



Full wwPDB EM Validation Report ⓘ

Nov 16, 2024 – 07:16 AM EST

PDB ID : 9DF0
EMDB ID : EMD-46805
Title : PDCoV S RBD bound to PD41 Fab (local refinement)
Authors : Asarnow, D.; Rexhepaj, M.; Seattle Structural Genomics Center for Infectious Disease (SSGCID); Veessler, D.
Deposited on : 2024-08-29
Resolution : 2.80 Å (reported)
Based on initial models : ., 6bfu

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 ⓘ 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:

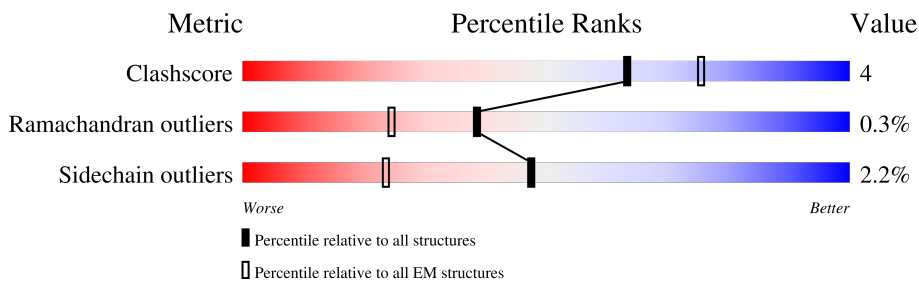
EMDB validation analysis : 0.0.1.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

1 Overall quality at a glance

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

The reported resolution of this entry is 2.80 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	A	1166	
2	H	118	
3	L	111	
4	B	3	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2509 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 Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	112	858	541	146	161	10	0	0

There are 69 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1099	GLY	-	expression tag	UNP A0A6M5ICE2
A	1100	SER	-	expression tag	UNP A0A6M5ICE2
A	1101	GLY	-	expression tag	UNP A0A6M5ICE2
A	1102	TYR	-	expression tag	UNP A0A6M5ICE2
A	1103	ILE	-	expression tag	UNP A0A6M5ICE2
A	1104	PRO	-	expression tag	UNP A0A6M5ICE2
A	1105	GLU	-	expression tag	UNP A0A6M5ICE2
A	1106	ALA	-	expression tag	UNP A0A6M5ICE2
A	1107	PRO	-	expression tag	UNP A0A6M5ICE2
A	1108	ARG	-	expression tag	UNP A0A6M5ICE2
A	1109	ASP	-	expression tag	UNP A0A6M5ICE2
A	1110	GLY	-	expression tag	UNP A0A6M5ICE2
A	1111	GLN	-	expression tag	UNP A0A6M5ICE2
A	1112	ALA	-	expression tag	UNP A0A6M5ICE2
A	1113	TYR	-	expression tag	UNP A0A6M5ICE2
A	1114	VAL	-	expression tag	UNP A0A6M5ICE2
A	1115	ARG	-	expression tag	UNP A0A6M5ICE2
A	1116	LYS	-	expression tag	UNP A0A6M5ICE2
A	1117	ASP	-	expression tag	UNP A0A6M5ICE2
A	1118	GLY	-	expression tag	UNP A0A6M5ICE2
A	1119	GLU	-	expression tag	UNP A0A6M5ICE2
A	1120	TRP	-	expression tag	UNP A0A6M5ICE2
A	1121	VAL	-	expression tag	UNP A0A6M5ICE2
A	1122	LEU	-	expression tag	UNP A0A6M5ICE2
A	1123	LEU	-	expression tag	UNP A0A6M5ICE2
A	1124	SER	-	expression tag	UNP A0A6M5ICE2
A	1125	THR	-	expression tag	UNP A0A6M5ICE2
A	1126	PHE	-	expression tag	UNP A0A6M5ICE2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1127	LEU	-	expression tag	UNP A0A6M5ICE2
A	1128	GLY	-	expression tag	UNP A0A6M5ICE2
A	1129	ARG	-	expression tag	UNP A0A6M5ICE2
A	1130	SER	-	expression tag	UNP A0A6M5ICE2
A	1131	LEU	-	expression tag	UNP A0A6M5ICE2
A	1132	GLU	-	expression tag	UNP A0A6M5ICE2
A	1133	VAL	-	expression tag	UNP A0A6M5ICE2
A	1134	LEU	-	expression tag	UNP A0A6M5ICE2
A	1135	PHE	-	expression tag	UNP A0A6M5ICE2
A	1136	GLN	-	expression tag	UNP A0A6M5ICE2
A	1137	GLY	-	expression tag	UNP A0A6M5ICE2
A	1138	PRO	-	expression tag	UNP A0A6M5ICE2
A	1139	GLY	-	expression tag	UNP A0A6M5ICE2
A	1140	SER	-	expression tag	UNP A0A6M5ICE2
A	1141	GLY	-	expression tag	UNP A0A6M5ICE2
A	1142	GLY	-	expression tag	UNP A0A6M5ICE2
A	1143	LEU	-	expression tag	UNP A0A6M5ICE2
A	1144	ASN	-	expression tag	UNP A0A6M5ICE2
A	1145	ASP	-	expression tag	UNP A0A6M5ICE2
A	1146	ILE	-	expression tag	UNP A0A6M5ICE2
A	1147	PHE	-	expression tag	UNP A0A6M5ICE2
A	1148	GLU	-	expression tag	UNP A0A6M5ICE2
A	1149	ALA	-	expression tag	UNP A0A6M5ICE2
A	1150	GLN	-	expression tag	UNP A0A6M5ICE2
A	1151	LYS	-	expression tag	UNP A0A6M5ICE2
A	1152	ILE	-	expression tag	UNP A0A6M5ICE2
A	1153	GLU	-	expression tag	UNP A0A6M5ICE2
A	1154	TRP	-	expression tag	UNP A0A6M5ICE2
A	1155	HIS	-	expression tag	UNP A0A6M5ICE2
A	1156	GLU	-	expression tag	UNP A0A6M5ICE2
A	1157	GLY	-	expression tag	UNP A0A6M5ICE2
A	1158	SER	-	expression tag	UNP A0A6M5ICE2
A	1159	GLY	-	expression tag	UNP A0A6M5ICE2
A	1160	HIS	-	expression tag	UNP A0A6M5ICE2
A	1161	HIS	-	expression tag	UNP A0A6M5ICE2
A	1162	HIS	-	expression tag	UNP A0A6M5ICE2
A	1163	HIS	-	expression tag	UNP A0A6M5ICE2
A	1164	HIS	-	expression tag	UNP A0A6M5ICE2
A	1165	HIS	-	expression tag	UNP A0A6M5ICE2
A	1166	HIS	-	expression tag	UNP A0A6M5ICE2
A	1167	HIS	-	expression tag	UNP A0A6M5ICE2

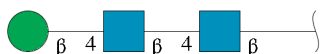
- Molecule 2 is a protein called PD41 Fab variable heavy-chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	H	116	859	562	144	151	2	0	0

- Molecule 3 is a protein called PD41 Fab variable light-chain.

