



wwPDB EM Validation Summary Report ⓘ

Oct 13, 2024 – 08:37 am BST

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, 6AFO, 6GMH

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.dev113
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

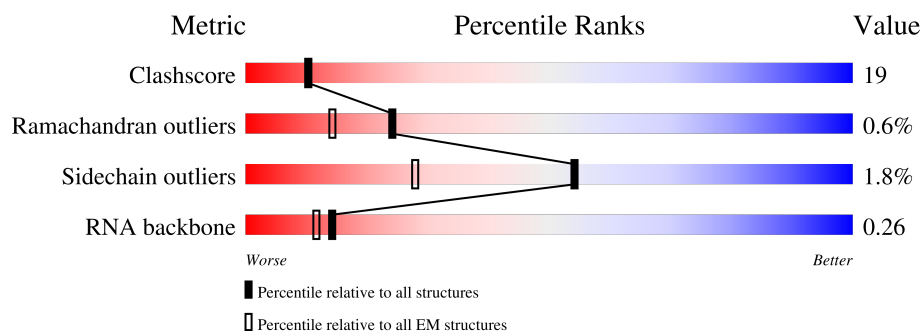
1 Overall quality at a glance

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.





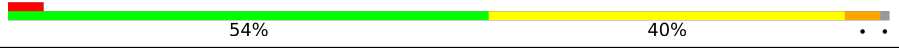

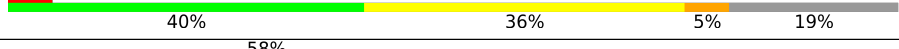

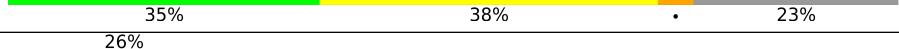

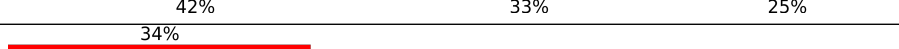
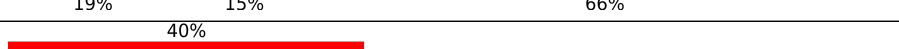


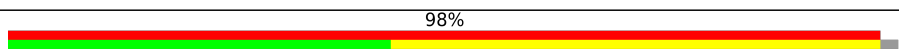

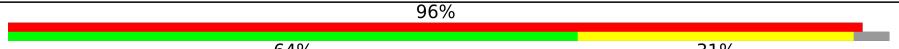


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

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
1	A	1426	Total	C	N	O	P	S	
			11255	7074	2014	2095	2	70	0

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	171	Total	C	N	O	S	0	0
			1333	866	214	245	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	149	Total	C	N	O	S	0	0
			1197	759	195	238	5		

- 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
			942	582	168	181	11		

- Molecule 10 is a protein called Uncharacterized protein.

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

- Molecule 11 is a protein called Uncharacterized protein.

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

- Molecule 12 is a protein called Uncharacterized protein.

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

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

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

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
14	N	37	Total	C	N	O	P	0	0
			773	361	158	217	37		

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

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

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

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

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
17	R	244	Total	C	N	O	S	0	0
			1832	1148	340	337	7		

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
18	T	48	Total	C	N	O	P	0	0
			974	462	168	296	48		

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

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

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

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

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

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

- Molecule 22 is a protein called Parafibromin.

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

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

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

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
24	Z	510	Total	C	N	O	P	S	0	0
			4023	2550	709	745	1	18		

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

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

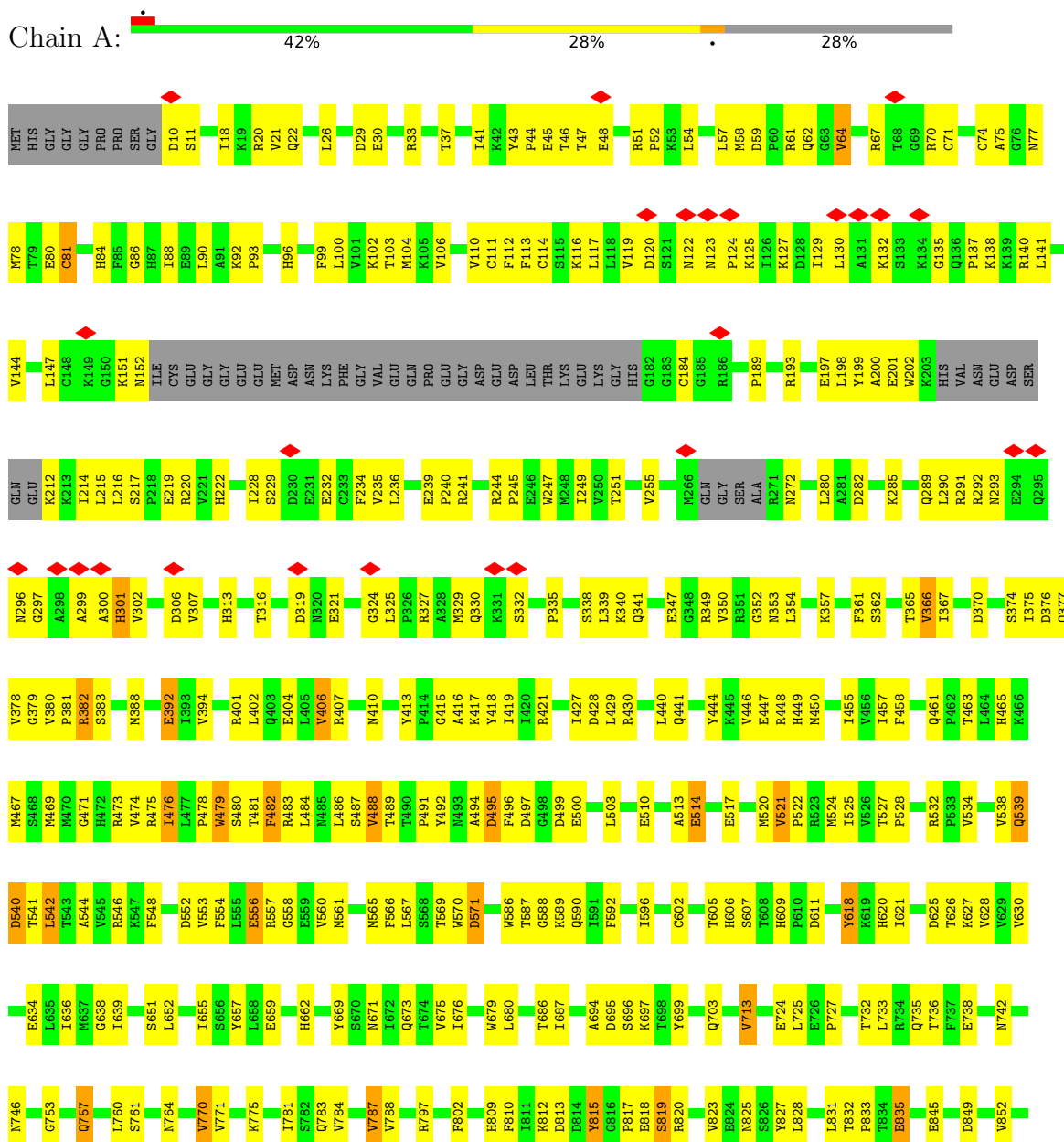
- Molecule 26 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
26	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 subunit

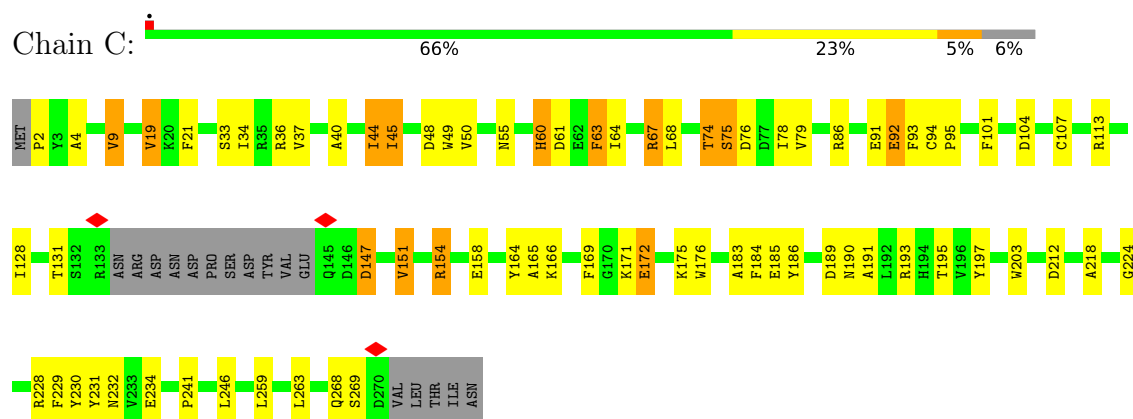




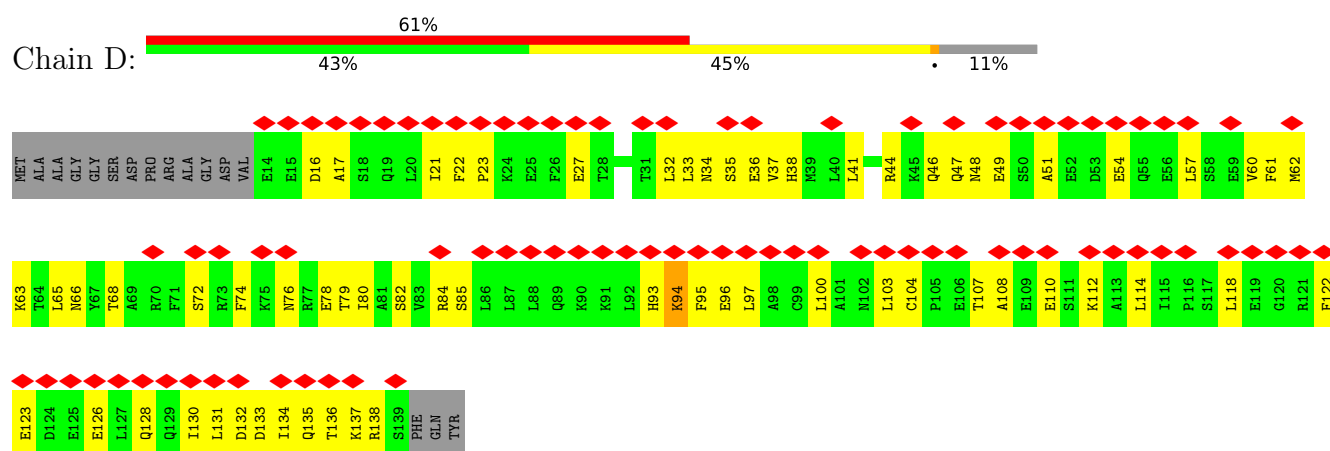
Chain B: 

