



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 11:50 AM UTC

PDB ID : 7UND / pdb_00007und
EMDB ID : EMD-26621
Title : Pol II-DSIF-SPT6-PAF1c-TFIIS-nucleosome complex (stalled at +38)
Authors : Filipovski, M.; Vos, S.M.; Farnung, L.
Deposited on : 2022-04-10
Resolution : 3.00 Å (reported)
Based on initial models : 3LZ0, 6TED

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
Mogul : 2022.3.0, CSD as543be (2022)
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

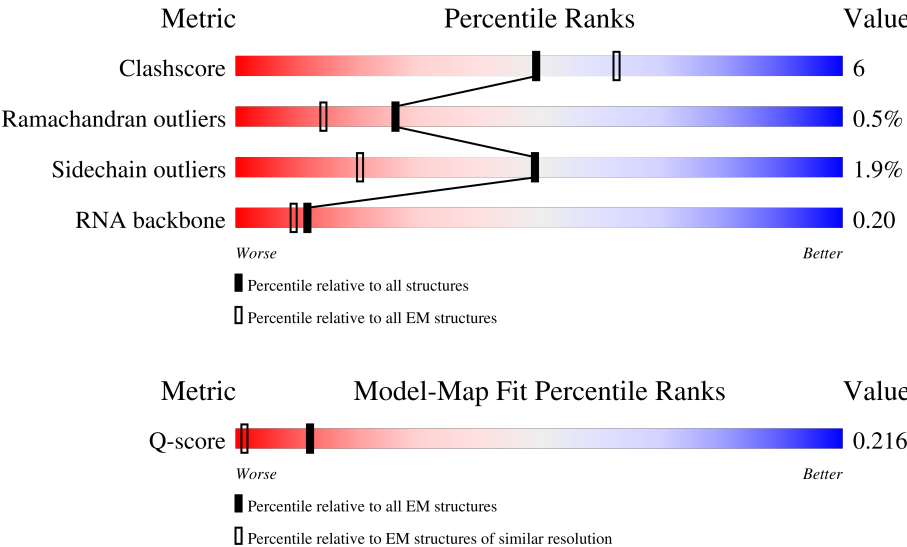
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	

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Mol	Chain	Length	Quality of chain
4	D	184	
5	E	210	
6	F	127	
7	G	172	
8	H	150	
9	I	125	
10	J	67	
11	K	117	
12	L	58	
13	M	1729	
14	N	209	
15	O	304	
16	P	18	
17	Q	1179	
18	R	713	
19	T	215	
20	U	666	
21	V	531	
22	W	305	
23	X	531	
24	Y	117	
25	Z	1087	
26	a	136	
26	e	136	
27	b	103	

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Mol	Chain	Length	Quality of chain
27	f	103	
28	c	130	
28	g	130	
29	d	123	
29	h	123	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
30	ZN	C	301	-	-	X	-

2 Entry composition [i](#)

There are 31 unique types of molecules in this entry. The entry contains 129470 atoms, of which 61557 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	H	N	O	P	S	0	0
			22640	7074	11385	2014	2095	2	70		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	1122	Total	C	H	N	O	S	0	0
			18004	5684	9024	1576	1656	64		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	258	Total	C	H	N	O	S	0	0
			4093	1300	2021	356	410	6		

- Molecule 4 is a protein called RPOL4c domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	126	Total	C	H	N	O	S	0	0
			1985	630	981	170	200	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	209	Total	C	H	N	O	S	0	0
			3456	1089	1736	300	323	8		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	78	Total	C	H	N	O	S	0	0
			1284	401	658	106	114	5		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	171	Total	C	H	N	O	S	0	0
			2654	866	1321	214	245	8		

- Molecule 8 is a protein called RPB8.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	H	149	Total	C	H	N	O	S	0	0
			2354	759	1157	195	238	5		

- Molecule 9 is a protein called RPB9.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	I	116	Total	C	H	N	O	S	0	0
			1816	582	874	168	181	11		

- Molecule 10 is a protein called RPB10.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	J	66	Total	C	H	N	O	S	0	0
			1065	339	541	88	91	6		

- Molecule 11 is a protein called RPB11.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	K	115	Total	C	H	N	O	S	0	0
			1862	593	942	152	173	2		

- Molecule 12 is a protein called RNA polymerase II subunit K.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	L	47	Total	C	H	N	O	S	0	0
			804	246	407	77	68	6		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
13	M	1002	Total	C	H	N	O	S	0	0
			7565	2738	2638	1074	1108	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 Non-template DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	N	120	Total	C	H	N	O	P	0	0
			3815	1169	1355	433	738	120		

- Molecule 15 is a protein called Transcription elongation factor A protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	161	Total	C	N	O	S	0	0
			1274	778	234	248	14		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	-2	SER	-	expression tag	UNP P23193
O	-1	ASN	-	expression tag	UNP P23193
O	0	ALA	-	expression tag	UNP P23193

- Molecule 16 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	P	18	Total	C	H	N	O	P	0	0
			572	169	191	61	133	18		

- Molecule 17 is a protein called RNA polymerase-associated protein CTR9 homolog.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	Q	890	Total	C	H	N	O	S	0	0
			14397	4579	7171	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

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	1178	PHE	-	expression tag	UNP Q6PD62
Q	1179	GLN	-	expression tag	UNP Q6PD62

- Molecule 18 is a protein called RNA polymerase-associated protein RTF1 homolog.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	R	244	Total	C	H	N	O	S	0	0
			3537	1152	1701	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 19 is a DNA chain called Template DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	T	131	Total	C	H	N	O	P	0	0
			4138	1267	1458	518	764	131		

- Molecule 20 is a protein called RNA polymerase-associated protein LEO1.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	U	125	Total	C	H	N	O	S	0	0
			1544	538	687	151	167	1		

- Molecule 21 is a protein called RNA polymerase II-associated factor 1 homolog.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	V	244	Total	C	H	N	O	S	0	0
			3161	1066	1450	306	335	4		

- Molecule 22 is a protein called WDR61.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	W	300	Total	C	H	N	O	S	0	0
			4580	1483	2247	392	454	4		

- Molecule 23 is a protein called Parafibromin.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	43	Total	C	H	N	O	0	0
			725	220	372	69	64		

- Molecule 24 is a protein called Transcription elongation factor SPT4.

Mol	Chain	Residues	Atoms					AltConf	Trace	
24	Y	116	Total	C	H	N	O	S	0	0
			1820	570	909	159	173	9		

- Molecule 25 is a protein called Transcription elongation factor SPT5.

Mol	Chain	Residues	Atoms							AltConf	Trace
25	Z	510	Total	C	H	N	O	P	S	0	0
			8071	2552	4046	709	745	1	18		

- Molecule 26 is a protein called Histone H3.2.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	a	97	Total	C	H	N	O	S	0	0
			1643	506	841	155	138	3		
26	e	97	Total	C	H	N	O	S	0	0
			1640	504	839	155	139	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	102	ALA	GLY	engineered mutation	UNP P84233
e	102	ALA	GLY	engineered mutation	UNP P84233

- Molecule 27 is a protein called Histone H4.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	b	83	Total	C	H	N	O	S	0	0
			1372	418	710	129	114	1		
27	f	78	Total	C	H	N	O	S	0	0
			1279	391	660	120	107	1		

- Molecule 28 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	103	Total	C	H	N	O	0	0
			1642	501	847	155	139		

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Mol	Chain	Residues	Atoms					AltConf	Trace
28	g	105	Total	C	H	N	O	0	0
			1674	510	865	158	141		

- Molecule 29 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	d	95	Total	C	H	N	O	S	0	0
			1519	469	774	134	140	2		
29	h	93	Total	C	H	N	O	S	0	0
			1475	457	749	130	137	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
d	0	MET	-	initiating methionine	UNP P02281
d	29	THR	SER	engineered mutation	UNP P02281
h	0	MET	-	initiating methionine	UNP P02281
h	29	THR	SER	engineered mutation	UNP P02281

- Molecule 30 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

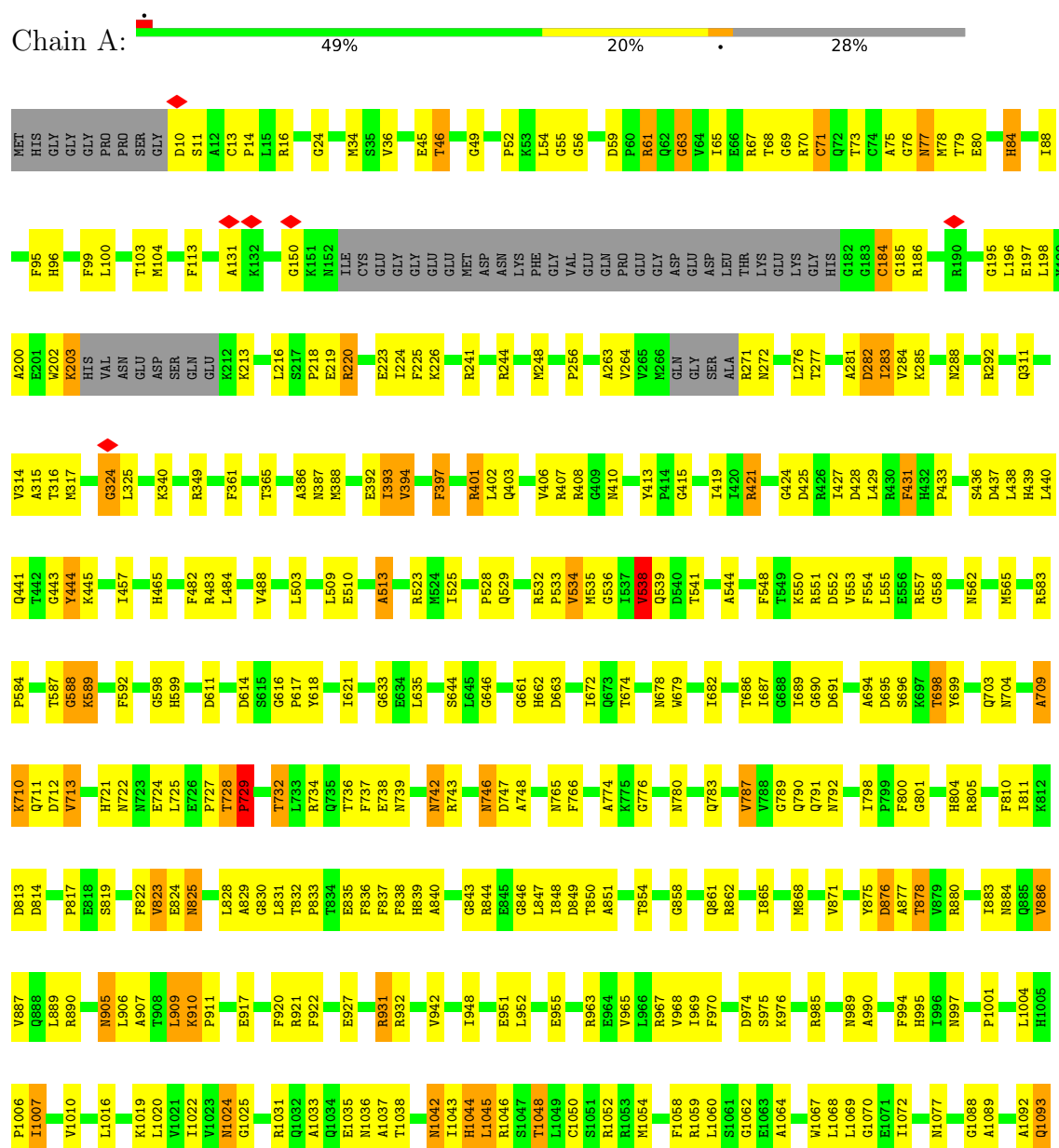
- Molecule 31 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

