



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 11:08 AM UTC

PDB ID : 5A22 / pdb_00005a22
EMDB ID : EMD-6337
Title : Structure of the L protein of vesicular stomatitis virus from electron cryomicroscopy
Authors : Liang, B.; Li, Z.; Jenni, S.; Rameh, A.A.; Morin, B.M.; Grant, T.; Grigorieff, N.; Harrison, S.C.; Whelan, S.P.J.
Deposited on : 2015-05-06
Resolution : 3.80 Å(reported)

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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

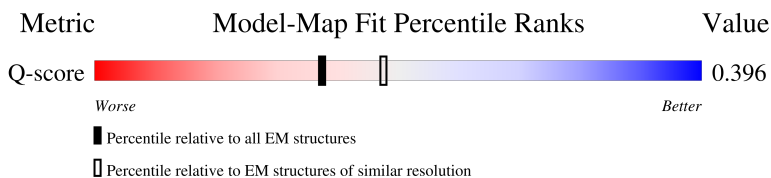
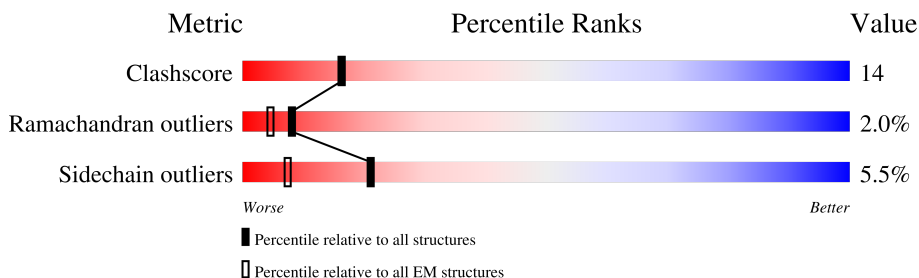
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	2109	24% 62% 29% • 5%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 32187 atoms, of which 16110 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 VESICULAR STOMATITIS VIRUS L POLYMERASE.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A	2002	32185	10249	16110	2803	2934	89	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	228	ARG	PRO	conflict	UNP P03523
A	467	ASP	HIS	conflict	UNP P03523
A	548	LEU	PHE	conflict	UNP P03523
A	549	ARG	PRO	conflict	UNP P03523
A	670	ARG	PRO	conflict	UNP P03523
A	910	PHE	SER	conflict	UNP P03523
A	1026	ALA	PRO	conflict	UNP P03523
A	1348	GLY	ALA	conflict	UNP P03523
A	1589	ALA	PRO	conflict	UNP P03523

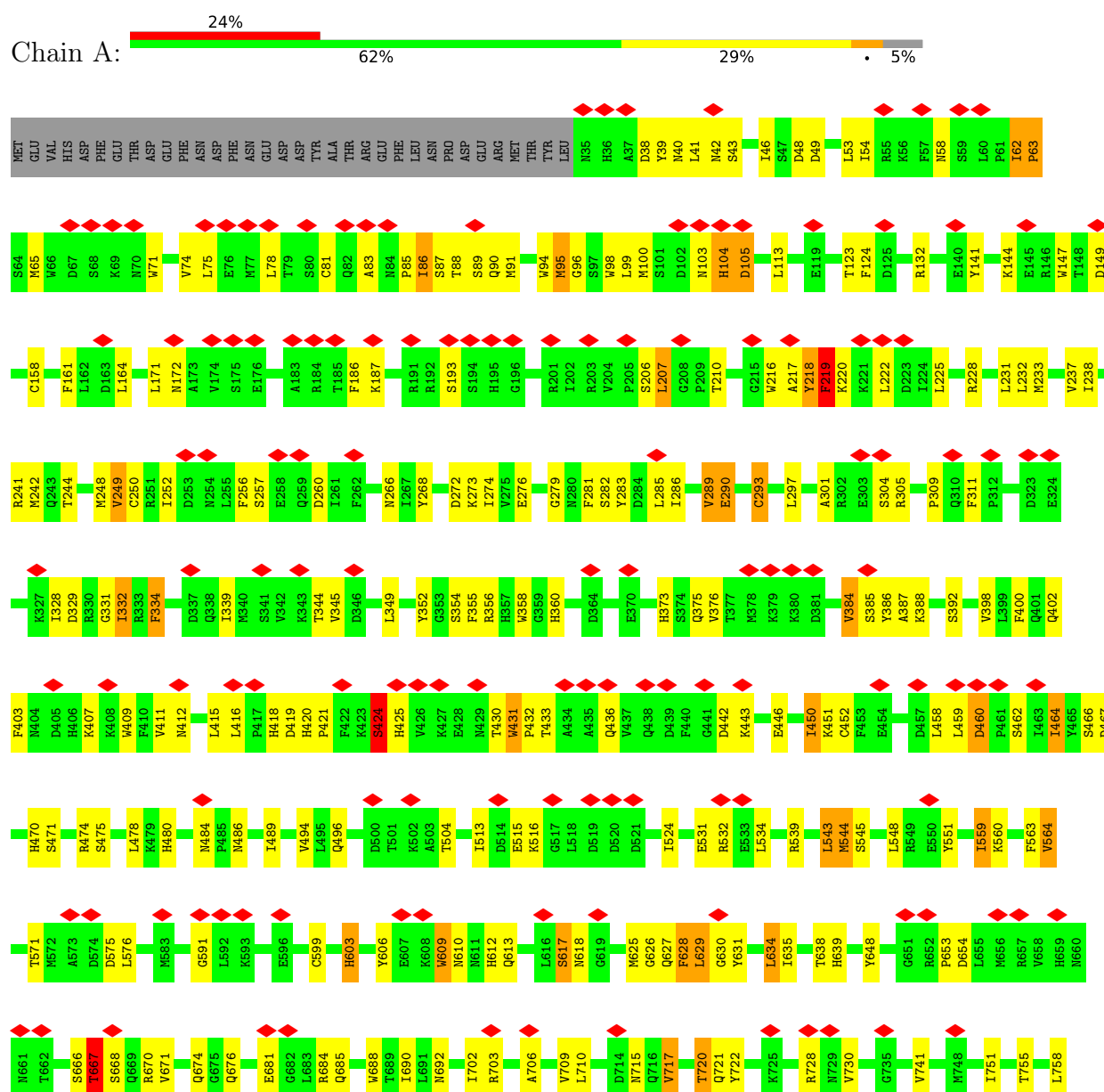
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

