



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 05:02 PM UTC

PDB ID : 6V85 / pdb_00006v85
EMDB ID : EMD-21095
Title : Parainfluenza virus 5 L-P complex
Authors : Abdella, R.; He, Y.
Deposited on : 2019-12-10
Resolution : 4.38 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:

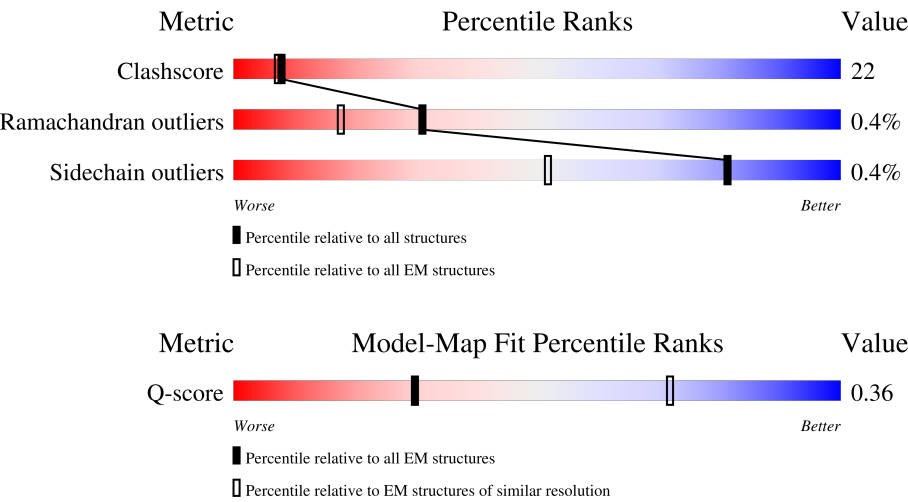
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.38 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	3702 (3.88 - 4.88)

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	2255	
2	B	392	
2	C	392	
2	D	392	

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Mol	Chain	Length	Quality of chain
2	E	392	14%15%81%
2	F	392	8%88%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 17878 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 RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1901	Total	C	N	O	S	0	0
			15200	9769	2578	2770	83		

- Molecule 2 is a protein called Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	F	47	Total	C	N	O	S	0	0
			374	238	64	70	2		
2	B	72	Total	C	N	O	S	4	0
			569	350	101	115	3		
2	C	74	Total	C	N	O	S	4	0
			582	357	103	119	3		
2	D	72	Total	C	N	O	S	4	0
			569	350	101	115	3		
2	E	74	Total	C	N	O	S	4	0
			582	357	103	119	3		

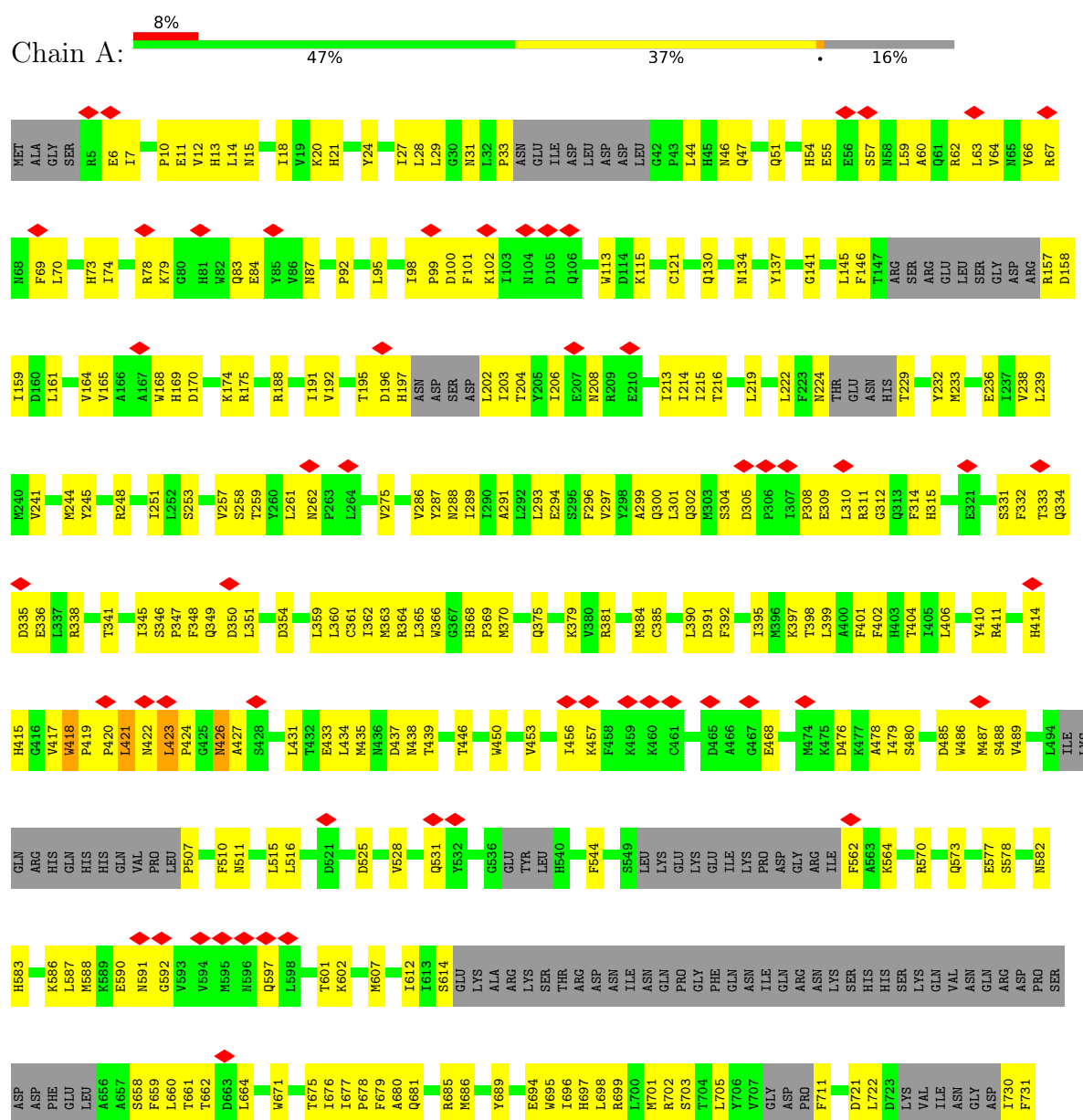
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	A	2	Total	Zn	0
			2	2	

