



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 01:51 PM UTC

PDB ID : 6UEB / pdb_00006ueb
EMDB ID : EMD-20753
Title : Structure of Rabies SAD-B19 L-P complex from cryo-EM
Authors : Horwitz, J.A.; Harrison, S.C.
Deposited on : 2019-09-20
Resolution : 3.30 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

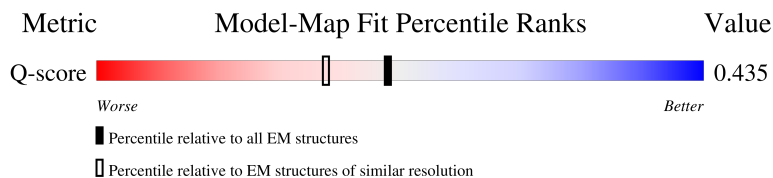
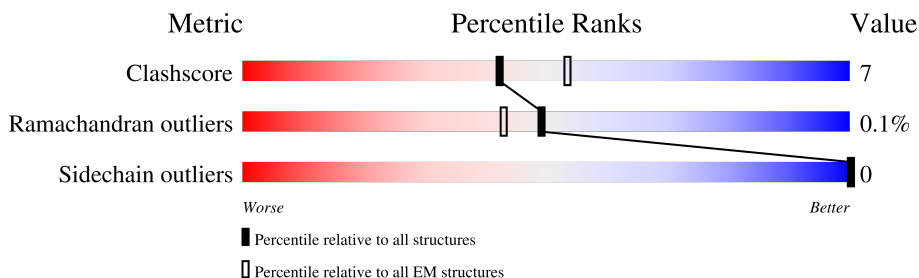
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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	2127	
2	B	42	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 34451 atoms, of which 17232 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 Large structural protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	2099	Total	C	H	N	O	S	0	0
			33865	10792	16965	2931	3097	80		

- Molecule 2 is a protein called Phosphoprotein,Phosphoprotein.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	42	Total	C	H	N	O	S	0	0
			584	190	267	57	68	2		

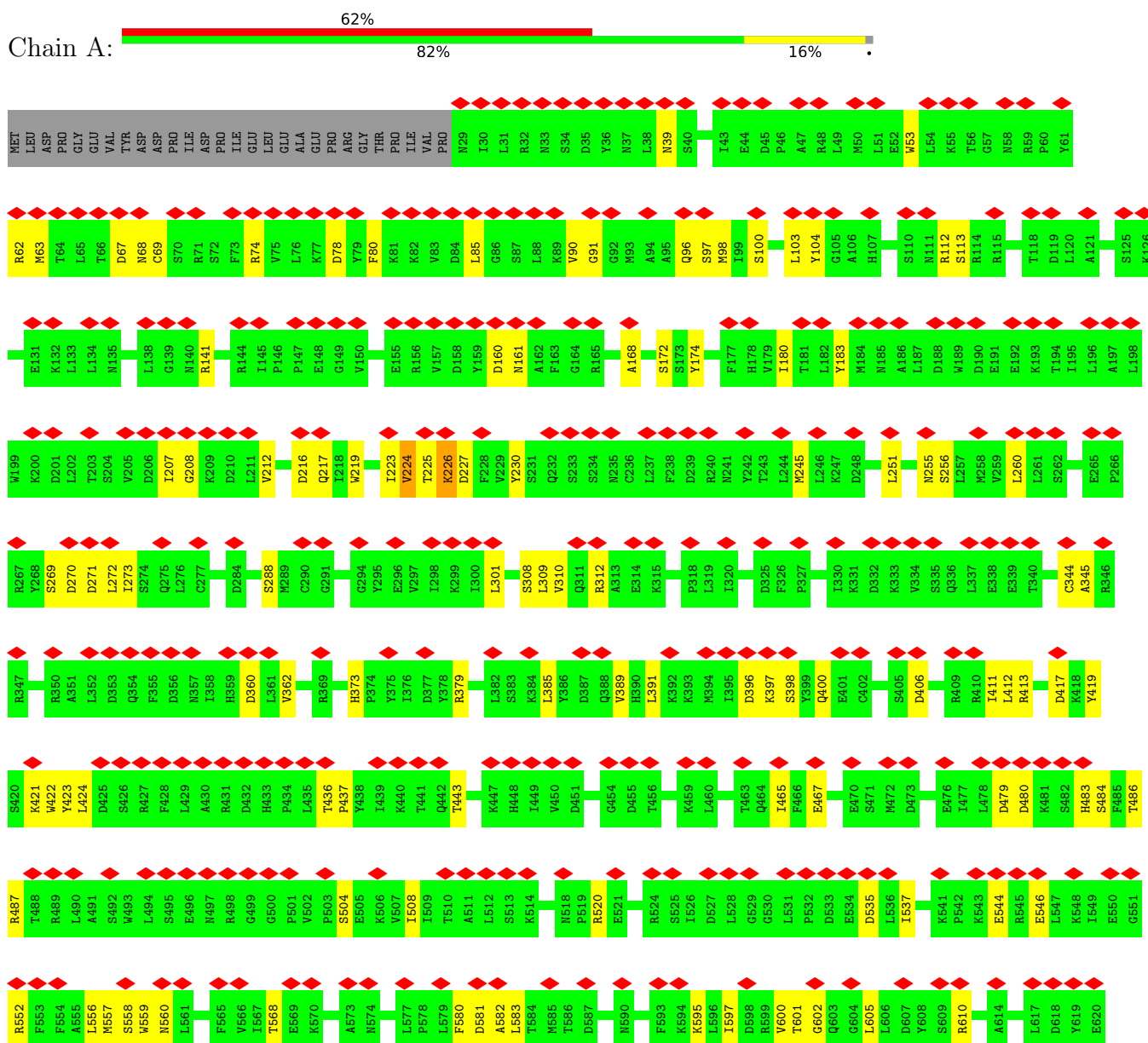
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

