



wwPDB EM Validation Summary Report ⓘ

Aug 5, 2025 – 01:28 pm BST

PDB ID : 9GD7 / pdb_00009gd7
EMDB ID : EMD-51249
Title : DNA-PK Ku80 mediated dimer bound to DNA polymerase Lambda and DNA
ligase 4/XRCC4
Authors : Chaplin, A.K.; Amin, H.; Zahid, S.; Hardwick, S.W.
Deposited on : 2024-08-05
Resolution : 4.25 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.dev126
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.45.1

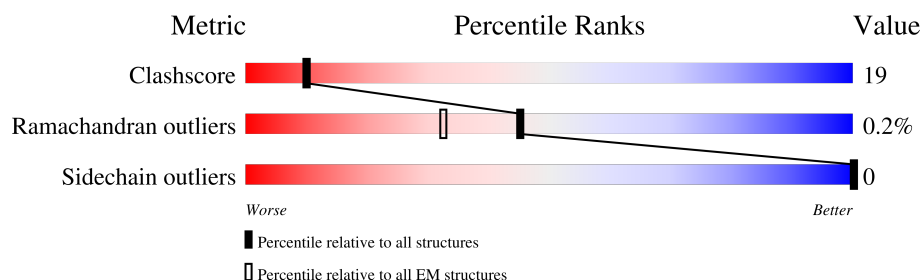
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.25 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	E	911	<div> <div>17%</div> <div>16%</div> <div>10%</div> <div>73%</div> </div>
2	L	732	<div> <div>19%</div> <div>53%</div> <div>35%</div> <div>12%</div> </div>
3	M	204	<div> <div>8%</div> <div>89%</div> </div>
4	P	336	<div> <div>16%</div> <div>9%</div> <div>8%</div> <div>83%</div> </div>
4	Q	336	<div> <div>15%</div> <div>10%</div> <div>7%</div> <div>83%</div> </div>
5	S	4128	<div> <div>50%</div> <div>35%</div> <div>14%</div> </div>
6	T	609	<div> <div>48%</div> <div>35%</div> <div>18%</div> </div>
7	i	25	<div> <div>40%</div> <div>60%</div> </div>

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Mol	Chain	Length	Quality of chain
8	j	25	<div><div></div><div>20%</div><div></div><div>80%</div></div>
9	A	575	<div><div></div><div>10%</div><div></div><div>7%</div><div></div><div>83%</div></div>

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 41717 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 DNA ligase 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	E	246	Total	C	N	O	S	0	0
			1956	1240	332	371	13		

- Molecule 2 is a protein called X-ray repair cross-complementing protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	641	Total	C	N	O	S	0	0
			5084	3250	859	950	25		

- Molecule 3 is a protein called Protein PAXX.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	M	23	Total	C	N	O	S	0	0
			160	102	27	30	1		

- Molecule 4 is a protein called DNA repair protein XRCC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	P	57	Total	C	N	O	S	0	0
			480	303	90	86	1		
4	Q	57	Total	C	N	O	S	0	0
			475	301	89	84	1		

- Molecule 5 is a protein called DNA-dependent protein kinase catalytic subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	S	3535	Total	C	N	O	S	0	0
			27773	17865	4705	5020	183		

- Molecule 6 is a protein called X-ray repair cross-complementing protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	T	501	Total	C	N	O	S	0	0
			4001	2561	679	743	18		

- Molecule 7 is a DNA chain called DNA.

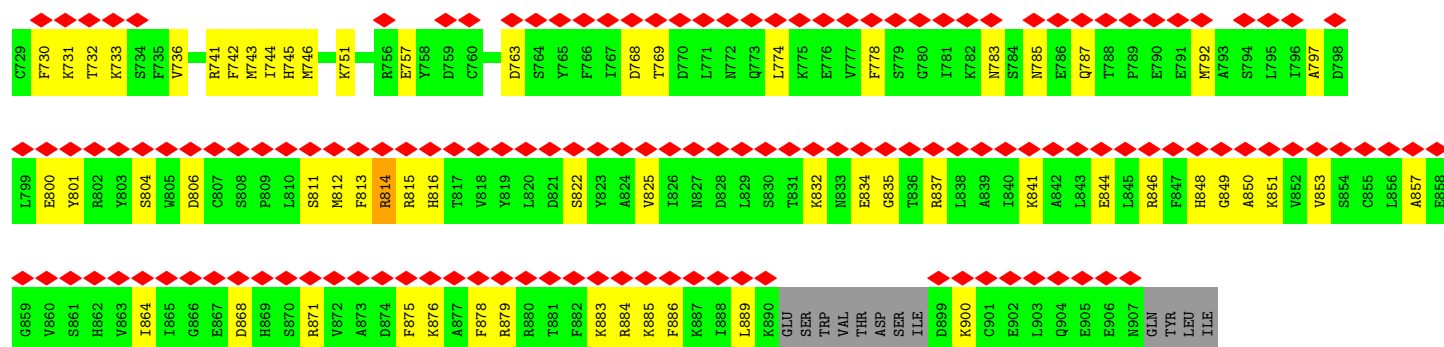
Mol	Chain	Residues	Atoms					AltConf	Trace
7	i	25	Total	C	N	O	P	0	0
			510	247	92	146	25		

- Molecule 8 is a DNA chain called DNA.

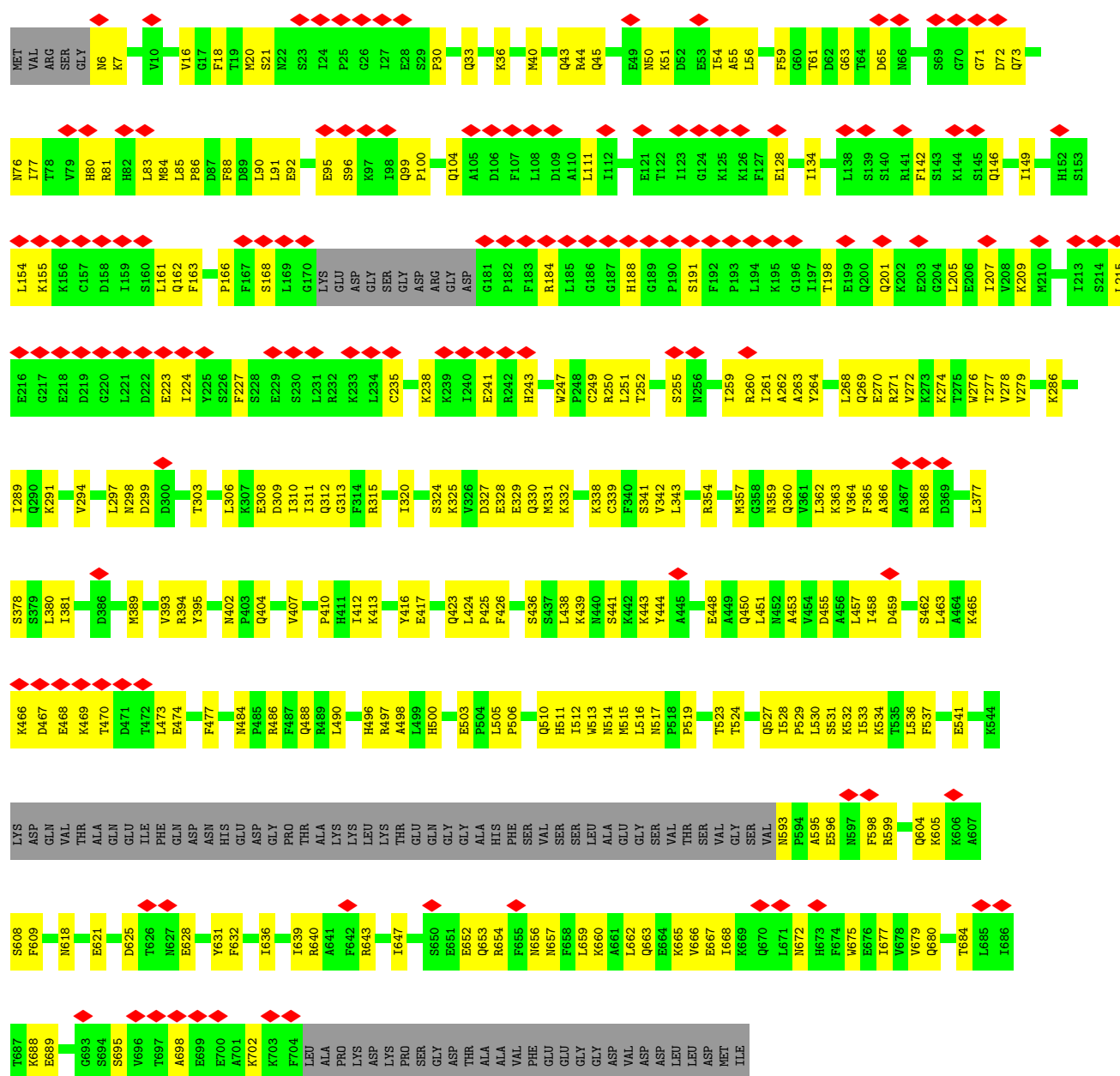
Mol	Chain	Residues	Atoms					AltConf	Trace
8	j	25	Total	C	N	O	P	0	0
			514	250	86	154	24		

- Molecule 9 is a protein called DNA polymerase lambda.

