



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 07:23 PM UTC

PDB ID : 4BTG / pdb_00004btg
EMDB ID : EMD-2364
Title : Coordinates of the bacteriophage phi6 capsid subunits (P1A and P1B) fitted into the cryoEM reconstruction of the procapsid at 4.4 Å resolution
Authors : Nemecek, D.; Boura, E.; Wu, W.; Cheng, N.; Plevka, P.; Qiao, J.; Mindich, L.; Heymann, J.B.; Hurley, J.H.; Steven, A.C.
Deposited on : 2013-06-17
Resolution : 4.40 Å (reported)
Based on initial model : 4K7H

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

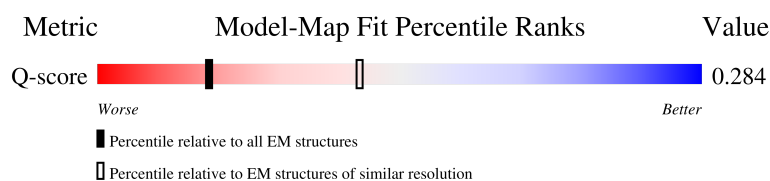
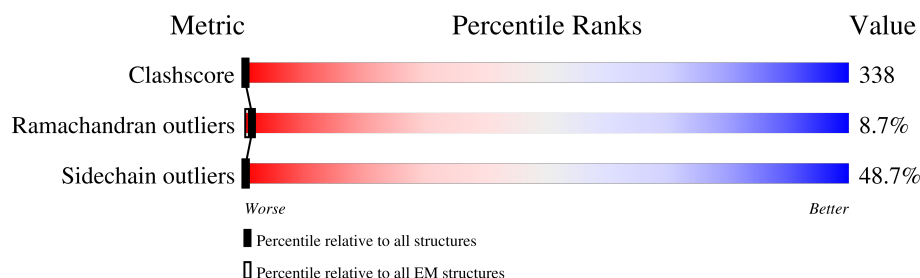
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.40 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	3132 (3.91 - 4.90)

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	761	
1	B	761	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 11840 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 MAJOR INNER PROTEIN P1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	761	Total	C	N	O	S	0	0
			5920	3741	1048	1109	22		
1	B	761	Total	C	N	O	S	0	0
			5920	3741	1048	1109	22		

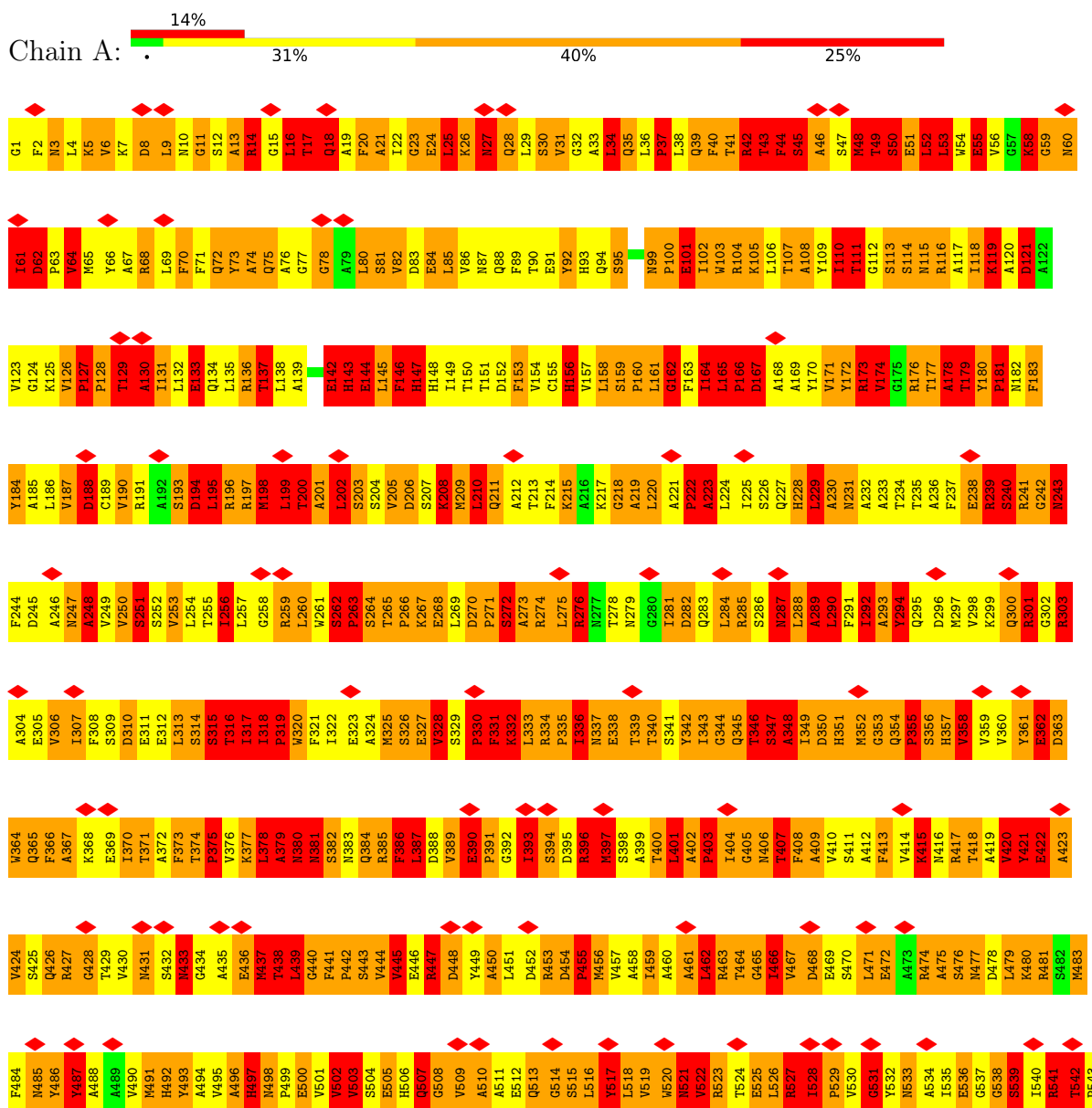
There are 2 discrepancies between the modelled and reference sequences:

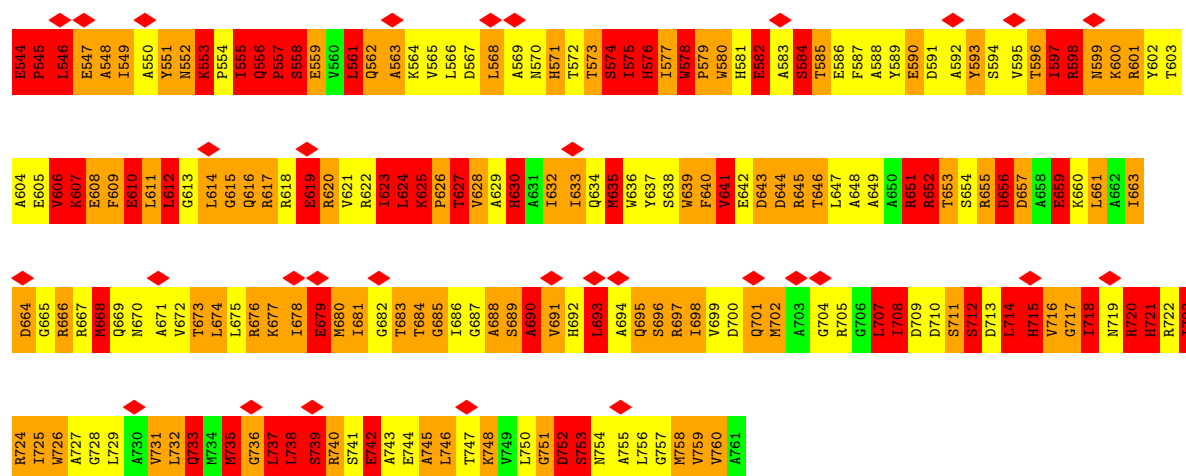
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP P11126
B	1	GLY	-	expression tag	UNP P11126

