



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:34 PM UTC

PDB ID : 8C8M / pdb_00008c8m
EMDB ID : EMD-16484
Title : In vitro structure of the Nitrosopumilus maritimus S-layer - Composite map
between two and six-fold symmetrised
Authors : von Kuegelgen, A.; Bharat, T.
Deposited on : 2023-01-20
Resolution : 2.87 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:

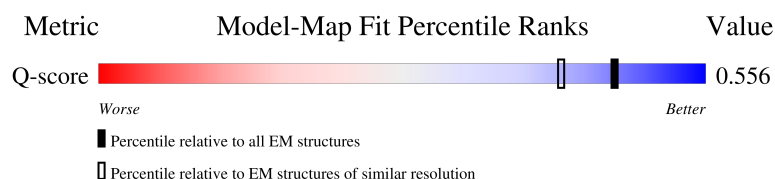
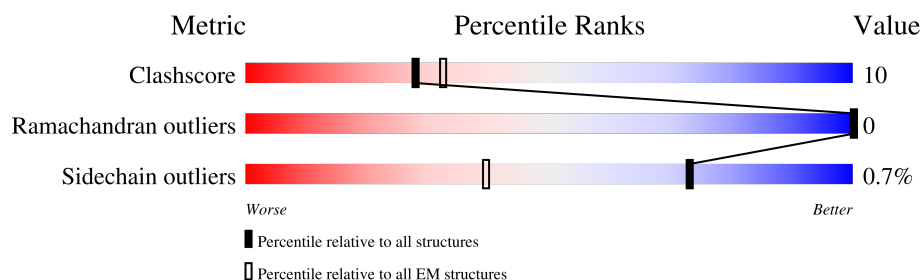
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.87 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	12062 (2.37 - 3.37)

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	1734	
1	B	1734	
1	C	1734	
1	D	1734	

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Mol	Chain	Length	Quality of chain
1	E	1734	 72% 19% 9%
1	F	1734	 72% 19% 9%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 70506 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.

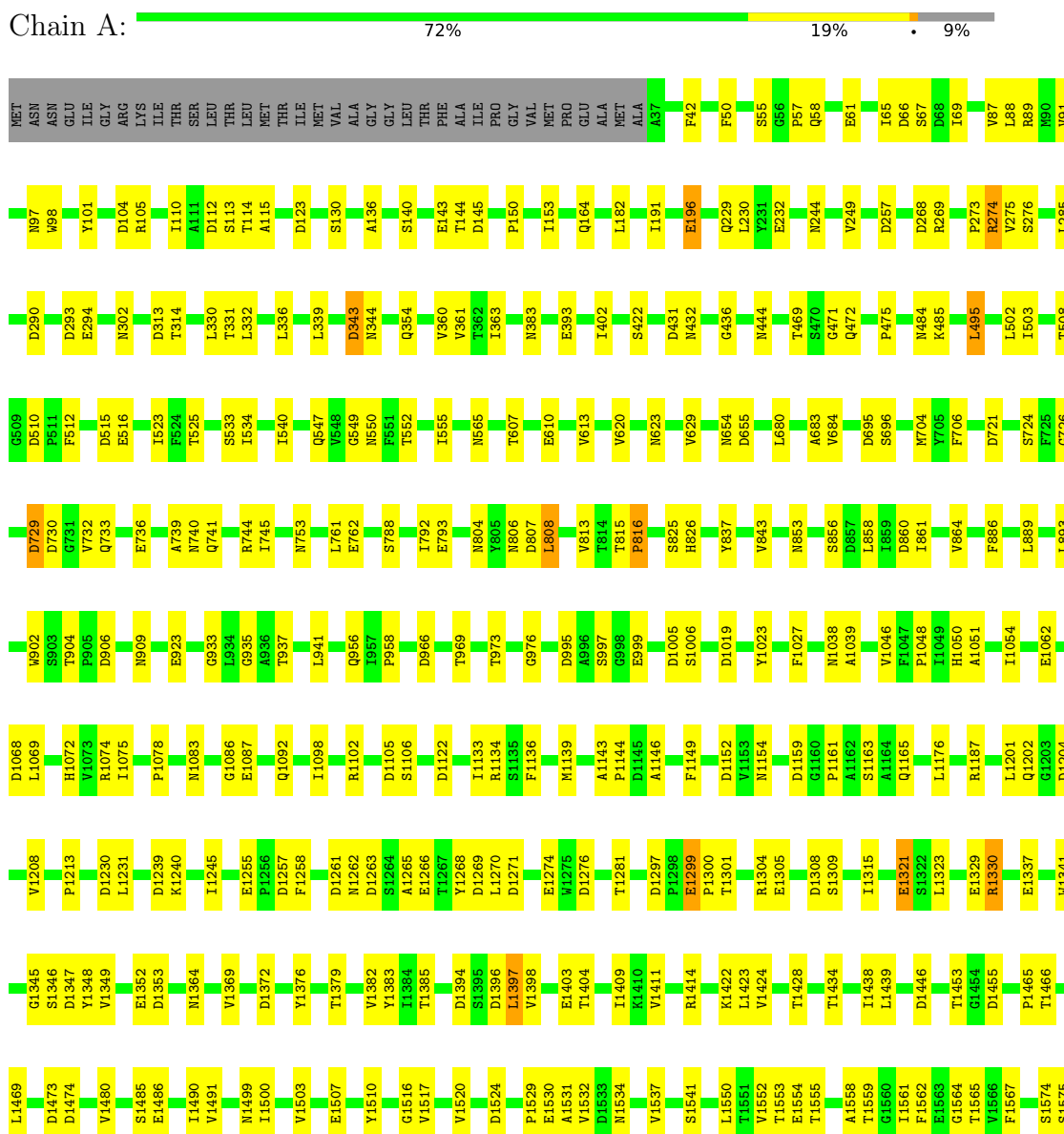
- Molecule 1 is a protein called Cell surface protein.

