



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 08:40 AM UTC

PDB ID : 7ZUF / pdb_00007zuf
EMDB ID : EMD-14975
Title : Saccharomyces cerevisiae L-BC virus, open particle, C5 reconstruction
Authors : Grybchuk, D.; Prochazkova, M.; Fuzik, T.; Konovalovas, A.; Serva, S.;
Yurchenko, V.; Plevka, P.
Deposited on : 2022-05-12
Resolution : 10.00 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:

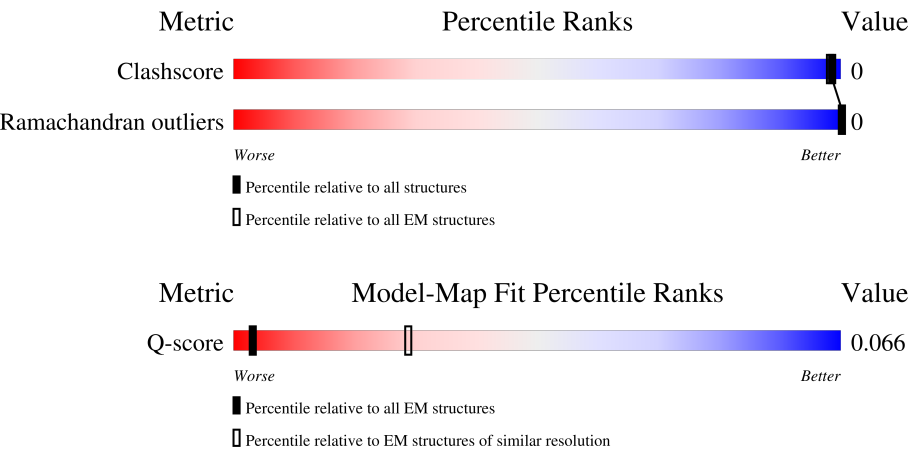
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 10.00 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.



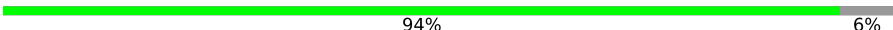
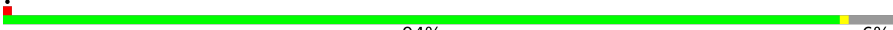
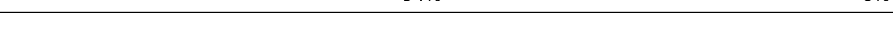
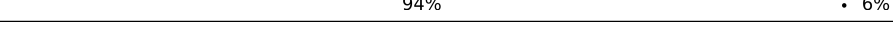
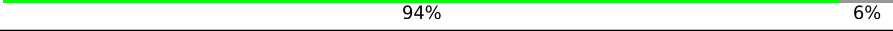
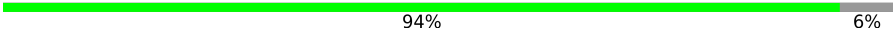
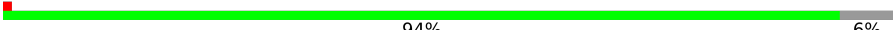
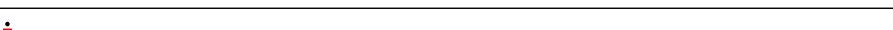
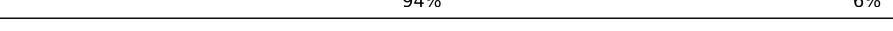
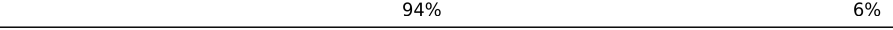
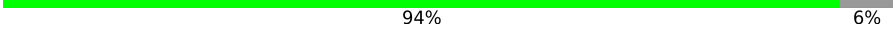
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	147 (9.50 - 10.50)

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	697	94% 6%
1	B	697	94% 6%
1	C	697	94% 6%
1	D	697	16% 94% 6%
1	E	697	88% 12%

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Mol	Chain	Length	Quality of chain
1	F	697	
1	G	697	
1	H	697	
1	I	697	
1	J	697	
1	K	697	
1	L	697	
1	M	697	
1	N	697	
1	O	697	
1	P	697	
1	Q	697	
1	R	697	
1	S	697	
1	T	697	
1	U	697	
1	V	697	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 56080 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 Major capsid protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	B	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	A	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	L	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	C	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	M	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	D	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	E	613	Total	C	N	O	0	0
			2452	1226	613	613		
1	N	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	F	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	O	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	G	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	P	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	H	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	Q	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	I	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	R	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	J	658	Total	C	N	O	0	0
			2632	1316	658	658		

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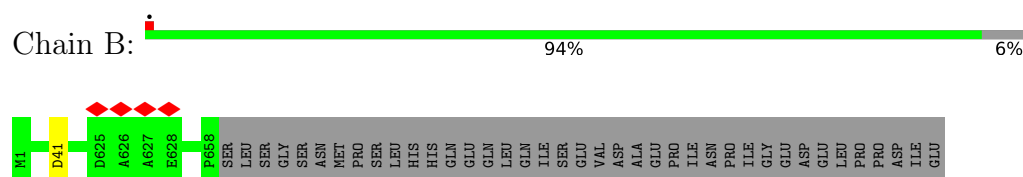
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Mol	Chain	Residues	Atoms				AltConf	Trace
1	S	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	K	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	T	593	Total	C	N	O	0	0
			2372	1186	593	593		
1	U	422	Total	C	N	O	1	0
			1692	846	423	423		
1	V	538	Total	C	N	O	0	0
			2152	1076	538	538		

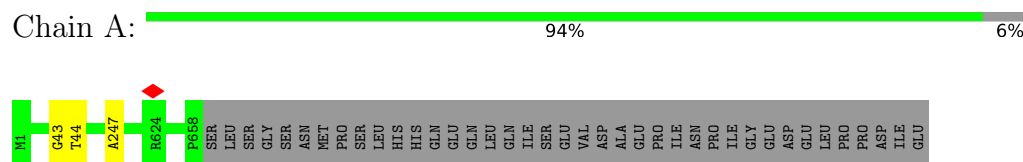
3 Residue-property plots [i](#)

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.

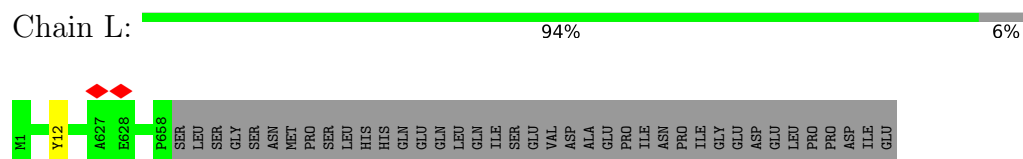
- Molecule 1: Major capsid protein



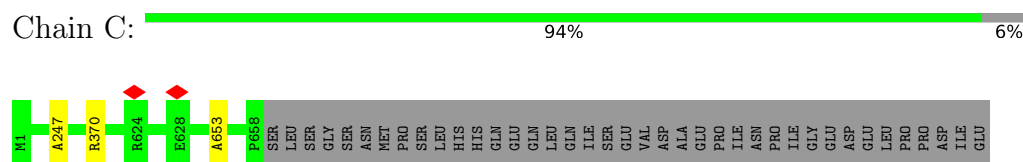
- Molecule 1: Major capsid protein



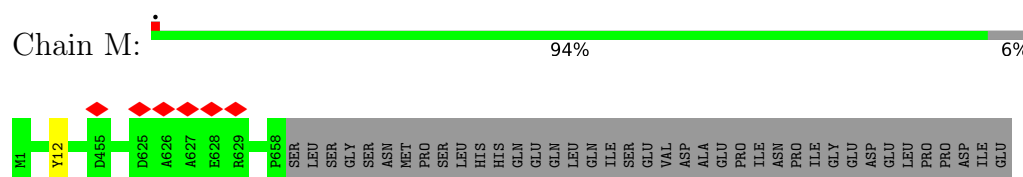
- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein

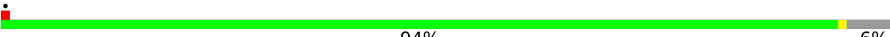


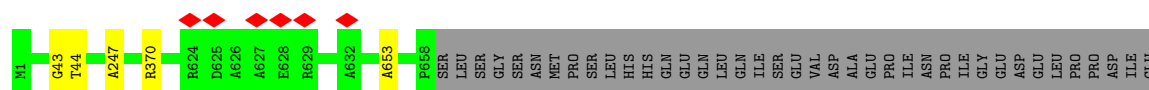
- Molecule 1: Major capsid protein



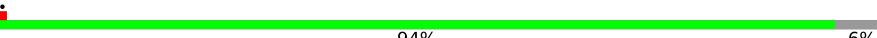
-  M1
  D41
  D625
  A626
  A627
  E628
  E629
  P658
 LEU
 SER
 GLY
 SER
 SER
 ASN
 MET
 PRO
 SER
 HIS
 HIS
 GLN
 GLU
 GLN
 LEU
 LEU
 GLN
 ILE
 SER
 SER
 GLU
 VAL
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 LEU
 PRO
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 THR