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: VESICULAR STOMATITIS VIRUS L POLYMERASE





K2089	D2028	S1957	V1878	K1806
E2090	S2029	D1958	Y1881	M1807
D2091	L2030	G1959	F1882	A1808
R2092	A2031	I1960	T1883	V1809
S2093	P2032	A1961	L1884	T1810
I2094	T2083	Q1962	T1885	I1811
L2095	G2034	M1963	G1886	L1812
M2096	T2035	V1964	I1887	G1813
L2097	W2036	G1965	P1888	
K2098	L2037	I1966		D1820
S2099	R2038	A1967	F1891	L1821
D2100	S2039		I1892	V1822
L2101	L2040	F1973	P1893	Q1823
H2102	E2041	W1974	D1894	T1824
E2103	L2042	L1975	P1895	E1825
	V2043	S1976	F1896	F1826
		L1977	V1897	S1827
		M1978	N1898	
	Q2046	H1979	I1899	V1834
	V2047	K1980	E1900	Y1835
	R2048	D1981	T1901	M1836
	L2049	I1982		V1837
	W2050	Y1985	I1905	C1838
	P2051		F1906	K1839
	F2052	C1988	V1912	GLY
	N2053	L1989	A1916	LEU
	E2054	A1990	A1917	LYS
	I2055	V1991	L1918	LYS
	L2056	I1992	K1919	LEU
	F2057	Q1993		ILE
	W2058			ASP
	Q2059	I1998	D1922	GLU
	L2060	R1999	R1923	PRO
	C2061	W2000	P1924	ASN
	R2062	E2001	A1925	P1850
	T2063		D1926	D1851
	V2064	S2004	L1927	W1852
	D2065	V2005		S1853
	N2066	K2006	I1930	S1854
	H2067	G2007	Y1934	I1855
	L2068	G2008		M1856
	K2069	Y2009	I1937	E1857
	W2070	K2010	I1943	S1858
	S2071	Q2011	N1944	W1859
	N2072	K2012	H1945	K1860
	L2073	S2014	I1946	M1861
	R2074	T2015	R1947	L1862
	R2075	R2016	V1948	Y1863
	N2076	G2017	G1949	A1864
	T2077	D2018	P1950	F1865
	G2078	P2021	I1951	
	N2079	K2022	P1952	E1869
	I2080	D2023	P1953	Q1870
	E2081	T2024	N1954	F1871
	W2082	R2025	P1955	F1872
	I2083	I2026	S2027	A1873
	N2084			R1874
	R2085			A1875
	R2086			K1876
	I2087			K1877
	S2088			

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	74940	Depositor
Resolution determination method	Not provided	
CTF correction method	INDIVIDUAL PARTICLES	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	100	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	40410	Depositor
Image detector	GATAN K2 (4k x 4k)	Depositor
Maximum map value	5.041	Depositor
Minimum map value	-2.928	Depositor
Average map value	0.052	Depositor
Map value standard deviation	0.385	Depositor
Recommended contour level	1.2	Depositor
Map size ($\text{\AA}$)	148.44, 148.44, 148.44	wwPDB
Map dimensions	120, 120, 120	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.237, 1.237, 1.237	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: 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	0.57	2/16456 (0.0%)	0.99	51/22270 (0.2%)