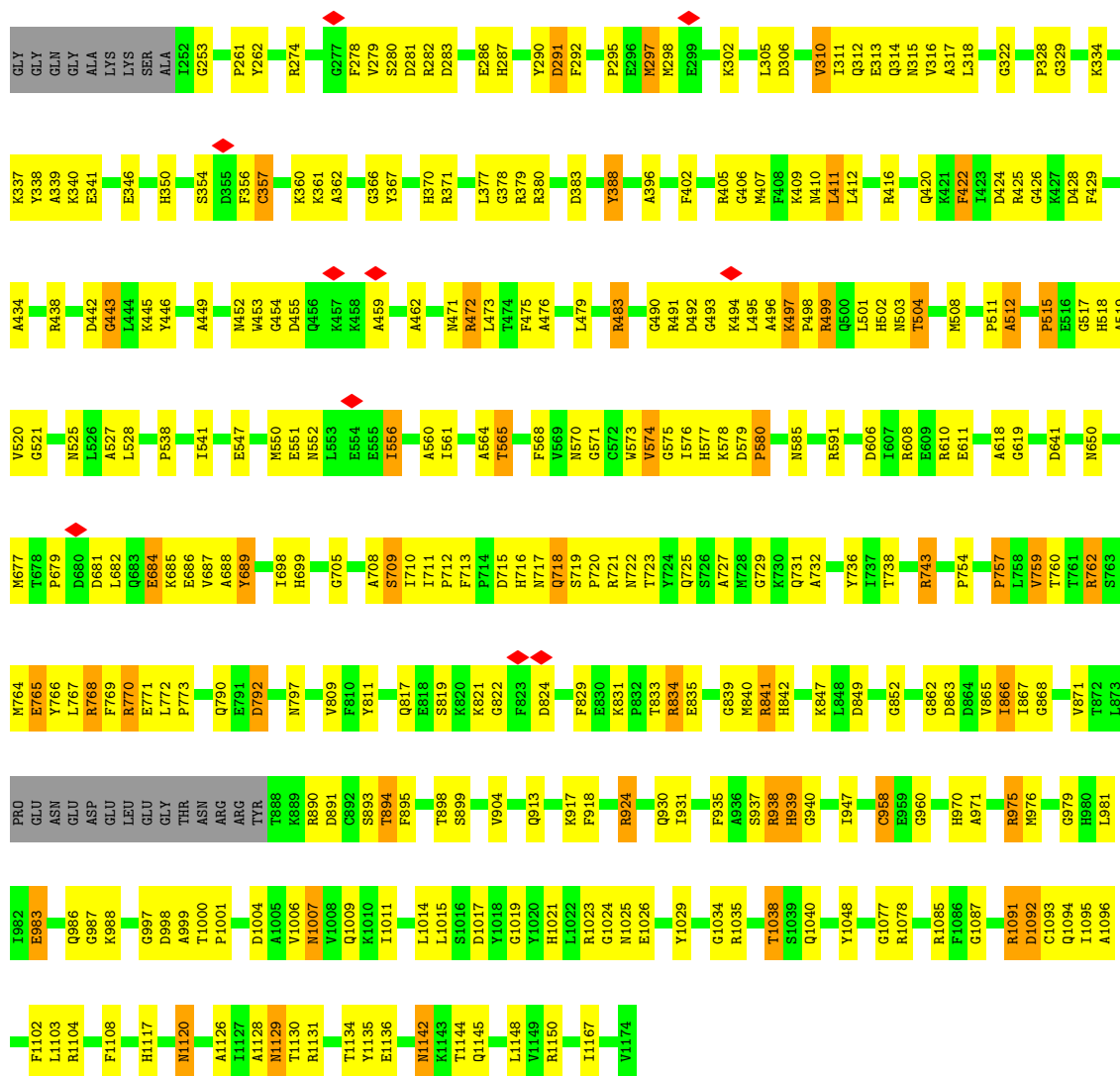
3 Residue-property plots

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

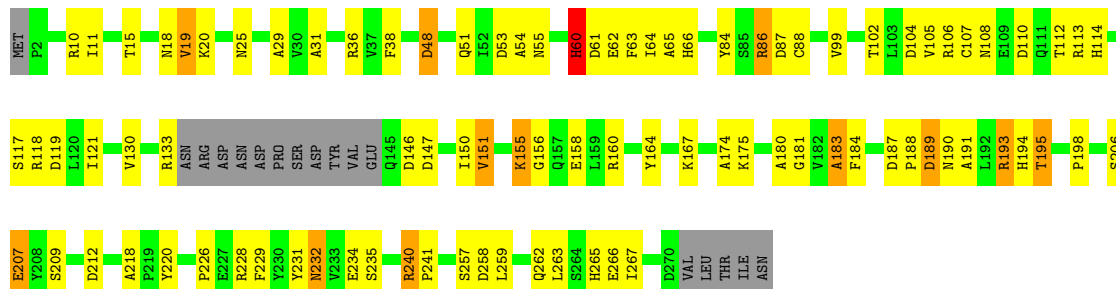






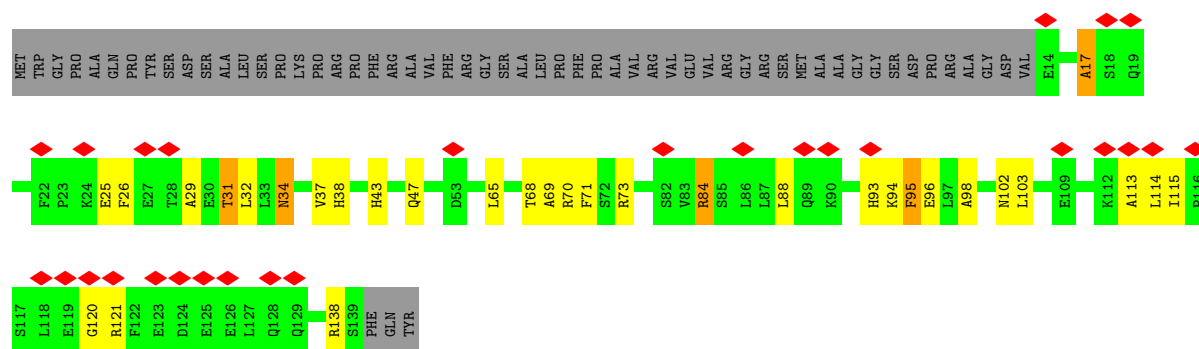
• Molecule 3: DNA-directed RNA polymerase II subunit RPB3

Chain C: 60% 29% 6%

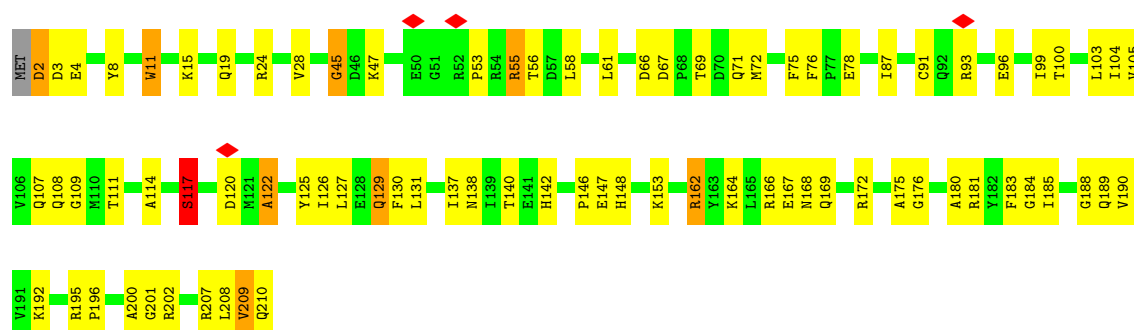


• Molecule 4: RPOL4c domain-containing protein

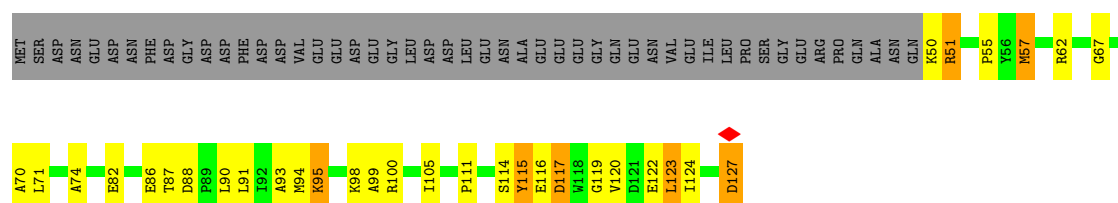
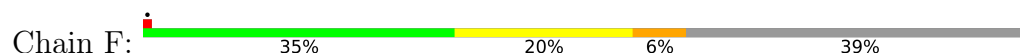
Chain D: 15% 51% 15% 32%



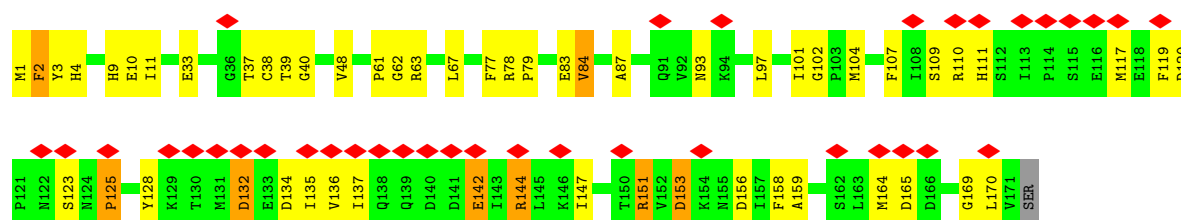
• Molecule 5: DNA-directed RNA polymerase II subunit E



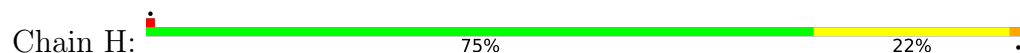
• Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2



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

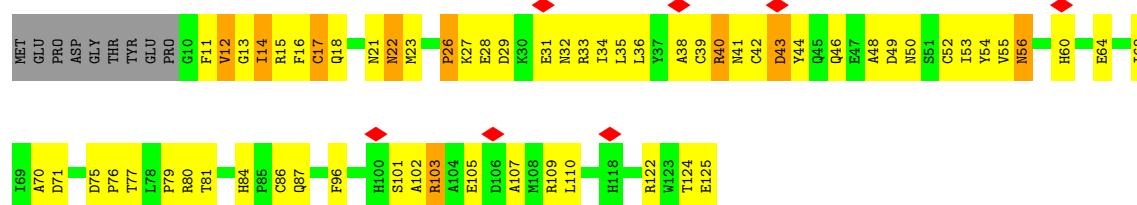
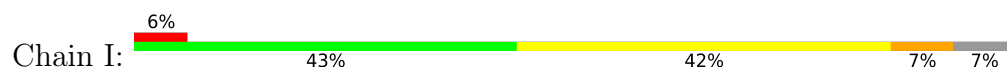


