



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2026 – 10:33 AM UTC

PDB ID : 8ZJI / pdb_00008zji
EMDB ID : EMD-60146
Title : Structure of DOCK5/ELMO1/Rac1 core (RhoG/DOCK5/ELMO1/Rac1 dataset, class 1)
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

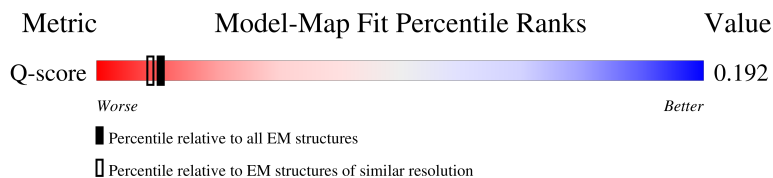
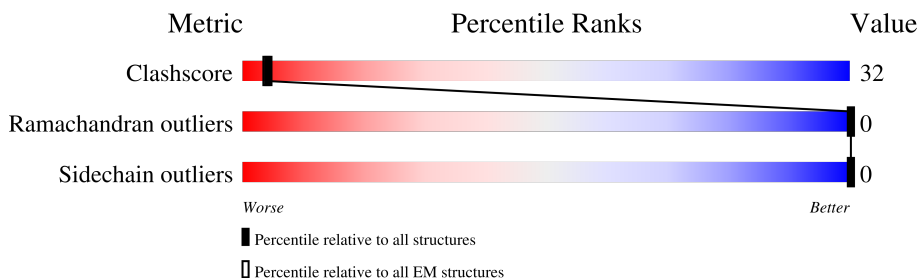
1 Overall quality at a glance

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	
1	D	733	
2	B	1648	
2	E	1648	

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Mol	Chain	Length	Quality of chain
3	C	184	 49% 47% .
3	F	184	 49% 47% .

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		

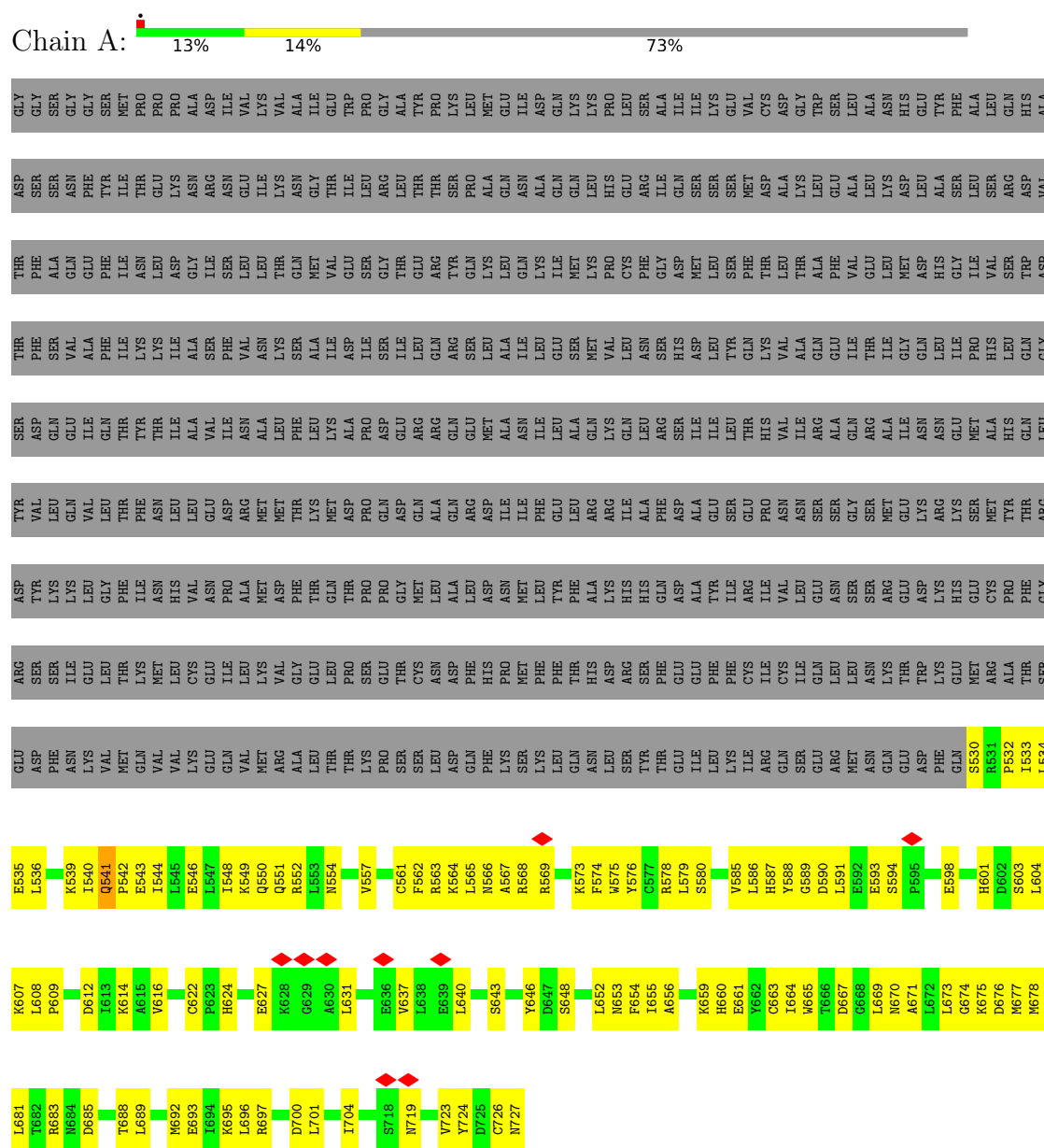
There are 16 discrepancies between the modelled and reference sequences:

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

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: Engulfment and cell motility protein 1



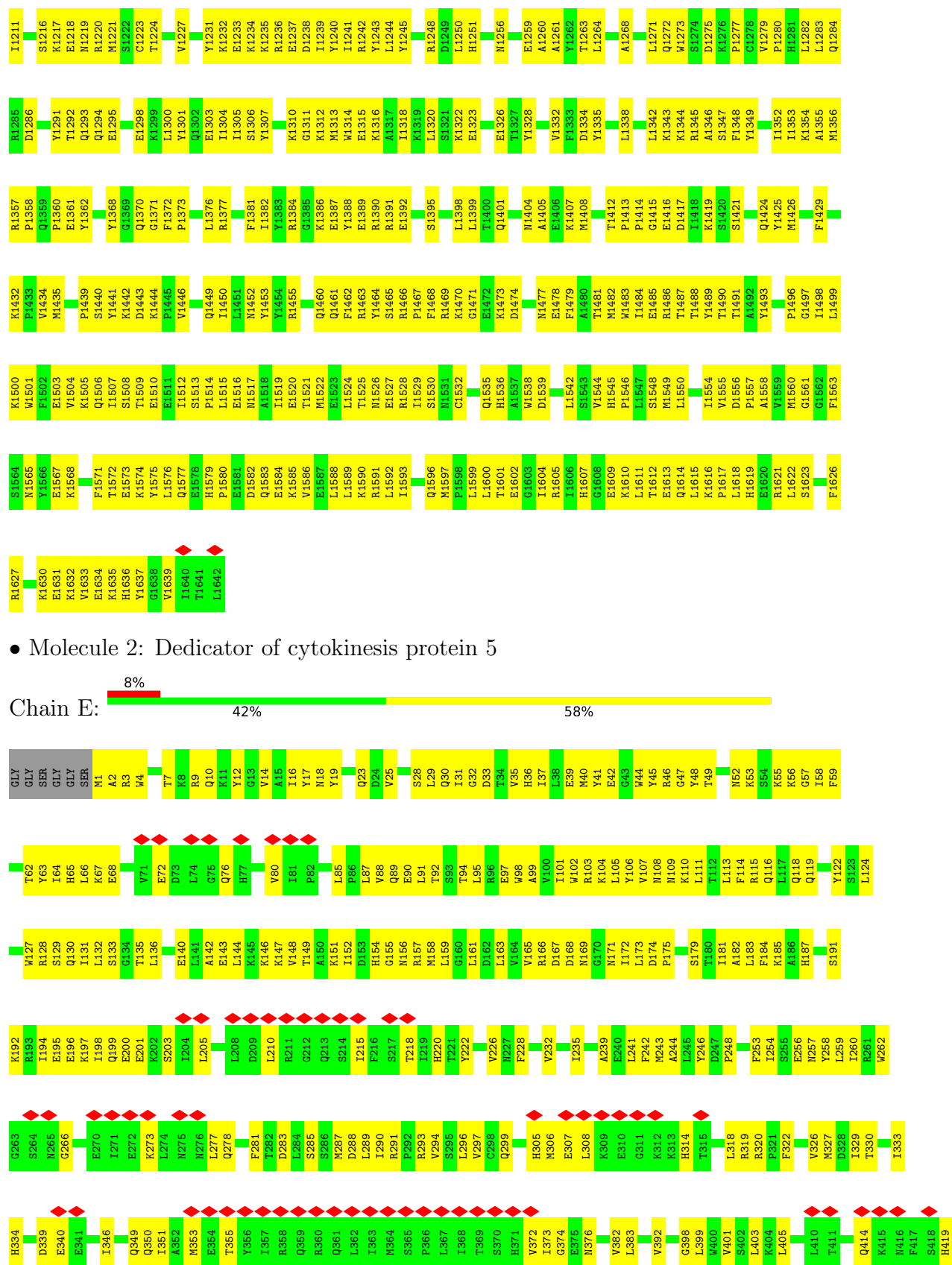
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Chain B:

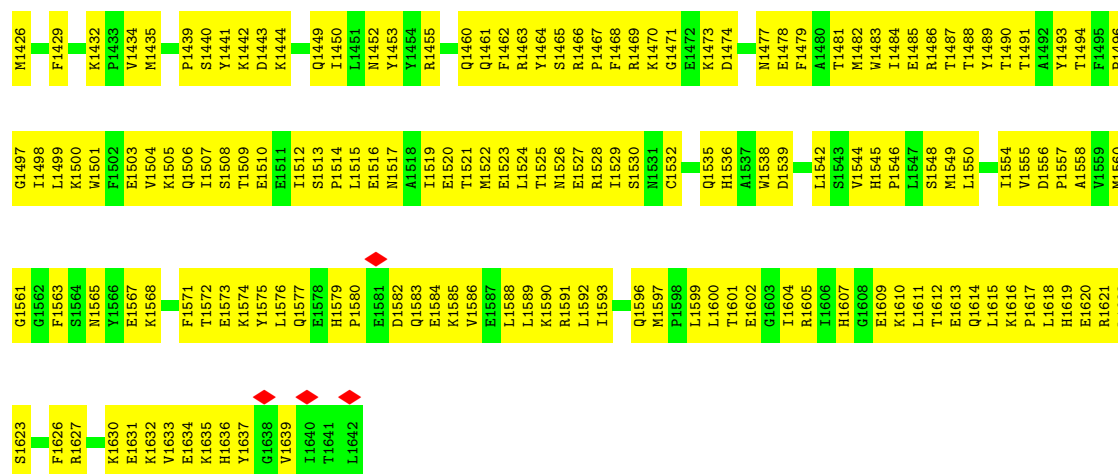
8% 42% 57%

GLY GLY SER GLY GLY GLY SER M1 A2 R3 W4 T7 K8 R9 Q10 Y12 K11 G13 V14 A15 I16 Y17 N18 Y19 Q23 D24 V25 S28 L29 Q30 I31 G32 G33 T34 V35 H36 I37 L38 E39 M40 Y41 E42 G43 W44 Y45 R46 G47 Y48 T49 N52 K53 S54 K55 K56 G57 I58 F59 P60 E61 T62 Y63 I64 H65 L66 K67 E68 V71 E72 D73 L74 G75 Q76 H77 V80 I81 P82 L85 P86 L87 V88 Q89 E90 L91 T92 S93 T94 L95 R96 E97 W98 A99 I100 I101 M102 R103 K104 L105 Y106 V107 N108 M109 K110 L111 T112 L113 F114 R115 Q116 L117 Q118 Q119 F122 E123 L124 W127 R128 S129 Q130 I131 L132 S133 G134 T135 L136 E140 L141 A142 E143 L144 K145 K146 K147 V148 T149 A150 K151 L152 D153 H154 G155 N156 L157 M158 L159 G160 L161 D162 L163 V164 V165 R166 D167 D168 M171 L172 L173 D174 P175 S179 T180 L181 A182 L183 F184 K185 A186 L187 S191

K192	R193	I194	E195	K196	K197	I198	Q199	E200	E201	K202	S203	I204	L205	L208	D209	L210	R211	Q212	Q213	S214	I215	F216	S217	T218	I219	H220	I221	Y222	Y225	V226	K227	F228	V232	I235	A239	E240	L241	F242	M243	A244	L245	Y246	D247	P248	D249	Q250	F253	I254	S255	E256	N257	Y258	L259						
I260	R261	W262	W265	G266	K269	I271	E272	K273	L274	N275	N276	L277	Q278	F281	T282	D283	L284	S285	S286	M287	D288	L289	I290	R291	P292	R293	P294	S295	L296	V297	C298	Q299	H305	M306	E307	L308	K309	E310	G311	K312	K313	H314	T315	L318	R319	R320	P321	F322	V326	N327	D328	I329							
T330	I333	H334	G335	D339	E340	E341	I346	Q349	Q350	I351	A352	M353	E354	T355	Y356	I357	R358	Q359	D360	Q361	L362	I363	M364	S365	P366	L367	K368	T369	S370	H371	V372	I373	G374	N376	V382	L383	V392	G398	L399	W400	W401	S402	L403	K404	K482	L405	Q414	K415	M416	F417	S418								
H419	L420	D422	R423	S424	T425	A426	I427	A428	R429	K430	M431	G432	I436	I437	L438	P439	G440	D441	V442	R443	N444	I446	L450	I451	K457	G458	K459	K460	K461	T462	P463	K464	N465	V466	E467	V468	T469	V472	D473	D474	E475	E476	G477	K478	L479	L480	E481	D483	A483	I484	H485	P486	G487						
A488	G489	Y490	E495	Y496	V500	Q503	Y510	E511	K514	V515	S516	I517	A518	I519	E520	E521	V522	T523	R524	C525	H526	I527	R528	F529	T530	F531	R532	H533	R534	Q537	E538	T539	R540	D541	K542	S543	E544	R545	A546	F547	G548	V549	V552	M555	N556	P557	D558	G559	T560	T561	L562								
L569	Y572	D575	N576	K577	K578	N579	E580	D581	A582	K583	F584	Y585	L586	T587	L588	P589	G590	Y591	K592	M593	E594	E597	K598	E599	L600	Q601	A602	S603	K604	N605	L606	V607	T608	F609	T610	P611	S612	K613	D614	S615	T616	K617	F620	A623	G627	S628	T629	K630	L631	T632	Q633	N634							
L637	L638	G639	L640	L641	N642	W643	W644	S645	N646	S647	Q648	L649	L650	K651	H652	L653	K655	K656	L657	W658	E659	V660	E664	K667	F668	L669	Q670	L673	L676	F677	N678	M680	M681	E682	D685	Y689	L692	V693	F694	D695	A696	L697	I700	I701	I704	F709													
Q710	H711	P714	V715	L716	E717	T718	Y719	W720	Y721	K722	H723	F724	S725	A726	L727	W728	Y729	Y730	Y731	K732	V736	L737	W738	F739	Y740	Y741	A742	N743	L744	D745	D746	S747	K748	K749	L753	L757	K758	A759	L760	K761	R765	F766	I767	T768	Q769	S770	Y771	Y772	L773	Y774	L775	R776	G779						
Q780	S781	K782	D783	D785	E786	F787	N788	W789	S790	T791	H792	Q793	L794	F795	L796	A797	F798	N799	M800	L801	M802	D803	R804	P805	E808	A809	W810	R811	L812	K813	A816	Y819	L820	P821	T824	N825	D826	W827	K828	L829	W830	F831	D832	P833	W834	L839	K842	F843	I844	D845	S846	I847							
L852	W853	R854	D855	K856	L857	R858	C859	M860	T861	K862	L863	W864	E865	S866	T867	L868	F869	R870	Q871	S872	E873	C874	R875	E876	W877	L878	Y879	P880	L881	L882	L883	Q885	D892	N895	K896	H899	L905	L906	S907	I908	Y909	T910	D911	V912	R915	V918	T921	A922	V923	H924									
I925	Q926	I927	R928	N929	E930	R931	L932	I933	R934	R935	R936	N937	R938	T939	Y940	F941	Q942	R943	W944	R945	I946	C956	N957	F958	A959	L960	L961	Q962	Q963	N964	P965	H968	Y969	S970	H971	Y972	I973	S974	T975	F976	R979	F985	W987	E988	T989	F990	I991												
M992	F993	K994	D995	L996	I997	Y1002	M1009	R1015	R1019	Q1023	F1024	L1027	L1028	T1029	R1030	F1031	S947	F1032	C874	R949	I950	F953	Y954	A955	L1043	N1044	L1045	Y1046	F1047	H1048	L1054	T1055	H1056	E1057	S1058	L1059	E1062	T1063	L1064	S1065	Q1066	A1067	K1068	N1069	W1070	K1071	I1072	V1073	K1074										
K1075	Y1076	G1077	D1078	R1079	M1080	K1081	E1082	R1086	W1089	D1090	W1091	Y1092	N1093	L1094	G1095	P1096	H1097	L1098	I1099	Q1100	Q1167	F1101	I1102	M1105	V1106	L1107	P1108	L1109	E1110	E1111	W1112	R1181	K1182	H1183	K1184	T1115	P1116	L1186	E1117	V1118	E1119	R1121	K1122	A1123	T1124	I1125	P1126	I1127	F1128	F1129	D1130	M1131	M1132	Q1133	C1134	E1135	F1136	T1209	S1139
N1143	H1144	F1145	M1146	R1147	E1148	N1149	E1150	K1154	D1155	L1156	Q1157	E1158	V1159	E1160	R1163	G1164	D1165	E1166	Q1167	Y1168	K1169	L1172	L1176	L1177	E1178	H1179	C1180	V1112	R1181	K1182	H1183	K1184	T1115	P1116	L1186	E1117	V1118	E1119	R1121	K1122	A1123	T1124	I1125	P1126	I1127	F1128	F1129	D1130	M1131	M1132	Q1133	C1134	E1135	F1136	T1209	S1139			

