wwPDB EM Validation Summary Report (i)

Oct 18, 2026 – 04:38 PM EDT

PDB ID	:	12TT / pdb_000012tt
EMDB ID	:	EMD-76753
Title	:	2 molecules of Fab NORO-320 bound to A-A' VP1 dimer of GII.4 Syd VLP (T=1) Right side
Authors	:	Apostol, C.V.; Anish, R.; Pham, S.; Prasad, B.V.V.
Deposited on	:	2026-04-18
Resolution	:	7.50 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:

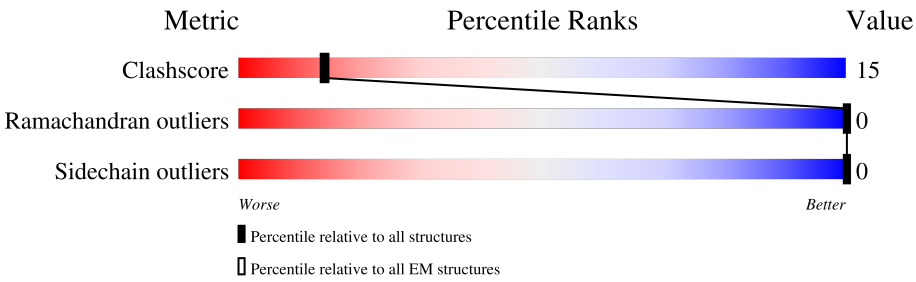
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

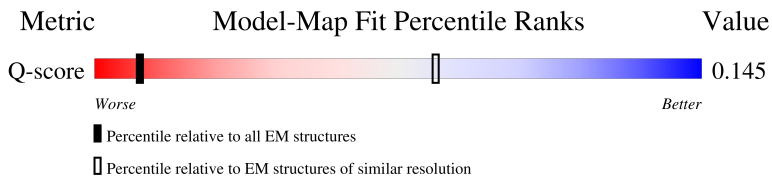
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 7.50 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	436 (7.00 - 8.00)

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	B	540	51% 40% 9%
1	F	540	56% 35% 9%
2	E	238	11% 73% 23% •
2	H	238	8% 67% 29% •

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Mol	Chain	Length	Quality of chain
3	G	219	26% 74% 25%
3	I	219	15% 77% 22%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 14372 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 VP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	B	491	3831	2446	653	718	14	0	0
1	F	492	3839	2450	655	720	14	0	0

- Molecule 2 is a protein called Fab NORO-320 Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	E	228	1688	1063	280	337	8	0	0
2	H	228	1688	1063	280	337	8	0	0

- Molecule 3 is a protein called Fab NORO-320 Light Chain.

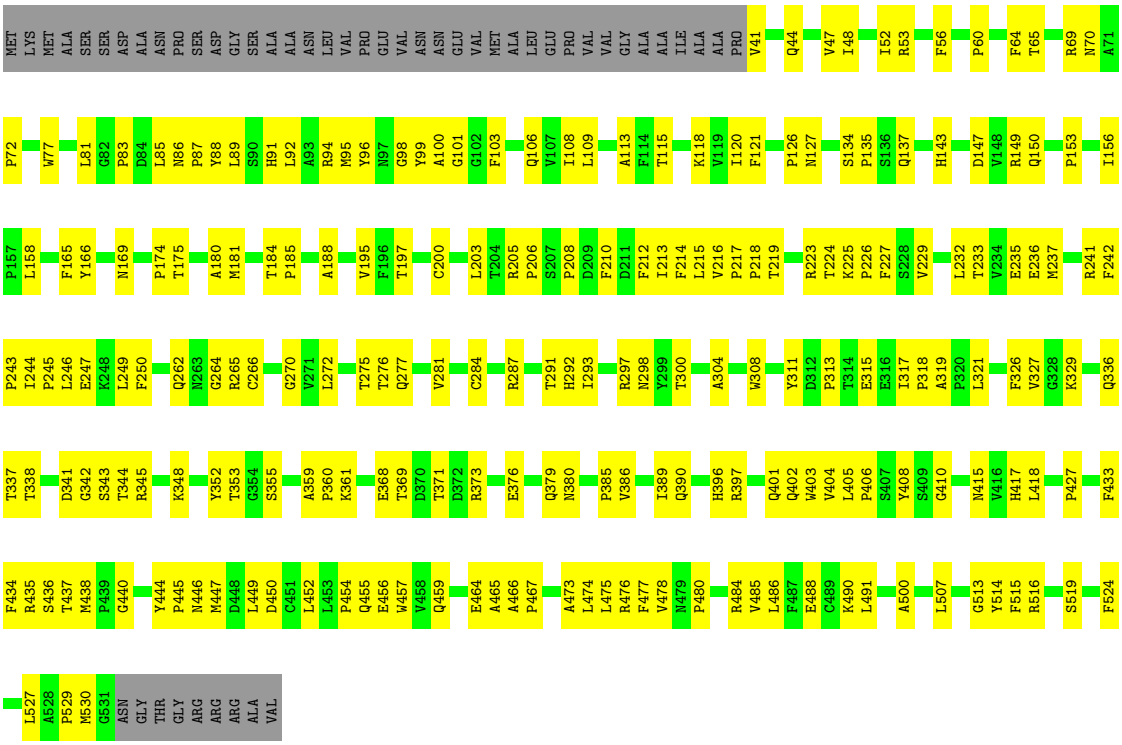
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	G	217	1663	1041	280	336	6	0	0
3	I	217	1663	1041	280	336	6	0	0

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.

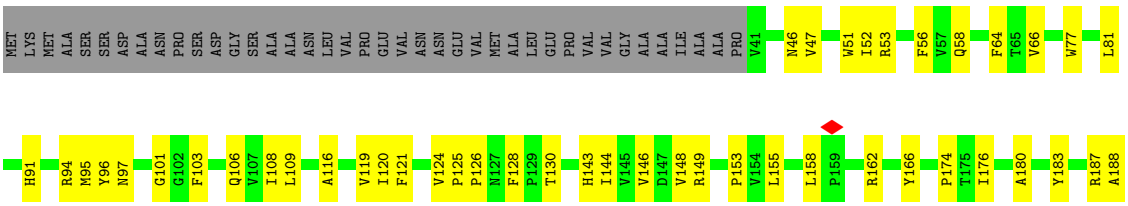
- Molecule 1: VP1

Chain B: 51% 40% 9%



- Molecule 1: VP1

Chain F: 56% 35% 9%



N189 N190 T197 L203 T204 R205 P208 D209 F210 D211 F214 L215 V216 P217 P218 V229 V234 M237 T238 N239 S240 R241 F242 P243 I244 P245 L246 L249 F250 T251 G252 V258 V259 Q260 P261 Q262 R265 C266 T267 T268 L273 G274 T275 T276 Q277 L278 S279 P280 V281

R287 V290 T291 H292 R297 N298 Y299 T300 M301 N302 L303 Q306 T314 I317 P318 A319 P320 D325 F326 V327 G328 K329 G332 V333 L334 T335 Q336 S343 T344 R345 G346 H347 K348 Y352 T353 G354 S355 A356 D357 F358 A359 P360 K361 L362 G363 R364 V365 Q366 F367 E368

