



wwPDB EM Validation Summary Report ⓘ

May 27, 2026 – 01:22 PM EDT

PDB ID : 13HS / pdb_000013hs
EMDB ID : EMD-77073
Title : Cryo-EM structure of Pseudomonas aeruginosa outer-membrane lipoprotein PA3214 in the open conformation
Authors : Giacometti, S.I.; Coudray, N.; Bhabha, G.; Ekiert, D.C.
Deposited on : 2026-05-06
Resolution : 3.70 Å(reported)
Based on initial model : .

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:

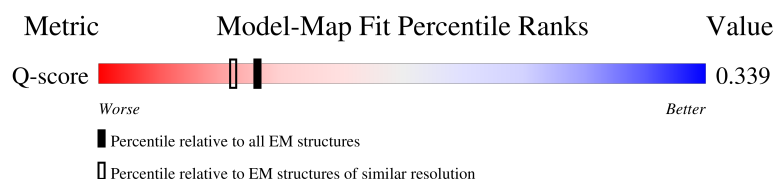
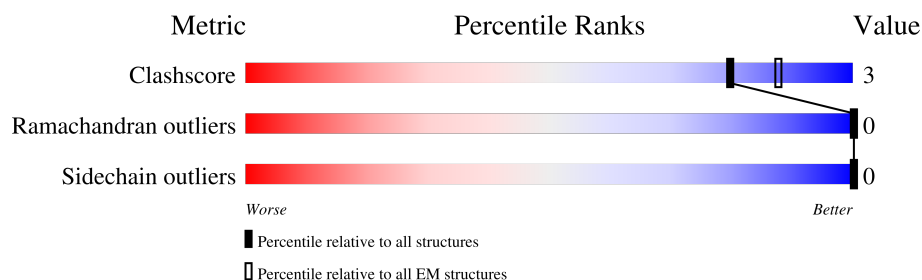
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 3.70 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	11569 (3.20 - 4.20)

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	214	<div> <div>34%</div> <div>72% 11% 17%</div> </div>
1	B	214	<div> <div>9%</div> <div>78% 6% 17%</div> </div>
1	C	214	<div> <div>•</div> <div>80% • 17%</div> </div>
1	D	214	<div> <div>•</div> <div>82% • 17%</div> </div>

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Mol	Chain	Length	Quality of chain
1	E	214	
1	F	214	
1	G	214	
1	H	214	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 11040 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.

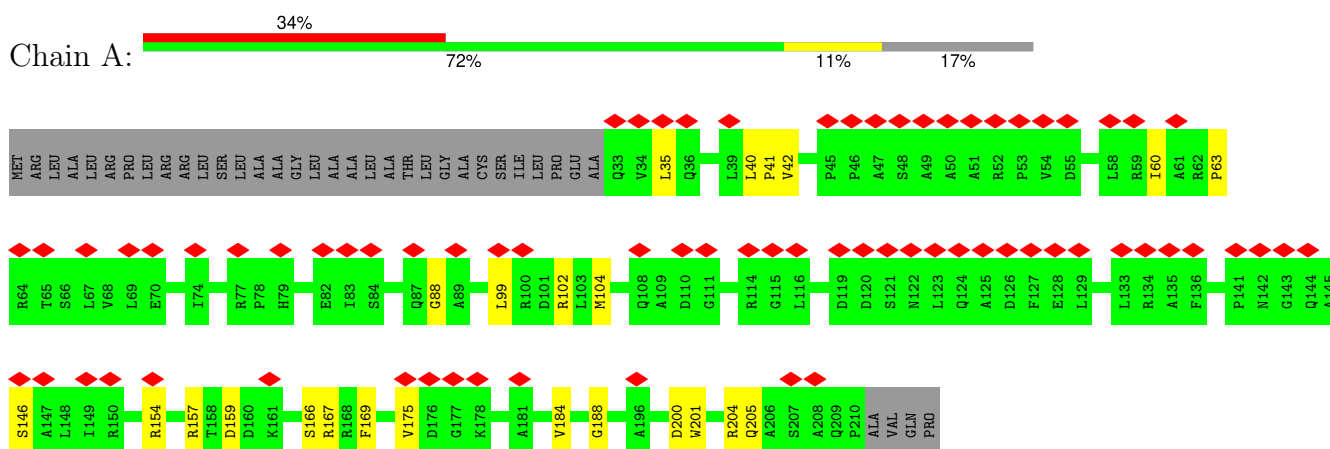
- Molecule 1 is a protein called ABC-type transport auxiliary lipoprotein component domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	178	Total	C	N	O	S	0	0
			1380	860	261	258	1		
1	B	178	Total	C	N	O	S	0	0
			1380	860	261	258	1		
1	C	178	Total	C	N	O	S	0	0
			1380	860	261	258	1		
1	D	178	Total	C	N	O	S	0	0
			1380	860	261	258	1		
1	E	178	Total	C	N	O	S	0	0
			1380	860	261	258	1		
1	F	178	Total	C	N	O	S	0	0
			1380	860	261	258	1		
1	G	178	Total	C	N	O	S	0	0
			1380	860	261	258	1		
1	H	178	Total	C	N	O	S	0	0
			1380	860	261	258	1		

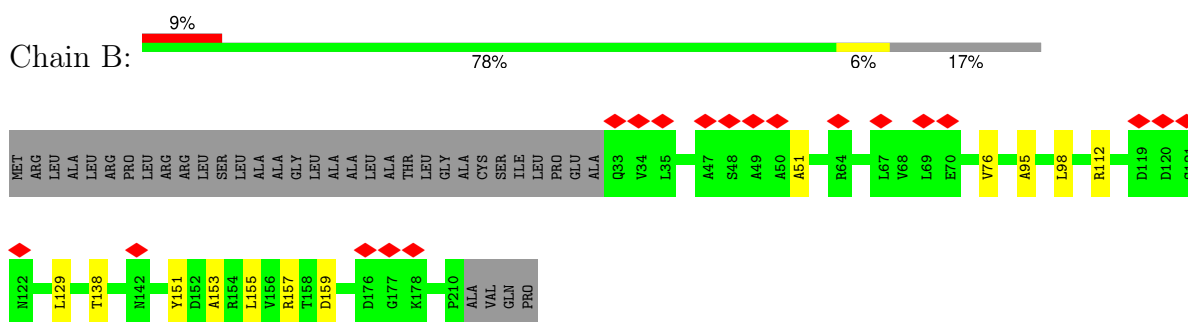
3 Residue-property plots

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.

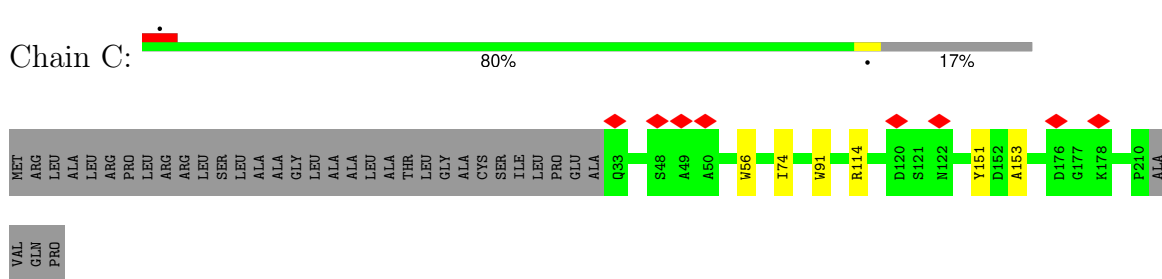
- Molecule 1: ABC-type transport auxiliary lipoprotein component domain-containing protein



- Molecule 1: ABC-type transport auxiliary lipoprotein component domain-containing protein

