



wwPDB EM Validation Summary Report ⓘ

Apr 22, 2025 – 06:17 PM JST

PDB ID : 9ITM / pdb_00009itm
EMDB ID : EMD-60871
Title : Chloroflexus aurantiacus ATP synthase, state 1, focused refinement of FO
Authors : Zhang, X.; Wu, J.; Xu, X.
Deposited on : 2024-07-20
Resolution : 3.16 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.dev117
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) : 2.42

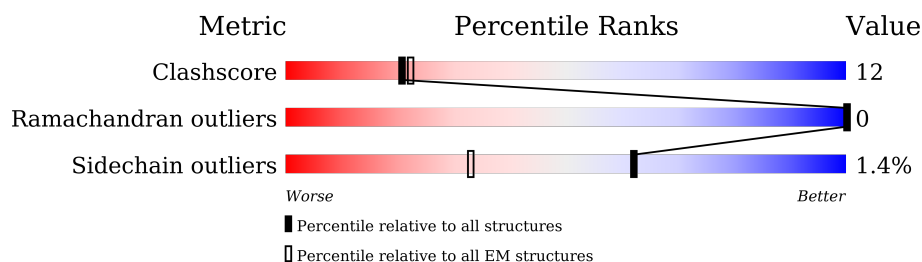
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.16 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	H	76	67% 28% 5%
1	I	76	66% 29% 5%
1	J	76	59% 36% 5%
1	K	76	59% 36% 5%
1	L	76	67% 28% 5%
1	M	76	53% 42% 5%
1	N	76	68% 26% 5%
1	O	76	74% 21% 5%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	P	76	 71%24%5%
1	Q	76	 59%36%5%
2	T	312	 63%22%15%
2	Z	312	 65%18%16%
3	U	164	 23%6%71%
3	V	164	 15%8%76%
3	X	164	 18%8%74%
3	Y	164	 26%71%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10692 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 ATP synthase subunit c.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	H	72	Total	C	N	O	S	0	0
			506	336	82	87	1		
1	I	72	Total	C	N	O	S	0	0
			513	340	82	89	2		
1	J	72	Total	C	N	O	S	0	0
			513	340	82	89	2		
1	K	72	Total	C	N	O	S	0	0
			513	340	82	89	2		
1	L	72	Total	C	N	O	S	0	0
			513	340	82	89	2		
1	M	72	Total	C	N	O	S	0	0
			513	340	82	89	2		
1	N	72	Total	C	N	O	S	0	0
			513	340	82	89	2		
1	O	72	Total	C	N	O	S	0	0
			513	340	82	89	2		
1	P	72	Total	C	N	O	S	0	0
			513	340	82	89	2		
1	Q	72	Total	C	N	O	S	0	0
			513	340	82	89	2		

- Molecule 2 is a protein called ATP synthase subunit a.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	T	266	Total	C	N	O	S	0	0
			2064	1405	317	336	6		
2	Z	261	Total	C	N	O	S	0	0
			2038	1392	312	328	6		

- Molecule 3 is a protein called ATP synthase subunit b.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	U	48	Total	C	N	O	S	0	0
			396	261	68	65	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
3	V	40	Total	C	N	O	S	0	0
			335	224	60	50	1		
3	X	42	Total	C	N	O	S	0	0
			348	233	62	52	1		
3	Y	47	Total	C	N	O	S	0	0
			388	256	67	64	1		

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.

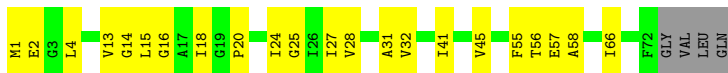
- Molecule 1: ATP synthase subunit c

Chain H: 



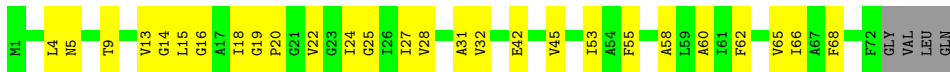
- Molecule 1: ATP synthase subunit c

Chain I: 



- Molecule 1: ATP synthase subunit c

Chain J: 



- Molecule 1: ATP synthase subunit c

Chain K: 



- Molecule 1: ATP synthase subunit c

Chain L: 



- Molecule 1: ATP synthase subunit c

H1	L4	N5	A9	T10	L11	A12	V13	G14	L15	G16	A17	L18	G19	P20	T24	G25	T26	L27	V28	A31	I35	N38	L41	E42	V45	F51	G52	I53	A54	F55	T56	E57	A58	L59	A60	T61	F62	G63	I66	F72	GLY VAL LEU
----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-------------

- Chain N: 68% 26% 5%

M1
N5
T9
V13
G14
L15
I18
G19
P20
I24
I27
V28
A31
V32
I36
I41
V45
F55
A58
F62
V65
I66
F72
GLY VAL LEU GLN

- Chain O:  74% 21% 5%

M1	L4	N5	L6	V13	G14	L15	I18	G19	G25	T26	I27	V32	I35	G36	I41	E42	N43	R44	V45	F72	GLY	VAL	LEU	GLN
----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Chain P: 71% 24% 5%

M1	V7	G14	G16	A17	I18	G19	P20	G25	I26	I27	A31	V32	N38	I41	E42	F55	A58	L59	A60	V65	I66	F72	GLY	VAL	LEU	GLN
----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

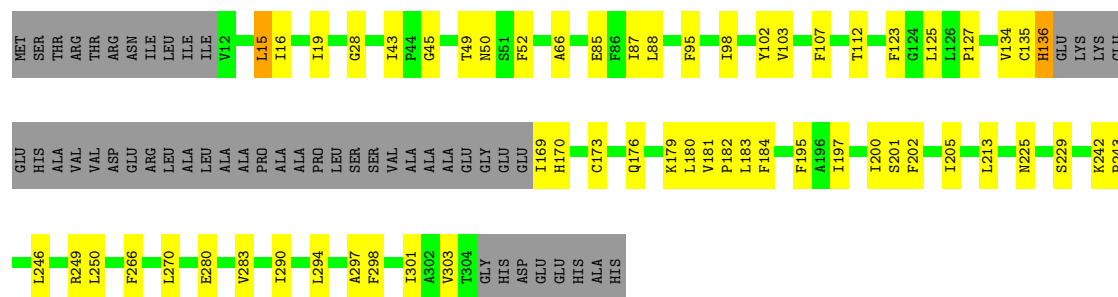
- Chain Q:  59% 36% 5%

H1
N5
T9
A12
V13
G14
L15
G16
G19
P20
G23
I24
G25
I26
I27
V28
V32
I35
G36
R37
I41
E42
Y48
I51
T56
E57
A58
I61
I66
A67
F72
GLY
VAL
LEU
IUN

