wwPDB EM Validation Summary Report

Oct 6, 2024 – 05:48 AM 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:

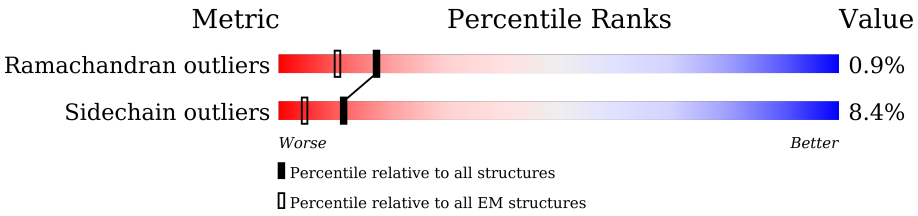
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance (i)

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	207382	16835
Sidechain outliers	206894	16415

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 <=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	30%, 25%, 5%, 70%
2	m	131	85%, 15%
3	d	270	14%, 43%, 16%, 41%
4	f	246	58%, 9%, 32%
5	g	233	53%, 17%, 29%
6	h	268	54%, 16%, 29%
7	r	208	74%, 18%, 8%
8	t	212	74%, 17%, 9%
9	j	135	7%, 79%, 10%, 10%

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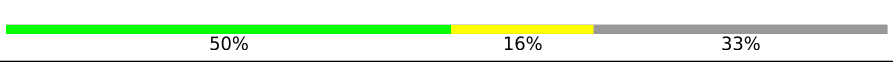
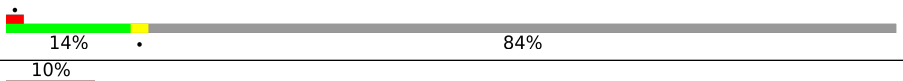
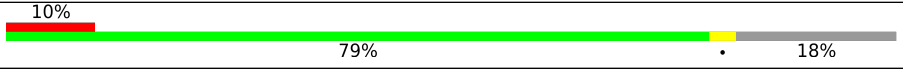
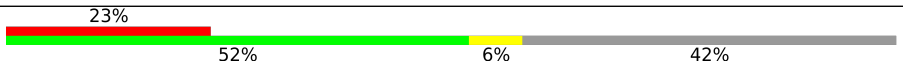
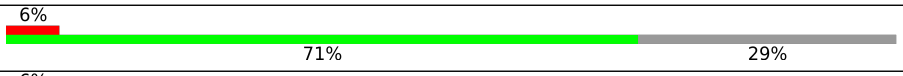
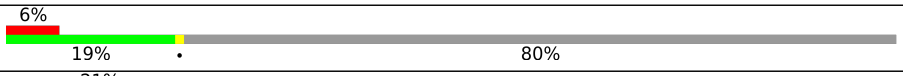
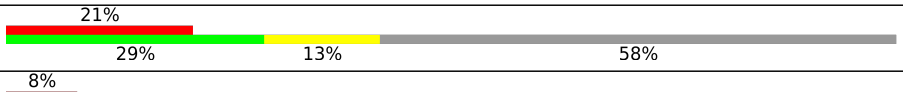
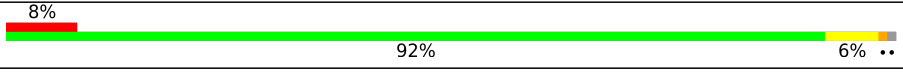
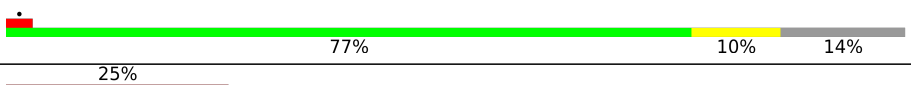
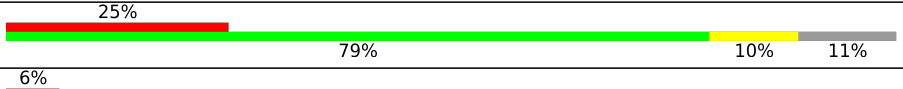
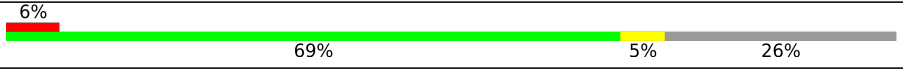
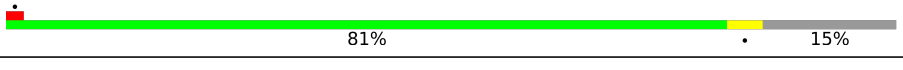
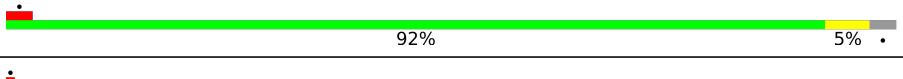
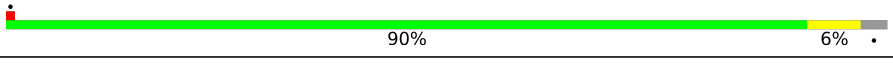
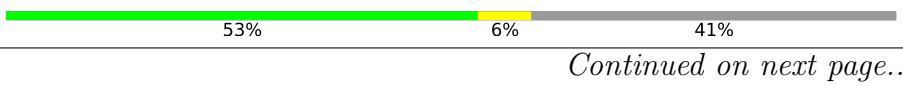
Mol	Chain	Length	Quality of chain
10	k	117	
11	n	1454	
12	q	651	
13	s	244	
14	u	144	
15	v	200	
16	z	600	
17	c	311	
18	e	178	
19	b	200	
20	l	178	
21	o	788	
22	i	146	
23	0	309	
24	8	346	
25	9	323	
26	1	548	
27	2	395	
28	3	308	
29	4	462	
30	5	71	
31	6	782	
32	7	760	
33	EA	439	
34	EB	291	

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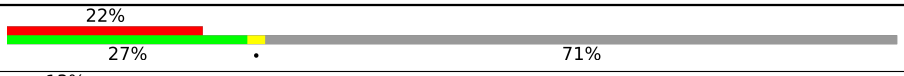
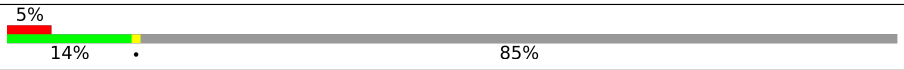
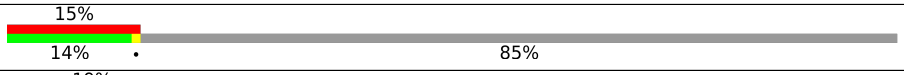
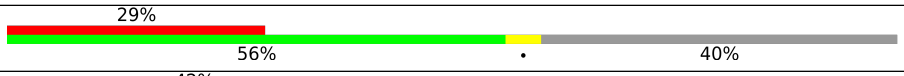
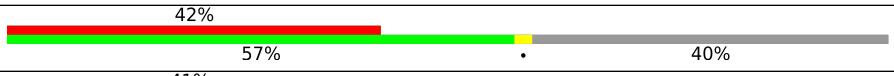
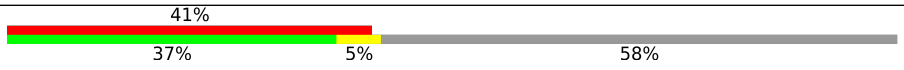
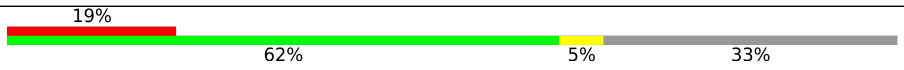
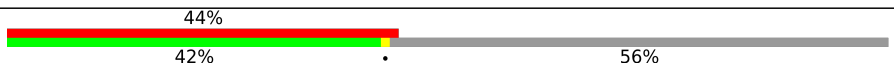
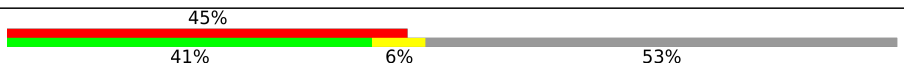
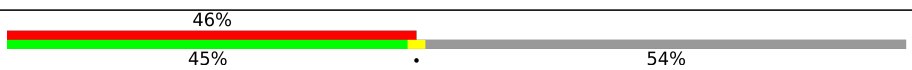
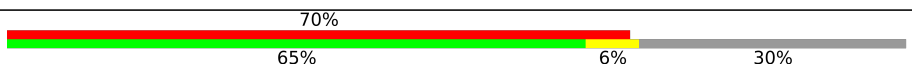
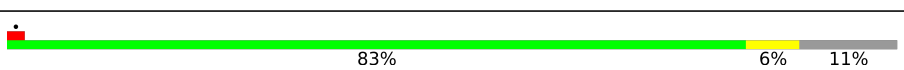
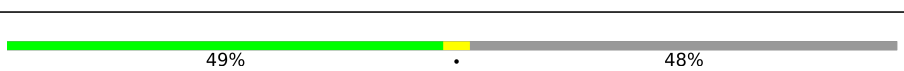
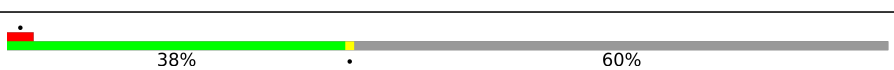
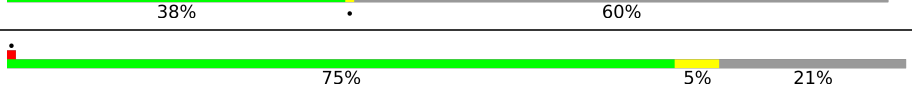
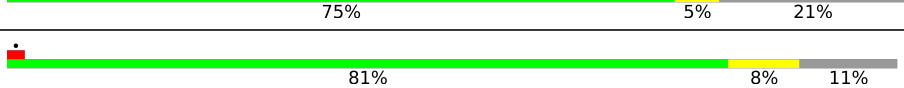
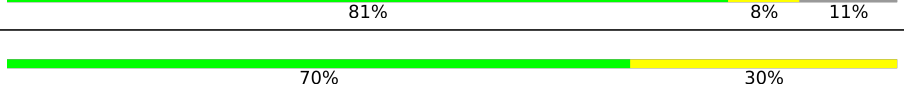
Mol	Chain	Length	Quality of chain
35	DA	1872	
36	DB	1199	
37	DD	1085	
37	Dd	1085	
38	DE	800	
38	De	800	
39	DF	677	
39	Df	677	
40	DG	349	
41	DH	310	
42	DI	264	
42	Di	264	
43	DJ	218	
43	Dj	218	
44	DL	161	
44	Dl	161	
45	Dc	929	
46	Dk	211	
47	Dm	124	
48	DO	109	
49	DP	339	
50	DQ	307	
51	BA	316	
52	FB	249	
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% 96%
69	x	989	87% 88% 9%
70	p	841	48% 47% 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
6	h	190	Total	C	N	O	S	0	0
			1486	925	262	295	4		

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

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

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

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

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

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

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

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

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

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

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
12	q	552	Total	C	N	O	S	0	0
			4261	2691	764	789	17		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 25 is a protein called Cyclin-H.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 50 is a protein called TFIIA-a.

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

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

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

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

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

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

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

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

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

- Molecule 55 is a protein called RPB1.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 64 is a protein called RPB10.

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

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

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

- 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	

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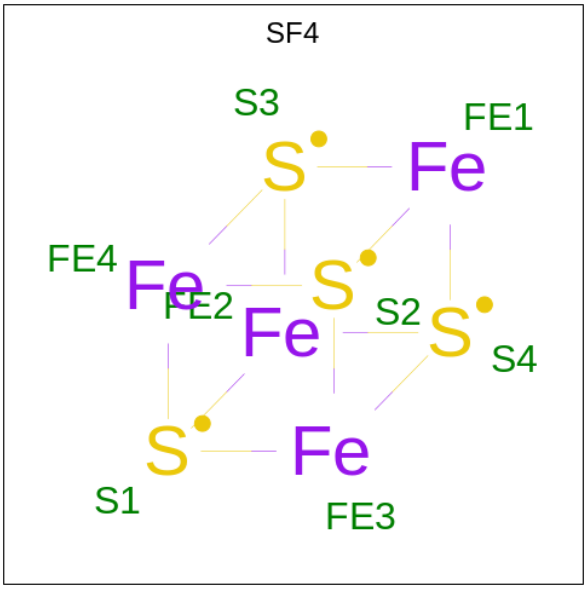
Mol	Chain	Residues	Atoms	AltConf
71	PB	1	Total Zn 1 1	0
71	PC	1	Total Zn 1 1	0
71	PI	2	Total Zn 2 2	0
71	PJ	1	Total Zn 1 1	0
71	PL	1	Total Zn 1 1	0

- Molecule 72 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).



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

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

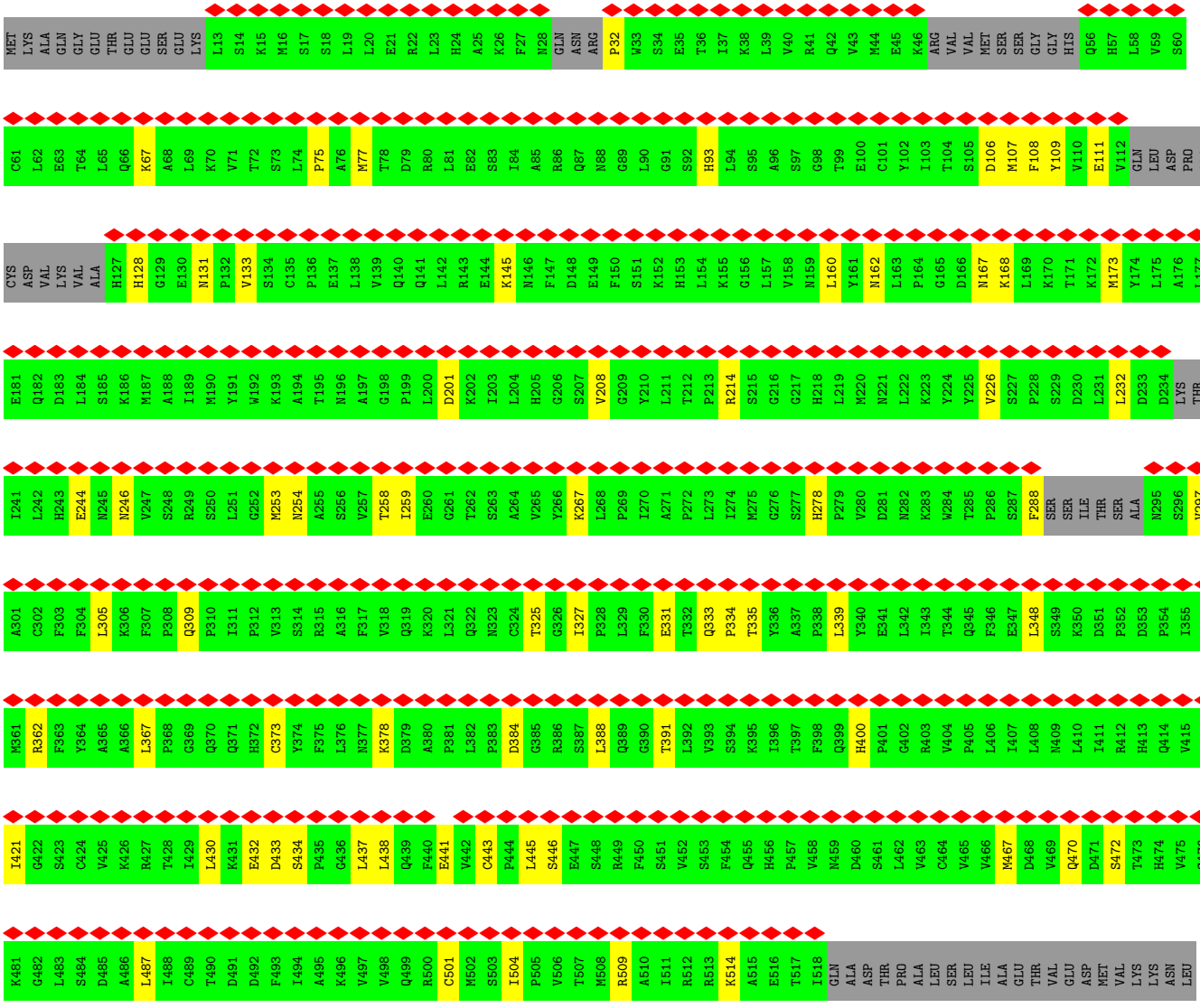
Mol	Chain	Residues	Atoms	AltConf
73	PA	1	Total Mg 1 1	0

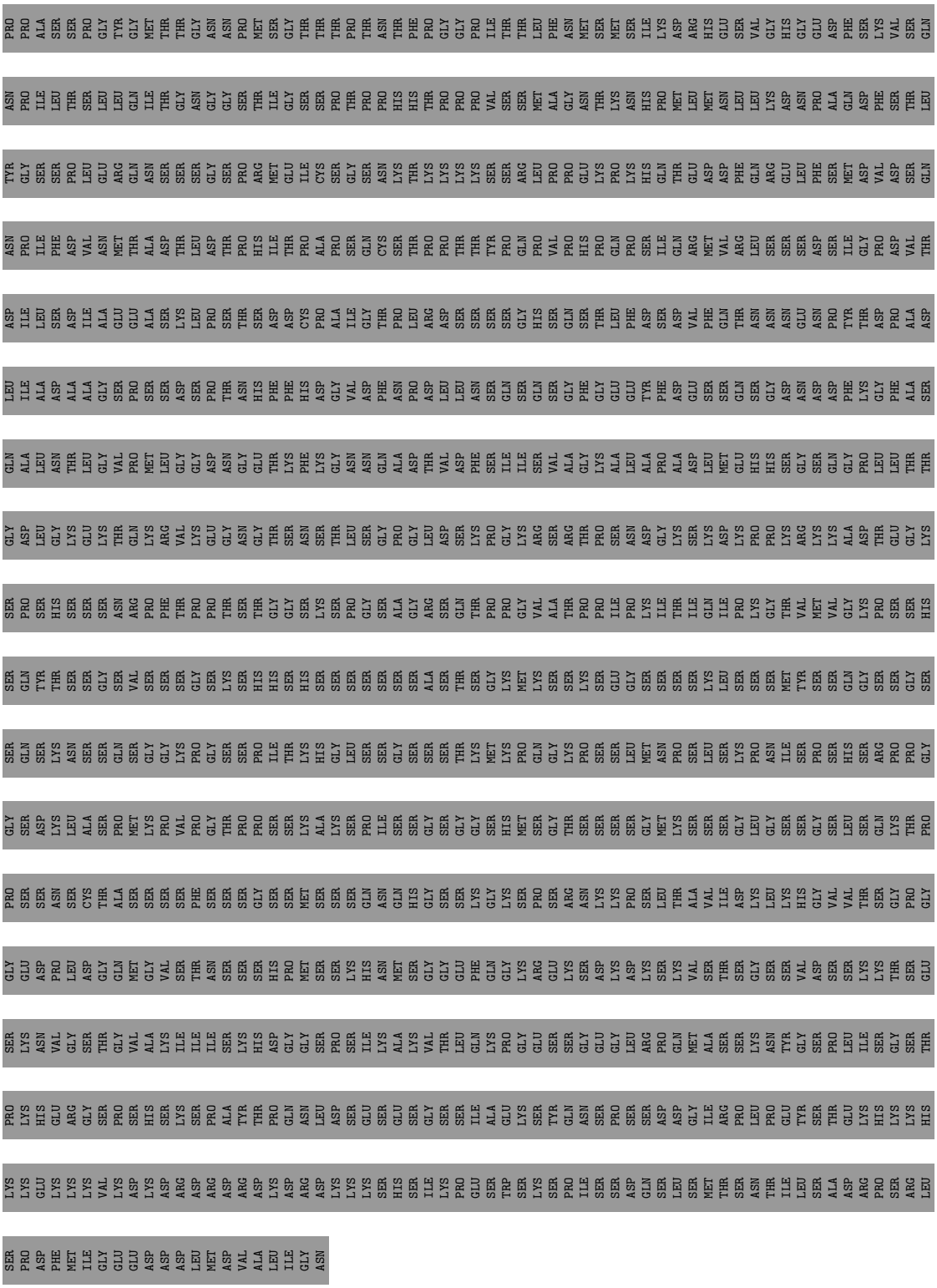
3 Residue-property plots (i)

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

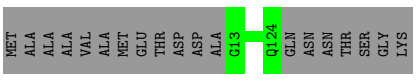
Chain a:





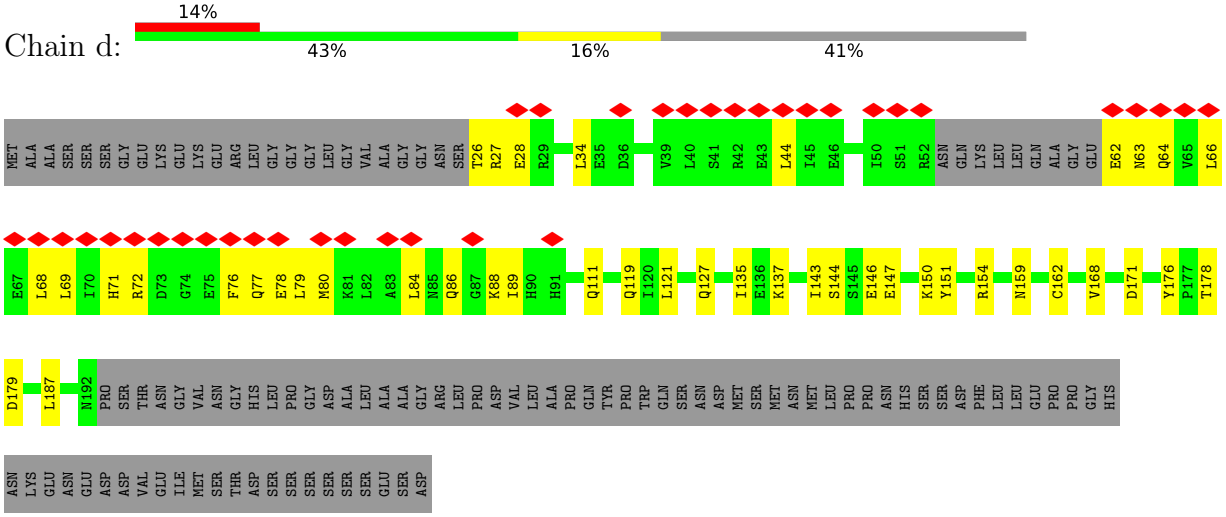
• Molecule 2: Mediator of RNA polymerase II transcription subunit 31

Chain m:



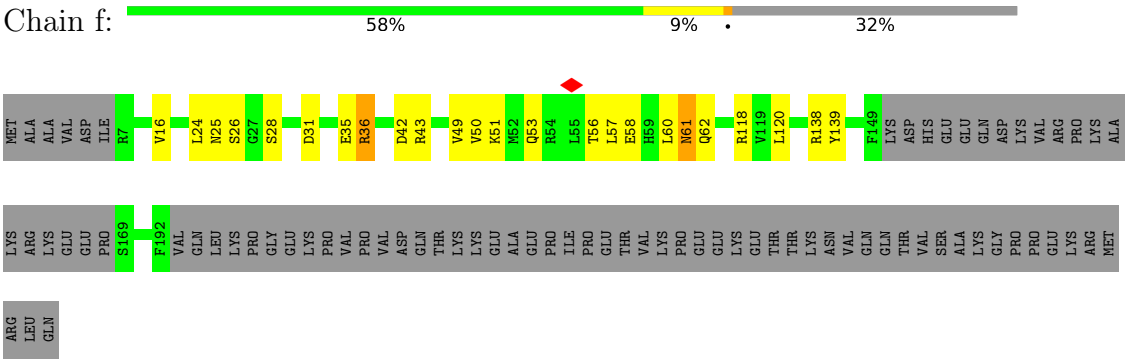
• Molecule 3: Mediator of RNA polymerase II transcription subunit 4

Chain d:



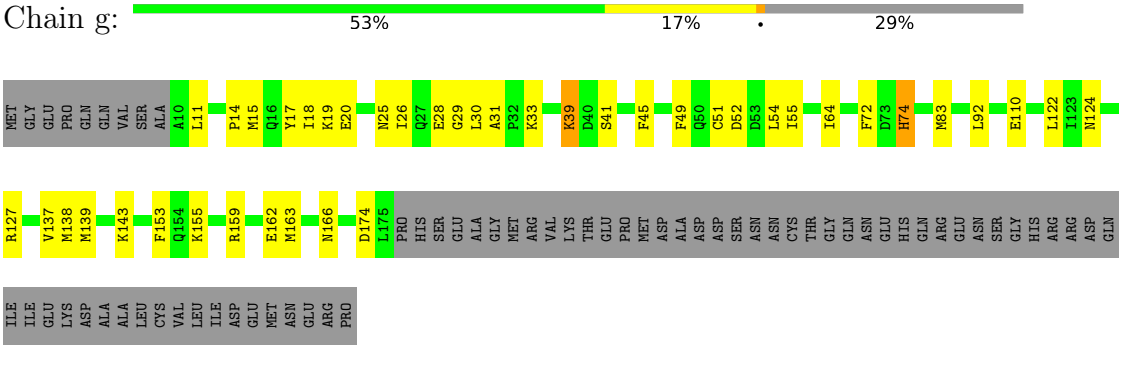
• Molecule 4: Mediator of RNA polymerase II transcription subunit 6

Chain f:



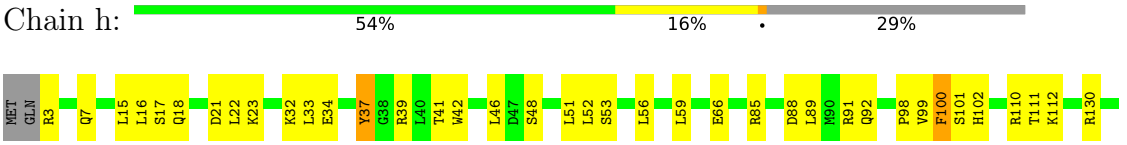
• Molecule 5: Mediator of RNA polymerase II transcription subunit 7

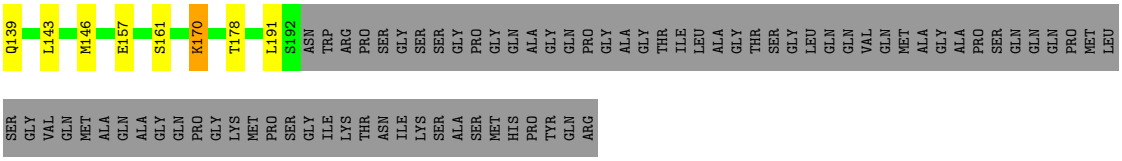
Chain g:



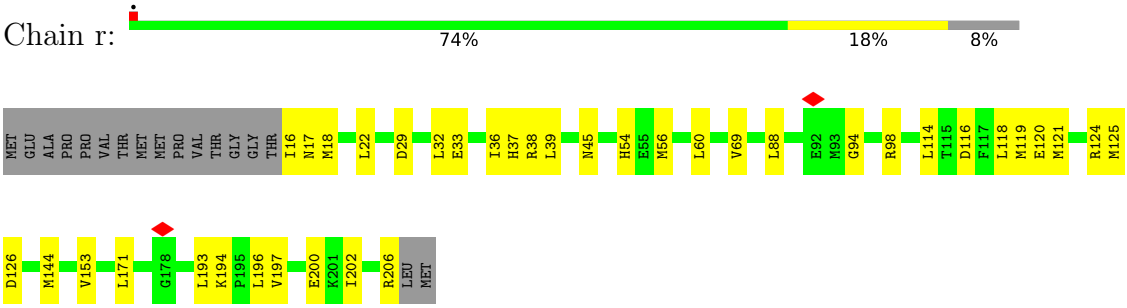
• Molecule 6: Isoform 2 of Mediator of RNA polymerase II transcription subunit 8

Chain h:

