



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 04:43 AM UTC

PDB ID : 7ENA / pdb_00007ena
EMDB ID : EMD-31204
Title : TFIID-based PIC-Mediator holo-complex in pre-assembled state (pre-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 : 4.07 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

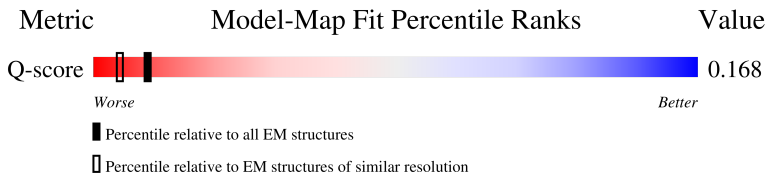
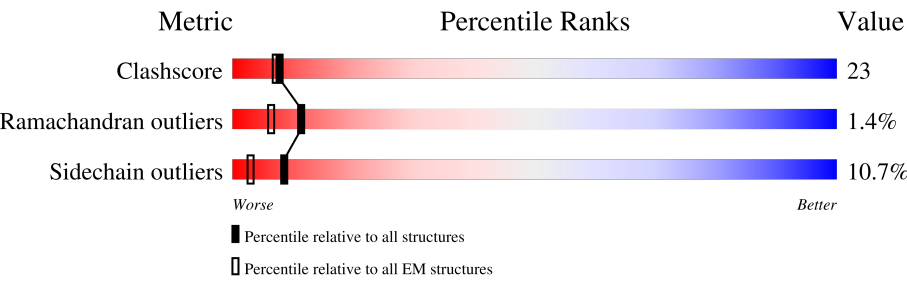
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.07 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.



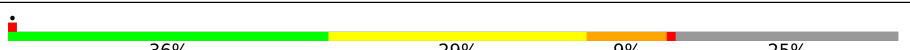
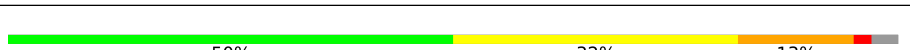
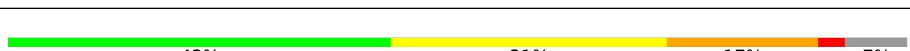
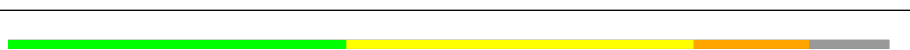
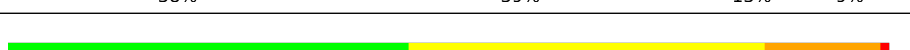
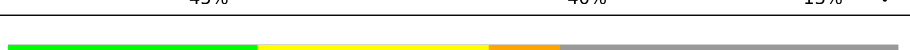
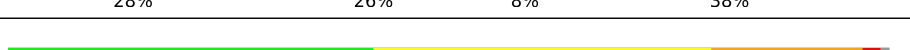
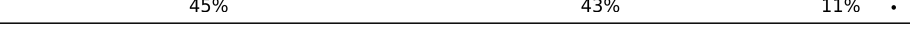
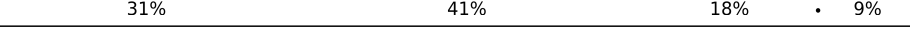
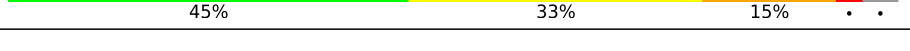
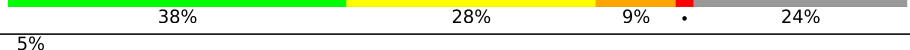
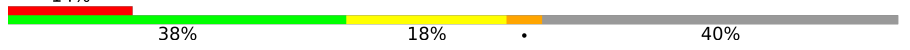
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	6427 (3.58 - 4.57)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	309	 17% 58% 28% 11% ..
2	8	346	 8% 34% 34% 17% • 14%
3	9	323	 33% 41% 30% 16% • 11%
4	DO	109	 • 56% 21% 11% • 11%

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Mol	Chain	Length	Quality of chain
5	DP	339	
6	DQ	307	
7	BA	316	
8	FA	517	
9	FB	249	
10	PA	1970	
11	PB	1174	
12	PC	275	
13	PD	142	
14	PE	210	
15	PF	127	
16	PG	172	
17	PH	150	
18	PI	125	
19	PJ	67	
20	PK	117	
21	PL	58	
22	DA	1872	
23	DB	1199	
24	DD	1085	
24	Dd	1085	
25	DE	800	
25	De	800	
26	DF	677	
26	Df	677	

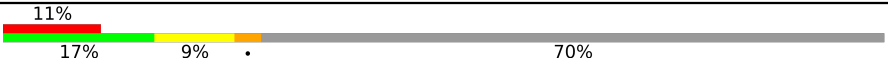
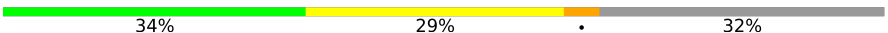
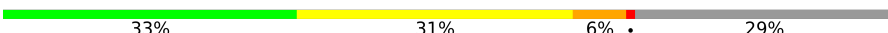
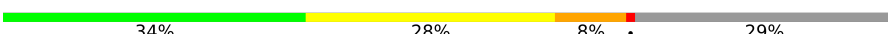
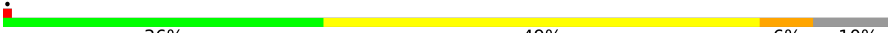
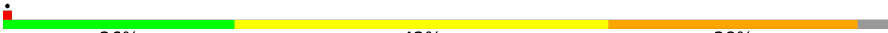
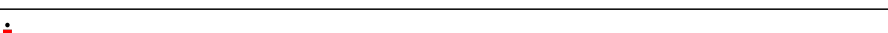
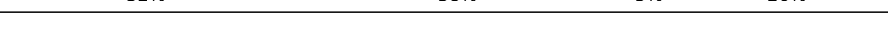
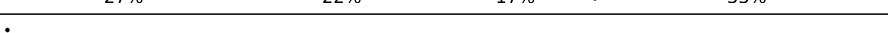
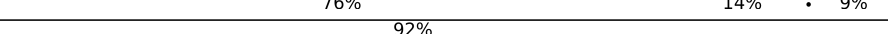
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Mol	Chain	Length	Quality of chain
27	DG	349	
28	DH	310	
29	DI	264	
29	Di	264	
30	DJ	218	
30	Dj	218	
31	DL	161	
31	Dl	161	
32	Dc	929	
33	Dk	211	
34	Dm	124	
35	EA	439	
36	EB	291	
37	1	548	
38	2	395	
39	3	308	
40	4	462	
41	5	71	
42	6	782	
43	7	760	
44	c	311	
45	e	178	
46	b	200	
47	l	178	
48	m	131	

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Mol	Chain	Length	Quality of chain
49	a	1581	
50	d	270	
51	f	246	
52	g	233	
53	h	268	
54	i	146	
55	j	135	
56	k	117	
57	n	1454	
58	o	788	
59	q	651	
60	r	208	
61	s	244	
62	t	212	
63	u	144	
64	v	200	
65	z	600	
66	x	989	
67	w	1368	
68	p	841	
69	X	69	
70	Y	69	

2 Entry composition

There are 73 unique types of molecules in this entry. The entry contains 173965 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 CDK-activating kinase assembly factor MAT1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	306	Total	C	N	O	S	0	0
			2255	1404	399	441	11		

- Molecule 2 is a protein called Cyclin-dependent kinase 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	8	299	Total	C	N	O	S	0	0
			2378	1535	406	426	11		

- Molecule 3 is a protein called Cyclin-H.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	9	287	Total	C	N	O	S	0	0
			2307	1477	398	417	15		

- Molecule 4 is a protein called Transcription initiation factor IIA subunit 2.

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

- Molecule 5 is a protein called TATA-box-binding protein.

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

- Molecule 6 is a protein called TFIIA-a.

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

- Molecule 7 is a protein called Transcription initiation factor IIB.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	BA	255	Total	C	N	O	S	0	0
			1959	1226	348	368	17		

- Molecule 8 is a protein called General transcription factor IIF subunit 1.

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

- Molecule 9 is a protein called General transcription factor IIF subunit 2.

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

- Molecule 10 is a protein called RPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	PA	1475	Total	C	N	O	S	0	0
			11662	7336	2071	2183	72		

- Molecule 11 is a protein called DNA-directed RNA polymerase subunit beta.

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

- Molecule 12 is a protein called DNA-directed RNA polymerase II subunit RPB3.

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

- Molecule 13 is a protein called DNA-directed RNA polymerase II subunit RPB4.

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

- Molecule 14 is a protein called DNA-directed RNA polymerase II subunit E.

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

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

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

- Molecule 16 is a protein called DNA-directed RNA polymerase II subunit RPB7.

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

- Molecule 17 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

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

- Molecule 18 is a protein called DNA-directed RNA polymerase II subunit RPB9.

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

- Molecule 19 is a protein called RPB10.

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

- Molecule 20 is a protein called RNA_pol_L_2 domain-containing protein.

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

- Molecule 21 is a protein called RPB12.

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

- Molecule 22 is a protein called Transcription initiation factor TFIID subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	DA	600	Total	C	N	O	S	0	0
			4918	3135	858	897	28		

- Molecule 23 is a protein called Transcription initiation factor TFIID subunit 2.

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

- Molecule 24 is a protein called Transcription initiation factor TFIID subunit 4.

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

- Molecule 25 is a protein called Transcription initiation factor TFIID subunit 5.

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

- Molecule 26 is a protein called Transcription initiation factor TFIID subunit 6.

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

- Molecule 27 is a protein called Transcription initiation factor TFIID subunit 7.

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

- Molecule 28 is a protein called Transcription initiation factor TFIID subunit 8.

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

- Molecule 29 is a protein called Transcription initiation factor TFIID subunit 9.

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

- Molecule 30 is a protein called Transcription initiation factor TFIID subunit 10.

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

- Molecule 31 is a protein called Transcription initiation factor TFIID subunit 12.

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

- Molecule 32 is a protein called Transcription initiation factor TFIID subunit 3.

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

- Molecule 33 is a protein called Transcription initiation factor TFIID subunit 11.

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

- Molecule 34 is a protein called Transcription initiation factor TFIID subunit 13.

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

- Molecule 35 is a protein called General transcription factor IIE subunit 1.

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

- Molecule 36 is a protein called Transcription initiation factor IIE subunit beta.

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

- Molecule 37 is a protein called General transcription factor IIH subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	1	433	Total	C	N	O	S	0	0
			3436	2153	602	664	17		

- Molecule 38 is a protein called General transcription factor IIH subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	2	385	Total	C	N	O	S	0	0
			3024	1909	524	564	27		

- Molecule 39 is a protein called General transcription factor IIH subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	3	295	Total	C	N	O	S	0	0
			2306	1477	384	426	19		

- Molecule 40 is a protein called General transcription factor IIH subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	4	457	Total	C	N	O	S	0	0
			3644	2341	641	648	14		

- Molecule 41 is a protein called General transcription factor IIH subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	5	66	Total	C	N	O	S	0	0
			522	336	83	100	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	6	652	Total	C	N	O	S	0	0
			5255	3345	898	980	32		

- Molecule 43 is a protein called General transcription and DNA repair factor IIH helicase subunit XPD.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	7	732	Total	C	N	O	S	0	0
			5861	3742	1023	1068	28		

- Molecule 44 is a protein called Mediator of RNA polymerase II transcription subunit 27.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	c	263	Total	C	N	O	S	0	0
			2108	1337	378	382	11		

- Molecule 45 is a protein called Mediator of RNA polymerase II transcription subunit 28.

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

- Molecule 46 is a protein called Mediator of RNA polymerase II transcription subunit 29.

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

- Molecule 47 is a protein called Mediator of RNA polymerase II transcription subunit 30.

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

- Molecule 48 is a protein called Mediator of RNA polymerase II transcription subunit 31.

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

- Molecule 49 is a protein called Mediator of RNA polymerase II transcription subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	a	469	Total	C	N	O	S	0	0
			3585	2283	615	663	24		

- Molecule 50 is a protein called Mediator of RNA polymerase II transcription subunit 4.

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

- Molecule 51 is a protein called Mediator of RNA polymerase II transcription subunit 6.

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

- Molecule 52 is a protein called Mediator of RNA polymerase II transcription subunit 7.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 53 is a protein called Isoform 2 of Mediator of RNA polymerase II transcription subunit 8.

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

- Molecule 54 is a protein called Mediator of RNA polymerase II transcription subunit 9.

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

- Molecule 55 is a protein called Mediator of RNA polymerase II transcription subunit 10.

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

- Molecule 56 is a protein called Mediator of RNA polymerase II transcription subunit 11.

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

- Molecule 57 is a protein called Mediator of RNA polymerase II transcription subunit 14.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 58 is a protein called Mediator of RNA polymerase II transcription subunit 15.

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

- Molecule 59 is a protein called Mediator of RNA polymerase II transcription subunit 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	q	555	Total	C	N	O	S	0	0
			4276	2700	767	792	17		

- Molecule 60 is a protein called Mediator of RNA polymerase II transcription subunit 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	r	206	Total	C	N	O	S	0	0
			1630	1033	285	294	18		

- Molecule 61 is a protein called Mediator of RNA polymerase II transcription subunit 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	s	81	Total	C	N	O	S	0	0
			505	312	91	100	2		

- Molecule 62 is a protein called Mediator of RNA polymerase II transcription subunit 20.

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

- Molecule 63 is a protein called Mediator of RNA polymerase II transcription subunit 21.

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

- Molecule 64 is a protein called Mediator of RNA polymerase II transcription subunit 22.

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

- Molecule 65 is a protein called Mediator of RNA polymerase II transcription subunit 26.

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

- Molecule 66 is a protein called Mediator of RNA polymerase II transcription subunit 24.

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

- Molecule 67 is a protein called Mediator of RNA polymerase II transcription subunit 23.

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

- Molecule 68 is a protein called Isoform 2 of Mediator of RNA polymerase II transcription subunit 16.

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

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

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

- Molecule 70 is a DNA chain called DNA(69-MER).

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

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

Mol	Chain	Residues	Atoms		AltConf
71	0	2	Total	Zn	0
			2	2	
71	BA	1	Total	Zn	0
			1	1	
71	PA	2	Total	Zn	0
			2	2	
71	PB	1	Total	Zn	0
			1	1	
71	PC	1	Total	Zn	0
			1	1	
71	PI	2	Total	Zn	0
			2	2	

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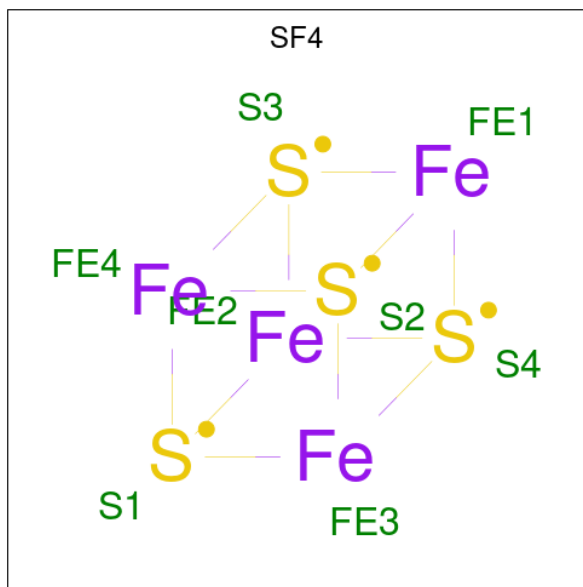
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
71	PJ	1	Total	Zn	0
			1	1	
71	PL	1	Total	Zn	0
			1	1	
71	EA	1	Total	Zn	0
			1	1	
71	2	3	Total	Zn	0
			3	3	
71	3	1	Total	Zn	0
			1	1	

- Molecule 72 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 73 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).

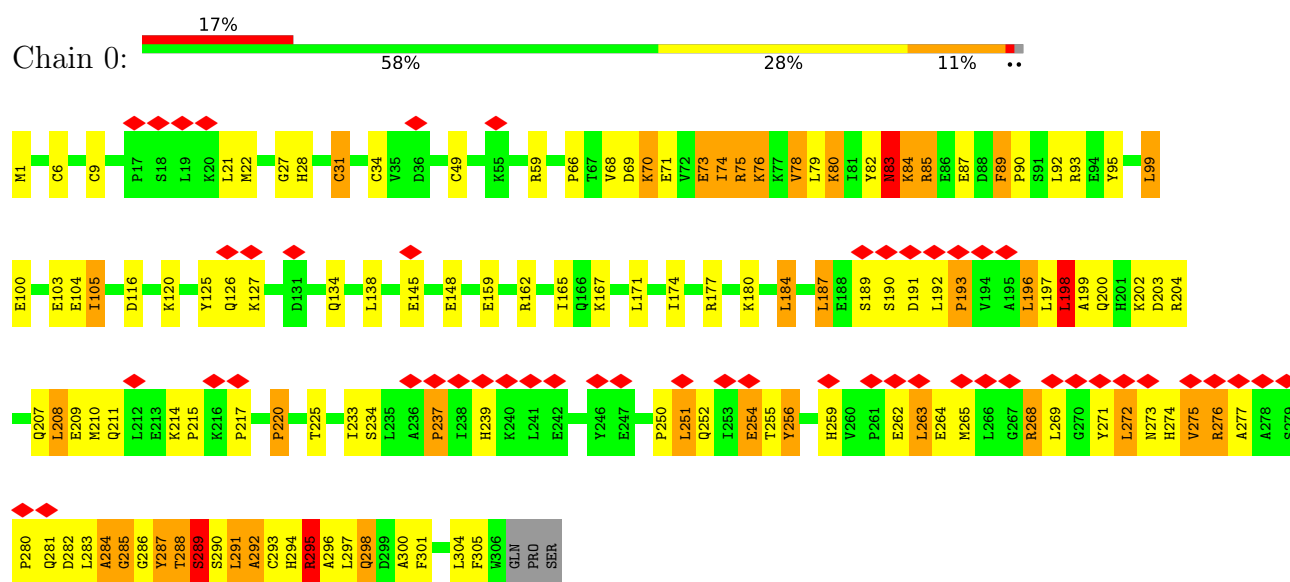


Mol	Chain	Residues	Atoms			AltConf
73	7	1	Total	Fe	S	0
			8	4	4	

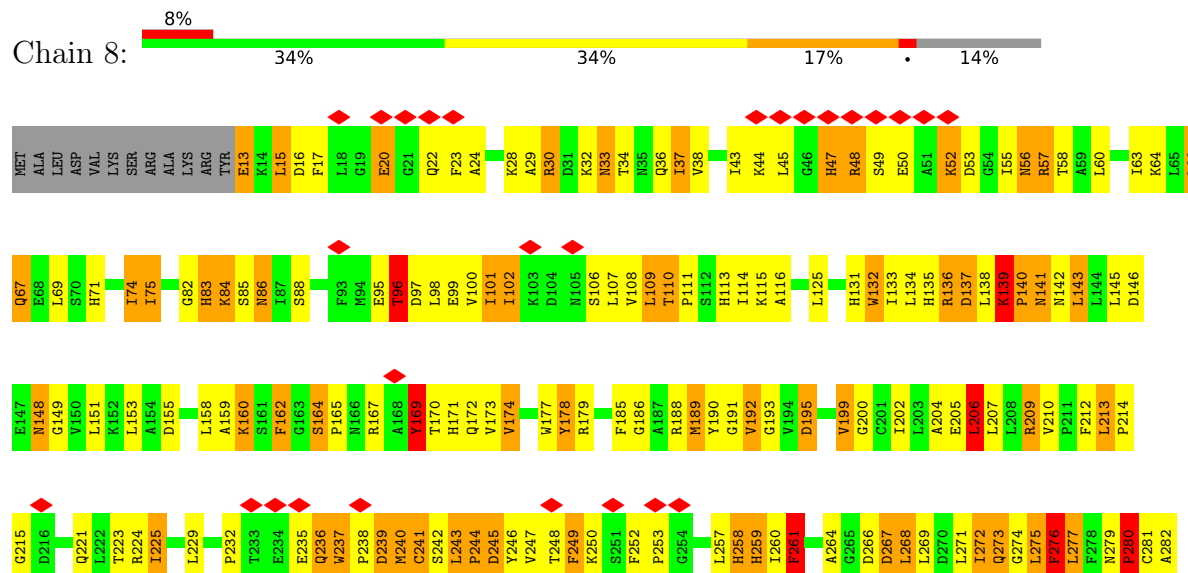
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

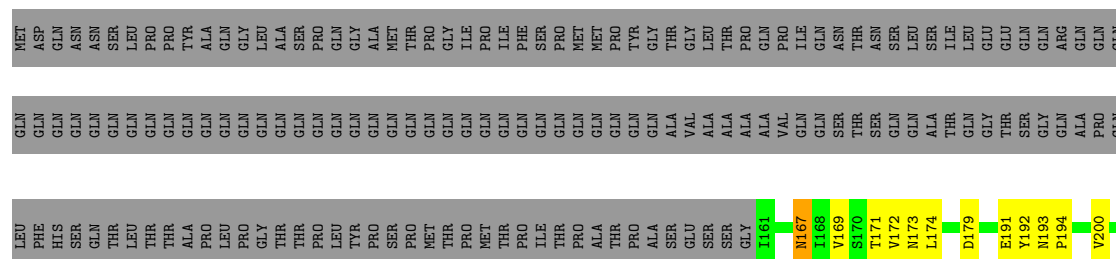
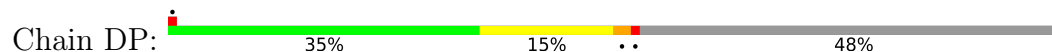
- Molecule 1: CDK-activating kinase assembly factor MAT1



