wwPDB EM Validation Summary Report (i)

Aug 6, 2026 – 08:46 AM JST

PDB ID	:	7ENC / pdb_00007enc
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 (i) 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 (1)) were used in the production of this report:

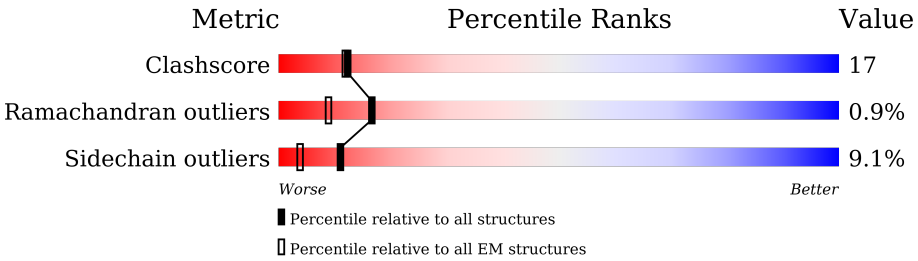
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

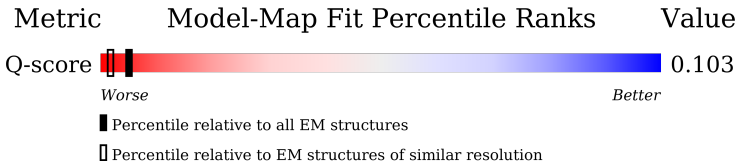
1 Overall quality at a glance (i)

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5607 (3.63 - 4.63)

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%; 17%, 9%, •, 70%
2	m	131	47%, 38%, 15%
3	d	270	14%; 24%, 24%, 10%, 41%
4	f	246	32%, 28%, 6%, •, 32%

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Mol	Chain	Length	Quality of chain
5	g	233	27% 33% 11% • 29%
6	h	268	33% 25% 12% 29%
7	r	208	• 43% 34% 14% 8%
8	t	212	• 38% 37% 14% • 9%
9	j	135	7% 33% 51% 5% • 10%
10	k	117	• 28% 40% 27% •
11	n	1454	10% 46% 20% • 32%
12	q	651	• 44% 31% 9% 15%
13	s	244	• 19% 11% •• 68%
14	u	144	32% 35% 5% • 26%
15	v	200	29% 26% 12% 33%
16	z	600	• 8% 6% • 84%
17	c	311	10% 59% 22% • 18%
18	e	178	38% 19% • 43%
19	b	200	23% 34% 23% • 42%
20	l	178	6% 48% 23% 29%
21	o	788	6% 11% 8% • 80%
22	i	146	21% 21% 15% 5% • 58%
23	0	309	8% 77% 19% ••
24	8	346	• 62% 21% • 14%
25	9	323	25% 68% 17% • 11%
26	1	548	6% 62% 9% • 26%
27	2	395	• 66% 16% • 16%
28	3	308	• 66% 19% • 15%
29	4	462	• 74% 20% ••

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Mol	Chain	Length	Quality of chain
30	5	71	54% 18% 24%
31	6	782	60% 16% 23%
32	7	760	75% 19%
33	EA	439	29% 10% 59%
34	EB	291	44% 13% 41%
35	DA	1872	22% 24% 5% 71%
36	DB	1199	13% 56% 22% 20%
37	DD	1085	5% 11% 85%
37	Dd	1085	15% 11% 85%
38	DE	800	19% 49% 17% 32%
38	De	800	67% 48% 17% 33%
39	DF	677	29% 46% 13% 40%
39	Df	677	42% 47% 12% 40%
40	DG	349	41% 31% 10% 58%
41	DH	310	19% 54% 13% 33%
42	DI	264	21% 36% 9% 55%
42	Di	264	46% 40% 5% 54%
43	DJ	218	17% 33% 7% 59%
43	Dj	218	44% 34% 9% 56%
44	DL	161	45% 27% 17% 53%
44	Dl	161	66% 41% 24% 34%
45	Dc	929	14% 11% 86%
46	Dk	211	46% 35% 12% 54%
47	Dm	124	70% 55% 14% 30%
48	DO	109	72% 13% 5% 11%

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Mol	Chain	Length	Quality of chain
49	DP	339	35% 17% 48%
50	DQ	307	35% 5% 60%
51	BA	316	63% 16% 21%
52	FB	249	70% 17% 11%
53	X	69	25% 65% 10%
54	Y	69	42% 52% 6%
55	PA	1970	56% 17% 25%
56	PB	1174	73% 21%
57	PC	275	71% 21% 7%
58	PD	142	66% 20% 9%
59	PE	210	77% 20%
60	PF	127	41% 17% 38%
61	PG	172	70% 25% 5%
62	PH	150	73% 25%
63	PI	125	72% 18% 9%
64	PJ	67	87% 7%
65	PK	117	83% 17%
66	PL	58	64% 10% 24%
67	FA	517	21% 5% 74%
68	w	1368	96% 78% 18%
69	x	989	87% 75% 15% 9%
70	p	841	48% 39% 9% 52%

2 Entry composition (i)

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

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

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

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

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

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

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

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

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

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

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

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

There are 2 discrepancies between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 25 is a protein called Cyclin-H.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 50 is a protein called TFIIA-a.

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

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

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

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

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

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

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

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

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

- Molecule 55 is a protein called RPB1.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 64 is a protein called RPB10.

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

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

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

- Molecule 66 is a protein called RPB12.

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
70	p	406	3124	1982	536	585	21	0	0

- Molecule 71 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

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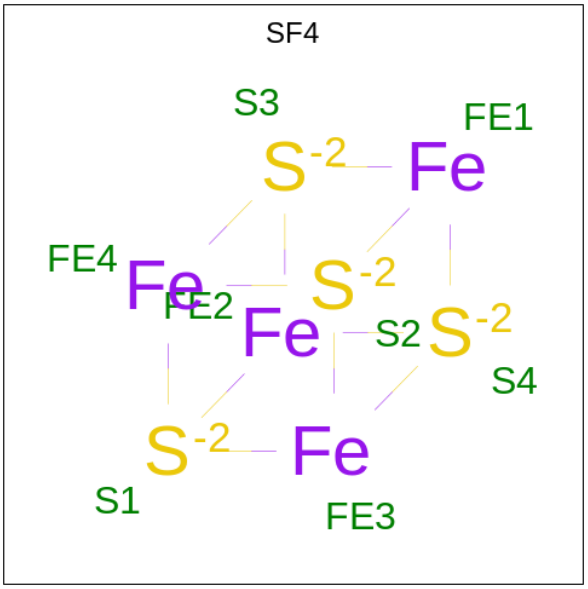
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
71	PB	1	1	1	0
71	PC	1	1	1	0
71	PI	2	2	2	0
71	PJ	1	1	1	0
71	PL	1	1	1	0

- Molecule 72 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



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

- Molecule 73 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

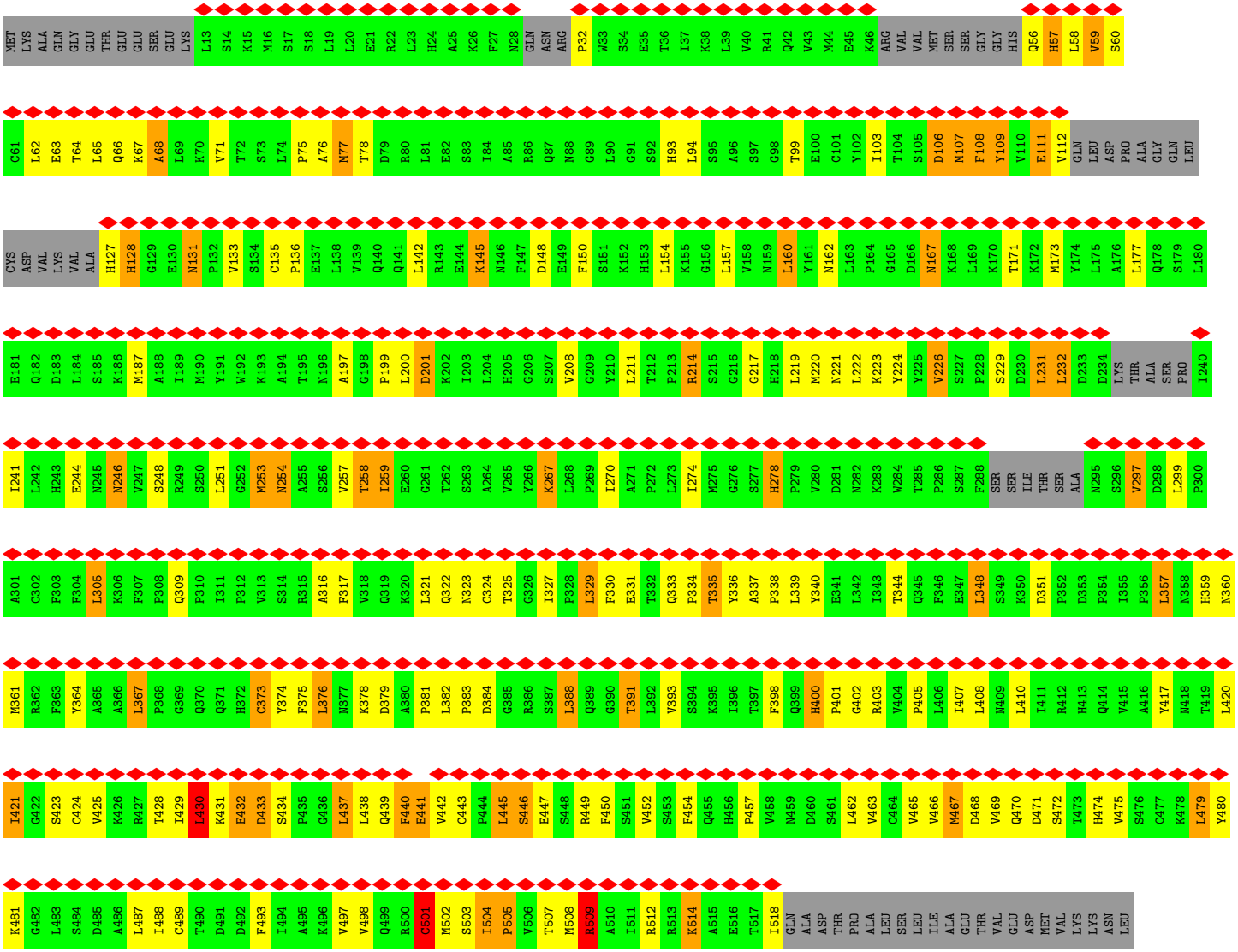
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
73	PA	1	1	1	0

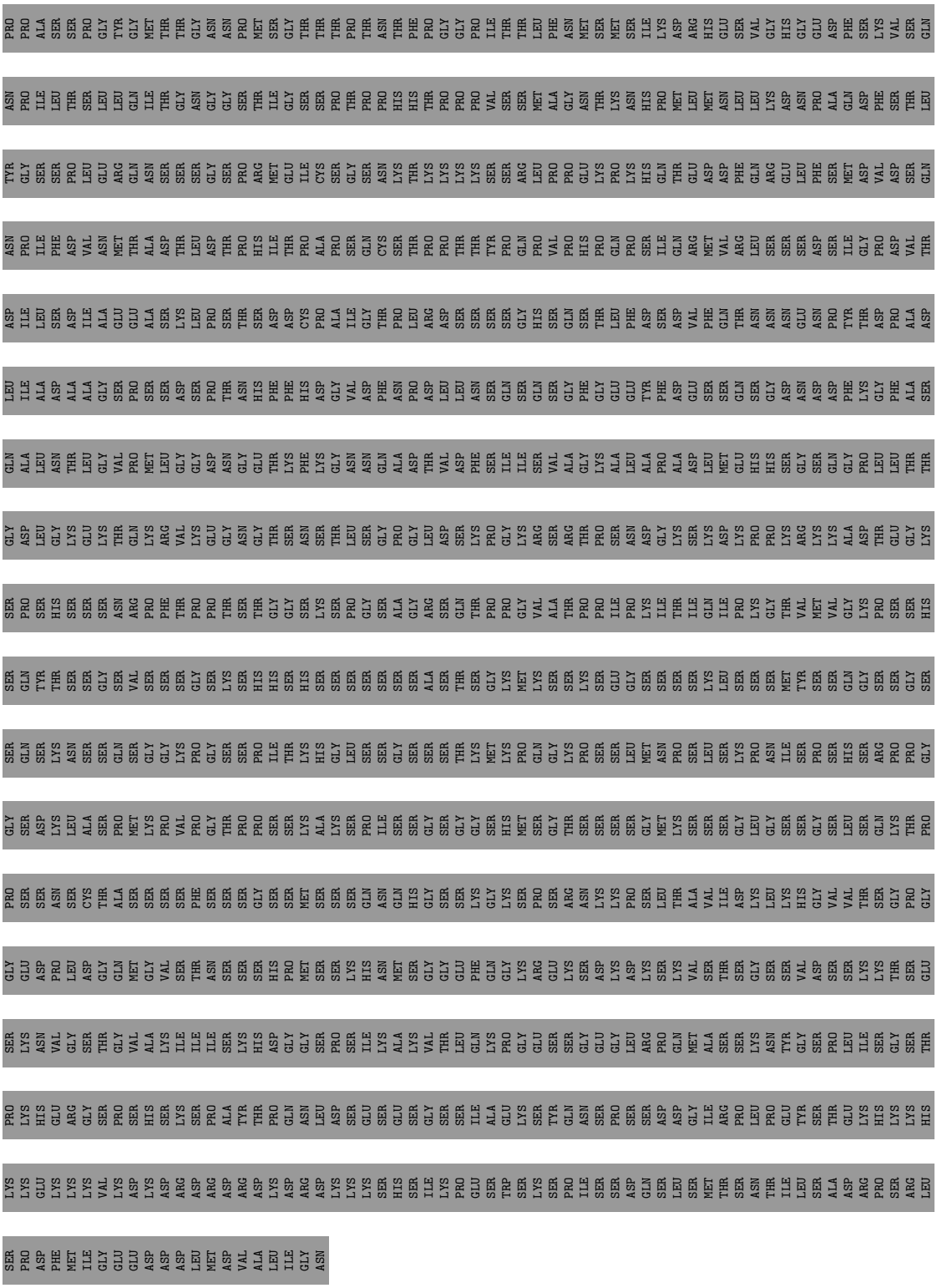
3 Residue-property plots (i)

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

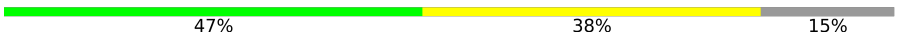
Chain a: 30% 17% 9% • 70%

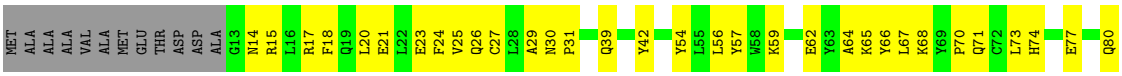


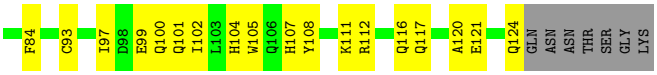


- Molecule 2: Mediator of RNA polymerase II transcription subunit 31

Chain m:

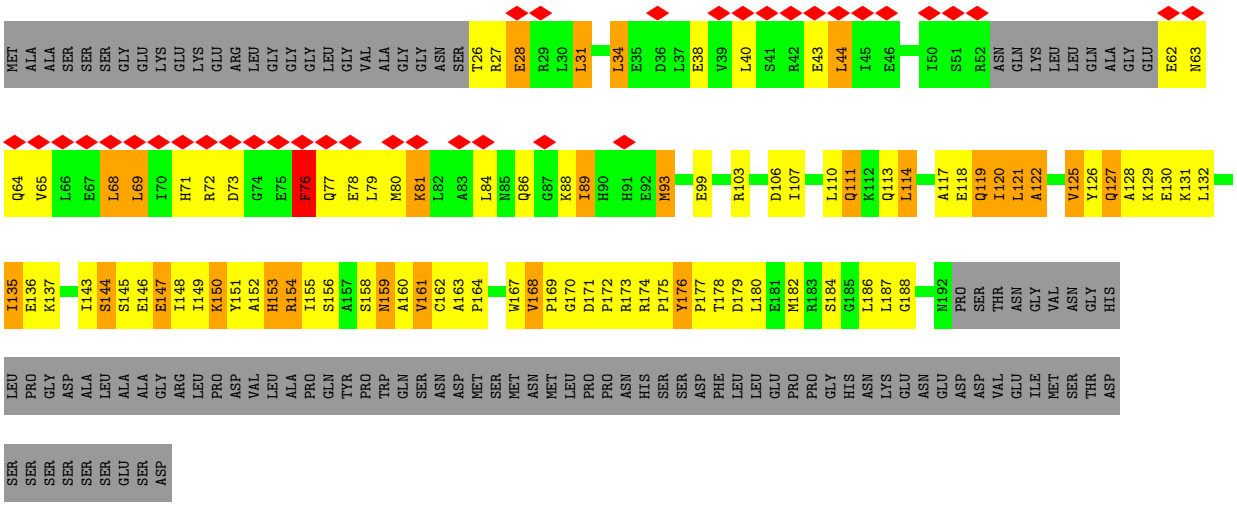






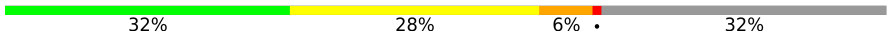
• Molecule 3: Mediator of RNA polymerase II transcription subunit 4

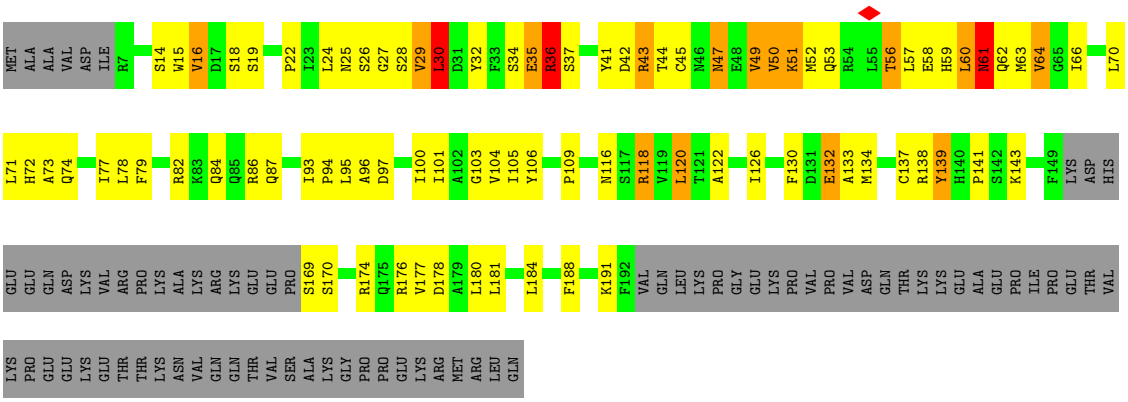
Chain d:



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

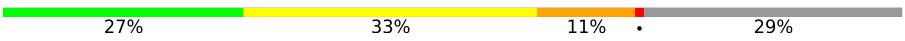
Chain f:

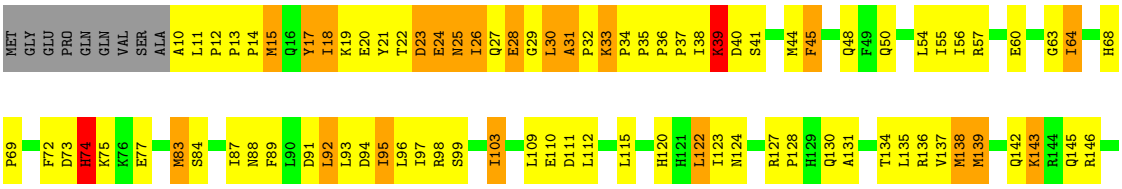


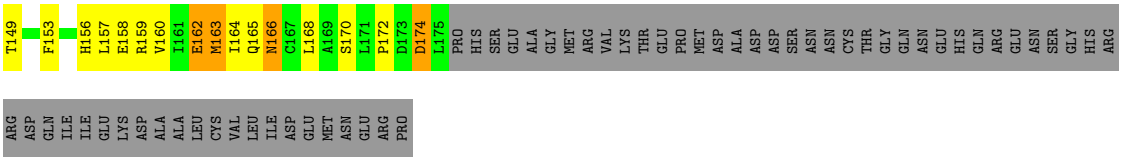


• Molecule 5: Mediator of RNA polymerase II transcription subunit 7

Chain g:

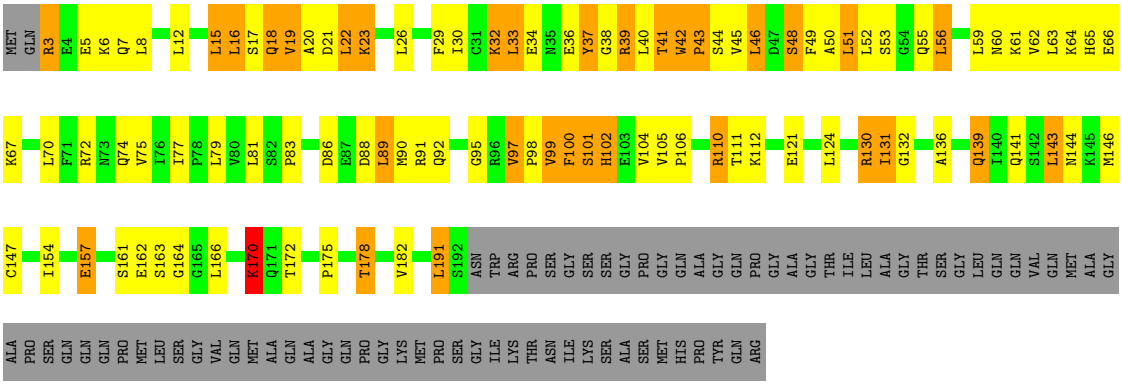






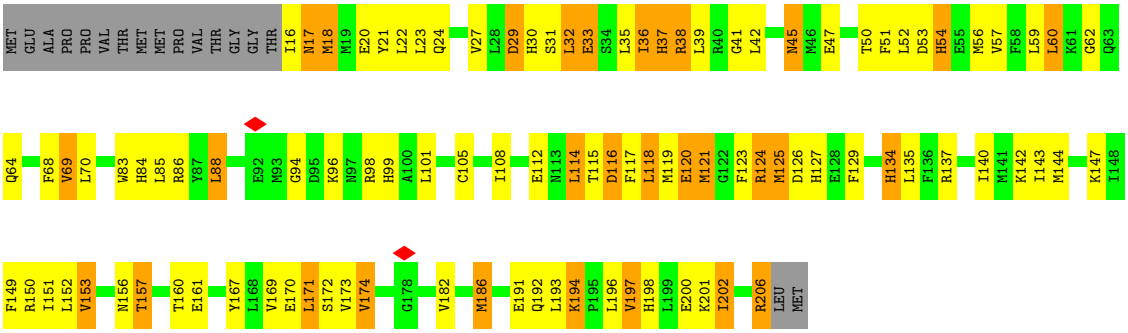
- Molecule 6: Isoform 2 of Mediator of RNA polymerase II transcription subunit 8

Chain h:



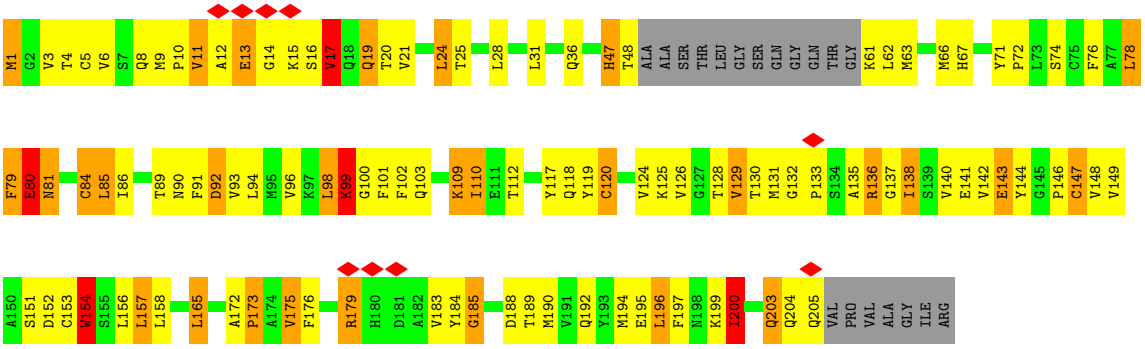
- Molecule 7: Mediator of RNA polymerase II transcription subunit 18

Chain r:



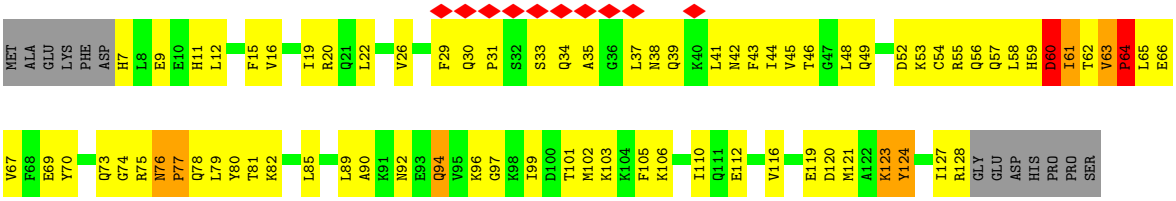
- Molecule 8: Mediator of RNA polymerase II transcription subunit 20

Chain t:



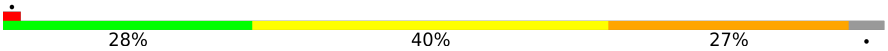
- Molecule 9: Mediator of RNA polymerase II transcription subunit 10

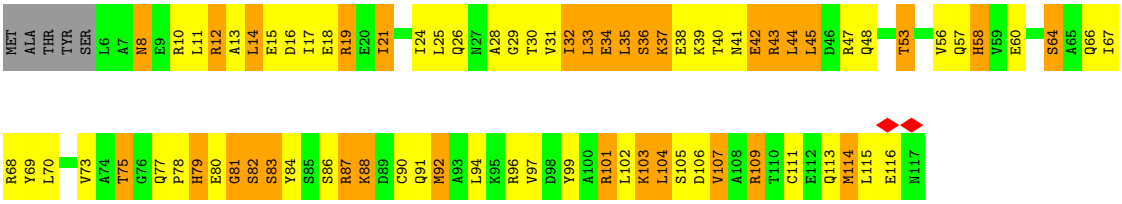
Chain j:



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

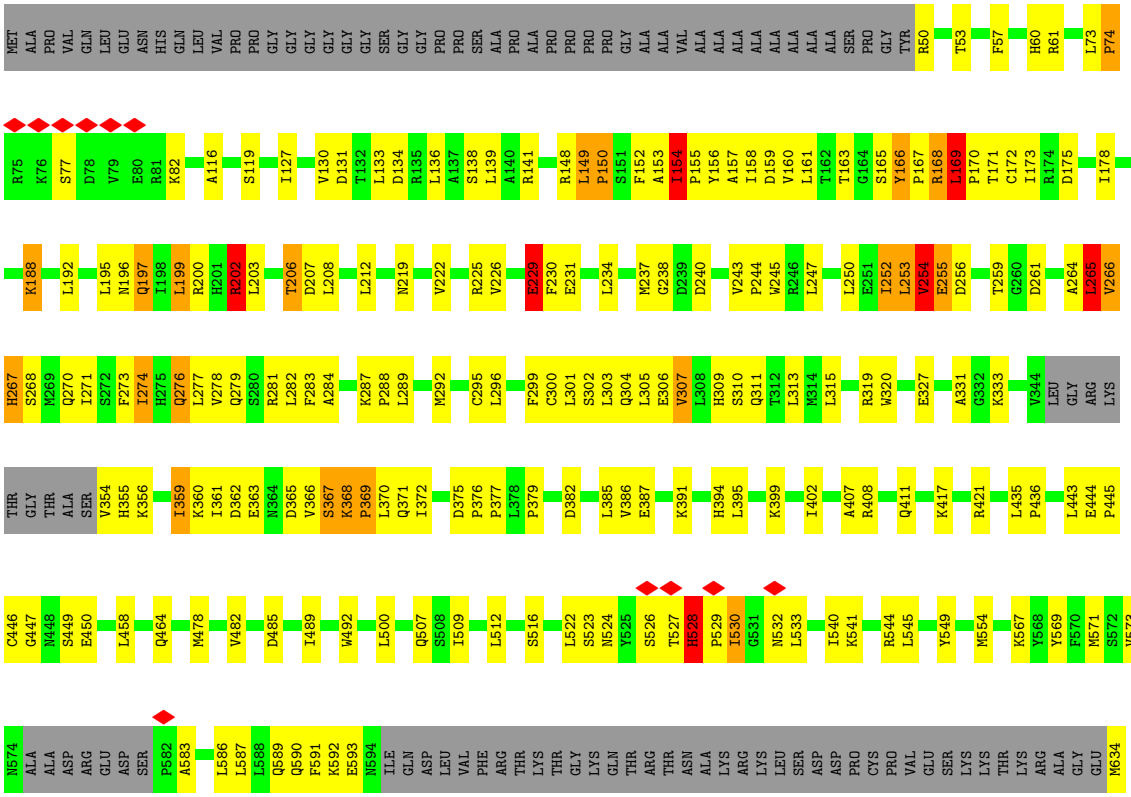
Chain k:

