



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 06:01 PM UTC

PDB ID : 8ZJM / pdb_00008zjm
EMDB ID : EMD-60150
Title : Structure of DOCK5/ELMO1/Rac1 core (RhoG/DOCK5/ELMO1/Rac1 dataset, class 5)
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 : 4.52 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

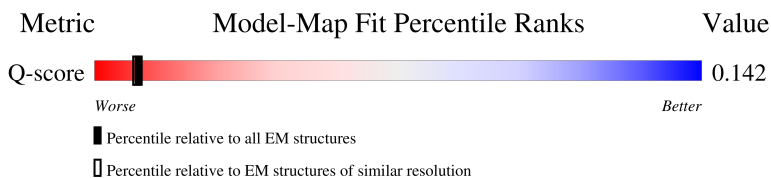
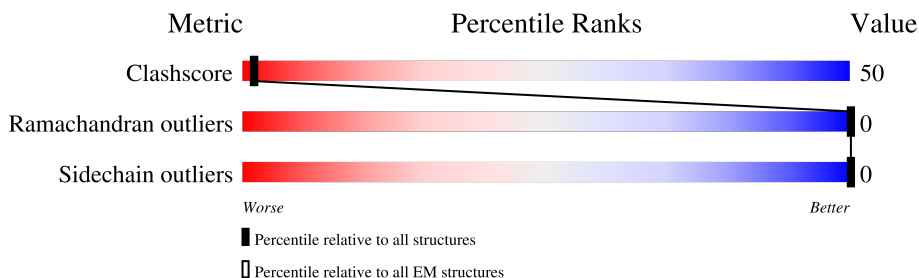
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

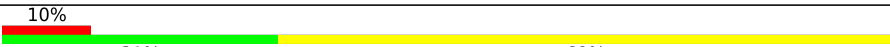
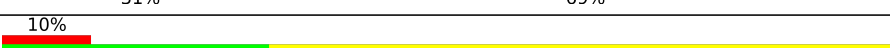
The reported resolution of this entry is 4.52 Å.

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	2506 (4.02 - 5.02)

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	 10% 31% 69%
2	E	1648	 10% 30% 70%

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Mol	Chain	Length	Quality of chain
3	C	184	8% 33% 63%
3	F	184	6% 34% 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:

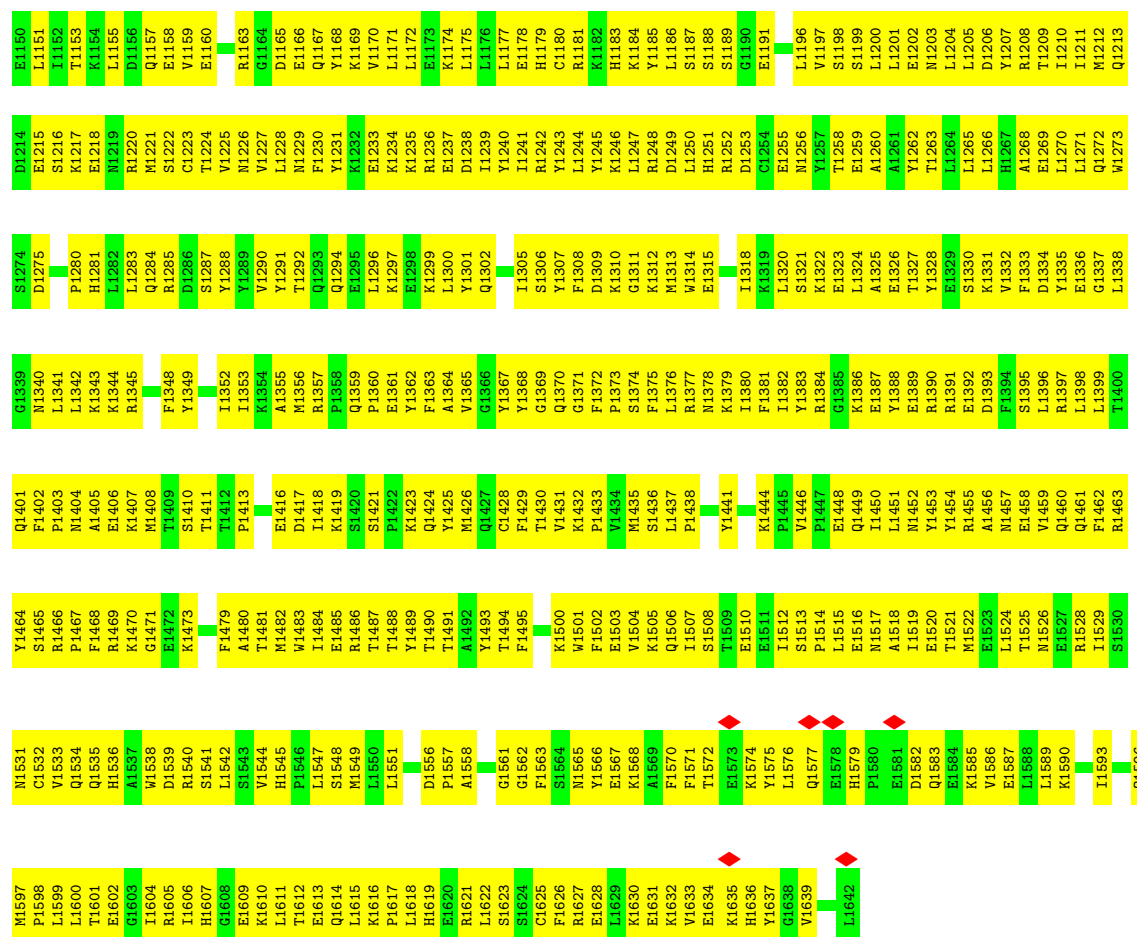
Residue	Category
GLY	Red
GLY	Red
SER	Red
GLY	Red
GLY	Red
SER	Red
M1	Red
A2	Green
R3	Green
W4	Green
I5	Green
P6	Green
T7	Green
K8	Green
R9	Green
Q10	Green
K11	Green
Y12	Green
G13	Green
V14	Green
A15	Green
I16	Green
Y17	Green
N18	Green
Y19	Green
N20	Green
Q23	Yellow
D24	Yellow
V25	Yellow
E26	Yellow
L27	Yellow
S28	Yellow
L29	Yellow
Q30	Yellow
I31	Yellow
G32	Yellow
S33	Yellow
T34	Yellow
V35	Yellow
H36	Yellow
I37	Yellow
L38	Yellow
E39	Yellow
N40	Yellow
V41	Yellow
W44	Yellow
Y45	Yellow
R46	Yellow
G47	Yellow
Y48	Yellow
T49	Yellow
L50	Yellow
I58	Red
F59	Red
P60	Red
L124	Red
I125	Red
E126	Red
W127	Red
I128	Red
S129	Red
Q130	Red
I131	Red
L136	Red
P137	Red
K138	Red
D139	Red
E140	Red
L141	Red
A142	Red
E143	Red
L144	Red
K145	Red
K146	Red
E147	Red
K148	Red
T149	Red
A150	Red
K151	Red
I152	Red
D153	Red
H154	Red
G155	Red
M156	Red
R157	Red
M158	Red
L159	Red
S160	Red
L161	Red
D162	Red
L163	Red
V164	Red
V165	Red
R166	Red
D167	Red
D168	Red
M169	Red
G170	Red
M171	Red
I172	Red
L173	Red
D174	Red
D176	Red
S179	Red
T180	Red
L86	Yellow
P86	Yellow
L87	Yellow
R88	Yellow
E89	Yellow
Q90	Yellow
L91	Yellow
S92	Yellow
T93	Yellow
T94	Yellow
L95	Yellow
R96	Yellow
E97	Yellow
W98	Yellow
A99	Yellow
V100	Yellow
I101	Yellow
W102	Yellow
R103	Yellow
K104	Yellow
L105	Yellow
Y106	Yellow
V107	Yellow
K110	Yellow
L111	Yellow
F114	Yellow