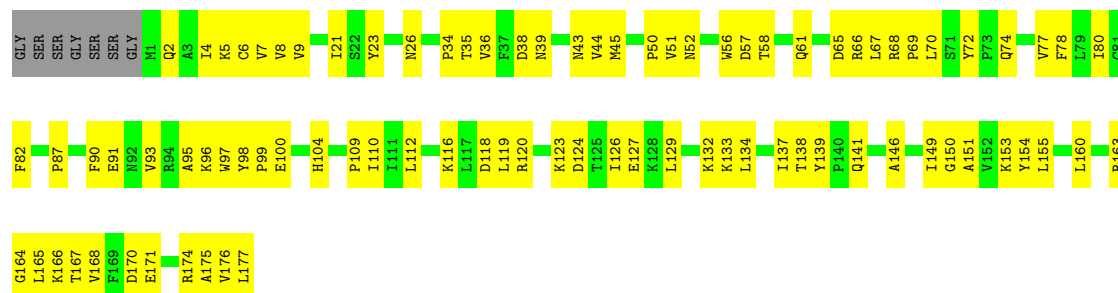


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A1355	Q1284	I1210	S1139	K1074	F993	L927	I847	S781	T632	T560	A488	V421
M1356	D1285	I1211	M1143	K1075	K994	I928	L852	D782	Q633	G489	D422	R423
Q1358	D1286		F1144	K1076	D995	M929	L852	K783	L638	Y490	R423	S424
Q1359		S1216	H1145	G1077	L996	E930	R853	G784	G639	E495	S424	T425
T1291	Y1291	K1217	H1146	D1078	L997	R931	R854	D785	L640	Y496	T425	A126
T1292	T1292	E1218	M1079	M1079		L932	Q855	D786	L641	K497	A126	I427
E1361	Q1293	M1219	K1080	K1080	Y1002	L933	Q856	F787	N642	S498	A428	R429
Y1362	Q1294	K1220	K1081	K1081	M1009	R934	L857	F787	W643	V500	K430	M431
	E1295	M1221	E1082	E1082		R935	N858	N788	R644	Q503	M431	G432
Y1368		E1149	E1082		R1015	I936	R935	N788	S645			
Q1369	E1298	C1223	R1086	R1086		N937	R860	S790	N646			
Q1370	A1299	T1224			R1019	R938	T861	S791	N646			
G1371	L1300	V1227	D1089	D1089		T939	K862	R792	S647			
P1372	Y1301		M1090	M1090	M1022	V940	I863	Q793	Q648			
P1373	Q1302	Y1231	Y1091	Y1091	Q1023	G942	V864	F794	N649			
L1376	E1303	K1232	N1093	N1093	F1024	M943	S866	L796	I650			
R1377	I1304	K1233	L1094	L1094	A1025	N944	T867	A797	K651			
	S1305	K1234	G1095	G1095	E1026	R945	L868	F798	H652			
F1381	Y1307	K1235	P1096	P1096	E1027	Q946	F869	N799	N653			
I1382	K1310	R1236	H1097	H1097	Q1027	Q947	R870	F799	L654			
Y1383	G1311	D1237	K1098	K1098	L1028	S947	R871	N800	K655			
R1384	M1312	T1238	I1099	I1099	T1029	P948	Q870	M800	L657			
G1385	M1313	I1239	K1100	K1100	R1030	H949	S872	L801	L657			
K1386	M1314	Y1240	F1101	F1101	F1031	R950	E873	M802	M658			
E1387	W1314	I1241	K1169	K1169	F1032	C874	C874	R804	E659			
Y1388	E1315	K1242			M1033	R875	R875	R804	V660			
K1389	K1316	Y1243	L1172	L1172	D1034	V954	E876	P805	E664			
R1390	A1317	K1244	M1105	M1105	Q1035	C956	V877	E808	K667			
R1391	Y1318	Y1245	V1106	V1106	A1036	R877	R877	A809	V741			
E1392	K1319	L1176	G1107	G1107	S1037	M957	V858	V810	F740			
D1393	L1177	L1177	P1108	P1108	F1038	E959	P880	V810	F668			
F1394	E1178	R1248	I1109	I1109	E1039	L881	L881	A742	N743			
S1395	L1320	D1249	L1110	L1110	L960	L960	T882	N743	E596			
	K1321	L1250	E1111	E1111	L961	L961	T883	D745	E597			
	E1223	H1251	V1112	V1112	W1043	Q962	D884	D746	K598			
			T1113	T1113	M1044	Q963	Q885	S747	E599			
			L1114	L1114	M1045	M964	L890	S748	L600			
			T1115	T1115	Y1046	D965	L890	K749	Q601			
			P1116	P1116	F1047	D966	K896	L753	A602			
			E1117	E1117	H1048	S967	H899	L757	S603			
			V1118	V1118	L1054	H968	H899	K758	Q604			
			E1119	E1119	T1055	S970	L905	A759	N605			
			L1120	L1120	T1056	H971	L905	L760	L606			
			R1121	R1121	E1057	Y972	D826	K761	V607			
			K1122	K1122	S1058	I973	V827	L697	T608			
			A1123	A1123	L1059	S974	K828	Y689	S541			
			T1124	T1124	E1062	T975	E911	L692	K542			
			I1125	I1125	F1063	F976	V912	V693	S543			
			P1126	P1126	T1064		R915	F831	E544			
			I1127	I1127	F1065	R979	R915	I768	R545			
			F1128	F1128	S1065		V918	Q769	R546			
			D1129	D1129	Q1066		V918	S770	R771			
			D1130	D1130	A1067		T921	R772	L614			
			M1131	M1131	A1067		A922	L773	S815			
			M1132	M1132	K1068		V923	Y774	D618			
			Q1133	Q1133	R1069		H987	L775	V549			
			C1134	C1134	F989		L986	T629	M555			
			E1135	E1135	K1071		L986	A623	N556			
			F1136	F1136	I1072		I991	G627	P557			
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								T629	A483			
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									P486			



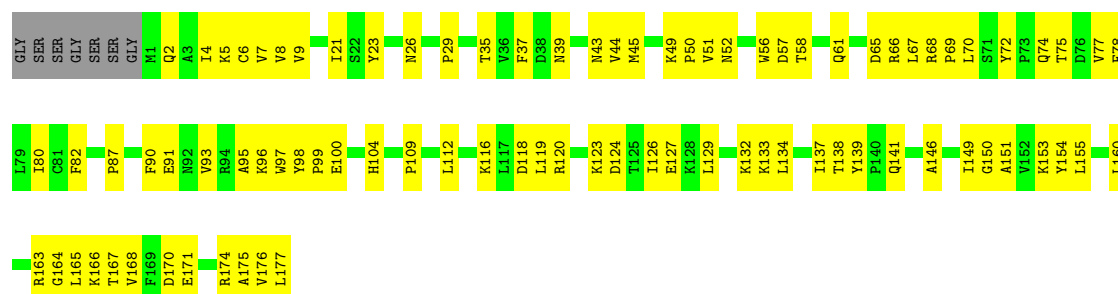
• Molecule 3: Ras-related C3 botulinum toxin substrate 1