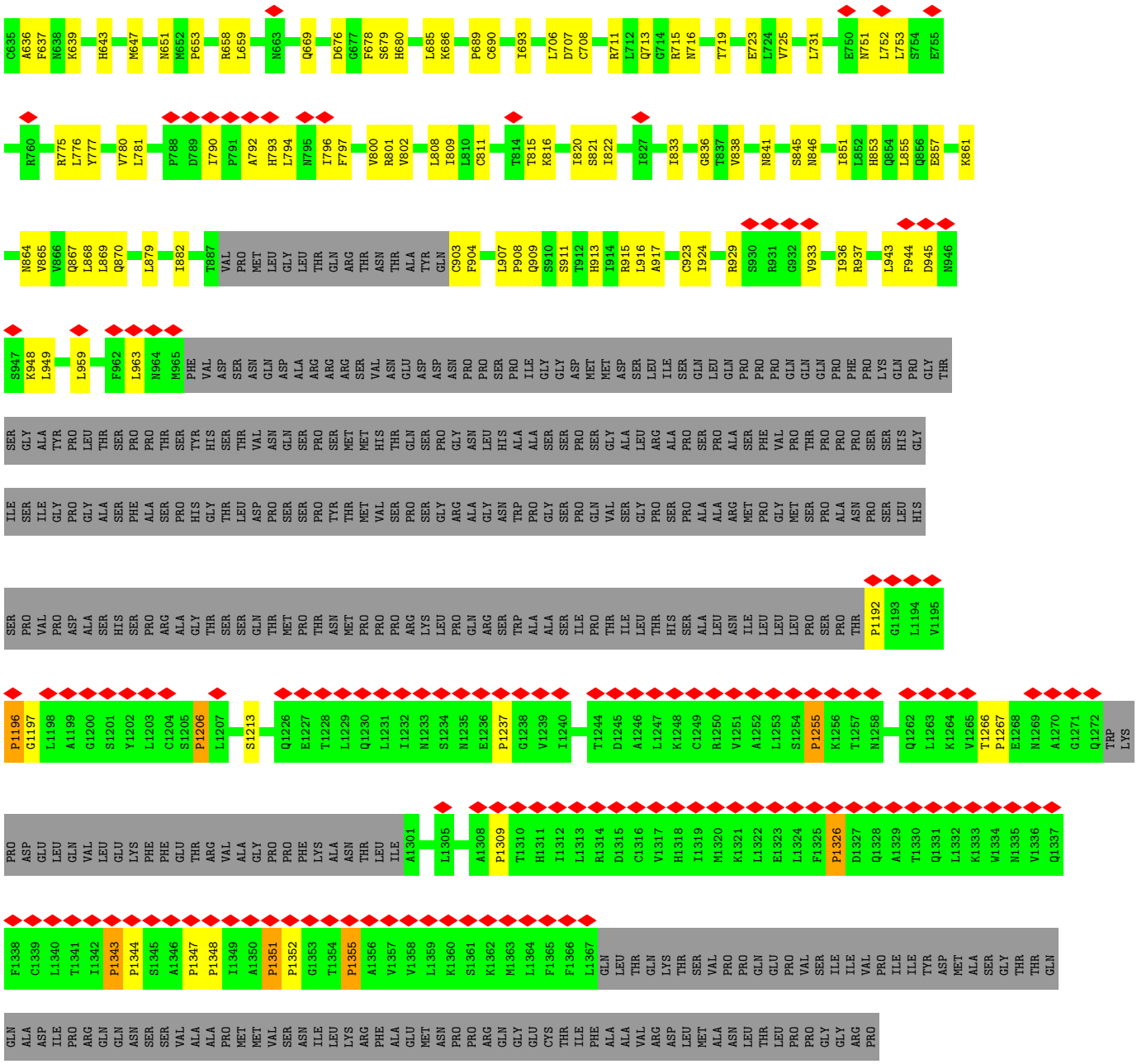




- Molecule 11: Mediator of RNA polymerase II transcription subunit 14

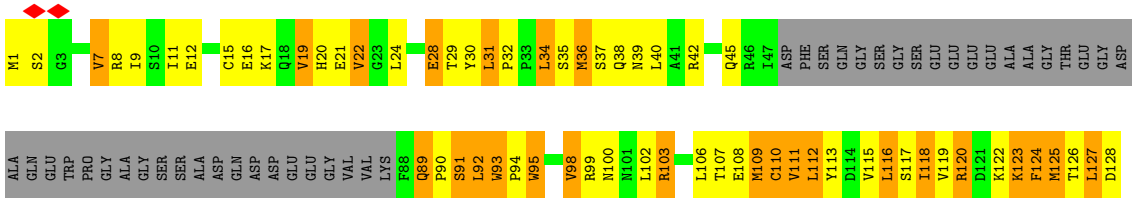
Chain n:

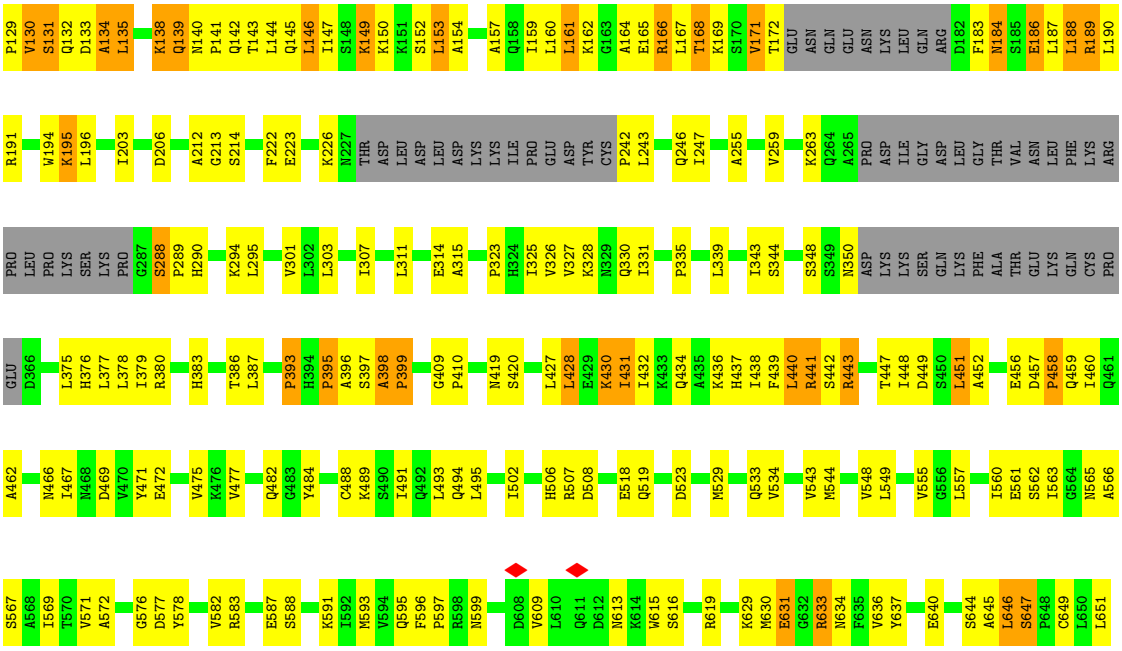




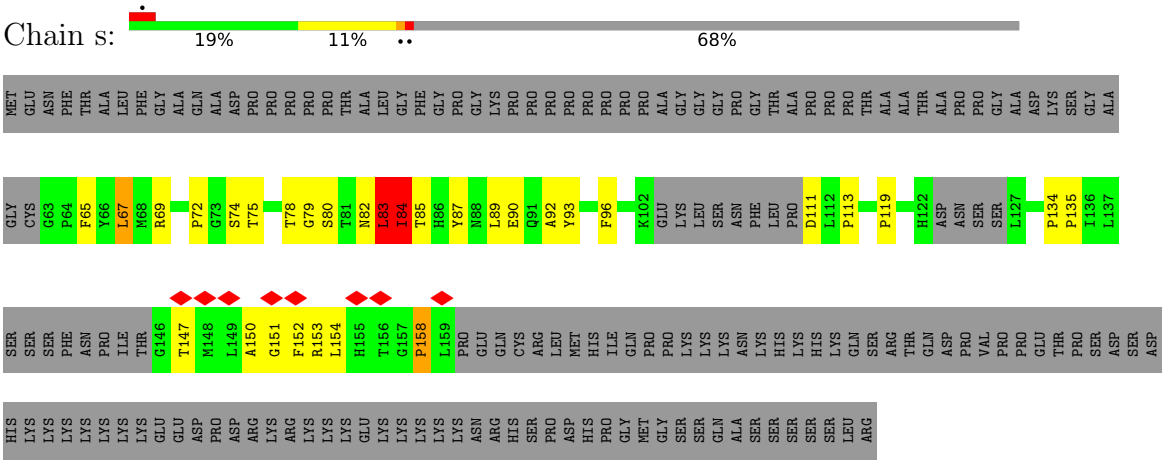
• Molecule 12: Mediator of RNA polymerase II transcription subunit 17

Chain q:

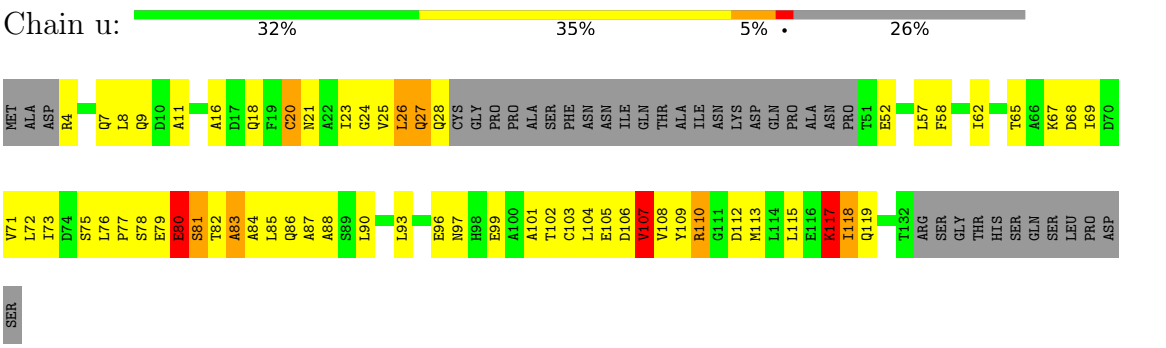




• Molecule 13: Mediator of RNA polymerase II transcription subunit 19

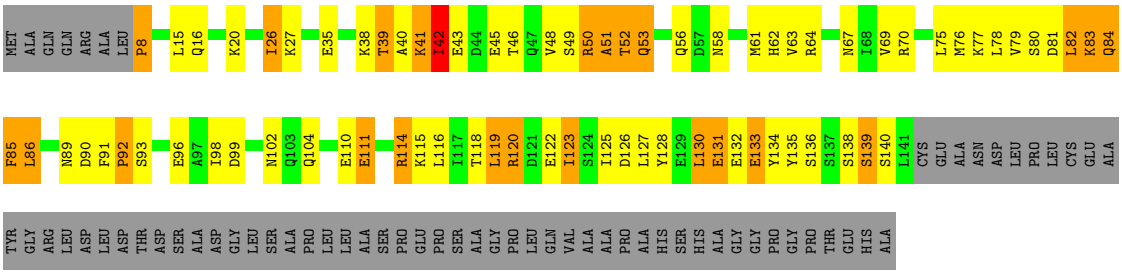


• Molecule 14: Mediator of RNA polymerase II transcription subunit 21



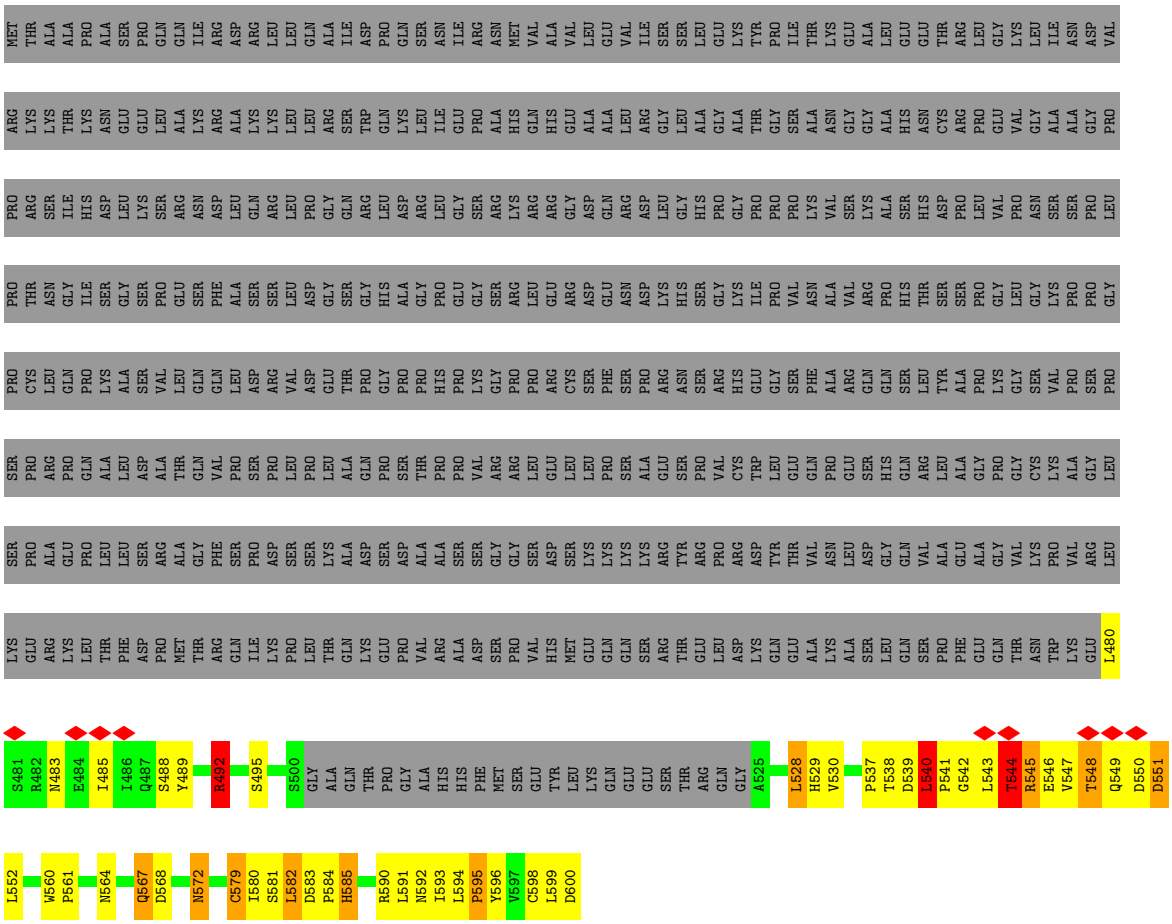
• Molecule 15: Mediator of RNA polymerase II transcription subunit 22

Chain v: 29% 26% 12% 33%



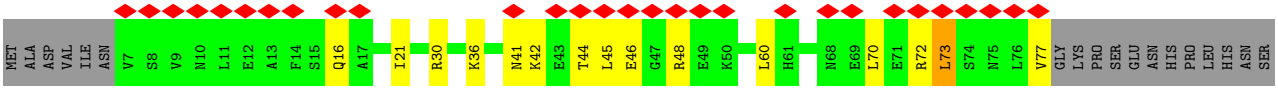
• Molecule 16: Mediator of RNA polymerase II transcription subunit 26

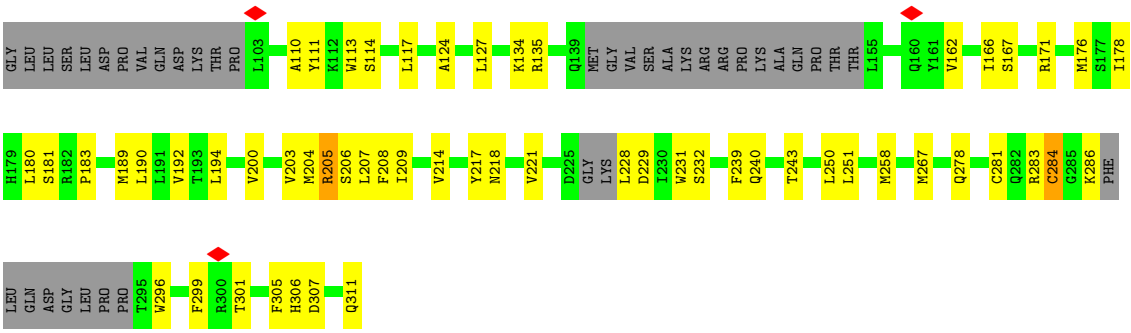
Chain z: 8% 6% • 84%



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

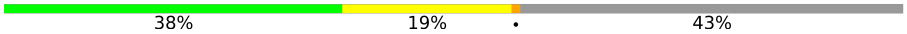
Chain c: 10% 59% 22% • 18%

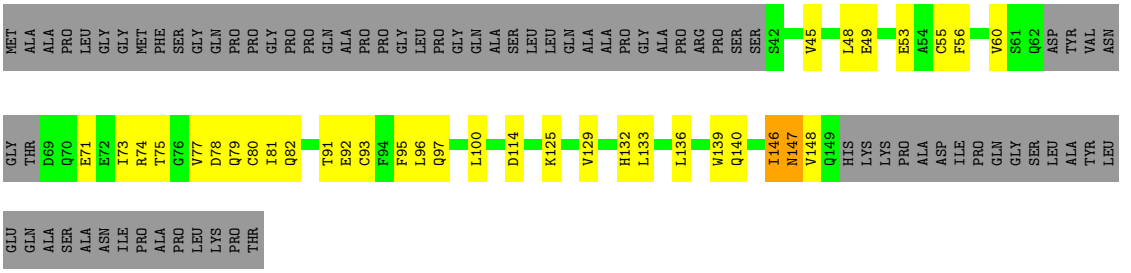




• Molecule 18: Mediator of RNA polymerase II transcription subunit 28

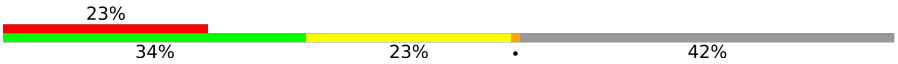
Chain e:

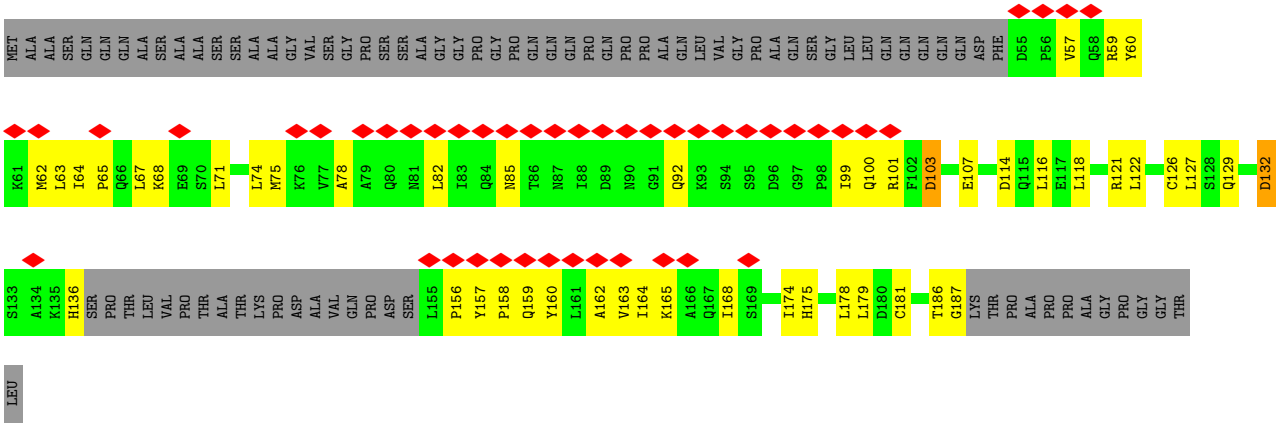




• Molecule 19: Mediator of RNA polymerase II transcription subunit 29

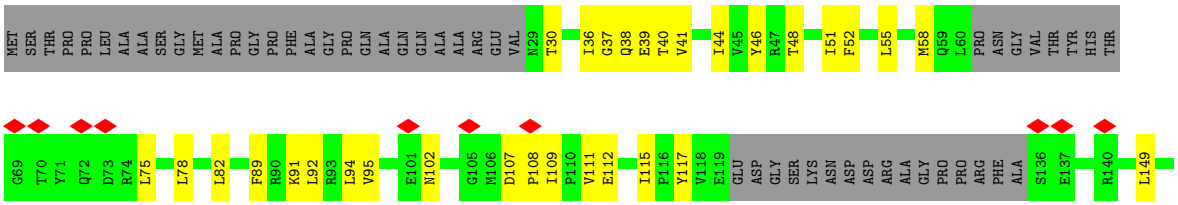
Chain b:



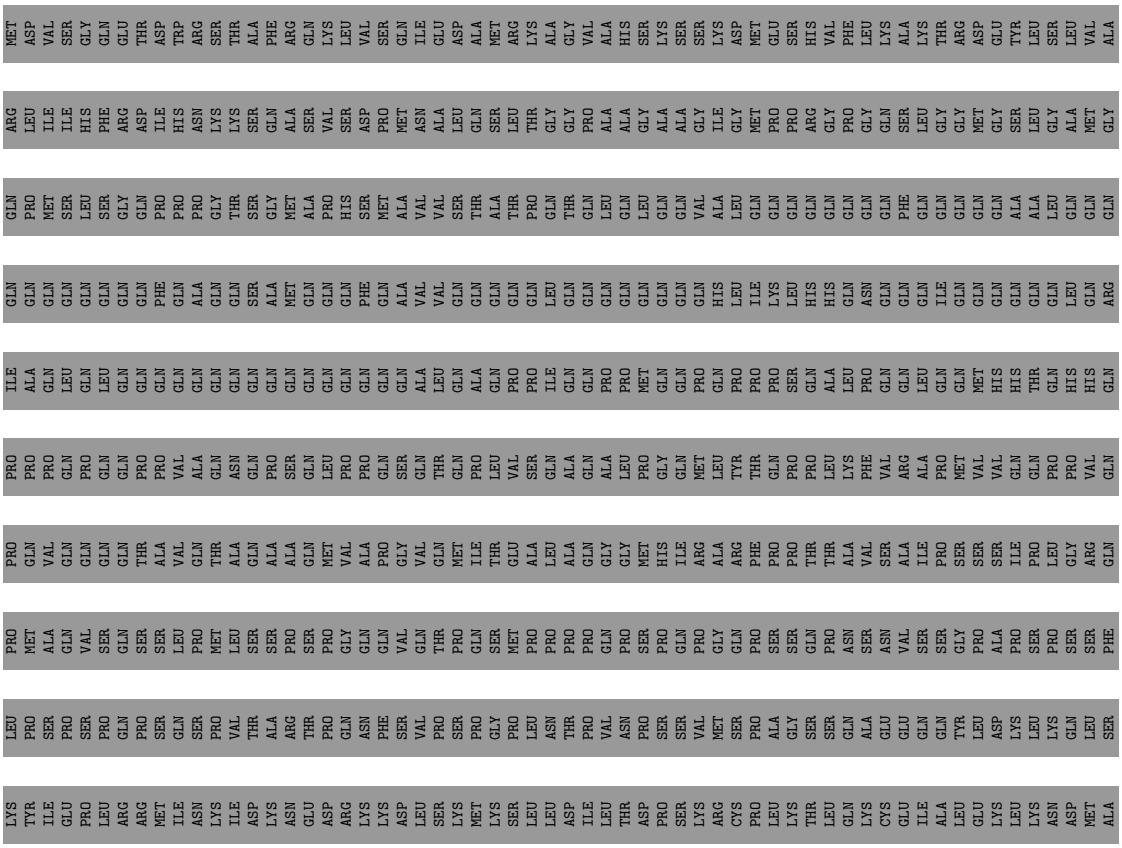


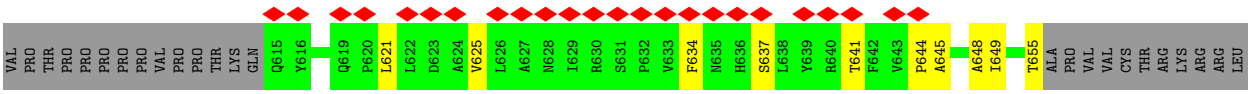
• Molecule 20: Mediator of RNA polymerase II transcription subunit 30

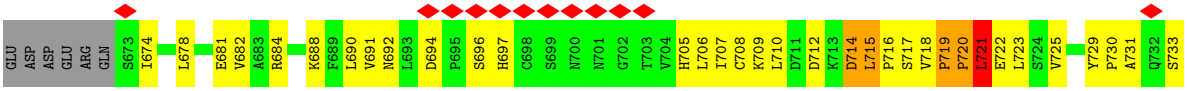
Chain l:

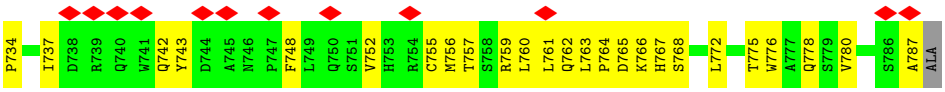


• Molecule 21: Mediator of RNA polymerase II transcription subunit 15

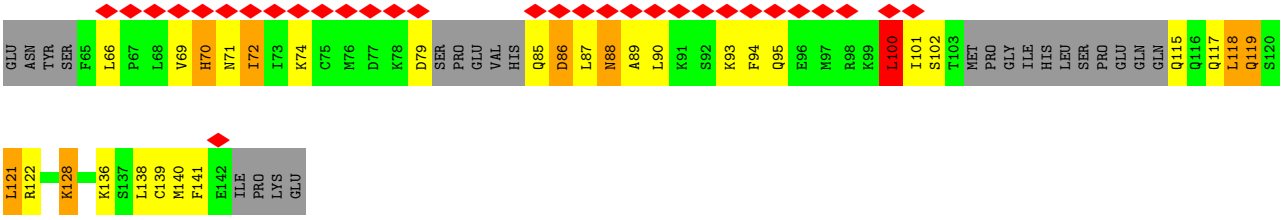






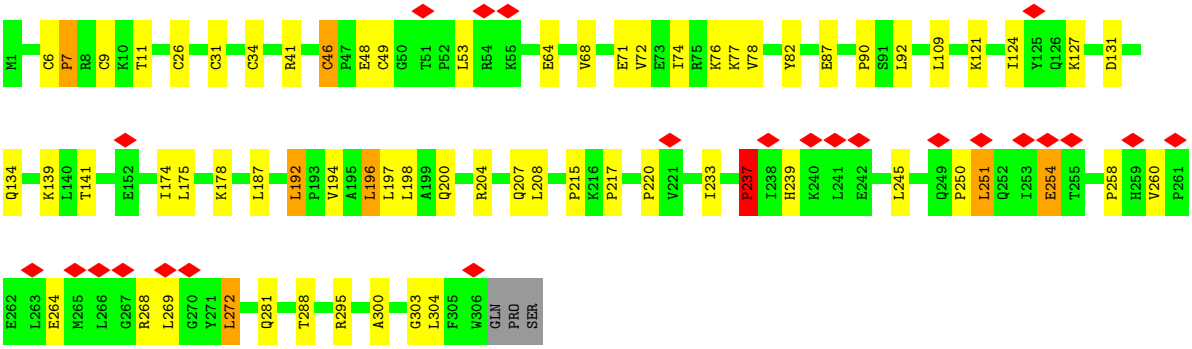


• Molecule 22: Mediator of RNA polymerase II transcription subunit 9



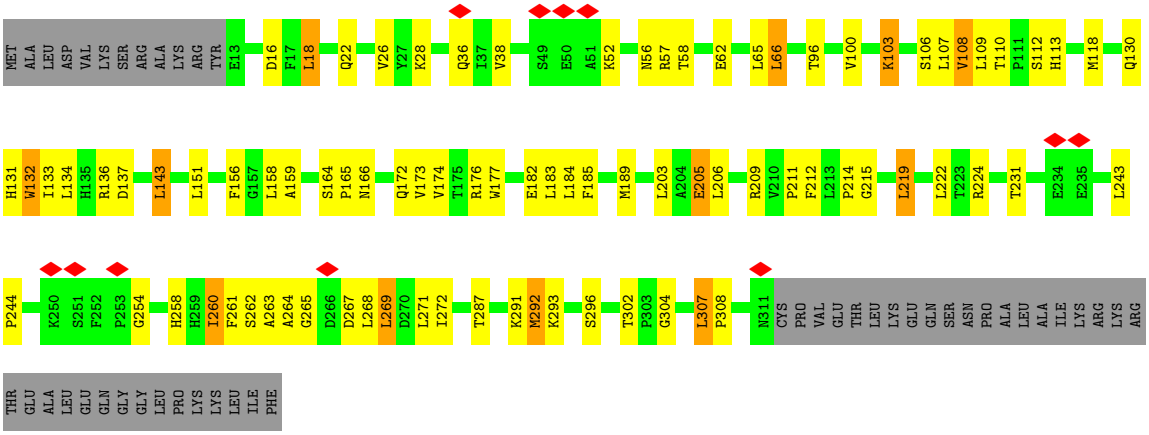
- Molecule 23: CDK-activating kinase assembly factor MAT1

Chain 0:



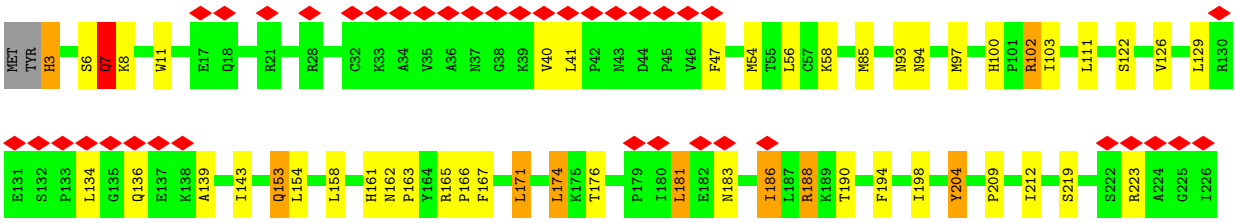
- Molecule 24: Cyclin-dependent kinase 7

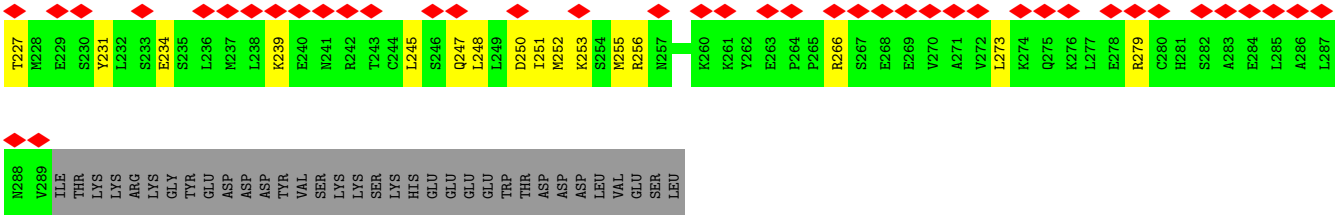
Chain 8:



- Molecule 25: Cyclin-H

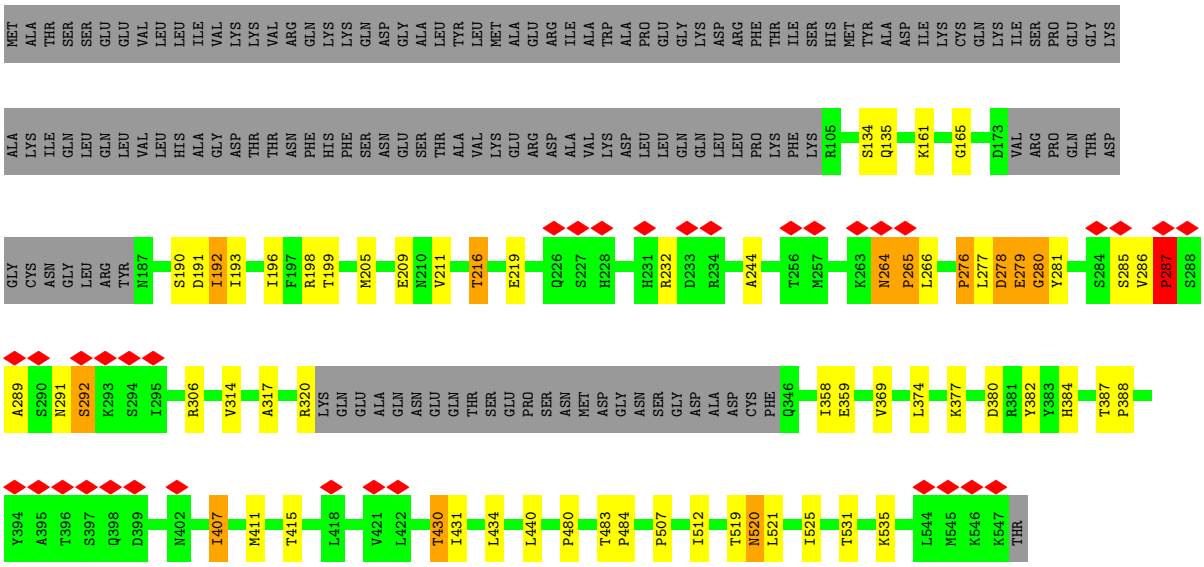
Chain 9:





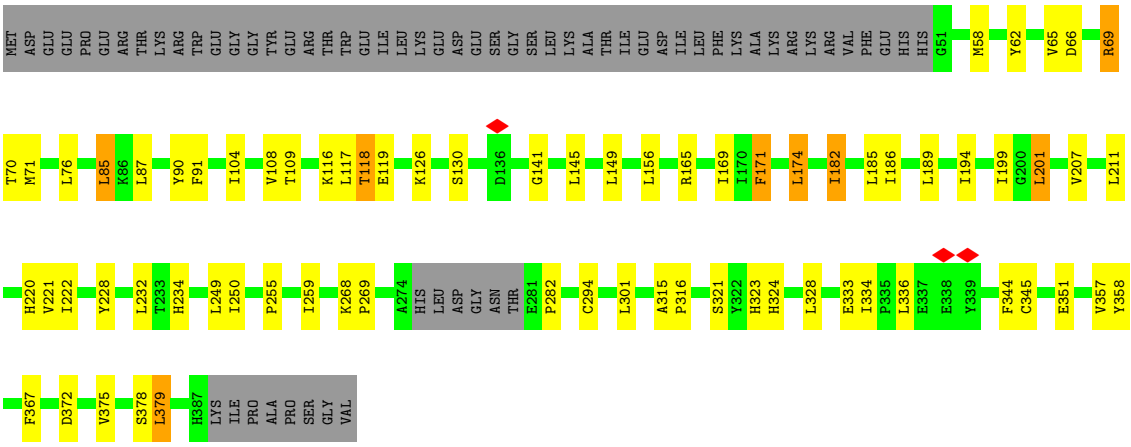
• Molecule 26: General transcription factor IIH subunit 1

Chain 1:



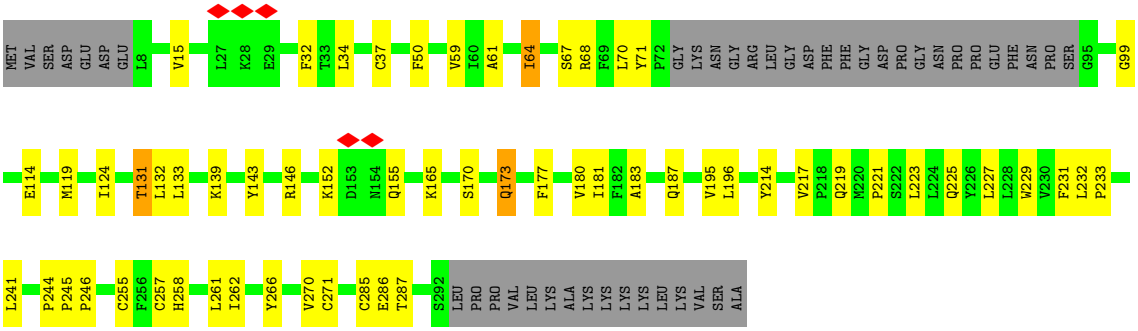
• Molecule 27: General transcription factor IIH subunit 2

Chain 2:



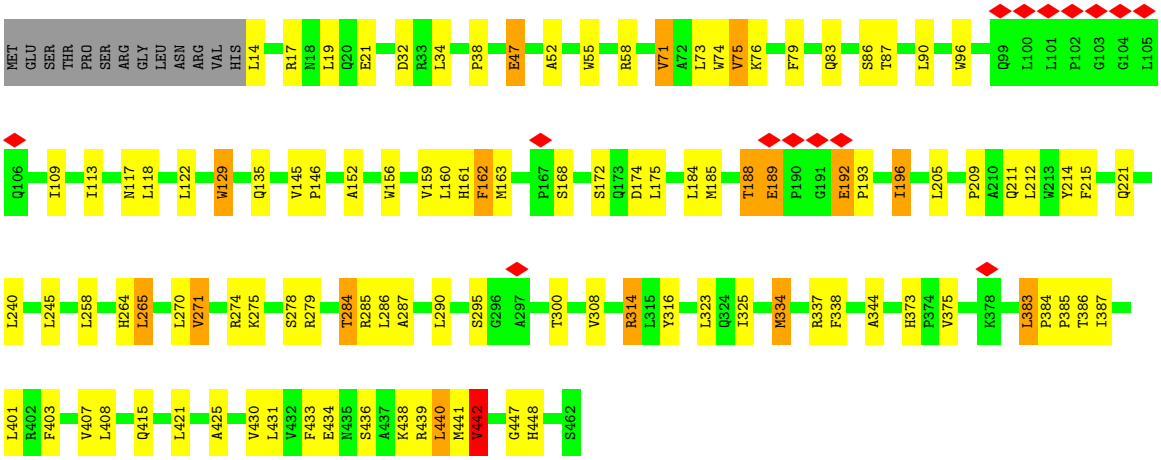
• Molecule 28: General transcription factor IIH subunit 3

Chain 3:



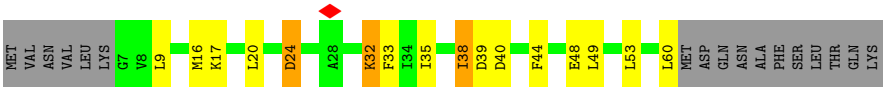
• Molecule 29: General transcription factor IIH subunit 4

Chain 4:



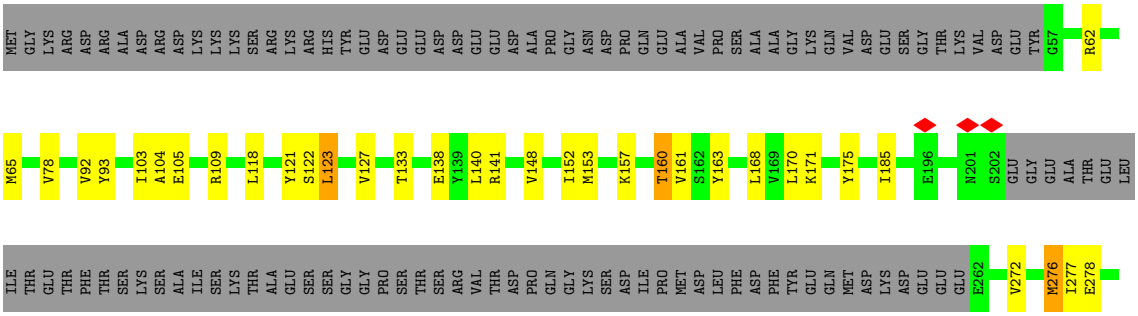
• Molecule 30: General transcription factor IIH subunit 5

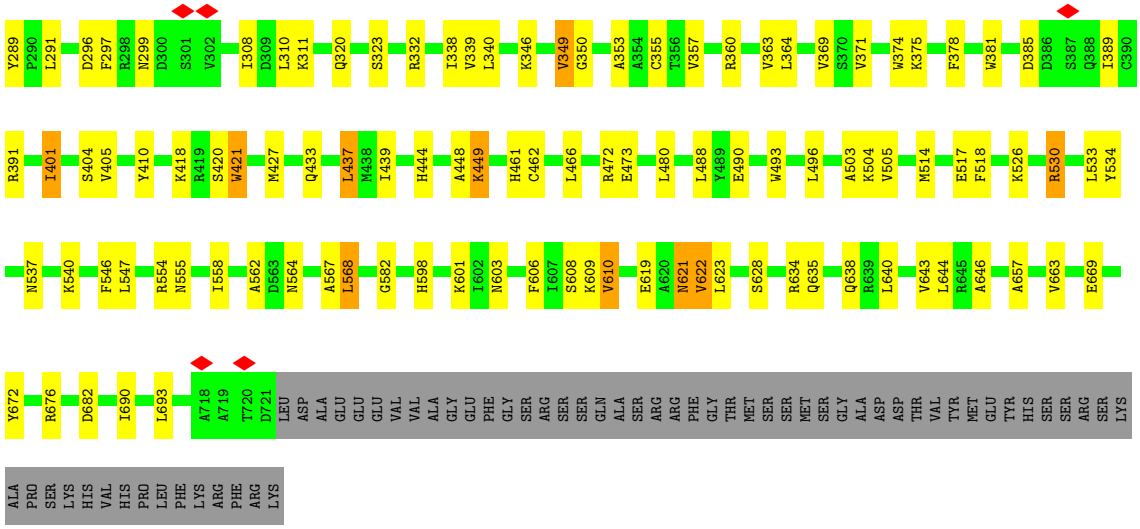
Chain 5:



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

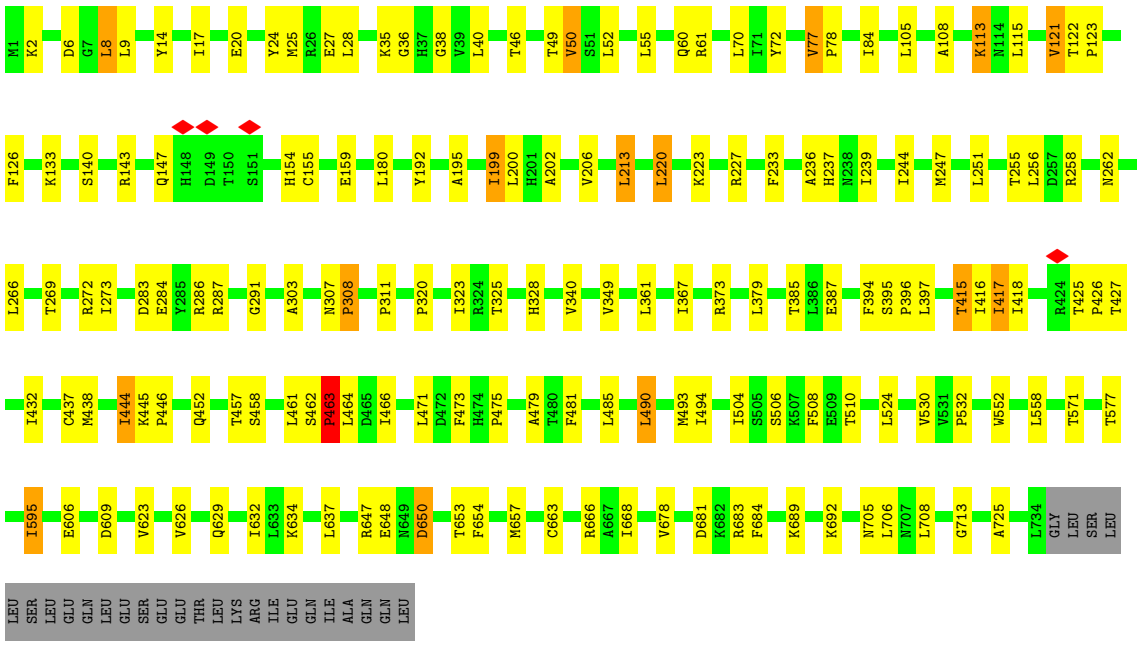
Chain 6:





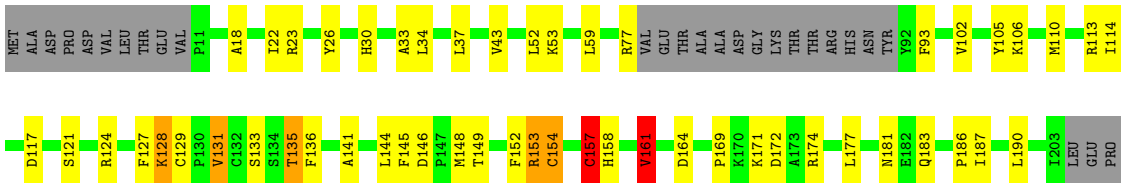
• Molecule 32: General transcription and DNA repair factor IIH helicase subunit XPD

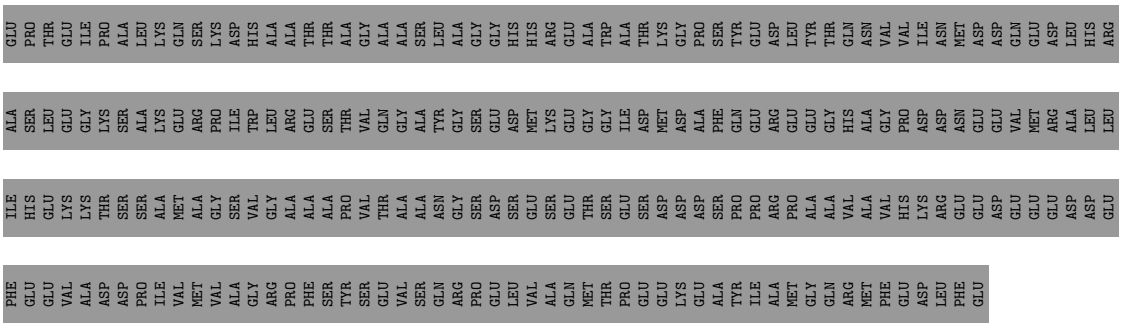
Chain 7:



• Molecule 33: General transcription factor IIE subunit 1

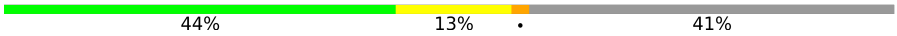
Chain EA:

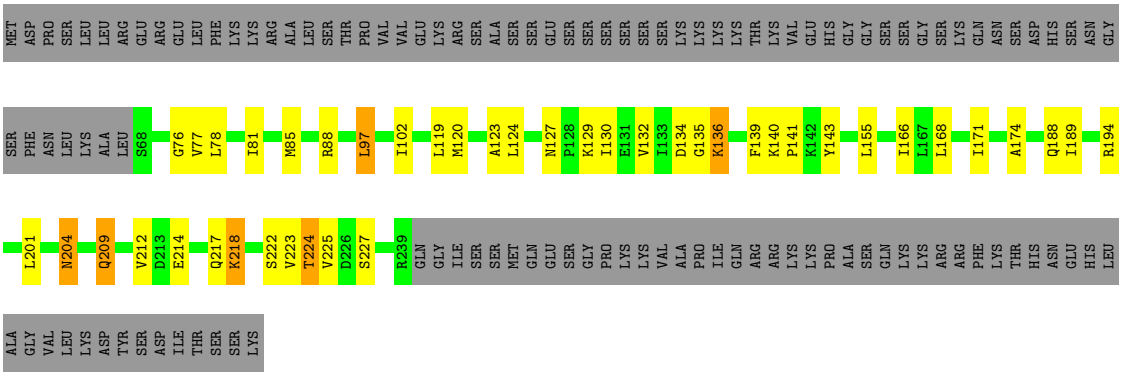




• Molecule 34: Transcription initiation factor IIE subunit beta

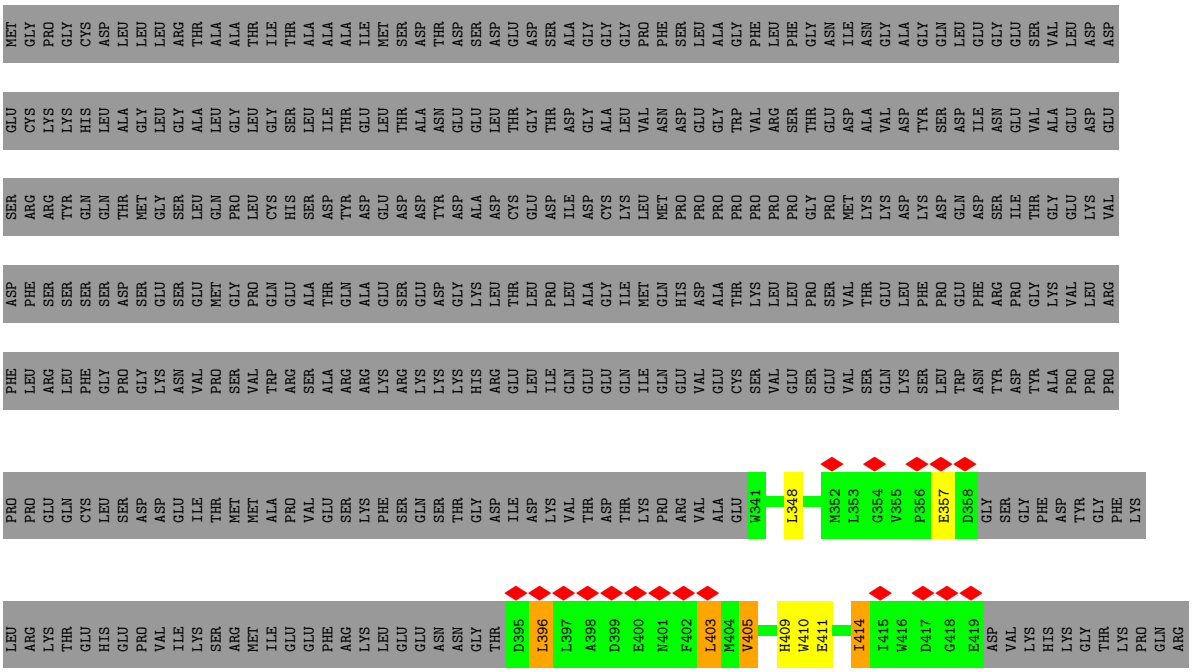
Chain EB:

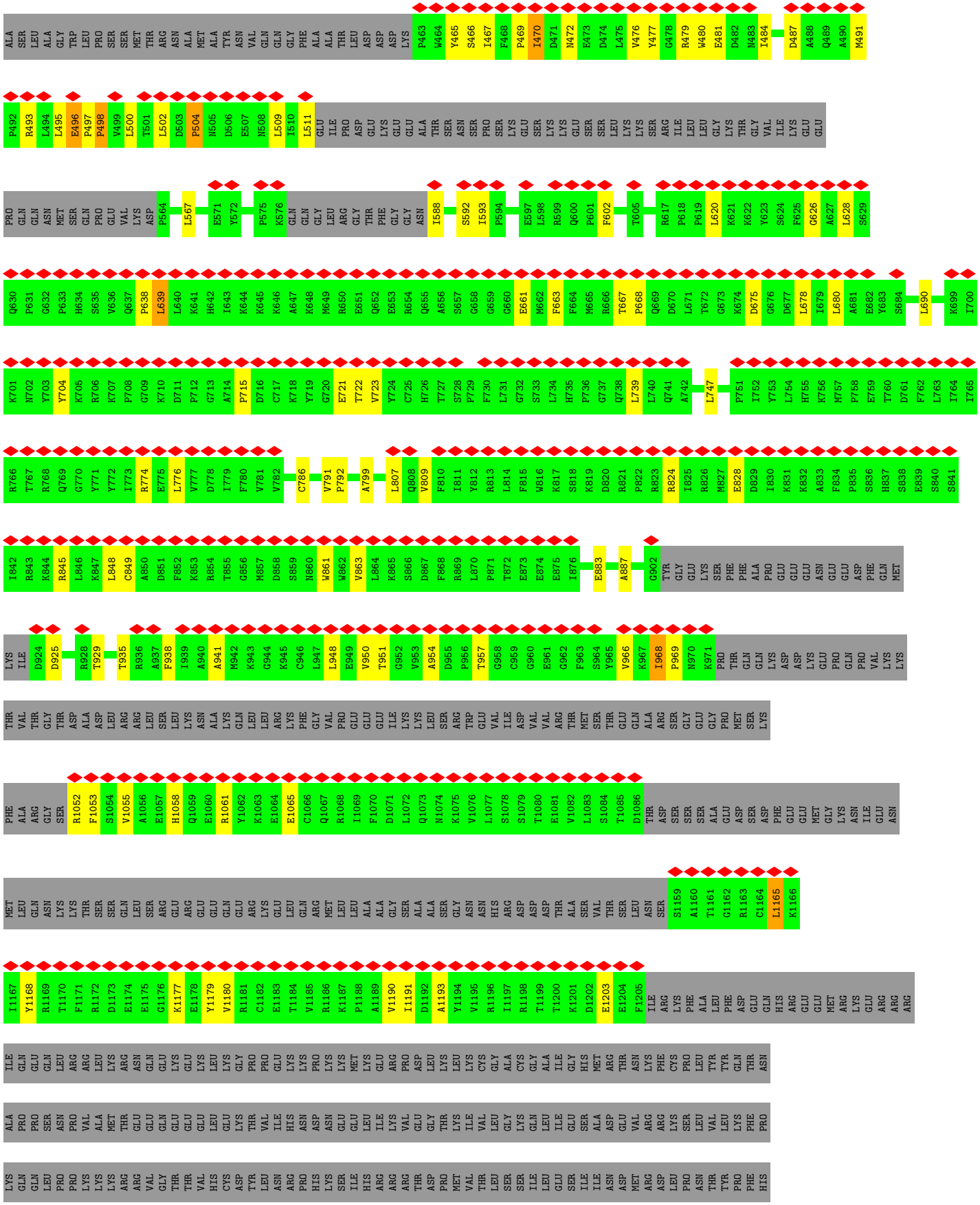


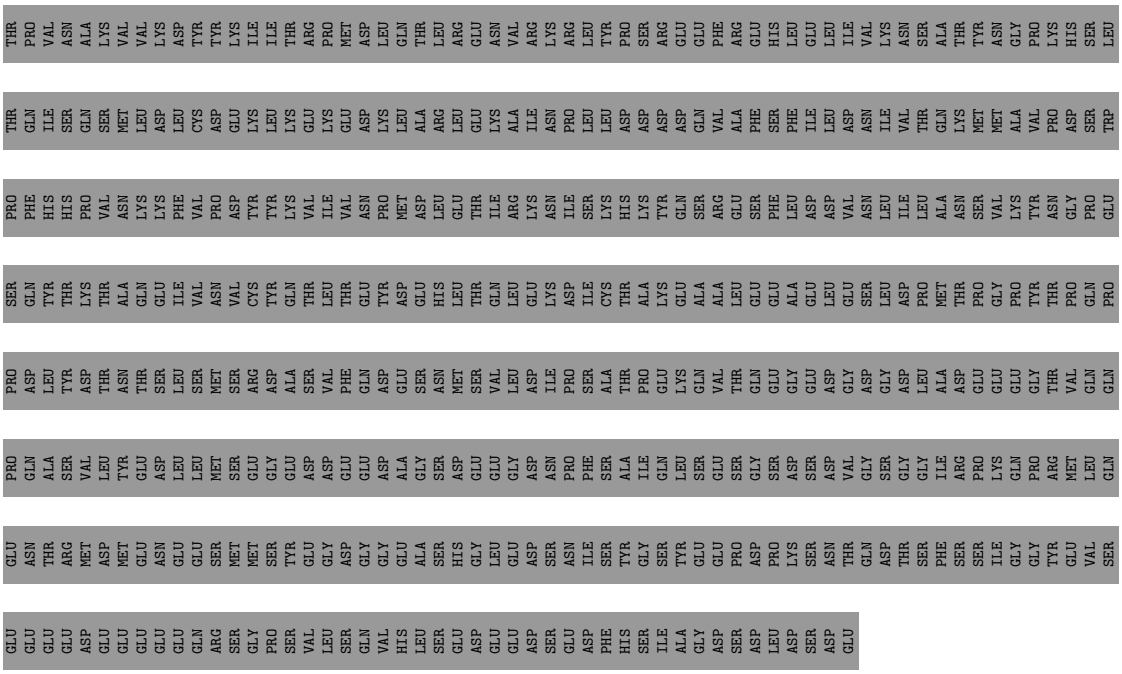


• Molecule 35: Transcription initiation factor TFIID subunit 1

Chain DA:

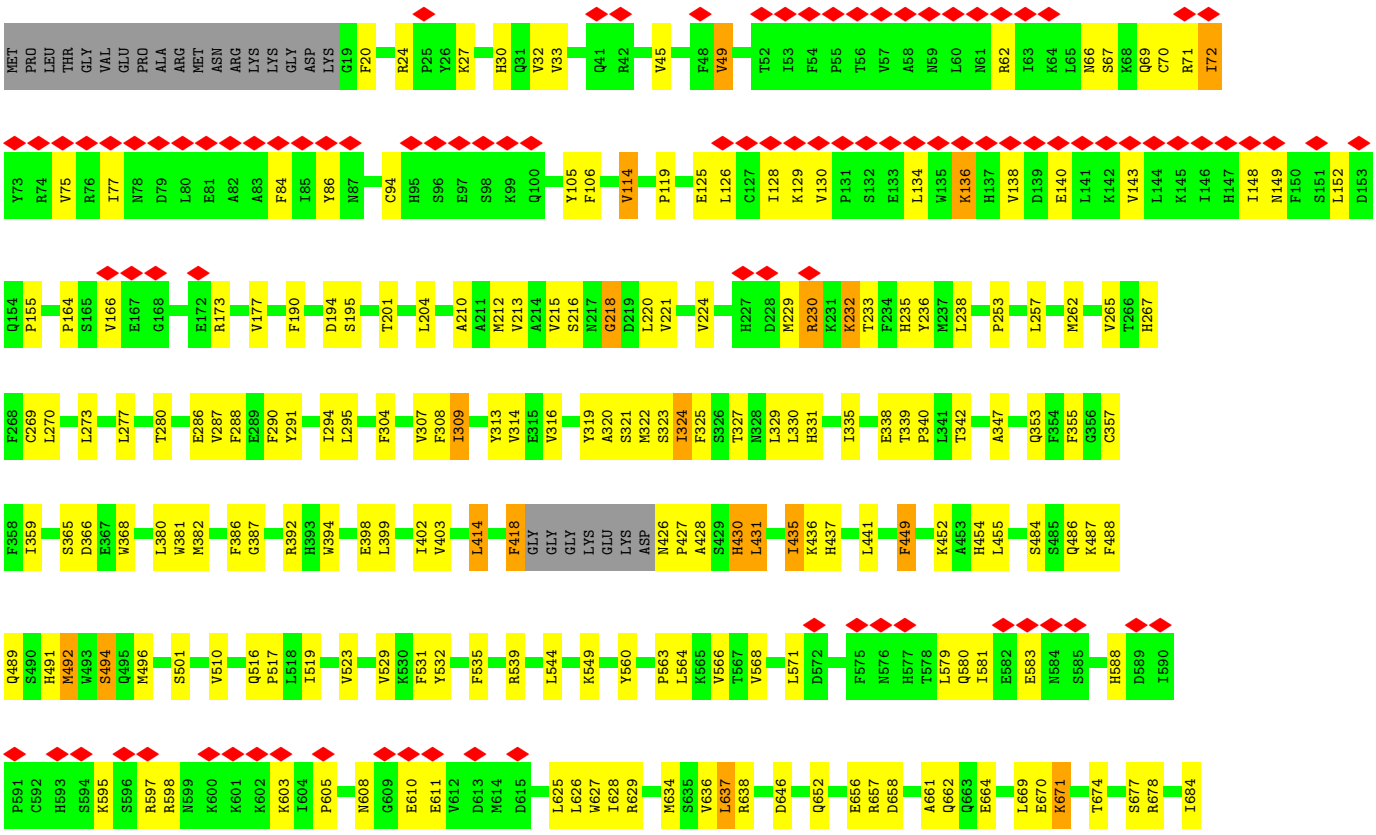


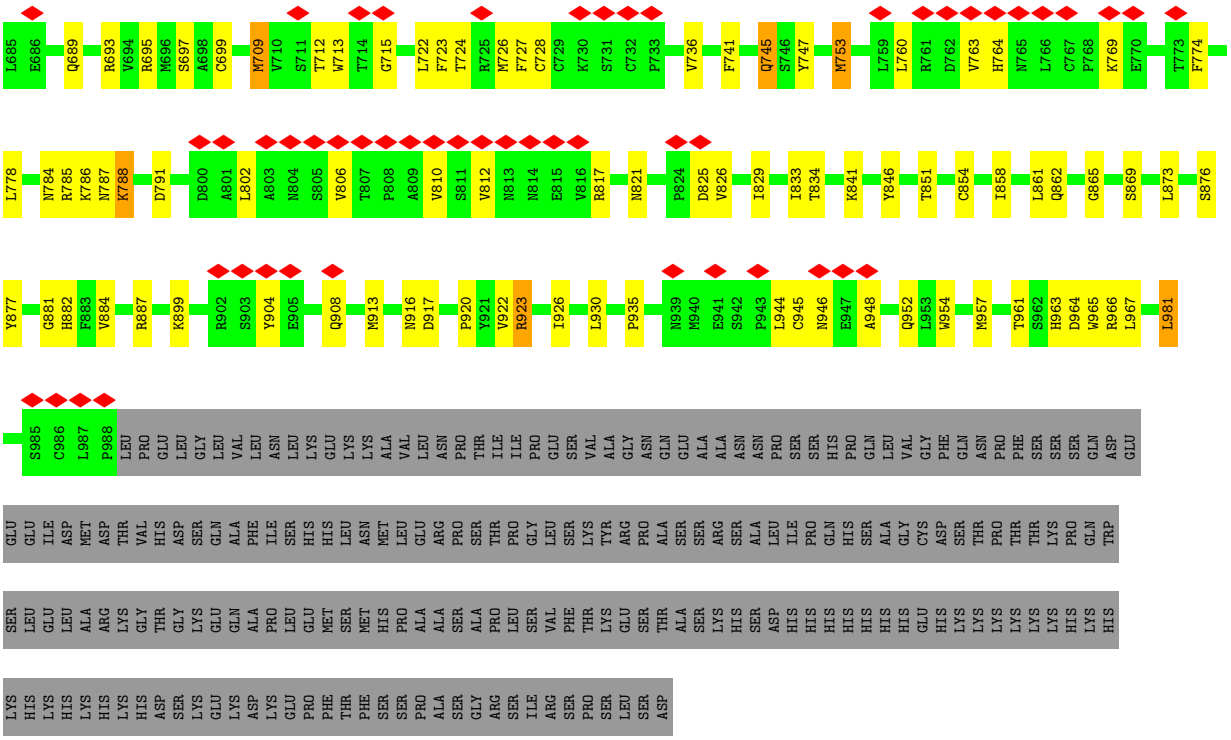

ALA SER LEU ALA GLY TRP LEU PRO SER SER MET THR ARG ASN ALA MET ALA TYR ASN VAL GLN GLN GLY PHE ALA ALA THR LEU ASP ASP ASP LYS P463 W464 Y465 S466 I467 F468 P469 I470 D471 N472 E473 D474 L475 V476 Y477 G478 R479 W480 E481 D482 N483 I484 D487 A488 Q489 A490 M491
P492 R493 L494 L495 E496 P497 P498 V499 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 L567 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 L690 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 L747 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 C786 V791 P792 A799 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 E883 A887 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 T929 T935 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 F963 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 ARG LEU SER LEU LYS ASN ALA LYS GLN LEU LEU ARG LYS PHE GLY VAL 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 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 A1193 Y1194 V1195 R1196 T1197 R1198 T1199 T1200 K1201 D1202 E1203 E1204 F1205 ILE ARG LYS PHE ALA LEU PHE ASP GLU GLN HIS ARG GLU GLU MET ARG LYS GLU ARG ARG ARG
ILE GLN GLU GLN LEU ARG ARG LEU LYS ARG ASN GLU GLN GLU LYS GLU LYS LEU LYS GLY PRO PRO GLU LYS LYS PRO LYS LYS MET LYS GLU ARG PRO ASP LEU LYS LEU LYS CYS GLY ALA CYS GLY ALA ILE GLY HIS MET ARG THR ASN LYS PHE CYS PRO LEU TYR TYR GLN THR ASN
ALA PRO PRO SER ASN PRO VAL ALA MET THR GLU GLU GLN GLU GLU GLU LEU GLU LYS THR VAL ILE HIS ASN ASP GLN LEU ILE GLU SER ALA ASP GLU VAL ARG ARG LYS SER LEU VAL LEU LYS PHE PRO
LYS GLN GLN LEU PRO PRO LYS LYS LYS ARG ARG VAL GLY THR THR VAL HIS CYS ASP TYR LEU ASN ARG PRO HIS LYS SER ILE HIS ARG ARG ARG THR ASP PRO MET VAL THR LEU SER SER ILE LEU GLU SER ILE ILE ASN ASP MET ARG ASP LEU PRO ASN THR TYR PRO PHE HIS



• Molecule 36: Transcription initiation factor TFIID subunit 2

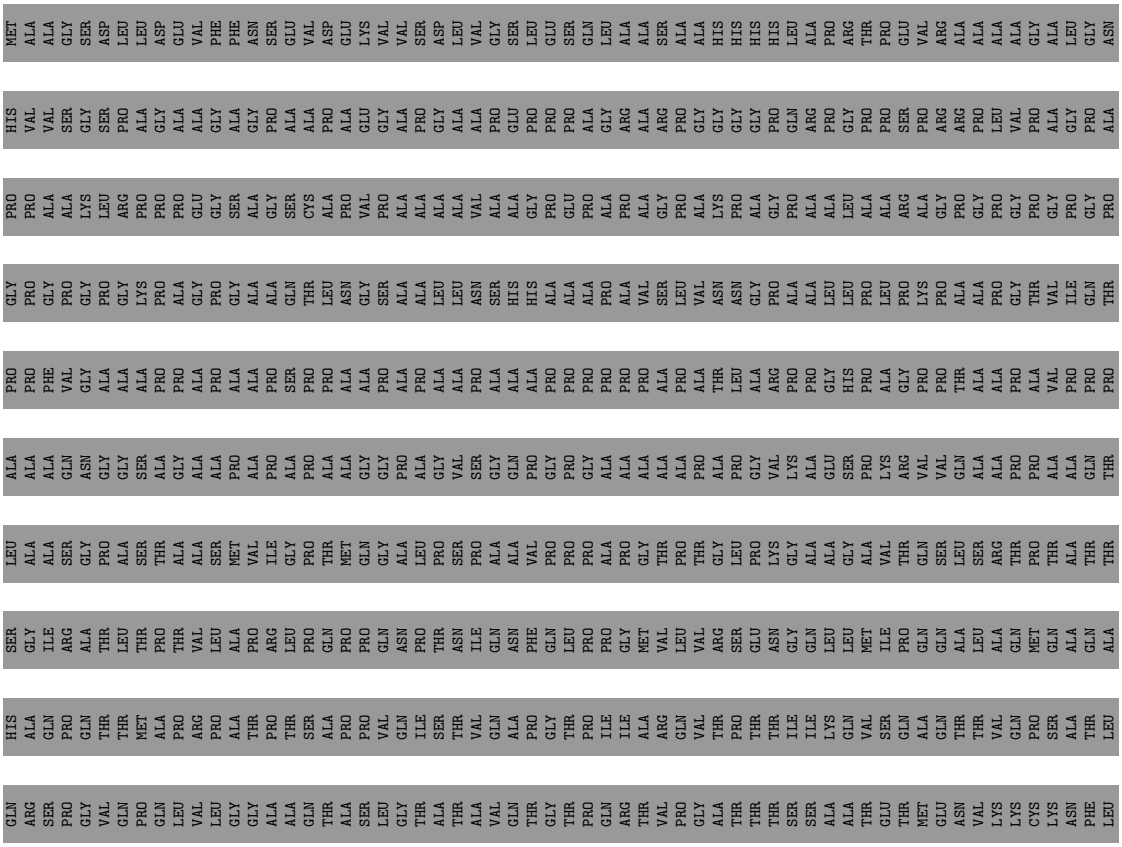
Chain DB:

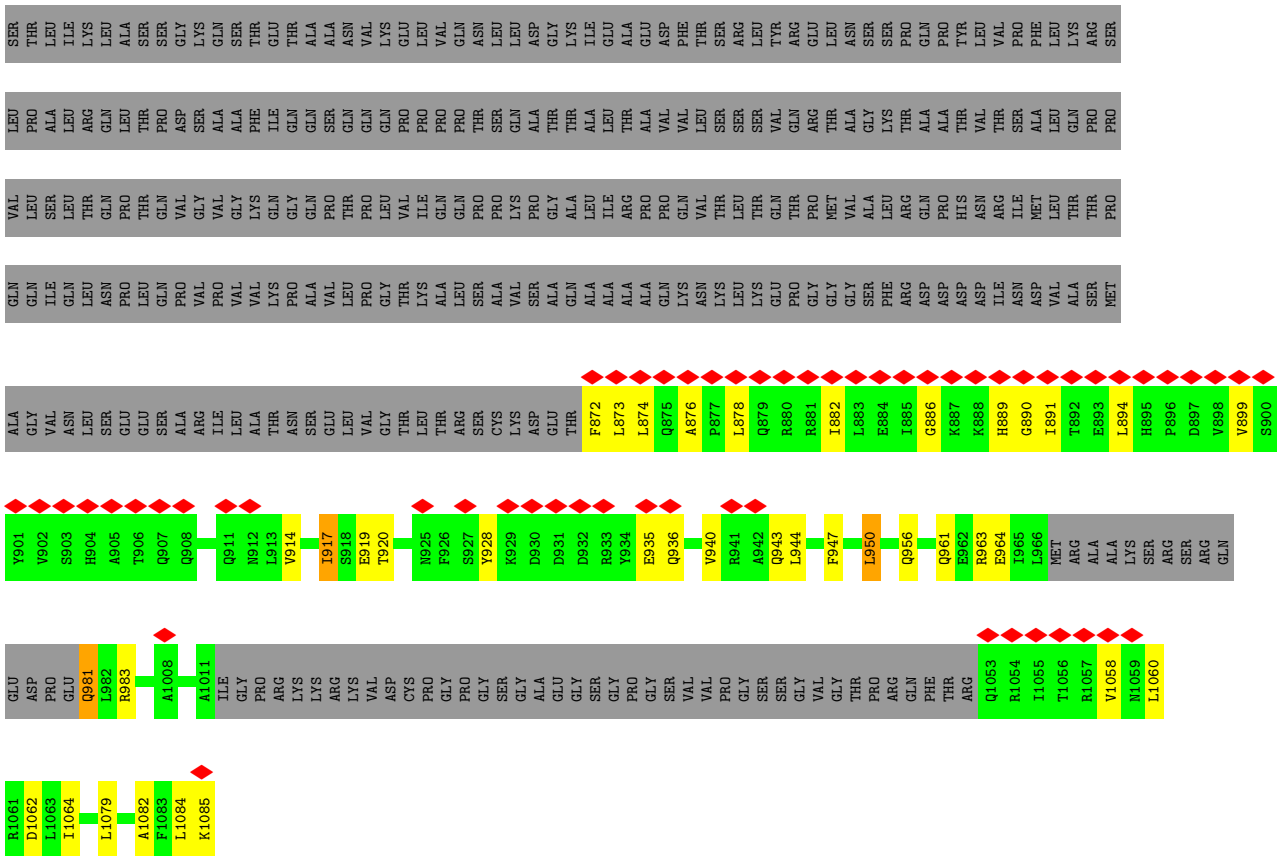




- Molecule 37: Transcription initiation factor TFIID subunit 4

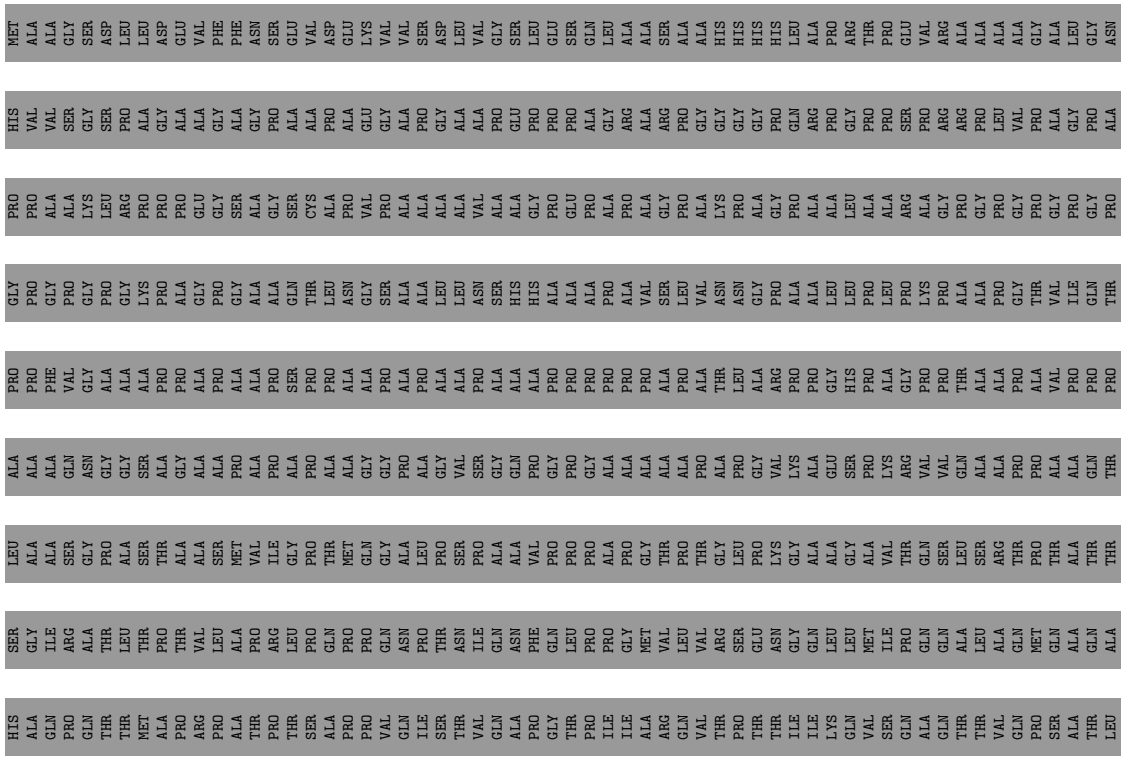
Chain DD:

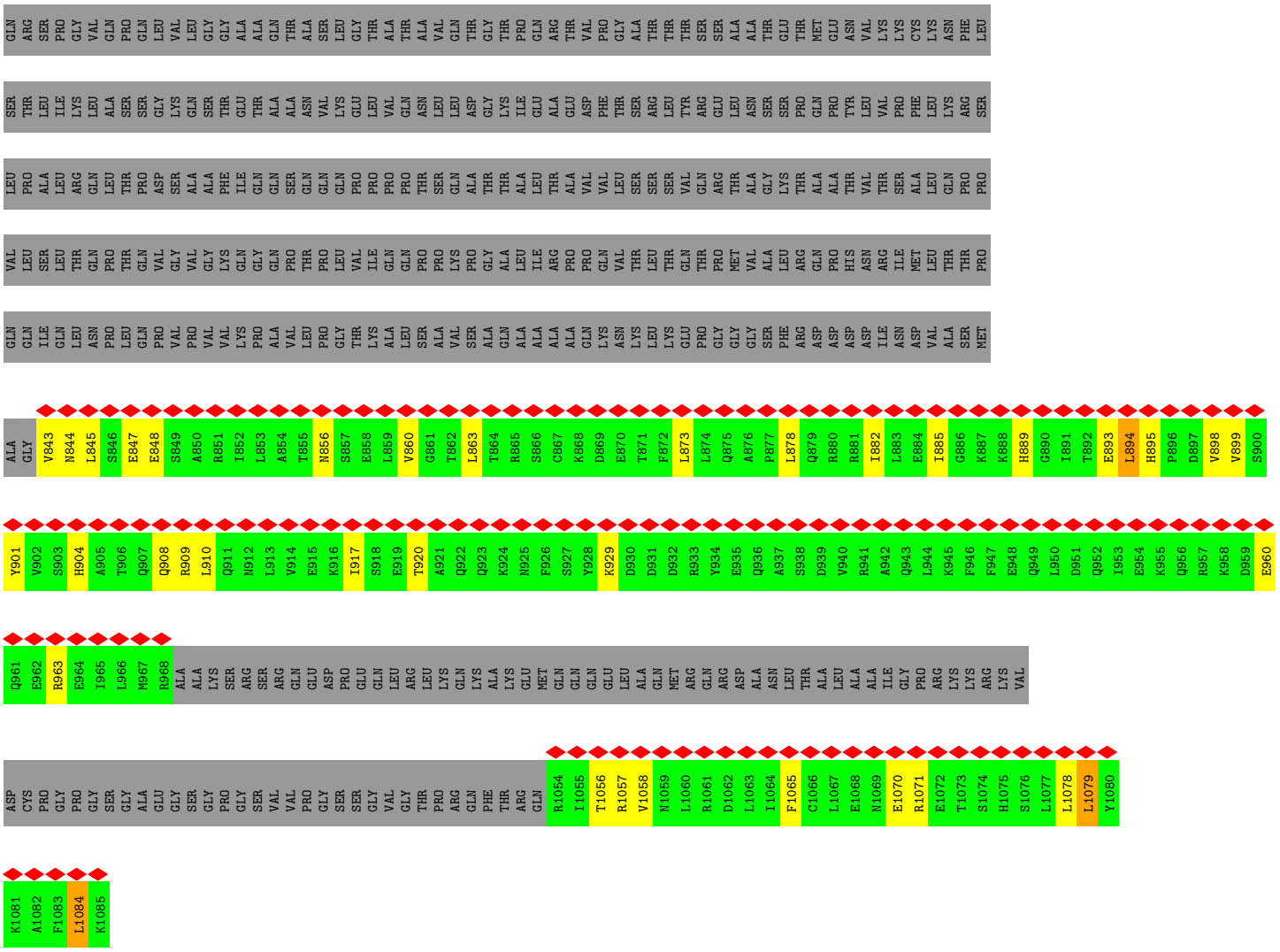




- Molecule 37: Transcription initiation factor TFIID subunit 4

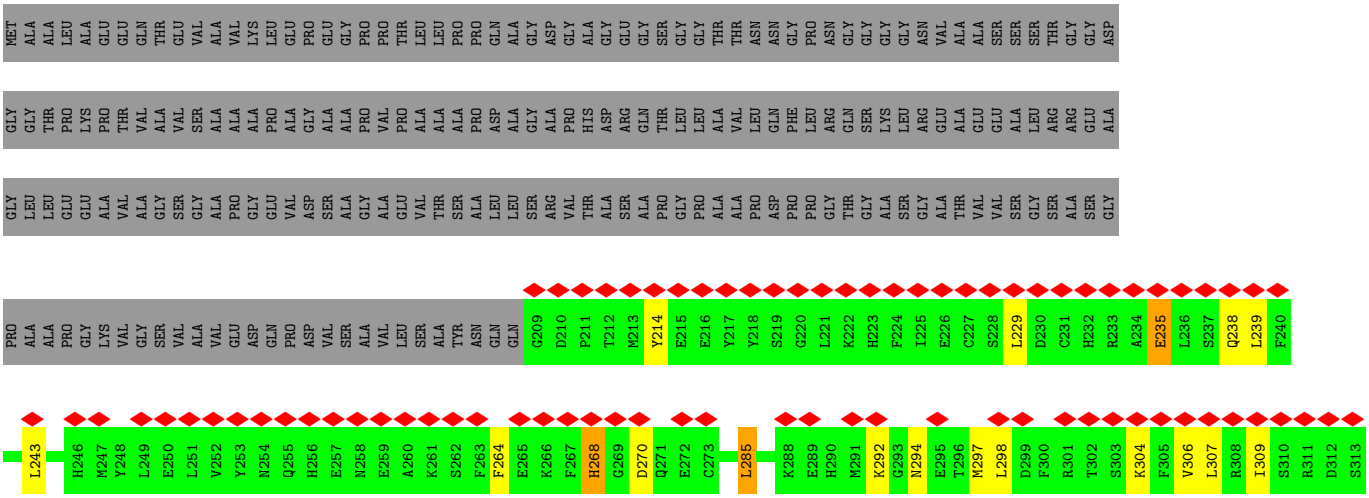
Chain Dd: 15% 11% • 85%





• Molecule 38: Transcription initiation factor TFIID subunit 5

Chain DE: 19% 49% 17% • 32%



Y314 Q315 L316 L317 K318 R319 H320 L321 Q322 E323 K324 Q325 N326 N327 Q328 I329 W330 N331 I332 V333 Q334 E335 H336 L337 Y338 I339 D340 I341 F342 D343 G344 M345 P346 R347 S348 K349 Q350 Q351 I352 D353 L359 A363 K364 R365 E366 A367 N368 K369 L376 L377 K378 GLU PRO GLU ILE GLU VAL

PRO LEU ASP ASP GLU ASP GLU GLU GLY GLU ASN GLU GLU GLY LYS PRO LYS LYS LYS LYS LYS PRO LYS LYS ASP SER ILE GLY SER LYS SER LYS LYS Q417 D418 P419 P422 P423 Q424 N425 R426 I427 P428 I441 K445 R450 V451 R452 L453 G454 P455 D456 C457 Y464 T465 F466

T474 A475 V476 T479 R495 V499 K503 V507 K508 Q509 A510 S511 D512 L513 S514 L515 I516 D521 D522 V523 E530 K531 T532 A533 S534 E535 L536 K537 H542 S543 Y547 G548 A549 S550 F551 R555 N556 Y557 L558 L559 S560 S561 S562 E563 V567 W570 S571

L572 Q573 L578 N585 Y586 P587 V588 W589 D590 T591 Q592 F593 Y599 F600 V601 G604 H605 A609 R610 L611 D615 H616 P619 L620 R621 I622 F623 D629 T633 R634 F635 H636 P637 Y641 V642 A643 T644 A647 D648 V651 R652 L653 L657 N658 R663 I664

F665 H668 K669 G670 P671 I672 H673 S674 L675 T676 F677 L684 A685 T686 T689 D690 G691 R692 V693 W696 D697 H700 G701 L707 K708 G709 H710 T713 V714 C715 S716 L717 R718 F719 E724 S728 W738 I741 K742 E745 D746 L747 GLU THR ASP ASP PHE THR

T754 A755 T756 N760 L761 P762 E763 N764 S765 Q766 E767 L768 V780 V781 H782 L783 H784 F785 R788 N789 L790 V791 L792 A793 A796 Y797 S798 PRO GLN

- Molecule 38: Transcription initiation factor TFIID subunit 5

Chain De:

MET ALA ALA LEU ALA GLU GLU GLN THR GLU VAL ALA VAL LYS LEU GLU PRO GLU GLY PRO PRO THR LEU LEU PRO PRO GLN ALA GLY ASP GLY ALA GLY GLU GLY SER GLY GLY THR THR ASN ASN GLY PRO ASN GLY GLY GLY GLY ASN VAL ALA ALA SER SER SER THR GLY GLY ASP

GLY GLY THR PRO LYS PRO THR VAL ALA VAL SER ALA ALA ALA PRO ALA GLY ALA ALA PRO VAL PRO ALA ALA ALA PRO ASP ALA GLY ALA PRO HIS ASP ARG GLN THR LEU LEU ALA VAL LEU GLN PHE LEU ARG GLN SER LYS LEU ARG GLU ALA GLU GLU ALA LEU ARG ARG GLU ALA

GLY LEU LEU GLU GLU ALA VAL ALA GLY SER GLY SER GLY ALA PRO GLY GLU VAL ASP SER ALA GLY ALA GLU VAL THR SER ALA LEU LEU SER ARG VAL THR ALA SER ALA PRO GLY PRO ALA ALA PRO ASP PRO PRO GLY THR GLY ALA SER GLY ALA THR VAL VAL SER GLY SER ALA SER GLY

PRO ALA ALA PRO GLY LYS VAL GLY SER VAL ALA VAL GLU ASP GLN PRO ASP VAL SER ALA VAL L202 S203 A204 Y205 N206 Q207 Q208 G209 D210 P211 T212 M213 Y214 E215 E216 Y217 Y218 S219 G220 L221 K222 H223 F224 I225 E226 C227 S228 L229 D230 C231 H232 R233 A234 E235 L236 S237 Q238 L239 F240

Y241 P242 L243 F244 V245 H246 M247 Y248 L249 E250 L251 V252 Y253 N254 Q255 H256 E257 N258 E259 A260 K261 S262 F263 F264 E265 K266 F267 H268 G269 D270 Q271 E272 C273 Y274 Y275 Q276 D277 D278 L279 R280 V281 L282 S283 S284 L285 T286 K287 K288 E289 H290 M291 K292 G293 N294 E295 T296 M297 L298 D299 E300

R301 T302 S303 K304 F305 V306 L307 R308 I309 S310 R311 D312 S313 Y314 Q315 L316 L317 K318 R319 H320 L321 Q322 E323 K324 Q325 N326 N327 Q328 I329 W330 N331 I332 V333 Q334 E335 H336 L337 Y338 I339 D340 I341 F342 D343 GLY MET PRO ARG SER LYS GLN GLN ILE ASP ALA MET VAL GLY SER LEU ALA

GLY GLU A363 K364 R365 E366 A367 N368 K369 S370 K371 V372 F373 F374 G375 L376 L377 K378 E379 P380 GLU ILE GLU VAL PRO LEU ASP ASP GLU ASP GLU GLU GLY GLU ASN GLU GLU GLY LYS PRO LYS LYS LYS LYS PRO LYS LYS ASP SER ILE GLY SER LYS SER LYS K416 Q417 D418 P419 N420

A421 P422 P423 Q424 N425 R426 I427 P428 L429 P430 E431 L432 K433 D434 S435 D436 K437 L438 D439 K440 I441 M442 N443 M444 K445 E446 T447 T448 K449 R450 V451 R452 L453 G454 P455 D456 C457 L458 P459 S460 I461 C462 F463 Y464 T465 F466 L467 N468 A469 Y470 Q471 G472 L473 T474 A475 V476 D477 V478 T479 D480

D481 S482 S483 L484 I485 A486 G487 G488 F489 A490 D491 S492 T493 V494 R495 V496 W497 S498 V499 T500 P501 K502 K503 L504 R505 S506 V507 K508 Q509 A510 S511 D512 L513 S514 L515 I516 D517 K518 E519 S520 D521 D522 V523 L524 E525 R526 I527 M528 D529 E530 K531 T532 A533 S534 E535 L536 K537 I538 L539 Y540

G541 H542 S543 G544 P545 V546 Y547 G548 A549 S550 F551 S552 P553 D554 R555 N556 Y557 L558 L559 S560 S561 S562 E563 D564 G565 T566 V567 R568 L569 W570 S571 L572 Q573 T574 F575 T576 C577 L578 V579 G580 Y581 K582 G583 H584 N585 Y586 P587 V588 W589 D590 T591 Q592 F593 S594 P595 Y596 G597 Y598 Y599 F600

V601 S602 G603 G604 H605 D606 R607 V608 A609 R610 L611 W612 A613 T614 D615 H616 Y617 Q618 P619 L620 R621 I622 F623 A624 G625 H626 L627 A628 D629 V630 M631 C632 T633 R634 F635 H636 P637 N638 S639 N640 Y641 V642 A643 T644 G645 S646 A647 D648 R649 T650 V651 R652 L653 W654 D655 V656 L657 N658 G659 N660

C661 V662 R663 I664 F665 T666 G667 H668 K669 G670 P671 I672 H673 S674 L675 T676 F677 S678 P679 N680 G681 R682 F683 L684 A685 T686 G687 A688 T689 D690 G691 R692 V693 L694 L695 W696 D697 I698 G699 H700 G701 L702 M703 V704 G705 E706 L707 K708 G709 H710 T711 D712 T713 V714 C715 S716 L717 R718 F719 S720

