



wwPDB EM Validation Summary Report ⓘ

Aug 6, 2026 – 08:39 PM JST

PDB ID : 8GXQ / pdb_00008gxq
EMDB ID : EMD-34359
Title : PIC-Mediator in complex with +1 nucleosome (T40N) in MH-binding state
Authors : Chen, X.; Wang, X.; Liu, W.; Ren, Y.; Qu, X.; Li, J.; Yin, X.; Xu, Y.
Deposited on : 2022-09-21
Resolution : 5.04 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.dev133
Mogul : 1.8.5 (274361), CSD as541be (2020)
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) : 2.50

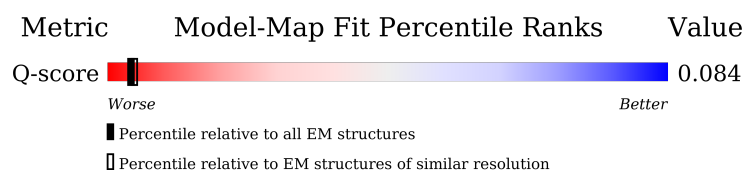
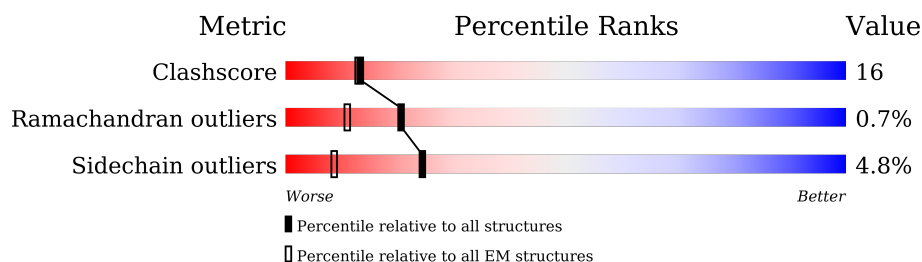
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.04 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.



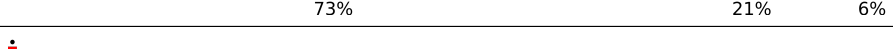
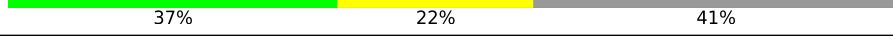
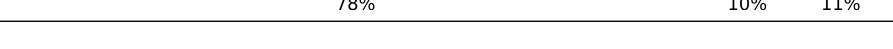
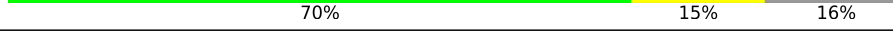
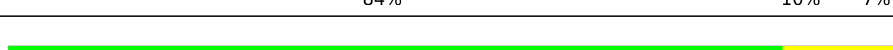
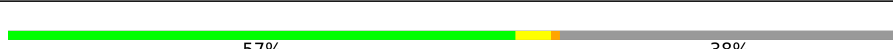
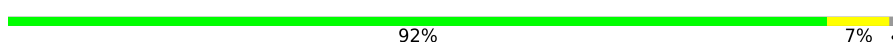
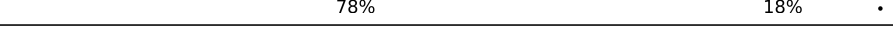
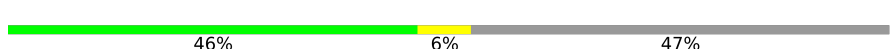
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	840 (4.54 - 5.51)

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	X	228	20% 9% 71%
2	Y	228	22% 7% 71%
3	BA	316	71% 9% 20%
4	DA	1872	24% 5% 70%

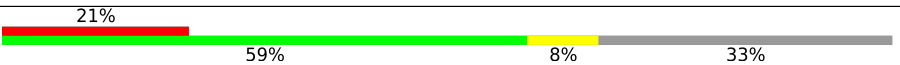
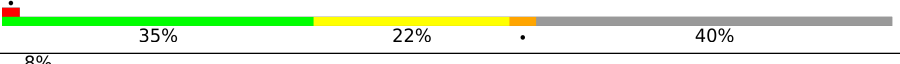
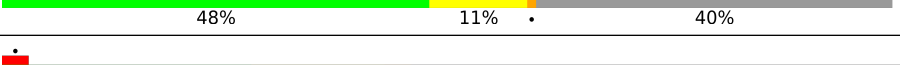
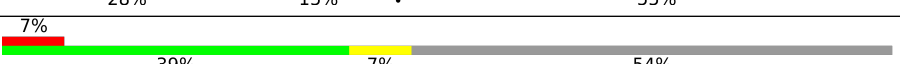
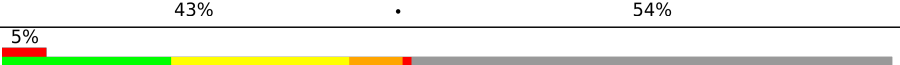
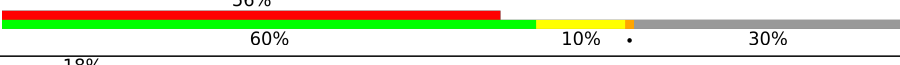
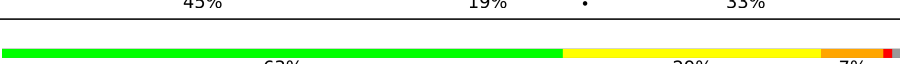
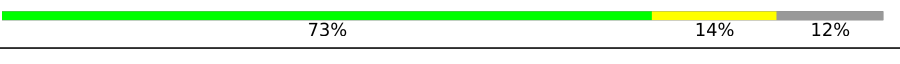
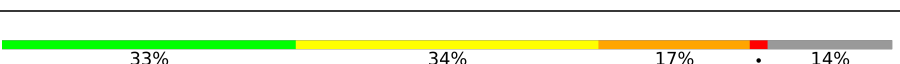
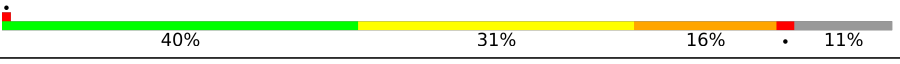
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Mol	Chain	Length	Quality of chain
5	EA	439	
6	FA	517	
7	HA	760	
8	NA	136	
8	NE	136	
9	PA	1970	
10	DB	1199	
11	EB	291	
12	FB	249	
13	HB	548	
14	NB	103	
14	NF	103	
15	PB	1174	
16	HC	462	
17	PC	275	
18	PE	210	
19	PF	127	
20	PH	150	
21	PI	125	
22	PJ	67	
23	PK	117	
24	PL	58	
25	DP	339	
26	DQ	376	
27	DO	109	

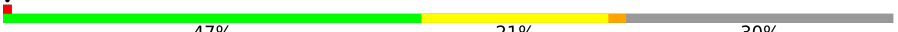
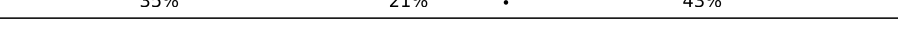
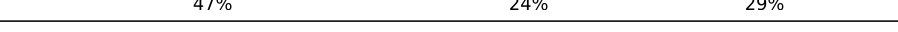
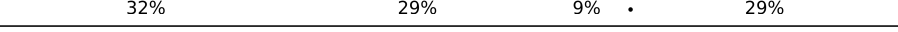
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Mol	Chain	Length	Quality of chain
28	Dc	929	
29	DD	1085	
29	Dd	1085	
30	DE	800	
30	De	800	
31	DF	677	
31	Df	677	
32	DI	264	
32	Di	264	
33	DJ	218	
33	Dj	218	
34	Dk	211	
35	DL	161	
35	DI	161	
36	Dm	124	
37	DG	349	
38	DH	310	
39	HD	309	
40	HE	308	
41	HG	395	
42	HH	782	
43	HF	71	
44	HI	346	
45	HJ	323	
46	PD	142	

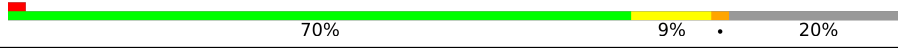
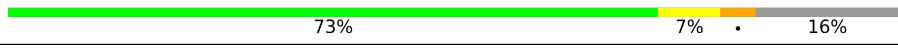
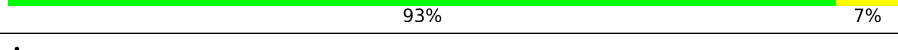
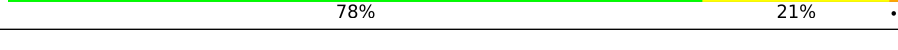
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Mol	Chain	Length	Quality of chain
47	PG	172	
48	g	233	
49	j	135	
50	n	1454	
51	s	244	
52	u	144	
53	a	1581	
54	d	270	
55	f	246	
56	i	146	
57	m	131	
58	q	651	
59	z	600	
60	b	200	
61	c	311	
62	e	178	
63	l	178	
64	o	788	
65	h	268	
66	k	117	
67	r	208	
68	t	212	
69	v	200	
70	p	841	
71	w	1368	

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Mol	Chain	Length	Quality of chain
72	x	989	
73	y	747	
74	NC	128	
74	NG	128	
75	ND	126	
75	NH	126	
76	NX	162	
77	NY	162	

2 Entry composition

There are 80 unique types of molecules in this entry. The entry contains 185972 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 DNA chain called DNA (228-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	X	67	Total	C	N	O	P	0	0
			1387	652	275	394	66		

- Molecule 2 is a DNA chain called DNA (228-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Y	67	Total	C	N	O	P	0	0
			1357	643	239	408	67		

- Molecule 3 is a protein called Transcription initiation factor IIB.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	BA	252	Total	C	N	O	S	0	0
			1953	1224	346	366	17		

- Molecule 4 is a protein called Transcription initiation factor TFIID subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	DA	558	Total	C	N	O	S	0	0
			4563	2913	791	832	27		

- Molecule 5 is a protein called General transcription factor IIE subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	EA	187	Total	C	N	O	S	0	0
			1535	964	275	285	11		

- Molecule 6 is a protein called General transcription factor IIF subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	FA	138	Total	C	N	O	S	0	0
			1138	719	208	208	3		

- Molecule 7 is a protein called General transcription and DNA repair factor IIIH helicase subunit XPD.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	HA	714	Total	C	N	O	S	0	0
			5751	3683	999	1040	29		

- Molecule 8 is a protein called Histone H3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	NA	100	Total	C	N	O		0	0
			498	298	100	100			
8	NE	103	Total	C	N	O		0	0
			511	305	103	103			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	PA	1471	Total	C	N	O	S	0	0
			11628	7314	2064	2178	72		

- Molecule 10 is a protein called Transcription initiation factor TFIID subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	DB	963	Total	C	N	O	S	0	0
			7796	5011	1315	1412	58		

- Molecule 11 is a protein called Transcription initiation factor IIE subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	EB	171	Total	C	N	O	S	0	0
			1403	895	243	261	4		

- Molecule 12 is a protein called General transcription factor IIF subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	FB	222	Total	C	N	O	S	0	0
			1788	1127	320	338	3		

- Molecule 13 is a protein called General transcription factor IIH subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	HB	265	Total	C	N	O	S	0	0
			2167	1382	378	395	12		

- Molecule 14 is a protein called Histone H4.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	NB	80	Total	C	N	O	0	0
			391	231	80	80		
14	NF	86	Total	C	N	O	0	0
			421	249	86	86		

- Molecule 15 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	PB	1136	Total	C	N	O	S	0	0
			9076	5739	1597	1676	64		

- Molecule 16 is a protein called General transcription factor IIH subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	HC	390	Total	C	N	O	S	0	0
			3158	2050	545	551	12		

- Molecule 17 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	PC	257	Total	C	N	O	S	0	0
			2059	1294	351	408	6		

- Molecule 18 is a protein called DNA-directed RNA polymerase II subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	PE	209	Total	C	N	O	S	0	0
			1721	1089	300	324	8		

- Molecule 19 is a protein called DNA-directed RNA polymerase II subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	PF	79	Total	C	N	O	S	0	0
			636	406	108	117	5		

- Molecule 20 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	PH	148	Total	C	N	O	S	0	0
			1186	750	194	237	5		

- Molecule 21 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	PI	114	Total	C	N	O	S	0	0
			928	571	166	180	11		

- Molecule 22 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	PJ	64	Total	C	N	O	S	0	0
			507	328	86	87	6		

- Molecule 23 is a protein called RNA_pol_L_2 domain-containing protein.

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

- Molecule 24 is a protein called RPB12.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	PL	44	Total	C	N	O	S	0	0
			373	231	72	64	6		

- Molecule 25 is a protein called TATA-box-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	DP	179	Total	C	N	O	S	0	0
			1422	923	251	241	7		

- Molecule 26 is a protein called Transcription initiation factor IIA subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	DQ	113	Total	C	N	O	S	0	0
			930	585	152	189	4		

- Molecule 27 is a protein called Transcription initiation factor IIA subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	DO	99	Total	C	N	O	S	0	0
			806	510	142	151	3		

- Molecule 28 is a protein called Transcription initiation factor TFIID subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Dc	127	Total	C	N	O	S	0	0
			1011	638	174	193	6		

- Molecule 29 is a protein called Transcription initiation factor TFIID subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Dd	158	Total	C	N	O	S	0	0
			1307	814	238	252	3		
29	DD	159	Total	C	N	O	S	0	0
			1330	830	248	249	3		

- Molecule 30 is a protein called Transcription initiation factor TFIID subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	De	539	Total	C	N	O	S	0	0
			4327	2746	748	814	19		
30	DE	546	Total	C	N	O	S	0	0
			4364	2766	757	820	21		

- Molecule 31 is a protein called Transcription initiation factor TFIID subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Df	403	Total	C	N	O	S	0	0
			3081	1954	533	576	18		
31	DF	408	Total	C	N	O	S	0	0
			3109	1970	542	579	18		

- Molecule 32 is a protein called Transcription initiation factor TFIID subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Di	121	Total	C	N	O	S	0	0
			967	615	167	178	7		
32	DI	120	Total	C	N	O	S	0	0
			959	610	166	177	6		

- Molecule 33 is a protein called Transcription initiation factor TFIID subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Dj	95	Total	C	N	O	S	0	0
			759	488	124	143	4		
33	DJ	90	Total	C	N	O	S	0	0
			720	466	115	135	4		

- Molecule 34 is a protein called Transcription initiation factor TFIID subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Dk	98	Total	C	N	O	S	0	0
			785	499	142	139	5		

- Molecule 35 is a protein called Transcription initiation factor TFIID subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Dl	107	Total	C	N	O	S	0	0
			876	547	158	166	5		
35	DL	74	Total	C	N	O	S	0	0
			605	379	105	118	3		

- Molecule 36 is a protein called Transcription initiation factor TFIID subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Dm	87	Total	C	N	O	S	0	0
			724	456	131	131	6		

- Molecule 37 is a protein called Transcription initiation factor TFIID subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	DG	145	Total	C	N	O	S	0	0
			1180	748	217	211	4		

- Molecule 38 is a protein called Transcription initiation factor TFIID subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	DH	209	Total	C	N	O	S	0	0
			1633	1034	283	311	5		

- Molecule 39 is a protein called CDK-activating kinase assembly factor MAT1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	HD	306	Total	C	N	O	S	0	0
			2400	1498	424	465	13		

- Molecule 40 is a protein called General transcription factor IIH subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	HE	263	Total	C	N	O	S	0	0
			2066	1323	344	380	19		

- Molecule 41 is a protein called General transcription factor IIH subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	HG	347	Total	C	N	O	S	0	0
			2732	1726	471	508	27		

- Molecule 42 is a protein called General transcription and DNA repair factor IIH helicase subunit XPB.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	HH	605	Total	C	N	O	S	0	0
			4890	3127	848	885	30		

- Molecule 43 is a protein called General transcription factor IIH subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	HF	66	Total	C	N	O	S	0	0
			523	337	83	100	3		

- Molecule 44 is a protein called Cyclin-dependent kinase 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	HI	299	Total	C	N	O	S	0	0
			2374	1532	405	426	11		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
HI	41	ALA	LYS	engineered mutation	UNP P50613

- Molecule 45 is a protein called Cyclin-H.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	HJ	287	Total	C	N	O	S	0	0
			2307	1477	398	417	15		

- Molecule 46 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	PD	128	Total	C	N	O	S	0	0
			1050	656	178	212	4		

- Molecule 47 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	PG	171	Total	C	N	O	S	0	0
			1351	875	219	249	8		

- Molecule 48 is a protein called Mediator of RNA polymerase II transcription subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	g	106	Total	C	N	O	S	0	0
			898	569	166	157	6		

- Molecule 49 is a protein called Mediator of RNA polymerase II transcription subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	j	122	Total	C	N	O	S	0	0
			840	527	151	159	3		

- Molecule 50 is a protein called Mediator of RNA polymerase II transcription subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	n	1015	Total	C	N	O	S	0	0
			7751	4941	1363	1405	42		

- Molecule 51 is a protein called Mediator of RNA polymerase II transcription subunit 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	s	93	Total	C	N	O	S	0	0
			723	463	121	135	4		

- Molecule 52 is a protein called Mediator of RNA polymerase II transcription subunit 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	117	Total	C	N	O	S	0	0
			886	552	146	184	4		

- Molecule 53 is a protein called Mediator of RNA polymerase II transcription subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	a	438	Total	C	N	O	S	0	0
			3430	2190	584	632	24		

- Molecule 54 is a protein called Mediator of RNA polymerase II transcription subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	d	158	Total	C	N	O	S	0	0
			1268	791	228	243	6		

- Molecule 55 is a protein called Mediator of RNA polymerase II transcription subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	f	167	Total	C	N	O	S	0	0
			1365	882	235	243	5		

- Molecule 56 is a protein called Mediator of RNA polymerase II transcription subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	i	73	Total	C	N	O	S	0	0
			605	382	107	110	6		

- Molecule 57 is a protein called Mediator of RNA polymerase II transcription subunit 31.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	m	112	Total	C	N	O	S	0	0
			983	641	172	165	5		

- Molecule 58 is a protein called Mediator of RNA polymerase II transcription subunit 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	q	555	Total	C	N	O	S	0	0
			4373	2765	783	805	20		

- Molecule 59 is a protein called Mediator of RNA polymerase II transcription subunit 26.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	z	97	Total	C	N	O	S	0	0
			765	472	136	154	3		

- Molecule 60 is a protein called Mediator of RNA polymerase II transcription subunit 29.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	b	115	Total	C	N	O	S	0	0
			899	563	155	172	9		

- Molecule 61 is a protein called Mediator of RNA polymerase II transcription subunit 27.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	c	263	Total	C	N	O	S	0	0
			2131	1356	379	385	11		

- Molecule 62 is a protein called Mediator of RNA polymerase II transcription subunit 28.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	e	102	Total	C	N	O	S	0	0
			832	520	146	163	3		

- Molecule 63 is a protein called Mediator of RNA polymerase II transcription subunit 30.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	l	126	Total	C	N	O	S	0	0
			1040	649	191	193	7		

- Molecule 64 is a protein called Mediator of RNA polymerase II transcription subunit 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	o	156	Total	C	N	O	S	0	0
			1221	780	212	222	7		

- Molecule 65 is a protein called Isoform 2 of Mediator of RNA polymerase II transcription subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	h	190	Total	C	N	O	S	0	0
			1465	913	259	289	4		

- Molecule 66 is a protein called Mediator of RNA polymerase II transcription subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	k	112	Total	C	N	O	S	0	0
			879	537	163	175	4		

- Molecule 67 is a protein called Mediator of RNA polymerase II transcription subunit 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	r	192	Total	C	N	O	S	0	0
			1535	973	271	276	15		

- Molecule 68 is a protein called Mediator of RNA polymerase II transcription subunit 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	t	193	Total	C	N	O	S	0	0
			1499	955	247	280	17		

- Molecule 69 is a protein called Mediator of RNA polymerase II transcription subunit 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	v	134	Total	C	N	O	S	0	0
			1083	668	185	226	4		

- Molecule 70 is a protein called Isoform 2 of Mediator of RNA polymerase II transcription subunit 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	p	766	Total	C	N	O	S	0	0
			5983	3816	1026	1092	49		

- Molecule 71 is a protein called Mediator of RNA polymerase II transcription subunit 23.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	w	1334	Total	C	N	O	S	0	0
			10774	6967	1827	1909	71		

- Molecule 72 is a protein called Mediator of RNA polymerase II transcription subunit 24.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	x	897	Total	C	N	O	S	0	0
			7061	4524	1190	1293	54		

- Molecule 73 is a protein called Mediator of RNA polymerase II transcription subunit 25.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	y	210	Total	C	N	O	S	0	0
			1605	1030	264	302	9		

- Molecule 74 is a protein called HISTONE H2A.Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	NG	107	Total	C	N	O		0	0
			524	310	107	107			
74	NC	103	Total	C	N	O		0	0
			506	300	103	103			

- Molecule 75 is a protein called Histone H2B.

Mol	Chain	Residues	Atoms				AltConf	Trace
75	ND	95	Total	C	N	O	0	0
			471	281	95	95		
75	NH	95	Total	C	N	O	0	0
			471	281	95	95		

- Molecule 76 is a DNA chain called DNA (162-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
76	NX	162	Total	C	N	O	P	0	0
			3078	1458	486	972	162		

- Molecule 77 is a DNA chain called DNA (162-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
77	NY	162	Total	C	N	O	P	0	0
			3561	1620	810	970	161		

- Molecule 78 is ZINC ION (CCD ID: ZN) (formula: Zn).

