



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 08:20 PM UTC

PDB ID : 8RN5 / pdb_00008rn5
EMDB ID : EMD-19387
Title : Pseudo-symmetrical influenza B polymerase apo-dimer, ENDO(R) moiety
(from "Influenza B polymerase pseudo-symmetrical dimer" | Local refinement)
Authors : Arragain, B.; Cusack, S.
Deposited on : 2024-01-09
Resolution : 2.88 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:

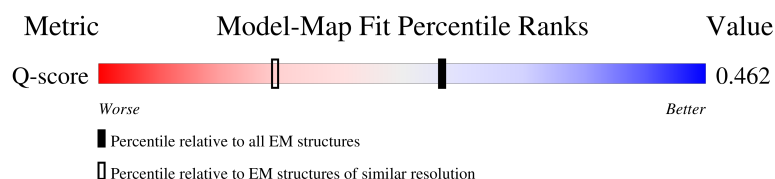
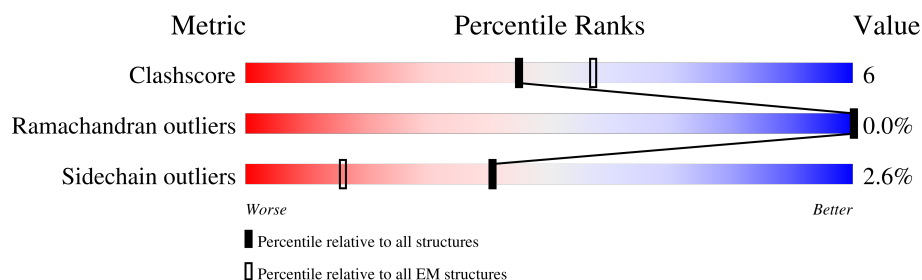
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.88 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	12111 (2.38 - 3.38)

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	726	29% 83% 13% ..
1	E	726	96%
2	B	752	13% 78% 16% 5%
2	D	752	97%

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Mol	Chain	Length	Quality of chain
3	C	799	52% 63% 13% 24%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 33083 atoms, of which 16596 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 Polymerase acidic protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	705	Total	C	H	N	O	S	0	0
			11308	3602	5644	949	1073	40		
1	E	29	Total	C	H	N	O	S	0	0
			446	143	218	35	47	3		

- Molecule 2 is a protein called RNA-directed RNA polymerase catalytic subunit.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	713	Total	C	H	N	O	S	0	0
			11167	3534	5570	961	1052	50		
2	D	23	Total	C	H	N	O	S	0	0
			379	118	198	31	30	2		

- Molecule 3 is a protein called Polymerase basic protein 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	604	Total	C	H	N	O	S	0	0
			9782	3041	4966	856	887	32		

There are 29 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	771	GLY	-	expression tag	UNP Q5V8X3
C	772	TRP	-	expression tag	UNP Q5V8X3
C	773	SER	-	expression tag	UNP Q5V8X3
C	774	HIS	-	expression tag	UNP Q5V8X3
C	775	PRO	-	expression tag	UNP Q5V8X3
C	776	GLN	-	expression tag	UNP Q5V8X3
C	777	PHE	-	expression tag	UNP Q5V8X3
C	778	GLU	-	expression tag	UNP Q5V8X3
C	779	LYS	-	expression tag	UNP Q5V8X3
C	780	GLY	-	expression tag	UNP Q5V8X3
C	781	GLY	-	expression tag	UNP Q5V8X3

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Chain	Residue	Modelled	Actual	Comment	Reference
C	782	GLY	-	expression tag	UNP Q5V8X3
C	783	SER	-	expression tag	UNP Q5V8X3
C	784	GLY	-	expression tag	UNP Q5V8X3
C	785	GLY	-	expression tag	UNP Q5V8X3
C	786	GLY	-	expression tag	UNP Q5V8X3
C	787	SER	-	expression tag	UNP Q5V8X3
C	788	GLY	-	expression tag	UNP Q5V8X3
C	789	GLY	-	expression tag	UNP Q5V8X3
C	790	SER	-	expression tag	UNP Q5V8X3
C	791	ALA	-	expression tag	UNP Q5V8X3
C	792	TRP	-	expression tag	UNP Q5V8X3
C	793	SER	-	expression tag	UNP Q5V8X3
C	794	HIS	-	expression tag	UNP Q5V8X3
C	795	PRO	-	expression tag	UNP Q5V8X3
C	796	GLN	-	expression tag	UNP Q5V8X3
C	797	PHE	-	expression tag	UNP Q5V8X3
C	798	GLU	-	expression tag	UNP Q5V8X3
C	799	LYS	-	expression tag	UNP Q5V8X3

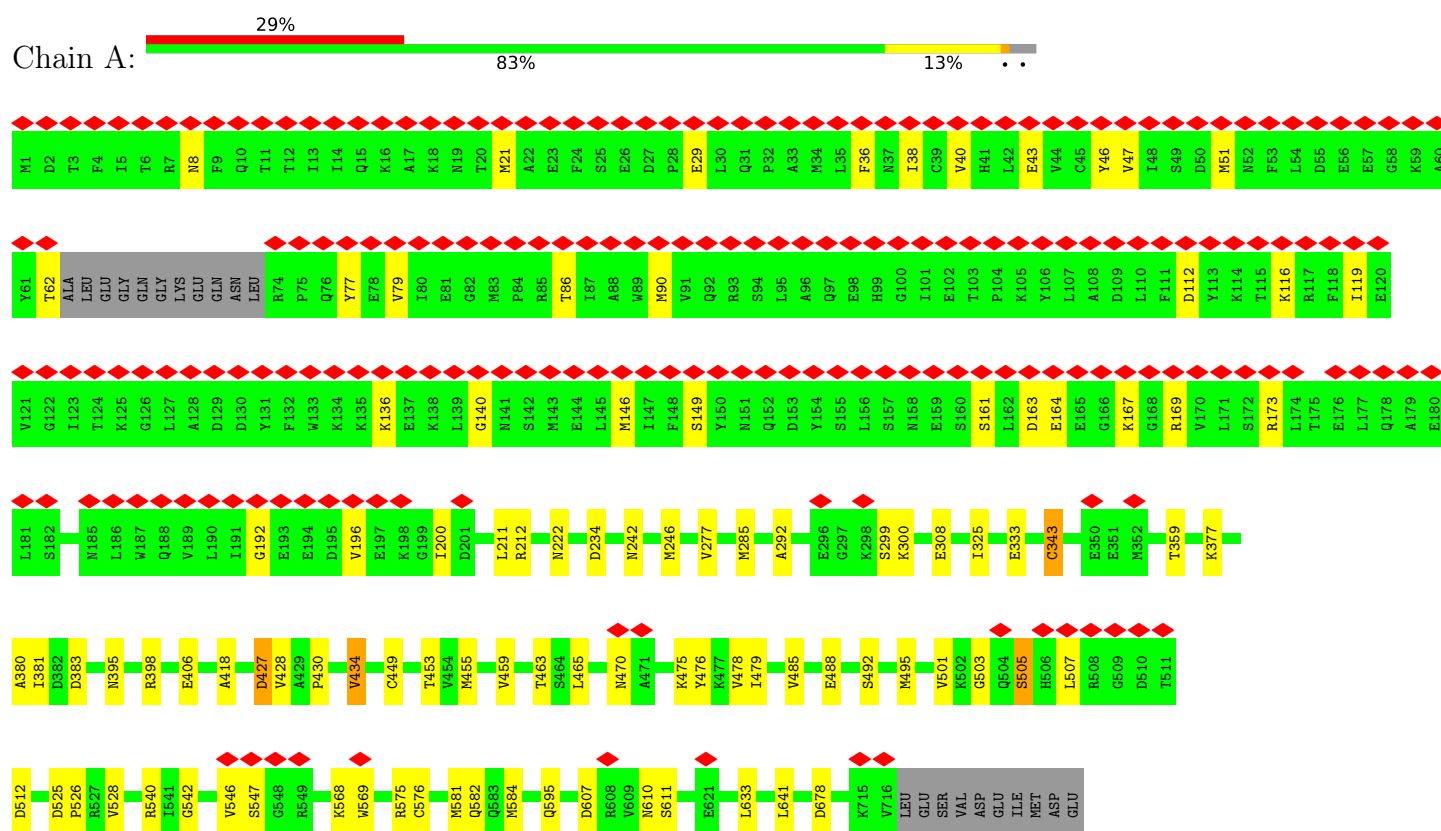
- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
4	B	1	Total Mg 1 1	0

