



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 05:21 AM UTC

PDB ID : 9EAG / pdb_00009eag
EMDB ID : EMD-47801
Title : The Structure of ApoB100 from Human Low-Density Lipoprotein
Authors : Berndsen, Z.T.; Cassidy, C.K.
Deposited on : 2024-11-11
Resolution : 9.00 Å (reported)
Based on initial model : .

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:

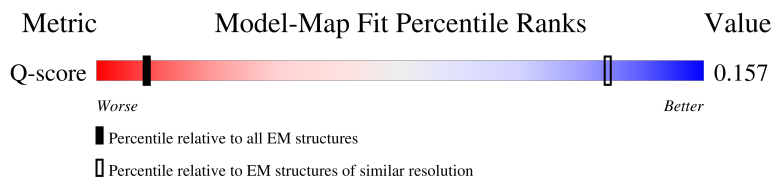
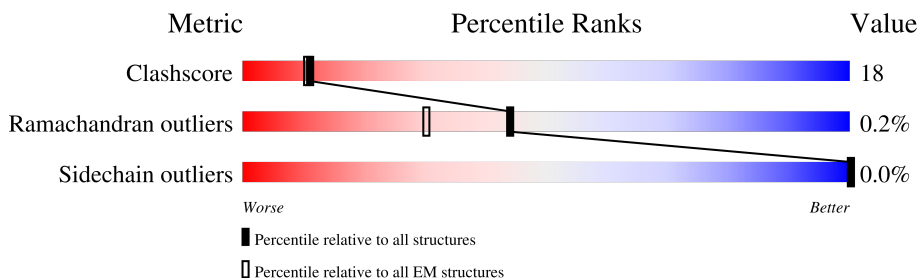
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 9.00 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	257 (8.50 - 9.50)

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	4563	<p>37% (red), 61% (green), 38% (yellow), . (grey)</p>

2 Entry composition

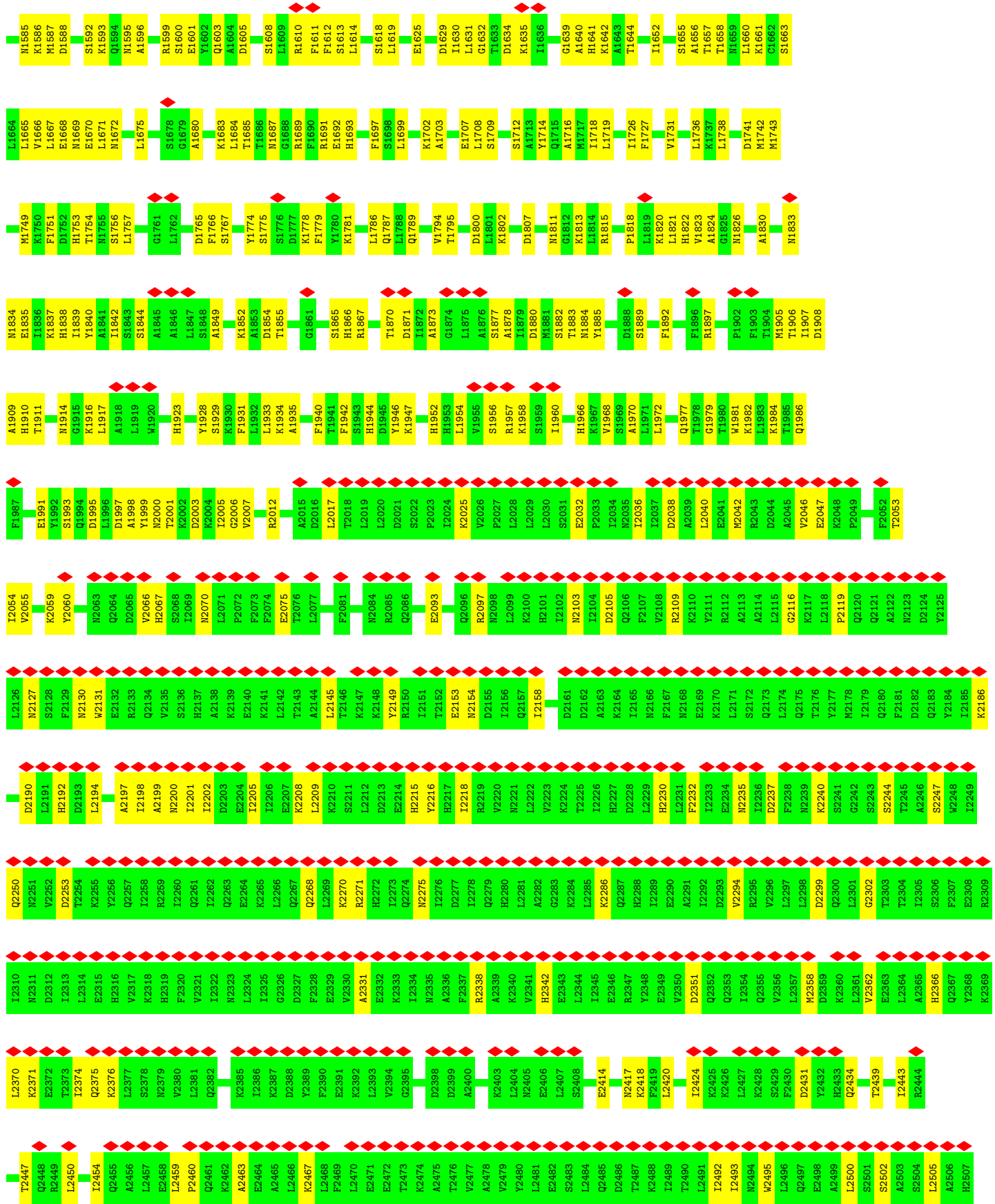
There is only 1 type of molecule in this entry. The entry contains 36083 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Apolipoprotein B 100.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	4526	36083	23018	6066	6897	102	0	0

K632	F633	S634	R635	M636	Q638	L639	Y640	K641	S642	V643	S644	L645	P646	S647	L648	D649	P650	A651	S652	A653	K654	I655	E656	G657	M658	L659	I660	P663	N664	M665	Y666	L667	P668	K669	E670	S671	M672	L673	K674	T675	L676	L677	F680	G681	F682	A683	S684	D686	L687	I688	E689	I690	G691	L692	E693				
G694	K695	G696	F697	E698	P699	T700	L701	E702	L704	F705	G706	K707	Q708	G709	F710	F711	P712	D713	S714	V715	N716	K717	A718	L719	G720	V721	W722	N723	G724	Q725	K726	P727	D728	G729	V730	S731	K732	V733	L734	V735	D736	H737	F738	G739	Y740	T741	K742	A685	D743	D744	K745	H746	E747	Q748	D749	M750	V751	N752	G753
I754	M755	L756	V758	E759	K760	L761	I762	K763	D764	L765	K766	S767	K768	E769	E772	A773	R774	A775	Y776	L777	R778	E783	L784	G785	N786	M789	Q790	D791	L795	G796	K797	L798	M801	R804	Q807	P810	I813	G814	E815	V816	I817	R818	K819	G820	S821	K822	F825	F826	L827	H828	Q900								
Y829	I830	F831	E833	L838	P839	T840	G841	L844	Q845	L846	Q847	V853	I854	A855	P856	G857	A858	K859	A860	G861	V862	L864	E865	V866	A867	N868	M869	Q870	V874	A875	K876	V879	S880	V881	E882	F883	V884	T885	N886	M887	G888	I889	I890	I891	P892	I817	D893	F894	A895	R896	V899	Q900							
M901	N902	T903	N904	F905	H906	E907	E908	G910	L911	E912	A913	H914	L915	A916	L917	K923	F924	I925	I926	P927	K928	P929	K930	R931	P932	V933	K934	L935	L936	S937	G938	G939	N940	T941	L942	H943	L944	V945	S946	T950	E951	V952	I953	N959	R960	Q968	V969	F970	P971	Y975	N983	A984							
S985	S986	T987	D988	S989	A990	S991	Y992	Y993	P994	L995	T996	D998	T999	R1000	L1001	E1002	L1003	E1004	L1005	R1006	P1007	E1010	Q1013	Y1014	S1015	Y1020	E1021	Q1023	R1024	E1025	A1028	L1029	L1033	T1037	G1041	A1042	K1043	Q1044	M1049	S1061	S1062	E1063	V1064	Q1065	I1066	V1071													
R1078	V1079	E1082	S1083	T1084	E1085	G1086	K1087	T1088	L1092	L1093	L1094	D1095	I1096	K1099	K1100	I1101	T1102	E1103	V1104	A1105	L1106	M1107	S1111	C1112	D1113	T1114	K1115	E1116	E1117	R1118	K1119	I1120	K1121	G1122	V1123	I1124	S1125	I1126	P1127	R1128	L1129	Q1130	A1131	E1132	A1133	R1134	S1135	E1136	I1137	H1140	W1141	A1144							
L1147	D1151	S1152	A1153	A1154	T1155	G1158	S1159	T1160	V1161	S1162	K1163	R1164	W1167	H1168	Y1169	D1170	E1171	E1172	K1173	I1174	E1175	F1176	E1177	W1178	M1179	D1185	L1186	K1187	K1188	N1189	L1197	S1198	D1199	Y1200	P1201	K1202	S1203	L1204	H1205	M1206	Y1207	R1210	L1211	L1212	E1213	H1214	R1215	V1216	P1217	Q1218	T1219	D1220							
F1223	R1224	H1225	V1226	G1227	L1230	I1231	V1232	A1233	M1234	S1235	S1236	W1237	L1238	Q1239	K1240	A1241	S1242	E1243	S1244	L1245	P1246	Y1247	T1248	Q1249	T1250	L1251	Q1252	D1253	L1255	M1256	S1257	E1260	F1261	M1262	L1263	Q1264	M1265	M1266	G1267	L1268	P1269	D1270	F1271	H1272	I1273	P1274	E1275	M1276	L1277	K1280	S1281	D1282	G1283	R1284					
V1285	K1286	Y1287	T1288	L1289	M1290	K1291	N1292	S1293	L1294	K1295	I1296	E1297	I1298	P1299	L1300	P1301	F1302	G1303	G1304	K1305	S1306	S1307	R1308	D1309	L1310	K1311	M1312	L1313	E1314	T1315	V1316	R1317	T1318	P1319	A1320	L1321	H1322	F1323	K1324	S1325	V1326	G1327	F1328	H1329	L1330	P1331	S1332	R1333	E1334	F1335	Q1336	V1337	P1338	T1339	F1340	T1341	I1342	P1343	K1344
L1345	Y1346	Q1347	L1348	Q1349	V1350	P1351	L1352	L1353	G1354	V1355	L1356	D1357	Y1367	M1368	V1369	S1370	Y1373	S1374	G1375	G1376	D1381	L1385	Y1389	H1390	M1391	K1392	A1393	D1394	S1395	V1396	V1397	D1398	L1399	S1401	Y1402	M1403	V1404	Q1405	E1409	T1410	T1411	Y1412	D1413	H1414	K1415	M1416	T1417	F1418	T1419	L1420	S1421								
G1424	S1425	L1426	R1427	H1428	K1429	F1430	L1431	D1432	S1433	N1434	I1435	K1436	F1437	S1438	H1439	V1440	L1443	G1444	N1445	N1446	P1447	Y1448	S1449	L1453	D1456	A1457	S1458	S1459	P1459	V1463	V1469	S1473	K1474	K1475	K1476	Q1477	H1478	L1479	F1480	V1481	V1484	Q1489	F1490	R1491	V1492	S1493	G1496	G1499	T1500	Y1501									
L1503	Q1506	R1507	D1508	P1509	R1513	L1514	M1515	L1520	R1521	F1522	M1523	S1524	L1527	Q1528	G1529	T1530	M1531	Q1532	I1533	T1534	G1535	R1536	Y1537	E1538	S1543	L1544	T1545	S1546	D1549	L1550	I1554	I1555	K1556	A1559	S1560	L1561	M1562	L1570	K1571	S1572	D1573	T1574	M1575	G1576	K1577	Y1578	A1582												



