Full wwPDB EM Validation Report (i)

Nov 19, 2022 – 08:57 am GMT

PDB ID	:	5LWI
EMDB ID	:	EMD-4115
Title	:	Israeli acute paralysis virus heated to 63 degree - empty particle
Authors	:	Mullapudi, E.; Fuzik, T.; Pridal, A.; Plevka, P.
Deposited on	:	2016-09-16
Resolution	:	3.80 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (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:

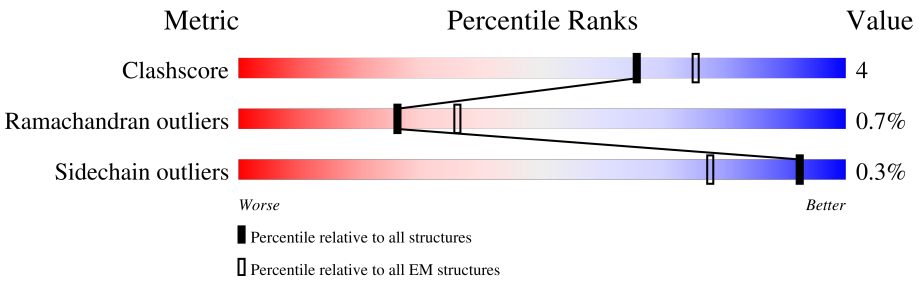
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 3.80 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	208	36% 87% 13%
2	C	300	38% 88% 12%
3	B	236	50% 90% 8% •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5876 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	A	208	1676	1061	287	322	6	0	0

- Molecule 2 is a protein called VP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	C	300	2337	1492	388	443	14	0	0

- Molecule 3 is a protein called Structural polyprotein.

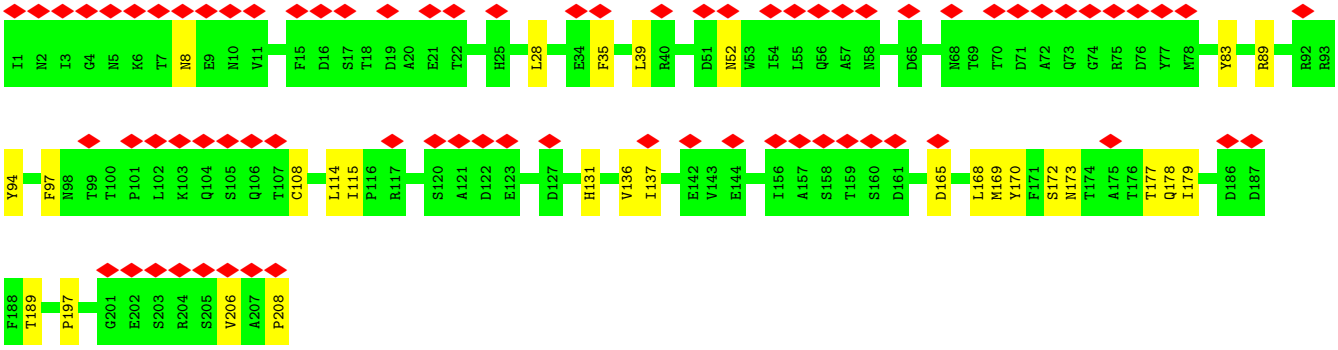
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	B	236	1863	1179	309	369	6	0	0

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.

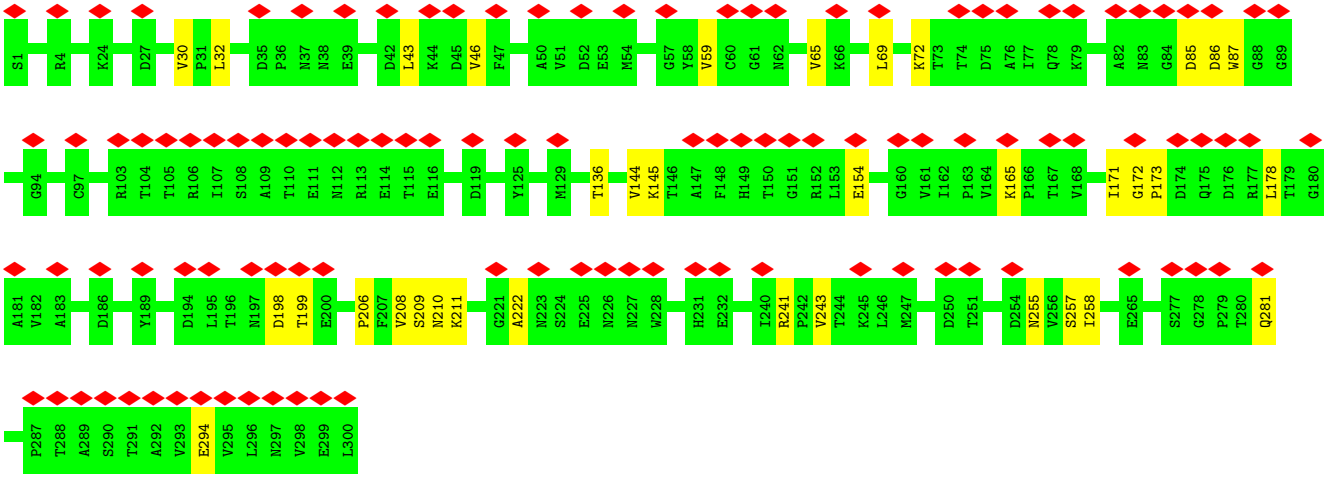
- Molecule 1: VP1

Chain A:



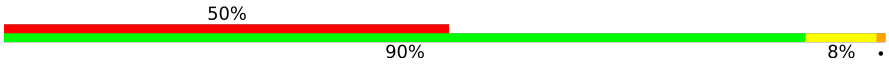
- Molecule 2: VP2

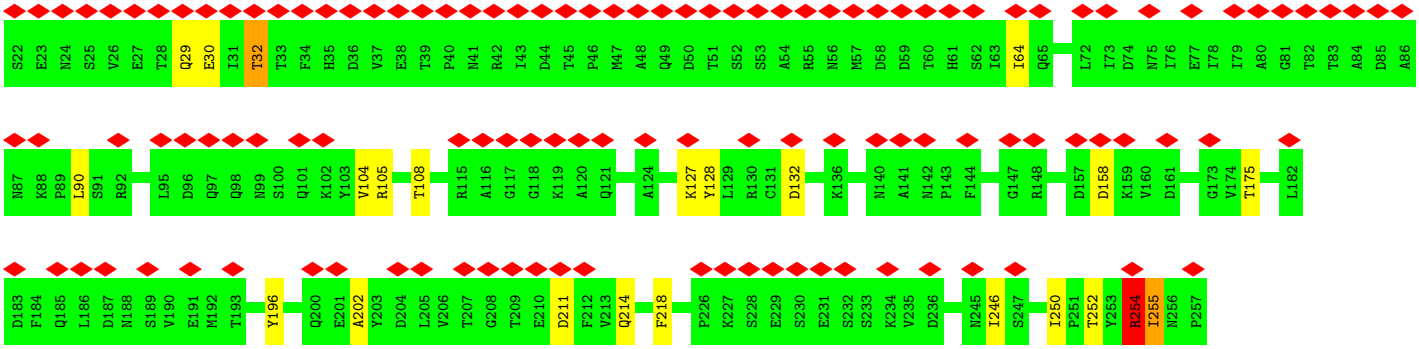
Chain C:



- Molecule 3: Structural polyprotein

Chain B:




S22 E23 N24 S25 V26 E27 T28 Q29 E30 I31 T32 T33 F34 H35 D36 V37 E38 T39 P40 N41 R42 I43 D44 T45 P46 M47 A48 Q49 D50 T51 S52 S53 A54 R55 N56 M57 D58 D59 T60 H61 S62 I63 I64 Q65 L72 I73 D74 N75 I76 E77 I78 I79 A80 G81 T82 T83 A84 D85 A86
N87 K88 P89 L90 S91 R92 L95 D96 Q97 Q98 N99 S100 Q101 K102 Y103 V104 R105 T108 R115 A116 G117 G118 K119 A120 Q121 A124 K127 Y128 L129 R130 C131 D132 K136 N140 A141 N142 P143 F144 G147 R148 D157 D158 K159 V160 D161 G173 V174 T175 L182
D183 F184 Q185 L186 D187 N188 S189 V190 E191 M192 T193 Y196 Q200 E201 A202 Y203 D204 L205 V206 T207 G208 T209 E210 D211 F212 V213 Q214 F218 P226 K227 S228 E229 S230 E231 S232 S233 K234 V235 D236 N245 I246 S247 I250 P251 T252 Y253 R254 I255 N256 P257

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	1138	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 ($e^-/Å^2$)	21	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	11.737	Depositor
Minimum map value	-7.249	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.4	Depositor
Map size (Å)	353.1, 353.1, 353.1	wwPDB
Map dimensions	330, 330, 330	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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	A	0.36	0/1718	0.61	0/2337
2	C	0.36	0/2400	0.61	0/3287
3	B	0.38	1/1902 (0.1%)	0.66	2/2595 (0.1%)
All	All	0.37	1/6020 (0.0%)	0.63	2/8219 (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
3	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	254	ARG	C-N	7.25	1.50	1.34

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	254	ARG	O-C-N	-11.75	103.90	122.70
3	B	254	ARG	CA-C-N	-7.51	100.68	117.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	B	254	ARG	Mainchain

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	A	1676	0	1618	18	0
2	C	2337	0	2300	20	0
3	B	1863	0	1834	17	0
All	All	5876	0	5752	48	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (48) 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)
3:B:158:ASP:OD1	3:B:214:GLN:NE2	2.10	0.83
3:B:158:ASP:OD1	3:B:214:GLN:OE1	2.06	0.72
3:B:158:ASP:OD1	3:B:214:GLN:CD	2.31	0.69
3:B:158:ASP:CG	3:B:214:GLN:HE22	2.00	0.65
3:B:254:ARG:O	3:B:255:ILE:HG23	1.97	0.65
1:A:83:TYR:HB3	1:A:197:PRO:HD2	1.82	0.62
3:B:64:ILE:HA	3:B:246:ILE:HD11	1.83	0.59
3:B:104:VAL:HG12	3:B:105:ARG:HG2	1.87	0.57
1:A:97:PHE:HB2	1:A:179:ILE:HB	1.89	0.55
3:B:128:TYR:HB3	3:B:202:ALA:HB1	1.89	0.54
1:A:170:TYR:OH	1:A:178:GLN:NE2	2.42	0.53
1:A:189:THR:HG21	2:C:43:LEU:HD21	1.91	0.53
3:B:29:GLN:HB2	3:B:32:THR:HB	1.90	0.52
1:A:52:ASN:OD1	1:A:177:THR:OG1	2.27	0.52
3:B:127:LYS:HD3	3:B:252:THR:HG21	1.92	0.51
2:C:65:VAL:HG23	3:B:175:THR:HG21	1.92	0.51
3:B:196:TYR:OH	3:B:202:ALA:N	2.43	0.50
2:C:69:LEU:HB2	2:C:258:ILE:HB	1.93	0.50
2:C:144:VAL:HB	2:C:257:SER:HB2	1.93	0.49
1:A:115:ILE:HG13	1:A:169:MET:HB2	1.93	0.49
2:C:87:TRP:HA	2:C:173:PRO:HG3	1.96	0.48
1:A:28:LEU:HD22	1:A:35:PHE:HD1	1.79	0.48
1:A:89:ARG:HD2	2:C:46:VAL:HG11	1.96	0.48
3:B:158:ASP:CG	3:B:214:GLN:OE1	2.52	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:178:LEU:O	2:C:241:ARG:NH1	2.48	0.46
2:C:171:ILE:HD12	2:C:222:ALA:HB1	1.98	0.46
2:C:85:ASP:N	2:C:86:ASP:HA	2.31	0.46
2:C:165:LYS:N	2:C:172:GLY:O	2.48	0.46
2:C:145:LYS:NZ	2:C:199:THR:OG1	2.50	0.45
1:A:206:VAL:HG22	1:A:208:PRO:HD2	1.98	0.45
1:A:136:VAL:HG13	1:A:137:ILE:HG23	1.98	0.45
2:C:209:SER:O	2:C:211:LYS:N	2.50	0.45
1:A:114:LEU:HD11	2:C:32:LEU:HB3	1.98	0.44
3:B:90:LEU:HD21	3:B:218:PHE:HB3	2.00	0.43
3:B:127:LYS:HB3	3:B:250:ILE:HB	2.00	0.43
3:B:132:ASP:OD1	3:B:196:TYR:N	2.52	0.43
1:A:165:ASP:N	1:A:165:ASP:OD1	2.52	0.43
1:A:172:SER:OG	1:A:173:ASN:N	2.52	0.43
1:A:39:LEU:HD12	2:C:59:VAL:HG21	2.01	0.42
2:C:72:LYS:HG2	2:C:255:ASN:HD22	1.85	0.42
2:C:154:GLU:HB2	2:C:243:VAL:HG23	2.02	0.41
2:C:281:GLN:NE2	2:C:294:GLU:O	2.53	0.41
1:A:8:ASN:ND2	2:C:198:ASP:OD1	2.54	0.41
1:A:108:CYS:HA	1:A:173:ASN:HD21	1.86	0.41
3:B:158:ASP:CG	3:B:214:GLN:NE2	2.66	0.41
1:A:94:TYR:HD2	1:A:168:LEU:HD22	1.85	0.41
2:C:136:THR:HG23	2:C:206:PRO:HA	2.03	0.41
1:A:131:HIS:NE2	2:C:30:VAL:HG21	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	206/208 (99%)	183 (89%)	23 (11%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	298/300 (99%)	273 (92%)	24 (8%)	1 (0%)	41	74
3	B	234/236 (99%)	201 (86%)	29 (12%)	4 (2%)	9	43
All	All	738/744 (99%)	657 (89%)	76 (10%)	5 (1%)	26	60