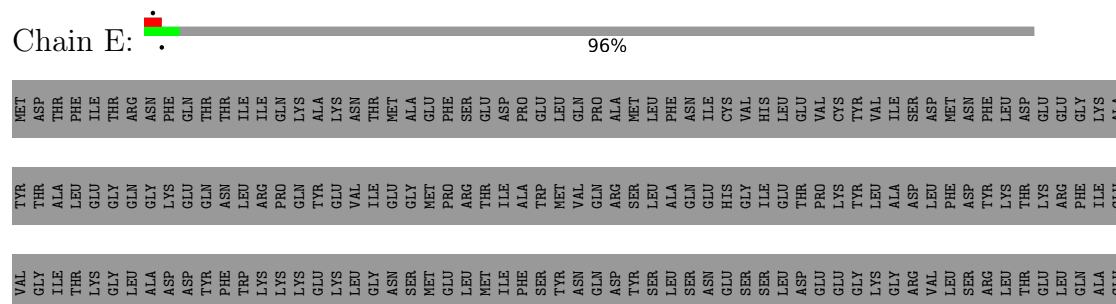
3 Residue-property plots

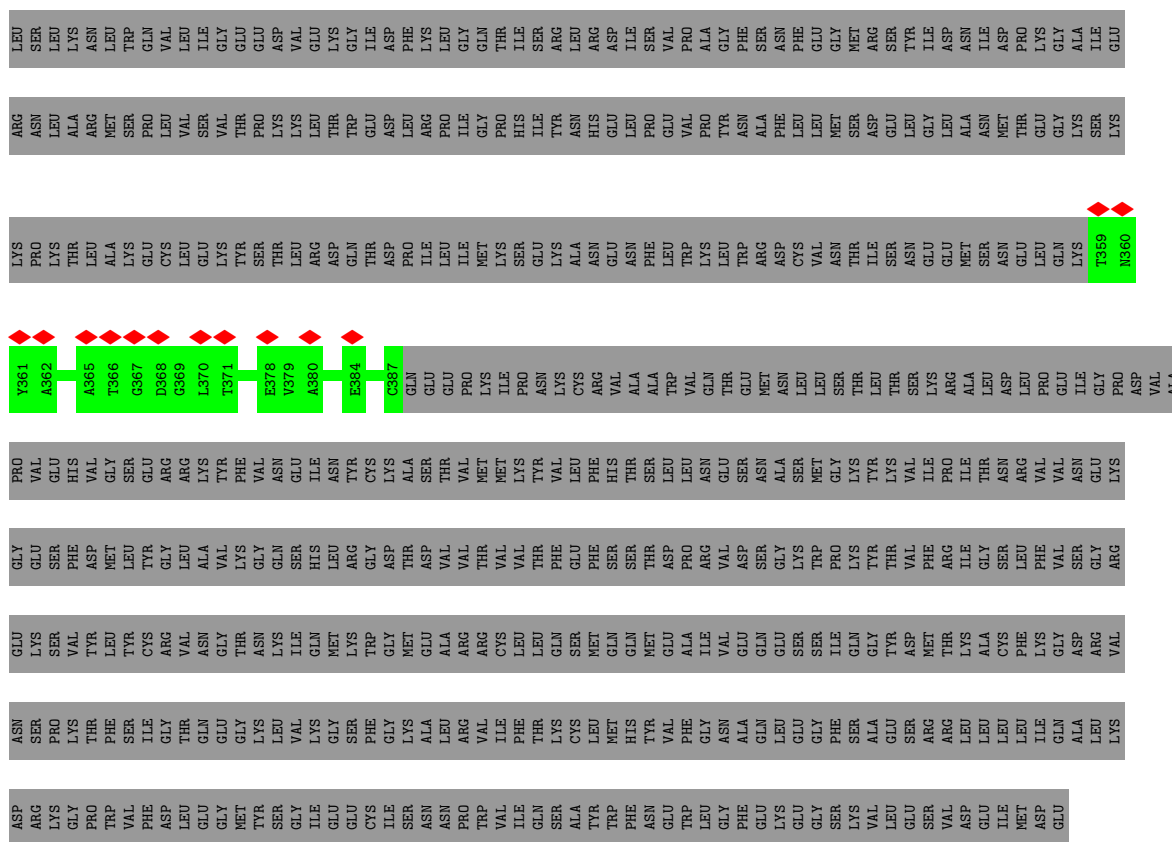
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Polymerase acidic protein

