



wwPDB EM Validation Summary Report ⓘ

Dec 11, 2022 – 11:58 pm GMT

PDB ID : 6TED
EMDB ID : EMD-10480
Title : Structure of complete, activated transcription complex Pol II-DSIF-PAF-SPT6
uncovers allosteric elongation activation by RTF1
Authors : Vos, S.M.; Farnung, L.; Cramer, P.
Deposited on : 2019-11-11
Resolution : 3.10 Å (reported)
Based on initial models : 4L1U, 6GMH, 6AFO

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:

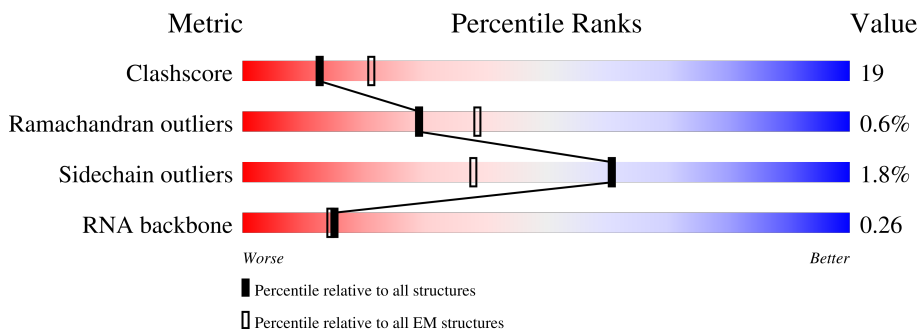
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

1 Overall quality at a glance

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

The reported resolution of this entry is 3.10 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.






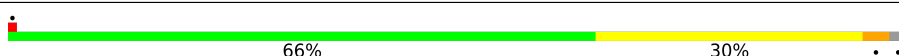
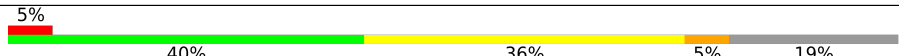

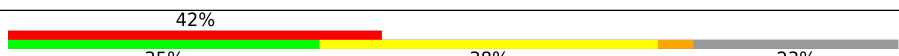
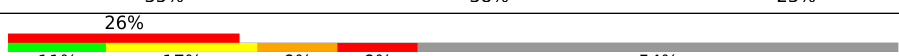
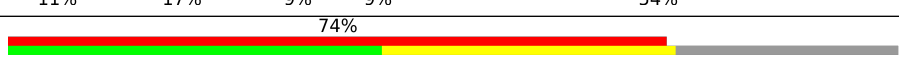

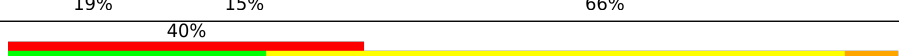
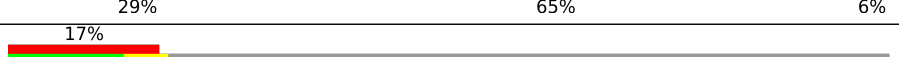

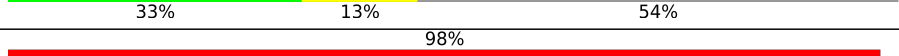

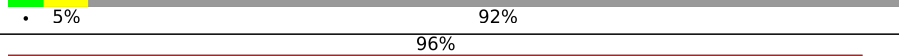

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	1984	
2	B	1251	
3	C	275	
4	D	142	
5	E	210	
6	F	127	
7	G	172	

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Mol	Chain	Length	Quality of chain
8	H	150	
9	I	125	
10	J	67	
11	K	117	
12	L	58	
13	M	1729	
14	N	48	
15	P	46	
16	Q	1179	
17	R	713	
18	T	48	
19	U	666	
20	V	531	
21	W	305	
22	X	531	
23	Y	121	
24	Z	1087	

2 Entry composition [i](#)

There are 26 unique types of molecules in this entry. The entry contains 57142 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 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	N	O	P			S
1	A	1426	Total	C	N	O	P	S	0	0
			11255	7074	2014	2095	2	70		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	1122	Total	C	N	O	S	0	0
			8980	5684	1576	1656	64		

- Molecule 3 is a protein called RNA polymerase II subunit C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	258	Total	C	N	O	S	0	0
			2072	1300	356	410	6		

- Molecule 4 is a protein called RNA polymerase II subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	126	Total	C	N	O	S	0	0
			1004	630	170	200	4		

- Molecule 5 is a protein called RNA polymerase II subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	209	Total	C	N	O	S	0	0
			1720	1089	300	323	8		

- Molecule 6 is a protein called RNA polymerase II subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	78	Total	C	N	O	S	0	0
			626	401	106	114	5		

- Molecule 7 is a protein called RNA polymerase II subunit G.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	171	1333	866	214	245	8	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	149	1197	759	195	238	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	116	942	582	168	181	11	0	0

- Molecule 10 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	66	524	339	88	91	6	0	0

- Molecule 11 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	K	115	920	593	152	173	2	0	0

- Molecule 12 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L	47	390	240	77	67	6	0	0

- Molecule 13 is a protein called Transcription elongation factor SPT6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	M	1002	4737	2583	1071	1076	7	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-2	SER	-	expression tag	UNP Q7KZ85
M	-1	ASN	-	expression tag	UNP Q7KZ85
M	0	ALA	-	expression tag	UNP Q7KZ85

- Molecule 14 is a DNA chain called DNA (37-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
14	N	37	773	361	158	217	37	0	0

- Molecule 15 is a RNA chain called RNA (5'-R(P*UP*AP*AP*CP*CP*GP*GP*AP*GP*AP*GP*GP*GP*AP*AP*CP*CP*CP*AP*CP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
15	P	21	452	202	87	142	21	0	0

- Molecule 16 is a protein called RNA polymerase-associated protein CTR9 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	Q	890	7226	4579	1264	1352	31	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	1174	GLU	-	expression tag	UNP Q6PD62
Q	1175	ASN	-	expression tag	UNP Q6PD62
Q	1176	LEU	-	expression tag	UNP Q6PD62
Q	1177	TYR	-	expression tag	UNP Q6PD62
Q	1178	PHE	-	expression tag	UNP Q6PD62
Q	1179	GLN	-	expression tag	UNP Q6PD62

- Molecule 17 is a protein called RNA polymerase-associated protein RTF1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	R	244	1832	1148	340	337	7	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-2	SER	-	expression tag	UNP Q92541
R	-1	ASN	-	expression tag	UNP Q92541
R	0	ALA	-	expression tag	UNP Q92541

- Molecule 18 is a DNA chain called Template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
18	T	48	974	462	168	296	48	0	0

- Molecule 19 is a protein called RNA polymerase-associated protein LEO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	U	125	852	534	151	166	1	0	0

- Molecule 20 is a protein called RNA polymerase II-associated factor 1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	V	244	1703	1061	305	333	4	0	0

- Molecule 21 is a protein called WD repeat-containing protein 61.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	W	300	2333	1483	392	454	4	0	0

- Molecule 22 is a protein called Parafibromin.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
22	X	43	353	220	69	64	0	0

- Molecule 23 is a protein called Transcription elongation factor SPT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	Y	116	911	570	159	173	9	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	-3	GLY	-	expression tag	UNP P63272
Y	-2	PRO	-	expression tag	UNP P63272
Y	-1	GLY	-	expression tag	UNP P63272
Y	0	SER	-	expression tag	UNP P63272

- Molecule 24 is a protein called Transcription elongation factor SPT5.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	N	O	P			S
24	Z	510	4023	2550	709	745	1	18	0	0

- Molecule 25 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

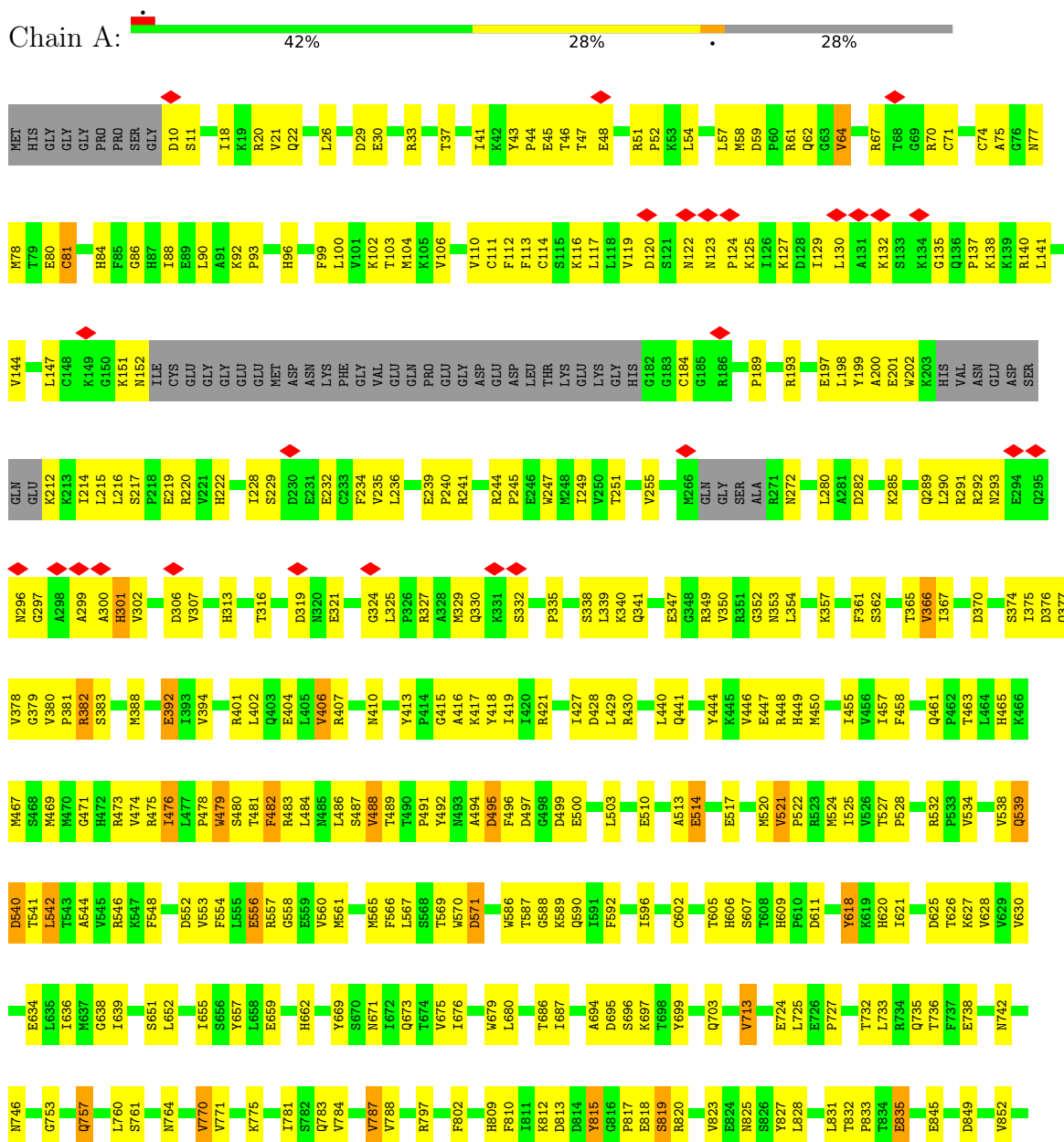
- Molecule 26 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

