



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 02:10 PM UTC

PDB ID : 6GYL / pdb_00006gyl
EMDB ID : EMD-0091
Title : Structure of a yeast closed complex with distorted DNA (core CCdist)
Authors : Dienemann, C.; Schwalb, B.; Schilbach, S.; Cramer, P.
Deposited on : 2018-06-30
Resolution : 4.80 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

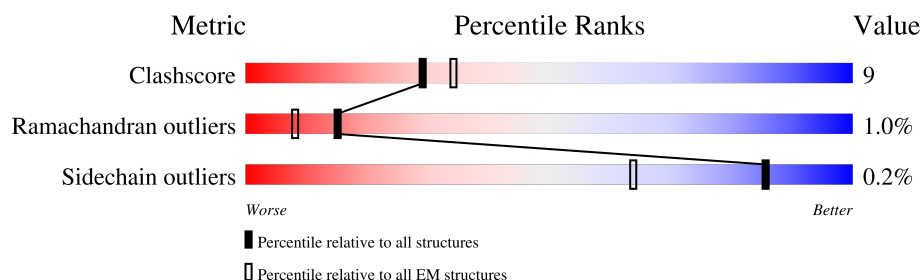
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.80 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)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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	1733	44% 66% 14% 19%
2	B	1224	53% 73% 21% 6%
3	C	318	42% 67% 15% 18%
4	D	221	56% 62% 9% 29%
5	E	215	57% 87% 12% .
6	F	155	26% 43% 10% 46%
7	G	171	57% 66% 34%
8	H	146	50% 70% 23% 7%

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Mol	Chain	Length	Quality of chain
9	I	122	
10	J	70	
11	K	120	
12	L	70	
13	M	345	
14	N	56	
15	O	240	
16	Q	735	
17	R	400	
18	T	56	
19	U	171	
20	V	129	
21	W	586	
22	X	328	

2 Entry composition

There are 24 unique types of molecules in this entry. The entry contains 43409 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 DNA-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1398	Total	C	N	O	S	0	0
			10997	6931	1927	2078	61		

- Molecule 2 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1152	Total	C	N	O	S	0	0
			9178	5807	1608	1708	55		

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	262	Total	C	N	O	S	0	0
			2061	1299	343	406	13		

- Molecule 4 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	157	Total	C	N	O	S	0	0
			1253	779	220	252	2		

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	213	Total	C	N	O	S	0	0
			1744	1107	308	318	11		

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	83	Total	C	N	O	S	0	0
			670	428	114	125	3		

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	171	Total	C	N	O	S	0	0
			1340	861	222	249	8		

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	136	Total	C	N	O	S	0	0
			1089	686	184	215	4		

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	116	Total	C	N	O	S	0	0
			944	581	172	181	10		

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	65	Total	C	N	O	S	0	0
			532	339	93	94	6		

- Molecule 11 is a protein called DNA-directed RNA polymerase II subunit RPB11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	112	Total	C	N	O	S	0	0
			904	580	154	168	2		

- Molecule 12 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	45	Total	C	N	O	S	0	0
			358	221	71	62	4		

- Molecule 13 is a protein called Transcription initiation factor IIB.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	279	Total	C	N	O	S	0	0
			2175	1382	373	403	17		

- Molecule 14 is a DNA chain called GAT1 promoter DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	56	Total	C	N	O	P	0	0
			1129	540	204	329	56		

- Molecule 15 is a protein called TATA-box-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	180	Total	C	N	O	S	0	0
			1416	921	242	247	6		

- Molecule 16 is a protein called Transcription initiation factor IIF subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	148	Total	C	N	O	S	0	0
			1144	733	195	212	4		

- Molecule 17 is a protein called Transcription initiation factor IIF subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	190	Total	C	N	O	S	0	0
			1303	812	238	246	7		

- Molecule 18 is a DNA chain called GAT1 promoter DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	56	Total	C	N	O	P	0	0
			1149	546	222	325	56		

- Molecule 19 is a protein called Transcription initiation factor IIA large subunit, Transcription initiation factor IIA large subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	U	92	Total	C	N	O	S	0	0
			757	474	130	150	3		

- Molecule 20 is a protein called Transcription initiation factor IIA subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	100	Total	C	N	O	S	0	0
			782	492	130	156	4		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	123	LYS	-	expression tag	UNP P32774
V	124	HIS	-	expression tag	UNP P32774
V	125	HIS	-	expression tag	UNP P32774
V	126	HIS	-	expression tag	UNP P32774
V	127	HIS	-	expression tag	UNP P32774
V	128	HIS	-	expression tag	UNP P32774
V	129	HIS	-	expression tag	UNP P32774

- Molecule 21 is a protein called Transcription initiation factor IIE subunit alpha,Tfa1,Tfa1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	191	Total	C	N	O	S	0	0
			1469	932	254	277	6		

- Molecule 22 is a protein called Transcription initiation factor IIE subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	160	Total	C	N	O	S	0	0
			1004	620	184	196	4		

- Molecule 23 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
23	A	2	Total	Zn	0
			2	2	
23	B	1	Total	Zn	0
			1	1	
23	C	1	Total	Zn	0
			1	1	
23	I	2	Total	Zn	0
			2	2	
23	J	1	Total	Zn	0
			1	1	
23	L	1	Total	Zn	0
			1	1	
23	M	1	Total	Zn	0
			1	1	
23	W	1	Total	Zn	0
			1	1	

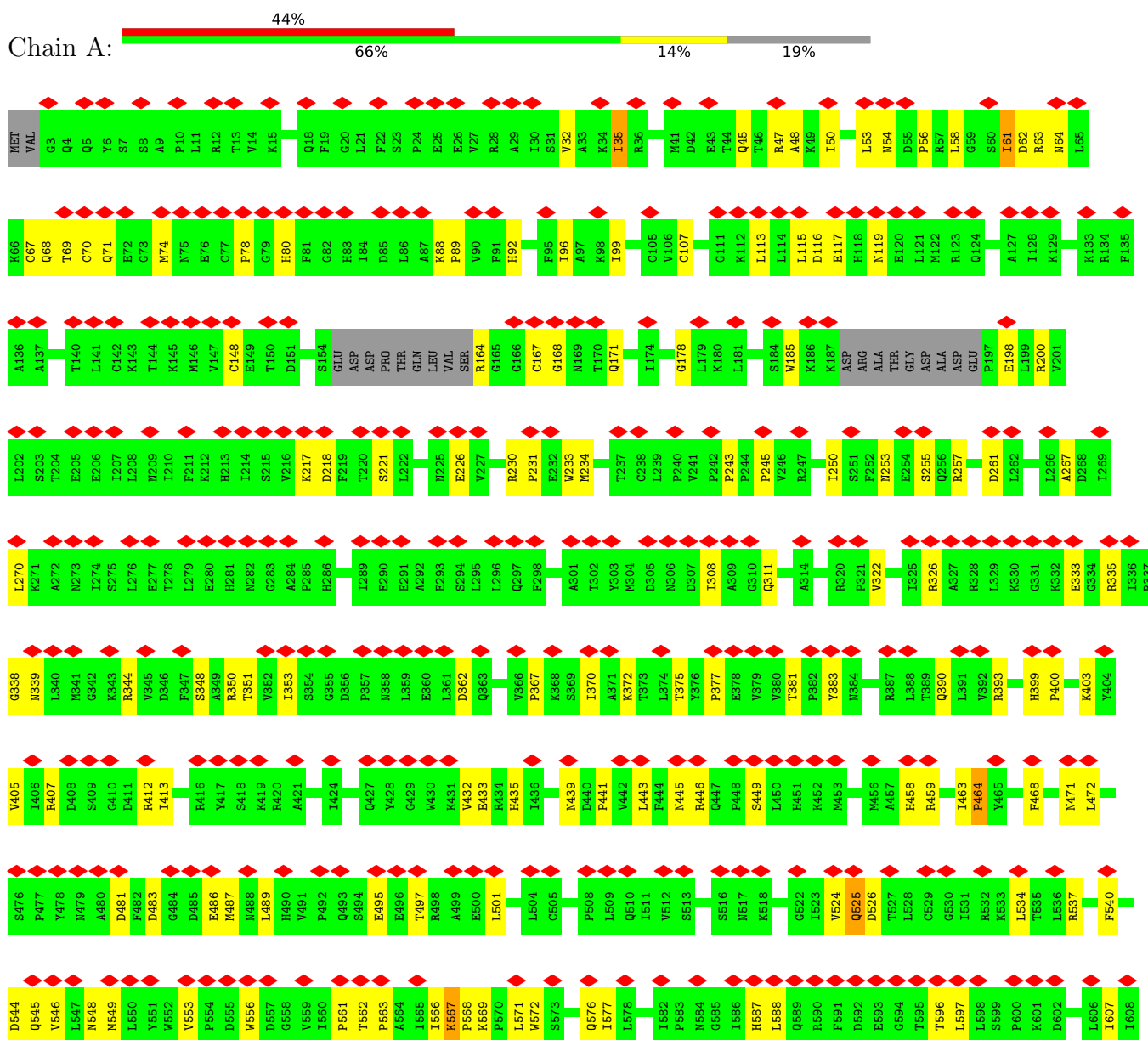
- Molecule 24 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
24	A	1	Total	Mg	0
			1	1	

3 Residue-property plots

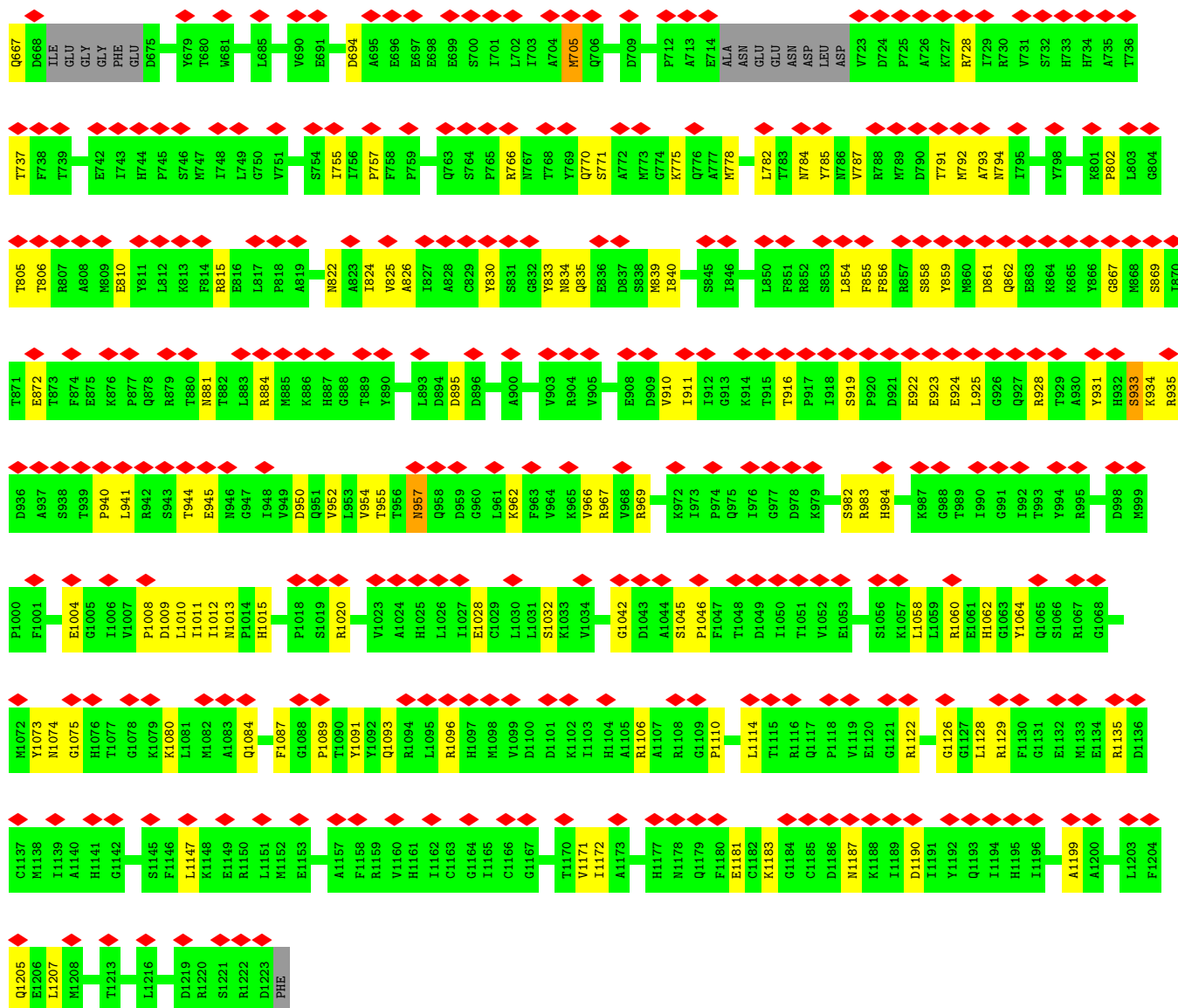
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: DNA-directed RNA polymerase II subunit RPB1

