



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 10:14 PM UTC

PDB ID : 8ZJK / pdb_00008zjk
EMDB ID : EMD-60148
Title : Structure of DOCK5/ELMO1/Rac1 core (RhoG/DOCK5/ELMO1/Rac1 dataset, class 3)
Authors : Kukimoto-Niino, M.; Katsura, K.; Ishizuka-Katsura, Y.; Mishima-Tsumagari, C.; Yonemochi, M.; Inoue, M.; Nakagawa, R.; Kaushik, R.; Zhang, K.Y.J.; Shirouzu, M.
Deposited on : 2024-05-15
Resolution : 4.23 Å(reported)
Based on initial model : 7DPA

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

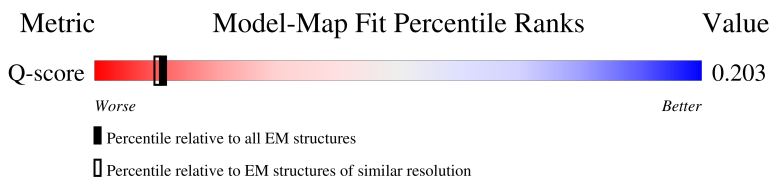
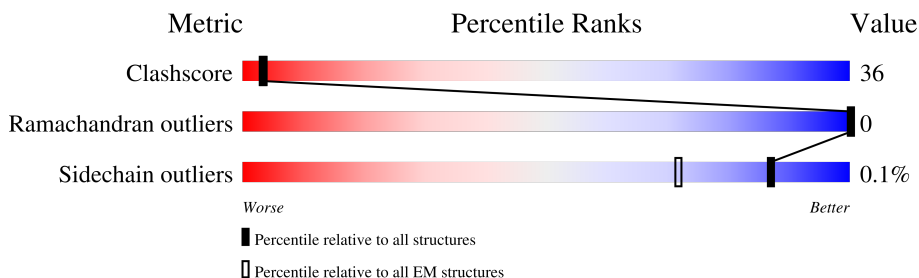
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.23 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	4685 (3.74 - 4.73)

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	733	 10% 17% 73%
1	D	733	 10% 17% 73%
2	B	1648	 7% 40% 60%
2	E	1648	 6% 39% 60%

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Mol	Chain	Length	Quality of chain
3	C	184	 34% 61% . .
3	F	184	 33% 62% . .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 32858 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 Engulfment and cell motility protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	198	Total	C	N	O	S	0	0
			1608	1018	277	303	10		
1	D	198	Total	C	N	O	S	0	0
			1608	1018	277	303	10		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	expression tag	UNP Q92556
A	-4	GLY	-	expression tag	UNP Q92556
A	-3	SER	-	expression tag	UNP Q92556
A	-2	GLY	-	expression tag	UNP Q92556
A	-1	GLY	-	expression tag	UNP Q92556
A	0	SER	-	expression tag	UNP Q92556
D	-5	GLY	-	expression tag	UNP Q92556
D	-4	GLY	-	expression tag	UNP Q92556
D	-3	SER	-	expression tag	UNP Q92556
D	-2	GLY	-	expression tag	UNP Q92556
D	-1	GLY	-	expression tag	UNP Q92556
D	0	SER	-	expression tag	UNP Q92556

- Molecule 2 is a protein called Deducator of cytokinesis protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1642	Total	C	N	O	S	0	0
			13436	8618	2264	2484	70		
2	E	1642	Total	C	N	O	S	0	0
			13436	8618	2264	2484	70		

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	GLY	-	expression tag	UNP Q9H7D0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	GLY	-	expression tag	UNP Q9H7D0
B	-3	SER	-	expression tag	UNP Q9H7D0
B	-2	GLY	-	expression tag	UNP Q9H7D0
B	-1	GLY	-	expression tag	UNP Q9H7D0
B	0	SER	-	expression tag	UNP Q9H7D0
B	1285	ARG	LYS	variant	UNP Q9H7D0
E	-5	GLY	-	expression tag	UNP Q9H7D0
E	-4	GLY	-	expression tag	UNP Q9H7D0
E	-3	SER	-	expression tag	UNP Q9H7D0
E	-2	GLY	-	expression tag	UNP Q9H7D0
E	-1	GLY	-	expression tag	UNP Q9H7D0
E	0	SER	-	expression tag	UNP Q9H7D0
E	1285	ARG	LYS	variant	UNP Q9H7D0

- Molecule 3 is a protein called Ras-related C3 botulinum toxin substrate 1.

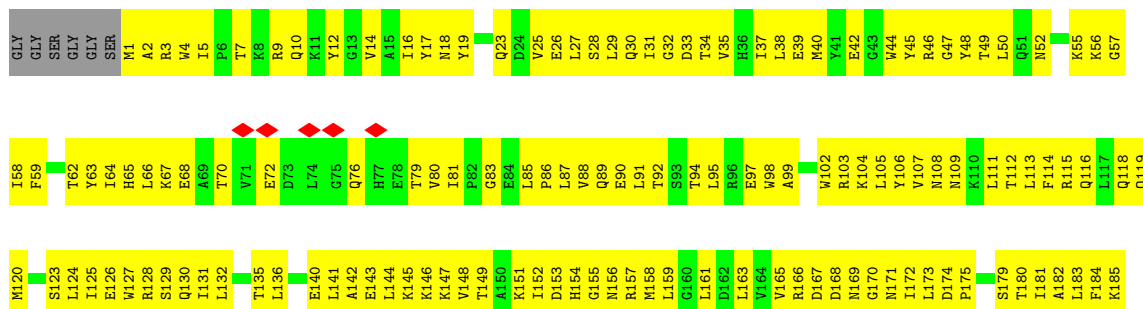
Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	177	Total	C	N	O	S	0	0
			1385	890	228	259	8		
3	F	177	Total	C	N	O	S	0	0
			1385	890	228	259	8		

There are 16 discrepancies between the modelled and reference sequences:

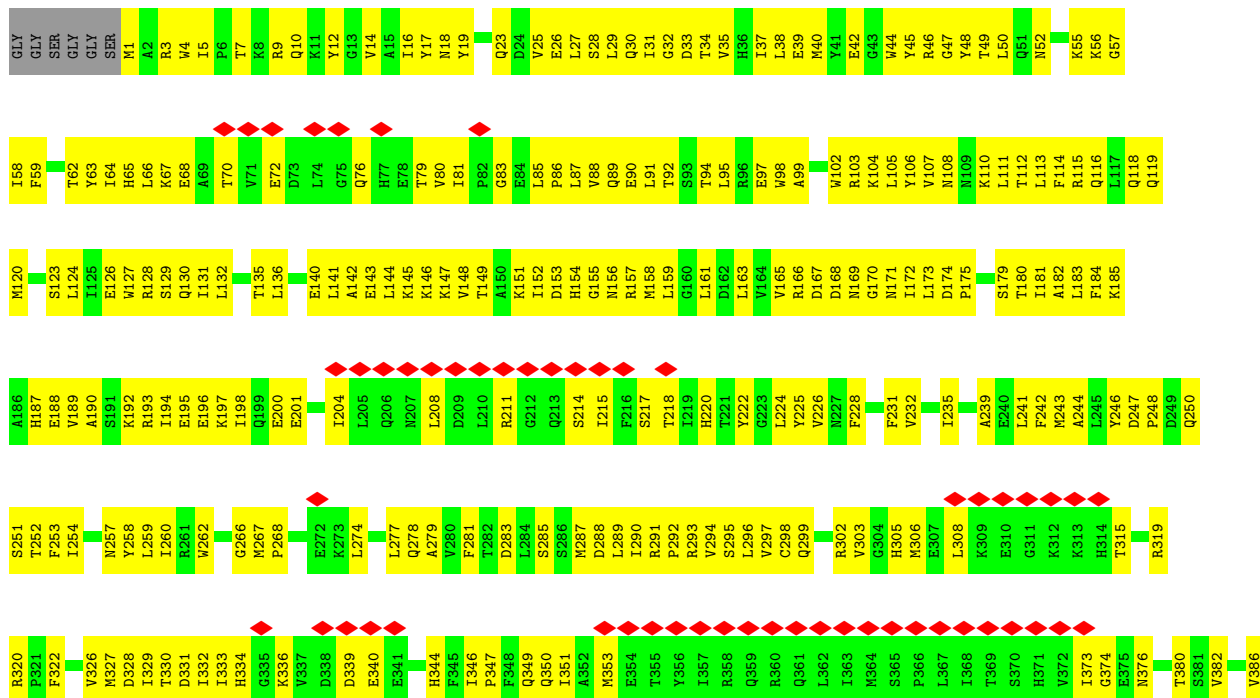
Chain	Residue	Modelled	Actual	Comment	Reference
C	-6	GLY	-	expression tag	UNP P63000
C	-5	SER	-	expression tag	UNP P63000
C	-4	SER	-	expression tag	UNP P63000
C	-3	GLY	-	expression tag	UNP P63000
C	-2	SER	-	expression tag	UNP P63000
C	-1	SER	-	expression tag	UNP P63000
C	0	GLY	-	expression tag	UNP P63000
C	15	ALA	GLY	engineered mutation	UNP P63000
F	-6	GLY	-	expression tag	UNP P63000
F	-5	SER	-	expression tag	UNP P63000
F	-4	SER	-	expression tag	UNP P63000
F	-3	GLY	-	expression tag	UNP P63000
F	-2	SER	-	expression tag	UNP P63000
F	-1	SER	-	expression tag	UNP P63000
F	0	GLY	-	expression tag	UNP P63000
F	15	ALA	GLY	engineered mutation	UNP P63000