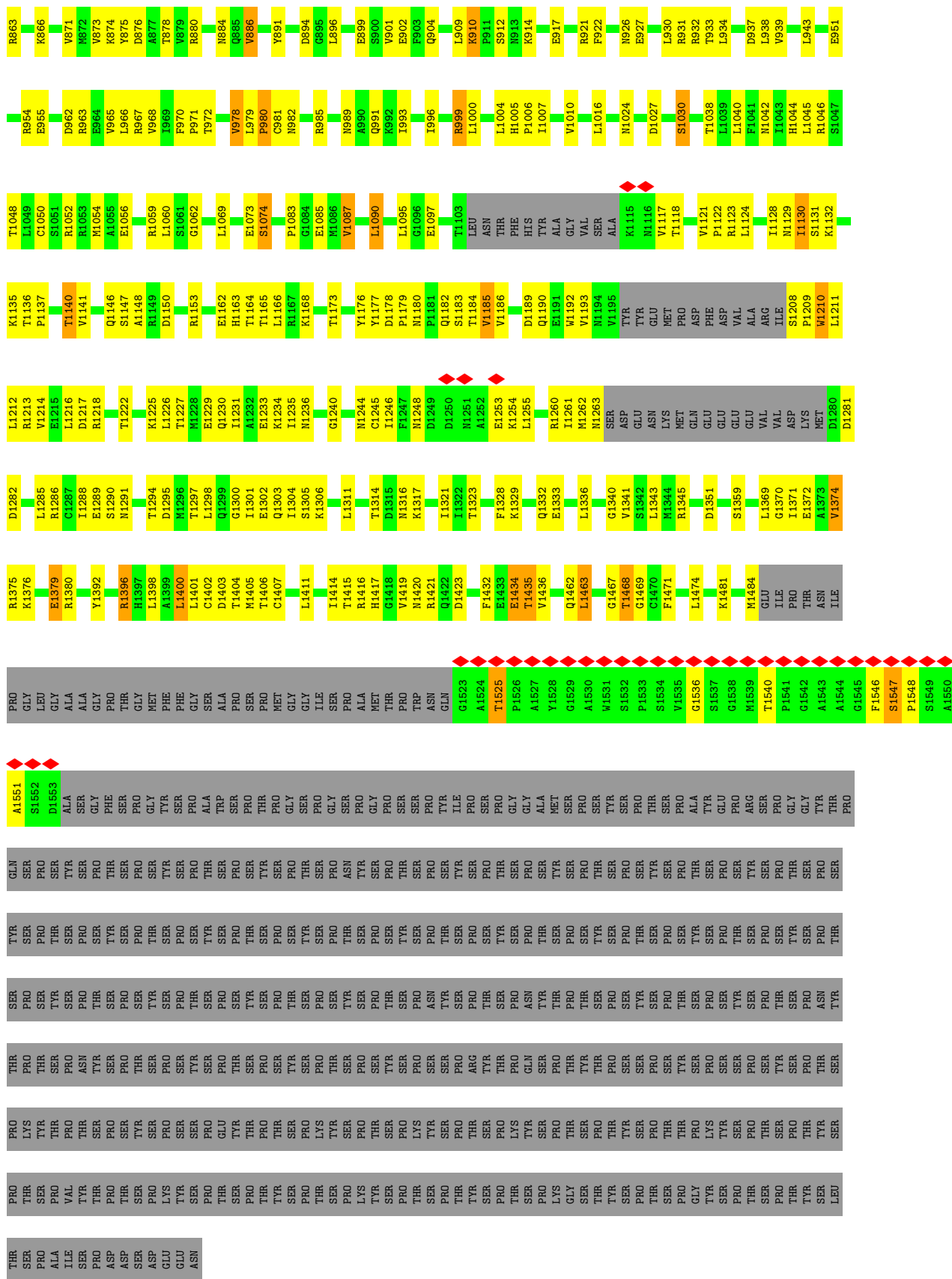
Mol	Chain	Residues	Atoms		AltConf
26	A	1	Total 1	Mg 1	0

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 subunit



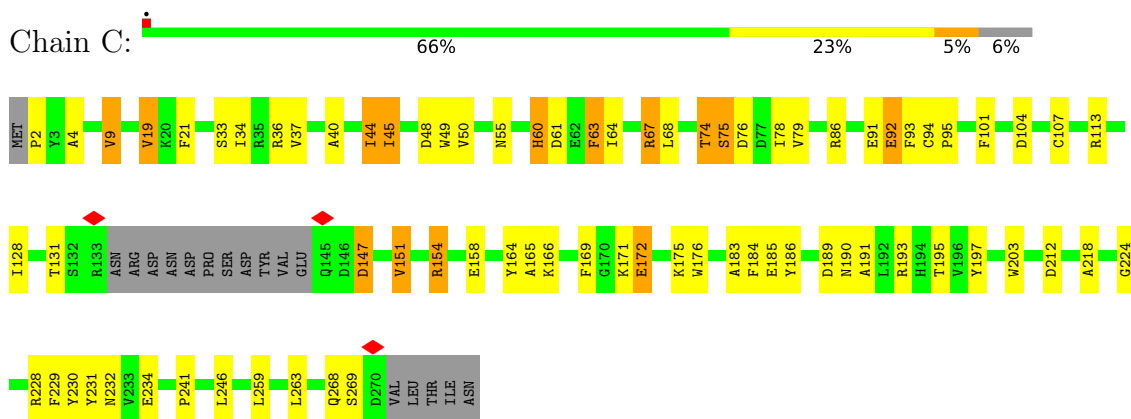


• Molecule 2: DNA-directed RNA polymerase subunit beta

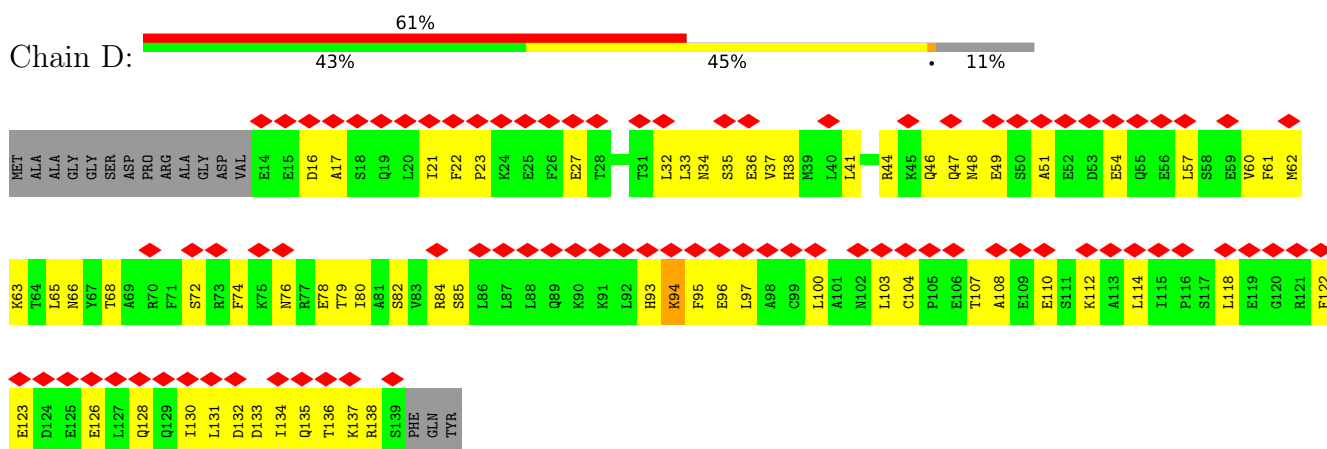


MET	CYS	SER	THR	VAL	ALA	GLN	ASN	LEU	SER	GLN	ALA	LEU	VAL	TYR	PHE	ARG	ALA	GLY	ALA	GLY	ALA	ASN	ASN	LEU	THR	ALA	GLY	PHE	ARG	GLY	ASP	SER	ARG	ARG	ARG	LYS	ARG	LYS	SER	LEU	CYS	LEU	ALA	ALA	LEU	ARG	PRG	GLY	GLY	ALA	CYS	ALA	ALA	CYS	TRP	ARG	TRP	LEU	LEU	ALA
VAL	SER	CYS	VAL	ALA	GLN	ASN	LEU	ARG	GLY	GLY	ALA	LEU	VAL	ALA	GLU	PRO	SER	GLY	GLY	P81	P82	R83	Y84	L85	L86	Q90	I91	Y92	L93	S94	K95	E100	ARG	D102	P105	M108	A113	R114	L115	Y120	S121	A122	P123	K130	T131	V132	I133	K134	E135	M53	S54	V55	Q56	R57	I58	V59	D66	L67		
GLN	ALA	GLU	ALA	GLN	HIS	ALA	ALA	VAL	GLU	GLY	GLU	GLY	P81	P82	R83	Y84	L85	L86	Q90	I91	Y92	L93	S94	K95	E100	ARG	D102	P105	M108	A113	R114	L115	Y120	S121	A122	P123	K130	T131	V132	I133	K134	E135	G136	E137	E138	Q139	L140	O141	T142	Q143	H144	Q145								
K146	T147	F148	P153	H154	M155	L156	L157	S158	T159	L163	M164	G165	L166	R169	D170	E176	C177	P178	L179	D180	Y184	F185	I186	I187	E191	K192	V193	E198	K199	K211	D212	T218	R222	S223	S228	S229	R230	L235	V236	V237	S238	R242	GLY	GLY	GLN	GLY														
ALA	LYS	LYS	SER	ALA	L252	G253	Q254	R255	T259	V267	F273	V279	S280	D281	L284	L285	M297	M298	E299	K302	P303	S304	L305	B306	E307	A308	F309	V310	I311	Q312	E313	Q314	N319	N315	V316	A317	L318	N319	F320	I321	G322	S323	A326	K327	F328	G329	V330	T331	K332	E333	K334									
A339	Y342	K346	M347	L348	F349	H350	V351	S354	D355	F356	C357	E358	T359	K360	K361	Y367	K368	V369	H370	R371	L377	D386	H387	Y388	L393	D394	L395	L399	L403	F404	R405	F408	L411	L412	K413	E414	Q420	K421	F422	R425	G426	K427	D428	F429	K430	E431	K432	E433	K434											
R438	L439	G451	H452	G454	H455	D456	H457	K458	K458	H460	Q461	Y466	S467	L472	L473	R472	V473	H474	L479	R483	R484	L485	D492	G493	K494	L495	A496	P498	R499	L501	T504	L505	W506	V509	C510	V520	V523	K524	R525	L528	I532	Q537	P538	L542	S543															
F544	L545	E546	E547	W548	E551	H552	L553	D556	S557	P558	A559	T565	K566	L567	F568	W573	V574	E575	L576	H577	F580	L583	T586	L587	R588	R592	D595	L596	L597	V601	E609	R610	R613	L614	V615	R620	L621	C622	R623	P624	L625	L626	E629	L633																
L634	R638	H639	L643	R646	E647	V648	H649	H650	W651	S652	D655	S659	G660	V661	V662	E663	Y664	L665	D666	T667	L668	E671	R677	T678	P679	D680	D681	L682	H684	E684	K685	E686	C690	S691	T692	V693	E697	L698	G705	V706	C707	H708	S709	P714	F715	Q718	S719													
R720	K721	M728	Q731	V735	Y736	L737	T738	H739	F740	H741	V742	R743	H744	D745	V750	L751	Y752	Y753	P754	Q755	K756	P757	T760	E765	V766	L767	R768	F769	D681	L682	H684	E684	K685	E686	C690	S691	T692	V693	E697	L698	G705	V706	C707	H708	S709	P714	F715	Q718	S719											
F810	Y811	Y814	K815	E816	Q817	R821	G822	F823	D824	T833	R834	E835	G839	H840	R841	H842	R847	L848	D851	R859	H860	D864	V865	I866	R867	G868	K869	T872	A783	S784	Y785	T786	G787	Y788	M789	Q790	E791	D792	S793	V794	L795	Y801	V801	F805	F806	R807	S808	H809	R897	T898										
S899	E900	T901	V904	V907	T910	L911	N912	F918	C919	R920	K921	R922	V923	R924	S925	V926	I931	G932	D933	S937	R938	H939	G940	Q941	K942	C945	Y949	R950	D953	T957	C958	E959	N968	S974	R975	C984	K993	G994	E995	I996	G997	P1001	F1002	N1003																
D1004	A1005	Y1006	M1007	K1010	I1011	L1014	L1015	Y1018	G1019	Y1020	H1021	L1022	R1023	V1027	L1028	Y1029	T1038	S1039	Q1040	Y1047	Y1048	Q1049	G1050	R1062	G1065	M1071	R1072	Q1073	P1074	E1088	C1093	Q1101	R1104	E1105	F1108	D1112	Q1115	V1116	H1117	V1118	C1119	M1120																		
M1125	N1129	T1130	R1131	T1134	Y1135	E1136	N1142	K1143	T1144	Q1145	L1148	V1149	R1150	M1151	F1152	Y1153	K1156	L1157	E1161	M1171	M1172	S1173	V1174																																					

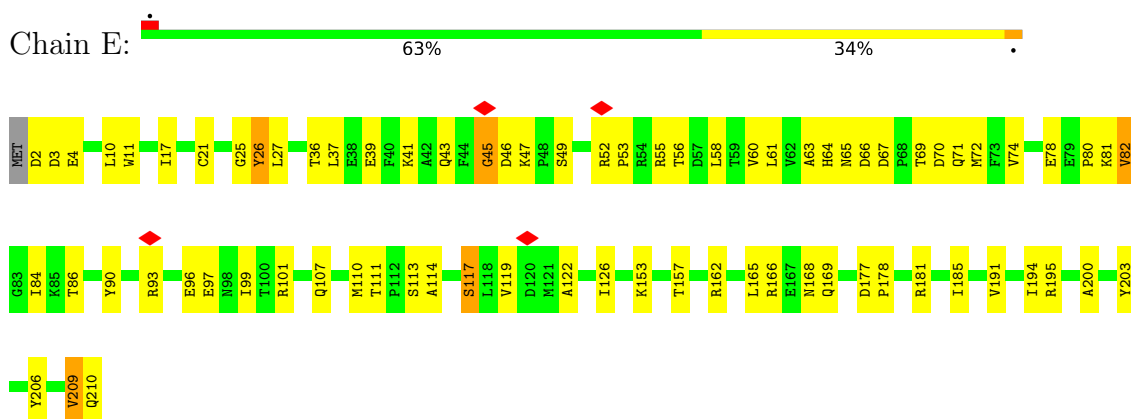
• Molecule 3: RNA polymerase II subunit C



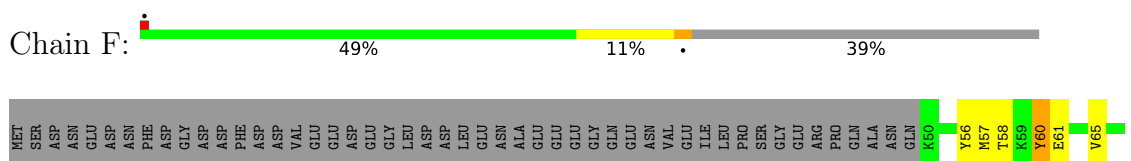
• Molecule 4: RNA polymerase II subunit D



