



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 07:13 PM UTC

PDB ID : 6GYK / pdb_00006gyk
EMDB ID : EMD-0090
Title : Structure of a yeast closed complex (core CC1)
Authors : Dienemann, C.; Schwalb, B.; Schilbach, S.; Cramer, P.
Deposited on : 2018-06-30
Resolution : 5.10 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

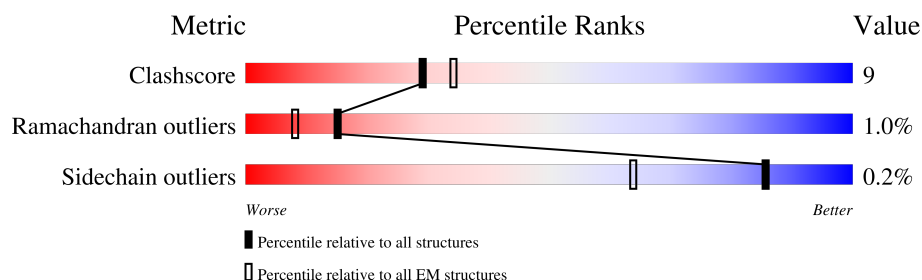
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.10 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	51% 66% 14% 19%
2	B	1224	60% 73% 20% 6%
3	C	318	45% 67% 15% 18%
4	D	220	70% 61% 10% 29%
5	E	215	64% 87% 12% .
6	F	154	31% 44% 10% 46%
7	G	171	92% 68% 32%
8	H	146	52% 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	

2 Entry composition

There are 22 unique types of molecules in this entry. The entry contains 40637 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	56	Total	C	N	O	P	0	0
			1126	541	206	323	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	132	Total	C	N	O	S	0	0
			1015	640	180	188	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
			1142	546	219	321	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 ZINC ION (CCD ID: ZN) (formula: Zn).

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

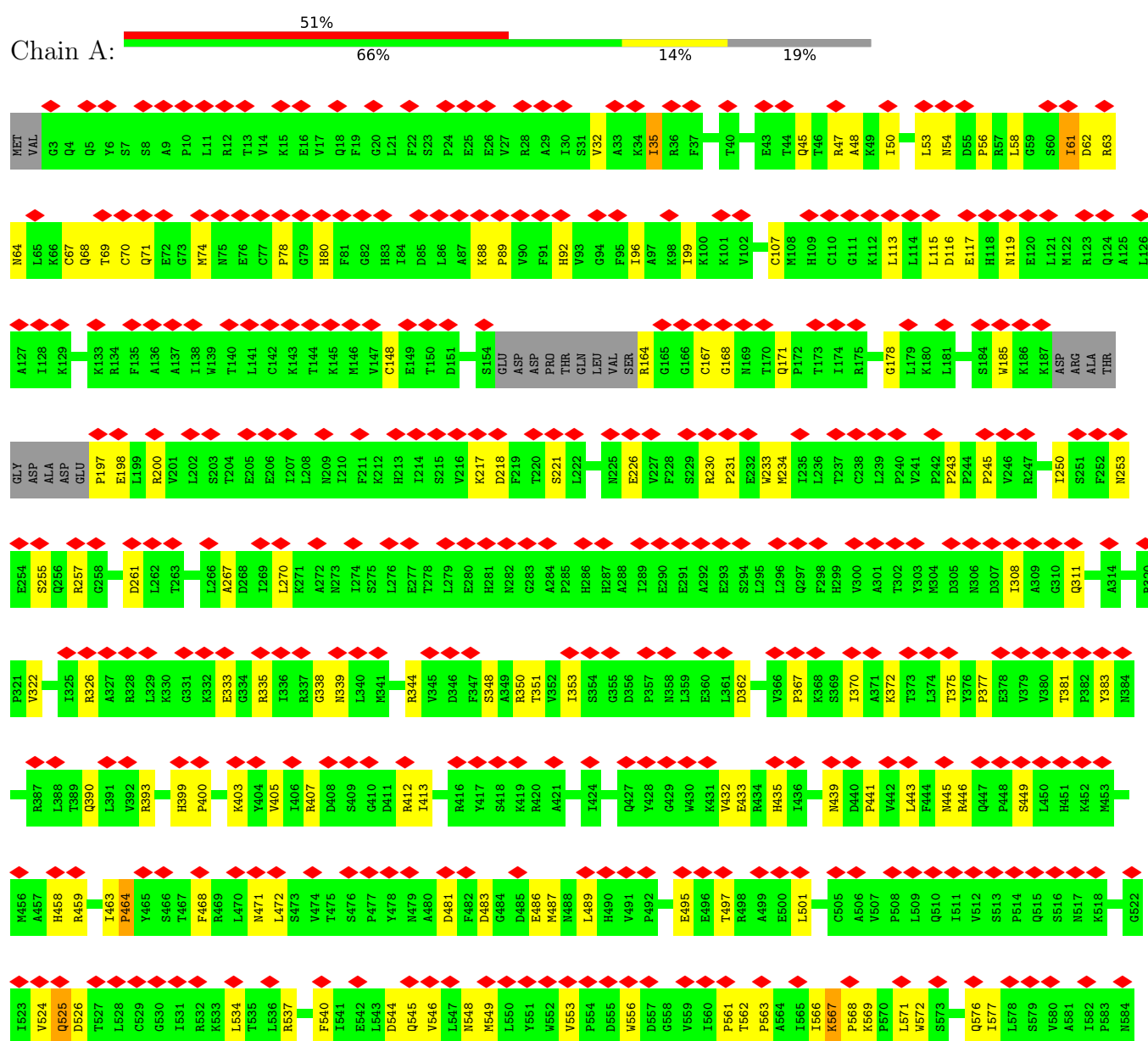
- Molecule 22 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

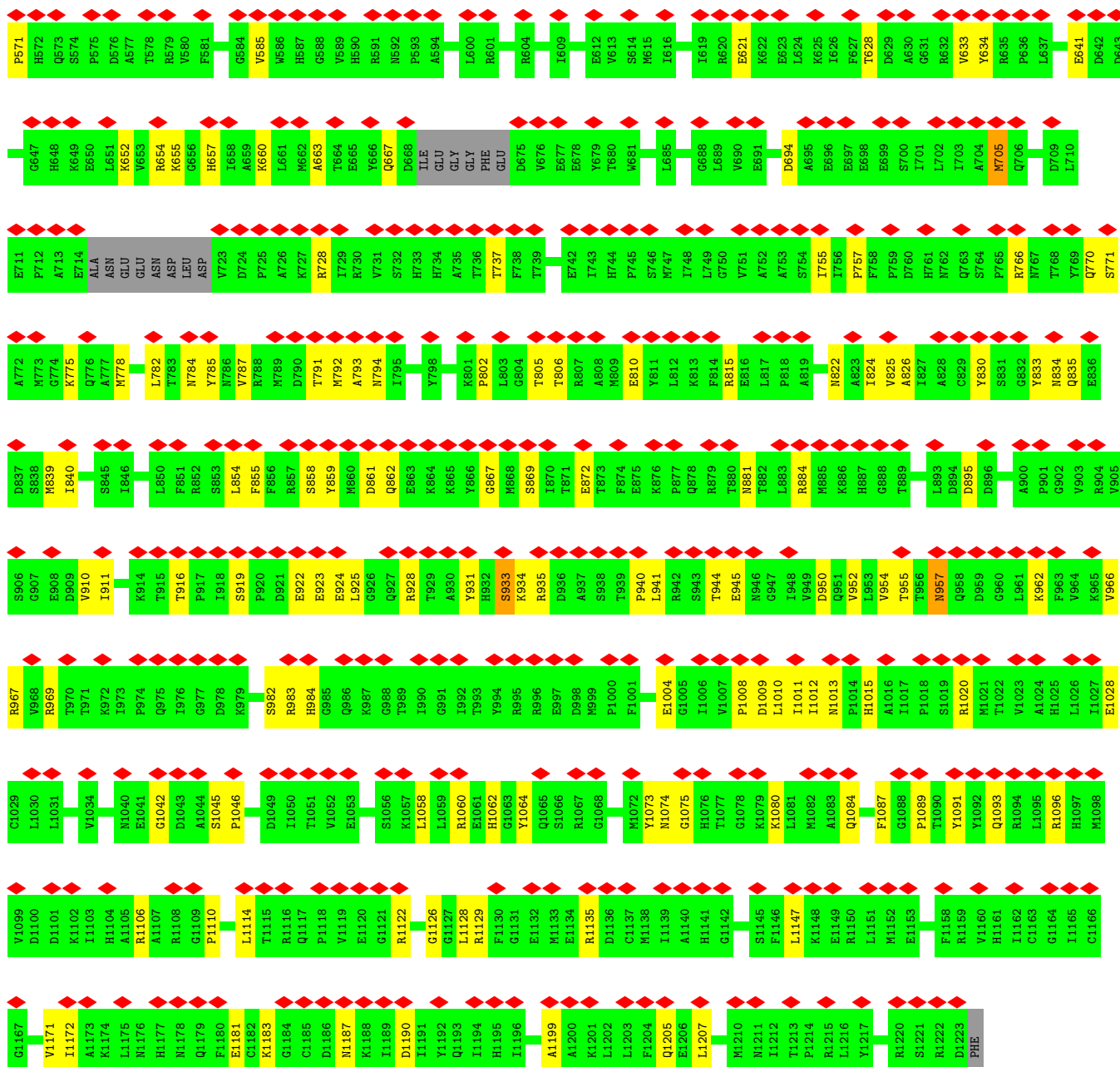
3 Residue-property plots

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.