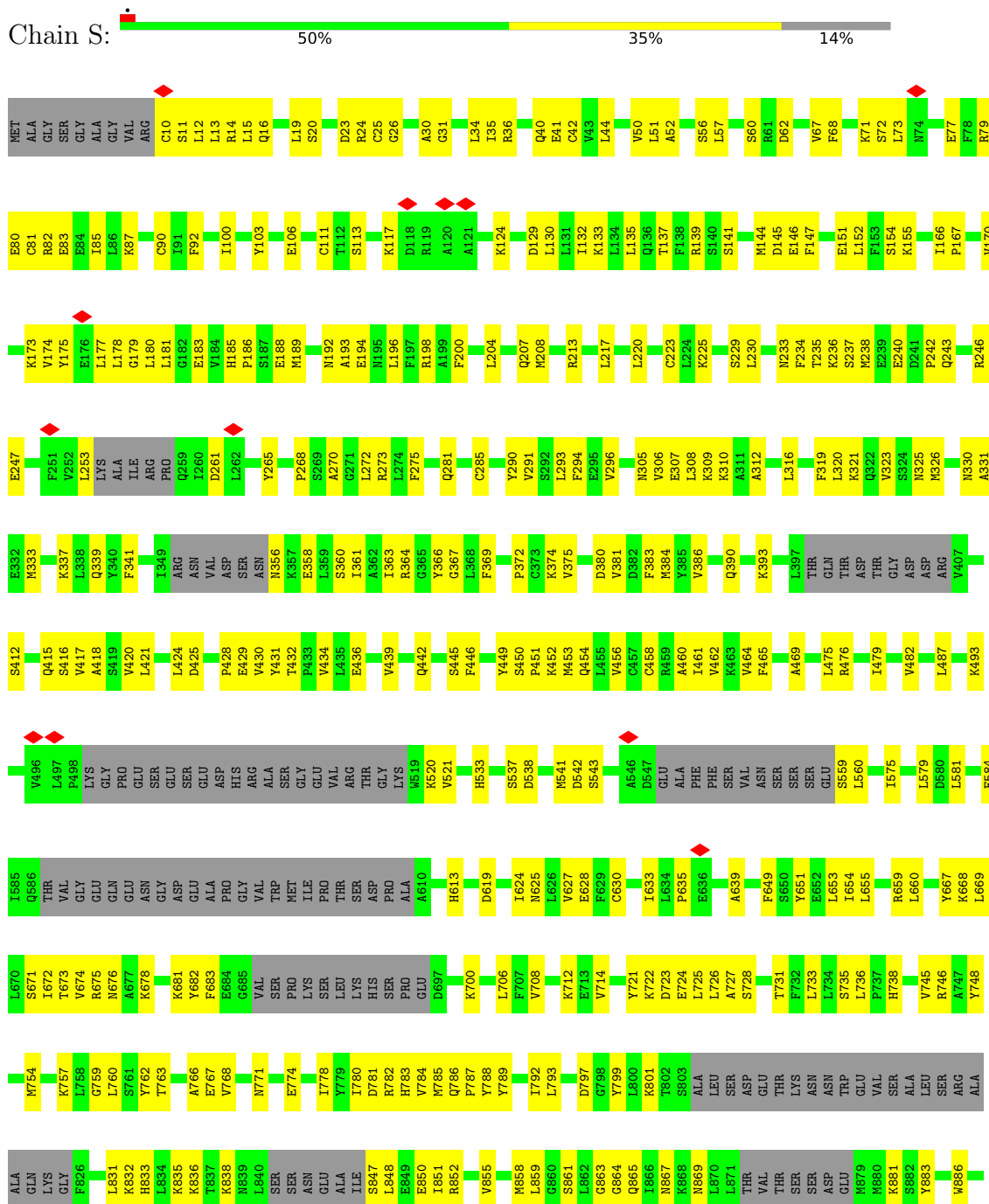
Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	98	Total	C	N	O	S	0	0
			764	487	142	132	3		



