



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 12:35 AM UTC

PDB ID : 6ZH2 / pdb_00006zh2
EMDB ID : EMD-11211
Title : Cryo-EM structure of DNA-PKcs (State 1)
Authors : Chaplin, A.K.; Hardwick, S.W.; Chirgadze, D.Y.; Blundell, T.L.
Deposited on : 2020-06-20
Resolution : 3.92 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

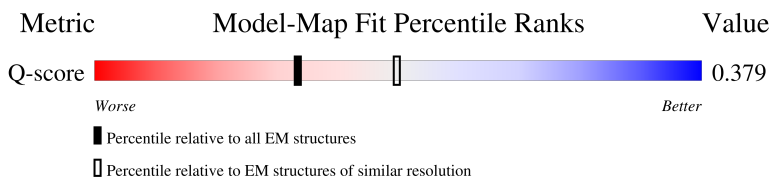
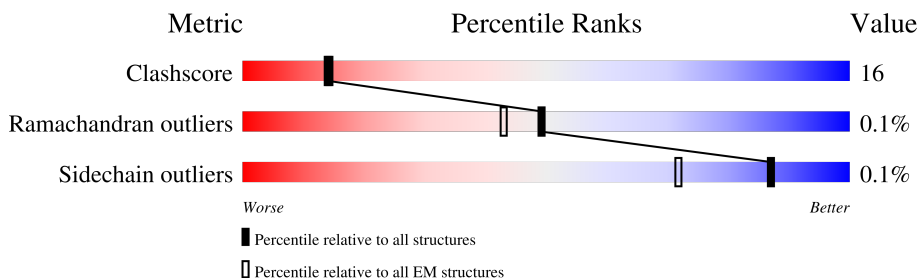
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.92 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	7862 (3.42 - 4.42)

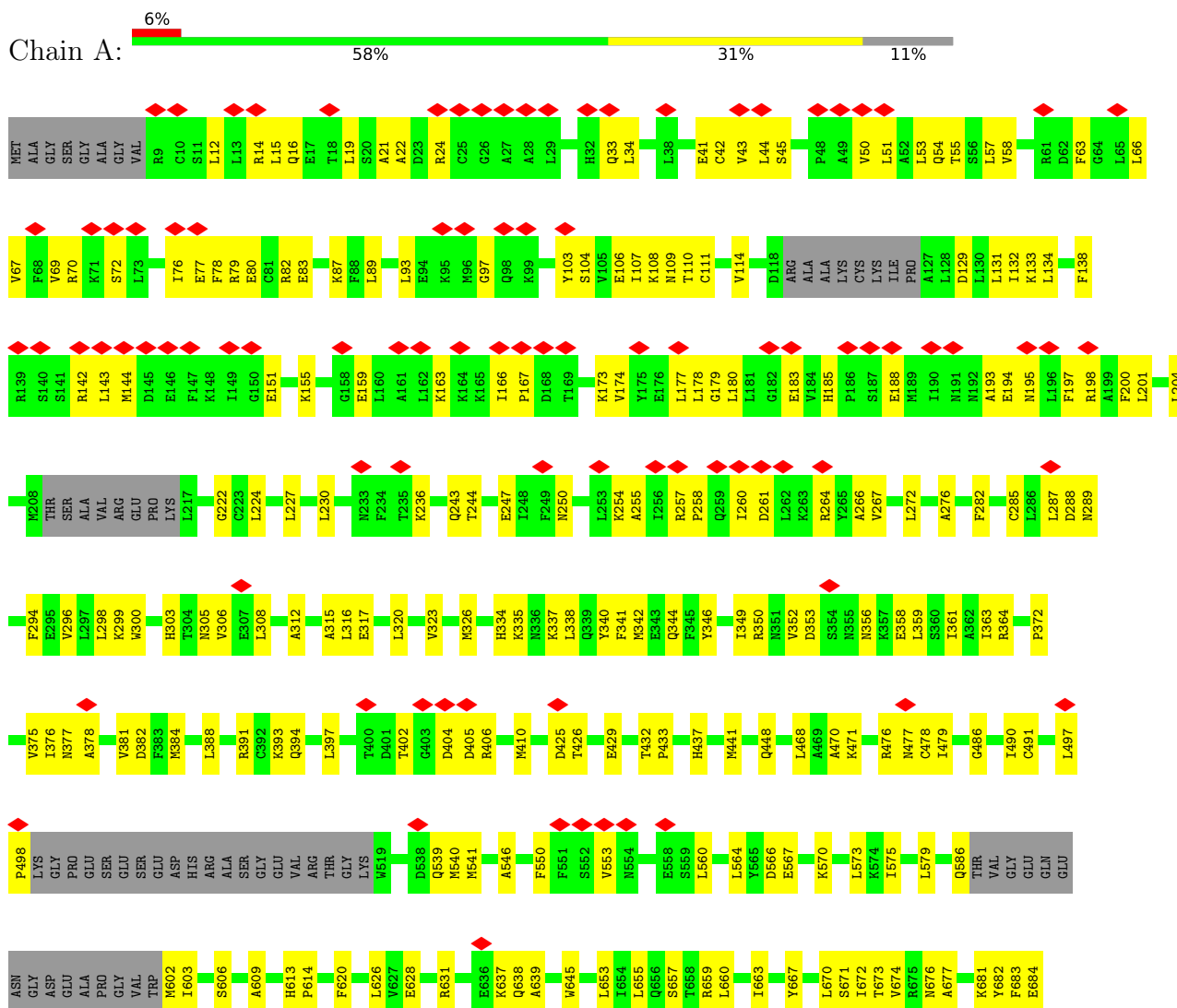
The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment 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	

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: DNA-dependent protein kinase catalytic subunit,DNA-dependent protein kinase catalytic subunit,DNA-dependent protein kinase catalytic subunit,DNA-dependent protein kinase catalytic subunit,DNA-dependent protein kinase catalytic subunit,DNA-dependent protein kinase catalytic subunit,DNA-PKcs



