



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 09:58 PM UTC

PDB ID : 6QWL / pdb_00006qwl
EMDB ID : EMD-4660
Title : Influenza B virus (B/Panama/45) polymerase Heterotrimer in complex with 3'5' cRNA promoter
Authors : Keown, J.R.; Carrique, L.; Fan, H.; Fodor, E.; Grimes, J.M.
Deposited on : 2019-03-05
Resolution : 4.10 Å(reported)
Based on initial model : 5EPI

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:

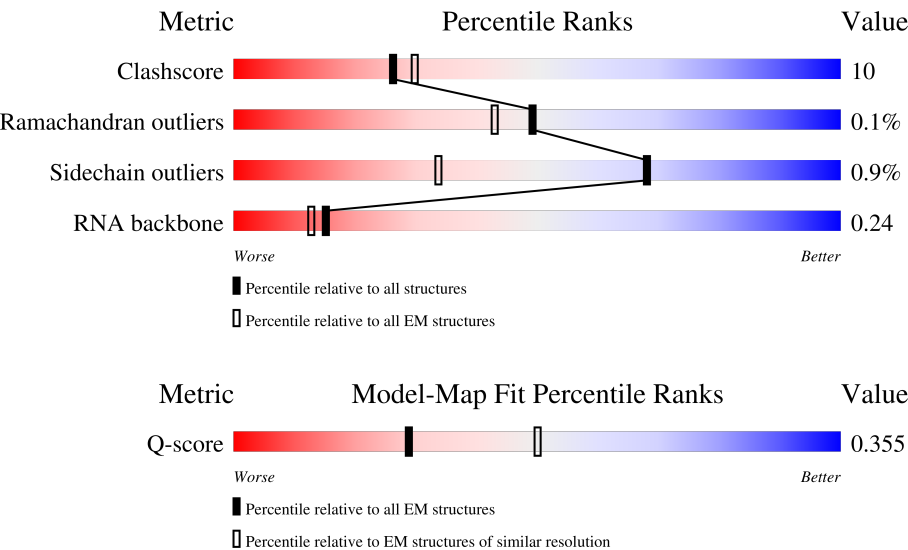
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.10 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	6458 (3.60 - 4.60)

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	E	726	54%16%30%
2	K	752	5%51%20%28%
3	Q	778	8%17%7%75%

Continued on next page...

Mol	Chain	Length	Quality of chain
4	T	15	
5	W	14	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10408 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 Polymerase acidic protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	E	511	Total	C	N	O	S	0	0
			4084	2593	696	765	30		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	K	539	Total	C	N	O	S	0	0
			4206	2656	717	799	34		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Q	194	Total	C	N	O	S	0	0
			1565	1002	276	277	10		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	771	ALA	-	expression tag	UNP O36431
Q	772	ARG	-	expression tag	UNP O36431
Q	773	GLU	-	expression tag	UNP O36431
Q	774	ASN	-	expression tag	UNP O36431
Q	775	LEU	-	expression tag	UNP O36431
Q	776	TYR	-	expression tag	UNP O36431
Q	777	PHE	-	expression tag	UNP O36431
Q	778	GLN	-	expression tag	UNP O36431

- Molecule 4 is a RNA chain called 3' cRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	T	12	Total	C	N	O	P	0	0
			249	111	36	90	12		

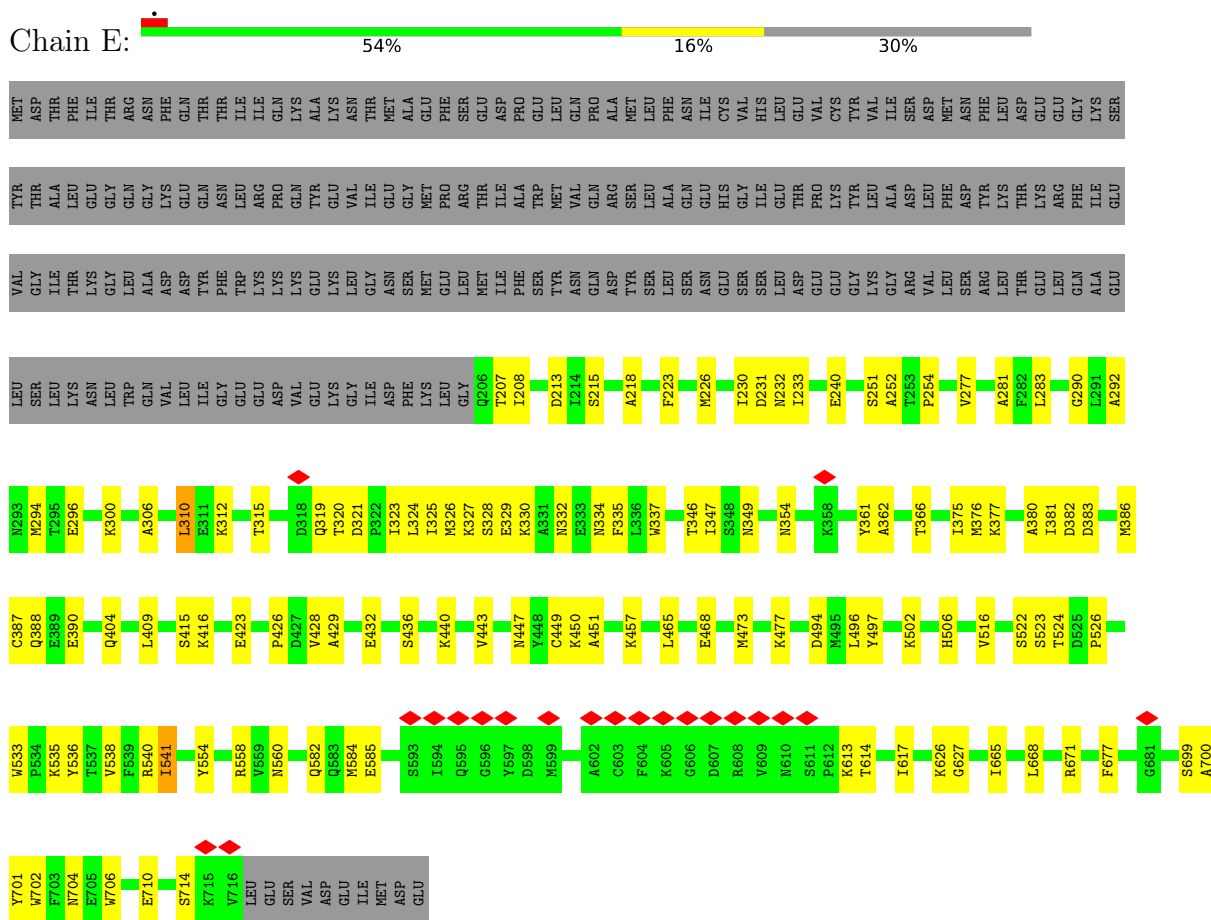
- Molecule 5 is a RNA chain called 5' cRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	W	14	Total	C	N	O	P	0	0
			304	136	62	92	14		