• Molecule 2: X-ray repair cross-complementing protein 5

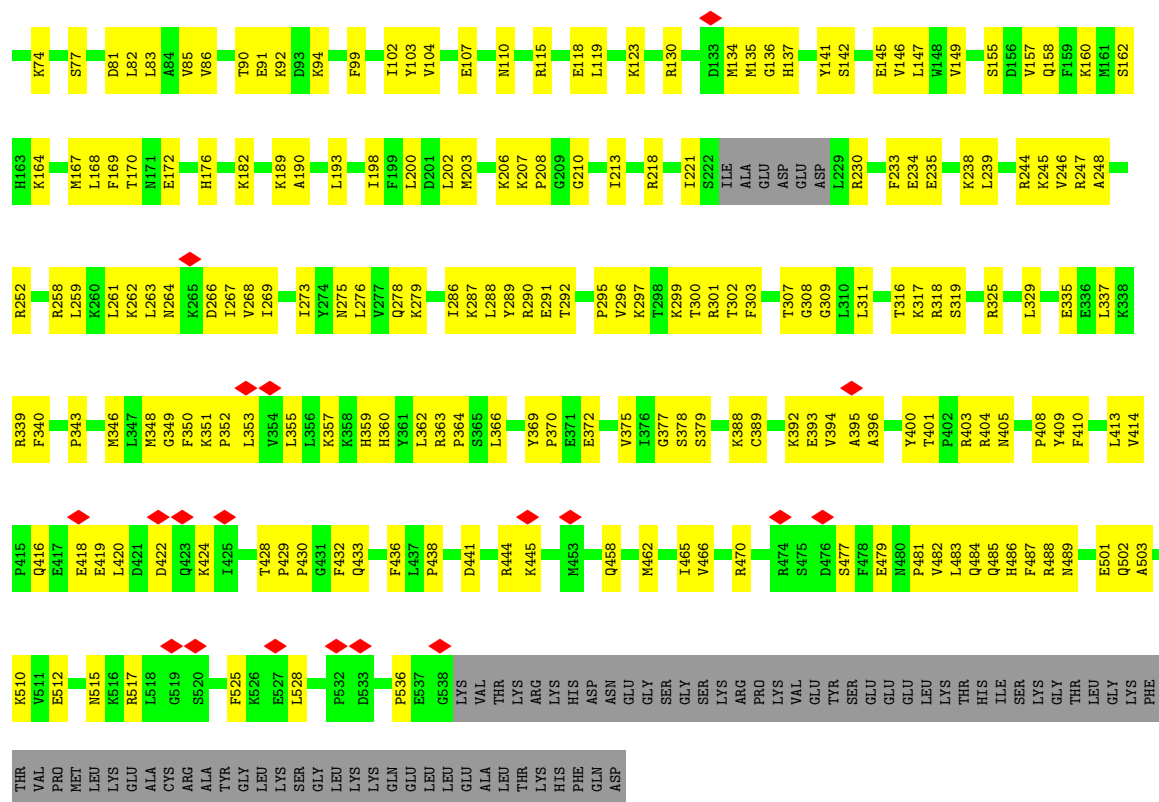


- Molecule 5: DNA-dependent protein kinase catalytic subunit



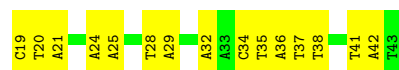
PHE	L1824	M1643	H1477	Q1287	E1215	T1137	Q1047	R971	E889
GLU	T1825	A1644	S1478	S1288	G1216	I1138	Q1048	C974	K890
ASN	T1826	V1645	V1479	S1289	V1217	I1139	Q1049	C975	K891
ILE	L1827	L1646	E1482	K1292	S1218	H1142	E1050	D975	L892
LEU	L1828	L1647	E1483	A1380	S1219	H1143	K1051	V976	S893
ASP	W1829	L1648	E1484	S1381	L1220	M1146	D977	D977	F894
LEU	H1830	L1649	K1489	A1295	L1221	M1147	S1052	Q978	A895
LYS	E1751	L1650	K1573	F1296	H1222	K1149	P1053	V979	V896
THR	L1752	K1651	L1491	F1297	T1223	K1150	V1054	T980	P897
ARG	Q1754	L1652	A1492	L1298	T1224	K1151	N1055	T981	F898
GLY	Q1755	L1653	L1577	E1299	F1224	P1154	T1056	V982	V904
N1909	R1837	L1654	PRO	S1300	E1225	P1155	K1057	V984	E900
ASN	M1757	L1655	GLY	E1300	E1226	A1155	E985	E985	M901
PHE	M1762	L1656	ASP	I1301	G1227	G1156	P986	P986	K902
PRO	V1844	L1657	GLU	H1304	G1228	F1157	K1061	L987	P903
D1921	V1845	M1583	ARG	M1392	G1229	P1158	R1062	V988	V904
A1922	M1762	L1658	GLN	A1393	G1230	P1159	K1057	V984	E900
F1923	L1766	D1588	CYS	I1307	G1231	P1160	K1057	V984	E900
T1924	C1767	W1659	LEU	A1308	T1232	S1162	S1065	L982	F906
E1925	D1849	S1660	THR	A1309	T1233	L1163	L1066	H993	L907
N1926	V1850	F1661	PRO	V1398	G1234	L1163	A1067	H994	V994
VAL	L1851	M1662	S1502	G1399	G1235	L1163	L1068	F995	F910
PRO	L1852	T1663	S1503	C1399	I1235	L1164	H1069	F995	F910
MET	SER	Q1771	D1504	K1311	L1236	L1165	T1070	H997	R913
ALA	ARG	H1772	L1589	F1312	L1236	L1166	N1071	K997	R913
GLY	PHE	H1665	L1595	F1313	A1237	D1167	N1071	K998	R913
GLU	THR	E1775	V1596	GLY	Q1238	L1167	A1072	K998	R913
ASN	LYS	E1776	S1506	THR	P1239	L1168	F1073	A999	L917
GLN	LEU	F1777	C1507	GLY	T1240	L1168	K1074	K1000	T926
LEU	ASN	L1778	K1508	ALA	L1240	W1171	R1075	F1001	T926
GLU	GLU	Q1779	Q1509	ALA	L1241	H1171	R1075	K1001	K927
SER	SER	P1697	D1602	ALA	L1242	H1172	Q1004	Q1004	C931
LEU	F1698	F1698	L1517	GLY	L1243	H1173	D1005	D1005	E932
THR	R1606	E1607	E1526	ASN	L1244	C1176	F1006	F1006	L933
A1786	R1608	R1527	R1527	ARG	L1245	G1177	N1084	N1084	L933
LEU	SER	A1609	L1415	GLY	L1246	R1178	I1085	I1085	H935
SER	LEU	R1609	A1536	S1323	L1247	T1181	Y1086	Y1086	S936
THR	THR	L1610	V1537	P1324	L1248	E1182	E1087	E1087	M937
GLY	GLY	Q1611	L1538	Q1325	S1249	C1183	F1089	F1089	V938
L1783	T1783	SER	SER	E1326	L1250	L1184	D1015	D1015	V938
Q1794	H1613	THR	THR	R1329	Q1251	K1185	G1016	G1016	M941
H1614	Q1614	ALA	ALA	A1425	A1252	K1186	T1017	T1017	L942
L1797	L1707	SER	SER	Q1426	L1253	S1187	V1018	V1018	G943
L1798	E1708	LEU	LEU	V1337	L1254	I1188	D1019	D1019	K944
LEU	K1617	GLY	GLY	L1427	C1255	F1191	P1020	P1020	V968
R1711	R1711	GLY	GLY	L1428	L1256	D1022	V1021	V1021	G951
E1803	E1803	SER	SER	L1431	L1257	V1195	S1023	S1023	G952
M1804	L1621	SER	SER	L1431	L1257	V1195	V1105	V1105	G952
F1805	L1622	GLN	GLN	L1431	D1258	P1196	R1026	R1026	Q953
R1806	L1714	GLY	GLY	V1452	L1259	L1197	M1108	M1108	G954
Q1716	Q1624	SER	SER	S1453	L1260	L1198	E1109	E1109	G954
LYS	W1626	VAL	VAL	T1345	L1261	P1199	S1110	S1110	A955
ASP	P1723	ASP	ILE	T1346	A1262	R1202	R1031	R1031	P956
LEU	M1724	PRO	THR	K1456	L1263	R1202	R1031	R1031	P957
THR	Q1725	ARG	THR	Q1457	L1264	R1202	R1031	R1031	P957
LEU	S1726	PHE	PHE	Q1457	E1265	R1202	R1031	R1031	P957
ALA	C1629	THR	THR	R1460	E1265	R1202	R1031	R1031	P957
GLY	S1726	THR	THR	R1460	E1265	R1202	R1031	R1031	P957
ASP	P1729	THR	THR	R1460	E1265	R1202	R1031	R1031	P957
LEU	F1729	THR	THR	R1460	E1265	R1202	R1031	R1031	P957
LYS	PHE	THR	THR	R1460	E1265	R1202	R1031	R1031	P957
GLU	T1815	THR	THR	R1460	E1265	R1202	R1031	R1031	P957
LEU	L1819	THR	THR	R1460	E1265	R1202	R1031	R1031	P957
ALA	S1818	THR	THR	R1460	E1265	R1202	R1031	R1031	P957
ASP	LYS	THR	THR	R1460	E1265	R1202	R1031	R1031	P957
S2034	ASN	THR	THR	R1460	E1265	R1202	R1031	R1031	P957
D2044	LEU	THR	THR	R1460	E1265	R1202	R1031	R1031	P957
T2045	GLN	THR	THR	R1460	E1265	R1202	R1031	R1031	P957





- Molecule 7: DNA

Chain i: 40% 60%



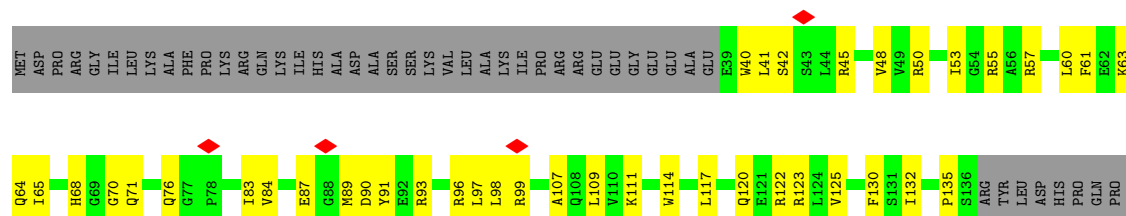
- Molecule 8: DNA

Chain j: 20% 80%



- Molecule 9: DNA polymerase lambda

Chain A: 10% 7% 83%



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	14964	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 ($e^-/\text{\AA}^2$)	51.96	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.696	Depositor
Minimum map value	-0.178	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.034	Depositor
Recommended contour level	0.211	Depositor
Map size (Å)	417.28, 417.28, 417.28	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.304, 1.304, 1.304	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	E	0.14	0/1997	0.40	0/2695
2	L	0.14	0/5182	0.36	0/6990
3	M	0.17	0/164	0.44	0/220
4	P	0.11	0/485	0.34	0/647
4	Q	0.13	0/480	0.35	0/640
5	S	0.19	0/28315	0.48	0/38300
6	T	0.17	0/4079	0.41	0/5499
7	i	0.28	0/572	0.50	0/879
8	j	0.32	0/575	0.58	0/888
9	A	0.16	0/780	0.44	0/1057
All	All	0.18	0/42629	0.46	0/57815

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 [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	E	1956	0	1905	76	0
2	L	5084	0	5080	206	0
3	M	160	0	148	6	0
4	P	480	0	501	27	0
4	Q	475	0	492	25	0
5	S	27773	0	27732	1057	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	T	4001	0	4050	188	0
7	i	510	0	285	18	0
8	j	514	0	290	20	0
9	A	764	0	785	35	0
All	All	41717	0	41268	1564	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 19.

The worst 5 of 1564 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)
5:S:2806:LYS:HG3	5:S:2857:CYS:HB3	1.59	0.84
1:E:757:GLU:HB3	1:E:763:ASP:H	1.42	0.83
5:S:835:LYS:HA	5:S:838:LYS:HG2	1.62	0.81
5:S:1300:SER:HA	5:S:1304:HIS:HB2	1.65	0.79
5:S:1820:VAL:HA	5:S:1824:LEU:HD23	1.64	0.79

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	E	242/911 (27%)	208 (86%)	32 (13%)	2 (1%)	16	53
2	L	635/732 (87%)	598 (94%)	36 (6%)	1 (0%)	44	78
3	M	21/204 (10%)	21 (100%)	0	0	100	100
4	P	55/336 (16%)	55 (100%)	0	0	100	100
4	Q	55/336 (16%)	55 (100%)	0	0	100	100
5	S	3459/4128 (84%)	3188 (92%)	263 (8%)	8 (0%)	44	78

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	T	497/609 (82%)	461 (93%)	36 (7%)	0	100	100
9	A	96/575 (17%)	96 (100%)	0	0	100	100
All	All	5060/7831 (65%)	4682 (92%)	367 (7%)	11 (0%)	45	78

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	814	ARG
5	S	4012	ASP
5	S	4013	TRP
5	S	1231	GLN
5	S	4010	SER

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	217/808 (27%)	217 (100%)	0	100	100
2	L	559/649 (86%)	559 (100%)	0	100	100
3	M	16/160 (10%)	16 (100%)	0	100	100
4	P	53/303 (18%)	53 (100%)	0	100	100
4	Q	51/303 (17%)	51 (100%)	0	100	100
5	S	2998/3671 (82%)	2998 (100%)	0	100	100
6	T	444/548 (81%)	444 (100%)	0	100	100
9	A	81/480 (17%)	81 (100%)	0	100	100
All	All	4419/6922 (64%)	4419 (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 59 such sidechains are listed below:

Mol	Chain	Res	Type
5	S	1611	GLN
6	T	484	GLN
5	S	2493	ASN
6	T	433	GLN
5	S	4055	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.

