



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 07:48 AM UTC

PDB ID : 7OGM / pdb_00007ogm
EMDB ID : EMD-12884
Title : A cooperative PNPase-Hfq-RNA carrier complex facilitates bacterial riboregulation. PNPase-3'ETS(leuZ)-Hfq
Authors : Dendooven, T.; Sinha, D.; Roesoleva, A.; Cameron, T.A.; De Lay, N.; Luisi, B.F.; Bandyra, K.
Deposited on : 2021-05-06
Resolution : 3.70 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.dev132
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) : 2.49

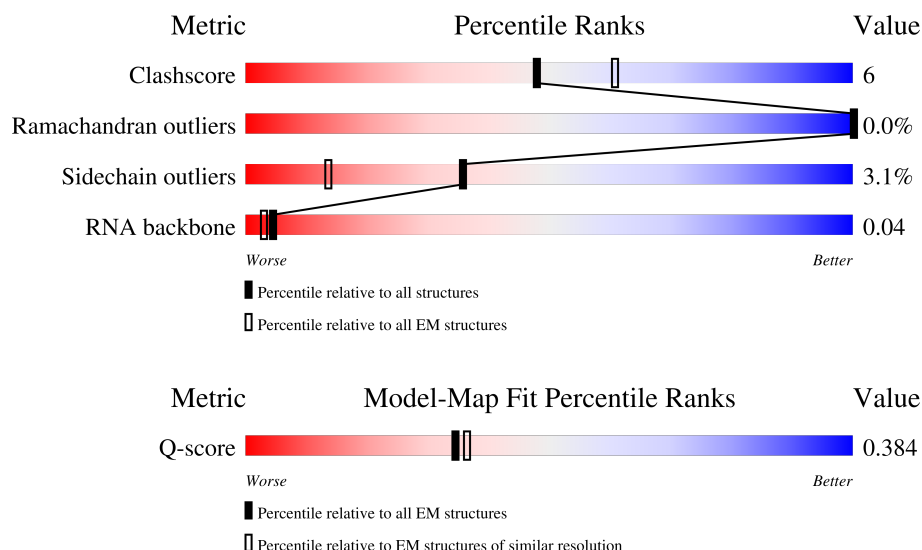
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	D	102	
1	E	102	
1	F	102	

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Mol	Chain	Length	Quality of chain
1	I	102	23%57%5%38%
1	J	102	22%56%6%38%
1	K	102	17%50%11%39%
2	L	711	6%85%11%..
2	N	711	10%88%8%. .
2	O	711	14%90%7%..
3	P	49	8%14%47%37%. .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 17683 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 RNA-binding protein Hfq.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	K	62	Total	C	N	O	0	0
			389	254	64	71		
1	J	63	Total	C	N	O	0	0
			404	266	65	73		
1	I	63	Total	C	N	O	0	0
			406	267	66	73		
1	D	67	Total	C	N	O	0	0
			438	289	69	80		
1	E	61	Total	C	N	O	0	0
			413	276	65	72		
1	F	61	Total	C	N	O	0	0
			390	257	63	70		

- Molecule 2 is a protein called Polyribonucleotide nucleotidyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	693	Total	C	N	O	S	0	0
			4777	3021	847	890	19		
2	N	689	Total	C	N	O	S	0	0
			4841	3046	860	915	20		
2	O	695	Total	C	N	O	S	0	0
			4672	2931	845	878	18		

- Molecule 3 is a RNA chain called 3'ETS(LeuZ).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	P	49	Total	C	N	O	P	0	0
			953	422	162	320	49		

ASN
THR
SER
ALA
GLN
GLN
ASP
SER
SER
GLU
GLU
THR
GLU

• Molecule 1: RNA-binding protein Hfq



MET
ALA
LYS
GLY
GLN
SER
SER
LEU
Q8
I30
I36
S51
H57
A58
T61
V62
V63
P64
S65
R66
P67
V68
SER
HIS
HIS
ASN
ASN
ALA
GLY
GLY
THR
SER
SER
ASN
TYR
HIS
HIS
GLY
SER
SER
SER
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ALA
GLN
GLN
ASP
SER
SER
GLU
GLU
THR
GLU

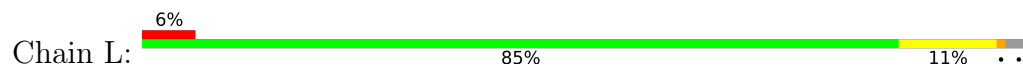
• Molecule 1: RNA-binding protein Hfq



MET
ALA
LYS
GLY
GLN
SER
SER
LEU
Q8
I24
Y25
L26
V27
N28
L32
Q35
I36
E37
V64
I59
S60
P64
R66
P67
V68
SER
HIS
HIS
SER
ASN
ASN
ALA
GLY
GLY
THR
SER
SER
SER
ASN
TYR
HIS
HIS
GLY
SER
SER
SER
ALA
GLN
ASN
THR
SER
ALA
GLN
GLN
ASP

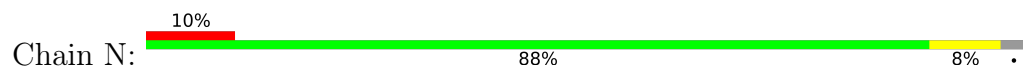
SER
GLU
GLU
THR
GLU

• Molecule 2: Polyribonucleotide nucleotidyltransferase

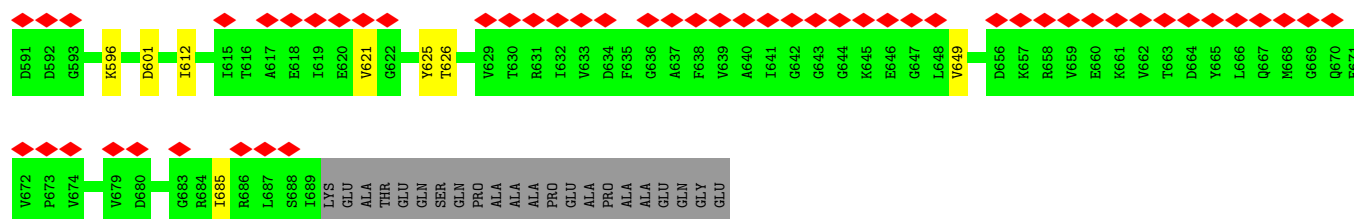


M1
L2
N3
P4
I5
V6
R7
K8
F9
Q10
Y11
G12
Q13
H14
T15
V16
L17
L18
M22
Q26
V33
I39
L102
F103
P104
F107
E110
G133
I143
P144
F145
N146
G147
P148
I157
V162
L163
N164
Q167
D168
E169
K174
V178
V206
I216
L222
A226
W231
N239
L242
V246
L254
V270
I273
L282
A283
E284
D285
E286
T287
L288
L293
I296
D317
G318
R319
R325
G326
L327
D328
V329
R330
L334
P335
R336
L342
F343
T344
R345
G346
Q349
A350
L351
H379
G394
S395
D417
I431
G436
M440
V455
G463
I481
R499
I533
V536
E550
R554
K559
I560
N561
K564
V568
I569
G570
K571
G572
V575
I576
T585
I589
E590
D591
D592
G593
T594
V595
D601
A617
E618
I619
E620
V621
G622
R623
T630
R631
I632
V633
D634
V639
G642
G643
G644
A655
D656
K657
R658
V659
T663
L666
Q667
M668
G669
Q670
E671
V672
P673
L677
E678
V679
D680
R681
A692
T693
GLU
GLN
SER
GLN
PRO
ALA
ALA
ALA
PRO
GLU
ALA
PRO
ALA
ALA
ALA
GLU
GLY
GLU