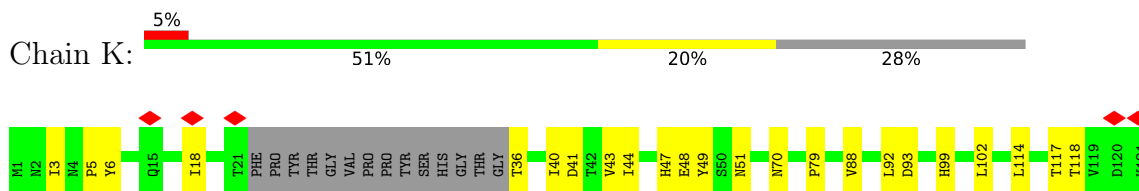
3 Residue-property plots

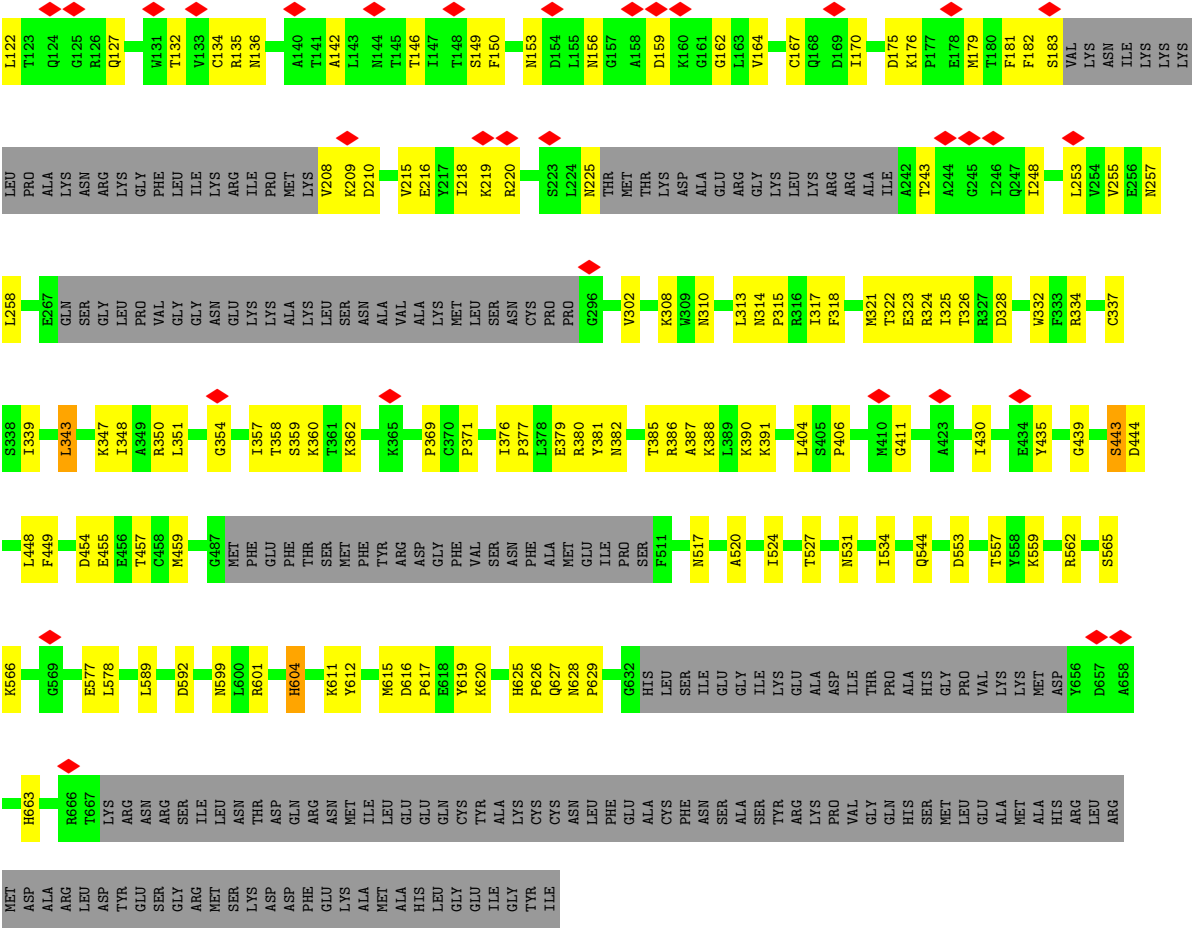
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

