



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 08:17 AM UTC

PDB ID : 9WBZ / pdb_00009wbz
EMDB ID : EMD-65851
Title : The structure of NCP-motor-ARP module of ncBAF-nucleosome complex
Authors : Chen, K.J.; Chen, Z.C.
Deposited on : 2025-08-15
Resolution : 2.90 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:

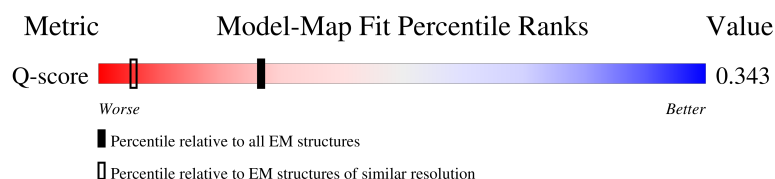
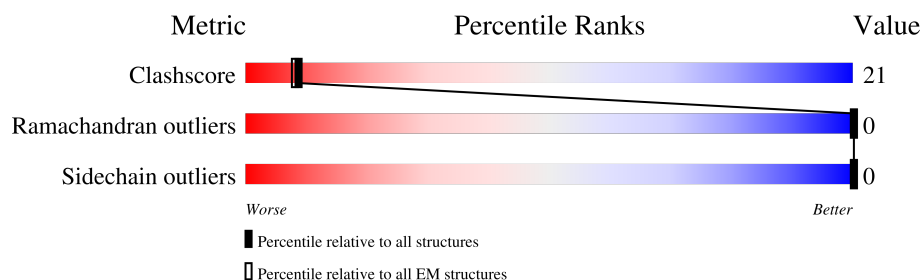
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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



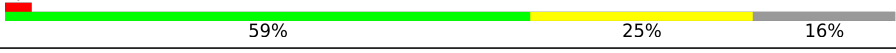

The reported resolution of this entry is 2.90 Å.

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.




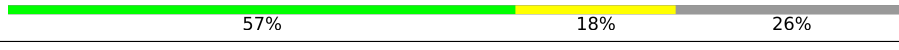
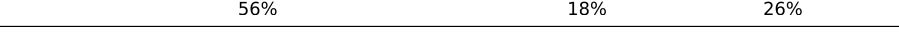

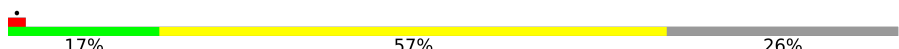
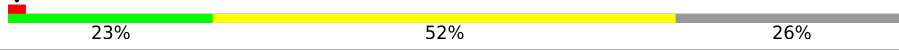

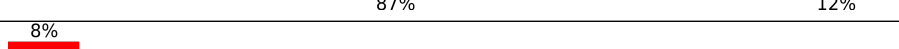


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	1614	
2	B	102	
2	F	102	
3	C	129	

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Mol	Chain	Length	Quality of chain
3	G	129	
4	D	125	
4	H	125	
5	E	135	
5	K	135	
6	I	207	
7	J	207	
8	L	375	
9	N	429	
10	O	210	

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 31470 atoms, of which 6897 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 Isoform 2 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 4.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	681	Total	C	H	N	O	S	0	0
			6178	3567	569	999	1016	27		

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	87	Total	C	N	O	S	0	0
			703	443	142	117	1		
2	F	86	Total	C	N	O	S	0	0
			672	424	130	117	1		

- Molecule 3 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	107	Total	C	N	O	0	0
			811	510	158	143		
3	G	108	Total	C	N	O	0	0
			828	522	162	144		

- Molecule 4 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	93	Total	C	N	O	S	0	0
			717	450	128	137	2		
4	H	93	Total	C	N	O	S	0	0
			725	456	130	137	2		

- Molecule 5 is a protein called Histone H3.2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	95	Total	C	N	O	S	0	0
			779	492	148	136	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	K	98	Total	C	N	O	S	0	0
			801	506	153	139	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	102	ALA	GLY	conflict	UNP P84233
K	102	ALA	GLY	conflict	UNP P84233

- Molecule 6 is a DNA chain called DNA (207-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	154	Total	C	N	O	P	0	0
			3139	1489	572	924	154		

- Molecule 7 is a DNA chain called DNA (207-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	154	Total	C	N	O	P	0	0
			3175	1501	596	924	154		

- Molecule 8 is a protein called Actin, cytoplasmic 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
8	L	375	Total	C	H	N	O	S	0	0
			5816	1850	2891	491	561	23		

- Molecule 9 is a protein called Actin-like protein 6A.

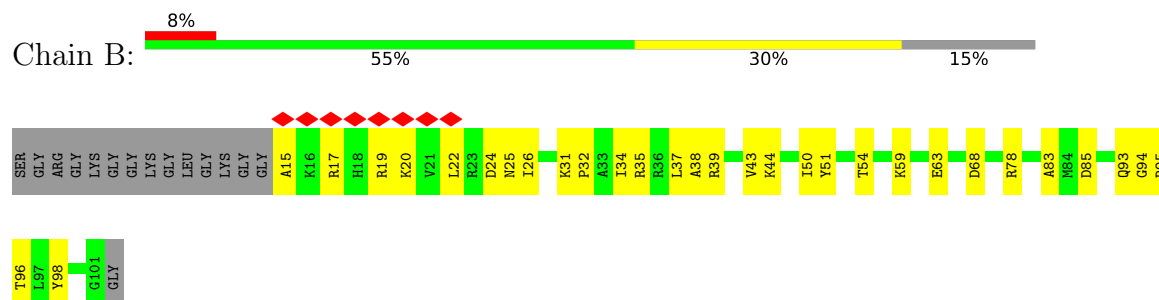
Mol	Chain	Residues	Atoms						AltConf	Trace
9	N	427	Total	C	H	N	O	S	0	0
			6555	2086	3242	565	637	25		

- Molecule 10 is a protein called B-cell CLL/lymphoma 7 protein family member A.

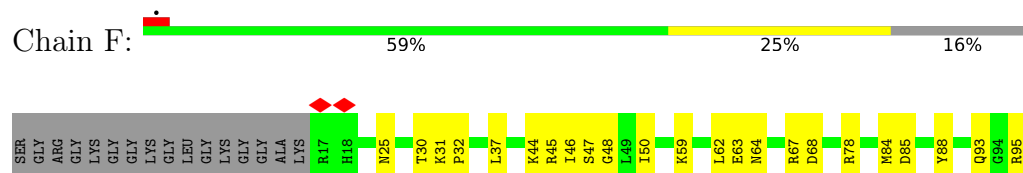
Mol	Chain	Residues	Atoms					AltConf	Trace	
10	O	44	Total	C	H	N	O	S	0	0
			571	240	195	72	63	1		