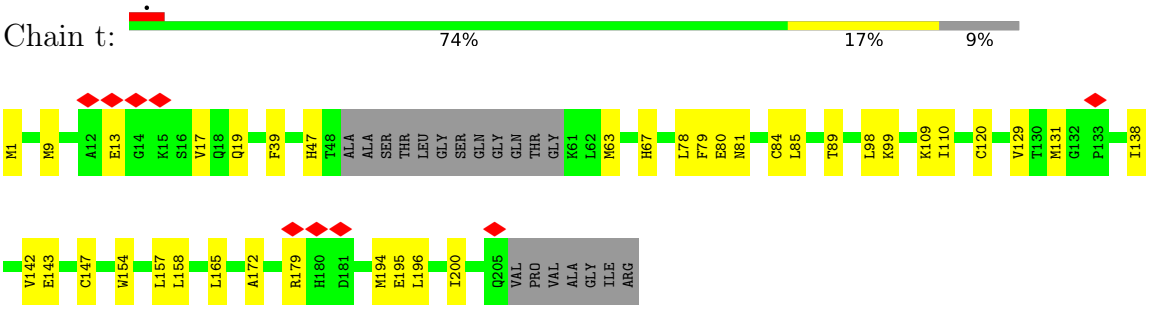




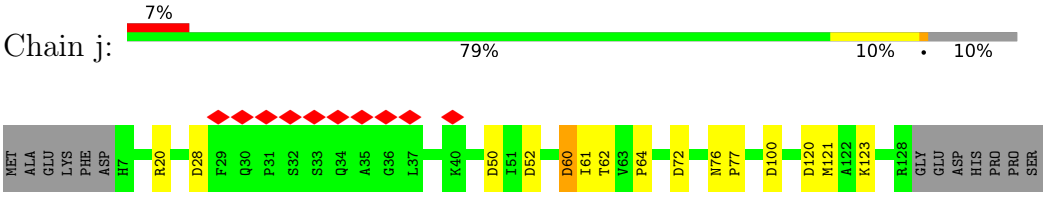
• Molecule 7: Mediator of RNA polymerase II transcription subunit 18



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

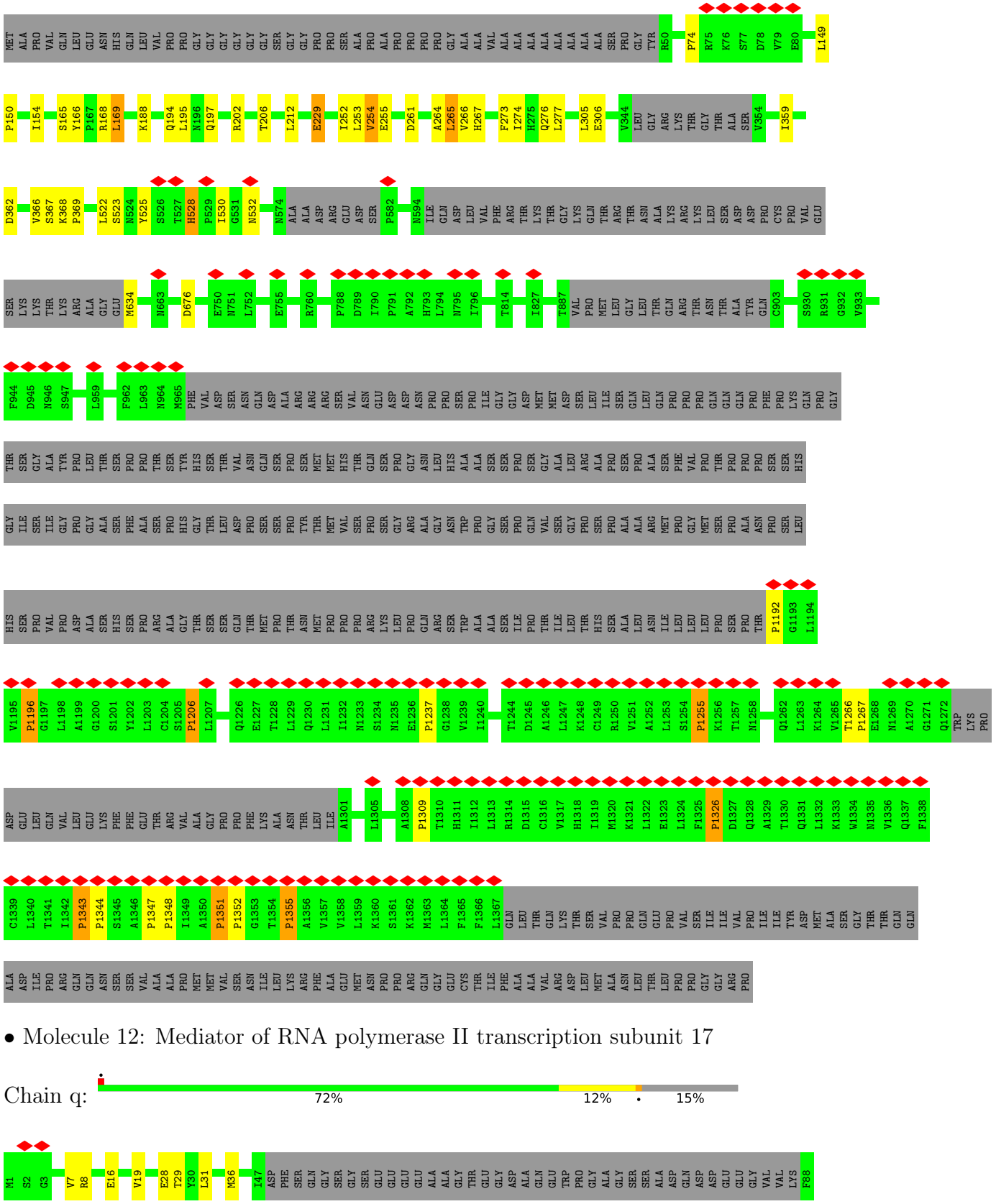


• Molecule 9: Mediator of RNA polymerase II transcription subunit 10



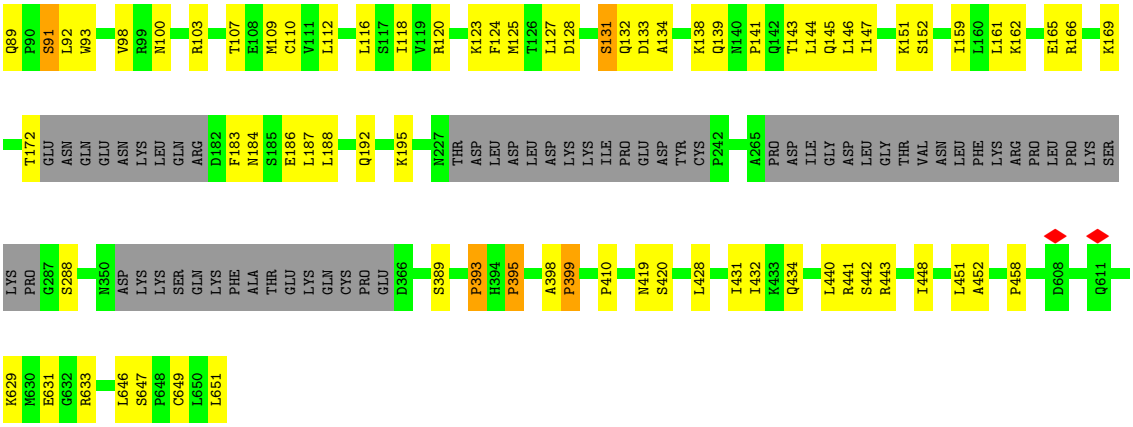
• Molecule 10: Mediator of RNA polymerase II transcription subunit 11

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



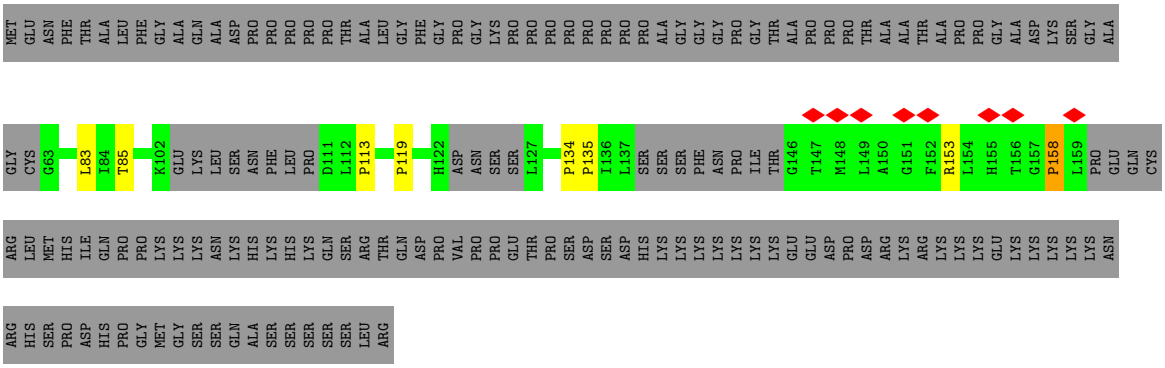
• Molecule 12: Mediator of RNA polymerase II transcription subunit 17

Chain q:



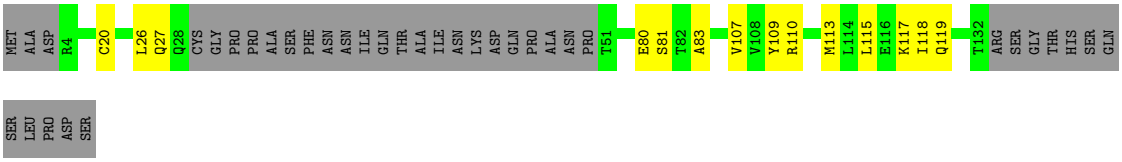
• Molecule 13: Mediator of RNA polymerase II transcription subunit 19

Chain s:



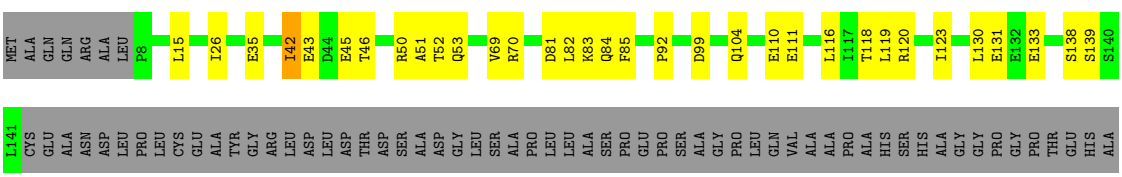
• Molecule 14: Mediator of RNA polymerase II transcription subunit 21

Chain u:



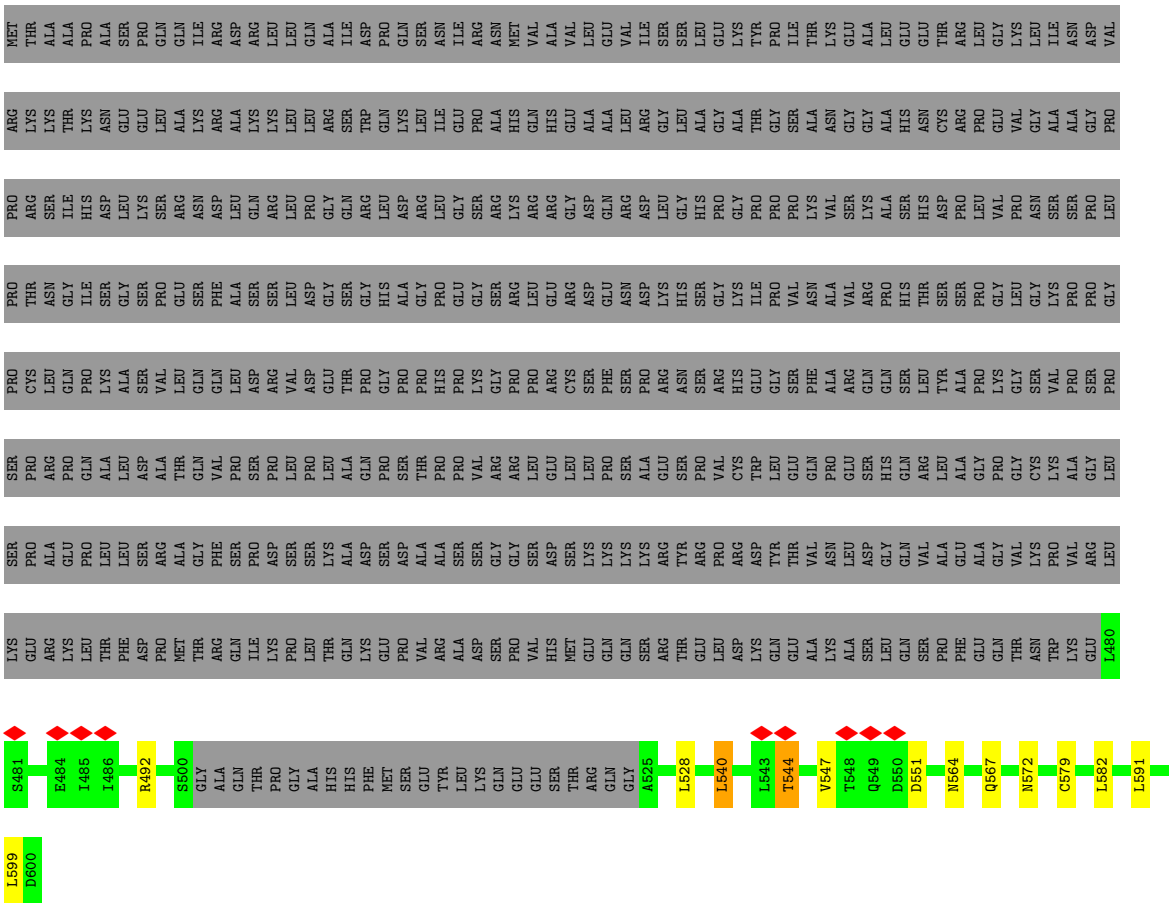
• Molecule 15: Mediator of RNA polymerase II transcription subunit 22

Chain v:



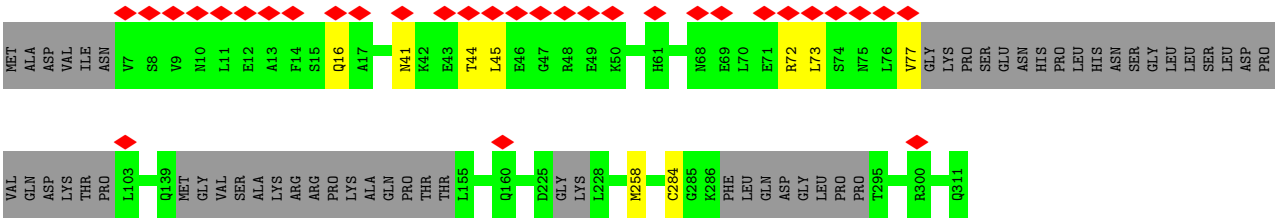
• Molecule 16: Mediator of RNA polymerase II transcription subunit 26

Chain z:



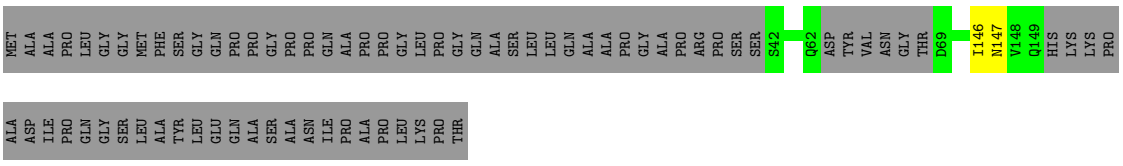
• Molecule 17: Mediator of RNA polymerase II transcription subunit 27

Chain c:



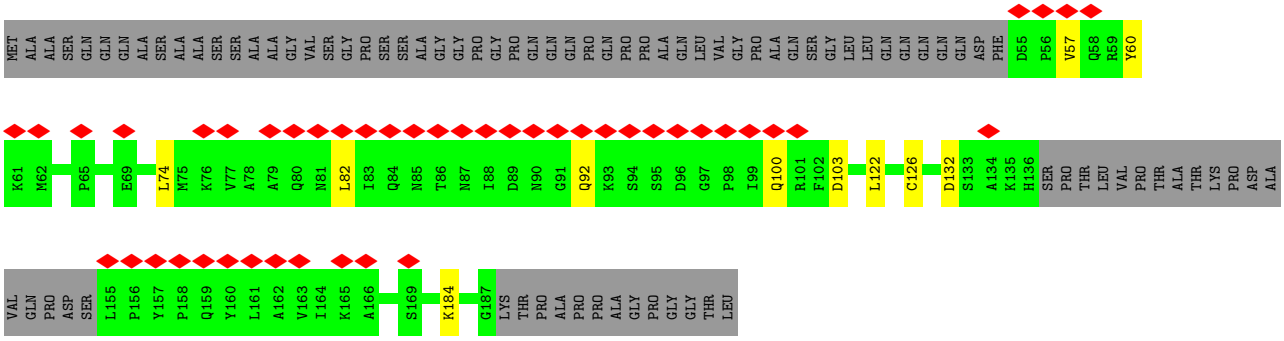
• Molecule 18: Mediator of RNA polymerase II transcription subunit 28

Chain e:



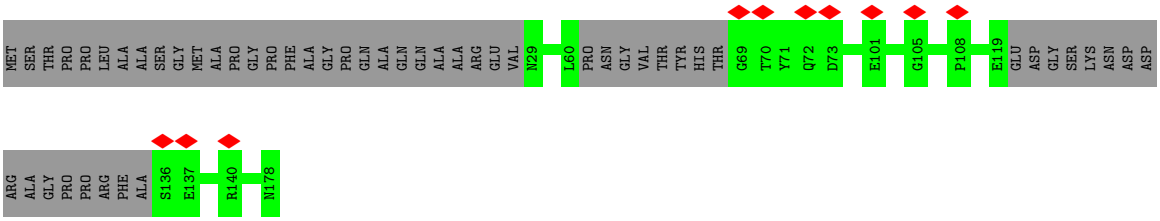
• Molecule 19: Mediator of RNA polymerase II transcription subunit 29

Chain b:



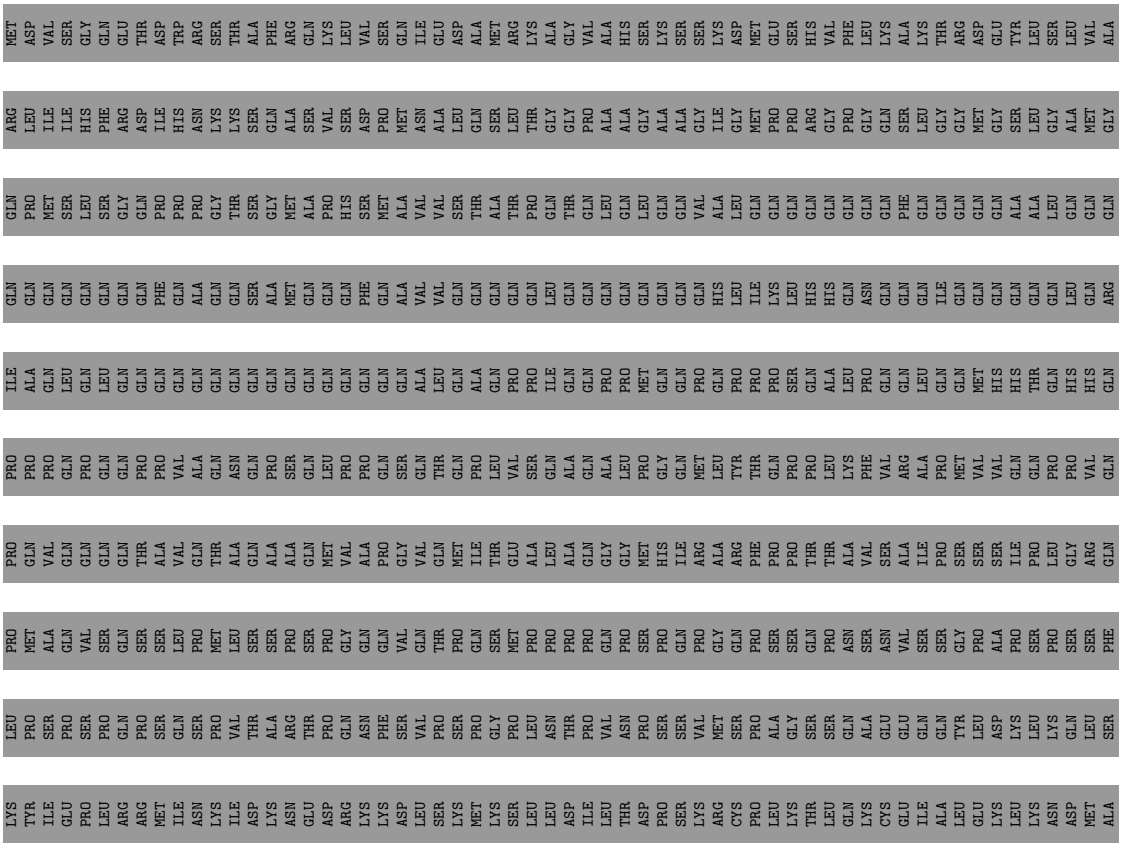
• Molecule 20: Mediator of RNA polymerase II transcription subunit 30

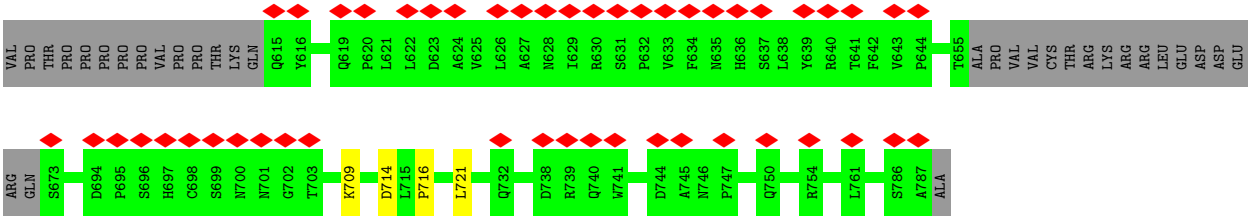
Chain l:



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

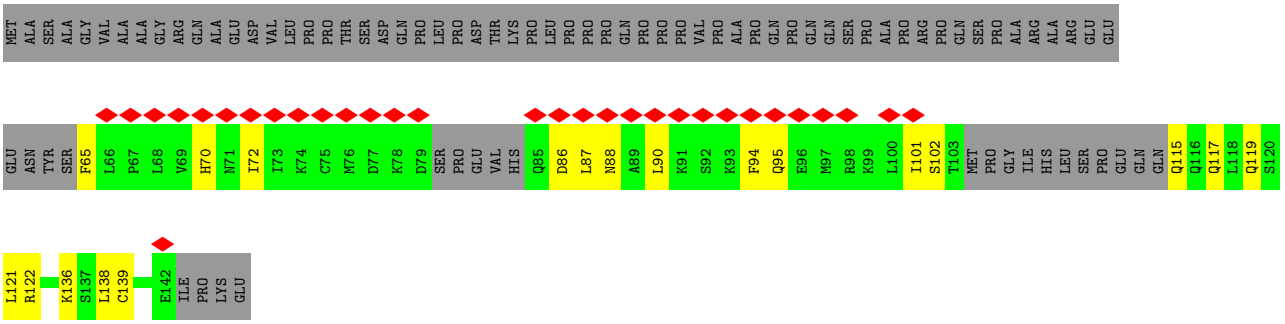
Chain o:





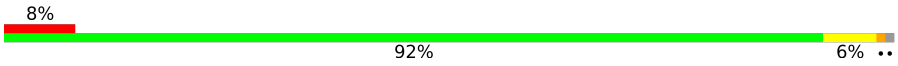
• Molecule 22: Mediator of RNA polymerase II transcription subunit 9

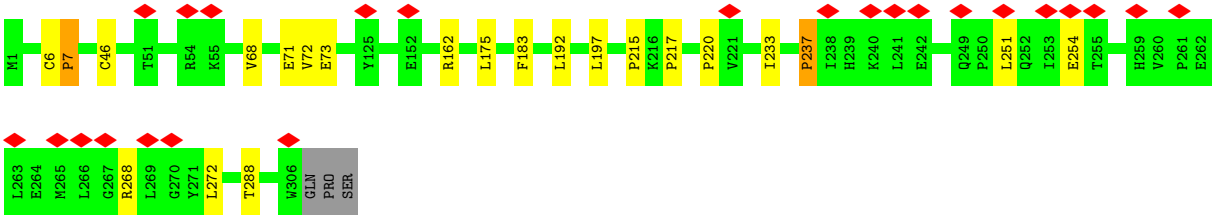
Chain i:



• Molecule 23: CDK-activating kinase assembly factor MAT1

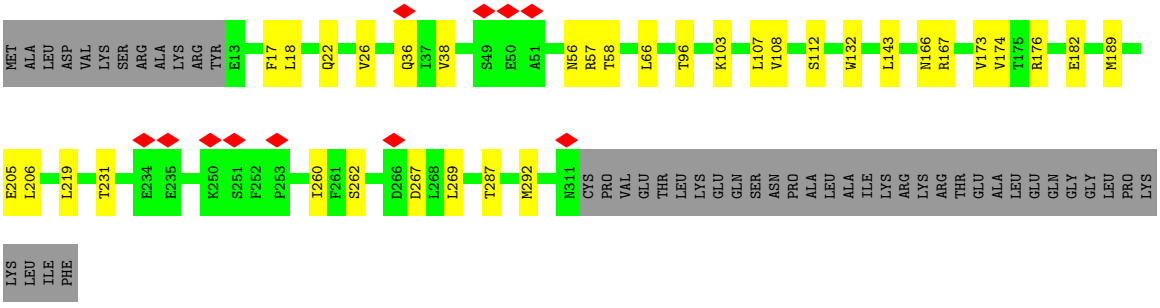
Chain 0:





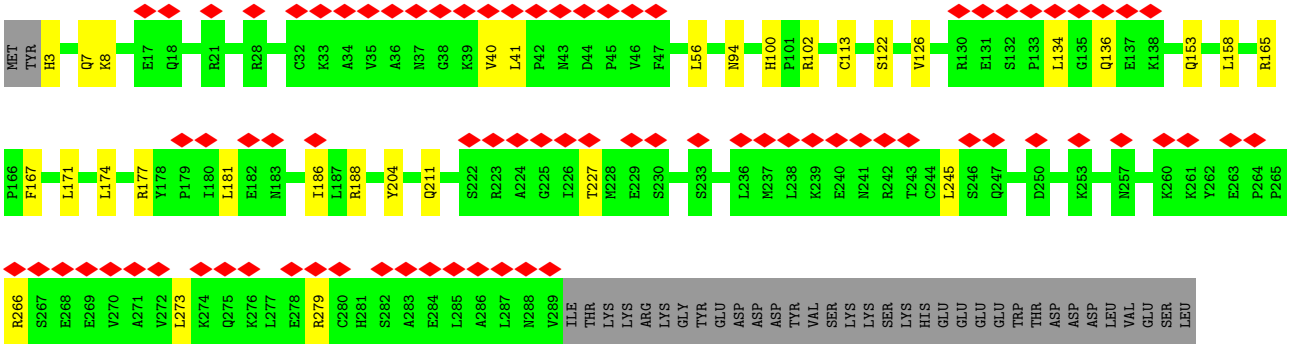
• Molecule 24: Cyclin-dependent kinase 7

Chain 8:



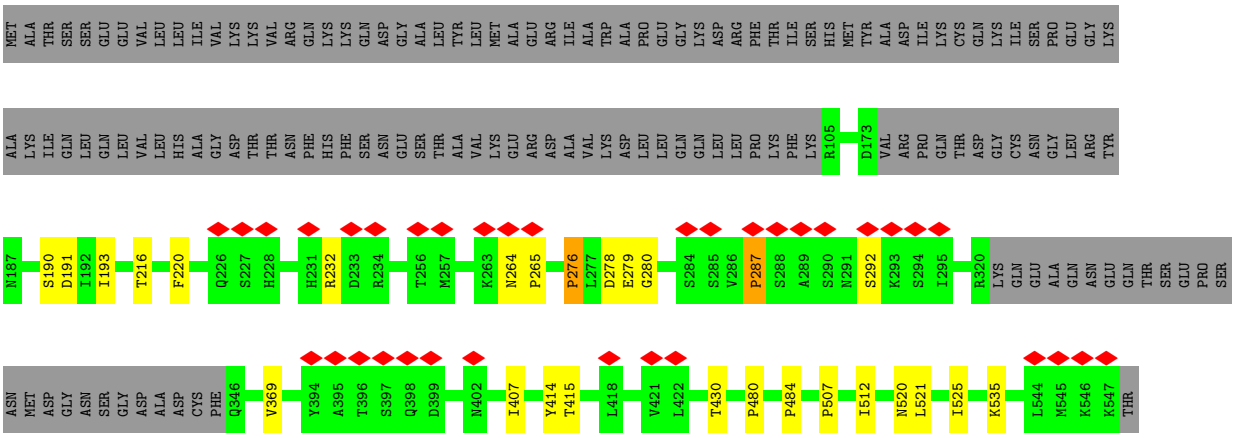
• Molecule 25: Cyclin-H

Chain 9:



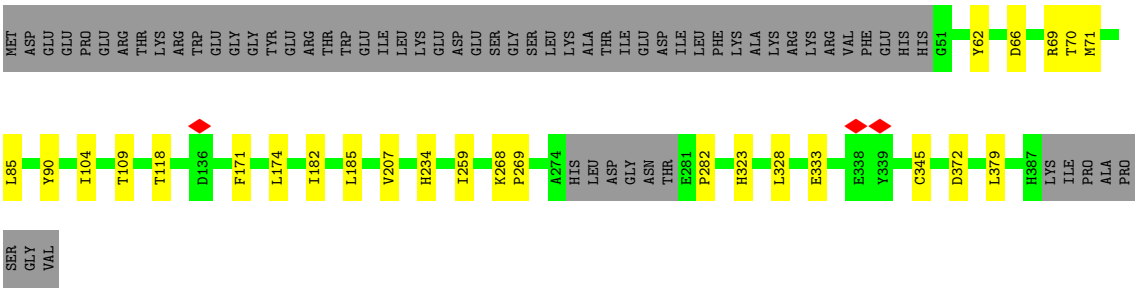
• Molecule 26: General transcription factor IIH subunit 1

Chain 1:



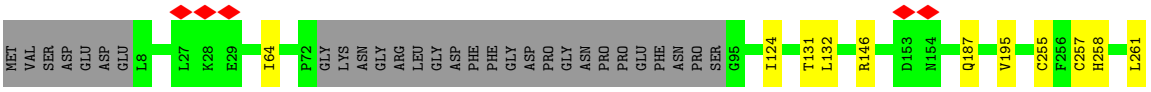
• Molecule 27: General transcription factor IIH subunit 2

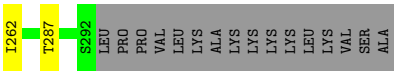
Chain 2:



• Molecule 28: General transcription factor IIH subunit 3

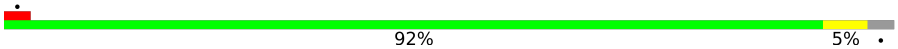
Chain 3:

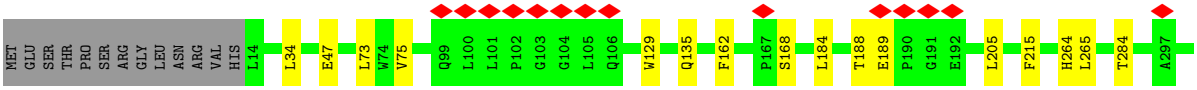


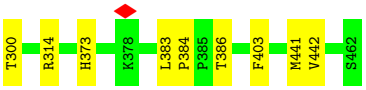


• Molecule 29: General transcription factor IIH subunit 4

Chain 4:

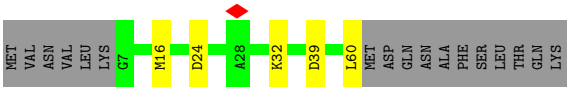






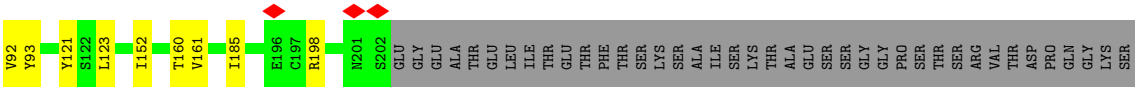
• Molecule 30: General transcription factor IIH subunit 5

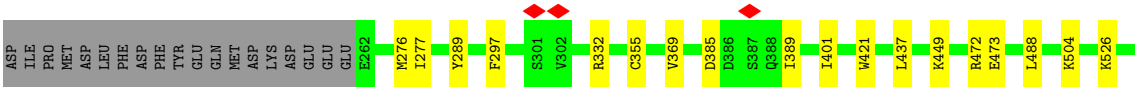
Chain 5:



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

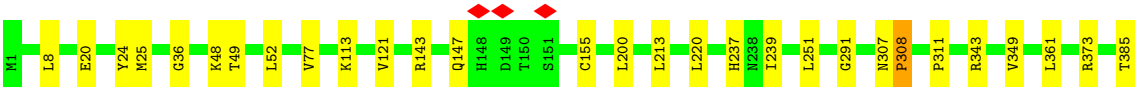
Chain 6:

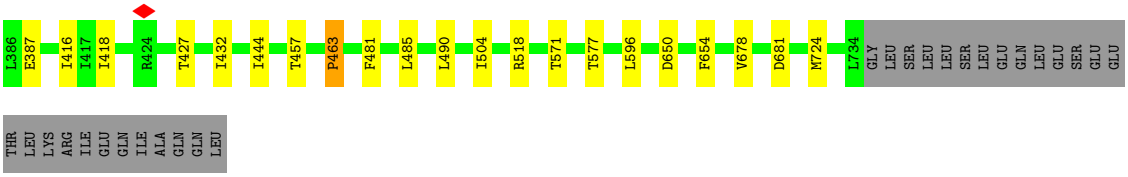




• Molecule 32: General transcription and DNA repair factor IIH helicase subunit XPD

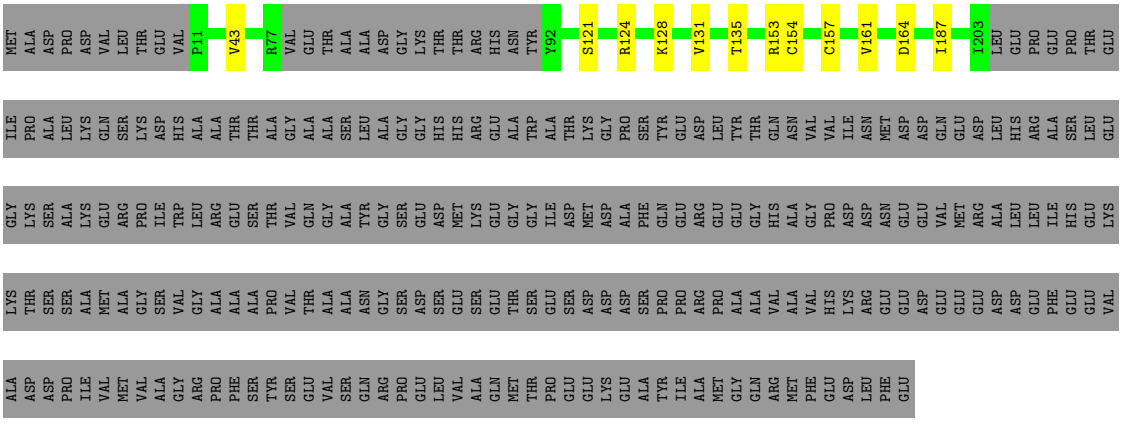
Chain 7:





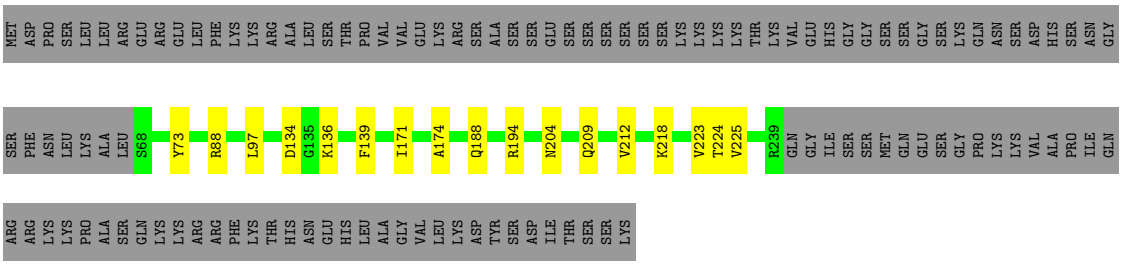
• Molecule 33: General transcription factor IIE subunit 1

Chain EA:



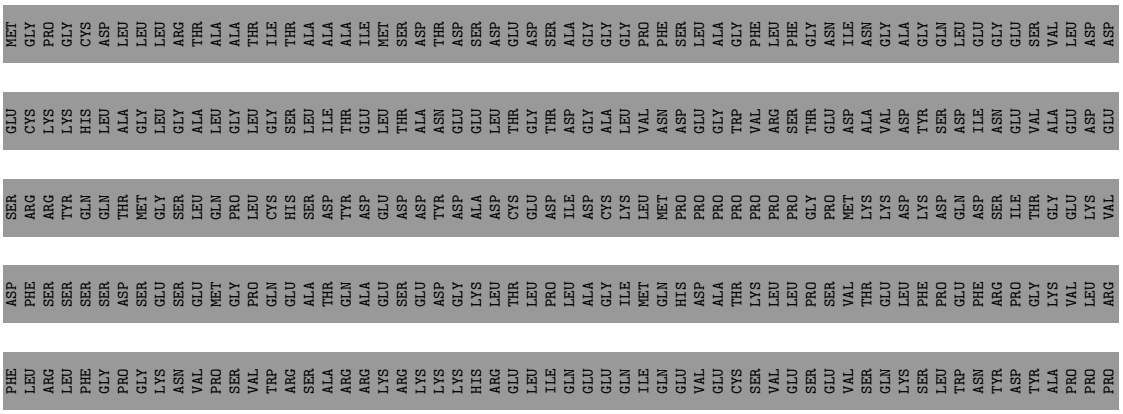
• Molecule 34: Transcription initiation factor IIE subunit beta

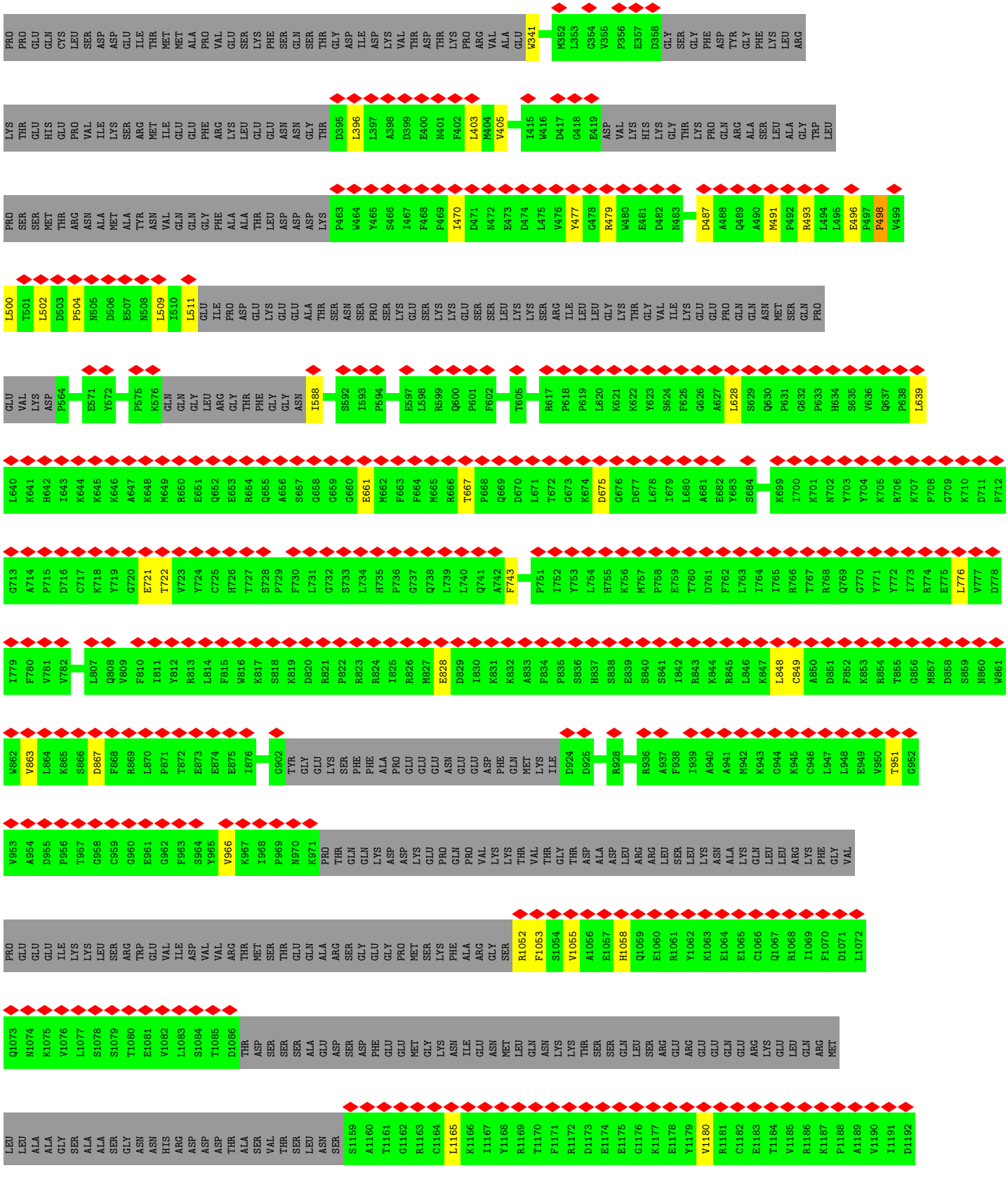
Chain EB:

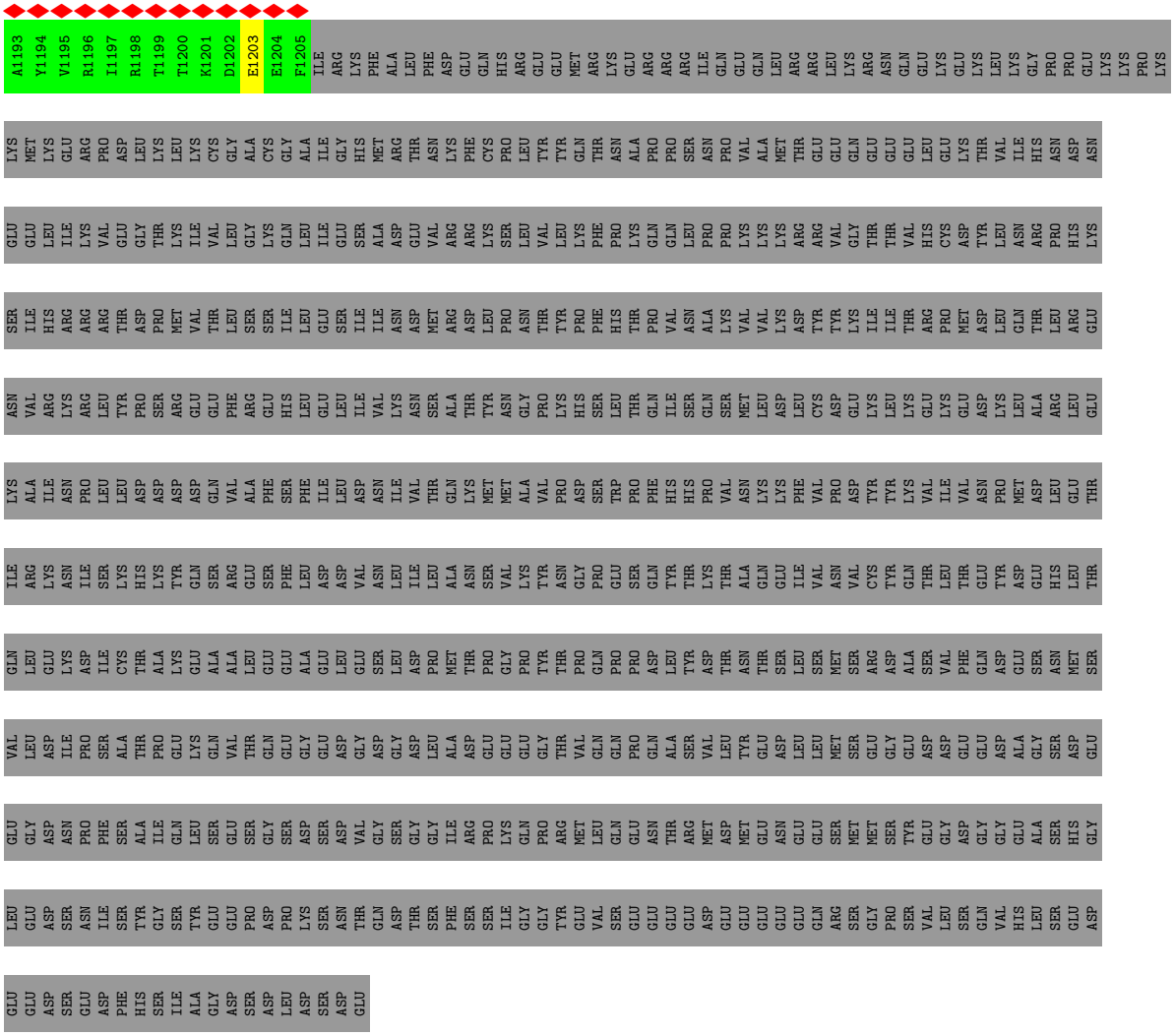


• Molecule 35: Transcription initiation factor TFIID subunit 1

Chain DA:

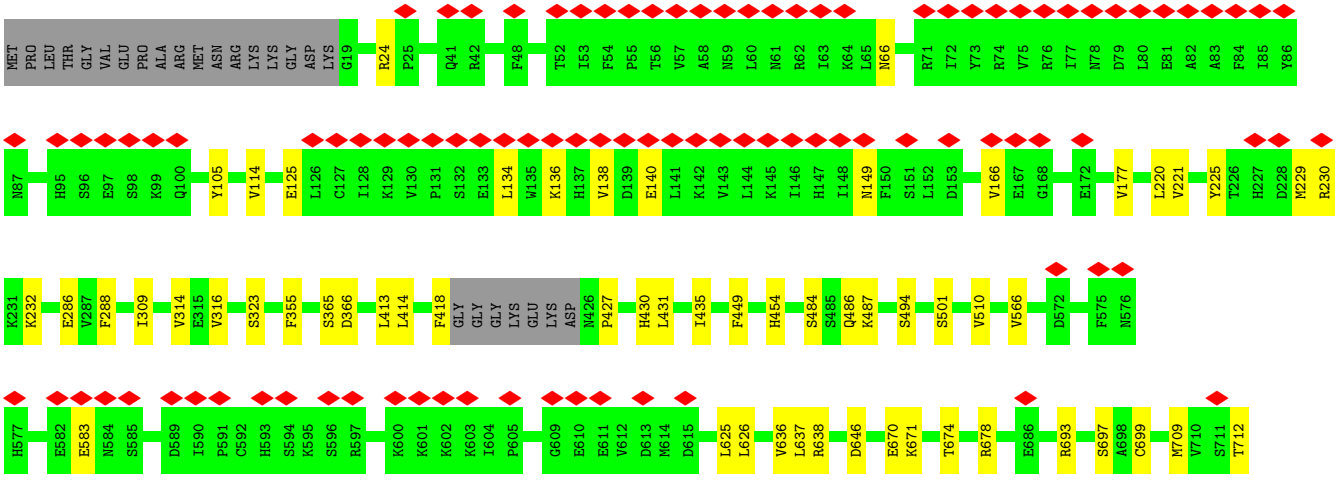


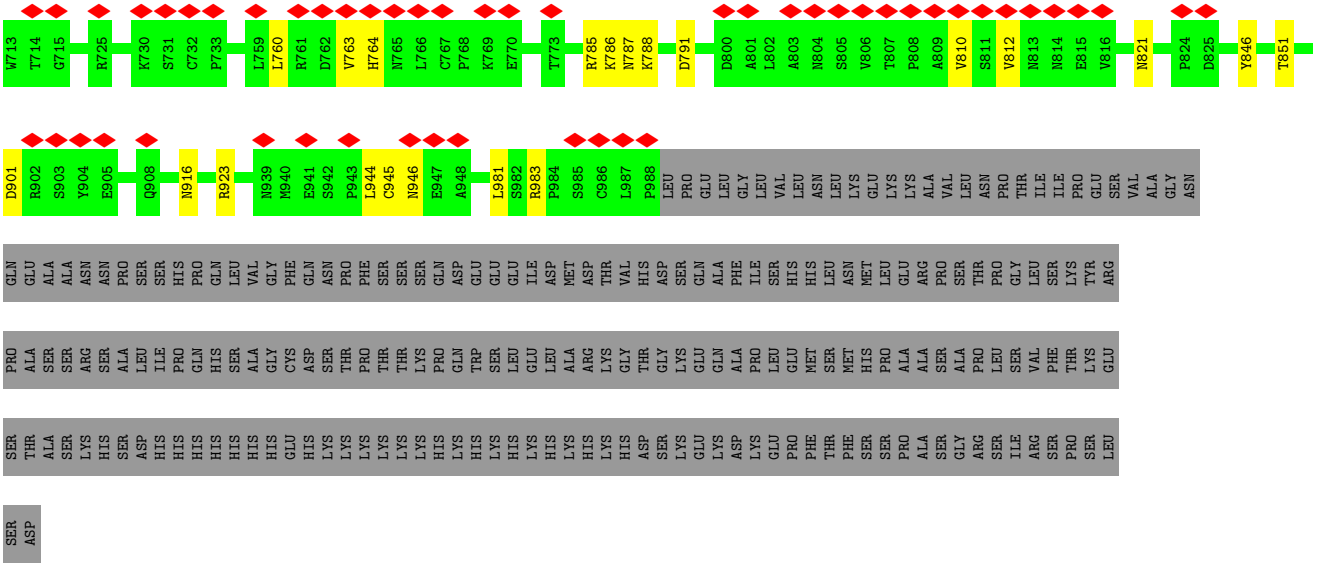

PRO PRO GLU GLN CYS LEU SER ASP ASP GLU ILE THR MET MET ALA PRO VAL GLU SER LYS PHE SER GLN SER THR GLY ASP ILE ASP LYS VAL THR ASP THR LYS PRO ARG VAL ALA GLU W341 M352 L353 G354 V355 P356 E357 D358 GLY SER GLY PHE ASP TYR GLY PHE LYS LEU ARG
LYS THR GLU HIS GLU PRO VAL ILE LYS SER ARG MET ILE GLU GLU PHE ARG LYS LEU GLU GLU ASN ASN GLY THR D395 L396 L397 A398 D399 E400 N401 F402 L403 M404 V405 I415 W416 D417 G418 E419 ASP VAL LYS HIS LYS GLY THR LYS PRO GLN ARG ALA SER LEU ALA GLY TRP LEU
PRO SER SER MET THR ARG ASN ALA MET ALA TYR ASN VAL GLN GLN GLY PHE ALA ALA THR LEU ASP ASP ASP LYS P463 W464 Y465 S466 I467 F468 P469 I470 D471 N472 E473 D474 L475 V476 Y477 G478 R479 W480 E481 D482 N483 D487 A488 Q489 A490 M491 P492 R493 L494 L495 E496 P497 P498 V499
L500 T501 L502 D503 P504 N505 D506 E507 N508 L509 I510 L511 GLU ILE PRO ASP GLU LYS GLU GLU ALA THR SER ASN SER PRO SER LYS GLU SER LYS LYS GLU SER SER LEU LYS LYS SER ARG ILE LEU LEU GLY LYS THR GLY VAL ILE LYS GLU GLU PRO GLN GLN ASN MET SER GLN PRO
GLU VAL LYS ASP P564 E571 Y572 P575 K576 GLN GLN GLY LEU ARG GLY THR PHE GLY GLY ASN I588 S592 I593 P594 E597 L598 R599 Q600 P601 F602 T605 R617 P618 P619 L620 K621 K622 Y623 S624 F625 G626 A627 L628 S629 Q630 P631 G632 P633 H634 S635 V636 Q637 P638 L639
L640 K641 H642 I643 K644 K645 K646 A647 K648 M649 R650 E651 Q652 E653 R654 Q655 A656 S657 G658 G659 G660 E661 M662 F663 F664 M665 R666 T667 P668 Q669 D670 L671 T672 G673 K674 D675 G676 D677 L678 I679 L680 A681 E682 Y683 S684 K699 I700 K701 N702 Y703 Y704 K705 R706 K707 P708 G709 K710 D711 P712
G713 A714 P715 D716 C717 K718 Y719 G720 E721 T722 V723 Y724 C725 H726 T727 S728 P729 F730 L731 G732 S733 L734 H735 P736 G737 Q738 L739 L740 Q741 A742 F743 P751 I752 Y753 L754 H755 K756 M757 P758 E759 T760 D761 F762 L763 I764 I765 R766 T767 R768 Q769 G770 Y771 Y772 I773 R774 E775 L776 V777 D778
I779 F780 V781 V782 L807 Q808 V809 F810 I811 Y812 R813 L814 F815 W816 K817 S818 K819 D820 R821 P822 R823 R824 I825 R826 M827 E828 D829 I830 K831 K832 A833 F834 P835 S836 H837 S838 E839 S840 S841 I842 R843 K844 R845 L846 K847 L848 C849 A850 D851 F852 K853 R854 T855 G856 M857 D858 S859 N860 W861
W862 V863 L864 K865 S866 D867 F868 R869 L870 P871 T872 E873 E874 E875 I876 G902 TYR GLY GLU LYS SER PHE PHE ALA PRO GLU GLU GLU ASN GLU GLU ASP PHE GLN MET LYS ILE D924 D925 R928 R936 A937 F938 I939 A940 A941 M942 K943 G944 K945 C946 L947 L948 E949 V950 T951 G952
V953 A954 D955 P956 T957 G958 C959 G960 E961 G962 P963 S964 Y965 V966 K967 I968 P969 N970 K971 PRO THR GLN GLN LYS ASP ASP LYS GLU PRO GLN PRO VAL LYS LYS THR VAL THR GLY THR ASP ALA ASP LEU ARG ARG LEU SER LEU LYS ASN ALA LYS GLN LEU LEU ARG LYS PHE GLY VAL
PRO GLU GLU GLU ILE LYS LYS LEU SER ARG TRP GLU VAL ILE ASP VAL VAL ARG THR MET SER THR GLU GLN ALA ARG SER GLY GLU GLY PRO MET SER LYS PHE ALA ARG GLY SER R1052 F1053 S1054 V1055 A1056 E1057 H1058 Q1059 E1060 R1061 Y1062 K1063 E1064 E1065 C1066 Q1067 R1068 I1069 F1070 D1071 L1072
Q1073 N1074 K1075 V1076 L1077 S1078 S1079 T1080 E1081 V1082 L1083 S1084 T1085 D1086 THR ASP SER SER SER ALA GLU ASP SER ASP PHE GLU GLU MET GLY LYS ASN ILE GLU ASN MET LEU GLN ASN LYS LYS THR SER SER GLN LEU SER ARG GLU ARG GLU GLU GLN GLU ARG LYS GLU LEU GLN ARG MET
LEU LEU ALA ALA GLY SER ALA ALA SER GLY ASN ASN HIS ARG ASP ASP ASP THR ALA SER VAL THR SER LEU ASN SER 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



