



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 11:07 AM UTC

PDB ID : 7AOD / pdb_00007aod
EMDB ID : EMD-11841
Title : Schizosaccharomyces pombe RNA polymerase I (dimer)
Authors : Heiss, F.; Daiss, J.; Becker, P.; Engel, C.
Deposited on : 2020-10-14
Resolution : 4.50 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

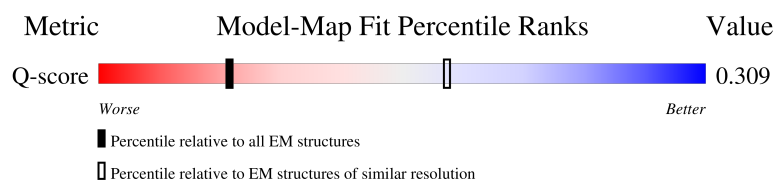
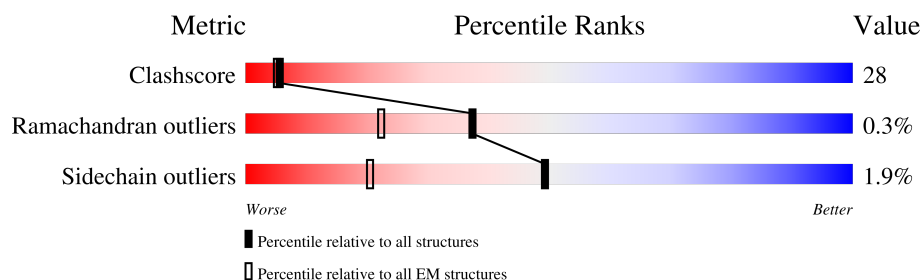
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 4.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2937 (4.00 - 5.00)

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	1689	
1	M	1689	
2	B	1174	
2	N	1174	

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Mol	Chain	Length	Quality of chain
3	C	348	
3	O	348	
4	D	147	
4	P	147	
5	E	210	
5	Q	210	
6	F	142	
6	R	142	
7	G	173	
7	S	173	
8	H	125	
8	T	125	
9	I	119	
9	U	119	
10	J	71	
10	V	71	
11	K	125	
11	W	125	
12	L	63	
12	X	63	

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 59256 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 I subunit rpa1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1384	Total	C	N	O	S	0	0
			10976	6965	1894	2059	58		
1	M	1384	Total	C	N	O	S	0	0
			10976	6965	1894	2059	58		

- Molecule 2 is a protein called Probable DNA-directed RNA polymerase I subunit RPA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1156	Total	C	N	O	S	0	0
			9127	5791	1592	1685	59		
2	N	1156	Total	C	N	O	S	0	0
			9127	5791	1592	1685	59		

- Molecule 3 is a protein called DNA-directed RNA polymerases I and III subunit RPAC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	317	Total	C	N	O	S	0	0
			2533	1621	430	475	7		
3	O	317	Total	C	N	O	S	0	0
			2533	1621	430	475	7		

- Molecule 4 is a protein called DNA-directed RNA polymerase I subunit rpa14.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	39	Total	C	N	O	S	0	0
			322	203	57	61	1		
4	P	39	Total	C	N	O	S	0	0
			322	203	57	61	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	207	Total	C	N	O	S	0	0
			1663	1050	301	306	6		
5	Q	207	Total	C	N	O	S	0	0
			1663	1050	301	306	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	82	Total	C	N	O	S	0	0
			650	413	111	123	3		
6	R	82	Total	C	N	O	S	0	0
			650	413	111	123	3		

- Molecule 7 is a protein called DNA-directed RNA polymerase I subunit rpa43.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	160	Total	C	N	O	S	0	0
			1267	817	210	236	4		
7	S	160	Total	C	N	O	S	0	0
			1267	817	210	236	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	123	Total	C	N	O	S	0	0
			990	628	166	193	3		
8	T	123	Total	C	N	O	S	0	0
			990	628	166	193	3		

- Molecule 9 is a protein called DNA-directed RNA polymerase I subunit RPA12.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	57	Total	C	N	O	S	0	0
			431	269	69	89	4		
9	U	57	Total	C	N	O	S	0	0
			431	269	69	89	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	68	Total	C	N	O	S	0	0
			550	350	93	100	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	V	68	Total	C	N	O	S	0	0
			550	350	93	100	7		

- Molecule 11 is a protein called DNA-directed RNA polymerases I and III subunit RPAC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	95	Total	C	N	O	S	0	0
			745	472	123	146	4		
11	W	95	Total	C	N	O	S	0	0
			745	472	123	146	4		

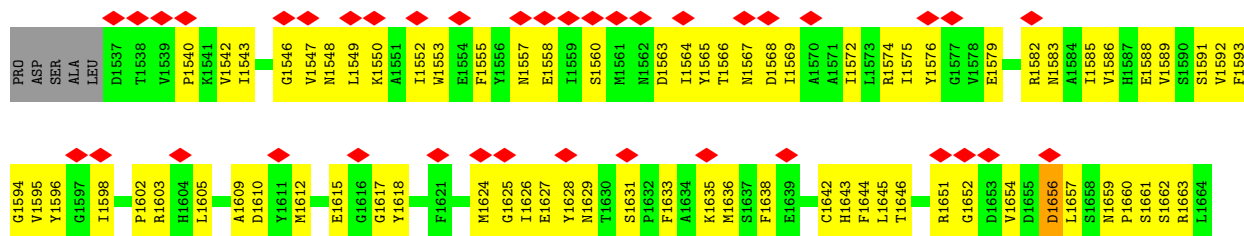
- Molecule 12 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	45	Total	C	N	O	S	0	0
			368	225	74	61	8		
12	X	45	Total	C	N	O	S	0	0
			368	225	74	61	8		

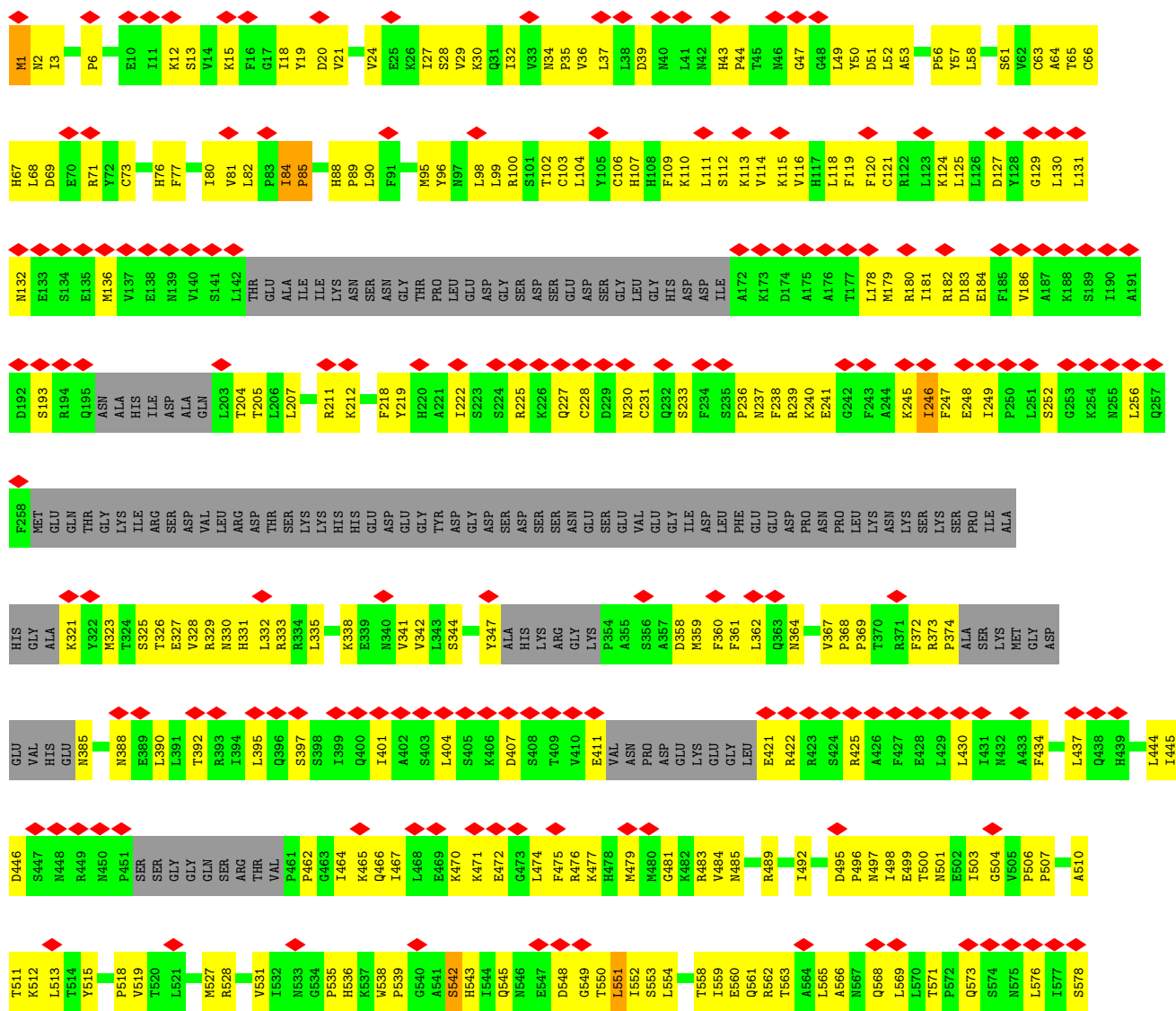
- Molecule 13 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
13	A	2	Total	Zn	0
			2	2	
13	B	1	Total	Zn	0
			1	1	
13	I	1	Total	Zn	0
			1	1	
13	J	1	Total	Zn	0
			1	1	
13	L	1	Total	Zn	0
			1	1	
13	M	2	Total	Zn	0
			2	2	
13	N	1	Total	Zn	0
			1	1	
13	U	1	Total	Zn	0
			1	1	
13	V	1	Total	Zn	0
			1	1	
13	X	1	Total	Zn	0
			1	1	