T369 D372 R373 D374 F375 E376 A377 T381 K382 F383 V388 I389 Q390 H396 R397 N398 E399 P400 Q401 Q402 W403 V404 L405 P406 S409 G410 R411 N412 V422 E429 Q430 L431 L432 F433 F434 R435 S436 Y444 P445 N446 L449 D450 C451 L452 L453 P454 Q455 E456 W457 V458 Q459

Y460 F461 E464 Q469 L475 R476 F477 V478 N479 P480 R484 K490 L491 H492 K493 S494 G495 Y496 V497 T498 V499 A500 Q504 H505 I509 P510 P511 Y514 F515 R516 W520 L527 N532 GLY THR GLY ARG ARG ARG ALA VAL

• Molecule 2: Fab NORO-320 Heavy Chain

Chain E: 11% 73% 23%

Q1 L4 V5 Q6 K19 K23 S30 S35 Q39 A40 Q43 G44 L45 E46 W47 M48 G49 G50 I51 I52 P53 I54 F55 T58 N59 Y60 D73 G77 T78 M81 R87 S88 E89 Y95 C96 A97 R98 D99 R100 V101 Y104 S107 ARG ARG PHE

SER THR LYS GLY A115 M116 W117 M122 D123 V124 W125 G126 P145 L146 A147 P148 S149 S150 K151 S152 T153 S154 G155 G156 T157 A158 A159 L160 V164 P169 V172 W176 F188 P189 A190 Y198 S199 L200 V206 P207 S208 S209 S210 L211 G212 T213 Q214 T215 Y216 I217 C218

N221 H222 K223 P224 K231 K232 V233 E234 P235 LYS SER CYS

• Molecule 2: Fab NORO-320 Heavy Chain

Chain H: 8% 67% 29%

Q1 L4 V5 Q6 K12 K19 S31 S35 W36 Q39 A40 Q43 G44 L45 E46 W47 M48 G49 G50 I51 F55 T58 N59 Y60 A61 T69 D73 E74 G77 M81 E82 R87 S88 E89 D90 T91 Y94 Y95 C96 A97 R100 V101 Y104

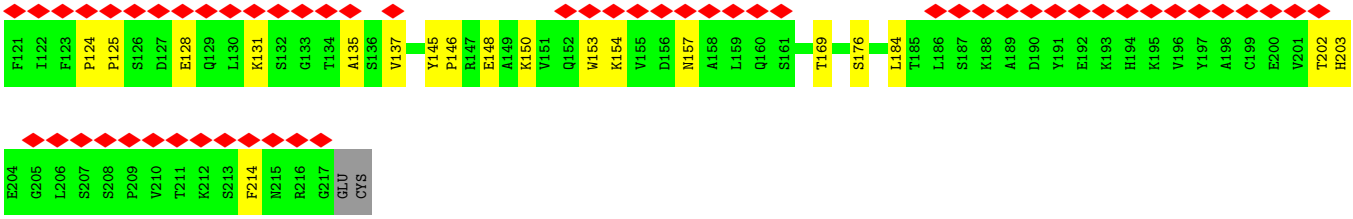
S107 ARG ARG PHE SER THR LYS GLY A115 M116 W117 Y120 G121 M122 W125 G126 V131 T132 V133 P145 S150 K151 S152 T153 S154 G155 G156 T157 A158 A159 L160 V164 V172 T173 V174 S175 W176 N177 L181 T187 A190 V191 L192 Q193 L197 Y198 S199 L200

S201 S202 V206 P207 S208 S209 S210 L211 G212 T213 Q214 T215 Y216 I217 C218 N219 V220 N221 H222 K223 P224 K231 K232 V233 E234 P235 LYS SER CYS

• Molecule 3: Fab NORO-320 Light Chain

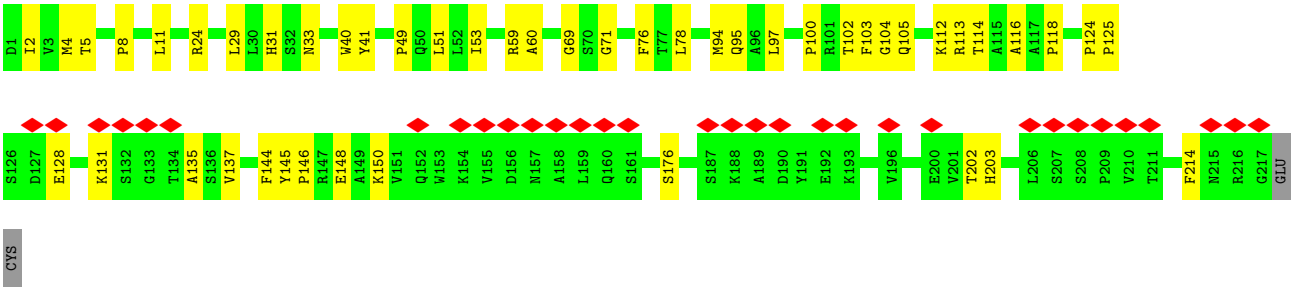
Chain G: 26% 74% 25%

D1 I2 T5 P8 L11 C23 Q27 Y35 L38 D39 W40 Y41 L42 Q43 K44 Q47 S48 P49 Q50 L51 L52 I53 R59 A60 V63 G71 F76 T77 L78 Y91 Y92 C93 M94 Q95 T102 F103 G104 Q105 K112 R113 T114 A115 A116 V120



- Molecule 3: Fab NORO-320 Light Chain

Chain I:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	72670	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 ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.193	Depositor
Minimum map value	-0.063	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	604.80005, 604.80005, 604.80005	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	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	B	0.16	0/3947	0.39	1/5410 (0.0%)
1	F	0.14	0/3955	0.38	0/5421
2	E	0.13	0/1728	0.33	0/2354
2	H	0.13	0/1728	0.31	0/2354
3	G	0.11	0/1699	0.27	0/2307
3	I	0.10	0/1699	0.26	0/2307
All	All	0.14	0/14756	0.35	1/20153 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	386	VAL	N-CA-C	-5.05	108.58	113.53

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	217	PRO	Peptide

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	B	3831	0	3699	160	0
1	F	3839	0	3705	143	0
2	E	1688	0	1658	43	0
2	H	1688	0	1658	48	0
3	G	1663	0	1623	43	0
3	I	1663	0	1623	31	0
All	All	14372	0	13966	439	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 15.

The worst 5 of 439 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:F:237:MET:HE3	1:F:238:THR:H	1.40	0.87
1:F:120:ILE:HD11	1:F:143:HIS:HB2	1.57	0.86
1:B:237:MET:HG2	1:B:246:LEU:HB2	1.60	0.84
1:F:357:ASP:HB3	1:F:366:GLN:HB2	1.62	0.81
1:B:440:GLY:HA2	1:B:447:MET:HE3	1.61	0.81

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	B	489/540 (91%)	460 (94%)	29 (6%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	490/540 (91%)	456 (93%)	34 (7%)	0	100	100
2	E	224/238 (94%)	212 (95%)	12 (5%)	0	100	100
2	H	224/238 (94%)	218 (97%)	6 (3%)	0	100	100
3	G	215/219 (98%)	213 (99%)	2 (1%)	0	100	100
3	I	215/219 (98%)	213 (99%)	2 (1%)	0	100	100
All	All	1857/1994 (93%)	1772 (95%)	85 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	424/459 (92%)	424 (100%)	0	100	100
1	F	425/459 (93%)	425 (100%)	0	100	100
2	E	192/201 (96%)	192 (100%)	0	100	100
2	H	192/201 (96%)	192 (100%)	0	100	100
3	G	190/192 (99%)	190 (100%)	0	100	100
3	I	190/192 (99%)	190 (100%)	0	100	100
All	All	1613/1704 (95%)	1613 (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. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	532	ASN
2	E	43	GLN
2	H	177	ASN
2	E	39	GLN
2	E	186	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)

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.

