



wwPDB EM Validation Summary Report ⓘ

May 6, 2025 – 09:11 AM EDT

PDB ID : 9CE0 / pdb_00009ce0
EMDB ID : EMD-45489
Title : DosP Apo Bent form
Authors : Kumar, P.; Kober, D.L.
Deposited on : 2024-06-25
Resolution : 3.97 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev118
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
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) : 2.43.1

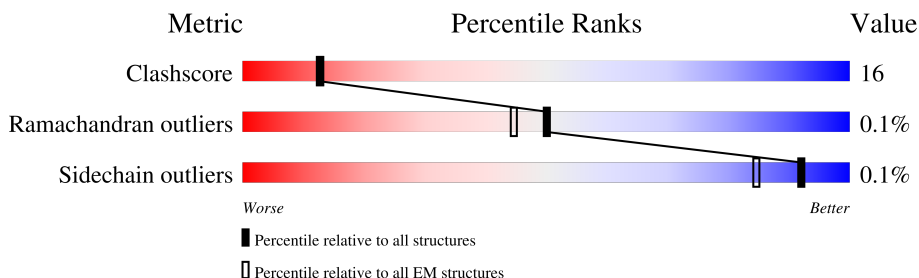
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.97 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	806	
1	B	806	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	OXY	A	902	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12551 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.

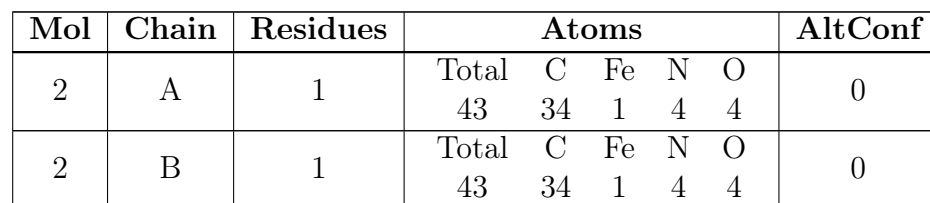
- Molecule 1 is a protein called Oxygen sensor protein DosP.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	787	Total	C	N	O	S	0	0
			6257	3961	1095	1168	33		
1	B	781	Total	C	N	O	S	0	0
			6204	3928	1085	1158	33		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP P76129
A	2	ARG	-	expression tag	UNP P76129
A	3	GLN	-	expression tag	UNP P76129
A	4	ASP	-	expression tag	UNP P76129
A	5	ALA	-	expression tag	UNP P76129
A	6	GLU	-	expression tag	UNP P76129
A	7	VAL	-	expression tag	UNP P76129
A	8	ILE	-	expression tag	UNP P76129
A	16	SER	ASN	conflict	UNP P76129
A	195	THR	ILE	conflict	UNP P76129
B	1	MET	-	expression tag	UNP P76129
B	2	ARG	-	expression tag	UNP P76129
B	3	GLN	-	expression tag	UNP P76129
B	4	ASP	-	expression tag	UNP P76129
B	5	ALA	-	expression tag	UNP P76129
B	6	GLU	-	expression tag	UNP P76129
B	7	VAL	-	expression tag	UNP P76129
B	8	ILE	-	expression tag	UNP P76129
B	16	SER	ASN	conflict	UNP P76129
B	195	THR	ILE	conflict	UNP P76129

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$) (labeled as "Ligand of Interest" by depositor).



- OXY
- O1 O = O O2

Mol	Chain	Residues	Atoms	AltConf
3	A	1	Total O 2 2	0



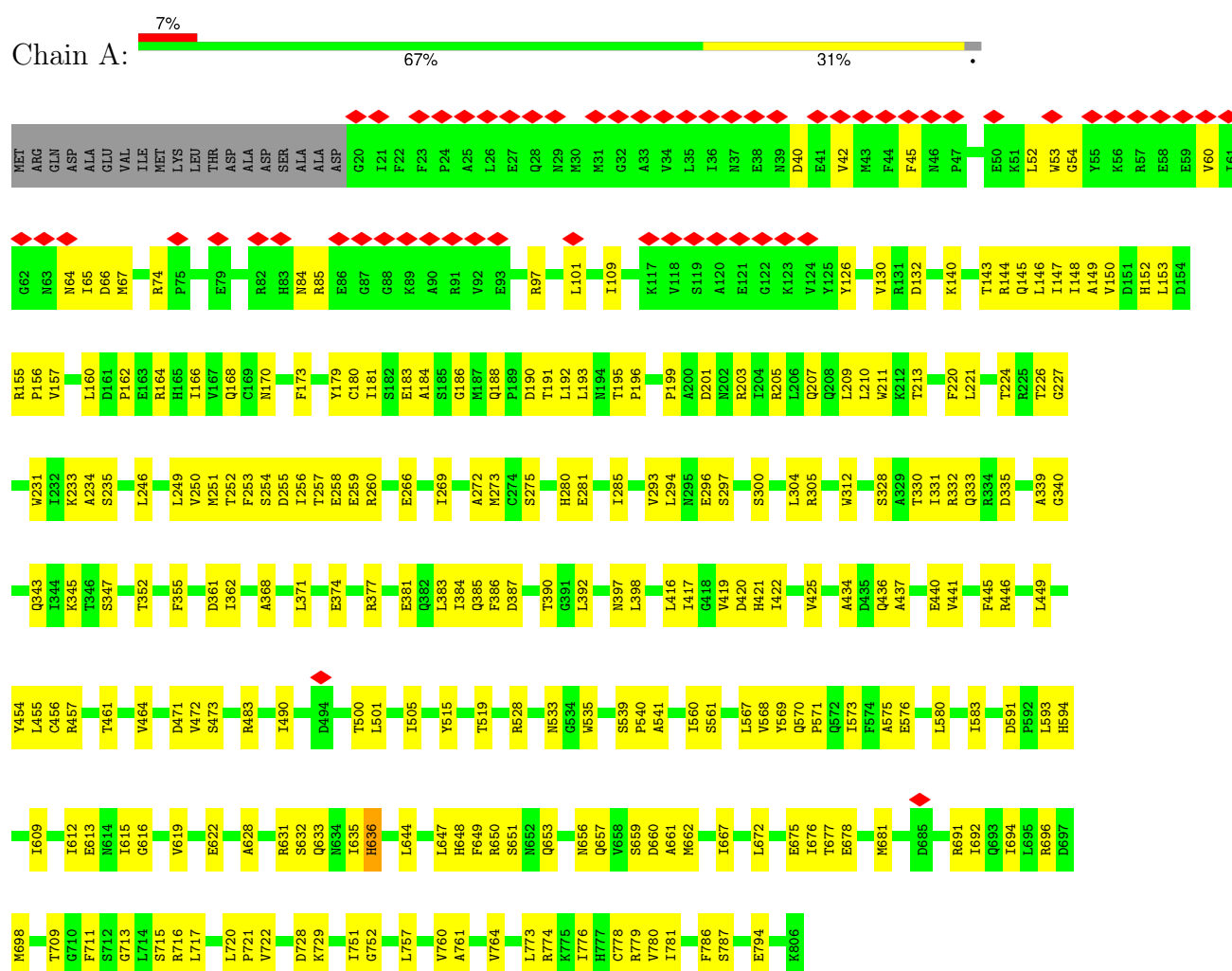
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
3	B	1	Total	O	0
			2	2	

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: Oxygen sensor protein DosP