Chain C: 49% 47%



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

Chain F: 49% 47%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	133323	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	0.065	Depositor
Minimum map value	-0.020	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	0.24	0/1641	0.46	0/2218
1	D	0.24	0/1641	0.46	0/2218
2	B	0.25	0/13722	0.47	0/18514
2	E	0.25	0/13722	0.47	0/18514
3	C	0.23	0/1415	0.47	0/1924
3	F	0.23	0/1415	0.47	0/1924
All	All	0.25	0/33556	0.47	0/45312

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	1
1	D	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	541	GLN	Peptide
1	D	541	GLN	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	1608	0	1617	106	0
1	D	1608	0	1617	112	0
2	B	13436	0	13516	896	0
2	E	13436	0	13516	897	0
3	C	1385	0	1407	84	0
3	F	1385	0	1407	91	0
All	All	32858	0	33080	2123	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 32.

The worst 5 of 2123 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)
2:B:1346:ALA:HB2	2:E:1342:LEU:HD11	1.27	1.09
1:A:536:LEU:HD21	2:B:17:TYR:HB2	1.40	1.03
1:A:697:ARG:HB3	2:B:31:ILE:HB	1.53	0.89
3:F:93:VAL:HA	3:F:97:TRP:HB2	1.59	0.85
2:E:144:LEU:HD13	2:E:147:LYS:HE2	1.60	0.83

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%)	180 (92%)	16 (8%)	0	100	100
1	D	196/733 (27%)	180 (92%)	16 (8%)	0	100	100
2	B	1640/1648 (100%)	1539 (94%)	101 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	1640/1648 (100%)	1540 (94%)	100 (6%)	0	100	100
3	C	175/184 (95%)	163 (93%)	12 (7%)	0	100	100
3	F	175/184 (95%)	163 (93%)	12 (7%)	0	100	100
All	All	4022/5130 (78%)	3765 (94%)	257 (6%)	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%)	153 (100%)	0	100	100
3	F	153/157 (98%)	153 (100%)	0	100	100
All	All	3662/4636 (79%)	3662 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	20	ASN
2	E	526	HIS
3	F	2	GLN
2	E	1460	GLN
2	E	108	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](#)

There are no chain breaks in this entry.

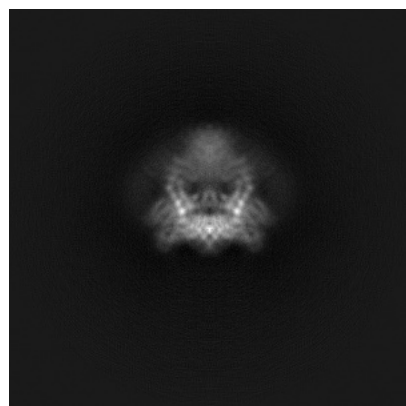
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60146. These allow visual inspection of the internal detail of the map and identification of artifacts.

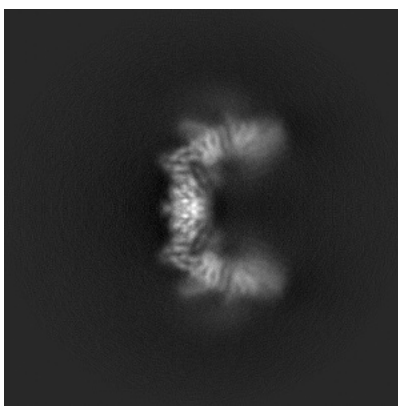
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

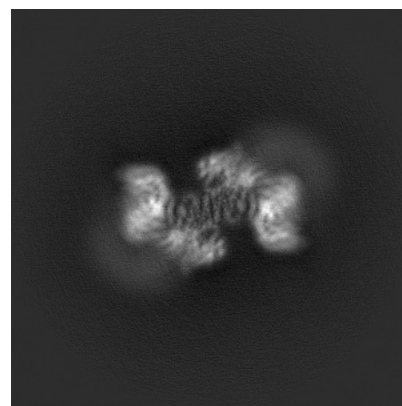
6.1.1 Primary map



X

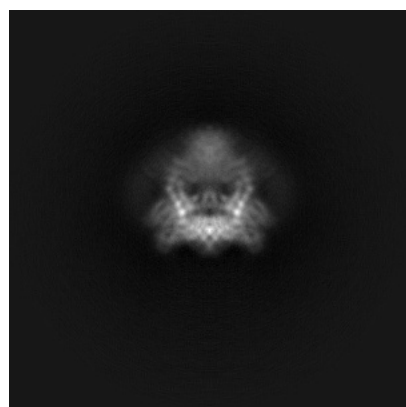


Y

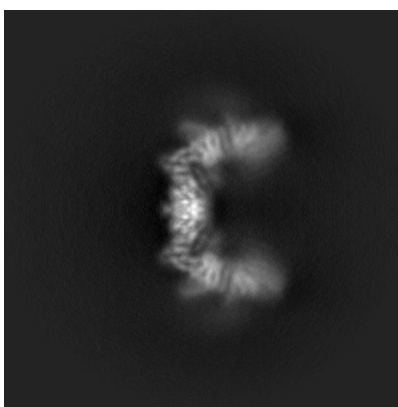


Z

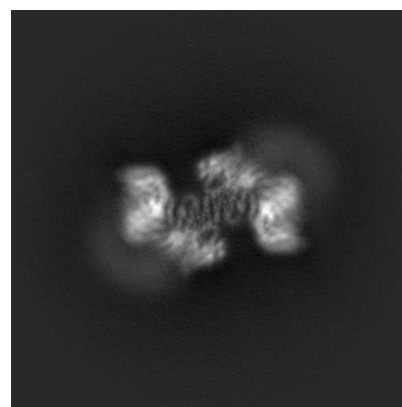
6.1.2 Raw map



X



Y

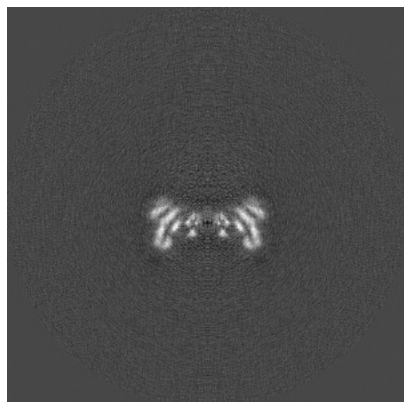


Z

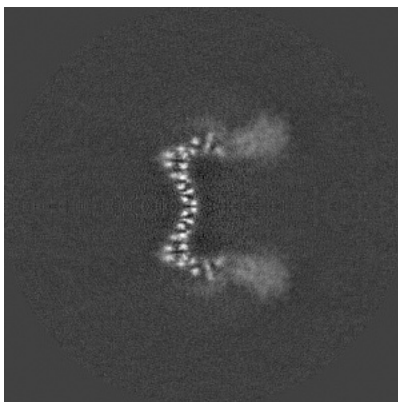
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