[illegible]

Chain B: 7% 40% 60%



I1099	I1100	F1101	I1102	V1106	G1107	F1108	I1109	L1110	E1111	L1114	T1115	P1116	E1117	V1118	E1119	L1120	R1121	K1122	A1123	T1124	I1125	P1126	I1127	F1128	F1129	D1130	M1131	M1132	Q1133	C1134	E1135	F1136	N1137	F1138	S1139	M1143	F1144	H1145	M1149	E1150	L1151	I1152	T1153	K1154	L1155	D1156	Q1157	V1158	V1159	R1163	G1164	D1165	E1166	Q1167
V1027	F1031	F1032	F1033	D1034	Q1035	F1038	E1039	L1040	S970	L1041	W1042	W1043	N1044	H1048	F1053	L1054	T1055	H1056	E1057	S1058	L1059	Q1060	L1061	E1062	T1063	M1064	S1065	Q1066	A1067	K1068	R1069	N1070	K1071	I1072	K1075	Y1076	G1077	D1078	M1079	R1080	K1081	E1082	I1083	R1086	I1087	R1088	D1089	M1090	G1095	P1096	H1097	K1098		
L886	S887	Q888	Q889	L890	D891	D892	K893	S894	K895	L896	H899	S902	S903	Q904	T905	L906	S907	N908	L909	L910	E911	L912	L913	D914	N917	L918	N919	V921	A922	V923	H924	L925	Q926	L927	N929	E930	R931	L932	L933	R934	M1010	M1011	T1012	T939	V940	T941	G942	N943	N944	L945	Q946	S947	T950	T954
I958	Q962	Q963	Q964	D965	D966	S967	H968	Y969	S970	H971	Y972	I973	S974	T975	F976	R979	I982	F985	L986	M987	E988	L989	F990	T991	M992	F993	K994	D995	L996	I997	Y1002	A1003	D1004	D1005	V1008	M1009	M1010	M1011	T1012	R1015	W1016	F1017	L1018	R1019	A1020	I1021	N1022	Q1023	F1024	A1025	E1026			
L820	P821	S822	L823	L824	N825	D826	V827	K828	L829	W830	F831	D832	P833	W834	E835	L839	F840	G841	K842	F843	L844	Q845	S846	L847	Q851	L852	W853	R854	Q855	L856	L857	N858	C859	M860	T863	S866	T867	L868	F869	R870	Q871	S872	E873	C874	R875	E876	V877	L878	L879	P880	L881	L882	D883	Q885
L763	F764	L765	L766	L767	S770	R771	V772	L773	W774	L775	R776	S781	K782	D783	G784	D785	F787	W788	N789	S790	L791	H792	L793	L794	F795	L796	A797	F798	N799	M800	L801	M802	D803	P805	L806	E807	E808	A809	L812	K813	C814	A815	A816	L817	K818	Y819								
N678	L679	N680	N681	E682	N683	Y689	L692	L693	F694	L697	I700	L701	S702	L703	I704	G705	L706	L707	K708	F709	Q710	H711	F712	N713	L716	E717	L718	Y719	L720	Y721	C722	H723	T727	L728	A729	Y730	Y731	K732	K735	V736	L737	N738	F739	Y740	V741	A742	N743	A744	D745	D746	K749			
L536	Q637	E538	Q639	R540	D541	K542	S543	E544	F547	G548	V549	A550	F551	V552	K553	L554	M555	P557	G558	T560	T561	L562	L569	V570	K578	D581	F584	T585	T587	L588	P589	G590	T591	H592	M593	E594	M595	E596	E597	K598	E599	Q601	A602	S603	K604									
N605	L606	V607	T608	F609	T610	P611	S612	K613	D614	K617	F620	Q621	L622	K623	L624	M625	T626	C627	S628	T629	K630	L631	T632	Q633	N634	L637	L638	G639	L640	L641	N642	W643	R644	S645	N646	S647	Q648	N649	I650	K651	H652	L653	L654	K655	K656	E659	D661	I665	F668	Q670				
M678	M680	M681	E682	M683	Y689	L692	L693	F694	L697	I700	L701	S702	L703	I704	G705	L706	L707	K708	F709	Q710	H711	F712	N713	L716	E717	L718	Y719	L720	Y721	C722	H723	T727	L728	A729	Y730	Y731	K732	K735	V736	L737	N738	F739	Y740	V741	A742	N743	A744	D745	D746	K749				
L753	F754	L757	L760	K761	F764	R765	F766	I767	S770	R771	V772	L773	W774	L775	R776	S781	K782	D783	G784	D785	F787	W788	N789	S790	L791	H792	L793	L794	F795	L796	A797	F798	N799	M800	L801	M802	D803	P805	L806	E807	E808	A809	L812	K813	C814	A815	A816	L817	K818	Y819				
L820	P821	S822	L823	L824	N825	D826	V827	K828	L829	W830	F831	D832	P833	W834	E835	L839	F840	G841	K842	F843	L844	Q845	S846	L847	Q851	L852	W853	R854	Q855	L856	L857	N858	C859	M860	T863	S866	T867	L868	F869	R870	Q871	S872	E873	C874	R875	E876	V877	L878	L879	P880	L881	L882	D883	Q885
L886	S887	Q888	Q889	L890	D891	D892	K893	S894	K895	L896	H899	S902	S903	Q904	T905	L906	S907	N908	L909	L910	E911	L912	L913	D914	N917	L918	N919	V921	A922	V923	H924	L925	Q926	L927	N929	E930	R931	L932	L933	R934	M1010	M1011	T1012	T939	V940	T941	G942	N943	N944	L945	Q946	S947	T950	T954
I958	Q962	Q963	Q964	D965	D966	S967	H968	Y969	S970	H971	Y972	I973	S974	T975	F976	R979	I982	F985	L986	M987	E988	L989	F990	T991	M992	F993	K994	D995	L996	I997	Y1002	A1003	D1004	D1005	V1008	M1009	M1010	M1011	T1012	R1015	W1016	F1017	L1018	R1019	A1020	I1021	N1022	Q1023	F1024	A1025	E1026			
V1027	F1031	F1032	F1033	D1034	Q1035	F1038	E1039	L1040	S970	L1041	W1042	W1043	N1044	H1048	F1053	L1054	T1055	H1056	E1057	S1058	L1059	Q1060	L1061	E1062	T1063	M1064	S1065	Q1066	A1067	K1068	R1069	N1070	K1071	I1072	K1075	Y1076	G1077	D1078	M1079	R1080	K1081	E1082	I1083	R1086	I1087	R1088	D1089	M1090	G1095	P1096	H1097	K1098		

