



wwPDB EM Validation Summary Report ⓘ

Nov 22, 2022 – 04:00 PM JST

PDB ID : 7ENC
EMDB ID : EMD-31207
Title : TFIID-based PIC-Mediator holo-complex in fully-assembled state (hPIC-MED)
Authors : Chen, X.; Qi, Y.; Wang, X.; Wu, Z.; Yin, X.; Li, J.; Liu, W.; Xu, Y.
Deposited on : 2021-04-16
Resolution : 4.13 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:

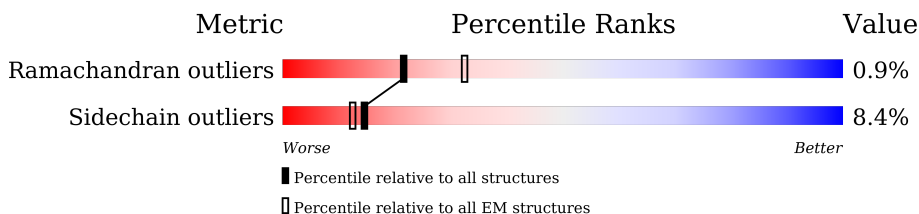
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

1 Overall quality at a glance

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

The reported resolution of this entry is 4.13 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.






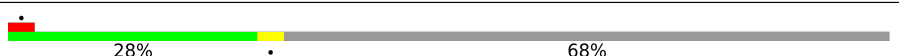
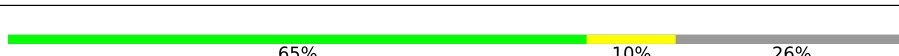

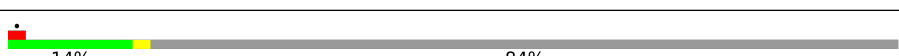
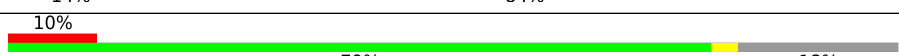
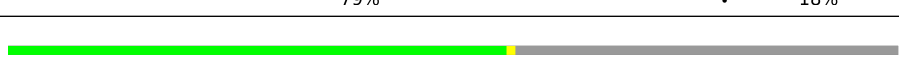

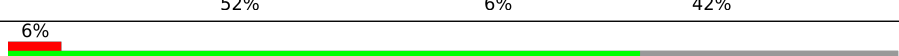
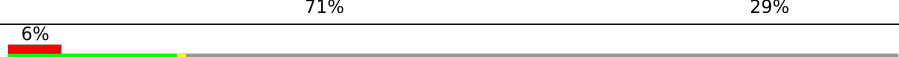

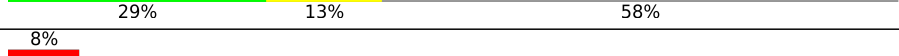
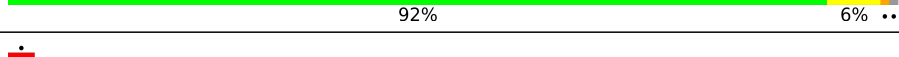




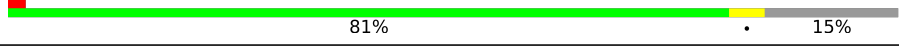
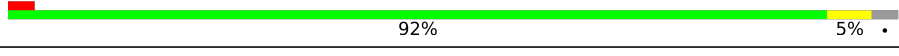
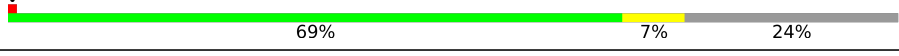

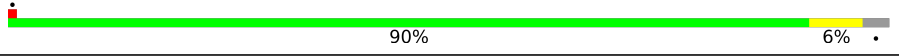

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	1581	
2	m	131	
3	d	270	
4	f	246	
5	g	233	
6	h	268	
7	r	208	
8	t	212	
9	j	135	

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Mol	Chain	Length	Quality of chain
10	k	117	
11	n	1454	
12	q	651	
13	s	244	
14	u	144	
15	v	200	
16	z	600	
17	c	311	
18	e	178	
19	b	200	
20	l	178	
21	o	788	
22	i	146	
23	0	309	
24	8	346	
25	9	323	
26	1	548	
27	2	395	
28	3	308	
29	4	462	
30	5	71	
31	6	782	
32	7	760	
33	EA	439	
34	EB	291	

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Mol	Chain	Length	Quality of chain
35	DA	1872	
36	DB	1199	
37	DD	1085	
37	Dd	1085	
38	DE	800	
38	De	800	
39	DF	677	
39	Df	677	
40	DG	349	
41	DH	310	
42	DI	264	
42	Di	264	
43	DJ	218	
43	Dj	218	
44	DL	161	
44	Dl	161	
45	Dc	929	
46	Dk	211	
47	Dm	124	
48	DO	109	
49	DP	339	
50	DQ	307	
51	BA	316	
52	FB	249	
53	X	69	

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Mol	Chain	Length	Quality of chain
54	Y	69	78% 22%
55	PA	1970	68% 7% 25%
56	PB	1174	88% 8%
57	PC	275	88% 6% 7%
58	PD	142	80% 11% 9%
59	PE	210	92% 7%
60	PF	127	56% 6% 38%
61	PG	172	86% 13%
62	PH	150	92% 7%
63	PI	125	86% 6% 9%
64	PJ	67	94%
65	PK	117	96%
66	PL	58	72% 24%
67	FA	517	26% 74%
68	w	1368	96%
69	x	989	87% 9%
70	p	841	48% 52%

2 Entry composition [i](#)

There are 73 unique types of molecules in this entry. The entry contains 171177 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	a	469	3570	2271	614	661	24	0	0

- Molecule 2 is a protein called Mediator of RNA polymerase II transcription subunit 31.

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

- Molecule 3 is a protein called Mediator of RNA polymerase II transcription subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	d	158	1264	788	227	243	6	0	0

- Molecule 4 is a protein called Mediator of RNA polymerase II transcription subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	f	167	1329	851	231	242	5	0	0

- Molecule 5 is a protein called Mediator of RNA polymerase II transcription subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	g	166	1382	880	244	248	10	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
g	10	ALA	LEU	conflict	UNP O43513
g	11	LEU	PRO	conflict	UNP O43513

- Molecule 6 is a protein called Isoform 2 of Mediator of RNA polymerase II transcription subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	h	190	1486	925	262	295	4	0	0

- Molecule 7 is a protein called Mediator of RNA polymerase II transcription subunit 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	r	191	1528	969	270	274	15	0	0

- Molecule 8 is a protein called Mediator of RNA polymerase II transcription subunit 20.

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

- Molecule 9 is a protein called Mediator of RNA polymerase II transcription subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	j	122	1001	636	174	187	4	0	0

- Molecule 10 is a protein called Mediator of RNA polymerase II transcription subunit 11.

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

- Molecule 11 is a protein called Mediator of RNA polymerase II transcription subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	n	994	7241	4576	1293	1334	38	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	133	LEU	ALA	conflict	UNP O60244

- Molecule 12 is a protein called Mediator of RNA polymerase II transcription subunit 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	q	552	4261	2691	764	789	17	0	0

- Molecule 13 is a protein called Mediator of RNA polymerase II transcription subunit 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	s	77	485	300	87	96	2	0	0

- Molecule 14 is a protein called Mediator of RNA polymerase II transcription subunit 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	u	107	792	492	132	165	3	0	0

- Molecule 15 is a protein called Mediator of RNA polymerase II transcription subunit 22.

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

- Molecule 16 is a protein called Mediator of RNA polymerase II transcription subunit 26.

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

- Molecule 17 is a protein called Mediator of RNA polymerase II transcription subunit 27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	c	255	2069	1314	370	374	11	0	0

- Molecule 18 is a protein called Mediator of RNA polymerase II transcription subunit 28.

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

- Molecule 19 is a protein called Mediator of RNA polymerase II transcription subunit 29.

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

- Molecule 20 is a protein called Mediator of RNA polymerase II transcription subunit 30.

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

- Molecule 21 is a protein called Mediator of RNA polymerase II transcription subunit 15.

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

- Molecule 22 is a protein called Mediator of RNA polymerase II transcription subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	i	62	520	329	92	94	5	0	0

- Molecule 23 is a protein called CDK-activating kinase assembly factor MAT1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	0	306	2255	1404	399	441	11	0	0

- Molecule 24 is a protein called Cyclin-dependent kinase 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	8	299	2378	1535	406	426	11	0	0

- Molecule 25 is a protein called Cyclin-H.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	9	287	2307	1477	398	417	15	0	0

- Molecule 26 is a protein called General transcription factor IIIH subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	1	405	2634	1640	486	501	7	0	0

- Molecule 27 is a protein called General transcription factor IIIH subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	2	331	2534	1597	441	470	26	0	0

- Molecule 28 is a protein called General transcription factor IIIH subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	3	263	2065	1323	344	379	19	0	0

- Molecule 29 is a protein called General transcription factor IIIH subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	4	449	3579	2303	624	638	14	0	0

- Molecule 30 is a protein called General transcription factor IIIH subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	5	54	428	277	67	82	2	0	0

- Molecule 31 is a protein called General transcription and DNA repair factor IIIH helicase subunit XPB.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	6	606	4880	3117	849	884	30	0	0

- Molecule 32 is a protein called General transcription and DNA repair factor IIIH helicase subunit XPD.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	7	734	5833	3727	1022	1055	29	0	0

- Molecule 33 is a protein called General transcription factor IIE subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	EA	179	1476	932	261	272	11	0	0

- Molecule 34 is a protein called Transcription initiation factor IIE subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	EB	172	1404	893	243	264	4	0	0

- Molecule 35 is a protein called Transcription initiation factor TFIID subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	DA	550	4511	2882	782	820	27	0	0

- Molecule 36 is a protein called Transcription initiation factor TFIID subunit 2.

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

- Molecule 37 is a protein called Transcription initiation factor TFIID subunit 4.

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

- Molecule 38 is a protein called Transcription initiation factor TFIID subunit 5.

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

- Molecule 39 is a protein called Transcription initiation factor TFIID subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	DF	408	3109	1970	542	579	18	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	Df	403	3081	1954	533	576	18	0	0

- Molecule 40 is a protein called Transcription initiation factor TFIID subunit 7.

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

- Molecule 41 is a protein called Transcription initiation factor TFIID subunit 8.

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

- Molecule 42 is a protein called Transcription initiation factor TFIID subunit 9.

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

- Molecule 43 is a protein called Transcription initiation factor TFIID subunit 10.

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

- Molecule 44 is a protein called Transcription initiation factor TFIID subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	DL	75	614	384	107	120	3	0	0
44	DI	107	876	547	158	166	5	0	0

- Molecule 45 is a protein called Transcription initiation factor TFIID subunit 3.

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

- Molecule 46 is a protein called Transcription initiation factor TFIID subunit 11.

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

- Molecule 47 is a protein called Transcription initiation factor TFIID subunit 13.

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

- Molecule 48 is a protein called Transcription initiation factor IIA subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	DO	97	771	491	133	145	2	0	0

- Molecule 49 is a protein called TATA-box-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	DP	177	1412	918	249	238	7	0	0

- Molecule 50 is a protein called TFIIA-a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	DQ	122	996	623	162	207	4	0	0

- Molecule 51 is a protein called Transcription initiation factor IIB.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	BA	251	1939	1214	344	364	17	0	0

- Molecule 52 is a protein called General transcription factor IIF subunit 2.

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

- Molecule 53 is a DNA chain called DNA (69-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
53	X	69	1429	672	279	409	69	0	0

- Molecule 54 is a DNA chain called DNA (69-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
54	Y	69	1400	664	248	419	69	0	0

- Molecule 55 is a protein called RPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	PA	1474	11655	7333	2070	2180	72	0	0

- Molecule 56 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	PB	1134	9062	5732	1595	1671	64	0	0

- Molecule 57 is a protein called DNA-directed RNA polymerase II subunit RPB3.

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

- Molecule 58 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	PD	129	1021	643	174	200	4	0	0

- Molecule 59 is a protein called DNA-directed RNA polymerase II subunit E.

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

- Molecule 60 is a protein called DNA-directed RNA polymerase II subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	PF	79	635	406	108	116	5	0	0

- Molecule 61 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	PG	171	1334	867	216	243	8	0	0

- Molecule 62 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

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

- Molecule 63 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	PI	114	927	571	166	179	11	0	0

- Molecule 64 is a protein called RPB10.

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

- Molecule 65 is a protein called RNA_pol_L_2 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	PK	117	937	604	154	177	2	0	0

- Molecule 66 is a protein called RPB12.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	PL	44	Total	C	N	O	S	0	0
			372	231	72	63	6		

- Molecule 67 is a protein called General transcription factor IIF subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	FA	134	Total	C	N	O	S	0	0
			1101	698	199	202	2		

- Molecule 68 is a protein called Mediator of RNA polymerase II transcription subunit 23.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	w	1334	Total	C	N	O	S	0	0
			10772	6965	1827	1909	71		

- Molecule 69 is a protein called Mediator of RNA polymerase II transcription subunit 24.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	x	896	Total	C	N	O	S	0	0
			7050	4516	1188	1292	54		

- 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	406	Total	C	N	O	S	0	0
			3124	1982	536	585	21		

- Molecule 71 is ZINC ION (three-letter code: ZN) (formula: Zn).

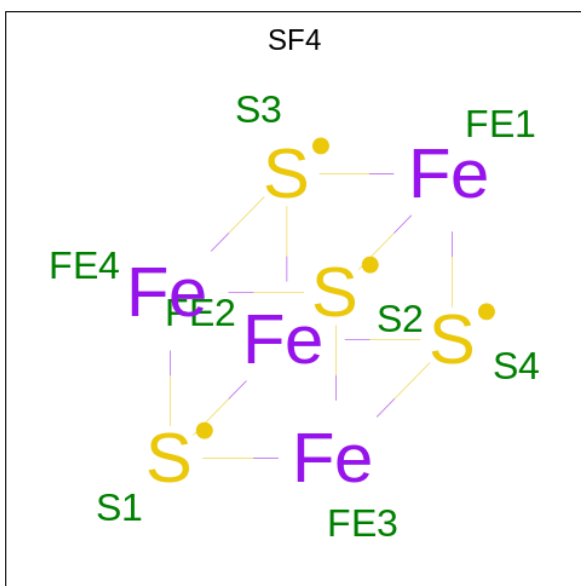
Mol	Chain	Residues	Atoms		AltConf
71	0	2	Total	Zn	0
			2	2	
71	2	3	Total	Zn	0
			3	3	
71	3	1	Total	Zn	0
			1	1	
71	EA	1	Total	Zn	0
			1	1	
71	BA	1	Total	Zn	0
			1	1	
71	PA	2	Total	Zn	0
			2	2	

Continued on next page...

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Mol	Chain	Residues	Atoms		AltConf
71	PB	1	Total	Zn	0
			1	1	
71	PC	1	Total	Zn	0
			1	1	
71	PI	2	Total	Zn	0
			2	2	
71	PJ	1	Total	Zn	0
			1	1	
71	PL	1	Total	Zn	0
			1	1	

- Molecule 72 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			AltConf
72	7	1	Total	Fe	S	0
			8	4	4	

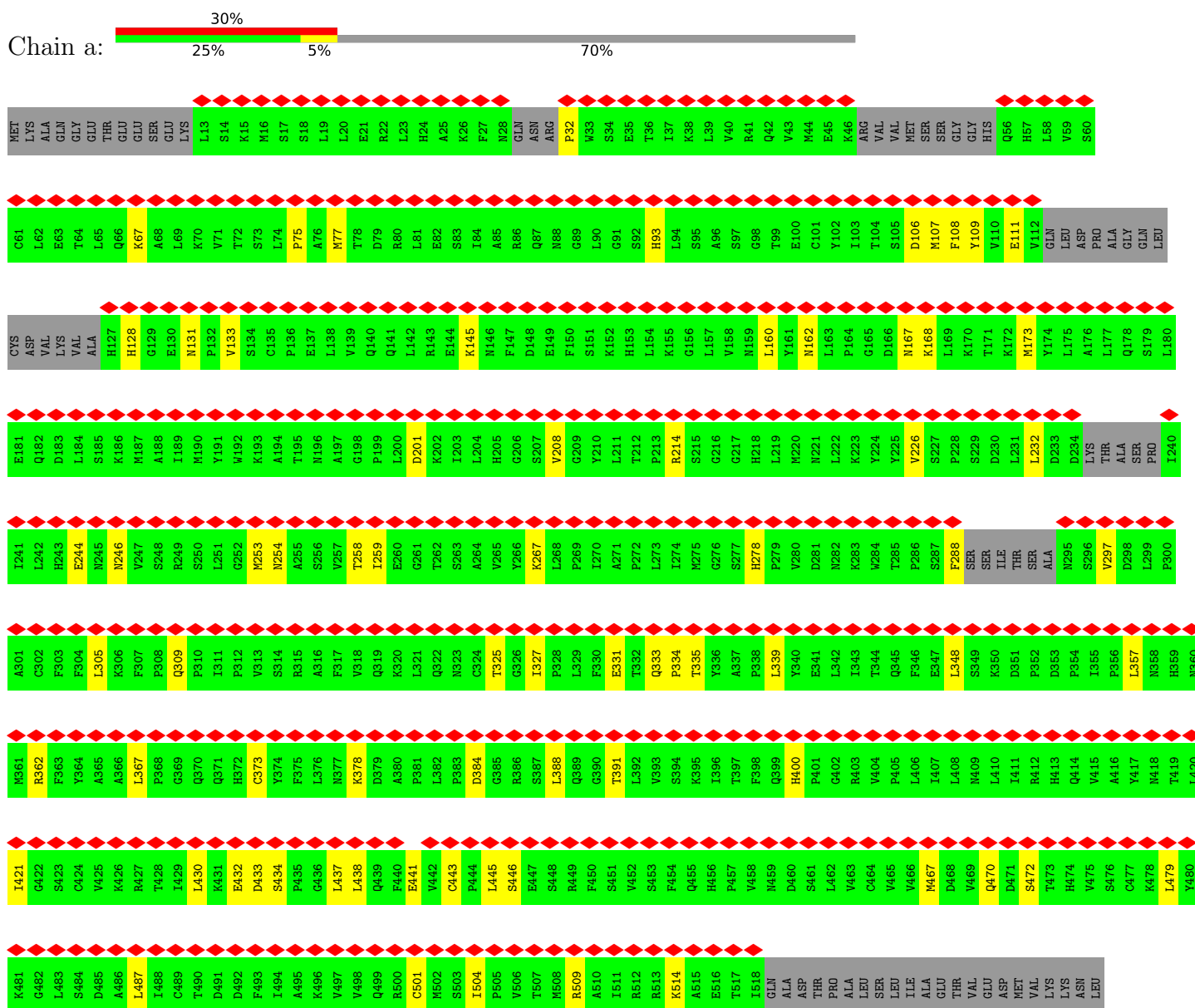
- Molecule 73 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

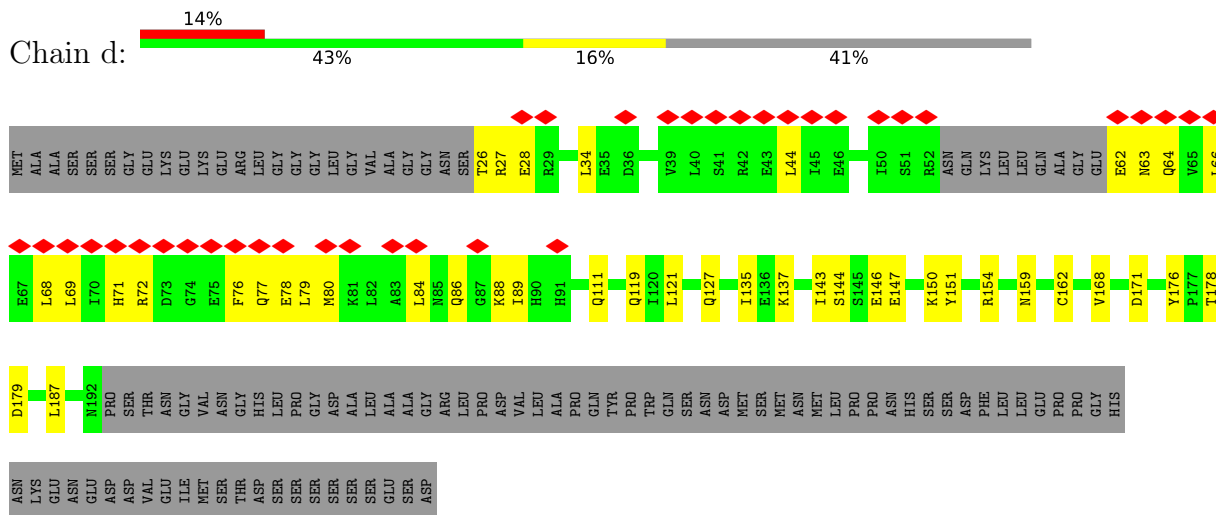
3 Residue-property plots

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.

