag	UNP P63092
A	48	ALA	-	expression tag	UNP P63092
A	49	ASP	-	expression tag	UNP P63092
A	50	ASN	-	expression tag	UNP P63092
A	51	SER	-	expression tag	UNP P63092
A	52	GLY	-	expression tag	UNP P63092
A	53	LYS	-	expression tag	UNP P63092
A	54	SER	-	expression tag	UNP P63092
A	55	THR	-	expression tag	UNP P63092
A	56	ILE	-	expression tag	UNP P63092
A	57	VAL	-	expression tag	UNP P63092
A	58	LYS	-	expression tag	UNP P63092
A	59	GLN	-	expression tag	UNP P63092
A	60	MET	-	expression tag	UNP P63092
A	61	ARG	-	expression tag	UNP P63092
A	193	ILE	-	expression tag	UNP P63092
A	194	LEU	-	expression tag	UNP P63092
A	195	HIS	-	expression tag	UNP P63092
A	196	GLY	-	expression tag	UNP P63092
A	197	GLY	-	expression tag	UNP P63092
A	198	SER	-	expression tag	UNP P63092
A	199	GLY	-	expression tag	UNP P63092
A	200	GLY	-	expression tag	UNP P63092
A	201	SER	-	expression tag	UNP P63092
A	202	GLY	-	expression tag	UNP P63092
A	203	GLY	-	expression tag	UNP P63092
A	249	ASP	ALA	conflict	UNP P63092
A	252	ASP	SER	conflict	UNP P63092

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ASN	deletion	UNP P63092
A	?	-	MET	deletion	UNP P63092
A	?	-	VAL	deletion	UNP P63092
A	?	-	ILE	deletion	UNP P63092
A	?	-	ARG	deletion	UNP P63092
A	?	-	GLU	deletion	UNP P63092
A	?	-	ASP	deletion	UNP P63092
A	?	-	ASN	deletion	UNP P63092
A	?	-	GLN	deletion	UNP P63092
A	?	-	THR	deletion	UNP P63092
A	372	ALA	ILE	conflict	UNP P63092
A	375	ILE	VAL	conflict	UNP P63092

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	322	Total	C	H	N	O	S	0	0
			4476	1459	2154	409	436	18		

There are 31 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-29	MET	-	initiating methionine	UNP P62873
B	-28	HIS	-	expression tag	UNP P62873
B	-27	HIS	-	expression tag	UNP P62873
B	-26	HIS	-	expression tag	UNP P62873
B	-25	HIS	-	expression tag	UNP P62873
B	-24	HIS	-	expression tag	UNP P62873
B	-23	HIS	-	expression tag	UNP P62873
B	-22	LEU	-	expression tag	UNP P62873
B	-21	GLU	-	expression tag	UNP P62873
B	-20	VAL	-	expression tag	UNP P62873
B	-19	LEU	-	expression tag	UNP P62873
B	-18	PHE	-	expression tag	UNP P62873
B	-17	GLN	-	expression tag	UNP P62873
B	-16	GLY	-	expression tag	UNP P62873
B	-15	PRO	-	expression tag	UNP P62873
B	-14	GLU	-	expression tag	UNP P62873
B	-13	ASP	-	expression tag	UNP P62873
B	-12	GLN	-	expression tag	UNP P62873
B	-11	VAL	-	expression tag	UNP P62873

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-10	ASP	-	expression tag	UNP P62873
B	-9	PRO	-	expression tag	UNP P62873
B	-8	ARG	-	expression tag	UNP P62873
B	-7	LEU	-	expression tag	UNP P62873
B	-6	ILE	-	expression tag	UNP P62873
B	-5	ASP	-	expression tag	UNP P62873
B	-4	GLY	-	expression tag	UNP P62873
B	-3	LYS	-	expression tag	UNP P62873
B	-2	GLY	-	expression tag	UNP P62873
B	-1	SER	-	expression tag	UNP P62873
B	0	SER	-	expression tag	UNP P62873
B	1	GLY	-	expression tag	UNP P62873

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	G	38	Total	C	H	N	O	S	0	0
			452	154	207	41	47	3		

- Molecule 4 is a protein called Nanobody 35.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	N	115	Total	C	H	N	O	S	0	0
			1640	537	789	147	161	6		

- Molecule 5 is a protein called Substance-P receptor.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	R	284	Total	C	H	N	O	S	0	0
			4522	1534	2253	351	364	20		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-10	ASP	-	expression tag	UNP P25103
R	-9	TYR	-	expression tag	UNP P25103
R	-8	LYS	-	expression tag	UNP P25103
R	-7	ASP	-	expression tag	UNP P25103
R	-6	ASP	-	expression tag	UNP P25103
R	-5	ASP	-	expression tag	UNP P25103
R	-4	ASP	-	expression tag	UNP P25103

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Chain	Residue	Modelled	Actual	Comment	Reference
R	-3	ALA	-	expression tag	UNP P25103
R	-2	SER	-	expression tag	UNP P25103
R	-1	ILE	-	expression tag	UNP P25103
R	0	ASP	-	expression tag	UNP P25103

- Molecule 6 is a protein called Protachykinin-1.

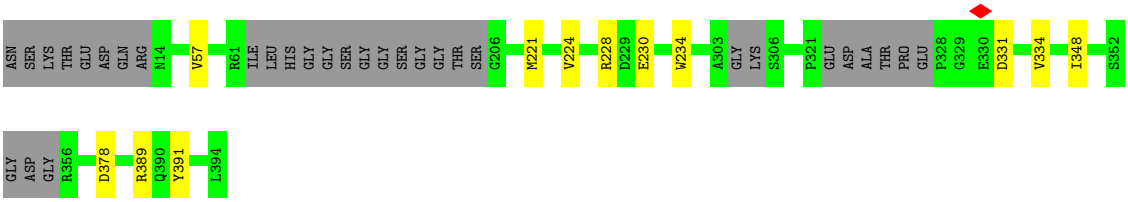
Mol	Chain	Residues	Atoms						AltConf	Trace
6	S	11	Total	C	H	N	O	S	0	0
			161	57	77	13	13	1		

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.

