



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 05:57 PM UTC

PDB ID : 6ZH6 / pdb_00006zh6
EMDB ID : EMD-11215
Title : Cryo-EM structure of DNA-PKcs:Ku80ct194
Authors : Chaplin, A.K.; Hardwick, S.W.; Chirgadze, D.Y.; Blundell, T.L.
Deposited on : 2020-06-21
Resolution : 3.93 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

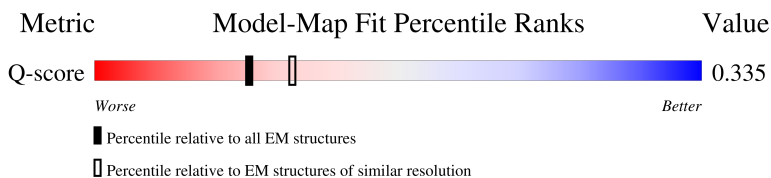
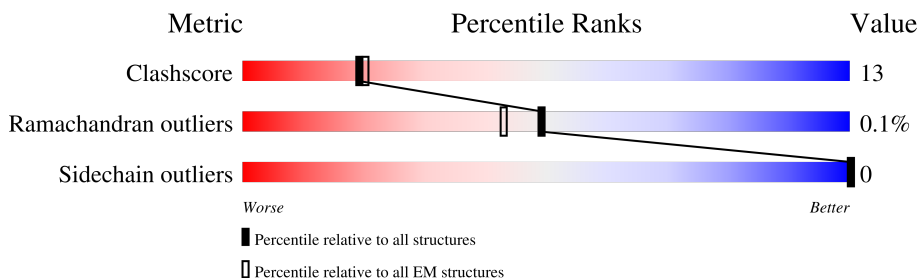
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.93 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	7811 (3.43 - 4.43)

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	4156	
2	B	192	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 29201 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-dependent protein kinase catalytic subunit,DNA-PKcs.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3692	Total	C	N	O	S	0	0
			29138	18697	4938	5311	192		

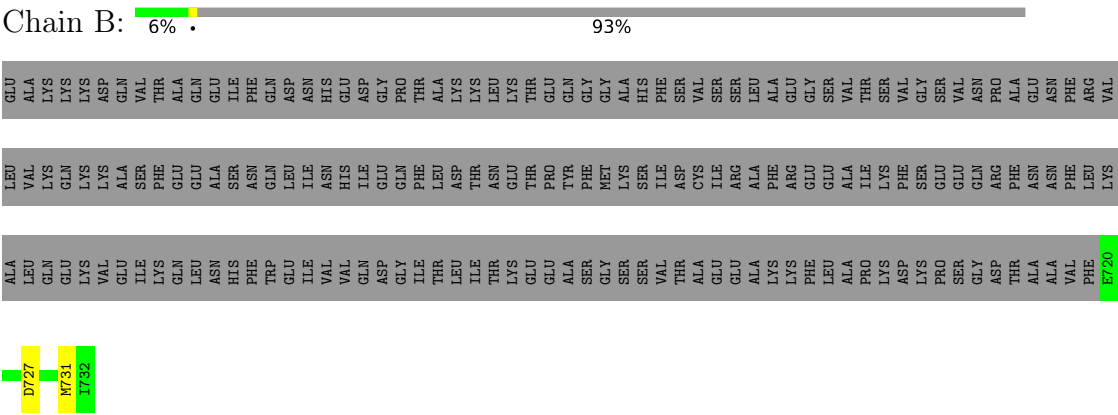
- Molecule 2 is a protein called X-ray repair cross-complementing protein 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	13	Total	C	N	O	0	0
			63	37	13	13		

L2480	F2383	L2219	GLY	SER	L1976	I1848	P1734	L1623	C1499	I1306	P1158	R1031
Y2484	L2386	M2220	PRO	GLN	M1980	D1849	R1735	C1629	L1500	I1307	L1163	R1034
S2489	H2222	H2222	GLN	PHE	L1981	V1850	M1738	W1632	P1501	K1311	C1164	L1037
E2490	V2223	V2223	GLY	PHE	H1986	K1852	M1743	W1633	S1502	C1312	L1165	T1045
N2493	G2391	F2224	GLY	SER	ARG	F1863	K1744	A1634	D1504	GLY	H1175	T1048
D2494	V2392	H2225	GLY	THR	TYR	D1864	K1745	A1634	L1505	PHE	R1178	Q1048
S2495	T2395	P2226	ASP	GLY	ASN	T1865	F1746	P1638	S1506	T1315	P1179	Q1049
Q2496	T2227	K2227	SER	VAL	PHE	Q1866	L1747	L1639	C1507	G1316	Q1180	E1050
L2506	R2404	V2230	VAL	SER	PRO	Q1867	L1750	E1640	S1512	A1317	T1181	V1054
L2510	Q2414	Y2253	GLY	TYR	VAL	T1868	L1750	T1641	S1512	A1318	E1182	V1054
T2511	L2415	H2254	VAL	GLY	VAL	K1869	S1753	K1642	A1518	G1319	C1183	K1057
D2512	K2418	L2255	GLU	GLY	GLU	K1870	Q1754	M1643	F1521	M1320	R1184	K1057
E2513	D2419	M2126	VAL	VAL	VAL	M1871	M1757	L1648	L1524	S1323	G1200	L1066
N2514	F2420	S2127	PRO	PRO	PRO	D1877	L1652	A1425	E1326	E1326	N1201	L1066
F2524	M2424	K2259	ARG	GLY	GLY	V1879	L1766	E1429	L1528	Y1330	R1202	M1071
P2532	D2428	L2276	ARG	ARG	ARG	M1880	Q1770	C1432	L1531	K1334	S1203	A1072
R2538	R2431	V2304	THR	ALA	LYS	S1882	Q1771	A1433	L1538	C1335	L1206	F1073
L2542	C2435	M2307	GLY	THR	TYR	R1883	E1775	Q1442	E1670	K1335	W1207	K1074
F2554	L2436	V2310	ARG	ARG	ILE	C1904	F1778	V1443	T1673	T1336	V1211	G1077
L2555	D2437	T2311	ARG	ARG	GLY	K1913	Y1675	D1444	A1541	V1337	N1084	N1084
S2556	R2438	R2311	ARG	ARG	ILE	K1913	T1785	R1445	SER	W1337	E1215	I1085
L2557	L2439	Y2312	ARG	ARG	ARG	T1914	A1786	L1448	LEU	R1340	I1086	Y1086
L2563	L2444	G1245	GLN	ALA	LYS	L1915	H1687	L1448	GLY	F1344	E1225	R1087
N2574	M2442	V2315	ARG	ARG	ALA	I1916	Y1802	V1452	SER	F1344	G1226	L1095
P2575	M2443	L2146	ASP	GLU	ARG	C1919	R1806	K1456	GLN	L1348	G1227	L1095
M2576	K2443	A2147	ALA	GLU	GLU	Y1920	Q1690	Q1457	S1549	P1353	G1228	F1099
F2577	P2444	K2148	ALA	ALA	ALA	Y1920	V1693	Q1457	F1553	W1356	S1233	E1102
E2578	L2454	N2152	ASN	GLY	ASN	F1923	T1694	H1459	F1553	W1356	L1236	A1103
H2579	N2456	K2183	GLY	GLY	GLY	L1933	L1696	L1464	T1566	K1361	A1237	T1106
P2580	P2457	V2186	SER	SER	ASP	L1934	P1697	L1467	T1567	K1361	Q1238	Y1107
L2581	F2461	L2345	ASP	ASP	SER	L1934	R1816	T1467	N1568	N1365	L1241	A1112
F2586	Q2347	A2346	VAL	VAL	ASP	E1935	Q1817	L1468	N1568	N1365	Y1243	A1112
Q2587	Q2348	K2349	LEU	LEU	ASP	R1936	S1818	L1476	L1575	N1369	L1244	I1124
E2588	L2349	L2344	GLY	GLY	PRO	R1936	F1819	H1479	L1700	R1370	P1247	H1133
Y2589	H2464	L2345	LEU	TYR	TYR	L1939	L1707	E1479	L1575	V1371	L1250	I1137
D2594	P2465	K2350	GLY	TYR	MET	L1939	E1708	E1482	M1583	E1378	L1261	L1145
TRP	T2467	K2350	GLY	TYR	MET	N1946	E1709	L1483	D1588	A1380	E1285	N1146
ARG	T2468	Q2353	M2085	GLY	SER	C1947	L1710	L1486	D1588	F1384	K1147	K1147
PHE	Q2469	K2347	L2088	SER	SER	C1947	L1710	L1486	D1588	N1385	E1285	A1148
ARG	R2470	L2348	L2088	SER	SER	C1947	L1710	L1486	D1588	N1385	E1285	A1148
ARG	E2471	L2348	L2088	SER	SER	C1947	L1710	L1486	D1588	N1385	E1285	A1148
THR	Q2472	K2348	L2088	SER	SER	C1947	L1710	L1486	D1588	N1385	E1285	A1148
VAL	M2473	L2374	L2100	LEU	LEU	F1956	F1840	P1493	G1599	F1384	L1261	L1145
L2478	M2478	D2376	M2104	SER	SER	F1956	F1840	P1493	G1599	F1384	L1261	L1145
THR	W2479	E2377	M2104	GLY	GLY	F1956	F1840	P1493	G1599	F1384	L1261	L1145
PRO		F2378	L2108	GLY	GLY	F1956	F1840	P1493	G1599	F1384	L1261	L1145