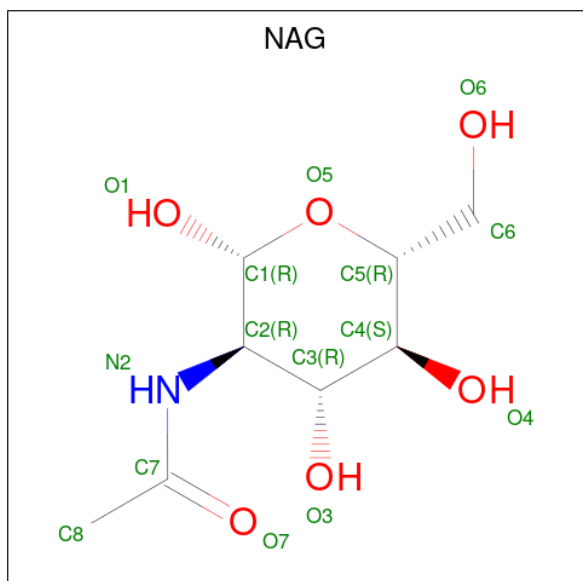
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	L	109	739	467	127	141	4	0	0

- Molecule 4 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	B	3	39	22	2	15	0	0

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).

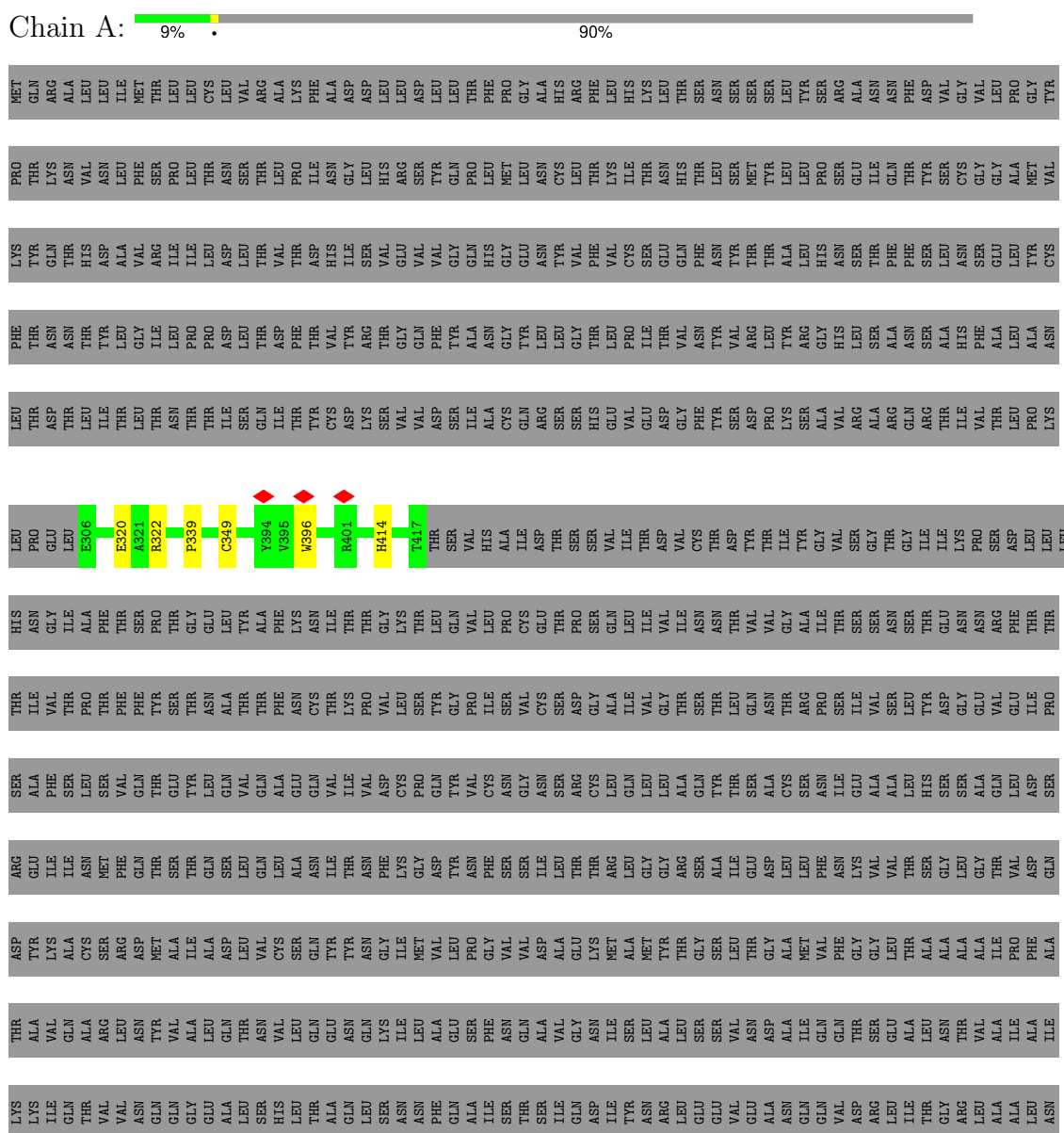


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
5	A	1	14	8	1	5	0

3 Residue-property plots

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: Spike glycoprotein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	438204	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 ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.207	Depositor
Minimum map value	-0.115	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	360.72, 360.72, 360.72	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.835, 0.835, 0.835	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: BMA, 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	0.37	0/873	0.53	0/1185
2	H	0.42	0/885	0.54	0/1217
3	L	0.42	0/757	0.52	0/1035
All	All	0.40	0/2515	0.53	0/3437

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	858	0	809	2	0
2	H	859	0	767	4	0
3	L	739	0	608	13	0
4	B	39	0	34	0	0
5	A	14	0	13	0	0
All	All	2509	0	2231	19	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 (19) 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:H:42:HIS:HD2	2:H:43:PRO:HD2	1.50	0.77
2:H:42:HIS:CD2	2:H:43:PRO:HD2	2.28	0.67
3:L:4:LEU:HB2	3:L:103:GLY:HA2	1.87	0.56
3:L:20:ILE:HD11	3:L:108:LEU:HD12	1.89	0.54
3:L:50:ILE:HD13	3:L:56:ARG:HB3	1.91	0.51
3:L:52:ASP:O	3:L:54:SER:N	2.45	0.50
3:L:28:ASP:HA	3:L:93:TYR:O	2.15	0.47
3:L:28:ASP:OD1	3:L:29:VAL:N	2.44	0.46
3:L:23:THR:HA	3:L:72:THR:HB	1.97	0.46
3:L:56:ARG:NE	3:L:62:ASN:HA	2.31	0.46
3:L:28:ASP:HA	3:L:94:ALA:HA	1.98	0.45
2:H:49:TRP:CZ2	2:H:51:GLY:HA2	2.53	0.44
3:L:56:ARG:HE	3:L:62:ASN:HA	1.83	0.43
3:L:6:GLN:HE21	3:L:6:GLN:HB3	1.64	0.42
1:A:320:GLU:OE1	1:A:322:ARG:NH2	2.53	0.42
2:H:40:ARG:HB2	2:H:50:ILE:HD11	2.03	0.41
1:A:339:PRO:O	1:A:414:HIS:HA	2.21	0.41
3:L:48:LEU:HD21	3:L:51:TYR:HB3	2.02	0.41
3:L:37:TRP:HB2	3:L:50:ILE:HB	2.03	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	110/1166 (9%)	107 (97%)	3 (3%)	0	100	100
2	H	114/118 (97%)	111 (97%)	2 (2%)	1 (1%)	14	42
3	L	107/111 (96%)	99 (92%)	8 (8%)	0	100	100
All	All	331/1395 (24%)	317 (96%)	13 (4%)	1 (0%)	38	67

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	102	VAL

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	92/1024 (9%)	90 (98%)	2 (2%)	47	79
2	H	76/102 (74%)	76 (100%)	0	100	100
3	L	58/90 (64%)	55 (95%)	3 (5%)	19	50
All	All	226/1216 (19%)	221 (98%)	5 (2%)	47	79

