



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 07:55 AM UTC

PDB ID : 7VWY / pdb_00007vwy
EMDB ID : EMD-32165
Title : Cryo-EM structure of Rob-dependent transcription activation complex in a unique conformation
Authors : Lin, W.; Feng, Y.
Deposited on : 2021-11-12
Resolution : 4.57 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:

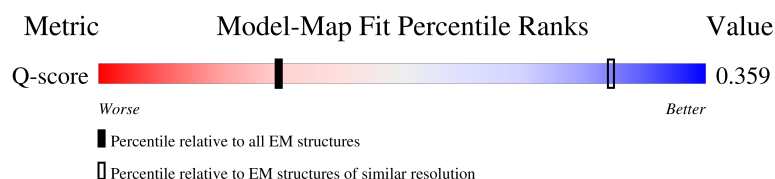
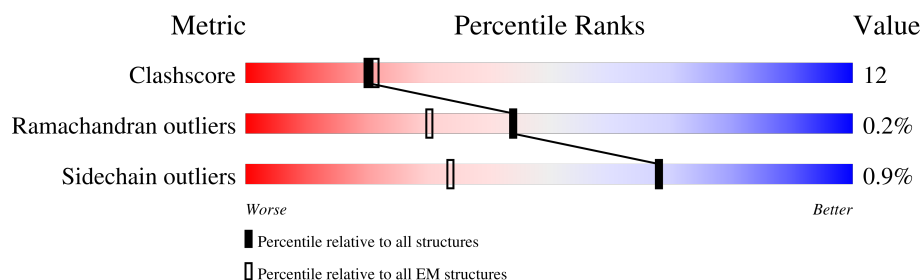
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.57 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.



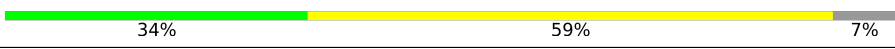
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2418 (4.07 - 5.07)

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	329	 74% 20% • 5%
1	B	329	 52% 17% 31%
2	C	1342	 79% 21%
3	D	1407	 71% 23% • 5%

Continued on next page...

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Mol	Chain	Length	Quality of chain
4	E	91	 74% 13% 13%
5	F	613	 58% 20% 21%
6	1	70	 34% 59% 7%
7	2	70	 47% 43% 9%
8	G	289	 71% 27% 2%

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 34628 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 DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	311	Total	C	N	O	S	0	0
			2418	1512	425	473	8		
1	B	228	Total	C	N	O	S	0	0
			1767	1100	312	349	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	1340	Total	C	N	O	S	0	0
			10557	6626	1835	2053	43		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	516	VAL	ASP	engineered mutation	UNP P0A8V2

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	1337	Total	C	N	O	S	0	0
			10391	6528	1853	1960	50		

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	79	Total	C	N	O	S	0	0
			627	382	118	126	1		

- Molecule 5 is a protein called RNA polymerase sigma factor RpoD.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	483	Total	C	N	O	S	0	0
			3913	2448	697	745	23		

- Molecule 6 is a DNA chain called micF promoter DNA scaffold forward strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1	65	Total	C	N	O	P	0	0
			1330	634	254	378	64		

- Molecule 7 is a DNA chain called micF promoter DNA scaffold reverse strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	2	64	Total	C	N	O	P	0	0
			1324	631	236	393	64		

- Molecule 8 is a protein called Right origin-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	283	Total	C	N	O	S	0	0
			2298	1469	402	417	10		

- Molecule 9 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
9	D	2	Total	Zn	0
			2	2	

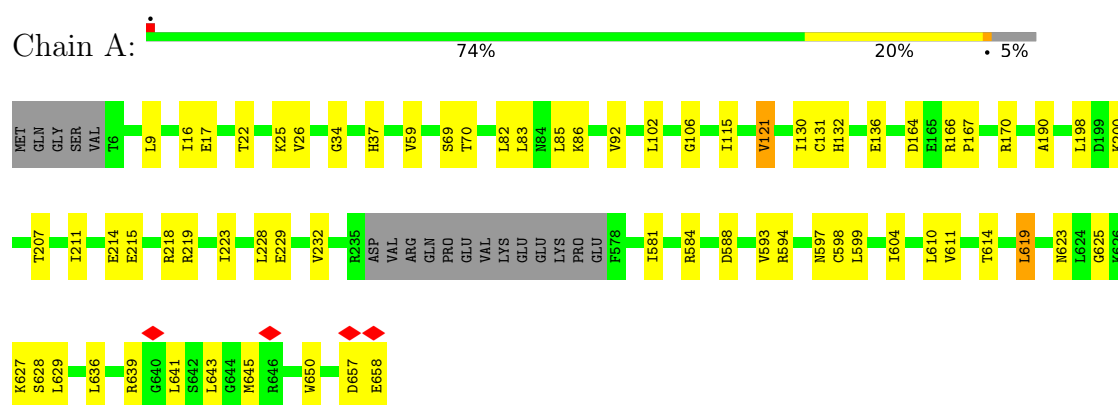
- Molecule 10 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
10	D	1	Total	Mg	0
			1	1	

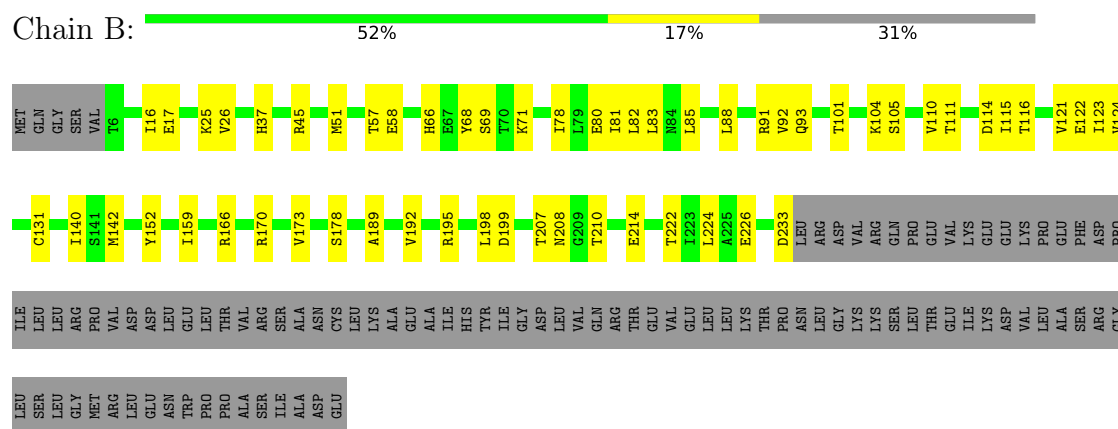
3 Residue-property plots

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.

