



wwPDB EM Validation Summary Report ⓘ

Sep 14, 2026 – 06:35 PM JST

PDB ID : 9U43 / pdb_00009u43
EMDB ID : EMD-63832
Title : Cryo-EM structure of D-peptide-GPCR-Gq complex
Authors : Liu, S.H.; Zhang, Y.J.; Hua, T.; Liu, Z.J.
Deposited on : 2025-03-19
Resolution : 3.02 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

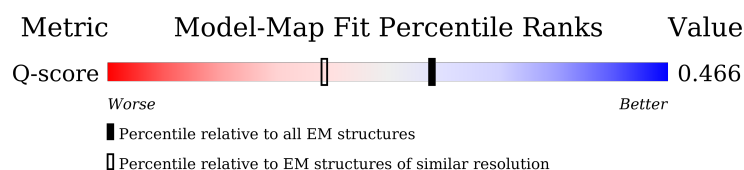
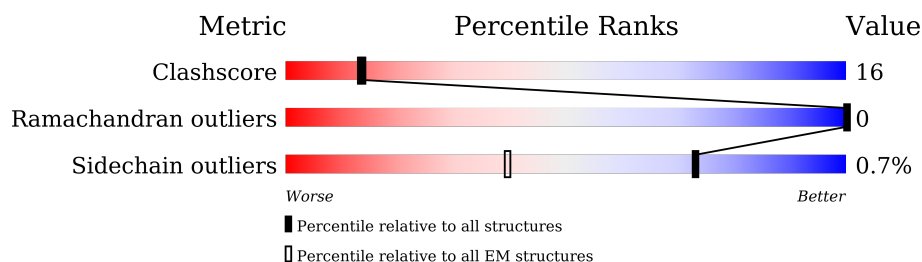
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.02 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	13913 (2.52 - 3.52)

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	R	855	
2	P	10	
3	A	246	
4	B	377	

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Mol	Chain	Length	Quality of chain
5	G	71	
6	N	157	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8211 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 exo-alpha-sialidase, Vasopressin V1a receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	290	Total	C	N	O	S	0	0
			2326	1529	394	380	23		

There are 47 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-458	MET	-	initiating methionine	UNP Q59310
R	-457	LYS	-	expression tag	UNP Q59310
R	-456	THR	-	expression tag	UNP Q59310
R	-455	ILE	-	expression tag	UNP Q59310
R	-454	ILE	-	expression tag	UNP Q59310
R	-453	ALA	-	expression tag	UNP Q59310
R	-452	LEU	-	expression tag	UNP Q59310
R	-451	SER	-	expression tag	UNP Q59310
R	-450	TYR	-	expression tag	UNP Q59310
R	-449	ILE	-	expression tag	UNP Q59310
R	-448	PHE	-	expression tag	UNP Q59310
R	-447	CYS	-	expression tag	UNP Q59310
R	-446	LEU	-	expression tag	UNP Q59310
R	-445	VAL	-	expression tag	UNP Q59310
R	-444	PHE	-	expression tag	UNP Q59310
R	-443	ALA	-	expression tag	UNP Q59310
R	-442	ASP	-	expression tag	UNP Q59310
R	-441	TYR	-	expression tag	UNP Q59310
R	-440	LYS	-	expression tag	UNP Q59310
R	-439	ASP	-	expression tag	UNP Q59310
R	-438	ASP	-	expression tag	UNP Q59310
R	-437	ASP	-	expression tag	UNP Q59310
R	-436	ASP	-	expression tag	UNP Q59310
R	-435	ALA	-	expression tag	UNP Q59310
R	-434	GLY	-	expression tag	UNP Q59310
R	-433	ARG	-	expression tag	UNP Q59310
R	-432	ALA	-	expression tag	UNP Q59310
R	-281	SER	GLY	conflict	UNP Q59310

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Chain	Residue	Modelled	Actual	Comment	Reference
R	112	LYS	ASP	engineered mutation	UNP P37288
R	379	LEU	-	expression tag	UNP P37288
R	380	GLU	-	expression tag	UNP P37288
R	381	VAL	-	expression tag	UNP P37288
R	382	LEU	-	expression tag	UNP P37288
R	383	PHE	-	expression tag	UNP P37288
R	384	GLN	-	expression tag	UNP P37288
R	385	GLY	-	expression tag	UNP P37288
R	386	PRO	-	expression tag	UNP P37288
R	387	HIS	-	expression tag	UNP P37288
R	388	HIS	-	expression tag	UNP P37288
R	389	HIS	-	expression tag	UNP P37288
R	390	HIS	-	expression tag	UNP P37288
R	391	HIS	-	expression tag	UNP P37288
R	392	HIS	-	expression tag	UNP P37288
R	393	HIS	-	expression tag	UNP P37288
R	394	HIS	-	expression tag	UNP P37288
R	395	HIS	-	expression tag	UNP P37288
R	396	HIS	-	expression tag	UNP P37288

- Molecule 2 is a protein called Arg-vasopressin.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	P	10	Total	C	N	O	S	0	1
			75	46	15	12	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	8	DAR	ARG	engineered mutation	UNP P01185
P	10	NH2	-	amidation	UNP P01185

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(q) subunit alpha-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	221	Total	C	N	O	S	0	0
			1813	1144	322	340	7		

- Molecule 4 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	338	Total	C	N	O	S	0	0
			2600	1604	467	508	21		

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	MET	-	initiating methionine	UNP P62873
B	-4	HIS	-	expression tag	UNP P62873
B	-3	HIS	-	expression tag	UNP P62873
B	-2	HIS	-	expression tag	UNP P62873
B	-1	HIS	-	expression tag	UNP P62873
B	0	HIS	-	expression tag	UNP P62873
B	1	HIS	-	expression tag	UNP P62873
B	2	GLY	-	expression tag	UNP P62873
B	3	SER	-	expression tag	UNP P62873
B	4	LEU	-	expression tag	UNP P62873
B	5	LEU	-	expression tag	UNP P62873
B	6	GLN	-	expression tag	UNP P62873
B	346	GLY	-	expression tag	UNP P62873
B	347	SER	-	expression tag	UNP P62873
B	348	SER	-	expression tag	UNP P62873
B	349	GLY	-	expression tag	UNP P62873
B	350	GLY	-	expression tag	UNP P62873
B	351	GLY	-	expression tag	UNP P62873
B	352	GLY	-	expression tag	UNP P62873
B	353	SER	-	expression tag	UNP P62873
B	354	GLY	-	expression tag	UNP P62873
B	355	GLY	-	expression tag	UNP P62873
B	356	GLY	-	expression tag	UNP P62873
B	357	GLY	-	expression tag	UNP P62873
B	358	SER	-	expression tag	UNP P62873
B	359	SER	-	expression tag	UNP P62873
B	360	GLY	-	expression tag	UNP P62873
B	361	VAL	-	expression tag	UNP P62873
B	362	SER	-	expression tag	UNP P62873
B	363	GLY	-	expression tag	UNP P62873
B	364	TRP	-	expression tag	UNP P62873
B	365	ARG	-	expression tag	UNP P62873
B	366	LEU	-	expression tag	UNP P62873
B	367	PHE	-	expression tag	UNP P62873
B	368	LYS	-	expression tag	UNP P62873
B	369	LYS	-	expression tag	UNP P62873
B	370	ILE	-	expression tag	UNP P62873