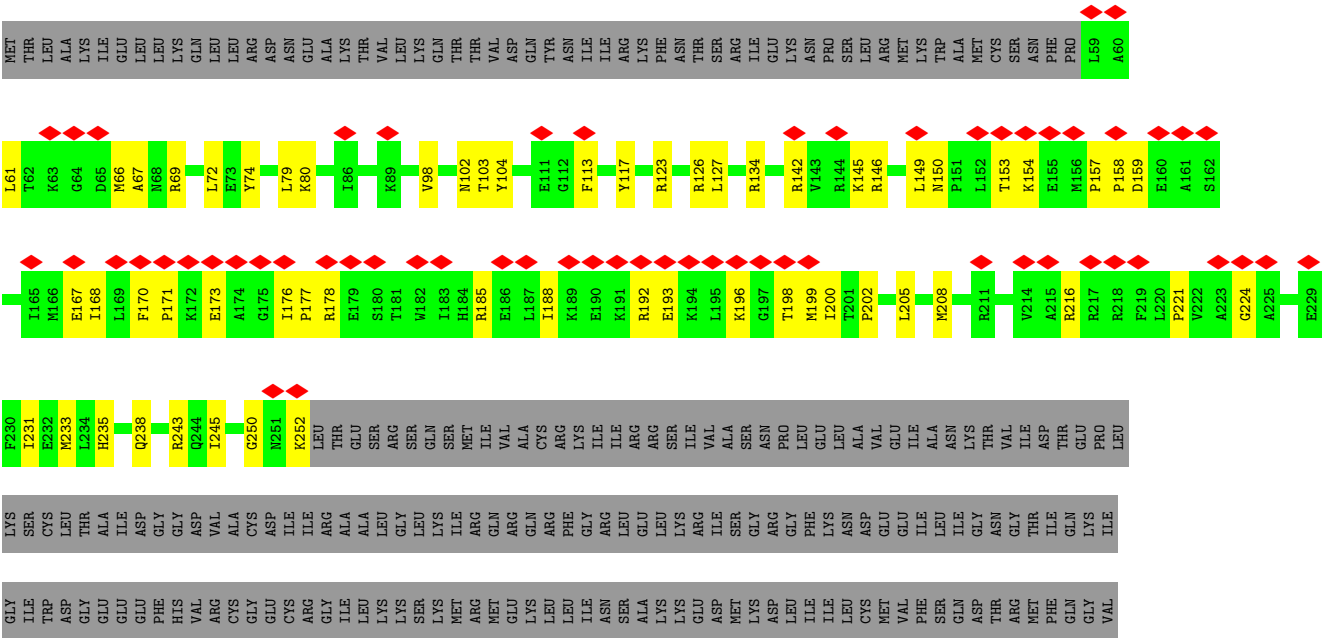


- Molecule 2: RNA-directed RNA polymerase catalytic subunit





● Molecule 3: Polymerase basic protein 2



PHE GLN	LEU	PRO	ALA	MET	LYS	ARG
	GLU	GLY	GLY	TRP	GLY	
PHE GLN	LEU	PRO	ALA	GLY	VAL	GLU
	LEU	PRO	VAL	LEU	MET	ILE
PHE GLN	PRO	ASN	LYS	LYS	THR	ASN
	GLY	PRO	GLN	THR	THR	LEU
PHE GLN	GLU	LYS	ARG	MET	LYS	ASN
	ALA	LYS	ASP	GLU	VAL	ARG
PHE GLN	ASN	VAL	GLN	VAL	ASP	GLY
	ILE	LEU	GLU	GLN	ASP	GLN
PHE GLN	LEU	THR	VAL	ASN	PHE	LEU
	LEU	ILE	MET	THR	THR	LEU
PHE GLN	GLN	CYS	LYS	GLN	THR	PRO
	GLY	ARG	ASP	TRP	GLU	MET
PHE GLN	LYS	MET	GLN	VAL	THR	TYR
	PRO	MET	PHE	LEU	GLU	GLN
PHE GLN	VAL	SER	ILE	LYS	LYS	LEU
	LYS	LYS	LYS	ASN	VAL	GLN
PHE GLN	VAL	LEU	LEU	LEU	SER	ARG
	VAL	GLY	LEU	VAL	ILE	TYR
PHE GLN	ARG	ILE	PHE	THR	THR	PHE
	LYS	GLY	CYS	ALA	ASN	LEU
PHE GLN	ARG	ASP	PHE	GLN	LEU	ASN
	TYR	GLU	SER	GLN	SER	SER
PHE GLN	SER	GLU	PRO	PHE	LEU	ASN
	ALA	ARG	PRO	LEU	ILE	ASP
PHE GLN	LEU	ASN	LYS	LEU	ARG	LEU
	SER	ARG	LEU	GLY	THR	PHE
PHE GLN	ASN	ASN	ARG	LYS	THR	ASP
	ASP	MET	SER	GLU	GLY	GLN
PHE GLN	ILE	GLY	ASN	ASP	GLU	TRP
	SER	ASN	GLY	MET	VAL	GLY
PHE GLN	GLN	ALA	GLU	PHE	ILE	TYR
	GLY	VAL	PRO	GLN	MET	GLU
PHE GLN	ILE	LEU	TYR	TRP	GLY	GLU
	LYS	ALA	GLN	ASP	ALA	SER
PHE GLN	ARG	GLY	PHE	ALA	ASN	PRO
	GLN	PHE	LEU	PHE	ASP	LYS
PHE GLN	ARG	LEU	ARG	GLU	VAL	ALA
	MET	VAL	LEU	ALA	SER	SER
PHE GLN	THR	SER	VAL	PHE	GLU	GLU
	VAL	GLY	LEU	GLU	LEU	LEU
PHE GLN	GLU	LYS	LYS	SER	GLU	HIS
	SER	TYR	GLY	ILE	SER	GLY
PHE GLN	MET	ASP	GLY	ILE	ILE	GLN
	GLY	PRO	GLY	PRO	ALA	ASN
PHE GLN	TRP	ASP	GLU	GLN	GLN	GLU
	ALA	LEU	ASN	LYS	LEU	LEU
PHE GLN	LEU	GLY	PHE	MET	MET	LEU
	SER	ASP	ILE	ALA	ILE	ASN
PHE GLN	ALA	PHE	GLU	GLY	THR	ALA
	ARG	LYS	VAL	GLN	TYR	SER
PHE GLN	ASN	THR	ARG	TYR	THR	ASP
	ASN	ILE	LYS	SER	ASP	TYR
PHE GLN	LEU	GLU	GLY	GLY	PRO	THR

- Molecule 4: 3' cRNA



- Molecule 5: 5' cRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	1012085	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.1	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	38.011	Depositor
Minimum map value	-25.019	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	5.6	Depositor
Map size ($\text{\AA}$)	276.48, 276.48, 276.48	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.08, 1.08, 1.08	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	E	0.41	0/4170	0.61	1/5624 (0.0%)
2	K	0.33	0/4282	0.58	0/5785
3	Q	0.22	0/1600	0.51	0/2159
4	T	0.39	0/275	0.61	0/425
5	W	0.35	0/341	0.55	0/530
All	All	0.35	0/10668	0.58	1/14523 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	E	347	ILE	N-CA-C	-5.08	107.85	112.12

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	E	4084	0	4086	87	0
2	K	4206	0	4176	112	0
3	Q	1565	0	1598	40	0
4	T	249	0	127	0	0
5	W	304	0	155	3	0
All	All	10408	0	10142	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 10.

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)
1:E:386:MET:HB3	2:K:357:ILE:HD12	1.71	0.72
2:K:517:ASN:HD21	2:K:520:ALA:H	1.35	0.71
2:K:99:HIS:HB3	2:K:102:LEU:HB2	1.73	0.70
1:E:526:PRO:HG3	1:E:538:VAL:HG11	1.78	0.65
1:E:449:CYS:SG	1:E:450:LYS:N	2.70	0.64

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	E	509/726 (70%)	445 (87%)	64 (13%)	0	100	100
2	K	525/752 (70%)	464 (88%)	60 (11%)	1 (0%)	43	76
3	Q	192/778 (25%)	183 (95%)	9 (5%)	0	100	100
All	All	1226/2256 (54%)	1092 (89%)	133 (11%)	1 (0%)	49	81

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	K	443	SER

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	E	452/645 (70%)	448 (99%)	4 (1%)	70	76
2	K	461/644 (72%)	456 (99%)	5 (1%)	65	74
3	Q	166/682 (24%)	165 (99%)	1 (1%)	78	80
All	All	1079/1971 (55%)	1069 (99%)	10 (1%)	68	76

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	K	348	ILE
2	K	604	HIS
3	Q	98	VAL
1	E	541	ILE
2	K	18	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
2	K	153	ASN
2	K	306	ASN
2	K	261	ASN
2	K	429	ASN
1	E	666	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	T	11/15 (73%)	9 (81%)	0
5	W	13/14 (92%)	6 (46%)	0
All	All	24/29 (82%)	15 (62%)	0

5 of 15 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	T	3	C
4	T	4	C
4	T	5	U
4	T	6	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	T	7	G

There are no RNA pucker outliers to report.