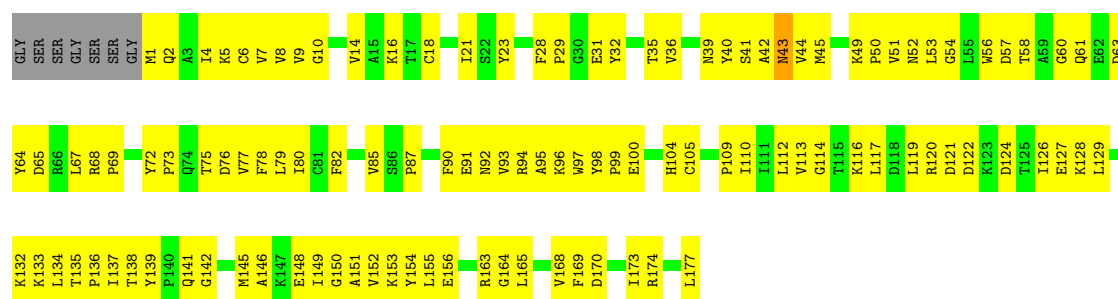


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D1392	K1235	Y1307	K1236	R1163	G1095	E1026	I958	S887	L886	I679	I679	N605	E538	K464	A389
F1393	R1236	G1311	R1237	D1165	H1097	L1028	Q962	Q888	S822	F754	M681	L606	T539	V466	K390
S1395	E1237	E1166	D1238	E1167	K1098	T1029	Q963	L990	I824	L757	E682	V607	R540	E467	E391
L1399	I1239	E1315	I1239	Q1167	K1099	R1030	Q964	D891	R825	L760	M683	T608	D541	V468	V392
T1400	Y1240	I1318	I1241	K1168	K1100	F1031	D965	D892	D826	K761	Y689	F609	K542	M470	H394
Q1401	F1101	K1169	R1242	K1169	F1101	F1032	D966	N893	K828	R764	L692	T610	S543	S471	Q397
F1402	Y1243	L1170	Y1243	F1170	M1033	Q1033	S967	S894	L829	R765	V693	S612	H473	V472	G398
M1404	Y1244	L1171	L1244	L1171	D1034	Q1034	H968	N895	V830	F766	F694	K613	D474	H473	L399
A1405	Y1245	L1172	Y1245	Q1035	Q1035	Q1035	S970	K896	F831	I767	L697	D614	G548	V400	V400
E1406	K1246	G1107	K1246	F1038	H971	F1038	H971	H899	D832	I767	L697	D614	G548	V400	V400
K1407	L1175	P1108	L1247	E1039	Y972	E1039	Y972	S902	P833	S770	L697	D614	G548	V400	V400
M1408	L1176	L1109	L1177	L1110	L1110	L1040	L1110	S903	P833	S770	L697	D614	G548	V400	V400
T1412	E1178	E1111	E1178	E1111	E1111	Q1041	S974	Q904	V834	R771	L697	D614	G548	V400	V400
P1413	H1179	Y1112	H1179	Y1112	Y1112	L1042	T975	L905	V772	V772	L697	D614	G548	V400	V400
E1416	C1180	T1113	C1180	T1113	T1113	W1043	T976	L906	L773	L773	L697	D614	G548	V400	V400
D1417	R1181	L1114	R1181	L1114	L1114	W1043	S974	L906	L773	L773	L697	D614	G548	V400	V400
I1418	K1182	T1115	K1182	T1115	T1115	N1045	T975	L906	L773	L773	L697	D614	G548	V400	V400
K1419	H1183	P1116	H1183	P1116	P1116	N1045	T975	L906	L773	L773	L697	D614	G548	V400	V400
S1420	Y1184	E1117	Y1184	E1117	E1117	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
A1421	K1185	Y1118	K1185	Y1118	Y1118	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
F1422	Y1186	E1119	Y1186	E1119	E1119	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
K1423	S1187	L1120	S1187	L1120	L1120	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
Q1424	S1188	R1121	S1188	R1121	R1121	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
Y1425	S1189	E1122	Y1189	E1122	E1122	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
E1426	K1184	T1124	K1184	T1124	T1124	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
F1427	Y1192	L1125	Y1192	L1125	L1125	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
C1428	F1193	T1126	C1428	F1193	F1193	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
P1430	L1196	E1127	P1430	L1196	E1127	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
Y1431	K1197	F1128	Y1431	K1197	F1128	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
K1432	V1197	S1274	K1432	V1197	S1274	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
P1433	E1198	D1130	P1433	E1198	D1130	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
V1434	S1199	M1131	V1434	S1199	M1131	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
S1436	L1200	M1132	S1436	L1200	M1132	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
L1437	Q1133	E1201	L1437	Q1133	E1201	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
P1438	E1202	L1204	P1438	E1202	L1204	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
F1439	N1203	K1206	F1439	N1203	K1206	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
S1440	L1205	D1206	S1440	L1205	D1206	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
Y1441	E1206	M1137	Y1441	E1206	M1137	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
K1442	F1138	S1139	K1442	F1138	S1139	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
D1443	L1376	E1209	D1443	L1376	E1209	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
K1444	R1377	K1378	K1444	R1377	K1378	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
E1448	G1379	T1291	E1448	G1379	T1291	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
Q1449	E1150	K1217	Q1449	E1150	K1217	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
I1450	E1218	E1218	I1450	E1218	E1218	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
M1451	L1151	K1081	M1451	L1151	K1081	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
N1452	F1017	L1018	N1452	F1017	L1018	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
Y1453	T1153	I1083	Y1453	T1153	I1083	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
K1386	K1154	L1154	K1386	K1154	L1154	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
E1387	L1155	L1155	E1387	L1155	L1155	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
Y1454	T1224	Y1231	Y1454	T1224	Y1231	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
K1455	E1238	E1238	K1455	E1238	E1238	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
E1456	Y1301	Y1301	E1456	Y1301	Y1301	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
D456	K457	K457	D456	K457	K457	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
K457	K457	K457	K457	K457	K457	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
G458	K458	K458	G458	K458	K458	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
K459	K459	K459	K459	K459	K459	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
K460	K460	K460	K460	K460	K460	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400
K461	K461	K461	K461	K461	K461	H1048	T975	L906	L773	L773	L697	D614	G548	V400	V400



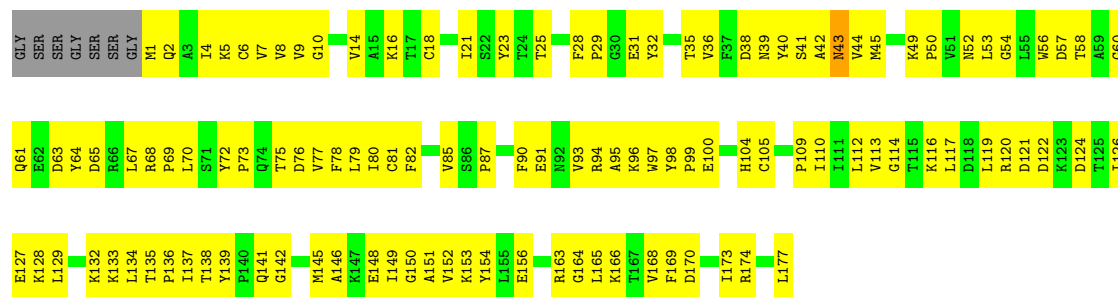
• Molecule 3: Ras-related C3 botulinum toxin substrate 1

Chain C: 34% 61%



• Molecule 3: Ras-related C3 botulinum toxin substrate 1

Chain F: 33% 62%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	120707	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	64000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.060	Depositor
Minimum map value	-0.022	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	452.2, 452.2, 452.2	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.33, 1.33, 1.33	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	0.23	0/1641	0.48	0/2218
1	D	0.23	0/1641	0.48	0/2218
2	B	0.32	1/13722 (0.0%)	0.51	4/18514 (0.0%)
2	E	0.32	1/13722 (0.0%)	0.51	4/18514 (0.0%)
3	C	0.26	0/1415	0.46	0/1924
3	F	0.26	0/1415	0.46	0/1924
All	All	0.31	2/33556 (0.0%)	0.51	8/45312 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	463	PRO	CG-CD	-13.93	1.03	1.50
2	B	463	PRO	CG-CD	-13.90	1.03	1.50

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	463	PRO	N-CD-CG	-17.32	77.21	103.20
2	E	463	PRO	N-CD-CG	-17.30	77.25	103.20
2	B	463	PRO	CA-CB-CG	-11.88	81.93	104.50
2	E	463	PRO	CA-CB-CG	-11.87	81.96	104.50
2	B	463	PRO	CB-CG-CD	8.19	132.31	106.10

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	1608	0	1617	142	0
1	D	1608	0	1617	145	0
2	B	13436	0	13516	954	0
2	E	13436	0	13516	986	0
3	C	1385	0	1407	109	0
3	F	1385	0	1407	120	0
All	All	32858	0	33080	2379	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 36.