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Chain	Residue	Modelled	Actual	Comment	Reference
B	371	SER	-	expression tag	UNP P62873

- Molecule 5 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	57	Total	C	N	O	S	0	0
			436	273	77	83	3		

- Molecule 6 is a protein called Nanobody 35.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	126	Total	C	N	O	S	0	0
			961	599	168	188	6		

ASP
THR
LEU
GLU
VAL
LEU
PHE
GLN
GLY
PRO
HIS
HIS
HIS
HIS
HIS
HIS
HIS

• Molecule 2: Arg-vasopressin

Chain P: 

G1
Y2
N5
C6
P7
R8
G9
H210

• Molecule 3: Guanine nucleotide-binding protein G(q) subunit alpha-1

Chain A: 

MET
GLY
SER
THR
VAL
SER
ALA
E8
D9
K10
A11
K17
L23
G27
E28
K29
R32
L38
G45
K46
S47
T48
I49
V50
LYS
GLN
MET
ARG
ILE
LEU
HIS
GLY
SER
GLY
GLY
SER
GLY
THR
GLY
I182
D190
V199
Q202
R207
K208
W209
I210

L220
S225
Y228
W229
R230
E233
A234
L235
F238
W242
Y243
N244
L247
V252
F255
L262
K265
S271
K272
L273
E274
D275
Y276
F277
E287
D288
A289
T290
P291
E295
T300
K303
Y304
K308
I313
S314
S317
G318
D319
G320

R338
F341
N342
D343
C344
K345
D346
I347
I348
N351
K352
L353
R354
E355
Y356
N357
L358
V359

• Molecule 4: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1

Chain B: 

MET
HIS
HIS
HIS
HIS
HIS
HIS
GLY
SER
LEU
LEU
GLN
SER
E8
L9
D10
Q11
L12
R13
Q14
E15
A16
E17
Q18
L19
Q22
R27
A31
D32
S36
T39
W47
I48
Q49
T52
R53
R54
T55
L56
L60
T63
N66
V76
S77
A78
G82
K83
L84

T92
I98
P99
L100
V105
M106
T107
C108
A109
V117
A119
L122
D123
N124
I128
Y129
N130
L131
K132
T133
R134
E135
G136
N137
Y140
S141
R142
H147
Y150
C153
L157
D158
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D168
T169
I170
C171
A172
L173
W174
D175
I176

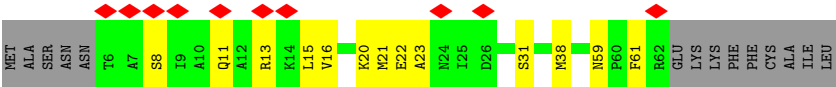
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A208
C209
D210
K214
L215
W216
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V218
V219
E220
G221
R224
Q225
H230
E231
I237
C238
F239
F240
F241
N242
T246
G249
S250
D251
A253
T254
C255
R256
L257
F258
D259
Q264
S265
L266
T267
T268
I274
L275
C276

T279
S280
V281
S282
F283
S284
R288
L289
L290
L291
D295
D303
A304
L305
K306
R319
V320
S321
C322
L323
K330
A331
V332
A333
T334
G335
S336
W337
L343
K344
K345
GLY
SER
SER
GLY
GLY
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GLY
VAL
SER
GLY
TRP
ARG
LEU
PHE
LYS

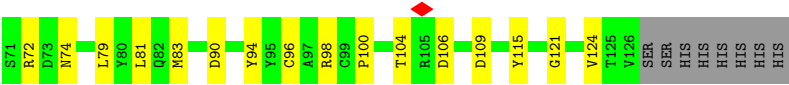
LYS
ILE
SER

• Molecule 5: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2

Chain G: 



• Molecule 6: Nanobody 35



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	310743	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.256	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.1	Depositor
Map size ($\text{\AA}$)	266.24, 266.24, 266.24	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.83199996, 0.83199996, 0.83199996	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: DAR, NH2

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	R	0.16	0/2395	0.32	0/3267
2	P	0.17	0/64	0.28	0/84
3	A	0.17	0/1846	0.30	0/2486
4	B	0.17	0/2647	0.34	0/3589
5	G	0.12	0/442	0.26	0/597
6	N	0.16	0/981	0.30	0/1329
All	All	0.16	0/8375	0.32	0/11352

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	R	2326	0	2359	84	0
2	P	75	0	64	5	0
3	A	1813	0	1791	63	0
4	B	2600	0	2505	99	0
5	G	436	0	448	12	0
6	N	961	0	928	34	0
All	All	8211	0	8095	259	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 16.

The worst 5 of 259 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:R:160:LEU:HD11	3:A:348:ILE:HD13	1.49	0.92
1:R:285:ALA:HB2	3:A:359:VAL:HA	1.56	0.86
1:R:288:ARG:NH2	3:A:357:ASN:ND2	2.28	0.81
3:A:355:GLU:OE1	3:A:355:GLU:C	2.23	0.80
4:B:39:THR:HB	4:B:305:LEU:HD13	1.65	0.77

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	R	286/855 (34%)	275 (96%)	11 (4%)	0	100	100
2	P	7/10 (70%)	6 (86%)	1 (14%)	0	100	100
3	A	217/246 (88%)	203 (94%)	14 (6%)	0	100	100
4	B	336/377 (89%)	325 (97%)	11 (3%)	0	100	100
5	G	55/71 (78%)	55 (100%)	0	0	100	100
6	N	124/157 (79%)	122 (98%)	2 (2%)	0	100	100
All	All	1025/1716 (60%)	986 (96%)	39 (4%)	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	R	253/734 (34%)	253 (100%)	0	100	100
2	P	7/7 (100%)	6 (86%)	1 (14%)	3	15
3	A	197/213 (92%)	196 (100%)	1 (0%)	81	88
4	B	281/308 (91%)	279 (99%)	2 (1%)	76	85
5	G	46/58 (79%)	46 (100%)	0	100	100
6	N	104/127 (82%)	102 (98%)	2 (2%)	50	75
All	All	888/1447 (61%)	882 (99%)	6 (1%)	73	85

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	B	239	PHE
6	N	35	ASN
6	N	96	CYS
3	A	50	VAL
2	P	6	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
4	B	345	ASN
6	N	3	GLN
3	A	236	ASN
3	A	244	ASN
3	A	357	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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-63832. These allow visual inspection of the internal detail of the map and identification of artifacts.