- Molecule 2: Dedicator of cytokinesis protein 5

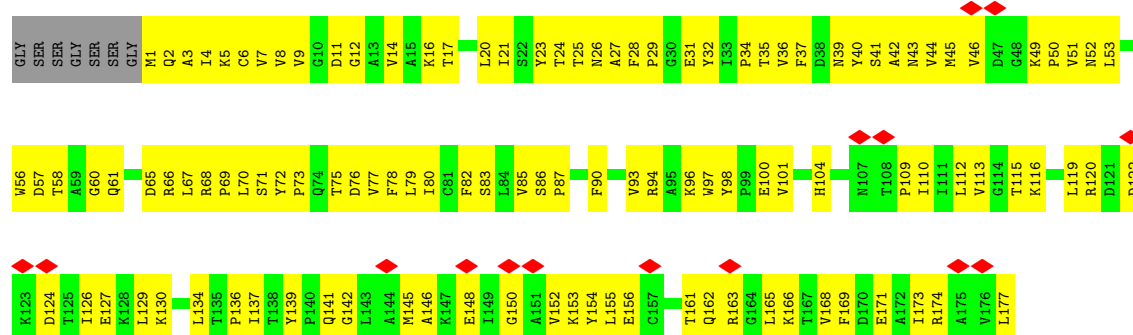


I1087	R1088	D1089	M1090	Y1091	Y1092	N1093	L1094	G1095	H1096	H1097	K1098	K1099	K1100	F1101	I1102	M1105	V1106	G1107	P1108	I1109	L1110	E1111	V1112	T1113	L1114	E1115	P1116	E1117	V1118	E1119	L1120	R1121	K1122	A1123	T1124	I1125	P1126	I1127	F1128	F1129	D1130	M1131	M1132	Q1133	C1134	E1135	F1136	M1137	F1138	S1139	G1140	M1143	F1144	H1145	E1148	N1149				
Q1023	F1024	A1025	E1026	L1027	Y1028	T1029	A1030	F1031	Y0969	M1032	D1034	Q1035	A1036	E1039	L1040	Q1041	L1042	V1043	I0982	N1045	L1110	F1047	H1048	L1049	L1113	A1050	C859	V1051	P1116	A1053	F1054	H1056	E1057	S1058	K0994	L1059	Q1060	L1061	E1062	T1063	F1064	S1065	Q1066	A1067	K1068	R1069	M1070	L1071	E1135	F1136	Y1076	G1077	D1078	M1079	R1080	F1081	I1082	I1083	G1084	R1086
K896	P897	D898	H899	S902	S903	Q904	L905	L906	S907	N908	H971	L910	Q845	E911	V912	L913	D914	R915	V918	G919	A920	T921	A922	V923	H924	L925	Q926	L927	R928	L929	H800	L801	M802	D803	R804	P805	E807	E808	R809	V810	K811	L812	A815	A816	L881	L882	T883	D884	Q885	L886	Q889	L890	N893	F957	L958	A959				
L960	L961	Q962	Q963	M964	D965	D966	S967	H968	L969	F970	S971	Y972	I973	S974	T975	F976	K977	T978	R979	I982	L983	D984	F985	L986	L987	L988	L989	Q989	F990	L991	M992	F993	L994	D995	L996	L997	G998	K999	Y1002	A1003	K1004	D1005	M1006	M1007	V1008	M1009	D945	Q946	S947	P948	H949	L950	F953	V954	P957	L958	A959			
Q1023	F1024	A1025	E1026	L1027	Y1028	T1029	A1030	F1031	Y0969	M1032	D1034	Q1035	A1036	E1039	L1040	Q1041	L1042	V1043	I0982	N1045	L1110	F1047	H1048	L1049	L1113	A1050	C859	V1051	P1116	A1053	F1054	H1056	E1057	S1058	K0994	L1059	Q1060	L1061	E1062	T1063	F1064	S1065	Q1066	A1067	K1068	R1069	M1070	L1071	E1135	F1136	Y1076	G1077	D1078	M1079	R1080	F1081	I1082	I1083	G1084	R1086
H314	T315	C316	R319	R320	R321	F322	V326	M327	D328	I329	T330	D331	I332	I333	K336	V337	D338	D339	E340	E341	K342	Q343	H344	F345	I346	P347	Q348	Q349	Q350	I351	A352	M353	E354	T355	Y356	I357	R358	Q359	R360	Q361	L362	I363	M364	S365	P366	I367	I368	T369	S370	H371	V372	I373	G374	E375	N376	E377				
P378	L379	T380	L383	V386	I387	A388	A389	K390	V392	N393	H394	K395	V400	V401	S402	L403	K404	L405	L406	P407	G408	D409	S471	L410	T411	Q412	V413	Q414	K415	M416	F417	S418	H419	L420	V421	D422	R423	S424	A426	I427	A428	R429	K430	M431	G432	F433	P434	E435	I436	V500	Y501	L502	D441	V503	R443					
N444	D445	I446	V447	V448	L449	L450	L451	F455	D456	K457	G458	K459	K460	K461	T462	P463	K464	M465	V466	E467	V468	T469	M470	S471	V472	H473	D474	E475	E476	G477	K478	L479	L480	E481	K482	A483	I484	H485	P486	G487	A488	G489	Y490	E491	G492	I493	E494	E495	N556	K497	S498	V499	V500	Y501	Q503	V504	K505			
Q506	W509	Y510	E511	T512	V513	K514	I517	A518	I519	E520	E521	V522	T523	R524	C525	H526	I527	R528	F529	T530	F531	R532	H533	R534	S535	S536	Q537	E538	T539	R540	D541	S603	K542	S603	K543	E544	R545	A546	F547	G548	V549	F551	V552	K553	L554	M555	N556	T560	T561	L562	G565	L569	V570	V571	Y572					
K573	G574	D575	N576	K577	K578	M579	E580	D581	A582	K583	F584	Y585	L586	T587	L588	P589	G590	T591	K592	N593	E594	M595	E596	E597	K598	Q599	L600	Q601	A602	S603	K604	N605	L606	V607	T608	F609	T610	S612	K613	D614	M555	S615	T616	K617	S619	F620	Q621	L622	A623	T624	L625	L626	C627	S628	T629	K630	L631	T632		
Q633	D636	L637	L638	G639	L640	L641	N642	R644	S645	N646	Q648	N649	L650	H651	H652	N653	L654	K655	L656	M658	L659	E659	V660	D661	G662	G663	E664	T665	V666	F668	L669	D670	D671	T672	L673	A675	L676	F677	N678	M680	M681	D690	F691	L692	V693	F694	D695	A696	L697	V698	F699	I700								
I701	K708	F709	Q710	H711	F712	N713	P714	L715	E717	T718	V719	I720	I721	K722	H723	F724	S725	A726	T727	L728	A729	V730	V731	K732	L733	S734	K735	V736	L737	N738	F739	V740	V741	A742	N743	A744	D745	D746	K749	T750	E751	L752	F753	F754	A755	A756	L757	K758	A759	L760	K761	V762	L763	F764	R765	F766				
L767	L768	Q769	S770	R771	V772	L773	V774	L775	F777	V778	G779	Q780	S781	D785	E786	F787	N788	S789	R854	S790	T791	R792	Q793	L794	F795	L796	R797	F798	V799	H800	L801	M802	D803	R804	P805	E807	E808	R809	V810	K811	L812	A815	A816	L881	L882	T883	D884	Q885	L886	Q889	L890	N893	F957	L958	A959					
V830	F831	D832	E835	L836	S837	V838	L839	F840	C841	R842	F843	L844	Q845	E846	L847	O851	L852	H853	R854	Q855	R856	L857	N858	C859	N860	T861	R862	L863	V864	E865	S866	T867	L868	F869	R870	Q871	C874	R875	E876	V877	L878	L879	P880	L881	L882	T883	D884	Q885	L886	Q889	L890	N893	F957	L958	A959					
K896	P897	D898	H899	S902	S903	Q904	L905	L906	S907	N908	H971	L910	Q845	E911	V912	L913	D914	R915	V918	G919	A920	T921	A922	V923	H924	L925	Q926	L927	R928	L929	H800	L801	M802	D803	R804	P805	E807	E808	R809	V810	K811	L812	A815	A816	L881	L882	T883	D884	Q885	L886	Q889	L890	N893	F957	L958	A959				
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L960	L961	Q962	Q963	M964	D965	D966	S967	H968	L969	F970	S971	Y972	I973	S974	T975	F976	K977	T978	R979	I982	L983	D984	F985	L986	L987	L988	L989	Q989	F990	L991	M992	F993	L994	D995	L996	L997	G998	K999	Y1002	A1003	K1004	D1005	M1006	M1007	V1008	M1009	D945	Q946	S947	P948	H949	L950	F953	V954	P957	L958	A959			
Q1023	F1024	A1025	E1026	L1027	Y1028	T1029	A1030	F1031	Y0969	M1032	D1034	Q1035	A1036	E1039	L1040	Q1041	L1042	V1043	I0982	N1045	L1110	F1047	H1048	L1049	L1113	A1050	C859	V1051	P1116	A1053	F1054	H1056	E1057	S1058	K0994	L1059	Q1060	L1061	E1062	T1063	F1064	S1065	Q1066	A1067	K1068	R1069	M1070	L1071	E1135	F1136	Y1076	G1077	D1078	M1079	R1080	F1081	I1082	I1083	G1084	R1086
H1087	R1088	D1089	M1090	Y1091	Y1092	N1093	L1094	G1095	H1096	H1097	K1098	K1099	K1100	F1101	I1102	M1105	V1106	G1107	P1108	I1109	L1110	E1111	V1112	T1113	L1114	E1115	P1116	E1117	V1118	E1119	L1120	R1121	K1122	A1123	T1124	I1125	P1126	I1127	F1128	F1129	D1130	M1131	M1132	Q1133	C1134	E1135	F1136	M1137	F1138	S1139	G1140	M1143	F1144	H1145	E1148	N1149				