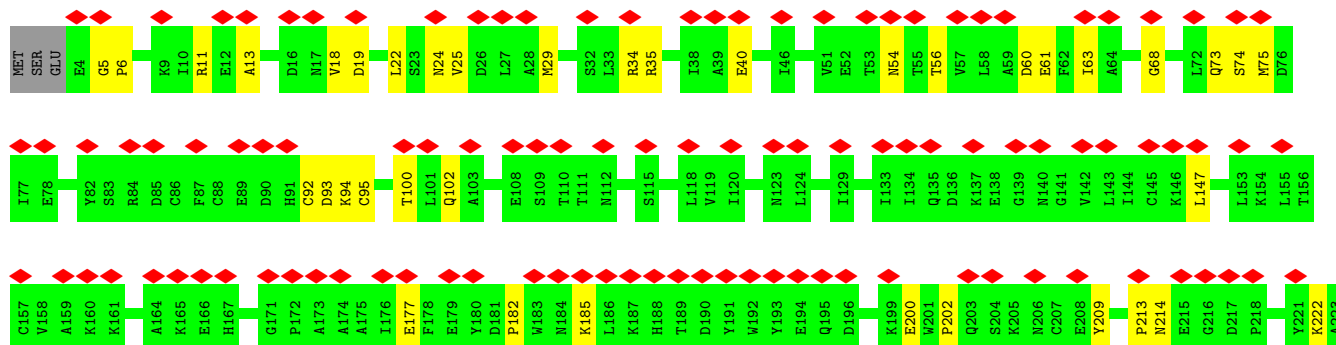
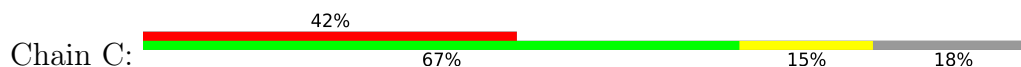


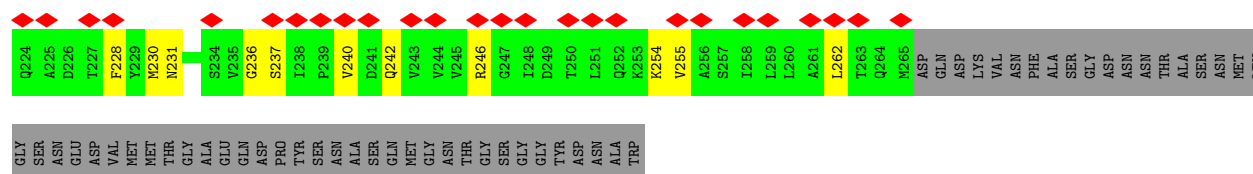
D609	E681	S751	V629	N903	T970	E1034	E1103	F1174	L1236	E1307	V1372	M1444
K830	T882	K752	K831	T904	F971	Y1035	I1104	S1175	I1237	T1308	D1373	I1445
I613	T882	G753	T831	D905	H972	R1036	L1105	LEU	I1238	D1309	V1374	D1446
G615	E685	S754	A832	D906	H973	L1037	N1106	LEU	R1239	G1310	T1377	E1447
V616	A686	F755	E833	T907	D974	K1039	V1107	ASP	G1240	R1241	G1380	E1448
V617	K887	T756	T834	L908	H975	Q1040	A1108	GLU	R1242	V1243	L1351	S1449
E618	K888	N757	G835	D909	P910	Q1041	A1041	ALA	R1243	ARG	T1365	L1450
K619	E619	N758	Y836	D909	P911	F1042	K1109	GLU	V1243	PRO	R1366	V1451
K620	K620	A759	I837	S911	N910	D1043	N1110	GLN	PRO	LYS	H1367	K1452
T621	T621	Q760	Q838	L912	D880	D1043	M1111	SER	LYS	SER	G1388	TYR
V622	V622	M761	R839	L913	L981	L1046	T1116	ASP	SER	ASP	H1389	MET
G623	G623	S762	R840	L913	T982	S1047	T1117	GLU	ASP	ALA	T1394	PRO
S624	S624	G766	L841	S917	K984	S1047	Y1118	ALA	ALA	THR	G1399	GLU
G627	G627	G767	A844	E918	D985	E1049	E1121	THR	GLU	GLU	N1399	GLN
G628	G628	Q767	L845	L920	D986	E1050	P1122	GLN	THR	THR	N1399	GLN
L629	L629	Q768	E946	G921	D987	A1051	G1123	GLU	GLU	GLU	N1399	GLN
I630	I630	E771	M849	D922	L988	R1055	H1124	GLU	GLU	GLU	N1399	GLN
H631	H631	G772	Y852	L923	G989	R1055	H1125	GLU	GLU	GLU	N1399	GLN
V632	V632	K773	Y852	L923	V990	R1055	A1126	GLU	GLU	GLU	N1399	GLN
V633	V633	Q773	D853	K924	K991	V1058	A1126	GLU	GLU	GLU	N1399	GLN
T634	T634	A776	D853	L925	D992	H1059	Q1128	GLU	GLU	GLU	N1399	GLN
R635	R635	F777	N854	Q926	L993	M1063	E1129	GLU	GLU	GLU	N1399	GLN
E636	E636	G778	T855	V927	Q994	V1064	Q1130	GLU	GLU	GLU	N1399	GLN
K637	K637	G781	T855	L928	D994	G1065	A1131	GLU	GLU	GLU	N1399	GLN
G638	G638	D781	R857	L929	N996	V1066	K1132	GLU	GLU	GLU	N1399	GLN
P639	P639	T709	R857	D930	L998	L1067	L1133	GLU	GLU	GLU	N1399	GLN
Q640	Q640	L710	L860	E931	L998	A1068	L1134	GLU	GLU	GLU	N1399	GLN
L645	L645	F714	V863	E932	R1001	A1069	S1136	GLU	GLU	GLU	N1399	GLN
F646	F646	E715	I864	Y933	G1002	I1072	A1137	GLU	GLU	GLU	N1399	GLN
G647	G647	D716	T865	K934	K1003	P1075	I1138	GLU	GLU	GLU	N1399	GLN
G647	G647	N717	F865	V937	N1004	A1076	E1138	GLU	GLU	GLU	N1399	GLN
N648	N648	N717	I867	K938	E1005	T1077	T1141	GLU	GLU	GLU	N1399	GLN
I649	I649	E795	Y868	D939	I1006	Q1078	S1145	GLU	GLU	GLU	N1399	GLN
V652	V652	R720	G869	R940	I1007	Q1078	V1146	GLU	GLU	GLU	N1399	GLN
V653	V653	F721	E870	K941	Q1008	THR	T1147	GLU	GLU	GLU	N1399	GLN
N654	N654	L722	D871	R942	N1009	LEU	Y1153	GLU	GLU	GLU	N1399	GLN
F655	F655	N723	G872	L943	R1012	ASN	D1155	GLU	GLU	GLU	N1399	GLN
W656	W656	N724	M873	E945	D1013	THR	P1156	GLU	GLU	GLU	N1399	GLN
G661	G661	A725	A876	V945	A1014	PHE	D1157	GLU	GLU	GLU	N1399	GLN
S663	S663	R726	S882	F947	T1015	HIS	P1158	GLU	GLU	GLU	N1399	GLN
T664	T664	R727	T885	V948	T1016	ALA	R1159	GLU	GLU	GLU	N1399	GLN
G665	G665	K728	I886	D949	F1017	GLY	R1159	GLU	GLU	GLU	N1399	GLN
I666	I666	R731	D890	G950	F1018	ALA	S1160	GLU	GLU	GLU	N1399	GLN
G667	G667	E734	A891	N953	C1019	SER	T1161	GLU	GLU	GLU	N1399	GLN
D668	D668	V735	A892	N954	C1020	LYS	V1162	GLU	GLU	GLU	N1399	GLN
T669	T669	E735	A892	N954	L1021	K1093	I1163	GLU	GLU	GLU	N1399	GLN
I670	I670	R738	D890	N954	L1022	V1094	P1164	GLU	GLU	GLU	N1399	GLN
A671	A671	D739	A891	N954	R1023	T1095	E1165	GLU	GLU	GLU	N1399	GLN
D672	D672	R821	A891	N954	R1024	S1096	E1166	GLU	GLU	GLU	N1399	GLN
G673	G673	R821	A891	N954	R1025	P1099	E1167	GLU	GLU	GLU	N1399	GLN
P674	P674	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
T675	T675	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
M676	M676	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
R677	R677	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
E678	E678	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
E681	E681	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
E682	E682	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
E685	E685	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
A686	A686	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
K887	K887	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
K888	K888	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
K889	K889	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
D692	D692	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
V693	V693	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
T694	T694	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
K695	K695	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
E696	E696	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
A699	A699	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
N700	N700	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
L701	L701	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
T702	T702	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
T703	T703	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
A704	A704	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
K705	K705	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
H706	H706	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
G707	G707	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
M708	M708	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
T709	T709	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
L710	L710	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
F714	F714	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
E715	E715	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
D716	D716	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
N717	N717	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
R720	R720	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
F721	F721	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
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A725	A725	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
R726	R726	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
D727	D727	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
K728	K728	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
R731	R731	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
L732	L732	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
A733	A733	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
E734	E734	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
V735	V735	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
K738	K738	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
D739	D739	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
V743	V743	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
K744	K744	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
V747	V747	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
M748	M748	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
A749	A749	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
G750	G750	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
E681	E681	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
E682	E682	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
E685	E685	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
A686	A686	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
K887	K887	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
K888	K888	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
K889	K889	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
D692	D692	R821	A891	N954	L1026	R1100	I1169	GLU	GLU	GLU	N1399	GLN
V693	V693	R821	A891	N954	L1026</							