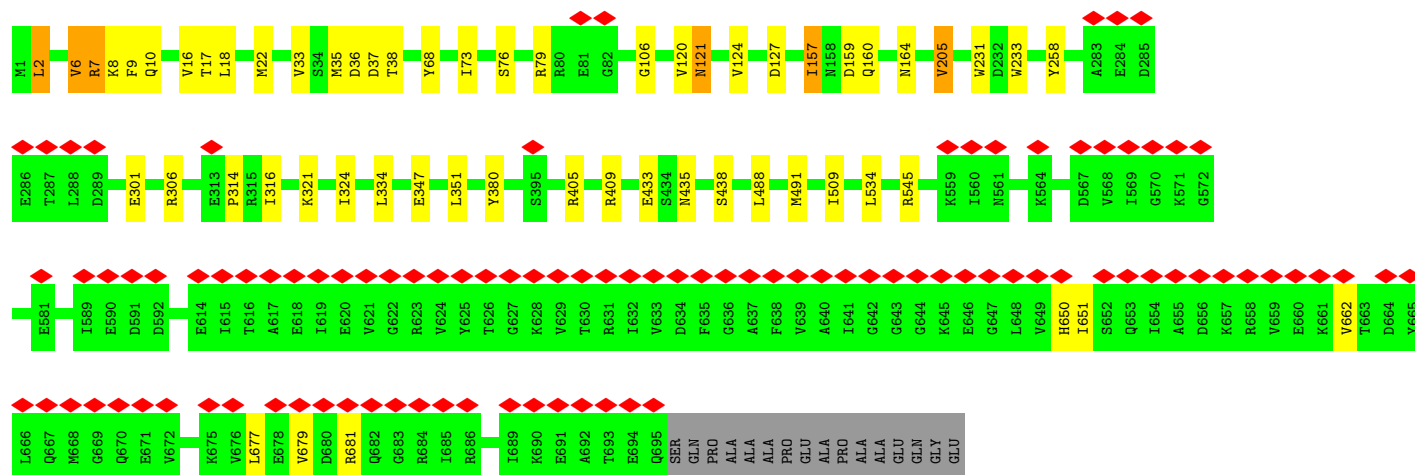
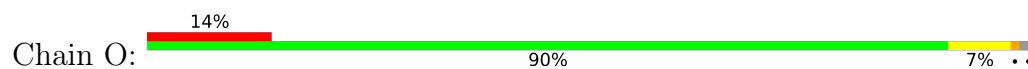
• Molecule 2: Polyribonucleotide nucleotidyltransferase



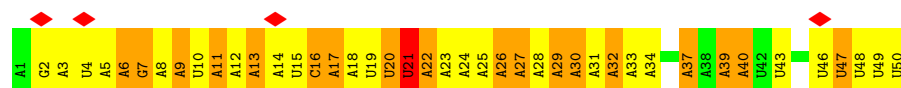
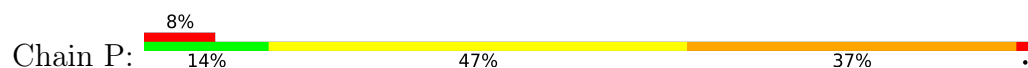
M1
L2
N3
P4
R7
K8
F9
V16
M22
M23
V40
D55
F56
F78
R79
R80
L102
V118
S119
V120
N121
A130
N218
E221
K228
P229
R230
V238
A241
L254
L282
A283
E284
D285
E286
T287
L288
D289
L293
E301
A311
G312
E313
P314
R315
I316
D317
G318
R319
E320
K321
M322
M323
D328
V329
R330
T344
T348
Q349
A359
R360
D361
A362
Q363
V364
R372
V387
V428
E433
G467
L478
I481
E485
L488
G489
D490
I555
D563
K571
G584
E588
I589
E590



• Molecule 2: Polyrribonucleotide nucleotidyltransferase



• Molecule 3: 3'ETS(LeuZ)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	133607	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	53.6	Depositor
Minimum defocus (nm)	-1	Depositor
Maximum defocus (nm)	-2.6	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.176	Depositor
Minimum map value	-1.698	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.065	Depositor
Recommended contour level	0.41	Depositor
Map size ($\text{\AA}$)	319.50003, 319.50003, 319.50003	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.065, 1.065, 1.065	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	D	1.28	1/446 (0.2%)	1.35	0/619
1	E	1.33	1/422 (0.2%)	1.39	0/585
1	F	1.29	0/396	1.37	0/552
1	I	1.30	1/412 (0.2%)	1.43	1/573 (0.2%)
1	J	1.32	0/411	1.36	0/572
1	K	1.35	0/393	1.39	0/547
2	L	1.16	4/4844 (0.1%)	1.47	27/6629 (0.4%)
2	N	1.13	0/4913	1.44	13/6704 (0.2%)
2	O	1.19	2/4739 (0.0%)	1.46	21/6487 (0.3%)
3	P	0.42	0/1063	0.90	4/1651 (0.2%)
All	All	1.15	9/18039 (0.0%)	1.41	66/24919 (0.3%)

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	O	38	THR	C-O	-7.64	1.14	1.23
2	O	164	ASN	C-O	-7.34	1.14	1.24
1	D	45	LEU	C-O	-6.82	1.15	1.24
2	L	330	ARG	C-O	-6.74	1.15	1.23
2	L	18	LEU	C-O	-6.01	1.16	1.23

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	P	20	U	C1'-C2'-O2'	-8.58	98.93	111.80
2	L	9	PHE	CA-C-O	-8.11	112.17	121.58
2	L	9	PHE	CA-CB-CG	7.83	121.63	113.80
2	L	5	ILE	CA-C-O	-7.74	113.46	121.67
2	O	7	ARG	CA-C-N	-7.36	111.85	122.67

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	438	0	394	12	0
1	E	413	0	379	5	0
1	F	390	0	355	5	0
1	I	406	0	375	2	0
1	J	404	0	360	3	0
1	K	389	0	355	8	0
2	L	4777	0	4567	69	0
2	N	4841	0	4617	60	0
2	O	4672	0	4268	47	0
3	P	953	0	484	20	0
All	All	17683	0	16154	201	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 6.

The worst 5 of 201 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)
2:N:555:ILE:HG21	2:N:596:LYS:CE	1.58	1.31
2:N:555:ILE:HG21	2:N:596:LYS:HE2	1.26	1.14
2:N:555:ILE:CG2	2:N:596:LYS:CE	2.25	1.14
2:L:569:ILE:HA	2:L:576:ILE:CD1	1.82	1.09
2:N:555:ILE:CG2	2:N:596:LYS:HE3	1.81	1.08

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	D	65/102 (64%)	62 (95%)	3 (5%)	0	100	100
1	E	59/102 (58%)	58 (98%)	1 (2%)	0	100	100
1	F	59/102 (58%)	57 (97%)	2 (3%)	0	100	100
1	I	61/102 (60%)	59 (97%)	2 (3%)	0	100	100
1	J	61/102 (60%)	60 (98%)	1 (2%)	0	100	100
1	K	60/102 (59%)	60 (100%)	0	0	100	100
2	L	691/711 (97%)	657 (95%)	34 (5%)	0	100	100
2	N	687/711 (97%)	666 (97%)	20 (3%)	1 (0%)	48	78
2	O	693/711 (98%)	668 (96%)	25 (4%)	0	100	100
All	All	2436/2745 (89%)	2347 (96%)	88 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	N	4	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	39/89 (44%)	39 (100%)	0	100	100
1	E	38/89 (43%)	38 (100%)	0	100	100
1	F	34/89 (38%)	31 (91%)	3 (9%)	9	33
1	I	37/89 (42%)	37 (100%)	0	100	100
1	J	35/89 (39%)	33 (94%)	2 (6%)	18	45
1	K	34/89 (38%)	32 (94%)	2 (6%)	18	44
2	L	438/575 (76%)	418 (95%)	20 (5%)	24	49
2	N	454/575 (79%)	448 (99%)	6 (1%)	61	71
2	O	397/575 (69%)	383 (96%)	14 (4%)	32	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1506/2259 (67%)	1459 (97%)	47 (3%)	36 57