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

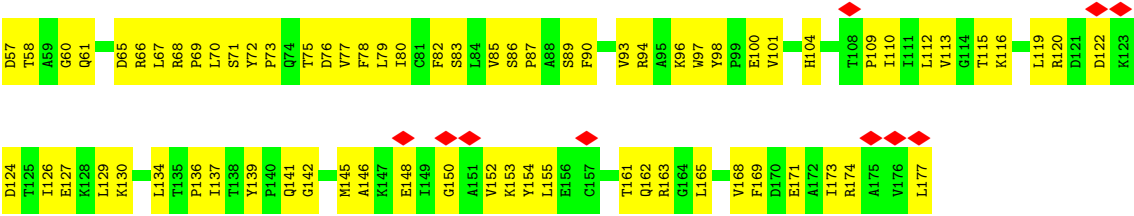
Chain C: 8% 33% 63%



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

Chain F: 6% 34% 62%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	156585	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	0.052	Depositor
Minimum map value	-0.015	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	0.25	0/1641	0.50	0/2218
1	D	0.25	0/1641	0.50	0/2218
2	B	0.30	0/13722	0.53	0/18514
2	E	0.30	0/13722	0.53	0/18514
3	C	0.22	0/1415	0.51	1/1924 (0.1%)
3	F	0.22	0/1415	0.51	1/1924 (0.1%)
All	All	0.29	0/33556	0.53	2/45312 (0.0%)

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
2	B	0	1
2	E	0	1
All	All	0	4

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	46	VAL	N-CA-C	-6.60	106.58	112.12
3	F	46	VAL	N-CA-C	-6.54	106.62	112.12

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	541	GLN	Peptide

Continued on next page...

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Mol	Chain	Res	Type	Group
2	B	1041	GLN	Peptide
1	D	541	GLN	Peptide
2	E	1041	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	142	0
1	D	1608	0	1617	156	0
2	B	13436	0	13516	1413	0
2	E	13436	0	13516	1434	0
3	C	1385	0	1407	136	0
3	F	1385	0	1407	132	0
All	All	32858	0	33080	3322	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 50.

The worst 5 of 3322 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:E:929:MET:HA	2:E:933:LEU:HD13	1.43	1.01
1:A:701:LEU:HD23	2:B:31:ILE:HG23	1.43	1.00
2:B:929:MET:HA	2:B:933:LEU:HD13	1.43	0.99
2:E:1545:HIS:HB2	3:F:5:LYS:HE2	1.49	0.95
2:B:929:MET:HB2	2:B:964:MET:HE1	1.50	0.94

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%)	170 (87%)	26 (13%)	0	100	100
1	D	196/733 (27%)	170 (87%)	26 (13%)	0	100	100
2	B	1640/1648 (100%)	1476 (90%)	164 (10%)	0	100	100
2	E	1640/1648 (100%)	1476 (90%)	164 (10%)	0	100	100
3	C	175/184 (95%)	160 (91%)	15 (9%)	0	100	100
3	F	175/184 (95%)	160 (91%)	15 (9%)	0	100	100
All	All	4022/5130 (78%)	3612 (90%)	410 (10%)	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	1449/1497 (97%)	1449 (100%)	0	100	100
2	E	1495/1497 (100%)	1495 (100%)	0	100	100
3	C	147/157 (94%)	147 (100%)	0	100	100
3	F	153/157 (98%)	153 (100%)	0	100	100
All	All	3610/4636 (78%)	3610 (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 63 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	1517	ASN

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Mol	Chain	Res	Type
2	E	1045	ASN
2	E	109	ASN
2	E	1044	ASN
2	E	1427	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.

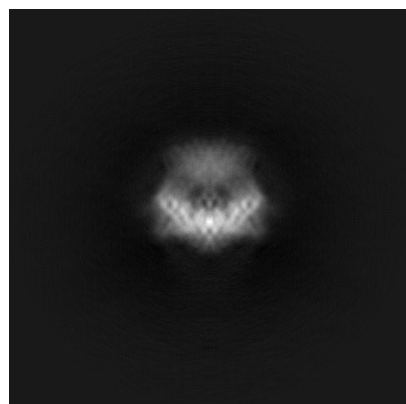
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60150. These allow visual inspection of the internal detail of the map and identification of artifacts.