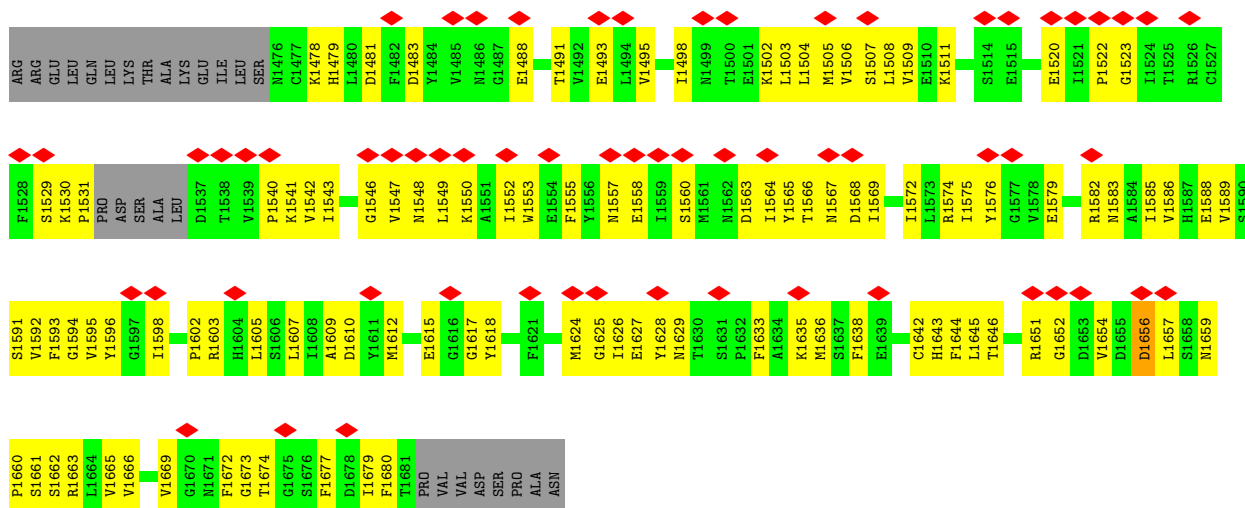




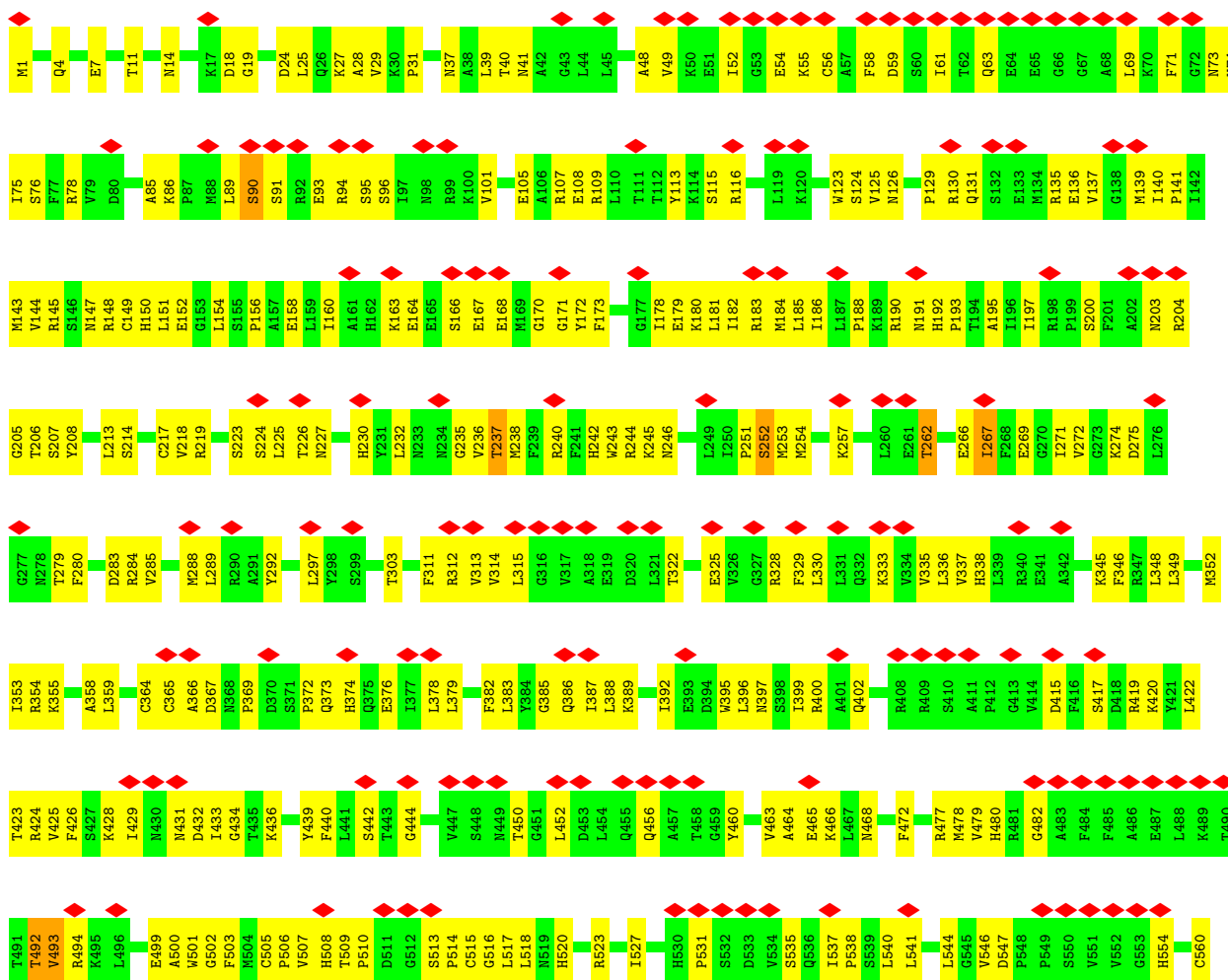
• Molecule 1: DNA-directed RNA polymerase I subunit rpa1

