



wwPDB EM Validation Summary Report ⓘ

Jul 10, 2026 – 12:41 PM JST

PDB ID : 9XSM / pdb_00009xsm
EMDB ID : EMD-67183
Title : CydDC in nanodisc with heme-bound I
Authors : Zhang, C.; Luo, Y.; Yang, L.
Deposited on : 2025-11-21
Resolution : 3.40 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.dev133
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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) : 2.50

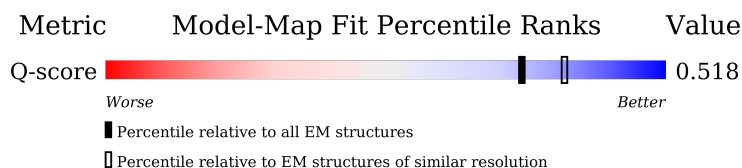
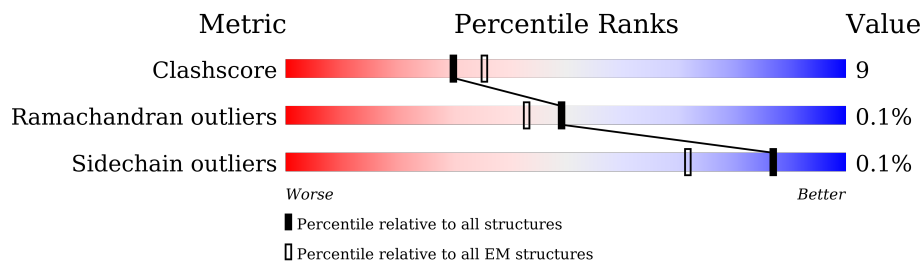
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	C	584	57% 76% 22% .
2	D	588	59% 79% 20% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8977 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 Glutathione/L-cysteine transport system ATP-binding/permease protein CydC.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	572	Total	C	N	O	S	0	0
			4425	2831	780	799	15		

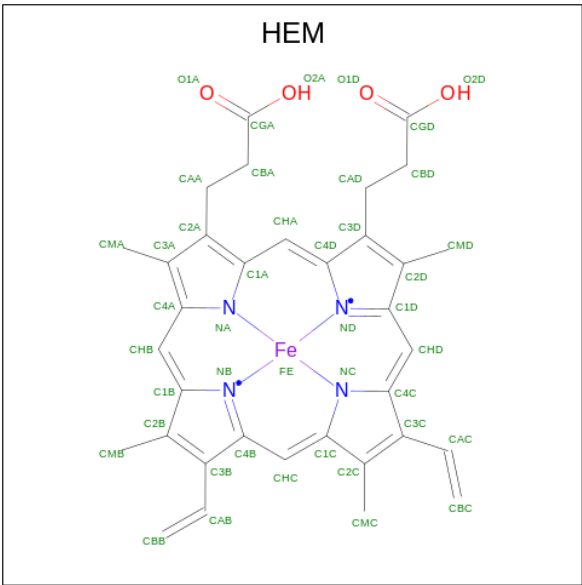
There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	574	GLY	-	expression tag	UNP P23886
C	575	SER	-	expression tag	UNP P23886
C	576	SER	-	expression tag	UNP P23886
C	577	HIS	-	expression tag	UNP P23886
C	578	HIS	-	expression tag	UNP P23886
C	579	HIS	-	expression tag	UNP P23886
C	580	HIS	-	expression tag	UNP P23886
C	581	HIS	-	expression tag	UNP P23886
C	582	HIS	-	expression tag	UNP P23886
C	583	HIS	-	expression tag	UNP P23886
C	584	HIS	-	expression tag	UNP P23886

- Molecule 2 is a protein called Glutathione/L-cysteine transport system ATP-binding/permease protein CydD.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	582	Total	C	N	O	S	0	0
			4509	2893	793	809	14		

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: C₃₄H₃₂FeN₄O₄) (labeled as "Ligand of Interest" by depositor).

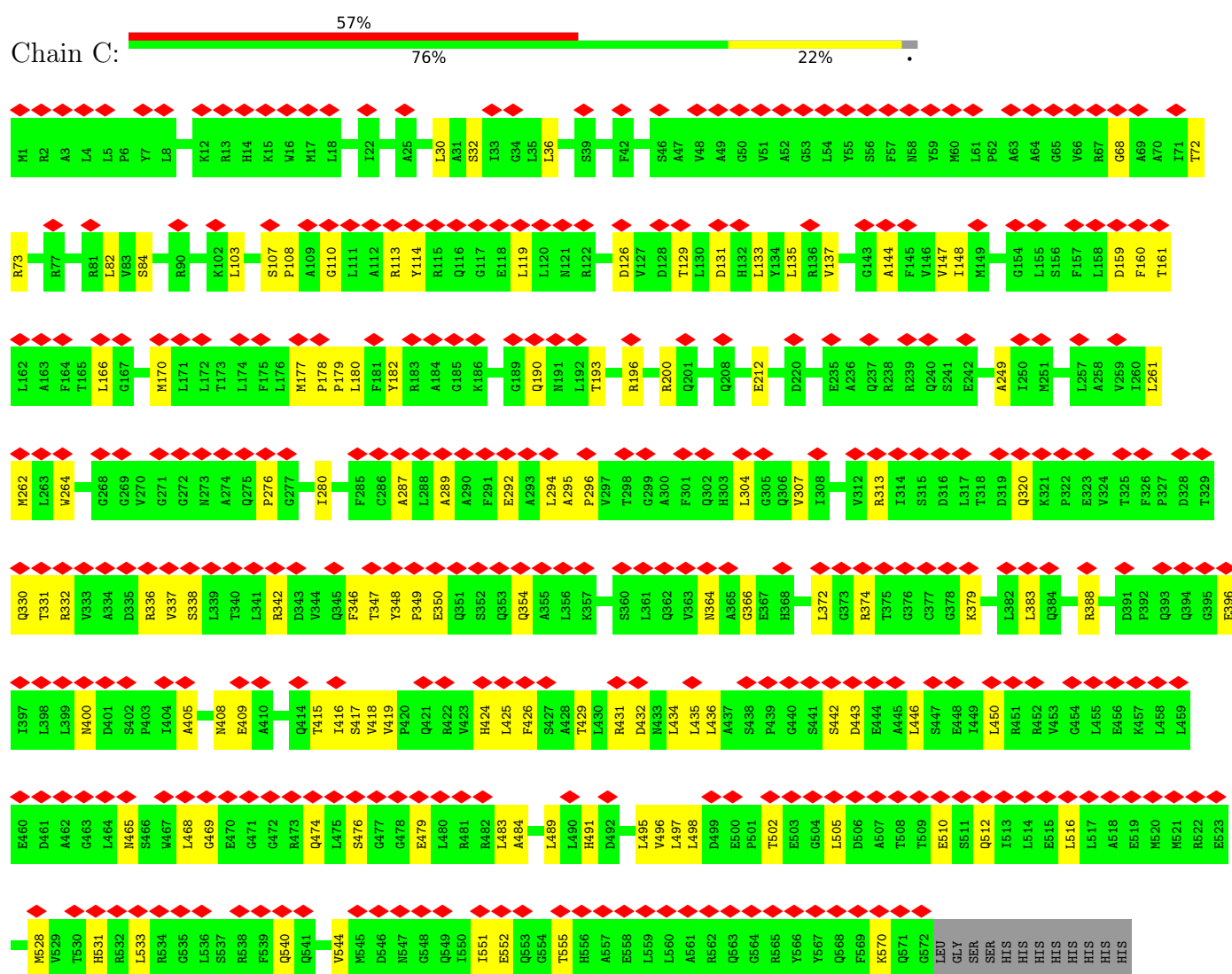


Mol	Chain	Residues	Atoms					AltConf
			Total	C	Fe	N	O	
3	D	1	43	34	1	4	4	0

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: Glutathione/L-cysteine transport system ATP-binding/permease protein CydC