W4027	M3858	R3734	G3626	Y3531	P3405	N3310	G1N	Q3104	L2939	A2796	LEU
E4030	Y3859	P3735	A3627	P3532	A3406	N3311	GLU	N3105	ARG	R2800	ARG
R4041	R3864	R3736	R3630	I3534	M3414	S3109	GLU	Q3108	ARG	D2801	ARG
L4051	V3868	R3737	Q3634	I3535	L3416	F3110	D3226	F3110	ARG	A2805	ARG
A4054	E3875	D3744	F3642	S3541	L3424	R3324	K3235	M3111	PHE	L2837	MET
L4064	V3878	L3751	D3640	G3548	N3430	Q3326	F3236	L3120	ARG	N2841	ASP
L4065	P3879	D3757	K3642	H3549	ALA	S3237	K3238	L3121	ARG	N2845	GLN
L4066	A3880	L3758	H3643	K3550	SER	N3327	K3242	K3128	ASP	C2857	LEU
E4069	D3881	R3759	K3646	N3551	VAL	L3328	I3243	Q3133	ASP	S2862	LEU
D4086	L3882	Q3760	F3553	K3552	ASP	T3333	D3244	T3136	GLN	Q2864	ALA
H4087	R3889	R3763	S3649	F3554	SER	Y3334	R3247	E3137	GLU	H2865	SER
M4088	K3650	R3767	K3655	V3555	ALA	R3335	K3250	L3142	LEU	L2868	GLY
E4093	S3657	M3771	L3562	A3556	GLU	A3338	K3251	I3145	THR	D2872	ALA
E4100	R3657	L3774	K3561	R3557	A3440	N3339	N3250	L3151	ARG	V2876	GLU
E4101	D3661	L3775	L3562	R3557	A3441	S3342	K3251	L3151	GLY	D2879	ALA
T4102	F3659	A3776	V3567	I3568	K3449	L3348	K3256	W3164	VAL	A3006	GLN
Q4103	D3661	A3777	I3568	Q3569	L3451	I3351	K3257	P3169	ARG	E2995	ARG
L4104	N3664	Q3777	Q3570	F3571	F3472	E3352	L3259	W3179	PRO	C2879	PRO
K4105	N3670	Q3787	N3572	F3571	I3472	E3353	K3260	P3180	LEU	S2883	GLY
C4106	M3670	Q3787	N3572	N3572	I3472	K3355	E3261	K3180	GLN	E2894	VAL
L4107	M3670	V3793	A3574	A3574	K3483	K3356	L3262	P3181	SER	P2902	GLY
M4108	D3922	V3794	L3575	L3575	T3484	R3357	R3269	I3182	THR	A3022	ILE
D4113	R3923	P3795	D3576	D3576	K3485	R3358	D3270	R3186	ALA	N3028	ALA
E4122	F3942	M3796	L3577	L3577	I3487	I3359	D3271	K3196	ASP	K3029	SER
G4123	Q3951	L3800	E3582	E3582	P3491	L3361	V3274	L3197	PHE	T3030	GLN
M4124	G3801	G3801	K3586	K3586	C3492	D3369	Q3278	THR	GLN	E3033	HIS
E4125	L3802	L3802	K3586	K3586	C3492	S3370	Q3278	PRO	LYS	P3034	LYS
P4126	L3803	L3803	K3586	K3586	W3493	E3371	L3283	LEU	ARG	MET	PHE
M4128	M3806	L3806	M3886	M3887	F3495	K3372	S3284	PRO	LEU	ARG	THR
X5009	R3965	L3806	M3887	V3592	K3502	G3376	H3285	GLU	VAL	VAL	LEU
X6004	L3970	T3809	L3699	E3595	L3505	G3376	C3286	ASP	ARG	GLY	THR
X6005	M3971	L3812	E3700	L3596	L3505	R3380	R3287	ASN	GLY	Q2788	GLN
X6006	P3973	N3818	I3701	A3597	D3509	R3380	S3288	SER	LYS	R2773	THR
X6015	K3974	M3820	G3702	K3598	Q3510	Q3383	R3289	MET	ASP	S2774	ASP
X6019	K3975	S3821	Q3704	K3598	A3513	E3387	S3290	ASN	VAL	Y2775	VAL
X6023	M3980	K3825	P3711	V3601	V3514	V3389	S3294	GLN	ASP	R2776	ASP
	Y3981	L3829	L3712	N3602	S3517	E3396	Q3296	ASP	ASN	H2777	SER
	M3984	R3717	V3717	I3606	I3521	GLN	E3295	GLY	LYS	G2778	SER
	R3989	R3718	R3718	E3607	T3522	PRO	V3297	ASP	VAL	K2786	PHE
	R3992	D3723	D3723	M3609	T3522	SER	L3299	PRO	LYS	R2922	ASP
	P3995	E3724	E3724	M3612	Y3525	TRP	V3300	ASP	ALA	W2923	GLY
		V3728	V3728	M3613	I3529	GLY	L3301	ARG	ALA	W2924	THR
		M3729	M3729	L3617	V3530	CYS	D3308	MET	GLY	L2790	GLY
		A3730	A3730			GLY	E3309	GLU	THR	T2792	SER
								VAL	ASP	P2793	THR

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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	43995	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 ($e^-/\text{\AA}^2$)	54.49	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	0.504	Depositor
Minimum map value	-0.138	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.125	Depositor
Map size (Å)	336.64, 336.64, 336.64	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.052, 1.052, 1.052	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	0.16	0/29593	0.38	1/40028 (0.0%)
2	B	0.16	0/62	0.43	0/84
All	All	0.16	0/29655	0.38	1/40112 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1659	VAL	N-CA-C	-6.32	107.70	113.71

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	A	29138	0	29130	702	0
2	B	63	0	27	1	0
All	All	29201	0	29157	703	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 13.