The worst 5 of 2379 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:D:697:ARG:HH21	2:E:30:GLN:HB2	1.33	0.91
1:D:670:ASN:ND2	1:D:676:ASP:O	2.06	0.88
2:E:1579:HIS:HB3	2:E:1582:ASP:HB2	1.56	0.88
1:A:670:ASN:ND2	1:A:676:ASP:O	2.06	0.87
1:A:697:ARG:HH21	2:B:30:GLN:HB2	1.42	0.85

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	196/733 (27%)	179 (91%)	17 (9%)	0	100	100
1	D	196/733 (27%)	179 (91%)	17 (9%)	0	100	100
2	B	1640/1648 (100%)	1512 (92%)	128 (8%)	0	100	100
2	E	1640/1648 (100%)	1512 (92%)	128 (8%)	0	100	100
3	C	175/184 (95%)	164 (94%)	11 (6%)	0	100	100

Continued on next page...

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	F	175/184 (95%)	165 (94%)	10 (6%)	0	100	100
All	All	4022/5130 (78%)	3711 (92%)	311 (8%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	183/664 (28%)	183 (100%)	0	100	100
1	D	183/664 (28%)	183 (100%)	0	100	100
2	B	1495/1497 (100%)	1495 (100%)	0	100	100
2	E	1495/1497 (100%)	1495 (100%)	0	100	100
3	C	153/157 (98%)	152 (99%)	1 (1%)	76	78
3	F	153/157 (98%)	152 (99%)	1 (1%)	76	78
All	All	3662/4636 (79%)	3660 (100%)	2 (0%)	87	88

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

Mol	Chain	Res	Type
3	C	43	ASN
3	F	43	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	187	HIS
2	E	738	ASN
2	E	257	ASN
2	E	556	ASN
2	E	885	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.

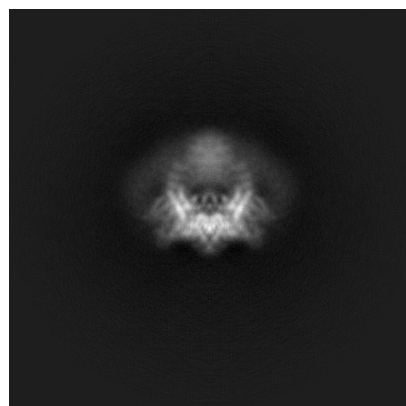
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60148. These allow visual inspection of the internal detail of the map and identification of artifacts.

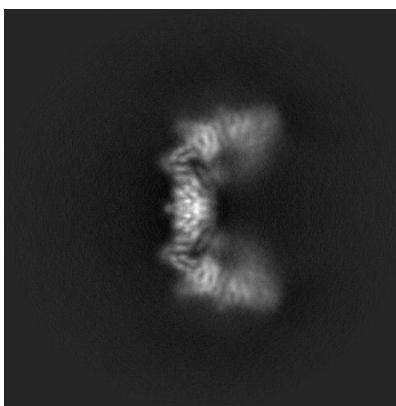
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

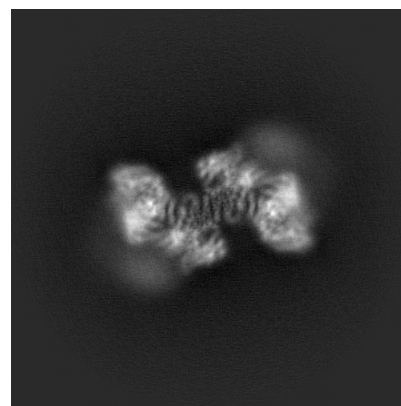
6.1.1 Primary map



X

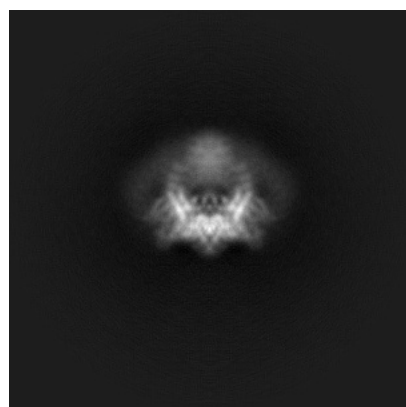


Y

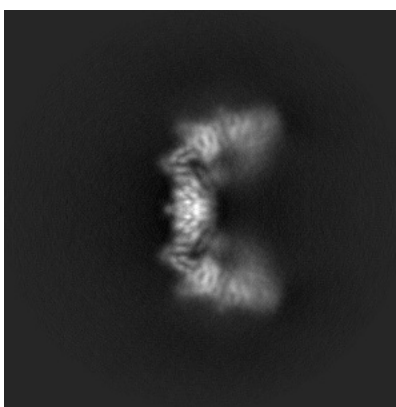


Z

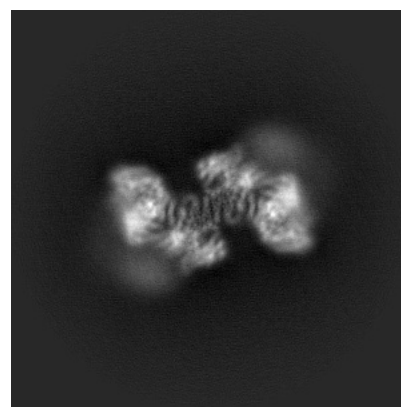
6.1.2 Raw map



X



Y

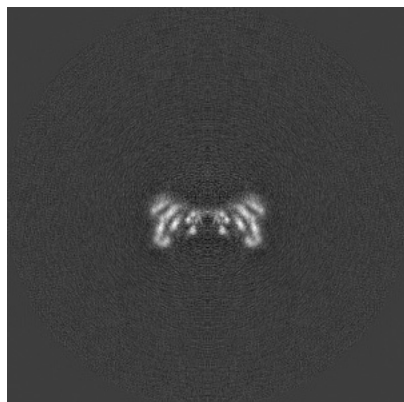


Z

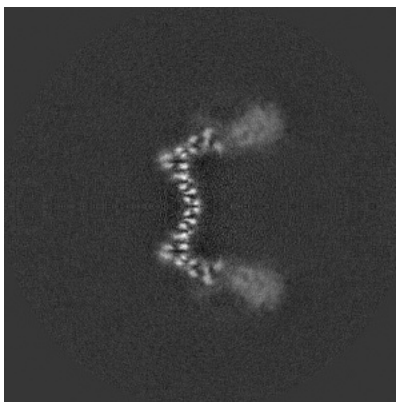
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

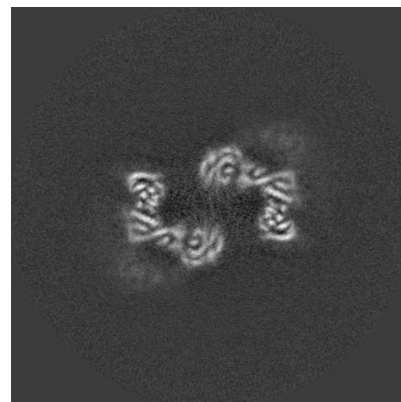
6.2.1 Primary map



X Index: 170

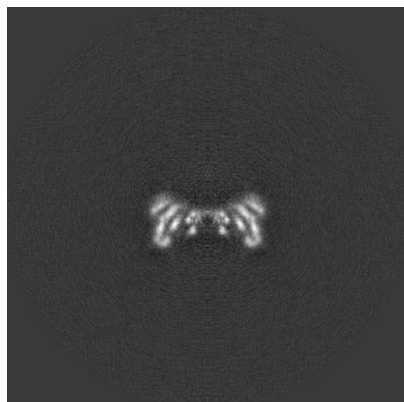


Y Index: 170

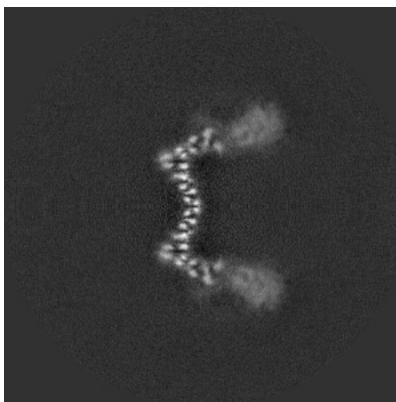


Z Index: 170

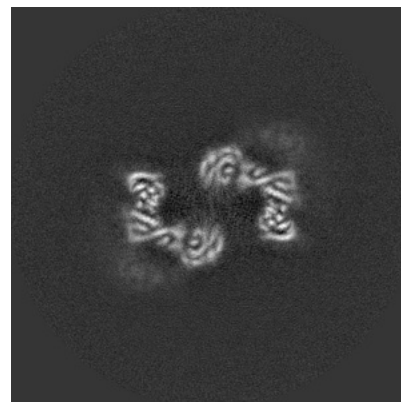
6.2.2 Raw map



X Index: 170



Y Index: 170

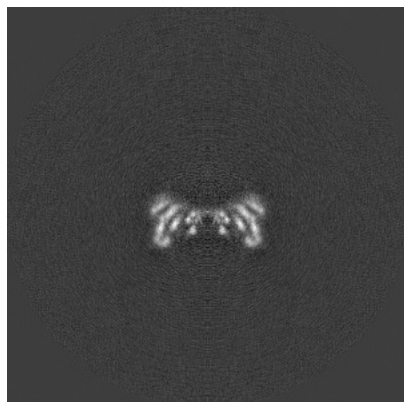


Z Index: 170

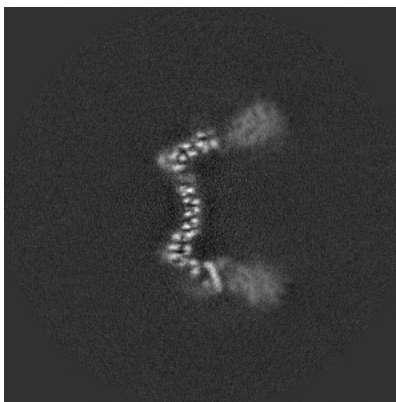
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