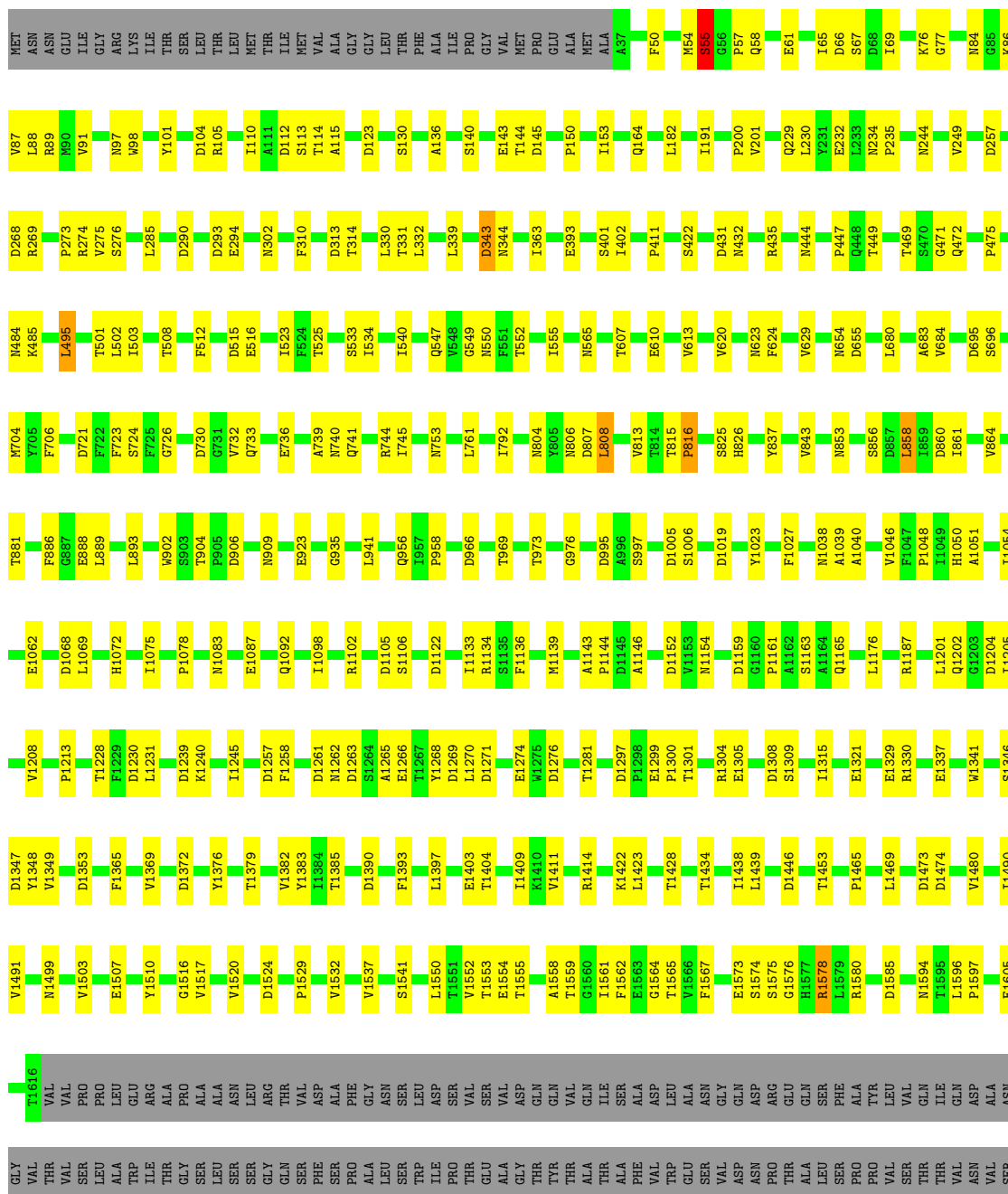
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1580	Total	C	N	O	S	0	0
			11751	7234	1888	2610	19		
1	B	1580	Total	C	N	O	S	0	0
			11751	7234	1888	2610	19		
1	C	1580	Total	C	N	O	S	0	0
			11751	7234	1888	2610	19		
1	D	1580	Total	C	N	O	S	0	0
			11751	7234	1888	2610	19		
1	E	1580	Total	C	N	O	S	0	0
			11751	7234	1888	2610	19		
1	F	1580	Total	C	N	O	S	0	0
			11751	7234	1888	2610	19		

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.