The worst 5 of 703 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:1175:HIS:HB3	1:A:1178:ARG:HH21	1.41	0.85
1:A:1396:PRO:HB3	1:A:1457:GLN:HE22	1.40	0.85
1:A:1178:ARG:NH1	1:A:1183:CYS:SG	2.55	0.80
1:A:3256:MET:HE3	1:A:3287:ARG:HH21	1.47	0.79
1:A:166:ILE:HG13	1:A:167:PRO:HD3	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	A	3630/4156 (87%)	3335 (92%)	292 (8%)	3 (0%)	48	81
2	B	11/192 (6%)	11 (100%)	0	0	100	100
All	All	3641/4348 (84%)	3346 (92%)	292 (8%)	3 (0%)	49	81

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	102	PRO
1	A	2787	HIS
1	A	101	ALA

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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	3168/3671 (86%)	3168 (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 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2795	GLN
1	A	3093	GLN
1	A	2841	ASN
1	A	3177	ASN
1	A	1098	GLN

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 ⓘ

There are no ligands in this entry.

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
1	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	4128:MET	C	5009:UNK	N	96.24
1	A	5016:UNK	C	6004:UNK	N	50.57

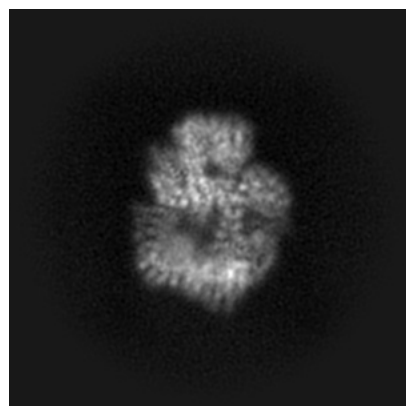
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11215. These allow visual inspection of the internal detail of the map and identification of artifacts.

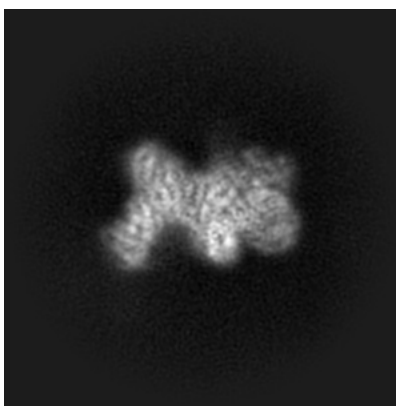
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

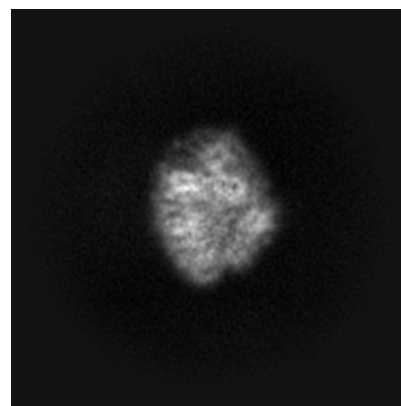
6.1.1 Primary map



X

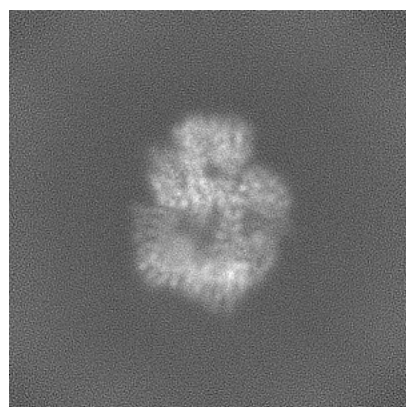


Y

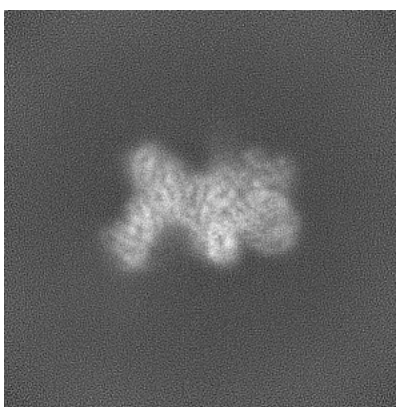


Z

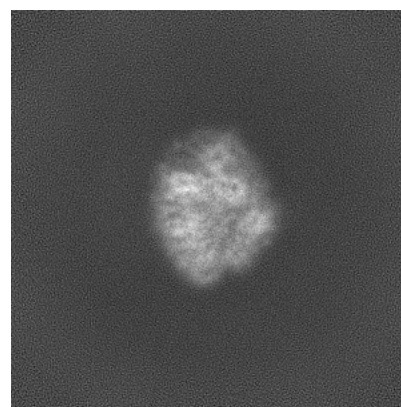
6.1.2 Raw map



X



Y

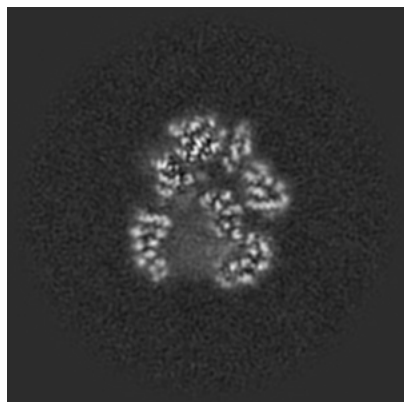


Z

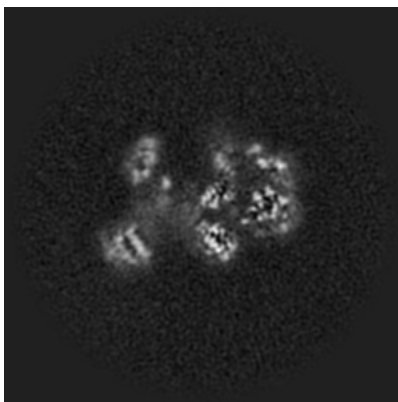
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