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	14

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	289	VAL	CA-CB	6.60	1.61	1.54
1	A	865	ILE	CA-CB	5.08	1.60	1.54

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1165	GLN	CA-C-N	-9.65	107.78	119.84
1	A	1165	GLN	C-N-CA	-9.65	107.78	119.84
1	A	1447	PRO	N-CA-C	8.12	120.60	110.70
1	A	1954	ASN	CA-C-N	-7.92	112.22	120.38
1	A	1954	ASN	C-N-CA	-7.92	112.22	120.38

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1071	LEU	Peptide

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Mol	Chain	Res	Type	Group
1	A	1125	THR	Peptide
1	A	431	TRP	Peptide
1	A	63	PRO	Peptide
1	A	766	GLU	Peptide

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	16075	16110	16109	458	0
2	A	2	0	0	0	0
All	All	16077	16110	16109	458	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 14.

The worst 5 of 458 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:100:MET:SD	1:A:241:ARG:NH1	2.51	0.84
1:A:88:THR:O	1:A:91:MET:N	2.21	0.73
1:A:977:ARG:O	1:A:986:LYS:NZ	2.22	0.72
1:A:419:ASP:HB2	1:A:421:PRO:HD2	1.71	0.71
1:A:1361:GLN:OE1	1:A:1364:ARG:NH2	2.23	0.70

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	1994/2109 (94%)	1678 (84%)	277 (14%)	39 (2%)	6	32

5 of 39 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	63	PRO
1	A	355	PHE
1	A	730	VAL
1	A	1381	ALA
1	A	2066	ASN

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	1794/1890 (95%)	1695 (94%)	99 (6%)	19	45

5 of 99 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1072	ARG
1	A	1408	LEU
1	A	1105	HIS
1	A	1257	MET
1	A	1452	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2050	ASN
1	A	2076	ASN
1	A	862	GLN
1	A	932	ASN
1	A	1277	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 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 [i](#)

There are no chain breaks in this entry.

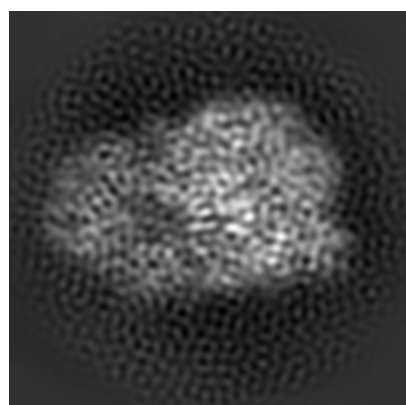
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6337. These allow visual inspection of the internal detail of the map and identification of artifacts.

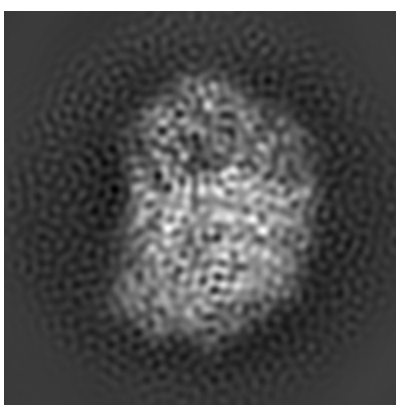
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

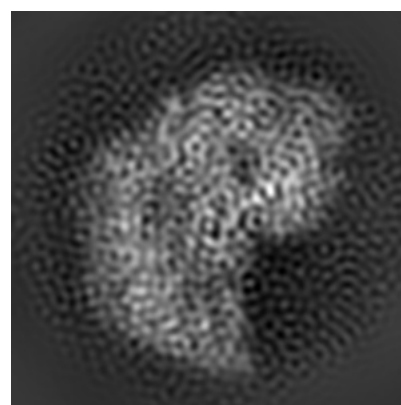
6.1.1 Primary map



X



Y

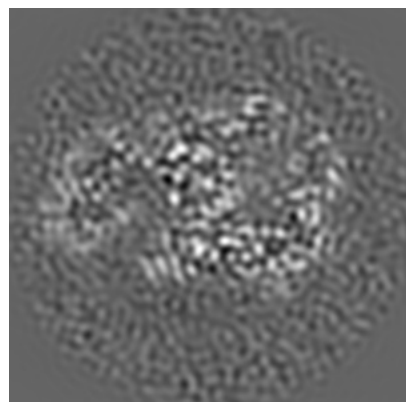


Z

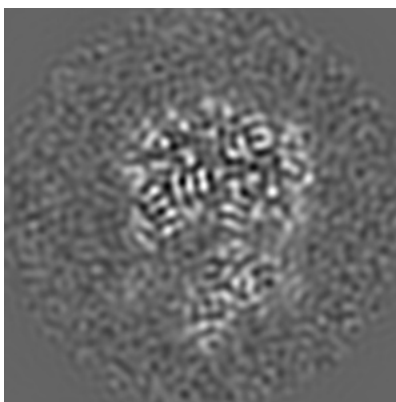
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