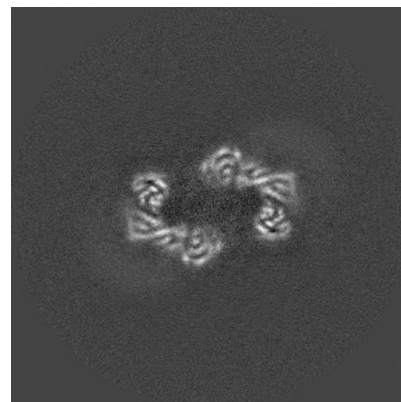
6.2.1 Primary map



X Index: 170

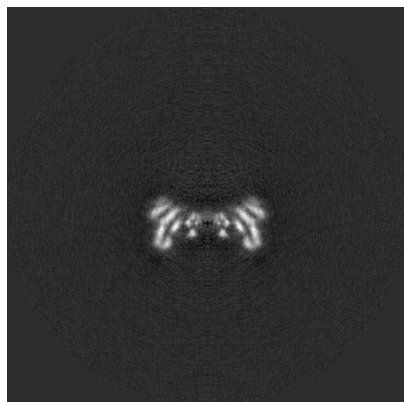


Y Index: 170

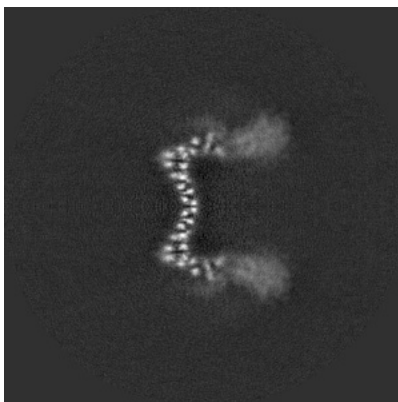


Z Index: 170

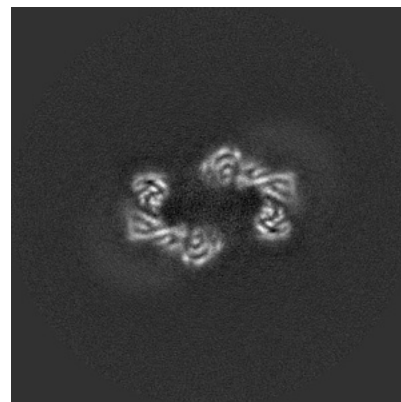
6.2.2 Raw map



X Index: 170



Y Index: 170

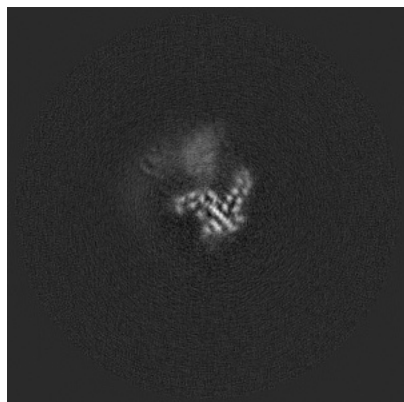


Z Index: 170

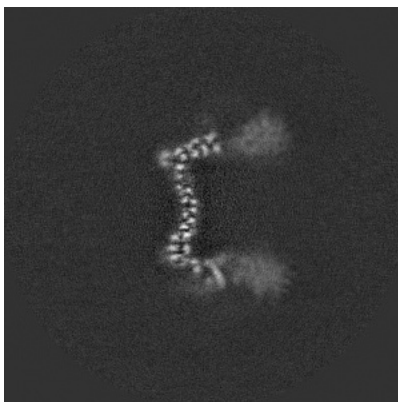
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

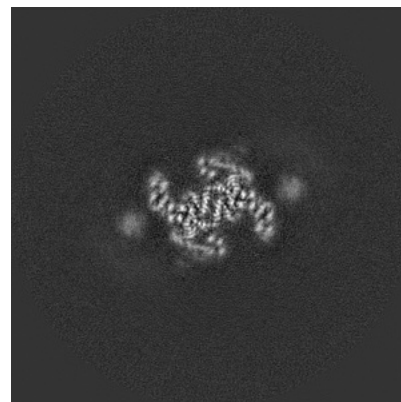
6.3.1 Primary map



X Index: 120

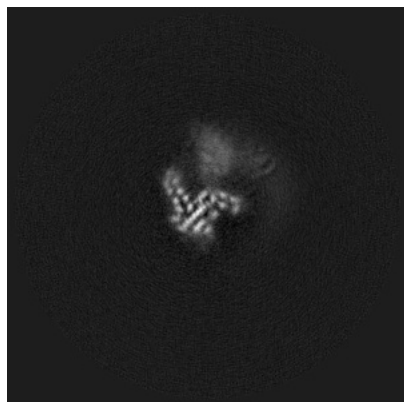


Y Index: 167

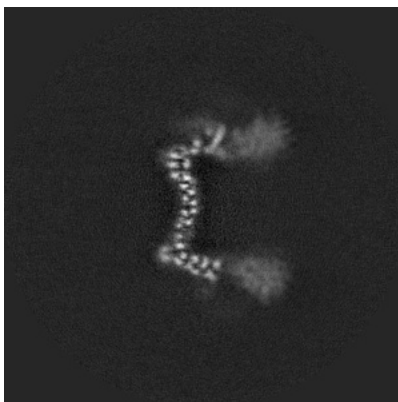


Z Index: 153

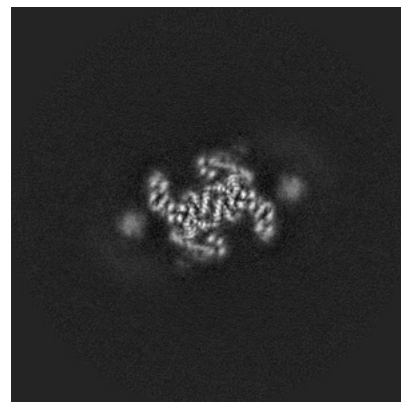
6.3.2 Raw map



X Index: 220



Y Index: 173

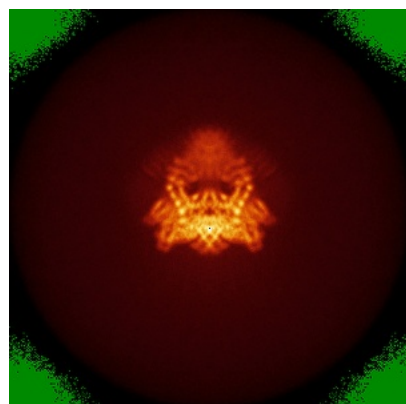


Z Index: 153

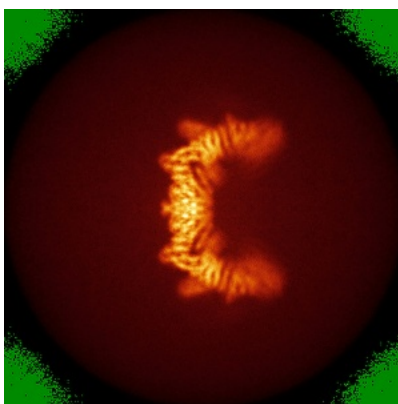
The images above show the largest variance slices of the map in three orthogonal directions.

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

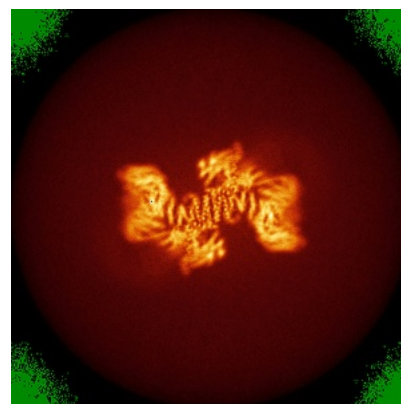
6.4.1 Primary map



X



Y



Z

6.4.2 Raw map



X



Y

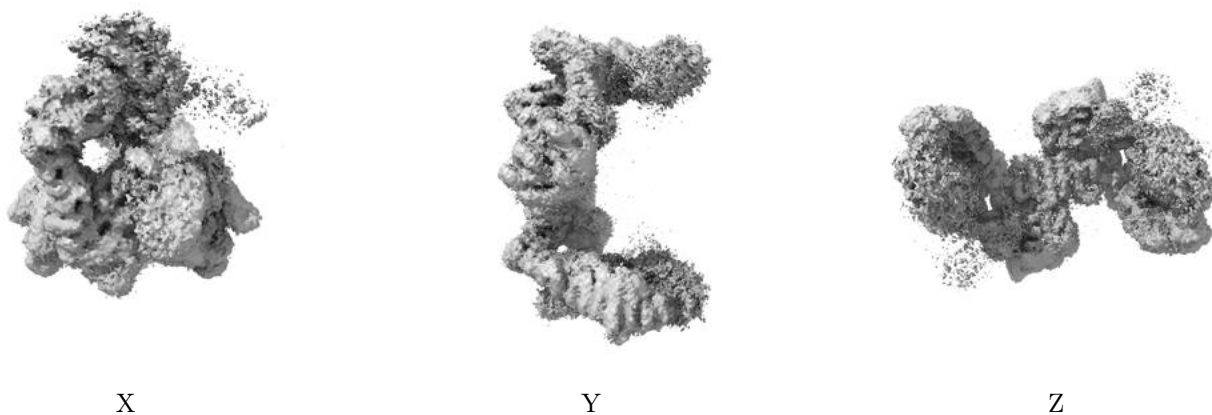


Z

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.