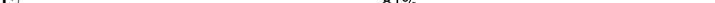


- Molecule 1: ABC-type transport auxiliary lipoprotein component domain-containing protein

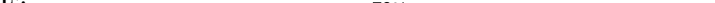


- Molecule 1: ABC-type transport auxiliary lipoprotein component domain-containing protein

MET	ARG	LEU	ALA	LEU	ARG	PRO	LEU	ARG	ARG	LEU	SER	LEU	ALA	GLY	LEU	ALA	ALA	LEU	ALA	THR	LEU	GLY	ALA	CYS	SSR	ILE	LEU	PRO	GLU	ALA	Q33	A49	A50	W56	I74	W91	D119	D120	D176	P210	ALA	VAL	GLN	PRO
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- Chain E:  81% • 17%

MET	ARG	LEU	ALA	LEU	ARG	PRO	LEU	ARG	ARG	LEU	SER	LEU	ALA	ALA	GLY	ALA	ALA	LEU	ALA	THR	LEU	GLY	ALA	CYS	SER	ILE	LEU	PRO	GLU	ALA	Q33	A49	A50	W56	I74	W91	D120	Y151	D152	A153	D176	G177	K178	P210	ALA	VAL	GLN
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- Chain F:  6% 79% 17%

MET ARG LEU LEU ARG PRO LEU ARG LEU SER LEU ALA ALA GLY LEU ALA ALA LEU THR LEU LEU CYS SER ILE LEU PRO GLU ALA
 Q33 L40 P41 S48 A49 A50 A51 L69 I74 A75 W91 R114 D119 D120 G131 R134 Y151

A diagram showing a protein sequence segment. The residues are A153, V175, D176, G177, and P210. A red diamond highlights the D176 residue. The residues are color-coded: A153, V175, and G177 are yellow; D176 is green; and P210 is green. The residues are connected by lines, and the D176 residue is highlighted with a red diamond.

- Chain G: 

MET	ARG	LEU	ALA	LEU	ARG	PRO	LEU	ARG	ARG	SER	LEU	ALA	ALA	GLY	LEU	ALA	ALA	LEU	LEU	ALA	THR	LEU	GLY	ALA	CYS	SER	ILE	LEU	PRO	GLU	ALA	Q33	V34	L35	L39	L40	P41	V42	P46	A47	S48	A49	A50	A51	A52	R51	L60	A61	R62	P63	R64	L67	V68	L69	E70
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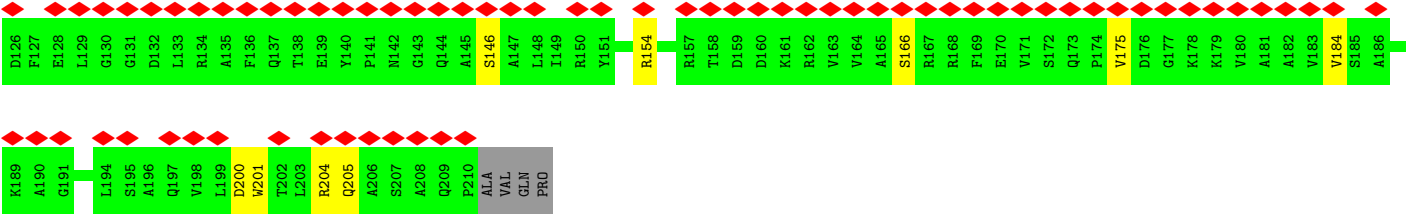
I74	A75	R76	V77	G80	D81	E82	I83	S84	V85	Y86	Q87	G88	W91	S92	D93	P94	L99	R102	Q105	R114	G115	L116	D119	N122	E128	L129	G130	G131	R134	A135	F136	N142	S146	Y151	R154	R157	T158	D159	R162	S166	R167	P168
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Diagram illustrating the structure of the 12S ribosomal subunit, showing various proteins (F169, E170, V175, D176, G177, K178, F187, D200, W201, R204, Q205, A208, Q209, P210, ALA, VAL, GLN, PRO) and their interactions, with red diamonds indicating specific sites of interest.

- Chain H: 

MET	ARG	LEU	ALA	LEU	ARG	PRO	LEU	ARG	ARG	LEU	SER	LEU	ALA	ALA	LEU	ALA	THR	LEU	GLY	ALA	CYS	ILE	LEU	PRO	GLU	ALA	Q33	Q34	L35	Y38	L39	L40	P41	V42	H43	N44	P45	P46	A47	S48	A49	A50	A51	R52	P53	V54	D55	W56	R59	T60	A61	...
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P63	R64	T65	S66	L67	V68	L69	E70	S71	T72	R73	L74	A75	V76	R77	F78	H79	G80	D81	S82	L83	S84	V85	Y86	O87	C88	A89	R90	W91	S92	D93	P94	A95	L99	R102	L103	M104	Q105	A106	F107	Q108	A109	D110	G111	R112	V113	R114	G115	L116	S117	S118	D119	D120	S121	M122	L123	Q124	L125	A126	R127	L128	S129	L130	R131	L132	S133	L134	R135	L136	S137	L138	R139	L140	S141	L142	R143	L144	S145	L146	R147	L148	S149	L150	R151	L152	S153	L154	R155	L156	S157	L158	R159	L160	S161	L162	R163	L164	S165	L166	R167	L168	S169	L170	R171	L172	S173	L174	R175	L176	S177	L178	R179	L180	S181	L182	R183	L184	S185	L186	R187	L188	S189	L190	R191	L192	S193	L194	R195	L196	S197	L198	R199	L200	S201	L202	R203	L204	S205	L206	R207	L208	S209	L210	R211	L212	S213	L214	R215	L216	S217	L218	R219	L220	S221	L222	R223	L224	S225	L226	R227	L228	S229	L230	R231	L232	S233	L234	R235	L236	S237	L238	R239	L240	S241	L242	R243	L244	S245	L246	R247	L248	S249	L250	R251	L252	S253	L254	R255	L256	S257	L258	R259	L260	S261	L262	R263	L264	S265	L266	R267	L268	S269	L270	R271	L272	S273	L274	R275	L276	S277	L278	R279	L280	S281	L282	R283	L284	S285	L286	R287	L288	S289	L290	R291	L292	S293	L294	R295	L296	S297	L298	R299	L300	S301	L302	R303	L304	S305	L306	R307	L308	S309	L310	R311	L312	S313	L314	R315	L316	S317	L318	R319	L320	S321	L322	R323	L324	S325	L326	R327	L328	S329	L330	R331	L332	S333	L334	R335	L336	S337	L338	R339	L340	S341	L342	R343	L344	S345	L346	R347	L348	S349	L350	R351	L352	S353	L354	R355	L356	S357	L358	R359	L360	S361	L362	R363	L364	S365	L366	R367	L368	S369	L370	R371	L372	S373	L374	R375	L376	S377	L378	R379	L380	S381	L382	R383	L384	S385	L386	R387	L388	S389	L390	R391	L392	S393	L394	R395	L396	S397	L398	R399	L400	S401	L402	R403	L404	S405	L406	R407	L408	S409	L410	R411	L412	S413	L414	R415	L416	S417	L418	R419	L420	S421	L422	R423	L424	S425	L426	R427	L428	S429	L430	R431	L432	S433	L434	R435	L436	S437	L438	R439	L440	S441	L442	R443	L444	S445	L446	R447	L448	S449	L450	R451	L452	S453	L454	R455	L456	S457	L458	R459	L460	S461	L462	R463	L464	S465	L466	R467	L468	S469	L470	R471	L472	S473	L474	R475	L476	S477	L478	R479	L480	S481	L482	R483	L484	S485	L486	R487	L488	S489	L490	R491	L492	S493	L494	R495	L496	S497	L498	R499	L500	S501	L502	R503	L504	S505	L506	R507	L508	S509	L510	R511	L512	S513	L514	R515	L516	S517	L518	R519	L520	S521	L522	R523	L524	S525	L526	R527	L528	S529	L530	R531	L532	S533	L534	R535	L536	S537	L538	R539	L540	S541	L542	R543	L544	S545	L546	R547	L548	S549	L550	R551	L552	S553	L554	R555	L556	S557	L558	R559	L560	S561	L562	R563	L564	S565	L566	R567	L568	S569	L570	R571	L572	S573	L574	R575	L576	S577	L578	R579	L580	S581	L58
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	187311	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 ($e^-/\text{\AA}^2$)	51.51, 51.43	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k), GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.121	Depositor
Minimum map value	-0.390	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.044	Depositor
Recommended contour level	0.399	Depositor
Map size (Å)	277.248, 277.248, 277.248	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.083, 1.083, 1.083	Depositor