VAL	LYS	GLN	CYS	LYS	ARG	ASP	D1257	I1193	L1126	L1063	I996	K934	L870	R801	A735	GLN
LYS	ASP	ASP	GLN	ASP	LYS	ALA	E1258	Q1196	D1127	G1064	K997	S935	A871	I902	H736	ALA
SER	SER	ALA	ALA	ASP	ARG	GLU	E1259	N1197	G1128	F1065	C998	C936	K872	N803	A737	ALA
SER	SER	VAL	GLN	SER	SER	VAL	E1260	E1198	T1129	T1066	D999	S937	I873	G804	V738	PRO
GLY	ARG	ASP	THR	GLY	ASP	GLU	D1261	R1199	E1133	G1067	L1003	T938	M875	P805	T739	THR
GLN	LEU	ARG	LEU	GLY	ALA	LEU	E1262	R1200	D1134	G1068	V1006	F939	K376	F806	E740	LEU
LEU	GLY	THR	THR	CYS	GLY	THR	V1263	V1201	R1135	T1069	R1009	Q941	Y877	I808	R741	PRO
THR	SER	GLY	GLY	GLY	L1204	GLY	F1264	M1137	G1136	Q1071	H1010	E940	M878	Y877	V742	VAL
VAL	PHE	GLU	GLY	THR	L1206	GLU	E1265	L1138	L1137	L1072	A1013	Q941	M879	D743	D743	GLY
PHE	THR	GLU	GLY	THR	T1206	GLU	D1266	L1139	D1074	L1073	K1014	W942	I879	K744	K744	LYS
ILE	THR	GLU	GLY	THR	E1267	GLU	E1267	T1140	L1075	L1076	G1015	F943	V880	S813	Q745	LYS
GLN	SER	GLU	GLY	THR	V1207	GLU	V1268	T1141	L1077	L1078	V1016	N944	D882	L815	S746	LYS
PRO	ARG	THR	THR	THR	E1208	ARG	V1269	F1142	L1077	L1078	L1017	P946	D886	L748	A747	ILE
LEU	ASP	ARG	ARG	ARG	S1209	GLY	N1270	M1143	L1077	S1079	L1018	F947	N888	M749	M749	PRO
SER	SER	ARG	SER	SER	V1210	SER	Q1271	E1211	A1078	L1078	L1019	A948	H889	A819	K755	ASP
ARG	ARG	ASP	ILE	ARG	E1212	ASP	M1272	E1212	S1079	L1078	T1019	W949	H890	Y820	Q756	ASP
LYS	LYS	LYS	VAL	LYS	A1274	LYS	I1273	E1214	L1081	F1082	D1020	T950	C891	F822	Q758	VAL
LEU	LEU	ASP	GLN	ASP	K1213	ASP	R1275	I1214	E1082	E1083	G1021	G951	C892	D823	I759	SER
PRO	PRO	ASP	SER	ASP	I1218	GLU	H1276	K1219	E1148	L1084	S1022	E952	L893	P826	K760	VAL
VAL	THR	GLU	VAL	GLY	K1219	GLY	E1277	E1220	F1149	L1085	GLY	K953	T894	S828	G761	GLY
TYR	TYR	SER	PHE	SER	K1342	SER	E1278	L1153	E1152	D1086	LYS	E954	Q895	V829	L762	VAL
TYR	TYR	LYS	THR	LYS	K1343	LYS	E1279	L1154	F1152	L1087	LYS	V954	Q896	V830	E763	ASP
GLY	GLY	GLY	VAL	GLN	V1344	GLY	F1280	L1155	L1156	L1088	GLY	L956	N898	K831	W764	ALA
LEU	LEU	GLY	VAL	ILE	L1346	LYS	E1281	L1156	T1156	L1089	LYS	N957	T899	E763	W764	ARG
ARG	ARG	LYS	GLN	ARG	V1282	LYS	L1282	L1157	A1158	L1090	GLY	E958	H900	K835	L765	HIS
LYS	LYS	ARG	ILE	ARG	D1225	GLY	F1283	V1224	A1158	L1089	GLY	E959	Y901	W766	W766	ILE
PRO	PRO	GLY	GLY	GLY	Q1226	GLY	M1284	D1226	G1159	K1091	G1031	E960	Y902	S767	S767	ILE
VAL	VAL	THR	THR	THR	K1227	THR	R1285	Q1226	G1160	A1094	T1032	E960	A903	G336	L768	GLY
VAL	VAL	GLY	GLY	VAL	V1228	LYS	M1286	K1228	L1161	T1095	K1033	T961	R806	P838	N771	ASN
PHE	PHE	ALA	LYS	PHE	L1228	GLN	D1287	G1162	T1095	L1096	L1034	I962	L907	A839	A772	ALA
ASP	ASP	GLY	ASP	ASP	L1230	GLY	L1288	G1163	H1097	L1096	L1035	I963	L908	A840	N773	LYS
ASP	ASP	LEU	SER	LEU	A1231	LEU	D1289	M1164	K1098	L1098	M1036	I964	L909	R841	L774	GLN
GLY	GLY	LYS	GLY	LYS	R1290	LYS	E1289	L1165	V1099	L1099	N1037	I965	T910	R842	G775	ASP
GLY	GLY	ALA	GLY	SER	R1291	ALA	R1291	L1166	L1100	L1100	M1037	I965	G911	A843	G775	VAL
GLY	GLY	PRO	GLY	PRO	R1292	PRO	R1292	S1167	L1101	L1101	M1040	R966	G911	R966	I776	ASP
ILE	ILE	ASN	GLY	ASN	Q1235	ILE	R1292	A1168	F1102	F1102	Q1041	R967	L914	P846	I777	ASP
ARG	ARG	PRO	GLY	PRO	Q1236	GLY	E1293	D1169	C1103	C1103	L1042	L968	Q915	Q847	L777	GLY
ASN	ASN	GLY	GLY	ASN	K1237	GLY	E1294	T1170	Q1104	Q1104	R1043	H969	Q915	L848	D779	TYR
HIS	HIS	THR	GLY	ASN	S1238	THR	A1295	V1171	M1105	Q1104	R1043	K970	N916	R849	E780	GLY
TYR	TYR	LEU	GLY	LEU	S1239	LEU	R1296	I1172	L1107	L1106	M1105	V971	K917	R849	M781	VAL
ARG	ARG	THR	GLY	THR	S1240	THR	M1297	L1173	S1107	T1106	L1045	L972	L918	N854	G782	SER
LYS	LYS	LYS	GLY	LYS	H1241	LYS	P1298	F1174	L1108	L1108	C1046	L972	L918	N854	G782	GLN
MET	MET	GLY	GLY	MET	K1299	GLY	K1299	D1177	L1109	L1109	M1047	L974	P919	V855	L783	ALA
ASN	ASN	GLY	GLY	ASN	E1242	GLY	R1300	W1178	T1110	T1110	H1048	P974	P919	V855	G784	ALA
LEU	LEU	GLY	GLY	LEU	R1243	GLY	K1301	M1178	I1111	I1111	P1049	L975	E920	L856	K785	LEU
ASP	ASP	VAL	GLY	ASP	R1244	VAL	P1302	M1179	M1112	M1112	Y1050	L976	L921	T858	T786	ALA
GLY	GLY	VAL	GLY	GLY	A1245	VAL	R1303	P1180	E1113	F1052	M1051	L977	W922	I787	I787	ARG
LYS	LYS	ASP	SER	LYS	F1246	ASP	L1304	D1180	D1114	F1052	R978	L978	A923	Q788	Q788	LEU
ASP	ASP	ALA	GLY	ASP	L1247	GLN	L1304	L1246	D1114	Q1053	R979	L979	L925	E861	T789	GLN
VAL	VAL	VAL	GLY	VAL	Q1248	LYS	M1305	Q1185	F1115	H1054	L980	K981	L925	Y862	I790	SER
MET	MET	ILE	GLY	MET	E1306	LYS	E1306	A1186	Y1115	F1116	L980	K981	L925	Y862	A791	LYS
LEU	LEU	LYS	ARG	LEU	D1248	ARG	E1307	Q1187	F1116	H1054	L980	K981	L925	Y862	Y732	Y731
LEU	LEU	TYR	ARG	LEU	A1249	ARG	D1308	D1188	F1116	H1054	L980	K981	L925	Y862	I791	Y731
LEU	LEU	TYR	ARG	LEU	L1251	ARG	E1309	R1189	F1116	H1054	L980	K981	L925	Y862	I791	Y731
LEU	LEU	LYS	ARG	LEU	L1252	ARG	E1310	A1190	F1116	H1054	L980	K981	L925	Y862	I791	Y731
LEU	LEU	LYS	ARG	LEU	E1252	ARG	L1310	H1191	F1116	H1054	L980	K981	L925	Y862	I791	Y731
LEU	LEU	LYS	ARG	LEU	E1253	ARG	S1312	R1192	F1116	H1054	L980	K981	L925	Y862	I791	Y731
LEU	LEU	LYS	ARG	LEU	E1254	ARG	W1313	F1116	F1116	H1054	L980	K981	L925	Y862	I791	Y731
LEU	LEU	LYS	ARG	LEU	E1255	ARG	I1314	F1116	F1116	H1054	L980	K981	L925	Y862	I791	Y731
LEU	LEU	LYS	ARG	LEU	Q1256	ARG	I1315	F1116	F1116	H1054	L980	K981	L925	Y862	I791	Y731
LEU	LEU	LYS	ARG	LEU		LYS	K1316	F1116	F1116	H1054	L980	K981	L925	Y862	I791	Y731