- Molecule 2: DNA-directed RNA polymerase II subunit RPB2

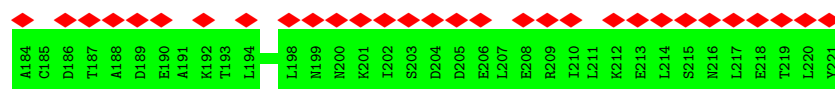
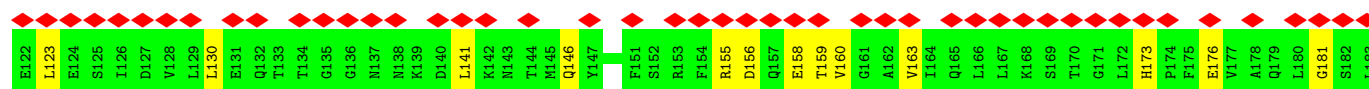
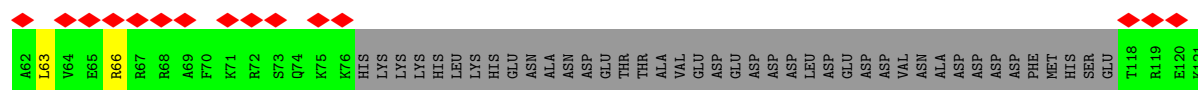
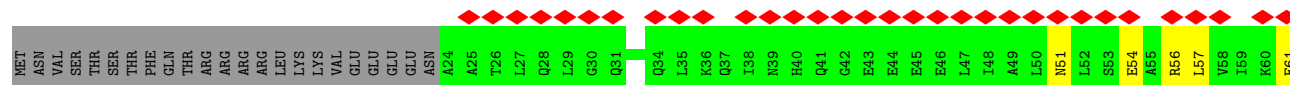


• Molecule 3: DNA-directed RNA polymerase II subunit RPB3

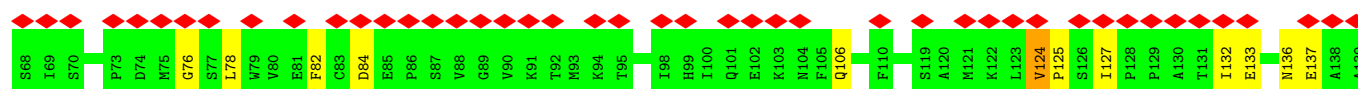
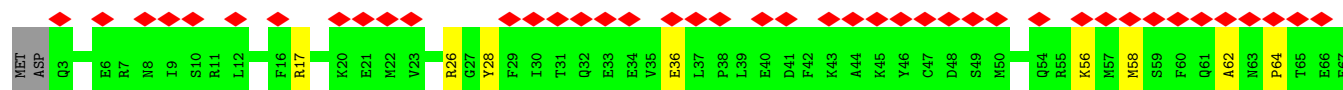
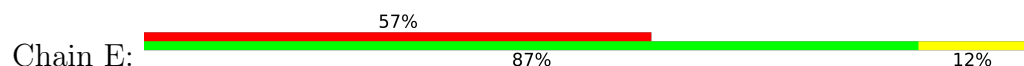




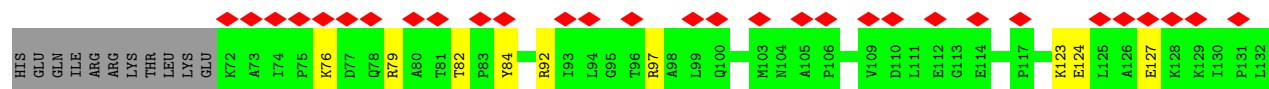
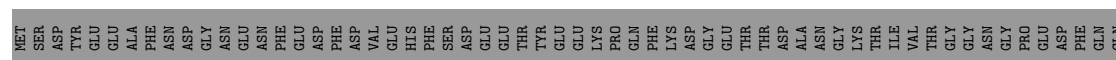
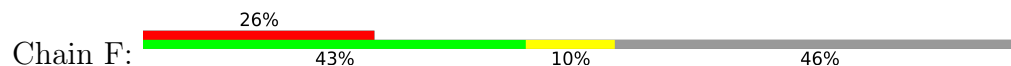
• Molecule 4: DNA-directed RNA polymerase II subunit RPB4



• Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1

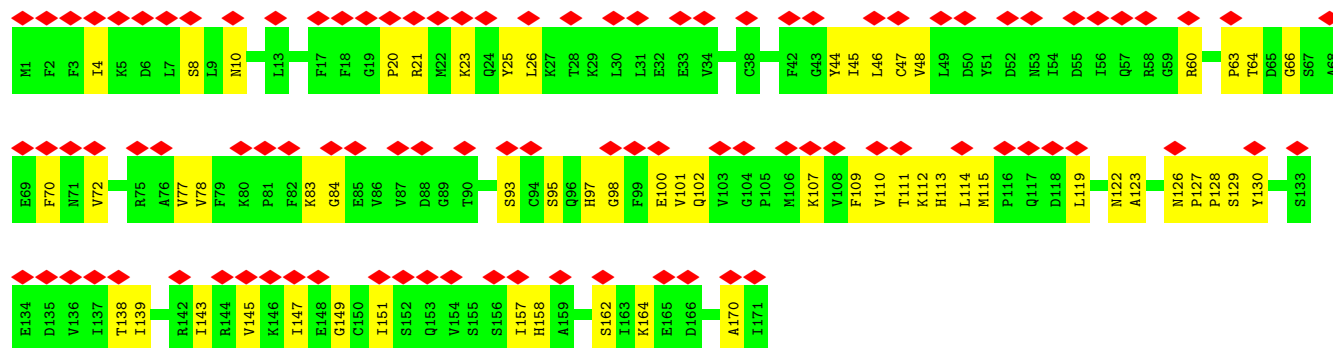


• Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2

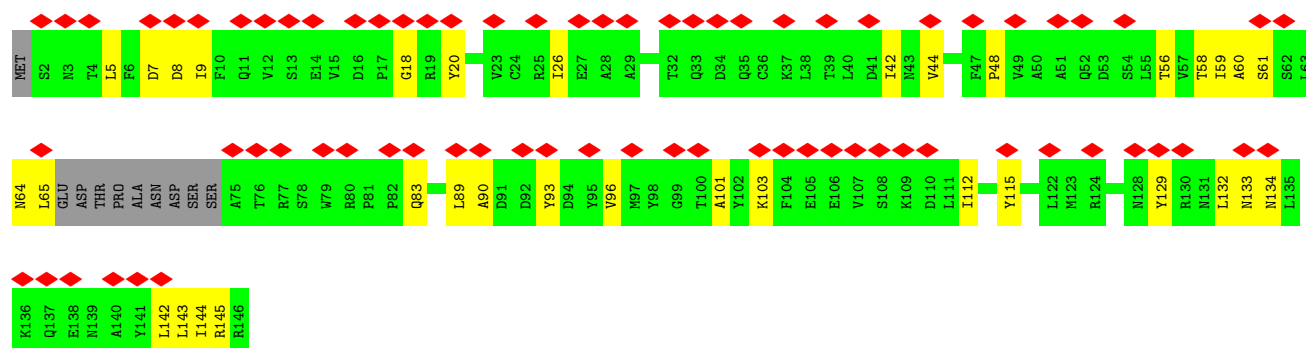




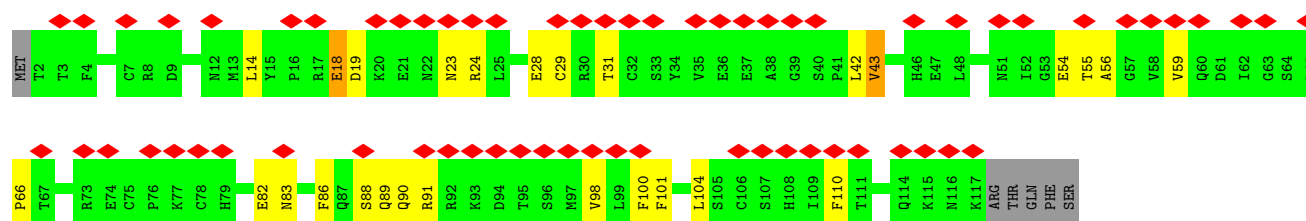
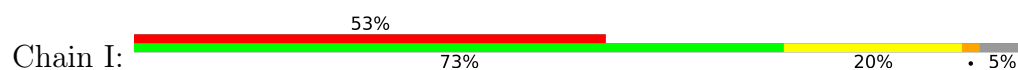
- Molecule 7: DNA-directed RNA polymerase II subunit RPB7



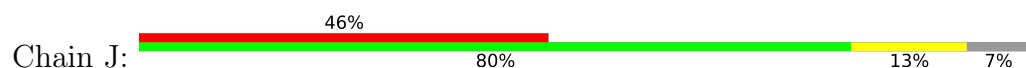
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3

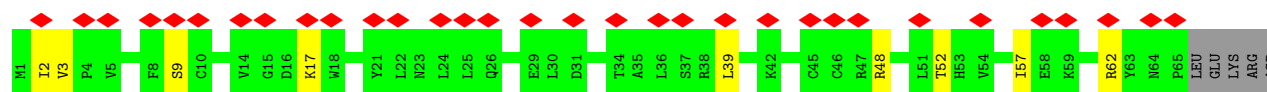


- Molecule 9: DNA-directed RNA polymerase II subunit RPB9

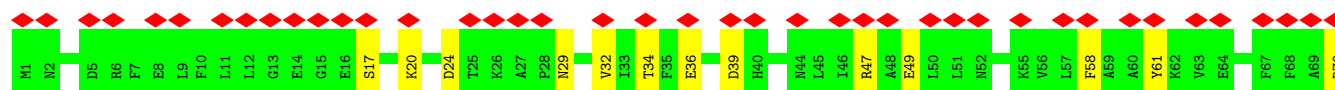
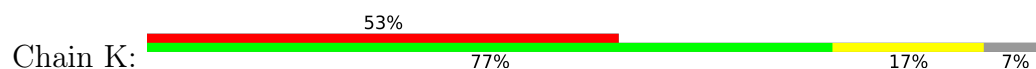


- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5

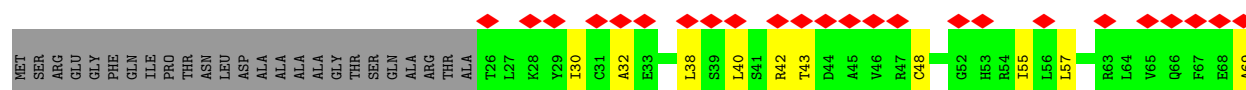




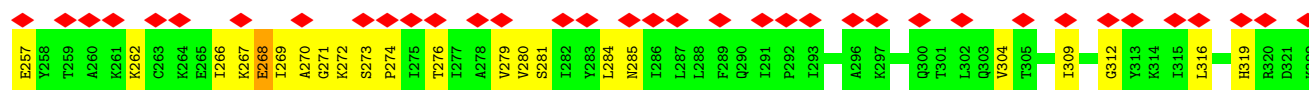
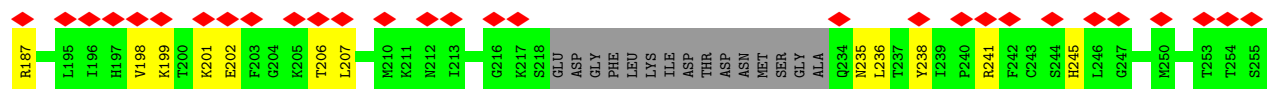
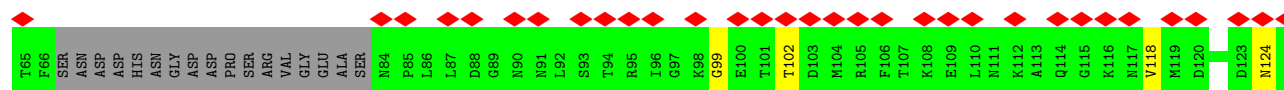
- Molecule 11: DNA-directed RNA polymerase II subunit RPB11