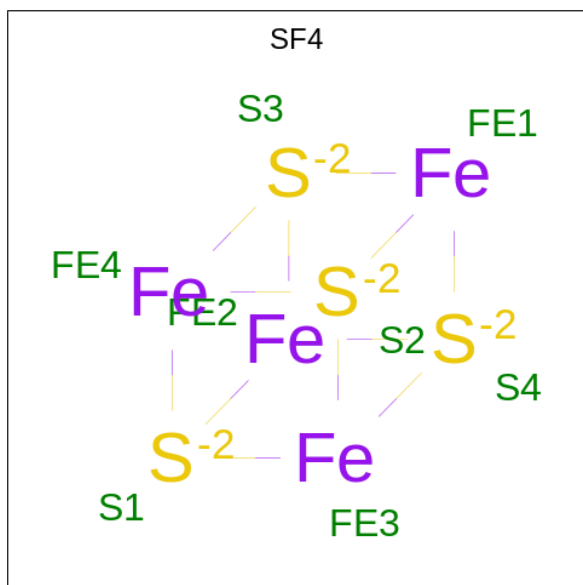
Mol	Chain	Residues	Atoms		AltConf
78	BA	1	Total	Zn	0
			1	1	
78	EA	1	Total	Zn	0
			1	1	
78	PA	2	Total	Zn	0
			2	2	
78	PB	1	Total	Zn	0
			1	1	
78	PC	1	Total	Zn	0
			1	1	
78	PI	2	Total	Zn	0
			2	2	
78	PJ	1	Total	Zn	0
			1	1	
78	PL	1	Total	Zn	0
			1	1	
78	HD	2	Total	Zn	0
			2	2	
78	HE	2	Total	Zn	0
			2	2	

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Mol	Chain	Residues	Atoms		AltConf
78	HG	3	Total	Zn	0
			3	3	
78	c	1	Total	Zn	0
			1	1	
78	p	1	Total	Zn	0
			1	1	

- Molecule 79 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms			AltConf
79	HA	1	Total	Fe	S	0
			8	4	4	

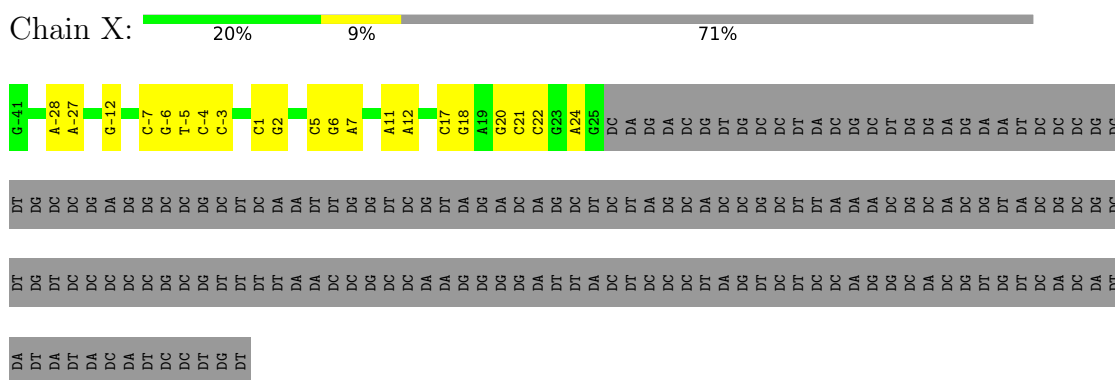
- Molecule 80 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
80	PA	1	Total	Mg	0
			1	1	

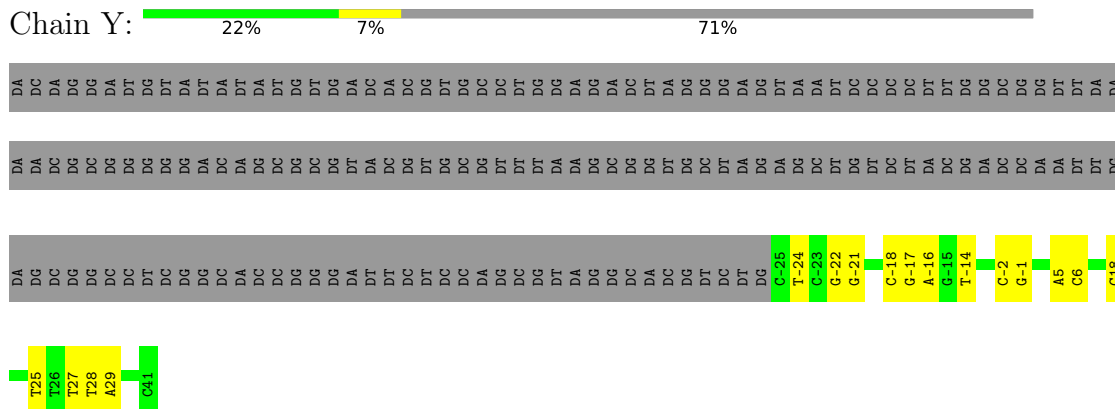
3 Residue-property plots

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.

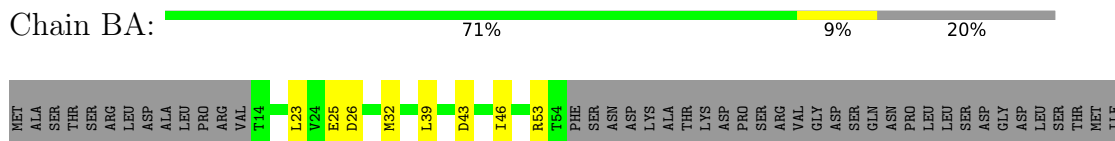
• Molecule 1: DNA (228-mer)



• Molecule 2: DNA (228-mer)

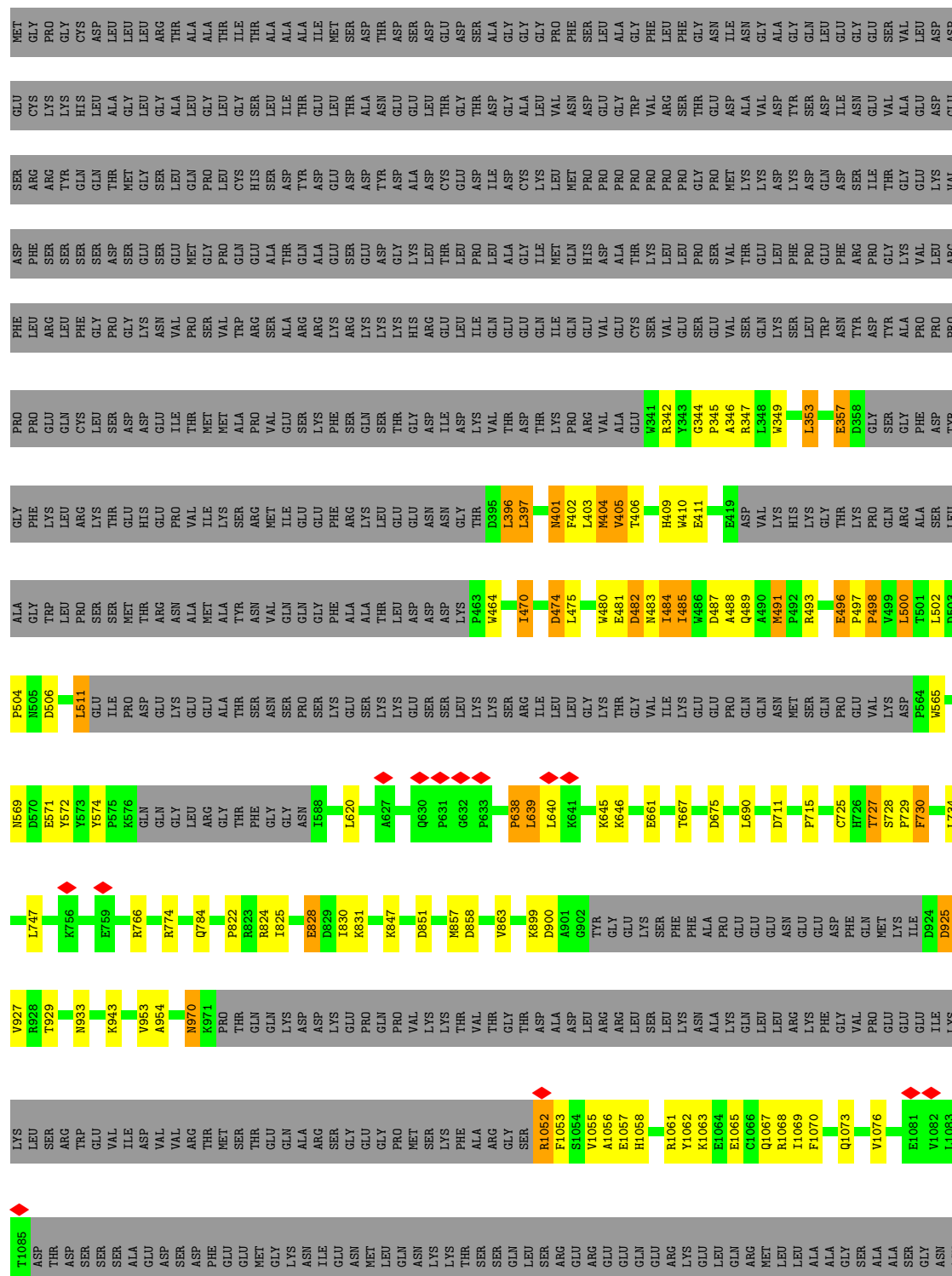


• Molecule 3: Transcription initiation factor IIB





● Molecule 4: Transcription initiation factor TFIID subunit 1



HIS	ARG	ASP	ASP	T1150	A1151	S1152	V1153	T1154	S1155	L1156	N1157	S1158	S1159	A1160	T1161	G1162	R1163	C1164	L1165	K1166	I1167	Y1168	R1169	T1170	F1171	R1172	D1173	E1174	E1175	G1176	K1177	E1178	Y1179	V1180	R1181	C1182	E1183	T1184	V1185	R1186	K1187	P1188	A1189	V1190	I1191	D1192	A1193	Y1194	V1195	R1196	I1197	R1198	T1199	T1200	K1201	D1202	E1203	E1204																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																

● Molecule 5: General transcription factor IIE subunit 1



ASP	GLN	GLU	ASP	HIS	ARG	ALA	SER	LEU	GLY	LYS	SER	ALA	LYS	GLN	SER	ARG	PRO	ILE	THR	LEU	ARG	GLU	SER	GLY	ASP	GLY	GLU	ASP	MET	LYS	GLU	GLY	GLY	ILE	ASP	MET	ARG	GLU	THR	HIS	ALA	GLY	GLY	PHE	GLN	GLU	GLY	ASP	ARG	GLU	GLY	GLY	GLY	HIS	ALA	GLY	VAL	VAL	ASP	ASN	ASP	ASN	ASP	GLU
ALA	THR	ILE	LEU	GLU	PRO	GLU	PRO	THR	GLU	PRO	ALA	LEU	LYS	GLN	SER	SER	PRO	ASP	HIS	ALA	ALA	ALA	THR	THR	ALA	GLY	ALA	SER	LEU	ALA	GLY	GLY	ALA	TRP	ALA	GLY	HIS	HIS	ARG	GLU	ALA	TRP	ALA	THR	LYS	GLY	PRO	SER	THR	GLY	GLY	THR	GLN	ASN	VAL	VAL	ILE	ASN	MET	ASP				
I114	T122	F127	K128	V131	C132	S133	T137	D138	L139	N142	Q143	L144	F145	M148	T149	F152	R153	C154	T155	F156	C157	H158	S166	K170	K171	R174	T175	L176	L177	A178	R179	F180	N181	E185	P186	I187	Y188	A189	L190	L191	T194	E195	D196	VAL	ASN	LEU																		
MET	ALA	ASP	PRO	VAL	LEU	THR	GLY	V10	L17	Y20	V21	I22	Y26	G27	I28	E29	L34	V43	K44	E45	M48	L49	L52	R56	K57	Q58	L59	D69	D83	G84	K85	T86	T87	R88	H89	I90	F91	Y92	F93	I94	V103	K104	Y105	K106	L107	R111																		

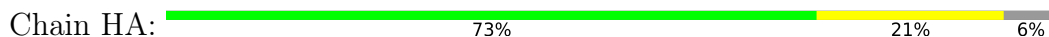
[illegible]

- Molecule 6: General transcription factor IIF subunit 1



GLU	ASP	THR	ARG	GLY	SER	K109	MET
	ALA	SER	ARG	SER	SER	ALA	ALA
	VAL	SER	LYS	SER	ASP	F127	ALA
	ARG	THR	ASP	SER	ALA		LEU
	ARG	LEU	SER	SER	SER	N142	G5
	TVR	ARG	SER	GLN	ASP	W143	
	LEU	ALA	GLU	GLU	ALA		V15
	THR	ALA	GLU	GLU	SER	L149	V16
	ARG	ALA	ASP	PRO	GLY	A150	
	ARG	ALA	SER	GLU	GLU	R151	N43
	LYS	SER	ASP	GLU	GLY	H152	Q44
	PRO	LEU	SER	SER	GLU		
	MET	LEU	SER	LYS	GLY	R153	
	THR	GLU	GLU	ALA	GLY		L47
	THR	GLN	GLU	LYS	ARG	E163	
	LYS	GLY	SER	ALA	VAL		D50
	ASP	ARG	PRO	PRO	PRO		
	LEU	ARG	ILE	GLN	LYS	R166	N53
	LEU	VAL	ASP	GLN	ALA	R167	K54
	LYS	SER	SER	GLU	LYS		LYS
	LYS	GLU	GLU	GLU	LYS		ILE
	PHE	MET	ALA	GLY	LYS	L171	TYR
	GLN	PRO	SER	PRO	ALA	M177	GLN
	THR	ALA	SER	LYS	PRO		GLU
	LYS	ALA	ALA	GLY	LEU	R180	GLU
	LYS	LYS	LEU	VAL	ALA	ARG	GLU
	THR	ARG	PHE	ASP	LYS		LEU
	GLY	LEU	MET	GLU	GLY	LYS	MET
	LEU	ARG	ALA	GLN	GLY	ASP	GLU
	SER	LEU	LYS	SER	ARG	GLN	SER
	SER	ASP	LYS	ASP	LYS	ASP	GLY
	GLU	THR	LYS	SER	LYS	GLN	ALA
	GLN	GLY	THR	SER	LYS	ASP	GLY
	THR	PRO	PRO	GLU	LYS	GLU	SER
	VAL	GLN	PRO	GLU	LYS	ASP	GLU
	ASN	SER	LYS	SER	LYS	GLU	PHE
	VAL	LEU	ARG	GLU	GLY	GLU	ASN
	LEU	SER	GLU	GLU	SER	GLU	ARG
	ALA	GLY	ARG	GLU	ASP	GLY	LYS
	GLN	LYS	LYS	LYS	ASP	LYS	ARG
	ILE	SER	PRO	PRO	GLU	ALA	LEU
	LEU	THR	SER	PRO	GLU	LYS	ARG
	LYS	PRO	GLY	GLU	ALA	ARG	GLU
	ARG	GLN	GLY	GLU	PHE	GLY	GLU
	LEU	GLN	GLY	GLU	GLU	ARG	GLU
	LEU	PRO	SER	ASP	ASP	ARG	ALA
	ASN	SER	SER	LYS	SER	LYS	ARG
	PRO	PRO	ARG	GLU	ASP	ALA	LYS
	GLU	GLY	GLY	GLU	ASP	SER	LYS
	ARG	LYS	ASN	GLU	GLY	GLU	TYR
	LYS	THR	THR	GLU	ASP	LEU	GLY
	MET	THR	ARG	GLU	PHE	ARG	VAL
	ILE	PRO	PRO	LYS	GLU	ILE	VAL
	ASN	ASN	GLY	LYS	GLN	HIS	LEU
	ASN	SER	THR	ALA	GLY	ASP	LYS
	LYS	GLY	PRO	PRO	GLU	LEU	GLU
	MET	ASP	ALA	VAL	VAL	LEU	PHE
	HIS	VAL	ALA	PRO	THR	GLU	ARG
	PHE	GLN	GLU	GLN	TYR	ASP	
	SER	VAL	GLY	GLU	MET	ASP	P93
	LEU	THR	SER	LYS	GLU	LEU	
	LYS	GLU	GLY	LYS	ASP	MET	W98

- Molecule 7: General transcription and DNA repair factor IIH helicase subunit XPD



L382	L383	L384	L385	L386	L387	L388	L389	L390	L391	L392	L393	L394	L395	L396	L397	L398	L399	L400	L401	L402	L403	L404	L405	L406	L407	L408	L409	L410	L411	L412	L413	L414	L415	L416	L417	L418	L419	L420	L421	L422	L423	L424	L425	L426	L427	L428	L429	L430	L431	L432	L433	L434	L435	L436	L437	L438	L439	L440	L441	L442	L443	L444	L445	L446	L447	L448	L449	L450	L451	L452	L453	L454	L455	L456	L457	L458	L459	L460	L461	L462	L463	L464	L465	L466	L467	L468	L469	L470	L471	L472	L473	L474	L475	L476	L477	L478	L479	L480	L481	L482	L483	L484	L485	L486	L487	L488	L489	L490	L491	L492	L493	L494	L495	L496	L497	L498	L499	L500	L501	L502	L503	L504	L505	L506	L507	L508	L509	L510	L511	L512	L513	L514	L515	L516	L517	L518	L519	L520	L521	L522	L523	L524	L525	L526	L527	L528	L529	L530	L531	L532	L533	L534	L535	L536	L537	L538	L539	L540	L541	L542	L543	L544	L545	L546	L547	L548	L549	L550	L551	L552	L553	L554	L555	L556	L557	L558	L559	L560	L561	L562	L563	L564	L565	L566	L567	L568	L569	L570	L571	L572	L573	L574	L575	L576	L577	L578	L579	L580	L581	L582	L583	L584	L585	L586	L587	L588	L589	L590	L591	L592	L593	L594	L595	L596	L597	L598	L599	L600	L601	L602	L603	L604	L605	L606	L607	L608	L609	L610	L611	L612	L613	L614	L615	L616	L617	L618	L619	L620	L621	L622	L623	L624	L625	L626	L627	L628	L629	L630	L631	L632	L633	L634	L635	L636	L637	L638	L639	L640	L641	L642	L643	L644	L645	L646	L647	L648	L649	L650	L651	L652	L653	L654	L655	L656	L657	L658	L659	L660	L661	L662	L663	L664	L665	L666	L667	L668	L669	L670	L671	L672	L673	L674	L675	L676	L677	L678	L679	L680	L681	L682	L683	L684	L685	L686	L687	L688	L689	L690	L691	L692	L693	L694	L695	L696	L697	L698	L699	L700	L701	L702	L703	L704	L705	L706	L707	L708	L709	L710	L711	L712	L713	L714	L715	L716	L717	L718	L719	L720	L721	L722	L723	L724	L725	L726	L727	L728	L729	L730	L731	L732	L733	L734	L735	L736	L737	L738	L739	L740	L741	L742	L743	L744	L745	L746	L747	L748	L749	L750	L751	L752	L753	L754	L755	L756	L757	L758	L759	L760	L761	L762	L763	L764	L765	L766	L767	L768	L769	L770	L771	L772	L773	L774	L775	L776	L777	L778	L779	L780	L781	L782	L783	L784	L785	L786	L787	L788	L789	L790	L791	L792	L793	L794	L795	L796	L797	L798	L799	L800	L801	L802	L803	L804	L805	L806	L807	L808	L809	L810	L811	L812	L813	L814	L815	L816	L817	L818	L819	L820	L821	L822	L823	L824	L825	L826	L827	L828	L829	L830	L831	L832	L833	L834	L835	L836	L837	L838	L839	L840	L841	L842	L843	L844	L845	L846	L847	L848	L849	L850	L851	L852	L853	L854	L855	L856	L857	L858	L859	L860	L861	L862	L863	L864	L865	L866	L867	L868	L869	L870	L871	L872	L873	L874	L875	L876	L877	L878	L879	L880	L881	L882	L883	L884	L885	L886	L887	L888	L889	L890	L891	L892	L893	L894	L895	L896	L897	L898	L899	L900	L901	L902	L903	L904	L905	L906	L907	L908	L909	L910	L911	L912	L913	L914	L915	L916	L917	L918	L919	L920	L921	L922	L923	L924	L925	L926	L927	L928	L929	L930	L931	L932	L933	L934	L935	L936	L937	L938	L939	L940	L941	L942	L943	L944	L945	L946	L947	L948	L949	L950	L951	L952	L953	L954	L955	L956	L957	L958	L959	L960	L961	L962	L963	L964	L965	L966	L967	L968	L969	L970	L971	L972	L973	L974	L975	L976	L977	L978	L979	L980	L981	L982	L983	L984	L985	L986	L987	L988	L989	L990	L991	L992	L993	L994	L995	L996	L997	L998	L999	L1000
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SER
LEU
GLU
GLN
GLY
GLU
SER
GLU
GLU
THR
LYS
THR
LYS
LYS
GLY
ILE
GLU
GLN
ILE
ALA
GLN
LEU

● Molecule 8: Histone H3

Chain NA:  68% 26%

MET
ALA
ARG
THR
GLY
LYS
GLN
THR
ALA
ARG
LYS
SER
THR
LYS
GLY
GLY
LYS
ALA
PRO
ARG
LYS
GLN
LEU
THR
LYS
ALA
ALA
ARG
LYS
SER
SER
ALA
PRO
THR
GLY
GLY
VAL
K436
K437
P438
K464
V517
T518
E533
R594
A535

● Molecule 8: Histone H3

Chain NE:  69% 6% 24%

MET
ALA
THR
GLY
LYS
PRO
ARG
LYS
SER
THR
LYS
GLY
GLY
LYS
ALA
PRO
ARG
LYS
SER
SER
ALA
PRO
THR
GLY
GLY
G833
G834
V835
K636
P643
Q655
K664
Q685
V717
R734
A735

● Molecule 9: DNA-directed RNA polymerase subunit

Chain PA:  63% 11% 25%

MET
HIS
GLY
GLY
THR
LEU
GLY
PRO
PRO
SER
GLY
LYS
ASP
HIS
S11
Q22
F23
G24
D29
R33
L57
T68
Q72
E89
F95
K105
V106
V110
C111
M122
K127
R140
L141
C154
E155
GLY
GLY
GLU
GLU
MET
ASP
ASN
LYS
PHE
GLY
VAL
GLU
GLN
PRO
GLU

GLY
ASP
GLU
ASP
THR
LYS
GLU
GLY
HIS
G182
Q188
R193
S194
G195
V202
LYS
HIS
VAL
ASN
GLU
ASP
SER
GLN
GLU
K212
E219
E223
T224
F225
L228
C233
F234
R244
R261
Q273
T277
H278
K279
T283
N287
Q311
L322

R327
R340
G348
R349
V350
R351
G352
N353
K357
D360
F361
A363
L373
D400
R401
D425
D428
L429
R430
I457
F458
N459
R460
P478
L484
N485
L486
S487
V488
P491
D495
F496
D497
M501
N502
L509
E510
T511
R512
A513
S514
I515
V521

M535
V538
Q539
L542
T543
A544
V546
T549
V560
L564
L567
W570
P575
V586
K589
L594
H609
I621
S622
D625
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F668
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I676
L680
T689
I693
I706
K710
R734
A774
A786
V787

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M872
Y875
D876
V879
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E893
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F903
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K910
P911
S912
N913
R963
C981
R985
H1005
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HIS
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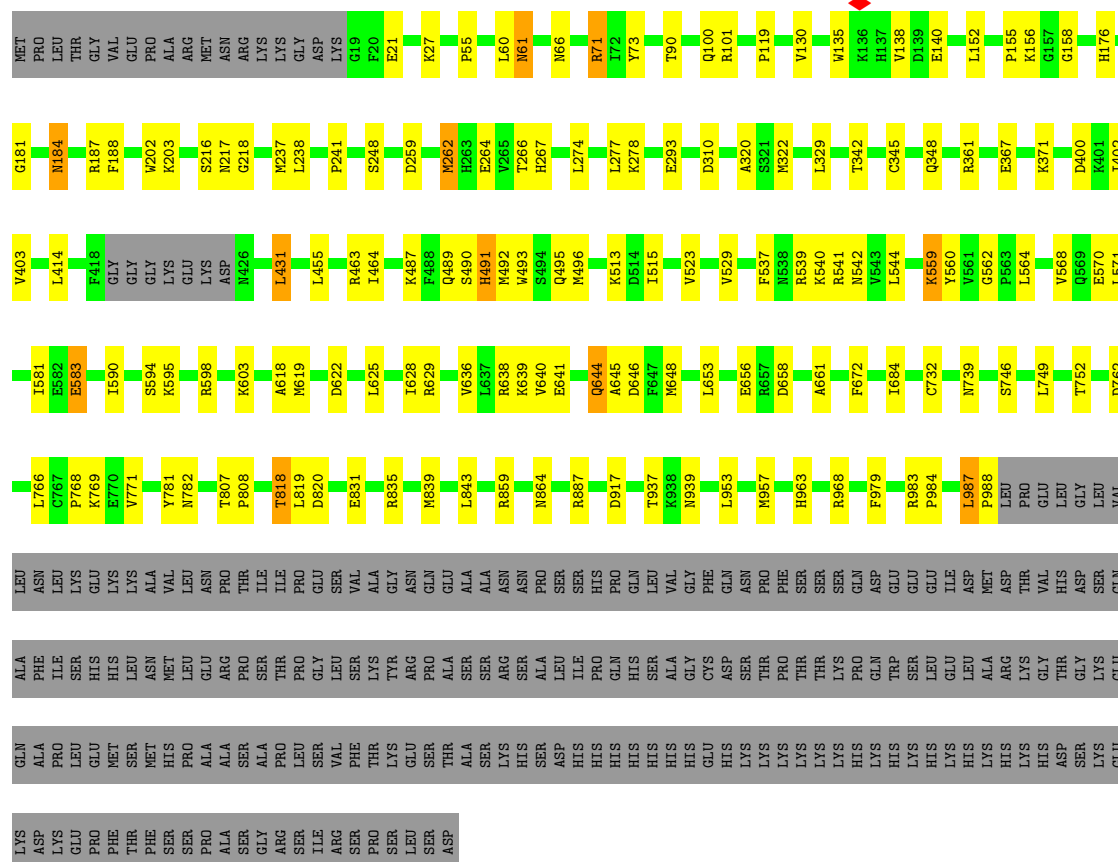
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G1340
GLY
D1375
T1378
F1386
D1203
V1204
R1213
V1214
E1215
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K1234
D1242
I1243
N1244
C1245
I1246
F1247
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A1252
E1253
K1254
R1260
I1261
M1262
T1435
V1436
D1437
E1441
A1442
A1443
G1446
G1453