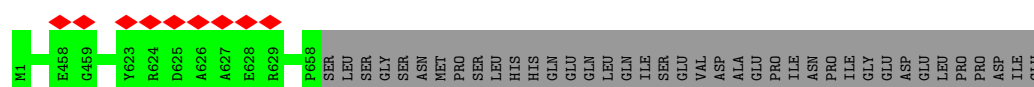
- Molecule 1: Major capsid protein

Chain G:  94% 6%

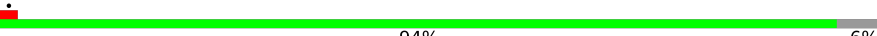


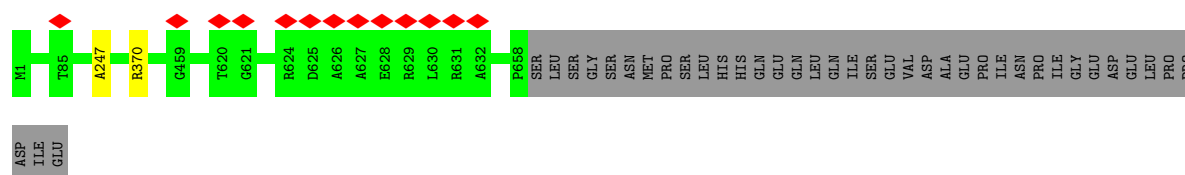
- Molecule 1: Major capsid protein

Chain P:  94% 6%

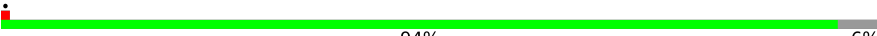


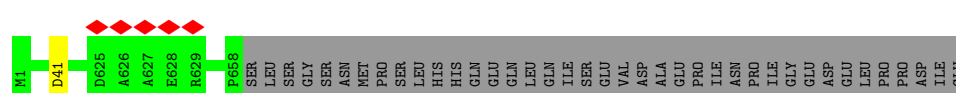
- Molecule 1: Major capsid protein

Chain H:  94% 6%



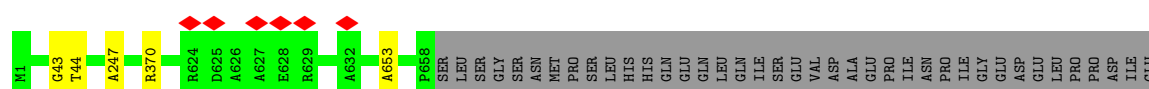
- Molecule 1: Major capsid protein

Chain Q:  94% 6%



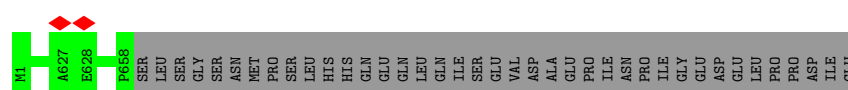
- Molecule 1: Major capsid protein

Chain I:  94% 6%

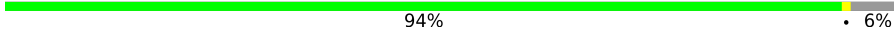


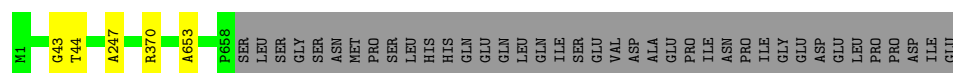
- Molecule 1: Major capsid protein

Chain R:  94% 6%

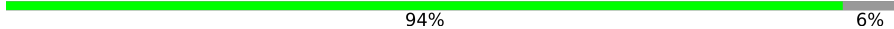


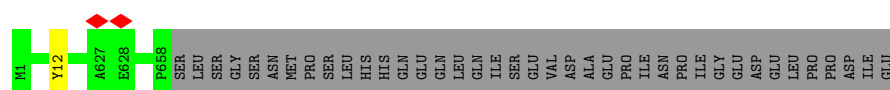
- Molecule 1: Major capsid protein

Chain J:  94% 6%

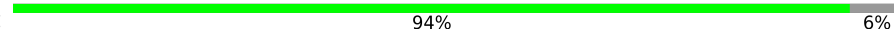


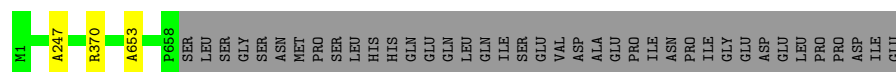
- Molecule 1: Major capsid protein

Chain S:  94% 6%



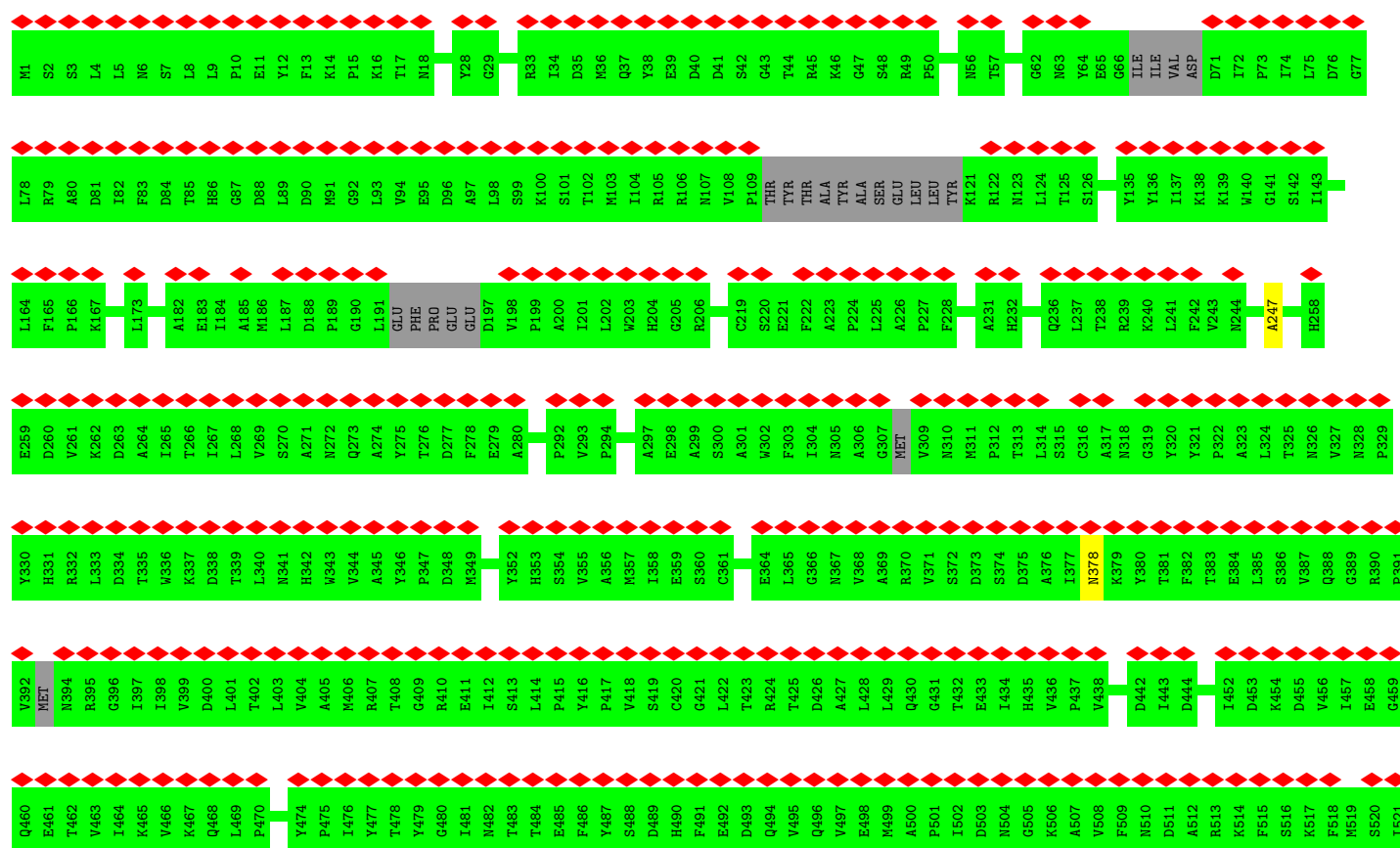
- Molecule 1: Major capsid protein

Chain K:  94% 6%

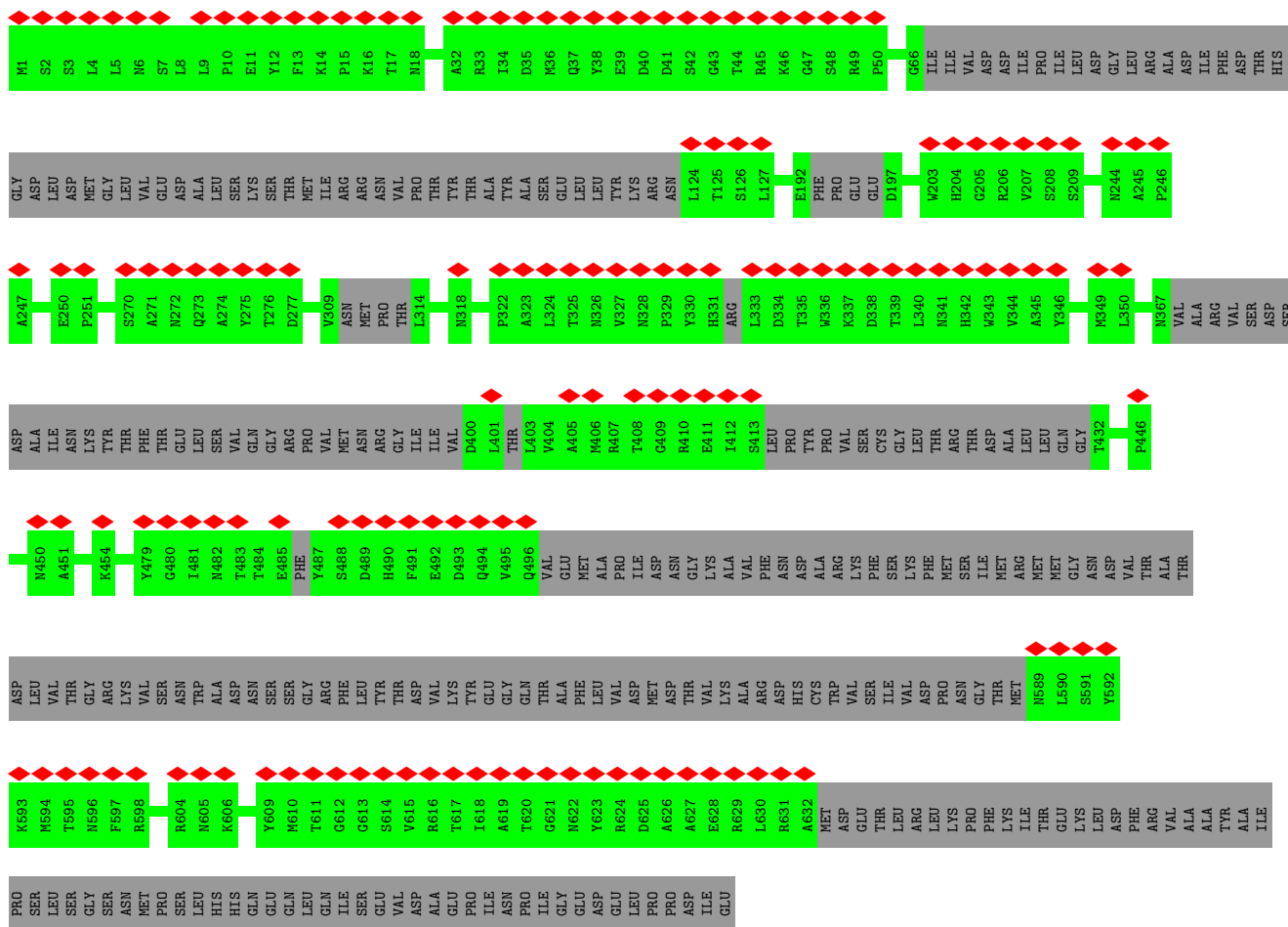


- Molecule 1: Major capsid protein

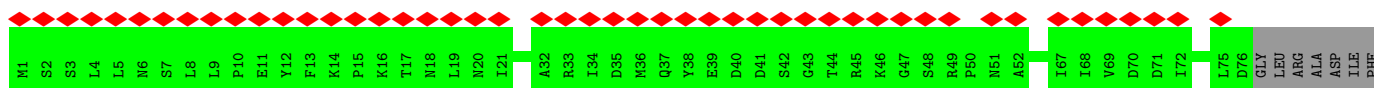
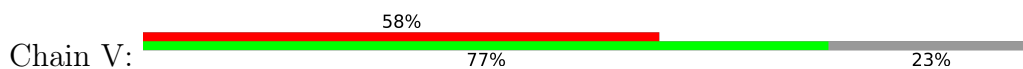
Chain T:  59% 85% 15%



- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein



L639	K640	P641	F642	K643	I644	T645	E646	K647	L648	D649	F650	R651	V652	A653	A654	Y655	A656	I657	P658	SER	LEU	SER	GLY	SER	ASN	MET	PRO	SER	LEU	HIS	HIS	GLN	GLU	GLN	LEU	GLN	ILE	ILE	SER	GLU	VAL	THR	ASP	ILE	ALA	ALA	THR	GLY	ASN	TYR	PRO	PRO	ILE	GLY	GLU	ASP	GLU	LEU	PRO	PRO	PRO	ASP	ILE	GLU
E559	G560	Q561	T562	A563	F564	L565	V566	K572	N579	D583	F584	N585	G586	T587	M588	N589	L590	S591	Y592	K593	M594	T595	N596	F597	P607	L608	Y609	G612	GLY	SER	VAL	ARG	THR	THR	ILE	ASP	ALA	ALA	THR	GLY	ASN	TYR	PRO	PRO	ILE	ASP	ALA	A627	E628	R629	L630	R631	A632	M633	D634	E635	T636	L637	R638					
D489	H490	F491	E492	D493	Q494	V495	Q496	V497	E498	M499	A500	P501	I502	D503	N504	G505	K506	A507	V508	F509	N510	D511	A512	R513	K514	F515	S516	K517	F518	M519	S520	T521	M522	R523	M524	A531	T532	D533	L534	V535	T536	G537	R538	K539	V540	S541	M542	G549	R550	F551	L552	Y553	T554	D555	V556	K557	Y558							
T423	R424	T425	Q430	G431	T432	E433	I434	H435	V436	P437	V438	V439	V440	M445	P446	Q447	Y448	Y449	M450	A451	I452	D453	K454	D455	V456	I457	E458	G459	Q460	E461	T462	V463	I464	K465	V466	K467	Q468	L469	P470	P471	A472	M473	Y474	P475	I476	Y477	T478	Y479	G480	I481	N482	T483	T484	E485	F486	Y487	S488							
