



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 10:06 AM UTC

PDB ID : 7LBM / pdb_00007lbm
EMDB ID : EMD-23255
Title : Structure of the human Mediator-bound transcription pre-initiation complex
Authors : Abdella, R.; Talyzina, A.; He, Y.
Deposited on : 2021-01-08
Resolution : 4.80 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:

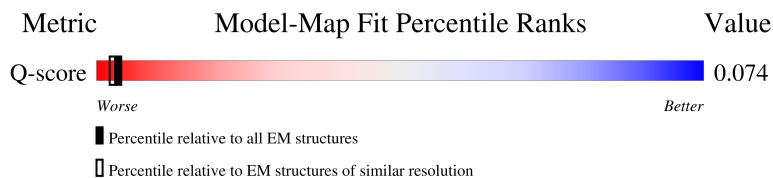
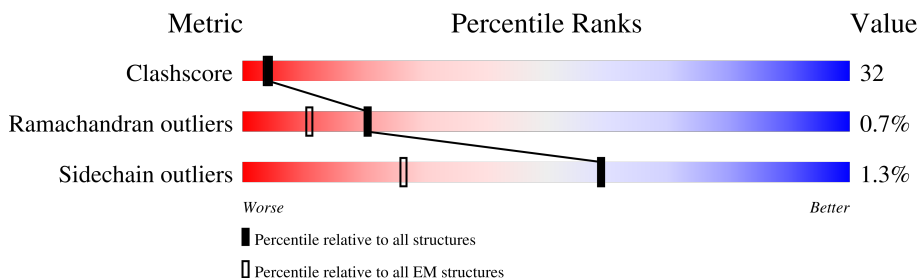
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 4.80 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	1575 (4.30 - 5.30)

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	841	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">14%</div> <div style="width: 100%; height: 20px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">46%</div> <div style="text-align: center;">40%</div> <div style="text-align: center;">••</div> <div style="text-align: center;">11%</div> </div>
2	1	1368	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">48%</div> <div style="width: 100%; height: 20px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">60%</div> <div style="text-align: center;">36%</div> <div style="text-align: center;">•</div> </div>
3	2	989	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">31%</div> <div style="width: 100%; height: 20px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">52%</div> <div style="text-align: center;">38%</div> <div style="text-align: center;">•</div> <div style="text-align: center;">9%</div> </div>
4	3	747	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">10%</div> <div style="width: 100%; height: 20px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">12%</div> <div style="text-align: center;">13%</div> <div style="text-align: center;">•</div> <div style="text-align: center;">74%</div> </div>

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Mol	Chain	Length	Quality of chain
5	A	1970	47% 26% 26%
6	B	1174	65% 31%
7	C	275	10% 63% 34%
8	D	142	8% 47% 42% 9%
9	E	210	65% 35%
10	F	127	6% 43% 24% 32%
11	G	172	60% 40%
12	H	150	7% 73% 27%
13	I	125	6% 60% 30% 7%
14	J	67	9% 82% 18%
15	K	117	5% 79% 21%
16	L	58	59% 21% 21%
17	M	376	12% 11% 19% 70%
18	N	109	32% 42% 47% 9%
19	O	316	8% 53% 28% 18%
20	P	339	12% 25% 29% 45%
21	Q	439	6% 22% 19% 58%
22	R	291	11% 23% 33% 43%
23	S	517	8% 11% 13% 75%
24	T	249	22% 45% 42% 11%
25	U	100	16% 42% 22% 36%
26	V	100	17% 39% 25% 36%
27	W	782	67% 52% 21% 27%
28	X	760	58% 75% 24%
29	Y	548	32% 22% 17% 60%

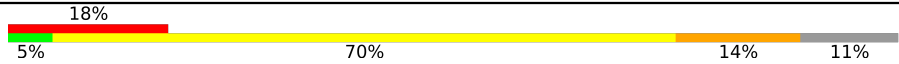

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Mol	Chain	Length	Quality of chain
30	Z	462	79% 67% 26% 6%
31	a	395	72% 65% 18% 16%
32	b	308	66% 56% 29% 15%
33	c	71	76% 58% 31% 7%
34	d	309	50% 74% 15% 11%
35	e	346	46% 56% 29% 14%
36	f	323	54% 63% 24% 13%
37	g	246	23% 30% 47%
38	h	268	29% 28% 41%
39	i	117	50% 44% 6%
40	j	651	32% 38% 6% 23%
41	k	208	8% 51% 36% 11%
42	l	212	12% 47% 39% 13%
43	m	200	32% 31% 38%
44	n	311	49% 39% 9%
45	o	178	30% 30% 39%
46	p	200	36% 22% 43%
47	q	178	31% 38% 31%
48	r	1454	12% 31% 35% 29%
49	s	270	26% 10% 36% 50%
50	t	233	16% 42% 5% 50%
51	u	146	24% 14% 26% 59%
52	v	135	48% 7% 79% 10%
53	w	244	9% 12% 84%
54	x	144	32% 5% 60% 11% 23%

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Mol	Chain	Length	Quality of chain
55	y	131	 <p>5% 18% 70% 14% 11%</p>
56	z	788	 <p>8% 8% 81%</p>

2 Entry composition [i](#)

There are 59 unique types of molecules in this entry. The entry contains 129277 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 Isoform 2 of Mediator of RNA polymerase II transcription subunit 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	752	Total	C	N	O	S	0	0
			5864	3744	1005	1068	47		

- Molecule 2 is a protein called Mediator of RNA polymerase II transcription subunit 23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	1317	Total	C	N	O	S	0	0
			10636	6878	1809	1880	69		

- Molecule 3 is a protein called Mediator of RNA polymerase II transcription subunit 24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	897	Total	C	N	O	S	0	0
			7007	4487	1180	1284	56		

- Molecule 4 is a protein called Mediator of RNA polymerase II transcription subunit 25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	3	195	Total	C	N	O	S	0	0
			1504	969	249	277	9		

- Molecule 5 is a protein called DNA-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	A	1455	Total	C	N	O	S	0	0
			11519	7241	2052	2154	72		

- Molecule 6 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	B	1142	Total	C	N	O	S	0	0
			9129	5769	1604	1692	64		

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	C	267	2147	1344	370	426	7	0	0

- Molecule 8 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	D	129	1062	665	179	214	4	0	0

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	E	210	1723	1088	301	325	9	0	0

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	F	86	689	437	120	127	5	0	0

- Molecule 11 is a protein called DNA-directed RNA polymerase II subunit RPB7.

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

- Molecule 12 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		
12	H	150	1205	764	196	239	6	0	0

- Molecule 13 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	I	116	942	582	168	181	11	0	0

- Molecule 14 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	67	Total	C	N	O	S	0	0
			533	345	90	92	6		

- Molecule 15 is a protein called DNA-directed RNA polymerase II subunit RPB11-a.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	116	Total	C	N	O	S	0	0
			928	599	153	174	2		

- Molecule 16 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	46	Total	C	N	O	S	0	0
			388	241	75	66	6		

- Molecule 17 is a protein called Transcription initiation factor IIA subunit 1.

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

- Molecule 18 is a protein called Transcription initiation factor IIA subunit 2.

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

- Molecule 19 is a protein called Transcription initiation factor IIB.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	260	Total	C	N	O	S	0	0
			2018	1265	360	376	17		

- Molecule 20 is a protein called TATA-box-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	185	Total	C	N	O	S	0	0
			1462	946	257	252	7		

- Molecule 21 is a protein called General transcription factor IIE subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	Q	184	1520	957	272	280	11	0	0

- Molecule 22 is a protein called Transcription initiation factor IIE subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	R	165	1357	865	235	253	4	0	0

- Molecule 23 is a protein called General transcription factor IIF subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	S	127	1059	671	196	189	3	0	0

- Molecule 24 is a protein called General transcription factor IIF subunit 2.

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

- Molecule 25 is a DNA chain called super core promoter sense strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
25	U	64	1321	623	256	379	63	0	0

- Molecule 26 is a DNA chain called super core promoter antisense strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
26	V	64	1300	616	233	387	64	0	0

- Molecule 27 is a protein called TFIIF basal transcription factor complex helicase XPB subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	W	574	4645	2973	807	835	30	0	0

- Molecule 28 is a protein called TFIIF basal transcription factor complex helicase XPD subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	X	760	6109	3899	1066	1115	29	0	0

- Molecule 29 is a protein called General transcription factor IIH subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	Y	218	1631	1028	290	305	8	0	0

- Molecule 30 is a protein called General transcription factor IIH subunit 4, p52.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	Z	436	3473	2239	609	611	14	0	0

- Molecule 31 is a protein called General transcription factor IIH subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	a	331	2580	1628	443	482	27	0	0

- Molecule 32 is a protein called General transcription factor IIH subunit 3.

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

- Molecule 33 is a protein called General transcription factor IIH subunit 5.

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

- Molecule 34 is a protein called CDK-activating kinase assembly factor MAT1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	d	275	2104	1315	368	410	11	0	0

- Molecule 35 is a protein called Cyclin-dependent kinase 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	e	298	2376	1537	404	423	12	0	0

- Molecule 36 is a protein called Cyclin-H.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	f	281	2293	1465	394	416	18	0	0

- Molecule 37 is a protein called Mediator of RNA polymerase II transcription subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	g	130	1035	664	174	192	5	0	0

- Molecule 38 is a protein called Mediator of RNA polymerase II transcription subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	h	158	1230	767	214	246	3	0	0

- Molecule 39 is a protein called Mediator of RNA polymerase II transcription subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	i	110	863	527	160	172	4	0	0

- Molecule 40 is a protein called Mediator of RNA polymerase II transcription subunit 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	j	504	4005	2530	719	739	17	0	0

- Molecule 41 is a protein called Mediator of RNA polymerase II transcription subunit 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	k	185	1484	942	259	268	15	0	0

- Molecule 42 is a protein called Mediator of RNA polymerase II transcription subunit 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	l	184	1425	907	235	267	16	0	0

- Molecule 43 is a protein called Mediator of RNA polymerase II transcription subunit 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	m	125	1024	632	175	213	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	n	283	2279	1445	406	417	11	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	o	108	887	553	155	176	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	p	114	893	559	154	171	9	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	q	122	1007	628	188	182	9	0	0

- Molecule 48 is a protein called Mediator of RNA polymerase II transcription subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	r	1034	8174	5239	1427	1461	47	0	0

- Molecule 49 is a protein called Mediator of RNA polymerase II transcription subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	s	135	1084	676	191	212	5	0	0

- Molecule 50 is a protein called Mediator of RNA polymerase II transcription subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	t	116	975	621	175	173	6	0	0

- Molecule 51 is a protein called Mediator of RNA polymerase II transcription subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	u	60	501	314	93	90	4	0	0

- Molecule 52 is a protein called Mediator of RNA polymerase II transcription subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	v	131	1067	676	182	204	5	0	0

- Molecule 53 is a protein called Mediator of RNA polymerase II transcription subunit 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	w	39	309	198	52	57	2	0	0

- Molecule 54 is a protein called Mediator of RNA polymerase II transcription subunit 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	x	111	852	528	142	178	4	0	0

- Molecule 55 is a protein called Mediator of RNA polymerase II transcription subunit 31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	y	116	1003	649	177	172	5	0	0

- Molecule 56 is a protein called Mediator of RNA polymerase II transcription subunit 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	z	149	1168	747	204	210	7	0	0

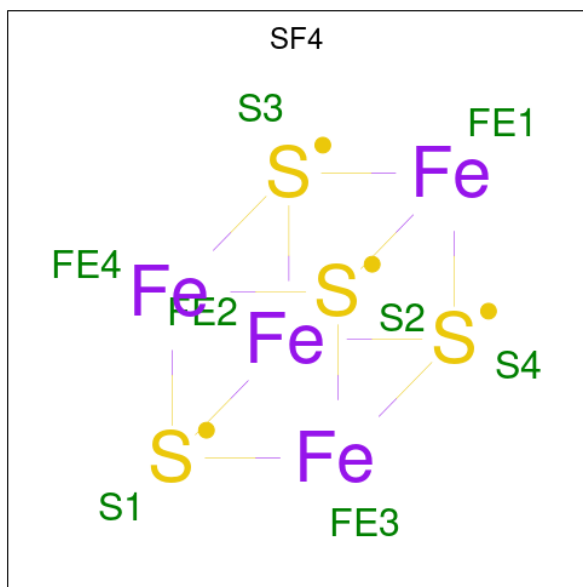
- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	A	2	Total	Mg	0
			2	2	

- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
58	A	2	Total	Zn	0
			2	2	
58	B	1	Total	Zn	0
			1	1	
58	C	1	Total	Zn	0
			1	1	
58	I	2	Total	Zn	0
			2	2	
58	J	1	Total	Zn	0
			1	1	
58	L	1	Total	Zn	0
			1	1	
58	O	1	Total	Zn	0
			1	1	
58	Q	1	Total	Zn	0
			1	1	
58	a	3	Total	Zn	0
			3	3	
58	b	1	Total	Zn	0
			1	1	
58	d	2	Total	Zn	0
			2	2	

- Molecule 59 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).

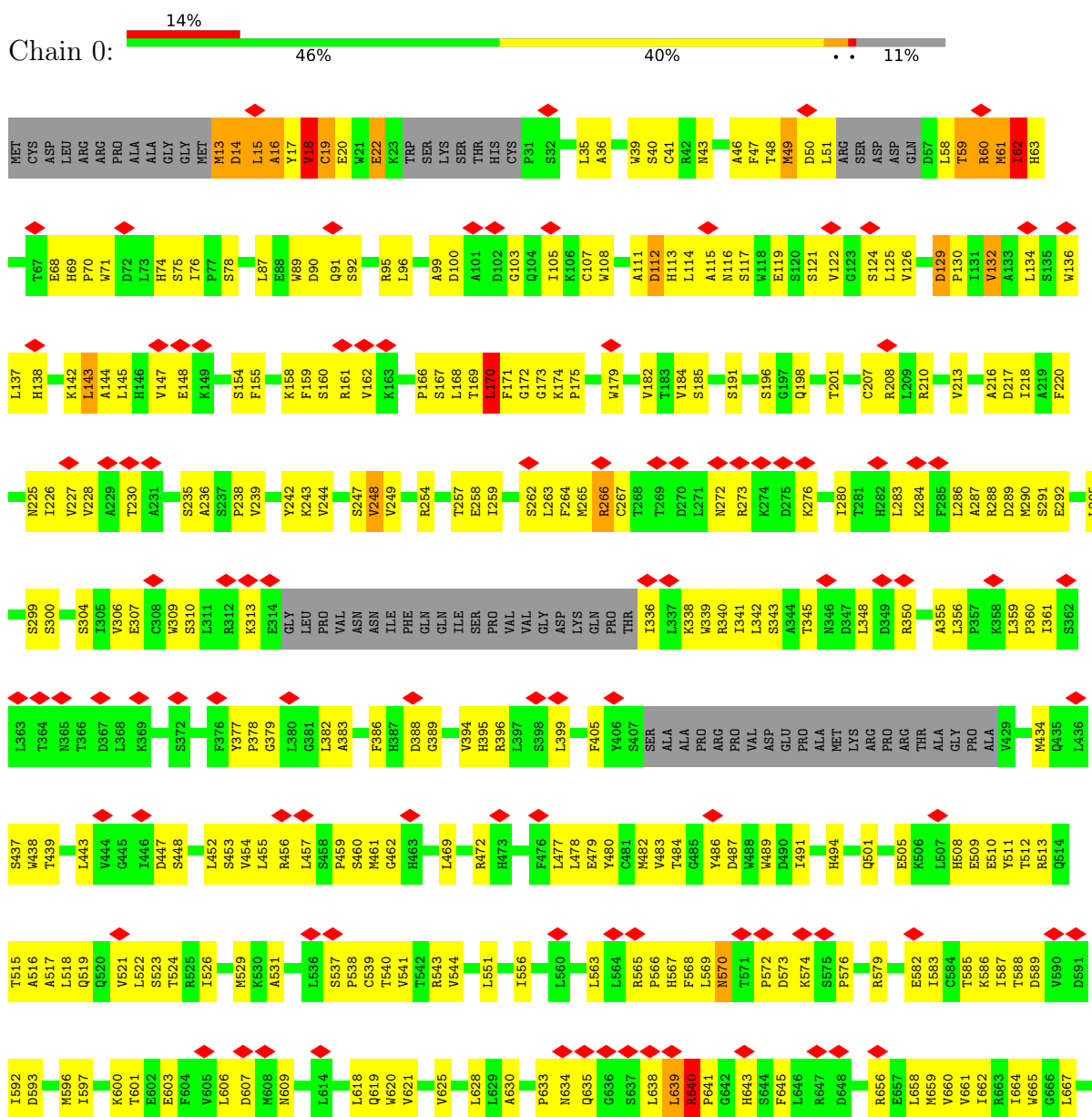


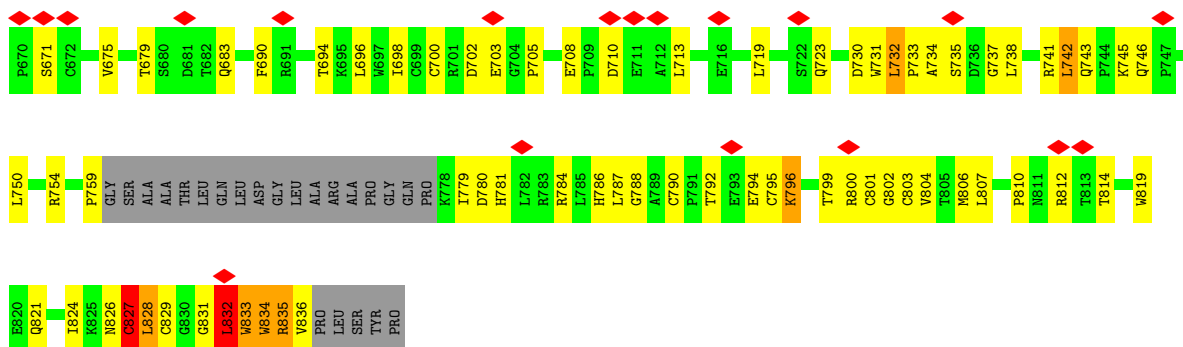
Mol	Chain	Residues	Atoms			AltConf
59	X	1	Total	Fe	S	0
			8	4	4	