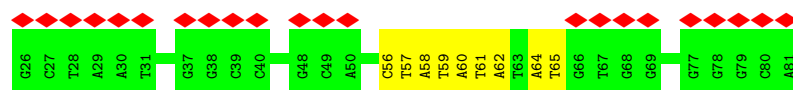
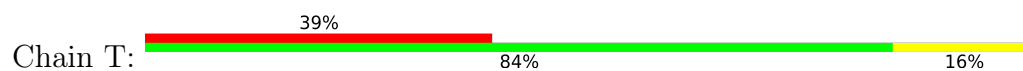
- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4



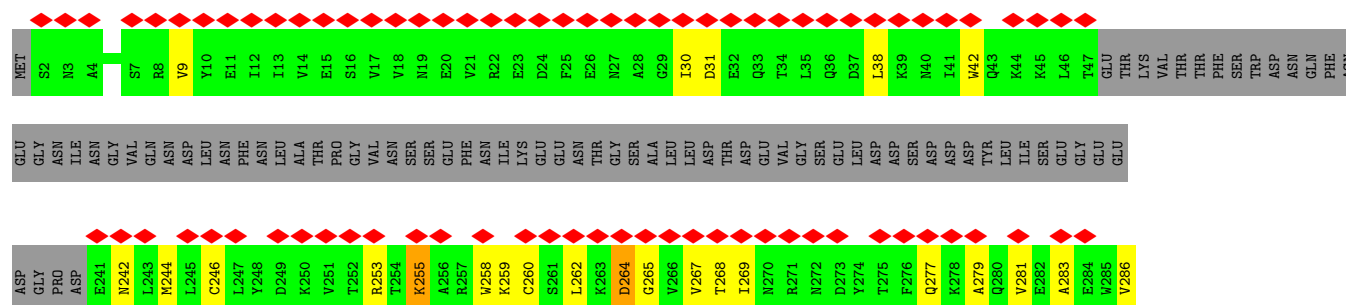
- Molecule 13: Transcription initiation factor IIB



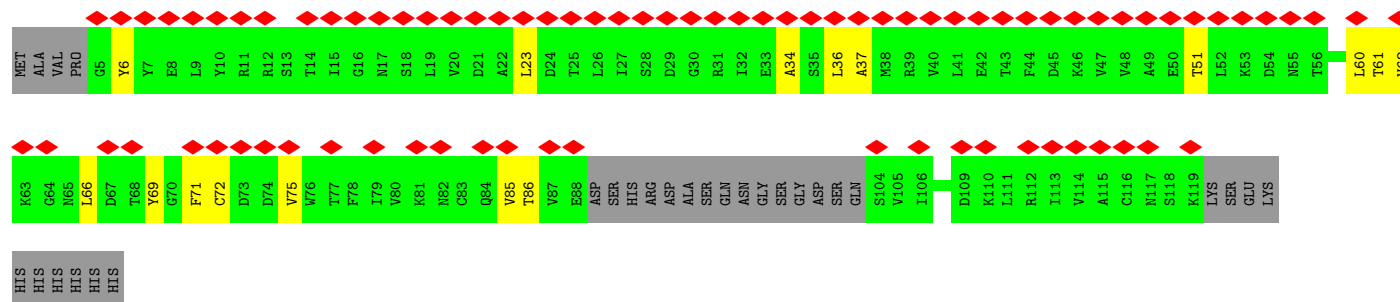
- Molecule 18: GAT1 promoter DNA



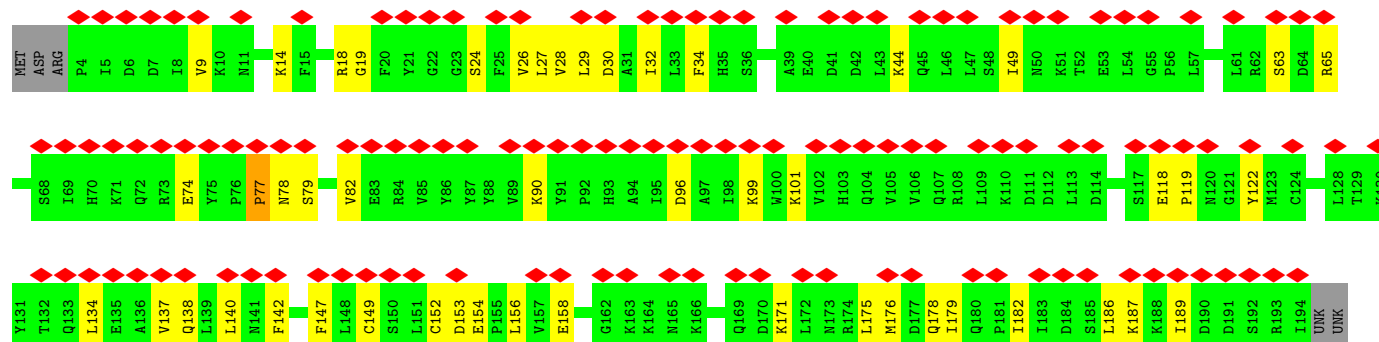
- Molecule 19: Transcription initiation factor IIA large subunit, Transcription initiation factor IIA large subunit



- Molecule 20: Transcription initiation factor IIA subunit 2



- Molecule 21: Transcription initiation factor IIE subunit alpha, Tfa1, Tfa1



[illegible]

- Molecule 22: Transcription initiation factor IIE subunit beta

Chain X:  39% 42% 6% 13%

GLY	G249	◆	T183	LYS	◆
LYS	G250	◆	Y184	SER	◆
ILE	N251	◆	D185	ALA	◆
THR	L252	◆	Y186	LYS	◆
THR	K253	◆	H187	PRO	◆
MET	C254	◆	S188	VAL	◆
THR	T255	◆	P189	LEU	◆
GLY	D256	◆	S190	VAL	◆
THR	E257	◆	E191	ALA	◆
ILE	E258	◆	L192	ILE	◆
LEU	E259	◆	L193	ASN	◆
LYS	F260	◆	K194	LYS	◆
ASP	K261	◆	L195	GLU	◆
TYR	N262	◆	L196	ALA	◆
THR	K263	◆	R197	GLY	◆
HIS	E264	◆	S198	Y134	◆
SER	N265	◆	P199	T135	◆
HIS	V266	◆	V200	K138	◆
ARG	Q267	◆	T201	GLN	◆
VAL	L268	◆	F202	K140	◆
		◆	K203	P141	◆
		◆	G204	V142	◆
		◆	T205	L143	◆
		◆	S206	V144	◆
		◆	C207	N145	◆
		◆	K208	E146	◆
		◆	D209	L147	◆
		◆	L210	L148	◆
		◆	K211	D149	◆
		◆	W214	Y150	◆
		◆	P215	L151	◆
		◆	Q216	S152	◆
		◆	C217	K155	◆
		◆	D218	D156	◆
		◆	E219	D157	◆
		◆	T220	K158	◆
		◆	T221	V159	◆
		◆	N222	I160	◆
		◆	Q223	E161	◆
		◆	L224	L162	◆
		◆	E225	L163	◆
		◆	E226	K164	◆
		◆	D227	K165	◆
		◆	S228	L166	◆
		◆	K229	D167	◆
		◆	V232	R168	◆
		◆	L233	I169	◆
		◆	R234	E170	◆
		◆	D238	F171	◆
		◆	K239	D172	◆
		◆	T240	P173	◆
		◆	V244	K174	◆
		◆	W246	K175	◆
		◆	N247	G176	◆
		◆	S248	T177	◆
		◆		F178	◆
		◆		K179	◆
		◆		Y180	◆
		◆		L181	◆
		◆		SER	◆

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	38000	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 ($e^-/\text{\AA}^2$)	37	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.022	Depositor
Minimum map value	-0.011	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0028	Depositor
Map size (Å)	315.0, 315.0, 315.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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	0.12	0/11192	0.30	2/15128 (0.0%)
2	B	0.11	0/9357	0.27	0/12618
3	C	0.09	0/2099	0.24	0/2845
4	D	0.08	0/1262	0.22	0/1693
5	E	0.11	0/1780	0.32	2/2395 (0.1%)
6	F	0.10	0/682	0.26	0/922
7	G	0.10	0/1368	0.24	0/1844
8	H	0.11	0/1107	0.28	0/1499
9	I	0.11	0/962	0.32	0/1295
10	J	0.14	0/541	0.33	0/727
11	K	0.08	0/922	0.21	0/1244
12	L	0.14	0/360	0.43	0/478
13	M	0.12	0/2204	0.30	0/2963
14	N	0.15	0/1264	0.30	0/1933
15	O	0.12	0/1443	0.28	0/1942
16	Q	0.22	0/1168	0.43	0/1579
17	R	0.13	0/1312	0.33	0/1777
18	T	0.16	0/1292	0.28	0/1981
19	U	0.09	0/766	0.25	0/1032
20	V	0.08	0/789	0.22	0/1066
21	W	0.10	0/1490	0.26	0/2014
22	X	0.12	0/1013	0.33	0/1385
All	All	0.12	0/44373	0.29	4/60360 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	127	ILE	CA-C-N	6.55	124.37	119.66
5	E	127	ILE	C-N-CA	6.55	124.37	119.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1146	VAL	CA-C-N	-6.33	114.35	122.77
1	A	1146	VAL	C-N-CA	-6.33	114.35	122.77

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	10997	0	11081	173	0
2	B	9178	0	9195	166	0
3	C	2061	0	2029	32	0
4	D	1253	0	1275	12	0
5	E	1744	0	1772	15	0
6	F	670	0	690	11	0
7	G	1340	0	1357	75	0
8	H	1089	0	1062	21	0
9	I	944	0	899	28	0
10	J	532	0	542	6	0
11	K	904	0	911	14	0
12	L	358	0	381	7	0
13	M	2175	0	2283	51	0
14	N	1129	0	629	8	0
15	O	1416	0	1493	77	0
16	Q	1144	0	1034	28	0
17	R	1303	0	1110	29	0
18	T	1149	0	627	51	0
19	U	757	0	747	23	0
20	V	782	0	790	15	0
21	W	1469	0	1431	97	0
22	X	1004	0	730	38	0
23	A	2	0	0	0	0
23	B	1	0	0	0	0
23	C	1	0	0	0	0
23	I	2	0	0	0	0
23	J	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	L	1	0	0	0	0
23	M	1	0	0	0	0
23	W	1	0	0	0	0
24	A	1	0	0	0	0
All	All	43409	0	42068	769	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 9.