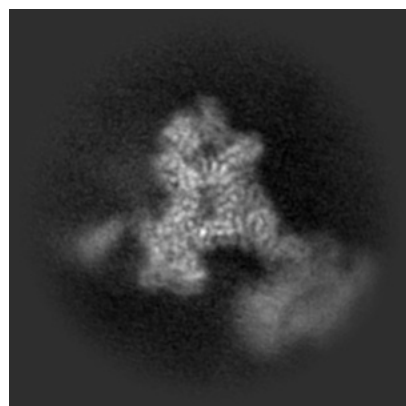
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51249. These allow visual inspection of the internal detail of the map and identification of artifacts.

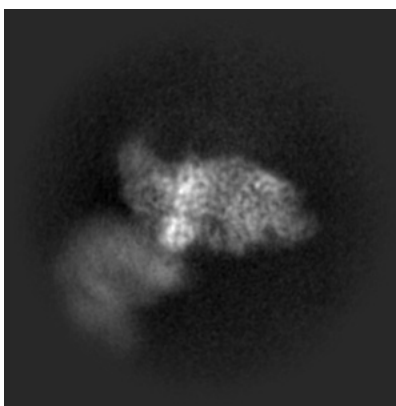
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

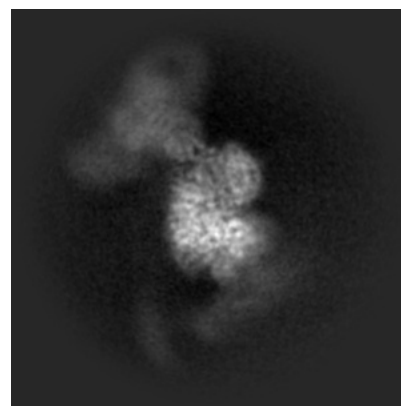
6.1.1 Primary map



X

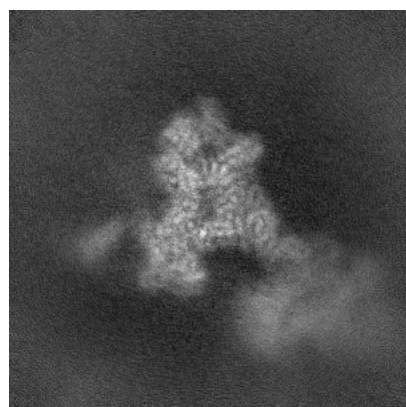


Y

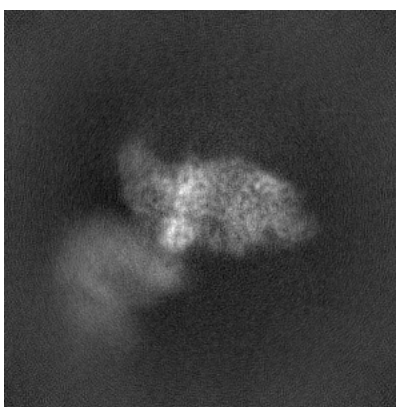


Z

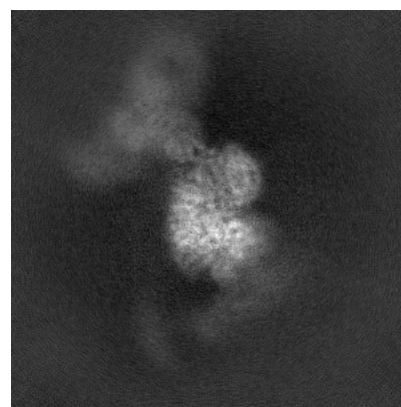
6.1.2 Raw map



X



Y

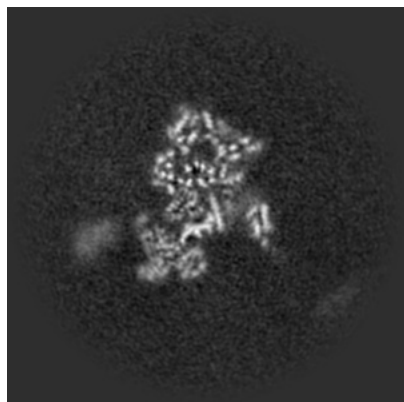


Z

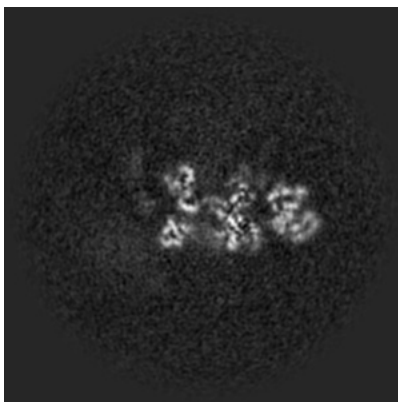
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

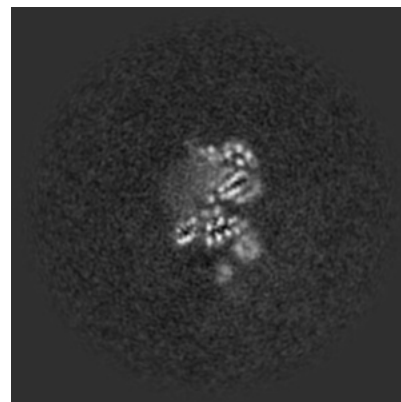
6.2.1 Primary map



X Index: 160

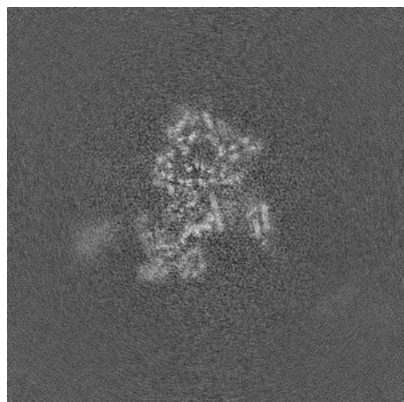


Y Index: 160

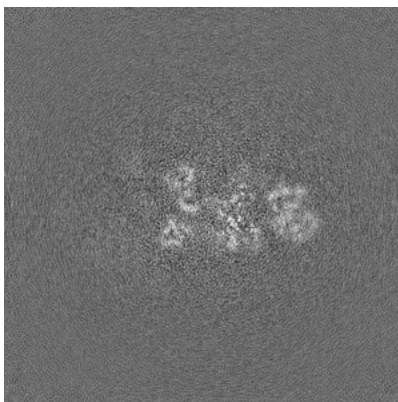


Z Index: 160

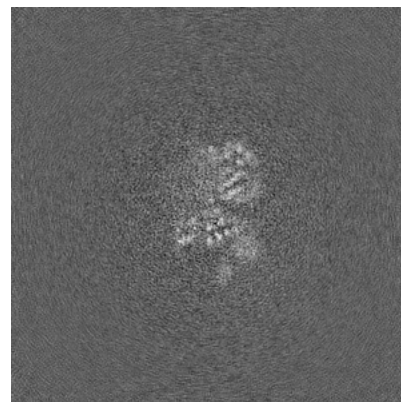
6.2.2 Raw map



X Index: 160



Y Index: 160

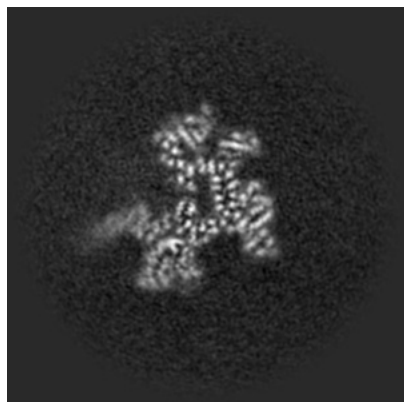


Z Index: 160

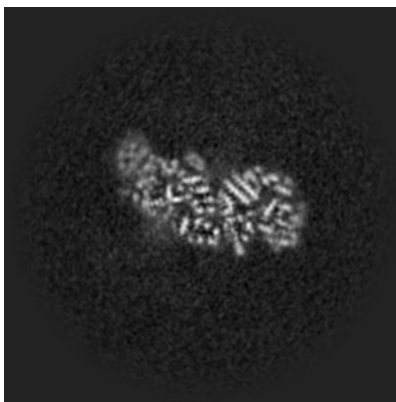
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