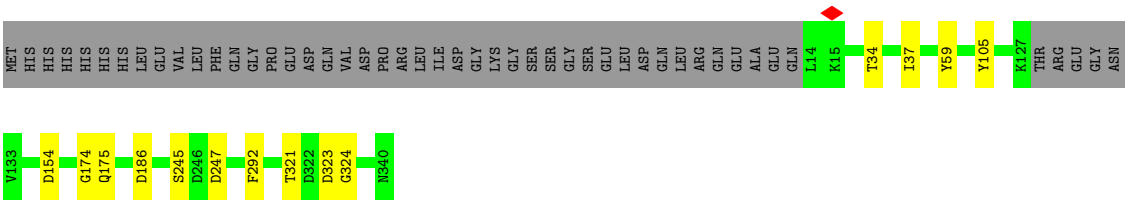
• Molecule 1: Guanine nucleotide-binding protein G(s) subunit alpha isoforms short

Chain A:



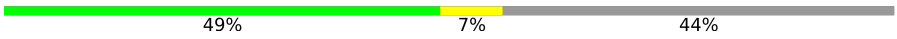
• Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1

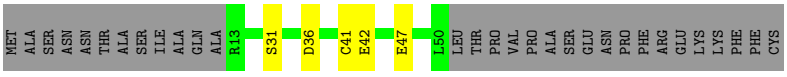
Chain B:



• Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2

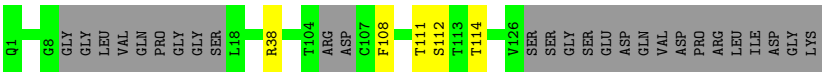
Chain G:





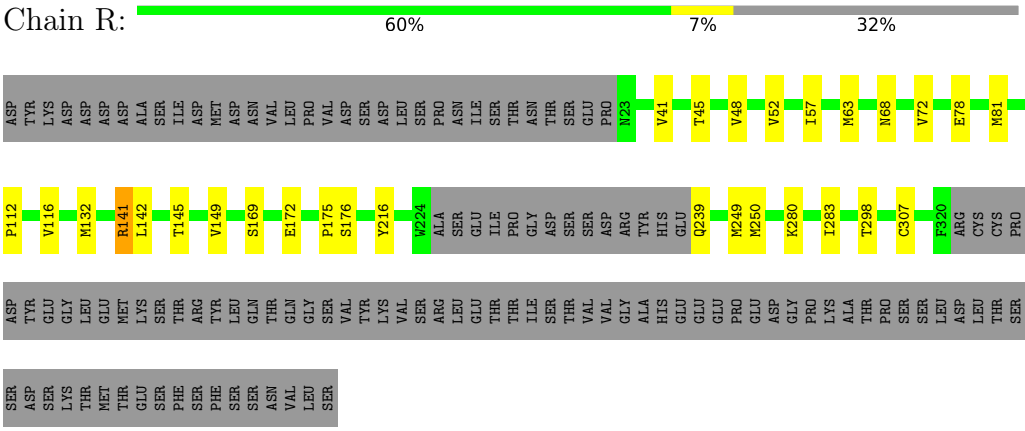
• Molecule 4: Nanobody 35

Chain N:



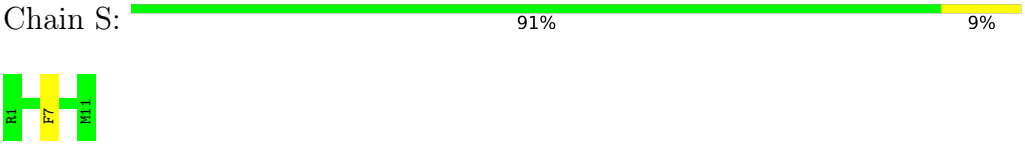
• Molecule 5: Substance-P receptor

Chain R:



• Molecule 6: Protachykinin-1

Chain S:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	288659	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	30	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	31.966	Depositor
Minimum map value	-17.381	Depositor
Average map value	0.001	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.0	Depositor
Map size (Å)	275.04, 275.04, 275.04	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.146, 1.146, 1.146	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	A	0.25	0/1698	0.49	0/2299
2	B	0.24	0/2368	0.51	0/3229
3	G	0.26	0/247	0.36	0/339
4	N	0.26	0/868	0.51	0/1178
5	R	0.27	0/2345	0.44	0/3219
6	S	0.34	0/87	0.39	0/117
All	All	0.25	0/7613	0.48	0/10381

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	1665	1552	1548	7	0
2	B	2322	2154	2152	9	0
3	G	245	207	206	2	0
4	N	851	789	787	2	0
5	R	2269	2253	2251	18	0
6	S	84	77	77	1	0
All	All	7436	7032	7021	36	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 2.

The worst 5 of 36 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:R:175:PRO:O	5:R:176:SER:OG	2.03	0.75
1:A:228:ARG:NH2	1:A:230:GLU:OE2	2.21	0.73
2:B:321:THR:HG23	2:B:324:GLY:H	1.61	0.65
5:R:96:ASN:ND2	6:S:7:PHE:O	2.33	0.61
2:B:245:SER:OG	2:B:247:ASP:OD1	2.19	0.59

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	206/248 (83%)	199 (97%)	7 (3%)	0	100	100
2	B	318/370 (86%)	311 (98%)	7 (2%)	0	100	100
3	G	36/68 (53%)	36 (100%)	0	0	100	100
4	N	109/142 (77%)	106 (97%)	3 (3%)	0	100	100
5	R	280/418 (67%)	273 (98%)	7 (2%)	0	100	100
6	S	9/11 (82%)	6 (67%)	3 (33%)	0	100	100
All	All	958/1257 (76%)	931 (97%)	27 (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	154/219 (70%)	152 (99%)	2 (1%)	69 87
2	B	225/309 (73%)	222 (99%)	3 (1%)	69 87
3	G	18/56 (32%)	16 (89%)	2 (11%)	6 11
4	N	85/118 (72%)	83 (98%)	2 (2%)	49 74
5	R	237/374 (63%)	233 (98%)	4 (2%)	60 82
6	S	8/10 (80%)	8 (100%)	0	100 100
All	All	727/1086 (67%)	714 (98%)	13 (2%)	61 81

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	N	38	ARG
4	N	108	PHE
5	R	307	CYS
5	R	141	ARG
5	R	239	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 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.

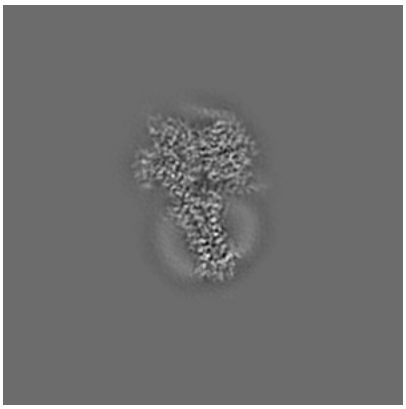
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-41840. These allow visual inspection of the internal detail of the map and identification of artifacts.