The worst 5 of 769 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)
15:O:99:PHE:CD2	18:T:58:DA:H1'	1.23	1.65
15:O:98:ARG:HG2	18:T:58:DA:C5'	1.46	1.43
15:O:99:PHE:CG	18:T:58:DA:H1'	1.57	1.37
15:O:99:PHE:CZ	18:T:58:DA:N3	1.95	1.35
7:G:158:HIS:HB2	21:W:138:GLN:NE2	1.40	1.32

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	1386/1733 (80%)	1298 (94%)	77 (6%)	11 (1%)	16	52
2	B	1136/1224 (93%)	1064 (94%)	62 (6%)	10 (1%)	14	49
3	C	260/318 (82%)	236 (91%)	20 (8%)	4 (2%)	8	38
4	D	153/221 (69%)	145 (95%)	7 (5%)	1 (1%)	18	55
5	E	211/215 (98%)	202 (96%)	8 (4%)	1 (0%)	24	63
6	F	81/155 (52%)	79 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	G	169/171 (99%)	156 (92%)	12 (7%)	1 (1%)	21	58
8	H	132/146 (90%)	117 (89%)	12 (9%)	3 (2%)	5	28
9	I	114/122 (93%)	99 (87%)	15 (13%)	0	100	100
10	J	63/70 (90%)	58 (92%)	3 (5%)	2 (3%)	3	21
11	K	110/120 (92%)	109 (99%)	1 (1%)	0	100	100
12	L	43/70 (61%)	37 (86%)	6 (14%)	0	100	100
13	M	273/345 (79%)	252 (92%)	16 (6%)	5 (2%)	6	33
15	O	178/240 (74%)	164 (92%)	13 (7%)	1 (1%)	21	58
16	Q	140/735 (19%)	119 (85%)	17 (12%)	4 (3%)	3	23
17	R	176/400 (44%)	160 (91%)	15 (8%)	1 (1%)	21	58
19	U	88/171 (52%)	82 (93%)	4 (4%)	2 (2%)	5	28
20	V	96/129 (74%)	92 (96%)	3 (3%)	1 (1%)	12	47
21	W	189/586 (32%)	183 (97%)	4 (2%)	2 (1%)	11	45
22	X	156/328 (48%)	129 (83%)	23 (15%)	4 (3%)	4	25
All	All	5154/7499 (69%)	4781 (93%)	320 (6%)	53 (1%)	15	47

5 of 53 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	Q	127	ILE
21	W	77	PRO
2	B	830	TYR
2	B	933	SER
7	G	63	PRO

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	1221/1520 (80%)	1221 (100%)	0	100	100
2	B	1000/1061 (94%)	999 (100%)	1 (0%)	88	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	230/274 (84%)	229 (100%)	1 (0%)	84	83
4	D	139/200 (70%)	139 (100%)	0	100	100
5	E	195/197 (99%)	195 (100%)	0	100	100
6	F	73/137 (53%)	73 (100%)	0	100	100
7	G	152/152 (100%)	152 (100%)	0	100	100
8	H	119/128 (93%)	119 (100%)	0	100	100
9	I	110/116 (95%)	106 (96%)	4 (4%)	31	52
10	J	60/65 (92%)	60 (100%)	0	100	100
11	K	97/102 (95%)	97 (100%)	0	100	100
12	L	40/57 (70%)	40 (100%)	0	100	100
13	M	245/299 (82%)	245 (100%)	0	100	100
15	O	152/205 (74%)	152 (100%)	0	100	100
16	Q	109/641 (17%)	108 (99%)	1 (1%)	70	77
17	R	107/363 (30%)	107 (100%)	0	100	100
19	U	84/154 (54%)	84 (100%)	0	100	100
20	V	90/115 (78%)	90 (100%)	0	100	100
21	W	155/244 (64%)	155 (100%)	0	100	100
22	X	62/295 (21%)	62 (100%)	0	100	100
All	All	4440/6325 (70%)	4433 (100%)	7 (0%)	85	86

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	I	42	LEU
9	I	43	VAL
16	Q	334	VAL
9	I	59	VAL
9	I	18	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 91 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	264	GLN
11	K	112	GLN
4	D	179	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
8	H	35	GLN
15	O	91	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 11 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

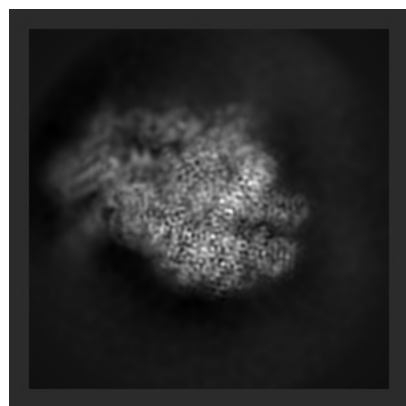
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0091. These allow visual inspection of the internal detail of the map and identification of artifacts.

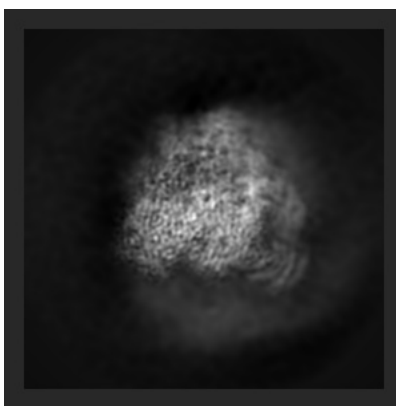
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

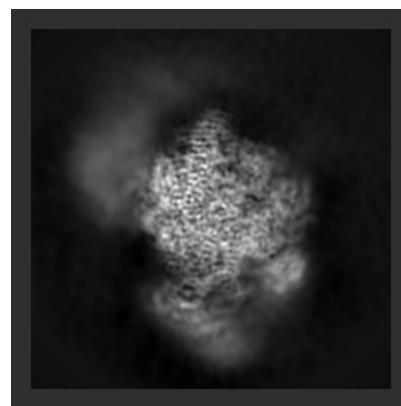
6.1.1 Primary map



X

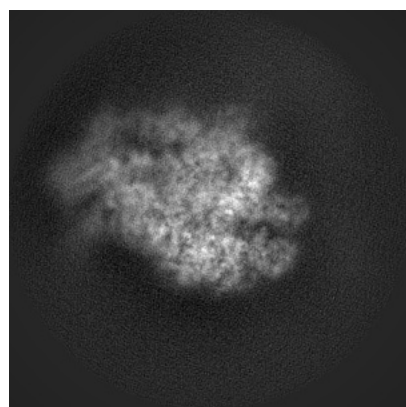


Y

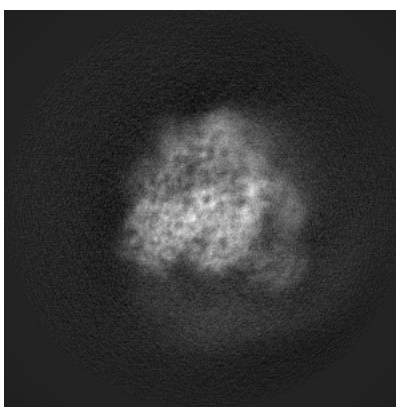


Z

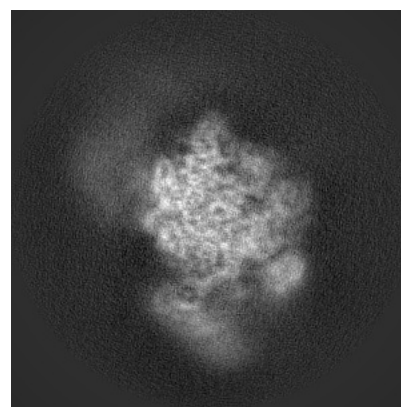
6.1.2 Raw map



X



Y

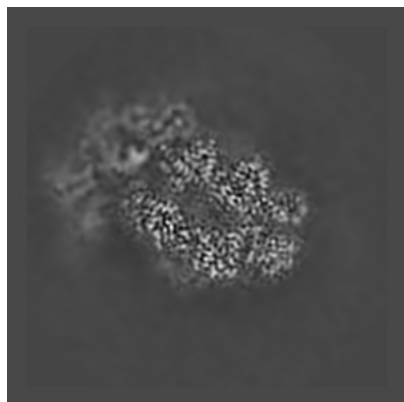


Z

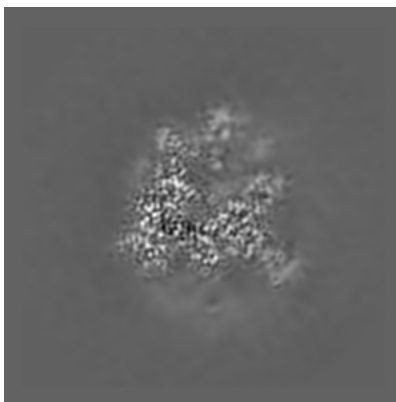
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

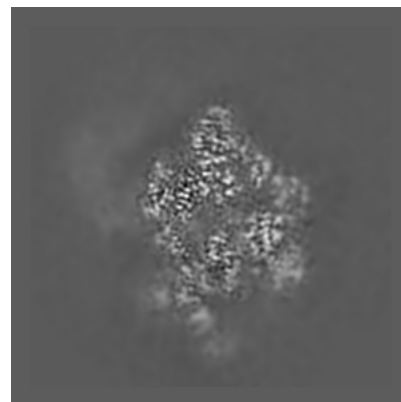
6.2.1 Primary map



X Index: 150

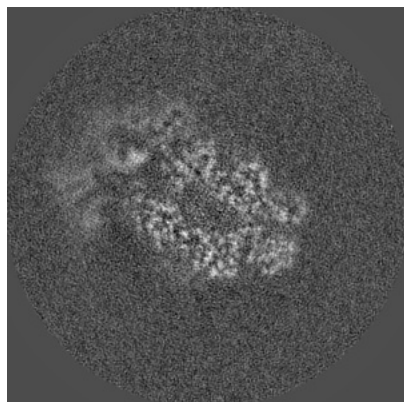


Y Index: 150

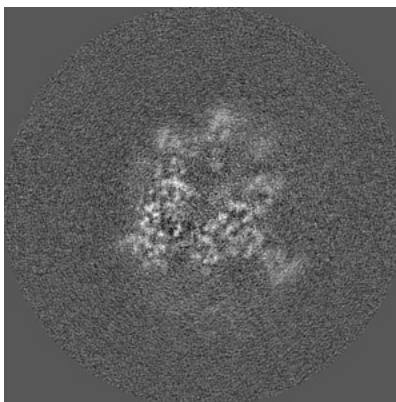


Z Index: 150

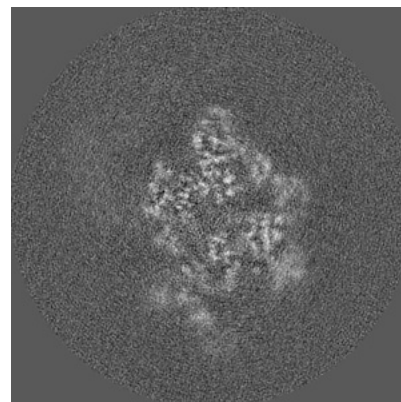
6.2.2 Raw map



X Index: 150



Y Index: 150

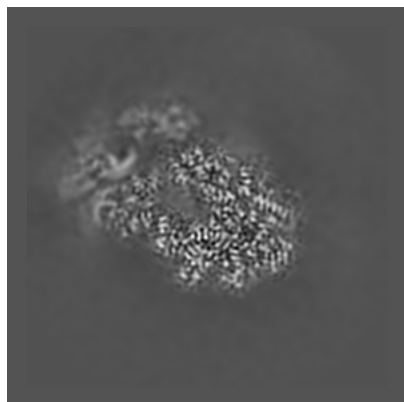


Z Index: 150

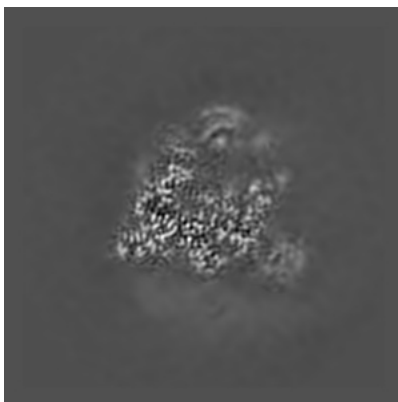
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