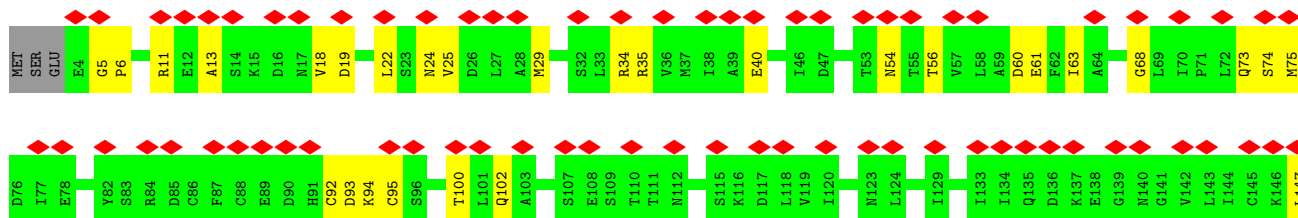
- Molecule 1: DNA-directed RNA polymerase II subunit RPB1

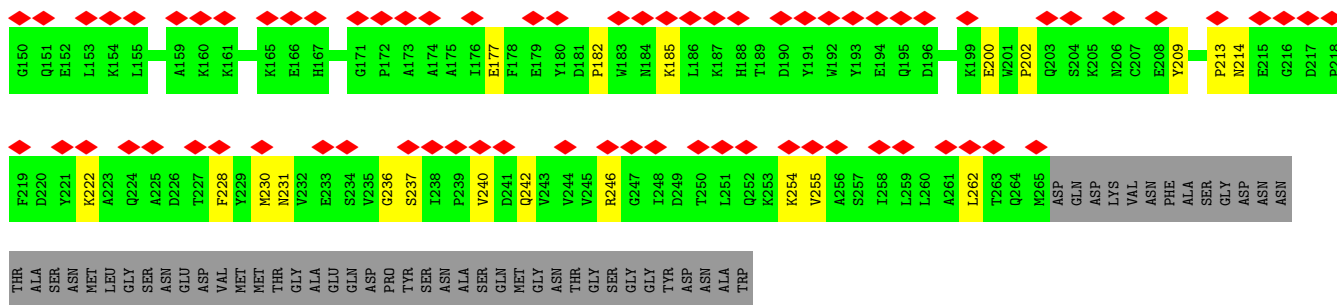


H1387	G1388	F1389	N1390	R1391	S1392	N1393	T1394	G1395	A1396	L1397	M1398	R1399	F1402	E1403	A1404	T1405	V1406	E1407	I1408	L1409	F1410	E1411	A1412	A1413	A1414	S1415	A1416	E1417	L1418	D1419	D1420	C1421	R1422	G1423	V1424	S1425	E1426	N1427	N1428	I1429	L1430	M1431	Q1432	M1433	A1434	P1435	I1436	G1437	T1438	A1439	A1440	F1441	M1444	T1445	D1446	E1447	E1448	
P1320	G1321	I1322	D1323	P1324	T1325	R1326	I1327	Y1328	T1329	N1330	S1331	D1334	I1335	M1336	E1337	V1338	L1339	G1340	I1341	A1342	A1343	A1346	A1347	L1348	Y1349	K1350	E1351	V1352	Y1353	N1354	A1357	S1358	D1359	G1360	S1361	Y1362	V1363	N1364	Y1365	R1366	H1367	M1368	A1369	L1370	L1371	V1372	V1373	T1377	G1380	L1381	T1385	R1386						
ARG	PRO	LYS	SER	LEU	ALA	GLU	THR	GLY	A1254	E1255	D1256	H1258	M1259	L1260	K1261	K1262	I1263	E1264	M1265	T1266	M1267	L1268	E1269	M1270	R1274	G1275	V1276	E1277	V1283	R1289	K1290	V1291	P1292	S1293	P1294	T1295	G1296	V1299	K1300	E1301	L1306	E1307	T1308	V1311	S1314	E1315	V1316	M1317	T1318	V1319								
ALA	GLU	GLN	SER	PHE	ASP	Q1187	Q1188	S1189	P1190	W1191	L1192	I1193	R1194	L1197	D1198	R1199	A1200	A1201	M1202	M1203	D1204	K1205	L1206	L1207	T1208	M1209	G1210	Q1211	V1212	G1213	E1214	R1215	I1216	K1217	Q1218	K1221	M1222	D1223	L1224	F1225	V1226	I1227	W1228	S1229	E1230	D1231	D1233	E1234	K1235	I1238	R1239	C1240	R1241	V1242	V1243			
T1117	V1118	Y1119	L1120	E1121	P1122	G1123	H1124	A1125	D1127	Q1128	E1129	Q1130	A1131	K1132	L1133	I1134	R1135	S1136	A1137	I1138	E1139	H1140	T1141	L1142	L1143	K1144	S1145	V1146	T1147	Y1153	Y1154	D1155	P1156	D1157	P1158	R1159	S1160	T1161	V1162	I1163	P1164	E1165	D1166	E1167	E1168	I1169	I1170	Q1171	L1172	H1173	F1174	S1175	LEU	ASP	GLU	GLU		
I1049	E1050	A1051	Q1052	F1053	L1054	R1055	V1058	H1059	M1063	V1064	G1065	V1066	L1067	A1068	A1069	I1072	P1075	A1076	T1077	Q1078	M1079	THR	LEU	ASN	THR	PHE	HIS	PHE	ALA	GLY	VAL	ALA	SER	LYS	K1093	V1094	T1095	S1096	G1097	V1098	P1099	R1100	L1101	K1102	E1103	T1104	L1105	M1106	V1107	A1108	K1109	M1110	M1111	L1116				
V987	L988	G989	V990	K991	D992	L993	Q994	E995	N996	L997	L998	R1001	G1002	K1003	N1004	E1005	I1006	I1007	Q1008	N1009	A1010	Q1011	R1012	D1013	A1014	V1015	T1016	L1017	F1018	C1019	C1020	L1021	L1022	N959	R1023	R961	D900	L901	L902	N903	T904	D905	G835	Y836	T907	L908	D909	P910	S911	L912	L913	S917	E918	I919	L920	G921	D922	L923
K924	L925	Q926	V927	L928	L929	D930	E931	E932	Y933	K934	Q935	L936	V937	K938	D939	R940	K941	F942	L943	R944	E945	V946	F947	V948	D949	A952	N953	W954	P955	L956	P957	V958	N959	I960	R961	R962	L963	I964	Q965	N966	A967	Q968	Q969	T970	F971	H972	I973	D974	H975	T976	D980	L981	I982	Y983	K984	D985	L986	
T855	T856	R857	L860	V863	I864	Q865	F866	I867	Y868	G869	E870	D871	G872	M873	D874	A875	E876	E879	S882	L883	D884	T885	S889	D890	A891	A892	F893	E894	K895	R898	V899	D900	L901	L902	N903	T904	D905	G835	Y836	T907	L908	D909	P910	S911	L912	L913	S917	E918	I919	L920	G921	D922	L923					
D790	D791	Y792	S793	F794	K797	G798	F799	V800	E801	N802	S803	Y804	R805	G807	L808	T809	P810	Q811	F814	F815	H816	A817	M818	G819	G820	R821	E822	G823	L824	I825	D826	T827	A828	V829	K830	T831	E832	E833	T834	G835	Y836	I837	Q838	R839	R840	L841	A844	L845	E846	M849	Y852	D853	N854					
L722	N723	E724	A725	R726	D727	K728	R731	L732	A733	E734	V735	N736	L737	K738	D739	L740	N741	N742	V743	K744	V747	M748	A749	G750	S751	K752	G753	S754	F755	I756	N757	I758	A759	S762	A763	G766	Q767	Q768	S769	V770	E771	G772	K773	I774	I775	A776	G777	F779	V780	D781	F787	S788	K789					
N654	F655	W656	L657	G661	F662	S663	T664	G665	I666	G667	D668	T669	I670	A671	P674	T675	M676	R677	E678	I679	T680	E681	T682	E685	A686	K687	K688	K689	D692	V693	S694	K695	E696	N700	L701	L702	T703	A704	K705	H706	G707	M708	T709	L710	R711	E712	S713	F714	E715	D716	N717	R720	F721					
G585	I586	H587	L588	Q589	R590	F591	D592	E593	G594	T595	T596	L597	S598	S599	P600	K601	D602	L606	I607	I608	I613	F614	V617	E618	K619	K620	T621	V622	G623	S624	S625	M626	G627	G628	L629	V632	V633	T634	R635	E636	K637	G638	P639	A643	K644	L645	F646	G647	I649	Q650	K651	V652	V653					

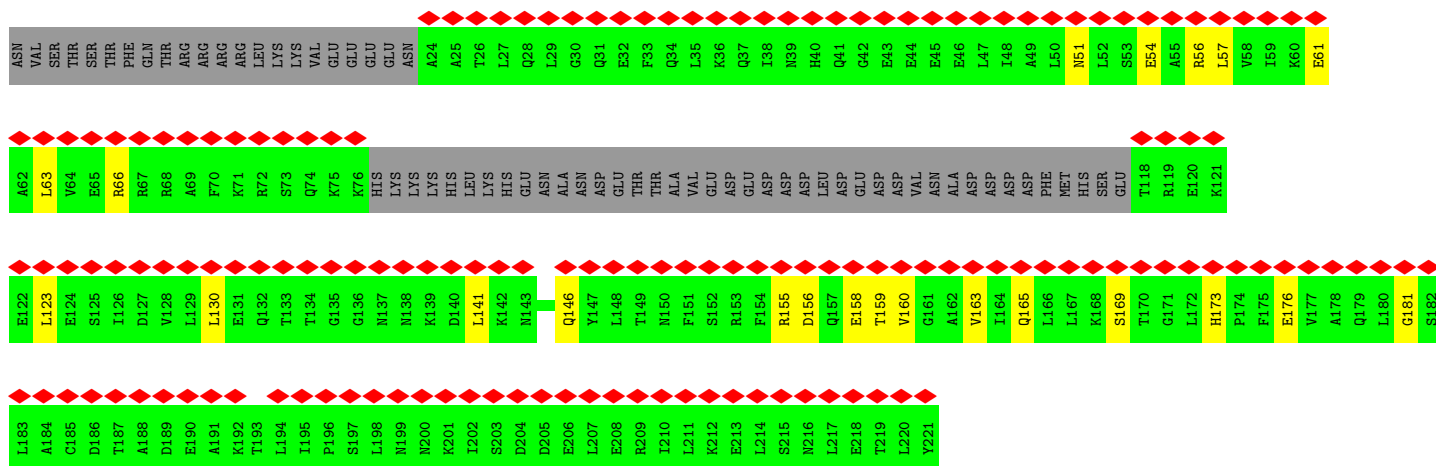


● Molecule 3: DNA-directed RNA polymerase II subunit RPB3

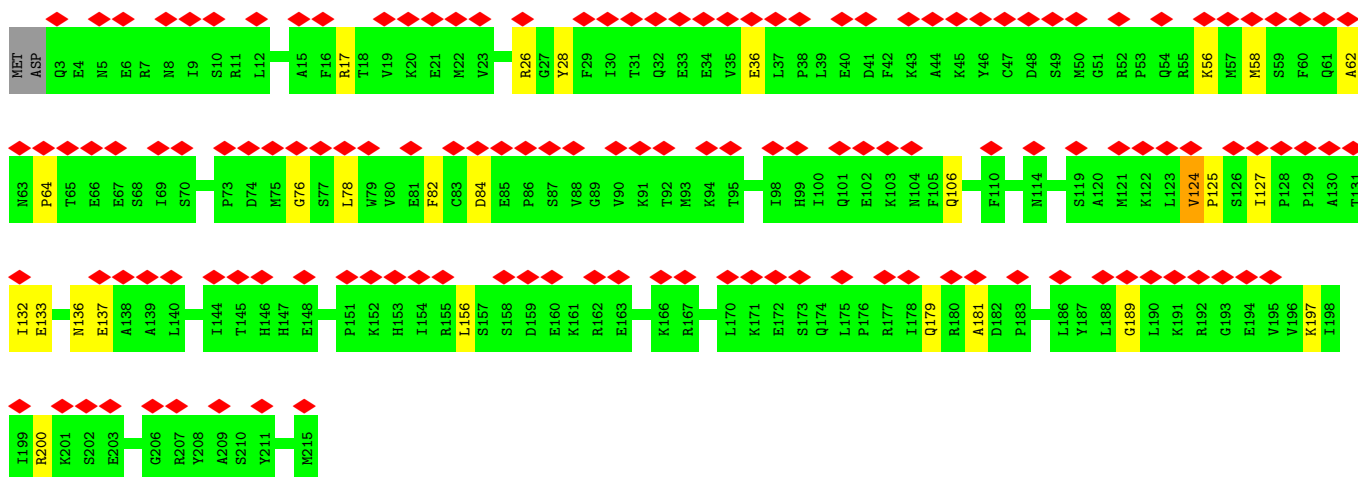
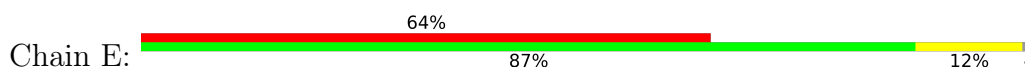