F3293	F3294	Y3295	T3296	L3297	L3298	L3299	F3300	S3301	L3302	L3304	F3305	F3306	L3307	H3308	F3309	F3310	R3311	L3312	L3313	K3314	L3315	S3316	N3257	F3258	E3259	F3260	S3261	F3262	F3263	T3264	L3265	E3266	F3267	F3268	F3269	F3270	F3271	F3272	F3273	F3274	F3275	F3276	F3277	F3278	F3279	F3280	F3281	F3282	F3283	F3284	F3285	F3286	F3287	F3288	F3289	F3290	R3291	F3292						
Y3233	K3234	A3235	E3236	K3237	S3238	H3239	D3240	E3241	L3242	R3243	R3244	F3245	Q3247	I3248	P3249	G3250	Y3251	T3252	V3253	P3254	F3255	V3256	V3256	N3257	F3258	E3259	F3260	S3261	F3262	F3263	T3264	L3265	E3266	F3267	F3268	F3269	F3270	S3271	F3272	D3273	R3274	F3275	F3276	F3277	F3278	F3279	F3280	F3281	F3282	F3283	F3284	F3285	F3286	F3287	F3288	F3289	F3290	R3291	F3292					
D3170	L3171	Q3176	Y3177	K3178	K3179	N3180	R3183	H3184	S3185	L3186	T3187	N3188	P3189	L3190	A3191	V3192	L3193	C3194	E3195	F3196	L3197	S3198	Q3199	S3200	L3201	K3202	S3203	F3204	D3205	R3206	H3207	F3208	E3209	K3210	N3211	R3212	N3213	N3214	A3215	L3216	D3217	F3218	V3219	T3220	K3221	S3222	Y3223	N3224	E3225	T3226	K3227	L3228	F3229	F3230	D3231	K3232								
A3104	G3105	N3106	N3107	E3108	N3109	I3110	N3111	H3114	V3115	G3116	I3117	E3120	L3123	D3124	F3125	L3126	N3127	I3128	F3129	L3130	F3131	I3132	F3133	E3134	N3135	L3136	L3137	F3138	F3139	I3140	I3141	I3142	I3143	T3144	F3145	L3146	L3147	K3148	D3149	F3150	S3151	F3152	K3155	L3158	K3159	E3160	F3161	L3162	K3163	T3164	K3165	Q3167												
F3038	F3039	S3040	A3041	Q3042	E3045	L3046	T3047	A3048	S3049	T3050	N3051	H3052	E3053	L3056	F3060	P3061	L3062	R3063	L3064	T3065	G3066	K3067	I3068	D3069	F3070	L3071	N3072	S3000	L3002	T3003	A3004	K3005	G3006	N3007	A3008	E3016	F3017	T3018	G3019	R3020	H3021	D3022	A3023	H3024	L3025	N3026	G3031	T3032	L3033	K3034	N3035	S3036	L3037											
L2966	H2967	L2968	R2969	V2970	N2971	Q2972	N2973	L2974	V2975	Y2976	E2977	S2980	S2984	K2985	L2986	E2987	L2988	Q2989	Q2990	Q2991	V2992	D2993	S2994	Q2995	H2996	V2997	G2998	H2999	S3000	L3002	T3003	A3004	K3005	G3006	N3007	A3008	E3016	F3017	T3018	G3019	R3020	H3021	D3022	A3023	H3024	L3025	N3026	G3031	T3032	L3033	K3034	N3035	S3036	L3037										
L2898	D2899	Q2903	A2904	D2905	L2906	R2907	N2908	S2841	E2842	N2843	L2844	L2845	F2846	G2847	A2849	G2917	H2918	I2919	A2920	W2921	T2922	G2927	L2860	H2861	W2929	K2930	E2864	N2865	T2866	L2867	E2868	S2799	S2937	N2870	N2871	V2875	K2876	L2877	N2878	N2879	Q2880	L2881	L2882	D2884	S2885	N2886	T2887	K2888	Y2889	F2890	H2891	L2892	L2893	N2894	L2895	P2896	K2897							
Q2765	S2766	P2767	L2768	F2769	T2770	L2701	P2702	L2703	A2704	L2705	L2706	T2707	L2708	P2709	D2710	F2711	R2712	L2713	P2714	E2715	L2716	A2717	L2718	P2719	E2720	F2721	L2722	L2723	P2724	T2725	L2726	N2727	L2728	N2729	D2730	F2731	Q2732	T2733	P2734	D2735	L2736	H2737	L2738	P2739	S2682	E2683	L2684	Q2685	W2686	P2687	V2688	P2689	D2690	L2691	Y2692	L2693	D2622	L2623	L2624	R2625	S2628	V2629	Q2630	L2631
S2831	S2832	K2833	R2836	H2839	G2840	S2841	E2842	N2843	L2844	L2845	F2846	G2847	A2849	G2917	H2918	I2919	A2920	W2921	T2922	G2927	L2860	H2861	W2929	K2930	E2864	N2865	T2866	L2867	E2868	S2799	S2937	N2870	N2871	V2875	K2876	L2877	N2878	N2879	Q2880	L2881	L2882	D2884	S2885	N2886	T2887	K2888	Y2889	F2890	H2891	L2892	L2893	N2894	L2895	P2896	K2897									
L2898	D2899	Q2903	A2904	D2905	L2906	R2907	N2908	S2841	E2842	N2843	L2844	L2845	F2846	G2847	A2849	G2917	H2918	I2919	A2920	W2921	T2922	G2927	L2860	H2861	W2929	K2930	E2864	N2865	T2866	L2867	E2868	S2799	S2937	N2870	N2871	V2875	K2876	L2877	N2878	N2879	Q2880	L2881	L2882	D2884	S2885	N2886	T2887	K2888	Y2889	F2890	H2891	L2892	L2893	N2894	L2895	P2896	K2897							
S2831	S2832	K2833	R2836	H2839	G2840	S2841	E2842	N2843	L2844	L2845	F2846	G2847	A2849	G2917	H2918	I2919	A2920	W2921	T2922	G2927	L2860	H2861	W2929	K2930	E2864	N2865	T2866	L2867	E2868	S2799	S2937	N2870	N2871	V2875	K2876	L2877	N2878	N2879	Q2880	L2881	L2882	D2884	S2885	N2886	T2887	K2888	Y2889	F2890	H2891	L2892	L2893	N2894	L2895	P2896	K2897									
L2898	D2899	Q2903	A2904	D2905	L2906	R2907	N2908	S2841	E2842	N2843	L2844	L2845	F2846	G2847	A2849	G2917	H2918	I2919	A2920	W2921	T2922	G2927	L2860	H2861	W2929	K2930	E2864	N2865	T2866	L2867	E2868	S2799	S2937	N2870	N2871	V2875	K2876	L2877	N2878	N2879	Q2880	L2881	L2882	D2884	S2885	N2886	T2887	K2888	Y2889	F2890	H2891	L2892	L2893	N2894	L2895	P2896	K2897							
L2898	D2899	Q2903	A2904	D2905	L2906	R2907	N2908	S2841	E2842	N2843	L2844	L2845	F2846	G2847	A2849	G2917	H2918	I2919	A2920	W2921	T2922	G2927	L2860	H2861	W2929	K2930	E2864	N2865	T2866	L2867	E2868	S2799	S2937	N2870	N2871	V2875	K2876	L2877	N2878	N2879	Q2880	L2881	L2882	D2884	S2885	N2886	T2887	K2888	Y2889	F2890	H2891	L2892	L2893	N2894	L2895	P2896	K2897							
L2898	D2899	Q2903	A2904	D2905	L2906	R2907	N2908	S2841	E2842	N2843	L2844	L2845	F2846	G2847	A2849	G2917	H2918	I2919	A2920	W2921	T2922	G2927	L2860	H2861	W2929	K2930	E2864	N2865	T2866	L2867	E2868	S2799	S2937	N2870	N2871	V2875	K2876	L2877	N2878	N2879	Q2880	L2881	L2882	D2884	S2885	N2886	T2887	K2888	Y2889	F2890	H2891	L2892	L2893	N2894	L2895	P2896	K2897							
L2898	D2899	Q2903	A2904	D2905	L2906	R2907	N2908	S2841	E2842	N2843	L2844	L2845	F2846	G2847	A2849	G2917	H2918	I2919	A2920	W2921	T2922	G2927	L2860	H2861	W2929	K2930	E2864	N2865	T2866	L2867	E2868	S2799	S2937	N2870	N2871	V2875	K2876	L2877	N2878	N2879	Q2880	L2881	L2882	D2884	S2885	N2886	T2887	K2888	Y2889	F2890	H2891	L2892	L2893	N2894	L2895	P2896	K2897							
L2898	D2899	Q2903	A2904	D2905	L2906	R2907	N2908	S2841	E2842	N2843	L2844	L2845	F2846	G2847	A2849	G2917	H2918	I2919	A2920	W2921	T2922	G2927	L2860	H2861	W2929	K2930	E2864	N2865	T2866	L2867	E2868	S2799	S2937	N2870	N2871	V2875	K2876	L2877	N2878	N2879	Q2880	L2881	L2882	D2884	S2885	N2886	T2887	K2888	Y2889	F2890	H2891	L2892	L2893	N2894	L2895	P2896	K2897							
L2898	D2899	Q2903	A2904	D2905	L2906	R2907	N2908	S2841	E2842	N2843	L2844	L2845	F2846	G2847	A2849	G2917	H2918	I2919	A2920	W2921	T2922	G2927	L2860	H2861	W2929	K2930	E2864	N2865	T2866	L2867	E2868	S2799	S2937	N2870	N2871	V2875	K2876	L2877	N2878	N2879	Q2880	L2881	L2882	D2884	S2885	N2886	T2887	K2888	Y2889	F2890	H2891	L2892	L2893	N2894	L2895	P2896	K2897							
L2898	D2899	Q2903	A2904	D2905	L2906	R2907	N2908	S2841	E2842	N2843	L2844	L2845	F2846	G2847	A2849	G2917	H2918	I2919	A2920	W2921	T2922	G2927	L2860	H2861	W2929	K2930	E2864	N2865	T2866	L2867	E2868	S2799	S2937	N2870	N2871	V2875	K2876	L2877	N2878	N2879	Q2880	L2881	L2882	D2884	S2885	N2886	T2887	K2888	Y2889	F2890	H2891	L2892	L2893	N2894	L2895	P2896	K2897							
L2898	D2899	Q2903	A2904	D2905	L2906	R2907	N2908	S2841	E2842	N2843	L2844	L2845	F2846	G2847	A2849	G2917	H2918	I2919	A2920	W2921	T2922	G2927	L2860	H2861	W2929	K2930	E2864	N2865	T2866	L2867	E2868	S2799	S2937	N2870	N2871	V2875	K2876	L2877	N2878	N2879	Q2880	L2881	L2882	D2884	S2885	N2886	T2887	K2888	Y2889	F2890	H2891	L2892	L2893	N2894	L2895	P2896	K2897							
L2898	D2899	Q2903	A2904	D2905	L2906	R2907	N2908	S2841	E2842	N2843	L2844	L2845	F2846	G2847	A2849	G2917	H2918	I2919	A2920	W2921	T2922	G2927	L2860	H2861	W2929	K2930	E2864	N2865	T2866	L2867	E2868	S2799	S2937	N2870	N2871	V2875	K2876	L2877	N2878	N2879	Q2880	L2881	L2882	D2884	S2885	N2886	T2887	K2888	Y2889	F2890	H2891	L2892	L2893	N2894	L2895	P2896	K2897							
L2898	D2899	Q2903	A2904	D2905	L2906	R2907	N2908	S2841	E2842	N2843	L2844	L2845	F2846	G2847	A2849	G2917	H2918	I2919	A2920	W2921	T2922	G2927	L2860	H2861	W2929	K2930	E2864	N2865	T2866	L2867	E2868	S2799	S2937	N2870	N2871	V2875	K2876	L2877	N2878	N2879	Q2880	L2881	L2882	D2884	S2885	N2886	T2887	K2888	Y2889	F2890	H2891	L2892	L2893	N2894	L2895	P2896	K2897							
L2898	D2899	Q2903	A2904	D2905	L2906	R2907	N2908	S2841	E2842	N2843	L2844	L2845	F2846	G2847	A2849	G2917	H2918	I2919	A2920	W2921	T2922	G2927	L2860	H2861	W2929	K2930	E2864	N2865	T2866	L2867	E2868	S2799	S2937	N2870	N2871	V2875	K2876	L2877	N2878	N2879	Q2880	L2881	L2882	D2884	S2885	N2886	T2887	K2888	Y2889	F2890	H2891	L2892	L2893	N2894	L2895	P2896	K2897							
L2898	D2899	Q2903	A2904	D2905	L2906	R2907	N2908	S2841	E2842	N2843	L2844	L2845	F2846	G2847	A2849	G2917	H2918	I2919	A2920	W2921	T2922	G2927	L2860	H2861	W2929	K2930	E2864	N2865	T2866	L2867	E2868	S2799	S2937	N2870	N2871	V2875	K2876	L2877	N2878	N2879	Q2880	L2881	L2882	D2884	S2885	N2886	T2887	K2888	Y2889	F2890	H2891	L2892	L2893	N2894	L2895	P2896	K2897							
L2898	D2899	Q2903	A2904	D2905	L2906	R2907																																																										