• Molecule 8: RPB8

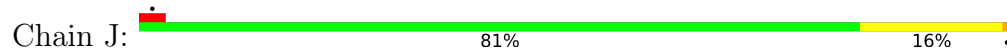




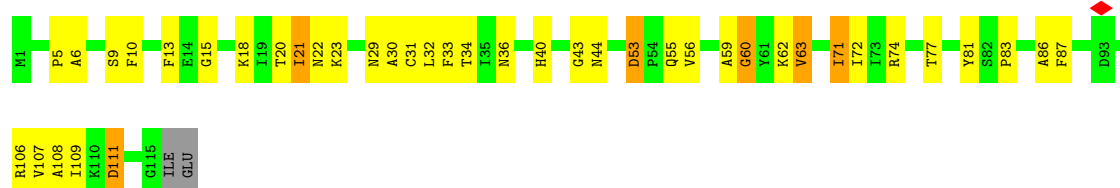
- Molecule 9: RPB9



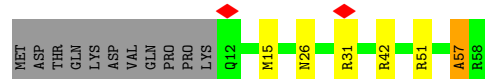
- Molecule 10: RPB10



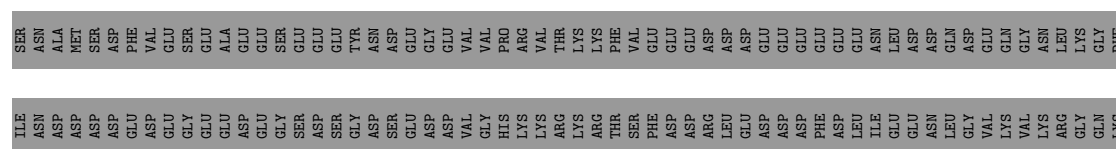
- Molecule 11: RPB11



- Molecule 12: RNA polymerase II subunit K

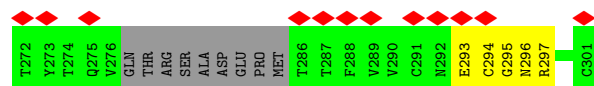
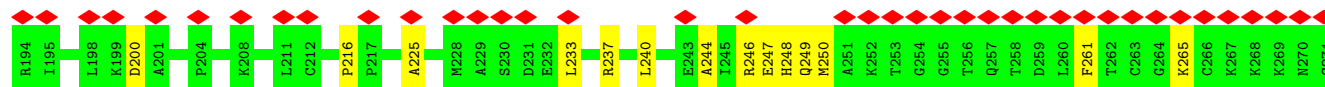
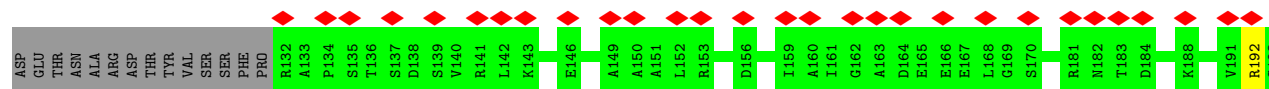


- Molecule 13: Transcription elongation factor SPT6

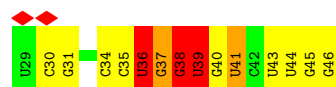
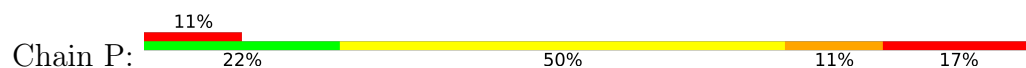




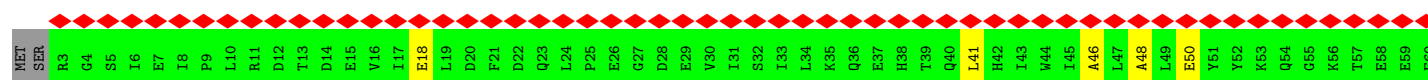
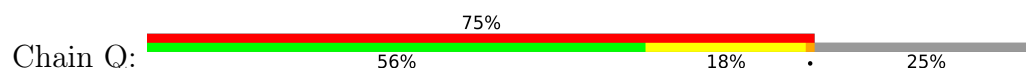
- Molecule 15: Transcription elongation factor A protein 1



- Molecule 16: RNA



- Molecule 17: RNA polymerase-associated protein CTR9 homolog



L841	R842	A843	K844	Q845	P846	Q847	L788	K849	E850	L851	L852	R853	Q854	R855	L856	L857	K858	E859	Q860	E861	P862	R863	R864	R865	R866	R867	K868	E869	P870	A810	A811	T812	E813	A814	R815	Q816	C817	S818	D819	L820	L821	S822	Q823	A824	Q825	Y826	H827	V828	A829	R830	A831	R832	K833	Q834	THR	D835	E836	E837	E838	R839	E840
L721	Y722	L723	A724	R725	L726	L727	F728	K729	G730	G731	K732	F733	Q734	E735	G736	K737	Q738	T739	L740	L741	K742	R743	R744	H745	L746	A747	P748	S749	D750	L751	V752	L753	A754	F755	N756	Y757	A758	L759	V760	L761	Q762	R763	A764	A765	T766	S767	V768	L769	K770	A771	E772	K773	S774	N775	L776	K777	E778	Y779	L780		
M781	A782	V783	K784	E785	L786	E787	L788	A789	H790	R791	Y792	F793	S794	Y795	L796	S797	K798	Y799	G800	D801	K802	M803	R804	F805	D806	L807	A808	L809	A810	A811	T812	E813	A814	R815	Q816	C817	S818	D819	L820	L821	S822	Q823	A824	Q825	Y826	H827	V828	A829	R830	A831	R832	K833	Q834	THR	D835	E836	E837	E838	R839	E840	
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T601	Y602	S603	M604	L605	A606	L607	G608	N609	V610	M611	L612	Q613	T614	L615	H616	Q617	P618	T619	D620	D621	R622	E623	K624	E625	K626	R627	H628	Q629	D630	R631	A632	L633	A634	L635	Y636	K637	D638	V639	L640	R641	N642	D643	D644	K645	N646	L647	Y648	A649	N650	N651	G652	L653	O654	P655	S656	T597	Q598	S659	R660		
A541	R542	D543	K544	G545	N546	F547	Y548	E549	A550	S551	D552	M553	F554	K555	E556	A557	L558	Q559	T560	N561	Q562	D563	H564	P565	D566	A567	V568	S569	L570	L571	G572	N573	L574	H575	L576	A577	K578	Q579	E580	M581	G582	P583	G584	K585	E586	K587	F588	E589	E590	L591	L592	K593	O594	P595	S596	T597	Q598	S599	D600		
A481	K482	A483	E484	A485	E486	H487	D488	E489	H490	Y491	Y492	N493	A494	T495	S496	Y497	T498	T499	S500	L501	N502	L503	A504	R505	L506	Y507	E508	A509	N510	C511	E512	F513	H514	E515	A516	E517	K518	L519	Y520	K521	N522	L523	L524	R525	E526	H527	P528	N529	Y530	V531	D532	C533	Y534	L535	R536	L537	Q538	A539	N540		
I421	L422	E423	Q424	T425	D426	T427	Q428	G429	A430	L431	S432	A433	Y434	G435	T436	A437	T438	R439	L440	L441	Q442	E443	K444	V445	Q446	A447	D448	V449	P450	P451	E452	I453	L454	N455	N456	G457	G458	A459	L460	H461	F462	R463	L464	G465	N466	L467	G468	A469	Y470	K471	K472	Y473	F474	L475	A476	S477	L478	D479	R480		
S361	Q362	C363	F364	E365	K366	V367	L368	K369	A370	Y371	P372	N373	N374	Y375	E376	T377	M378	K379	I380	L381	G382	S383	L384	Y385	A386	A387	S388	E389	D390	Q391	E392	K393	R394	D395	I396	A397	K398	G399	H400	L401	K402	K403	V404	T405	A406	Q407	Y408	P409	D410	D411	V412	E413	A414	N415	T416	E417	L418	A419	Q420		
V301	E302	A303	M304	Q305	A306	E307	S308	C309	Y310	Q311	L312	A313	R314	S315	F316	H317	V318	Q319	E320	D321	Y322	D323	Q324	A325	F326	Q327	Y328	Y329	Y330	Q331	A332	T333	Q334	F335	A336	S337	S338	S339	F340	V341	L342	F343	F344	G345	L347	G348	Q349	M350	Y351	I352	Y353	R354	G355	D356	K357	N358	N359	A360			
L241	E242	L243	N244	K245	K246	E247	A248	D249	S250	I251	K252	N253	G254	V255	Q256	L257	L258	S259	R260	A261	Y262	T263	I264	D265	P266	S267	N268	P269	M270	K271	L272	N273	H274	L275	A276	N277	H278	F279	L279	A220	F221	N222	K223	A224	L225	L226	L227	N228	S229	K229	H290	L291	A292	L293	H294	A295	F296	H297	N298	T299	E300
G181	A182	L183	A184	Y185	Y186	K187	K188	A189	L190	R191	T192	N193	P194	G195	C196	P197	A198	E199	V200	R201	L202	G203	M204	G205	H206	C207	F208	V209	K210	L211	N212	K213	L214	E215	K216	A217	R218	L219	A220	F221	N222	K223	A224	L225	L226	L227	N228	S229	K229	H290	L291	A292	L293	H294	A295	F296	H297	N298	T299	E300	
D121	K122	I123	I124	M125	Y126	D127	Q128	N129	H130	L131	L132	G133	R134	A135	C136	F137	C138	L139	L140	E141	G142	D143	K144	M145	D146	Q147	A148	D149	A150	Q151	F152	H153	F154	V155	L156	M157	K158	S159	P160	N161	N162	I163	P164	A165	L166	L167	G168	K169	A170	C171	I172	S173	F174	N175	K176	K177	D178	Y179	R180		
V61	K62	L63	L64	E65	A66	A67	R68	I69	D70	G71	N72	L73	D74	Y75	R76	D77	H78	E79	K80	D81	Q82	M83	T84	C85	L86	D87	T88	L89	A90	A91	Y92	Y93	V94	Q95	Q96	A97	R98	K99	E100	K101	N102	K103	D104	N105	K106	K107	D108	L109	I110	T111	Q112	A113	T114	L115	L116	Y117	T118	M119	A120		

[illegible]

- Molecule 18: RNA polymerase-associated protein RTF1 homolog

[illegible]

- Molecule 19: Template DNA

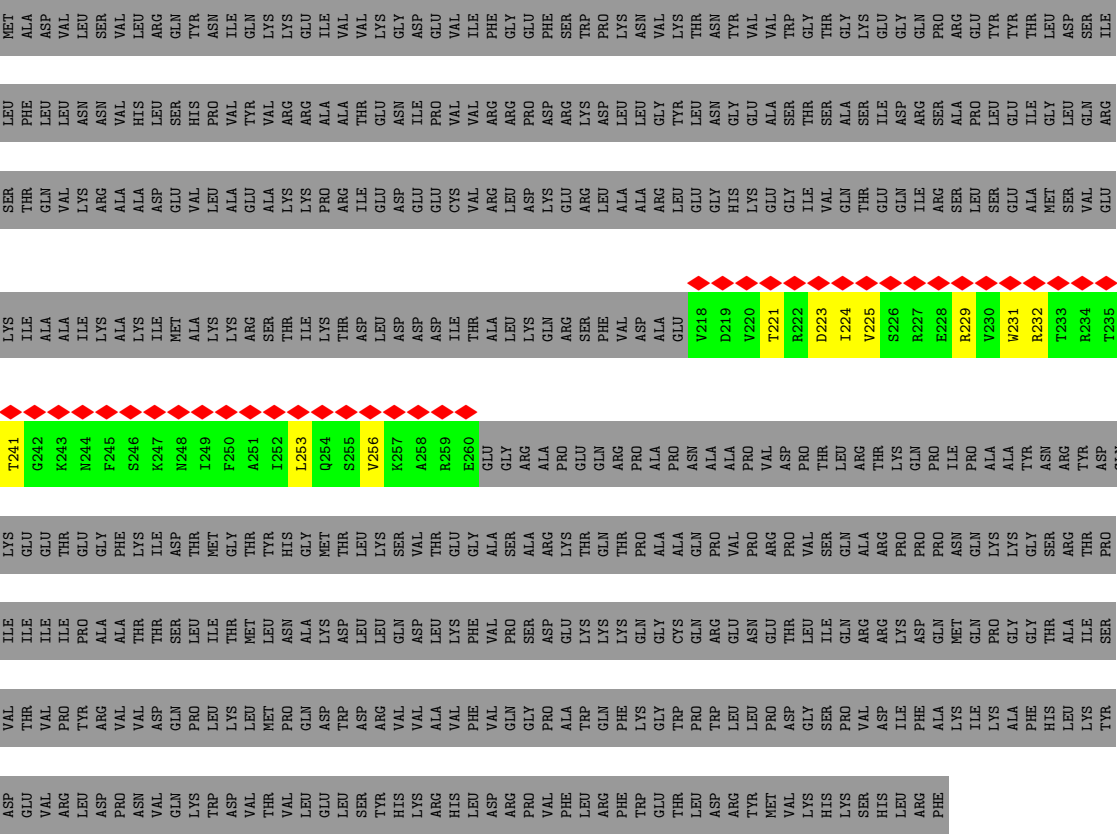
DA	C-36	G-110	DT
DC		T-109	DA
DA	A-32	A-108	DC
DG	C-31	G-107	DG
DG	A-30	A-106	DT
DG	C-29	C-105	DA
DG		A-104	DT
DT	G-21	G-103	DA
	A-20	C-102	DA
	G-19	T-101	DT
	A-18	C-100	DG
	C-17	T-99	DC
	A-16	A-98	DC
	G-15	G-97	DG
	A-14	G-92	DT
DA		C-91	DA
DA		T-90	DG
DA		T-89	DT
DA		A-88	DC
DA		A-87	DC
DA		A-86	DA
DA		C-85	DC
DA		G-84	DG
DA		C-83	DC
DA		A-82	DG
DG		C-81	DC
DA		G-80	DA
DA		T-79	DT
DA		A-78	DA
DA		C-77	DA
DC		G-76	DC
DG		C-73	T-144
DG		T-72	C-143
DC		G-71	A-142
DC		T-70	G-141
DA		C-69	A-140
DC		C-68	A-139
DC		C-67	T-138
DC		C-66	C-137
DC		G-62	C-136
DC		A-61	C-135
DA		A-60	G-134
DG		A-57	G-133
DC		A-56	T-132
DA		C-55	G-131
DC		C-54	C-130
DA		G-53	G-129
DC		C-52	A-127
DC		G-48	G-122
DA		G-47	C-121
DA		G-46	T-120
DC		A-41	A-117
DA		C-40	T-116
DC			G-113
DA			T-112
DC			C-111
DC			