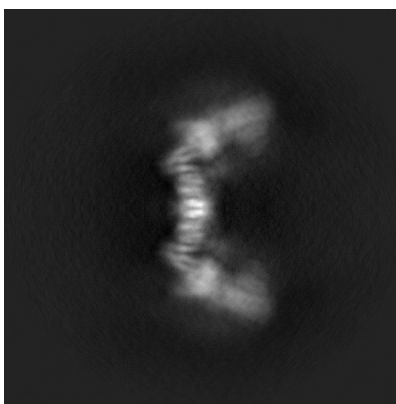
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

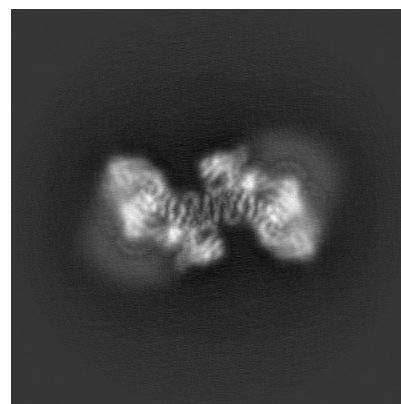
6.1.1 Primary map



X

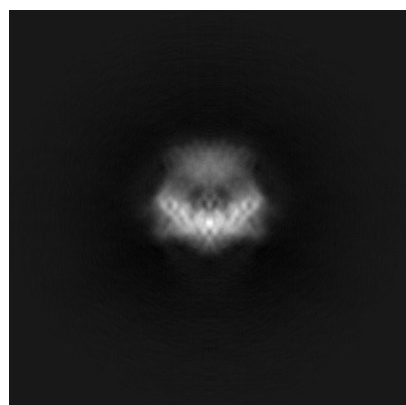


Y

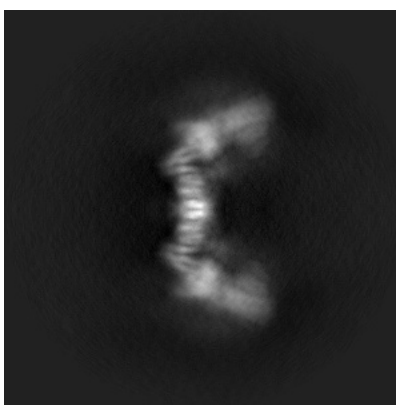


Z

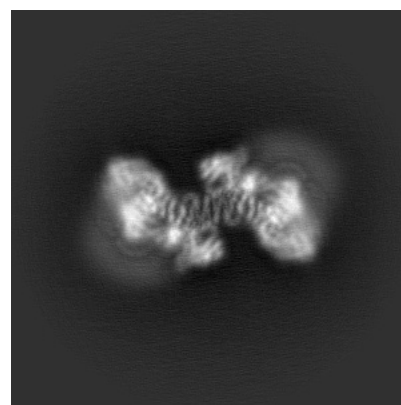
6.1.2 Raw map



X



Y

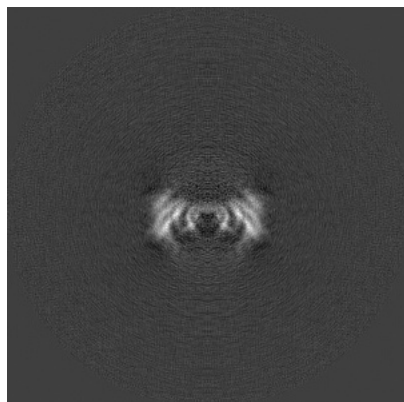


Z

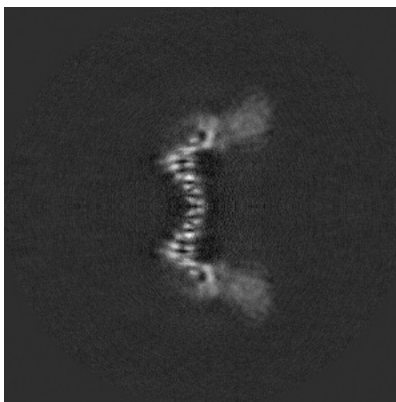
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

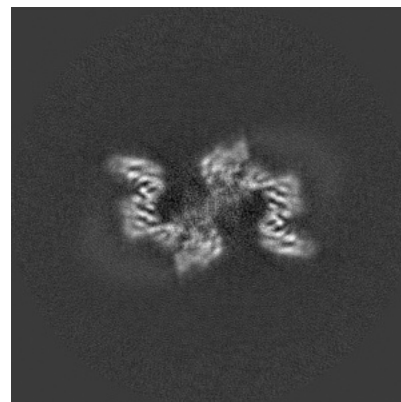
6.2.1 Primary map



X Index: 170

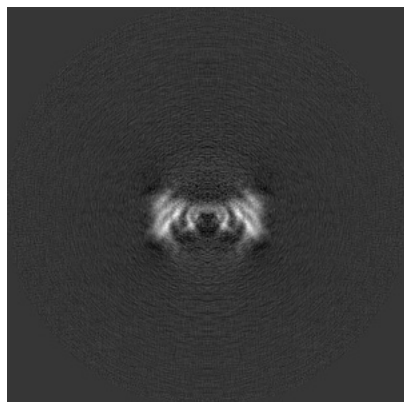


Y Index: 170

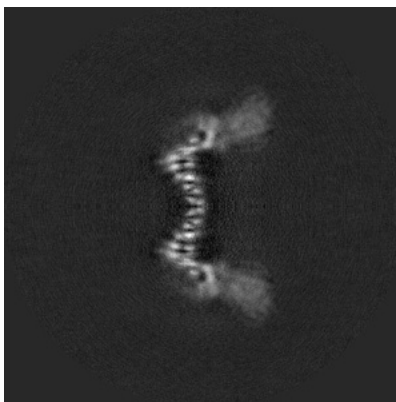


Z Index: 170

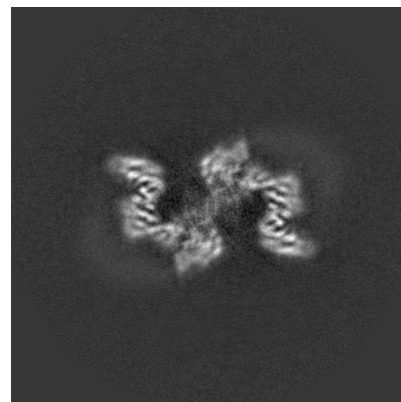
6.2.2 Raw map



X Index: 170



Y Index: 170

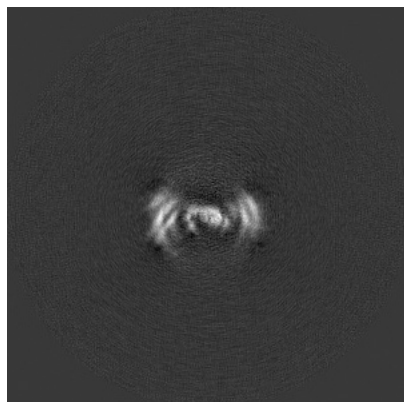


Z Index: 170

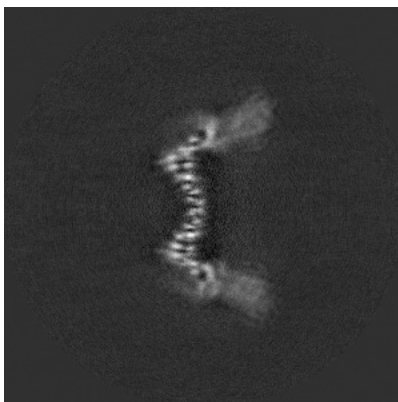
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