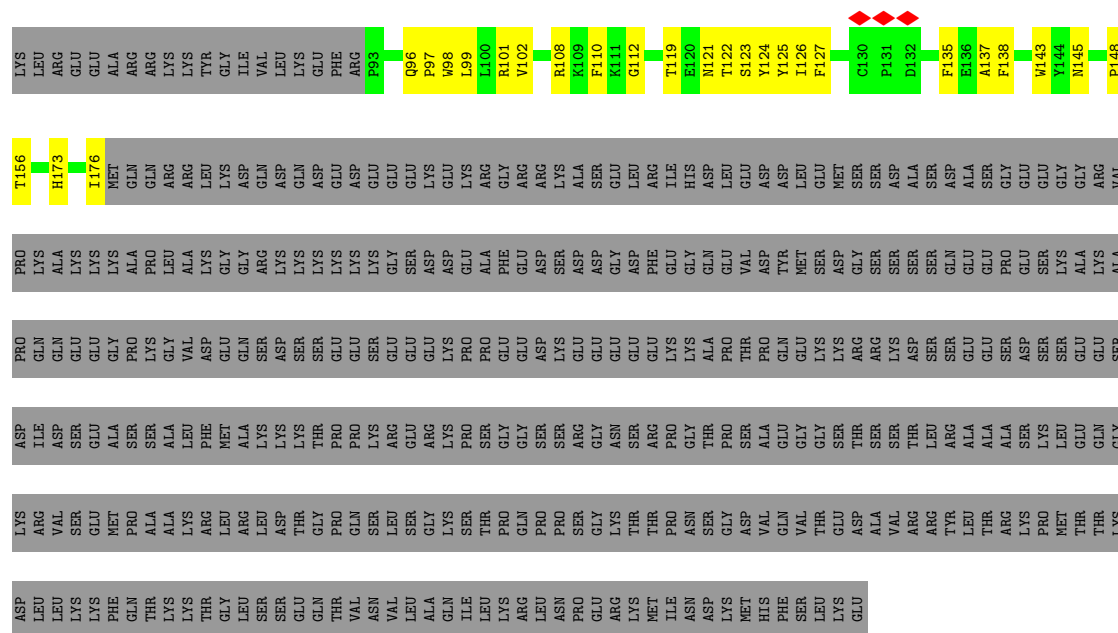
- Molecule 2: Cyclin-dependent kinase 7



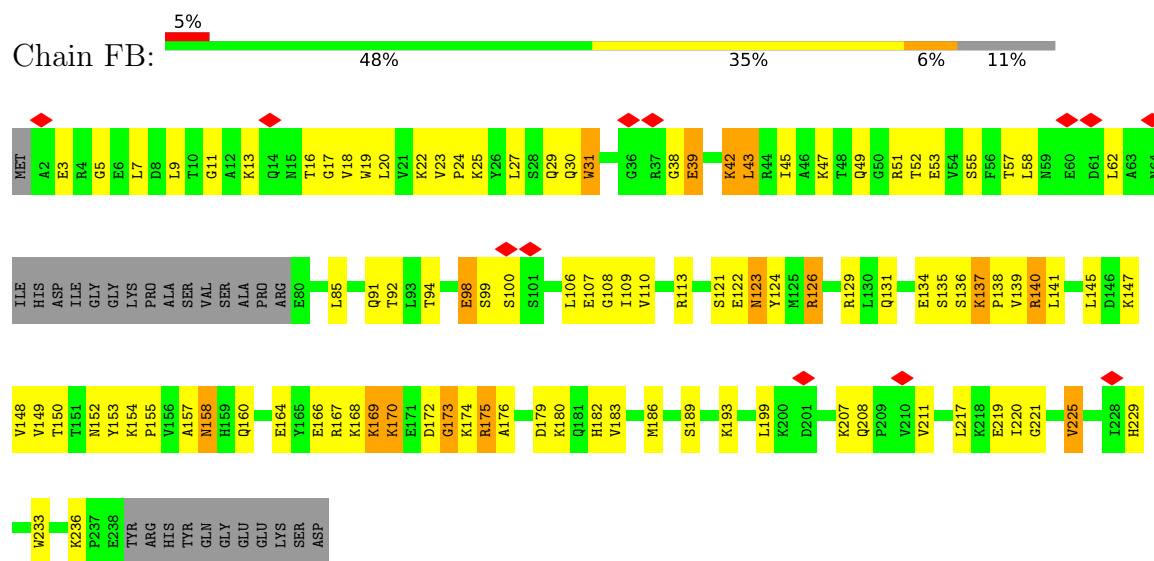
Chain 9:



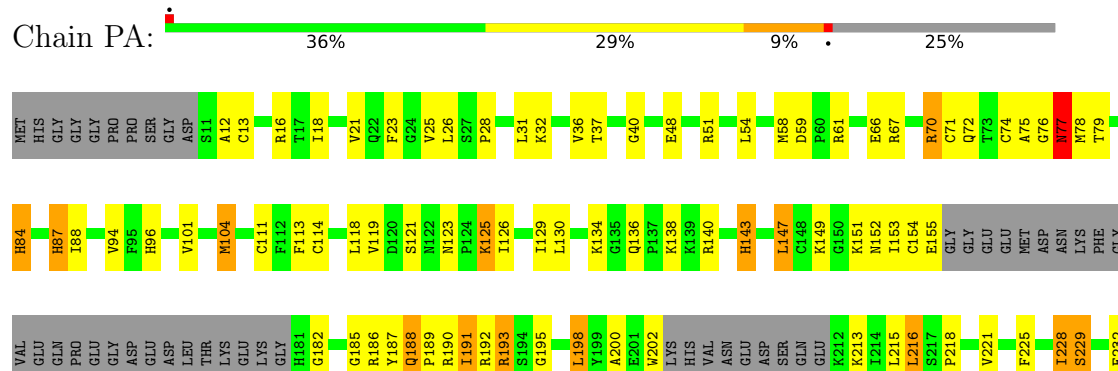




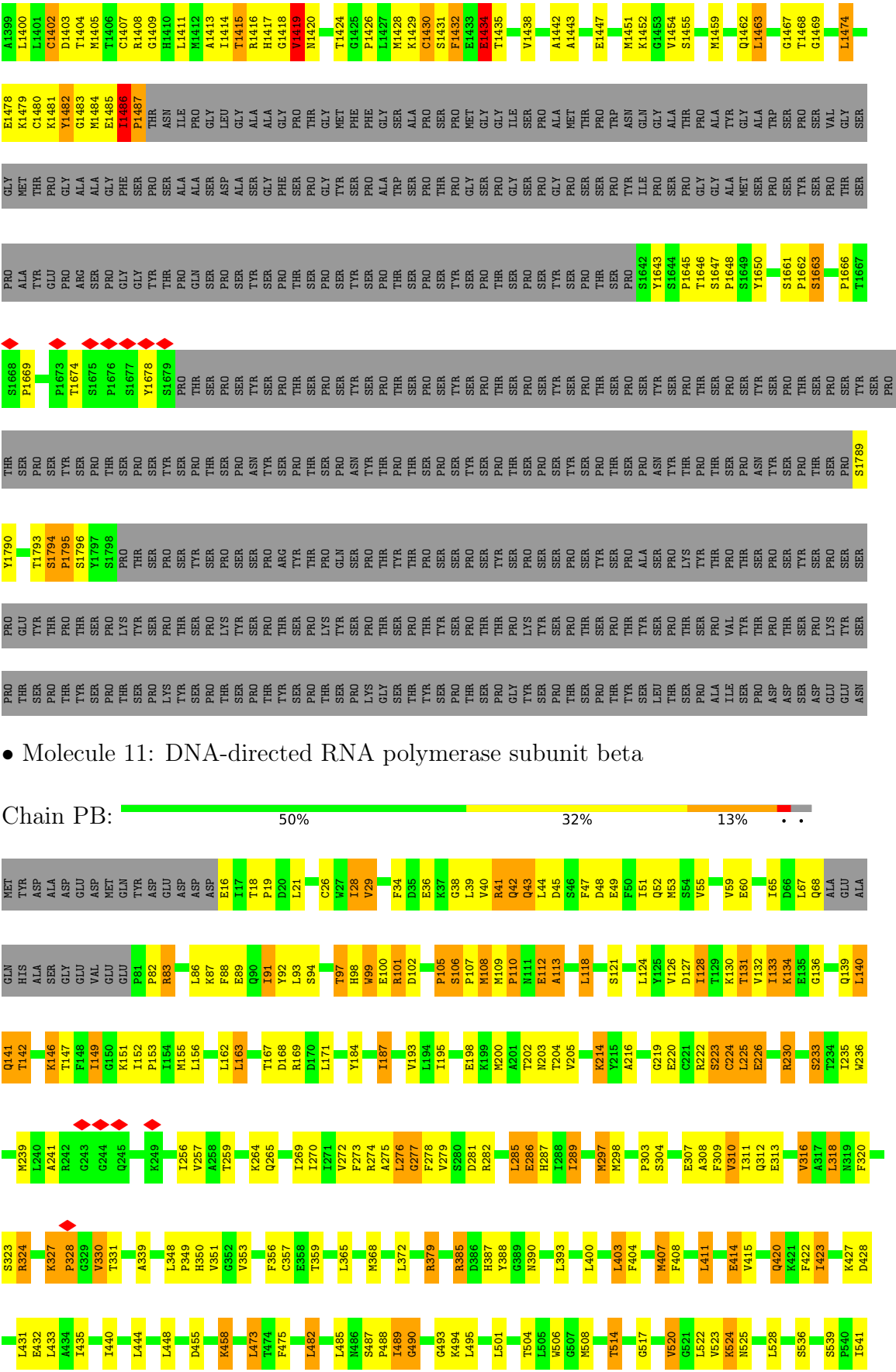
- Molecule 9: General transcription factor IIF subunit 2



- Molecule 10: RPB1

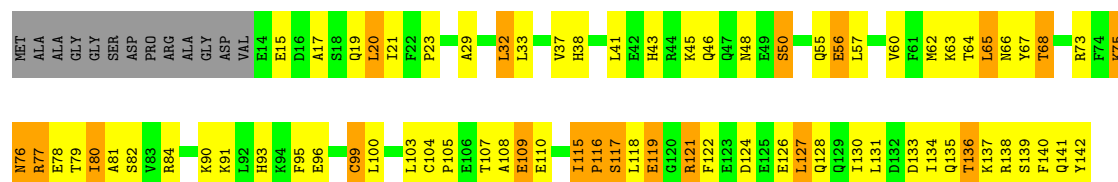


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E1327	L1243	A1174	L952	T878	W793	T698	K619	Y594	Q461	I393	H313	
A1330	I1175	Y1175	E955	Y879	K796	T699	S622	G536	P462	V394	T316	L236
L1331	Y1176	F1176	E956	R880	K797	Q700	D625	G537	T463	T395	M317	G237
Q1332	D1177	D1177	E957	N881	R797	Q703	T626	Y538	L464	P396	V318	M238
E1333	F1247	P1179	R958	S882	T798	Q703	T627	F539	H465	F397	E239	
W1334	N1248	Q1182	R959	T883	F799	N794	T628	Q539	S468	K388	E321	P240
I1335	D1249	S1183	R960	N884	F800	T705	V628	D540		I399	L322	
L1336	D1250	S1184	E961	Q885		T706	V629	T541	M469	D400	P323	A243
E1337		T1184	D962	V887	T806	K707	V630	T542	M470	R401	L325	R244
T1338	K1254	V1185	R963	Q888	L807	K708	E631	T543		L402		R245
L1339	L1255	V1186	E964	Q889	P808	D712	E634	A544	R473	Q403	M329	E246
G1340	V1256	A1187	V965	R890	V713	W713	E635	Y545	R474	E404	Q247	
V1341	V1257	E1188	L966	R891	F714	E715	L636	K547	R475	L405	Q350	M248
S1342	I1259	D1189	I969	E893	T811	E715	L637	F548	L476	V406	K331	L249
L1343	K1115	G1190	T972	E894	F817	H721	E638	T549		R408		
M1344	N1116	L1191	G973	G895			M637	W478				T251
R1345	V1117	W1192	D974	L896	G821	P729	L640	W479		P414		
V1346	T1118	Y1193	R975	A897	W823	G730	C641			G415	K340	V255
E1349	L1119	L1194	S976	E898	W823	N731	C641	K550		R417	Q341	
K1350	G1120	T1048	K976	E899	T732	T732	L645	S480		Y418	R342	
D1351	P1122	L1049	V977	S900	G830	L733	L655	T481		I419	K344	
V1352	R1123	C1050	N978	F903	E835	R734				I420	K345	
P1353	L1124	R1052	L979		F836	Q735	E659	Y492		R421	G345	P262
P1354		R1053	P980	L906	F837	T736	E660	A494		D422	K346	A263
		M1054	C981	L907	F838	E738	G661	F566		N423	E347	V264
		E1055	N982	A907	F839	E739	G662	L567		R426	G348	P265
		L1056	L983	T908	H862	N739	D663	D497		I427	R349	M266
		F1057	L984	L909	A840			G498		D428	V350	Q267
		F1058	R985	K910	M841	T752		D499		L429	R351	G268
		R1059	N986	P911		G753	R666	E500		R430	M355	S269
		L1060	I987	S912	L847	S754	F668	M501		F431	G356	A270
		S1061	W988	N913	F848	S755	Y669	H432		R431	K357	Q273
		G1062	N989	K914	D849	A756		L503		H433	R358	D274
		E1063	A990	A915		Q757		L504		P435	D275	D275
		A1064	Q991	F916	V852			H504		D437	L276	L276
		F1065	K992	E917	K853	E762	Q673	P506		S436	T277	
		W1067	I993			Y763		L505		D360	F361	H278
		L1068	R999	F920	T857	N765		Q507		H439	R364	L283
		L1069	R921	R921	Y859			S508		L438	A363	V284
			P1001	Y924	T860	V770		L509		L440	T365	K285
					Q861			T511		Q441	V366	I286
					R862	K775		R512			I367	
					R863	K778		A513		Y444	L373	Q289
					L864	K778		E514		V446		
					T865			S593		E447		A299
					K866	W781		R604		R448	D376	
					S867	S782		A519		H449	Q377	A300
					R868	Q783		M520		M450	V378	V302
					E869	W784		T605			P381	
					S870	T785		H606			R382	V307
					W871	A786		V521				K308
					M872	V787		P522				L309
					W873			R523				L310
					A874	Q789		M524				Q311
					W875	Q790		F458				
					D876	Q791		I525				F312



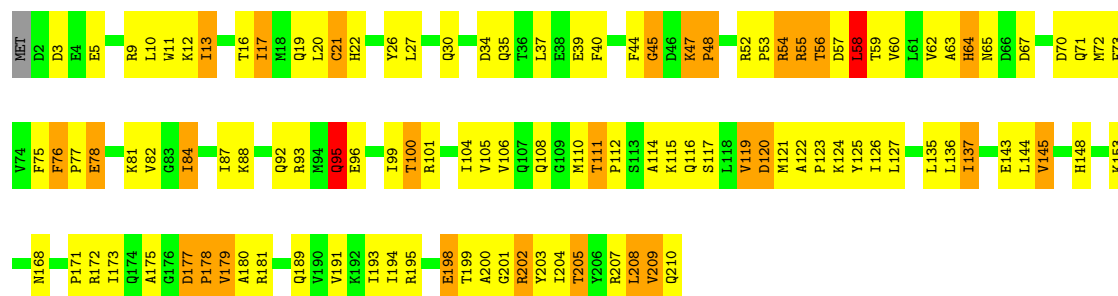
● Molecule 11: DNA-directed RNA polymerase subunit beta

Chain PB: 50% 32% 13% . .



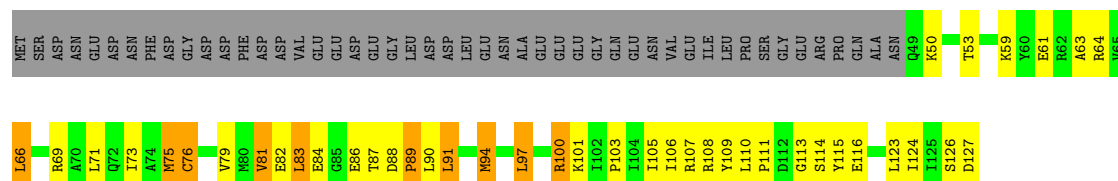
• Molecule 14: DNA-directed RNA polymerase II subunit E

Chain PE: 45% 40% 13%



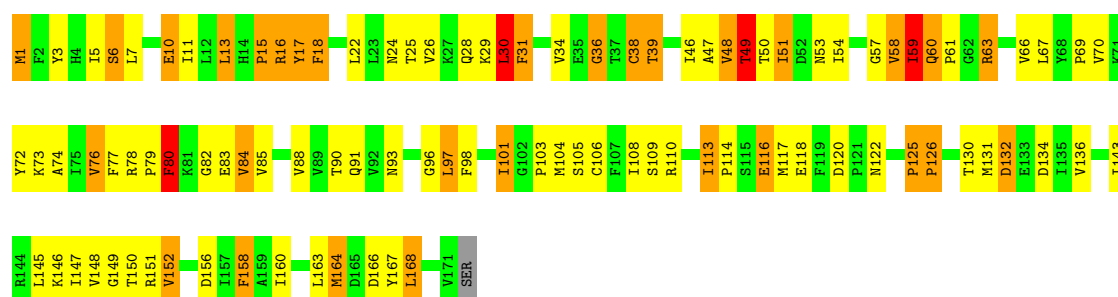
• Molecule 15: DNA-directed RNA polymerase II subunit F

Chain PF: 28% 26% 8% 38%



• Molecule 16: DNA-directed RNA polymerase II subunit RPB7

Chain PG: 41% 38% 17%



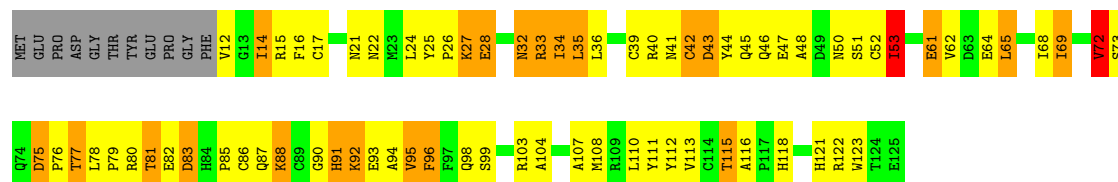
• Molecule 17: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain PH: 45% 43% 11%





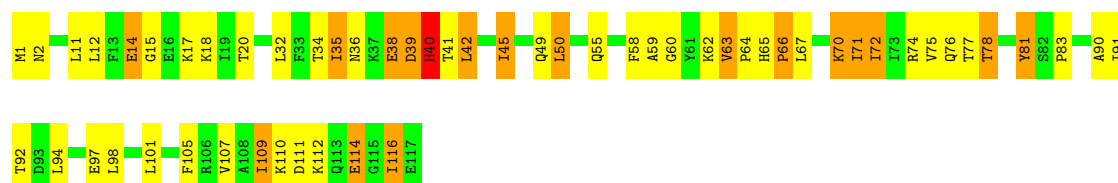
• Molecule 18: DNA-directed RNA polymerase II subunit RPB9



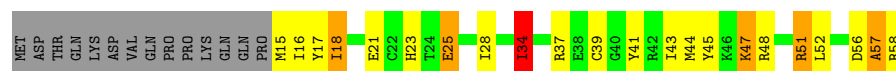
• Molecule 19: RPB10



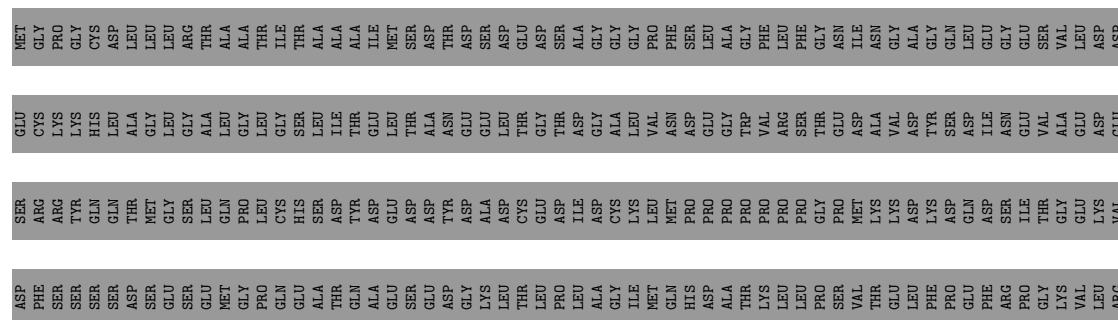
• Molecule 20: RNA_pol_L_2 domain-containing protein



• Molecule 21: RPB12



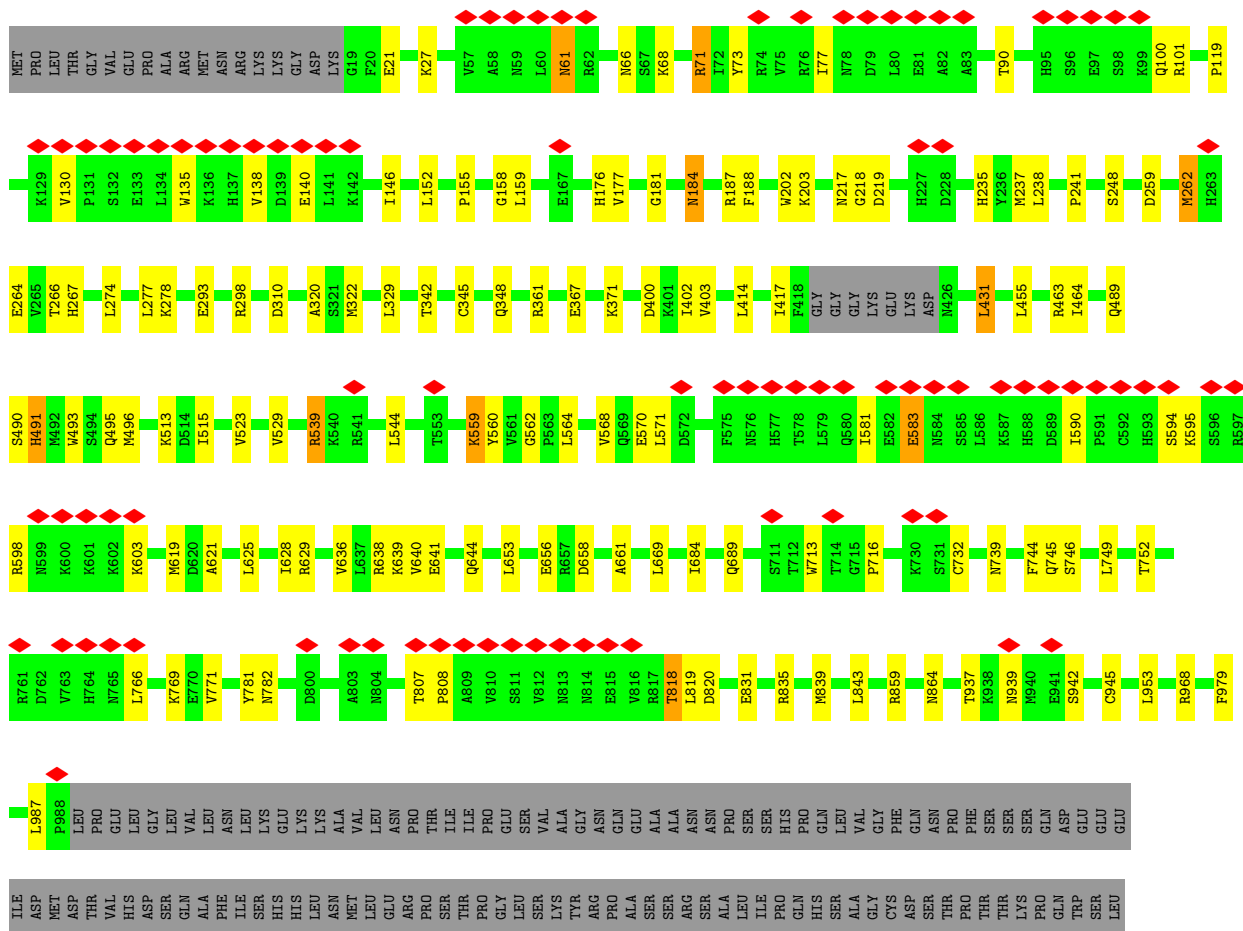
• Molecule 22: Transcription initiation factor TFIID subunit 1