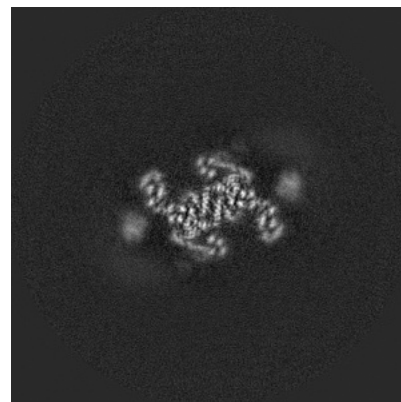
6.3.1 Primary map



X Index: 170

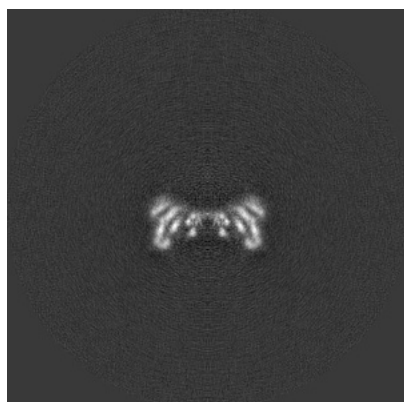


Y Index: 166

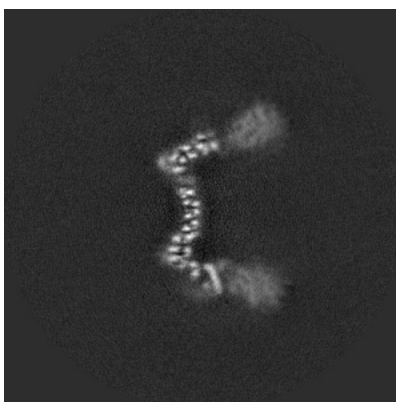


Z Index: 155

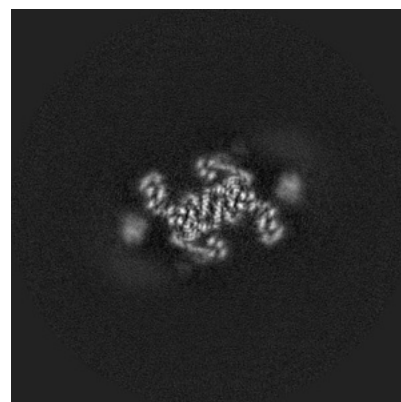
6.3.2 Raw map



X Index: 170



Y Index: 166

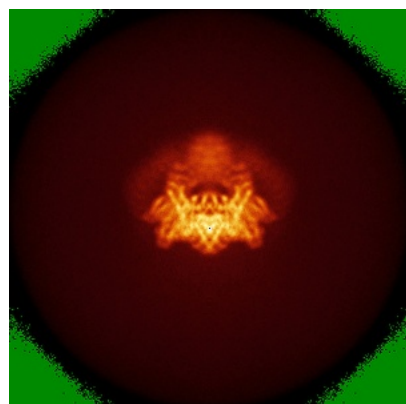


Z Index: 155

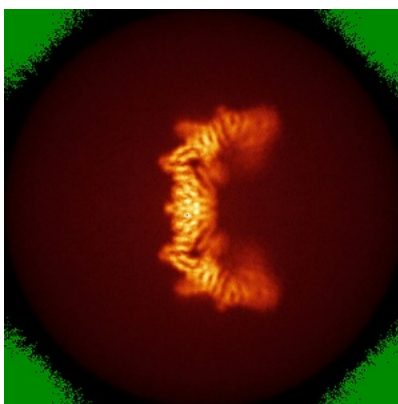
The images above show the largest variance slices of the map in three orthogonal directions.

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

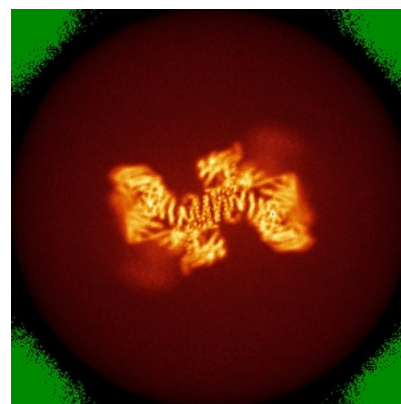
6.4.1 Primary map



X



Y



Z

6.4.2 Raw map



X



Y

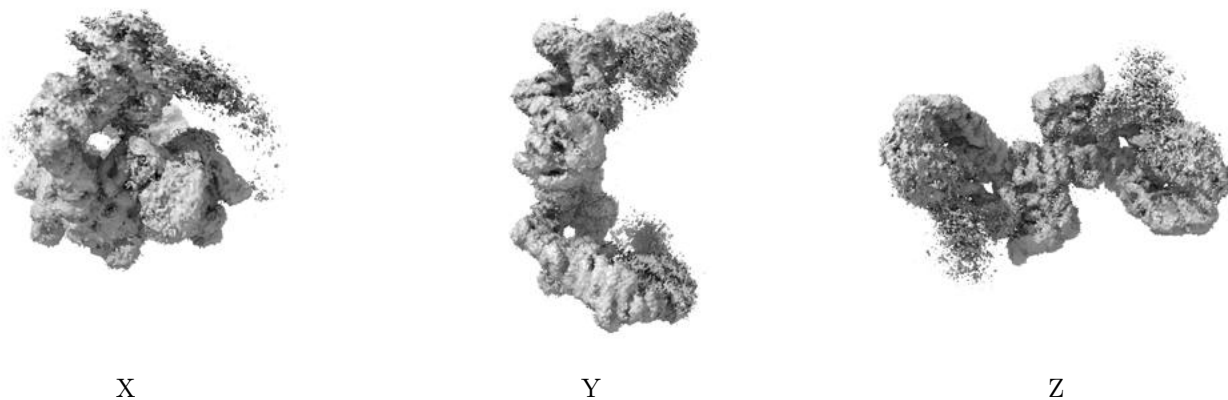


Z

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.

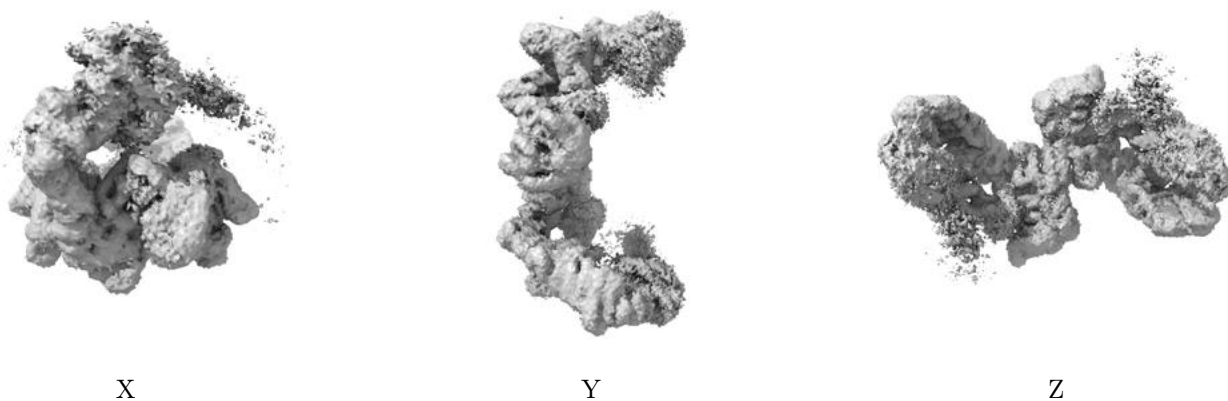
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. 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.