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	349	CYS
1	A	396	TRP
3	L	20	ILE
3	L	72	THR
3	L	90	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	H	42	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

3 monosaccharides are 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
4	NAG	B	1	4,1	14,14,15	0.79	0	17,19,21	1.02	1 (5%)
4	NAG	B	2	4	14,14,15	0.72	0	17,19,21	0.88	1 (5%)
4	BMA	B	3	4	11,11,12	0.84	0	15,15,17	1.84	1 (6%)

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
4	NAG	B	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	B	2	4	-	0/6/23/26	0/1/1/1
4	BMA	B	3	4	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	3	BMA	C1-O5-C5	6.02	120.25	112.19
4	B	1	NAG	O5-C1-C2	-2.48	107.45	111.29
4	B	2	NAG	C1-O5-C5	2.32	115.29	112.19

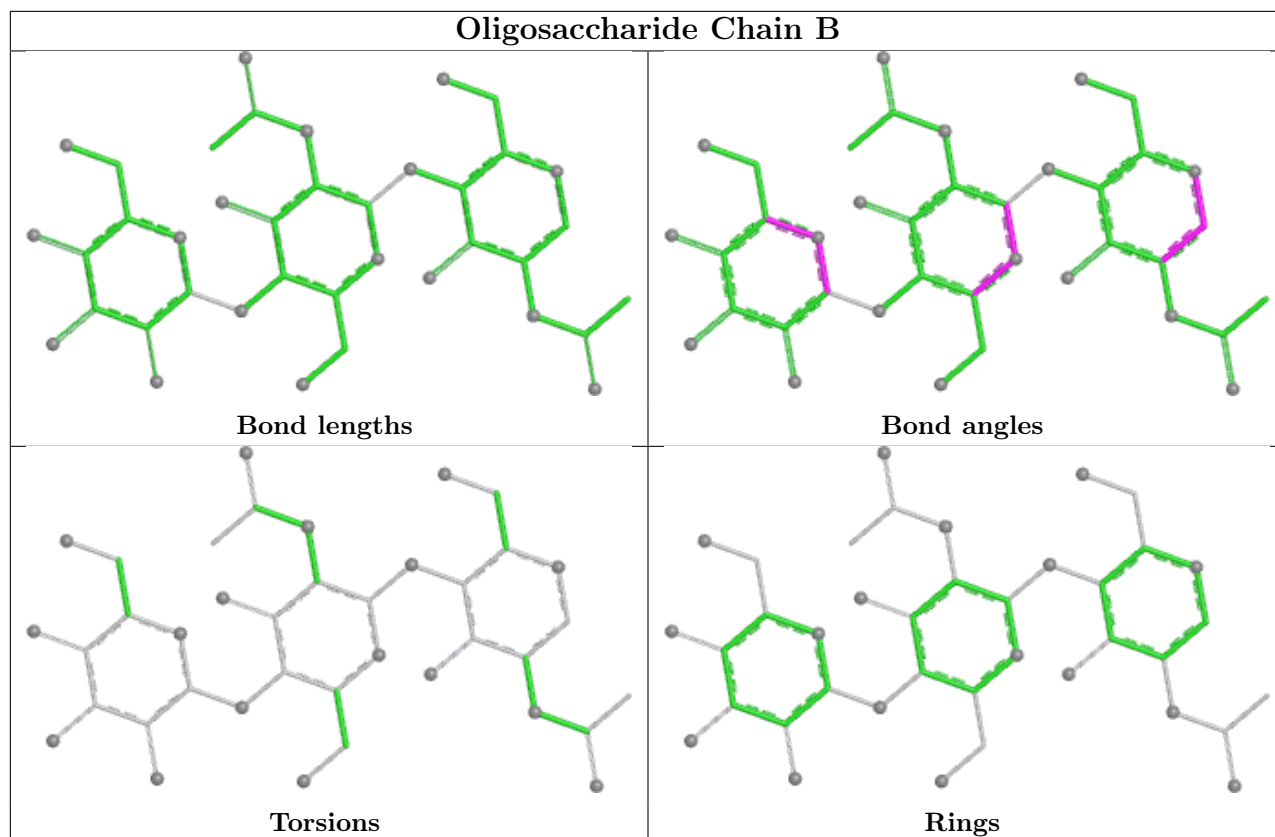
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



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	$\# Z > 2$
5	NAG	A	1201	1	14,14,15	0.64	0	17,19,21	0.96	1 (5%)

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
5	NAG	A	1201	1	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
5	A	1201	NAG	O5-C1-C2	-2.16	107.95	111.29

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1201	NAG	C1-C2-N2-C7

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.

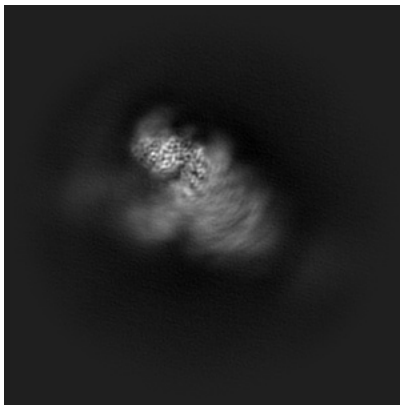
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-46805. These allow visual inspection of the internal detail of the map and identification of artifacts.

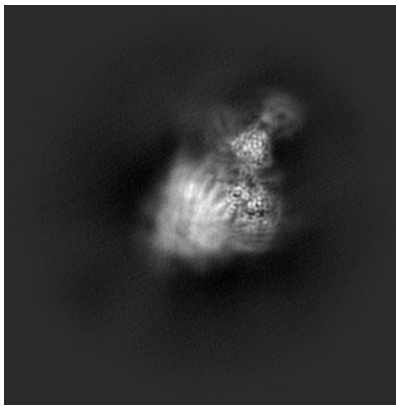
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