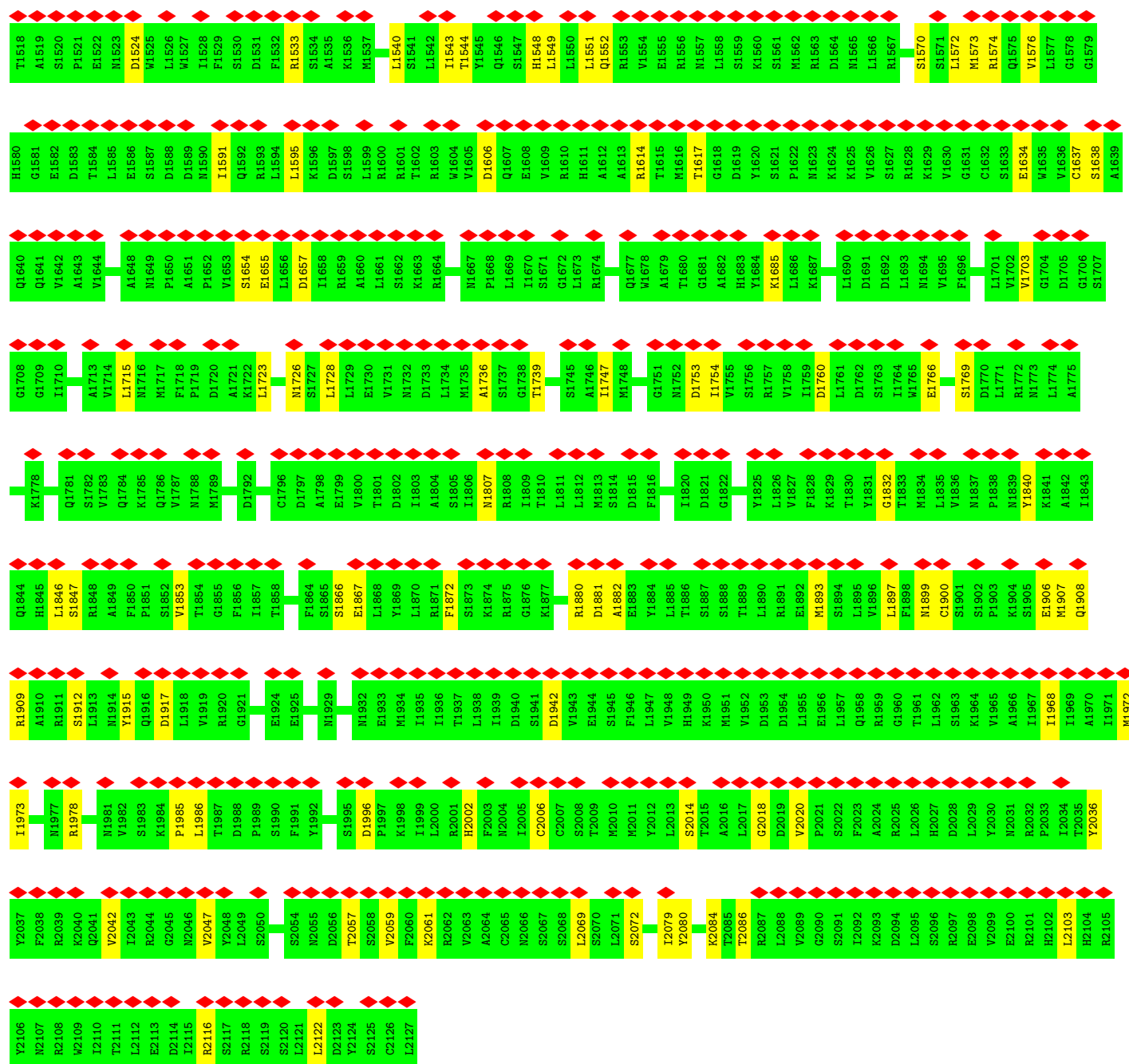
3 Residue-property plots

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.

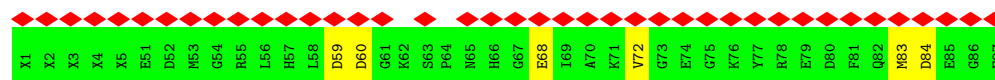
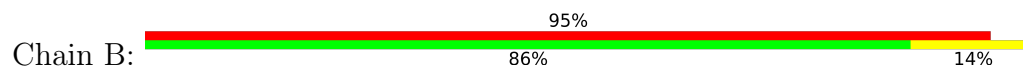
- Molecule 1: Large structural protein



V1453	G1361	K1244	E1041	H910	T836	R757	G694	K621
I1457	S1362	S1245	S1042	R912	Q339	N758	L695	W622
L1458	L1366	A1246	I1043	Q13	H940	W623	E996	N623
L1459	H1395	R1247	I1044	F914	S941	R627	G997	R627
R1460	L1396	Y1248	G1045	S915	Q942	L628	L698	L628
L1461	S1397	S1249	I1047	D916	S843	E929	R699	E929
D1462	G1398	E1250	I1049	P917	L844	T631	Q700	S630
N1463	S1399	G1251	W1049	E920	I845	T631	K701	T631
H1464	Y1253	G1252	S1050	G921	K946	E632	G702	E632
L1467	C1257	L1193	R1051	R926	R847	D633	W703	D633
Y1468	P1258	S1194	I1052	R927	M848	V634	L705	V634
M1470	L1261	S1195	I1053	E928	R849	F635	L709	F635
L1471	S1262	L1196	R1054	W929	D850	D639	M710	D639
R1472	H1263	E1197	R1055	I928	I777	Q640	I711	Q640
P1474	S1265	S1198	Q1056	L930	K778	L644	D712	L644
P1477	D1269	I1199	F1057	S932	K779	K645	R713	K645
L1476	W1201	M1200	R1058	Q933	E781	V647	S715	V647
R1477	F1270	W1202	K1059	E934	Y862	F648	Q716	F648
G1478	M1271	R1205	S1060	E935	L863	S649	I717	S649
E1479	S1272	D1206	S1061	W996	L864	R650	R718	R650
I1480	S1273	S1207	L1062	S997	F865	E653	T720	E653
F1481	D1274	M1208	S1063	E998	P867	F654	R721	F654
S1482	T1275	A1210	L1064	F999	K870	F655	R722	F655
I1483	Q1276	Q1211	T1065	R1000	G871	W659	K723	W659
P1484	D1277	A1212	E1066	E1001	L796	S663	I724	S663
Q1485	G1278	L1213	S1068	A1002	K797	D664	A726	D664
K1486	K1279	I1214	F1069	L1003	R798	R665	Q727	R665
A1489	N1280	R1215	Y1070	N946	L802	S666	D728	S666
A1490	Y1281	R1216	N1071	P947	E805	D667	D729	D667
Y1491	D1282	M1216	S1072	D948	S906	L668	G734	L668
P1492	D1283	I1217	E1073	L949	K807	I669	L671	I669
T1493	F1285	M1218	I1074	G950	W809	G670	L671	G670
L1494	M1284	S1219	H1075	E951	A810	L672	T736	L672
M1495	F1285	G1219	G1076	R952	R811	E673	Y737	E673
K1496	L1288	G1222	R1079	T953	V812	D674	M738	D674
E1497	M1289	P1223	M1080	L954	S816	Q675	S740	Q675
G1498	L1290	D1224	T1081	S955	N817	I676	G742	I676
L1499	Y1291	F1225	Q1082	S956	D818	C678	L679	C678
R1500	A1292	P1226	Q1085	T958	Q819	L679	S744	Q819
S1501	T1296	L1227	R1086	R959	I820	D680	Q745	D680
I1502	S1297	E1228	R1087	L961	V821	A681	Q746	A681
L1503	E1298	A1229	G1088	L962	N822	S682	G747	S682
C1504	Q1301	P1231	G1089	L963	I901	N683	E748	N683
Y1505	R1302	F1232	V1090	N968	S902	G684	L748	G684
L1506	D1303	W1233	E1096	I969	G903	W688	Y749	W688
S1507	D1304	K1234	R1097	R970	M904	N689	L750	N689
H1508	R1305	R1235	A1098	G971	S905	G690	L751	G690
R1511	L1306	T1236	D1099	A973	L906	Q691	L752	Q691
Y1512	R1307	G1237	L1100	S974	F907	D692	R754	D692
E1513	F1307	S1238	L1101	P975	R908	G693	I755	G693
R1514	D1308	L1240	E1102	T976	F909	S756	S756	S756
E1515	S1309	H1241	R1103					
I1516	F1310	R1242	L1031					
I1517	F1311	F1243	F1032					
	H1312		S1033					
			F1036					
			L1037					
			I1039					
			P1040					



• Molecule 2: Phosphoprotein, Phosphoprotein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	44500	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	72	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	23.362	Depositor
Minimum map value	-12.309	Depositor
Average map value	0.015	Depositor
Map value standard deviation	1.889	Depositor
Recommended contour level	7	Depositor
Map size (Å)	143.144, 143.144, 143.144	wwPDB
Map dimensions	116, 116, 116	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.234, 1.234, 1.234	Depositor

5 Model quality

5.1 Standard geometry

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	0.26	0/17290	0.43	0/23418
2	B	0.19	0/296	0.49	0/392
All	All	0.26	0/17586	0.43	0/23810

There are no bond length outliers.