3 Residue-property plots

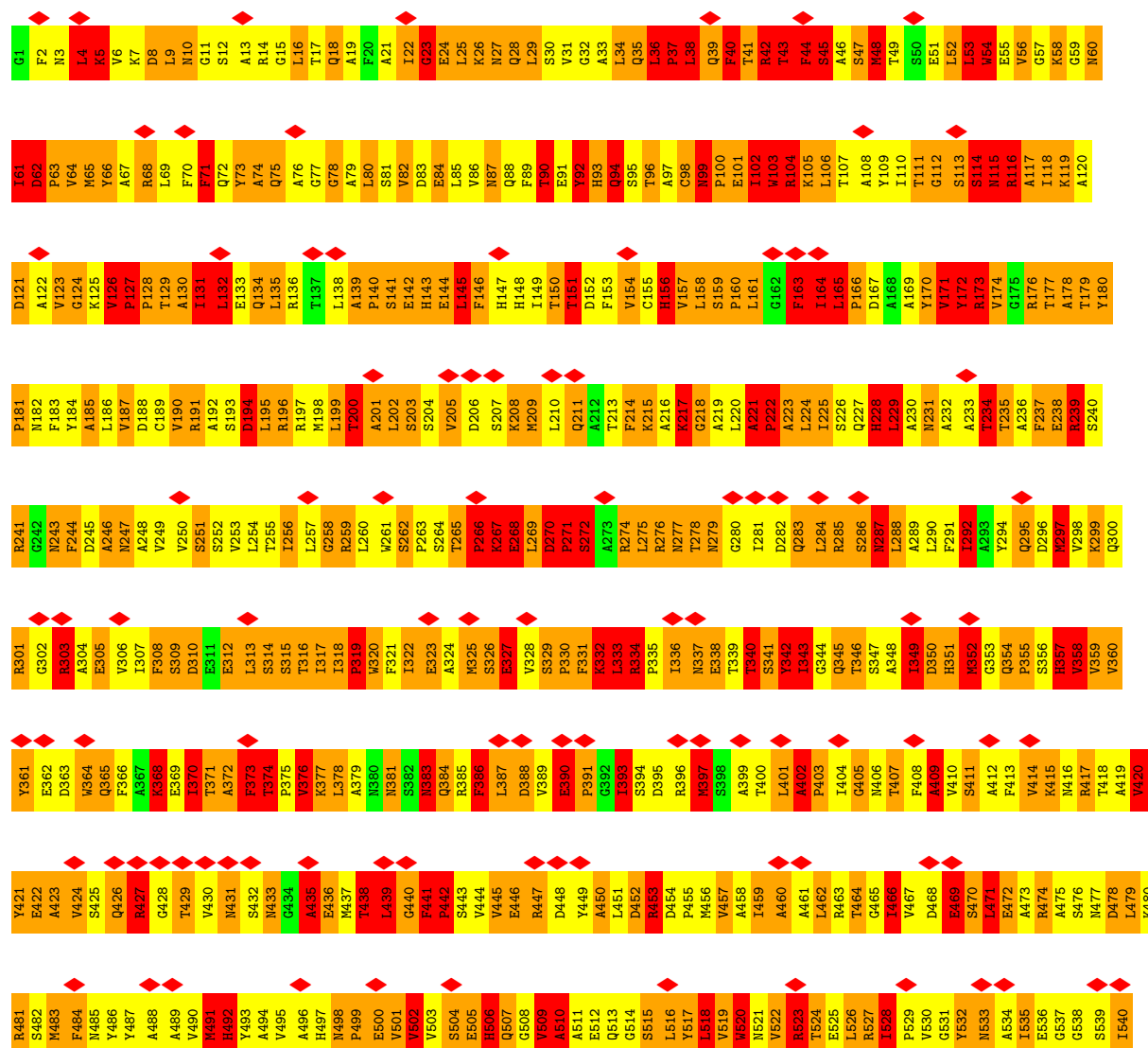
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: MAJOR INNER PROTEIN P1