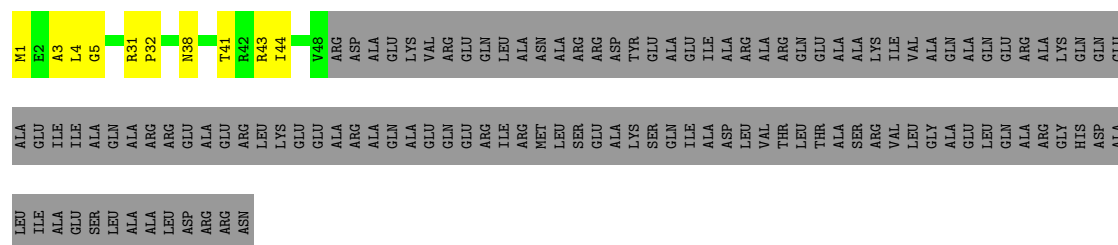
- Chain T:  63% 22% . 15%

L125	L246	L260	L286	L293	L300	L303	L304	L309	L310	L311	L312	L313	L314	L315	L316	L317	L318	L319	L320	L321	L322	L323	L324	L325	L326	L327	L328	L329	L330	L331	L332	L333	L334	L335	L336	L337	L338	L339	L340	L341	L342	L343	L344	L345	L346	L347	L348	L349	L350	L351	L352	L353	L354	L355	L356	L357	L358	L359	L360	L361	L362	L363	L364	L365	L366	L367	L368	L369	L370	L371	L372	L373	L374	L375	L376	L377	L378	L379	L380	L381	L382	L383	L384	L385	L386	L387	L388	L389	L390	L391	L392	L393	L394	L395	L396	L397	L398	L399	L400	L401	L402	L403	L404	L405	L406	L407	L408	L409	L410	L411	L412	L413	L414	L415	L416	L417	L418	L419	L420	L421	L422	L423	L424	L425	L426	L427	L428	L429	L430	L431	L432	L433	L434	L435	L436	L437	L438	L439	L440	L441	L442	L443	L444	L445	L446	L447	L448	L449	L450	L451	L452	L453	L454	L455	L456	L457	L458	L459	L460	L461	L462	L463	L464	L465	L466	L467	L468	L469	L470	L471	L472	L473	L474	L475	L476	L477	L478	L479	L480	L481	L482	L483	L484	L485	L486	L487	L488	L489	L490	L491	L492	L493	L494	L495	L496	L497	L498	L499	L500	L501	L502	L503	L504	L505	L506	L507	L508	L509	L510	L511	L512	L513	L514	L515	L516	L517	L518	L519	L520	L521	L522	L523	L524	L525	L526	L527	L528	L529	L530	L531	L532	L533	L534	L535	L536	L537	L538	L539	L540	L541	L542	L543	L544	L545	L546	L547	L548	L549	L550	L551	L552	L553	L554	L555	L556	L557	L558	L559	L560	L561	L562	L563	L564	L565	L566	L567	L568	L569	L570	L571	L572	L573	L574	L575	L576	L577	L578	L579	L580	L581	L582	L583	L584	L585	L586	L587	L588	L589	L590	L591	L592	L593	L594	L595	L596	L597	L598	L599	L600	L601	L602	L603	L604	L605	L606	L607	L608	L609	L610	L611	L612	L613	L614	L615	L616	L617	L618	L619	L620	L621	L622	L623	L624	L625	L626	L627	L628	L629	L630	L631	L632	L633	L634	L635	L636	L637	L638	L639	L640	L641	L642	L643	L644	L645	L646	L647	L648	L649	L650	L651	L652	L653	L654	L655	L656	L657	L658	L659	L660	L661	L662	L663	L664	L665	L666	L667	L668	L669	L670	L671	L672	L673	L674	L675	L676	L677	L678	L679	L680	L681	L682	L683	L684	L685	L686	L687	L688	L689	L690	L691	L692	L693	L694	L695	L696	L697	L698	L699	L700	L701	L702	L703	L704	L705	L706	L707	L708	L709	L710	L711	L712	L713	L714	L715	L716	L717	L718	L719	L720	L721	L722	L723	L724	L725	L726	L727	L728	L729	L730	L731	L732	L733	L734	L735	L736	L737	L738	L739	L740	L741	L742	L743	L744	L745	L746	L747	L748	L749	L750	L751	L752	L753	L754	L755	L756	L757	L758	L759	L760	L761	L762	L763	L764	L765	L766	L767	L768	L769	L770	L771	L772	L773	L774	L775	L776	L777	L778	L779	L780	L781	L782	L783	L784	L785	L786	L787	L788	L789	L790	L791	L792	L793	L794	L795	L796	L797	L798	L799	L800	L801	L802	L803	L804	L805	L806	L807	L808	L809	L810	L811	L81
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----

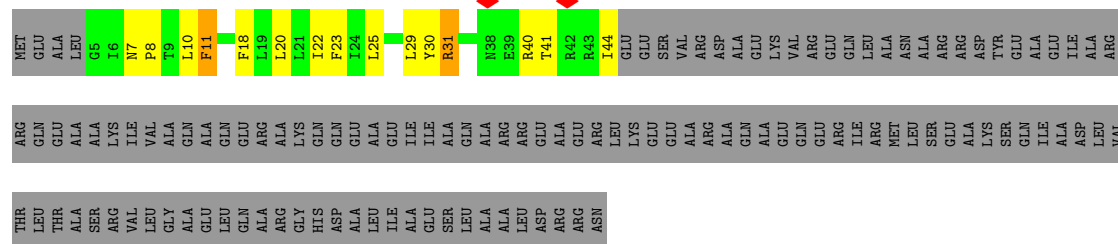
- Chain Z:  65% 18% • 16%



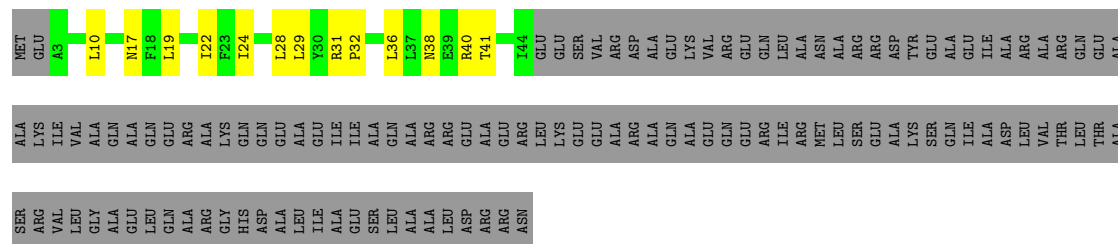
• Molecule 3: ATP synthase subunit b



• Molecule 3: ATP synthase subunit b

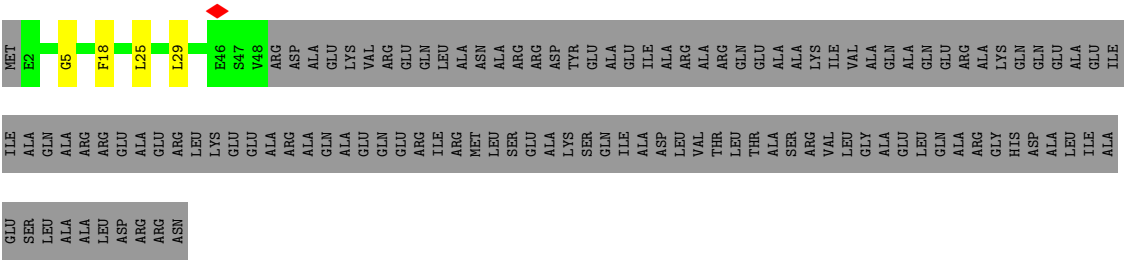


• Molecule 3: ATP synthase subunit b



• Molecule 3: ATP synthase subunit b





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	231462	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.644	Depositor
Minimum map value	-0.292	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	372.0, 372.0, 372.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.93, 0.93, 0.93	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	H	0.32	0/513	0.45	0/698
1	I	0.33	0/520	0.46	0/706
1	J	0.32	0/520	0.46	0/706
1	K	0.32	0/520	0.45	0/706
1	L	0.33	0/520	0.46	0/706
1	M	0.32	0/520	0.45	0/706
1	N	0.32	0/520	0.46	0/706
1	O	0.32	0/520	0.46	0/706
1	P	0.30	0/520	0.45	0/706
1	Q	0.32	0/520	0.47	0/706
2	T	0.28	0/2125	0.46	0/2898
2	Z	0.29	0/2098	0.44	0/2861
3	U	0.24	0/401	0.47	0/542
3	V	0.25	0/340	0.51	0/460
3	X	0.26	0/353	0.50	0/478
3	Y	0.24	0/393	0.48	0/532
All	All	0.30	0/10903	0.46	0/14823

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	H	506	0	535	18	0
1	I	513	0	546	20	0
1	J	513	0	546	25	0
1	K	513	0	546	22	0
1	L	513	0	546	19	0
1	M	513	0	546	29	0
1	N	513	0	546	20	0
1	O	513	0	546	17	0
1	P	513	0	546	18	0
1	Q	513	0	546	25	0
2	T	2064	0	2113	52	0
2	Z	2038	0	2102	46	0
3	U	396	0	433	6	0
3	V	335	0	373	12	0
3	X	348	0	389	10	0
3	Y	388	0	421	3	0
All	All	10692	0	11280	259	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 12.

