



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 12:29 AM UTC

PDB ID : 6F5O / pdb_00006f5o
EMDB ID : EMD-4190
Title : A mechanism for the activation of the influenza virus transcriptase
Authors : Serna Martin, I.; Grimes, J.M.
Deposited on : 2017-12-02
Resolution : 9.80 Å(reported)

This is a Full wwPDB EM Validation 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:

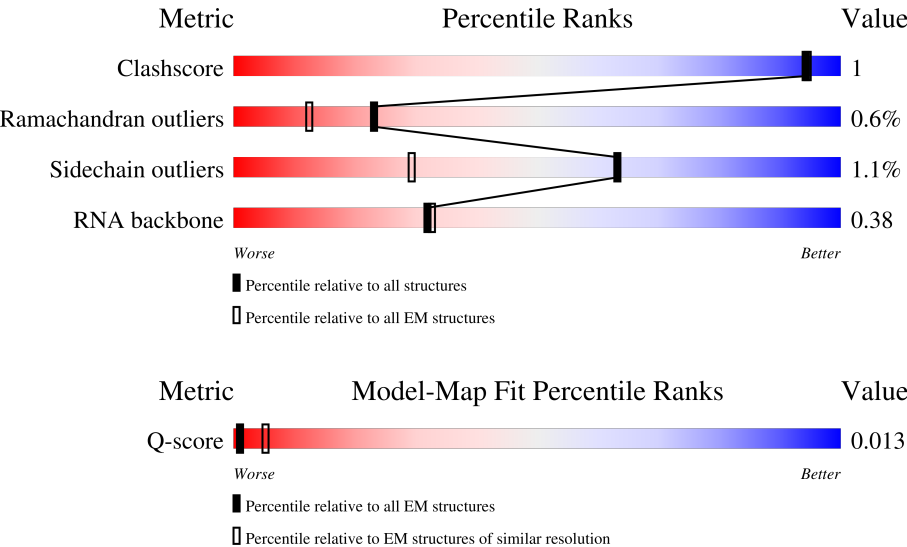
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 9.80 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	157 (9.30 - 10.30)

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	727	59% 94% • •
2	B	752	39% 95% • •
3	C	770	44% 88% 7% 5%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	R	14	
5	V	14	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 17940 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	A	716	Total	C	N	O	S	0	0
			5747	3651	962	1094	40		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP Q5V8Z9

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	733	Total	C	N	O	S	0	0
			5761	3636	999	1074	52		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	730	Total	C	N	O	S	0	0
			5843	3715	1023	1065	40		

- Molecule 4 is a RNA chain called 3' promoter vRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	R	14	Total	C	N	O	P	0	0
			282	128	42	99	13		

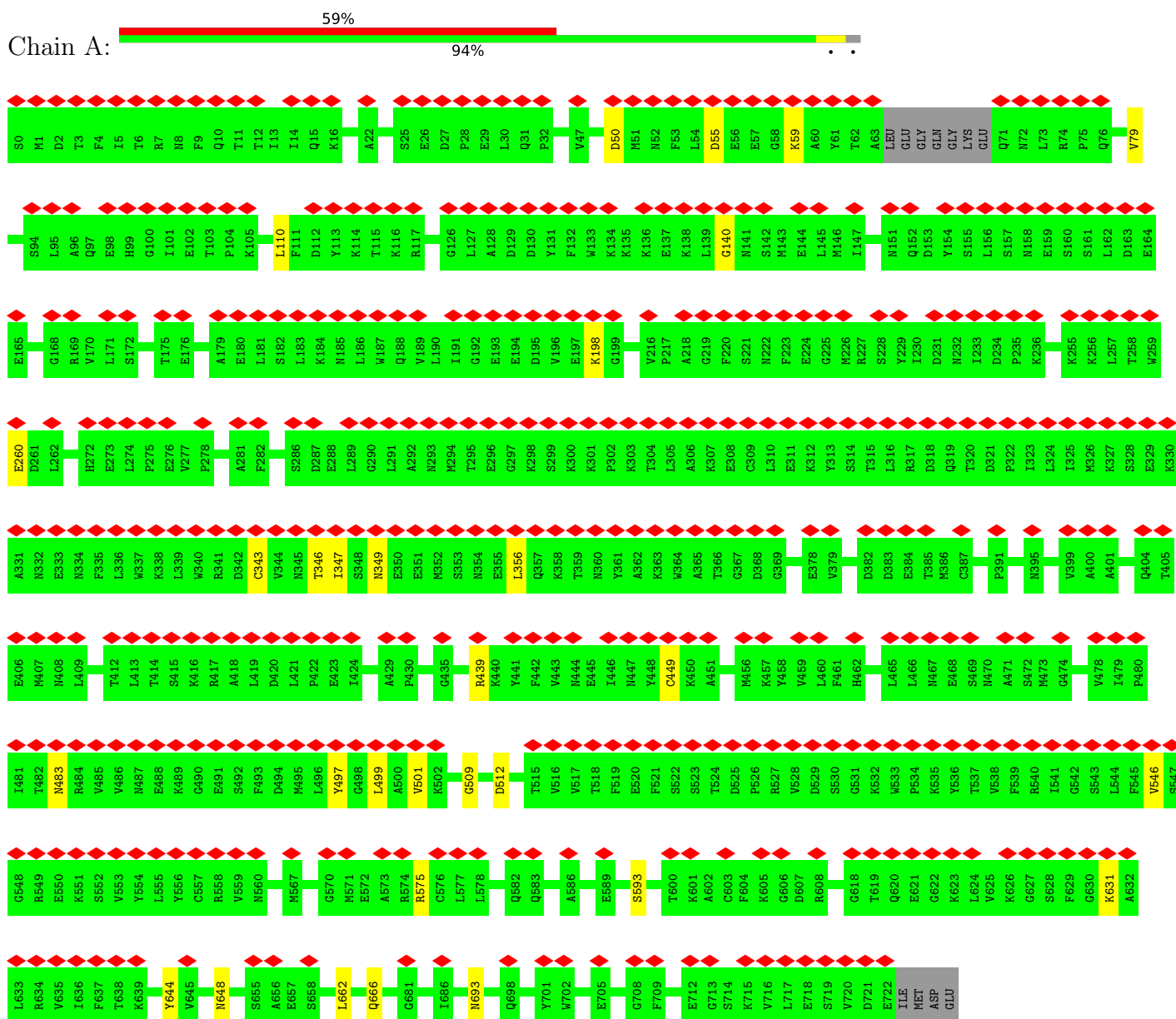
- Molecule 5 is a RNA chain called 5' promoter vRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	V	14	Total	C	N	O	P	0	0
			307	137	62	94	14		