• Molecule 1: MAJOR INNER PROTEIN P1



H721	R541	R601	L661	H726	R547	R607	L666	H729	R552	R613	L674	H730	R553	R614	L677	H731	R554	R615	L678	H732	R555	R616	L679	H733	R556	R617	L680	H734	R557	R618	L681	H735	R558	R619	L682	H736	R559	R620	L683	H737	R560	R621	L684	H738	R561	R622	L685	H739	R562	R623	L686	H740	R563	R624	L687	H741	R564	R625	L688	H742	R565	R626	L689	H743	R566	R627	L690	H744	R567	R628	L691	H745	R568	R629	L692	H746	R569	R630	L693	H747	R570	R631	L694	H748	R571	R632	L695	H749	R572	R633	L696	H750	R573	R634	L697	H751	R574	R635	L698	H752	R575	R636	L699	H753	R576	R637	L700	H754	R577	R638	L701	H755	R578	R639	L702	H756	R579	R640	L703	H757	R580	R641	L704	H758	R581	R642	L705	H759	R582	R643	L706	H760	R583	R644	L707	H761	R584	R645	L708	R585	R646	L709	R586	R647	L710	R587	R648	L711	R588	R649	L712	R589	R650	L713	R590	R651	L714	R591	R652	L715	R592	R653	L716	R593	R654	L717	R594	R655	L718	R595	R656	L719	R596	R657	L720	R597	R658	L721	R598	R659	L722	R599	R660	L723	R600	L724	R601	L725	R602	L726	R603	L727	R604	L728	R605	L729	R606	L730	R607	L731	R608	L732	R609	L733	R610	L734	R611	L735	R612	L736	R613	L737	R614	L738	R615	L739	R616	L740	R617	L741	R618	L742	R619	L743	R620	L744	R621	L745	R622	L746	R623	L747	R624	L748	R625	L749	R626	L750	R627	L751	R628	L752	R629	L753	R630	L754	R631	L755	R632	L756	R633	L757	R634	L758	R635	L759	R636	L760	R637	L761	R638	L762	R639	L763	R640	L764	R641	L765	R642	L766	R643	L767	R644	L768	R645	L769	R646	L770	R647	L771	R648	L772	R649	L773	R650	L774	R651	L775	R652	L776	R653	L777	R654	L778	R655	L779	R656	L780	R657	L781	R658	L782	R659	L783	R660	L784	R661	L785	R662	L786	R663	L787	R664	L788	R665	L789	R666	L790	R667	L791	R668	L792	R669	L793	R670	L794	R671	L795	R672	L796	R673	L797	R674	L798	R675	L799	R676	L800	R677	L801	R678	L802	R679	L803	R680	L804	R681	L805	R682	L806	R683	L807	R684	L808	R685	L809	R686	L810	R687	L811	R688	L812	R689	L813	R690	L814	R691	L815	R692	L816	R693	L817	R694	L818	R695	L819	R696	L820	R697	L821	R698	L822	R699	L823	R700	L824	R701	L825	R702	L826	R703	L827	R704	L828	R705	L829	R706	L830	R707	L831	R708	L832	R709	L833	R710	L834	R711	L835	R712	L836	R713	L837	R714	L838	R715	L839	R716	L840	R717	L841	R718	L842	R719	L843	R720	L844	R721	L845	R722	L846	R723	L847	R724	L848	R725	L849	R726	L850	R727	L851	R728	L852	R729	L853	R730	L854	R731	L855	R732	L856	R733	L857	R734	L858	R735	L859	R736	L860	R737	L861	R738	L862	R739	L863	R740	L864	R741	L865	R742	L866	R743	L867	R744	L868	R745	L869	R746	L870	R747	L871	R748	L872	R749	L873	R750	L874	R751	L875	R752	L876	R753	L877	R754	L878	R755	L879	R756	L880	R757	L881	R758	L882	R759	L883	R760	L884	R761	L885	R762	L886	R763	L887	R764	L888	R765	L889	R766	L890	R767	L891	R768	L892	R769	L893	R770	L894	R771	L895	R772	L896	R773	L897	R774	L898	R775	L899	R776	L900	R777	L901	R778	L902	R779	L903	R780	L904	R781	L905	R782	L906	R783	L907	R784	L908	R785	L909	R786	L910	R787	L911	R788	L912	R789	L913	R790	L914	R791	L915	R792	L916	R793	L917	R794	L918	R795	L919	R796	L920	R797	L921	R798	L922	R799	L923	R800	L924	R801	L925	R802	L926	R803	L927	R804	L928	R805	L929	R806	L930	R807	L931	R808	L932	R809	L933	R810	L934	R811	L935	R812	L936	R813	L937	R814	L938	R815	L939	R816	L940	R817	L941	R818	L942	R819	L943	R820	L944	R821	L945	R822	L946	R823	L947	R824	L948	R825	L949	R826	L950	R827	L951	R828	L952	R829	L953	R830	L954	R831	L955	R832	L956	R833	L957	R834	L958	R835	L959	R836	L960	R837	L961	R838	L962	R839	L963	R840	L964	R841	L965	R842	L966	R843	L967	R844	L968	R845	L969	R850	L970	R851	L971	R852	L972	R853	L973	R854	L974	R855	L975	R856	L976	R857	L977	R858	L978	R859	L979	R860	L980	R861	L981	R862	L982	R863	L983	R864	L984	R865	L985	R866	L986	R867	L987	R868	L988	R869	L989	R870	L990	R871	L991	R872	L992	R873	L993	R874	L994	R875	L995	R876	L996	R877	L997	R878	L998	R879	L999	R880	L1000	R881	L1001	R882	L1002	R883	L1003	R884	L1004	R885	L1005	R886	L1006	R887	L1007	R888	L1008	R889	L1009	R890	L1010	R891	L1011	R892	L1012	R893	L1013	R894	L1014	R895	L1015	R896	L1016	R897	L1017	R898	L1018	R899	L1019	R900	L1020	R901	L1021	R902	L1022	R903	L1023	R904	L1024	R905	L1025	R906	L1026	R907	L1027	R908	L1028	R909	L1029	R910	L1030	R911	L1031	R912	L1032	R913	L1033	R914	L1034	R915	L1035	R916	L1036	R917	L1037	R918	L1038	R919	L1039	R920	L1040	R921	L1041	R922	L1042	R923	L1043	R924	L1044	R925	L1045	R926	L1046	R927	L1047	R928	L1048	R929	L1049	R930	L1050	R931	L1051	R932	L1052	R933	L1053	R934	L1054	R935	L1055	R936	L1056	R937	L1057	R938	L1058	R939	L1059	R940	L1060	R941	L1061	R942	L1062	R943	L1063	R944	L1064	R945	L1065	R946	L1066	R947	L1067	R948	L1068	R949	L1069	R950	L1070	R951	L1071	R952	L1072	R953	L1073	R954	L1074	R955	L1075	R956	L1076	R957	L1077	R958	L1078	R959	L1079	R960	L1080	R961	L1081	R962	L1082	R963	L1083	R964	L1084	R965	L1085	R966	L1086	R967	L1087	R968	L1088	R969	L1089	R970	L1090	R971	L1091	R972	L1092	R973	L1093	R974	L1094	R975	L1095	R976	L1096	R977	L1097	R978	L1098	R979	L1099	R980	L1100	R981	L1101	R982	L1102	R983	L1103	R984	L1104	R985	L1105	R986	L1106	R987	L1107	R988	L1108	R989	L1109	R990	L1110	R991	L1111	R992	L1112	R993	L1113	R994	L1114	R995	L1115	R996	L1116	R997	L1117	R998	L1118	R999	L1119	R1000	L1120	R1001	L1121	R1002	L1122	R1003	L1123	R1004	L1124	R1005	L1125	R1006	L1126	R1007	L1127	R1008	L1128	R1009	L1129	R1010	L1130	R1011	L1131	R1012	L1132	R1013	L1133	R1014	L1134	R1015	L1135	R1016	L1136	R1017	L1137	R1018	L1138	R1019	L1139	R1020	L1140	R1021	L1141	R1022	L1142	R1023	L1143	R1024	L1144	R1025	L1145	R1026	L1146	R1027	L1147	R1028	L1148	R1029	L1149	R1030	L1150	R1031	L1151	R1032	L1152	R1033	L1153	R1034	L1154	R1035	L1155	R1036	L1156	R1037	L1157	R1038	L1158	R1039	L1159	R1040	L1160	R1041	L1161	R1042	L1162	R1043	L1163	R1044	L1164	R1045	L1165	R1046	L1166	R1047	L1167	R1048	L1168	R1049	L1169	R1050	L1170	R1051	L1171	R1052	L1172	R1053	L1173	R1054	L1174	R1055	L1175	R1056	L1176	R1057	L1177	R1058	L1178	R1059	L1179	R1060	L1180	R1061	L1181	R1062	L1182	R1063	L1183	R1064	L1184	R1065	L1185	R1066	L1186	R1067	L1187	R1068	L1188	R1069	L1189	R1070	L1190	R1071	L1191	R1072	L1192	R1073	L1193	R1074	L1194	R1075	L1195	R1076	L1196	R1077	L1197	R1078	L1198	R1079	L1199	R1080	L1200	R1081	L1201	R1082	L1202	R1083	L1203	R1084	L1204	R1085	L1205	R1086	L1206	R1087	L1207	R1088	L1208	R1089	L1209	R1090	L1210	R1091	L1211	R1092	L1212	R1093	L1213	R1094	L1214	R1095	L1215	R1096	L1216	R1097	L1217	R1098	L1218	R1099	L1219	R1100	L1220	R1101	L1221	R1102	L1222	R1103	L1223	R1104	L1224	R1105	L1225	R1106	L1226	R1107	L1227	R1108	L1228	R1109	L1229	R1110	L1230	R1111	L1231	R1112	L1232	R1113	L1233	R1114	L1234	R1115	L1235	R1116	L1236	R1117	L1237	R1118	L1238	R1119	L1239	R1120	L1240	R1121	L1241	R1122	L1242	R1123	L1243	R1124	L1244	R1125	L1245	R1126	L1246	R1127	L1247	R1128	L1248	R1129	L1249	R1130	L1250	R1131	L1251	R1132	L1252	R1133	L1253	R1134	L1254	R1135	L1255	R1136	L1256	R1137	L1257	R1138	L1258	R1139	L1259	R1140	L1260	R1141	L1261	R1142	L1262	R1143	L1263	R1144	L1264	R1145	L1265	R1146	L1266	R1147	L1267	R1148	L1268	R1149	L1269	R1150	L1270	R1151	L1271	R1152	L1272	R1153	L1273	R1154	L1274	R1155	L1275	R1156	L1276	R1157	L1277	R1158	L1278	R1159	L1279	R1160	L1280	R1161	L1281	R1162	L1282	R1163	L1283	R1164	L1284	R1165	L1285	R1166	L1286	R1167	L1287	R1168	L1288	R1169	L1289	R1170	L1290	R1171	L1291	R1172	L1292	R1173	L1293	R1174	L1294	R1175	L1295	R1176	L1296	R1177	L1297	R1178	L1298	R1179	L1299	R1180	L1300	R1181	L1301	R1182	L1302	R1183	L1303	R1184	L1304	R1185	L1305	R1186	L1306	R1187	L1307	R1188	L1308	R1189	L1309	R1190	L1310	R1191	L1311	R1192	L1312	R1193	L1313	R1194	L1314	R1195	L1315	R1196	L1316	R1197	L1317	R1198	L1318	R1199	L1319	R1200	L1320	R1201	L1321	R1202	L1322	R1203	L1323	R1204	L1324	R1205	L1325	R1206	L1326	R1207	L1327	R1208	L1328	R1209	L1329	R1210	L1330	R1211	L1331	R1212	L1332	R1213	L1333	R1214	L1334	R1215	L1335	R1216	L1336	R1217	L1337	R1218	L1338	R1219	L1339	R1220	L1340	R1221	L1341	R1222	L1342	R1223	L1343	R1224	L1344	R1225	L1345	R1226	L1346	R1227	L1347	R1228	L1348	R1229	L1349	R1230	L1350	R1231	L1351	R1232	L1352	R1233	L1353	R1234	L1354	R1235	L1355	R1236	L1356	R1237	L1357	R1238	L1358	R1239
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	18326	Depositor
Resolution determination method	Not provided	
CTF correction method	PARTICLES FROM EACH MICRO-GRAPH	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	15	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	44739	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	21.125	Depositor
Minimum map value	-8.041	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2	Depositor
Map size ($\text{\AA}$)	586.74, 586.74, 586.74	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.397, 1.397, 1.397	Depositor

5 Model quality

5.1 Standard geometry

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	1.85	128/6038 (2.1%)	2.27	402/8200 (4.9%)
1	B	1.58	61/6039 (1.0%)	1.99	284/8203 (3.5%)
All	All	1.72	189/12077 (1.6%)	2.13	686/16403 (4.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	67
1	B	0	45
All	All	0	112

The worst 5 of 189 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	127	PRO	C-N	74.32	1.91	1.33
1	A	466	ILE	C-N	-61.06	0.50	1.33
1	A	437	MET	C-N	19.50	1.61	1.33
1	A	75	GLN	CA-CB	-14.19	1.29	1.53
1	B	172	TYR	CA-C	12.97	1.70	1.53

The worst 5 of 686 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	441	PHE	C-N-CD	-26.13	17.89	125.00
1	A	542	THR	CA-C-N	-22.22	89.63	120.96
1	A	542	THR	C-N-CA	-22.22	89.63	120.96
1	B	127	PRO	CA-C-N	-20.18	97.94	120.94
1	B	127	PRO	C-N-CA	-20.18	97.94	120.94

There are no chirality outliers.