E4223	V4224	G4225	T4226	V4227	L4228	V4231	V4232	S4233	K4234	V4235	H4236	N4237	G4238	S4239	E4240	I4241	L4242	F4243	S4244	V4245	F4246	Q4247	D4248	L4249	V4250	I4251	T4252	L4253	P4254	F4255	E4256	L4257	R4258	K4259	H4260	K4261	L4262	L4263	D4264	V4265	L4266	S4267	M4268	V4269	R4270	E4271	L4272	L4273	K4274	D4275	L4276	S4277	K4278	E4279	A4280	Q4281	F4282	V4283
E4159	G4160	Q4161	A4162	S4163	G4166	L4167	K4168	D4169	N4170	V4171	F4172	G4173	L4174	S4175	V4176	T4177	F4182	H4183	M4184	K4185	V4186	K4187	H4188	L4189	I4190	L4193	I4194	D4195	F4196	L4197	M4198	F4199	P4200	R4201	F4202	Q4203	F4204	P4205	G4206	K4207	P4208	G4209	I4210	Y4211	Q4153	E4154	L4155	L4156	T4157	Q4158	C4217	T4218	M4219	F4220	I4221	R4222		
K4087	Y4088	H4089	V4090	E4091	H4092	L4095	R4098	S4101	S4102	K4103	L4104	R4105	R4106	Q4109	N4110	M4111	A4112	Y4116	Q4117	G4118	A4119	I4120	R4121	Q4122	I4123	D4124	S4125	D4127	V4128	R4129	F4130	T4137	T4138	Y4141	Q4142	E4143	M4144	K4145	D4146	K4147	A4148	L4151	Y4152	Q4153	L4155	L4156	T4157	Q4158	T4218	M4219	F4220	I4221	R4222					
D4017	S4020	K4021	W4022	N4023	F4024	Y4025	Y4026	S4027	P4028	Q4029	S4030	A4031	P4032	D4033	K4034	K4035	L4036	T4037	L4038	F4039	K4040	L4043	R4046	E4047	S4048	D4049	E4050	F4051	T4052	Q4053	L4054	K4055	W4058	E4059	E4060	E4061	A4062	A4063	S4064	G4065	L4066	L4067	T4068	S4069	L4070	K4071	D4072	M4073	V4074	P4075	K4076	D4083	Y4084					
A3942	S3943	K3946	G3947	T3948	F3949	A3950	H3951	R3952	D3953	F3954	S3955	E3957	Y3958	Y3964	E3965	G3966	L3967	Q3968	K3970	E3971	G3972	K3973	L3976	N3977	N3977	L3978	K3979	S3980	P3981	T3984	D3985	L3986	H3987	L3988	K3992	D3993	K3994	I3997	S3998	T3999	S4000	A4001	A4002	S4003	P4004	A4005	V4006	G4010	M4011	M4013								
A3942	E3443	L3444	K3449	S3450	K3451	V3454	S3455	S3456	S457	M3458	E3459	F3460	K3461	Y3462	D3463	F3464	A3473	K3474	G3475	A3476	V3477	D3478	H3479	K3480	L3481	S482	K3483	E3484	Y3489	F3490	E3493	S3494	S495	T3496	K3497	V3500	S3506	R3507	S3510	G3511	T3512	A3513	A3514	T3519	Y3520	L3521	S3522	N3523	R3527									
S3528	S3529	V3530	K3531	L3532	Q3533	G3534	T3535	S3536	K3537	L3538	D3539	D3540	I3541	W3542	N3543	L3544	K3547	E3548	M3549	F3550	E3553	I3559	L3562	W3563	Q3564	K3565	S3566	T3567	K3568	N3569	H3570	L3571	Q3572	L3573	E3574	F3577	F3578	T3579	N3580	H3583	T3584	S3585	K3586	N3587	S3588	E3590	L3591	S3592	P3593	N3522	K3437	N3438	F3440	K3441				
S3597	A3598	L3599	V3600	L3601	Q3602	H3603	P3607	S3608	S3609	D3612	F3613	P3614	D3615	L3616	G3617	Q3618	A3621	L3622	R3625	T3626	K3627	N3628	Q3629	K3630	I3631	R3632	W3633	K3634	N3635	R3638	I3639	H3640	S3641	G3642	S3643	Q3644	S3645	S3646	Q3647	V3648	E3649	L3650	S3651	N3652	D3653	Q3654	E3655	A3657	H3658	L3659	A3662	G3663						
S3664	L3665	H3668	L3669	R3670	F3671	L3672	K3673	N3674	L3675	L3676	Y3680	D3681	K3682	S3683	L3684	W3685	D3686	F3687	T3689	S3694	S3695	I3696	G3697	R3698	R3699	Q3700	H3701	L3702	R3703	K3694	S3705	F3708	V3709	Y3710	T3711	K3712	M3713	P3714	M3715	G3716	Y3717	F3718	F3719	S3720	I3721	P3722	L3723	V3725	L3726	A3727	D3728	K3729	F3730	I3731				
I3732	P3733	G3734	L3735	K3736	L3737	N3738	Q3739	L3740	S3742	V3743	L3744	V3745	K3746	F3747	T3748	F3749	H3750	V3751	P3752	F3753	T3754	D3755	L3756	Q3757	V3758	F3759	S3760	C3761	K3762	L3763	D3764	F3765	K3766	E3767	L3768	Q3769	I3770	Y3771	K3772	T3776	S3777	S3778	L3779	K3780	L3781	N3782	L3783	F3784	T3785	L3786	E3788	V3789	K3790	F3791	F3792	E3793		
T3798	K3799	S3800	S3801	Q3802	P3803	E3804	D3805	S3806	L3807	I3808	P3809	F3810	F3811	V3815	P3816	E3817	S3818	Q3819	L3820	T3821	S3822	S3823	Q3824	F3825	R3826	L3827	P3828	K3829	S3830	V3831	S3832	D3833	G3834	I3835	A3836	A3837	L3838	D3839	L3840	N3841	A3842	V3843	A3844	N3845	K3846	I3847	A3848	L3849	F3850	E3851	L3852	I3855	L3856	V3857	P3858	E3859		
Q3860	T3861	L3862	F3863	G3864	P3865	S3866	L3867	K3868	F3869	S3870	V3871	P3872	A3873	G3874	L3875	V3876	L3877	P3878	L3883	T3884	A3885	R3886	F3887	E3888	V3889	D3890	S3901	L3902	K3903	N3904	K3905	A3906	D3907	E3910	T3911	V3912	C3917	S3918	S3919	T3920	V3921	Q3922	F3923	L3924	A4005	E3925	L3928	H3934	E3937	D3938	G3939	T3940	L3941					
A3942	S3943	K3946	G3947	T3948	F3949	A3950	H3951	R3952	D3953	F3954	S3955	E3957	Y3958	Y3964	E3965	G3966	L3967	Q3968	K3970	E3971	G3972	K3973	L3976	N3977	N3977	L3978	K3979	S3980	P3981	T3984	D3985	L3986	H3987	L3988	K3992	D3993	K3994	I3997	S3998	T3999	S4000	A4001	A4002	S4003	P4004	A4005	V4006	G4010	M4011	M4013								
D4017	S4020	K4021	W4022	N4023	F4024	Y4025	Y4026	S4027	P4028	Q4029	S4030	A4031	P4032	D4033	K4034	K4035	L4036	T4037	L4038	F4039	K4040	L4043	R4046	E4047	S4048	D4049	E4050	F4051	T4052	Q4053	L4054	K4055	W4058	E4059	E4060	E4061	A4062	A4063	S4064	G4065	L4066	L4067	T4068	S4069	L4070	K4071	D4072	M4073	V4074	P4075	K4076	D4083	Y4084					
K4087	Y4088	H4089	V4090	E4091	H4092	L4095	R4098	S4101	S4102	K4103	L4104	R4105	R4106	Q4109	N4110	M4111	A4112	Y4116	Q4117	G4118	A4119	I4120	R4121	Q4122	I4123	D4124	S4125	D4127	V4128	R4129	F4130	T4137	T4138	Y4141	Q4142	E4143	M4144	K4145	D4146	K4147	A4148	L4151	Y4152	Q4153	L4155	L4156	T4157	Q4158	T4218	M4219	F4220	I4221	R4222					