K1852	S1853	R1854	F1855	T1856	K1857	L1858	M1859	E1860	S1861	F1862	T1763	D1764	T1765	Q1766	T1767	E1768	V1769	C1770	V1771	L1772	V1773	T1774	E1775	F1776	Q1777	F1778	R1779	R1780	I1781	A1782	R1783	R1784	R1785	A1786	R1787	Q1788	T1789	V1790	C1791	V1792	T1793	Q1794	L1795	V1801	F1805	D1809	P1810	S1813	E1814	E1815	I1816	V1819	M1880	R1883	L1884	F1885	D1886	S1887	V1888	R1889	H1890	A1891	K1892	E1893	S1894	K1895	V1899	F1900	H1901	C1904	I1905	T1906	G1908	N1909	E1910	L1911	T1912	K1913	T1914	L1915	K1917
Q1770	Q1771	H1772	V1773	M1774	E1775	F1776	Q1777	F1778	R1779	R1780	I1781	A1782	R1783	R1784	R1785	A1786	R1787	Q1788	T1789	V1790	C1791	V1792	T1793	Q1794	L1795	V1801	F1805	D1809	P1810	S1813	E1814	E1815	I1816	V1819	M1880	R1883	L1884	F1885	D1886	S1887	V1888	R1889	H1890	A1891	K1892	E1893	S1894	K1895	V1899	F1900	H1901	C1904	I1905	T1906	G1908	N1909	E1910	L1911	T1912	K1913	T1914	L1915	K1917																		
S1664	H1665	G1666	S1667	F1668	P1669	V1670	F1671	S1672	D1685	G1690	Q1691	A1692	V1693	T1694	L1695	L1696	T1700	T1703	G1704	L1707	E1708	E1709	L1710	R1711	V1712	V1713	E1714	E1715	I1718	P1723	M1724	E1728	G1732	R1735	F1736	N1737	M1743	F1746	L1747	S1753	Q1754	M1762	L1766																																						
V1550	E1557	L1572	L1575	A1578	L1582	S1585	S1586	V1587	N1589	M1592	L1601	E1607	R1608	M1609	Q1611	Q1614	K1617	L1623	K1627	K1628	C1629	V1632	K1635	D1636	S1637	P1638	L1639	E1640	T1641	K1642	M1643	L1646	K1651	S1657	S1658	V1659	S1660	T1663																																											
S1470	Q1471	T1473	D1474	L1475	H1476	H1477	S1478	V1479	E1482	S1485	L1486	V1487	Y1488	I1491	A1492	G1493	D1495	E1496	Q1497	Q1498	C1499	S1502	D1504	L1505	S1506	C1507	K1508	Q1509	L1510	A1511	S1512	G1513	L1514	L1515	E1516	G1523	V1529	S1530	L1531	L1532	A1541	SER	LEU	GLY	SER	SER	GLN	S1549																																	
S1381	I1382	M1385	I1386	G1387	D1388	V1389	Q1390	V1391	M1392	L1395	P1396	D1397	V1398	C1399	N1401	L1402	M1403	K1404	K1407	P1410	Y1411	K1412	D1413	I1414	L1415	E1416	T1417	H1418	L1419	E1420	E1421	K1422	S1427	E1430	Y1437	G1438	P1439	Q1442	V1443	D1444	R1445	S1446	R1447	A1448	A1449	V1452	L1463																																		
M1303	H1304	D1305	I1306	I1307	A1308	E1310	K1311	C1312	GLY	T1315	G1316	A1317	A1318	G1319	M1320	R1321	T1322	S1323	P1324	Q1325	E1326	G1327	E1328	K1334	V1338	V1339	R1340	I1341	M1342	L1348	T1351	S1352	P1353	M1356	K1357	L1358	L1359	K1361	D1362	H1367	L1368	M1369	R1370	V1371	L1372	V1373	E1378	A1380																																	
K1213	S1218	F1219	L1220	I1221	T1222	T1223	F1224	E1225	Q1231	P1232	S1233	G1234	I1235	L1236	A1237	Q1238	Y1243	L1244	R1245	G1246	F1248	S1249	L1250	Q1251	A1252	T1253	L1259	L1260	L1261	L1264	Y1267	V1281	L1282	G1283	T1284	E1285	Q1287	S1288	S1289	L1291	K1292	F1297	L1298	E1299	S1300	T1301	A1302																																		
R1075	L1080	F1082	T1085	A1087	R1087	R1090	E1091	V1100	F1101	E1102	V1105	L1106	Y1107	M1108	A1112	D1117	E1139	D1005	D1006	T1006	V1007	L1010	I1013	I1017	V1018	D1019	P1020	I1021	D1022	R1026	R1031	W1039	K1042	Y1064	A1067	S1203	P1204	N1205	L1206	W1207	K1209																																								
GLN	G954	A955	P956	P957	K958	Y959	P967	V968	L972	Q978	R981	Y984	L991	F995	K999	K1000	Q1004	D1005	T1006	V1007	L1010	I1013	I1017	V1018	D1019	P1020	I1021	D1022	R1026	R1031	W1039	K1042	Y1064	A1067	S1203	P1204	N1205	L1206	W1207	K1209																																									
R852	I853	V854	L859	G860	K868	N869	L870	L871	T872	S875	S876	D877	E878	M879	M880	K881	S882	Y883	W886	D887	R888	R891	F894	R899	E900	M901	P903	V904	I905	D908	L911	T915	D923	R924	Q925	L933	S936	M937	M948	PRO	GLY	GLY	E849																																						
D781	R782	Y789	K790	D791	I792	Y799	K801	T802	S803	A804	L805	SER	ASP	GLU	THR	LYS	ASN	ASN	TRP	GLU	VAL	SER	ALA	ALA	GLN	LYS	GLY	PHE	ASN	L1019	V904	VAL	LEU	LYS	LYS	THR	ASN	LEU	SER	SER	ASN	GLU	ALA	I1E	S847	L848	E849																																		
P688	LYS	SER	LEU	LYS	HIS	SER	PRO	GLU	D697	K700	Y701	V708	K709	E713	V714	M718	Y721	L725	L726	L730	F732	L733	L736	P737	I740	R746	A747	Y748	A751	L752	Q753	G759	Y762	T763	P764	A766	E767	L770	N771	E774																																									