- Molecule 20: RNA polymerase-associated protein LEO1

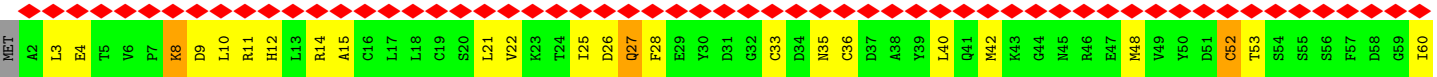
[illegible]



● Molecule 23: Parafibromin

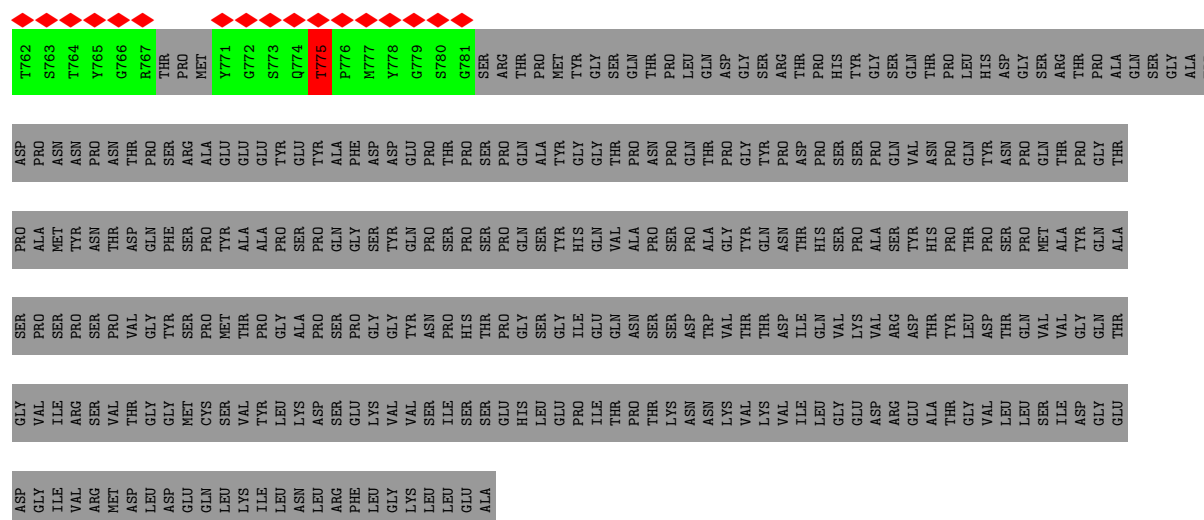


● Molecule 24: Transcription elongation factor SPT4

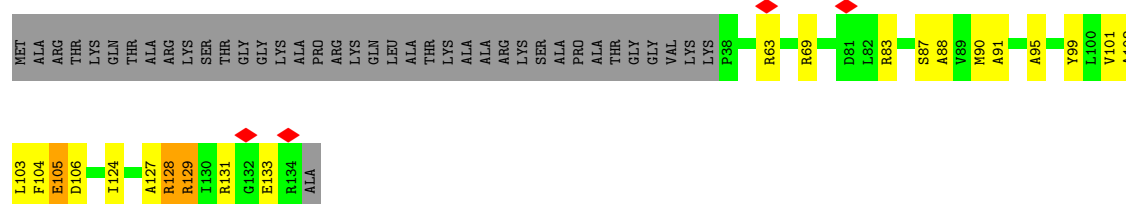


Chain Z: 40% 35% 11% 53%

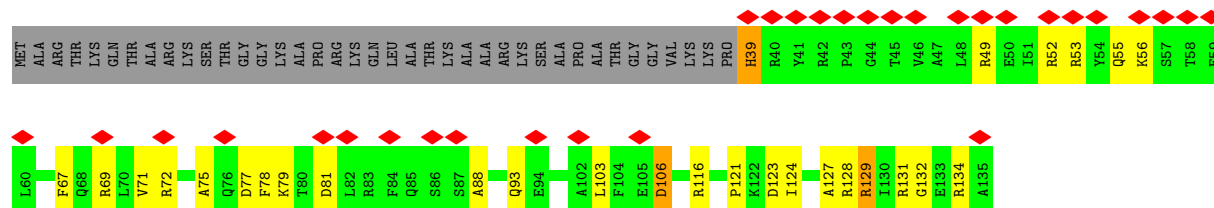




• Molecule 26: Histone H3.2



• Molecule 26: Histone H3.2

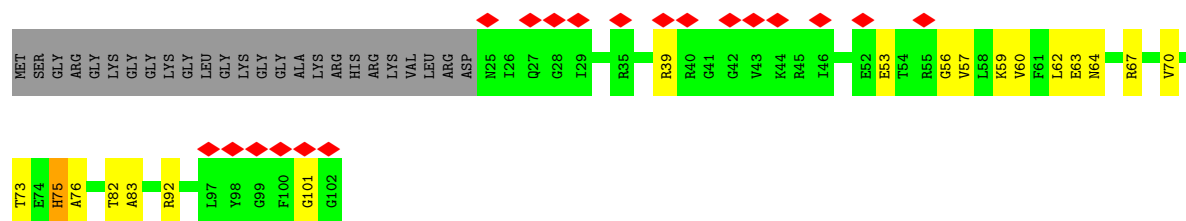


• Molecule 27: Histone H4

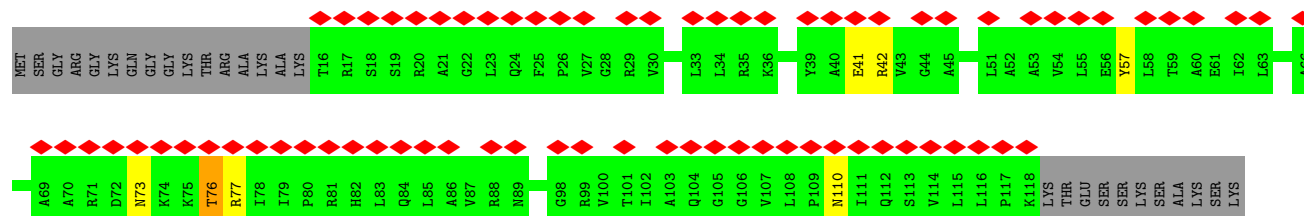
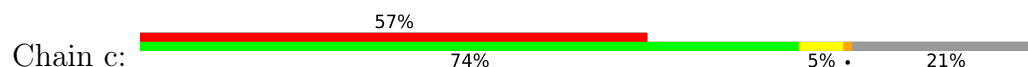


• Molecule 27: Histone H4





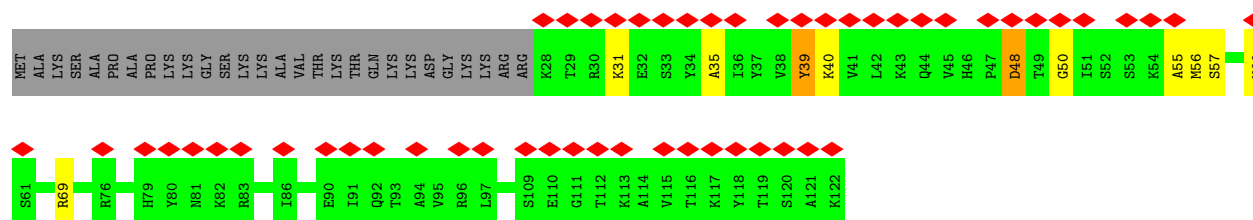
• Molecule 28: Histone H2A



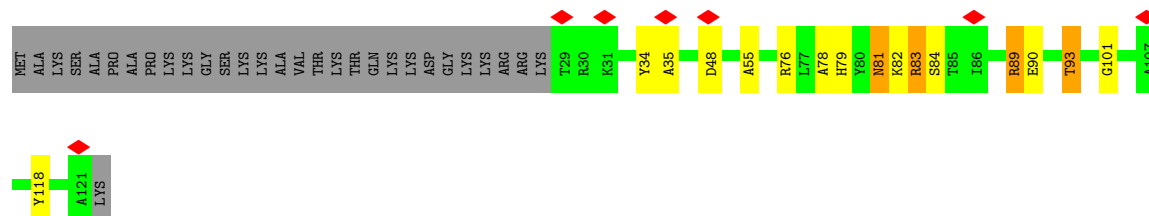
• Molecule 28: Histone H2A



• Molecule 29: Histone H2B 1.1



• Molecule 29: Histone H2B 1.1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	105420	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 ($e^-/\text{\AA}^2$)	52	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.935	Depositor
Minimum map value	-0.271	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.0832	Depositor
Map size (Å)	373.5, 373.5, 373.5	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	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, TPO, MG, SEP

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	1.98	207/11437 (1.8%)	2.01	435/15433 (2.8%)
2	B	2.01	191/9158 (2.1%)	2.00	329/12360 (2.7%)
3	C	2.14	42/2115 (2.0%)	2.13	107/2873 (3.7%)
4	D	1.83	22/1017 (2.2%)	1.86	33/1368 (2.4%)
5	E	2.08	48/1751 (2.7%)	1.97	72/2366 (3.0%)
6	F	2.52	17/636 (2.7%)	2.31	38/859 (4.4%)
7	G	1.98	21/1364 (1.5%)	2.02	56/1853 (3.0%)
8	H	1.65	16/1219 (1.3%)	1.72	32/1644 (1.9%)
9	I	2.14	25/964 (2.6%)	2.07	59/1305 (4.5%)
10	J	1.26	2/533 (0.4%)	1.49	5/719 (0.7%)
11	K	2.29	14/939 (1.5%)	2.29	50/1271 (3.9%)
12	L	1.56	7/403 (1.7%)	1.58	4/536 (0.7%)
13	M	1.24	13/4988 (0.3%)	1.78	61/6450 (0.9%)
14	N	0.97	35/2752 (1.3%)	1.96	36/4246 (0.8%)
15	O	0.72	0/1287	1.19	1/1721 (0.1%)
16	P	1.42	0/423	1.51	4/657 (0.6%)
17	Q	1.21	55/7365 (0.7%)	1.22	125/9927 (1.3%)
18	R	1.66	21/1866 (1.1%)	1.87	84/2519 (3.3%)
19	T	1.00	42/3012 (1.4%)	1.69	26/4641 (0.6%)
20	U	1.68	15/872 (1.7%)	1.89	34/1187 (2.9%)
21	V	1.55	14/1739 (0.8%)	1.88	62/2375 (2.6%)
22	W	0.49	1/2392 (0.0%)	0.56	9/3257 (0.3%)
23	X	0.64	0/356	0.79	0/478
24	Y	1.95	17/927 (1.8%)	2.00	46/1250 (3.7%)
25	Z	1.50	35/4084 (0.9%)	1.64	105/5498 (1.9%)
26	a	1.55	11/814 (1.4%)	1.84	26/1092 (2.4%)
26	e	1.96	21/812 (2.6%)	2.09	33/1088 (3.0%)
27	b	1.71	10/669 (1.5%)	1.92	22/894 (2.5%)
27	f	1.57	8/626 (1.3%)	1.82	18/837 (2.2%)
28	c	1.29	6/805 (0.7%)	1.62	8/1088 (0.7%)
28	g	1.40	12/819 (1.5%)	1.68	12/1106 (1.1%)
29	d	1.27	3/756 (0.4%)	1.68	6/1015 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
29	h	1.61	12/737 (1.6%)	1.76	13/993 (1.3%)
All	All	1.66	943/69637 (1.4%)	1.80	1951/94906 (2.1%)