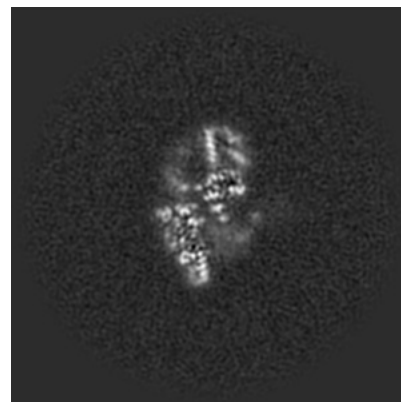
6.2.1 Primary map



X Index: 160

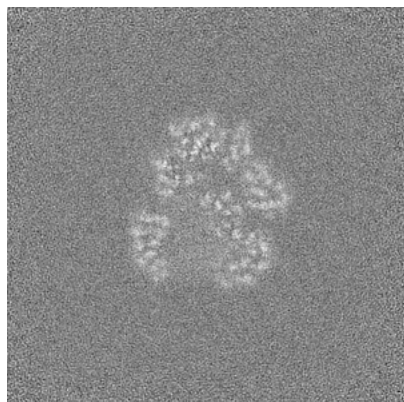


Y Index: 160



Z Index: 160

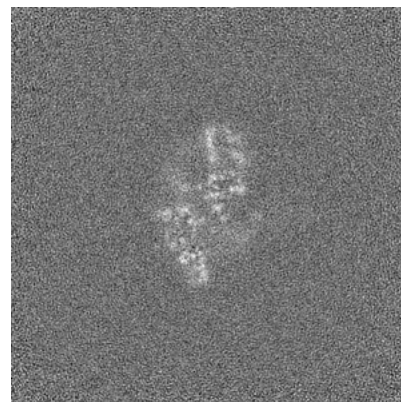
6.2.2 Raw map



X Index: 160



Y Index: 160

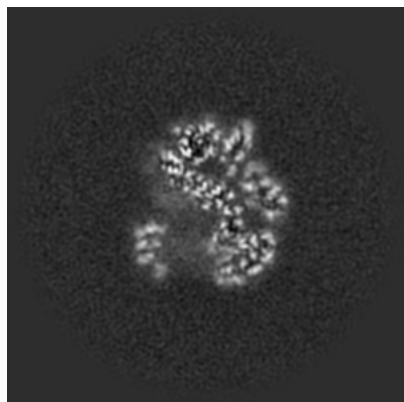


Z Index: 160

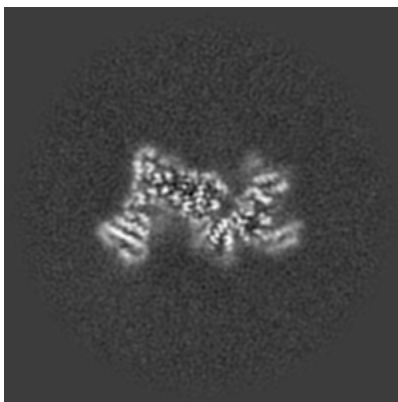
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

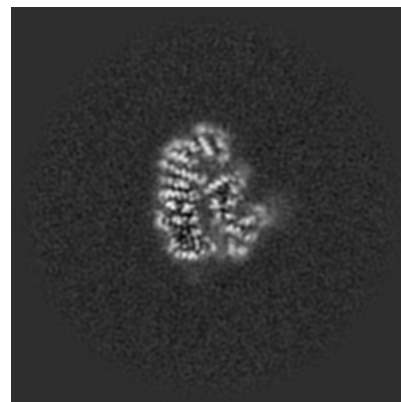
6.3.1 Primary map



X Index: 165

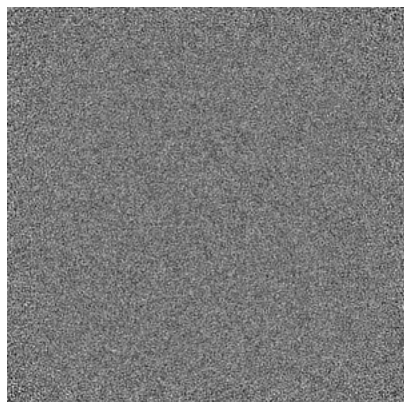


Y Index: 176

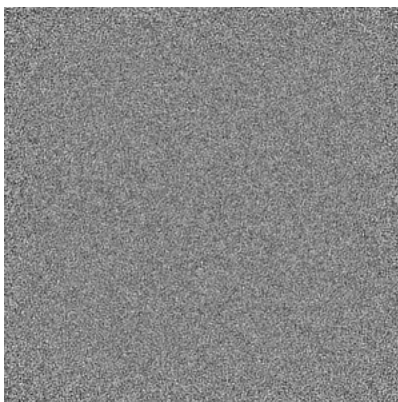


Z Index: 169

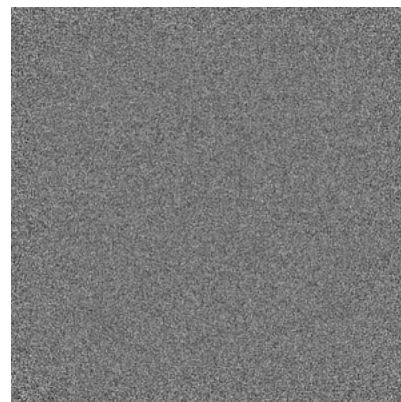
6.3.2 Raw map



X Index: 0



Y Index: 0

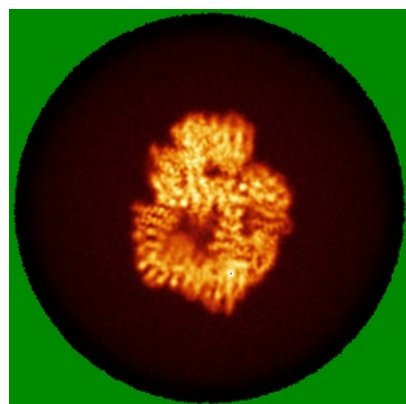


Z Index: 0

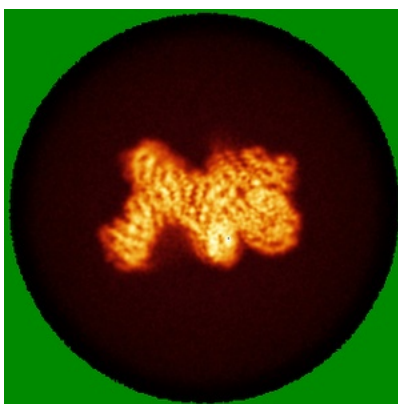
The images above show the largest variance slices of the map in three orthogonal directions.