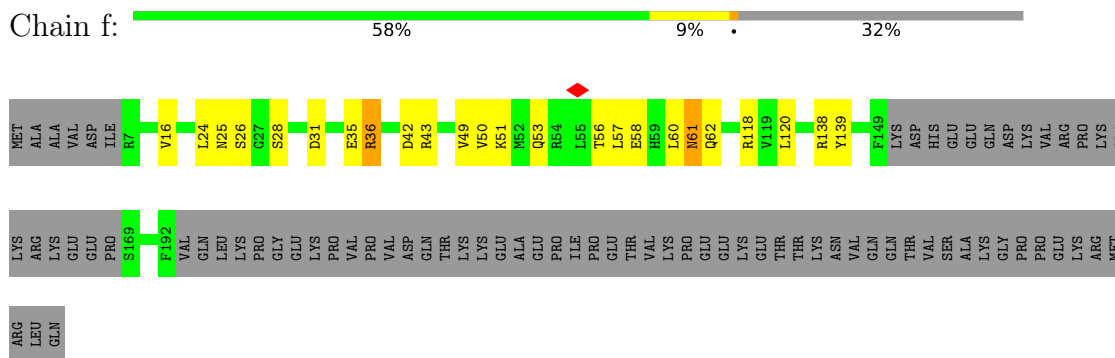
• Molecule 1: Mediator of RNA polymerase II transcription subunit 1



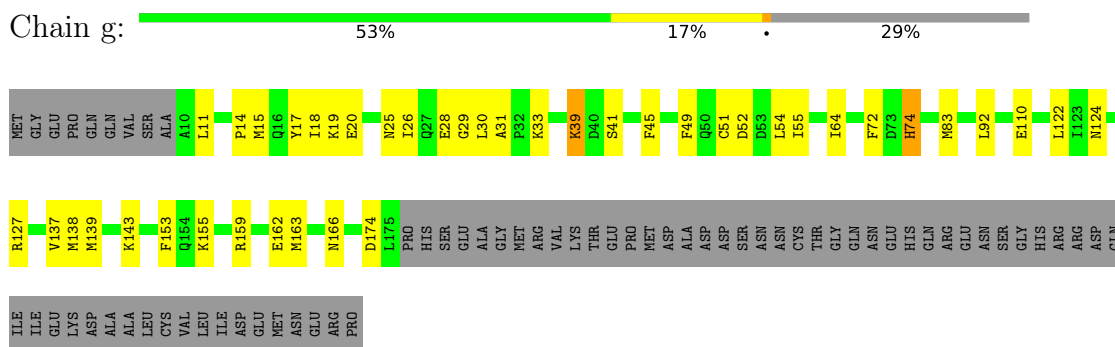
- Molecule 3: Mediator of RNA polymerase II transcription subunit 4



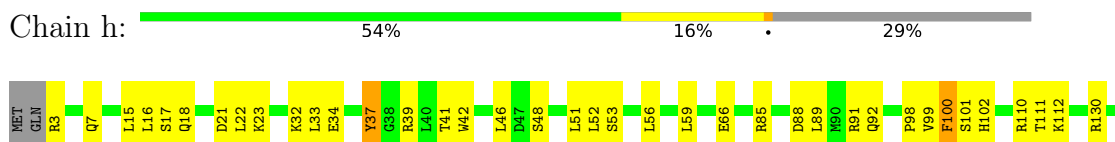
- Molecule 4: Mediator of RNA polymerase II transcription subunit 6

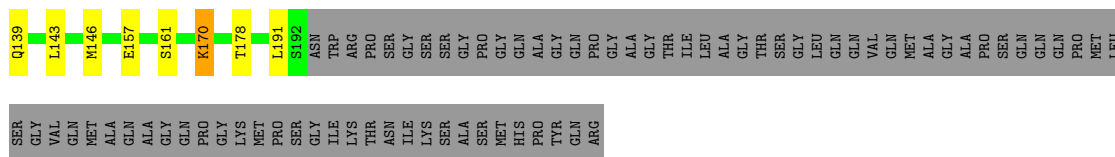


- Molecule 5: Mediator of RNA polymerase II transcription subunit 7

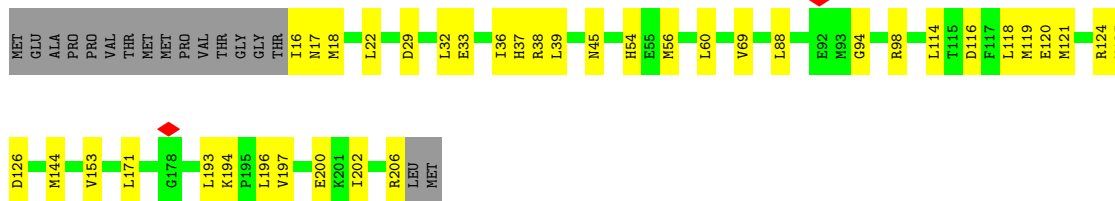


- Molecule 6: Isoform 2 of RNA polymerase II transcription subunit 8

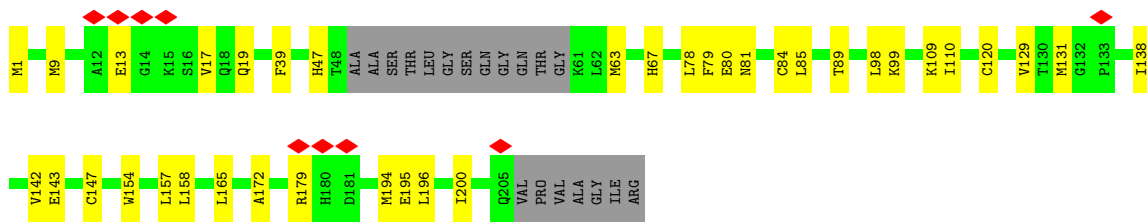




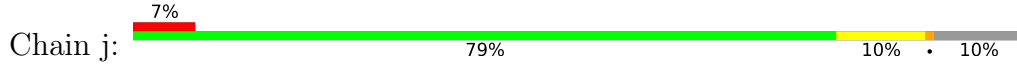
• Molecule 7: Mediator of RNA polymerase II transcription subunit 18



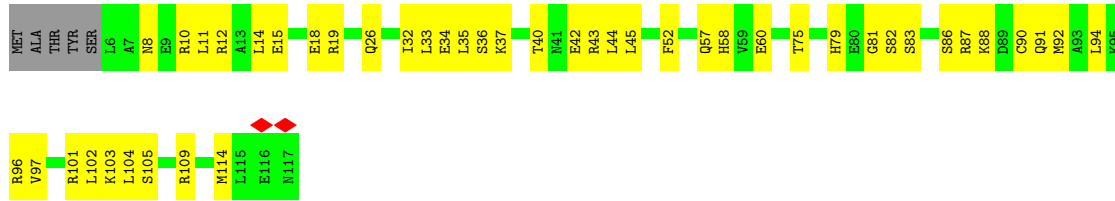
• Molecule 8: Mediator of RNA polymerase II transcription subunit 20



• Molecule 9: Mediator of RNA polymerase II transcription subunit 10

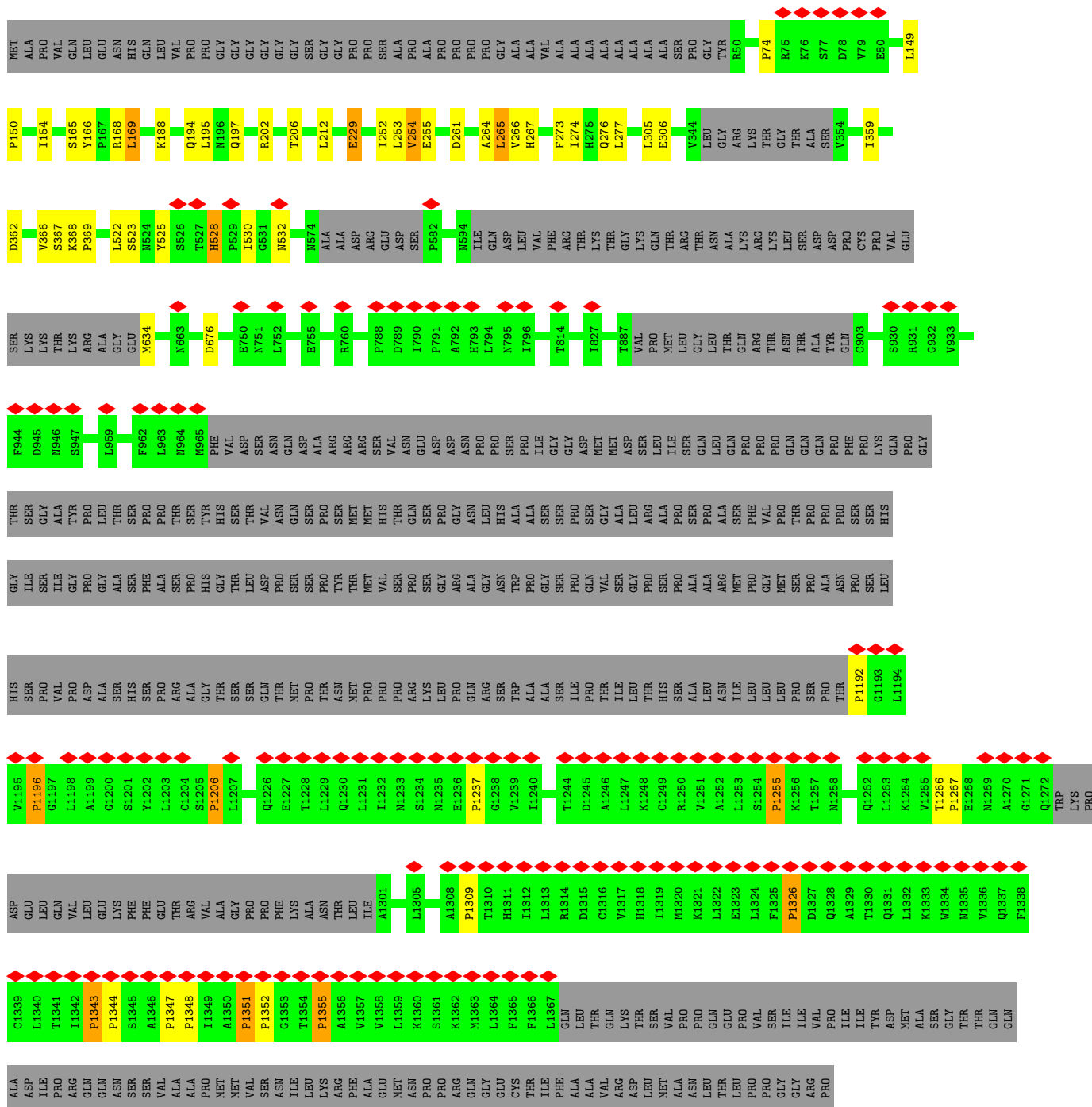


• Molecule 10: Mediator of RNA polymerase II transcription subunit 11

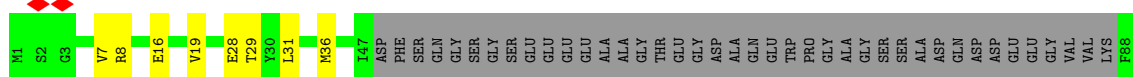


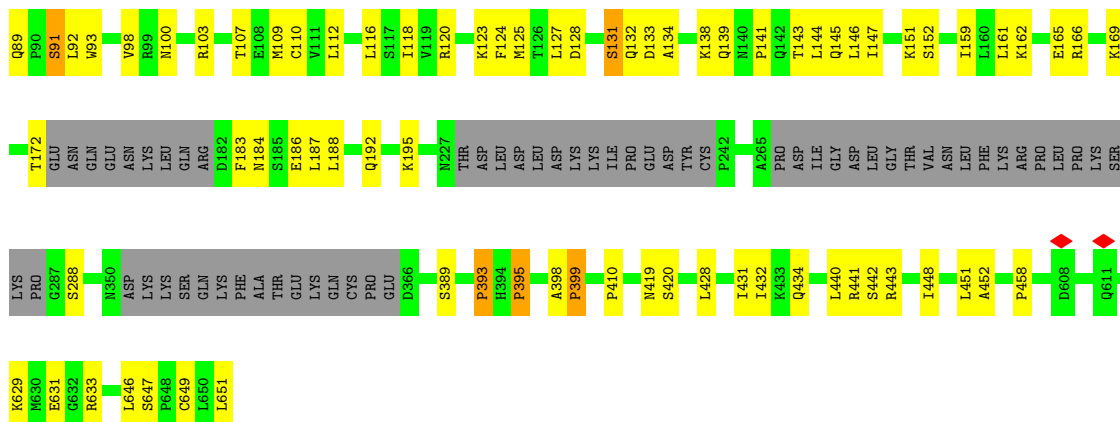
• Molecule 11: Mediator of RNA polymerase II transcription subunit 14



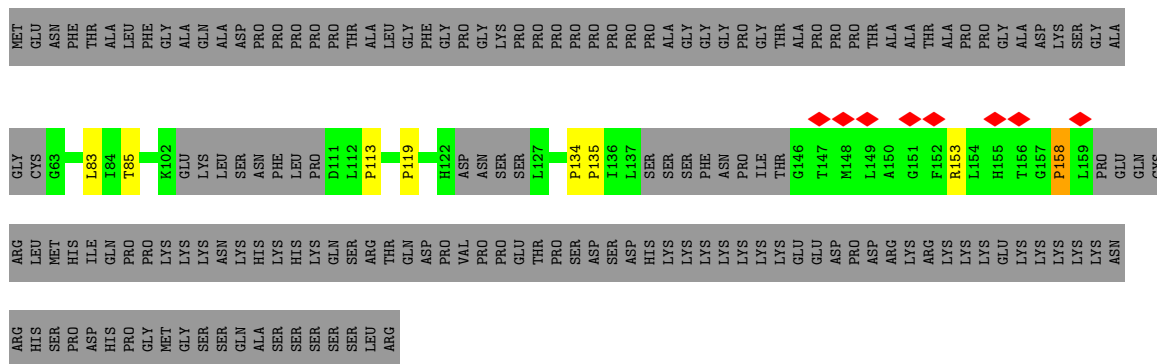


• Molecule 12: Mediator of RNA polymerase II transcription subunit 17

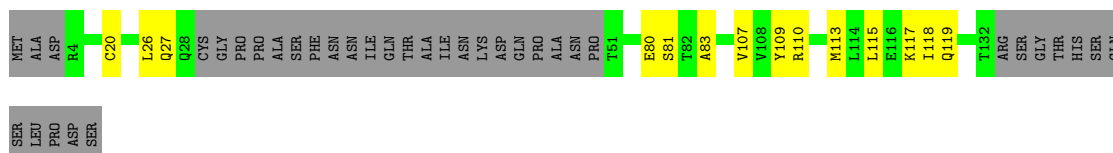




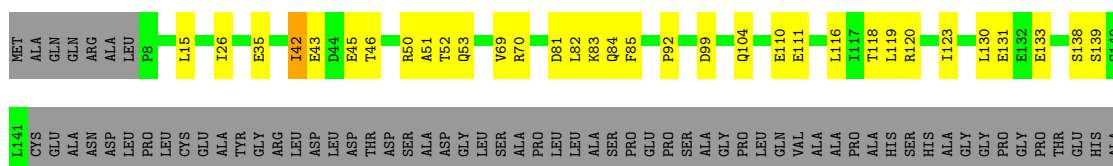
● Molecule 13: Mediator of RNA polymerase II transcription subunit 19



● Molecule 14: Mediator of RNA polymerase II transcription subunit 21

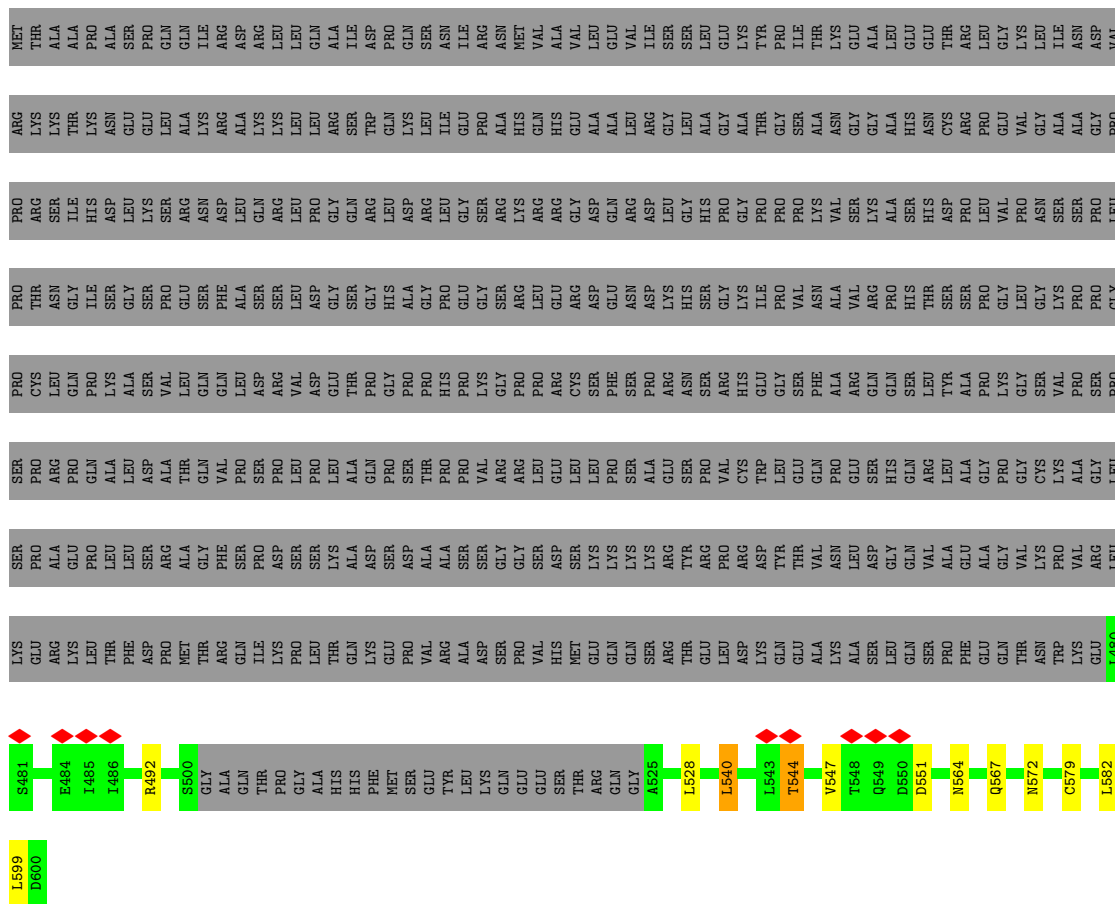


● Molecule 15: Mediator of RNA polymerase II transcription subunit 22

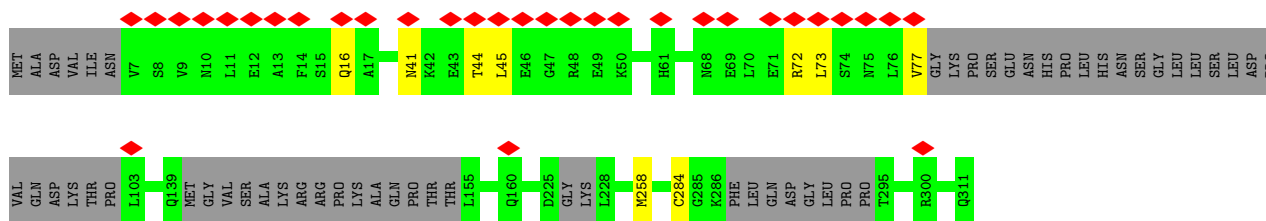
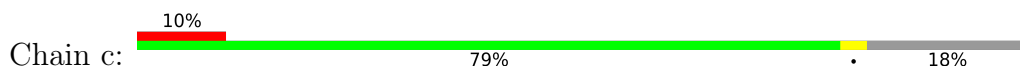