MET	VAL	GLN	K146	ALA	A339	F544	L634	P720	F810	S899	D1004	M1125
CYS	SER	ALA	T147	LYS	V342	L545	R638	R721	Y811	E900	A1005	N1129
THR	VAL	GLN	F148	SER	E346	E546	R639	M728	Y814	T901	M1006	T1130
LEU	ASN	HIS	P153	ALA	K347	W548	L643	Q731	E815	V904	M1007	R1131
SER	LEU	ALA	I154	G253	L348	E551	R646	V735	Q816	V907	I1010	T1134
GLN	ARG	ALA	M155	Q254	F349	R552	E647	Y736	R821	T910	L1014	Y1135
LEU	ARG	SER	L156	R255	K350	L553	E648	T737	G822	L911	L1015	E1136
ALA	GLY	GLY	R157	Q256	V351	E556	R649	T738	F823	N912	L1016	N1142
LEU	GLY	GLY	S158	T259	Q352	S557	R650	W739	F824	F918	Y1018	K1143
ALA	ALA	GLU	T159	V267	S354	P558	W651	H740	D824	C919	G1019	T1144
THR	PRO	GLU	L163	F273	D355	R559	S652	V742	R834	R920	H1021	T1145
PHE	GLY	SER	M164	G279	F356	A559	D655	W743	E835	I921	L1022	L1148
ARG	SER	CYS	G165	V279	C357	T565	S659	R744	R841	R922	R1023	V1149
ALA	ALA	CYS	L166	W280	K359	T567	G660	W745	H842	V923	R1024	R1150
ALA	ASN	ASN	R83	S280	T359	I567	V661	P754	R847	R924	V1027	M1151
ALA	ASN	ASN	Y84	L86	K360	F568	V662	Q755	L848	S925	L1028	P1152
LEU	LEU	THR	L86	D281	K361	F569	E661	W756	D851	V926	Y1029	Y1153
THR	THR	ASP	D170	T284	Y367	W573	V662	Y757	R859	I931	T1038	K1156
ALA	ALA	ALA	E176	L285	L472	V574	E663	Y758	R860	G932	Q1039	L1157
ALA	ASP	ASP	C177	L285	R473	V575	E664	Y759	R861	G933	Q1040	E1161
ALA	GLU	GLU	P178	L285	L473	G575	E665	Y760	R862	H934	Y1047	M1171
LEU	LEU	ASP	L179	L285	L473	G576	E666	Y761	R863	G935	Y1048	M1172
TRP	TRP	MET	D180	L285	L473	G577	E667	Y762	R864	D936	Q1049	S1173
ALA	ALA	GLN	Y184	L285	L473	G578	E668	Y763	R865	K941	R1062	V1174
GLY	THR	TYR	F185	L285	L473	G579	E669	Y764	R866	K942	G1065	
PHE	PHE	ASP	I187	L285	L473	G580	E670	Y765	R867	C945	G1066	
ARG	ARG	ASP	I187	L285	L473	G581	E671	Y766	R868	C946	M1071	
ARG	ARG	ASP	E191	L285	L473	G582	E672	Y767	R869	C947	R1072	
LYS	LYS	ASP	K192	L285	L473	G583	E673	Y768	R870	C948	Q1073	
LYS	LYS	ASP	V193	L285	L473	G584	E674	Y769	R871	C949	P1074	
SER	SER	ASP	E198	L285	L473	G585	E675	Y770	R872	C950	E1088	
LEU	LEU	ASP	K199	L285	L473	G586	E676	Y771	R873	C951	C1093	
CYS	CYS	ASP	D211	L285	L473	G587	E677	Y772	R874	C952	Q1101	
LEU	LEU	ASP	D212	L285	L473	G588	E678	Y773	R875	C953	R1104	
ALA	ALA	ASP	T218	L285	L473	G589	E679	Y774	R876	C954	E1105	
LEU	LEU	ASP	R222	L285	L473	G590	E680	Y775	R877	C955	F1108	
LEU	LEU	ASP	R223	L285	L473	G591	E681	Y776	R878	C956	D1112	
LEU	LEU	ASP	S228	L285	L473	G592	E682	Y777	R879	C957	Q1115	
ARG	ARG	ASP	S229	L285	L473	G593	E683	Y778	R880	C958	Q1116	
PRO	PRO	ASP	R230	L285	L473	G594	E684	Y779	R881	C959	H1117	
GLY	GLY	ASP	E135	L285	L473	G595	E685	Y780	R882	C960	V1118	
GLY	GLY	ASP	G136	L285	L473	G596	E686	Y781	R883	C961	M1119	
ALA	ALA	ASP	E137	L285	L473	G597	E687	Y782	R884	C962	N1120	
CYS	CYS	ASP	E138	L285	L473	G598	E688	Y783	R885	C963		
TRP	TRP	ASP	Q139	L285	L473	G599	E689	Y784	R886	C964		
ARG	ARG	ASP	L140	L285	L473	G600	E690	Y785	R887	C965		
TRP	TRP	ASP	E141	L285	L473	G601	E691	Y786	R888	C966		
LEU	LEU	ASP	Q142	L285	L473	G602	E692	Y787	R889	C967		
ALA	ALA	ASP	Q143	L285	L473	G603	E693	Y788	R890	C968		
ALA	ALA	ASP	Q144	L285	L473	G604	E694	Y789	R891	C969		
ALA	ALA	ASP	Q145	L285	L473	G605	E695	Y790	R892	C970		
		ASP		L285	L473	G606	E696	Y791	R893	C971		
		ASP		L285	L473	G607	E697	Y792	R894	C972		
		ASP		L285	L473	G608	E698	Y793	R895	C973		
		ASP		L285	L473	G609	E699	Y794	R896	C974		
		ASP		L285	L473	G610	E700	Y795	R897	C975		
		ASP		L285	L473	G611	E701	Y796	R898	C976		
		ASP		L285	L473	G612	E702	Y797	R899	C977		
		ASP		L285	L473	G613	E703	Y798	R900	C978		
		ASP		L285	L473	G614	E704	Y799	R901	C979		
		ASP		L285	L473	G615	E705	Y800	R902	C980		
		ASP		L285	L473	G616	E706	Y801	R903	C981		
		ASP		L285	L473	G617	E707	Y802	R904	C982		
		ASP		L285	L473	G618	E708	Y803	R905	C983		
		ASP		L285	L473	G619	E709	Y804	R906	C984		
		ASP		L285	L473	G620	E710	Y805	R907	C985		
		ASP		L285	L473	G621	E711	Y806	R908	C986		
		ASP		L285	L473	G622	E712	Y807	R909	C987		
		ASP		L285	L473	G623	E713	Y808	R910	C988		
		ASP		L285	L473	G624	E714	Y809	R911	C989		
		ASP		L285	L473	G625	E715	Y810	R912	C990		
		ASP		L285	L473	G626	E716	Y811	R913	C991		
		ASP		L285	L473	G627	E717	Y812	R914	C992		
		ASP		L285	L473	G628	E718	Y813	R915	C993		
		ASP		L285	L473	G629	E719	Y814	R916	C994		
		ASP		L285	L473	G630	E720	Y815	R917	C995		
		ASP		L285	L473	G631	E721	Y816	R918	C996		
		ASP		L285	L473	G632	E722	Y817	R919	C997		
		ASP		L285	L473	G633	E723	Y818	R920	C998		
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		ASP		L285	L473	G635	E725	Y820	R922	C1000		
		ASP		L285	L473	G636	E726	Y821	R923	C1001		
		ASP		L285	L473	G637	E727	Y822	R924	C1002		
		ASP		L285	L473	G638	E728	Y823	R925	C1003		
		ASP		L285	L473	G639	E729	Y824	R926	C1004		
		ASP		L285	L473	G640	E730	Y825	R927	C1005		
		ASP		L285	L473	G641	E731	Y826	R928	C1006		
		ASP		L285	L473	G642	E732	Y827	R929	C1007		
		ASP		L285	L473	G643	E733	Y828	R930	C1008		
		ASP		L285	L473	G644	E734	Y829	R931	C1009		
		ASP		L285	L473	G645	E735	Y830	R932	C1010		
		ASP		L285	L473	G646	E736	Y831	R933	C1011		
		ASP		L285	L473	G647	E737	Y832	R934	C1012		
		ASP		L285	L473	G648	E738	Y833	R935	C1013		
		ASP		L285	L473	G649	E739	Y834	R936	C1014		
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		ASP		L285	L473	G654	E744	Y839	R941	C1019		
		ASP		L285	L473	G655	E745	Y840	R942	C1020		
		ASP		L285	L473	G656	E746	Y841	R943	C1021		
		ASP		L285	L473	G657	E747	Y842	R944	C1022		
		ASP		L285	L473	G658	E748	Y843	R945	C1023		
		ASP		L285	L473	G659	E749	Y844	R946	C1024		
		ASP		L285	L473	G660	E750	Y845	R947	C1025		
		ASP		L285	L473	G661	E751	Y846	R948	C1026		
		ASP		L285	L473	G662	E752	Y847	R949	C1027		
		ASP		L285	L473	G663	E753	Y848	R950	C1028		
		ASP		L285	L473	G664	E754	Y849	R951	C1029		
		ASP		L285	L473	G665	E755	Y850	R952	C1030		
		ASP		L285	L473	G666	E756	Y851	R953	C1031		
		ASP		L285	L473	G667	E757	Y852	R954	C1032		
		ASP		L285	L473	G668	E758	Y853	R955	C1033		
		ASP		L285	L473	G669	E759	Y854	R956	C1034		
		ASP		L285	L473	G670	E760	Y855	R957	C1035		
		ASP		L285	L473	G671	E761	Y856	R958	C1036		
		ASP		L285	L473	G672	E762	Y857	R959	C1037		
		ASP		L285	L473	G673	E763	Y858	R960	C1038		
		ASP		L285	L473	G674	E764	Y859	R961	C1039		
		ASP		L285	L473	G675	E765	Y860	R962	C1040		
		ASP		L285	L473	G676	E766	Y861	R963	C1041		
		ASP		L285	L473	G677	E767	Y862	R964	C1042		
		ASP		L285	L473	G678	E768	Y863	R965	C1043		
		ASP		L285	L473	G679	E769	Y864	R966	C1044		
		ASP		L285	L473	G680	E770	Y865	R967	C1045		
		ASP		L285	L473	G681	E771	Y866	R968	C1046		

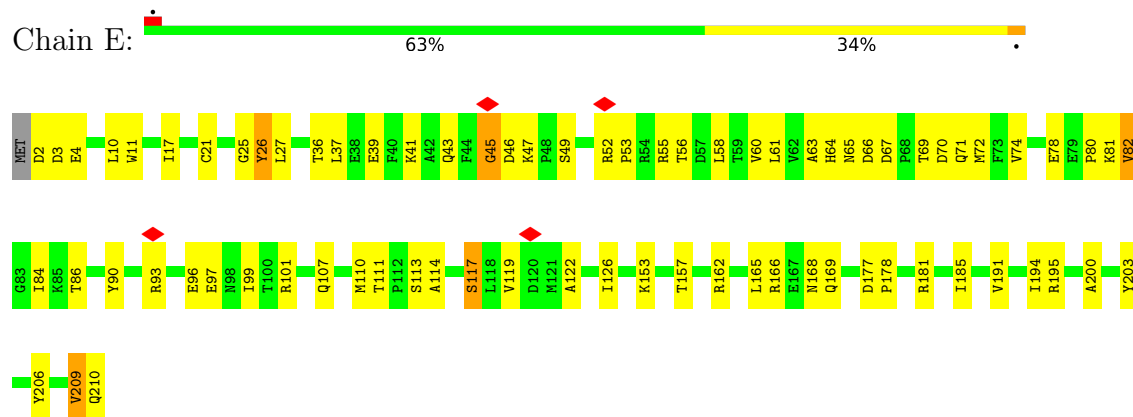
- Molecule 3: RNA polymerase II subunit C



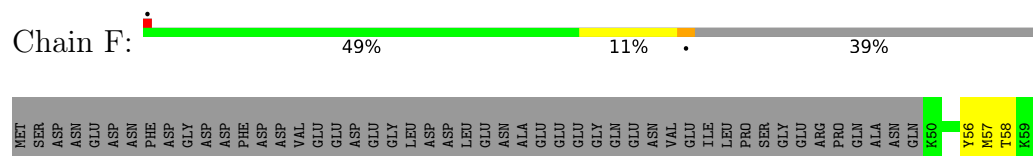
- Molecule 4: RNA polymerase II subunit D