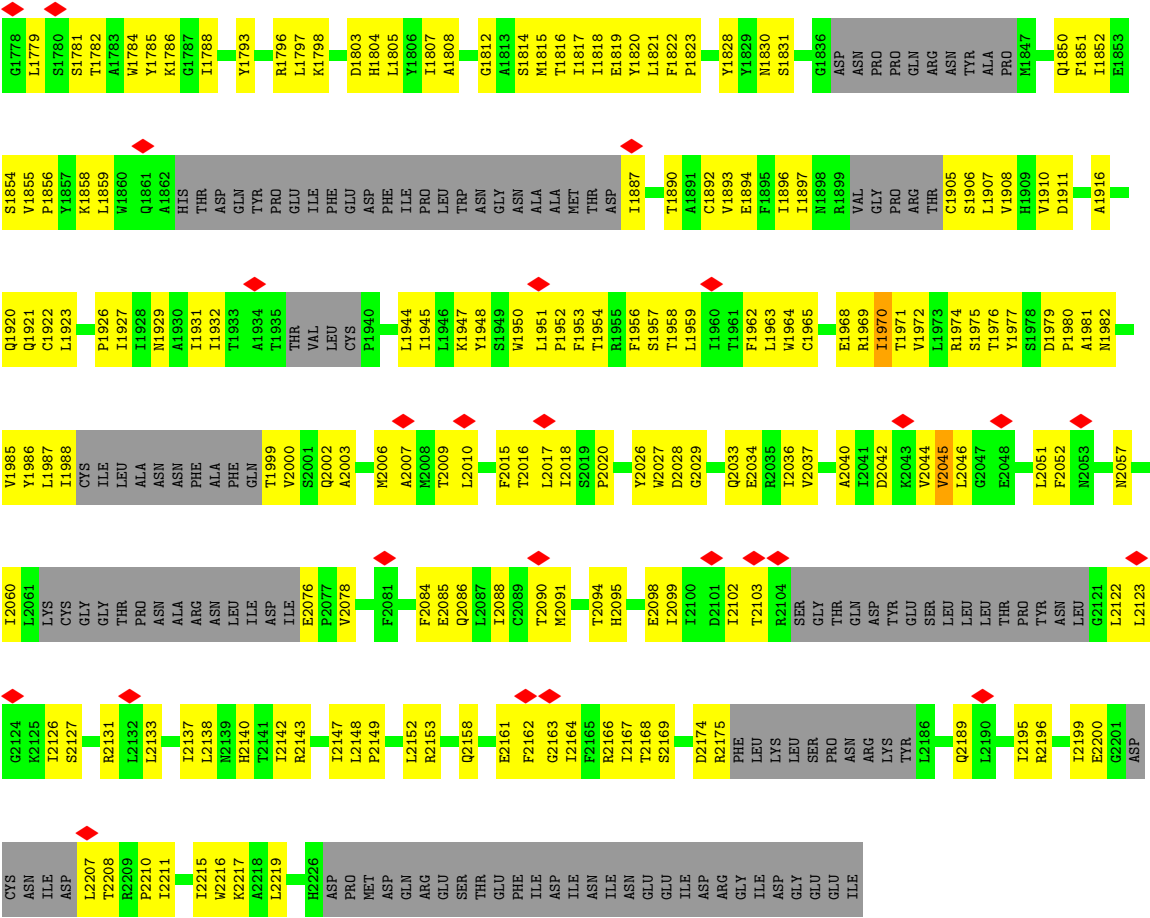
3 Residue-property plots [i](#)

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: RNA-directed RNA polymerase L