5 of 112 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	23	GLY	Peptide
1	A	25	LEU	Peptide
1	A	34	LEU	Peptide
1	A	52	LEU	Peptide
1	A	60	ASN	Peptide

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	5920	0	5870	3872	0
1	B	5920	0	5883	4136	0
All	All	11840	0	11753	7970	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 338.

The worst 5 of 7970 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:61:ILE:HG22	1:A:156:HIS:CD2	1.18	1.68
1:A:732:LEU:CD1	1:A:738:LEU:HD22	1.23	1.67
1:B:373:PHE:CD2	1:B:583:ALA:HB1	1.31	1.66
1:B:670:ASN:HD21	1:B:749:VAL:CG1	1.07	1.65
1:A:2:PHE:CG	1:A:459:ILE:HG21	1.28	1.65

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	755/761 (99%)	575 (76%)	109 (14%)	71 (9%)	0	8
1	B	757/761 (100%)	591 (78%)	105 (14%)	61 (8%)	1	9
All	All	1512/1522 (99%)	1166 (77%)	214 (14%)	132 (9%)	1	8

5 of 132 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	34	LEU
1	A	61	ILE
1	A	119	LYS
1	A	123	VAL
1	A	144	GLU

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	629/629 (100%)	335 (53%)	294 (47%)	0	0
1	B	629/629 (100%)	310 (49%)	319 (51%)	0	0
All	All	1258/1258 (100%)	645 (51%)	613 (49%)	0	0

5 of 613 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	397	MET
1	B	661	LEU
1	B	433	ASN
1	B	393	ILE
1	B	533	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	156	HIS
1	B	295	GLN
1	B	634	GLN
1	B	182	ASN
1	B	231	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	5
1	B	2

The worst 5 of 7 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	51:GLU	C	52:LEU	N	2.98
1	A	357:HIS	C	358:VAL	N	2.72

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	336:ILE	C	337:ASN	N	2.72
1	B	127:PRO	C	128:PRO	N	1.91
1	A	437:MET	C	438:THR	N	1.61

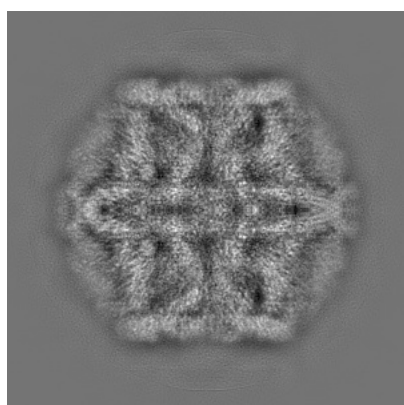
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2364. These allow visual inspection of the internal detail of the map and identification of artifacts.

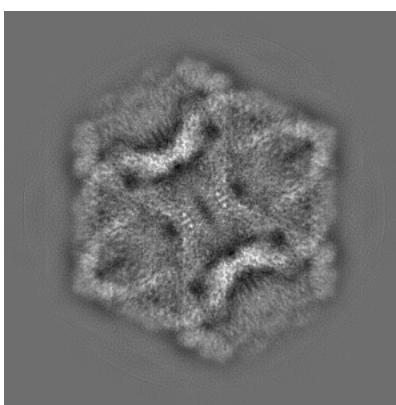
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

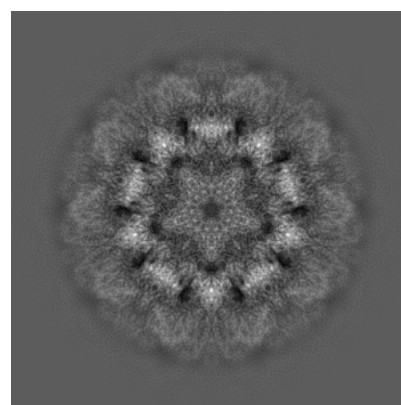
6.1.1 Primary map



X



Y

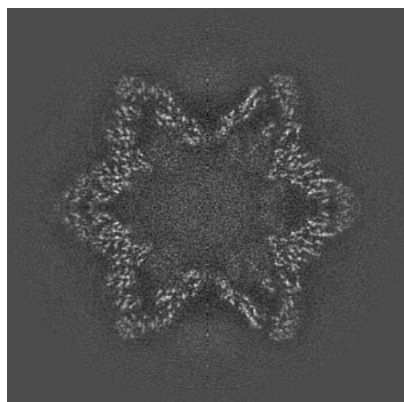


Z

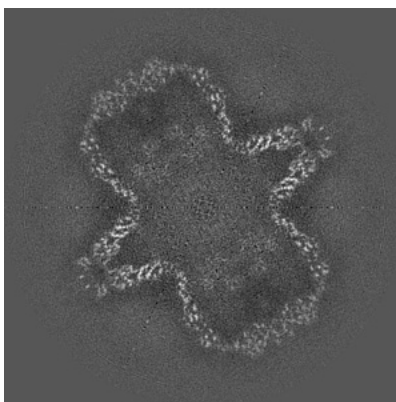
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

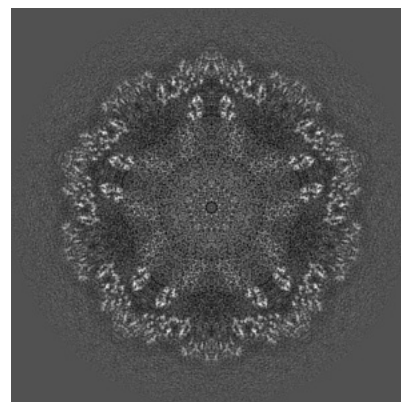
6.2.1 Primary map



X Index: 210



Y Index: 210

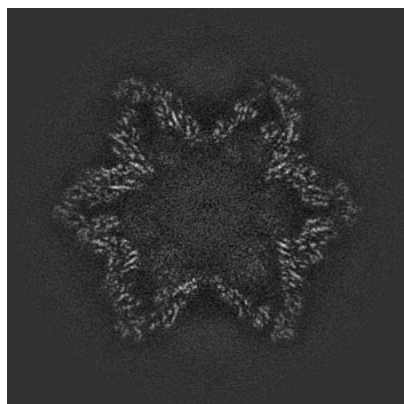


Z Index: 210

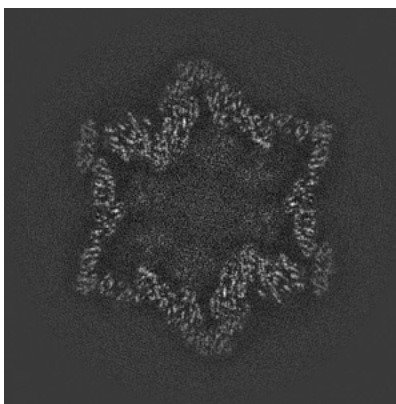
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