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	10
2	B	0	10
3	C	0	3
4	D	0	1
9	I	0	1
10	J	0	4
13	M	0	3
14	N	0	37
16	P	0	1
18	R	0	1
19	T	0	32
25	Z	0	1
26	a	0	1
28	c	0	1
28	g	0	4
29	h	0	1
All	All	0	111

The worst 5 of 943 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	103	LEU	C-N	14.30	1.51	1.33
5	E	126	ILE	C-N	13.06	1.53	1.33
2	B	496	ALA	C-N	12.90	1.60	1.33
1	A	225	PHE	C-N	-9.12	1.22	1.33
1	A	96	HIS	ND1-CE1	-9.06	1.23	1.32

The worst 5 of 1951 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	N	107	DC	OP1-P-O3'	-34.40	4.81	108.00
14	N	85	DG	OP1-P-O3'	-34.14	5.57	108.00
19	T	-71	DG	OP1-P-O3'	-34.14	5.57	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	N	86	DT	OP1-P-O3'	-34.14	5.58	108.00
19	T	-133	DG	OP1-P-O3'	-34.12	5.63	108.00

There are no chirality outliers.

5 of 111 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	413	TYR	Sidechain
1	A	727	PRO	Mainchain
1	A	84	HIS	Sidechain
1	A	862	ARG	Sidechain
1	A	910	LYS	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	11385	11373	213	0
2	B	8980	9024	9022	65	0
3	C	2072	2021	2022	18	0
4	D	1004	981	980	8	0
5	E	1720	1736	1737	22	0
6	F	626	658	657	10	0
7	G	1333	1321	1321	13	0
8	H	1197	1157	1156	5	0
9	I	942	874	872	17	0
10	J	524	541	542	2	0
11	K	920	942	942	6	0
12	L	397	407	405	3	0
13	M	4927	2638	2622	24	0
14	N	2460	1355	1345	23	0
15	O	1274	0	1277	107	0
16	P	381	191	186	34	0
17	Q	7226	7171	7169	97	0
18	R	1836	1701	1699	28	0
19	T	2680	1458	1441	39	0
20	U	857	687	684	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	V	1711	1450	1446	18	0
22	W	2333	2247	2246	47	0
23	X	353	372	371	8	0
24	Y	911	909	907	10	0
25	Z	4025	4046	4041	48	0
26	a	802	841	841	1	0
26	e	801	839	838	2	0
27	b	662	710	709	0	0
27	f	619	660	659	3	0
28	c	795	847	846	0	0
28	g	809	865	864	0	0
29	d	745	774	773	2	0
29	h	726	749	747	4	0
30	A	2	0	0	0	0
30	B	1	0	0	0	0
30	C	1	0	0	2	0
30	I	2	0	0	0	0
30	J	1	0	0	0	0
30	R	1	0	0	0	0
30	Y	1	0	0	0	0
31	A	1	0	0	0	0
All	All	67913	61557	62740	714	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 6.

The worst 5 of 714 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)
1:A:1314:THR:CG2	15:O:297:ARG:HE	0.95	1.59
1:A:1314:THR:C	15:O:295:GLY:HA3	1.09	1.50
1:A:1314:THR:C	15:O:295:GLY:CA	1.91	1.40
1:A:1223:ASP:CG	15:O:244:ALA:HB2	1.45	1.39
1:A:1314:THR:HG22	15:O:297:ARG:NE	1.31	1.38

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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%)	1296 (92%)	105 (8%)	7 (0%)	24	60
2	B	1112/1251 (89%)	1024 (92%)	85 (8%)	3 (0%)	36	70
3	C	254/275 (92%)	239 (94%)	13 (5%)	2 (1%)	16	50
4	D	124/184 (67%)	122 (98%)	2 (2%)	0	100	100
5	E	207/210 (99%)	197 (95%)	8 (4%)	2 (1%)	12	45
6	F	76/127 (60%)	71 (93%)	5 (7%)	0	100	100
7	G	169/172 (98%)	155 (92%)	13 (8%)	1 (1%)	21	56
8	H	147/150 (98%)	137 (93%)	10 (7%)	0	100	100
9	I	114/125 (91%)	104 (91%)	10 (9%)	0	100	100
10	J	64/67 (96%)	61 (95%)	2 (3%)	1 (2%)	7	34
11	K	113/117 (97%)	108 (96%)	5 (4%)	0	100	100
12	L	45/58 (78%)	40 (89%)	4 (9%)	1 (2%)	5	26
13	M	976/1729 (56%)	860 (88%)	98 (10%)	18 (2%)	6	31
15	O	157/304 (52%)	154 (98%)	3 (2%)	0	100	100
17	Q	888/1179 (75%)	838 (94%)	50 (6%)	0	100	100
18	R	240/713 (34%)	224 (93%)	16 (7%)	0	100	100
20	U	119/666 (18%)	93 (78%)	24 (20%)	2 (2%)	7	32
21	V	236/531 (44%)	200 (85%)	33 (14%)	3 (1%)	9	38
22	W	298/305 (98%)	269 (90%)	29 (10%)	0	100	100
23	X	41/531 (8%)	40 (98%)	1 (2%)	0	100	100
24	Y	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
25	Z	497/1087 (46%)	452 (91%)	43 (9%)	2 (0%)	30	65
26	a	95/136 (70%)	92 (97%)	3 (3%)	0	100	100
26	e	95/136 (70%)	90 (95%)	5 (5%)	0	100	100
27	b	81/103 (79%)	79 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	f	76/103 (74%)	70 (92%)	6 (8%)	0	100	100
28	c	101/130 (78%)	99 (98%)	2 (2%)	0	100	100
28	g	103/130 (79%)	93 (90%)	10 (10%)	0	100	100
29	d	93/123 (76%)	89 (96%)	4 (4%)	0	100	100
29	h	91/123 (74%)	83 (91%)	8 (9%)	0	100	100
All	All	8134/12866 (63%)	7488 (92%)	604 (7%)	42 (0%)	26	60

5 of 42 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
13	M	294	LEU
13	M	373	VAL
13	M	376	ILE
13	M	385	GLU
13	M	779	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1245/1761 (71%)	1217 (98%)	28 (2%)	45	74
2	B	986/1084 (91%)	956 (97%)	30 (3%)	36	69
3	C	235/252 (93%)	231 (98%)	4 (2%)	53	78
4	D	109/160 (68%)	108 (99%)	1 (1%)	70	85
5	E	191/192 (100%)	186 (97%)	5 (3%)	40	72
6	F	68/111 (61%)	67 (98%)	1 (2%)	57	80
7	G	146/153 (95%)	141 (97%)	5 (3%)	32	66
8	H	130/131 (99%)	127 (98%)	3 (2%)	44	74
9	I	104/112 (93%)	102 (98%)	2 (2%)	50	76
10	J	55/56 (98%)	54 (98%)	1 (2%)	51	77
11	K	104/106 (98%)	100 (96%)	4 (4%)	29	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	L	44/55 (80%)	43 (98%)	1 (2%)	44	74
13	M	207/1524 (14%)	206 (100%)	1 (0%)	81	89
15	O	140/268 (52%)	140 (100%)	0	100	100
17	Q	761/1011 (75%)	756 (99%)	5 (1%)	76	86
18	R	170/625 (27%)	168 (99%)	2 (1%)	63	82
20	U	66/590 (11%)	65 (98%)	1 (2%)	57	80
21	V	148/462 (32%)	145 (98%)	3 (2%)	48	76
22	W	255/260 (98%)	252 (99%)	3 (1%)	63	82
23	X	40/467 (9%)	39 (98%)	1 (2%)	42	72
24	Y	102/103 (99%)	101 (99%)	1 (1%)	68	84
25	Z	435/939 (46%)	431 (99%)	4 (1%)	70	85
26	a	85/111 (77%)	83 (98%)	2 (2%)	43	73
26	e	84/111 (76%)	81 (96%)	3 (4%)	31	65
27	b	68/79 (86%)	67 (98%)	1 (2%)	57	80
27	f	63/79 (80%)	62 (98%)	1 (2%)	55	79
28	c	82/102 (80%)	81 (99%)	1 (1%)	63	82
28	g	83/102 (81%)	82 (99%)	1 (1%)	63	82
29	d	81/103 (79%)	78 (96%)	3 (4%)	30	64
29	h	79/103 (77%)	76 (96%)	3 (4%)	29	63
All	All	6366/11212 (57%)	6245 (98%)	121 (2%)	49	76

5 of 121 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	1148	LEU
29	d	39	TYR
7	G	67	LEU
28	c	76	THR
29	h	83	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 79 such sidechains are listed below:

Mol	Chain	Res	Type
17	Q	860	GLN

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Mol	Chain	Res	Type
25	Z	234	HIS
17	Q	887	ASN
21	V	300	ASN
28	c	112	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	P	17/18 (94%)	6 (35%)	2 (11%)

5 of 6 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
16	P	30	C
16	P	31	G
16	P	36	U
16	P	37	G
16	P	39	U

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	P	36	U
16	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$
1	TPO	A	1525	1	8,10,11	2.12	2 (25%)	10,14,16	2.05	2 (20%)
1	SEP	A	1547	1	8,9,10	2.09	2 (25%)	7,12,14	1.42	1 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
25	TPO	Z	775	25	8,10,11	1.73	1 (12%)	10,14,16	2.13	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
1	TPO	A	1525	1	-	4/9/11/13	-
1	SEP	A	1547	1	-	0/6/8/10	-
25	TPO	Z	775	25	-	2/9/11/13	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1525	TPO	O-C	3.90	1.34	1.20
25	Z	775	TPO	O-C	3.88	1.34	1.20
1	A	1547	SEP	O-C	3.87	1.34	1.20
1	A	1547	SEP	P-O1P	3.54	1.61	1.50
1	A	1525	TPO	P-O1P	3.52	1.61	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	Z	775	TPO	P-OG1-CB	-5.99	107.06	123.33
1	A	1525	TPO	P-OG1-CB	-5.62	108.06	123.33
1	A	1547	SEP	OG-CB-CA	3.20	111.26	108.14
1	A	1525	TPO	CG2-CB-CA	-2.17	109.03	113.26

There are no chirality outliers.

5 of 6 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
1	A	1525	TPO	O-C-CA-CB
25	Z	775	TPO	O-C-CA-CB

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1525	TPO	2	0
25	Z	775	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

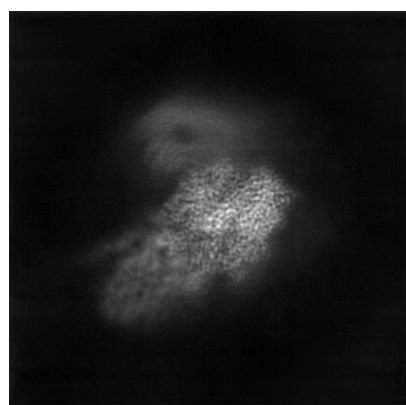
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26621. These allow visual inspection of the internal detail of the map and identification of artifacts.