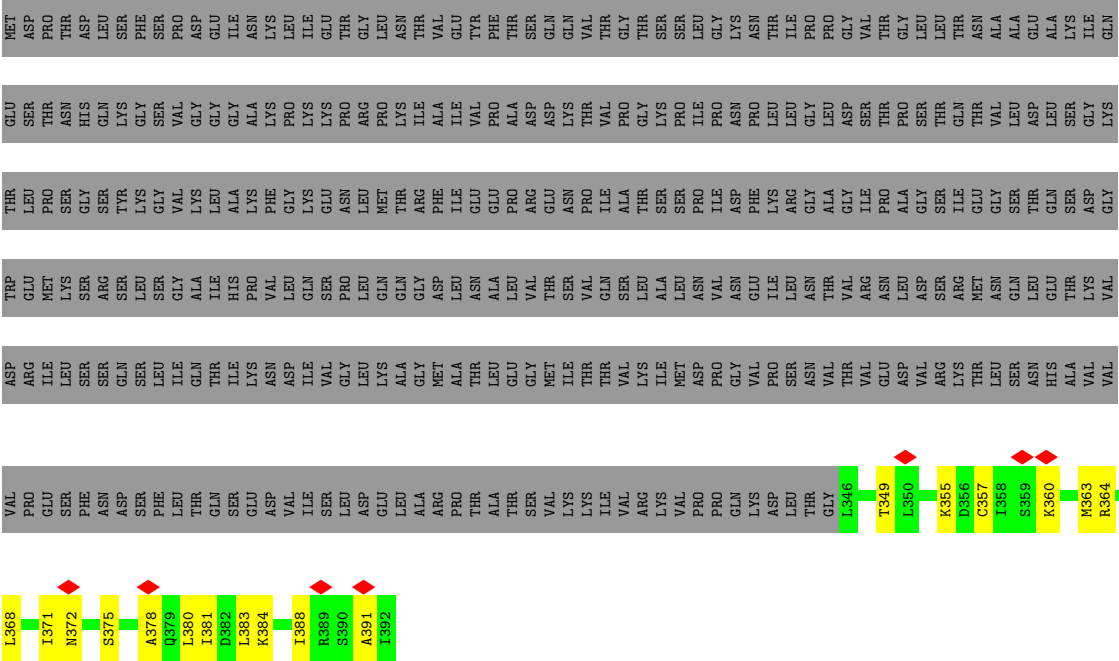






• Molecule 2: Phosphoprotein

Chain F: 8% . 88%



LYS	GLU	THR	TRP	THR	GLU	MET
MET	ASP	LEU	GLU	LEU	THR	ASP
ASP	PRO	THR	MET	PRO	THR	PRO
THR	ASN	GLY	LYS	SER	ASN	THR
GLU	TYR	ASP	ARG	GLY	HIS	ASP
LEU	SER	SER	SER	TYR	LYS	SER
LEU	PHE	LEU	LEU	LYS	GLY	PHE
LYS	ILE	THR	SER	GLY	SER	LYS
ASN	GLN	ASN	ALA	LEU	VAL	GLU
ALA	GLU	SER	ILE	LYS	GLY	ILE
GLN	ASP	LEU	GLN	GLY	LYS	GLU
ASP	ASP	GLU	SER	ASN	PRO	THR
GLU	ILE	GLU	P199	LEU	ARG	GLY
ILE	ASP	LEU	L200	MET	PRO	LEU
ASP	LEU	ALA	L257	THR	LYS	ASN
LYS	LYS	ARG	V258	THR	ILE	THR
LYS	LYS	ARG	G259	ARG	ALA	VAL
ALA	ALA	THR	L260	PHE	ILE	GLU
ILE	ILE	ALA	K261	GLU	VAL	TYR
ILE	ILE	THR	A262	GLU	PRO	PHE
ARG	ARG	SER	G263	PRO	ALA	THR
SER	SER	VAL	M264	ARG	ASP	SER
ILE	ILE	LYS	A265	GLU	LYS	GLN
ALA	ALA	ILE	L266	ASN	THR	VAL
		ILE	L267	PRO	THR	THR
		VAL		ILE	VAL	THR
		VAL		ALA	PRO	GLY
		ARG	M270	THR	GLY	THR
		LYS	ILE	SER	LYS	SER
		VAL	THR	PRO	PRO	SER
		PRO	VAL	PRO	ILE	LEU
		GLN	LYS	ILE	PRO	GLY
		LYS	ILE	ASP	ASN	LYS
		ASP	MET	PHE	PRO	ASN
		LEU	THR	LYS	LEU	THR
		THR	PRO	ARG	LEU	THR
		GLY	GLY	GLY	LEU	ILE
		LEU	VAL	ALA	LEU	PRO
		LYS	PRO	ILE	ASP	GLY
		ILE	SER	ILE	SER	VAL
		THR	ASN	PRO	THR	THR
		LEU	VAL	ALA	PRO	GLY
		LEU	THR	GLY	SER	THR
		GLN	VAL	SER	THR	LEU
		LEU	VAL	ILE	GLN	LEU
		ALA	ASP	GLU	THR	ASN
		LYS	VAL	LYS	THR	ALA
		ASP	ARG	SER	VAL	ALA
		CYS	LYS	THR	ASP	GLU
		ILE	THR	THR	GLN	ALA
		SER	LEU	SER	SER	LYS
		LYS	SER	ASP	ASP	ILE
		PRO	HIS	GLY	GLY	GLN
			ASN	ASP	ASP	
			ALA	THR	LEU	
			VAL	GLN	LEU	
			VAL	VAL	ASP	
			VAL	VAL	LEU	
			VAL	VAL	SER	
					GLY	
					LYS	
					THR	
					ARG	
					M227	
					N228	
					L229	
					D230	
					S231	
					R232	
					M233	
					N234	
					Q235	
					L236	
					E237	
					T238	
					K239	
					M240	

[illegible]

WORLDWIDE
PDB
PROTEIN DATA BANK

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	102493	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL 3200FS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	80.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.091	Depositor
Minimum map value	-0.048	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.027	Depositor
Map size (Å)	403.2, 403.2, 403.2	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.12, 1.12, 1.12	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.31	0/15514	0.56	5/21035 (0.0%)
2	B	0.32	0/575	0.52	0/776
2	C	0.25	0/588	0.46	0/794
2	D	0.28	0/575	0.44	0/776
2	E	0.28	0/588	0.49	0/794
2	F	0.19	0/375	0.33	0/498
All	All	0.30	0/18215	0.55	5/24673 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1374	CYS	CA-C-N	7.14	129.97	122.97
1	A	1374	CYS	C-N-CA	7.14	129.97	122.97
1	A	1375	VAL	O-C-N	6.71	126.95	121.85
1	A	2045	VAL	N-CA-C	-5.32	106.33	112.98
1	A	1375	VAL	N-CA-C	-5.26	106.53	111.48

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	15200	0	15373	750	0
2	B	569	0	600	25	0
2	C	582	0	611	20	0
2	D	569	0	600	18	0
2	E	582	0	611	26	0
2	F	374	0	414	12	0
3	A	2	0	0	0	0
All	All	17878	0	18209	809	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 22.

The worst 5 of 809 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:A:410:TYR:CE1	1:A:414:HIS:HD2	1.32	1.48
1:A:1950:TRP:CE3	1:A:1956:PHE:CE1	2.16	1.33
1:A:1950:TRP:HE3	1:A:1956:PHE:CD1	1.47	1.31
1:A:410:TYR:CE1	1:A:414:HIS:CD2	2.17	1.29
1:A:1746:LEU:HB3	1:A:1748:LYS:NZ	1.50	1.25

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	1843/2255 (82%)	1542 (84%)	292 (16%)	9 (0%)	24	62
2	B	74/392 (19%)	74 (100%)	0	0	100	100
2	C	76/392 (19%)	76 (100%)	0	0	100	100
2	D	74/392 (19%)	74 (100%)	0	0	100	100
2	E	76/392 (19%)	76 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	F	45/392 (12%)	43 (96%)	2 (4%)	0	100	100
All	All	2188/4215 (52%)	1885 (86%)	294 (13%)	9 (0%)	31	66

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	418	TRP
1	A	1134	GLU
1	A	1738	TRP
1	A	1029	MET
1	A	1739	ILE

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	1701/2019 (84%)	1692 (100%)	9 (0%)	81	81
2	B	68/342 (20%)	68 (100%)	0	100	100
2	C	70/342 (20%)	70 (100%)	0	100	100
2	D	68/342 (20%)	68 (100%)	0	100	100
2	E	70/342 (20%)	70 (100%)	0	100	100
2	F	42/342 (12%)	42 (100%)	0	100	100
All	All	2019/3729 (54%)	2010 (100%)	9 (0%)	81	82

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1743	ASN
1	A	1970	ILE
1	A	689	TYR
1	A	1294	LEU
1	A	1373	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1338	GLN
1	A	1919	ASN
1	A	1366	HIS
1	A	1659	ASN
1	A	2024	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 2 ligands modelled in this entry, 2 are 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 ⓘ

There are no chain breaks in this entry.