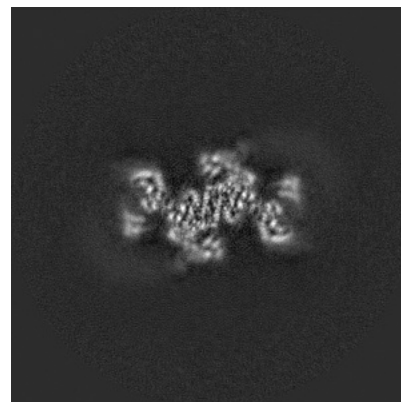
6.3.1 Primary map



X Index: 166

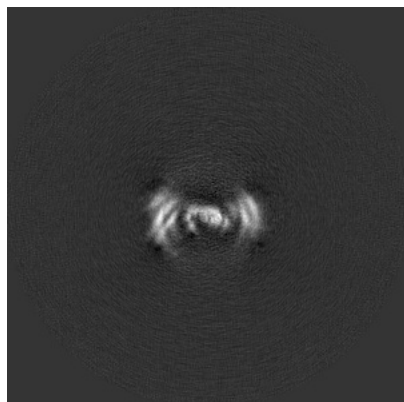


Y Index: 169

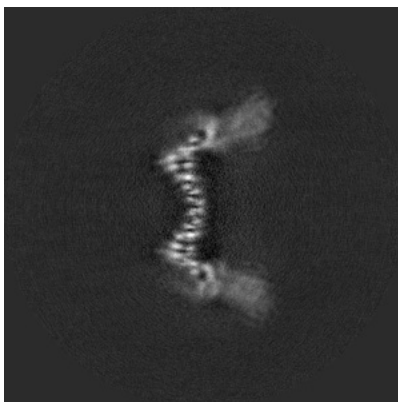


Z Index: 159

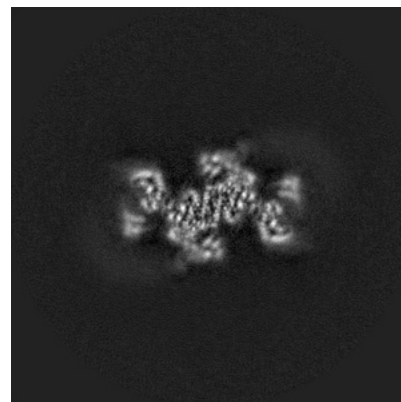
6.3.2 Raw map



X Index: 166



Y Index: 169

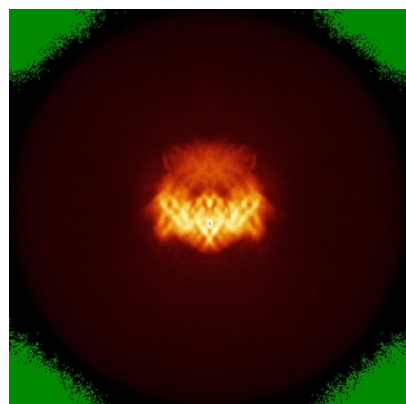


Z Index: 159

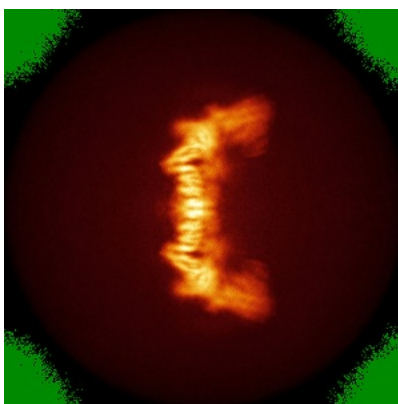
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

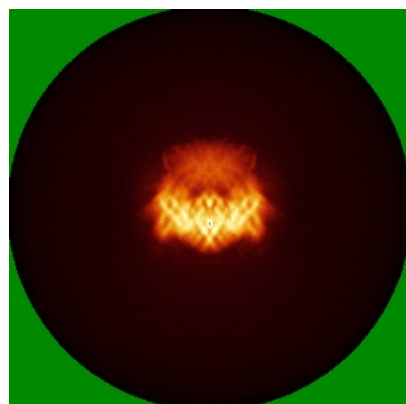


Y



Z

6.4.2 Raw map



X



Y

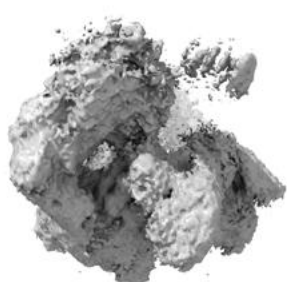


Z

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



X



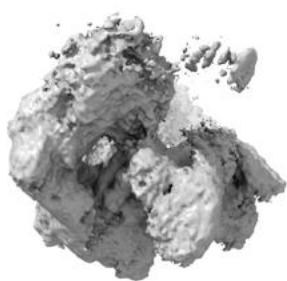
Y



Z

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



X



Y



Z

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.

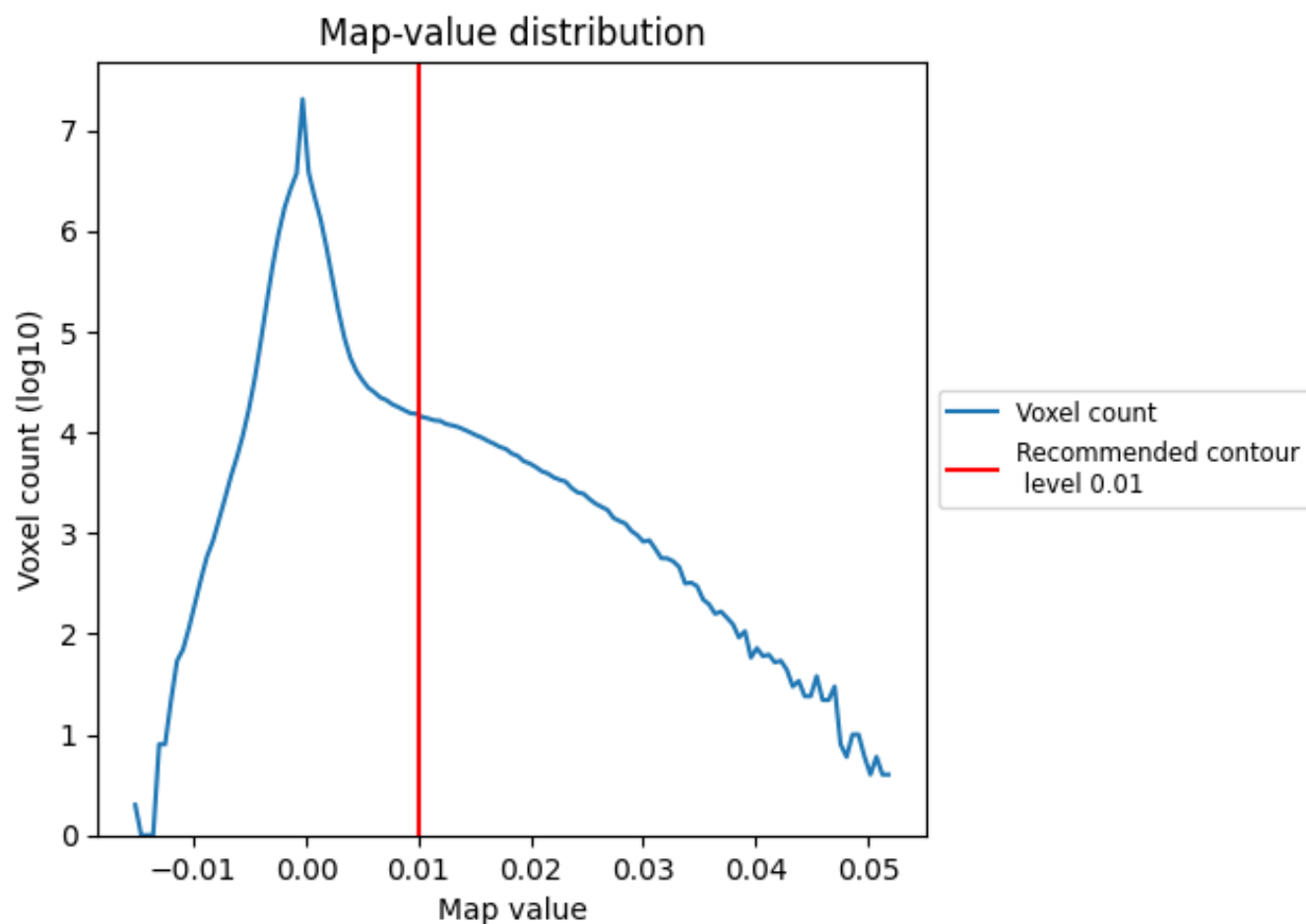
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