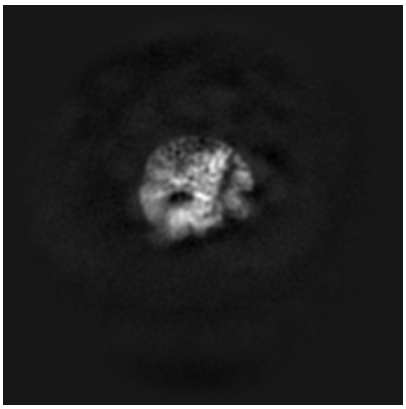
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-76753. These allow visual inspection of the internal detail of the map and identification of artifacts.

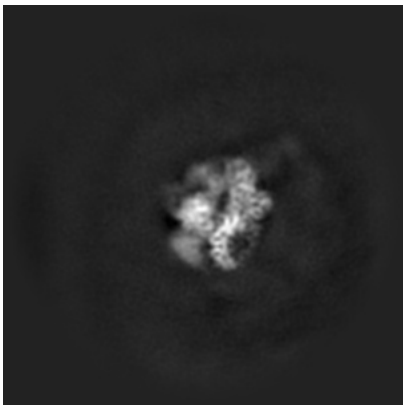
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

6.1.1 Primary map



X



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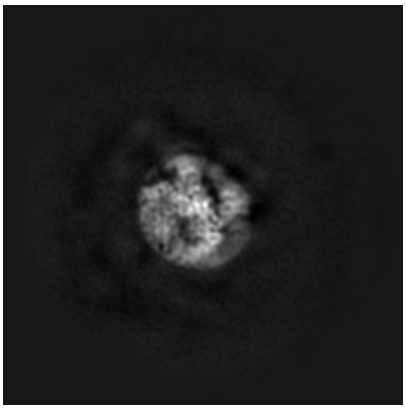
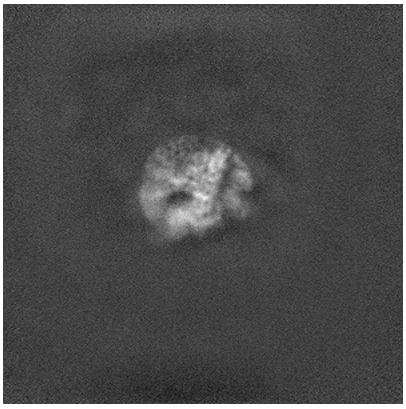


Z

6.1.2 Raw map



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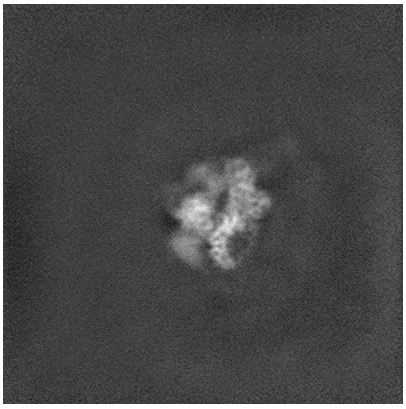
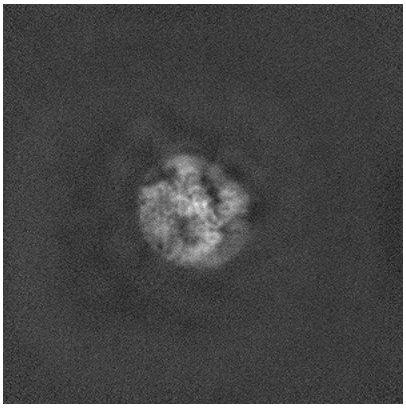


Y

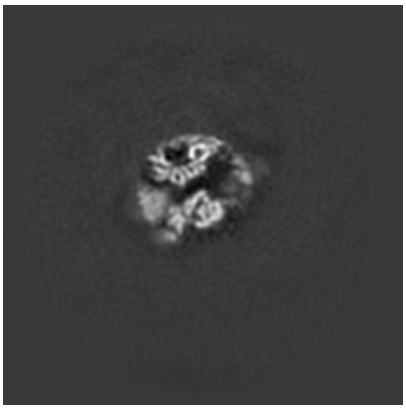


Z

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

6.2 Central slices (i)

6.2.1 Primary map



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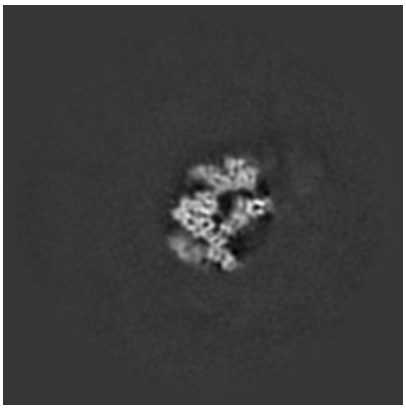

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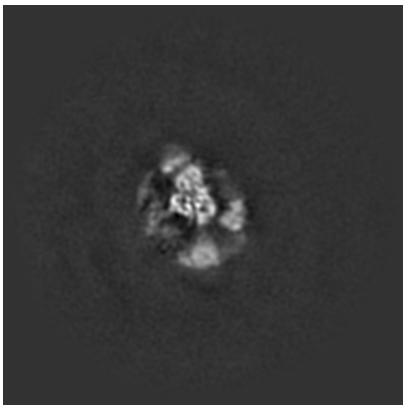
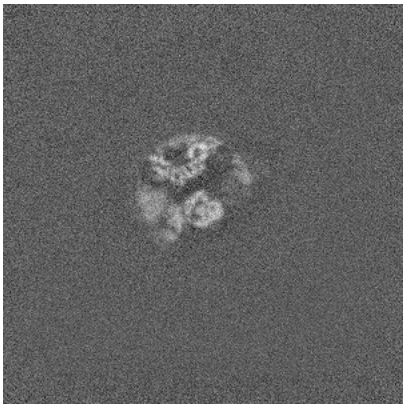
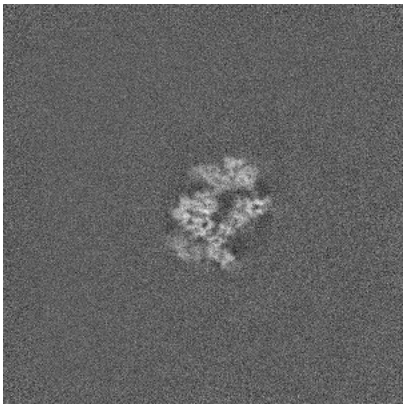