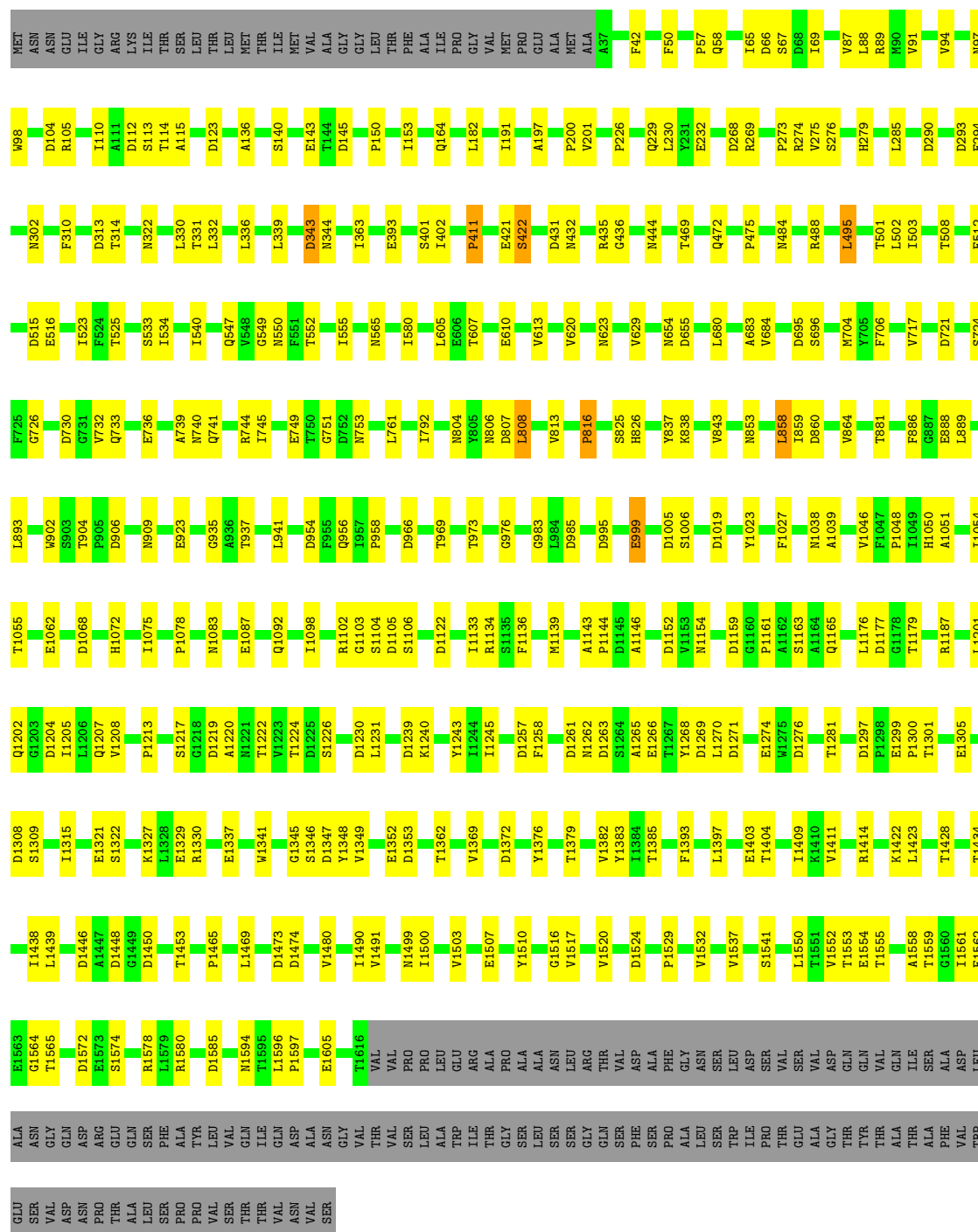
• Molecule 1: Cell surface protein





- Molecule 1: Cell surface protein

Chain C:  72% 19% 9%



- Molecule 1: Cell surface protein

Chain D:  72% 19% 9%

V275	L495	D721	F986	E1062	D1204	Y1348	D1473	H1594	GLN	THR
S276	T501	F722	L889	D1068	V1208	V1349	D1474	T1595	ILE	THR
L285	L502	F723	L893	L1069	P1213	E1352	V1480	L1596	GLN	THR
D290	I503	F724	L902	H1072	D1230	D1353	V1491	P1597	ASP	ASN
D293	T508	F725	S903	R1074	L1231	F1365	V1499	E1605	ALA	VAL
E294	F512	D730	T904	I1075	D1239	V1369	I1500	T1616	GLY	VAL
N302	D515	G731	P905	P1078	K1240	D1372	V1503	VAL	THR	THR
F310	E516	Q733	N909	N1083	I1245	Y1376	E1507	PRO	LEU	LEU
D313	I523	E736	E923	E1087	D1257	T1379	Y1510	GLU	ALA	THR
T314	F524	A739	G935	Q1092	F1258	V1382	Y1510	ARG	THR	THR
T331	T525	N740	G935	Q1092	D1261	Y1382	G1516	ALA	ALA	ALA
L332	S533	Q741	L941	I1098	N1262	Y1384	V1517	ALA	ALA	ALA
L336	I534	R744	Q956	R1102	D1263	T1385	V1520	ASN	ALA	ALA
L339	I540	I745	P957	D1105	S1264	D1390	D1524	LEU	LEU	LEU
D343	Q547	N753	P958	S1106	T1267	F1393	P1529	THR	THR	THR
N344	G549	L761	I957	S1106	E1268	L1397	V1532	VAL	THR	THR
I363	N550	E762	T969	D1122	D1289	V1398	V1537	ALA	ALA	ALA
N363	F551	S788	T973	I1133	L1270	G1399	S1541	PHE	ALA	ALA
E393	T552	I792	G976	S1135	D1274	E1403	L1550	PRO	ALA	ALA
S401	I555	N804	D995	F1136	V1275	T1404	T1551	GLY	ALA	ALA
I402	T607	N806	E999	M139	T1281	I1409	V1552	THR	ALA	ALA
P411	E610	D807	I1000	A1143	D1297	V1411	T1553	GLN	ALA	ALA
S422	V613	L808	D1005	D1145	P1298	R1414	E1554	ASP	ALA	ALA
D431	V620	T814	S1006	A1146	E1299	K1422	T1555	GLN	ALA	ALA
N432	N623	T815	D1019	F1149	T1301	L1423	A1558	VAL	ALA	ALA
R435	F624	P816	Y1023	N1154	R1304	T1428	G1560	ILE	ALA	ALA
N444	V629	H826	F1027	N1154	E1305	T1434	I1561	SER	ALA	ALA
P447	N654	Y837	N1038	D1159	D1308	T1438	E1563	ASP	ALA	ALA
Q448	D655	V843	A1039	G1160	S1309	L1439	G1564	VAL	ALA	ALA
T449	L680	N853	A1040	P1161	I1315	D1446	V1566	GLY	ALA	ALA
T469	A683	S856	V1046	S1163	E1321	D1447	F1567	GLN	ALA	ALA
S470	V684	F1047	F1047	Q1165	E1329	D1448	S1574	ASP	ALA	ALA
G471	P1048	P1048	P1048	L1176	R1330	G1449	S1575	ARG	ALA	ALA
D695	L858	I1049	I1049	L1176	E1337	D1450	G1576	GLU	ALA	ALA
S696	H1050	H1050	H1050	R1187	E1341	T1453	H1577	GLN	ALA	ALA
N485	D860	I861	A1051	R1187	W1341	P1465	L1579	SER	ALA	ALA
	T704	L1201	I1054	L1201	S1346	L1469	R1580	PHE	ALA	ALA
	F706	Q1202	T1055	Q1202	D1347		D1585	TYR	ALA	ALA
		G1203		G1203				LEU	VAL	VAL

● Molecule 1: Cell surface protein

Chain F:  72% 19% 9%

MET	W98	D290	F512	MET	ASN	THR	THR	THR	THR	THR
ASN	D104	D293	D515	ASN	ASN	THR	THR	THR	THR	THR
GLU	R105	E294	E516	GLU	GLU	THR	THR	THR	THR	THR
ILE	I110	N302	I523	ILE	ILE	THR	THR	THR	THR	THR
ASN	A111	F310	F524	ASN	ASN	THR	THR	THR	THR	THR
GLY	D112	D313	T525	GLY	GLY	THR	THR	THR	THR	THR
ARG	S113	T314	S533	ARG	ARG	THR	THR	THR	THR	THR
LYS	A115	N322	I534	LYS	LYS	THR	THR	THR	THR	THR
THR	D123	L330	I540	THR	THR	THR	THR	THR	THR	THR
LEU	S130	T331	Q547	LEU	LEU	THR	THR	THR	THR	THR
ALA	A136	R333	V548	ALA	ALA	THR	THR	THR	THR	THR
VAL	S140	T334	G549	VAL	VAL	THR	THR	THR	THR	THR
SER	E143	T335	N550	SER	SER	THR	THR	THR	THR	THR
THR	D145	T336	F551	THR	THR	THR	THR	THR	THR	THR
LEU	T144	L336	T552	LEU	LEU	THR	THR	THR	THR	THR
THR	D145	N344	I555	THR	THR	THR	THR	THR	THR	THR
ASP	P150	T363	N565	ASP	ASP	THR	THR	THR	THR	THR
ALA	T153	E393	I580	ALA	ALA	THR	THR	THR	THR	THR
PRO	Q164	S401	T607	PRO	PRO	THR	THR	THR	THR	THR
GLY	L182	I402	E610	GLY	GLY	THR	THR	THR	THR	THR
THR	T191	P411	V613	THR	THR	THR	THR	THR	THR	THR
ILE	A197	E421	V620	ILE	ILE	THR	THR	THR	THR	THR
ALA	P200	S422	N623	ALA	ALA	THR	THR	THR	THR	THR
ASP	V201	D431	V629	ASP	ASP	THR	THR	THR	THR	THR
GLN	P226	M432	N654	GLN	GLN	THR	THR	THR	THR	THR
THR	Q229	R435	D655	THR	THR	THR	THR	THR	THR	THR
ALA	L230	C436	L680	ALA	ALA	THR	THR	THR	THR	THR
VAL	Y231	M444	A683	VAL	VAL	THR	THR	THR	THR	THR
ASP	E232	T469	V684	ASP	ASP	THR	THR	THR	THR	THR
THR	S251	Q472	D695	THR	THR	THR	THR	THR	THR	THR
GLU	D268	P475	S696	GLU	GLU	THR	THR	THR	THR	THR
VAL	R269	M484	T704	VAL	VAL	THR	THR	THR	THR	THR
ASP	P273	R274	F706	ASP	ASP	THR	THR	THR	THR	THR
ASN	L88	R89	V717	ASN	ASN	THR	THR	THR	THR	THR
PRO	V275	S276	D721	PRO	PRO	THR	THR	THR	THR	THR
LEU	N90	L495	S724	LEU	LEU	THR	THR	THR	THR	THR
THR	V91	T501		THR	THR	THR	THR	THR	THR	THR
ALA	V94	L502		ALA	ALA	THR	THR	THR	THR	THR
PRO	N97	I503		PRO	PRO	THR	THR	THR	THR	THR
VAL				VAL	VAL	THR	THR	THR	THR	THR