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	N	321	LYS
2	O	10	GLN
2	N	348	THR
2	N	621	VAL
2	O	33	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
2	O	200	GLN
2	O	269	GLN
2	O	217	GLN
2	N	291	ASN
2	O	64	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	P	47/49 (95%)	40 (85%)	5 (10%)

5 of 40 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	P	2	G
3	P	3	A
3	P	4	U
3	P	5	A
3	P	6	A

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	P	2	G
3	P	9	A

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Mol	Chain	Res	Type
3	P	10	U
3	P	29	A
3	P	31	A

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	P	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	P	40:A	O3'	42:U	P	9.61

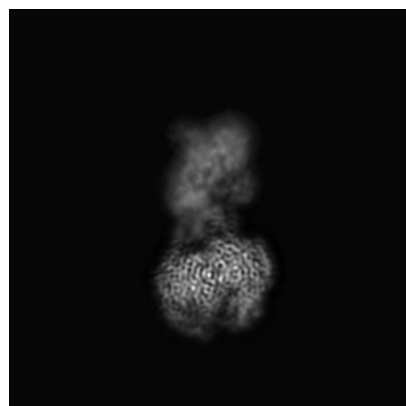
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12884. These allow visual inspection of the internal detail of the map and identification of artifacts.

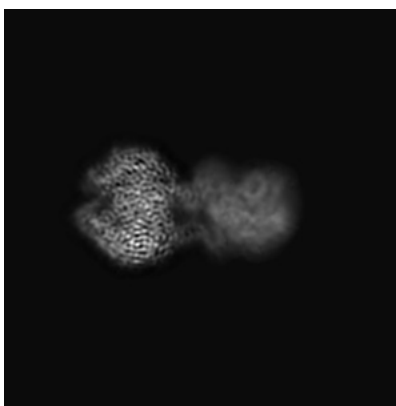
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

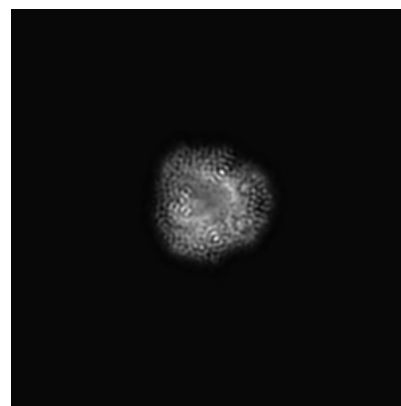
6.1.1 Primary map



X

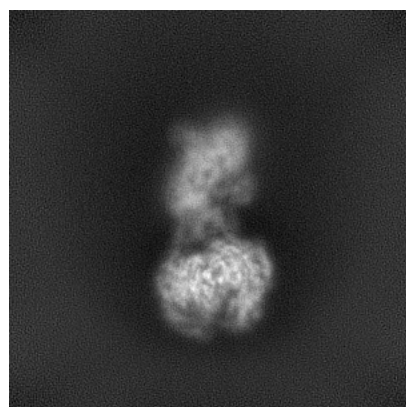


Y

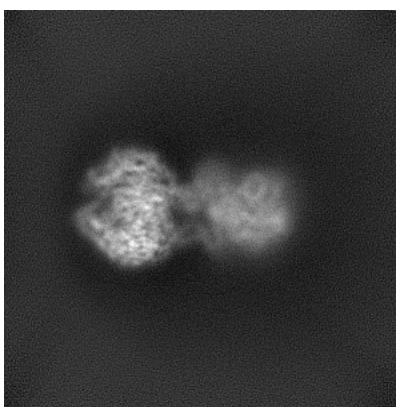


Z

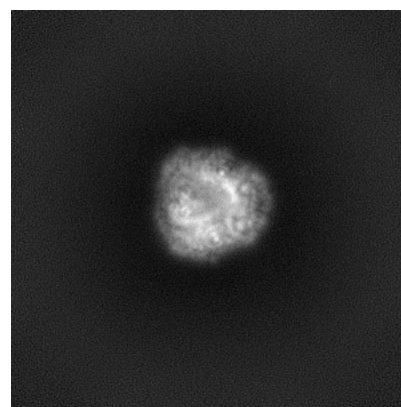
6.1.2 Raw map



X



Y

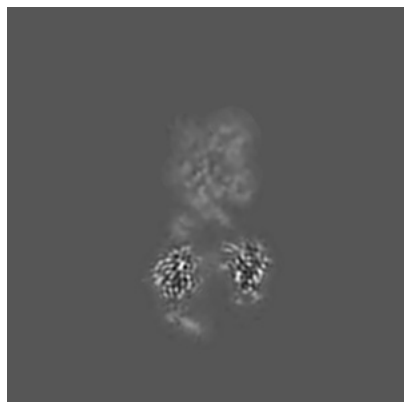


Z

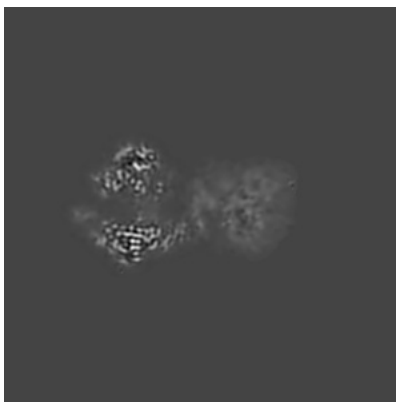
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