There are no bond angle outliers.

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	16900	16965	16964	227	0
2	B	317	267	268	5	0
3	A	2	0	0	0	0
All	All	17219	17232	17232	229	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 7.

The worst 5 of 229 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:180:ILE:HD12	1:A:224:VAL:HG21	1.53	0.89
1:A:2042:VAL:HG12	1:A:2047:VAL:HG12	1.58	0.82
1:A:1469:ILE:HD11	1:A:1739:THR:HG21	1.61	0.82
1:A:255:ASN:ND2	1:A:809:TRP:O	2.13	0.81
1:A:68:ASN:HB3	1:A:227:ASP:OD2	1.83	0.78

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	2097/2127 (99%)	2085 (99%)	10 (0%)	2 (0%)	48	75
2	B	35/42 (83%)	34 (97%)	1 (3%)	0	100	100
All	All	2132/2169 (98%)	2119 (99%)	11 (0%)	2 (0%)	49	75

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	224	VAL
1	A	226	LYS

5.3.2 Protein sidechains [i](#)

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1901/1927 (99%)	1901 (100%)	0	100	100
2	B	30/30 (100%)	30 (100%)	0	100	100
All	All	1931/1957 (99%)	1931 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	800	ASN
1	A	857	GLN
1	A	1932	ASN
1	A	1623	ASN
1	A	497	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	5:UNK	C	51:GLU	N	20.90

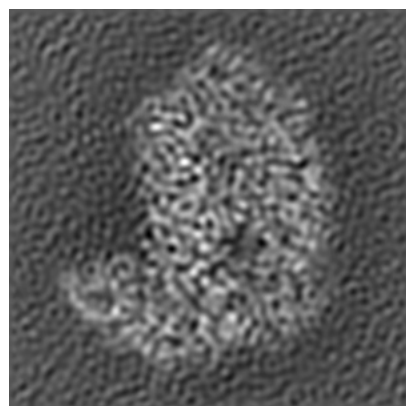
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20753. These allow visual inspection of the internal detail of the map and identification of artifacts.

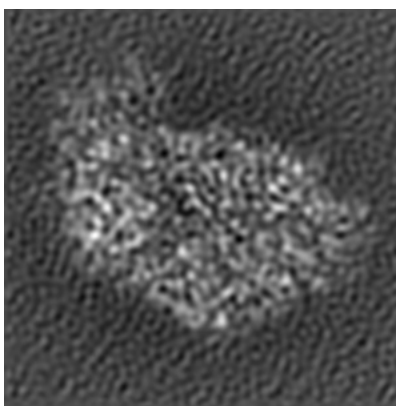
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

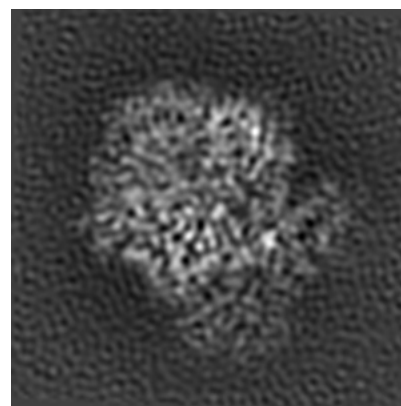
6.1.1 Primary map



X

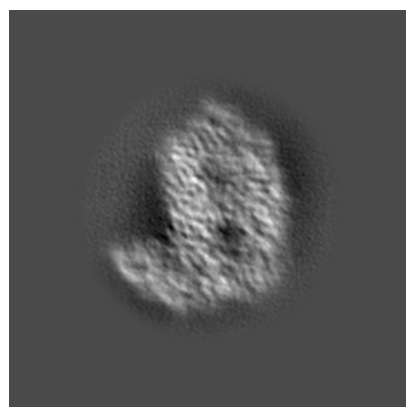


Y

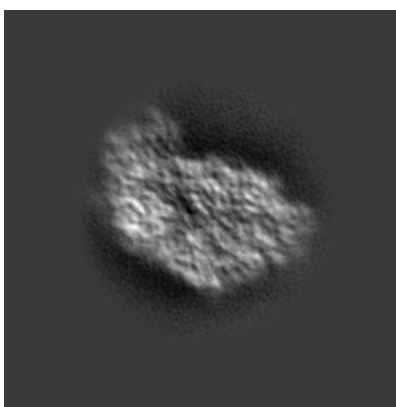


Z

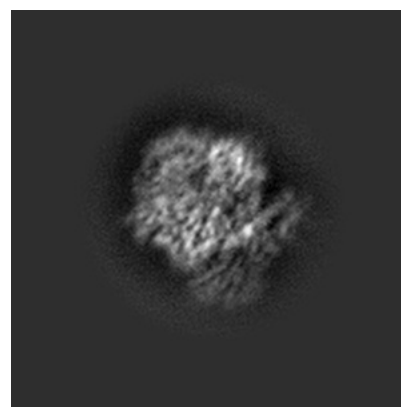
6.1.2 Raw map



X



Y

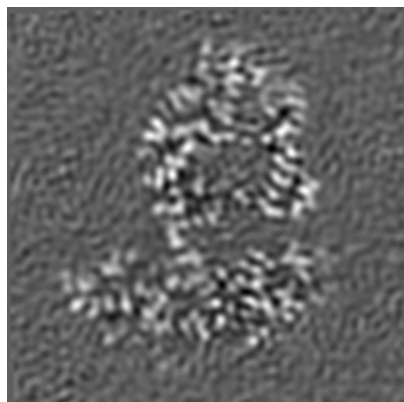


Z

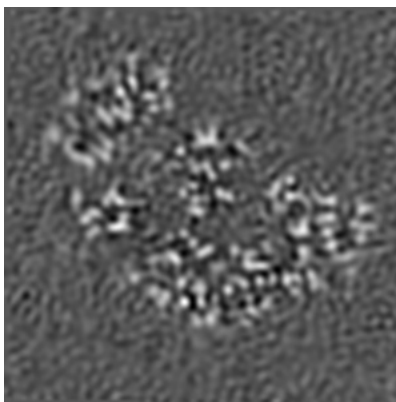
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