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

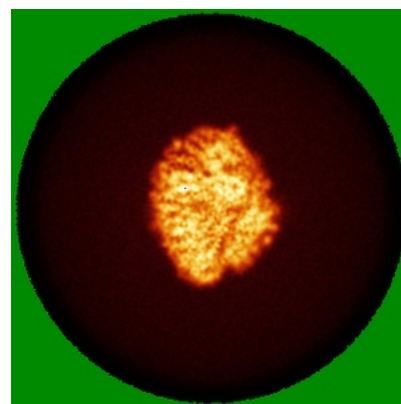
6.4.1 Primary map



X

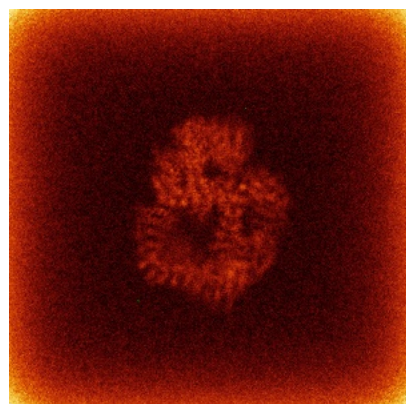


Y

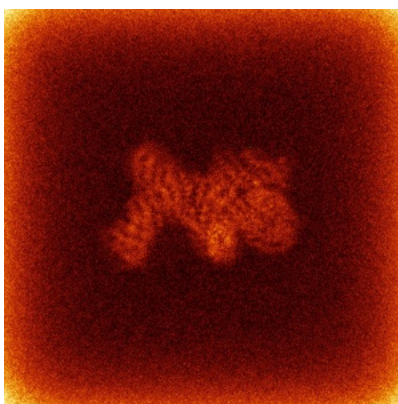


Z

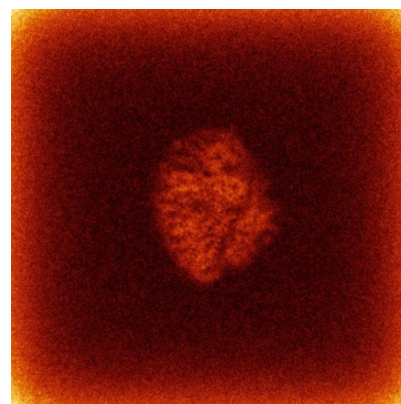
6.4.2 Raw map



X



Y

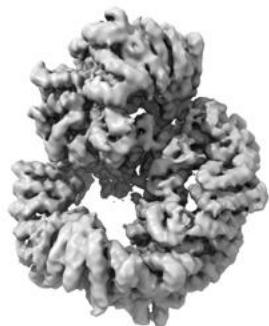


Z

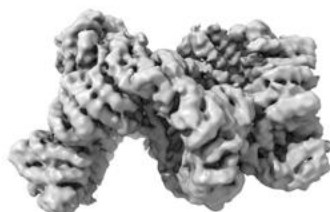
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



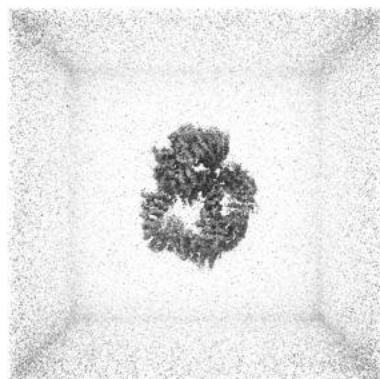
Y



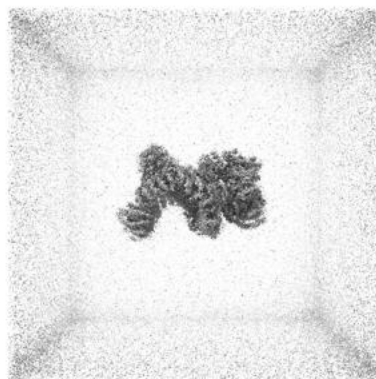
Z

The images above show the 3D surface view of the map at the recommended contour level 0.125. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

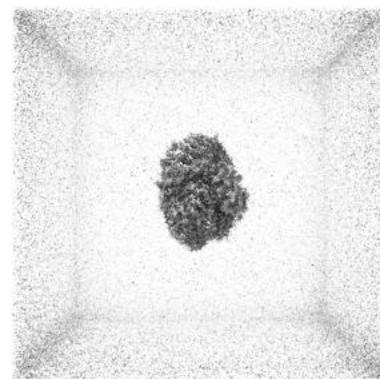
6.5.2 Raw map



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.

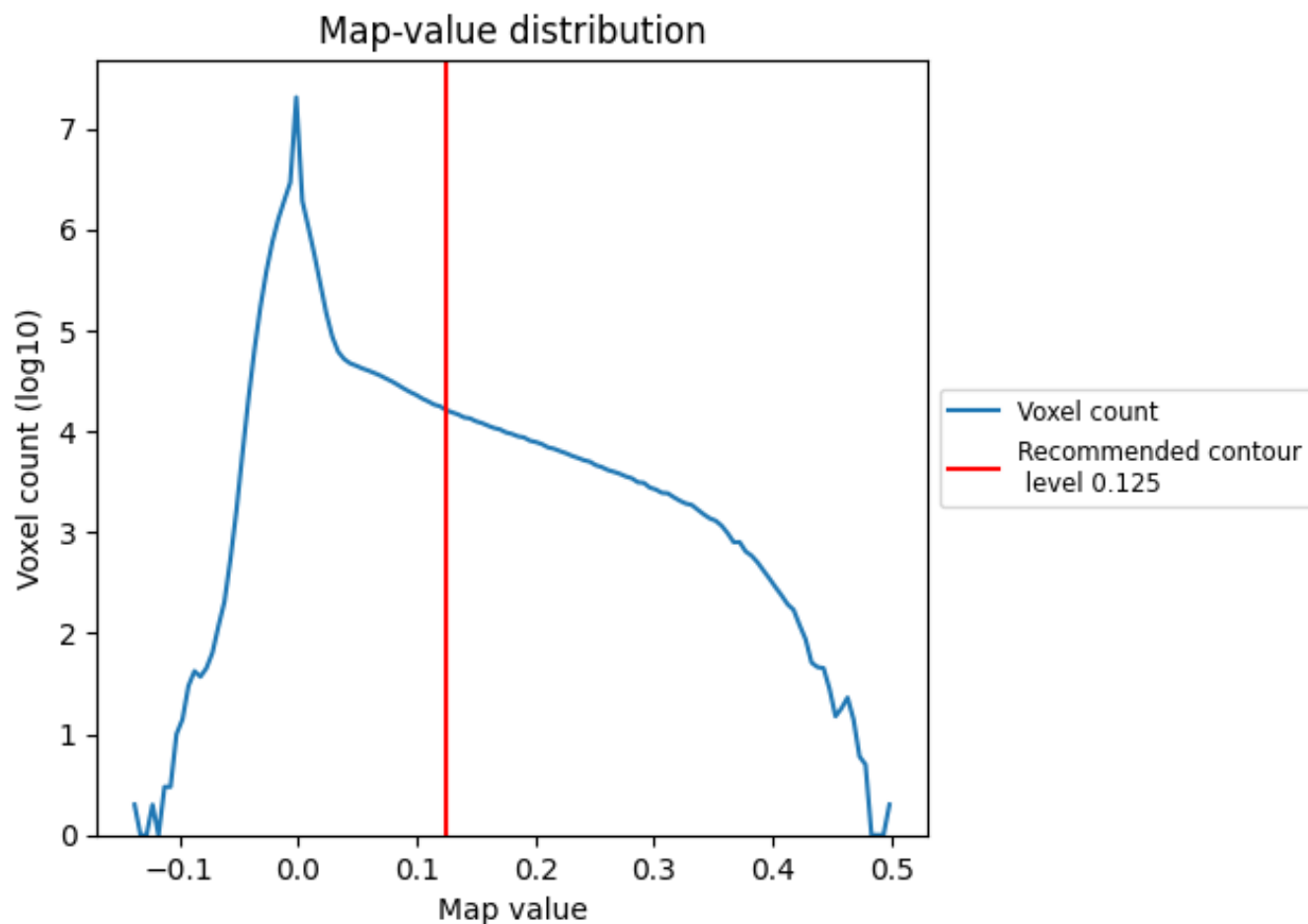
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