F4284	K4358	L4418	S4479	L4554
K4285	F4359	K4419	Q4480	A4555
A4286	M4360	D4420	A4481	P4556
I4287	E4361	F4421	I4482	Q4557
Q4288	F4362	H4422	A4483	E4558
S4289	I4363	S4423	T4484	L4559
L4290	I4364	E4424	I4488	T4560
L4291	M4365	Y4425	Y4491	L4563
K4291	E4366	I4426	Y4491	
T4292	L4367	V4427	Q4494	
T4293	L4367	S4428	F4495	
E4294	Q4368	A4429	R4496	
W4295	E4369	S4430	Y4497	
L4296	A4370	M4431	K4498	
R4297	S4371	F4432	L4499	
M4298	Q4372	T4433	F4502	
L4299	E4373	S4434	S4503	
Q4300	L4374	Q4435	D4504	
D4301	Q4375	L4436	Q4505	
L4302	Q4376	S4437	L4506	
L4303	I4377	S4438	Y4509	
Q4304	H4378	Q4439	Y4510	
F4305	Q4379	V4440	E4511	
I4306	Y4380	E4441	K4512	
I4310	I4381	Q4442	F4513	
K4315	M4382	F4443	I4514	
K4318	A4383	L4444	A4515	
E4319	L4384	H4445	L4520	
M4320	R4385	R4446	I4521	
K4321	E4386	M4447	S4524	
F4322	E4387	I4448	I4525	
T4323	Y4388	Q4449	Q4526	
F4324	F4389	E4450	M4527	
Y4324	D4390	Y4451	Y4528	
L4325	P4391	L4452	T4529	
I4326	S4392	S4453	T4530	
M4327	I4393	I4454	F4531	
Y4328	V4394	L4455	L4532	
I4329	G4395	T4456	I4533	
Q4330	W4396	D4457	Y4534	
D4331	T4397	P4458	I4535	
F4337	Y4398	D4459	L4538	
S4338	K4399	Q4460	L4539	
D4339	Y4400	K4461	L4539	
Y4340	Y4401	K4462	K4540	
I4341	E4402	E4464	K4541	
P4342	L4403	R4465	L4542	
Y4343	E4404	R4466	Q4543	
K4346	I4407	I4466	S4544	
E4350	V4408	A4467	T4545	
M4351	S4409	L4469	Y4551	
C4353	L4410	T4472	M4552	
L4354	I4411	A4473	K4553	
M4355	K4412	Q4474		
L4356	N4413	E4475		
L4356	L4414	I4476		
M4356	L4415	I4477		
L4356	V4416	K4478		
L4356	A4417			

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	52843	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.148	Depositor
Minimum map value	-0.560	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.182	Depositor
Map size (Å)	490.5, 490.5, 490.5	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09, 1.09, 1.09	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	0/36813	0.37	0/49814

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	A	36083	0	36243	1315	0
All	All	36083	0	36243	1315	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 18.

The worst 5 of 1315 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:825:PHE:O	1:A:857:GLY:HA2	1.68	0.93
1:A:3918:SER:HA	1:A:3925:GLU:HG2	1.52	0.92
1:A:322:ALA:O	1:A:325:VAL:HB	1.70	0.92
1:A:4138:THR:HG22	1:A:4142:GLN:HE22	1.37	0.88
1:A:3965:GLU:O	1:A:3969:GLU:HB2	1.73	0.86

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	4524/4563 (99%)	4297 (95%)	219 (5%)	8 (0%)	43 78

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	137	GLU
1	A	1477	GLN
1	A	3828	PRO
1	A	375	SER
1	A	1200	TYR

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	4051/4080 (99%)	4050 (100%)	1 (0%)	100 100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	76	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3035	ASN
1	A	3442	GLN
1	A	3099	ASN
1	A	3127	ASN
1	A	3533	GLN

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.

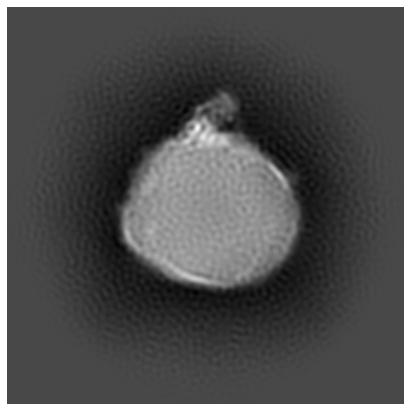
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47801. These allow visual inspection of the internal detail of the map and identification of artifacts.

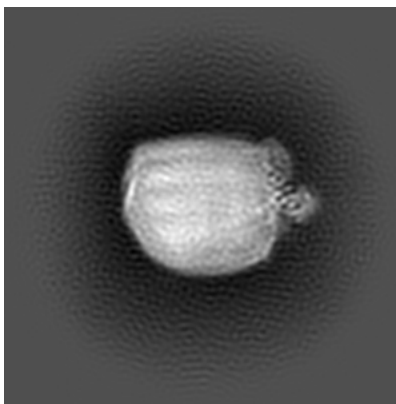
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