L1918	L1919	L1920	L1928	L1929	L1930	L1931	L1932	L1933	L1934	L1935	L1936	L1937	L1938	L1939	Y1945	L1949	L1950	L1951	Y1955	L1976	L1977	L1978	L1979	L1980	L1981	L1985	ARG	TYR	ASN	TYR	PRO	PRO	VAL	GLU	VAL	GLU	VAL	ASP	PRO	MET	ARG	GLU	LYS	LYS	THR	ILE	ARG	GLU	ILE	ARG	GLU	LYS	ALA	ARG
L2146	A2147	K2148	L2149	L2150	L2151	L2152	L2153	L2158	L2159	Y2160	H2163	L2168	A2172	A2173	S2174	E2175	G2178	H2183	Y2184	M2185	Y2186	L2187	E2188	L2189	V2190	L2193	L2194	S2195	W2196	T2197	K2207	V2210	N2213	R2214	L2215	L2216	N2217	F2218	M2220	K2221	H2222	V2223	K2227	V2230	C2244									
W2245	K2246	D2247	C2248	L2249	S2250	L2251	R2254	L2255	L2256	F2257	E2258	K2259	F2260	S2261	D2269	N2270	G2273	T2274	L2277	M2281	A2282	L2283	D2284	L2285	F2286	T2287	T2288	D2289	P2290	Q2291	C2292	G2293	T2294	Q2295	S2296	E2298	F2299	F2300	Q2301	A2302	L2303	Y2312	K2313	E2314	V2315	A2317	A2318	A2319	A2320	E2321	V2322			
L2323	L2326	W2330	L2331	E2332	R2333	K2334	N2335	E2338	E2339	S2340	L2341	C2342	E2343	L2344	V2345	L2349	H2352	Q2353	M2356	E2357	D2358	K2359	N2365	T2368	K2369	A2375	D2376	R2377	F2378	M2379	N2380	A2381	V2382	F2383	F2384	K2388	F2389	H2390	K2394	C2397	L2398	E2399	V2400	V2401	V2405									
T2409	E2410	L2411	Y2412	Q2413	Q2414	L2415	K2418	D2419	F2420	V2421	V2423	M2424	H2426	R2431	Q2432	L2433	V2434	C2435	I2438	L2439	Y2440	K2441	M2442	M2443	P2444	K2445	L2446	K2447	P2448	V2449	E2450	L2451	L2454	L2455	N2456	P2457	V2458	F2461	V2462	S2466	T2467	T2468	E2471	Q2472	M2473	V2474	N2475	L2476	L2477	M2478				
Y2479	L2480	H2481	D2482	R2485	D2486	F2487	E2488	S2489	D2490	T2491	D2492	N2493	D2494	S2495	Q2496	F2499	K2500	L2501	V2505	Q2508	L2511	L2517	Q2518	L2519	R2522	N2523	T2529	R2530	R2538	L2539	L2540	K2541	L2542	N2543	K2549	L2550	F2554	L2555	A2558	F2561	L2562	L2563	S2569	Y2572										
P2573	R2574	P2575	M2576	F2577	F2586	Y2589	D2592	S2593	D2594	W2595	P2596	PHE	ARG	GLY	THR	V2601	M2605	F2606	V2607	GLU	THR	ALA	GLN	GLY	LEU	GLN	THR	ARG	THR	GLU	GLY	LEU	ARG	ALA	VAL	ALA	GLY	ILE	ARG	ALA	THR	GLN	GLN	GLN	HIS	ASP								
PHE	THR	LEU	THR	GLN	THR	ALA	ASP	GLY	ARG	SER	SER	PHE	ASP	TRP	GLY	THR	SER	ASP	THR	ASP	PRO	LEU	VAL	ASP	HIS	ARG	THR	ALA	HIS	LYS	ARG	ALA	ARG	GLY	PRO	ALA	LEU	LYS	SER	VAL	GLY	ALA	PRO	PHE	GLY	LYS	LYS							
ARG	LEU	GLY	PRO	GLY	ASP	GLU	VAL	ASN	ASP	LYS	LYS	GLY	ALA	ALA	GLY	THR	ARG	THR	ASP	LEU	ARG	LEU	ARG	GLN	LEU	LEU	LEU	LEU	PHE	ALA	LEU	HIS	TYR	ALA	ARG	ARG	LYS	ALA	GLY	VAL	ILE	LYS	SER	GLU	LEU	LYS	MET							
LYS	GLN	ASP	ALA	Q2768	R2773	Y2774	Y2775	R2776	H2777	D2782	I2783	Q2784	L2785	K2786	H2787	S2788	S2789	T2792	P2793	L2794	Q2795	A2796	S2810	S2811	L2812	F2813	M2820	D2821	E2828	K2829	T2832	T2833	Q2834	K2835	L2836	L2837	Q2838	D2839	R2842	F2843	L2844	C2857	I2861	L2869	A2875	Q2886								
I2890	R2891	L2892	L2893	E2894	E2895	A2896	L2897	L2898	R2899	P2902	ALA	GLU	LEU	PRO	ALA	LYS	ARG	VAL	ARG	GLY	LYS	ALA	ARG	L2916	P2917	L2918	K3067	D2919	V2920	L2929	I2933	R2940	F2943	I2947	L2957	R2962	S2963	D2964	Y2965	N2977	K2978	Q2979	L3005	A3006	F3007	W3008	L3011							
S3021	E3022	R3023	D3026	L3027	R3028	V3031	F3035	S3047	K3048	L3049	K3050	L3051	E3056	K3057	D3058	Q3059	S3060	L3061	L3062	T3065	D3066	K3067	A3068	K3069	G3070	L3072	L3073	Q3074	L3078	E3085	L3089	Y3090	Q3093	D3094	D3095	V3096	D3097	R3098	K3099	I3100	I3103	I3107	Q3108	Y3114										

E4035	R3889	L3666	P3581	S3488	PRO	N3310	ASP	D3118
K4036	M3890	L3667	E3582	S3489	SER	S3314	ARG	V3119
K4050	A3896	K3668	L3583	W3493	TRP	Y3315	MET	L3120
A4054	L3900	M3670	W3588	I3496	GLU	L3316	VAL	L3121
M4055	L3910	K3671	W3589	S3497	CYS	N3319	GLN	R3125
P4056	L3913	M3672	V3592	W3498	GLY	I3320	GLU	L3126
L4059	L3916	K3673	R3593	I3499	P3405	L3321	GLN	A3134
L4064	W3916	S3674	E3595	S3500	A3406	A3322	GLU	L3135
L4065	A3931	K3675	L3596	H3501	V3409	F3323	GLU	T3136
F4074	M3932	P3676	L3597	S3502	I3410	R3324	GLU	E3137
R4075	E3933	P3677	K3598	M3503	E3411	R3325	GLU	I3138
D4076	L3902	G3678	T3599	A3504	A3412	I3328	GLU	R3139
Y4077	L3806	M3679	P3600	D3507	Y3413	I3328	GLU	E3140
G4083	L3807	E3680	V3601	K3508	L3416	T3332	GLU	G3148
S4084	E3807	C3683	N3602	A3511	R3425	T3333	GLU	R3149
K4085	M3808	S3684	K3603	V3512	E3429	Y3334	GLU	N3150
D4086	T3809	P3685	K3604	V3513	N3430	R3335	GLU	V3155
H4087	T3809	W3686	N3605	V3514	ALA	A3346	GLU	K3158
N4088	T3809	M3687	T3606	Q3515	SER	C3347	GLU	W3164
I4089	T3819	F3694	K3607	I3521	VAL	L3348	GLU	P3169
M3959	M3820	L3695	K3608	T3522	ILE	A3349	GLU	K3176
R3965	E3838	R3696	Y3610	I3529	ASP	E3350	GLU	W3179
Q3966	Y3839	M3697	E3611	V3530	SER	I3351	GLU	I3182
A4091	E3838	E3698	R3612	V3531	ALA	L3354	GLU	I3183
Q4092	Y3839	L3699	K3613	P3532	GLU	E3355	GLU	R3186
E4100	K3845	E3700	A3616	I3535	L3439	R3356	GLU	L3190
Q4103	M3846	I3701	D3619	F3542	L3445	S3357	GLU	S3191
L4107	K3849	P3702	P3620	K3543	K3449	L3358	GLU	K3192
M4108	H3850	Q3704	K3621	T3544	M3450	I3359	GLU	L3197
D4109	D3851	D3706	A3622	T3545	K3455	L3360	GLU	THR
Q4110	Y3855	G3707	L3625	T3546	L3456	E3361	GLU	PRO
D4113	M3858	R3708	G3626	S3546	N3459	S3363	GLU	LEU
P4114	A3862	G3709	R3629	G3548	R3462	G3364	GLU	PRO
N4115	N3863	K3710	K3629	H3549	L3463	S3365	GLU	ASP
I4116	K3864	L3711	F3636	K3550	K3464	S3366	GLU	ASN
R4119	T3865	P3713	G3637	M3553	F3465	S3367	GLU	VAL
W4124	E3866	H3716	K3638	E3552	K3465	E3368	GLU	ASP
W4127	T3867	H3716	E3639	E3553	L3468	E3371	GLU	GLY
X5009	Y3868	I3719	F3640	D3563	I3472	R3380	GLU	ASP
X6017	R3874	D3723	H3643	Q3564	E3473	L3385	GLU	ASN
X6020	E3875	E3724	K3653	G3565	R3474	S3386	GLU	ASN
	P3879	R3733	M3654	I3568	Y3475	V3389	GLU	VAL
	A3880	K3733	K3655	F3571	E3478	A3392	GLU	ASP
	D3881	R3737	L3656	L3575	T3479	E3393	GLU	GLN
	L3882	E3747	S3657	L3578	L3480	A3394	GLU	ASP
	F3887	D3757	F3659	N3579	M3483	E3395	GLU	ASP
	Y3888	R3763	T3663	N3580	I3487	A3396	GLU	PRO
						GLN	GLU	SER
						PRO	GLU	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	38575	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 ($e^-/\text{\AA}^2$)	53.95	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.199	Depositor
Minimum map value	-0.071	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.055	Depositor
Map size (Å)	280.36002, 280.36002, 280.36002	wwPDB
Map dimensions	430, 430, 430	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.652, 0.652, 0.652	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	0.15	0/29777	0.37	1/40278 (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	1306	ILE	N-CA-C	-5.86	108.14	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	29313	0	29356	907	0
All	All	29313	0	29356	907	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 16.