Z Index: 280

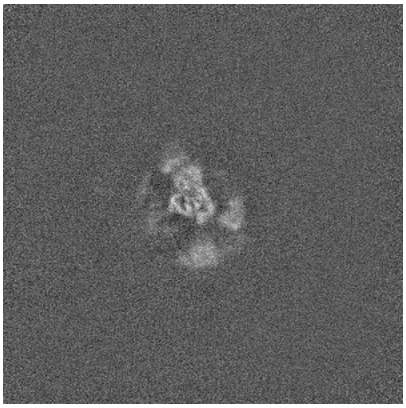
6.2.2 Raw map



X Index: 280



Y Index: 280

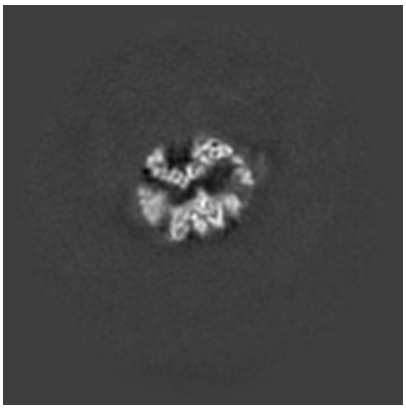


Z Index: 280

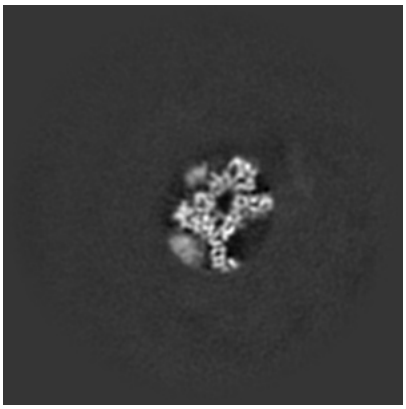
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 272



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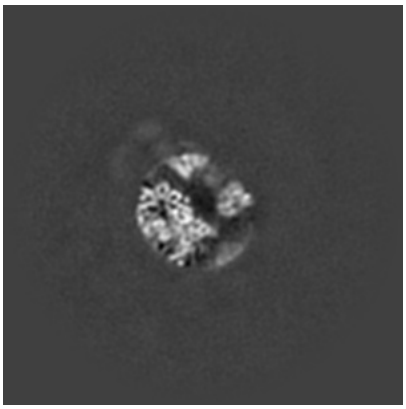
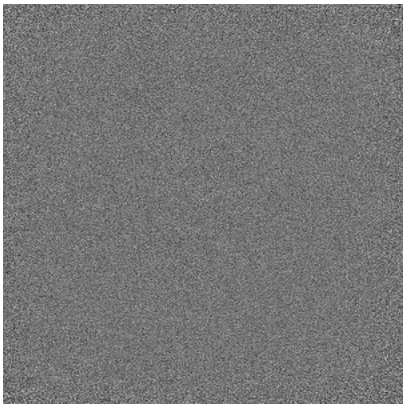
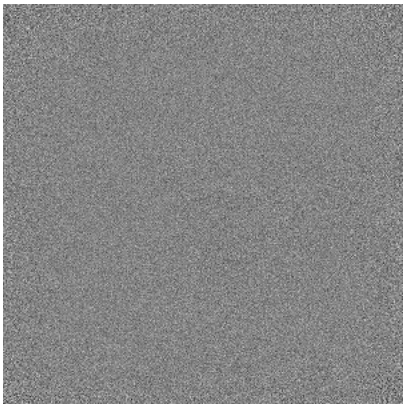


Z Index: 313

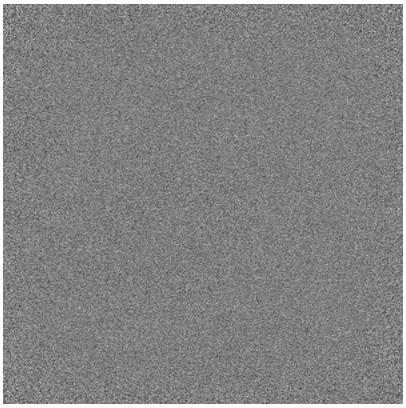
6.3.2 Raw map



X Index: 559



Y Index: 559

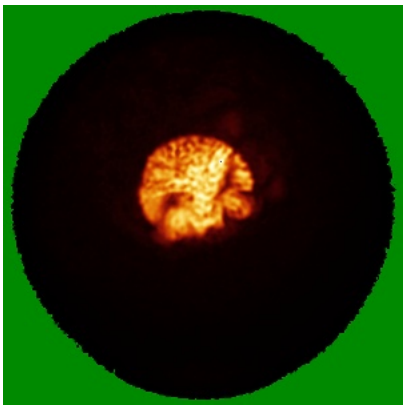


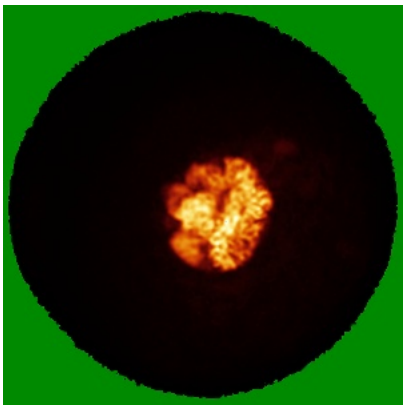
Z Index: 559

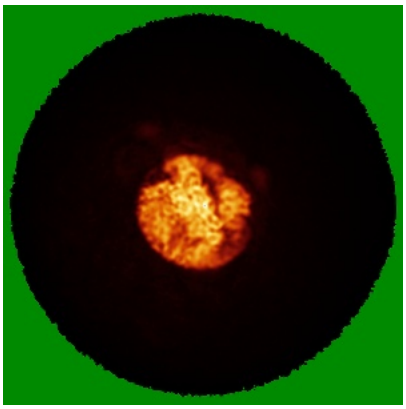
The images above show the largest variance slices of the map in three orthogonal directions.