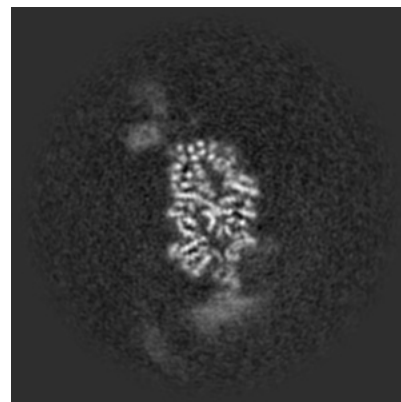
6.3.1 Primary map



X Index: 175

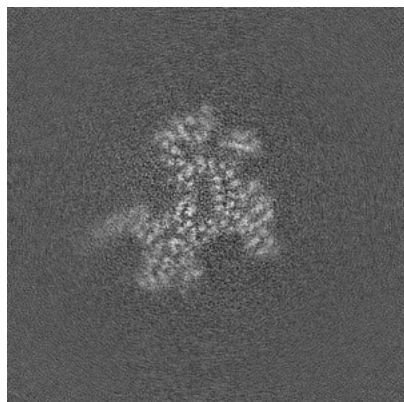


Y Index: 138

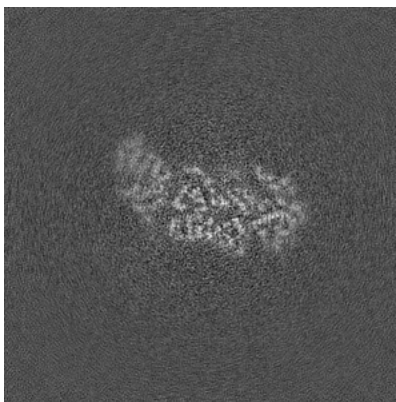


Z Index: 142

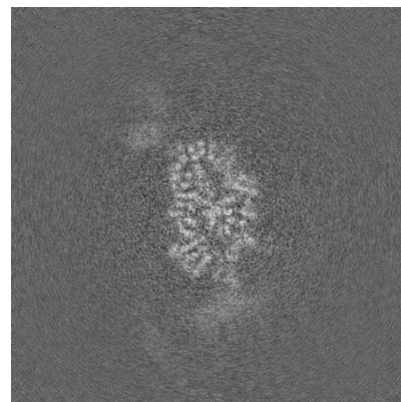
6.3.2 Raw map



X Index: 174



Y Index: 143

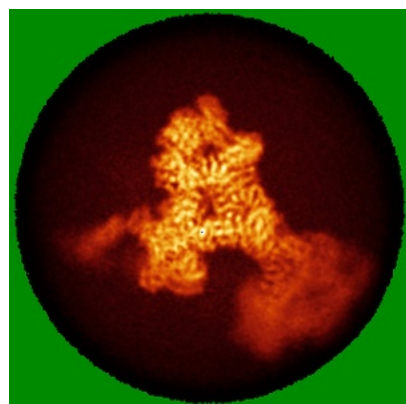


Z Index: 142

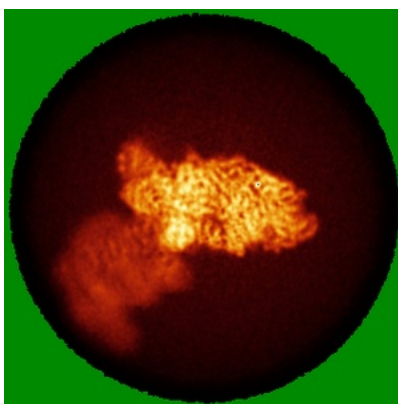
The images above show the largest variance slices of the map in three orthogonal directions.

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

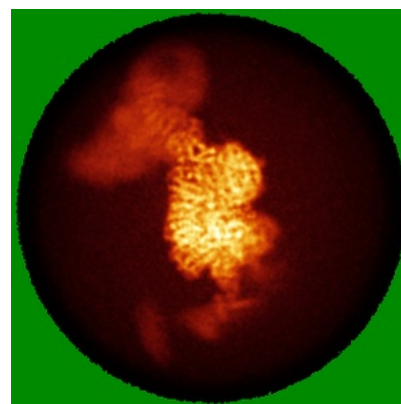
6.4.1 Primary map



X

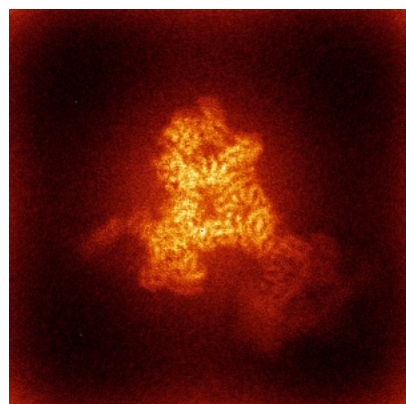


Y

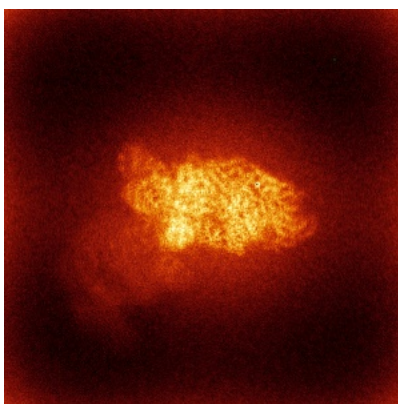


Z

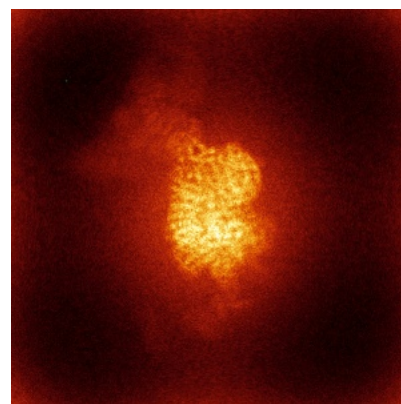
6.4.2 Raw map



X



Y

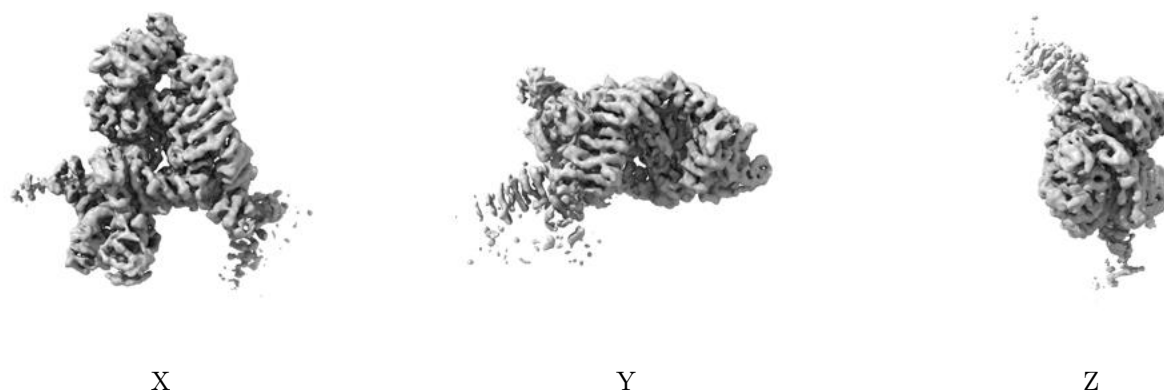


Z

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.

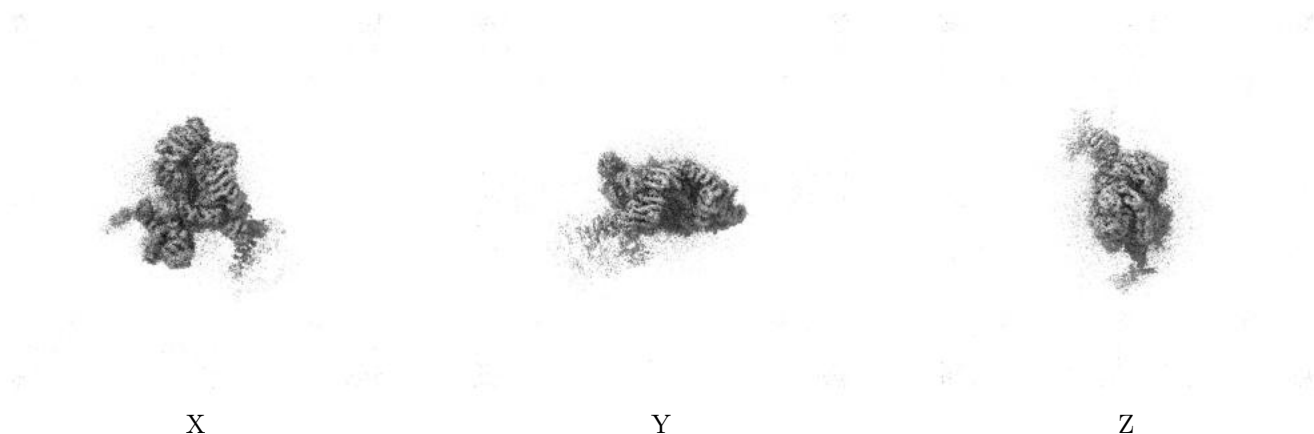
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.211. 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.