The worst 5 of 259 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:M:56:THR:HG22	1:N:24:ILE:HG13	1.61	0.82
1:P:66:ILE:HG13	1:Q:13:VAL:HG21	1.64	0.80
1:H:19:GLY:HA3	1:I:18:ILE:HA	1.66	0.78
1:L:66:ILE:HG13	1:M:13:VAL:HG21	1.68	0.76
1:I:27:ILE:HG13	1:J:25:GLY:HA2	1.68	0.76

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	H	70/76 (92%)	68 (97%)	2 (3%)	0	100	100
1	I	70/76 (92%)	68 (97%)	2 (3%)	0	100	100
1	J	70/76 (92%)	67 (96%)	3 (4%)	0	100	100
1	K	70/76 (92%)	65 (93%)	5 (7%)	0	100	100
1	L	70/76 (92%)	67 (96%)	3 (4%)	0	100	100
1	M	70/76 (92%)	69 (99%)	1 (1%)	0	100	100
1	N	70/76 (92%)	70 (100%)	0	0	100	100
1	O	70/76 (92%)	66 (94%)	4 (6%)	0	100	100
1	P	70/76 (92%)	69 (99%)	1 (1%)	0	100	100
1	Q	70/76 (92%)	69 (99%)	1 (1%)	0	100	100
2	T	262/312 (84%)	243 (93%)	19 (7%)	0	100	100
2	Z	257/312 (82%)	242 (94%)	15 (6%)	0	100	100
3	U	46/164 (28%)	45 (98%)	1 (2%)	0	100	100
3	V	38/164 (23%)	37 (97%)	1 (3%)	0	100	100
3	X	40/164 (24%)	40 (100%)	0	0	100	100
3	Y	45/164 (27%)	43 (96%)	2 (4%)	0	100	100
All	All	1388/2040 (68%)	1328 (96%)	60 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	H	48/53 (91%)	48 (100%)	0	100	100
1	I	50/53 (94%)	50 (100%)	0	100	100
1	J	50/53 (94%)	49 (98%)	1 (2%)	50	72
1	K	50/53 (94%)	49 (98%)	1 (2%)	50	72
1	L	50/53 (94%)	50 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	M	50/53 (94%)	50 (100%)	0	100	100
1	N	50/53 (94%)	50 (100%)	0	100	100
1	O	50/53 (94%)	50 (100%)	0	100	100
1	P	50/53 (94%)	50 (100%)	0	100	100
1	Q	50/53 (94%)	49 (98%)	1 (2%)	50	72
2	T	213/251 (85%)	208 (98%)	5 (2%)	45	69
2	Z	212/251 (84%)	209 (99%)	3 (1%)	62	80
3	U	44/131 (34%)	43 (98%)	1 (2%)	45	69
3	V	37/131 (28%)	34 (92%)	3 (8%)	9	32
3	X	38/131 (29%)	38 (100%)	0	100	100
3	Y	43/131 (33%)	43 (100%)	0	100	100
All	All	1085/1556 (70%)	1070 (99%)	15 (1%)	62	80

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	T	277	TYR
2	Z	136	HIS
3	U	43	ARG
2	Z	195	PHE
3	V	31	ARG

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

Mol	Chain	Res	Type
2	T	253	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

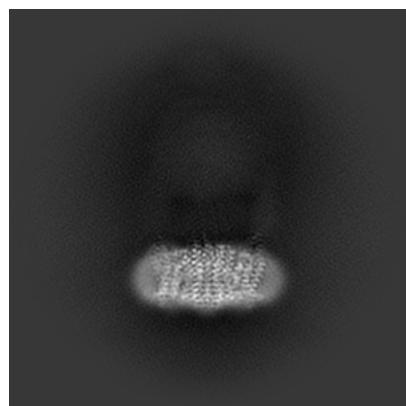
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60871. These allow visual inspection of the internal detail of the map and identification of artifacts.

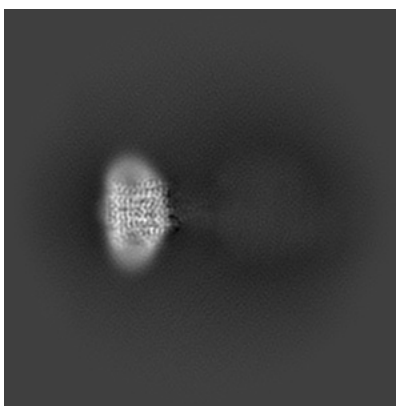
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

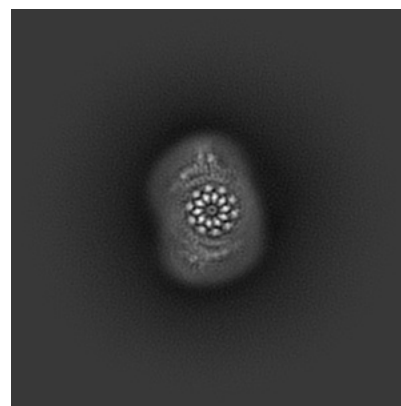
6.1.1 Primary map



X

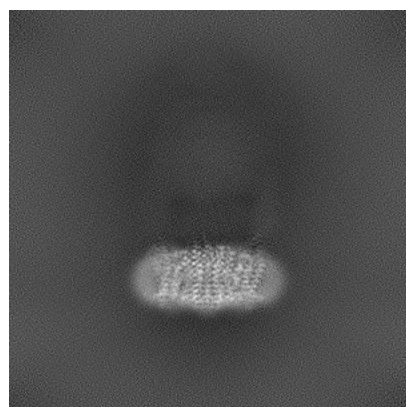


Y

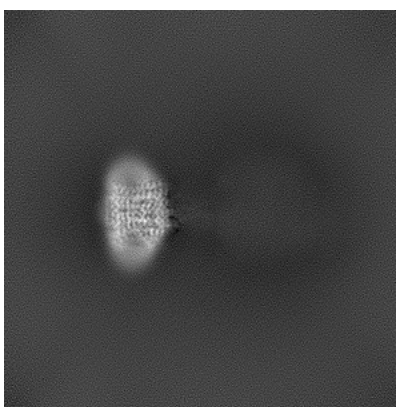


Z

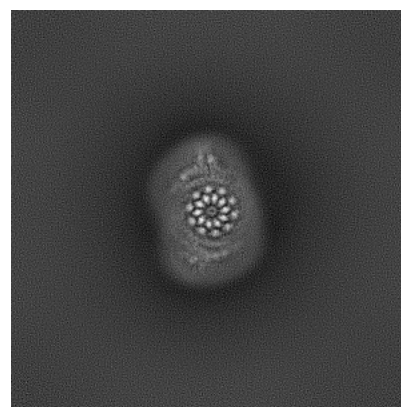
6.1.2 Raw map



X



Y

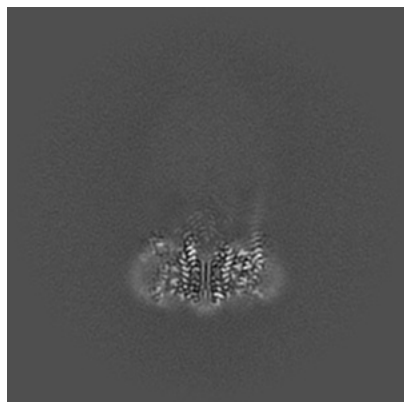


Z

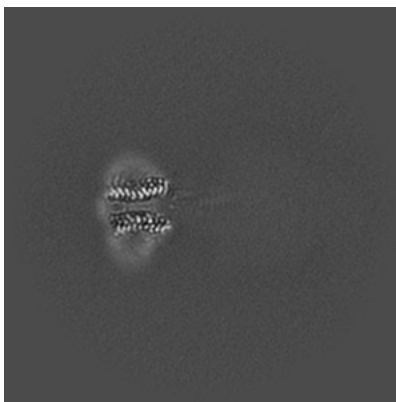
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