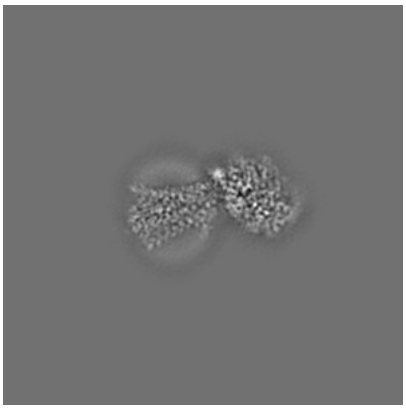
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

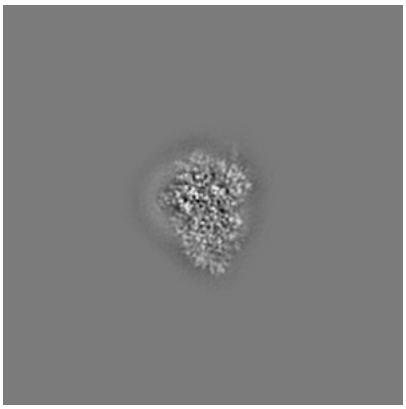
6.1.1 Primary map



X

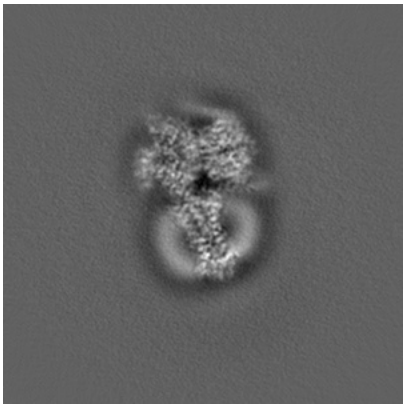


Y

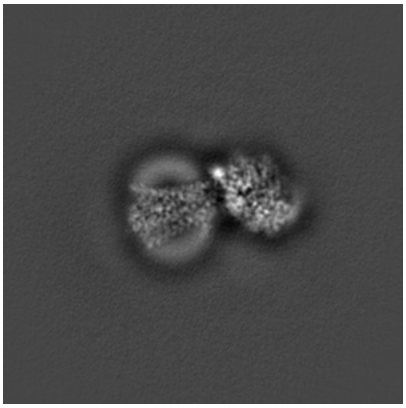


Z

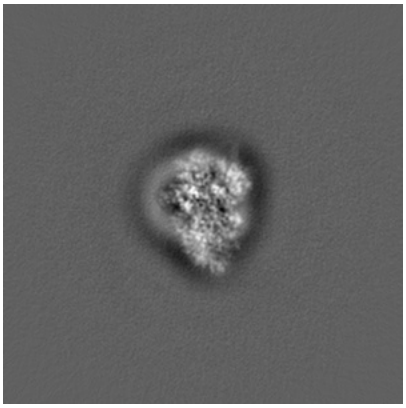
6.1.2 Raw map



X



Y



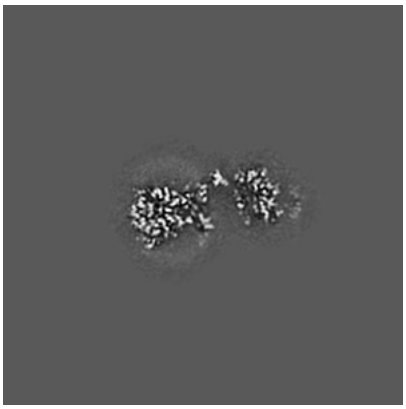
Z

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

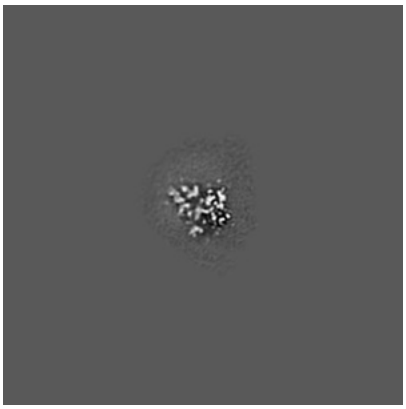
6.2 Central slices (i)