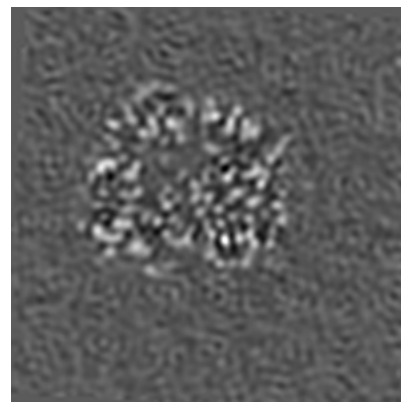
6.2.1 Primary map



X Index: 58

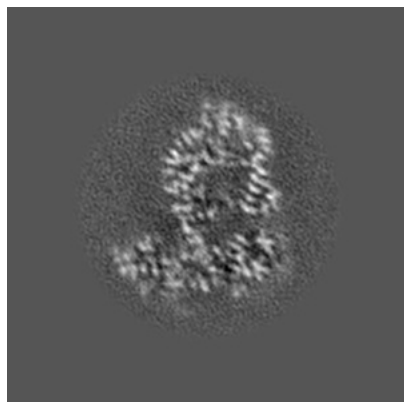


Y Index: 58

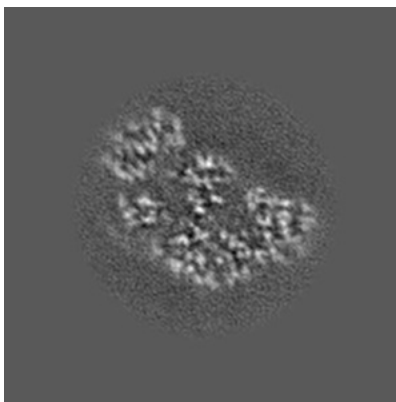


Z Index: 58

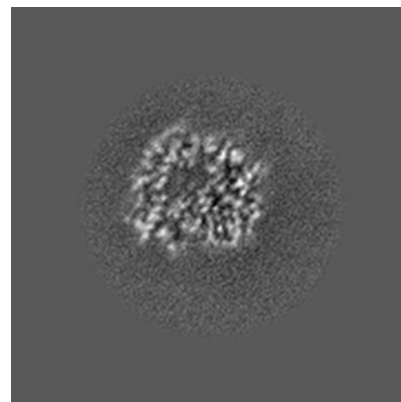
6.2.2 Raw map



X Index: 90



Y Index: 90

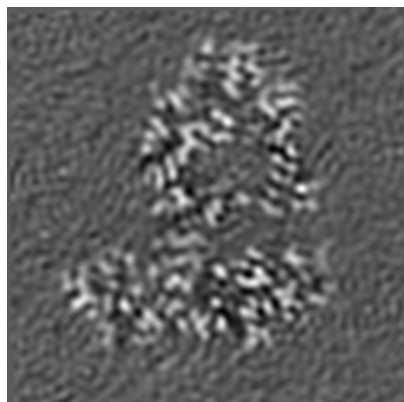


Z Index: 90

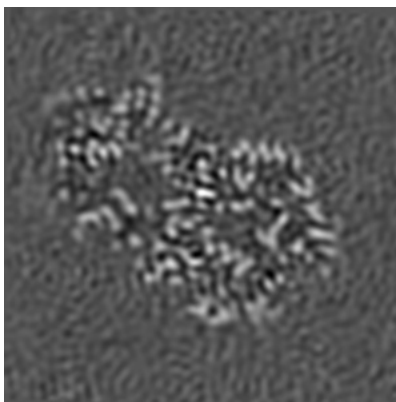
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

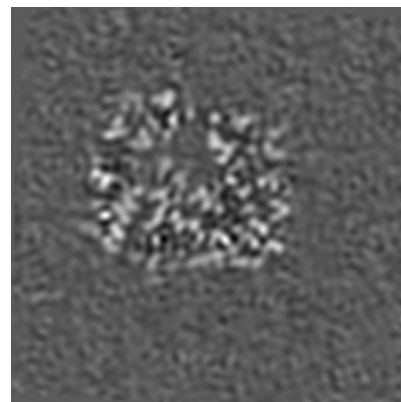
6.3.1 Primary map



X Index: 57

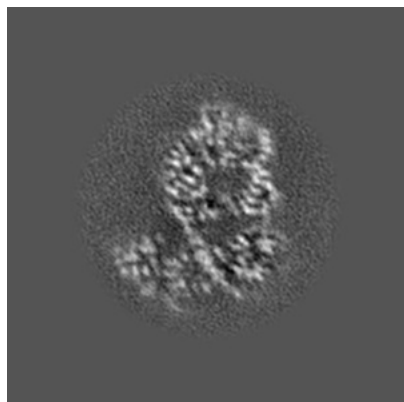


Y Index: 48

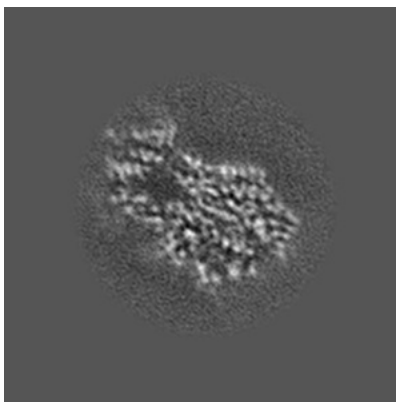


Z Index: 56

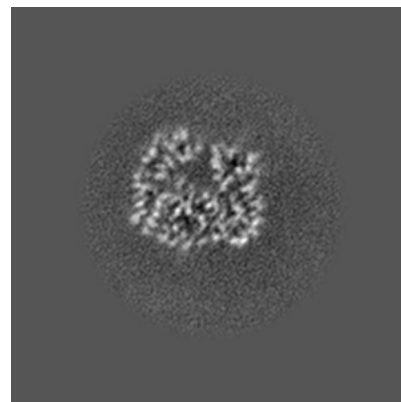
6.3.2 Raw map



X Index: 91



Y Index: 82

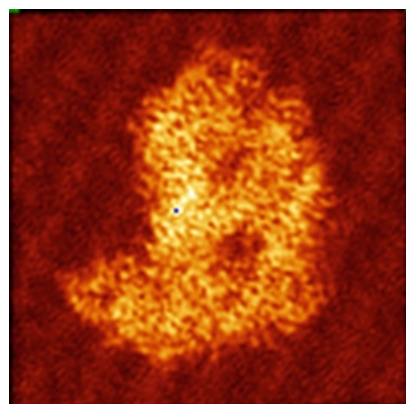


Z Index: 87

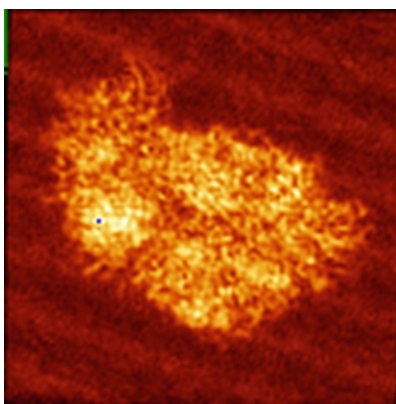
The images above show the largest variance slices of the map in three orthogonal directions.