- Molecule 5: RNA polymerase II subunit E

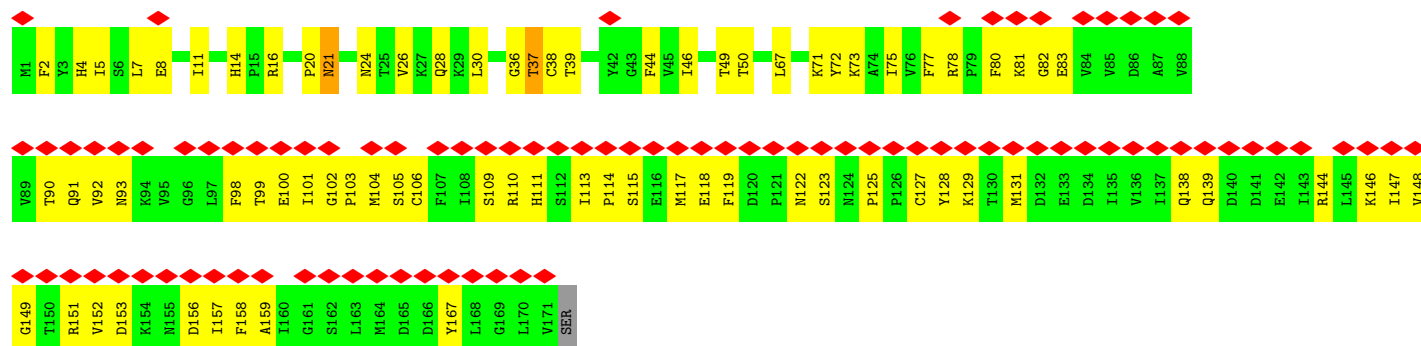


- Molecule 6: RNA polymerase II subunit F

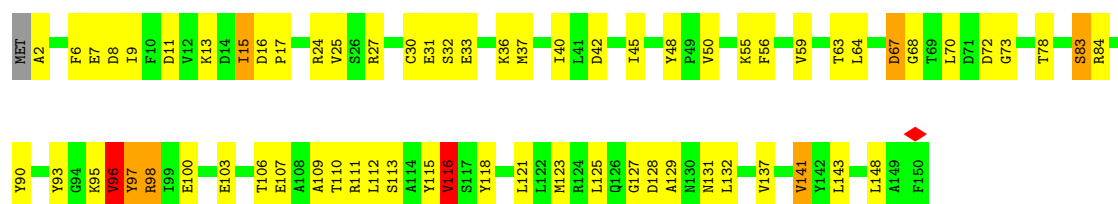




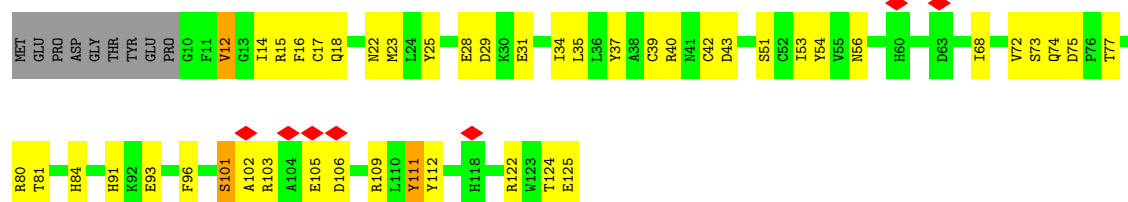
• Molecule 7: RNA polymerase II subunit G



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



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

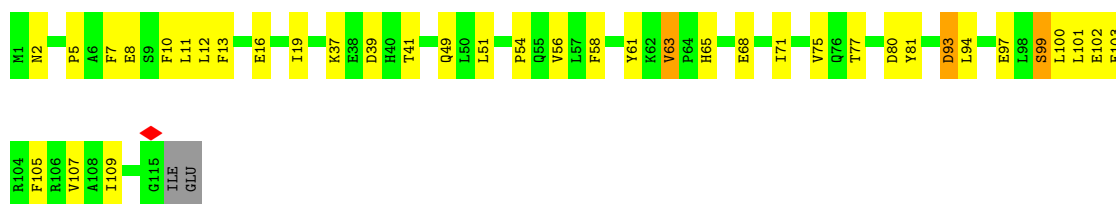


• Molecule 10: Uncharacterized protein



• Molecule 11: Uncharacterized protein

Chain K: 



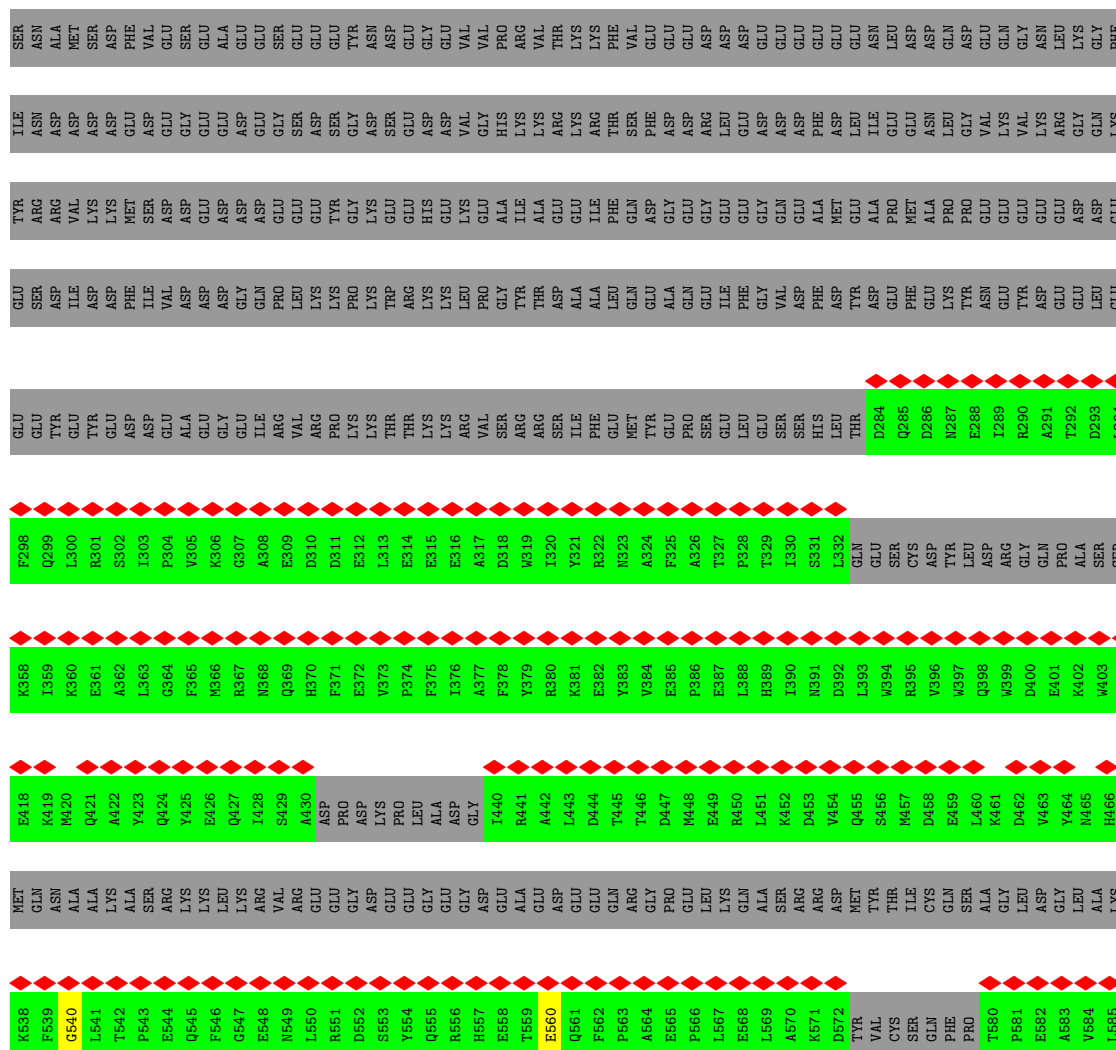
• Molecule 12: Uncharacterized protein

Chain L: 



• Molecule 13: Transcription elongation factor SPT6

Chain M: 



ARG	LYS	GLN	ARG	THR	THR	ILE	LYS	ARG	VAL	I1327	A1328	H1329	P1330	S1331	F1332	H1333	N1334	I1338	N1339	F1340	K1341	Q1342	A1343	E1344	K1345	M1346	M1347	E1348	T1349	M1350	D1351	Q1352	G1353	D1354	V1355	I1356	I1357	R1358	P1359	S1360	S1361	K1362	G1363	E1364	N1365	H1366	L1367	T1368	V1369	T1370	K1372	V1373	S1374	D1375	G1376	I1377																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
K1258	V1259	G1260	M1261	T1262	V1263	H1264	C1265	L1266	I1267	M1268	K1269	I1270	D1271	I1272	E1273	K1274	F1275	S1276	A1277	D1278	L1279	T1280	C1281	R1282	T1283	S1284	D1285	L1286	M1287	ASP	ASN	ASN	GLU	TRP	LYS	LEU	LYS	PRO	ASP	THR	TYR	ASP	PHE	ASP	ALA	GLU	ALA	ASP	HIS	LYS	GLN	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU



[illegible]

- Molecule 17: RNA polymerase-associated protein RTF1 homolog



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

[illegible]