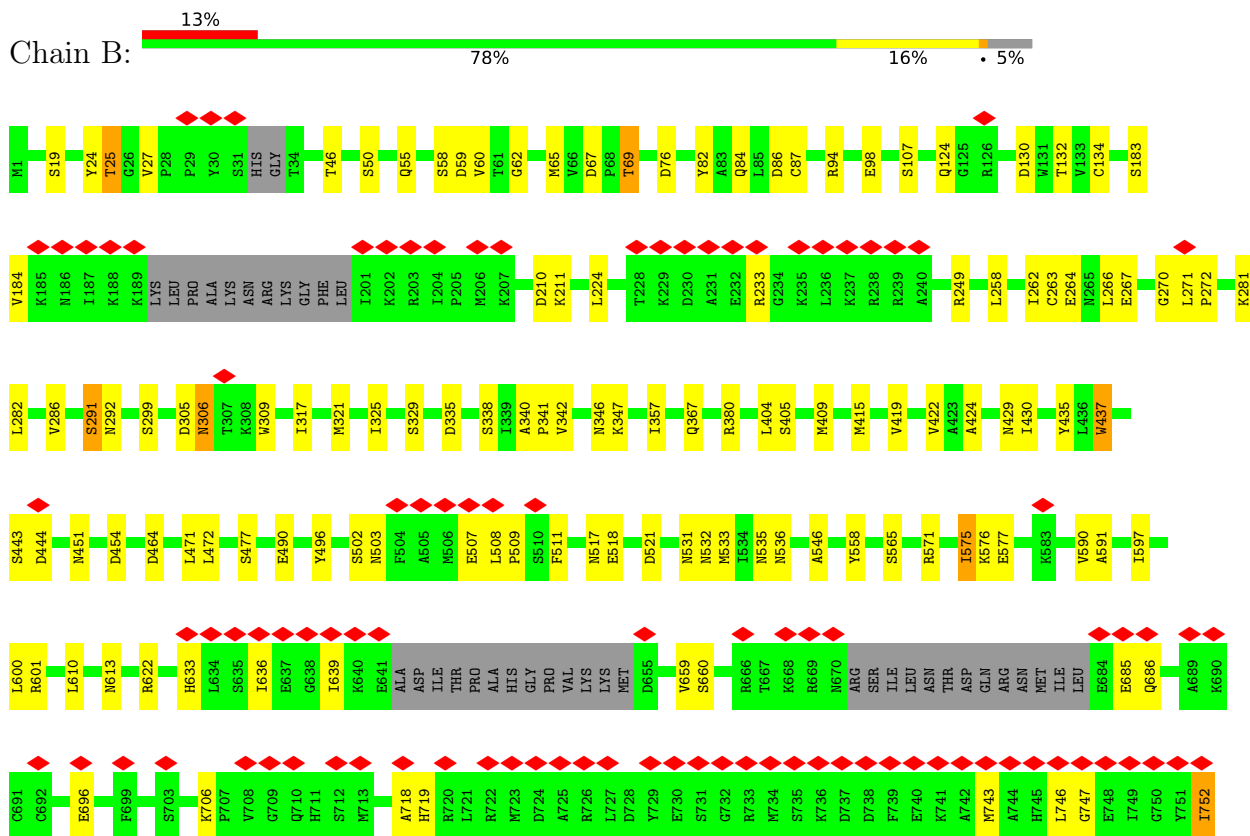


• Molecule 1: Polymerase acidic protein





- Molecule 2: RNA-directed RNA polymerase catalytic subunit



Chain D: 97%



T761	S701	VAL	PHE	E521	E461	I401	K341	L281	K196
V762	G702	LEU	GLU	L522	L462	L402	N342	A282	G197
E763	K703	LYS	SER	E523	H463	C403	D343	V283	
S764	Y704	GLY	ILE	S524	G464	M404	E344	E284	T201
M765	D705	GLY	PRO	Q525	I465	V405	E345	I285	P202
G766	P706	GLU	GLN	A526	M466	F406	I346	A286	I203
TRP	D707	ASN	LYS	Q527	E467	S407	I347	N287	Y207
ALA	L708	ILE	ALA	L528	S468	Q408	I348	N288	M208
LEU	G709	GLU	GLY	M529	M469	D409	G349	T289	
SER	D710	VAL	GLN	I530	N470	T410	N350	V290	R211
TRP	F711	ARG	TYR		A471	R411	G351	I291	
SER	K712	LYS	SER	T531	S472	M412	T352	D292	A215
HIS	T713	SER	PHE	Y532	D473	F413	I353	T293	R216
PRO	L714	PRO	ALA	D533	Y474	Q414	Q354	E294	R217
GLN		ARG	ARG	THR					
PHE	E715	PHE	ALA	PRO	T475	G415	K355	P295	R218
GLY	E716	SER	VAL	LYS	L476	V416	I356	L296	F219
GLY	L717	TYR	LYS	MET	K477	R417	G357	K297	L220
GLY	E718	ASN	LEU	TRP	G478	G418	I358	S298	P221
GLY	K719	PRO	GLN	GLY	V479	G418	W359	C299	V222
SER	L720	GLN	MET	GLY					A223
GLY		THR	ARG	THR	V480	I420	D360	L300	G224
GLY	K721	GLU	ASP	THR	V481	N421	G361	A301	Q238
GLY	P722	VAL	GLN	THR					
GLY	G723	LEU	GLU	LYS	T482	F422	E362	A302	R243
GLY	E724	THR	VAL	GLY	R483	L423	I303	I303	
GLY	G725	ILE	MET	LEU	N484	M424	E364	D304	
SER	K726	CYS	LYS	VAL	V485		F365	G305	
ALA	A726	GLN	THR	GLN			H366	G306	
ALA	N727	ASN	ASP	ASN	I486	A426	V367	D307	G249
TRP		ARG	GLN	THR	D487				GLY
SER	L728	MET	PHE	TYR			R368	V308	ASN
SER	G729	THR	ILE	GLN	D488	Q428	C369	A309	LYS
PRO	L730	LEU	LYS	TRP	F489	L429	G370	C310	THR
GLN	Y731	LYS	LEU	VAL	S490	L430	E371	D311	GLU
PHE	Q732	GLY	LEU	LEU	S491	S431			
LYS		LYS	PRO	LYS	T492	P432	C372	I312	R257
	G733	ILE	PHE	ASN	E493	M433	R373	I313	S258
	K734	GLU	CYS	LEU	T494	M433	I374	R314	Q259
	P735	ASP	PHE	VAL	E495	Y434	I375	A315	M261
	G736	GLU	SER	THR	K496	Q435	I376	A316	I262
	L737	GLU	PRO	LEU		L436	K377	L317	V263
	K737	ARG	LYS	LEU	V497	Q437	R378	G318	A264
	V738	ASN	LEU	ALA		R438	S379	L319	C265
	G739	ARG	ARG	PHE	I499	Y439	K380	K320	R266
	R740	SER	SER	LEU	T500	F440	M381	I321	K267
	K741	M690	ASN	LEU	K501	L441	K382	R322	I268
	L742	G691	GLY	GLY	N502	L441	L383	Q323	I269
	R743	M692	GLU	GLU	L503	M442	E384	Q325	R270
	Y744	A693	PRO	ASP	S504	R443	K385	R326	E271
	S745	V694	GLN	MET		S444	I386	R324	R272
	A746	L695	PHE	PHE	L505	M445	I387	G328	I273
	L747	G697	LEU	GLN	I506	N445	L386	R329	V274
	S748	F698	LYS	TRP	K507	D446	K395	L330	A275
	N749	L699	ALA	ALA	R508	L447	I388	E331	S276
	D750	V700	PHE	PHE	T509	F448	N389	N277	P278
	I751		GLU	GLU	G510	D449	S390	K333	L279
	S752		ALA	ALA	E511	Q450	A391	R334	E280
	Q753				V512	W451	K392	I335	
	G754				I513	G452	K393	G337	
	I755				M514	Y453	E394	G339	
	K756				G515	E454	D395	I336	
	R757				A516	E455	H396	S336	
	Q758				N517	S456	R397	G337	
	R759				D518	P457	I398	G339	
	M760				V519	K458	L400	F340	
					S520	A459			

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	92684	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	4.488	Depositor
Minimum map value	-3.325	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.094	Depositor
Recommended contour level	0.6	Depositor
Map size (Å)	403.19998, 403.19998, 403.19998	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.84, 0.84, 0.84	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.11	0/5780	0.25	0/7794
1	E	0.07	0/231	0.17	0/311
2	B	0.12	0/5704	0.26	0/7685
2	D	0.09	0/184	0.22	0/244
3	C	0.10	0/4888	0.25	0/6565
All	All	0.11	0/16787	0.25	0/22599

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5664	5644	5643	65	0
1	E	228	218	218	0	0
2	B	5597	5570	5591	98	0
2	D	181	198	198	0	0
3	C	4816	4966	4965	69	0
4	B	1	0	0	0	0
All	All	16487	16596	16615	208	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 6.

The worst 5 of 208 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:B:267:GLU:O	2:B:281:LYS:NZ	2.09	0.85
2:B:521:ASP:OD2	2:B:558:TYR:OH	1.95	0.83
2:B:613:ASN:OD1	3:C:124:LYS:NZ	2.15	0.79
3:C:371:GLU:O	3:C:373:ARG:NH1	2.15	0.79
2:B:696:GLU:OE2	3:C:30:TYR:OH	2.00	0.79

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	701/726 (97%)	676 (96%)	25 (4%)	0	100	100
1	E	27/726 (4%)	27 (100%)	0	0	100	100
2	B	703/752 (94%)	680 (97%)	23 (3%)	0	100	100
2	D	21/752 (3%)	21 (100%)	0	0	100	100
3	C	598/799 (75%)	567 (95%)	30 (5%)	1 (0%)	43	70
All	All	2050/3755 (55%)	1971 (96%)	78 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	526	ALA

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	627/645 (97%)	612 (98%)	15 (2%)	43	73
1	E	24/645 (4%)	24 (100%)	0	100	100
2	B	612/645 (95%)	593 (97%)	19 (3%)	35	66
2	D	21/645 (3%)	21 (100%)	0	100	100
3	C	527/693 (76%)	514 (98%)	13 (2%)	42	72
All	All	1811/3273 (55%)	1764 (97%)	47 (3%)	41	71

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	477	SER
3	C	56	ASN
2	B	490	GLU
2	B	590	VAL
3	C	94	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	247	HIS
3	C	435	GLN
3	C	502	ASN
2	B	156	ASN
2	B	257	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

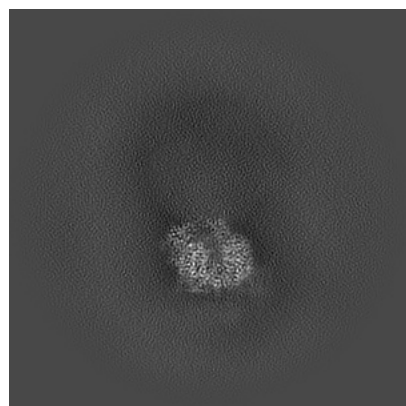
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19387. These allow visual inspection of the internal detail of the map and identification of artifacts.

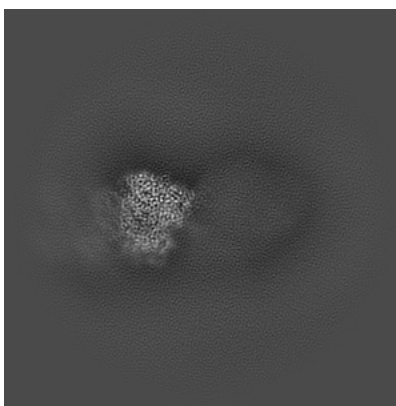
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

