wwPDB EM Validation Summary Report (i)

Oct 12, 2026 – 06:04 PM EDT

PDB ID	:	10NE / pdb_000010ne
EMDB ID	:	EMD-75302
Title	:	Cryo-EM structure of human IL-10RA and IL-10RB in complex with tandem VHHs E07-A05
Authors	:	Xu, H.
Deposited on	:	2026-01-28
Resolution	:	3.14 Å(reported)
Based on initial models	:	1Y6K, 3LQM, 7PIJ

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 (1)) were used in the production of this report:

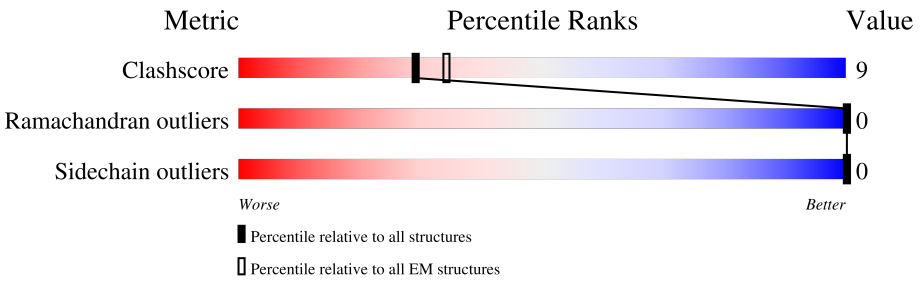
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

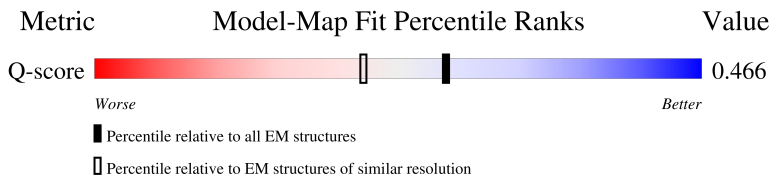
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.14 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	14483 (2.64 - 3.64)

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	227	22%; 68%; 22%; 11%
2	B	258	•; 74%; 21%; 5%
3	C	214	•; 72%; 18%; 9%
4	H	239	72%; 20%; 8%

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Mol	Chain	Length	Quality of chain
5	L	215	77% 20% •

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 8358 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 Interleukin-10 receptor subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	203	1630	1037	281	306	6	0	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	236	GLY	-	expression tag	UNP Q13651
A	237	GLY	-	expression tag	UNP Q13651
A	238	GLY	-	expression tag	UNP Q13651
A	239	GLY	-	expression tag	UNP Q13651
A	240	SER	-	expression tag	UNP Q13651
A	241	HIS	-	expression tag	UNP Q13651
A	242	HIS	-	expression tag	UNP Q13651
A	243	HIS	-	expression tag	UNP Q13651
A	244	HIS	-	expression tag	UNP Q13651
A	245	HIS	-	expression tag	UNP Q13651
A	246	HIS	-	expression tag	UNP Q13651
A	247	HIS	-	expression tag	UNP Q13651
A	248	HIS	-	expression tag	UNP Q13651

- Molecule 2 is a protein called tandem VHHs E07-A05.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	246	1859	1164	321	365	9	0	0

- Molecule 3 is a protein called Interleukin-10 receptor subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	194	1598	1020	263	305	10	0	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	221	GLY	-	expression tag	UNP Q08334
C	222	GLY	-	expression tag	UNP Q08334
C	223	GLY	-	expression tag	UNP Q08334
C	224	GLY	-	expression tag	UNP Q08334
C	225	SER	-	expression tag	UNP Q08334
C	226	HIS	-	expression tag	UNP Q08334
C	227	HIS	-	expression tag	UNP Q08334
C	228	HIS	-	expression tag	UNP Q08334
C	229	HIS	-	expression tag	UNP Q08334
C	230	HIS	-	expression tag	UNP Q08334
C	231	HIS	-	expression tag	UNP Q08334
C	232	HIS	-	expression tag	UNP Q08334
C	233	HIS	-	expression tag	UNP Q08334

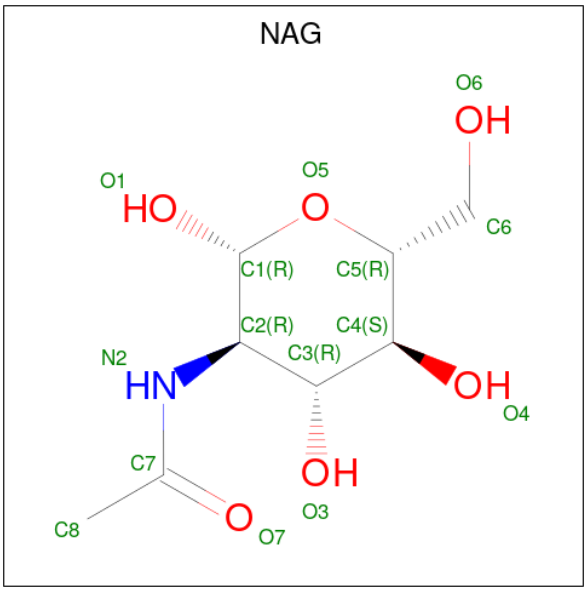
- Molecule 4 is a protein called Fab Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	H	220	1675	1069	276	325	5	0	0

- Molecule 5 is a protein called Fab Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	L	208	1582	987	267	323	5	0	0

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



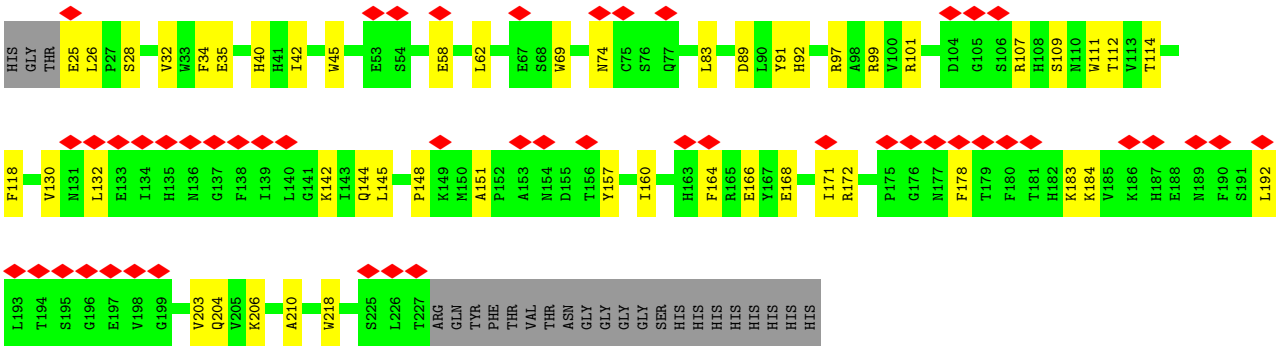
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
6	H	1	14	8	1	5	0

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.