- Molecule 23: Transcription initiation factor TFIID subunit 2

Chain DB:



[illegible]

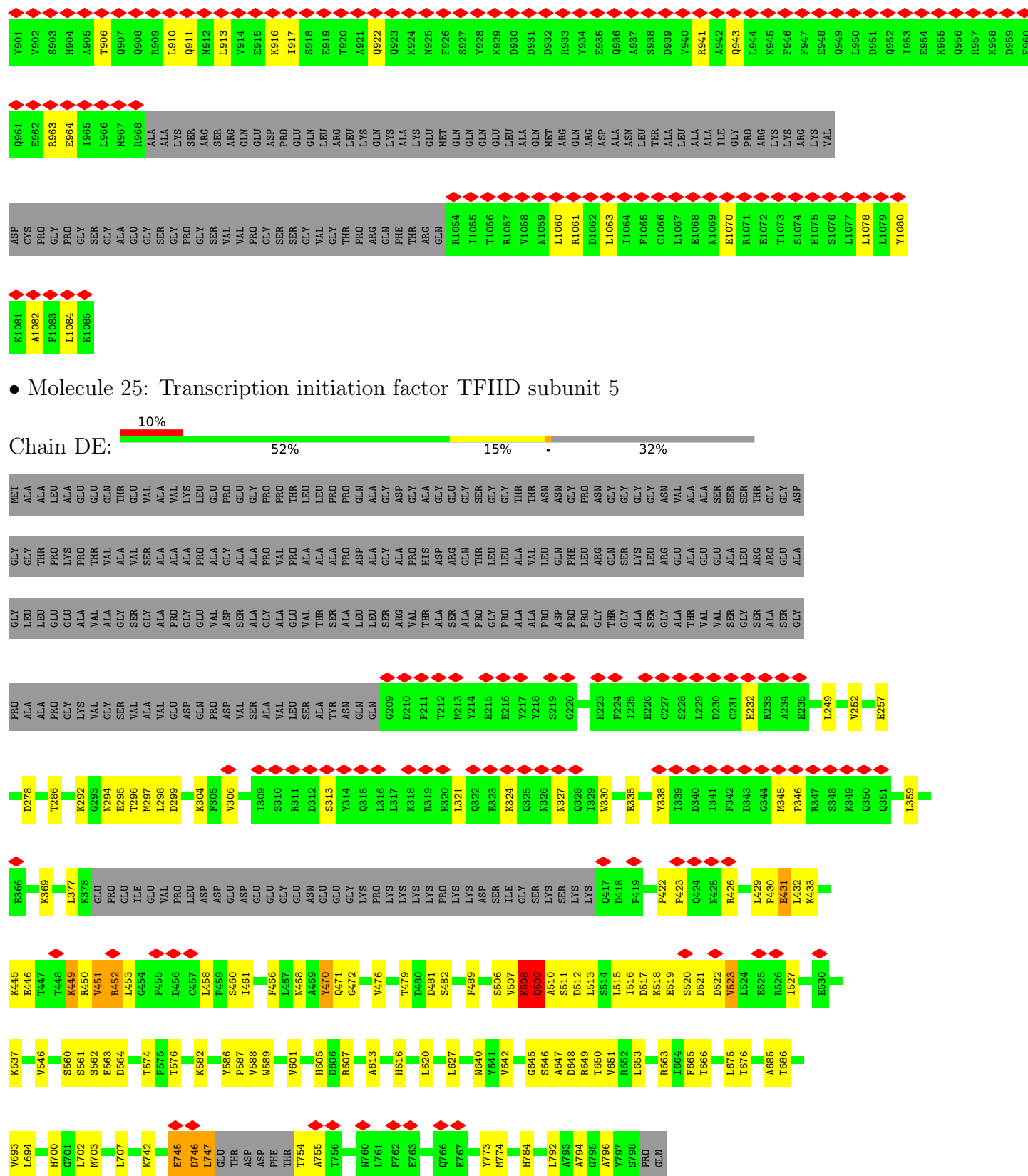
- Molecule 24: Transcription initiation factor TFIID subunit 4

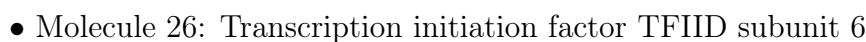
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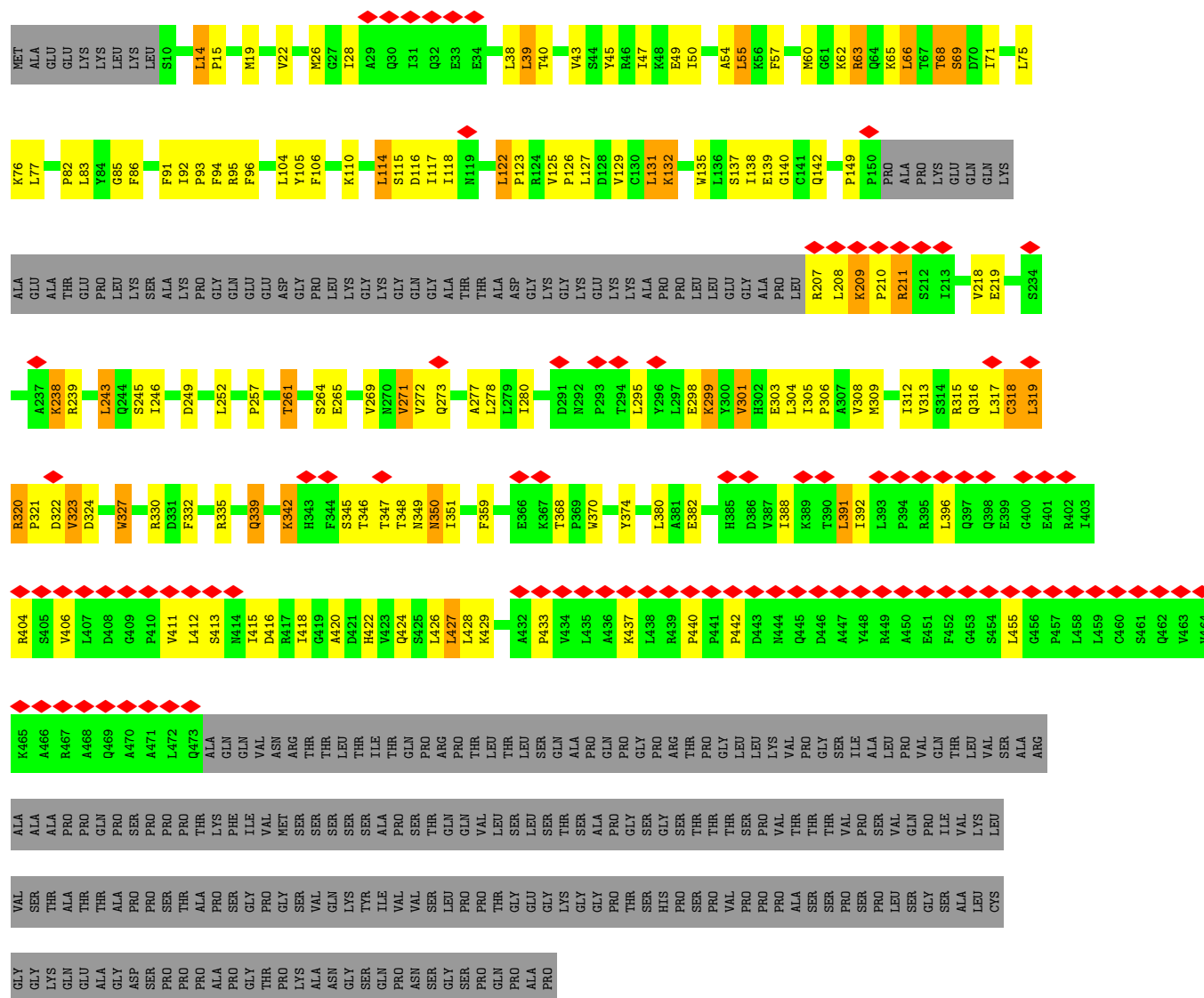
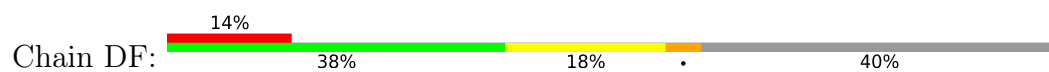


Chain Dd: 15%
13% 85%

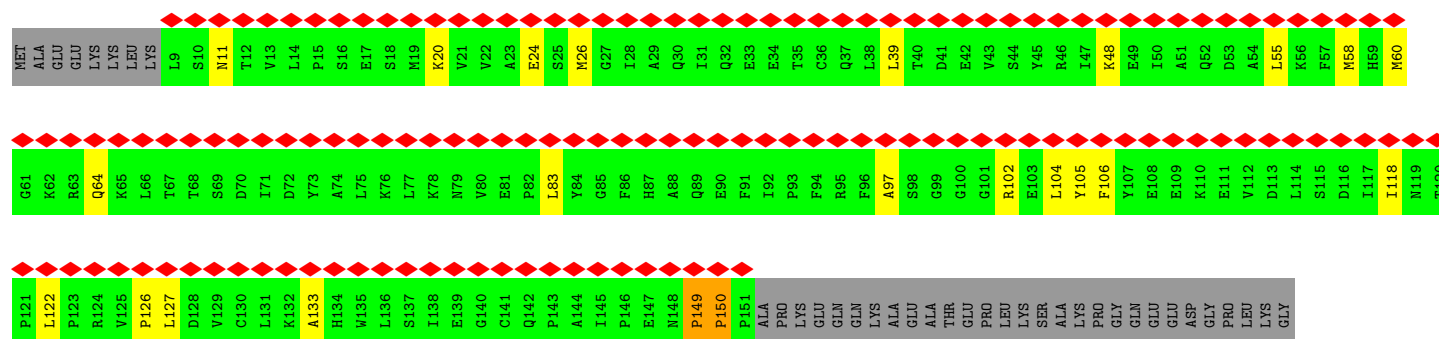




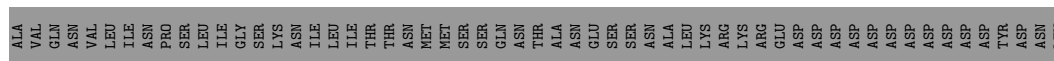
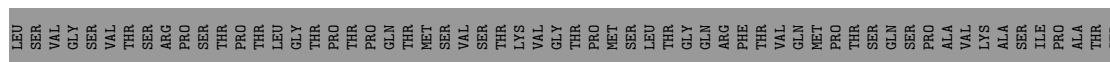




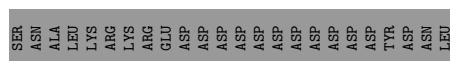
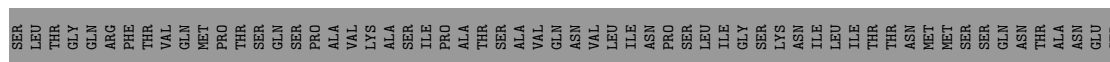
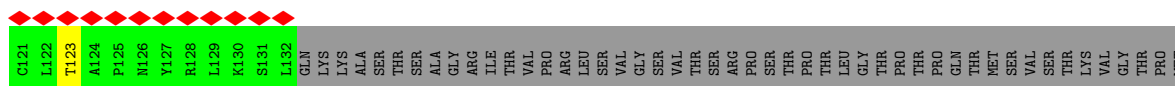
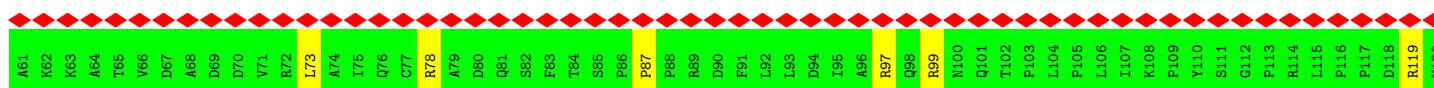
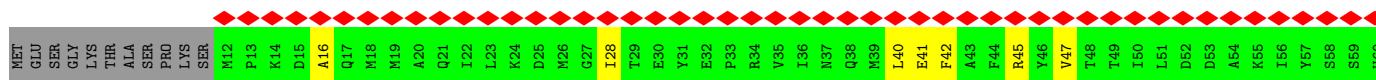
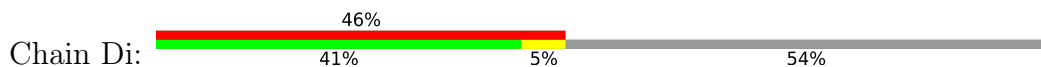
• Molecule 26: Transcription initiation factor TFIID subunit 6



- Molecule 29: Transcription initiation factor TFIID subunit 9

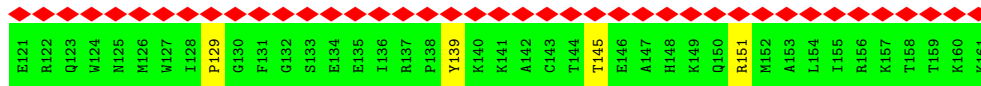


- Molecule 29: Transcription initiation factor TFIID subunit 9

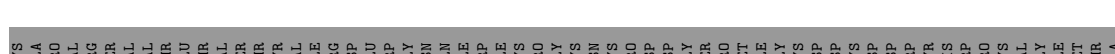
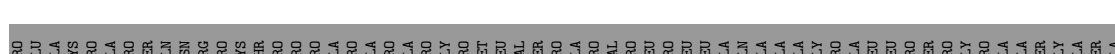
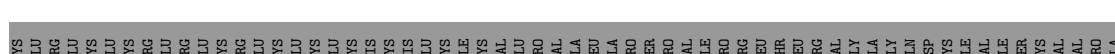
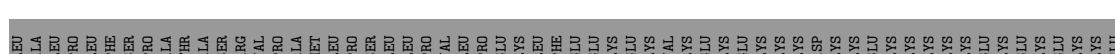
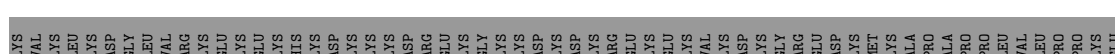
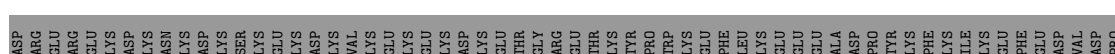
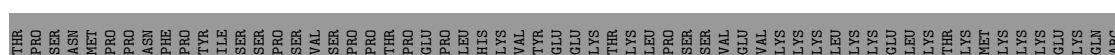
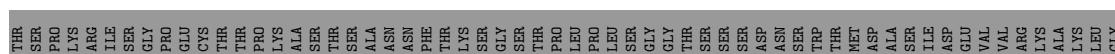
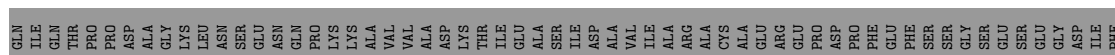
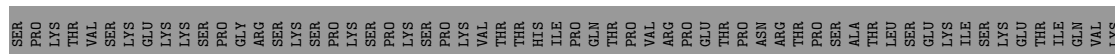
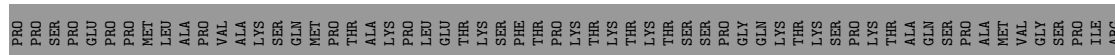
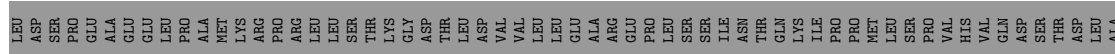
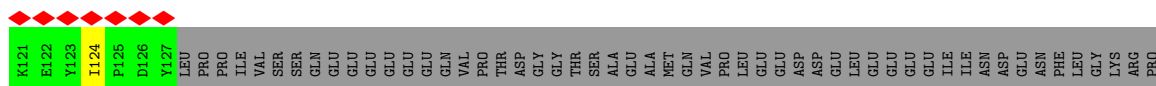
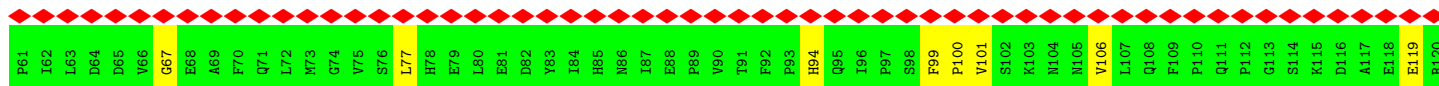