3 Residue-property plots

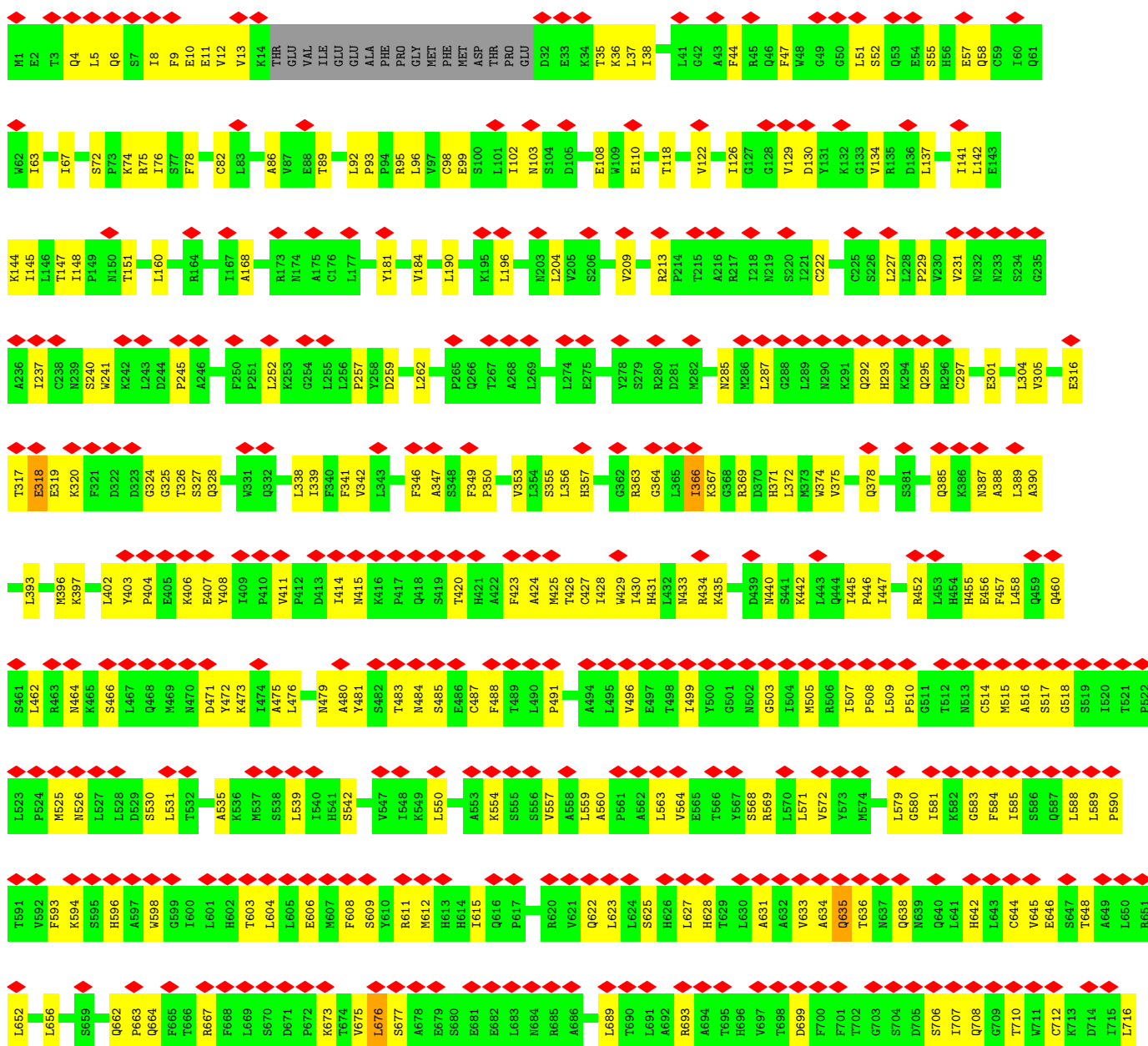
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

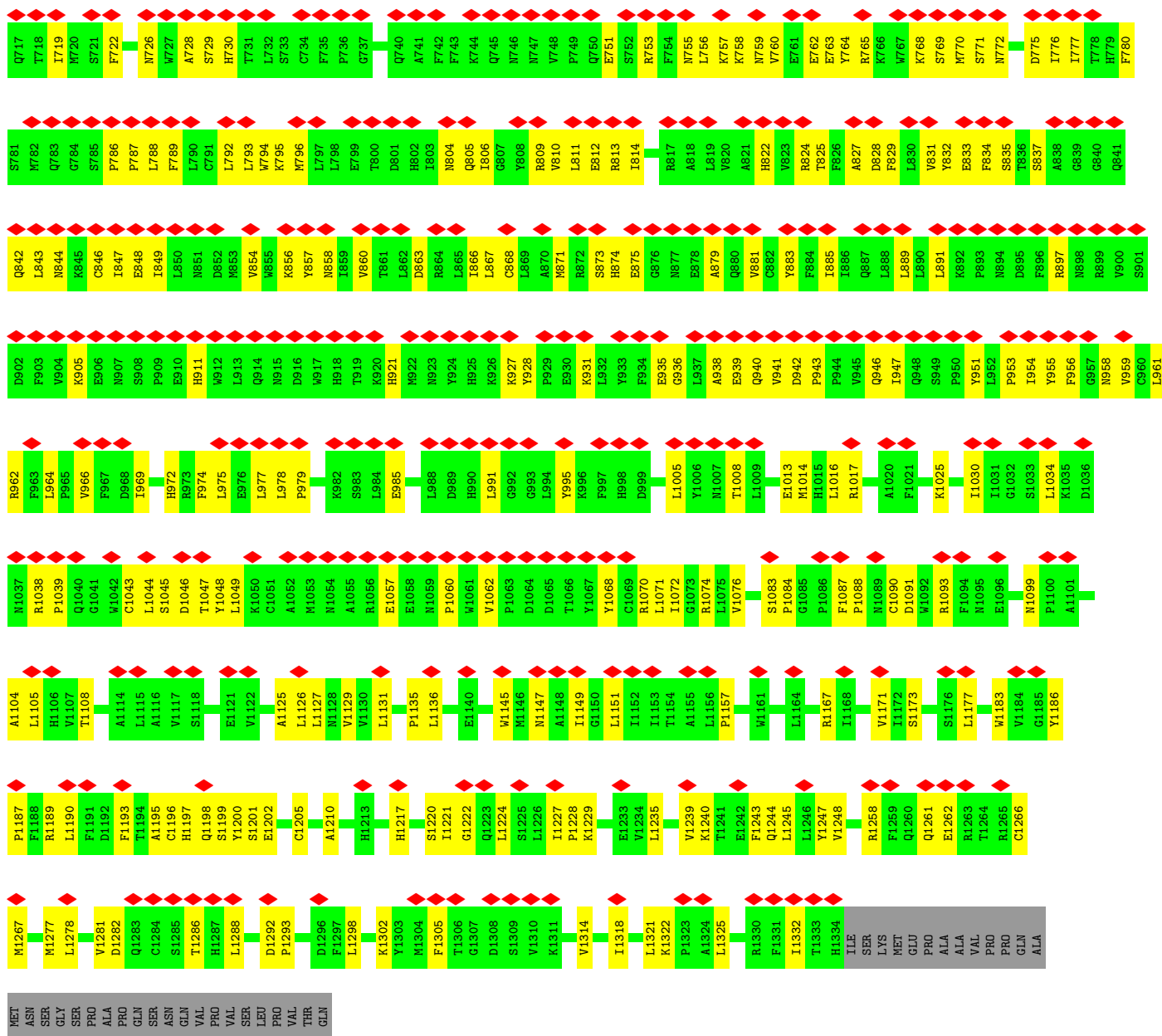
- Molecule 1: Isoform 2 of Mediator of RNA polymerase II transcription subunit 16



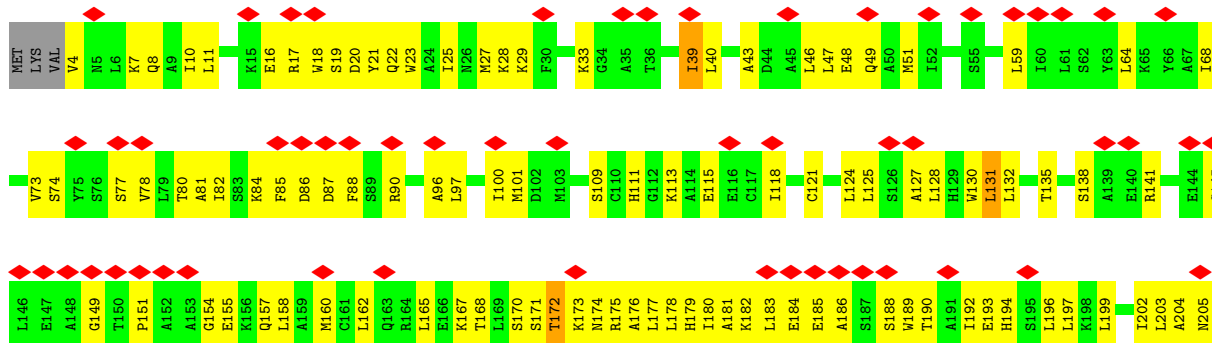


• Molecule 2: Mediator of RNA polymerase II transcription subunit 23

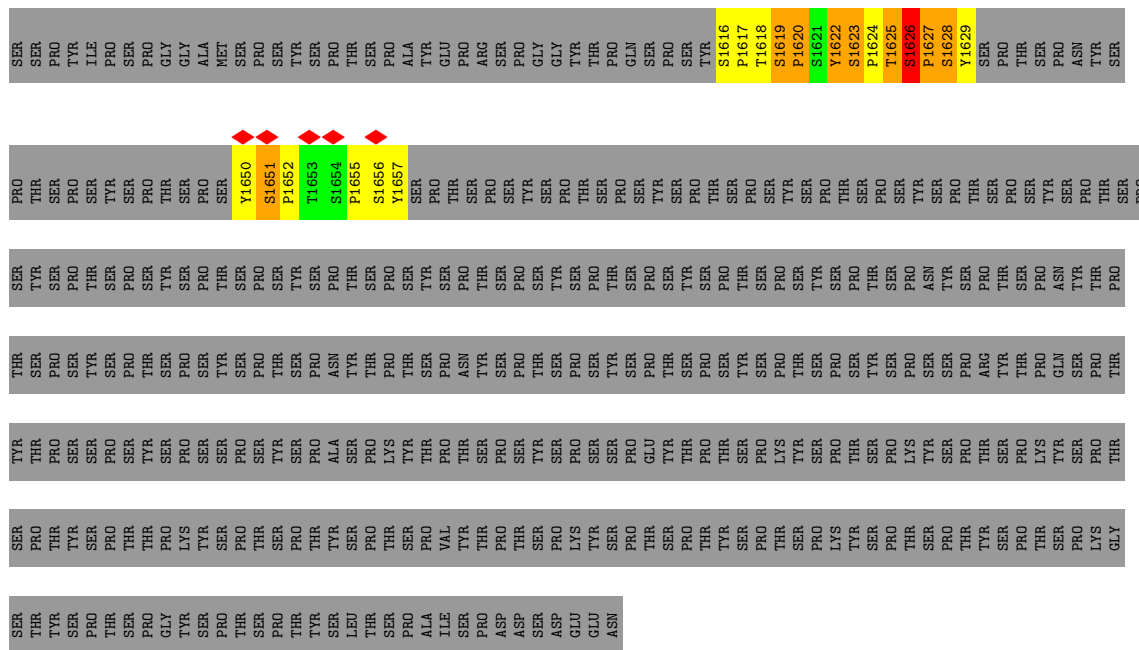




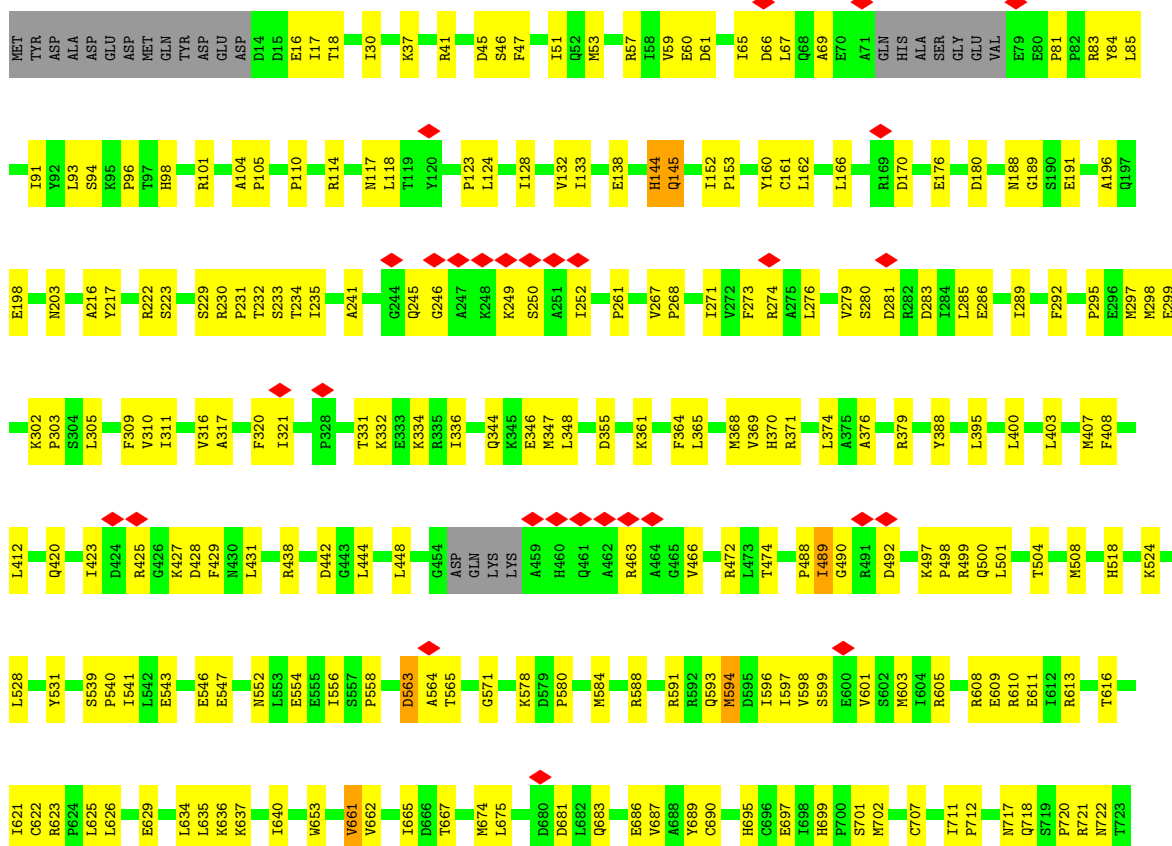
• Molecule 3: Mediator of RNA polymerase II transcription subunit 24