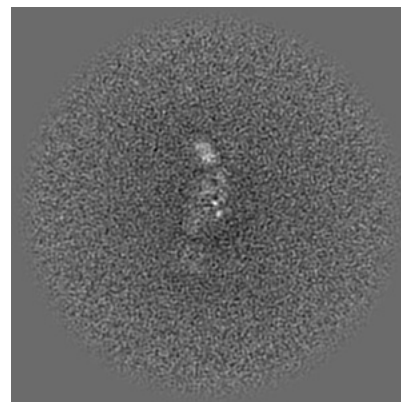
6.2.1 Primary map



X Index: 200

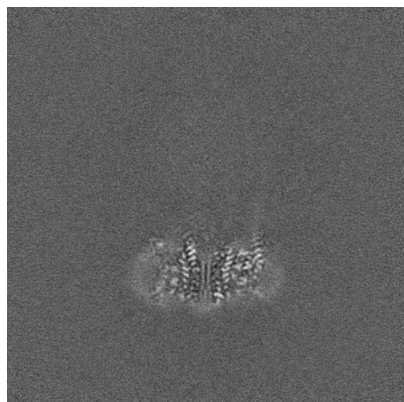


Y Index: 200

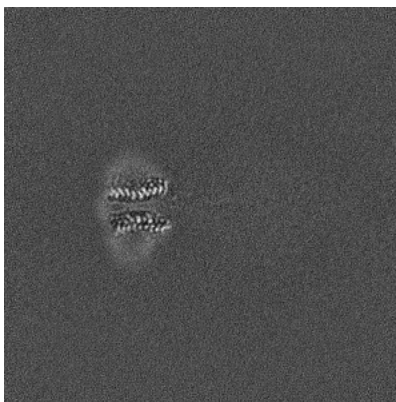


Z Index: 200

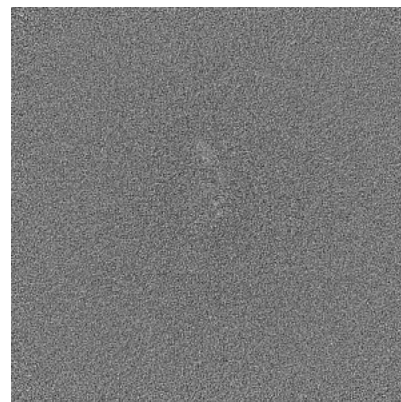
6.2.2 Raw map



X Index: 200



Y Index: 200

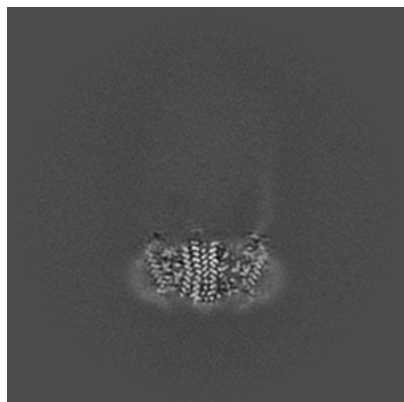


Z Index: 200

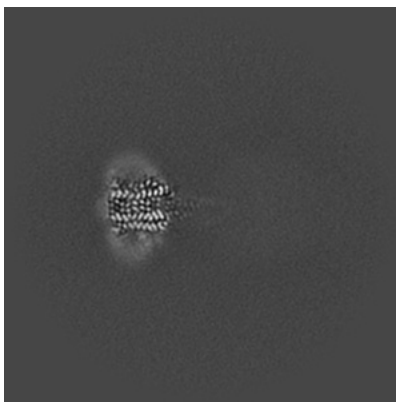
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

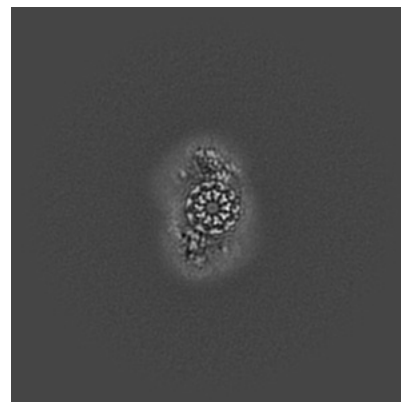
6.3.1 Primary map



X Index: 189

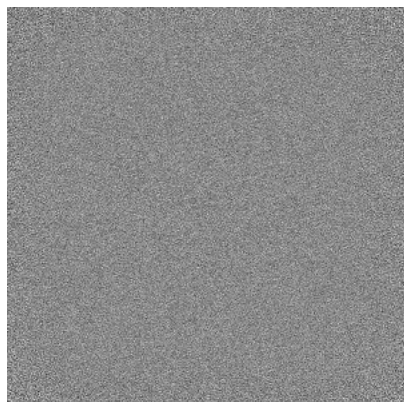


Y Index: 190

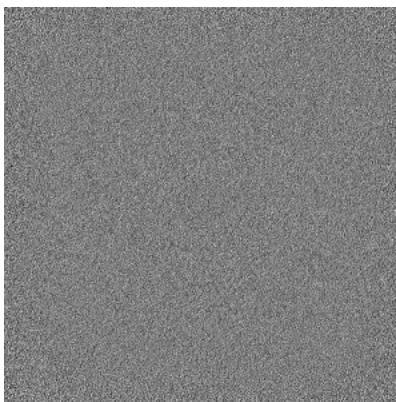


Z Index: 145

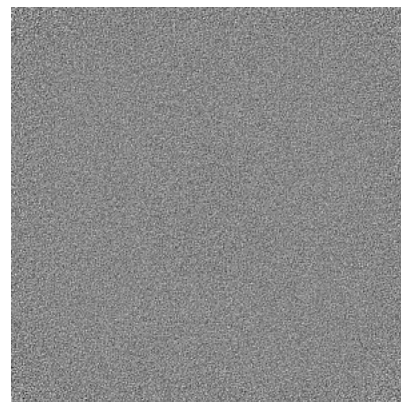
6.3.2 Raw map



X Index: 0



Y Index: 0

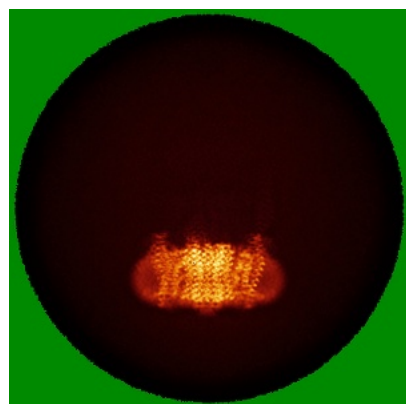


Z Index: 0

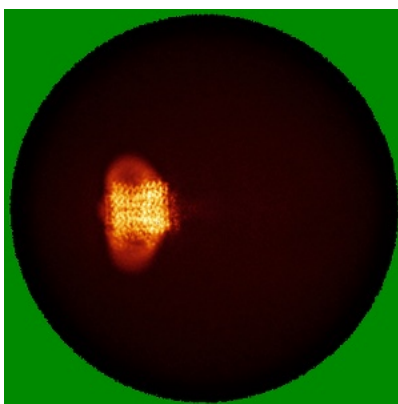
The images above show the largest variance slices of the map in three orthogonal directions.