- Molecule 30: Transcription initiation factor TFIID subunit 10

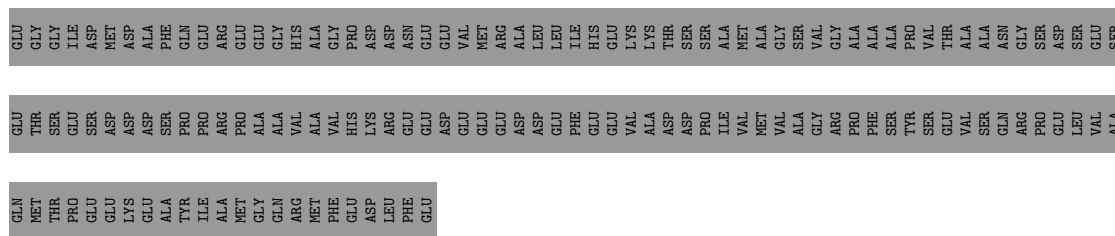




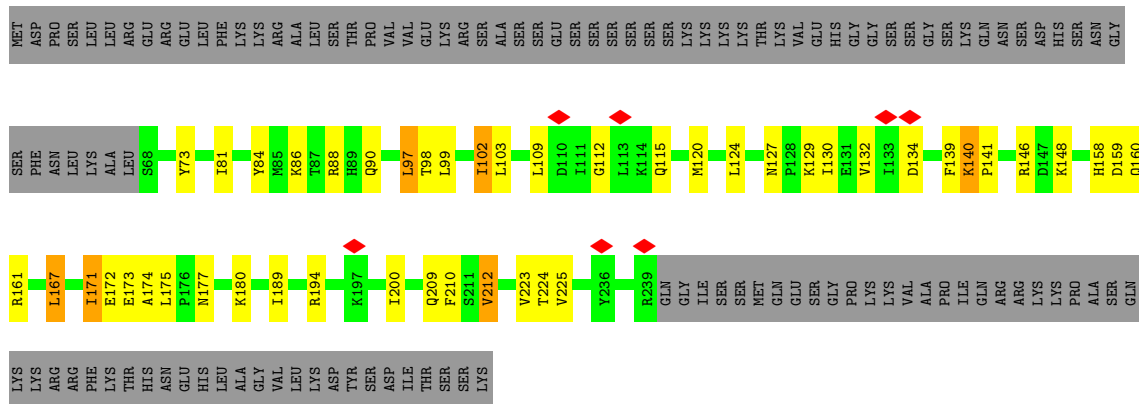
Chain Dc: 14% 12% 86%



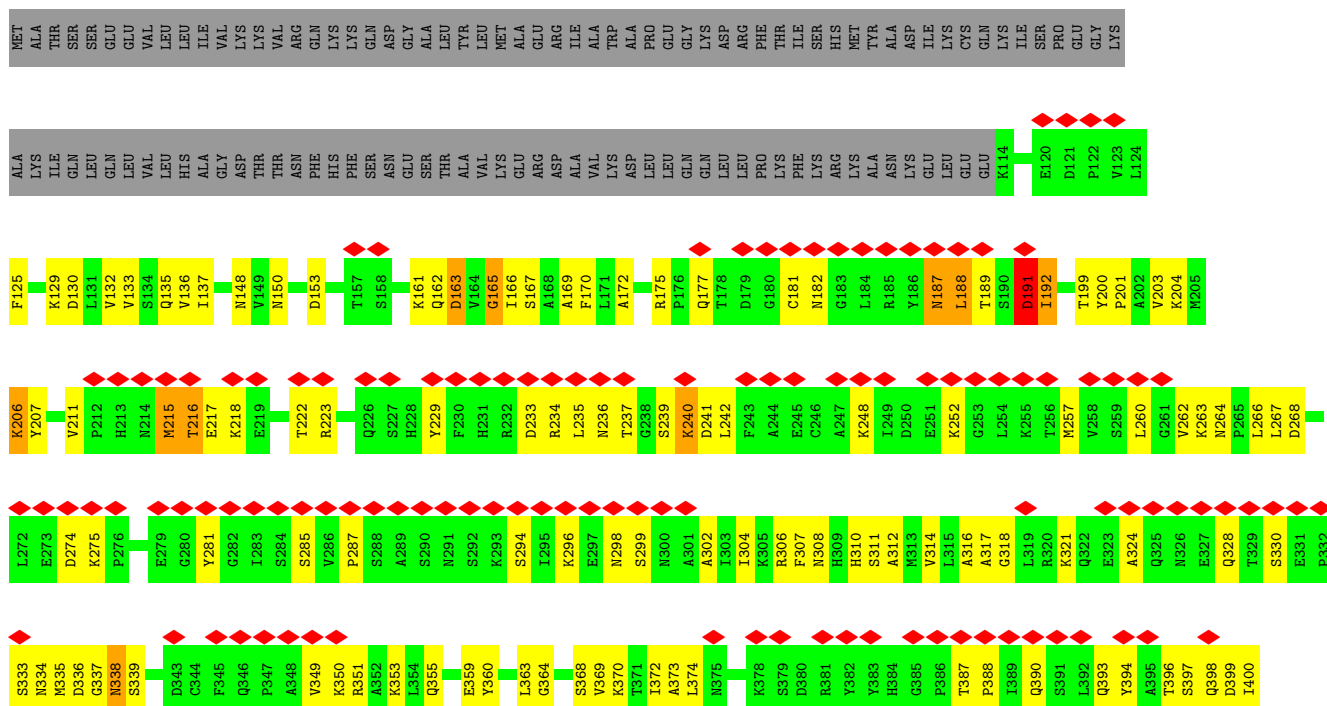


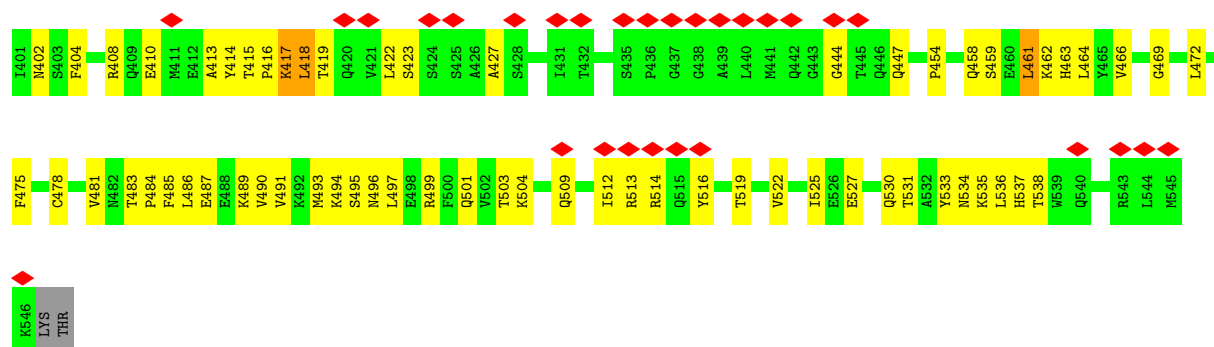


- Molecule 36: Transcription initiation factor IIE subunit beta

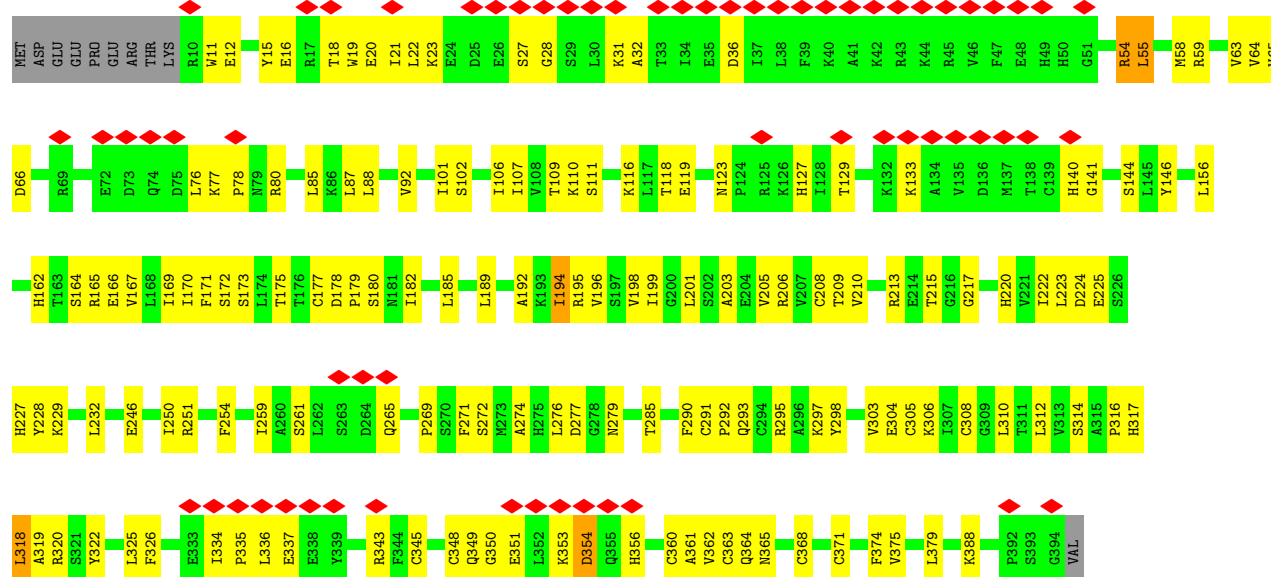


- Molecule 37: General transcription factor IIH subunit 1

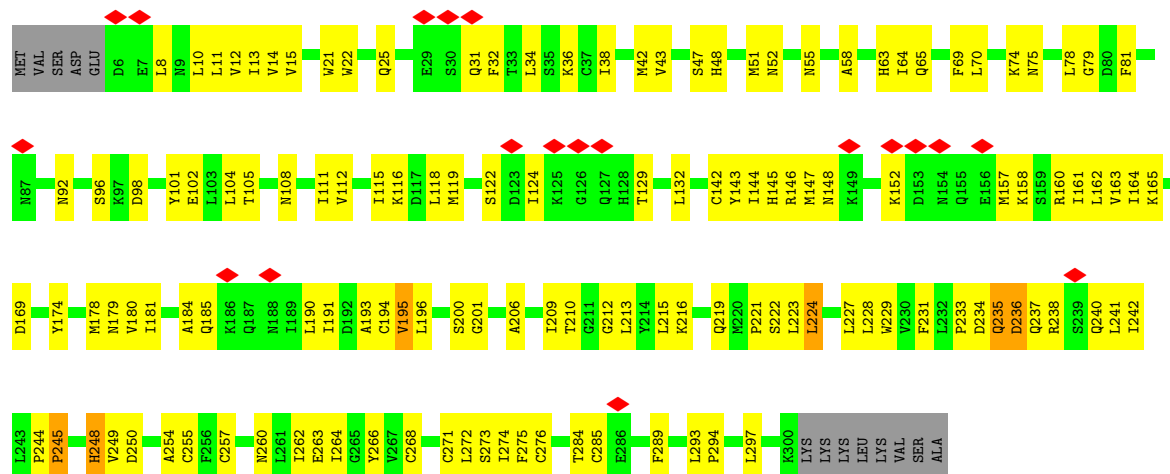




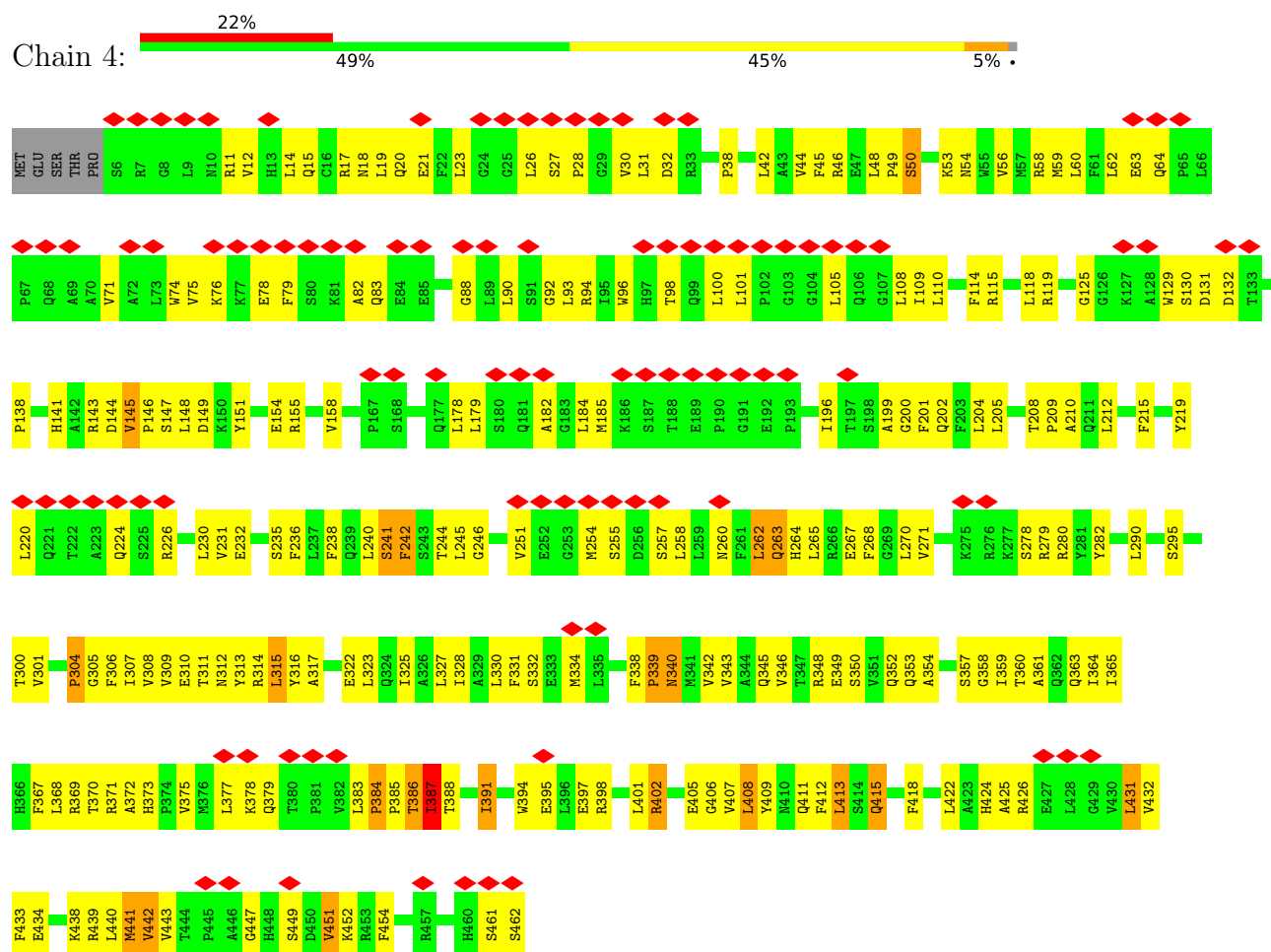
• Molecule 38: General transcription factor IIH subunit 2



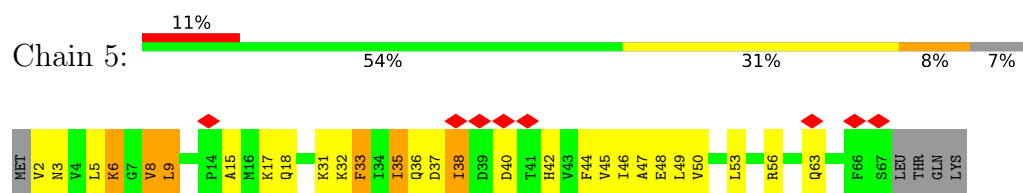
• Molecule 39: General transcription factor IIH subunit 3



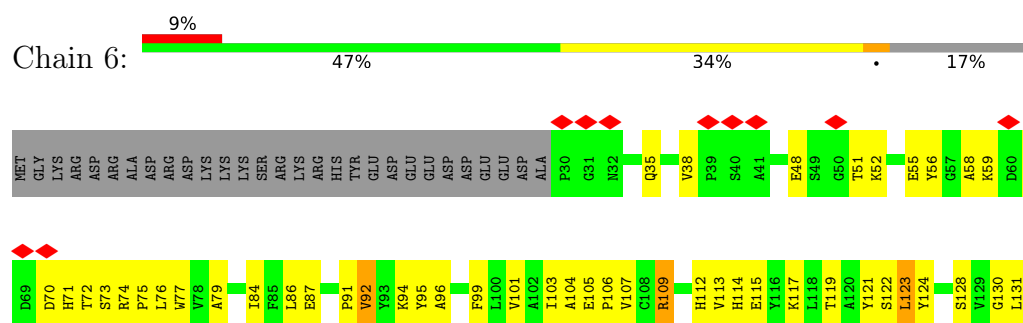
• Molecule 40: General transcription factor IIH subunit 4

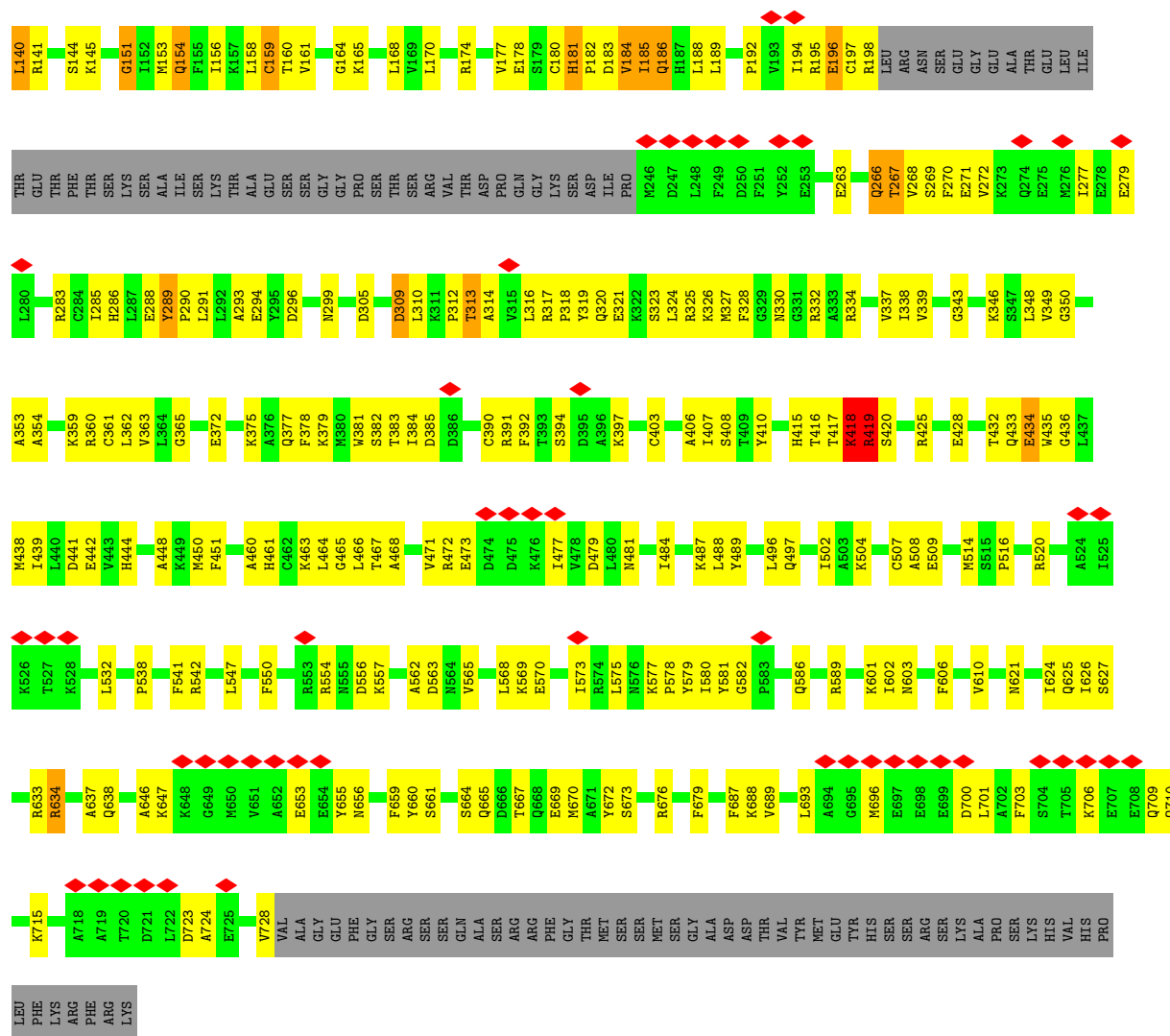


• Molecule 41: General transcription factor IIH subunit 5



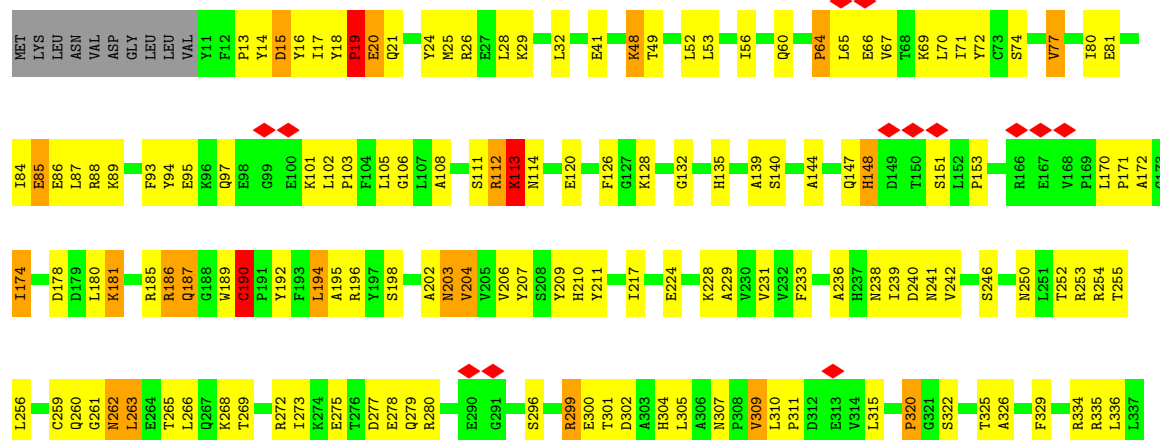
• Molecule 42: General transcription and DNA repair factor IIH helicase subunit XPB

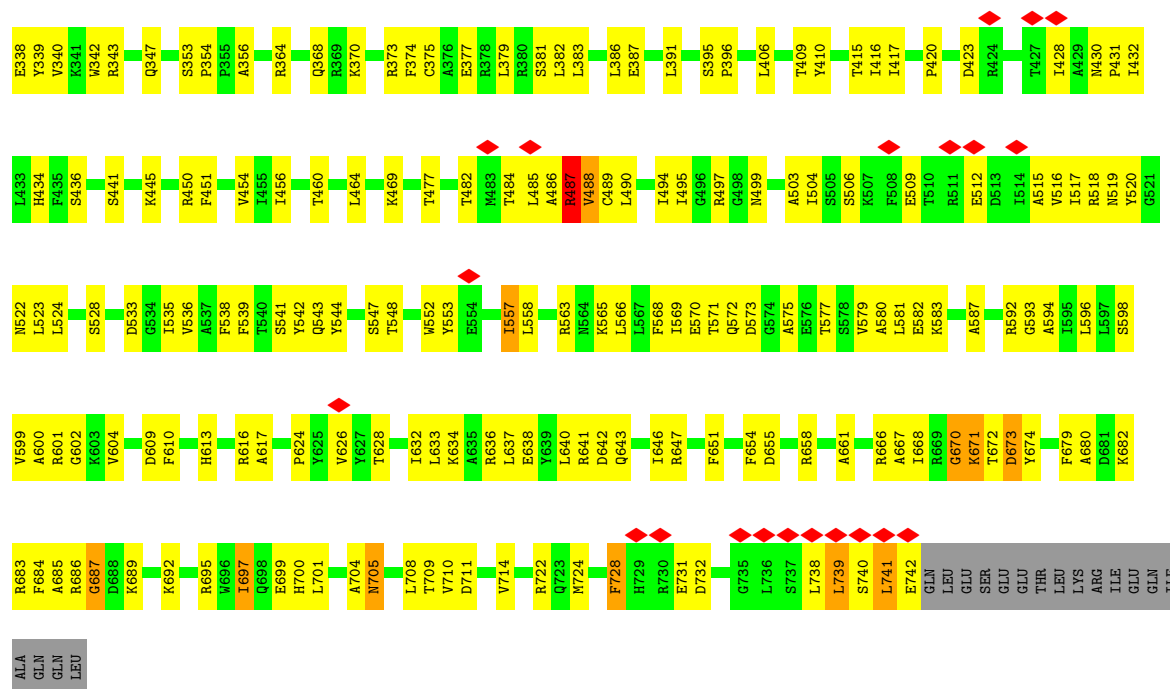




- Molecule 43: General transcription and DNA repair factor IIH helicase subunit XPD

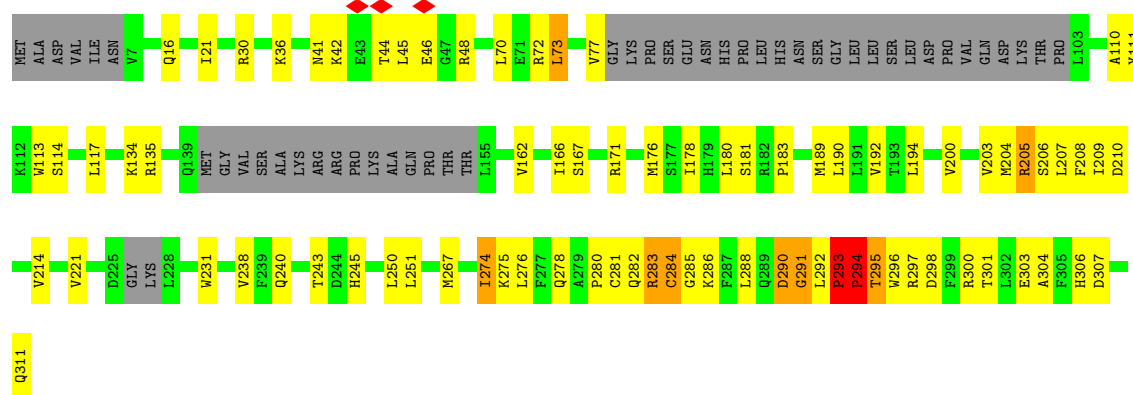
Chain 7: 53% 39% . . .