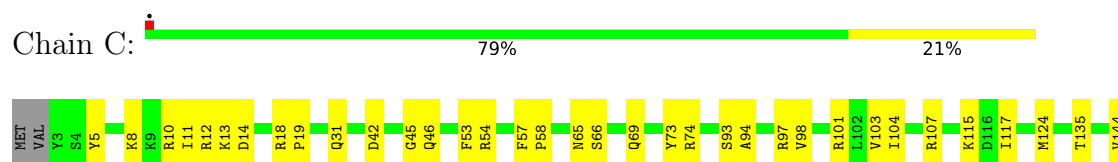
• Molecule 1: DNA-directed RNA polymerase subunit alpha

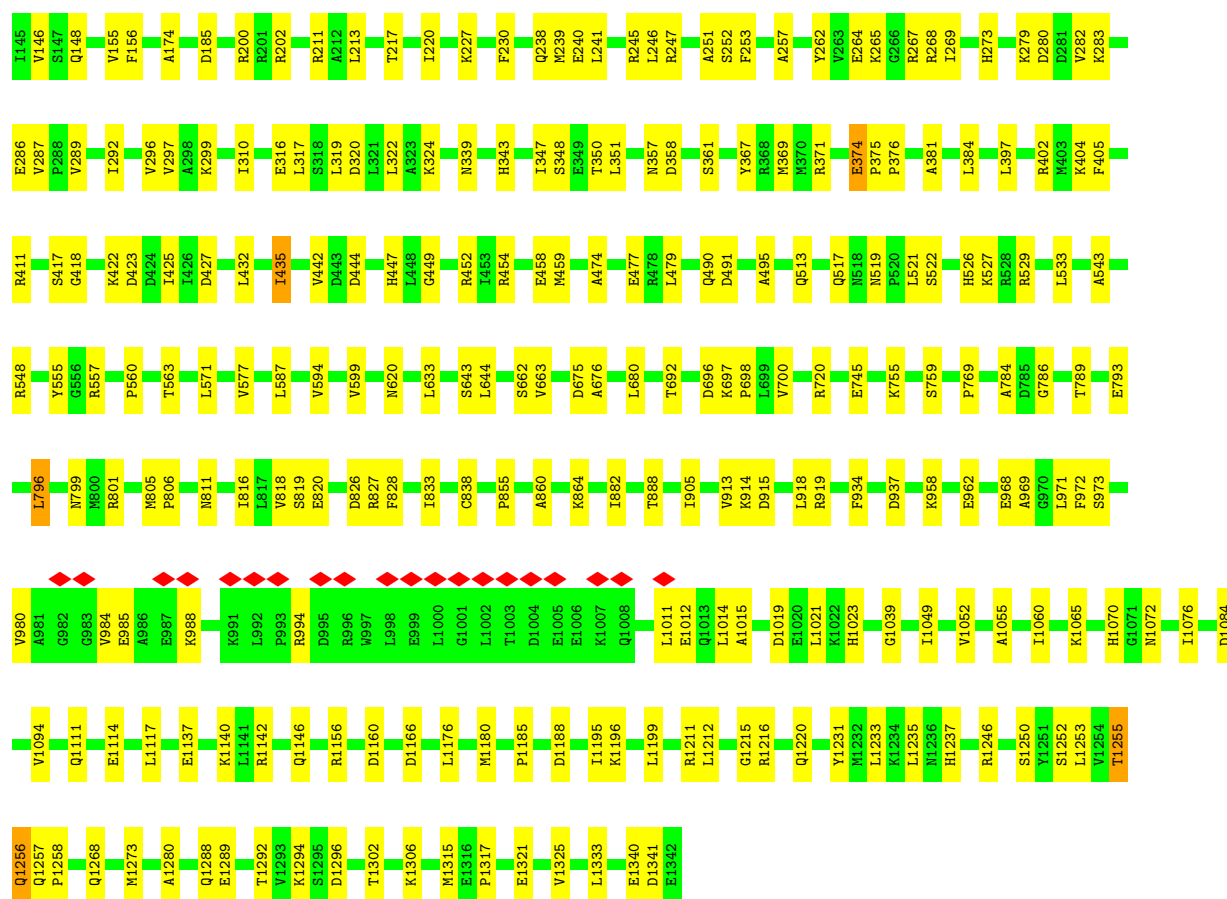


• Molecule 1: DNA-directed RNA polymerase subunit alpha



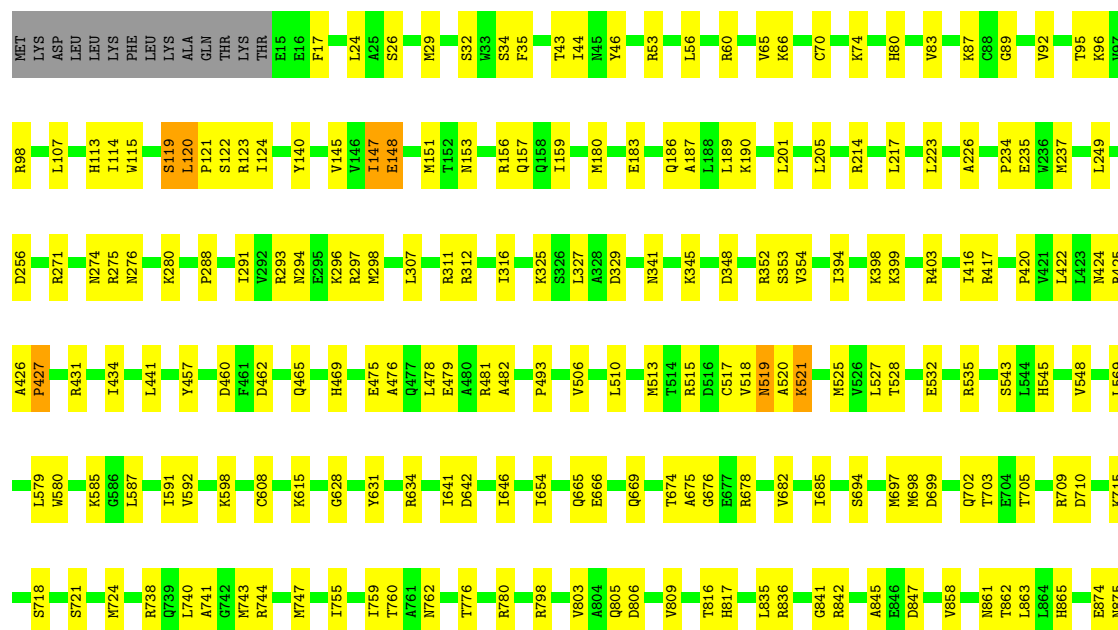
• Molecule 2: DNA-directed RNA polymerase subunit beta