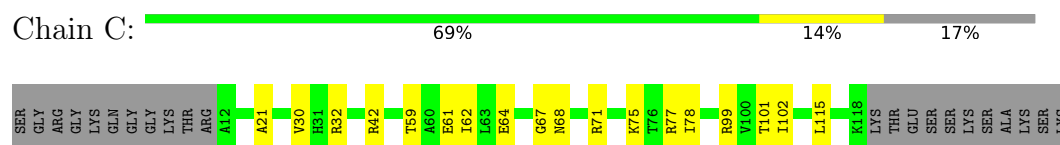
- Molecule 2: Histone H4



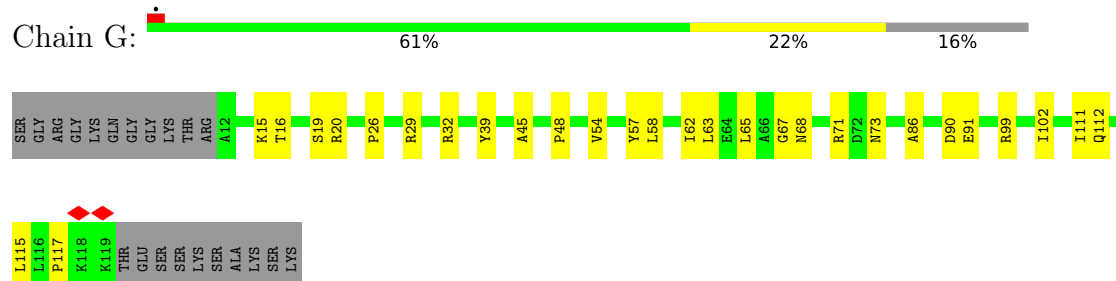
- Molecule 2: Histone H4



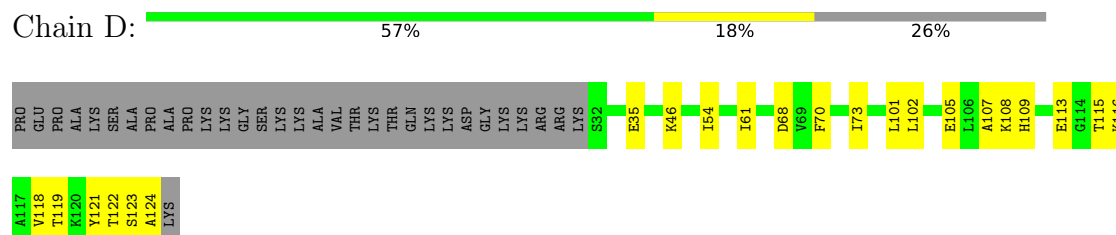
- Molecule 3: Histone H2A



- Molecule 3: Histone H2A



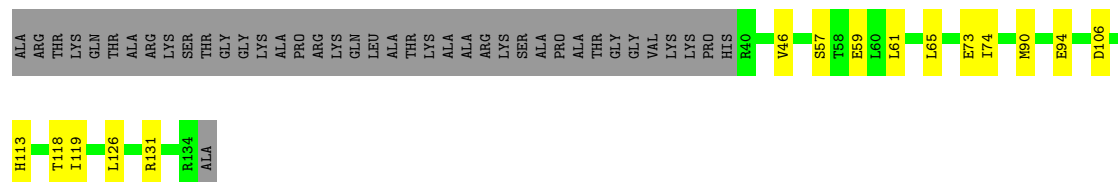
- Molecule 4: Histone H2B 1.1



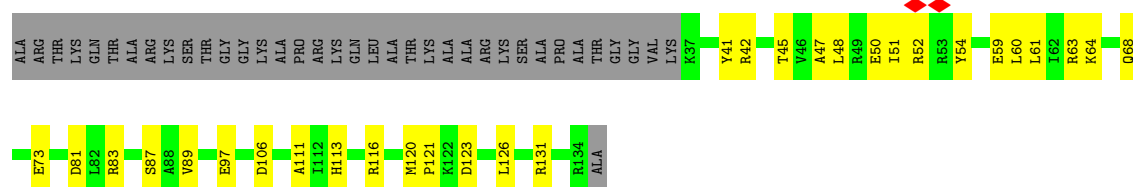
- Molecule 4: Histone H2B 1.1



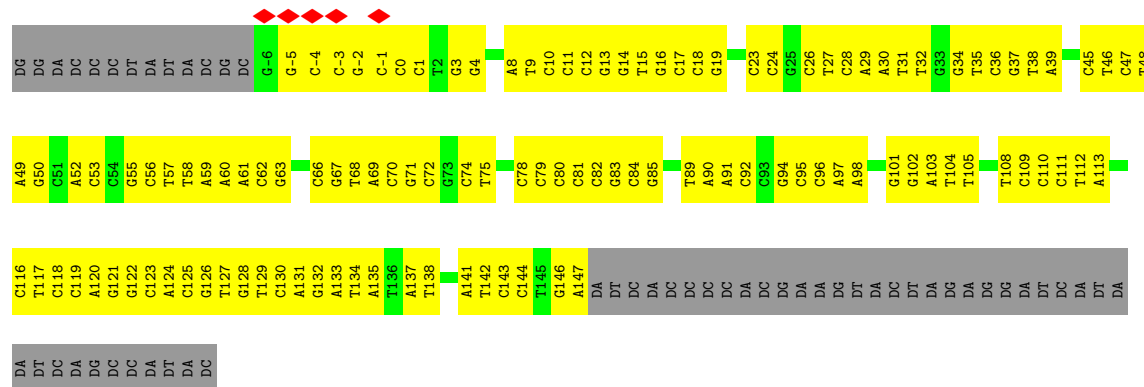
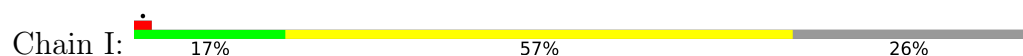
- Molecule 5: Histone H3.2



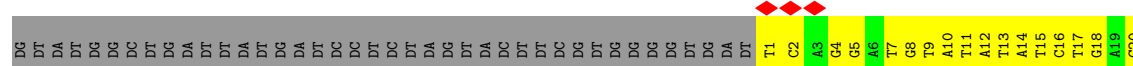
- Molecule 5: Histone H3.2



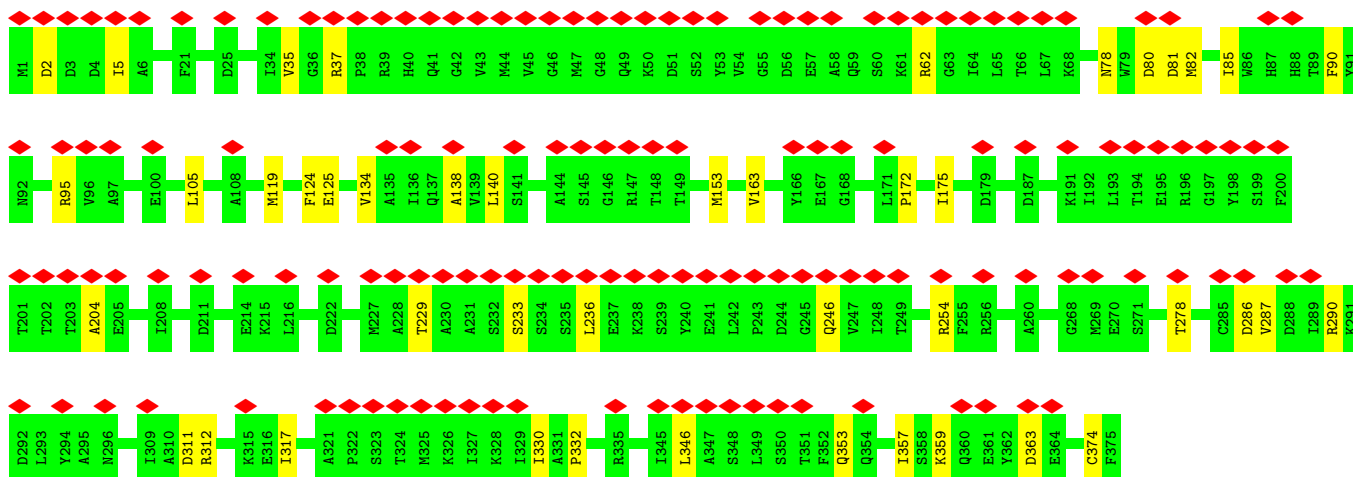
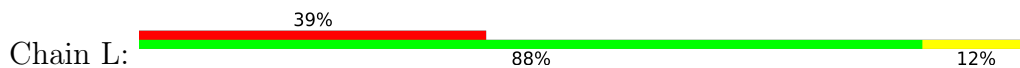
- Molecule 6: DNA (207-MER)



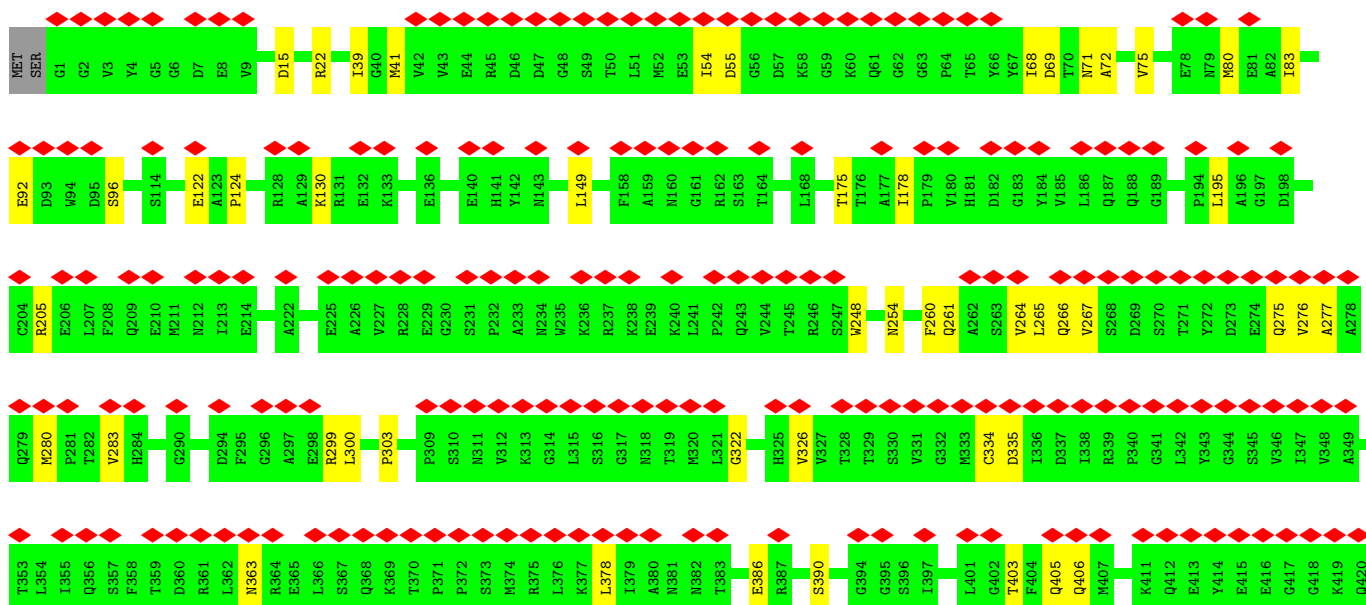
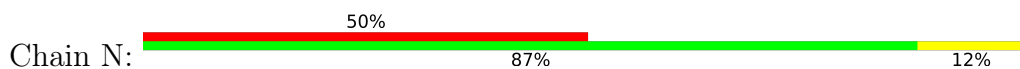
- Molecule 7: DNA (207-MER)