V363	E364	L365	G366	N367	V368	A369	R370	V371	S372	D373	S374	D375	A376	I377	N378	K379	V380	T381	F382	T383	E384	L385	S386	V387	Q388	G389	R390	P391	V392	M393	N394	R395	G396	I397	I398	V399	D400	L401	T402	L403	V404	A405	M406	R407	T408	G409	R410	E411	I412	S413	L414	P415	Y416	P417	V418	S419	C420	G421	L422					
A299	S300	A301	I304	V309	N310	M311	P312	T313	L314	S315	C316	A317	ASN	GLY	TYR	TYR	PRO	ALA	PRO	ALA	ILE	LEU	THR	ASN	VAL	ASN	PRO	TYR	HIS	ARG	LEU	ASP	THR	LYS	ASP	ALA	ALA	THR	ILE	LEU	VAL	ASN	ALA	GLN	ALA	T276	E279	A280	A281	Y282	L283	M284	L285	A286	Q287	E298								
K147	D148	A149	I150	H156	M161	R162	Q163	L164	F165	P166	K167	S168	R169	S172	L173	E174	S175	S176	L177	E181	A182	E183	I184	A185	M186	L187	D188	PRO	G190	L191	E192	F193	P194	E195	E196	D197	V198	I201	LEU	TRP	HIS	GLY	ARG	VAL	SER	ARG	ALA	T212	C213	I214	L215	A218												
ASP	THR	HIS	GLY	ASP	LEU	ASP	MET	GLY	LEU	VAL	GLU	ASP	ALA	LEU	SER	LYS	SER	THR	MET	THR	ILE	ARG	ASN	VAL	PRO	THR	THR	T112	A113	Y114	A115	S116	E117	L118	L119	Y120	K121	L124	T125	S126	L127	F128	Y129	M130	M131	L132	R133	L134	Y135	Y136	I137	K138	K139	W140	G141	Y145	E146							

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1120	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 ($e^-/\text{\AA}^2$)	36	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	8.452	Depositor
Minimum map value	-3.718	Depositor
Average map value	-0.229	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	0.8	Depositor
Map size (Å)	603.97125, 603.97125, 603.97125	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07852, 1.07852, 1.07852	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	1.46	0/2631	1.99	2/3287 (0.1%)
1	B	1.47	0/2635	2.00	0/3292
1	C	1.47	0/2631	1.99	2/3287 (0.1%)
1	D	1.47	0/2631	1.99	2/3287 (0.1%)
1	E	1.46	0/2451	1.99	2/3062 (0.1%)
1	F	1.47	0/2631	1.99	2/3287 (0.1%)
1	G	1.47	0/2631	1.99	2/3287 (0.1%)
1	H	1.46	0/2631	1.99	2/3287 (0.1%)
1	I	1.47	0/2631	1.99	2/3287 (0.1%)
1	J	1.46	0/2631	1.99	2/3287 (0.1%)
1	K	1.46	0/2631	1.99	2/3287 (0.1%)
1	L	1.47	0/2635	2.00	0/3292
1	M	1.46	0/2635	2.00	0/3292
1	N	1.47	0/2635	2.00	0/3292
1	O	1.47	0/2635	2.00	0/3292
1	P	1.46	0/2635	2.00	0/3292
1	Q	1.47	0/2635	2.00	0/3292
1	R	1.46	0/2635	2.00	0/3292
1	S	1.46	0/2635	2.00	0/3292
1	T	1.46	0/2366	1.98	4/2947 (0.1%)
1	U	1.45	0/1682	2.00	0/2085
1	V	1.46	0/2145	1.96	0/2669
All	All	1.46	0/56038	1.99	24/69974 (0.0%)

There are no bond length outliers.