R721 D722 G723 E724 I725 L726 A727 S728 G729 S730 M731 D732 N733 T734 V735 R736 L737 W738 D739 A740 I741 K742 A743 F744 E745 D746 L747 E748 THR ASP ASP PHE THR T754 A755 T756 G757 H758 I759 N760 L761 P762 E763 N764 S765 Q766 E767 L768 L769 L770 G771 T772 Y773 M774 T775 K776 S777 T778 P779 V780

V781 H782 L783 H784 F785 T786 R787 R788 N789 L790 V791 L792 A793 A794 G795 A796 Y797 S798 P799 GLN

- Molecule 39: Transcription initiation factor TFIID subunit 6

Chain DF: 29% 46% 13% • 40%

MET ALA GLU GLU LYS LYS LEU LYS LEU S10 N11 T12 V13 L14 P15 S16 E17 S18 M19 K20 V21 V22 A23 E24 S25 M26 G27 I28 A29 Q30 I31 Q32 E33 E34 T35 C36 Q37 L38 L39 L55 M58 H59 M60 G61 K62 R63 Q64 K65 L66 L75 P82 L83 E90 F91 I92

P93 F106 Y107 E108 E109 K110 E111 V112 D113 L114 S115 D116 I117 I118 N119 T120 P121 L122 P123 V129 C130 L131 L136 S137 I138 E139 I145 N148 P149 P150 PRO ALA PRO LYS GLU GLN LYS ALA GLU ALA THR GLU PRO LEU LYS SER ALA LYS PRO GLY GLN GLU GLU ASP

GLY PRO LEU LYS GLY LYS GLY GLN GLY ALA THR THR ALA ASP GLY LYS GLY LYS GLU LYS LYS ALA PRO PRO LEU LEU GLU GLY ALA PRO LEU R207 L208 K209 P210 R211 S212 I213 H214 E215 L216 S217 V218 E219 V232 G233 S234 C235 E236 A237 K238 R239 L243 I246 L252 Y253

Q254 M255 L256 P257 R258 T261 F262 I263 S264 E265 G266 V267 R268 V269 N270 V271 V272 Q273 N274 N275 L276 A277 L278 L279 I280 Y281 M285 V286 K287 A288 L289 M290 T294 L295 Y296 L297 E298 K299 Y300 V301 L304 T310 R315 Q316 L317 C318 L319 R320 P321 D322 V323 D324 N325 H326

W327 A328 L329 R330 D331 F332 R335 I340 H343 F344 S345 T346 T347 T348 N349 N350 I351 R354 F359 T360 K361 V364 D365 E366 K367 T368 P369 W370 I377 A378 G379 L380 A381 E382 L383 G384 H385 D386 V387 I388 K389 T390 L391 I392 L393 P394 R395 L396 Q397 Q398 E399 G400 E401

R402 I403 R404 S405 V406 L407 D408 G409 P410 V411 L412 S413 N414 I415 D416 R417 I418 G419 A420 D421 H422 V423 Q424 S425 L426 L427 L428 K429 H430 C431 A432 P433 V434 L435 A436 K437 L438 R439 P440 P441 P442 D443 N444 Q445 D446 A447 Y448 R449 A450 E451 F452 G453 S454 L455 G456 P457 L458 L459 C460 S461

Q462 V463 V464 K465 A466 R467 A468 Q469 A470 A471 L472 Q473 ALA GLN GLN VAL ASN ARG THR THR LEU THR ILE THR GLN PRO ARG PRO THR LEU THR LEU SER GLN ALA PRO GLN PRO GLY PRO ARG THR PRO GLY LEU LEU LYS VAL PRO GLY SER ILE ALA LEU PRO VAL GLN THR LEU VAL

SER ALA ARG ALA ALA ALA PRO PRO GLN PRO SER PRO PRO PRO THR LYS PHE ILE VAL MET SER SER SER SER SER SER ALA PRO SER THR GLN GLN VAL LEU SER LEU SER THR SER ALA PRO GLY SER GLY SER THR THR SER PRO VAL THR THR THR VAL PRO SER VAL GLN PRO ILE

VAL LYS LEU VAL SER THR ALA THR THR ALA ALA PRO PRO SER SER THR ALA PRO SER SER GLY PRO GLY SER VAL GLN LYS TYR ILE VAL VAL SER LEU PRO PRO THR GLY GLU GLU GLY LYS GLY GLY PRO THR SER HIS PRO SER PRO VAL PRO PRO PRO ALA SER SER PRO SER PRO LEU SER GLY SER

ALA LEU CYS GLY GLY LYS GLN GLU ALA GLY ASP SER PRO PRO PRO ALA PRO GLY THR PRO LYS ALA ASN GLY SER GLN PRO ASN SER GLY SER PRO GLN PRO ALA PRO

- Molecule 39: Transcription initiation factor TFIID subunit 6

Chain Df: 42% 47% 12% • 40%

MET ALA GLU GLU LYS LYS LEU LYS L9 S10 N11 T12 V13 L14 P15 S16 E17 S18 M19 K20 V21 V22 A23 E24 S25 M26 G27 I28 A29 Q30 I31 Q32 E33 E34 T35 C36 Q37 L38 L39 T40 D41 E42 V43 S44 Y45 R46 I47 K48 E49 I50 A51 Q52 D53 A54 L55 K56 F57 M58 H59 M60

G61 K62 R63 Q64 K65 L66 T67 T68 S69 D70 I71 D72 Y73 A74 L75 K76 L77 K78 N79 V80 E81 P82 L83 Y84 G85 F86 H87 A88 Q89 E90 F91 I92 P93 F94 R95 F96 A97 S98 G99 G100 G101 R102 E103 L104 Y105 F106 Y107 E108 E109 K110 E111 V112 D113 L114 S115 D116 I117 I118 N119 T120

P121 L122 P123 R124 V125 P126 L127 D128 V129 C130 L131 K132 A133 H134 W135 L136 S137 I138 E139 G140 C141 Q142 P143 A144 I145 P146 E147 N148 P149 P150 P151 ALA PRO LYS GLU GLN GLN LYS ALA GLU ALA THR GLU PRO LEU LYS SER ALA LYS PRO GLY GLN GLU GLU ASP GLY PRO LEU LYS GLY

LYS GLY GLN GLY ALA THR THR ALA ASP GLY LYS GLY LYS GLU LYS LYS LYS ALA PRO PRO LEU LEU GLU GLY ALA PRO LEU ARG LEU LYS PRO ARG SER ILE H214 V218 E219 Q220 Q221 L222 Y223 Y224 K225 E226 I227 T228 E229 A230 C231 V232 G233 S234 C235 E236 A237 K238 R239 A240 M255

I263 V267 V272 Q273 N274 N275 L276 A277 L278 L279 I280 Y281 L282 V286 M290 D291 N292 L295 Y296 L297 E298 K299 H302 E303 P306 A307 V308 M309 T310 C311 I312 R315 Q316 L317 C318 L319 R320 P321 D322 V323 D324 N325 H326 W327 A328 L329 R330 A334 R335 L336

V337 I340 C341 K342 H343 F344 S345 T346 T347 T348 N349 N350 I351 Q352 S353 R354 I355 T356 K357 T358 F359 T360 K361 S362 W363 V364 D365 E366 K367 T368 P369 W370 T371 T372 R373 Y374 G375 S376 G379 L380 A381 E382 L383 D386 V387 I388 K389 T390 L391 I392 L393 P394 R395 L396 Q397 Q398 E399

G400 E401 R402 I403 R404 S405 V406 L407 D408 G409 P410 V411 L412 S413 N414 I415 D416 R417 I418 G419 A420 D421 H422 V423 Q424 S425 L426 L427 L428 K429 H430 C431 A432 P433 V434 L435 A436 K437 L438 R439 P440 P441 P442 D443 N444 Q445 D446 A447 Y448 R449 A450 E451 F452 G453 S454 L455 G456 P457 L458 L459

C460 S461 Q462 V463 V464 K465 A466 R467 A468 Q469 A470 A471 L472 Q473 ALA GLN GLN VAL ASN ARG THR THR LEU THR ILE THR GLN PRO ARG PRO THR LEU THR LEU SER GLN ALA PRO GLN PRO GLY PRO ARG THR PRO GLY LEU LEU LYS VAL PRO GLY SER ILE ALA LEU PRO VAL GLN THR

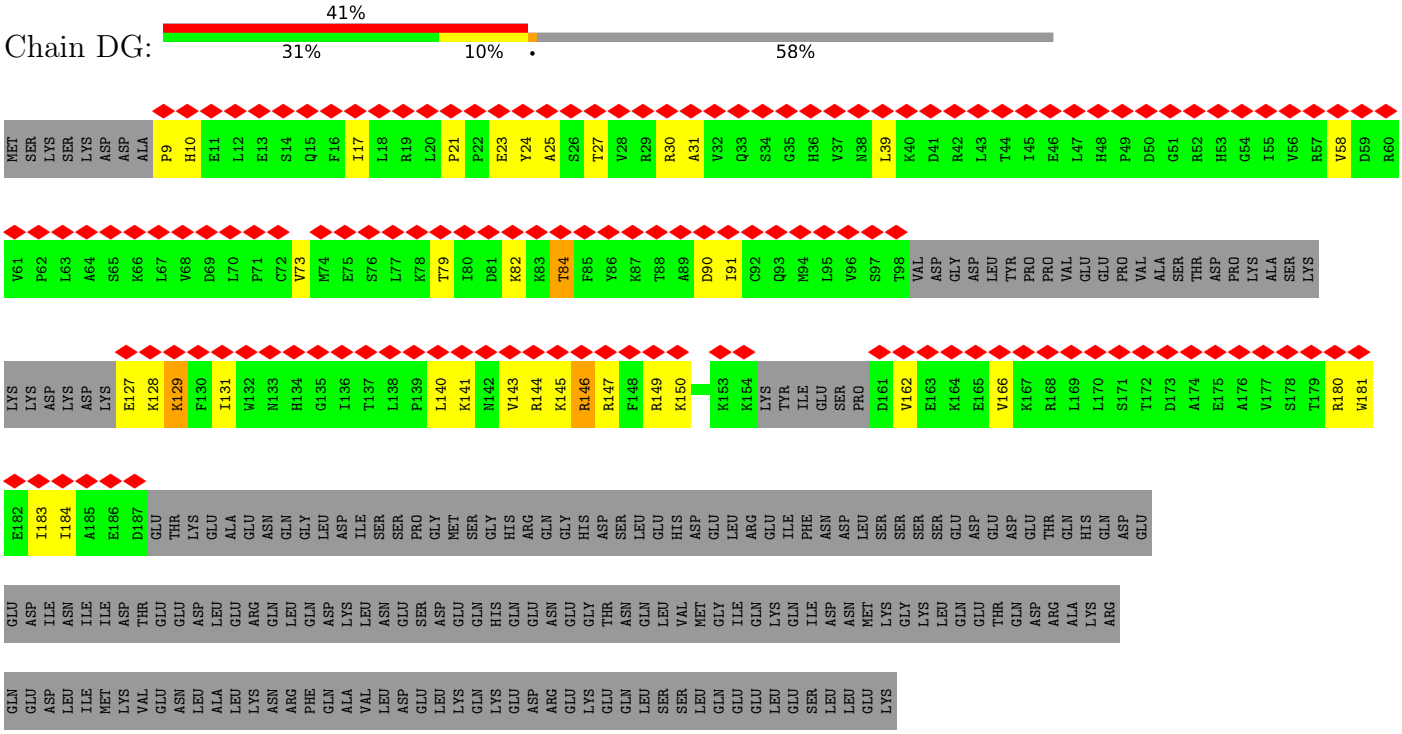
LEU VAL SER ALA ARG ALA ALA ALA PRO PRO GLN PRO SER PRO PRO PRO PRO THR LYS PHE ILE VAL MET SER SER SER SER SER ALA PRO SER THR GLN GLN VAL LEU SER LEU SER THR SER ALA PRO GLY SER GLY SER THR THR THR SER PRO VAL THR THR THR VAL PRO SER VAL GLN

PRO ILE VAL LYS LEU VAL SER THR ALA THR THR ALA ALA PRO PRO SER THR ALA PRO SER GLY PRO GLY SER VAL GLN LYS TYR ILE VAL VAL SER LEU PRO PRO THR GLY GLU GLY LYS GLY GLY PRO THR SER HIS PRO SER PRO VAL PRO PRO PRO PRO ALA SER SER PRO SER PRO LEU SER

GLY SER ALA LEU CYS GLY GLY LYS GLN GLU ALA GLY ASP SER PRO PRO PRO ALA PRO GLY THR PRO LYS ALA ASN GLY SER GLY SER PRO GLN PRO ALA PRO

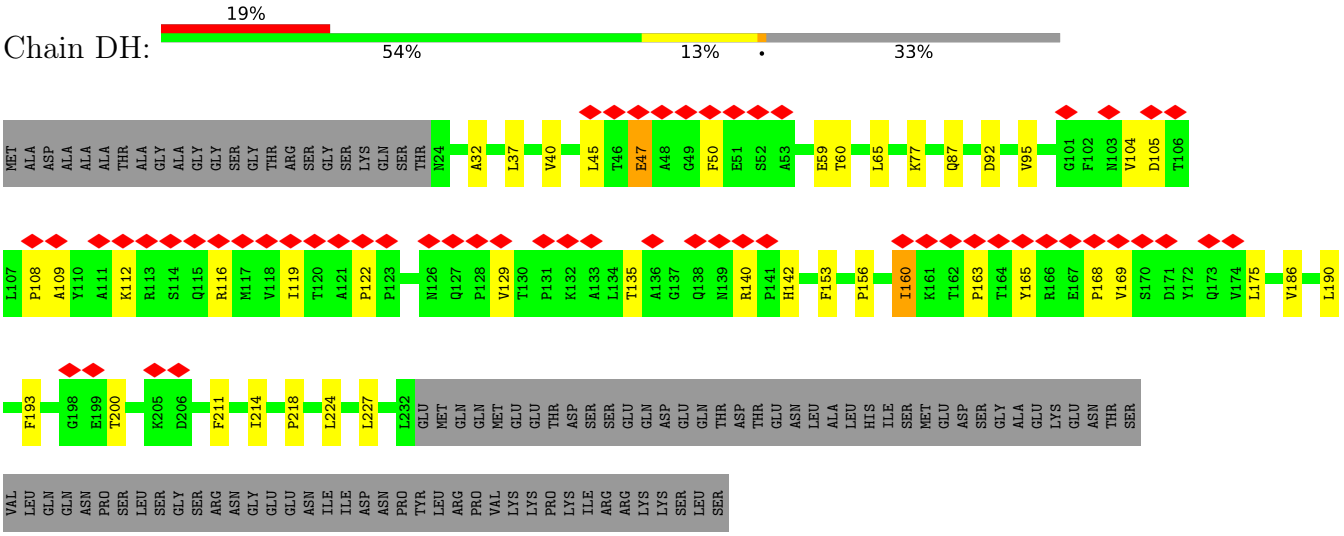
- Molecule 40: Transcription initiation factor TFIID subunit 7

Chain DG:



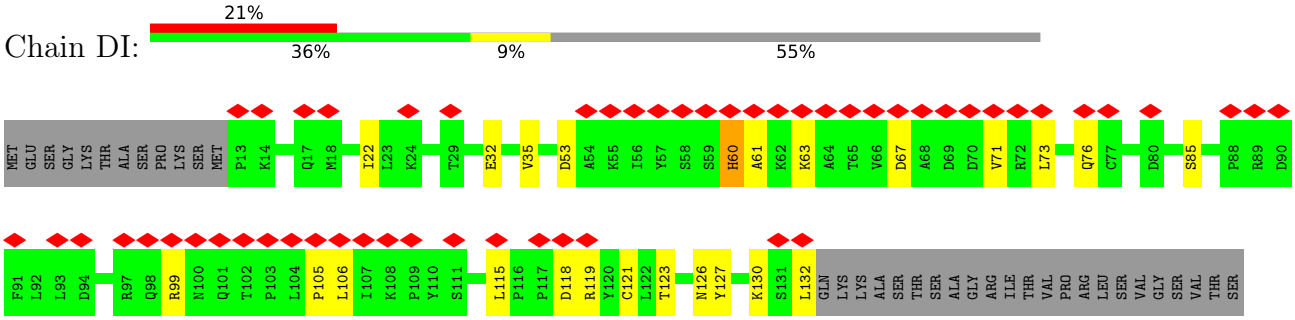
- Molecule 41: Transcription initiation factor TFIID subunit 8

Chain DH:



- Molecule 42: Transcription initiation factor TFIID subunit 9

Chain DI:



ARG PRO SER THR PRO THR LEU GLY THR PRO THR PRO GLN THR MET SER VAL SER THR LYS VAL GLY THR PRO MET SER LEU THR GLY GLN ARG PHE THR VAL GLN MET PRO THR SER GLN SER PRO ALA VAL LYS ALA SER ILE PRO ALA THR SER ALA VAL GLN ASN VAL LEU ILE ASN

PRO SER LEU ILE GLY SER LYS ASN ILE LEU ILE THR THR ASN MET MET SER SER GLN ASN THR ALA ASN GLU SER SER ASN ALA LEU LYS ARG LYS ARG GLU ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP TYR ASP ASN LEU

- Molecule 42: Transcription initiation factor TFIID subunit 9

Chain Di:

MET GLU SER GLY LYS THR ALA SER PRO LYS SER M12 P13 K14 D15 A16 Q17 M18 M19 A20 Q21 I22 L23 K24 D25 M26 G27 I28 T29 E30 Y31 E32 P33 R34 V35 I36 N37 Q38 M39 L40 E41 F42 A43 F44 R45 Y46 V47 T48 T49 I50 L51 D52 D53 A54 K55 I56 Y57 S58 S59 H60

A61 K62 K63 A64 T65 V66 D67 A68 D69 D70 V71 R72 L73 A74 I75 Q76 C77 R78 A79 D80 Q81 S82 F83 T84 S85 P86 P87 P88 R89 D90 F91 L92 L93 D94 I95 A96 R97 Q98 R99 N100 Q101 T102 P103 L104 P105 L106 I107 K108 P109 Y110 S111 G112 P113 R114 L115 P116 P117 D118 R119 Y120

C121 L122 T123 A124 P125 N126 Y127 R128 L129 K130 S131 L132 GLN LYS LYS ALA SER THR SER ALA GLY ARG ILE THR VAL PRO ARG LEU SER VAL GLY SER VAL THR SER ARG PRO SER THR PRO THR LEU GLY THR PRO THR PRO GLN THR MET SER VAL SER THR LYS VAL GLY THR PRO MET

SER LEU THR GLY GLN ARG PHE THR VAL GLN MET PRO THR SER GLN SER PRO ALA VAL LYS ALA SER ILE PRO ALA THR SER ALA VAL GLN ASN VAL LEU ILE ASN PRO SER LEU ILE GLY SER LYS ASN ILE LEU ILE THR THR ASN MET MET SER SER GLN ASN THR ALA ASN GLU SER

SER ASN ALA LEU LYS ARG LYS ARG GLU ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP TYR ASP ASN LEU

- Molecule 43: Transcription initiation factor TFIID subunit 10

Chain DJ:

MET SER CYS SER GLY SER GLY ALA ASP PRO GLU ALA ALA PRO ALA SER ALA ALA SER ALA PRO GLY PRO ALA PRO PRO VAL SER ALA PRO ALA ALA LEU PRO SER SER THR ALA ALA GLU ASN LYS ALA SER PRO ALA GLY THR ALA GLY GLY PRO GLY ALA GLY ALA ALA ALA GLY GLY

THR GLY PRO LEU ALA ALA ARG ALA GLY GLU PRO ALA GLU ARG ARG GLY ALA ALA PRO VAL SER ALA GLY GLY GLY ALA ALA PRO PRO GLU GLY ALA ILE SER ASN GLY VAL TYR VAL LEU PRO SER ALA ALA ASN GLY ASP VAL LYS PRO VAL VAL SER SER T114 P115 D118 M121 Q122

L123 E124 D125 Y126 T127 P128 T129 I130 P131 D132 A133 L139 F144 E145 A146 I152 A159 Q160 D165 I166 A167 N168 D169 A170 L171 Q172 H173 C174 K175 M176 K177 GLY THR ALA SER GLY SER SER ARG SER LYS SER LYS ASP ARG K192 Y193 T194 L195 T196 M197 E198 D199 P202

A203 L204 S205 E206 Y207 G208 I209 N210 V211 F217 THR

- Molecule 43: Transcription initiation factor TFIID subunit 10

Chain Dj:

MET SER CYS SER GLY SER GLY ALA ASP PRO GLU ALA ALA PRO ALA SER ALA ALA SER ALA PRO GLY PRO ALA PRO PRO VAL SER ALA PRO ALA ALA LEU PRO SER SER THR ALA ALA GLU ASN LYS ALA SER PRO ALA GLY THR ALA GLY GLY PRO GLY ALA GLY ALA ALA ALA GLY GLY

THR GLY PRO LEU ALA ALA ARG ALA GLY GLU PRO ALA GLU ARG ARG GLY ALA ALA PRO VAL SER ALA GLY GLY ALA ALA PRO PRO GLU GLY ALA ILE SER ASN GLY VAL TYR VAL LEU PRO SER ALA ALA ASN GLY ASP VAL LYS PRO VAL VAL SER SER T114 P115 L116 V117 D118 F119 L120

M121 Q122 L123 E124 D125 Y126 T127 P128 T129 I130 P131 D132 A133 V134 T135 G136 Y137 Y138 L139 N140 R141 A142 G143 F144 E145 A146 S147 D148 P149 R150 I151 I152 R153 L154 I155 S156 L157 A158 A159 Q160 K161 F162 I163 S164 D165 I166 A167 N168 D169 A170 L171 Q172 H173 C174 K175 M176 K177 G178 THR ALA

SER GLY SER SER ARG SER LYS SER K189 D190 R191 K192 Y193 T194 L195 T196 M197 E198 D199 L200 T201 P202 A203 L204 S205 E206 Y207 G208 I209 N210 V211 K212 K213 P214 H215 Y216 F217 T218

- Molecule 44: Transcription initiation factor TFIID subunit 12

Chain DL: 45% 27% 17% 53%

MET ASN GLN PHE GLY PRO SER ALA LEU ILE ASN LEU SER ASN PHE SER SER ILE LYS PRO GLU PRO ALA SER THR PRO PRO GLN GLY SER MET ALA ASN SER THR ALA VAL VAL LYS ILE PRO GLY THR PRO GLY ALA GLY GLY ARG LEU SER PRO GLU ASN ASN Q56 V57 L58 T59 K60

K61 K62 L63 Q64 D65 L66 V67 R68 E69 V70 D71 P72 N73 E74 Q75 L76 D77 E78 D79 V80 E81 E82 M83 L84 L85 Q86 I87 A88 D89 D90 F91 I92 E93 S94 V95 V96 T97 A98 A99 C100 Q101 L102 A103 R104 H105 R106 K107 S108 S109 T110 L111 E112 V113 K114 D115 V116 Q117 L118 H119 L120

E121 R122 Q123 W124 N125 M126 W127 I128 P129 G130 PHE GLY SER GLU GLU ILE ARG PRO TYR LYS LYS ALA CYS THR THR GLU ALA HIS LYS GLN ARG MET ALA LEU ILE ARG LYS THR THR LYS LYS

- Molecule 44: Transcription initiation factor TFIID subunit 12

Chain Dl: 66% 41% 24% 34%

MET ASN GLN PHE GLY PRO SER ALA LEU ILE ASN LEU SER ASN PHE SER SER ILE LYS PRO GLU PRO ALA SER THR PRO PRO GLN GLY SER MET ALA ASN SER THR ALA VAL VAL LYS ILE PRO GLY THR PRO GLY ALA GLY GLY ARG LEU SER PRO GLU ASN N55 Q56 V57 L58 T59 K60

K61 K62 L63 Q64 D65 L66 V67 R68 E69 V70 D71 P72 N73 E74 Q75 L76 D77 E78 D79 V80 E81 E82 M83 L84 L85 Q86 I87 A88 D89 D90 F91 I92 E93 S94 V95 V96 T97 A98 A99 C100 Q101 L102 A103 R104 H105 R106 K107 S108 S109 T110 L111 E112 V113 K114 D115 V116 Q117 L118 H119 L120

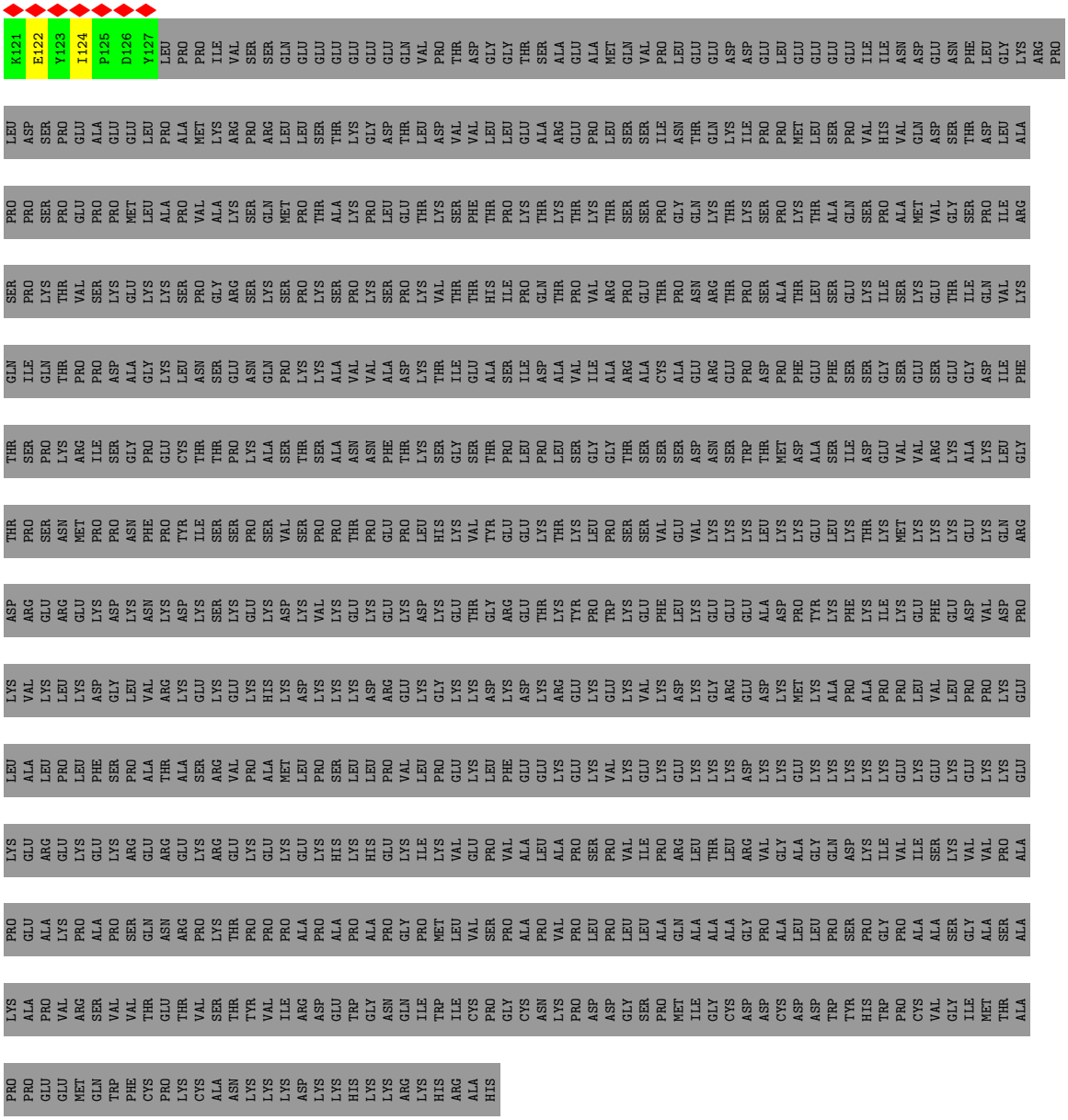
E121 R122 Q123 W124 N125 M126 W127 I128 P129 G130 F131 G132 S133 E134 E135 I136 R137 P138 Y139 K140 K141 A142 C143 T144 T145 E146 A147 H148 K149 Q150 R151 M152 A153 L154 I155 R156 K157 T158 T159 K160 K161

- Molecule 45: Transcription initiation factor TFIID subunit 3

Chain Dc: 14% 11% 86%

M1 C2 E3 S4 Y5 S6 R7 S8 L9 L10 R11 V12 S13 V14 A15 Q16 I17 C18 Q19 A20 L21 G22 W23 D24 S25 V26 Q27 L28 S29 A30 C31 H32 L33 L34 T35 D36 V37 L38 Q39 R40 Y41 L42 Q43 Q44 L45 G46 R47 G48 C49 H50 R51 Y52 S53 E54 L55 Y56 G57 R58 T59 D60

P61 I62 L63 D64 D65 V66 G67 E68 A69 F70 Q71 L72 M73 G74 V75 S76 L77 H78 E79 L80 E81 D82 Y83 I84 H85 N86 I87 E88 P89 V90 T91 F92 P93 H94 Q95 I96 P97 S98 F99 P100 V101 S102 K103 N104 N105 V106 L107 Q108 F109 P110 Q111 P112 G113 S114 K115 D116 A117 E118 E119 R120