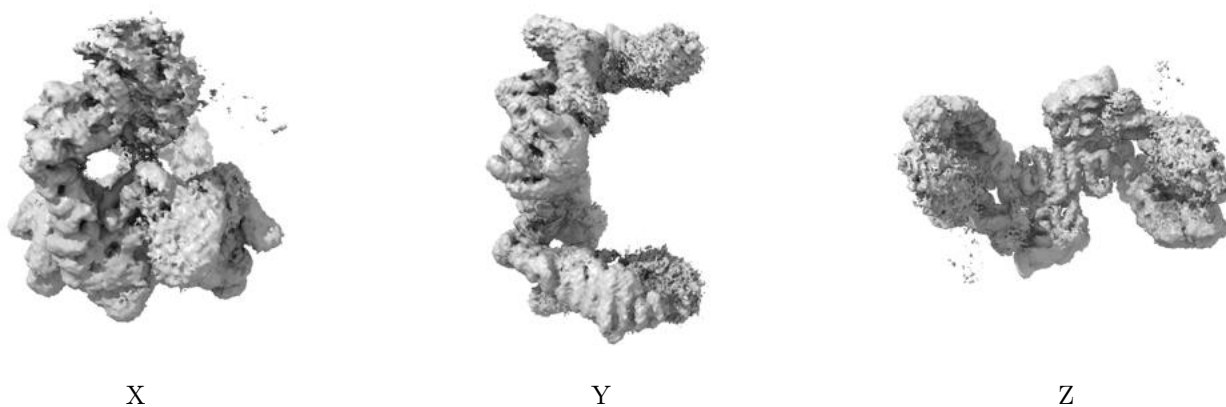
6.5 Orthogonal surface views [i](#)

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.

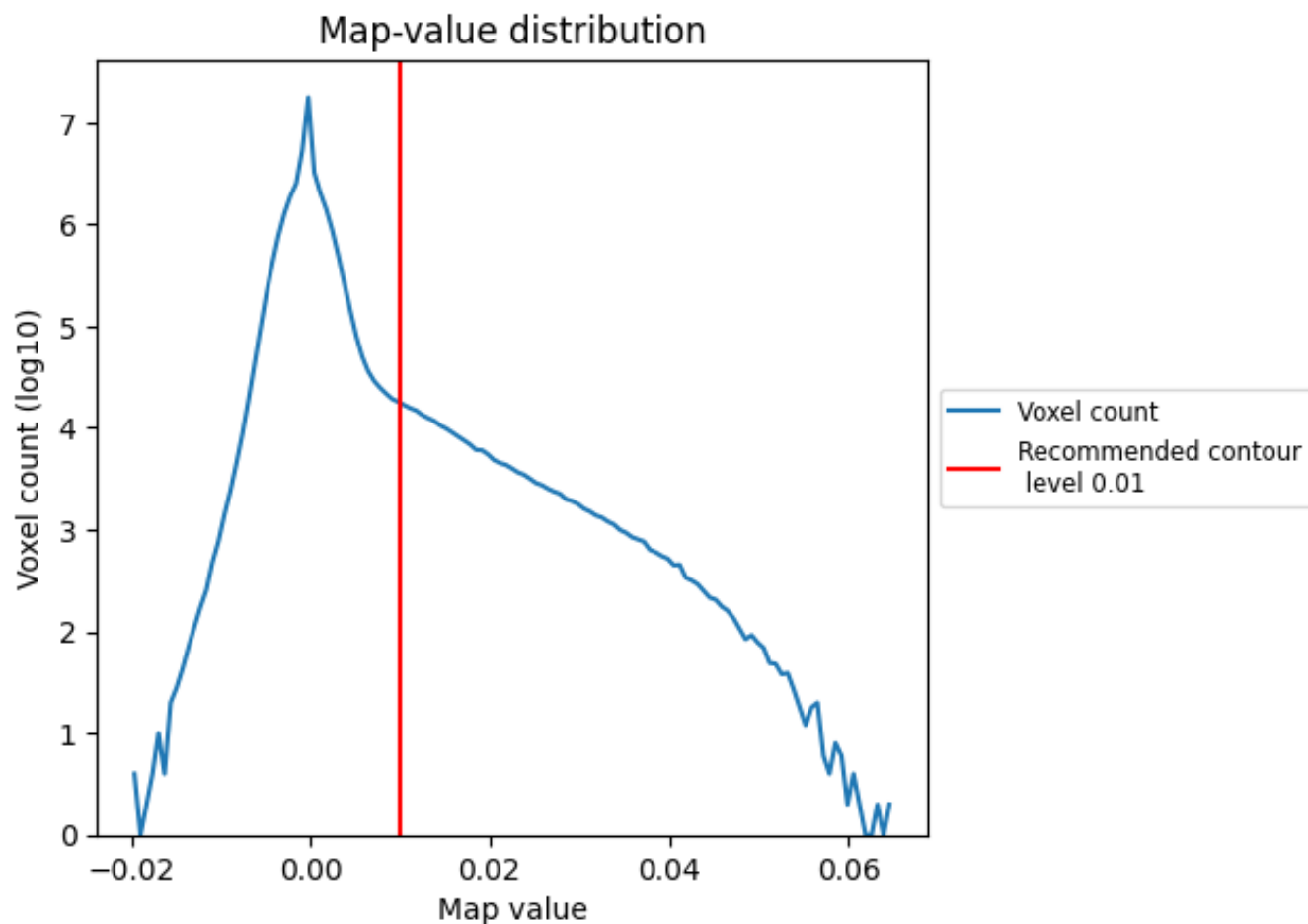
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

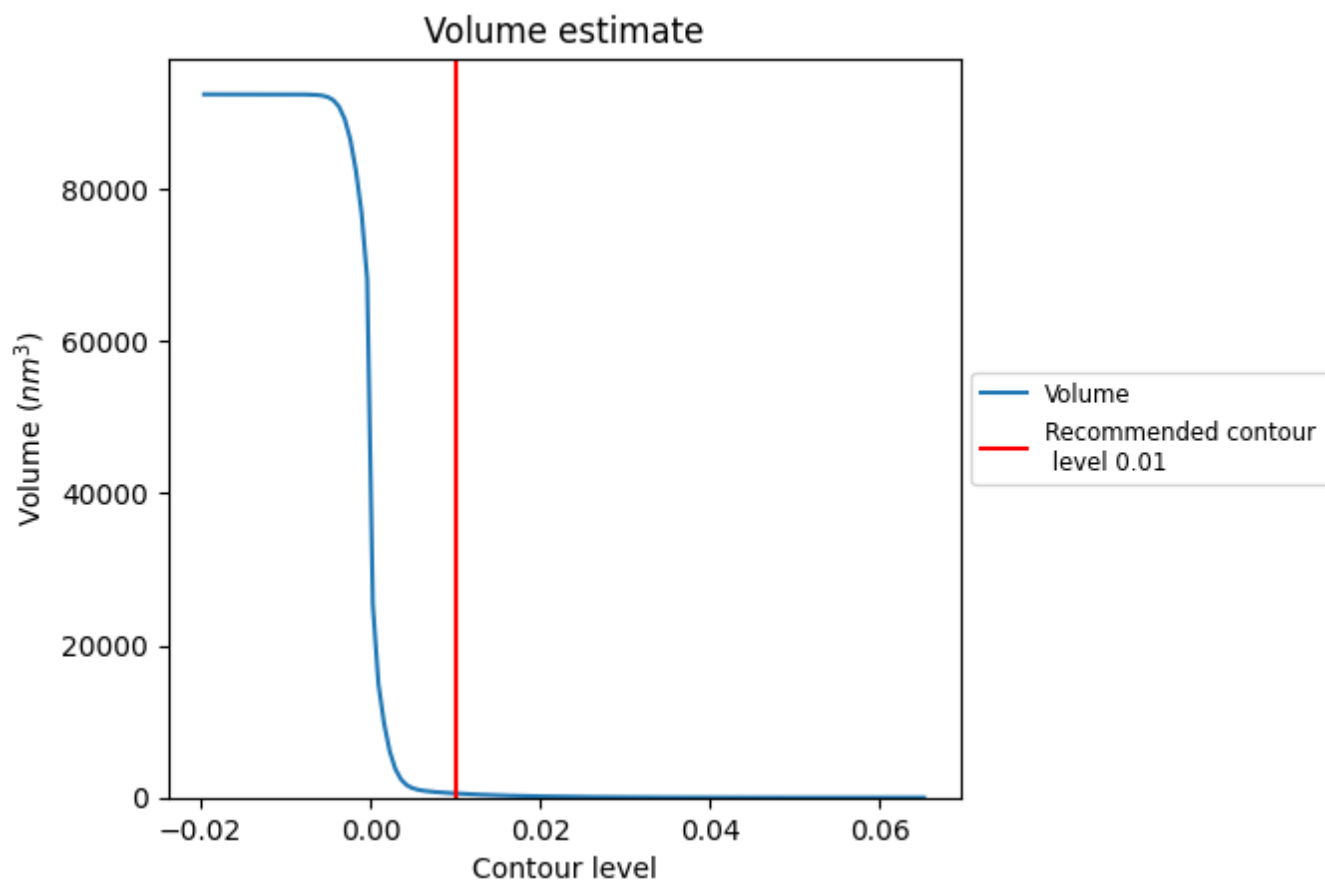
This section contains the results of statistical analysis of the map.