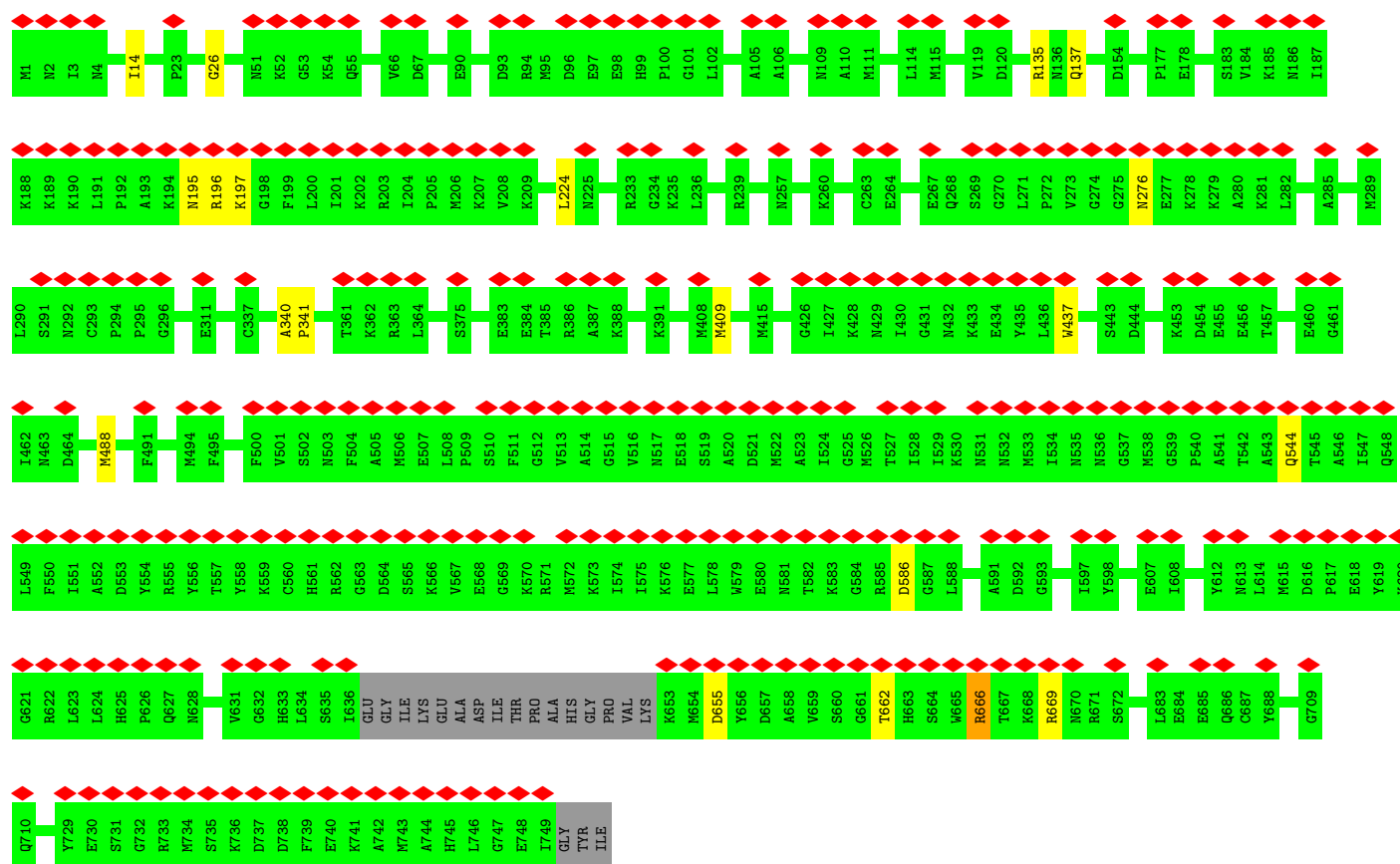
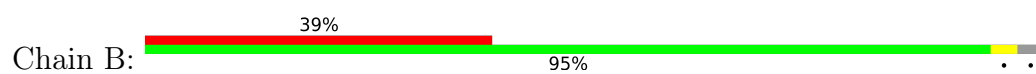
3 Residue-property plots [i](#)

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.

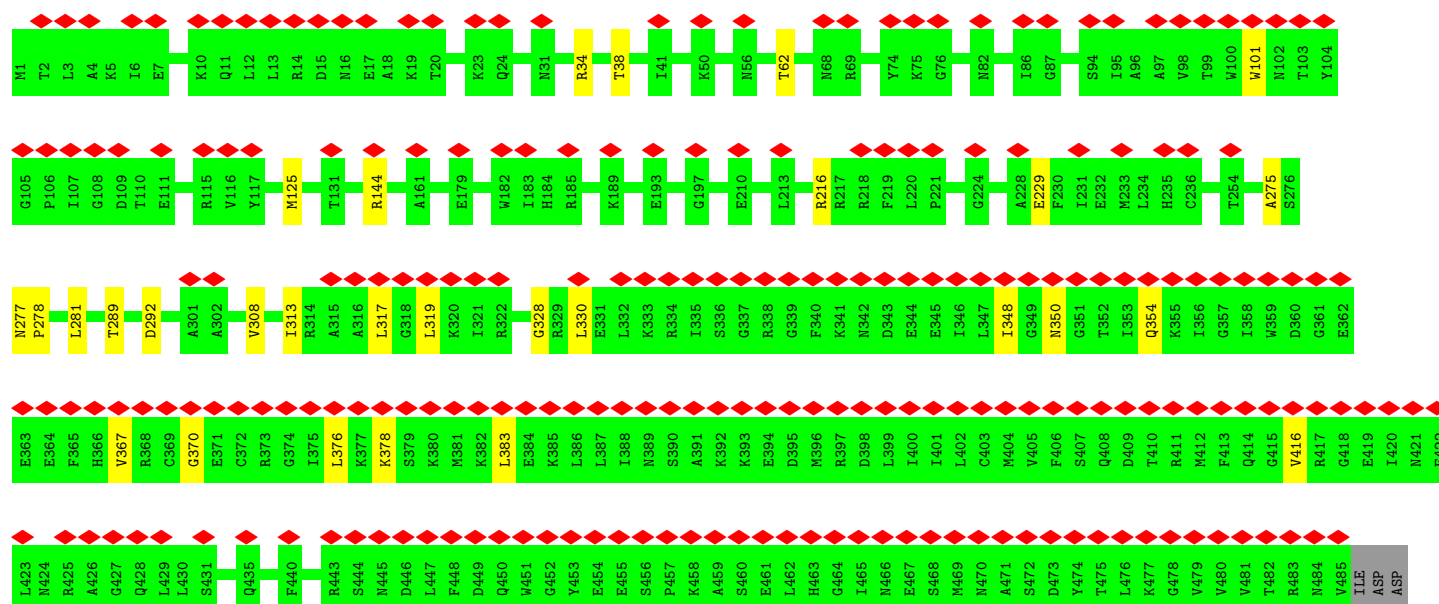
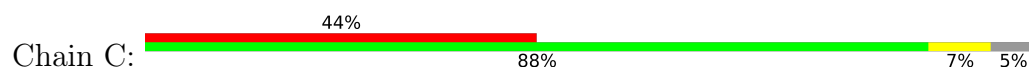
- Molecule 1: Polymerase acidic protein