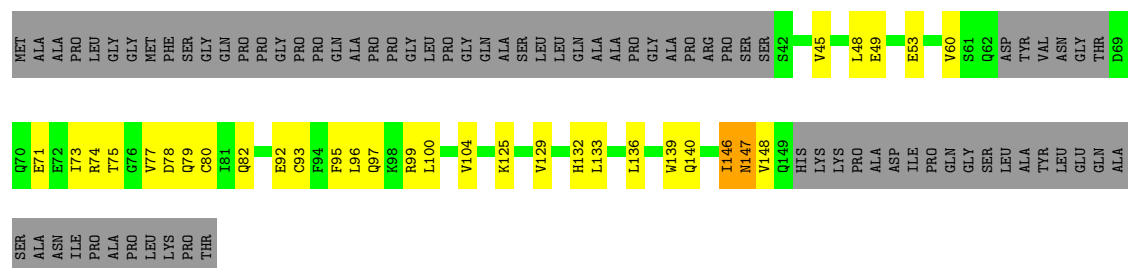
• Molecule 44: Mediator of RNA polymerase II transcription subunit 27

Chain c: 59% 23% 15%

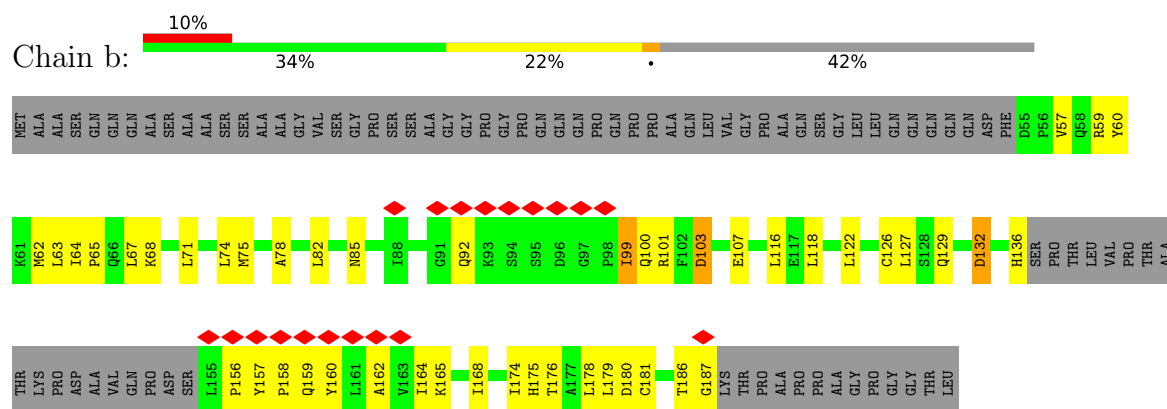


• Molecule 45: Mediator of RNA polymerase II transcription subunit 28

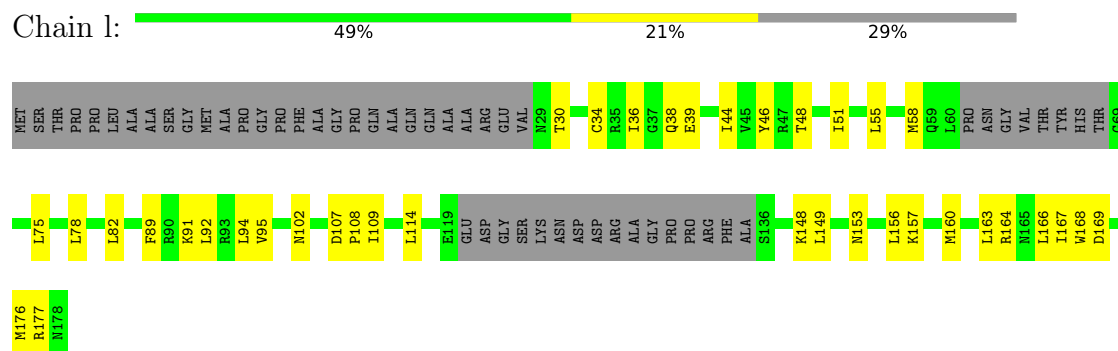
Chain e: 39% 17% 43%



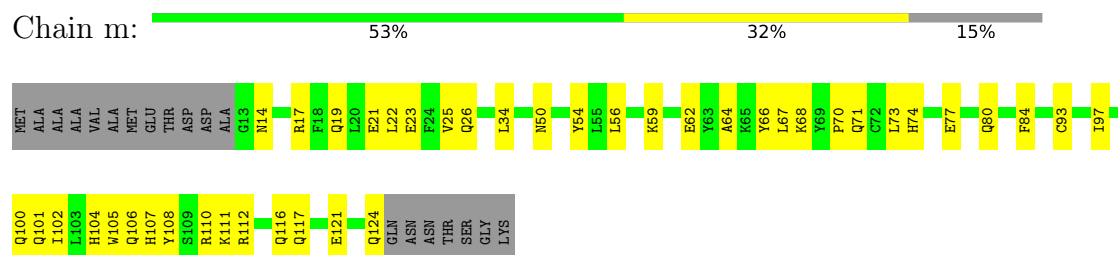
- Molecule 46: Mediator of RNA polymerase II transcription subunit 29



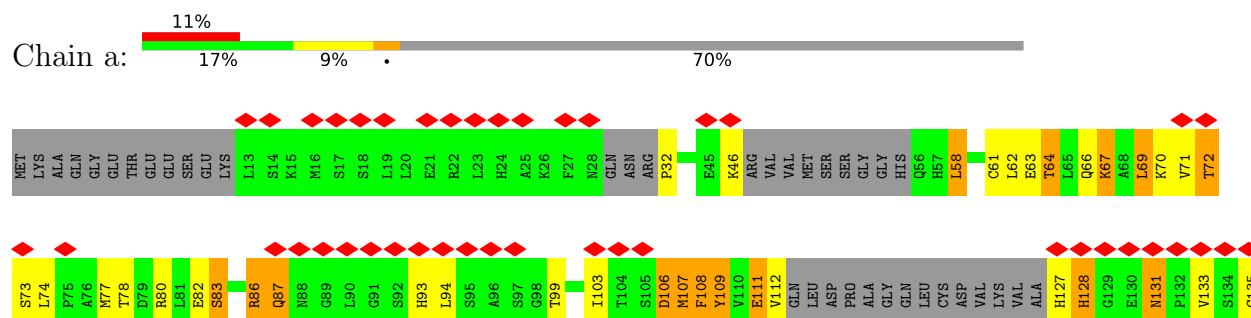
- Molecule 47: Mediator of RNA polymerase II transcription subunit 30



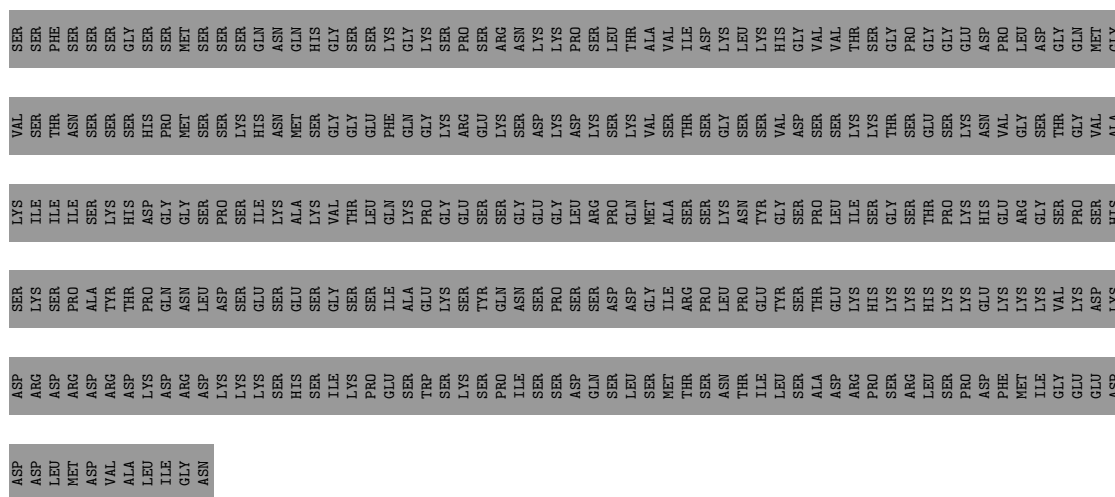
- Molecule 48: Mediator of RNA polymerase II transcription subunit 31



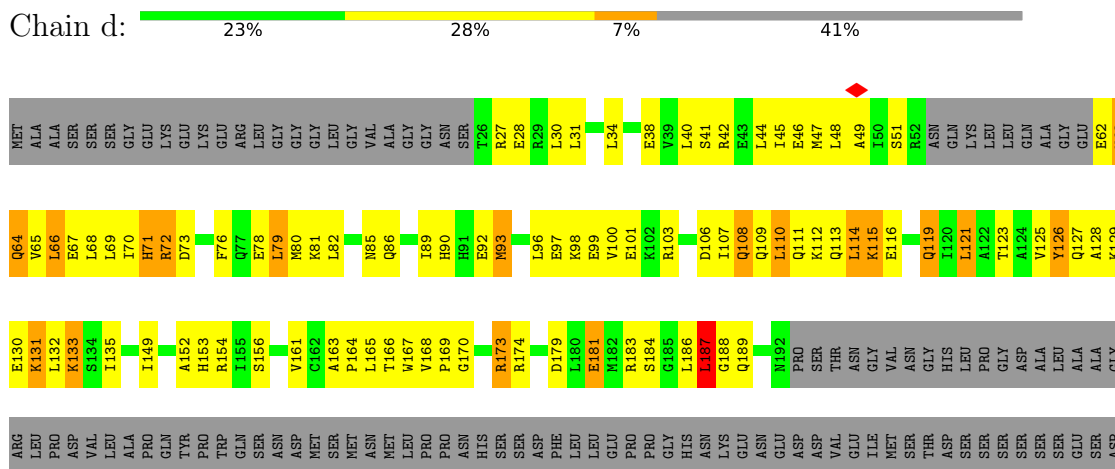
- Molecule 49: Mediator of RNA polymerase II transcription subunit 1



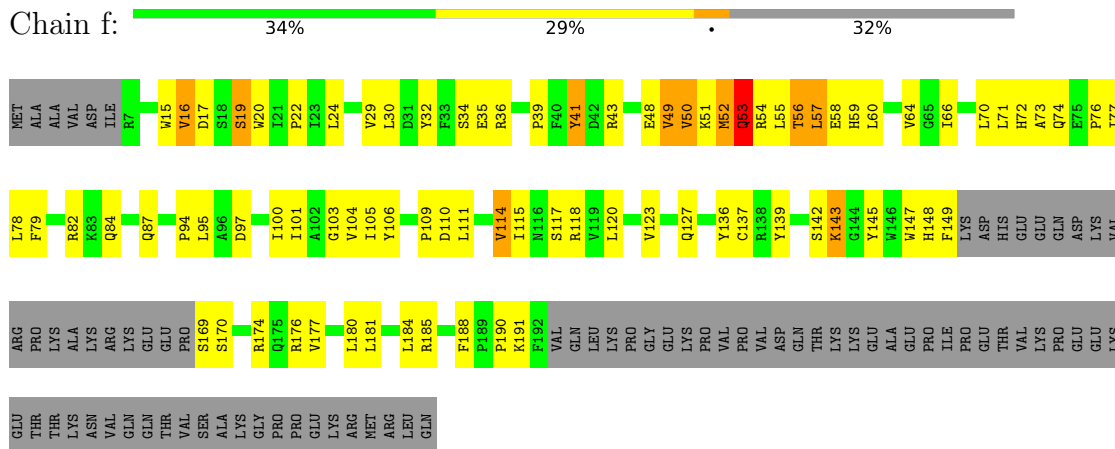
PRO	VAL	GLY	SER	PHE	ARG	LEU	SER	ASP	SER	THR	THR	D485	I421	S349	P279	G217	P136
VAL	PRO	PRO	GLY	THR	VAL	GLY	GLY	THR	SER	GLY	THR	A486	G422	K350	V280	H218	E137
GLY	GLY	GLY	PRO	PRO	GLY	GLY	ASP	ASP	GLY	ASN	GLY	L487	S423	D351	D281	L219	L138
PRO	THR	THR	THR	THR	ASN	ASN	THR	THR	SER	ASN	GLY	I488	C424	P352	N282	M220	V139
PRO	PRO	PRO	GLY	THR	GLY	GLY	PRO	PRO	PRO	PRO	THR	C489	V425	P354	K283	L221	Q140
SER	ILE	ILE	THR	THR	THR	THR	THR	THR	THR	THR	THR	F493	K427	P354	V284	Y224	
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	V497	T428	I355	T285	Y225	R143
ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	V498	L430	P356	P286	V226	K145
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	C501	K431	N357	S287	S227	K146
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	S502	A432	N358	F288	F147	E144
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	S503	D433	H359	SER	D230	D148
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	S504	S434	N360	ILE	L231	E149
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	S505	P435	K361	THR	L232	F150
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	V506	G436	G436	SER	D233	S151
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	T507	L437	Y364	ALA	D234	K152
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	N508	L438	L367	THR	LYS	K157
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	R509	L439	L367	THR	THR	H153
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	F440	Q439	C373	SER	ALA	K155
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	E441	E441	Y374	V297	SER	G156
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	C443	C443	F375	D298	PRO	L157
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	P444	P444	N377	I241	I241	V158
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	L445	L445	K378	I242	I242	N159
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	S446	S446	D379	H243	H243	L160
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	E447	E447	A380	E244	E244	Y161
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	F450	F450	P308	N245	N245	M162
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	S451	S451	Q309	N246	N246	L163
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	V452	V452	P310	V247	V247	P164
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	S453	S453	G384	S248	S248	G165
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	F454	F454	G385	R249	R249	D166
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	G455	G455	F317	G249	G249	N167
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	H456	H456	V318	S250	S250	K168
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	P457	P457	Q319	L251	L251	L170
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	V458	V458	Q319	G252	G252	K172
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	M459	M459	K320	N253	N253	M173
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	D460	D460	L321	E260	E260	L177
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	S461	S461	Q322	G261	G261	M187
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	L462	L462	N323	T262	T262	V192
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	V463	V463	G324	S263	S263	K193
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	C464	C464	T325	A264	A264	A194
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	V465	V465	G325	V265	V265	T195
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	M466	M466	T325	V266	V266	N196
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	D468	D468	G326	K267	K267	A197
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	V469	V469	I327	I270	I270	G198
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	D469	D469	P328	A271	A271	P199
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	Q470	Q470	R403	P272	P272	L200
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	S472	S472	V404	L273	L273	D201
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	V475	V475	P405	L274	L274	V208
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR			L406	M275	M275	L211
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	L479	L479	I407	G276	G276	L212
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	V480	V480	T332	S277	S277	P213
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	K481	K481	Q333	R214	R214	
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	G482	G482	T335			
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	L483	L483	Y336			
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	S484	S484	P338			
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR			L339			
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR			Y340			
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR			E341			
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR			T344			
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR			Q345			
THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR			L348			



- Molecule 50: Mediator of RNA polymerase II transcription subunit 4

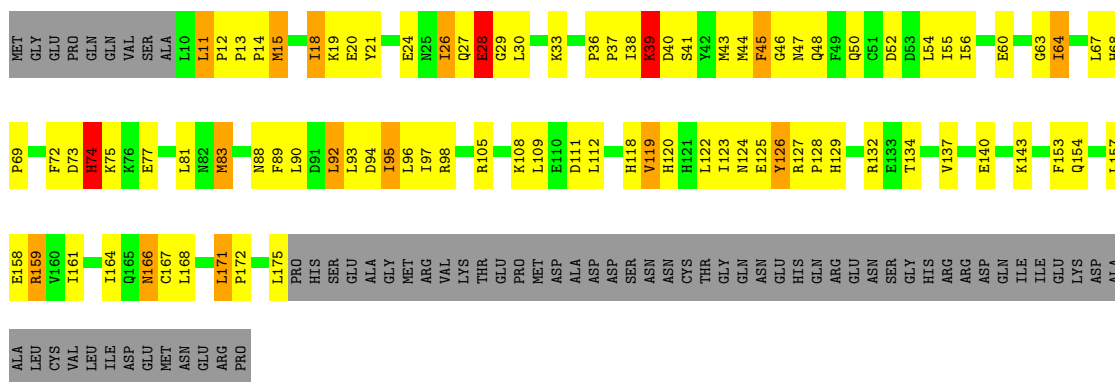


- Molecule 51: Mediator of RNA polymerase II transcription subunit 6

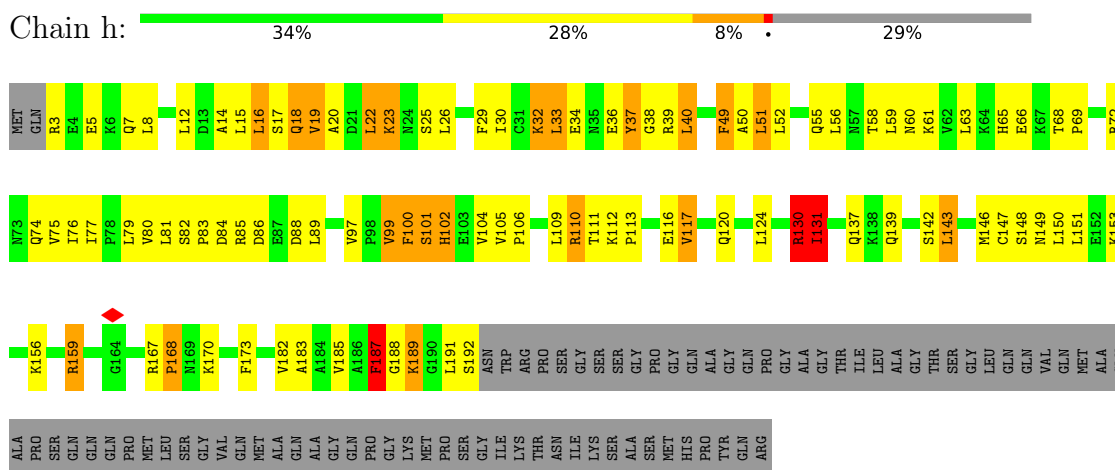


- Molecule 52: Mediator of RNA polymerase II transcription subunit 7

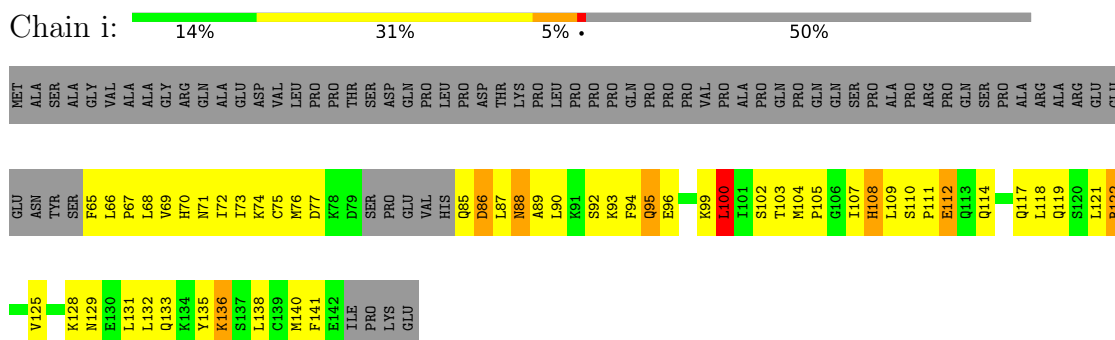




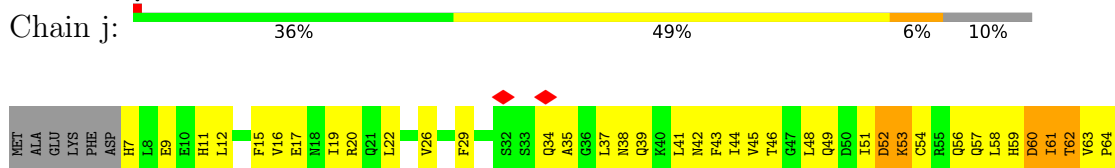
- Molecule 53: Isoform 2 of Mediator of RNA polymerase II transcription subunit 8



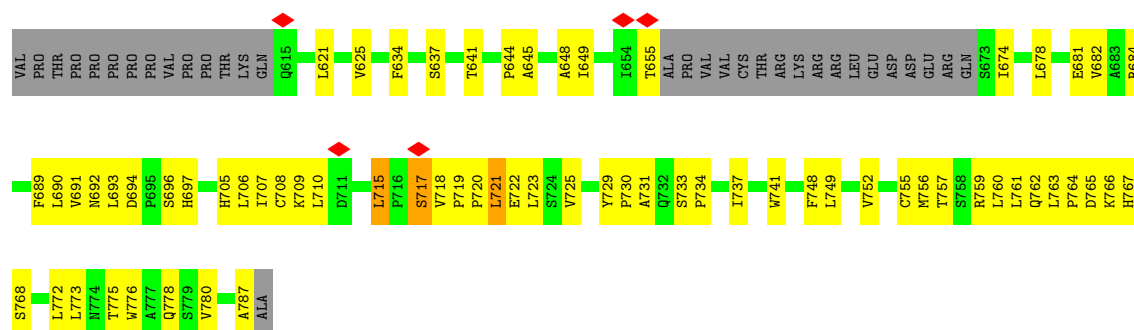
- Molecule 54: Mediator of RNA polymerase II transcription subunit 9