GLU
GLU
VAL
VAL
ASP
K1278
M1279
D1280
D1281
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T1357
F1366
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E1379
L1382
V1385
L1398
L1411
T1415
R1416
M1420
R1421
K1429
C1430
T1435
V1436
D1437
E1441
A1442
A1443
G1446
G1453

V1454
S1455
E1456
N1457
I1458
T1468
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L1475
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M1484
F1487
THR
ASN
TLE
PRO
GLY
SER
ALA
SER
GLY
PHE
SER
PRO
THR
GLY
TYR
SER
PRO
PHE
GLY
TRP
SER
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GLY
MET
SER
THR
TRP
ASN
ILE
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SER
ALA
PRO
GLY
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MET
SER

TRP
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PHE
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SER
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THR
PRO
GLY
MET
SER
THR
TRP
ASN
ILE
PRO
SER
ALA
PRO
GLY
TYR
ALA
MET
SER

- Molecule 10: Transcription initiation factor TFIID subunit 2



Chain EB: 37% 22% 41%

MET	SER	V145	LYS
ASP	PHE	R146	VAL
PRO	ASN	D147	ALA
SER	LEU	K148	PRO
LEU	LYS	L151	ILE
LEU	ALA	L151	GLN
ARG	LEU	L167	ARG
GLU	SER	L168	ARG
ARG	GLY	L171	LYS
GLU	SER	I171	LYS
LEU	LEU	A174	PRO
PHE	G72	L175	ALA
LYS	Y73	L176	SER
LYS	K74	L177	GLN
ARG	F75	A181	LYS
ALA	G76	L193	LYS
LEU	Y82	R194	ARG
SER	N83	K198	ARG
THR	Y84	L195	THR
PRO	M85	I189	LYS
VAL	K86	HIS	HIS
GLU	T87	ASN	ASN
LYS	R88	GLU	GLU
ARG	H89	L213	HIS
SER	Q90	L214	LYS
ALA	R91	E214	ASP
LYS	G92	E215	SER
SER	D93	F216	SER
GLU	L99	W220	ASP
SER	L103	L225	THR
SER	D104	S227	SER
SER	E105	W228	SER
SER	H108	D229	LYS
LYS	I111	E230	LYS
LYS	M120	K232	THR
THR	L121	L233	LYS
LYS	A122	Y236	VAL
VAL	L124	L237	GLU
GLU	V125	I242	VAL
HIS	M126	SER	GLN
GLY	E131	SER	ASN
GLY	V132	GLN	SER
SER	I133	MET	SER
SER	D134	GLU	GLY
GLN	Y137	SER	GLY
ASN	A138	PRO	LYS
SER	F139	LYS	
HIS	K140		
SER	P141		
ASN	Y144		

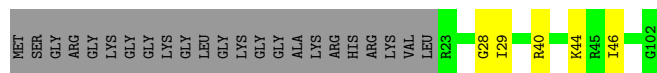
Chain FB:

Amino Acid	Percentage
MET	11%
A2	11%
V21	10%
Q30	10%
W31	10%
L43	10%
S55	10%
F56	10%
T57	10%
L58	10%
L62	10%
A63	10%
N64	10%
ILE	10%
HIS	10%
ASP	10%
ILE	10%
GLY	10%
GLY	10%
LYS	10%
PRO	10%
ALA	10%
SER	10%
VAL	10%
SER	10%
ALA	10%
PRO	10%
ARG	10%
E80	10%
H81	10%
T94	10%
I109	10%
N123	10%
D179	10%
H182	10%
M186	10%
L187	10%
F188	10%
S189	10%
E192	10%
K193	10%
H194	10%
Q195	10%
Y196	10%
K214	10%
T270	10%
G221	78%
N224	78%
H229	78%
E234	78%
E238	78%
TYR	78%
ARG	78%
HIS	78%
TYR	78%
GLN	78%
GLY	78%
GLU	78%
GLU	78%
LYS	78%
SER	78%
ASP	78%

[illegible]

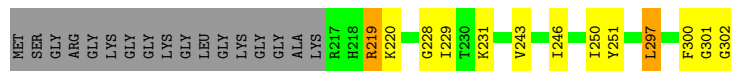
- Molecule 14: Histone H4

Chain NB:  73% 5% 22%



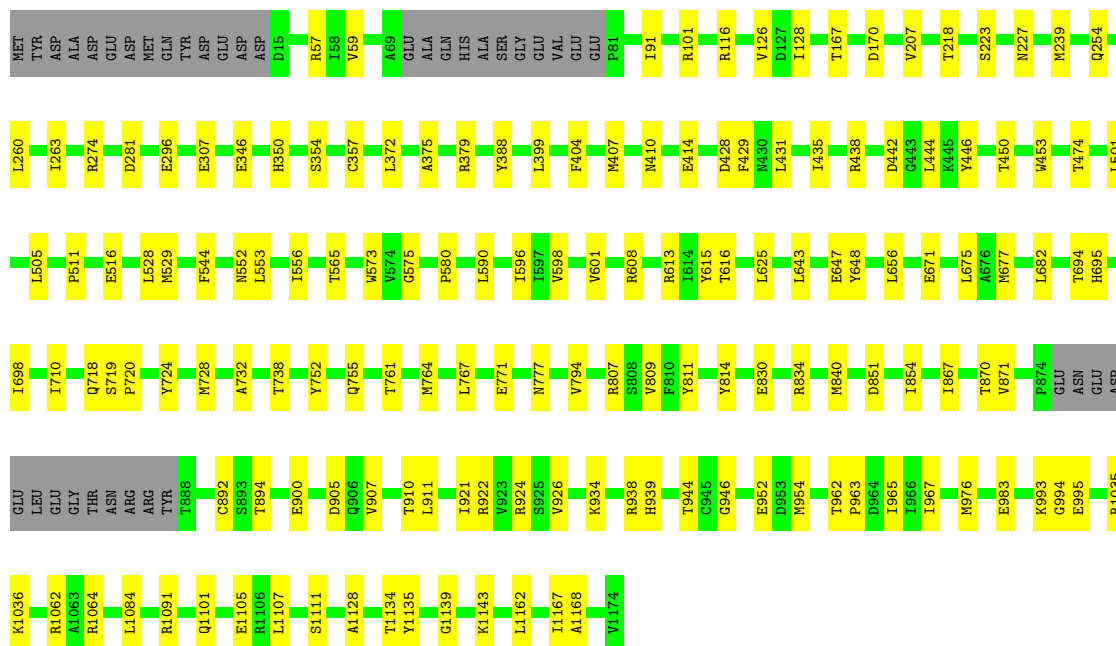
- Molecule 14: Histone H4

Chain NF:  71% 11% 17%



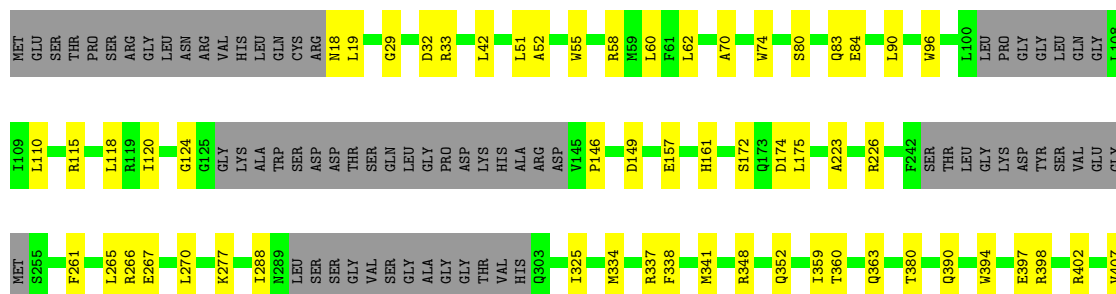
- Molecule 15: DNA-directed RNA polymerase subunit beta

Chain PB:  84% 13% .



- Molecule 16: General transcription factor IIH subunit 4

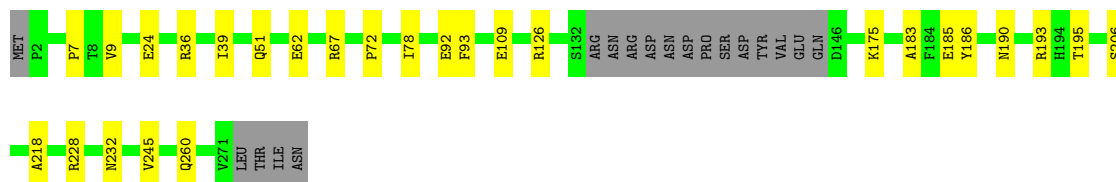
Chain HC:  70% 15% 16%





- Molecule 17: DNA-directed RNA polymerase II subunit RPB3

Chain PC: 84% 10% 7%



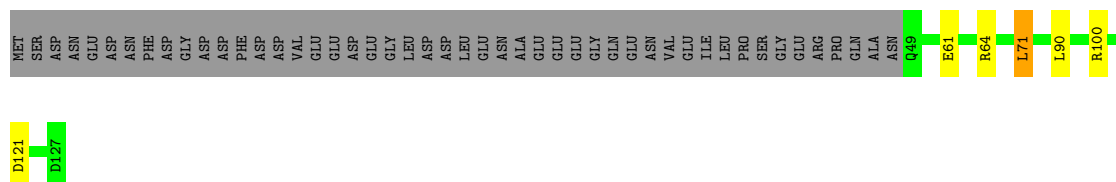
- Molecule 18: DNA-directed RNA polymerase II subunit E

Chain PE: 87% 13%



- Molecule 19: DNA-directed RNA polymerase II subunit F

Chain PF: 57% 38%



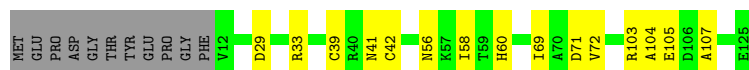
- Molecule 20: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain PH: 92% 7%



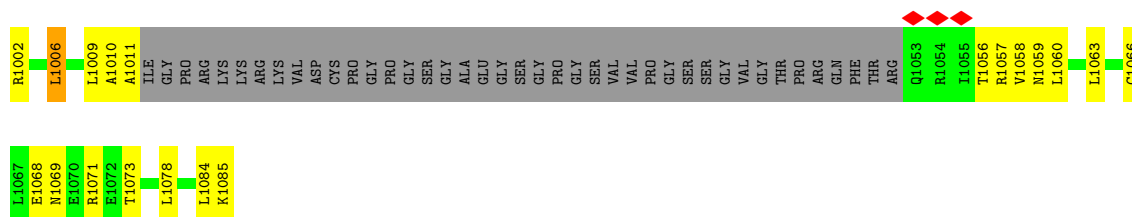
- Molecule 21: DNA-directed RNA polymerase II subunit RPB9

Chain PI: 79% 12% 9%

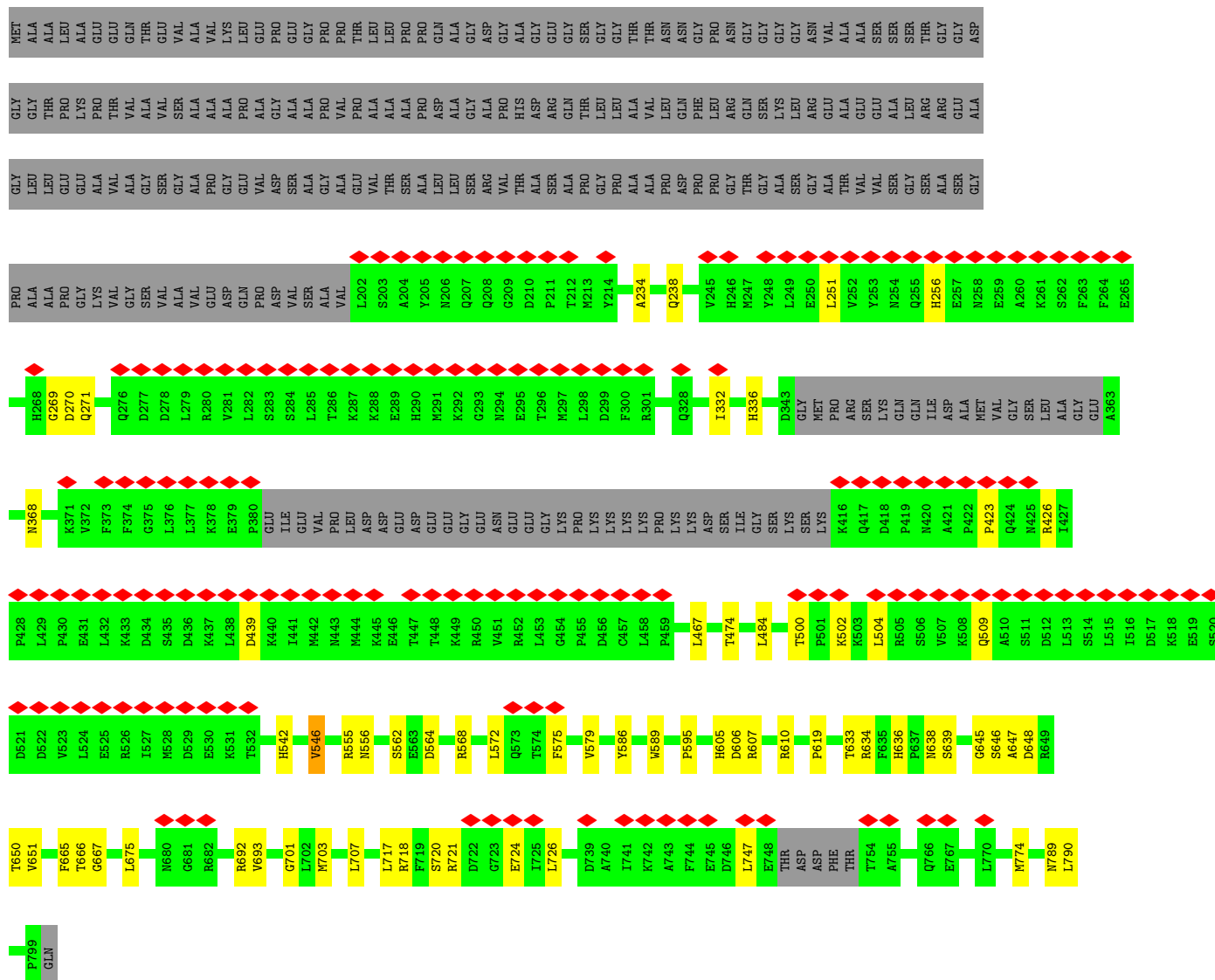


- Molecule 22: DNA-directed RNA polymerases I, II, and III subunit RPABC5

Chain PJ: 78% 18%

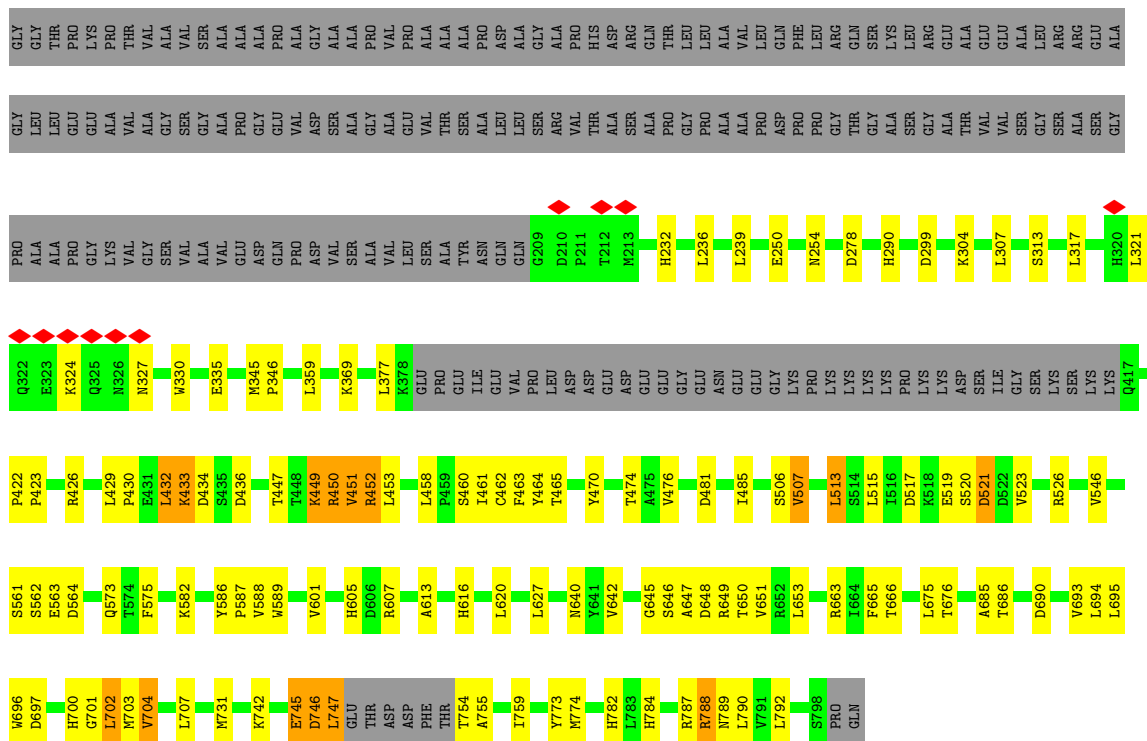


• Molecule 30: Transcription initiation factor TFIID subunit 5

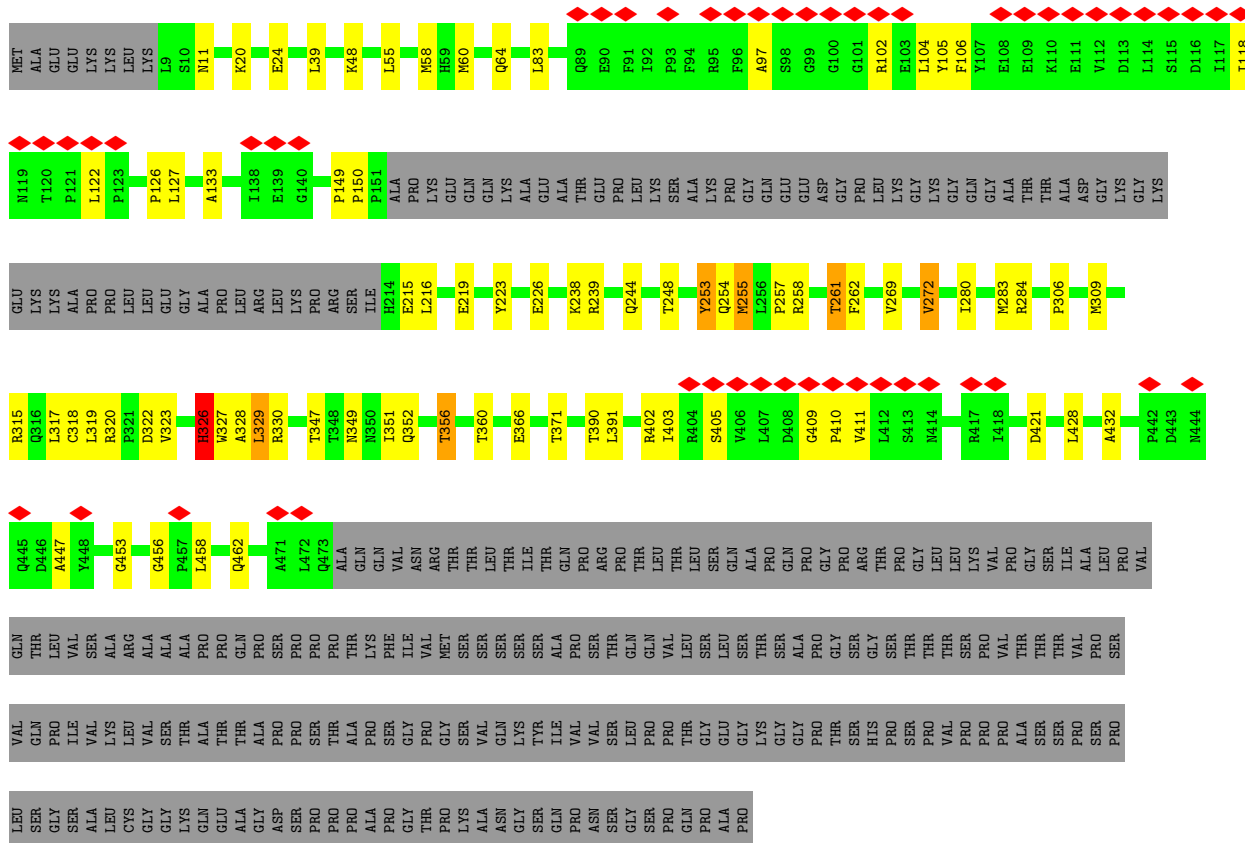


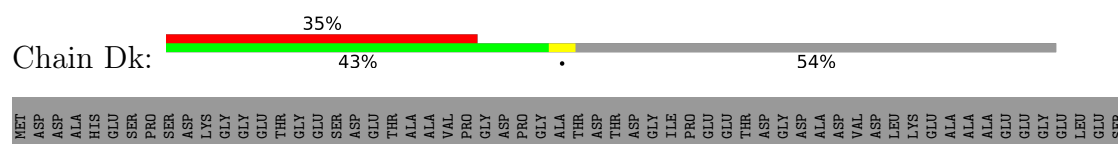
• Molecule 30: Transcription initiation factor TFIID subunit 5

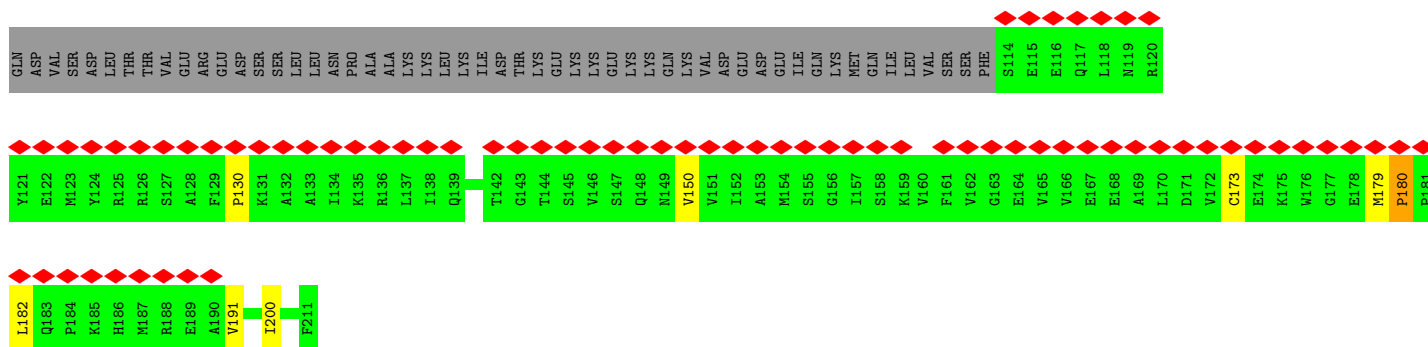




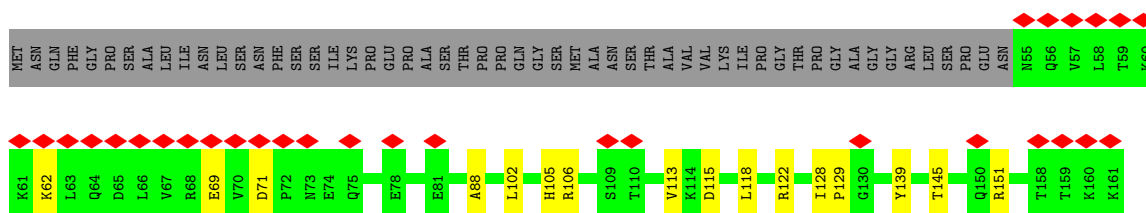
- Molecule 31: Transcription initiation factor TFIID subunit 6



