



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 05:08 AM UTC

PDB ID : 7DPA / pdb_00007dpa
EMDB ID : EMD-30802
Title : Cryo-EM structure of the human ELMO1-DOCK5-Rac1 complex
Authors : Kukimoto-Niino, M.; Katsura, K.; Kaushik, R.; Ehara, H.; Yokoyama, T.;
Uchikubo-Kamo, T.; Mishima-Tsumagari, C.; Yonemochi, M.; Ikeda, M.;
Hanada, K.; Zhang, K.Y.J.; Shirouzu, M.
Deposited on : 2020-12-18
Resolution : 3.80 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

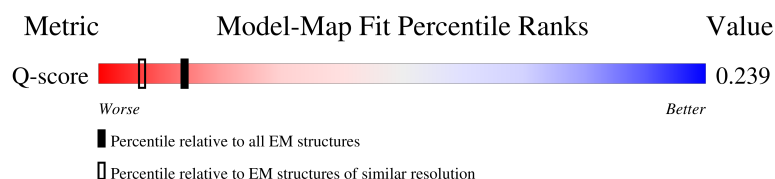
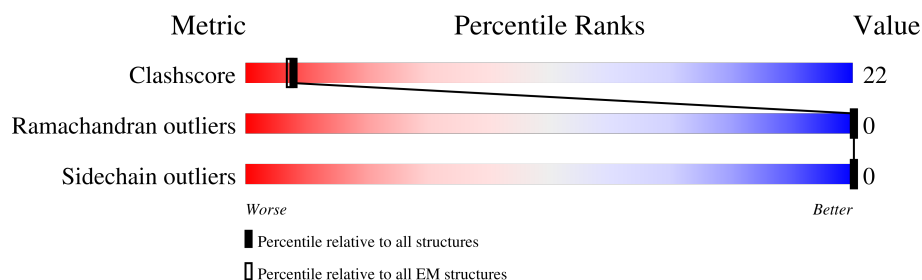
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.80 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	10198 (3.30 - 4.30)

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	1648	
1	D	1648	
2	B	184	
2	E	184	

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Mol	Chain	Length	Quality of chain
3	C	733	15%12%73%
3	F	733	15%12%73%

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 Dedicator of cytokinesis protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1642	Total	C	N	O	S	0	0
			13436	8618	2264	2484	70		
1	D	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
A	-5	GLY	-	expression tag	UNP Q9H7D0
A	-4	GLY	-	expression tag	UNP Q9H7D0
A	-3	SER	-	expression tag	UNP Q9H7D0
A	-2	GLY	-	expression tag	UNP Q9H7D0
A	-1	GLY	-	expression tag	UNP Q9H7D0
A	0	SER	-	expression tag	UNP Q9H7D0
A	1285	ARG	LYS	variant	UNP Q9H7D0
D	-5	GLY	-	expression tag	UNP Q9H7D0
D	-4	GLY	-	expression tag	UNP Q9H7D0
D	-3	SER	-	expression tag	UNP Q9H7D0
D	-2	GLY	-	expression tag	UNP Q9H7D0
D	-1	GLY	-	expression tag	UNP Q9H7D0
D	0	SER	-	expression tag	UNP Q9H7D0
D	1285	ARG	LYS	variant	UNP Q9H7D0

- Molecule 2 is a protein called Ras-related C3 botulinum toxin substrate 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	177	Total	C	N	O	S	0	0
			1385	890	228	259	8		
2	E	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
B	-6	GLY	-	expression tag	UNP P63000
B	-5	SER	-	expression tag	UNP P63000
B	-4	SER	-	expression tag	UNP P63000
B	-3	GLY	-	expression tag	UNP P63000
B	-2	SER	-	expression tag	UNP P63000
B	-1	SER	-	expression tag	UNP P63000
B	0	GLY	-	expression tag	UNP P63000
B	15	ALA	GLY	engineered mutation	UNP P63000
E	-6	GLY	-	expression tag	UNP P63000
E	-5	SER	-	expression tag	UNP P63000
E	-4	SER	-	expression tag	UNP P63000
E	-3	GLY	-	expression tag	UNP P63000
E	-2	SER	-	expression tag	UNP P63000
E	-1	SER	-	expression tag	UNP P63000
E	0	GLY	-	expression tag	UNP P63000
E	15	ALA	GLY	engineered mutation	UNP P63000

- Molecule 3 is a protein called Engulfment and cell motility protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	198	Total	C	N	O	S	0	0
			1608	1018	277	303	10		
3	F	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
C	-5	GLY	-	expression tag	UNP Q92556
C	-4	GLY	-	expression tag	UNP Q92556
C	-3	SER	-	expression tag	UNP Q92556
C	-2	GLY	-	expression tag	UNP Q92556
C	-1	GLY	-	expression tag	UNP Q92556
C	0	SER	-	expression tag	UNP Q92556
F	-5	GLY	-	expression tag	UNP Q92556
F	-4	GLY	-	expression tag	UNP Q92556
F	-3	SER	-	expression tag	UNP Q92556
F	-2	GLY	-	expression tag	UNP Q92556
F	-1	GLY	-	expression tag	UNP Q92556
F	0	SER	-	expression tag	UNP Q92556

3 Residue-property plots

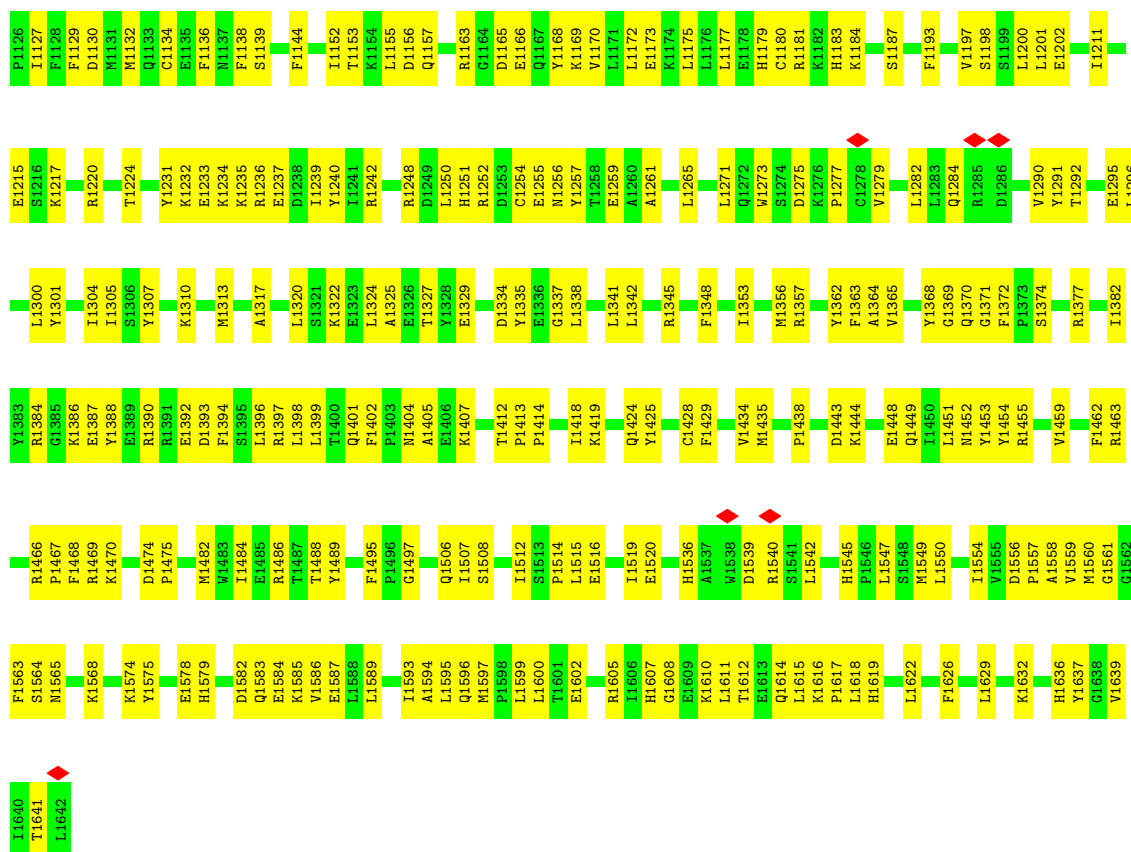
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Dedicator of cytokinesis protein 5