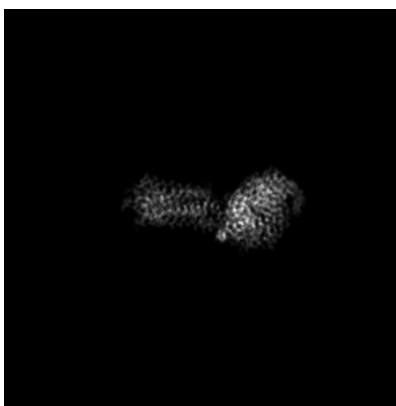
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

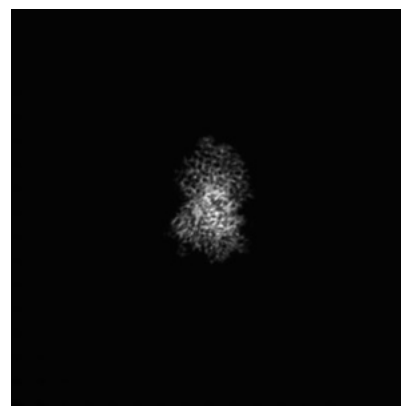
6.1.1 Primary map



X

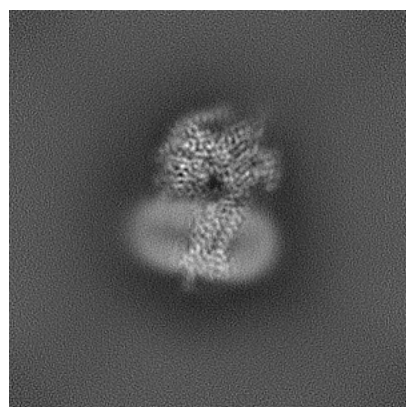


Y

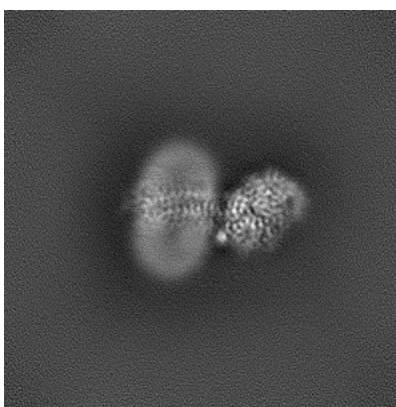


Z

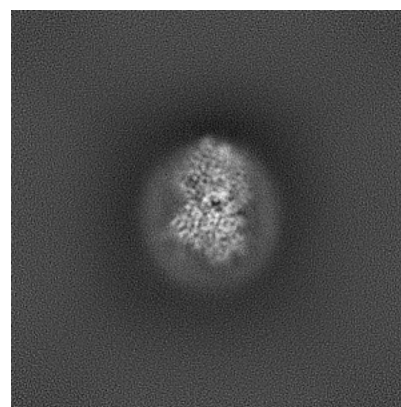
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices [i](#)