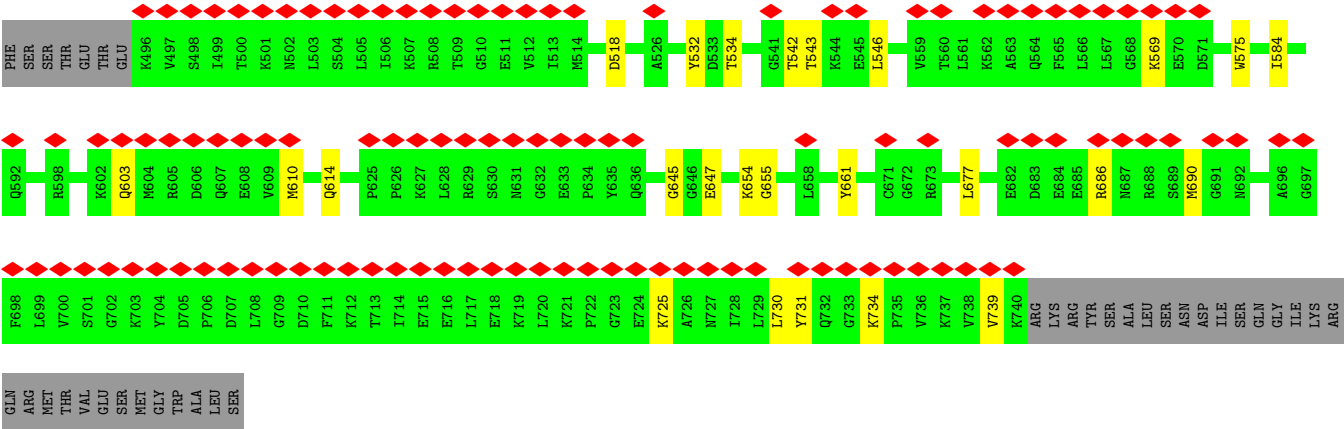


- Molecule 2: RNA-directed RNA polymerase catalytic subunit



• Molecule 3: Polymerase basic protein 2

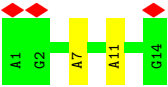
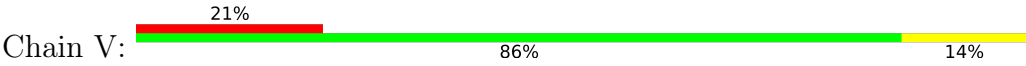




● Molecule 4: 3' promoter vRNA



● Molecule 5: 5' promoter vRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	9159	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.09	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	0.115	Depositor
Minimum map value	-0.077	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.0267	Depositor
Map size (Å)	216.0, 216.0, 216.0	wwPDB
Map dimensions	160, 160, 160	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.35, 1.35, 1.35	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	A	0.28	0/5862	0.64	0/7904
2	B	0.29	0/5873	0.65	0/7915
3	C	0.29	0/5943	0.65	0/7987
4	R	0.17	0/312	0.35	0/482
5	V	0.13	0/345	0.32	0/535
All	All	0.28	0/18335	0.63	0/24823

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	5747	0	5718	13	0
2	B	5761	0	5783	15	0
3	C	5843	0	6015	22	0
4	R	282	0	146	0	0
5	V	307	0	153	0	0
All	All	17940	0	17815	41	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 1.

All (41) 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:195:ASN:O	2:B:197:LYS:N	2.32	0.62
1:A:648:ASN:OD1	1:A:693:ASN:ND2	2.40	0.54
1:A:346:THR:O	1:A:349:ASN:ND2	2.40	0.54
1:A:509:GLY:N	1:A:512:ASP:OD2	2.42	0.52
1:A:666:GLN:HB2	2:B:14:ILE:HD12	1.93	0.51
3:C:330:LEU:HD11	3:C:367:VAL:CG1	2.41	0.51
2:B:669:ARG:NH1	3:C:38:THR:OG1	2.44	0.49
1:A:439:ARG:NH1	2:B:544:GLN:OE1	2.45	0.49
3:C:725:LYS:HG2	3:C:739:VAL:HG22	1.94	0.49
2:B:276:ASN:OD1	3:C:144:ARG:NH1	2.45	0.49
2:B:340:ALA:HB3	2:B:341:PRO:HD3	1.94	0.48
3:C:661:TYR:CE1	3:C:677:LEU:HD12	2.48	0.48
1:A:662:LEU:HB3	2:B:14:ILE:HD13	1.97	0.47
3:C:546:LEU:HB2	3:C:584:ILE:HD11	1.98	0.46
1:A:644:TYR:HA	2:B:26:GLY:HA2	1.99	0.45
3:C:367:VAL:HG21	3:C:376:LEU:HB2	1.99	0.44
3:C:543:THR:HG23	3:C:584:ILE:HG21	1.99	0.44
2:B:655:ASP:OD2	3:C:216:ARG:NH2	2.50	0.44
1:A:79:VAL:HA	1:A:110:LEU:HD23	2.00	0.43
3:C:313:ILE:HG22	3:C:317:LEU:HD12	2.01	0.43
2:B:437:TRP:C	2:B:437:TRP:CD1	2.97	0.43
1:A:55:ASP:OD1	1:A:59:LYS:N	2.47	0.42
2:B:224:LEU:HD13	2:B:409:MET:HG3	2.01	0.42
3:C:289:THR:HG22	3:C:532:TYR:CD1	2.55	0.42
3:C:614:GLN:HB2	3:C:690:MET:HE1	2.00	0.42
2:B:586:ASP:N	2:B:586:ASP:OD1	2.50	0.42
1:A:347:ILE:HD12	1:A:499:LEU:HD13	2.00	0.42
2:B:135:ARG:NH1	2:B:137:GLN:OE1	2.52	0.42
3:C:654:LYS:HG2	3:C:655:GLY:N	2.35	0.42
3:C:277:ASN:N	3:C:278:PRO:HD3	2.35	0.41
3:C:350:ASN:HB3	3:C:416:VAL:HG12	2.02	0.41
2:B:666:ARG:NH2	3:C:62:THR:OG1	2.53	0.41
1:A:483:ASN:HB3	1:A:497:TYR:HE1	1.85	0.41
1:A:347:ILE:CD1	1:A:499:LEU:HD22	2.51	0.41
3:C:348:ILE:HD12	3:C:354:GLN:HG3	2.02	0.40
3:C:546:LEU:CB	3:C:584:ILE:HD11	2.51	0.40
2:B:662:THR:HG21	3:C:101:TRP:CD1	2.56	0.40
3:C:275:ALA:HB3	3:C:281:LEU:HD12	2.04	0.40
1:A:343:CYS:SG	1:A:501:VAL:HG22	2.61	0.40
3:C:532:TYR:O	3:C:534:THR:N	2.48	0.40
3:C:731:TYR:CE2	3:C:734:LYS:HG3	2.57	0.40