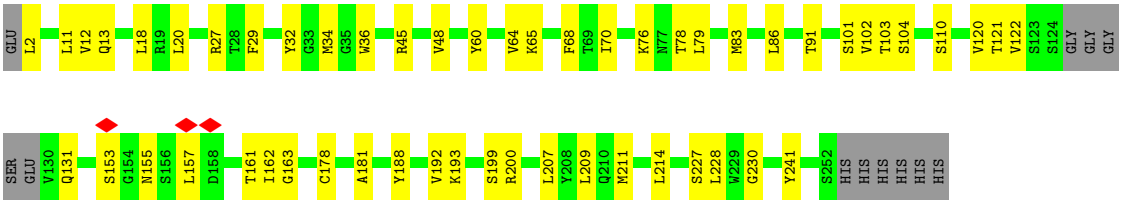
- Molecule 1: Interleukin-10 receptor subunit alpha

Chain A:



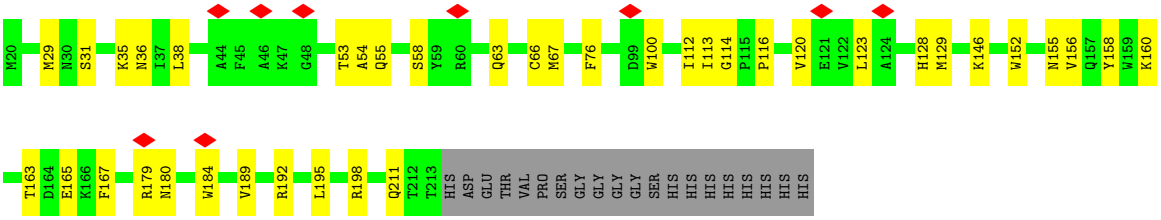
- Molecule 2: tandem VHHs E07-A05

Chain B:



- Molecule 3: Interleukin-10 receptor subunit beta

Chain C:



- Molecule 4: Fab Heavy Chain

Chain H: 72% 20% 8%

GLU ILE SER GLU V2 V12 A40 K43 W47 Y50 I51 S52 Y56 T57 S58 Y59 A60 K75 N76 T77 M82 L82C T87 A93 W99 L100K T110 K117 G118 P119 P123 L124 A125 P126 S127 SER LYS SER THR SER GLY GLY T135 A136

A137 L138 L141 V142 K143 D144 Y145 E148 P149 V152 S153 W154 N155 S156 L159 T165 L178 S179 S180 V181 V182 T183 N197 H200 K201 P202 K209 P213 LYS SER CYS ASP LYS THR HIS THR

• Molecule 5: Fab Light Chain

Chain L: 77% 20% •

SER ASP ILE GLN M4 S7 P8 V19 R24 V29 A32 V33 Q37 Q38 K39 K42 L47 A51 T74 A84 Q89 L95 I96 I106 K107 R108 F116 P120 V132 V133 C134 L135 L136 P141 R142 E143 A144 W148 K149 V150

Q155 N158 V163 S171 A184 K188 H189 K190 V196 T197 H198 Q199 R211 GLY GLU CYS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	101358	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	165000	Depositor
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.641	Depositor
Minimum map value	-0.356	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.075	Depositor
Map size (Å)	349.91998, 349.91998, 349.91998	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.729, 0.729, 0.729	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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	0.13	0/1676	0.42	0/2280
2	B	0.23	0/1901	0.48	0/2574
3	C	0.17	0/1646	0.48	0/2246
4	H	0.19	0/1724	0.38	0/2356
5	L	0.20	0/1614	0.44	0/2190
All	All	0.19	0/8561	0.44	0/11646

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 (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	1630	0	1572	32	0
2	B	1859	0	1787	44	0
3	C	1598	0	1498	24	0
4	H	1675	0	1598	30	0
5	L	1582	0	1551	30	0
6	H	14	0	13	0	0
All	All	8358	0	8019	153	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 9.

The worst 5 of 153 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:B:91:THR:HG22	2:B:122:VAL:H	1.29	0.95
5:L:7:SER:HB2	5:L:24:ARG:HH12	1.38	0.88
4:H:52:SER:HB2	4:H:56:TYR:HB2	1.65	0.78
1:A:168:GLU:HB3	1:A:206:LYS:HB3	1.67	0.76
2:B:32:TYR:HE2	2:B:102:VAL:HG12	1.53	0.74

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	201/227 (88%)	196 (98%)	5 (2%)	0	100	100
2	B	242/258 (94%)	237 (98%)	5 (2%)	0	100	100
3	C	192/214 (90%)	184 (96%)	8 (4%)	0	100	100
4	H	216/239 (90%)	210 (97%)	6 (3%)	0	100	100
5	L	206/215 (96%)	197 (96%)	9 (4%)	0	100	100
All	All	1057/1153 (92%)	1024 (97%)	33 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	184/203 (91%)	184 (100%)	0	100	100
2	B	197/206 (96%)	197 (100%)	0	100	100
3	C	178/195 (91%)	178 (100%)	0	100	100
4	H	183/200 (92%)	183 (100%)	0	100	100
5	L	184/190 (97%)	184 (100%)	0	100	100
All	All	926/994 (93%)	926 (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 9 such sidechains are listed below:

Mol	Chain	Res	Type
5	L	155	GLN
5	L	166	GLN
3	C	147	ASN
3	C	190	GLN
4	H	82(A)	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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
6	NAG	H	301	4	14,14,15	0.69	0	17,19,21	0.84	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	H	301	4	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	H	301	NAG	C8-C7-N2-C2
6	H	301	NAG	O7-C7-N2-C2

There are no ring outliers.

No monomer is involved in short contacts.

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.

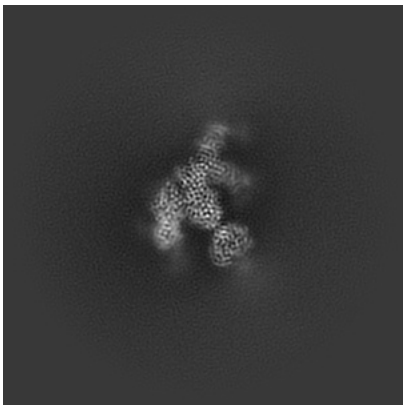
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-75302. These allow visual inspection of the internal detail of the map and identification of artifacts.