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	210	ASN
3	B	30	GLU
3	B	32	THR
3	B	211	ASP
3	B	255	ILE

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	186/186 (100%)	186 (100%)	0	100	100
2	C	262/262 (100%)	261 (100%)	1 (0%)	91	95
3	B	212/212 (100%)	211 (100%)	1 (0%)	88	94
All	All	660/660 (100%)	658 (100%)	2 (0%)	92	96

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	208	VAL
3	B	108	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	C	67	HIS
2	C	255	ASN

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.

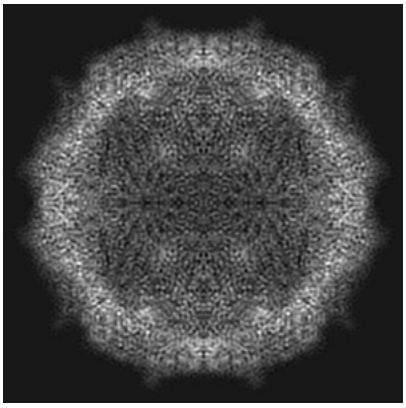
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-4115. These allow visual inspection of the internal detail of the map and identification of artifacts.

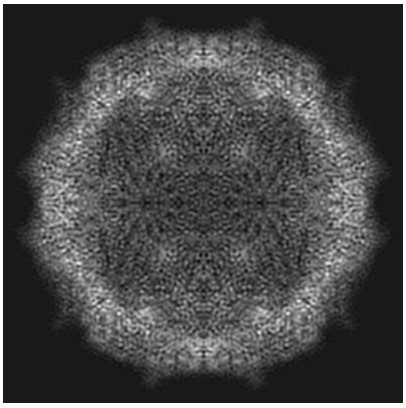
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

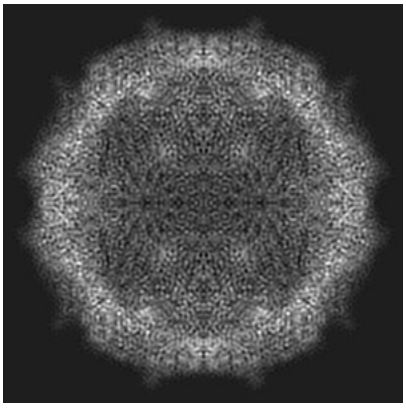
6.1.1 Primary map



X



Y

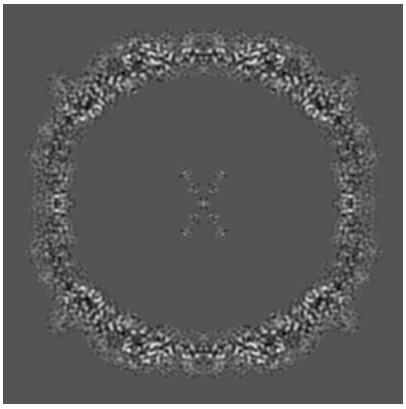


Z

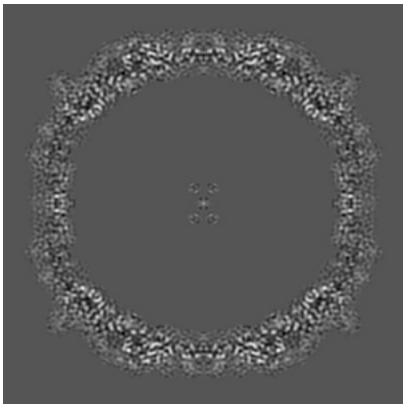
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