GLU	LEU	LEU	ALA	LYS	GLN	PRO	PRO	LYS	THR	SER	GLU	VAL	TYR	SER	ASP	ASP	GLU	GLU	GLU	GLU	GLU	ASP	ASP	LYS	SER	SER	SER	GLU	LYS	SER	ASP	ARG	SER	SER	ARG	ARG	THR	THR	SER	SER	SER	ASP	ASP	GLU	GLU	GLU	GLU	GLU	LYS	GLU	GLU	ILE	PRO	PRO	LYS	SER	GLN	PRO	353	354	355	356	357
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E358	L359	N360	R361	V362	R363	L364	S365	R366	H367	K368	L369	E370	R371	W372	C373	H374	N375	F376	F377	F378	A379	K380	T381	V382	T383	C384	C385	F386	V387	R388	R389	I390	G391	I391	G392	ASN	HIS	ASN	ASN	SER	K397	P398	V399	Y400	R401	V402	A403	A404	E405	I406	T407	V408	V409	E410	T411	A412	K413	V414	Y415	Q416	L417
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G418	G419	T420	R421	T422	N423	K424	G425	L426	Q427	L428	R429	H430	G431	N432	D433	Q434	R435	V436	F437	R438	L439	E440	F441	V442	S443	N444	Q445	E446	F447	T448	E449	S450	E451	F452	N453	K454	W455	K456	F457	A458	M459	F460	A461	A462	Q463	M464	Q465	L466	P467	T468	L469	D470	E471	T472	N473	K474	K475	E476	L477
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S478	1479	F481	A482	L483	N484	Y485	K486	F487	N488	D489	Q490	D491	L492	E493	E494	L495	V496	K497	E498	K499	E500	R501	F502	R503	K504	A505	F506	F507	N508	Y509	A510	N511	K512	K513	T514	Q515	L516	L517	K518	F519	K520	A521	M522	A523	E524	D525	L526	G527	D528	Q529	D530	K531	K532	A533	Q534	L535	Q536	D537
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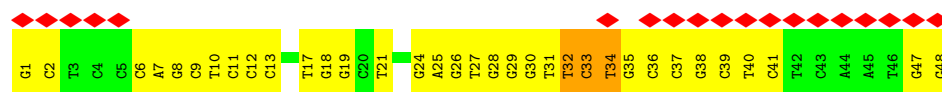
Q538	L539	N540	E541	E543	E544	R545	E547	L549	D550	R551	Q552	R553	T554	K555	N556	L557	S558	A559	S560	Y562	T563	N564	Q565	E566	N567	R568	E569	W570	N571	L572	V573	E574	S575	E576	K577	A578	L579	V580	A581	E582	S583	H584	N585	M586	K587	N588	Q589	Q590	M591	D592	P593	F594	T595	R596	R597
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Q598	C599	K600	PRO	THR	TLE	VAL	SER	SER	ASN	SER	ARG	ASP	PRO	ALA	VAL	GLN	ALA	ALA	TLE	LEU	ALA	GLN	LEU	ASN	LYS	TYR	GLY	SER	GLY	VAL	LEU	PRO	ASP	ALA	PRO	LYS	GLU	MET	SER	LYS	GLY	GLN	GLY	LYS	ASP	LEU	ASN	SER	LYS	SER	ALA	SER	ASP	LEU	SER	GLU	ASP
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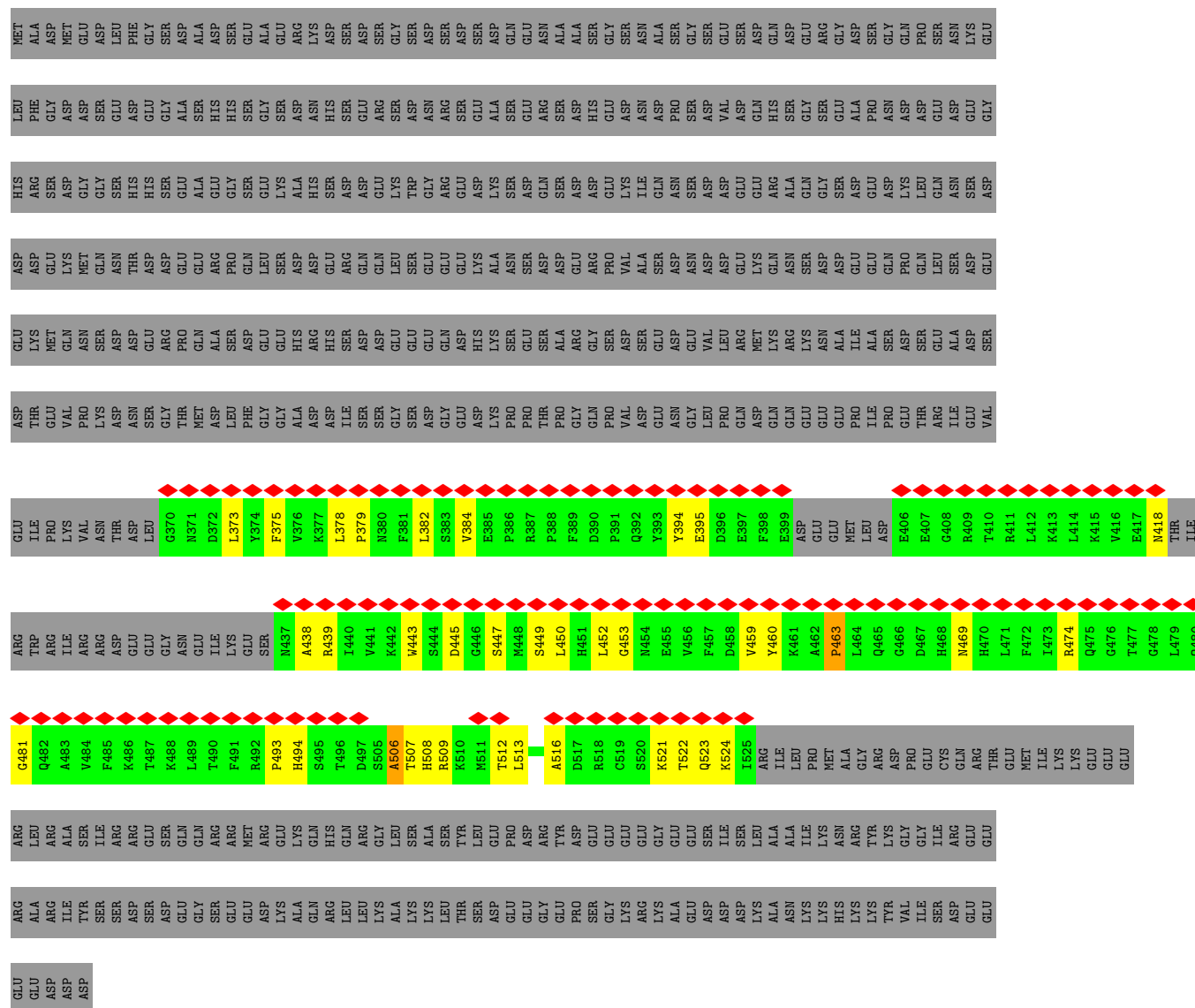
LEU PHE LYS VAL HIS ASP PHE ASP VAL LYS ILE LEU LEU GLN VAL VAL PRO SER SER SER GLU LEU LEU ALA ALA ILE THR SER SER LYS ALA ALA PRO PRO PRO ALA ALA LYS ASP ASP GLY GLY ALA ALA PRO PRO ARG ARG SER SER ASN LEU LEU LEU LEU ASP ASP TYR LYS LYS ARG ARG GLY GLY LEU LEU

- Molecule 18: Template DNA

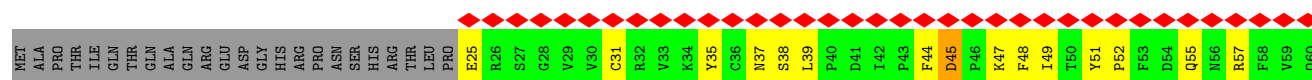
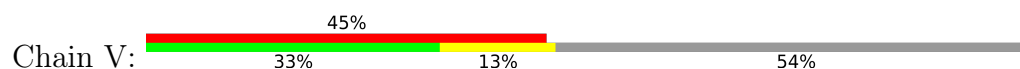




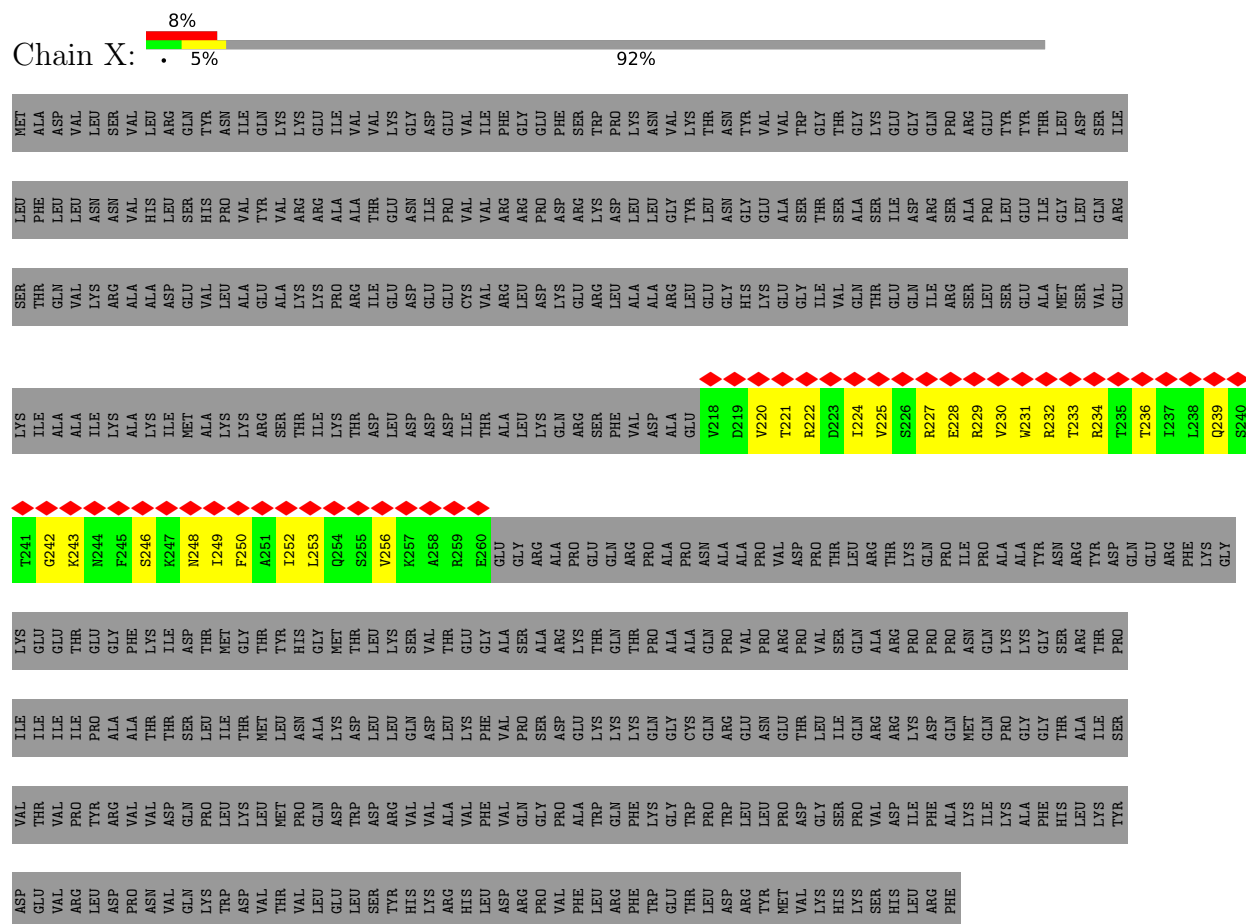
• Molecule 19: RNA polymerase-associated protein LEO1



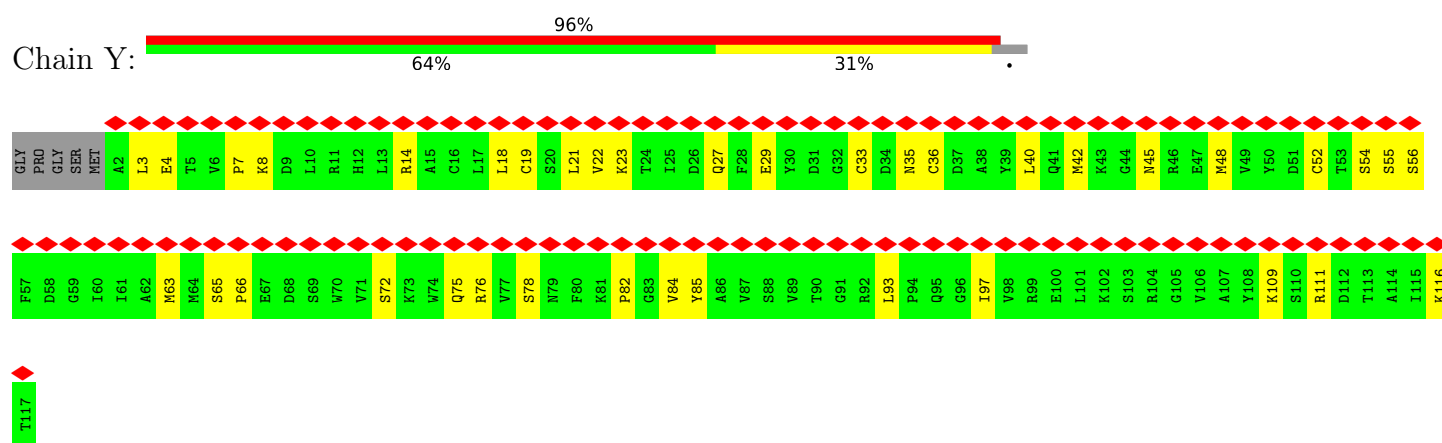
• Molecule 20: RNA polymerase II-associated factor 1 homolog



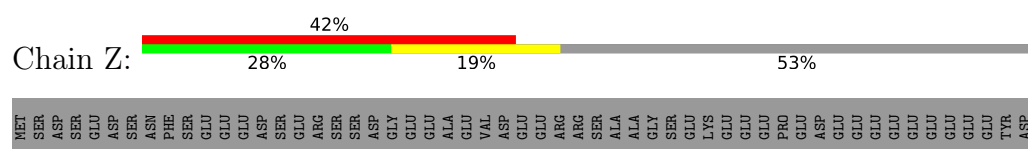
● Molecule 22: Parafibromin



● Molecule 23: Transcription elongation factor SPT4



● Molecule 24: Transcription elongation factor SPT5





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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SEP, ZN, TPO, 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	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%)	19	51
2	B	1112/1251 (89%)	998 (90%)	105 (9%)	9 (1%)	16	48
3	C	254/275 (92%)	232 (91%)	19 (8%)	3 (1%)	11	38
4	D	124/142 (87%)	118 (95%)	6 (5%)	0	100	100
5	E	207/210 (99%)	199 (96%)	7 (3%)	1 (0%)	25	58
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%)	19	51
9	I	114/125 (91%)	104 (91%)	10 (9%)	0	100	100
10	J	64/67 (96%)	60 (94%)	2 (3%)	2 (3%)	3	19
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%)	48	79
16	Q	888/1179 (75%)	836 (94%)	52 (6%)	0	100	100
17	R	240/713 (34%)	225 (94%)	14 (6%)	1 (0%)	30	63
19	U	117/666 (18%)	88 (75%)	21 (18%)	8 (7%)	1	6
20	V	234/531 (44%)	199 (85%)	31 (13%)	4 (2%)	7	30