● Molecule 16: Mediator of RNA polymerase II transcription subunit 26

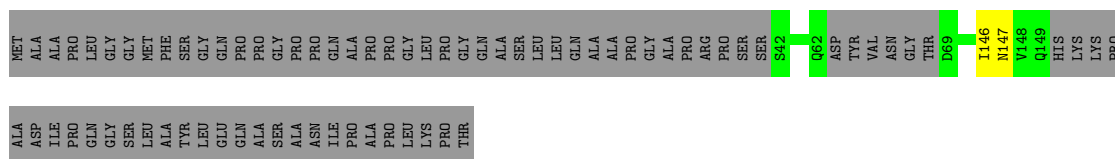




• Molecule 17: Mediator of RNA polymerase II transcription subunit 27

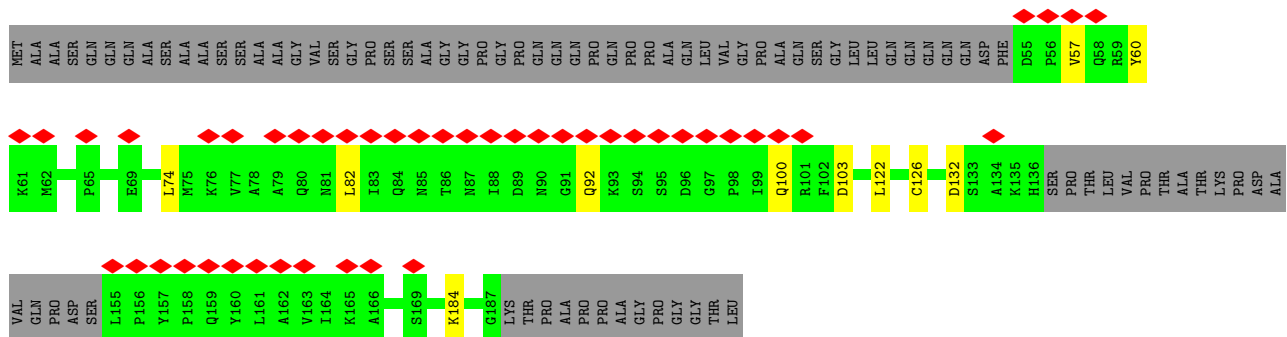


• Molecule 18: Mediator of RNA polymerase II transcription subunit 28

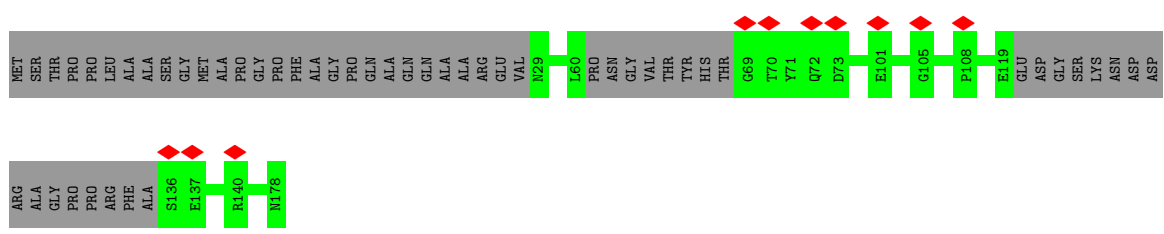


• Molecule 19: Mediator of RNA polymerase II transcription subunit 29

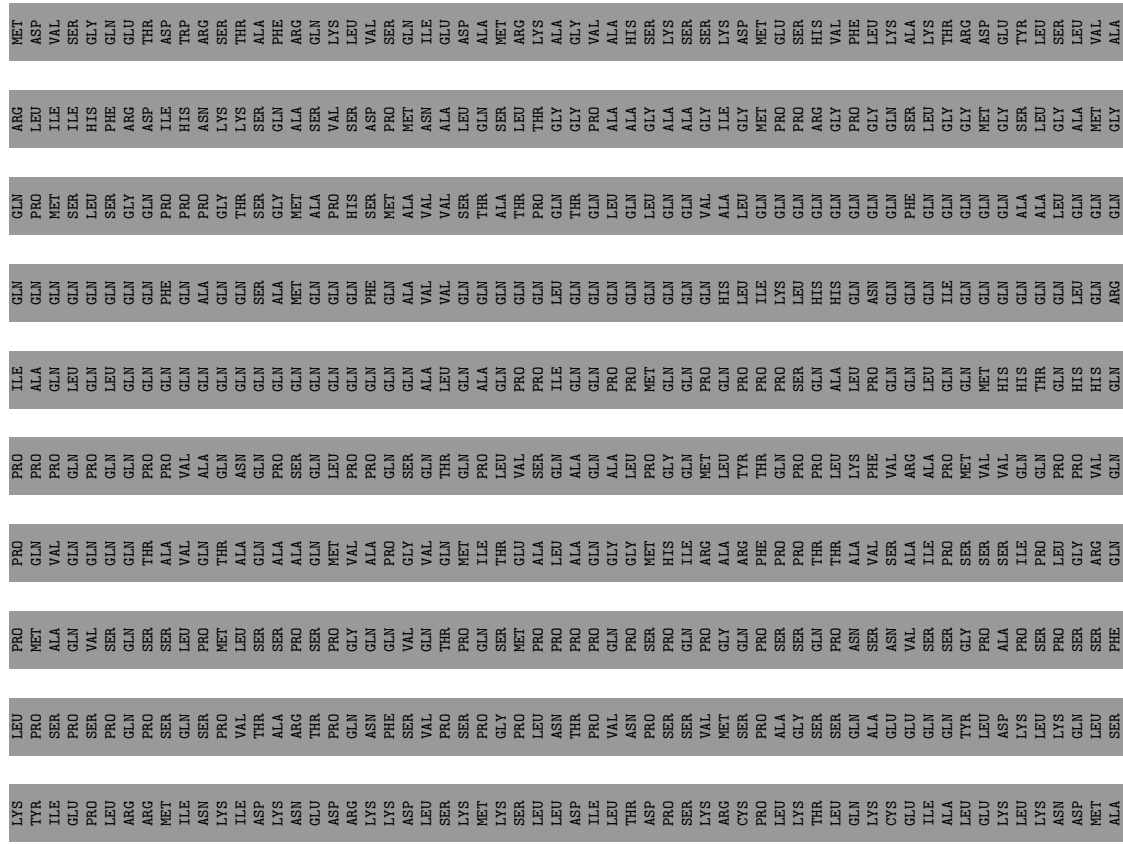


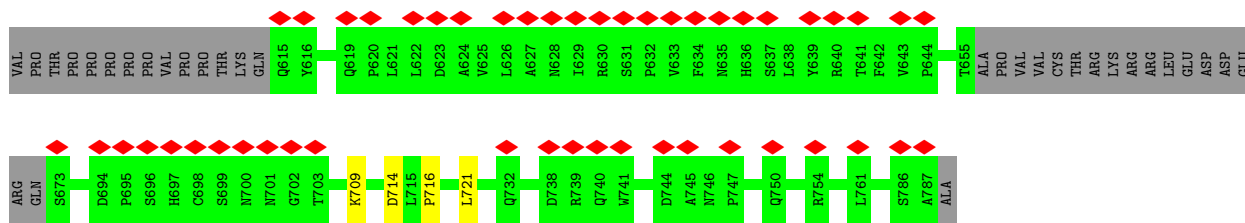


• Molecule 20: Mediator of RNA polymerase II transcription subunit 30

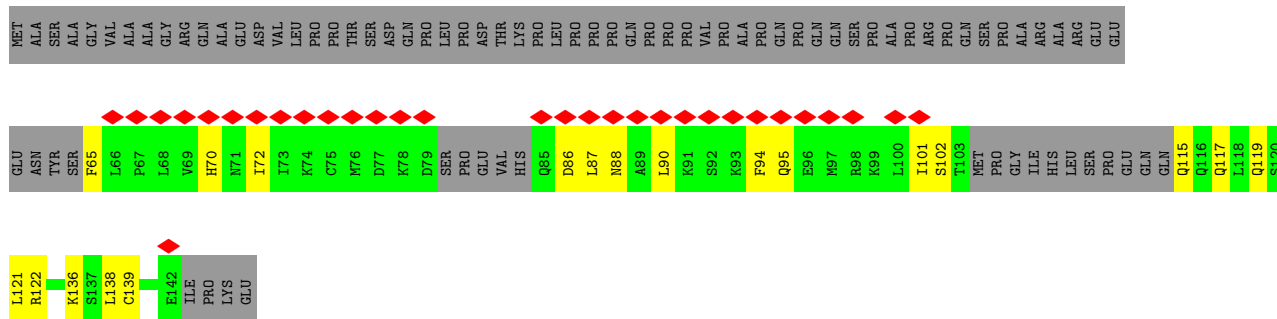


• Molecule 21: Mediator of RNA polymerase II transcription subunit 15

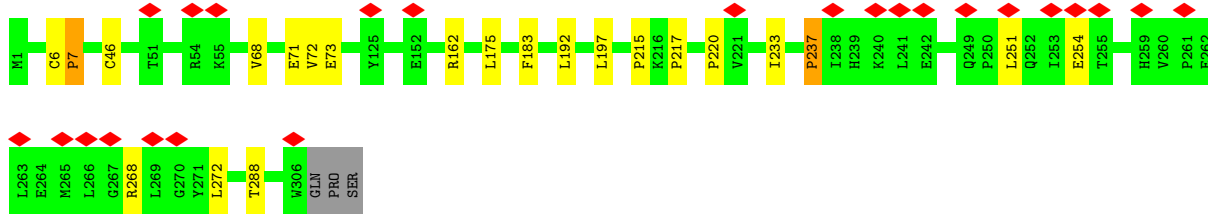
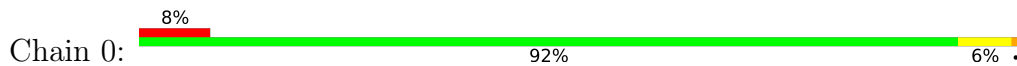




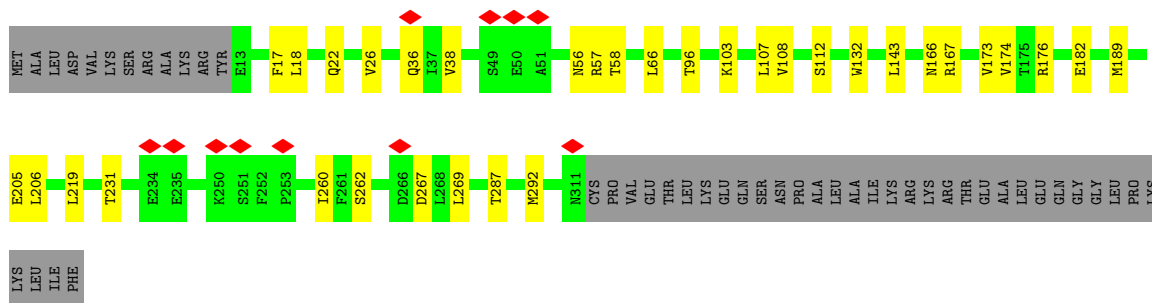
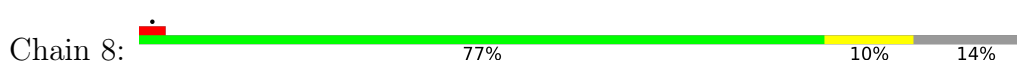
• Molecule 22: Mediator of RNA polymerase II transcription subunit 9



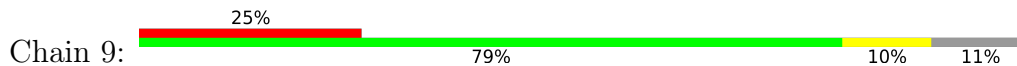
• Molecule 23: CDK-activating kinase assembly factor MAT1

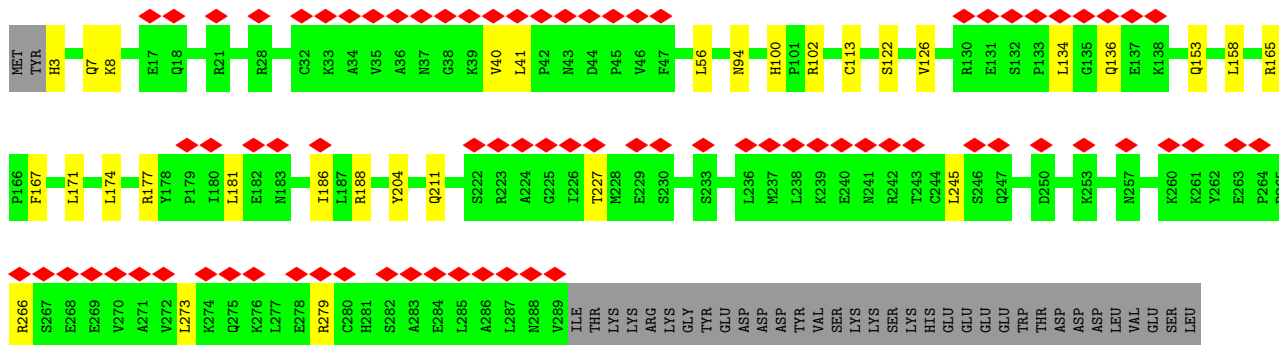


• Molecule 24: Cyclin-dependent kinase 7

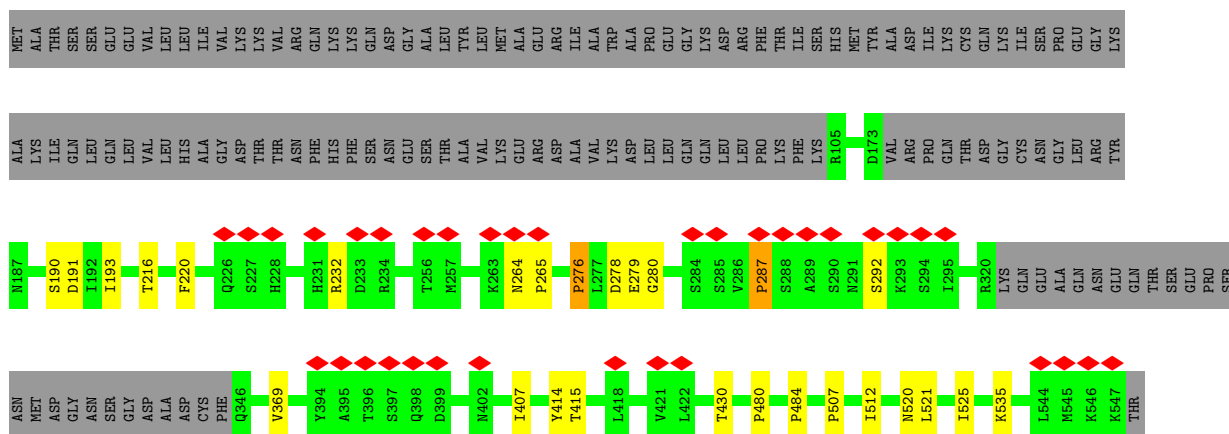


• Molecule 25: Cyclin-H

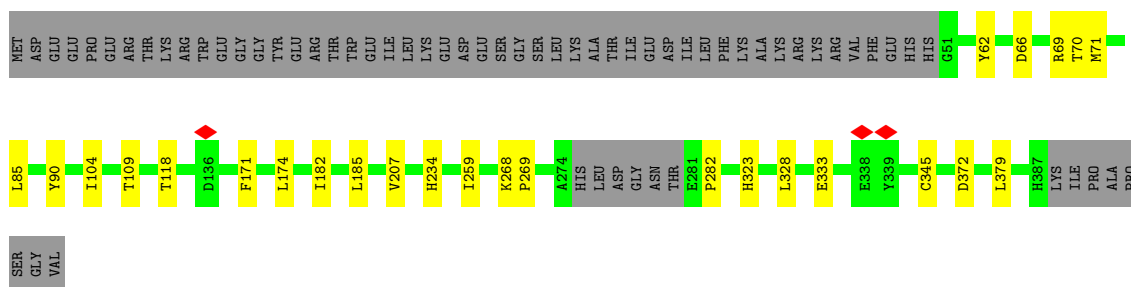
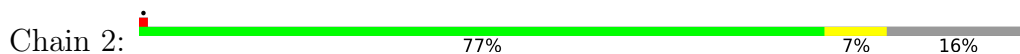




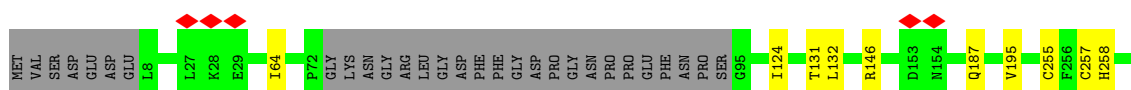
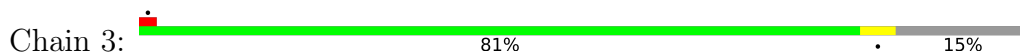
• Molecule 26: General transcription factor IIH subunit 1

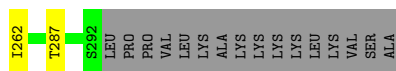


• Molecule 27: General transcription factor IIH subunit 2

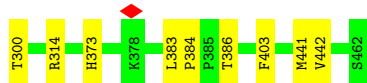
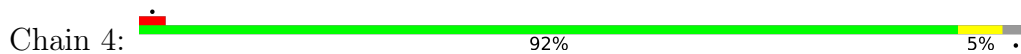


• Molecule 28: General transcription factor IIH subunit 3

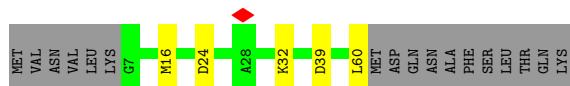




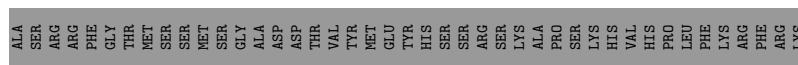
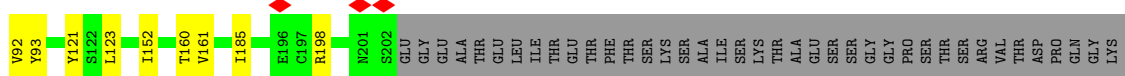
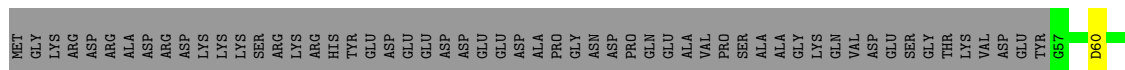
• Molecule 29: General transcription factor IIIH subunit 4



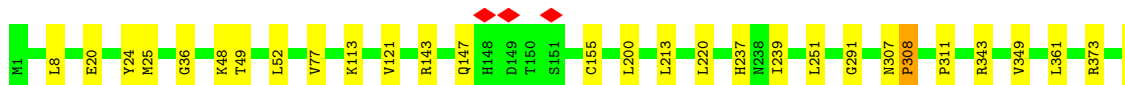
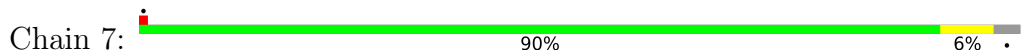
• Molecule 30: General transcription factor IIIH subunit 5

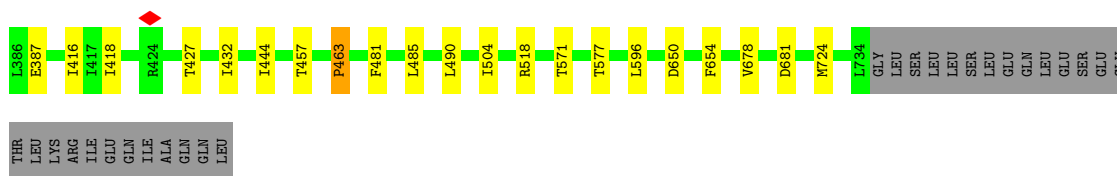


• Molecule 31: General transcription and DNA repair factor IIIH helicase subunit XPB

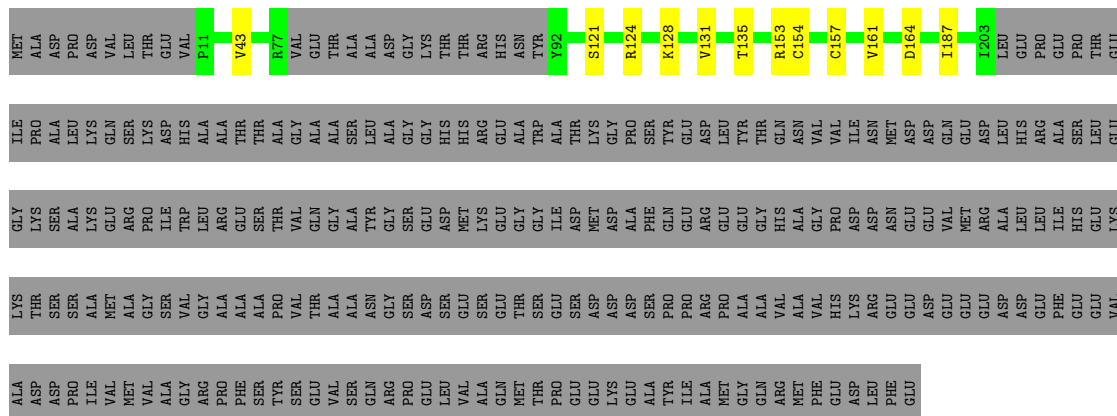


• Molecule 32: General transcription and DNA repair factor IIIH helicase subunit XPD

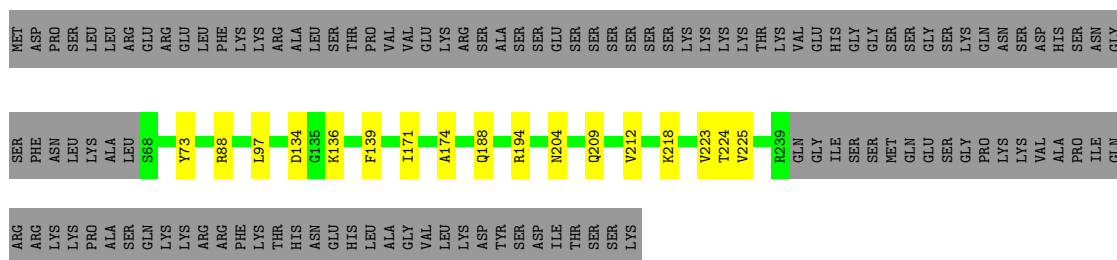




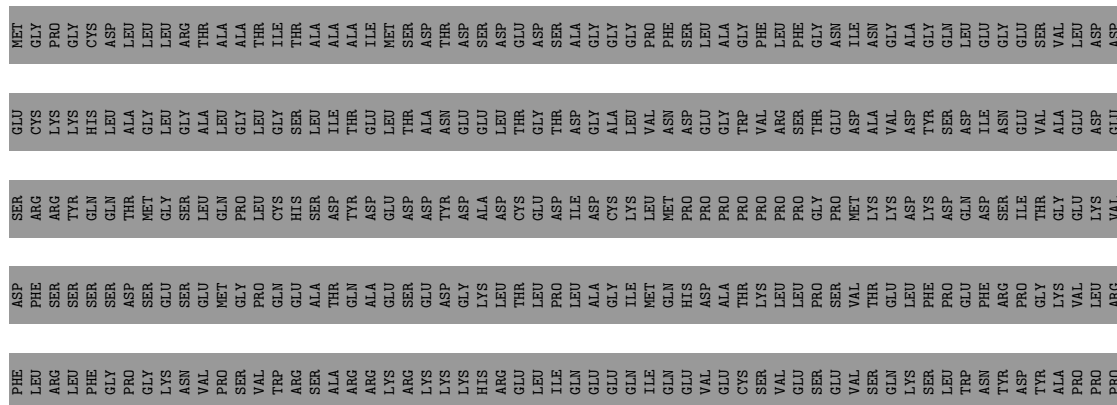
• Molecule 33: General transcription factor IIE subunit 1