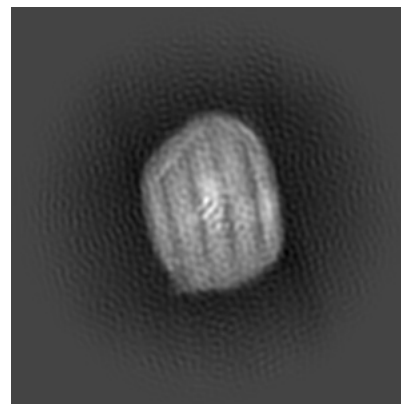
6.1.1 Primary map



X

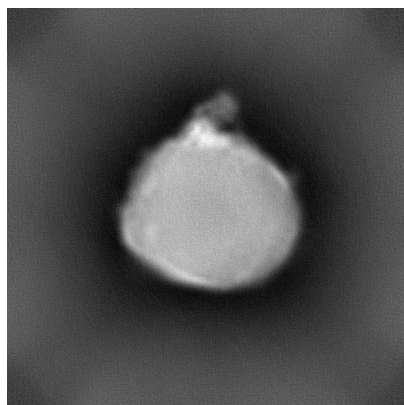


Y

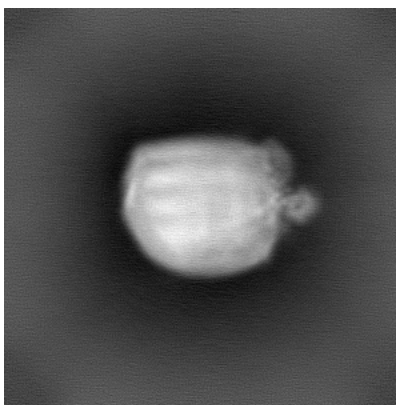


Z

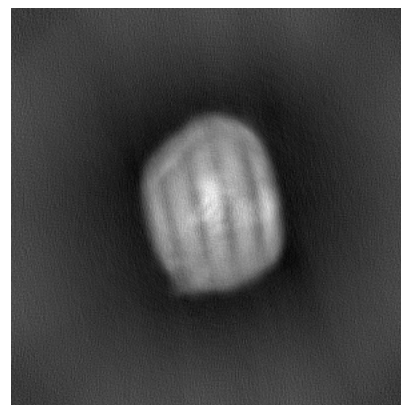
6.1.2 Raw map



X



Y

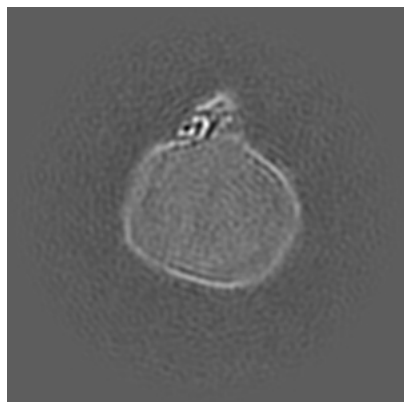


Z

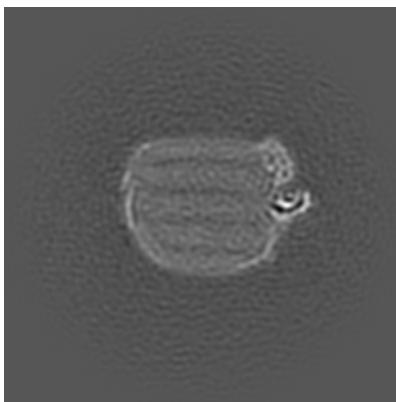
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

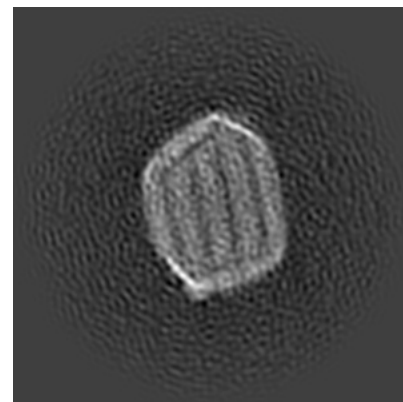
6.2.1 Primary map



X Index: 225

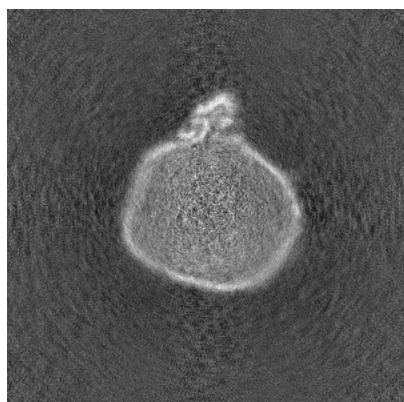


Y Index: 225

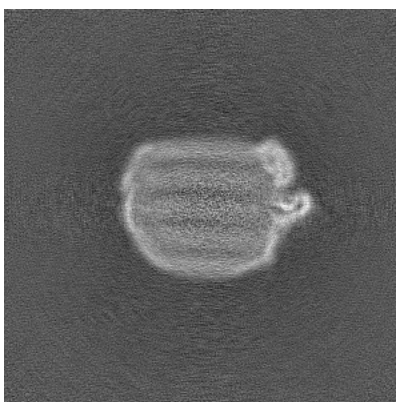


Z Index: 225

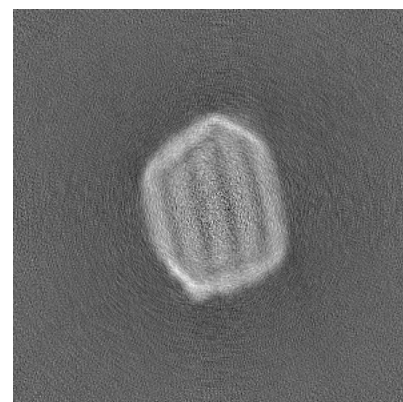
6.2.2 Raw map



X Index: 225



Y Index: 225

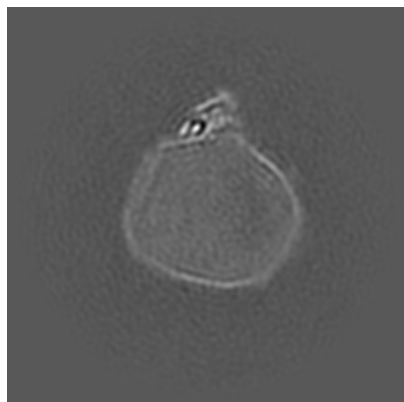


Z Index: 225

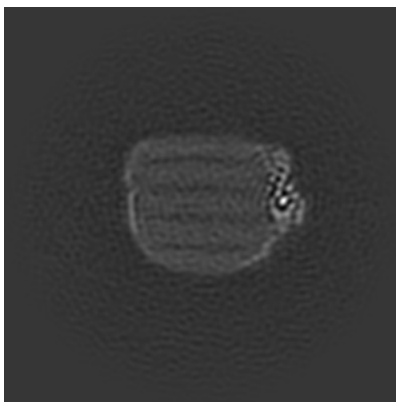
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

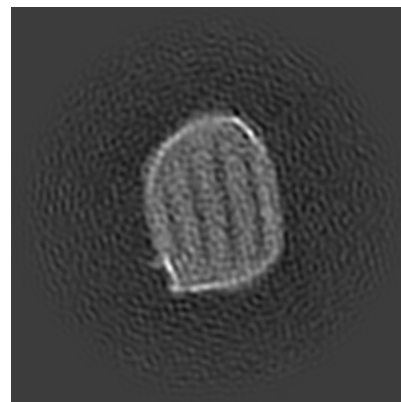
6.3.1 Primary map



X Index: 230



Y Index: 213

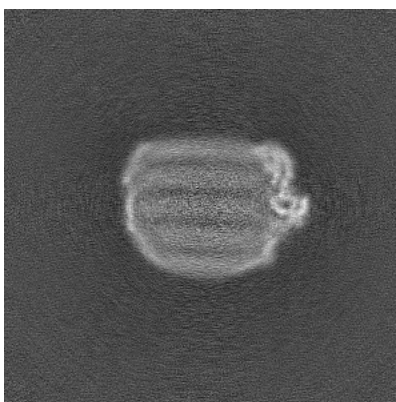


Z Index: 196

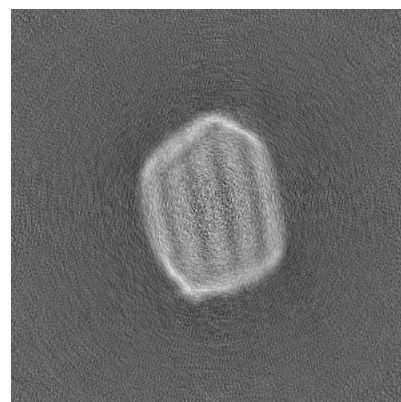
6.3.2 Raw map



X Index: 227



Y Index: 219

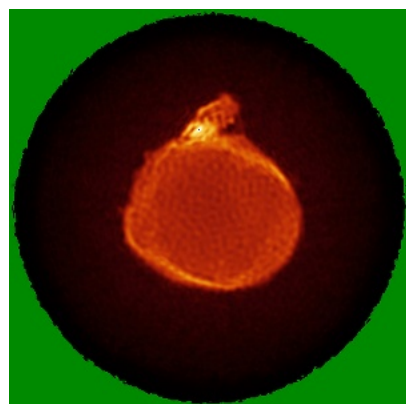


Z Index: 219

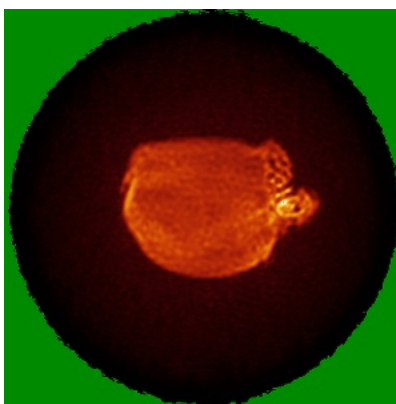
The images above show the largest variance slices of the map in three orthogonal directions.