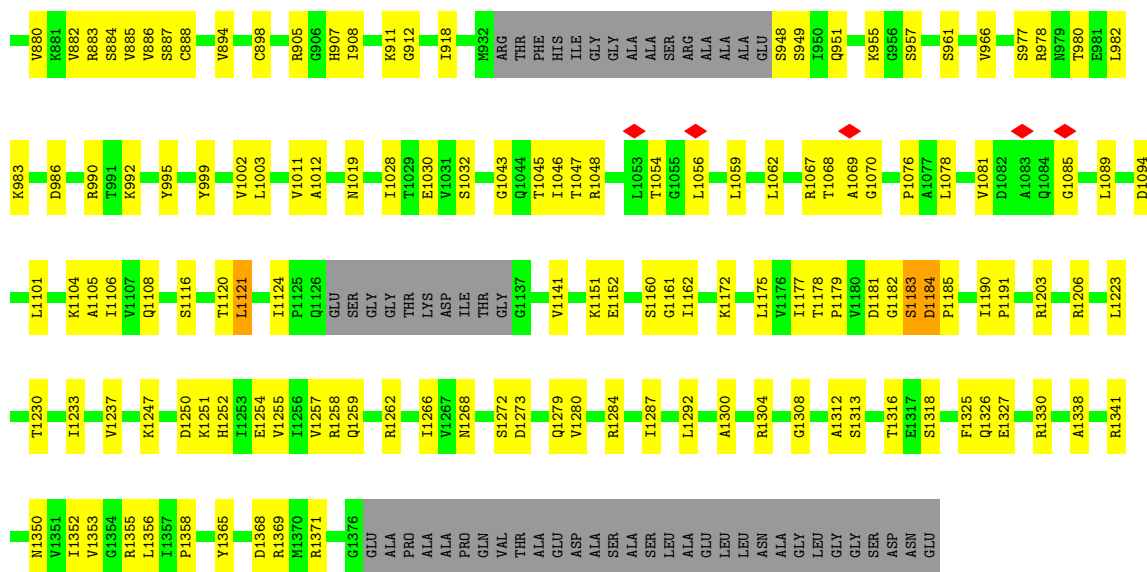




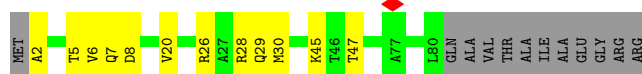
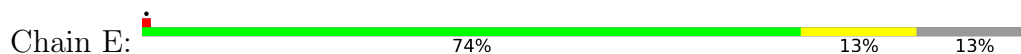
• Molecule 3: DNA-directed RNA polymerase subunit beta'

Chain D: 71% 23% 5%

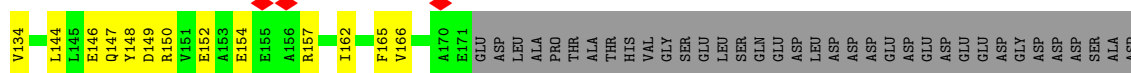
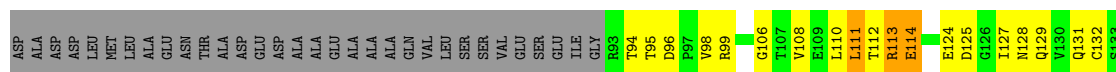
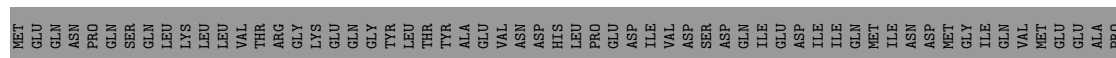




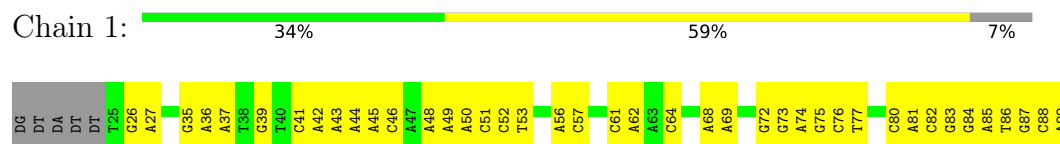
- Molecule 4: DNA-directed RNA polymerase subunit omega



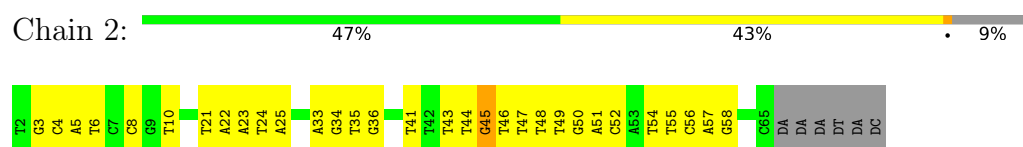
- Molecule 5: RNA polymerase sigma factor RpoD



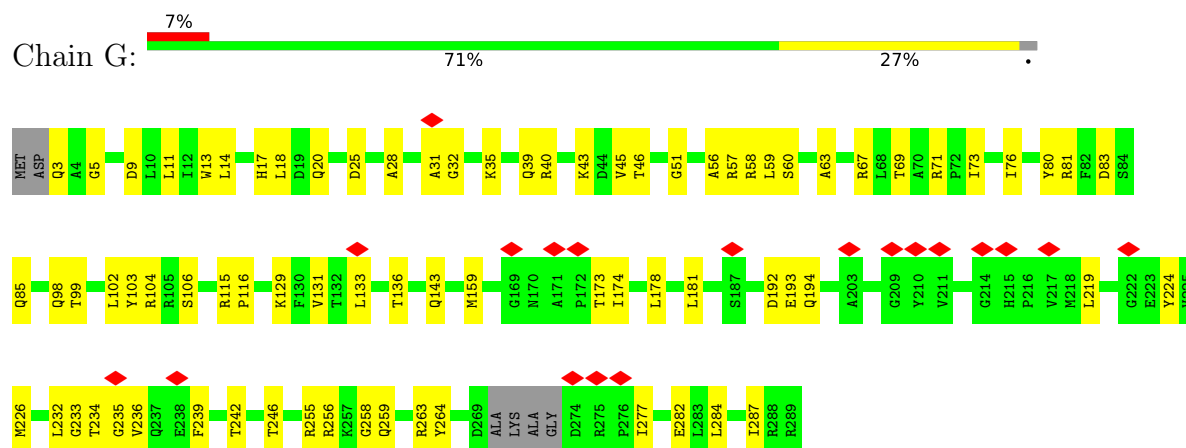
- Molecule 6: micF promoter DNA scaffold forward strand