• Molecule 34: Transcription initiation factor IIE subunit beta

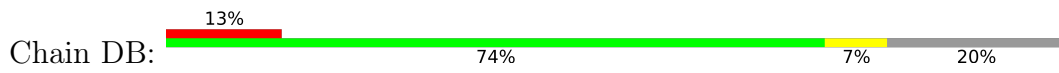


• Molecule 35: Transcription initiation factor TFIID subunit 1

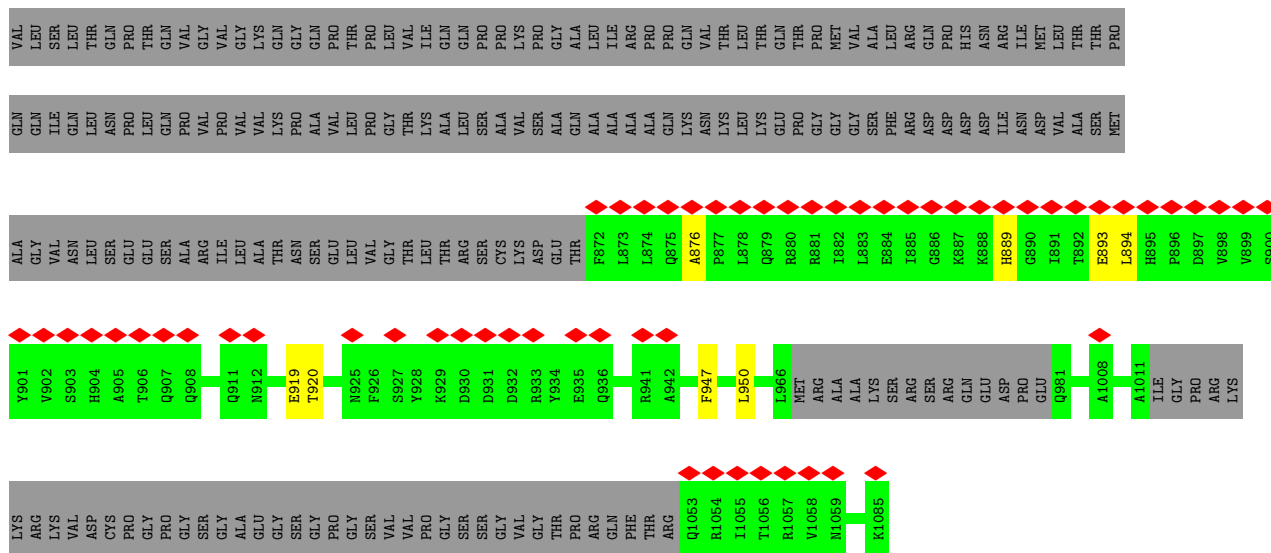


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LYS	MET	LYS	GLU	LYS	ARG	PRO	VAL	GLY	ALA	CYS	GLY	ALA	ALA	ILE	ILE	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
GLY	GLY	ILE	VAL	VAL	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
SER	ILE	HIS	ARG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

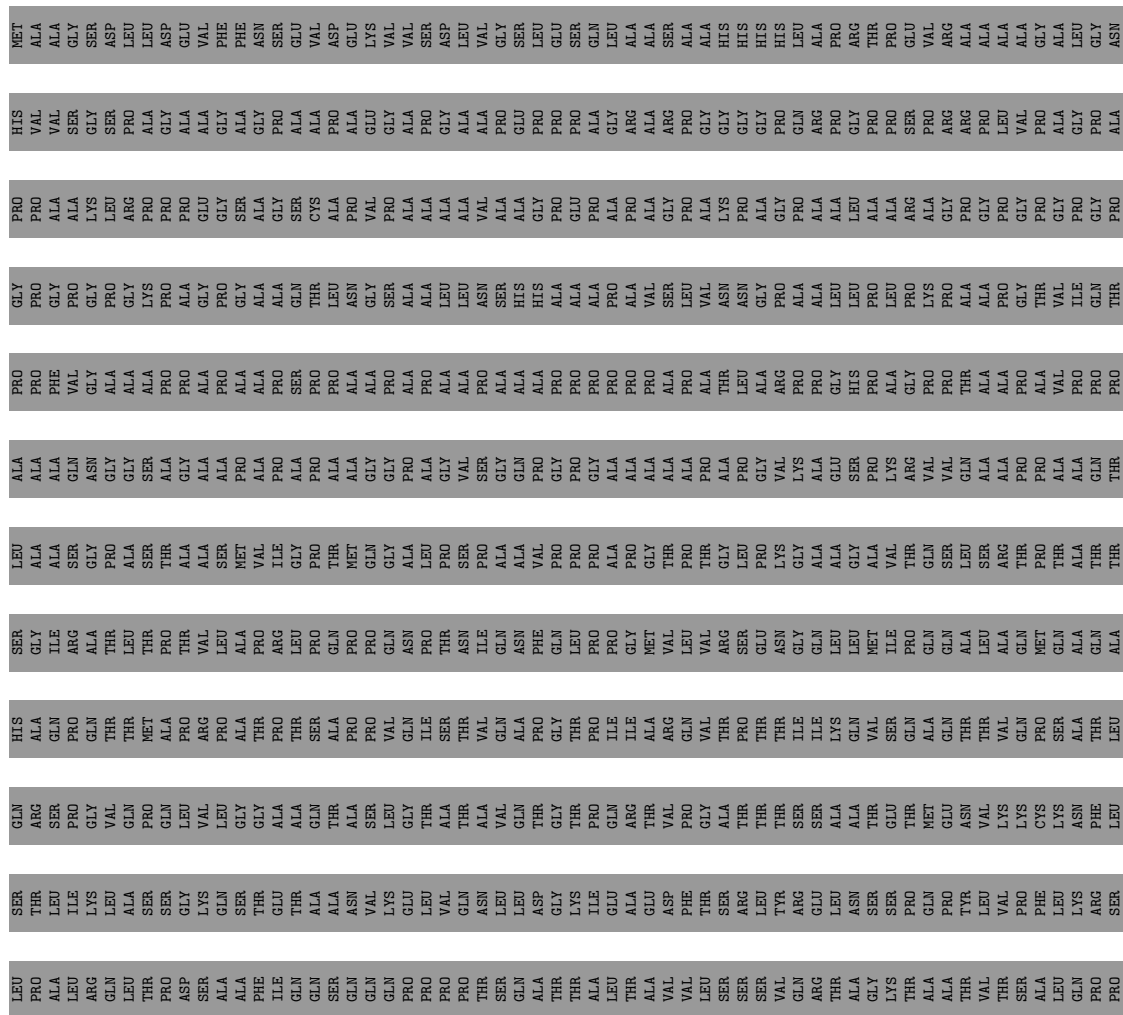
● Molecule 36: Transcription initiation factor TFIID subunit 2

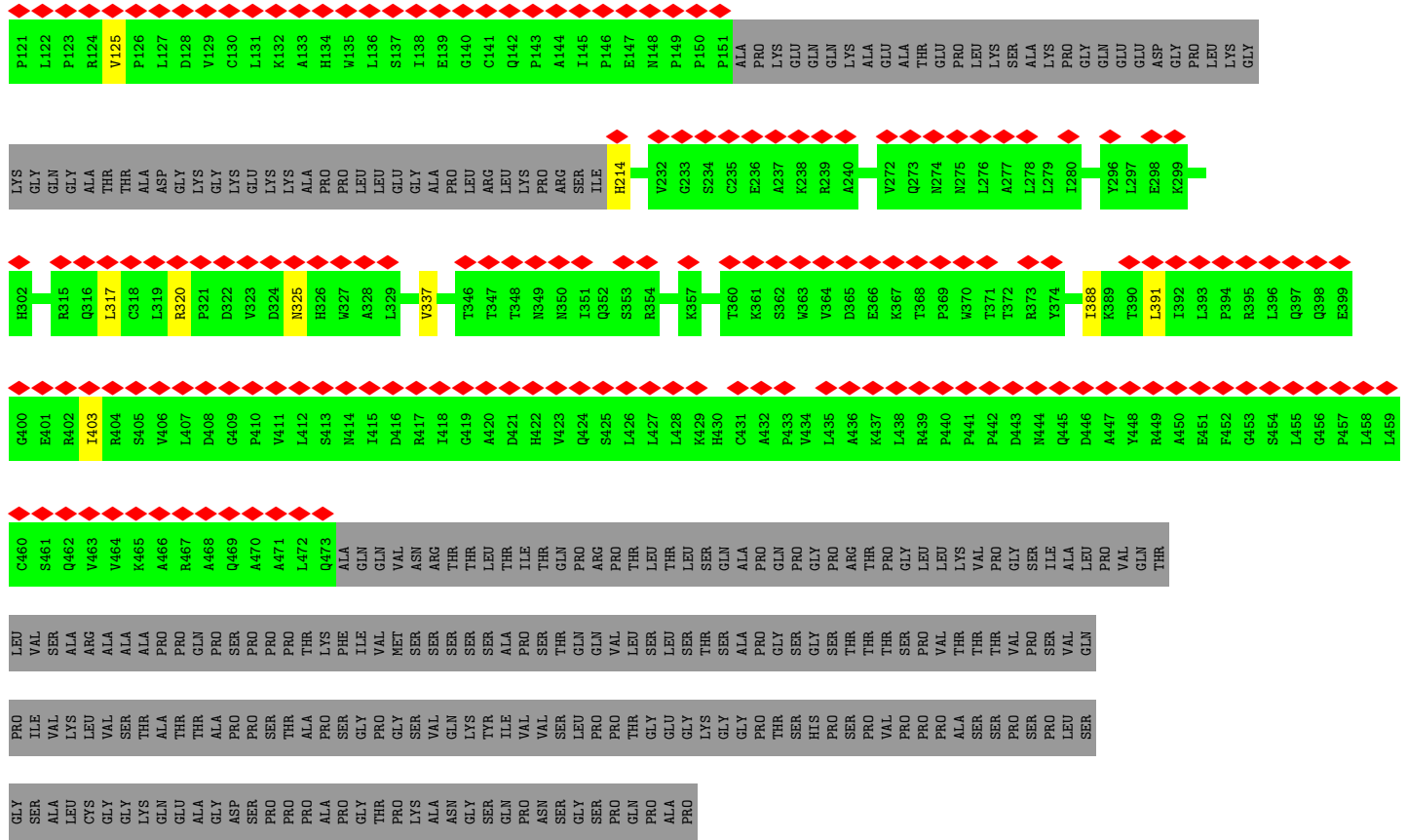


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MET	PRO	LEU	THR	VAL	PRO	ALA	ARG	MET	LYS	LYS	GLY	ASP	G19	R24	P25	Q41	R42	F48	T52	I53	F54	P55	T56	V57	A58	N59	L60	R61	R62	I63	K64	L65	N66	R71	I72	Y73	R74	V75	R76	I77	N78	D79	L80	E81	A82	A83	F84	I85	Y86	N87	H95	S96	E97	S98	K99	Q100	Y105	V114	E125	L126	C127	I128	V130	P131	S132	E133	L134	W135	K136	H137	V138	D139	E140	L141	K142	V143	L144	K145	I146	H147	I148	M149	F150	S151	L152	D153	V166	E167	G168	E172	V177	L220	V221	Y225	T226	H227	D228	M229	R230			
MET	PRO	LEU	THR	VAL	PRO	ALA	ARG	MET	LYS	LYS	GLY	ASP	G19	R24	P25	Q41	R42	F48	T52	I53	F54	P55	T56	V57	A58	N59	L60	R61	R62	I63	K64	L65	N66	R71	I72	Y73	R74	V75	R76	I77	N78	D79	L80	E81	A82	A83	F84	I85	Y86	N87	H95	S96	E97	S98	K99	Q100	Y105	V114	E125	L126	C127	I128	V130	P131	S132	E133	L134	W135	K136	H137	V138	D139	E140	L141	K142	V143	L144	K145	I146	H147	I148	M149	F150	S151	L152	D153	V166	E167	G168	E172	V177	L220	V221	Y225	T226	H227	D228	M229	R230			
K931	K232	E286	V287	F288	I309	V314	E315	V316	S323	F355	S365	D366	L413	L414	F418	G419	R24	P25	Q41	R42	F48	T52	I53	F54	P55	T56	V57	A58	N59	L60	R61	R62	I63	K64	L65	N66	R71	I72	Y73	R74	V75	R76	I77	N78	D79	L80	E81	A82	A83	F84	I85	Y86	N87	H95	S96	E97	S98	K99	Q100	Y105	V114	E125	L126	C127	I128	V130	P131	S132	E133	L134	W135	K136	H137	V138	D139	E140	L141	K142	V143	L144	K145	I146	H147	I148	M149	F150	S151	L152	D153	V166	E167	G168	E172	V177	L220	V221	Y225	T226	H227	D228	M229	R230
H577	E582	E583	N584	S585	D589	I590	F591	C592	H593	S594	K595	S596	R597	K600	K601	K602	I604	P605	G609	E610	E611	V612	M614	D615	L625	L626	V636	L637	R638	D646	E670	K671	T674	R678	E686	R693	S697	A698	C699	M709	W710	S711	T712																																																											

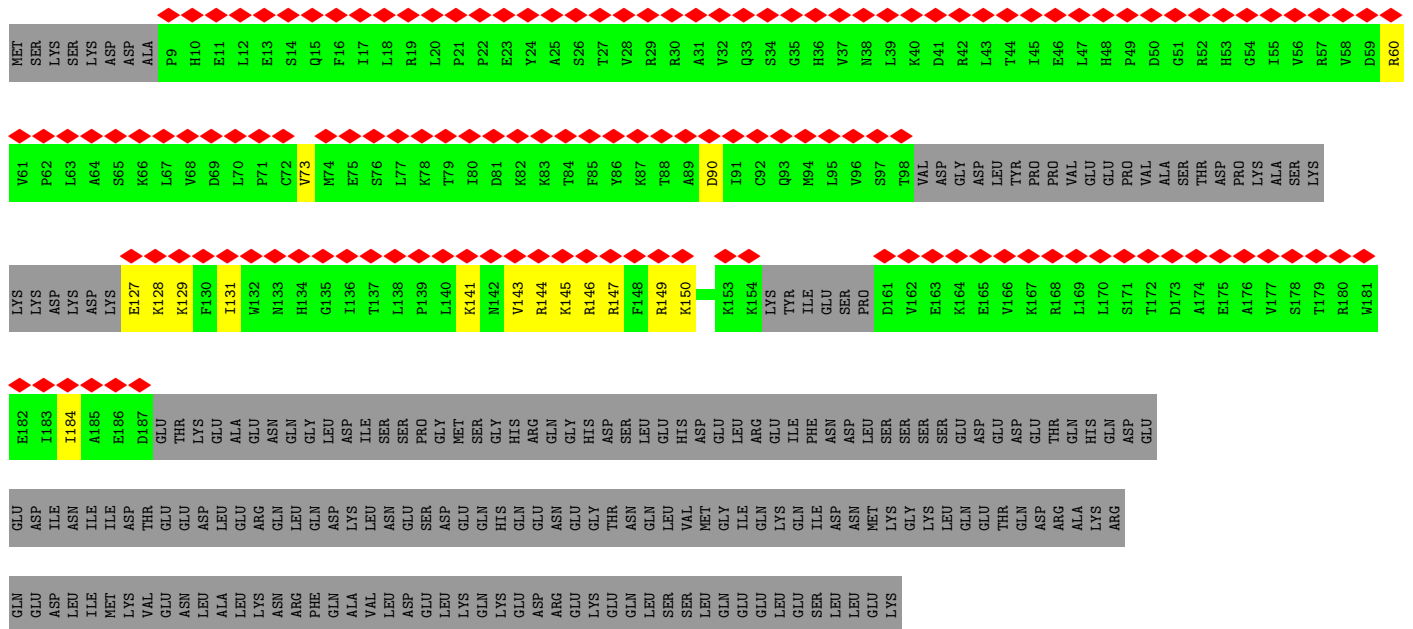
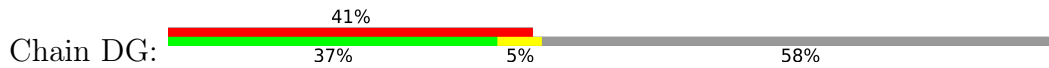


• Molecule 37: Transcription initiation factor TFIID subunit 4



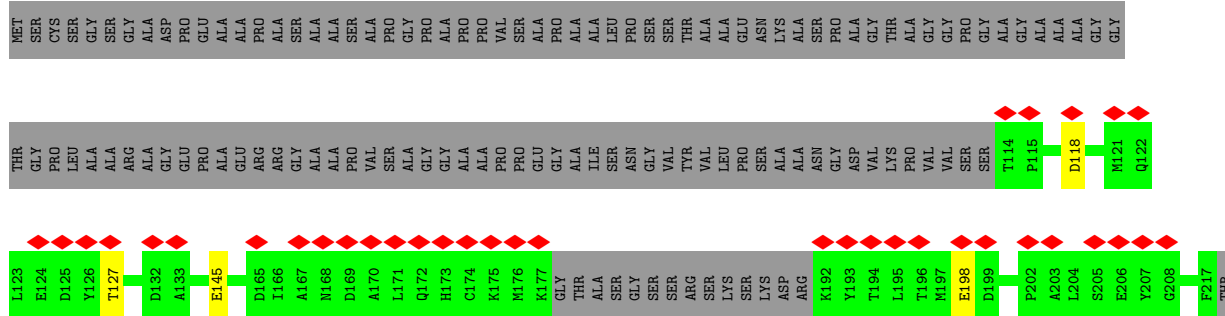


● Molecule 40: Transcription initiation factor TFIID subunit 7

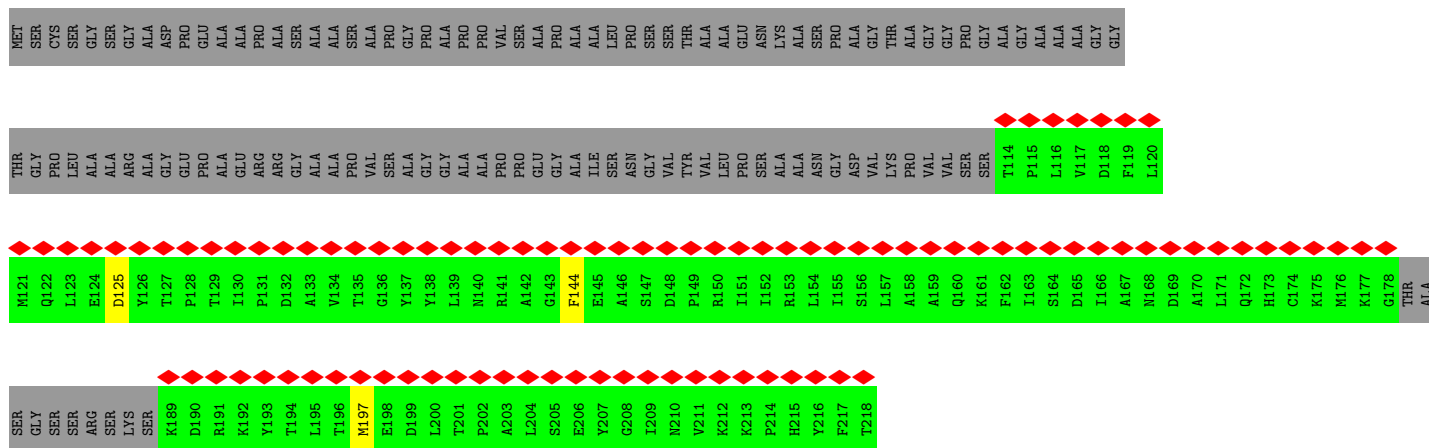
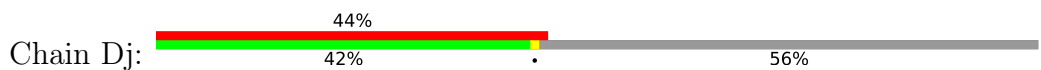


● Molecule 41: Transcription initiation factor TFIID subunit 8

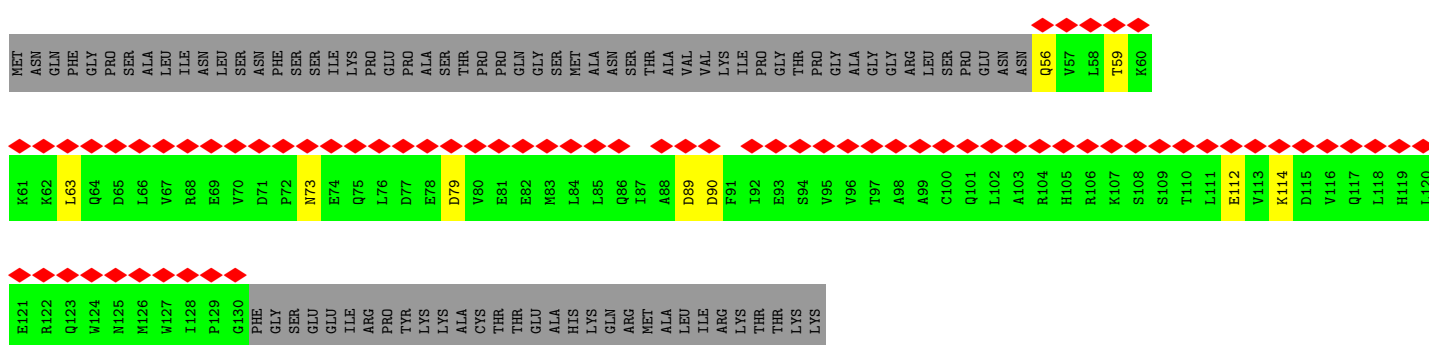
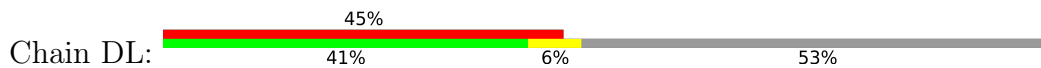
• Molecule 43: Transcription initiation factor TFIID subunit 10