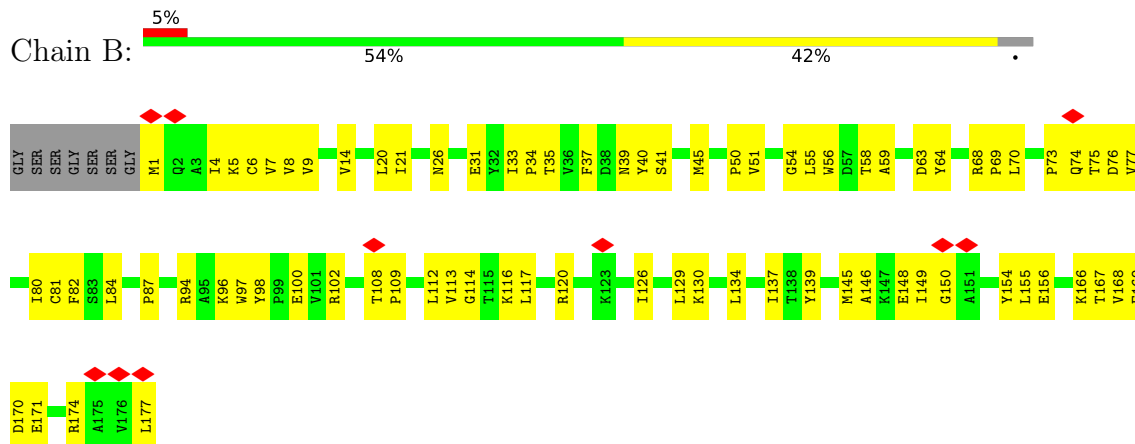




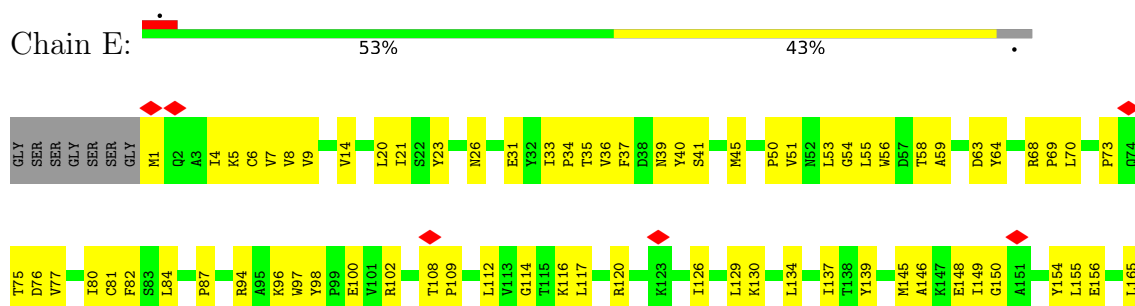
F1047	H857	L879	M802	F724	L640	K573	Y502	K430	L362	S295	F231	H154	F1048	H858	L880	M803	F725	L641	K574	Y503	K431	L363	S296	F232	H155	F1049	H859	L881	M804	F726	L642	K575	Y504	K432	L364	S297	F233	H156	F1050	H860	L882	M805	F727	L643	K576	Y505	K433	L365	S298	F234	H157	F1051	H861	L883	M806	F728	L644	K577	Y506	K434	L366	S299	F235	H158	F1052	H862	L884	M807	F729	L645	K578	Y507	K435	L367	S300	F236	H159	F1053	H863	L885	M808	F730	L646	K579	Y508	K436	L368	S301	F237	H160	F1054	H864	L886	M809	F731	L647	K580	Y509	K437	L369	S302	F238	H161	F1055	H865	L887	M810	F732	L648	K581	Y510	K438	L370	S303	F239	H162	F1056	H866	L888	M811	F733	L649	K582	Y511	K439	L371	S304	F240	H163	F1057	H867	L889	M812	F734	L650	K583	Y512	K440	L372	S305	F241	H164	F1058	H868	L890	M813	F735	L651	K584	Y513	K441	L373	S306	F242	H165	F1059	H869	L891	M814	F736	L652	K585	Y514	K442	L374	S307	F243	H166	F1060	H870	L892	M815	F737	L653	K586	Y515	K443	L375	S308	F244	H167	F1061	H871	L893	M816	F738	L654	K587	Y516	K444	L376	S309	F245	H168	F1062	H872	L894	M817	F739	L655	K588	Y517	K445	L377	S310	F246	H169	F1063	H873	L895	M818	F740	L656	K589	Y518	K446	L378	S311	F247	H170	F1064	H874	L896	M819	F741	L657	K590	Y519	K447	L379	S312	F248	H171	F1065	H875	L897	M820	F742	L658	K591	Y520	K448	L380	S313	F249	H172	F1066	H876	L898	M821	F743	L659	K592	Y521	K449	L381	S314	F250	H173	F1067	H877	L899	M822	F744	L660	K593	Y522	K450	L382	S315	F251	H174	F1068	H878	L900	M823	F745	L661	K594	Y523	K451	L383	S316	F252	H175	F1069	H879	L901	M824	F746	L662	K595	Y524	K452	L384	S317	F253	H176	F1070	H880	L902	M825	F747	L663	K596	Y525	K453	L385	S318	F254	H177	F1071	H881	L903	M826	F748	L664	K597	Y526	K454	L386	S319	F255	H178	F1072	H882	L904	M827	F749	L665	K598	Y527	K455	L387	S320	F256	H179	F1073	H883	L905	M828	F750	L666	K599	Y528	K456	L388	S321	F257	H180	F1074	H884	L906	M829	F751	L667	K600	Y529	K457	L389	S322	F258	H181	F1075	H885	L907	M830	F752	L668	K601	Y530	K458	L390	S323	F259	H182	F1076	H886	L908	M831	F753	L669	K602	Y531	K459	L391	S324	F260	H183	F1077	H887	L909	M832	F754	L670	K603	Y532	K460	L392	S325	F261	H184	F1078	H888	L910	M833	F755	L671	K604	Y533	K461	L393	S326	F262	H185	F1079	H889	L911	M834	F756	L672	K605	Y534	K462	L394	S327	F263	H186	F1080	H890	L912	M835	F757	L673	K606	Y535	K463	L395	S328	F264	H187	F1081	H891	L913	M836	F758	L674	K607	Y536	K464	L396	S329	F265	H188	F1082	H892	L914	M837	F759	L675	K608	Y537	K465	L397	S330	F266	H189	F1083	H893	L915	M838	F760	L676	K609	Y538	K466	L398	S331	F267	H190	F1084	H894	L916	M839	F761	L677	K610	Y539	K467	L399	S332	F268	H191	F1085	H895	L917	M840	F762	L678	K611	Y540	K468	L400	S333	F269	H192	F1086	H896	L918	M841	F763	L679	K612	Y541	K469	L401	S334	F270	H193	F1087	H897	L919	M842	F764	L680	K613	Y542	K470	L402	S335	F271	H194	F1088	H898	L920	M843	F765	L681	K614	Y543	K471	L403	S336	F272	H195	F1089	H899	L921	M844	F766	L682	K615	Y544	K472	L404	S337	F273	H196	F1090	H900	L922	M845	F767	L683	K616	Y545	K473	L405	S338	F274	H197	F1091	H901	L923	M846	F768	L684	K617	Y546	K474	L406	S339	F275	H198	F1092	H902	L924	M847	F769	L685	K618	Y547	K475	L407	S340	F276	H199	F1093	H903	L925	M848	F770	L686	K619	Y548	K476	L408	S341	F277	H200	F1094	H904	L926	M849	F771	L687	K620	Y549	K477	L409	S342	F278	H201	F1095	H905	L927	M850	F772	L688	K621	Y550	K478	L410	S343	F279	H202	F1096	H906	L928	M851	F773	L689	K622	Y551	K479	L411	S344	F280	H203	F1097	H907	L929	M852	F774	L690	K623	Y552	K480	L412	S345	F281	H204	F1098	H908	L930	M853	F775	L691	K624	Y553	K481	L413	S346	F282	H205	F1099	H909	L931	M854	F776	L692	K625	Y554	K482	L414	S347	F283	H206	F1100	H910	L932	M855	F777	L693	K626	Y555	K483	L415	S348	F284	H207	F1101	H911	L933	M856	F778	L694	K627	Y556	K484	L416	S349	F285	H208	F1102	H912	L934	M857	F779	L695	K628	Y557	K485	L417	S350	F286	H209	F1103	H913	L935	M858	F780	L696	K629	Y558	K486	L418	S351	F287	H210	F1104	H914	L936	M859	F781	L697	K630	Y559	K487	L419	S352	F288	H211	F1105	H915	L937	M860	F782	L698	K631	Y560	K488	L420	S353	F289	H212	F1106	H916	L938	M861	F783	L699	K632	Y561	K489	L421	S354	F290	H213	F1107	H917	L939	M862	F784	L700	K633	Y562	K490	L422	S355	F291	H214	F1108	H918	L940	M863	F785	L701	K634	Y563	K491	L423	S356	F292	H215	F1109	H919	L941	M864	F786	L702	K635	Y564	K492	L424	S357	F293	H216	F1110	H920	L942	M865	F787	L703	K636	Y565	K493	L425	S358	F294	H217	F1111	H921	L943	M866	F788	L704	K637	Y566	K494	L426	S359	F295	H218	F1112	H922	L944	M867	F789	L705	K638	Y567	K495	L427	S360	F296	H219	F1113	H923	L945	M868	F790	L706	K639	Y568	K496	L428	S361	F297	H220	F1114	H924	L946	M869	F791	L707	K640	Y569	K497	L429	S362	F298	H221	F1115	H925	L947	M870	F792	L708	K641	Y570	K498	L430	S363	F299	H222	F1116	H926	L948	M871	F793	L709	K642	Y571	K499	L431	S364	F300	H223	F1117	H927	L949	M872	F794	L710	K643	Y572	K500	L432	S365	F301	H224	F1118	H928	L950	M873	F795	L711	K644	Y573	K501	L433	S366	F302	H225	F1119	H929	L951	M874	F796	L712	K645	Y574	K502	L434	S367	F303	H226	F1120	H930	L952	M875	F797	L713	K646	Y575	K503	L435	S368	F304	H227	F1121	H931	L953	M876	F798	L714	K647	Y576	K504	L436	S369	F305	H228	F1122	H932	L954	M877	F799	L715	K648	Y577	K505	L437	S370	F306	H229	F1123	H933	L955	M878	F800	L716	K649	Y578	K506	L438	S371	F307	H230	F1124	H934	L956	M879	F801	L717	K650	Y579	K507	L439	S372	F308	H231	F1125	H935	L957	M880	F802	L718	K651	Y580	K508	L440	S373	F309	H232	F1126	H936	L958	M881	F803	L719	K652	Y581	K509	L441	S374	F310	H233	F1127	H937	L959	M882	F804	L720	K653	Y582	K510	L442	S375	F311	H234	F1128	H938	L960	M883	F805	L721	K654	Y583	K511	L443	S376	F312	H235	F1129	H939	L961	M884	F806	L722	K655	Y584	K512	L444	S377	F313	H236	F1130	H940	L962	M885	F807	L723	K656	Y585	K513	L445	S378	F314	H237	F1131	H941	L963	M886	F808	L724	K657	Y586	K514	L446	S379	F315	H238	F1132	H942	L964	M887	F809	L725	K658	Y587	K515	L447	S380	F316	H239	F1133	H943	L965	M888	F810	L726	K659	Y588	K516	L448	S381	F317	H240	F1134	H944	L966	M889	F811	L727	K660	Y589	K517	L449	S382	F318	H241	F1135	H945	L967	M890	F812	L728	K661	Y590	K518	L450	S383	F319	H242	F1136	H946	L968	M891	F813	L729	K662	Y591	K519	L451	S384	F320	H243	F1137	H947	L969	M892	F814	L730	K663	Y592	K520	L452	S385	F321	H244	F1138	H948	L970	M893	F815	L731	K664	Y593	K521	L453	S386	F322	H245	F1139	H949	L971	M894	F816	L732	K665	Y594	K522	L454	S387	F323	H246	F1140	H950	L972	M895	F817	L733	K666	Y595	K523	L455	S388	F324	H247	F1141	H951	L973	M896	F818	L734	K667	Y596	K524	L456	S389	F325	H248	F1142	H952	L974	M897	F819	L735	K668	Y597	K525	L457	S390	F326	H249	F1143	H953	L975	M898	F820	L736	K669	Y598	K526	L458	S391	F327	H250	F1144	H954	L976	M899	F821	L737	K670	Y599	K527	L459	S392	F328	H251	F1145	H955	L977	M900	F822	L738	K671	Y600	K528	L460	S393	F329	H252	F1146	H956	L978	M901	F823	L739	K672	Y601	K529	L461	S394	F330	H253	F1147	H957	L979	M902	F824	L740	K673	Y602	K530	L462	S395	F331	H254	F1148	H958	L980	M903	F825	L741	K674	Y603	K531	L463	S396	F332	H255	F1149	H959	L981	M904	F826	L742	K675	Y604	K532	L464	S397	F333	H256	F1150	H960	L982	M905	F827	L743	K676	Y605	K533	L465	S398	F334	H257	F1151	H961	L983	M906	F828	L744	K677	Y606	K534	L466	S399	F335	H258	F1152	H962	L984	M907	F829	L745	K678	Y607	K535	L467	S400	F336	H259	F1153	H963	L985	M908	F830	L746	K679	Y608	K536	L468	S401	F337	H260	F1154	H964	L986	M909	F831	L747	K680	Y609	K537	L469	S402	F338	H261	F1155	H965	L987	M910	F832	L748	K681	Y610	K538	L470	S403	F339	H262	F1156	H966	L988	M911	F833	L749	K682	Y611	K539	L471	S404	F340	H263	F1157	H967	L989	M912	F834	L750	K683	Y612	K540	L472	S405	F341	H264	F1158	H968	L990	M913	F835	L751	K684	Y613	K541	L473	S406	F342	H265	F1159	H969	L991	M914	F836	L752	K685	Y614	K542	L474	S407	F343	H266	F1160	H970	L992	M915	F837	L753	K686	Y615	K543	L475	S408	F344	H267	F1161	H971	L993	M916	F838	L754	K687	Y616	K544	L476	S409	F345	H268	F1162	H972	L994	M917	F839	L755	K688
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• Molecule 2: Ras-related C3 botulinum toxin substrate 1