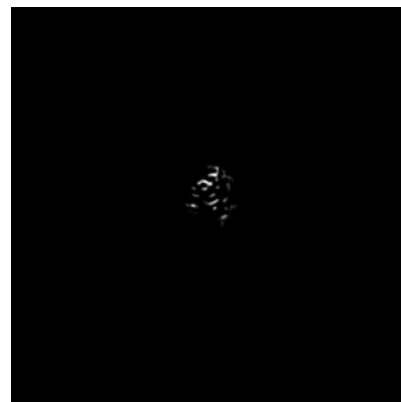
6.2.1 Primary map



X Index: 160

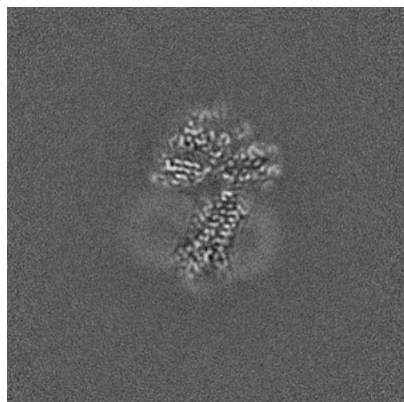


Y Index: 160

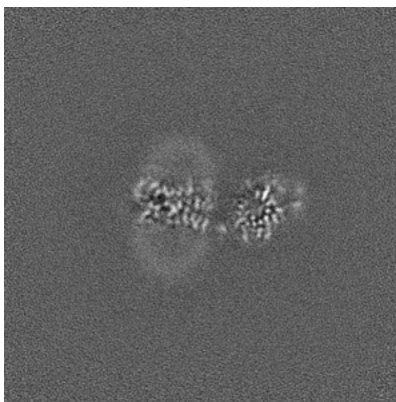


Z Index: 160

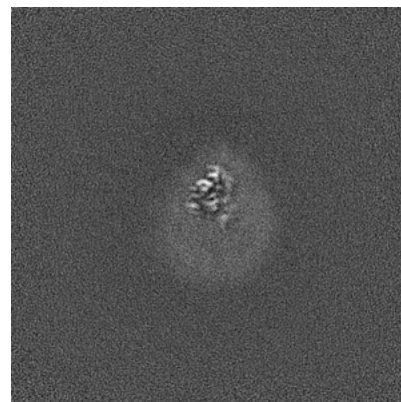
6.2.2 Raw map



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: 158

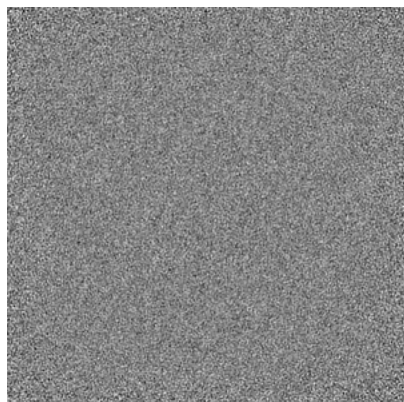


Y Index: 146

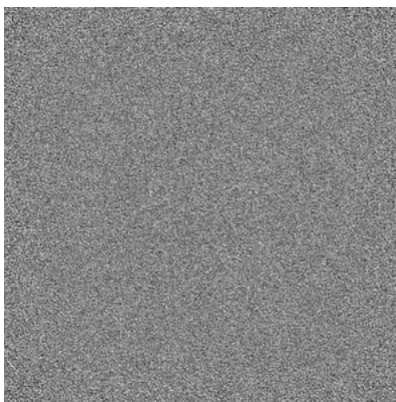


Z Index: 190

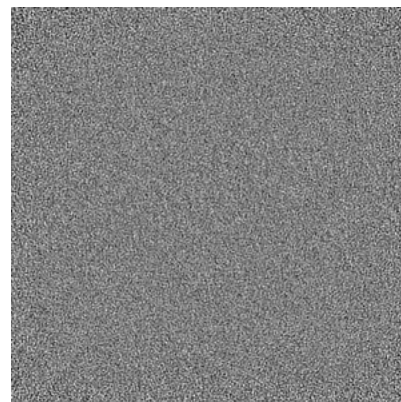
6.3.2 Raw map



X Index: 0



Y Index: 0

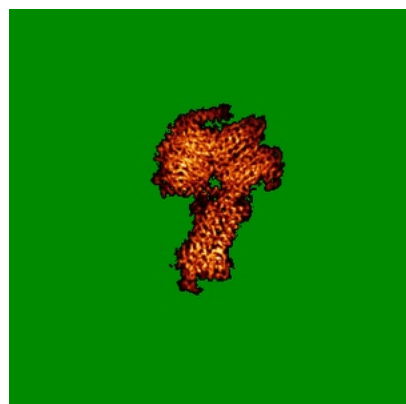


Z Index: 0

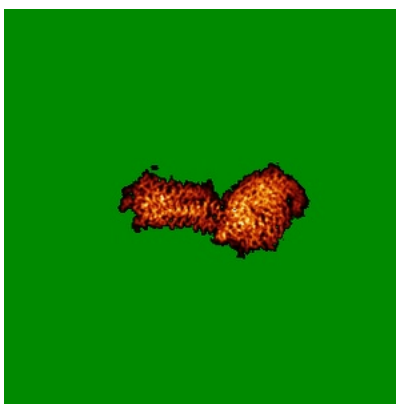
The images above show the largest variance slices of the map in three orthogonal directions.