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	354860	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; RELION refinement with in-built CTF correction. The function is similar to a Wiener filter, so amplitude correction included.	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48.5	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	10.250	Depositor
Minimum map value	-4.662	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.422	Depositor
Recommended contour level	1.05514	Depositor
Map size ($\text{\AA}$)	349.44, 349.44, 349.44	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.092, 1.092, 1.092	Depositor

5 Model quality

5.1 Standard geometry

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	1.02	13/11941 (0.1%)	1.13	20/16339 (0.1%)
1	B	1.01	9/11941 (0.1%)	1.11	14/16339 (0.1%)
1	C	1.01	8/11941 (0.1%)	1.11	15/16339 (0.1%)
1	D	0.99	6/11941 (0.1%)	1.11	15/16339 (0.1%)
1	E	1.01	9/11941 (0.1%)	1.11	12/16339 (0.1%)
1	F	1.01	9/11941 (0.1%)	1.11	15/16339 (0.1%)
All	All	1.01	54/71646 (0.1%)	1.11	91/98034 (0.1%)

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	2
1	B	0	1
All	All	0	3

The worst 5 of 54 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	858	LEU	C-O	-13.63	1.07	1.23
1	C	858	LEU	C-O	-13.58	1.07	1.23
1	D	858	LEU	C-O	-12.68	1.08	1.23
1	A	858	LEU	C-O	-12.51	1.08	1.23
1	B	858	LEU	C-O	-12.04	1.09	1.23

The worst 5 of 91 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	729	ASP	CA-CB-CG	18.17	130.77	112.60
1	D	58	GLN	CB-CA-C	-8.51	96.00	109.70
1	A	58	GLN	CB-CA-C	-8.49	96.03	109.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	58	GLN	CB-CA-C	-8.39	96.20	109.70
1	B	58	GLN	CB-CA-C	-7.88	97.01	109.70

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	196	GLU	Sidechain
1	A	729	ASP	Sidechain
1	B	55	SER	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	11751	0	10951	253	0
1	B	11751	0	10951	228	0
1	C	11751	0	10951	259	0
1	D	11751	0	10951	265	0
1	E	11751	0	10949	230	0
1	F	11751	0	10951	256	0
All	All	70506	0	65704	1301	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 10.

The worst 5 of 1301 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:C:1217:SER:CB	1:D:1424:VAL:HG21	1.65	1.25
1:A:1424:VAL:HG21	1:F:1217:SER:CB	1.65	1.24
1:C:816:PRO:HD2	1:D:1083:ASN:HD21	1.01	1.14
1:A:1424:VAL:CG2	1:F:1217:SER:HB2	1.82	1.09
1:C:1217:SER:HB2	1:D:1424:VAL:CG2	1.83	1.08

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	1578/1734 (91%)	1517 (96%)	61 (4%)	0	100	100
1	B	1578/1734 (91%)	1518 (96%)	60 (4%)	0	100	100
1	C	1578/1734 (91%)	1520 (96%)	58 (4%)	0	100	100
1	D	1578/1734 (91%)	1518 (96%)	60 (4%)	0	100	100
1	E	1578/1734 (91%)	1518 (96%)	60 (4%)	0	100	100
1	F	1578/1734 (91%)	1520 (96%)	58 (4%)	0	100	100
All	All	9468/10404 (91%)	9111 (96%)	357 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	1312/1438 (91%)	1303 (99%)	9 (1%)	76	90
1	B	1312/1438 (91%)	1303 (99%)	9 (1%)	76	90
1	C	1312/1438 (91%)	1303 (99%)	9 (1%)	76	90
1	D	1312/1438 (91%)	1302 (99%)	10 (1%)	73	89
1	E	1312/1438 (91%)	1301 (99%)	11 (1%)	73	89
1	F	1312/1438 (91%)	1302 (99%)	10 (1%)	73	89
All	All	7872/8628 (91%)	7814 (99%)	58 (1%)	73	90

5 of 58 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	274	ARG
1	F	565	ASN
1	D	1414	ARG
1	F	523	ILE
1	F	58	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 120 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	909	ASN
1	F	682	ASN
1	D	484	ASN
1	F	662	ASN
1	F	1094	ASN

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 [i](#)

There are no chain breaks in this entry.

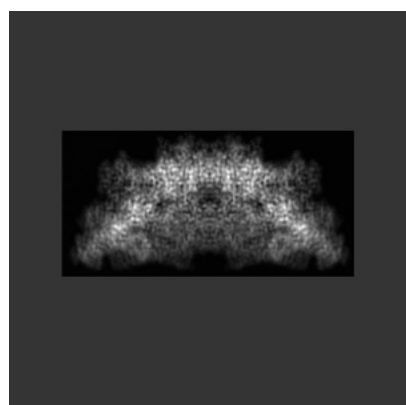
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16484. These allow visual inspection of the internal detail of the map and identification of artifacts.