The worst 5 of 907 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:3472:ILE:HA	1:A:3479:THR:HG21	1.22	1.15
1:A:3472:ILE:HG23	1:A:3479:THR:HB	1.38	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3472:ILE:HA	1:A:3479:THR:CG2	1.93	0.98
1:A:2085:MET:N	1:A:2184:TYR:HH	1.76	0.84
1:A:3475:TYR:HB3	1:A:3478:GLU:OE2	1.77	0.84

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	3640/4156 (88%)	3354 (92%)	284 (8%)	2 (0%)	48 81

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3480	LEU
1	A	2787	HIS

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	3203/3671 (87%)	3201 (100%)	2 (0%)	88 89

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2283	ASN
1	A	3478	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3162	ASN
1	A	3177	ASN
1	A	3850	HIS
1	A	1374	GLN
1	A	1367	HIS

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](#)

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	93.18
1	A	5016:UNK	C	6001:UNK	N	48.96

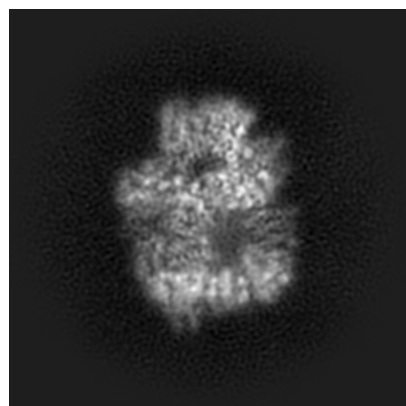
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11211. These allow visual inspection of the internal detail of the map and identification of artifacts.

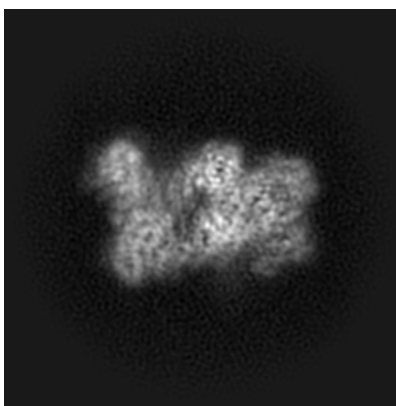
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

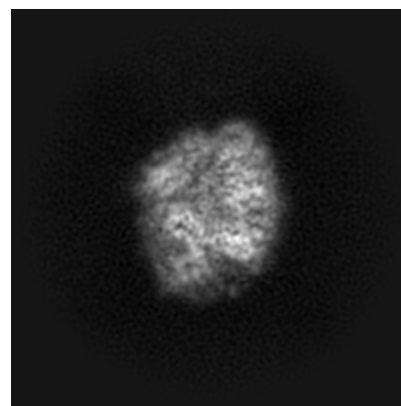
6.1.1 Primary map



X

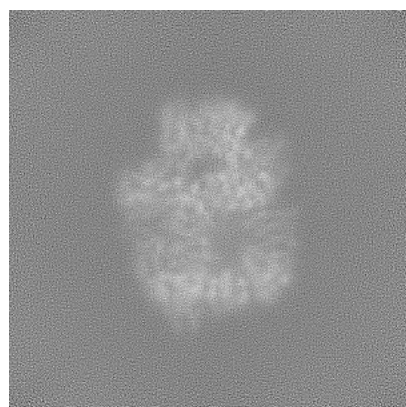


Y

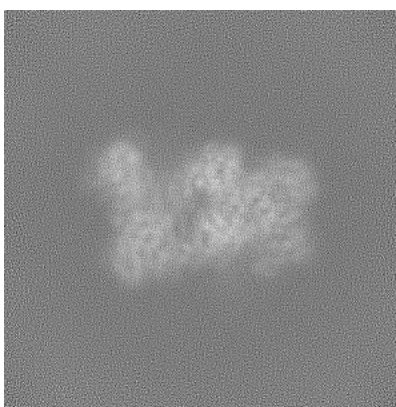


Z

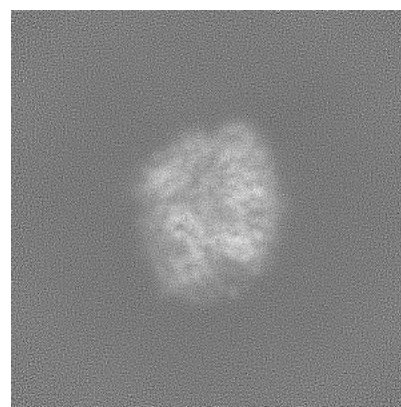
6.1.2 Raw map



X



Y

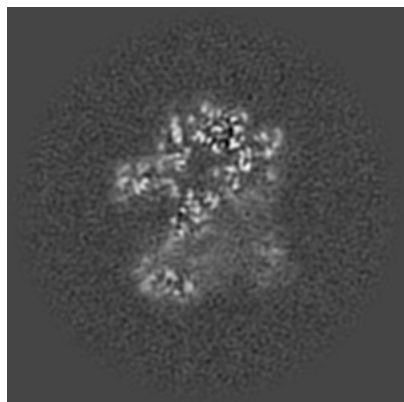


Z

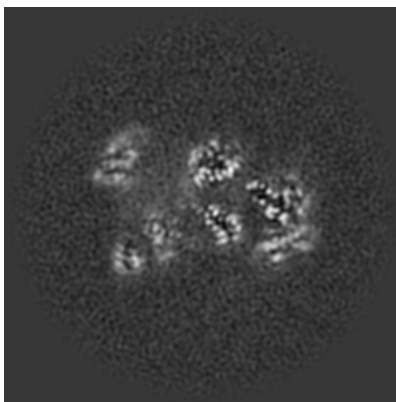
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