6.2.1 Primary map

X Index: 120

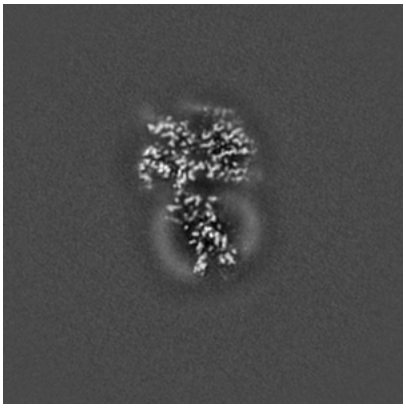


Y Index: 120

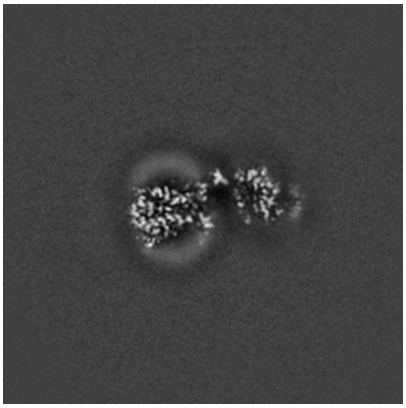


Z Index: 120

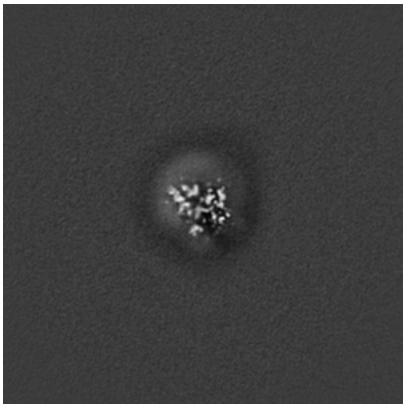
6.2.2 Raw map



X Index: 120



Y Index: 120



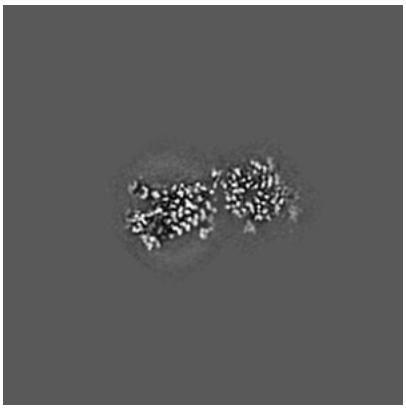
Z Index: 120

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

6.3 Largest variance slices (i)

6.3.1 Primary map

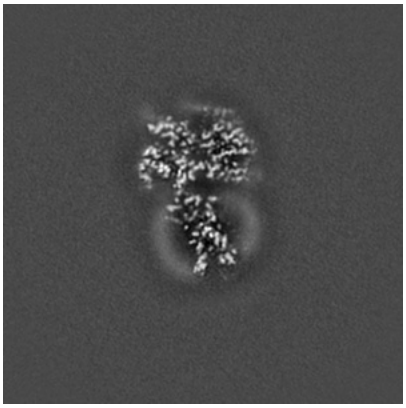
X Index: 120



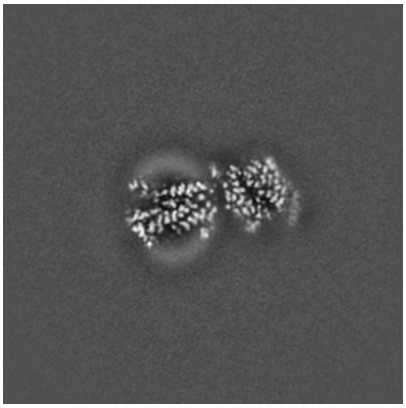
Y Index: 126

Z Index: 143

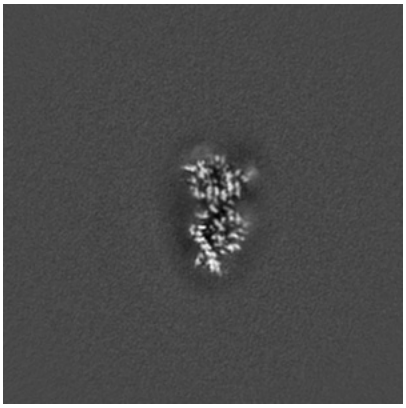
6.3.2 Raw map



X Index: 120



Y Index: 127

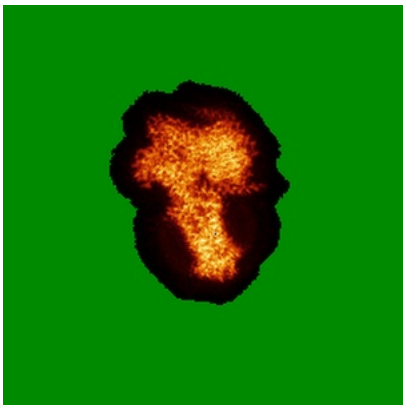


Z Index: 139

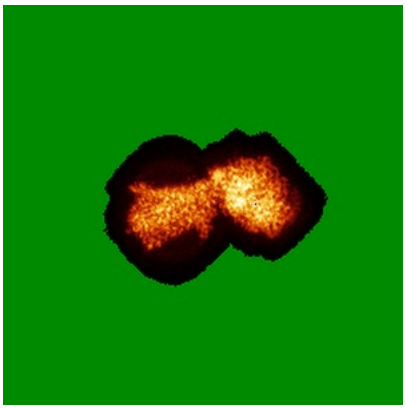
The images above show the largest variance slices of the map in three orthogonal directions.

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

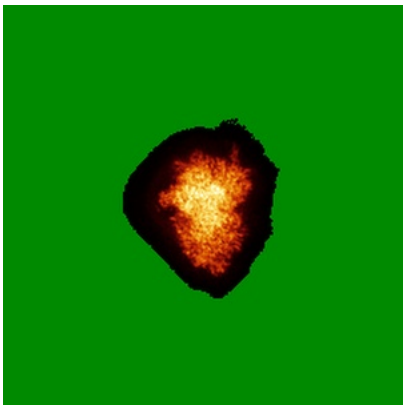
6.4.1 Primary map



X

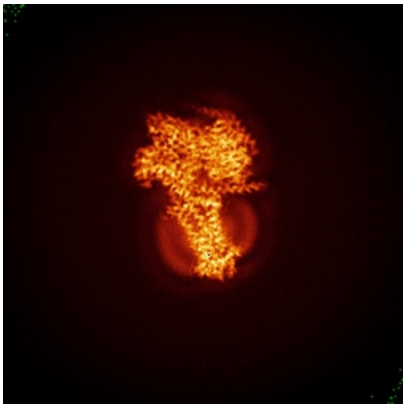


Y

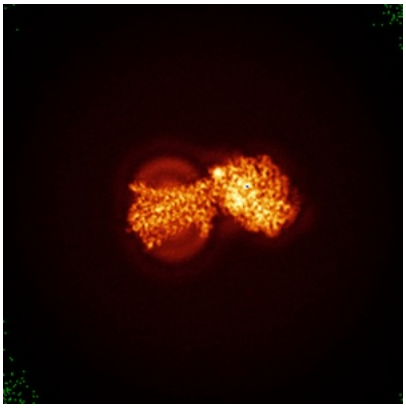


Z

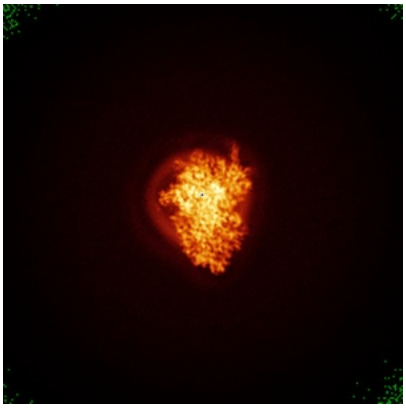
6.4.2 Raw map



X



Y

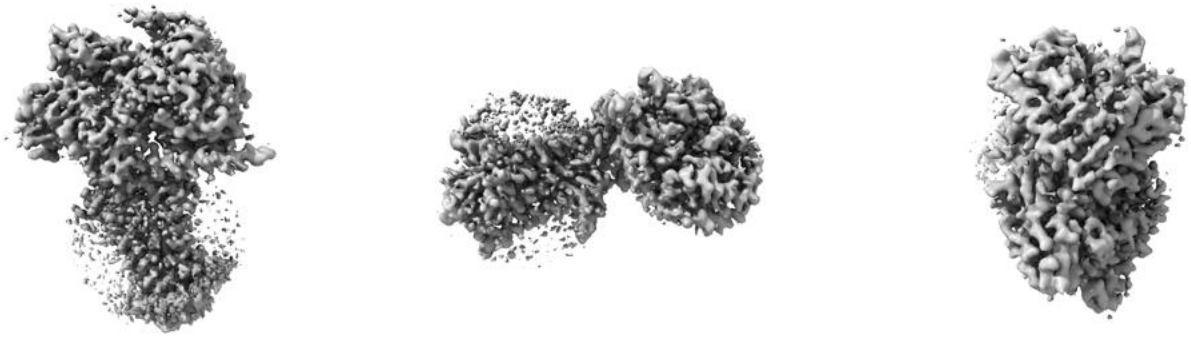


Z

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)