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	247	ALA	CA-C-N	5.47	125.29	120.10
1	D	247	ALA	C-N-CA	5.47	125.29	120.10
1	C	247	ALA	CA-C-N	5.46	125.28	120.10
1	C	247	ALA	C-N-CA	5.46	125.28	120.10
1	I	247	ALA	CA-C-N	5.44	125.27	120.10

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	2632	0	694	2	0
1	B	2636	0	696	1	0
1	C	2632	0	694	2	0
1	D	2632	0	694	1	0
1	E	2452	0	649	0	0
1	F	2632	0	694	2	0
1	G	2632	0	694	4	0
1	H	2632	0	694	1	0
1	I	2632	0	694	4	0
1	J	2632	0	694	4	0
1	K	2632	0	694	2	0
1	L	2636	0	696	1	0
1	M	2636	0	696	1	0
1	N	2636	0	696	0	0
1	O	2636	0	696	1	0
1	P	2636	0	696	0	0
1	Q	2636	0	696	1	0
1	R	2636	0	696	0	0
1	S	2636	0	696	1	0
1	T	2372	0	625	0	0
1	U	1692	0	436	0	0
1	V	2152	0	556	0	0
All	All	56080	0	14776	14	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 0.

The worst 5 of 14 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:G:43:GLY:HA3	1:I:44:THR:O	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:44:THR:O	1:I:43:GLY:HA3	2.04	0.57
1:A:43:GLY:HA3	1:J:44:THR:O	2.04	0.57
1:A:44:THR:O	1:J:43:GLY:HA3	2.04	0.56
1:I:370:ARG:O	1:K:653:ALA:N	2.44	0.47

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	B	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	C	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	D	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	E	611/697 (88%)	566 (93%)	45 (7%)	0	100	100
1	F	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	G	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	H	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	I	656/697 (94%)	604 (92%)	52 (8%)	0	100	100
1	J	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	K	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	L	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	M	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	N	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	O	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	P	657/697 (94%)	614 (94%)	43 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Q	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	R	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	S	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	T	581/697 (83%)	538 (93%)	43 (7%)	0	100	100
1	U	403/697 (58%)	376 (93%)	27 (7%)	0	100	100
1	V	524/697 (75%)	489 (93%)	35 (7%)	0	100	100
All	All	13936/15334 (91%)	12923 (93%)	1013 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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](#)

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 ⓘ

There are no chain breaks in this entry.

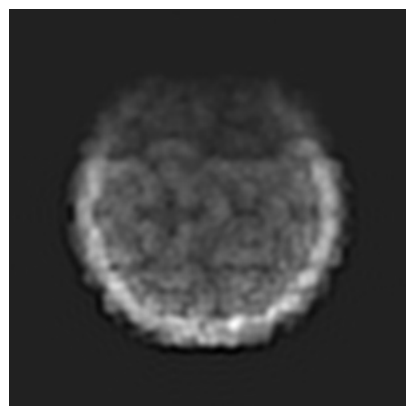
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14975. These allow visual inspection of the internal detail of the map and identification of artifacts.

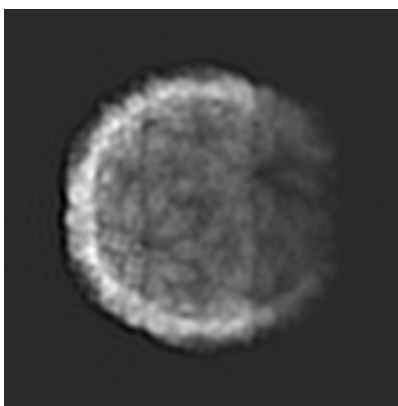
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

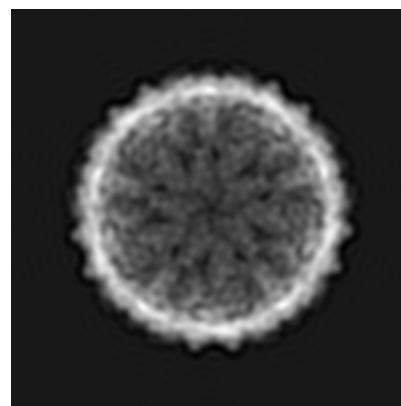
6.1.1 Primary map



X

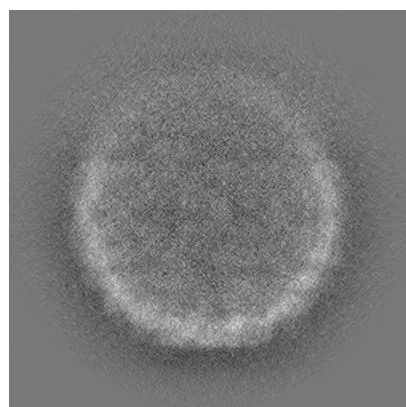


Y

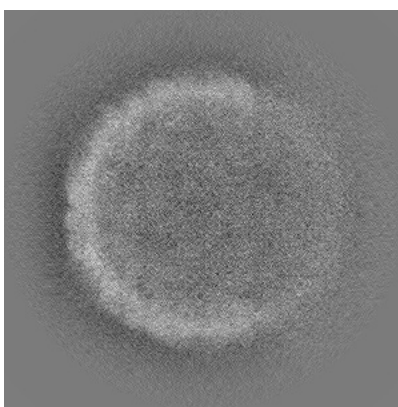


Z

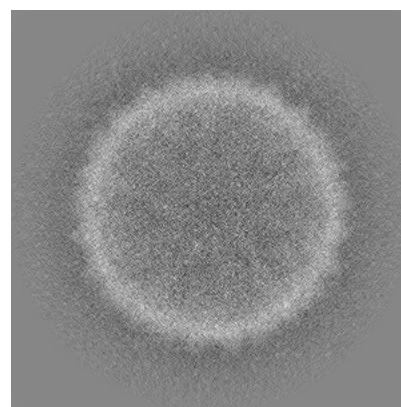
6.1.2 Raw map



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: 280

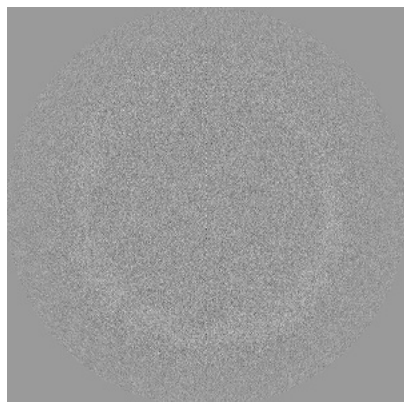


Y Index: 280

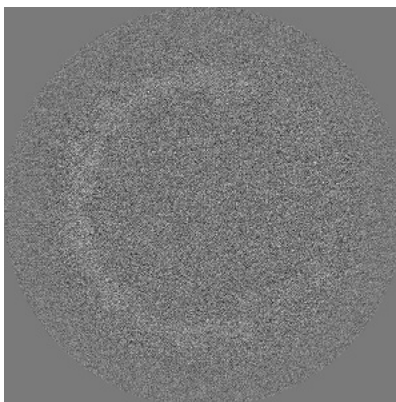


Z Index: 280

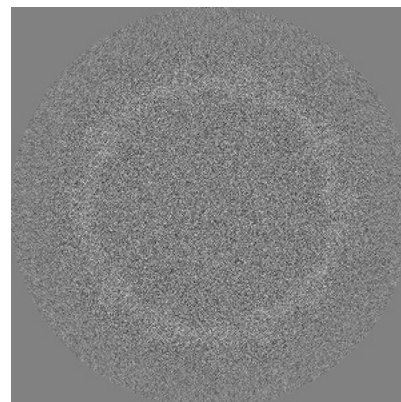
6.2.2 Raw map



X Index: 280



Y Index: 280

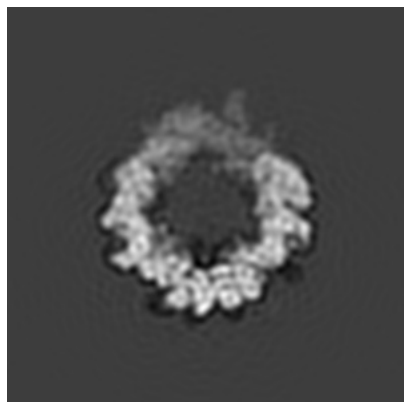


Z Index: 280

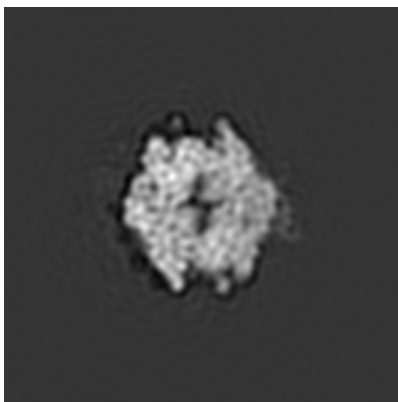
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