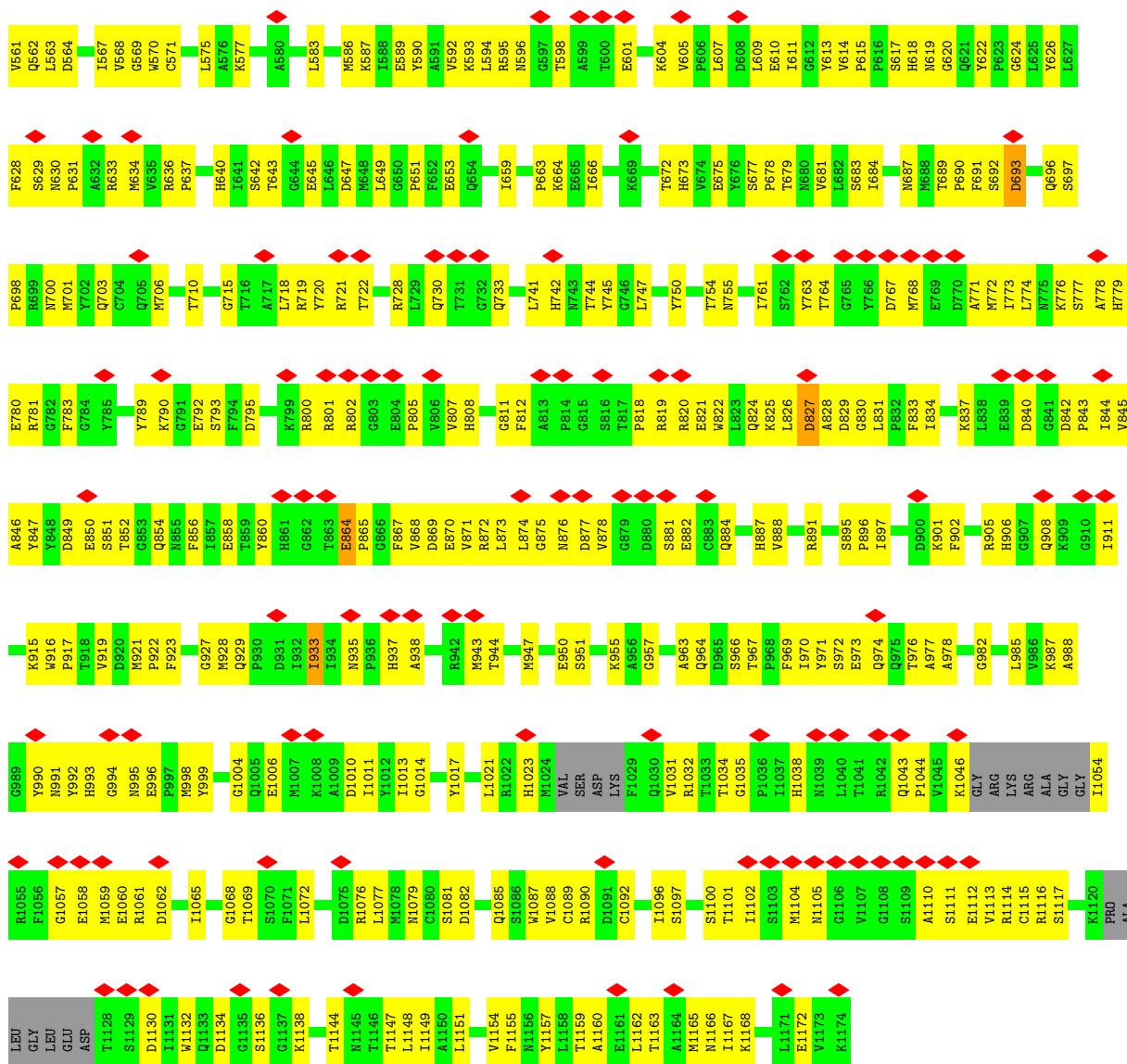




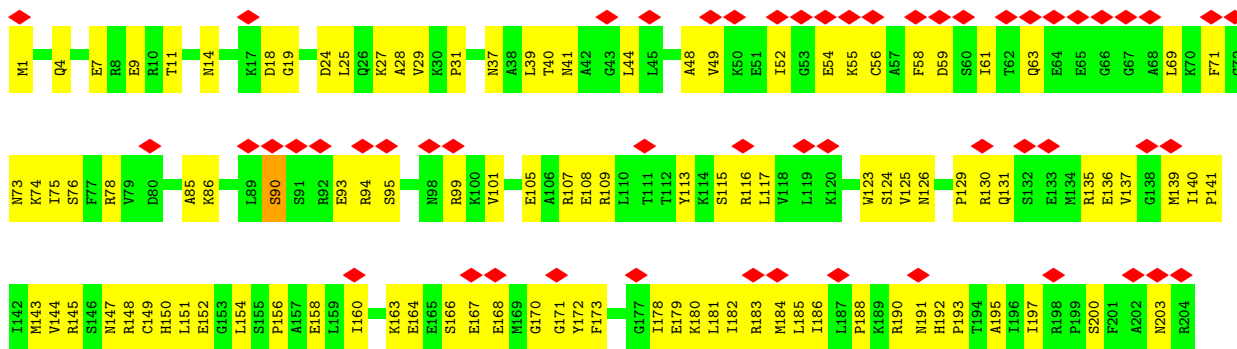


• Molecule 2: Probable DNA-directed RNA polymerase I subunit RPA2

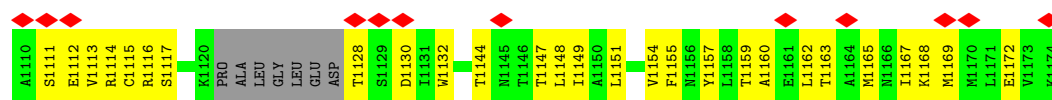




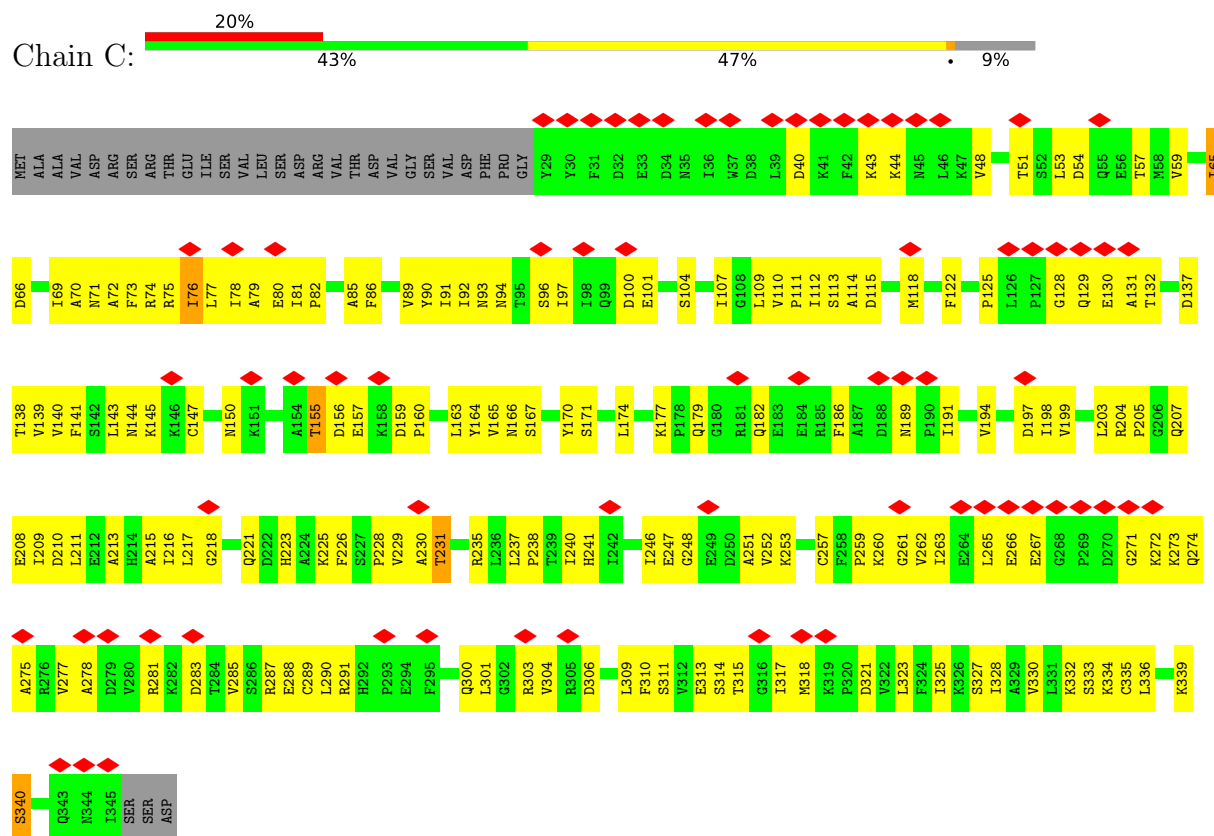
• Molecule 2: Probable DNA-directed RNA polymerase I subunit RPA2



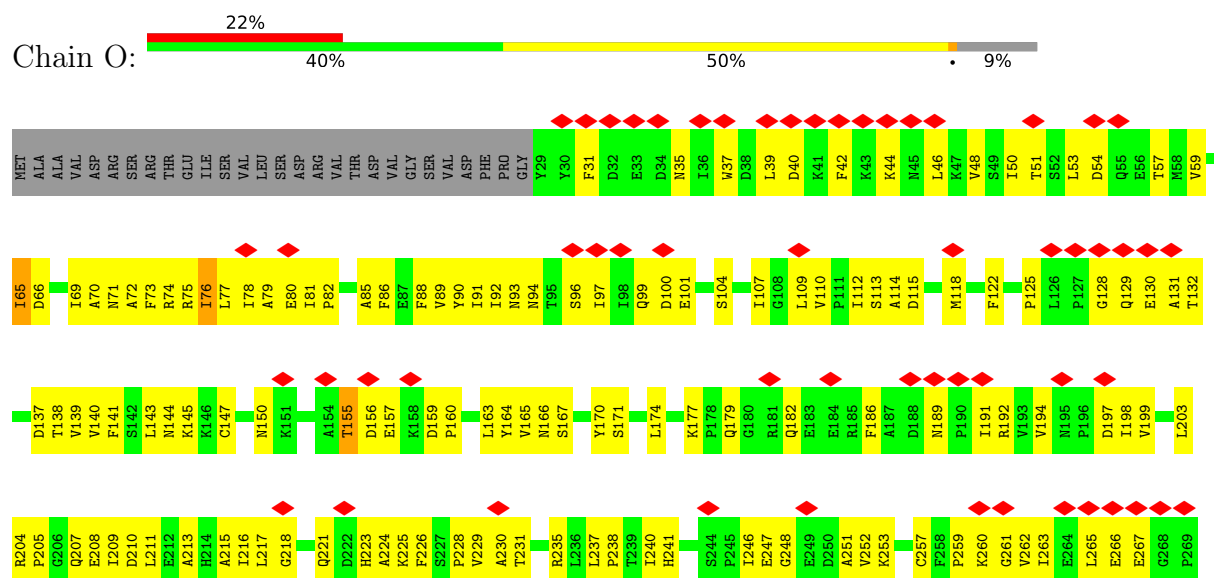
L1040	Y971	P896	F833	M768	M687	M618	D547	G482	S417	L348	L276	G205
Q1043	S972	I897	I834	E769	M688	M619	P848	A483	D418	L349	G277	T206
P1044	E973	D900	G835	D770	T689	G620	P849	F484	R419	M352	N278	S207
V1045	Q974	K901	T836	A771	Y622	D621	S550	F485	K420	I353	T279	Y208
K1046	G875	P902	K837	M772	P623	Y623	V551	A486	Y421	R354	D283	L213
GLY	T976	F902	L838	M773	G624	Y625	V552	A487	L422	K355	R284	S214
ARG	A977	R905	E839	L774	L625	Y626	G553	L488	T423	L356	R285	C217
LYS	A978	H906	D840	M775	Y627	L627	H554	L489	R424	A358	V218	V181
ALA	G982	G907	G841	K776	F628	S629	C560	T490	V425	L359	R219	R219
GLY	L985	Q908	D842	S777	S629	Y630	V561	T491	F426	E286	L287	Q222
I1054	Y986	P909	P843	A778	N630	Y632	S562	T492	R428	M288	Q223	S223
G1057	K987	G910	I844	H779	P631	Y633	L563	V493	N430	L289	S224	S224
E1058	G988	I911	V845	E780	M701	A632	D564	R494	I429	R290	S225	S225
M1059	A988	T911	A846	G782	G703	R633	S564	K495	N431	A291	L226	L226
E1060	Y990	K915	Y848	F783	G704	M634	L567	L496	D432	Y292	T226	T226
R1061	N991	W916	D849	G784	G705	V635	G569	E499	G434	L297	N227	N227
D1062	H992	P917	S851	Y785	M706	R636	G570	A500	T435	S298	H230	H230
I1065	G994	M921	T852	Y789	T710	P637	C571	W501	K436	S299	Y231	Y231
G1066	N995	P922	G853	G790	G715	H640	L575	G502	Y439	T303	W233	W233
H1067	E996	Q922	K854	G791	G716	L641	A576	F503	F440	L307	N234	N234
G1068	F997	M928	T855	E792	G717	S642	K577	F504	L441	G375	G235	G235
T1069	M998	Q929	S856	F794	L718	G644	A580	W507	H443	G376	T236	T236
S1070	N999	P930	T857	F795	R719	E645	L583	H508	T443	L378	W238	W238
F1071	G1004	H931	H861	K799	Y720	L646	L583	T509	G444	L379	F239	F239
L1072	Q1005	R932	R862	R800	R721	D647	L583	P510	Y447	L382	R240	R240
R1076	E1006	I933	G863	R801	T722	W648	L586	D511	S448	L383	H242	H242
M1079	A1008	T934	T863	R802	R728	G650	K587	G512	N449	G316	W243	W243
C1080	K1009	N935	E864	G803	L729	P651	E589	S513	T450	V317	R244	R244
S1081	P936	E865	E866	E804	Q730	E652	Y590	P514	G451	G385	K245	K245
D1082	H867	P867	G866	P805	T731	G654	V591	C515	L452	Q386	N246	N246
Q1085	W868	A938	W868	W806	G732	L654	V592	G516	L453	I387	L249	L249
S1086	D869	H942	D870	H807	Q733	L659	K993	L517	D454	L388	I250	I250
W1087	E871	M943	E870	H808	T734	A660	L594	L518	Q455	K389	P251	P251
V1088	W871	T944	R872	H809	L741	C661	N596	N519	Q456	T392	S252	S252
C1089	L874	T944	L873	F812	H742	P662	G597	H520	A457	E393	M253	M253
R1090	L874	M947	L874	A813	Y745	P663	T598	R523	T458	D394	M254	M254
D1091	G875	E950	G875	P814	G746	L666	A599	K524	G459	L396	K257	K257
S1092	N876	S951	N876	G815	L747	X669	T600	I527	Y460	N397	L260	L260
L1096	D877	S951	D877	G816	L747	X669	T600	H530	A464	F329	E261	E261
S1097	V878	K955	V878	T817	Y750	H672	E601	P531	A464	L330	T262	T262
S1100	G879	A956	G879	P818	Y750	H673	K604	S532	A464	K333	E266	E266
T1101	D880	G957	D880	R819	T754	H674	V605	P532	A465	V334	I267	I267
I1102	S881	Q957	S881	R820	W755	V674	P606	S532	E465	V335	F268	F268
S1103	E821	G961	E821	E822	A756	E675	L607	D533	K466	V337	E269	E269
M1104	C883	I962	C883	W822	V757	V676	D608	V534	N468	H338	G270	G270
M1105	Q884	L962	Q884	L823	S677	S677	L609	V535	R471	A411	I271	I271
M1106	Q885	A963	Q885	Q824	P678	E610	S535	Q536	F472	P412	V272	V272
V1107	T1034	Q964	T1034	K825	T679	G612	G613	Q537	H475	G413	G273	G273
G1108	I1036	S966	I1036	L826	W763	L682	G614	I537	R477	V414	K274	K274
S1109	I1037	T967	I1037	T764	G615	L682	V613	S539	M478	D415	D275	D275
	M1039	P968	M1039	G765	Y766	T684	P616	L541	W479	F416		
		I970		G766	D767		S617	L544	H480			
								G545	R481			
								V546				