• Molecule 1: Oxygen sensor protein DosP



MET	ARG	GLN	ASP	ALA	GLU	VAL	ILE	MET	LYS	LEU	THR	ASP	ALA	ASP	SER	ALA	ASP	G20	I21	F22	F23	P24	G28	N29	M30	M31	G32	A33	V34	L35	I36	N37	E38	N39	D40	M43	M46	W53	G54	Y55	K56	R57	E58	E59	V60	I61	G62	N63	N64	I65	D66	M67	L68	I69
P70	R71	D72	L73	R74	I81	R82	H83	N84	R85	E86	G87	G88	K89	A90	R91	V92	E93	G94	E98	L101	E102	I109	R112	K117	V118	S119	A120	E121	G122	K123	R131	Q139	K140	E141	Q142	T143	R144	Q145	L146	I147	I148	A149	V150	D151	H152	L153	D154	R155	P156	V157	I158			
V159	L160	R164	Q168	C169	M170	R171	T174	G178	Y179	C180	I181	S182	E183	M187	Q188	P189	D190	T191	L192	L193	T195	F198	R203	I204	R205	L206	Q207	Q208	L209	L210	W211	R215	D216	Q217	D218	E219	F220	L221	L222	W231	I232	K233	A234	S235	I236	D241	H245							
N248	L249	V250	M251	T252	F253	I256	E259	R260	Q261	I262	R263	Q264	L265	E266	Q267	M268	I269	L270	A271	A272	M273	P277	M282	L285	I286	N289	V293	L304	W312	Q322	N323	S326	W327	I331	P338	A339	Q343	G349	S353	E357	R358													
V359	A360	D361	I362	S363	M366	Q373	R377	GLN	HIS	ILE	GLU	GLN	LEU	I384	Q385	T390	L398	D404	D407	K408	I417	G418	V419	D420	H421	A437	L438	L439	E440	V441	C456	R457	T461	V464	L482	R483	V484	V485	V486	S487	I490	M491	I492	L499										
T500	L501	N512	R513	D514	Y515	L516	T519	M524	D525	Y526	I527	R528	K529	N530	Q536	F537	F538	S539	M542	G553	N562	N563	Q564	L565	K566	Q572	I573	T577	Y581	G582	I583	R588	W589	H590	D591	P592	L593	V597	P598	P599	F602	L605	E611	I612										
E613	M614	W618	E622	R631	S632	K633	F634	I635	H636	I637	H648	P649	R650	S651	M652	Q653	L654	P655	N656	Q657	V658	S659	M662	D668	Q671	M680	H684	D685	I688	F689	K690	R691	I692	Q693	I694	L695	R696	L702	D706	D707	F707	G708	T709	S712	S715									
R716	L717	V722	K726	I727	D728	K729	S730	F731	I732	D733	R734	E738	I741	L744	L745	E746	A747	S750	I751	V760	A761	E762	G763	V764	L773	R774	K775	I776	H777	C778	R779	V780	I781	F786	E793	E794	L803	P804	L805	K806														

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	154173	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.985	Depositor
Minimum map value	-0.226	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.123	Depositor
Map size (Å)	413.30002, 413.30002, 413.30002	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.6144532, 1.6144532, 1.6144532	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: HEM, OXY

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	0.22	0/6385	0.41	0/8650
1	B	0.22	0/6330	0.42	0/8574
All	All	0.22	0/12715	0.41	0/17224

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	6257	0	6236	213	0
1	B	6204	0	6184	213	0
2	A	43	0	30	5	0
2	B	43	0	30	6	0
3	A	2	0	0	2	0
3	B	2	0	0	0	0
All	All	12551	0	12480	410	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 16.

The worst 5 of 410 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:A:140:LYS:O	1:A:143:THR:OG1	1.93	0.87
1:B:326:SER:OG	1:B:343:GLN:NE2	2.10	0.85
1:B:164:ARG:NE	1:B:210:LEU:O	2.09	0.84
1:B:536:GLN:OE1	1:B:537:PHE:N	2.10	0.84
1:A:422:ILE:HG21	1:A:461:THR:HG21	1.56	0.84

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	785/806 (97%)	730 (93%)	53 (7%)	2 (0%)	37	70
1	B	777/806 (96%)	732 (94%)	45 (6%)	0	100	100
All	All	1562/1612 (97%)	1462 (94%)	98 (6%)	2 (0%)	50	81

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	53	TRP
1	A	636	HIS

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	683/698 (98%)	683 (100%)	0	100	100
1	B	677/698 (97%)	675 (100%)	2 (0%)	91	92
All	All	1360/1396 (97%)	1358 (100%)	2 (0%)	92	95

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

Mol	Chain	Res	Type
1	B	153	LEU
1	B	384	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	343	GLN
1	B	693	GLN
1	A	648	HIS
1	A	663	HIS
1	A	670	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](#)

4 ligands 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	$\# Z > 2$
3	OXY	B	902	2	1,1,1	0.17	0	-		
3	OXY	A	902	2	1,1,1	0.17	0	-		
2	HEM	A	901	3	42,50,50	1.52	6 (14%)	46,82,82	1.25	4 (8%)
2	HEM	B	901	1,3	42,50,50	1.52	6 (14%)	46,82,82	1.33	6 (13%)

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
2	HEM	A	901	3	-	5/12/54/54	-
2	HEM	B	901	1,3	-	1/12/54/54	-

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	901	HEM	C3C-C2C	-4.53	1.34	1.40
2	A	901	HEM	C3C-C2C	-4.53	1.34	1.40
2	B	901	HEM	C3C-CAC	3.38	1.55	1.47
2	A	901	HEM	C3C-CAC	3.36	1.55	1.47
2	A	901	HEM	C3C-C4C	3.08	1.45	1.41

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	901	HEM	C4B-CHC-C1C	2.71	126.13	122.56
2	A	901	HEM	C4D-ND-C1D	2.53	108.20	105.21
2	B	901	HEM	C4D-ND-C1D	2.49	108.15	105.21
2	B	901	HEM	C4C-CHD-C1D	2.40	125.73	122.56
2	B	901	HEM	C1B-NB-C4B	2.36	108.00	105.21

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	901	HEM	C2A-CAA-CBA-CGA

Continued on next page...

Continued from previous page...

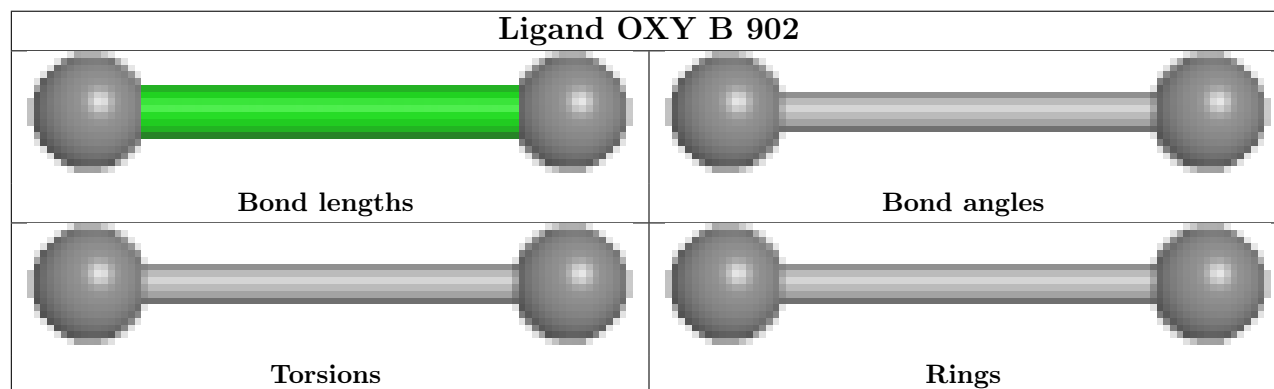
Mol	Chain	Res	Type	Atoms
2	A	901	HEM	C4D-C3D-CAD-CBD
2	A	901	HEM	C2D-C3D-CAD-CBD
2	A	901	HEM	CAA-CBA-CGA-O1A
2	A	901	HEM	CAA-CBA-CGA-O2A