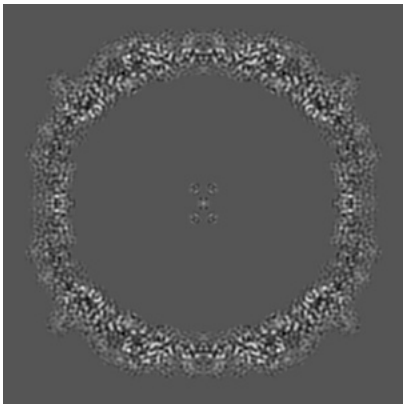
6.2.1 Primary map



X Index: 165



Y Index: 165

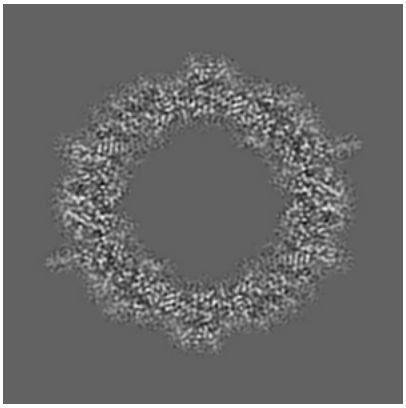


Z Index: 165

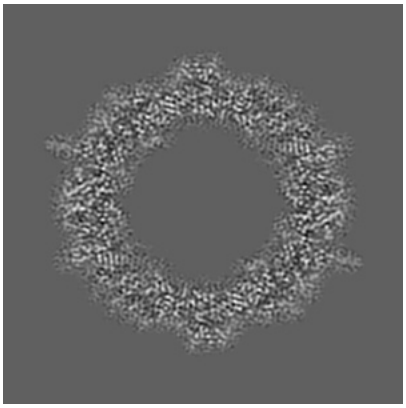
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

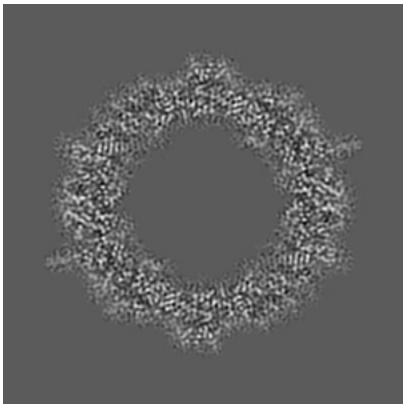
6.3.1 Primary map



X Index: 253



Y Index: 77

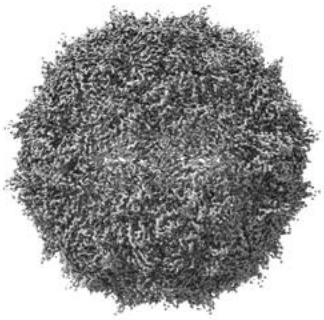


Z Index: 253

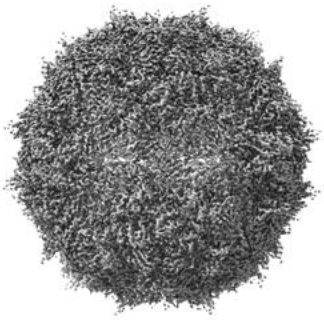
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

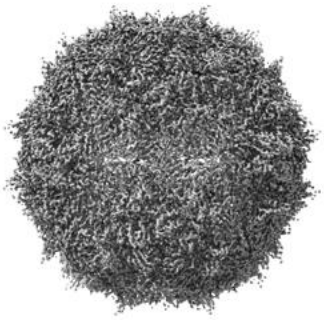
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

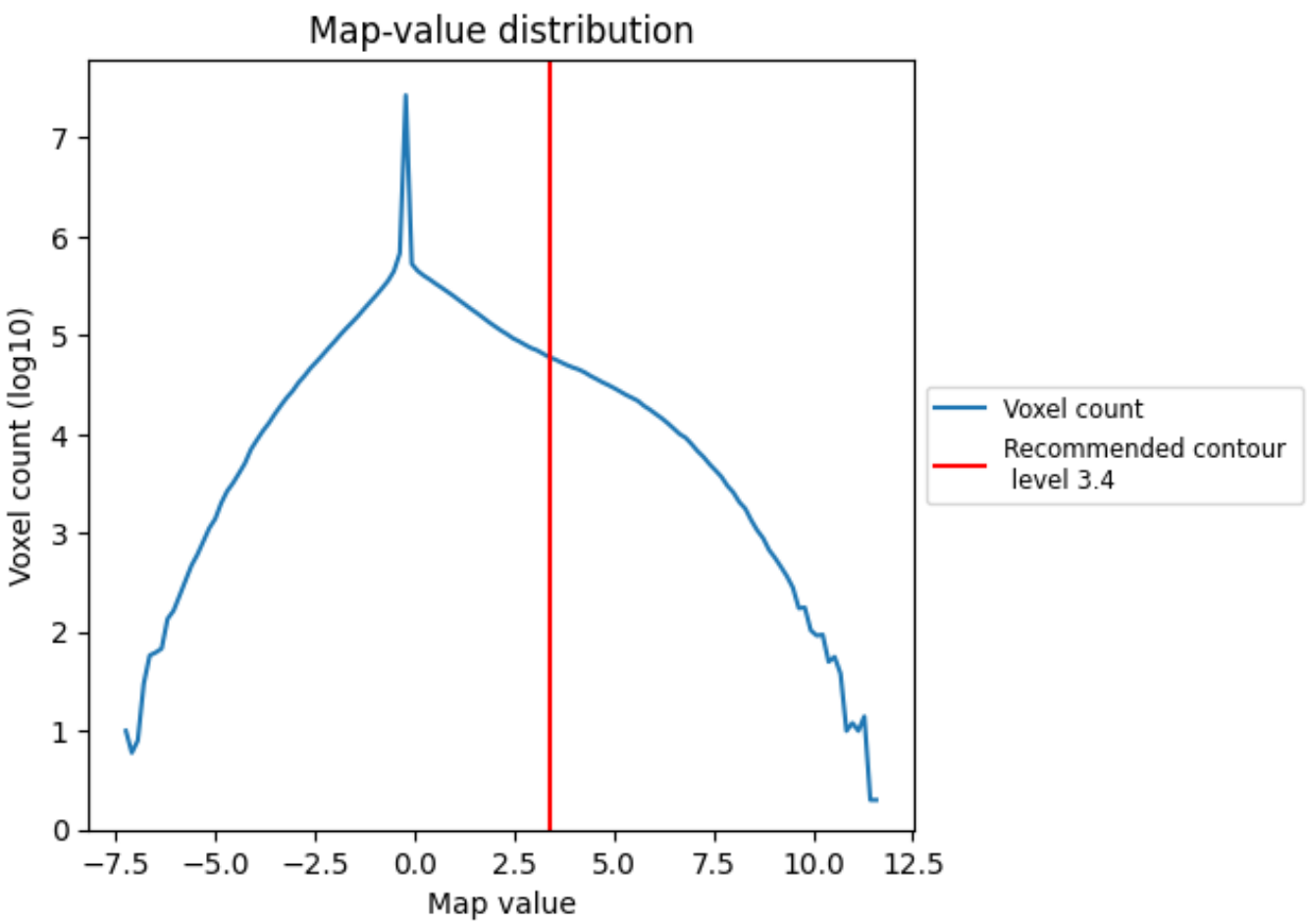
6.5 Mask visualisation (i)