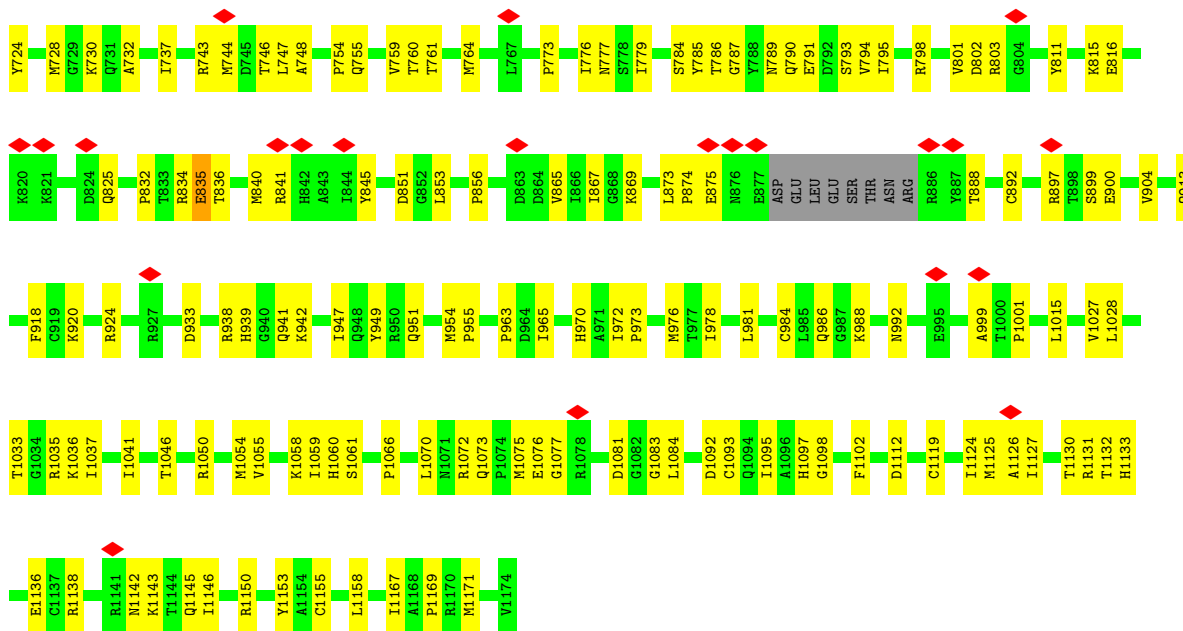


THR	V1436	R1345	M1263	W1192	G1120	P998	R890	N780	C641	V838	K445	K344	P262
PRO	V1346	V1193	S1264	V1193	V1121	P998	R891	I781	L645	V839	V446	G345	A263
TRP	L1347	M1194	D1265	M1194	S782	D1003	G892	S782	L645	Q539	V447	G346	V264
ASN	A1442	V1195	E1266	V1195	R1123	D1003	E893	A786	L652	D540	E447	V265	V265
GLN	A1443	V1196	M1267	V1196	R1124	L1020	Q904	V787	V653	Q541	R349	V350	M266
GLY	K1350	Y1197	K1268	E1198	K1125	L1020	N905	Q790	V654	V545	R351	G352	Q267
ALA	D1449	E1198	K1268	E1198	K1125	L1020	N905	Q790	H654	V545	R351	G352	Q267
THR	D1450	M1199	M1269	M1199	I1128	V1023	L906	I907	I655	R946	R352	G353	G268
PRO	P1451	P1200	GLN	P1200	R1129	S1030	A907	E794	E659	K547	R459	M355	S269
ALA	L1460	D1201	GLU	D1201	S1130	F1041	T908	R797	M659	F548	F458	M355	A270
ALA	G1461	F1202	GLU	F1202	S1131	N1042	L909	R797	E663	T549	N459	R362	R271
ALA	Q1462	D1203	GLU	D1203	K1132	I1043	E917	F800	I664	R850	R460	M272	M272
TRP	M1380	R1206	V1275	R1206	P1133	H1044	F920	R600	I664	R851	A363	R364	D275
PRO	D1361	S1207	V1276	S1207	P1137	H1044	R921	R605	I667	R857	K466	I367	D275
SER	I1362	S1209	M1279	S1209	P1137	H1044	R921	R605	I667	R857	K466	I367	D275
SER	V1363	M1279	M1279	M1279	P1137	H1044	R921	R605	I667	R857	K466	I367	D275
VAL	E1364	D1210	V1277	D1210	P1137	H1044	R921	R605	I667	R857	K466	I367	D275
GLY	V1368	L1211	M1279	L1211	F1142	L1049	Y924	P808	F668	V560	M479	I375	K379
GLY	L1369	L1212	M1279	L1212	L1143	C1050	Y924	H809	F668	V560	M479	I375	K379
MET	E1372	E1215	F1284	E1215	L1144	S1051	E927	F810	V675	M565	M479	V380	V284
PRO	E1381	L1216	F1284	L1216	G1145	R1052	R928	K812	I676	F566	S480	V380	V284
ALA	L1382	R1286	C1287	R1286	Q1146	R1052	R928	K812	N677	P575	T481	L290	L290
ALA	V1385	I1288	I1288	I1288	S1147	M1054	R932	D814	N677	P575	R483	Q295	Q295
GLY	I1386	M1292	M1292	M1292	A1148	M1054	R933	D814	N677	P575	R483	Q295	Q295
PHE	I1386	M1292	M1292	M1292	R1149	A1056	T933	P817	L680	A578	L484	M296	M296
PRO	Y1392	L1298	L1298	L1298	D1150	E1056	T933	P817	L680	A578	L484	M296	M296
SER	Y1392	L1298	L1298	L1298	D1150	E1056	T933	P817	L680	A578	L484	M296	M296
ASN	H1387	Q1299	Q1299	Q1299	D1156	R1059	V939	R820	I687	L880	M486	H301	H301
ALA	L1398	L1298	L1298	L1298	I1157	L1060	V942	V823	G688	K881	M486	V302	V302
ALA	L1398	L1298	L1298	L1298	I1157	L1060	V942	V823	G688	K881	M486	V302	V302
PRO	L1401	L1304	L1304	L1304	L1161	M1086	L952	L828	T698	Q590	P491	D306	D306
LEU	L1401	S1305	S1305	S1305	E1162	V1087	L952	L828	T698	Q590	P491	D306	D306
ALA	L1411	R1906	R1906	R1906	H1163	V1087	L952	L828	T698	Q590	P491	D306	D306
ALA	M1412	V1307	V1307	V1307	T1164	Q1093	F956	M841	I702	S892	A494	G409	G409
GLY	A1413	I1231	I1231	I1231	T1165	Q1093	F956	M841	I702	S892	A494	G409	G409
PRO	I1414	E1232	E1232	E1232	R1166	S1094	M959	E945	K710	L594	E500	N320	N320
GLY	H1417	K1312	K1312	K1312	R1167	L1095	M959	E945	K710	L594	E500	N320	N320
THR	G1418	Q1313	Q1313	Q1313	K1168	L1095	M959	E945	K710	L594	E500	N320	N320
PRO	V1419	M1316	M1316	M1316	V1169	P1098	D962	D849	N722	I595	M501	D319	D319
ALA	N1420	N1236	N1236	N1236	T1170	A1099	E964	D849	N722	I595	M501	D319	D319
SER	R1421	G1240	G1240	G1240	A1171	T1100	V965	V852	E724	P897	Q507	E321	E321
PRO	Q1422	D1241	D1241	D1241	N1172	GLN	L966	K853	P727	N601	Q507	E321	E321
THR	D1423	D1242	D1242	D1242	T1173	MET	L966	K853	P727	N601	Q507	E321	E321
PRO	P1426	L1243	L1243	L1243	A1174	THR	V968	E856	L733	T605	R512	L325	L325
GLY	L1427	M1244	M1244	M1244	V1176	LEU	V968	E856	L733	T605	R512	L325	L325
PRO	M1429	C1245	C1245	C1245	Y1177	ASN	V968	E856	L733	T605	R512	L325	L325
SER	C1430	L1246	L1246	L1246	D1178	THR	V977	I860	R734	H609	Q516	P326	P326
PRO	S1431	F1247	F1247	F1247	P1179	PHE	V978	I860	R734	H609	Q516	P326	P326
PRO	F1432	N1248	N1248	N1248	P1179	HIS	L979	I665	T752	Y618	V521	Q350	Q350
GLY	M1433	E1253	E1253	E1253	Q1182	ALA	N982	M668	Q757	I621	V521	Q350	Q350
GLY	L1434	K1254	K1254	K1254	S1183	VAL	N982	M668	Q757	I621	V521	Q350	Q350
SER	L1434	L1255	L1255	L1255	T1184	SER	N985	V871	K767	D625	R523	R336	R336
PRO	S1434	L1255	L1255	L1255	V1185	ALA	N985	V871	K767	D625	R523	R336	R336
ALA	F1433	R1256	R1256	R1256	V1186	K1115	N988	I881	V770	N632	P528	H432	H432
PRO	F1433	R1256	R1256	R1256	V1186	K1115	N988	I881	V770	N632	P528	H432	H432
PRO	E1434	L1261	L1261	L1261	D1189	T1118	N989	I883	K778	G638	V534	L339	L339
PRO	T1435	M1262	M1262	M1262	E1191	L1119	N989	I883	K778	G638	V534	L339	L339

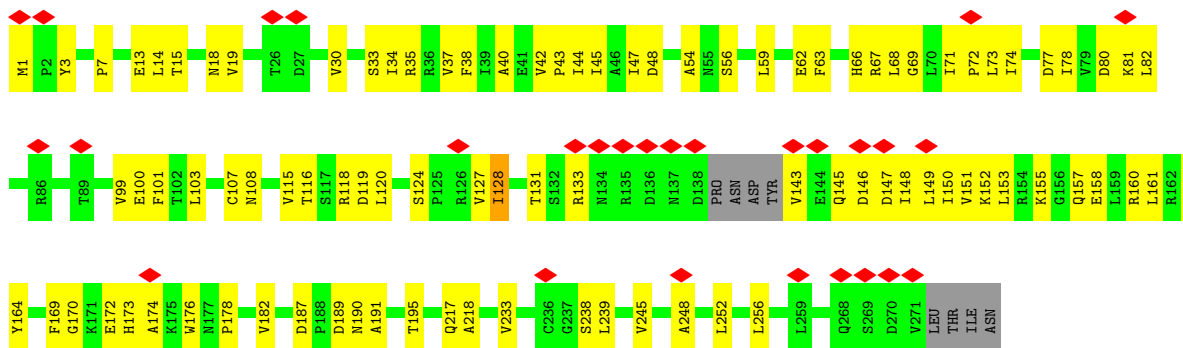


● Molecule 6: DNA-directed RNA polymerase II subunit RPB2

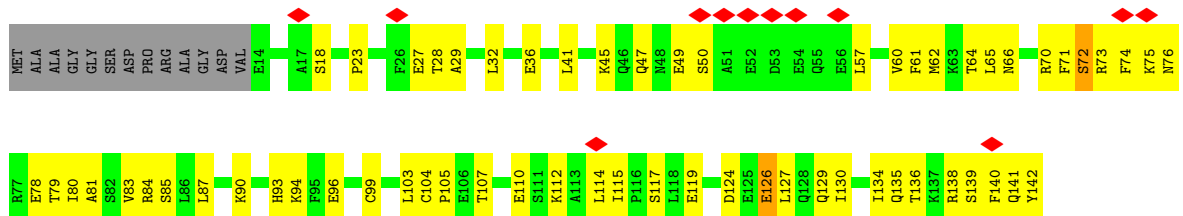




• Molecule 7: DNA-directed RNA polymerase II subunit RPB3

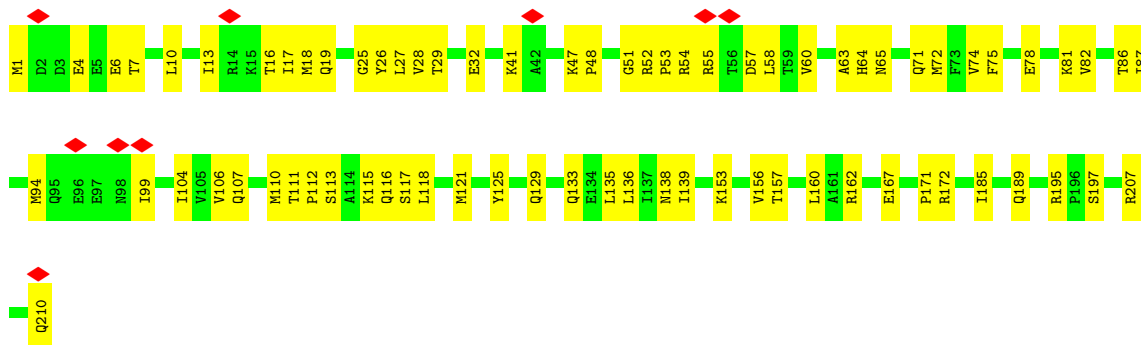


• Molecule 8: DNA-directed RNA polymerase II subunit RPB4

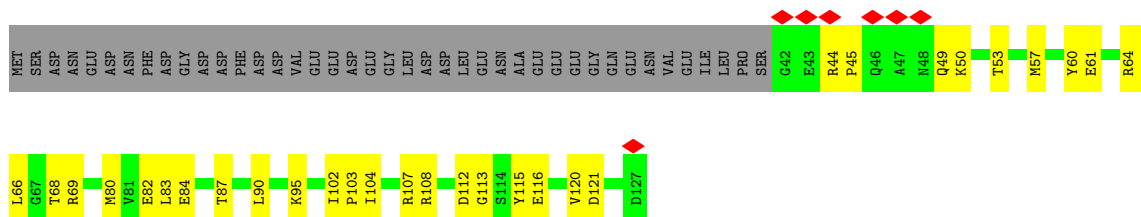
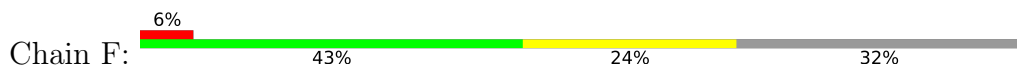


• Molecule 9: DNA-directed RNA polymerase II subunit RPB5

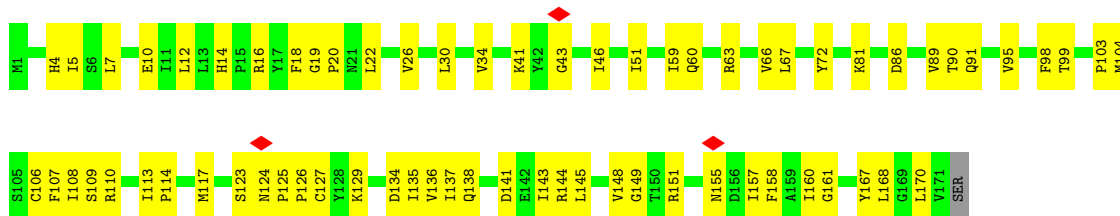




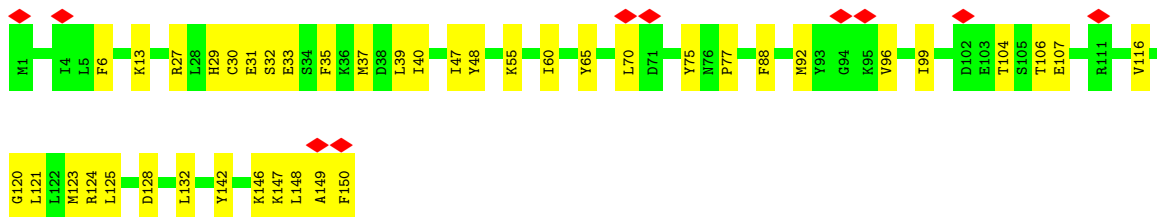
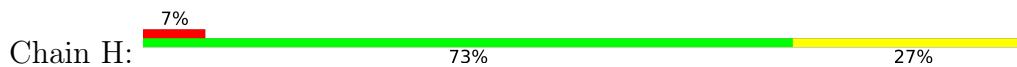
- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC2