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	710/727 (98%)	666 (94%)	41 (6%)	3 (0%)	30	67
2	B	729/752 (97%)	689 (94%)	39 (5%)	1 (0%)	48	83
3	C	726/770 (94%)	676 (93%)	42 (6%)	8 (1%)	11	46
All	All	2165/2249 (96%)	2031 (94%)	122 (6%)	12 (1%)	23	59

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	196	ARG
3	C	292	ASP
3	C	569	LYS
3	C	730	LEU
1	A	50	ASP
3	C	308	VAL
1	A	140	GLY
1	A	546	VAL
3	C	686	ARG
3	C	645	GLY
3	C	328	GLY
3	C	370	GLY

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	637/646 (99%)	630 (99%)	7 (1%)	65	76
2	B	631/645 (98%)	629 (100%)	2 (0%)	86	86
3	C	638/674 (95%)	626 (98%)	12 (2%)	50	67
All	All	1906/1965 (97%)	1885 (99%)	21 (1%)	63	76

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	198	LYS
1	A	260	GLU
1	A	356	LEU
1	A	449	CYS
1	A	575	ARG
1	A	593	SER
1	A	631	LYS
2	B	488	MET
2	B	666	ARG
3	C	34	ARG
3	C	125	MET
3	C	229	GLU
3	C	319	LEU
3	C	378	LYS
3	C	383	LEU
3	C	518	ASP
3	C	542	THR
3	C	575	TRP
3	C	603	GLN
3	C	610	MET
3	C	647	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	GLN
1	A	188	GLN
1	A	268	HIS
1	A	566	GLN
1	A	610	ASN

Continued on next page...

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Mol	Chain	Res	Type
1	A	643	HIS
1	A	666	GLN
2	B	710	GLN
3	C	389	ASN
3	C	414	GLN
3	C	442	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	R	13/14 (92%)	4 (30%)	1 (7%)
5	V	13/14 (92%)	2 (15%)	0
All	All	26/28 (92%)	6 (23%)	1 (3%)

All (6) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	R	4	A
4	R	5	C
4	R	6	C
4	R	14	C
5	V	7	A
5	V	11	A

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	R	1	U

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 ⓘ

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	164:GLU	C	165:GLU	N	3.00

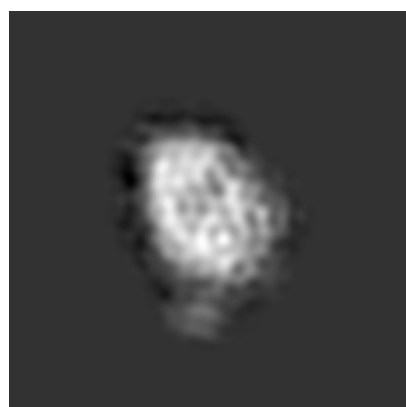
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4190. 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

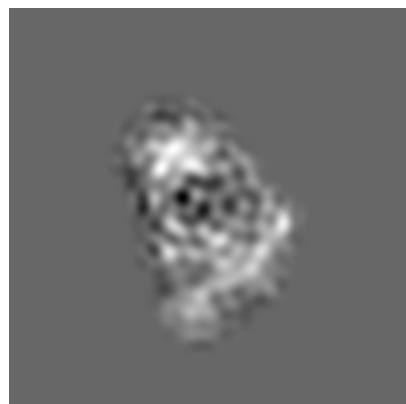


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 80



Y Index: 80



Z Index: 80

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: 102



Y Index: 77

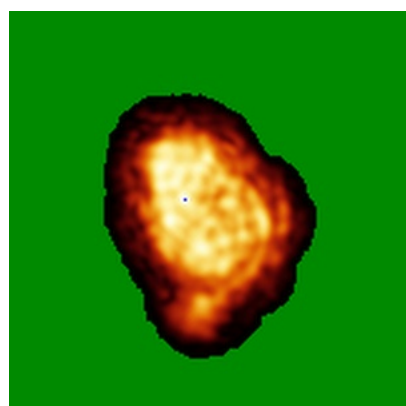


Z Index: 76

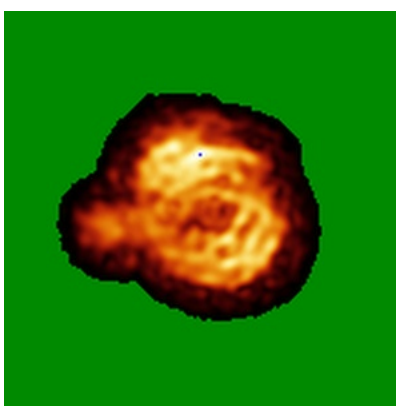
The images above show the largest variance slices of the map in three orthogonal directions.