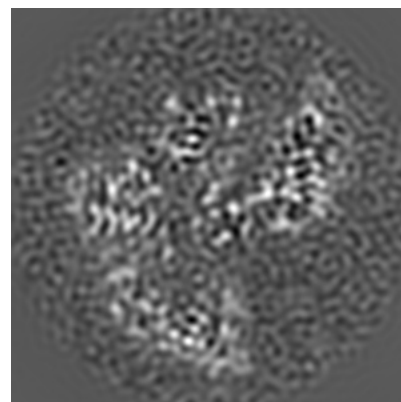
6.2.1 Primary map



X Index: 60



Y Index: 60

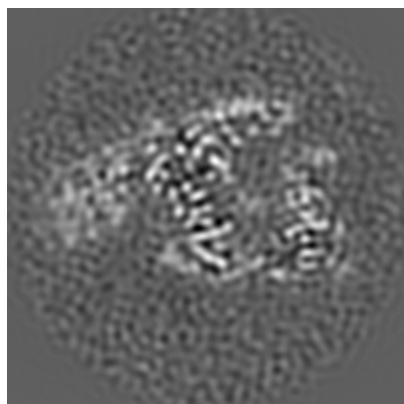


Z Index: 60

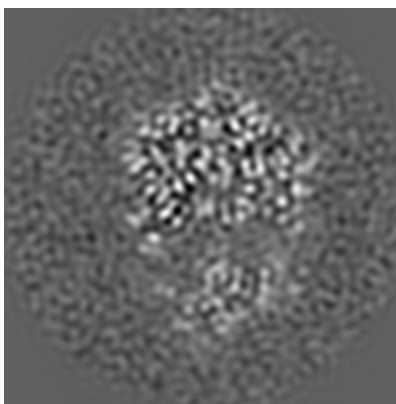
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

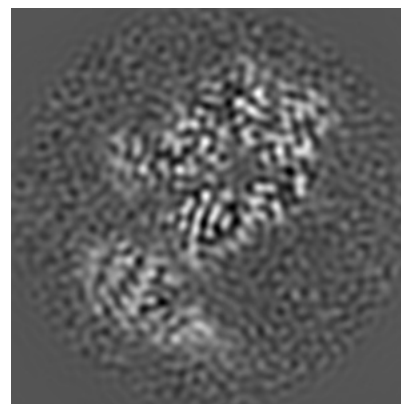
6.3.1 Primary map



X Index: 65



Y Index: 63

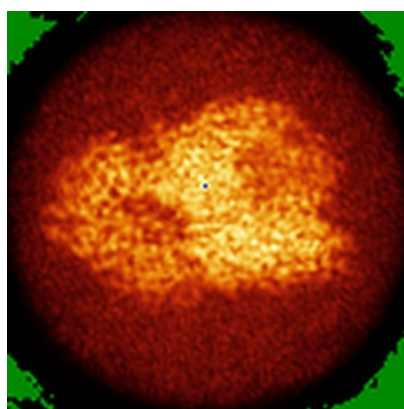


Z Index: 48

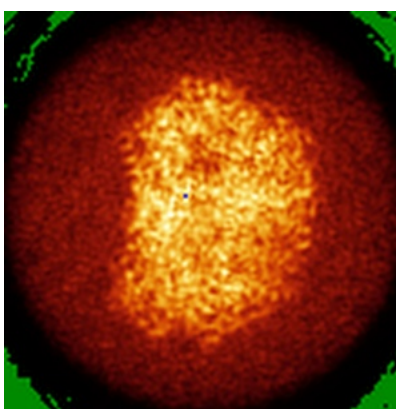
The images above show the largest variance slices of the map in three orthogonal directions.

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

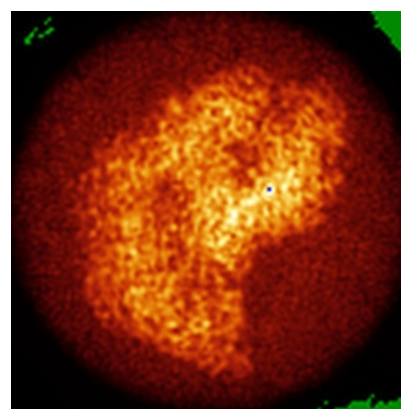
6.4.1 Primary map



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.