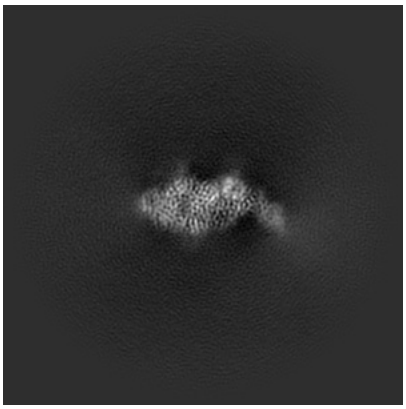
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

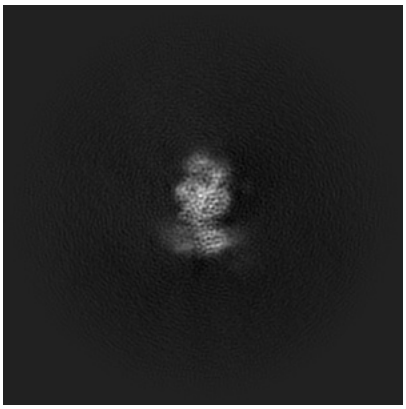
6.1.1 Primary map



X

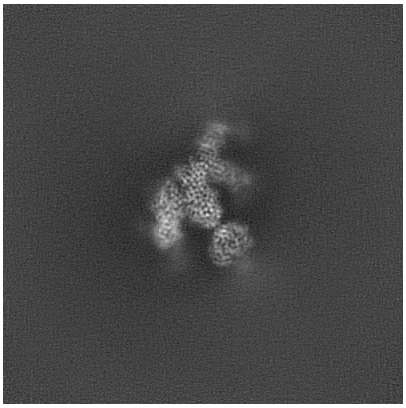


Y



Z

6.1.2 Raw map



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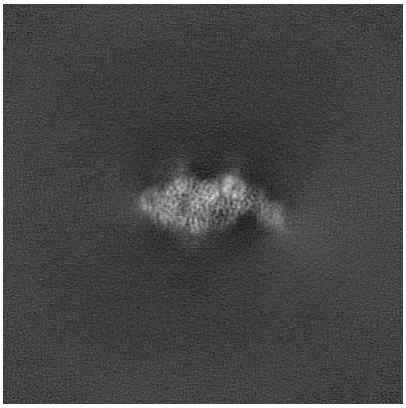
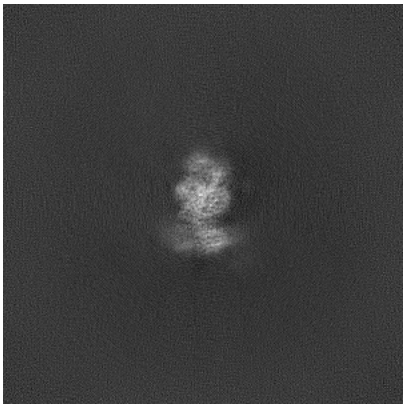


Y

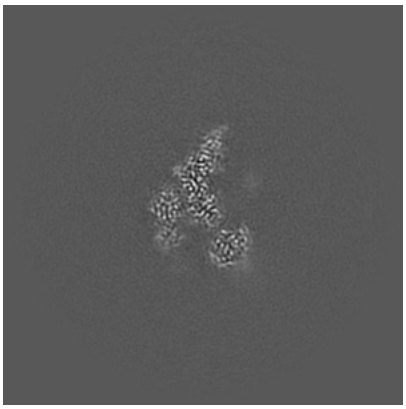


Z

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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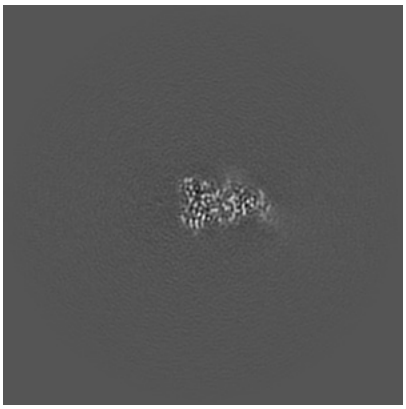
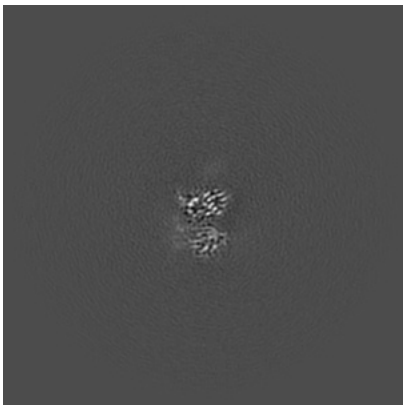

Y Index: 240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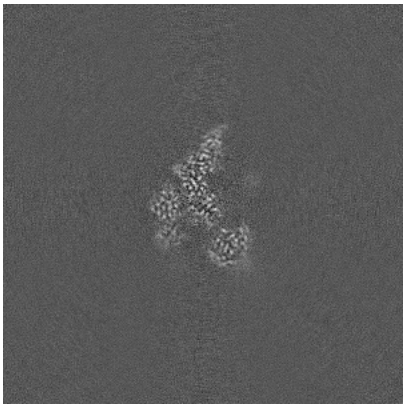
6.2.2 Raw map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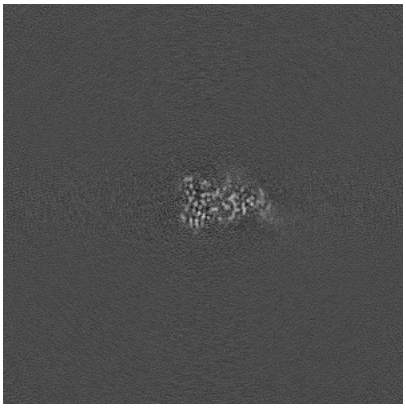
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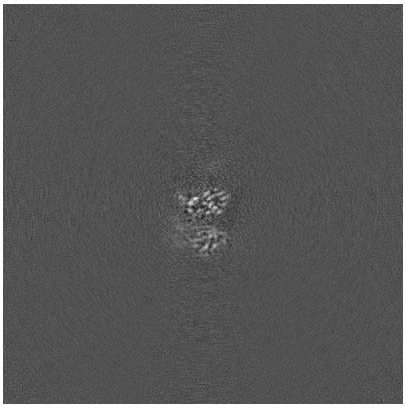
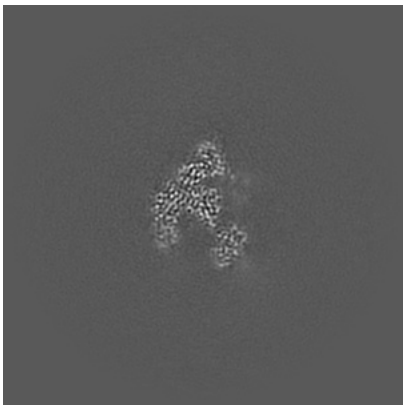
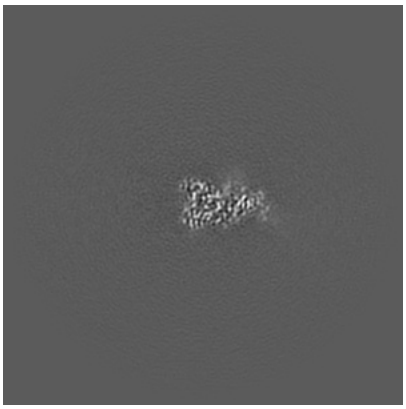