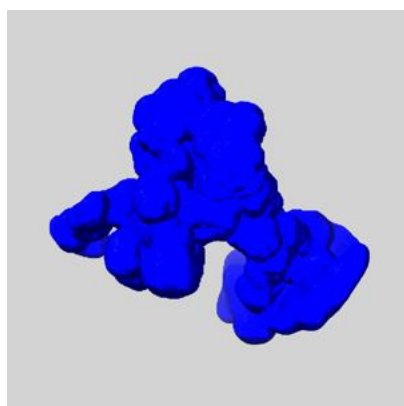
6.6 Mask visualisation [i](#)

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

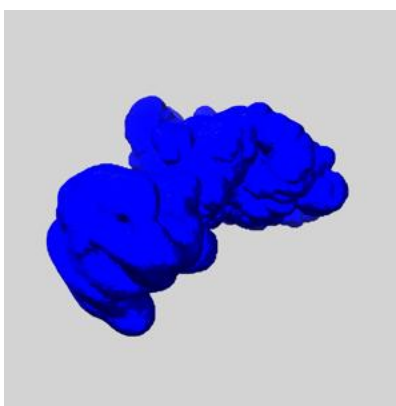
A mask typically either:

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

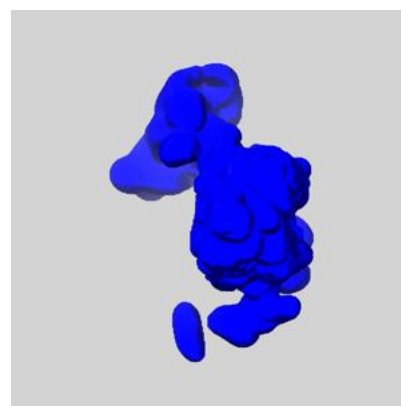
6.6.1 emd_51249_msk_1.map [i](#)



X



Y

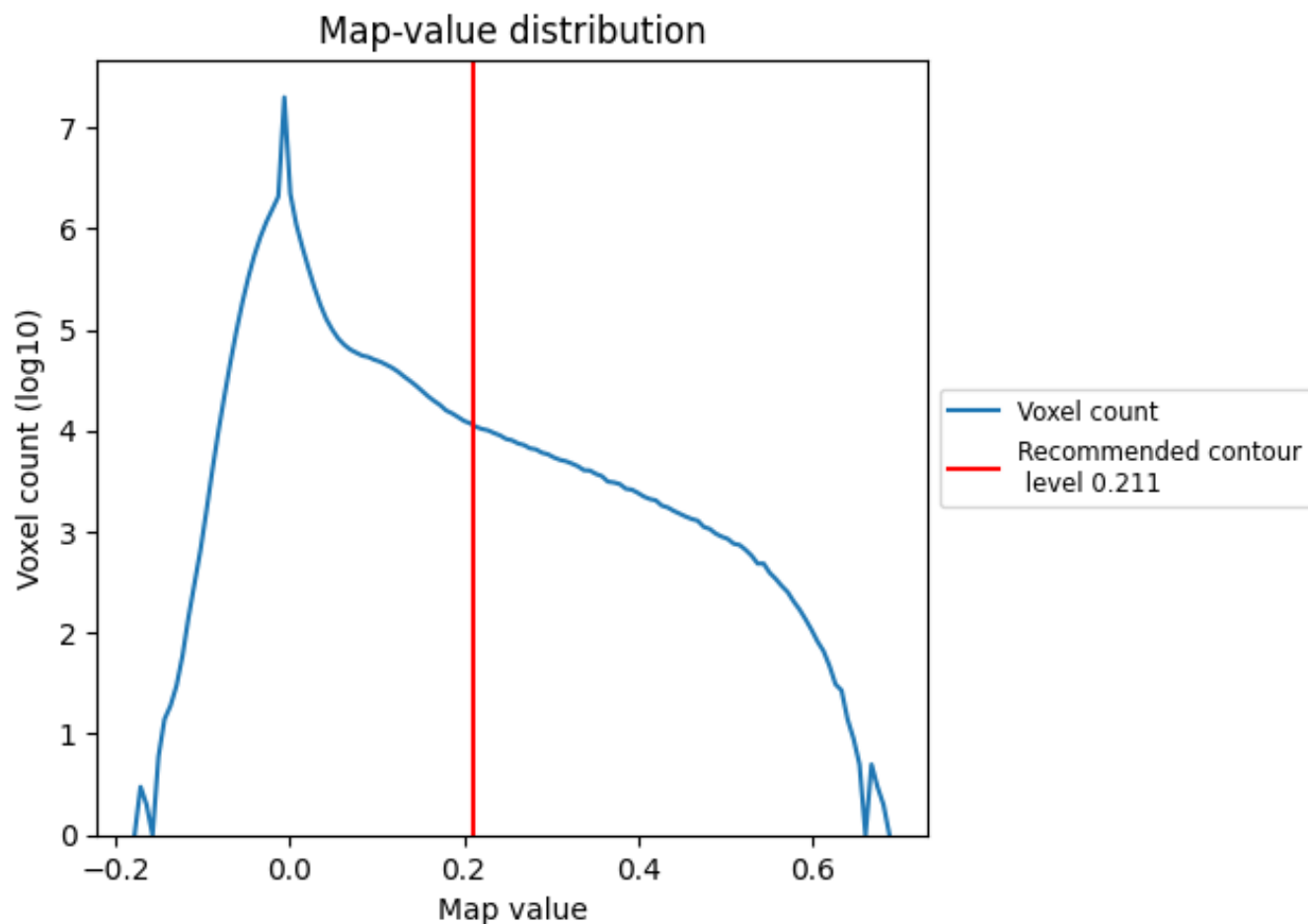


Z

7 Map analysis [i](#)

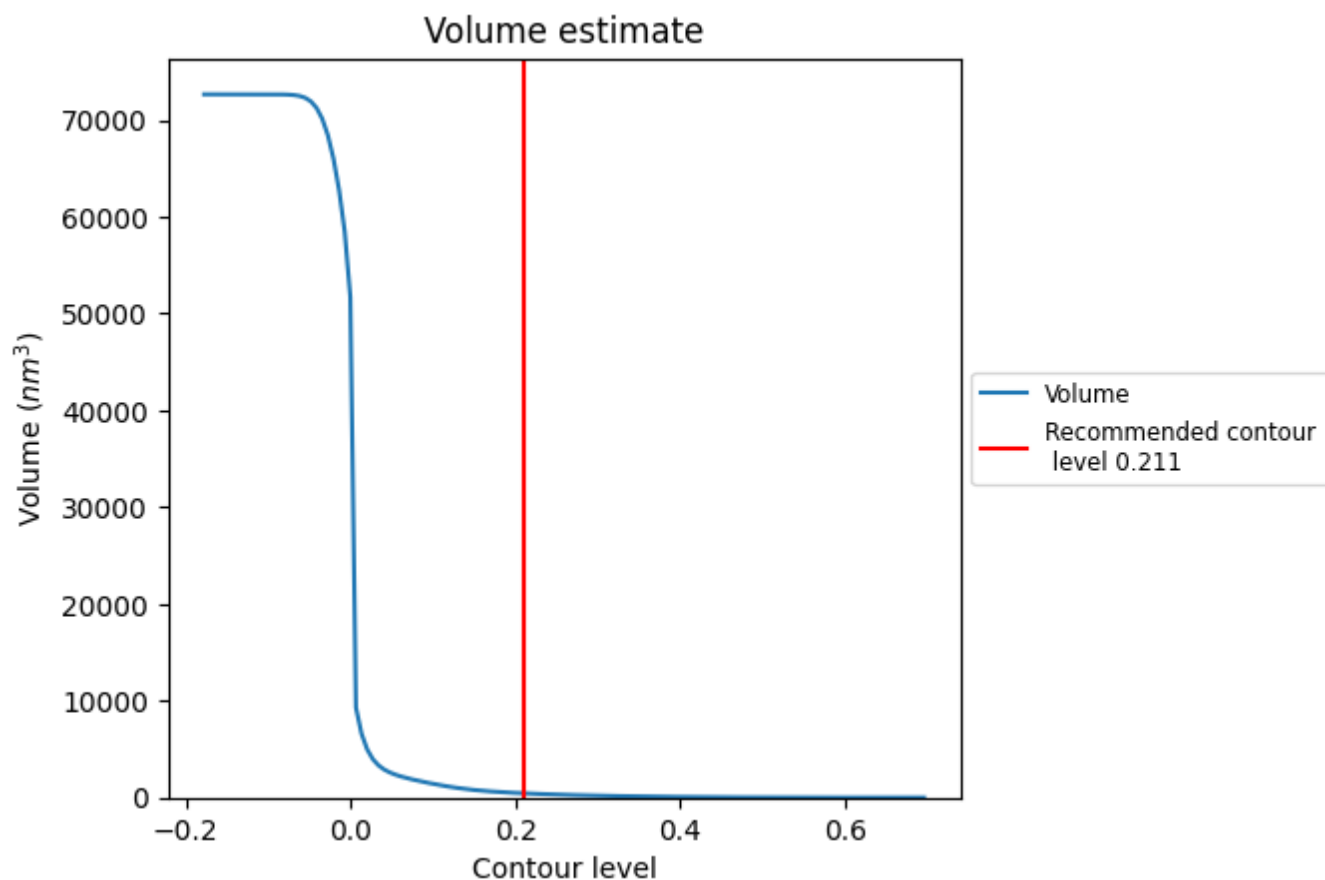
This section contains the results of statistical analysis of the map.

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.