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

This section was not generated.

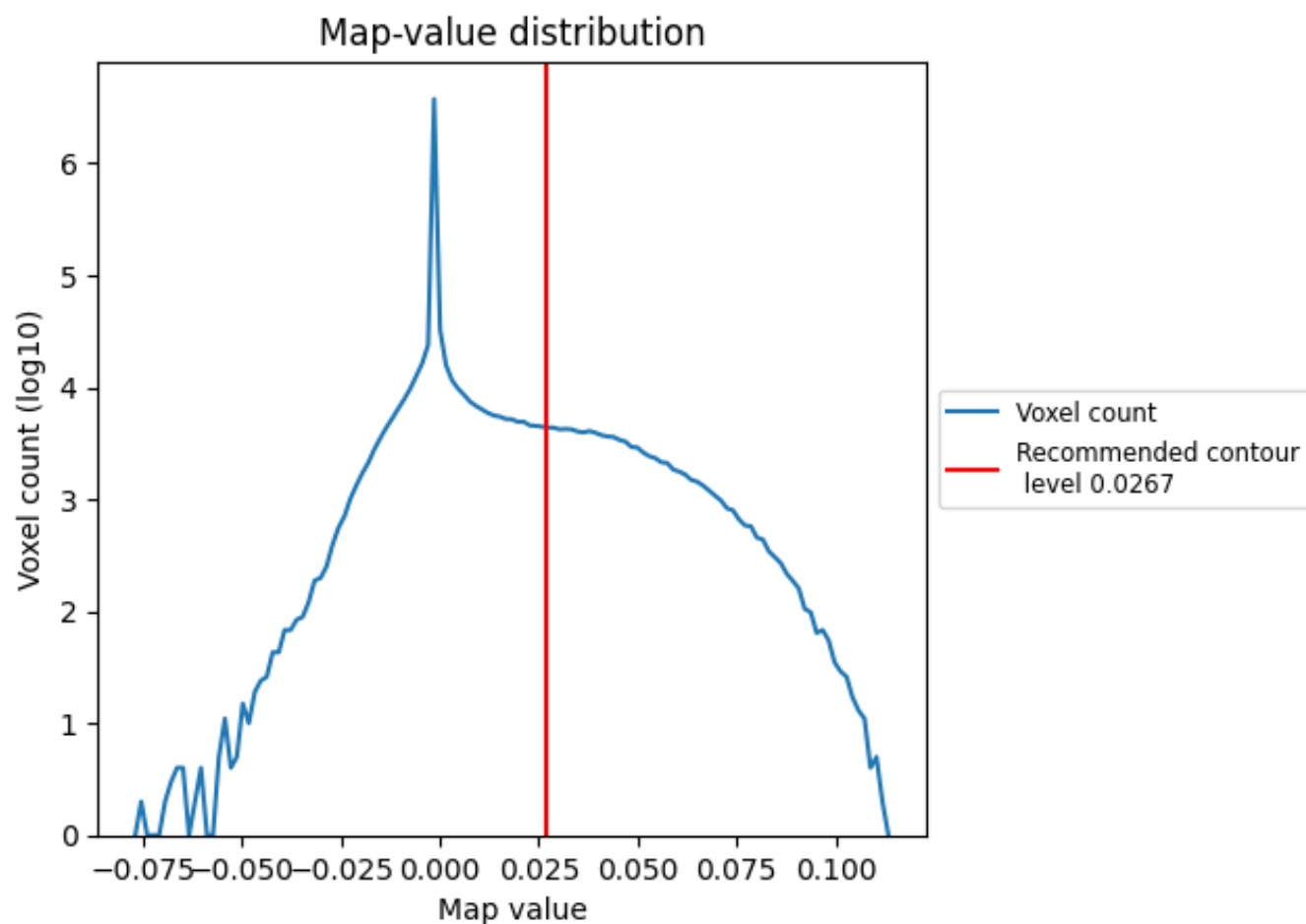
6.6 Mask visualisation

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

7 Map analysis [i](#)

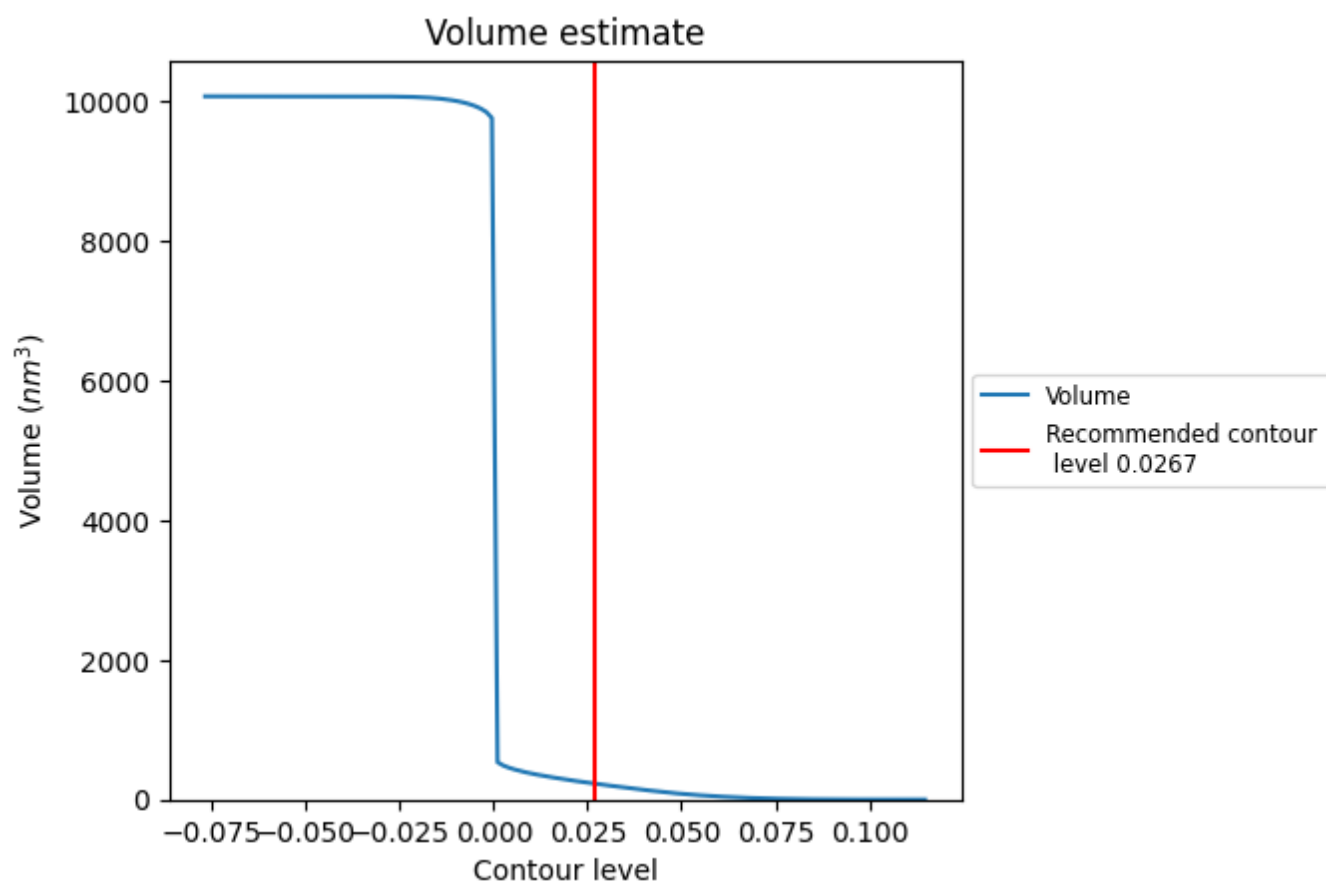
This section contains the results of statistical analysis of the map.