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

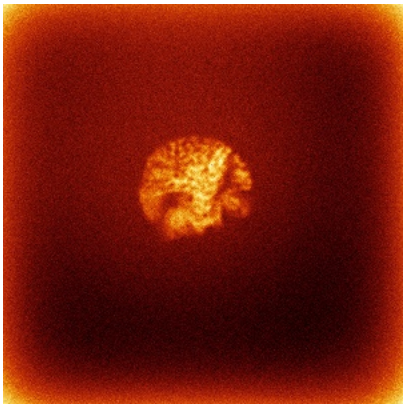
6.4.1 Primary map

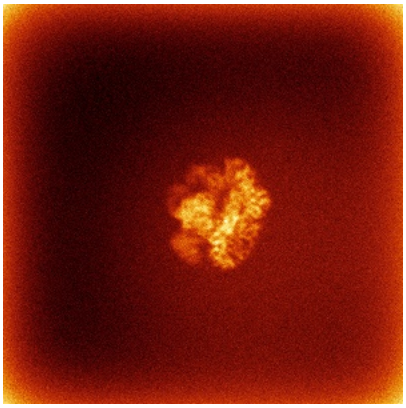

X

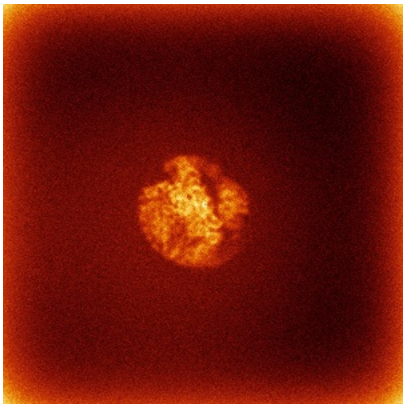

Y


Z

6.4.2 Raw map


X

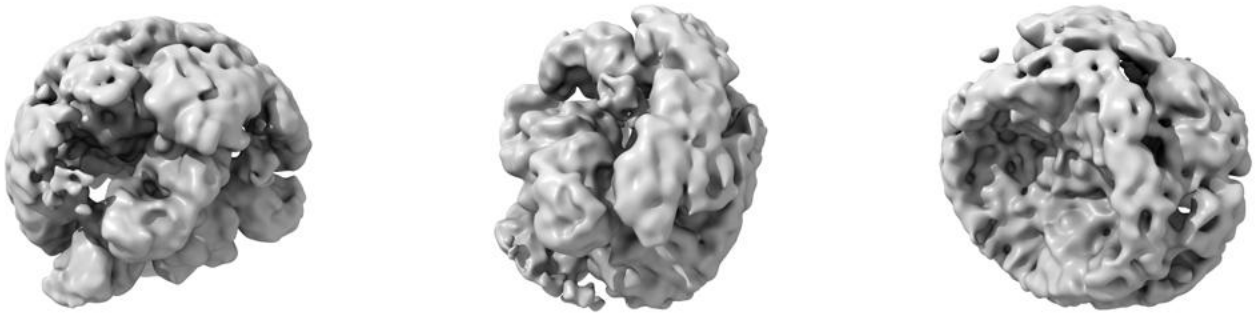

Y


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)

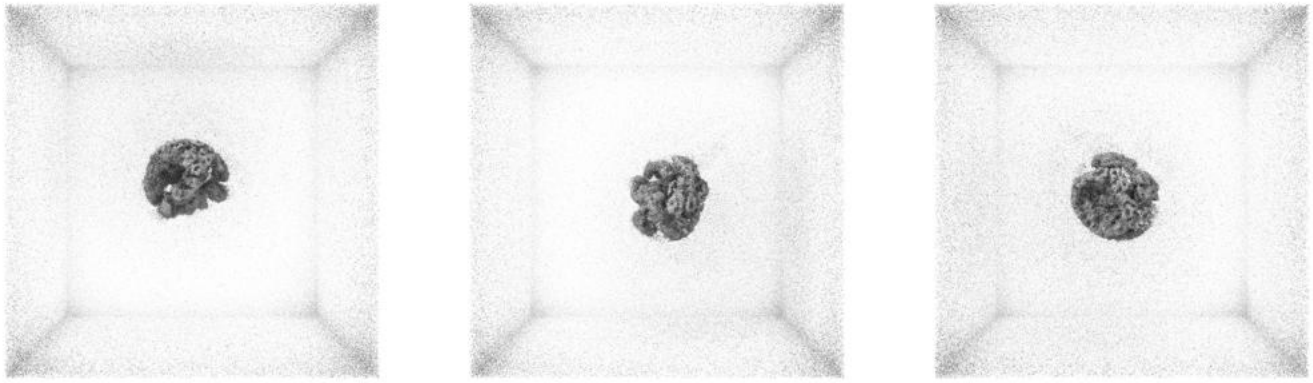
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. 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.

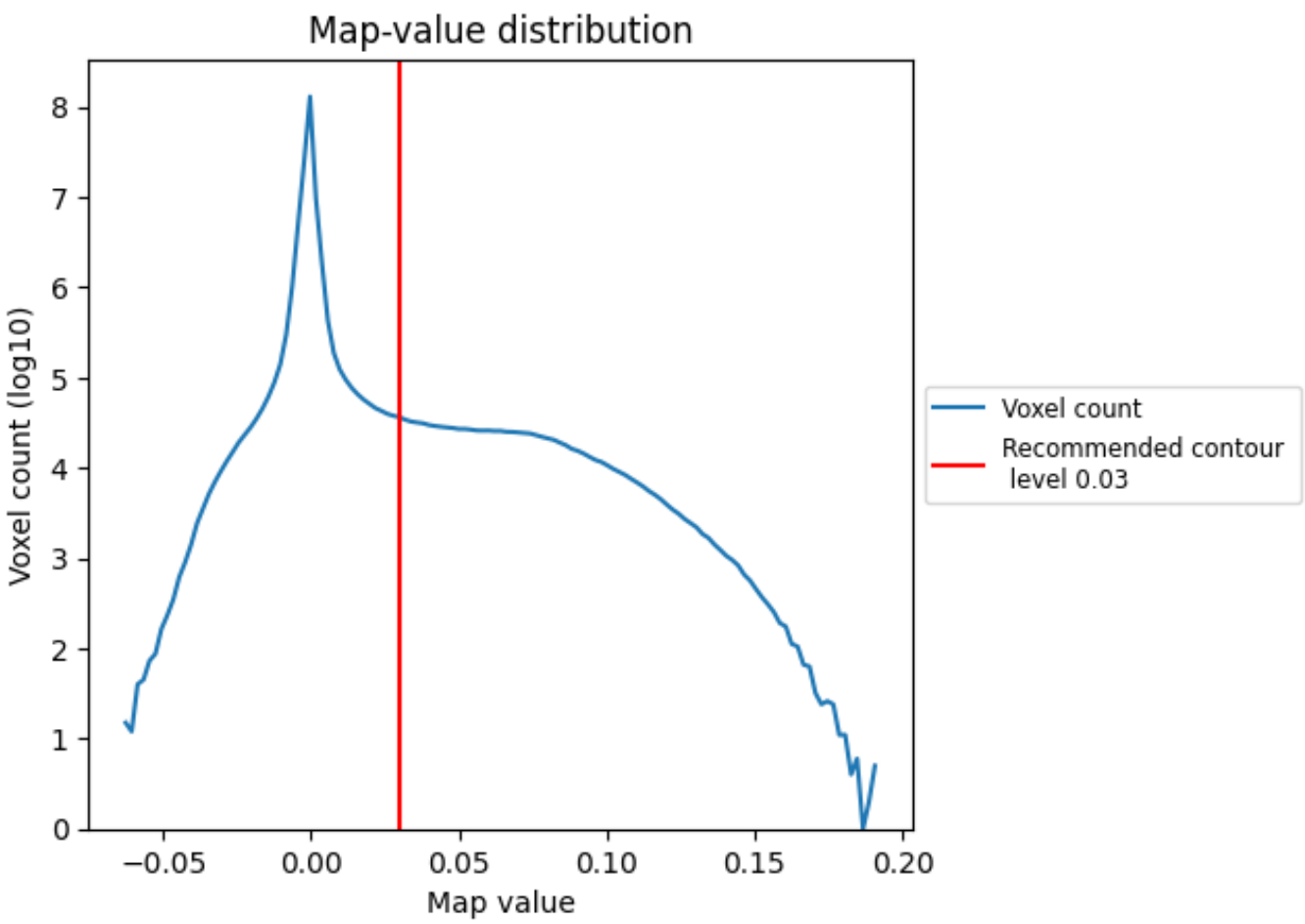
6.6 Mask visualisation (i)