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

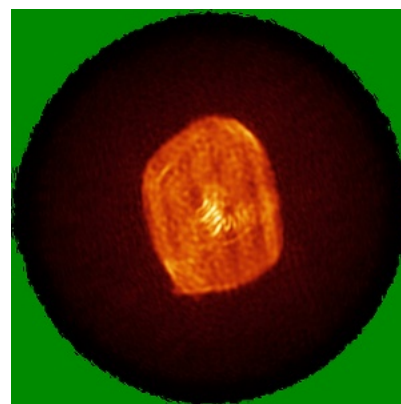
6.4.1 Primary map



X

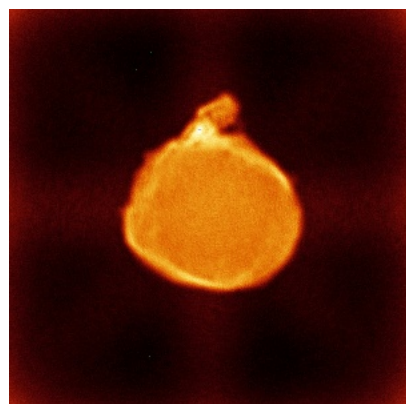


Y

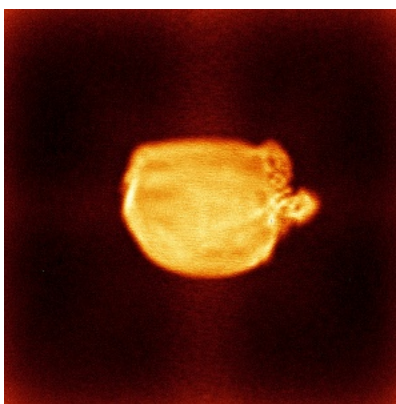


Z

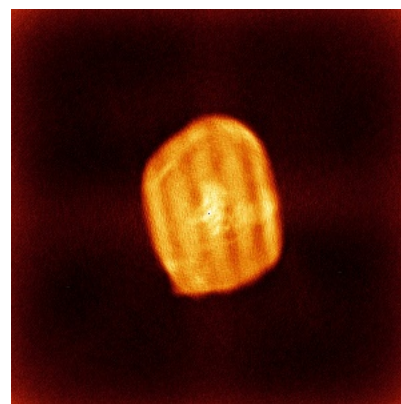
6.4.2 Raw map



X



Y

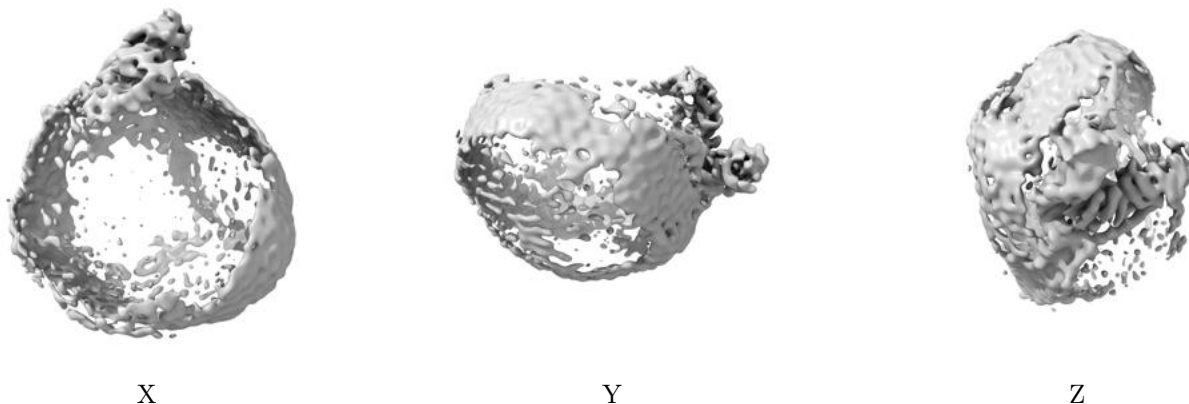


Z

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.

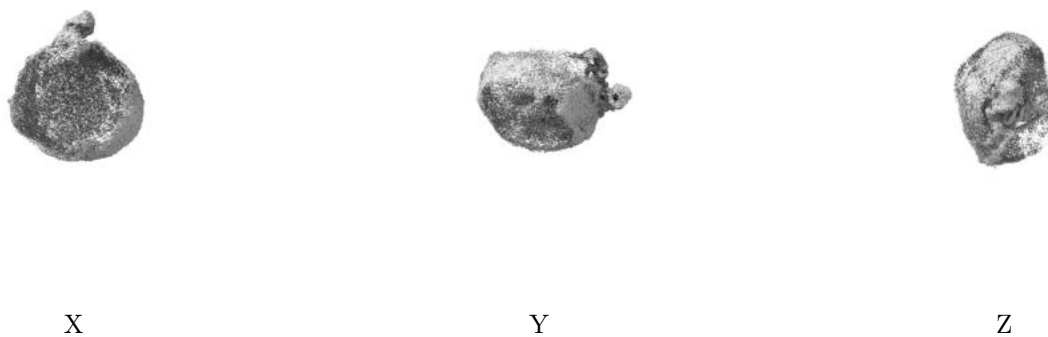
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.182. 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.

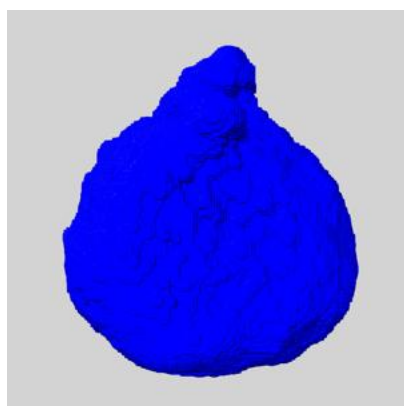
6.6 Mask visualisation [i](#)

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

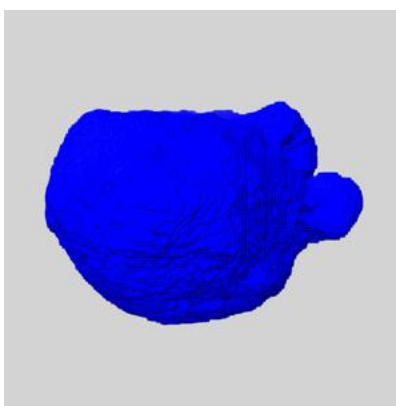
A mask typically either:

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

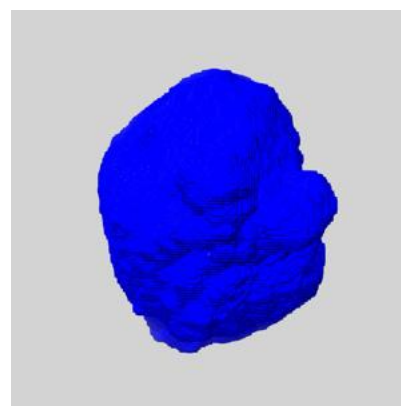
6.6.1 emd_47801_msk_1.map [i](#)



