



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 07:45 AM UTC

PDB ID : 6L42 / pdb_00006l42
EMDB ID : EMD-0828
Title : Structure of severe fever with thrombocytopenia syndrome virus L protein
Authors : Wang, P.; Lou, Z.
Deposited on : 2019-10-15
Resolution : 3.40 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

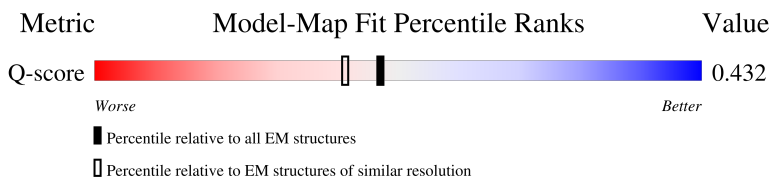
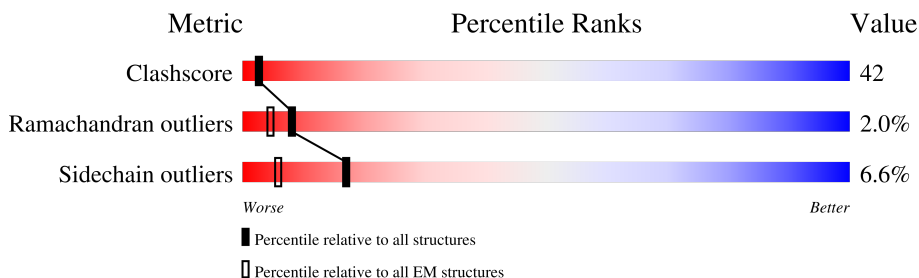
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	2109	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 14827 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 polymerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1864	Total	C	N	O	S	0	0
			14826	9388	2574	2773	91		

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-24	MET	-	initiating methionine	UNP I0DF35
A	-23	SER	-	expression tag	UNP I0DF35
A	-22	TYR	-	expression tag	UNP I0DF35
A	-21	TYR	-	expression tag	UNP I0DF35
A	-20	HIS	-	expression tag	UNP I0DF35
A	-19	HIS	-	expression tag	UNP I0DF35
A	-18	HIS	-	expression tag	UNP I0DF35
A	-17	HIS	-	expression tag	UNP I0DF35
A	-16	HIS	-	expression tag	UNP I0DF35
A	-15	HIS	-	expression tag	UNP I0DF35
A	-14	ASP	-	expression tag	UNP I0DF35
A	-13	TYR	-	expression tag	UNP I0DF35
A	-12	ASP	-	expression tag	UNP I0DF35
A	-11	ILE	-	expression tag	UNP I0DF35
A	-10	PRO	-	expression tag	UNP I0DF35
A	-9	THR	-	expression tag	UNP I0DF35
A	-8	THR	-	expression tag	UNP I0DF35
A	-7	GLU	-	expression tag	UNP I0DF35
A	-6	ASN	-	expression tag	UNP I0DF35
A	-5	LEU	-	expression tag	UNP I0DF35
A	-4	TYR	-	expression tag	UNP I0DF35
A	-3	PHE	-	expression tag	UNP I0DF35
A	-2	GLN	-	expression tag	UNP I0DF35
A	-1	GLY	-	expression tag	UNP I0DF35
A	0	ALA	-	expression tag	UNP I0DF35
A	1321	GLU	GLN	engineered mutation	UNP I0DF35

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total	Mg	0
			1	1	



A1902	E1973	M2041
K1906	G1974	E2046
T1907	S1975	R2049
Q1908	L1976	PRO
G1909	D1977	PHE
I1910	F1982	LEU
D1911	A1985	ILE
M1912	L1988	PHE
R1913	W1989	LEU
A1914	S1990	GLN
M1915	ALA	ILE
F1919	GLU	PRO
R1920	VAL	GLU
E1924	VAL	ASP
G1925	GLU	SER
S1926	GLU	ILE
L1927	PHE	SER
R1928	GLY	TRP
K1929	GLU	VAL
Q1930	GLY	SER
R1934	VAL	ASP
S1935	ALA	GLN
K1936	V2003	PHE
L1937	S2004	CYS
T1938	Y2005	ASP
E1939	S2006	SER
M1940	S2007	ARG
V1941	K2008	GLY
E1942	Y2009	LEU
K1943	Y2010	ASP
M1944	H2011	GLU
V1945	L2012	SER
V1946	M2015	THR
P1947	A2019	ILE
L1948	ILE	MET
T1949	THR	CYS
T1950	MET	ALA
Q1951	CYS	ILE
E1952	ALA	MET
L1953	ILE	GLY
V1954	GLY	K2028
P1955	K2028	E2029
L1956	E2029	G2030
L1957	G2030	C2031
E1958	C2031	R2032
E1959	R2032	G2033
D1960	G2033	L2034
I1961	L2034	LEU
D1962	LEU	THR
F1963	THR	GLU
S1964	GLU	LYS
D1965	LYS	R2039
V1969	R2039	C2040
E1970	C2040	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	147344	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40, 40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k), GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.061	Depositor
Minimum map value	-0.028	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0085	Depositor
Map size ($\text{\AA}$)	237.6, 237.6, 237.6	wwPDB
Map dimensions	220, 220, 220	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