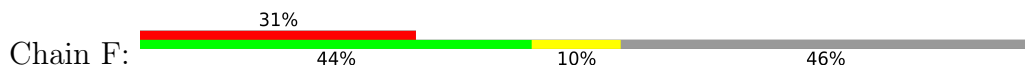
- Molecule 4: DNA-directed RNA polymerase II subunit RPB4

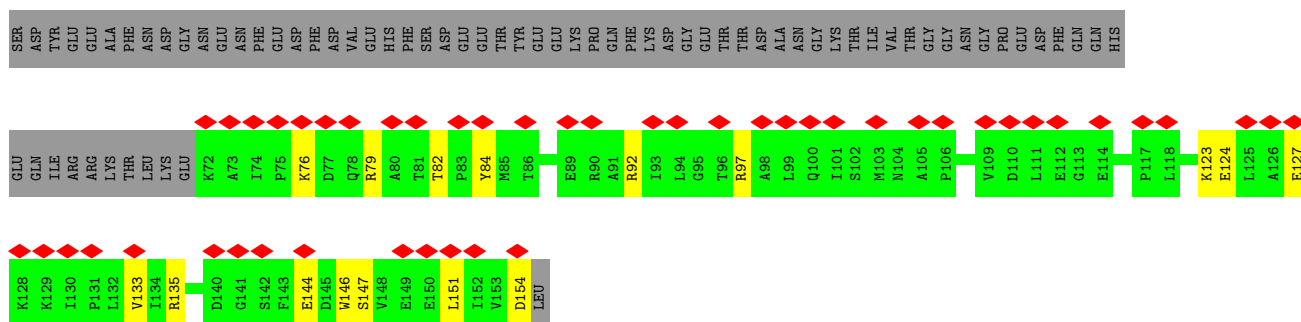


- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1

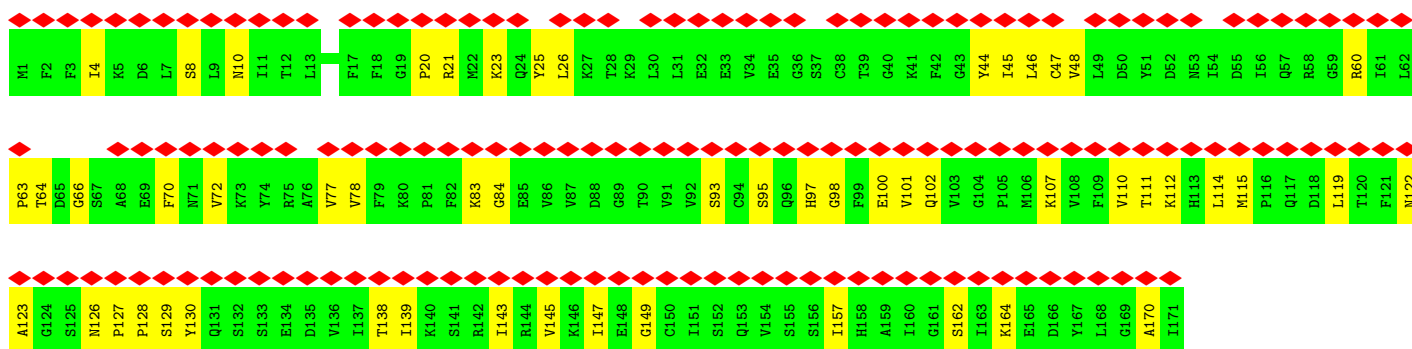


- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2

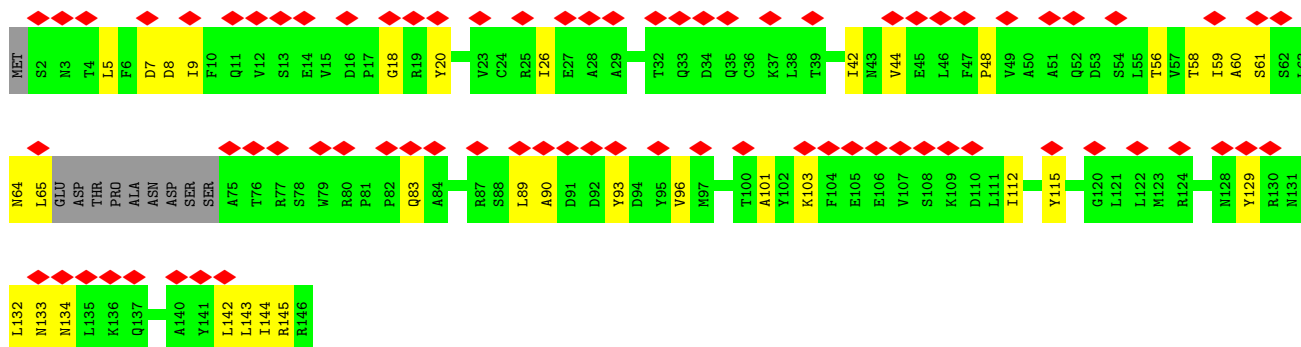




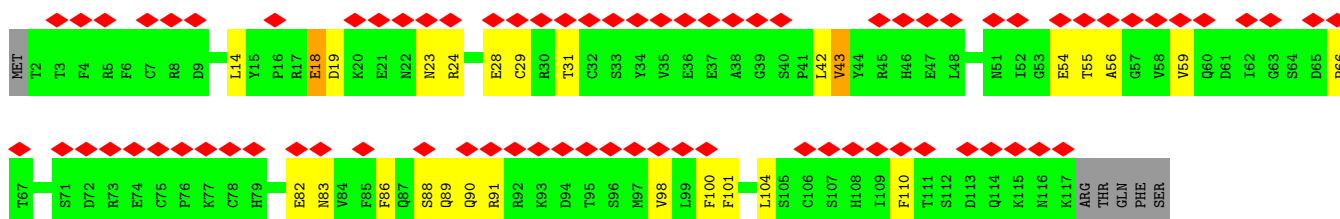
• Molecule 7: DNA-directed RNA polymerase II subunit RPB7



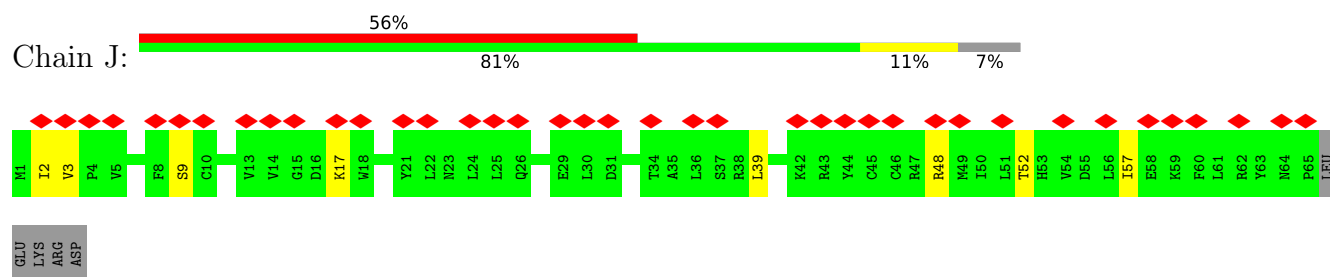
• Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3



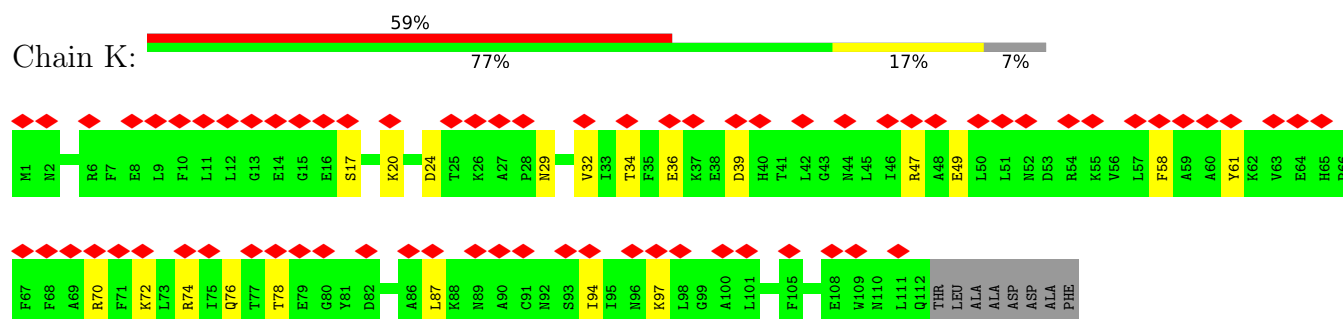
• Molecule 9: DNA-directed RNA polymerase II subunit RPB9



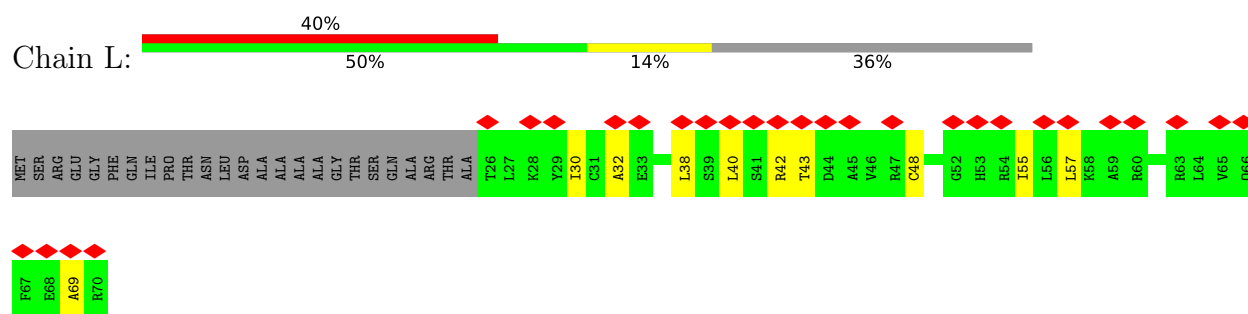
- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5