• Molecule 5: RNA polymerase II subunit E

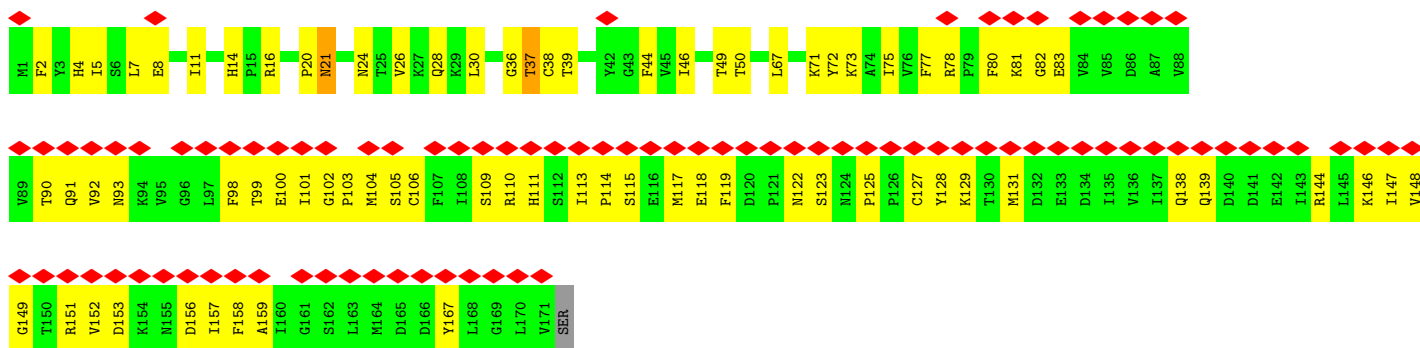


• Molecule 6: RNA polymerase II subunit F

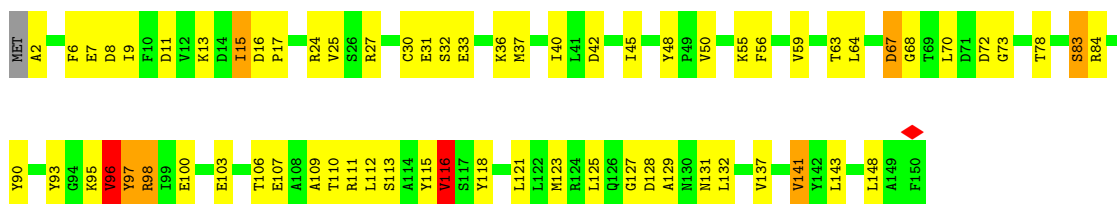




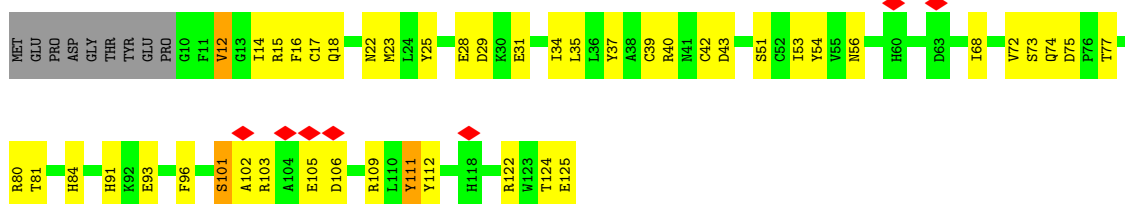
• Molecule 7: RNA polymerase II subunit G



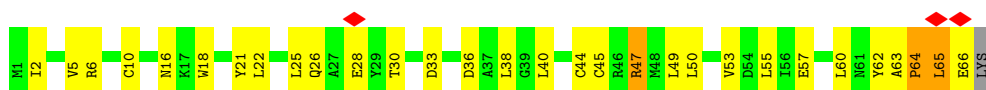
• Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3



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

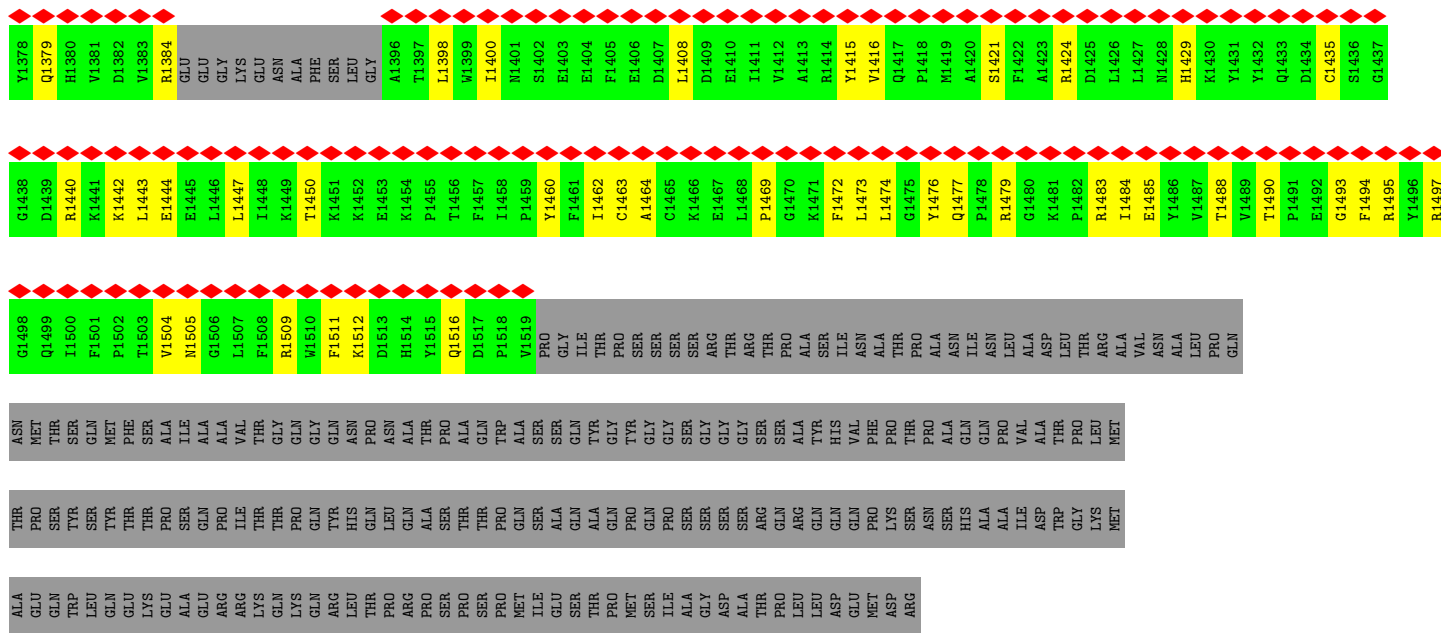


• Molecule 10: Uncharacterized protein

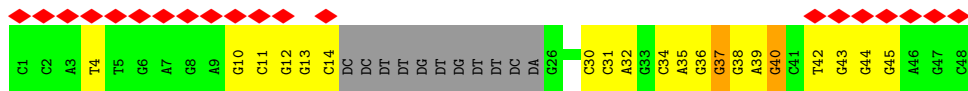


• Molecule 11: Uncharacterized protein

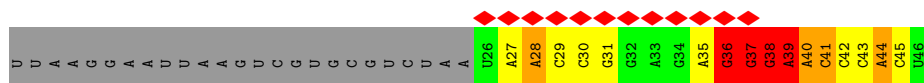
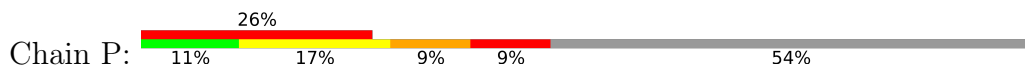
ARG	L658	Q718	G778	K638	K898	L958	V1018	E1078	R1138	CYS	K1258	I1327	ARG
LYS	A659	Q719	I779	F839	S899	Y959	T1019	S1079	T1139	PRO	V1259	A1328	LYS
GLN	E660	Q720	R780	L840	E900	C960	M1020	A1080	A1140	PHE	G1260	A1329	GLN
GLN	D661	L721	V781	L841	A901	E961	C1021	E1081	Y1141	CYS	M1261	I1330	GLN
THR	E662	L722	G783	N842	E902	F962	H1022	A1082	R1142	GLN	T1262	I1331	THR
THR	G663	V723	L784	K843	F903	I963	M1023	A1083	S1143	ASP	S1263	I1332	THR
ASN	Q604	Q724	I785	K844	R904	N964	G1024	N1084	P1144	ASN	H1264	I1333	ASN
PRO	V605	M725	A785	P845	D905	R965	P1025	P1085	M1145	PRO	C1265	I1334	PRO
LEU	L606	A726	F786	H846	Y906	V966	K1026	A1086	T1146	LEU	L1266	I1335	LEU
GLU	R607	K727	S787	V847	P907	E967	M1027	G1087	E1147	SER	I1267	I1336	GLU
SER	Q608	E728	S788	V848	P908	E968	F1028	A1088	E1148	GLU	M1268	I1337	SER
VAL	T609	L729	A789	T849	V909	V969	M1029	L1089	I1149	VAL	K1269	I1338	VAL
ASN	F610	K730	R790	V850	L910	F970	M1030	E1090	F1150	ASN	I1270	I1339	ASN
HIS	E611	N731	D791	A851	R911	G971	C1031	I1091	M1151	HIS	D1271	I1340	HIS
PHE	E612	K732	H792	G852	Q912	D972	A1032	I1092	M1152	PHE	I1272	I1341	PHE
ASP	R613	L733	P793	E853	A913	V973	G1033	L1093	L1153	ASP	E1273	I1342	ASP
GLY	A614	L734	P794	N854	V914	N974	F1034	E1094	T1154	GLY	K1274	I1343	GLY
CYS	K615	A735	F795	R855	S915	R975	L1035	N1095	K1155	CYS	F1275	I1344	CYS
PRO	L616	E736	C796	D856	L916	A976	K1036	P1096	E1156	PRO	S1276	I1345	PRO
GLY	N617	A737	A797	A857	A917	I977	I1037	E1097	T1157	GLY	A1277	I1346	GLY
TYR	L618	K738	L798	Q858	R918	A978	D1038	R1098	P1158	TYR	L1278	I1347	TYR
GLY	T619	E739	V799	M859	R919	H979	M1039	L1099	E1159	GLY	L1279	I1348	GLY
ASN	P620	Y740	N800	L860	I920	P980	ALA	K1100	T1160	ASN	I1226	I1349	ASN
ASP	T621	V741	G801	I861	Q921	Y981	SER	D1101	F1161	ASP	G1227	I1350	ASP
GLM	K622	I742	E802	E862	D922	S982	GLY	L1102	F1162	GLM	V1228	I1351	GLM
K623	T884	K743	G803	D863	P923	Q983	ASP	D1103	I1163	K623	K1229	I1352	K623
G624	F685	A744	E904	V864	L924	A984	SER	L1104	G1164	G624	S1230	I1353	G624
R625	F686	C745	V905	K865	I925	L985	THR	D1105	K1165	R625	R1231	I1354	R625
K626	E687	S746	T806	R866	E926	I986	ASP	A1106	L1166	K626	L1232	I1355	K626
D627	E688	R747	D807	I867	F927	Q987	TYR	F1107	I1167	D627	L1233	I1356	D627
V628	K689	K748	F808	V868	A928	Y988	ILE	A1108	I1168	V628	N1234	I1357	V628
D629	K690	L749	L809	H869	Q929	V989	V1051	E1109	C1169	D629	G1235	I1358	D629
E630	Q691	Y750	R810	E870	V930	C990	E1052	E1110	M1170	E630	V1236	I1359	E630
A631	F692	N751	L811	H871	V931	G991	L1053	L1111	V1171	A631	T1237	I1360	A631
H632	Y693	W752	P812	D872	S832	L982	D1054	E1112	T1172	H632	G1238	I1361	H632
Y633	Y694	L753	H813	Q873	SER	G983	G1055	R1113	G1173	Y633	F1239	I1362	Y633
Y635	D696	R754	H814	G874	ASP	P994	S1056	Q1114	I1174	Y635	I1240	I1363	Y635
S636	F697	A756	T815	Q875	E935	K995	R1057	G1115	A1175	S636	P1241	I1364	S636
F637	F698	W757	LYS	Q876	D936	K996	V1058	Y1116	H1176	F637	T1242	I1365	F637
K638	S699	Y758	ARG	L877	I937	G997	H1059	G1117	ARG	K638	K1243	I1366	K638
Y639	H700	ALA	THR	S878	L938	T998	P1060	D1118	PRO	Y639	F1244	I1367	Y639
L640	Q701	P760	ALA	S879	C939	H999	E1061	K1119	GLN	L640	L1245	I1368	L640
K641	V702	D761	TRP	I880	L940	L1000	T1062	H1120	GLY	K641	S1246	I1369	K641
W703	Q703	Q762	ARG	G881	K941	L1001	Y1063	I1121	GLU	W703	D1247	I1370	W703
E704	E704	Q763	GLU	V882	F942	K1002	E1064	T1122	SER	E704	K1248	I1371	E704
W705	W705	VAL	E824	E883	H943	I1003	M1065	L1123	TYR	W705	V1249	I1372	W705
N706	N706	GLU	E825	L884	P944	L1004	A1066	Y1124	GLN	N706	V1250	I1373	N706
R707	R707	GLU	R826	V885	L945	K1005	R1067	D1125	ALA	R707	K1251	I1374	R707
K646	Q708	ASP	E827	V886	Q946	K1006	K1068	I1126	ILE	K646	R1252	I1375	K646
E647	R709	ASP	N887	N886	E947	Q1006	M1069	I1127	ARG	E647	P1253	I1376	E647
L648	T710	PHE	K829	E888	H948	M1008	A1070	A1128	ASN	L648	E1254	I1377	L648
R649	M711	MET	Q831	L889	V949	T1009	V1071	L1129	THR	R649	GLU	I1378	R649
D650	A712	ASP	Q832	A890	V950	R1010	D1072	L1130	GLY	D650	L1255	I1379	D650
Q652	E714	GLU	I833	I891	K951	E1012	A1073	S1131	LEU	Q652	R1256	I1380	Q652
F653	E715	ASN	E834	L892	E952	E1013	L1074	C1132	TRP	F653	V1257	I1381	F653
L654	A716	ASP	Y893	L893	E953	S1013	E1076	R1133	GLN	L654		I1382	L654
K655	L717	ASN	M894	N895	L955	T1015	D1077	K1135		K655		I1383	K655
I656	L717	ASP	S896	K897	A857	Q1016	D1077	L1137		I656		I1384	I656