- Molecule 2: Glutathione/L-cysteine transport system ATP-binding/permease protein CydD



MET	ASN	LYS	SER	R5	Q6	K7	E8	L9	T10	R11	K14	Q15	Q16	S20	Q21	R22	W23	N25	R28	L29	L30	G31	F32	V33	Q41	R47	H51	M52	I53	M54	E55	N56	I57	P58	R59	E60	A61	L62	L63	L64	T67	L68	L69	V70	L71	T72	F73	V74	W81	L82					
R83	E84	R85	V86	R89	R100	Q101	D104	R105	Q108	A109	A112	W113	I114	Q115	G116	K117	L124	P118	A119	G120	S121	W122	E128	Q129	I130	D131	D132	D135	R139	Y140	L141	P142	Q143	M144	A145	L146	P151	L152	A157	I158	F159	P160	S161	N162	W163	A164	A165	A166	L167	I168	L169				
L170	G171	T172	A173	P174	L175	I176	P177	L178	F179	M180	A181	L182	W183	G184	G186	A187	A188	D189	A190	N191	R192	R193	N194	F195	L196	A197	L198	A199	R200	L201	S202	G203	H204	F205	L206	D207	R208	L209	R210	G211	W212	R216	T217	R220	G221	E222	A223	E224	I225	E226	S227	I228	R229	E233	D234
R238	E241	R244	L245	S250	E254	F255	F256	T257	S258	L259	S260	L263	V266	G269	F270	S271	Y272	L273	G274	E275	L276	D277	F278	G279	H280	Y281	D282	T283	G284	V285	T286	L287	A288	A289	G290	F291	L294	I295	E299	F300	F301	L304	R305	D306	L307	F310	F311								
H312	Q316	G319	A320	A321	D322	S323	L324	K325	T326	F327	M328	E329	T330	P331	L332	A333	H334	P335	Q336	R337	G338	E339	A340	E341	L342	A343	S344	T345	D346	E351	A352	E353	E354	L355	F356	I357	T358	S359	P360	E361	G362	K363	T364	L365	A366	G367	P368	L369	N370	F371	T372	A375	G376	Q377	R378
L381	V382	G383	R384	S385	G386	S387	G388	K389	S390	S391	L392	F399	L400	S401	Y402	Q403	G404	S405	L406	R407	I408	N409	G410	I411	E412	L413	R414	D415	L416	S417	P418	E419	L425	G429	Q430	N431	P432	Q433	L434	A437	T438	L439	R440	D441	L444	L445	A446	R447	P448	D449	A450	S451	E452		
Q453	E454	L455	Q456	A457	A458	L459	D460	N461	A462	W463	E466	F467	L468	P469	L470	L471	P472	Q473	G474	W475	D476	T477	P478	V479	G480	D481	Q482	A483	A484	R485	L486	S487	V488	G489	Q490	L500	L501	N502	S505	L506	D510	E511	P512	A513	A514	S515	L516	D517	A518	H519	S520	E521	Q522	R523	V524
M525	E526	A530	A531	R534	Q535	T536	M539	V540	T541	H542	Q543	L544	E545	D546	L547	A548	D549	W550	W554	W555	M556	Q557	D558	Q559	R560	I561	I562	E563	Q564	Q565	R566	Y567	A568	E569	L570	S571	V572	A573	O574	O575	P576	F577	A578	T579	L580	L581	A582	H583	R584	Q585	E586	GLU	ILE		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	2883634	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 ($e^-/\text{\AA}^2$)	59.7	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.830	Depositor
Minimum map value	-0.407	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.365	Depositor
Map size (Å)	299.2, 299.2, 299.2	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	Depositor

5 Model quality

5.1 Standard geometry

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

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	C	0.30	0/4502	0.47	0/6109
2	D	0.30	0/4607	0.48	0/6267
All	All	0.30	0/9109	0.48	0/12376

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

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	C	4425	0	4565	88	0
2	D	4509	0	4533	79	0
3	D	43	0	30	4	0
All	All	8977	0	9128	164	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 164 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:D:518:ALA:O	2:D:523:ARG:NH2	2.09	0.84
1:C:36:LEU:HD23	1:C:289:ALA:HB2	1.69	0.75
1:C:431:ARG:NH2	1:C:465:ASN:OD1	2.21	0.73
1:C:337:VAL:HA	1:C:400:ASN:HD21	1.54	0.72
1:C:469:GLY:O	1:C:474:GLN:NE2	2.25	0.70

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	C	570/584 (98%)	501 (88%)	68 (12%)	1 (0%)	43	71
2	D	580/588 (99%)	495 (85%)	85 (15%)	0	100	100
All	All	1150/1172 (98%)	996 (87%)	153 (13%)	1 (0%)	49	78

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	555	THR

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	C	465/476 (98%)	465 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	462/477 (97%)	461 (100%)	1 (0%)	87	85
All	All	927/953 (97%)	926 (100%)	1 (0%)	87	89

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	500	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	194	ASN
2	D	204	HIS
2	D	557	GLN
2	D	280	HIS
1	C	306	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	$\# Z > 2$
3	HEM	D	601	2,1	50,50,50	1.28	6 (12%)	66,82,82	1.14	2 (3%)

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
3	HEM	D	601	2,1	-	6/14/54/54	-

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	601	HEM	CAB-C3B	2.80	1.55	1.47
3	D	601	HEM	CAC-C3C	2.73	1.54	1.47
3	D	601	HEM	FE-NA	2.45	2.03	1.95
3	D	601	HEM	FE-ND	2.33	2.02	1.94
3	D	601	HEM	C3C-C2C	-2.20	1.32	1.37

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	601	HEM	C4D-ND-C1D	2.36	107.51	105.07
3	D	601	HEM	CAD-CBD-CGD	-2.24	108.77	113.60