- Molecule 7: micF promoter DNA scaffold reverse strand



- Molecule 8: Right origin-binding protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	89382	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 ($e^-/\text{\AA}^2$)	50	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	0.097	Depositor
Minimum map value	-0.029	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.015	Depositor
Map size ($\text{\AA}$)	256.172, 256.172, 256.172	wwPDB
Map dimensions	196, 196, 196	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.307, 1.307, 1.307	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, 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	0.26	0/2449	0.55	0/3318
1	B	0.23	0/1789	0.55	1/2425 (0.0%)
2	C	0.29	0/10726	0.54	0/14474
3	D	0.28	0/10547	0.59	2/14239 (0.0%)
4	E	0.22	0/629	0.51	0/847
5	F	0.25	0/3967	0.60	1/5336 (0.0%)
6	1	0.33	0/1495	0.48	0/2304
7	2	0.36	0/1484	0.52	1/2293 (0.0%)
8	G	0.25	0/2356	0.58	0/3194
All	All	0.28	0/35442	0.56	5/48430 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	124	ILE	N-CA-C	-8.44	105.26	113.53
1	B	192	VAL	N-CA-C	-7.37	102.01	110.05
5	F	602	SER	N-CA-C	-6.04	107.74	114.62
7	2	45	DG	C5'-C4'-O4'	-5.42	101.26	109.40
3	D	519	ASN	N-CA-C	5.08	116.81	111.28

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	2418	0	2467	44	0
1	B	1767	0	1789	39	0
2	C	10557	0	10565	190	0
3	D	10391	0	10605	254	0
4	E	627	0	634	12	0
5	F	3913	0	3964	113	0
6	1	1330	0	730	106	0
7	2	1324	0	727	119	0
8	G	2298	0	2265	49	0
9	D	2	0	0	0	0
10	D	1	0	0	0	0
All	All	34628	0	33746	826	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 12.

The worst 5 of 826 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)
6:1:50:DA:H2''	6:1:51:DC:C6	1.62	1.35
3:D:518:VAL:CG2	3:D:709:ARG:HG2	1.61	1.29
3:D:858:VAL:HG11	3:D:862:THR:CG2	1.65	1.25
3:D:858:VAL:CG1	3:D:862:THR:HG22	1.68	1.22
6:1:36:DA:C6	6:1:37:DA:C2	2.27	1.20

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	307/329 (93%)	277 (90%)	30 (10%)	0	100	100
1	B	226/329 (69%)	206 (91%)	20 (9%)	0	100	100
2	C	1338/1342 (100%)	1240 (93%)	97 (7%)	1 (0%)	48	83
3	D	1331/1407 (95%)	1216 (91%)	113 (8%)	2 (0%)	43	77
4	E	77/91 (85%)	74 (96%)	3 (4%)	0	100	100
5	F	479/613 (78%)	436 (91%)	39 (8%)	4 (1%)	16	53
8	G	279/289 (96%)	263 (94%)	16 (6%)	0	100	100
All	All	4037/4400 (92%)	3712 (92%)	318 (8%)	7 (0%)	44	77

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	F	507	MET
2	C	1258	PRO
5	F	114	GLU
5	F	264	LYS
3	D	1184	ASP

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	269/286 (94%)	266 (99%)	3 (1%)	65	74
1	B	196/286 (68%)	196 (100%)	0	100	100
2	C	1153/1157 (100%)	1146 (99%)	7 (1%)	78	80
3	D	1118/1168 (96%)	1106 (99%)	12 (1%)	65	74
4	E	67/75 (89%)	67 (100%)	0	100	100
5	F	426/540 (79%)	420 (99%)	6 (1%)	59	71
8	G	244/247 (99%)	242 (99%)	2 (1%)	73	77
All	All	3473/3759 (92%)	3443 (99%)	30 (1%)	68	76

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	148	GLU
5	F	333	VAL
3	D	642	ASP
8	G	131	VAL
5	F	113	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
3	D	865	HIS
5	F	227	GLN
3	D	1049	GLN
3	D	1350	ASN
5	F	406	GLN

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 3 ligands modelled in this entry, 3 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 [i](#)

There are no chain breaks in this entry.

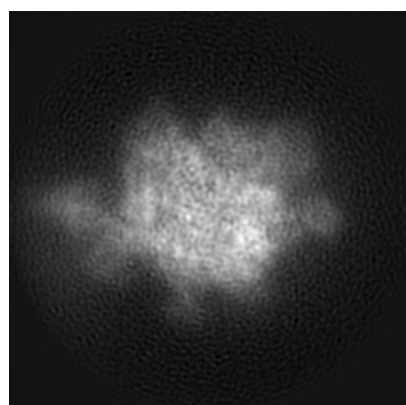
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32165. These allow visual inspection of the internal detail of the map and identification of artifacts.

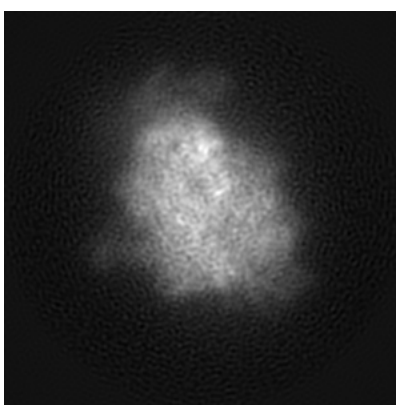
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

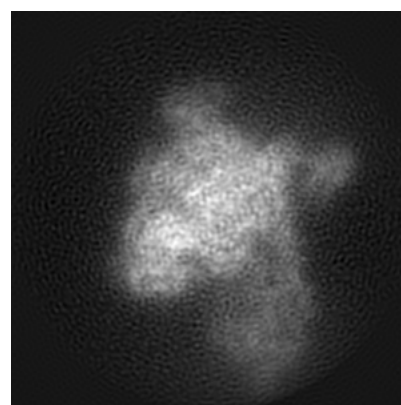
6.1.1 Primary map



X



Y

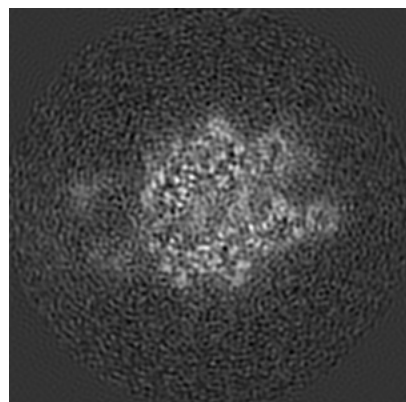


Z

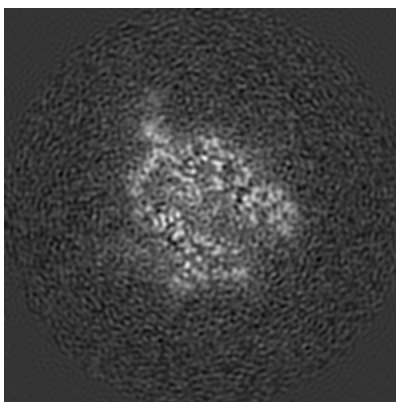
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