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

7 Map analysis (i)

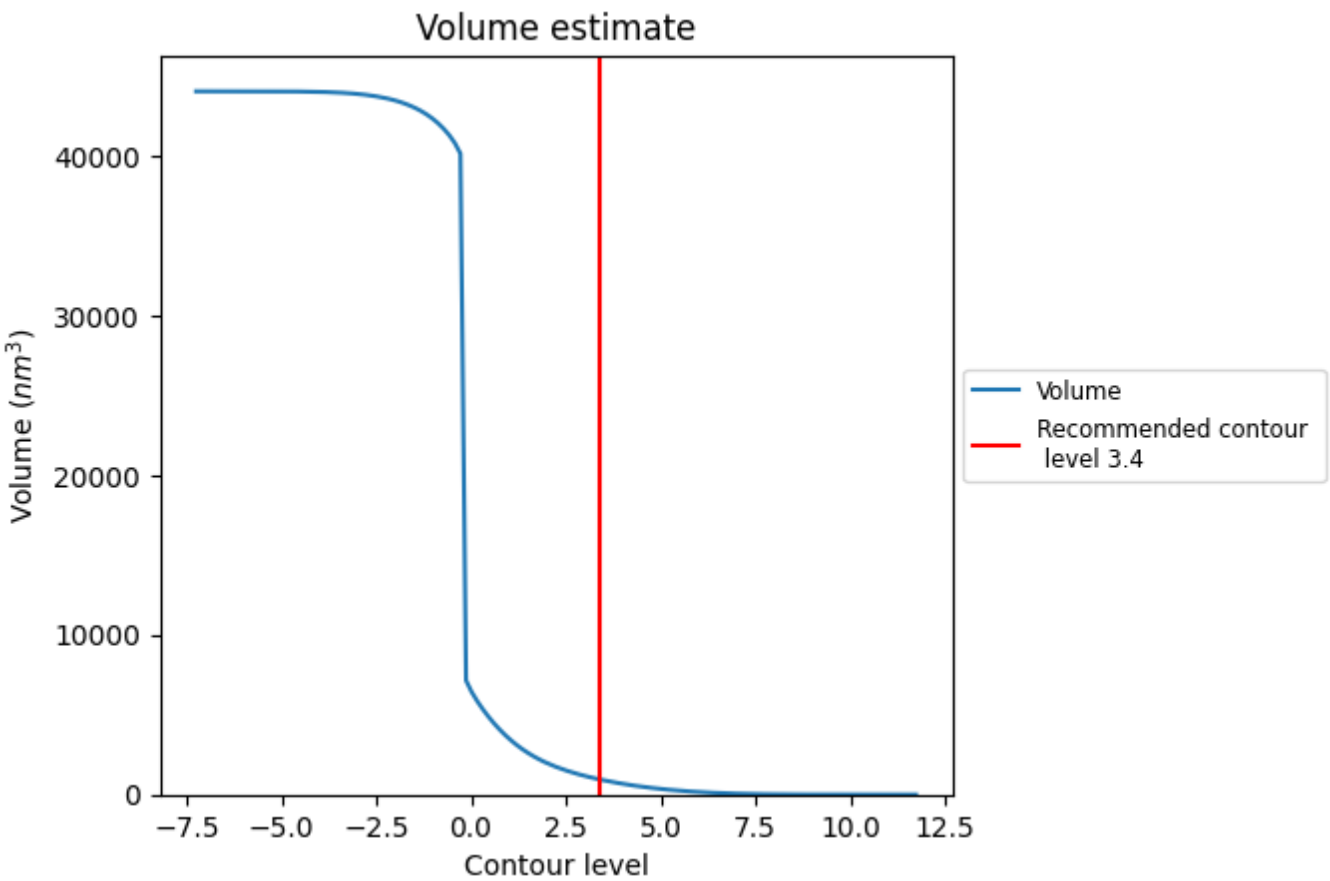
This section contains the results of statistical analysis of the map.

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.