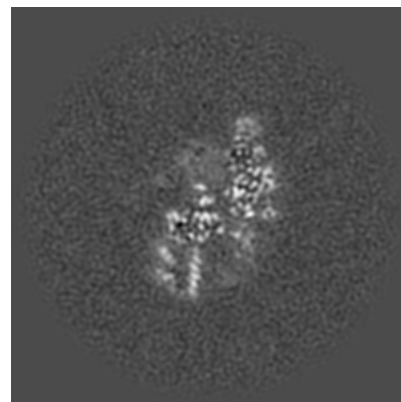
6.2.1 Primary map



X Index: 215

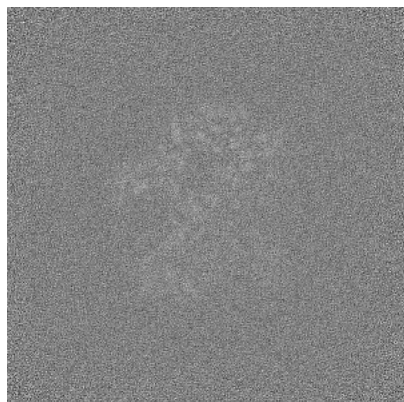


Y Index: 215

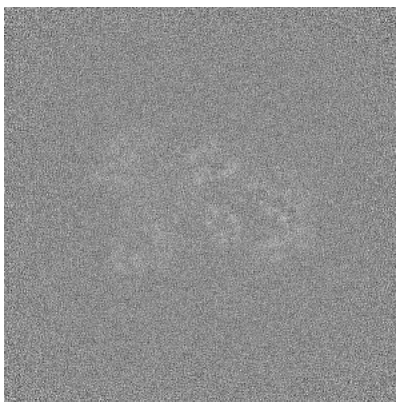


Z Index: 215

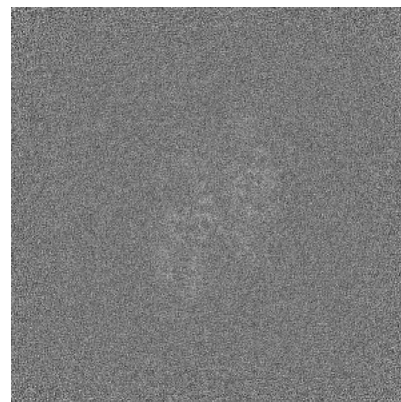
6.2.2 Raw map



X Index: 215



Y Index: 215

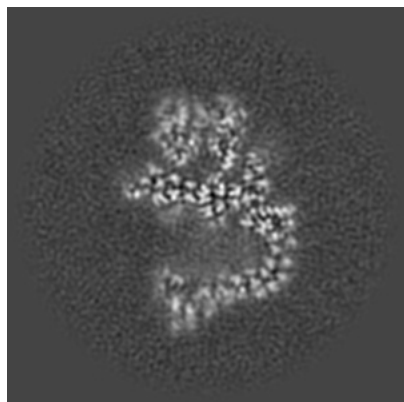


Z Index: 215

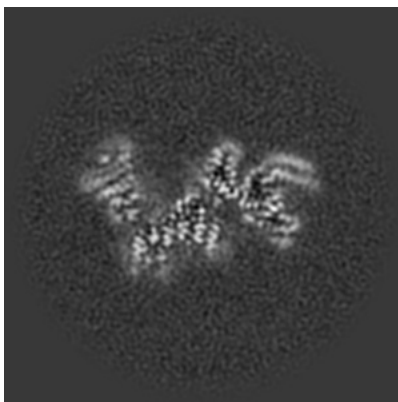
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

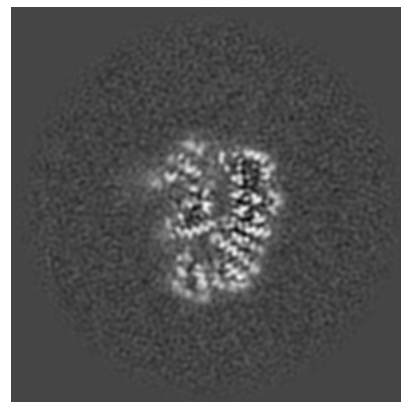
6.3.1 Primary map



X Index: 246

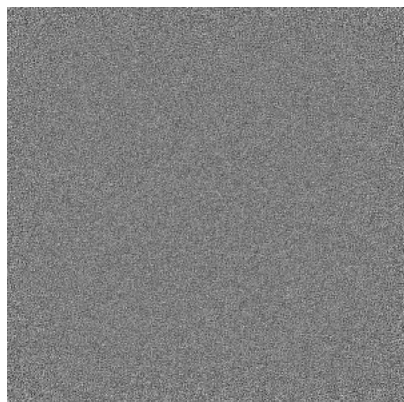


Y Index: 185

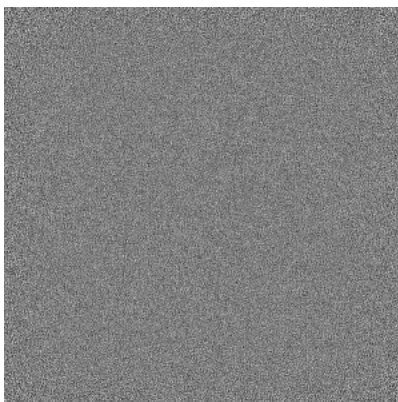


Z Index: 228

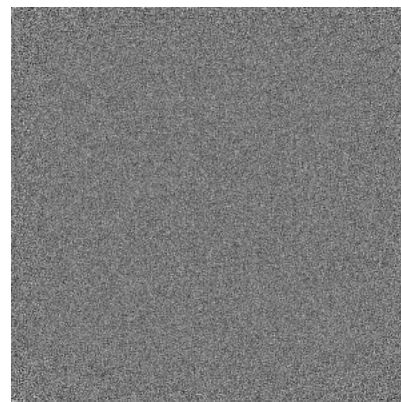
6.3.2 Raw map



X Index: 0



Y Index: 0

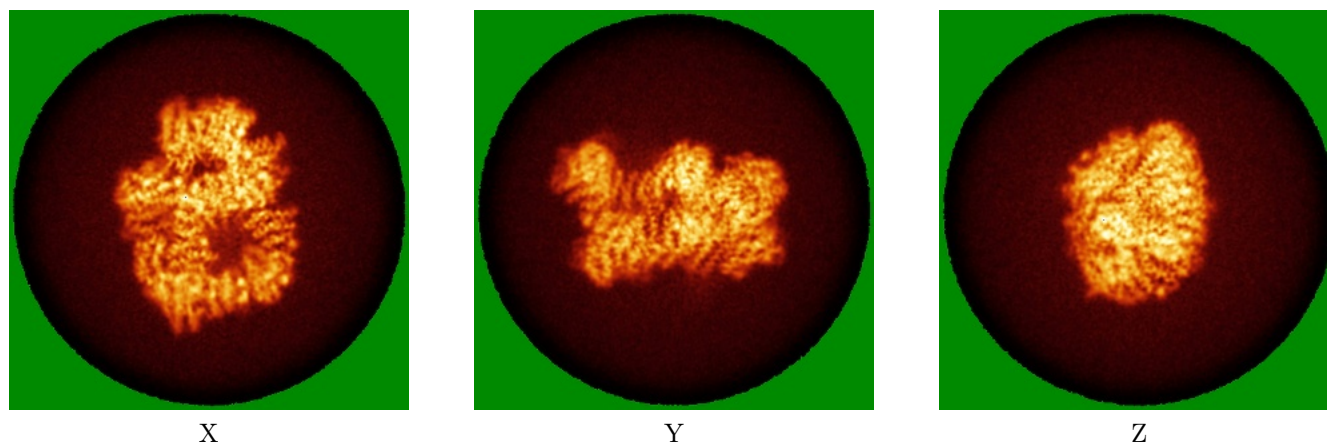


Z Index: 0

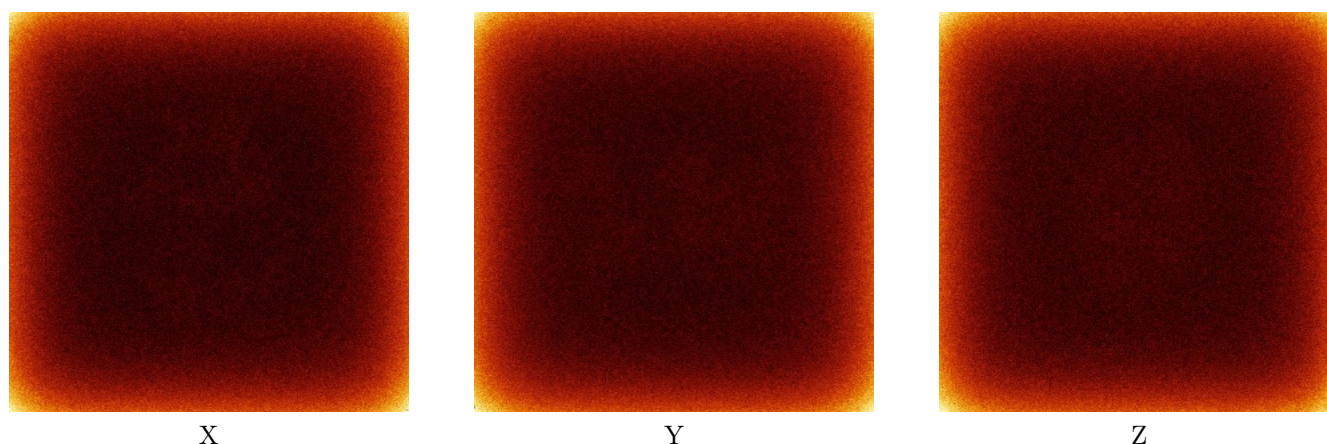
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