- Molecule 11: DNA-directed RNA polymerase II subunit RPB7

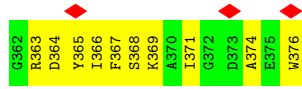


- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC3

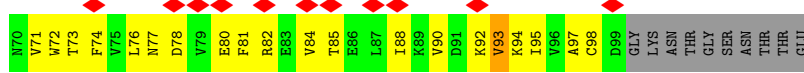
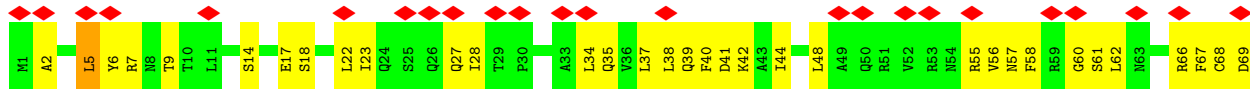
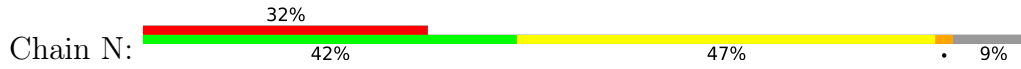


- Molecule 13: DNA-directed RNA polymerase II subunit RPB9

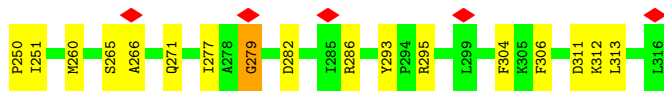
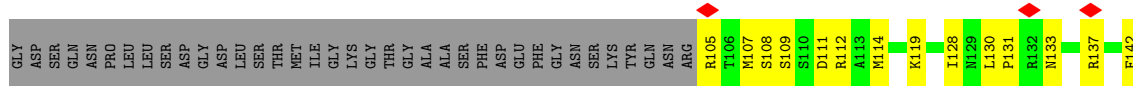
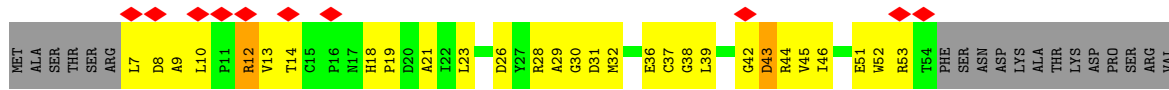




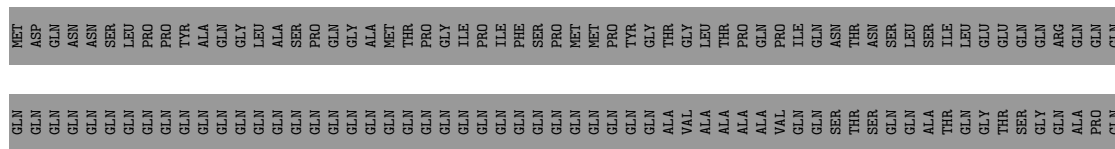
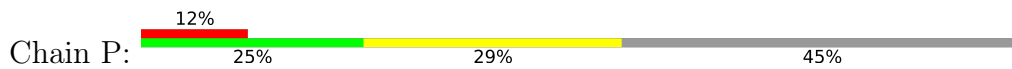
• Molecule 18: Transcription initiation factor IIA subunit 2

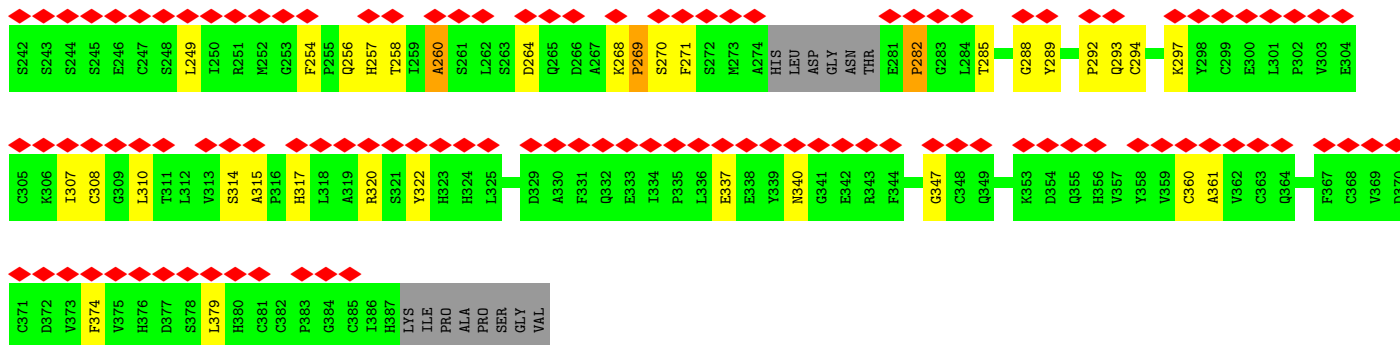


• Molecule 19: Transcription initiation factor IIB

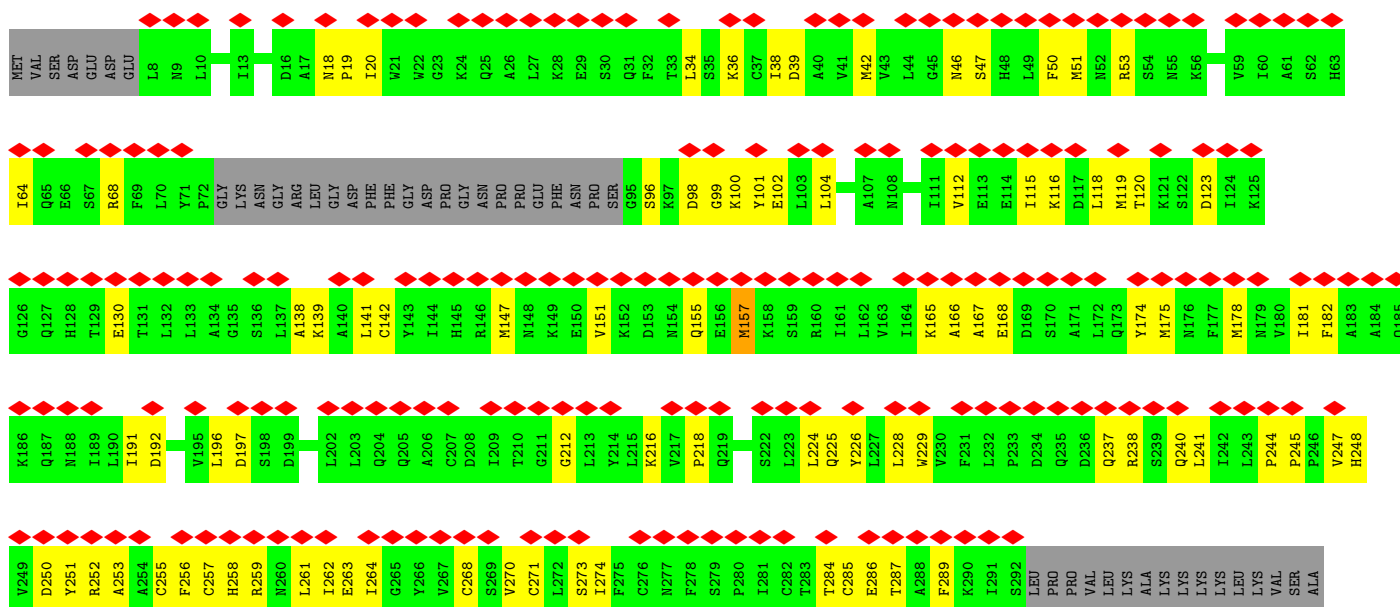


• Molecule 20: TATA-box-binding protein

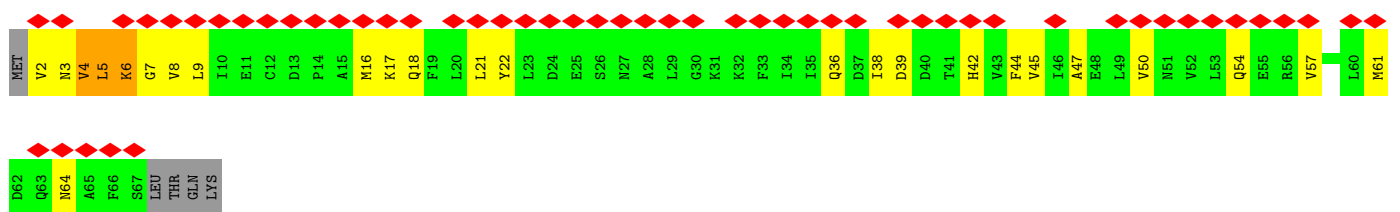




• Molecule 32: General transcription factor IIH subunit 3

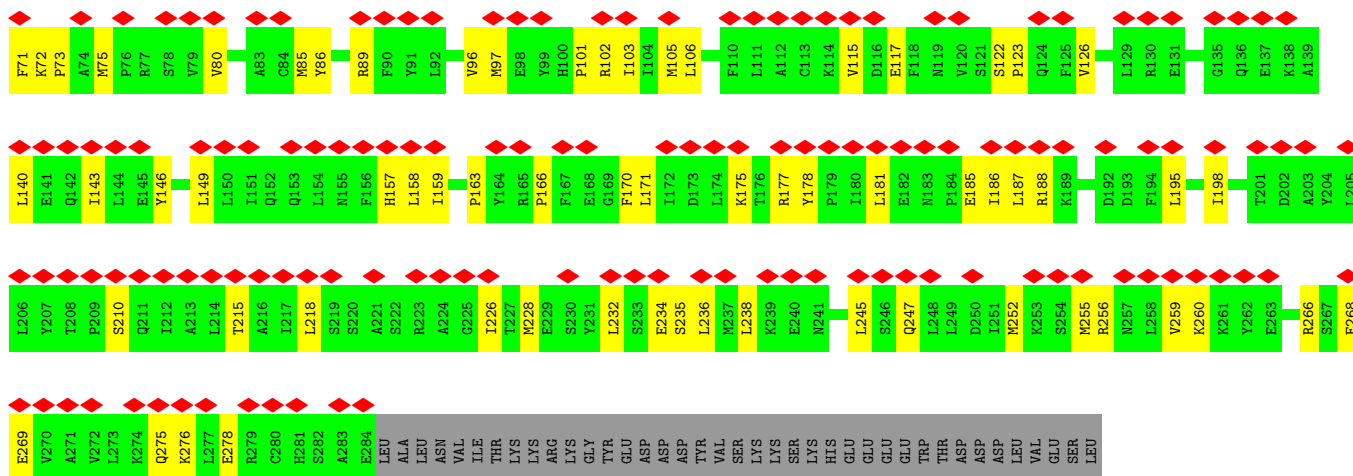


• Molecule 33: General transcription factor IIH subunit 5

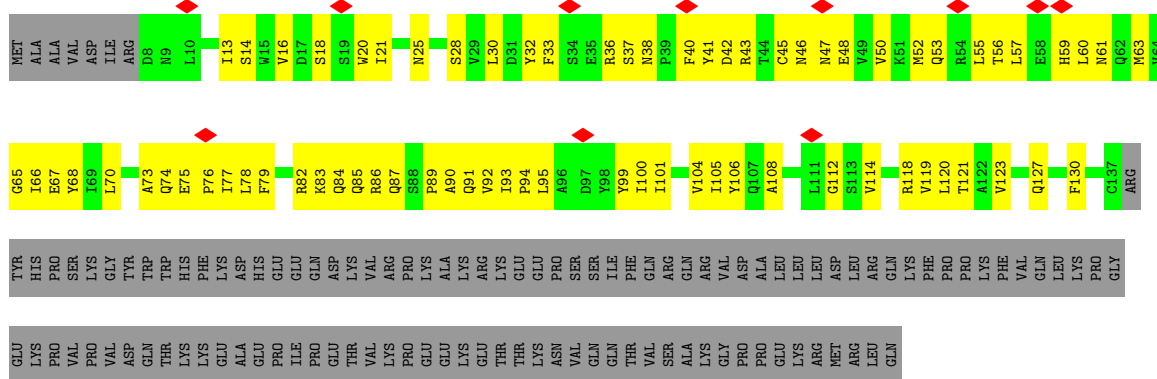
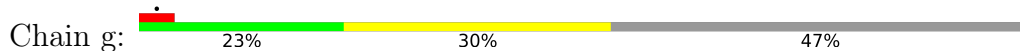


• Molecule 34: CDK-activating kinase assembly factor MAT1

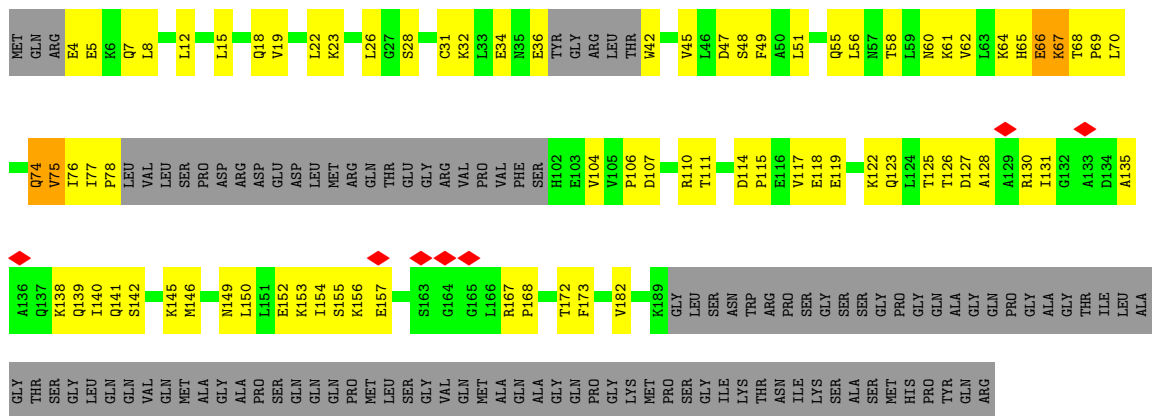
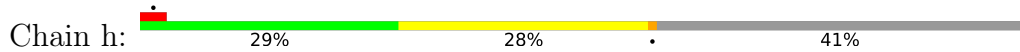




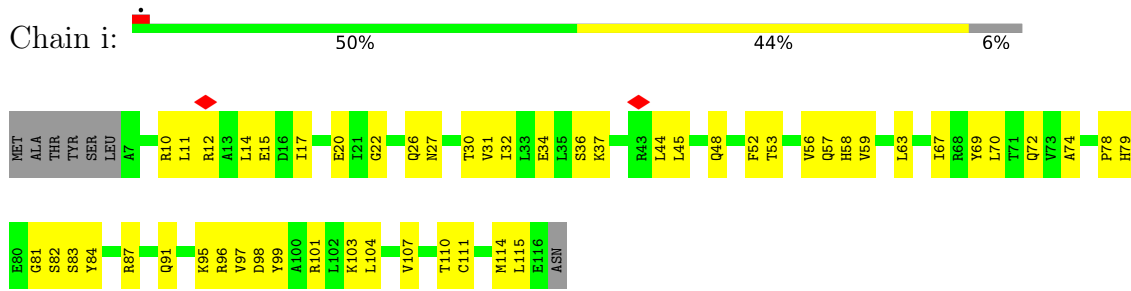
• Molecule 37: Mediator of RNA polymerase II transcription subunit 6