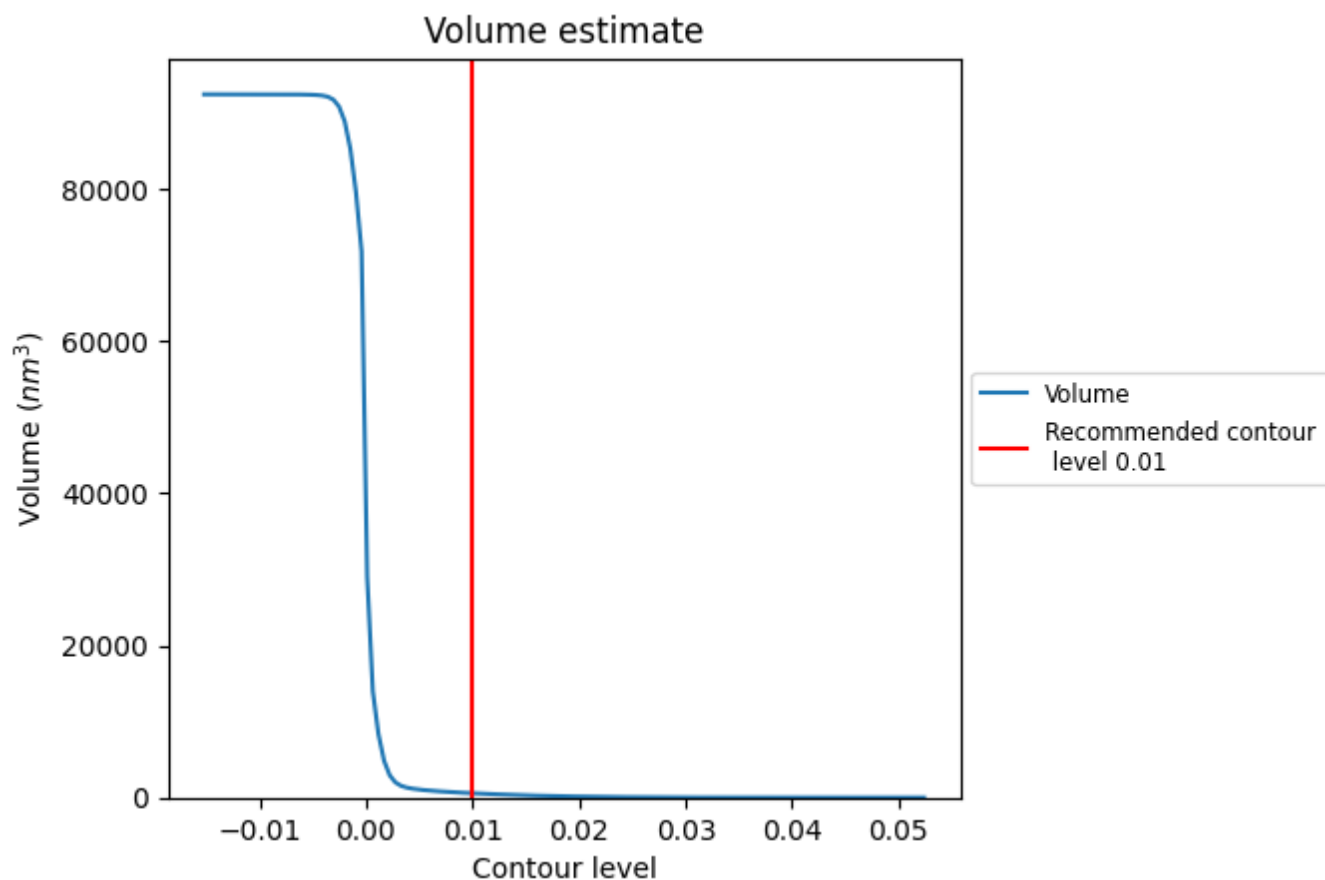
This section contains the results of statistical analysis of the map.

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.

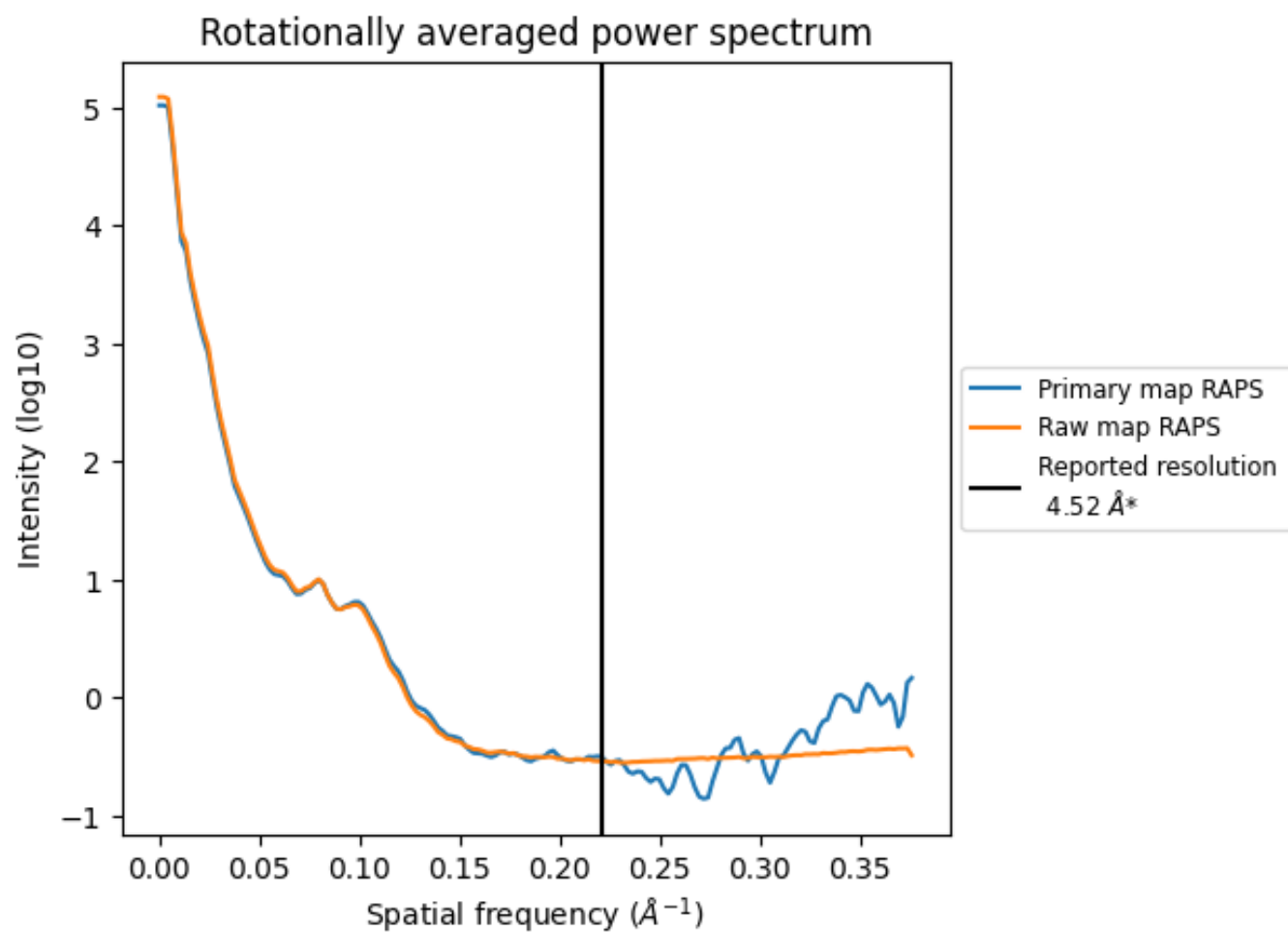
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 568 nm³; this corresponds to an approximate mass of 513 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 ⓘ