X



Y

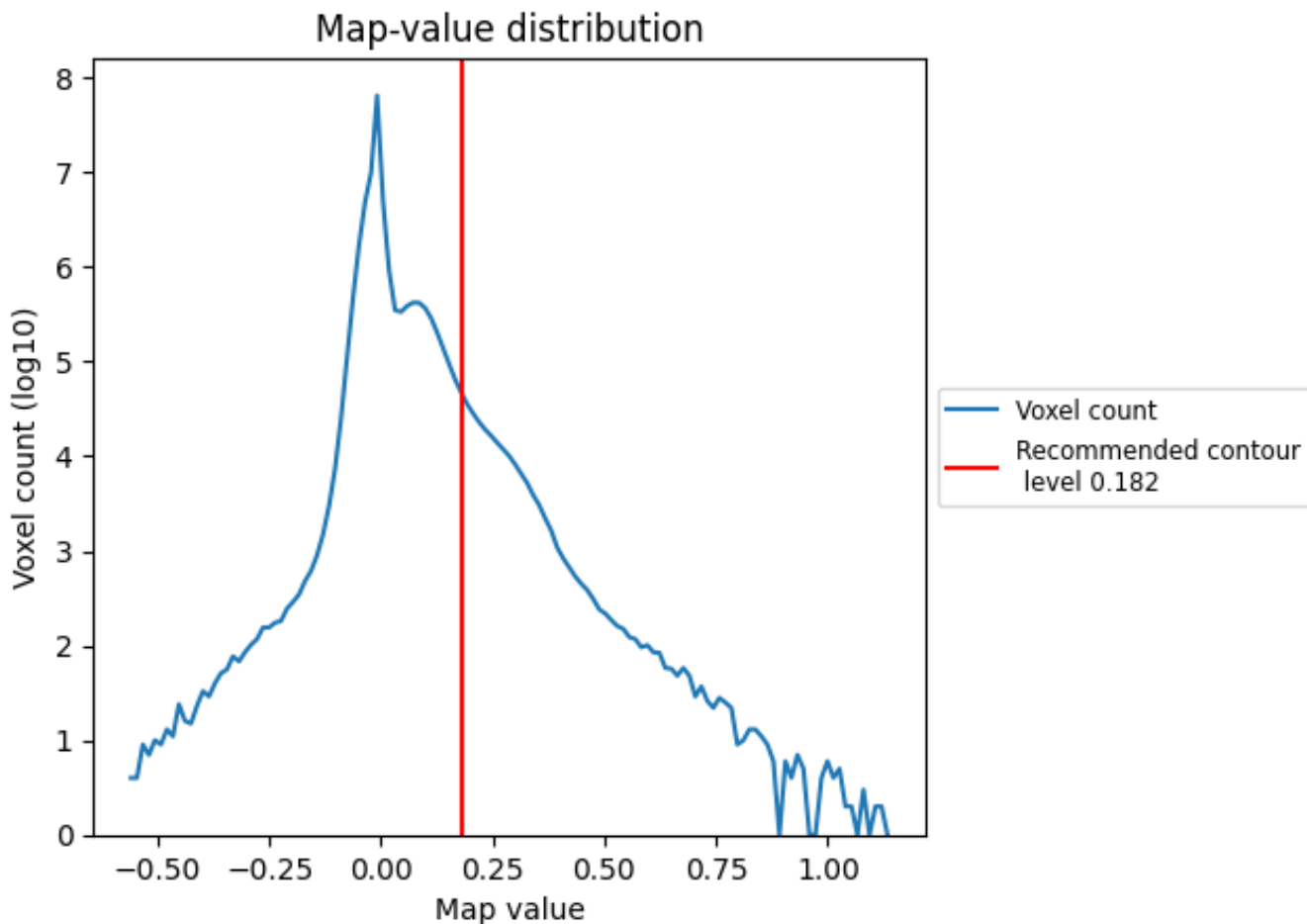


Z

7 Map analysis [i](#)

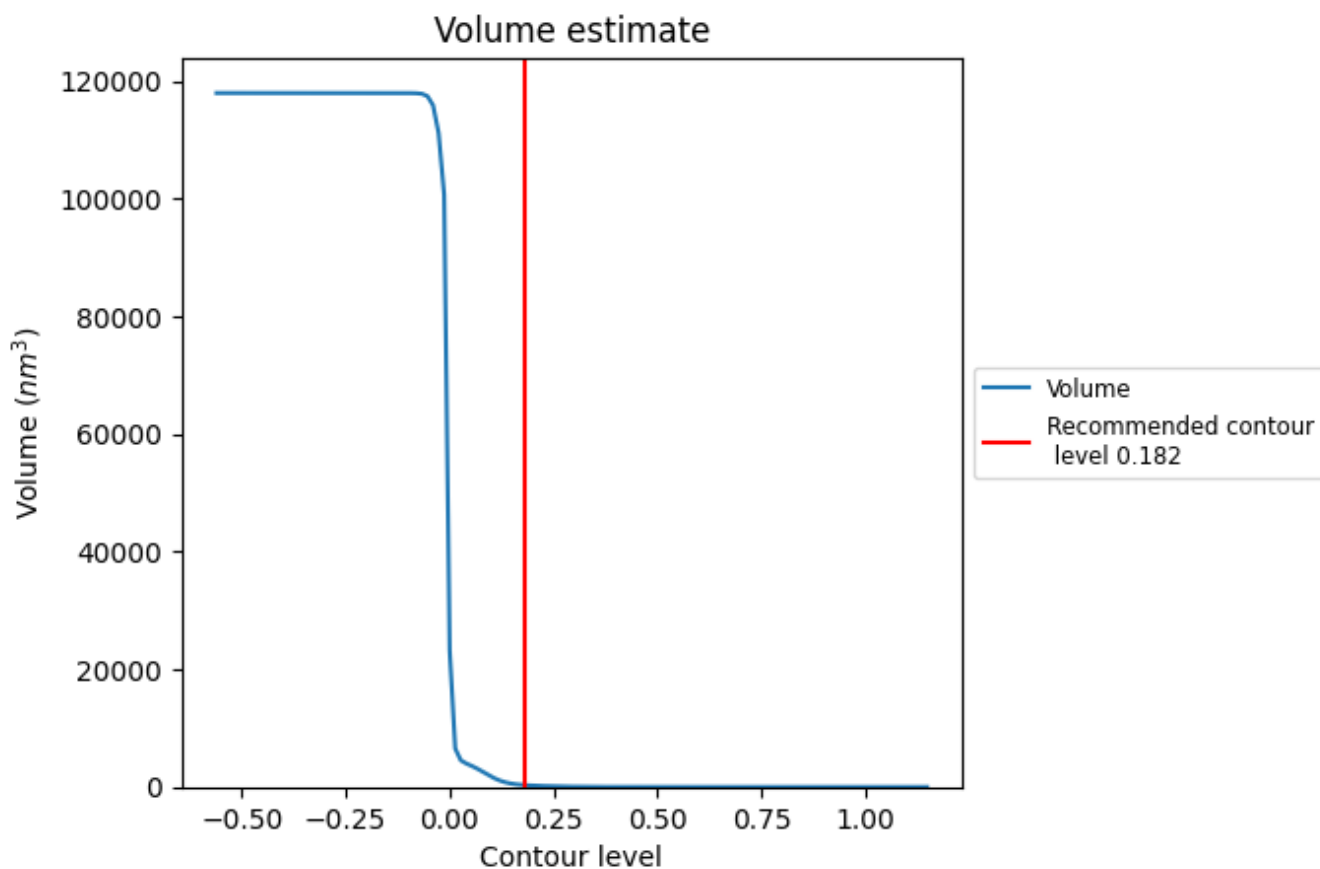
This section contains the results of statistical analysis of the map.

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.

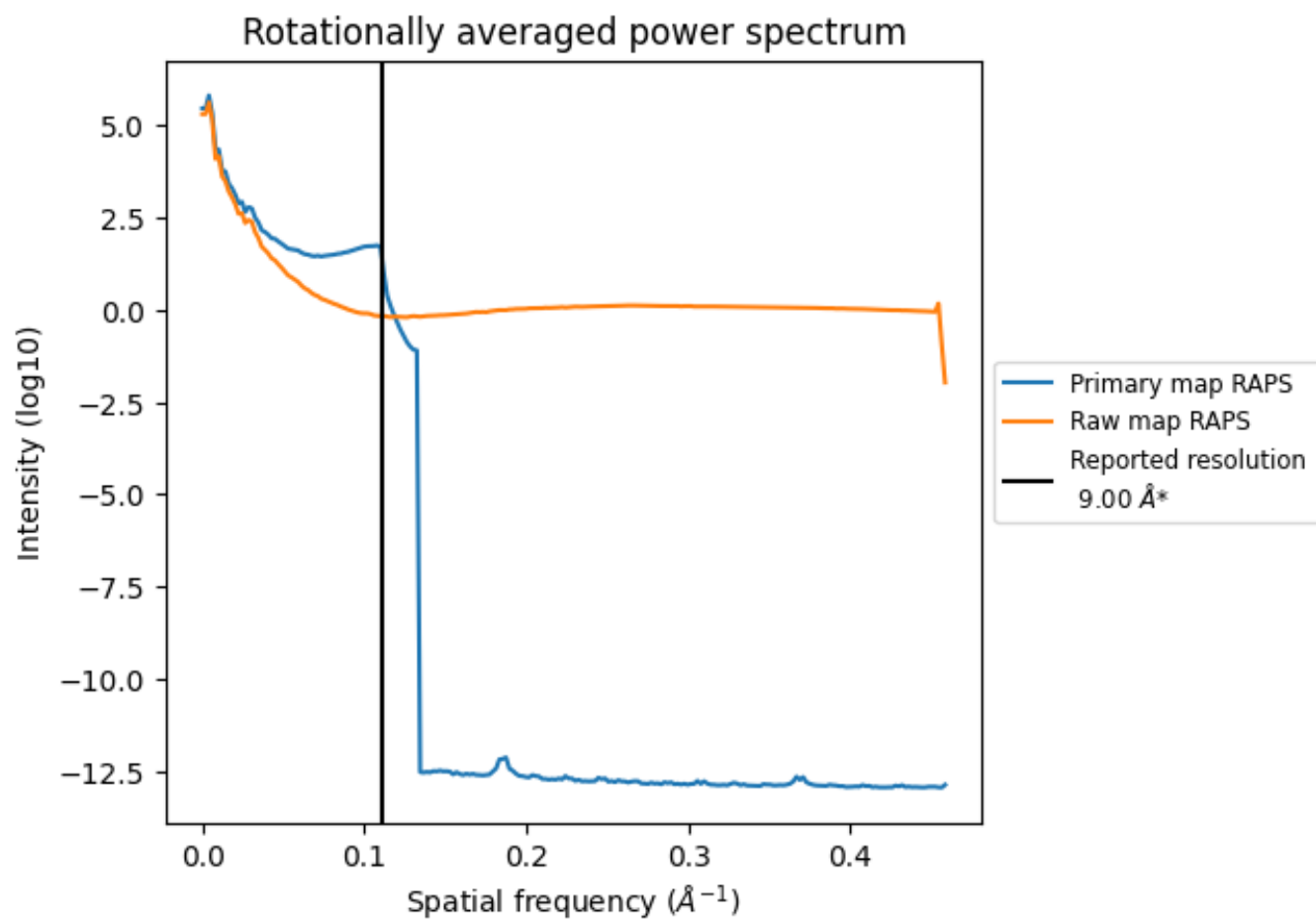
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 304 nm³; this corresponds to an approximate mass of 275 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 [i](#)