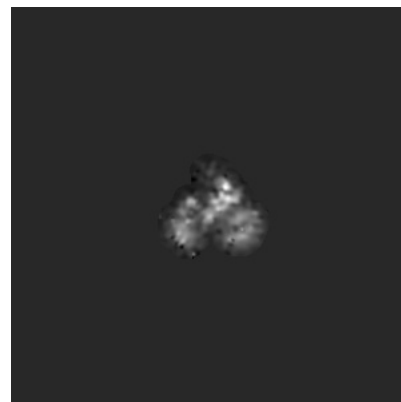
6.2.1 Primary map



X Index: 150

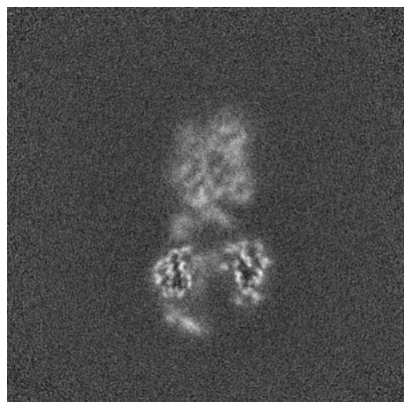


Y Index: 150

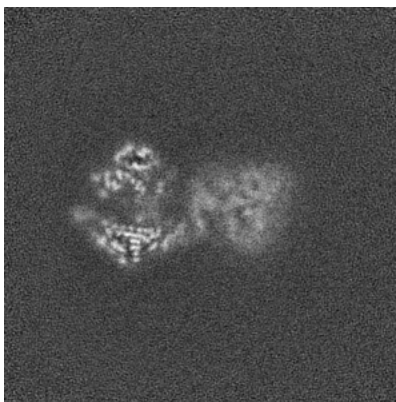


Z Index: 150

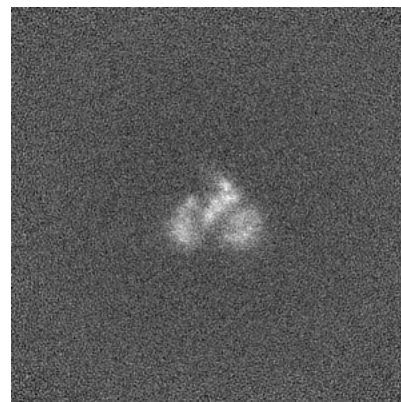
6.2.2 Raw map



X Index: 150



Y Index: 150

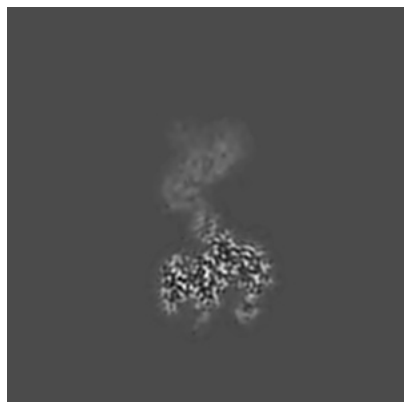


Z Index: 150

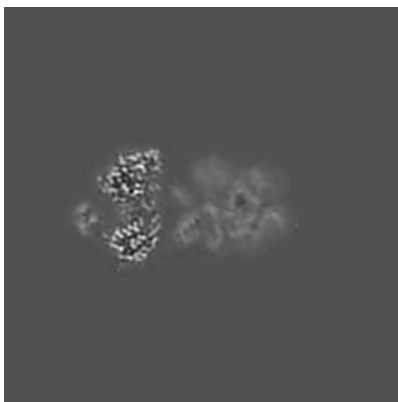
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

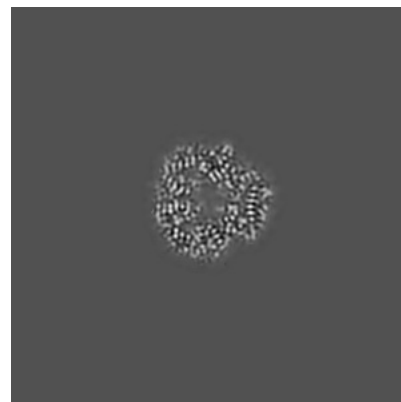
6.3.1 Primary map



X Index: 128

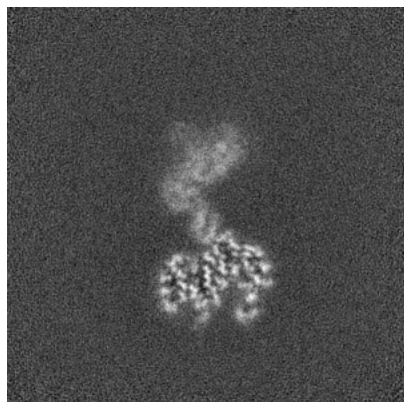


Y Index: 141

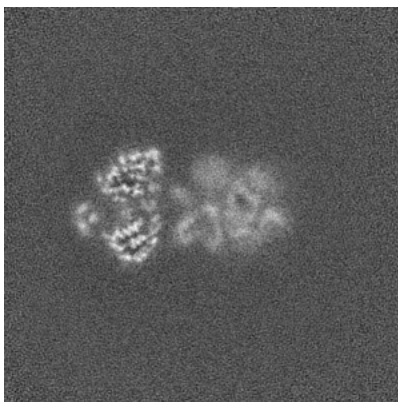


Z Index: 100

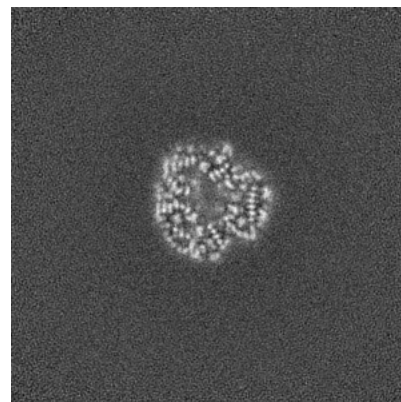
6.3.2 Raw map



X Index: 128



Y Index: 141

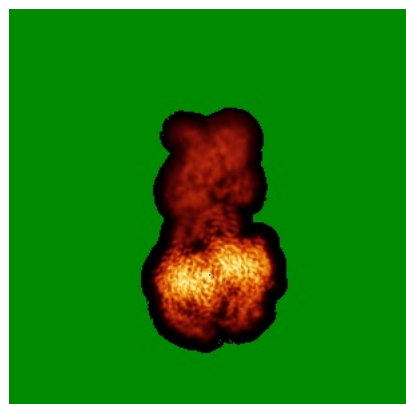


Z Index: 99

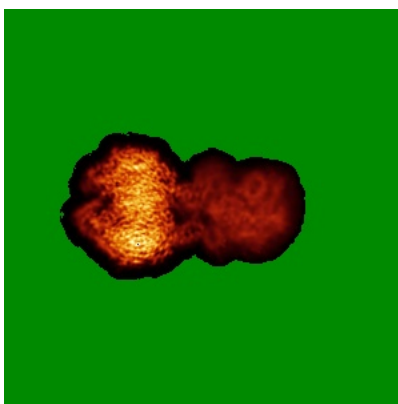
The images above show the largest variance slices of the map in three orthogonal directions.