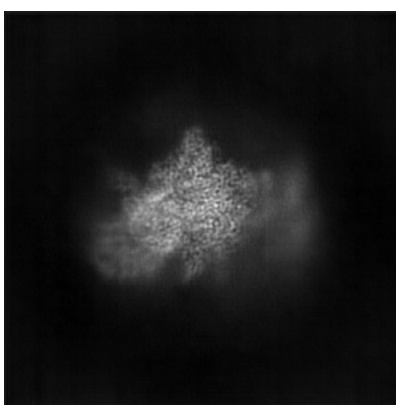
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

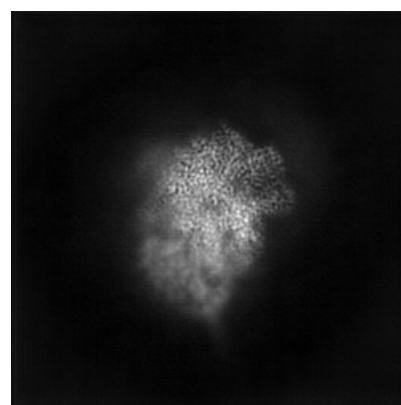
6.1.1 Primary map



X



Y

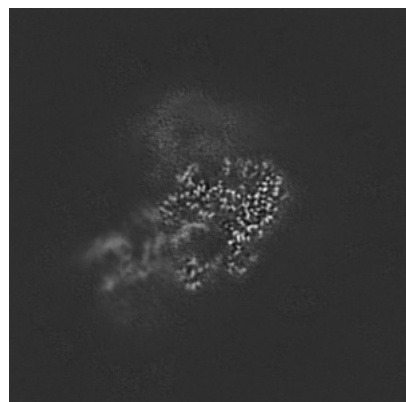


Z

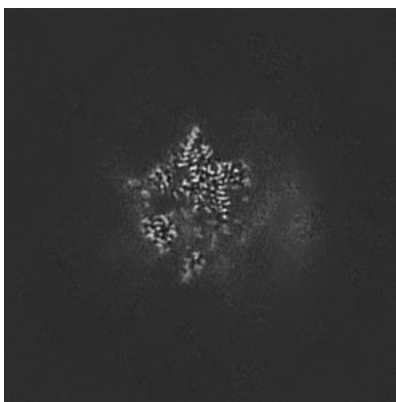
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

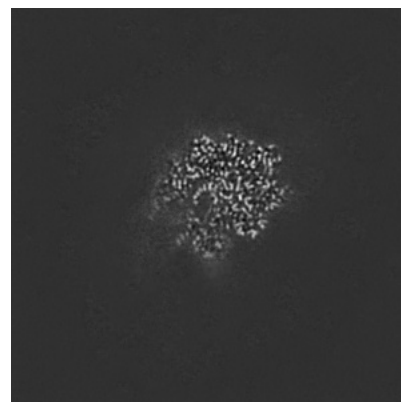
6.2.1 Primary map



X Index: 225



Y Index: 225

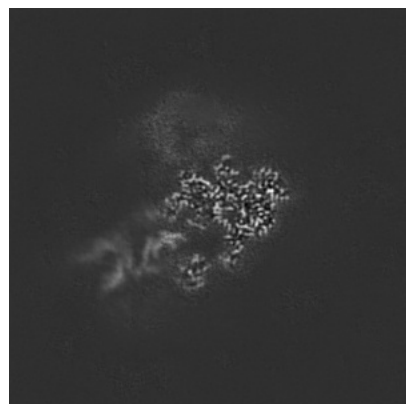


Z Index: 225

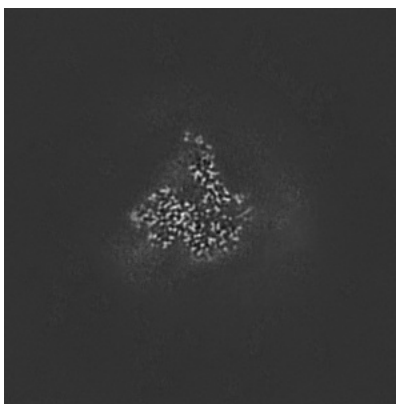
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

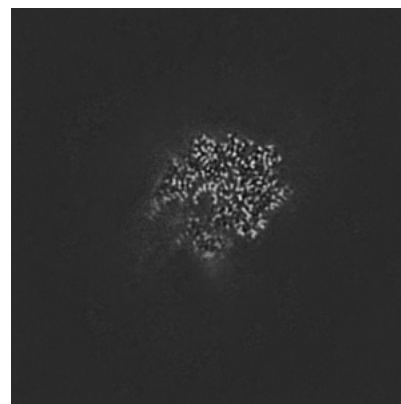
6.3.1 Primary map



X Index: 230



Y Index: 257

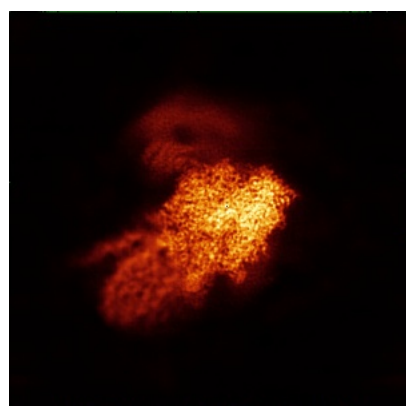


Z Index: 224

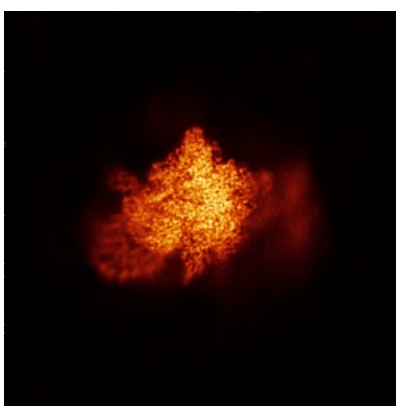
The images above show the largest variance slices of the map in three orthogonal directions.

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

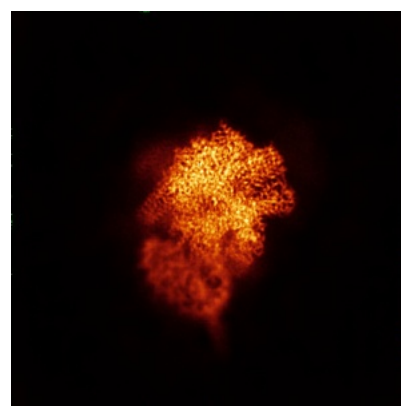
6.4.1 Primary map



X



Y

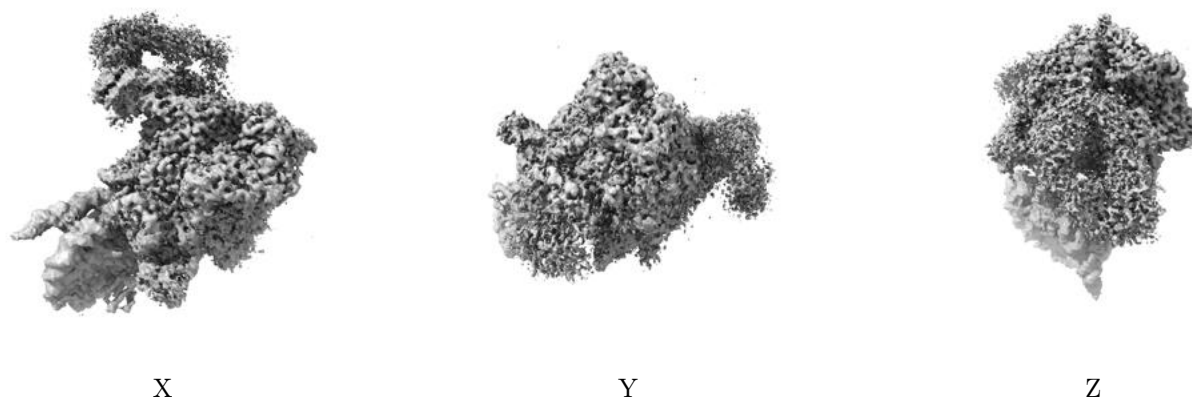


Z

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 0.0832. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

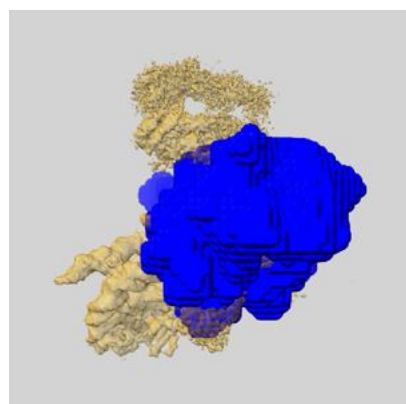
6.6 Mask visualisation [i](#)

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

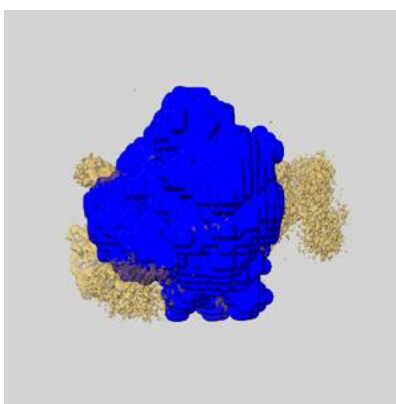
A mask typically either:

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

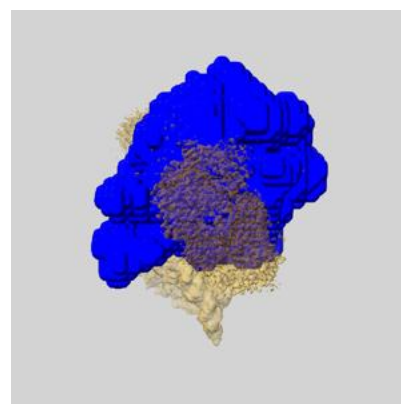
6.6.1 emd_26621_msk_1.map [i](#)



X

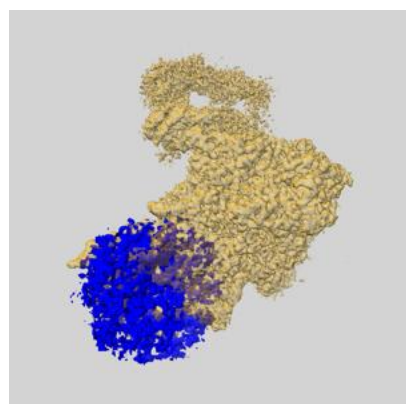


Y

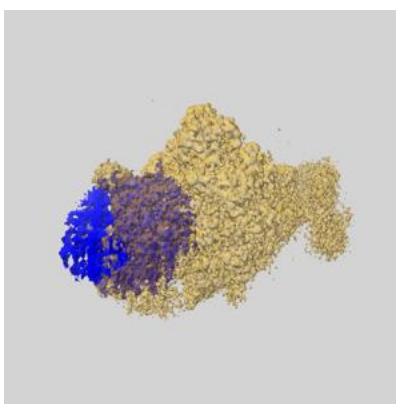


Z

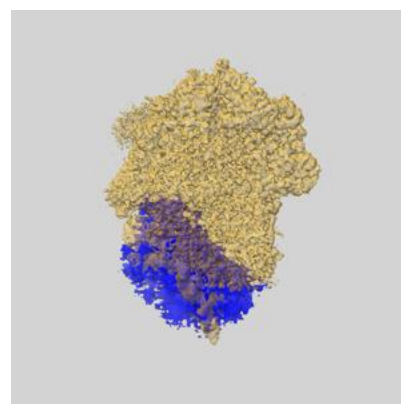
6.6.2 emd_26621_msk_2.map [i](#)