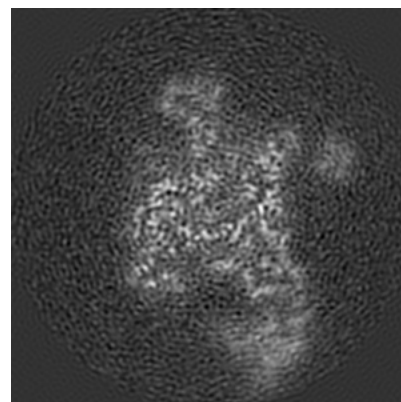
6.2.1 Primary map



X Index: 98



Y Index: 98

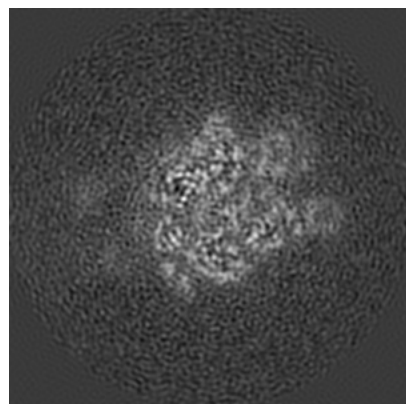


Z Index: 98

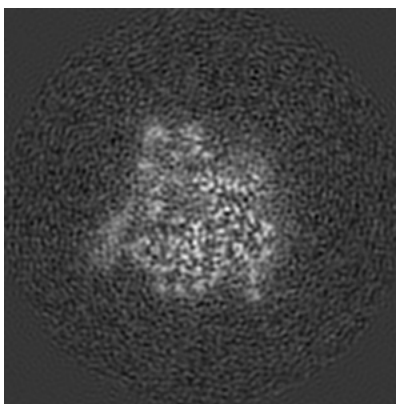
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

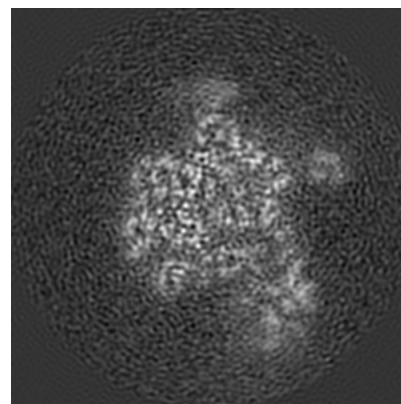
6.3.1 Primary map



X Index: 96



Y Index: 88

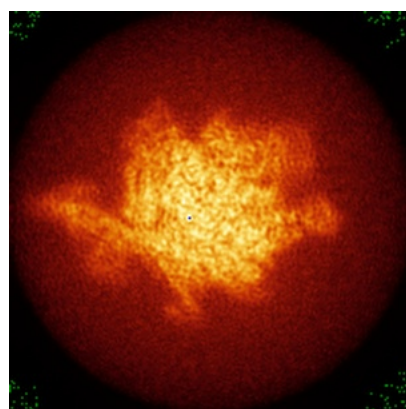


Z Index: 87

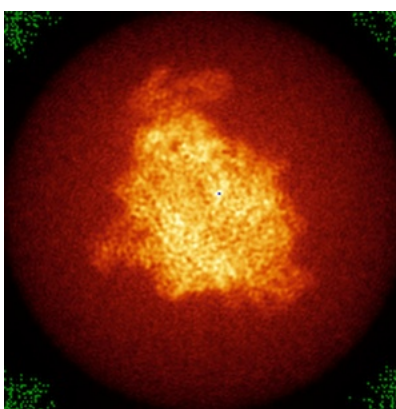
The images above show the largest variance slices of the map in three orthogonal directions.