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

7 Map analysis (i)

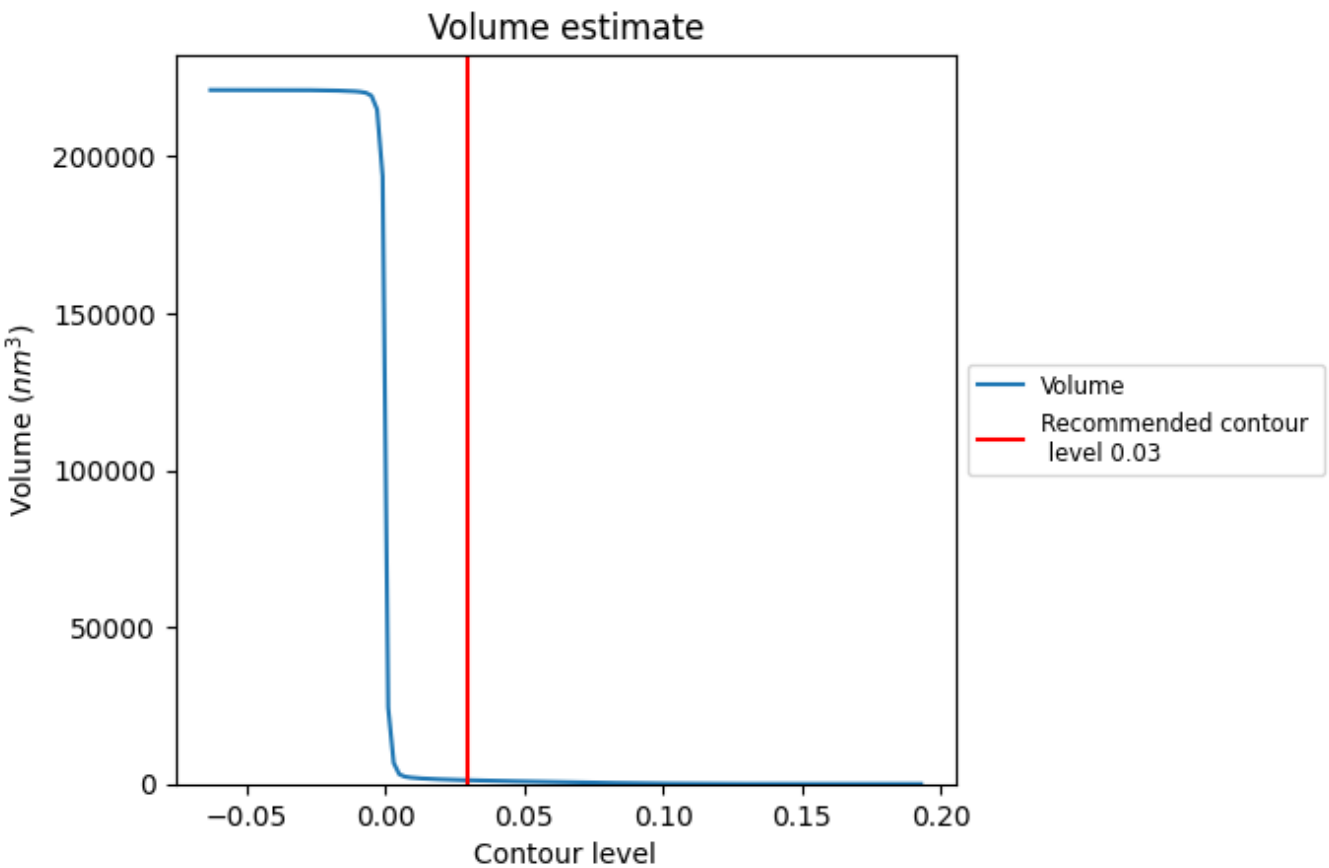
This section contains the results of statistical analysis of the map.

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.

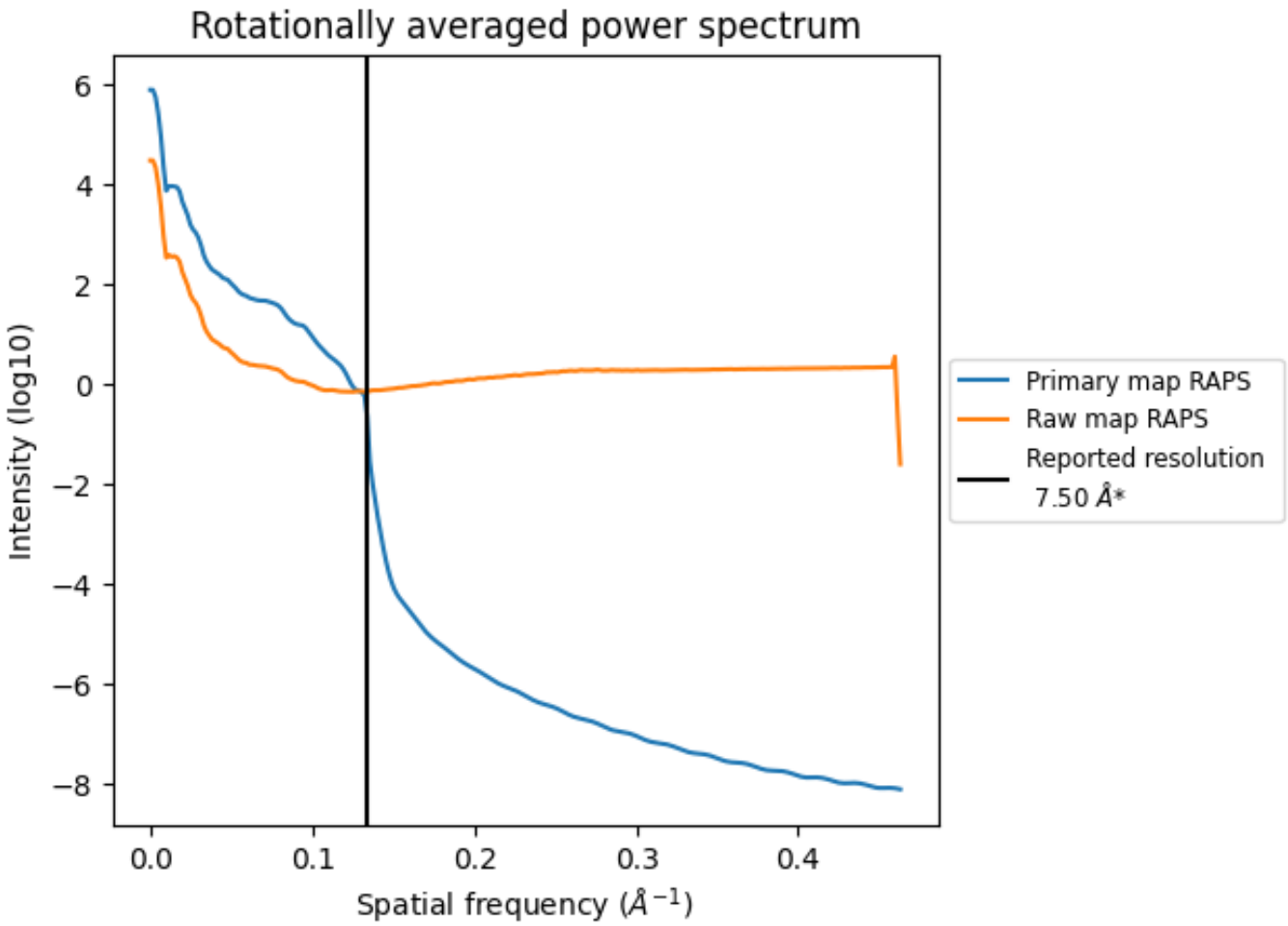
7.2 Volume estimate (i)