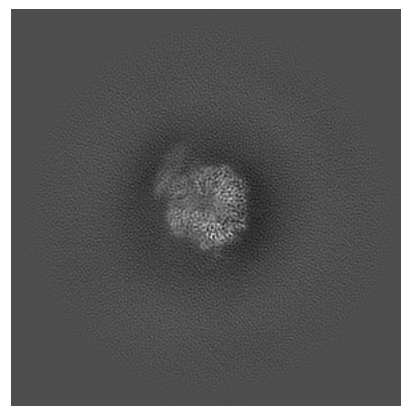
6.1.1 Primary map



X

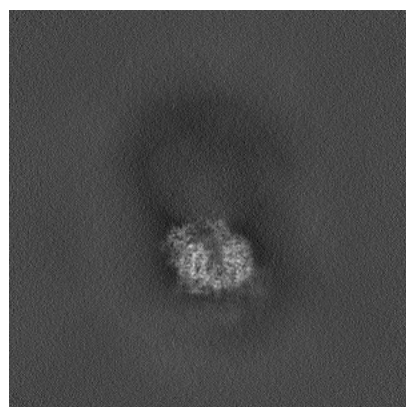


Y

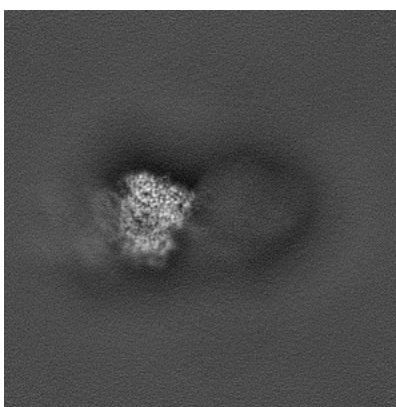


Z

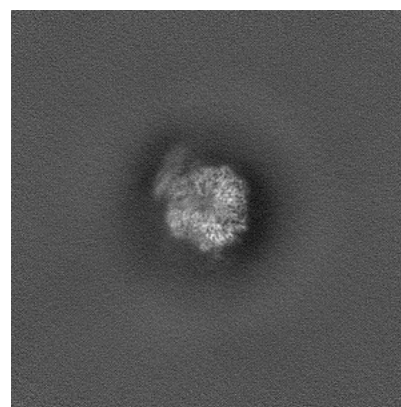
6.1.2 Raw map



X



Y

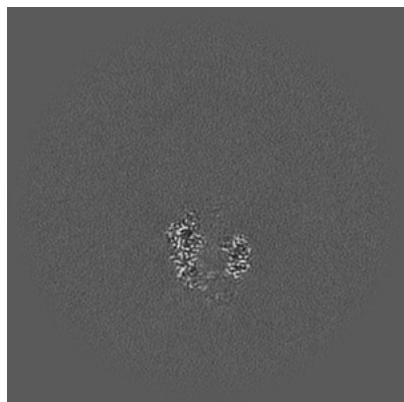


Z

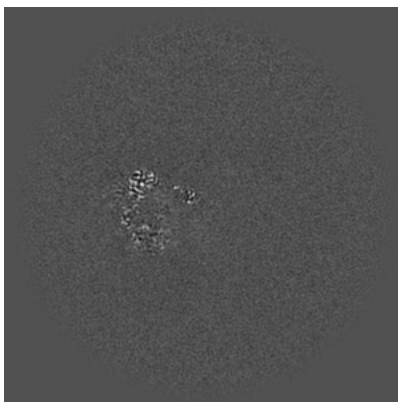
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

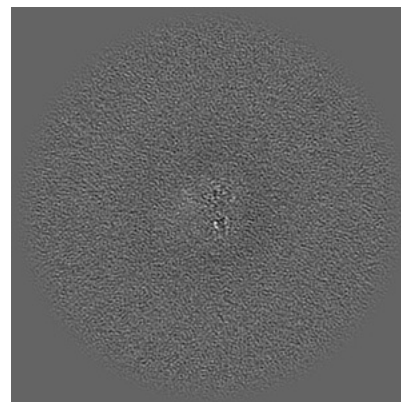
6.2.1 Primary map



X Index: 240

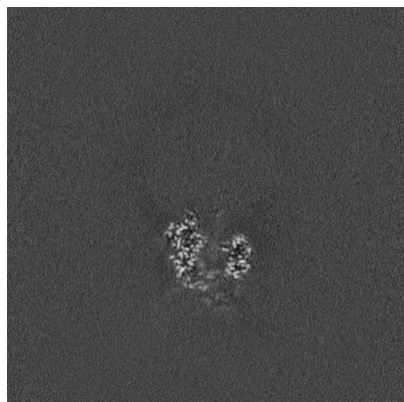


Y Index: 240

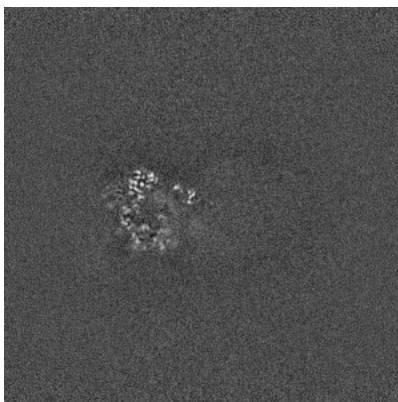


Z Index: 240

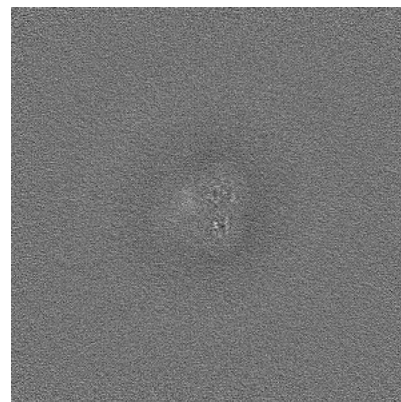
6.2.2 Raw map



X Index: 240



Y Index: 240

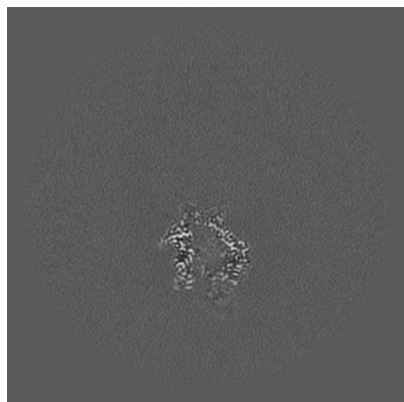


Z Index: 240

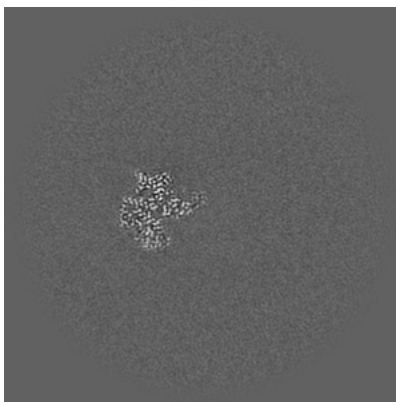
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