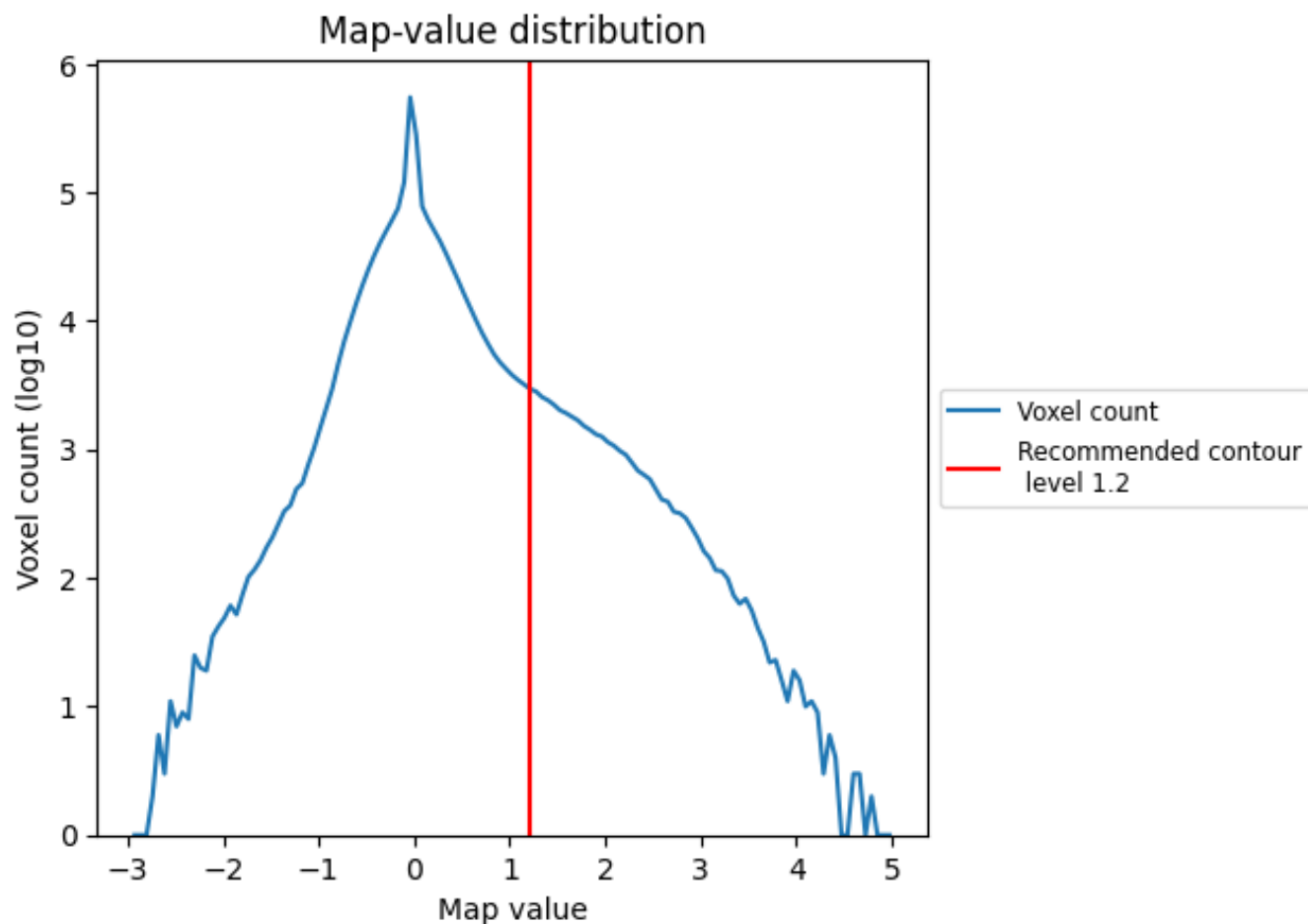
6.6 Mask visualisation

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

7 Map analysis [i](#)

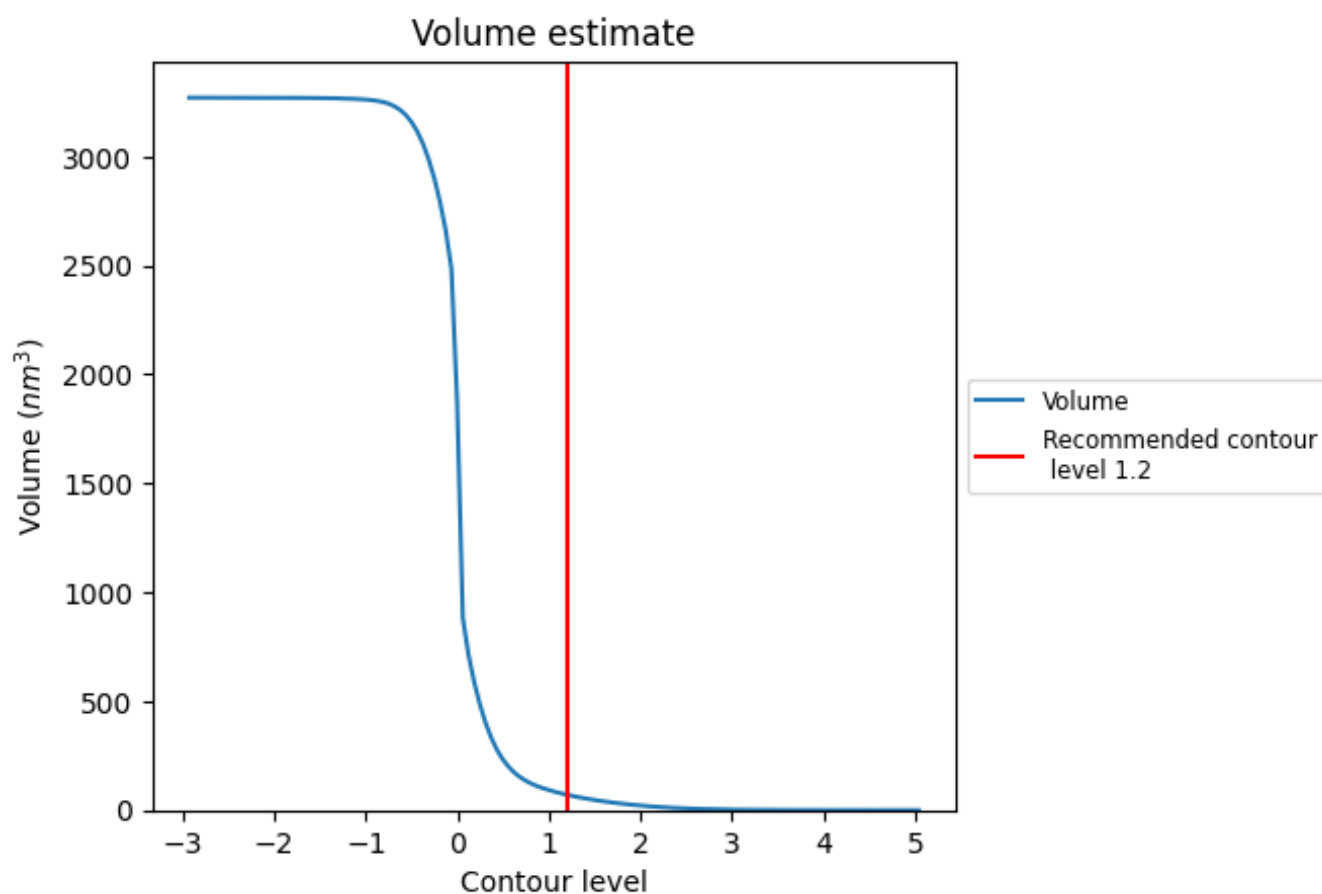
This section contains the results of statistical analysis of the map.

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.