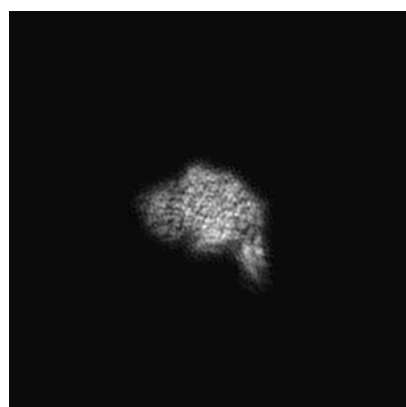
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21095. These allow visual inspection of the internal detail of the map and identification of artifacts.

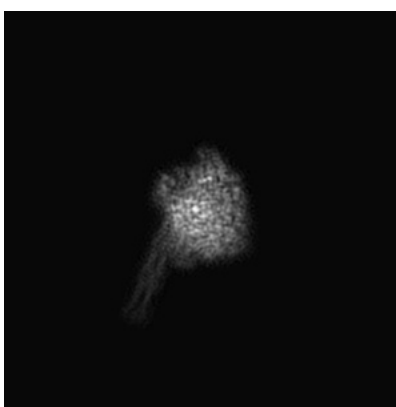
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y



Z

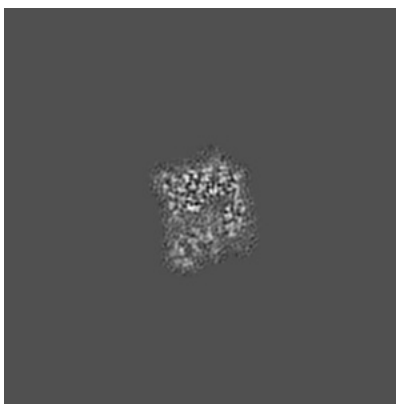
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

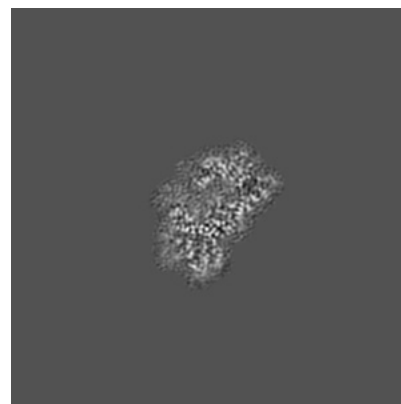
6.2.1 Primary map



X Index: 180



Y Index: 180



Z Index: 180

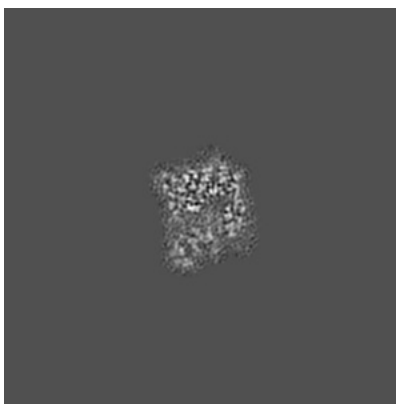
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

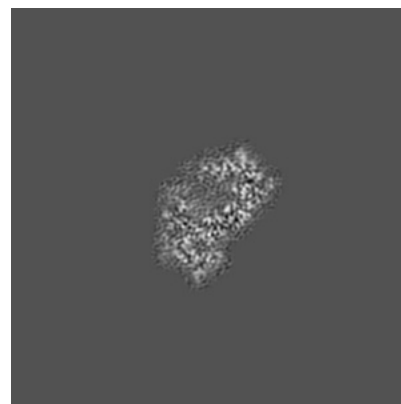
6.3.1 Primary map



X Index: 180



Y Index: 180

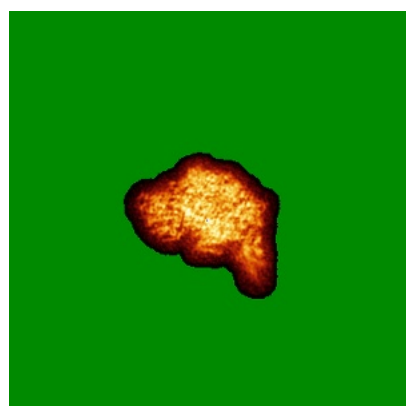


Z Index: 185

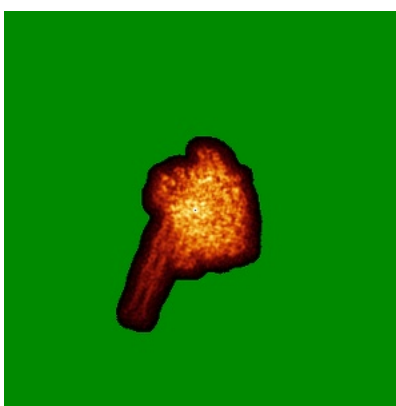
The images above show the largest variance slices of the map in three orthogonal directions.