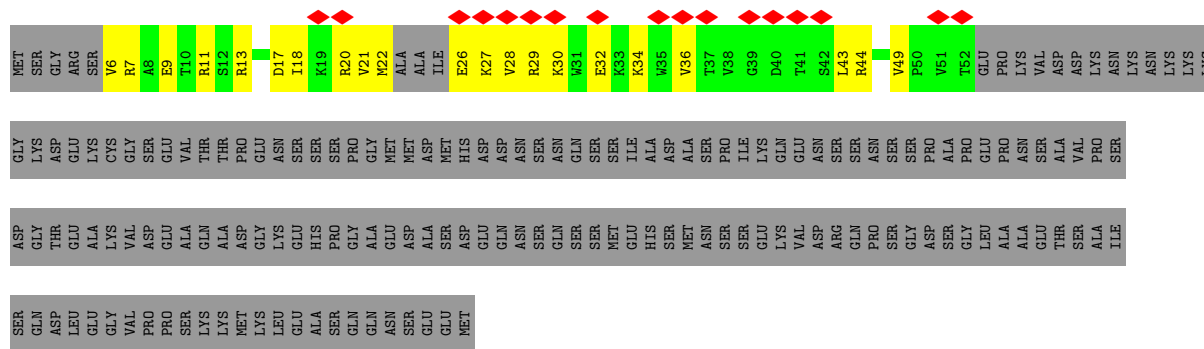


- Molecule 8: Actin, cytoplasmic 1



- Molecule 9: Actin-like protein 6A





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	175820	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.0	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.664	Depositor
Minimum map value	-0.242	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.05	Depositor
Map size (\AA)	389.69998, 389.69998, 389.69998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.0825, 1.0825, 1.0825	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	0.09	0/5715	0.26	0/7683
2	B	0.17	0/711	0.27	0/950
2	F	0.17	0/680	0.28	0/912
3	C	0.14	0/821	0.23	0/1112
3	G	0.14	0/838	0.27	0/1131
4	D	0.15	0/728	0.28	0/983
4	H	0.15	0/736	0.24	0/991
5	E	0.15	0/789	0.24	0/1059
5	K	0.15	0/813	0.27	0/1093
6	I	0.20	0/3517	0.36	0/5421
7	J	0.20	0/3565	0.33	0/5505
8	L	0.09	0/2988	0.23	0/4045
9	N	0.10	0/3386	0.26	0/4587
10	O	0.11	0/382	0.36	0/511
All	All	0.14	0/25669	0.29	0/35983

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	5609	569	5687	481	0
2	B	703	0	757	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	672	0	698	20	0
3	C	811	0	849	25	0
3	G	828	0	884	31	0
4	D	717	0	723	24	0
4	H	725	0	745	22	0
5	E	779	0	815	14	0
5	K	801	0	831	34	0
6	I	3139	0	1727	165	0
7	J	3175	0	1727	150	0
8	L	2925	2891	2891	36	0
9	N	3313	3242	3244	31	0
10	O	376	195	399	23	0
All	All	24573	6897	21977	984	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 21.

The worst 5 of 984 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:780:GLU:HB2	1:A:783:LEU:HD13	1.31	1.09
1:A:994:TYR:HB2	1:A:1272:MET:HE3	1.26	1.09
1:A:1088:ILE:HD12	1:A:1273:ILE:HD11	1.33	1.08
7:J:49:DC:H2''	7:J:50:DT:H71	1.39	1.04
6:I:13:DG:H2''	6:I:14:DG:H5''	1.40	1.03

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	671/1614 (42%)	629 (94%)	42 (6%)	0	100	100
2	B	85/102 (83%)	81 (95%)	4 (5%)	0	100	100
2	F	84/102 (82%)	83 (99%)	1 (1%)	0	100	100
3	C	105/129 (81%)	103 (98%)	2 (2%)	0	100	100
3	G	106/129 (82%)	105 (99%)	1 (1%)	0	100	100
4	D	91/125 (73%)	91 (100%)	0	0	100	100
4	H	91/125 (73%)	89 (98%)	2 (2%)	0	100	100
5	E	93/135 (69%)	93 (100%)	0	0	100	100
5	K	96/135 (71%)	92 (96%)	4 (4%)	0	100	100
8	L	373/375 (100%)	369 (99%)	4 (1%)	0	100	100
9	N	425/429 (99%)	417 (98%)	8 (2%)	0	100	100
10	O	40/210 (19%)	38 (95%)	2 (5%)	0	100	100
All	All	2260/3610 (63%)	2190 (97%)	70 (3%)	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	610/1396 (44%)	610 (100%)	0	100	100
2	B	72/78 (92%)	72 (100%)	0	100	100
2	F	67/78 (86%)	67 (100%)	0	100	100
3	C	81/101 (80%)	81 (100%)	0	100	100
3	G	84/101 (83%)	84 (100%)	0	100	100
4	D	77/105 (73%)	77 (100%)	0	100	100
4	H	79/105 (75%)	79 (100%)	0	100	100
5	E	82/110 (74%)	82 (100%)	0	100	100
5	K	84/110 (76%)	84 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	L	318/318 (100%)	318 (100%)	0	100	100
9	N	362/364 (100%)	362 (100%)	0	100	100
10	O	41/182 (22%)	41 (100%)	0	100	100
All	All	1957/3048 (64%)	1957 (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 16 such sidechains are listed below:

Mol	Chain	Res	Type
9	N	212	ASN
9	N	108	HIS
1	A	1248	GLN
8	L	73	HIS
1	A	1230	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 ⓘ

There are no chain breaks in this entry.

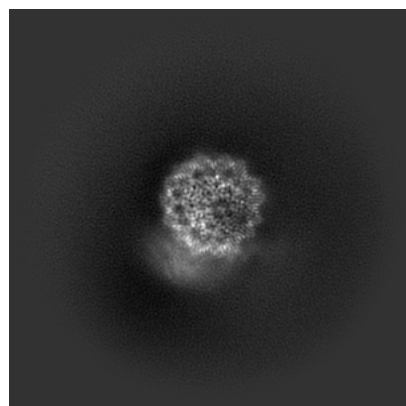
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-65851. These allow visual inspection of the internal detail of the map and identification of artifacts.

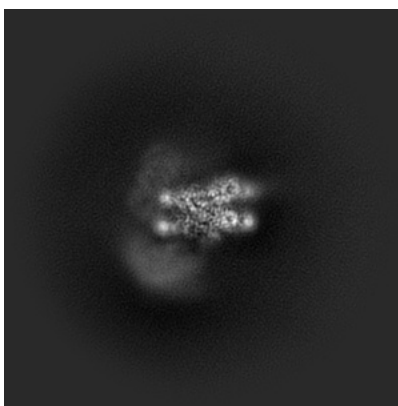
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