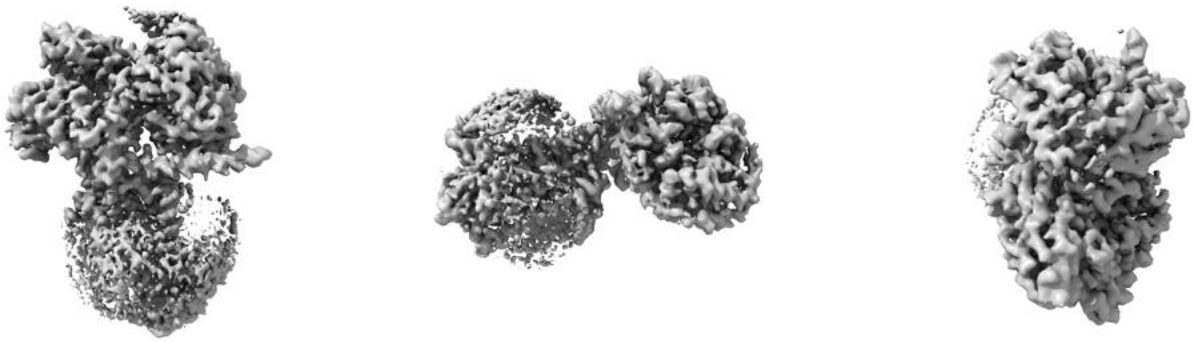
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 3.0. 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.

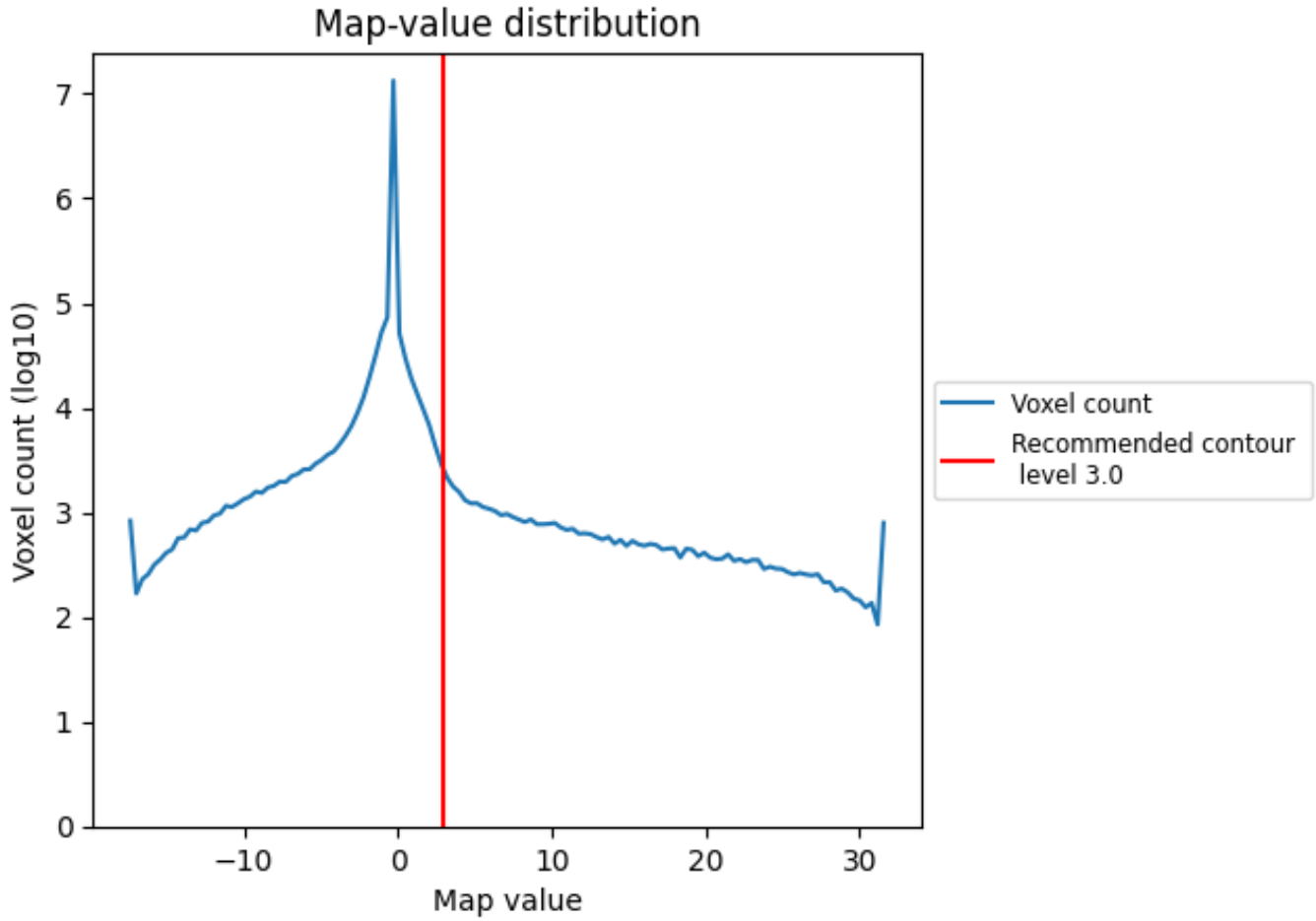
6.6 Mask visualisation (i)