- Molecule 55: Mediator of RNA polymerase II transcription subunit 10

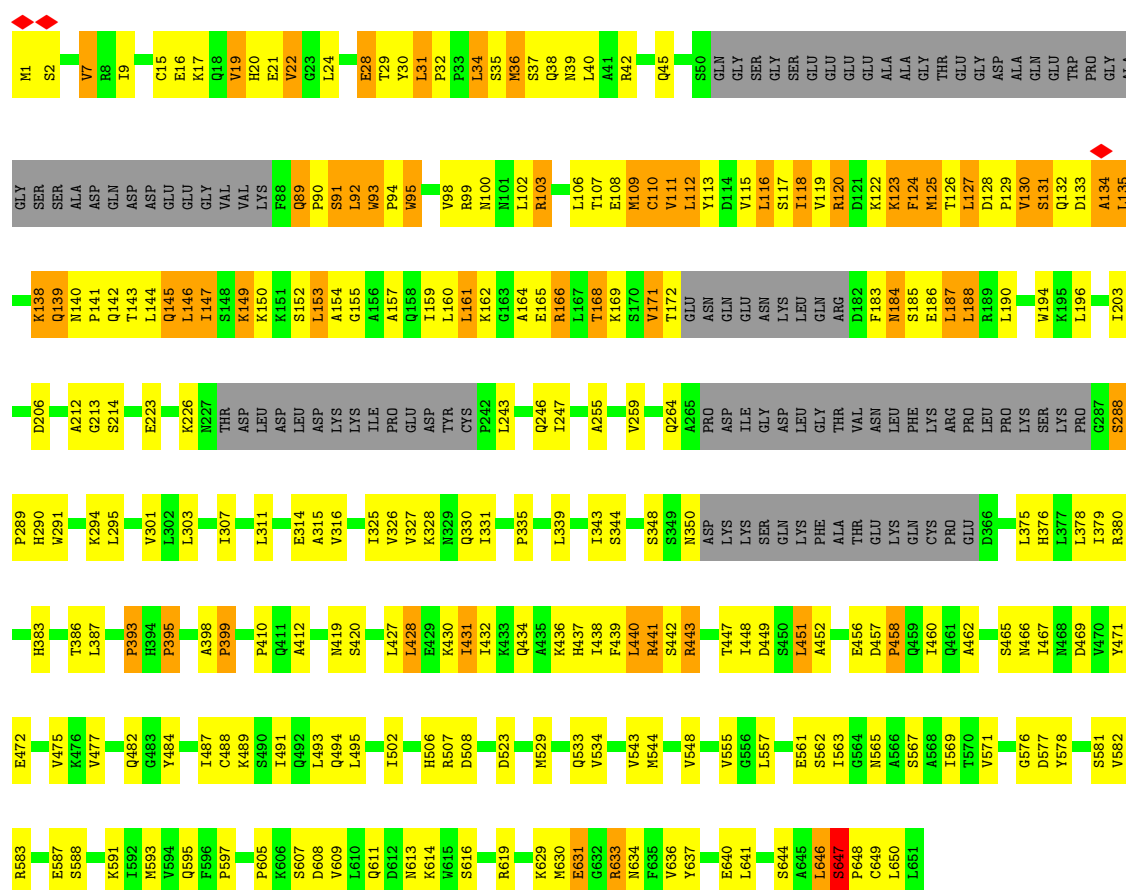






• Molecule 59: Mediator of RNA polymerase II transcription subunit 17

Chain q: 46% 30% 9% 15%



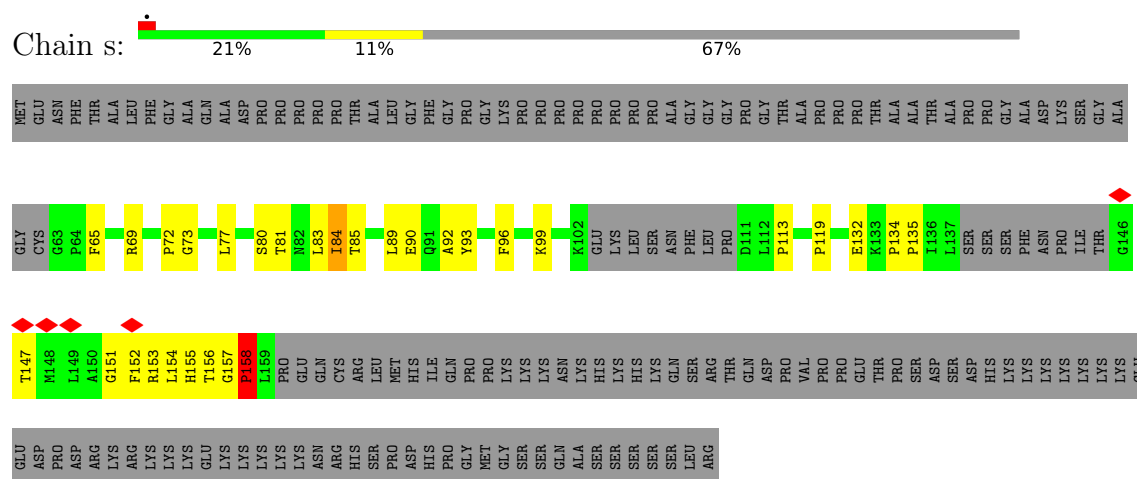
• Molecule 60: Mediator of RNA polymerase II transcription subunit 18

Chain r: 65% 27% 6%

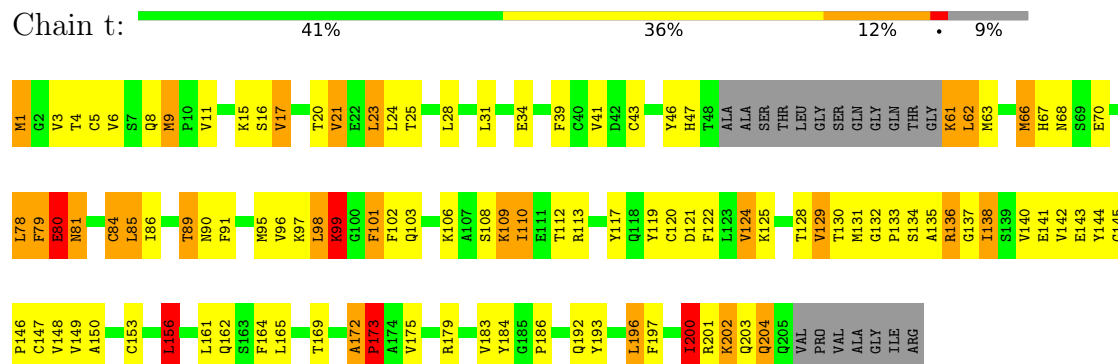




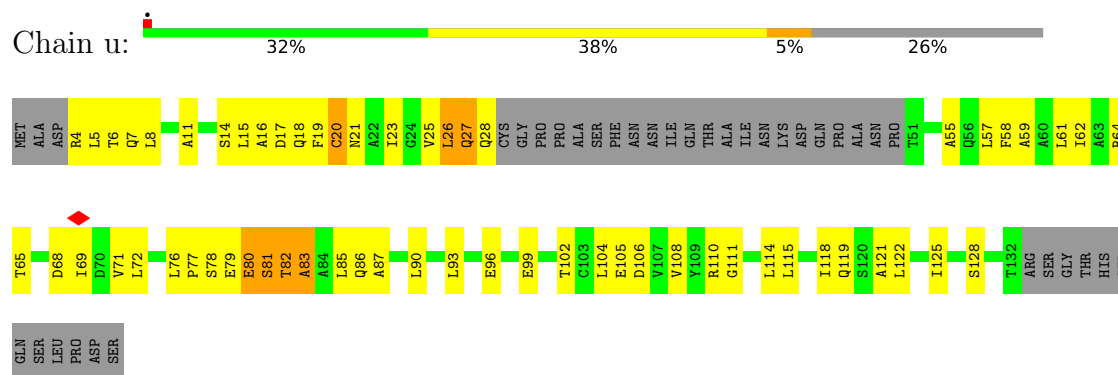
• Molecule 61: Mediator of RNA polymerase II transcription subunit 19



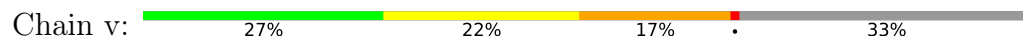
• Molecule 62: Mediator of RNA polymerase II transcription subunit 20

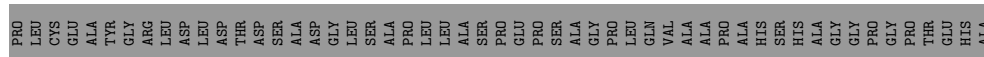


• Molecule 63: Mediator of RNA polymerase II transcription subunit 21

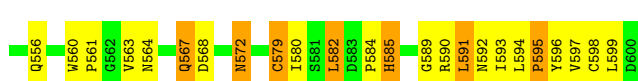


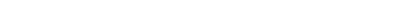
• Molecule 64: Mediator of RNA polymerase II transcription subunit 22

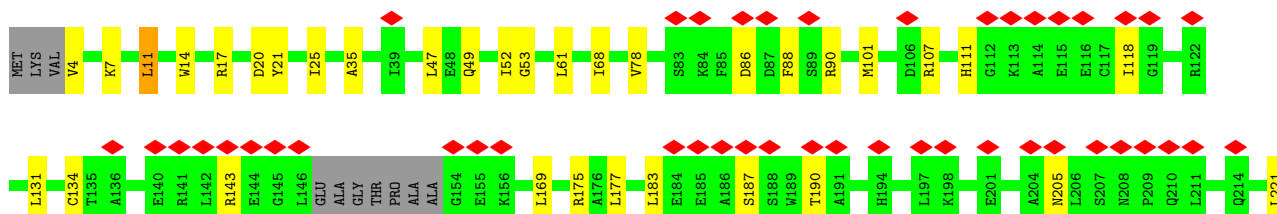


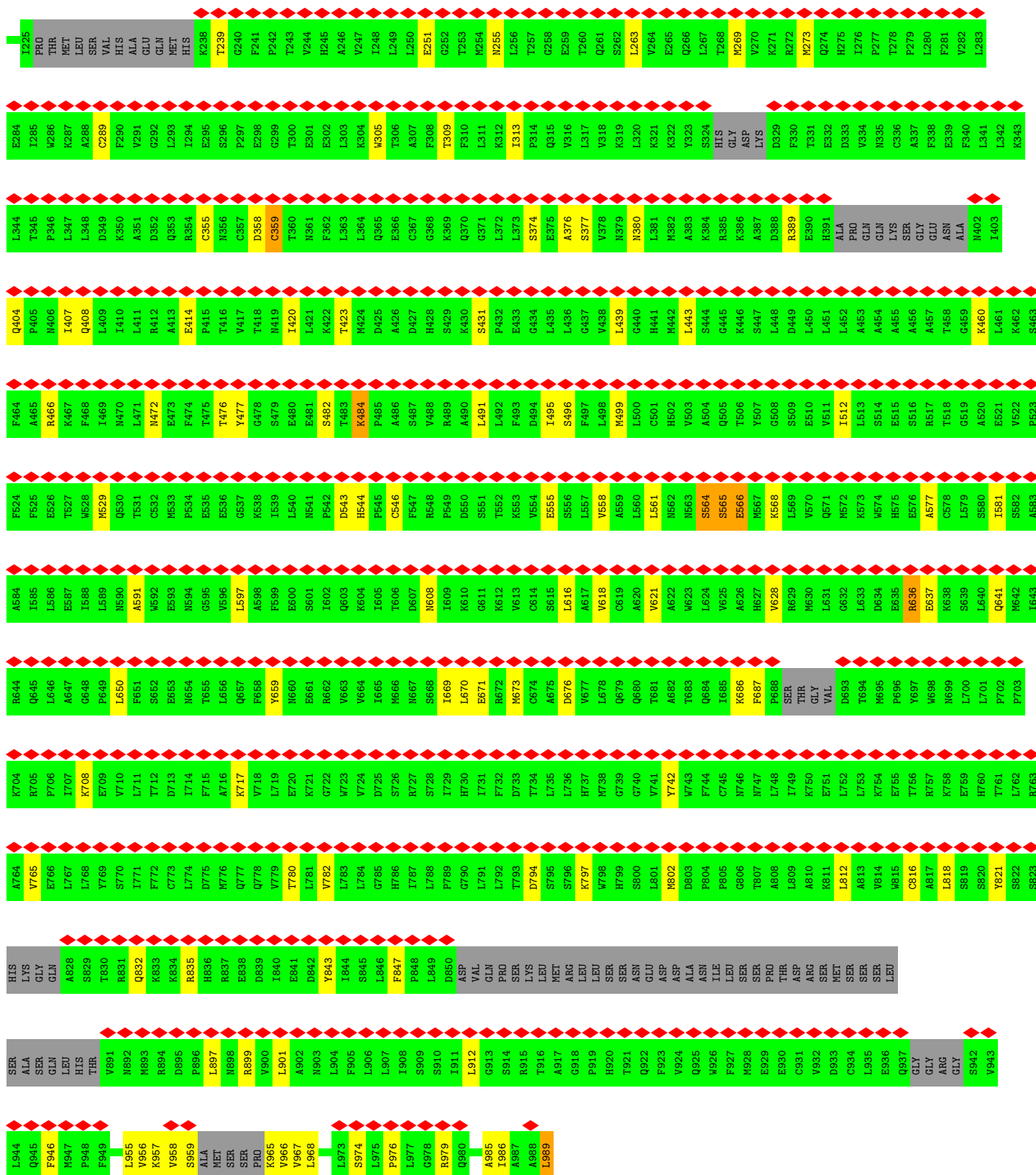


Chain z: 9% 5% 84%



Chain x:  71% 76% 14% 9%

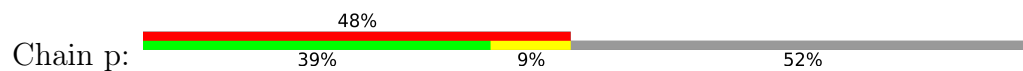




• Molecule 67: Mediator of RNA polymerase II transcription subunit 23

T1333	A1273	H1213	I1153	R1093	S1033	R973	L913	M853
H1334	F1274	A1214	T1154	F1094	L1034	F974	Q914	M854
ILE	Y1275	V1215	A1155	N1095	K1035	L975	N915	M855
SER	D1276	W1216	L1156	E1096	D1036	E976	D916	M856
MET	M1277	H1217	P1157	F1097	N1037	L977	W917	M857
GLJ	L1278	H1218	E1158	P1098	R1038	L978	H918	M858
PRO	L1279	S1219	P1159	N1099	P1039	P979	T919	M859
ALA	N1280	S1220	Y1160	P1100	Q1040	V980	K920	M860
ALA	V1281	I1221	W1161	A1101	G1041	S981	H921	M861
PRO	D1282	G1222	I1162	A1102	W1042	K982	K922	M862
PRO	Q1283	L1223	V1163	H1103	C1043	S983	N923	M863
GLN	C1284	L1224	L1164	A1104	L1044	L984	Y924	M864
ALA	S1285	S1225	H1165	L1105	S1045	E985	H925	M865
ASN	T1286	L1226	D1166	H1106	D1046	T986	K926	M866
SER	H1287	I1227	R1167	V1107	T1047	L987	K927	M867
GLY	L1288	P1228	I1168	T1108	Y1048	L988	Y928	M868
SER	L1289	K1229	V1169	C1109	L1049	D989	P929	M869
PRO	N1289	F1230	S1170	V1110	K1050	H990	E930	M870
ALA	Y1290	L1231	I1171	E1111	C1051	L991	K931	M871
PRO	M1291	T1232	I1172	L1112	A1052	G992	L932	M872
SER	D1292	E1233	S1173	M1113	M1053	G993	Y933	M873
ASN	P1293	V1234	S1174	A1114	N1054	L994	F934	M874
GLN	I1294	L1235	P1175	L1115	A1055	Y995	E935	M875
VAL	C1295	L1236	S1176	A1116	R1056	K996	G936	M876
PRO	D1296	L1237	S1177	V1117	E1057	F997	L937	M877
SER	F1297	P1237	L1177	V1117	E1058	H998	A938	M878
LEU	L1298	I1238	T1178	S1118	G1119	D999	E939	M879
PRO	L1299	V1239	S1179	G1119	P1060	R1000	Q940	M880
VAL	H1300	K1240	E1180	K1120	W1061	P1001	V941	M881
THR	M1301	T1241	T1181	E1121	V1062	V1002	D942	M882
GLN	K1302	E1242	E1182	V1122	P1063	T1003	P943	M883
	Y1303	F1243	W1183	G1123	D1064	Y1004	P944	M884
M1304	M1304	Q1244	V1184	A1124	D1065	L1005	P945	M885
F1305	F1305	L1245	G1185	A1125	T1066	Y1006	Q946	M886
T1306	T1306	L1246	Y1186	L1126	Y1067	N1007	I947	M887
G1307	G1307	V1247	P1187	L1127	Y1068	T1008	Q948	M888
D1308	D1308	V1248	F1188	N1128	C1069	L1009	S949	M889
S1309	S1309	Y1249	R1189	V1129	R1070	H1010	P950	M890
V1310	V1310	H1250	L1190	V1130	L1071	Y1011	Y951	M891
K1311	K1311	L1251	F1191	L1131	I1072	Y1012	L952	M892
E1312	E1312	V1252	D1192	K1132	S1133	E1013	P953	M893
Q1313	Q1313	G1253	F1193	S1133	G1073	M1014	Y954	M894
V1314	V1314	P1254	T1194	Q1134	R1074	H1015	Y955	M895
E1315	E1315	F1255	A1195	P1135	L1075	L1016	F956	M896
K1316	K1316	L1256	C1196	L1136	V1076	R1017	G957	M897
I1317	I1317	Q1257	H1197	V1137	D1077	D1018	N958	M898
L1318	L1318	R1258	Q1198	P1138	T1078	R1019	V959	M899
C1319	C1319	F1259	S1199	R1139	M1079	A1020	C960	M900
N1320	N1320	Q1260	Y1200	E1140	A1080	F1021	L961	M901
L1321	L1321	Q1261	S1201	N1141	K1081	L1022	R962	M902
K1322	K1322	E1262	E1202	I1142	K1082	K1023	F963	M903
P1323	P1323	R1263	M1203	T1143	S1083	R1024	V904	M904
A1324	A1324	T1264	S1204	A1144	P1084	K1025	P965	M905
L1325	L1325	R1265	C1205	W1145	G1085	L1026	V966	M906
K1326	K1326	C1266	S1206	M1146	P1086	V1027	F967	M907
L1327	L1327	M1267	Y1207	N1147	F1087	H1028	D968	M908
R1328	R1328	I1268	T1208	A1148	P1088	A1029	P969	M909
L1329	L1329	E1269	L1209	I1149	M1089	I1030	V970	M910
R1330	R1330	I1270	A1210	G1150	C1090	H911	H971	M911
F1331	F1331	G1271	L1211	L1151	D1091	T1031	H972	M912
I1332	I1332	V1272	A1212	T1152	W1092	G1032		

• Molecule 68: Isoform 2 of Mediator of RNA polymerase II transcription subunit 16



MET	CYS	ASP	LEU	ARG	ARG	PRO	ALA	ALA	GLY	GLY	MET	M13	D14	L15	A16	V17	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	F77	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	I104	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	D162	G163	F164	S165	P166	S167	L168	T169	L170	F171	G172	G173	K174	P175	M176	E177	G178	W179	I180

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	48654	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	8.884	Depositor
Minimum map value	-4.573	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.113	Depositor
Recommended contour level	0.5	Depositor
Map size ($\text{\AA}$)	674.56, 674.56, 674.56	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.3175, 1.3175, 1.3175	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.89	3/2288 (0.1%)	1.34	29/3101 (0.9%)
2	8	1.01	0/2437	1.65	50/3306 (1.5%)
3	9	1.10	3/2356 (0.1%)	1.72	53/3185 (1.7%)
4	DO	0.84	0/781	1.20	6/1061 (0.6%)
5	DP	0.95	0/1438	1.25	4/1935 (0.2%)
6	DQ	0.79	0/1013	1.12	2/1366 (0.1%)
7	BA	0.70	1/1987 (0.1%)	1.26	22/2684 (0.8%)
8	FA	0.69	0/1130	0.96	0/1528
9	FB	0.84	0/1817	1.17	5/2445 (0.2%)
10	PA	1.12	37/11888 (0.3%)	1.70	214/16066 (1.3%)
11	PB	1.19	39/9243 (0.4%)	1.68	167/12475 (1.3%)
12	PC	1.34	15/2102 (0.7%)	1.88	63/2857 (2.2%)
13	PD	0.90	0/1036	1.80	16/1397 (1.1%)
14	PE	0.89	1/1751 (0.1%)	1.59	22/2366 (0.9%)
15	PF	1.28	3/645 (0.5%)	1.71	10/871 (1.1%)
16	PG	1.01	2/1365 (0.1%)	1.79	22/1853 (1.2%)
17	PH	1.02	0/1207	1.70	25/1628 (1.5%)
18	PI	0.93	0/948	1.72	19/1284 (1.5%)
19	PJ	1.32	2/516 (0.4%)	1.83	13/696 (1.9%)
20	PK	1.30	8/956 (0.8%)	1.75	25/1294 (1.9%)
21	PL	1.09	1/377 (0.3%)	1.56	3/500 (0.6%)
22	DA	0.65	0/5037	0.93	8/6794 (0.1%)
23	DB	0.50	1/7993 (0.0%)	0.71	6/10836 (0.1%)
24	DD	0.86	1/1343 (0.1%)	1.25	4/1795 (0.2%)
24	Dd	0.24	0/1321	0.44	0/1772
25	DE	0.54	1/4469 (0.0%)	0.77	7/6050 (0.1%)
25	De	0.31	0/4433	0.53	0/6004
26	DF	0.79	0/3167	1.12	6/4303 (0.1%)
26	Df	0.56	0/3140	0.86	9/4268 (0.2%)
27	DG	0.71	0/1199	0.94	0/1612
28	DH	0.64	0/1673	0.86	0/2285
29	DI	0.69	1/981 (0.1%)	0.90	2/1332 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
29	Di	0.23	0/989	0.41	0/1343
30	DJ	0.66	0/736	0.91	0/998
30	Dj	0.24	0/775	0.45	0/1049
31	DL	0.62	0/622	0.98	1/841 (0.1%)
31	Dl	0.34	0/888	0.60	0/1194
32	Dc	0.49	0/1035	0.67	0/1406
33	Dk	0.30	0/799	0.53	1/1070 (0.1%)
34	Dm	0.32	0/733	0.56	0/977
35	EA	0.92	0/1499	1.32	5/2012 (0.2%)
36	EB	0.96	0/1428	1.20	1/1917 (0.1%)
37	1	0.43	1/3502 (0.0%)	0.90	6/4731 (0.1%)
38	2	0.43	0/3094	0.85	4/4188 (0.1%)
39	3	0.48	0/2353	0.96	7/3187 (0.2%)
40	4	0.62	1/3729 (0.0%)	1.04	11/5053 (0.2%)
41	5	0.72	0/528	1.14	3/713 (0.4%)
42	6	0.45	0/5365	0.90	12/7247 (0.2%)
43	7	0.57	3/5984 (0.1%)	0.96	25/8104 (0.3%)
44	c	0.63	0/2146	1.00	14/2899 (0.5%)
45	e	0.19	0/840	0.34	0/1128
46	b	0.75	0/911	1.08	0/1229
47	l	0.18	0/1048	0.36	0/1405
48	m	0.18	0/1010	0.38	0/1359
49	a	0.94	1/3660 (0.0%)	1.33	11/4971 (0.2%)
50	d	0.92	0/1281	1.30	1/1718 (0.1%)
51	f	0.80	1/1359 (0.1%)	1.07	3/1845 (0.2%)
52	g	0.90	0/1411	1.43	4/1901 (0.2%)
53	h	0.92	0/1485	1.31	5/2008 (0.2%)
54	i	0.99	1/612 (0.2%)	1.31	0/815
55	j	0.56	1/1016 (0.1%)	0.84	5/1363 (0.4%)
56	k	0.98	0/885	1.28	0/1190
57	n	0.42	0/7371	0.68	18/10037 (0.2%)
58	o	0.42	0/1256	0.82	1/1724 (0.1%)
59	q	0.68	2/4351 (0.0%)	0.87	5/5886 (0.1%)
60	r	0.93	1/1663 (0.1%)	1.35	7/2241 (0.3%)
61	s	0.84	0/510	1.18	6/694 (0.9%)
62	t	1.08	3/1530 (0.2%)	1.51	13/2066 (0.6%)
63	u	0.48	0/797	0.72	0/1082
64	v	0.97	0/1092	1.42	5/1468 (0.3%)
65	z	0.94	0/781	1.34	2/1067 (0.2%)
66	x	0.56	0/7179	0.70	5/9712 (0.1%)
67	w	0.56	0/11053	0.73	8/15018 (0.1%)
68	p	0.71	0/3191	0.78	2/4333 (0.0%)
69	X	0.60	1/1607 (0.1%)	0.92	6/2481 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
70	Y	0.57	0/1565	0.92	9/2410 (0.4%)
All	All	0.77	135/177706 (0.1%)	1.14	1018/241029 (0.4%)