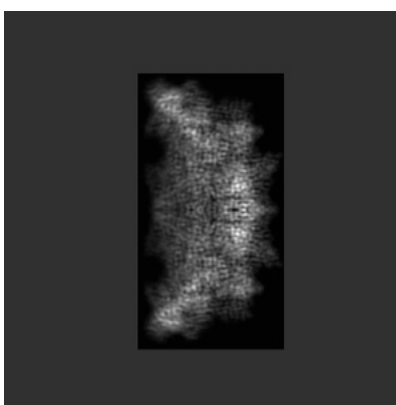
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

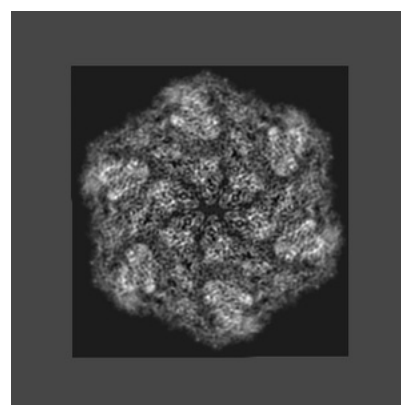
6.1.1 Primary map



X



Y

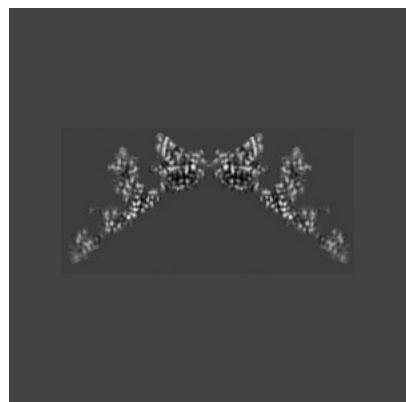


Z

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

6.2 Central slices [i](#)

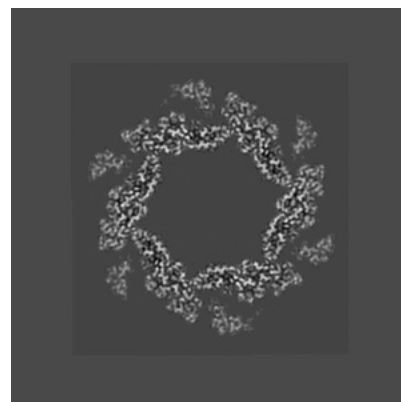
6.2.1 Primary map



X Index: 160



Y Index: 160



Z Index: 160

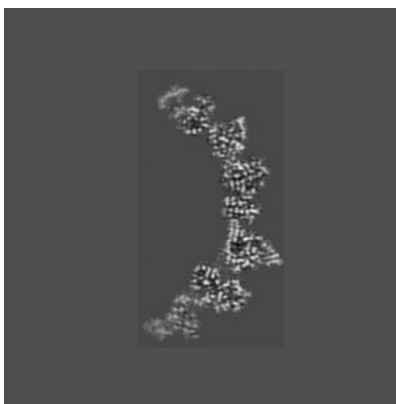
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 156



Y Index: 175

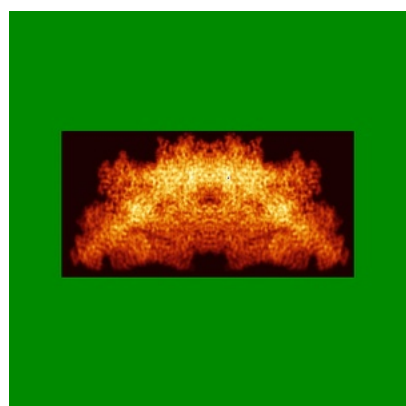


Z Index: 186

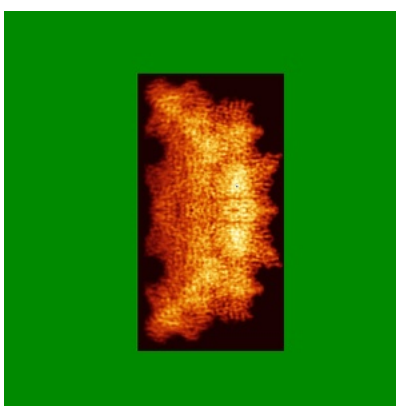
The images above show the largest variance slices of the map in three orthogonal directions.

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

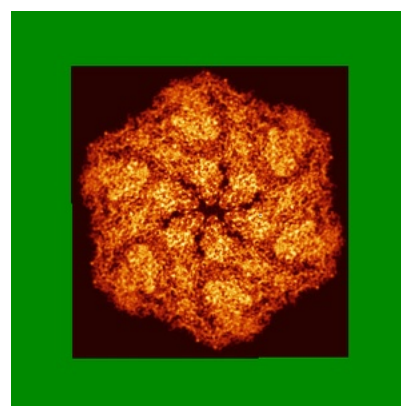
6.4.1 Primary map



X



Y

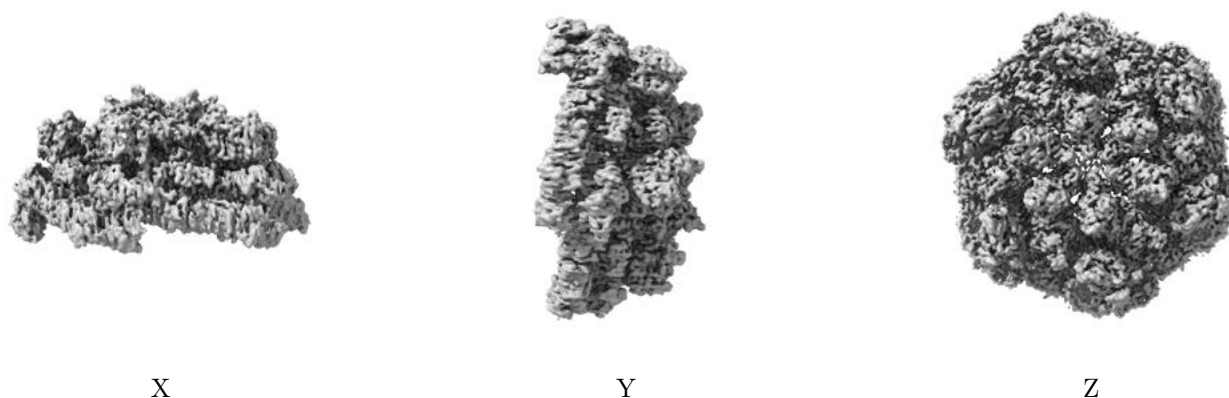


Z

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 1.05514. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