• Molecule 36: Transcription initiation factor TFIID subunit 2

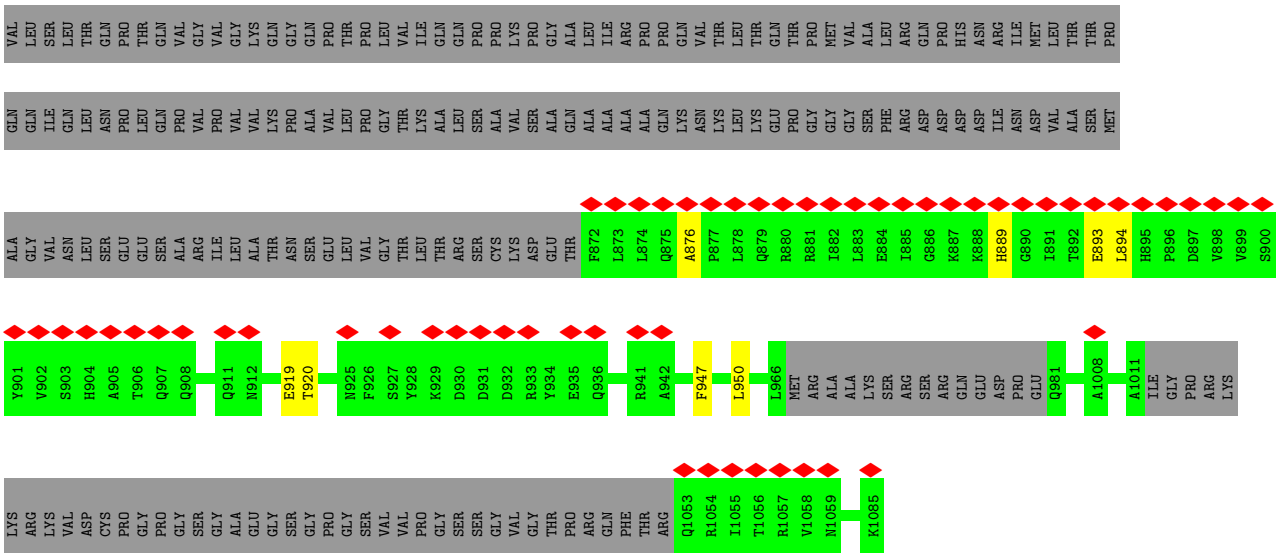
Chain DB:



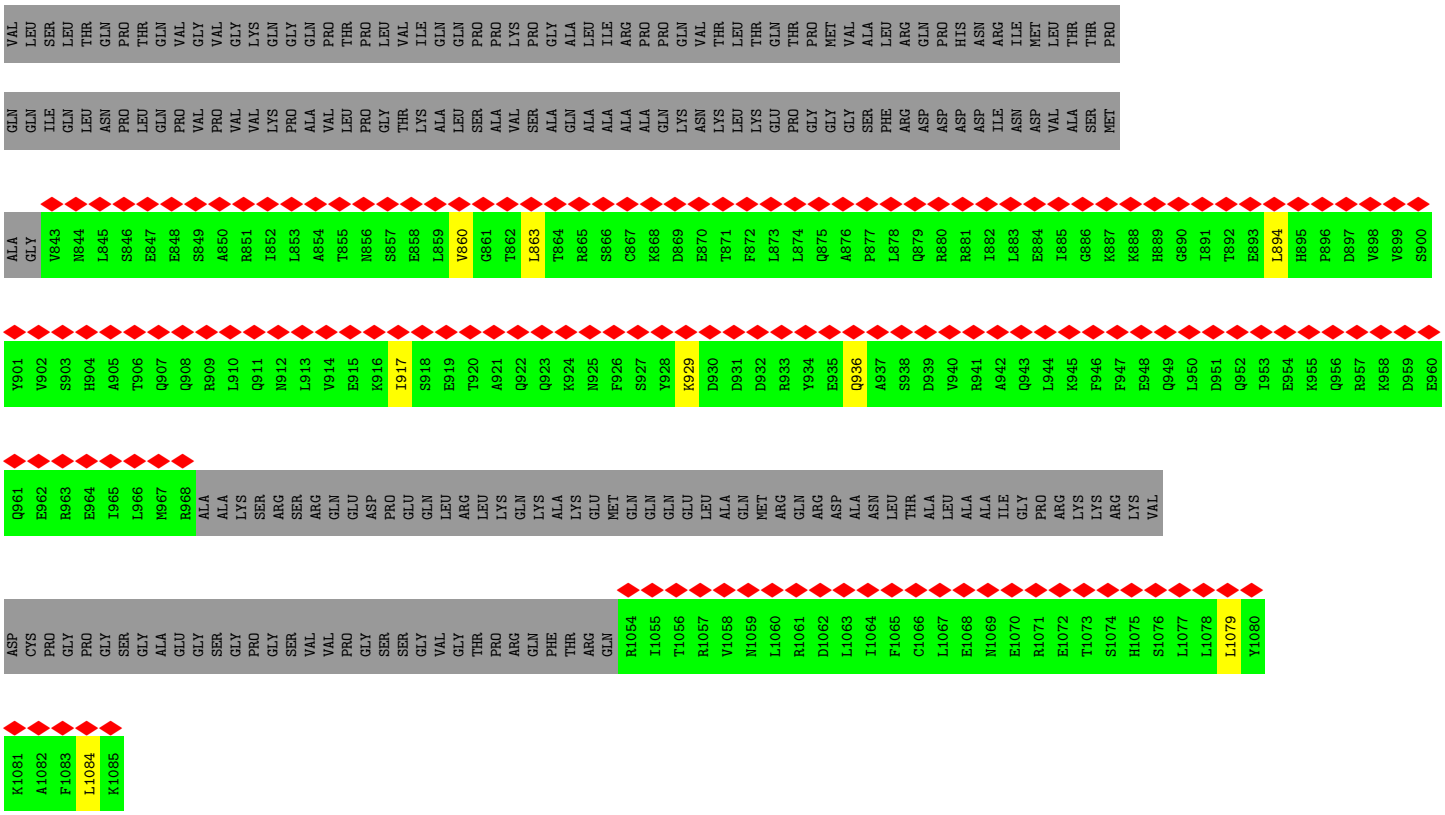

W713 T714 G715 R725 K730 S731 C732 P733 L759 L760 R761 D762 V763 H764 N765 L766 C767 P768 K769 E770 T773 R785 K786 N787 K788 D791 D800 A801 L802 A803 N804 S805 V806 T807 P808 A809 V810 S811 V812 N813 N814 E815 V816 N821 P824 D825 Y846 T851
D901 R902 S903 Y904 E905 Q908 N916 R923 N939 M940 E941 S942 P943 L944 C945 N946 E947 A948 L981 S982 R983 P984 S985 C986 L987 P988
GLN GLU ALA ALA ASN ASN PRO SER SER HIS PRO GLN LEU VAL GLY PHE GLN ASN PRO PHE SER SER SER GLN ASP GLU GLU GLU ILE ASP MET ASP THR VAL HIS ASP SER GLN ALA PHE ILE SER HIS HIS LEU ASN MET LEU GLU ARG PRO SER THR PRO GLY LEU SER VAL PHE THR LYS TYR ARG
PRO ALA SER SER ARG SER ALA LEU ILE PRO GLN HIS SER ALA GLY CYS ASP SER THR PRO THR THR LYS PRO GLN TRP SER LEU GLU LEU ALA ARG LYS GLY THR GLY LYS GLU GLN ALA PRO LEU GLU MET SER MET HIS PRO ALA ALA SER ALA PRO LEU SER VAL PHE THR LYS GLU
SER THR ALA SER LYS HIS SER ASP HIS HIS HIS HIS HIS GLU HIS LYS LYS LYS LYS LYS HIS LYS HIS LYS HIS LYS HIS LYS HIS ASP SER LYS GLU LYS ASP LYS GLU PRO PHE THR PHE SER SER PRO ALA SER GLY ARG SER ILE ARG SER PRO SER LEU
SER ASP

• Molecule 37: Transcription initiation factor TFIID subunit 4

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

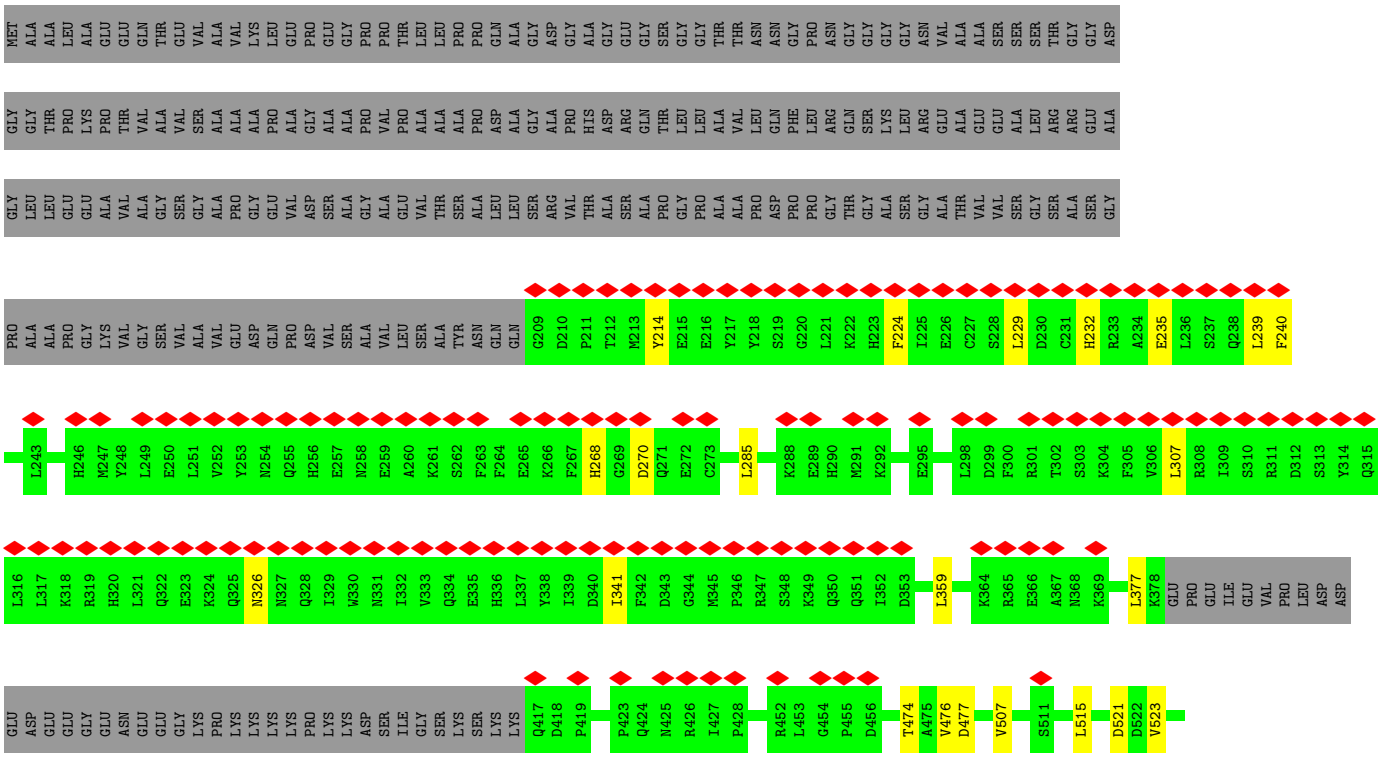


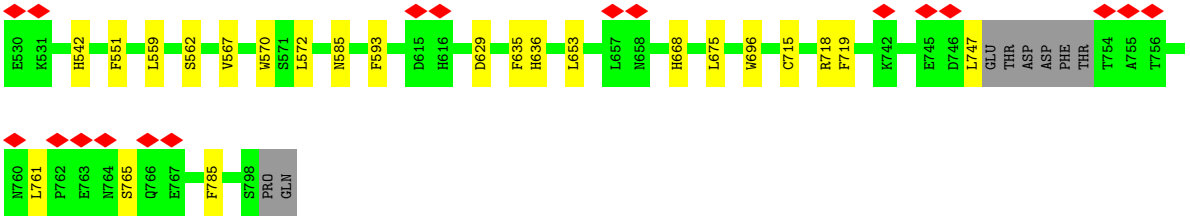
• Molecule 37: Transcription initiation factor TFIID subunit 4



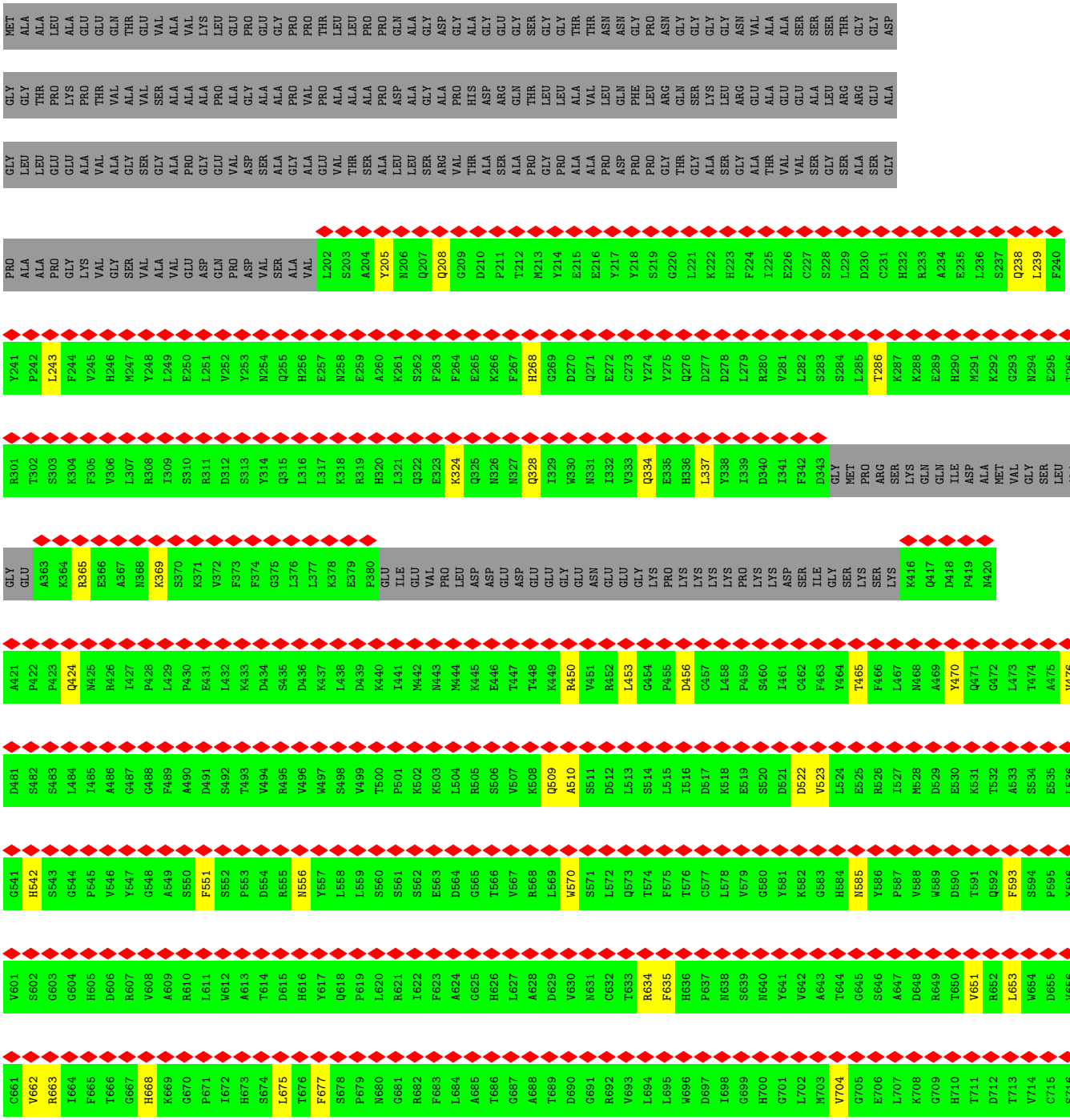
• Molecule 38: Transcription initiation factor TFIID subunit 5

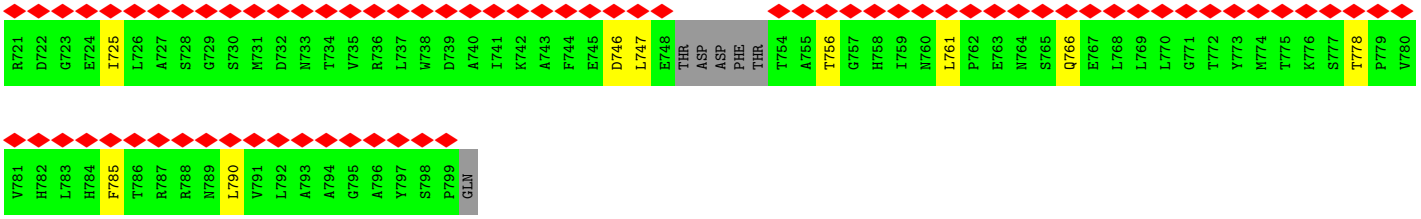
Chain DE:





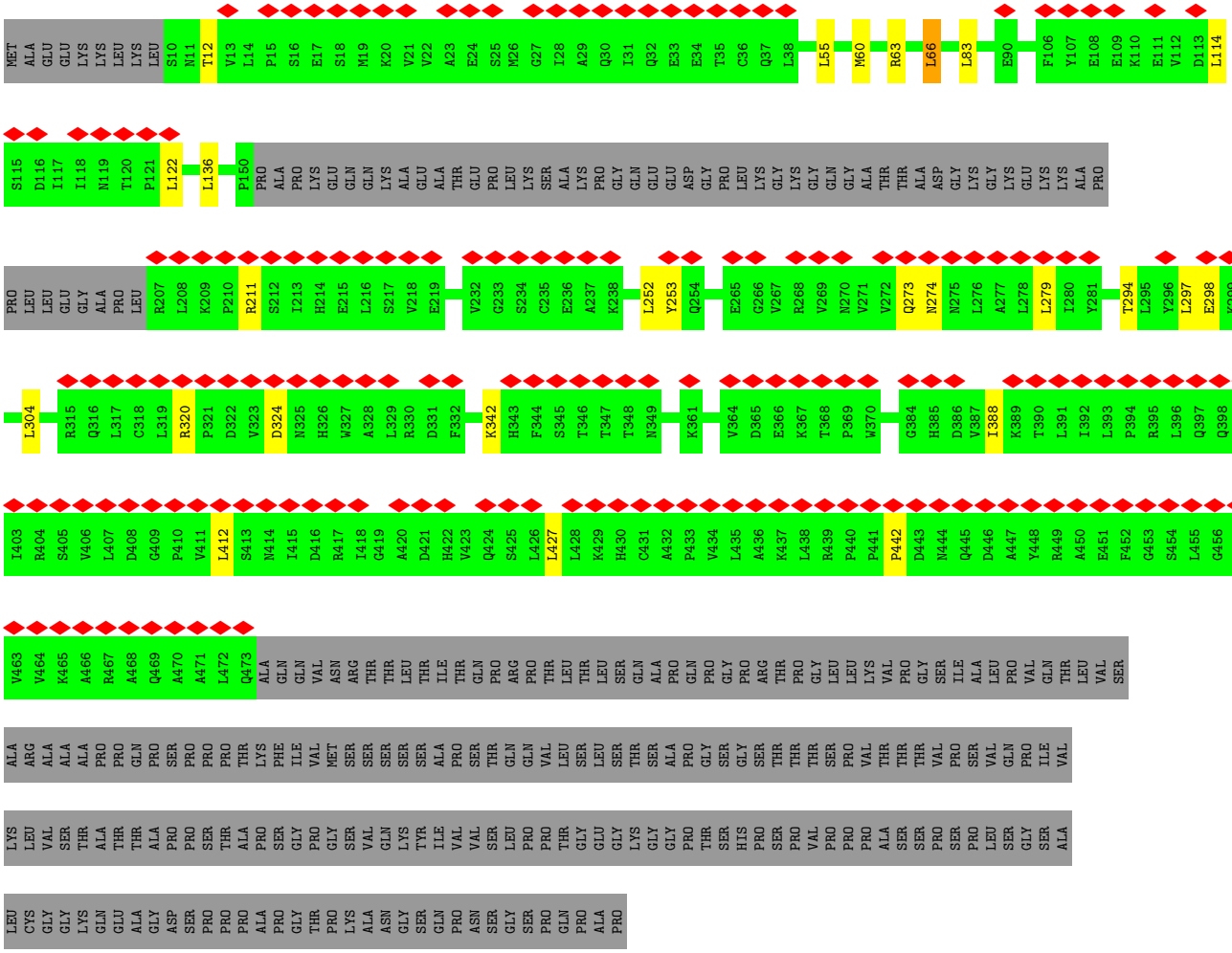
• Molecule 38: Transcription initiation factor TFIID subunit 5





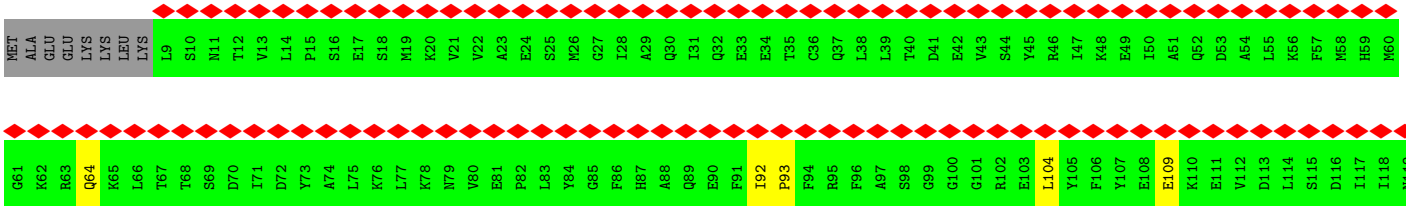
• Molecule 39: Transcription initiation factor TFIID subunit 6

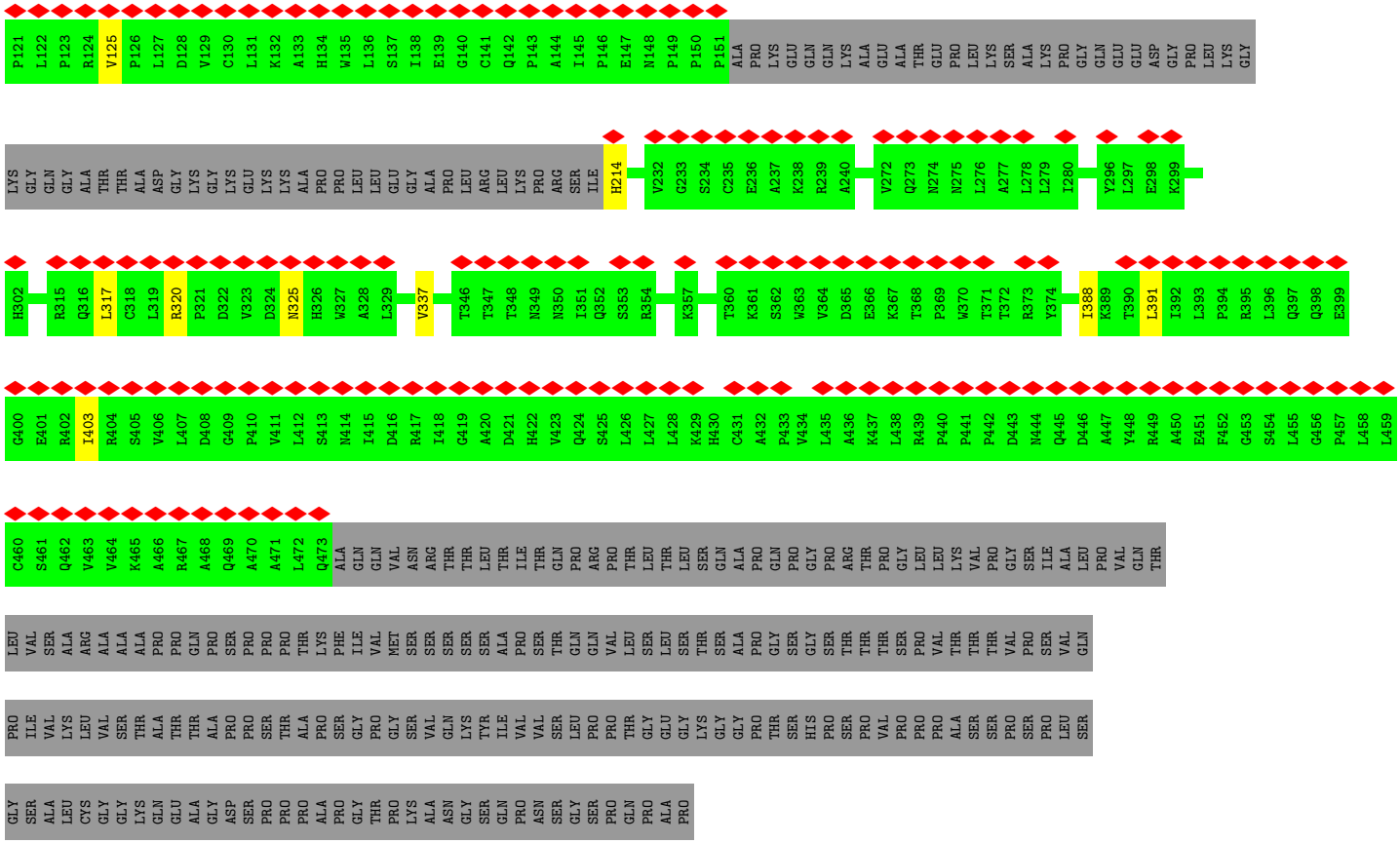
Chain DF:



• Molecule 39: Transcription initiation factor TFIID subunit 6

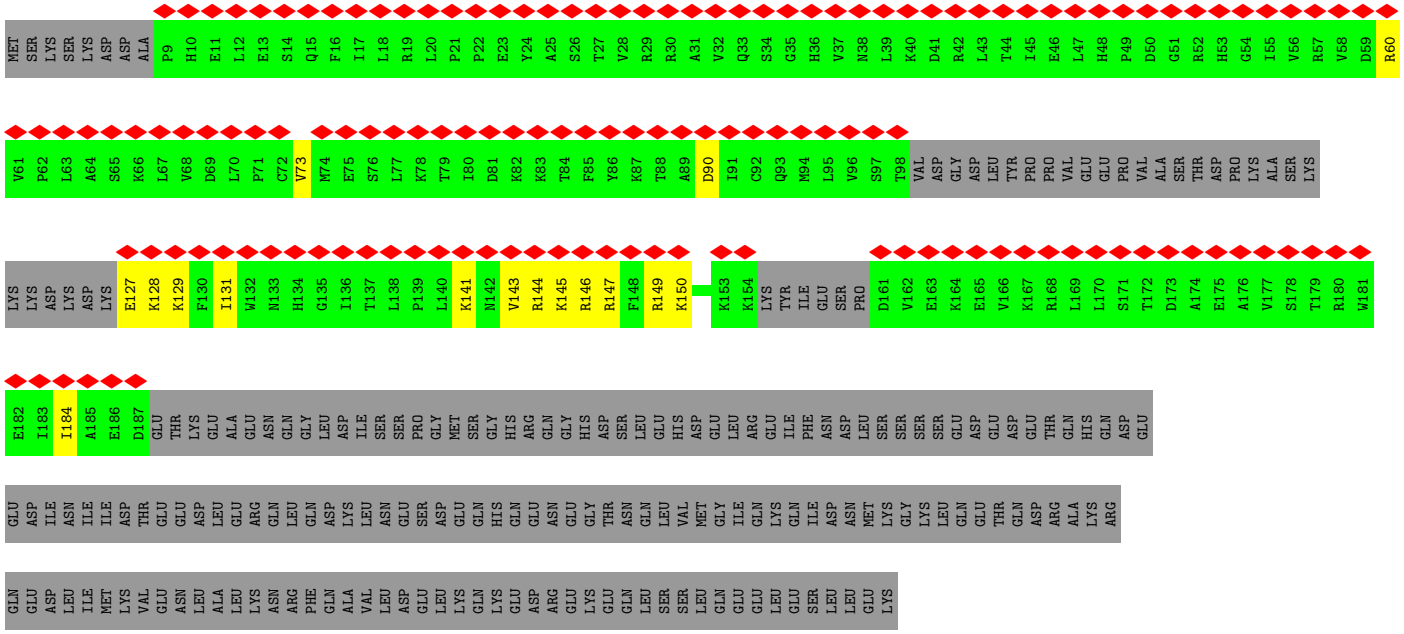
Chain Df:





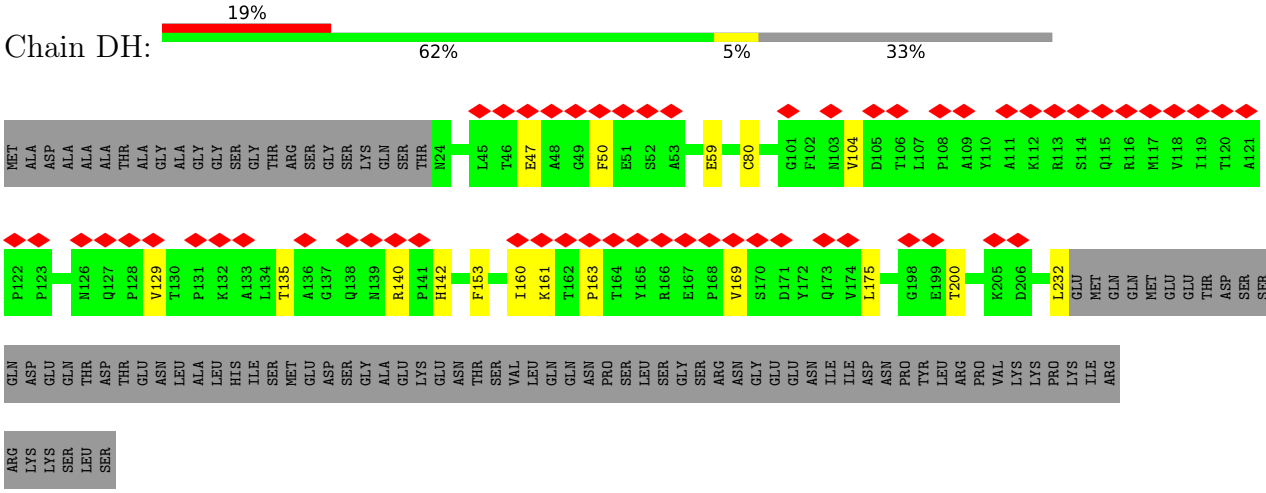
• Molecule 40: Transcription initiation factor TFIID subunit 7

Chain DG:



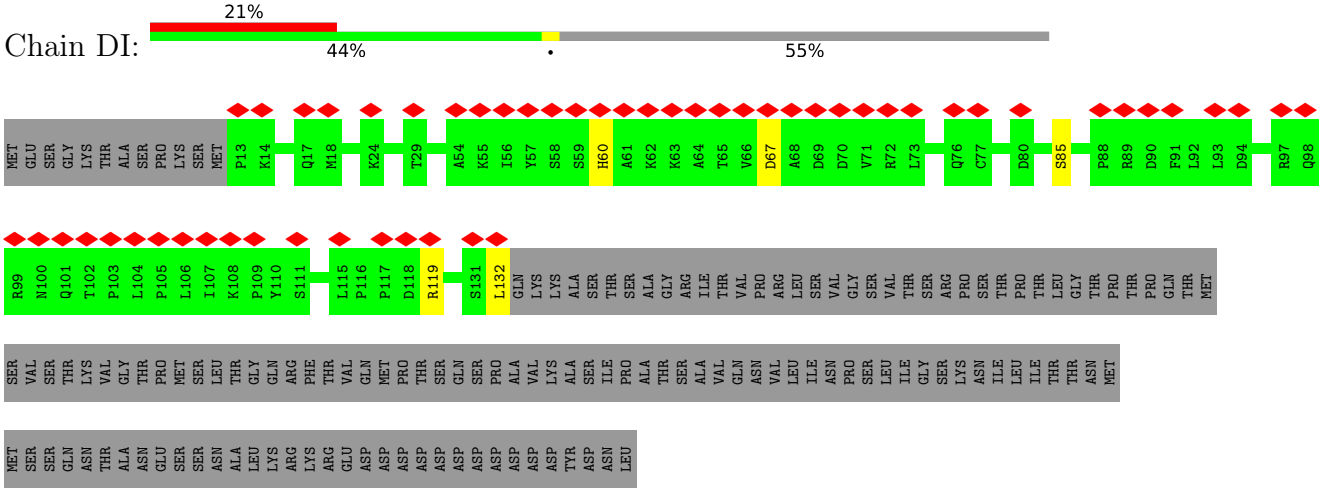
• Molecule 41: Transcription initiation factor TFIID subunit 8

Chain DH:



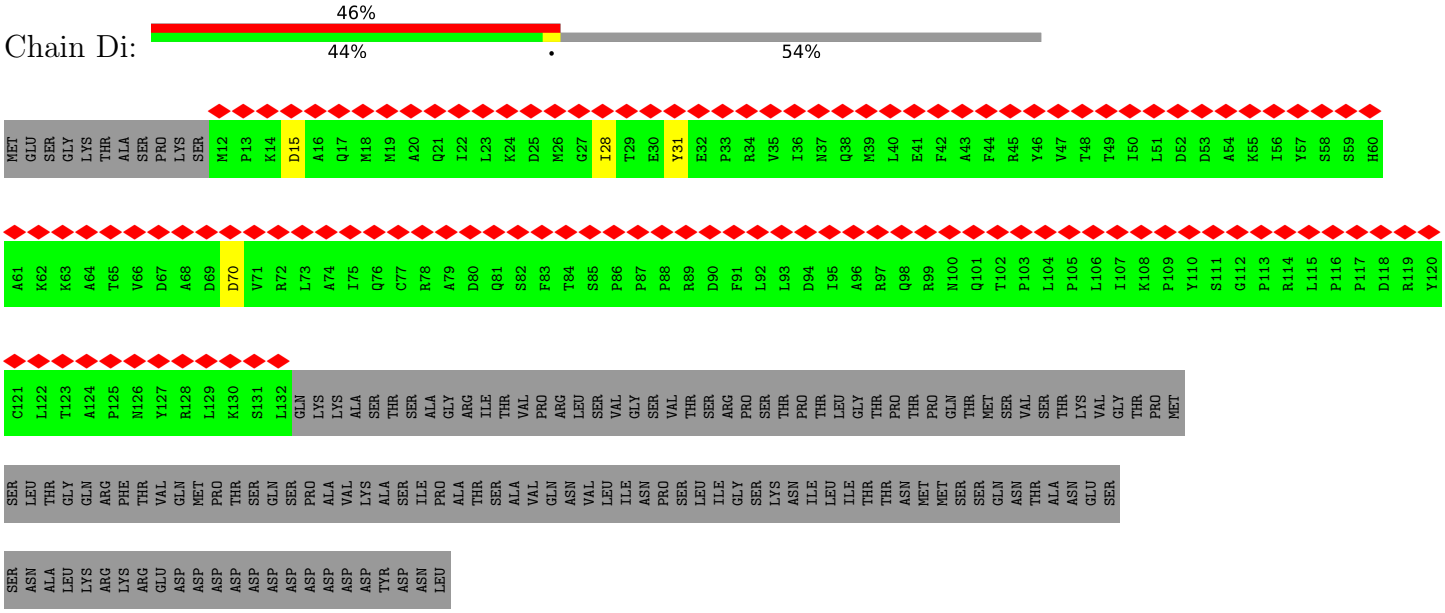
• Molecule 42: Transcription initiation factor TFIID subunit 9

Chain DI:



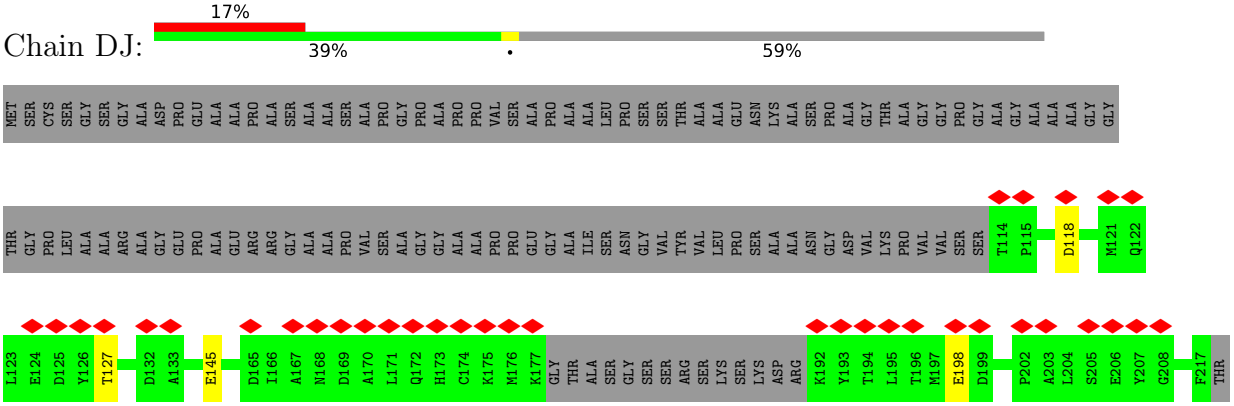
• Molecule 42: Transcription initiation factor TFIID subunit 9

Chain Di:



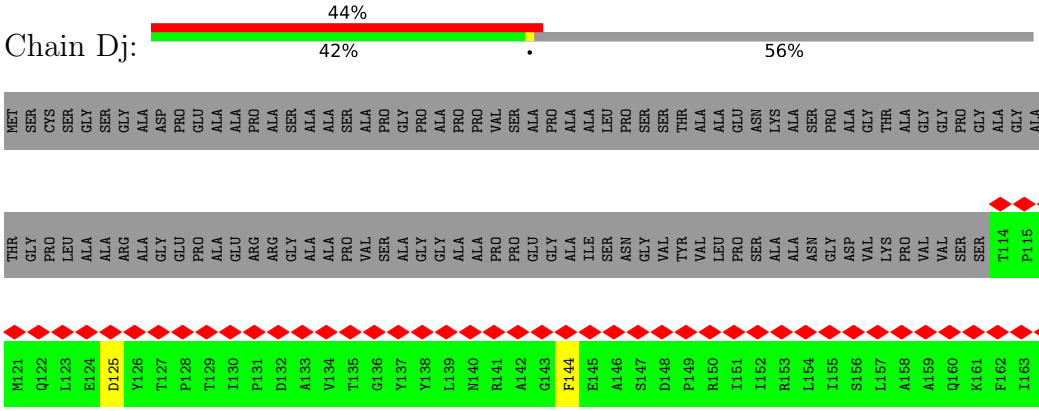
• Molecule 43: Transcription initiation factor TFIID subunit 10

Chain DJ:



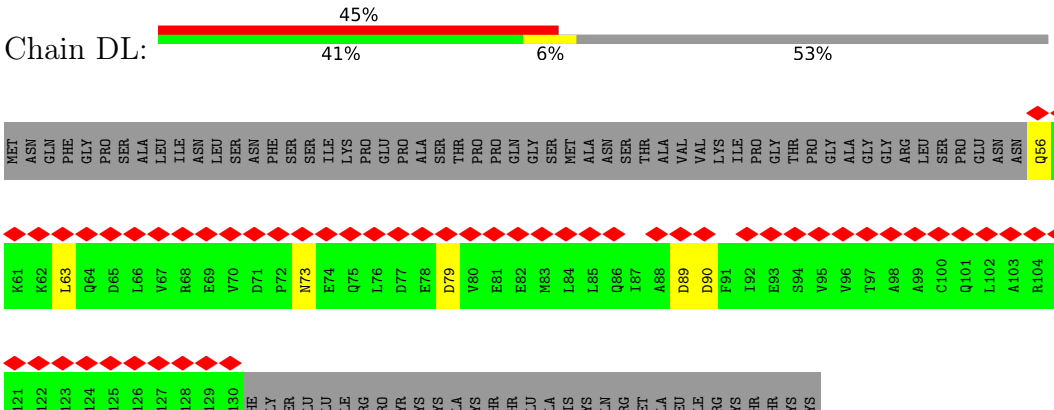
• Molecule 43: Transcription initiation factor TFIID subunit 10

Chain Dj:



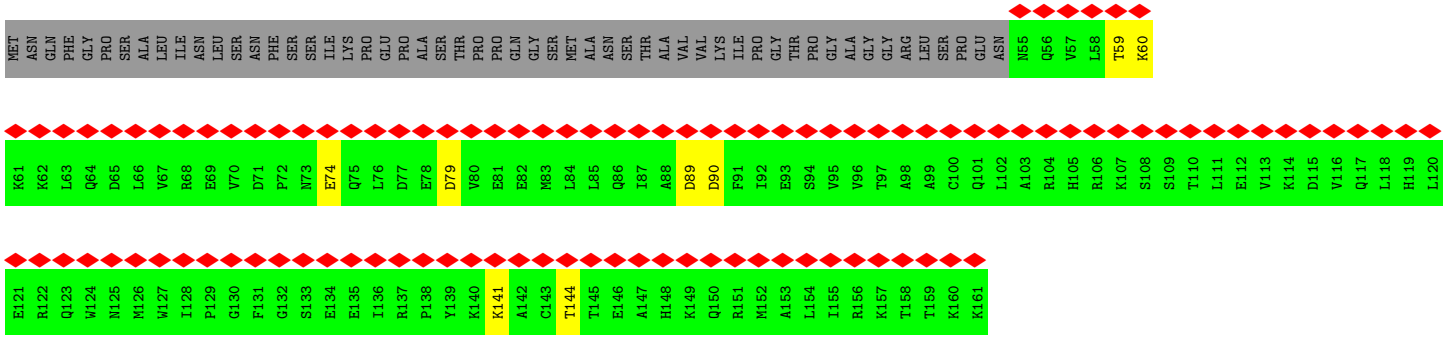
• Molecule 44: Transcription initiation factor TFIID subunit 12

Chain DL:

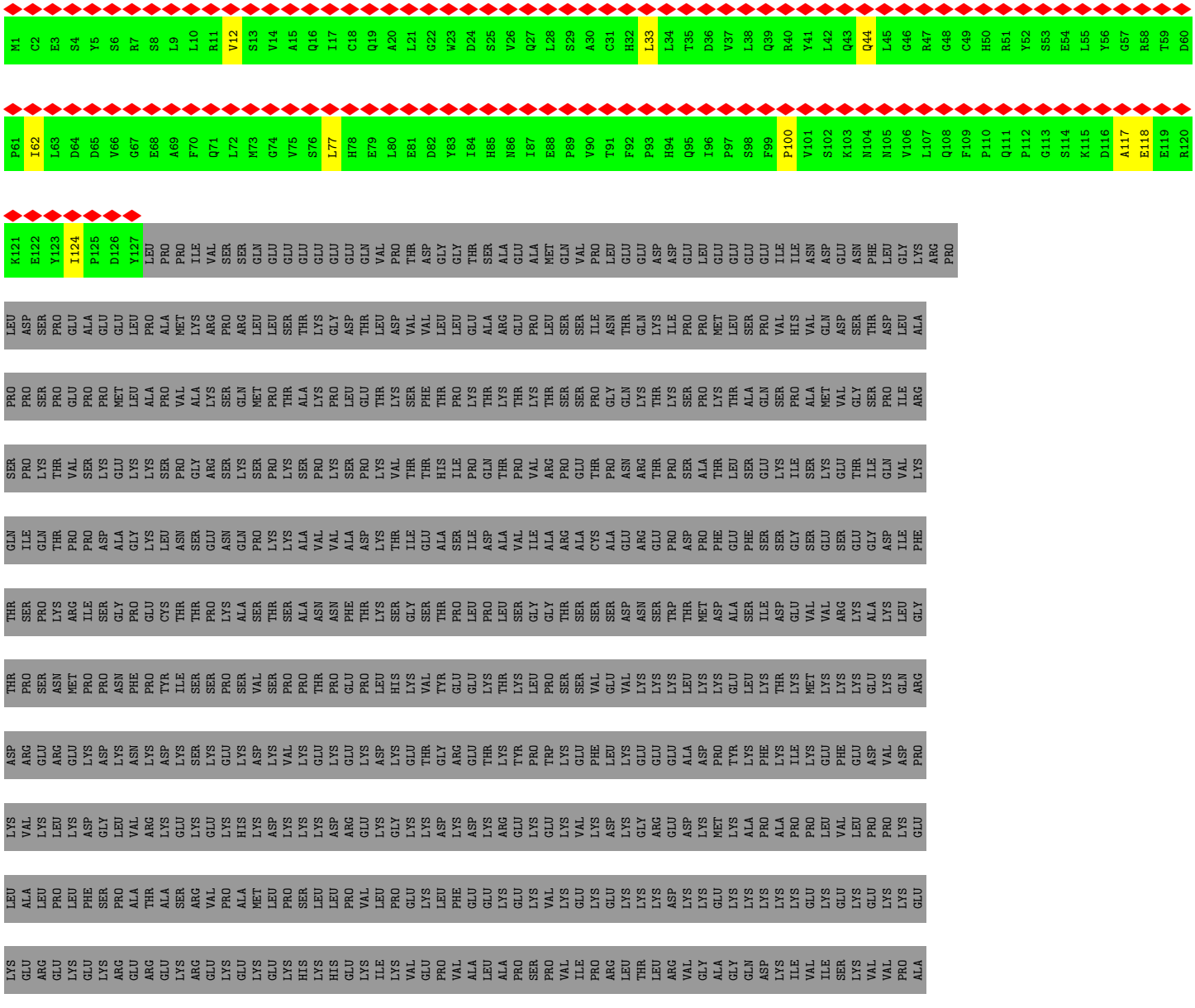


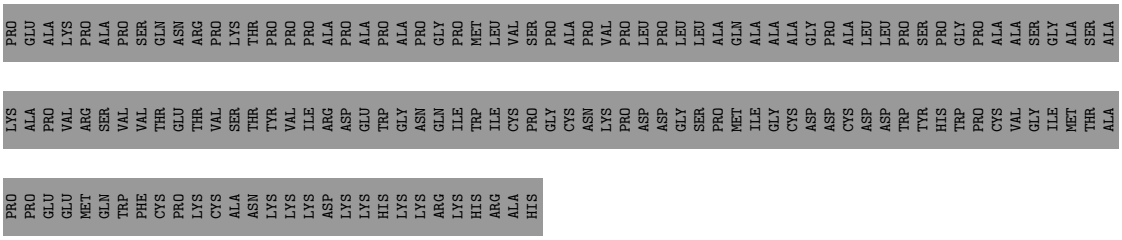
• Molecule 44: Transcription initiation factor TFIID subunit 12

Chain Dl:



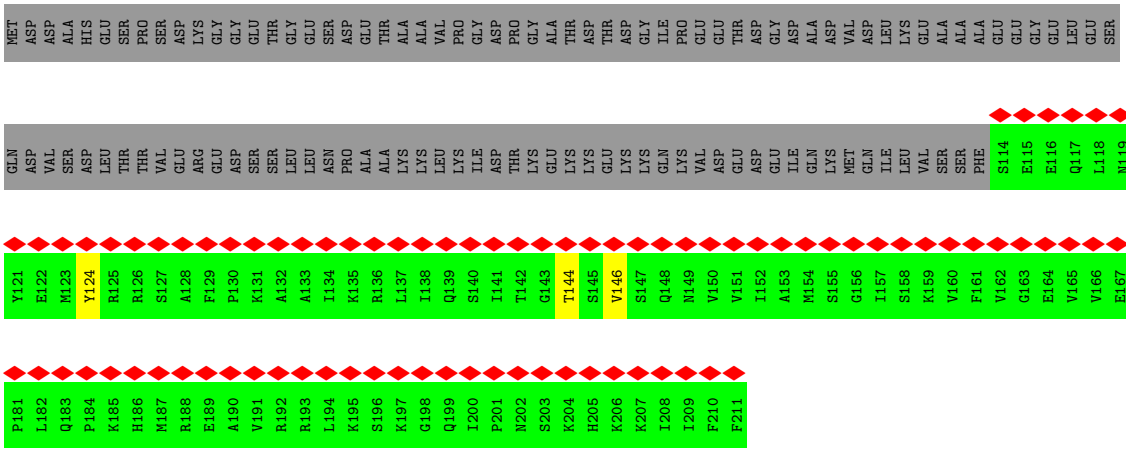
• Molecule 45: Transcription initiation factor TFIID subunit 3





• Molecule 46: Transcription initiation factor TFIID subunit 11

Chain Dk:

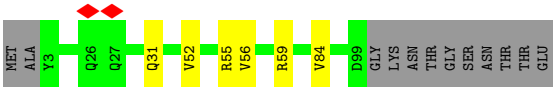


• Molecule 47: Transcription initiation factor TFIID subunit 13

Chain Dm:

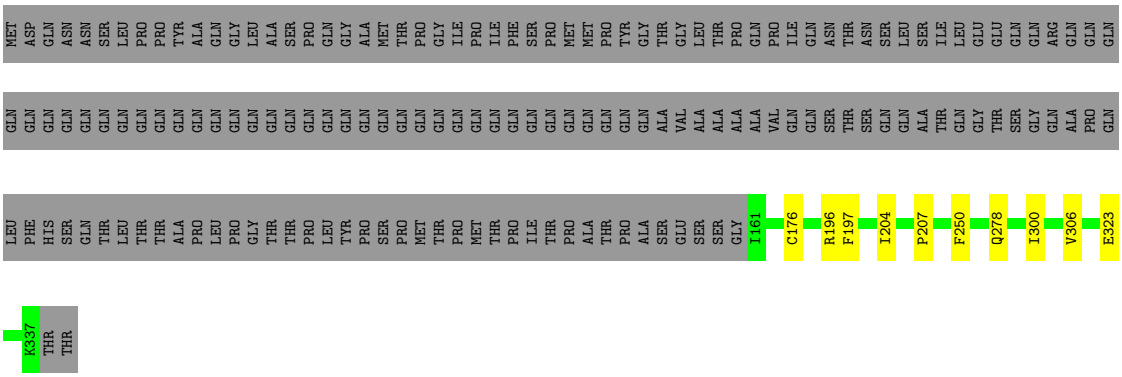
• Molecule 48: Transcription initiation factor IIA subunit 2

Chain DO:



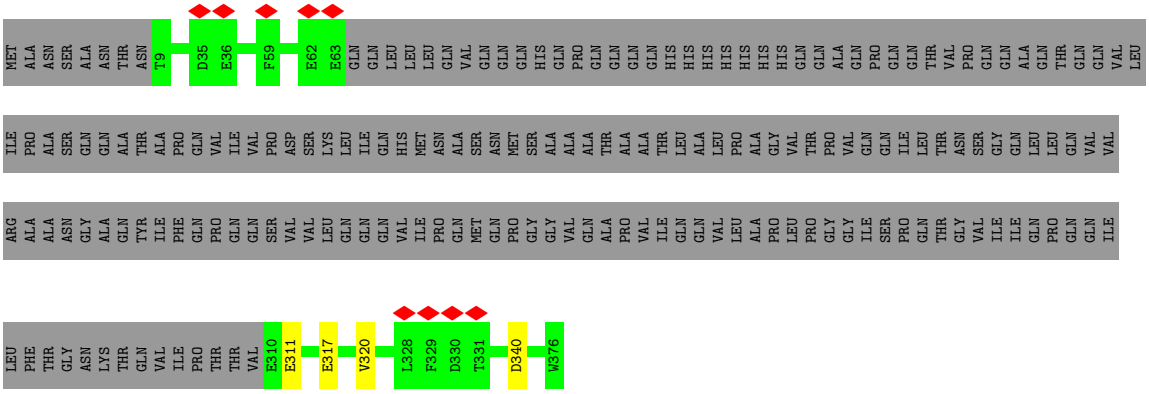
• Molecule 49: TATA-box-binding protein

Chain DP:



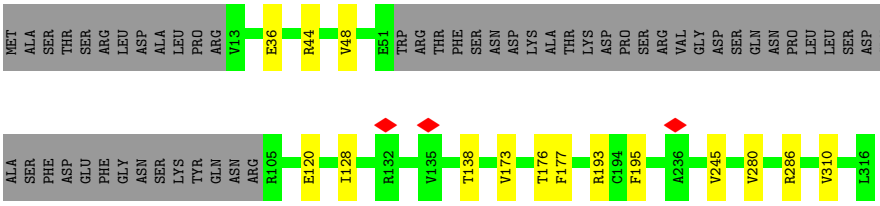
• Molecule 50: TFIIA-a

Chain DQ:



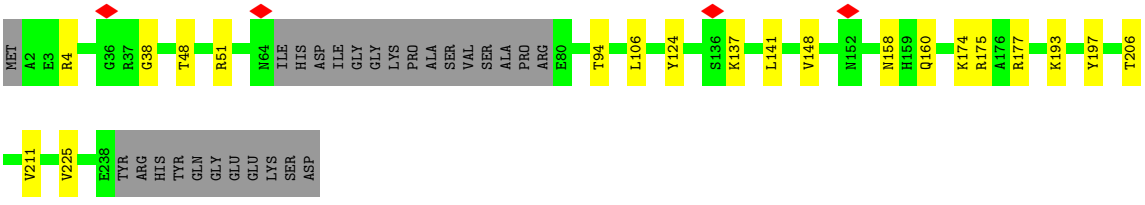
• Molecule 51: Transcription initiation factor IIB

Chain BA:



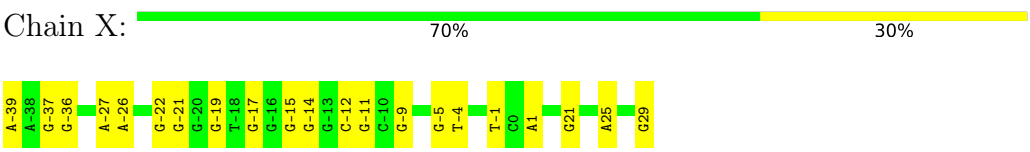
• Molecule 52: General transcription factor IIF subunit 2

Chain FB:



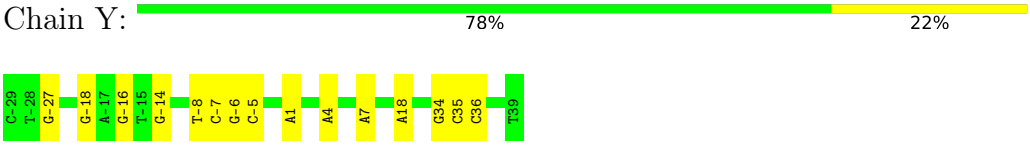
• Molecule 53: DNA (69-MER)

Chain X:



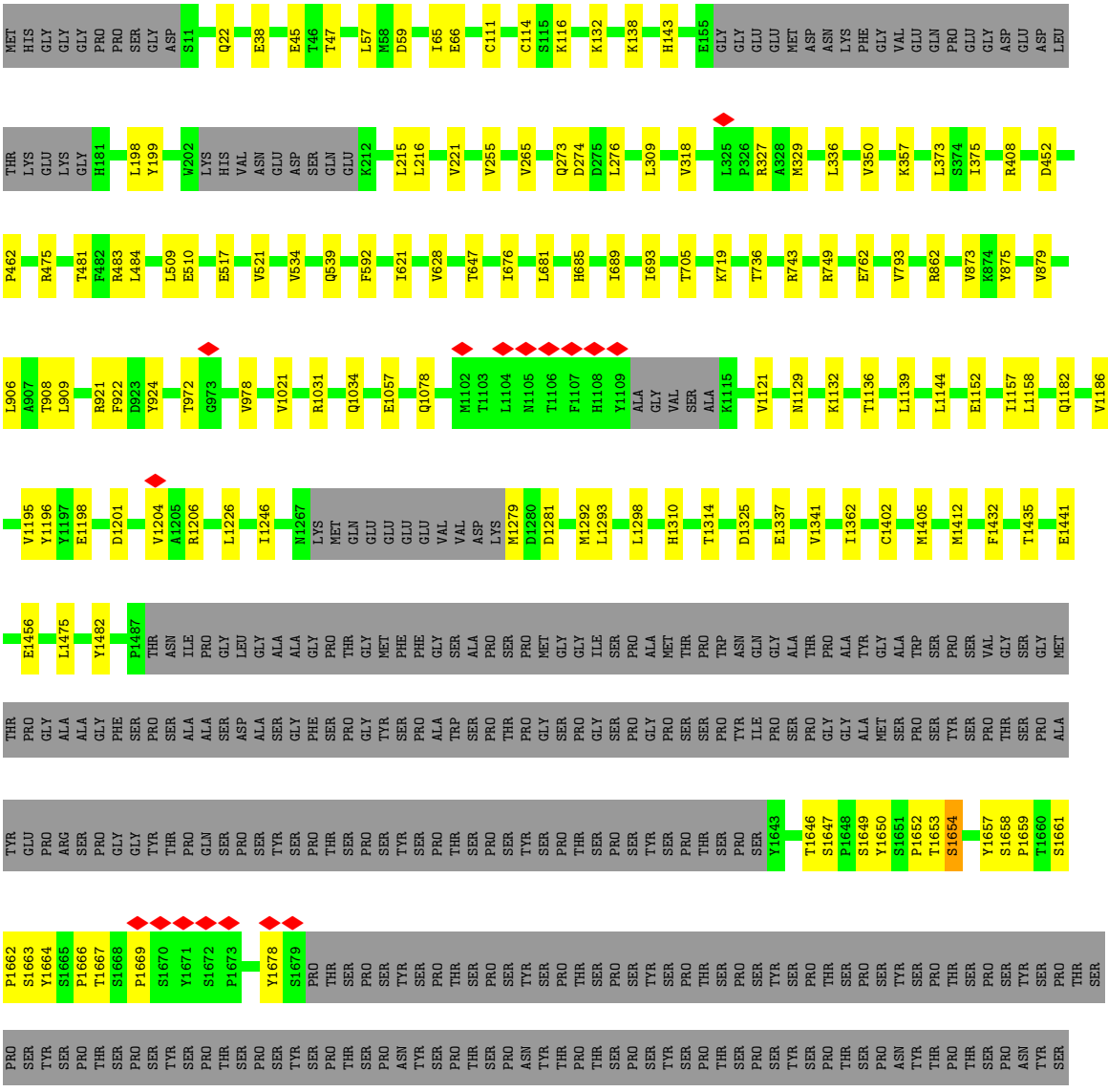
• Molecule 54: DNA (69-MER)