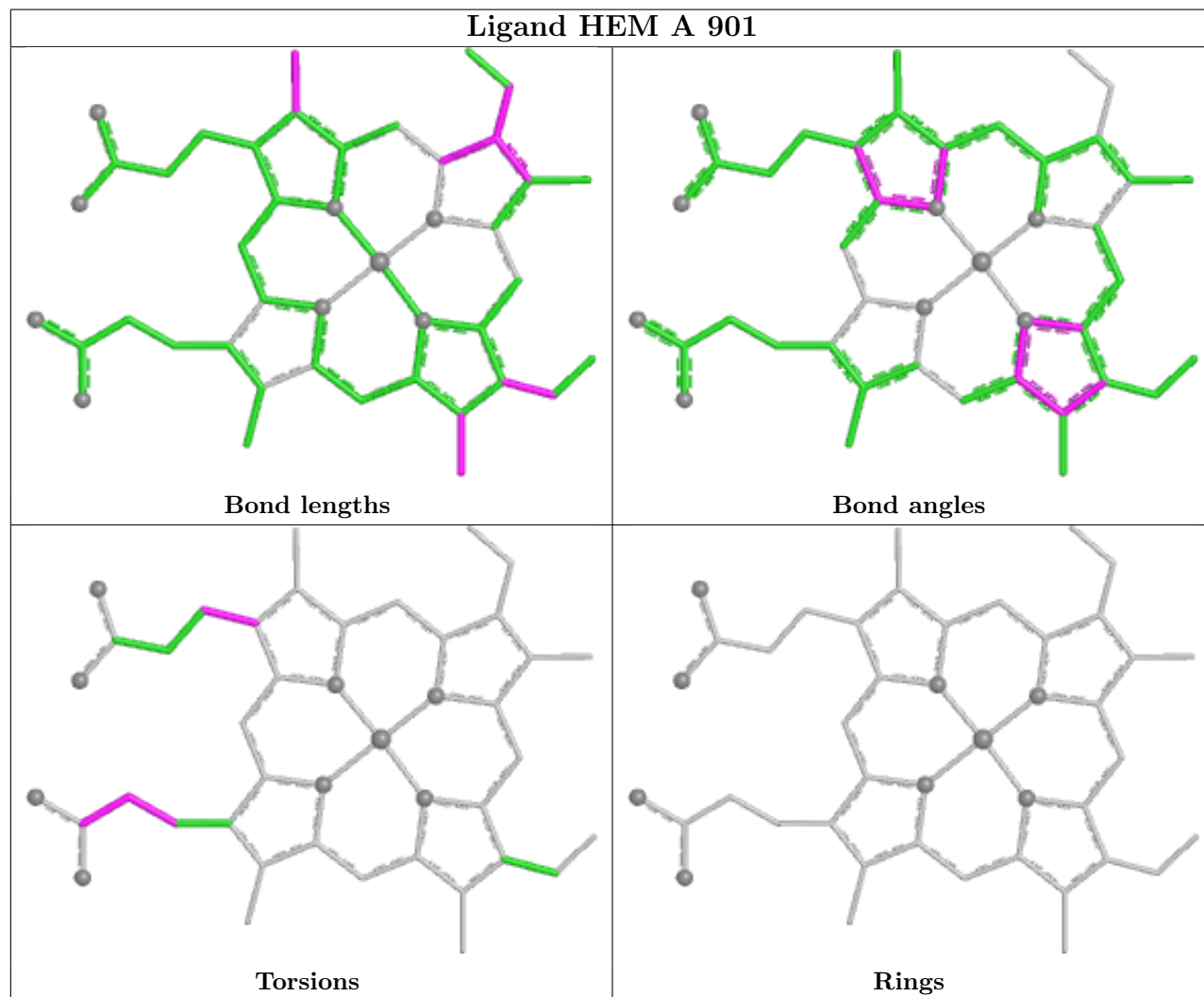
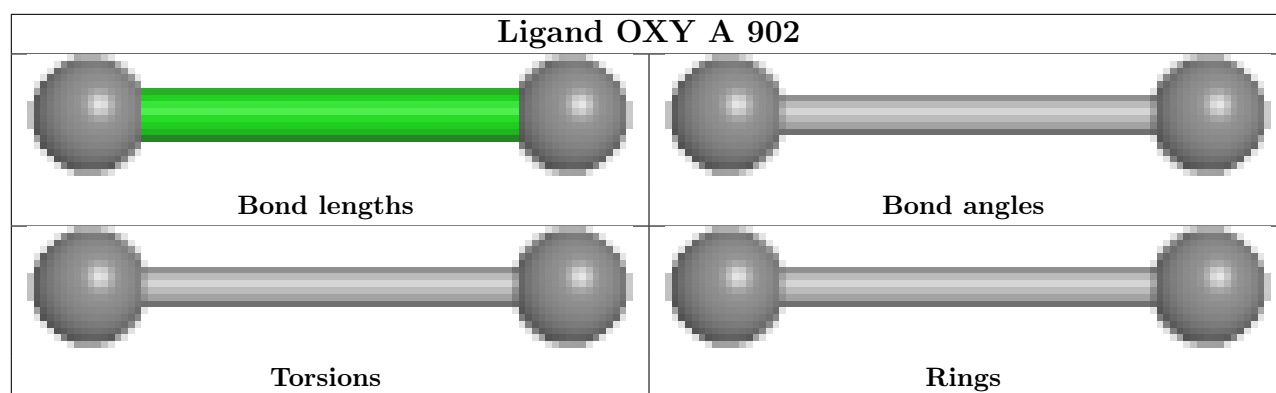
There are no ring outliers.

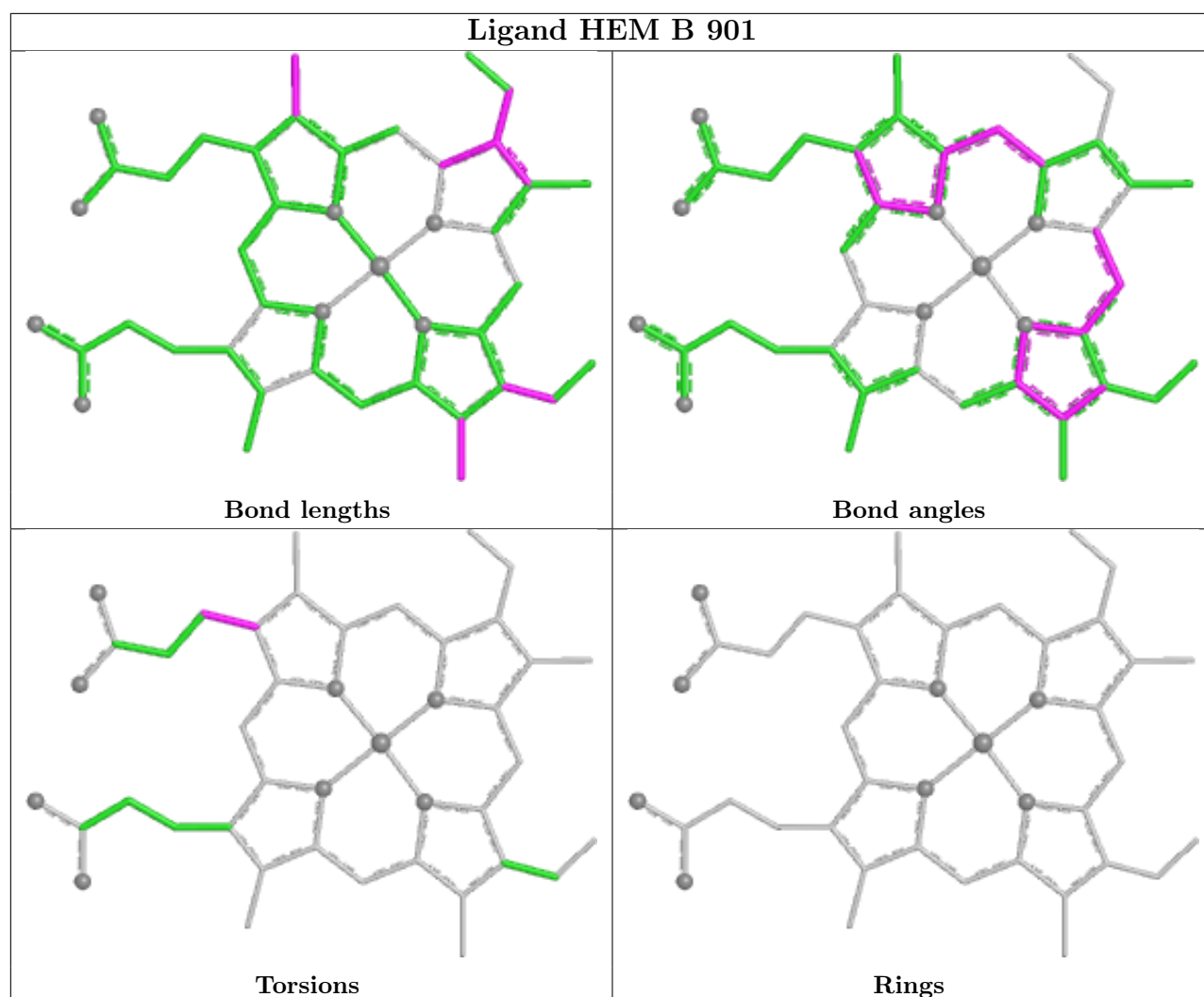
3 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	902	OXY	2	0
2	A	901	HEM	5	0
2	B	901	HEM	6	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







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.