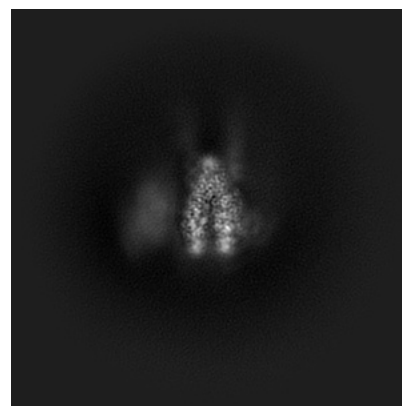
6.1.1 Primary map



X

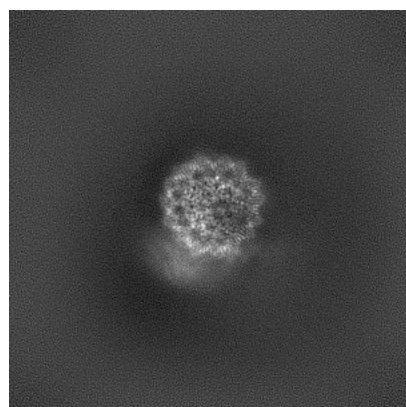


Y

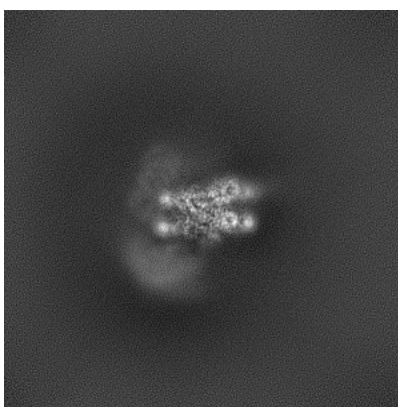


Z

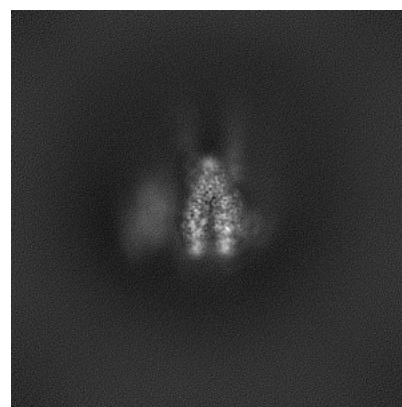
6.1.2 Raw map



X



Y

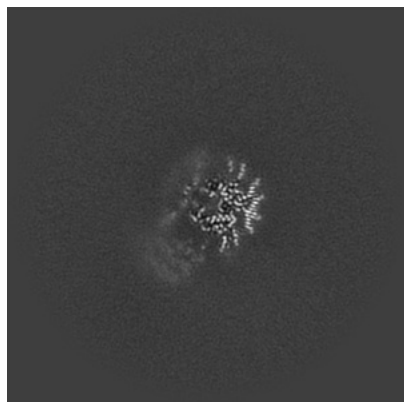


Z

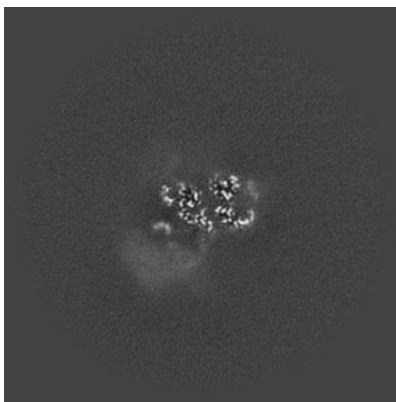
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

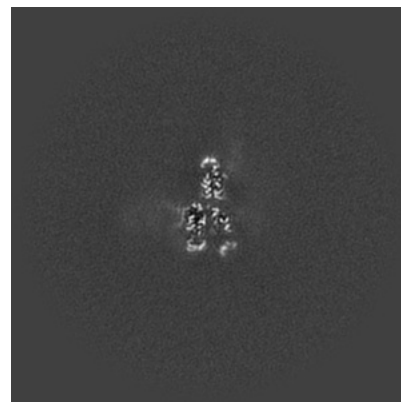
6.2.1 Primary map



X Index: 180

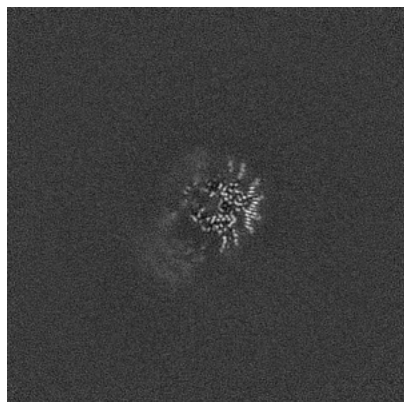


Y Index: 180

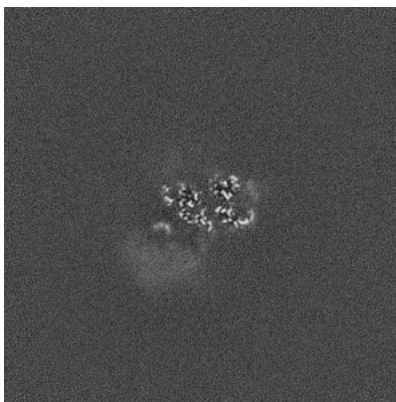


Z Index: 180

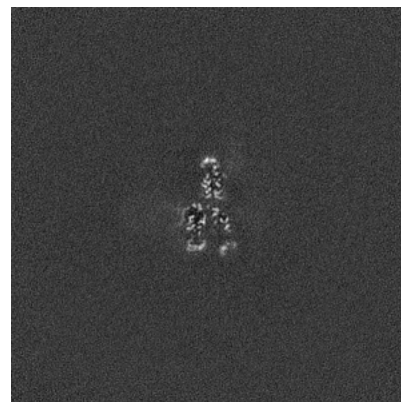
6.2.2 Raw map



X Index: 180



Y Index: 180

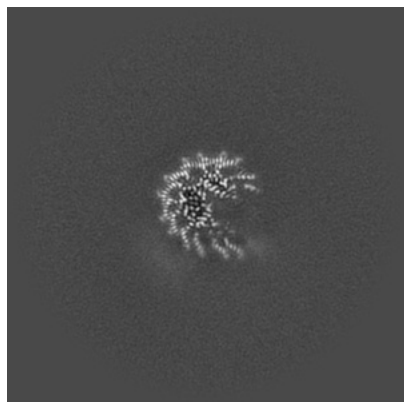


Z Index: 180

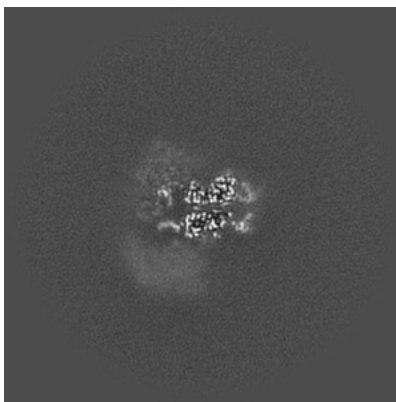
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