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

7 Map analysis

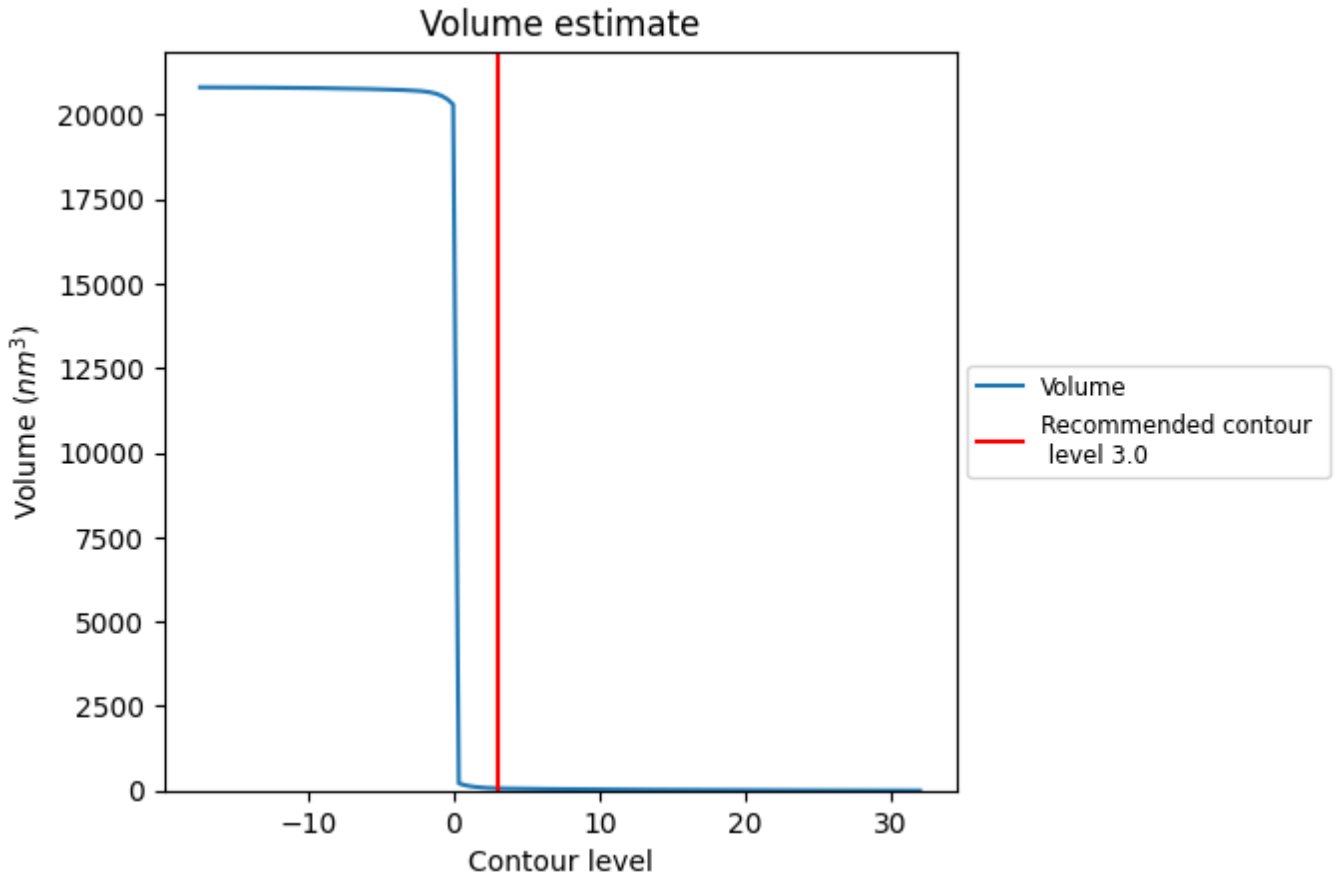
This section contains the results of statistical analysis of the map.

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.

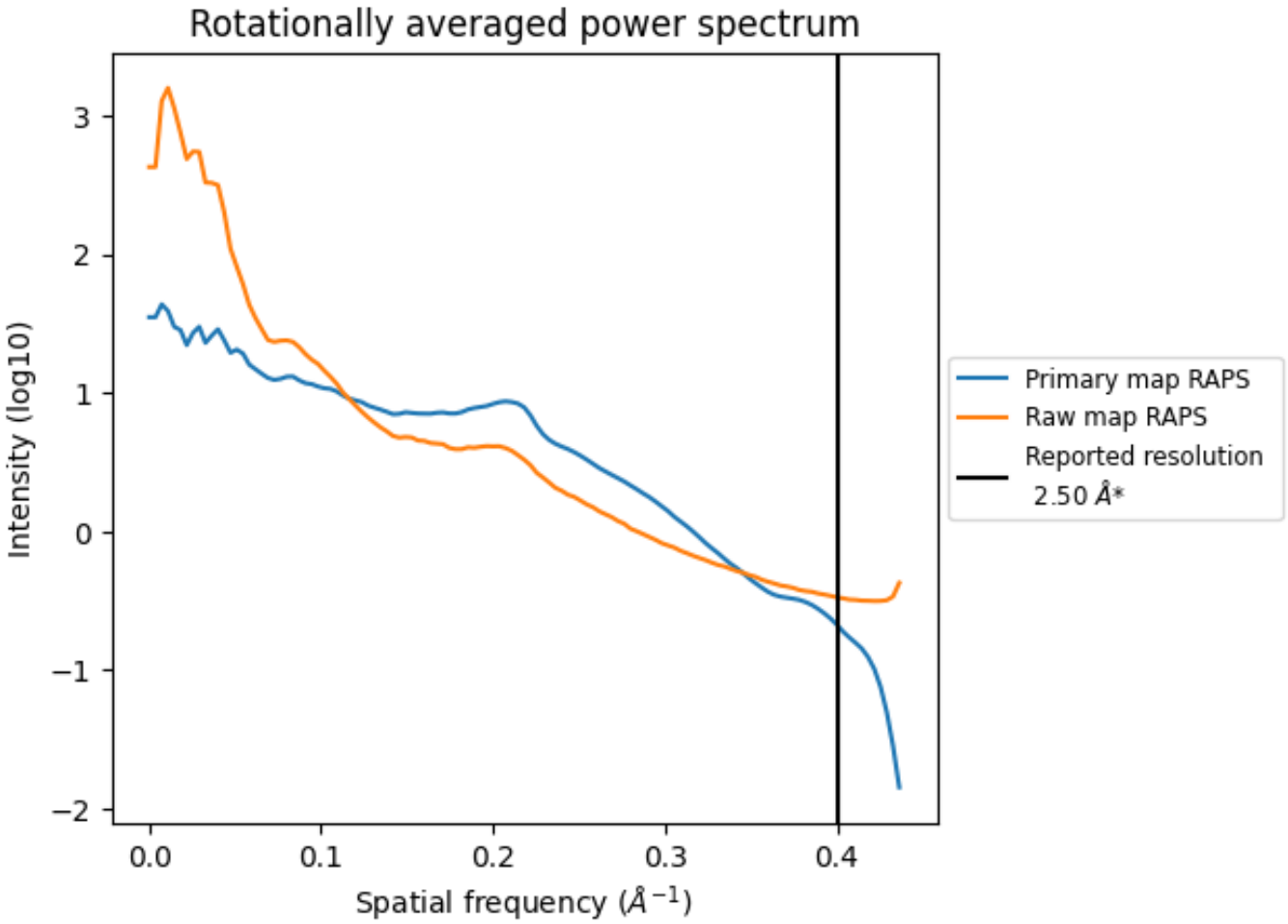
7.2 Volume estimate (i)