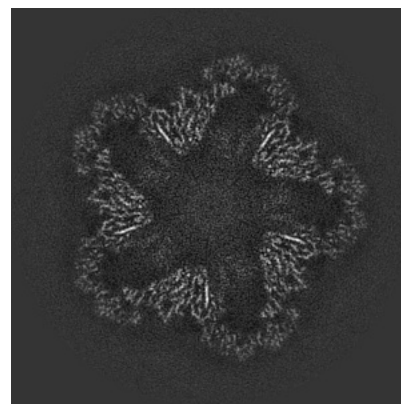
6.3.1 Primary map



X Index: 214



Y Index: 176

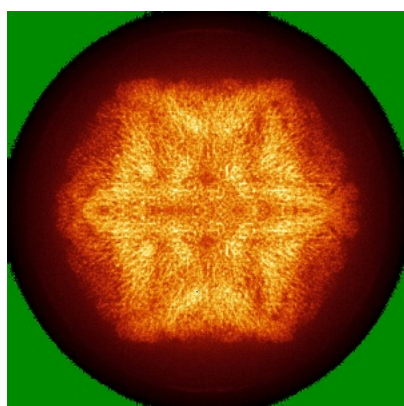


Z Index: 189

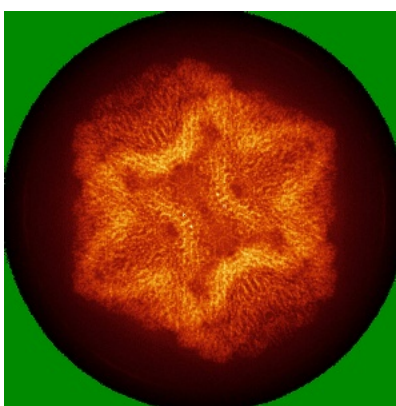
The images above show the largest variance slices of the map in three orthogonal directions.

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

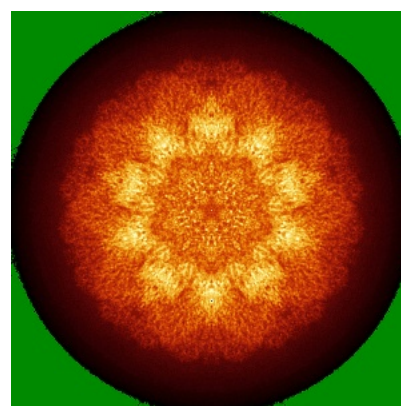
6.4.1 Primary map



X



Y



Z

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 2.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

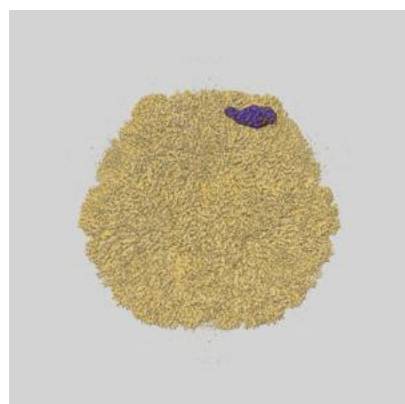
6.6 Mask visualisation [i](#)

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

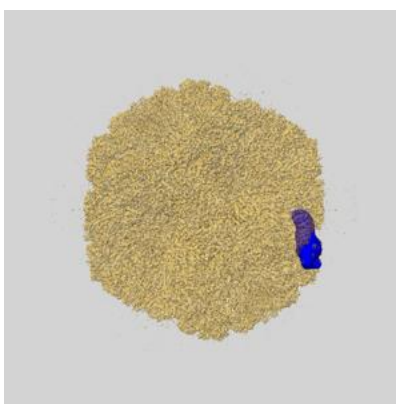
A mask typically either:

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

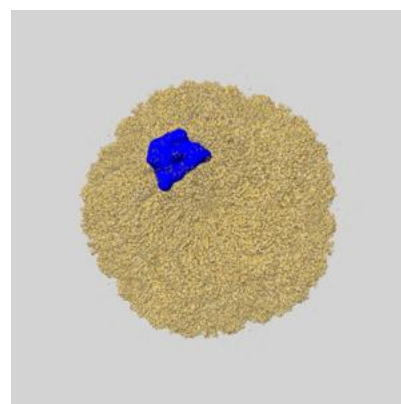
6.6.1 emd_2364_msk_1.map [i](#)



X

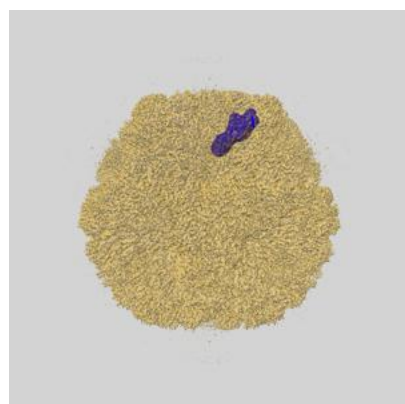


Y

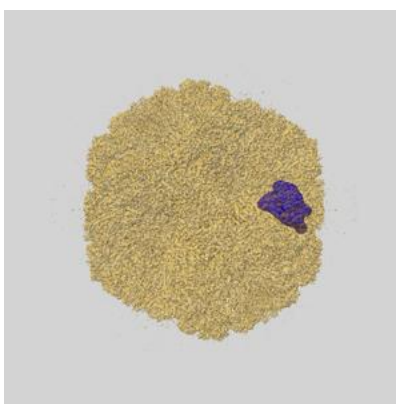


Z

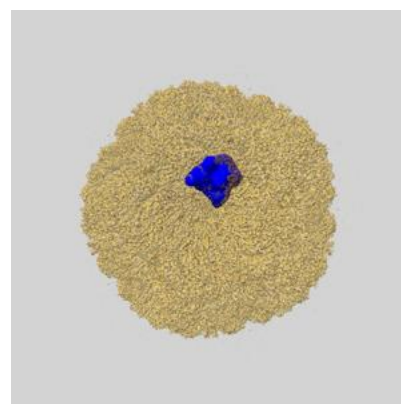
6.6.2 emd_2364_msk_2.map [i](#)