Z Index: 240

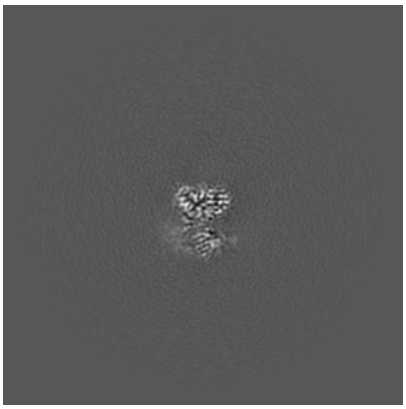
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

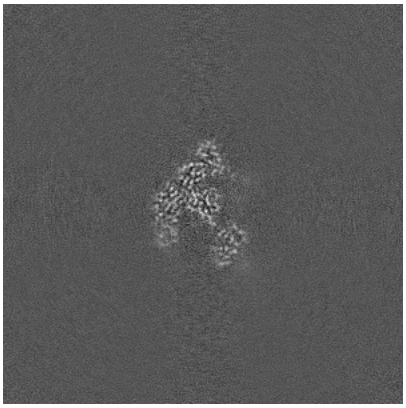
6.3.1 Primary map

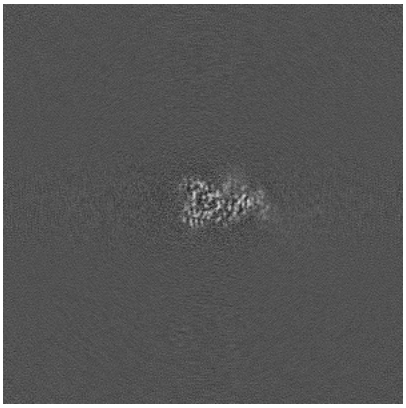

X Index: 248

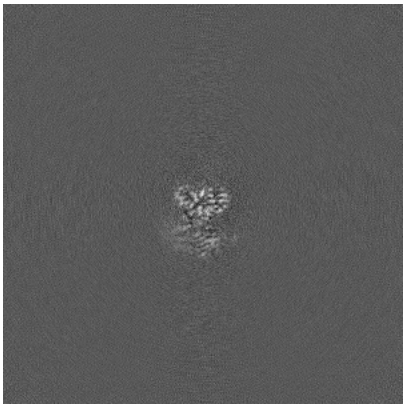

Y Index: 238


Z Index: 232

6.3.2 Raw map


X Index: 247

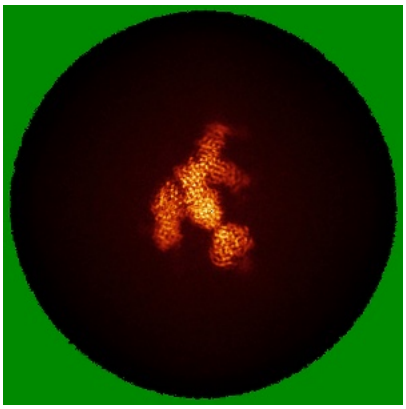

Y Index: 238

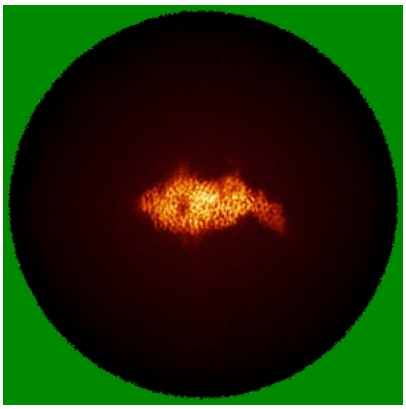

Z Index: 233

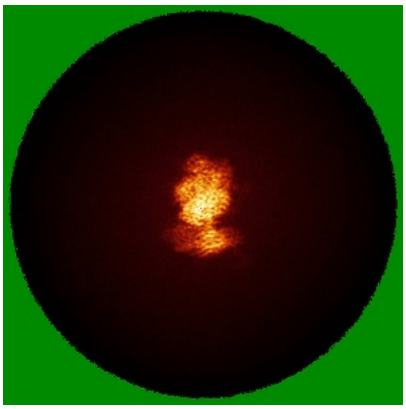
The images above show the largest variance slices of the map in three orthogonal directions.

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

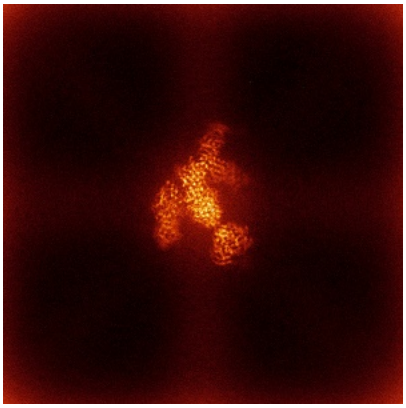
6.4.1 Primary map

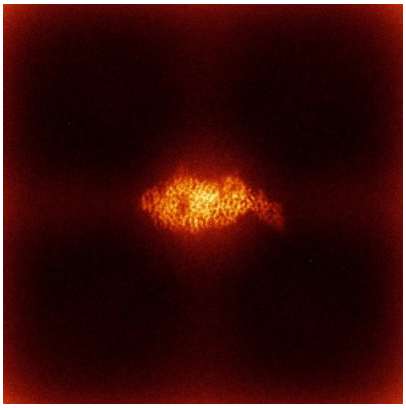

X

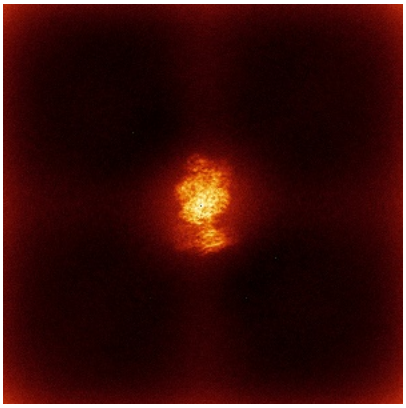

Y


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 0.075. 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.