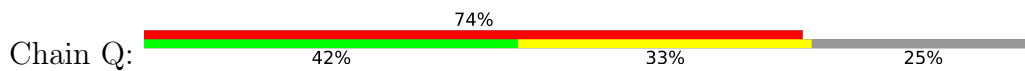
• Molecule 14: DNA (37-MER)



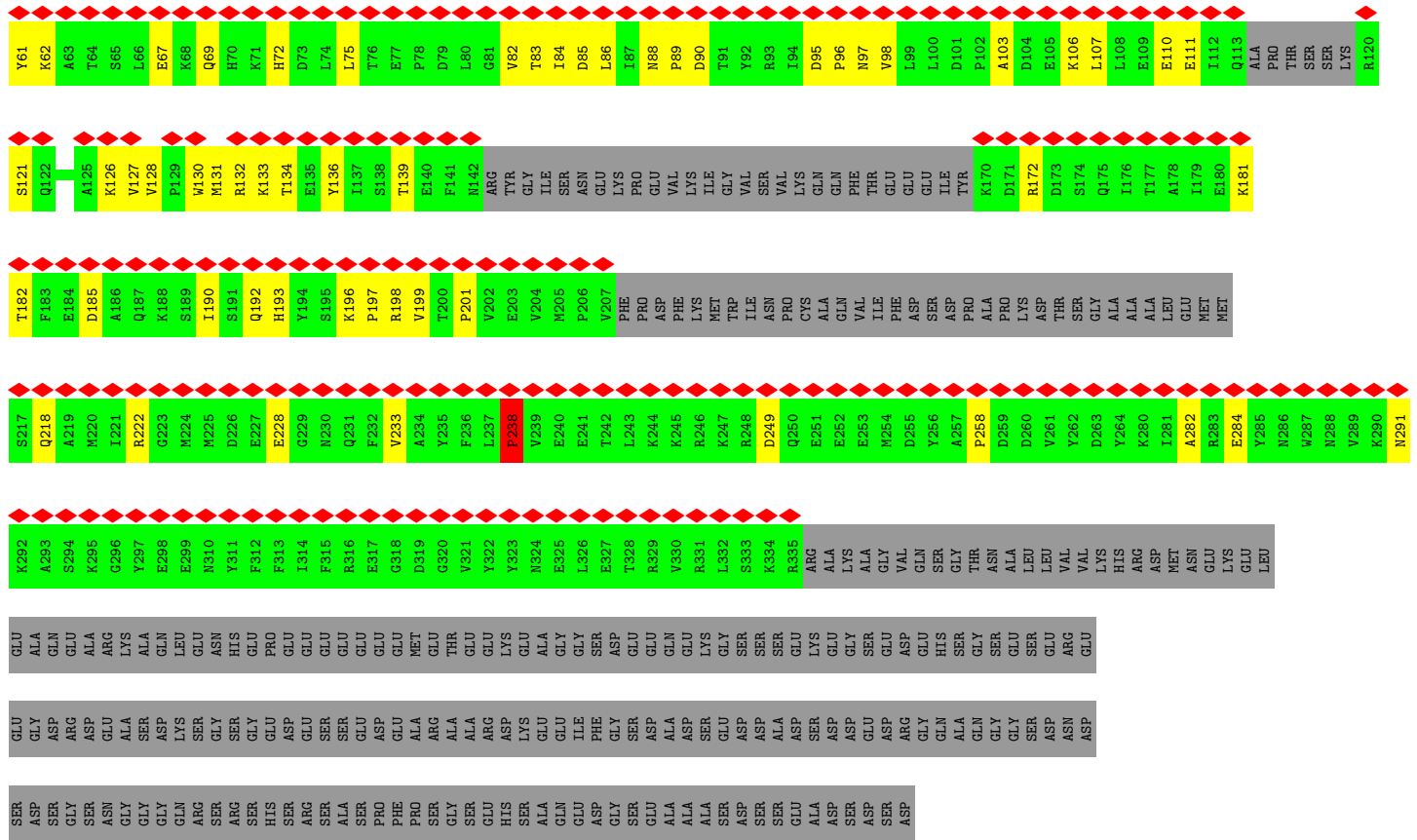
• Molecule 15: RNA (5'-R(P*UP*AP*AP*CP*CP*GP*GP*AP*GP*AP*GP*GP*GP*AP*AP*CP*CP*CP*AP*CP*U)-3')



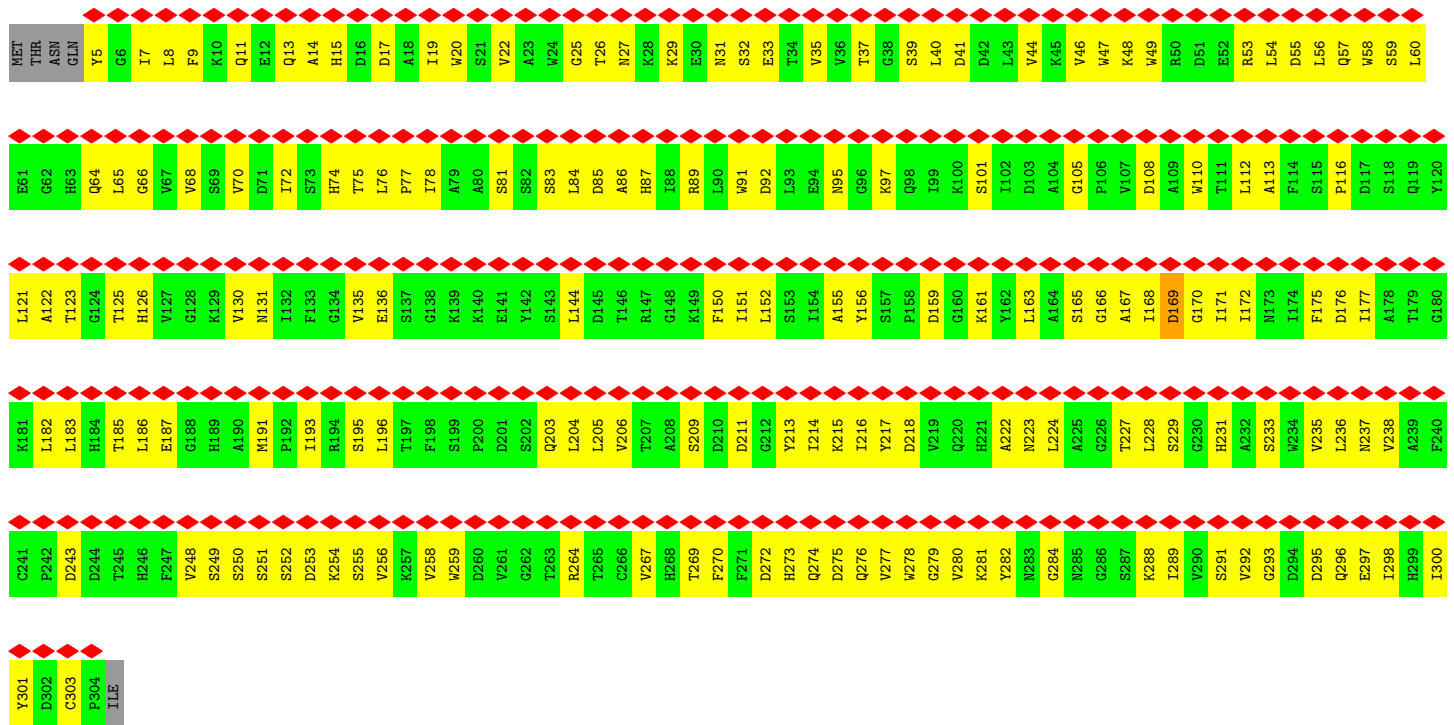
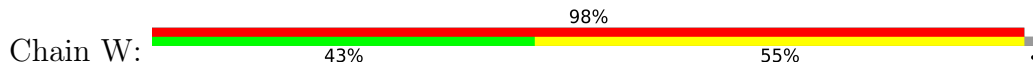
• Molecule 16: RNA polymerase-associated protein CTR9 homolog



ASP	GLU	L241	G181
ASP	GLY	E242	A182
LYS	GLY	L243	L183
LEU	GLY	N244	A184
ILE	GLY	N245	Y185
ALA	GLY	K246	Y186
ASP	SER	E247	K187
GLU	ASP	A248	K188
GLY	ASP	D249	A189
HIS	ASP	S250	L190
PRO	GLU	L251	R191
ARG	GLY	K252	T192
ASN	GLU	N253	N193
ASP	ASN	G254	P194
GLY	GLY	V255	G195
PRO	PRO	Q256	C196
ASN	PHE	L257	P197
VAL	VAL	L258	A198
ASP	ASN	S259	E199
ASP	ASP	R260	V200
ASP	ASP	A261	R201
GLN	ASP	Y262	L202
GLY	LEU	T263	G203
LEU	ALA	L264	M204
LEU	ALA	D265	G205
SER	ALA	P266	H206
ALA	ALA	S267	C207
SER	PRO	N268	F208
PRO	LYS	Y269	V209
PRO	ARG	M270	K210
PRO	ARG	V271	L211
LEU	LEU	L272	N212
LEU	GLY	N273	K213
GLN	GLY	H274	K214
ASN	ASN	F275	E215
ASN	ASN	A276	A216
ASN	MET	N277	A217
LEU	GLY	S278	R218
GLY	GLY	S279	L219
GLY	GLY	F280	A220
GLY	GLY	F281	F221
PRO	ILE	L282	S222
PRO	ARG	K283	R223
PRO	ARG	D284	A224
ARG	SER	Y285	L225
ARG	ASP	E286	E226
GLN	ASP	K287	L227
SER	SER	V288	N228
SER	SER	Q289	S229
SER	SER	H290	K230
SER	THR	L291	C231
THR	THR	V292	V232
GLU	THR	A293	G233
GLU	GLU	L294	G234
ALA	ALA	R295	L235
THR	THR	A295	L235
LYS	LYS	F296	V236
GLY	GLY	H297	G237
LYS	LYS	L298	L238
LYS	LYS	T299	A239
LYS	LYS	E300	V240
LYS	LYS	V301	V301
LYS	LYS	E302	E302
LEU	LYS	A303	A303
LYS	GLY	M304	M304
LEU	GLY	Q305	Q305
LEU	GLY	A306	A306
LEU	GLY	E307	E307
ALA	GLY	S308	S308
ALA	GLY	C309	C309
ALA	GLY	S310	S310
ASN	ASN	L312	L312
ASN	ASN	A313	A313
LEU	LEU	R314	R314
LEU	LEU	S315	S315
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ASP	ASP	H317	H317
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THR	THR	E320	E320
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ASP	ASP	V341	V341



● Molecule 21: WD repeat-containing protein 61



THR ASP ILE GLN VAL LYS VAL ARG ASP THR TYR LEU ASP THR GLN VAL VAL GLY GLN THR GLY VAL ILE ARG SER VAL THR GLY GLY MET CYS SER VAL TYR LEU LYS ASP SER GLU VAL VAL SER LYS ILE SER SER HIS LEU LEU PRO ILE THR PRO THR LYS ASN ASN VAL

LYS VAL ILE LEU GLY ASP ARG GLU ALA THR GLY VAL LEU LEU SER ILE ASP GLY GLU ASP GLY ILE VAL ARG MET ASP LEU ASP GLU GLN LEU LYS ILE LEU ASN LEU ARG PHE LEU GLY LYS LEU LEU GLU ALA

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	446195	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	130000	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.165	Depositor
Minimum map value	-0.086	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.022	Depositor
Map size (Å)	377.64, 377.64, 377.64	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.049, 1.049, 1.049	Depositor