• Molecule 2: Ras-related C3 botulinum toxin substrate 1



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	149846	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	0.5	Depositor
Maximum defocus (nm)	3.0	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.023	Depositor
Minimum map value	-0.008	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.004	Depositor
Map size (Å)	431.6, 431.6, 431.6	wwPDB
Map dimensions	520, 520, 520	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	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	0.26	0/13722	0.50	0/18514
1	D	0.26	0/13722	0.50	0/18514
2	B	0.20	0/1415	0.43	0/1924
2	E	0.21	0/1415	0.43	0/1924
3	C	0.18	0/1641	0.44	0/2218
3	F	0.18	0/1641	0.44	0/2218
All	All	0.25	0/33556	0.49	0/45312

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	13436	0	13516	624	0
1	D	13436	0	13516	625	0
2	B	1385	0	1407	70	0
2	E	1385	0	1407	69	0
3	C	1608	0	1617	87	0
3	F	1608	0	1617	90	0
All	All	32858	0	33080	1474	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 22.

The worst 5 of 1474 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:166:ARG:HB2	1:D:174:ASP:HB2	1.50	0.93
1:A:1342:LEU:HD12	1:D:1342:LEU:HD12	1.51	0.92
1:A:166:ARG:HB2	1:A:174:ASP:HB2	1.50	0.91
1:A:10:GLN:HG3	1:A:37:ILE:HB	1.53	0.88
1:D:10:GLN:HG3	1:D:37:ILE:HB	1.53	0.88

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	1640/1648 (100%)	1434 (87%)	206 (13%)	0	100	100
1	D	1640/1648 (100%)	1437 (88%)	203 (12%)	0	100	100
2	B	175/184 (95%)	158 (90%)	17 (10%)	0	100	100
2	E	175/184 (95%)	157 (90%)	18 (10%)	0	100	100
3	C	196/733 (27%)	170 (87%)	26 (13%)	0	100	100
3	F	196/733 (27%)	170 (87%)	26 (13%)	0	100	100
All	All	4022/5130 (78%)	3526 (88%)	496 (12%)	0	100	100

There are no Ramachandran outliers to report.