The worst 5 of 135 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	q	264	GLN	C-N	13.59	1.52	1.33
62	t	119	TYR	C-N	11.68	1.48	1.33
59	q	452	ALA	C-N	9.14	1.47	1.33
10	PA	685	HIS	C-O	-8.97	1.14	1.23
11	PB	965	ILE	C-O	-8.96	1.14	1.23

The worst 5 of 1018 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
69	X	3	DT	P-O3'-C3'	-11.23	103.35	120.20
58	o	719	PRO	N-CA-C	11.13	124.28	110.70
11	PB	982	ILE	N-CA-C	-10.98	101.24	111.45
11	PB	805	PHE	CA-CB-CG	10.80	124.60	113.80
12	PC	63	PHE	N-CA-C	-10.56	99.99	113.72

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	0	2255	0	2006	146	0
2	8	2378	0	2397	191	0
3	9	2307	0	2314	148	0
4	DO	771	0	764	41	0
5	DP	1412	0	1506	97	0
6	DQ	996	0	926	31	0
7	BA	1959	0	1987	118	0
8	FA	1101	0	1065	88	0
9	FB	1788	0	1819	133	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	PA	11662	0	11737	501	0
11	PB	9062	0	9110	381	0
12	PC	2059	0	2007	108	0
13	PD	1021	0	979	131	0
14	PE	1720	0	1737	79	0
15	PF	635	0	665	22	0
16	PG	1334	0	1333	76	0
17	PH	1186	0	1147	43	0
18	PI	927	0	859	64	0
19	PJ	507	0	523	22	0
20	PK	937	0	959	33	0
21	PL	372	0	378	11	0
22	DA	4918	0	4854	122	0
23	DB	7796	0	7751	135	0
24	DD	1330	0	1351	70	0
24	Dd	1307	0	1318	21	0
25	DE	4364	0	4244	106	0
25	De	4327	0	4197	46	0
26	DF	3109	0	3045	151	0
26	Df	3081	0	3012	81	0
27	DG	1180	0	1235	16	0
28	DH	1633	0	1621	53	0
29	DI	959	0	969	118	0
29	Di	967	0	977	31	0
30	DJ	720	0	719	70	0
30	Dj	759	0	759	18	0
31	DL	614	0	614	93	0
31	Di	876	0	893	59	0
32	Dc	1011	0	975	25	0
33	Dk	785	0	818	9	0
34	Dm	724	0	744	12	0
35	EA	1476	0	1487	43	0
36	EB	1404	0	1424	25	0
37	1	3436	0	3403	166	0
38	2	3024	0	2991	128	0
39	3	2306	0	2332	109	0
40	4	3644	0	3687	221	0
41	5	522	0	528	60	0
42	6	5255	0	5247	269	0
43	7	5861	0	5869	252	0
44	c	2108	0	2095	101	0
45	e	832	0	824	70	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
46	b	899	0	908	108	0
47	l	1040	0	1065	65	0
48	m	983	0	968	148	0
49	a	3585	0	3524	348	0
50	d	1268	0	1305	239	0
51	f	1329	0	1302	164	0
52	g	1382	0	1407	224	0
53	h	1465	0	1460	291	0
54	i	605	0	628	226	0
55	j	1001	0	1023	255	0
56	k	879	0	886	226	0
57	n	7241	0	6673	513	0
58	o	1221	0	1212	147	0
59	q	4276	0	4243	528	0
60	r	1630	0	1644	77	0
61	s	505	0	361	74	0
62	t	1499	0	1482	142	0
63	u	792	0	749	247	0
64	v	1083	0	1059	188	0
65	z	765	0	727	115	0
66	x	7050	0	7205	166	0
67	w	10772	0	10832	284	0
68	p	3124	0	3133	58	0
69	X	1429	0	769	119	0
70	Y	1400	0	774	105	0
71	0	2	0	0	0	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	PA	1	0	0	0	0
73	7	8	0	0	0	0
All	All	173965	0	171540	7785	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 23.

The worst 5 of 7785 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)
50:d:49:ALA:HB2	54:i:76:MET:SD	1.22	1.67
67:w:394:PRO:HA	68:p:171:PHE:CZ	1.29	1.66
49:a:493:PHE:CE2	49:a:514:LYS:HG3	1.29	1.65
54:i:65:PHE:CD1	54:i:99:LYS:HG2	1.16	1.63
52:g:161:ILE:HA	54:i:140:MET:CE	1.15	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	0	304/309 (98%)	242 (80%)	51 (17%)	11 (4%)	2	23
2	8	297/346 (86%)	266 (90%)	20 (7%)	11 (4%)	2	22
3	9	285/323 (88%)	268 (94%)	14 (5%)	3 (1%)	11	44
4	DO	95/109 (87%)	83 (87%)	11 (12%)	1 (1%)	11	44
5	DP	175/339 (52%)	166 (95%)	7 (4%)	2 (1%)	11	44
6	DQ	118/307 (38%)	105 (89%)	8 (7%)	5 (4%)	2	20
7	BA	251/316 (79%)	237 (94%)	10 (4%)	4 (2%)	7	38
8	FA	130/517 (25%)	117 (90%)	12 (9%)	1 (1%)	16	52
9	FB	218/249 (88%)	200 (92%)	13 (6%)	5 (2%)	5	31
10	PA	1461/1970 (74%)	1363 (93%)	81 (6%)	17 (1%)	10	43
11	PB	1128/1174 (96%)	1029 (91%)	83 (7%)	16 (1%)	9	39
12	PC	253/275 (92%)	229 (90%)	18 (7%)	6 (2%)	4	30
13	PD	127/142 (89%)	123 (97%)	3 (2%)	1 (1%)	16	52
14	PE	207/210 (99%)	201 (97%)	5 (2%)	1 (0%)	24	61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	PF	77/127 (61%)	72 (94%)	3 (4%)	2 (3%)	4	28
16	PG	169/172 (98%)	159 (94%)	8 (5%)	2 (1%)	10	43
17	PH	146/150 (97%)	129 (88%)	16 (11%)	1 (1%)	18	55
18	PI	112/125 (90%)	102 (91%)	8 (7%)	2 (2%)	6	35
19	PJ	62/67 (92%)	59 (95%)	2 (3%)	1 (2%)	7	38
20	PK	115/117 (98%)	106 (92%)	8 (7%)	1 (1%)	14	49
21	PL	42/58 (72%)	38 (90%)	3 (7%)	1 (2%)	4	30
22	DA	582/1872 (31%)	539 (93%)	33 (6%)	10 (2%)	7	36
23	DB	959/1199 (80%)	912 (95%)	47 (5%)	0	100	100
24	DD	153/1085 (14%)	144 (94%)	6 (4%)	3 (2%)	6	33
24	Dd	154/1085 (14%)	150 (97%)	4 (3%)	0	100	100
25	DE	540/800 (68%)	500 (93%)	36 (7%)	4 (1%)	18	55
25	De	531/800 (66%)	484 (91%)	47 (9%)	0	100	100
26	DF	404/677 (60%)	369 (91%)	29 (7%)	6 (2%)	8	39
26	Df	399/677 (59%)	371 (93%)	27 (7%)	1 (0%)	36	70
27	DG	139/349 (40%)	135 (97%)	4 (3%)	0	100	100
28	DH	207/310 (67%)	183 (88%)	20 (10%)	4 (2%)	6	34
29	DI	118/264 (45%)	103 (87%)	14 (12%)	1 (1%)	16	52
29	Di	119/264 (45%)	115 (97%)	4 (3%)	0	100	100
30	DJ	86/218 (39%)	82 (95%)	4 (5%)	0	100	100
30	Dj	91/218 (42%)	89 (98%)	2 (2%)	0	100	100
31	DL	73/161 (45%)	65 (89%)	5 (7%)	3 (4%)	2	21
31	DI	105/161 (65%)	101 (96%)	4 (4%)	0	100	100
32	Dc	125/929 (14%)	116 (93%)	9 (7%)	0	100	100
33	Dk	96/211 (46%)	91 (95%)	5 (5%)	0	100	100
34	Dm	85/124 (68%)	79 (93%)	6 (7%)	0	100	100
35	EA	175/439 (40%)	160 (91%)	12 (7%)	3 (2%)	7	36
36	EB	170/291 (58%)	160 (94%)	6 (4%)	4 (2%)	4	30
37	1	431/548 (79%)	350 (81%)	73 (17%)	8 (2%)	6	34
38	2	383/395 (97%)	311 (81%)	72 (19%)	0	100	100
39	3	293/308 (95%)	238 (81%)	51 (17%)	4 (1%)	9	39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	4	455/462 (98%)	374 (82%)	70 (15%)	11 (2%)	4	30
41	5	64/71 (90%)	57 (89%)	6 (9%)	1 (2%)	7	38
42	6	648/782 (83%)	514 (79%)	123 (19%)	11 (2%)	7	36
43	7	730/760 (96%)	600 (82%)	112 (15%)	18 (2%)	4	29
44	c	255/311 (82%)	235 (92%)	17 (7%)	3 (1%)	10	43
45	e	98/178 (55%)	92 (94%)	4 (4%)	2 (2%)	6	33
46	b	111/200 (56%)	109 (98%)	1 (1%)	1 (1%)	14	49
47	l	120/178 (67%)	115 (96%)	5 (4%)	0	100	100
48	m	110/131 (84%)	106 (96%)	4 (4%)	0	100	100
49	a	457/1581 (29%)	421 (92%)	31 (7%)	5 (1%)	11	44
50	d	154/270 (57%)	143 (93%)	9 (6%)	2 (1%)	9	41
51	f	163/246 (66%)	145 (89%)	13 (8%)	5 (3%)	3	25
52	g	164/233 (70%)	150 (92%)	11 (7%)	3 (2%)	6	35
53	h	188/268 (70%)	163 (87%)	15 (8%)	10 (5%)	1	18
54	i	69/146 (47%)	65 (94%)	2 (3%)	2 (3%)	3	26
55	j	120/135 (89%)	107 (89%)	9 (8%)	4 (3%)	3	24
56	k	110/117 (94%)	98 (89%)	10 (9%)	2 (2%)	6	35
57	n	980/1454 (67%)	876 (89%)	83 (8%)	21 (2%)	5	32
58	o	152/788 (19%)	138 (91%)	13 (9%)	1 (1%)	18	55
59	q	543/651 (83%)	476 (88%)	53 (10%)	14 (3%)	4	28
60	r	204/208 (98%)	190 (93%)	10 (5%)	4 (2%)	6	33
61	s	75/244 (31%)	64 (85%)	7 (9%)	4 (5%)	1	18
62	t	189/212 (89%)	168 (89%)	17 (9%)	4 (2%)	5	32
63	u	103/144 (72%)	99 (96%)	0	4 (4%)	2	21
64	v	132/200 (66%)	117 (89%)	9 (7%)	6 (4%)	2	20
65	z	93/600 (16%)	84 (90%)	6 (6%)	3 (3%)	3	25
66	x	876/989 (89%)	824 (94%)	50 (6%)	2 (0%)	43	75
67	w	1332/1368 (97%)	1266 (95%)	62 (5%)	4 (0%)	36	70
68	p	400/841 (48%)	366 (92%)	33 (8%)	1 (0%)	36	70
All	All	21285/34555 (62%)	19303 (91%)	1689 (8%)	293 (1%)	11	39

5 of 293 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	214	LYS
1	0	220	PRO
1	0	237	PRO
10	PA	539	GLN
10	PA	980	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	209/283 (74%)	171 (82%)	38 (18%)	2	11
2	8	259/299 (87%)	180 (70%)	79 (30%)	0	2
3	9	252/296 (85%)	173 (69%)	79 (31%)	0	2
4	DO	84/98 (86%)	68 (81%)	16 (19%)	1	10
5	DP	153/293 (52%)	141 (92%)	12 (8%)	11	34
6	DQ	111/269 (41%)	93 (84%)	18 (16%)	2	13
7	BA	214/268 (80%)	198 (92%)	16 (8%)	12	35
8	FA	117/448 (26%)	109 (93%)	8 (7%)	14	39
9	FB	196/218 (90%)	159 (81%)	37 (19%)	1	10
10	PA	1305/1748 (75%)	1045 (80%)	260 (20%)	1	9
11	PB	993/1027 (97%)	800 (81%)	193 (19%)	1	9
12	PC	234/252 (93%)	194 (83%)	40 (17%)	2	12
13	PD	108/126 (86%)	87 (81%)	21 (19%)	1	9
14	PE	191/192 (100%)	151 (79%)	40 (21%)	1	7
15	PF	69/111 (62%)	53 (77%)	16 (23%)	1	5
16	PG	147/153 (96%)	111 (76%)	36 (24%)	1	5
17	PH	129/131 (98%)	105 (81%)	24 (19%)	1	10
18	PI	103/112 (92%)	78 (76%)	25 (24%)	1	5
19	PJ	53/56 (95%)	42 (79%)	11 (21%)	1	7
20	PK	106/106 (100%)	88 (83%)	18 (17%)	2	12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	PL	41/55 (74%)	29 (71%)	12 (29%)	0	3
22	DA	532/1665 (32%)	482 (91%)	50 (9%)	8	28
23	DB	876/1083 (81%)	859 (98%)	17 (2%)	50	67
24	DD	144/815 (18%)	126 (88%)	18 (12%)	4	20
24	Dd	146/815 (18%)	146 (100%)	0	100	100
25	DE	478/657 (73%)	460 (96%)	18 (4%)	29	51
25	De	475/657 (72%)	474 (100%)	1 (0%)	87	87
26	DF	324/574 (56%)	260 (80%)	64 (20%)	1	9
26	Df	322/574 (56%)	300 (93%)	22 (7%)	14	39
27	DG	133/322 (41%)	124 (93%)	9 (7%)	14	39
28	DH	181/270 (67%)	156 (86%)	25 (14%)	3	17
29	DI	106/235 (45%)	90 (85%)	16 (15%)	3	15
29	Di	107/235 (46%)	107 (100%)	0	100	100
30	DJ	79/154 (51%)	68 (86%)	11 (14%)	3	17
30	Dj	83/154 (54%)	83 (100%)	0	100	100
31	DL	70/141 (50%)	59 (84%)	11 (16%)	2	14
31	DI	98/141 (70%)	98 (100%)	0	100	100
32	Dc	113/833 (14%)	111 (98%)	2 (2%)	51	68
33	Dk	87/182 (48%)	87 (100%)	0	100	100
34	Dm	80/106 (76%)	79 (99%)	1 (1%)	61	72
35	EA	163/373 (44%)	126 (77%)	37 (23%)	1	6
36	EB	155/261 (59%)	143 (92%)	12 (8%)	12	34
37	1	384/484 (79%)	367 (96%)	17 (4%)	25	48
38	2	342/352 (97%)	335 (98%)	7 (2%)	48	66
39	3	259/272 (95%)	255 (98%)	4 (2%)	57	71
40	4	394/399 (99%)	376 (95%)	18 (5%)	24	47
41	5	59/64 (92%)	54 (92%)	5 (8%)	10	32
42	6	576/688 (84%)	552 (96%)	24 (4%)	26	49
43	7	630/664 (95%)	595 (94%)	35 (6%)	19	43
44	c	231/280 (82%)	218 (94%)	13 (6%)	19	43
45	e	94/152 (62%)	94 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	b	102/163 (63%)	92 (90%)	10 (10%)	7	27
47	l	116/155 (75%)	116 (100%)	0	100	100
48	m	102/115 (89%)	102 (100%)	0	100	100
49	a	393/1391 (28%)	313 (80%)	80 (20%)	1	8
50	d	139/230 (60%)	93 (67%)	46 (33%)	0	2
51	f	144/223 (65%)	123 (85%)	21 (15%)	3	16
52	g	157/216 (73%)	131 (83%)	26 (17%)	2	13
53	h	161/225 (72%)	129 (80%)	32 (20%)	1	9
54	i	71/133 (53%)	62 (87%)	9 (13%)	4	19
55	j	113/124 (91%)	109 (96%)	4 (4%)	32	54
56	k	94/98 (96%)	44 (47%)	50 (53%)	0	0
57	n	689/1272 (54%)	662 (96%)	27 (4%)	28	51
58	o	141/697 (20%)	138 (98%)	3 (2%)	47	66
59	q	461/577 (80%)	385 (84%)	76 (16%)	2	13
60	r	180/183 (98%)	148 (82%)	32 (18%)	2	12
61	s	31/208 (15%)	28 (90%)	3 (10%)	8	27
62	t	166/178 (93%)	124 (75%)	42 (25%)	0	4
63	u	78/119 (66%)	73 (94%)	5 (6%)	16	40
64	v	122/173 (70%)	77 (63%)	45 (37%)	0	1
65	z	89/512 (17%)	75 (84%)	14 (16%)	2	14
66	x	787/864 (91%)	770 (98%)	17 (2%)	45	65
67	w	1202/1232 (98%)	1184 (98%)	18 (2%)	57	71
68	p	353/736 (48%)	346 (98%)	7 (2%)	48	66
All	All	18686/29967 (62%)	16683 (89%)	2003 (11%)	8	24

5 of 2003 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	PH	96	VAL
59	q	128	ASP
26	DF	319	LEU
59	q	92	LEU
62	t	183	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 476 such sidechains are listed below:

Mol	Chain	Res	Type
36	EB	95	HIS
66	x	799	HIS
43	7	304	HIS
66	x	402	ASN
68	p	272	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	$\# Z > 2$
73	SF4	7	801	43	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
73	SF4	7	801	43	-	-	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.

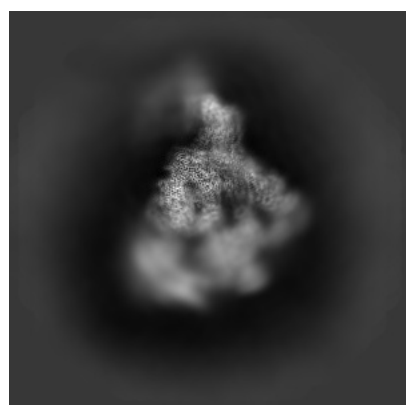
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31204. These allow visual inspection of the internal detail of the map and identification of artifacts.

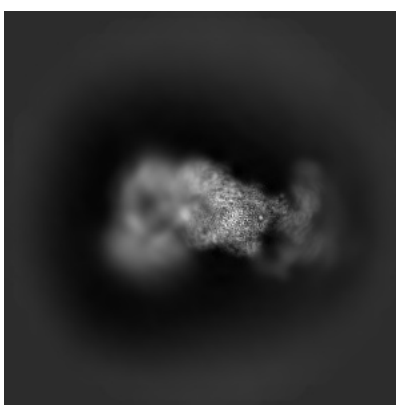
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

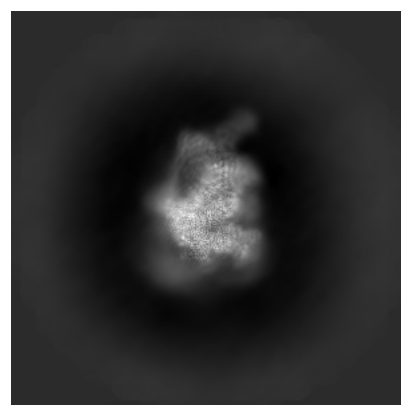
6.1.1 Primary map



X



Y

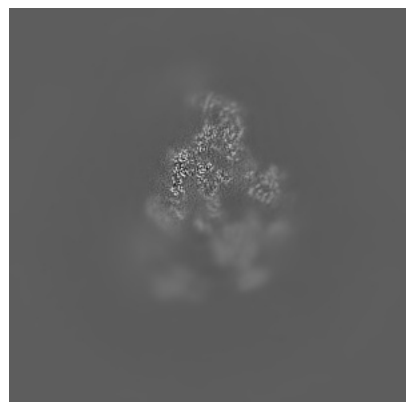


Z

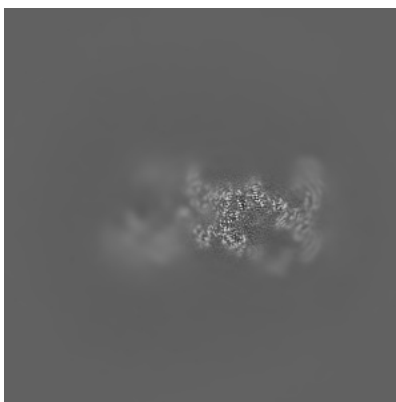
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

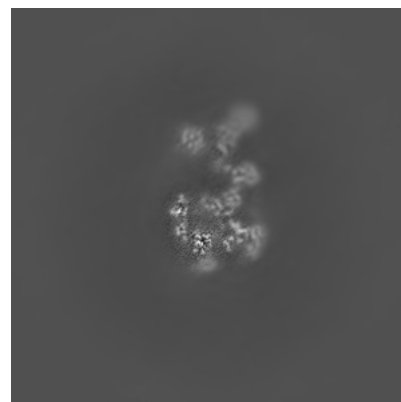
6.2.1 Primary map



X Index: 256



Y Index: 256

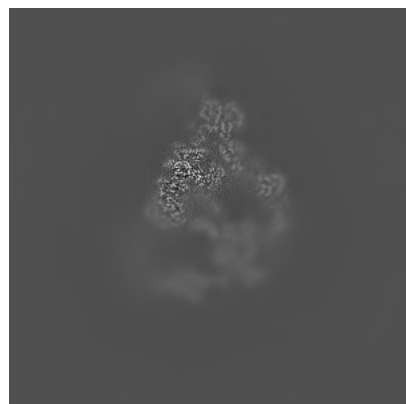


Z Index: 256

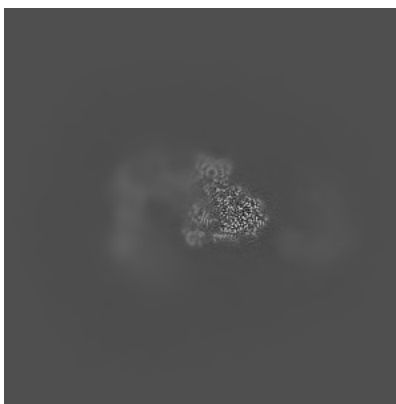
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

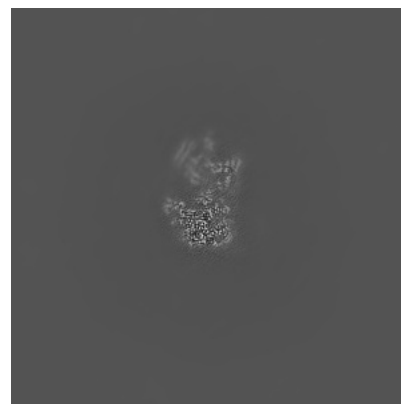
6.3.1 Primary map



X Index: 245



Y Index: 219

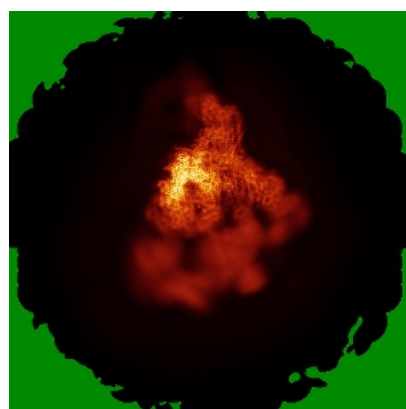


Z Index: 301

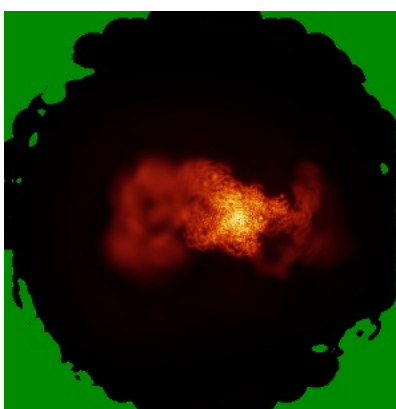
The images above show the largest variance slices of the map in three orthogonal directions.