5 Model quality i

5.1 Standard geometry i

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

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	1.40	97/11437 (0.8%)	0.89	18/15433 (0.1%)
2	B	1.63	126/9158 (1.4%)	0.97	28/12360 (0.2%)
3	C	1.77	44/2115 (2.1%)	0.96	7/2873 (0.2%)
4	D	0.42	0/1017	0.51	0/1368
5	E	1.29	10/1751 (0.6%)	0.81	1/2366 (0.0%)
6	F	1.69	9/636 (1.4%)	0.89	0/859
7	G	0.75	0/1364	0.62	0/1853
8	H	1.78	31/1219 (2.5%)	0.92	1/1644 (0.1%)
9	I	1.25	4/964 (0.4%)	0.79	0/1305
10	J	1.82	9/533 (1.7%)	1.03	3/719 (0.4%)
11	K	1.68	8/939 (0.9%)	0.92	2/1271 (0.2%)
12	L	1.57	5/395 (1.3%)	1.00	2/525 (0.4%)
13	M	0.26	0/4763	0.48	1/6084 (0.0%)
14	N	0.98	1/870 (0.1%)	0.87	1/1341 (0.1%)
15	P	1.34	3/506 (0.6%)	1.82	22/787 (2.8%)
16	Q	0.36	0/7365	0.51	0/9927
17	R	0.39	0/1860	0.56	2/2509 (0.1%)
18	T	1.68	11/1087 (1.0%)	1.13	6/1674 (0.4%)
19	U	0.34	0/864	0.58	2/1173 (0.2%)
20	V	0.32	0/1728	0.52	2/2357 (0.1%)
21	W	0.37	0/2392	0.53	0/3257
22	X	0.34	0/356	0.52	0/478
23	Y	0.27	0/927	0.48	0/1250
24	Z	0.45	0/4081	0.55	1/5493 (0.0%)
All	All	1.15	358/58327 (0.6%)	0.79	99/78906 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
2	B	0	3
17	R	0	1
All	All	0	6

The worst 5 of 358 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	791	GLU	CA-CB	-15.42	1.20	1.53
2	B	94	SER	C-N	-11.45	1.07	1.34
8	H	116	VAL	CB-CG1	-9.52	1.32	1.52
2	B	690	CYS	CB-SG	-8.84	1.67	1.82
2	B	1047	TYR	CD1-CE1	-8.57	1.26	1.39

The worst 5 of 99 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	P	40	A	C8-N9-C4	-13.77	100.29	105.80
15	P	40	A	N7-C8-N9	12.63	120.11	113.80
15	P	41	C	C6-N1-C2	-11.07	115.87	120.30
3	C	224	GLY	C-N-CA	10.22	147.25	121.70
15	P	40	A	C5-N7-C8	-9.32	99.24	103.90

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1434	GLU	Peptide
1	A	910	LYS	Peptide
2	B	20	ASP	Peptide
2	B	547	GLU	Peptide
2	B	686	GLU	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	11255	0	11374	435	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	8980	0	9017	295	0
3	C	2072	0	2019	45	0
4	D	1004	0	980	55	0
5	E	1720	0	1737	73	0
6	F	626	0	657	11	0
7	G	1333	0	1321	80	0
8	H	1197	0	1156	44	0
9	I	942	0	873	38	0
10	J	524	0	541	19	0
11	K	920	0	942	28	0
12	L	390	0	397	13	0
13	M	4737	0	2262	46	0
14	N	773	0	412	38	0
15	P	452	0	229	24	0
16	Q	7226	0	7169	355	0
17	R	1832	0	1687	114	0
18	T	974	0	541	39	0
19	U	852	0	668	31	0
20	V	1703	0	1426	85	0
21	W	2333	0	2246	155	0
22	X	353	0	371	28	0
23	Y	911	0	908	27	0
24	Z	4023	0	4035	181	0
25	A	2	0	0	0	0
25	B	1	0	0	0	0
25	C	1	0	0	0	0
25	I	2	0	0	0	0
25	J	1	0	0	0	0
25	L	1	0	0	0	0
25	Y	1	0	0	0	0
26	A	1	0	0	0	0
All	All	57142	0	52968	2040	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 19.

The worst 5 of 2040 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)
8:H:37:MET:HE2	8:H:127:GLY:HA3	1.42	0.99
2:B:953:ASP:OD1	3:C:36:ARG:NH2	1.96	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:609:HIS:HD1	1:A:626:THR:HG1	1.04	0.94
16:Q:505:ARG:HH21	20:V:44:PHE:HB2	1.32	0.93
1:A:904:GLN:NE2	1:A:981:CYS:O	2.01	0.91

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	1408/1984 (71%)	1281 (91%)	117 (8%)	10 (1%)	22	57
2	B	1112/1251 (89%)	998 (90%)	105 (9%)	9 (1%)	19	54
3	C	254/275 (92%)	232 (91%)	19 (8%)	3 (1%)	13	44
4	D	124/142 (87%)	118 (95%)	6 (5%)	0	100	100
5	E	207/210 (99%)	199 (96%)	7 (3%)	1 (0%)	29	64
6	F	76/127 (60%)	70 (92%)	6 (8%)	0	100	100
7	G	169/172 (98%)	157 (93%)	12 (7%)	0	100	100
8	H	147/150 (98%)	130 (88%)	16 (11%)	1 (1%)	22	57
9	I	114/125 (91%)	104 (91%)	10 (9%)	0	100	100
10	J	64/67 (96%)	60 (94%)	2 (3%)	2 (3%)	4	23
11	K	113/117 (97%)	107 (95%)	6 (5%)	0	100	100
12	L	45/58 (78%)	39 (87%)	6 (13%)	0	100	100
13	M	976/1729 (56%)	903 (92%)	72 (7%)	1 (0%)	51	83
16	Q	888/1179 (75%)	836 (94%)	52 (6%)	0	100	100
17	R	240/713 (34%)	225 (94%)	14 (6%)	1 (0%)	34	69
19	U	117/666 (18%)	88 (75%)	21 (18%)	8 (7%)	1	7
20	V	234/531 (44%)	199 (85%)	31 (13%)	4 (2%)	9	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	W	298/305 (98%)	268 (90%)	30 (10%)	0	100	100
22	X	41/531 (8%)	41 (100%)	0	0	100	100
23	Y	114/121 (94%)	109 (96%)	5 (4%)	0	100	100
24	Z	497/1087 (46%)	460 (93%)	36 (7%)	1 (0%)	47	79
All	All	7238/11540 (63%)	6624 (92%)	573 (8%)	41 (1%)	29	59

5 of 41 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	540	ASP
1	A	1185	VAL
1	A	1468	THR
2	B	19	PRO
3	C	93	PHE

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1245/1761 (71%)	1226 (98%)	19 (2%)	65	85
2	B	986/1084 (91%)	949 (96%)	37 (4%)	33	66
3	C	235/252 (93%)	228 (97%)	7 (3%)	41	71
4	D	109/126 (86%)	108 (99%)	1 (1%)	78	91
5	E	191/192 (100%)	189 (99%)	2 (1%)	76	90
6	F	68/111 (61%)	67 (98%)	1 (2%)	65	85
7	G	146/153 (95%)	143 (98%)	3 (2%)	53	79
8	H	130/131 (99%)	122 (94%)	8 (6%)	18	49
9	I	104/112 (93%)	101 (97%)	3 (3%)	42	72
10	J	55/56 (98%)	54 (98%)	1 (2%)	59	82
11	K	104/106 (98%)	103 (99%)	1 (1%)	76	90
12	L	43/55 (78%)	40 (93%)	3 (7%)	15	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	M	154/1524 (10%)	154 (100%)	0	100	100
16	Q	761/1011 (75%)	755 (99%)	6 (1%)	81	92
17	R	168/625 (27%)	166 (99%)	2 (1%)	71	88
19	U	63/590 (11%)	63 (100%)	0	100	100
20	V	144/462 (31%)	141 (98%)	3 (2%)	53	79
21	W	255/260 (98%)	254 (100%)	1 (0%)	91	96
22	X	40/467 (9%)	40 (100%)	0	100	100
23	Y	102/105 (97%)	102 (100%)	0	100	100
24	Z	434/939 (46%)	432 (100%)	2 (0%)	88	94
All	All	5537/10122 (55%)	5437 (98%)	100 (2%)	61	82

5 of 100 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	63	PHE
8	H	67	ASP
24	Z	720	TYR
3	C	75	SER
5	E	117	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 98 such sidechains are listed below:

Mol	Chain	Res	Type
16	Q	359	ASN
16	Q	887	ASN
16	Q	407	GLN
16	Q	585	GLN
17	R	585	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
15	P	20/46 (43%)	7 (35%)	3 (15%)

5 of 7 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
15	P	28	A
15	P	29	C
15	P	30	C
15	P	31	G
15	P	36	G

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
15	P	28	A
15	P	36	G
15	P	38	G

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

3 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	TPO	Z	775	24	8,10,11	1.54	1 (12%)	10,14,16	1.99	1 (10%)
1	TPO	A	1525	1	8,10,11	1.60	1 (12%)	10,14,16	1.83	1 (10%)
1	SEP	A	1547	1	8,9,10	1.49	1 (12%)	8,12,14	1.39	2 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	TPO	Z	775	24	-	1/9/11/13	-
1	TPO	A	1525	1	-	4/9/11/13	-
1	SEP	A	1547	1	-	0/5/8/10	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1525	TPO	P-O1P	3.41	1.61	1.50
24	Z	775	TPO	P-O1P	3.34	1.61	1.50
1	A	1547	SEP	P-O1P	3.25	1.61	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	Z	775	TPO	P-OG1-CB	-5.85	105.53	123.21
1	A	1525	TPO	P-OG1-CB	-4.96	108.22	123.21
1	A	1547	SEP	P-OG-CB	-2.69	110.89	118.30
1	A	1547	SEP	OG-CB-CA	2.01	110.10	108.14

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1525	TPO	N-CA-CB-CG2
1	A	1525	TPO	N-CA-CB-OG1
1	A	1525	TPO	C-CA-CB-CG2
24	Z	775	TPO	C-CA-CB-CG2
1	A	1525	TPO	O-C-CA-CB

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	Z	775	TPO	2	0
1	A	1525	TPO	1	0
1	A	1547	SEP	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	3
19	U	1
20	V	1
13	M	1
1	A	1

The worst 5 of 7 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	U	497:ASP	C	505:SER	N	25.86
1	V	299:GLU	C	310:ASN	N	12.74
1	M	1334:ASN	C	1338:ILE	N	5.29
1	B	755:GLN	C	756:LYS	N	1.18
1	B	108:MET	C	109:MET	N	1.17

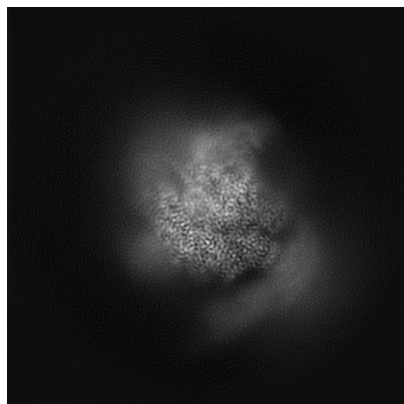
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10480. These allow visual inspection of the internal detail of the map and identification of artifacts.

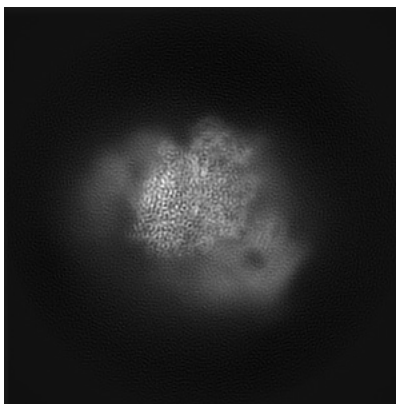
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

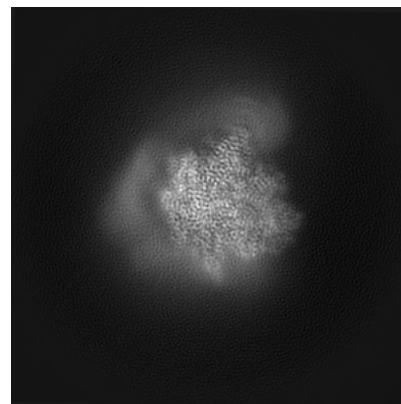
6.1.1 Primary map



X

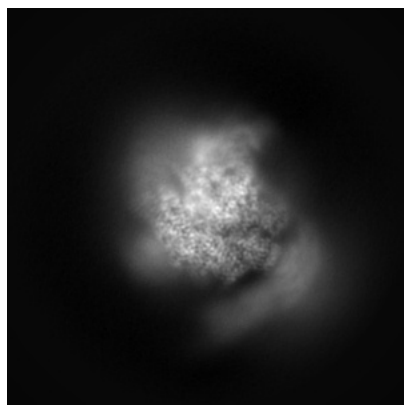


Y

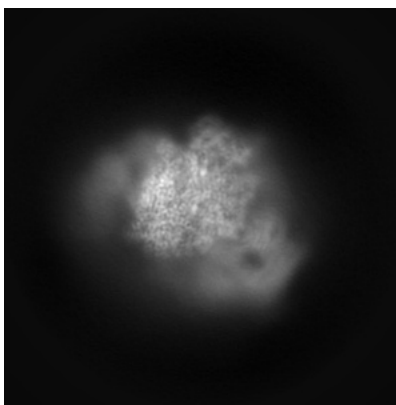


Z

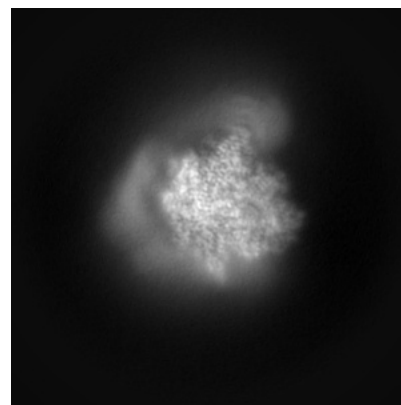
6.1.2 Raw map



X



Y

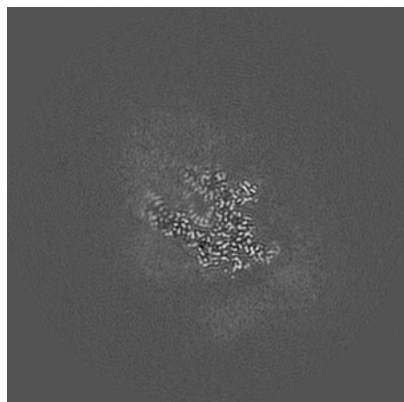


Z

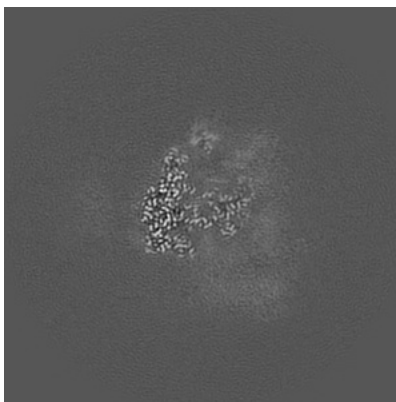
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