X

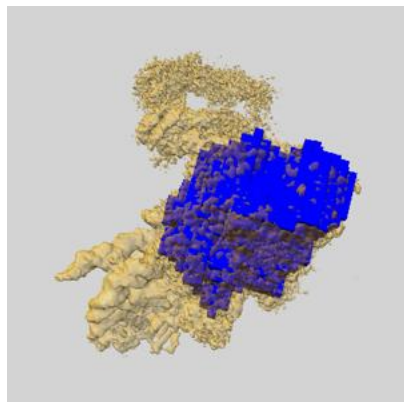


Y

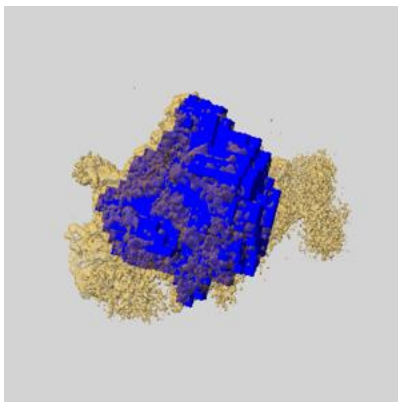


Z

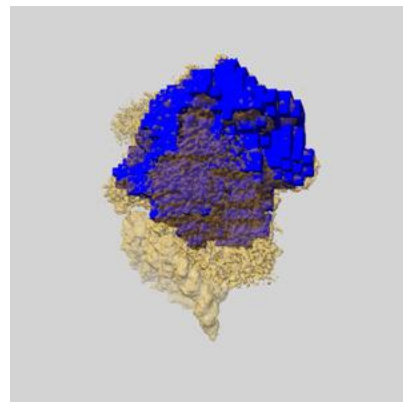
6.6.3 emd_26621_msk_3.map [i](#)



X



Y

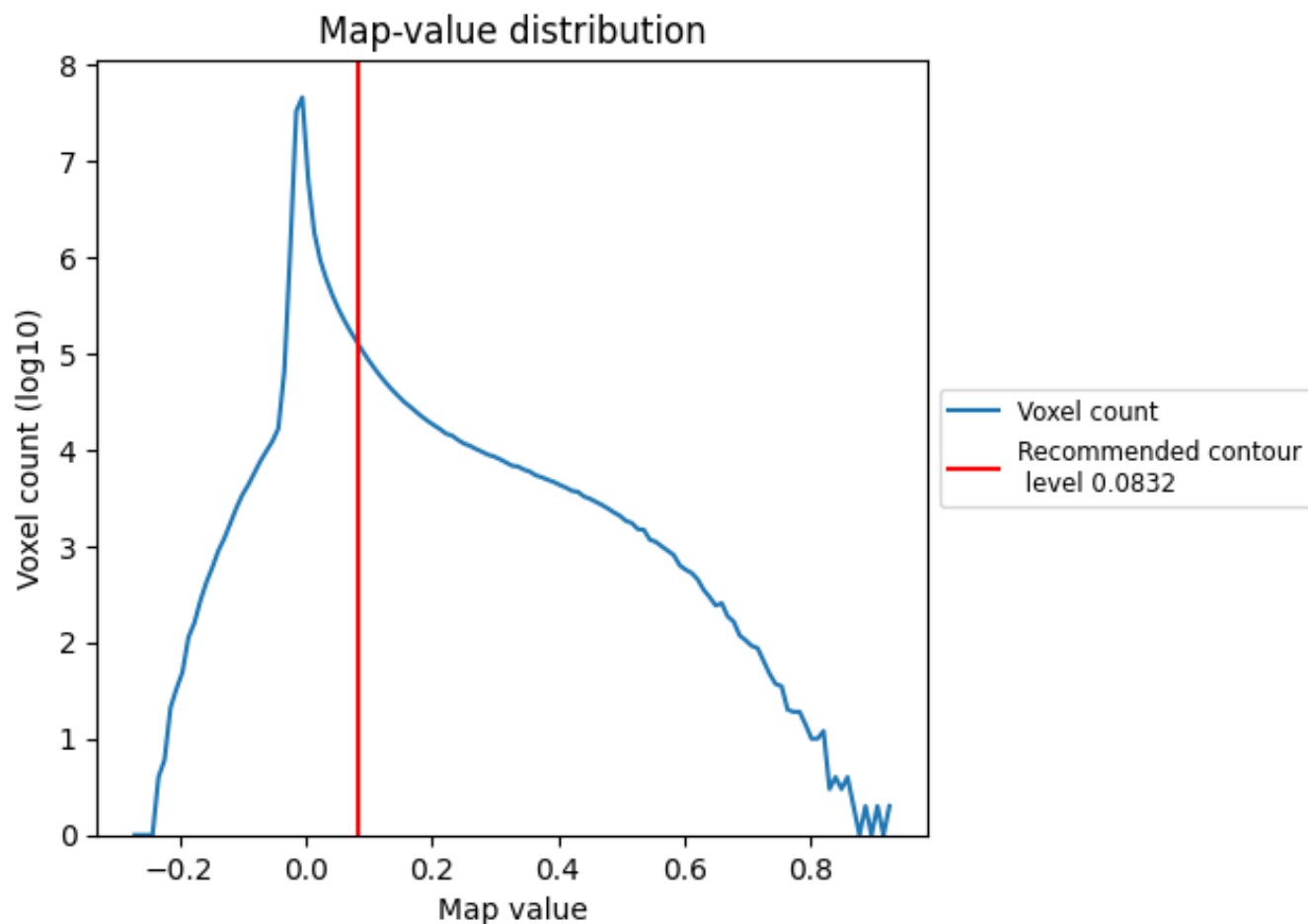


Z

7 Map analysis [i](#)

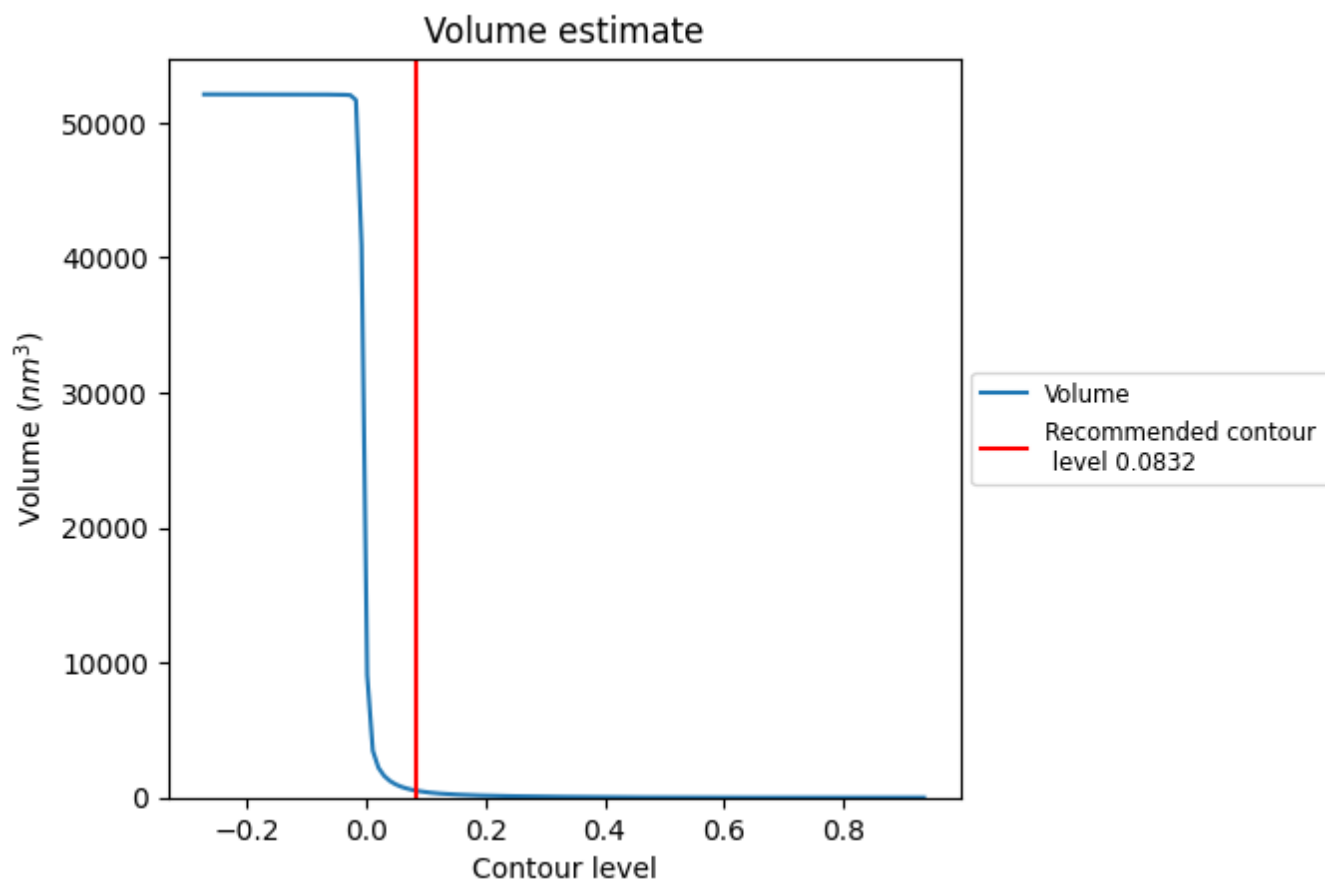
This section contains the results of statistical analysis of the map.

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.

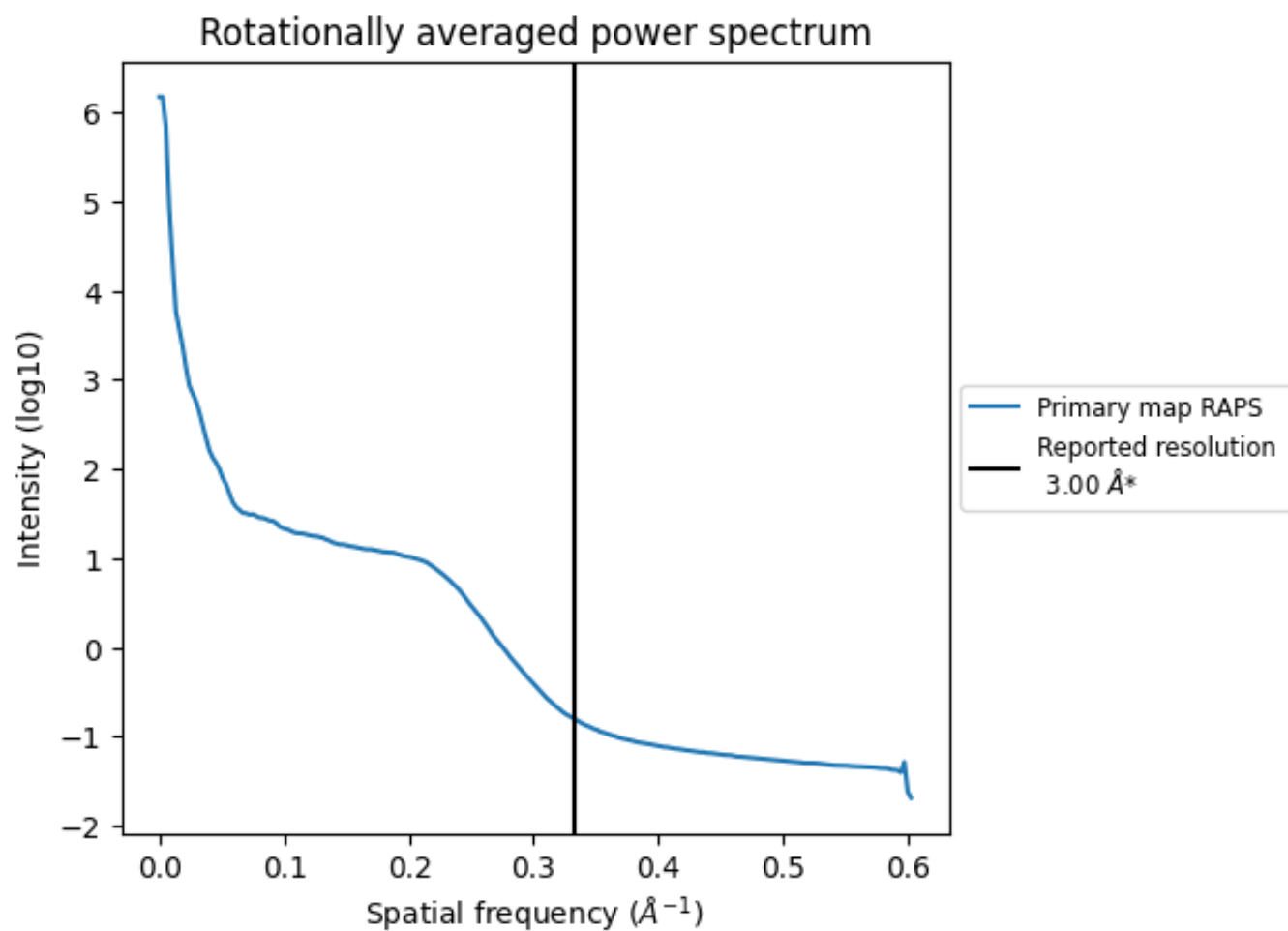
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 522 nm³; this corresponds to an approximate mass of 472 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 0.333 Å⁻¹