5.1 Standard geometry

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	0.93	105/15117 (0.7%)	2.15	569/20379 (2.8%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	94

The worst 5 of 105 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1520	VAL	CA-C	-23.22	1.17	1.52
1	A	892	ALA	C-N	21.80	1.59	1.34
1	A	348	THR	C-N	19.57	1.60	1.33
1	A	348	THR	CA-C	18.66	1.64	1.53
1	A	1	MET	C-N	17.37	1.58	1.33

The worst 5 of 569 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	348	THR	O-C-N	-55.41	79.92	121.47
1	A	1580	SER	O-C-N	-32.21	78.20	122.97
1	A	1584	LEU	O-C-N	-31.75	89.16	123.13
1	A	1581	VAL	O-C-N	30.97	161.28	122.57
1	A	1567	PHE	O-C-N	-30.23	83.09	122.39

There are no chirality outliers.

5 of 94 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1	MET	Mainchain
1	A	11	ASN	Mainchain
1	A	2	ASN	Mainchain
1	A	3	LEU	Mainchain
1	A	95	LEU	Mainchain

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	14826	0	14795	1230	0
2	A	1	0	0	0	0
All	All	14827	0	14795	1230	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 42.

The worst 5 of 1230 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:1556:LEU:HD11	1:A:1564:HIS:CD2	1.27	1.67
1:A:917:GLY:CA	1:A:920:ARG:HD3	1.26	1.65
1:A:1568:ARG:CA	1:A:1568:ARG:N	1.67	1.55
1:A:193:TYR:CE1	1:A:197:ILE:HD11	1.40	1.55
1:A:380:VAL:CG2	1:A:411:PHE:CE1	1.83	1.55

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	1832/2109 (87%)	1586 (87%)	209 (11%)	37 (2%)	6	25

5 of 37 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	163	PRO
1	A	356	MET
1	A	978	ILE
1	A	1424	SER
1	A	1426	SER

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	1635/1848 (88%)	1527 (93%)	108 (7%)	15	41

5 of 108 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1134	ILE
1	A	1514	GLU
1	A	1694	ARG
1	A	1137	LYS
1	A	1399	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	618	ASN
1	A	1457	ASN
1	A	895	GLN
1	A	1564	HIS
1	A	1204	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 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.

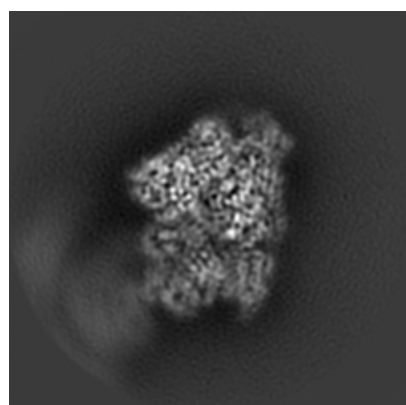
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0828. These allow visual inspection of the internal detail of the map and identification of artifacts.

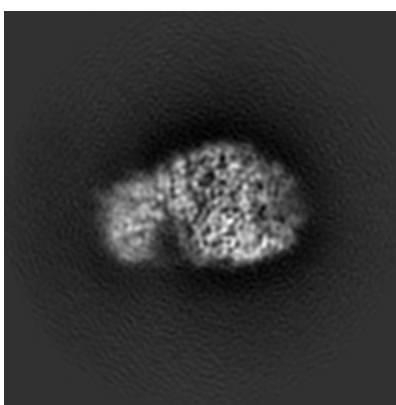
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