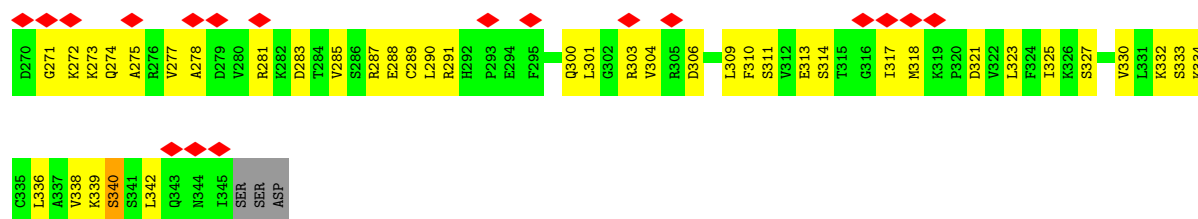


• Molecule 3: DNA-directed RNA polymerases I and III subunit RPAC1



• Molecule 3: DNA-directed RNA polymerases I and III subunit RPAC1

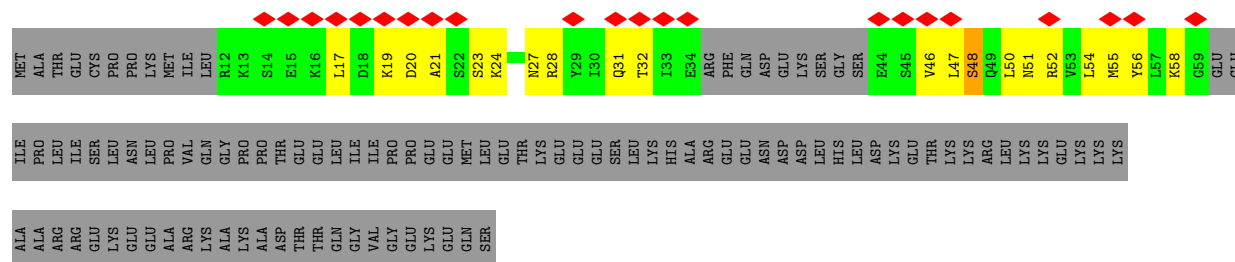




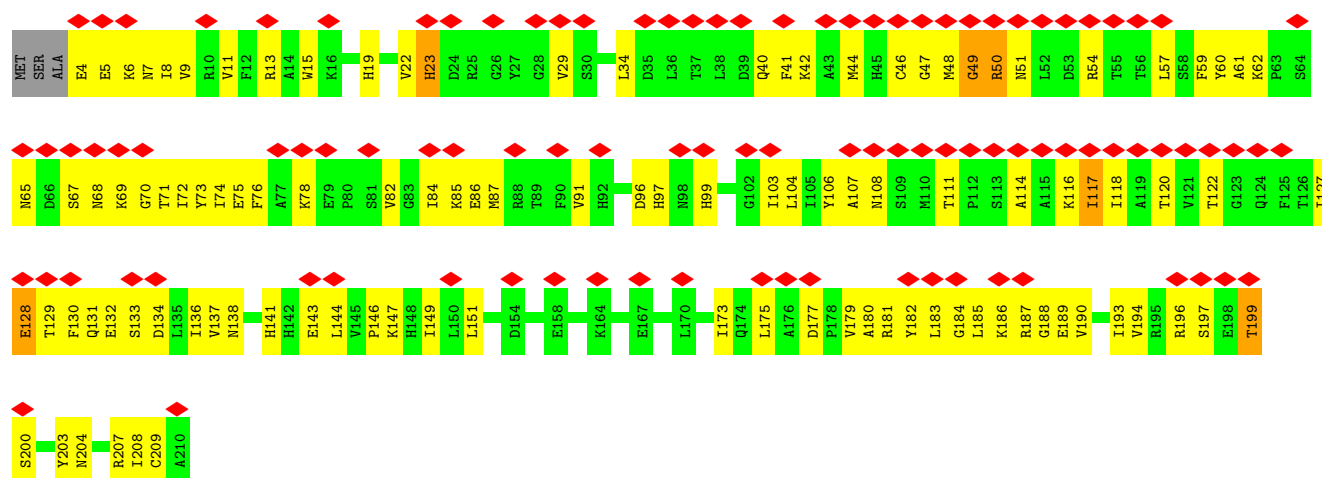
• Molecule 4: DNA-directed RNA polymerase I subunit rpa14



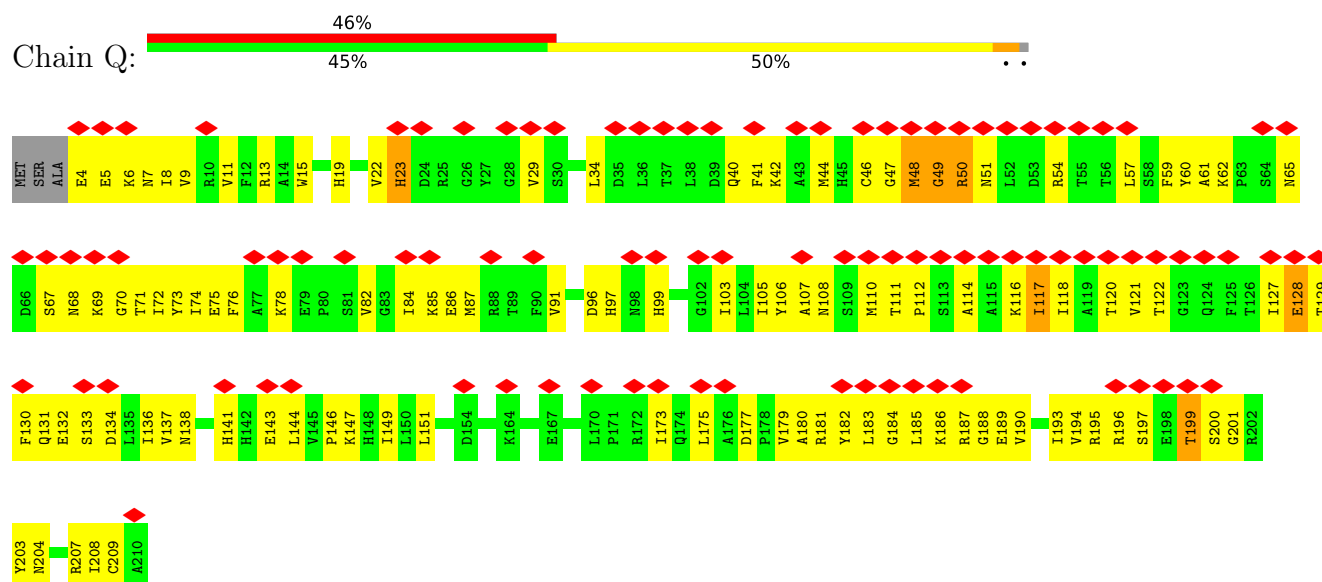
• Molecule 4: DNA-directed RNA polymerase I subunit rpa14



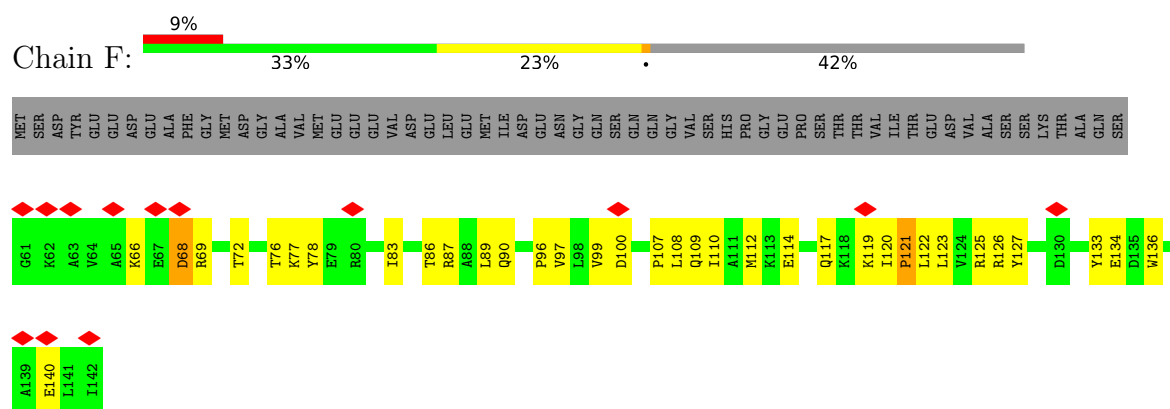
• Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1



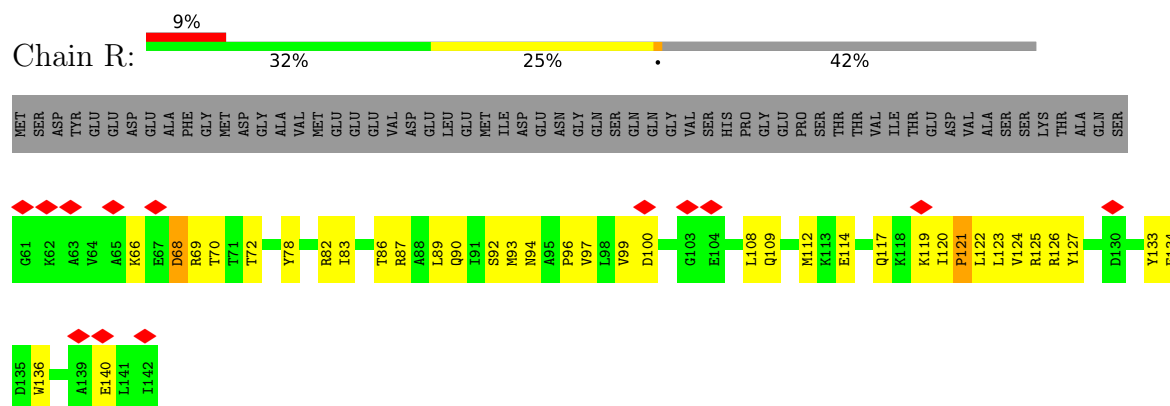
- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1



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

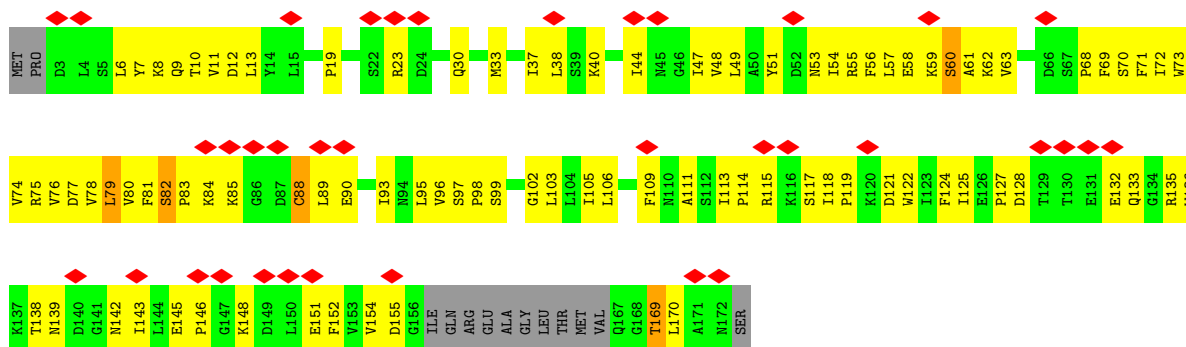


- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2

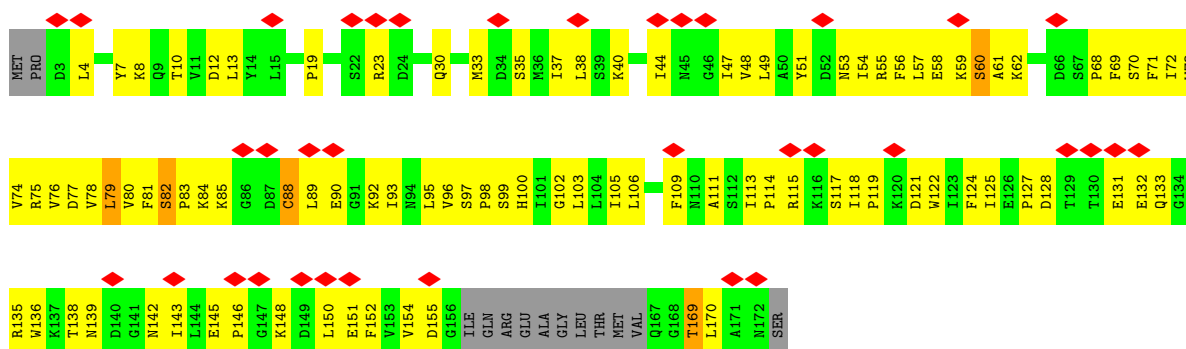


- Molecule 7: DNA-directed RNA polymerase I subunit rpa43

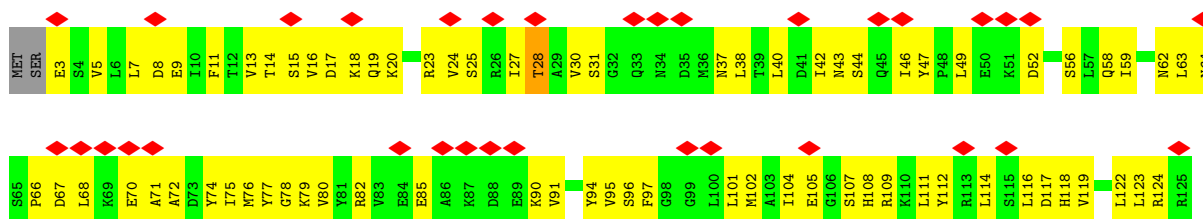




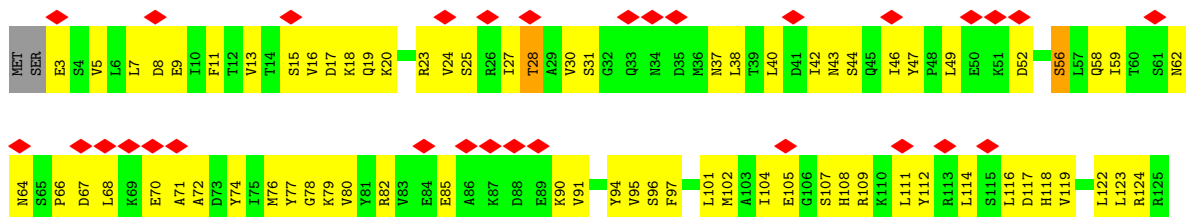
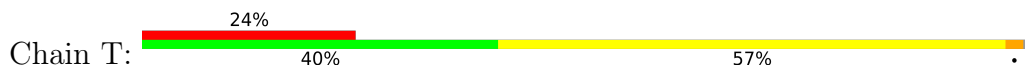
• Molecule 7: DNA-directed RNA polymerase I subunit rpa43