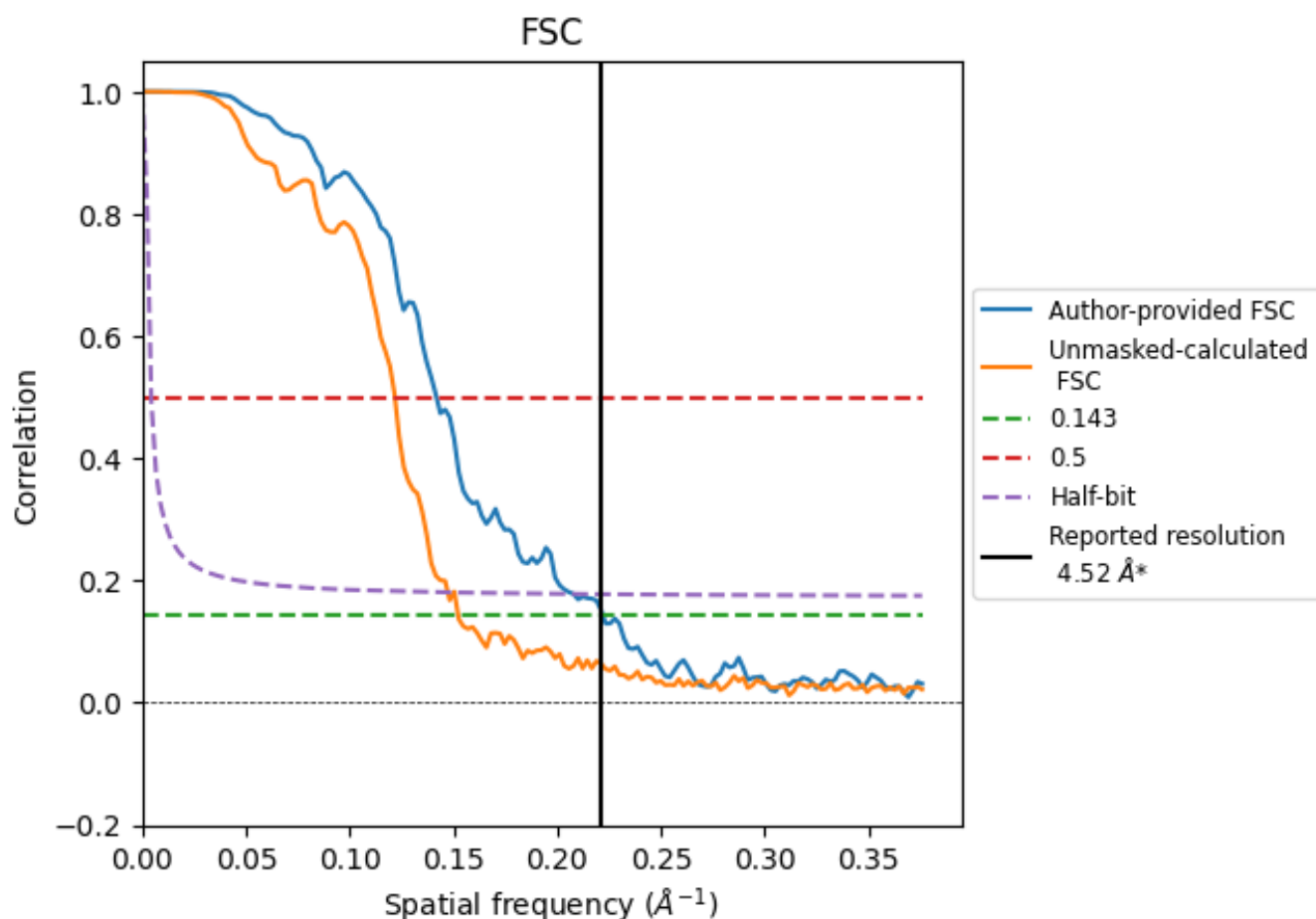


*Reported resolution corresponds to spatial frequency of 0.221 Å⁻¹

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 0.221 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

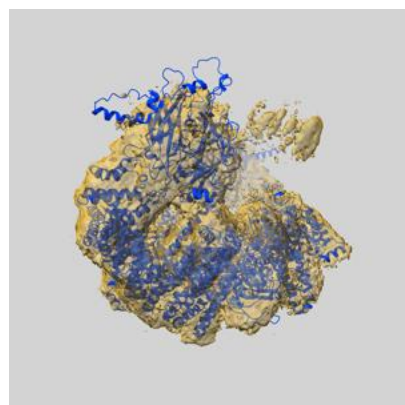
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.52	-	-
Author-provided FSC curve	4.50	7.05	4.81
Unmasked-calculated*	6.57	8.21	6.79

*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 6.57 differs from the reported value 4.52 by more than 10 %

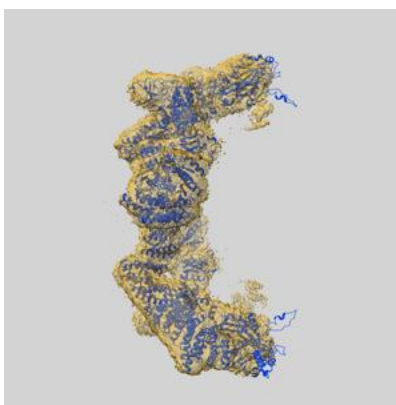
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-60150 and PDB model 8ZJM. Per-residue inclusion information can be found in section [3](#) on page [6](#).