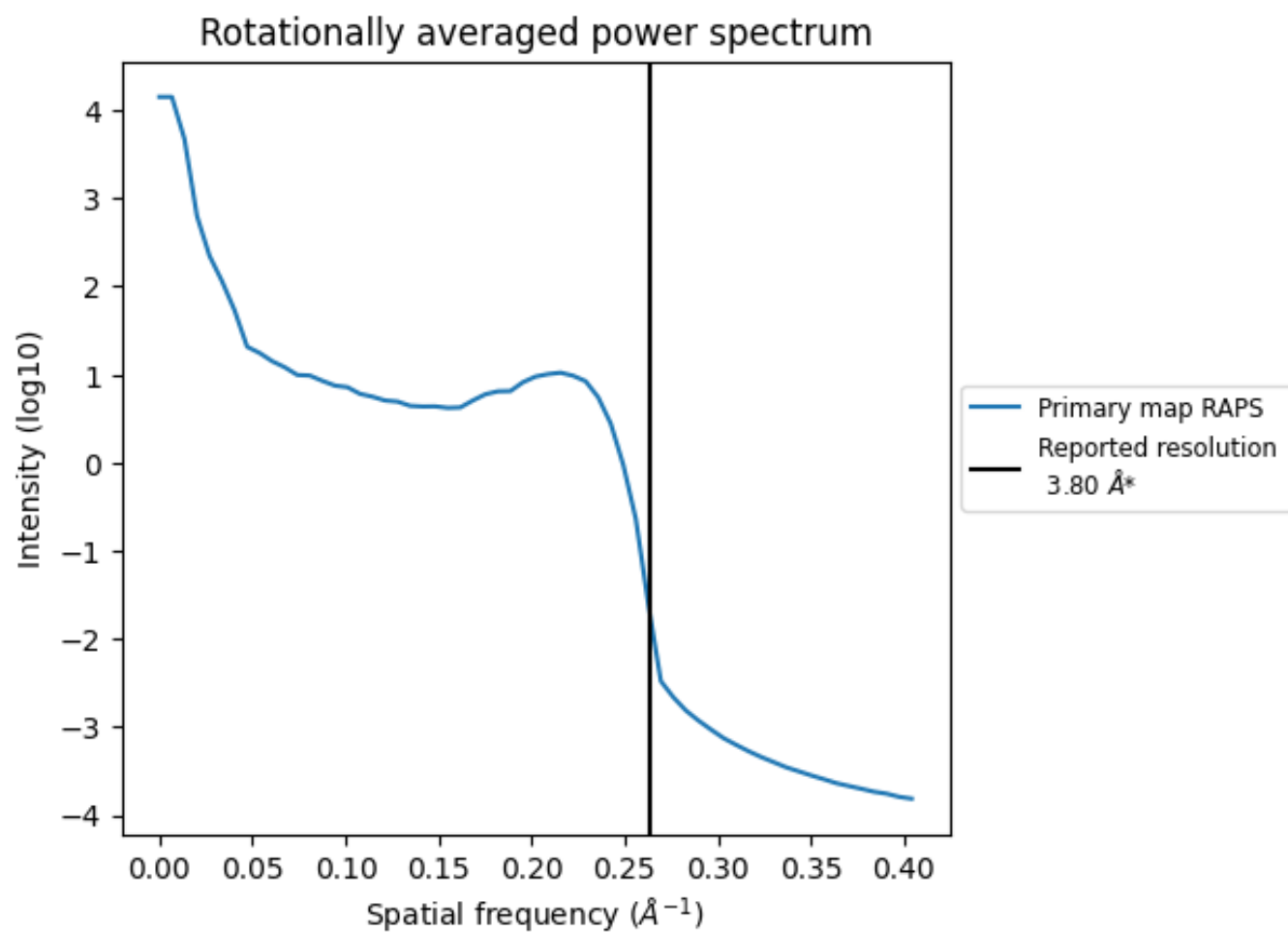
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 71 nm³; this corresponds to an approximate mass of 64 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 0.263 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