5 Model quality

5.1 Standard geometry

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	0.15	0/1408	0.31	0/1915
1	B	0.24	0/1408	0.48	0/1915
1	C	0.24	0/1408	0.41	0/1915
1	D	0.24	0/1408	0.38	0/1915
1	E	0.24	0/1408	0.43	0/1915
1	F	0.22	0/1408	0.38	0/1915
1	G	0.18	0/1408	0.33	0/1915
1	H	0.12	0/1408	0.28	0/1915
All	All	0.21	0/11264	0.38	0/15320

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	A	1380	0	1375	13	0
1	B	1380	0	1375	7	0
1	C	1380	0	1375	4	0
1	D	1380	0	1375	3	0
1	E	1380	0	1375	3	0
1	F	1380	0	1375	6	0
1	G	1380	0	1375	14	0
1	H	1380	0	1375	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	11040	0	11000	59	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 3.

The worst 5 of 59 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:G:40:LEU:HD12	1:G:41:PRO:HD2	1.82	0.62
1:A:40:LEU:HD12	1:A:41:PRO:HD2	1.83	0.60
1:B:151:TYR:CE2	1:B:153:ALA:HB2	2.40	0.57
1:F:134:ARG:HD2	1:G:105:GLN:HE21	1.69	0.57
1:D:74:ILE:HG12	1:D:91:TRP:NE1	2.20	0.56

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	176/214 (82%)	173 (98%)	3 (2%)	0	100	100
1	B	176/214 (82%)	172 (98%)	4 (2%)	0	100	100
1	C	176/214 (82%)	171 (97%)	5 (3%)	0	100	100
1	D	176/214 (82%)	173 (98%)	3 (2%)	0	100	100
1	E	176/214 (82%)	172 (98%)	4 (2%)	0	100	100
1	F	176/214 (82%)	173 (98%)	3 (2%)	0	100	100
1	G	176/214 (82%)	173 (98%)	3 (2%)	0	100	100
1	H	176/214 (82%)	173 (98%)	3 (2%)	0	100	100
All	All	1408/1712 (82%)	1380 (98%)	28 (2%)	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	A	145/170 (85%)	145 (100%)	0	100	100
1	B	145/170 (85%)	145 (100%)	0	100	100
1	C	145/170 (85%)	145 (100%)	0	100	100
1	D	145/170 (85%)	145 (100%)	0	100	100
1	E	145/170 (85%)	145 (100%)	0	100	100
1	F	145/170 (85%)	145 (100%)	0	100	100
1	G	145/170 (85%)	145 (100%)	0	100	100
1	H	145/170 (85%)	145 (100%)	0	100	100
All	All	1160/1360 (85%)	1160 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	124	GLN
1	H	87	GLN
1	F	105	GLN
1	H	33	GLN
1	F	43	HIS

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.

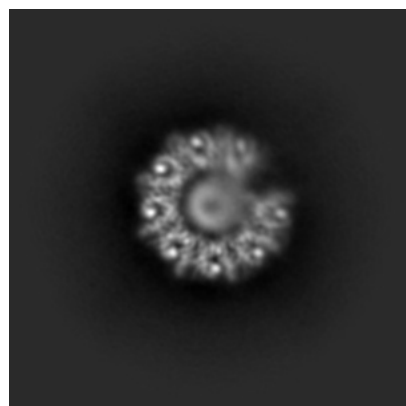
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-77073. These allow visual inspection of the internal detail of the map and identification of artifacts.

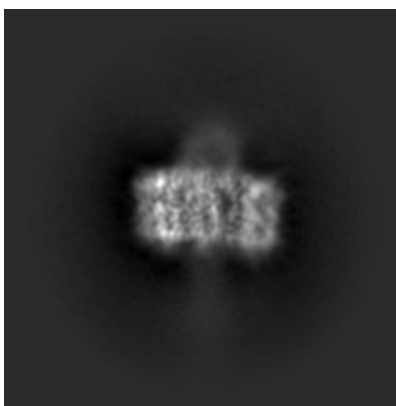
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

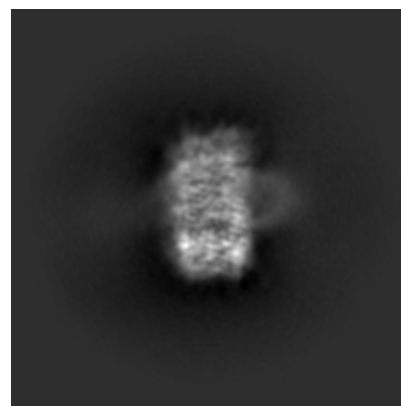
6.1.1 Primary map



X

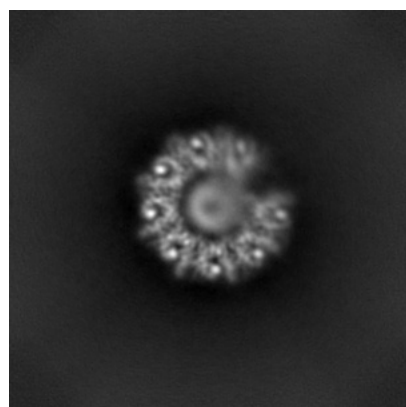


Y

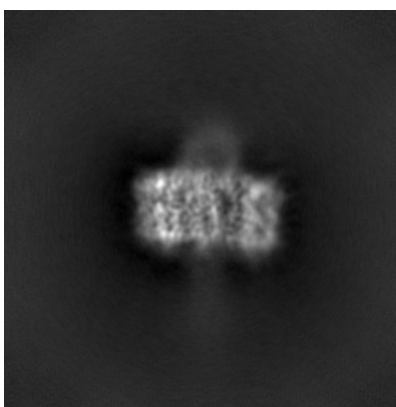


Z

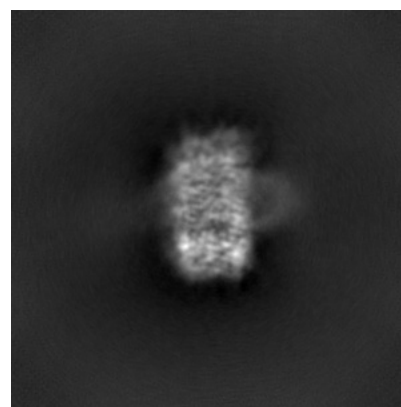
6.1.2 Raw map



X



Y

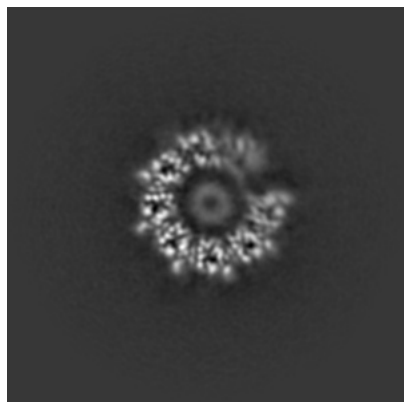


Z

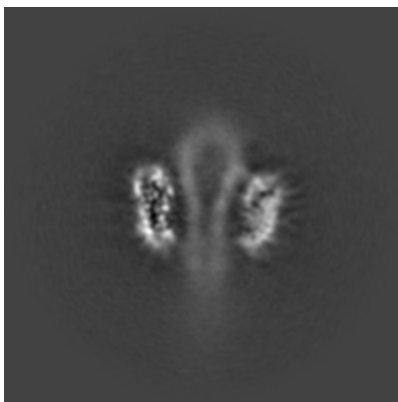
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