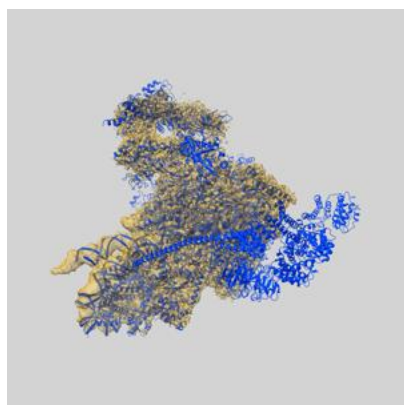
8 Fourier-Shell correlation

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

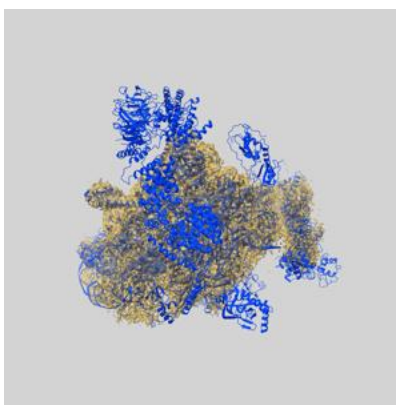
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-26621 and PDB model 7UND. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

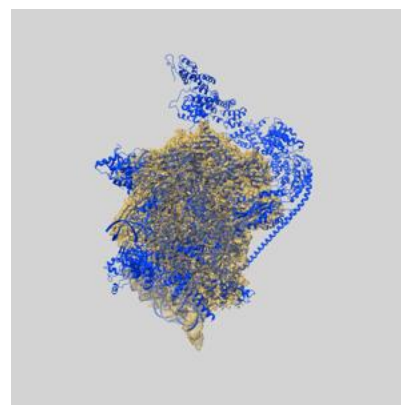
9.1 Map-model overlay [i](#)



X



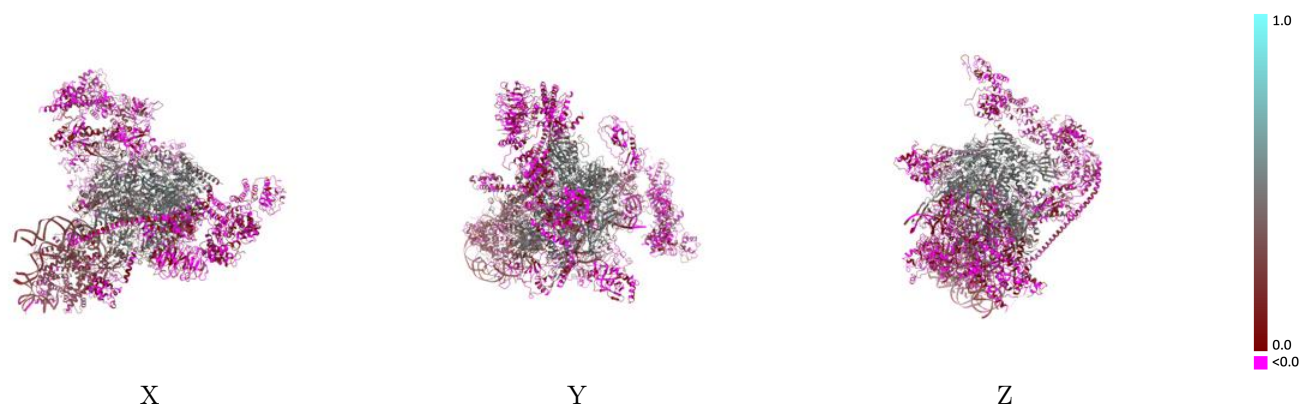
Y



Z

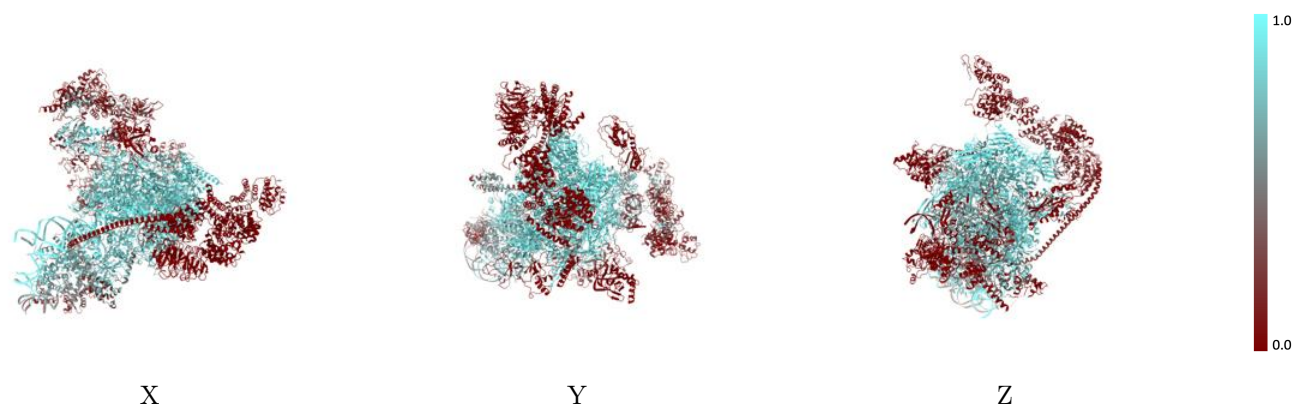
The images above show the 3D surface view of the map at the recommended contour level 0.0832 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



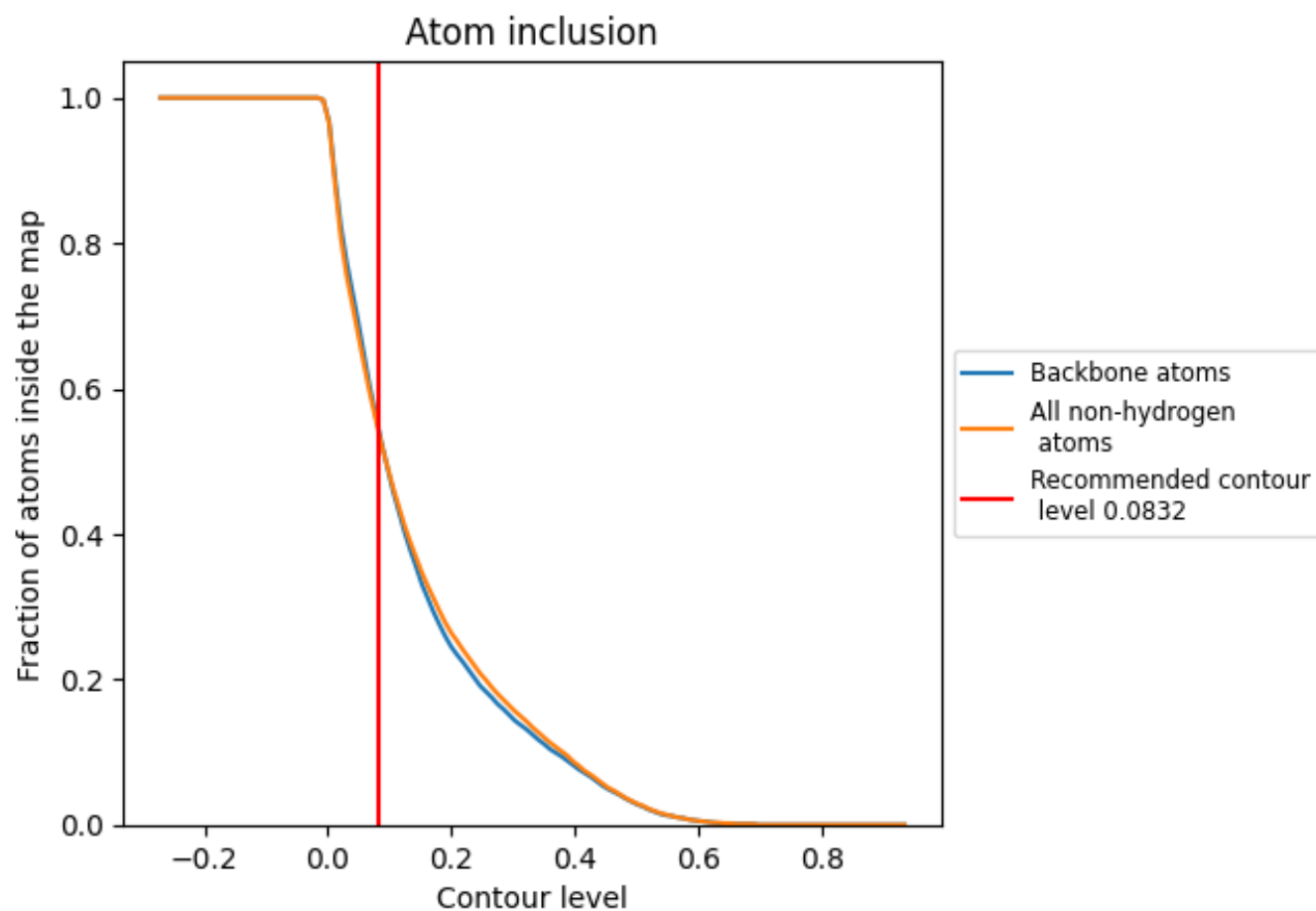
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0832).

9.4 Atom inclusion [i](#)



At the recommended contour level, 54% of all backbone atoms, 54% 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 (0.0832) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5370	 0.2160
A	 0.8900	 0.4080
B	 0.9010	 0.4260
C	 0.9340	 0.4660
D	 0.6280	 0.0950
E	 0.8750	 0.3370
F	 0.9130	 0.4550
G	 0.6570	 0.1730
H	 0.9020	 0.4280
I	 0.8040	 0.2330
J	 0.9060	 0.4630
K	 0.9260	 0.4680
L	 0.8530	 0.3870
M	 0.0870	 0.0240
N	 0.7610	 0.1640
O	 0.4130	 0.0160
P	 0.7660	 0.2450
Q	 0.0010	 0.0130
R	 0.0160	 0.0010
T	 0.8040	 0.2060
U	 0.2170	 0.0850
V	 0.0900	 0.0480
W	 0.0000	 -0.0010
X	 0.0000	 0.0470
Y	 0.0000	 0.0160
Z	 0.1410	 0.0610
a	 0.7450	 0.1410
b	 0.6760	 0.1640
c	 0.2520	 0.1160
d	 0.3350	 0.1300
e	 0.5610	 0.0830
f	 0.6350	 0.1020
g	 0.7810	 0.1820
h	 0.7240	 0.1610