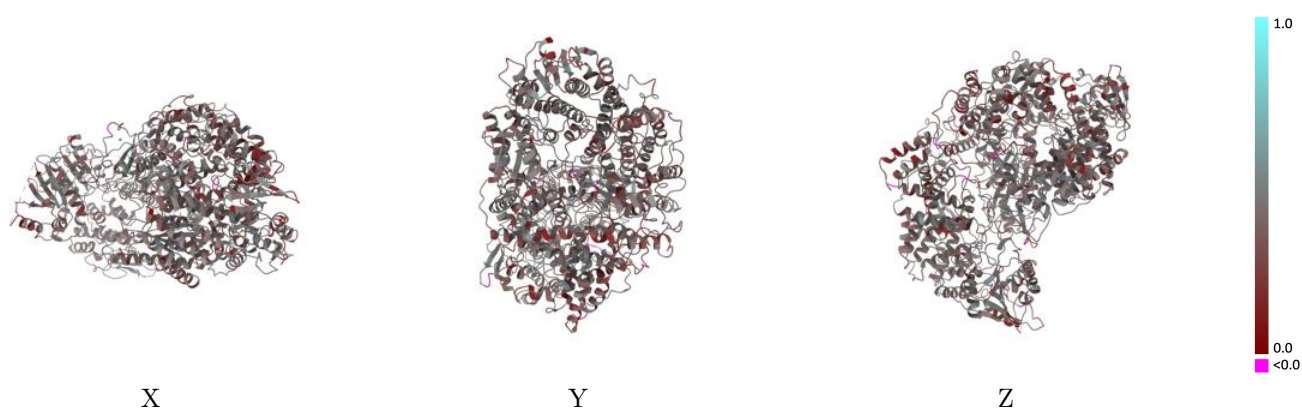
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6337 and PDB model 5A22. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

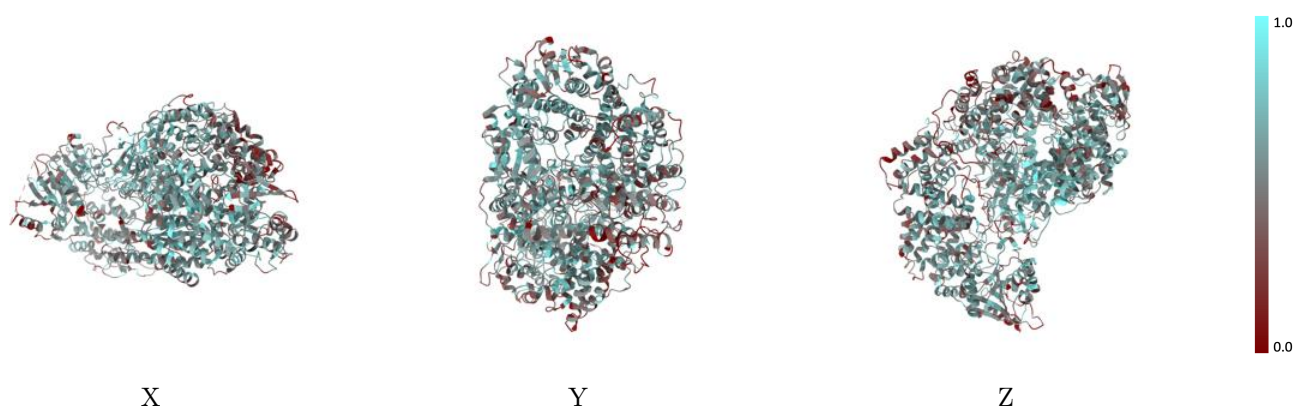
This section was not generated.