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.

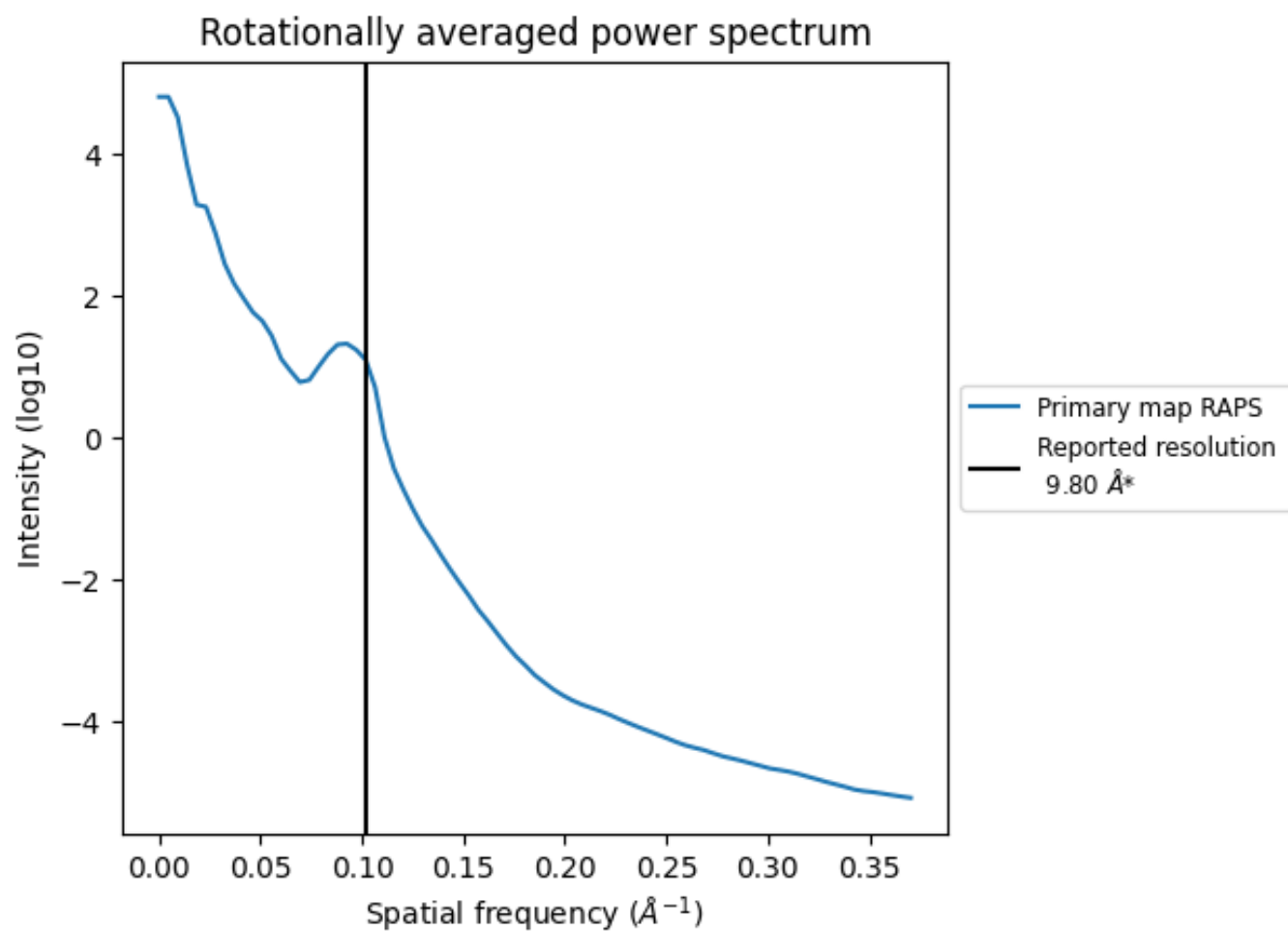
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 230 nm³; this corresponds to an approximate mass of 208 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 ⓘ