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](#)

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.

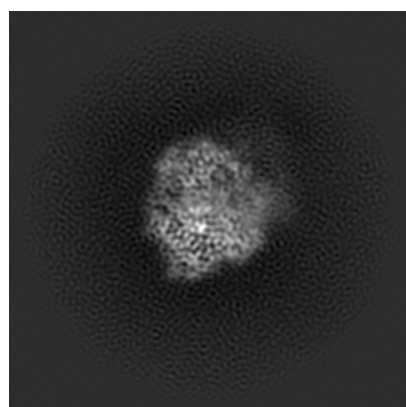
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4660. These allow visual inspection of the internal detail of the map and identification of artifacts.

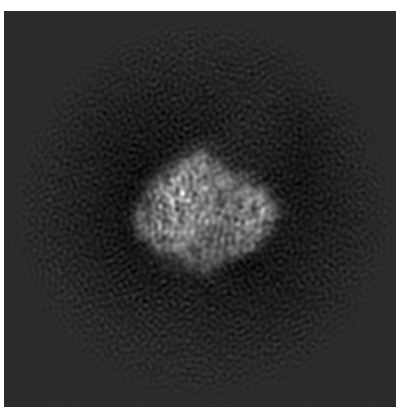
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

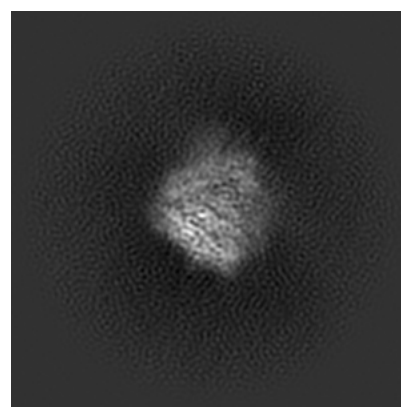
6.1.1 Primary map



X



Y

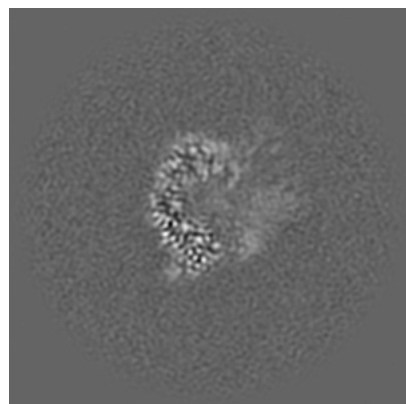


Z

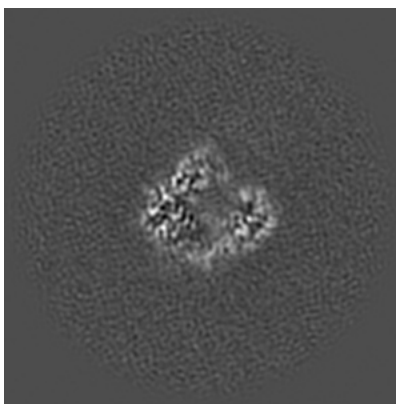
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

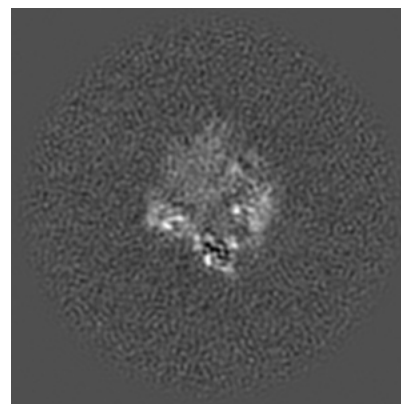
6.2.1 Primary map



X Index: 128



Y Index: 128

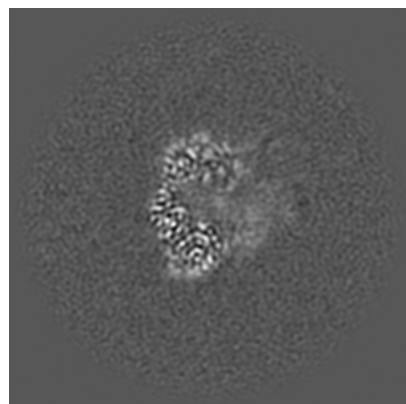


Z Index: 128

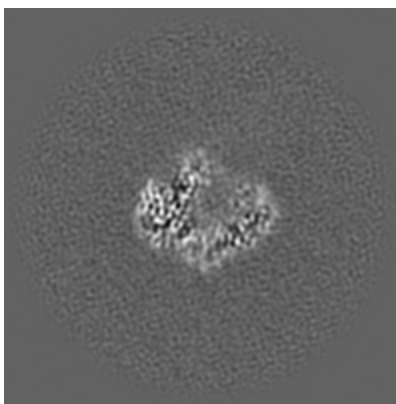
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

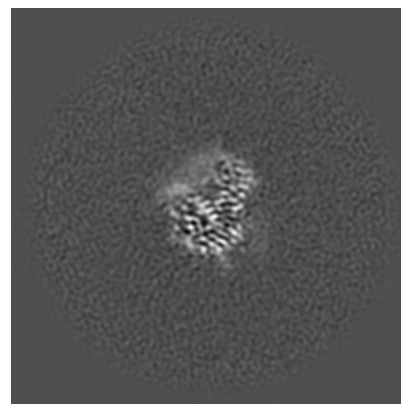
6.3.1 Primary map



X Index: 125



Y Index: 120

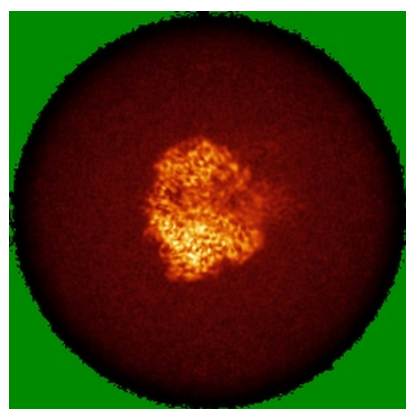


Z Index: 108

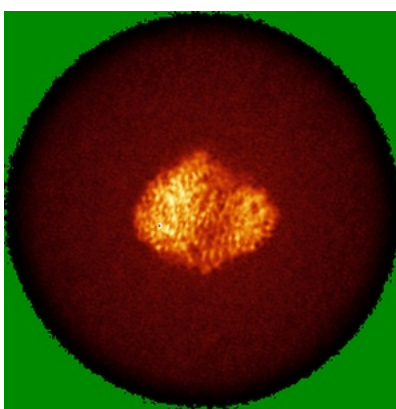
The images above show the largest variance slices of the map in three orthogonal directions.