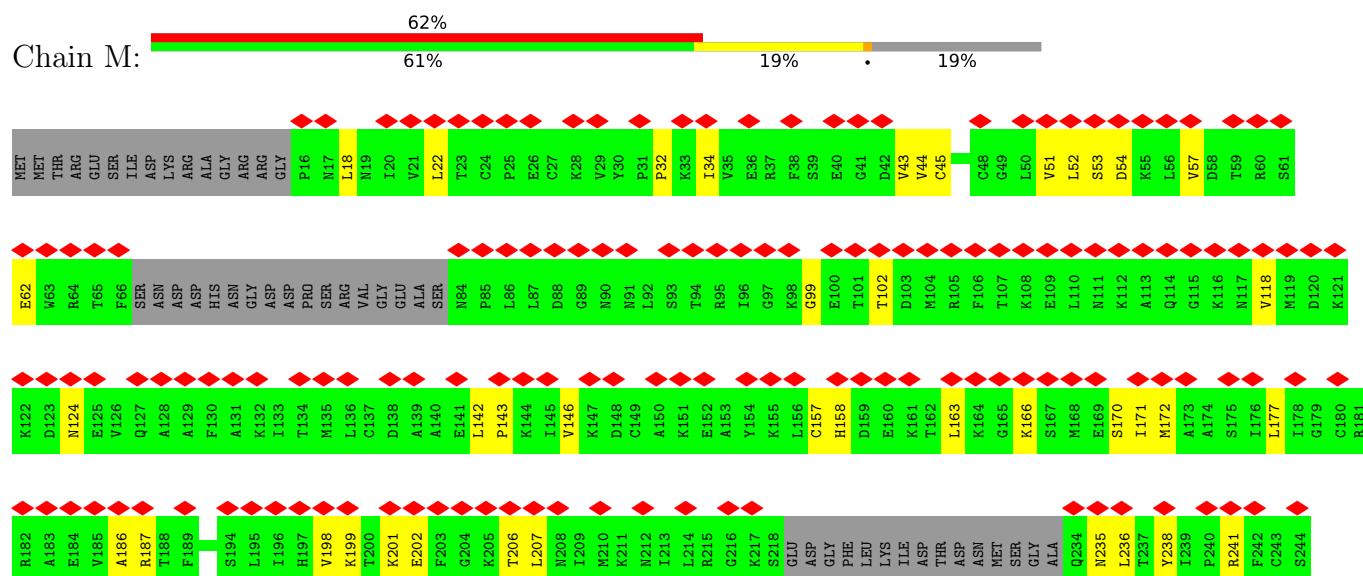
- Molecule 11: DNA-directed RNA polymerase II subunit RPB11

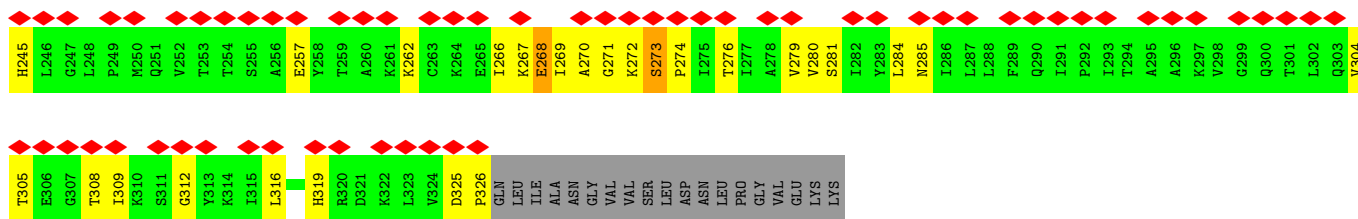


- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4



- Molecule 13: Transcription initiation factor IIB

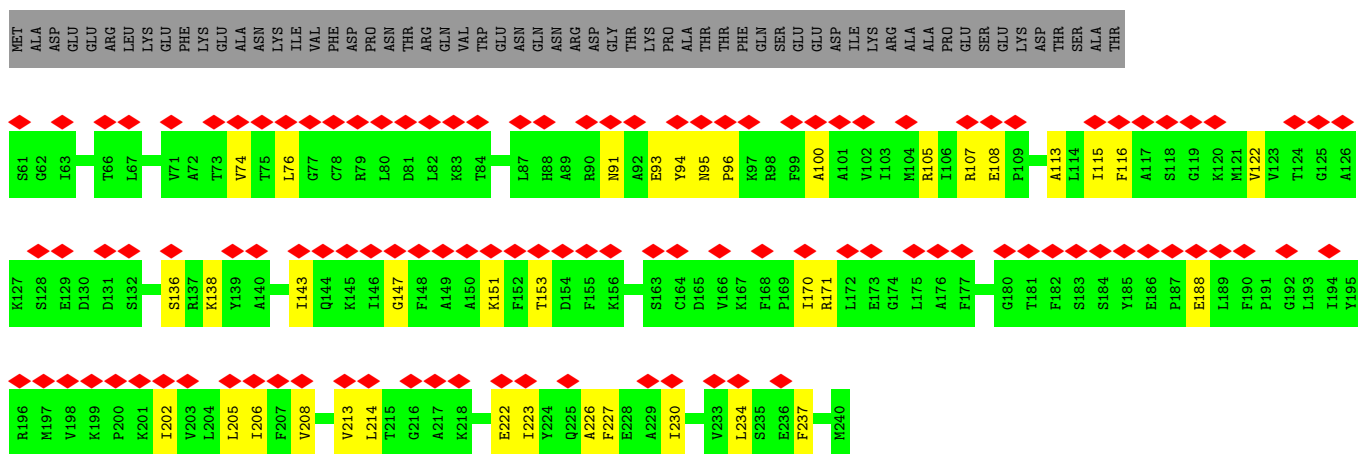




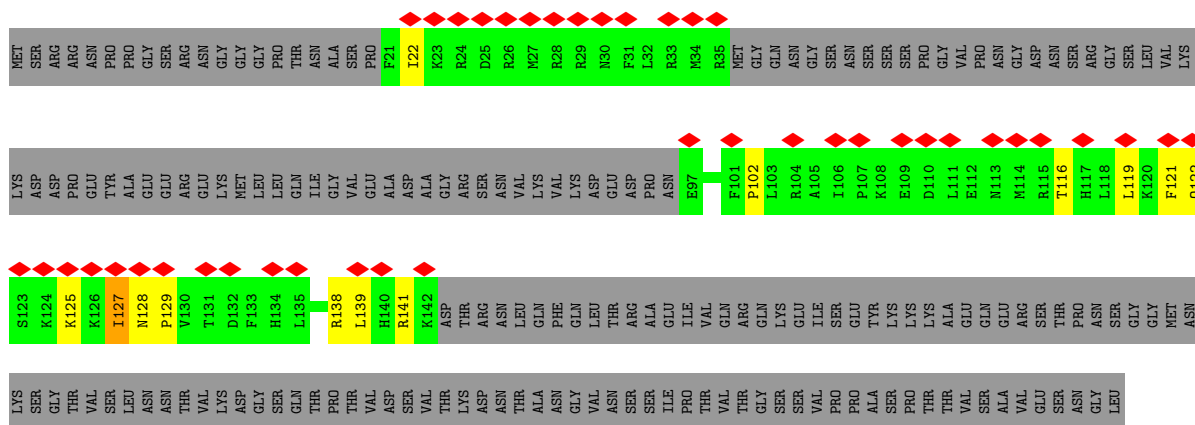
• Molecule 14: GAT1 Promoter



• Molecule 15: TATA-box-binding protein



• Molecule 16: Transcription initiation factor IIF subunit alpha



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	39000	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	0.017	Depositor
Minimum map value	-0.009	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.003	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	0.10	0/2099	0.24	0/2845
4	D	0.09	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	0.11	0/1368	0.25	0/1844
8	H	0.11	0/1107	0.28	0/1499
9	I	0.12	0/962	0.32	0/1295
10	J	0.15	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	0.27	0/1262	0.64	0/1923
15	O	0.13	0/1443	0.28	0/1942
16	Q	0.22	0/1168	0.43	0/1579
17	R	0.14	0/1025	0.35	0/1378
18	T	0.29	0/1284	0.63	0/1961
19	U	0.10	0/766	0.25	0/1032
20	V	0.08	0/789	0.22	0/1066
All	All	0.14	0/41573	0.32	4/56532 (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	6.51	124.35	119.66
5	E	127	ILE	C-N-CA	6.51	124.35	119.66
1	A	1146	VAL	CA-C-N	-6.36	114.31	122.77
1	A	1146	VAL	C-N-CA	-6.36	114.31	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	176	0
2	B	9178	0	9195	165	0
3	C	2061	0	2029	32	0
4	D	1253	0	1275	13	0
5	E	1744	0	1772	15	0
6	F	670	0	690	11	0
7	G	1340	0	1357	33	0
8	H	1089	0	1062	21	0
9	I	944	0	899	28	0
10	J	532	0	542	5	0
11	K	904	0	911	14	0
12	L	358	0	381	7	0
13	M	2175	0	2283	77	0
14	N	1126	0	629	49	0
15	O	1416	0	1492	88	0
16	Q	1144	0	1034	30	0
17	R	1015	0	987	32	0
18	T	1142	0	628	48	0
19	U	757	0	747	46	0
20	V	782	0	790	14	0
21	A	2	0	0	0	0
21	B	1	0	0	0	0
21	C	1	0	0	0	0
21	I	2	0	0	0	0
21	J	1	0	0	0	0
21	L	1	0	0	0	0
21	M	1	0	0	0	0
22	A	1	0	0	0	0
All	All	40637	0	39784	745	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 745 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)
13:M:267:LYS:CE	15:O:208:VAL:CG1	1.81	1.58
13:M:267:LYS:HE2	15:O:208:VAL:CG1	1.34	1.50
15:O:105:ARG:NE	19:U:253:ARG:NH2	1.74	1.30
15:O:105:ARG:NH2	19:U:253:ARG:CZ	1.96	1.28
15:O:105:ARG:CZ	19:U:253:ARG:CZ	2.15	1.25