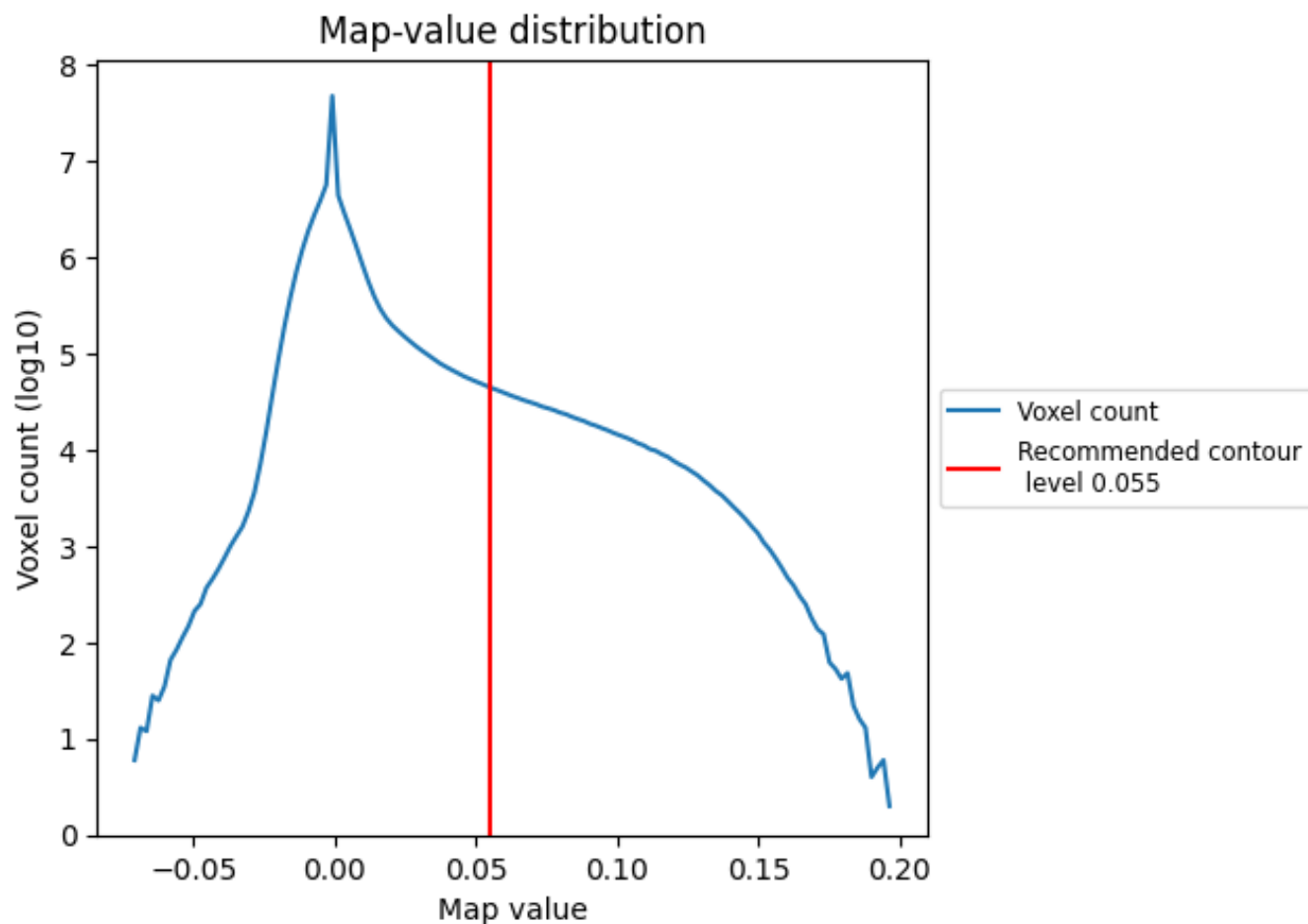
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

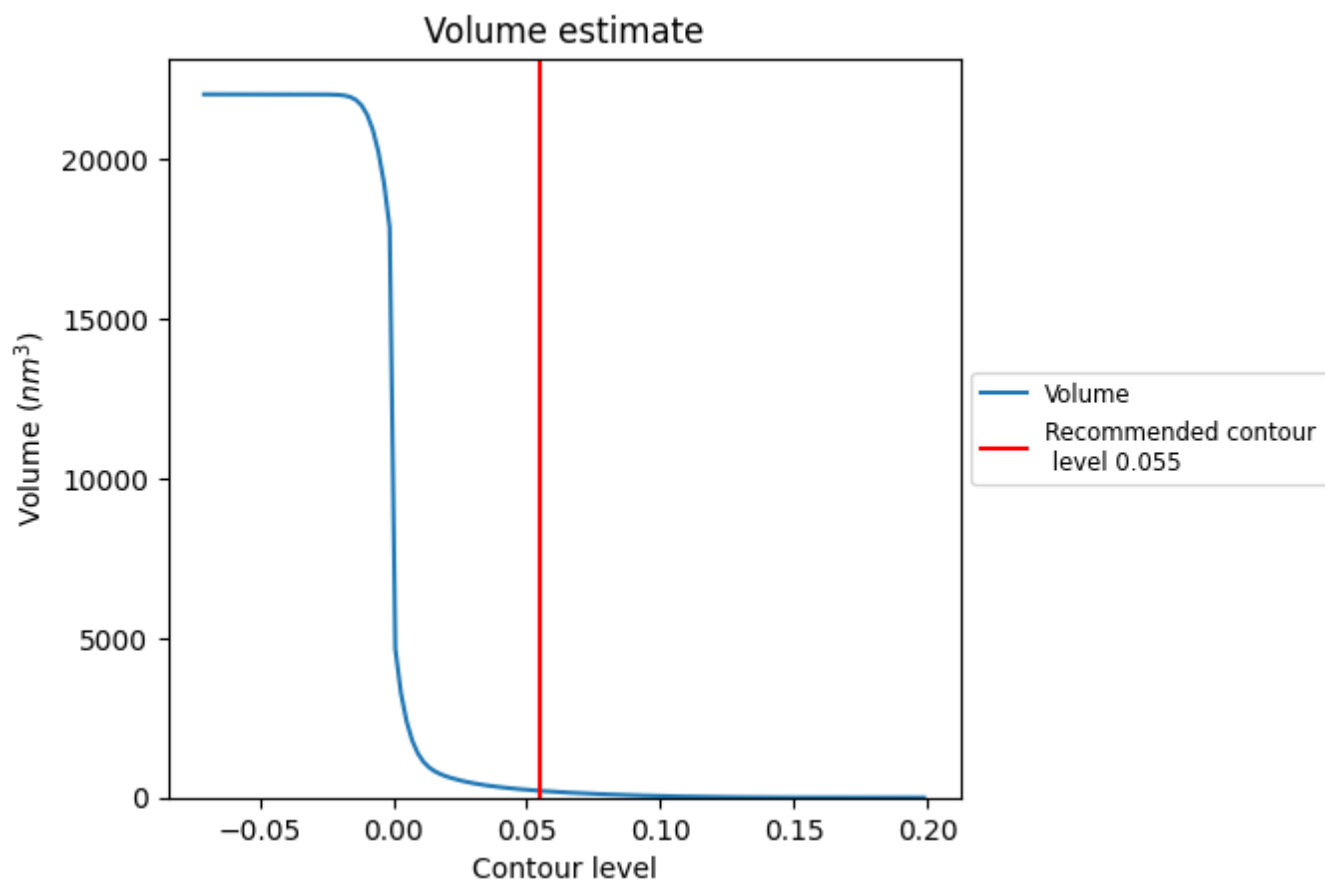
This section contains the results of statistical analysis of the map.