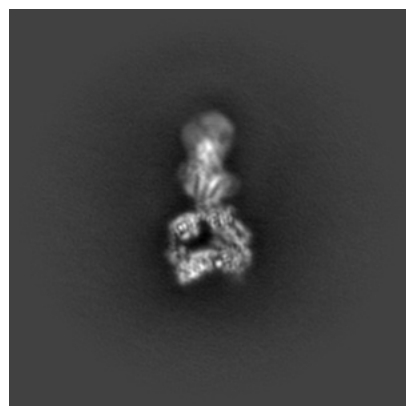
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-45489. These allow visual inspection of the internal detail of the map and identification of artifacts.

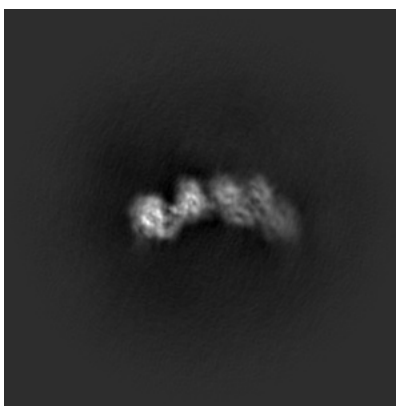
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

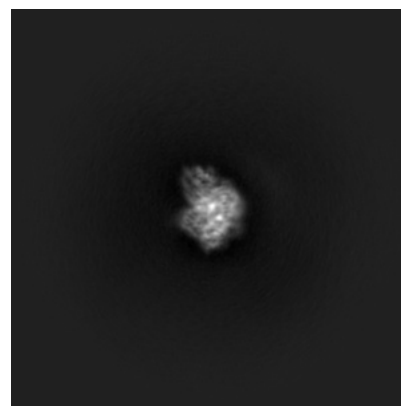
6.1.1 Primary map



X

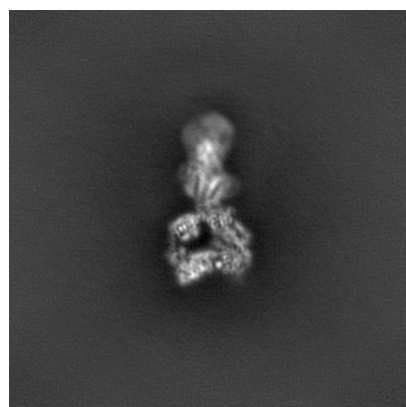


Y

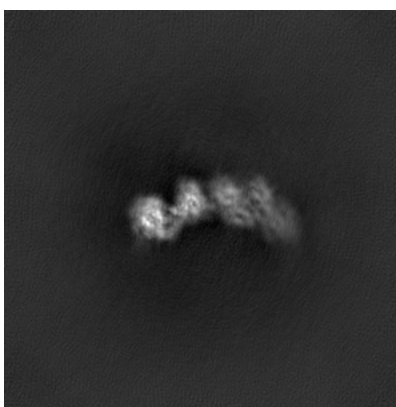


Z

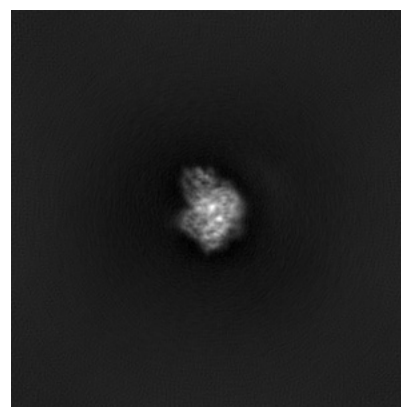
6.1.2 Raw map



X



Y

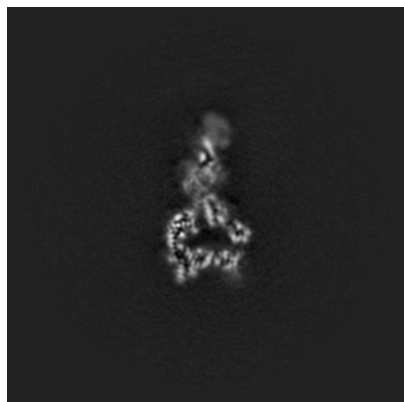


Z

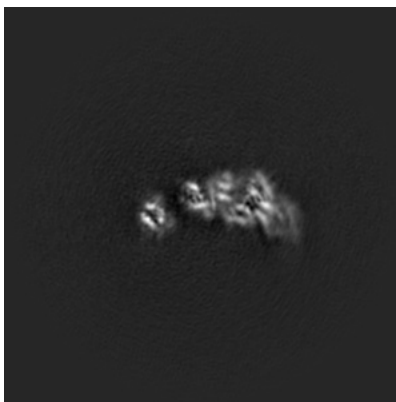
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

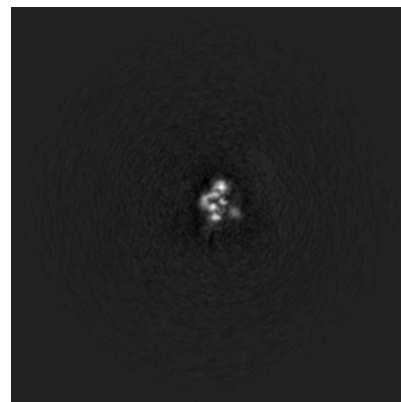
6.2.1 Primary map



X Index: 128

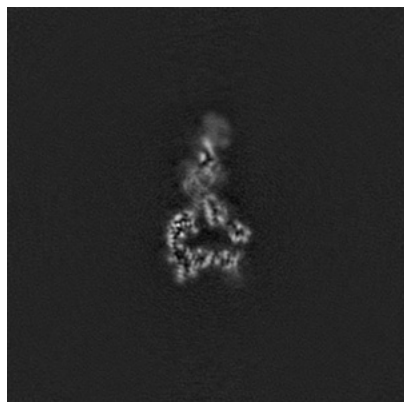


Y Index: 128

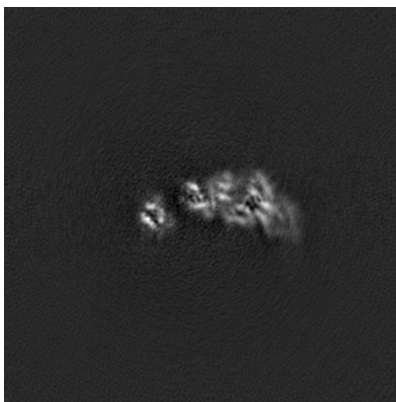


Z Index: 128

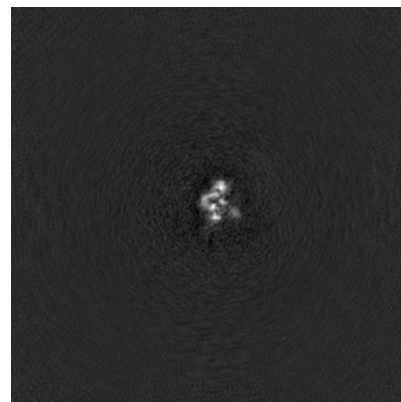
6.2.2 Raw map



X Index: 128



Y Index: 128

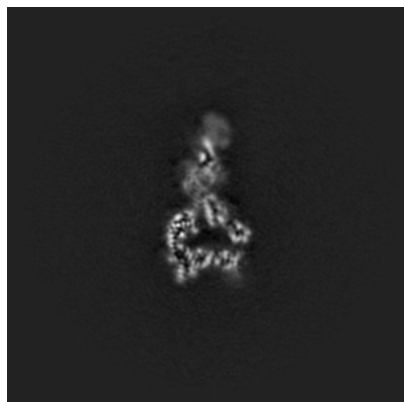


Z Index: 128

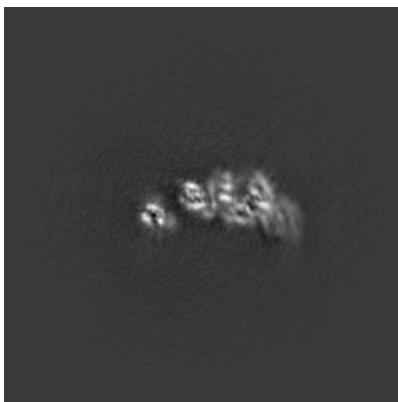
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