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

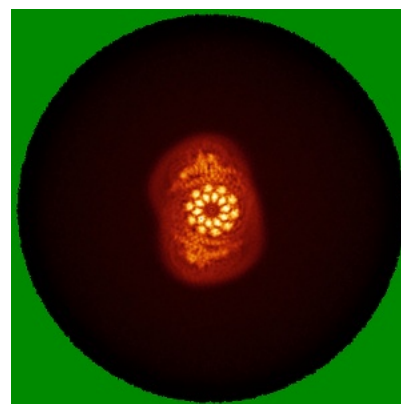
6.4.1 Primary map



X

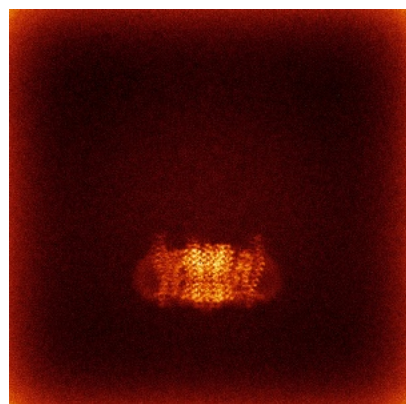


Y

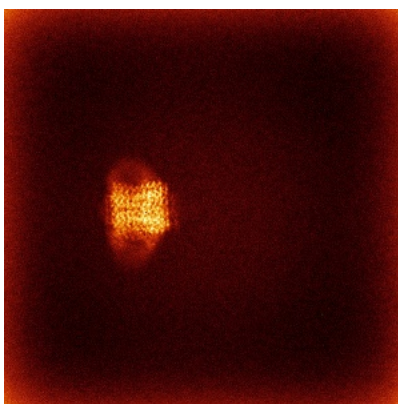


Z

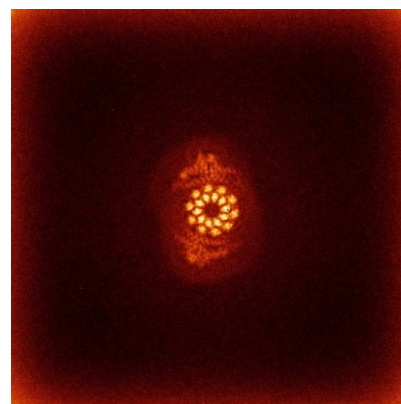
6.4.2 Raw map



X



Y

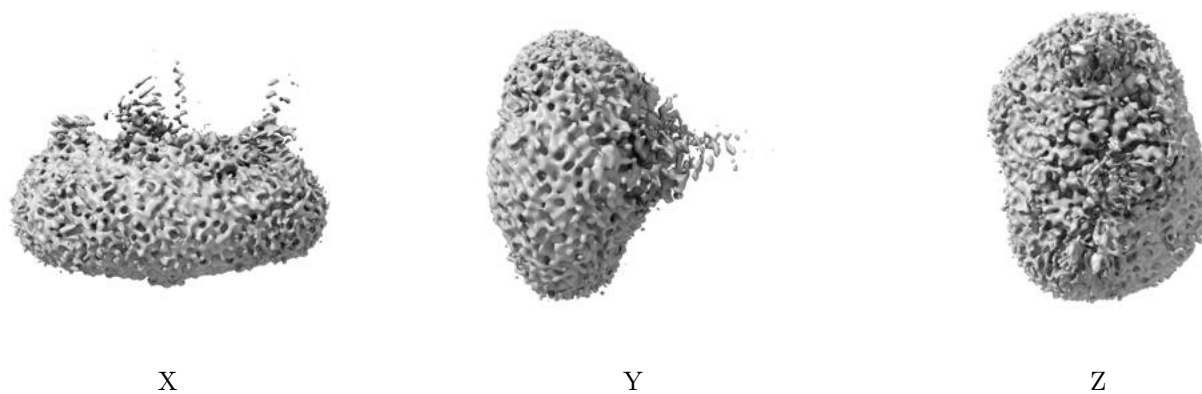


Z

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.

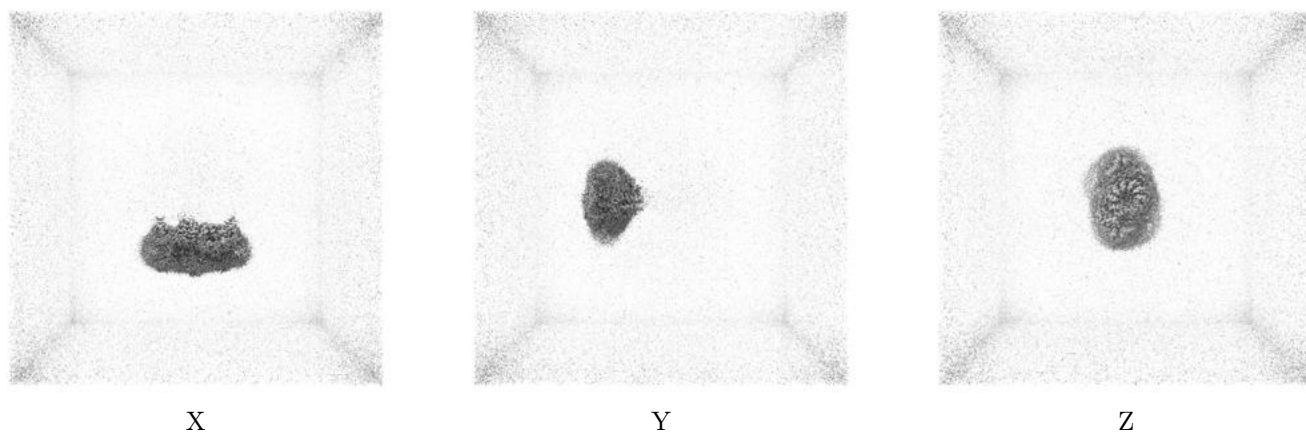
6.5 Orthogonal surface views [i](#)

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.

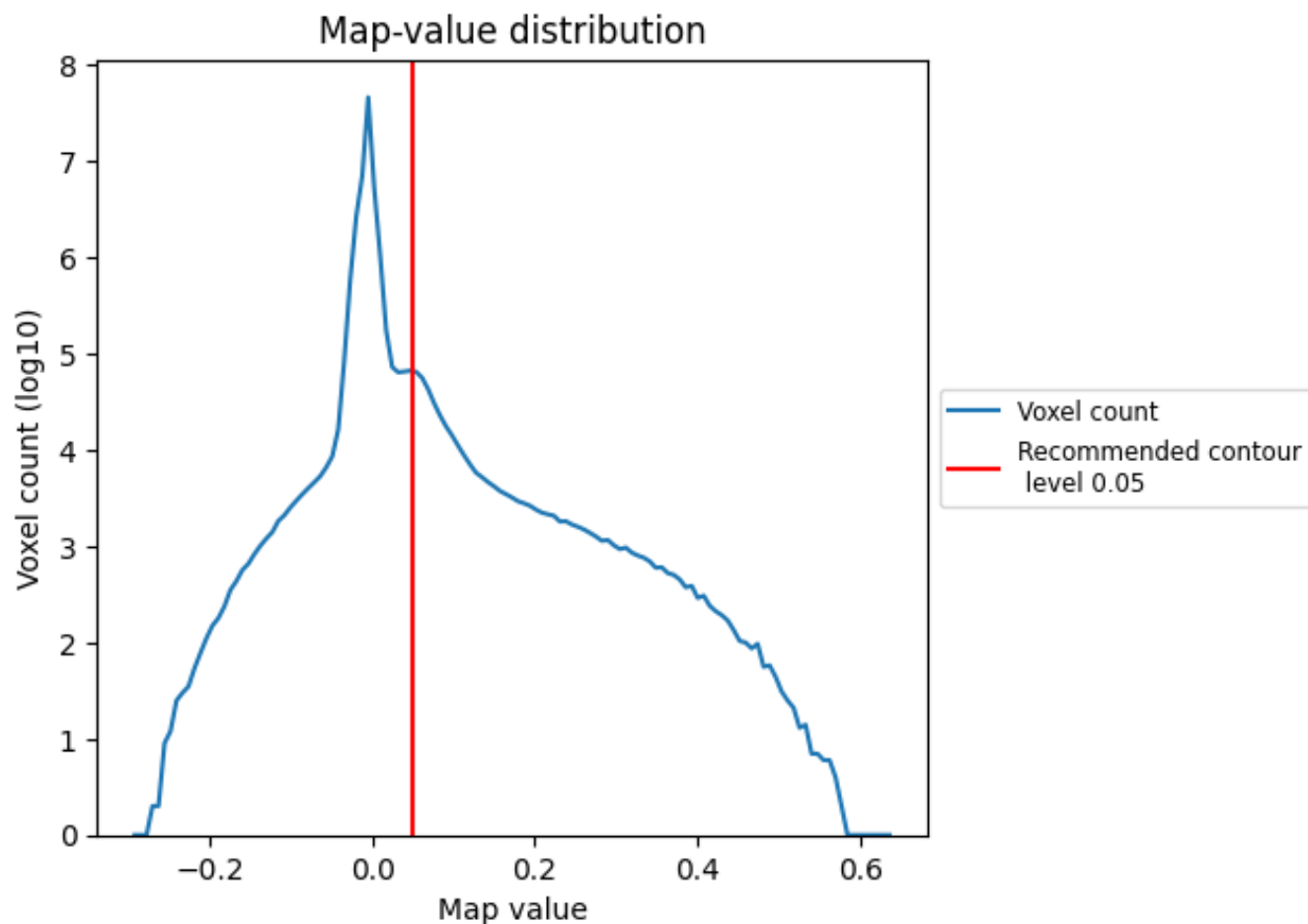
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