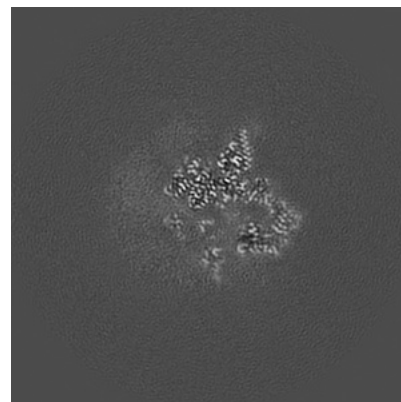
6.2.1 Primary map



X Index: 180

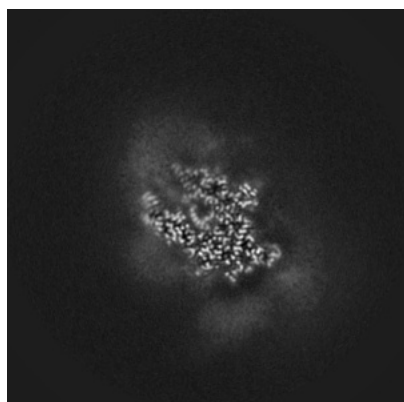


Y Index: 180

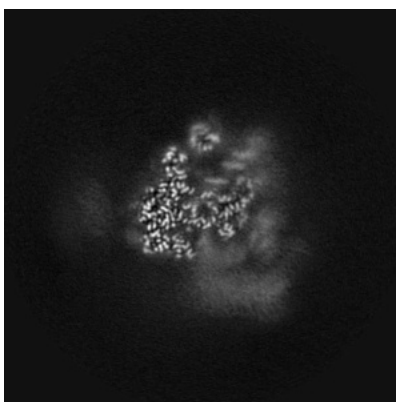


Z Index: 180

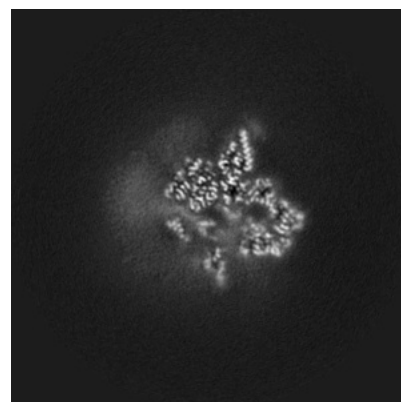
6.2.2 Raw map



X Index: 180



Y Index: 180

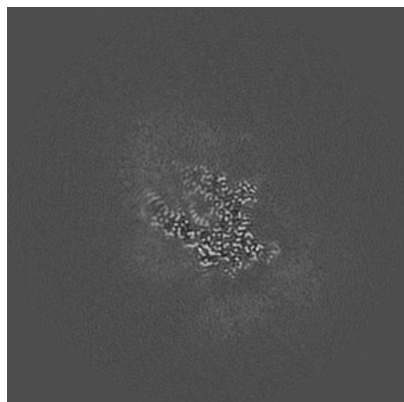


Z Index: 180

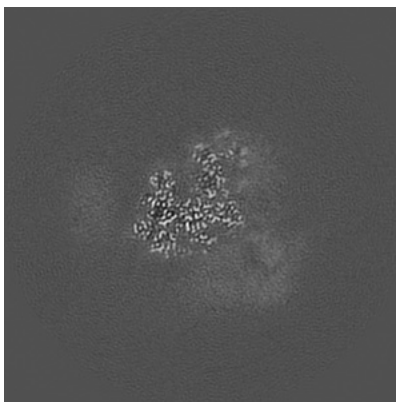
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

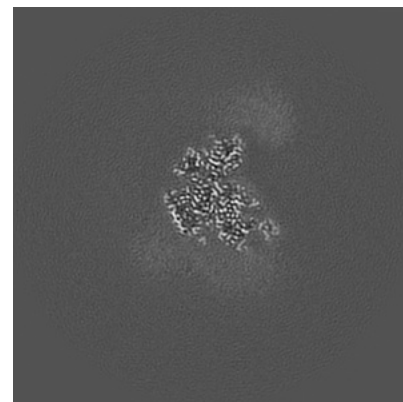
6.3.1 Primary map



X Index: 179

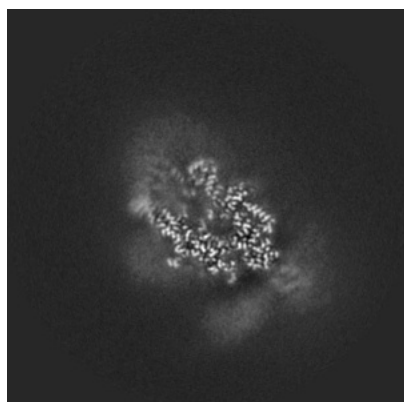


Y Index: 193

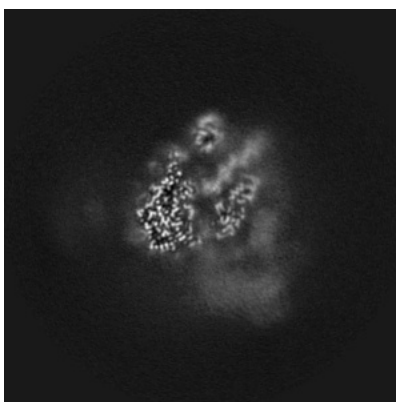


Z Index: 143

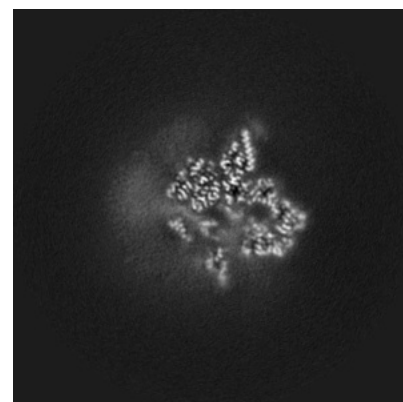
6.3.2 Raw map



X Index: 189



Y Index: 174

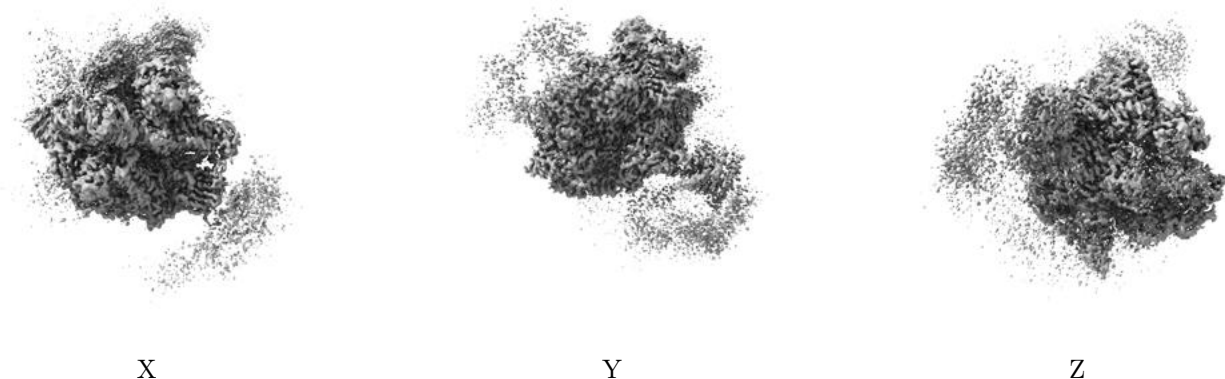


Z Index: 180

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

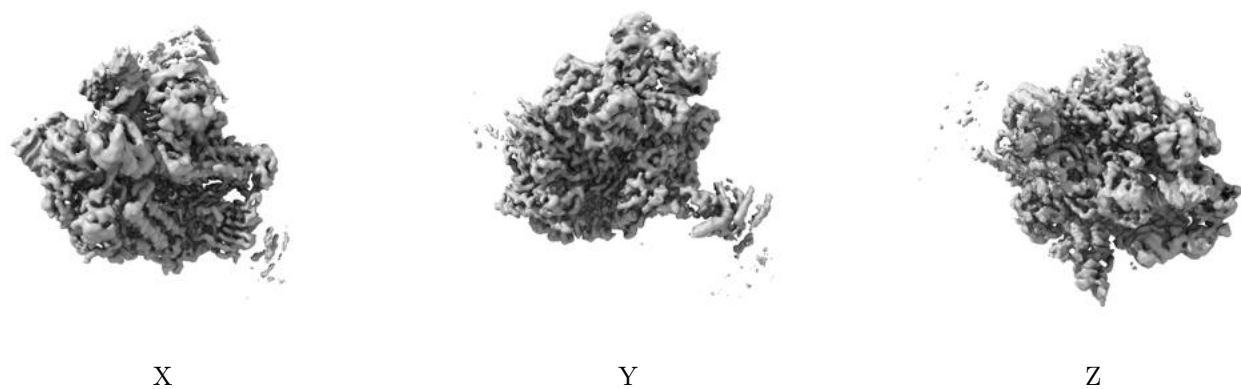
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.022. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

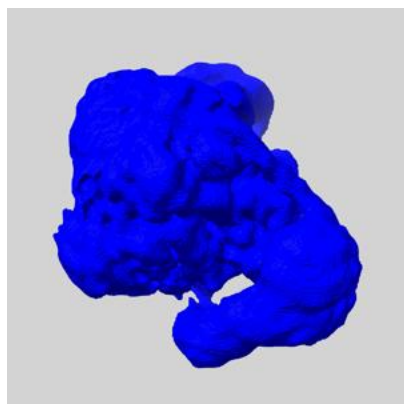
6.5 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

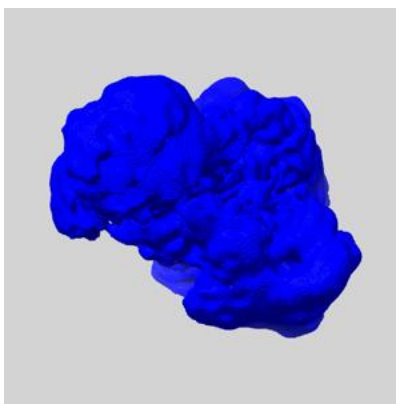
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

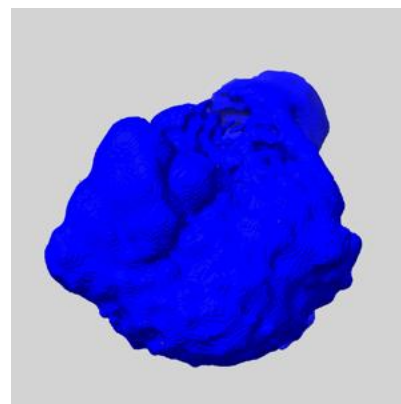
6.5.1 emd_10480_msk_1.map [i](#)



X

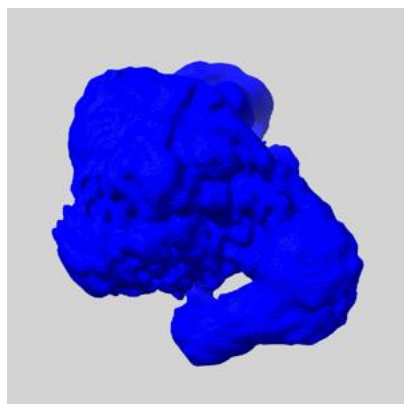


Y

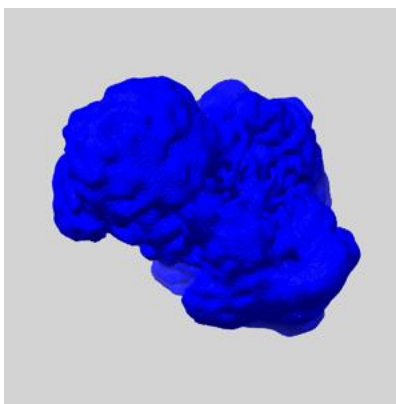


Z

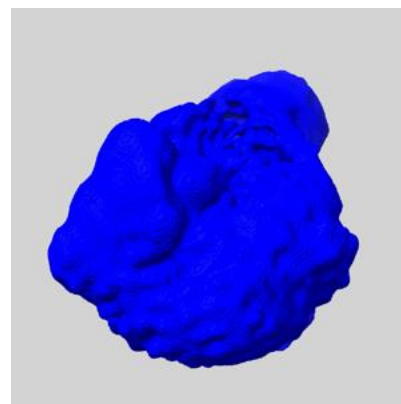
6.5.2 emd_10480_msk_2.map [i](#)