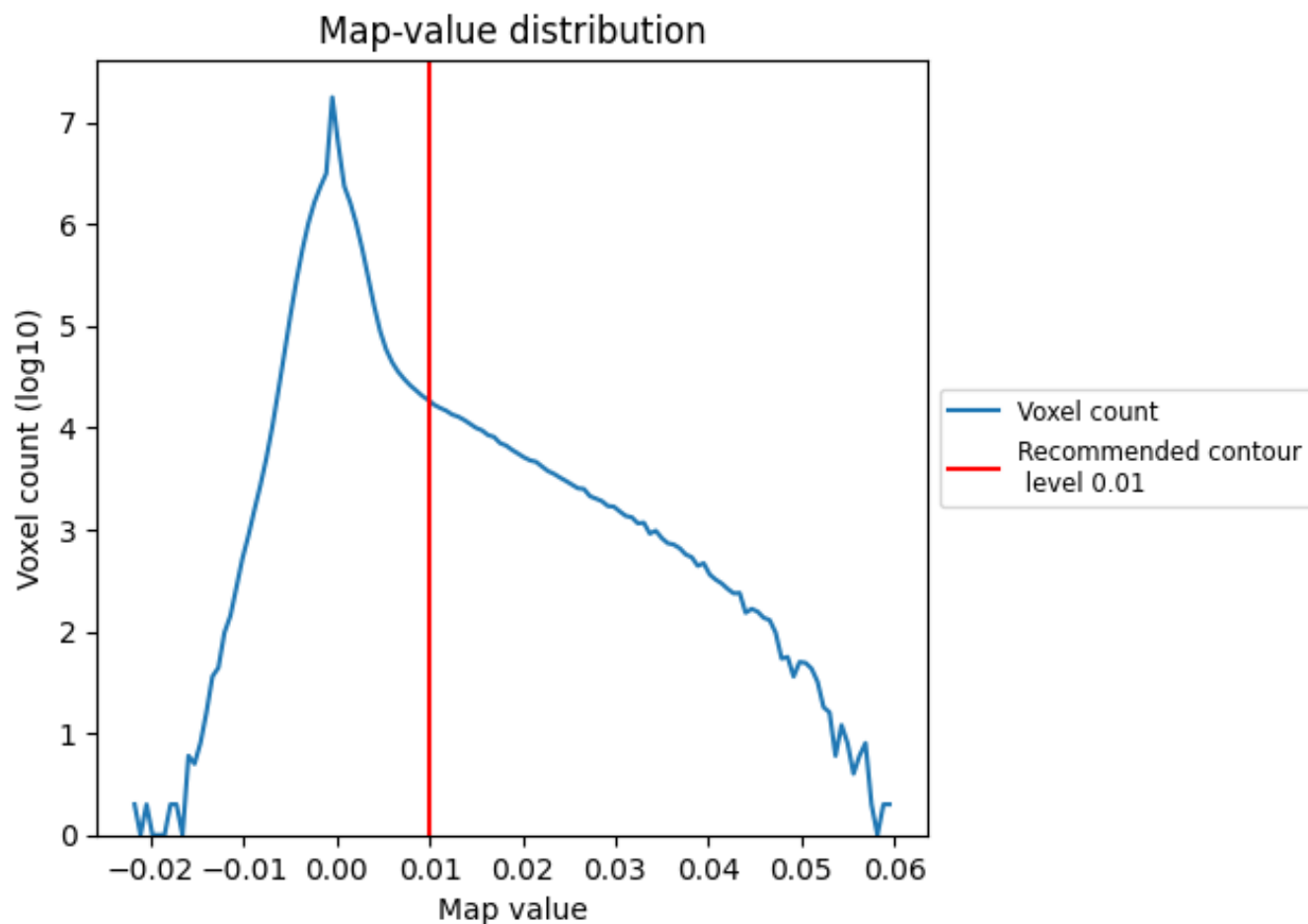
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

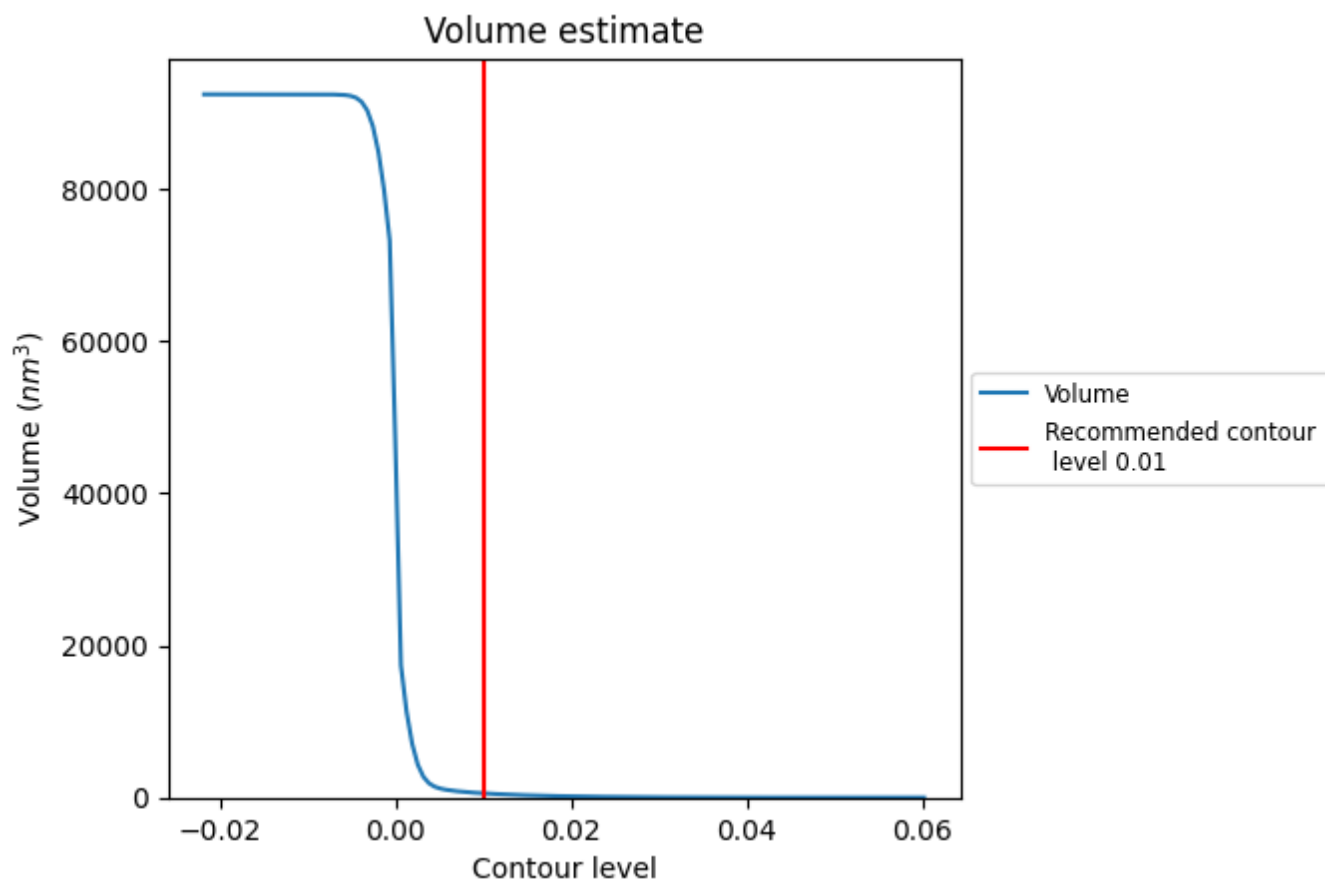
This section contains the results of statistical analysis of the map.

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.