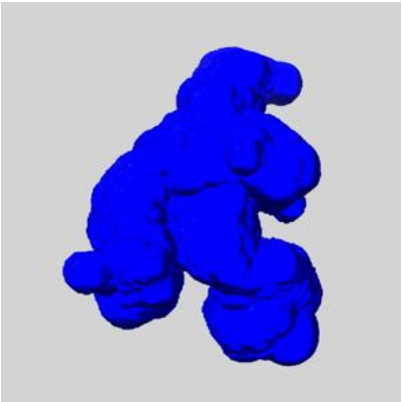
6.6 Mask visualisation (i)

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

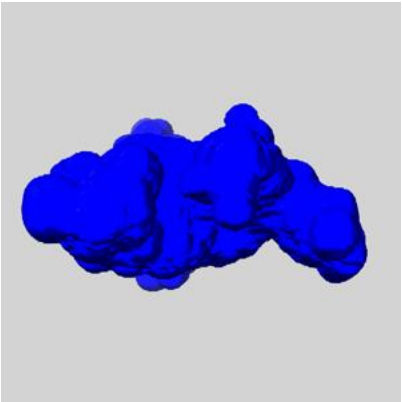
A mask typically either:

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

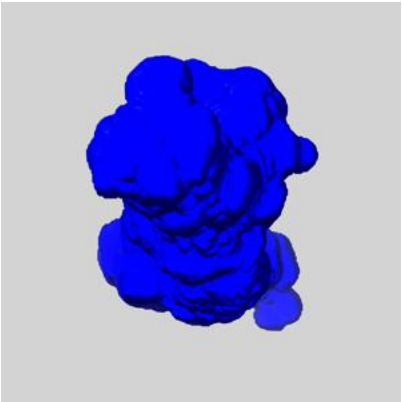
6.6.1 emd_75302_msk_1.map (i)