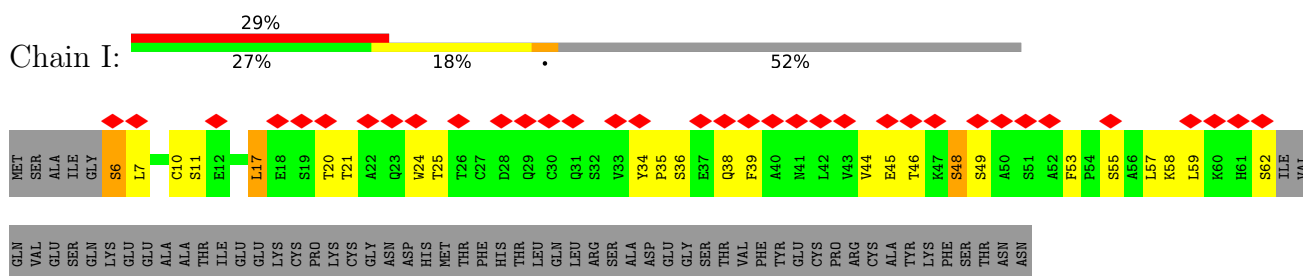
• Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3



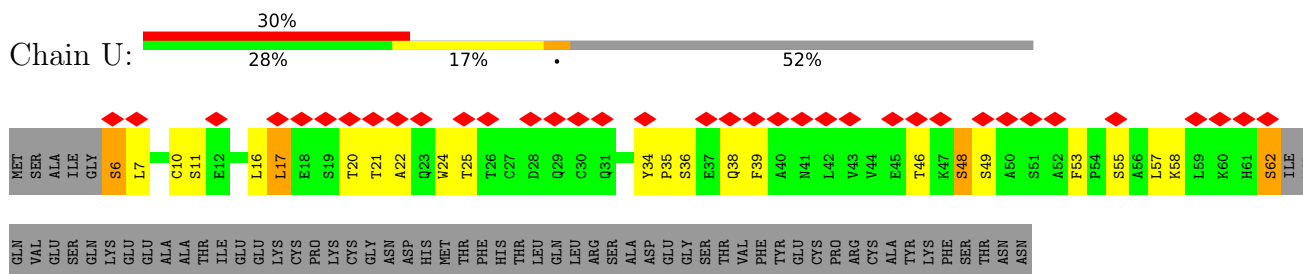
• Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3



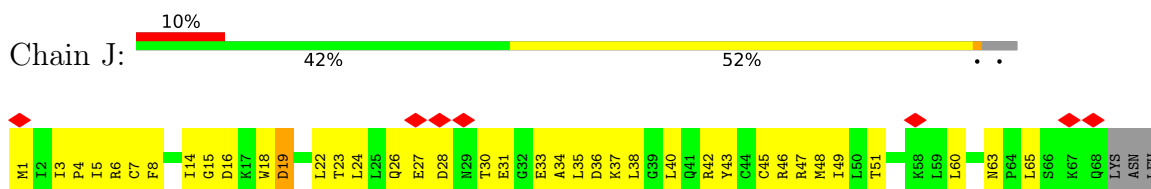
• Molecule 9: DNA-directed RNA polymerase I subunit RPA12



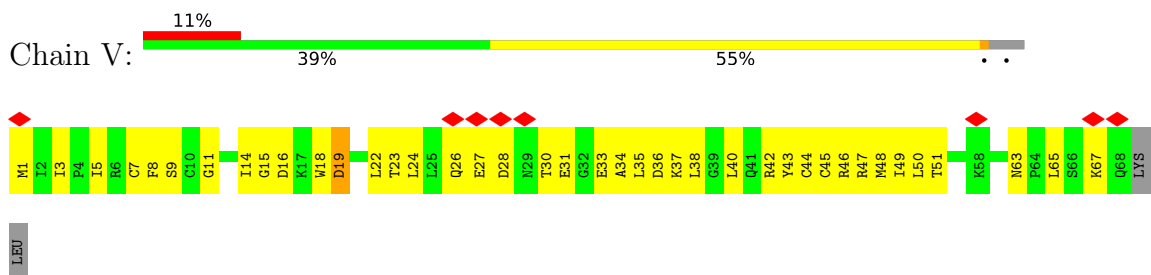
- Molecule 9: DNA-directed RNA polymerase I subunit RPA12



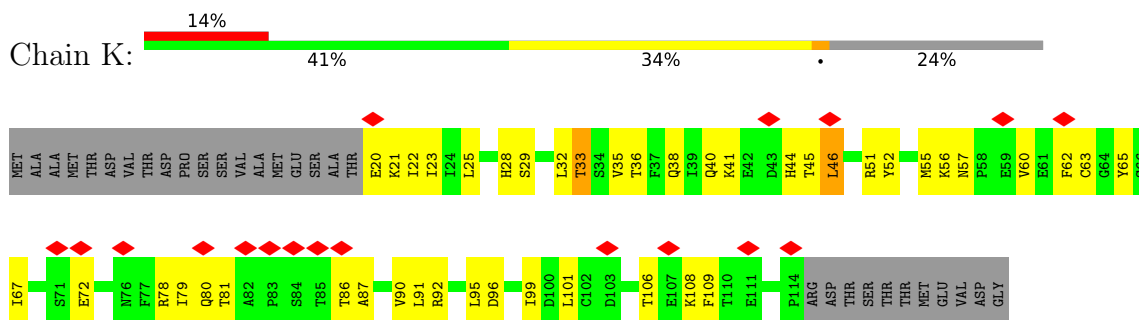
- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5



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

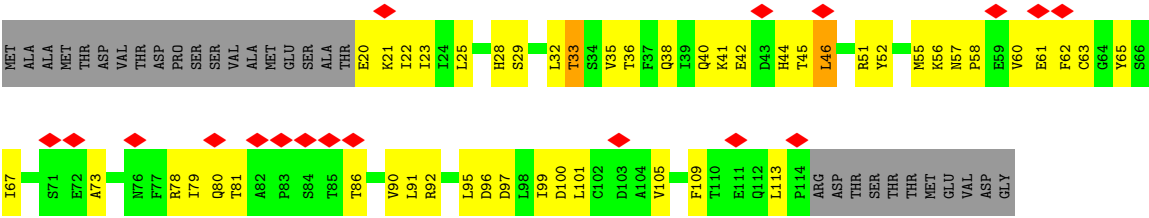


- Molecule 11: DNA-directed RNA polymerases I and III subunit RPAC2



- Molecule 11: DNA-directed RNA polymerases I and III subunit RPAC2

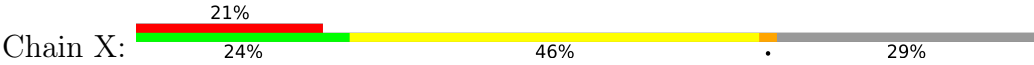




• Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4



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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	17102	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	86.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.099	Depositor
Minimum map value	-0.045	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.033	Depositor
Map size ($\text{\AA}$)	382.86002, 382.86002, 382.86002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0635, 1.0635, 1.0635	Depositor

5 Model quality

5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.31	0/11194	0.53	0/15122
1	M	0.31	0/11194	0.53	0/15122
2	B	0.34	0/9332	0.54	0/12615
2	N	0.34	0/9332	0.54	0/12615
3	C	0.31	0/2588	0.49	0/3505
3	O	0.31	0/2588	0.49	0/3505
4	D	0.25	0/323	0.49	0/427
4	P	0.25	0/323	0.49	0/427
5	E	0.28	0/1695	0.57	3/2287 (0.1%)
5	Q	0.28	0/1695	0.57	3/2287 (0.1%)
6	F	0.41	0/660	0.52	0/893
6	R	0.41	0/660	0.52	0/893
7	G	0.31	0/1295	0.53	0/1755
7	S	0.31	0/1295	0.53	0/1755
8	H	0.29	0/1004	0.59	0/1355
8	T	0.29	0/1004	0.60	0/1355
9	I	0.25	0/439	0.51	0/596
9	U	0.25	0/439	0.51	0/596
10	J	0.37	0/558	0.64	0/751
10	V	0.37	0/558	0.64	0/751
11	K	0.33	0/759	0.48	0/1030
11	W	0.33	0/759	0.48	0/1030
12	L	0.35	0/371	0.56	0/491
12	X	0.35	0/371	0.56	0/491
All	All	0.32	0/60436	0.53	6/81654 (0.0%)

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	4
1	M	0	4
2	B	0	1
2	N	0	1
5	E	0	4
5	Q	0	4
7	G	0	1
7	S	0	1
All	All	0	20

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	Q	49	GLY	CA-C-N	5.63	131.83	121.70
5	Q	49	GLY	C-N-CA	5.63	131.83	121.70
5	E	49	GLY	CA-C-N	5.62	131.82	121.70
5	E	49	GLY	C-N-CA	5.62	131.82	121.70
5	E	91	VAL	N-CA-C	-5.16	107.54	111.62

There are no chirality outliers.

5 of 20 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1656	ASP	Peptide
1	A	246	ILE	Peptide
1	A	84	ILE	Peptide
1	A	896	TYR	Peptide
2	B	90	SER	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	10976	0	10980	648	0
1	M	10976	0	10980	660	0
2	B	9127	0	9092	522	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	N	9127	0	9092	571	0
3	C	2533	0	2540	155	0
3	O	2533	0	2540	174	0
4	D	322	0	338	21	0
4	P	322	0	338	19	0
5	E	1663	0	1684	79	0
5	Q	1663	0	1684	86	0
6	F	650	0	674	36	0
6	R	650	0	674	38	0
7	G	1267	0	1278	93	0
7	S	1267	0	1278	99	0
8	H	990	0	1001	67	0
8	T	990	0	1001	65	0
9	I	431	0	410	17	0
9	U	431	0	410	21	0
10	J	550	0	564	38	0
10	V	550	0	564	42	0
11	K	745	0	745	42	0
11	W	745	0	745	53	0
12	L	368	0	377	27	0
12	X	368	0	377	52	0
13	A	2	0	0	0	0
13	B	1	0	0	0	0
13	I	1	0	0	0	0
13	J	1	0	0	0	0
13	L	1	0	0	0	0
13	M	2	0	0	0	0
13	N	1	0	0	0	0
13	U	1	0	0	0	0
13	V	1	0	0	0	0
13	X	1	0	0	0	0
All	All	59256	0	59366	3265	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 28.