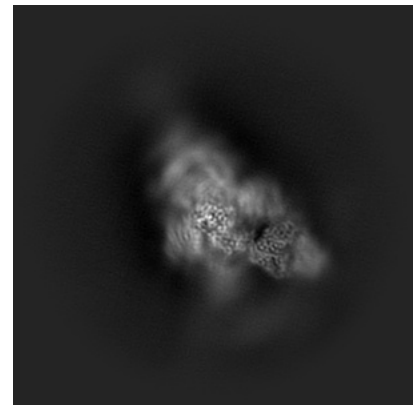
6.1.1 Primary map



X

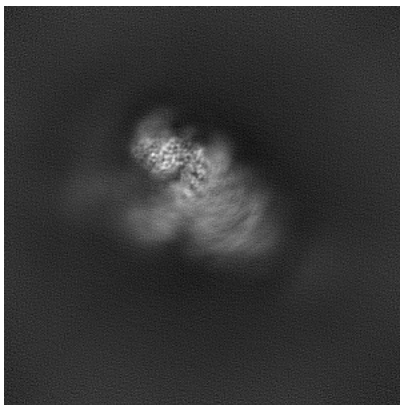


Y

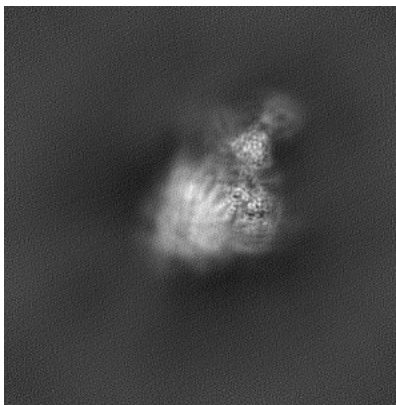


Z

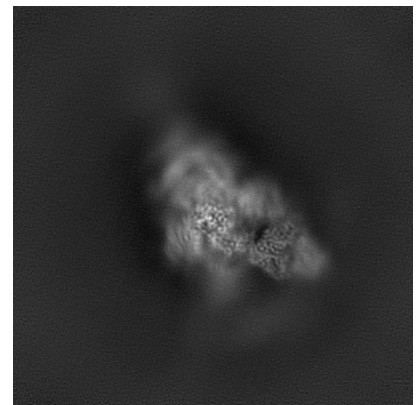
6.1.2 Raw map



X



Y

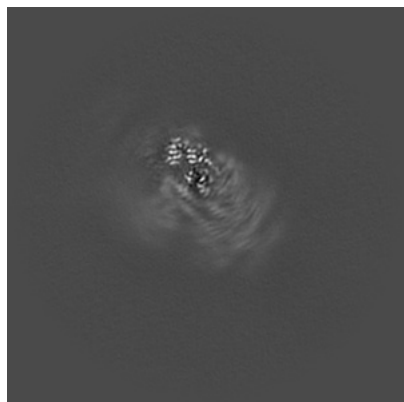


Z

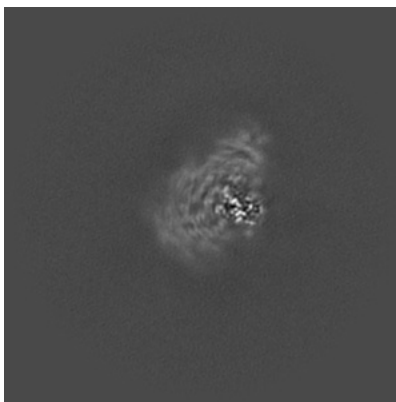
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

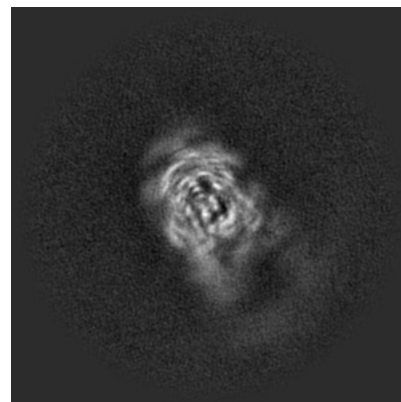
6.2.1 Primary map



X Index: 216

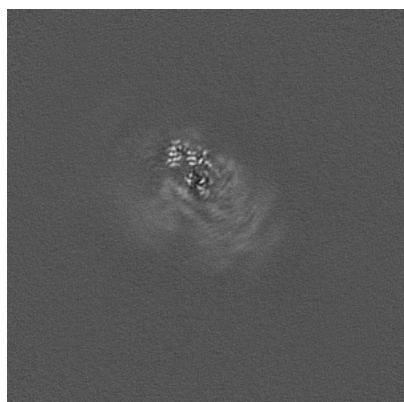


Y Index: 216

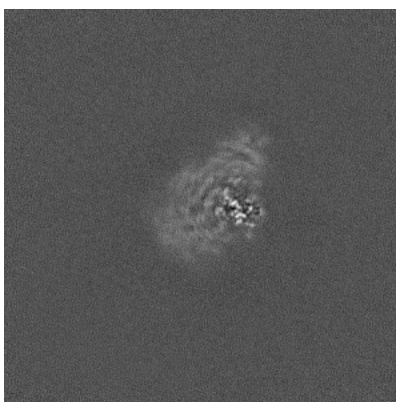


Z Index: 216

6.2.2 Raw map



X Index: 216



Y Index: 216

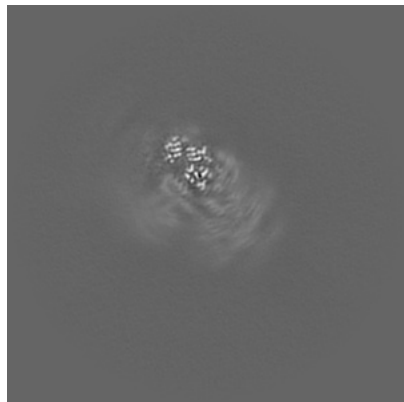


Z Index: 216

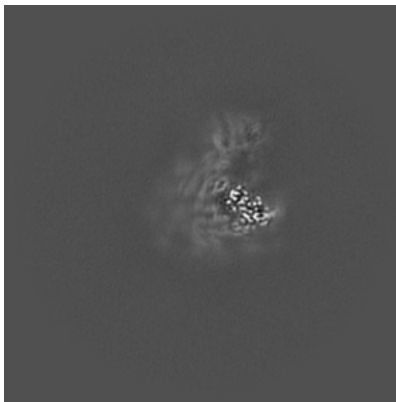
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

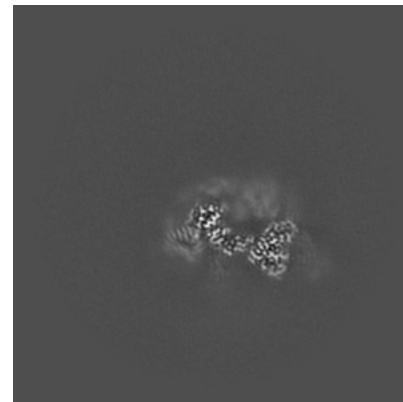
6.3.1 Primary map



X Index: 218

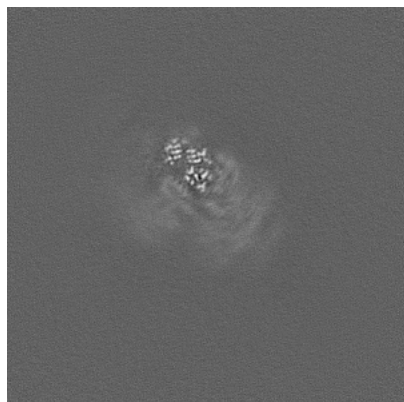


Y Index: 200

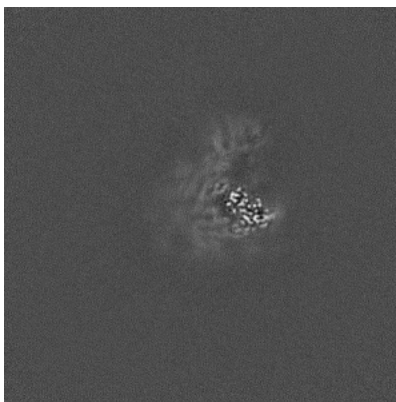


Z Index: 270

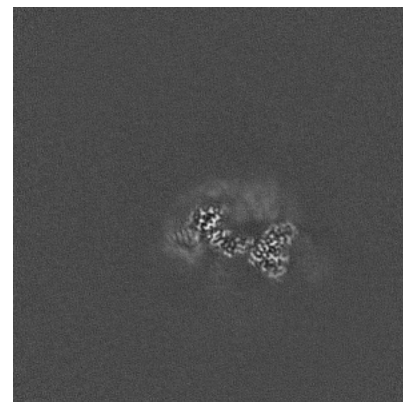
6.3.2 Raw map



X Index: 218



Y Index: 200

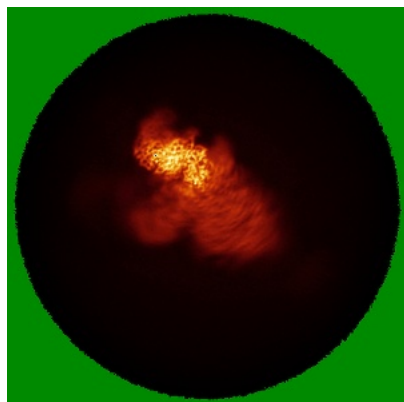


Z Index: 270

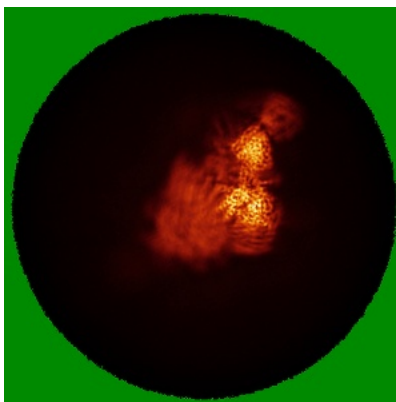
The images above show the largest variance slices of the map in three orthogonal directions.