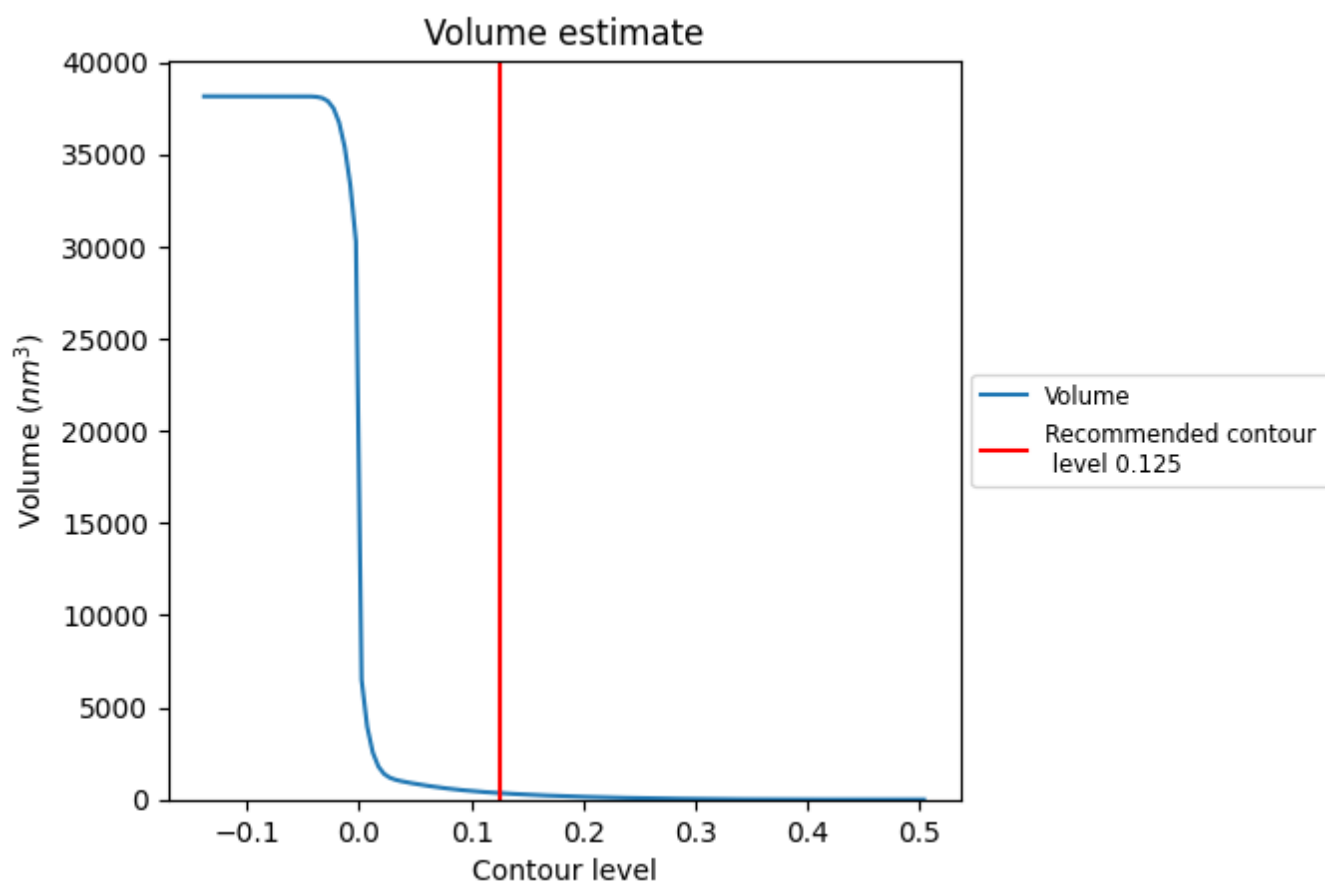
This section contains the results of statistical analysis of the map.

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.

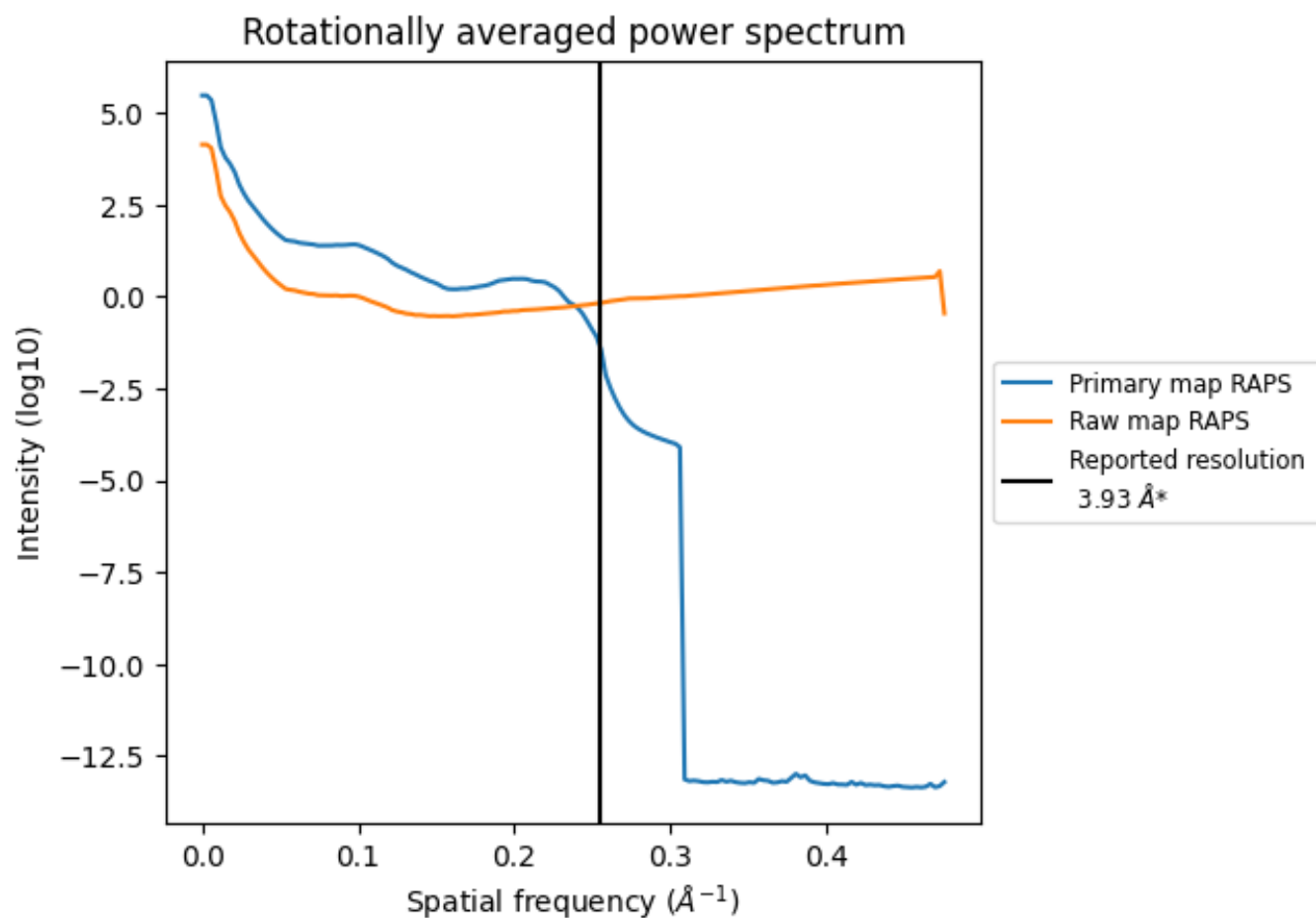
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 352 nm³; this corresponds to an approximate mass of 318 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 ⓘ