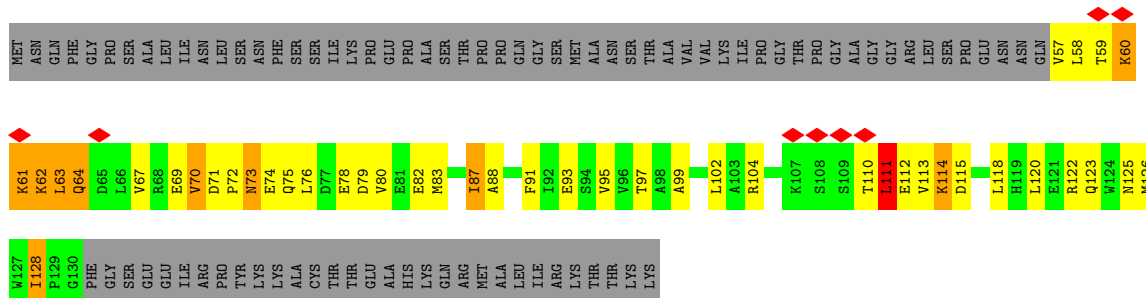
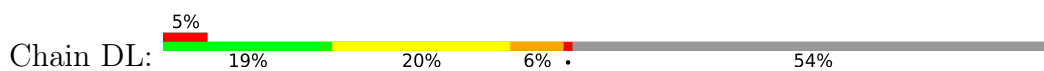




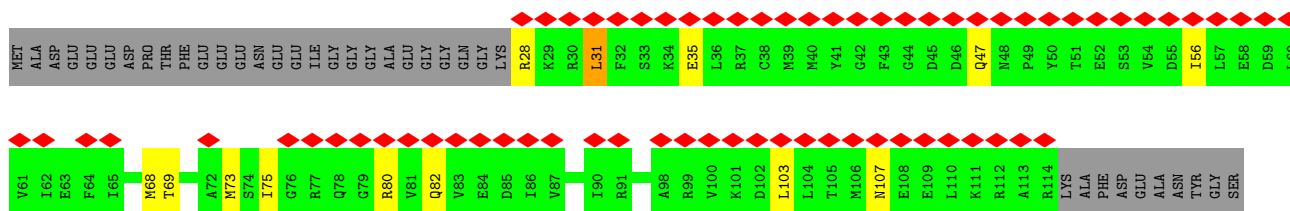
• Molecule 35: Transcription initiation factor TFIID subunit 12



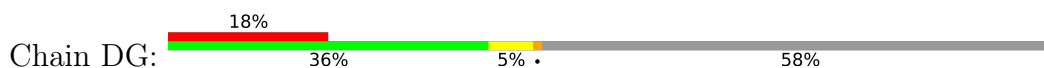
• Molecule 35: Transcription initiation factor TFIID subunit 12

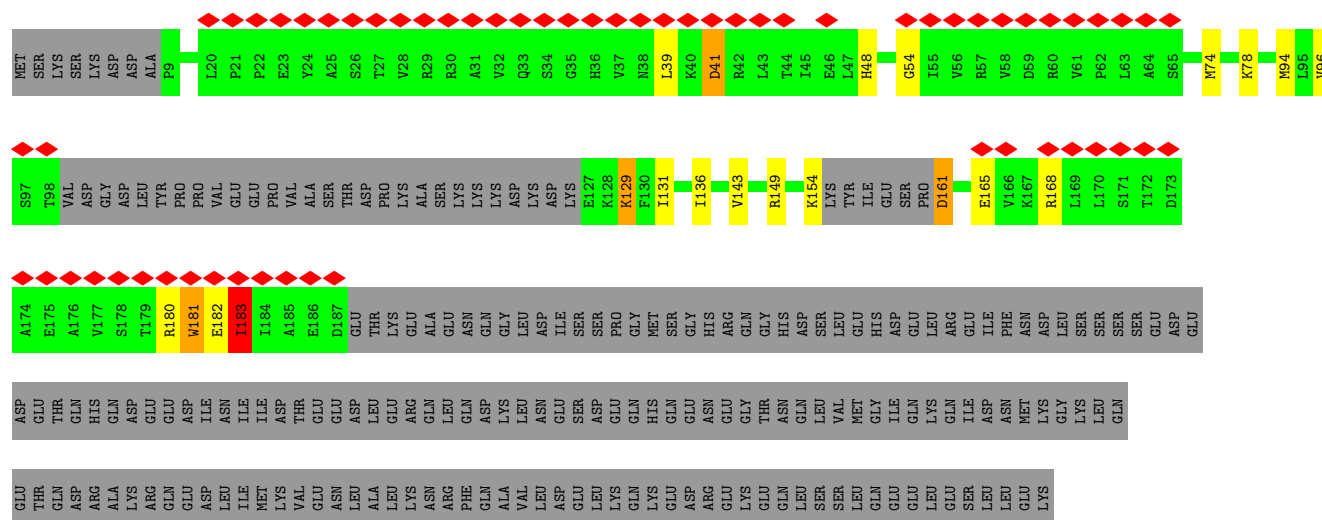


• Molecule 36: Transcription initiation factor TFIID subunit 13



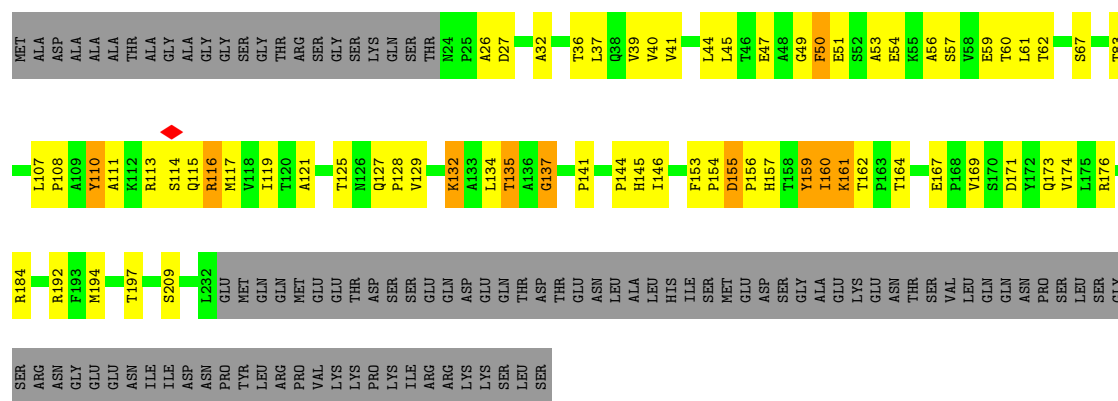
• Molecule 37: Transcription initiation factor TFIID subunit 7





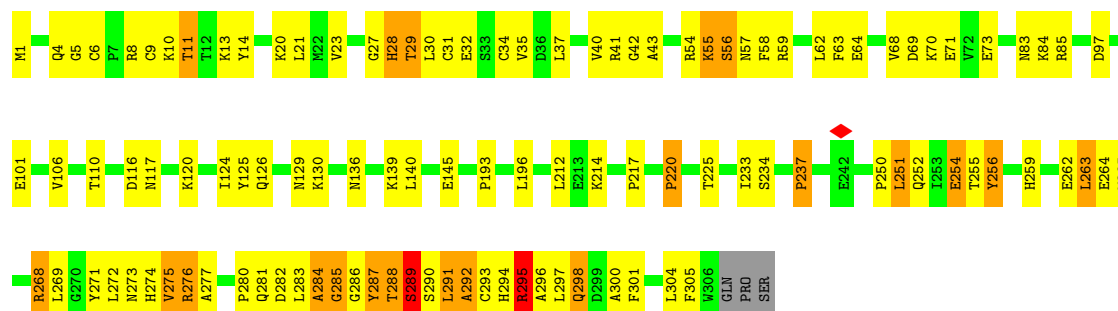
• Molecule 38: Transcription initiation factor TFIID subunit 8

Chain DH: 45% 19% 33%



• Molecule 39: CDK-activating kinase assembly factor MAT1

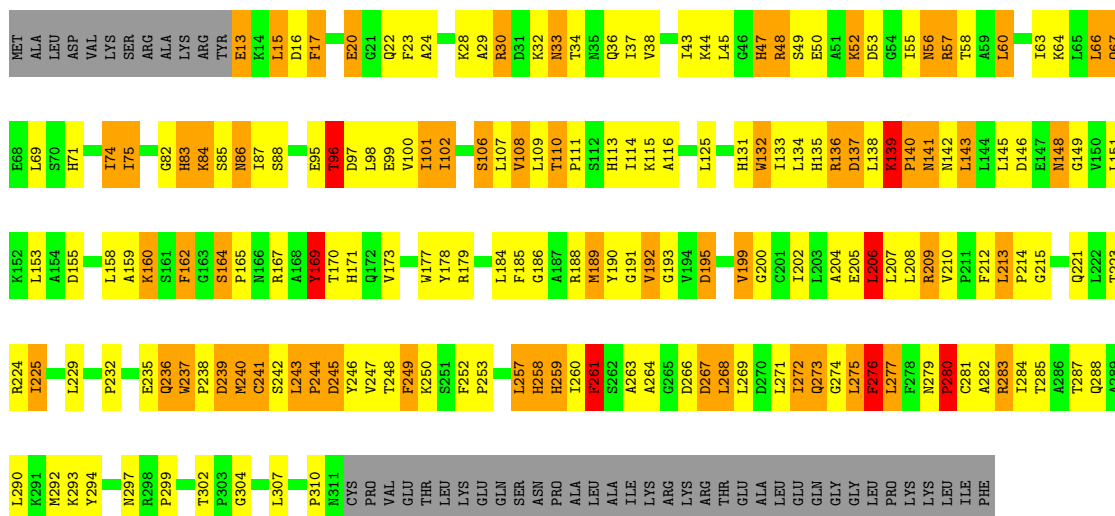
Chain HD: 63% 29% 7%



• Molecule 40: General transcription factor IIH subunit 3

Chain HE: 66% 18% 15%

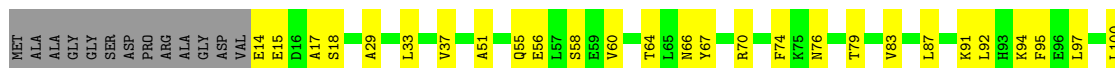
- Molecule 44: Cyclin-dependent kinase 7



- Molecule 45: Cyclin-H



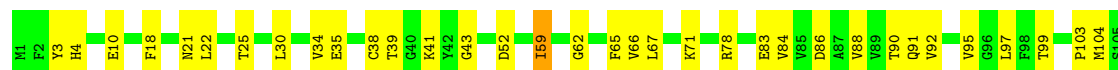
- Molecule 46: DNA-directed RNA polymerase II subunit RPB4





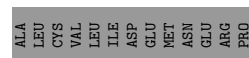
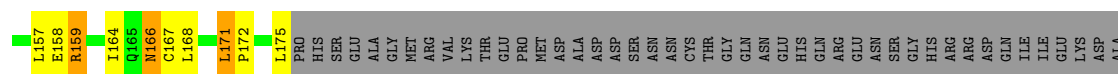
• Molecule 47: DNA-directed RNA polymerase II subunit RPB7

Chain PG: 67% 32% ..



• Molecule 48: Mediator of RNA polymerase II transcription subunit 7

Chain g: 26% 15% .. 55%



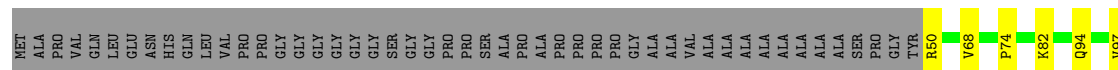
• Molecule 49: Mediator of RNA polymerase II transcription subunit 10

Chain j: 77% 13% • 10%

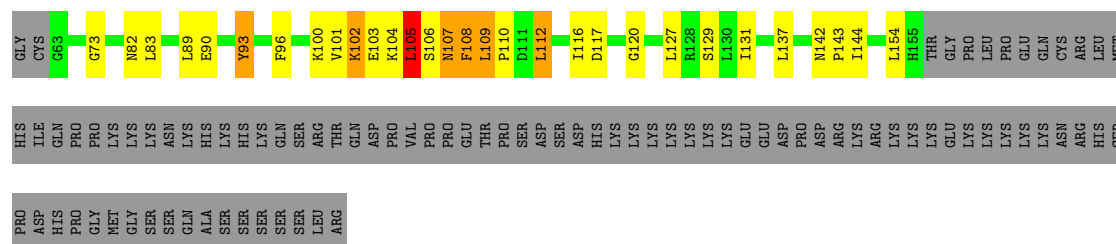


• Molecule 50: Mediator of RNA polymerase II transcription subunit 14

Chain n: 47% 21% • 30%

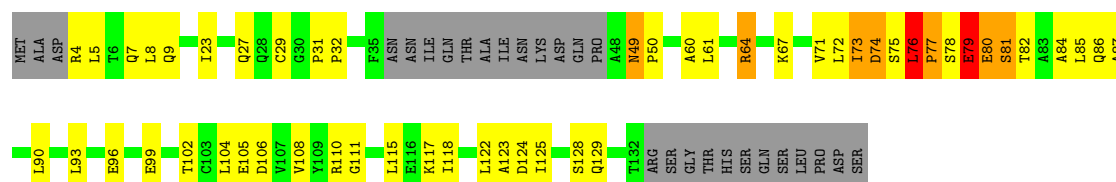






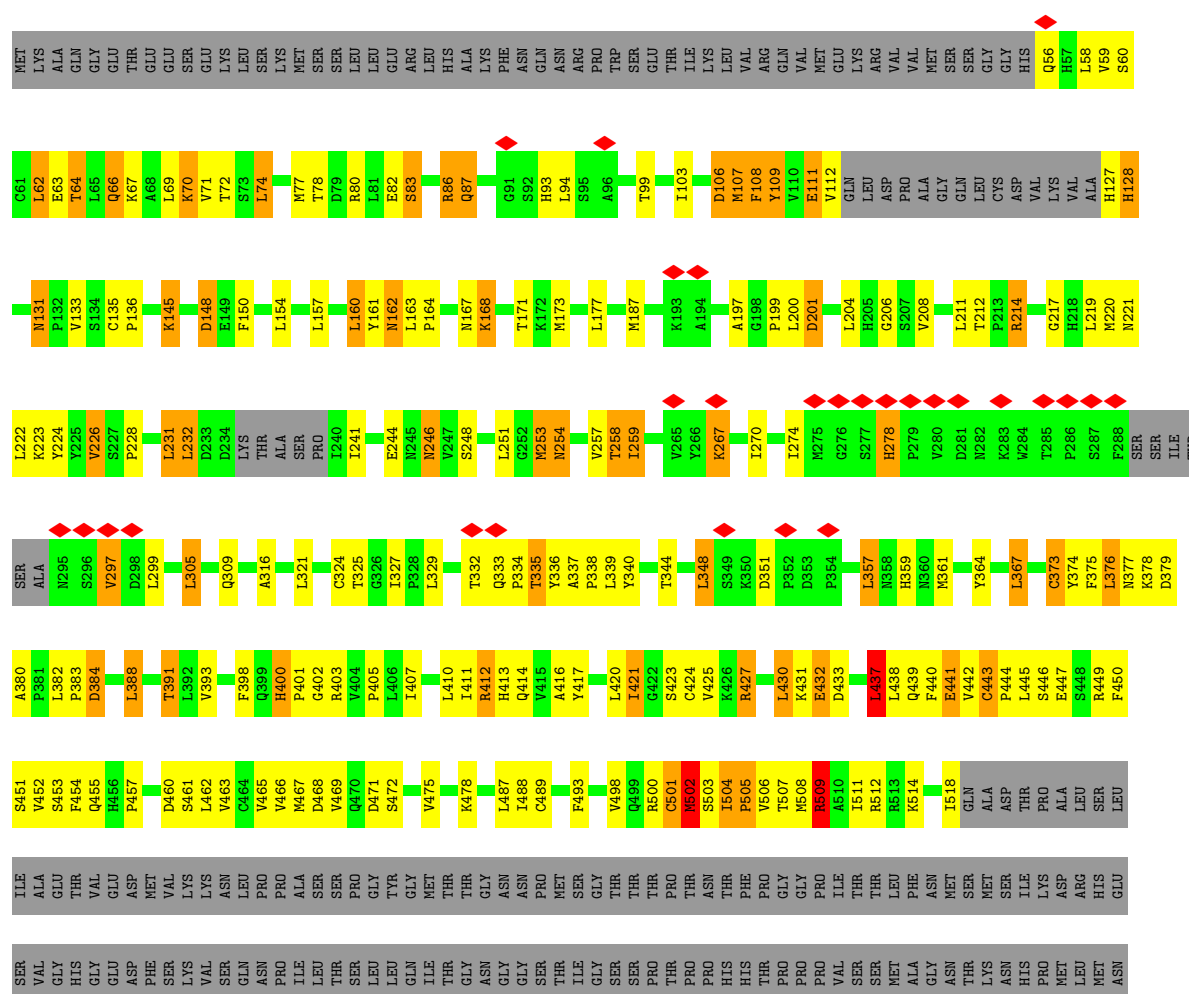
• Molecule 52: Mediator of RNA polymerase II transcription subunit 21

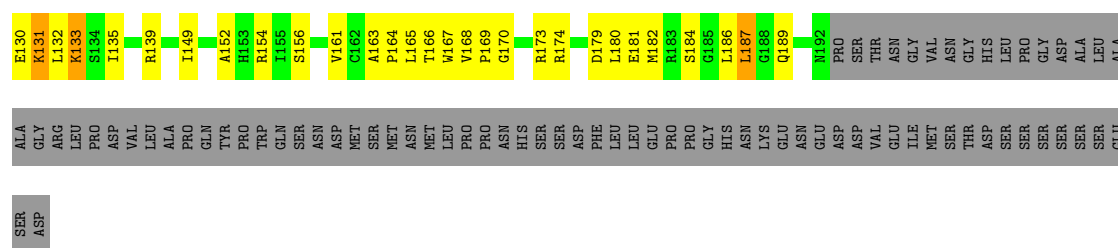
Chain u: 45% 30% 5% 19%



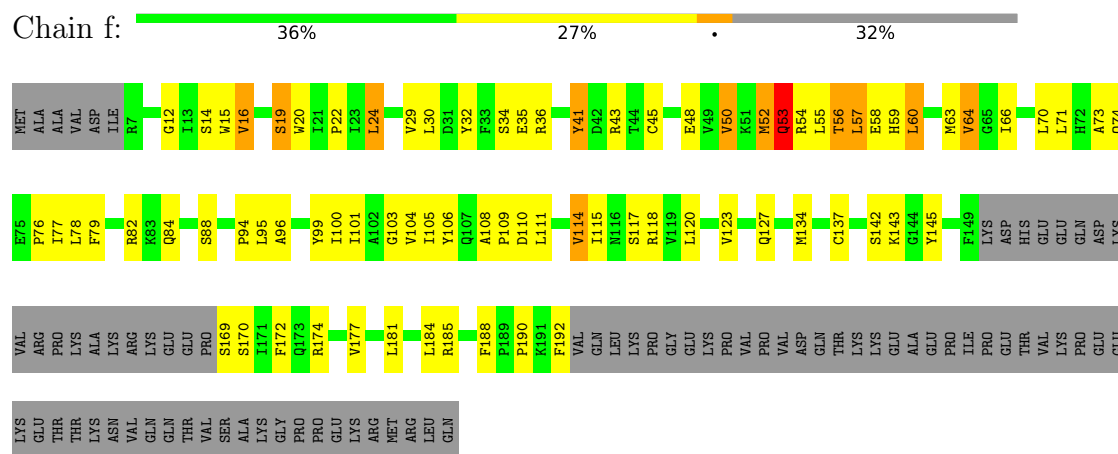
• Molecule 53: Mediator of RNA polymerase II transcription subunit 1

Chain a: 15% 9% 72%

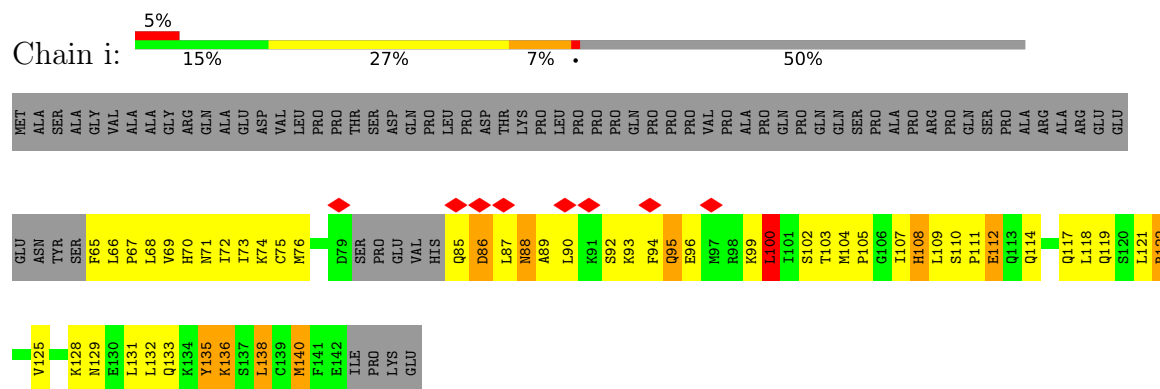




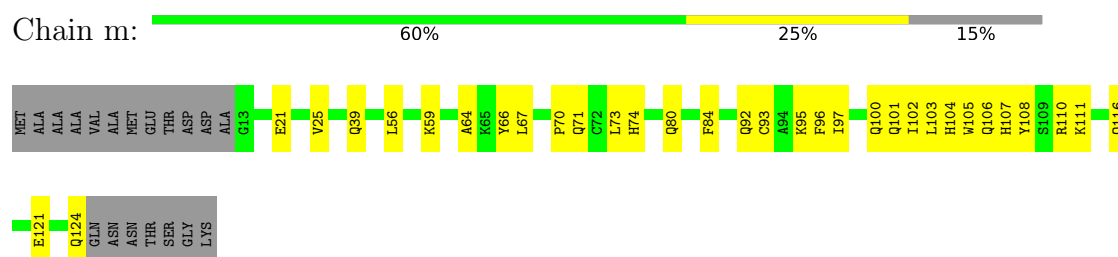
• Molecule 55: Mediator of RNA polymerase II transcription subunit 6