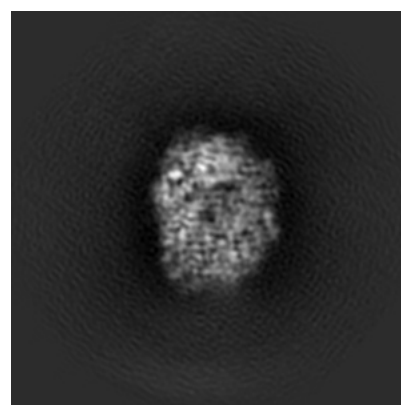
6.1.1 Primary map



X



Y

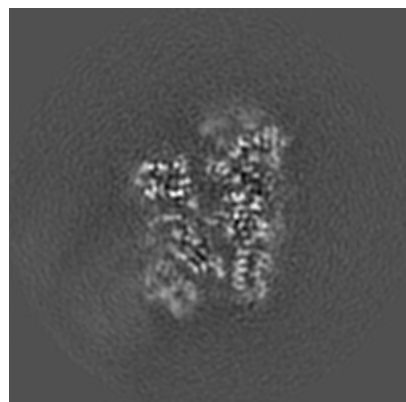


Z

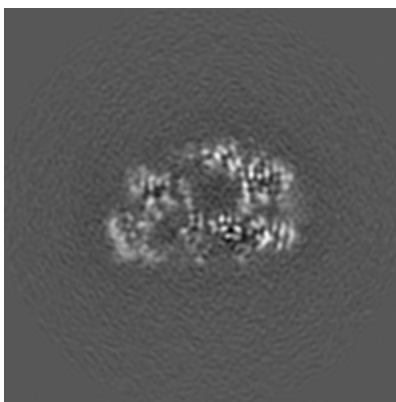
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

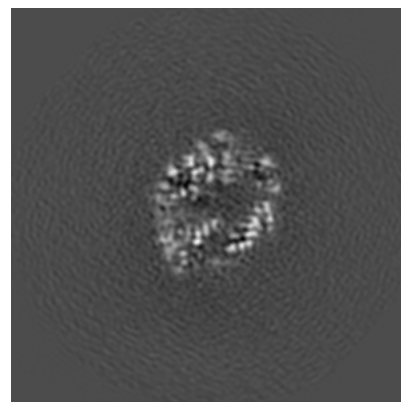
6.2.1 Primary map



X Index: 110



Y Index: 110

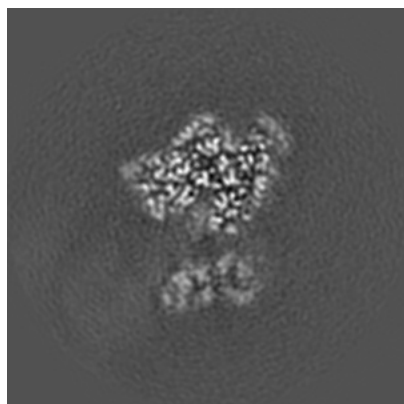


Z Index: 110

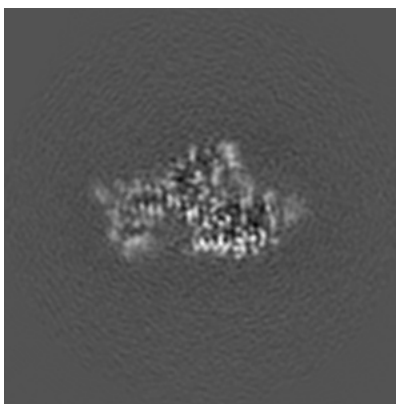
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

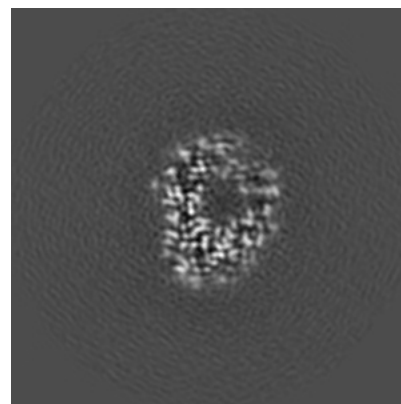
6.3.1 Primary map



X Index: 94



Y Index: 129

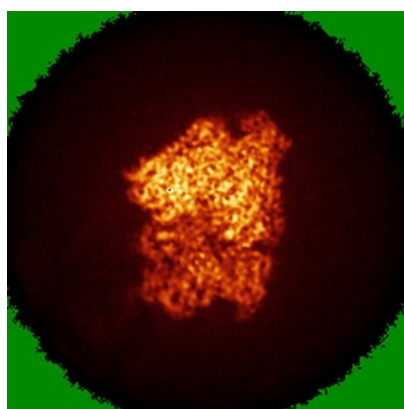


Z Index: 121

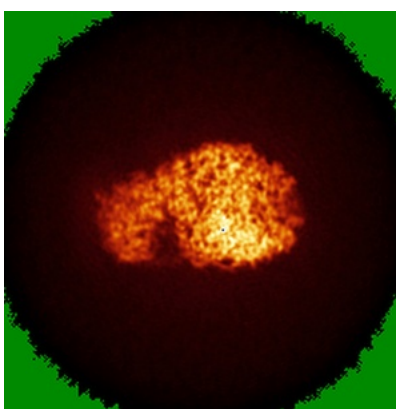
The images above show the largest variance slices of the map in three orthogonal directions.