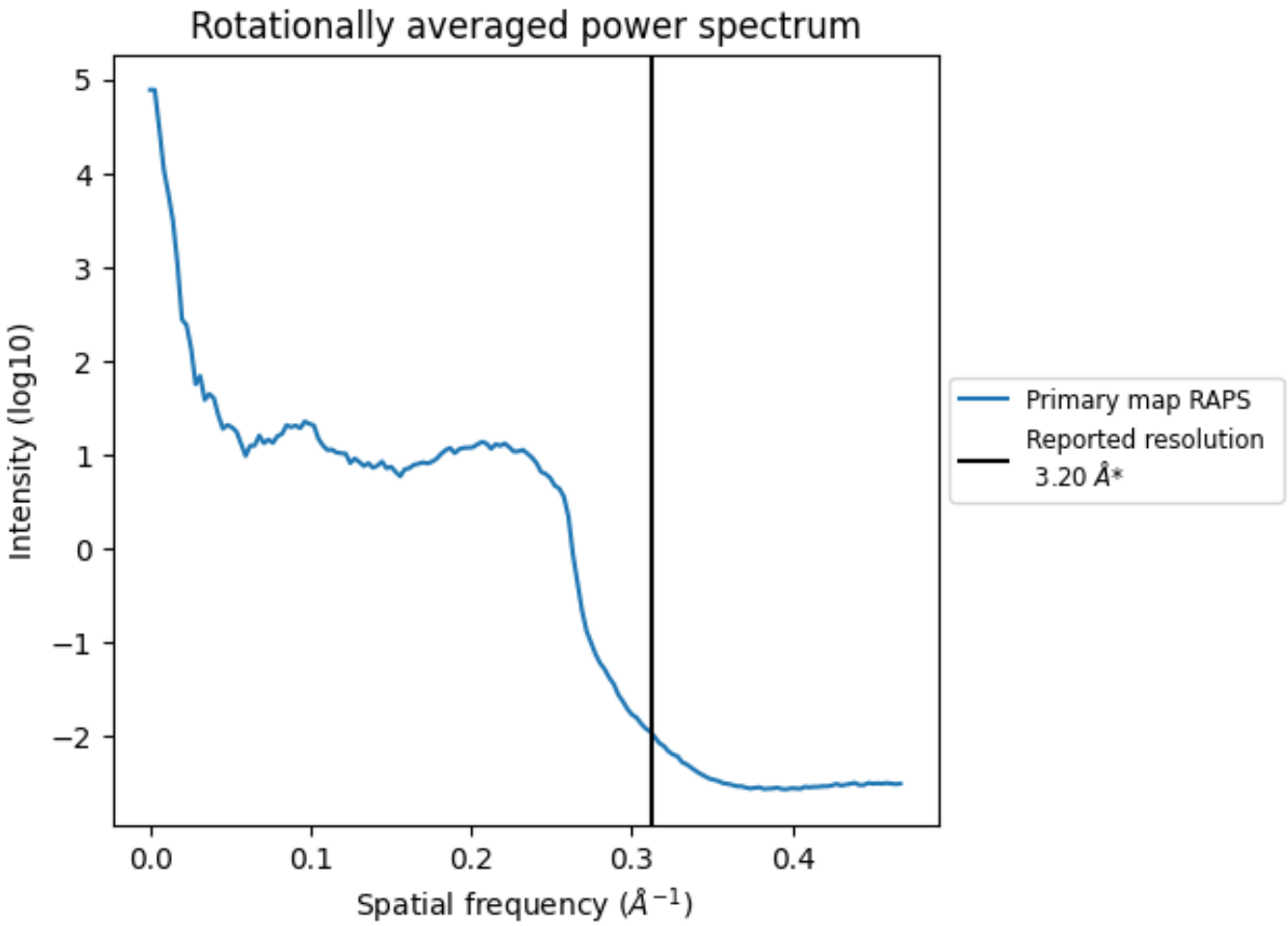
7.2 Volume estimate (i)



The volume at the recommended contour level is 944 nm^3; this corresponds to an approximate mass of 853 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