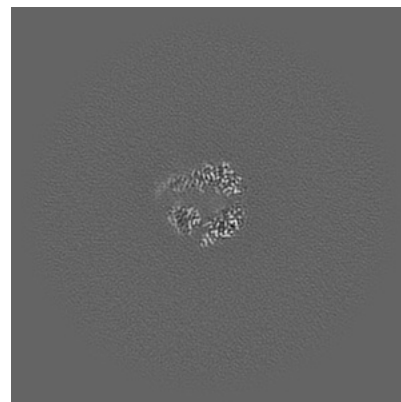
6.3.1 Primary map



X Index: 249

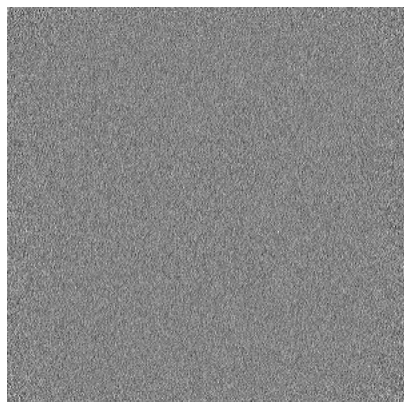


Y Index: 221

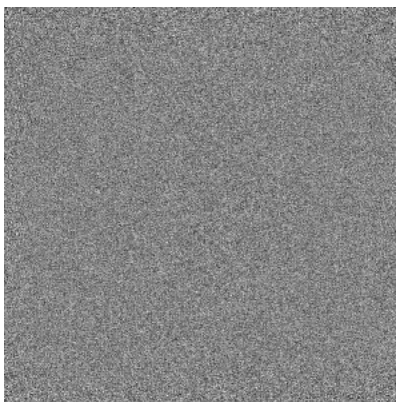


Z Index: 180

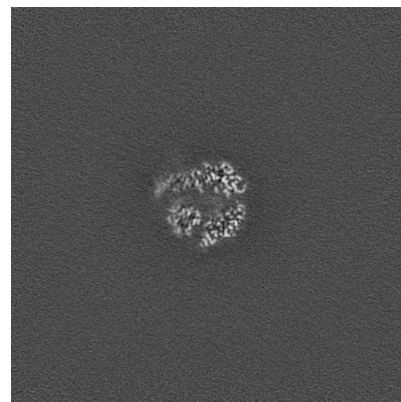
6.3.2 Raw map



X Index: 0



Y Index: 0

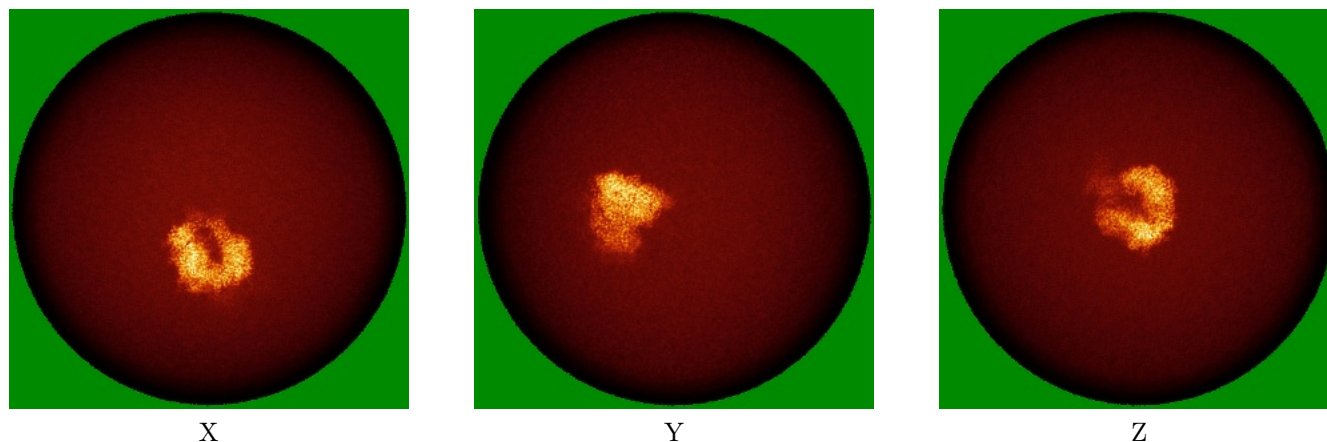


Z Index: 179

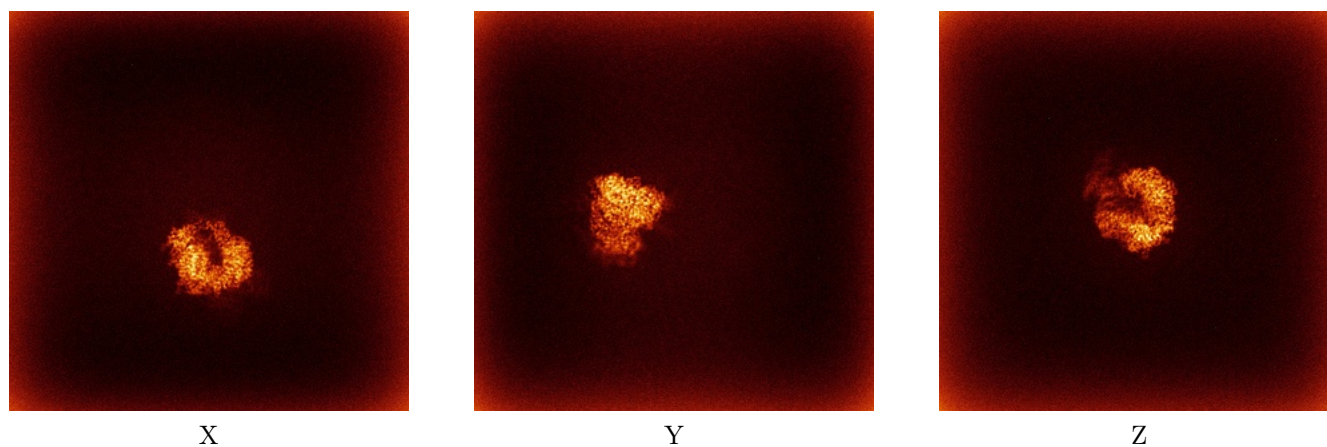
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



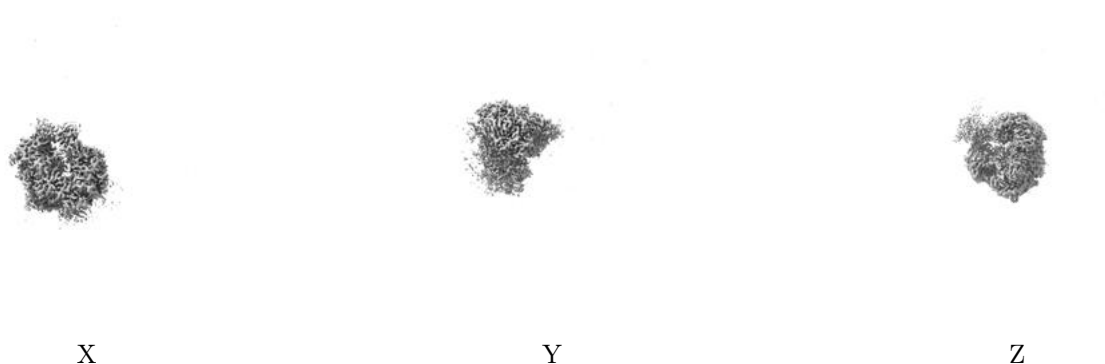
6.4.2 Raw map



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.

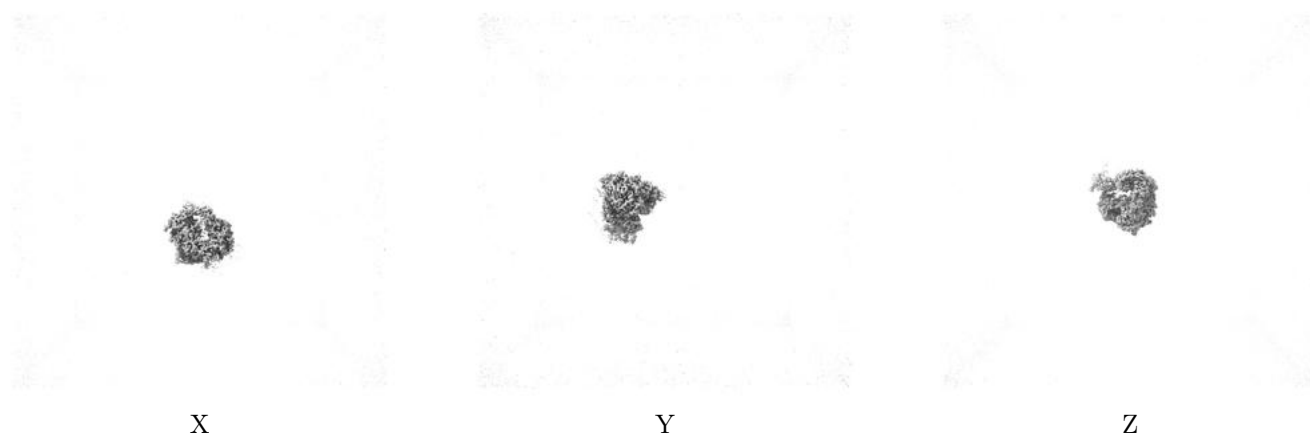
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.6. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

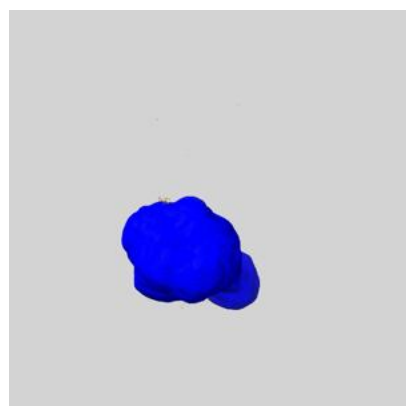
6.6 Mask visualisation [i](#)

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

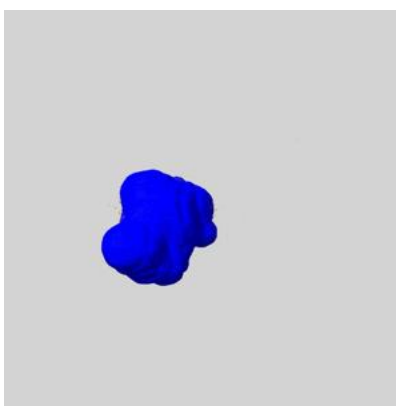
A mask typically either:

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

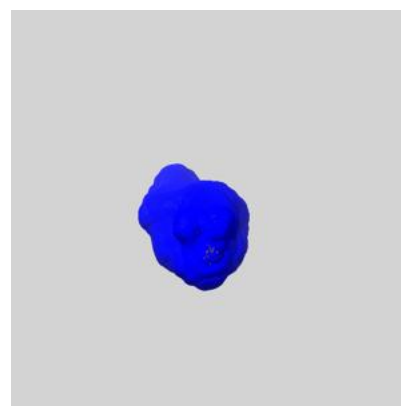
6.6.1 emd_19387_msk_1.map [i](#)