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.

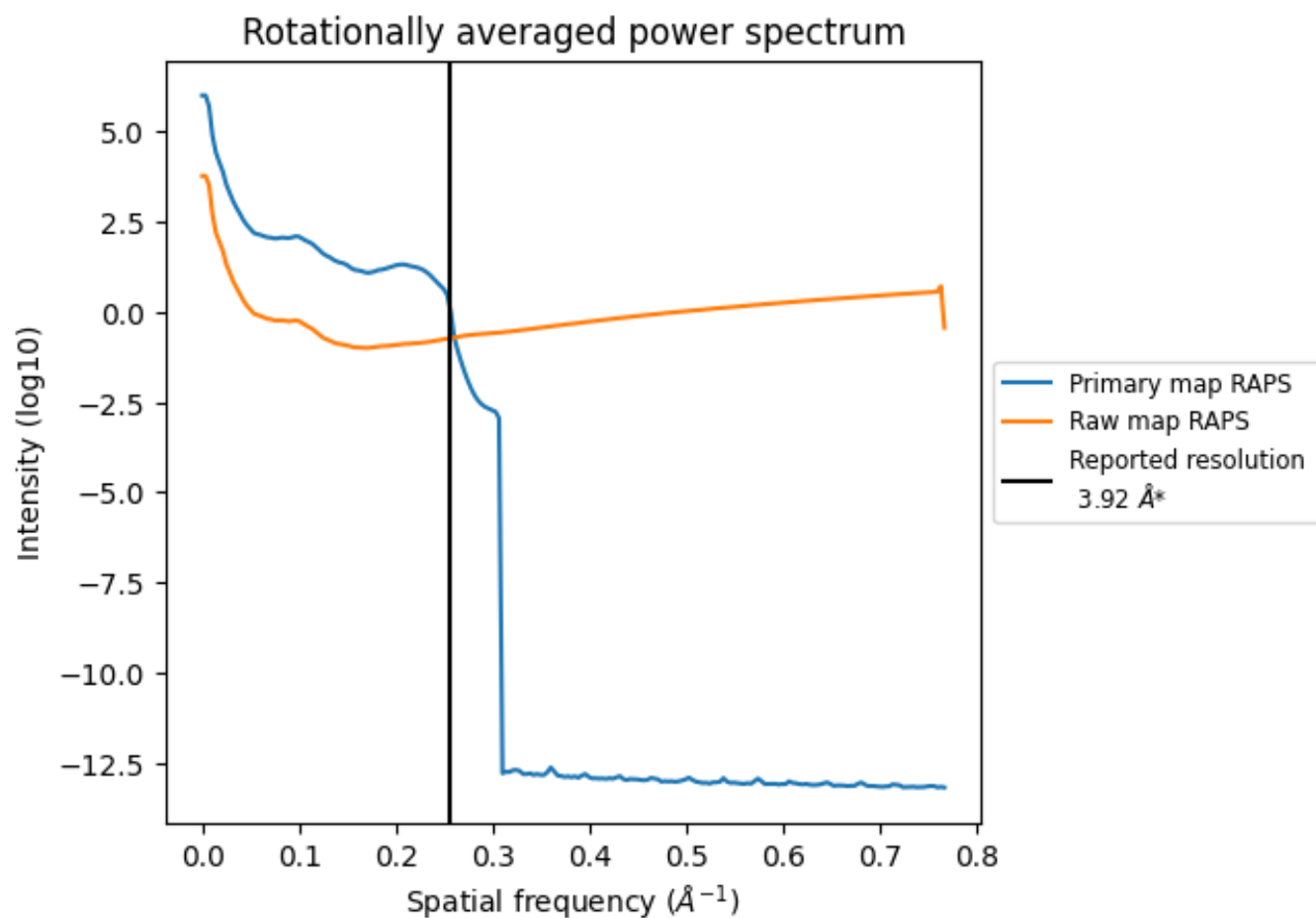
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 212 nm³; this corresponds to an approximate mass of 191 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 ⓘ