The volume at the recommended contour level is 66 nm^3; this corresponds to an approximate mass of 60 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)

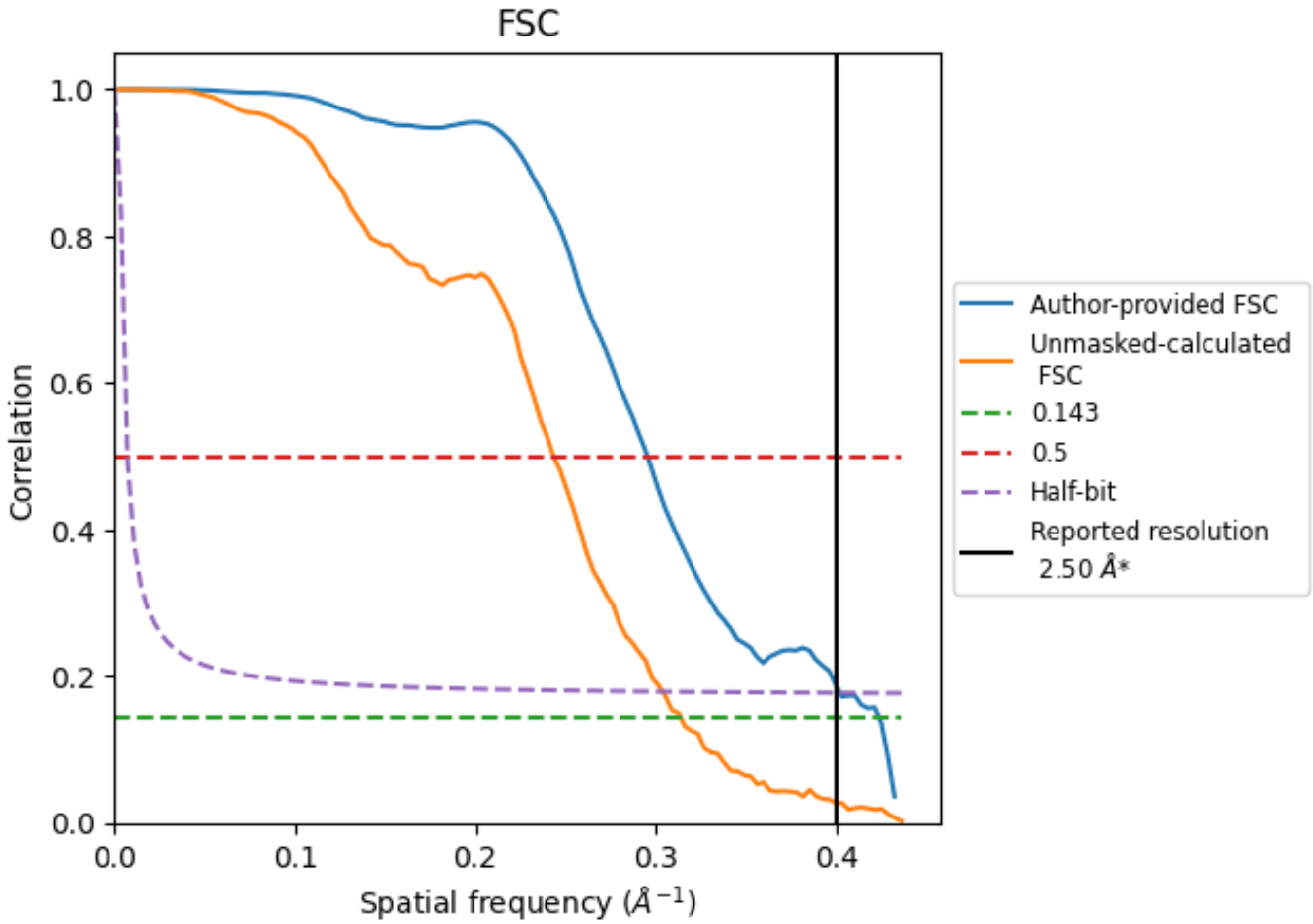


*Reported resolution corresponds to spatial frequency of 0.400 $Å^{-1}$

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 0.400 Å^{-1}

8.2 Resolution estimates (i)

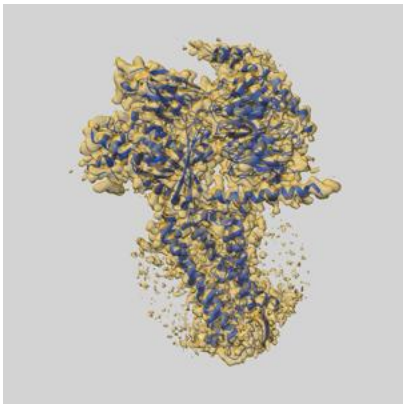
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.50	-	-
Author-provided FSC curve	2.36	3.38	2.49
Unmasked-calculated*	3.18	4.11	3.29

*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 3.18 differs from the reported value 2.5 by more than 10 %

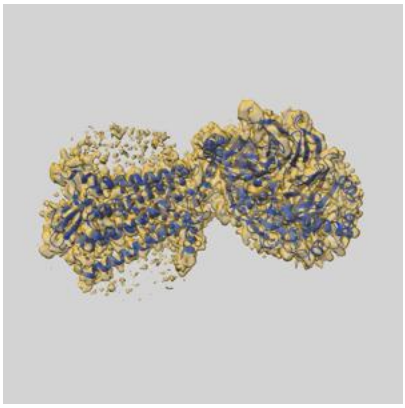
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-41840 and PDB model 8U26. Per-residue inclusion information can be found in section 3 on page 8.