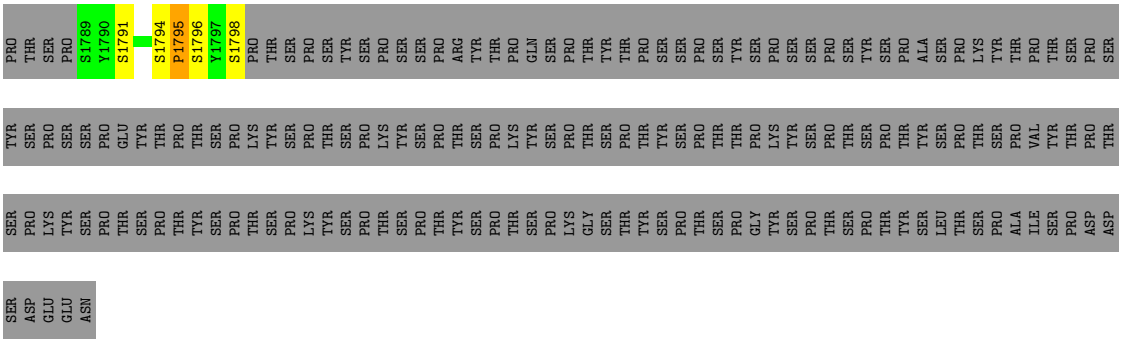
Chain Y:



• Molecule 55: RPB1

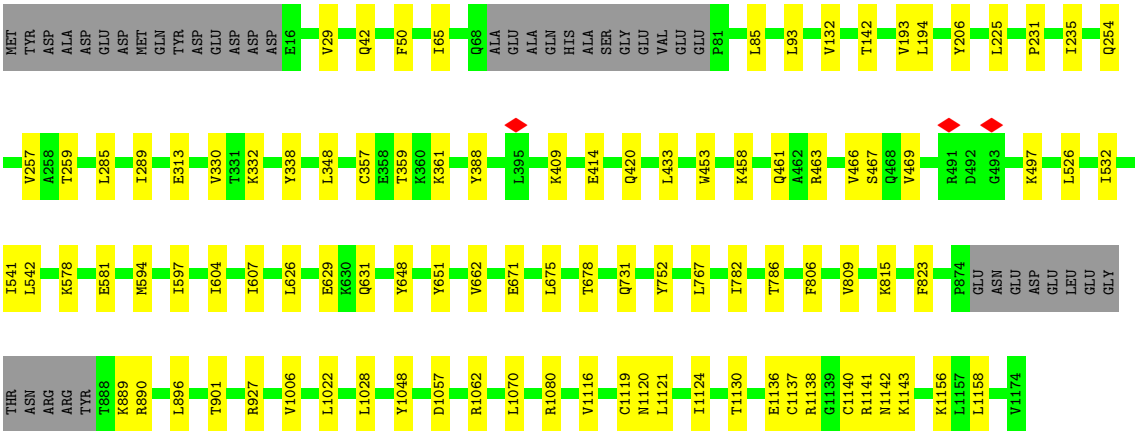
Chain PA:





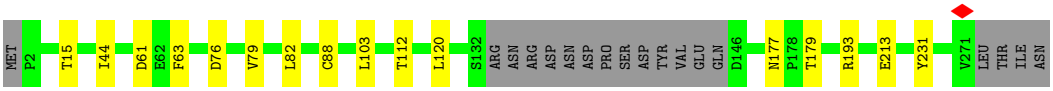
• Molecule 56: DNA-directed RNA polymerase subunit beta

Chain PB:



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

Chain PC:

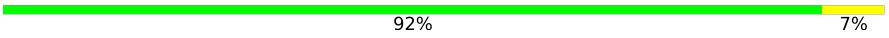


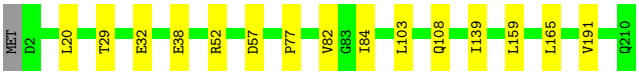
• Molecule 58: DNA-directed RNA polymerase II subunit RPB4

Chain PD:

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

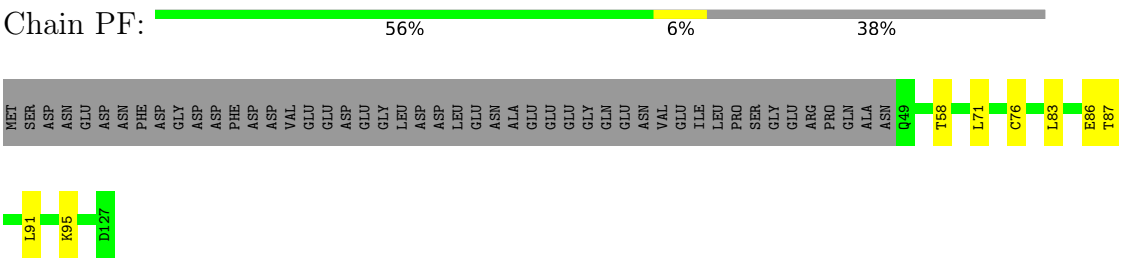
Chain PE:





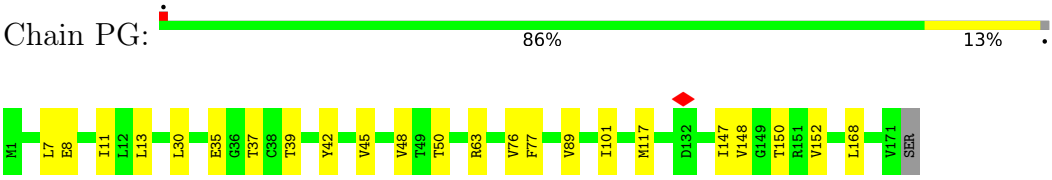
• Molecule 60: DNA-directed RNA polymerase II subunit F

Chain PF:



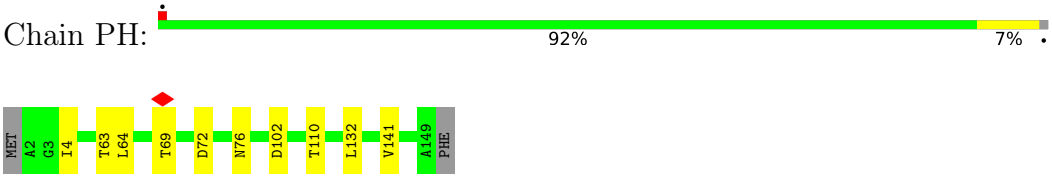
• Molecule 61: DNA-directed RNA polymerase II subunit RPB7

Chain PG:



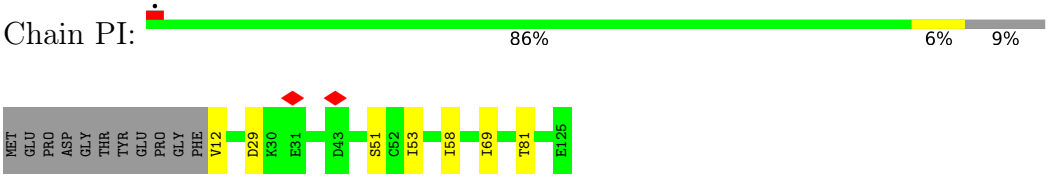
• Molecule 62: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain PH:



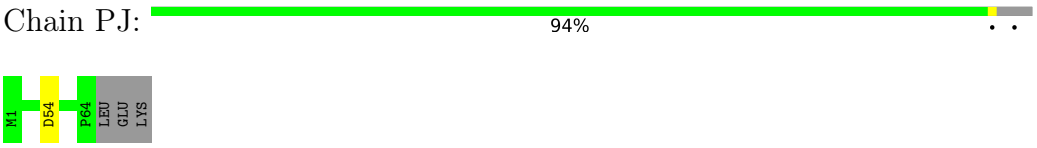
• Molecule 63: DNA-directed RNA polymerase II subunit RPB9

Chain PI:



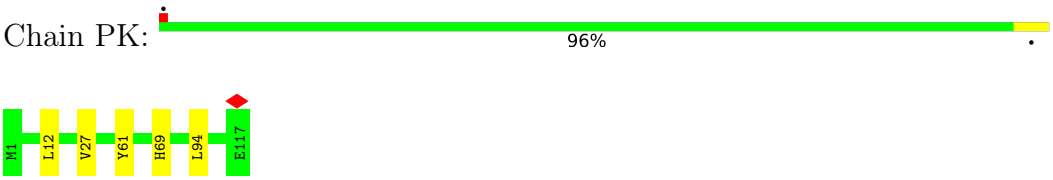
• Molecule 64: RPB10

Chain PJ:



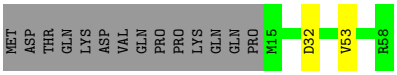
• Molecule 65: RNA_pol_L_2 domain-containing protein

Chain PK:



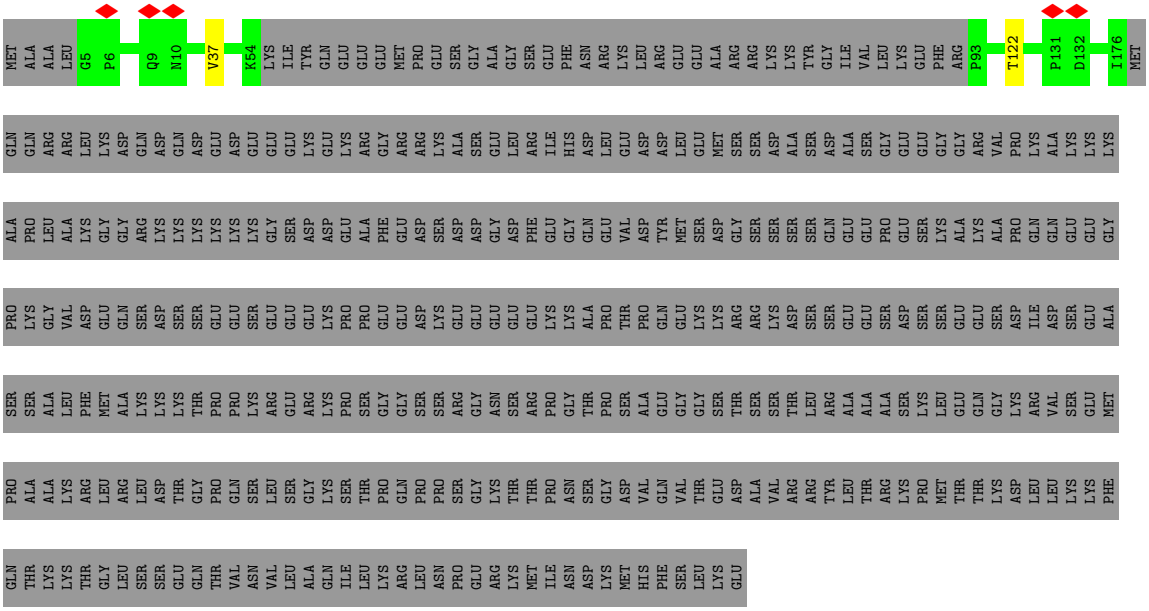
• Molecule 66: RPB12

Chain PL:



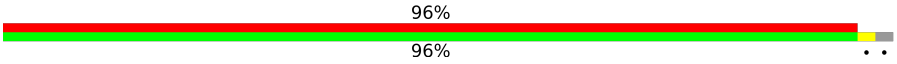
• Molecule 67: General transcription factor IIF subunit 1

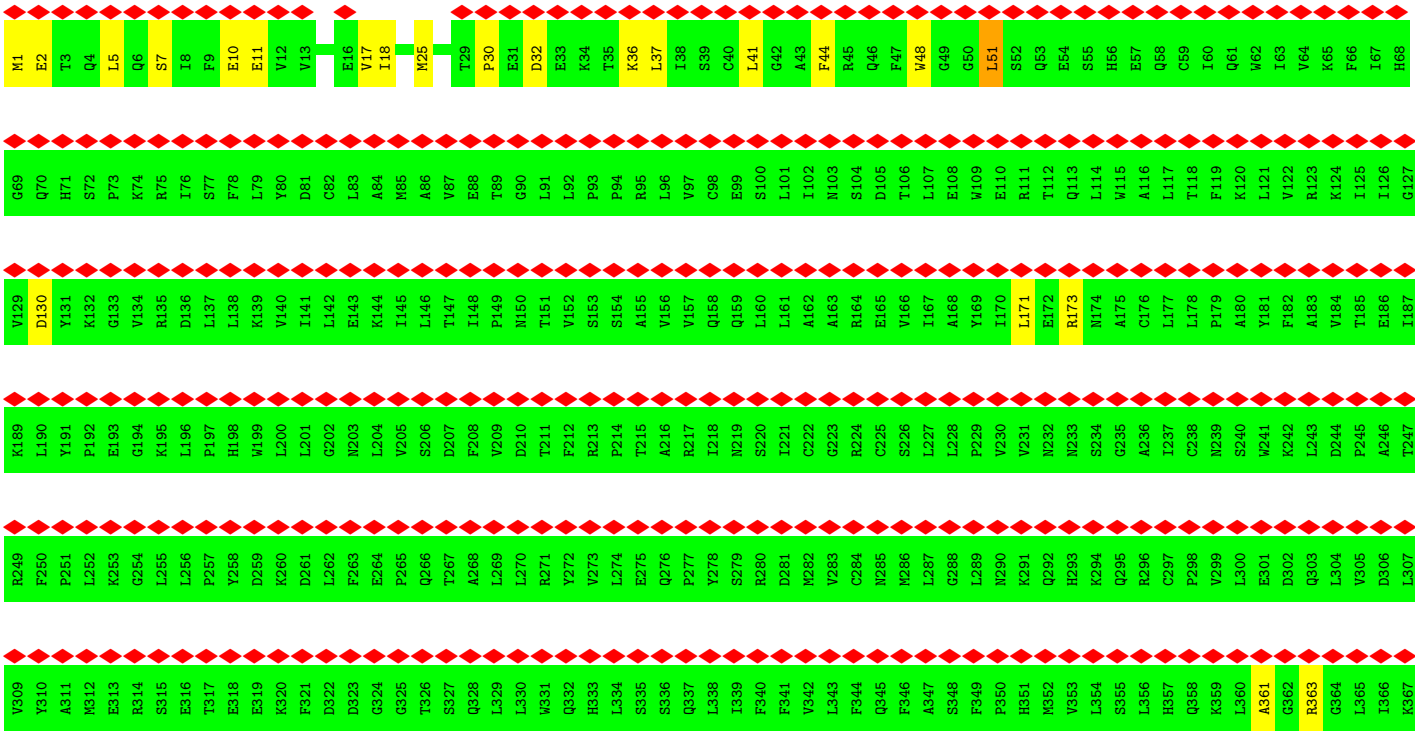
Chain FA:

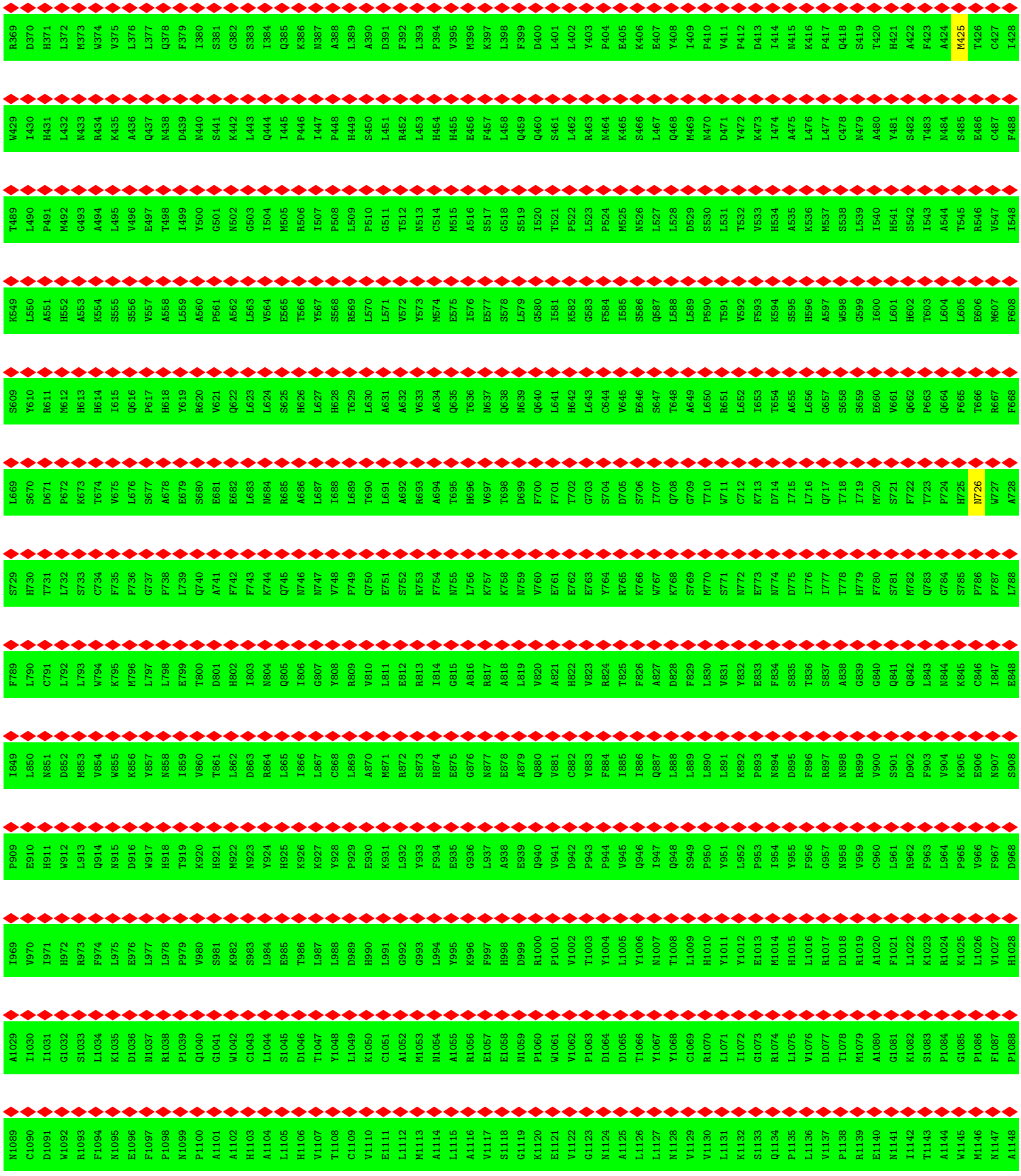


• Molecule 68: Mediator of RNA polymerase II transcription subunit 23

Chain w:



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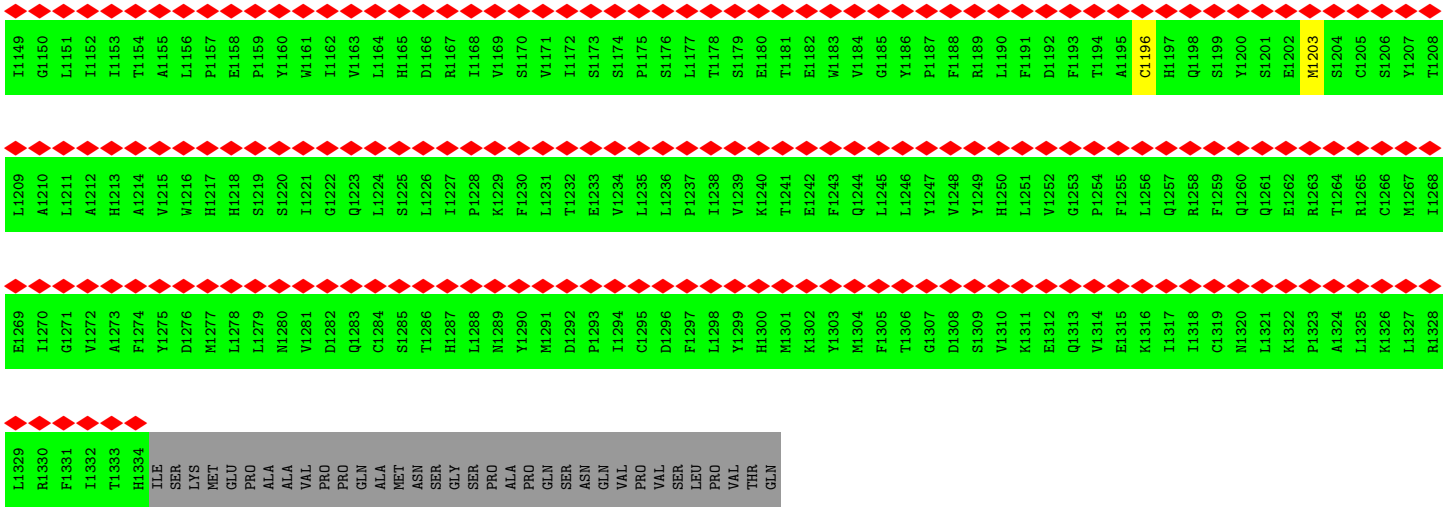
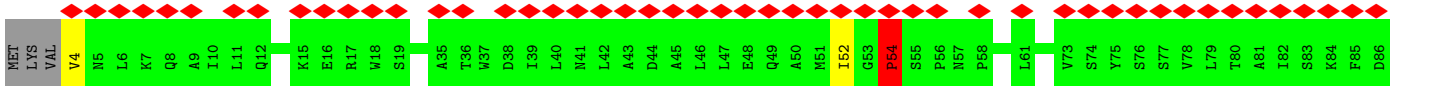
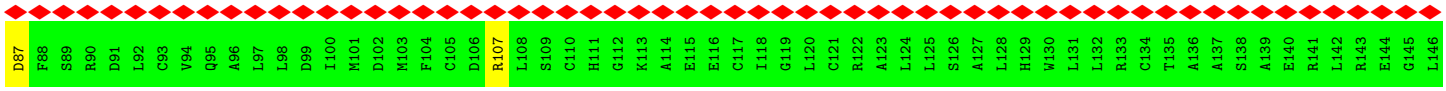
W429 I430 H431 L432 N433 R434 K435 A436 Q437 N438 D439 N440 S441 K442 L443 Q444 I445 P446 I447 P448 H449 S450 L451 R452 L453 H454 H455 E456 F457 L458 Q459 Q460 S461 L462 R463 N464 K465 S466 L467 Q468 M469 N470 D471 Y472 K473 I474 A475 L476 L477 C478 N479 A480 Y481 S482 T483 N484 S485 E486 C487 F488
T489 L490 P491 M492 G493 A494 L495 V496 E497 T498 I499 Y500 G501 N502 G503 I504 M505 R506 I507 P508 L509 P510 G511 T512 N513 C514 M515 A516 S517 G518 S519 I520 T521 P522 L523 P524 M525 N526 L527 L528 D529 S530 L531 T532 V533 H534 A535 K536 M537 S538 L539 I540 H541 S542 I543 A544 T545 R546 V547 I548
K549 L550 A551 H552 A553 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 I585 S586 Q587 L588 L589 P590 T591 V592 F593 K594 S595 H596 A597 W598 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 L643 C644 V645 E646 S647 T648 A649 L650 R651 L652 I653 T654 A655 L656 G657 S658 S659 E660 V661 Q662 P663 Q664 F665 T666 R667 F668
L669 S670 D671 P672 K673 T674 V675 L676 S677 A678 E679 S680 E681 E682 L683 N684 R685 A686 L687 I688 L689 T690 L691 A692 R693 A694 T695 H696 V697 T698 D699 F700 F701 T702 G703 S704 D705 S706 I707 Q708 G709 T710 W711 C712 K713 D714 I715 L716 Q717 T718 I719 M720 S721 F722 T723 P724 H725 N726 W727 A728
S729 H730 T731 L732 S733 C734 F735 P736 G737 P738 L739 Q740 A741 F742 F743 K744 Q745 N746 N747 V748 P749 Q750 E751 S752 R753 F754 N755 L756 K757 K758 N759 V760 E761 E762 E763 Y764 R765 K766 W767 K768 S769 M770 S771 N772 E773 N774 D775 I776 I777 T778 H779 F780 S781 M782 Q783 G784 S785 P786 F787 L788
F789 L790 C791 L792 L793 W794 K795 M796 L797 L798 E799 T800 D801 H802 I803 N804 Q805 I806 G807 Y808 R809 V810 L811 E812 R813 I814 G815 A816 R817 A818 L819 V820 A821 H822 V823 R824 T825 F826 A827 D828 F829 L830 V831 Y832 E833 F834 S835 T836 S837 A838 G839 G840 Q841 Q842 L843 N844 K845 C846 I847 E848
I849 L850 N851 D852 M853 V854 W855 K856 Y857 N858 I859 V860 T861 L862 D863 R864 L865 I866 L867 C868 L869 A870 M871 R872 S873 H874 E875 G876 N877 E878 A879 Q880 V881 C882 Y883 F884 I885 I886 Q887 L888 L889 L890 L891 K892 P893 N894 D895 F896 R897 N898 R899 V900 S901 D902 F903 V904 K905 E906 N907 S908
P909 E910 H911 W912 L913 Q914 N915 D916 W917 H918 T919 K920 H921 M922 N923 Y924 H925 K926 K927 Y928 P929 E930 K931 L932 Y933 F934 E935 G936 L937 A938 E939 Q940 V941 D942 P943 P944 V945 Q946 I947 Q948 S949 P950 Y951 L952 P953 I954 Y955 F956 G957 N958 V959 C960 L961 R962 F963 L964 P965 V966 F967 D968
I969 V970 I971 W972 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 Y1006 N1007 T1008 L1009 H1010 Y1011 Y1012 E1013 M1014 H1015 L1016 R1017 D1018 R1019 A1020 F1021 L1022 K1023 R1024 K1025 L1026 V1027 H1028
A1029 I1030 I1031 G1032 S1033 L1034 K1035 D1036 N1037 R1038 P1039 Q1040 G1041 W1042 C1043 L1044 S1045 D1046 T1047 Y1048 L1049 K1050 C1051 A1052 M1053 N1054 A1055 R1056 E1057 E1058 N1059 P1060 W1061 V1062 P1063 D1064 D1065 T1066 Y1067 Y1068 C1069 R1070 L1071 I1072 G1073 R1074 L1075 V1076 D1077 T1078 M1079 A1080 G1081 K1082 S1083 P1084 G1085 P1086 F1087 P1088
N1089 C1090 D1091 W1092 R1093 F1094 N1095 E1096 F1097 P1098 N1099 P1100 A1101 A1102 H1103 A1104 L1105 H1106 V1107 T1108 C1109 V1110 E1111 L1112 M1113 A1114 L1115 A1116 V1117 S1118 G1119 K1120 E1121 V1122 G1123 N1124 A1125 L1126 L1127 N1128 V1129 V1130 L1131 K1132 S1133 Q1134 P1135 L1136 V1137 P1138 R1139 E1140 N1141 I1142 T1143 A1144 W1145 M1146 N1147 A1148