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%)	1297 (94%)	78 (6%)	11 (1%)	16	53
2	B	1136/1224 (93%)	1064 (94%)	62 (6%)	10 (1%)	14	50
3	C	260/318 (82%)	236 (91%)	20 (8%)	4 (2%)	8	38
4	D	153/220 (70%)	145 (95%)	7 (5%)	1 (1%)	18	55
5	E	211/215 (98%)	202 (96%)	8 (4%)	1 (0%)	24	63
6	F	81/154 (53%)	79 (98%)	2 (2%)	0	100	100
7	G	169/171 (99%)	155 (92%)	13 (8%)	1 (1%)	21	58
8	H	132/146 (90%)	117 (89%)	12 (9%)	3 (2%)	5	27
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	32
15	O	178/240 (74%)	164 (92%)	13 (7%)	1 (1%)	21	58

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	Q	140/735 (19%)	119 (85%)	16 (11%)	5 (4%)	2	19
17	R	120/400 (30%)	107 (89%)	12 (10%)	1 (1%)	16	53
19	U	88/171 (52%)	82 (93%)	4 (4%)	2 (2%)	5	27
20	V	96/129 (74%)	92 (96%)	3 (3%)	1 (1%)	12	47
All	All	4753/6583 (72%)	4414 (93%)	291 (6%)	48 (1%)	15	47

5 of 48 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	Q	127	ILE
2	B	830	TYR
2	B	933	SER
7	G	63	PRO
13	M	269	ILE

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
3	C	230/274 (84%)	229 (100%)	1 (0%)	84	83
4	D	139/199 (70%)	139 (100%)	0	100	100
5	E	195/197 (99%)	195 (100%)	0	100	100
6	F	73/136 (54%)	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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
All	All	4223/5784 (73%)	4216 (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 82 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	264	GLN
13	M	90	ASN
4	D	179	GLN
8	H	83	GLN
15	O	158	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 10 ligands modelled in this entry, 10 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

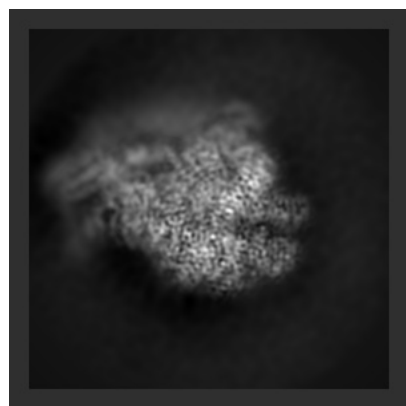
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0090. These allow visual inspection of the internal detail of the map and identification of artifacts.

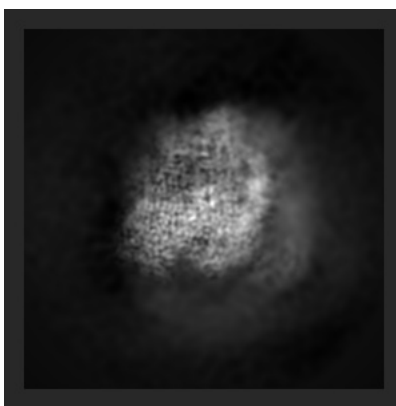
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

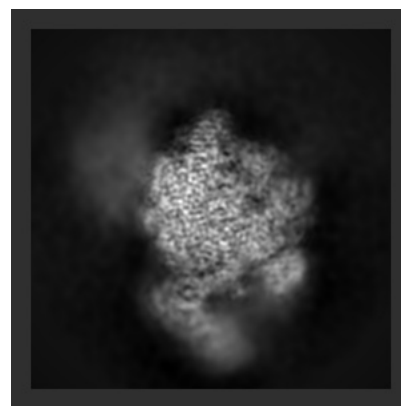
6.1.1 Primary map



X

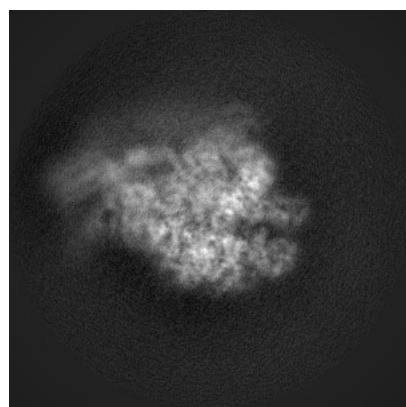


Y

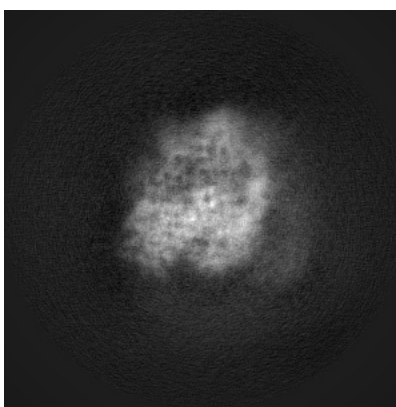


Z

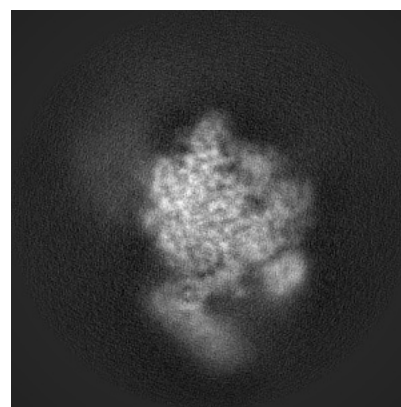
6.1.2 Raw map



X



Y

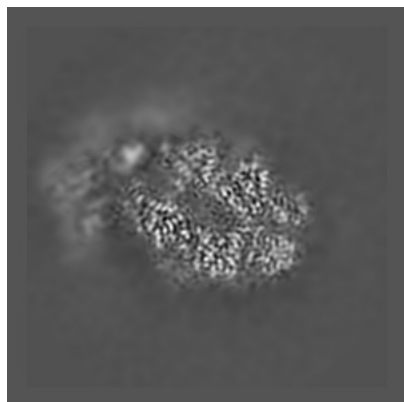


Z

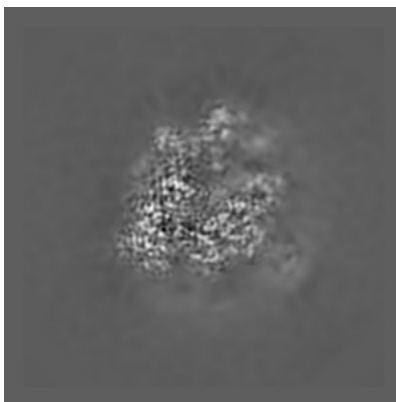
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

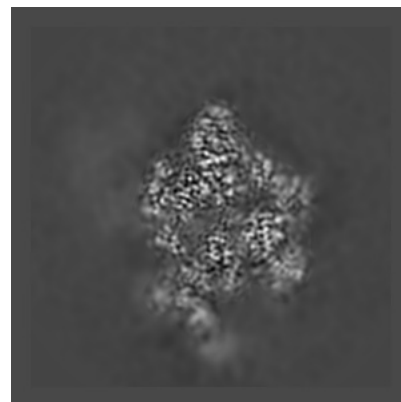
6.2.1 Primary map



X Index: 150

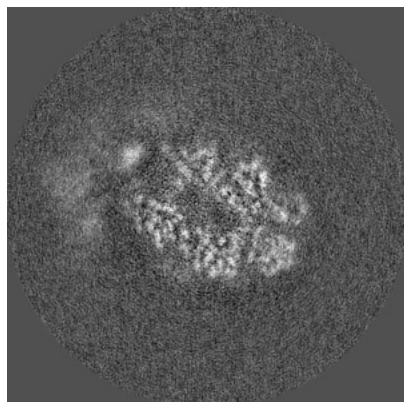


Y Index: 150

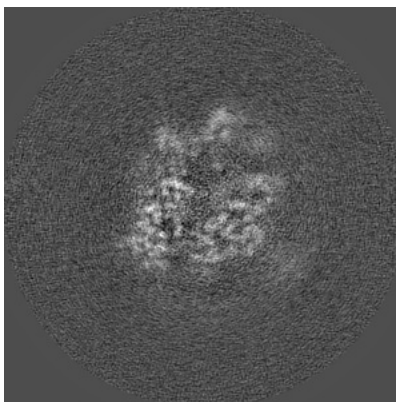


Z Index: 150

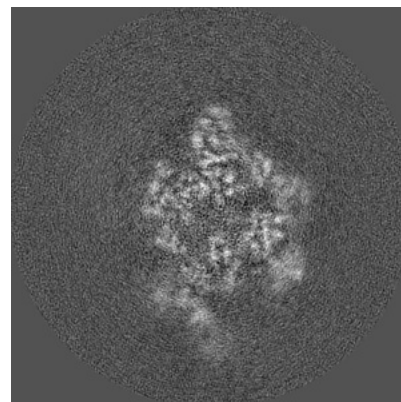
6.2.2 Raw map



X Index: 150



Y Index: 150

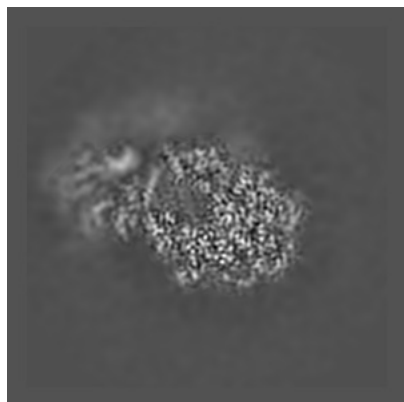


Z Index: 150

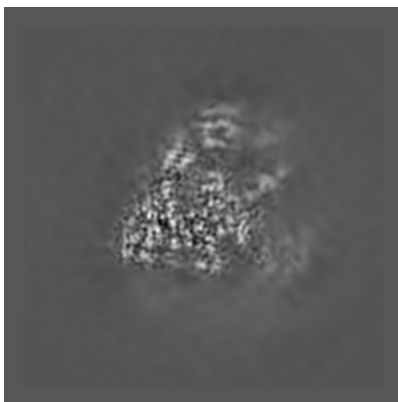
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