X



Y

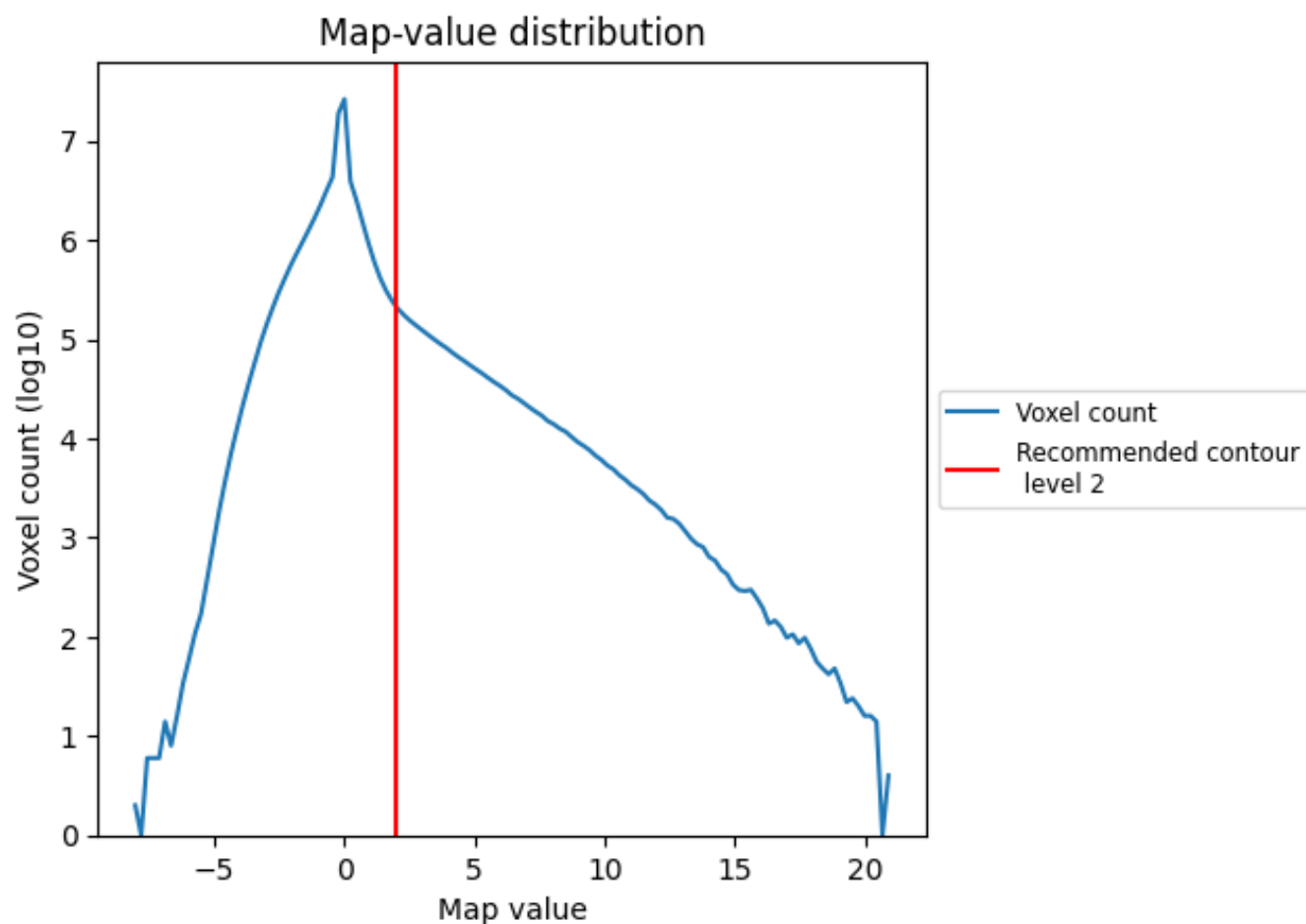


Z

7 Map analysis [i](#)

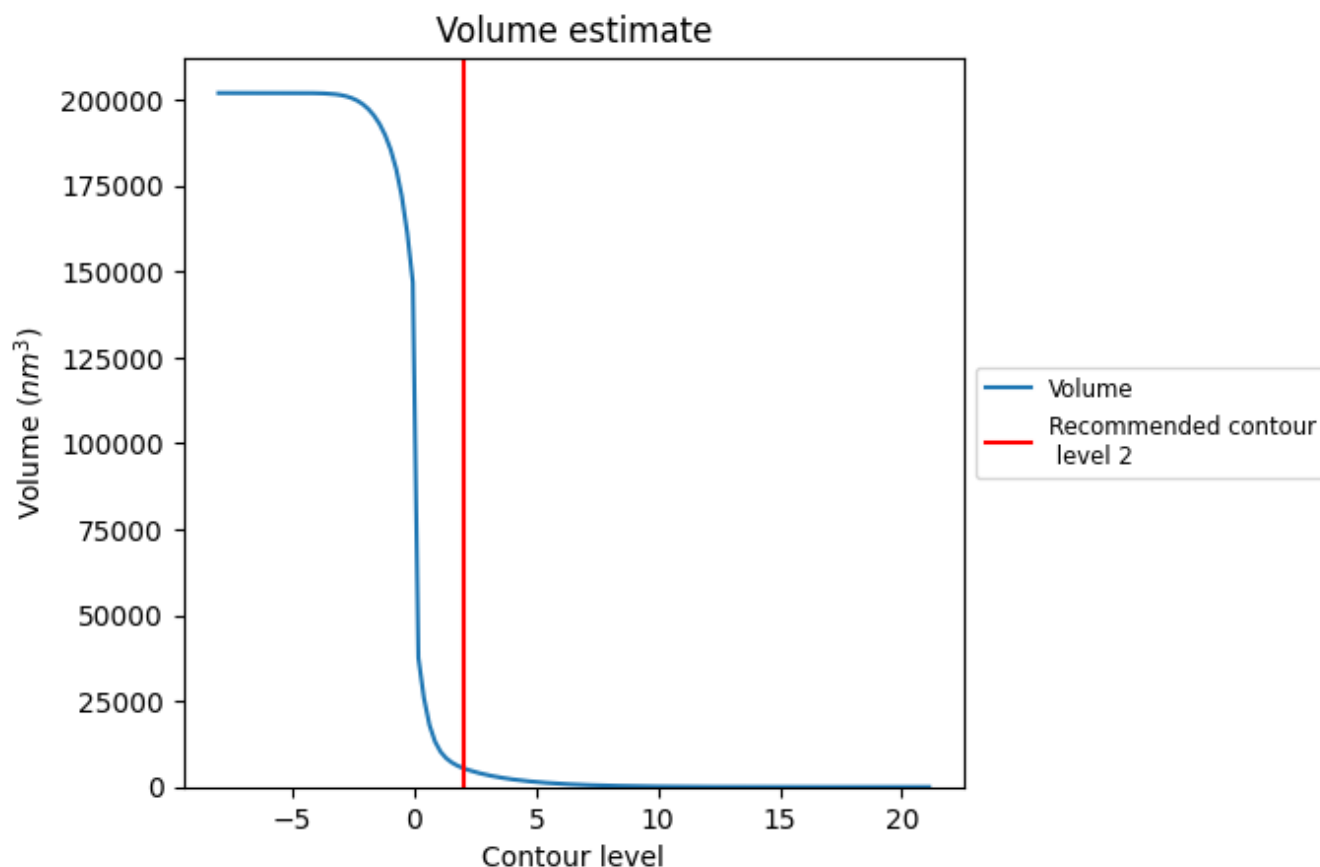
This section contains the results of statistical analysis of the map.

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.

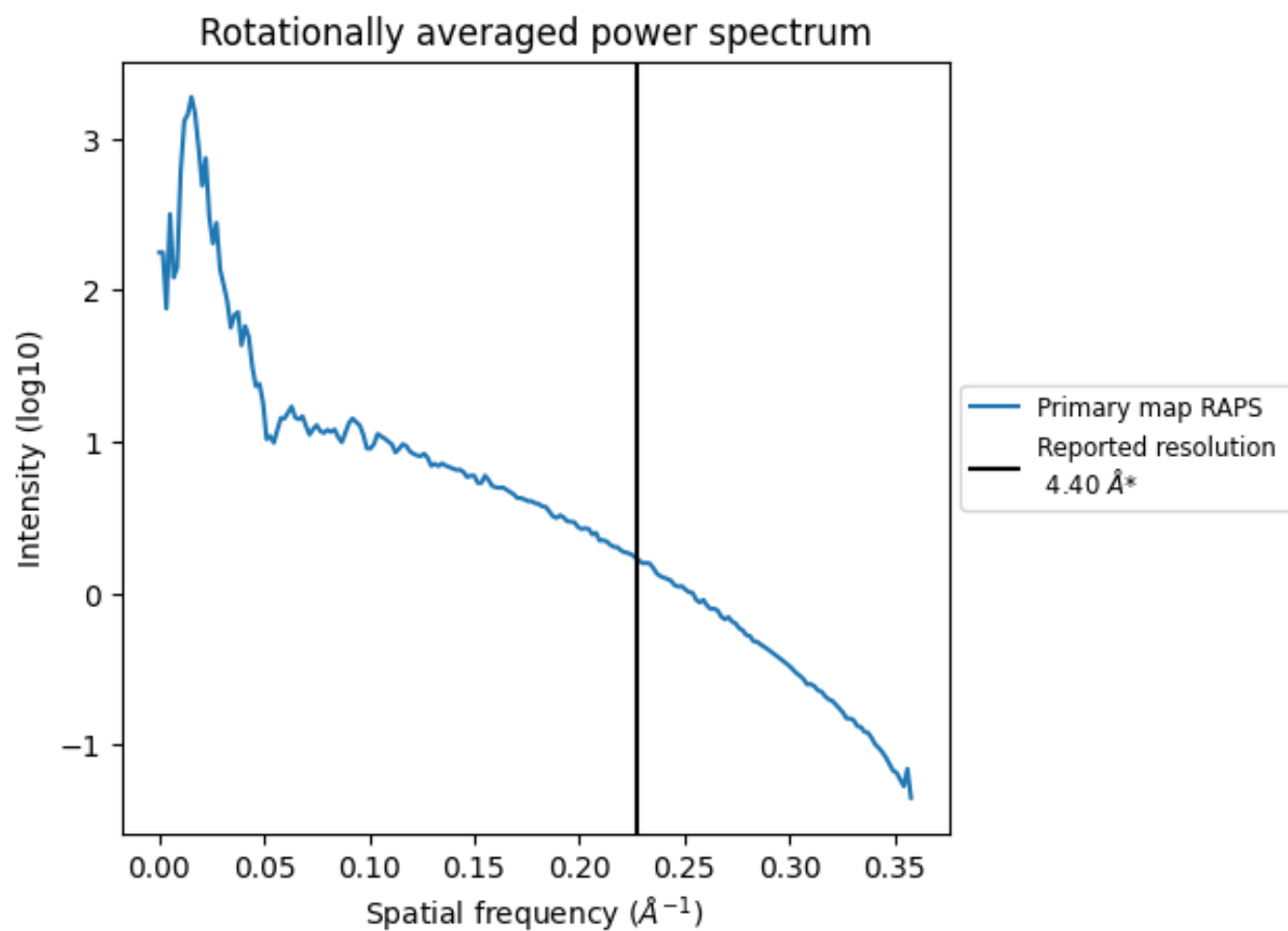
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5485 nm^3 ; this corresponds to an approximate mass of 4954 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 ⓘ