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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%)	44	74
All	All	7238/11540 (63%)	6624 (92%)	573 (8%)	41 (1%)	24	53

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 ⓘ

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%)	60	80
2	B	986/1084 (91%)	949 (96%)	37 (4%)	28	59
3	C	235/252 (93%)	228 (97%)	7 (3%)	36	64
4	D	109/126 (86%)	108 (99%)	1 (1%)	75	88
5	E	191/192 (100%)	189 (99%)	2 (1%)	73	86
6	F	68/111 (61%)	67 (98%)	1 (2%)	60	80
7	G	146/153 (95%)	143 (98%)	3 (2%)	48	72
8	H	130/131 (99%)	122 (94%)	8 (6%)	15	43
9	I	104/112 (93%)	101 (97%)	3 (3%)	37	65
10	J	55/56 (98%)	54 (98%)	1 (2%)	54	76
11	K	104/106 (98%)	103 (99%)	1 (1%)	73	86
12	L	43/55 (78%)	40 (93%)	3 (7%)	12	39

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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%)	79	89
17	R	168/625 (27%)	166 (99%)	2 (1%)	67	83
19	U	63/590 (11%)	63 (100%)	0	100	100
20	V	144/462 (31%)	141 (98%)	3 (2%)	48	72
21	W	255/260 (98%)	254 (100%)	1 (0%)	89	94
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%)	86	92
All	All	5537/10122 (55%)	5437 (98%)	100 (2%)	54	76

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 ⓘ

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 ⓘ

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	SEP	A	1547	1	8,9,10	1.49	1 (12%)	8,12,14	1.39	2 (25%)
1	TPO	A	1525	1	8,10,11	1.60	1 (12%)	10,14,16	1.83	1 (10%)

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	SEP	A	1547	1	-	0/5/8/10	-
1	TPO	A	1525	1	-	4/9/11/13	-

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	1547	SEP	1	0
1	A	1525	TPO	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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

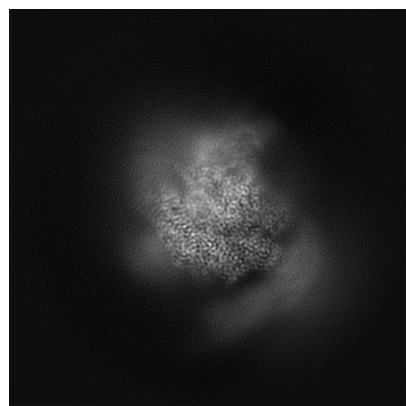
6 Map visualisation [i](#)

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.

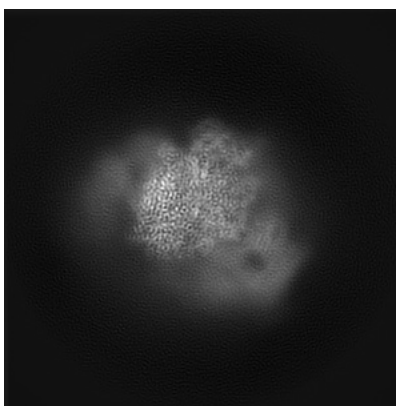
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

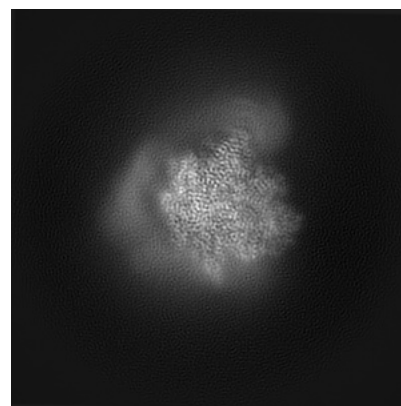
6.1.1 Primary map



X

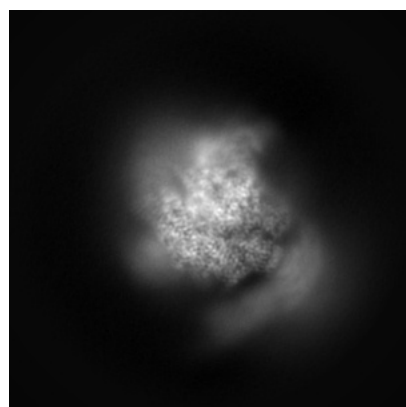


Y

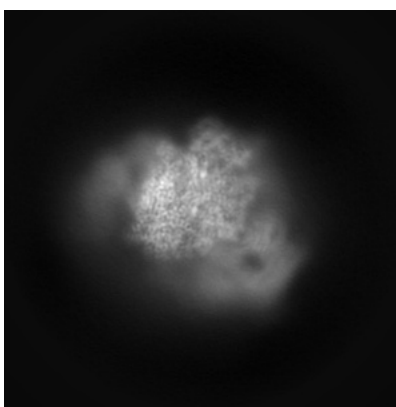


Z

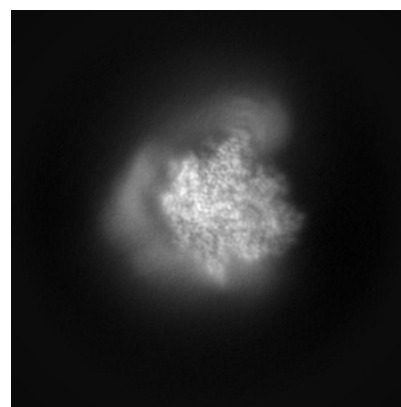
6.1.2 Raw map



X



Y

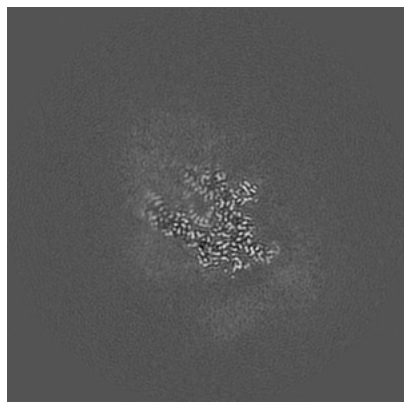


Z

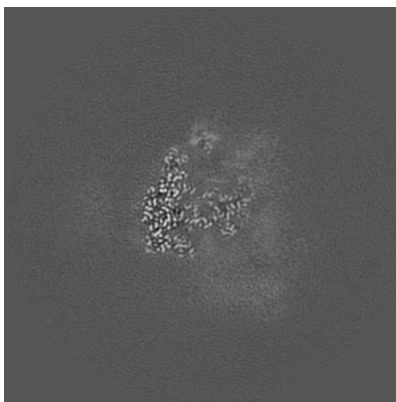
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

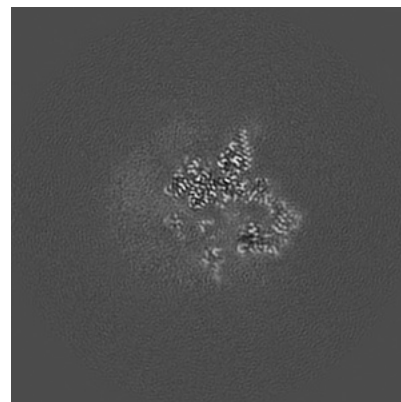
6.2.1 Primary map



X Index: 180

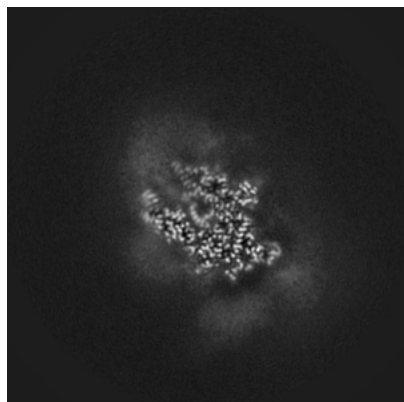


Y Index: 180

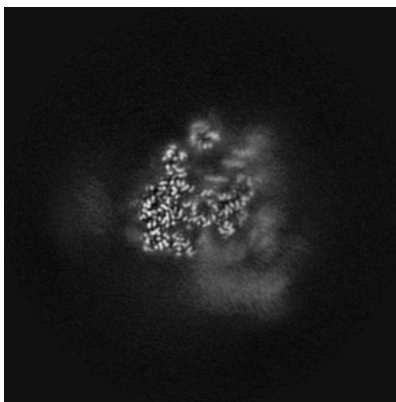


Z Index: 180

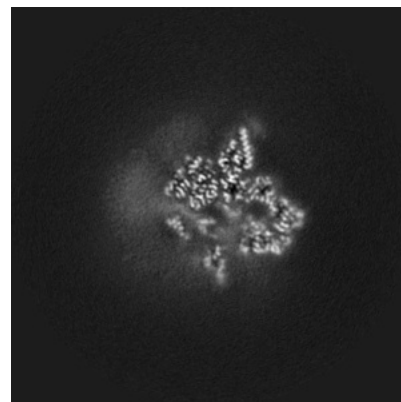
6.2.2 Raw map



X Index: 180



Y Index: 180

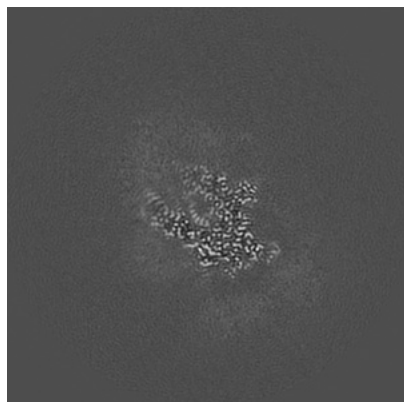


Z Index: 180

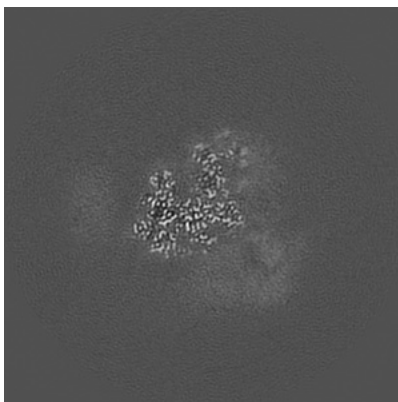
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

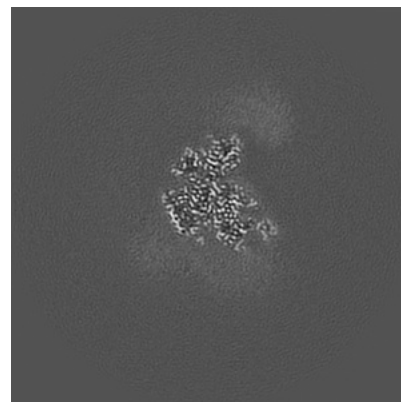
6.3.1 Primary map



X Index: 179

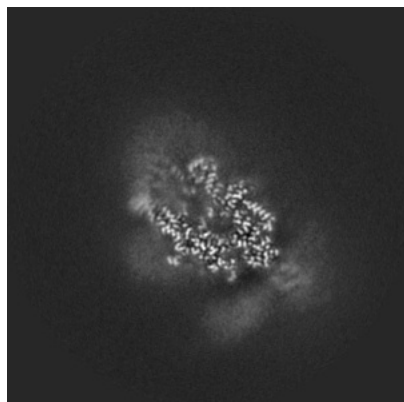


Y Index: 193

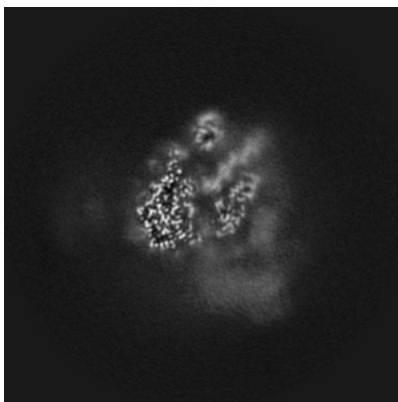


Z Index: 143

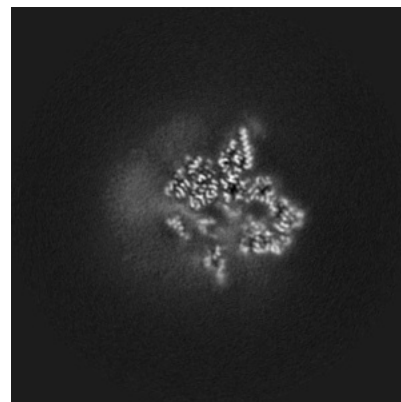
6.3.2 Raw map



X Index: 189



Y Index: 174

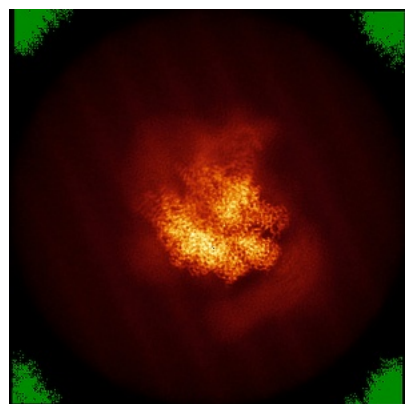


Z Index: 180

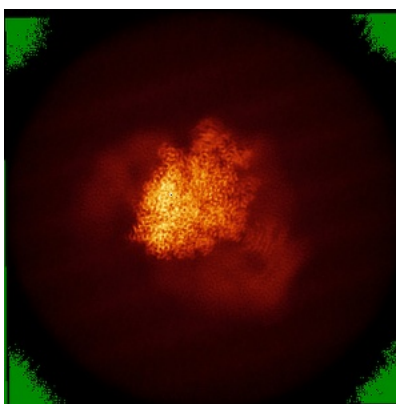
The images above show the largest variance slices of the map in three orthogonal directions.