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



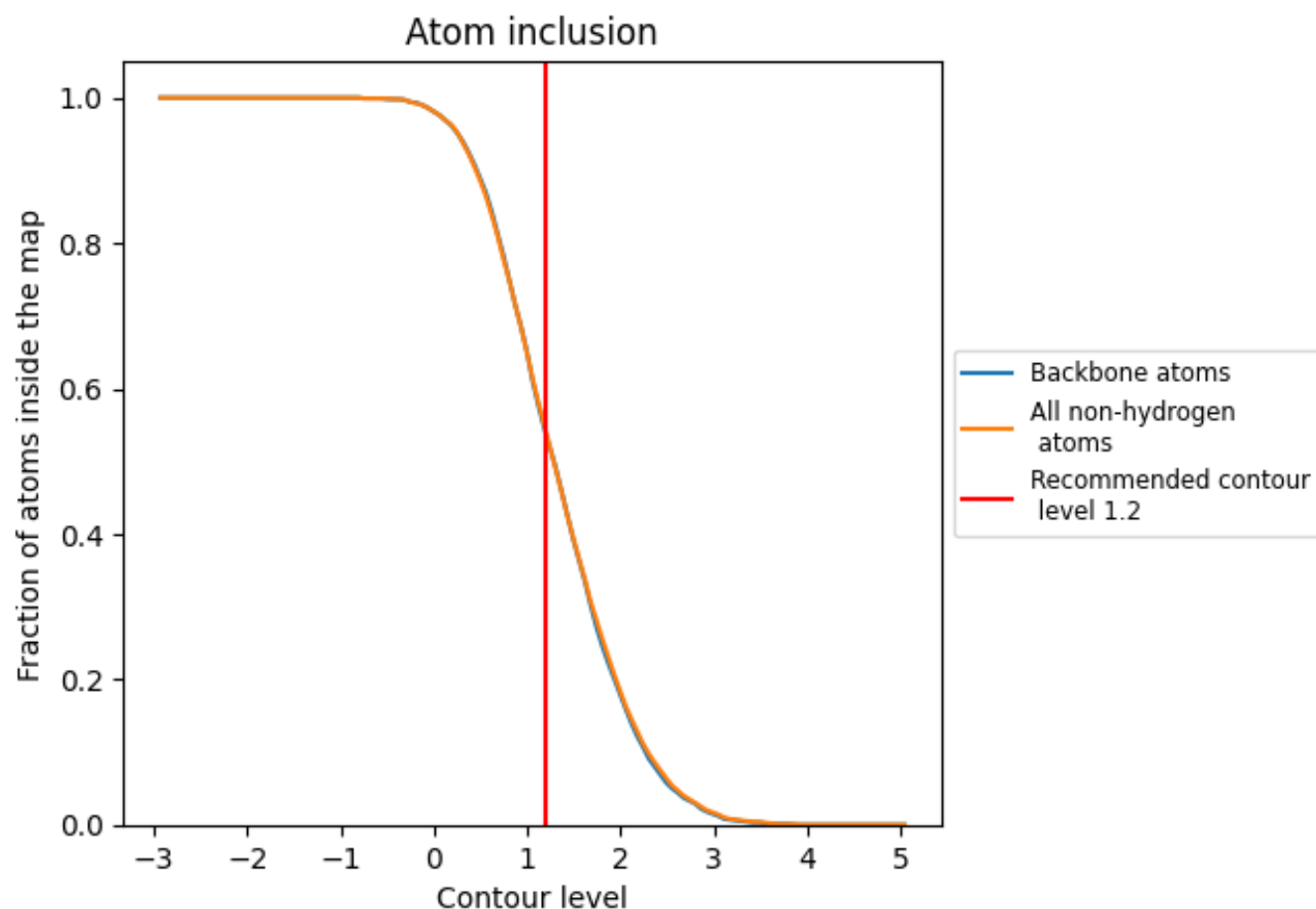
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 54% of all backbone atoms, 54% 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 (1.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5410	0.3960
A	0.5510	0.3960