X



Y

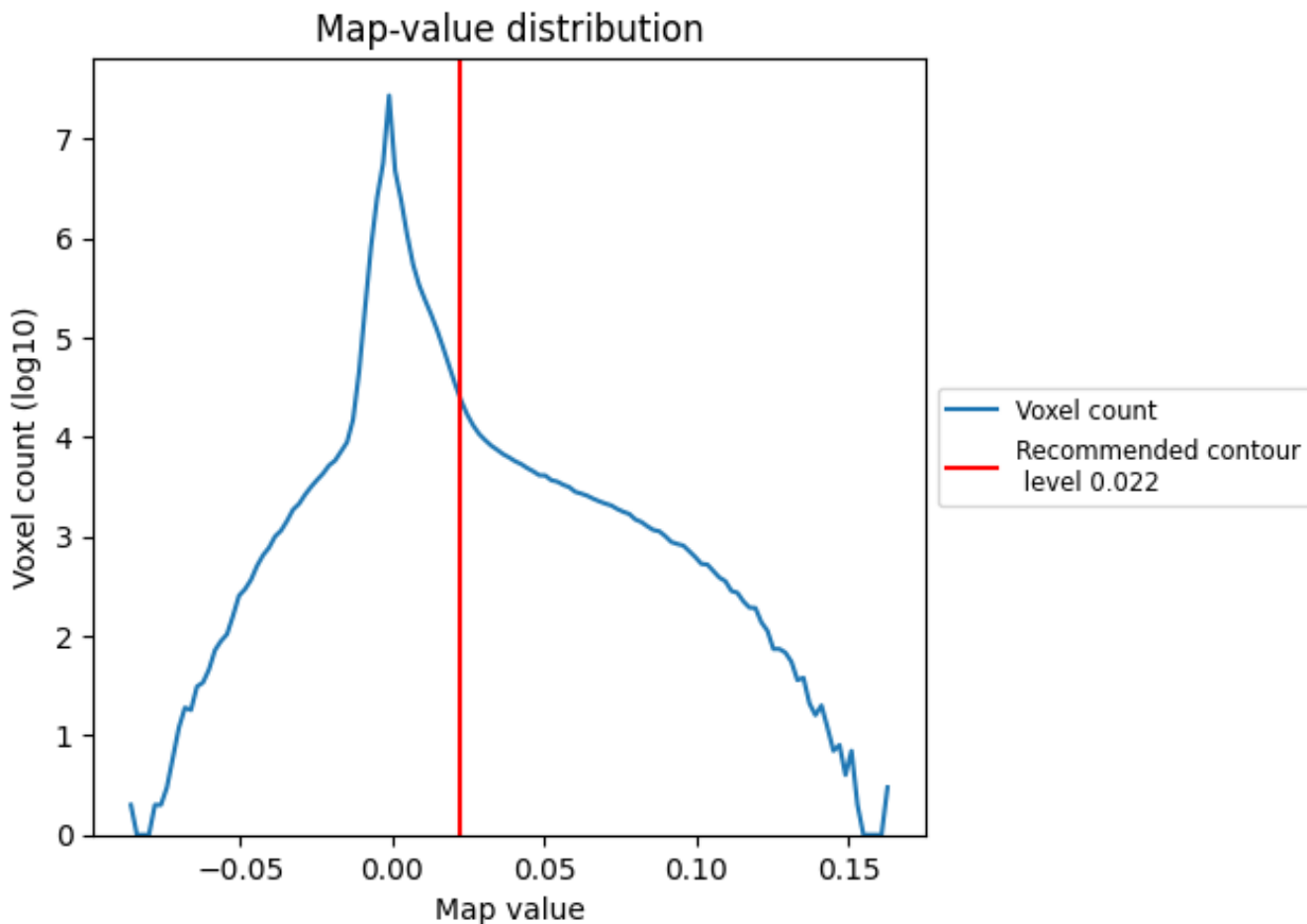


Z

7 Map analysis [i](#)

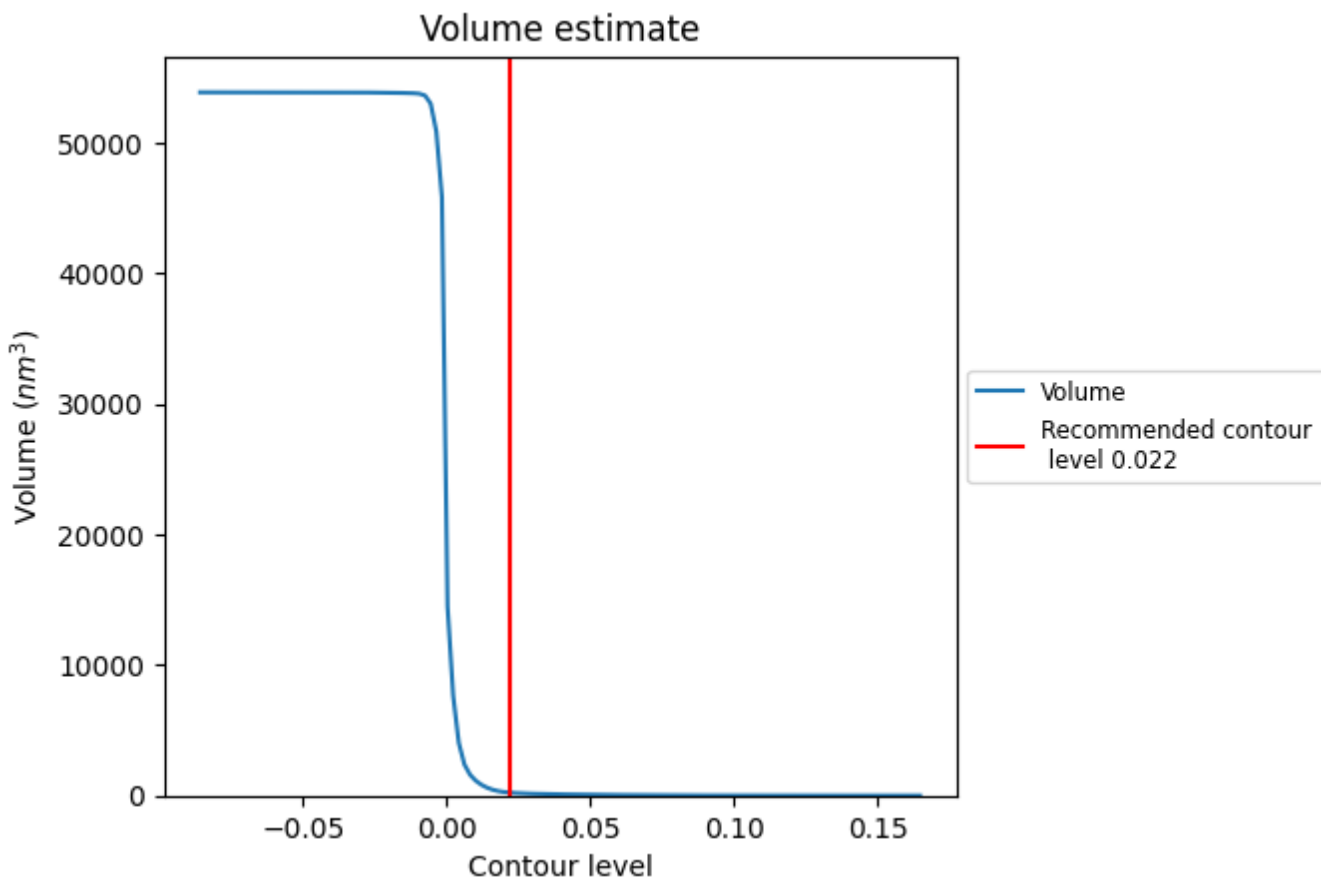
This section contains the results of statistical analysis of the map.

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.

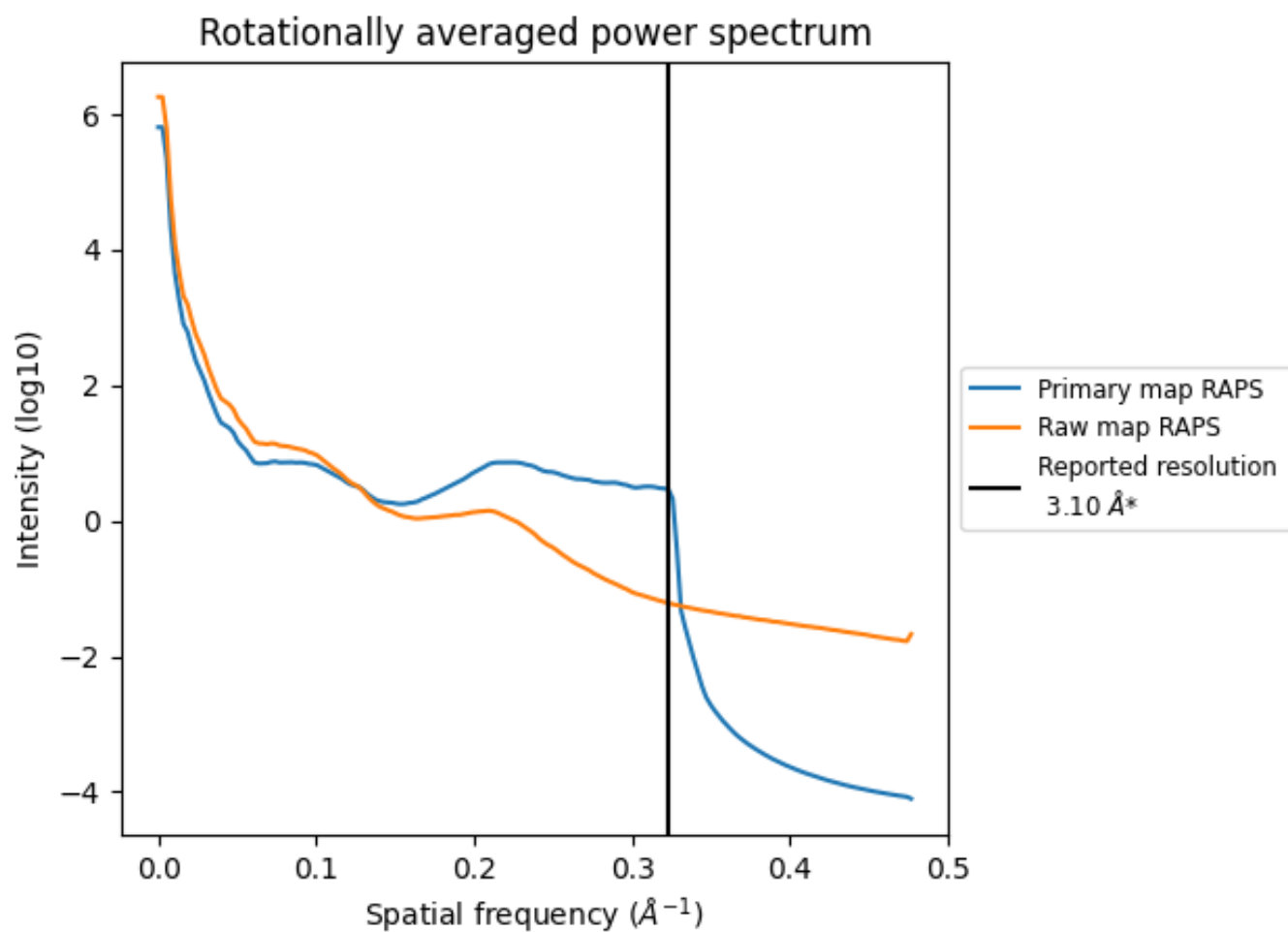
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 223 nm³; this corresponds to an approximate mass of 202 kDa.