• Molecule 43: Transcription initiation factor TFIID subunit 10

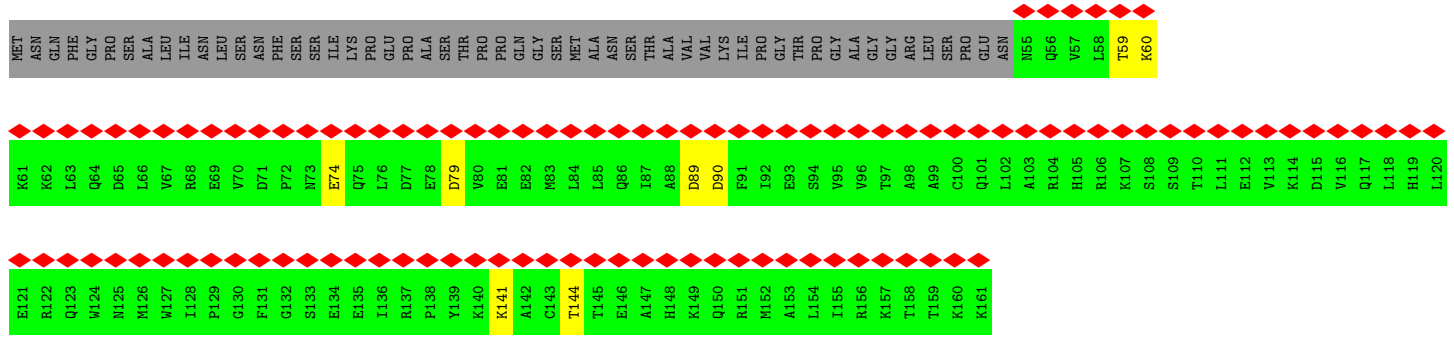


• Molecule 44: Transcription initiation factor TFIID subunit 12

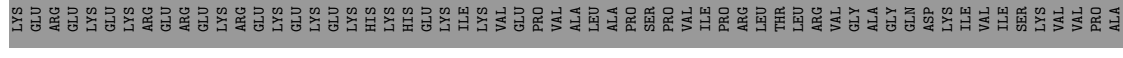
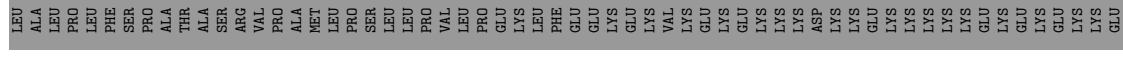
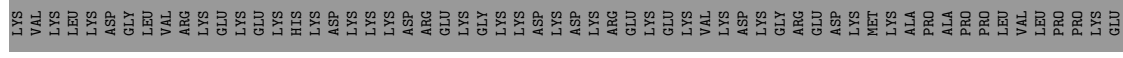
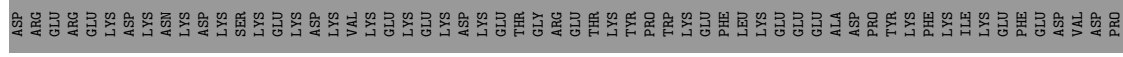
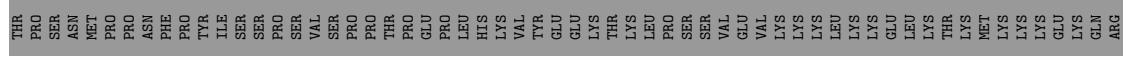
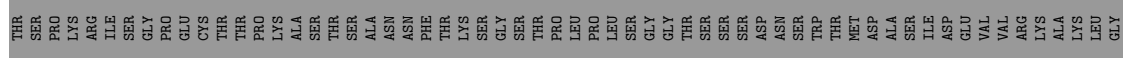
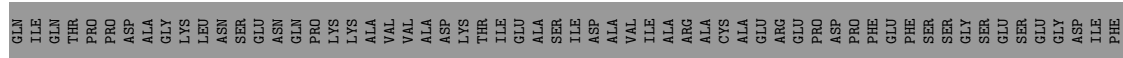
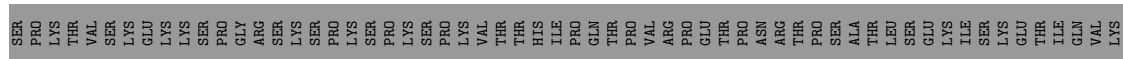
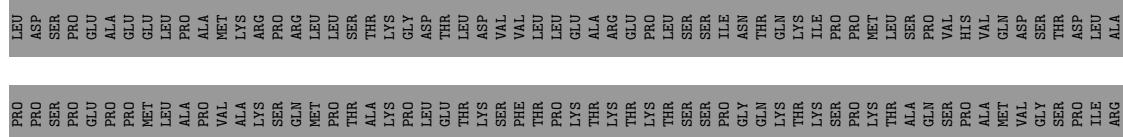
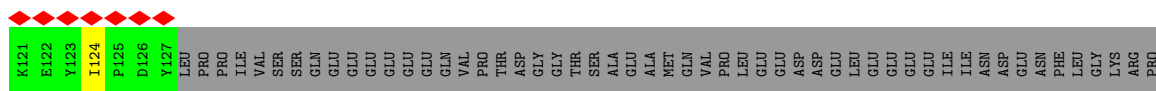


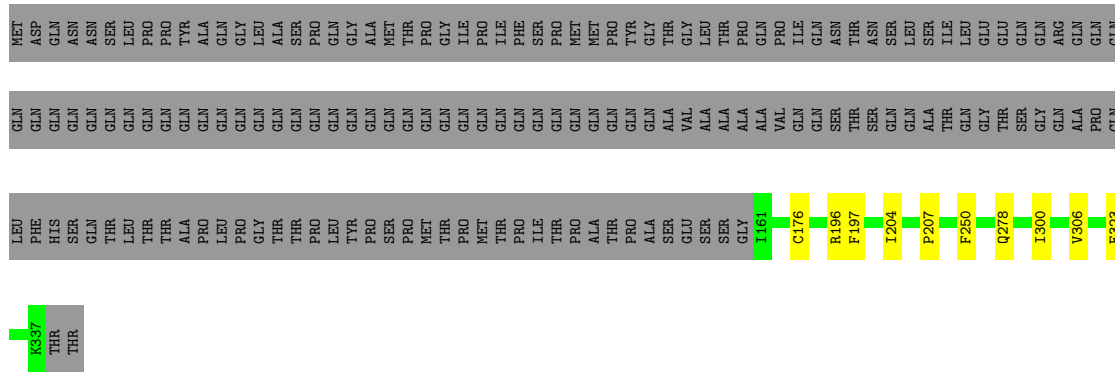
• Molecule 44: Transcription initiation factor TFIID subunit 12



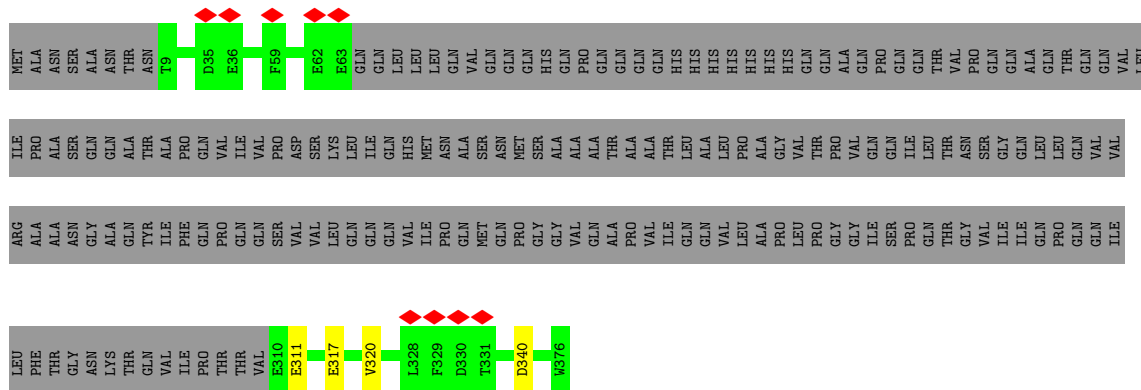


● Molecule 45: Transcription initiation factor TFIID subunit 3

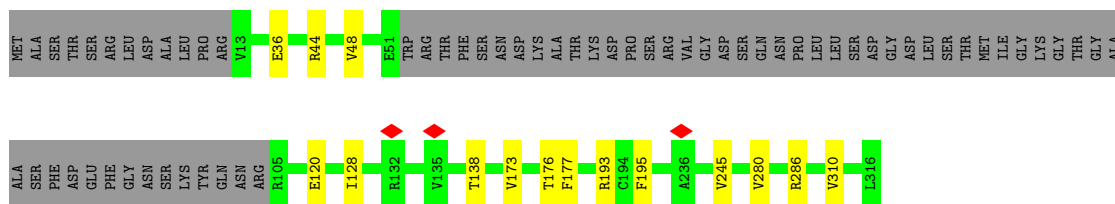
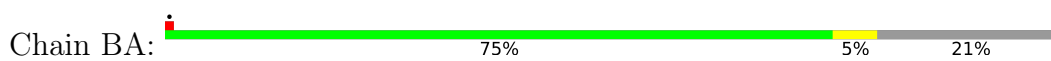




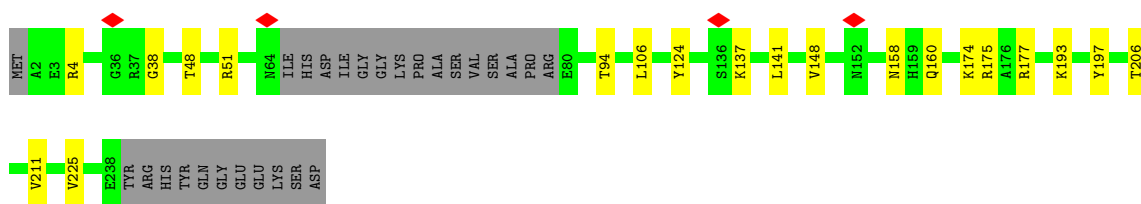
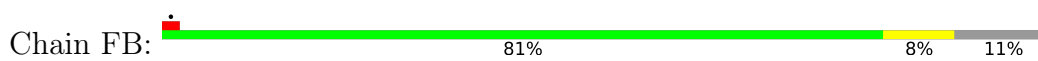
• Molecule 50: TFIIA-a



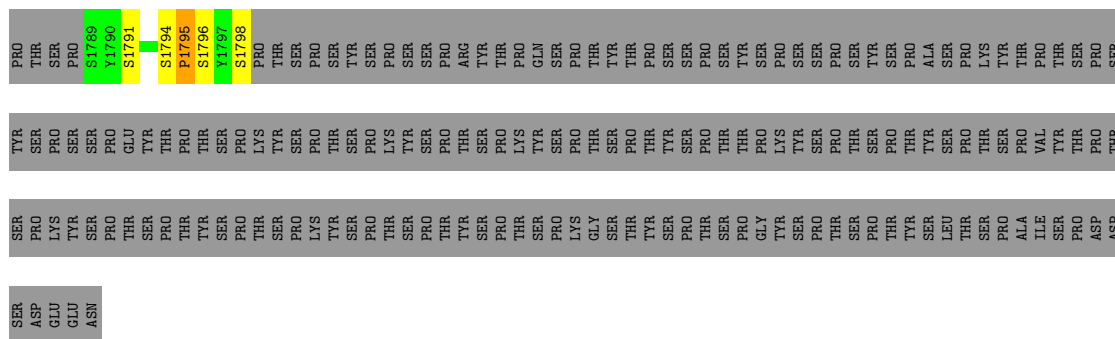
• Molecule 51: Transcription initiation factor IIB



• Molecule 52: General transcription factor IIF subunit 2

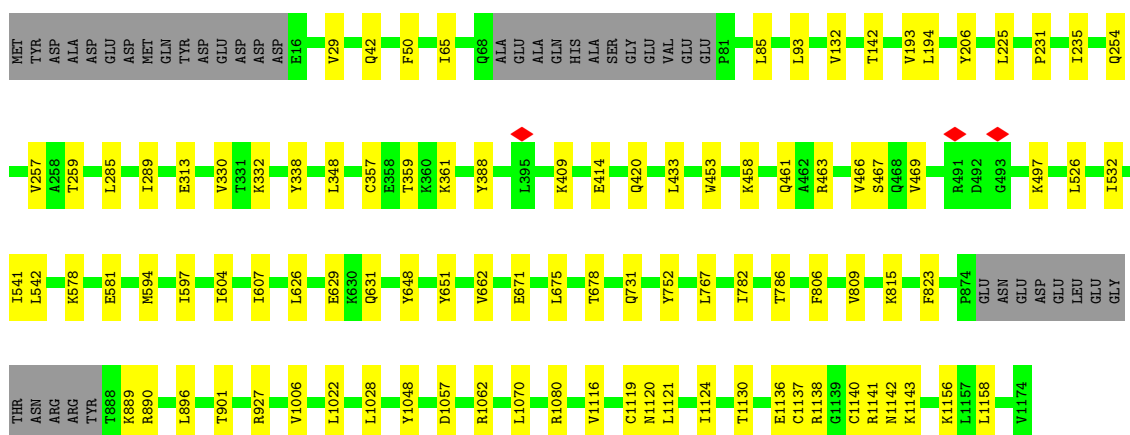


• Molecule 53: DNA (69-MER)



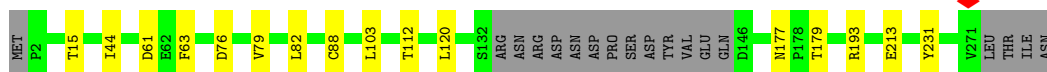
- Molecule 56: DNA-directed RNA polymerase subunit beta

Chain PB: 88% 8%



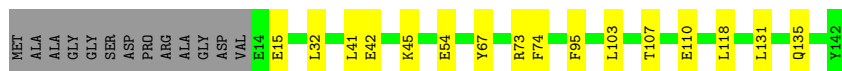
- Molecule 57: DNA-directed RNA polymerase II subunit RPB3

Chain PC: 88% 6% 7%



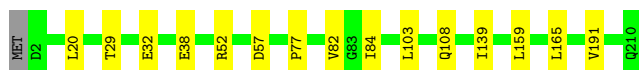
- Molecule 58: DNA-directed RNA polymerase II subunit RPB4

Chain PD: 80% 11% 9%

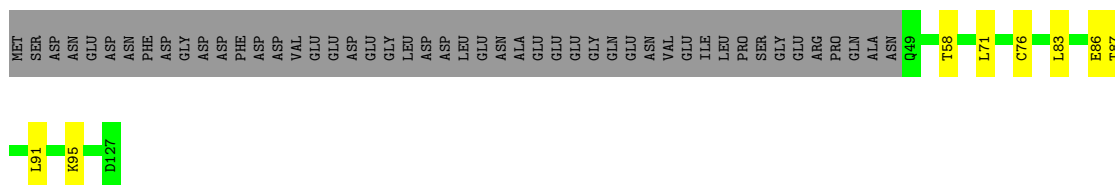


- Molecule 59: DNA-directed RNA polymerase II subunit E

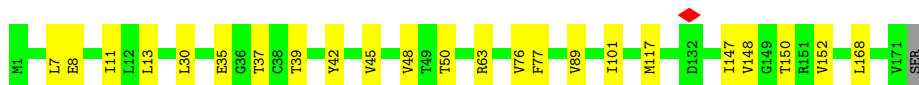
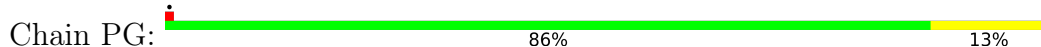
Chain PE: 92% 7%



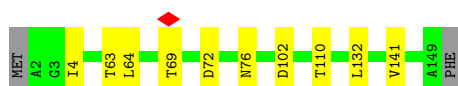
- Molecule 60: DNA-directed RNA polymerase II subunit F



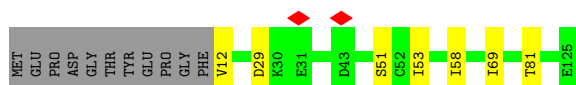
- Molecule 61: DNA-directed RNA polymerase II subunit RPB7



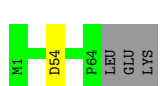
- Molecule 62: DNA-directed RNA polymerases I, II, and III subunit RPABC3



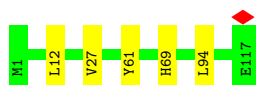
- Molecule 63: DNA-directed RNA polymerase II subunit RPB9



- Molecule 64: RPB10

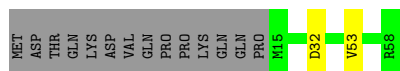


- Molecule 65: RNA_pol_L_2 domain-containing protein



- Molecule 66: RPB12

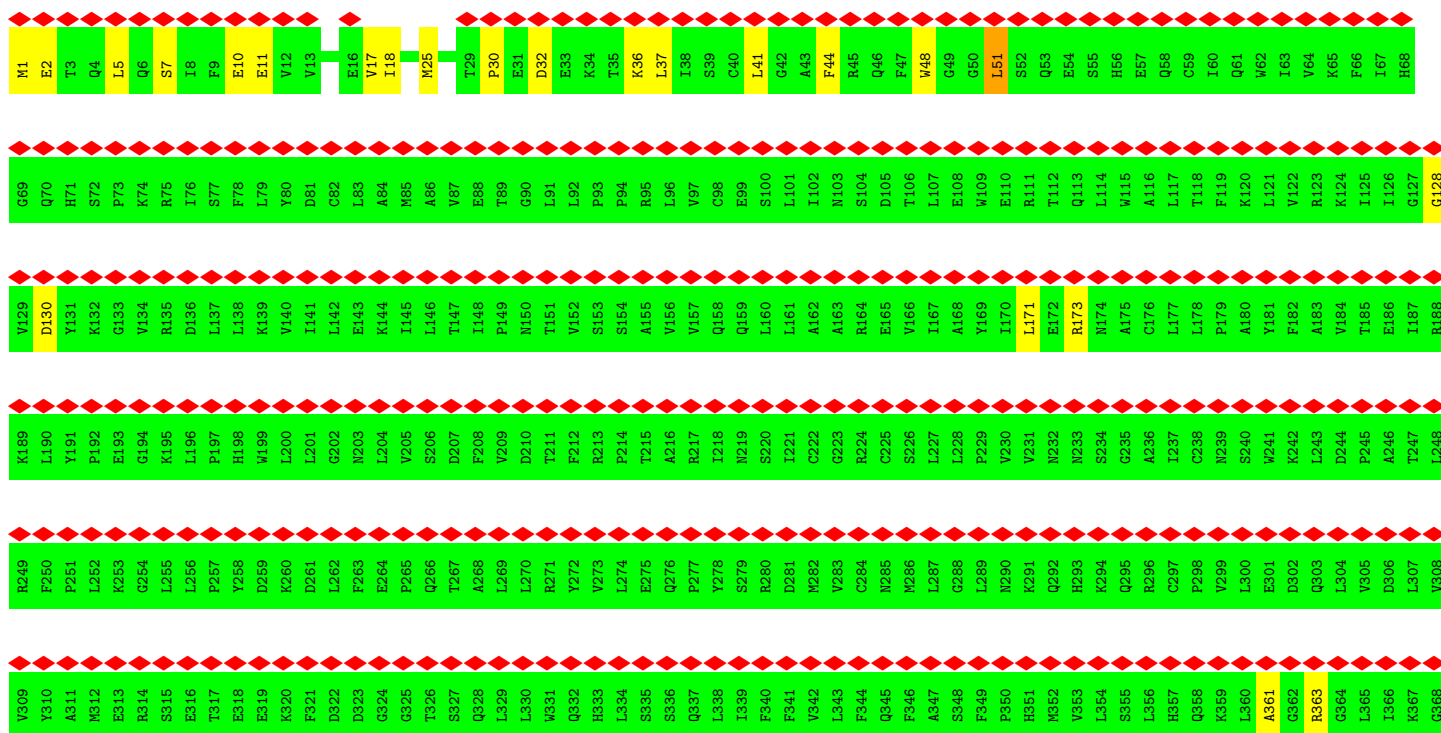




● Molecule 67: General transcription factor IIF subunit 1



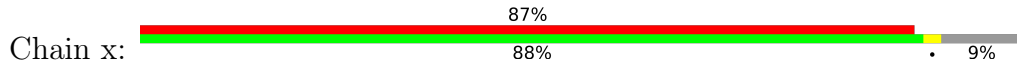
● Molecule 68: Mediator of RNA polymerase II transcription subunit 23