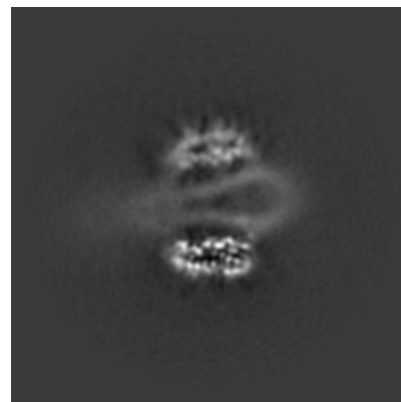
6.2.1 Primary map



X Index: 128

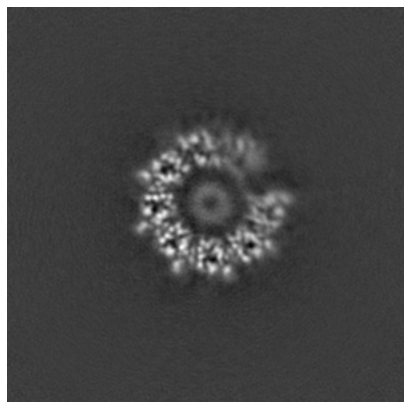


Y Index: 128

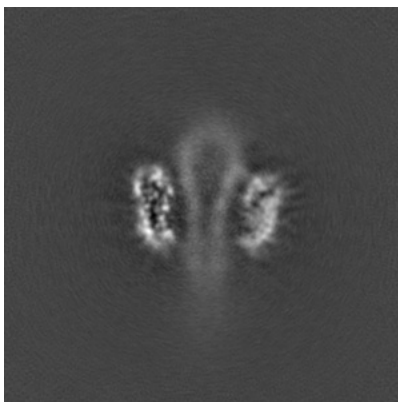


Z Index: 128

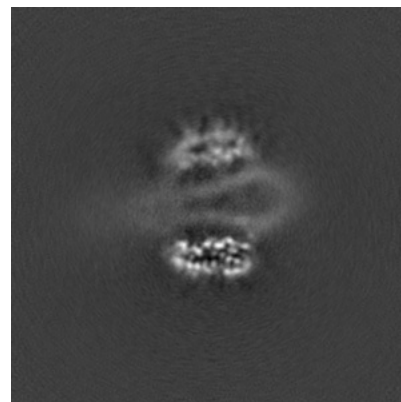
6.2.2 Raw map



X Index: 128



Y Index: 128

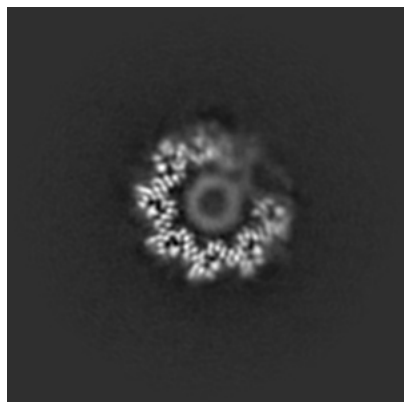


Z Index: 128

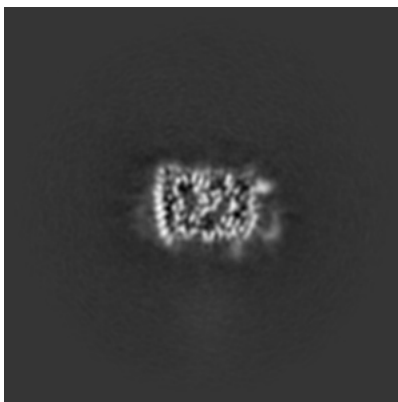
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

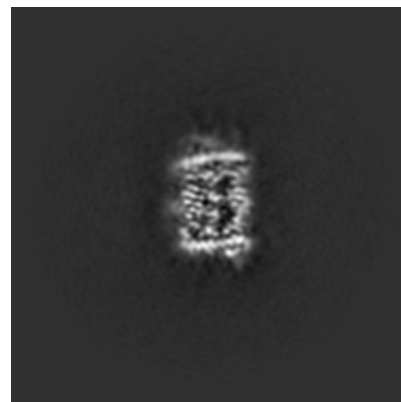
6.3.1 Primary map



X Index: 143

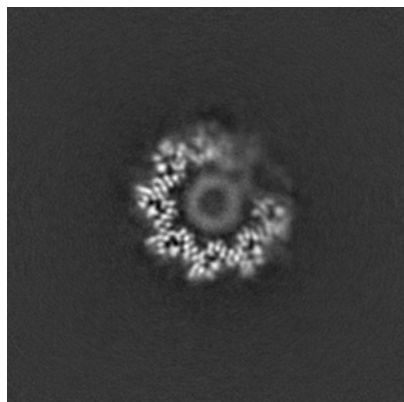


Y Index: 104

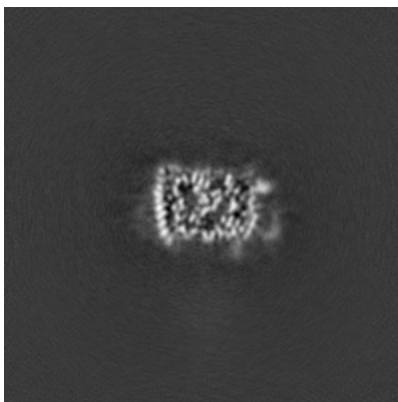


Z Index: 100

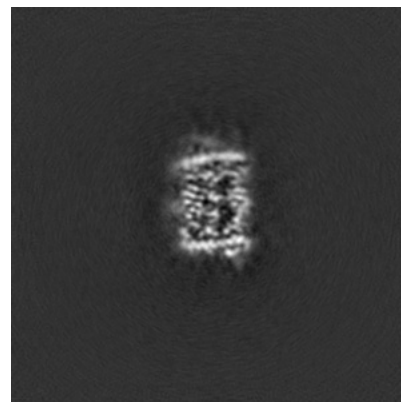
6.3.2 Raw map



X Index: 143



Y Index: 104



Z Index: 100

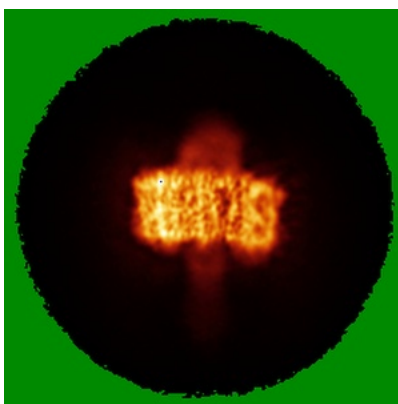
The images above show the largest variance slices of the map in three orthogonal directions.