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

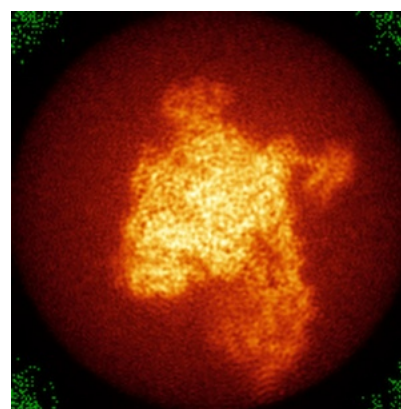
6.4.1 Primary map



X



Y

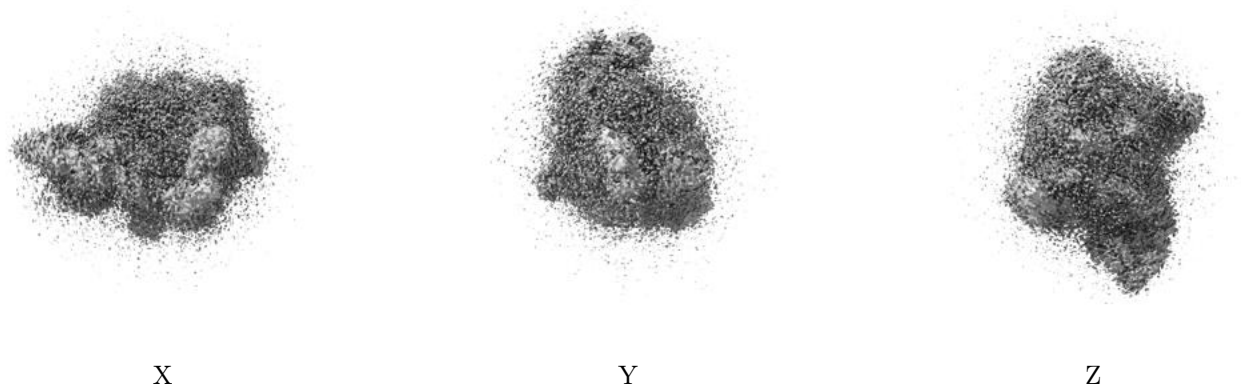


Z

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

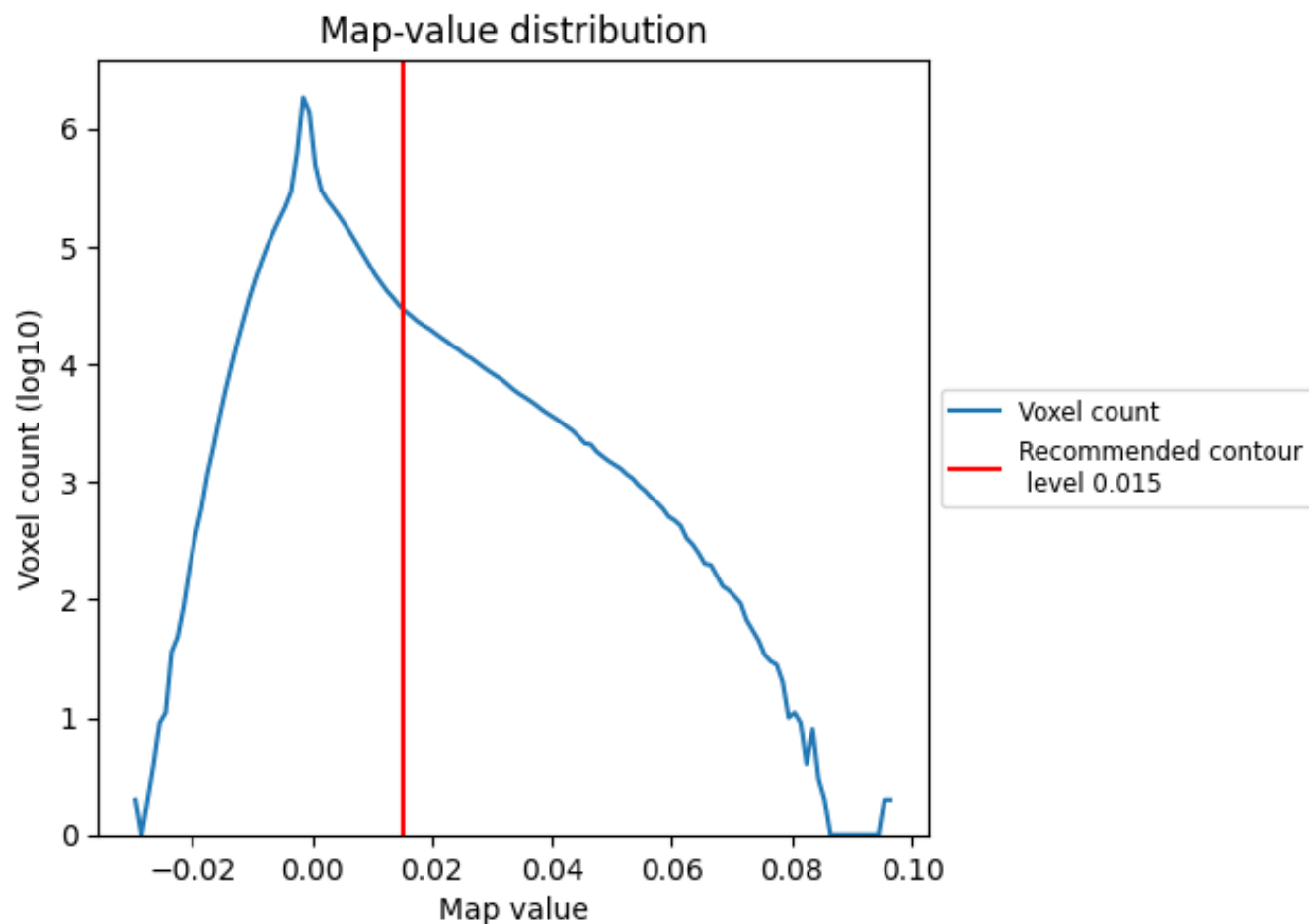
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

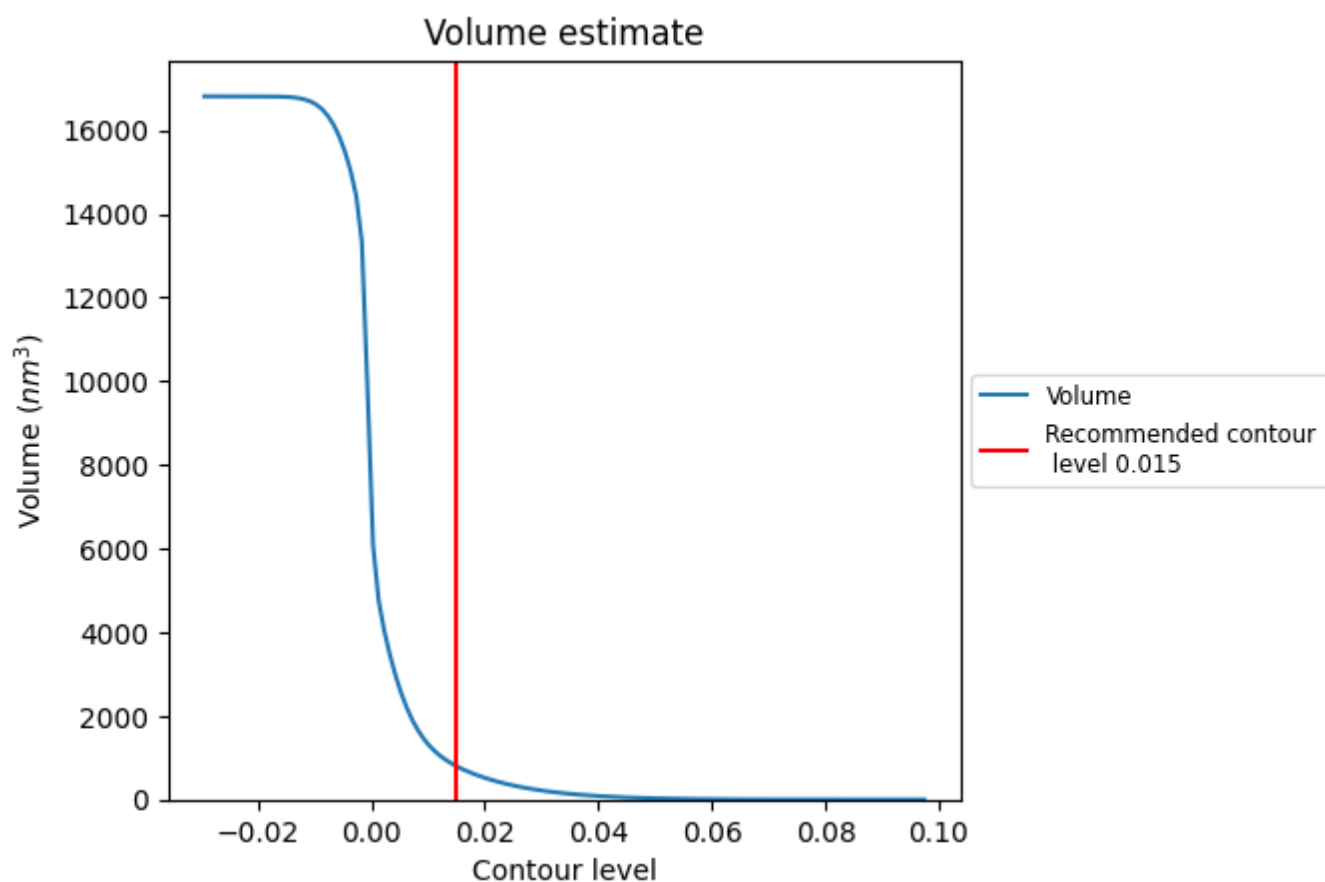
This section contains the results of statistical analysis of the map.

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.