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

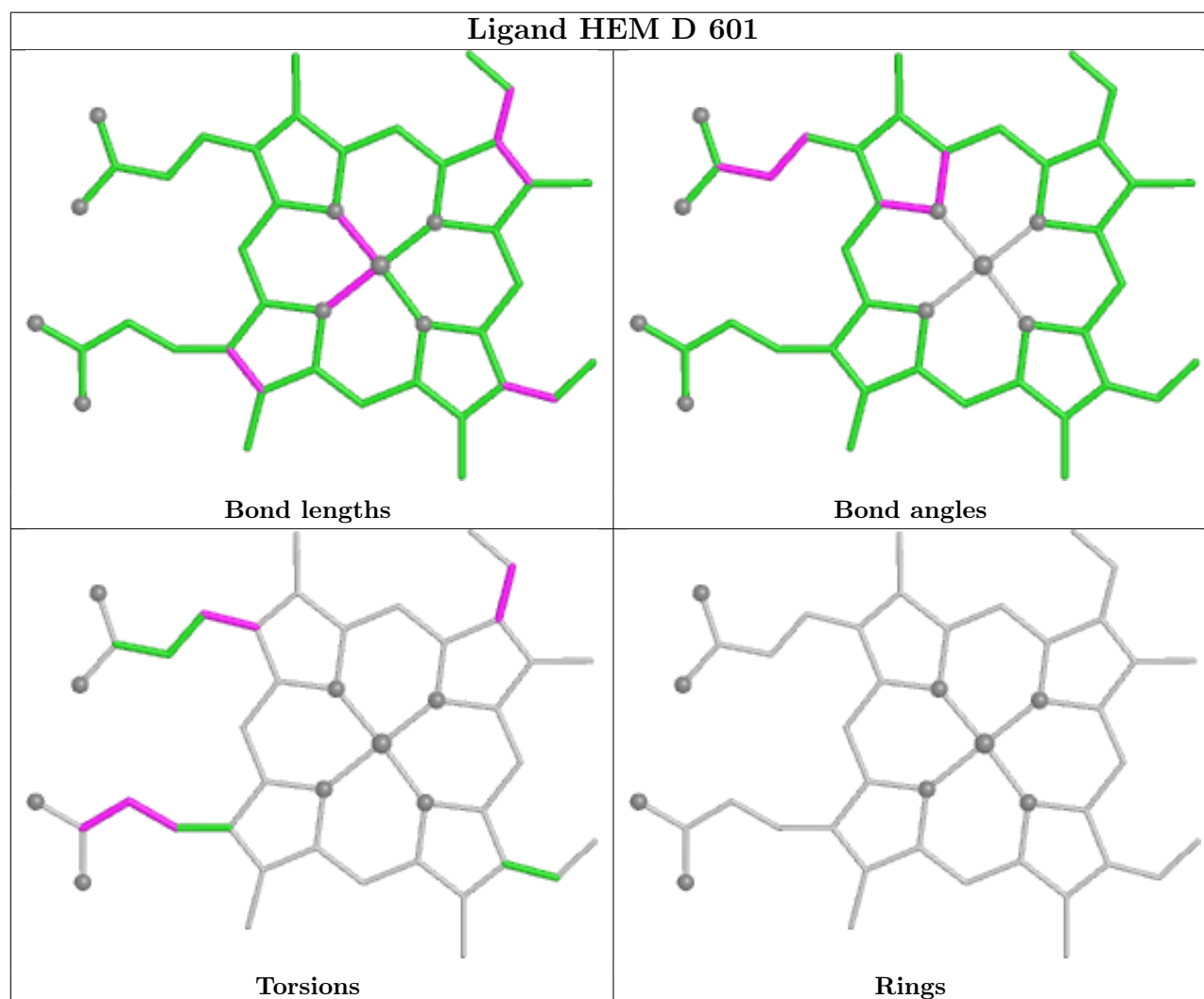
Mol	Chain	Res	Type	Atoms
3	D	601	HEM	C2A-CAA-CBA-CGA
3	D	601	HEM	C4C-C3C-CAC-CBC
3	D	601	HEM	C4D-C3D-CAD-CBD
3	D	601	HEM	C2D-C3D-CAD-CBD
3	D	601	HEM	CAA-CBA-CGA-O1A

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	601	HEM	4	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.

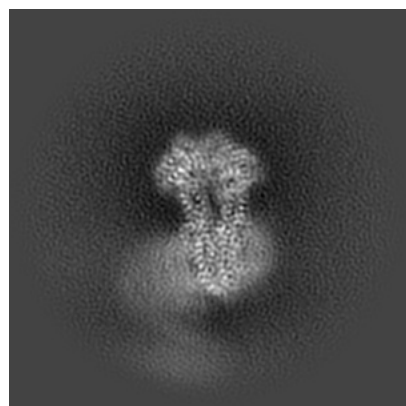
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-67183. These allow visual inspection of the internal detail of the map and identification of artifacts.

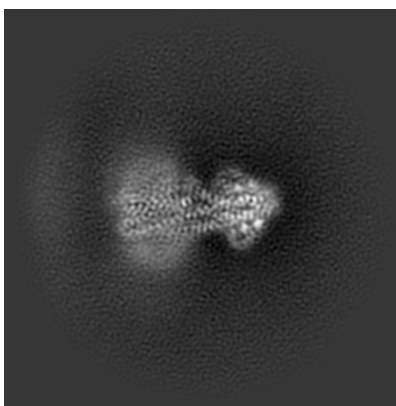
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

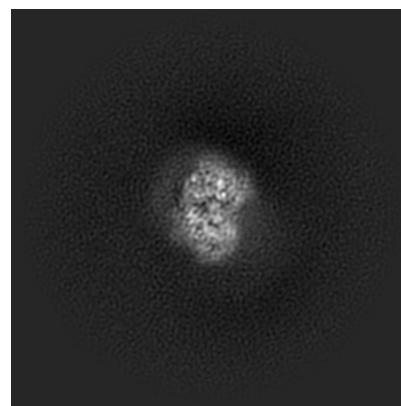
6.1.1 Primary map



X

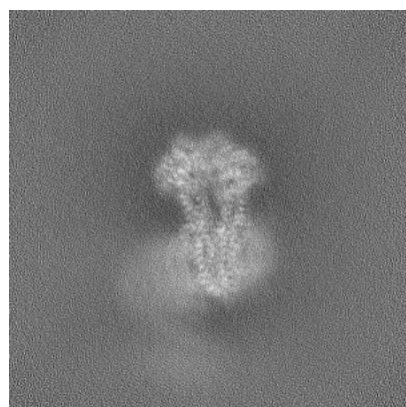


Y

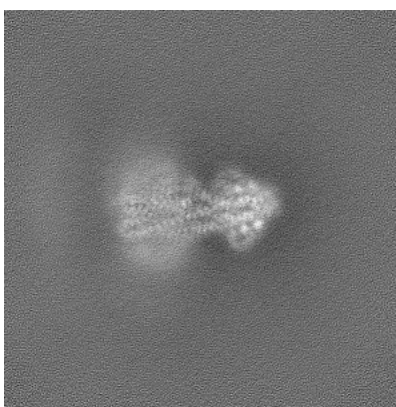


Z

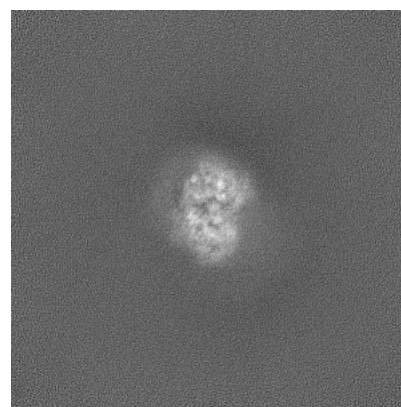
6.1.2 Raw map



X



Y

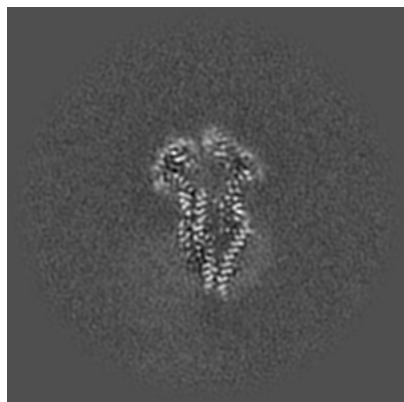


Z

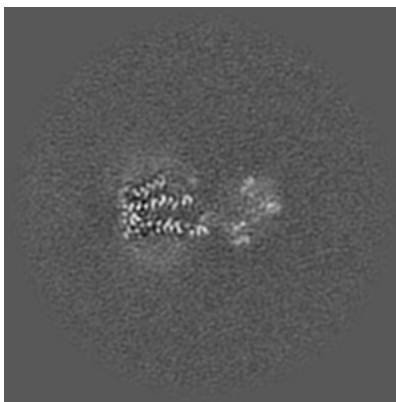
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