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

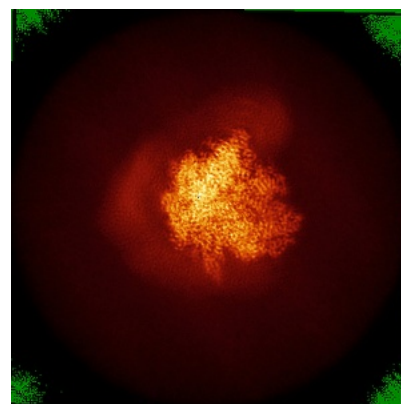
6.4.1 Primary map



X

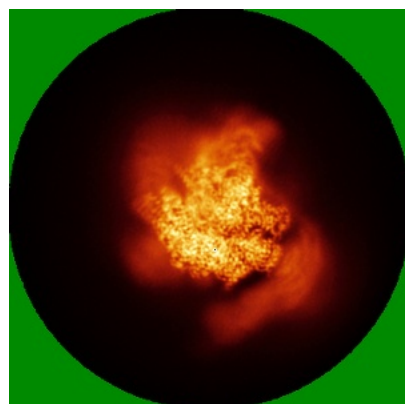


Y

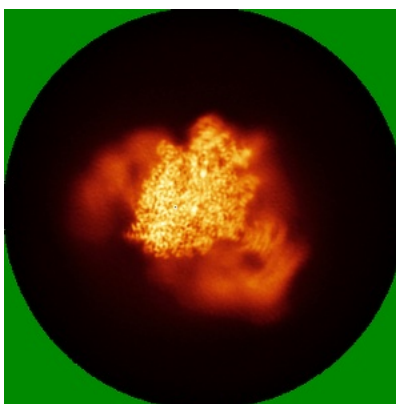


Z

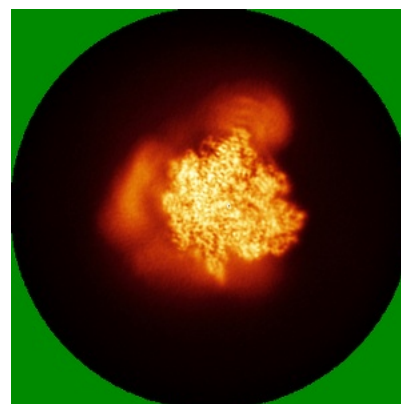
6.4.2 Raw map



X



Y

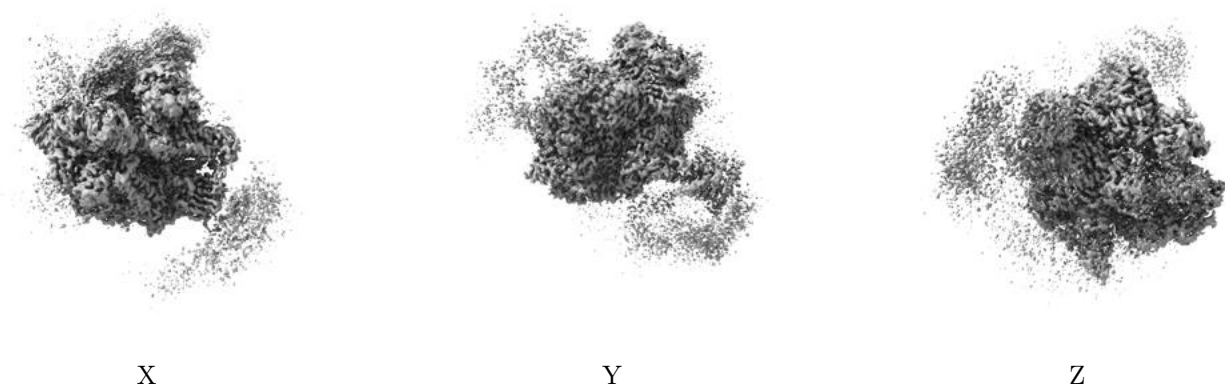


Z

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.

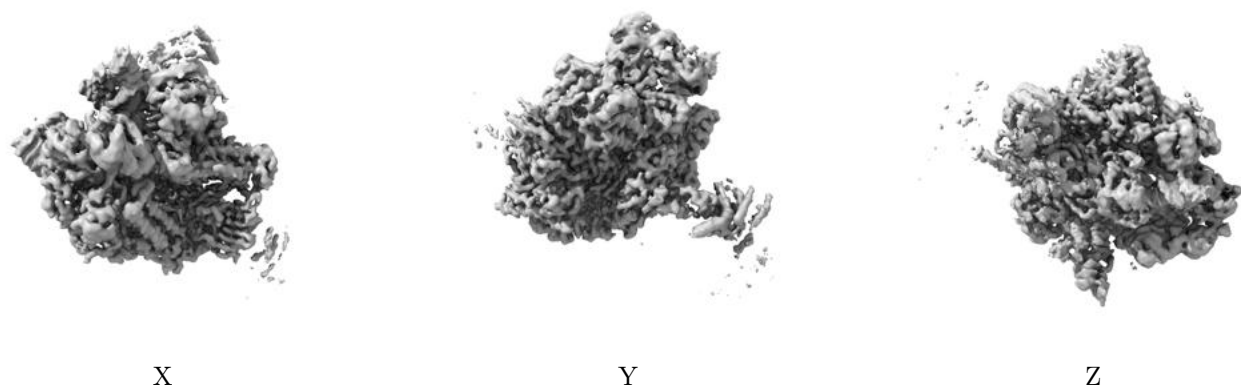
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.022. 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.

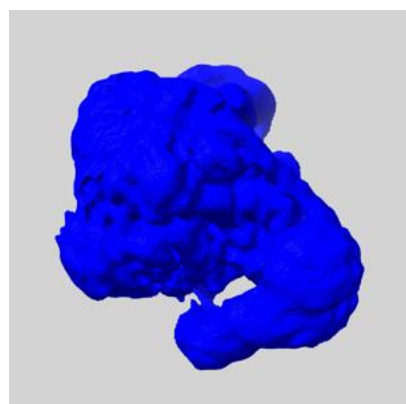
6.6 Mask visualisation [i](#)

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

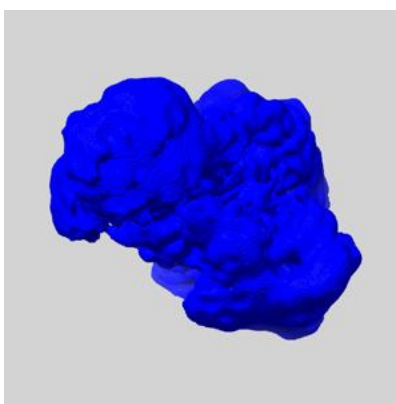
A mask typically either:

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

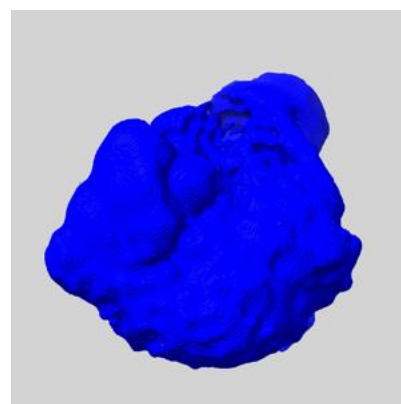
6.6.1 emd_10480_msk_1.map [i](#)



X

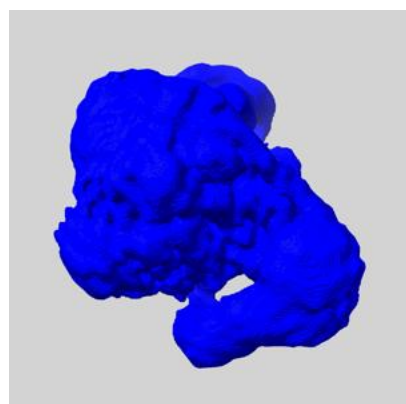


Y

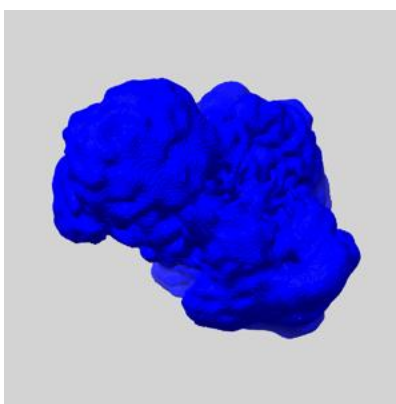


Z

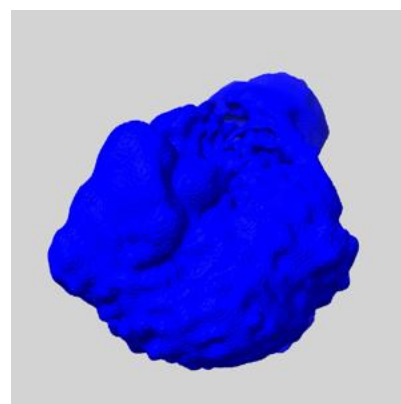
6.6.2 emd_10480_msk_2.map [i](#)