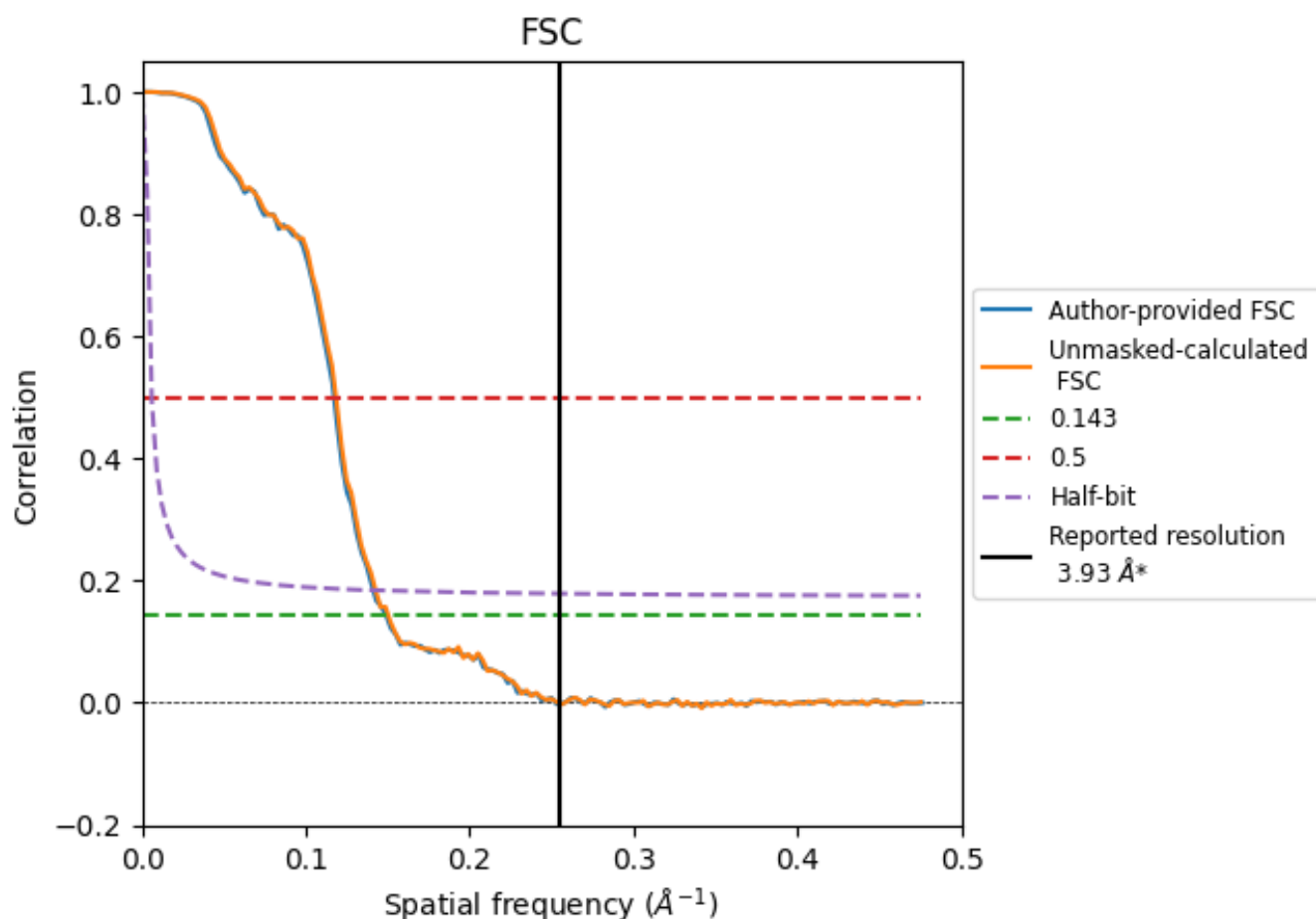


*Reported resolution corresponds to spatial frequency of 0.254 Å⁻¹

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 $0.254 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.93	-	-
Author-provided FSC curve	6.72	8.54	7.09
Unmasked-calculated*	6.66	8.45	7.02

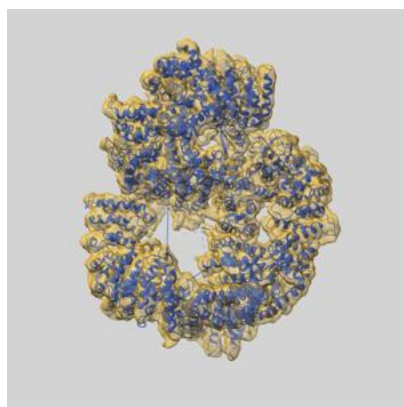
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 6.72 differs from the reported value 3.93 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.66 differs from the reported value 3.93 by more than 10 %

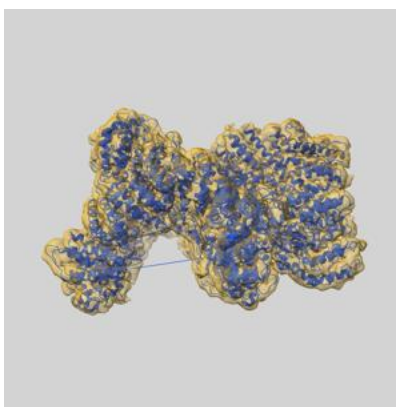
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11215 and PDB model 6ZH6. Per-residue inclusion information can be found in section [3](#) on page [4](#).