X



Y

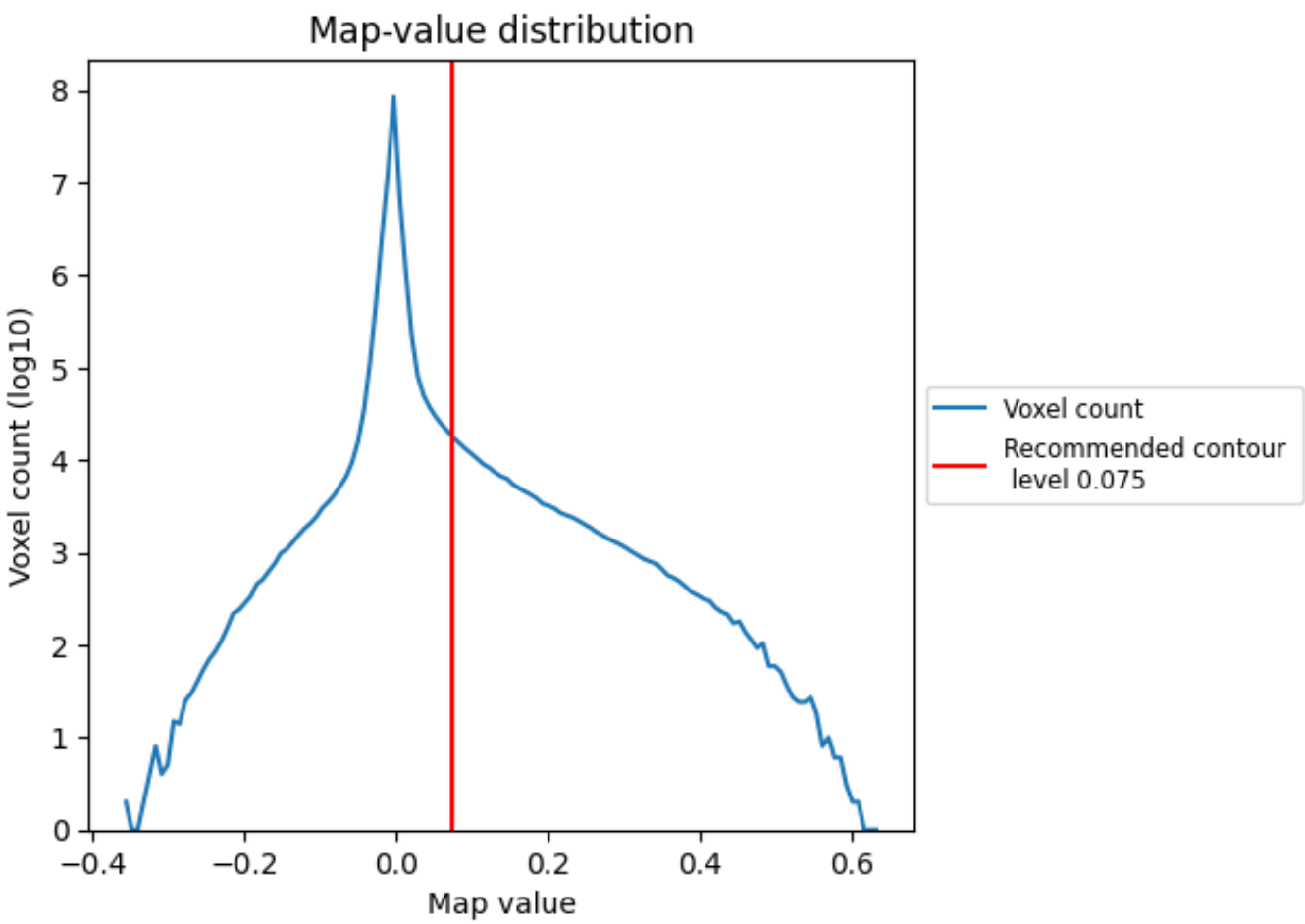


Z

7 Map analysis (i)

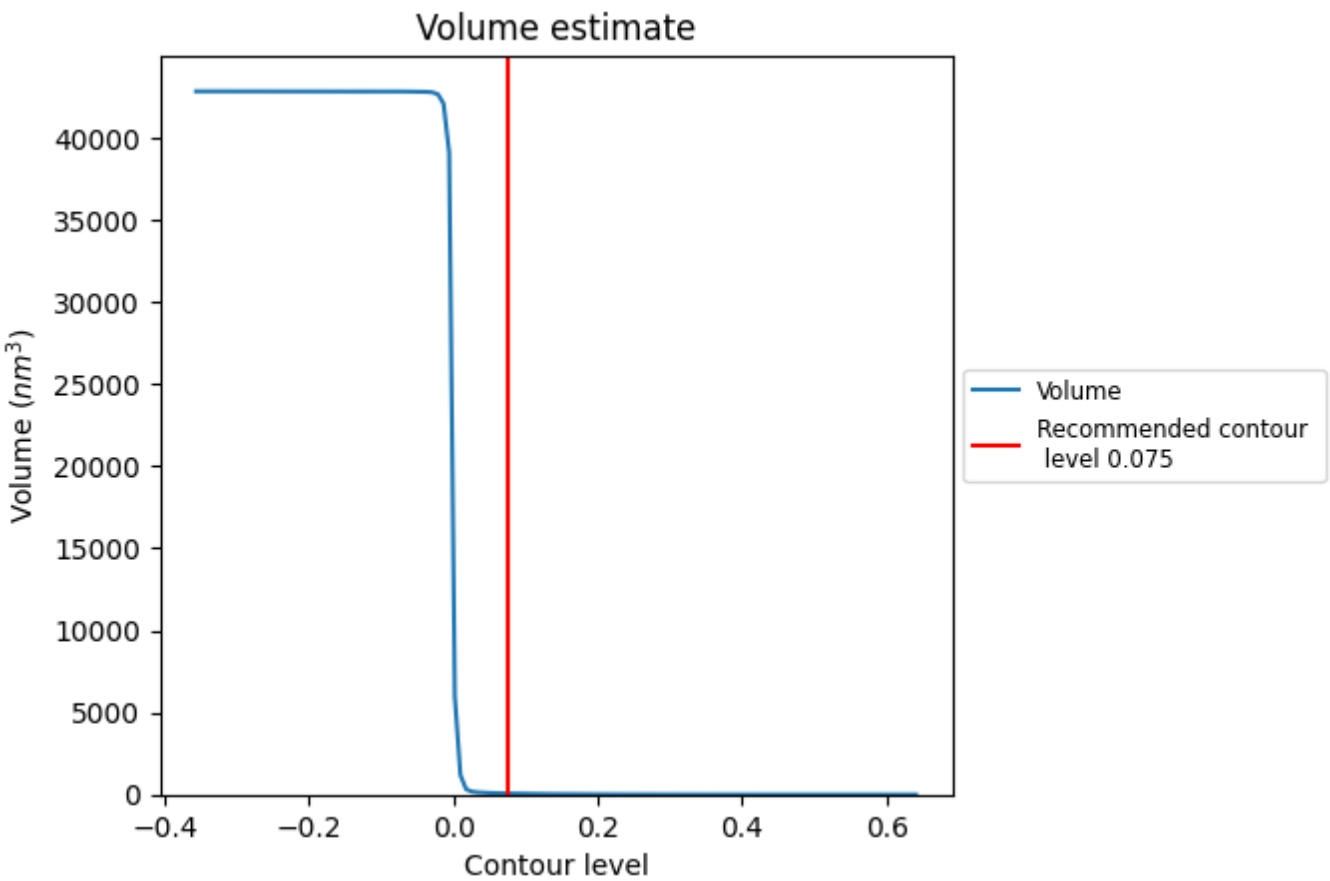
This section contains the results of statistical analysis of the map.

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.

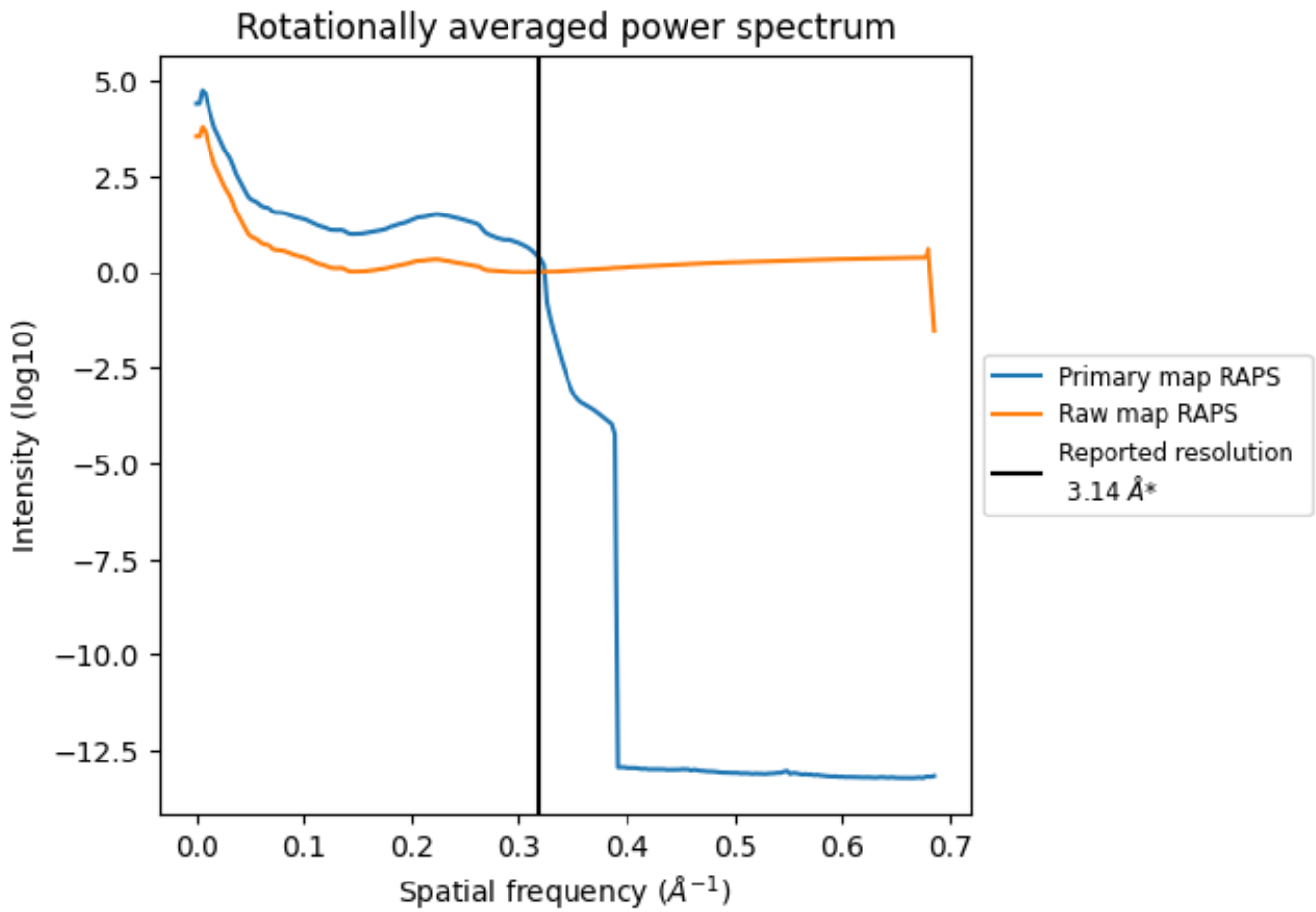
7.2 Volume estimate (i)



The volume at the recommended contour level is 67 nm^3; this corresponds to an approximate mass of 60 kDa.