The worst 5 of 3265 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)
2:N:696:GLN:HG2	2:N:698:PRO:HD2	1.45	0.98
2:B:696:GLN:HG2	2:B:698:PRO:HD2	1.45	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:735:GLN:HE22	8:H:77:TYR:HB2	1.30	0.95
1:A:1279:VAL:O	9:I:48:SER:OG	1.86	0.94
8:H:17:ASP:HA	8:H:18:LYS:HB2	1.51	0.92

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	1356/1689 (80%)	1213 (90%)	136 (10%)	7 (0%)	24	63
1	M	1356/1689 (80%)	1214 (90%)	135 (10%)	7 (0%)	24	63
2	B	1148/1174 (98%)	1015 (88%)	129 (11%)	4 (0%)	36	71
2	N	1148/1174 (98%)	1015 (88%)	129 (11%)	4 (0%)	36	71
3	C	315/348 (90%)	290 (92%)	25 (8%)	0	100	100
3	O	315/348 (90%)	290 (92%)	25 (8%)	0	100	100
4	D	35/147 (24%)	34 (97%)	1 (3%)	0	100	100
4	P	35/147 (24%)	34 (97%)	1 (3%)	0	100	100
5	E	205/210 (98%)	180 (88%)	25 (12%)	0	100	100
5	Q	205/210 (98%)	179 (87%)	26 (13%)	0	100	100
6	F	80/142 (56%)	75 (94%)	4 (5%)	1 (1%)	9	41
6	R	80/142 (56%)	75 (94%)	4 (5%)	1 (1%)	9	41
7	G	156/173 (90%)	139 (89%)	17 (11%)	0	100	100
7	S	156/173 (90%)	139 (89%)	17 (11%)	0	100	100
8	H	121/125 (97%)	95 (78%)	26 (22%)	0	100	100
8	T	121/125 (97%)	95 (78%)	26 (22%)	0	100	100
9	I	55/119 (46%)	50 (91%)	5 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	U	55/119 (46%)	50 (91%)	5 (9%)	0	100	100
10	J	66/71 (93%)	46 (70%)	20 (30%)	0	100	100
10	V	66/71 (93%)	46 (70%)	20 (30%)	0	100	100
11	K	93/125 (74%)	90 (97%)	3 (3%)	0	100	100
11	W	93/125 (74%)	90 (97%)	3 (3%)	0	100	100
12	L	43/63 (68%)	40 (93%)	3 (7%)	0	100	100
12	X	43/63 (68%)	40 (93%)	3 (7%)	0	100	100
All	All	7346/8772 (84%)	6534 (89%)	788 (11%)	24 (0%)	37	71

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1066	ASP
1	M	1066	ASP
1	A	1154	ASP
1	M	1154	ASP
2	B	206	THR

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	1225/1484 (82%)	1214 (99%)	11 (1%)	70	76
1	M	1225/1484 (82%)	1214 (99%)	11 (1%)	70	76
2	B	1001/1013 (99%)	989 (99%)	12 (1%)	63	73
2	N	1001/1013 (99%)	989 (99%)	12 (1%)	63	73
3	C	281/308 (91%)	271 (96%)	10 (4%)	31	52
3	O	281/308 (91%)	271 (96%)	10 (4%)	31	52
4	D	37/134 (28%)	36 (97%)	1 (3%)	39	59
4	P	37/134 (28%)	36 (97%)	1 (3%)	39	59
5	E	182/184 (99%)	174 (96%)	8 (4%)	25	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	Q	182/184 (99%)	174 (96%)	8 (4%)	25	47
6	F	70/121 (58%)	67 (96%)	3 (4%)	26	48
6	R	70/121 (58%)	67 (96%)	3 (4%)	26	48
7	G	143/154 (93%)	138 (96%)	5 (4%)	32	53
7	S	143/154 (93%)	138 (96%)	5 (4%)	32	53
8	H	112/114 (98%)	110 (98%)	2 (2%)	51	67
8	T	112/114 (98%)	110 (98%)	2 (2%)	51	67
9	I	51/105 (49%)	44 (86%)	7 (14%)	3	15
9	U	51/105 (49%)	44 (86%)	7 (14%)	3	15
10	J	63/66 (96%)	61 (97%)	2 (3%)	34	55
10	V	63/66 (96%)	61 (97%)	2 (3%)	34	55
11	K	86/111 (78%)	84 (98%)	2 (2%)	44	63
11	W	86/111 (78%)	84 (98%)	2 (2%)	44	63
12	L	39/53 (74%)	38 (97%)	1 (3%)	40	60
12	X	39/53 (74%)	38 (97%)	1 (3%)	40	60
All	All	6580/7694 (86%)	6452 (98%)	128 (2%)	49	66

5 of 128 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	T	56	SER
9	U	48	SER
7	G	143	ILE
7	G	88	CYS
9	U	57	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 138 such sidechains are listed below:

Mol	Chain	Res	Type
2	N	1038	HIS
3	O	182	GLN
7	S	30	GLN
3	C	166	ASN
2	B	1043	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 12 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

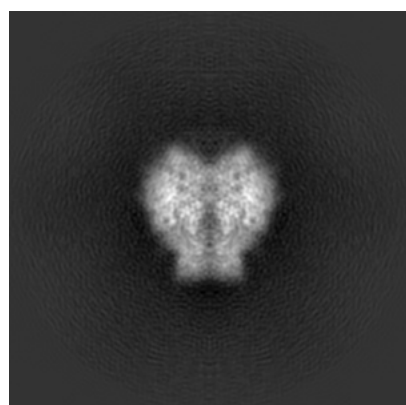
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11841. These allow visual inspection of the internal detail of the map and identification of artifacts.

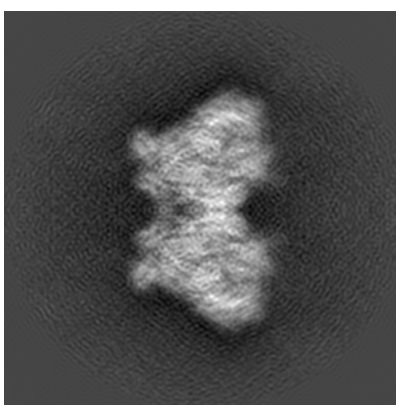
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

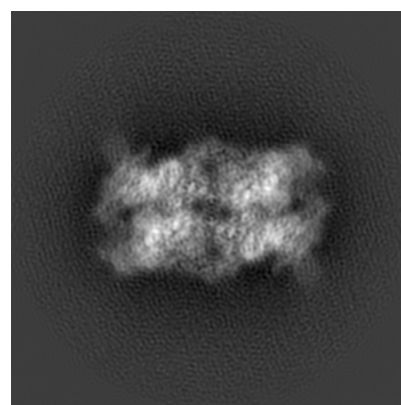
6.1.1 Primary map



X



Y

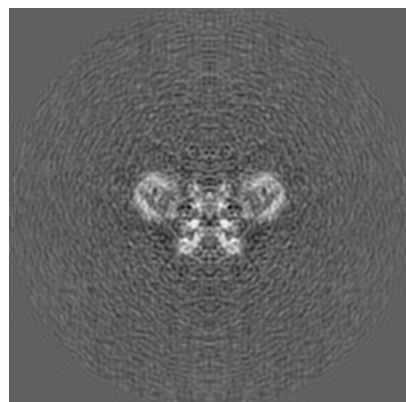


Z

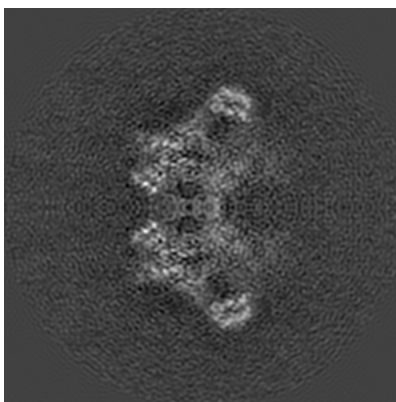
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

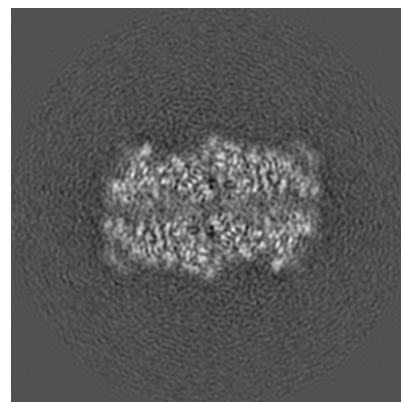
6.2.1 Primary map



X Index: 180



Y Index: 180

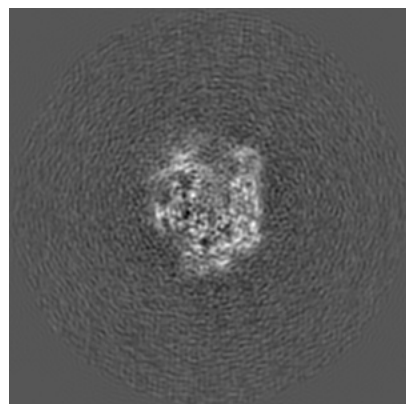


Z Index: 180

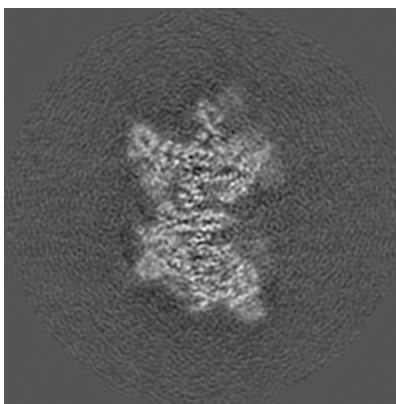
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

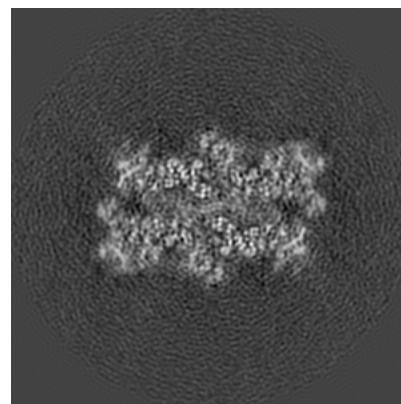
6.3.1 Primary map



X Index: 145



Y Index: 200

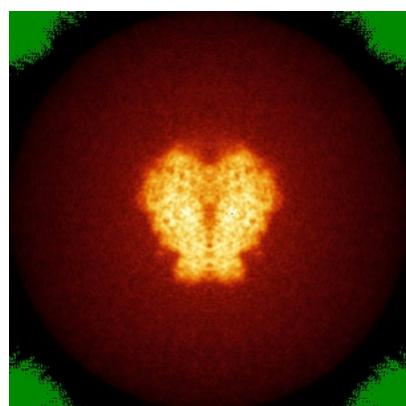


Z Index: 189

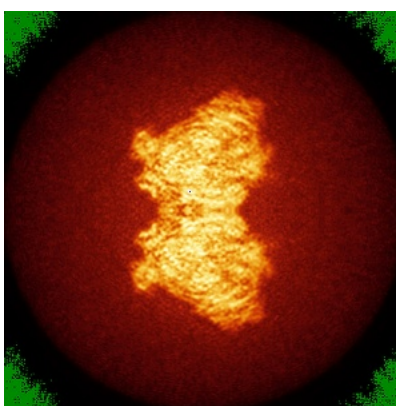
The images above show the largest variance slices of the map in three orthogonal directions.