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

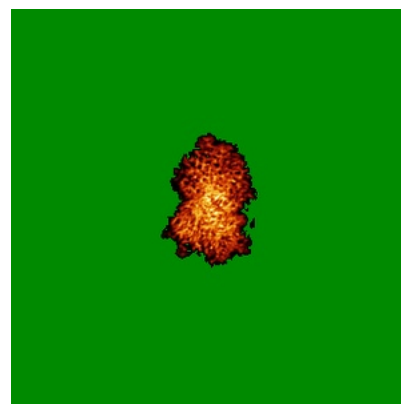
6.4.1 Primary map



X

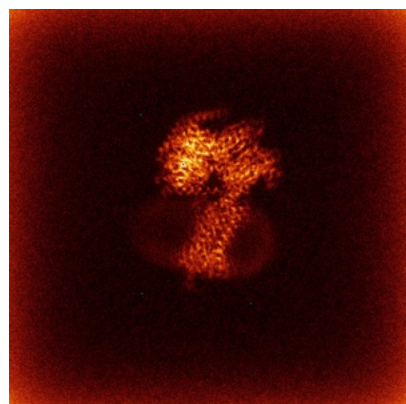


Y

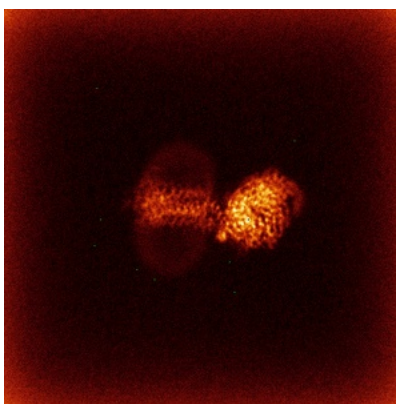


Z

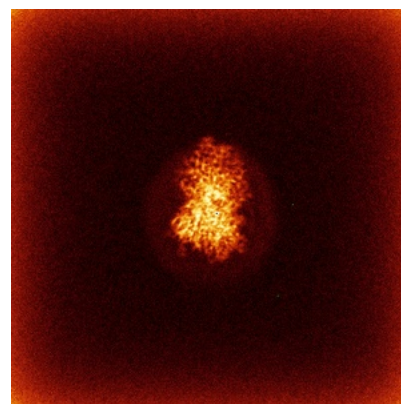
6.4.2 Raw map



X



Y

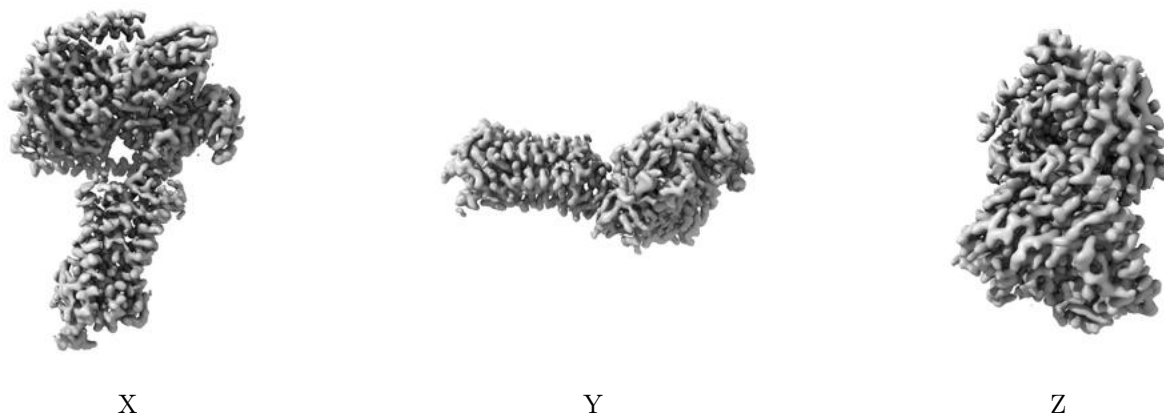


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

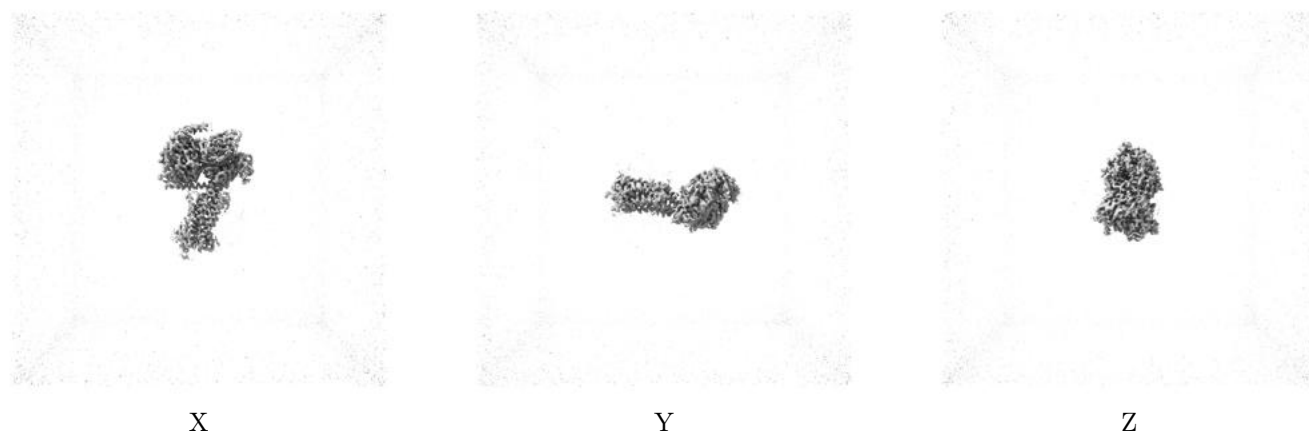
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. 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.

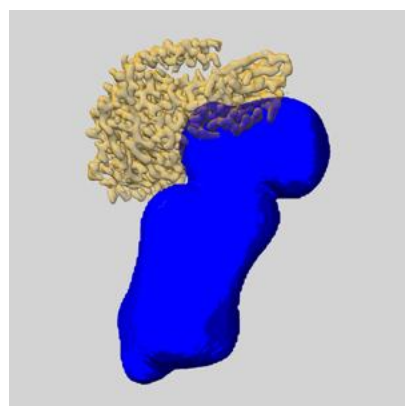
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

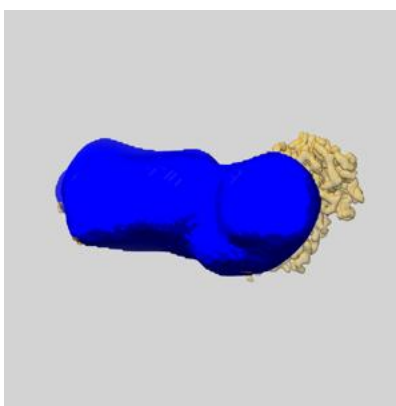
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

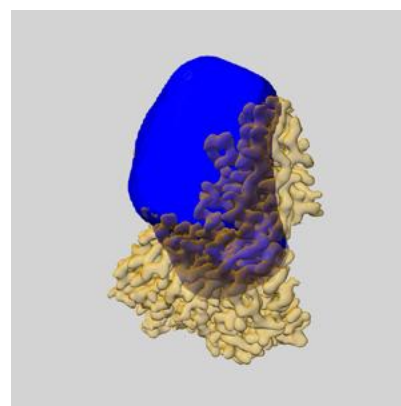
6.6.1 emd_63832_msk_1.map [i](#)