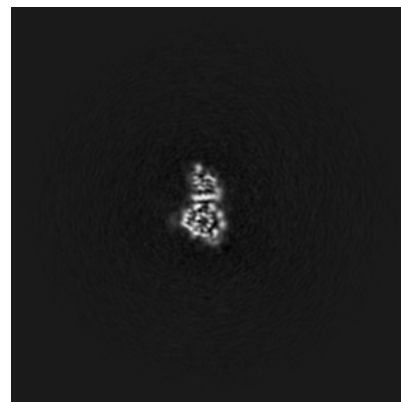
6.3.1 Primary map



X Index: 128

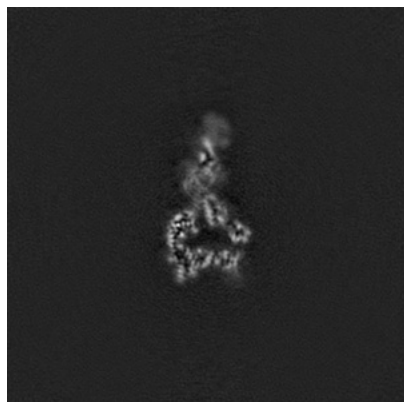


Y Index: 129

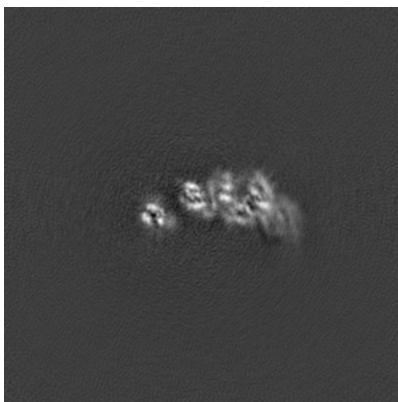


Z Index: 92

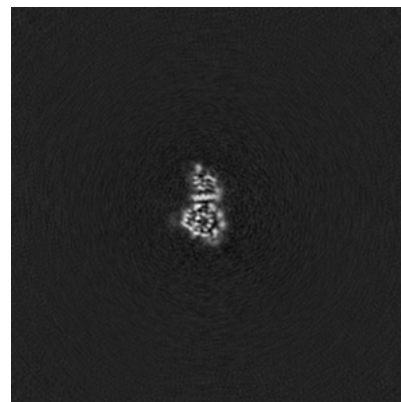
6.3.2 Raw map



X Index: 128



Y Index: 129



Z Index: 92

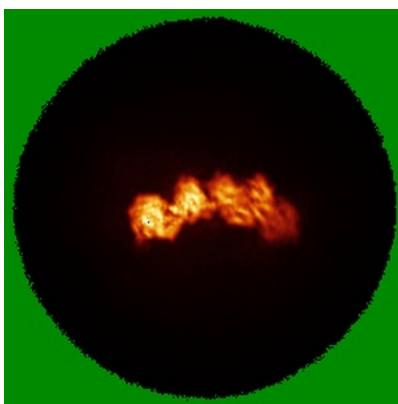
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

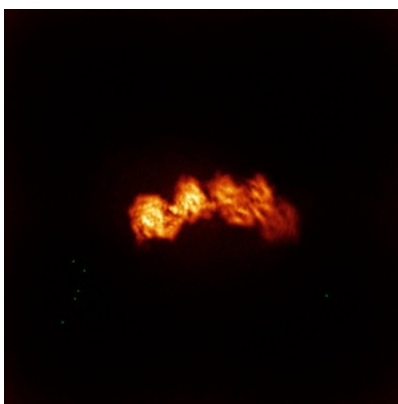


Z

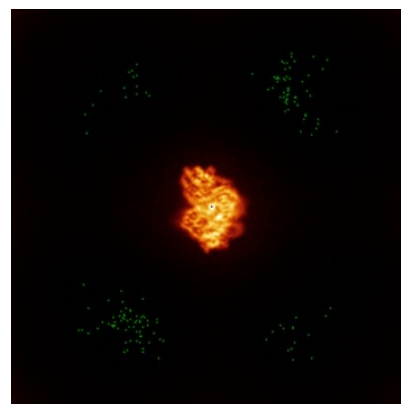
6.4.2 Raw map



X



Y

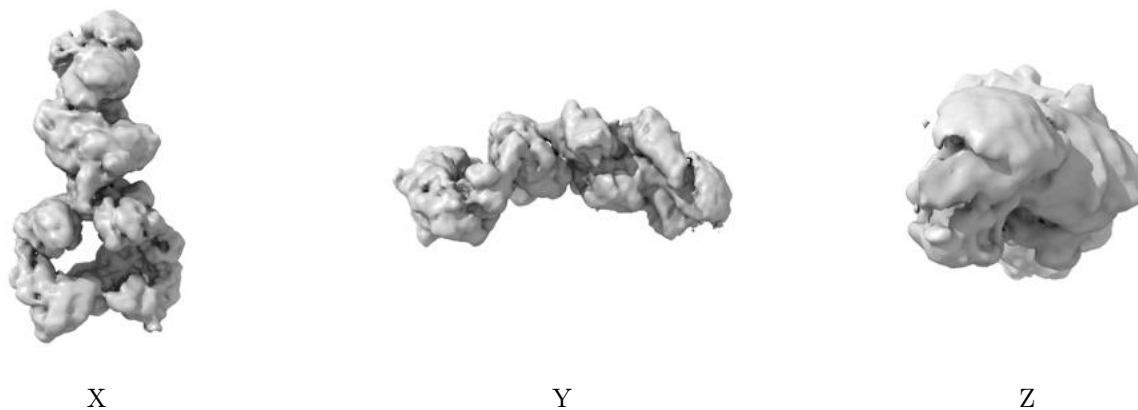


Z

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.

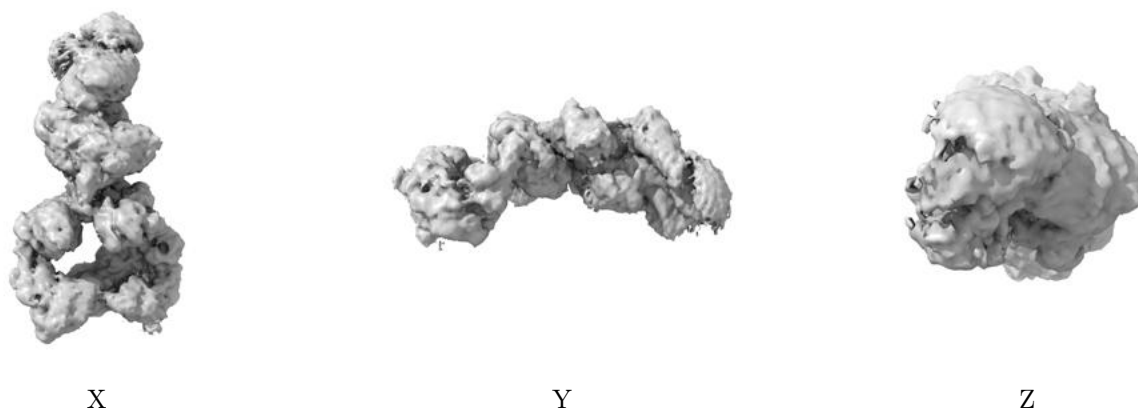
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.123. 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.