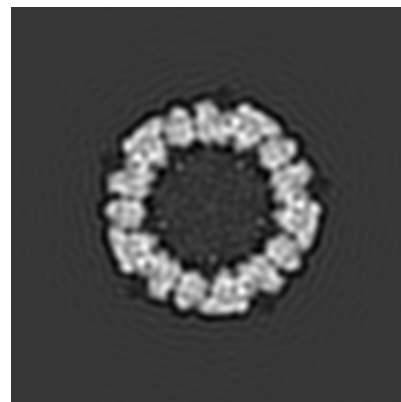
6.3.1 Primary map



X Index: 141

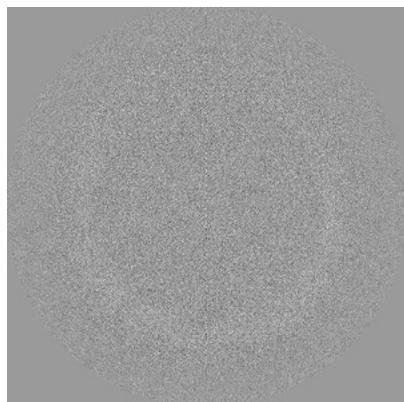


Y Index: 117

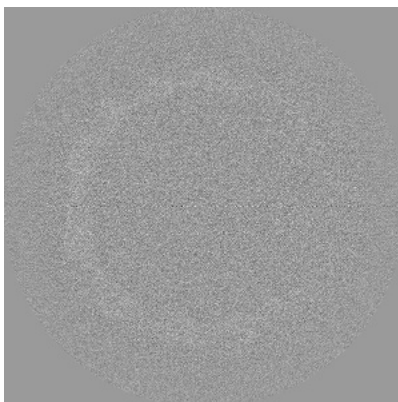


Z Index: 143

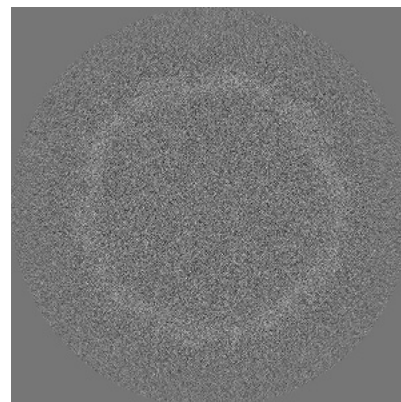
6.3.2 Raw map



X Index: 280



Y Index: 279

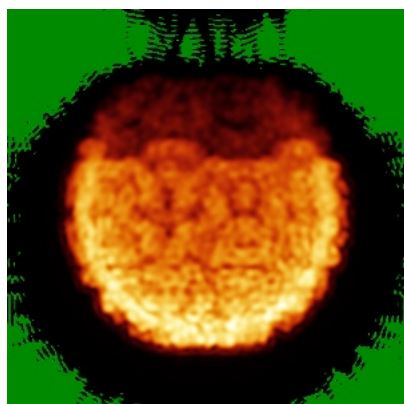


Z Index: 261

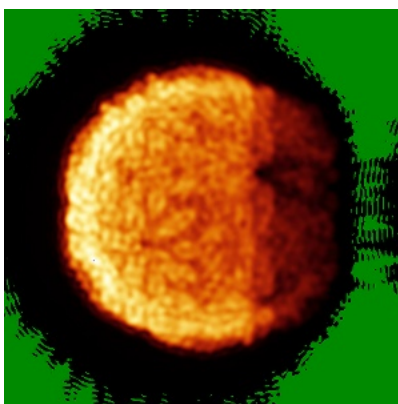
The images above show the largest variance slices of the map in three orthogonal directions.

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

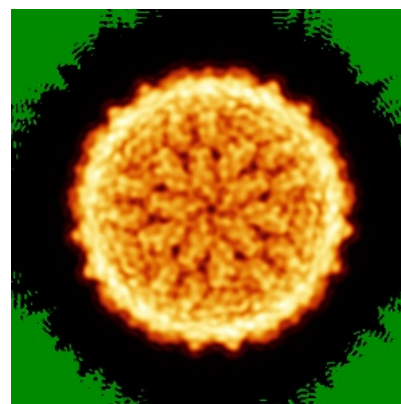
6.4.1 Primary map



X

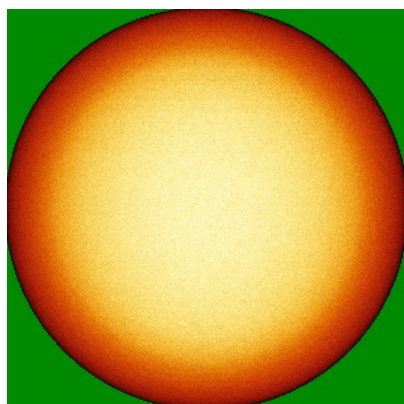


Y

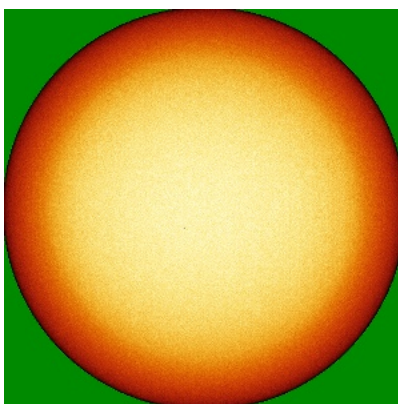


Z

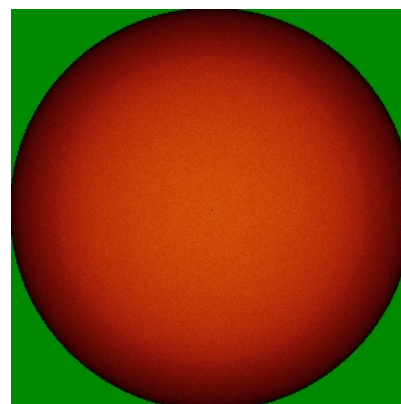
6.4.2 Raw map



X



Y

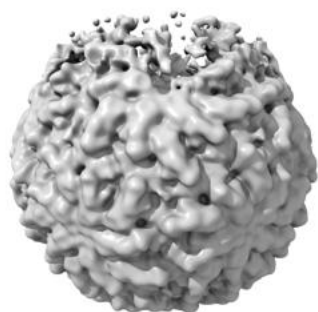


Z

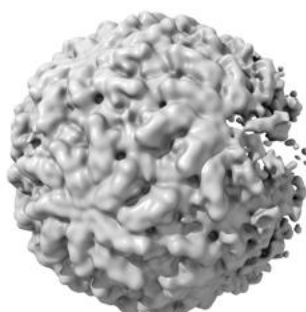
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

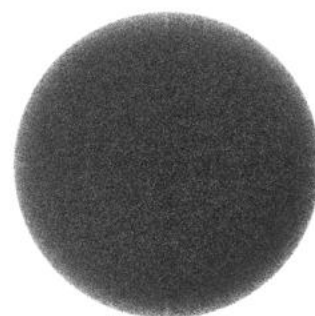
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

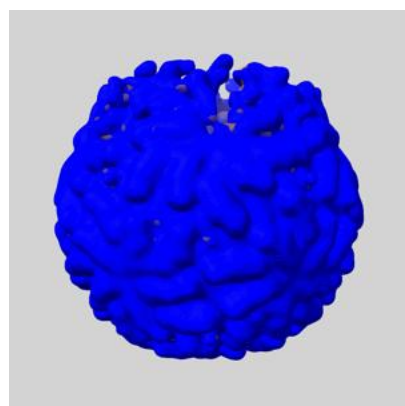
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

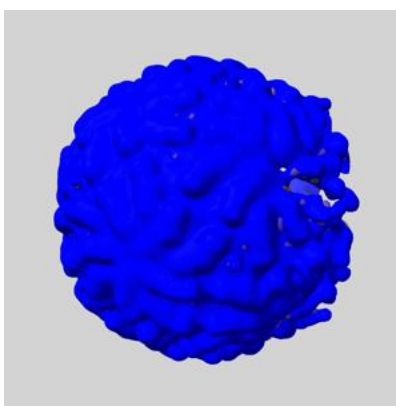
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