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	1495/1497 (100%)	1495 (100%)	0	100	100
1	D	1495/1497 (100%)	1495 (100%)	0	100	100
2	B	153/157 (98%)	153 (100%)	0	100	100
2	E	153/157 (98%)	153 (100%)	0	100	100
3	C	183/664 (28%)	183 (100%)	0	100	100
3	F	183/664 (28%)	183 (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 54 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	250	GLN
1	D	799	ASN
1	D	1596	GLN
1	D	275	ASN
1	D	563	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.

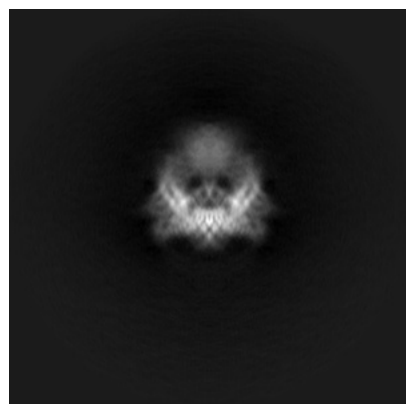
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30802. These allow visual inspection of the internal detail of the map and identification of artifacts.

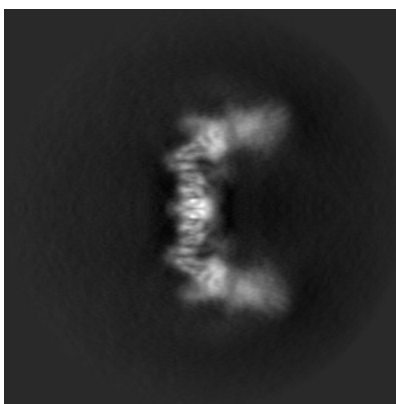
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

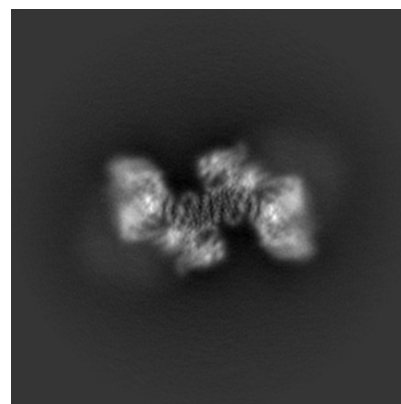
6.1.1 Primary map



X

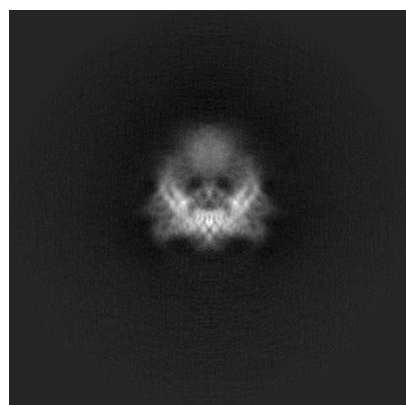


Y

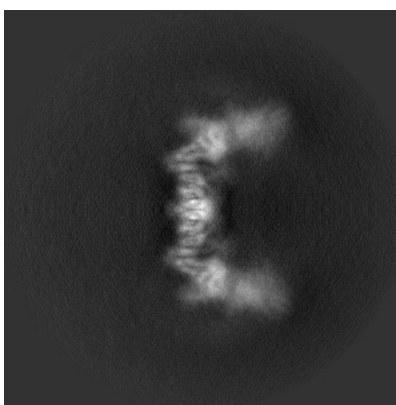


Z

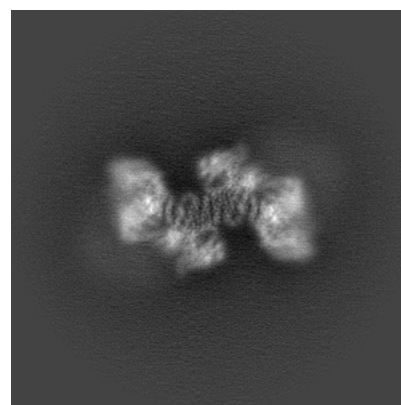
6.1.2 Raw map



X



Y

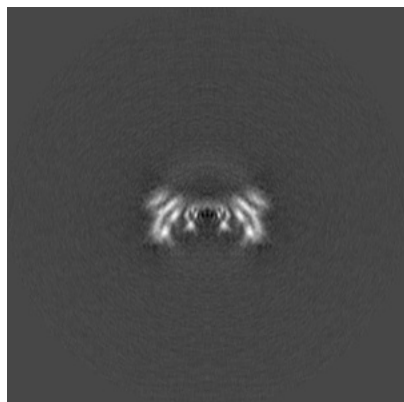


Z

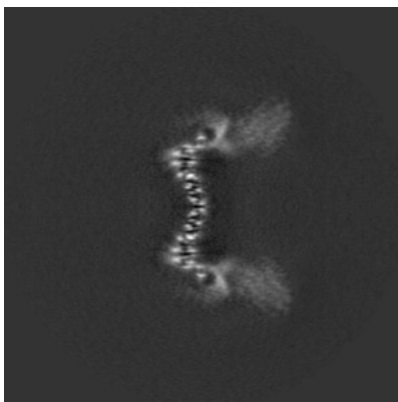
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

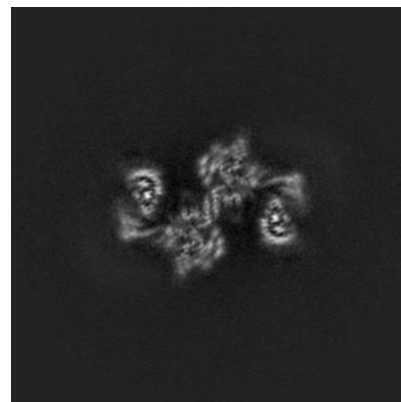
6.2.1 Primary map



X Index: 260

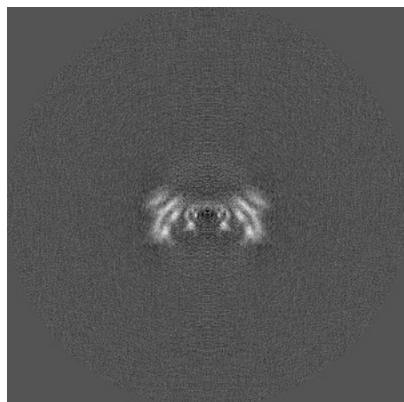


Y Index: 260

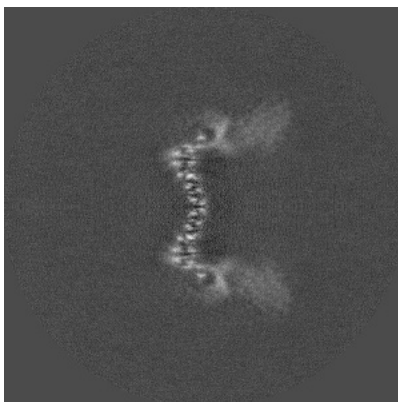


Z Index: 260

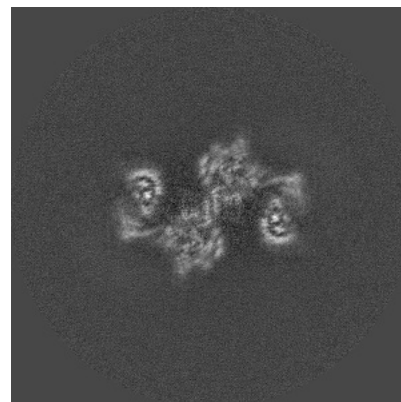
6.2.2 Raw map



X Index: 260



Y Index: 260

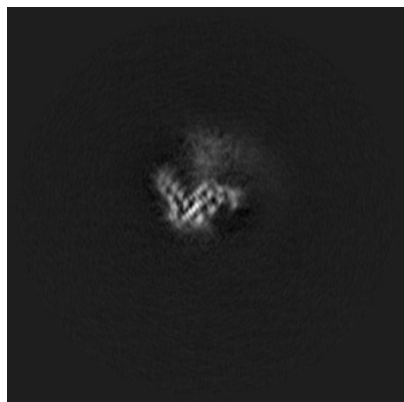


Z Index: 260

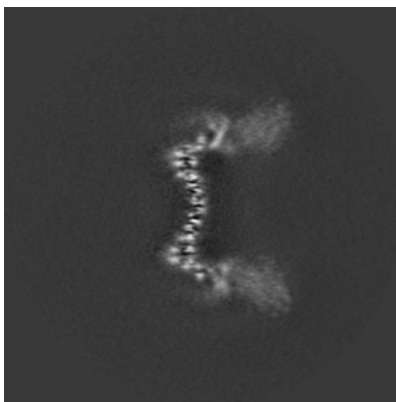
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