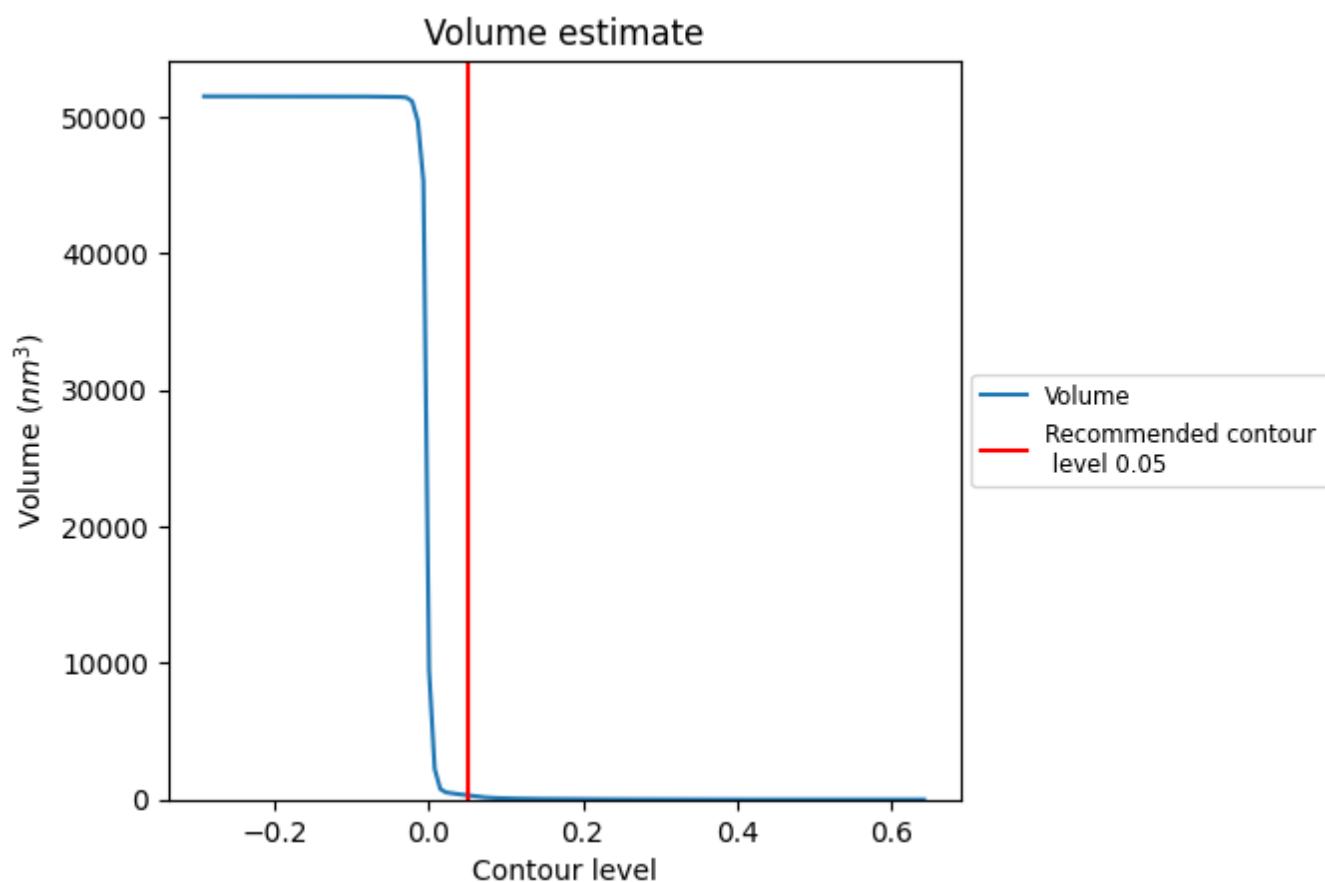
This section contains the results of statistical analysis of the map.

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.

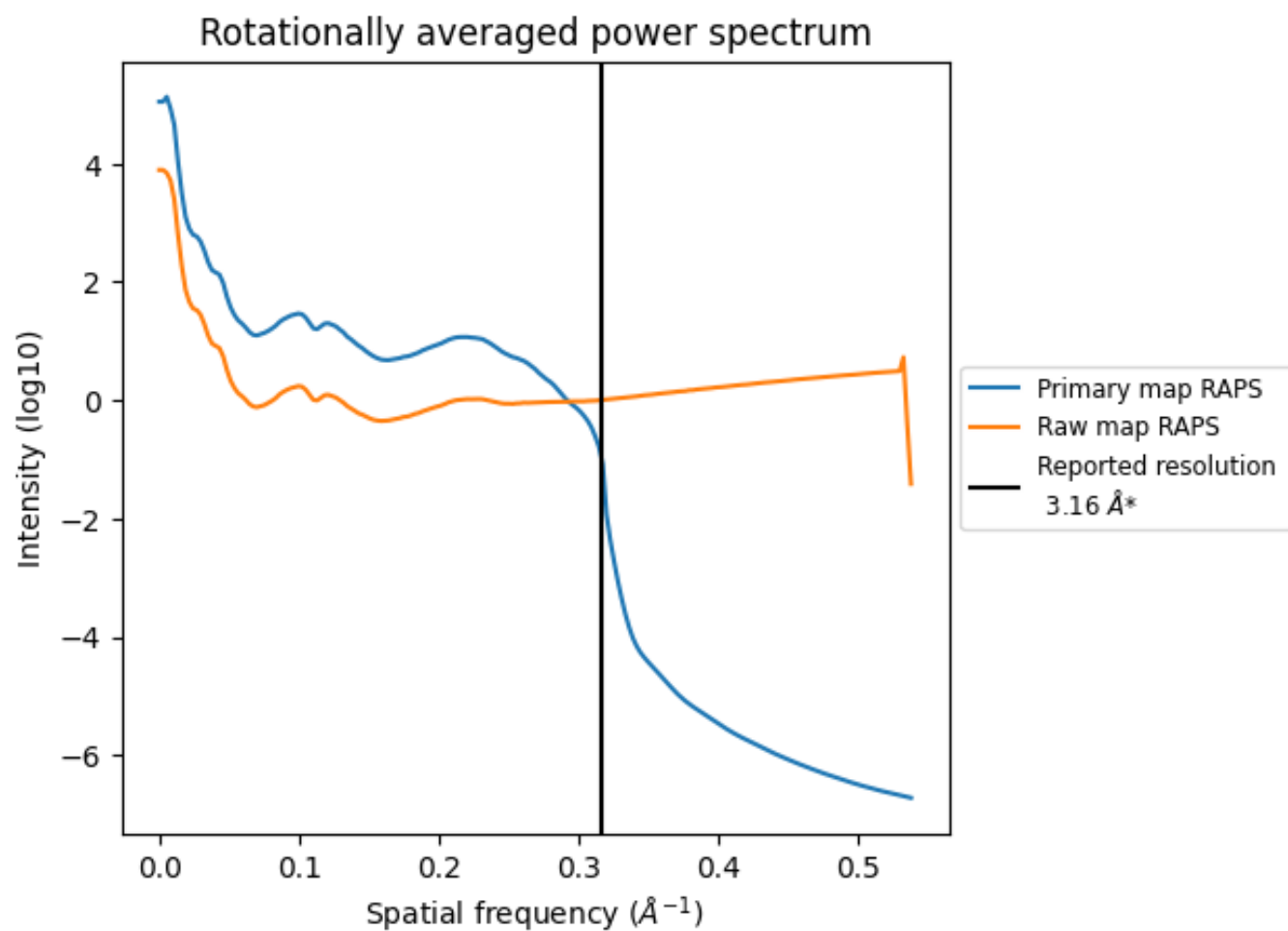
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 311 nm³; this corresponds to an approximate mass of 281 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 ⓘ