K121 E122 Y123 I124 P125 D126 Y127
LEU PRO PRO ILE VAL SER SER GLN GLU GLU GLU GLU GLU GLN VAL PRO THR ASP GLY GLY THR SER ALA GLU ALA MET GLN VAL PRO LEU GLU GLU ASP ASP GLU LEU GLU GLU GLU GLU ILE ILE ASN ASP GLU ASN PHE LEU GLY LYS ARG PRO
LEU ASP SER PRO GLU ALA GLU GLU LEU PRO ALA MET LYS ARG PRO ARG LEU LEU SER THR LYS GLY ASP THR LEU ASP VAL VAL LEU LEU GLU ALA ARG GLU PRO LEU SER SER ILE ASN THR GLN LYS ILE PRO PRO MET LEU SER PRO VAL HIS VAL GLN ASP SER THR ASP LEU ALA
PRO PRO SER PRO GLU PRO PRO MET LEU ALA PRO VAL ALA LYS SER GLN MET PRO THR ALA LYS PRO LEU GLU THR LYS SER PHE THR PRO LYS THR LYS THR LYS THR SER SER PRO GLY GLN LYS THR LYS SER PRO LYS THR ALA GLN SER PRO ALA MET VAL GLY SER PRO ILE ARG
SER PRO LYS THR VAL SER LYS GLU LYS LYS SER PRO GLY ARG SER LYS SER PRO LYS SER PRO LYS VAL THR THR HIS ILE PRO GLN THR PRO VAL ARG PRO GLU THR PRO ASN ARG THR PRO SER ALA THR LEU SER GLU LYS ILE SER LYS GLU THR ILE GLN VAL LYS
GLN ILE GLN THR PRO PRO ASP ALA GLY LYS LYS LEU ASN SER GLU ASN GLN PRO LYS LYS ALA VAL VAL ALA ASP LYS THR ILE GLU ALA SER ILE ASP ALA VAL ILE ALA ARG ALA CYS ALA GLU ARG GLU PRO ASP PRO PHE GLU PHE SER SER GLY SER GLU SER GLU ASP ILE PHE
THR SER PRO LYS ARG ILE SER GLY PRO GLU CYS THR THR PRO LYS ALA SER THR SER ALA ASN ASN PHE THR LYS SER GLY SER THR PRO LEU PRO LEU SER GLY GLY THR SER SER SER SER ASP ASN SER TRP THR MET ASP ALA SER ILE ASP GLU VAL LYS ALA LYS LEU GLY
THR PRO SER ASN MET PRO PRO ASN PHE PRO TYR ILE SER SER PRO SER VAL PRO THR PRO GLU PRO LEU HIS LYS VAL TYR GLU GLU LYS THR LYS LYS LEU PRO SER SER VAL GLU VAL LYS LYS LYS LEU LYS LYS LYS LYS LYS GLU LYS LYS GLN ARG
ASP ARG GLU ARG GLU LYS ASP LYS ASN LYS ASP LYS SER LYS GLU LYS ASP LYS VAL LYS LYS GLU THR GLY ARG GLU THR LYS TYR PRO TRP LYS GLU PHE LEU LYS GLU GLU GLU ALA ASP PRO TYR LYS PHE LYS ILE LYS ASP VAL ASP PRO
LYS VAL LYS LEU LYS ASP GLY LEU VAL ARG LYS GLU LYS GLU LYS HIS LYS ASP LYS LYS LYS LYS ARG GLU LYS LYS GLY LYS LYS ASP LYS ARG GLU LYS ASP LYS ARG GLU LYS LYS LYS VAL LYS ASP LYS GLY ARG GLU ASP LYS MET LYS ALA PRO ALA PRO PRO LEU VAL LEU PRO PRO LYS GLU
LEU ALA LEU PRO LEU PHE SER PRO ALA THR ALA SER ARG VAL PRO ALA MET LEU PRO SER LEU LEU PRO VAL LEU PRO GLU LYS LEU PHE GLU GLU LYS GLU LYS VAL LYS GLU LYS VAL LYS ASP LYS LYS LYS ASP LYS LYS LYS LYS LYS

P181 L182 Q183 P184 K185 H186 M187 R188 E189 A190 V191 R192 R193 L194 K195 S196 K197 G198 Q199 I200 P201 N202 S203 K204 H205 K206 K207 I208 I209 F210 F211

• Molecule 47: Transcription initiation factor TFIID subunit 13

Chain Dm: 70% | 55% 14% • 30%

MET ALA ASP GLU GLU GLU ASP PRO THR PHE GLU GLU GLU ASN GLU GLU ILE GLY GLY GLY ALA GLU GLY GLY GLN GLY LYS R28 K29 R30 L31 F32 S33 K34 E35 L36 R37 C38 M39 M40 Y41 G42 F43 G44 D45 D46 Q47 N48 P49 Y50 T51 E52 S53 V54 D55 I56 L57 E58 D59 L60

V61 I62 E63 F64 I65 T66 E67 M68 T69 H70 K71 A72 M73 S74 I75 G76 R77 Q78 G79 R80 V81 Q82 V83 E84 D85 I86 V87 F88 L89 I90 R91 K92 D93 P94 R95 K96 F97 A98 R99 V100 K101 D102 L103 L104 T105 M106 N107 E108 E109 L110 K111 R112 A113 R114 LYS ALA PHE ASP GLU ALA

ASN TYR GLY SER

• Molecule 48: Transcription initiation factor IIA subunit 2

Chain DO: • | 72% 13% 5% 11%

MET ALA Y3 L22 Q26 Q27 I28 T29 P30 Q31 L32 V52 R55 V56 R59 L76 V79 R82 E83 V84 L87 I88 K92 V93 A97 C98 D99 GLY LYS ASN THR GLY SER ASN THR THR GLU

• Molecule 49: TATA-box-binding protein

Chain DP: 35% 17% • 48%

MET ASP GLN ASN ASN SER LEU PRO PRO TYR ALA GLN GLY LEU ALA SER PRO GLN GLY ALA MET THR PRO GLY ILE PRO ILE PHE SER PRO MET MET PRO TYR GLY THR GLY LEU THR PRO GLN PRO ILE GLN ASN THR ASN SER LEU SER ILE LEU GLU GLU GLN GLN ARG GLN GLN

GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN GLN ALA VAL ALA ALA ALA ALA VAL GLN GLN SER THR SER GLN ALA THR GLN GLY THR SER GLY GLN ALA PRO GLN

LEU PHE HIS SER GLN THR LEU THR THR ALA PRO LEU PRO GLY THR THR PRO LEU TYR PRO SER PRO MET THR PRO MET THR PRO ILE THR PRO ALA THR PRO ALA SER GLU SER SER GLY I161 V162 P163 Q164 L165 I168 V169 S170 T171 V172 N173 L174 G175 C176 K177 L178 N193 P194

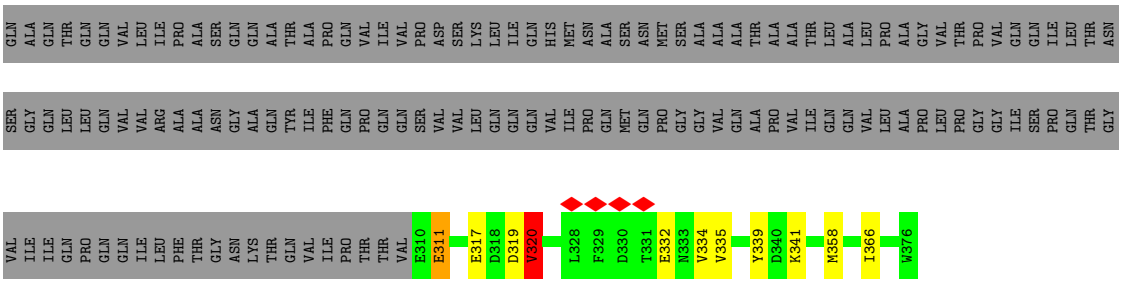
K195 R196 F197 V200 I204 R205 E206 P207 I213 V220 G223 A224 K225 S226 E227 L232 R235 K236 R239 V240 K243 L244 F250 F253 C262 D263 V264 K265 F266 P267 I268 R269 H277 Q278 Q279 F280 S281 S282 Y293 R294 M295 P298 R299 I300 V301

V306 K309 G314 A315 E323 A324 Y329 P330 I331 L332 K337 THR THR

• Molecule 50: TFIIA-a

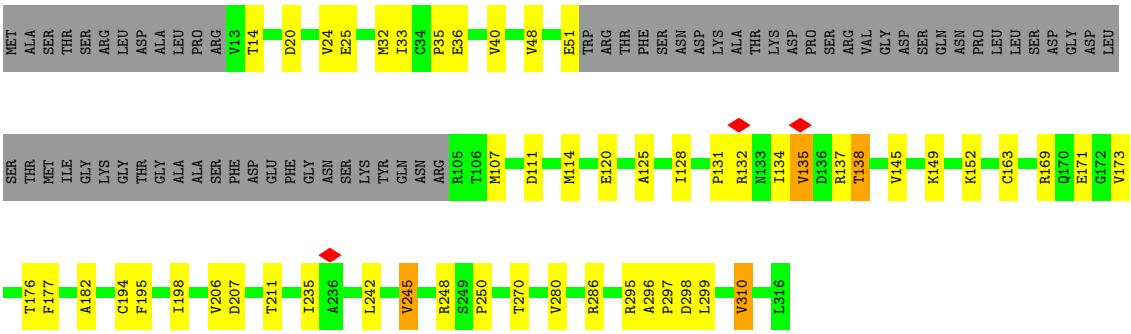
Chain DQ: • | 35% 5% 60%

MET ALA ASN SER ALA ASN THR ASN T9 V10 D35 E36 L39 L42 S53 R54 F59 E62 E63 GLN GLN LEU LEU LEU GLN VAL GLN GLN GLN HIS GLN PRO GLN GLN GLN GLN HIS HIS HIS HIS HIS HIS HIS GLN GLN ALA GLN PRO GLN GLN THR VAL PRO GLN



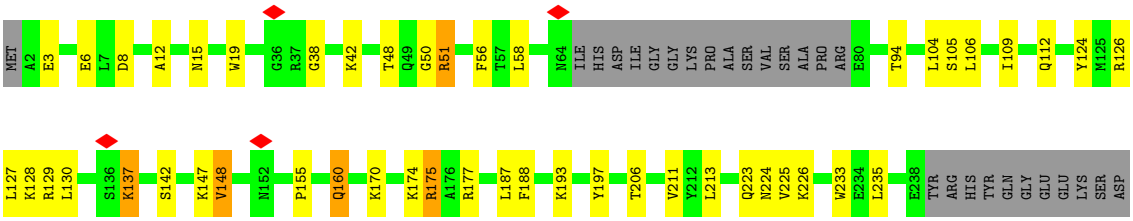
• Molecule 51: Transcription initiation factor IIB

Chain BA:



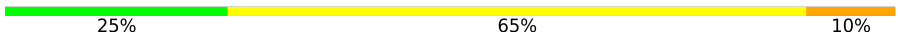
• Molecule 52: General transcription factor IIF subunit 2

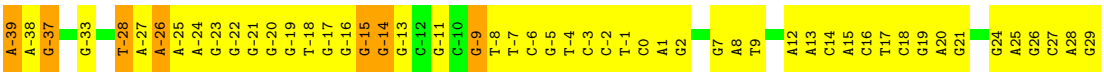
Chain FB:



• Molecule 53: DNA (69-MER)

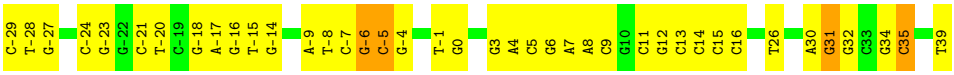
Chain X:





• Molecule 54: DNA (69-MER)

Chain Y:



• Molecule 55: RPB1

Chain PA: 56% 17% • 25%

MET HIS GLY GLY GLY PRO PRO SER GLY ASP S11 L15 Q22 V25 L26 S27 E30 M34 S35 V36 T37 E38 E45 T46 T47 L57 M58 G63 V64 I65 E66 G69 R70 C71 G76 N77 M78 T79 E80 L90 P93 V101 K102 T103 M104 C111

C114 S115 K116 V119 L130 H143 L147 E155 GLY GLY GLU GLU MET ASP ASN LYS PHE GLY VAL GLU GLN PRO GLU GLY ASP GLU ASP LEU THR LYS GLU LYS GLY H181 R192 R193 L198 Y199 A200 E201 W202 LYS HIS VAL ASN GLU ASP SER GLN GLU K212 K213

L216 E219 R220 V221 L236 A243 R244 P245 W248 T249 V250 V255 L258 V265 R271 N272 Q273 D274 D275 L276 D282 K285 A300 H301 V302 I303 L309 V318 L322 P323 G324 L325 P326 R327 A328 M329 L336 L339 V350 N353

K357 B358 S362 A363 I367 L373 S374 I375 P381 R382 S383 I384 F390 D400 Q403 R408 A416 I420 L429 K445 I457 F458 N459 R460 Q461 P462 H465 K466 M467 S468 M469 I476 S480 T481 F482 R483 L484 N485 V488 P491 A494

D495 F496 L503 Q507 S508 L509 E510 T511 Q516 E517 M520 V521 V526 Q529 S530 N531 R532 P533 V534 Q539 L542 R546 K550 R551 D552 V560 L563 F566 L567 P575 Q576 P577 L580 K581 W586 L594 I595 C602 I603 R604 T605 H606

H609 I621 V628 M637 L640 G641 K642 I647 I655 G661 R666 V675 I676 L681 H685 T686 I687 G688 I689 I693 T698 T705 T736 R749 T752 S759 L760 S761 E762 N765 I781 A786 G789 Q790 Q791 N792 V793

F802 R805 T806 L807 P808 H809 F810 I811 K812 F822 L828 A829 G830 H839 K853 V871 M872 V873 V879 I883 N884 Q885 V886 V887 Q888 L889 G892 E893 D894 G895 L896 L906 A907 T908 L909 K910 R921 F922 D923 Y924 E927 R928 A929 L934 L938

I948 L952 M959 D962 R963 L966 R967 T972 G973 V978 L983 N997 L1000 P1001 S1002 H1005 P1006 I1007 L1016 L1020 V1021 I1022 V1023 P1028 L1029 Q1034 A1037 I1043 H1044 L1045 R1052 R1053 M1054 E1057 F1058 R1059 E1073 Q1078 A1079

I1080 V1087 G1088 M1102 T1103 L1104 N1105 T1106 F1107 H1108 Y1109 ALA GLY VAL SER ALA K1115 N1116 V1121 P1122 N1129 K1132 K1133 P1134 K1135 T1136 P1137 L1143 L1144 S1147 A1148 R1153 I1157 L1158 L1161 E1162 H1163 T1170 N1180 P1181 Q1182 S1183 T1184 V1185 V1186 Q1190

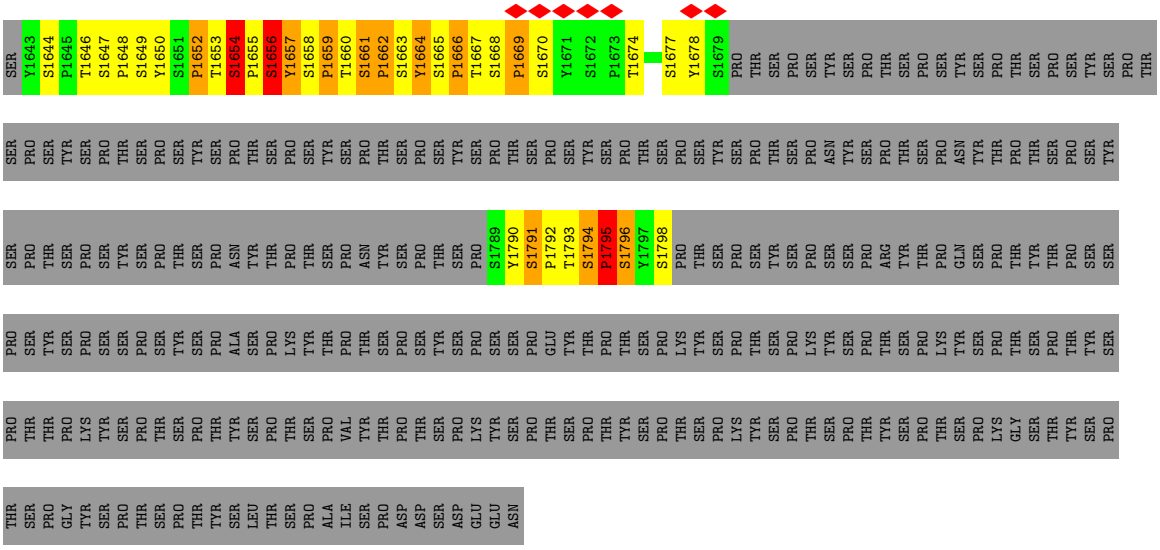
V1193 N1194 V1195 E1198 D1201 V1204 A1205 R1206 L1212 R1213 V1214 E1215 L1216 D1217 M1221 L1226 I1231 D1242 L1243 I1246 E1253 L1257 R1258 I1259 R1260 I1261 M1262 N1267 LYS MET GLN GLU GLU GLU GLU VAL VAL ASP LYS M1279 D1280 D1281 M1292 L1293 L1298 Q1299

G1300 I1301 I1304 V1307 Y1308 M1309 H1310 L1311 T1314 D1325 E1337 V1341 L1347 P1354 I1362 I1365 L1369 G1370 V1374 L1382 V1393 R1396 H1397 L1398 A1399 L1400 M1405 L1411 M1412 D1423 L1427 M1428 K1429 T1435 E1441 A1444 P1450

M1451 V1454 S1455 E1456 L1460 P1465 T1468 F1471 D1472 L1473 L1474 L1475 K1479 C1480 K1481 Y1482 G1483 M1484 P1487 THR ASN ILE PRO GLY LEU GLY ALA ALA GLY PRO THR GLY MET PHE PHE GLY SER ALA PRO SER PRO MET GLY GLY ILE SER PRO ALA MET THR PRO TRP ASN

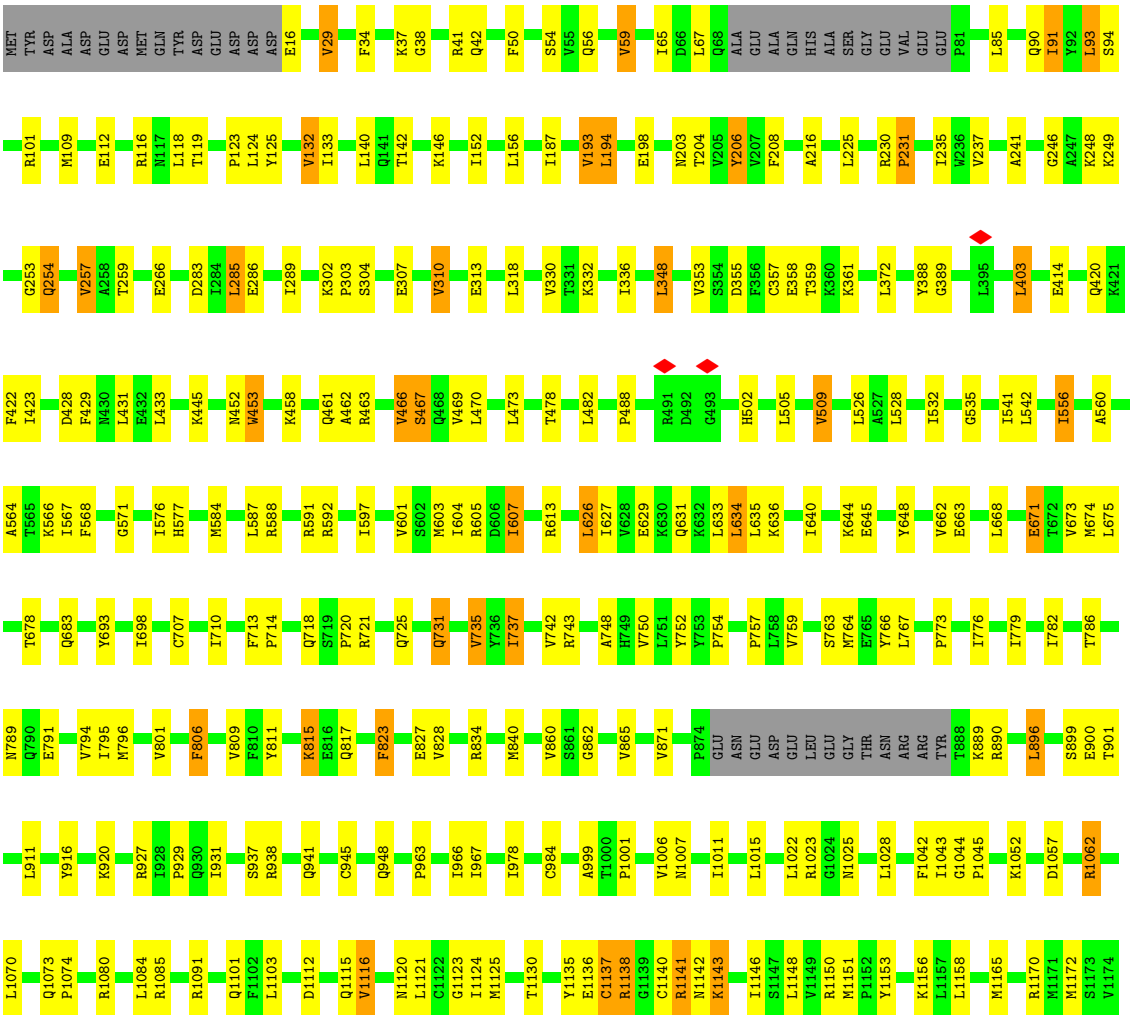
GLN GLY ALA THR PRO ALA TYR GLY ALA TRP SER PRO SER VAL GLY SER GLY MET THR PRO GLY ALA ALA GLY PHE SER PRO SER ALA ALA SER ASP ALA SER GLY PHE SER PRO GLY TYR SER PRO ALA TRP SER PRO SER PRO THR PRO GLY SER PRO GLY GLY SER PRO SER PRO GLY MET THR PRO SER SER PRO TYR

ILE PRO SER PRO GLY GLY ALA MET SER PRO SER TYR SER PRO THR SER PRO ALA TYR GLU PRO ARG SER PRO GLY GLY TYR THR PRO GLN SER PRO SER TYR THR SER PRO THR SER PRO SER SER PRO THR SER PRO SER TYR SER PRO THR SER PRO SER SER PRO TYR SER PRO THR SER PRO SER PRO TYR SER PRO THR SER PRO SER PRO TYR



- Molecule 56: DNA-directed RNA polymerase subunit beta

Chain PB: 73% 21%



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

Chain PC: 71% 21% • 7%

MET P2 T15 I23 E24 N25 V37 A40 E41 V42 P43 I44 I45 A46 I47 I52 D53 V58 L73 T74 S75 D76 D77 I78 V79 D80 K81 L82 C88 F101 T102 L103 R106 D110 Q111 T112 L120 V127 I128 S132 ARG ASN ARG ASP ASN ASP

PRO SER ASP TYR VAL GLU GLN D146 L149 K152 L153 R154 K155 E158 A165 F169 G170 K171 E172 N177 P178 T179 F184 D189 N190 R193 S206 S209 E213 Q217 A218 P219 Y220 K225 P226 E227 R228 F229 L239 I244 A248 Q260

T261 Q262 V271 LEU THR ILE ASN

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

Chain PD: 66% 20% • 9%

MET ALA ALA GLY GLY SER ASP PRO ARG ALA GLY ASP VAL E14 E15 D16 A17 S18 Q19 L20 P23 L32 V37 H38 M39 L40 L41 E42 K45 A51 E54 V60 F61 M62 Y67 R70 N76 T79 I80 R84 K90 F95 L103 T107

E110 I115 L118 I130 L131 Q135 T136 K137 F140 Q141 Y142

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

Chain PE: 77% 20% •

MET D2 D3 K12 M18 Q19 L20 C21 Y26 L27 V28 T29 E32 E38 G45 D46 K47 P53 R54 R55 T56 D57 L61 H64 Q71 M72 F73 V74 F75 F76 F77 P80 K81 V82 G83 I84 R93 I99 L103 I104 Q107 Q108 G109 L127

L136 T137 N138 I139 T140 E141 L159 R162 Y163 K164 L165 Q169 V179 V191 K192 I193 A200 V209 Q210

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

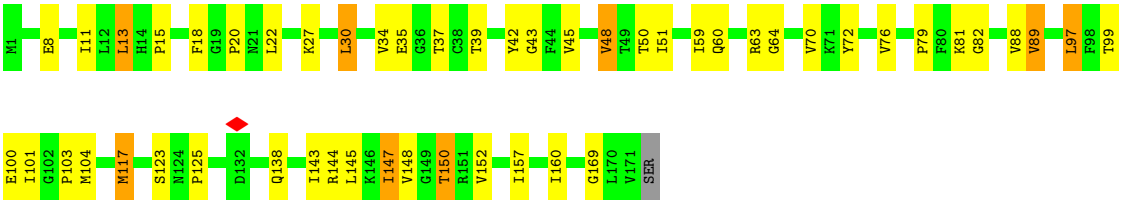
Chain PF: 41% 17% • 38%

MET SER ASP ASN GLU ASP ASN PHE ASP GLY ASP ASP PHE ASP ASP VAL GLU GLU GLU ASP GLU GLY LEU ASP ASP LEU GLU ASN ALA GLU GLU GLU GLY GLN GLU ASN VAL GLU ILE LEU PRO SER GLY GLU ARG PRO GLN ALA ASN Q49 I52 T58 K59 Y60 E61 R69 A70 L71

Q72 I73 A74 M75 C76 A77 V81 E82 L83 E86 T87 L91 I92 K95 R100 K101 R107 L110 P111 S114 Y115 E116 D121 D127

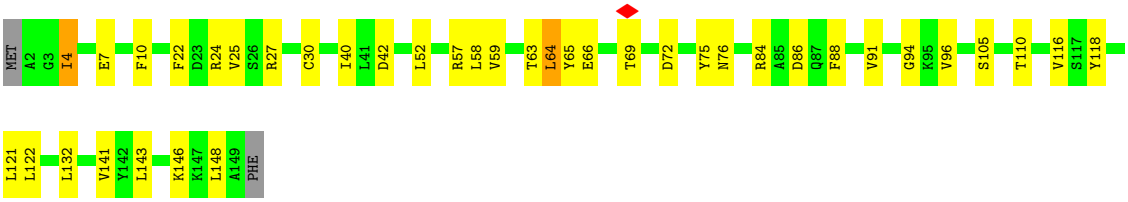
• Molecule 61: DNA-directed RNA polymerase II subunit RPB7

Chain PG: 70% 25% 5% •



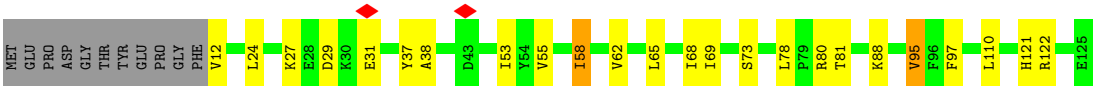
• Molecule 62: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain PH:



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

Chain PI:



• Molecule 64: RPB10

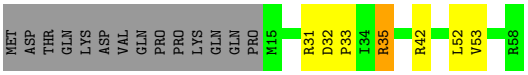
Chain PJ:

• Molecule 65: RNA_pol_L_2 domain-containing protein

Chain PK:

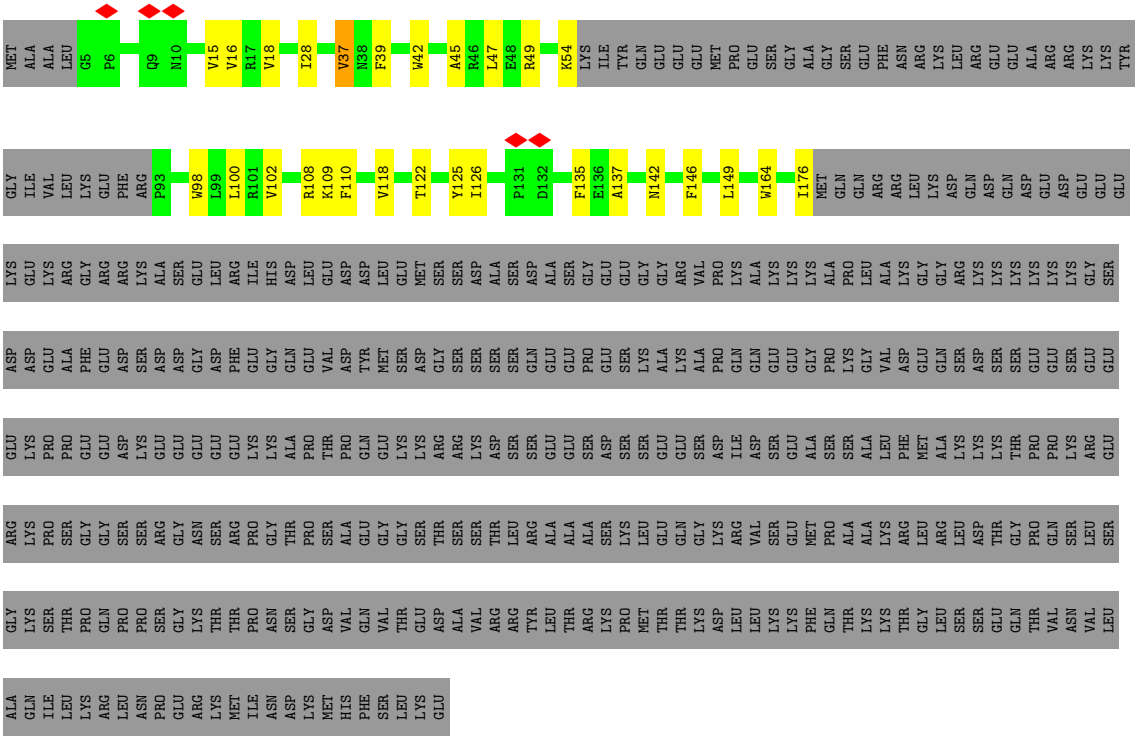
• Molecule 66: RPB12

Chain PL:



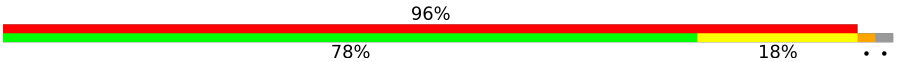
• Molecule 67: General transcription factor IIF subunit 1

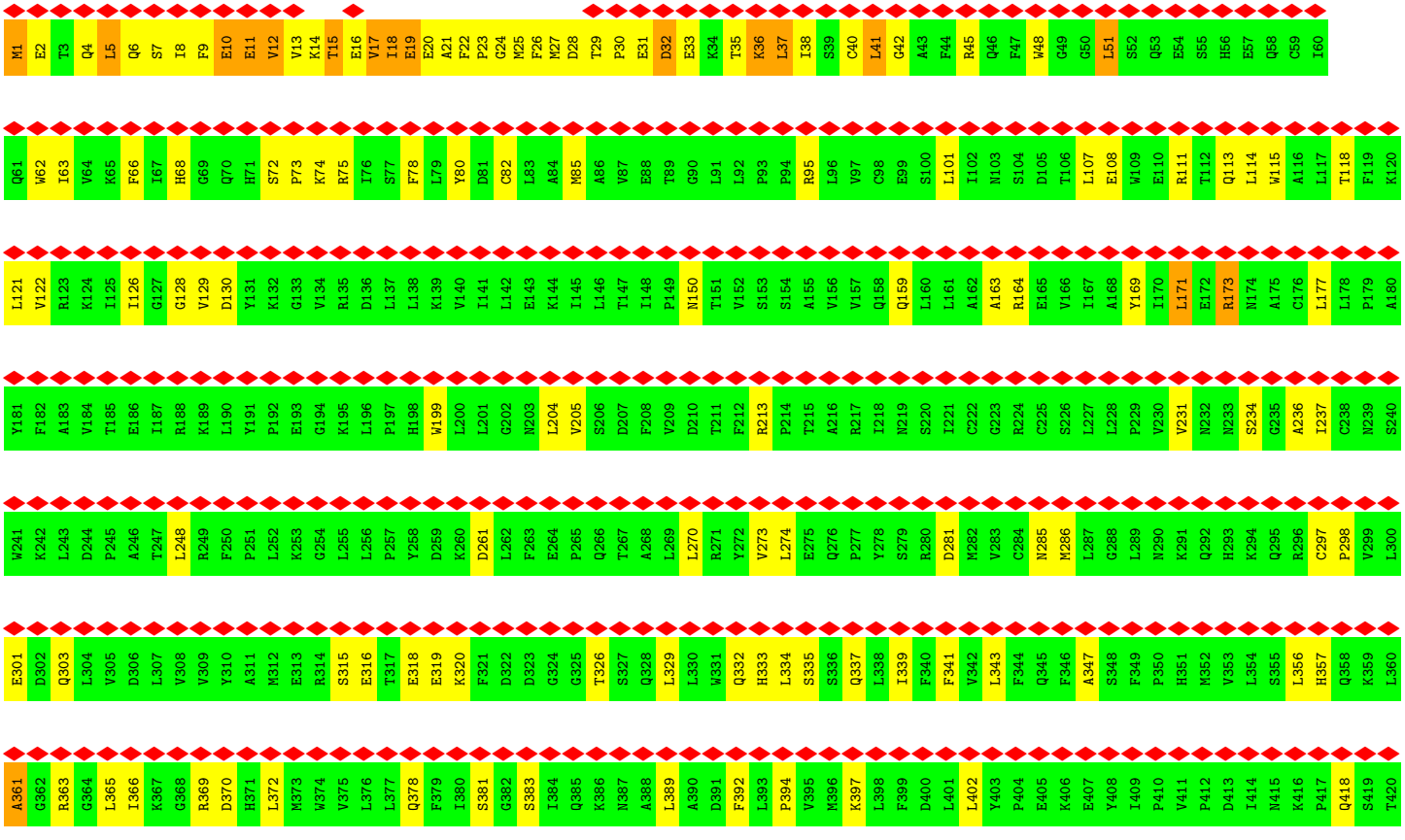
Chain FA:



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

Chain w:





H421 A422 F423 A424 M425 T426 C427 I428 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 M639 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 P787 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 H972 R973 F974 L975 E976 L977 L978 P979 V980 S981 K982 S983 L984 E985 T986 L987 L988 D989 H990 L991 G992 G993 L994 Y995 K996 F997 H998 D999 R1000 P1001 V1002 T1003 Y1004 L1005 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 I1149 G1150 L1151 I1152 I1153 T1154 A1155 L1156 P1157 E1158 P1159 Y1160 W1161 I1162 V1163 L1164 H1165 D1166 R1167 I1168 V1169 S1170 V1171 I1172 S1173 S1174 P1175 S1176 L1177 T1178 S1179 E1180 T1181 E1182 W1183 V1184 G1185 Y1186 P1187 F1188 R1189 L1190 F1191 D1192 F1193 T1194 A1195 C1196 H1197 Q1198 S1199 Y1200

S1201 E1202 M1203 S1204 C1205 S1206 Y1207 T1208 L1209 A1210 L1211 A1212 H1213 A1214 V1215 W1216 H1217 H1218 S1219 S1220 I1221 G1222 Q1223 L1224 S1225 L1226 I1227 P1228 K1229 F1230 L1231 T1232 E1233 V1234 L1235 L1236 P1237 I1238 V1239 K1240 T1241 E1242 F1243 Q1244 L1245 L1246 Y1247 V1248 Y1249 H1250 L1251 V1252 G1253 P1254 F1255 L1256 Q1257 R1258 F1259 Q1260

Q1261 E1262 R1263 T1264 R1265 C1266 M1267 I1268 E1269 I1270 G1271 V1272 A1273 F1274 Y1275 D1276 M1277 L1278 L1279 N1280 V1281 D1282 Q1283 C1284 S1285 T1286 H1287 L1288 N1289 Y1290 M1291 D1292 P1293 I1294 C1295 D1296 F1297 L1298 Y1299 H1300 M1301 K1302 Y1303 M1304 F1305 T1306 G1307 D1308 S1309 V1310 K1311 E1312 Q1313 V1314 E1315 K1316 I1317 I1318 C1319 N1320

L1321 K1322 P1323 A1324 L1325 K1326 L1327 R1328 L1329 R1330 F1331 I1332 T1333 H1334 ILE SER LYS MET GLU PRO ALA ALA VAL PRO PRO GLN ALA MET ASN SER GLY SER PRO ALA PRO GLN SER ASN GLN VAL PRO VAL SER LEU PRO VAL THR GLN

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

Chain x: 87% 75% 15% 9%

MET LYS VAL V4 N5 L6 K7 Q8 A9 I10 L11 Q12 A13 W14 K15 E16 R17 W18 S19 D20 Y21 I25 A35 T36 W37 D38 T39 L40 N41 L42 A43 D44 A45 L46 L47 E48 Q49 A50 M51 I52 C53 P54 S55 P56 N57 P58 L61 Y66 A67 I68 V73 S74 Y75 S76 S77

V78 L79 T80 A81 I82 S83 K84 F85 D86 D87 F88 S89 R90 D91 L92 C93 V94 Q95 A96 L97 L98 D99 I100 M101 D102 M103 F104 C105 D106 R107 L108 S109 C110 H111 G112 K113 A114 E115 E116 C117 I118 G119 L120 C121 R122 A123 L124 L125 S126 A127 L128 H129 W130 L131 L132 R133 C134 T135 A136 A137

S138 A139 E140 R141 L142 R143 E144 G145 L146 GLU ALA GLY THR PRO ALA ALA G154 E155 K156 Q157 L158 A159 M160 C161 L162 Q163 R164 L165 E166 K167 T168 L169 S170 S171 T172 K173 N174 R175 A176 L177 L178 H179 I180 A181 K182 L183 E184 E185 A186 S187 S188 W189 T190 A191 I192 E193 H194 S195 L196 L197

K198 L199 G200 E201 I202 L203 A204 N205 L206 S207 N208 P209 Q210 L211 R212 S213 Q214 A215 E216 Q217 C218 G219 T220 L221 I222 R223 S224 I225 PRO THR MET LEU SER VAL HIS ALA GLU GLN MET HIS K238 T239 G240 F241 P242 T243 V244 H245 A246 V247 I248 L249 L250 E251 G252 T253 M254 N255 L256 T257

G258 E259 T260 Q261 S262 L263 V264 E265 Q266 L267 T268 M269 V270 K271 R272 M273 Q274 H275 I276 P277 T278 P279 L280 F281 V282 L283 E284 I285 W286 K287 A288 C289 F290 V291 G292 L293 I294 E295 S296 P297 E298 G299 T300 E301 E302 L303 K304 W305 T306 A307 F308 T309 F310 L311 K312 I313 P314 Q315 V316 L317

V318 K319 L320 K321 K322 Y323 S324 HIS GLY ASP LYS D329 F330 T331 E332 D333 V334 N335 C336 A337 F338 E339 F340 L341 L342 K343 L344 T345 P346 L347 L348 D349 K350 A351 D352 Q353 R354 C355 M356 C357 D358 C359 T360 N361 F362 L363 L364 Q365 E366 C367 G368 K369 Q370 G371 L372 L373 S374 E375 A376 S377

V378 N379 N380 L381 M382 A383 K384 R385 K386 A387 D388 R389 E390 H391 ALA PRO GLN GLN LYS SER GLY GLU ASN ALA N402 I403 Q404 P405 N406 I407 Q408 L409 I410 L411 R412 A413 E414 P415 T416 V417 T418 N419 I420 L421 K422 T423 M424 D425 A426 D427 H428 S429 K430 S431 P432 E433 G434 L435 L436 G437

V438 L439 G440 H441 M442 L443 S444 G445 K446 S447 L448 D449 L450 L451 L452 A453 A454 A455 A456 A457 T458 G459 K460 L461 K462 S463 F464 A465 R466 K467 F468 I469 M470 L471 N472 E473 F474 T475 T476 Y477 G478 S479 E480 E481 S482 T483 K484 P485 A486 S487 V488 R489 A490 L491 L492 F493 D494 I495 S496 F497

L498 M499 L500 C501 H502 V503 A504 Q505 T506 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 M747 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 P929 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: 48% 39% 9% 52%

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 N225 I226 V227 V228 A229 T230 A231 D232 G233 S234 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 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 PHE LEU ILE ALA ILE SER SER THR LEU LYS SER 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 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 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 LEU VAL 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: ZN, MG, SF4

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	0.98	3/3645 (0.1%)	1.37	15/4952 (0.3%)
2	m	0.19	0/1010	0.38	0/1359
3	d	0.97	0/1277	1.50	11/1714 (0.6%)
4	f	0.76	0/1359	1.04	4/1845 (0.2%)
5	g	0.94	0/1411	1.38	2/1901 (0.1%)
6	h	0.94	1/1507 (0.1%)	1.31	2/2036 (0.1%)
7	r	0.94	1/1558 (0.1%)	1.27	5/2096 (0.2%)
8	t	1.05	2/1530 (0.1%)	1.54	20/2066 (1.0%)
9	j	0.55	1/1016 (0.1%)	0.91	6/1363 (0.4%)
10	k	0.96	0/885	1.26	0/1190
11	n	0.45	2/7371 (0.0%)	0.73	20/10037 (0.2%)
12	q	0.67	2/4336 (0.0%)	0.89	4/5865 (0.1%)
13	s	0.73	0/489	1.27	8/663 (1.2%)
14	u	0.68	0/797	1.12	5/1082 (0.5%)
15	v	1.00	2/1092 (0.2%)	1.58	8/1468 (0.5%)
16	z	0.92	0/781	1.39	5/1067 (0.5%)
17	c	0.51	0/2106	0.79	3/2842 (0.1%)
18	e	0.18	0/840	0.34	0/1128
19	b	0.75	0/911	1.08	0/1229
20	l	0.18	0/1048	0.36	0/1405
21	o	0.39	0/1256	0.76	2/1724 (0.1%)
22	i	0.98	1/523 (0.2%)	1.25	0/692
23	0	0.99	0/2288	1.27	4/3101 (0.1%)
24	8	0.97	0/2437	1.19	1/3306 (0.0%)
25	9	0.95	0/2356	1.23	1/3185 (0.0%)
26	1	1.06	0/2674	1.28	7/3660 (0.2%)
27	2	1.00	0/2588	1.18	2/3509 (0.1%)
28	3	0.99	0/2102	1.17	0/2844
29	4	0.97	0/3663	1.18	2/4965 (0.0%)
30	5	0.99	0/433	1.22	0/585
31	6	0.97	0/4983	1.18	1/6731 (0.0%)
32	7	0.97	0/5957	1.19	3/8071 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	EA	0.95	1/1499 (0.1%)	1.21	2/2012 (0.1%)
34	EB	0.96	0/1428	1.21	0/1917
35	DA	0.96	0/4627	1.17	3/6248 (0.0%)
36	DB	0.97	0/7993	1.16	5/10836 (0.0%)
37	DD	0.94	0/1343	1.22	2/1795 (0.1%)
37	Dd	0.95	0/1321	1.17	0/1772
38	DE	0.98	0/4469	1.19	3/6050 (0.0%)
38	De	0.98	0/4433	1.18	2/6004 (0.0%)
39	DF	1.00	0/3167	1.22	1/4303 (0.0%)
39	Df	1.00	0/3140	1.21	1/4268 (0.0%)
40	DG	1.00	0/1199	1.15	0/1612
41	DH	0.99	0/1673	1.18	0/2285
42	DI	0.98	0/981	1.20	0/1332
42	Di	0.95	0/989	1.18	0/1343
43	DJ	0.94	0/736	1.18	0/998
43	Dj	0.93	0/775	1.19	0/1049
44	DL	0.94	0/622	1.23	0/841
44	Dl	0.95	0/888	1.22	1/1194 (0.1%)
45	Dc	0.98	0/1035	1.16	0/1406
46	Dk	0.96	0/799	1.19	1/1070 (0.1%)
47	Dm	0.94	0/733	1.20	0/977
48	DO	1.00	0/781	1.20	0/1061
49	DP	0.98	0/1438	1.14	0/1935
50	DQ	0.96	0/1013	1.19	0/1366
51	BA	0.98	0/1967	1.21	0/2656
52	FB	0.98	0/1817	1.17	1/2445 (0.0%)
53	X	0.73	4/1607 (0.2%)	0.69	6/2481 (0.2%)
54	Y	0.57	0/1565	0.73	5/2410 (0.2%)
55	PA	0.99	0/11881	1.21	8/16057 (0.0%)
56	PB	0.99	0/9243	1.17	4/12475 (0.0%)
57	PC	1.00	0/2102	1.17	0/2857
58	PD	0.97	0/1036	1.20	0/1397
59	PE	0.97	0/1751	1.18	0/2366
60	PF	0.95	0/645	1.20	1/871 (0.1%)
61	PG	1.02	0/1365	1.18	1/1853 (0.1%)
62	PH	0.99	0/1207	1.14	0/1628
63	PI	0.99	0/948	1.15	1/1284 (0.1%)
64	PJ	0.96	0/516	1.19	0/696
65	PK	0.96	0/956	1.16	0/1294
66	PL	0.98	0/377	1.07	0/500
67	FA	0.96	0/1130	1.13	0/1528
68	w	0.56	0/11053	0.73	8/15018 (0.1%)
69	x	0.57	0/7179	0.72	5/9712 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
70	p	0.72	0/3191	0.78	0/4333
All	All	0.89	20/174847 (0.0%)	1.11	202/237216 (0.1%)

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	X	-39	DA	O3'-P	-13.42	1.41	1.61
12	q	452	ALA	C-N	9.04	1.46	1.33
7	r	174	VAL	C-O	-8.00	1.15	1.24
9	j	94	GLN	C-N	-7.89	1.24	1.33
1	a	57	HIS	C-O	7.62	1.32	1.24

The worst 5 of 202 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	d	161	VAL	N-CA-C	-12.81	100.00	112.17
3	d	130	GLU	N-CA-C	-11.44	98.89	111.36
54	Y	35	DC	C2'-C3'-O3'	-10.79	95.32	111.50
8	t	11	VAL	N-CA-C	-9.86	100.96	110.42
9	j	77	PRO	CA-N-CD	-9.34	98.92	112.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	3570	0	3480	309	0
2	m	983	0	967	231	0
3	d	1264	0	1293	227	0
4	f	1329	0	1302	173	0
5	g	1382	0	1410	307	0
6	h	1486	0	1500	230	0
7	r	1528	0	1538	139	0
8	t	1499	0	1482	132	0
9	j	1001	0	1021	364	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	k	879	0	886	200	0
11	n	7241	0	6673	623	0
12	q	4261	0	4237	508	0
13	s	485	0	352	101	0
14	u	792	0	749	231	0
15	v	1083	0	1059	169	0
16	z	765	0	727	162	0
17	c	2069	0	2079	101	0
18	e	832	0	824	112	0
19	b	899	0	908	110	0
20	l	1040	0	1065	81	0
21	o	1221	0	1212	125	0
22	i	520	0	545	46	0
23	0	2255	0	2007	80	0
24	8	2378	0	2397	79	0
25	9	2307	0	2314	34	0
26	1	2634	0	2042	38	0
27	2	2534	0	2455	33	0
28	3	2065	0	2098	33	0
29	4	3579	0	3620	67	0
30	5	428	0	434	11	0
31	6	4880	0	4924	66	0
32	7	5833	0	5798	72	0
33	EA	1476	0	1489	41	0
34	EB	1404	0	1424	26	0
35	DA	4511	0	4429	44	0
36	DB	7796	0	7751	213	0
37	DD	1330	0	1351	27	0
37	Dd	1307	0	1318	51	0
38	DE	4364	0	4244	86	0
38	De	4327	0	4197	77	0
39	DF	3109	0	3045	57	0
39	Df	3081	0	3012	58	0
40	DG	1180	0	1235	19	0
41	DH	1633	0	1621	27	0
42	DI	959	0	969	28	0
42	Di	967	0	977	25	0
43	DJ	720	0	719	12	0
43	Dj	759	0	759	19	0
44	DL	614	0	614	86	0
44	Dl	876	0	893	91	0
45	Dc	1011	0	975	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
46	Dk	785	0	818	18	0
47	Dm	724	0	744	14	0
48	DO	771	0	764	9	0
49	DP	1412	0	1506	42	0
50	DQ	996	0	926	8	0
51	BA	1939	0	1979	29	0
52	FB	1788	0	1819	27	0
53	X	1429	0	770	120	0
54	Y	1400	0	775	90	0
55	PA	11655	0	11726	248	0
56	PB	9062	0	9107	131	0
57	PC	2059	0	2008	33	0
58	PD	1021	0	979	33	0
59	PE	1720	0	1737	25	0
60	PF	635	0	665	16	0
61	PG	1334	0	1333	39	0
62	PH	1186	0	1147	19	0
63	PI	927	0	859	9	0
64	PJ	507	0	523	4	0
65	PK	937	0	959	13	0
66	PL	372	0	379	4	0
67	FA	1101	0	1065	20	0
68	w	10772	0	10832	335	0
69	x	7050	0	7203	154	0
70	p	3124	0	3133	62	0
71	0	2	0	0	1	0
71	2	3	0	0	0	0
71	3	1	0	0	0	0
71	BA	1	0	0	0	0
71	EA	1	0	0	0	0
71	PA	2	0	0	0	0
71	PB	1	0	0	0	0
71	PC	1	0	0	0	0
71	PI	2	0	0	0	0
71	PJ	1	0	0	0	0
71	PL	1	0	0	0	0
72	7	8	0	0	0	0
73	PA	1	0	0	0	0
All	All	171177	0	168176	5752	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 17.

The worst 5 of 5752 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:EA:129:CYS:SG	33:EA:131:VAL:HG23	1.29	1.73
3:d:121:LEU:CD1	5:g:160:VAL:HG21	1.18	1.64
68:w:394:PRO:HA	70:p:171:PHE:CZ	1.29	1.63
3:d:121:LEU:HD11	5:g:160:VAL:CG2	1.21	1.62
9:j:82:LYS:HG2	13:s:96:PHE:CD1	1.17	1.62

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	a	457/1581 (29%)	421 (92%)	29 (6%)	7 (2%)	8	38
2	m	110/131 (84%)	106 (96%)	4 (4%)	0	100	100
3	d	154/270 (57%)	143 (93%)	6 (4%)	5 (3%)	3	24
4	f	163/246 (66%)	142 (87%)	15 (9%)	6 (4%)	2	22
5	g	164/233 (70%)	145 (88%)	10 (6%)	9 (6%)	1	17
6	h	188/268 (70%)	167 (89%)	12 (6%)	9 (5%)	2	18
7	r	189/208 (91%)	176 (93%)	10 (5%)	3 (2%)	7	37
8	t	189/212 (89%)	166 (88%)	15 (8%)	8 (4%)	2	20
9	j	120/135 (89%)	110 (92%)	6 (5%)	4 (3%)	3	24
10	k	110/117 (94%)	99 (90%)	9 (8%)	2 (2%)	6	34
11	n	980/1454 (67%)	877 (90%)	86 (9%)	17 (2%)	7	36
12	q	540/651 (83%)	474 (88%)	53 (10%)	13 (2%)	4	29
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	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	v	132/200 (66%)	119 (90%)	10 (8%)	3 (2%)	5	30
16	z	93/600 (16%)	84 (90%)	7 (8%)	2 (2%)	5	31
17	c	245/311 (79%)	232 (95%)	13 (5%)	0	100	100
18	e	98/178 (55%)	92 (94%)	4 (4%)	2 (2%)	6	33
19	b	111/200 (56%)	109 (98%)	1 (1%)	1 (1%)	14	48
20	l	120/178 (67%)	115 (96%)	5 (4%)	0	100	100
21	o	152/788 (19%)	138 (91%)	10 (7%)	4 (3%)	4	28
22	i	56/146 (38%)	54 (96%)	1 (2%)	1 (2%)	6	34
23	0	304/309 (98%)	285 (94%)	15 (5%)	4 (1%)	9	41
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%)	21	58
28	3	259/308 (84%)	257 (99%)	2 (1%)	0	100	100
29	4	447/462 (97%)	431 (96%)	12 (3%)	4 (1%)	14	48
30	5	52/71 (73%)	50 (96%)	2 (4%)	0	100	100
31	6	602/782 (77%)	585 (97%)	14 (2%)	3 (0%)	24	61
32	7	732/760 (96%)	704 (96%)	23 (3%)	5 (1%)	18	54
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	65
36	DB	959/1199 (80%)	932 (97%)	25 (3%)	2 (0%)	43	76
37	DD	153/1085 (14%)	148 (97%)	4 (3%)	1 (1%)	18	54
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%)	43	76
39	DF	404/677 (60%)	393 (97%)	9 (2%)	2 (0%)	24	61
39	Df	399/677 (59%)	394 (99%)	4 (1%)	1 (0%)	36	70
40	DG	139/349 (40%)	137 (99%)	2 (1%)	0	100	100
41	DH	207/310 (67%)	199 (96%)	5 (2%)	3 (1%)	9	39
42	DI	118/264 (45%)	116 (98%)	1 (1%)	1 (1%)	16	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	20
44	Dl	105/161 (65%)	104 (99%)	0	1 (1%)	12	46
45	Dc	125/929 (14%)	122 (98%)	1 (1%)	2 (2%)	7	37
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%)	21	58
50	DQ	118/307 (38%)	115 (98%)	2 (2%)	1 (1%)	16	52
51	BA	247/316 (78%)	244 (99%)	3 (1%)	0	100	100
52	FB	218/249 (88%)	210 (96%)	7 (3%)	1 (0%)	24	61
55	PA	1460/1970 (74%)	1415 (97%)	38 (3%)	7 (0%)	24	61
56	PB	1128/1174 (96%)	1104 (98%)	22 (2%)	2 (0%)	43	76
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%)	24	61
60	PF	77/127 (61%)	76 (99%)	0	1 (1%)	9	41
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%)	24	61
69	x	876/989 (89%)	820 (94%)	51 (6%)	5 (1%)	21	58
70	p	400/841 (48%)	367 (92%)	32 (8%)	1 (0%)	36	70
All	All	20999/34555 (61%)	19990 (95%)	829 (4%)	180 (1%)	16	48

5 of 180 Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	a	387/1391 (28%)	322 (83%)	65 (17%)	2	12
2	m	102/115 (89%)	102 (100%)	0	100	100
3	d	138/230 (60%)	98 (71%)	40 (29%)	0	3
4	f	144/223 (65%)	122 (85%)	22 (15%)	3	14
5	g	157/215 (73%)	126 (80%)	31 (20%)	1	9
6	h	168/225 (75%)	126 (75%)	42 (25%)	0	4
7	r	168/183 (92%)	126 (75%)	42 (25%)	0	4
8	t	166/178 (93%)	136 (82%)	30 (18%)	2	11
9	j	113/124 (91%)	108 (96%)	5 (4%)	25	48
10	k	94/98 (96%)	45 (48%)	49 (52%)	0	0
11	n	689/1272 (54%)	654 (95%)	35 (5%)	21	44
12	q	461/577 (80%)	383 (83%)	78 (17%)	2	12
13	s	31/208 (15%)	27 (87%)	4 (13%)	4	18
14	u	78/119 (66%)	66 (85%)	12 (15%)	2	14
15	v	122/173 (70%)	88 (72%)	34 (28%)	0	3
16	z	89/512 (17%)	74 (83%)	15 (17%)	2	12
17	c	231/280 (82%)	225 (97%)	6 (3%)	40	60
18	e	94/152 (62%)	94 (100%)	0	100	100
19	b	102/163 (63%)	92 (90%)	10 (10%)	7	26
20	l	116/155 (75%)	116 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	o	141/697 (20%)	139 (99%)	2 (1%)	59	71
22	i	61/133 (46%)	42 (69%)	19 (31%)	0	2
23	0	209/283 (74%)	194 (93%)	15 (7%)	13	36
24	8	259/299 (87%)	225 (87%)	34 (13%)	4	18
25	9	252/296 (85%)	224 (89%)	28 (11%)	6	22
26	1	176/484 (36%)	162 (92%)	14 (8%)	11	33
27	2	279/352 (79%)	251 (90%)	28 (10%)	7	25
28	3	234/272 (86%)	219 (94%)	15 (6%)	16	40
29	4	387/399 (97%)	355 (92%)	32 (8%)	10	32
30	5	48/64 (75%)	42 (88%)	6 (12%)	4	19
31	6	533/688 (78%)	487 (91%)	46 (9%)	10	31
32	7	616/664 (93%)	565 (92%)	51 (8%)	10	32
33	EA	163/373 (44%)	148 (91%)	15 (9%)	8	29
34	EB	155/261 (59%)	143 (92%)	12 (8%)	12	34
35	DA	488/1665 (29%)	441 (90%)	47 (10%)	8	27
36	DB	876/1083 (81%)	790 (90%)	86 (10%)	7	26
37	DD	144/815 (18%)	134 (93%)	10 (7%)	14	38
37	Dd	146/815 (18%)	138 (94%)	8 (6%)	19	43
38	DE	478/657 (73%)	435 (91%)	43 (9%)	9	30
38	De	475/657 (72%)	420 (88%)	55 (12%)	5	21
39	DF	324/574 (56%)	295 (91%)	29 (9%)	9	30
39	Df	322/574 (56%)	307 (95%)	15 (5%)	23	46
40	DG	133/322 (41%)	117 (88%)	16 (12%)	5	20
41	DH	181/270 (67%)	170 (94%)	11 (6%)	17	41
42	DI	106/235 (45%)	101 (95%)	5 (5%)	23	46
42	Di	107/235 (46%)	104 (97%)	3 (3%)	38	59
43	DJ	79/154 (51%)	76 (96%)	3 (4%)	29	51
43	Dj	83/154 (54%)	82 (99%)	1 (1%)	63	73
44	DL	70/141 (50%)	64 (91%)	6 (9%)	10	31
44	Dl	98/141 (70%)	94 (96%)	4 (4%)	27	49
45	Dc	113/833 (14%)	106 (94%)	7 (6%)	16	40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	Dk	87/182 (48%)	84 (97%)	3 (3%)	32	55
47	Dm	80/106 (76%)	75 (94%)	5 (6%)	16	40
48	DO	84/98 (86%)	75 (89%)	9 (11%)	6	23
49	DP	153/293 (52%)	143 (94%)	10 (6%)	15	40
50	DQ	111/269 (41%)	105 (95%)	6 (5%)	20	44
51	BA	214/268 (80%)	197 (92%)	17 (8%)	11	33
52	FB	196/218 (90%)	179 (91%)	17 (9%)	9	31
55	PA	1303/1748 (74%)	1163 (89%)	140 (11%)	6	23
56	PB	993/1027 (97%)	887 (89%)	106 (11%)	6	23
57	PC	234/252 (93%)	218 (93%)	16 (7%)	14	38
58	PD	108/126 (86%)	91 (84%)	17 (16%)	2	14
59	PE	191/192 (100%)	174 (91%)	17 (9%)	9	30
60	PF	69/111 (62%)	60 (87%)	9 (13%)	4	18
61	PG	147/153 (96%)	125 (85%)	22 (15%)	3	15
62	PH	129/131 (98%)	118 (92%)	11 (8%)	10	31
63	PI	103/112 (92%)	93 (90%)	10 (10%)	8	26
64	PJ	53/56 (95%)	51 (96%)	2 (4%)	29	51
65	PK	106/106 (100%)	101 (95%)	5 (5%)	23	46
66	PL	41/55 (74%)	38 (93%)	3 (7%)	13	36
67	FA	117/448 (26%)	115 (98%)	2 (2%)	53	68
68	w	1202/1232 (98%)	1181 (98%)	21 (2%)	53	68
69	x	787/864 (91%)	769 (98%)	18 (2%)	44	63
70	p	353/736 (48%)	347 (98%)	6 (2%)	53	68
All	All	18247/29966 (61%)	16589 (91%)	1658 (9%)	11	29

5 of 1658 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	DB	487	LYS
38	De	675	LEU
63	PI	81	THR
36	DB	784	ASN
36	DB	486	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 486 such sidechains are listed below:

Mol	Chain	Res	Type
36	DB	450	GLN
68	w	358	GLN
44	DL	117	GLN
67	FA	141	HIS
69	x	402	ASN

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.