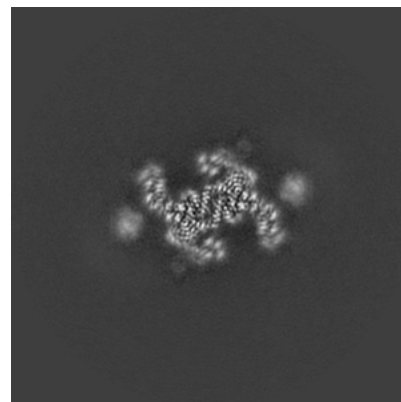
6.3.1 Primary map



X Index: 343

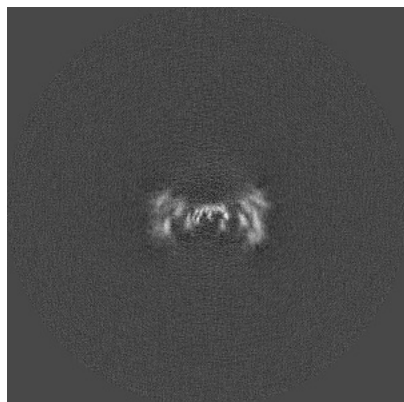


Y Index: 262

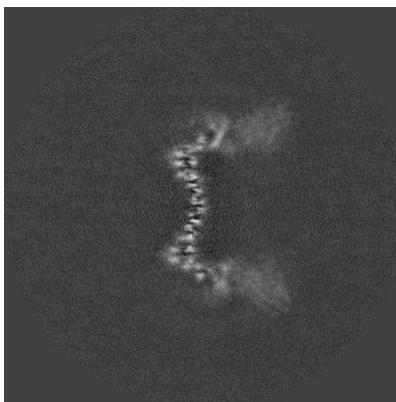


Z Index: 244

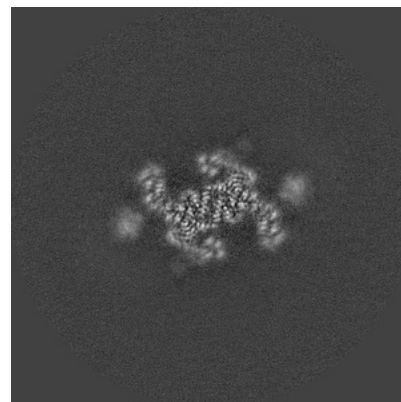
6.3.2 Raw map



X Index: 264



Y Index: 262



Z Index: 245

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

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

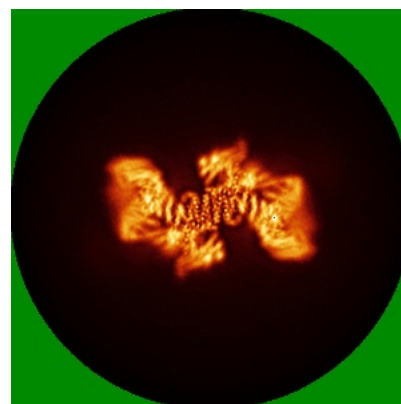
6.4.1 Primary map



X

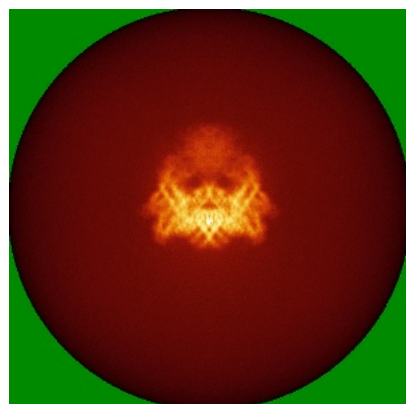


Y

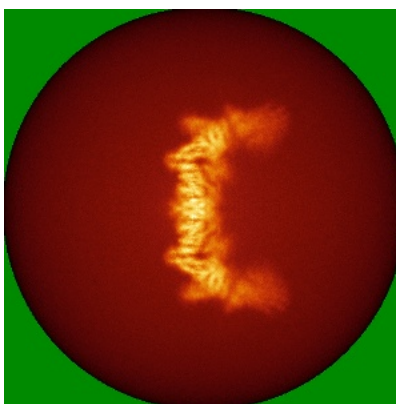


Z

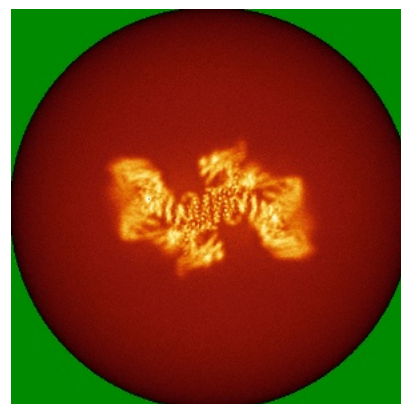
6.4.2 Raw map



X



Y

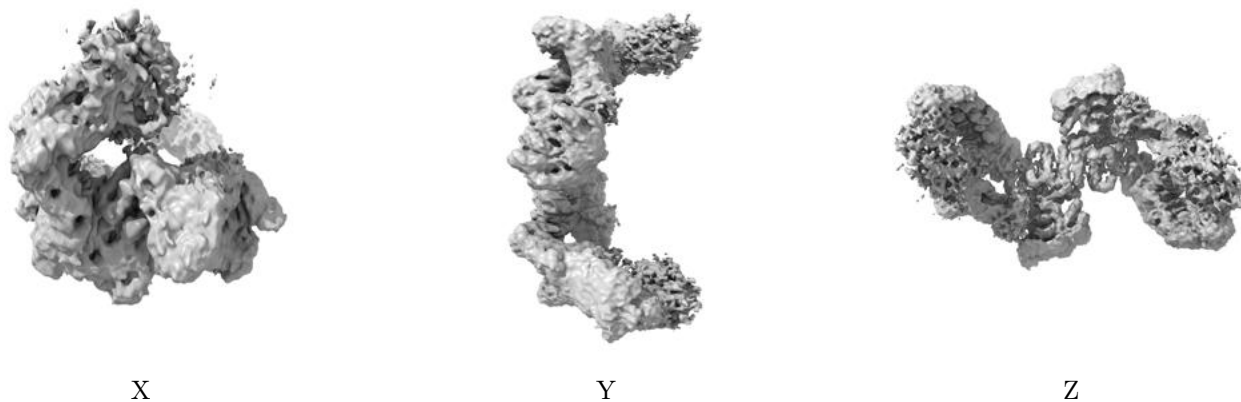


Z

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.

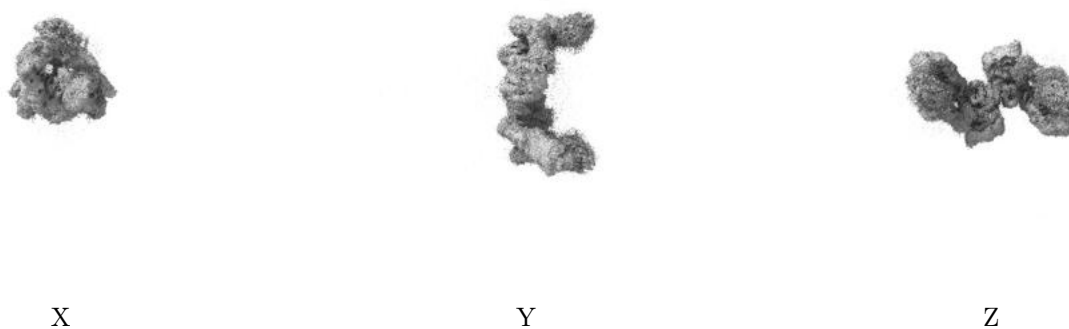
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.004. 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.