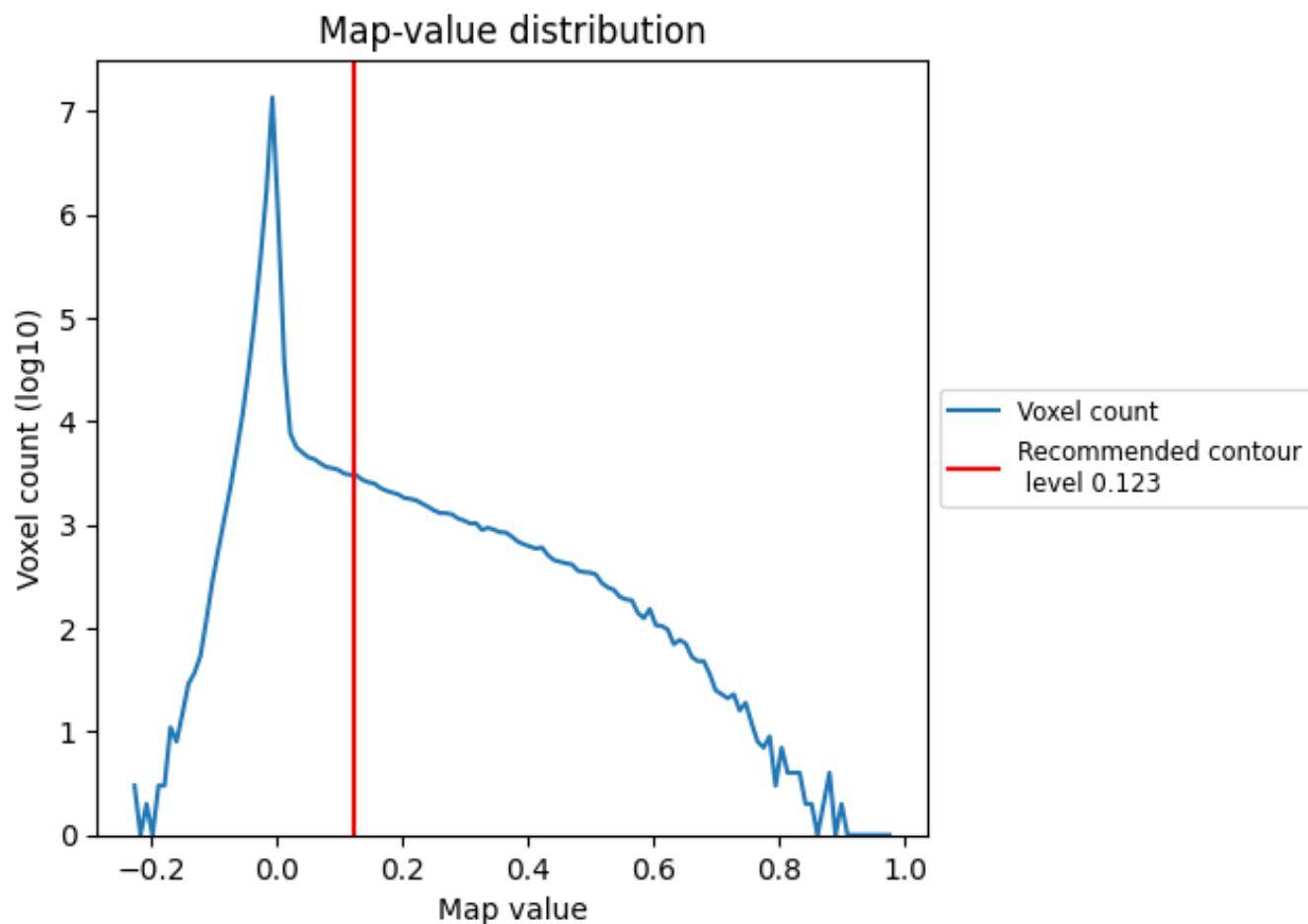
6.6 Mask visualisation [i](#)

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

7 Map analysis ⓘ

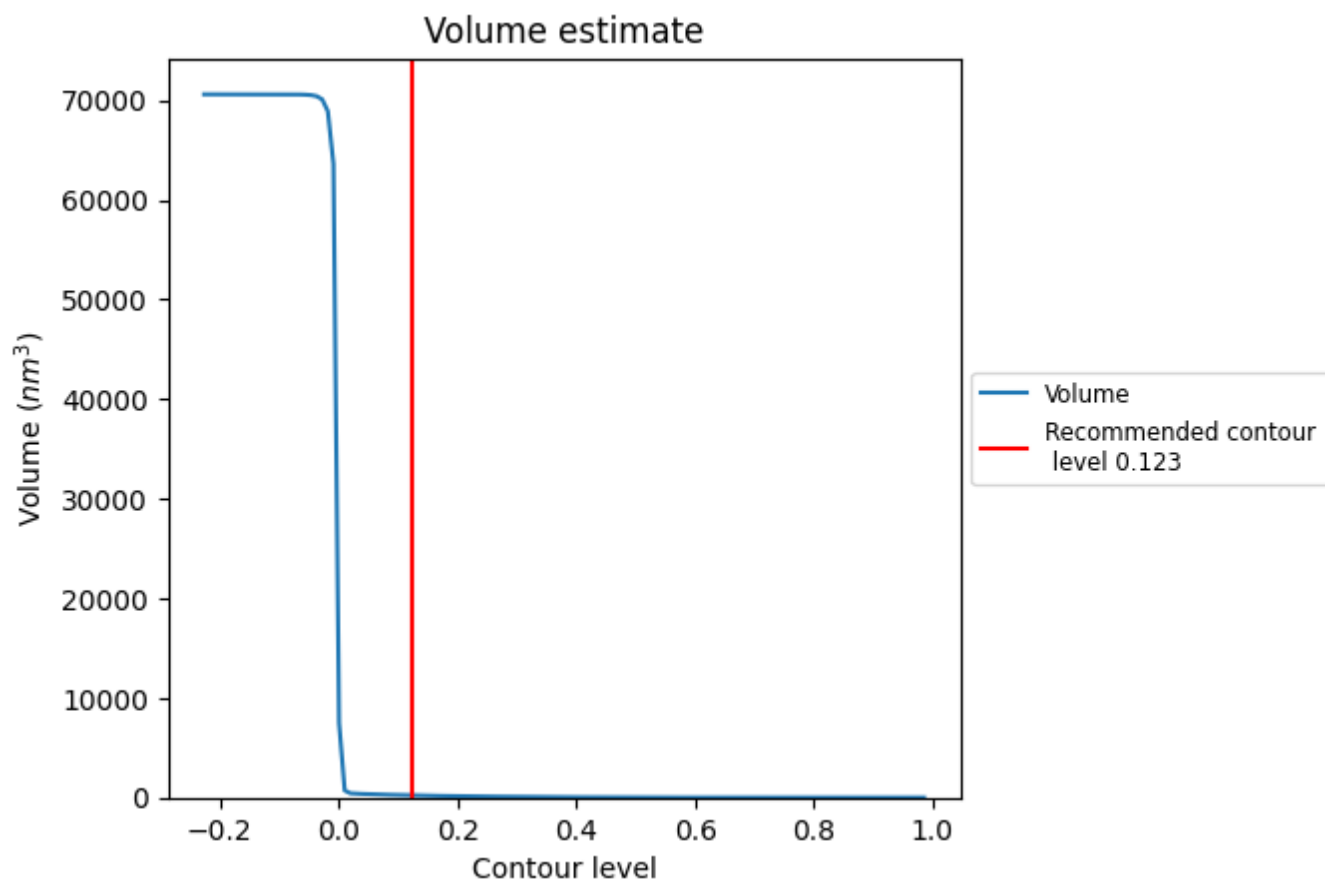
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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.