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.

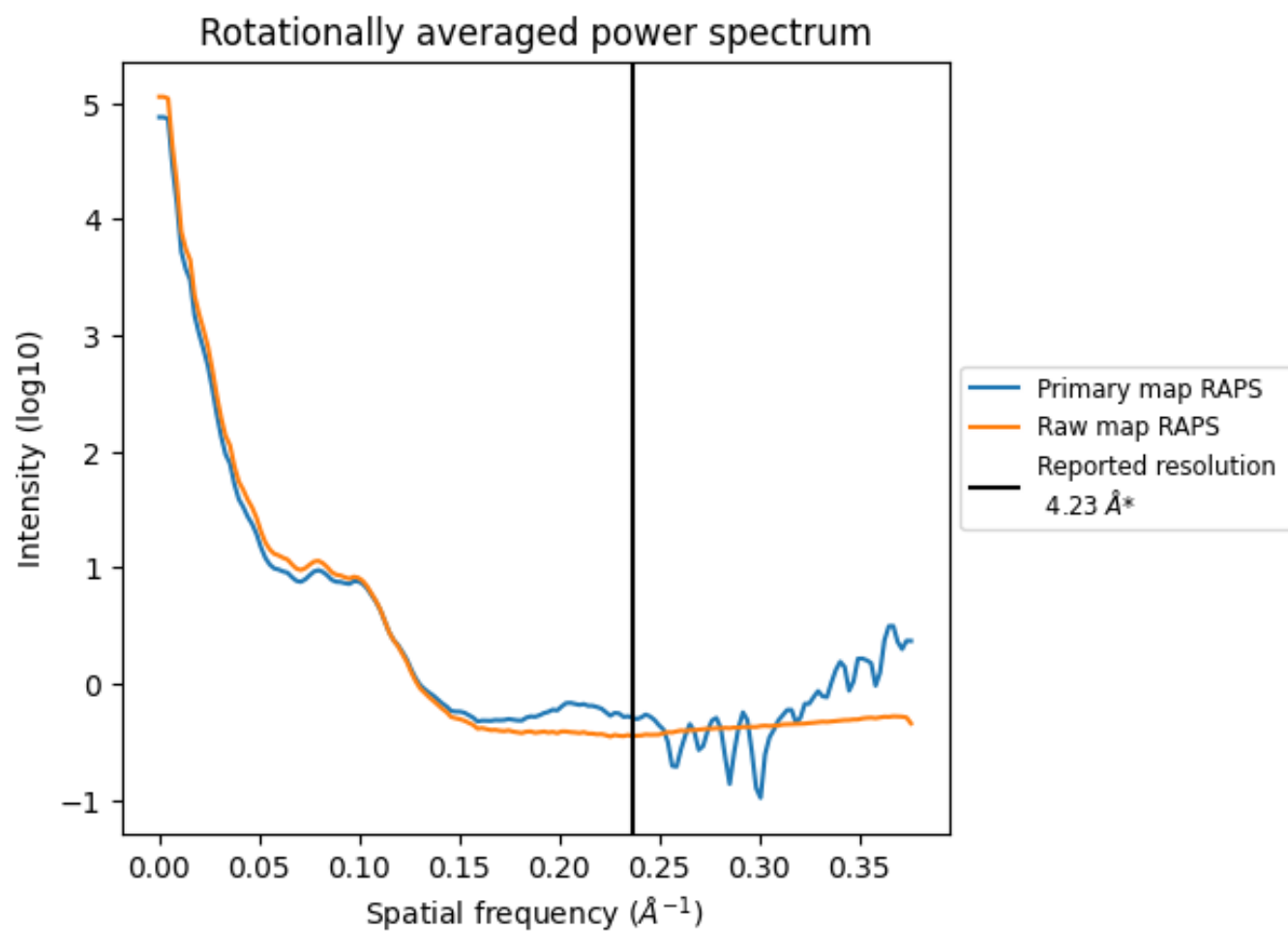
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 546 nm³; this corresponds to an approximate mass of 494 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 ⓘ

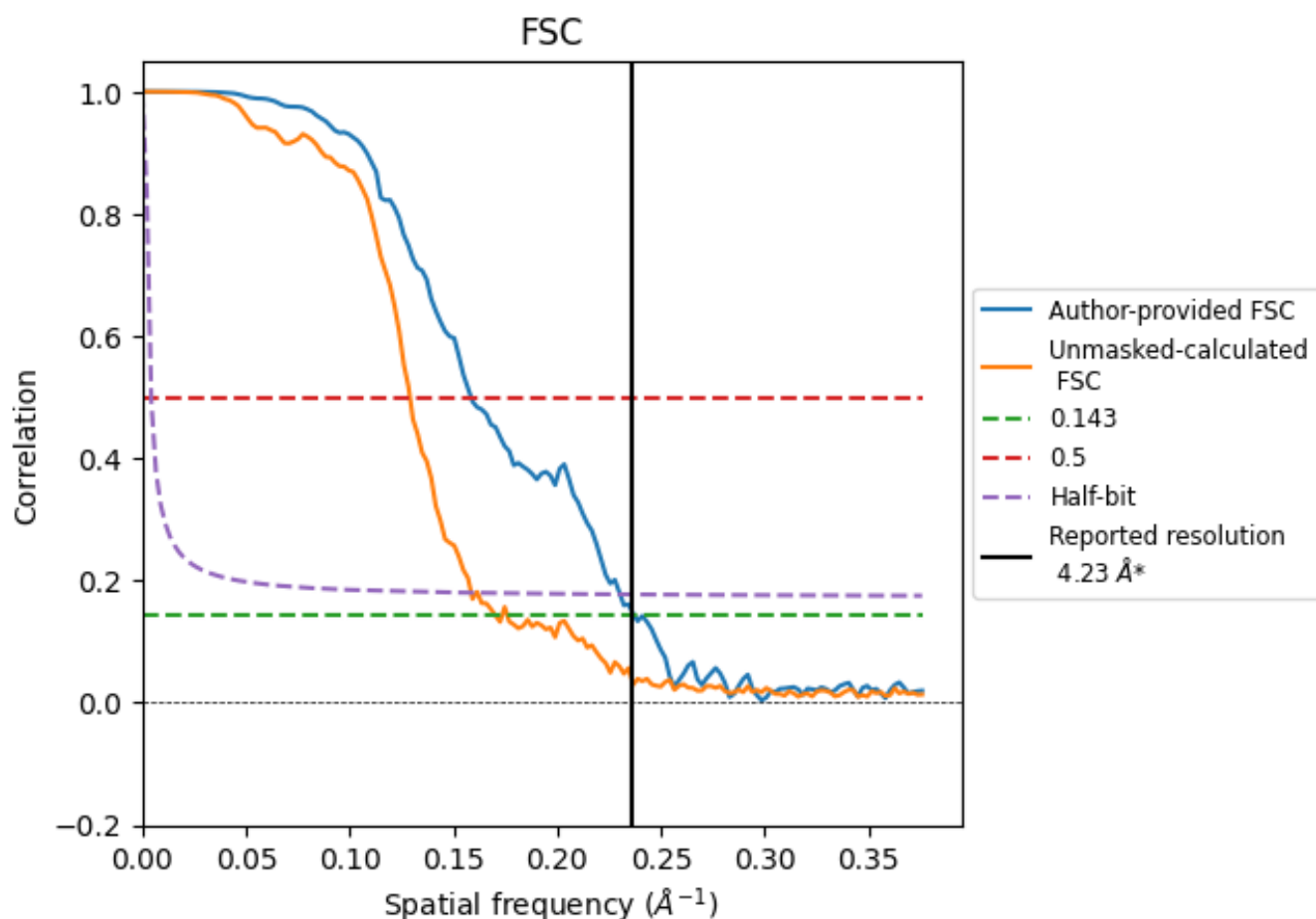


*Reported resolution corresponds to spatial frequency of 0.236 Å⁻¹

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](#)