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

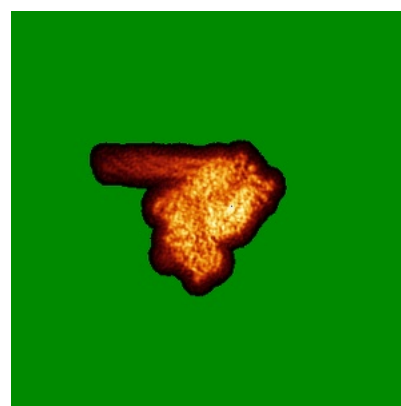
6.4.1 Primary map



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

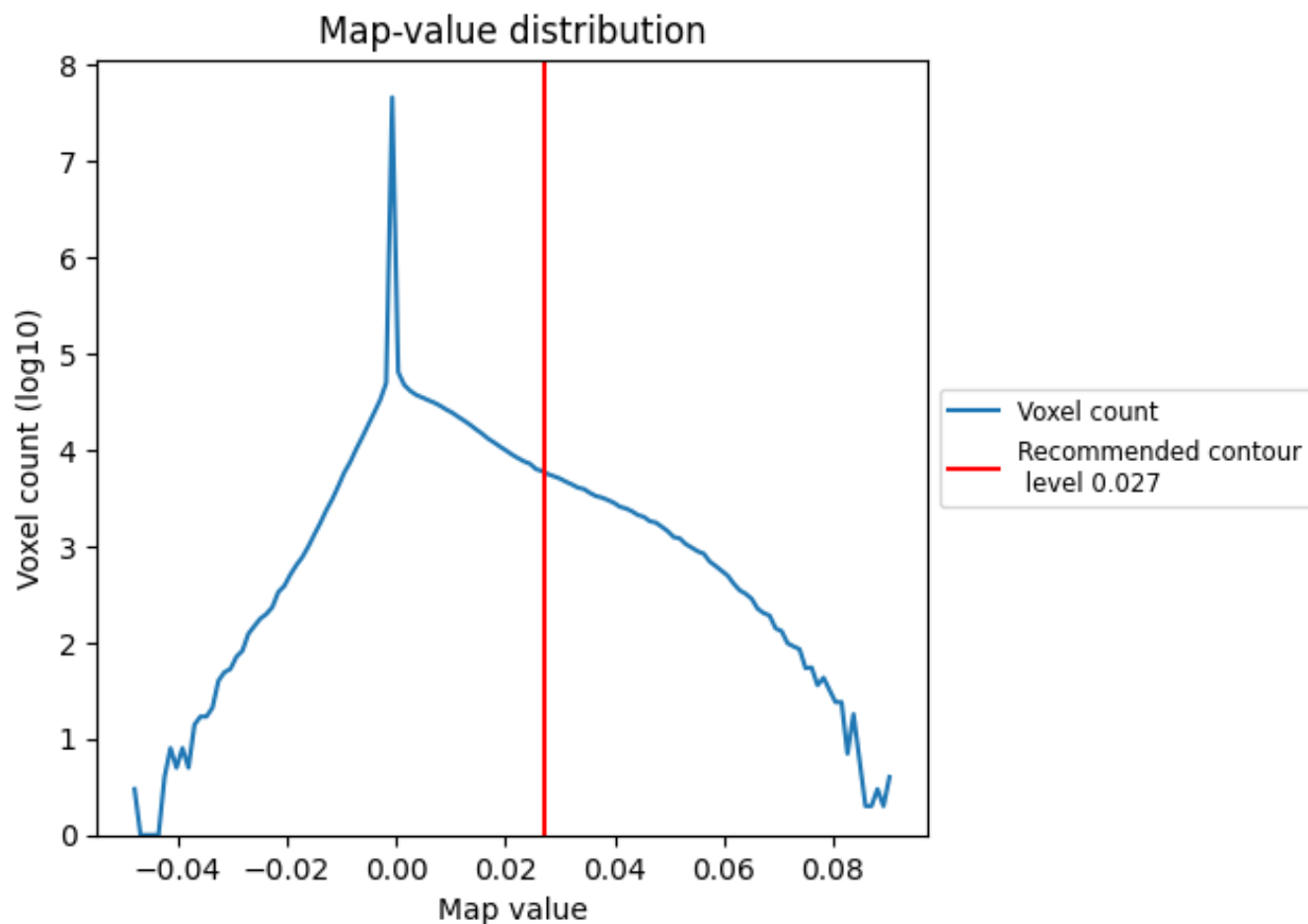
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

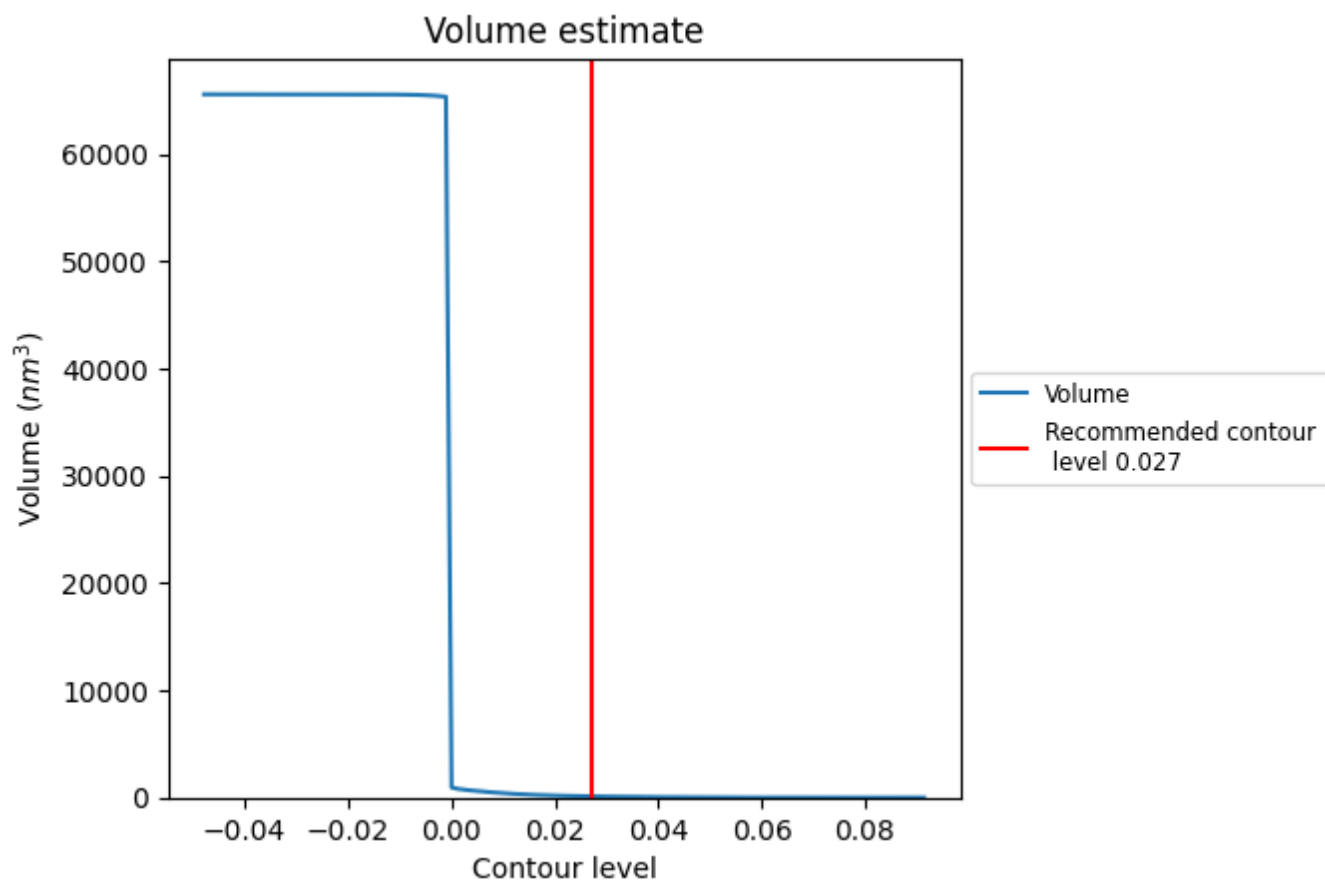
This section contains the results of statistical analysis of the map.