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

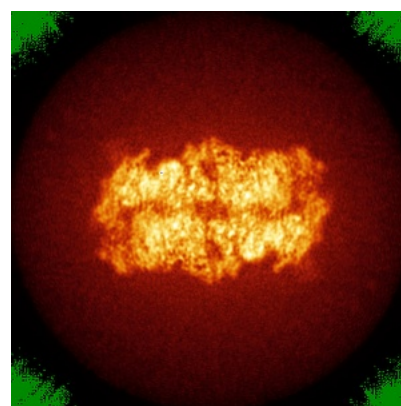
6.4.1 Primary map



X



Y

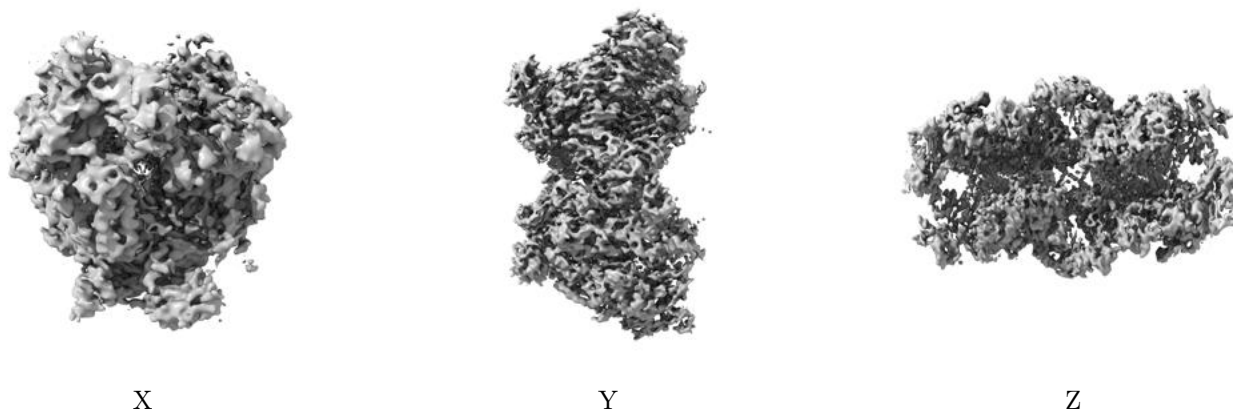


Z

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 0.033. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

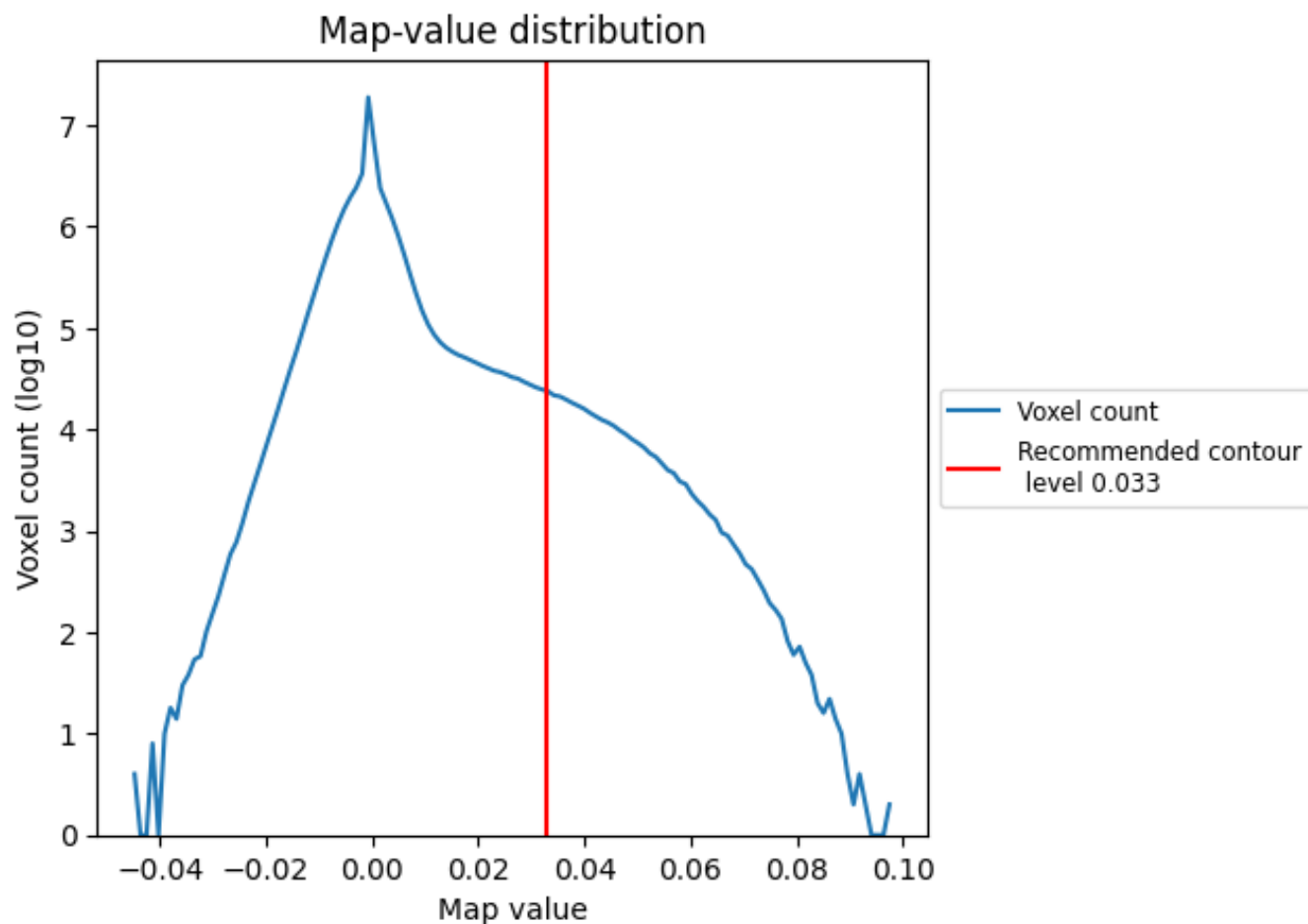
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

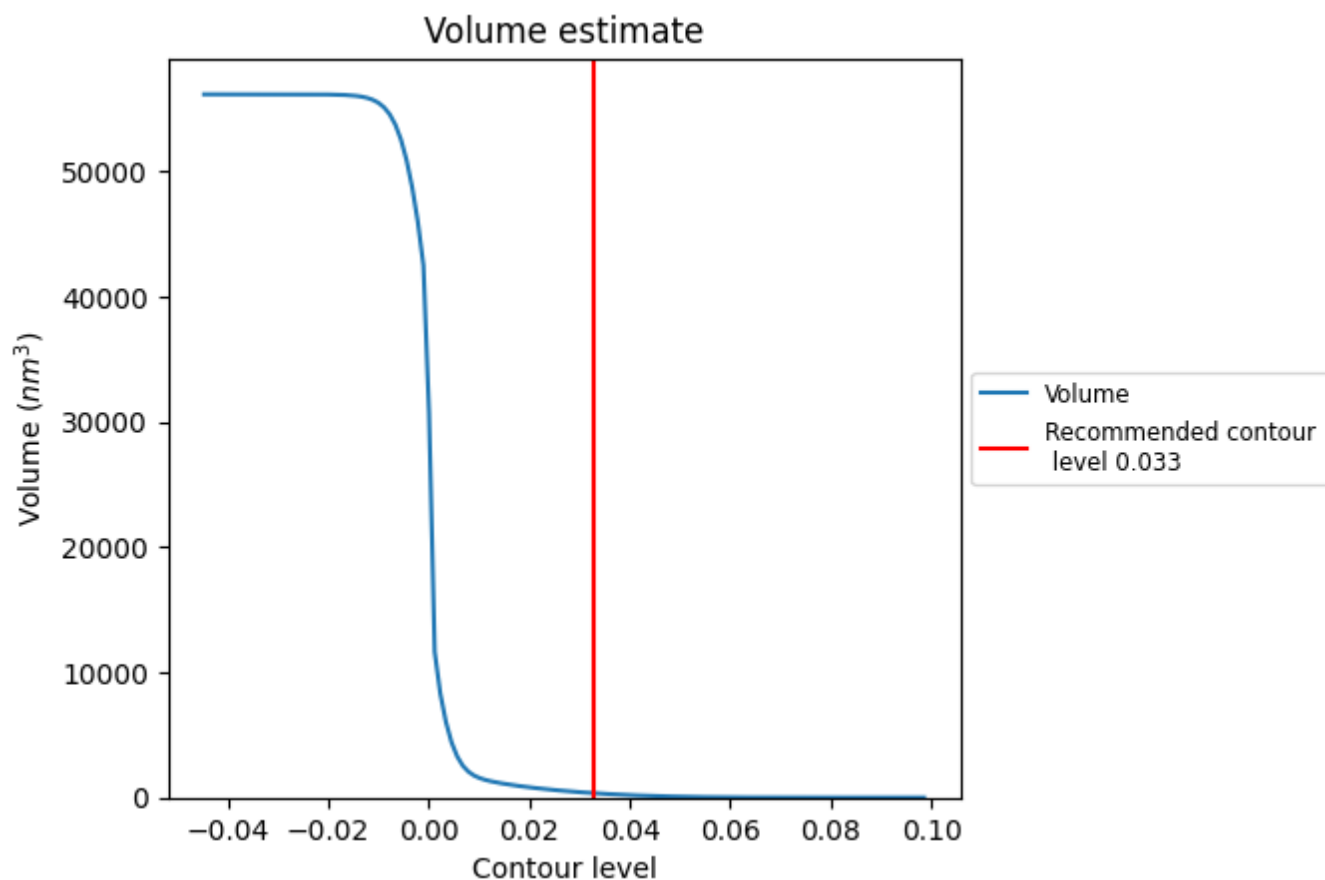
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

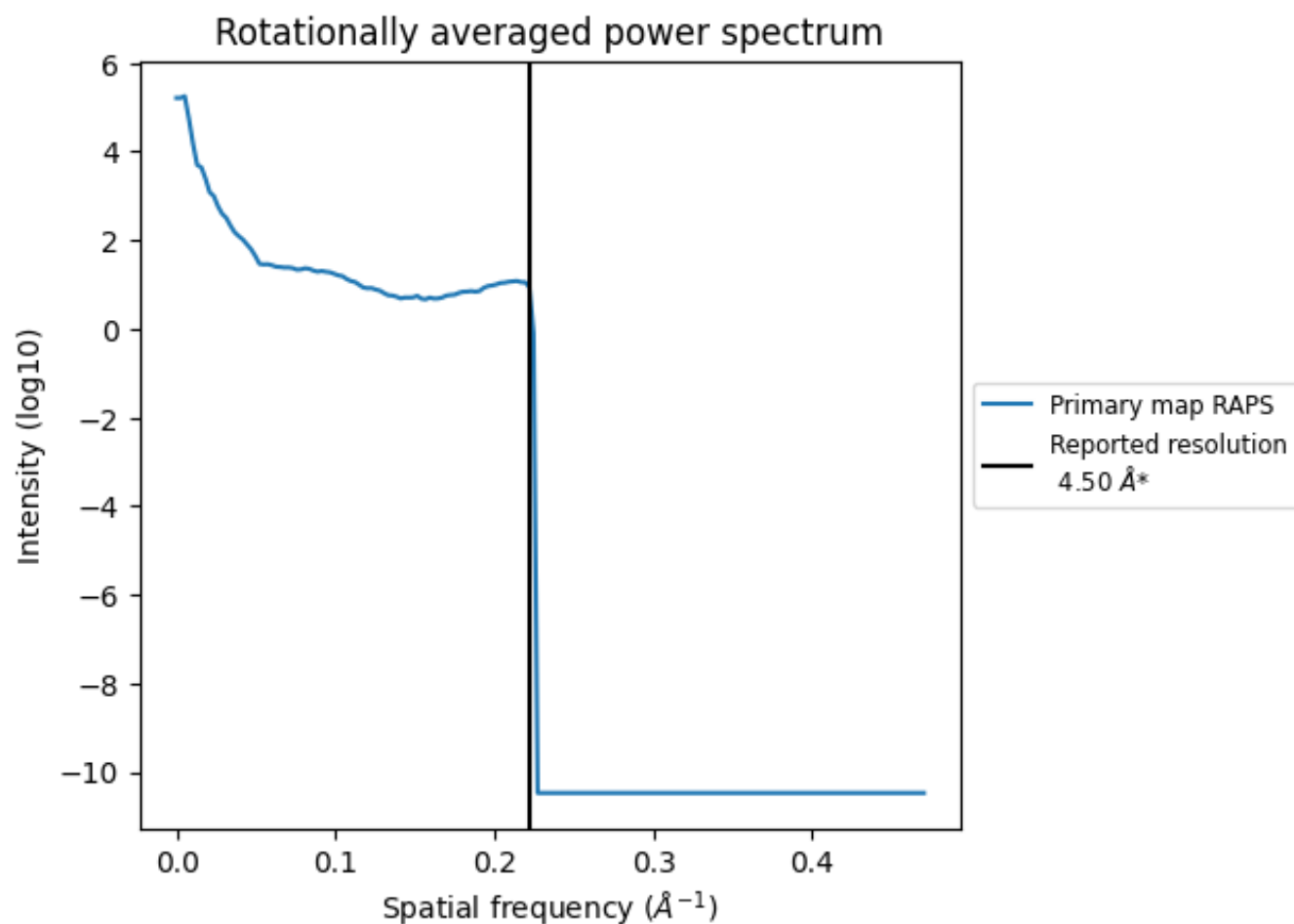
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 347 nm³; this corresponds to an approximate mass of 314 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 0.222 Å⁻¹