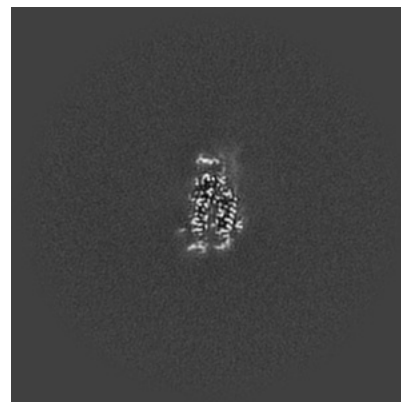
6.3.1 Primary map



X Index: 168

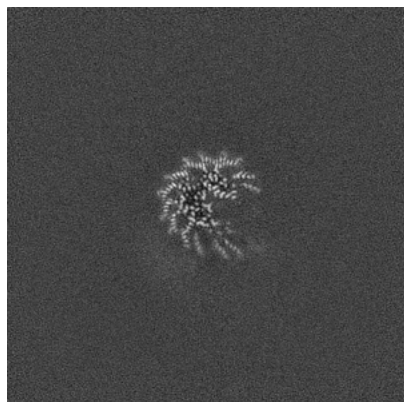


Y Index: 165

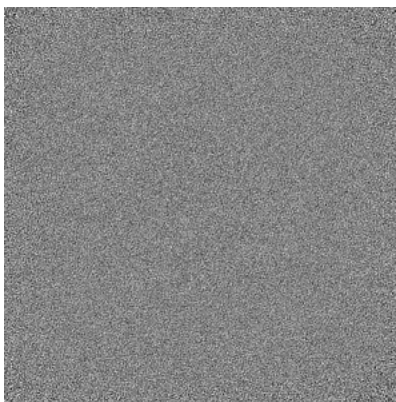


Z Index: 196

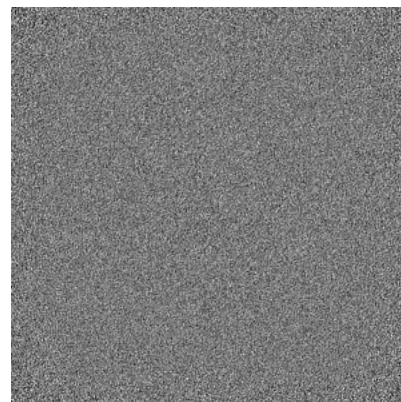
6.3.2 Raw map



X Index: 169



Y Index: 0

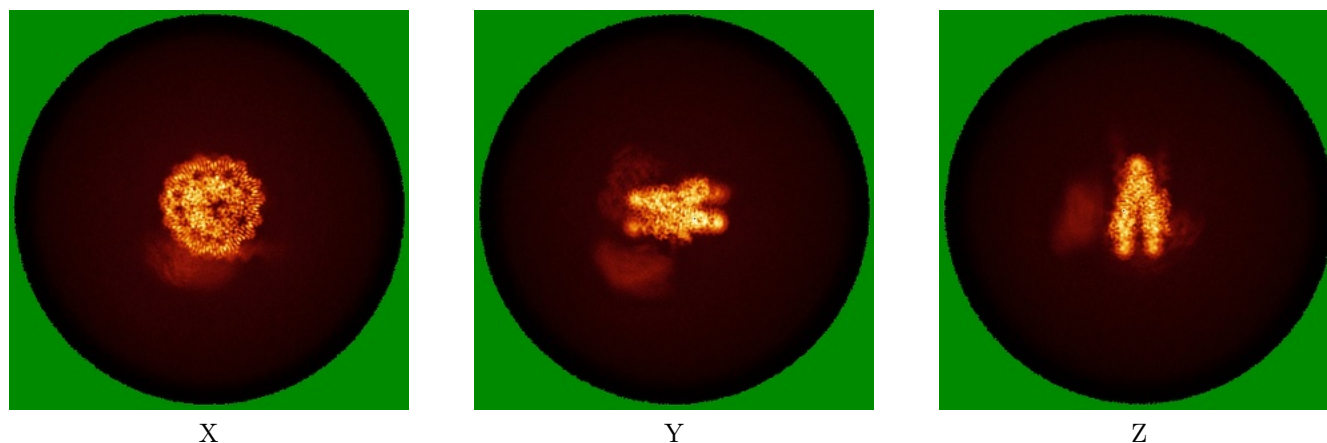


Z Index: 0

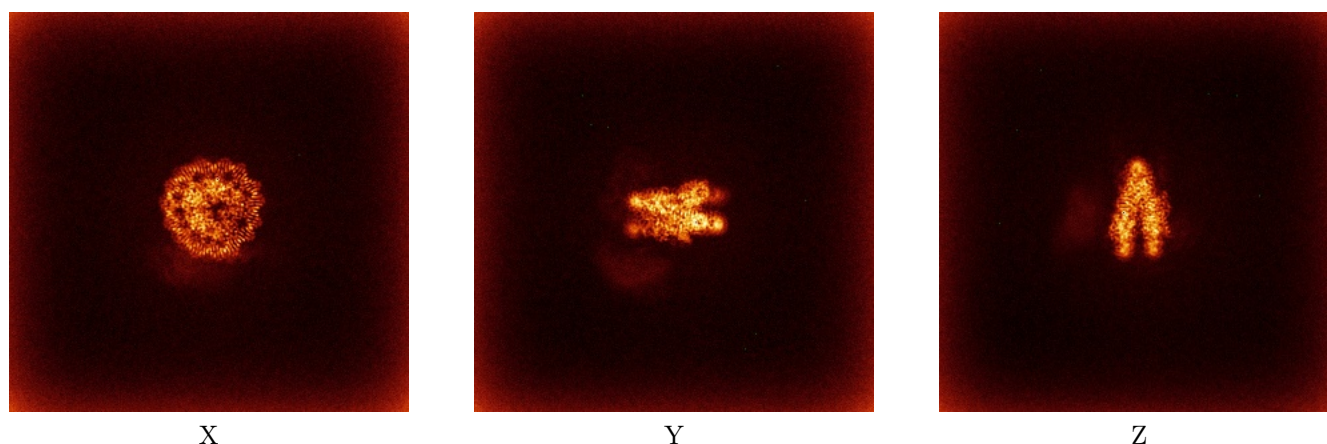
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

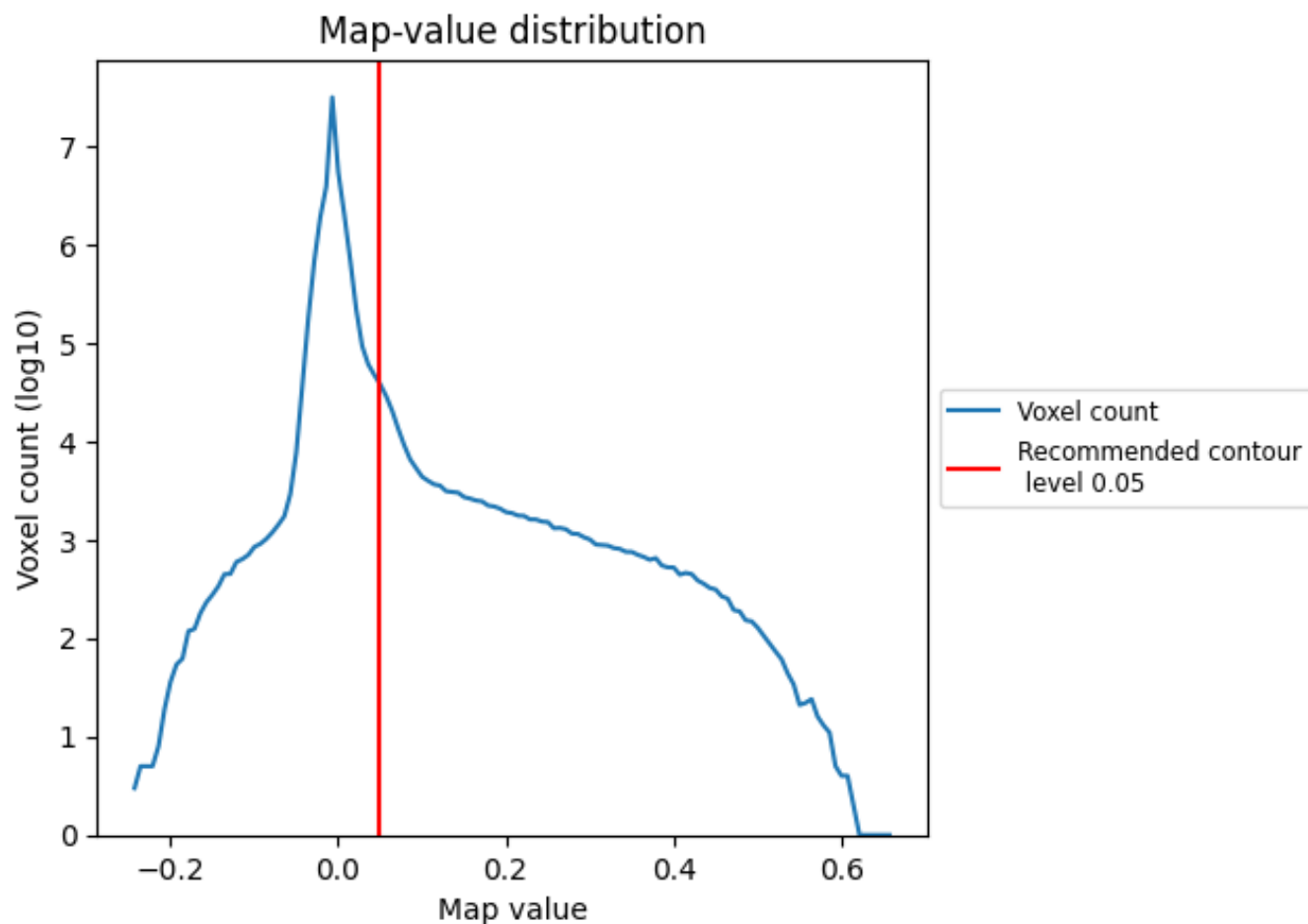
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

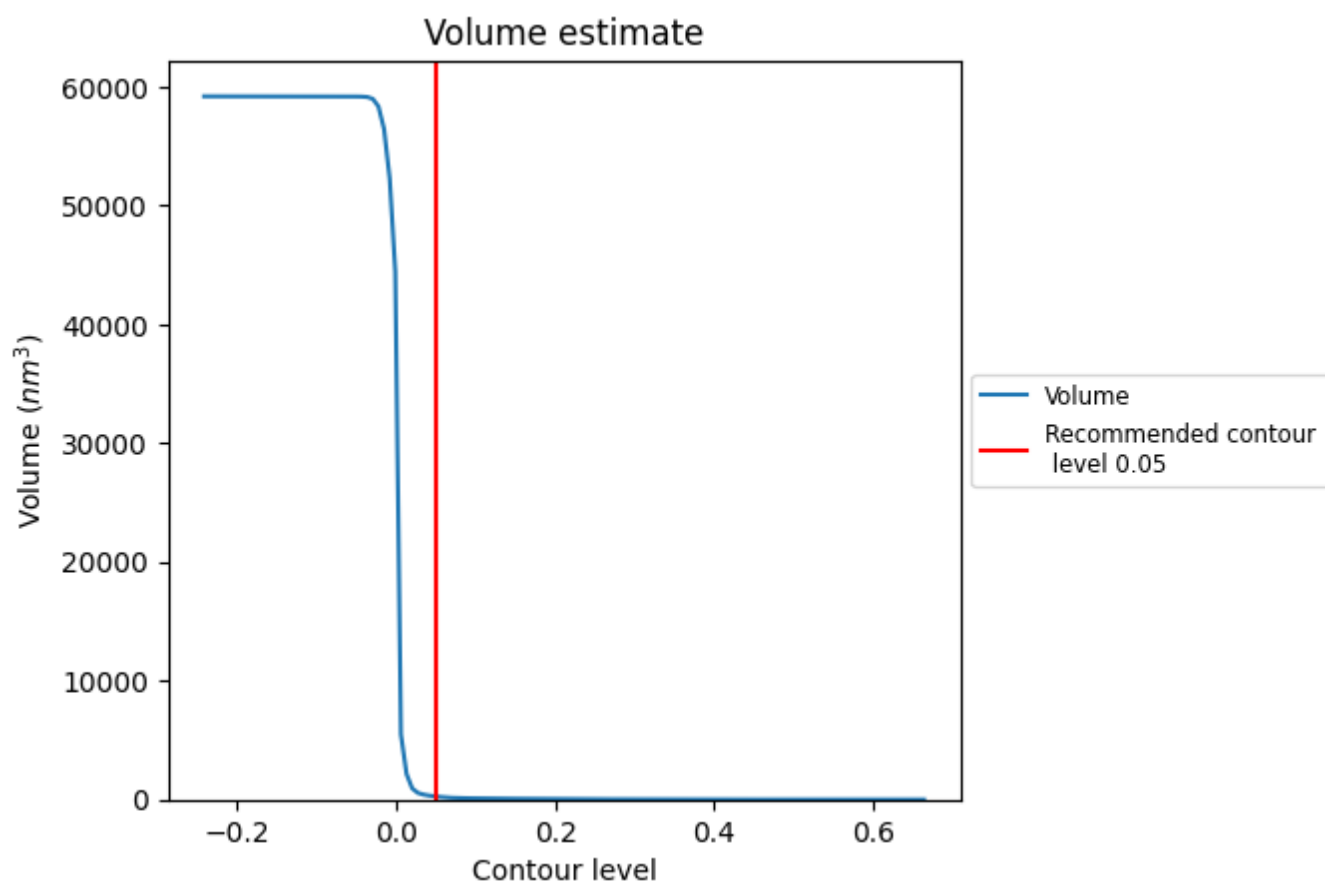
This section contains the results of statistical analysis of the map.