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

7.3 Rotationally averaged power spectrum (i)

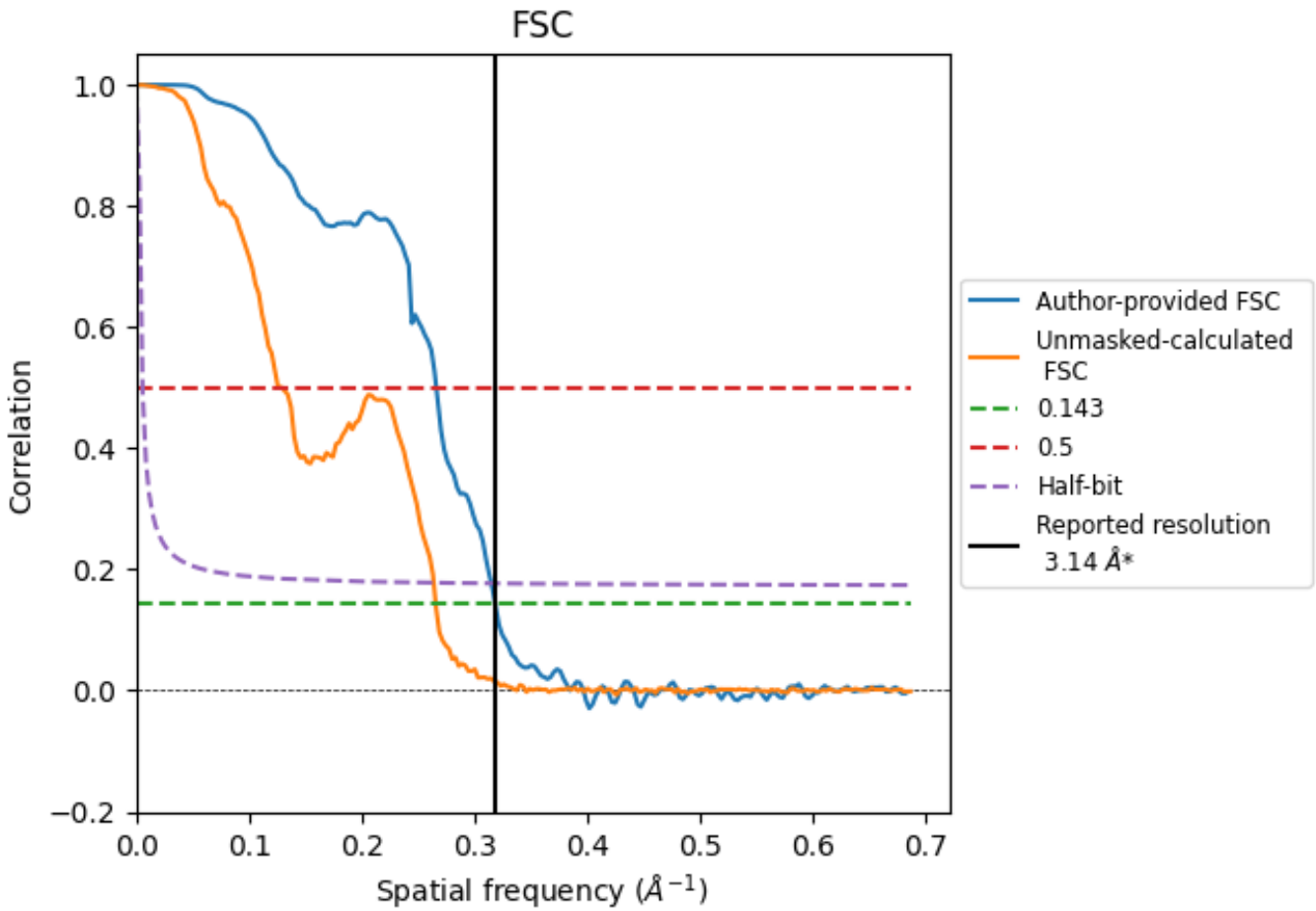


*Reported resolution corresponds to spatial frequency of 0.318 Å^{-1}

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 0.318 Å^{-1}

8.2 Resolution estimates (i)

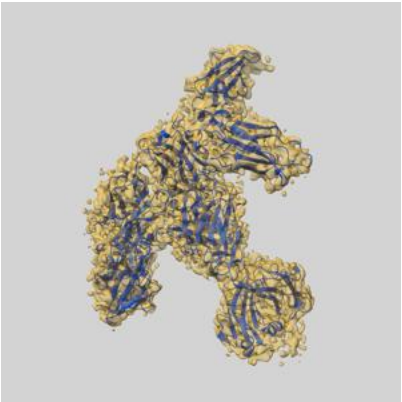
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.14	-	-
Author-provided FSC curve	3.14	3.76	3.18
Unmasked-calculated*	3.77	7.75	3.79

*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 3.77 differs from the reported value 3.14 by more than 10 %

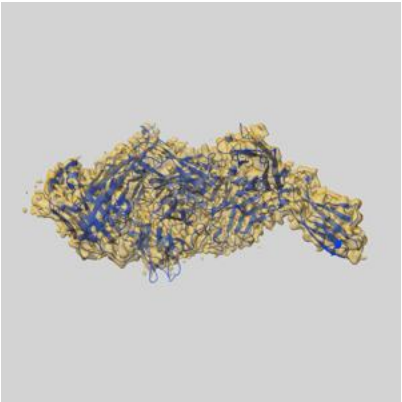
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-75302 and PDB model 10NE. Per-residue inclusion information can be found in section 3 on page 7.

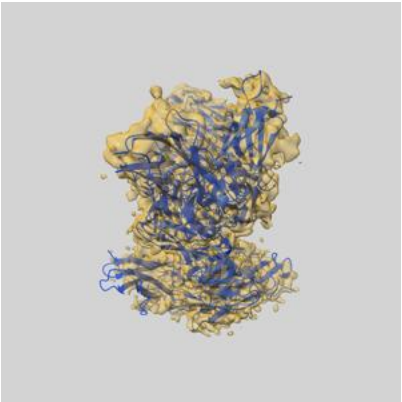
9.1 Map-model overlay (i)