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

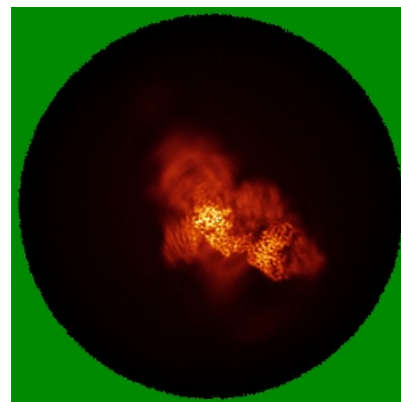
6.4.1 Primary map



X

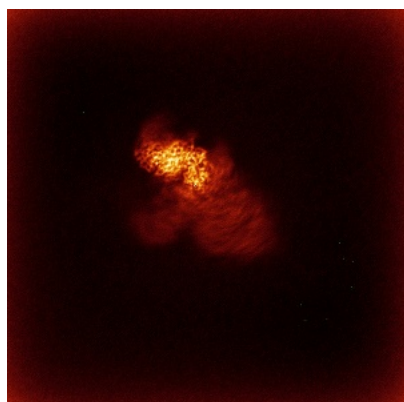


Y

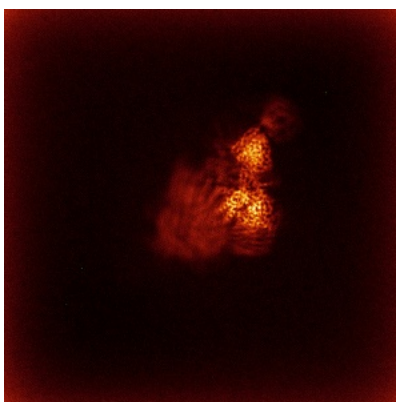


Z

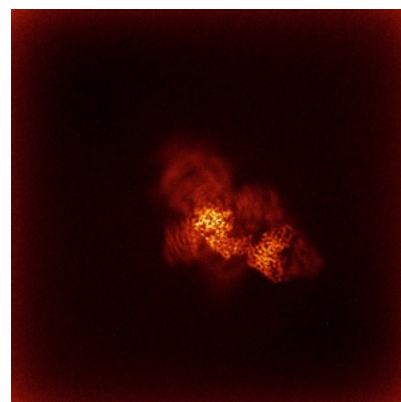
6.4.2 Raw map



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 0.05. 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.

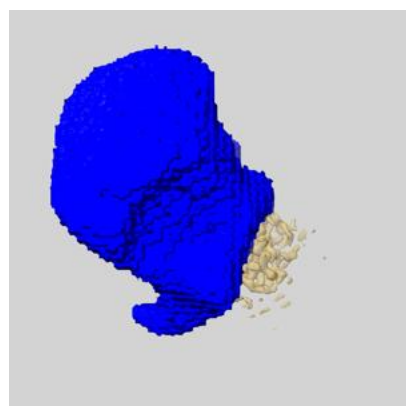
6.6 Mask visualisation [i](#)

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

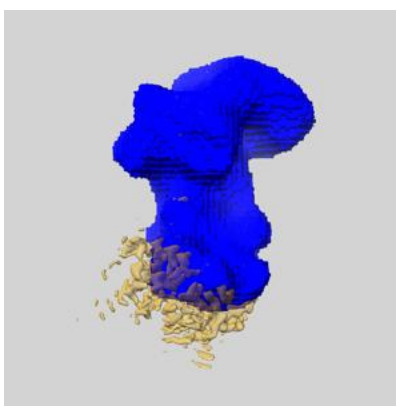
A mask typically either:

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

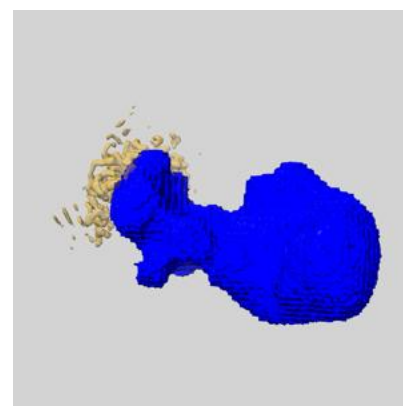
6.6.1 emd_46805_msk_1.map [i](#)



X

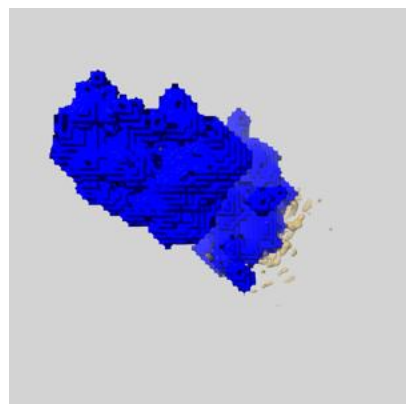


Y

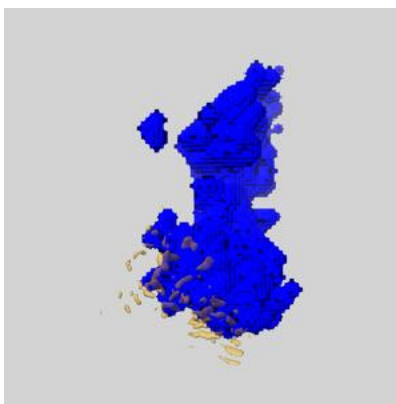


Z

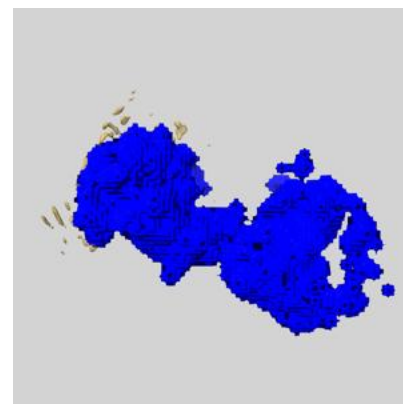
6.6.2 emd_46805_msk_2.map [i](#)