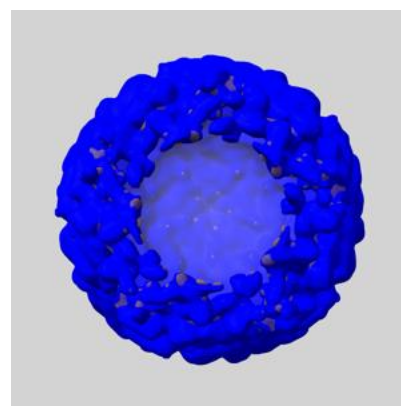
6.6.1 emd_14975_msk_1.map [i](#)



X



Y

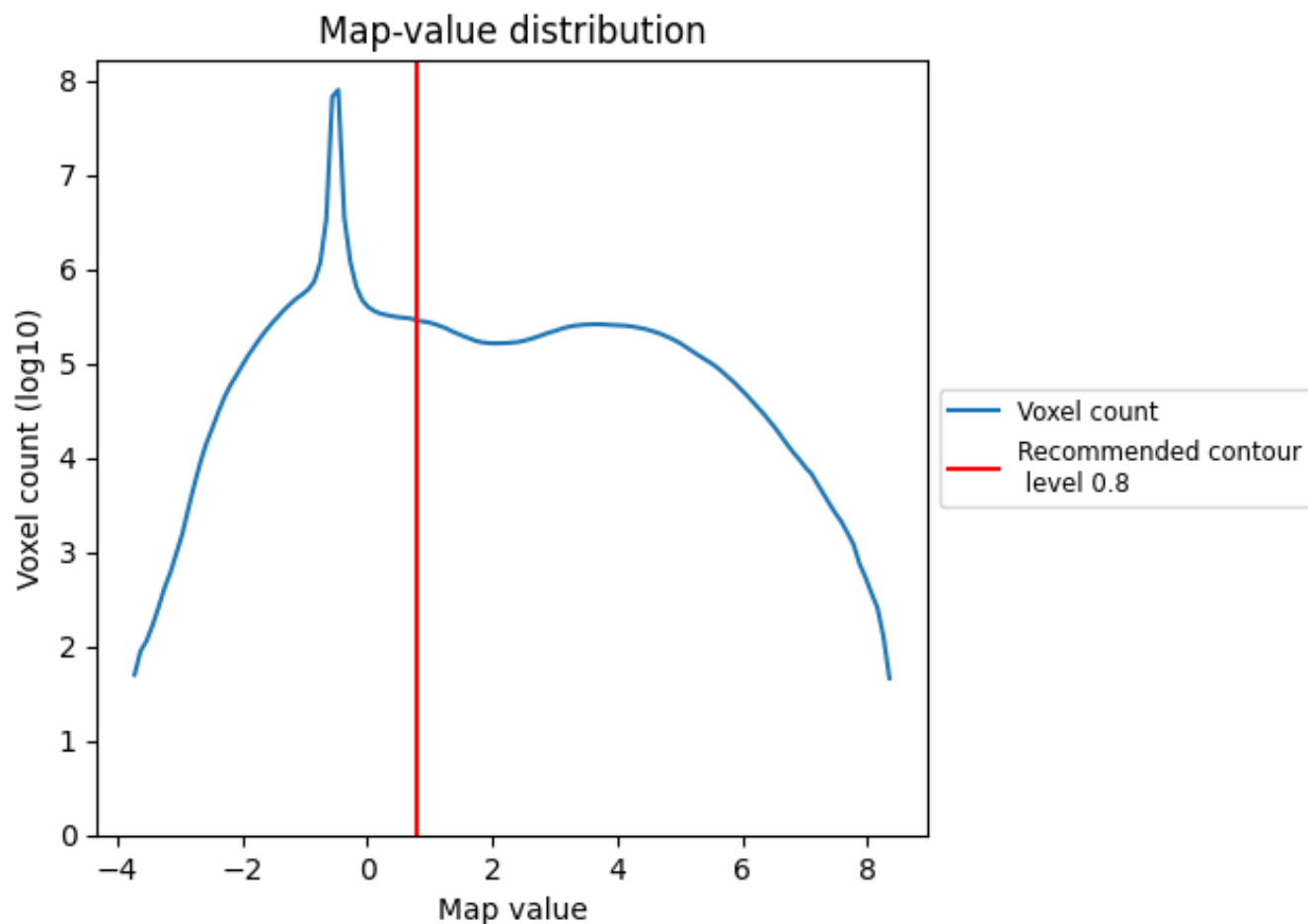


Z

7 Map analysis [i](#)

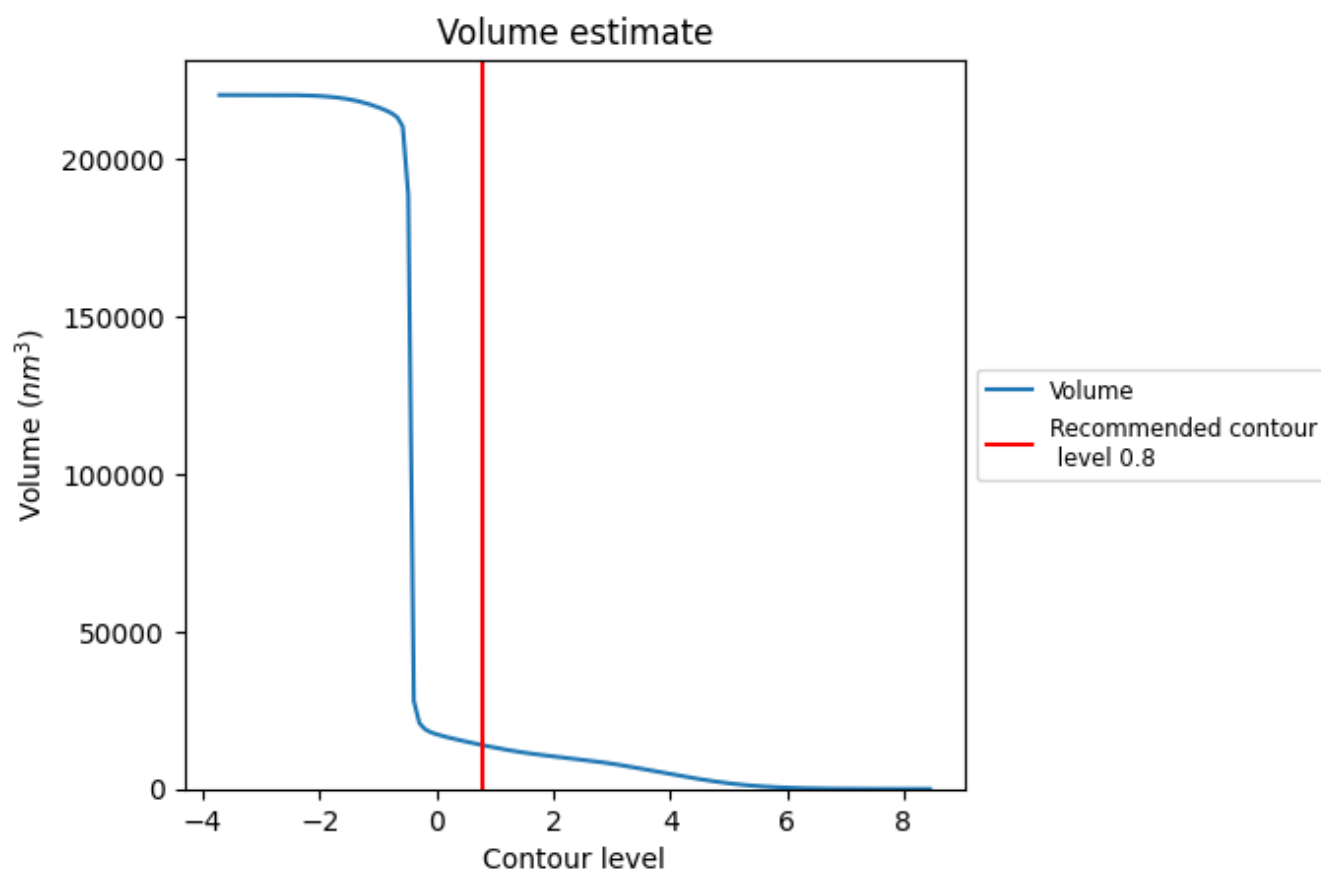
This section contains the results of statistical analysis of the map.

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.