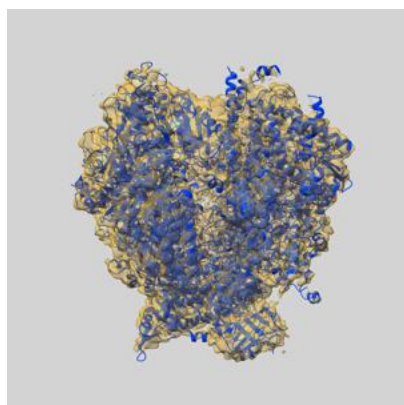
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

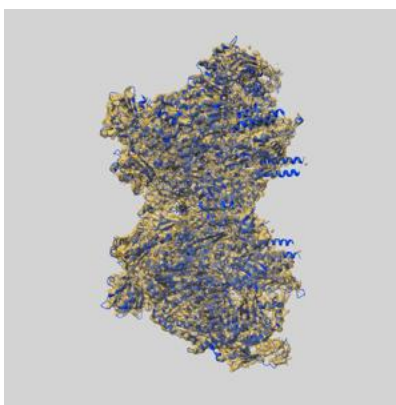
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11841 and PDB model 7AOD. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

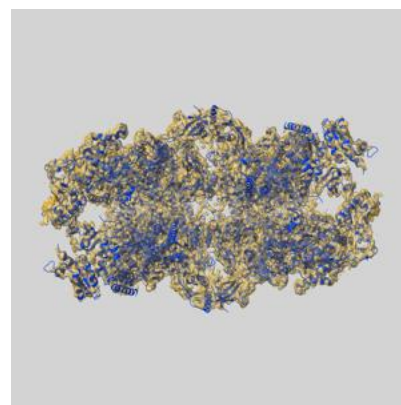
9.1 Map-model overlay [i](#)



X



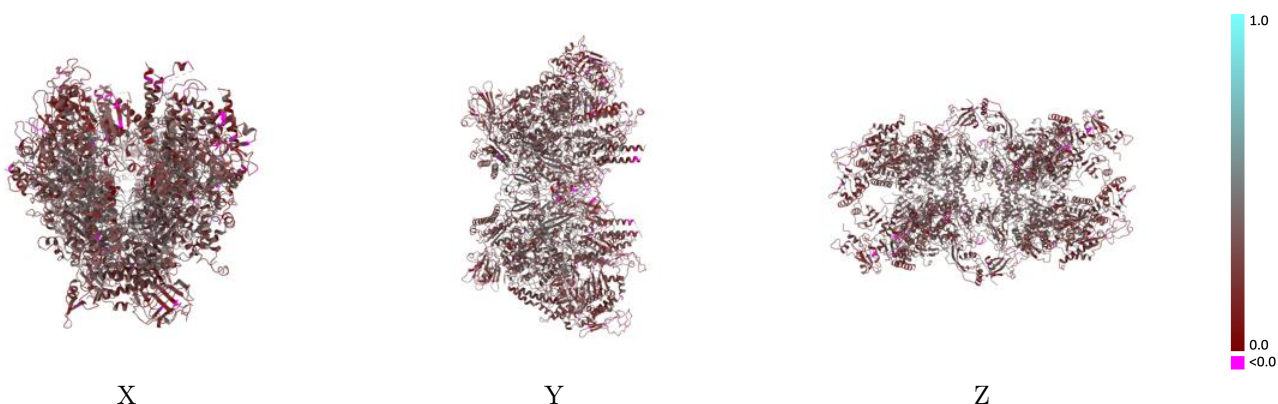
Y



Z

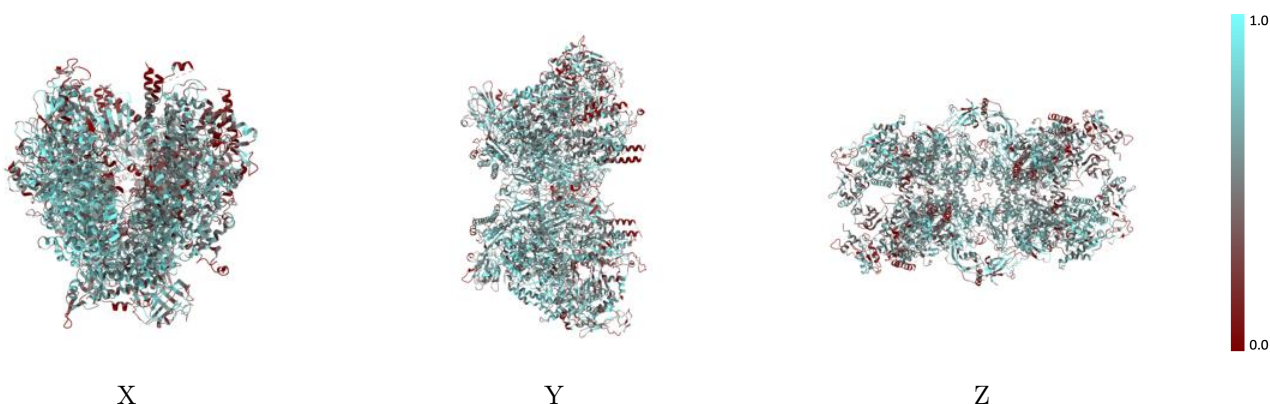
The images above show the 3D surface view of the map at the recommended contour level 0.033 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



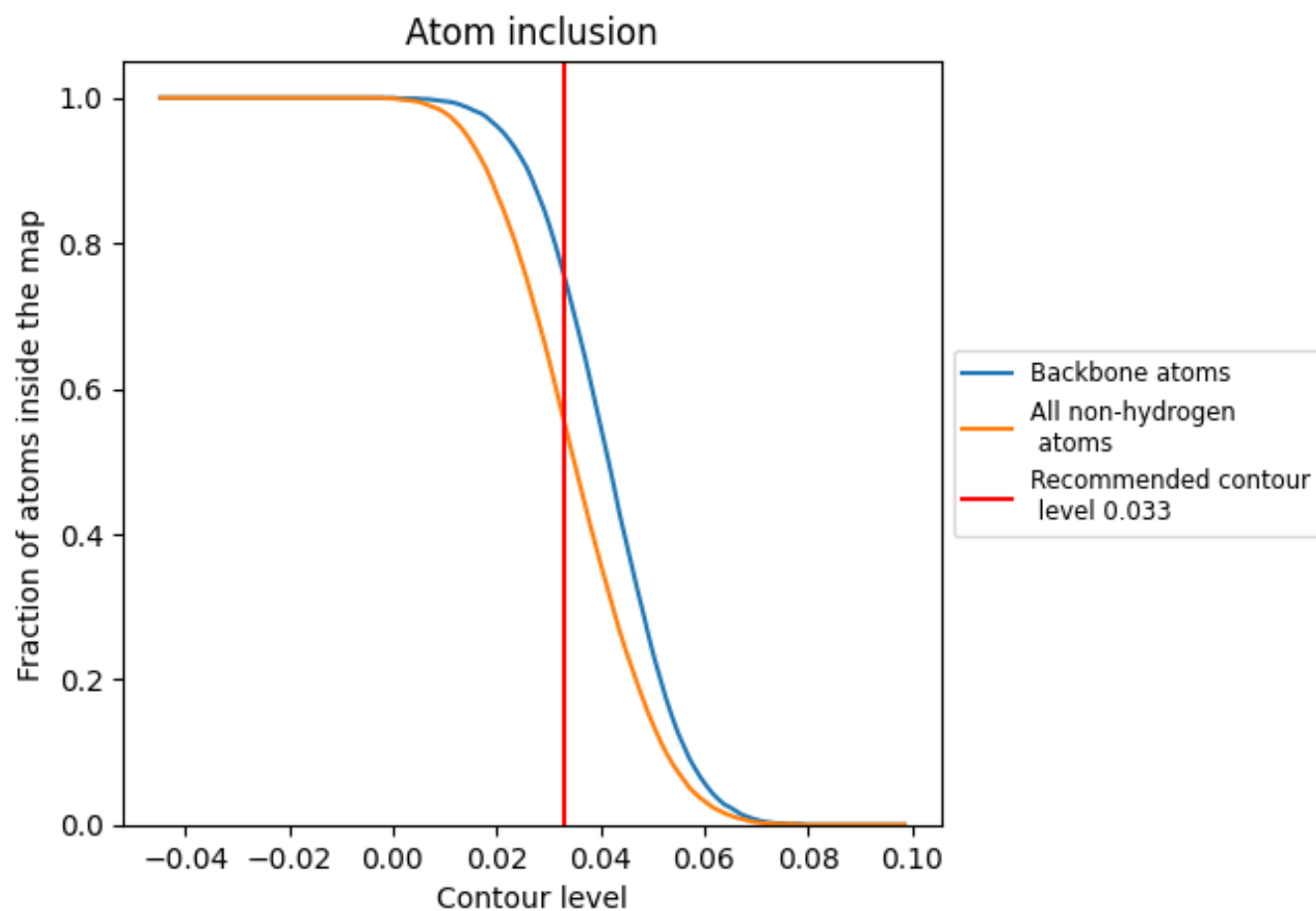
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.033).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 56% 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 (0.033) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5550	 0.3090
A	 0.5320	 0.3070
B	 0.5950	 0.3230
C	 0.5730	 0.3120
D	 0.3950	 0.2420
E	 0.4360	 0.2740
F	 0.6220	 0.3460
G	 0.5960	 0.2870
H	 0.5440	 0.2730
I	 0.3300	 0.2280
J	 0.7010	 0.3360
K	 0.6010	 0.2960
L	 0.5440	 0.3340
M	 0.5300	 0.3070
N	 0.5950	 0.3220
O	 0.5750	 0.3190
P	 0.3820	 0.2390
Q	 0.4460	 0.2780
R	 0.6160	 0.3530
S	 0.5990	 0.2910
T	 0.5520	 0.2720
U	 0.3330	 0.2410
V	 0.7070	 0.3460
W	 0.6000	 0.2950
X	 0.5500	 0.3400