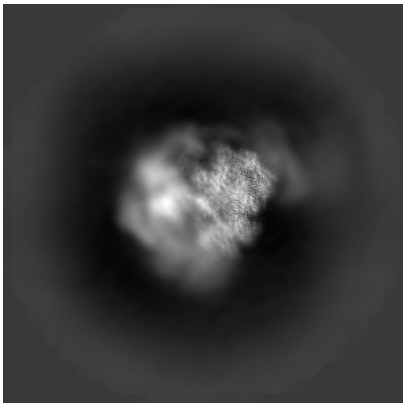
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-31207. These allow visual inspection of the internal detail of the map and identification of artifacts.

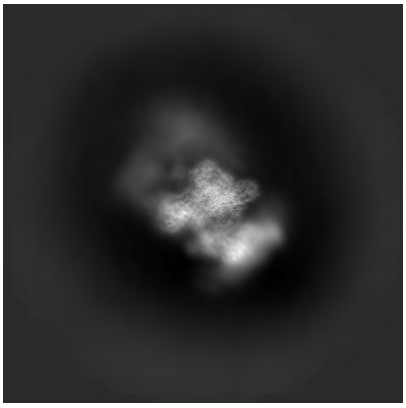
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

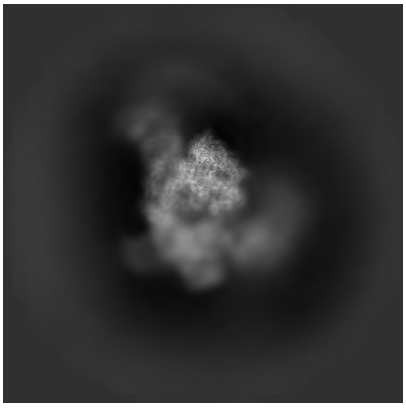
6.1.1 Primary map



X



Y

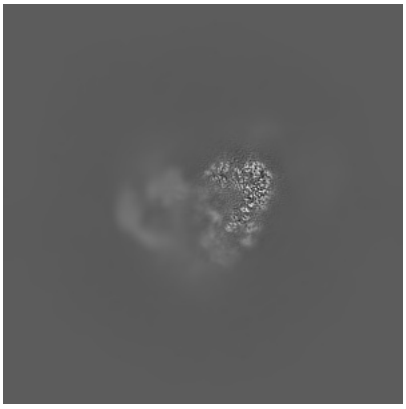


Z

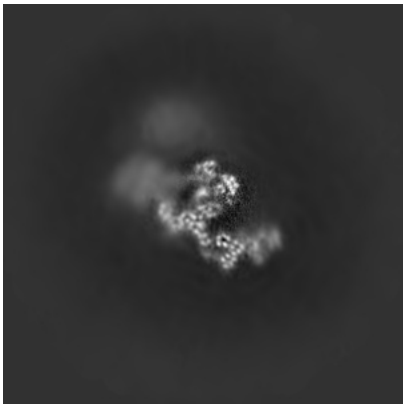
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

6.2.1 Primary map



X Index: 240



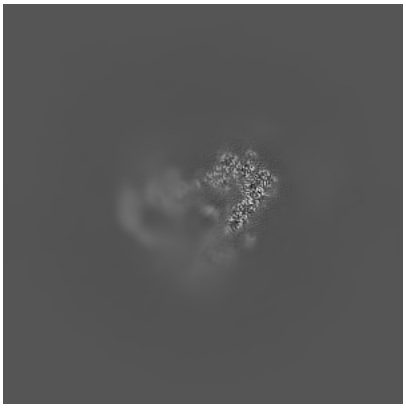
Y Index: 240

Z Index: 240

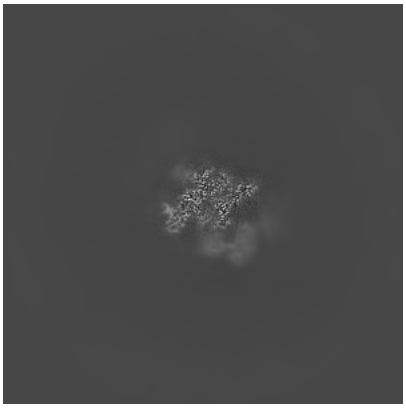
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

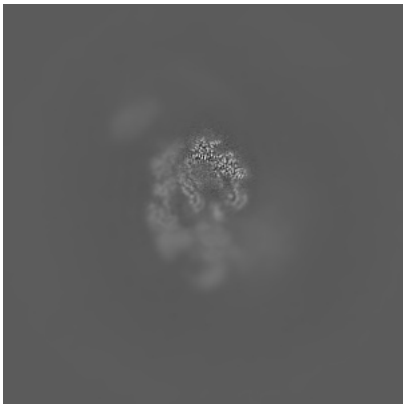
6.3.1 Primary map



X Index: 246



Y Index: 287

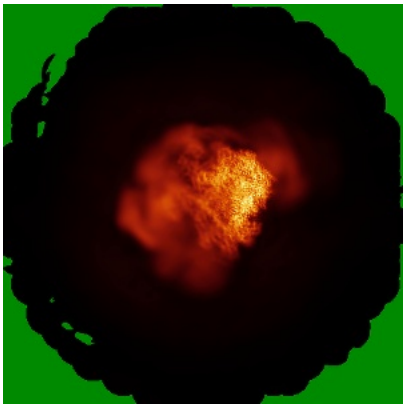


Z Index: 247

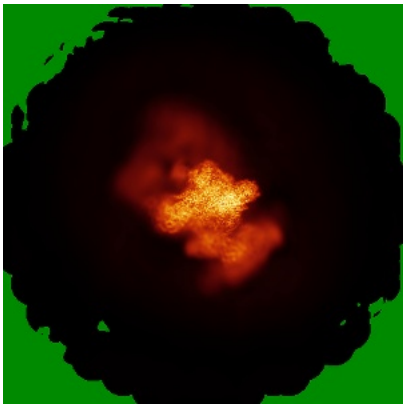
The images above show the largest variance slices of the map in three orthogonal directions.

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

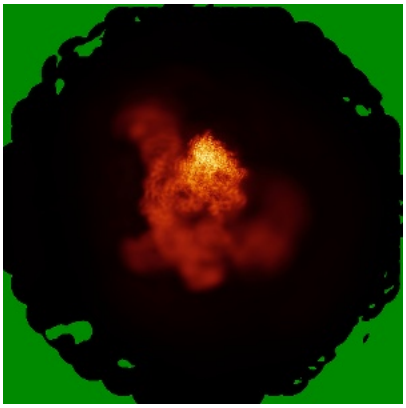
6.4.1 Primary map



X



Y

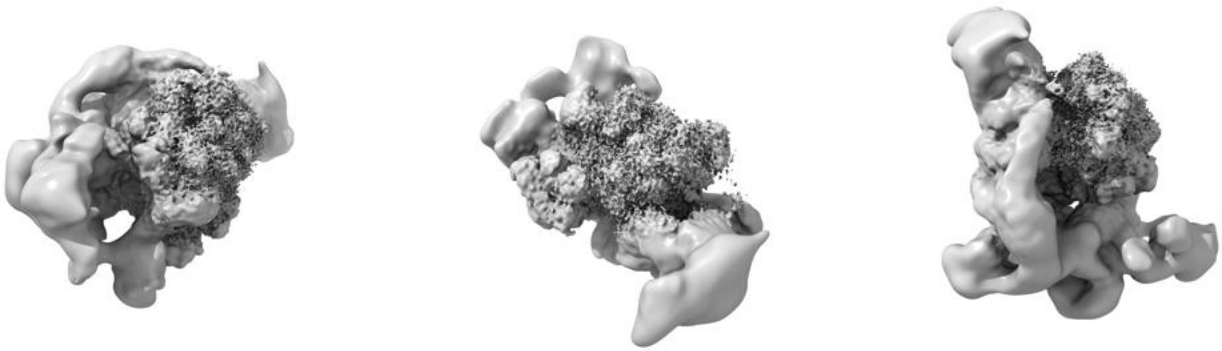


Z

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.

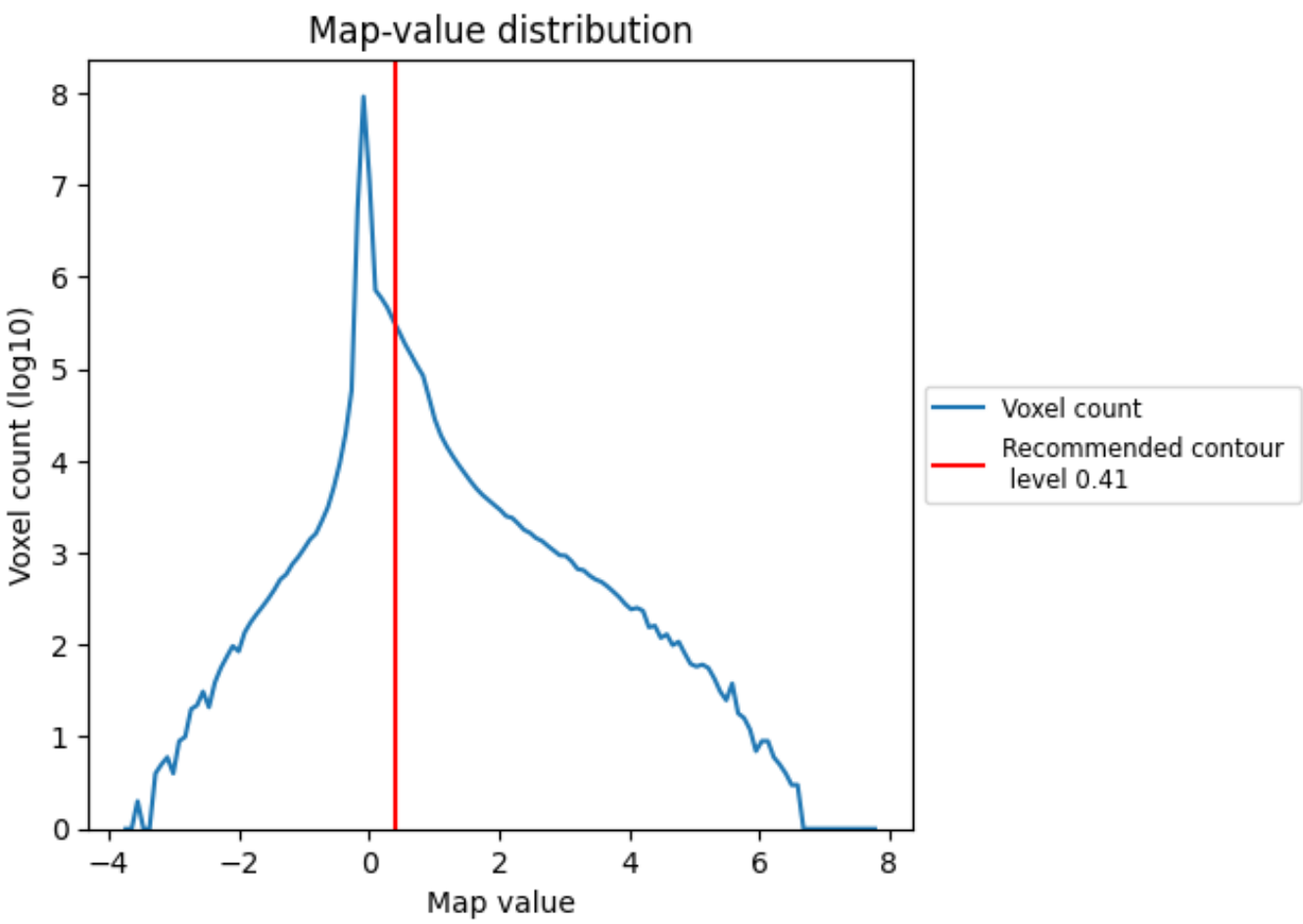
6.6 Mask visualisation (i)

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

7 Map analysis (i)

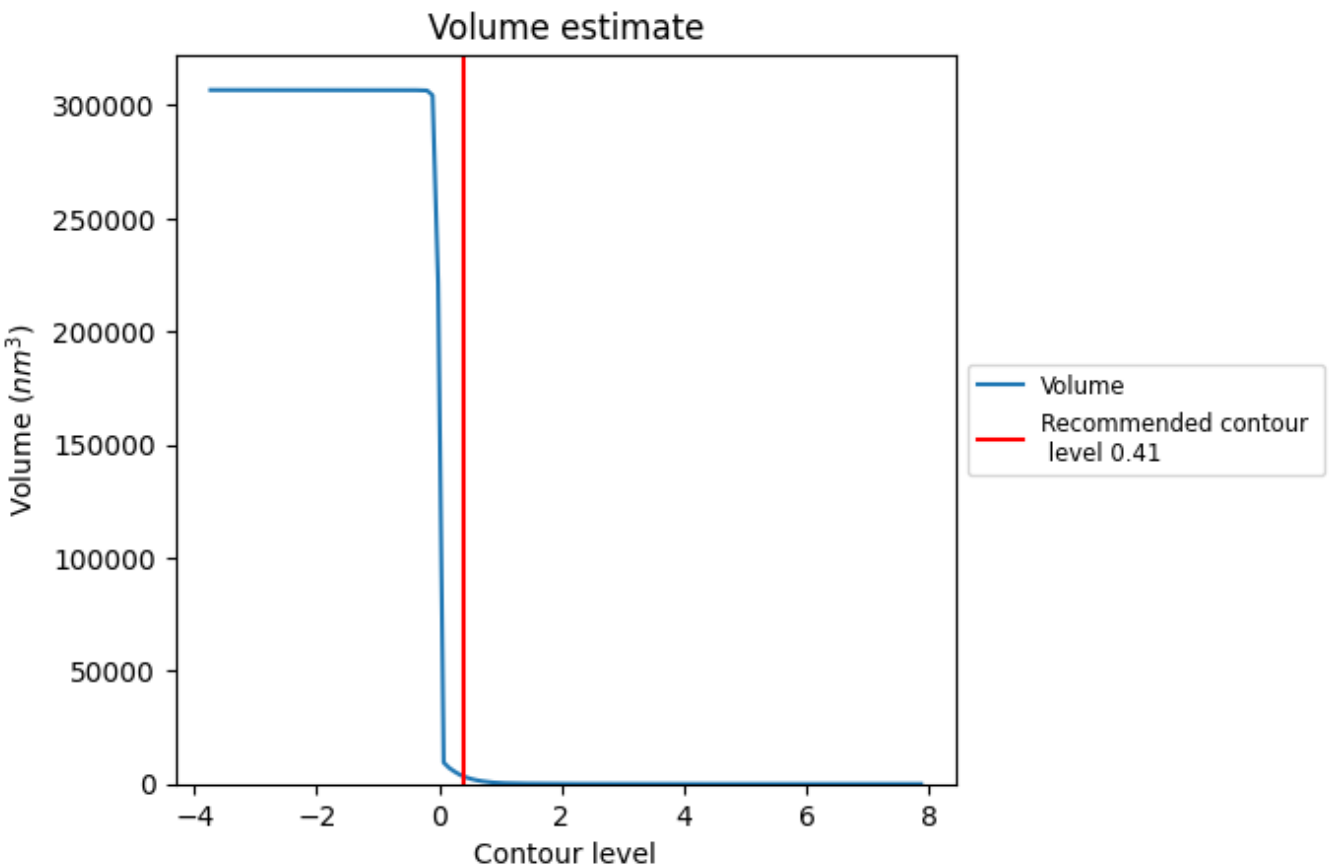
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

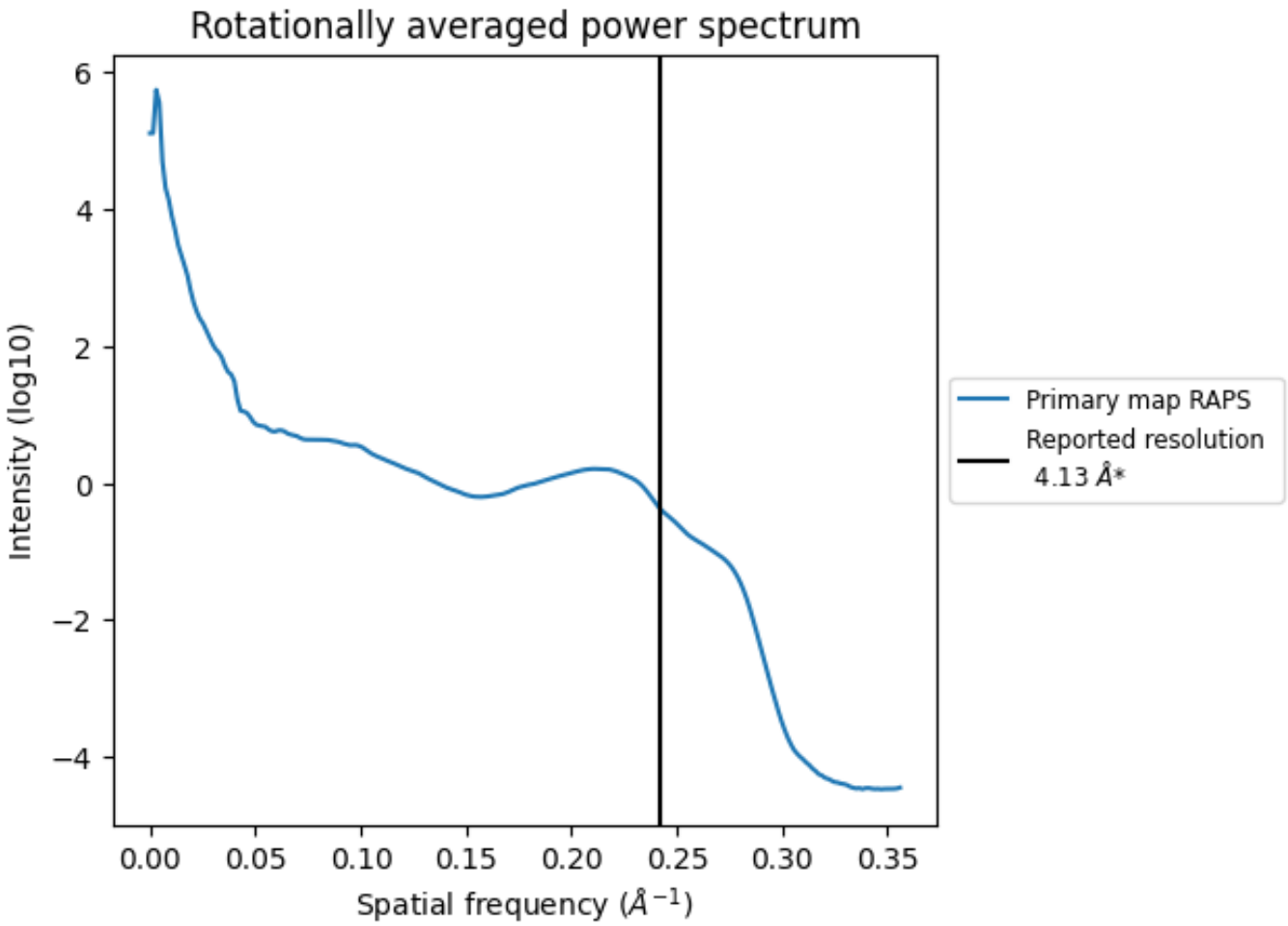
7.2 Volume estimate (i)



The volume at the recommended contour level is 3240 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}

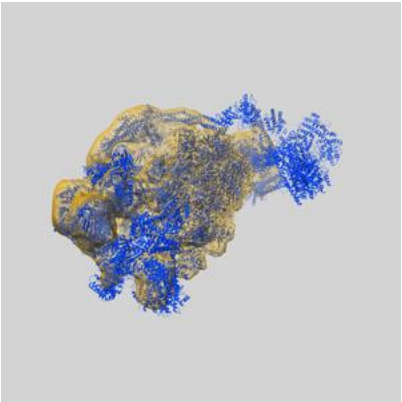
8 Fourier-Shell correlation (i)

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

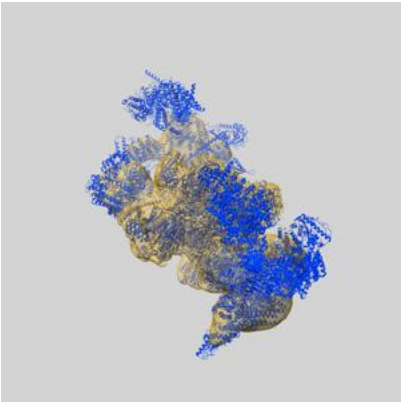
9 Map-model fit (i)

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

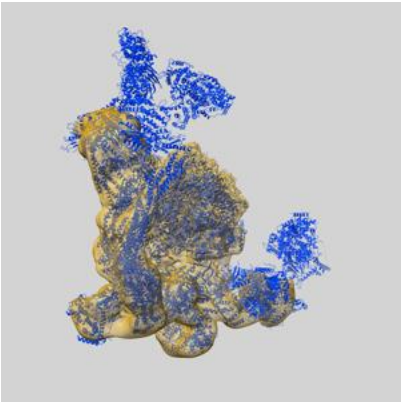
9.1 Map-model overlay (i)



X



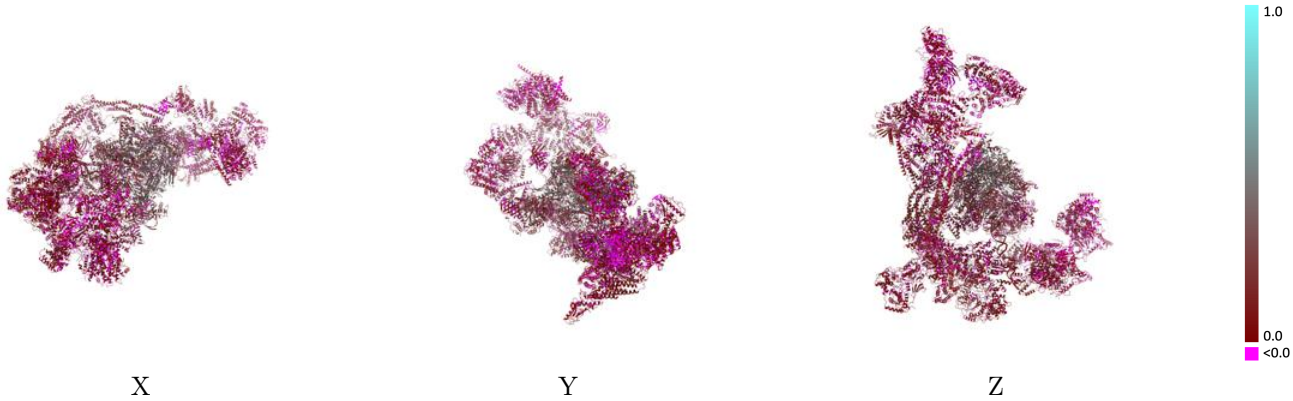
Y



Z

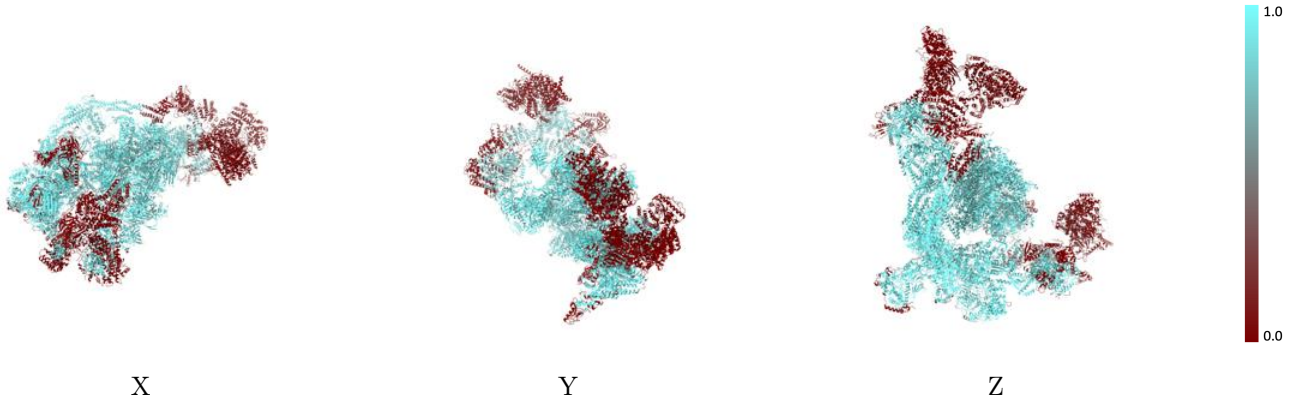
The images above show the 3D surface view of the map at the recommended contour level 0.41 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



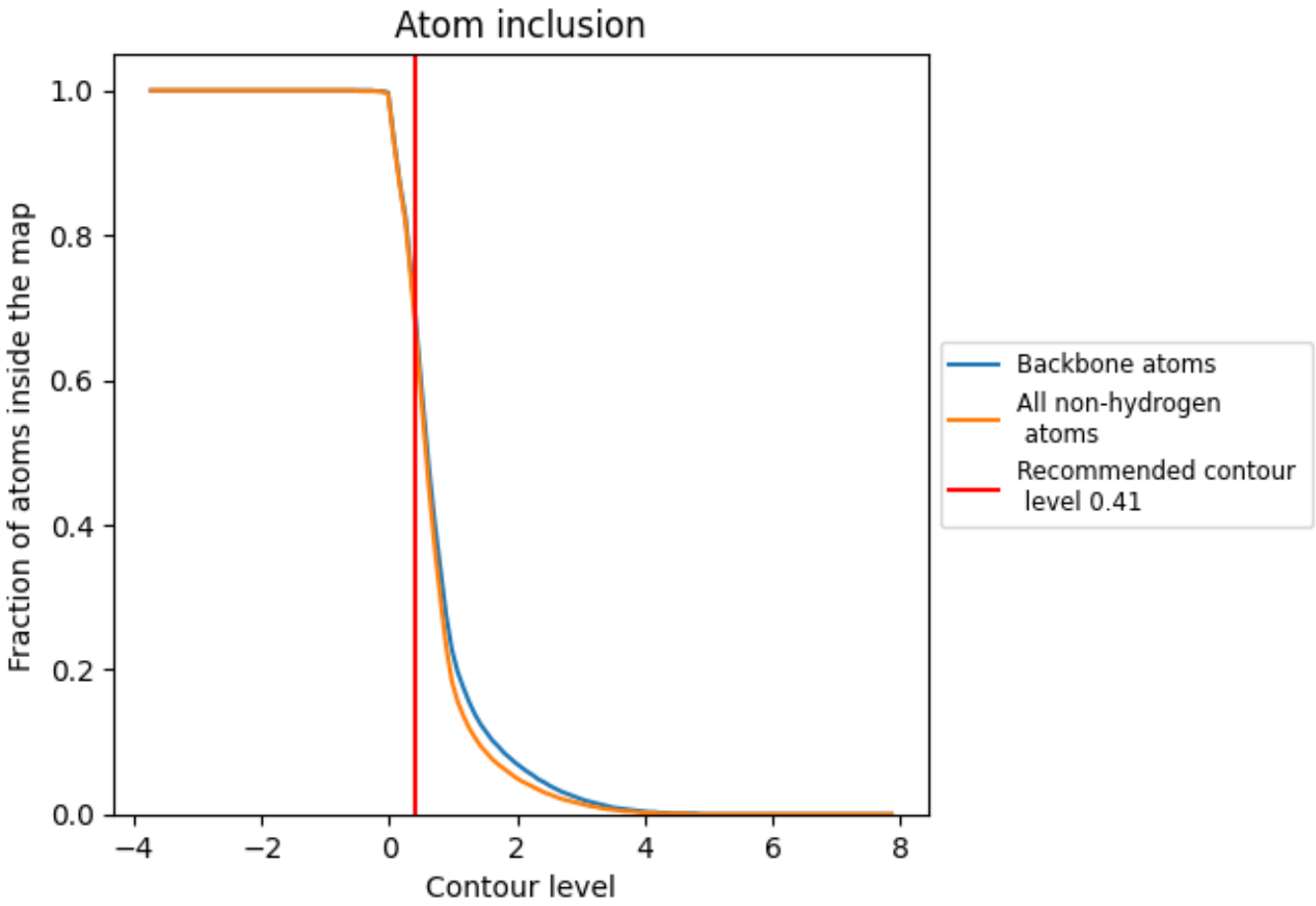
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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