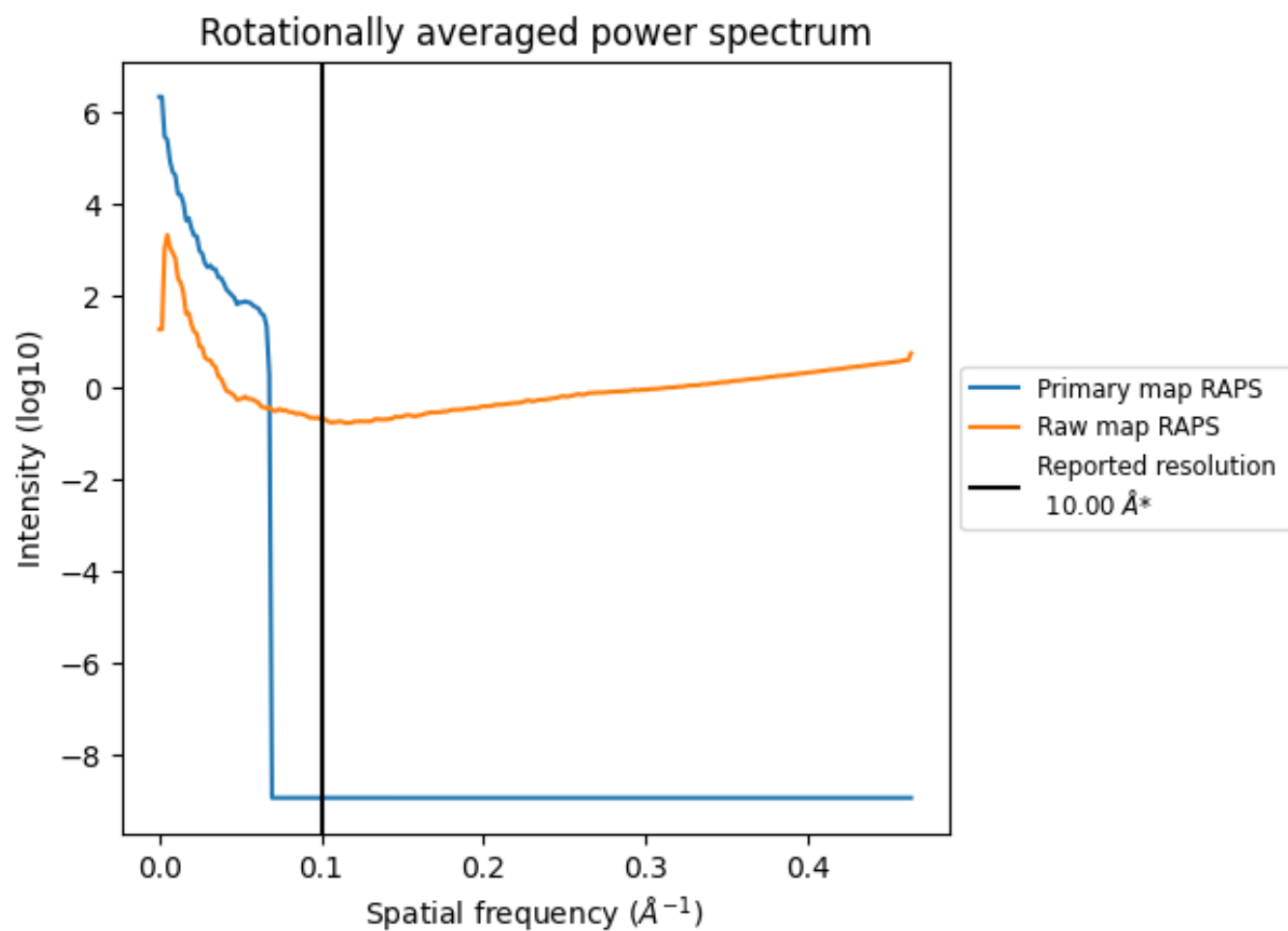
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 13861 nm^3 ; this corresponds to an approximate mass of 12521 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 ⓘ

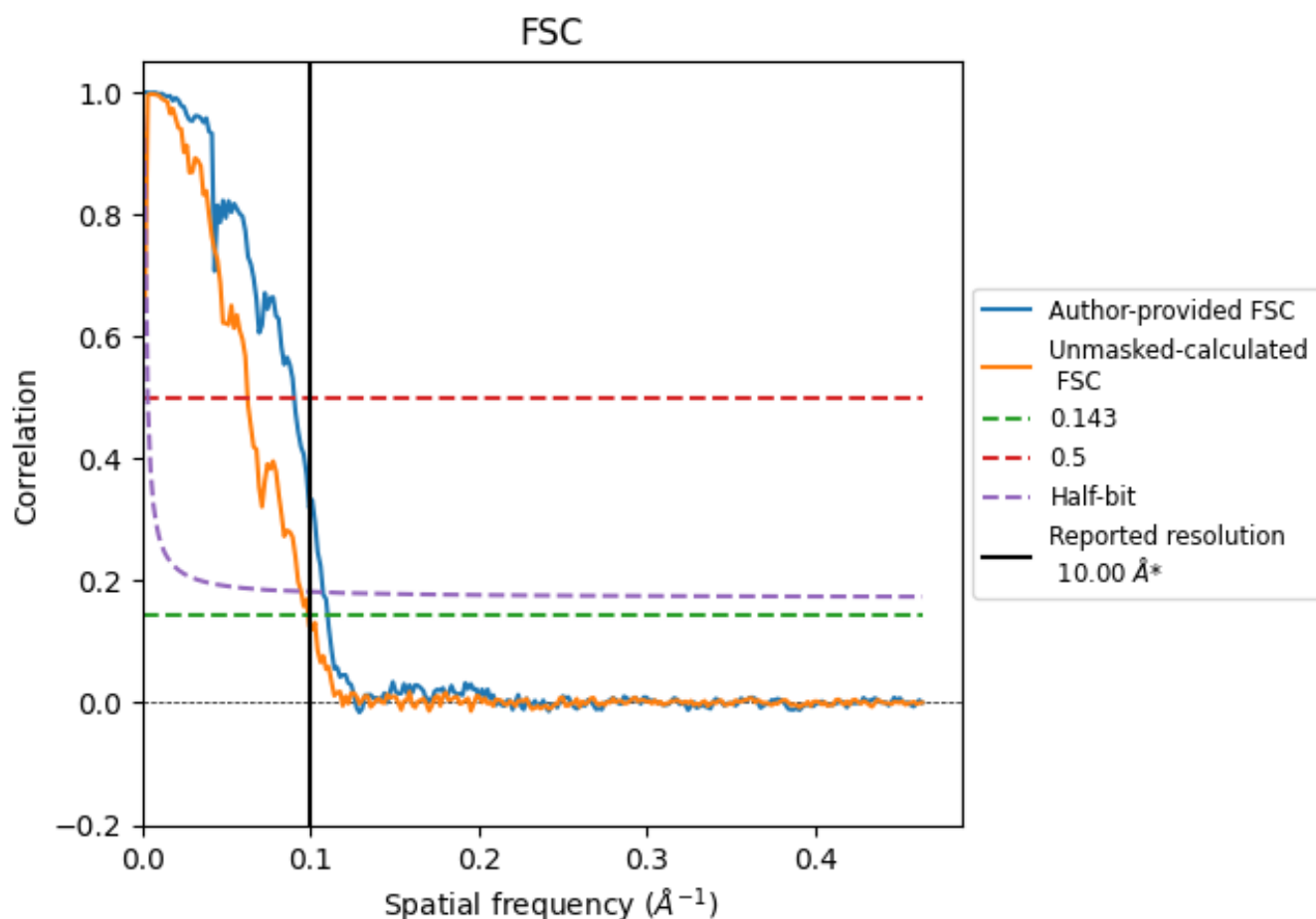


*Reported resolution corresponds to spatial frequency of 0.100 $\text{\AA}^{-1}$

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 0.100 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	10.00	-	-
Author-provided FSC curve	9.07	11.07	9.30
Unmasked-calculated*	10.13	15.95	476.19

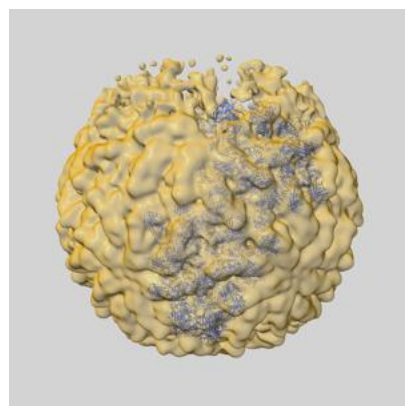
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

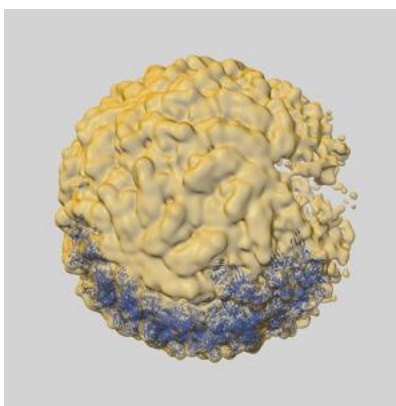
This section contains information regarding the fit between EMDB map EMD-14975 and PDB model 7ZUF. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlays