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.

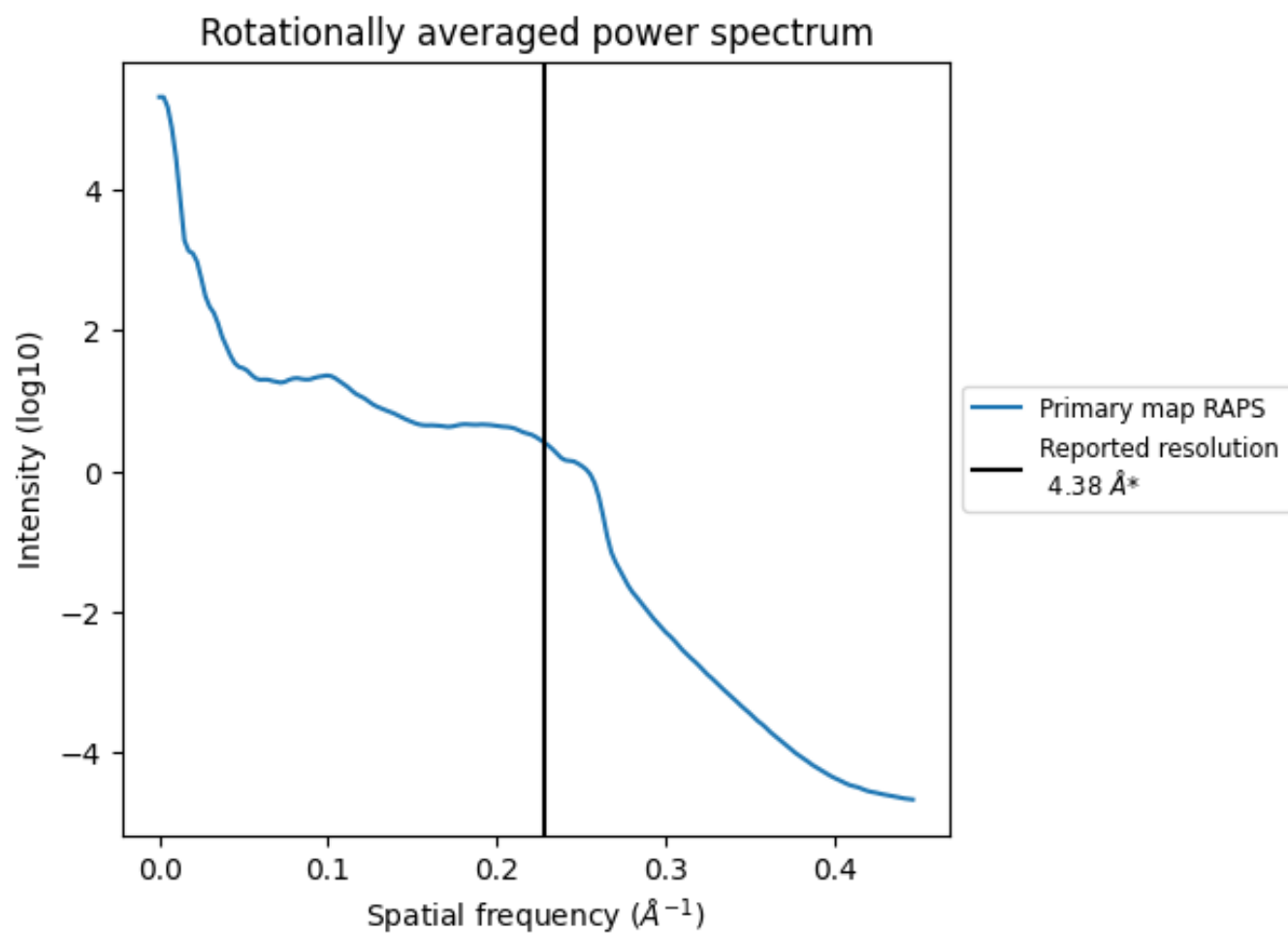
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 116 nm³; this corresponds to an approximate mass of 105 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 ⓘ