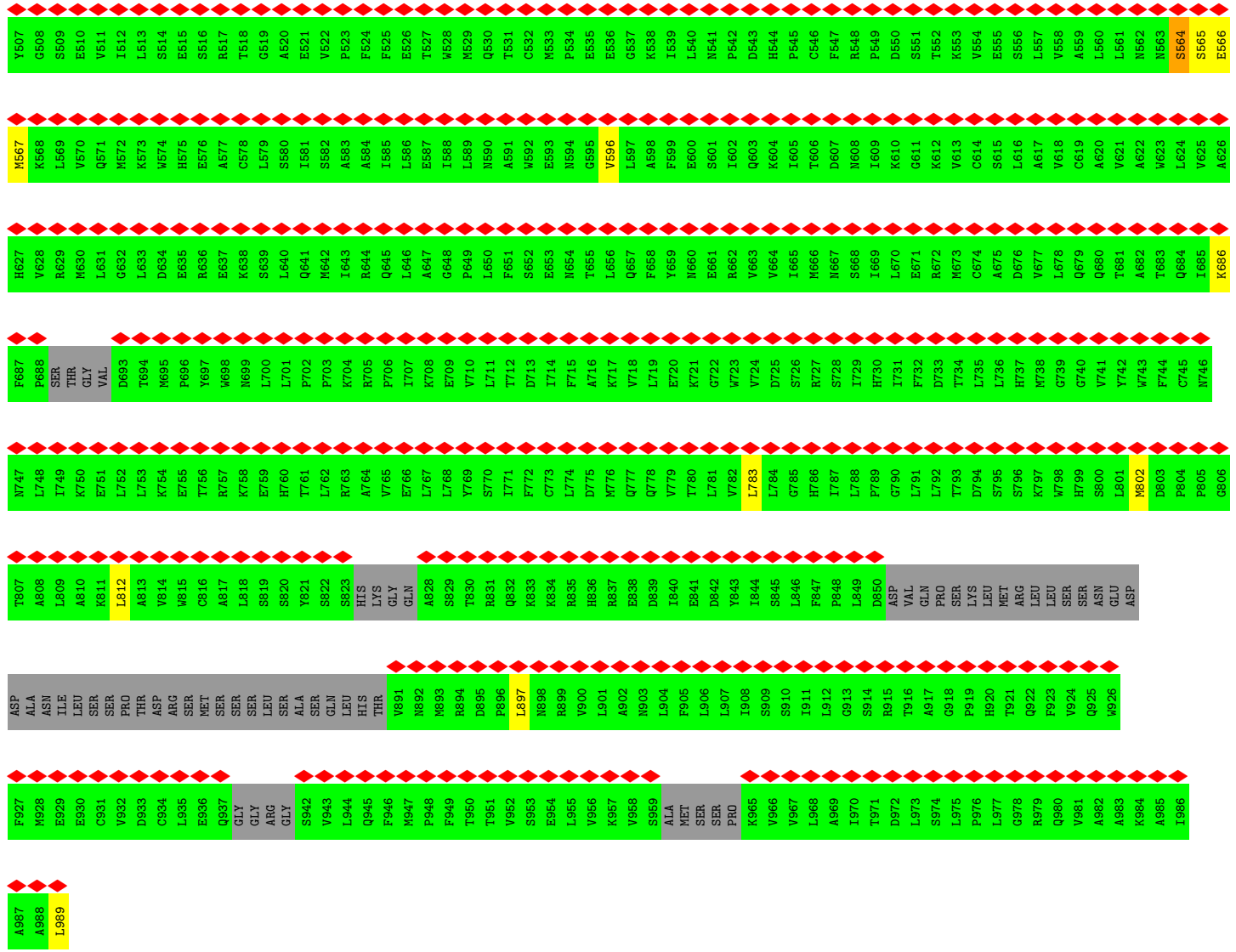
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I969	V970	I971	H972	R973	F974	L975	E976	L977	L978	P979	V980	S981	K982	S983	L984	E985	T986	L987	L988	D989	H990	L991	G992	G993	L994	Y995	K996	F997	H998	D999	R1000	P1001	V1002	T1003	Y1004	L1005	L1006	N1007	T1008	L1009	R1010	Y1011	Y1012	E1013	M1014	H1015	L1016	R1017	R1018	R1019	A1020	F1021	K1022	S1023	R1024	G1025	W1026	L1027	H1028
A1029	I1030	I1031	G1032	S1033	L1034	K1035	D1036	M1037	R1038	P1039	Q1040	G1041	W1042	C1043	L1044	S1045	D1046	T1047	Y1048	L1049	K1050	C1051	A1052	M1053	N1054	A1055	R1056	E1057	E1058	M1059	P1060	M1061	V1062	P1063	D1064	T1065	D1066	Y1067	Y1068	C1069	R1070	L1071	I1072	G1073	R1074	L1075	V1076	D1077	T1078	M1079	A1080	G1081	K1082	S1083	P1084	G1085	W1086	F1087	P1088
R369	D370	H371	L372	M373	V374	V375	L376	L377	Q378	F379	I380	S381	G382	S383	I384	Q385	K386	N387	A388	L389	A390	D391	F392	L393	P394	V395	M396	K397	L398	F399	D400	L401	Y402	Y403	P404	E405	K406	E407	Y408	I409	P410	V411	P412	D413	I414	M415	K416	P417	Q418	S419	T420	H421	A422	F423	A424	M425	T426	C427	I428
W429	I430	H431	L432	M433	R434	K435	A436	Q437	N438	D439	M440	S441	K442	L443	Q444	I445	A446	I447	P448	H449	S450	L451	R452	L453	H454	H455	E456	F457	L458	Q459	Q460	S461	L462	R463	M464	K465	S466	L467	Q468	M469	N470	D471	Y472	K473	I474	A475	L476	L477	C478	N479	A480	Y481	S482	T483	M484	S485	E486	C487	F488
T489	L490	P491	M492	G493	A494	L495	V496	E497	L498	I499	Y500	G501	N502	G503	I504	M505	R506	I507	P508	L509	P510	G511	T512	N513	C514	M515	A516	S517	G518	S519	I520	T521	L522	L523	P524	M525	N526	L527	L528	D529	S530	L531	T532	V533	H534	A535	K536	M537	S538	L539	I540	H541	S542	I543	A544	T545	E546	V547	I548
K549	L550	A551	H552	G553	K554	S555	S556	V557	A558	L559	A560	P561	A562	L563	V564	E565	T566	Y567	S568	R569	L570	L571	V572	Y573	M574	E575	I576	E577	S578	L579	G580	I581	K582	G583	F584	S585	S586	Q587	L588	L589	P590	T591	V592	F593	K594	S595	H596	A597	M598	G599	I600	L601	H602	T603	L604	L605	E606	M607	F608
S609	Y610	R611	M612	H613	H614	I615	Q616	P617	H618	Y619	R620	V621	Q622	L623	L624	S625	H626	L627	H628	T629	L630	A631	A632	V633	A634	Q635	T636	N637	Q638	N639	Q640	L641	H642	H643	C644	V645	E646	S647	T648	A649	L650	R651	L652	I653	T654	A655	L656	G657	S658	S659	E660	V661	Q662	P663	Q664	L665	F666	T667	F668
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S729	H730	I731	L732	S733	C734	F735	P736	G737	P738	L739	Q740	A741	F742	F743	K744	Q745	N746	M747	V748	P749	Q750	E751	S752	R753	F754	M755	L756	K757	K758	M759	V760	E761	E762	E763	Y764	R765	K766	M767	K768	S769	M770	S771	N772	E773	N774	D775	I776	I777	T778	H779	F780	S781	M782	Q783	G784	S785	P786	P787	L788
F789	L790	C791	L792	L793	W794	K795	M796	L797	L798	E799	T800	D801	H802	L803	N804	Q805	L806	G807	Y808	R809	V810	L811	E812	R813	L814	G815	A816	R817	A818	L819	V820	A821	H822	G823	R824	T825	F826	A827	D828	F829	L830	V831	G832	E833	F834	S835	T836	S837	A838	G839	G840	Q841	Q842	L843	N844	K845	C846	I847	E848
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P909	E910	H911	W912	L913	Q914	N915	D916	W917	H918	T919	K920	H921	N922	N923	Y924	H925	K926	K927	Y928	P929	E930	K931	L932	Y933	F934	E935	G936	L937	A938	E939	Q940	V941	D942	P943	P944	Y945	Y946	Q947	Q948	S949	P950	Y951	L952	P953	L954	Y955	F956	G957	N958	Y959	C960	L961	R962	F963	L964	P965	Y966	F967	D968
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P1158	P1158
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I1168	I1168
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S1176	S1176
L1177	L1177
T1178	T1178
S1179	S1179
E1180	E1180
T1181	T1181
E1182	E1182
M1183	M1183
V1184	V1184
G1185	G1185
Y1186	Y1186
P1187	P1187
F1188	F1188
R1189	R1189
L1190	L1190
F1191	F1191
D1192	D1192
F1193	F1193
T1194	T1194
A1195	A1195
C1196	C1196
H1197	H1197
O1198	O1198
S1199	S1199
Y1200	Y1200
S1201	S1201
E1202	E1202
M1203	M1203
S1204	S1204
C1205	C1205
S1206	S1206
Y1207	Y1207
L1208	L1208
L1209	L1209
A1210	A1210
L1211	L1211
A1212	A1212
H1213	H1213
A1214	A1214
V1215	V1215
W1216	W1216
H1217	H1217
H1218	H1218
S1219	S1219
S1220	S1220
I1221	I1221
G1222	G1222
Q1223	Q1223
L1224	L1224
S1225	S1225
L1226	L1226
I1227	I1227
K1228	K1228
P1229	P1229
K1229	K1229
V1230	V1230
L1231	L1231
T1232	T1232
E1233	E1233
V1234	V1234
L1235	L1235
L1236	L1236
P1237	P1237
I1238	I1238
V1239	V1239
K1240	K1240
T1241	T1241
E1242	E1242
F1243	F1243
Q1244	Q1244
L1245	L1245
L1246	L1246
Y1247	Y1247
D1248	D1248
Y1249	Y1249
H1250	H1250
L1251	L1251
V1252	V1252
G1253	G1253
P1254	P1254
F1255	F1255
L1256	L1256
Q1257	Q1257
R1258	R1258
F1259	F1259
Q1260	Q1260
Q1261	Q1261
E1262	E1262
R1263	R1263
T1264	T1264
R1265	R1265
C1266	C1266
M1267	M1267
L1268	L1268
E1269	E1269
I1270	I1270
G1271	G1271
V1272	V1272
A1273	A1273
F1274	F1274
Y1275	Y1275
D1276	D1276
M1277	M1277
H1278	H1278
L1279	L1279
M1280	M1280
V1281	V1281
D1282	D1282
Q1283	Q1283
C1284	C1284
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T1286	T1286
H1287	H1287
L1288	L1288
M1289	M1289
Y1290	Y1290
M1291	M1291
D1292	D1292
P1293	P1293
I1294	I1294
C1295	C1295
D1296	D1296
F1297	F1297
L1298	L1298
Y1299	Y1299
H1300	H1300
M1301	M1301
K1302	K1302
Y1303	Y1303
M1304	M1304
F1305	F1305
T1306	T1306
G1307	G1307
D1308	D1308
S1309	S1309
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K1311	K1311
E1312	E1312
V1313	V1313
Q1314	Q1314
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K1316	K1316
I1317	I1317
I1318	I1318
C1319	C1319
M1320	M1320
L1321	L1321
K1322	K1322
A1324	A1324
P1323	P1323
L1325	L1325
K1326	K1326
L1327	L1327
R1328	R1328
L1329	L1329
R1330	R1330
F1331	F1331
I1332	I1332
H1333	H1333
H1334	H1334
I1335	I1335
SER	SER
LEU	LEU
PRO	PRO
ALA	ALA
ALA	ALA
VAL	VAL
PRO	PRO
PRO	PRO
GLN	GLN
ALA	ALA
MET	MET
ASN	ASN
SER	SER
GLY	GLY
SER	SER
PRO	PRO
ALA	ALA
PRO	PRO
ALA	ALA
GLN	GLN
ASN	ASN
GLN	GLN
VAL	VAL
VAL	VAL
SER	SER
LEU	LEU
VAL	VAL
PRO	PRO
VAL	VAL
THR	THR
GLN	GLN

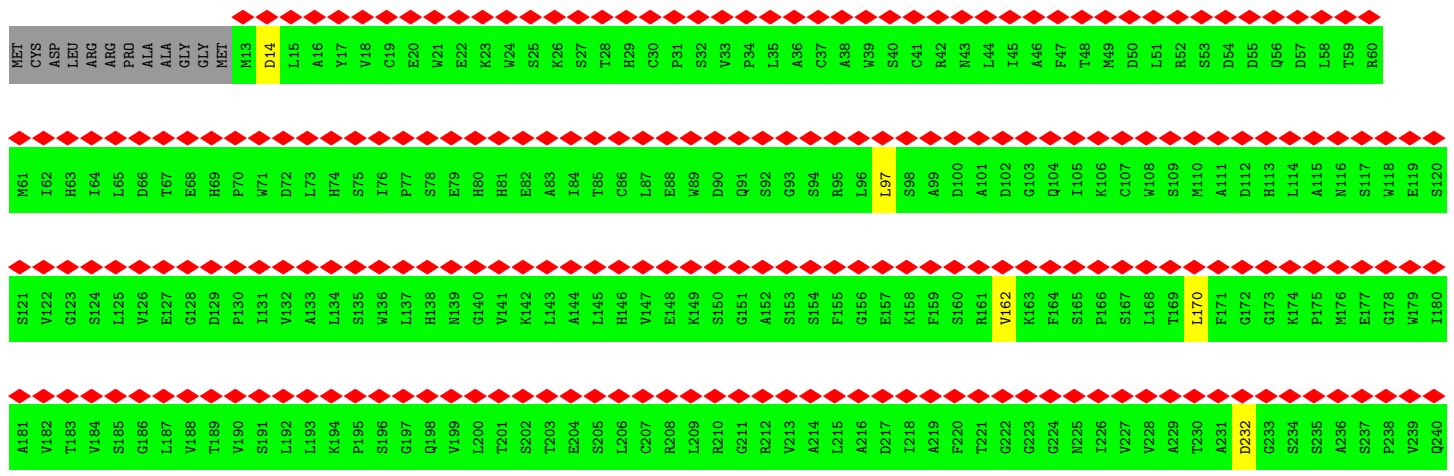
• Molecule 69: Mediator of RNA polymerase II transcription subunit 24



MET	L61
LYS	V73
VAL	S74
V4	Y75
N5	S76
L6	S77
K7	V78
Q8	L79
A9	T80
I10	A81
L11	I82
Q12	S83
K15	K84
E16	D86
R17	
W18	
S19	
A35	
T36	
W37	
D38	
I39	
L40	
N41	
L42	
A43	
G44	
A45	
E46	
L47	
L48	
E48	
Q49	
A50	
I52	
G53	
P54	
S55	
P56	
N57	
P58	
L61	
V73	
S74	
Y75	
S76	
S77	
V78	
L79	
T80	
A81	
I82	
S83	
K84	
D86	
F87	
S88	
R89	
D91	
L92	
C93	
V94	
K95	
I96	
L97	
L98	
D99	
I100	
M101	
D102	
M103	
F104	
C105	
D106	
R107	
S108	
C110	
H111	
G112	
K113	
A114	
E115	
E116	
C117	
I118	
G119	
M120	
C121	
R122	
E123	
L124	
L125	
S126	
L127	
H128	
H129	
V130	
L131	
L132	
R133	
C134	
L135	
L136	
A137	
S138	
E139	
I140	
R141	
L142	
R143	
E144	
G145	
L146	
G154	
E155	
K156	
Q157	
L158	
A159	
M160	
C161	
L162	
Q163	
R164	
L165	
E166	
K167	
T168	
L169	
S170	
T172	
K173	
N174	
R175	
A176	
L177	
L178	
H179	
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A181	
K182	
L183	
E184	
E185	
A186	
S187	
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I192	
E193	
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T211	
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E216	
Q217	
C218	
G219	
T220	
L221	
I222	
R223	
S224	
I225	
THR	
MET	
LEU	
SER	
VAL	
HIS	
GLU	
GLN	
MET	
HIS	
K238	
T239	
G240	
F241	
P242	
V243	
H244	
A246	
V247	
L248	
L249	
L250	
E251	
T253	
N254	
N255	
L256	
T257	
G258	
E259	
T260	
Q261	
S262	
L263	
V264	
E265	
Q266	
L267	
M268	
E269	
T270	
T331	
E332	
V334	
N335	
C336	
A337	
F338	
E339	
F340	
L341	
L342	
K343	
L344	
T345	
F346	
L347	
L348	
D349	
K350	
A351	
D352	
Q353	
R354	
C355	
N356	
C357	
D358	
C359	
T360	
N361	
F362	
L363	
L364	
Q365	
E366	
E367	
G368	
Q370	
G371	
L372	
L373	
S374	
E375	
A376	
S377	
V378	
N379	
N380	
L381	
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A383	
K384	
R385	
K386	
A387	
R388	
E390	
H391	
ALA	
PRO	
GLN	
GLN	
LYS	
SER	
GLY	
GLU	
ASN	
ALA	
M402	
I403	
Q404	
P405	
M406	
I407	
Q408	
L409	
L410	
L411	
R412	
A413	
E414	
P415	
T416	
V417	
T418	
N419	
D420	
L421	
K422	
T423	
M424	
D425	
A426	
D427	
H428	
S429	
K430	
S431	
P432	
E433	
G434	
L435	
L436	
G437	
V438	
L439	
G440	
H441	
M442	
L443	
S444	
G445	
K446	
S447	
L448	
M449	
L500	
C501	
H502	
V503	
A504	
Q505	
T506	
HIS	
GLY	



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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	67732	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)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	7.867	Depositor
Minimum map value	-3.734	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.101	Depositor
Recommended contour level	0.41	Depositor
Map size (\AA)	674.39996, 674.39996, 674.39996	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.405, 1.405, 1.405	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: SF4, MG, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a	0.65	0/3645	0.77	1/4952 (0.0%)
2	m	0.27	0/1010	0.37	0/1359
3	d	0.64	0/1277	0.82	0/1714
4	f	0.54	0/1359	0.70	2/1845 (0.1%)
5	g	0.61	0/1411	0.80	0/1901
6	h	0.62	0/1507	0.75	0/2036
7	r	0.61	0/1558	0.73	0/2096
8	t	0.69	0/1530	0.90	0/2066
9	j	0.41	0/1016	0.73	8/1363 (0.6%)
10	k	0.65	0/885	0.60	0/1190
11	n	0.36	0/7371	0.56	18/10037 (0.2%)
12	q	0.48	1/4336 (0.0%)	0.57	4/5865 (0.1%)
13	s	0.54	0/489	0.83	5/663 (0.8%)
14	u	0.48	0/797	0.72	1/1082 (0.1%)
15	v	0.67	0/1092	0.86	0/1468
16	z	0.62	0/781	0.81	0/1067
17	c	0.40	0/2106	0.53	1/2842 (0.0%)
18	e	0.26	0/840	0.36	0/1128
19	b	0.51	0/911	0.62	0/1229
20	l	0.26	0/1048	0.41	0/1405
21	o	0.35	0/1256	0.60	0/1724
22	i	0.66	0/523	0.67	0/692
23	0	0.66	0/2288	0.69	4/3101 (0.1%)
24	8	0.62	0/2437	0.63	0/3306
25	9	0.63	0/2356	0.63	0/3185
26	1	0.72	0/2674	0.66	6/3660 (0.2%)
27	2	0.65	0/2588	0.63	2/3509 (0.1%)
28	3	0.64	0/2102	0.61	0/2844
29	4	0.63	0/3663	0.62	0/4965
30	5	0.64	0/433	0.62	0/585
31	6	0.63	0/4983	0.62	0/6731
32	7	0.63	0/5957	0.62	2/8071 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	EA	0.62	0/1499	0.63	0/2012
34	EB	0.64	0/1428	0.63	0/1917
35	DA	0.62	0/4627	0.63	1/6248 (0.0%)
36	DB	0.63	0/7993	0.61	0/10836
37	DD	0.62	0/1343	0.64	1/1795 (0.1%)
37	Dd	0.63	0/1321	0.58	0/1772
38	DE	0.64	0/4469	0.64	0/6050
38	De	0.64	0/4433	0.63	0/6004
39	DF	0.65	0/3167	0.65	0/4303
39	Df	0.65	0/3140	0.63	0/4268
40	DG	0.62	0/1199	0.61	0/1612
41	DH	0.64	0/1673	0.62	0/2285
42	DI	0.62	0/981	0.63	0/1332
42	Di	0.61	0/989	0.60	0/1343
43	DJ	0.62	0/736	0.63	1/998 (0.1%)
43	Dj	0.62	0/775	0.62	0/1049
44	DL	0.63	0/622	0.72	3/841 (0.4%)
44	DI	0.63	0/888	0.69	3/1194 (0.3%)
45	Dc	0.64	0/1035	0.61	0/1406
46	Dk	0.64	0/799	0.59	0/1070
47	Dm	0.63	0/733	0.61	0/977
48	DO	0.65	0/781	0.64	0/1061
49	DP	0.64	0/1438	0.61	0/1935
50	DQ	0.64	0/1013	0.62	0/1366
51	BA	0.65	0/1967	0.62	0/2656
52	FB	0.63	0/1817	0.62	0/2445
53	X	1.14	21/1607 (1.3%)	0.98	1/2481 (0.0%)
54	Y	0.97	11/1565 (0.7%)	1.02	9/2410 (0.4%)
55	PA	0.64	0/11881	0.65	0/16057
56	PB	0.64	0/9243	0.62	0/12475
57	PC	0.63	0/2102	0.62	0/2857
58	PD	0.64	0/1036	0.60	0/1397
59	PE	0.62	0/1751	0.62	0/2366
60	PF	0.63	0/645	0.63	0/871
61	PG	0.65	0/1365	0.64	0/1853
62	PH	0.64	0/1207	0.63	0/1628
63	PI	0.64	0/948	0.63	0/1284
64	PJ	0.63	0/516	0.63	0/696
65	PK	0.62	0/956	0.60	0/1294
66	PL	0.64	0/377	0.60	0/500
67	FA	0.61	0/1130	0.60	0/1528
68	w	0.58	0/11053	0.62	1/15018 (0.0%)
69	x	0.59	0/7179	0.65	6/9712 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
70	p	0.71	0/3191	0.73	4/4333 (0.1%)
All	All	0.62	33/174847 (0.0%)	0.65	84/237216 (0.0%)