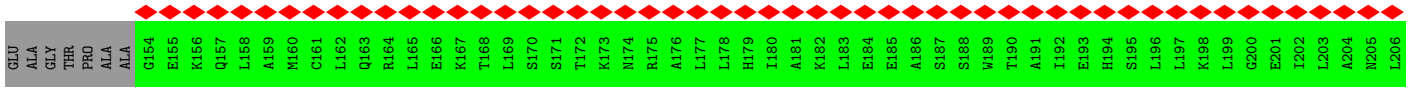


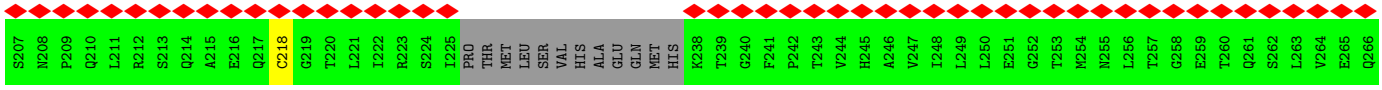
• Molecule 69: Mediator of RNA polymerase II transcription subunit 24

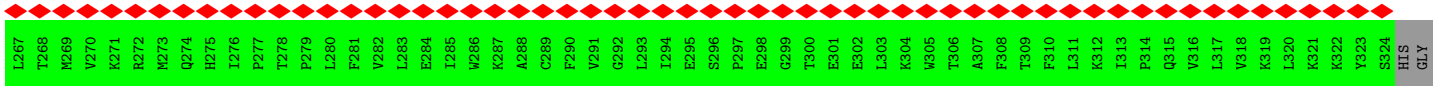
Chain x:

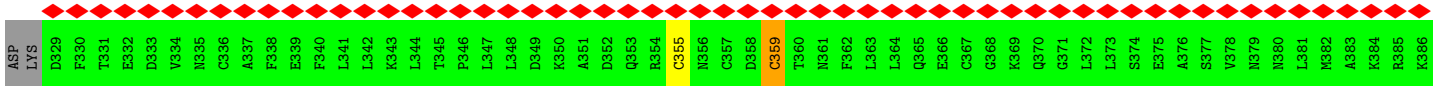


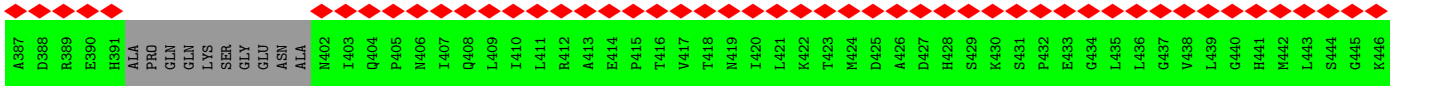


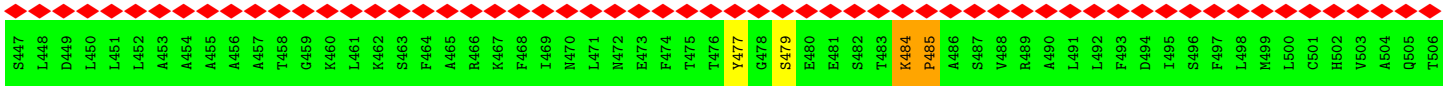












Y507 G508 S509 E510 V511 I512 L513 S514 E515 S516 R517 T518 G519 A520 E521 V522 P523 F524 F525 E526 T527 W528 M529 Q530 T531 C532 M533 P534 E535 E536 G537 K538 I539 L540 N541 P542 D543 H544 P545 C546 F547 R548 P549 D550 S551 T552 K553 V554 E555 S556 L557 V558 A559 L560 L561 N562 N563 S564 S565 E566

M567 K568 L569 V570 Q571 M572 K573 W574 H575 E576 A577 C578 L579 S580 I581 S582 A583 A584 I585 L586 E587 I588 L589 N590 A591 W592 E593 N594 G595 V596 L597 A598 F599 E600 S601 I602 Q603 K604 I605 T606 D607 N608 I609 K610 G611 K612 V613 C614 S615 L616 A617 V618 C619 A620 V621 A622 W623 L624 V625 A626

H627 V628 R629 M630 L631 G632 L633 D634 E635 R636 E637 K638 S639 L640 Q641 M642 I643 R644 Q645 L646 A647 G648 P649 L650 F651 S652 E653 N654 T655 L656 Q657 F658 Y659 N660 E661 R662 V663 V664 I665 M666 N667 S668 I669 L670 E671 R672 M673 C674 A675 D676 V677 L678 Q679 Q680 T681 A682 T683 Q684 I685 K686

F687 P688 SER THR GLY VAL D693 T694 M695 P696 Y697 W698 N699 L700 L701 P702 P703 K704 R705 P706 I707 K708 E709 V710 L711 T712 D713 I714 F715 A716 K717 V718 L719 E720 K721 G722 W723 V724 D725 S726 R727 S728 I729 H730 I731 F732 D733 T734 L735 L736 H737 M738 G739 G740 V741 Y742 W743 F744 C745 N746

N747 L748 I749 K750 E751 L752 L753 K754 E755 T756 R757 K758 E759 H760 T761 L762 R763 A764 V765 E766 L767 L768 Y769 S770 I771 F772 C773 L774 D775 M776 Q777 Q778 V779 T780 L781 V782 L783 L784 G785 H786 I787 L788 P789 G790 L791 L792 T793 D794 S795 S796 K797 W798 H799 S800 L801 M802 D803 P804 P805 G806

T807 A808 L809 A810 K811 L812 A813 V814 W815 C816 A817 L818 S819 S820 Y821 S822 S823 HIS LYS GLY GLN A828 S829 T830 R831 Q832 K833 K834 R835 H836 R837 E838 D839 I840 E841 D842 Y843 I844 S845 L846 F847 P848 L849 D850 ASP VAL GLN PRO SER LYS LEU MET ARG LEU LEU SER SER ASN GLU ASP

ASP ALA ASN ILE LEU SER SER PRO THR ASP ARG SER MET SER SER SER LEU SER ALA SER GLN LEU HIS THR V891 N892 M893 R894 D895 P896 L897 N898 R899 V900 L901 A902 N903 L904 F905 L906 L907 I908 S909 S910 I911 L912 G913 S914 R915 T916 A917 G918 P919 H920 T921 Q922 F923 V924 Q925 W926

F927 M928 E929 E930 C931 V932 D933 C934 L935 E936 Q937 GLY GLY ARG GLY S942 V943 L944 Q945 F946 M947 P948 F949 T950 T951 V952 S953 E954 L955 V956 K957 V958 S959 ALA MET SER SER PRO K965 V966 V967 L968 A969 I970 T971 D972 L973 S974 L975 P976 L977 G978 R979 Q980 V981 A982 A983 K984 A985 I986

A987 A988 L989

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

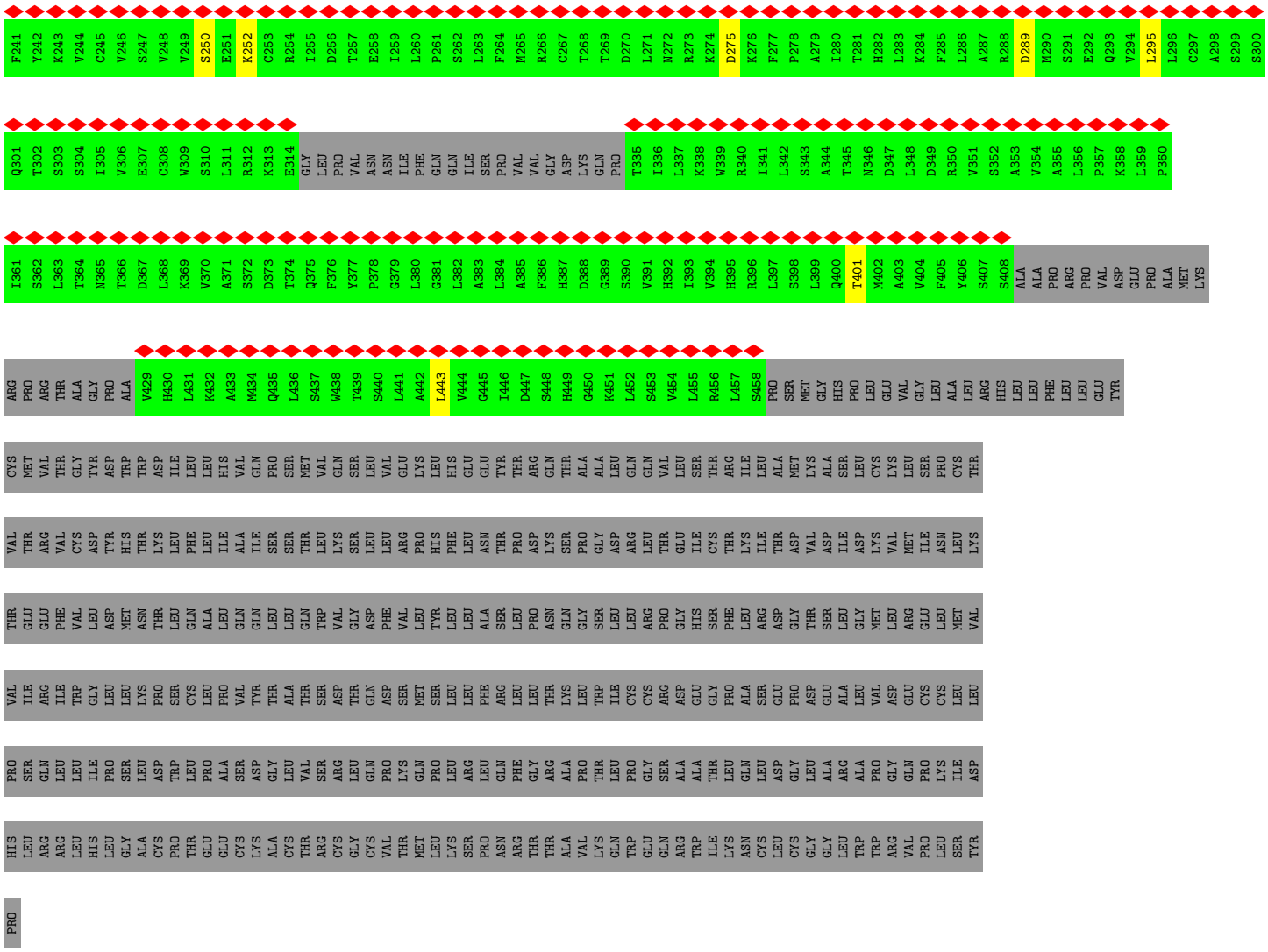
Chain p:

MET CYS ASP LEU ARG ARG PRO ALA ALA GLY GLY MET M13 D14 L15 A16 Y17 V18 C19 E20 W21 E22 K23 W24 S25 K26 S27 T28 H29 C30 P31 S32 V33 P34 L35 A36 C37 A38 W39 S40 C41 R42 N43 L44 I45 A46 F47 T48 M49 D50 L51 R52 S53 D54 D55 Q56 D57 L58 T59 R60

M61 I62 H63 I64 L65 D66 T67 E68 H69 P70 W71 D72 L73 H74 S75 I76 P77 S78 E79 H80 H81 E82 A83 I84 T85 C86 L87 E88 W89 D90 Q91 S92 G93 S94 R95 L96 L97 S98 A99 D100 A101 D102 G103 Q104 I105 K106 C107 W108 S109 M110 A111 D112 H113 L114 A115 N116 S117 W118 E119 S120

S121 V122 G123 S124 L125 V126 E127 G128 D129 P130 I131 V132 A133 L134 S135 W136 L137 H138 N139 G140 V141 K142 L143 A144 L145 H146 V147 E148 K149 S150 G151 A152 S153 S154 F155 G156 E157 K158 F159 S160 R161 V162 K163 F164 S165 P166 S167 L168 T169 L170 F171 G172 G173 K174 P175 M176 E177 G178 W179 I180

A181 V182 T183 V184 S185 G186 L187 V188 T189 V190 S191 L192 L193 K194 P195 S196 G197 Q198 V199 L200 T201 S202 T203 E204 S205 L206 C207 R208 L209 R210 G211 R212 V213 A214 L215 A216 D217 I218 A219 F220 T221 G222 G223 G224 W225 I226 V227 V228 A229 T230 A231 D232 G233 K234 S235 A236 S237 P238 V239 Q240


F241 Y242 K243 V244 C245 V246 S247 V248 V249 S250 E251 K252 C253 R254 I255 D256 T257 E258 I259 L260 P261 S262 L263 F264 M265 R266 C267 T268 T269 D270 L271 N272 R273 K274 D275 K276 F277 P278 A279 I280 T281 H282 L283 K284 F285 L286 A287 R288 D289 M290 S291 E292 Q293 V294 L295 L296 C297 A298 S299 S300
Q301 T302 S303 S304 I305 V306 E307 C308 W309 S310 L311 R312 K313 E314 GLY LEU PRO VAL ASN ASN ILE PHE GLN GLN ILE SER PRO VAL VAL GLY ASP LYS GLN PRO T335 I336 L337 K338 W339 R340 I341 L342 S343 A344 T345 N346 D347 L348 D349 R350 V351 S352 A353 V354 A355 L356 P357 K358 L359 P360
I361 S362 L363 T364 N365 T366 D367 L368 K369 V370 A371 S372 D373 T374 Q375 F376 Y377 P378 G379 L380 G381 L382 A383 L384 A385 F386 H387 D388 G389 S390 V391 H392 I393 V394 H395 R396 L397 S398 L399 Q400 T401 M402 A403 V404 F405 Y406 S407 S408 ALA ALA PRO ARG PRO VAL ASP GLU PRO ALA MET LYS
ARG PRO ARG THR ALA GLY PRO ALA V429 H430 L431 K432 A433 M434 Q435 L436 S437 W438 T439 S440 L441 A442 L443 V444 G445 I446 D447 S448 H449 G450 K451 L452 S453 V454 L455 R456 L457 S458 PRO SER MET GLY HIS PRO LEU GLU VAL GLY LEU ALA LEU ARG HIS LEU LEU PHE LEU LEU GLU TYR
CYS MET VAL THR GLY TYR ASP TRP TRP ASP ILE LEU LEU HIS VAL GLN PRO SER MET VAL GLN SER LEU VAL GLU LYS LEU HIS GLU GLU TYR THR ARG GLN THR ALA ALA LEU GLN GLN VAL LEU SER THR ARG ILE LEU ALA MET LYS ALA SER LEU CYS LYS LEU SER PRO CYS THR
VAL THR ARG VAL CYS ASP TYR HIS THR LYS LEU LEU PHE LEU ILE ALA ILE SER SER THR LEU LYS SER LEU LEU LEU ARG PRO HIS PHE LEU ASN THR PRO ASP LYS SER PRO GLY ASP ARG LEU THR GLU ILE CYS THR LYS ILE THR ASP VAL ASP ILE ASP LYS VAL MET ILE ASN LEU LYS
THR GLU GLU PHE VAL LEU ASP MET ASN THR LEU GLN ALA LEU GLN GLN LEU LEU LEU GLN TRP VAL GLY ASP PHE VAL LEU TYR LEU LEU ALA SER LEU PRO ASN GLN GLY SER LEU LEU ARG PRO GLY HIS SER PHE LEU ARG ASP GLY THR SER LEU GLY MET LEU ARG GLU LEU MET VAL
VAL ILE ARG ILE TRP GLY LEU LEU LYS PRO SER CYS LEU PRO VAL TYR THR ALA THR SER ASP THR GLN ASP SER MET SER LEU LEU PHE ARG LEU LEU THR LYS LEU TRP ILE CYS CYS ARG ASP GLU GLY PRO ALA SER GLU PRO ASP GLU ALA ALA LEU VAL ASP GLU CYS CYS LEU LEU
PRO SER GLN LEU LEU ILE PRO SER LEU ASP TRP LEU PRO ALA SER ASP GLY LEU VAL SER ARG LEU GLN PRO LYS GLN PRO LEU ARG LEU GLN PHE GLY ARG ALA PRO THR LEU PRO GLY SER ALA ALA THR LEU GLN LEU ASP GLY LEU ALA ARG ALA PRO GLY GLN PRO LYS ILE ASP
HIS LEU ARG ARG LEU HIS LEU GLY ALA CYS PRO THR GLU GLU CYS LYS ALA CYS THR ARG CYS GLY CYS VAL THR MET LEU LYS SER PRO ASN ARG THR THR ALA VAL LYS GLN TRP GLU GLN ARG TRP ILE LYS ASN CYS LEU CYS GLY GLY LEU TRP TRP ARG VAL PRO LEU SER TYR
PRO

4 Experimental information (i)

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 ($e^-/Å^2$)	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 (Å)	674.39996, 674.39996, 674.39996	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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, ZN, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	a	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	Dl	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(^{o})	Ideal(^{o})
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

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

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	a	457/1581 (29%)	421 (92%)	29 (6%)	7 (2%)	8 39
2	m	110/131 (84%)	106 (96%)	4 (4%)	0	100 100
3	d	154/270 (57%)	143 (93%)	6 (4%)	5 (3%)	3 25
4	f	163/246 (66%)	142 (87%)	15 (9%)	6 (4%)	2 23
5	g	164/233 (70%)	145 (88%)	10 (6%)	9 (6%)	1 18
6	h	188/268 (70%)	167 (89%)	12 (6%)	9 (5%)	2 19
7	r	189/208 (91%)	176 (93%)	10 (5%)	3 (2%)	8 38
8	t	189/212 (89%)	166 (88%)	15 (8%)	8 (4%)	2 21
9	j	120/135 (89%)	110 (92%)	6 (5%)	4 (3%)	3 24
10	k	110/117 (94%)	99 (90%)	9 (8%)	2 (2%)	7 35
11	n	980/1454 (67%)	877 (90%)	86 (9%)	17 (2%)	7 37
12	q	540/651 (83%)	474 (88%)	53 (10%)	13 (2%)	5 30
13	s	69/244 (28%)	60 (87%)	7 (10%)	2 (3%)	3 26
14	u	103/144 (72%)	93 (90%)	8 (8%)	2 (2%)	6 34
15	v	132/200 (66%)	119 (90%)	10 (8%)	3 (2%)	5 31
16	z	93/600 (16%)	84 (90%)	7 (8%)	2 (2%)	5 32
17	c	245/311 (79%)	232 (95%)	13 (5%)	0	100 100
18	e	98/178 (55%)	92 (94%)	4 (4%)	2 (2%)	6 34
19	b	111/200 (56%)	109 (98%)	1 (1%)	1 (1%)	14 50
20	l	120/178 (67%)	115 (96%)	5 (4%)	0	100 100
21	o	152/788 (19%)	138 (91%)	10 (7%)	4 (3%)	4 29
22	i	56/146 (38%)	54 (96%)	1 (2%)	1 (2%)	7 35
23	0	304/309 (98%)	285 (94%)	15 (5%)	4 (1%)	10 42
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%)	4 29
27	2	327/395 (83%)	315 (96%)	10 (3%)	2 (1%)	22 59
28	3	259/308 (84%)	257 (99%)	2 (1%)	0	100 100
29	4	447/462 (97%)	431 (96%)	12 (3%)	4 (1%)	14 50
30	5	52/71 (73%)	50 (96%)	2 (4%)	0	100 100
31	6	602/782 (77%)	585 (97%)	14 (2%)	3 (0%)	25 62
32	7	732/760 (96%)	704 (96%)	23 (3%)	5 (1%)	19 56

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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%)	3	26
35	DA	534/1872 (28%)	523 (98%)	9 (2%)	2 (0%)	30	67
36	DB	959/1199 (80%)	932 (97%)	25 (3%)	2 (0%)	44	77
37	DD	153/1085 (14%)	148 (97%)	4 (3%)	1 (1%)	19	56
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%)	44	77
39	DF	404/677 (60%)	393 (97%)	9 (2%)	2 (0%)	25	62
39	Df	399/677 (59%)	394 (99%)	4 (1%)	1 (0%)	37	71
40	DG	139/349 (40%)	137 (99%)	2 (1%)	0	100	100
41	DH	207/310 (67%)	199 (96%)	5 (2%)	3 (1%)	9	40
42	DI	118/264 (45%)	116 (98%)	1 (1%)	1 (1%)	16	53
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%)	2	21
44	Dl	105/161 (65%)	104 (99%)	0	1 (1%)	13	47
45	Dc	125/929 (14%)	122 (98%)	1 (1%)	2 (2%)	8	38
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%)	5	32
49	DP	175/339 (52%)	170 (97%)	4 (2%)	1 (1%)	22	59
50	DQ	118/307 (38%)	115 (98%)	2 (2%)	1 (1%)	16	53
51	BA	247/316 (78%)	244 (99%)	3 (1%)	0	100	100
52	FB	218/249 (88%)	210 (96%)	7 (3%)	1 (0%)	25	62
55	PA	1460/1970 (74%)	1415 (97%)	38 (3%)	7 (0%)	25	62
56	PB	1128/1174 (96%)	1104 (98%)	22 (2%)	2 (0%)	44	77
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%)	25	62

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
60	PF	77/127 (61%)	76 (99%)	0	1 (1%)	10 42
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%)	25 62
69	x	876/989 (89%)	820 (94%)	51 (6%)	5 (1%)	22 59
70	p	400/841 (48%)	367 (92%)	32 (8%)	1 (0%)	37 71
All	All	20999/34555 (61%)	19990 (95%)	829 (4%)	180 (1%)	17 50

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%)	1 11
2	m	102/115 (89%)	102 (100%)	0	100 100
3	d	138/230 (60%)	100 (72%)	38 (28%)	0 2
4	f	144/223 (65%)	126 (88%)	18 (12%)	3 17
5	g	157/215 (73%)	122 (78%)	35 (22%)	1 5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
6	h	168/225 (75%)	128 (76%)	40 (24%)	0 4
7	r	168/183 (92%)	133 (79%)	35 (21%)	1 6
8	t	166/178 (93%)	137 (82%)	29 (18%)	1 10
9	j	113/124 (91%)	109 (96%)	4 (4%)	31 53
10	k	94/98 (96%)	51 (54%)	43 (46%)	0 0
11	n	689/1272 (54%)	651 (94%)	38 (6%)	18 42
12	q	461/577 (80%)	391 (85%)	70 (15%)	2 13
13	s	31/208 (15%)	29 (94%)	2 (6%)	14 37
14	u	78/119 (66%)	67 (86%)	11 (14%)	3 15
15	v	122/173 (70%)	91 (75%)	31 (25%)	0 3
16	z	89/512 (17%)	76 (85%)	13 (15%)	2 14
17	c	231/280 (82%)	223 (96%)	8 (4%)	31 53
18	e	94/152 (62%)	94 (100%)	0	100 100
19	b	102/163 (63%)	92 (90%)	10 (10%)	6 23
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%)	10 32
24	8	259/299 (87%)	225 (87%)	34 (13%)	3 17
25	9	252/296 (85%)	221 (88%)	31 (12%)	4 18
26	1	176/484 (36%)	163 (93%)	13 (7%)	11 33
27	2	279/352 (79%)	257 (92%)	22 (8%)	10 31
28	3	234/272 (86%)	221 (94%)	13 (6%)	17 41
29	4	387/399 (97%)	366 (95%)	21 (5%)	18 42
30	5	48/64 (75%)	43 (90%)	5 (10%)	5 22
31	6	533/688 (78%)	488 (92%)	45 (8%)	9 30
32	7	616/664 (93%)	571 (93%)	45 (7%)	11 33
33	EA	163/373 (44%)	151 (93%)	12 (7%)	11 33
34	EB	155/261 (59%)	143 (92%)	12 (8%)	10 32
35	DA	488/1665 (29%)	449 (92%)	39 (8%)	10 31
36	DB	876/1083 (81%)	798 (91%)	78 (9%)	8 27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	DD	144/815 (18%)	138 (96%)	6 (4%)	25	48
37	Dd	146/815 (18%)	138 (94%)	8 (6%)	18	42
38	DE	478/657 (73%)	433 (91%)	45 (9%)	7	24
38	De	475/657 (72%)	424 (89%)	51 (11%)	5	21
39	DF	324/574 (56%)	298 (92%)	26 (8%)	10	31
39	Df	322/574 (56%)	309 (96%)	13 (4%)	27	49
40	DG	133/322 (41%)	117 (88%)	16 (12%)	4	18
41	DH	181/270 (67%)	167 (92%)	14 (8%)	10	32
42	DI	106/235 (45%)	102 (96%)	4 (4%)	28	51
42	Di	107/235 (46%)	103 (96%)	4 (4%)	29	52
43	DJ	79/154 (51%)	76 (96%)	3 (4%)	28	51
43	Dj	83/154 (54%)	80 (96%)	3 (4%)	30	52
44	DL	70/141 (50%)	67 (96%)	3 (4%)	25	48
44	Dl	98/141 (70%)	94 (96%)	4 (4%)	26	49
45	Dc	113/833 (14%)	106 (94%)	7 (6%)	15	38
46	Dk	87/182 (48%)	83 (95%)	4 (5%)	23	46
47	Dm	80/106 (76%)	73 (91%)	7 (9%)	8	27
48	DO	84/98 (86%)	80 (95%)	4 (5%)	21	45
49	DP	153/293 (52%)	144 (94%)	9 (6%)	16	40
50	DQ	111/269 (41%)	108 (97%)	3 (3%)	40	60
51	BA	214/268 (80%)	199 (93%)	15 (7%)	12	34
52	FB	196/218 (90%)	177 (90%)	19 (10%)	6	23
55	PA	1303/1748 (74%)	1167 (90%)	136 (10%)	5	22
56	PB	993/1027 (97%)	899 (90%)	94 (10%)	7	24
57	PC	234/252 (93%)	218 (93%)	16 (7%)	13	36
58	PD	108/126 (86%)	92 (85%)	16 (15%)	2	14
59	PE	191/192 (100%)	177 (93%)	14 (7%)	11	33
60	PF	69/111 (62%)	62 (90%)	7 (10%)	6	22
61	PG	147/153 (96%)	124 (84%)	23 (16%)	2	13
62	PH	129/131 (98%)	119 (92%)	10 (8%)	10	31
63	PI	103/112 (92%)	96 (93%)	7 (7%)	13	36

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
64	PJ	53/56 (95%)	52 (98%)	1 (2%)	52 69
65	PK	106/106 (100%)	101 (95%)	5 (5%)	22 46
66	PL	41/55 (74%)	39 (95%)	2 (5%)	21 44
67	FA	117/448 (26%)	115 (98%)	2 (2%)	56 72
68	w	1202/1232 (98%)	1181 (98%)	21 (2%)	56 72
69	x	787/864 (91%)	769 (98%)	18 (2%)	45 64
70	p	353/736 (48%)	346 (98%)	7 (2%)	50 68
All	All	18247/29966 (61%)	16706 (92%)	1541 (8%)	11 30

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 (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 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 (i)

There are no chain breaks in this entry.

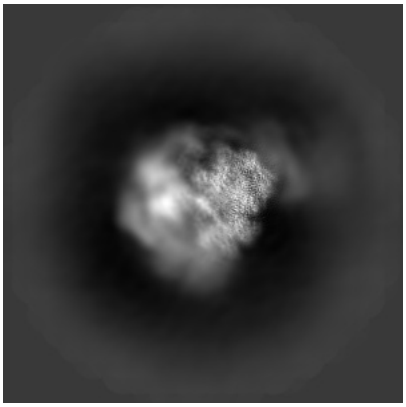
6 Map visualisation

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.

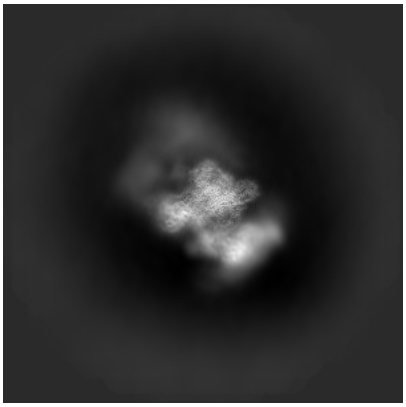
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

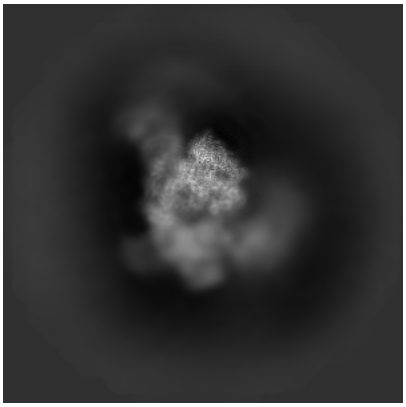
6.1.1 Primary map



X



Y

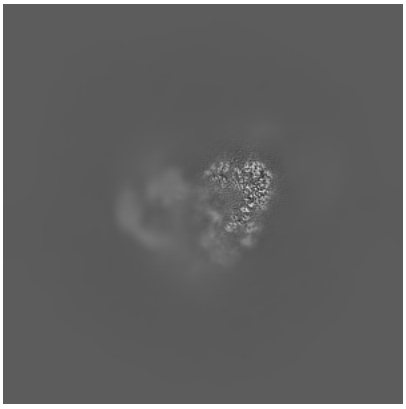


Z

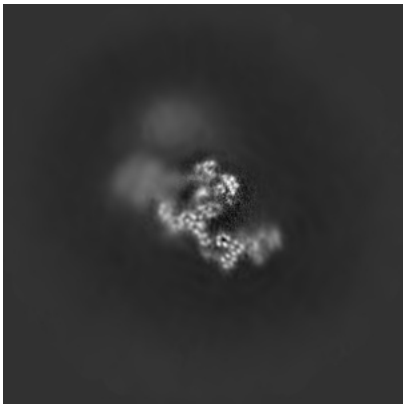
The images above show the map projected in three orthogonal directions.