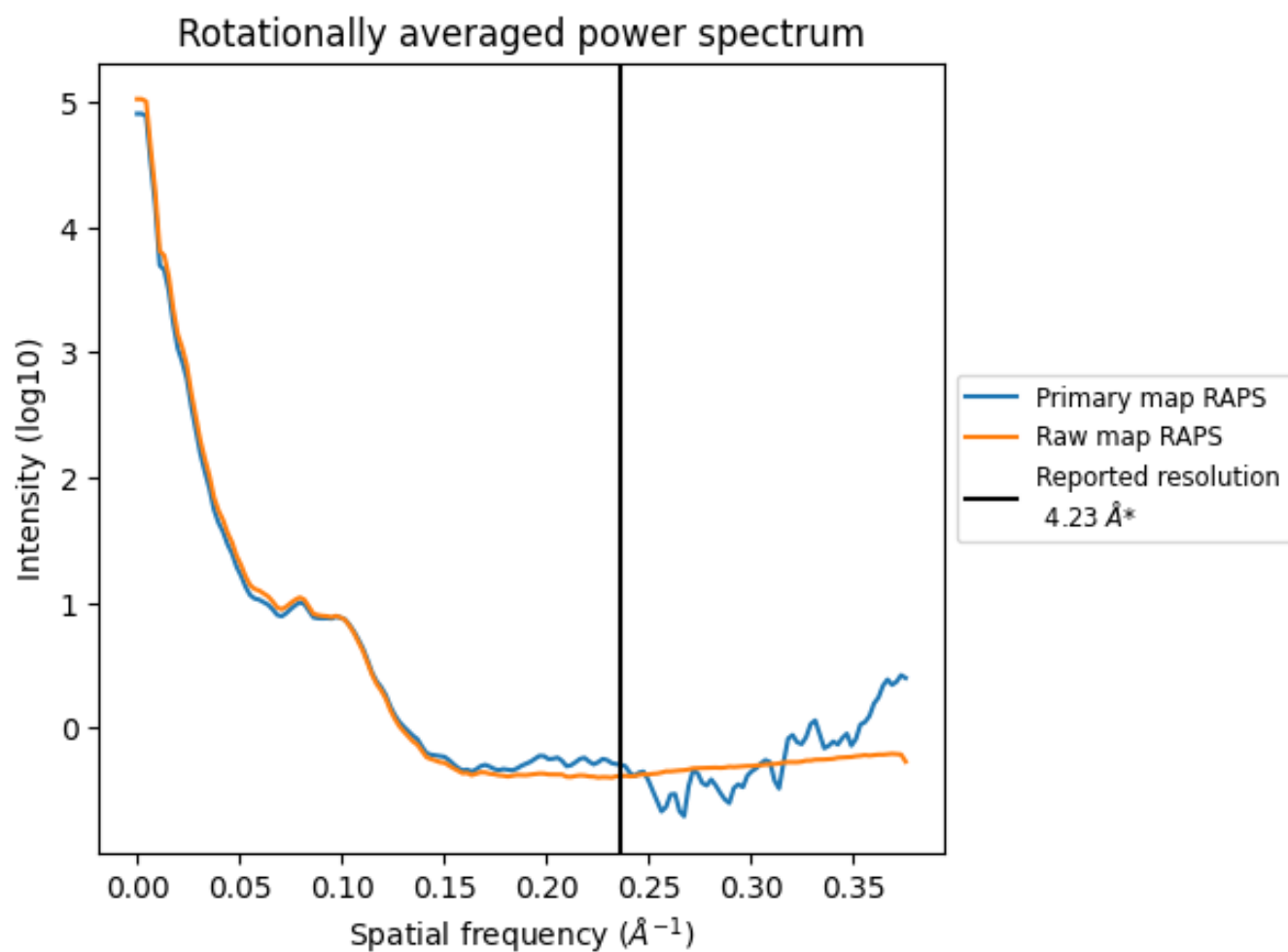
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 558 nm^3 ; this corresponds to an approximate mass of 504 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 ⓘ

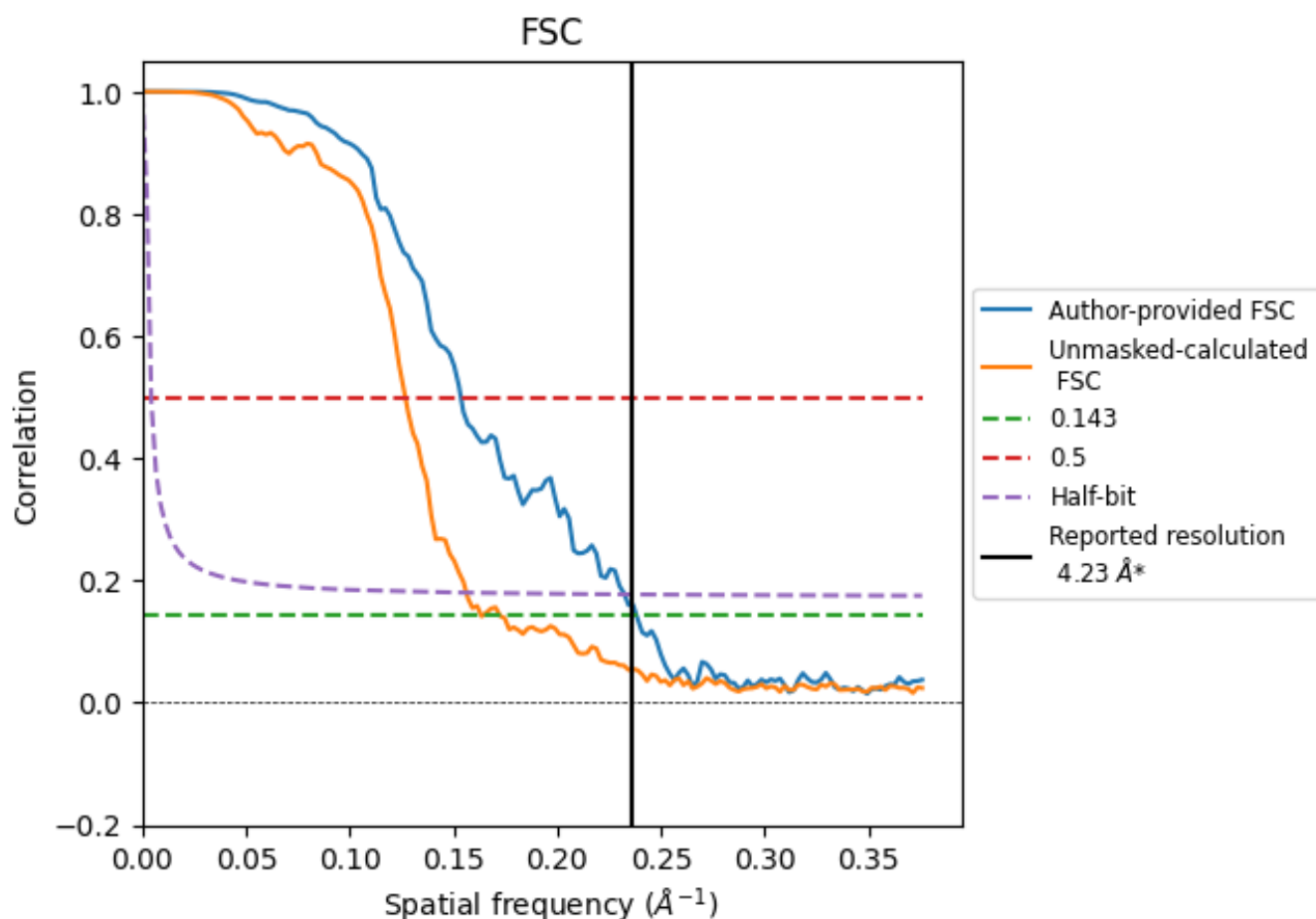


*Reported resolution corresponds to spatial frequency of 0.236 Å⁻¹

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 0.236 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

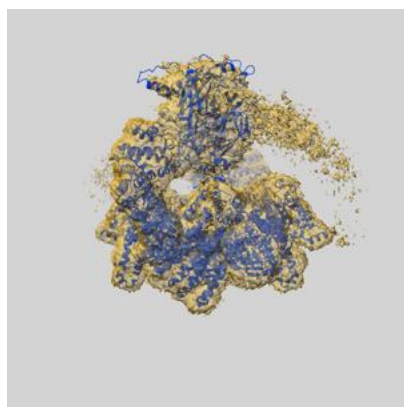
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.23	-	-
Author-provided FSC curve	4.20	6.51	4.30
Unmasked-calculated*	6.12	7.89	6.40

*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 6.12 differs from the reported value 4.23 by more than 10 %

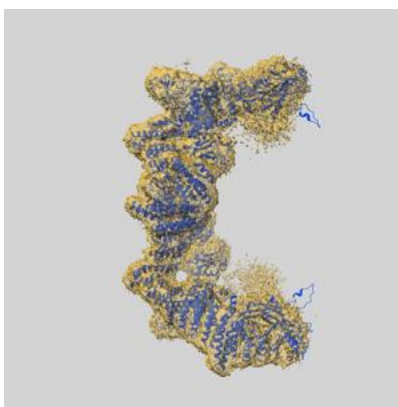
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-60148 and PDB model 8ZJK. Per-residue inclusion information can be found in section [3](#) on page [6](#).