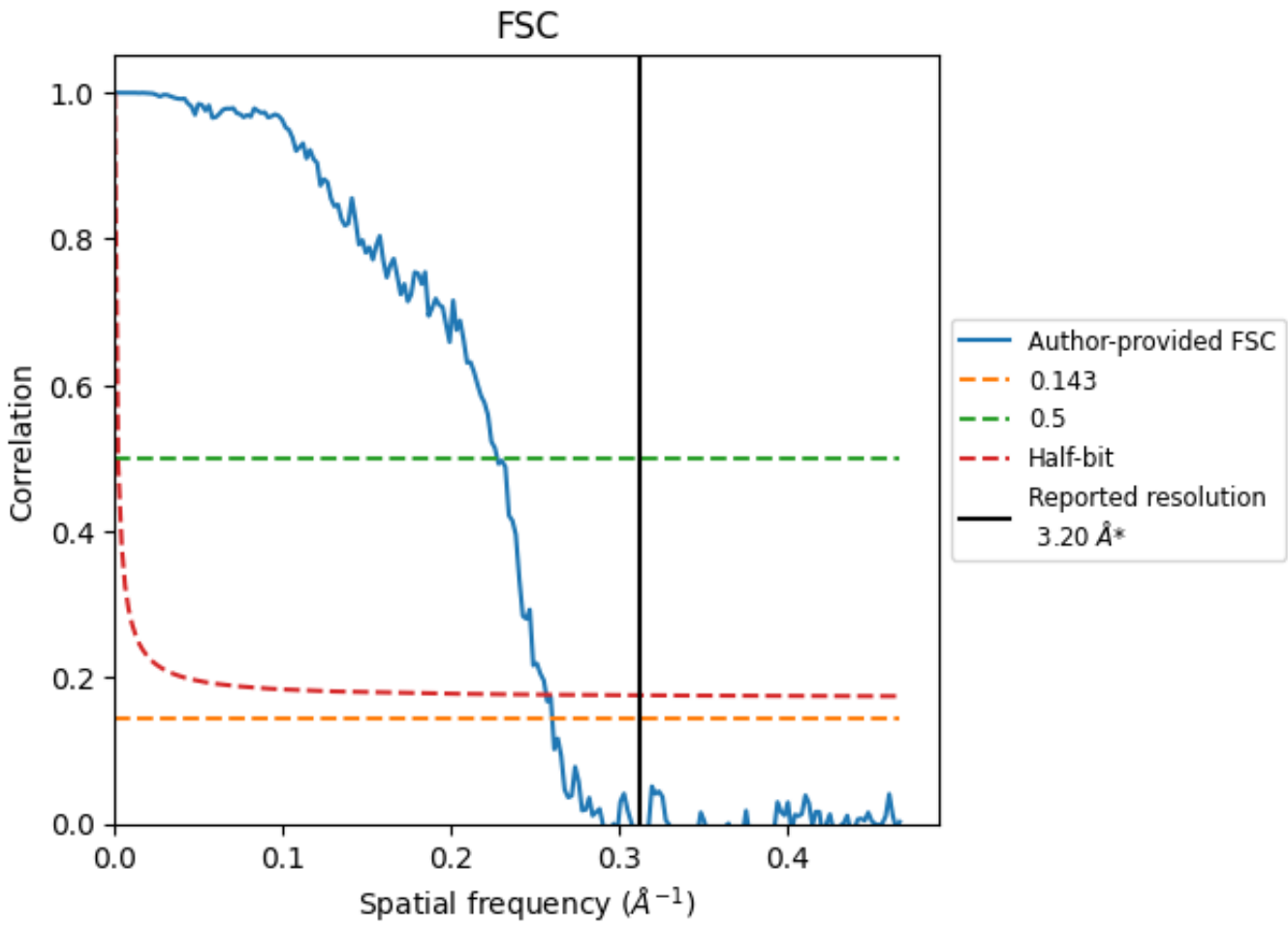


*Reported resolution corresponds to spatial frequency of 0.312 Å^{-1}

8 Fourier-Shell correlation (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 0.312 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.84	4.39	3.89
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.84 differs from the reported value 3.2 by more than 10 %

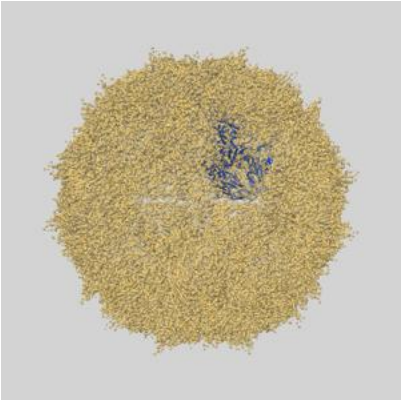
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-4115 and PDB model 5LWI. Per-residue inclusion information can be found in section 3 on page 4.

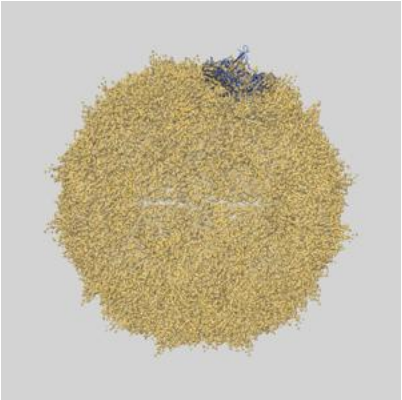
9.1 Map-model overlays

9.1.1 Map-model overlay (i)

X

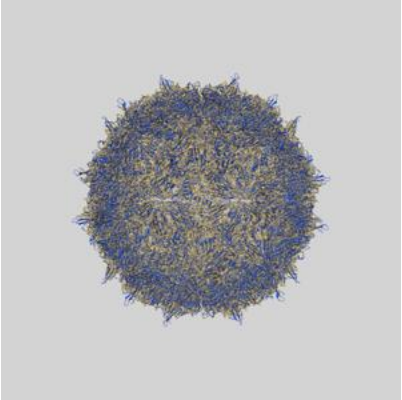


Y

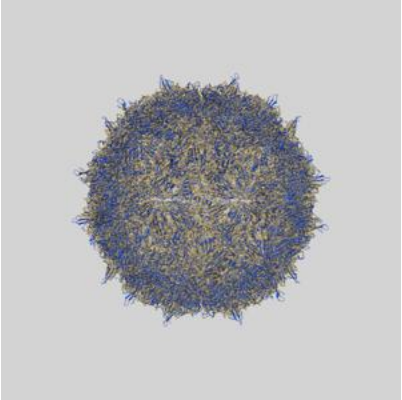


Z

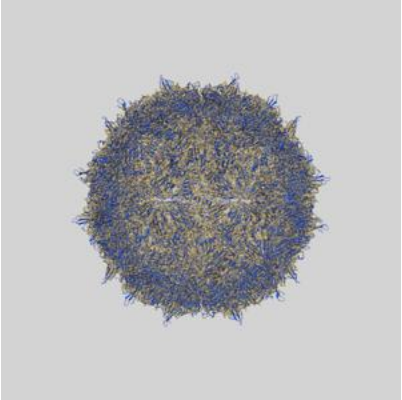
9.1.2 Map-model assembly overlay (i)