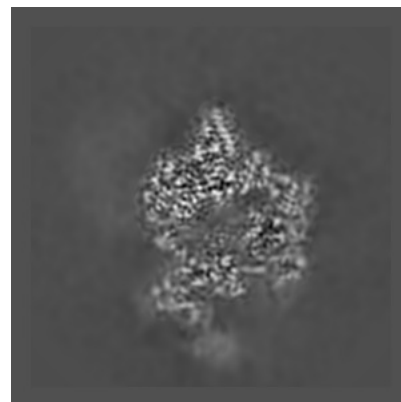
6.3.1 Primary map



X Index: 143

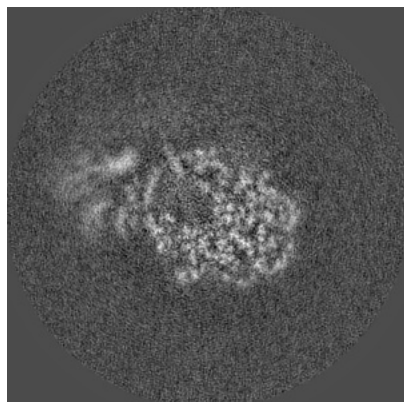


Y Index: 161

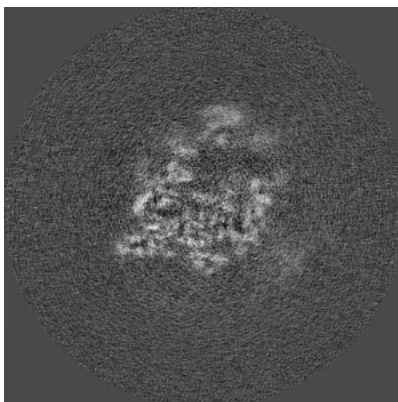


Z Index: 155

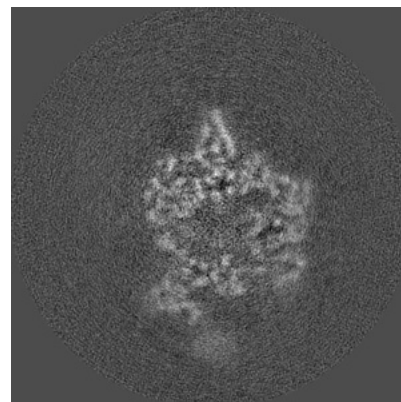
6.3.2 Raw map



X Index: 143



Y Index: 155

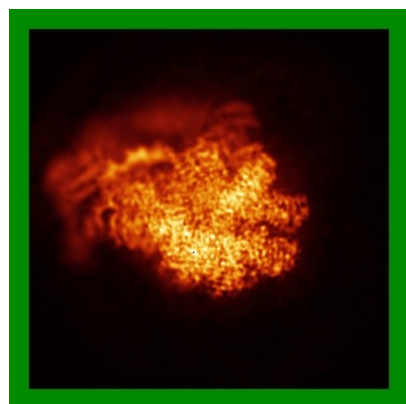


Z Index: 156

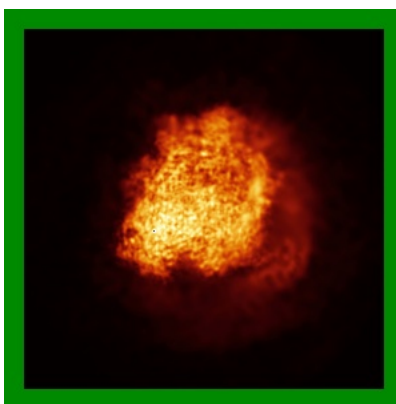
The images above show the largest variance slices of the map in three orthogonal directions.

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

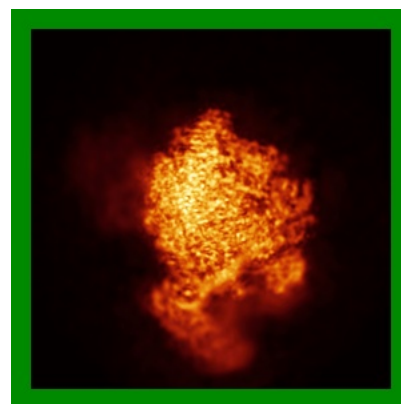
6.4.1 Primary map



X

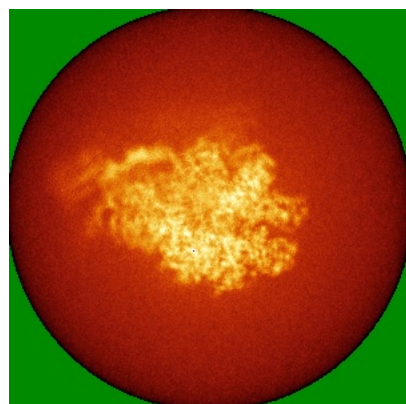


Y

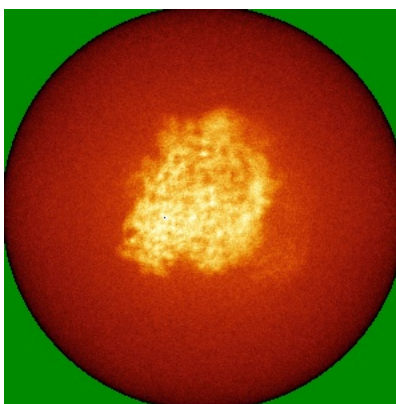


Z

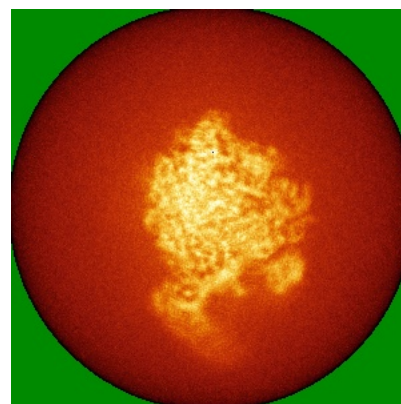
6.4.2 Raw map



X



Y

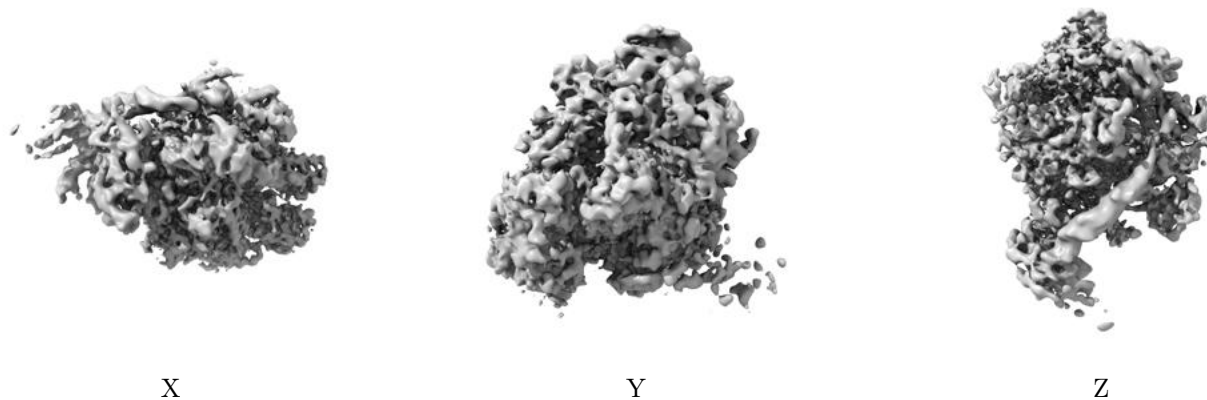


Z

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.

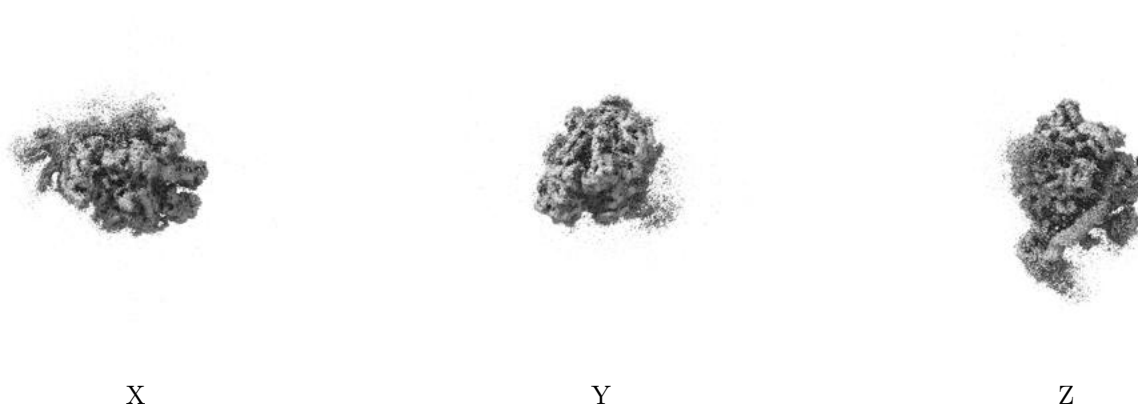
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.003. 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.

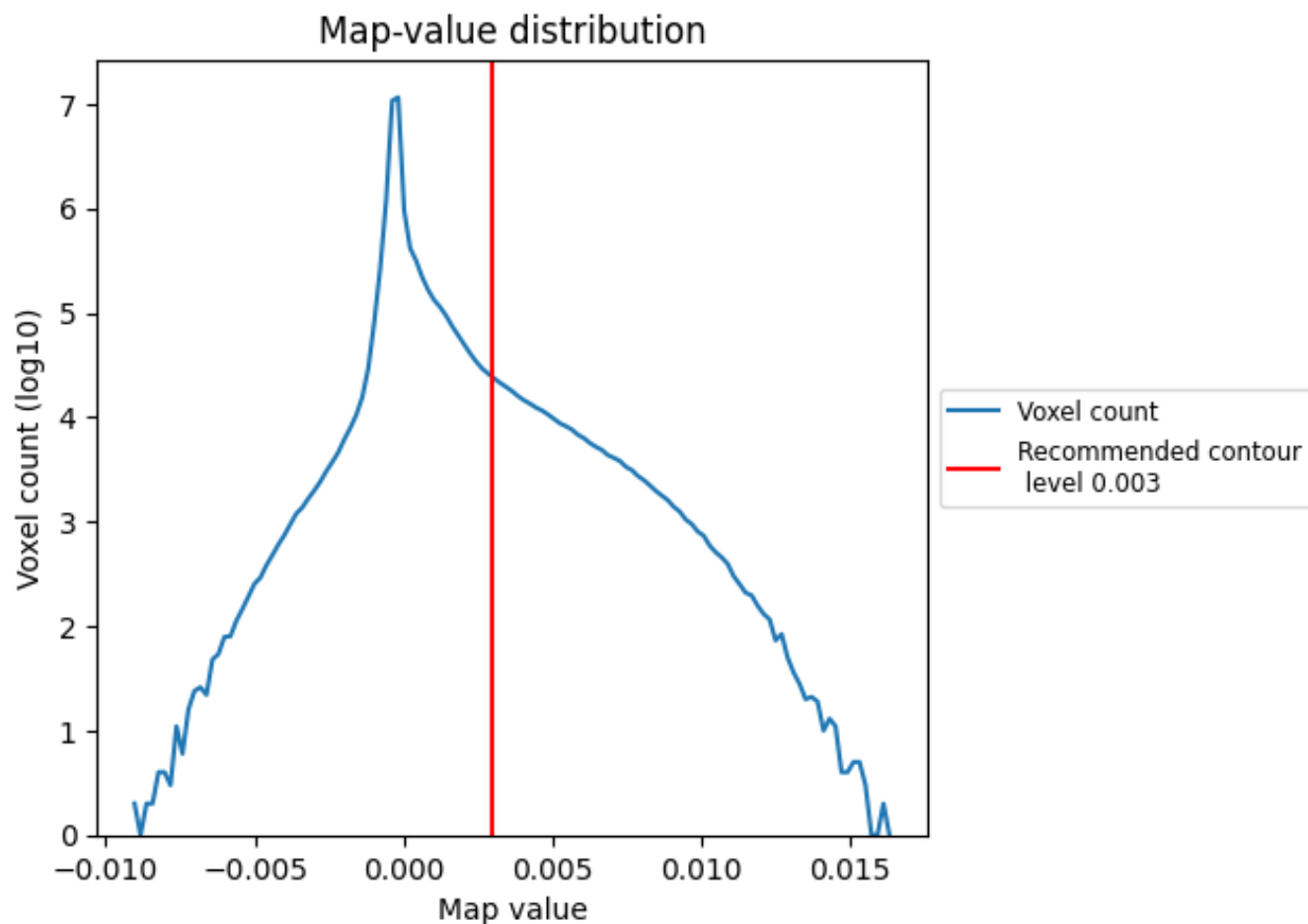
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