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

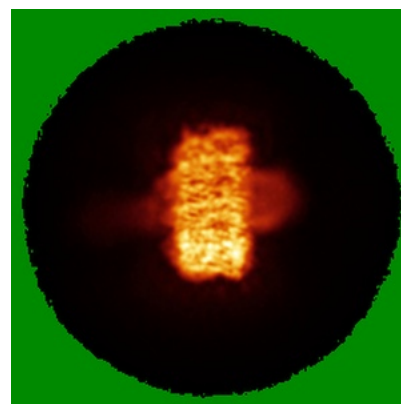
6.4.1 Primary map



X

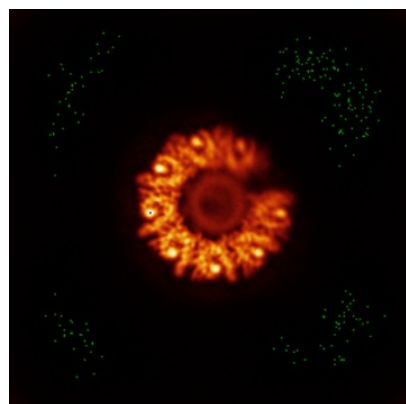


Y

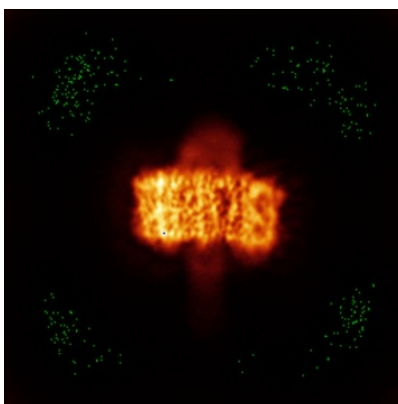


Z

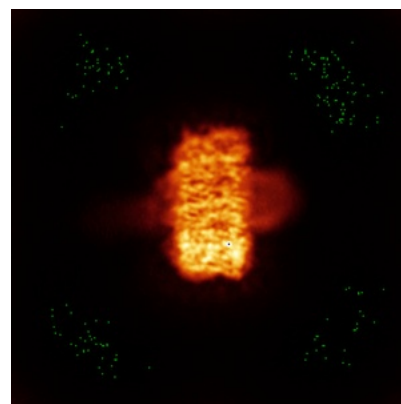
6.4.2 Raw map



X



Y

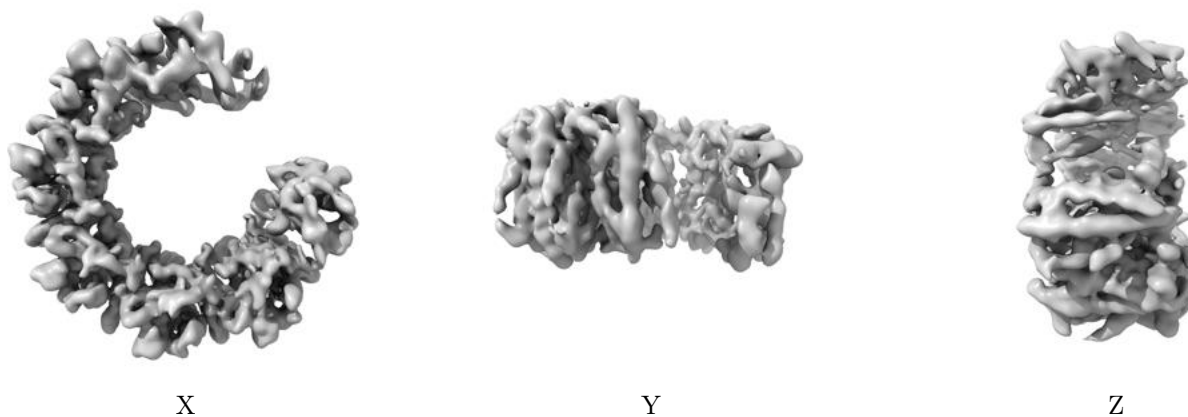


Z

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.

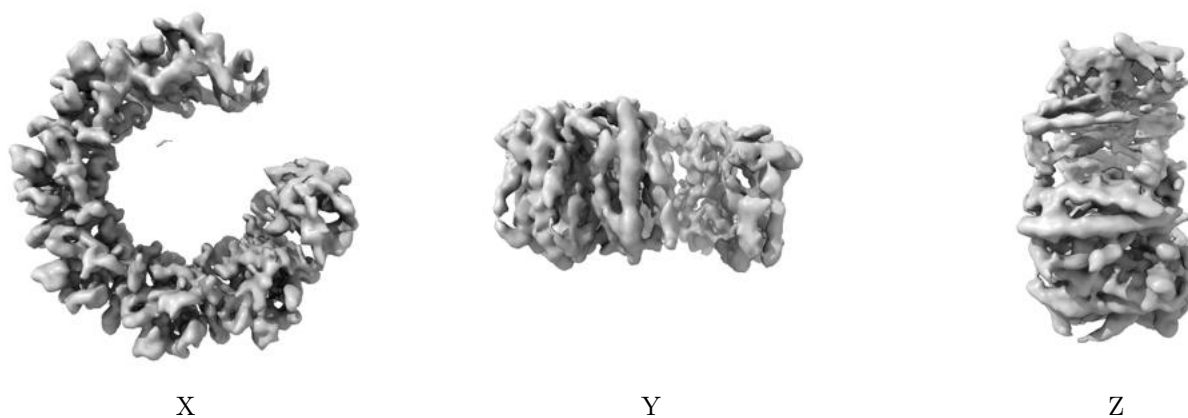
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.399. 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.

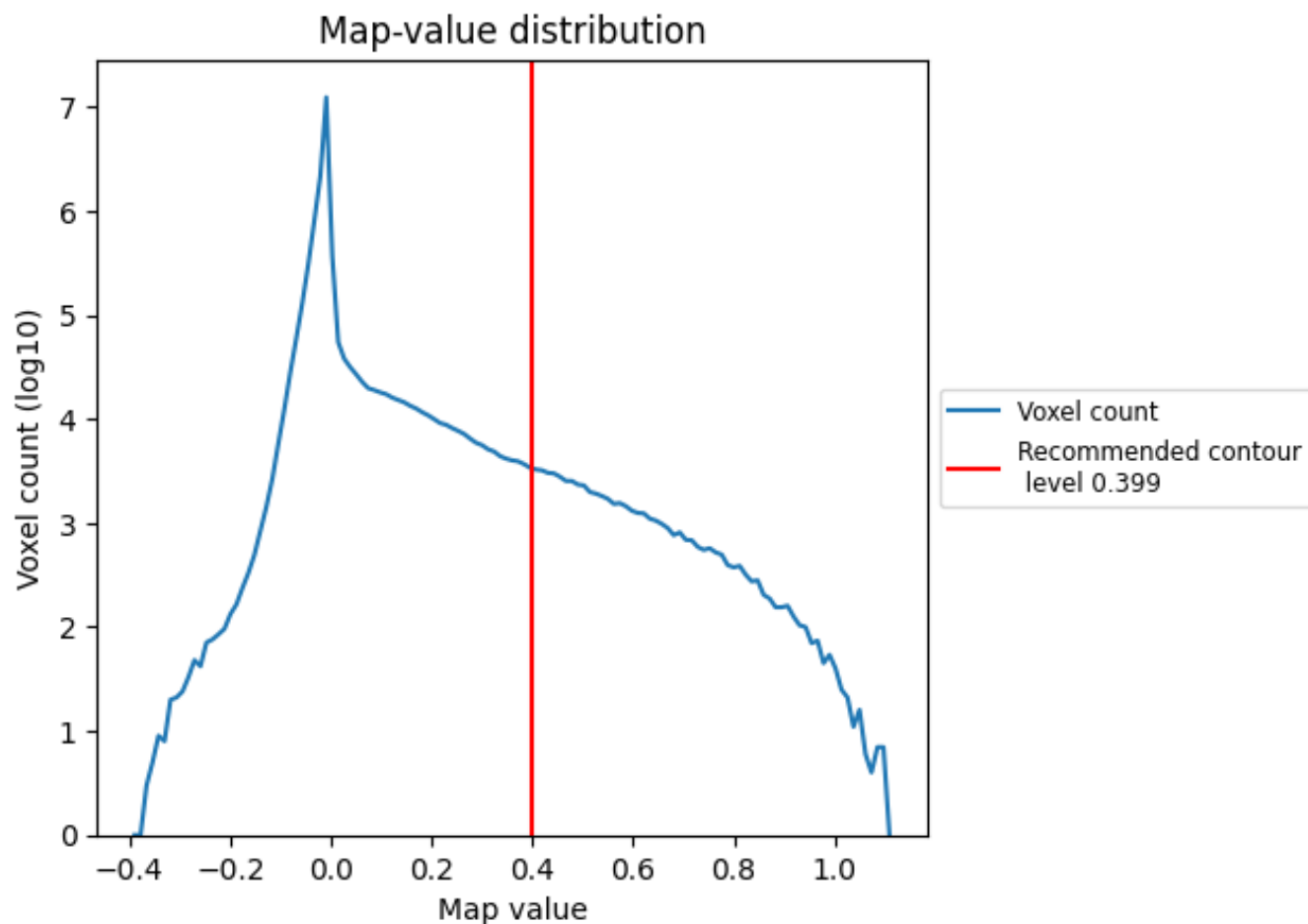
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