• Molecule 56: Mediator of RNA polymerase II transcription subunit 9



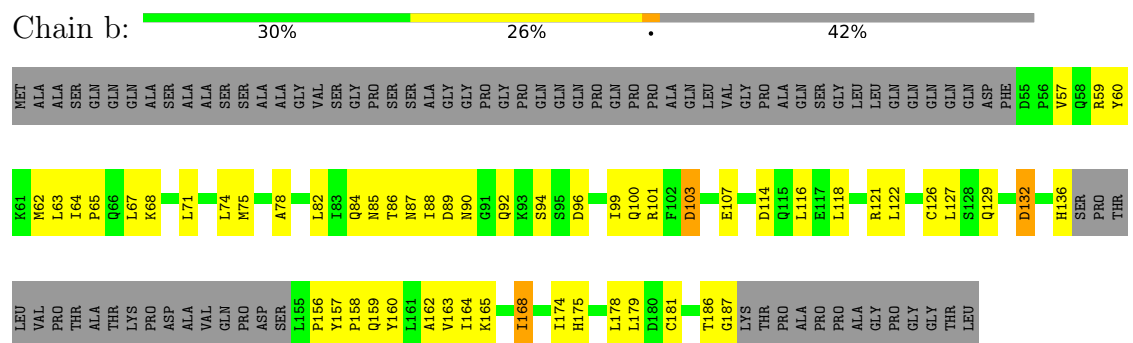
• Molecule 57: Mediator of RNA polymerase II transcription subunit 31



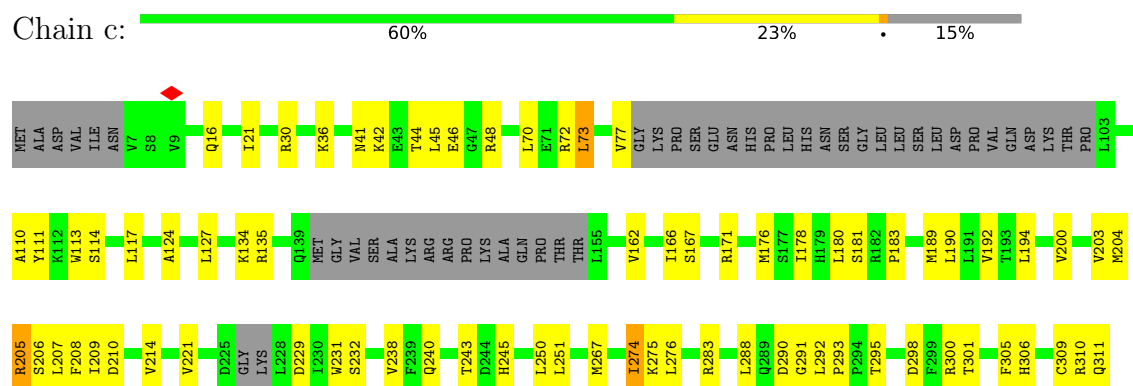
• Molecule 58: Mediator of RNA polymerase II transcription subunit 17



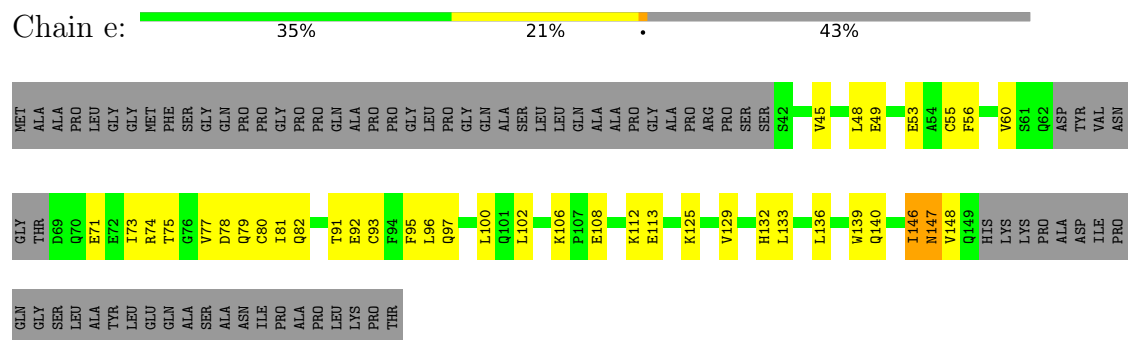
- Molecule 60: Mediator of RNA polymerase II transcription subunit 29



- Molecule 61: Mediator of RNA polymerase II transcription subunit 27



- Molecule 62: Mediator of RNA polymerase II transcription subunit 28

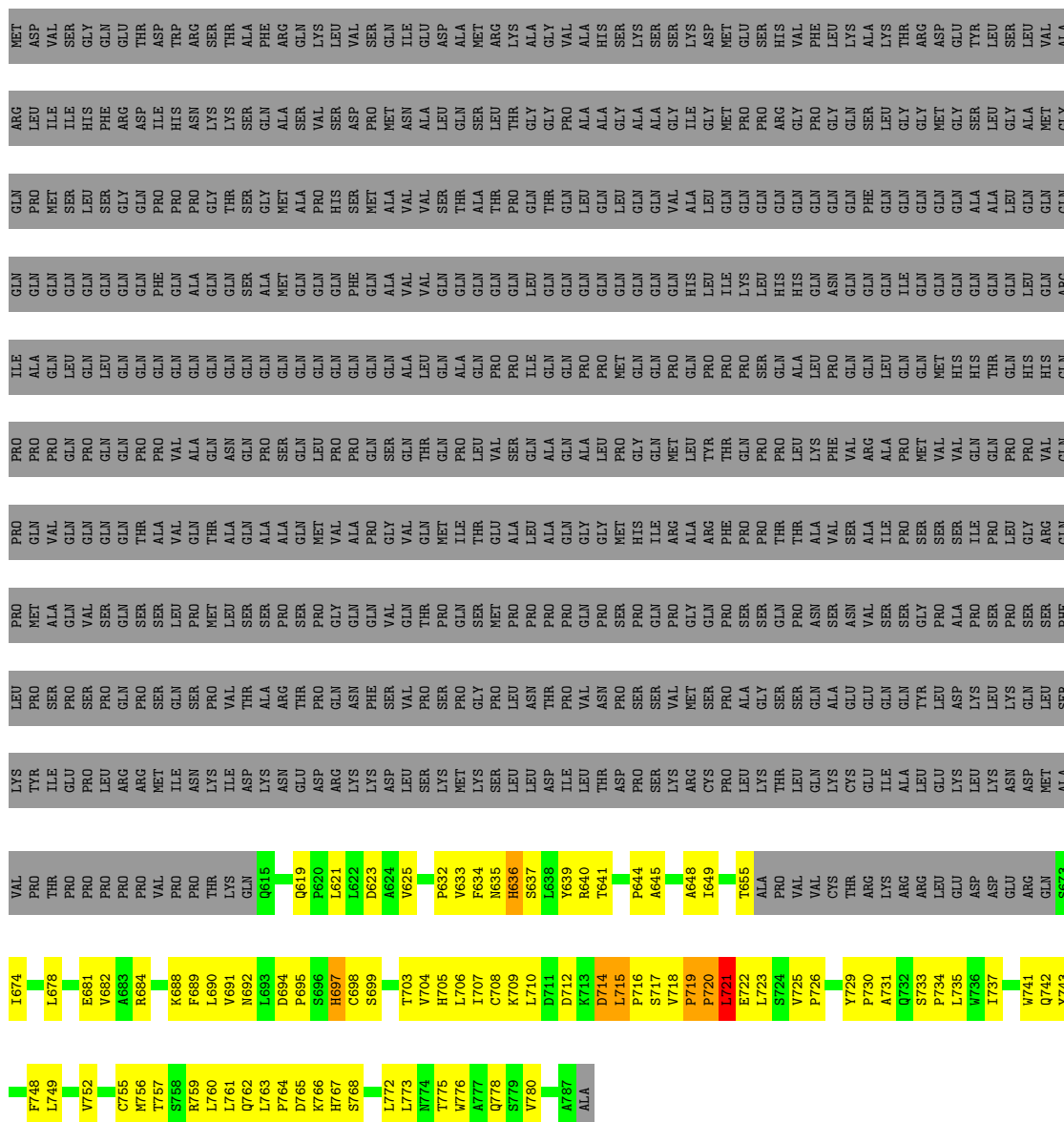


- Molecule 63: Mediator of RNA polymerase II transcription subunit 30

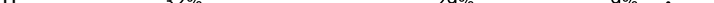


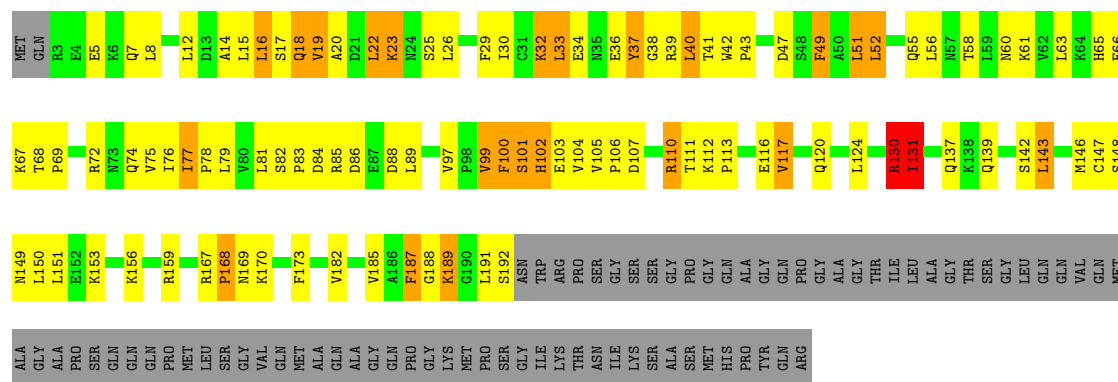
- Molecule 64: Mediator of RNA polymerase II transcription subunit 15

Chain o: 9% 10% 80%

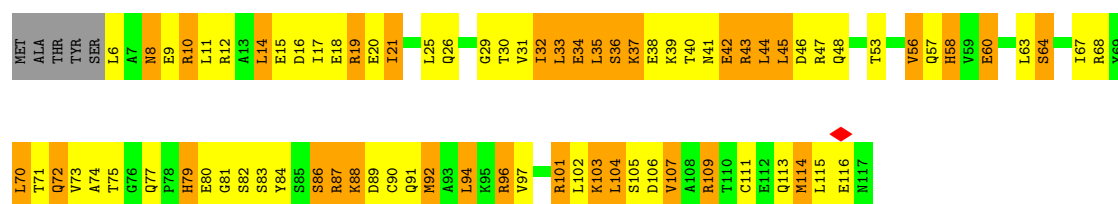
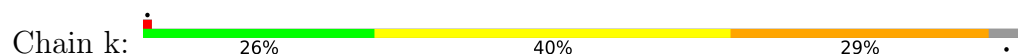


- Molecule 65: Isoform 2 of Mediator of RNA polymerase II transcription subunit 8

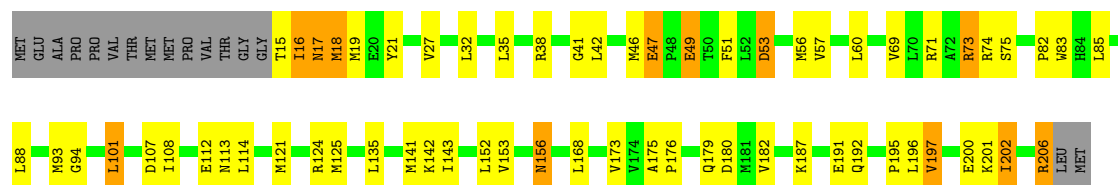
Chain h:  32% 29% 9% 1% 29%



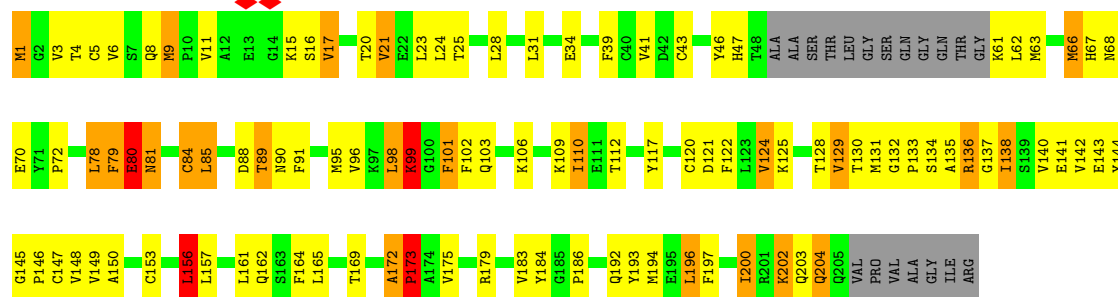
• Molecule 66: Mediator of RNA polymerase II transcription subunit 11



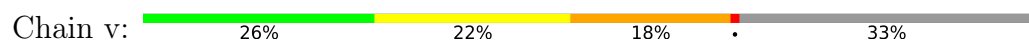
• Molecule 67: Mediator of RNA polymerase II transcription subunit 18



• Molecule 68: Mediator of RNA polymerase II transcription subunit 20

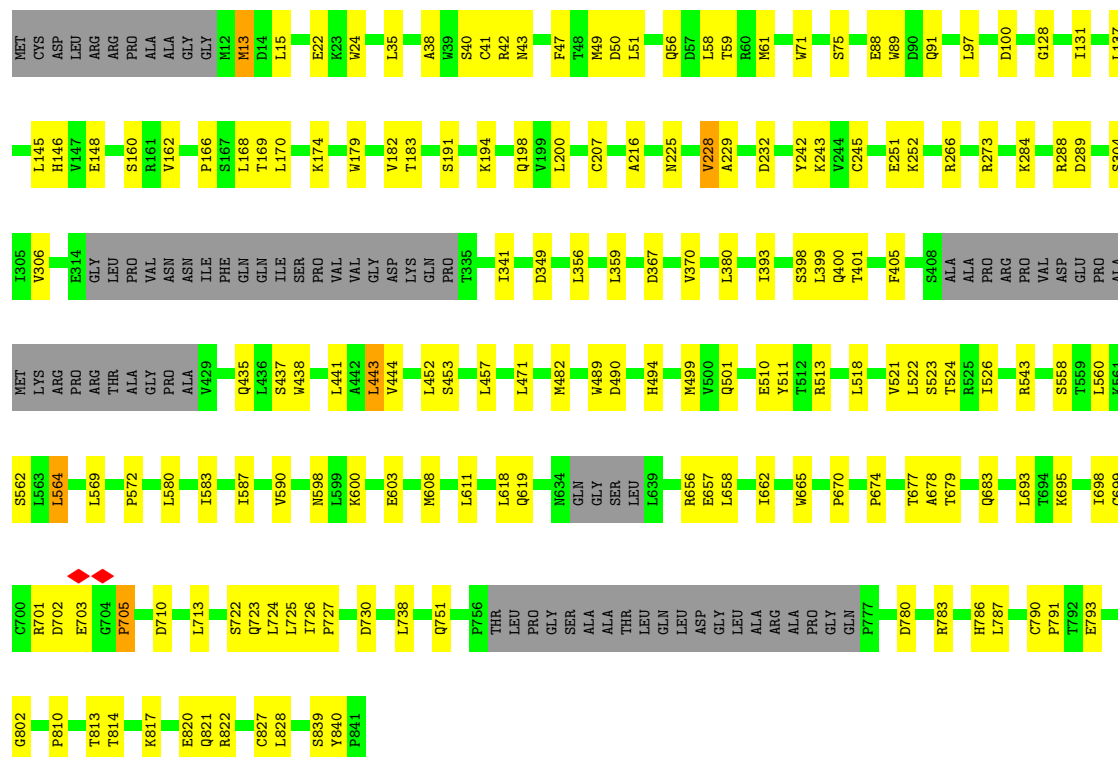


• Molecule 69: Mediator of RNA polymerase II transcription subunit 22

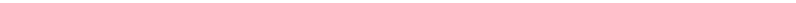


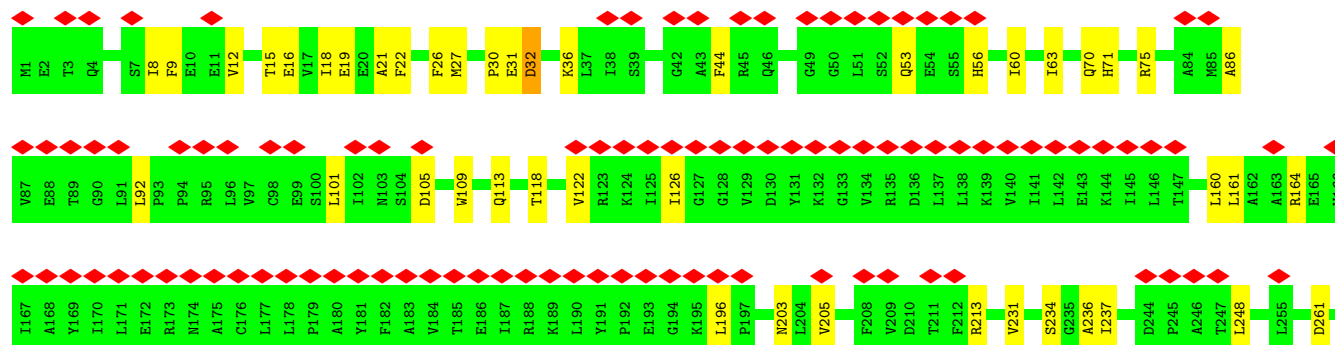
- Molecule 70: Isoform 2 of Mediator of RNA polymerase II transcription subunit 16

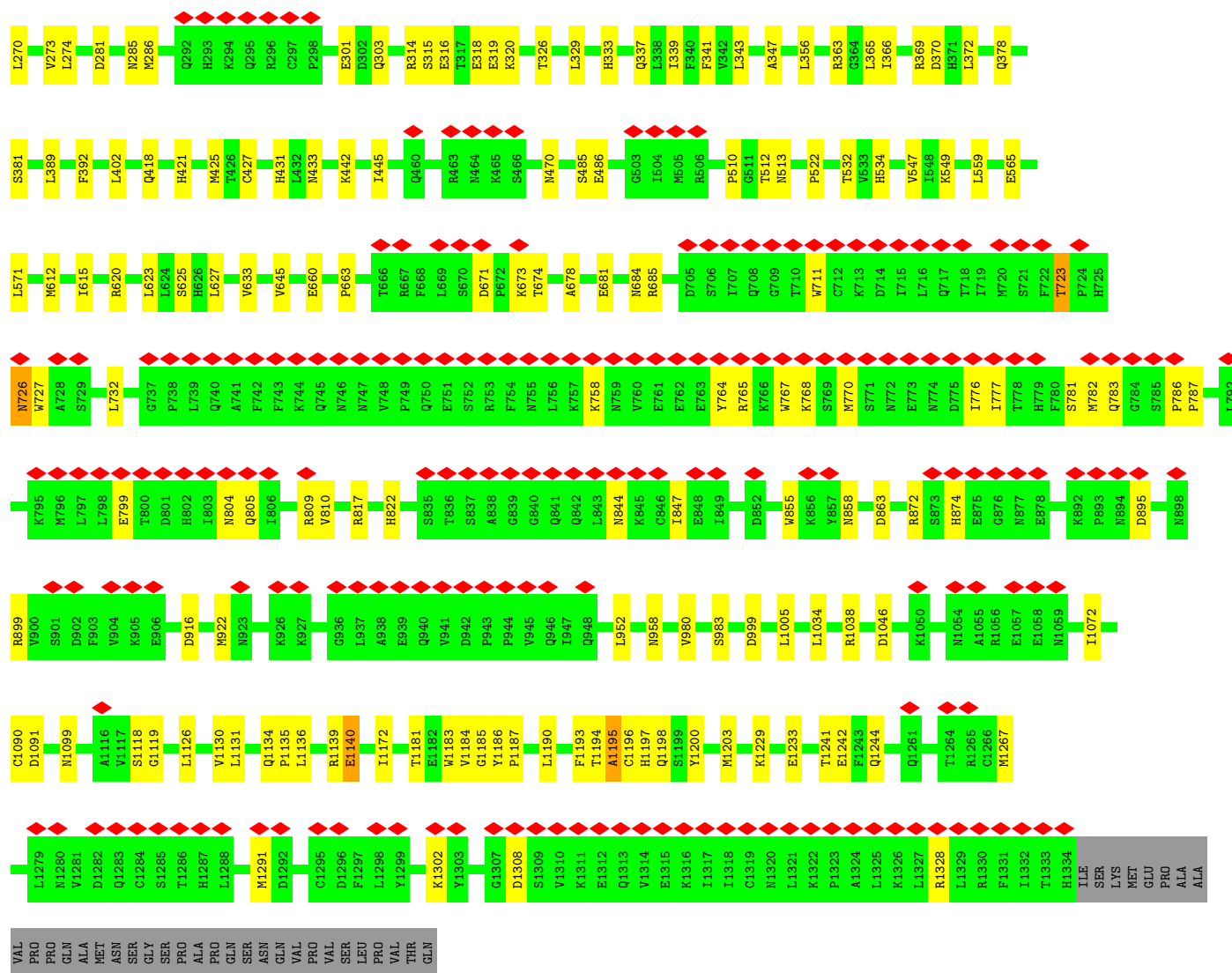
Chain p: 71% 20% • 9%



- Molecule 71: Mediator of RNA polymerase II transcription subunit 23

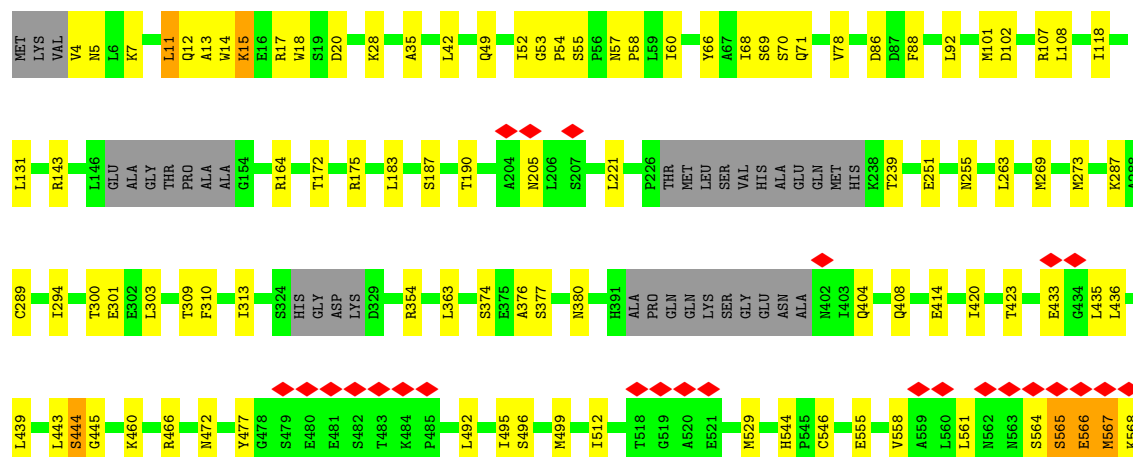
Chain w: 





• Molecule 72: Mediator of RNA polymerase II transcription subunit 24

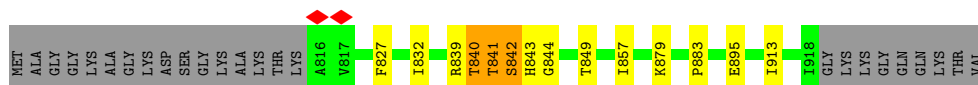
Chain x:



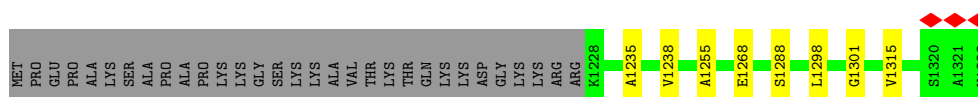




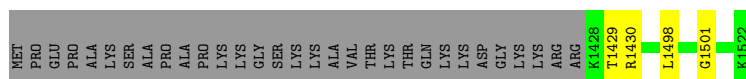
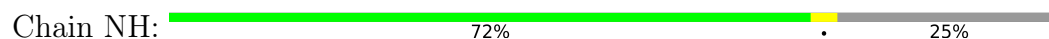
• Molecule 74: HISTONE H2A.Z