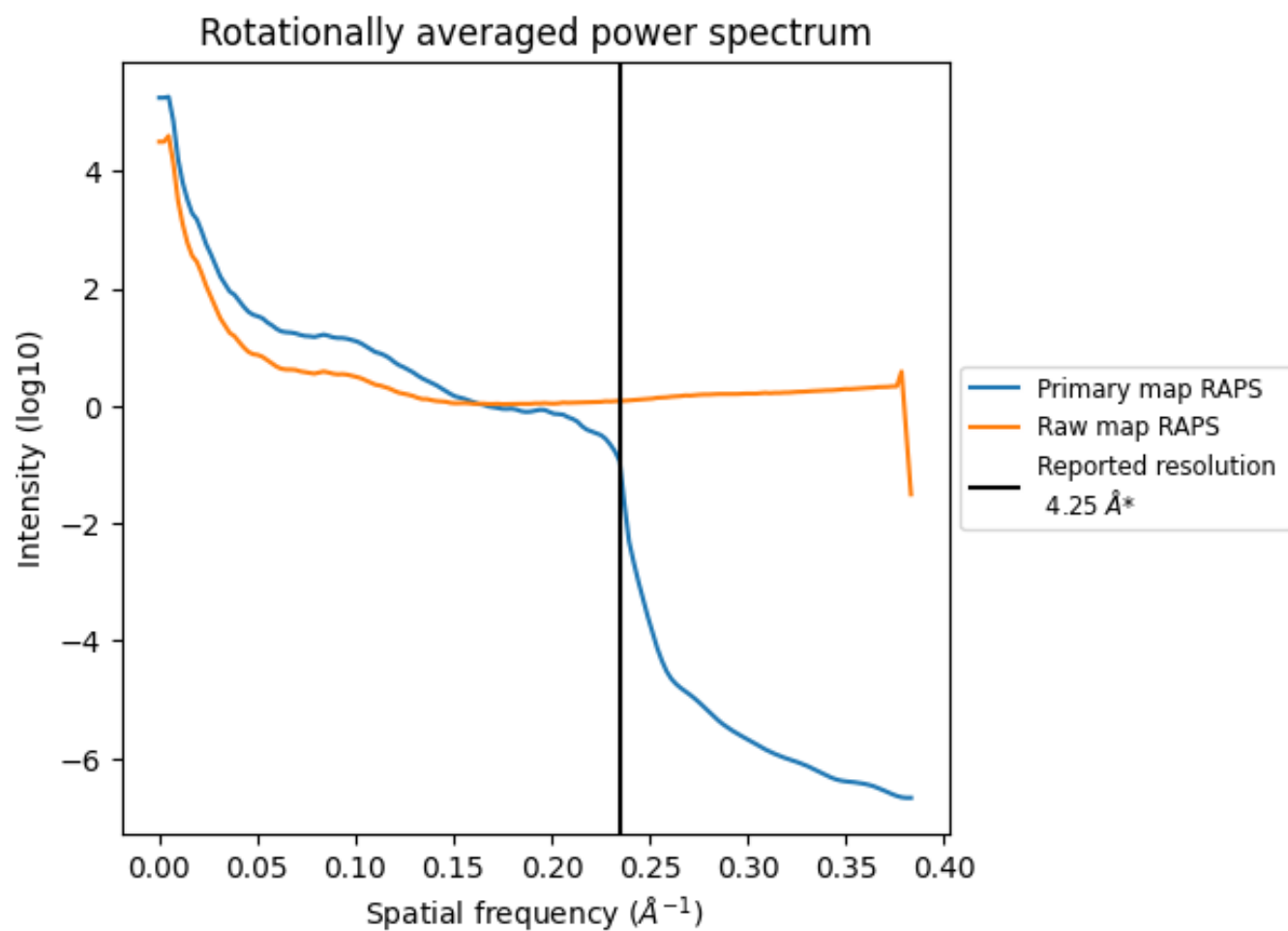
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 434 nm³; this corresponds to an approximate mass of 392 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 ⓘ

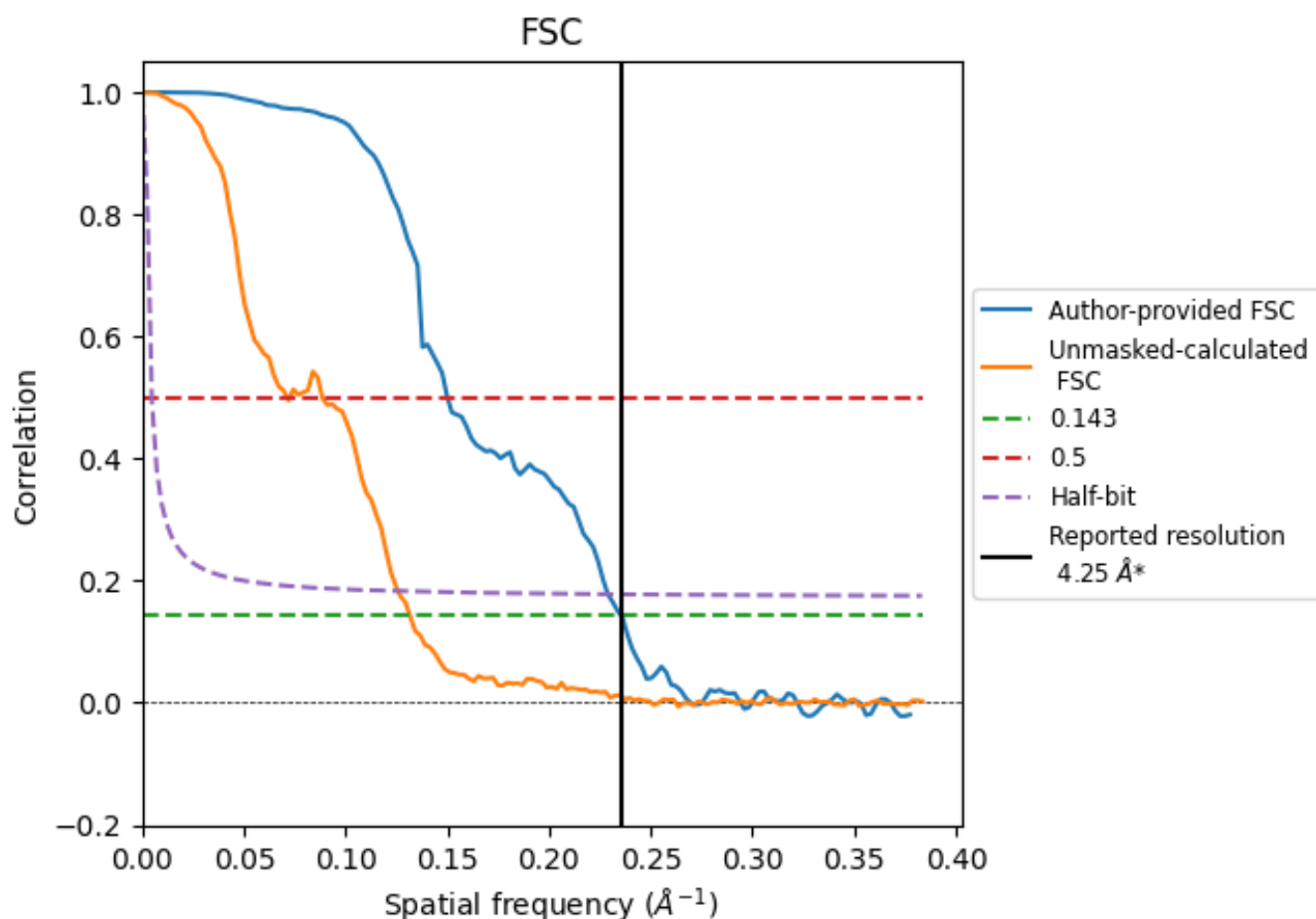


*Reported resolution corresponds to spatial frequency of 0.235 \AA^{-1}

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 0.235 \AA^{-1}

8.2 Resolution estimates [i](#)

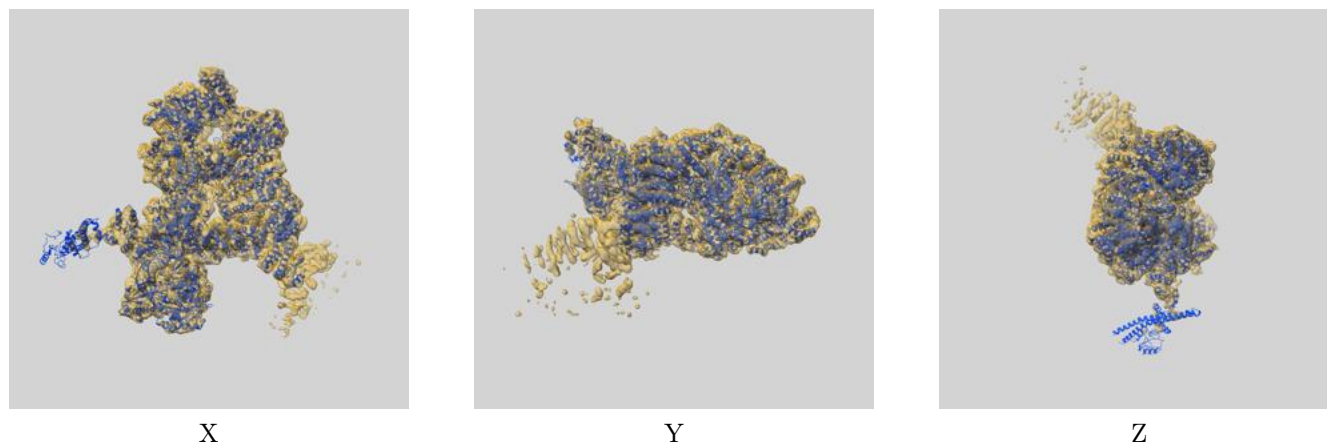
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.25	-	-
Author-provided FSC curve	4.25	6.66	4.37
Unmasked-calculated*	7.60	14.04	7.95