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

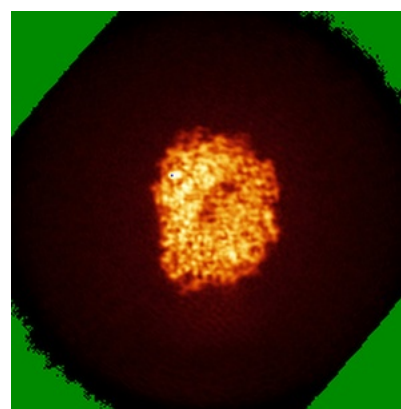
6.4.1 Primary map



X



Y

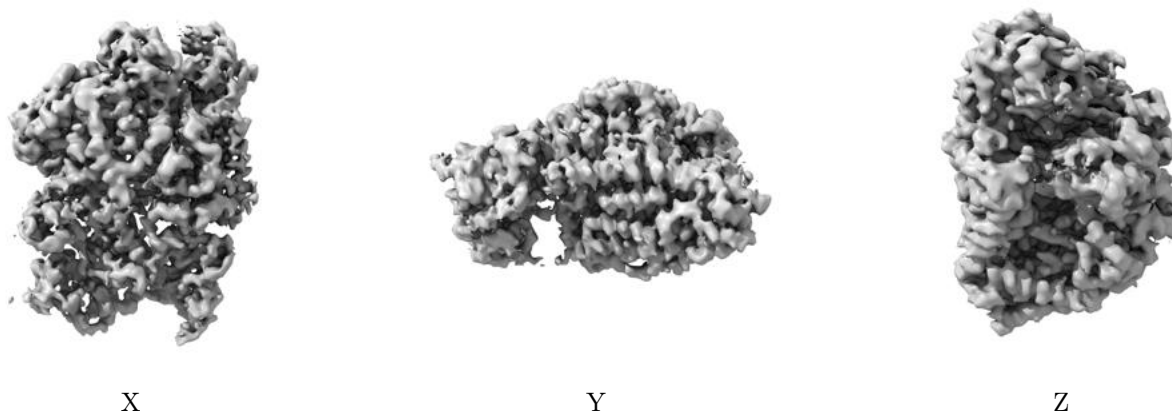


Z

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 0.0085. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

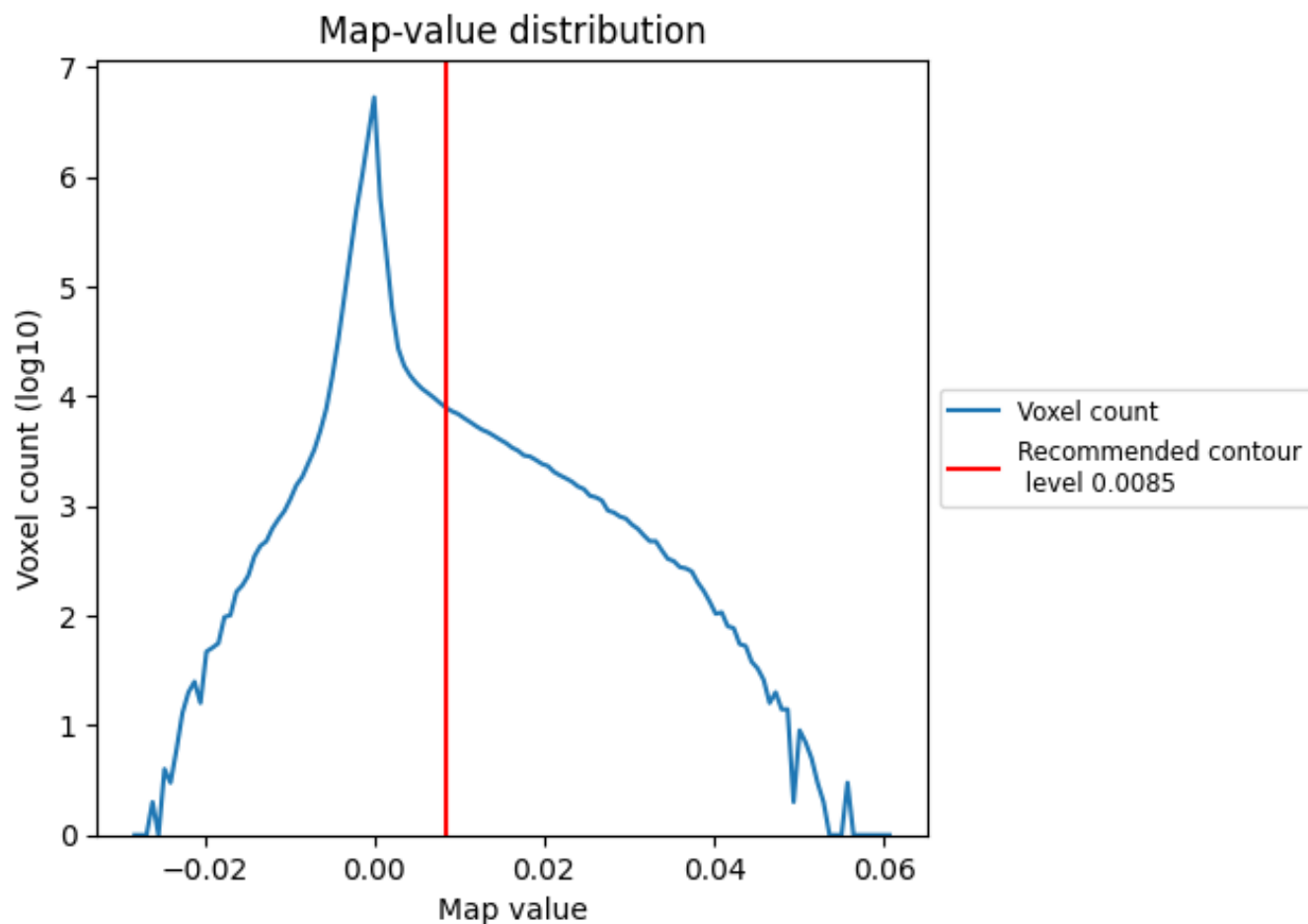
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