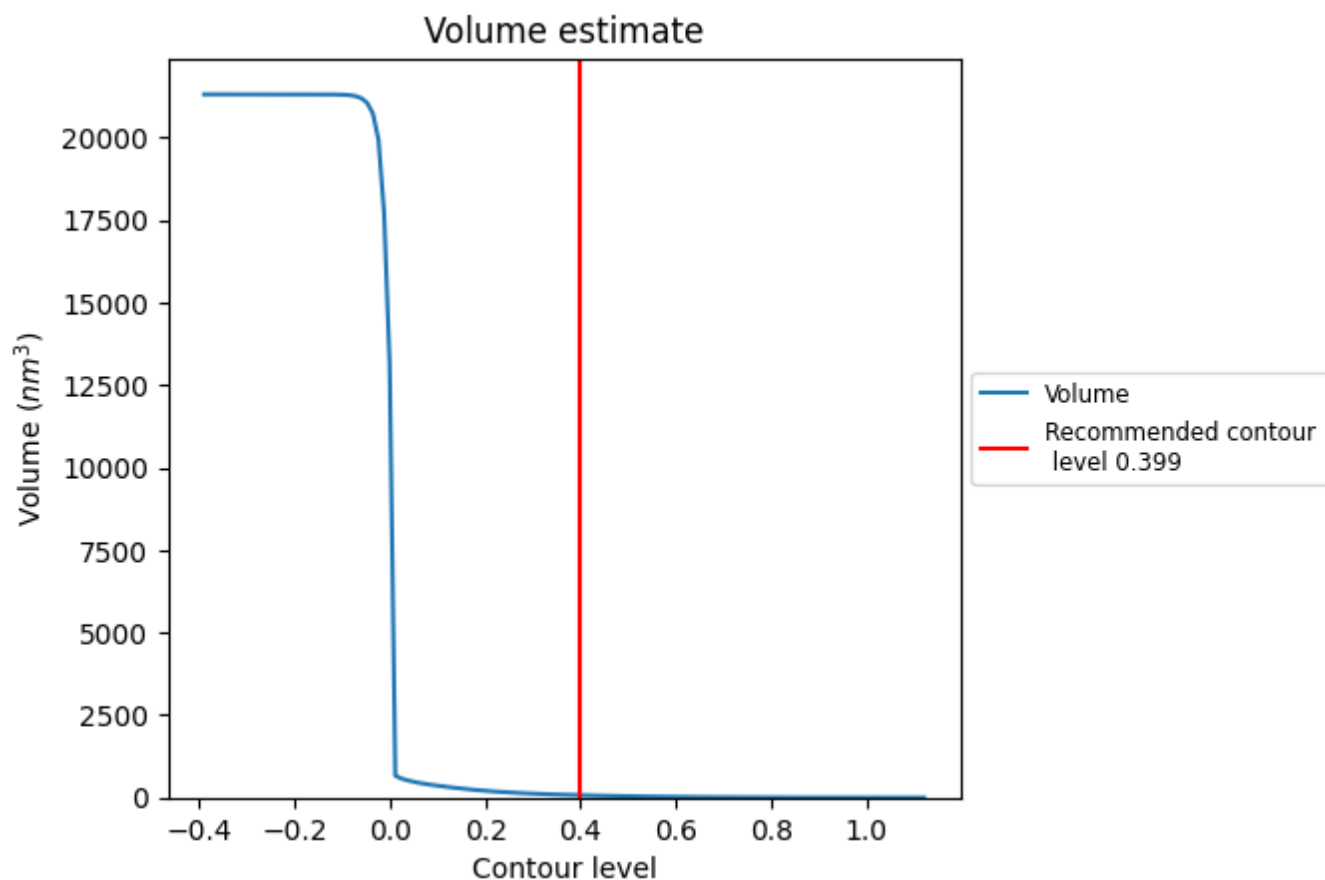
This section contains the results of statistical analysis of the map.

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.

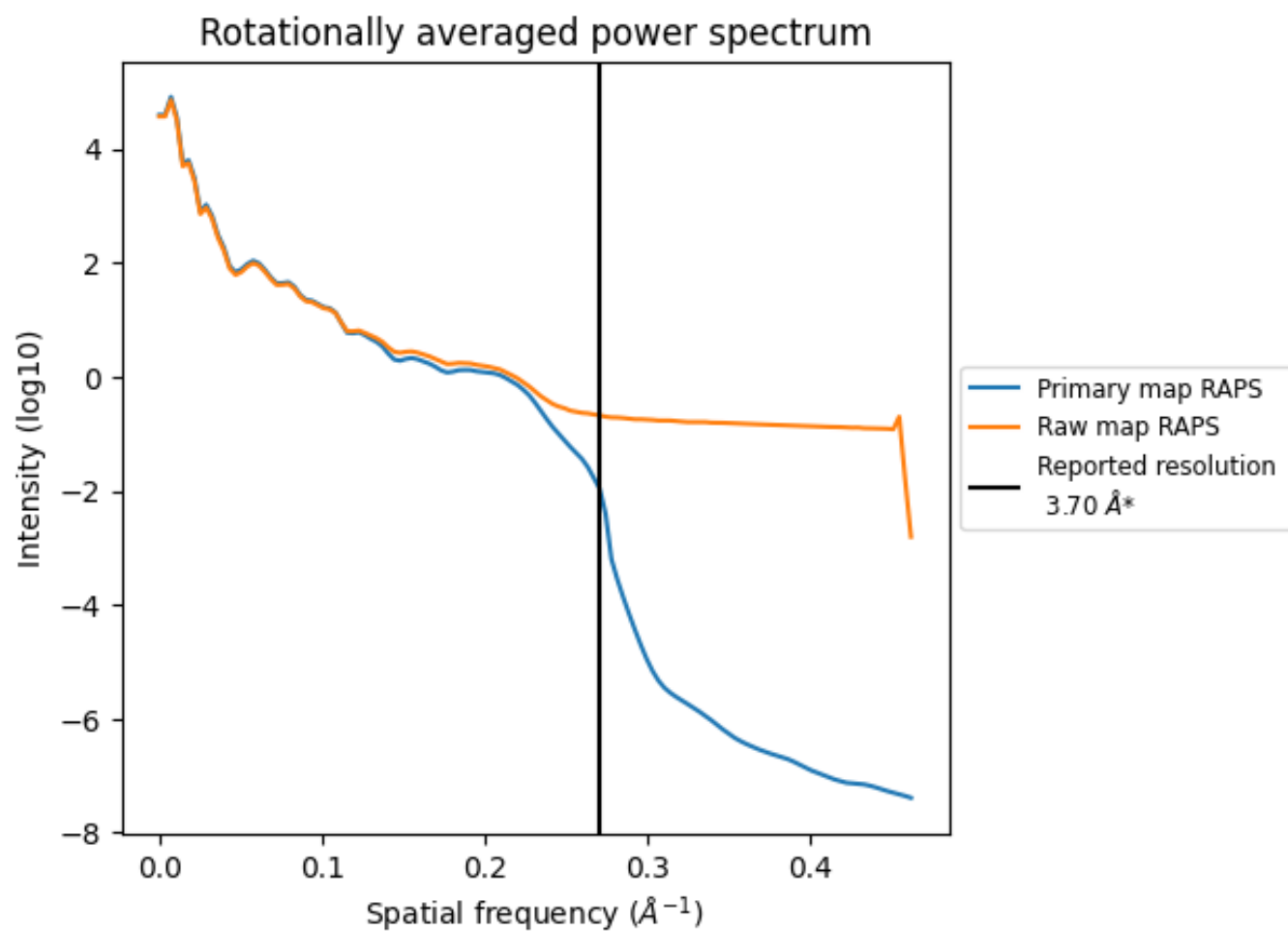
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 72 nm^3 ; this corresponds to an approximate mass of 65 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 ⓘ