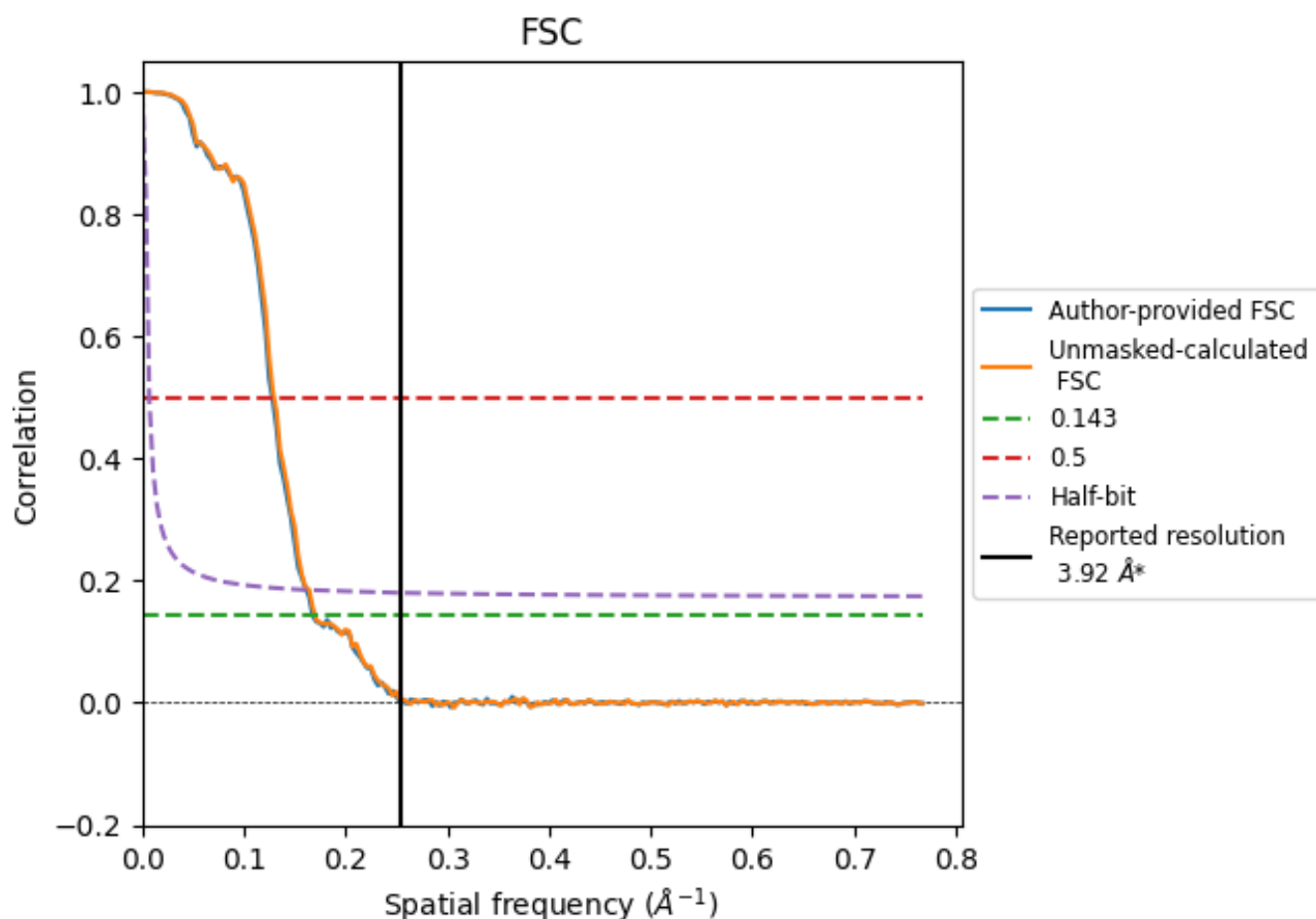


*Reported resolution corresponds to spatial frequency of 0.255 $\text{\AA}^{-1}$

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 $0.255 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.92	-	-
Author-provided FSC curve	5.97	7.82	6.20
Unmasked-calculated*	5.88	7.72	6.09

*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 5.97 differs from the reported value 3.92 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.88 differs from the reported value 3.92 by more than 10 %

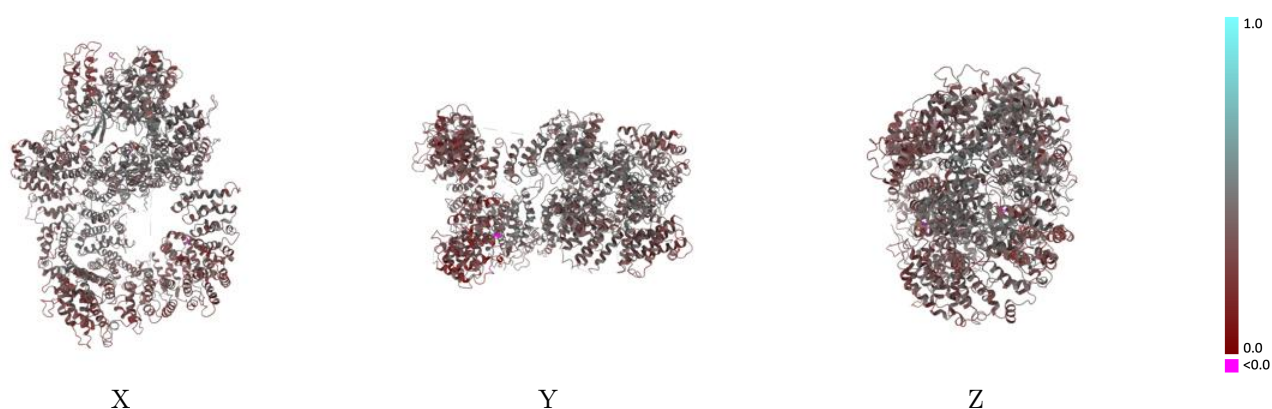
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11211 and PDB model 6ZH2. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

This section was not generated.

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

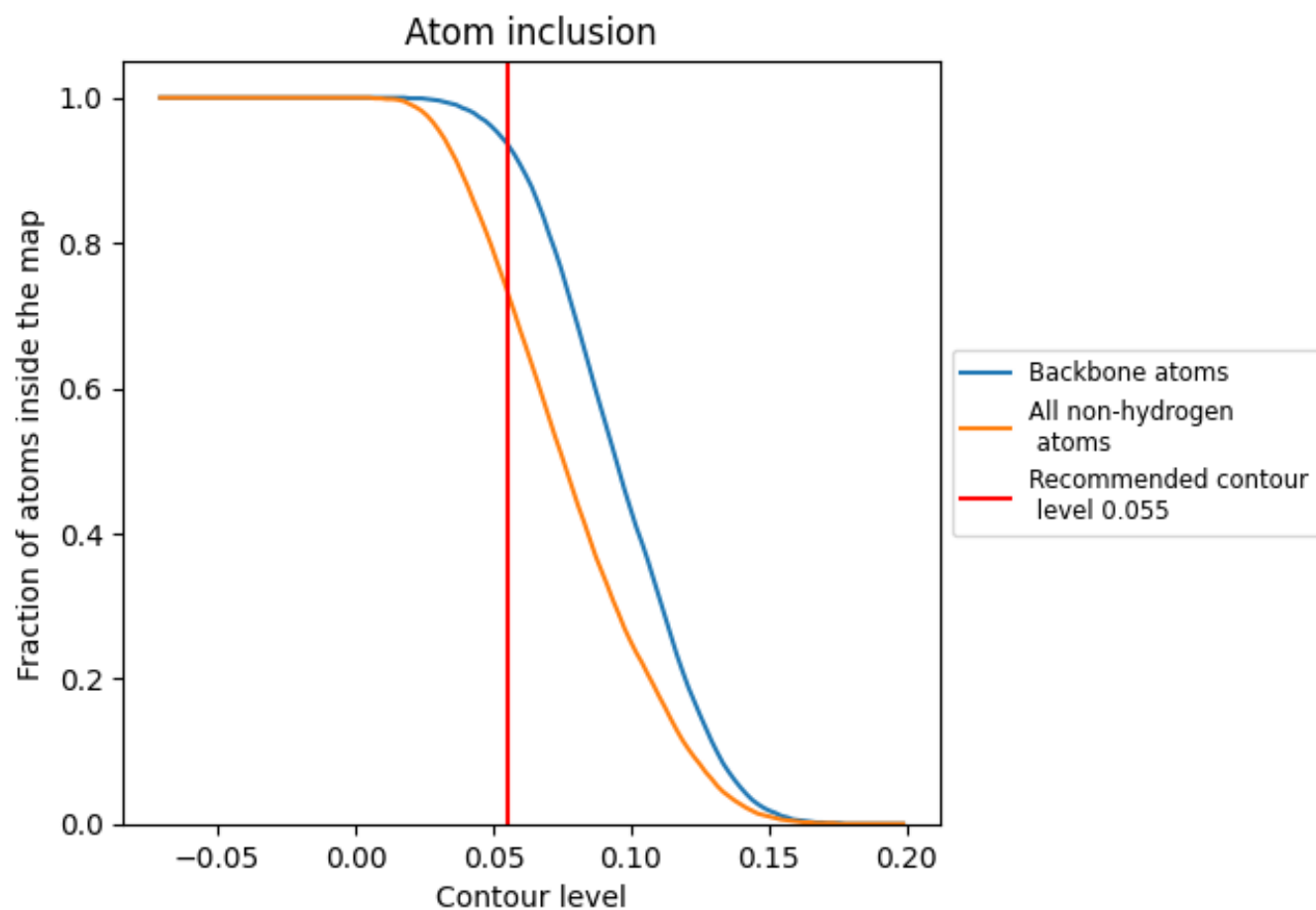


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 94% of all backbone atoms, 74% 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 (0.055) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7350	0.3790
A	0.7350	0.3790