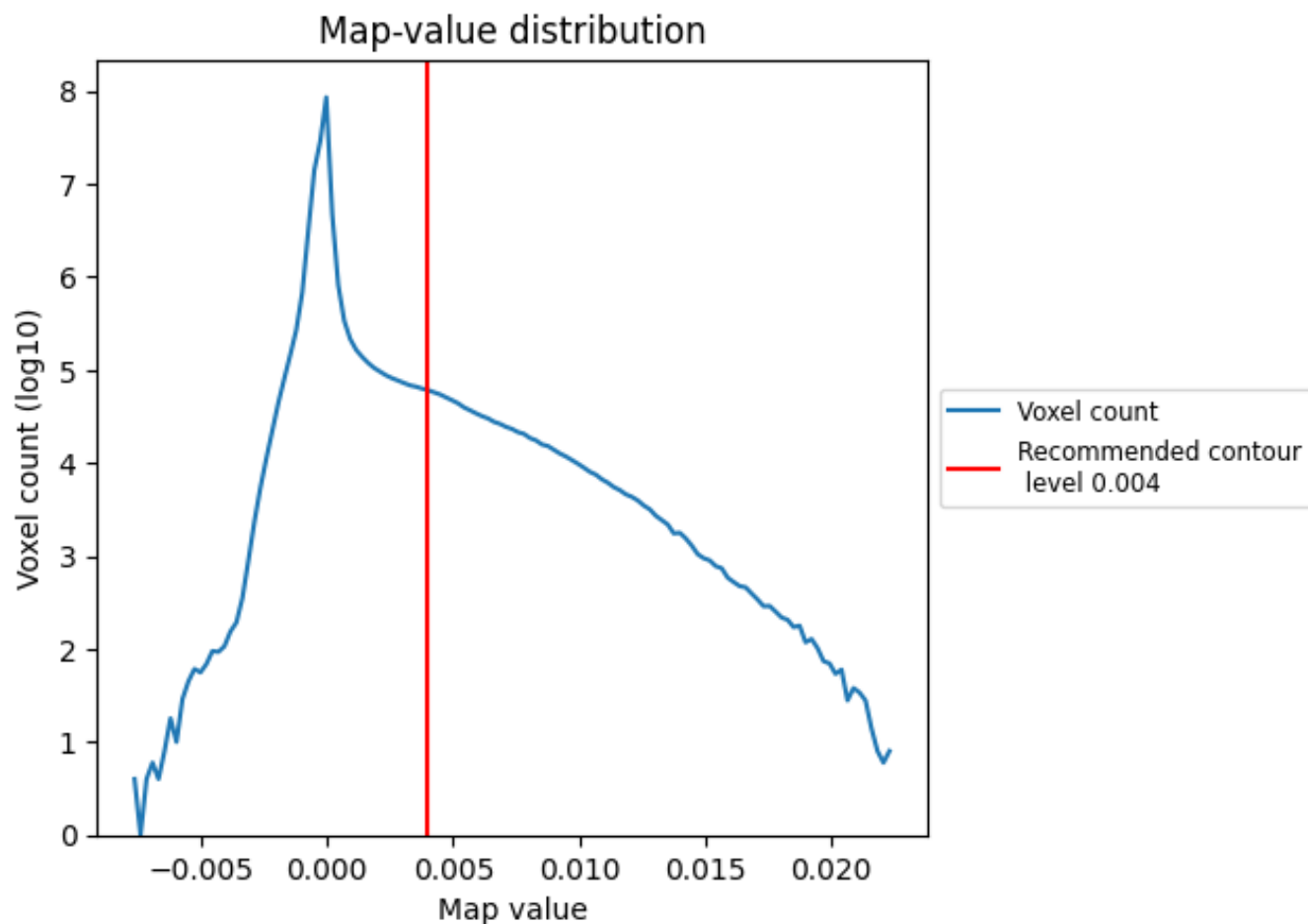
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

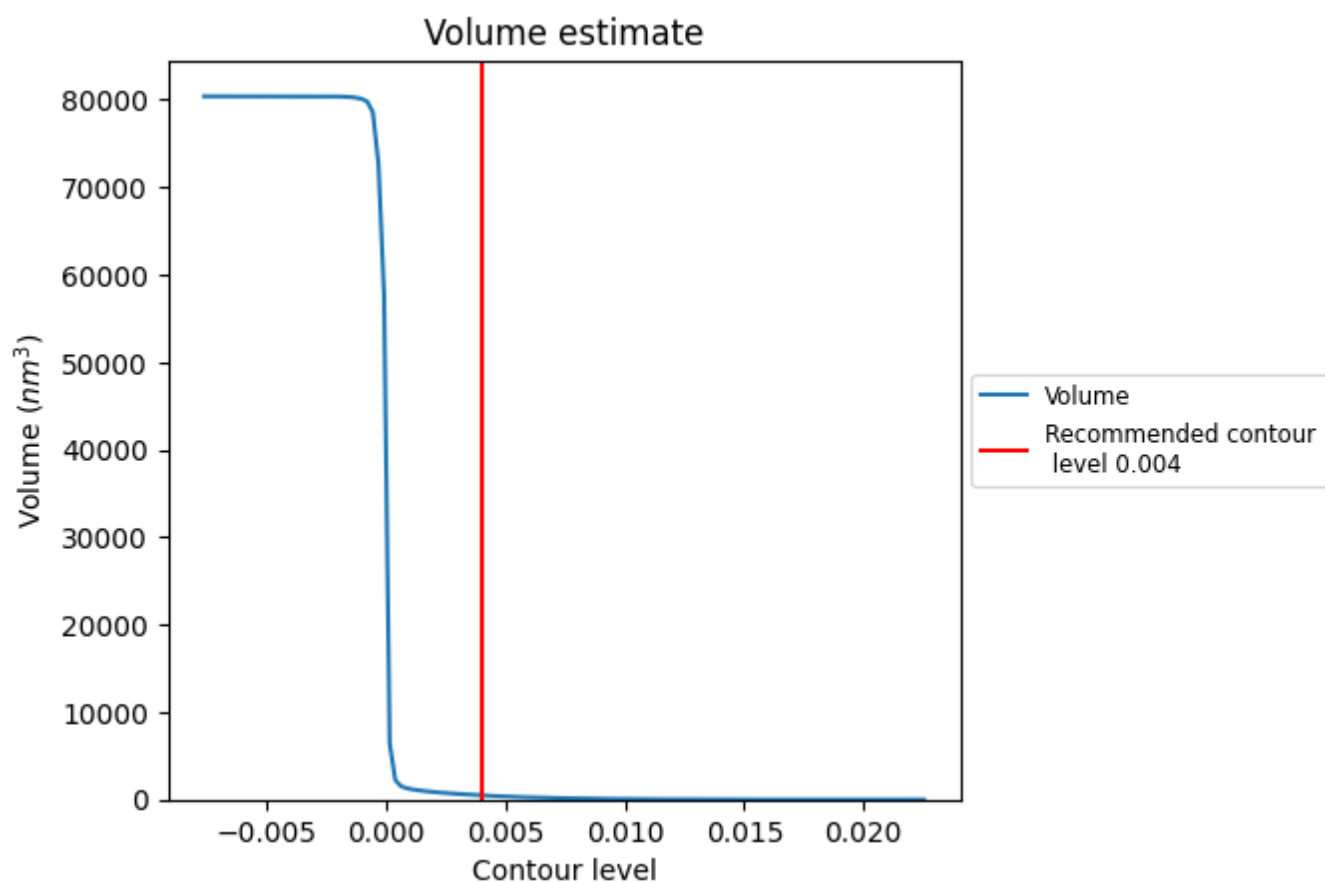
This section contains the results of statistical analysis of the map.

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.