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.

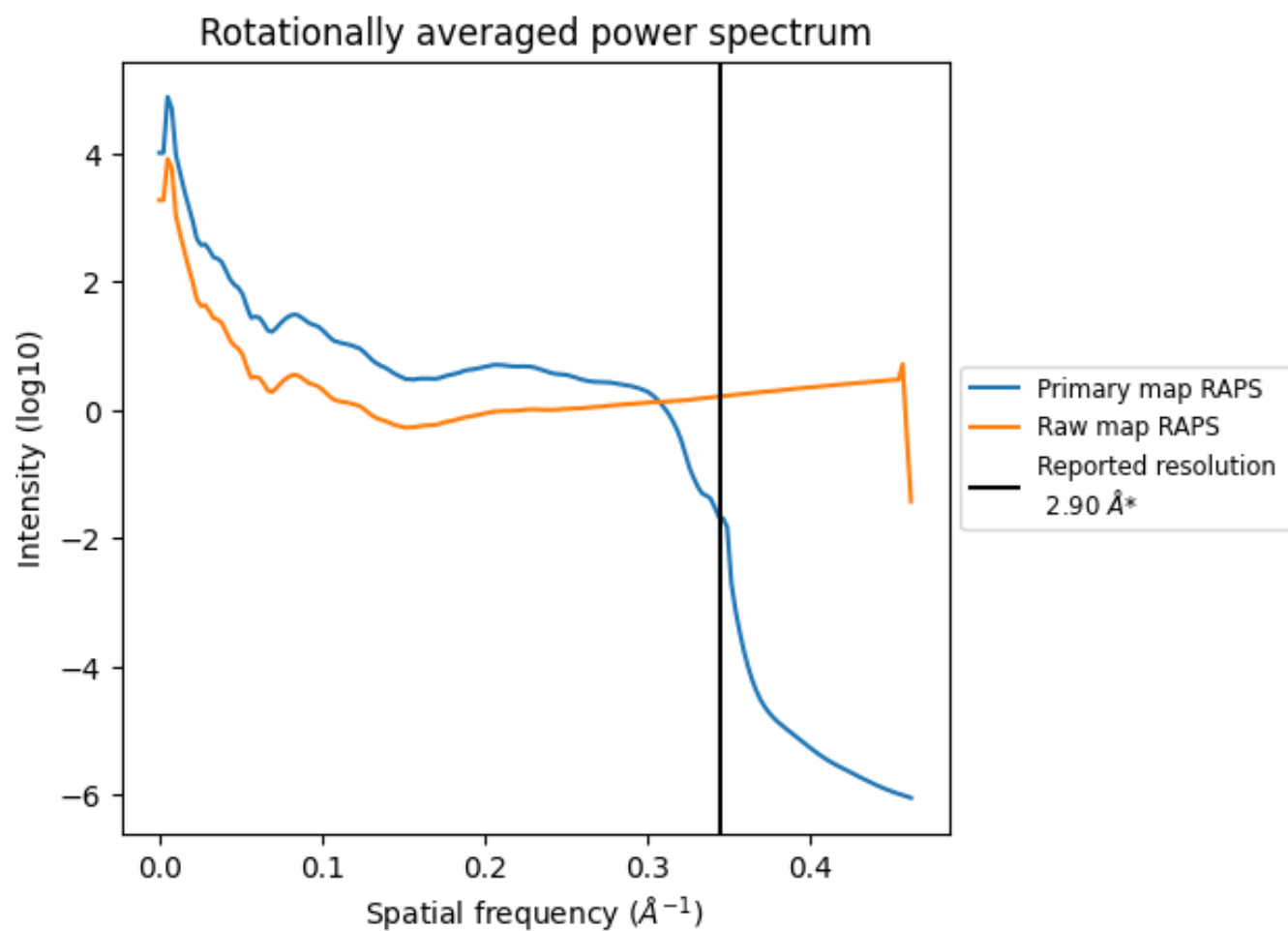
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 259 nm^3 ; this corresponds to an approximate mass of 234 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 ⓘ