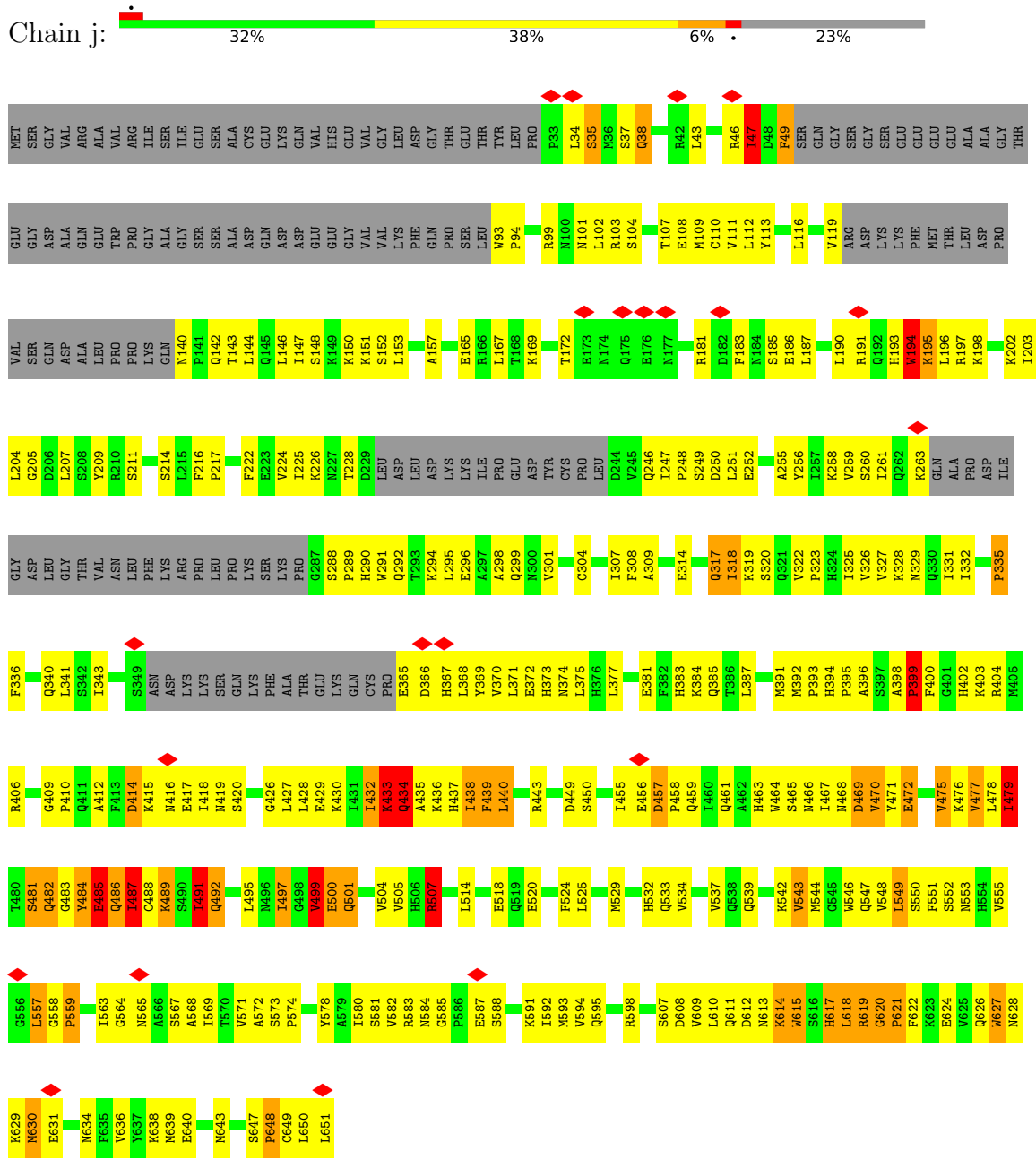
• Molecule 38: Mediator of RNA polymerase II transcription subunit 8



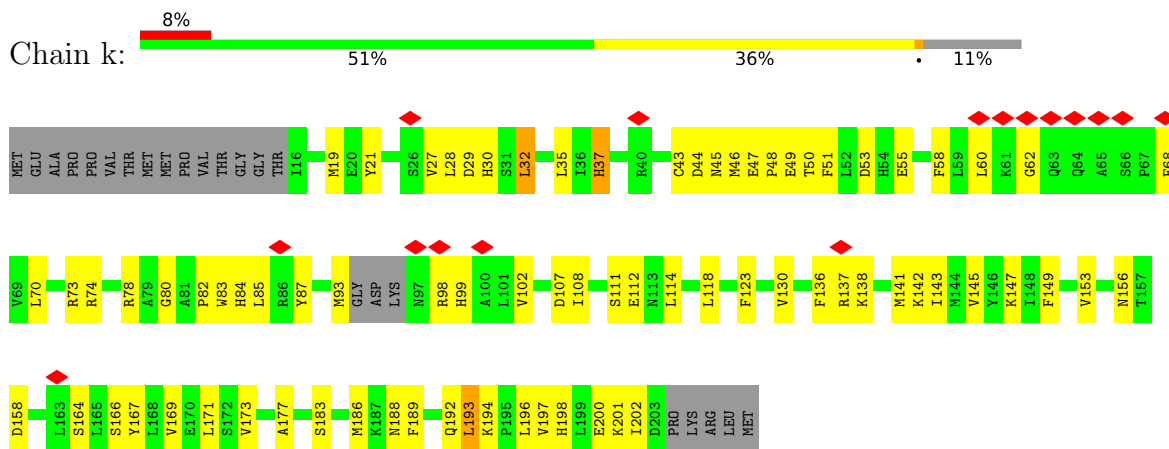
• Molecule 39: Mediator of RNA polymerase II transcription subunit 11



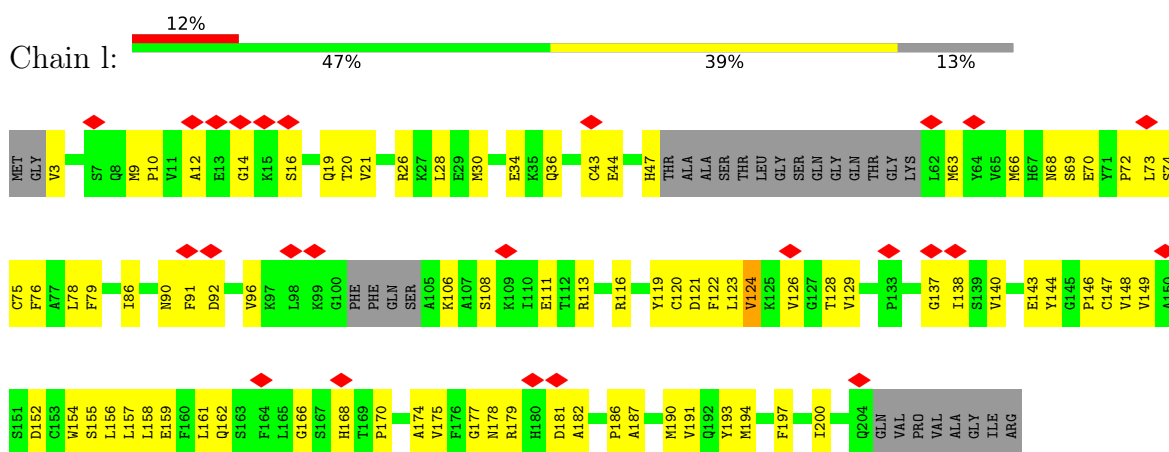
• Molecule 40: Mediator of RNA polymerase II transcription subunit 17



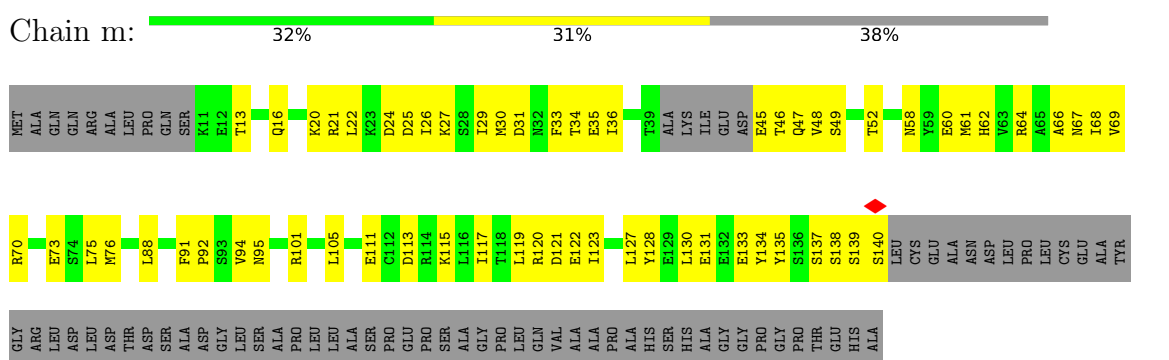
• Molecule 41: Mediator of RNA polymerase II transcription subunit 18



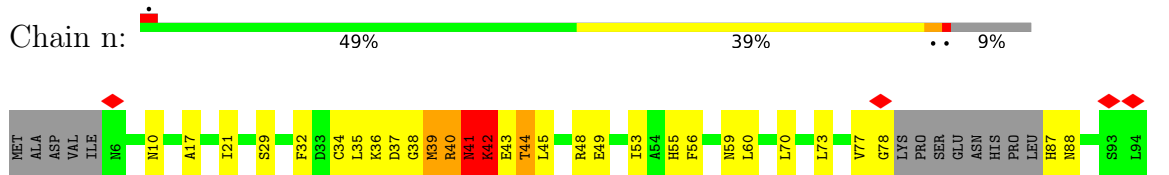
• Molecule 42: Mediator of RNA polymerase II transcription subunit 20

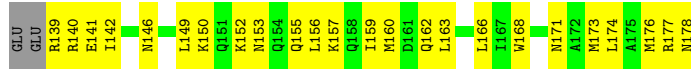


• Molecule 43: Mediator of RNA polymerase II transcription subunit 22

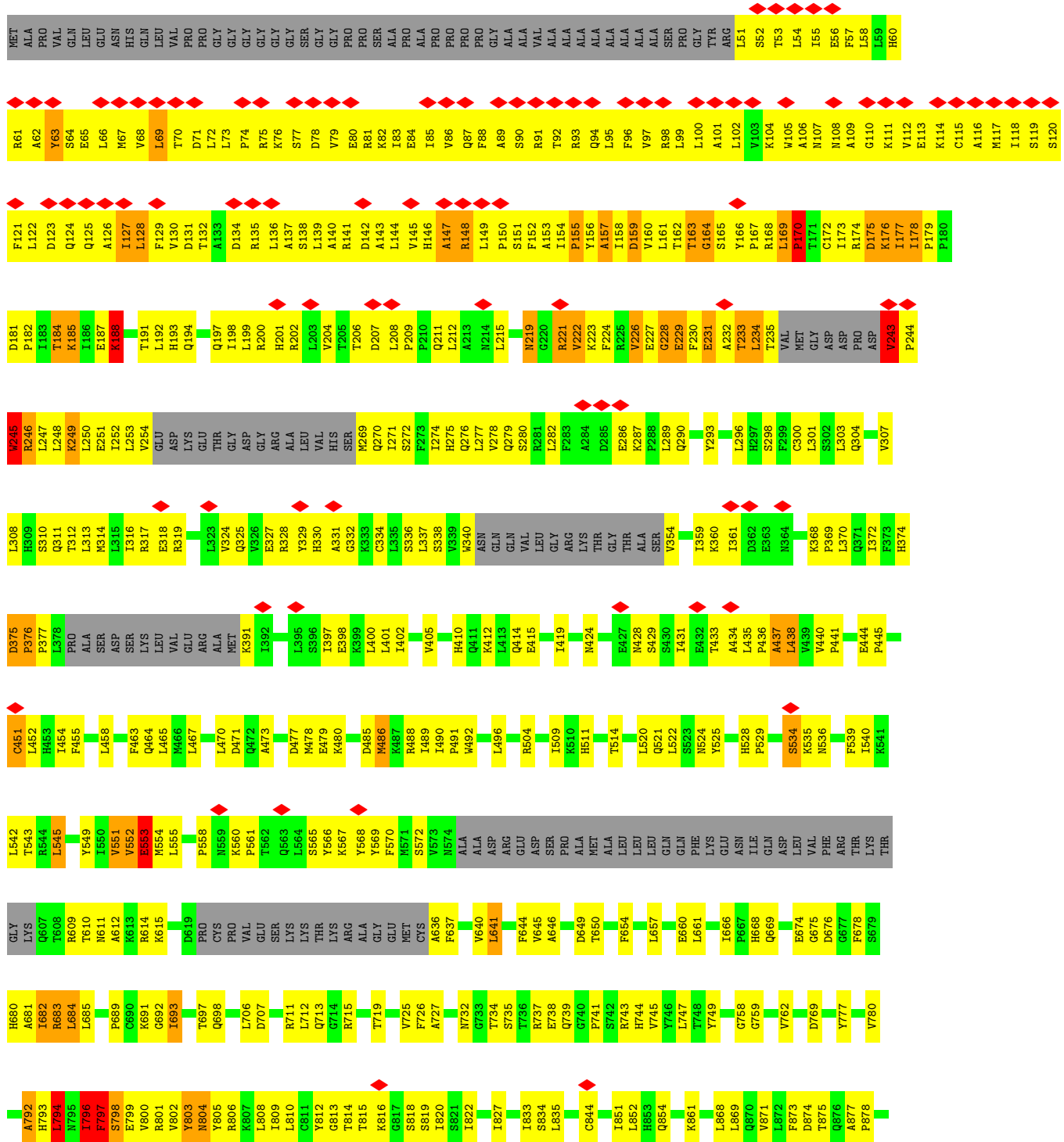


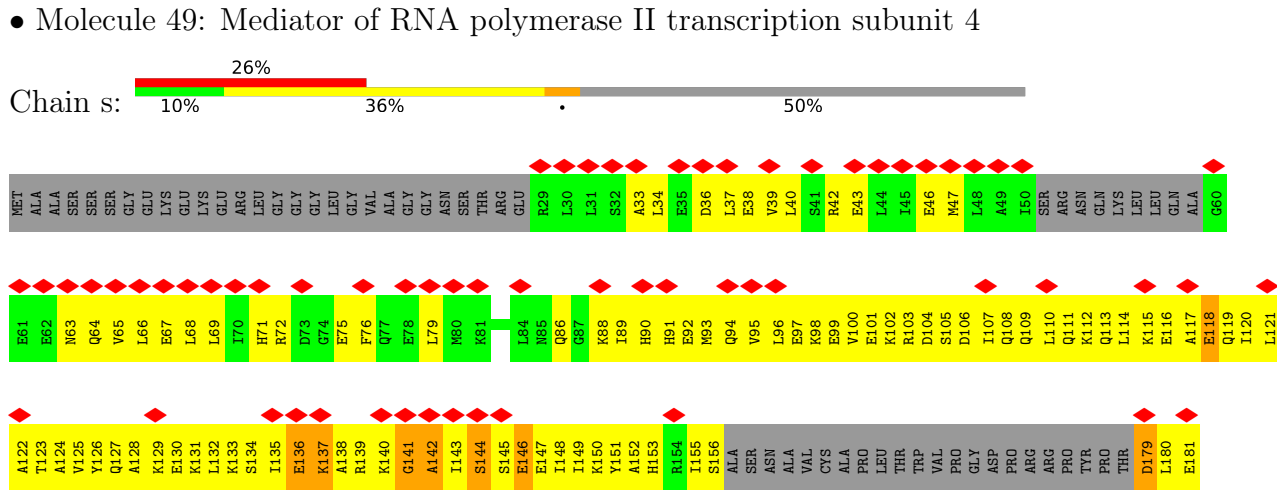
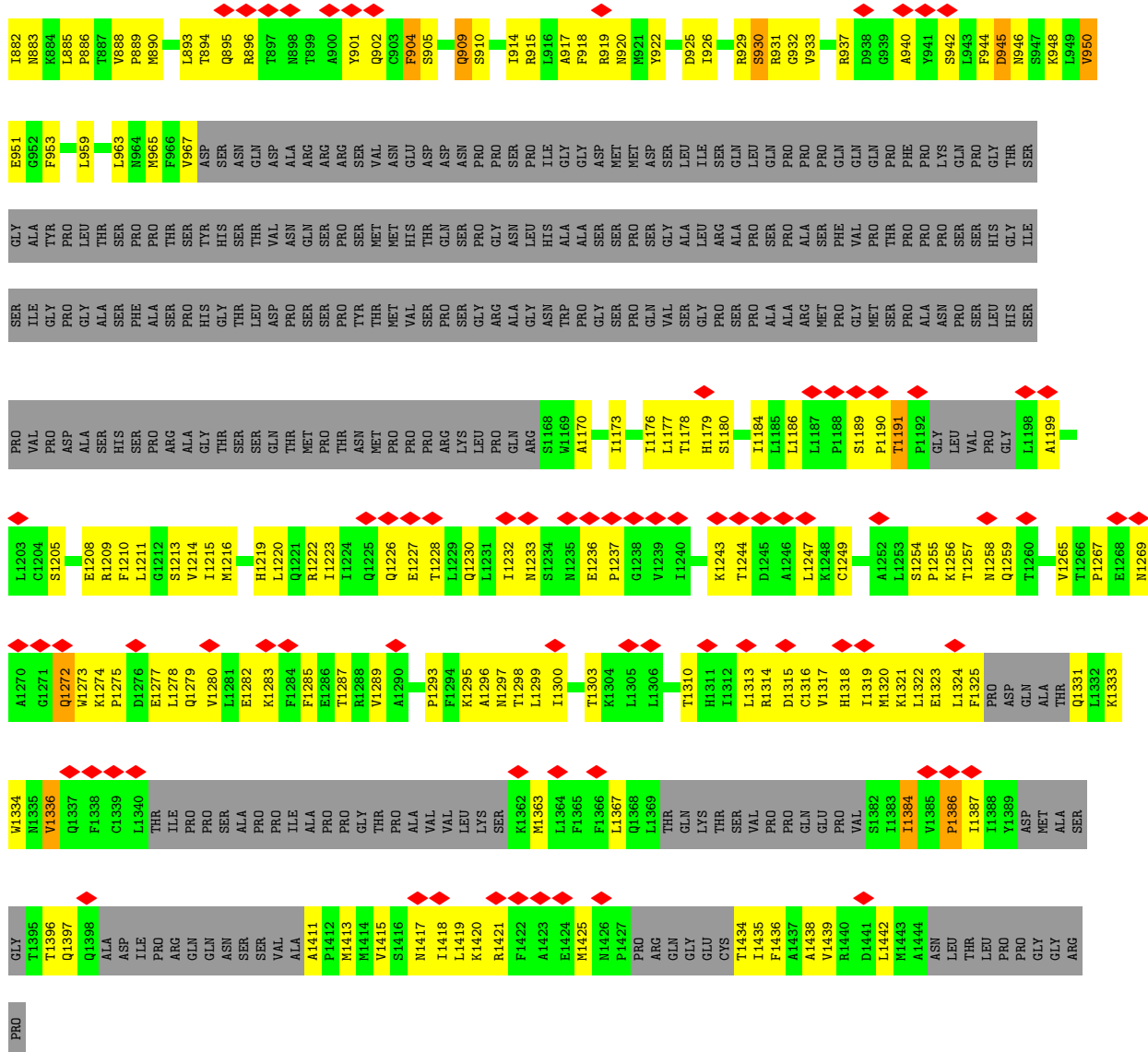
• Molecule 44: Mediator of RNA polymerase II transcription subunit 27