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

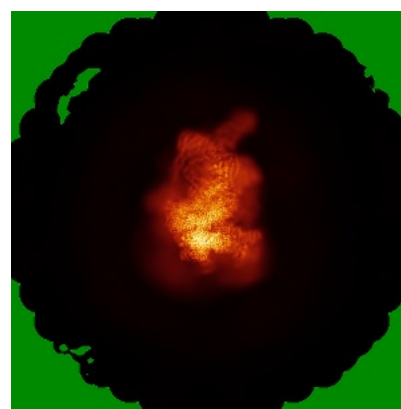
6.4.1 Primary map



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

This section was not generated.

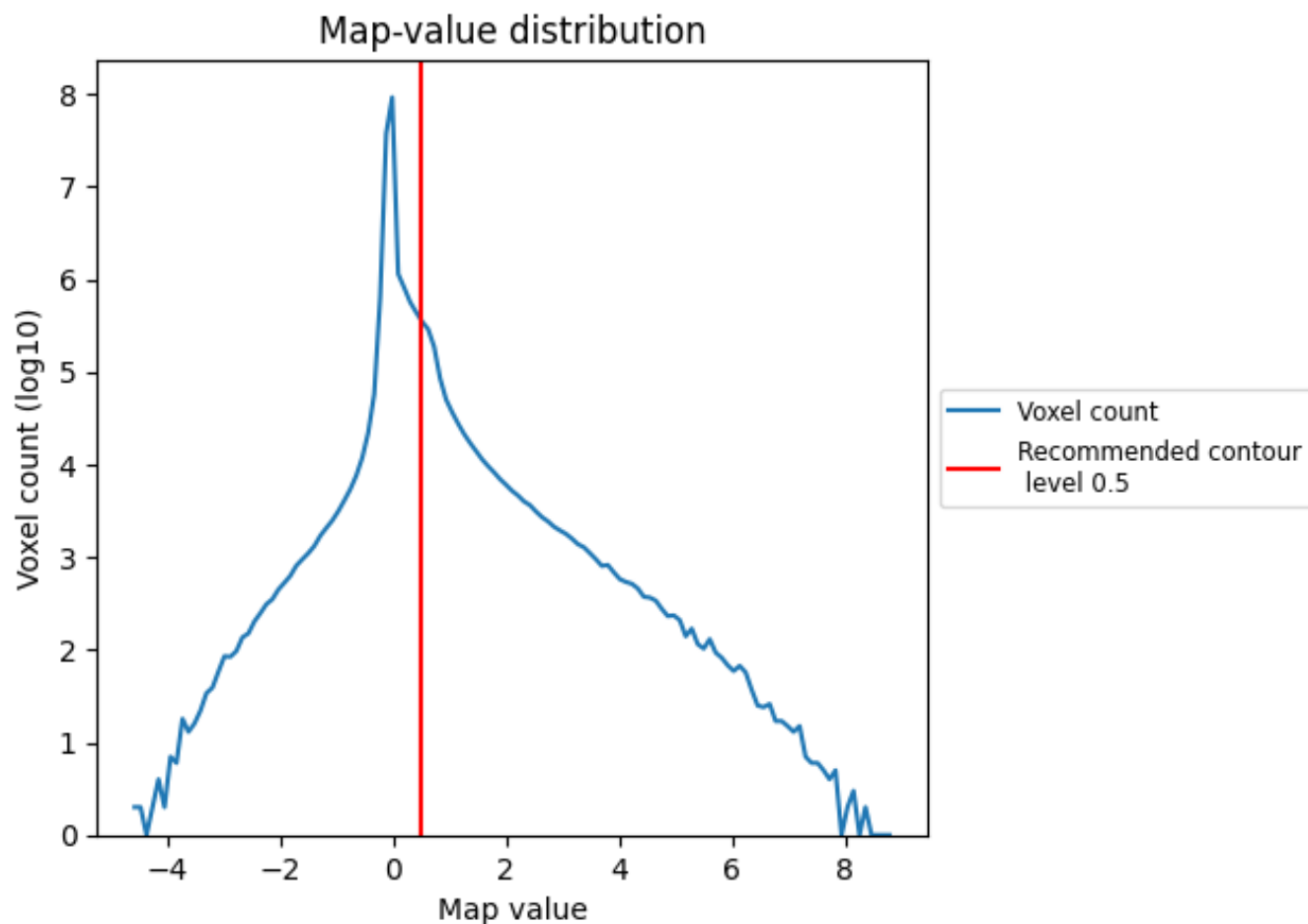
6.6 Mask visualisation

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

7 Map analysis [i](#)

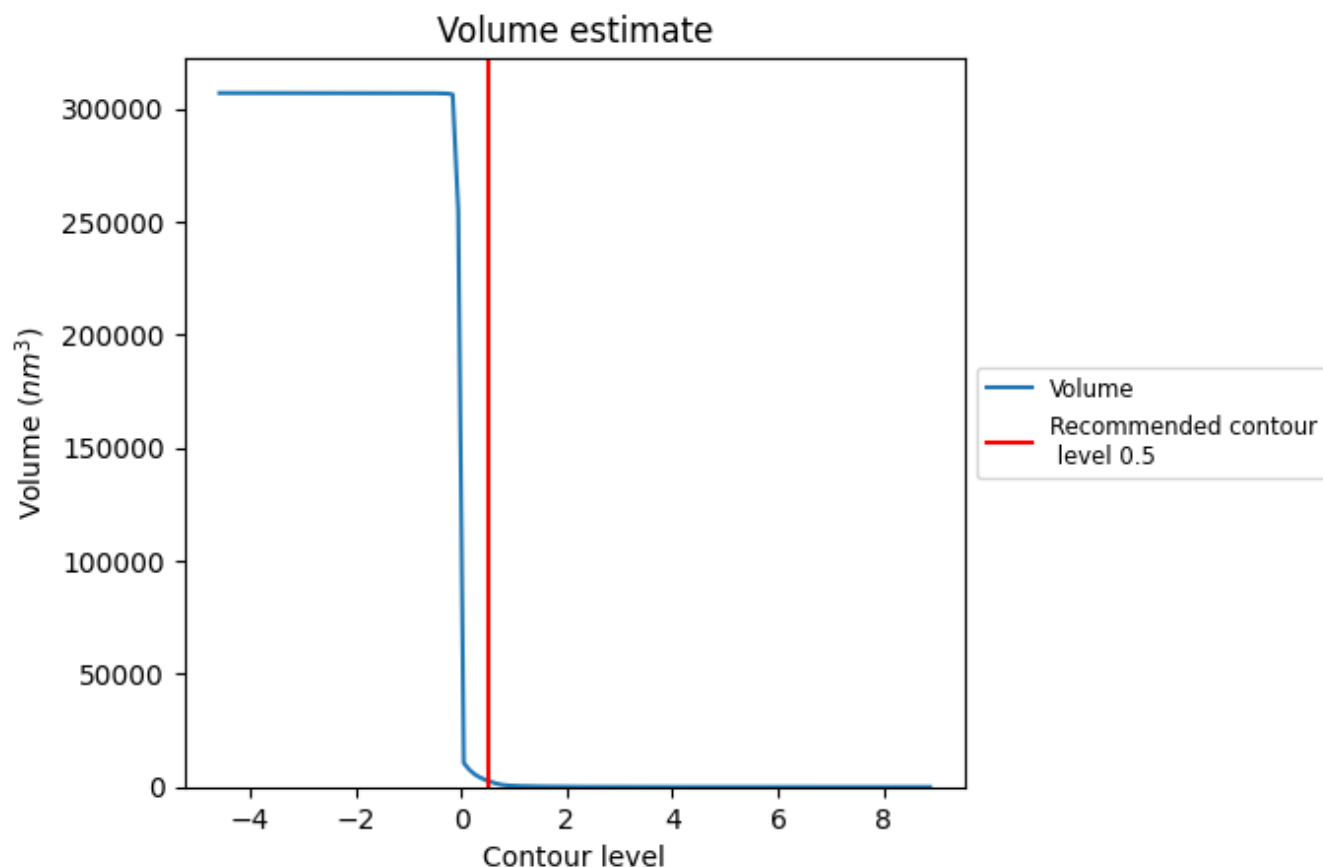
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

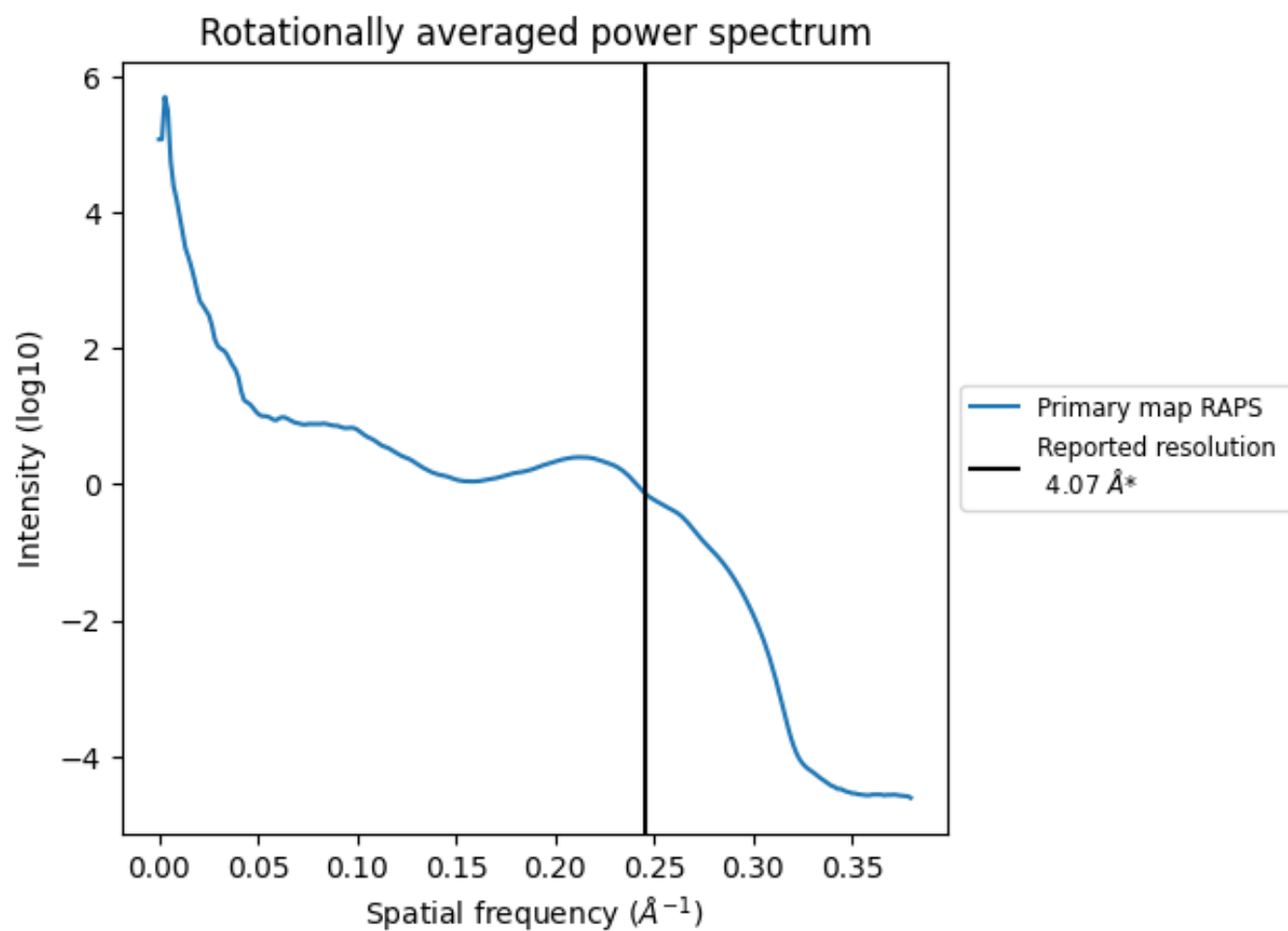
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2784 nm^3 ; this corresponds to an approximate mass of 2515 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.246 Å⁻¹

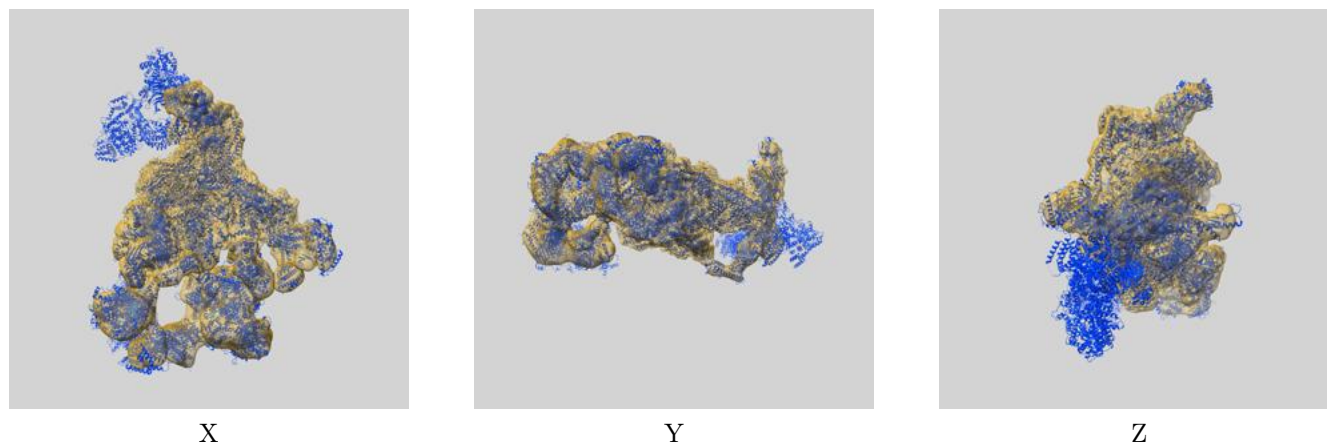
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-31204 and PDB model 7ENA. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.5 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](#)

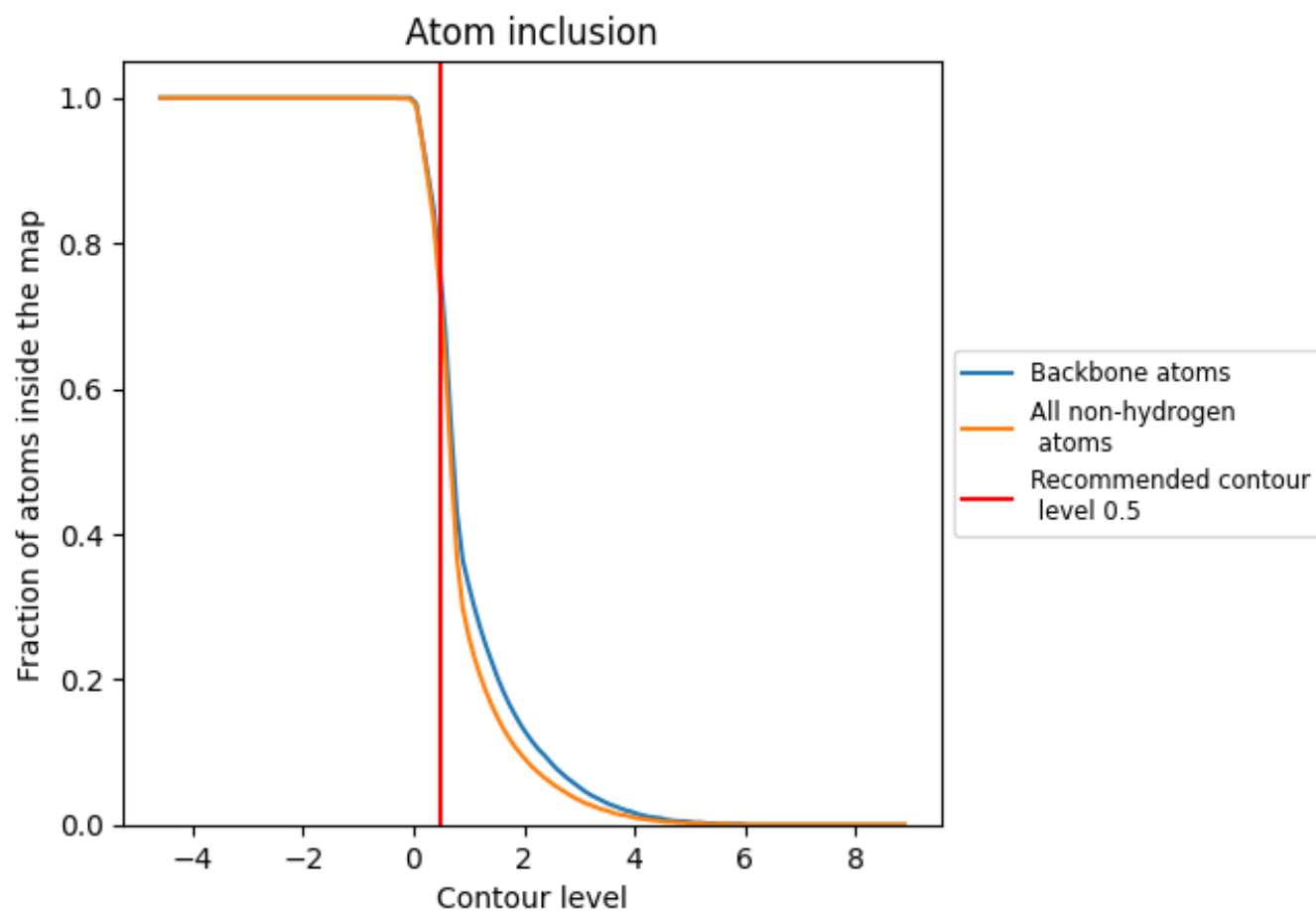


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 72% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7170	 0.1680
0	 0.7760	 0.1210
1	 0.6320	 0.0350
2	 0.8070	 0.0600
3	 0.9160	 0.0610
4	 0.7590	 0.0700
5	 0.8320	 0.0600
6	 0.8640	 0.0830
7	 0.9110	 0.1070
8	 0.8330	 0.1070
9	 0.6160	 0.0680
BA	 0.9210	 0.2770
DA	 0.8310	 0.0650
DB	 0.8880	 0.0600
DD	 0.7420	 0.0830
DE	 0.8120	 0.0650
DF	 0.7670	 0.0520
DG	 0.8530	 0.0550
DH	 0.8340	 0.0500
DI	 0.8170	 0.0540
DJ	 0.8740	 0.0580
DL	 0.5260	 0.0640
DO	 0.9130	 0.1060
DP	 0.9510	 0.1750
DQ	 0.7990	 0.1050
Dc	 0.0000	 0.0350
Dd	 0.0000	 0.0350
De	 0.0040	 0.0330
Df	 0.4390	 0.0530
Di	 0.0000	 0.0290
Dj	 0.0000	 0.0260
Dk	 0.0000	 0.0420
Dl	 0.0000	 0.0460
Dm	 0.0000	 0.0440
EA	 0.9470	 0.1860



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Chain	Atom inclusion	Q-score
EB	 0.9150	 0.1040
FA	 0.8960	 0.0700
FB	 0.8840	 0.1080
PA	 0.9540	 0.4180
PB	 0.9500	 0.4520
PC	 0.9630	 0.4890
PD	 0.9350	 0.4060
PE	 0.9720	 0.3600
PF	 0.9770	 0.5210
PG	 0.9610	 0.4380
PH	 0.9610	 0.4530
PI	 0.9710	 0.3540
PJ	 0.9740	 0.5150
PK	 0.9360	 0.4430
PL	 0.9580	 0.4470
X	 0.9510	 0.1560
Y	 0.9660	 0.1760
a	 0.5990	 0.0940
b	 0.7900	 0.1460
c	 0.8980	 0.2830
d	 0.9100	 0.1440
e	 0.8860	 0.1890
f	 0.9330	 0.2460
g	 0.9520	 0.1380
h	 0.8910	 0.2730
i	 0.9110	 0.1540
j	 0.9320	 0.1050
k	 0.9320	 0.2870
l	 0.9220	 0.1950
m	 0.9190	 0.1730
n	 0.8870	 0.1890
o	 0.9030	 0.1670
p	 0.0000	 -0.0140
q	 0.9170	 0.3040
r	 0.9260	 0.3830
s	 0.9400	 0.1130
t	 0.8860	 0.3610
u	 0.9390	 0.1550
v	 0.9140	 0.3410
w	 0.0420	 0.0510
x	 0.1950	 0.0640
z	 0.8980	 0.1220