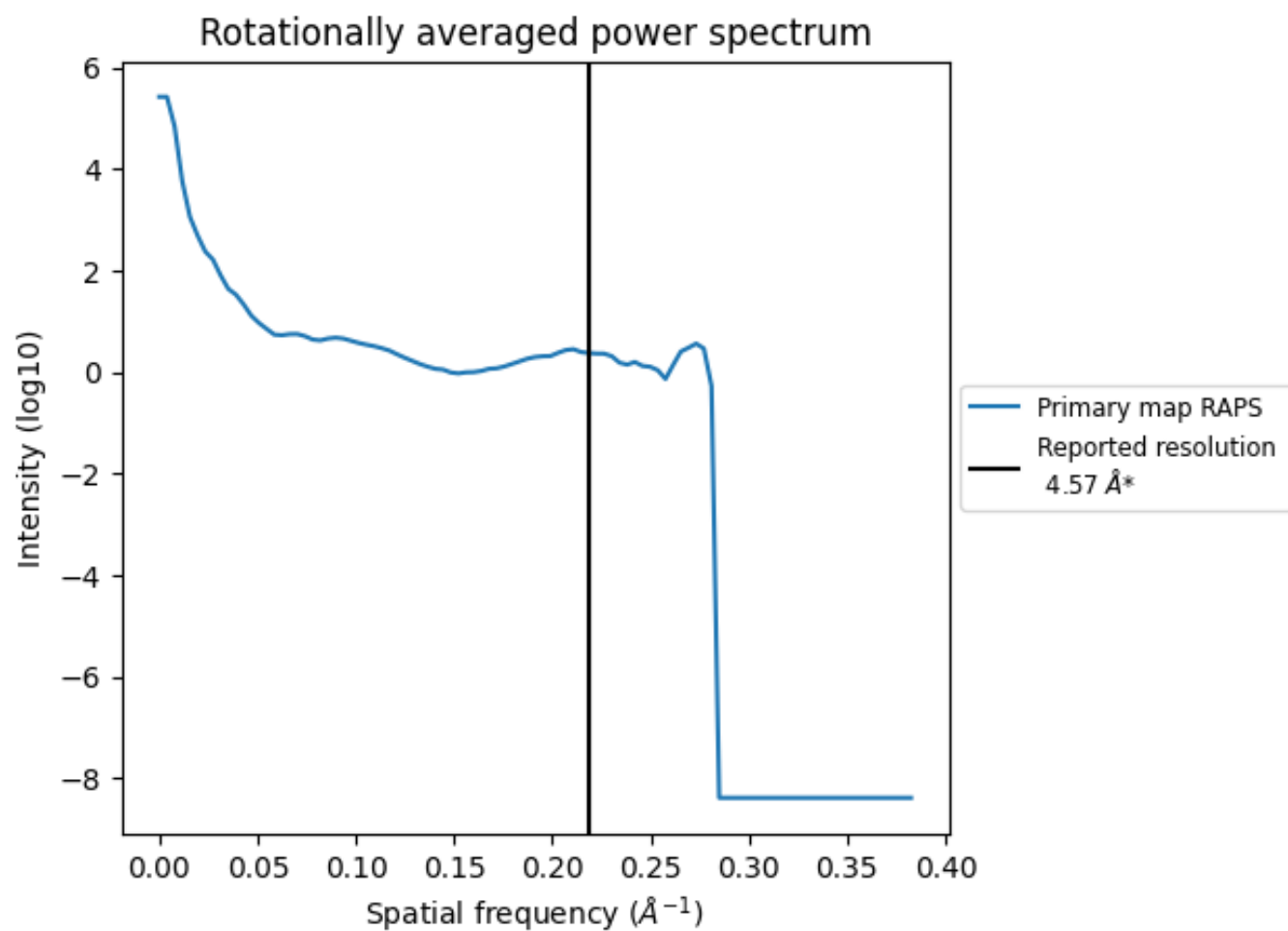
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 798 nm^3 ; this corresponds to an approximate mass of 721 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 0.219 Å⁻¹

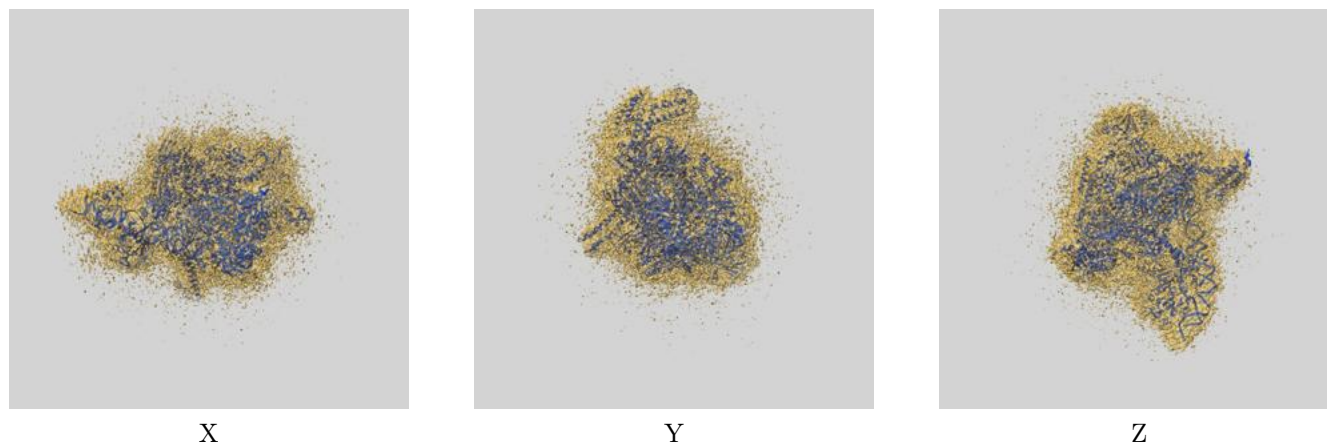
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

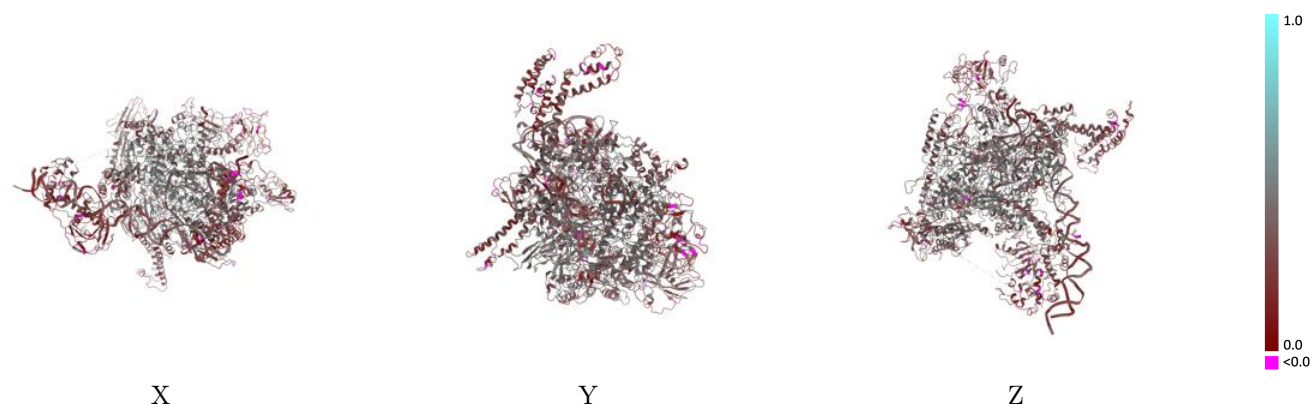
This section contains information regarding the fit between EMDB map EMD-32165 and PDB model 7VWY. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