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	X	-39	DA	O3'-P	-16.78	1.41	1.61
53	X	-37	DG	C1'-N9	-7.92	1.36	1.47
53	X	-9	DG	C1'-N9	-7.91	1.36	1.47
53	X	-26	DA	C1'-N9	-7.85	1.36	1.47
53	X	-19	DG	C1'-N9	-7.51	1.36	1.47

The worst 5 of 84 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	j	77	PRO	CA-N-CD	-8.98	98.92	111.50
69	x	485	PRO	CA-N-CD	-8.43	99.70	111.50
69	x	54	PRO	N-CA-CB	-8.18	93.49	103.30
54	Y	-6	DG	P-O3'-C3'	8.13	129.46	119.70
11	n	1355	PRO	N-CA-CB	6.84	111.51	103.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	a	457/1581 (29%)	421 (92%)	29 (6%)	7 (2%)	10	46
2	m	110/131 (84%)	106 (96%)	4 (4%)	0	100	100
3	d	154/270 (57%)	143 (93%)	6 (4%)	5 (3%)	4	30
4	f	163/246 (66%)	142 (87%)	15 (9%)	6 (4%)	3	28
5	g	164/233 (70%)	145 (88%)	10 (6%)	9 (6%)	2	21
6	h	188/268 (70%)	167 (89%)	12 (6%)	9 (5%)	2	23
7	r	189/208 (91%)	176 (93%)	10 (5%)	3 (2%)	9	44
8	t	189/212 (89%)	166 (88%)	15 (8%)	8 (4%)	3	25
9	j	120/135 (89%)	110 (92%)	6 (5%)	4 (3%)	4	30
10	k	110/117 (94%)	99 (90%)	9 (8%)	2 (2%)	8	41
11	n	980/1454 (67%)	877 (90%)	86 (9%)	17 (2%)	9	43
12	q	540/651 (83%)	474 (88%)	53 (10%)	13 (2%)	6	36
13	s	69/244 (28%)	60 (87%)	7 (10%)	2 (3%)	4	32
14	u	103/144 (72%)	93 (90%)	8 (8%)	2 (2%)	8	40
15	v	132/200 (66%)	119 (90%)	10 (8%)	3 (2%)	6	37
16	z	93/600 (16%)	84 (90%)	7 (8%)	2 (2%)	6	37
17	c	245/311 (79%)	232 (95%)	13 (5%)	0	100	100
18	e	98/178 (55%)	92 (94%)	4 (4%)	2 (2%)	7	40
19	b	111/200 (56%)	109 (98%)	1 (1%)	1 (1%)	17	55
20	l	120/178 (67%)	115 (96%)	5 (4%)	0	100	100
21	o	152/788 (19%)	138 (91%)	10 (7%)	4 (3%)	5	34
22	i	56/146 (38%)	54 (96%)	1 (2%)	1 (2%)	8	41
23	0	304/309 (98%)	285 (94%)	15 (5%)	4 (1%)	12	48
24	8	297/346 (86%)	290 (98%)	7 (2%)	0	100	100
25	9	285/323 (88%)	279 (98%)	6 (2%)	0	100	100
26	1	399/548 (73%)	336 (84%)	53 (13%)	10 (2%)	5	35
27	2	327/395 (83%)	315 (96%)	10 (3%)	2 (1%)	25	64
28	3	259/308 (84%)	257 (99%)	2 (1%)	0	100	100
29	4	447/462 (97%)	431 (96%)	12 (3%)	4 (1%)	17	55
30	5	52/71 (73%)	50 (96%)	2 (4%)	0	100	100
31	6	602/782 (77%)	585 (97%)	14 (2%)	3 (0%)	29	67
32	7	732/760 (96%)	704 (96%)	23 (3%)	5 (1%)	22	61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	EA	175/439 (40%)	163 (93%)	12 (7%)	0	100	100
34	EB	170/291 (58%)	161 (95%)	4 (2%)	5 (3%)	4	32
35	DA	534/1872 (28%)	523 (98%)	9 (2%)	2 (0%)	34	71
36	DB	959/1199 (80%)	932 (97%)	25 (3%)	2 (0%)	47	80
37	DD	153/1085 (14%)	148 (97%)	4 (3%)	1 (1%)	22	61
37	Dd	154/1085 (14%)	152 (99%)	2 (1%)	0	100	100
38	DE	540/800 (68%)	524 (97%)	16 (3%)	0	100	100
38	De	531/800 (66%)	514 (97%)	16 (3%)	1 (0%)	47	80
39	DF	404/677 (60%)	393 (97%)	9 (2%)	2 (0%)	29	67
39	Df	399/677 (59%)	394 (99%)	4 (1%)	1 (0%)	41	76
40	DG	139/349 (40%)	137 (99%)	2 (1%)	0	100	100
41	DH	207/310 (67%)	199 (96%)	5 (2%)	3 (1%)	11	46
42	DI	118/264 (45%)	116 (98%)	1 (1%)	1 (1%)	19	59
42	Di	119/264 (45%)	118 (99%)	1 (1%)	0	100	100
43	DJ	86/218 (39%)	84 (98%)	2 (2%)	0	100	100
43	Dj	91/218 (42%)	90 (99%)	1 (1%)	0	100	100
44	DL	73/161 (45%)	68 (93%)	2 (3%)	3 (4%)	3	25
44	Dl	105/161 (65%)	104 (99%)	0	1 (1%)	15	53
45	Dc	125/929 (14%)	122 (98%)	1 (1%)	2 (2%)	9	44
46	Dk	96/211 (46%)	93 (97%)	3 (3%)	0	100	100
47	Dm	85/124 (68%)	82 (96%)	3 (4%)	0	100	100
48	DO	95/109 (87%)	91 (96%)	2 (2%)	2 (2%)	7	38
49	DP	175/339 (52%)	170 (97%)	4 (2%)	1 (1%)	25	64
50	DQ	118/307 (38%)	115 (98%)	2 (2%)	1 (1%)	19	59
51	BA	247/316 (78%)	244 (99%)	3 (1%)	0	100	100
52	FB	218/249 (88%)	210 (96%)	7 (3%)	1 (0%)	29	67
55	PA	1460/1970 (74%)	1415 (97%)	38 (3%)	7 (0%)	29	67
56	PB	1128/1174 (96%)	1104 (98%)	22 (2%)	2 (0%)	47	80
57	PC	253/275 (92%)	252 (100%)	1 (0%)	0	100	100
58	PD	127/142 (89%)	127 (100%)	0	0	100	100
59	PE	207/210 (99%)	204 (99%)	2 (1%)	1 (0%)	29	67

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
60	PF	77/127 (61%)	76 (99%)	0	1 (1%)	12	48
61	PG	169/172 (98%)	165 (98%)	4 (2%)	0	100	100
62	PH	146/150 (97%)	144 (99%)	2 (1%)	0	100	100
63	PI	112/125 (90%)	111 (99%)	1 (1%)	0	100	100
64	PJ	62/67 (92%)	61 (98%)	1 (2%)	0	100	100
65	PK	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
66	PL	42/58 (72%)	42 (100%)	0	0	100	100
67	FA	130/517 (25%)	126 (97%)	4 (3%)	0	100	100
68	w	1332/1368 (97%)	1261 (95%)	65 (5%)	6 (0%)	29	67
69	x	876/989 (89%)	820 (94%)	51 (6%)	5 (1%)	25	64
70	p	400/841 (48%)	367 (92%)	32 (8%)	1 (0%)	41	76
All	All	20999/34555 (61%)	19990 (95%)	829 (4%)	180 (1%)	21	55

5 of 180 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	a	67	LYS
1	a	331	GLU
4	f	25	ASN
4	f	35	GLU
4	f	36	ARG

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	a	387/1391 (28%)	322 (83%)	65 (17%)	2	13
2	m	102/115 (89%)	102 (100%)	0	100	100
3	d	138/230 (60%)	100 (72%)	38 (28%)	0	3
4	f	144/223 (65%)	126 (88%)	18 (12%)	4	22
5	g	157/215 (73%)	122 (78%)	35 (22%)	1	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	h	168/225 (75%)	128 (76%)	40 (24%)	0	5
7	r	168/183 (92%)	133 (79%)	35 (21%)	1	7
8	t	166/178 (93%)	137 (82%)	29 (18%)	2	12
9	j	113/124 (91%)	109 (96%)	4 (4%)	36	60
10	k	94/98 (96%)	51 (54%)	43 (46%)	0	0
11	n	689/1272 (54%)	651 (94%)	38 (6%)	21	49
12	q	461/577 (80%)	391 (85%)	70 (15%)	3	17
13	s	31/208 (15%)	29 (94%)	2 (6%)	17	44
14	u	78/119 (66%)	67 (86%)	11 (14%)	3	19
15	v	122/173 (70%)	91 (75%)	31 (25%)	0	4
16	z	89/512 (17%)	76 (85%)	13 (15%)	3	18
17	c	231/280 (82%)	223 (96%)	8 (4%)	36	60
18	e	94/152 (62%)	94 (100%)	0	100	100
19	b	102/163 (63%)	92 (90%)	10 (10%)	8	29
20	l	116/155 (75%)	116 (100%)	0	100	100
21	o	141/697 (20%)	141 (100%)	0	100	100
22	i	61/133 (46%)	43 (70%)	18 (30%)	0	2
23	0	209/283 (74%)	193 (92%)	16 (8%)	13	39
24	8	259/299 (87%)	225 (87%)	34 (13%)	4	21
25	9	252/296 (85%)	221 (88%)	31 (12%)	4	22
26	1	176/484 (36%)	163 (93%)	13 (7%)	13	40
27	2	279/352 (79%)	257 (92%)	22 (8%)	12	38
28	3	234/272 (86%)	221 (94%)	13 (6%)	21	48
29	4	387/399 (97%)	366 (95%)	21 (5%)	22	49
30	5	48/64 (75%)	43 (90%)	5 (10%)	7	27
31	6	533/688 (78%)	488 (92%)	45 (8%)	11	36
32	7	616/664 (93%)	571 (93%)	45 (7%)	14	41
33	EA	163/373 (44%)	151 (93%)	12 (7%)	13	40
34	EB	155/261 (59%)	143 (92%)	12 (8%)	13	39
35	DA	488/1665 (29%)	449 (92%)	39 (8%)	12	38
36	DB	876/1083 (81%)	798 (91%)	78 (9%)	9	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	DD	144/815 (18%)	138 (96%)	6 (4%)	30	55
37	Dd	146/815 (18%)	138 (94%)	8 (6%)	21	49
38	DE	478/657 (73%)	433 (91%)	45 (9%)	8	30
38	De	475/657 (72%)	424 (89%)	51 (11%)	6	26
39	DF	324/574 (56%)	298 (92%)	26 (8%)	12	38
39	Df	322/574 (56%)	309 (96%)	13 (4%)	31	57
40	DG	133/322 (41%)	117 (88%)	16 (12%)	5	23
41	DH	181/270 (67%)	167 (92%)	14 (8%)	13	39
42	DI	106/235 (45%)	102 (96%)	4 (4%)	33	58
42	Di	107/235 (46%)	103 (96%)	4 (4%)	34	59
43	DJ	79/154 (51%)	76 (96%)	3 (4%)	33	58
43	Dj	83/154 (54%)	80 (96%)	3 (4%)	35	60
44	DL	70/141 (50%)	67 (96%)	3 (4%)	29	55
44	DI	98/141 (70%)	94 (96%)	4 (4%)	30	56
45	Dc	113/833 (14%)	106 (94%)	7 (6%)	18	45
46	Dk	87/182 (48%)	83 (95%)	4 (5%)	27	53
47	Dm	80/106 (76%)	73 (91%)	7 (9%)	10	34
48	DO	84/98 (86%)	80 (95%)	4 (5%)	25	52
49	DP	153/293 (52%)	144 (94%)	9 (6%)	19	47
50	DQ	111/269 (41%)	108 (97%)	3 (3%)	44	66
51	BA	214/268 (80%)	199 (93%)	15 (7%)	15	42
52	FB	196/218 (90%)	177 (90%)	19 (10%)	8	29
55	PA	1303/1748 (74%)	1167 (90%)	136 (10%)	7	27
56	PB	993/1027 (97%)	899 (90%)	94 (10%)	8	30
57	PC	234/252 (93%)	218 (93%)	16 (7%)	16	43
58	PD	108/126 (86%)	92 (85%)	16 (15%)	3	17
59	PE	191/192 (100%)	177 (93%)	14 (7%)	14	41
60	PF	69/111 (62%)	62 (90%)	7 (10%)	7	28
61	PG	147/153 (96%)	124 (84%)	23 (16%)	2	16
62	PH	129/131 (98%)	119 (92%)	10 (8%)	12	38
63	PI	103/112 (92%)	96 (93%)	7 (7%)	16	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
64	PJ	53/56 (95%)	52 (98%)	1 (2%)	57	74
65	PK	106/106 (100%)	101 (95%)	5 (5%)	26	53
66	PL	41/55 (74%)	39 (95%)	2 (5%)	25	52
67	FA	117/448 (26%)	115 (98%)	2 (2%)	60	78
68	w	1202/1232 (98%)	1181 (98%)	21 (2%)	60	78
69	x	787/864 (91%)	769 (98%)	18 (2%)	50	70
70	p	353/736 (48%)	346 (98%)	7 (2%)	55	73
All	All	18247/29966 (61%)	16706 (92%)	1541 (8%)	14	36

5 of 1541 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	DE	567	VAL
52	FB	94	THR
39	DF	136	LEU
38	DE	562	SER
38	De	450	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 353 such sidechains are listed below:

Mol	Chain	Res	Type
38	De	668	HIS
56	PB	639	HIS
42	Di	81	GLN
55	PA	22	GLN
57	PC	83	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 17 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
72	SF4	7	1000	32	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
72	SF4	7	1000	32	-	-	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

There are no chain breaks in this entry.

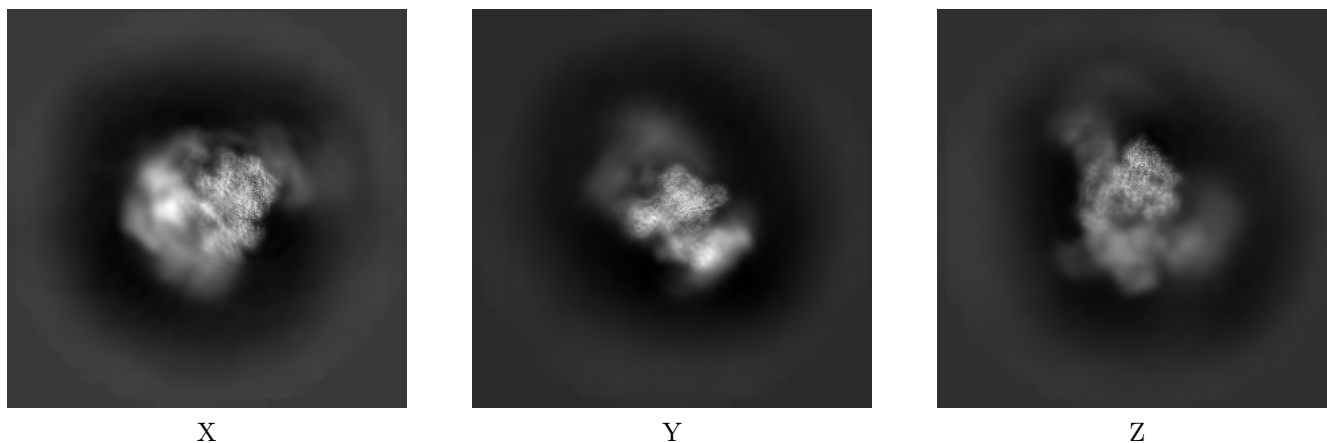
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31207. 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](#)

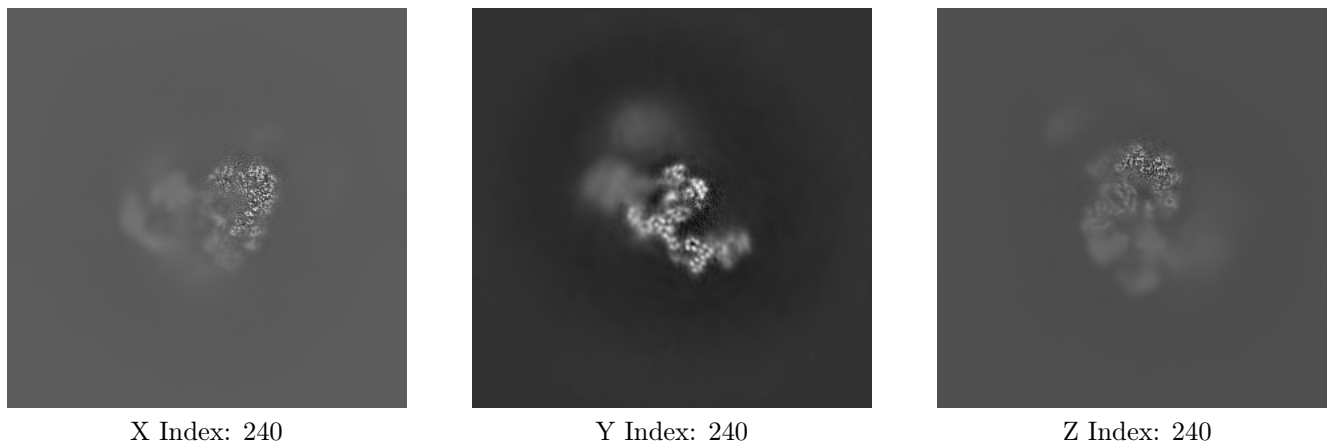
6.1.1 Primary map



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

6.2 Central slices [i](#)

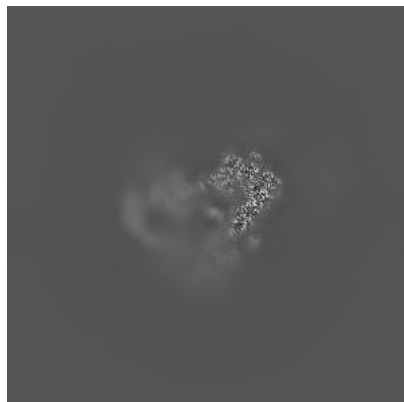
6.2.1 Primary map



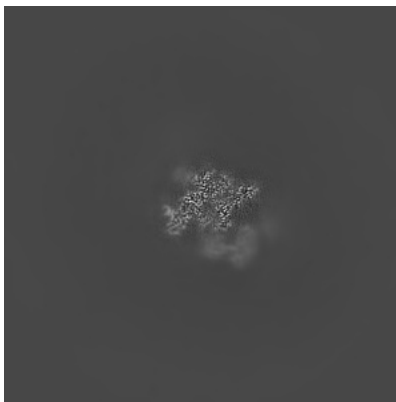
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

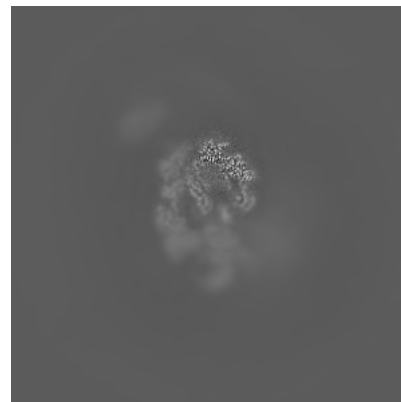
6.3.1 Primary map



X Index: 246



Y Index: 287

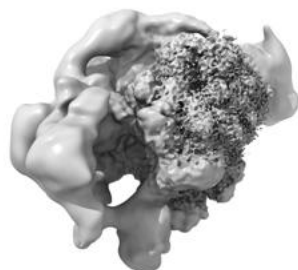


Z Index: 247

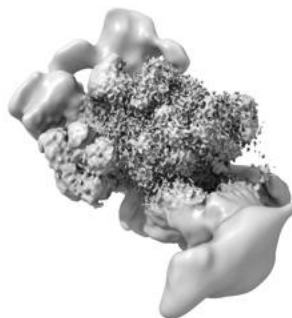
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.41. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