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

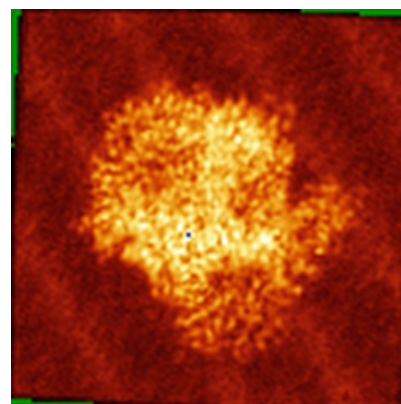
6.4.1 Primary map



X

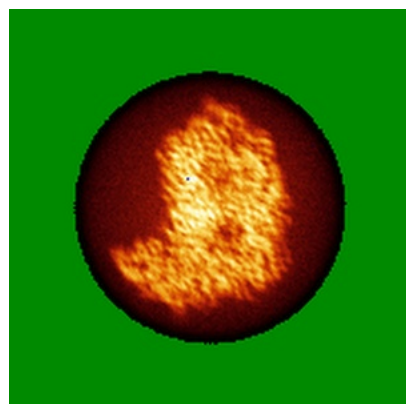


Y

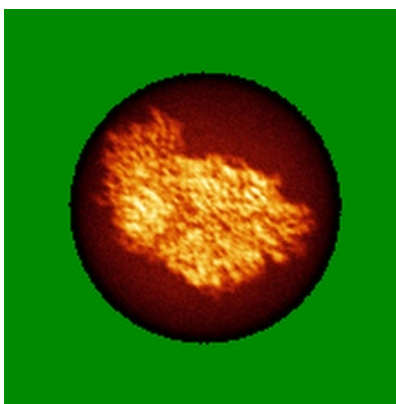


Z

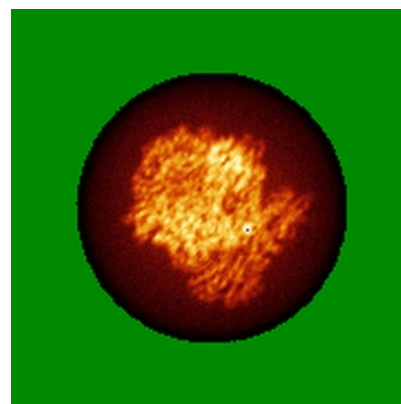
6.4.2 Raw map



X



Y

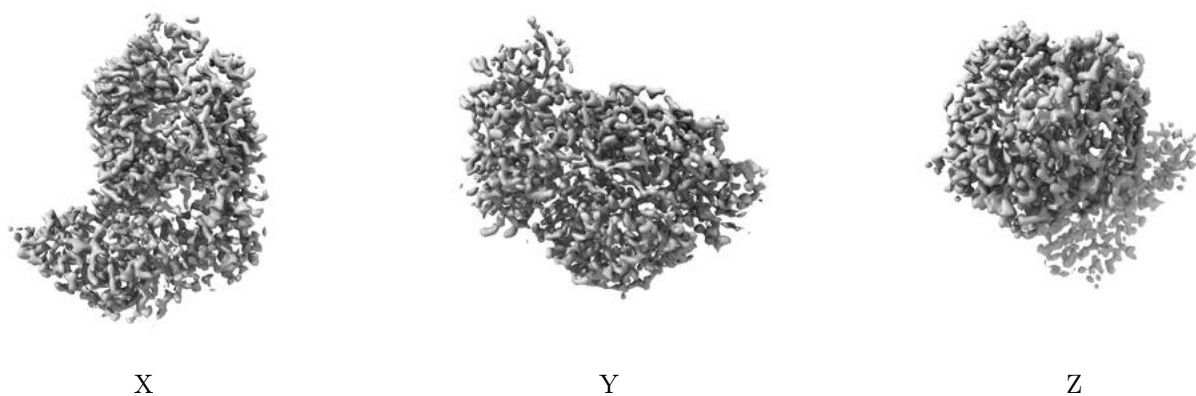


Z

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.

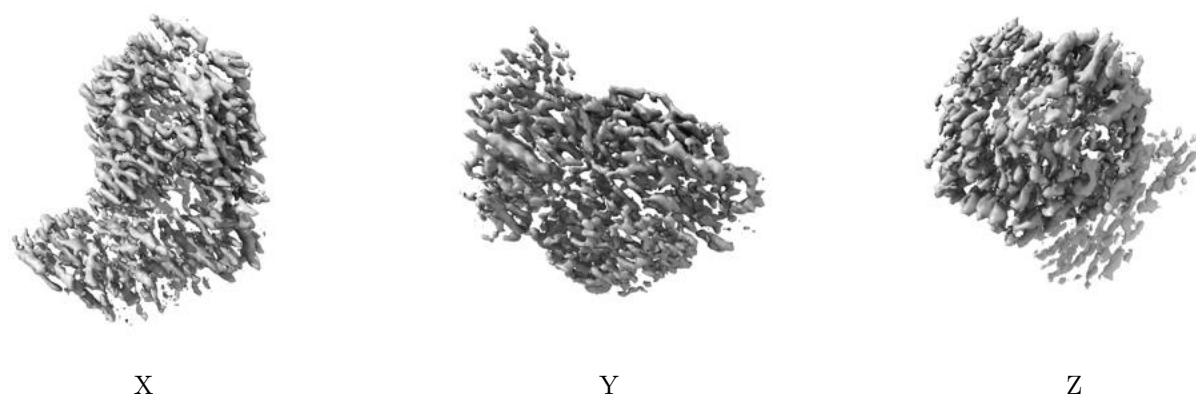
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 7.0. 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



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.