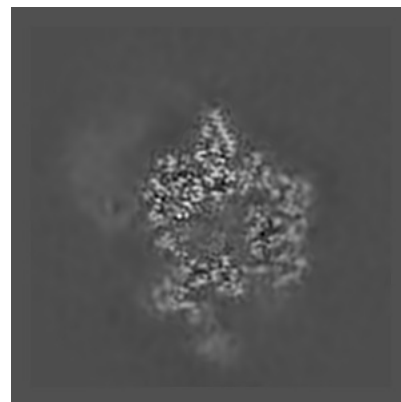
6.3.1 Primary map



X Index: 140

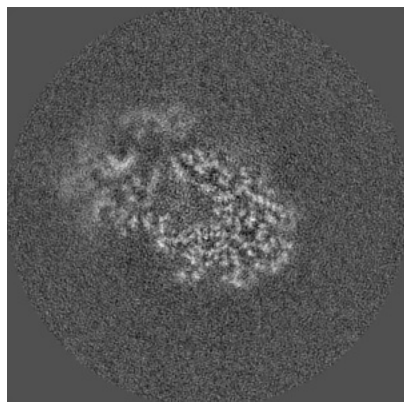


Y Index: 156

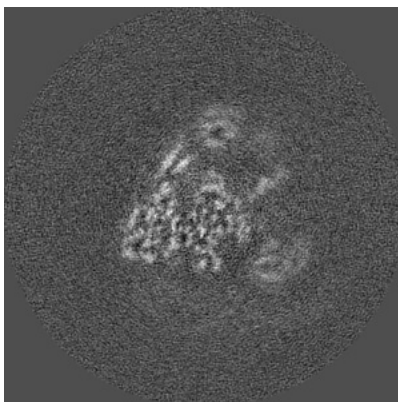


Z Index: 156

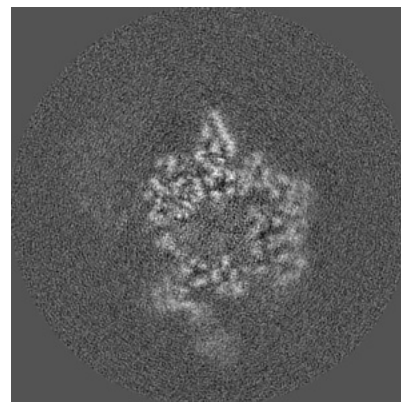
6.3.2 Raw map



X Index: 141



Y Index: 162

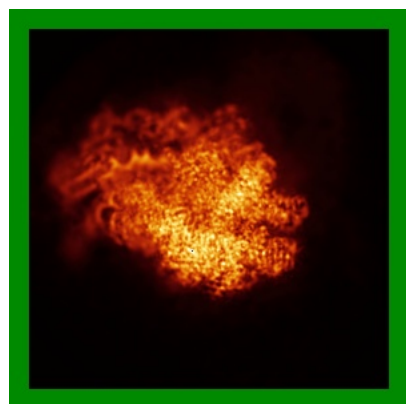


Z Index: 156

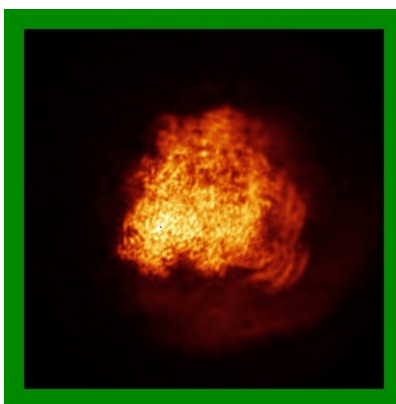
The images above show the largest variance slices of the map in three orthogonal directions.

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

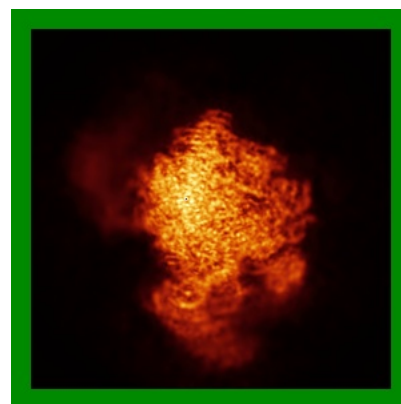
6.4.1 Primary map



X

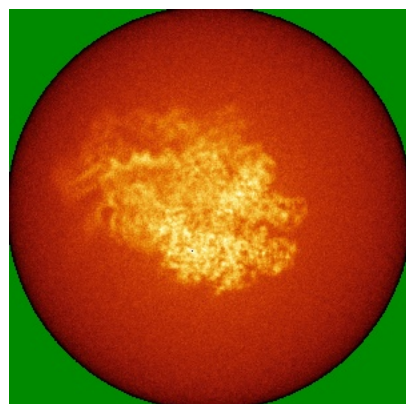


Y

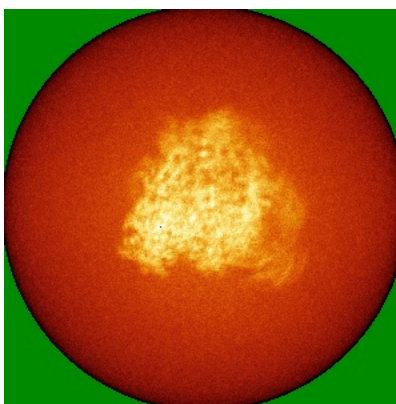


Z

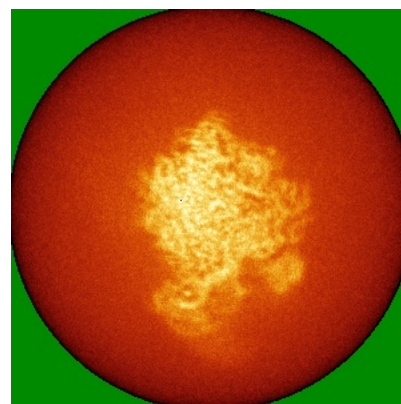
6.4.2 Raw map



X



Y

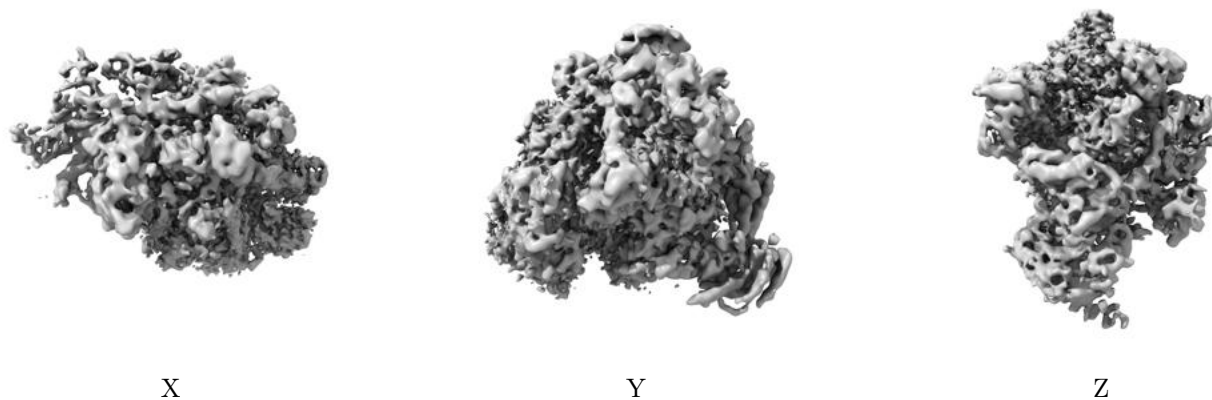


Z

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.

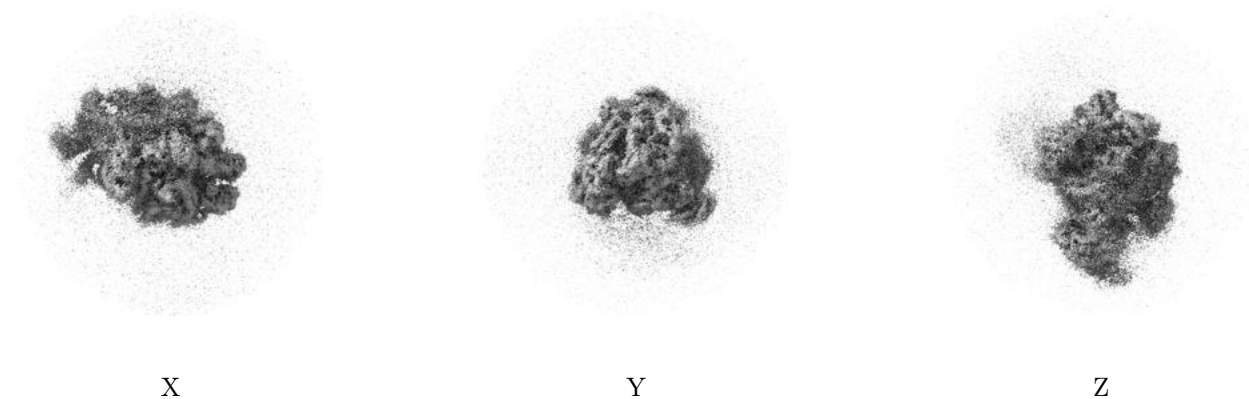
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0028. 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.

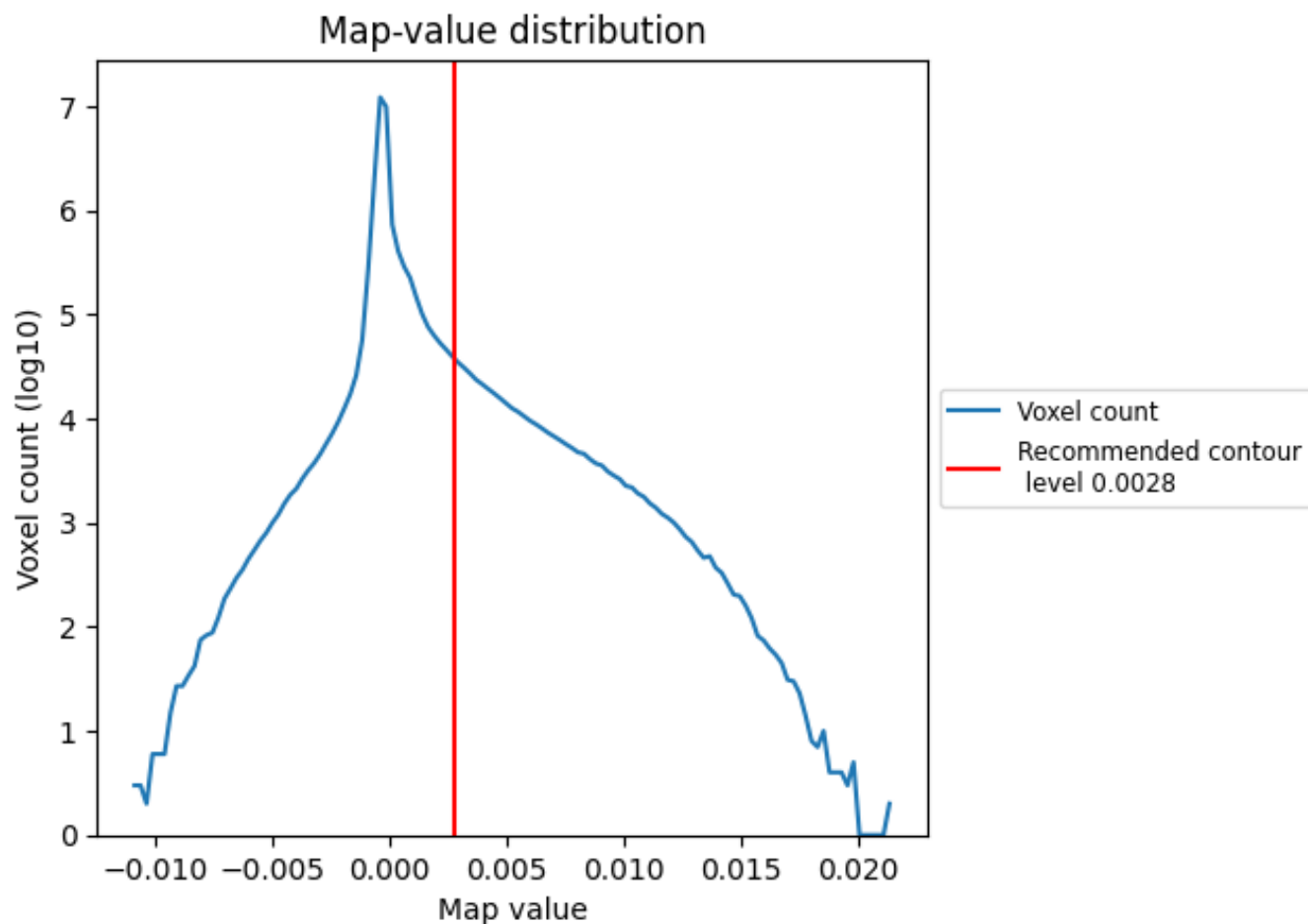
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