The volume at the recommended contour level is 1198 nm^3; this corresponds to an approximate mass of 1082 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)

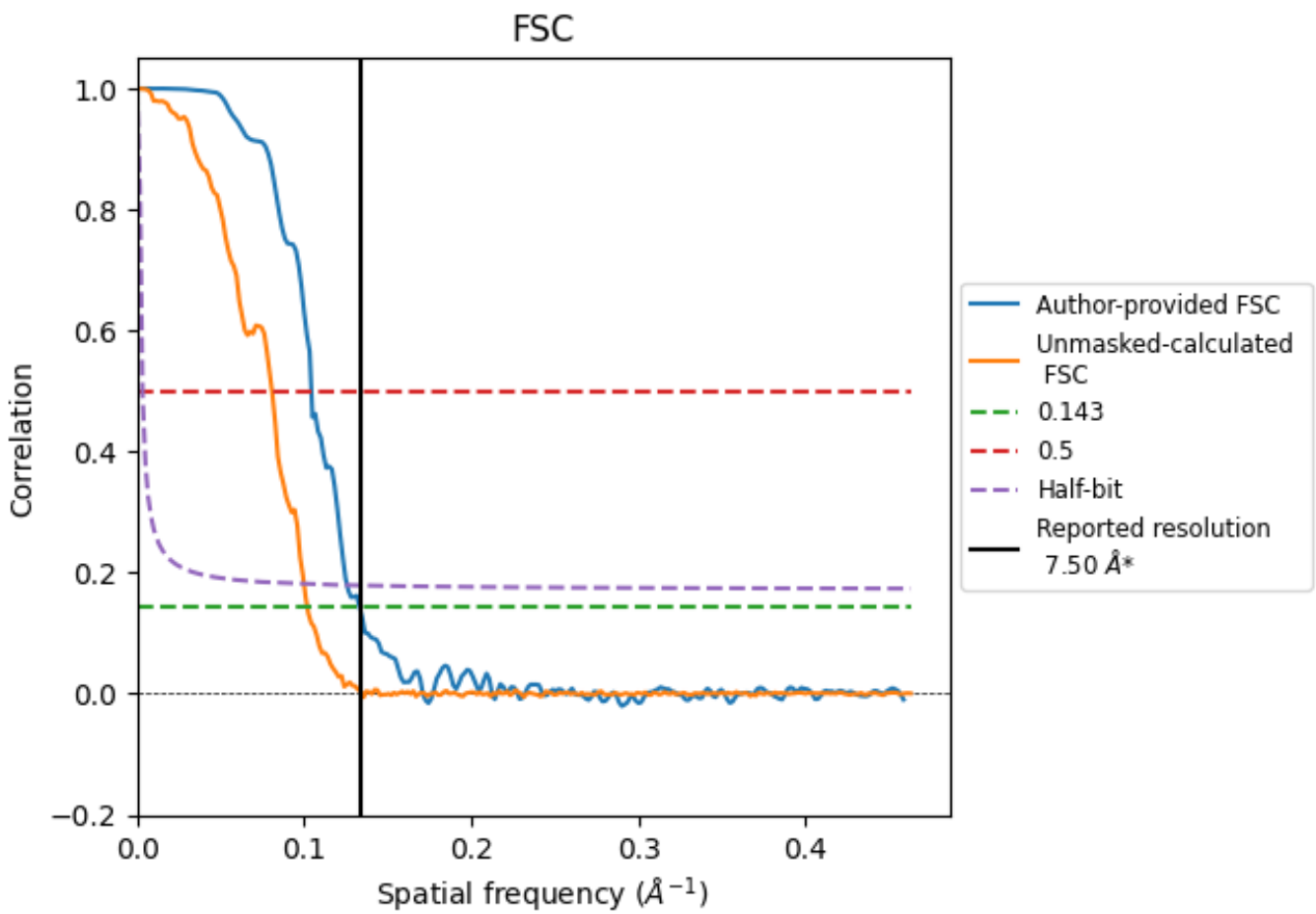


*Reported resolution corresponds to spatial frequency of 0.133 Å^{-1}

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 0.133 Å^{-1}

8.2 Resolution estimates (i)

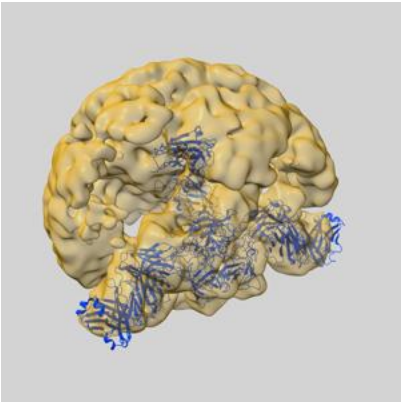
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.50	-	-
Author-provided FSC curve	7.51	9.59	7.96
Unmasked-calculated*	9.81	12.38	10.01

*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 9.81 differs from the reported value 7.5 by more than 10 %

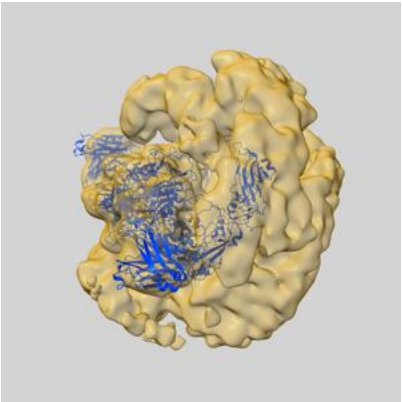
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-76753 and PDB model 12TT. Per-residue inclusion information can be found in section 3 on page 5.

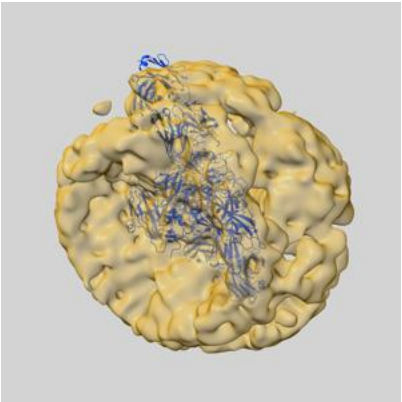
9.1 Map-model overlay (i)