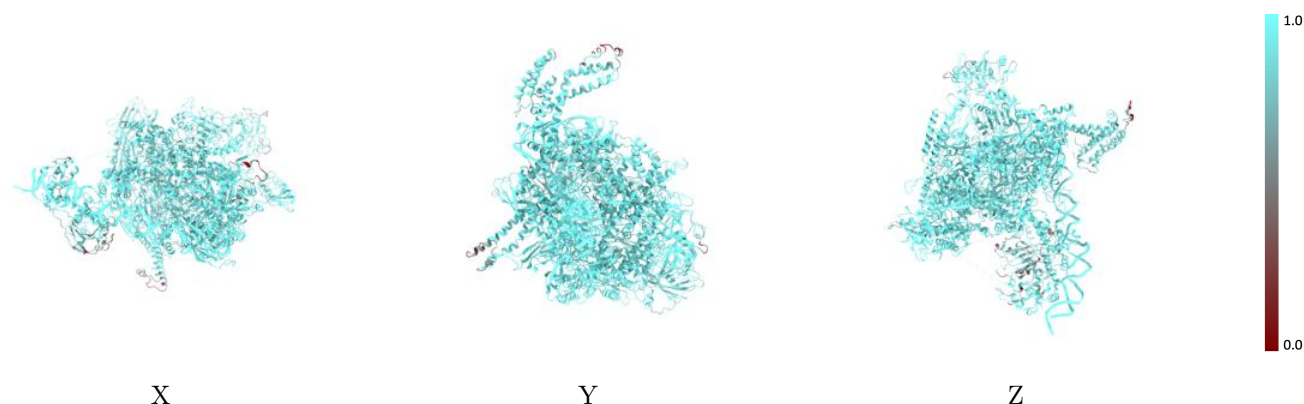
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



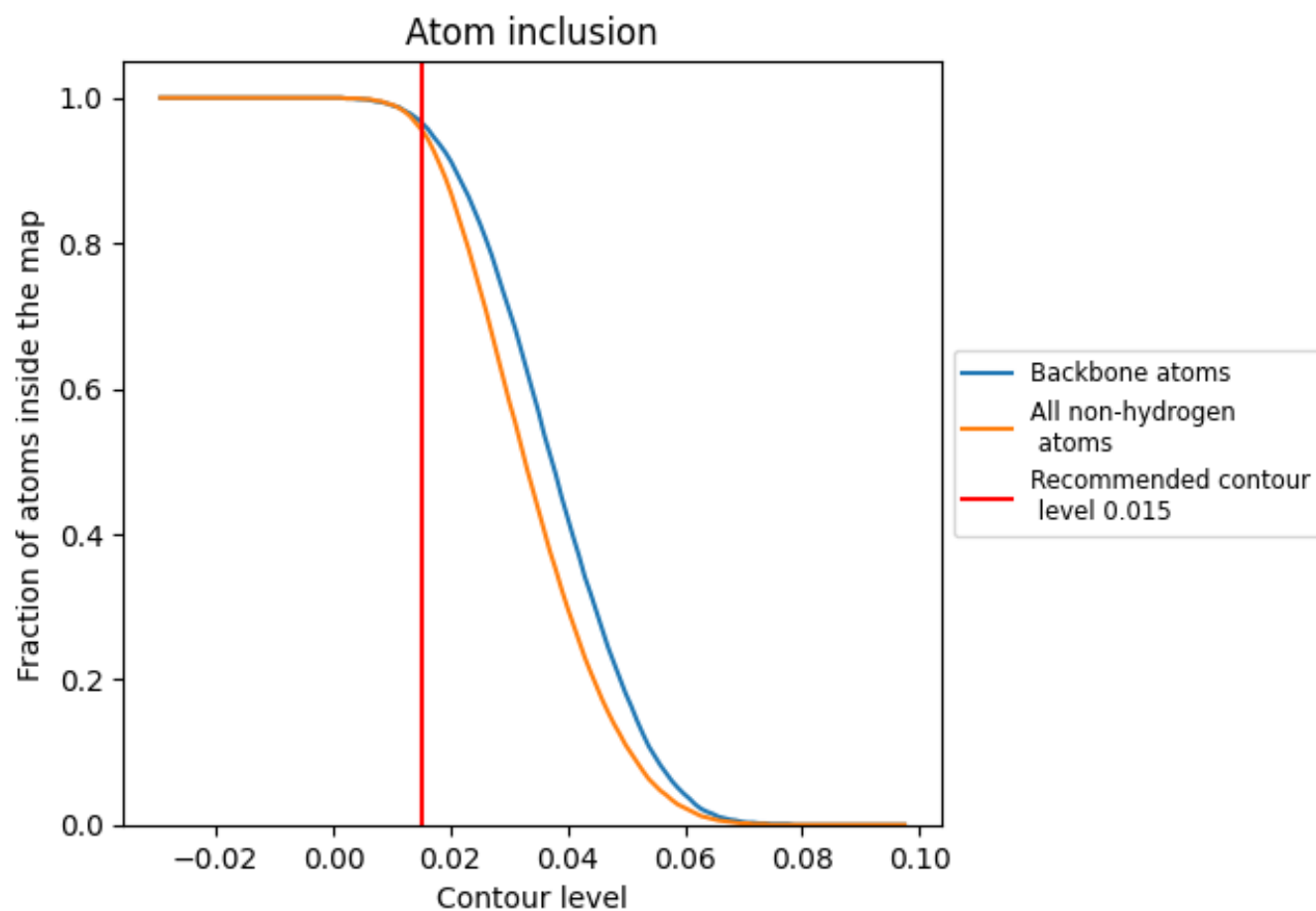
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 96% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9570	0.3590
1	0.9960	0.2940
2	0.9920	0.2860
A	0.9510	0.3510
B	0.9530	0.3440
C	0.9710	0.4000
D	0.9790	0.3850
E	0.9380	0.3820
F	0.9240	0.3030
G	0.8240	0.2350

1.0

0.0

<0.0