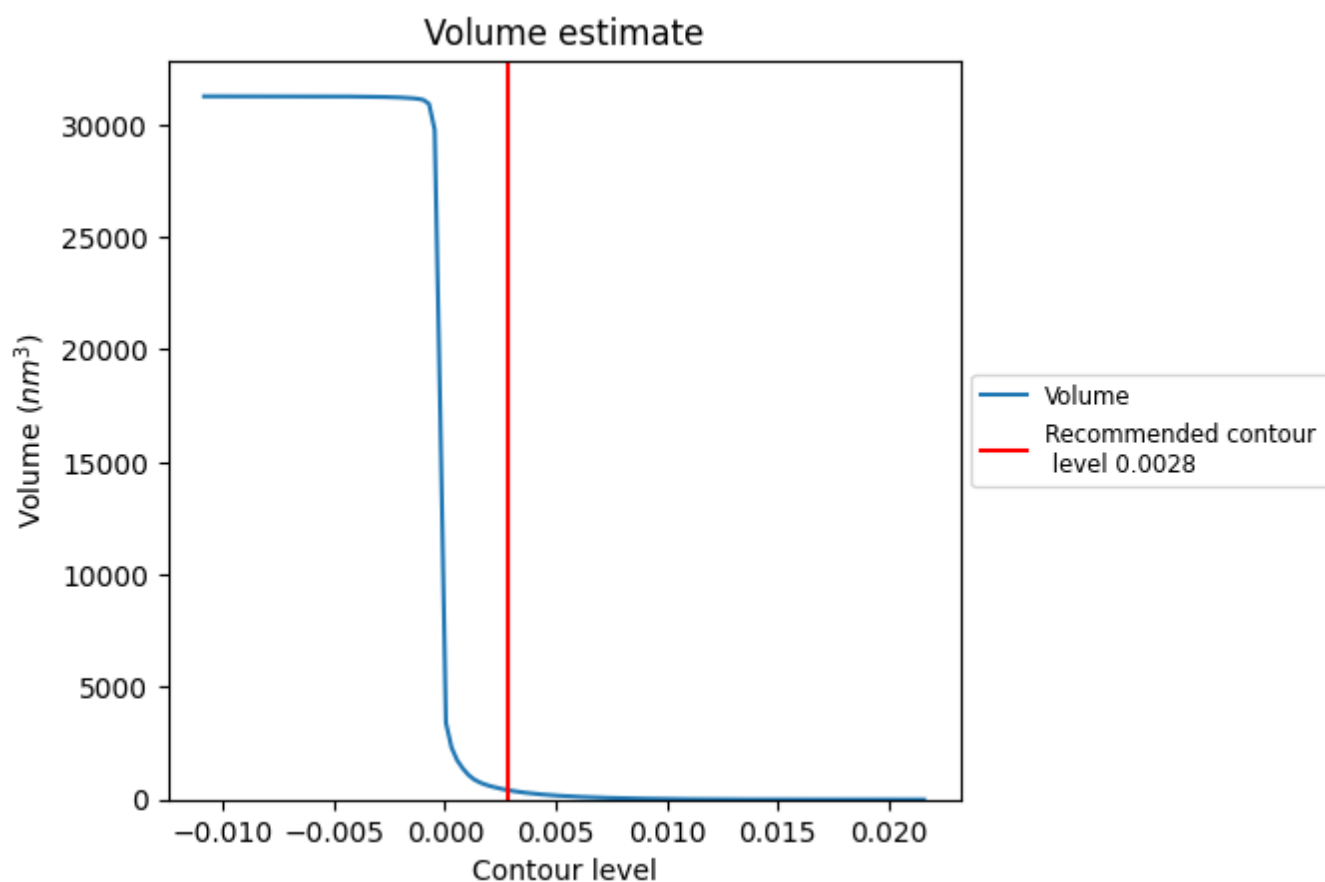
This section contains the results of statistical analysis of the map.

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.

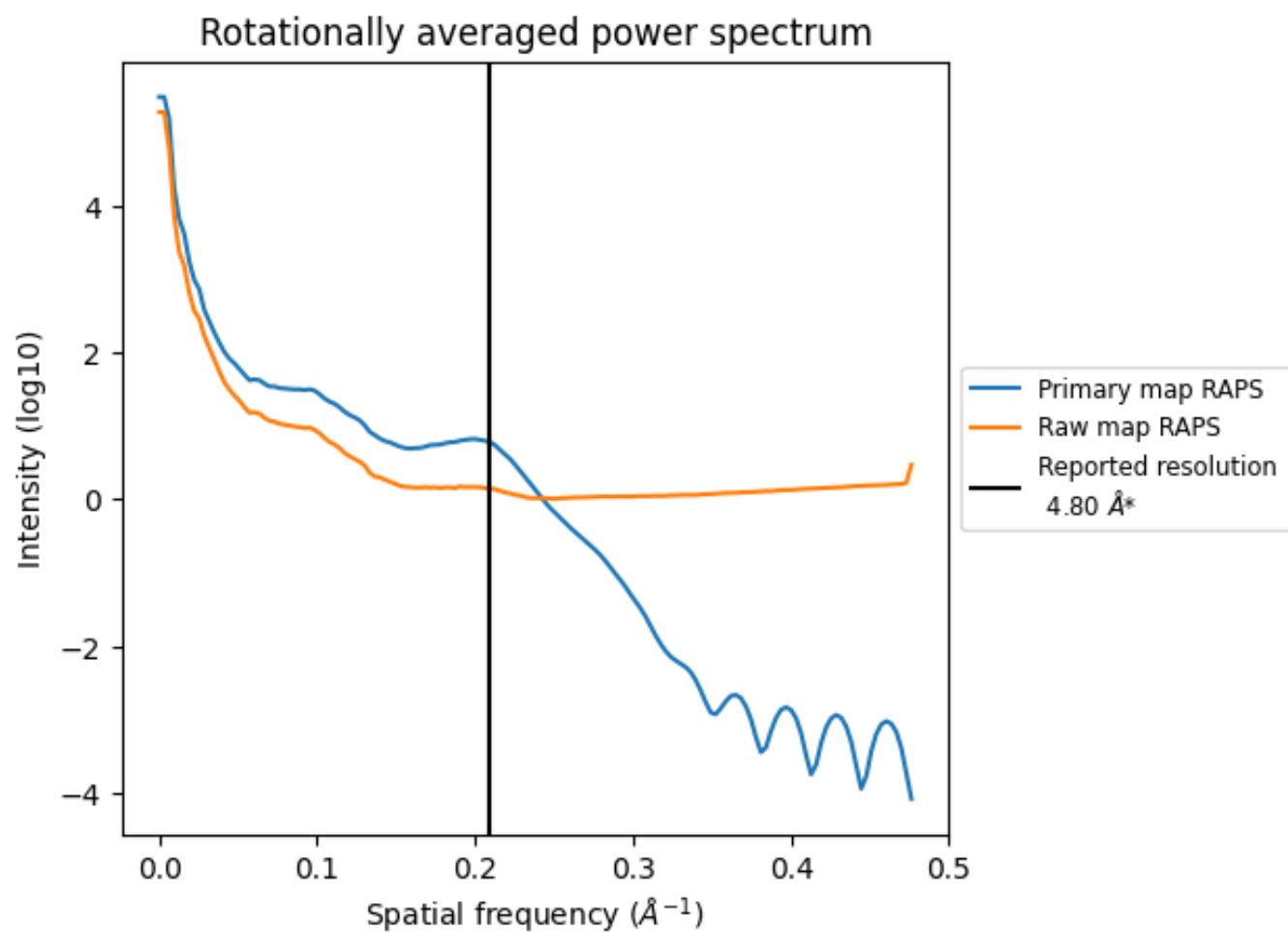
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 426 nm³; this corresponds to an approximate mass of 385 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 ⓘ