X



Y

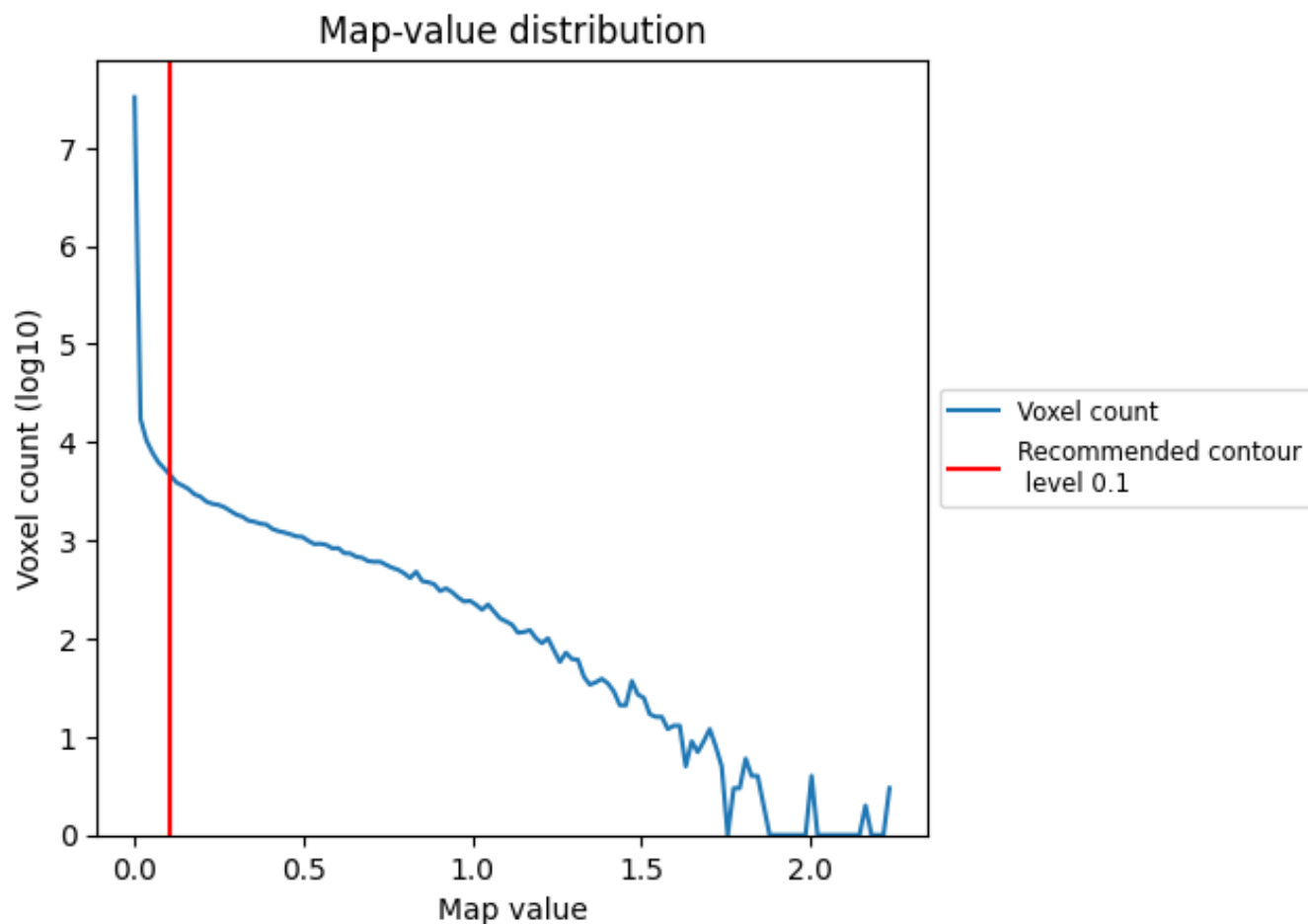


Z

7 Map analysis [i](#)

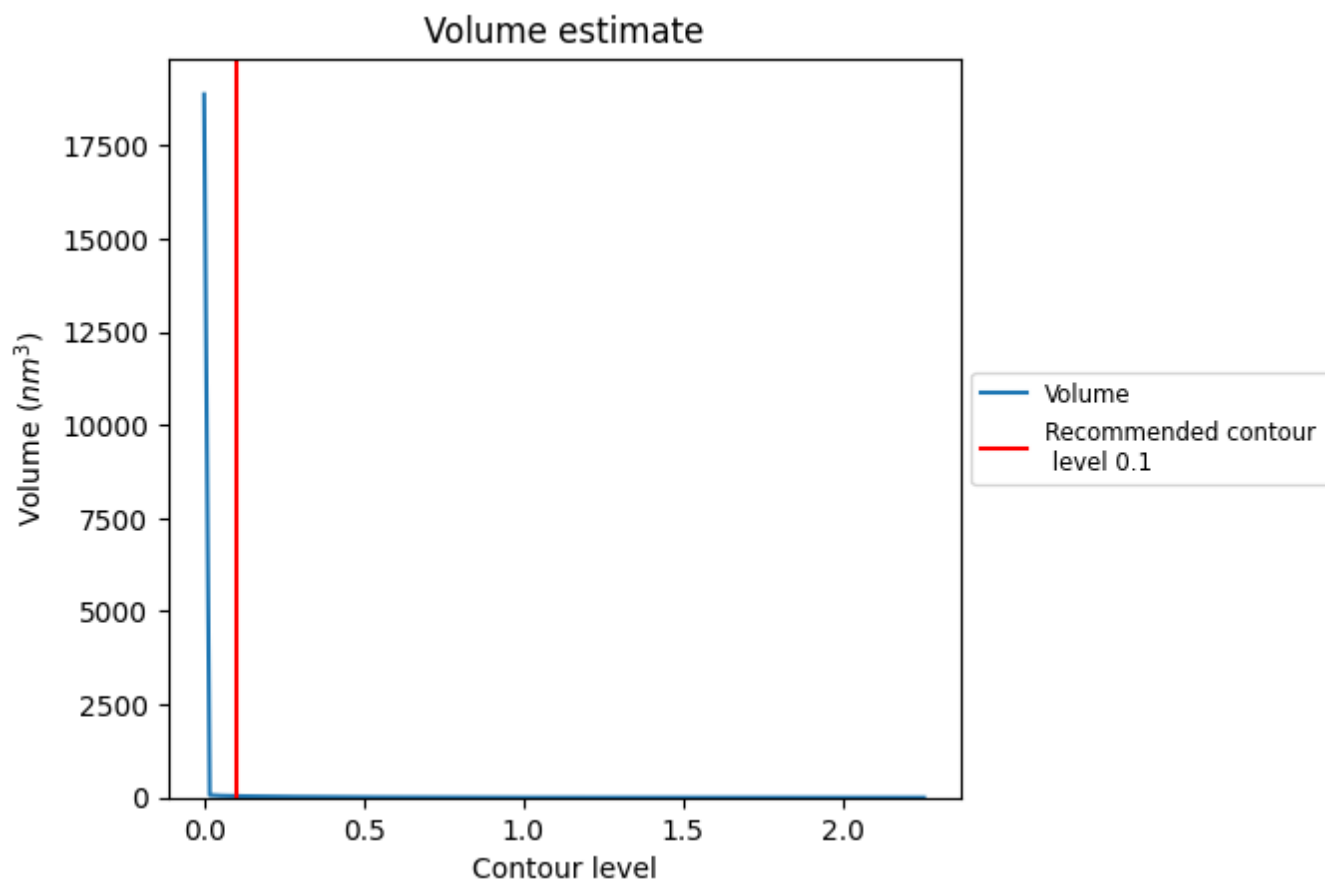
This section contains the results of statistical analysis of the map.

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.

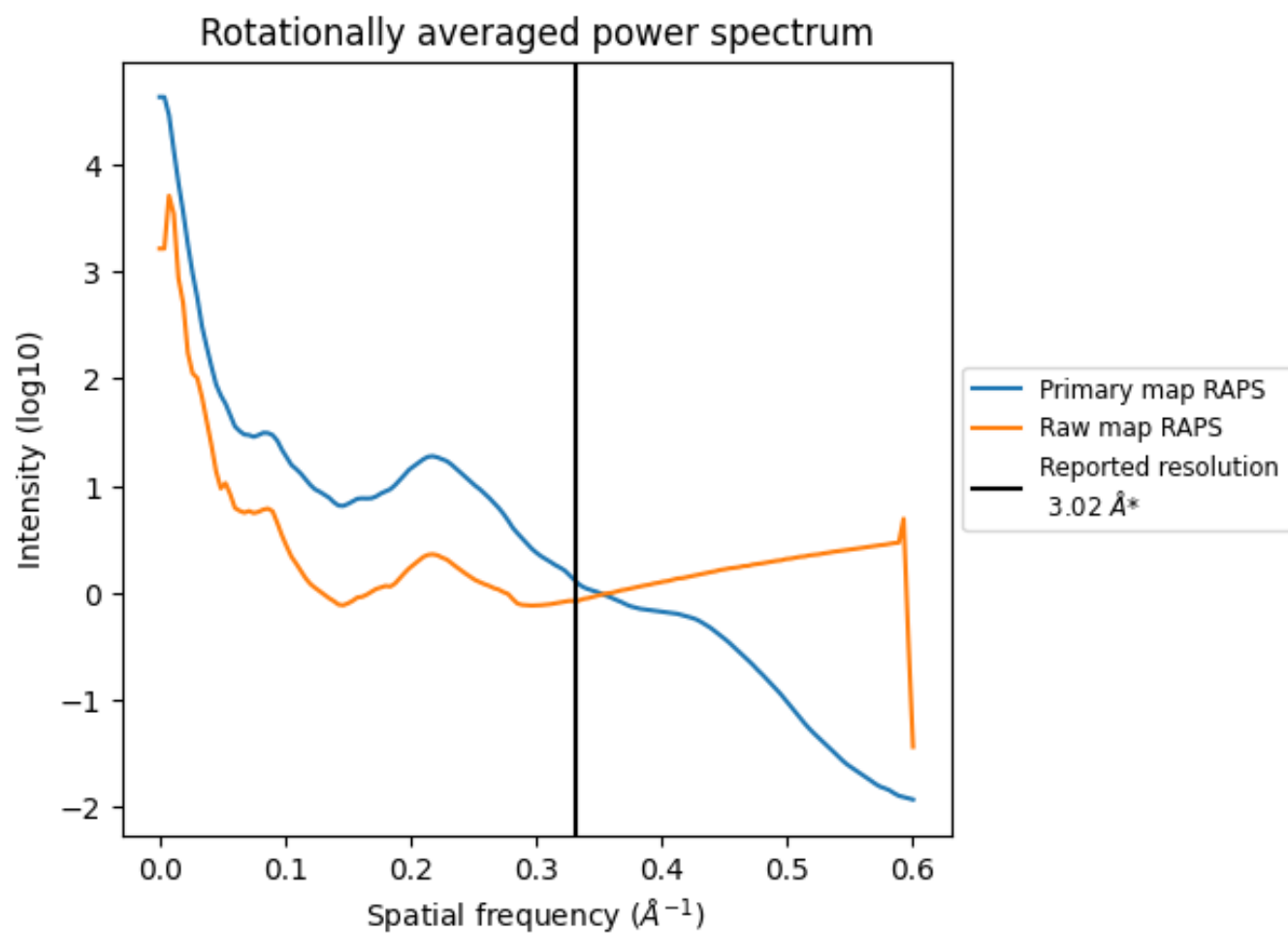
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 40 nm³; this corresponds to an approximate mass of 36 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 ⓘ