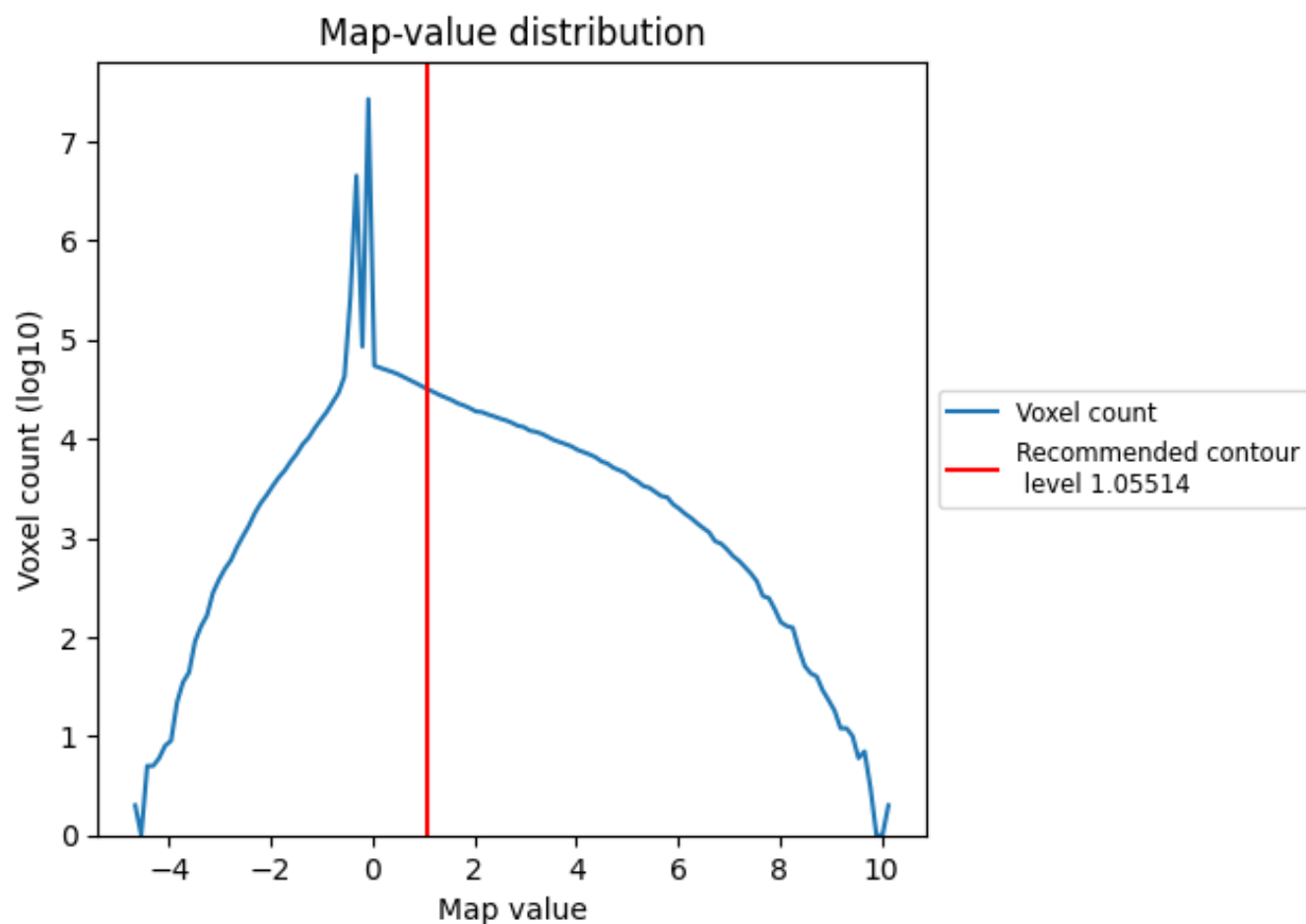
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

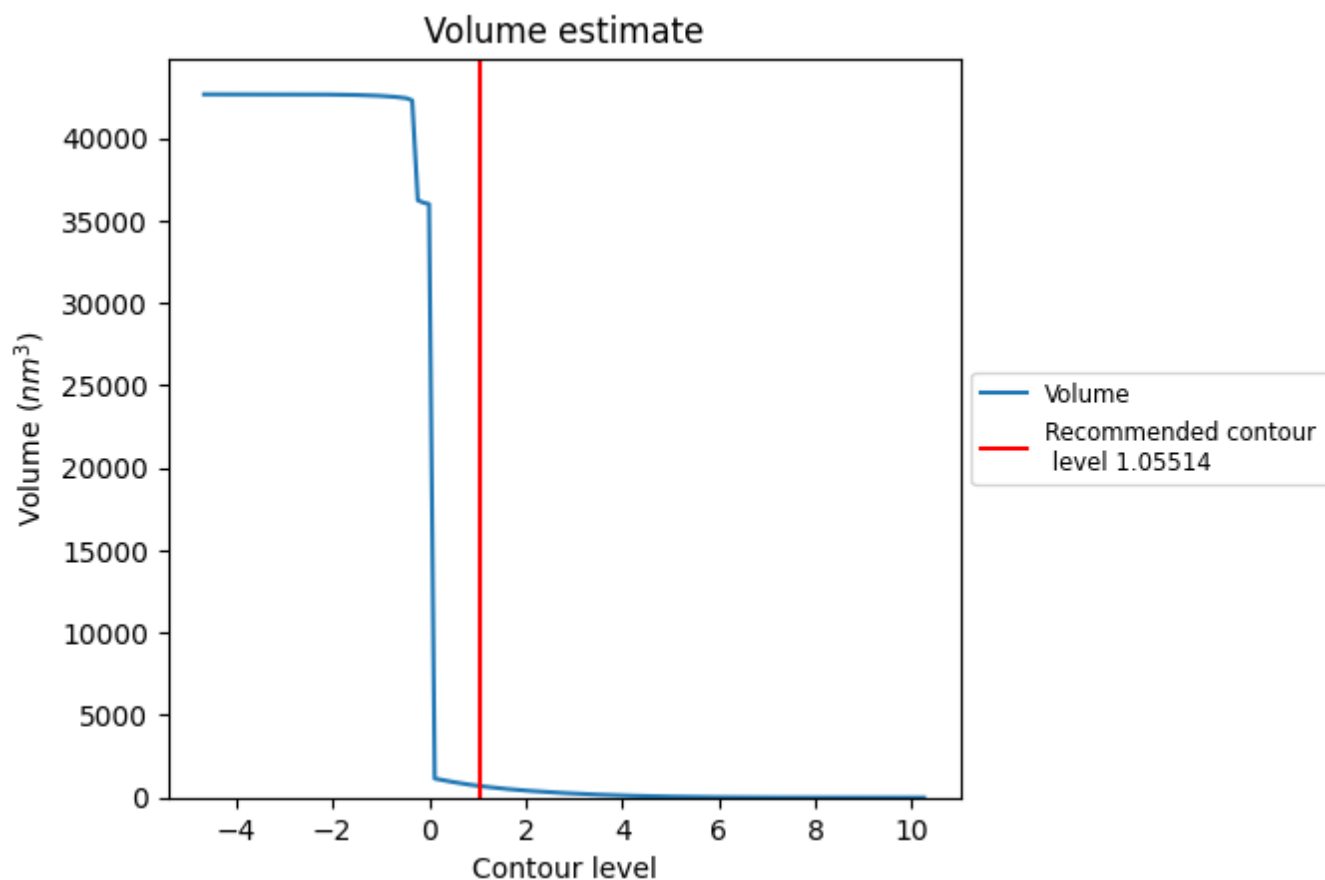
This section contains the results of statistical analysis of the map.