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

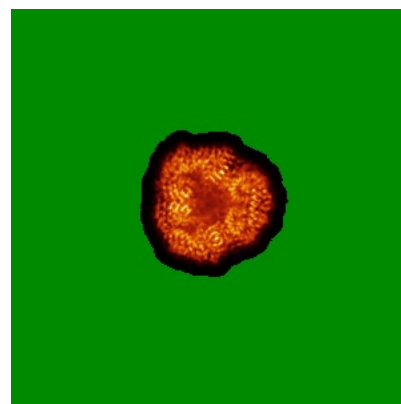
6.4.1 Primary map



X

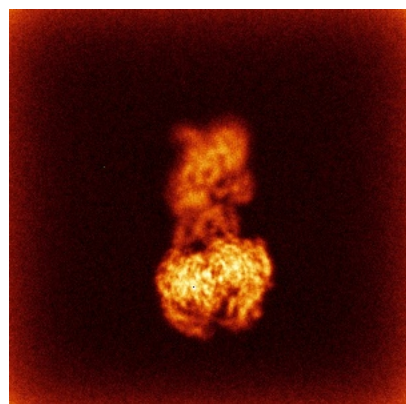


Y

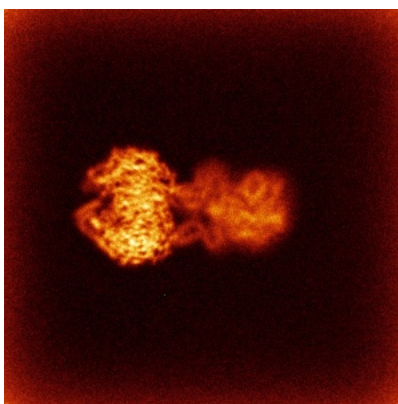


Z

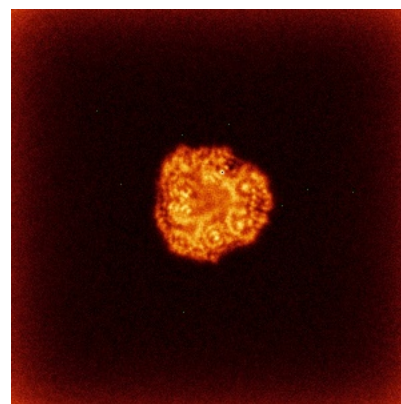
6.4.2 Raw map



X



Y

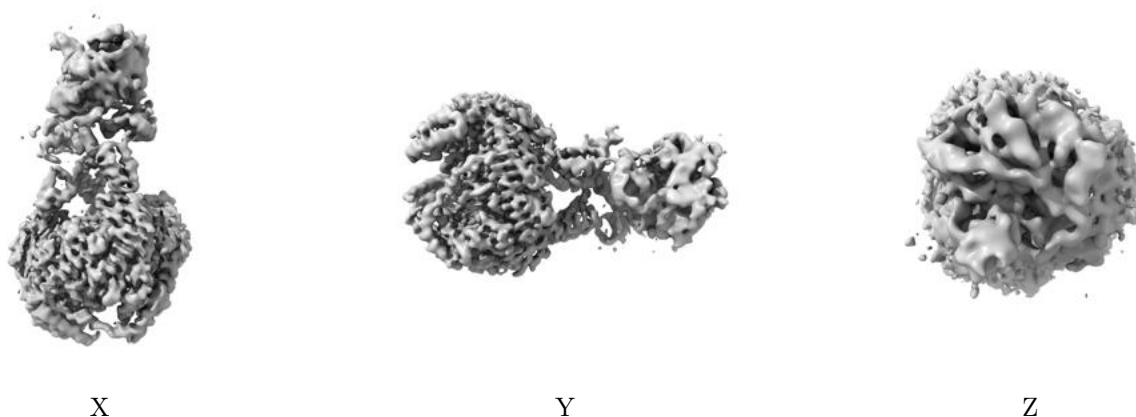


Z

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.

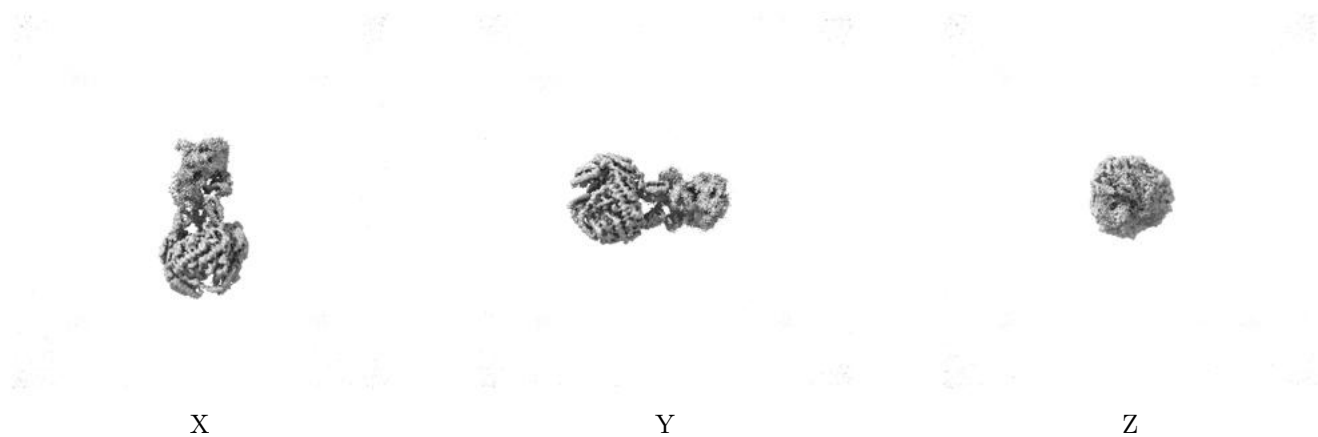
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.41. 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.

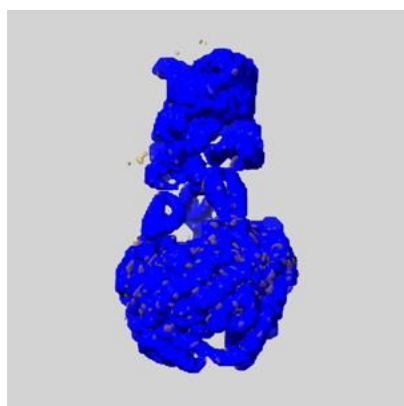
6.6 Mask visualisation [i](#)

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

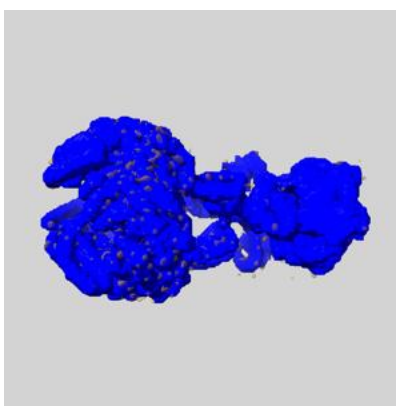
A mask typically either:

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

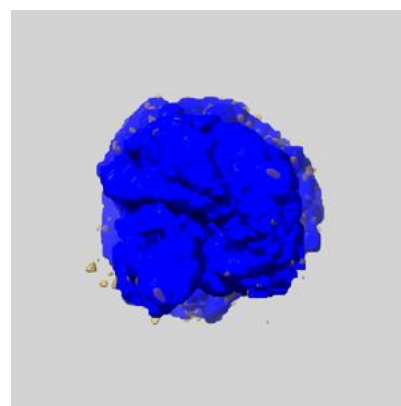
6.6.1 emd_12884_msk_1.map [i](#)