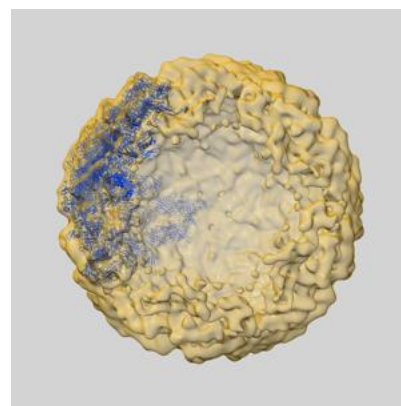
9.1.1 Map-model overlay [i](#)



X

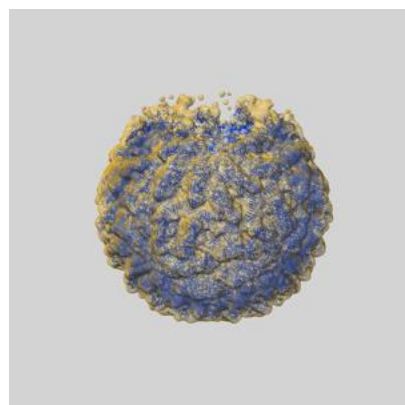


Y

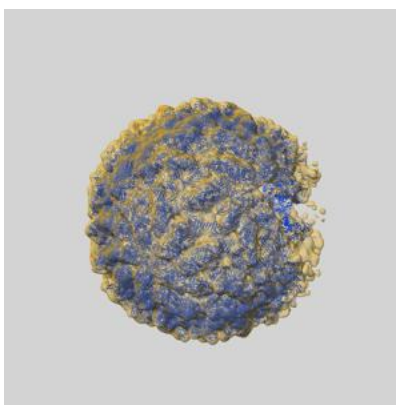


Z

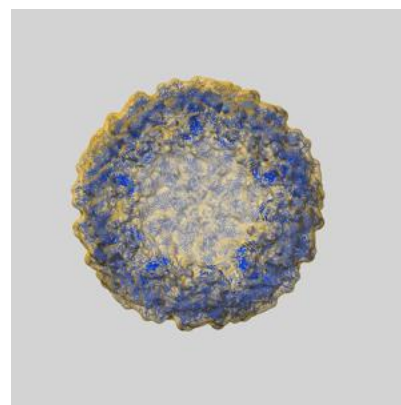
9.1.2 Map-model assembly overlay [i](#)



X



Y



Z

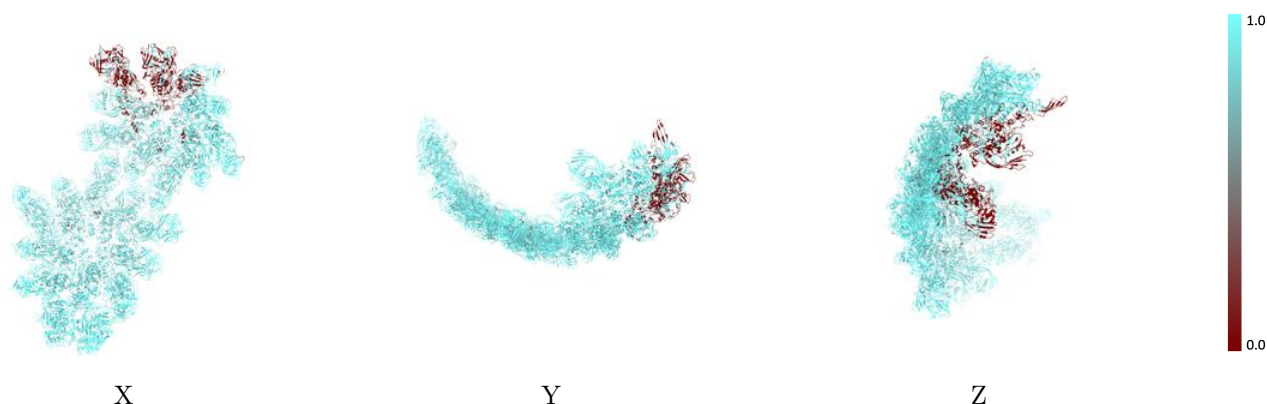
The images above show the 3D surface view of the map at the recommended contour level 0.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



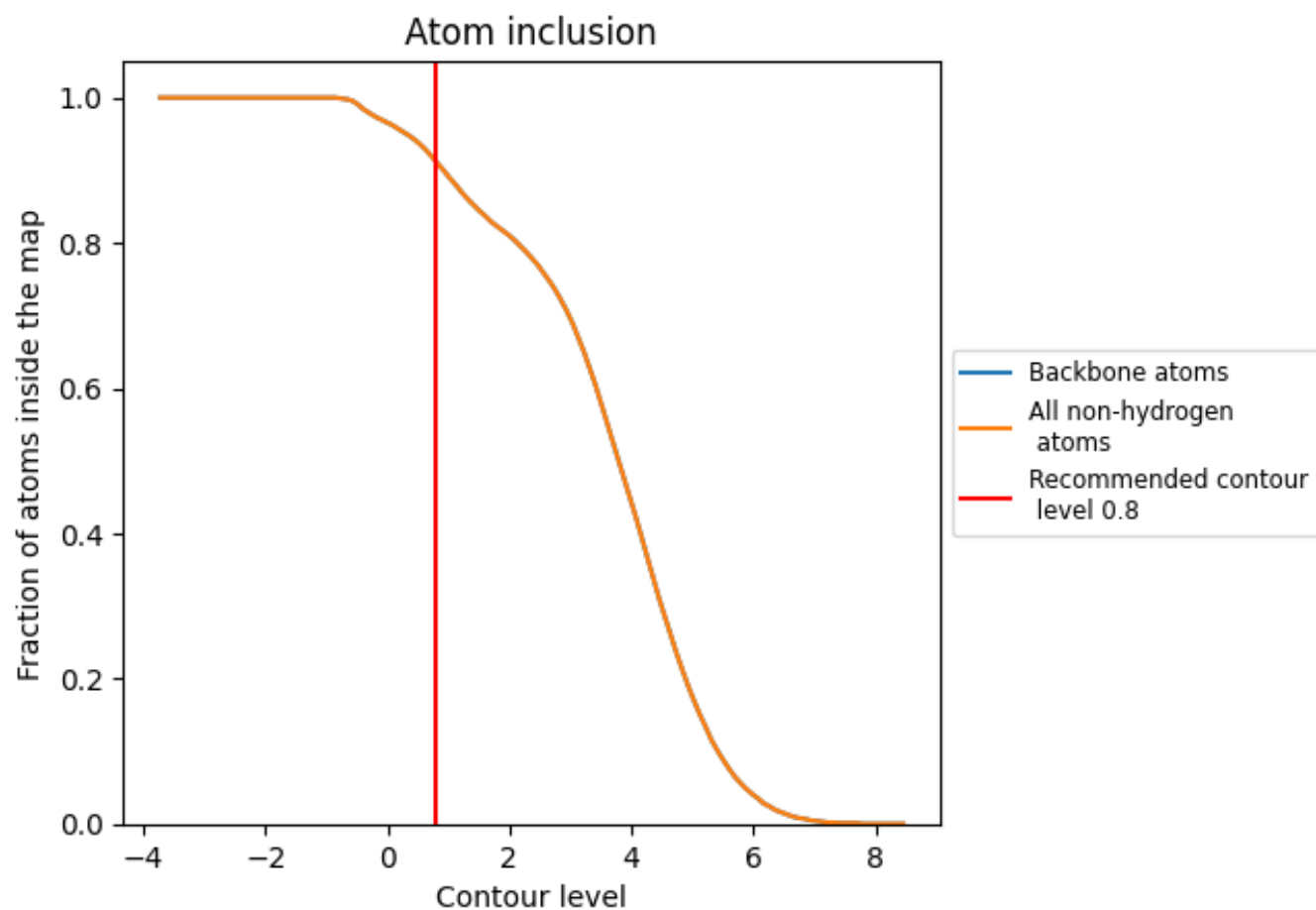
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.8).

9.4 Atom inclusion ⓘ



At the recommended contour level, 91% of all backbone atoms, 91% 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 (0.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9120	 0.0660
A	 0.9990	 0.0760
B	 0.9940	 0.0790
C	 0.9960	 0.0760
D	 0.8020	 0.0420
E	 0.9780	 0.0600
F	 0.9910	 0.0750
G	 0.9920	 0.0680
H	 0.9760	 0.0680
I	 0.9910	 0.0700
J	 0.9970	 0.0790
K	 0.9990	 0.0780
L	 0.9970	 0.0820
M	 0.9880	 0.0760
N	 0.9940	 0.0800
O	 0.9920	 0.0790
P	 0.9830	 0.0740
Q	 0.9920	 0.0750
R	 0.9970	 0.0830
S	 0.9950	 0.0780
T	 0.2770	 0.0080
U	 0.6210	 0.0000
V	 0.2310	 0.0060