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.

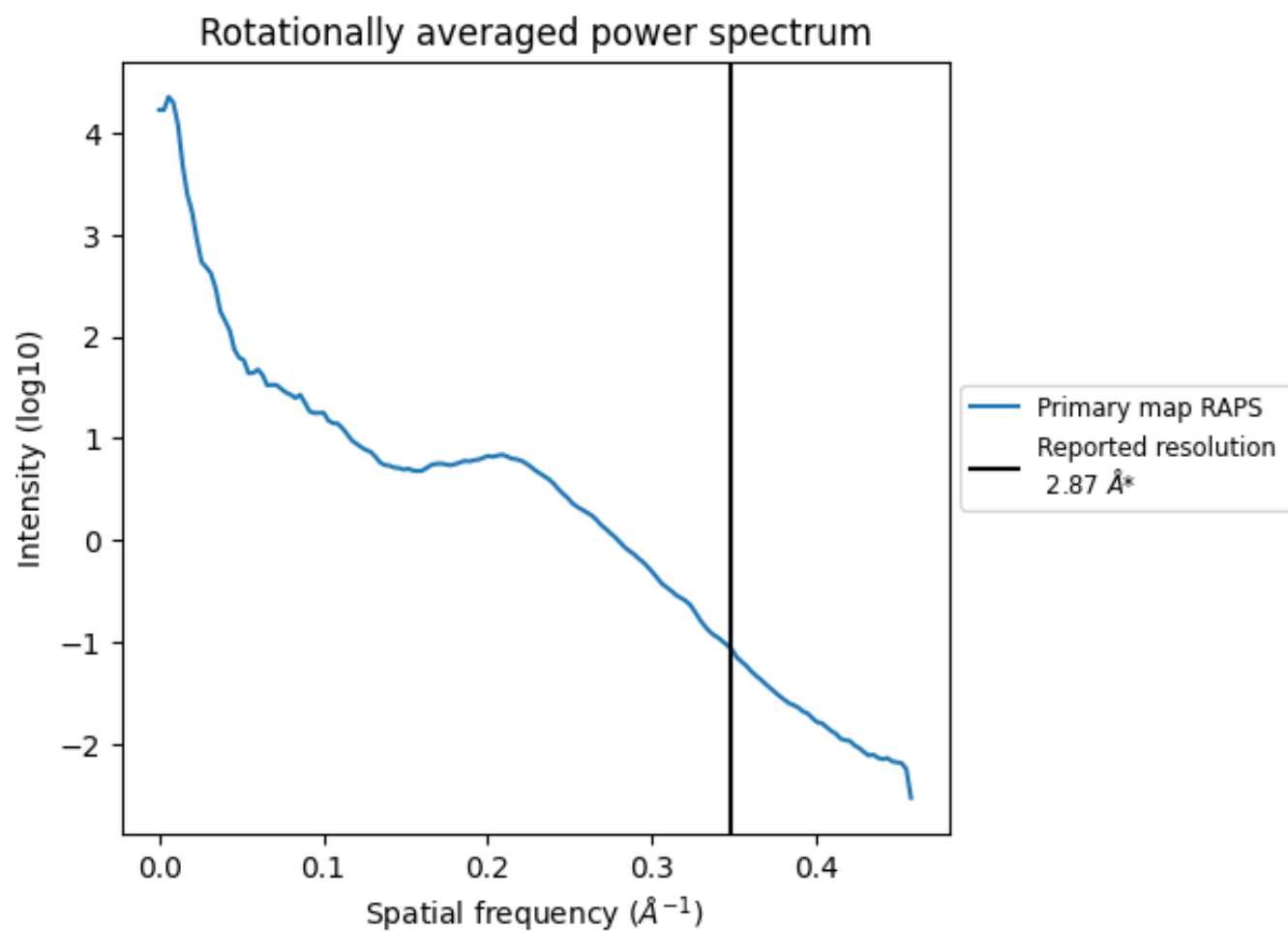
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 697 nm^3 ; this corresponds to an approximate mass of 630 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 0.348 Å⁻¹

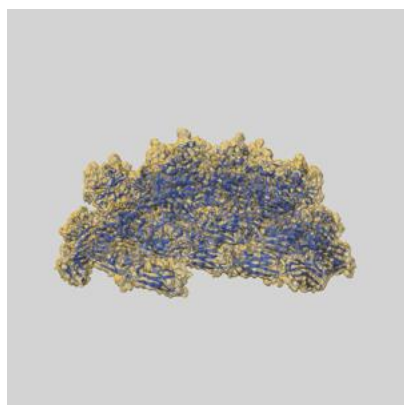
8 Fourier-Shell correlation

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

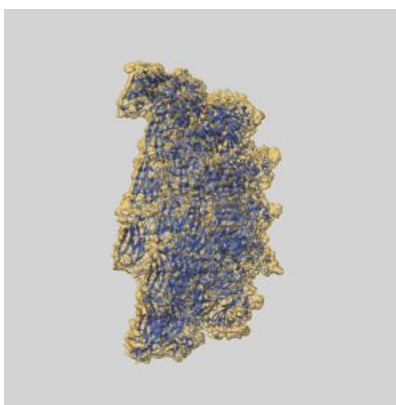
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-16484 and PDB model 8C8M. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

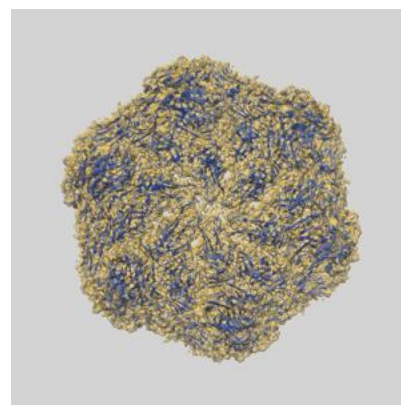
9.1 Map-model overlay [i](#)