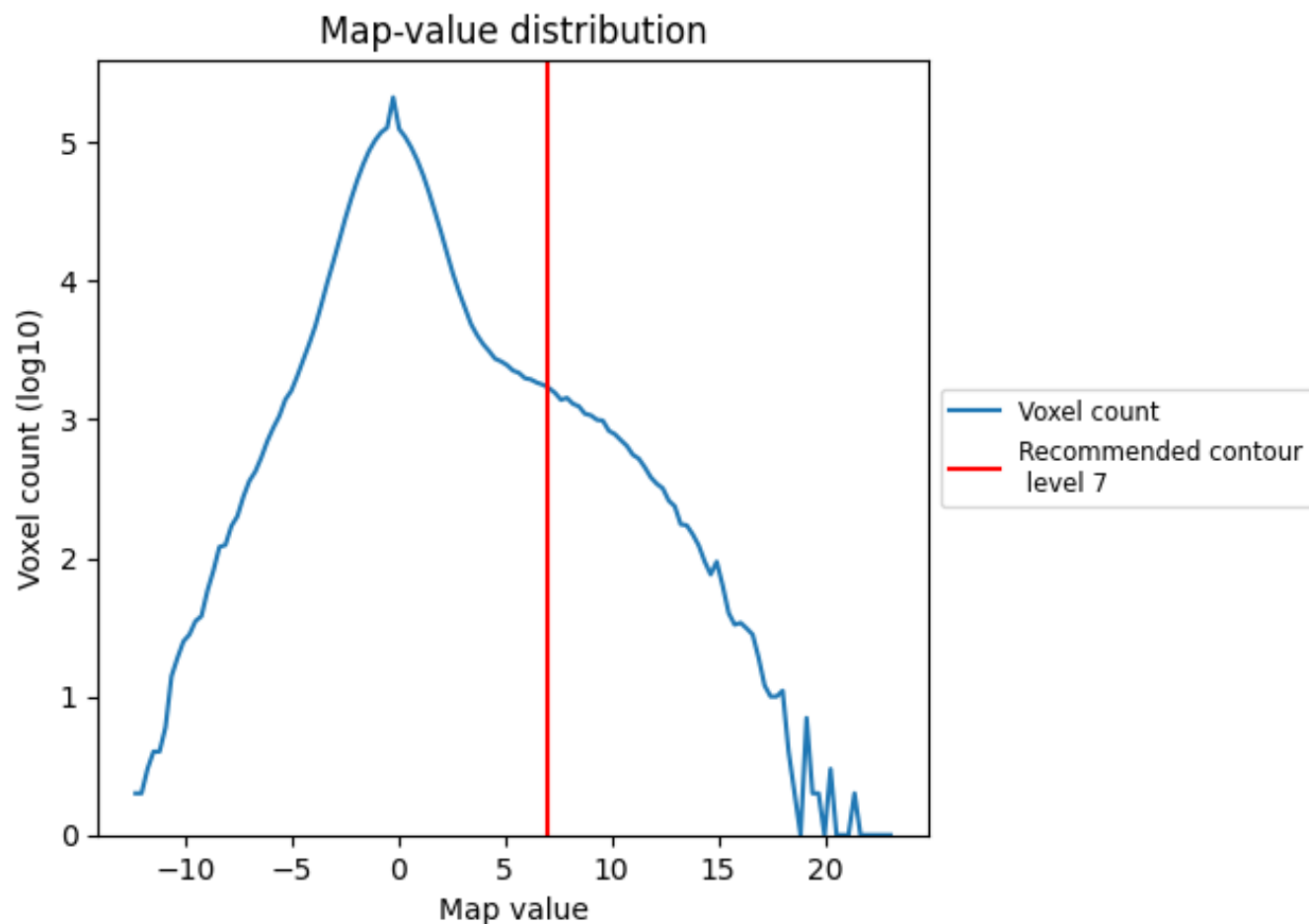
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

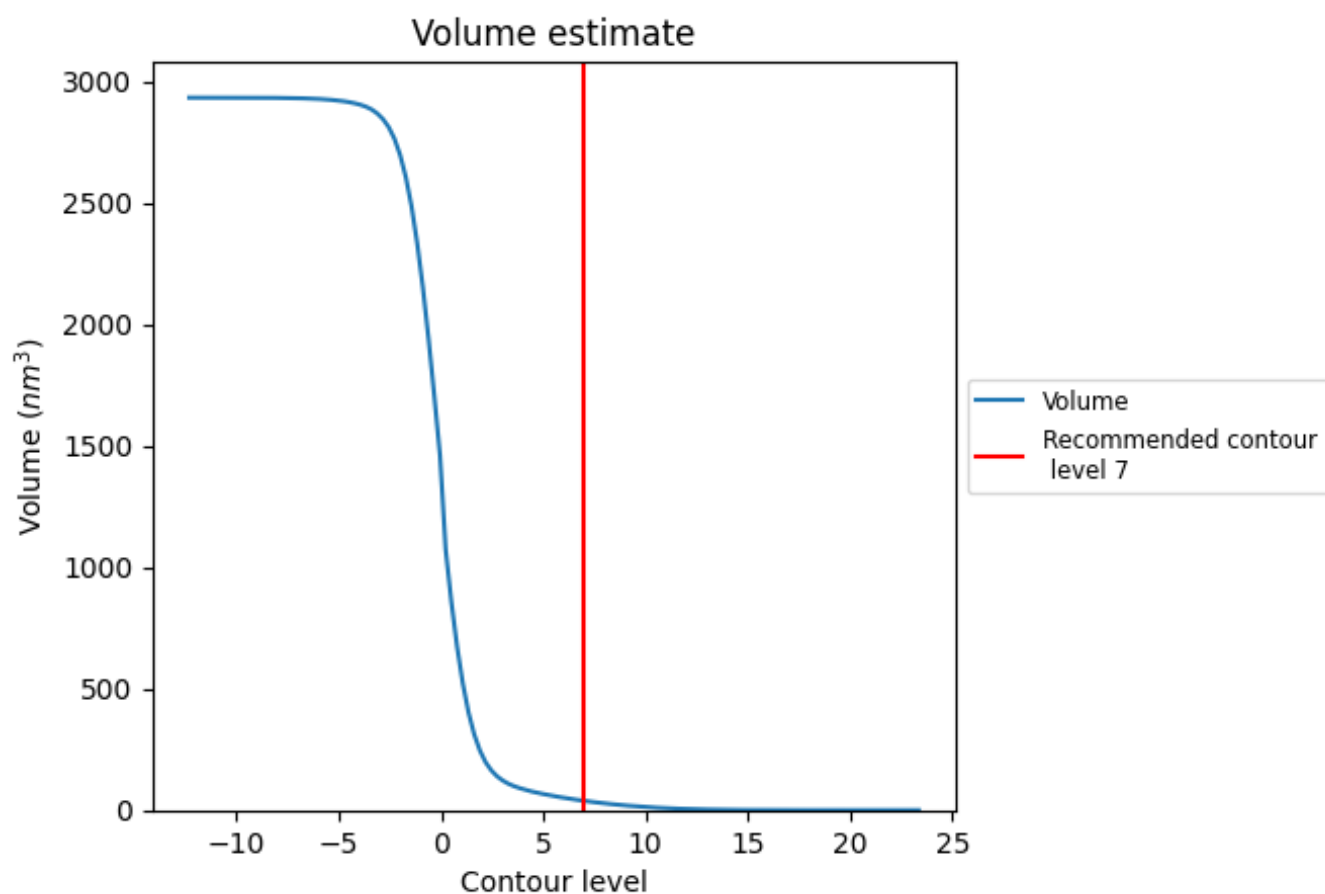
This section contains the results of statistical analysis of the map.

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.