X



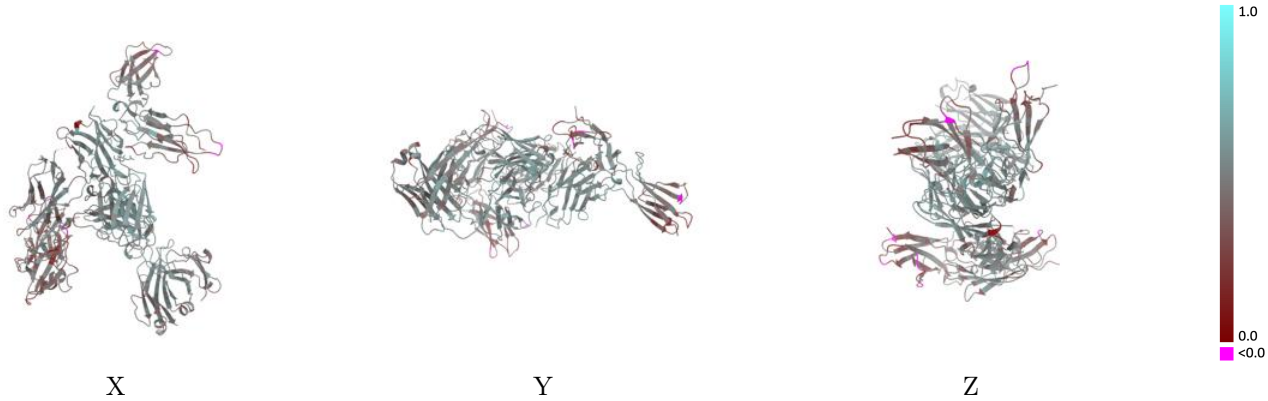
Y



Z

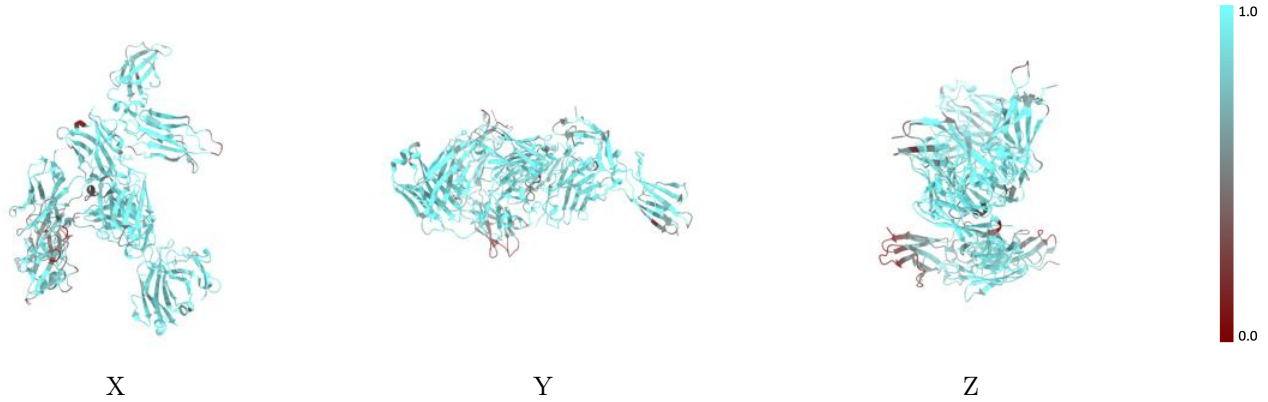
The images above show the 3D surface view of the map at the recommended contour level 0.075 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



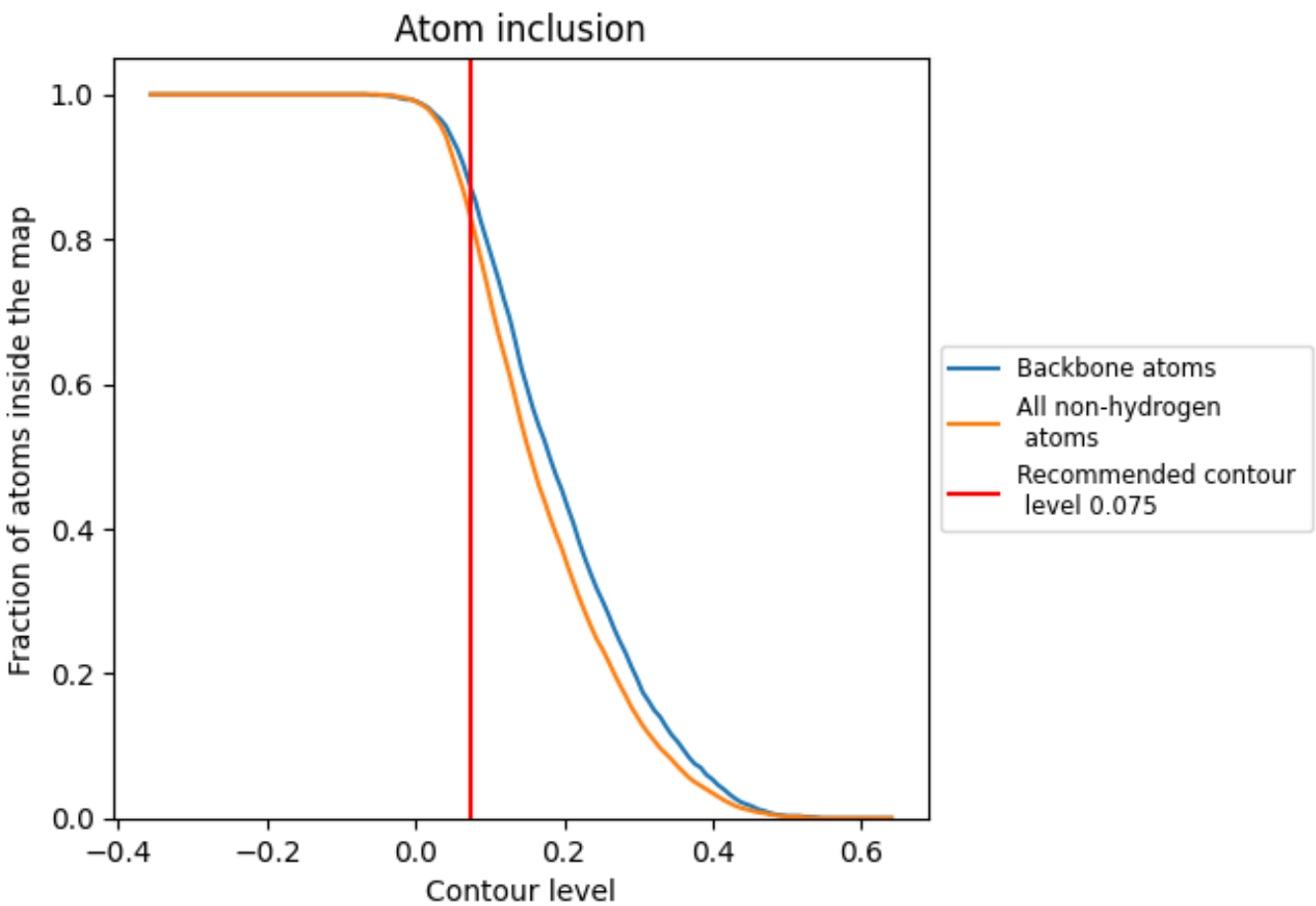
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.075).

9.4 Atom inclusion (i)



At the recommended contour level, 87% of all backbone atoms, 83% 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 (0.075) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8260	0.4660
A	0.6220	0.3610
B	0.8770	0.5010
C	0.8210	0.4290
H	0.9060	0.5200
L	0.8940	0.5120