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

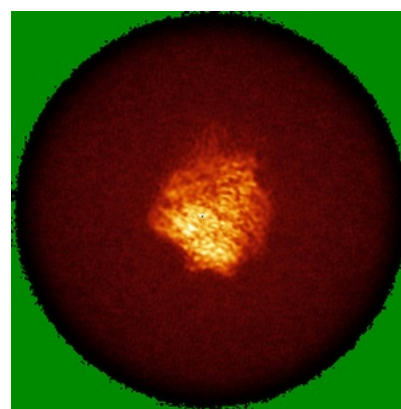
6.4.1 Primary map



X



Y

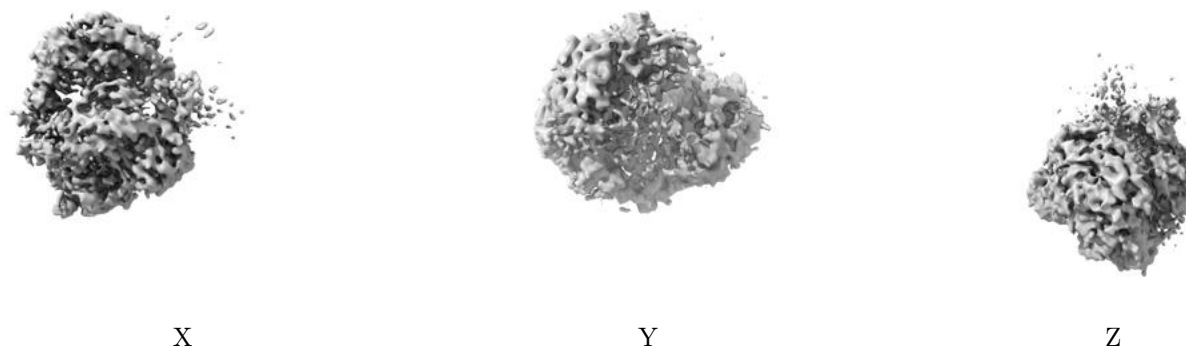


Z

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 5.6. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

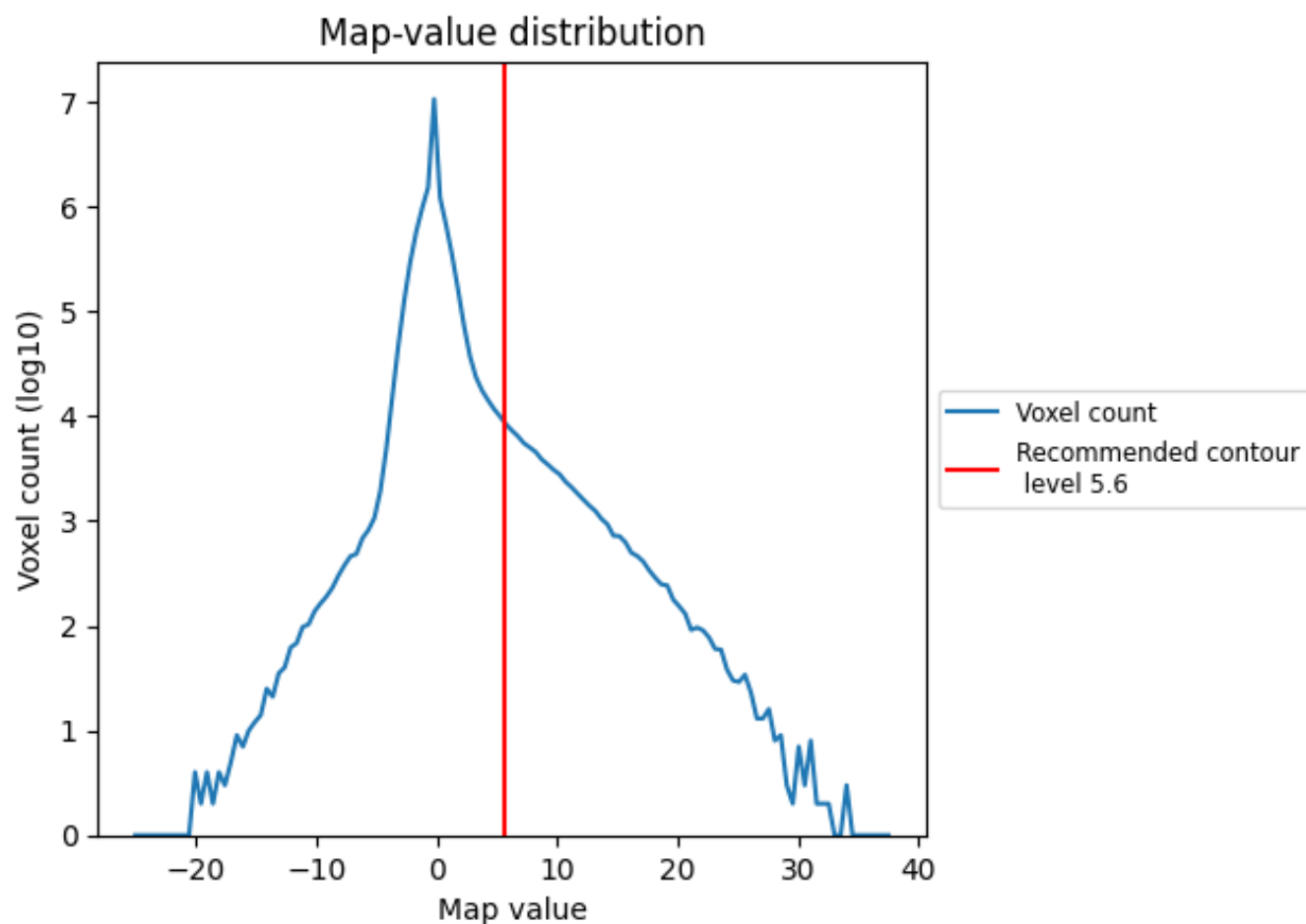
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