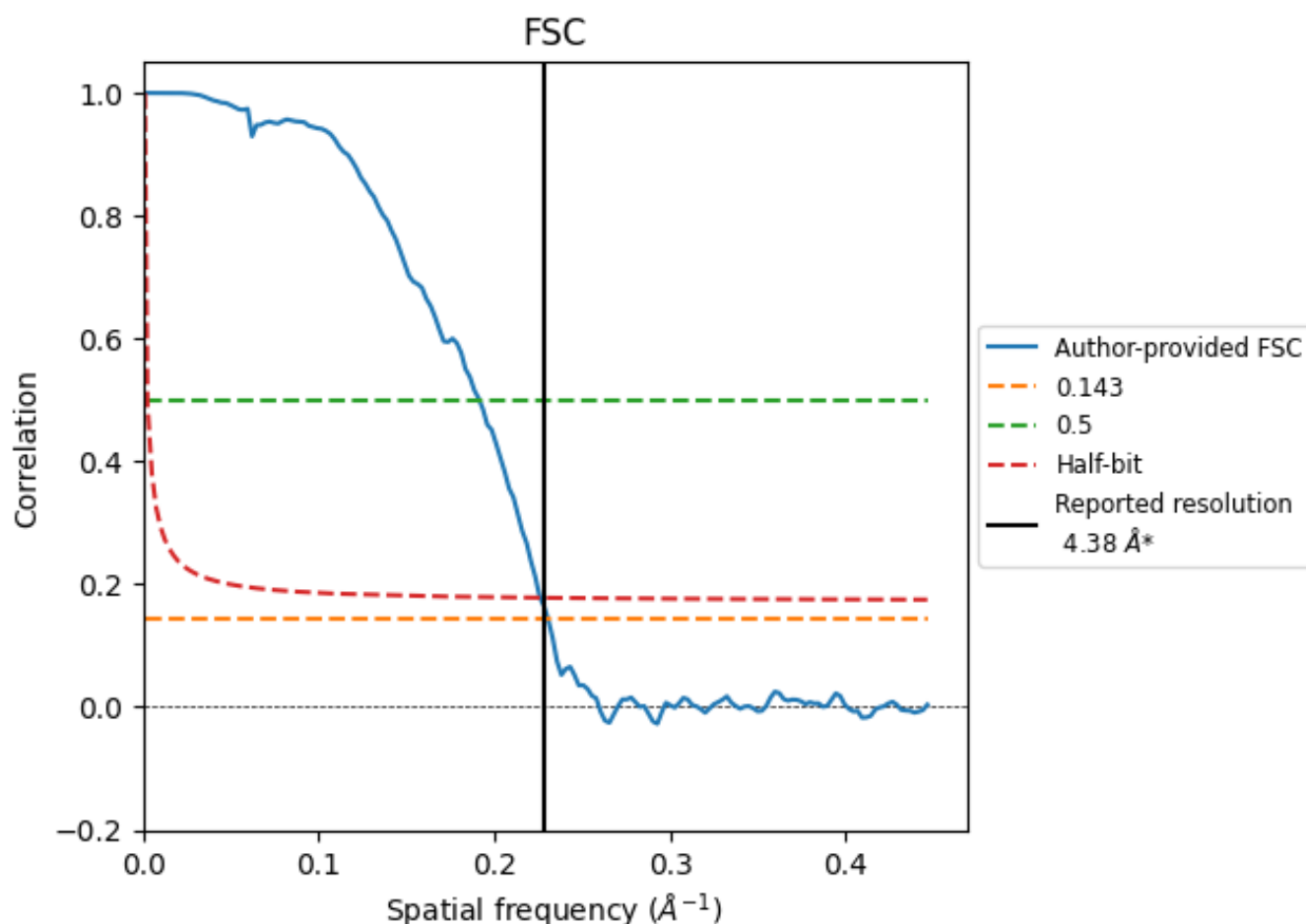


*Reported resolution corresponds to spatial frequency of 0.228 Å⁻¹

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 0.228 Å⁻¹

8.2 Resolution estimates [i](#)

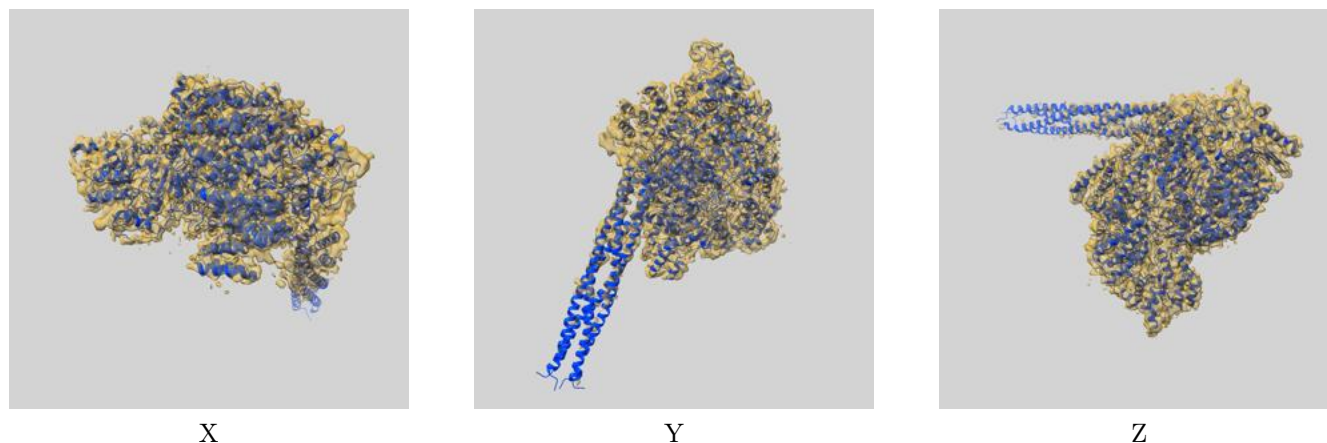
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.38	-	-
Author-provided FSC curve	4.34	5.23	4.43
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

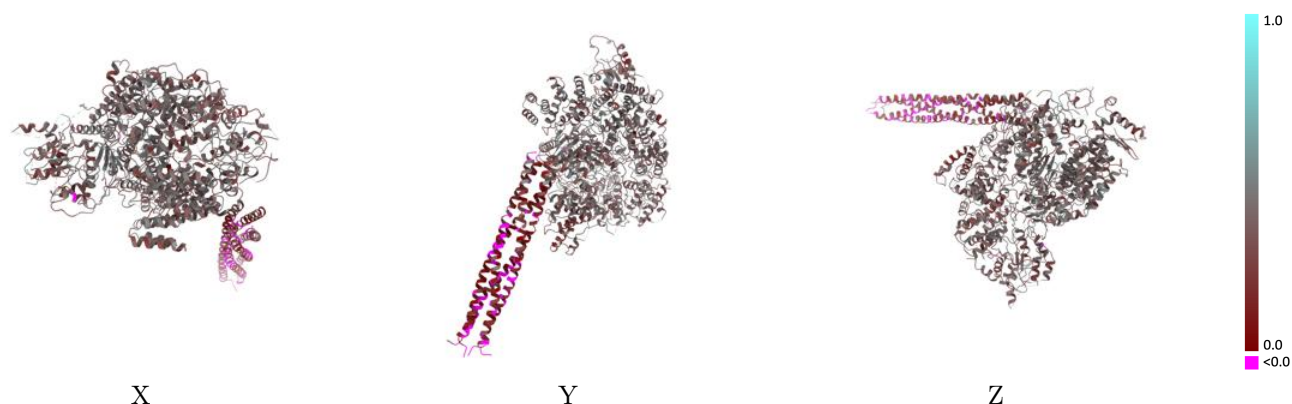
This section contains information regarding the fit between EMDB map EMD-21095 and PDB model 6V85. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