X



Y

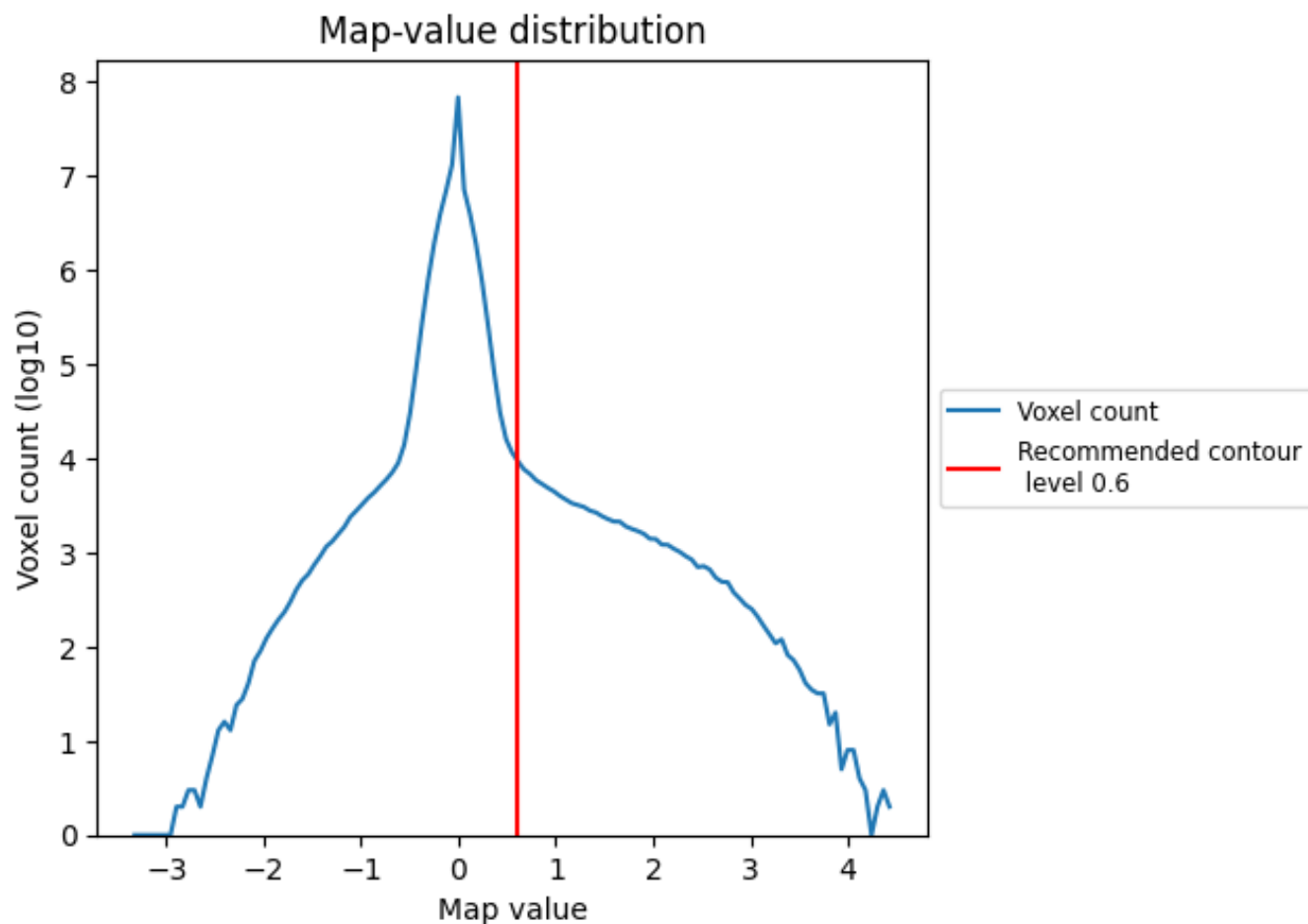


Z

7 Map analysis [i](#)

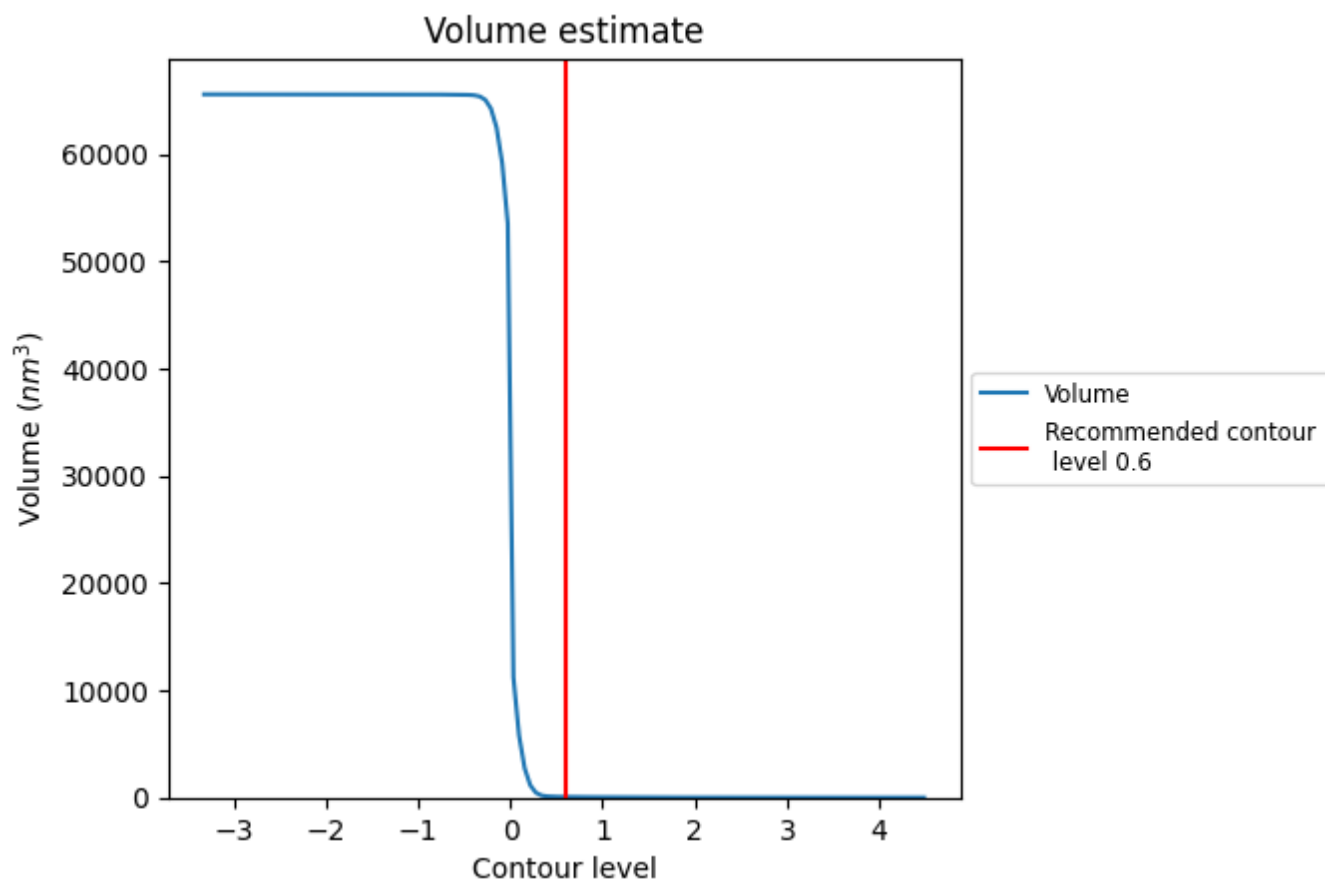
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