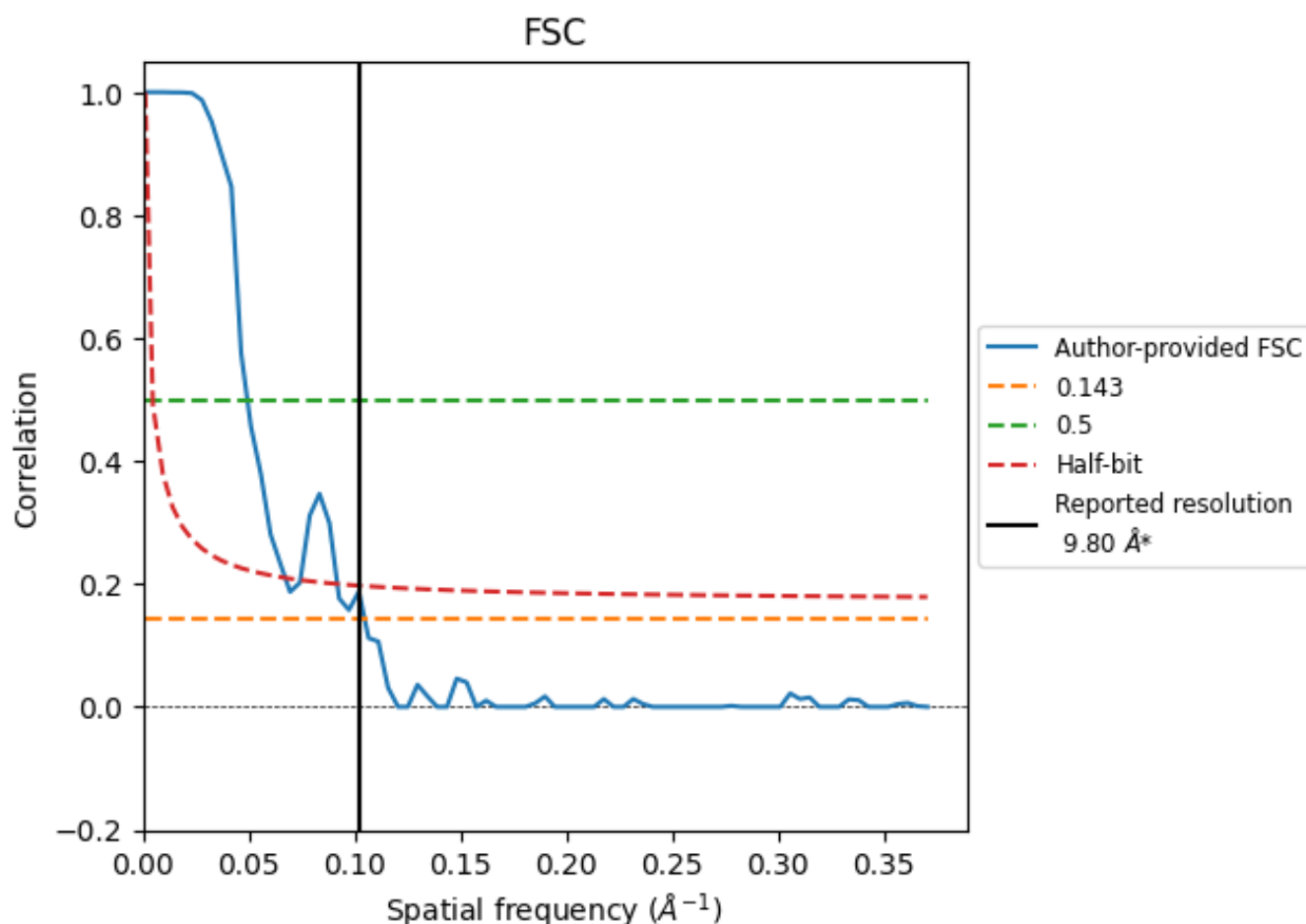


*Reported resolution corresponds to spatial frequency of 0.102 Å⁻¹

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 0.102 Å⁻¹

8.2 Resolution estimates [i](#)

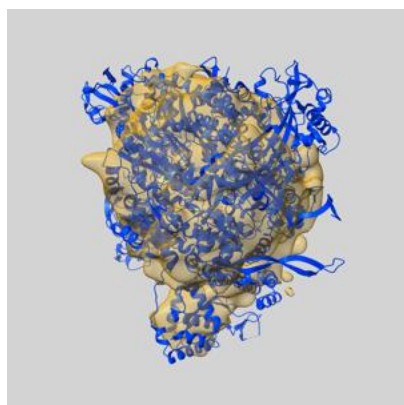
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.80	-	-
Author-provided FSC curve	9.56	20.33	14.90
Unmasked-calculated*	-	-	-

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

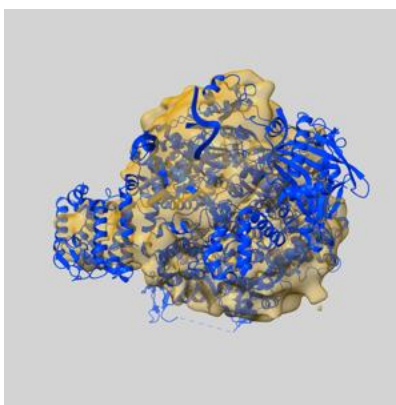
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4190 and PDB model 6F5O. Per-residue inclusion information can be found in section [3](#) on page [5](#).

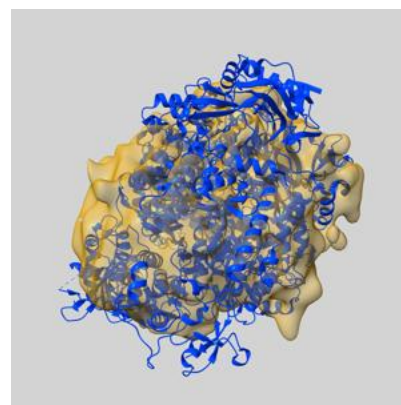
9.1 Map-model overlay [i](#)