X



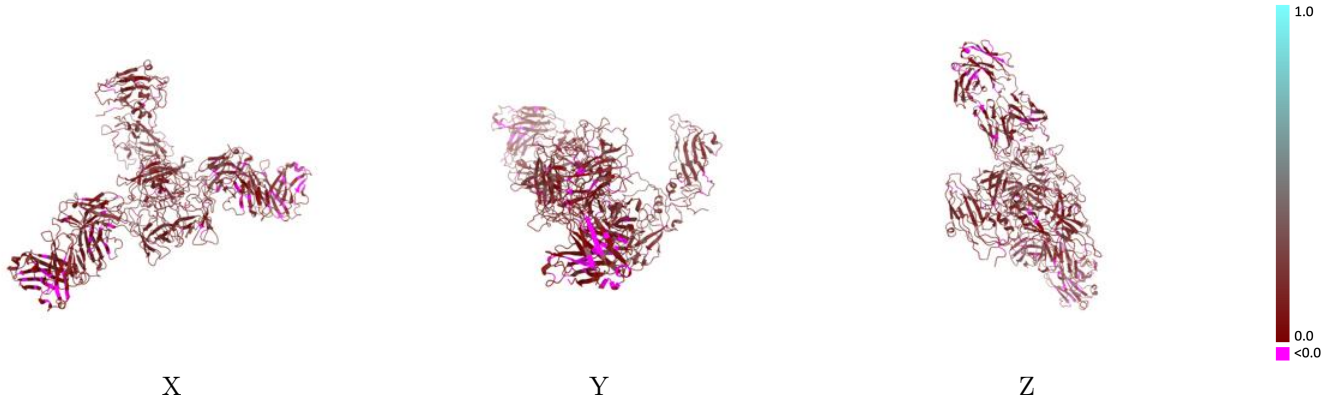
Y



Z

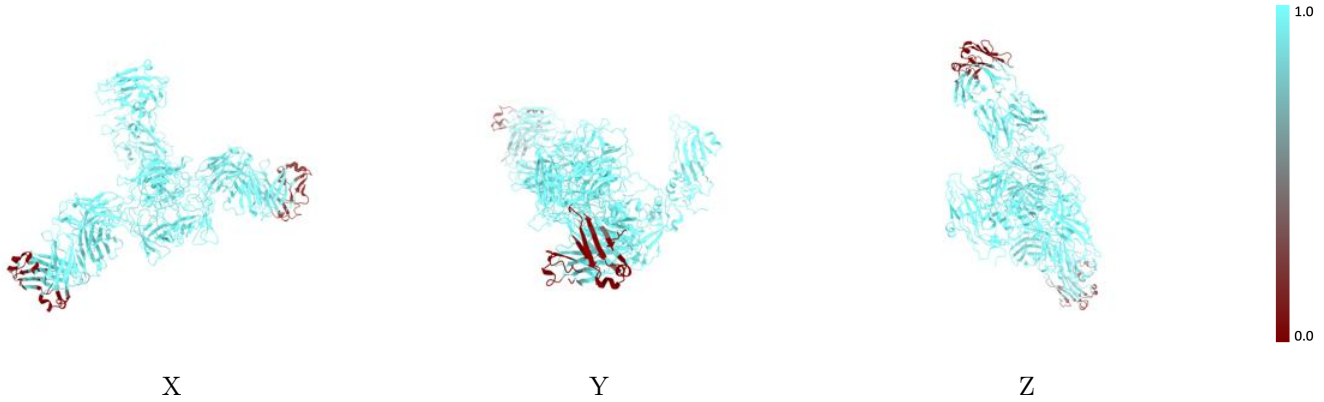
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



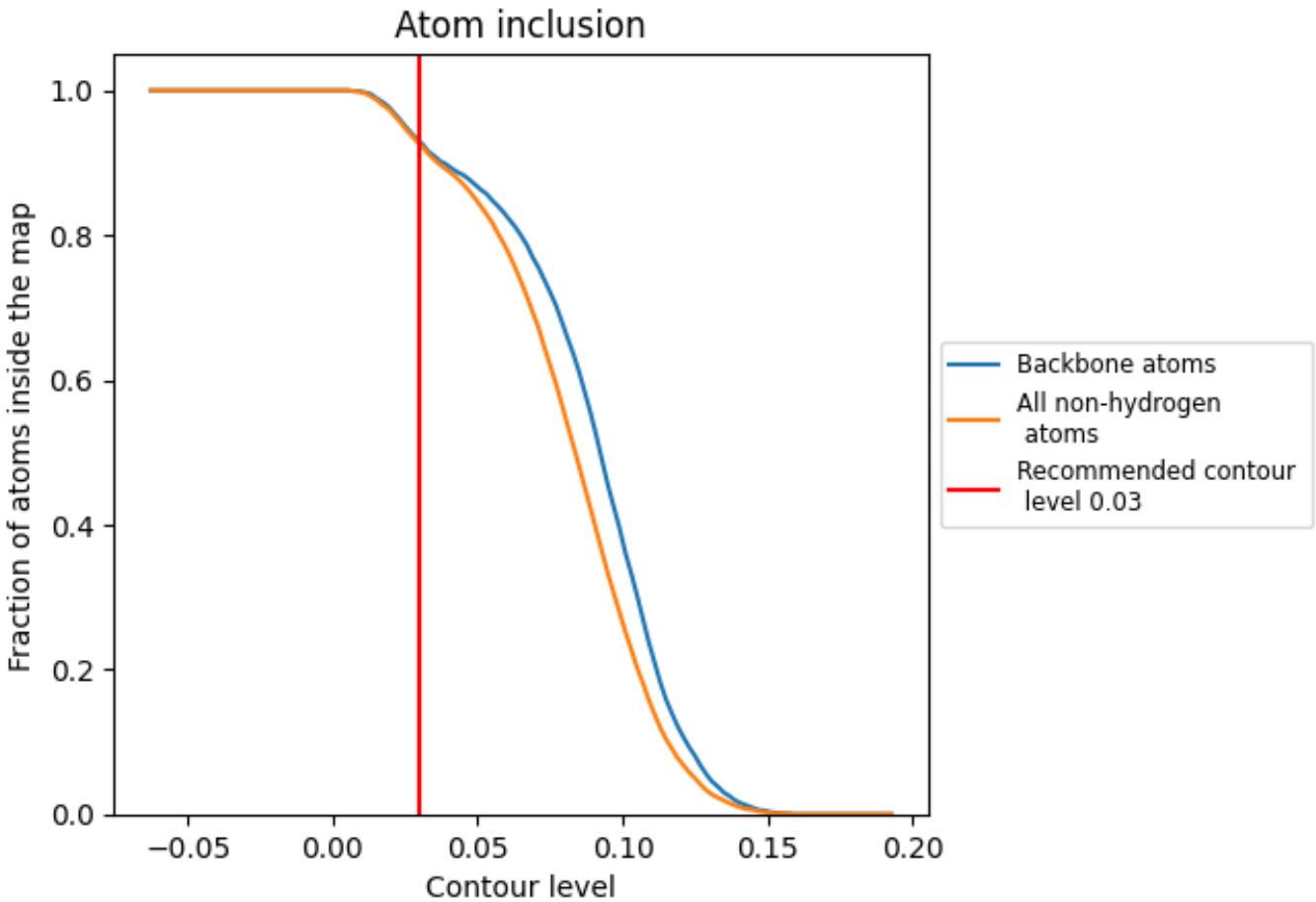
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion (i)



At the recommended contour level, 93% of all backbone atoms, 92% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9250	0.1450
B	0.9980	0.1770
E	0.8910	0.1200
F	0.9980	0.1670
G	0.7290	0.0980
H	0.9110	0.1140
I	0.8380	0.1200