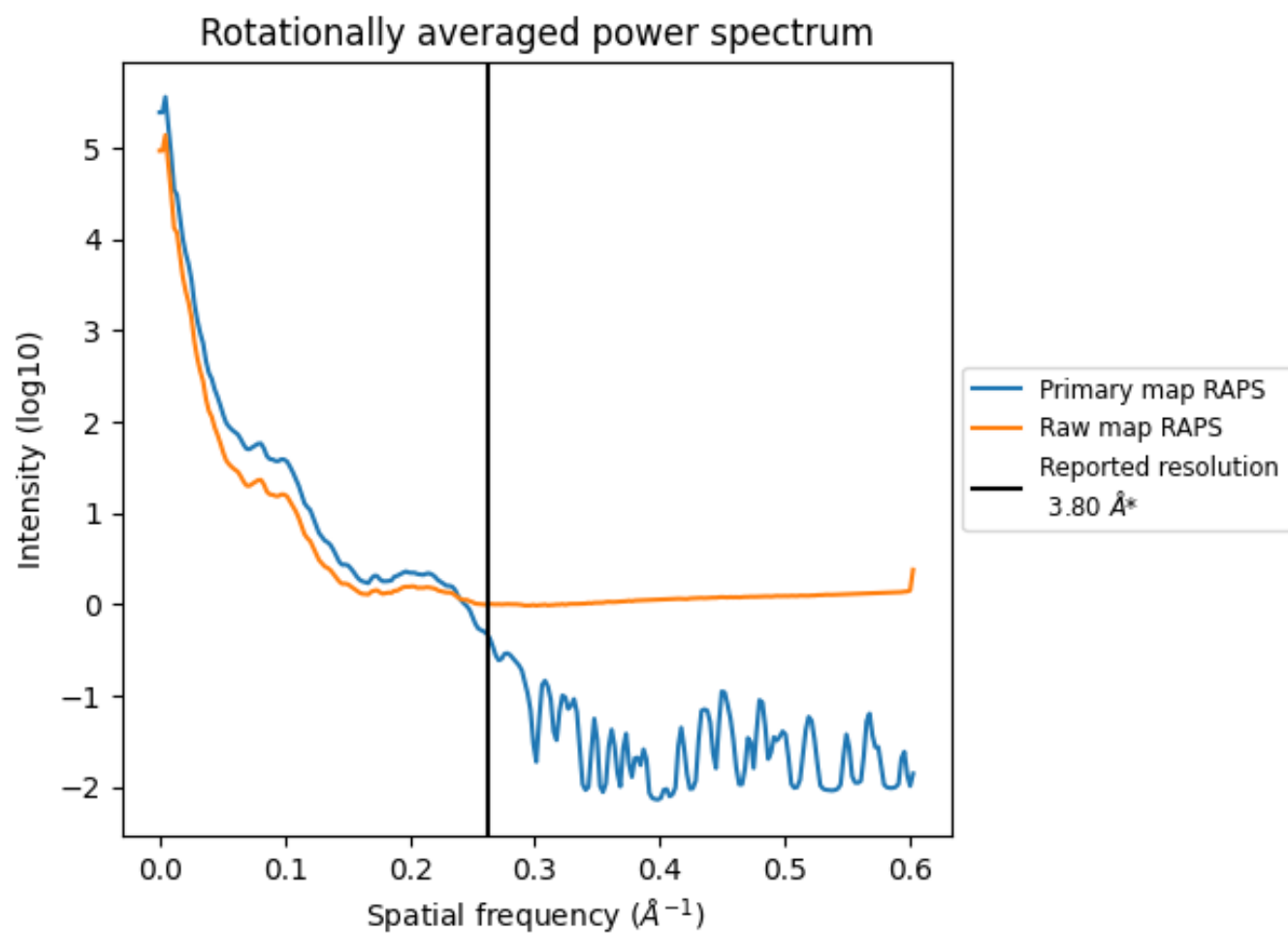
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 485 nm³; this corresponds to an approximate mass of 439 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

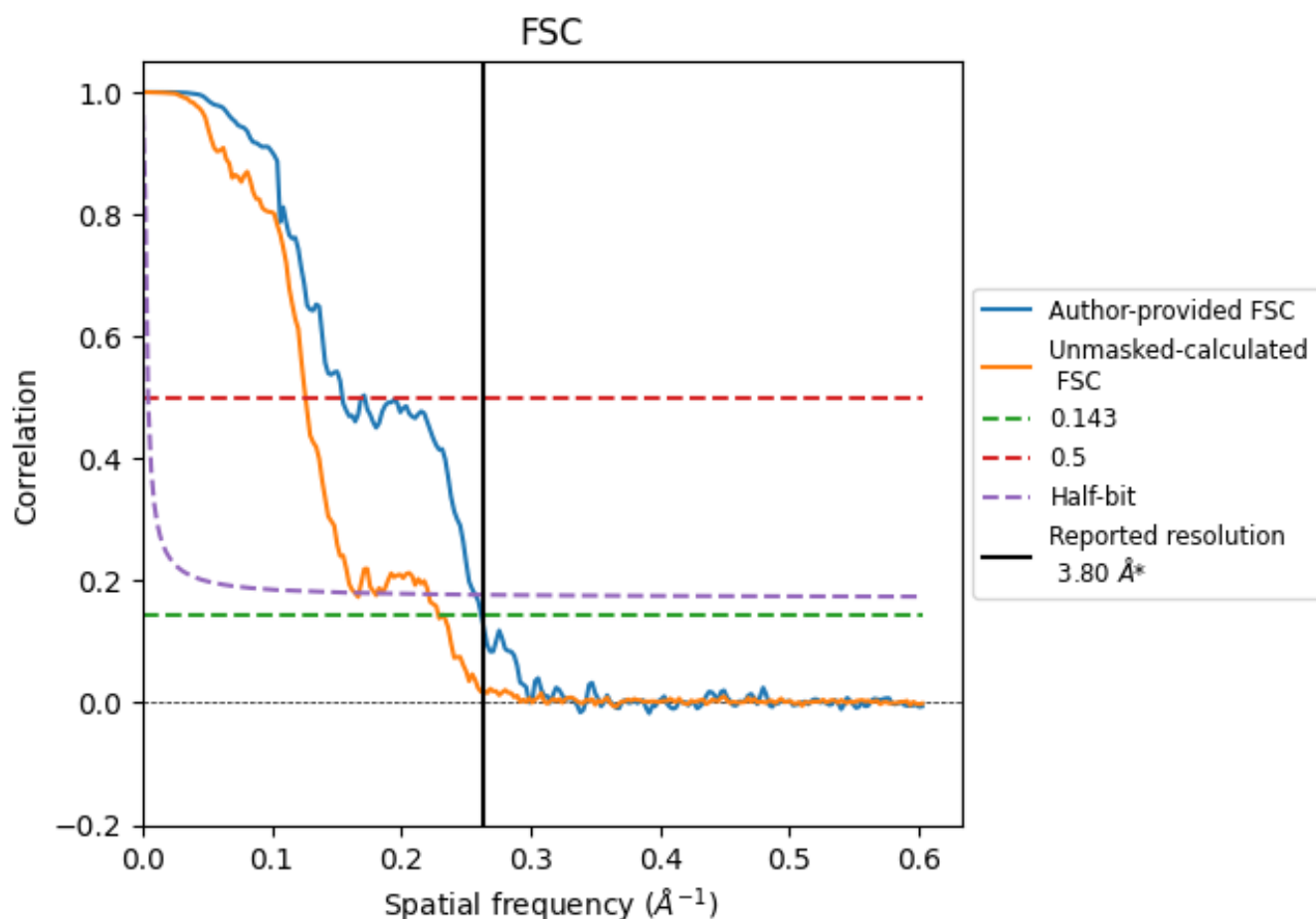


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

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 $0.263 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

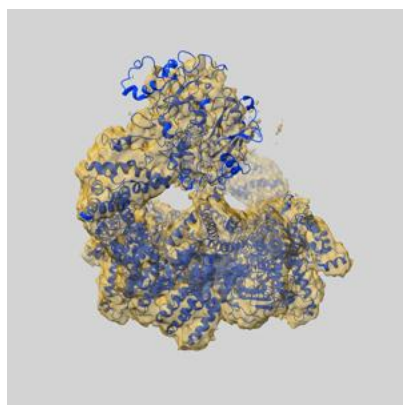
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.82	6.47	3.89
Unmasked-calculated*	4.37	7.93	6.08

*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 4.37 differs from the reported value 3.8 by more than 10 %

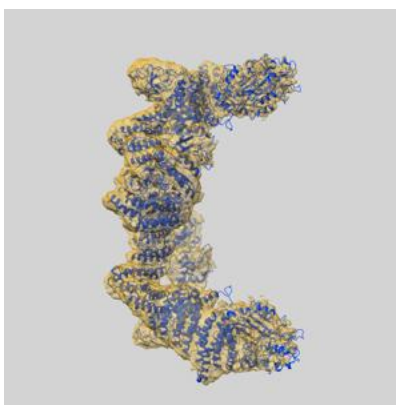
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30802 and PDB model 7DPA. Per-residue inclusion information can be found in section [3](#) on page [6](#).