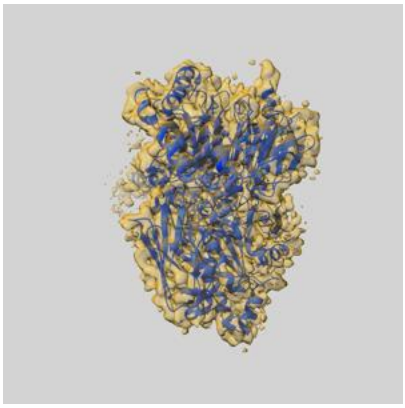
9.1 Map-model overlay



X



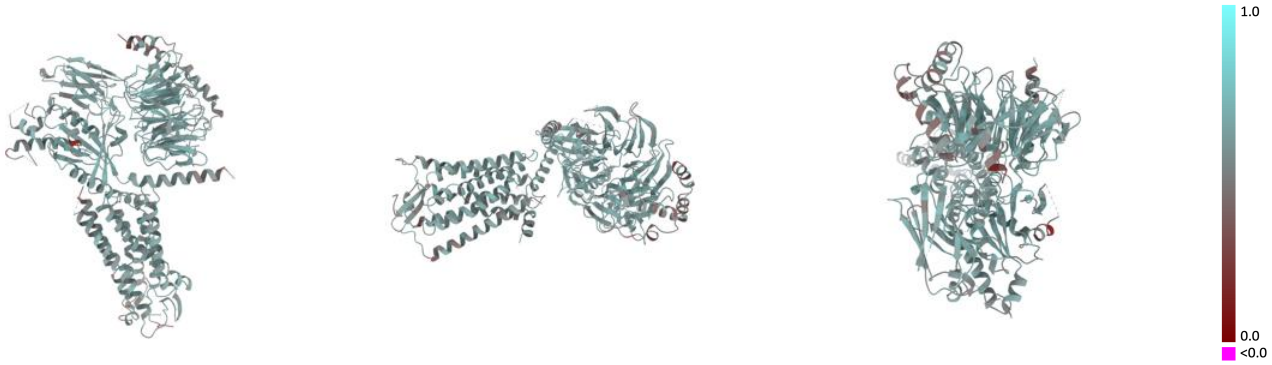
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.0 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

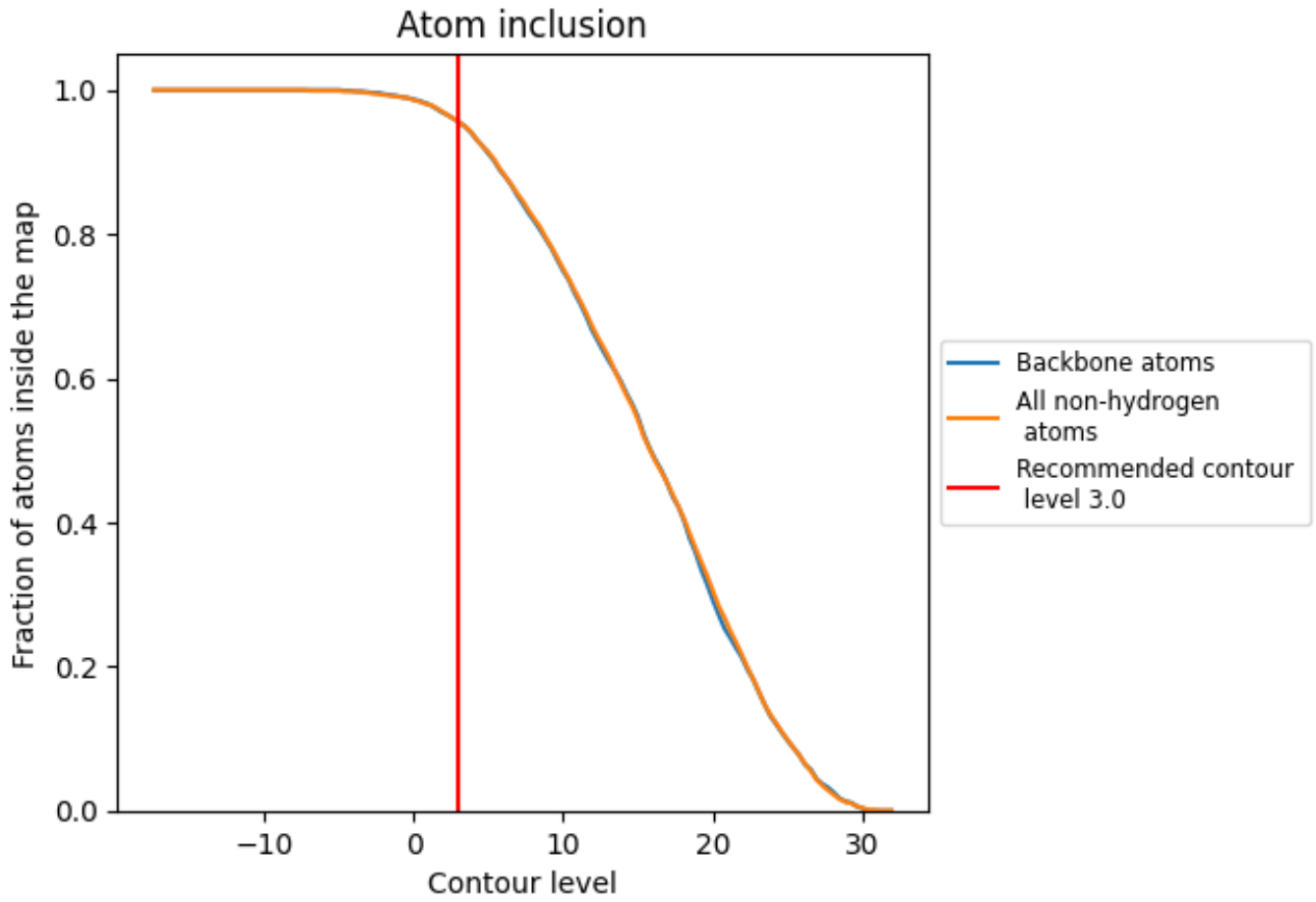
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.0).

9.4 Atom inclusion (i)



At the recommended contour level, 96% of all backbone atoms, 96% 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 (3.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9560	0.5720
A	0.9680	0.5790
B	0.9610	0.5850
G	0.8360	0.4840
N	0.9660	0.5840
R	0.9520	0.5620
S	0.8930	0.5070