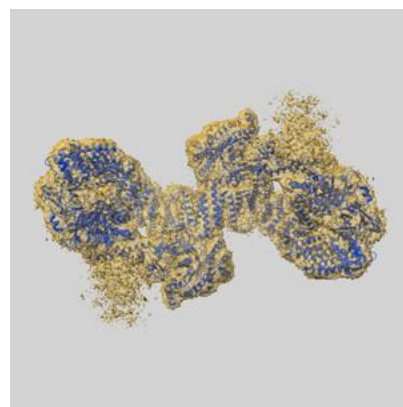
9.1 Map-model overlay [i](#)



X



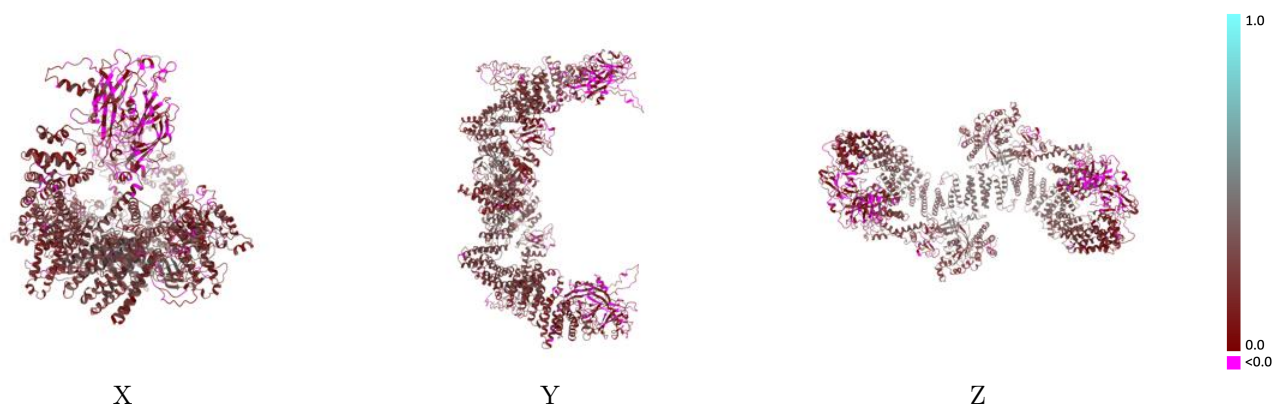
Y



Z

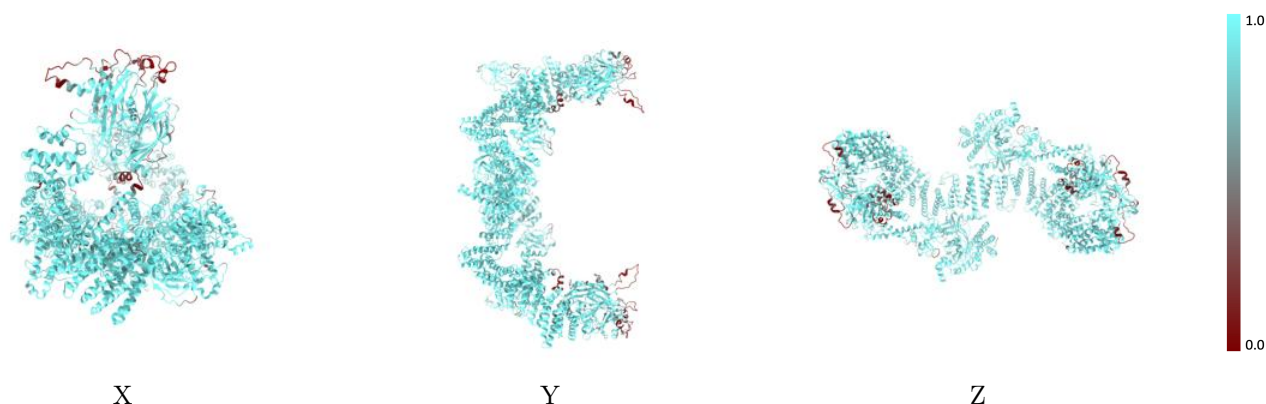
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



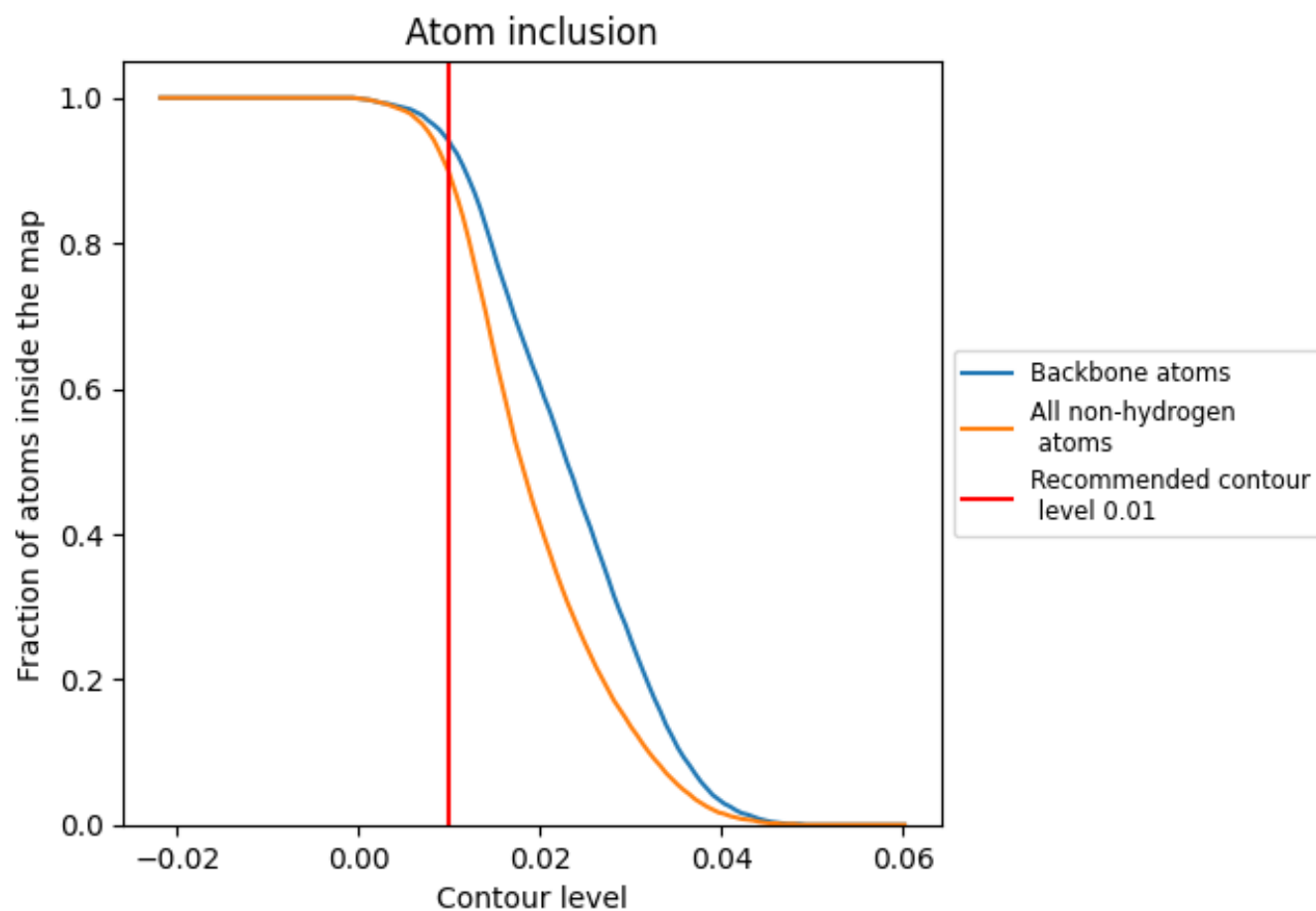
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 90% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8970	0.2030
A	0.8970	0.1680
B	0.8870	0.2030
C	0.9560	0.2450
D	0.9070	0.1610
E	0.8930	0.2040
F	0.9600	0.2420

1.0

0.0

<0.0