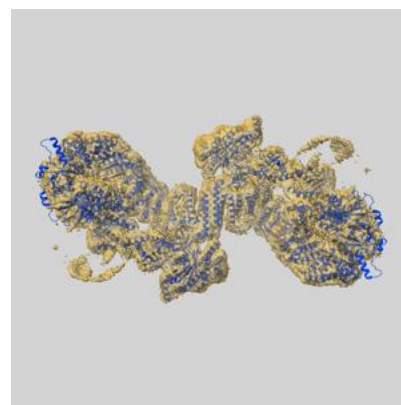
9.1 Map-model overlay [i](#)



X



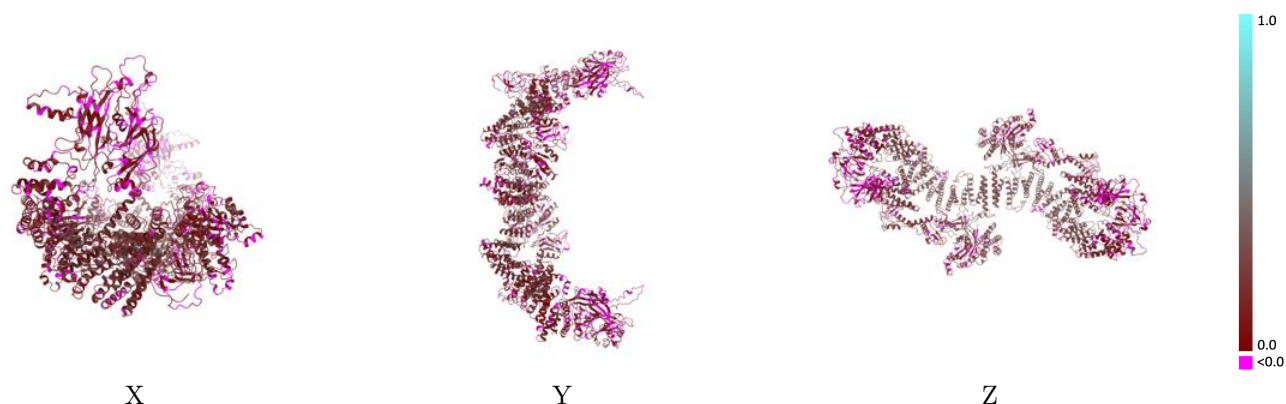
Y



Z

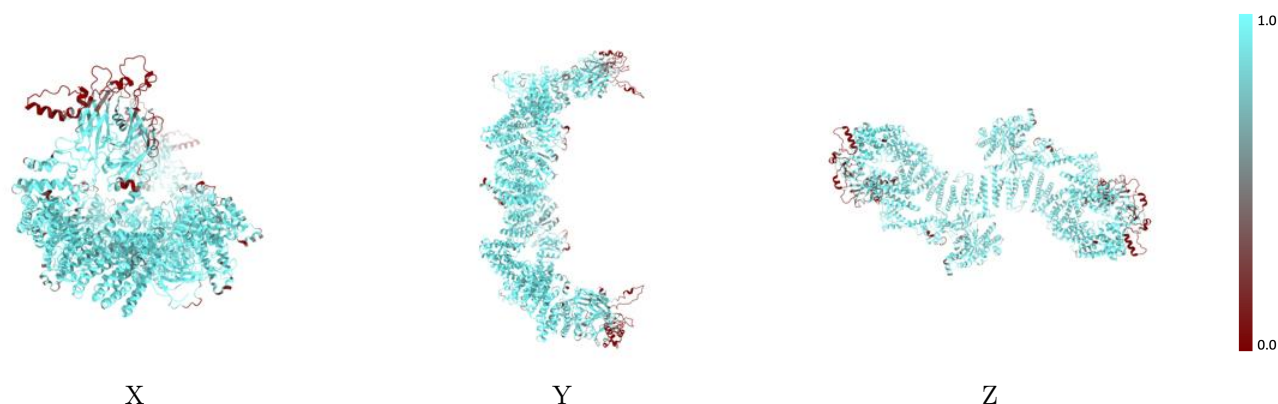
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



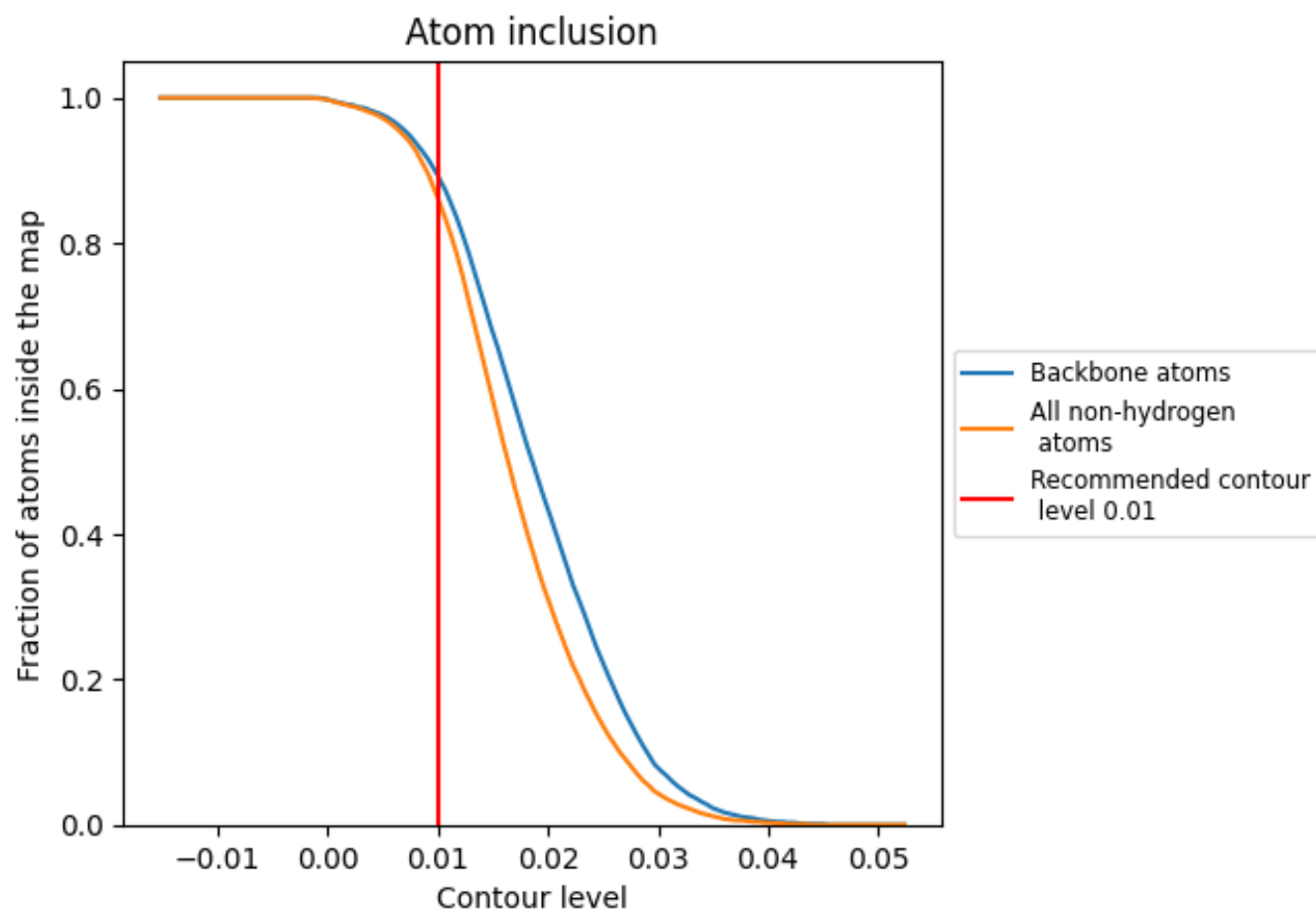
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 89% of all backbone atoms, 86% 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	0.8620	0.1420
A	0.8650	0.1090
B	0.8590	0.1490
C	0.8680	0.1320
D	0.8770	0.1070
E	0.8600	0.1450
F	0.8720	0.1300

1.0

0.0

<0.0