• Molecule 75: Histone H2B



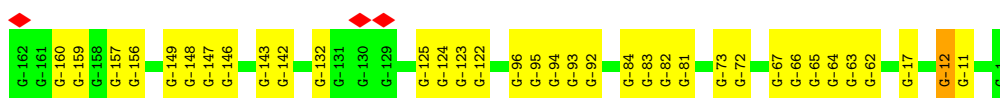
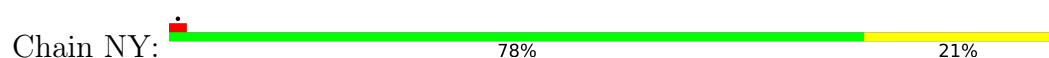
• Molecule 75: Histone H2B



• Molecule 76: DNA (162-mer)



• Molecule 77: DNA (162-mer)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	26458	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.678	Depositor
Minimum map value	-1.034	Depositor
Average map value	0.015	Depositor
Map value standard deviation	0.079	Depositor
Recommended contour level	0.156	Depositor
Map size ($\text{\AA}$)	560.27997, 560.27997, 560.27997	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.3339999, 1.3339999, 1.3339999	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, SF4, 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	X	0.42	0/1561	0.60	1/2411 (0.0%)
2	Y	0.48	0/1516	0.63	1/2334 (0.0%)
3	BA	0.13	0/1983	0.27	0/2679
4	DA	0.66	0/4679	0.90	6/6320 (0.1%)
5	EA	0.32	0/1560	0.58	1/2097 (0.0%)
6	FA	0.11	0/1167	0.27	0/1576
7	HA	0.14	0/5875	0.30	0/7955
8	NA	1.12	1/497 (0.2%)	1.43	2/693 (0.3%)
8	NE	1.27	0/510	1.55	6/710 (0.8%)
9	PA	0.24	0/11851	0.38	1/16014 (0.0%)
10	DB	0.49	1/7993 (0.0%)	0.71	8/10836 (0.1%)
11	EB	0.23	0/1427	0.44	0/1916
12	FB	0.19	0/1817	0.35	0/2445
13	HB	0.15	0/2210	0.31	0/2975
14	NB	1.23	0/390	1.46	5/539 (0.9%)
14	NF	1.39	5/420 (1.2%)	1.49	5/581 (0.9%)
15	PB	0.13	0/9257	0.28	0/12493
16	HC	0.21	0/3230	0.37	0/4376
17	PC	0.13	0/2102	0.29	0/2857
18	PE	0.12	0/1752	0.28	0/2366
19	PF	0.24	0/646	0.40	0/871
20	PH	0.11	0/1207	0.28	0/1628
21	PI	0.12	0/949	0.29	0/1284
22	PJ	0.14	0/516	0.25	0/696
23	PK	0.15	0/939	0.26	0/1271
24	PL	0.13	0/378	0.27	0/500
25	DP	0.14	0/1448	0.28	0/1948
26	DQ	0.16	0/945	0.35	0/1274
27	DO	0.15	0/816	0.29	0/1105
28	Dc	0.48	0/1035	0.67	0/1406
29	DD	0.56	0/1343	0.85	2/1795 (0.1%)
29	Dd	0.22	0/1321	0.44	0/1772

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	DE	0.43	0/4469	0.64	2/6050 (0.0%)
30	De	0.29	0/4433	0.53	0/6004
31	DF	0.70	1/3167 (0.0%)	1.07	10/4303 (0.2%)
31	Df	0.48	0/3140	0.81	6/4268 (0.1%)
32	DI	0.62	0/981	0.84	0/1332
32	Di	0.24	0/989	0.44	0/1343
33	DJ	0.24	0/736	0.46	0/998
33	Dj	0.23	0/775	0.45	0/1049
34	Dk	0.30	0/799	0.54	1/1070 (0.1%)
35	DL	0.65	0/613	1.03	1/829 (0.1%)
35	Dl	0.54	0/888	0.80	0/1194
36	Dm	0.32	0/733	0.55	0/977
37	DG	0.71	0/1199	0.95	1/1612 (0.1%)
38	DH	0.46	0/1673	0.75	2/2285 (0.1%)
39	HD	0.68	0/2436	1.05	23/3286 (0.7%)
40	HE	0.30	0/2103	0.42	0/2846
41	HG	0.13	0/2793	0.27	0/3780
42	HH	0.13	0/4994	0.29	0/6745
43	HF	0.19	0/529	0.43	1/714 (0.1%)
44	HI	1.02	0/2433	1.64	46/3302 (1.4%)
45	HJ	1.10	3/2356 (0.1%)	1.72	55/3185 (1.7%)
46	PD	0.28	0/1064	0.39	0/1428
47	PG	0.20	0/1382	0.33	0/1874
48	g	0.78	0/911	1.40	8/1219 (0.7%)
49	j	0.38	0/849	0.61	0/1150
50	n	0.43	0/7901	0.73	17/10731 (0.2%)
51	s	0.93	0/741	1.25	6/1002 (0.6%)
52	u	0.75	1/895 (0.1%)	1.10	9/1215 (0.7%)
53	a	0.93	0/3507	1.34	11/4760 (0.2%)
54	d	0.92	0/1281	1.30	1/1718 (0.1%)
55	f	0.75	1/1402 (0.1%)	1.00	2/1905 (0.1%)
56	i	0.99	1/612 (0.2%)	1.35	1/815 (0.1%)
57	m	0.21	0/1010	0.39	0/1359
58	q	0.66	1/4456 (0.0%)	0.87	0/6019
59	z	0.95	0/781	1.40	5/1067 (0.5%)
60	b	0.75	0/911	1.13	1/1229 (0.1%)
61	c	0.58	0/2172	0.88	4/2935 (0.1%)
62	e	0.25	0/840	0.44	0/1128
63	l	0.19	0/1048	0.40	0/1405
64	o	0.52	0/1256	0.86	3/1724 (0.2%)
65	h	0.93	0/1485	1.32	3/2008 (0.1%)
66	k	0.98	0/885	1.32	1/1190 (0.1%)
67	r	0.91	0/1565	1.27	2/2106 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
68	t	1.04	2/1530 (0.1%)	1.49	10/2066 (0.5%)
69	v	0.97	0/1092	1.43	6/1468 (0.4%)
70	p	0.65	0/6116	0.76	3/8311 (0.0%)
71	w	0.52	0/11056	0.65	4/15023 (0.0%)
72	x	0.59	0/7191	0.78	11/9728 (0.1%)
73	y	0.63	0/1645	0.83	0/2240
74	NC	1.27	2/505 (0.4%)	1.53	9/700 (1.3%)
74	NG	1.09	1/523 (0.2%)	1.44	10/724 (1.4%)
75	ND	1.22	2/470 (0.4%)	1.46	5/654 (0.8%)
75	NH	1.10	0/470	1.44	3/654 (0.5%)
76	NX	0.38	0/3401	0.67	2/5180 (0.0%)
77	NY	0.34	0/4046	0.57	1/6310 (0.0%)
All	All	0.53	22/190578 (0.0%)	0.77	324/259940 (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
39	HD	0	1

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	q	452	ALA	C-N	9.13	1.47	1.33
55	f	110	ASP	C-N	-8.18	1.22	1.33
45	HJ	244	CYS	C-O	6.98	1.32	1.24
68	t	136	ARG	C-O	-6.86	1.15	1.23
68	t	89	THR	C-O	6.61	1.32	1.24

The worst 5 of 324 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	g	128	PRO	N-CA-C	-13.40	91.97	114.75
8	NA	464	LYS	N-CA-C	12.62	124.58	111.07
48	g	130	GLN	N-CA-C	-11.90	98.33	111.07
72	x	12	GLN	N-CA-C	-11.47	99.24	113.01
8	NE	635	VAL	N-CA-C	-10.90	102.21	111.91

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
39	HD	126	GLN	Mainchain

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	X	1387	0	747	24	0
2	Y	1357	0	752	17	0
3	BA	1953	0	1987	20	0
4	DA	4563	0	4485	102	0
5	EA	1535	0	1539	133	0
6	FA	1138	0	1103	15	0
7	HA	5751	0	5794	104	0
8	NA	498	0	230	2	0
8	NE	511	0	238	3	0
9	PA	11628	0	11712	204	0
10	DB	7796	0	7751	116	0
11	EB	1403	0	1428	56	0
12	FB	1788	0	1819	33	0
13	HB	2167	0	2175	35	0
14	NB	391	0	185	0	0
14	NF	421	0	197	1	0
15	PB	9076	0	9116	123	0
16	HC	3158	0	3213	96	0
17	PC	2059	0	2007	23	0
18	PE	1721	0	1737	16	0
19	PF	636	0	665	7	0
20	PH	1186	0	1147	7	0
21	PI	928	0	859	11	0
22	PJ	507	0	523	14	0
23	PK	920	0	942	13	0
24	PL	373	0	378	8	0
25	DP	1422	0	1514	18	0
26	DQ	930	0	888	15	0
27	DO	806	0	818	31	0
28	Dc	1011	0	975	25	0
29	DD	1330	0	1351	127	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	Dd	1307	0	1318	14	0
30	DE	4364	0	4244	148	0
30	De	4327	0	4197	43	0
31	DF	3109	0	3045	310	0
31	Df	3081	0	3012	68	0
32	DI	959	0	969	133	0
32	Di	967	0	977	30	0
33	DJ	720	0	719	135	0
33	Dj	759	0	759	17	0
34	Dk	785	0	818	8	0
35	DL	605	0	606	77	0
35	DI	876	0	893	27	0
36	Dm	724	0	744	13	0
37	DG	1180	0	1235	18	0
38	DH	1633	0	1621	165	0
39	HD	2400	0	2295	197	0
40	HE	2066	0	2097	52	0
41	HG	2732	0	2698	43	0
42	HH	4890	0	4949	63	0
43	HF	523	0	530	50	0
44	HI	2374	0	2389	205	0
45	HJ	2307	0	2314	149	0
46	PD	1050	0	1033	52	0
47	PG	1351	0	1358	98	0
48	g	898	0	936	79	0
49	j	840	0	718	37	0
50	n	7751	0	7530	586	0
51	s	723	0	727	53	0
52	u	886	0	871	143	0
53	a	3430	0	3461	420	0
54	d	1268	0	1305	277	0
55	f	1365	0	1337	172	0
56	i	605	0	628	210	0
57	m	983	0	968	90	0
58	q	4373	0	4433	550	0
59	z	765	0	728	78	0
60	b	899	0	908	116	0
61	c	2131	0	2140	100	0
62	e	832	0	824	101	0
63	l	1040	0	1065	86	0
64	o	1221	0	1212	123	0
65	h	1465	0	1460	198	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
66	k	879	0	886	192	0
67	r	1535	0	1545	56	0
68	t	1499	0	1482	105	0
69	v	1083	0	1059	197	0
70	p	5983	0	6071	134	0
71	w	10774	0	10838	146	0
72	x	7061	0	7223	229	0
73	y	1605	0	1576	24	0
74	NC	506	0	250	4	0
74	NG	524	0	260	7	0
75	ND	471	0	221	0	0
75	NH	471	0	221	0	0
76	NX	3078	0	1783	7	0
77	NY	3561	0	1784	20	0
78	BA	1	0	0	0	0
78	EA	1	0	0	0	0
78	HD	2	0	0	0	0
78	HE	2	0	0	0	0
78	HG	3	0	0	0	0
78	PA	2	0	0	0	0
78	PB	1	0	0	0	0
78	PC	1	0	0	0	0
78	PI	2	0	0	0	0
78	PJ	1	0	0	0	0
78	PL	1	0	0	0	0
78	c	1	0	0	0	0
78	p	1	0	0	0	0
79	HA	8	0	0	0	0
80	PA	1	0	0	0	0
All	All	185972	0	179545	5909	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 16.

The worst 5 of 5909 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)
54:d:49:ALA:HB2	56:i:76:MET:SD	1.22	1.71
60:b:174:ILE:CD1	63:l:75:LEU:HD21	1.22	1.61
9:PA:1795:PRO:HD2	54:d:169:PRO:CB	1.24	1.61
58:q:451:LEU:CD1	58:q:529:MET:HE1	1.30	1.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EA:139:LEU:HD11	47:PG:151:ARG:CD	1.31	1.59

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	
3	BA	248/316 (78%)	246 (99%)	2 (1%)	0	100	100
4	DA	542/1872 (29%)	524 (97%)	15 (3%)	3 (1%)	21	58
5	EA	185/439 (42%)	183 (99%)	1 (0%)	1 (0%)	24	63
6	FA	134/517 (26%)	129 (96%)	5 (4%)	0	100	100
7	HA	710/760 (93%)	682 (96%)	28 (4%)	0	100	100
8	NA	98/136 (72%)	94 (96%)	2 (2%)	2 (2%)	6	30
8	NE	101/136 (74%)	96 (95%)	3 (3%)	2 (2%)	6	30
9	PA	1457/1970 (74%)	1406 (96%)	47 (3%)	4 (0%)	36	72
10	DB	959/1199 (80%)	910 (95%)	49 (5%)	0	100	100
11	EB	169/291 (58%)	164 (97%)	5 (3%)	0	100	100
12	FB	218/249 (88%)	213 (98%)	4 (2%)	1 (0%)	24	63
13	HB	253/548 (46%)	245 (97%)	8 (3%)	0	100	100
14	NB	78/103 (76%)	78 (100%)	0	0	100	100
14	NF	84/103 (82%)	77 (92%)	4 (5%)	3 (4%)	2	19
15	PB	1130/1174 (96%)	1093 (97%)	37 (3%)	0	100	100
16	HC	380/462 (82%)	363 (96%)	17 (4%)	0	100	100
17	PC	253/275 (92%)	241 (95%)	12 (5%)	0	100	100
18	PE	207/210 (99%)	203 (98%)	4 (2%)	0	100	100
19	PF	77/127 (61%)	76 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	PH	146/150 (97%)	143 (98%)	3 (2%)	0	100	100
21	PI	112/125 (90%)	104 (93%)	8 (7%)	0	100	100
22	PJ	62/67 (92%)	61 (98%)	1 (2%)	0	100	100
23	PK	113/117 (97%)	112 (99%)	1 (1%)	0	100	100
24	PL	42/58 (72%)	40 (95%)	2 (5%)	0	100	100
25	DP	177/339 (52%)	175 (99%)	2 (1%)	0	100	100
26	DQ	109/376 (29%)	102 (94%)	7 (6%)	0	100	100
27	DO	97/109 (89%)	95 (98%)	2 (2%)	0	100	100
28	Dc	125/929 (14%)	116 (93%)	9 (7%)	0	100	100
29	DD	153/1085 (14%)	146 (95%)	5 (3%)	2 (1%)	9	40
29	Dd	154/1085 (14%)	150 (97%)	4 (3%)	0	100	100
30	DE	540/800 (68%)	505 (94%)	33 (6%)	2 (0%)	30	67
30	De	531/800 (66%)	484 (91%)	47 (9%)	0	100	100
31	DF	404/677 (60%)	376 (93%)	21 (5%)	7 (2%)	7	34
31	Df	399/677 (59%)	378 (95%)	20 (5%)	1 (0%)	36	72
32	DI	118/264 (45%)	113 (96%)	3 (2%)	2 (2%)	7	34
32	Di	119/264 (45%)	115 (97%)	4 (3%)	0	100	100
33	DJ	86/218 (39%)	82 (95%)	4 (5%)	0	100	100
33	Dj	91/218 (42%)	89 (98%)	2 (2%)	0	100	100
34	Dk	96/211 (46%)	91 (95%)	5 (5%)	0	100	100
35	DL	72/161 (45%)	62 (86%)	6 (8%)	4 (6%)	1	14
35	Dl	105/161 (65%)	101 (96%)	4 (4%)	0	100	100
36	Dm	85/124 (68%)	79 (93%)	6 (7%)	0	100	100
37	DG	139/349 (40%)	135 (97%)	4 (3%)	0	100	100
38	DH	207/310 (67%)	190 (92%)	13 (6%)	4 (2%)	6	31
39	HD	304/309 (98%)	267 (88%)	27 (9%)	10 (3%)	3	20
40	HE	259/308 (84%)	252 (97%)	7 (3%)	0	100	100
41	HG	341/395 (86%)	329 (96%)	12 (4%)	0	100	100
42	HH	601/782 (77%)	575 (96%)	26 (4%)	0	100	100
43	HF	64/71 (90%)	62 (97%)	2 (3%)	0	100	100
44	HI	297/346 (86%)	267 (90%)	18 (6%)	12 (4%)	2	17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	HJ	285/323 (88%)	268 (94%)	14 (5%)	3 (1%)	11	45
46	PD	126/142 (89%)	122 (97%)	4 (3%)	0	100	100
47	PG	169/172 (98%)	166 (98%)	3 (2%)	0	100	100
48	g	104/233 (45%)	99 (95%)	4 (4%)	1 (1%)	12	47
49	j	120/135 (89%)	117 (98%)	1 (1%)	2 (2%)	7	34
50	n	993/1454 (68%)	894 (90%)	80 (8%)	19 (2%)	6	31
51	s	91/244 (37%)	82 (90%)	7 (8%)	2 (2%)	5	28
52	u	113/144 (78%)	105 (93%)	5 (4%)	3 (3%)	4	24
53	a	430/1581 (27%)	386 (90%)	39 (9%)	5 (1%)	10	42
54	d	154/270 (57%)	143 (93%)	9 (6%)	2 (1%)	9	40
55	f	163/246 (66%)	149 (91%)	12 (7%)	2 (1%)	10	42
56	i	69/146 (47%)	65 (94%)	2 (3%)	2 (3%)	3	23
57	m	110/131 (84%)	106 (96%)	4 (4%)	0	100	100
58	q	543/651 (83%)	484 (89%)	52 (10%)	7 (1%)	9	40
59	z	93/600 (16%)	84 (90%)	6 (6%)	3 (3%)	3	21
60	b	111/200 (56%)	109 (98%)	1 (1%)	1 (1%)	14	50
61	c	255/311 (82%)	241 (94%)	14 (6%)	0	100	100
62	e	98/178 (55%)	92 (94%)	4 (4%)	2 (2%)	6	30
63	l	120/178 (67%)	115 (96%)	5 (4%)	0	100	100
64	o	152/788 (19%)	136 (90%)	12 (8%)	4 (3%)	4	25
65	h	188/268 (70%)	165 (88%)	15 (8%)	8 (4%)	2	17
66	k	110/117 (94%)	96 (87%)	12 (11%)	2 (2%)	6	32
67	r	190/208 (91%)	180 (95%)	6 (3%)	4 (2%)	5	29
68	t	189/212 (89%)	169 (89%)	16 (8%)	4 (2%)	5	29
69	v	132/200 (66%)	116 (88%)	10 (8%)	6 (4%)	2	16
70	p	756/841 (90%)	704 (93%)	50 (7%)	2 (0%)	36	72
71	w	1332/1368 (97%)	1262 (95%)	66 (5%)	4 (0%)	36	72
72	x	877/989 (89%)	828 (94%)	44 (5%)	5 (1%)	21	58
73	y	206/747 (28%)	196 (95%)	9 (4%)	1 (0%)	24	63
74	NC	101/128 (79%)	93 (92%)	5 (5%)	3 (3%)	3	22
74	NG	105/128 (82%)	94 (90%)	8 (8%)	3 (3%)	3	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
75	ND	93/126 (74%)	91 (98%)	1 (1%)	1 (1%)	11	45
75	NH	93/126 (74%)	89 (96%)	3 (3%)	1 (1%)	11	45
All	All	22102/36357 (61%)	20865 (94%)	1075 (5%)	162 (1%)	20	55

5 of 162 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	DA	498	PRO
4	DA	1158	SER
8	NA	534	ARG
9	PA	1666	PRO
12	FB	229	HIS

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	
3	BA	215/268 (80%)	215 (100%)	0	100	100
4	DA	495/1665 (30%)	461 (93%)	34 (7%)	14	36
5	EA	169/373 (45%)	167 (99%)	2 (1%)	63	74
6	FA	121/448 (27%)	121 (100%)	0	100	100
7	HA	624/664 (94%)	624 (100%)	0	100	100
9	PA	1302/1749 (74%)	1296 (100%)	6 (0%)	81	82
10	DB	876/1083 (81%)	861 (98%)	15 (2%)	53	68
11	EB	154/261 (59%)	154 (100%)	0	100	100
12	FB	196/218 (90%)	196 (100%)	0	100	100
13	HB	241/484 (50%)	241 (100%)	0	100	100
15	PB	994/1027 (97%)	994 (100%)	0	100	100
16	HC	342/399 (86%)	342 (100%)	0	100	100
17	PC	234/252 (93%)	234 (100%)	0	100	100
18	PE	191/192 (100%)	191 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	PF	69/111 (62%)	68 (99%)	1 (1%)	59	72
20	PH	129/131 (98%)	129 (100%)	0	100	100
21	PI	103/112 (92%)	103 (100%)	0	100	100
22	PJ	53/56 (95%)	53 (100%)	0	100	100
23	PK	104/106 (98%)	104 (100%)	0	100	100
24	PL	41/55 (74%)	41 (100%)	0	100	100
25	DP	154/293 (53%)	154 (100%)	0	100	100
26	DQ	105/324 (32%)	105 (100%)	0	100	100
27	DO	90/98 (92%)	90 (100%)	0	100	100
28	Dc	113/833 (14%)	111 (98%)	2 (2%)	51	67
29	DD	144/815 (18%)	132 (92%)	12 (8%)	10	30
29	Dd	146/815 (18%)	146 (100%)	0	100	100
30	DE	478/657 (73%)	465 (97%)	13 (3%)	39	60
30	De	475/657 (72%)	473 (100%)	2 (0%)	84	83
31	DF	324/574 (56%)	295 (91%)	29 (9%)	9	28
31	Df	322/574 (56%)	312 (97%)	10 (3%)	35	56
32	DI	106/235 (45%)	97 (92%)	9 (8%)	10	29
32	Di	107/235 (46%)	107 (100%)	0	100	100
33	DJ	79/154 (51%)	77 (98%)	2 (2%)	42	62
33	Dj	83/154 (54%)	83 (100%)	0	100	100
34	Dk	87/182 (48%)	87 (100%)	0	100	100
35	DL	69/141 (49%)	58 (84%)	11 (16%)	2	12
35	DI	98/141 (70%)	98 (100%)	0	100	100
36	Dm	80/106 (76%)	79 (99%)	1 (1%)	61	72
37	DG	133/322 (41%)	125 (94%)	8 (6%)	17	39
38	DH	181/270 (67%)	170 (94%)	11 (6%)	17	39
39	HD	251/283 (89%)	233 (93%)	18 (7%)	13	35
40	HE	234/272 (86%)	229 (98%)	5 (2%)	47	65
41	HG	311/352 (88%)	311 (100%)	0	100	100
42	HH	536/688 (78%)	535 (100%)	1 (0%)	87	86
43	HF	59/64 (92%)	59 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	HI	258/298 (87%)	181 (70%)	77 (30%)	0	2
45	HJ	252/296 (85%)	173 (69%)	79 (31%)	0	2
46	PD	118/126 (94%)	117 (99%)	1 (1%)	73	78
47	PG	152/153 (99%)	151 (99%)	1 (1%)	76	80
48	g	102/216 (47%)	93 (91%)	9 (9%)	9	29
49	j	66/124 (53%)	65 (98%)	1 (2%)	57	71
50	n	807/1271 (64%)	785 (97%)	22 (3%)	39	60
51	s	83/208 (40%)	74 (89%)	9 (11%)	6	21
52	u	95/119 (80%)	91 (96%)	4 (4%)	26	48
53	a	393/1391 (28%)	316 (80%)	77 (20%)	1	8
54	d	139/230 (60%)	93 (67%)	46 (33%)	0	2
55	f	149/223 (67%)	131 (88%)	18 (12%)	5	18
56	i	71/133 (53%)	61 (86%)	10 (14%)	3	14
57	m	102/115 (89%)	101 (99%)	1 (1%)	68	76
58	q	491/577 (85%)	407 (83%)	84 (17%)	2	11
59	z	89/512 (17%)	74 (83%)	15 (17%)	2	11
60	b	102/163 (63%)	91 (89%)	11 (11%)	6	21
61	c	238/280 (85%)	227 (95%)	11 (5%)	24	46
62	e	94/152 (62%)	94 (100%)	0	100	100
63	l	116/155 (75%)	116 (100%)	0	100	100
64	o	141/697 (20%)	136 (96%)	5 (4%)	32	53
65	h	161/225 (72%)	123 (76%)	38 (24%)	1	5
66	k	94/98 (96%)	43 (46%)	51 (54%)	0	0
67	r	169/183 (92%)	140 (83%)	29 (17%)	2	11
68	t	166/178 (93%)	124 (75%)	42 (25%)	0	4
69	v	122/173 (70%)	76 (62%)	46 (38%)	0	1
70	p	681/736 (92%)	671 (98%)	10 (2%)	57	71
71	w	1203/1232 (98%)	1198 (100%)	5 (0%)	84	83
72	x	789/864 (91%)	779 (99%)	10 (1%)	61	72
73	y	175/601 (29%)	171 (98%)	4 (2%)	44	63
All	All	19036/30622 (62%)	18128 (95%)	908 (5%)	24	45

5 of 908 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
53	a	433	ASP
70	p	564	LEU
58	q	120	ARG
69	v	133	GLU
68	t	34	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 368 such sidechains are listed below:

Mol	Chain	Res	Type
56	i	117	GLN
65	h	60	ASN
58	q	262	GLN
59	z	483	ASN
68	t	180	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 21 ligands modelled in this entry, 20 are monoatomic - leaving 1 for Mogul analysis.