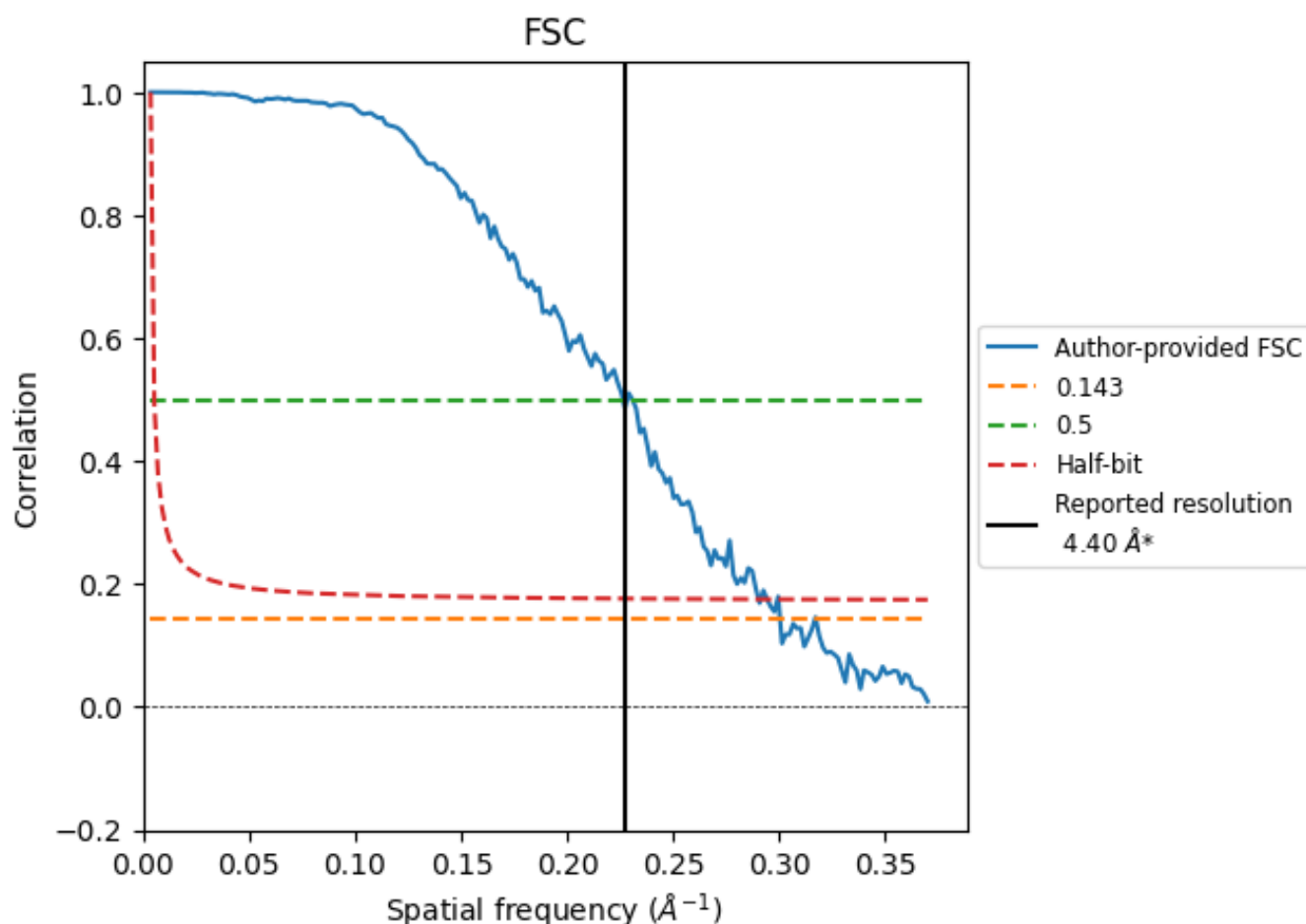


*Reported resolution corresponds to spatial frequency of 0.227 Å⁻¹

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 0.227 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	-	-
Author-provided FSC curve	3.33	4.42	3.44
Unmasked-calculated*	-	-	-

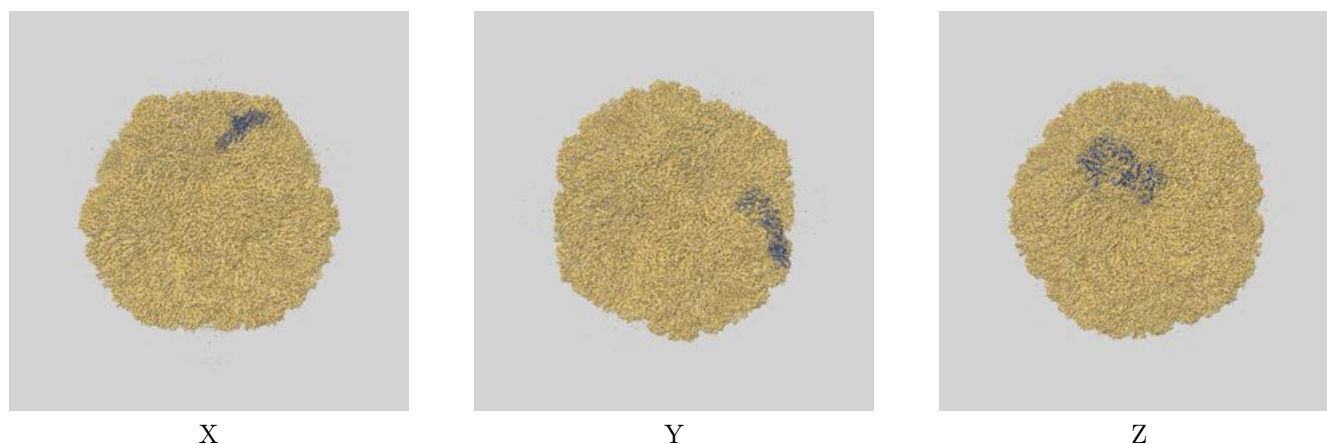
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

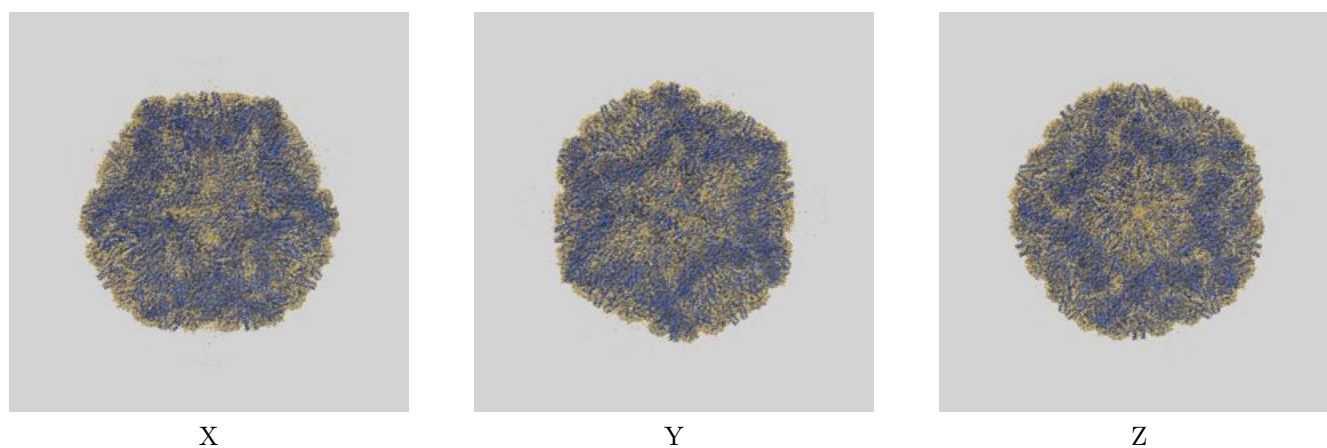
This section contains information regarding the fit between EMDB map EMD-2364 and PDB model 4BTG. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