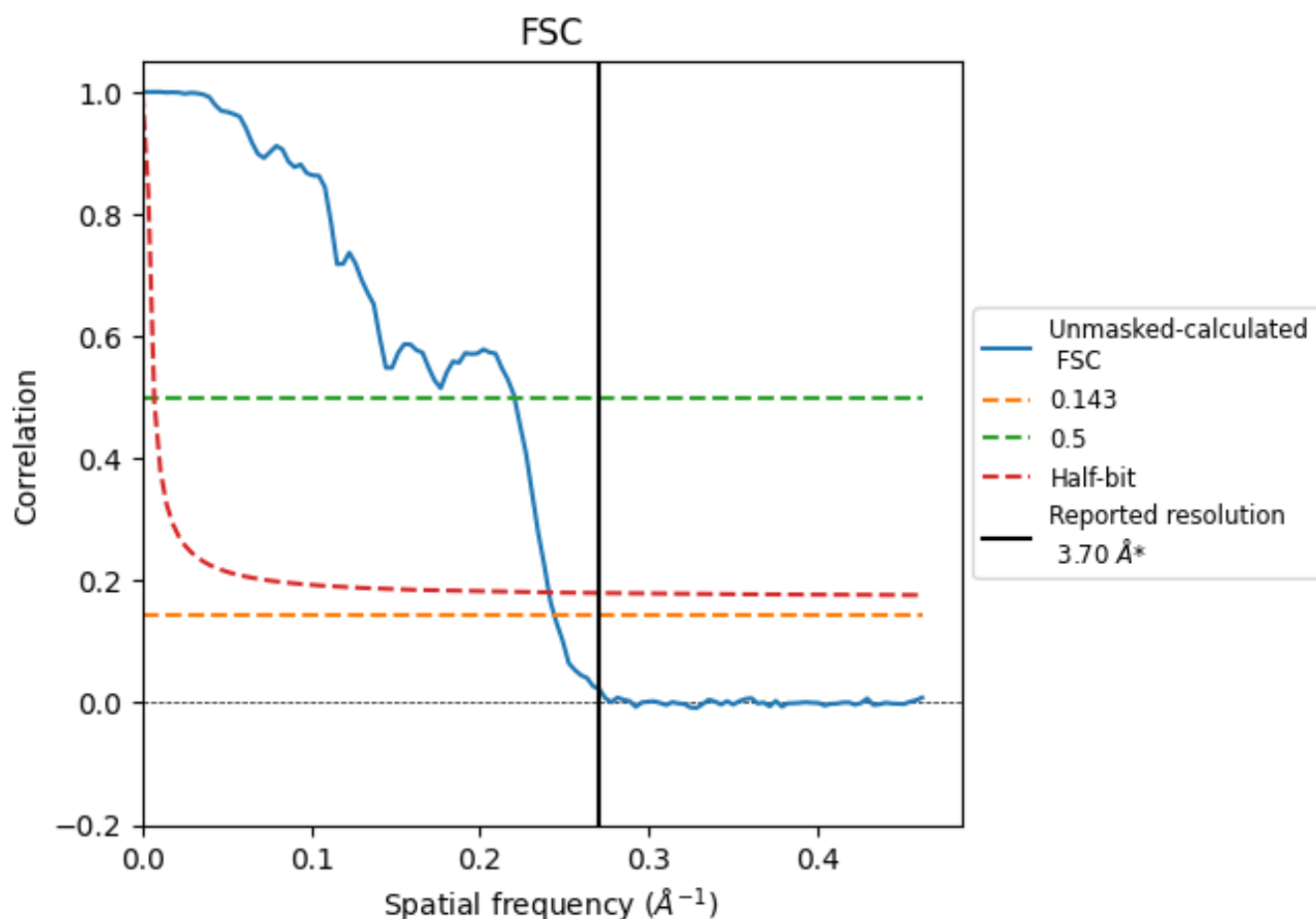


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

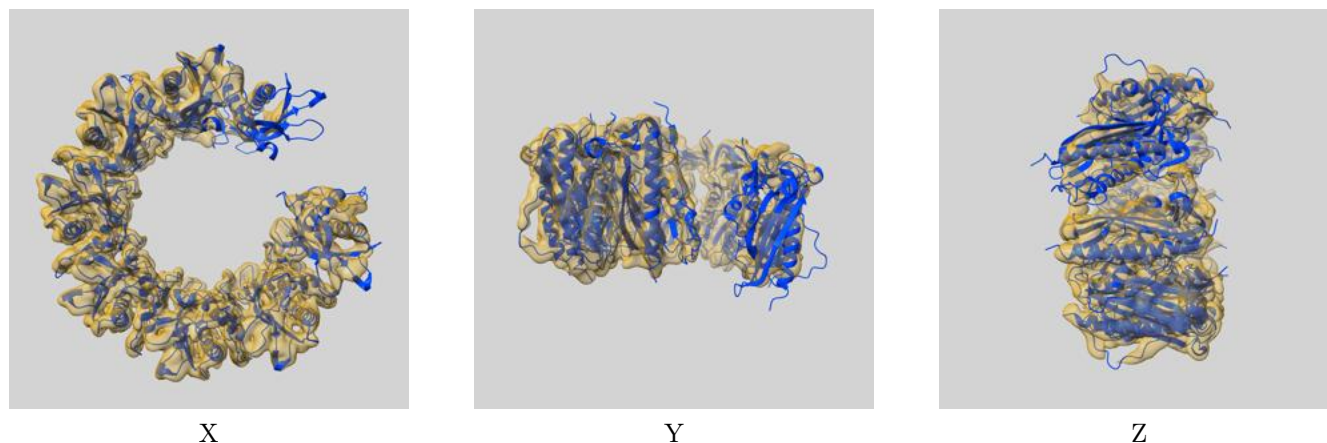
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.10	4.54	4.15

*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 4.10 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