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
79	SF4	HA	1000	7	0,12,12	-	-	-		

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
79	SF4	HA	1000	7	-	-	0/6/5/5

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.

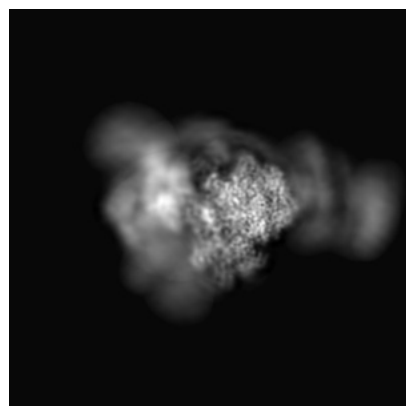
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34359. These allow visual inspection of the internal detail of the map and identification of artifacts.

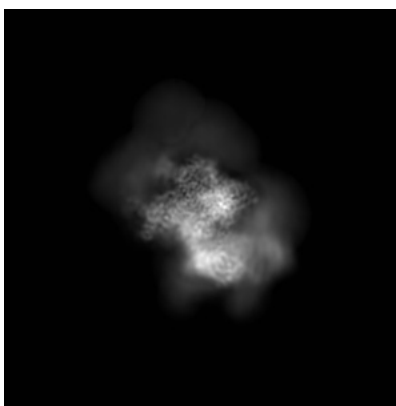
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

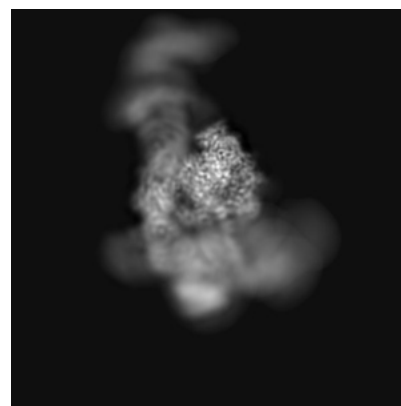
6.1.1 Primary map



X

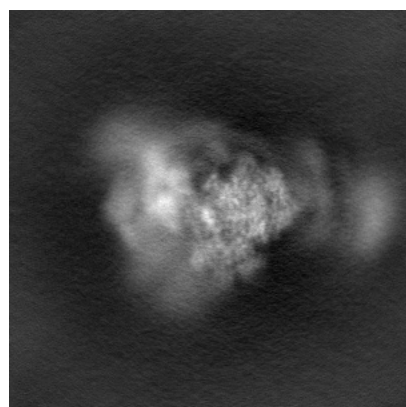


Y

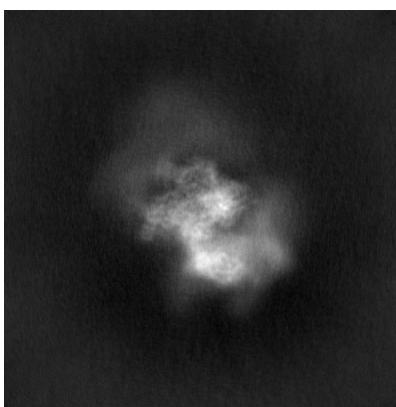


Z

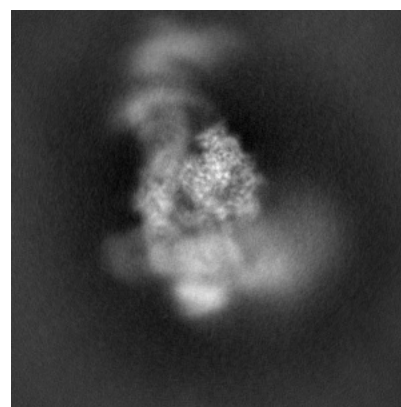
6.1.2 Raw map



X



Y

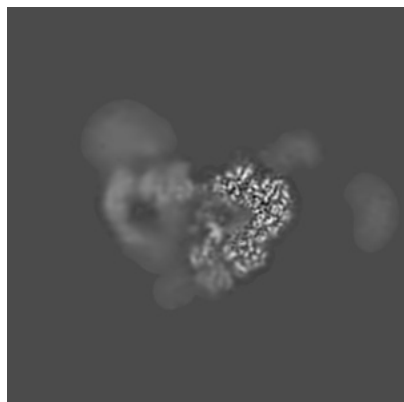


Z

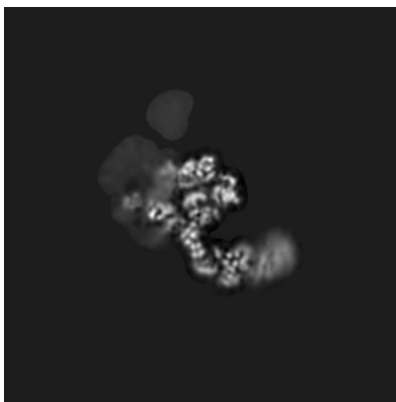
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

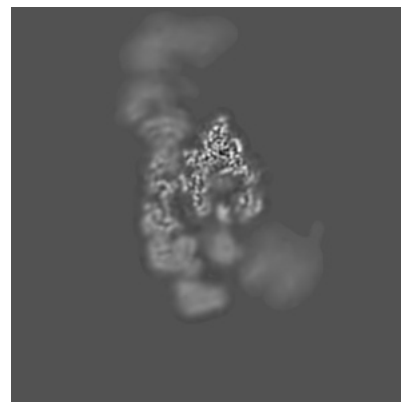
6.2.1 Primary map



X Index: 210

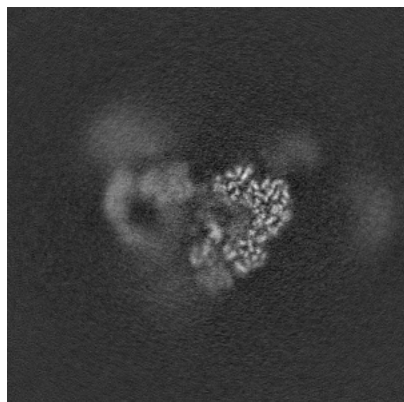


Y Index: 210

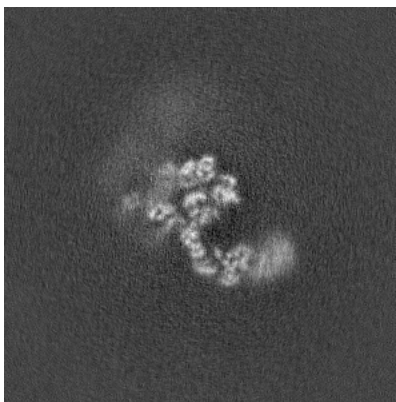


Z Index: 210

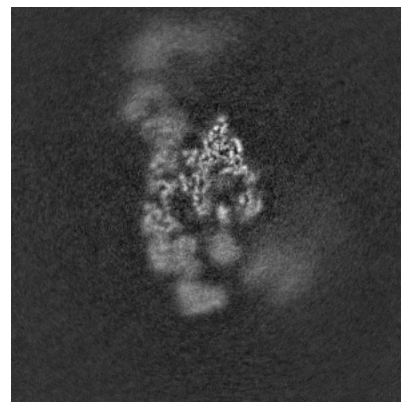
6.2.2 Raw map



X Index: 210



Y Index: 210

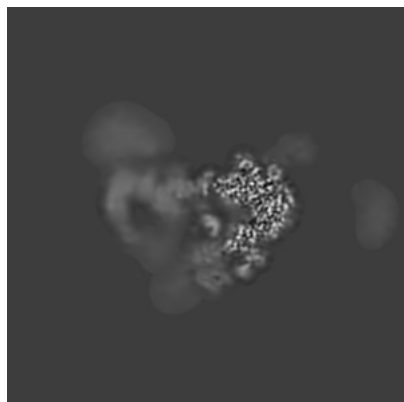


Z Index: 210

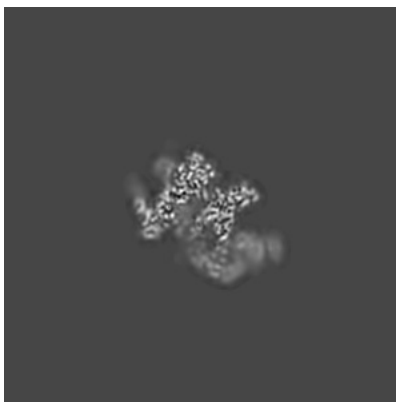
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

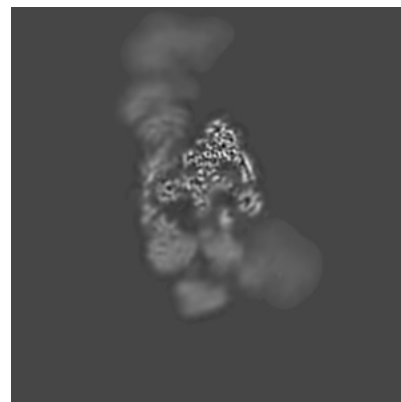
6.3.1 Primary map



X Index: 215

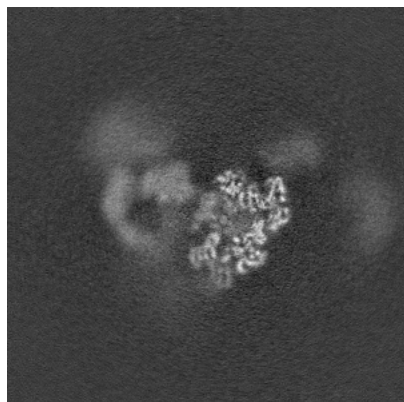


Y Index: 246

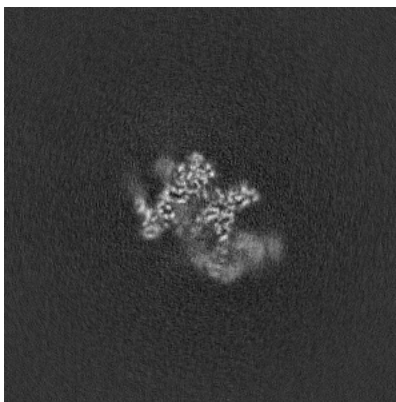


Z Index: 216

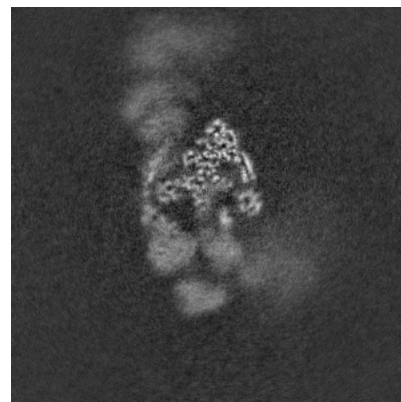
6.3.2 Raw map



X Index: 206



Y Index: 246

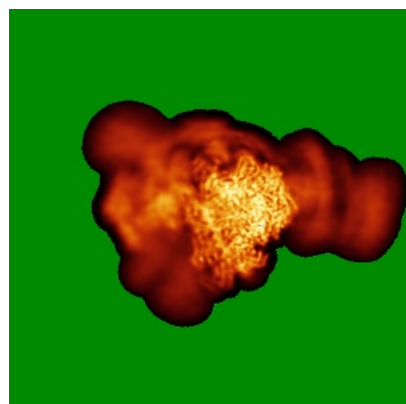


Z Index: 216

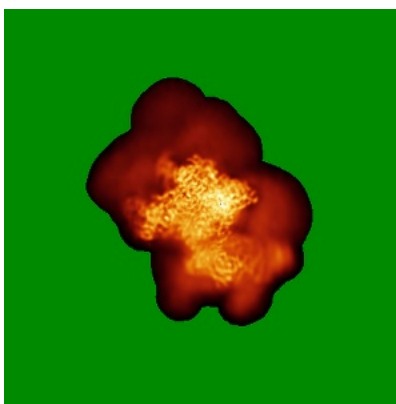
The images above show the largest variance slices of the map in three orthogonal directions.

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

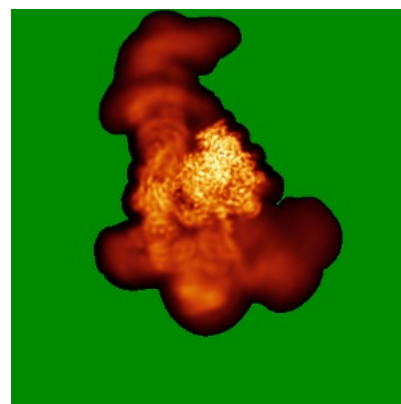
6.4.1 Primary map



X

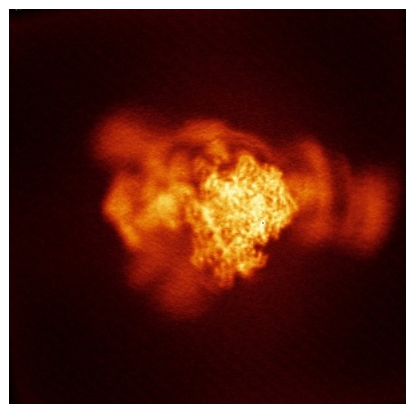


Y

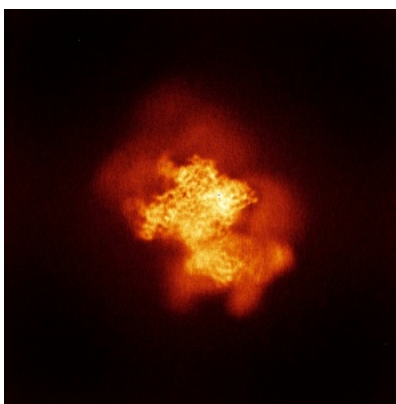


Z

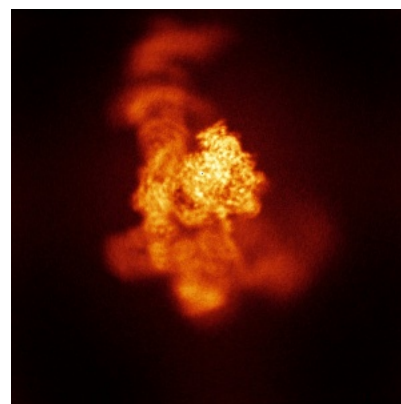
6.4.2 Raw map



X



Y

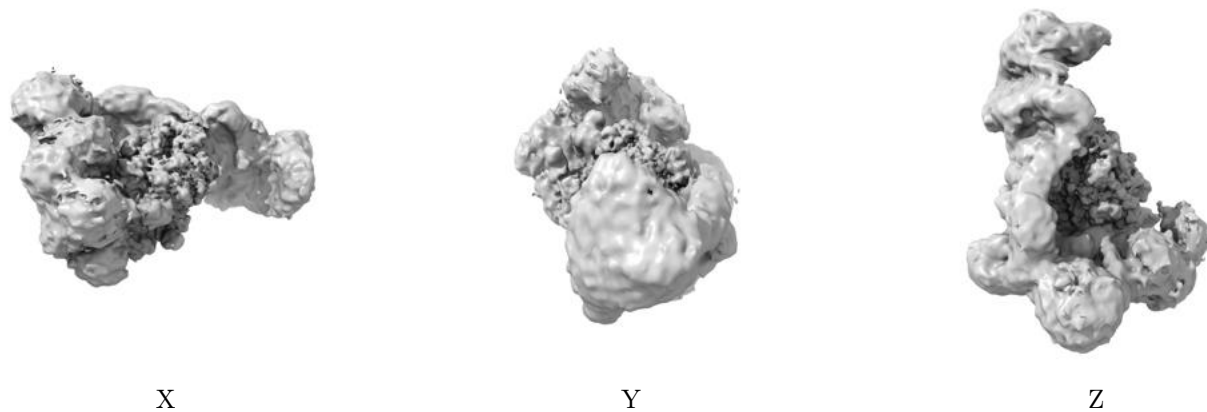


Z

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.

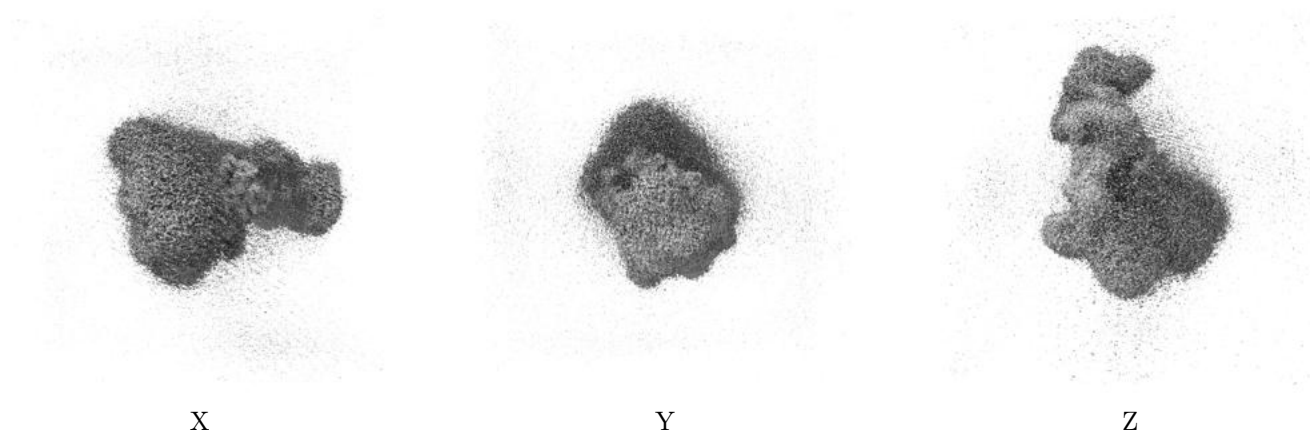
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.156. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

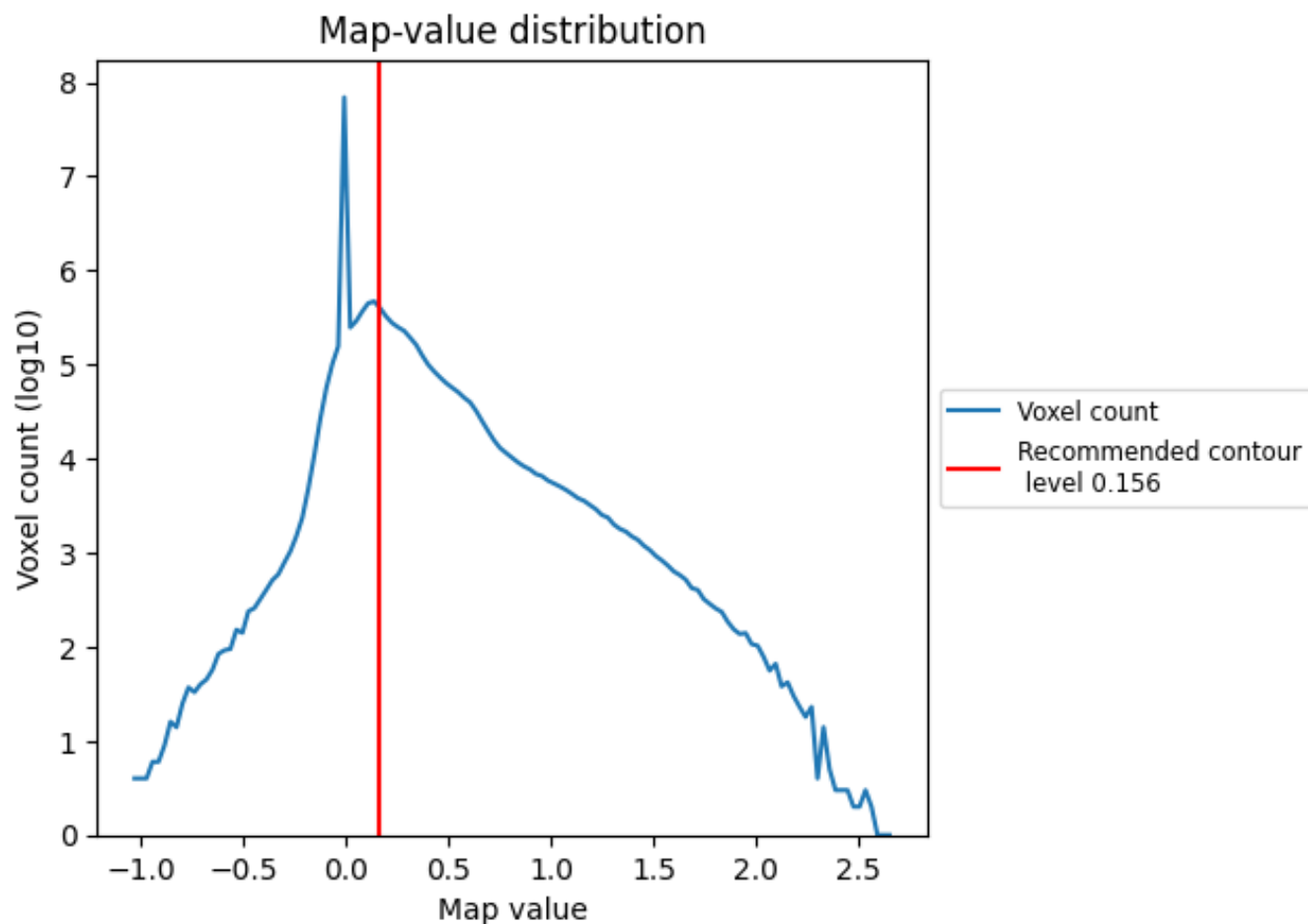
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