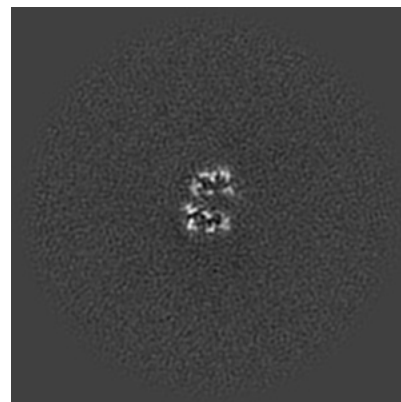
6.2.1 Primary map



X Index: 176

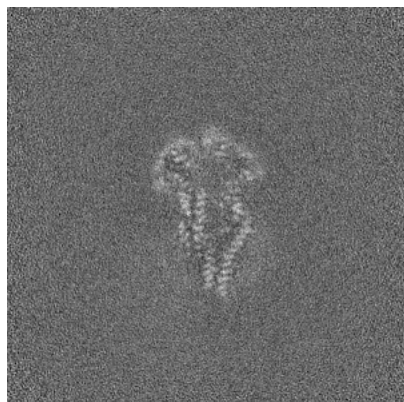


Y Index: 176

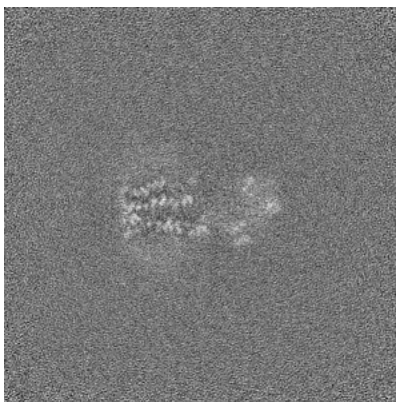


Z Index: 176

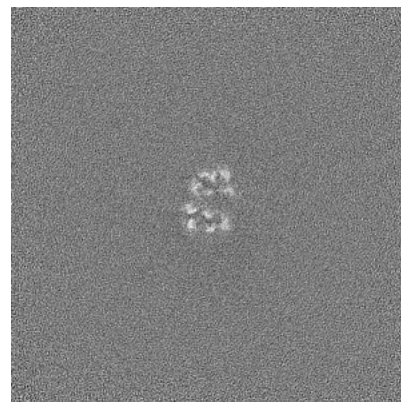
6.2.2 Raw map



X Index: 176



Y Index: 176

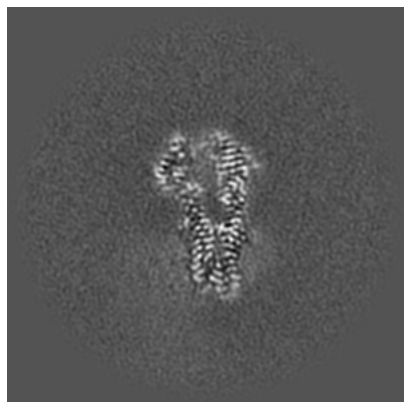


Z Index: 176

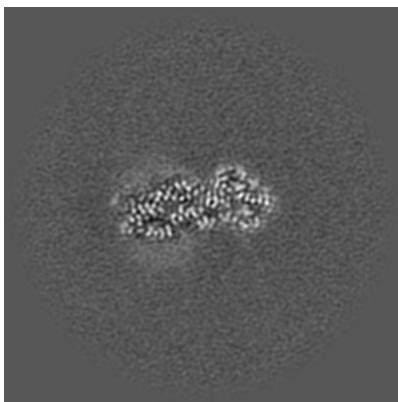
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

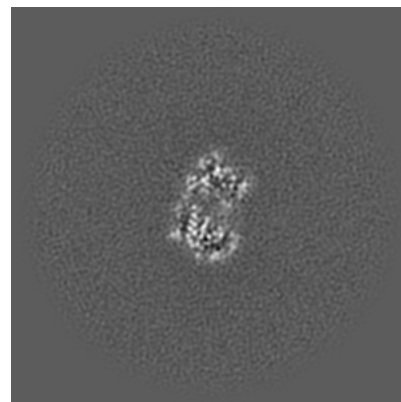
6.3.1 Primary map



X Index: 182

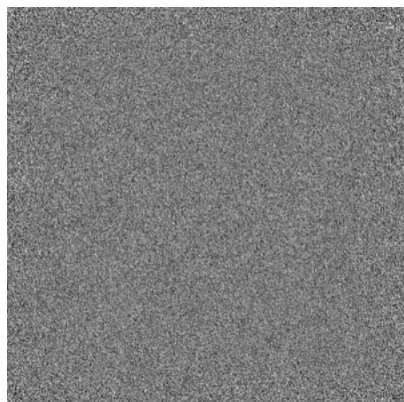


Y Index: 194

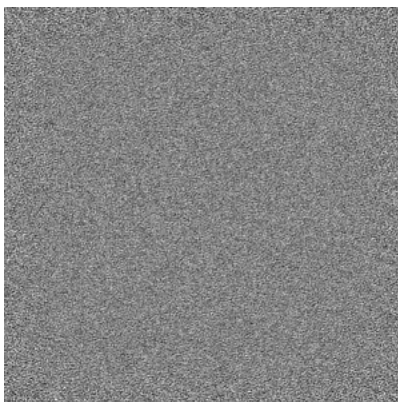


Z Index: 210

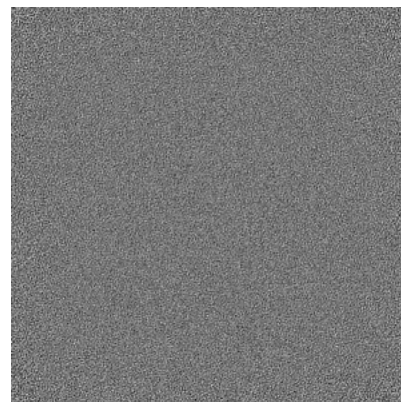
6.3.2 Raw map



X Index: 0



Y Index: 0

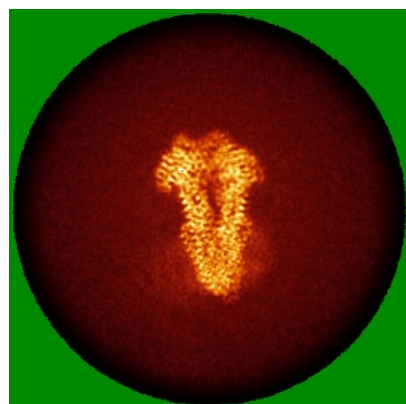


Z Index: 351

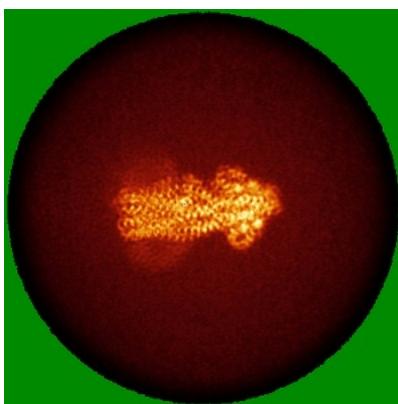
The images above show the largest variance slices of the map in three orthogonal directions.