● Molecule 48: Mediator of RNA polymerase II transcription subunit 14





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	156383	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	31.5	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	2.116	Depositor
Minimum map value	-0.039	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.035	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	444.78, 444.78, 444.78	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	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, SF4, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.70	18/5990 (0.3%)	0.75	13/8137 (0.2%)
2	1	0.35	0/10913	0.51	0/14828
3	2	0.48	9/7141 (0.1%)	0.59	2/9672 (0.0%)
4	3	0.74	4/1540 (0.3%)	0.73	2/2093 (0.1%)
5	A	0.33	0/11733	0.63	15/15844 (0.1%)
6	B	0.33	0/9310	0.50	2/12567 (0.0%)
7	C	0.34	0/2190	0.52	0/2975
8	D	0.22	0/1077	0.54	1/1446 (0.1%)
9	E	0.28	0/1753	0.50	0/2368
10	F	0.31	0/700	0.48	0/946
11	G	0.27	0/1382	0.53	0/1874
12	H	0.31	0/1227	0.53	0/1654
13	I	0.27	0/964	0.62	2/1305 (0.2%)
14	J	0.36	0/542	0.50	0/730
15	K	0.31	0/947	0.48	0/1282
16	L	0.28	0/394	0.61	0/524
17	M	0.21	0/945	0.60	1/1274 (0.1%)
18	N	0.22	0/816	0.52	0/1105
19	O	0.27	0/2049	0.54	0/2769
20	P	0.22	0/1489	0.47	0/2005
21	Q	0.23	0/1545	0.58	0/2075
22	R	0.22	0/1380	0.57	0/1854
23	S	0.23	0/1086	0.65	1/1461 (0.1%)
24	T	0.23	0/1817	0.61	1/2445 (0.0%)
25	U	0.25	0/1485	0.32	0/2293
26	V	0.26	0/1454	0.35	0/2239
27	W	0.35	0/4744	0.65	1/6402 (0.0%)
28	X	0.40	0/6236	0.73	2/8444 (0.0%)
29	Y	0.35	0/1660	0.79	5/2253 (0.2%)
30	Z	0.38	1/3552 (0.0%)	0.71	5/4814 (0.1%)
31	a	0.38	0/2637	0.67	2/3572 (0.1%)
32	b	0.35	0/2102	0.57	0/2844

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.33	0/528	0.71	0/713
34	d	0.30	0/2137	0.59	0/2890
35	e	0.34	0/2434	0.56	2/3300 (0.1%)
36	f	0.34	0/2342	0.45	0/3159
37	g	0.26	0/1058	0.53	0/1441
38	h	0.32	0/1245	0.60	0/1679
39	i	0.35	0/869	0.53	0/1168
40	j	0.94	32/4079 (0.8%)	0.92	17/5504 (0.3%)
41	k	0.37	0/1512	0.61	0/2034
42	l	0.35	0/1453	0.58	0/1963
43	m	0.41	0/1032	0.57	0/1385
44	n	0.58	2/2324 (0.1%)	0.73	5/3143 (0.2%)
45	o	0.39	0/897	0.59	0/1208
46	p	0.42	0/906	0.48	0/1222
47	q	0.41	0/1015	0.59	0/1360
48	r	0.72	11/8336 (0.1%)	0.89	32/11299 (0.3%)
49	s	0.99	1/1089 (0.1%)	1.05	2/1450 (0.1%)
50	t	1.22	1/991 (0.1%)	1.25	6/1331 (0.5%)
51	u	0.50	0/504	0.71	1/668 (0.1%)
52	v	1.04	3/1082 (0.3%)	1.09	5/1450 (0.3%)
53	w	0.89	0/311	1.02	0/412
54	x	1.22	0/858	1.28	8/1161 (0.7%)
55	y	1.23	3/1027 (0.3%)	1.16	6/1379 (0.4%)
56	z	1.14	8/1202 (0.7%)	1.29	11/1650 (0.7%)
All	All	0.50	93/132031 (0.1%)	0.67	150/179063 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	0	0	4
3	2	0	5
4	3	0	2
5	A	0	1
6	B	0	3
7	C	0	1
8	D	0	2
13	I	0	2
17	M	0	1
19	O	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
21	Q	0	1
23	S	0	1
27	W	0	3
28	X	0	3
29	Y	0	1
30	Z	0	2
31	a	0	2
34	d	0	1
37	g	0	1
38	h	0	1
39	i	0	1
40	j	0	9
44	n	0	4
45	o	0	2
48	r	0	13
49	s	0	5
50	t	0	3
52	v	0	1
53	w	0	4
54	x	0	5
55	y	0	1
56	z	0	1
All	All	0	88

The worst 5 of 93 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	z	719	PRO	CA-C	-15.14	1.42	1.52
48	r	245	TRP	C-N	14.21	1.53	1.33
40	j	440	LEU	CA-C	-10.54	1.39	1.52
56	z	721	LEU	CA-C	-9.09	1.42	1.52
40	j	497	ILE	CA-C	-8.21	1.43	1.52

The worst 5 of 150 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	z	715	LEU	CA-C-N	23.33	149.00	119.84
56	z	715	LEU	C-N-CA	23.33	149.00	119.84
5	A	1623	SER	CA-C-N	19.00	139.04	119.85
5	A	1623	SER	C-N-CA	19.00	139.04	119.85
48	r	245	TRP	CA-C-N	-13.47	102.58	122.65

There are no chirality outliers.

5 of 88 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	112	ASP	Peptide
1	0	170	LEU	Peptide
1	0	569	LEU	Peptide
1	0	732	LEU	Peptide
3	2	597	LEU	Peptide

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	0	5864	0	5967	384	0
2	1	10636	0	10706	350	0
3	2	7007	0	7171	331	0
4	3	1504	0	1492	119	0
5	A	11519	0	11611	513	0
6	B	9129	0	9143	291	0
7	C	2147	0	2091	78	0
8	D	1062	0	1042	125	0
9	E	1723	0	1744	58	0
10	F	689	0	715	29	0
11	G	1351	0	1358	63	0
12	H	1205	0	1168	35	0
13	I	942	0	871	43	0
14	J	533	0	554	12	0
15	K	928	0	953	23	0
16	L	388	0	394	10	0
17	M	930	0	888	76	0
18	N	806	0	818	60	0
19	O	2018	0	2061	80	0
20	P	1462	0	1549	118	0
21	Q	1520	0	1520	110	0
22	R	1357	0	1381	86	0
23	S	1059	0	1036	65	0
24	T	1788	0	1819	119	0
25	U	1321	0	716	44	0
26	V	1300	0	718	49	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	W	4645	0	4692	485	0
28	X	6109	0	6137	223	0
29	Y	1631	0	1532	267	0
30	Z	3473	0	3511	450	0
31	a	2580	0	2550	147	0
32	b	2065	0	2096	302	0
33	c	522	0	526	173	0
34	d	2104	0	1946	37	0
35	e	2376	0	2402	109	0
36	f	2293	0	2315	65	0
37	g	1035	0	1023	84	0
38	h	1230	0	1236	106	0
39	i	863	0	869	116	0
40	j	4005	0	4053	659	0
41	k	1484	0	1488	142	0
42	l	1425	0	1409	159	0
43	m	1024	0	1000	260	0
44	n	2279	0	2285	206	0
45	o	887	0	880	103	0
46	p	893	0	900	99	0
47	q	1007	0	1044	172	0
48	r	8174	0	8275	803	0
49	s	1084	0	1118	231	0
50	t	975	0	1005	284	0
51	u	501	0	530	56	0
52	v	1067	0	1080	307	0
53	w	309	0	309	82	0
54	x	852	0	842	255	0
55	y	1003	0	991	311	0
56	z	1168	0	1162	233	0
57	A	2	0	0	0	0
58	A	2	0	0	0	0
58	B	1	0	0	0	0
58	C	1	0	0	0	0
58	I	2	0	0	0	0
58	J	1	0	0	0	0
58	L	1	0	0	0	0
58	O	1	0	0	0	0
58	Q	1	0	0	0	0
58	a	3	0	0	0	0
58	b	1	0	0	0	0
58	d	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	X	8	0	0	0	0
All	All	129277	0	128692	8213	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 32.

The worst 5 of 8213 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)
30:Z:57:MET:HG2	32:b:51:MET:SD	1.28	1.71
27:W:85:PHE:HZ	30:Z:336:TYR:CD2	1.07	1.67
27:W:520:ARG:HA	33:c:22:TYR:CE1	1.19	1.64
27:W:85:PHE:CZ	30:Z:336:TYR:CD2	1.77	1.63
43:m:130:LEU:CB	47:q:160:MET:HE2	1.23	1.63

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	740/841 (88%)	619 (84%)	114 (15%)	7 (1%)	14	49
2	1	1313/1368 (96%)	1201 (92%)	108 (8%)	4 (0%)	36	71
3	2	885/989 (90%)	774 (88%)	105 (12%)	6 (1%)	18	55
4	3	189/747 (25%)	167 (88%)	22 (12%)	0	100	100
5	A	1443/1970 (73%)	1316 (91%)	119 (8%)	8 (1%)	21	58
6	B	1134/1174 (97%)	1028 (91%)	103 (9%)	3 (0%)	36	71
7	C	263/275 (96%)	240 (91%)	23 (9%)	0	100	100
8	D	127/142 (89%)	114 (90%)	12 (9%)	1 (1%)	16	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	E	208/210 (99%)	190 (91%)	18 (9%)	0	100	100
10	F	84/127 (66%)	80 (95%)	4 (5%)	0	100	100
11	G	169/172 (98%)	154 (91%)	15 (9%)	0	100	100
12	H	148/150 (99%)	134 (90%)	13 (9%)	1 (1%)	18	55
13	I	114/125 (91%)	95 (83%)	18 (16%)	1 (1%)	14	49
14	J	65/67 (97%)	61 (94%)	4 (6%)	0	100	100
15	K	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
16	L	44/58 (76%)	37 (84%)	7 (16%)	0	100	100
17	M	109/376 (29%)	91 (84%)	18 (16%)	0	100	100
18	N	97/109 (89%)	83 (86%)	14 (14%)	0	100	100
19	O	256/316 (81%)	232 (91%)	21 (8%)	3 (1%)	10	42
20	P	183/339 (54%)	178 (97%)	5 (3%)	0	100	100
21	Q	180/439 (41%)	153 (85%)	25 (14%)	2 (1%)	11	45
22	R	163/291 (56%)	139 (85%)	24 (15%)	0	100	100
23	S	123/517 (24%)	97 (79%)	25 (20%)	1 (1%)	16	52
24	T	218/249 (88%)	182 (84%)	33 (15%)	3 (1%)	9	39
27	W	568/782 (73%)	518 (91%)	49 (9%)	1 (0%)	43	78
28	X	758/760 (100%)	666 (88%)	92 (12%)	0	100	100
29	Y	214/548 (39%)	179 (84%)	35 (16%)	0	100	100
30	Z	432/462 (94%)	391 (90%)	39 (9%)	2 (0%)	24	63
31	a	327/395 (83%)	287 (88%)	40 (12%)	0	100	100
32	b	259/308 (84%)	244 (94%)	15 (6%)	0	100	100
33	c	64/71 (90%)	60 (94%)	4 (6%)	0	100	100
34	d	271/309 (88%)	236 (87%)	33 (12%)	2 (1%)	18	55
35	e	294/346 (85%)	277 (94%)	17 (6%)	0	100	100
36	f	277/323 (86%)	268 (97%)	9 (3%)	0	100	100
37	g	128/246 (52%)	111 (87%)	17 (13%)	0	100	100
38	h	152/268 (57%)	133 (88%)	16 (10%)	3 (2%)	6	31
39	i	108/117 (92%)	103 (95%)	5 (5%)	0	100	100
40	j	492/651 (76%)	409 (83%)	72 (15%)	11 (2%)	5	28
41	k	181/208 (87%)	159 (88%)	22 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	l	178/212 (84%)	150 (84%)	27 (15%)	1 (1%)	21	58
43	m	121/200 (60%)	118 (98%)	3 (2%)	0	100	100
44	n	277/311 (89%)	225 (81%)	46 (17%)	6 (2%)	5	28
45	o	106/178 (60%)	95 (90%)	9 (8%)	2 (2%)	6	32
46	p	110/200 (55%)	106 (96%)	4 (4%)	0	100	100
47	q	116/178 (65%)	107 (92%)	9 (8%)	0	100	100
48	r	1004/1454 (69%)	819 (82%)	165 (16%)	20 (2%)	6	31
49	s	129/270 (48%)	98 (76%)	27 (21%)	4 (3%)	3	21
50	t	110/233 (47%)	76 (69%)	32 (29%)	2 (2%)	6	33
51	u	54/146 (37%)	49 (91%)	5 (9%)	0	100	100
52	v	129/135 (96%)	92 (71%)	35 (27%)	2 (2%)	7	37
53	w	31/244 (13%)	21 (68%)	9 (29%)	1 (3%)	3	21
54	x	107/144 (74%)	81 (76%)	26 (24%)	0	100	100
55	y	112/131 (86%)	71 (63%)	36 (32%)	5 (4%)	2	17
56	z	145/788 (18%)	126 (87%)	14 (10%)	5 (3%)	3	20
All	All	15623/21786 (72%)	13748 (88%)	1768 (11%)	107 (1%)	20	55

5 of 107 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	170	LEU
1	0	570	ASN
3	2	687	PHE
5	A	1617	PRO
5	A	1620	PRO