X



Y

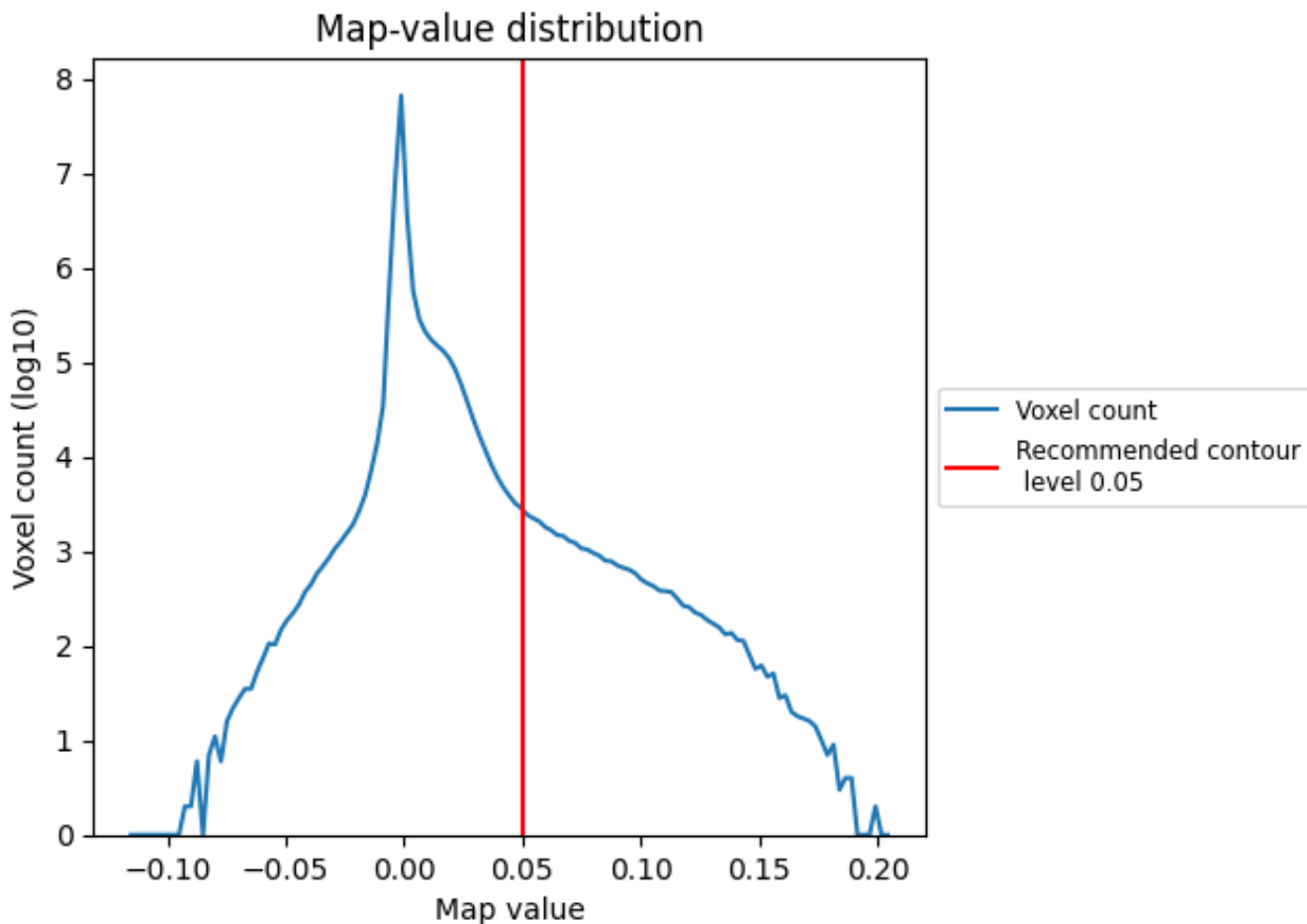


Z

7 Map analysis [i](#)

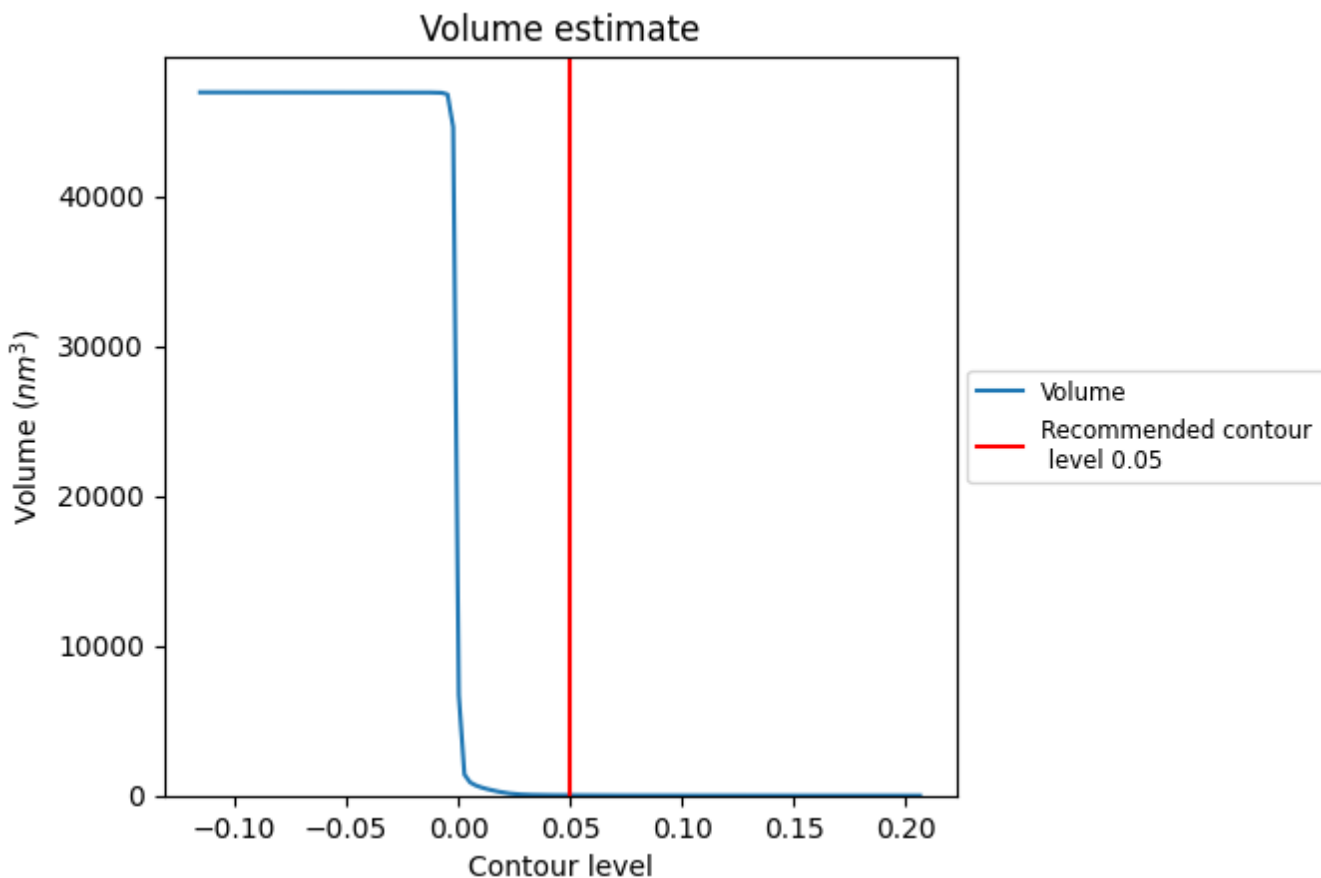
This section contains the results of statistical analysis of the map.

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.