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

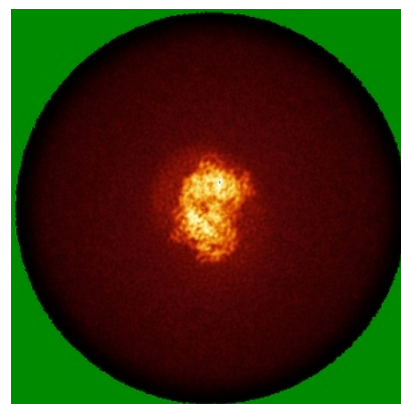
6.4.1 Primary map



X

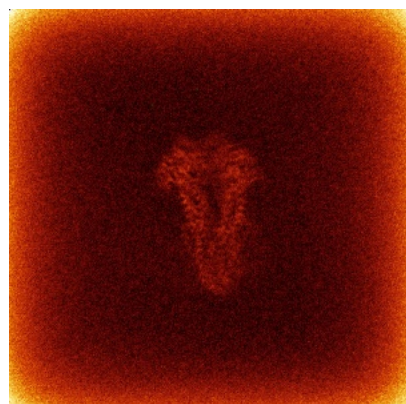


Y

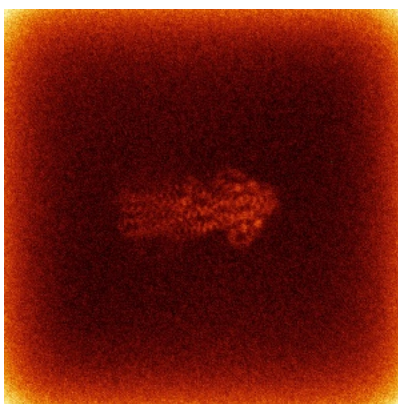


Z

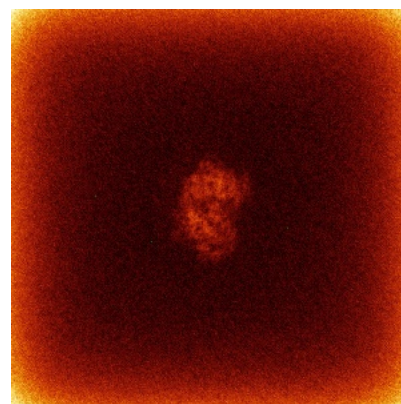
6.4.2 Raw map



X



Y

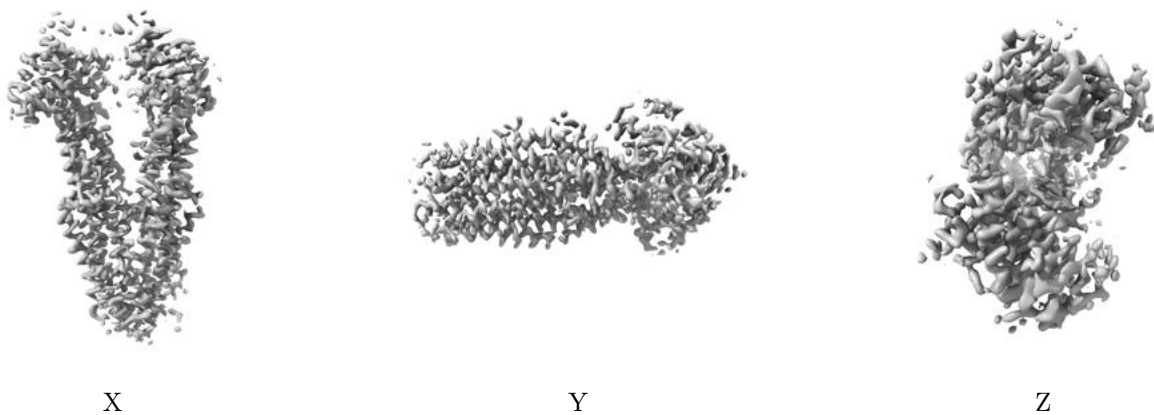


Z

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.

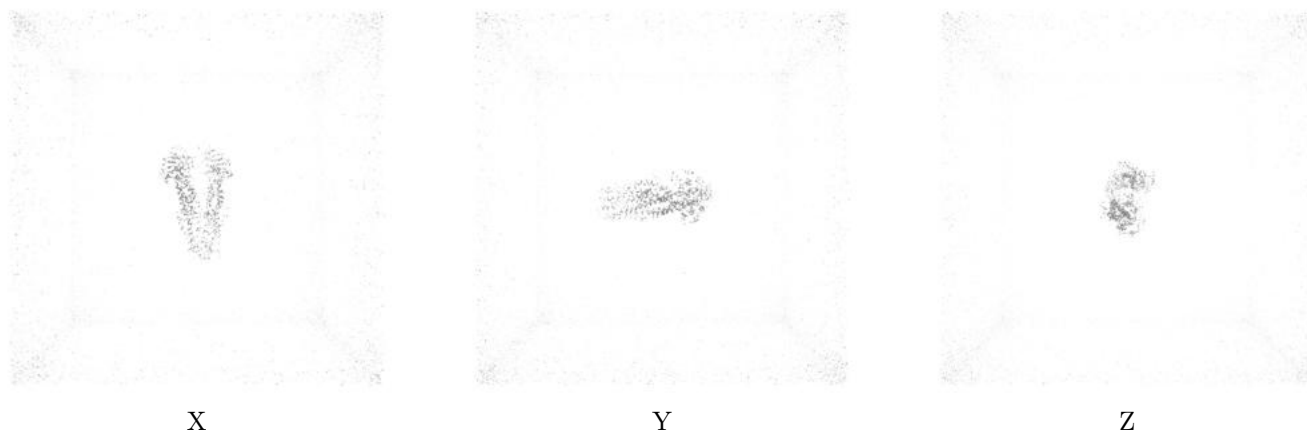
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.365. 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.

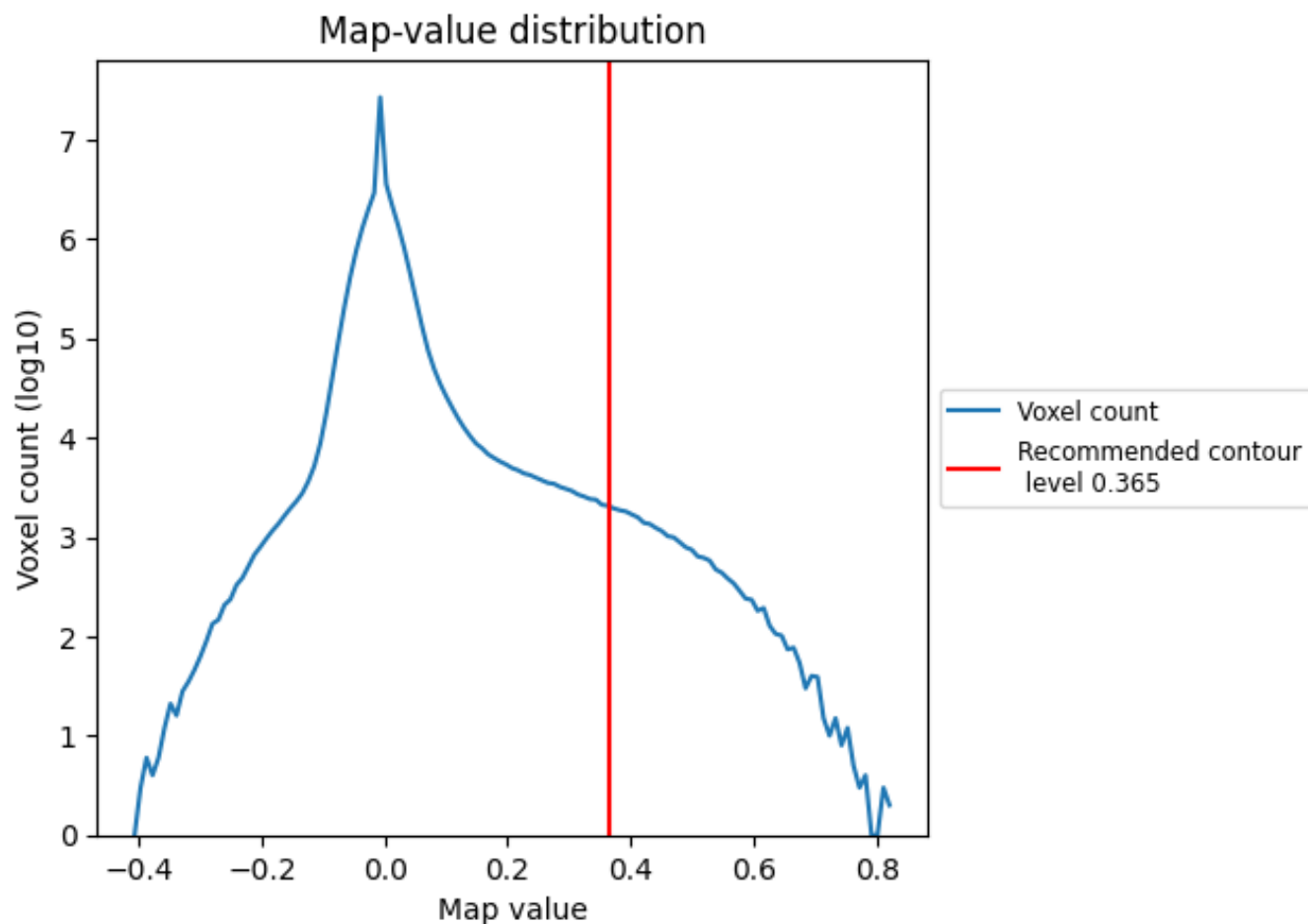
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