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	0	666/736 (90%)	644 (97%)	22 (3%)	33	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	1	1187/1232 (96%)	1183 (100%)	4 (0%)	86	84
3	2	780/864 (90%)	775 (99%)	5 (1%)	78	81
4	3	165/601 (28%)	155 (94%)	10 (6%)	17	39
5	A	1285/1748 (74%)	1278 (100%)	7 (0%)	81	82
6	B	999/1028 (97%)	999 (100%)	0	100	100
7	C	244/252 (97%)	244 (100%)	0	100	100
8	D	119/126 (94%)	119 (100%)	0	100	100
9	E	192/192 (100%)	192 (100%)	0	100	100
10	F	74/111 (67%)	74 (100%)	0	100	100
11	G	152/153 (99%)	152 (100%)	0	100	100
12	H	131/131 (100%)	131 (100%)	0	100	100
13	I	104/112 (93%)	104 (100%)	0	100	100
14	J	56/56 (100%)	56 (100%)	0	100	100
15	K	105/106 (99%)	105 (100%)	0	100	100
16	L	43/55 (78%)	43 (100%)	0	100	100
17	M	105/324 (32%)	105 (100%)	0	100	100
18	N	90/98 (92%)	88 (98%)	2 (2%)	45	64
19	O	222/268 (83%)	222 (100%)	0	100	100
20	P	159/293 (54%)	159 (100%)	0	100	100
21	Q	167/373 (45%)	167 (100%)	0	100	100
22	R	150/261 (58%)	149 (99%)	1 (1%)	76	79
23	S	111/448 (25%)	111 (100%)	0	100	100
24	T	196/218 (90%)	196 (100%)	0	100	100
27	W	508/688 (74%)	497 (98%)	11 (2%)	45	64
28	X	661/664 (100%)	659 (100%)	2 (0%)	86	84
29	Y	162/484 (34%)	162 (100%)	0	100	100
30	Z	372/399 (93%)	365 (98%)	7 (2%)	50	66
31	a	296/352 (84%)	296 (100%)	0	100	100
32	b	234/272 (86%)	233 (100%)	1 (0%)	84	83
33	c	59/64 (92%)	54 (92%)	5 (8%)	10	29
34	d	210/283 (74%)	210 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	e	259/299 (87%)	259 (100%)	0	100	100
36	f	256/296 (86%)	256 (100%)	0	100	100
37	g	115/223 (52%)	115 (100%)	0	100	100
38	h	139/225 (62%)	139 (100%)	0	100	100
39	i	92/98 (94%)	92 (100%)	0	100	100
40	j	452/577 (78%)	426 (94%)	26 (6%)	18	40
41	k	164/183 (90%)	161 (98%)	3 (2%)	51	67
42	l	158/178 (89%)	157 (99%)	1 (1%)	78	81
43	m	118/173 (68%)	118 (100%)	0	100	100
44	n	256/280 (91%)	254 (99%)	2 (1%)	73	78
45	o	102/152 (67%)	102 (100%)	0	100	100
46	p	102/163 (63%)	102 (100%)	0	100	100
47	q	114/155 (74%)	114 (100%)	0	100	100
48	r	905/1271 (71%)	875 (97%)	30 (3%)	33	55
49	s	119/230 (52%)	118 (99%)	1 (1%)	73	78
50	t	110/216 (51%)	109 (99%)	1 (1%)	70	77
51	u	59/133 (44%)	58 (98%)	1 (2%)	53	68
52	v	119/124 (96%)	113 (95%)	6 (5%)	22	43
53	w	34/208 (16%)	33 (97%)	1 (3%)	37	58
54	x	92/119 (77%)	82 (89%)	10 (11%)	6	21
55	y	105/115 (91%)	93 (89%)	12 (11%)	5	19
56	z	135/697 (19%)	129 (96%)	6 (4%)	25	47
All	All	14009/19107 (73%)	13832 (99%)	177 (1%)	59	72

5 of 177 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
48	r	188	LYS
52	v	48	LEU
48	r	227	GLU
48	r	693	ILE
54	x	9	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 316 such sidechains are listed below:

Mol	Chain	Res	Type
40	j	517	GLN
49	s	64	GLN
40	j	617	HIS
45	o	105	GLN
54	x	27	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 18 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
59	SF4	X	1000	28	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
59	SF4	X	1000	28	-	-	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.

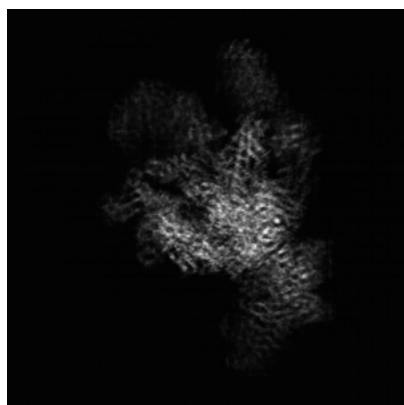
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23255. These allow visual inspection of the internal detail of the map and identification of artifacts.

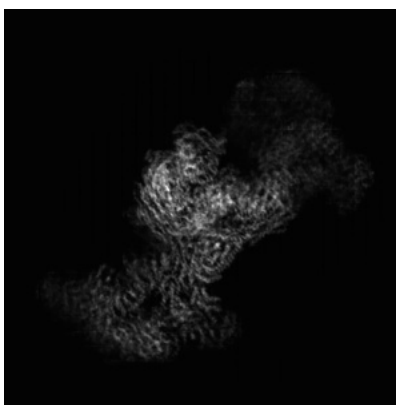
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

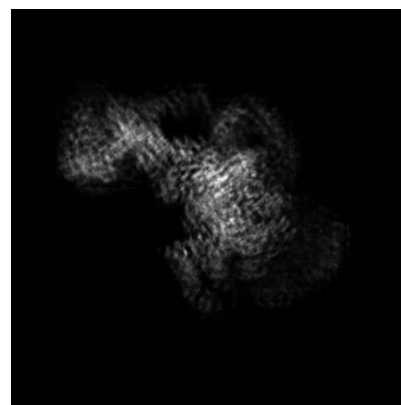
6.1.1 Primary map



X



Y

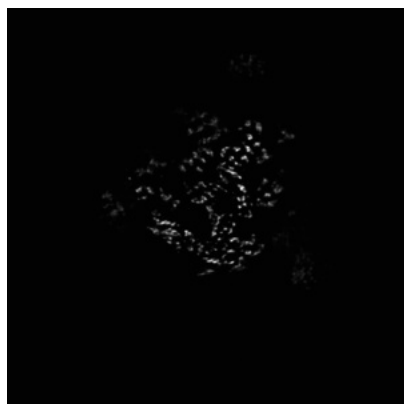


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 210



Y Index: 210

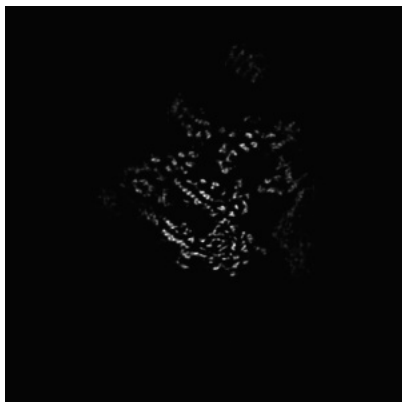


Z Index: 210

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

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 221



Y Index: 254

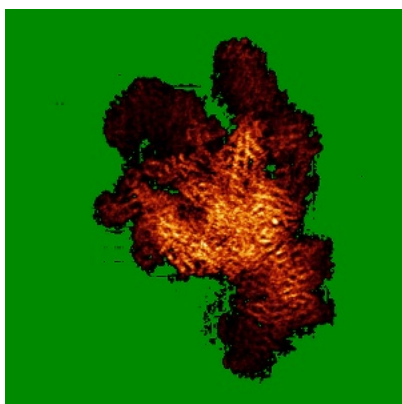


Z Index: 182

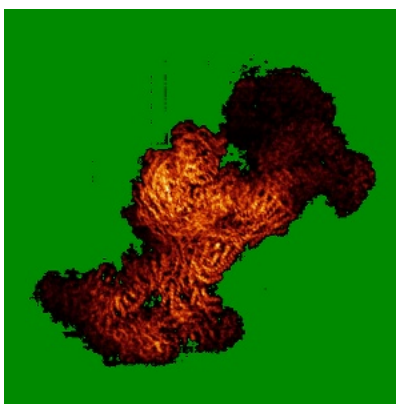
The images above show the largest variance slices of the map in three orthogonal directions.

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

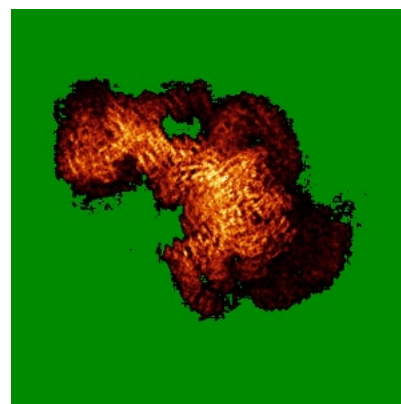
6.4.1 Primary map



X



Y

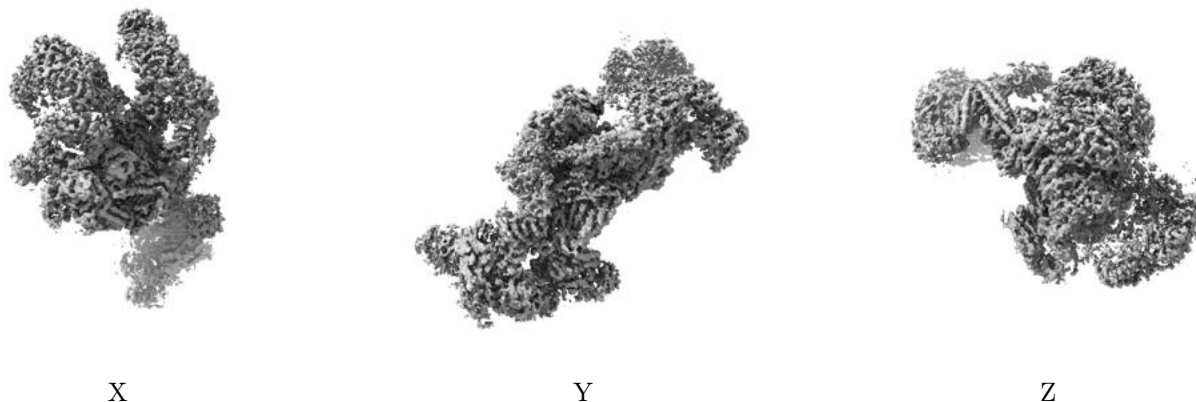


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

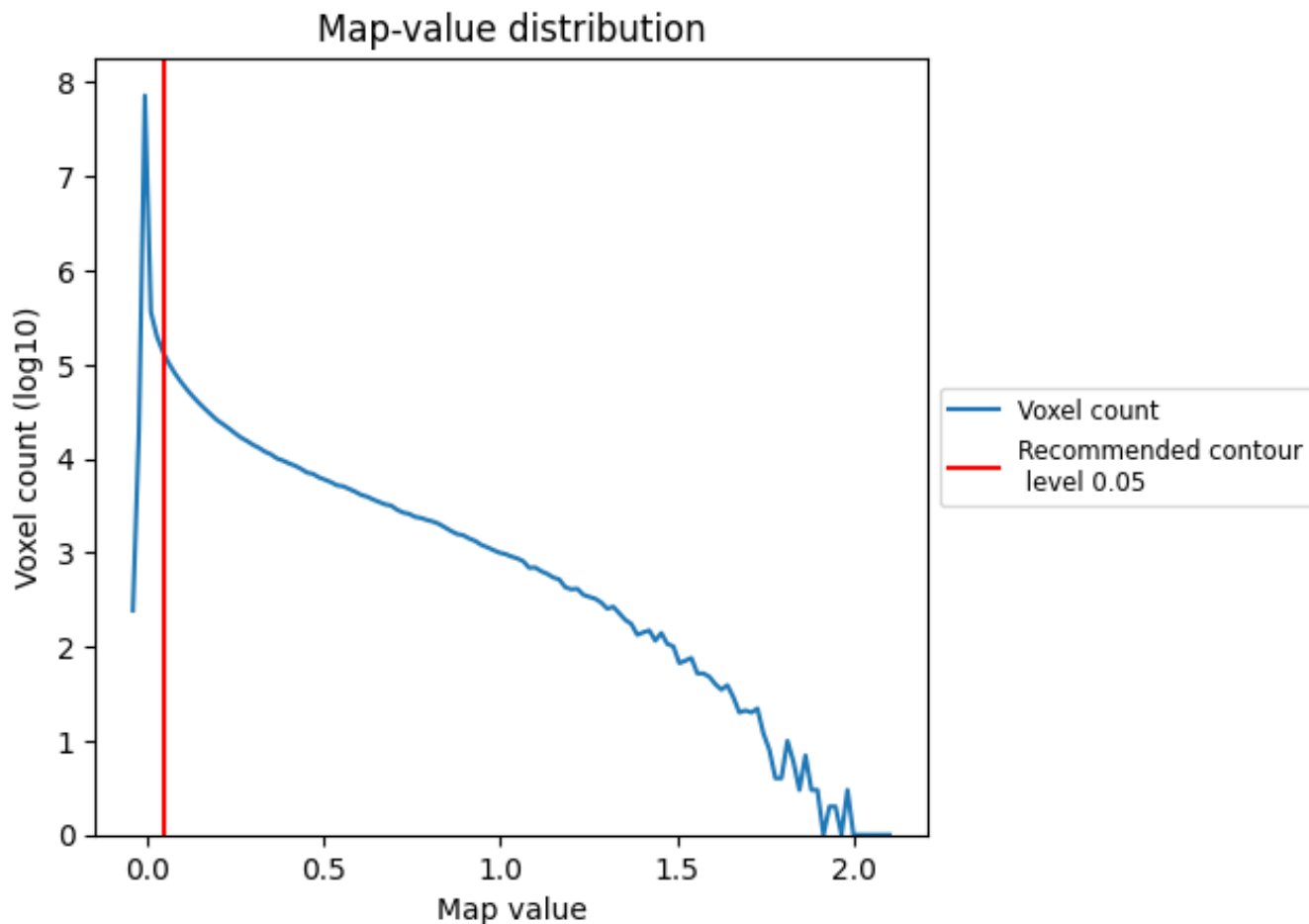
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

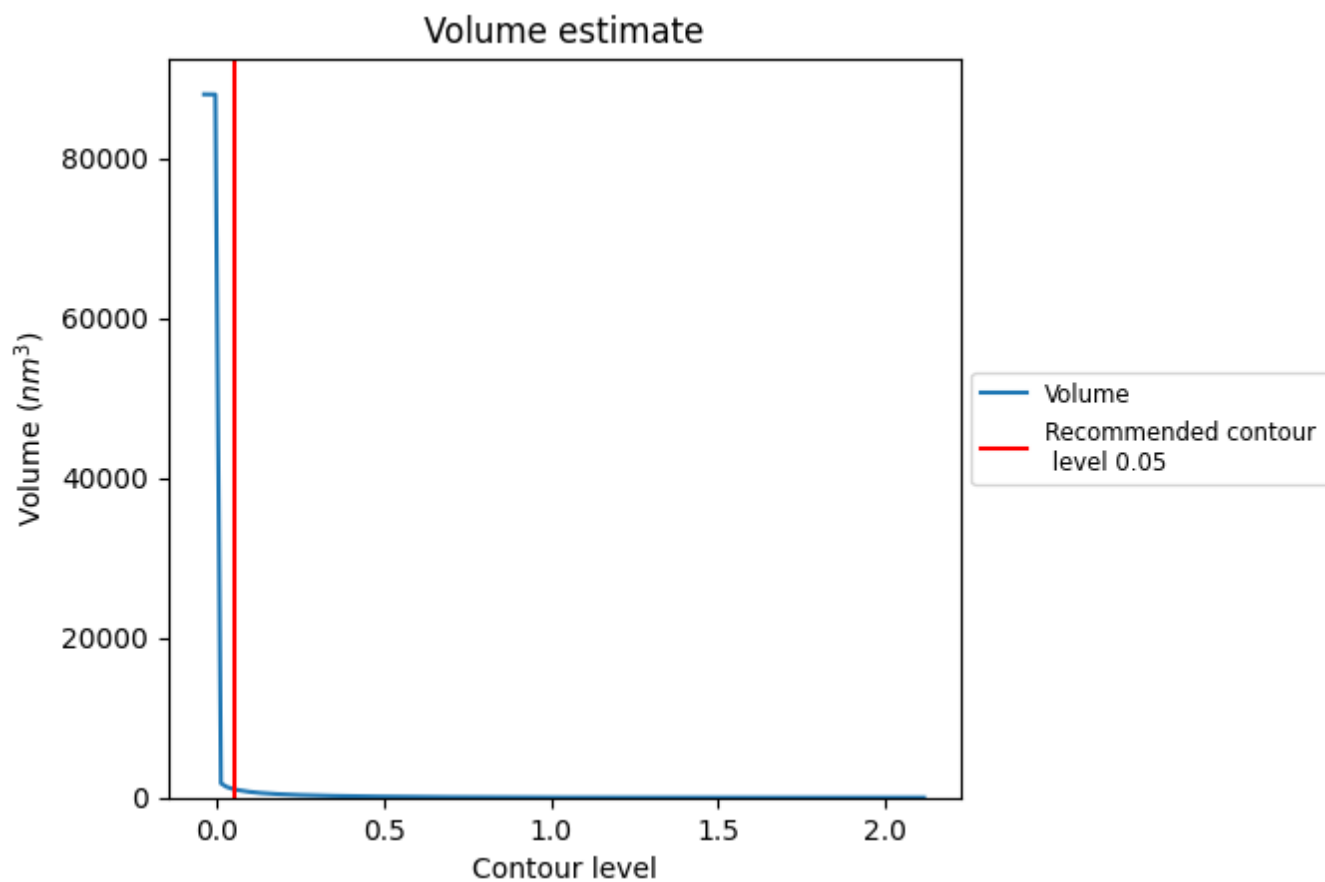
This section contains the results of statistical analysis of the map.