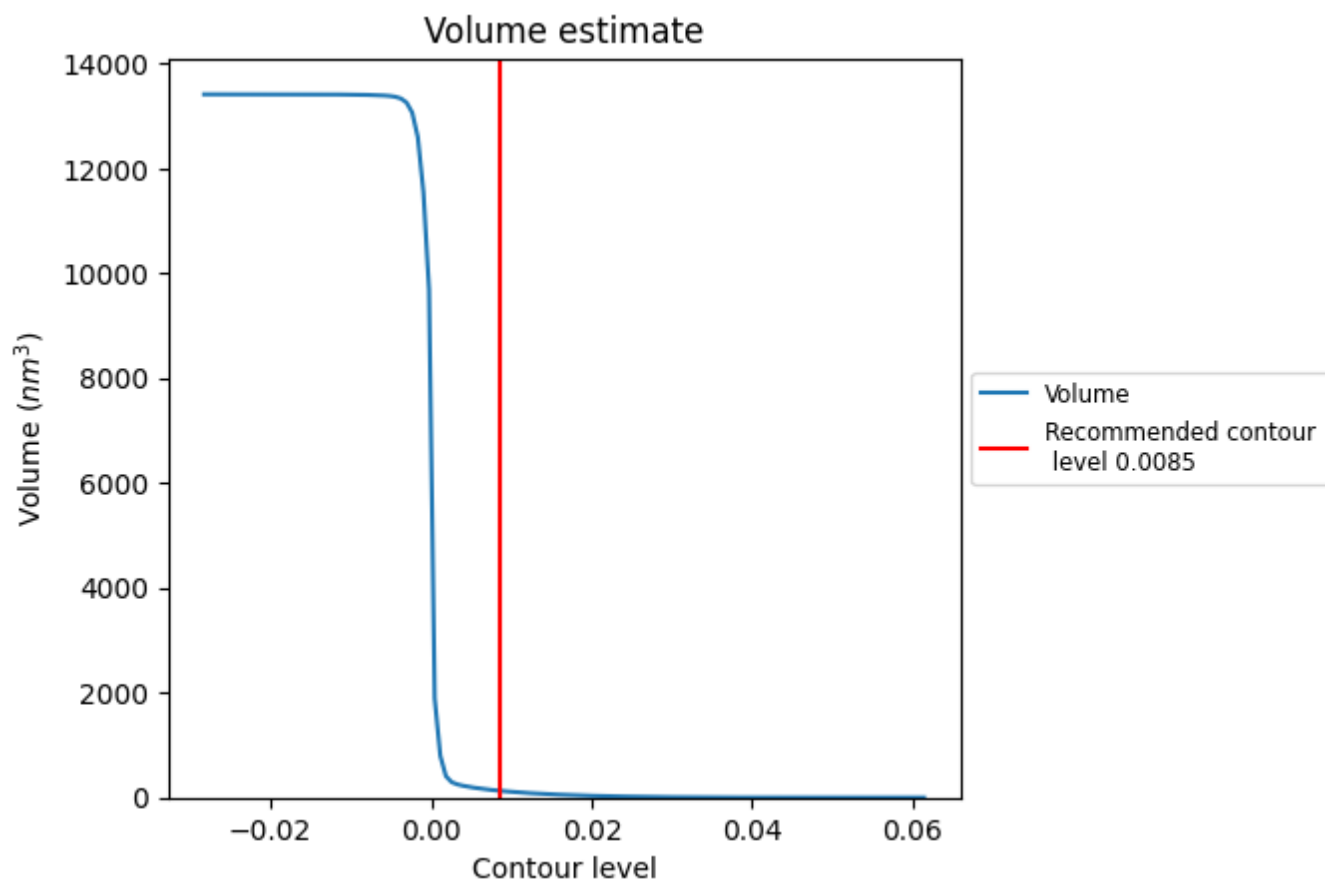
This section contains the results of statistical analysis of the map.