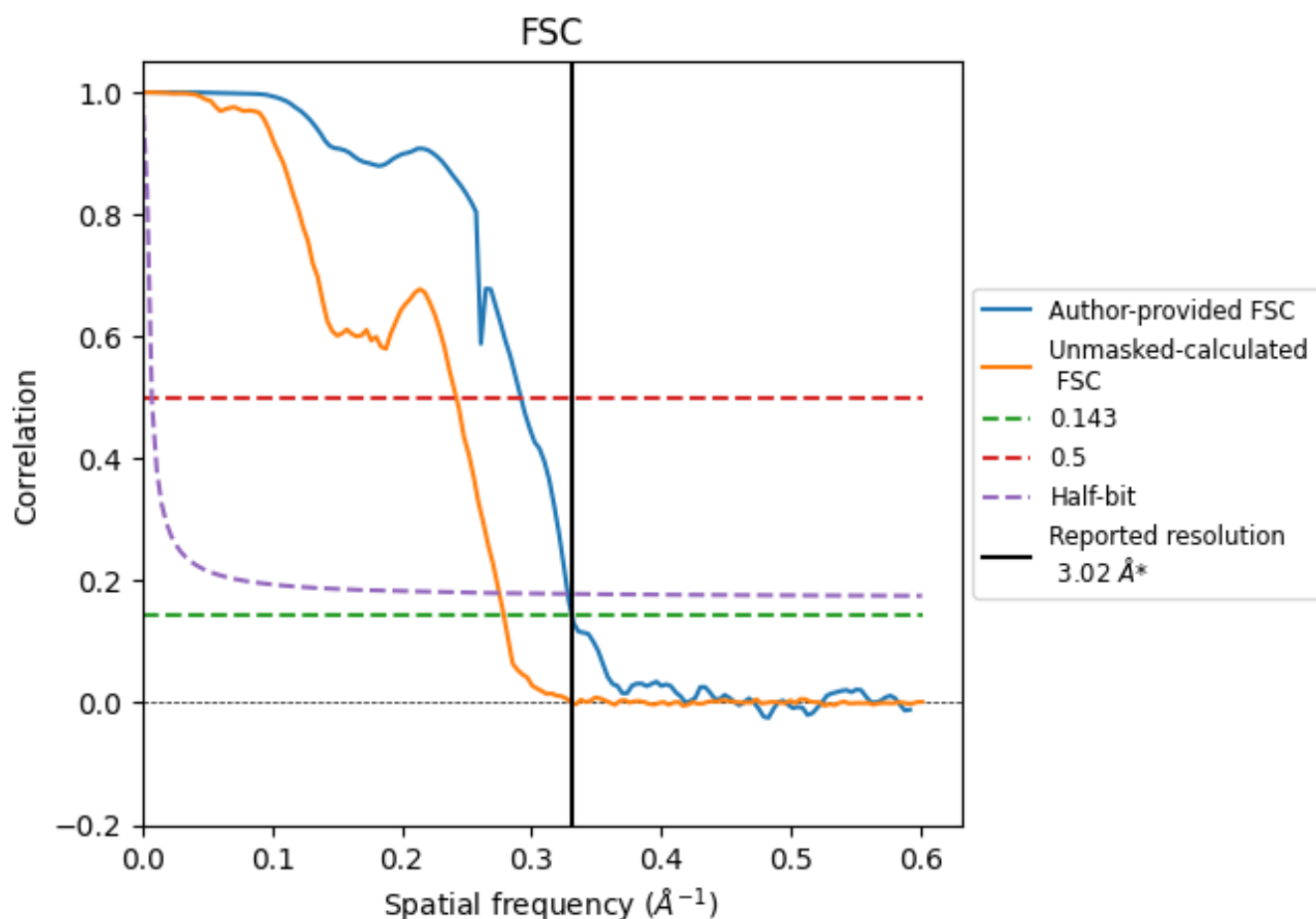


*Reported resolution corresponds to spatial frequency of 0.331 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.331 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

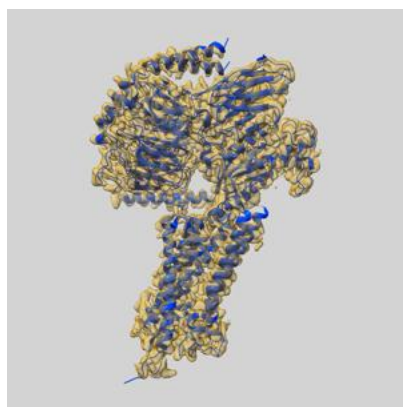
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.02	-	-
Author-provided FSC curve	3.02	3.43	3.05
Unmasked-calculated*	3.59	4.13	3.64

*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 3.59 differs from the reported value 3.02 by more than 10 %

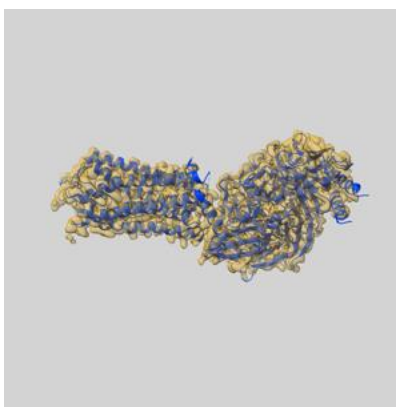
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-63832 and PDB model 9U43. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