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.

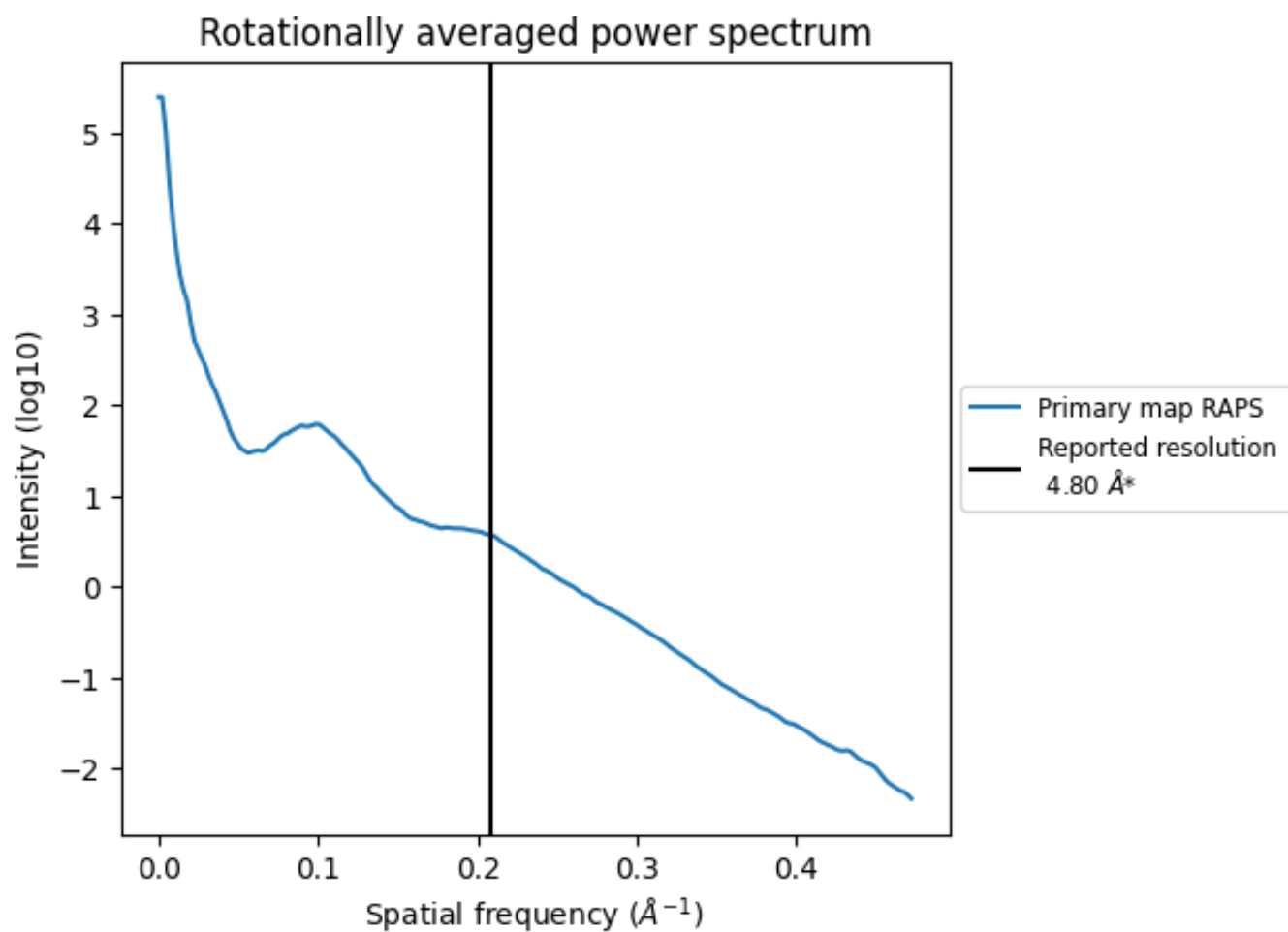
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1055 nm^3 ; this corresponds to an approximate mass of 953 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 0.208 Å⁻¹

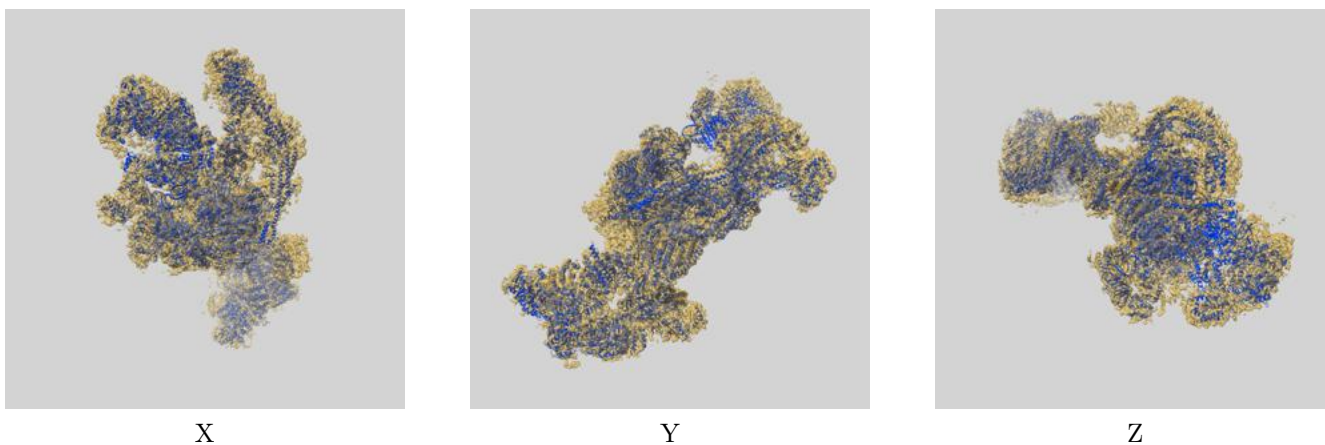
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

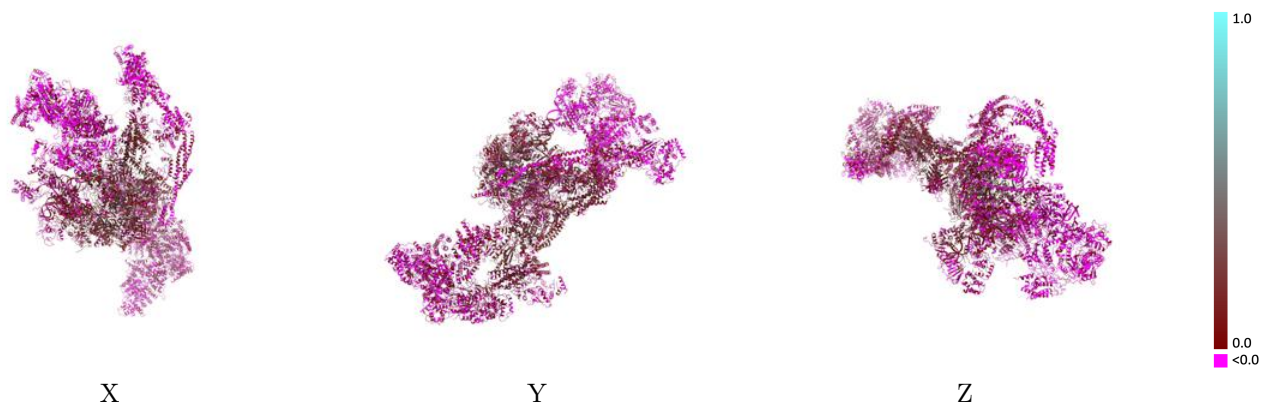
This section contains information regarding the fit between EMDB map EMD-23255 and PDB model 7LBM. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



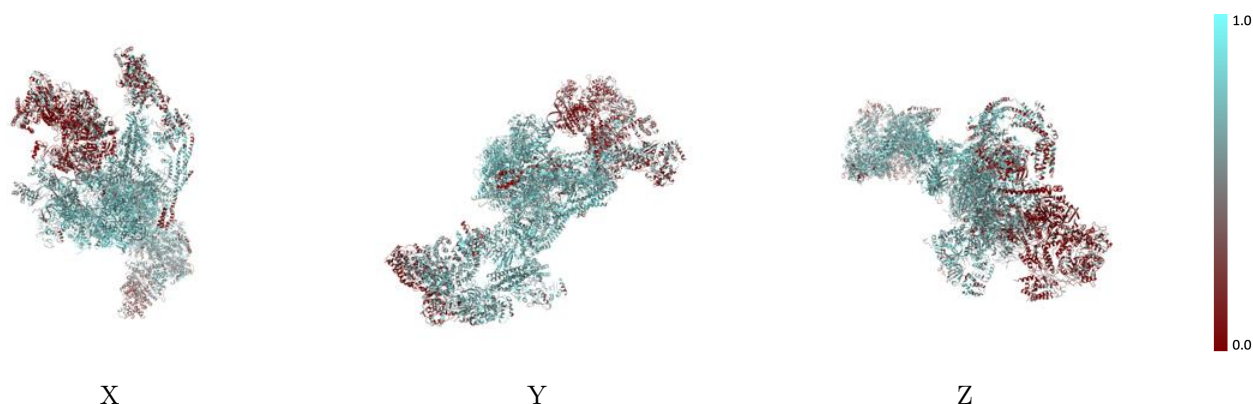
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



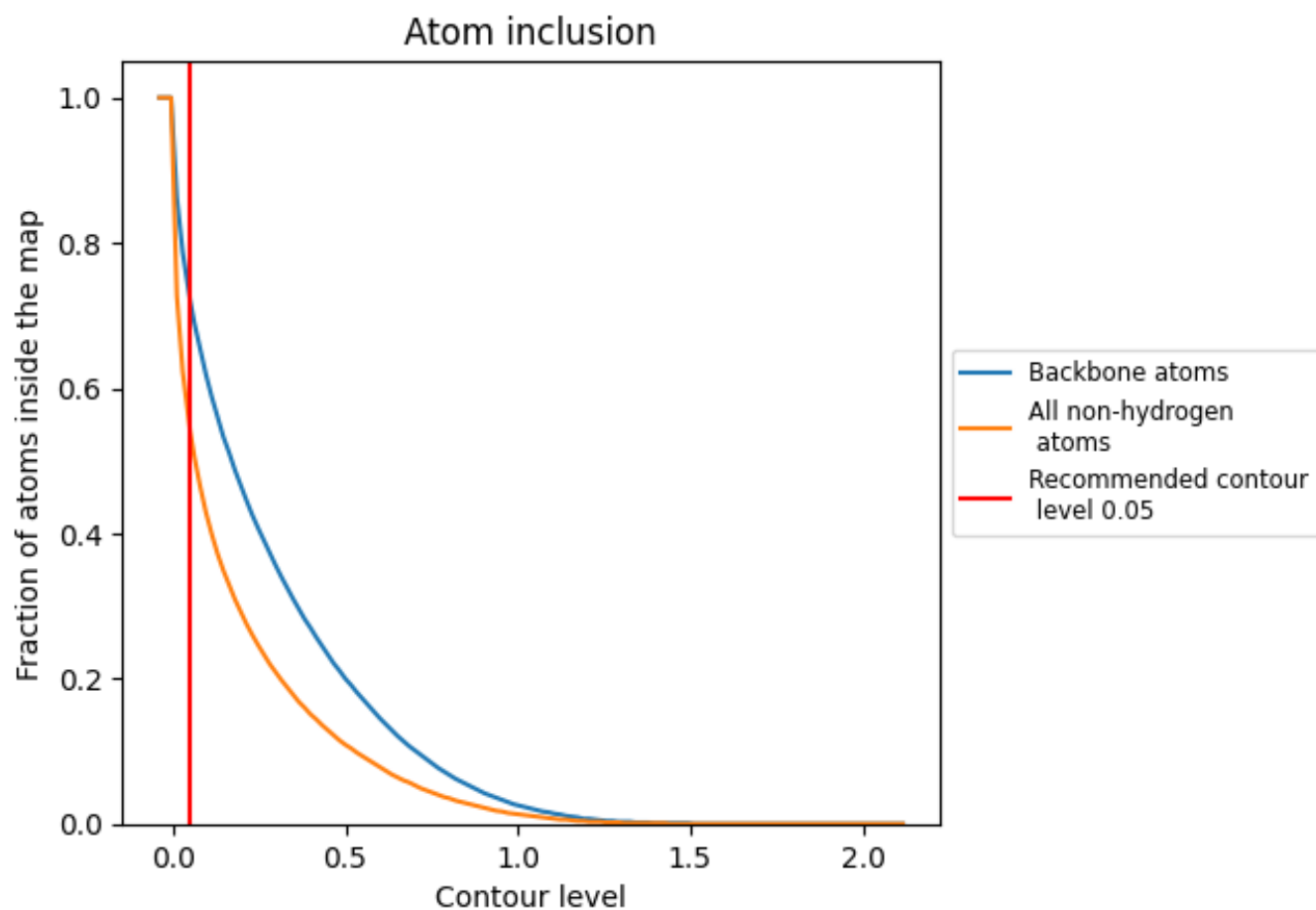
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 54% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5400	 0.0740
0	 0.6280	 0.0650
1	 0.4060	 -0.0060
2	 0.5140	 0.0300
3	 0.5240	 0.0330
A	 0.7150	 0.1930
B	 0.7240	 0.2010
C	 0.6720	 0.1450
D	 0.6640	 0.1400
E	 0.7060	 0.1630
F	 0.7070	 0.2010
G	 0.7280	 0.1730
H	 0.6740	 0.1380
I	 0.7120	 0.1510
J	 0.6810	 0.1180
K	 0.6870	 0.1510
L	 0.7020	 0.1860
M	 0.4900	 -0.0110
N	 0.4860	 0.0020
O	 0.6640	 0.1200
P	 0.6060	 0.0650
Q	 0.6220	 0.0780
R	 0.6070	 0.0470
S	 0.5410	 0.0520
T	 0.5720	 0.0580
U	 0.5970	 0.0640
V	 0.5890	 0.0520
W	 0.0960	 -0.0490
X	 0.3510	 -0.0060
Y	 0.2250	 -0.0660
Z	 0.1720	 -0.0670
a	 0.1290	 -0.0590
b	 0.2200	 -0.0550
c	 0.1850	 -0.0860
d	 0.3580	 -0.0120



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Chain	Atom inclusion	Q-score
e	 0.3920	 -0.0170
f	 0.3390	 -0.0590
g	 0.6910	 0.0790
h	 0.7060	 0.1450
i	 0.7250	 0.1740
j	 0.7350	 0.1960
k	 0.6540	 0.1170
l	 0.6410	 0.1080
m	 0.7310	 0.2080
n	 0.7070	 0.1790
o	 0.6650	 0.1300
p	 0.6440	 0.1040
q	 0.6880	 0.1560
r	 0.6350	 0.1010
s	 0.4180	 0.0040
t	 0.5380	 0.0180
u	 0.3480	 -0.0210
v	 0.4240	 -0.0400
w	 0.3930	 -0.0220
x	 0.5280	 0.0110
y	 0.6030	 0.0470
z	 0.7130	 0.1360