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

7.3 Rotationally averaged power spectrum i

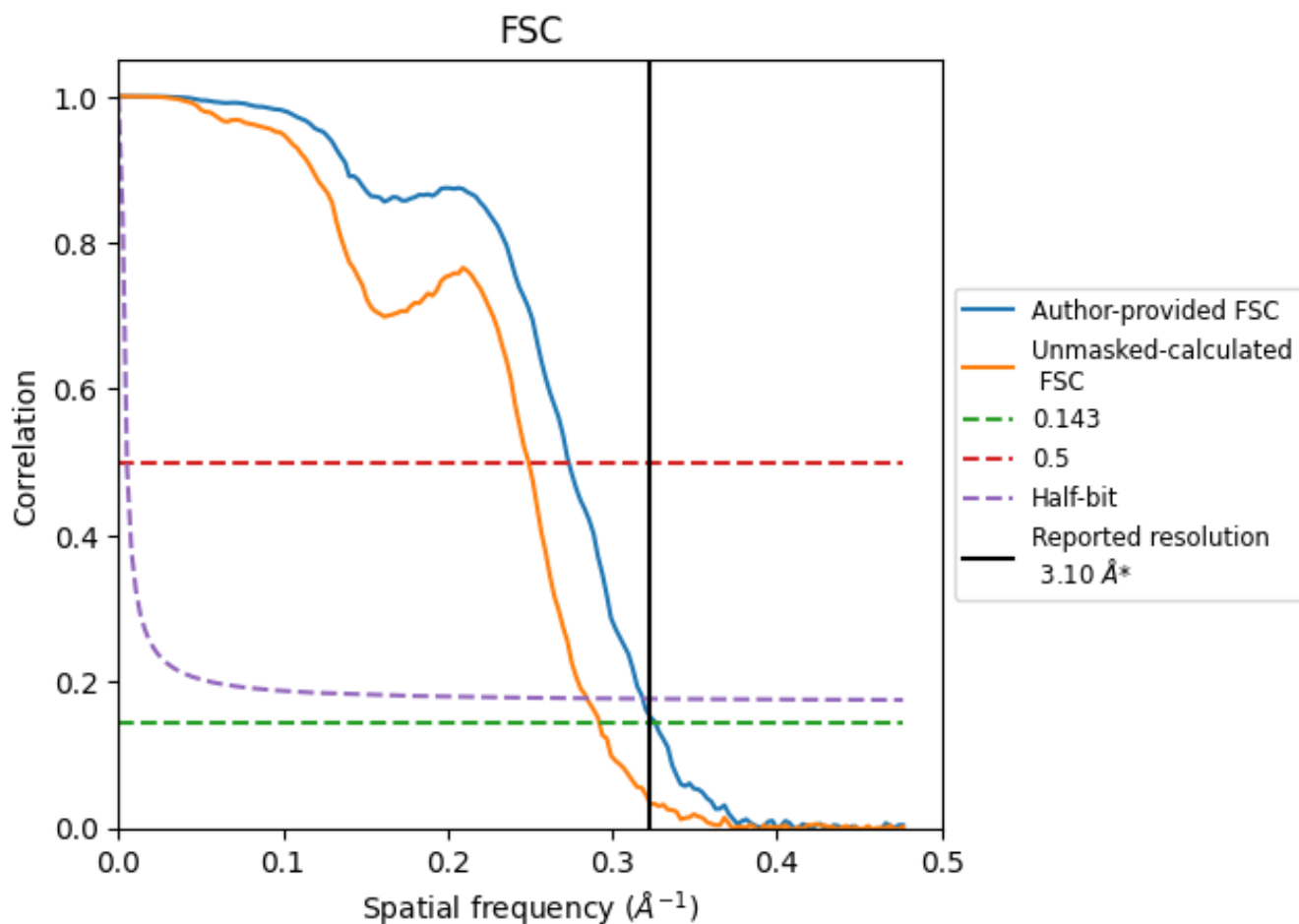


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

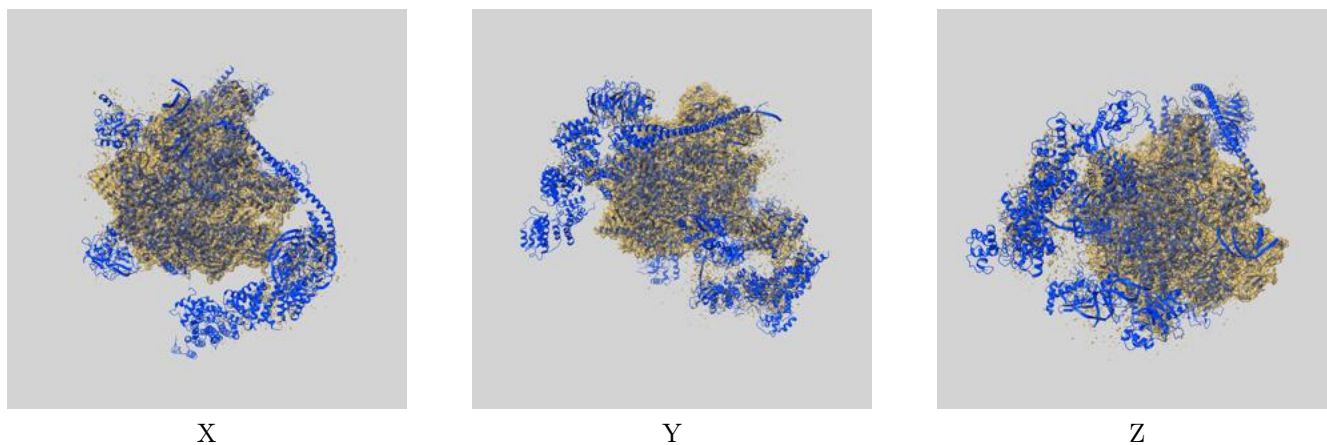
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.07	3.66	3.14
Unmasked-calculated*	3.42	4.01	3.51

*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 3.42 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

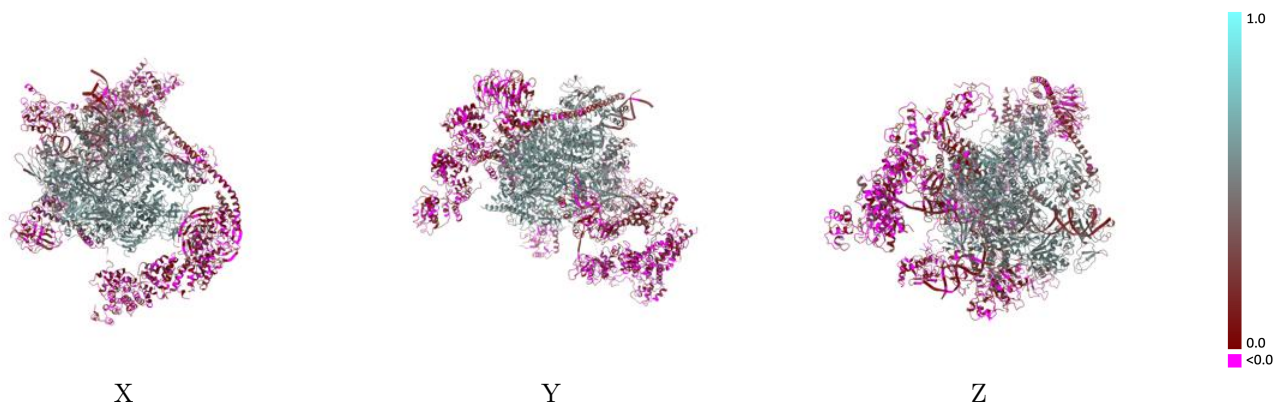
This section contains information regarding the fit between EMDB map EMD-10480 and PDB model 6TED. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)



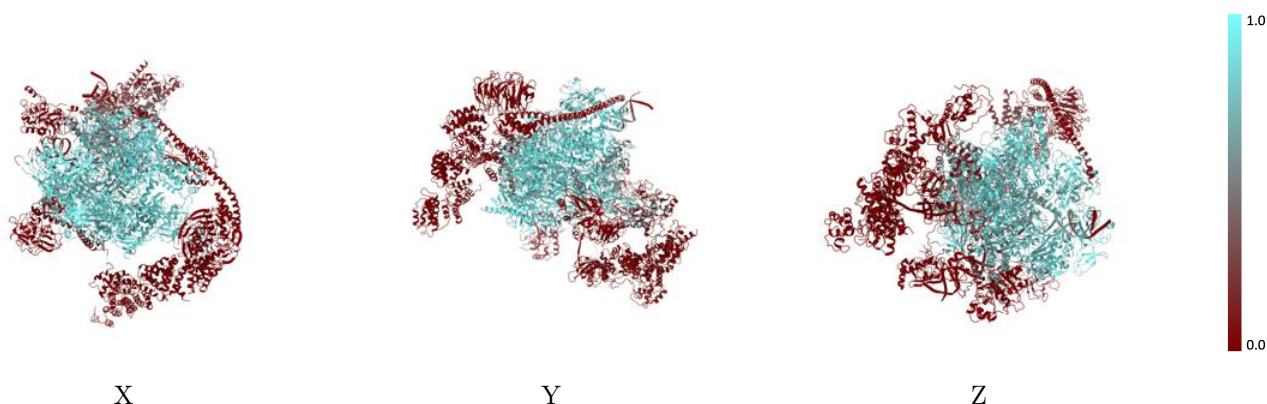
The images above show the 3D surface view of the map at the recommended contour level 0.022 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



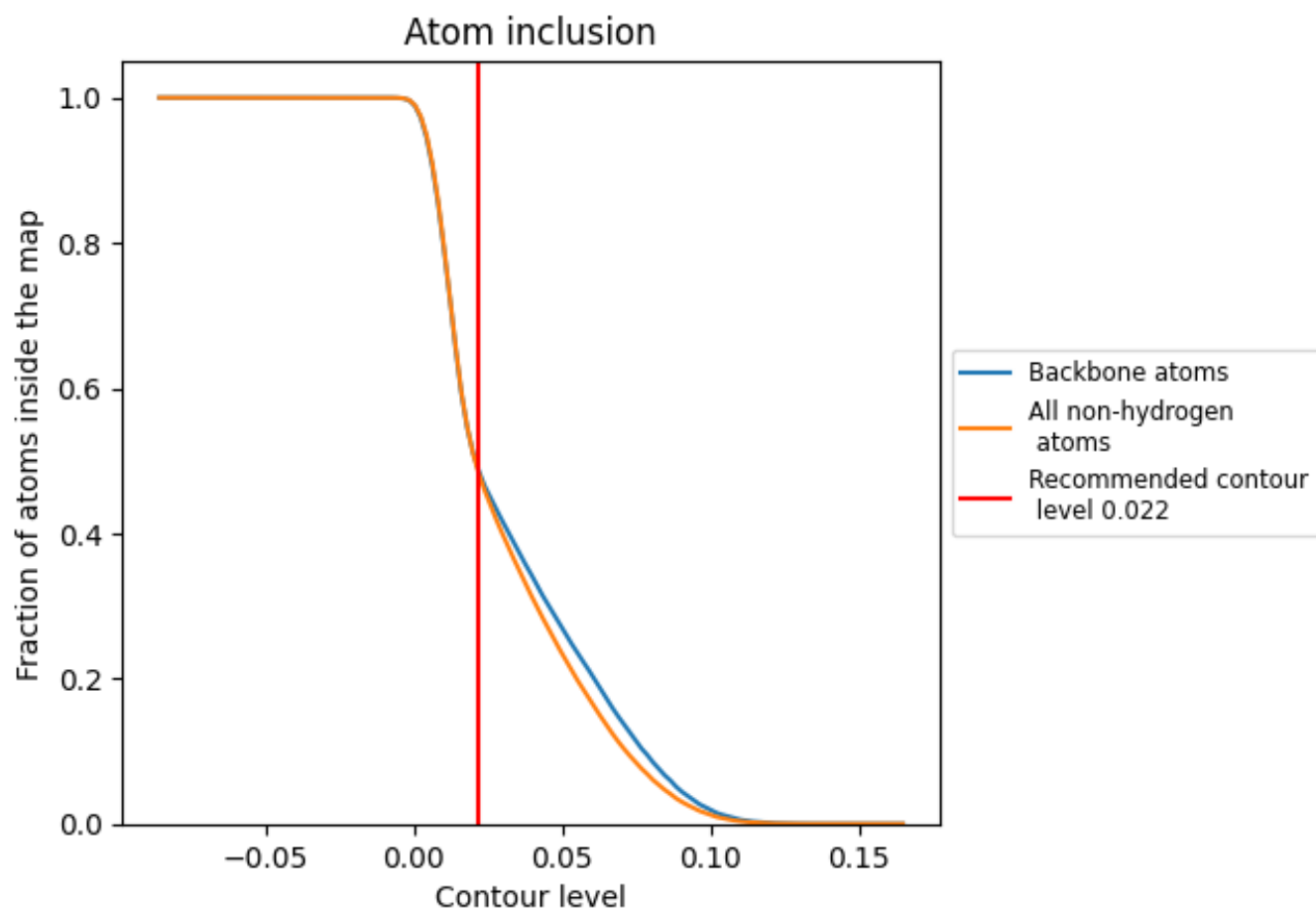
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.022).



















































9.4 Atom inclusion [i](#)



At the recommended contour level, 48% of all backbone atoms, 48% 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 (0.022) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4806	 0.3380
A	 0.8491	 0.5370
B	 0.8820	 0.5560
C	 0.9108	 0.5800
D	 0.2725	 0.1850
E	 0.8535	 0.5210
F	 0.8962	 0.5740
G	 0.4391	 0.3110
H	 0.8513	 0.5590
I	 0.8472	 0.5110
J	 0.9180	 0.5730
K	 0.9211	 0.5890
L	 0.8480	 0.5090
M	 0.0153	 0.0750
N	 0.3467	 0.2200
P	 0.4248	 0.2780
Q	 0.0282	 0.1020
R	 0.0117	 0.0880
T	 0.5195	 0.3100
U	 0.0548	 0.1140
V	 0.0256	 0.1270
W	 0.0109	 0.0430
X	 0.0235	 0.1060
Y	 0.0056	 0.0770
Z	 0.0993	 0.1660