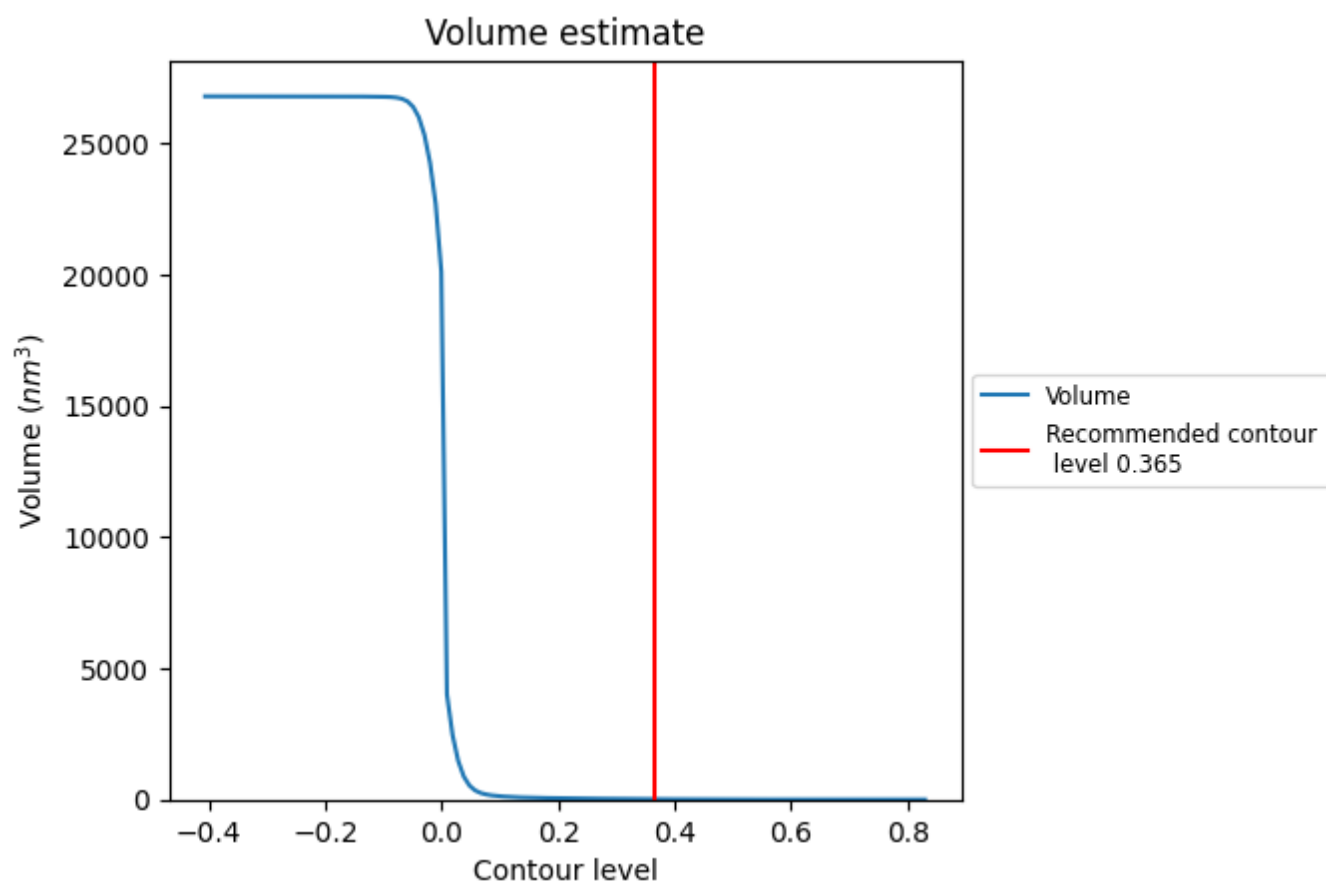
This section contains the results of statistical analysis of the map.

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.

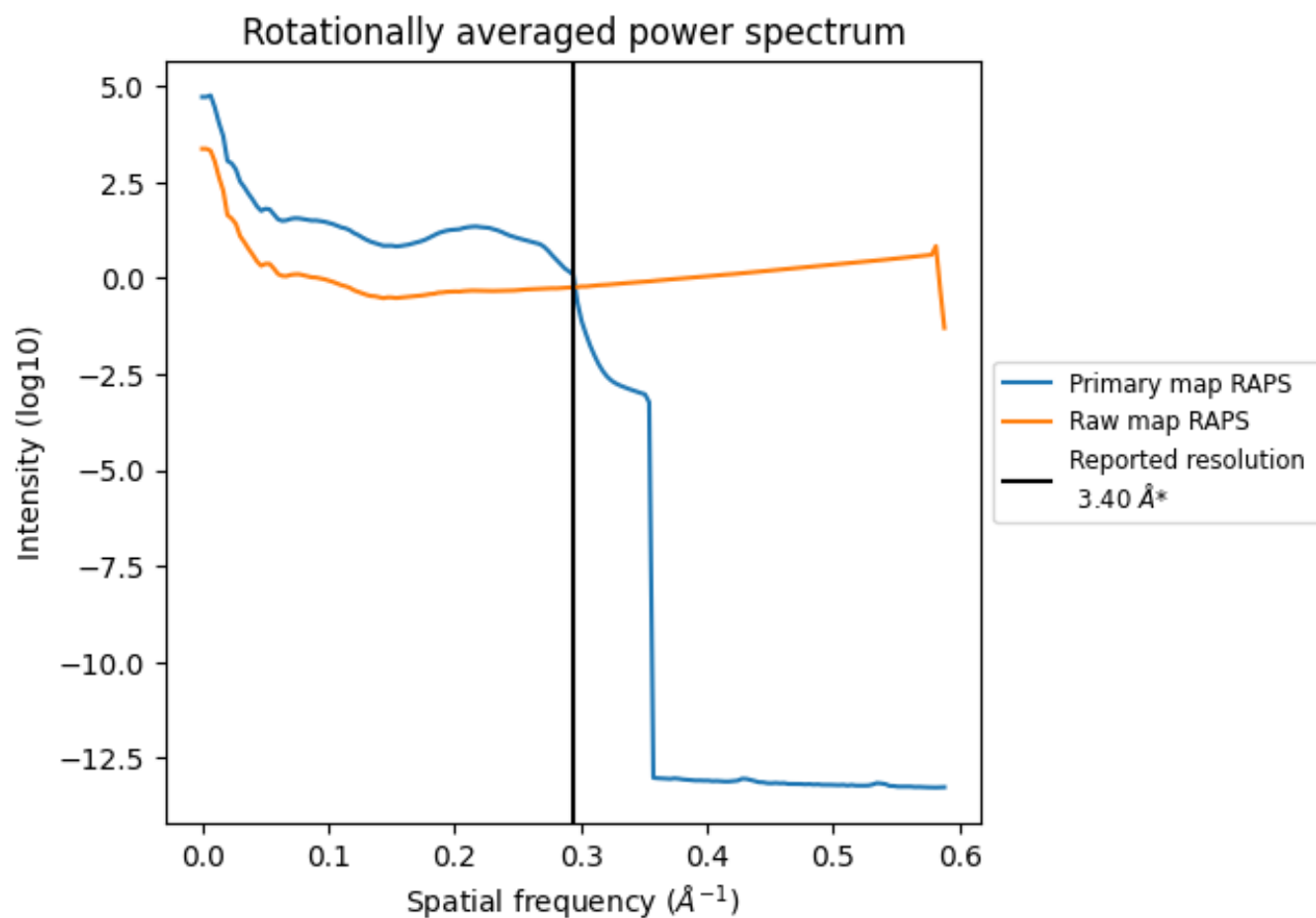
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 16 nm³; this corresponds to an approximate mass of 14 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 ⓘ