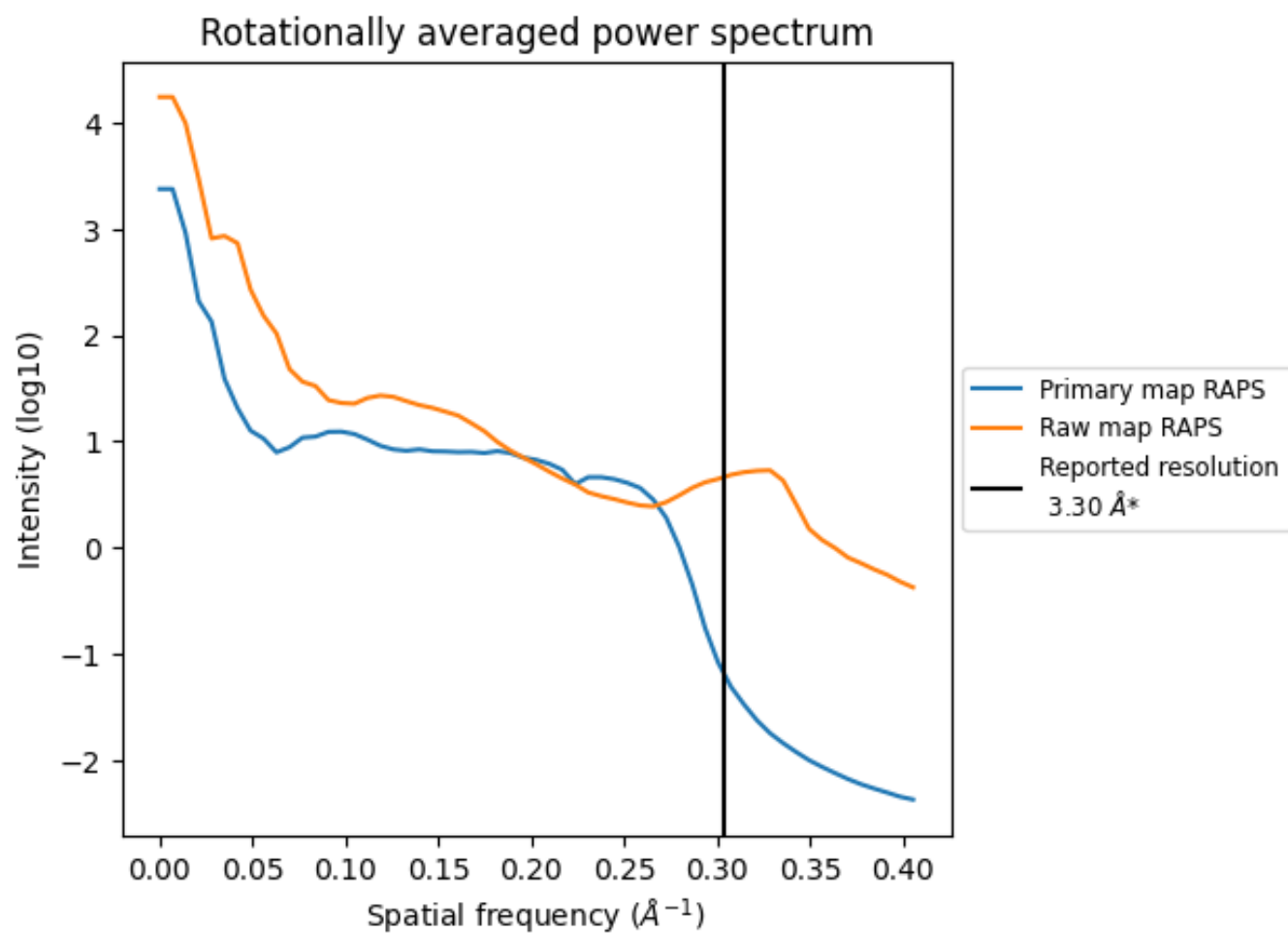
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 38 nm^3 ; this corresponds to an approximate mass of 35 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 ⓘ

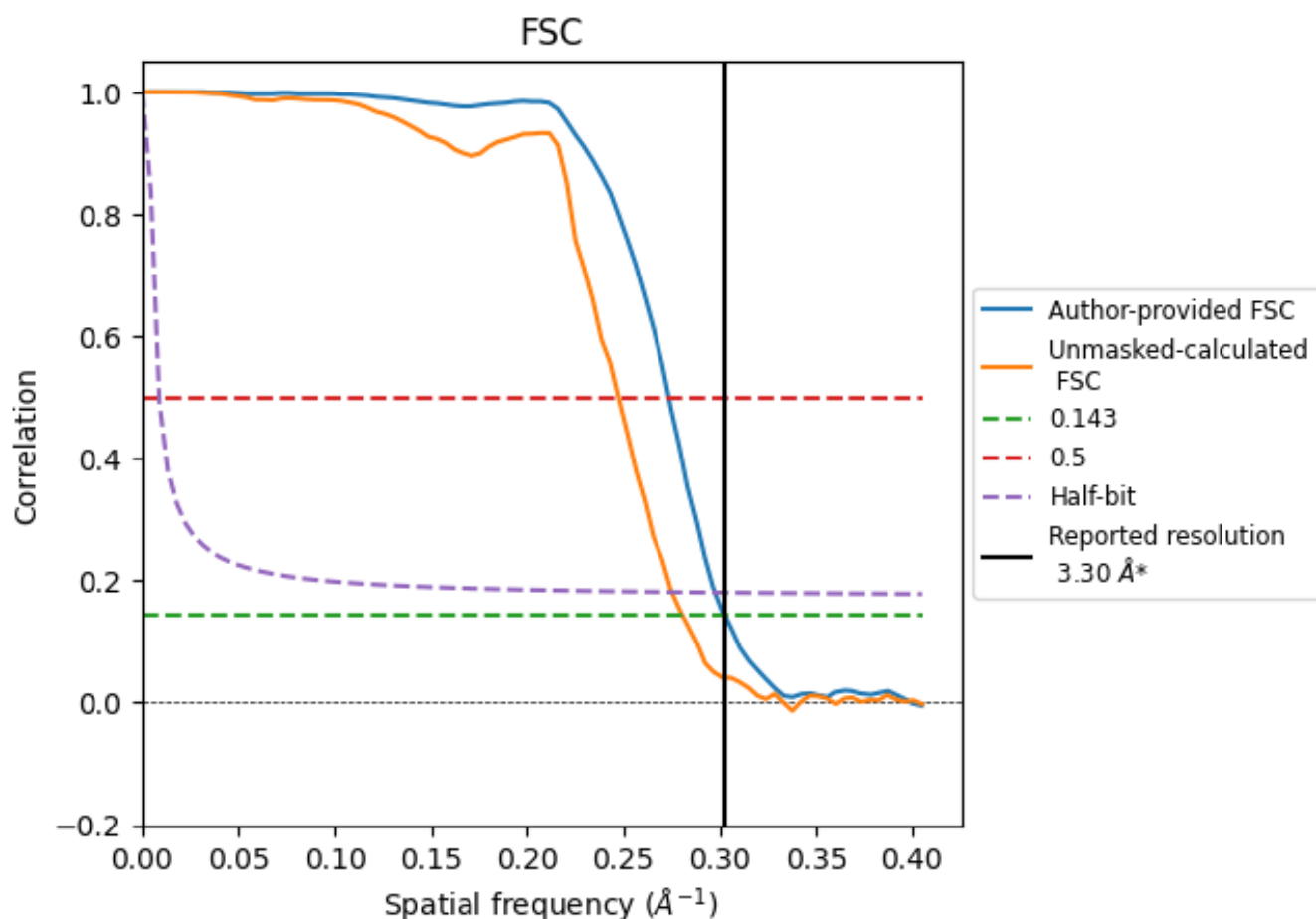


*Reported resolution corresponds to spatial frequency of 0.303 $\text{\AA}^{-1}$

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 0.303 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

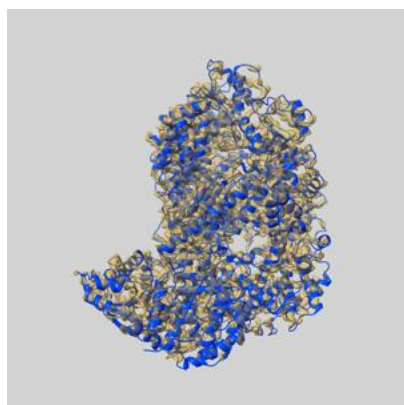
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.30	3.65	3.36
Unmasked-calculated*	3.56	4.04	3.63