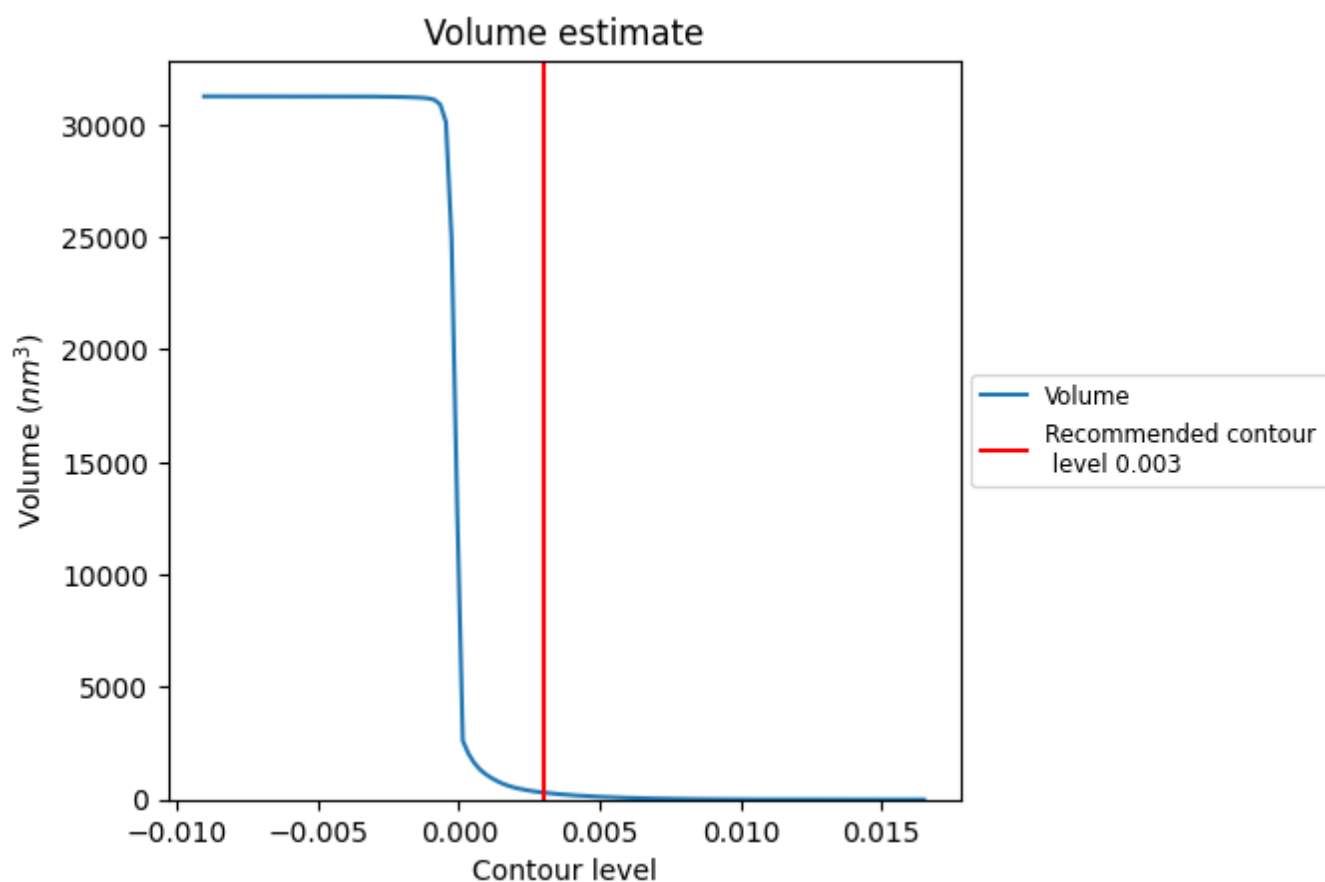
This section contains the results of statistical analysis of the map.

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.

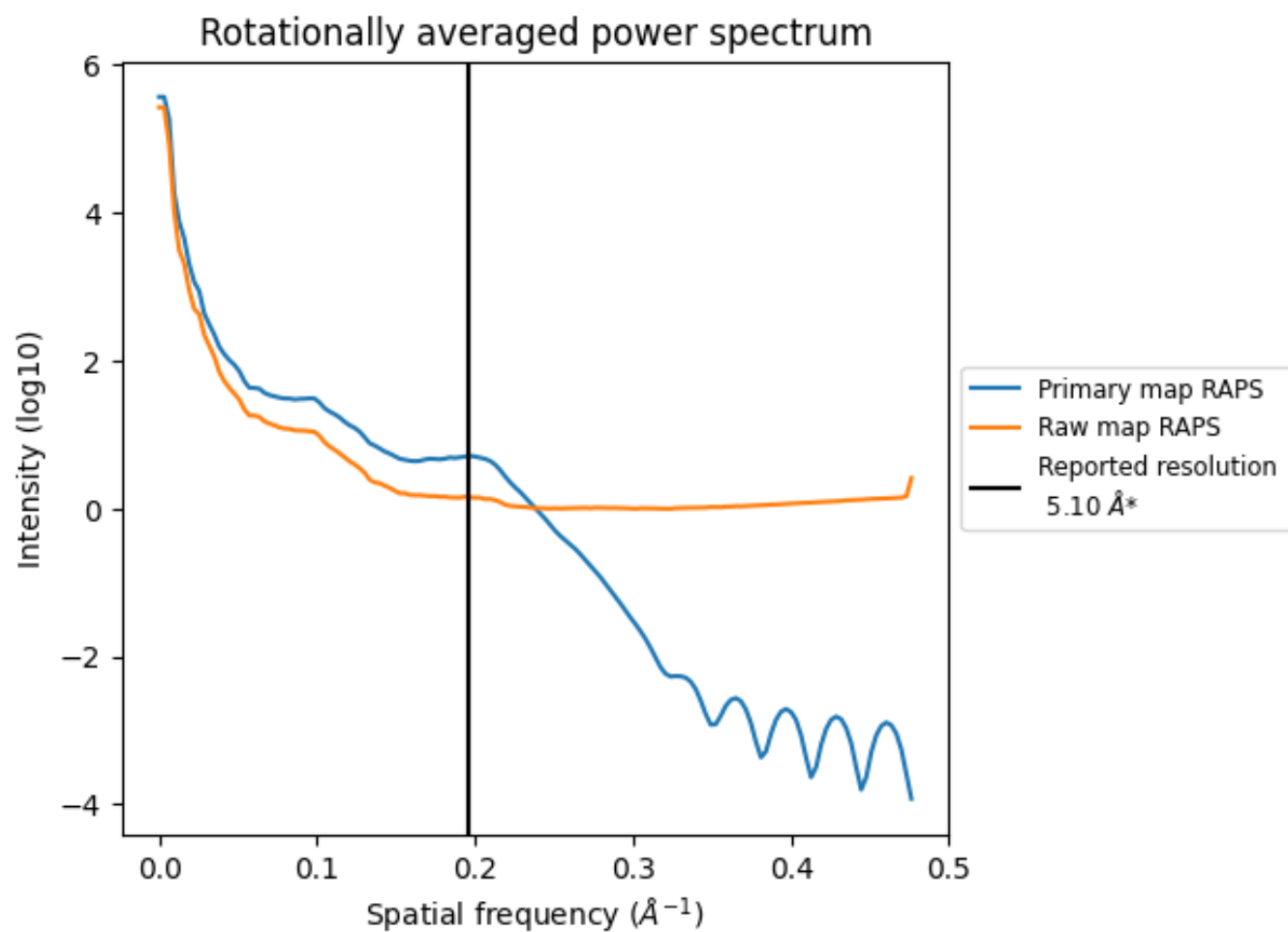
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 313 nm³; this corresponds to an approximate mass of 283 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 ⓘ