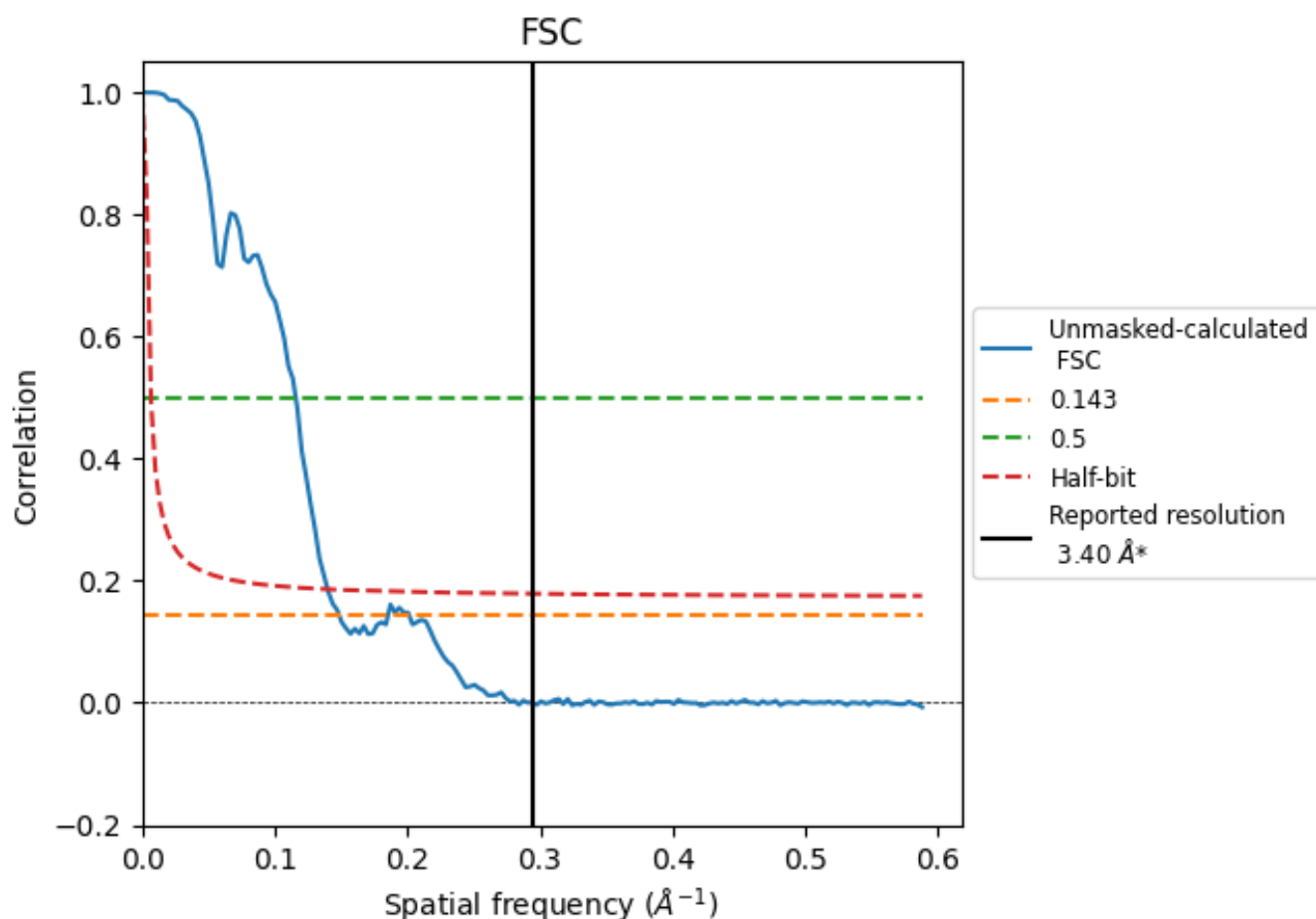


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

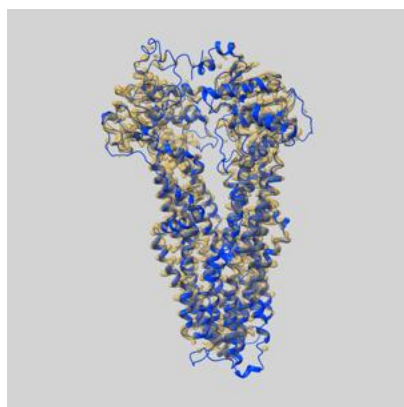
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.73	8.64	7.15

*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 6.73 differs from the reported value 3.4 by more than 10 %

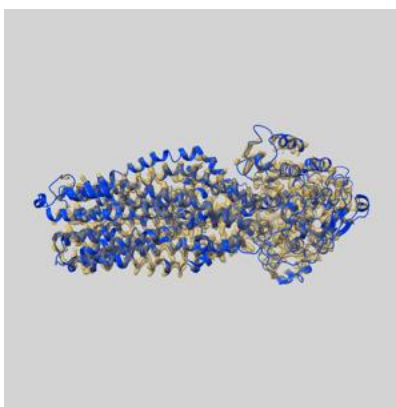
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-67183 and PDB model 9XSM. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

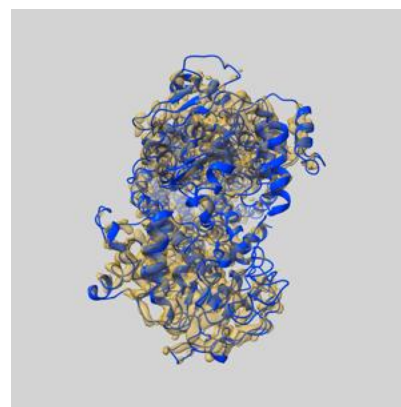
9.1 Map-model overlay [i](#)