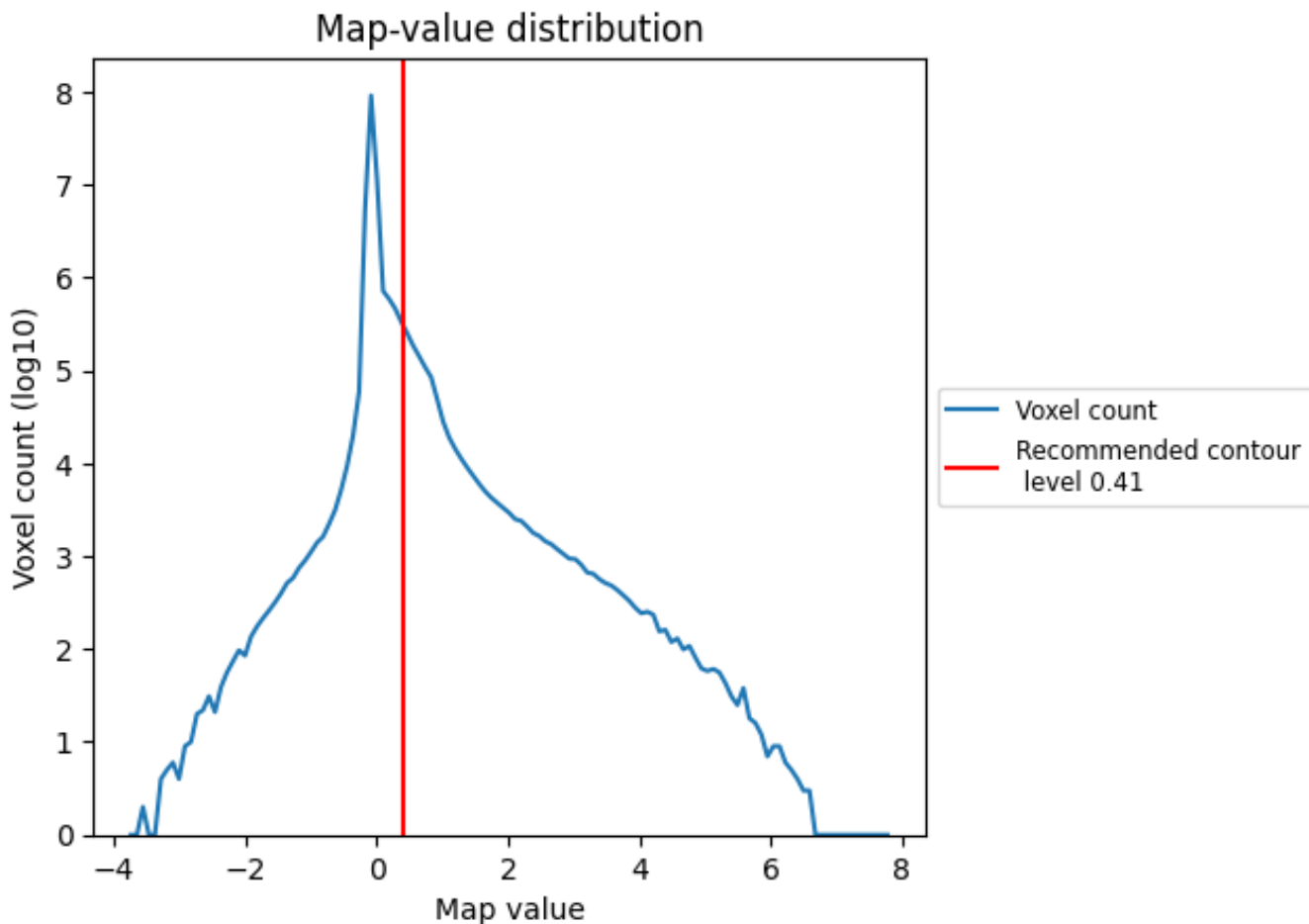
6.5 Mask visualisation

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

7 Map analysis [i](#)

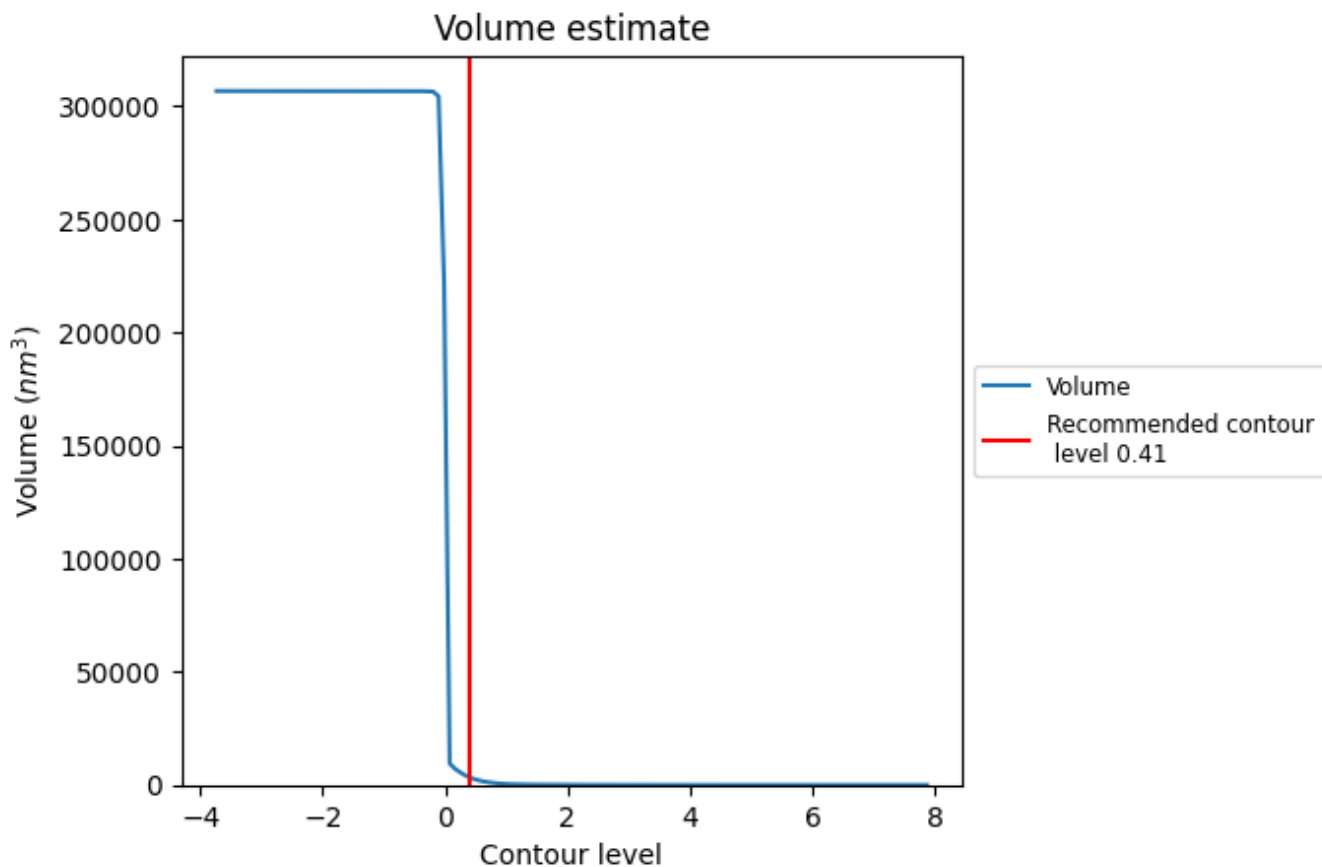
This section contains the results of statistical analysis of the map.

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.

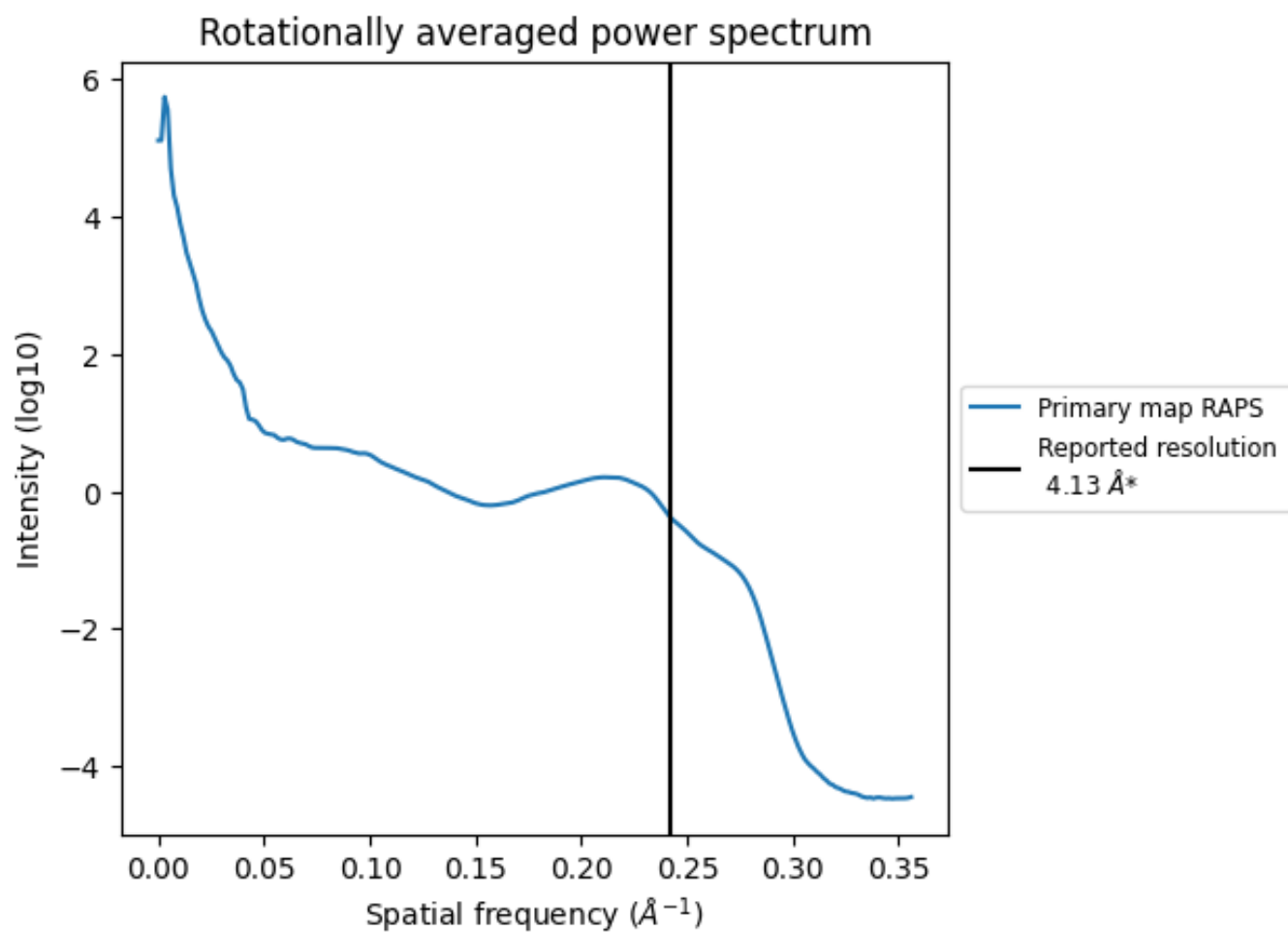
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3240 nm³; this corresponds to an approximate mass of 2927 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.242 Å⁻¹

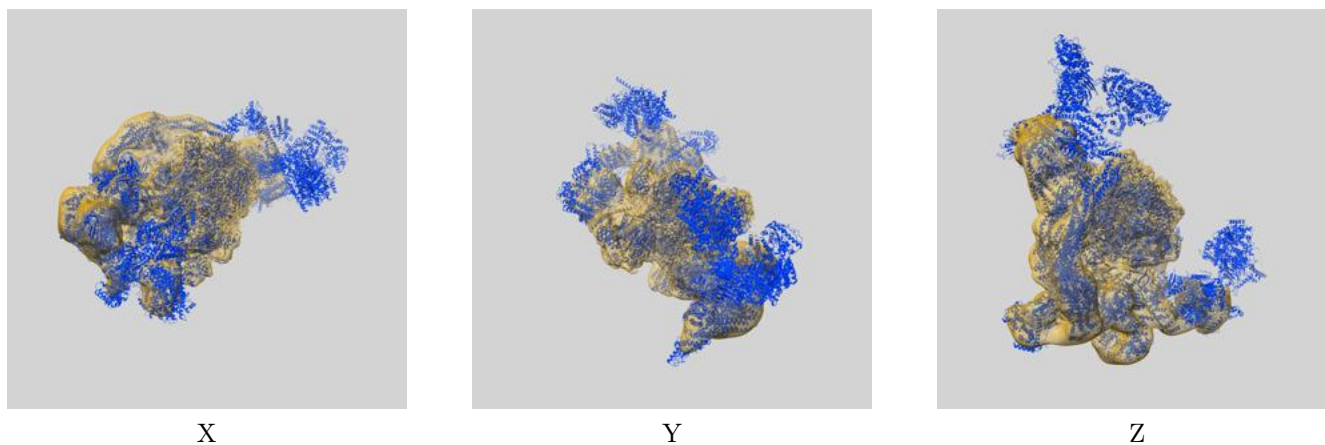
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

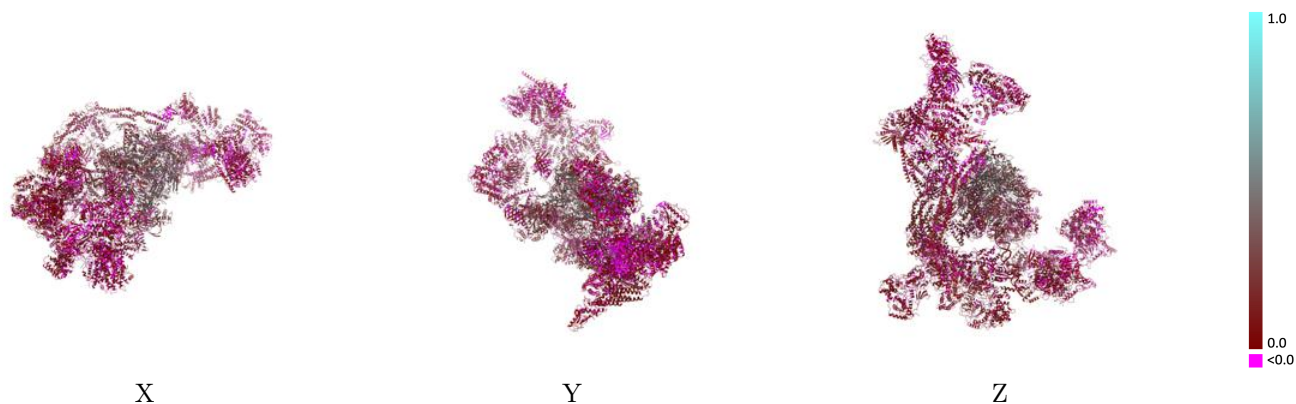
This section contains information regarding the fit between EMDB map EMD-31207 and PDB model 7ENC. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)



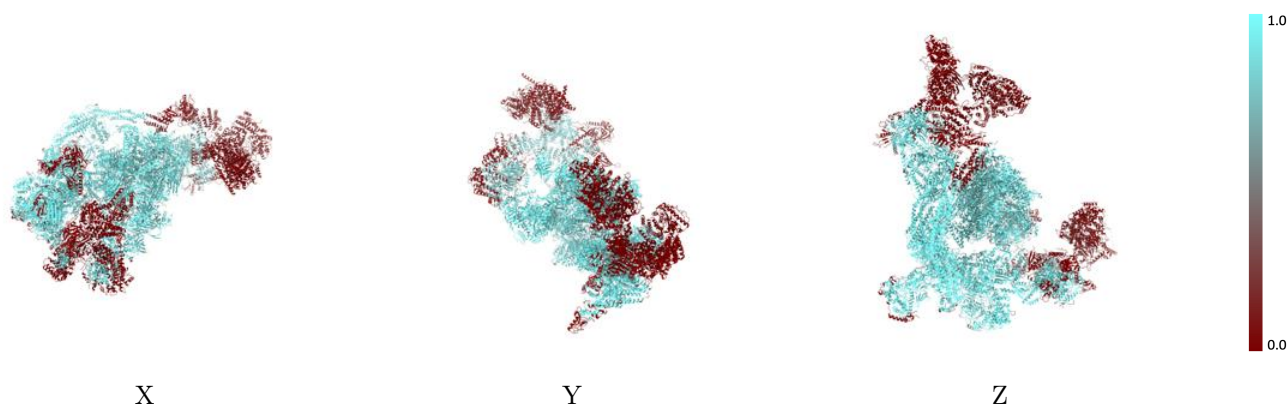
The images above show the 3D surface view of the map at the recommended contour level 0.41 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



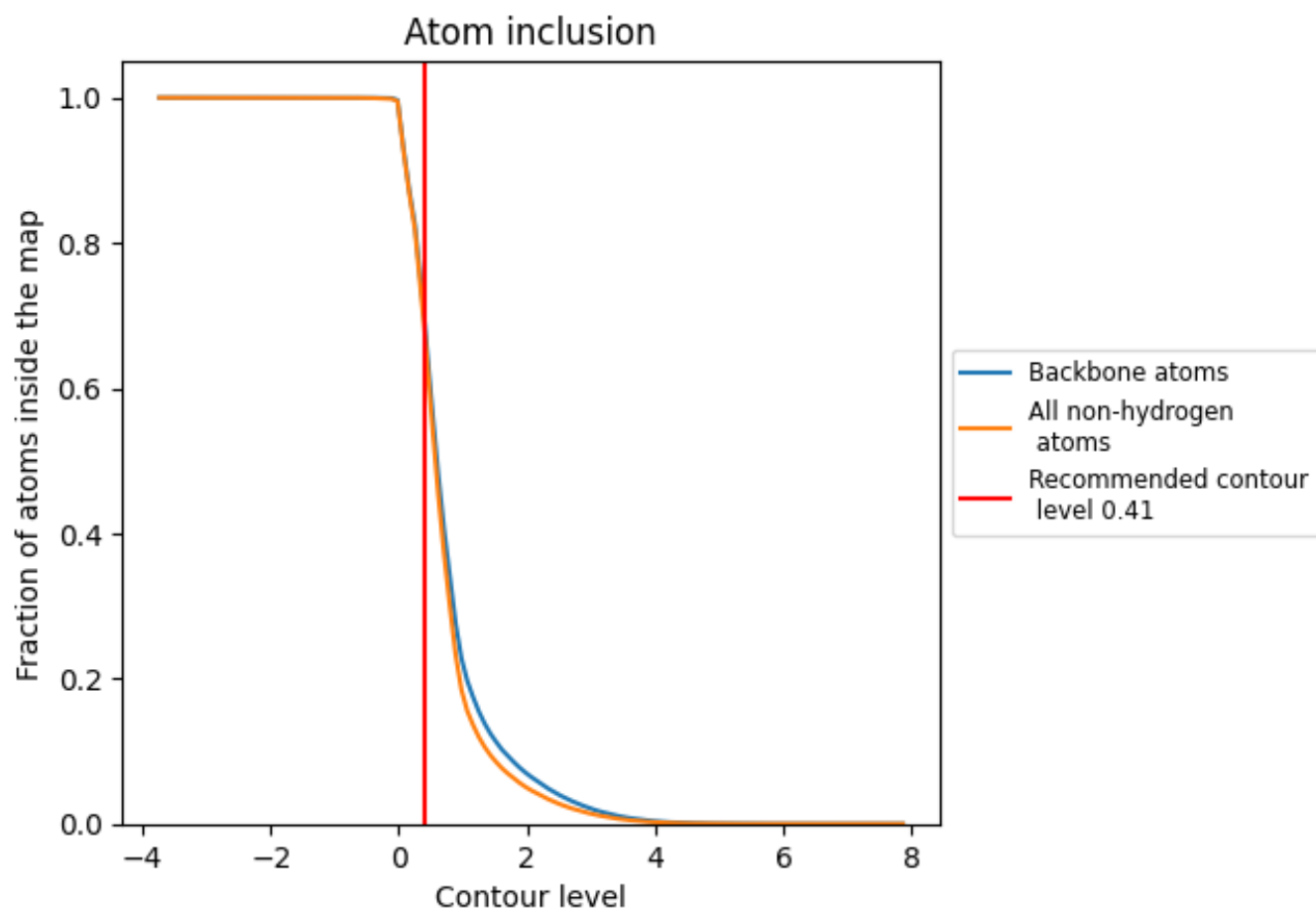
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.41).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 67% 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 (0.41) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6727	 0.1030
0	 0.8867	 0.0830
1	 0.8998	 0.0380
2	 0.9832	 0.0690
3	 0.9745	 0.0630
4	 0.9620	 0.0740
5	 0.9788	 0.0560
6	 0.9801	 0.0700
7	 0.9842	 0.0970
8	 0.9410	 0.0760
9	 0.7294	 0.0650
BA	 0.9130	 0.2020
DA	 0.2539	 0.0410
DB	 0.8243	 0.0560
DD	 0.6079	 0.0580
DE	 0.6887	 0.0520
DF	 0.5059	 0.0580
DG	 0.0200	 0.0240
DH	 0.6951	 0.0550
DI	 0.5241	 0.0260
DJ	 0.5819	 0.0500
DL	 0.0281	 0.0310
DO	 0.9353	 0.1010
DP	 0.9673	 0.1650
DQ	 0.8707	 0.0990
Dc	 0.0000	 0.0330
Dd	 0.0000	 0.0140
De	 0.0000	 0.0180
Df	 0.2937	 0.0470
Di	 0.0000	 0.0440
Dj	 0.0000	 0.0320
Dk	 0.0000	 -0.0020
Dl	 0.0000	 0.0200
Dm	 0.0000	 0.0190
EA	 0.9798	 0.1020



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Chain	Atom inclusion	Q-score
EB	 0.9870	 0.1230
FA	 0.9479	 0.0680
FB	 0.9521	 0.1150
PA	 0.9234	 0.2390
PB	 0.9390	 0.3370
PC	 0.9301	 0.3250
PD	 0.9373	 0.1590
PE	 0.9559	 0.2170
PF	 0.8880	 0.2560
PG	 0.9483	 0.1770
PH	 0.9241	 0.3110
PI	 0.9262	 0.1450
PJ	 0.9091	 0.3050
PK	 0.8805	 0.2840
PL	 0.9185	 0.2750
X	 0.9986	 0.1760
Y	 0.9950	 0.2000
a	 0.0028	 0.0340
b	 0.5512	 0.0380
c	 0.8450	 0.0550
d	 0.7480	 0.0840
e	 0.9597	 0.0930
f	 0.9869	 0.1340
g	 0.9808	 0.1050
h	 0.9870	 0.1610
i	 0.5010	 0.0850
j	 0.9189	 0.0640
k	 0.9556	 0.1540
l	 0.9171	 0.0710
m	 0.9990	 0.0910
n	 0.8740	 0.0690
o	 0.6689	 0.0440
p	 0.0000	 -0.0260
q	 0.9874	 0.0940
r	 0.9753	 0.0870
s	 0.9042	 0.0620
t	 0.9283	 0.0540
u	 0.9923	 0.0930
v	 0.9887	 0.1300
w	 0.0109	 0.0280
x	 0.0360	 0.0360
z	 0.8983	 0.0450