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.

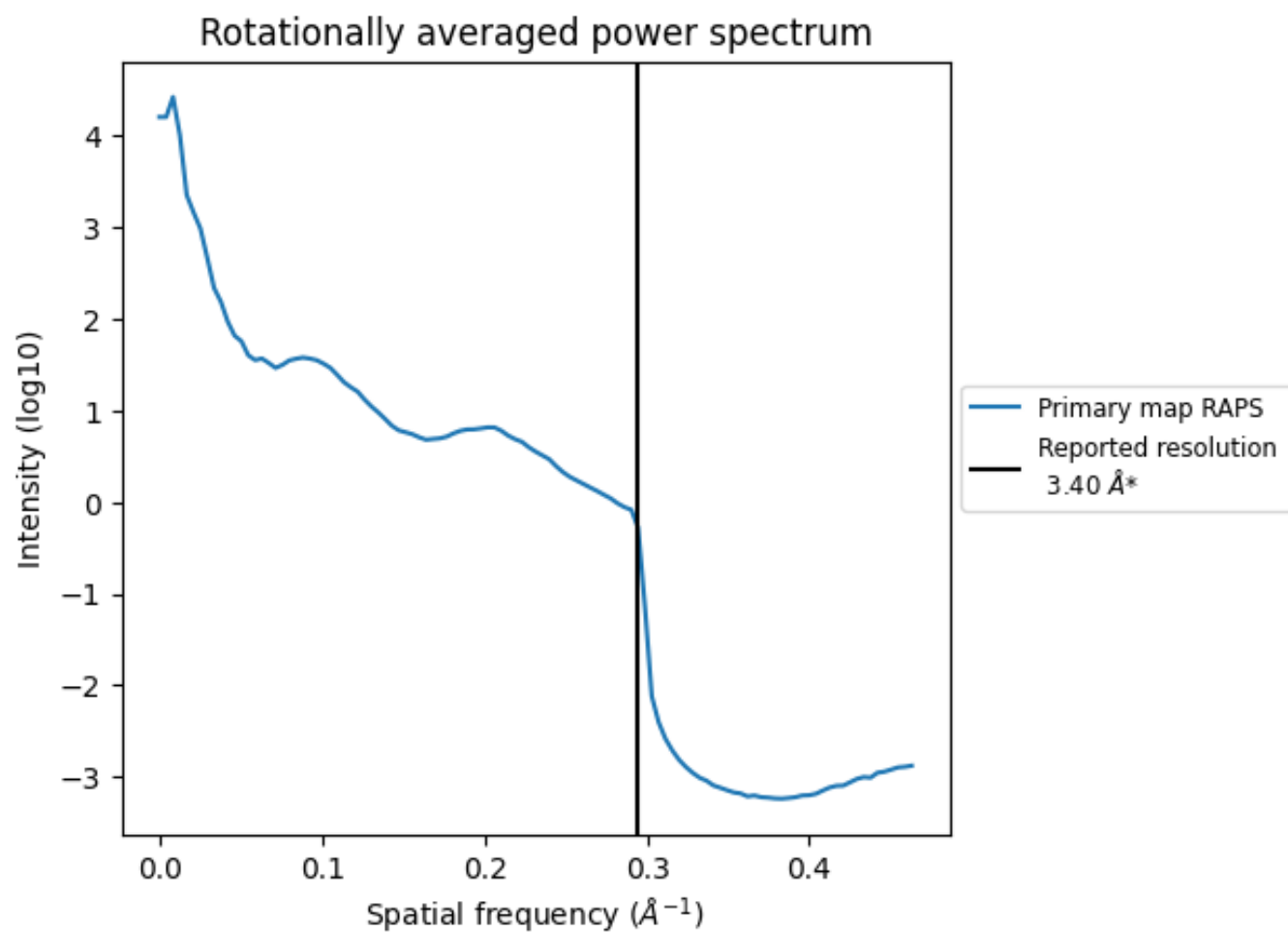
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 130 nm³; this corresponds to an approximate mass of 118 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 0.294 Å⁻¹