X



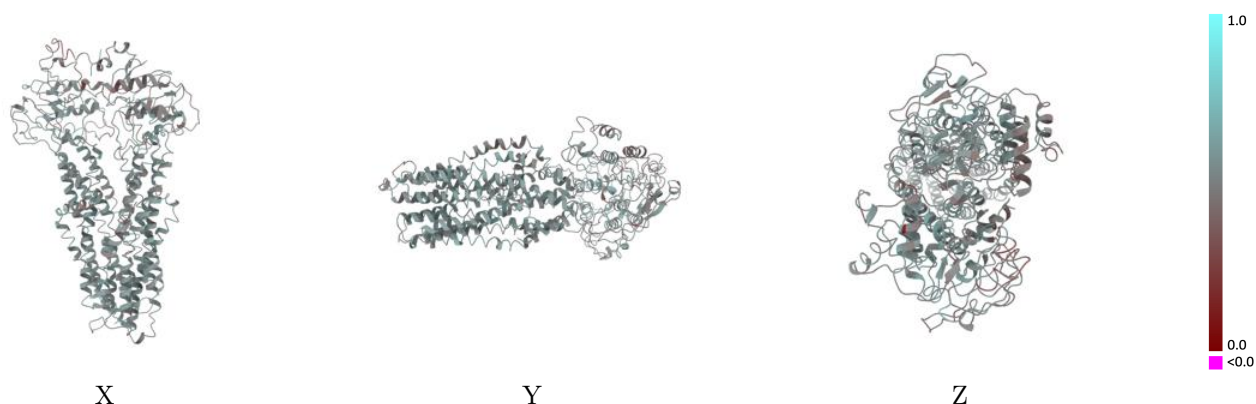
Y



Z

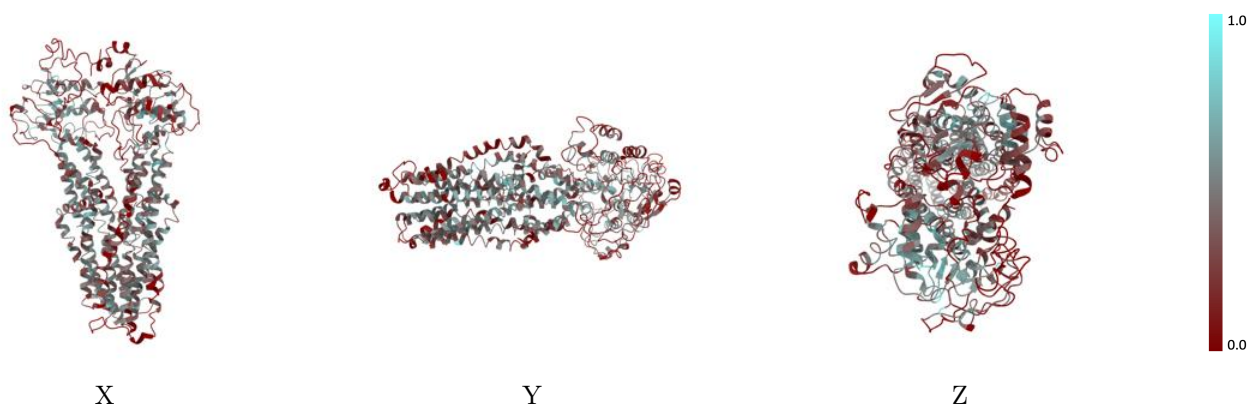
The images above show the 3D surface view of the map at the recommended contour level 0.365 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



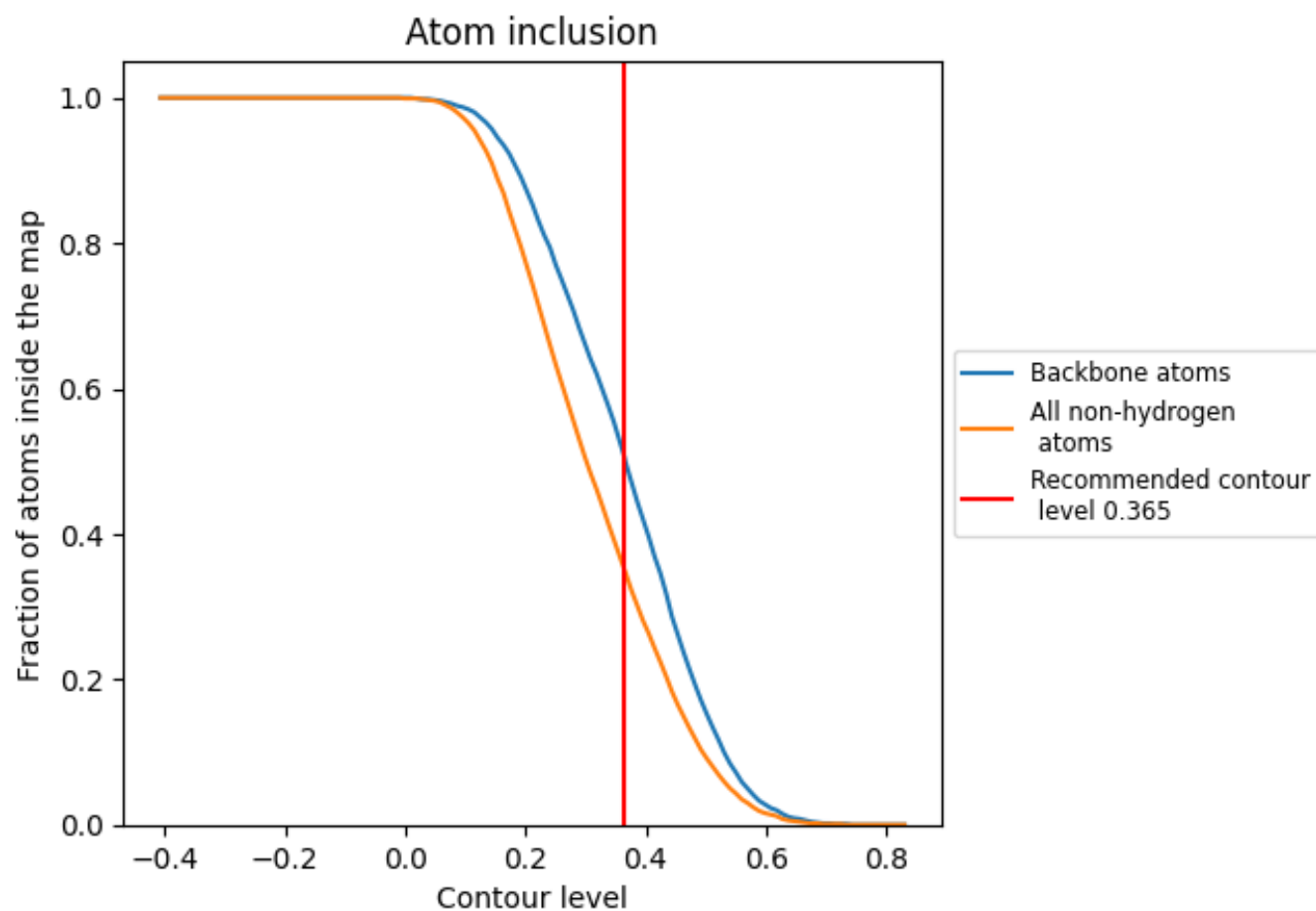
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.365).

9.4 Atom inclusion [i](#)



At the recommended contour level, 50% of all backbone atoms, 35% 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 (0.365) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3500	0.5180
C	0.3460	0.5200
D	0.3540	0.5160