X



Y

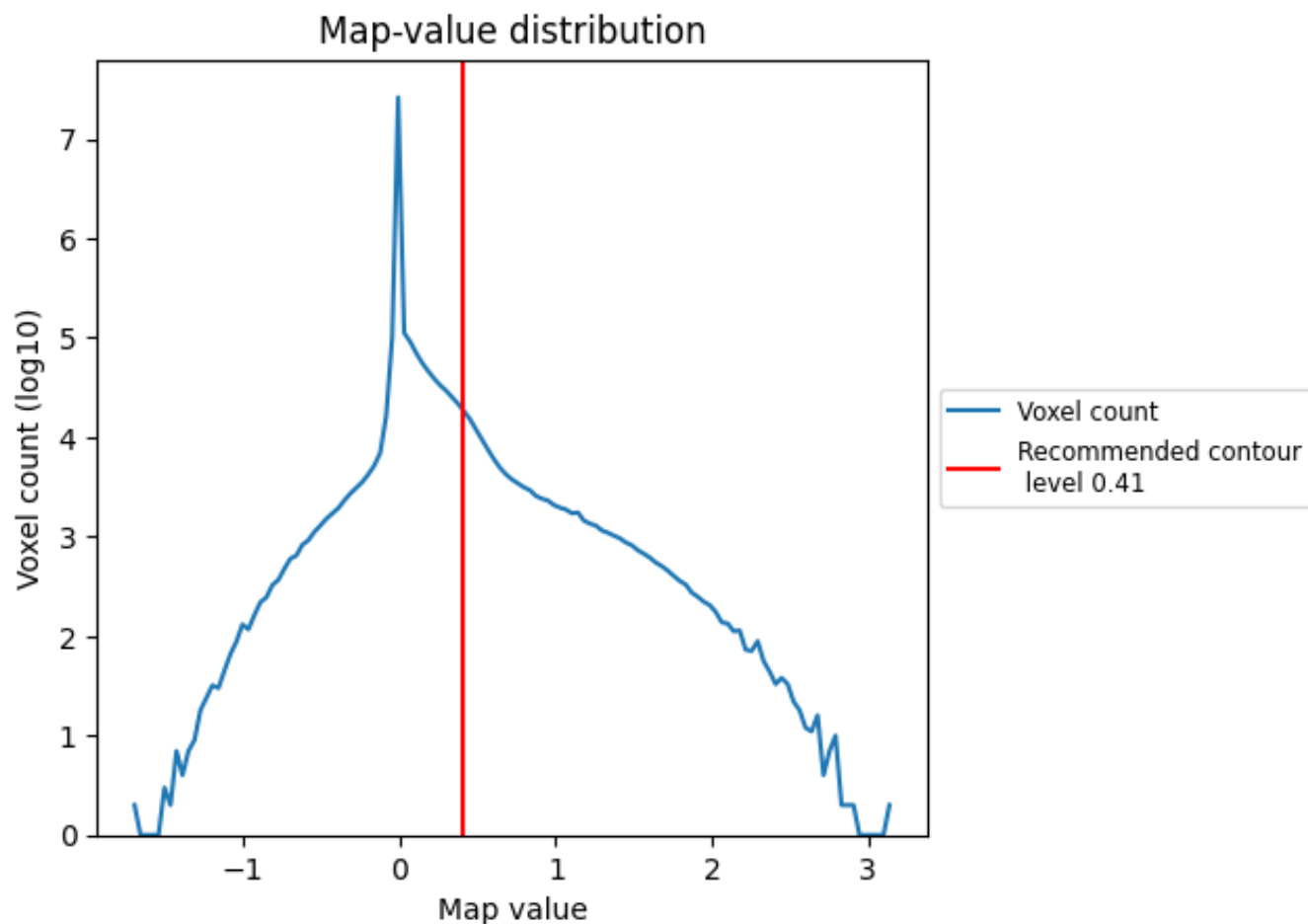


Z

7 Map analysis [i](#)

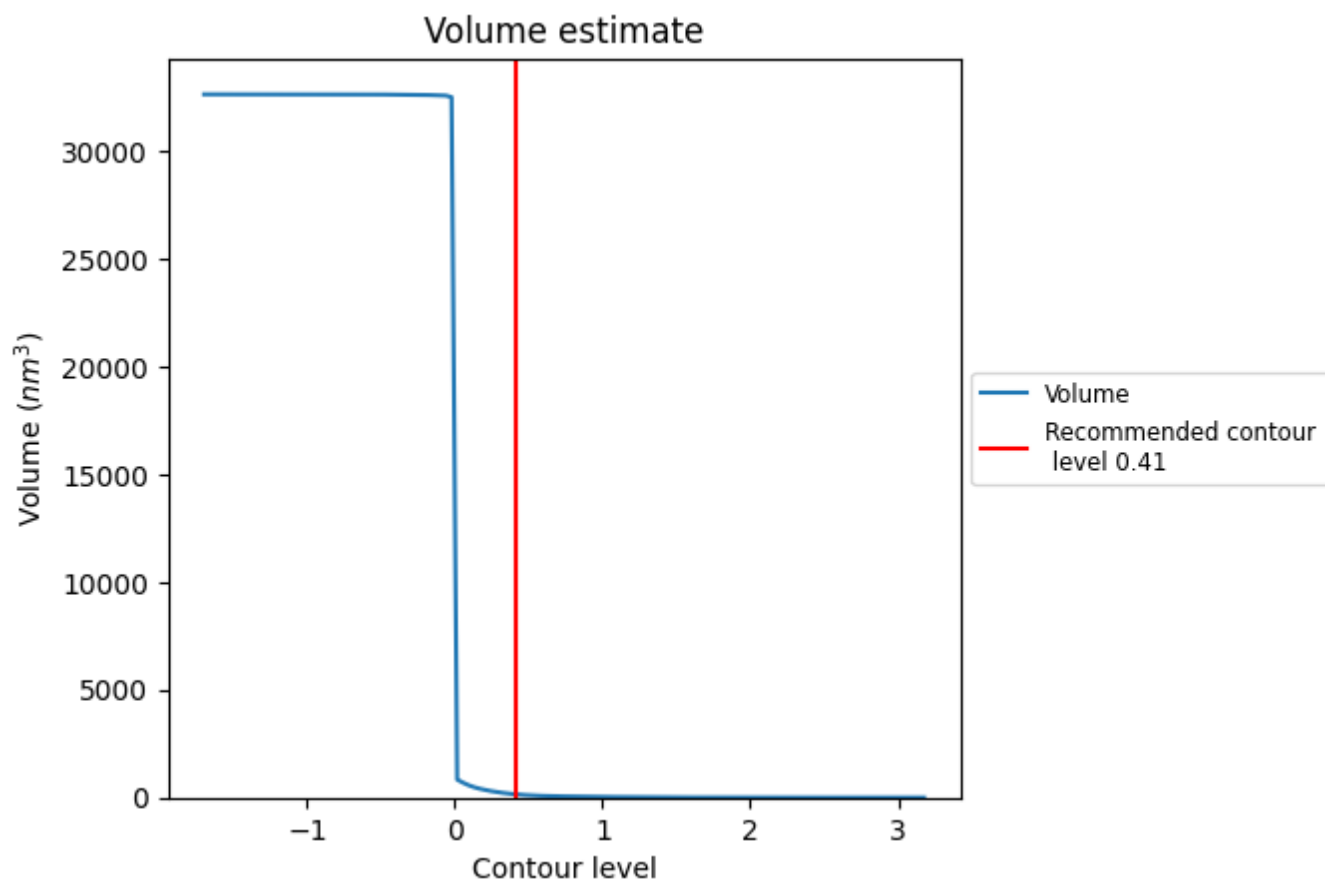
This section contains the results of statistical analysis of the map.

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.

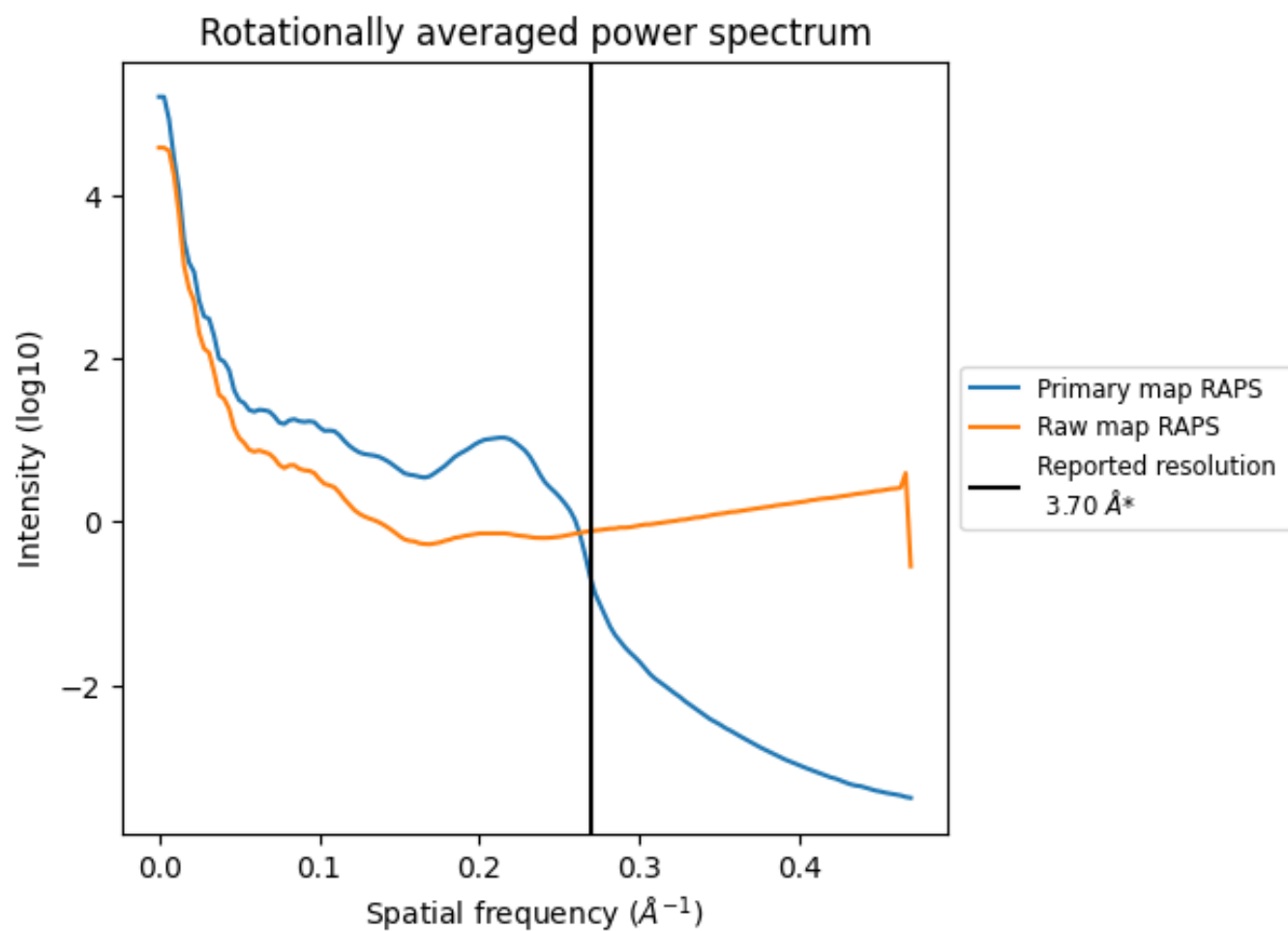
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 152 nm³; this corresponds to an approximate mass of 138 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 ⓘ