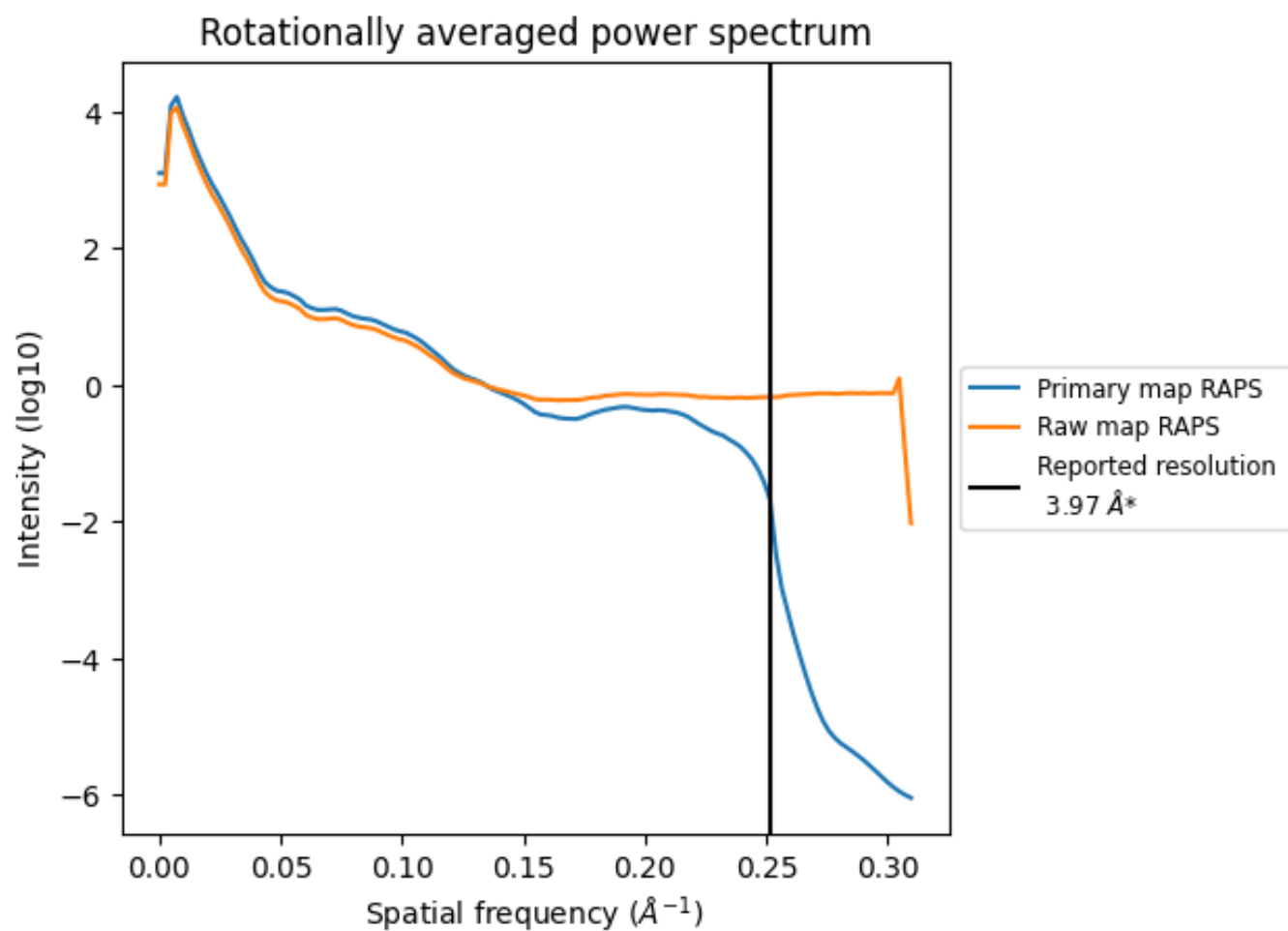
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 223 nm³; this corresponds to an approximate mass of 202 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

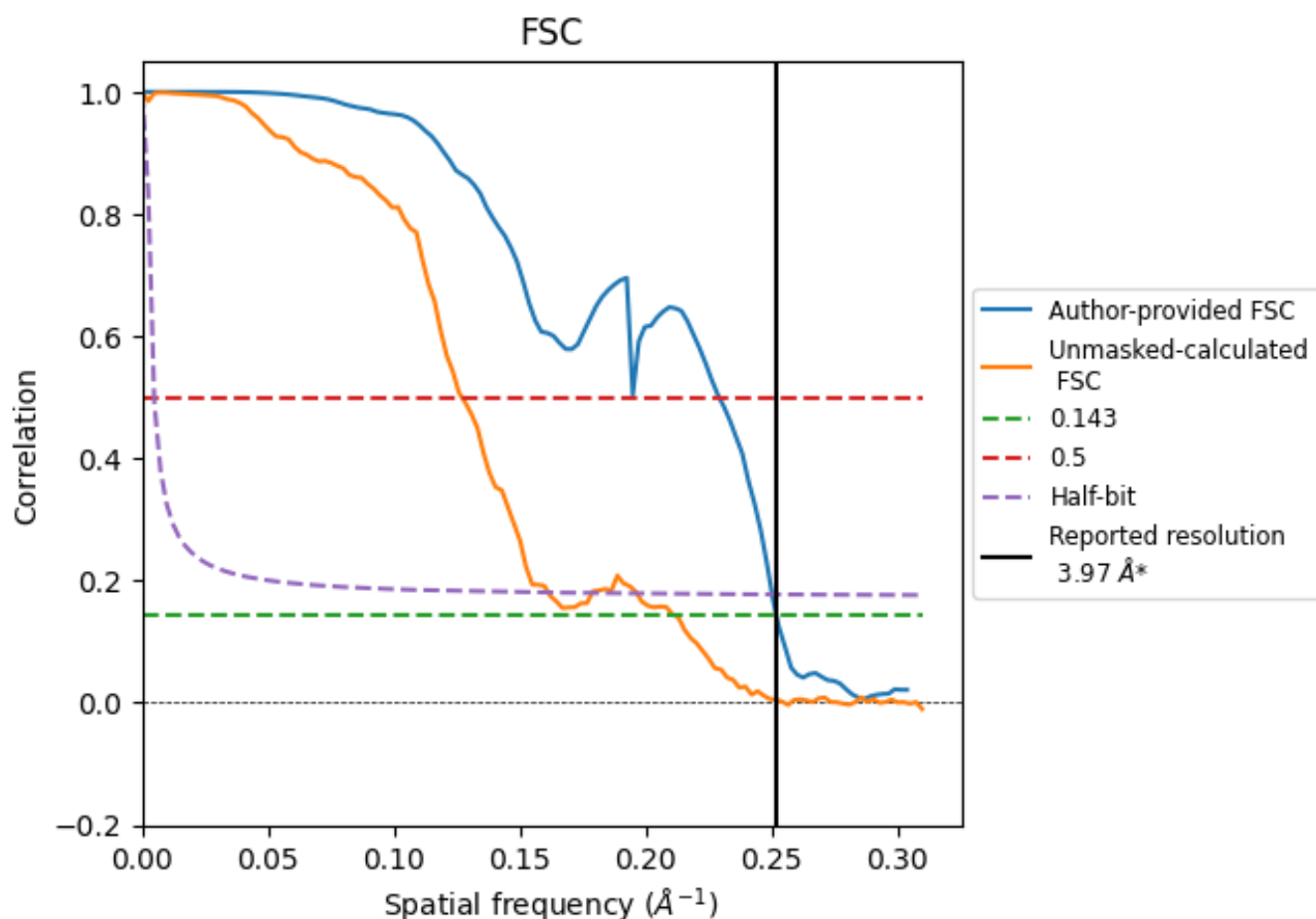


*Reported resolution corresponds to spatial frequency of 0.252 Å⁻¹

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 0.252 \AA^{-1}

8.2 Resolution estimates [i](#)

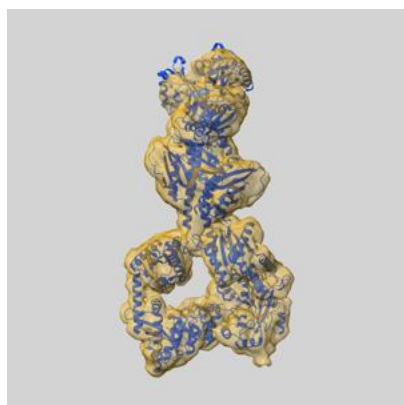
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.97	-	-
Author-provided FSC curve	3.97	4.36	4.00
Unmasked-calculated*	4.73	7.87	6.20

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.73 differs from the reported value 3.97 by more than 10 %

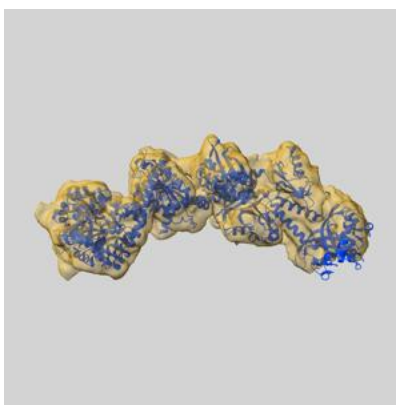
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-45489 and PDB model 9CE0. Per-residue inclusion information can be found in section [3](#) on page [6](#).