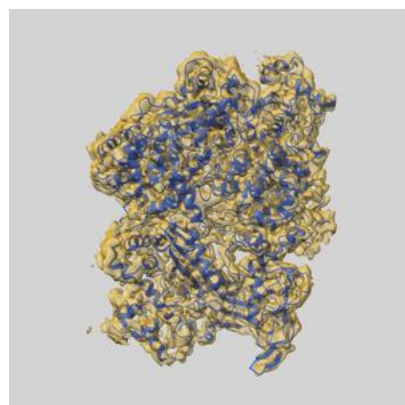
8 Fourier-Shell correlation

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

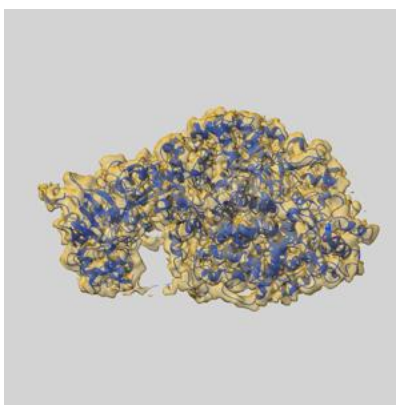
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0828 and PDB model 6L42. Per-residue inclusion information can be found in section 3 on page 5.

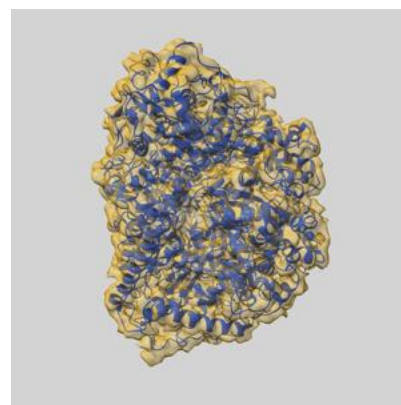
9.1 Map-model overlay [i](#)



X



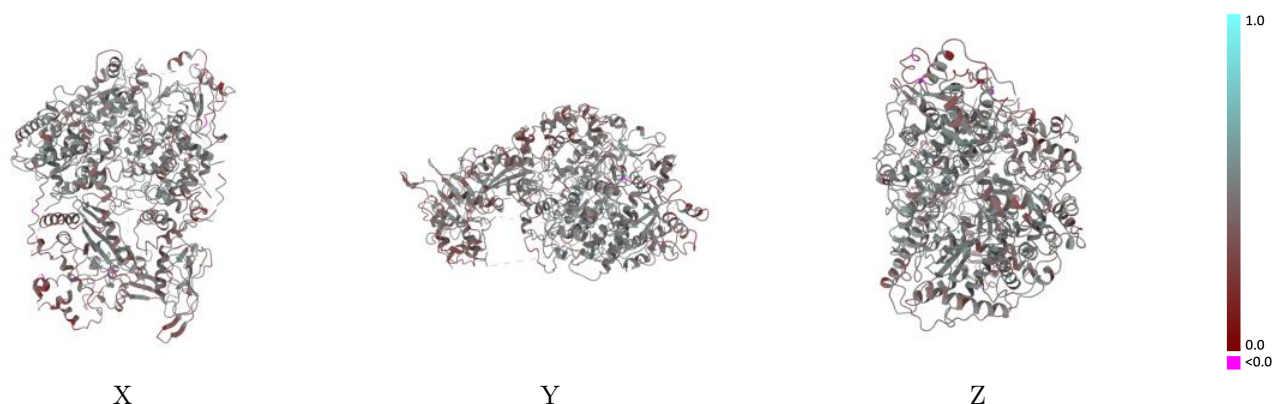
Y



Z

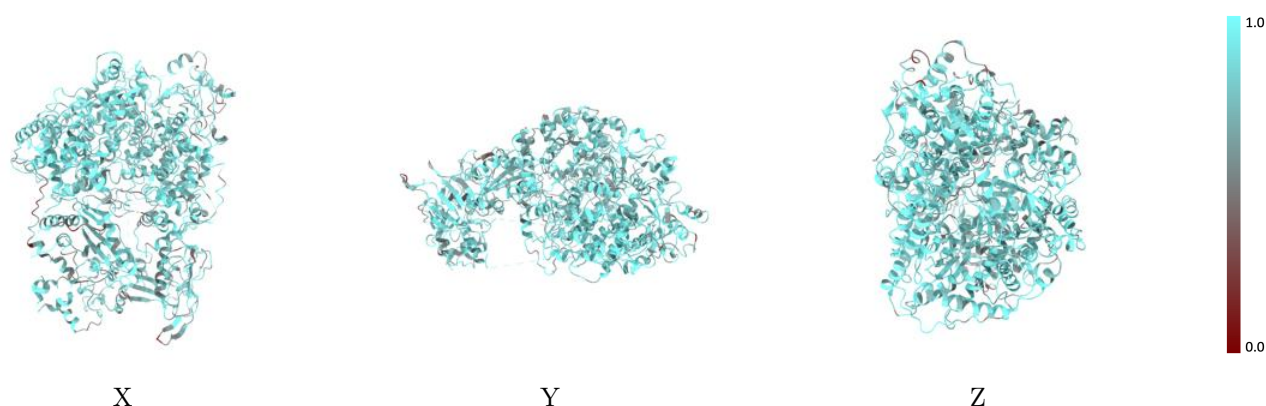
The images above show the 3D surface view of the map at the recommended contour level 0.0085 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