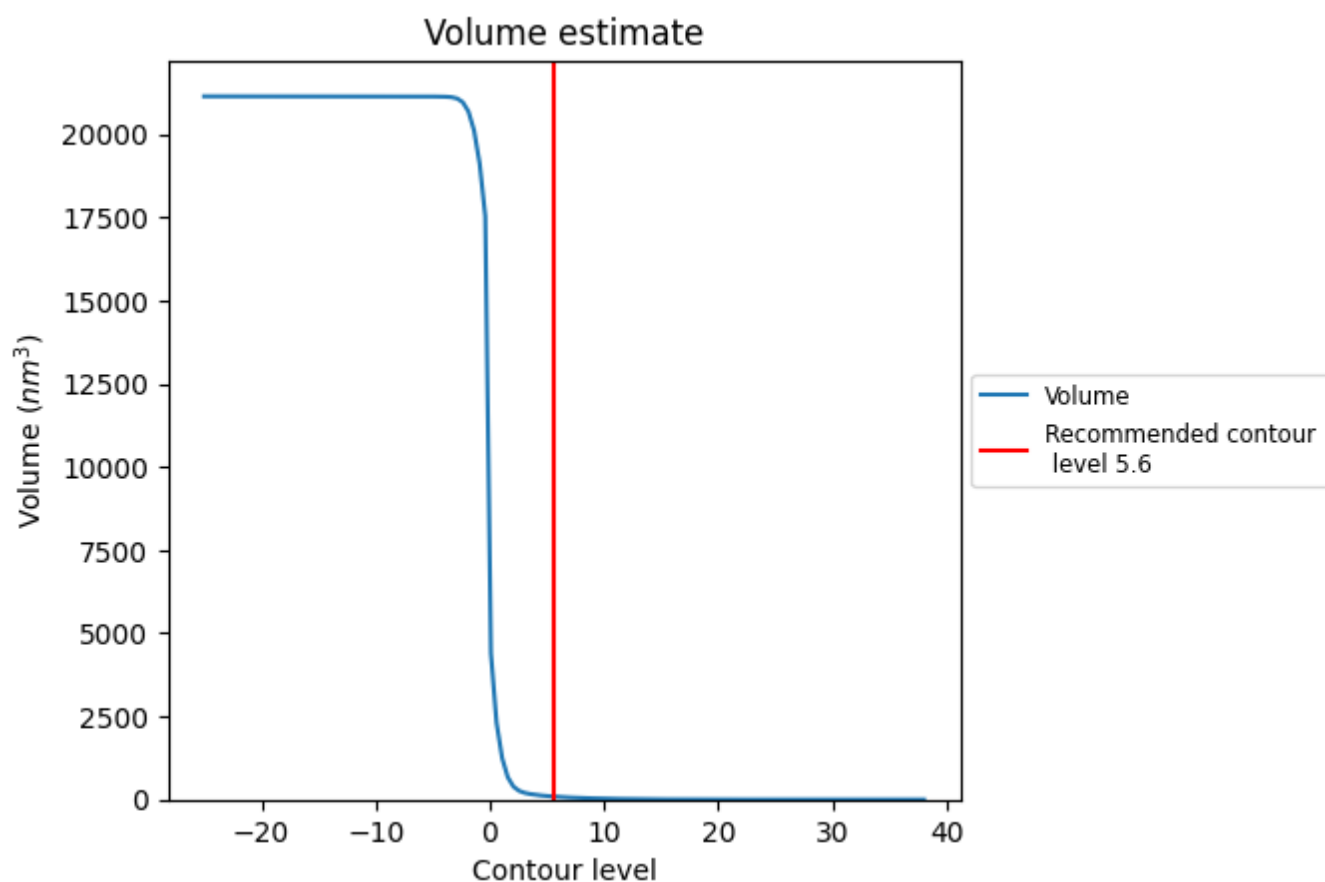
This section contains the results of statistical analysis of the map.

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.

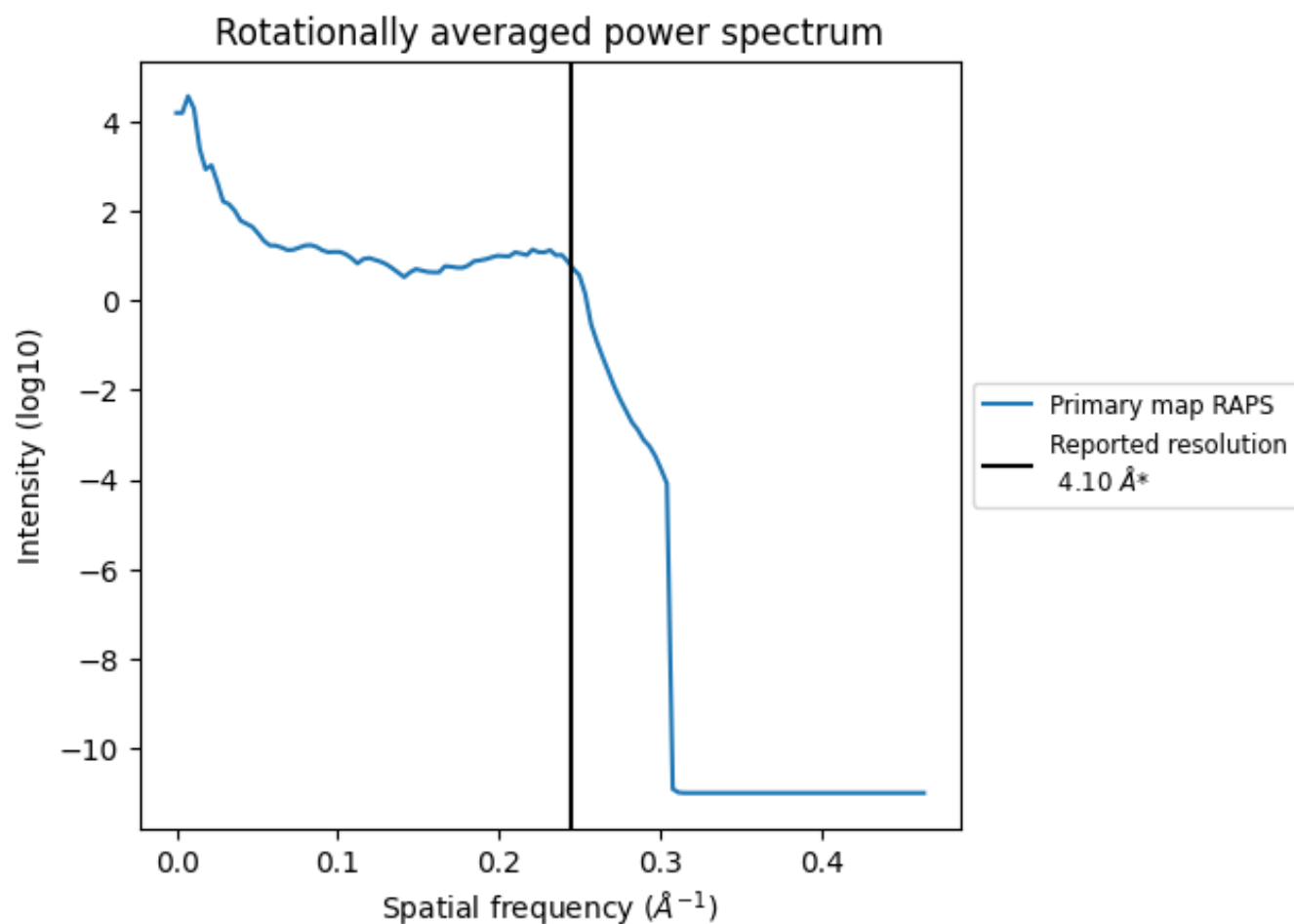
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 90 nm^3 ; this corresponds to an approximate mass of 81 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 ⓘ