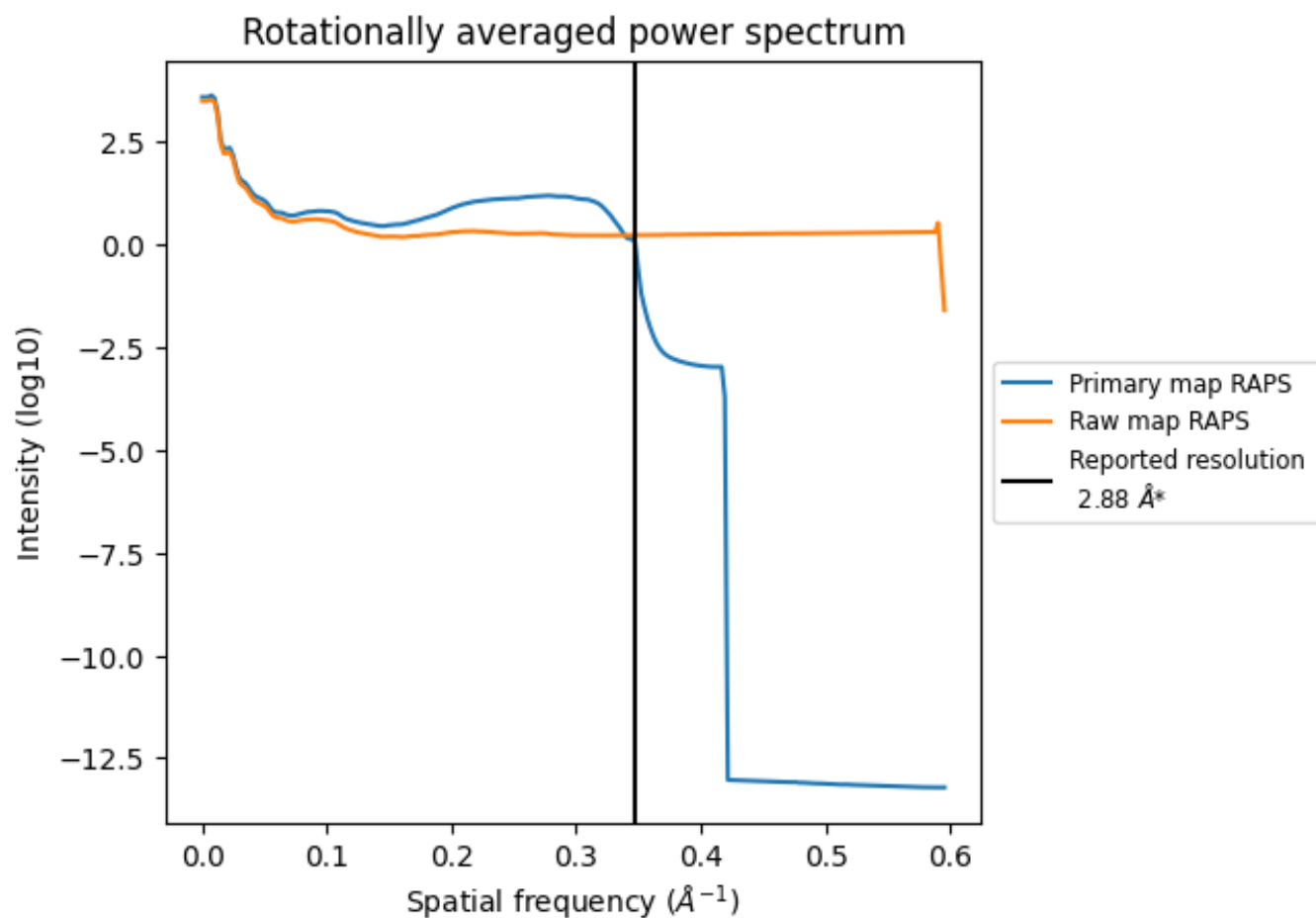
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 60 nm³; this corresponds to an approximate mass of 54 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 ⓘ

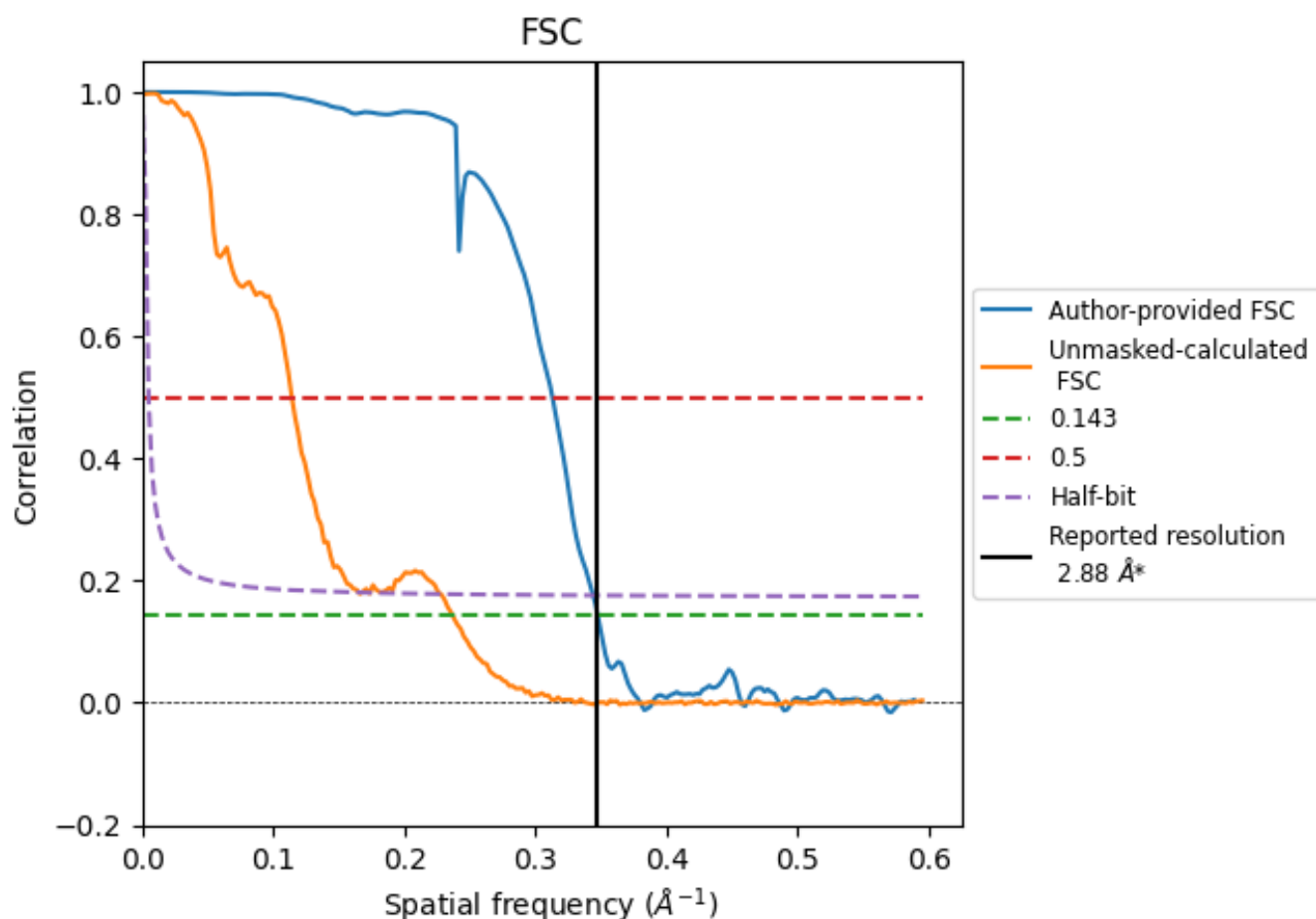


*Reported resolution corresponds to spatial frequency of 0.347 Å⁻¹

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 $0.347 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

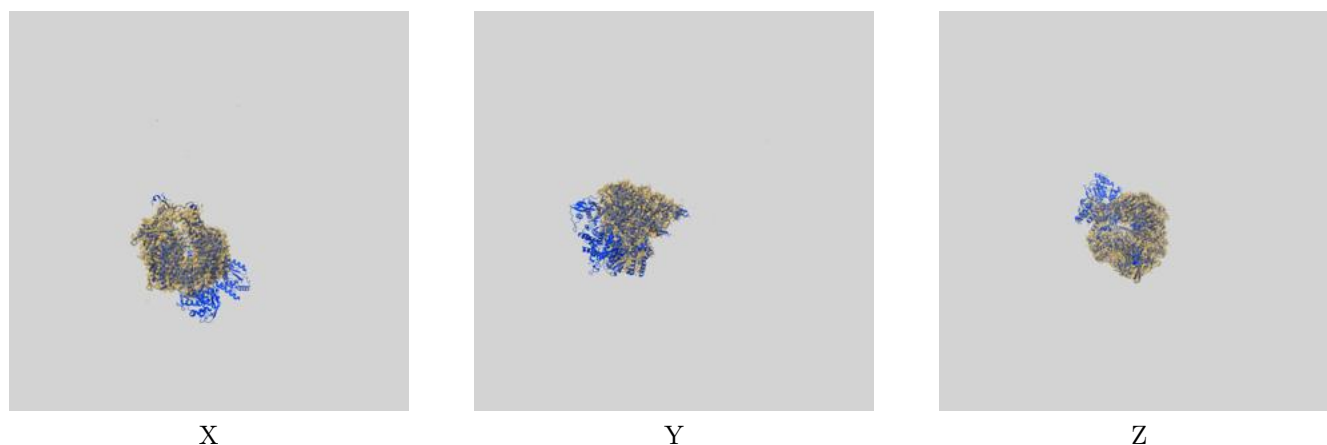
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.88	-	-
Author-provided FSC curve	2.88	3.19	2.91
Unmasked-calculated*	4.22	8.76	6.05