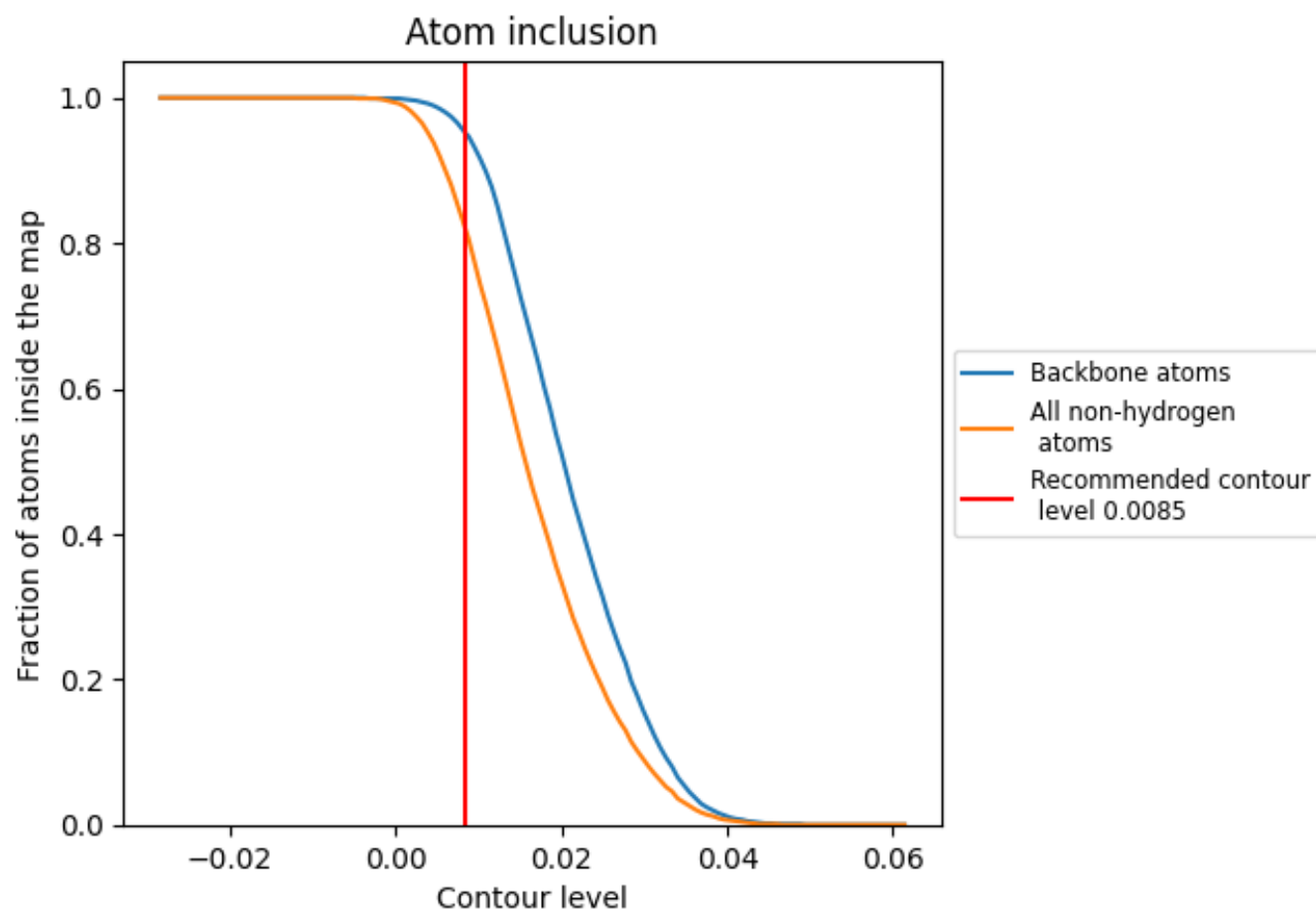
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0085).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 82% 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 (0.0085) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8170	0.4320
A	0.8170	0.4320