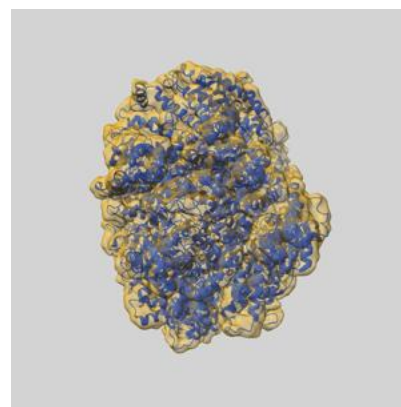
9.1 Map-model overlay [i](#)



X



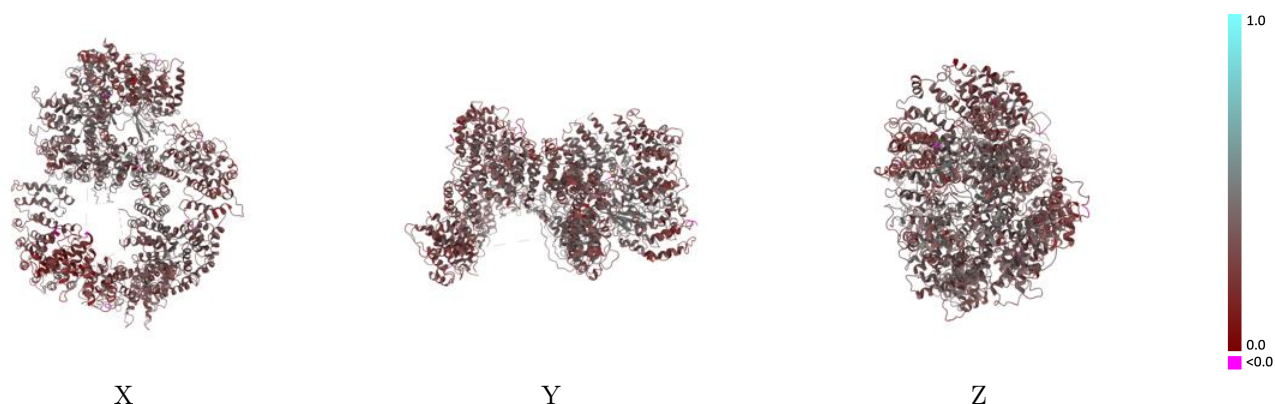
Y



Z

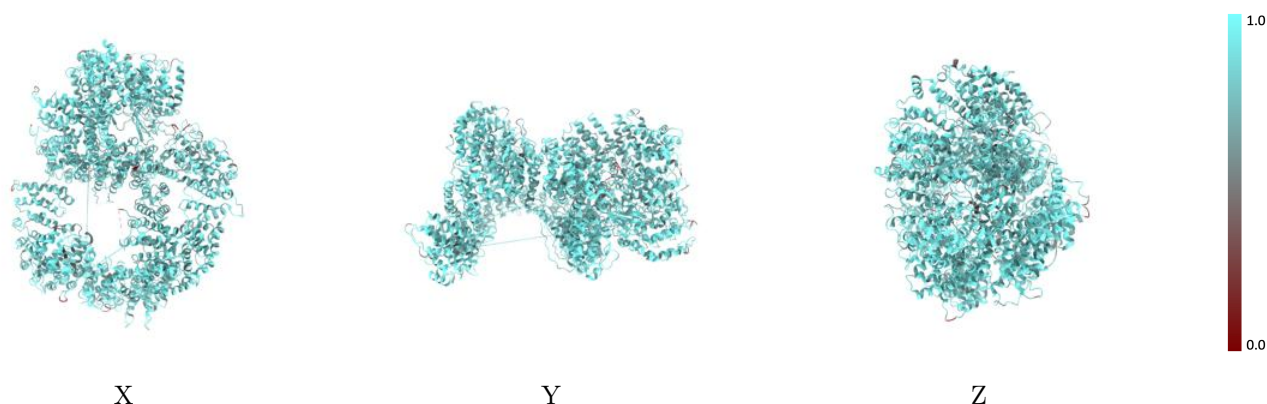
The images above show the 3D surface view of the map at the recommended contour level 0.125 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



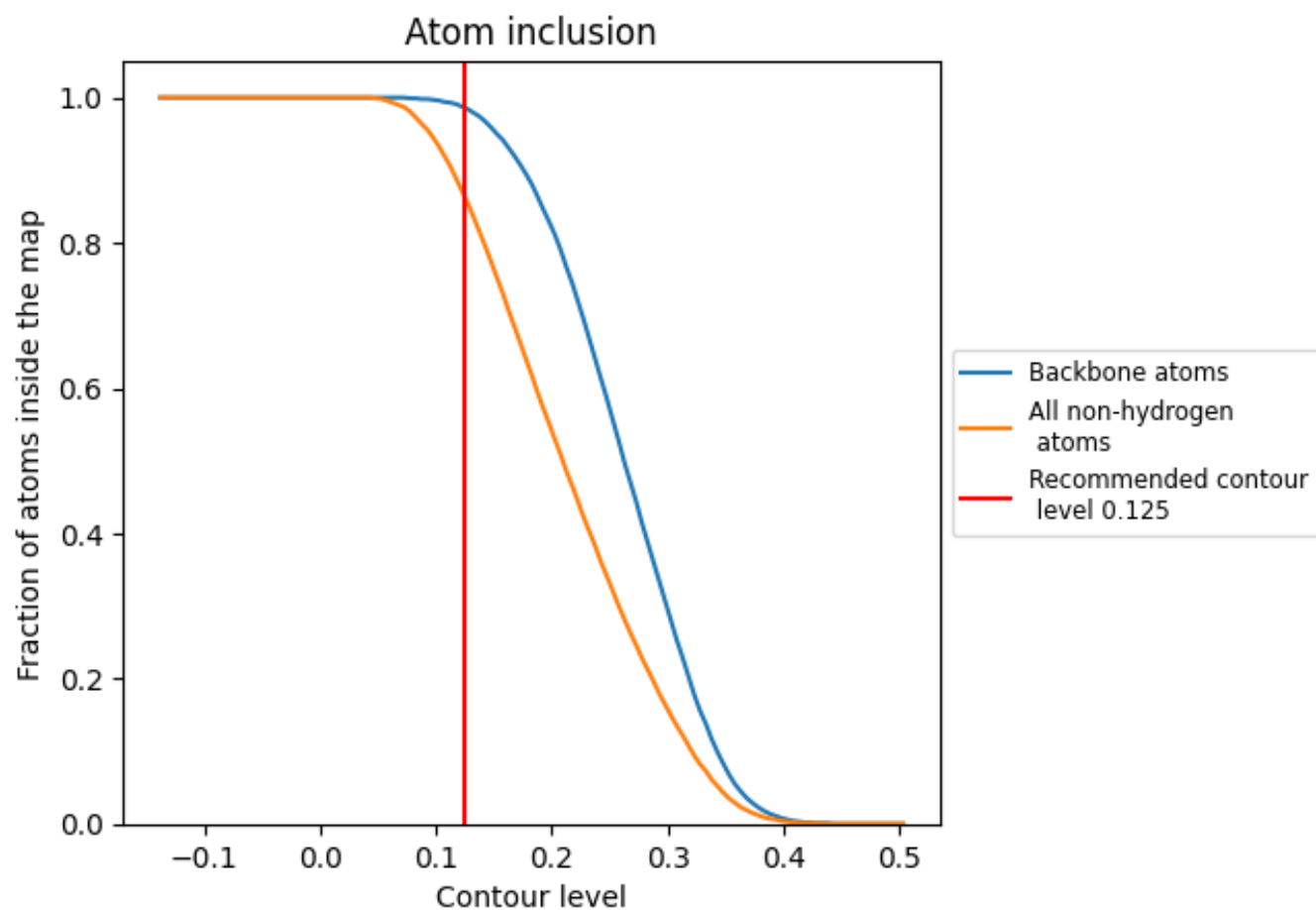
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.125).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 86% 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 (0.125) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8620	0.3350
A	0.8620	0.3350
B	0.9210	0.3380