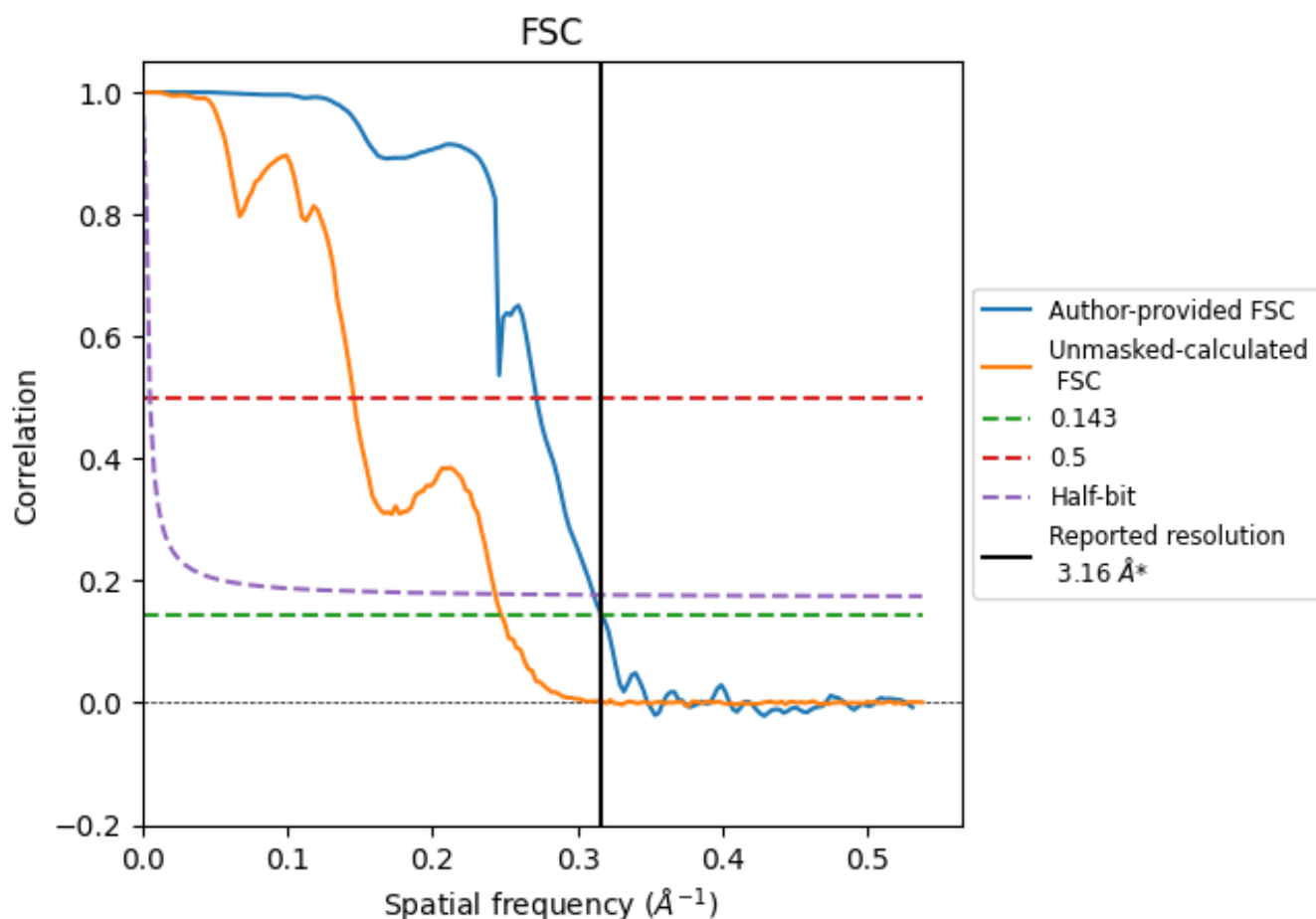


*Reported resolution corresponds to spatial frequency of 0.316 \AA^{-1}

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 0.316 \AA^{-1}

8.2 Resolution estimates [i](#)

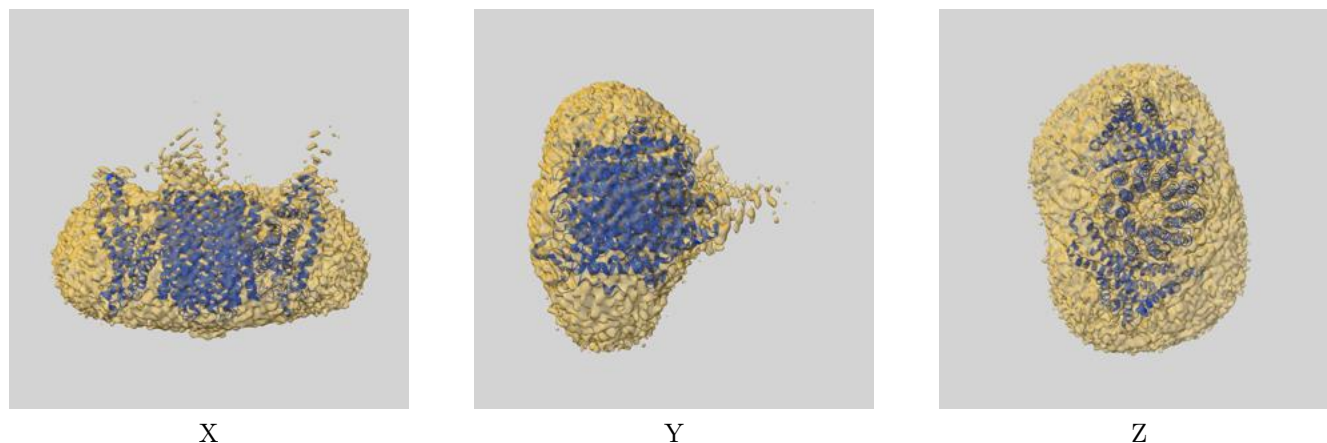
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.16	-	-
Author-provided FSC curve	3.16	3.68	3.21
Unmasked-calculated*	4.04	6.86	4.11

*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 4.04 differs from the reported value 3.16 by more than 10 %