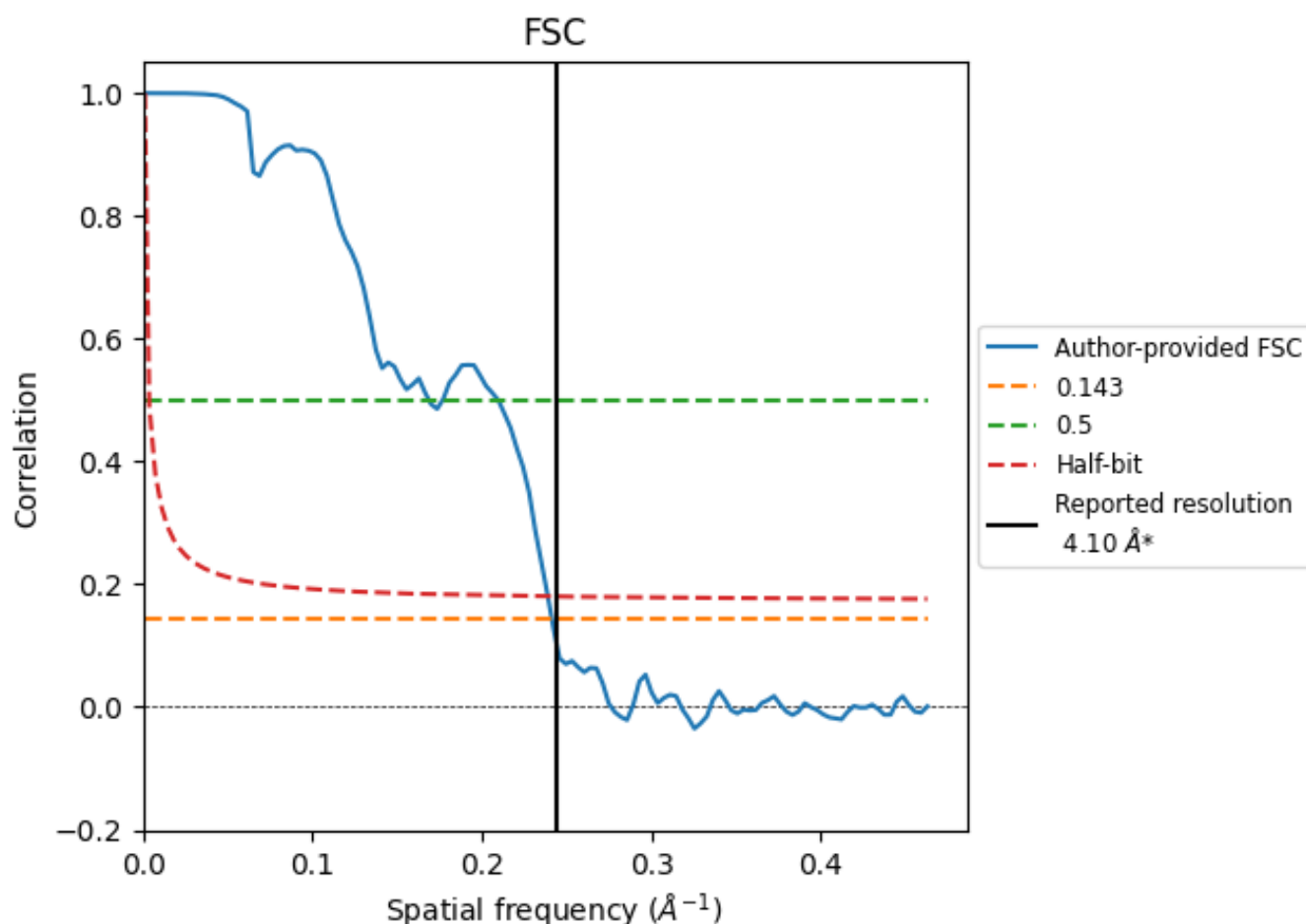


*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

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 0.244 Å⁻¹

8.2 Resolution estimates [i](#)

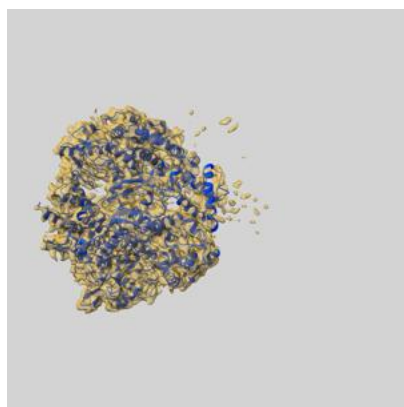
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.14	5.93	4.19
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

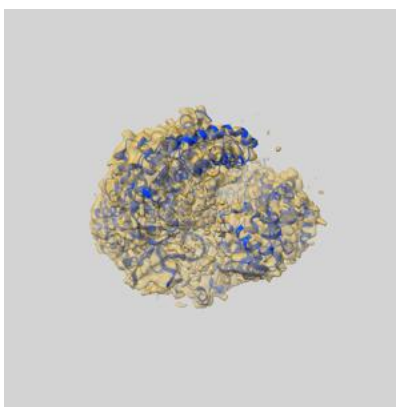
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4660 and PDB model 6QWL. Per-residue inclusion information can be found in section [3](#) on page [6](#).

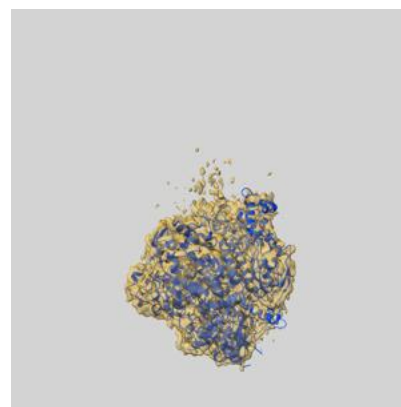
9.1 Map-model overlay [i](#)