X



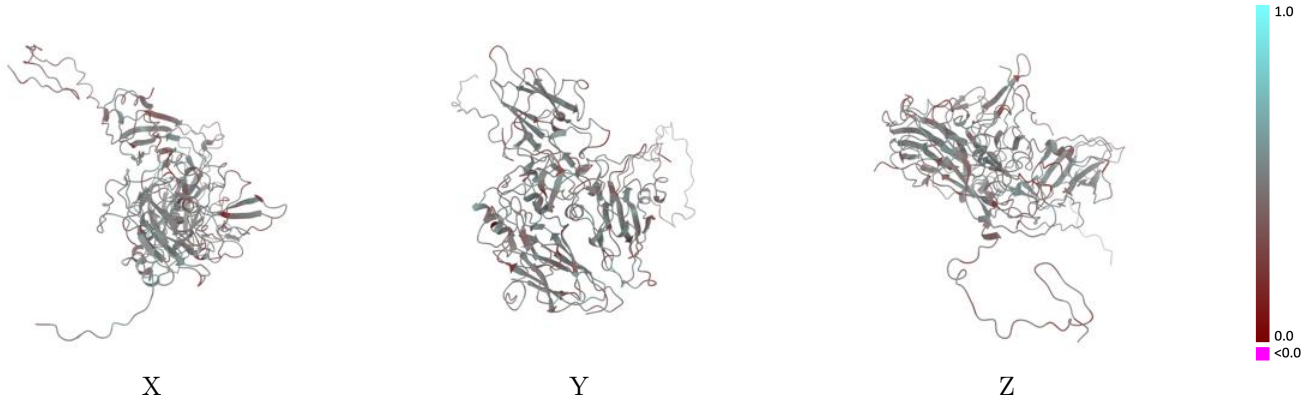
Y



Z

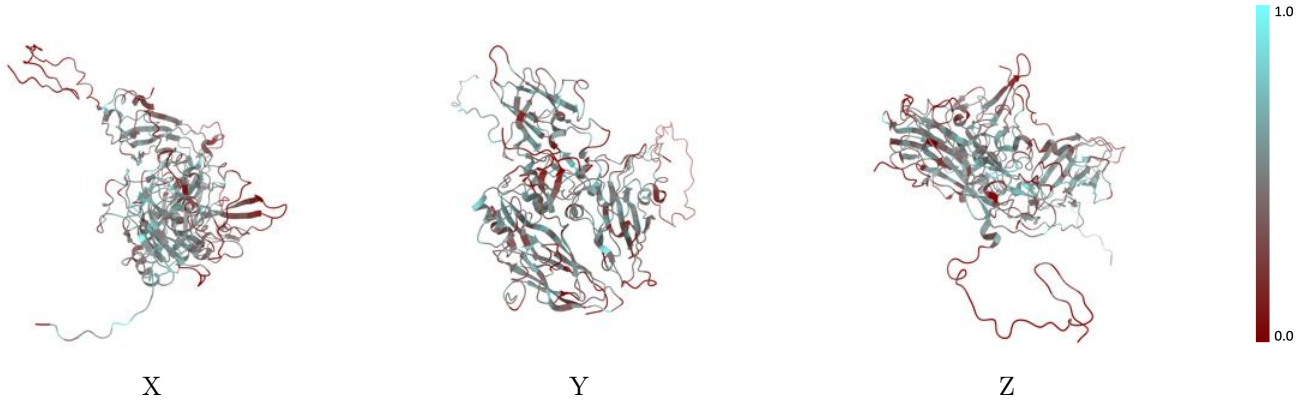
The images above show the 3D surface view of the map at the recommended contour level 3.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



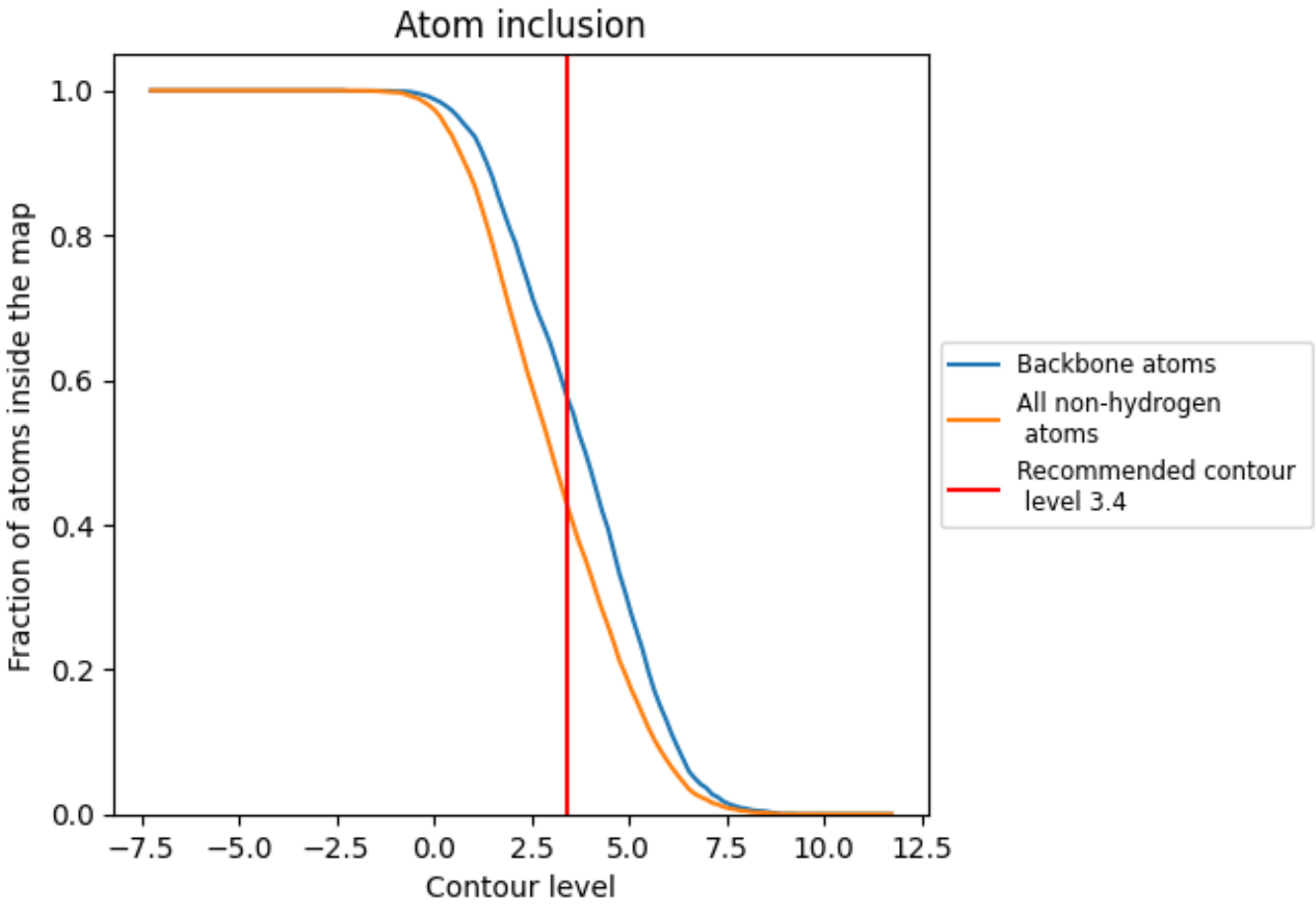
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.4).

9.4 Atom inclusion (i)



At the recommended contour level, 58% of all backbone atoms, 43% 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 (3.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4298	0.4570
A	0.4557	0.4650
B	0.3881	0.4470
C	0.4447	0.4590