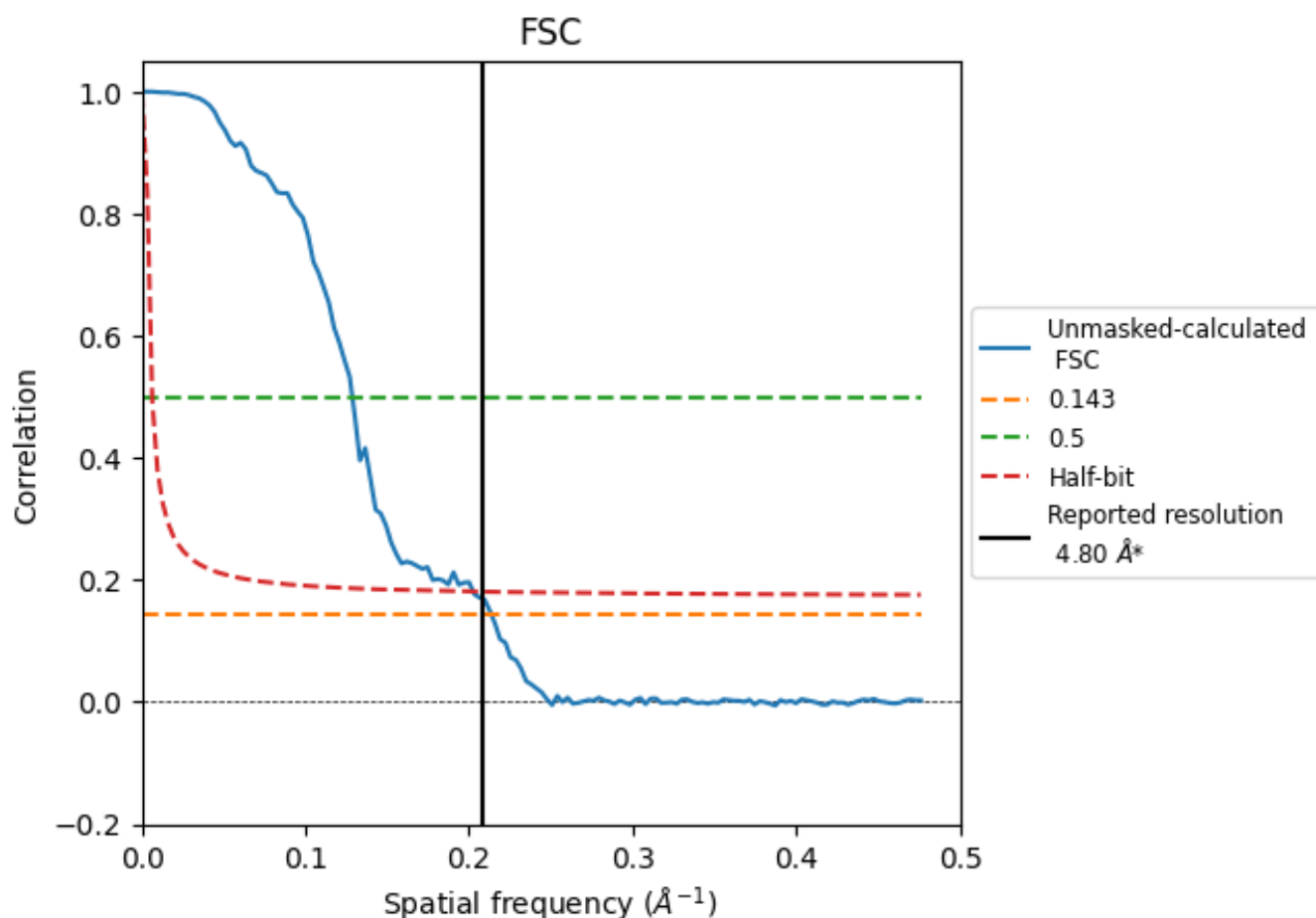


*Reported resolution corresponds to spatial frequency of 0.208 $\text{\AA}^{-1}$

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 0.208 Å⁻¹

8.2 Resolution estimates [i](#)

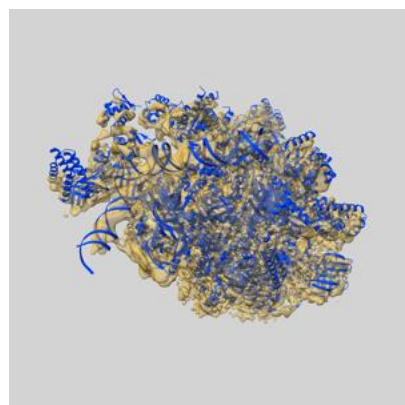
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.68	7.78	4.94

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

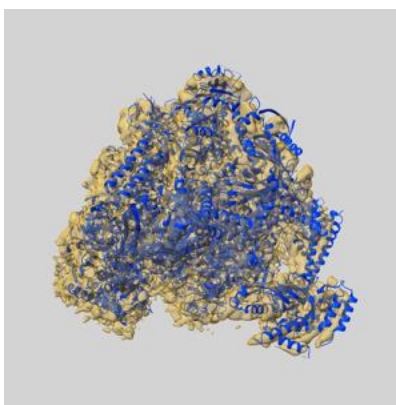
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0091 and PDB model 6GYL. Per-residue inclusion information can be found in section [3](#) on page [9](#).

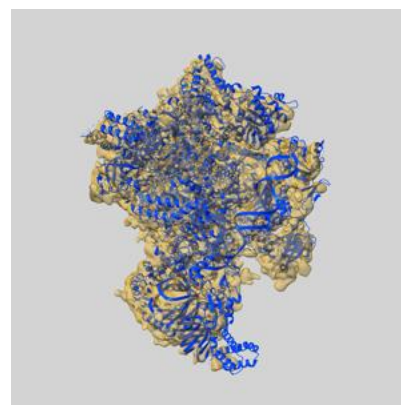
9.1 Map-model overlay [i](#)



X



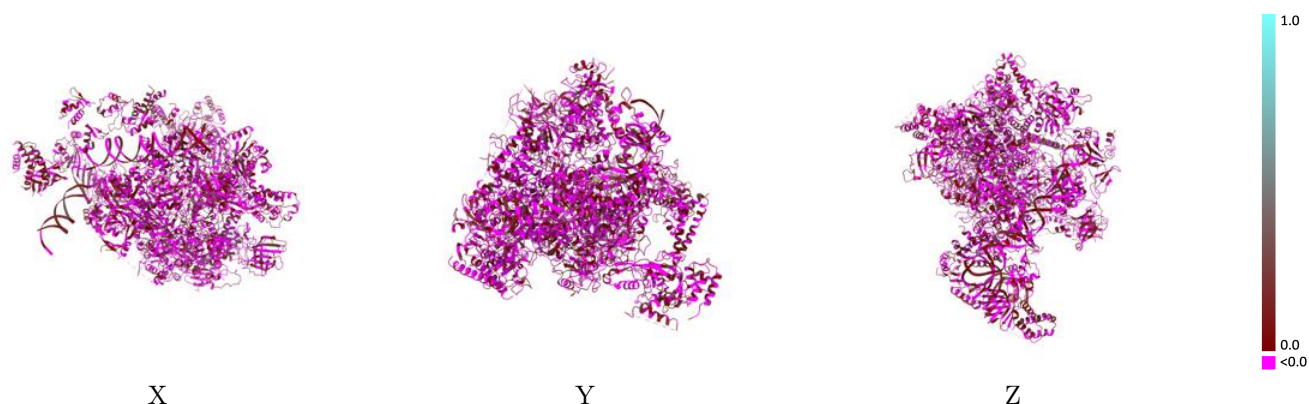
Y



Z

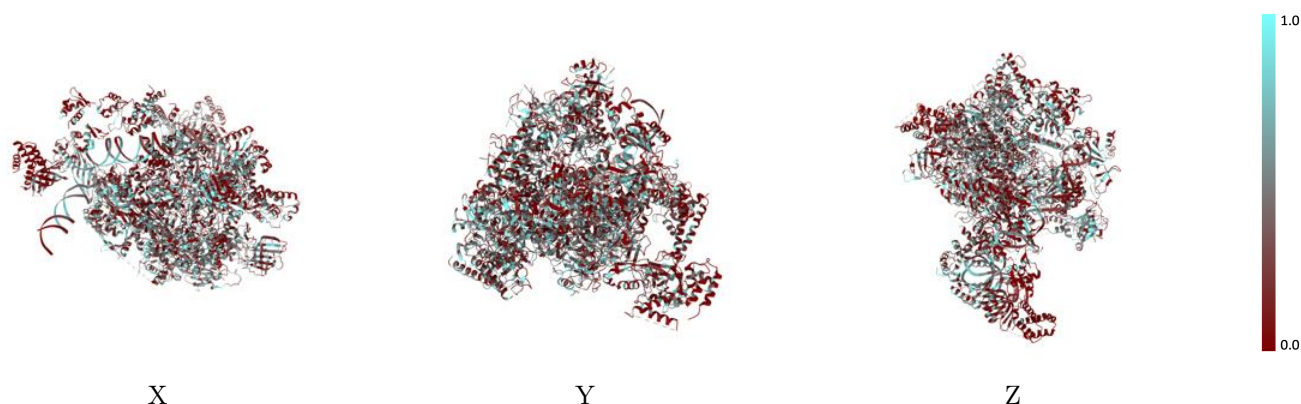
The images above show the 3D surface view of the map at the recommended contour level 0.0028 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



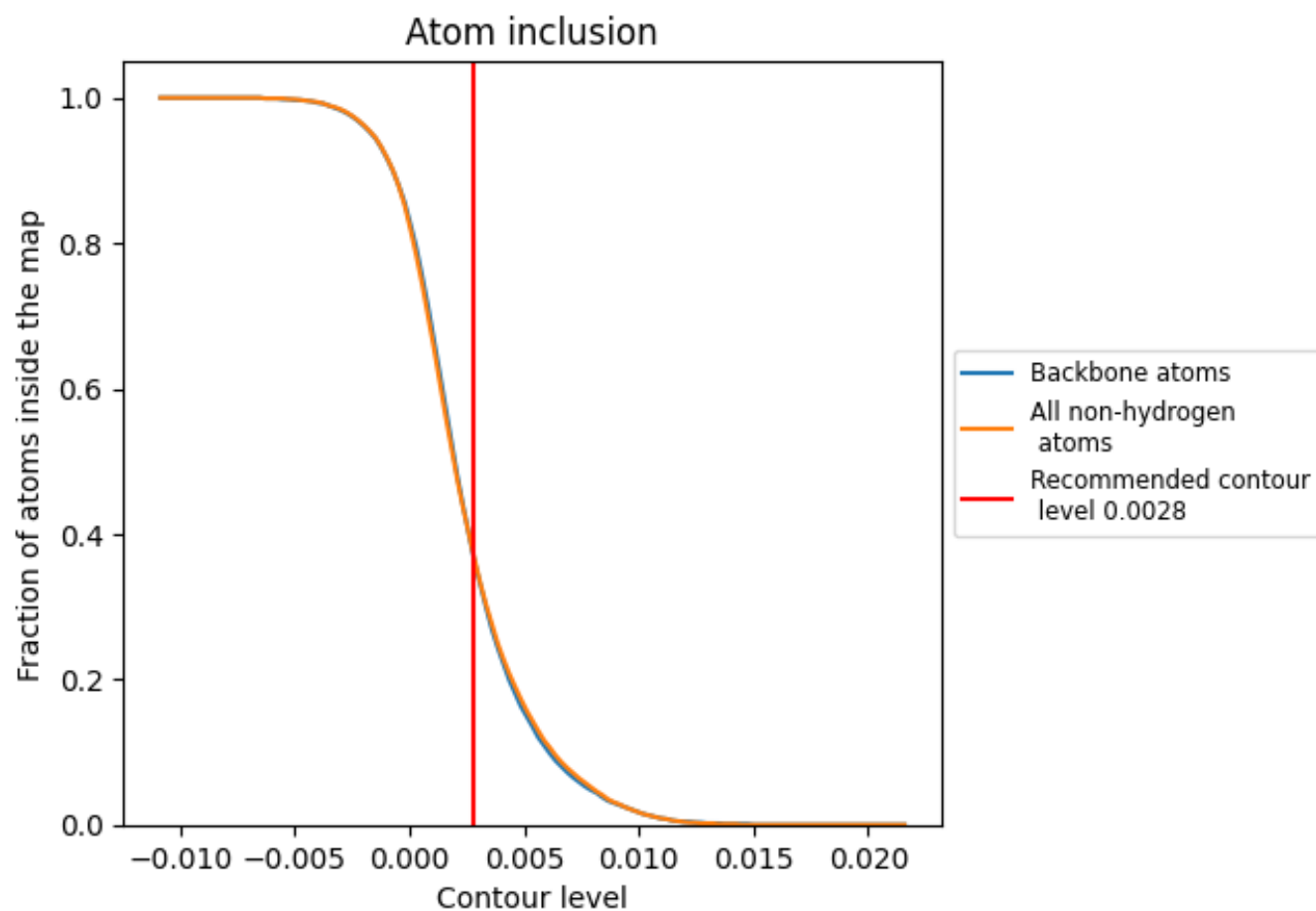
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0028).

9.4 Atom inclusion [i](#)



At the recommended contour level, 37% of all backbone atoms, 37% 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 (0.0028) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3700	 -0.0040
A	 0.3840	 -0.0110
B	 0.3770	 -0.0240
C	 0.4250	 -0.0310
D	 0.1990	 0.0040
E	 0.3740	 0.0120
F	 0.4200	 0.0230
G	 0.3480	 -0.0030
H	 0.3780	 -0.0040
I	 0.3820	 0.0160
J	 0.4330	 -0.0570
K	 0.3850	 -0.0410
L	 0.3640	 -0.0550
M	 0.3360	 -0.0170
N	 0.4180	 0.0710
O	 0.4780	 0.0280
Q	 0.3800	 0.0050
R	 0.4090	 -0.0100
T	 0.5000	 0.0660
U	 0.1610	 0.0330
V	 0.1630	 0.0540
W	 0.3140	 0.0240
X	 0.2140	 0.0330