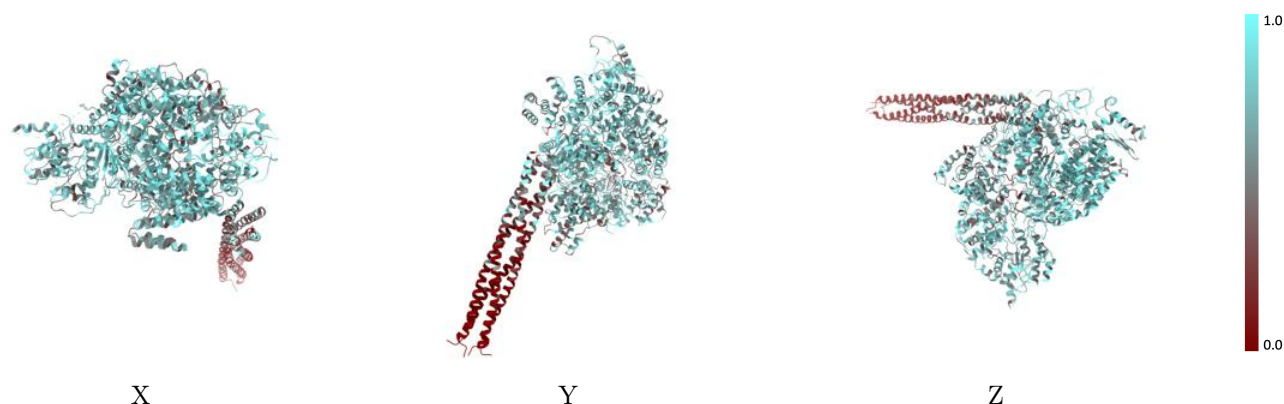
The images above show the 3D surface view of the map at the recommended contour level 0.027 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



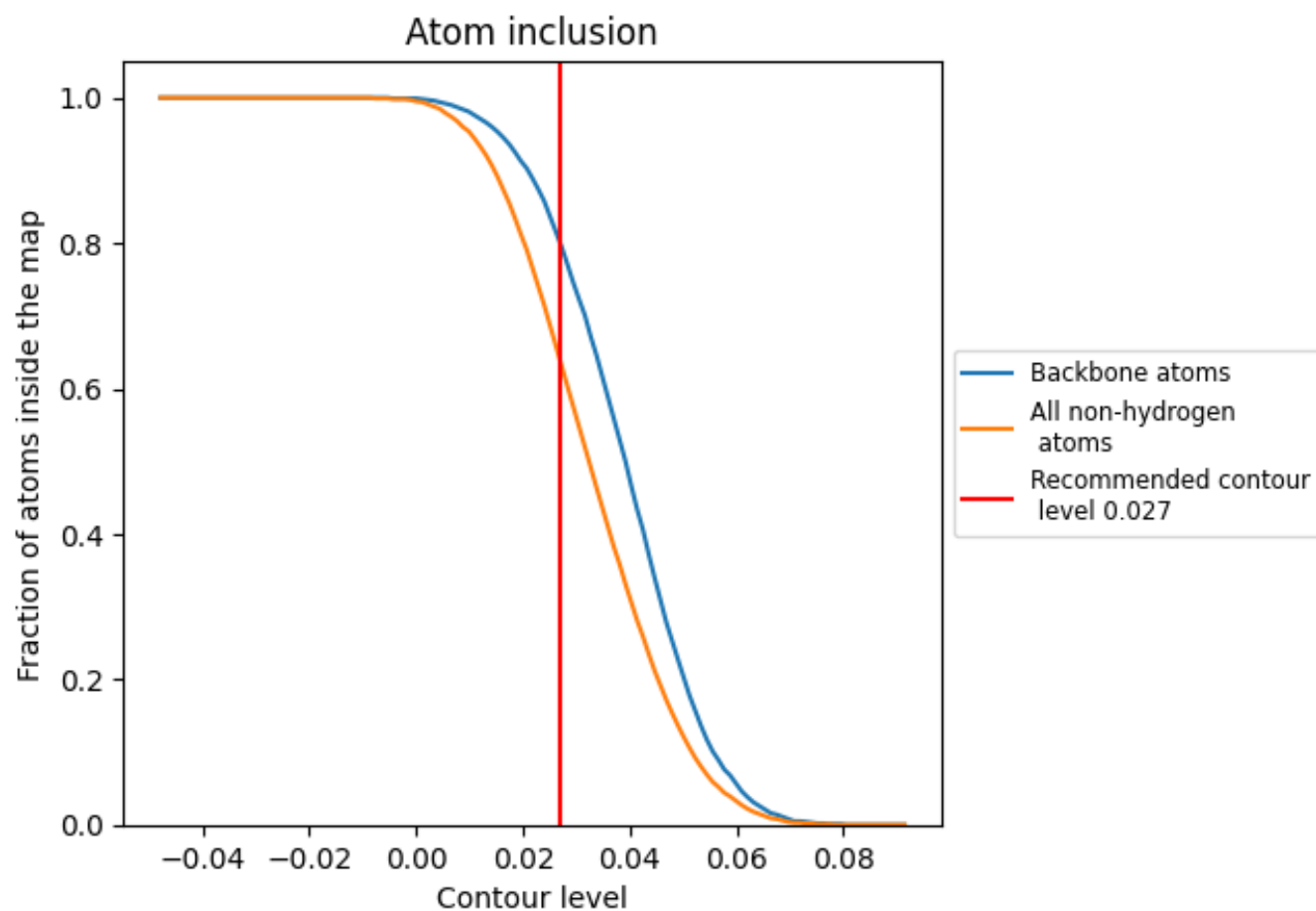
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.027).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 64% 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 (0.027) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6370	0.3600
A	0.7000	0.3960
B	0.1910	0.1040
C	0.2170	0.0960
D	0.1870	0.1180
E	0.2130	0.1110
F	0.6260	0.3970

1.0

0.0

<0.0