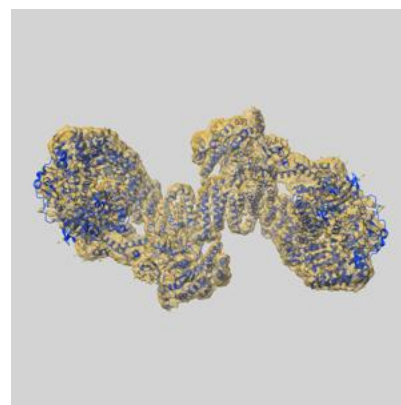
9.1 Map-model overlay [i](#)



X



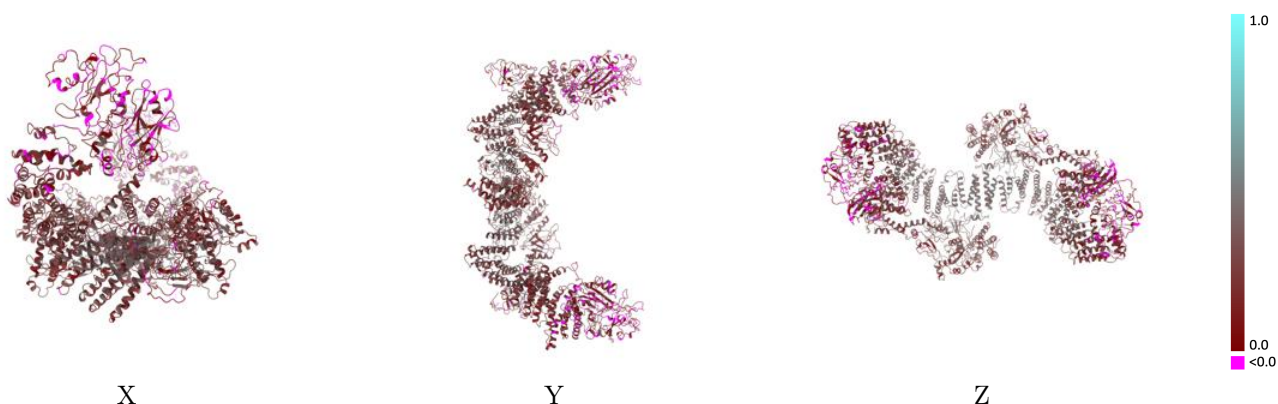
Y



Z

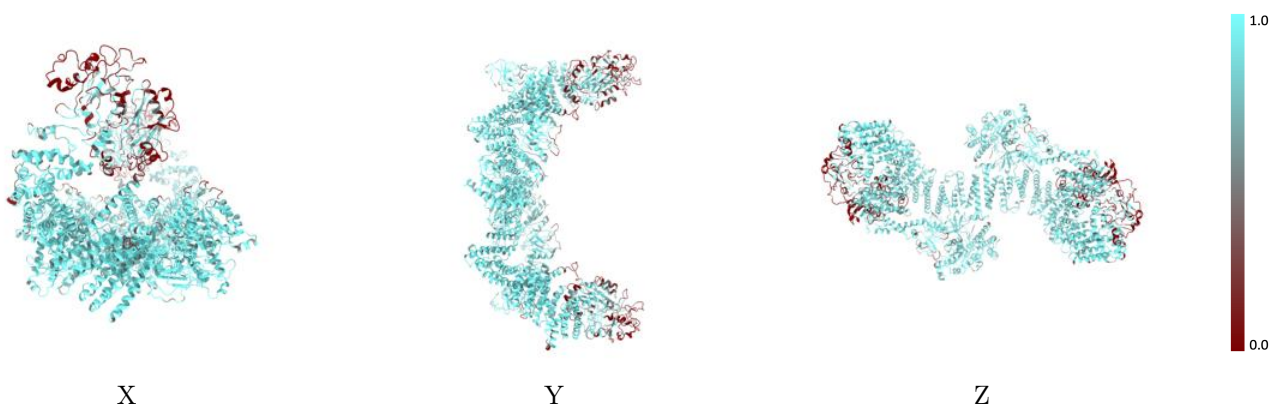
The images above show the 3D surface view of the map at the recommended contour level 0.004 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



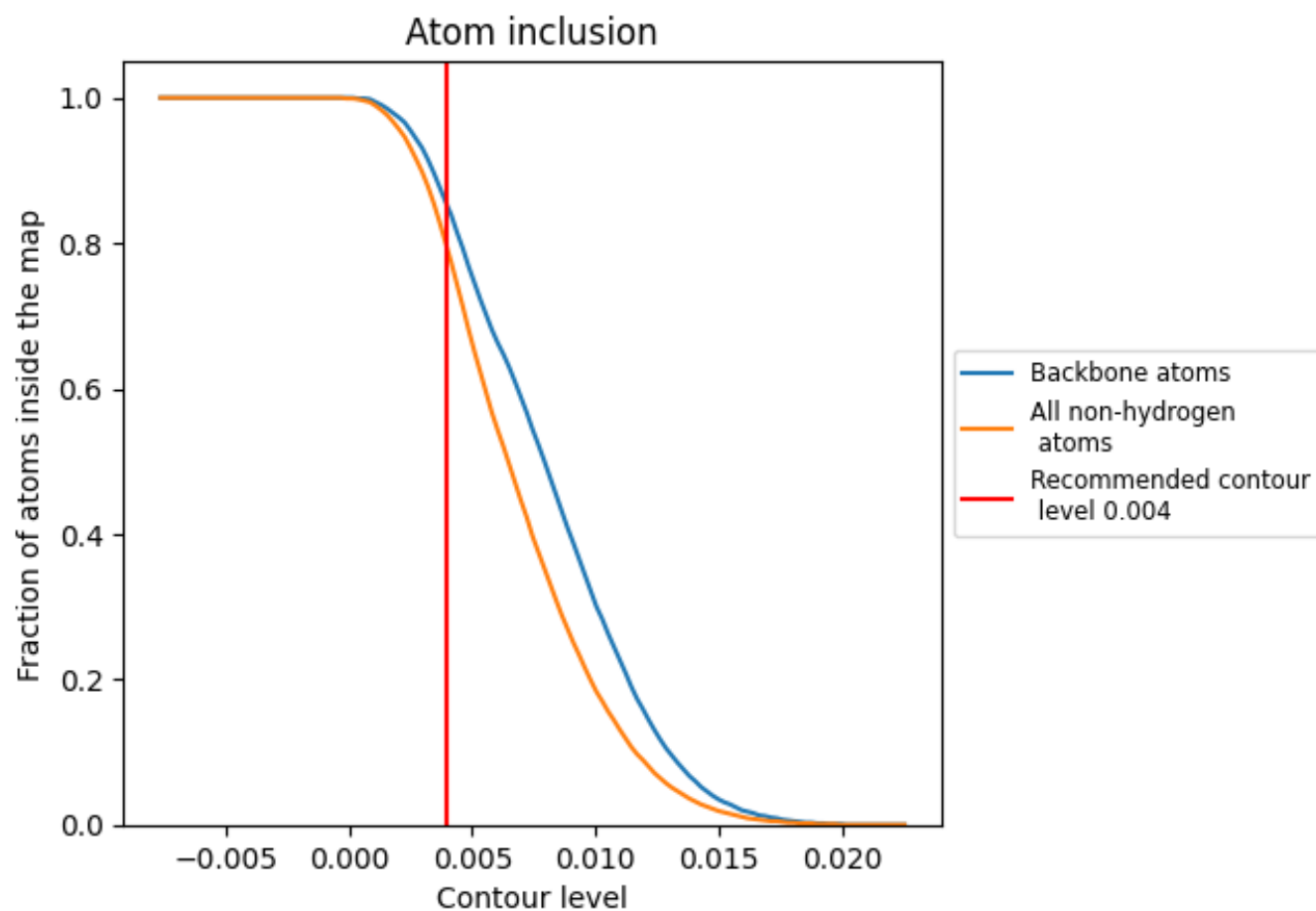
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.004).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 79% 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 (0.004) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7920	0.2390
A	0.7810	0.2390
B	0.8410	0.2650
C	0.8440	0.2220
D	0.7810	0.2380
E	0.8440	0.2710
F	0.8430	0.2230

1.0

0.0

<0.0