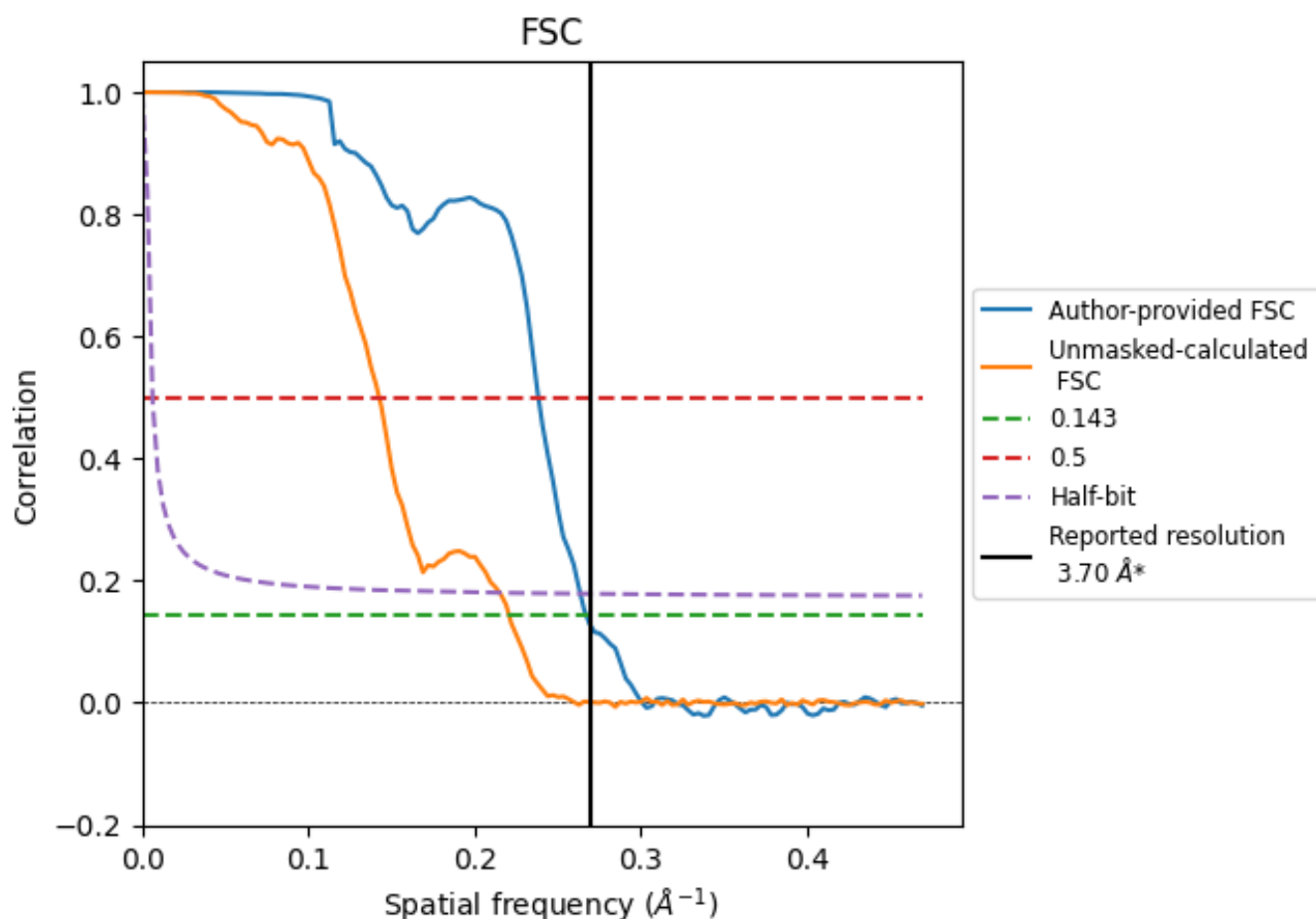


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

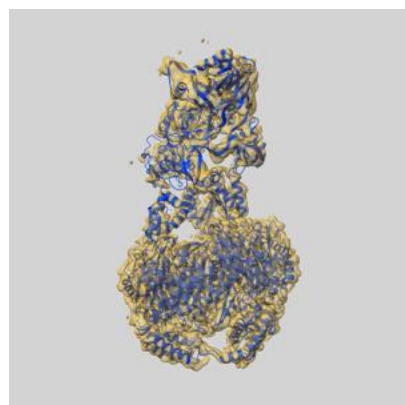
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.74	4.19	3.79
Unmasked-calculated*	4.53	7.01	4.65

*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 4.53 differs from the reported value 3.7 by more than 10 %

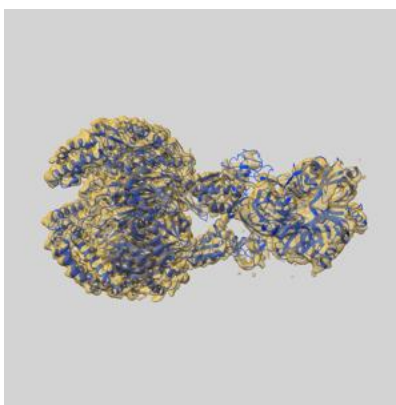
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12884 and PDB model 7OGM. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

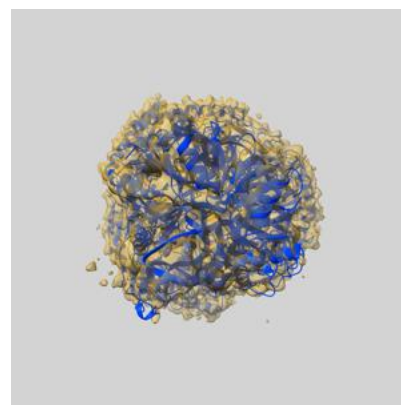
9.1 Map-model overlay [i](#)