9 Map-model fit [i](#)

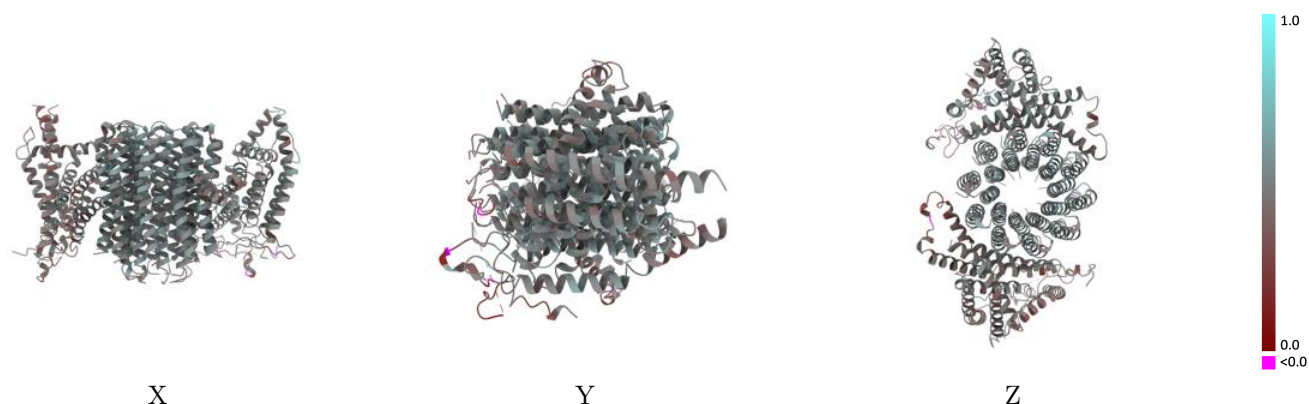
This section contains information regarding the fit between EMDB map EMD-60871 and PDB model 9ITM. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



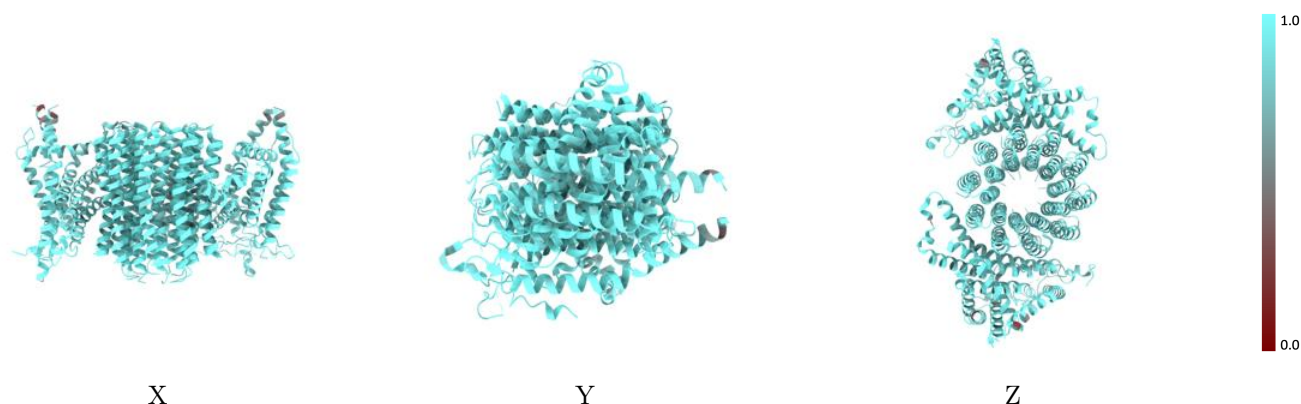
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



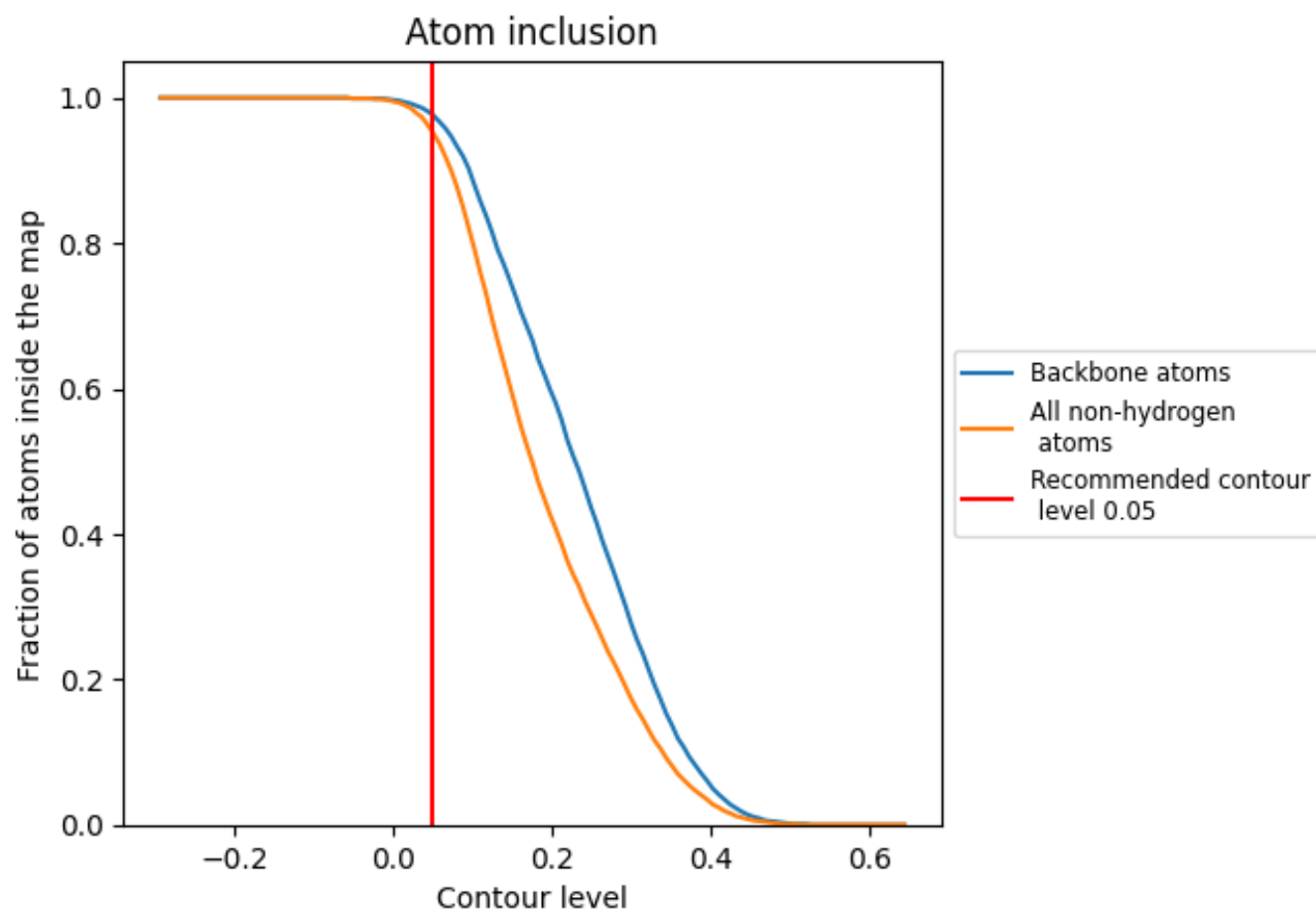
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 98% of all backbone atoms, 95% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9530	 0.4740
H	 0.9740	 0.5150
I	 0.9670	 0.5110
J	 0.9690	 0.5100
K	 0.9610	 0.5090
L	 0.9690	 0.5130
M	 0.9610	 0.5090
N	 0.9720	 0.5040
O	 0.9740	 0.5040
P	 0.9720	 0.5080
Q	 0.9740	 0.5090
T	 0.9640	 0.4550
U	 0.9250	 0.4730
V	 0.8670	 0.4210
X	 0.9080	 0.4690
Y	 0.9070	 0.4350
Z	 0.9360	 0.4240