6.2 Central slices

6.2.1 Primary map



X Index: 240



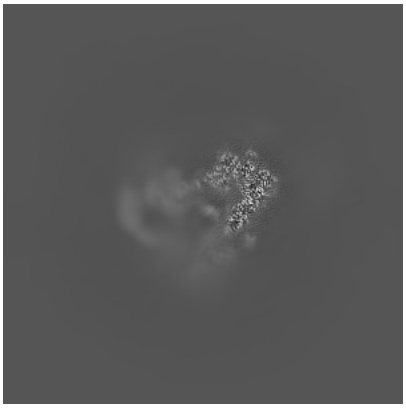
Y Index: 240

Z Index: 240

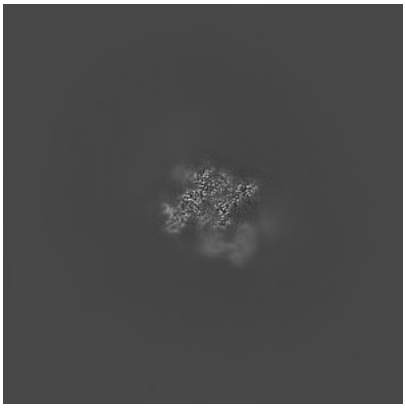
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

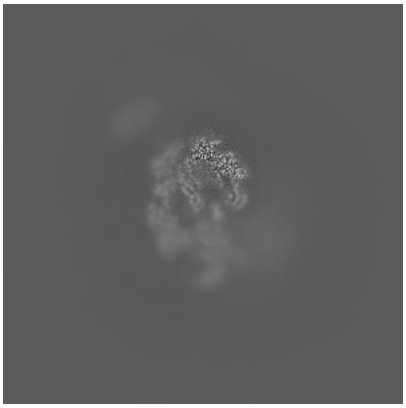
6.3.1 Primary map



X Index: 246



Y Index: 287

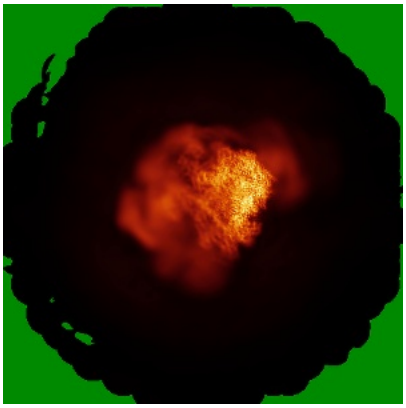


Z Index: 247

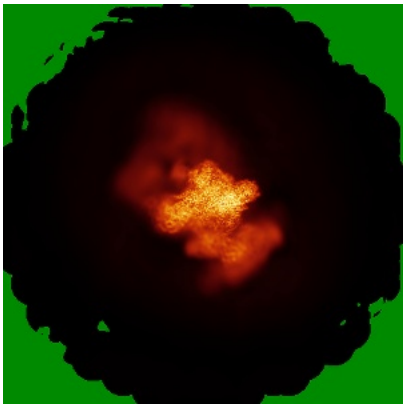
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

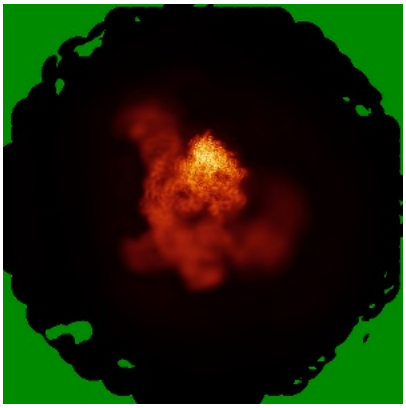
6.4.1 Primary map



X



Y

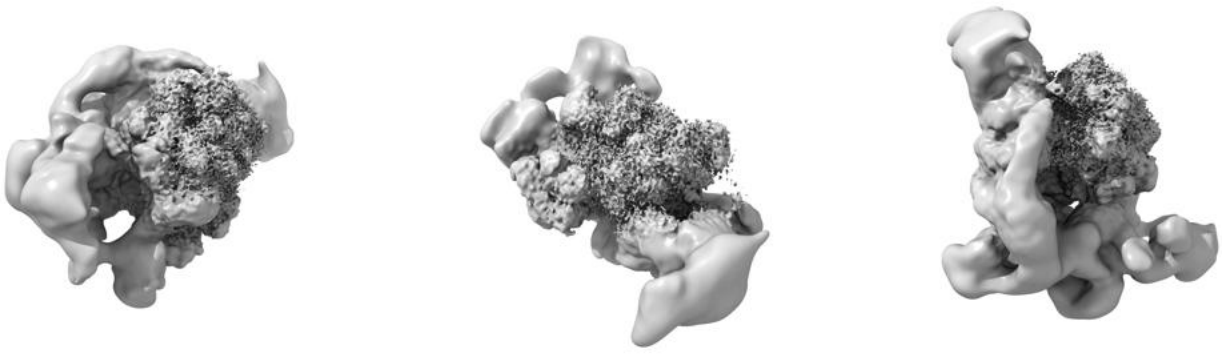


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map



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.

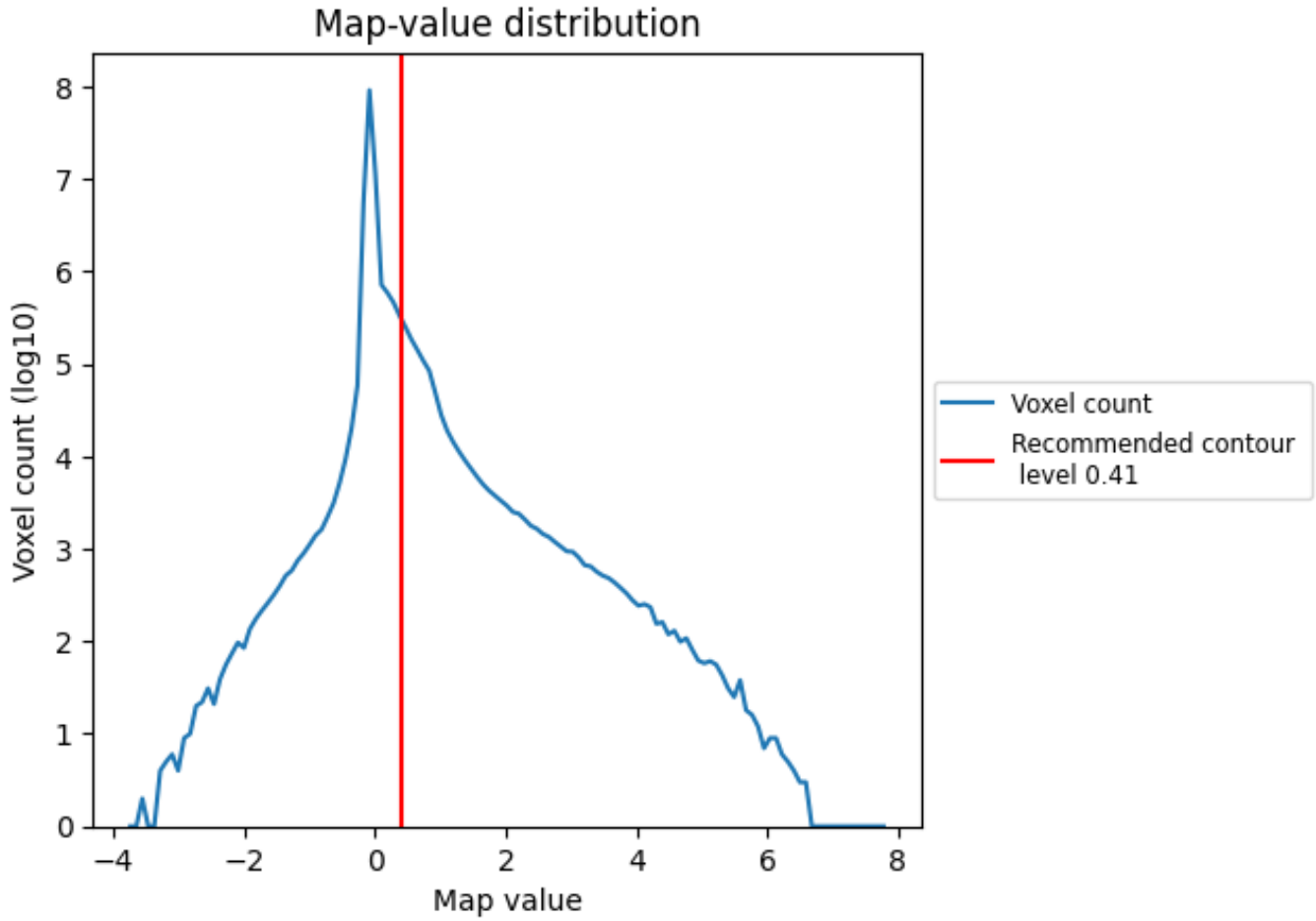
6.6 Mask visualisation (i)

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

7 Map analysis

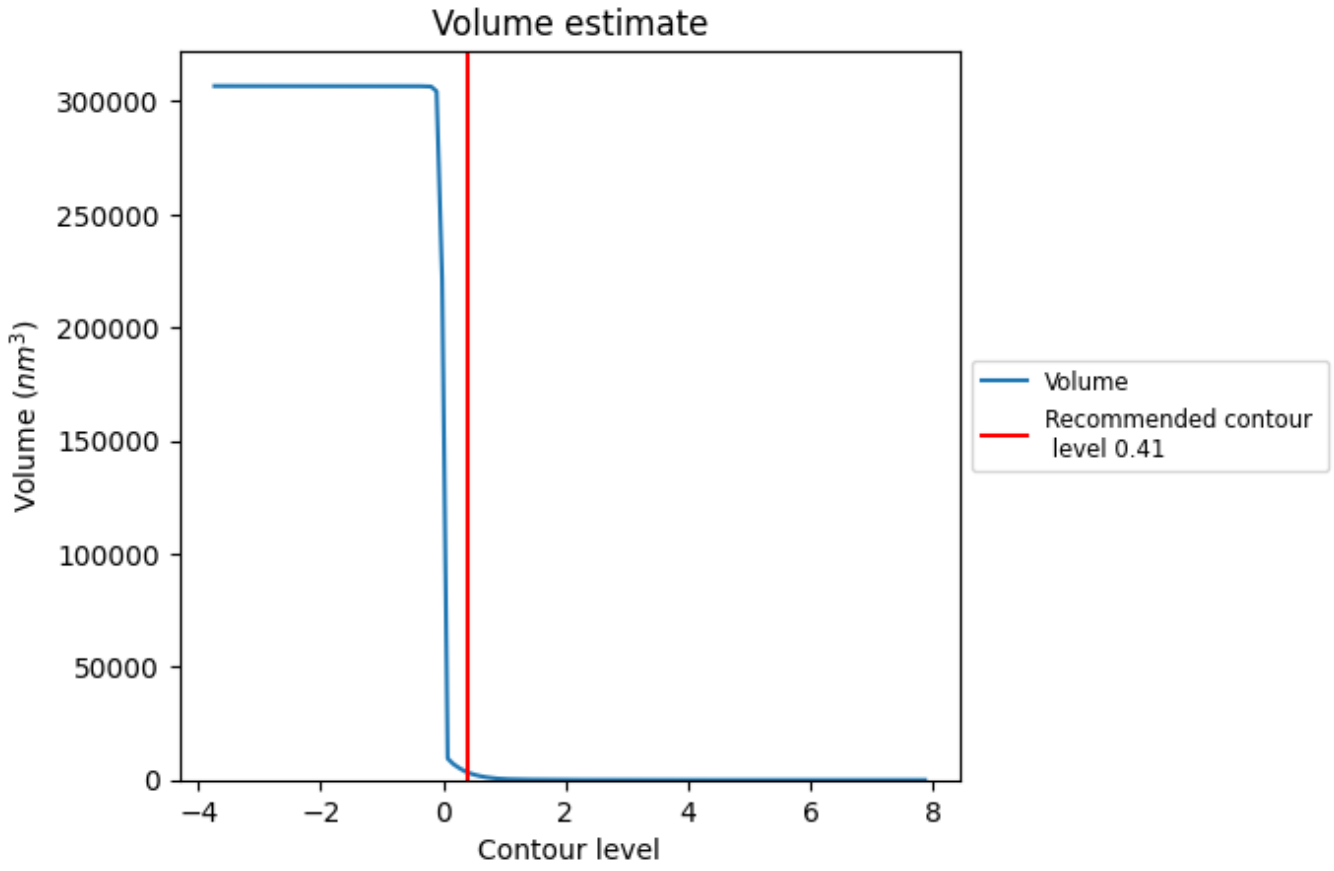
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

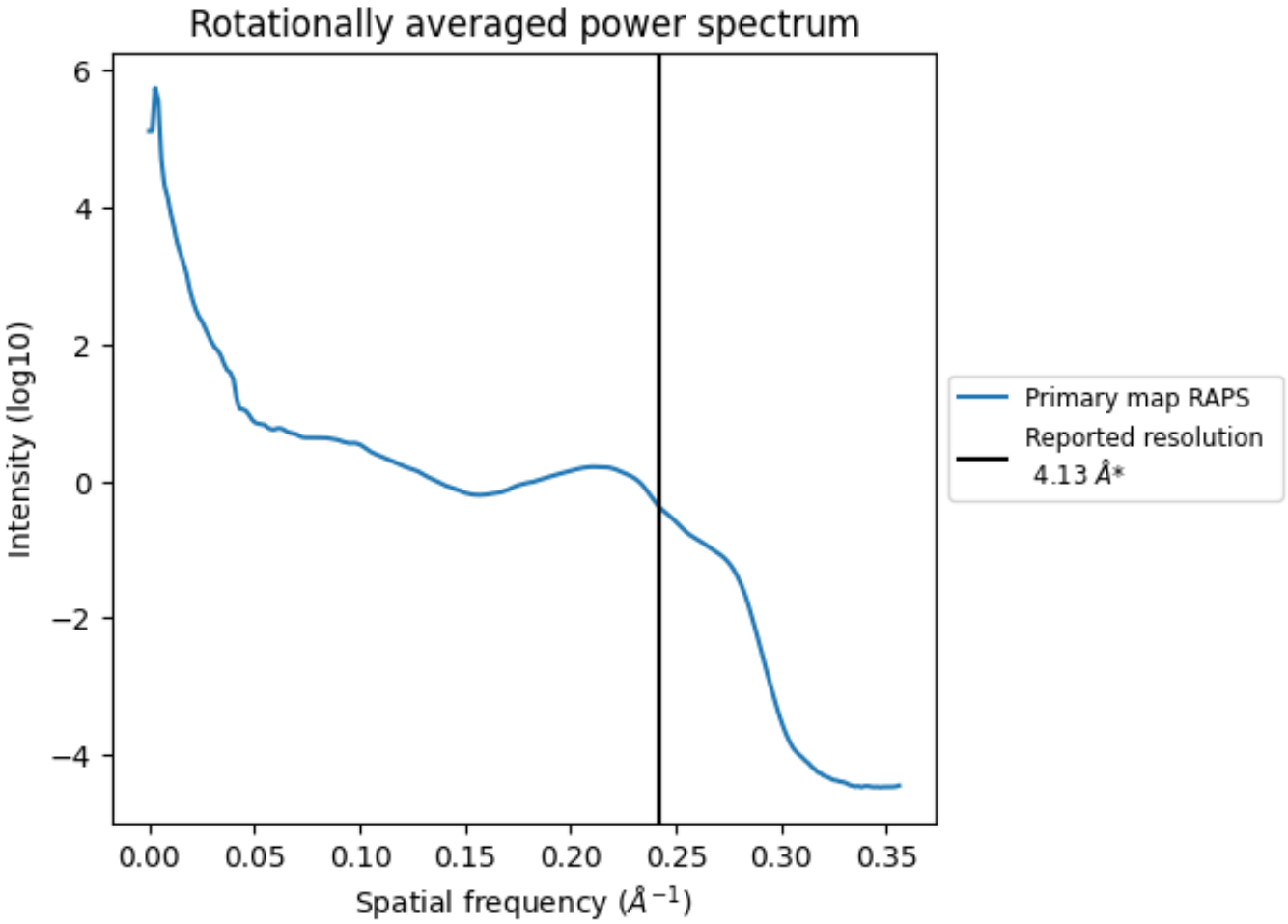
7.2 Volume estimate (i)



The volume at the recommended contour level is 3240 nm^3; 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}

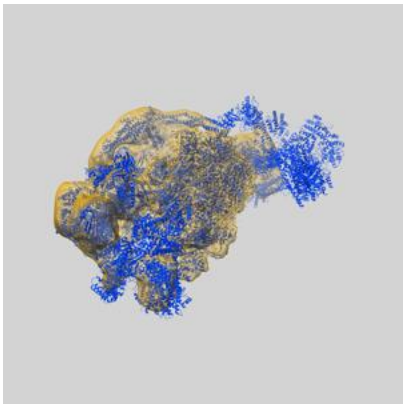
8 Fourier-Shell correlation (i)

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

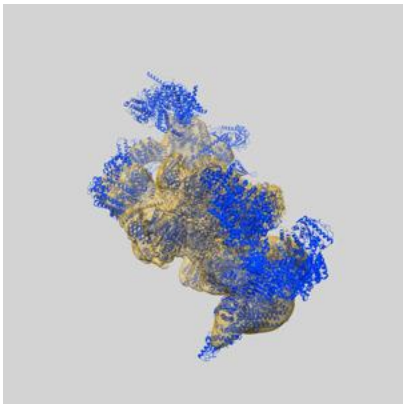
9 Map-model fit

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.

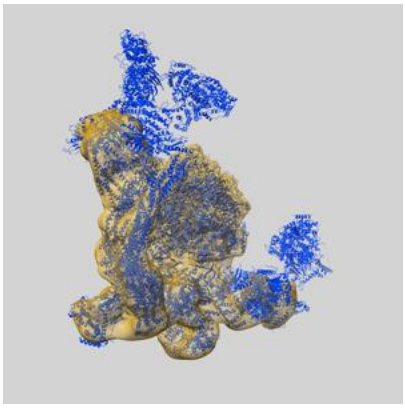
9.1 Map-model overlay



X



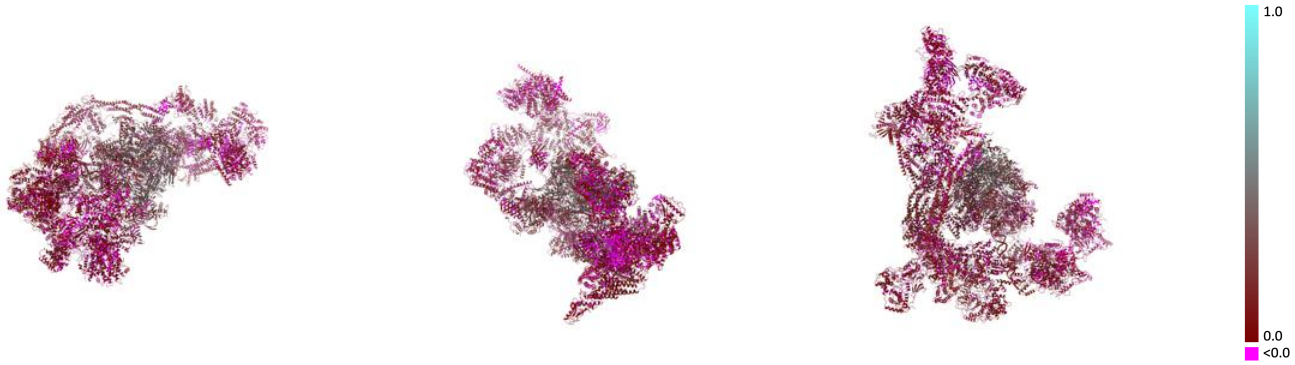
Y



Z

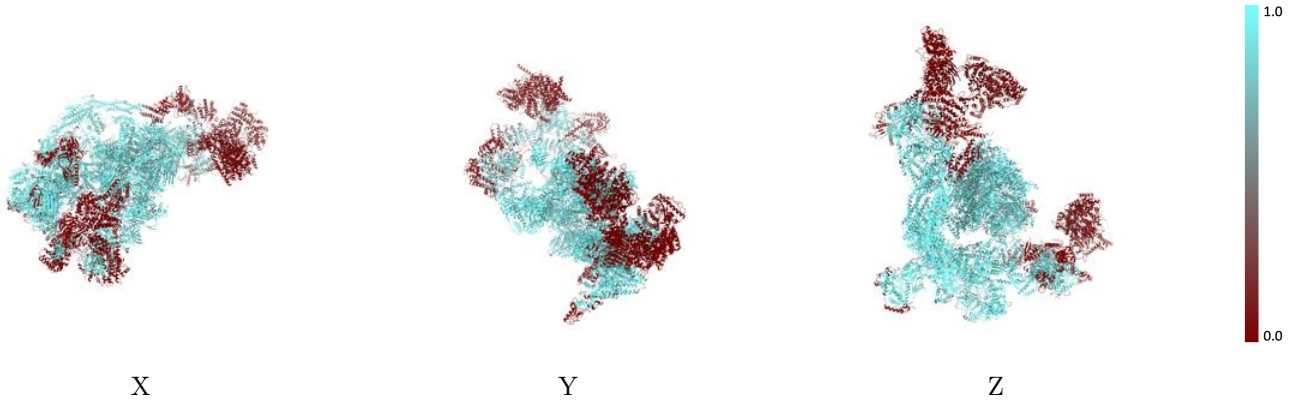
The images above show the 3D surface view of the map at the recommended contour level 0.41 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



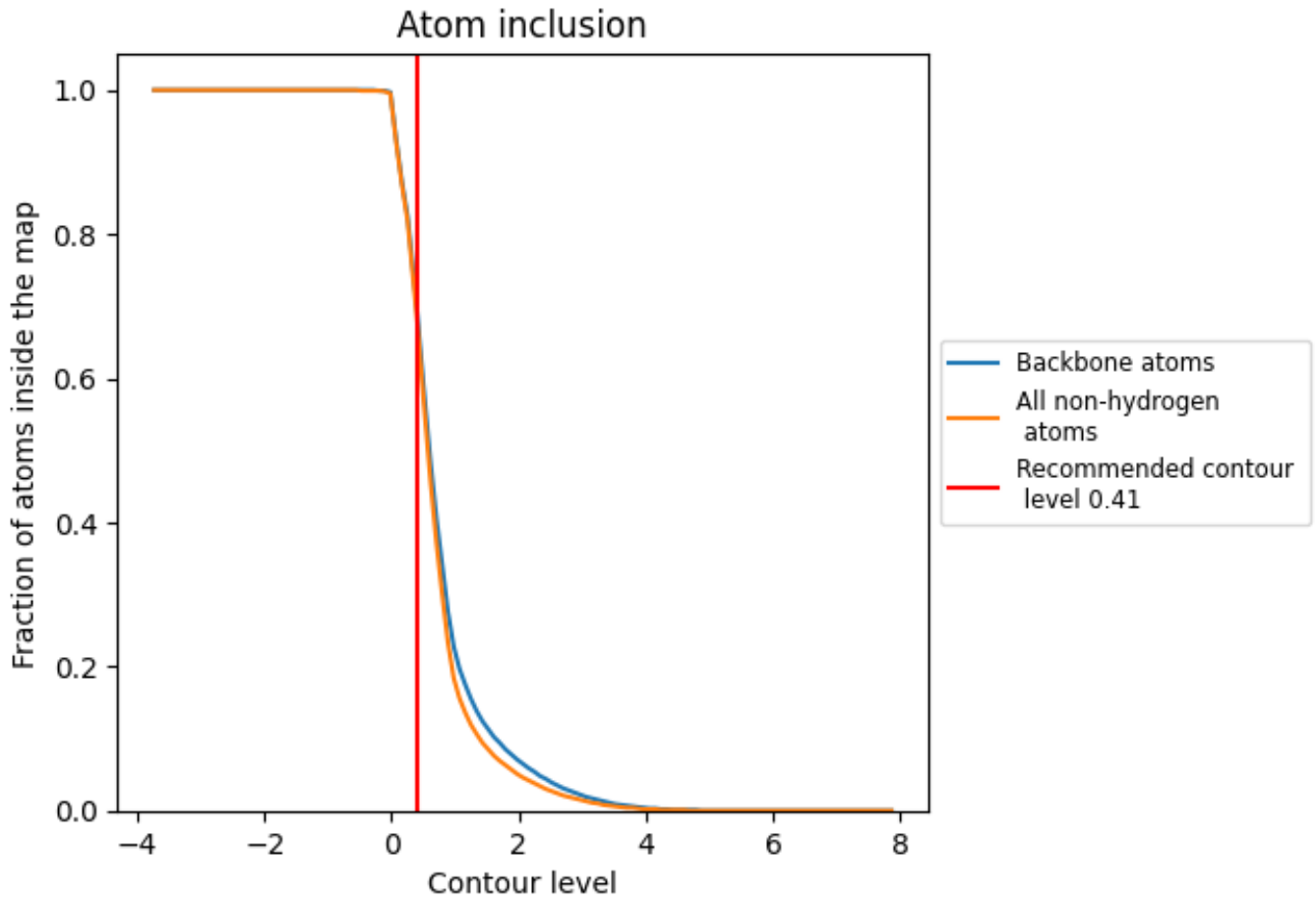
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	0.6730	0.1030
0	0.8870	0.0830
1	0.9000	0.0380
2	0.9830	0.0690
3	0.9750	0.0630
4	0.9620	0.0740
5	0.9790	0.0560
6	0.9800	0.0700
7	0.9840	0.0970
8	0.9410	0.0760
9	0.7290	0.0650
BA	0.9130	0.2020
DA	0.2540	0.0410
DB	0.8240	0.0560
DD	0.6080	0.0580
DE	0.6890	0.0520
DF	0.5060	0.0580
DG	0.0200	0.0240
DH	0.6950	0.0550
DI	0.5240	0.0260
DJ	0.5820	0.0500
DL	0.0280	0.0310
DO	0.9350	0.1010
DP	0.9670	0.1650
DQ	0.8710	0.0990
Dc	0.0000	0.0330
Dd	0.0000	0.0140
De	0.0000	0.0180
Df	0.2940	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	0.9800	0.1020

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Chain	Atom inclusion	Q-score
EB	0.9870	0.1230
FA	0.9480	0.0680
FB	0.9520	0.1150
PA	0.9230	0.2390
PB	0.9390	0.3370
PC	0.9300	0.3250
PD	0.9370	0.1590
PE	0.9560	0.2170
PF	0.8880	0.2560
PG	0.9480	0.1770
PH	0.9240	0.3110
PI	0.9260	0.1450
PJ	0.9090	0.3050
PK	0.8800	0.2840
PL	0.9180	0.2750
X	0.9990	0.1760
Y	0.9950	0.2000
a	0.0030	0.0340
b	0.5510	0.0380
c	0.8450	0.0550
d	0.7480	0.0840
e	0.9600	0.0930
f	0.9870	0.1340
g	0.9810	0.1050
h	0.9870	0.1610
i	0.5010	0.0850
j	0.9190	0.0640
k	0.9560	0.1540
l	0.9170	0.0710
m	0.9990	0.0910
n	0.8740	0.0690
o	0.6690	0.0440
p	0.0000	-0.0260
q	0.9870	0.0940
r	0.9750	0.0870
s	0.9040	0.0620
t	0.9280	0.0540
u	0.9920	0.0930
v	0.9890	0.1300
w	0.0110	0.0280
x	0.0360	0.0360
z	0.8980	0.0450