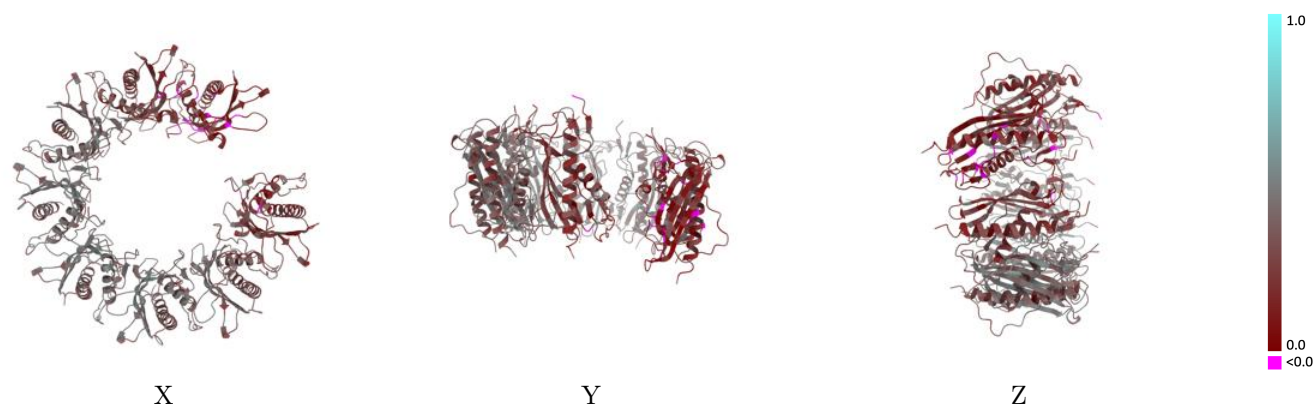
This section contains information regarding the fit between EMDB map EMD-77073 and PDB model 13HS. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



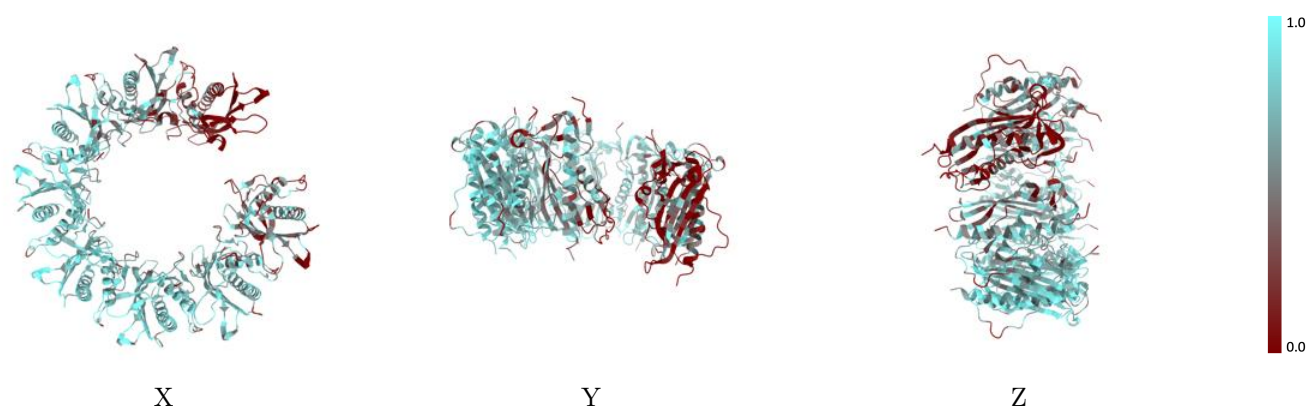
The images above show the 3D surface view of the map at the recommended contour level 0.399 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



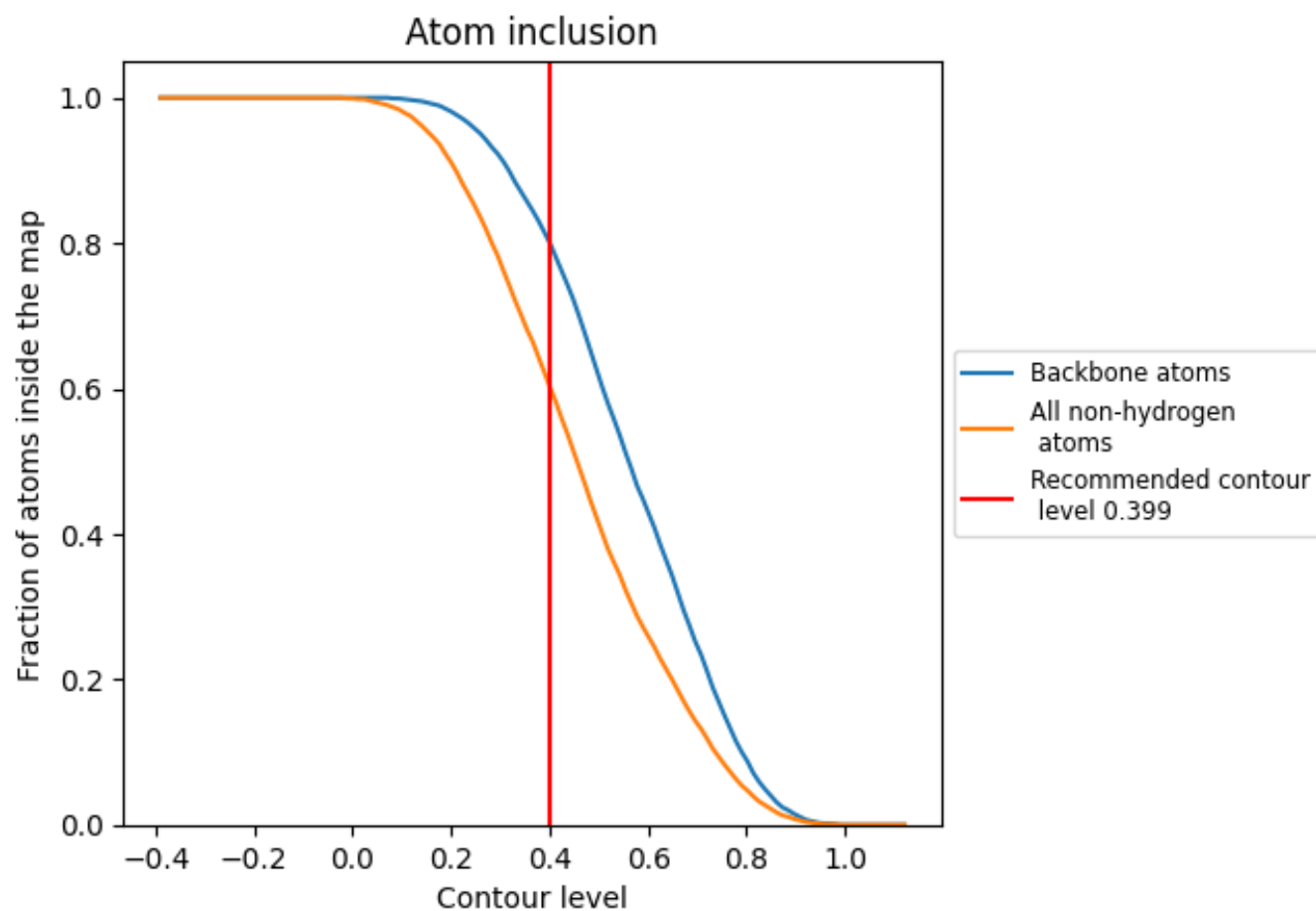
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.399).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 60% 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 (0.399) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6050	<div></div> 0.3390
A	<div></div> 0.4390	<div></div> 0.2530
B	<div></div> 0.6770	<div></div> 0.3800
C	<div></div> 0.7600	<div></div> 0.4190
D	<div></div> 0.7720	<div></div> 0.4280
E	<div></div> 0.7760	<div></div> 0.4220
F	<div></div> 0.7220	<div></div> 0.3950
G	<div></div> 0.5470	<div></div> 0.2730
H	<div></div> 0.1510	<div></div> 0.1430