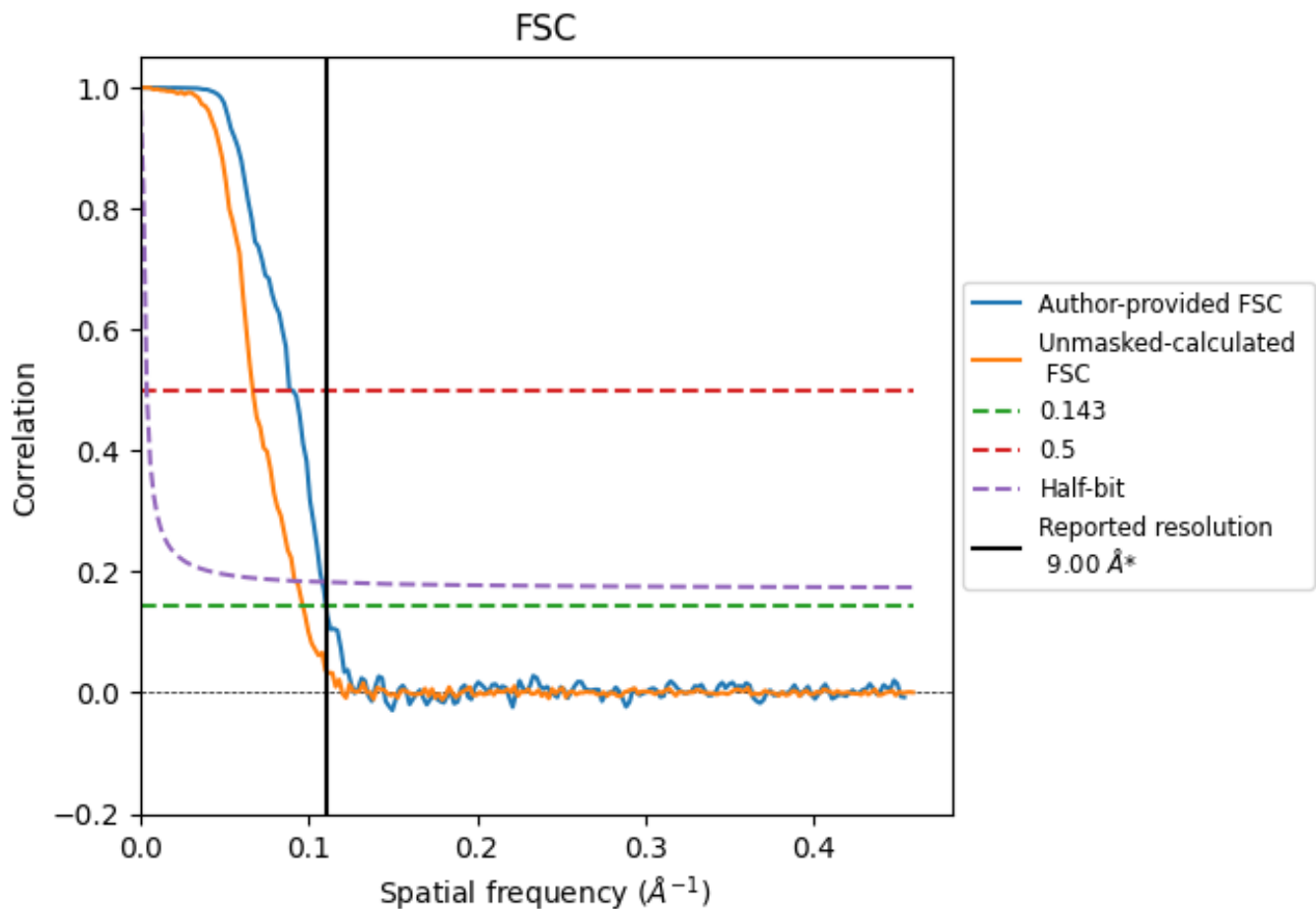


*Reported resolution corresponds to spatial frequency of 0.111 Å⁻¹

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 0.111 Å⁻¹

8.2 Resolution estimates [i](#)

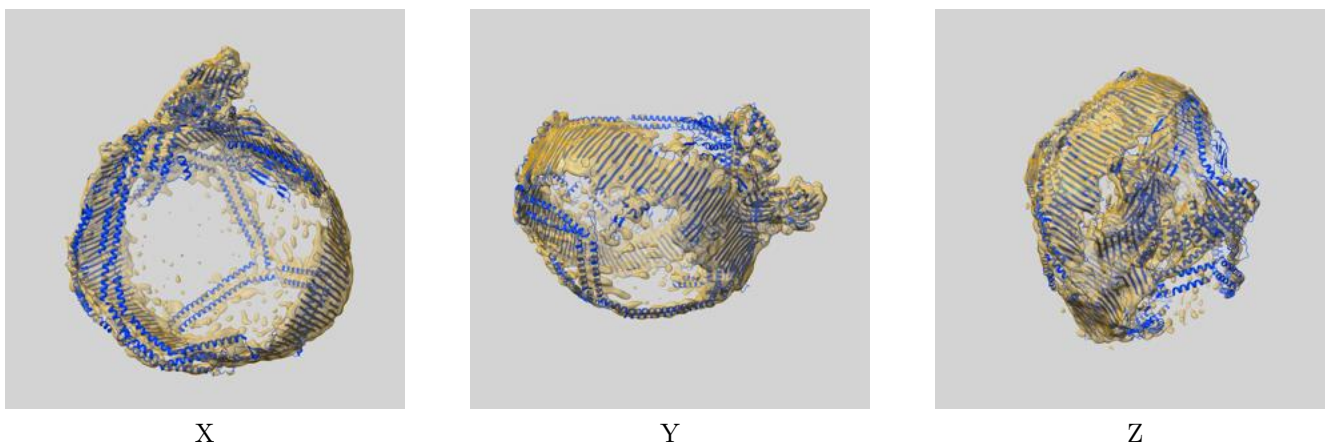
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.00	-	-
Author-provided FSC curve	9.06	11.27	9.24
Unmasked-calculated*	10.34	14.93	10.85

*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 10.34 differs from the reported value 9.0 by more than 10 %

9 Map-model fit [i](#)

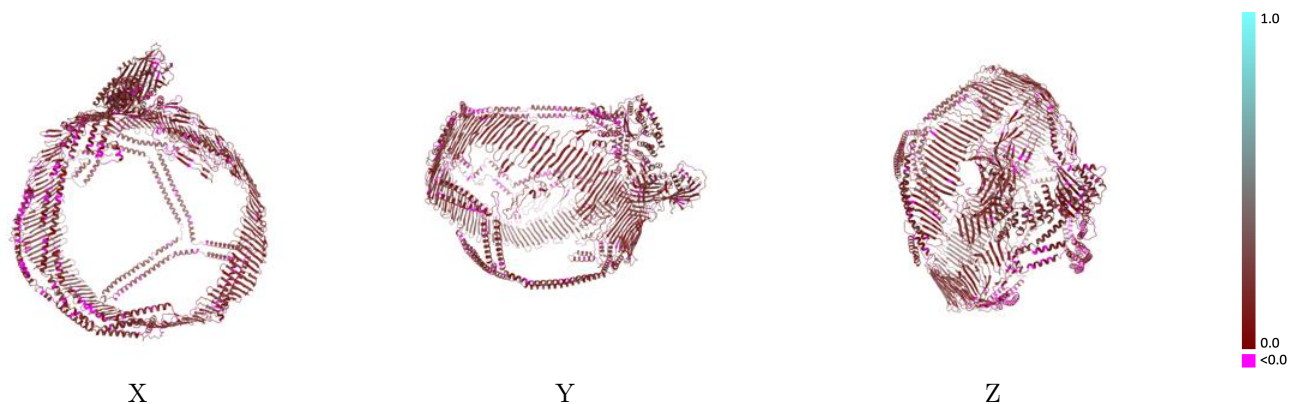
This section contains information regarding the fit between EMDB map EMD-47801 and PDB model 9EAG. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)



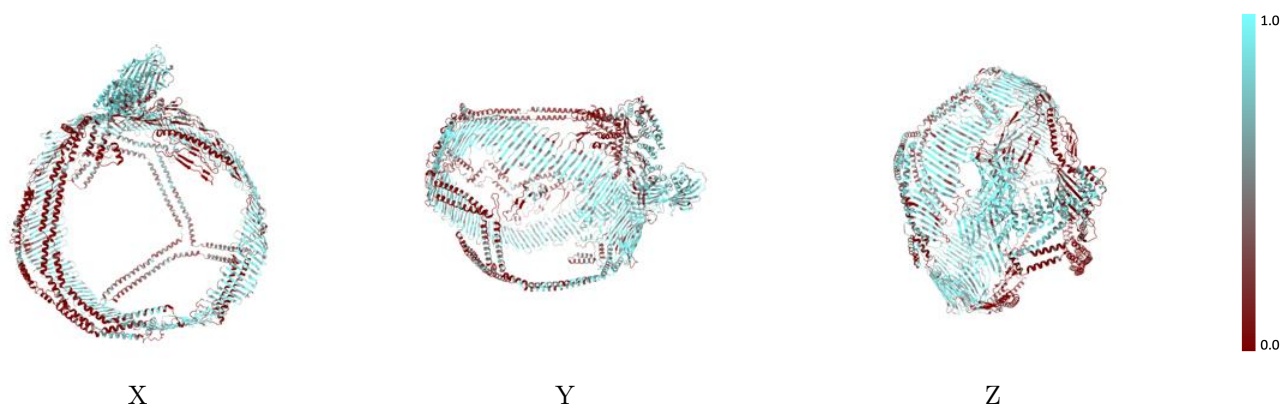
The images above show the 3D surface view of the map at the recommended contour level 0.182 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



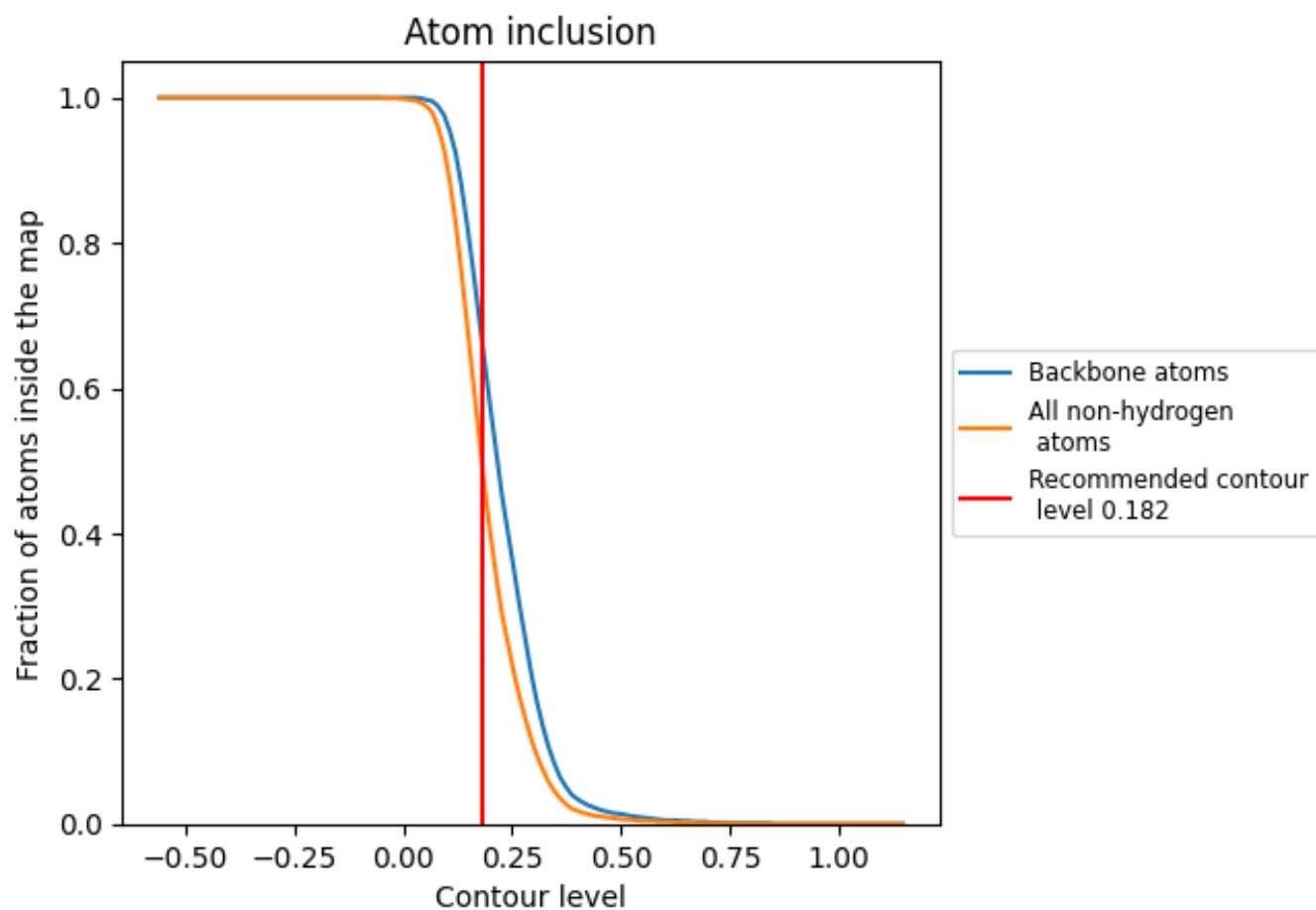
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.182).





9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 49% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.182) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4900	 0.1570
A	 0.4900	 0.1570