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.60 differs from the reported value 4.25 by more than 10 %

9 Map-model fit [i](#)

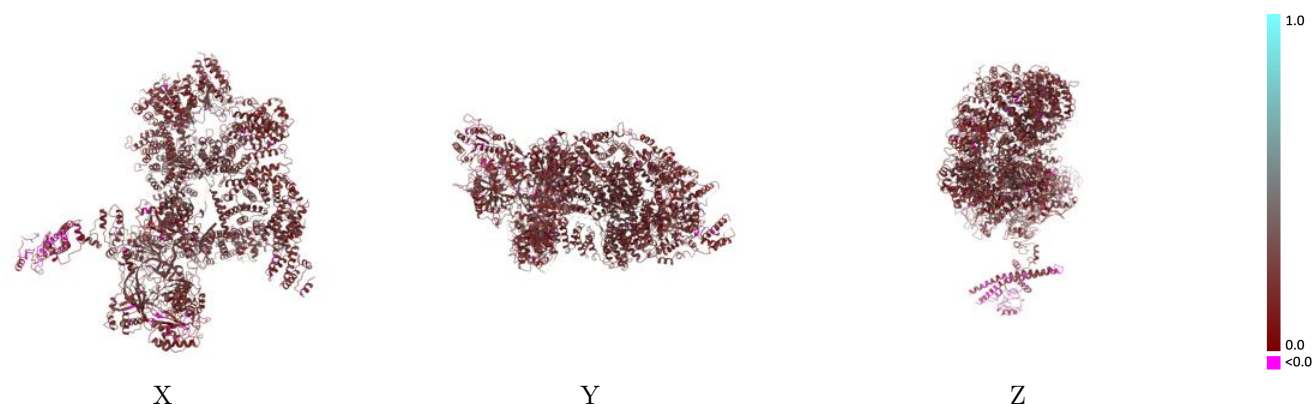
This section contains information regarding the fit between EMDB map EMD-51249 and PDB model 9GD7. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



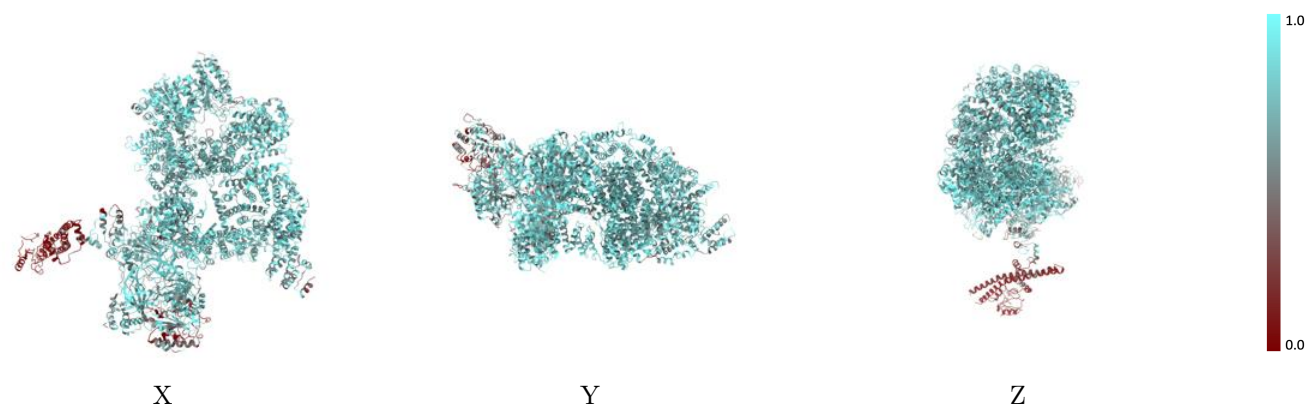
The images above show the 3D surface view of the map at the recommended contour level 0.211 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



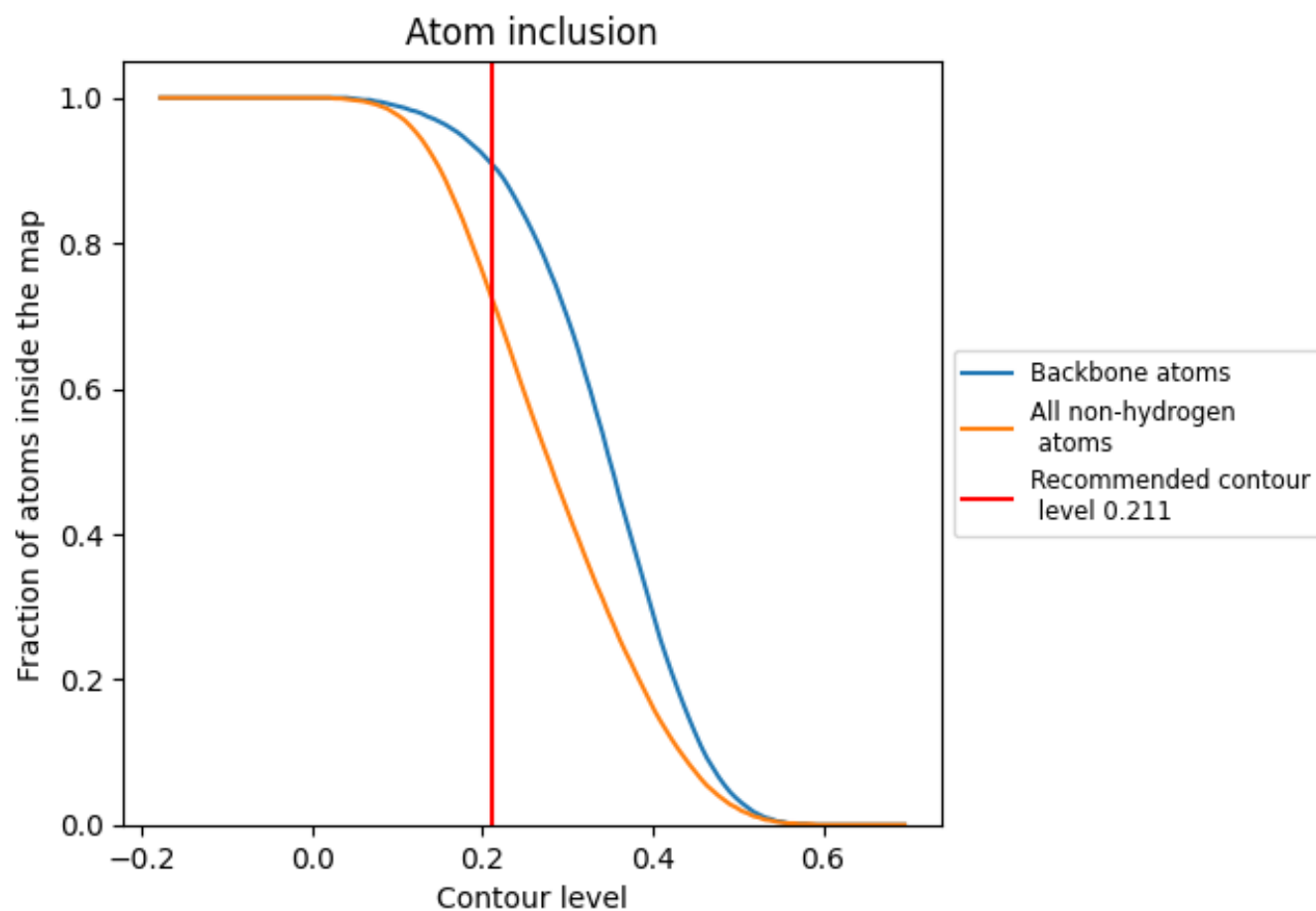
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.211).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 72% 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 (0.211) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7240	<div></div> 0.2280
A	<div></div> 0.7750	<div></div> 0.2160
E	<div></div> 0.2650	<div></div> 0.1390
L	<div></div> 0.6110	<div></div> 0.2070
M	<div></div> 0.6560	<div></div> 0.2950
P	<div></div> 0.0530	<div></div> 0.0970
Q	<div></div> 0.0970	<div></div> 0.0800
S	<div></div> 0.7870	<div></div> 0.2370
T	<div></div> 0.7420	<div></div> 0.2480
i	<div></div> 0.9770	<div></div> 0.3020
j	<div></div> 0.9810	<div></div> 0.2960

1.0

0.0

<0.0