*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 4.22 differs from the reported value 2.88 by more than 10 %

9 Map-model fit [i](#)

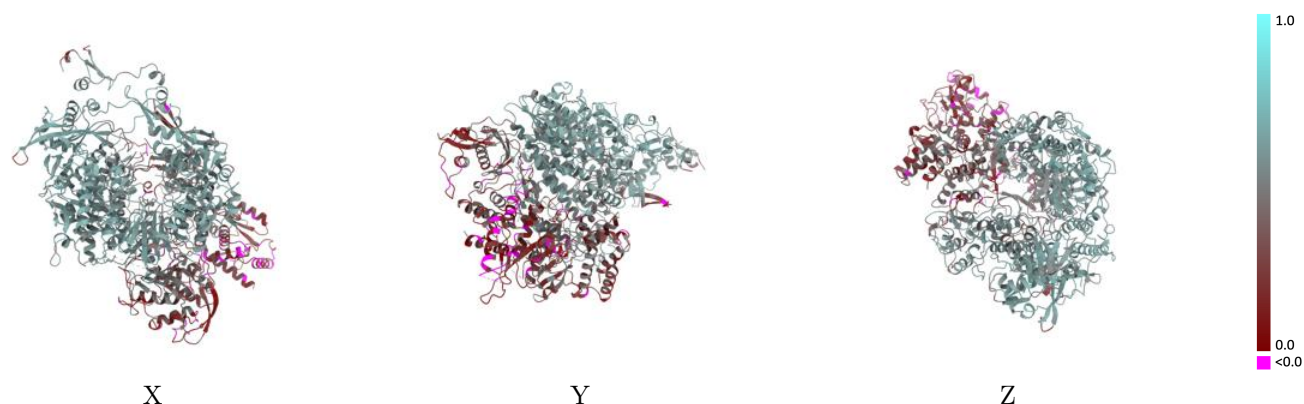
This section contains information regarding the fit between EMDB map EMD-19387 and PDB model 8RN5. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



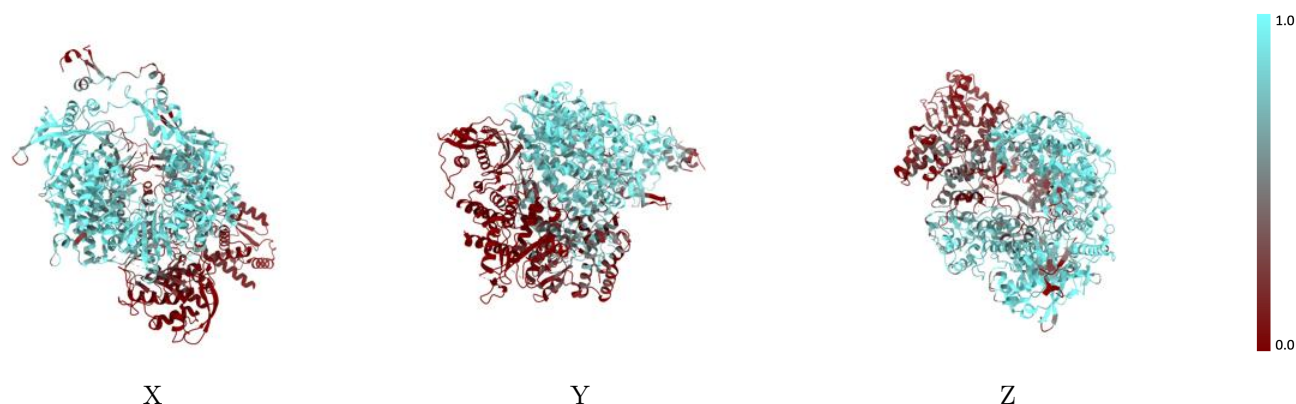
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



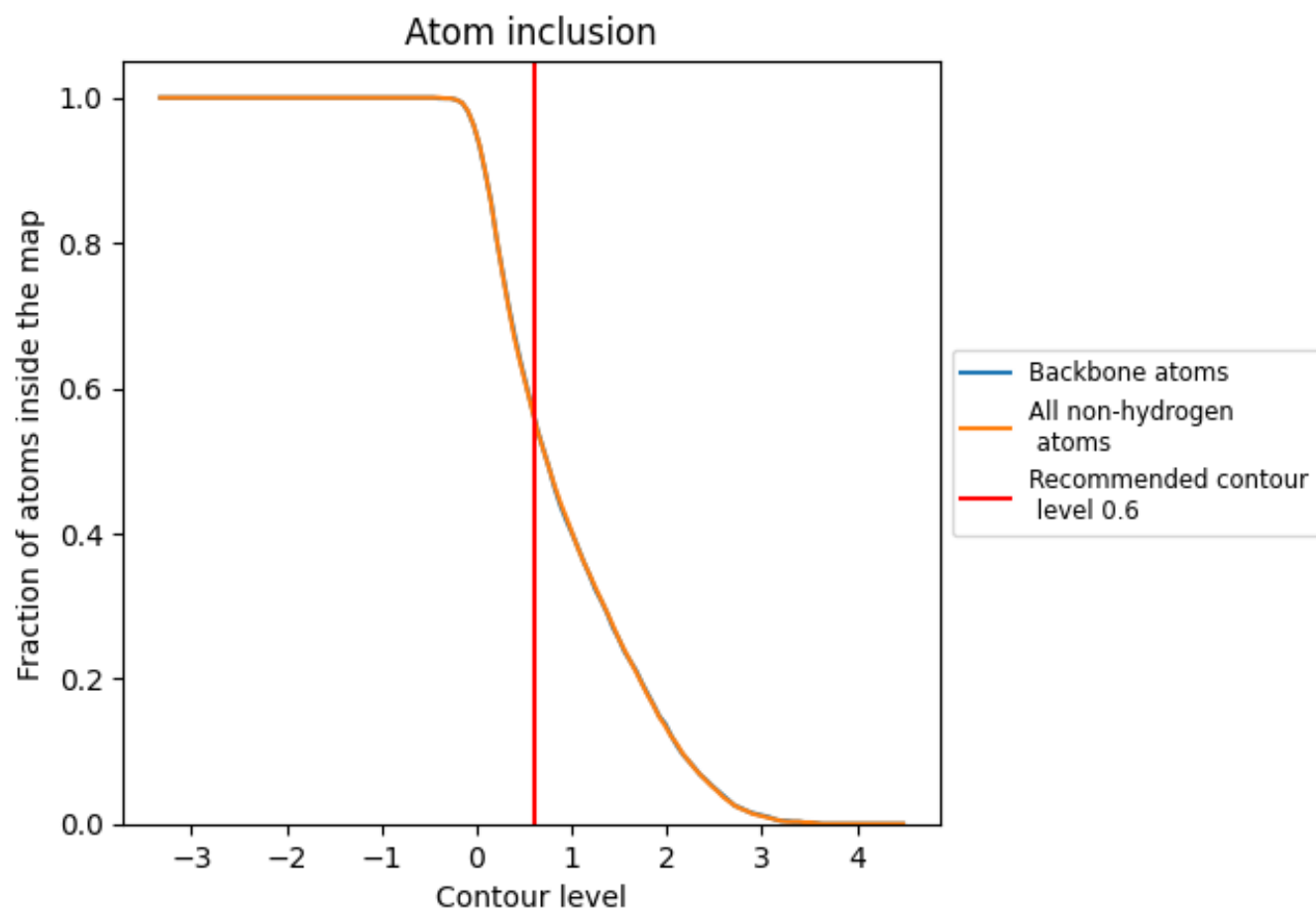
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.6).

9.4 Atom inclusion [i](#)



At the recommended contour level, 56% of all backbone atoms, 56% 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 (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5620	0.4620
A	0.6240	0.4730
B	0.7530	0.5350
C	0.2780	0.3620
D	0.3130	0.4810
E	0.4530	0.5330