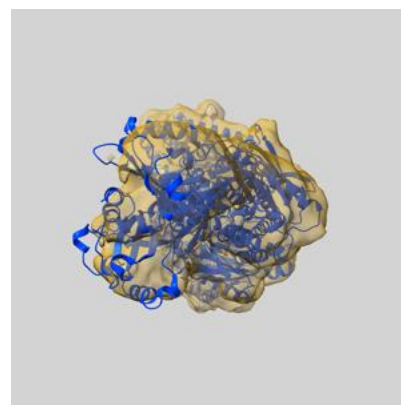
9.1 Map-model overlay [i](#)



X



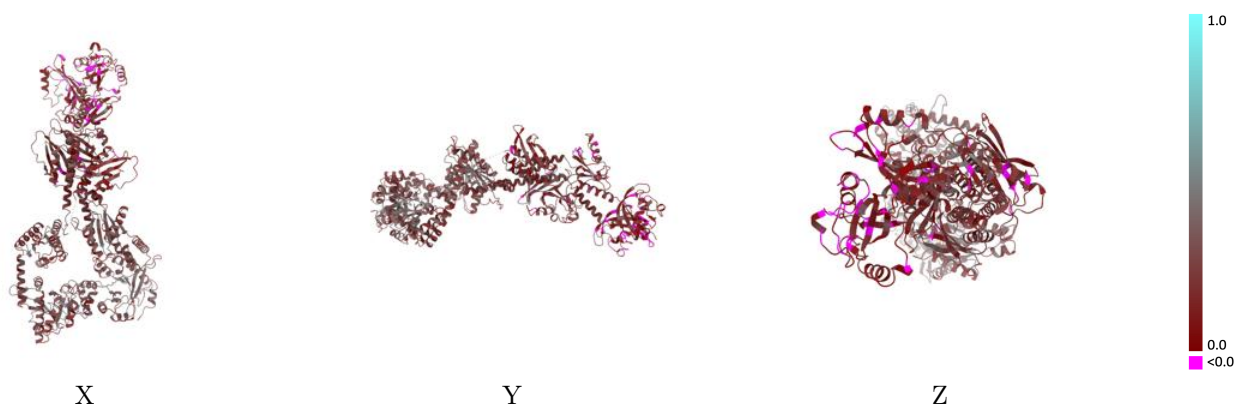
Y



Z

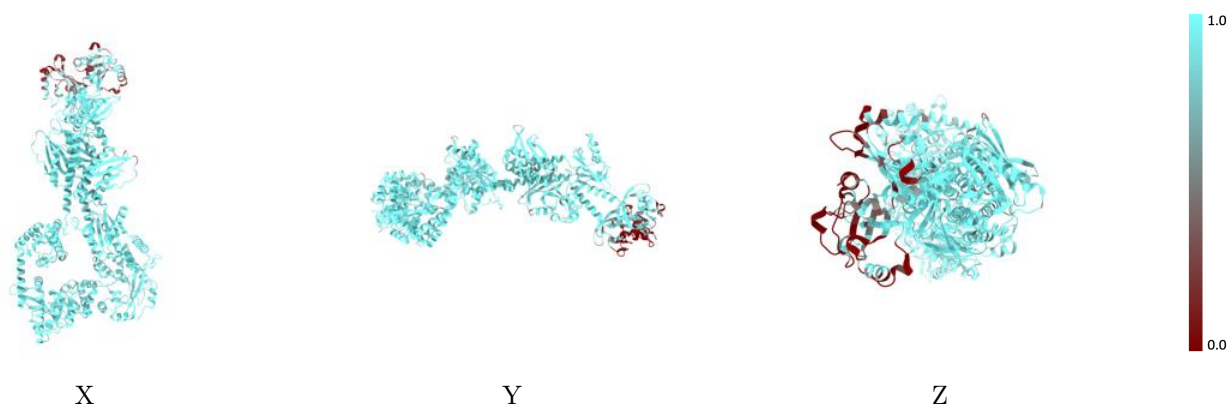
The images above show the 3D surface view of the map at the recommended contour level 0.123 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



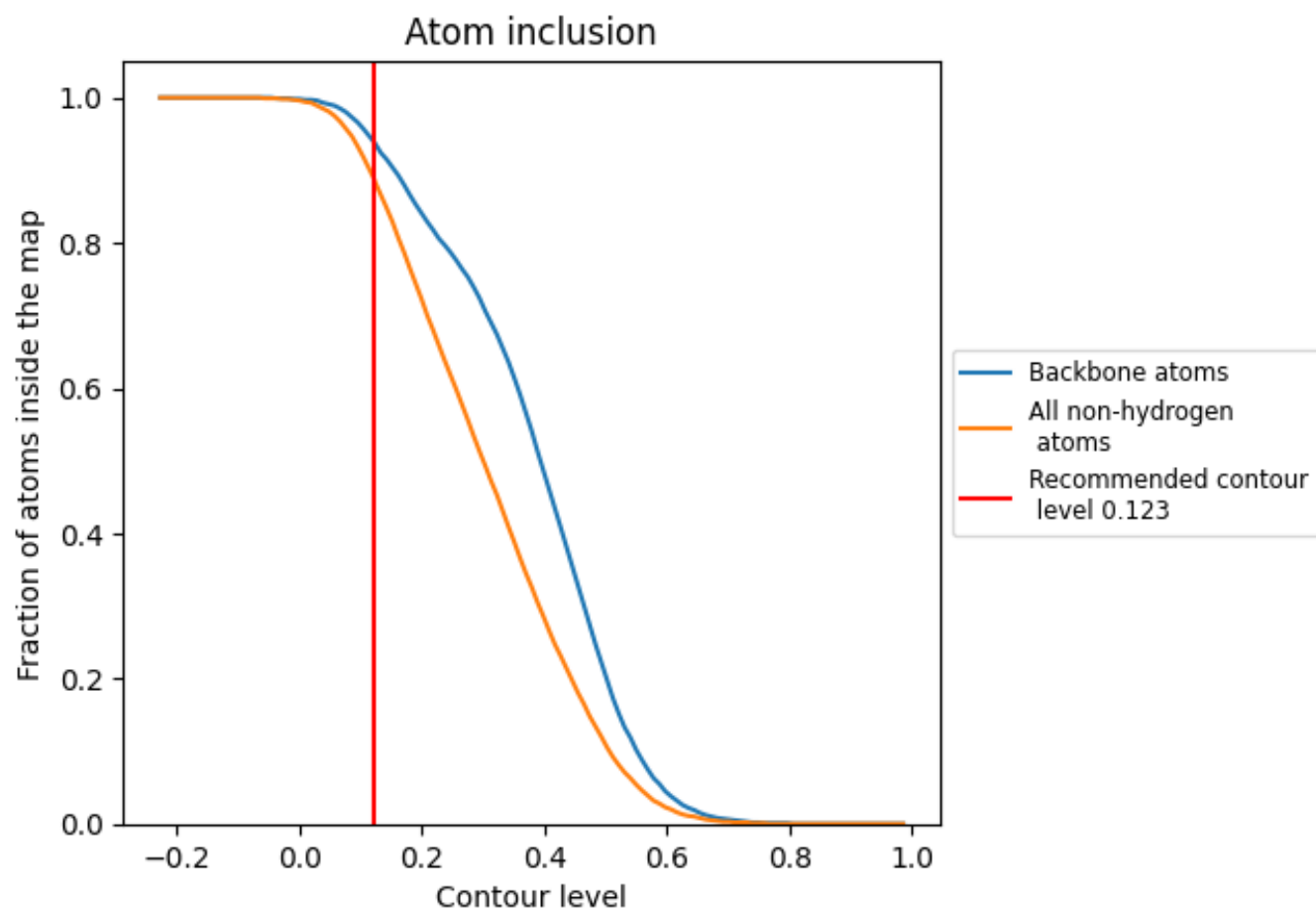
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.123).

9.4 Atom inclusion ⓘ



At the recommended contour level, 94% of all backbone atoms, 89% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.123) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8870	<div></div> 0.2480
A	<div></div> 0.8770	<div></div> 0.2490
B	<div></div> 0.8980	<div></div> 0.2470