X



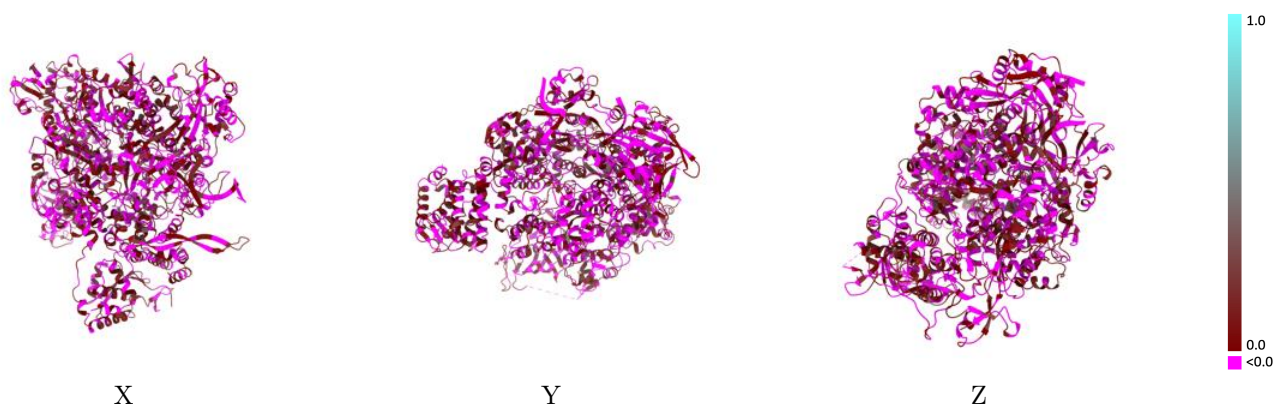
Y



Z

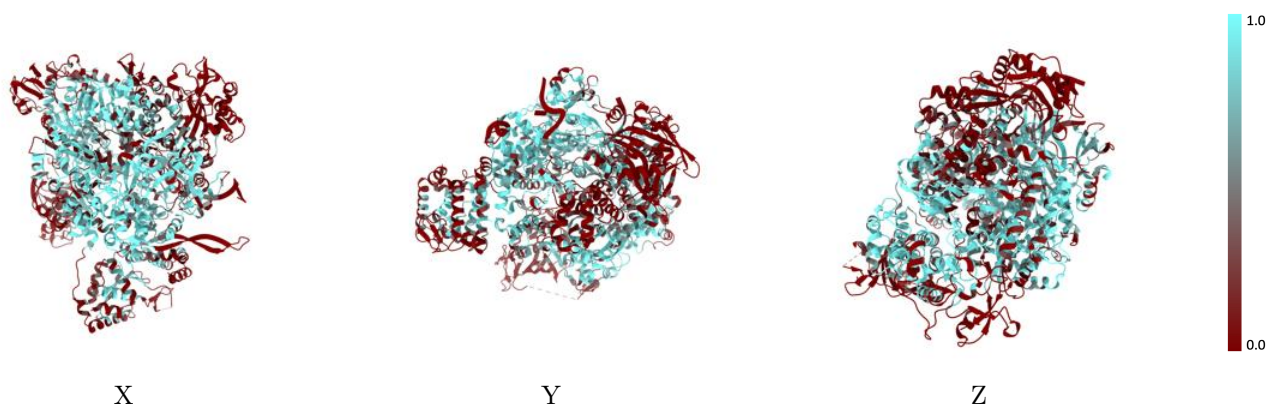
The images above show the 3D surface view of the map at the recommended contour level 0.0267 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



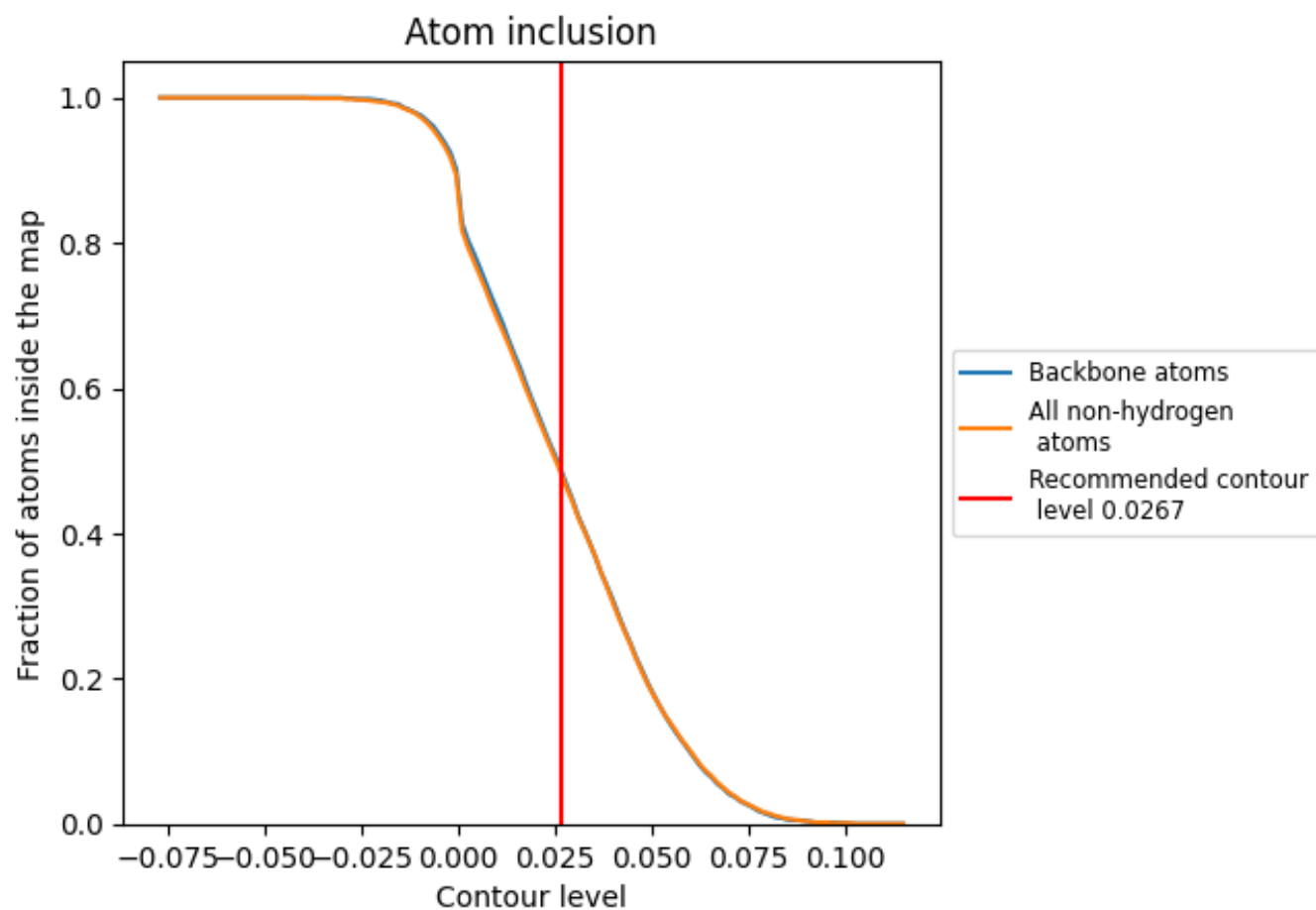
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0267).

9.4 Atom inclusion [i](#)



At the recommended contour level, 48% of all backbone atoms, 48% 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 (0.0267) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4810	0.0130
A	0.3750	0.0120
B	0.5640	0.0110
C	0.4930	0.0130
R	0.4040	0.0060
V	0.7560	0.0600