X



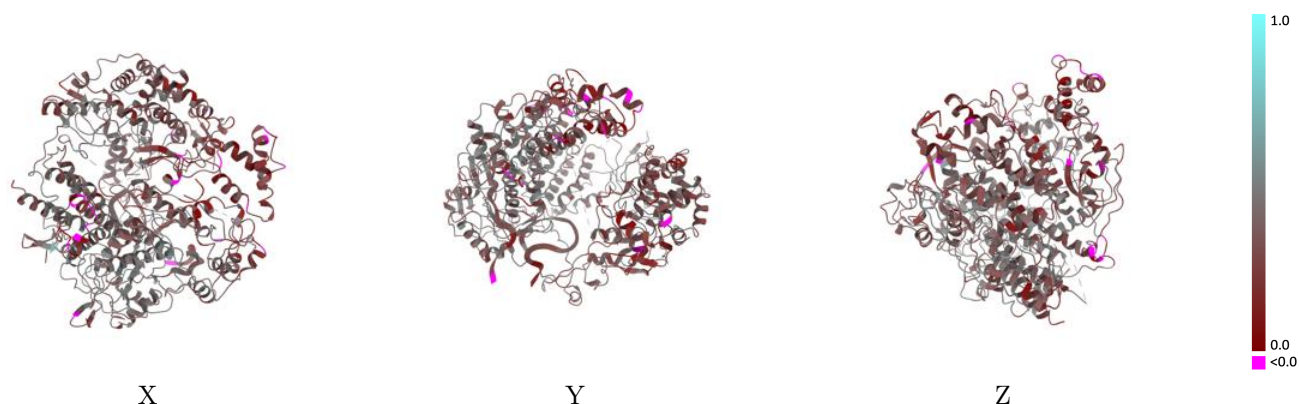
Y



Z

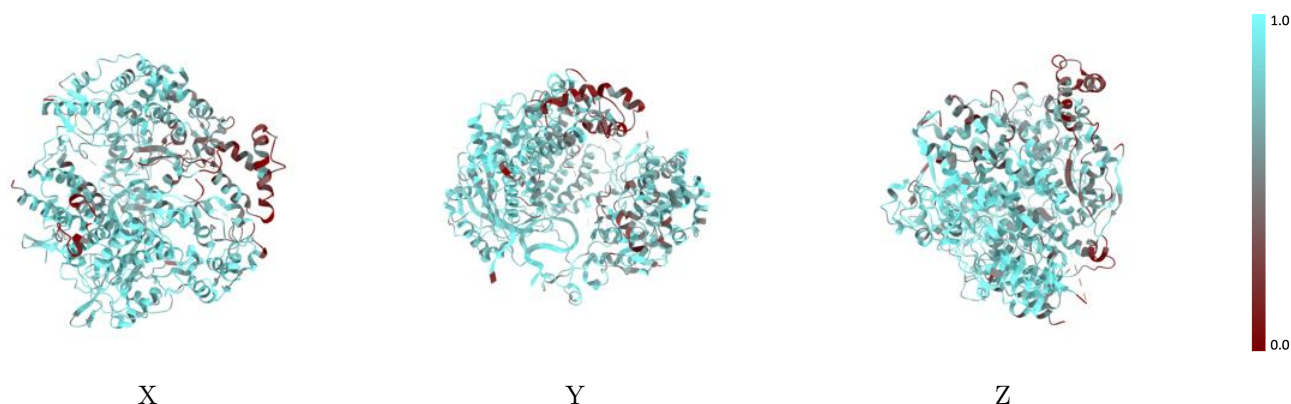
The images above show the 3D surface view of the map at the recommended contour level 5.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



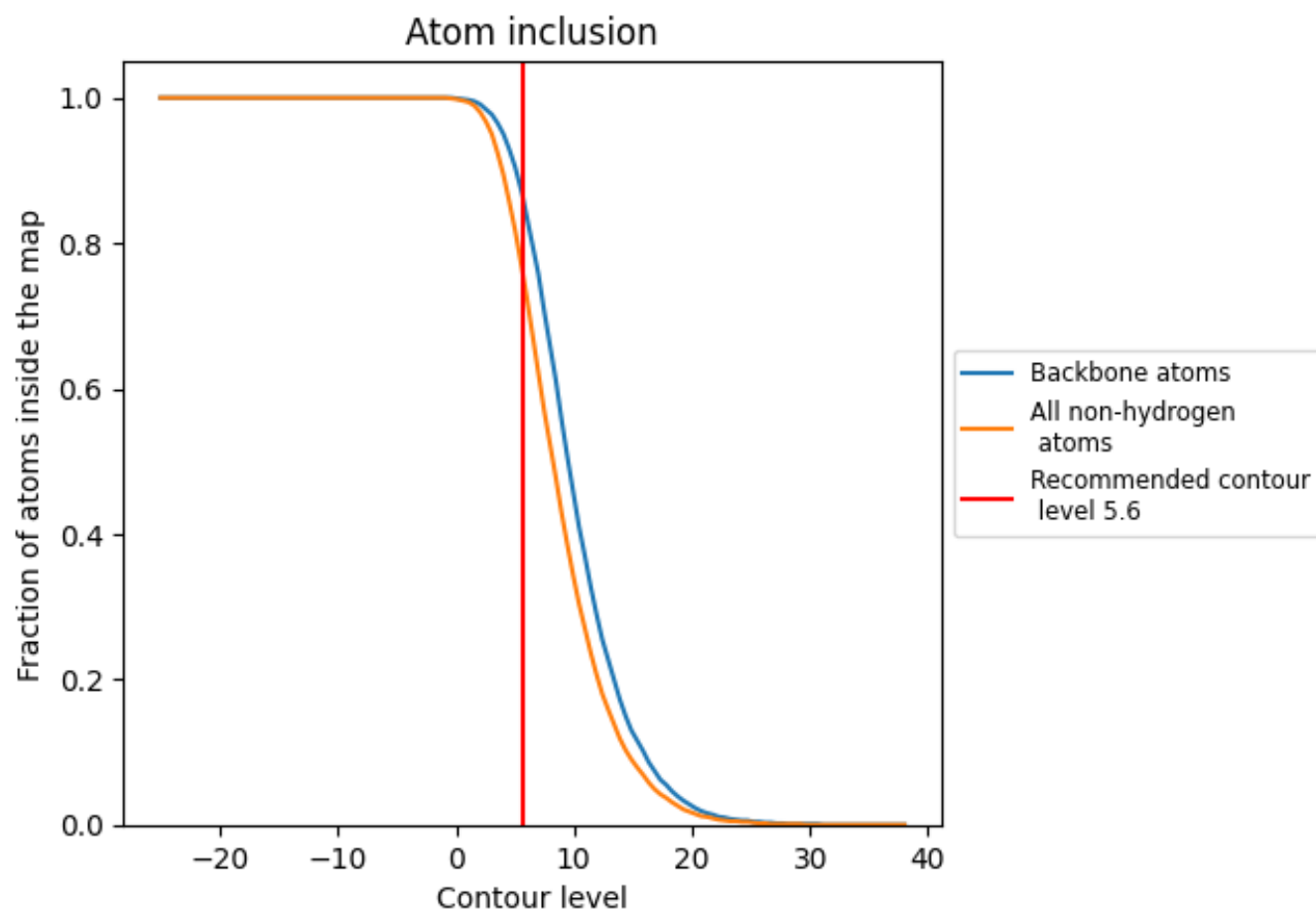
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (5.6).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 76% 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 (5.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7650	0.3550
E	0.8220	0.3950
K	0.7760	0.3590
Q	0.5620	0.2630
T	0.7670	0.3020
W	0.8850	0.3010