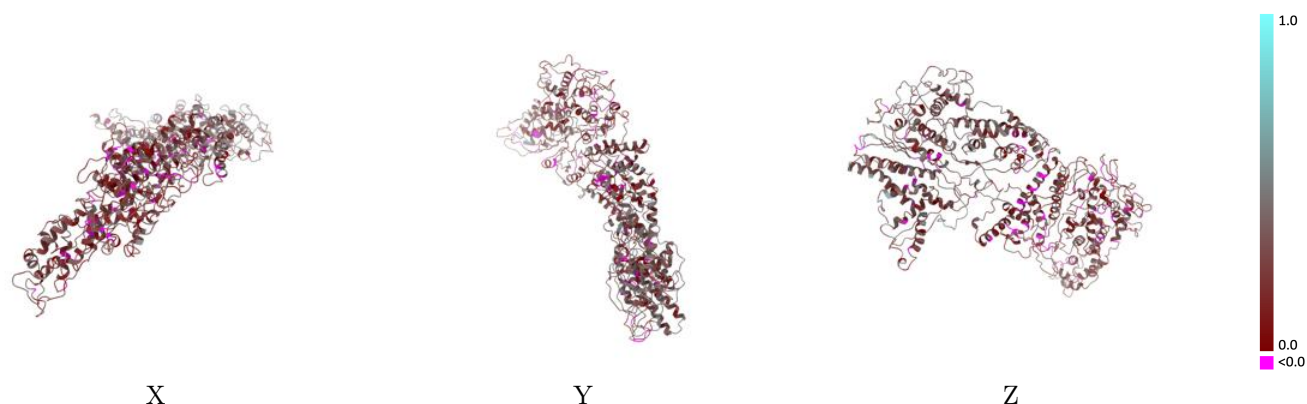


9.1.2 Map-model assembly overlay [i](#)



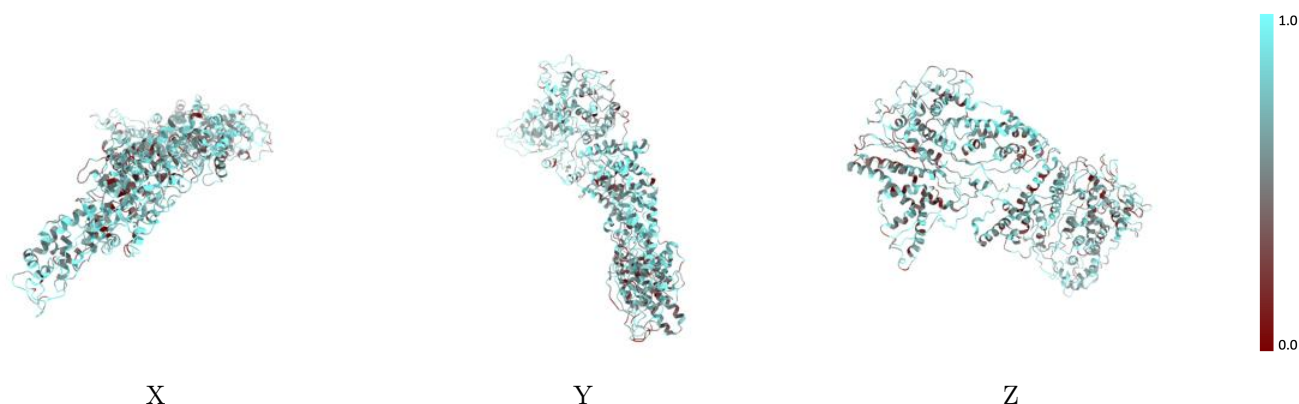
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



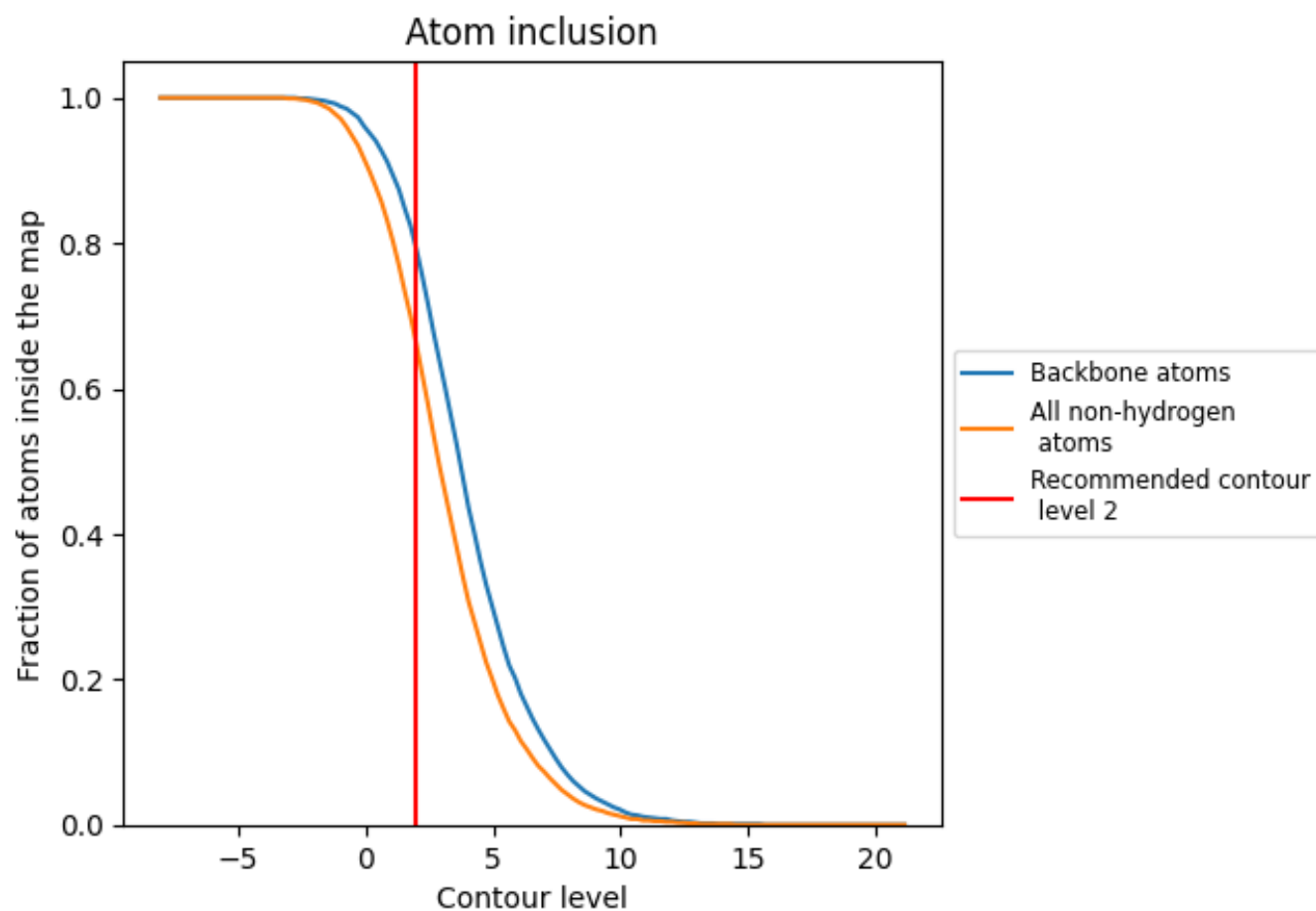
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



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 (2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 66% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6590	0.2840
A	0.6650	0.2390
B	0.6520	0.3280