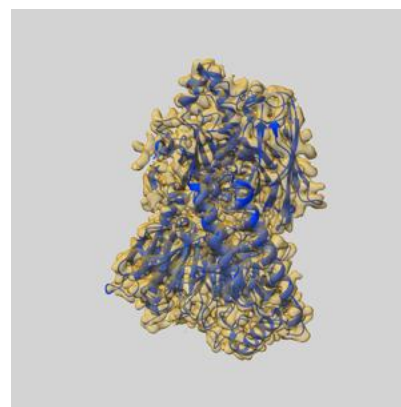
9.1 Map-model overlay [i](#)



X



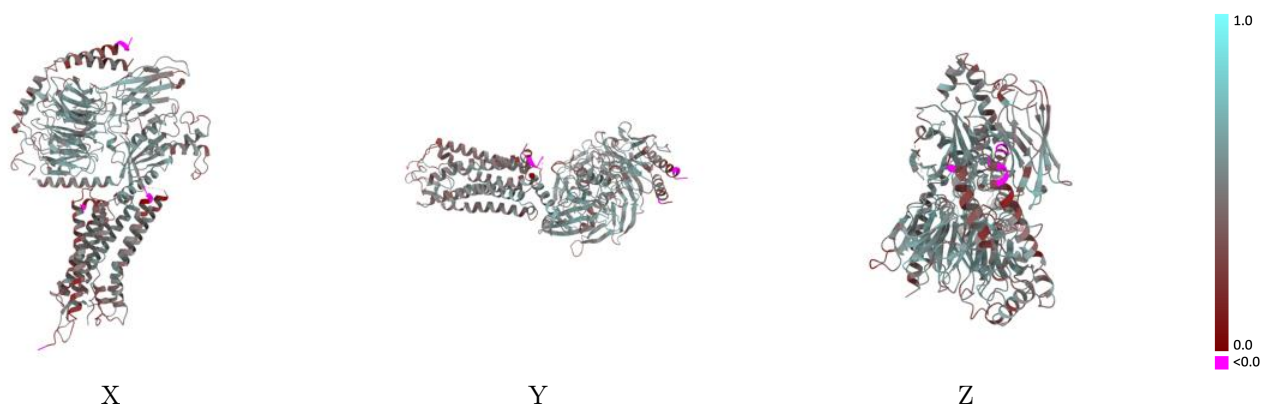
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.1 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](#)



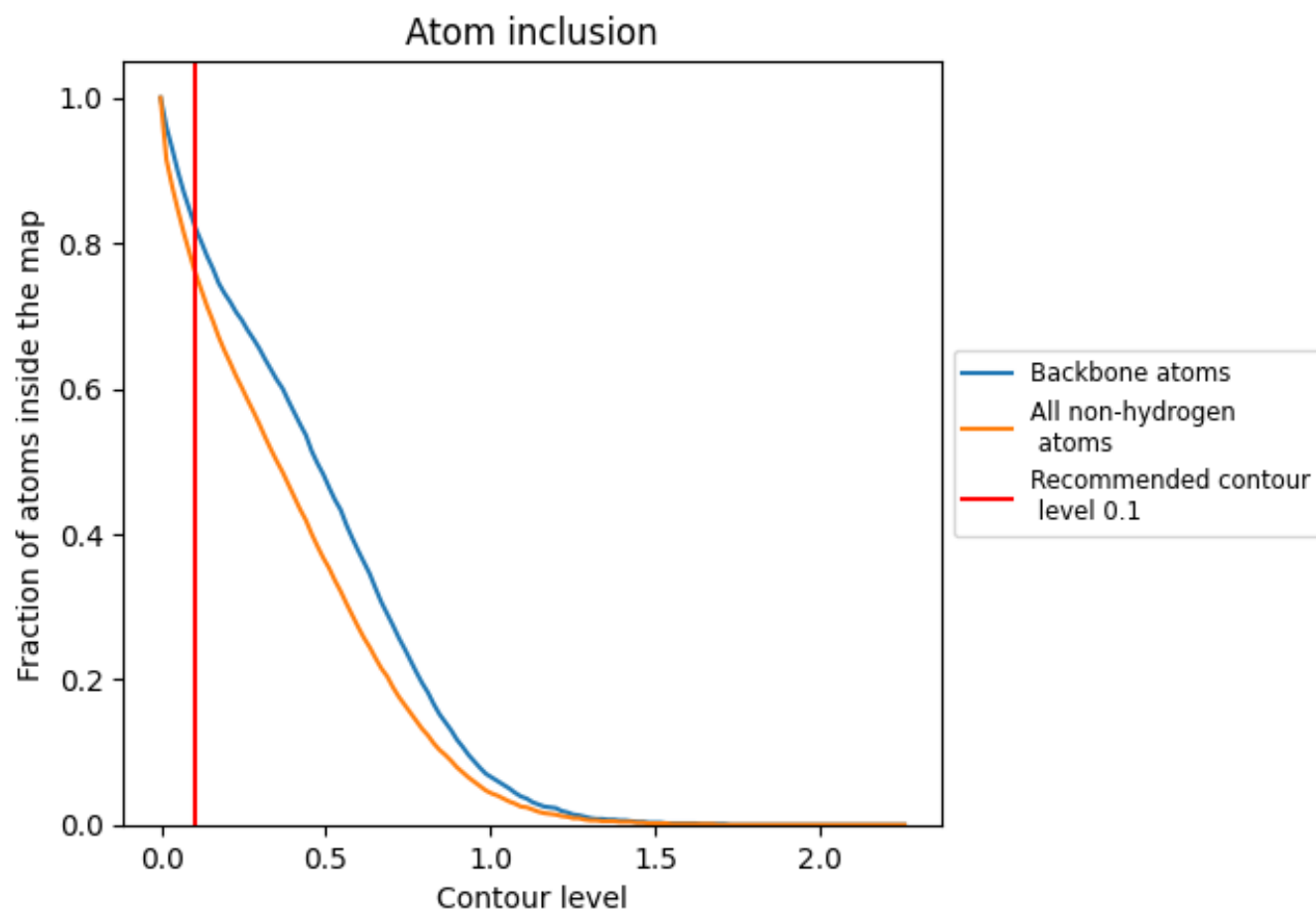
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 76% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7640	0.4660
A	0.7820	0.4940
B	0.8030	0.5070
G	0.6200	0.3710
N	0.7920	0.4890
P	0.9310	0.4750
R	0.7180	0.4040

1.0

0.0

<0.0