X



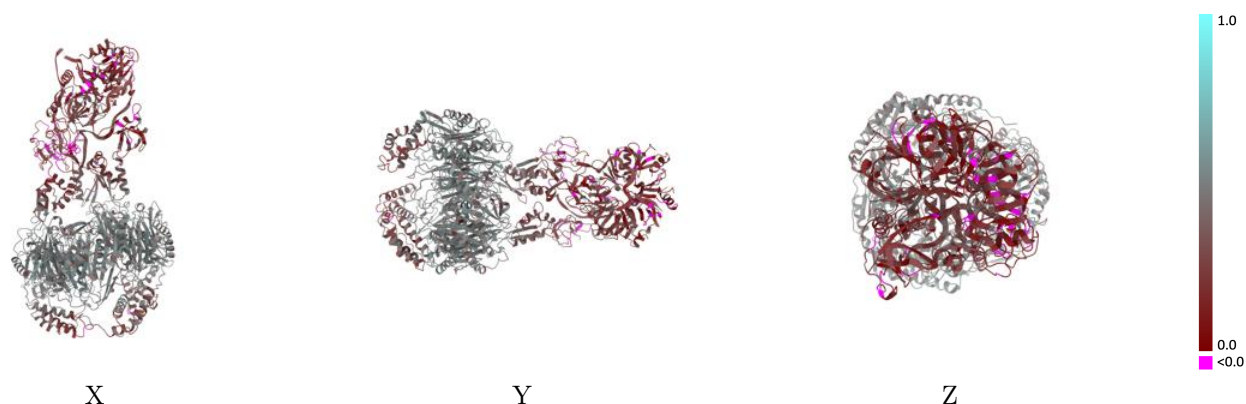
Y



Z

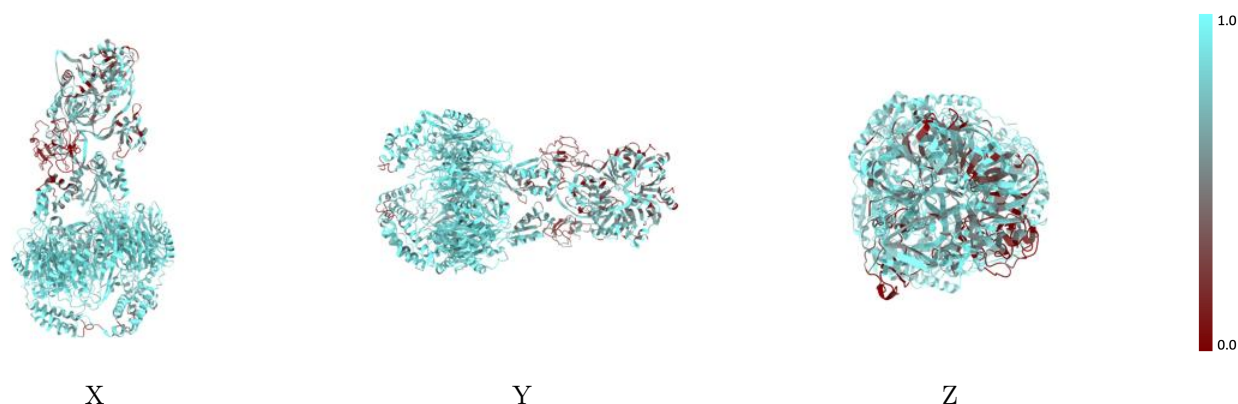
The images above show the 3D surface view of the map at the recommended contour level 0.41 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



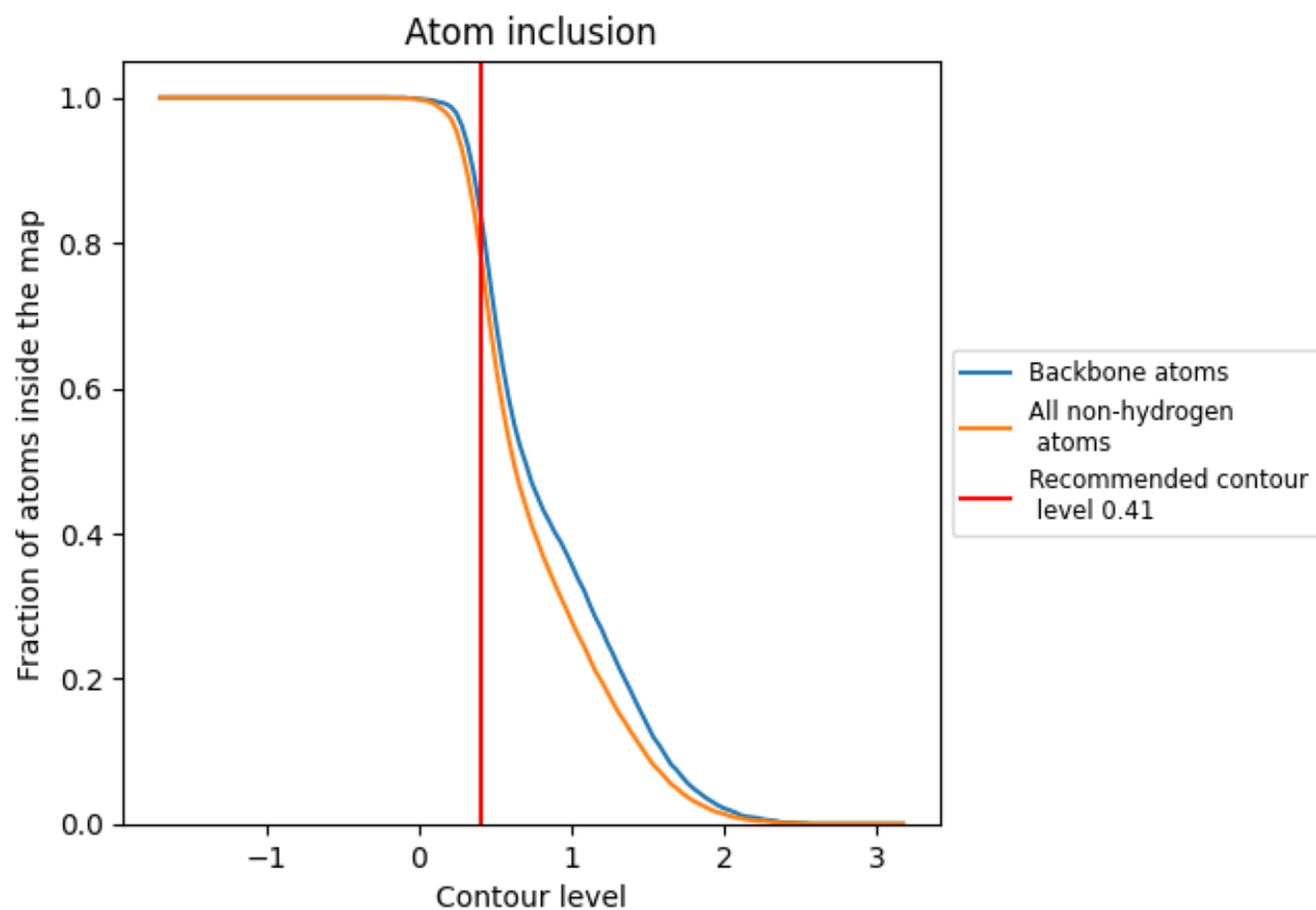
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.41).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 77% 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 (0.41) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7740	0.3840
D	0.6420	0.2450
E	0.7030	0.2840
F	0.6700	0.2220
I	0.5210	0.1750
J	0.5470	0.1710
K	0.5680	0.1420
L	0.8300	0.4310
N	0.8010	0.4210
O	0.7840	0.4210
P	0.7250	0.2290

1.0
0.0
<0.0