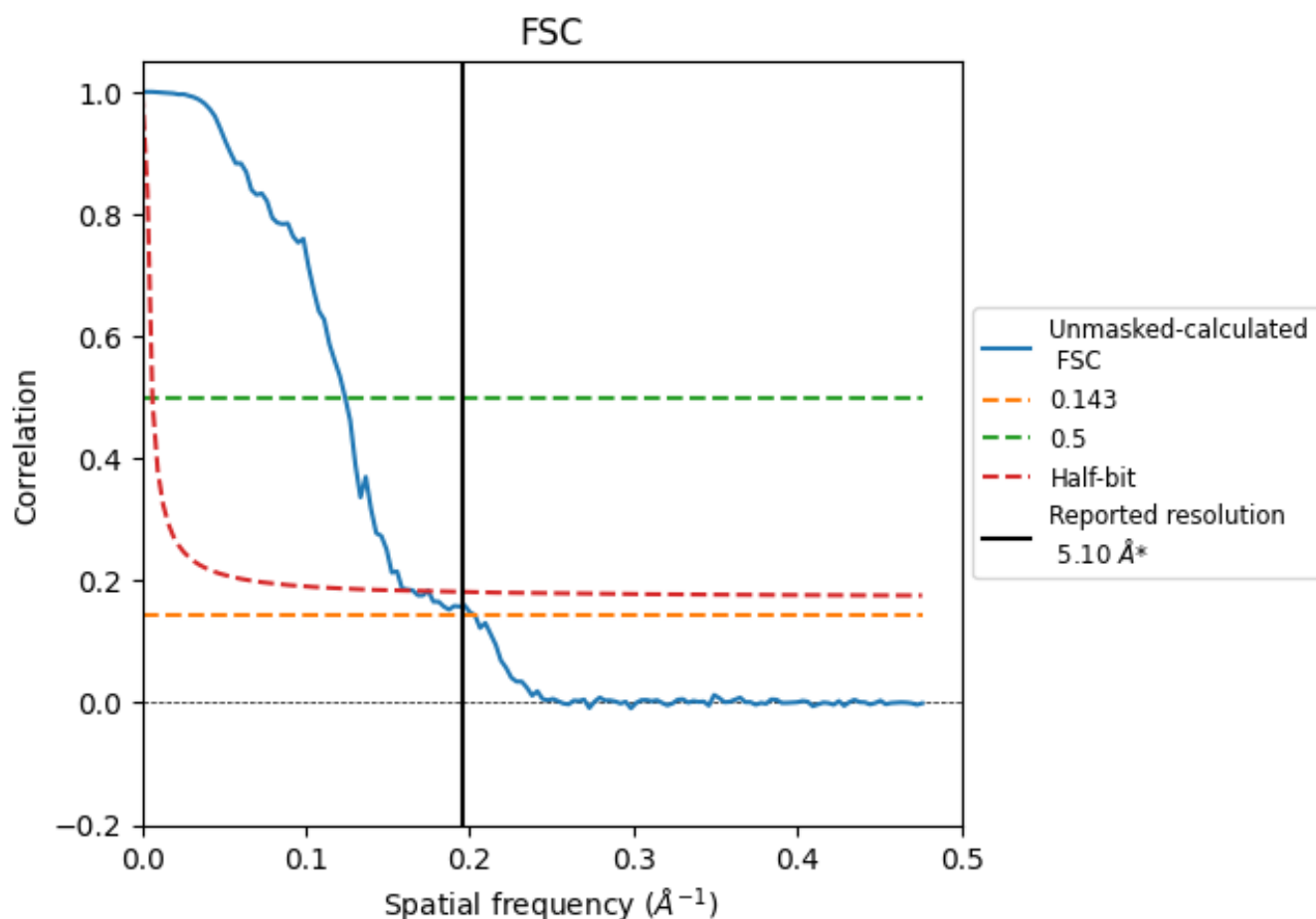


*Reported resolution corresponds to spatial frequency of 0.196 $\text{\AA}^{-1}$

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 0.196 Å⁻¹

8.2 Resolution estimates [i](#)

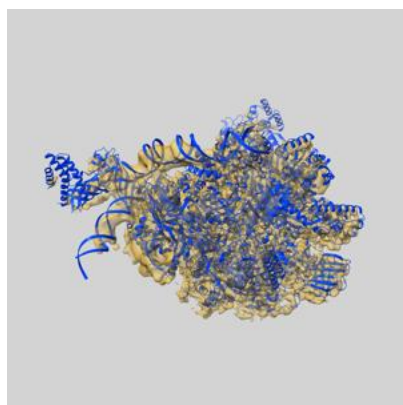
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.92	8.07	6.04

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

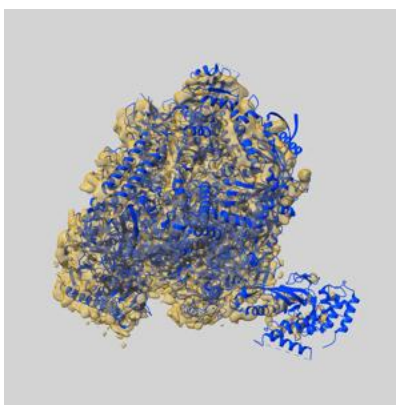
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0090 and PDB model 6GYK. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

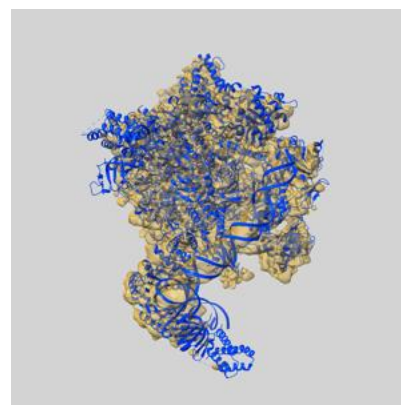
9.1 Map-model overlay [i](#)



X



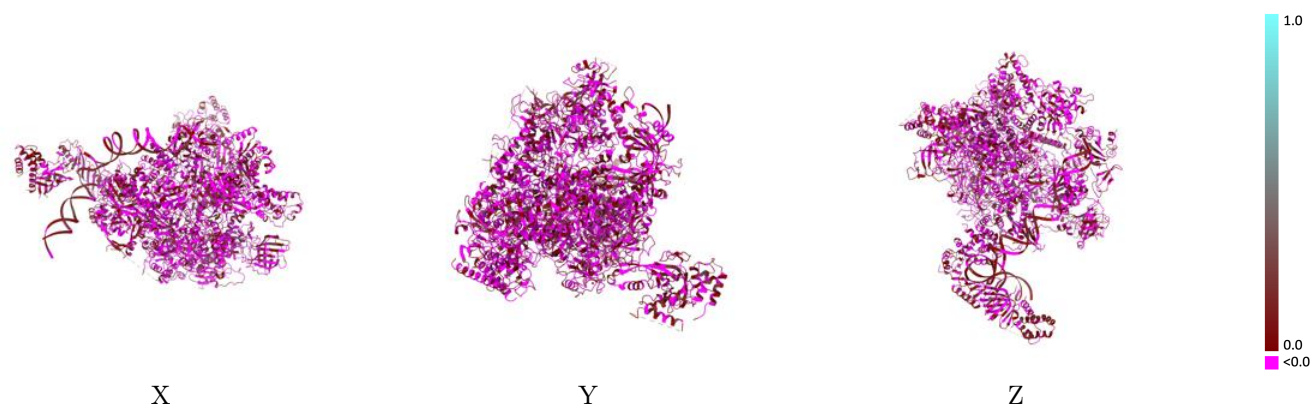
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.003 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](#)

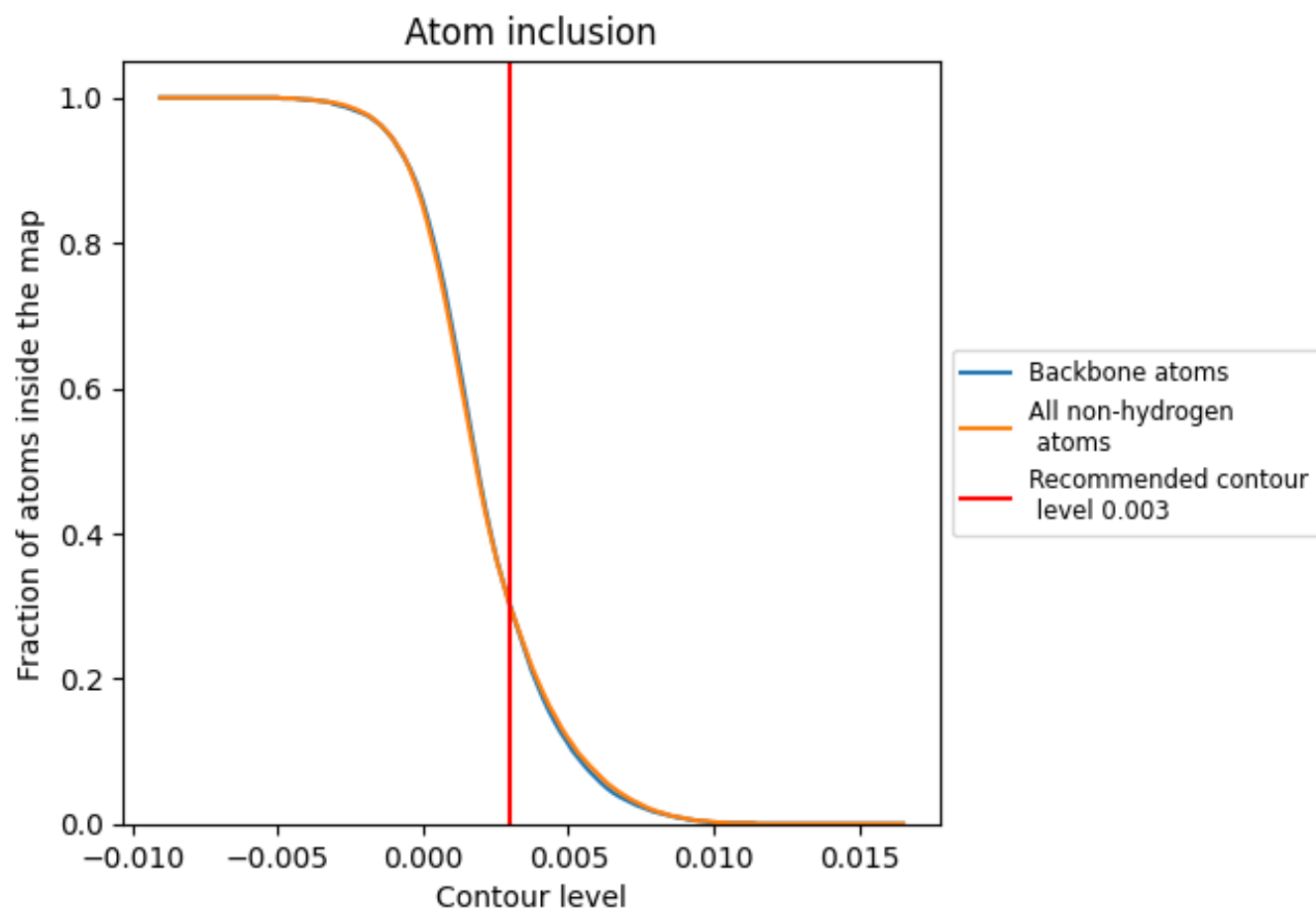


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 30% of all backbone atoms, 30% 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 (0.003) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.2990	 -0.0040
A	 0.3220	 -0.0130
B	 0.3190	 -0.0280
C	 0.3780	 -0.0240
D	 0.0230	 0.0410
E	 0.3160	 0.0030
F	 0.3500	 0.0340
G	 0.0790	 0.0150
H	 0.3550	 -0.0010
I	 0.3150	 0.0170
J	 0.3560	 -0.0750
K	 0.3110	 -0.0550
L	 0.3120	 -0.0360
M	 0.2270	 -0.0180
N	 0.3320	 0.0630
O	 0.3250	 0.0420
Q	 0.3230	 0.0270
R	 0.3660	 -0.0030
T	 0.4740	 0.0680
U	 0.0650	 0.0520
V	 0.0690	 0.0420