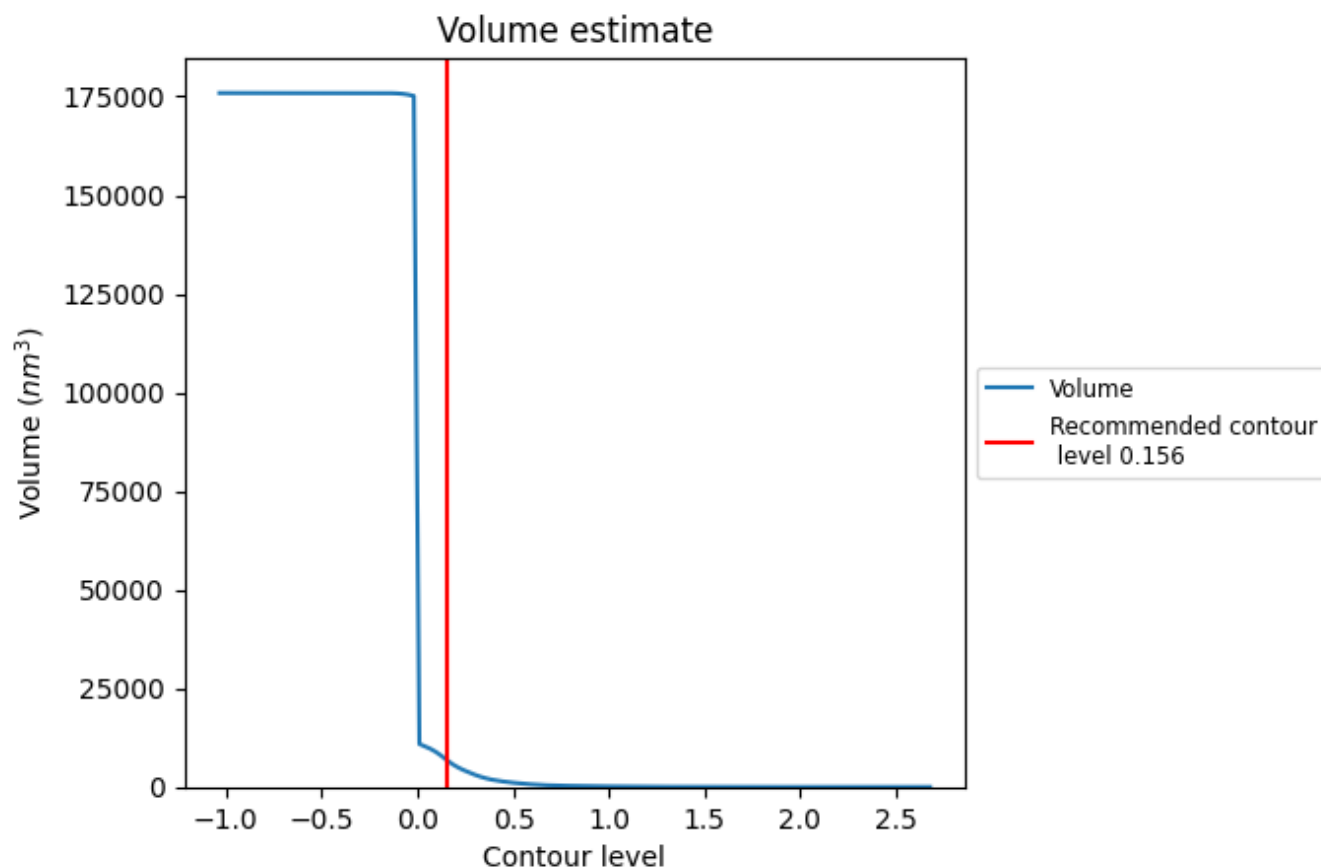
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

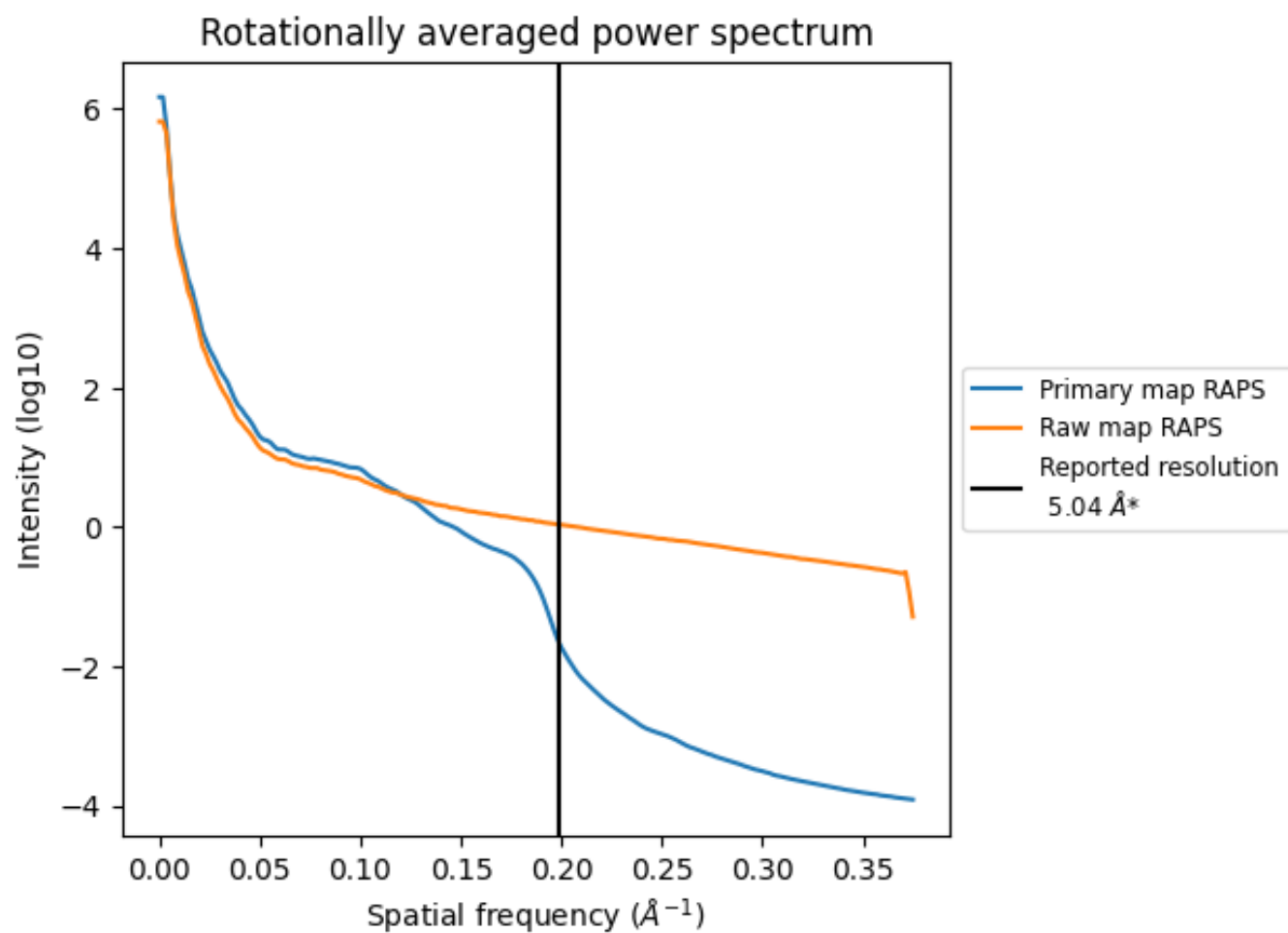
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6707 nm^3 ; this corresponds to an approximate mass of 6058 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 ⓘ

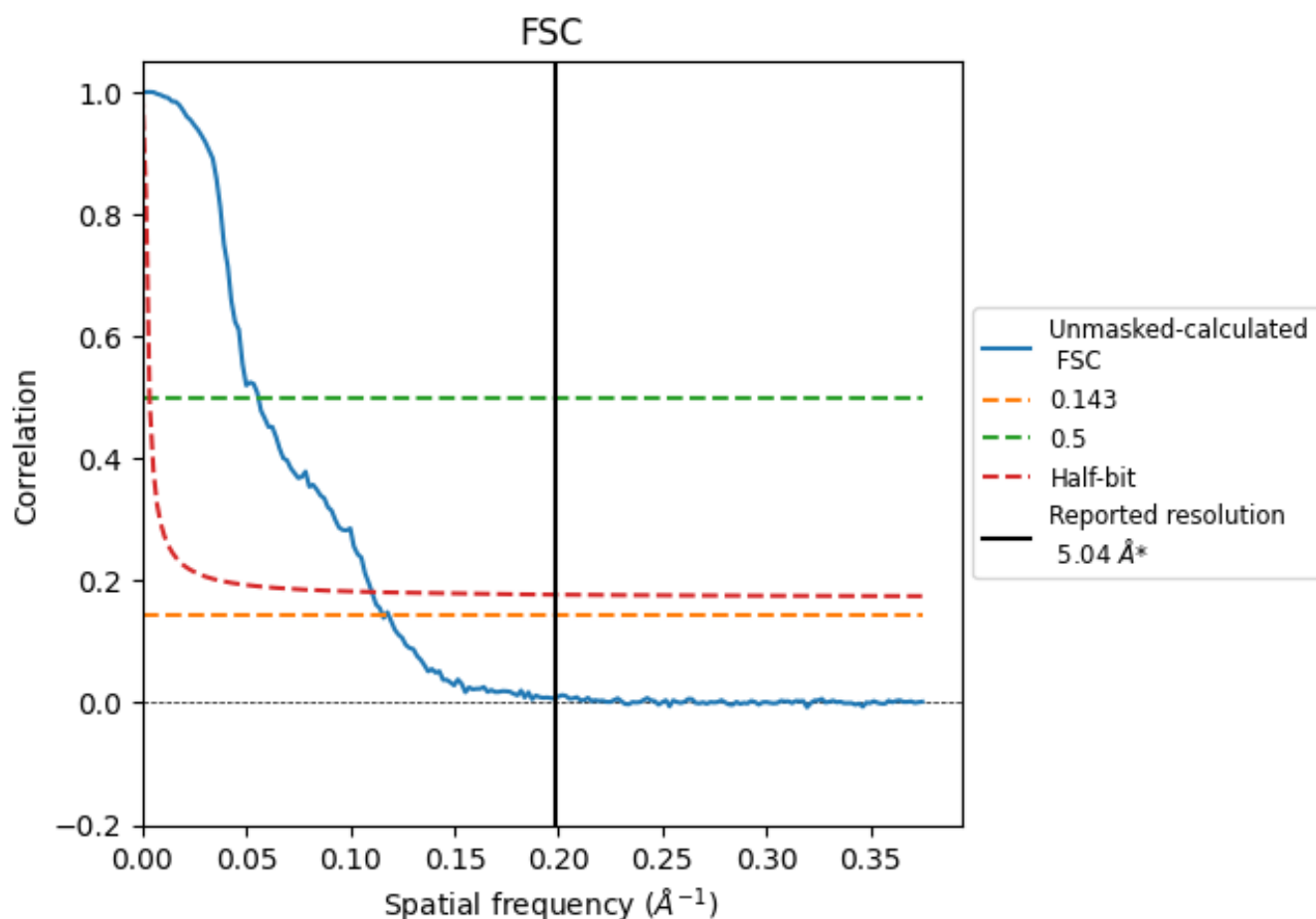


*Reported resolution corresponds to spatial frequency of 0.198 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.198 Å⁻¹

8.2 Resolution estimates [i](#)

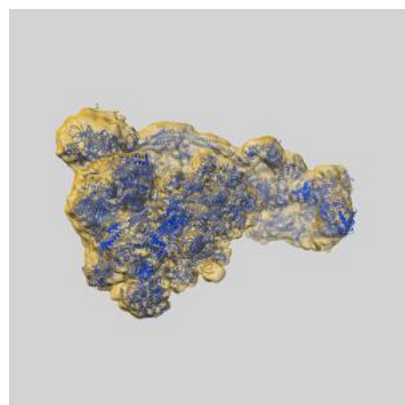
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.04	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	8.66	17.92	9.07

*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 8.66 differs from the reported value 5.04 by more than 10 %

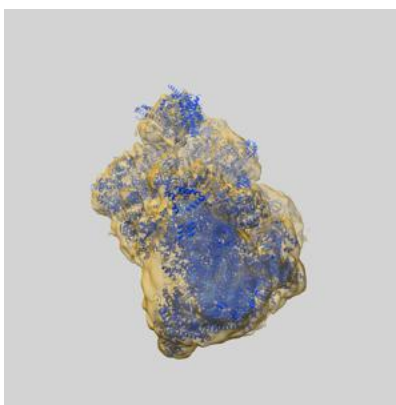
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-34359 and PDB model 8GXQ. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

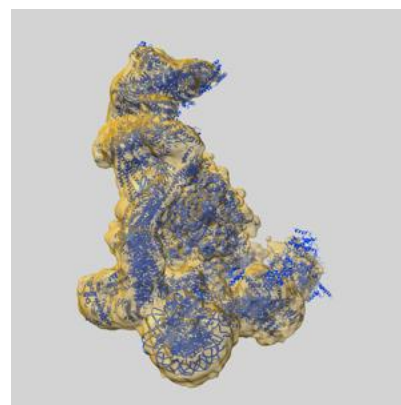
9.1 Map-model overlay [i](#)



X



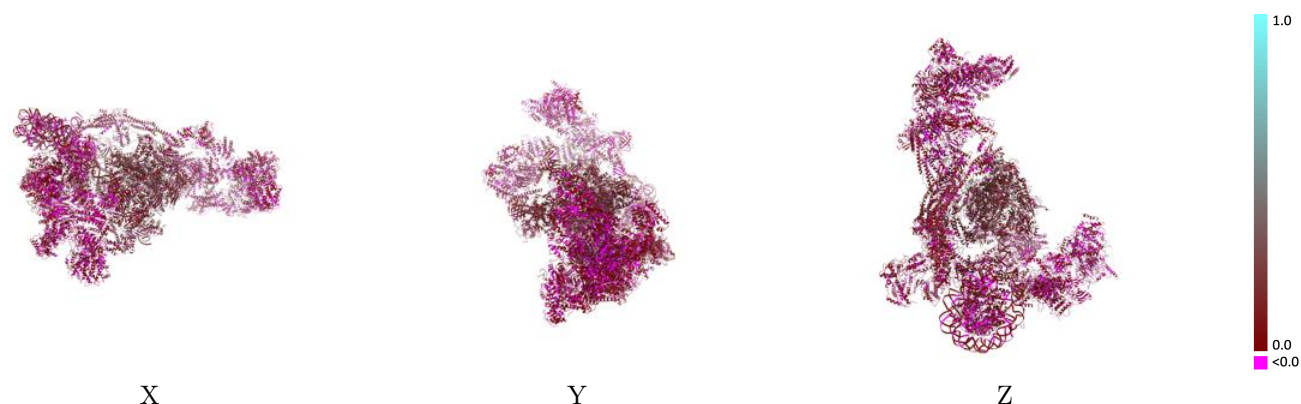
Y



Z

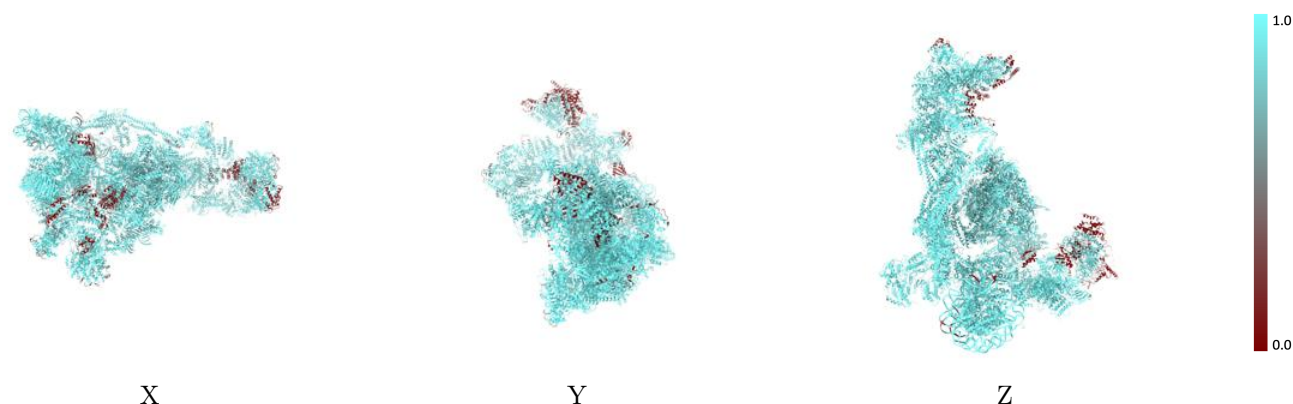
The images above show the 3D surface view of the map at the recommended contour level 0.156 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



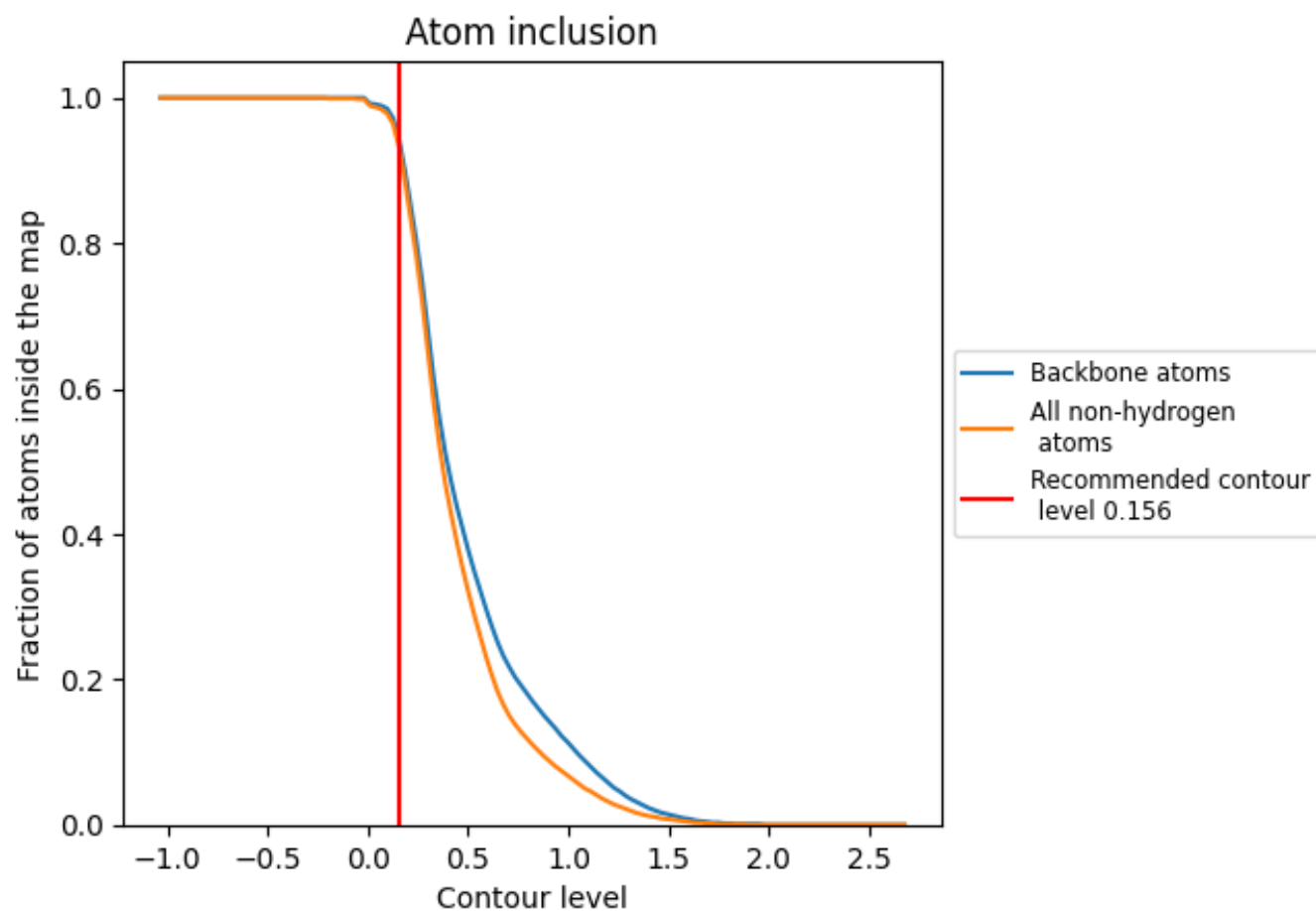
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.156).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 93% 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 (0.156) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9320	 0.0840
BA	 0.9710	 0.1780
DA	 0.8720	 0.0300
DB	 0.9940	 0.0440
DD	 0.9020	 0.0440
DE	 0.9790	 0.0430
DF	 0.9610	 0.0410
DG	 0.5770	 0.0150
DH	 0.9980	 0.0490
DI	 0.9200	 0.0360
DJ	 0.9960	 0.0450
DL	 0.8450	 0.0330
DO	 0.9730	 0.1060
DP	 0.9830	 0.1390
DQ	 0.9680	 0.1190
Dc	 0.6200	 0.0290
Dd	 0.3480	 0.0030
De	 0.6780	 0.0240
Df	 0.8640	 0.0370
Di	 0.8370	 0.0200
Dj	 0.6600	 0.0400
Dk	 0.2270	 0.0000
Dl	 0.6640	 0.0310
Dm	 0.2120	 0.0050
EA	 0.9500	 0.1120
EB	 0.9900	 0.1230
FA	 0.9870	 0.1360
FB	 0.9860	 0.1460
HA	 0.9980	 0.1150
HB	 0.9980	 0.0670
HC	 0.9970	 0.0860
HD	 0.9870	 0.1130
HE	 0.9980	 0.0490
HF	 1.0000	 0.0790
HG	 0.9990	 0.0690



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Chain	Atom inclusion	Q-score
HH	 0.9940	 0.0730
HI	 0.9980	 0.0630
HJ	 0.9830	 0.0630
NA	 0.9800	 0.0770
NB	 1.0000	 0.0420
NC	 0.9840	 0.0110
ND	 0.9700	 0.0500
NE	 0.9940	 0.0710
NF	 1.0000	 0.0330
NG	 1.0000	 0.0430
NH	 1.0000	 0.0020
NX	 0.9070	 0.0340
NY	 0.9400	 0.0460
PA	 0.9560	 0.1830
PB	 0.9530	 0.2030
PC	 0.9630	 0.2080
PD	 0.9630	 0.1720
PE	 0.9790	 0.1790
PF	 0.9290	 0.2020
PG	 0.9720	 0.1580
PH	 0.9600	 0.1920
PI	 0.9780	 0.1840
PJ	 0.9540	 0.1870
PK	 0.9450	 0.2030
PL	 0.9800	 0.2110
X	 1.0000	 0.1830
Y	 0.9990	 0.1940
a	 0.9250	 0.0510
b	 0.9970	 0.0400
c	 0.9890	 0.0500
d	 0.9730	 0.0590
e	 0.9990	 0.0910
f	 0.9990	 0.1300
g	 1.0000	 0.1080
h	 0.9880	 0.1470
i	 0.8660	 0.0960
j	 1.0000	 0.0750
k	 0.9880	 0.1390
l	 1.0000	 0.0690
m	 1.0000	 0.0690
n	 0.9880	 0.0610
o	 0.9970	 0.0280

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Chain	Atom inclusion	Q-score
p	 0.9960	 0.0430
q	 0.9970	 0.0780
r	 0.9950	 0.1020
s	 1.0000	 0.0400
t	 0.9870	 0.0680
u	 1.0000	 0.0900
v	 0.9840	 0.1110
w	 0.7510	 0.0240
x	 0.9500	 0.0400
y	 0.9750	 0.0310
z	 0.9480	 0.0340