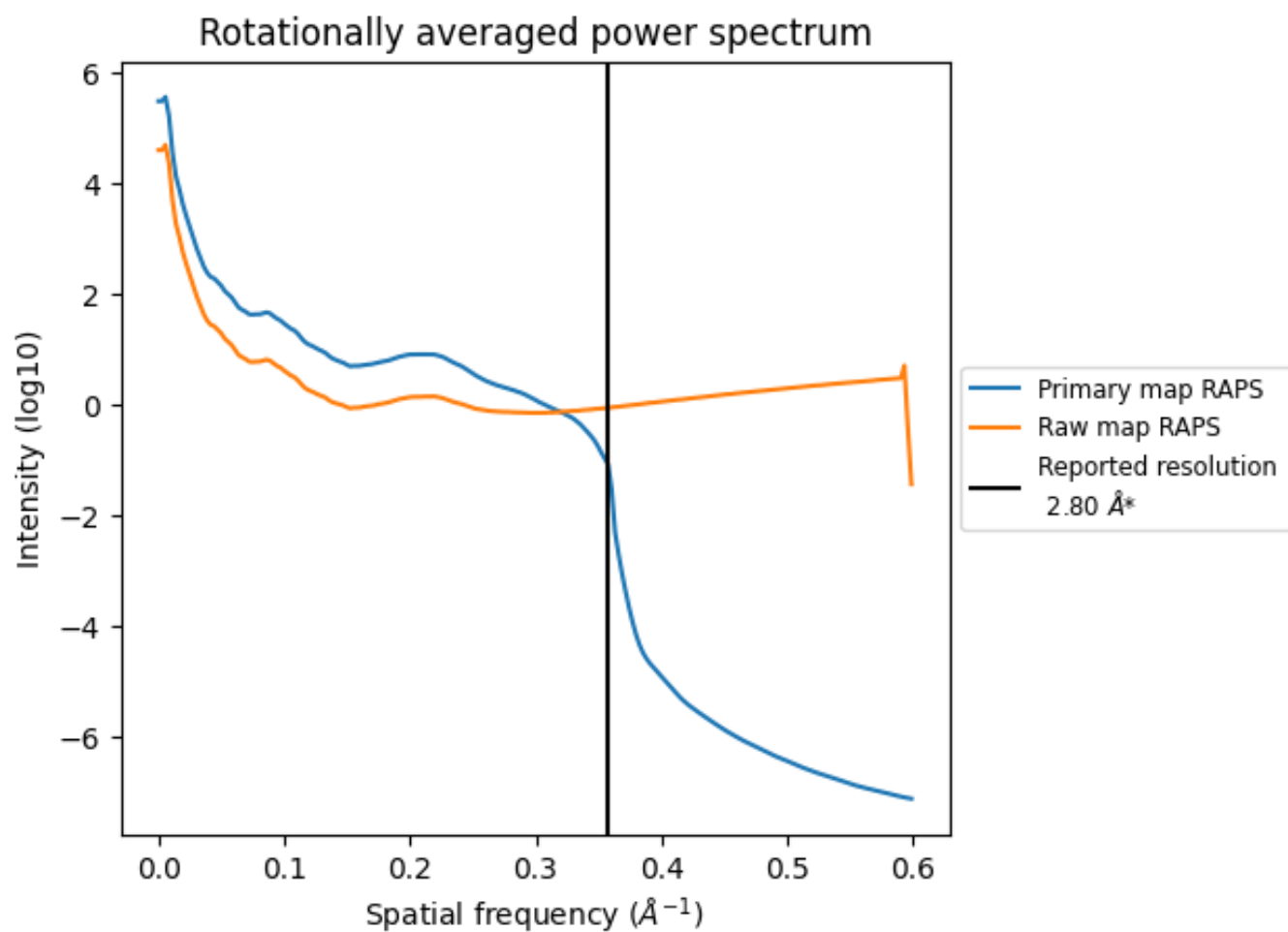
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 18 nm³; this corresponds to an approximate mass of 16 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](#)