X



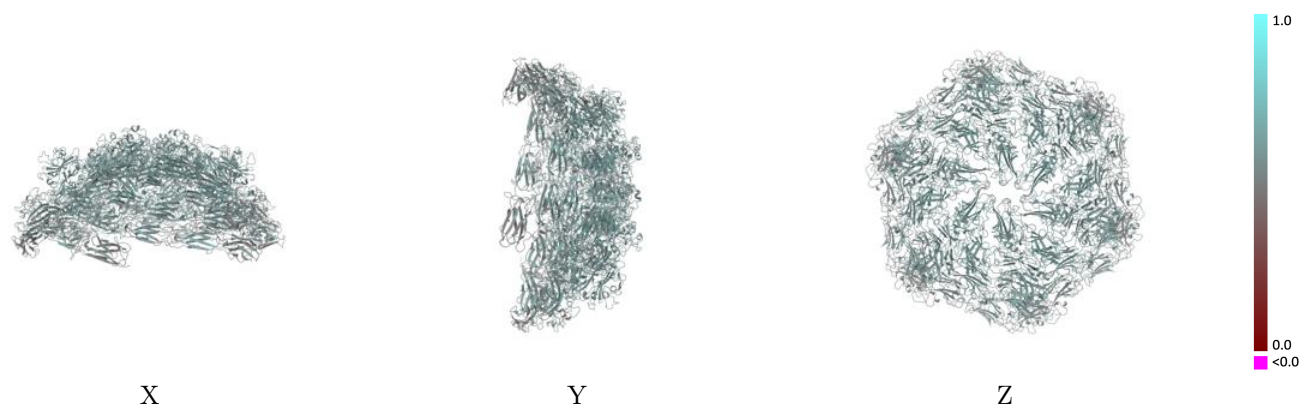
Y



Z

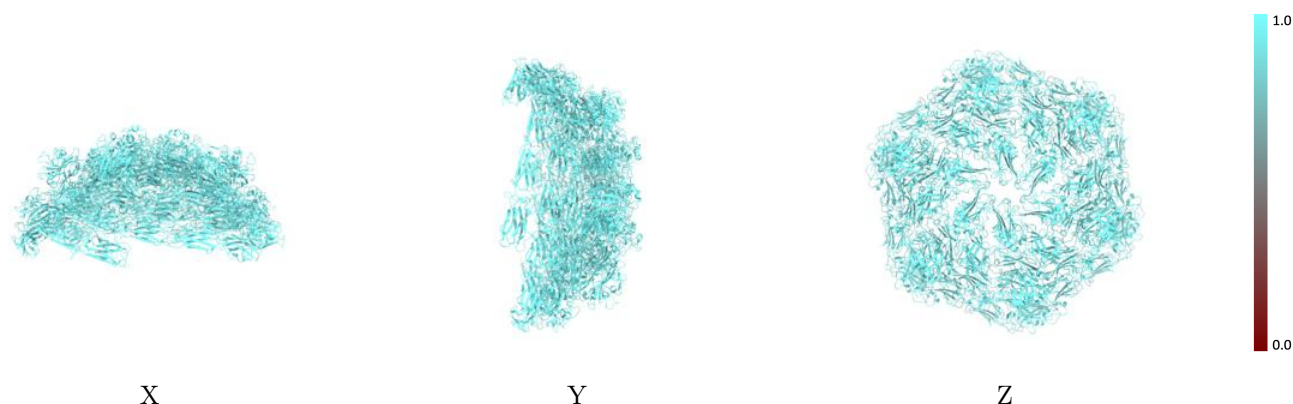
The images above show the 3D surface view of the map at the recommended contour level 1.05514 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



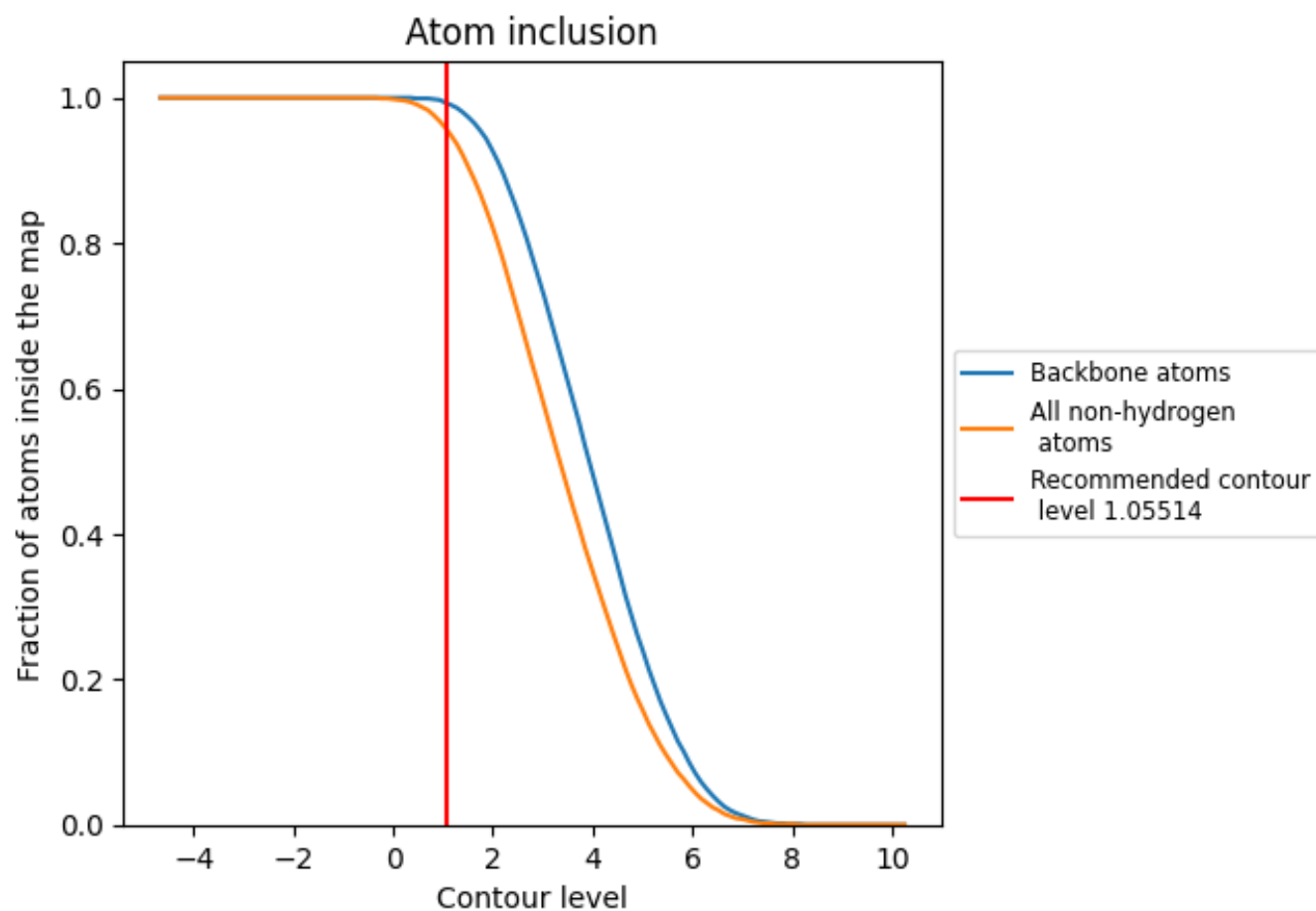
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.05514).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% 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 (1.05514) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9580	0.5560
A	0.9620	0.5630
B	0.9580	0.5530
C	0.9530	0.5520
D	0.9630	0.5620
E	0.9580	0.5530
F	0.9540	0.5520

1.0

0.0

<0.0