X



Y

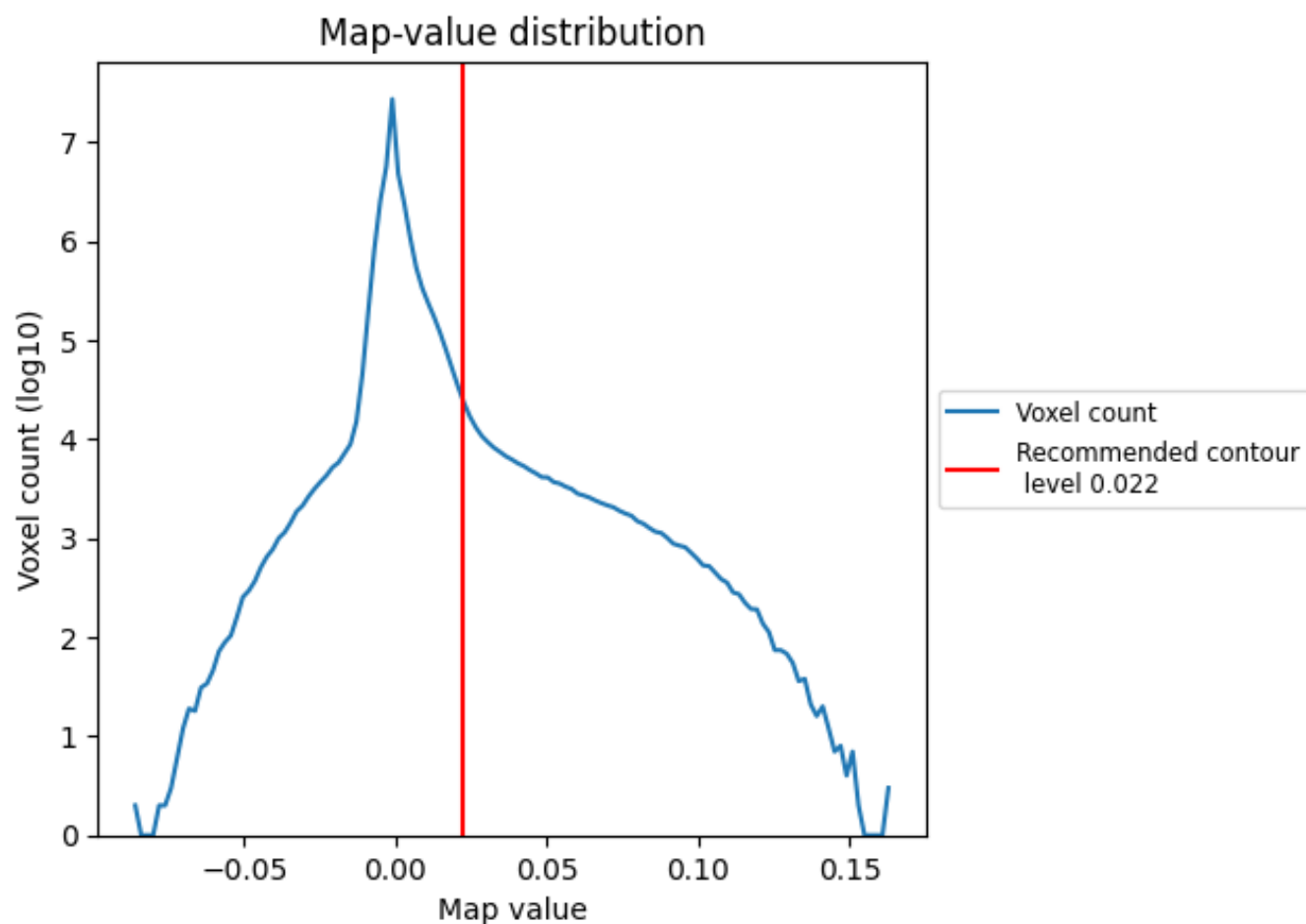


Z

7 Map analysis [i](#)

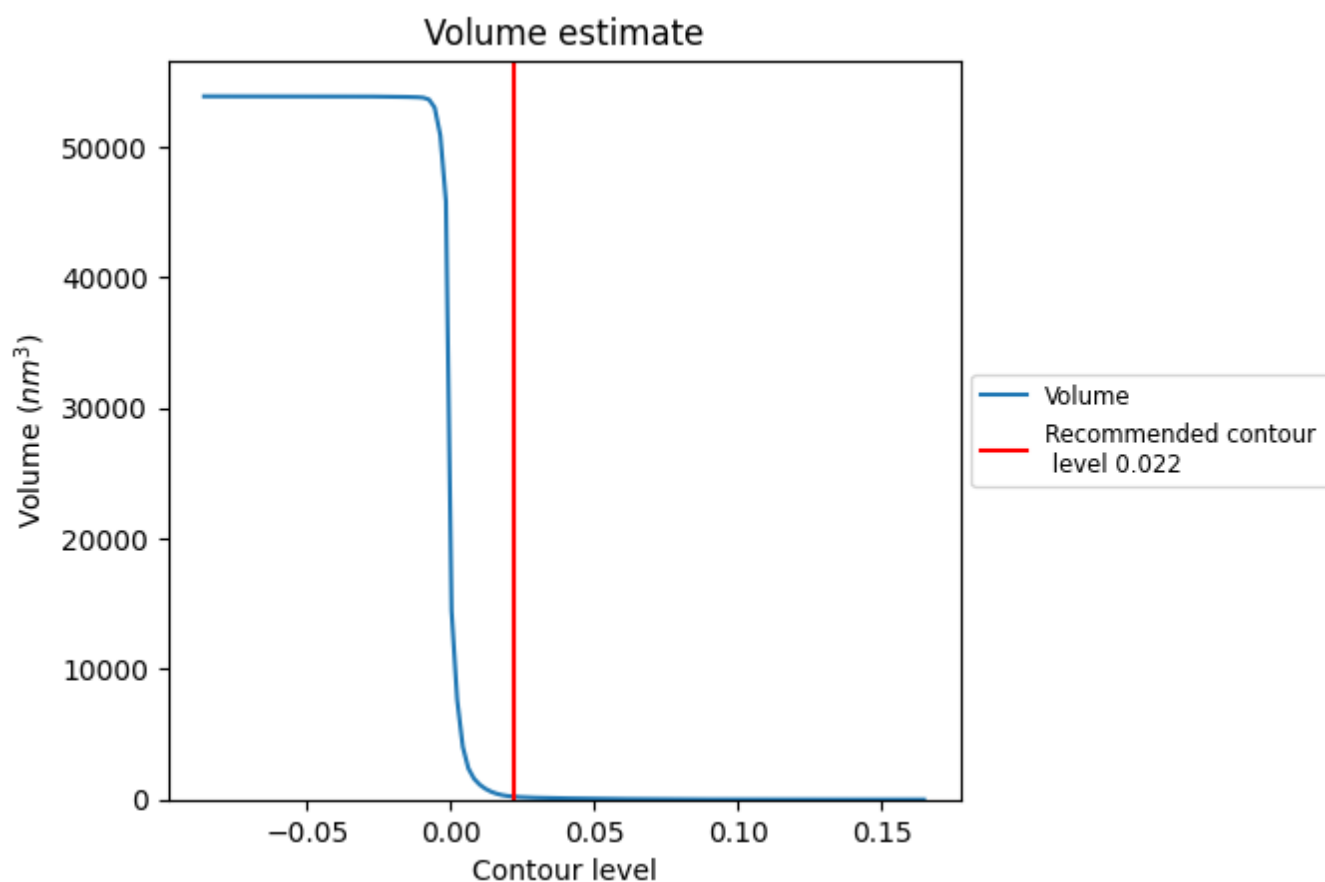
This section contains the results of statistical analysis of the map.

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.

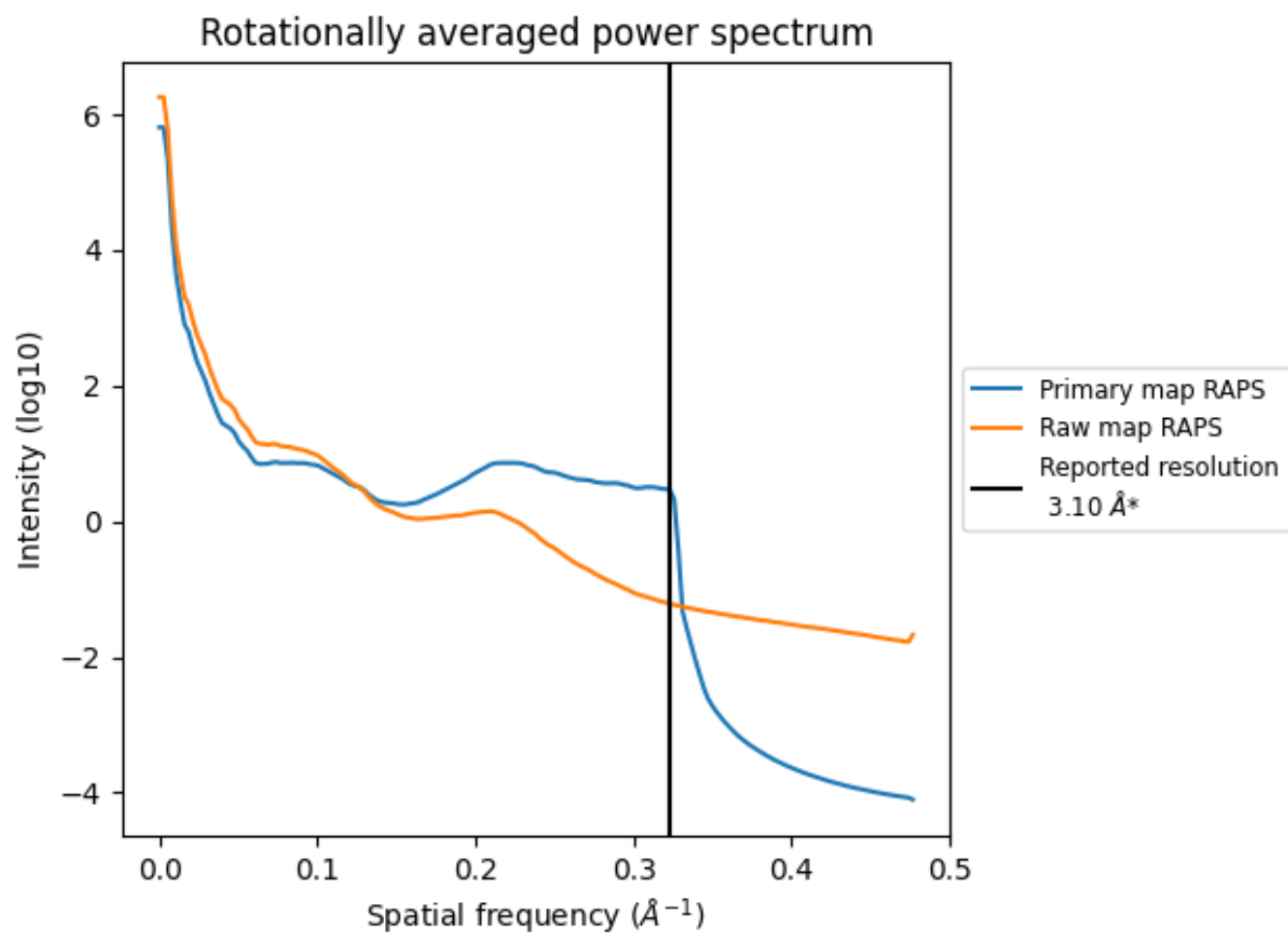
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 223 nm^3 ; 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 ⓘ