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

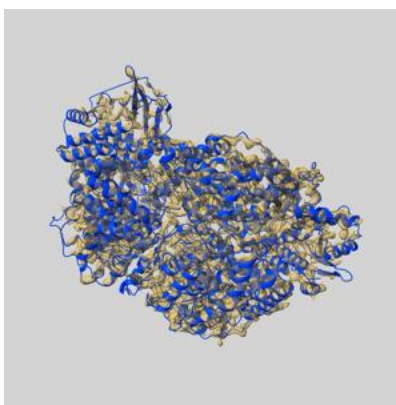
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20753 and PDB model 6UEB. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

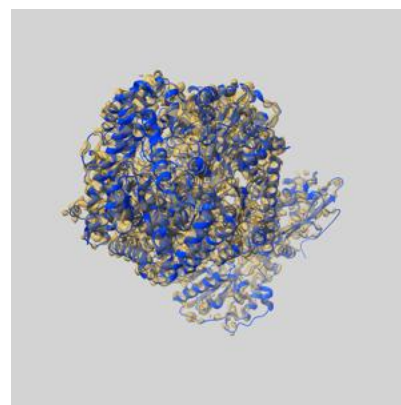
9.1 Map-model overlay [i](#)



X



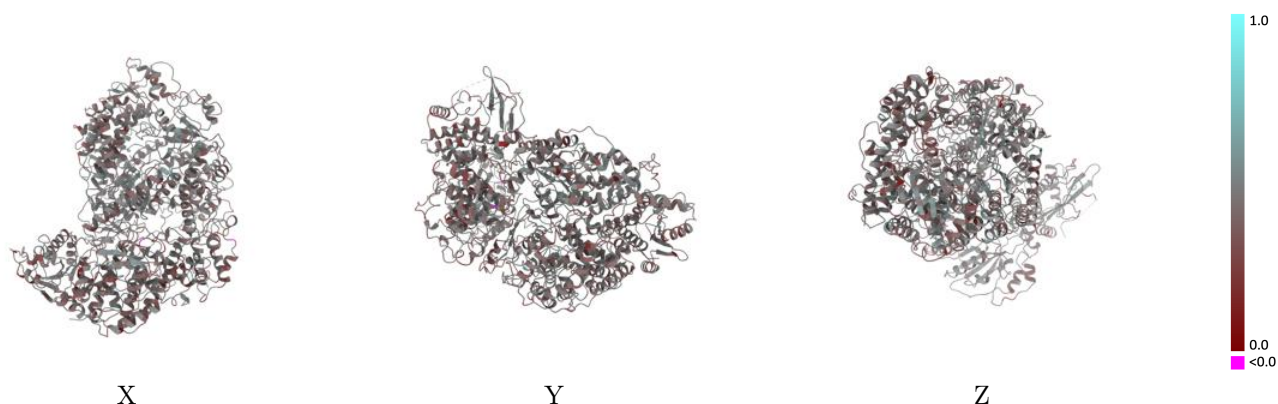
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 7.0 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](#)

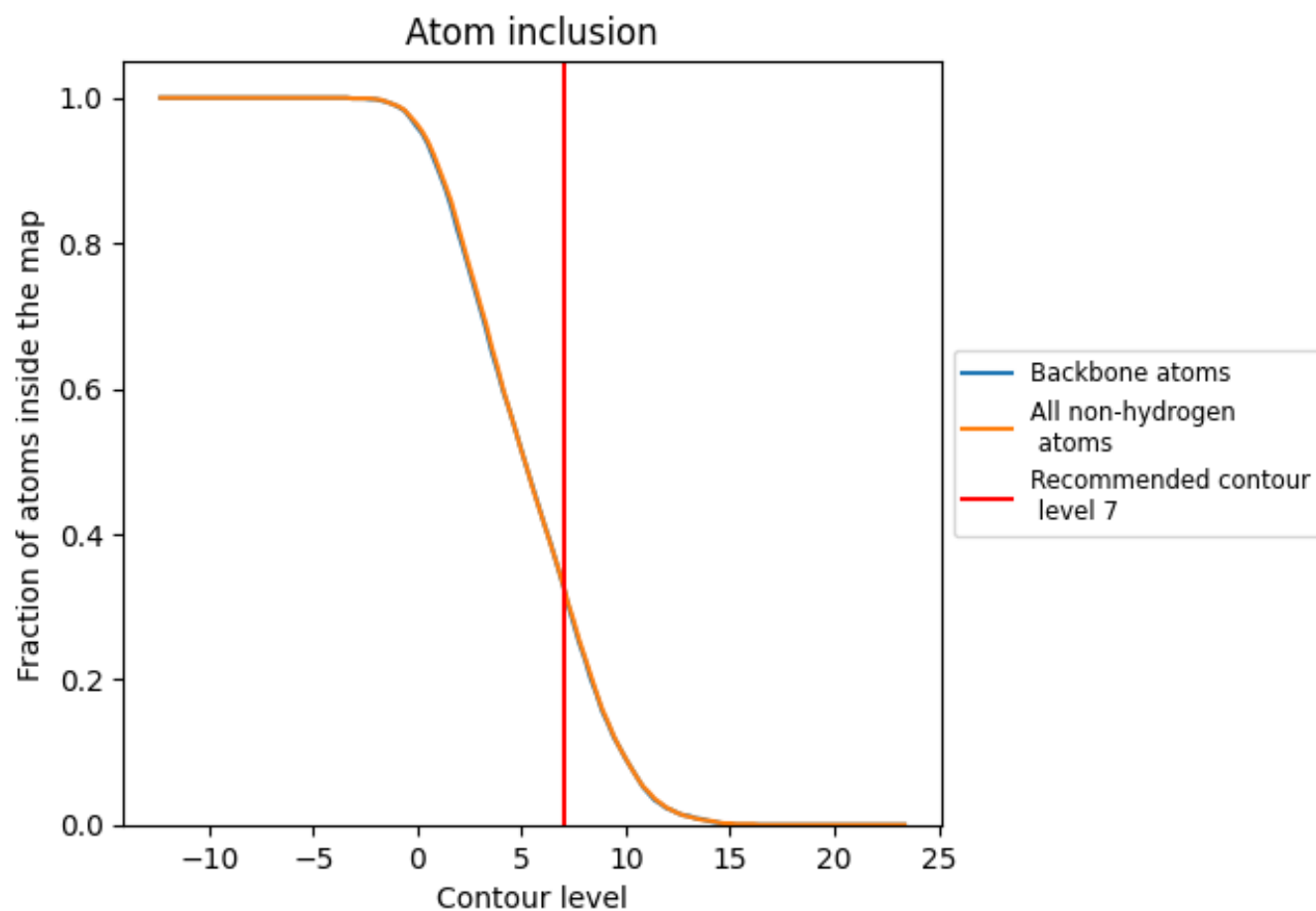


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 33% of all backbone atoms, 33% 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 (7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3300	0.4350
A	0.3390	0.4360
B	0.0900	0.3840