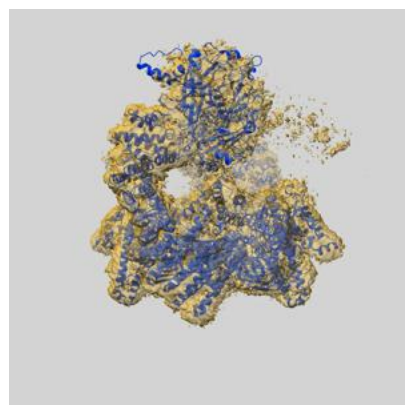
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.23	-	-
Author-provided FSC curve	4.22	6.31	4.34
Unmasked-calculated*	5.88	7.75	6.31

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

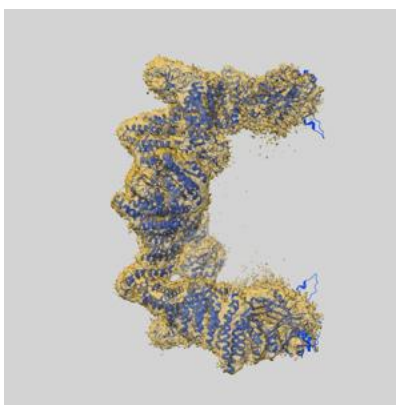
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-60146 and PDB model 8ZJI. Per-residue inclusion information can be found in section [3](#) on page [6](#).

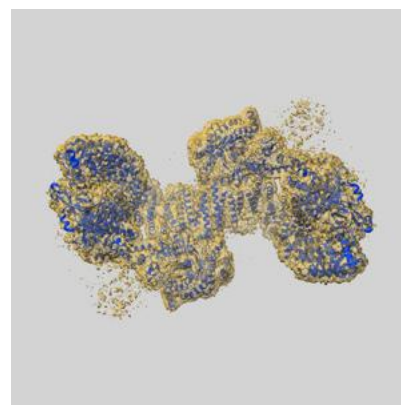
9.1 Map-model overlay [i](#)



X



Y



Z

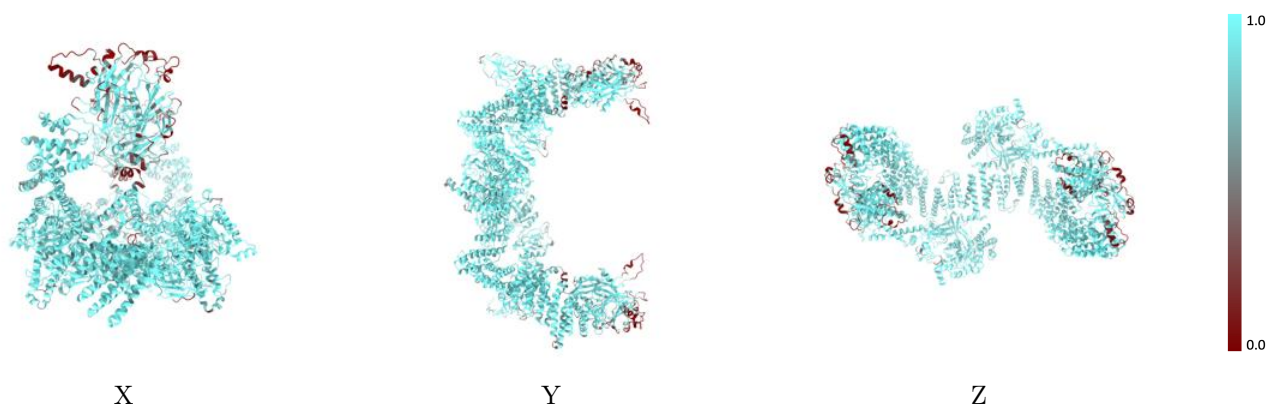
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



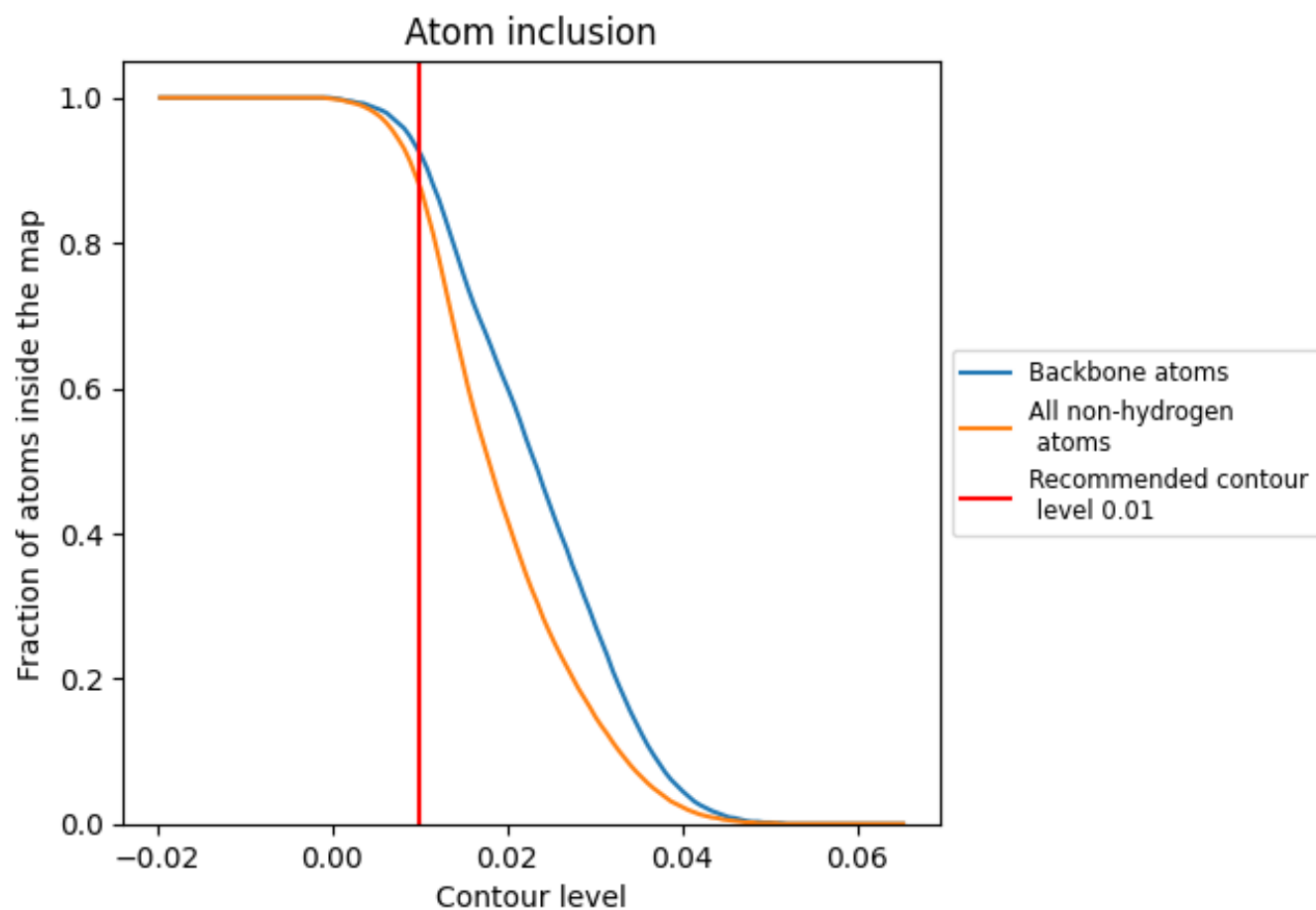
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



At the recommended contour level, 92% of all backbone atoms, 88% 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	0.8790	0.1920
A	0.9060	0.1590
B	0.8680	0.1910
C	0.9700	0.2480
D	0.9130	0.1580
E	0.8650	0.1900
F	0.9720	0.2490

1.0

0.0

<0.0