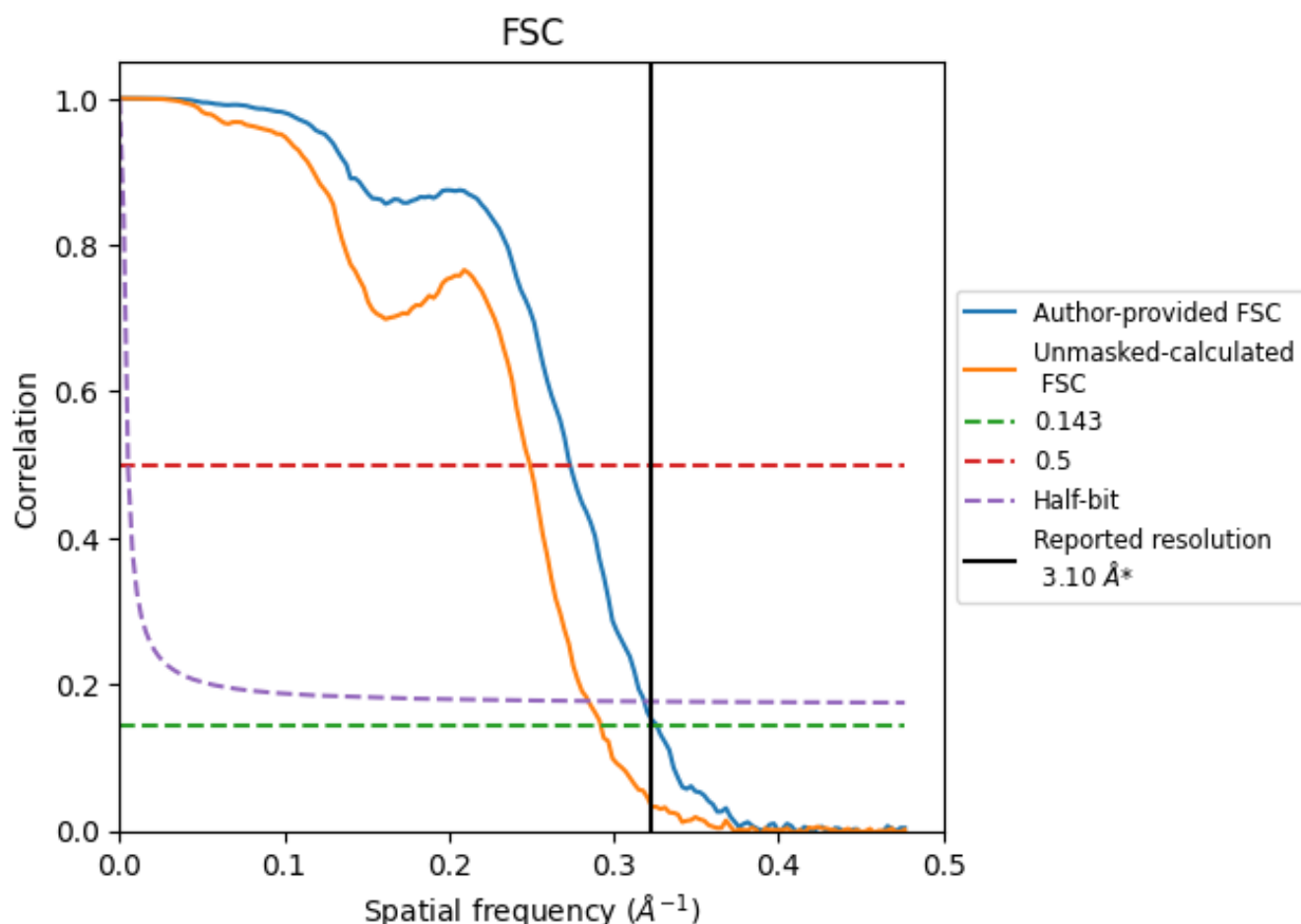


*Reported resolution corresponds to spatial frequency of 0.323 \AA^{-1}

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 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

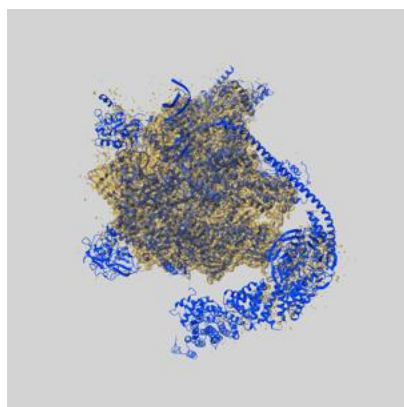
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.07	3.66	3.14
Unmasked-calculated*	3.42	4.01	3.51

*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 %

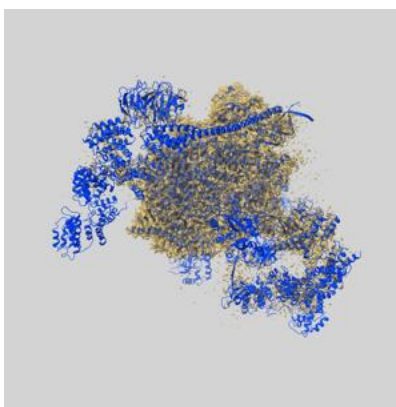
9 Map-model fit [i](#)

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](#).

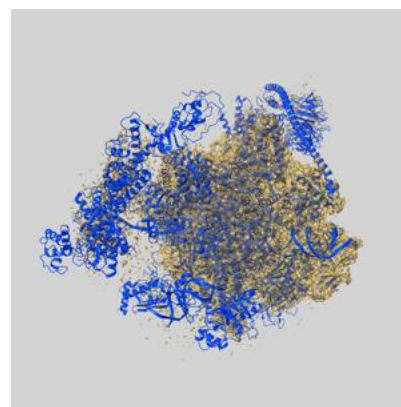
9.1 Map-model overlay [i](#)



X



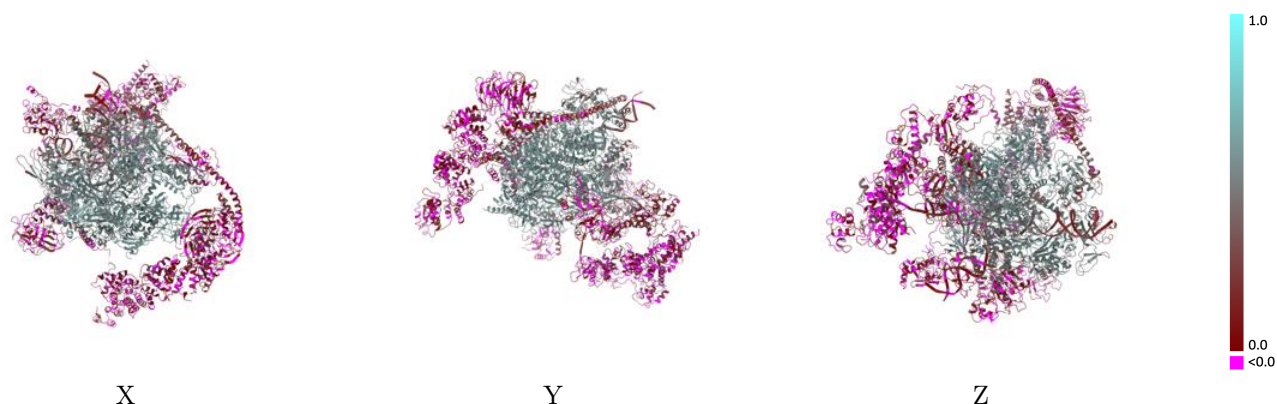
Y



Z

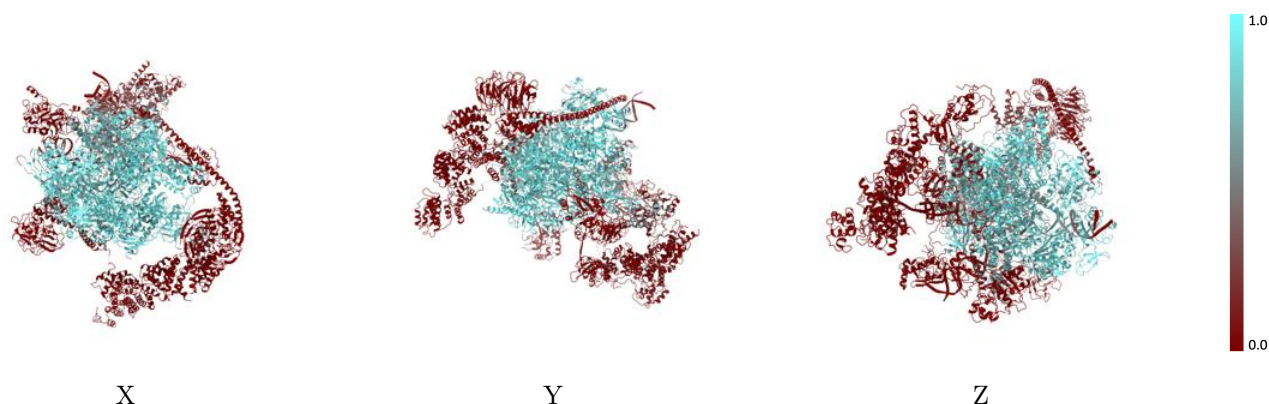
The images above show the 3D surface view of the map at the recommended contour level 0.022 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



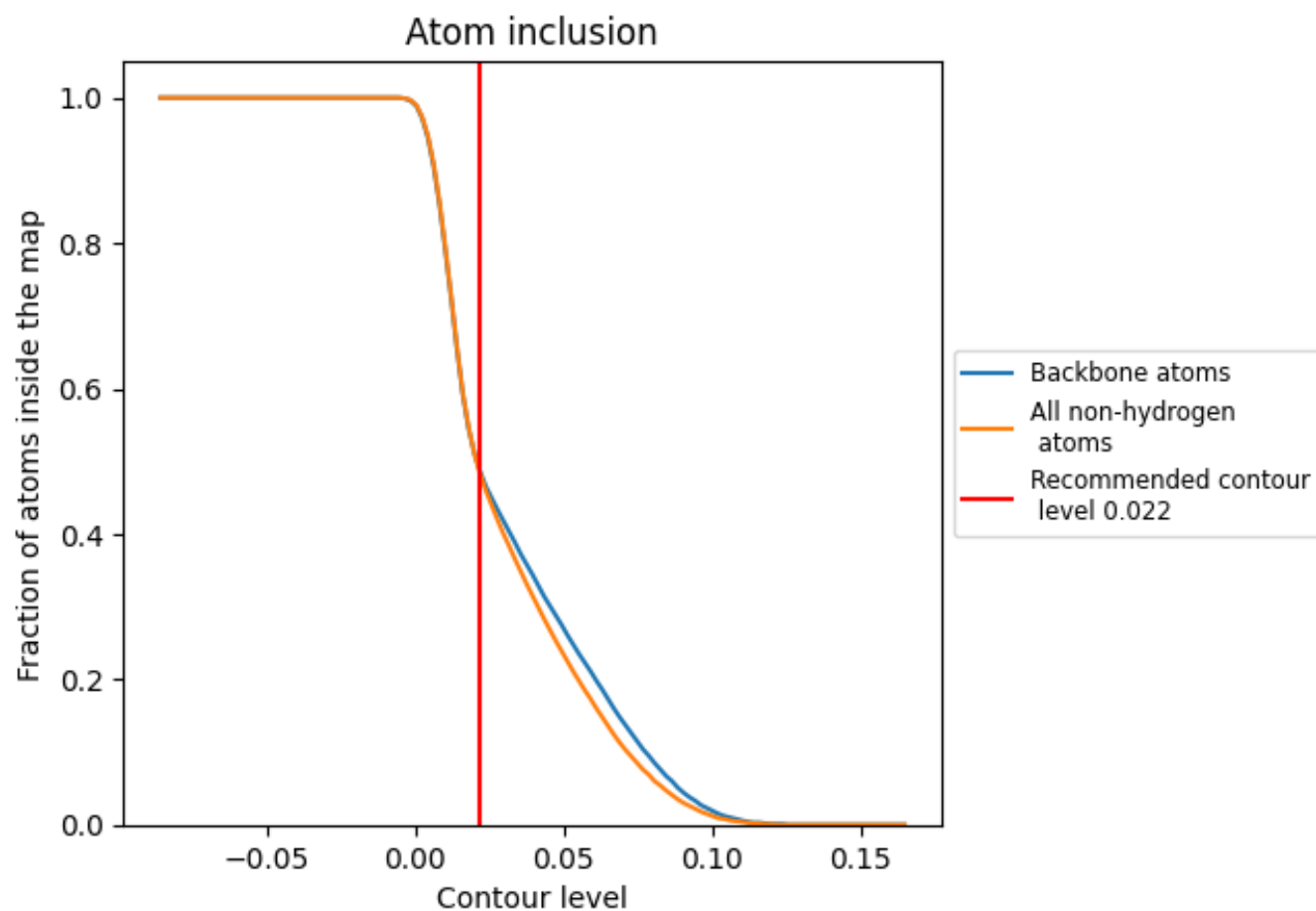
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.4810	 0.3380
A	 0.8490	 0.5370
B	 0.8820	 0.5560
C	 0.9110	 0.5800
D	 0.2730	 0.1850
E	 0.8540	 0.5210
F	 0.8960	 0.5740
G	 0.4390	 0.3110
H	 0.8510	 0.5590
I	 0.8470	 0.5110
J	 0.9180	 0.5730
K	 0.9210	 0.5890
L	 0.8480	 0.5090
M	 0.0150	 0.0750
N	 0.3470	 0.2200
P	 0.4250	 0.2780
Q	 0.0280	 0.1020
R	 0.0120	 0.0880
T	 0.5190	 0.3100
U	 0.0550	 0.1140
V	 0.0260	 0.1270
W	 0.0110	 0.0430
X	 0.0240	 0.1060
Y	 0.0060	 0.0770
Z	 0.0990	 0.1660