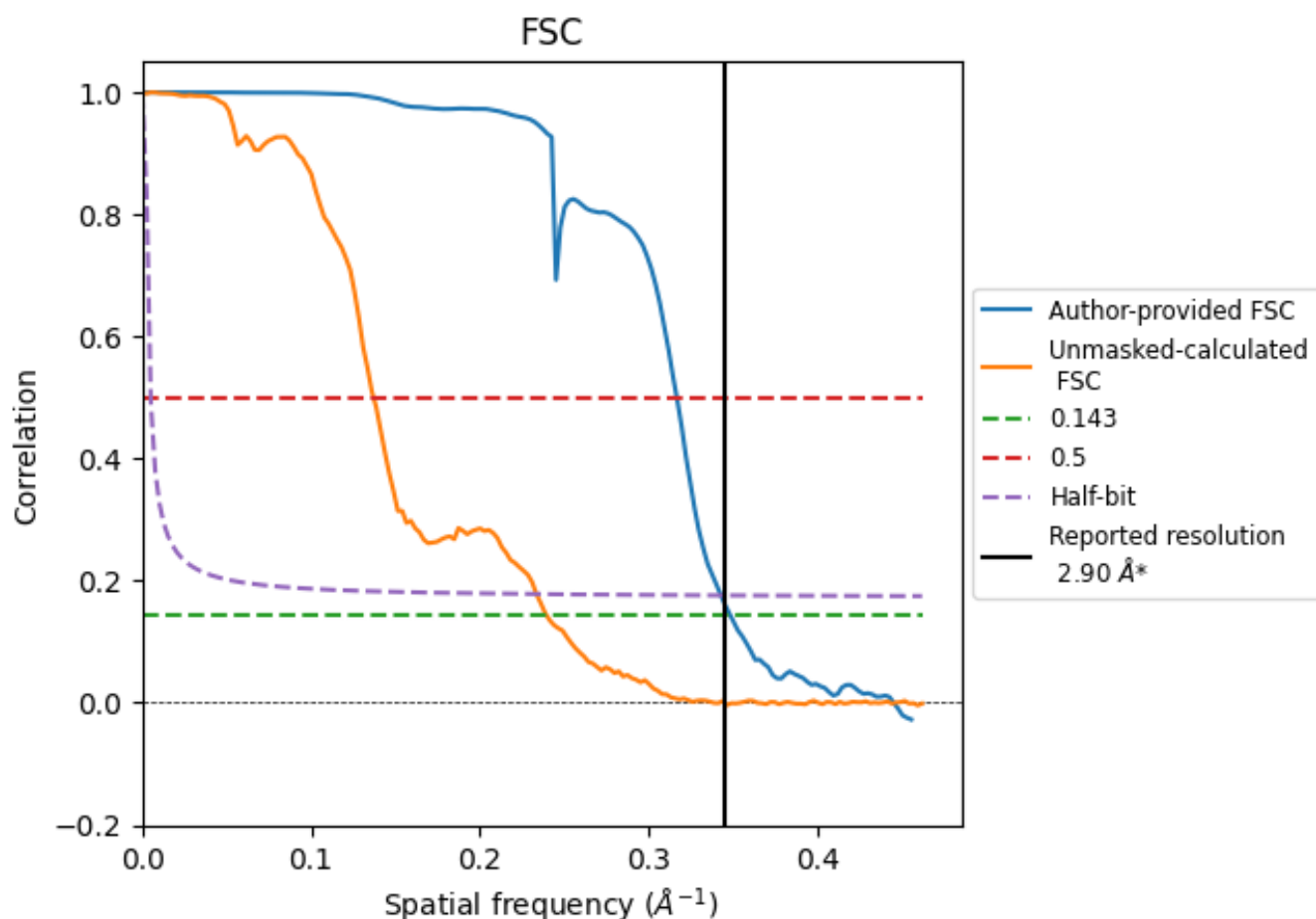


*Reported resolution corresponds to spatial frequency of 0.345 \AA^{-1}

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 0.345 \AA^{-1}

8.2 Resolution estimates [i](#)

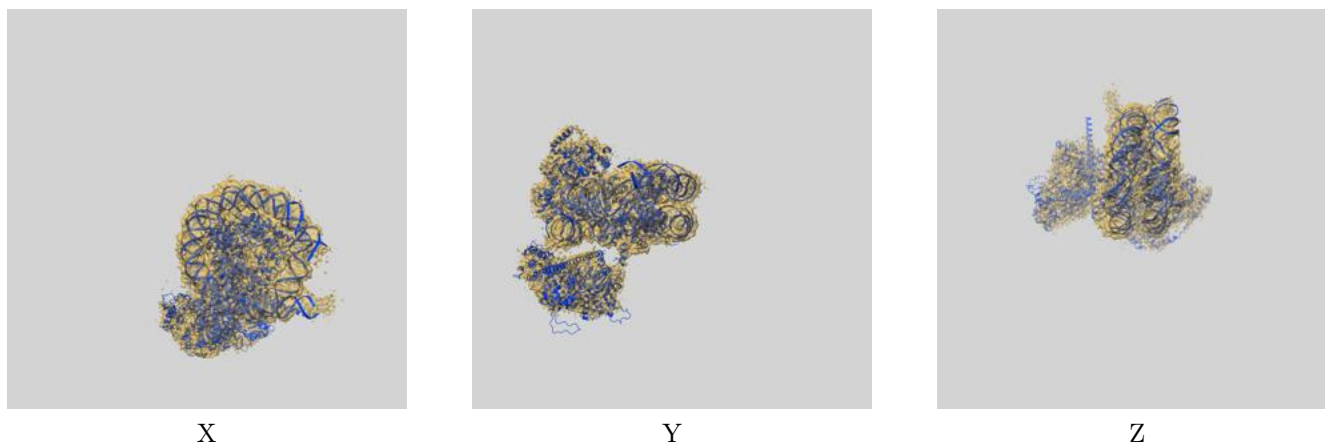
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.87	3.16	2.92
Unmasked-calculated*	4.17	7.30	4.28

*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 4.17 differs from the reported value 2.9 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-65851 and PDB model 9WBZ. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



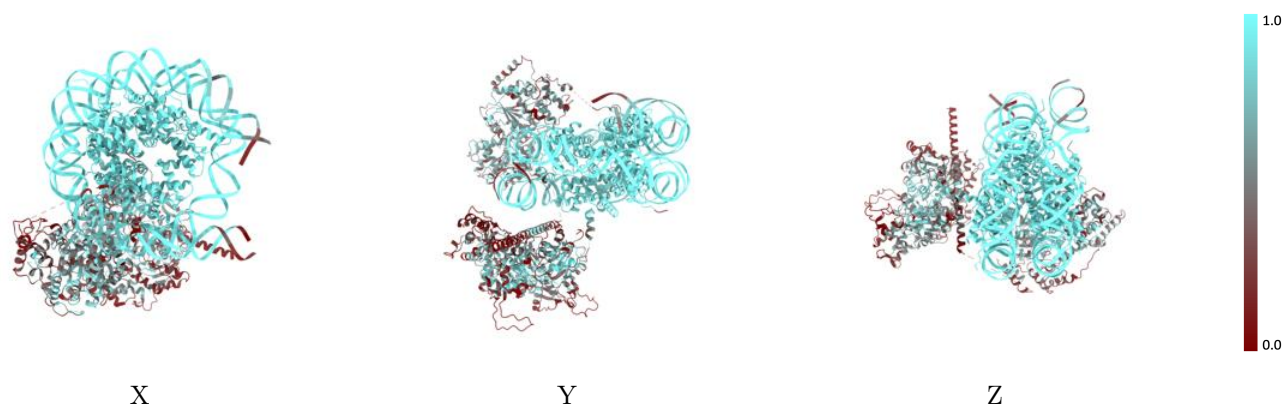
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



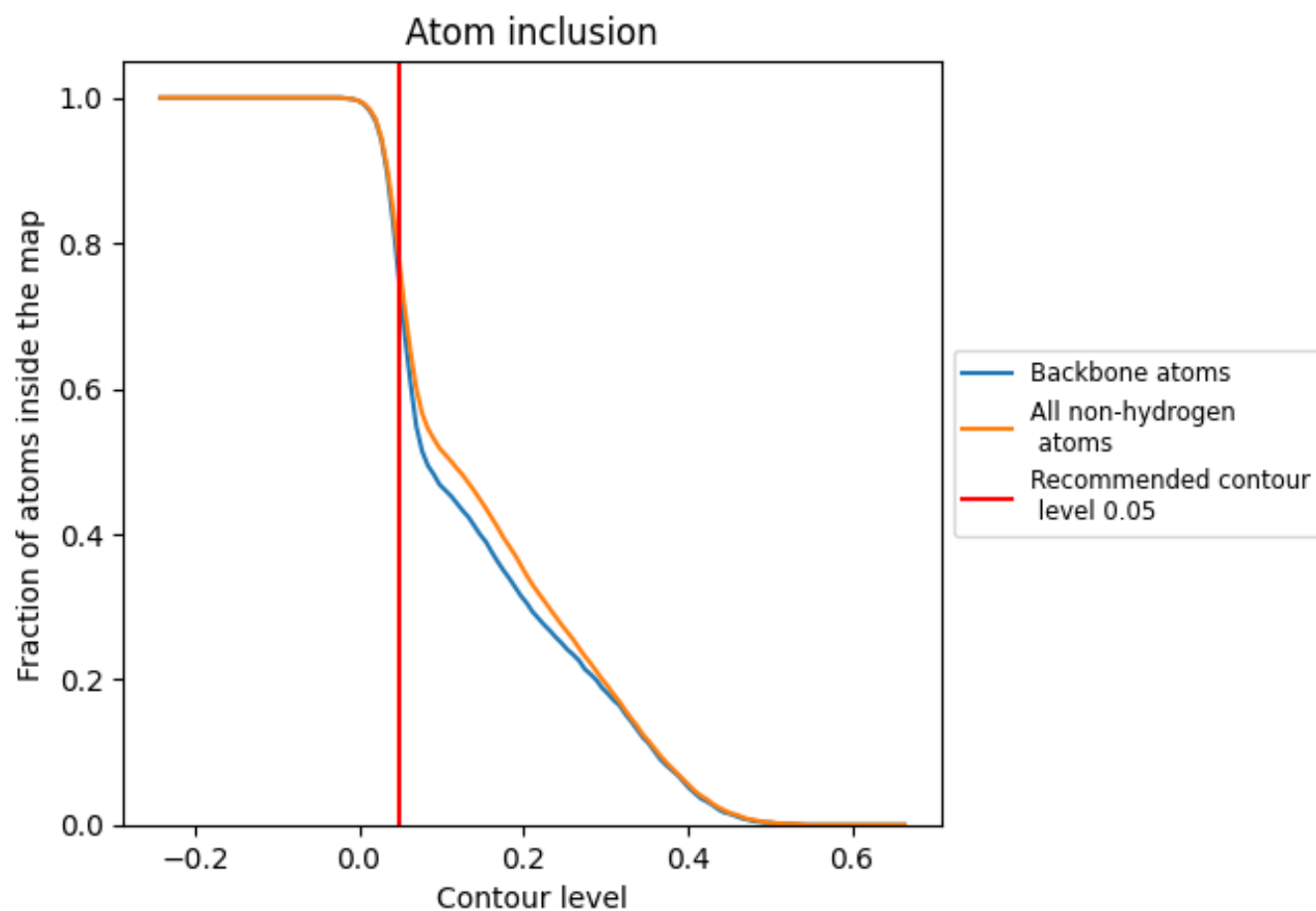
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 76% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7650	<div></div> 0.3430
A	<div></div> 0.4900	<div></div> 0.2550
B	<div></div> 0.8910	<div></div> 0.5200
C	<div></div> 0.9920	<div></div> 0.5570
D	<div></div> 0.9960	<div></div> 0.5500
E	<div></div> 0.9880	<div></div> 0.5680
F	<div></div> 0.9680	<div></div> 0.5560
G	<div></div> 0.9660	<div></div> 0.5530
H	<div></div> 0.9890	<div></div> 0.5570
I	<div></div> 0.9430	<div></div> 0.4920
J	<div></div> 0.9570	<div></div> 0.4950
K	<div></div> 0.9650	<div></div> 0.5390
L	<div></div> 0.5170	<div></div> 0.0920
N	<div></div> 0.4410	<div></div> 0.0620
O	<div></div> 0.5530	<div></div> 0.2100

1.0

0.0

<0.0