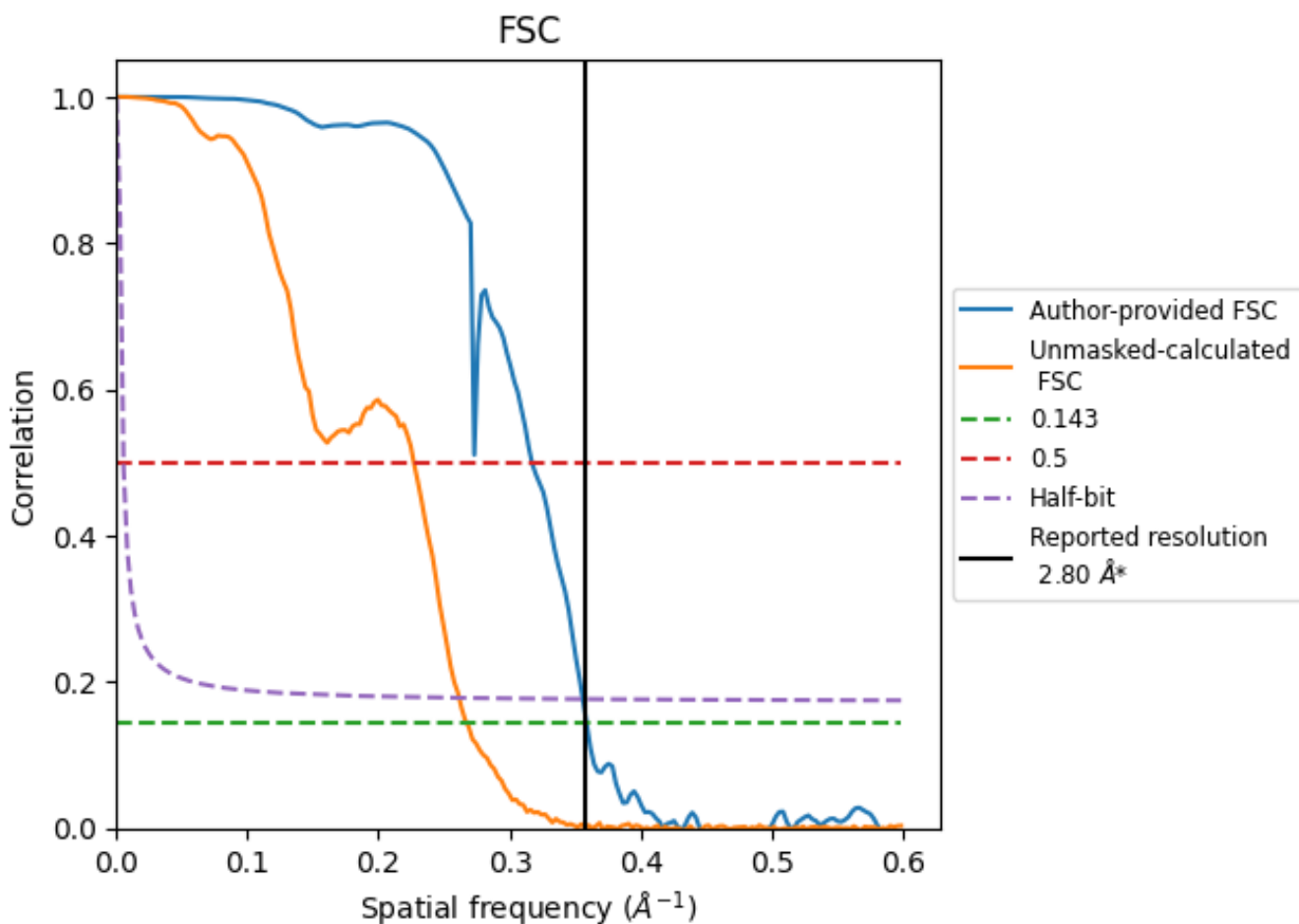


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

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 0.357\AA^{-1}

8.2 Resolution estimates [i](#)

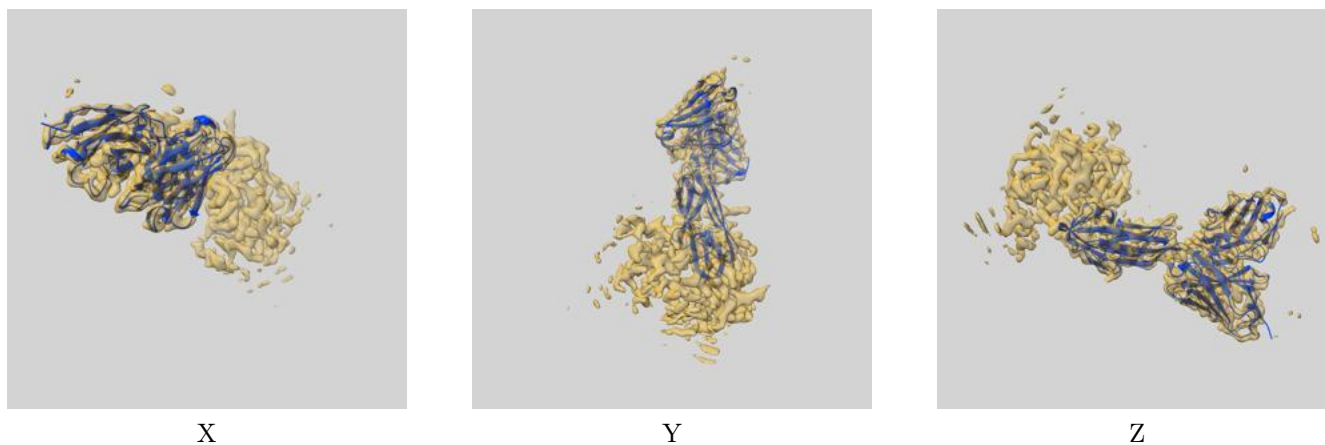
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.79	3.15	2.81
Unmasked-calculated*	3.74	4.41	3.82

*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 3.74 differs from the reported value 2.8 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-46805 and PDB model 9DF0. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



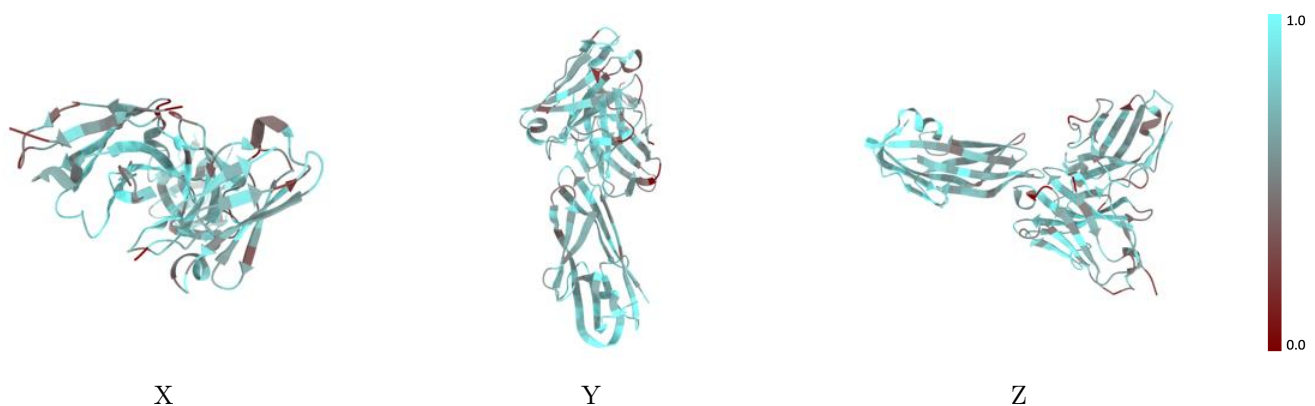
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



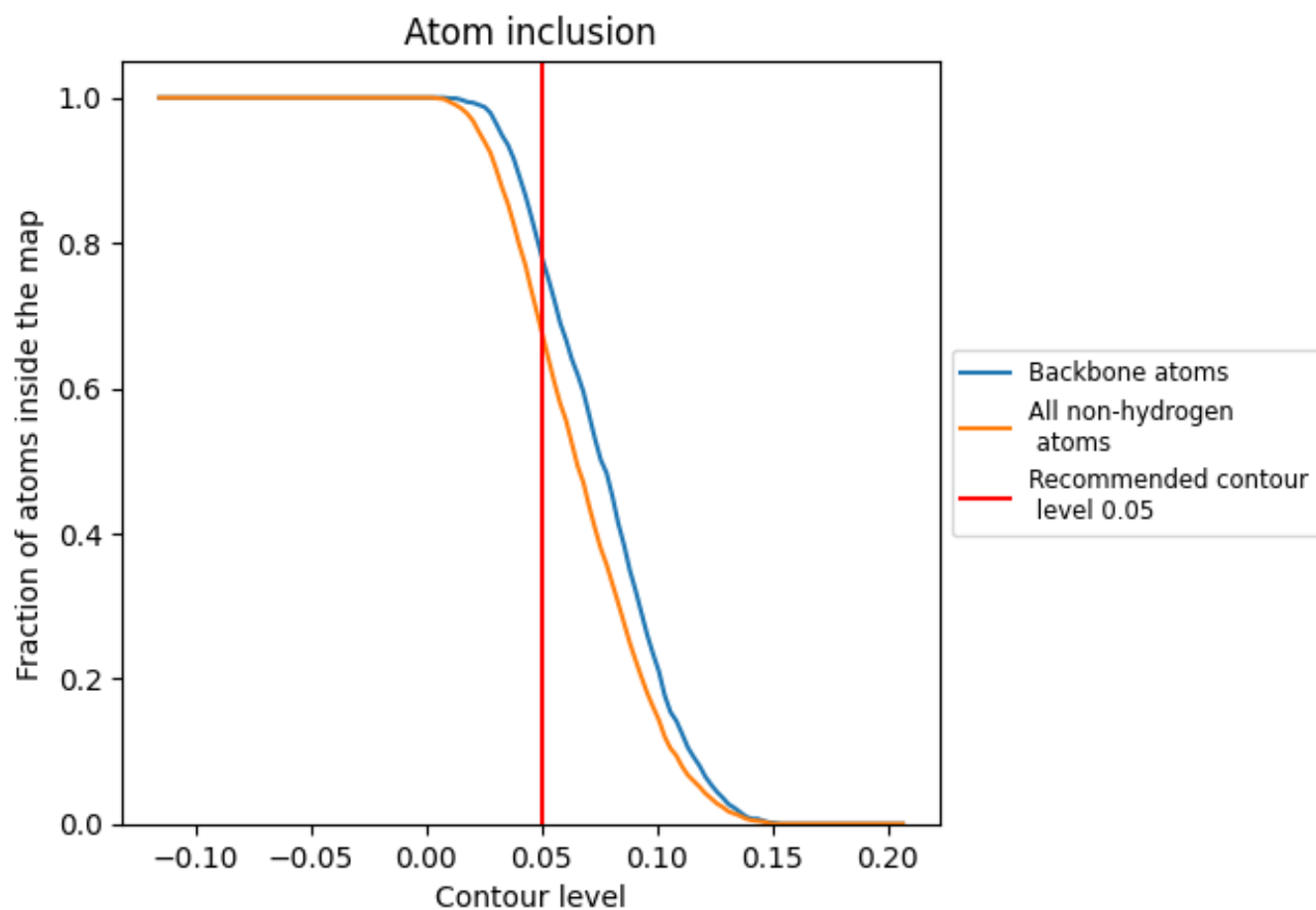
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).











9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 68% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6800	 0.5620
A	 0.6970	 0.5820
B	 0.3330	 0.4470
H	 0.7060	 0.5670
L	 0.6470	 0.5380

