



wwPDB EM Validation Summary Report ⓘ

Nov 2, 2022 – 09:04 PM EDT

PDB ID : 5U0S
EMDB ID : EMD-8480
Title : Cryo-EM structure of the Mediator-RNAPII complex
Authors : Tsai, K.-L.; Yu, X.; Gopalan, S.; Chao, T.-C.; Zhang, Y.; Florens, L.; Washburn, M.P.; Murakami, K.; Conaway, R.C.; Conaway, J.W.; Asturias, F.
Deposited on : 2016-11-26
Resolution : 7.80 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:

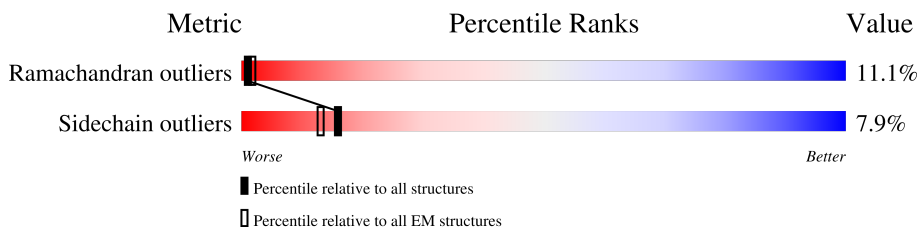
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance

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

The reported resolution of this entry is 7.80 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.



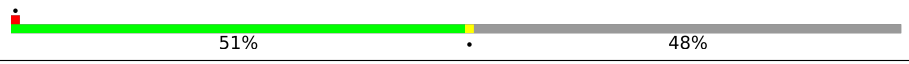





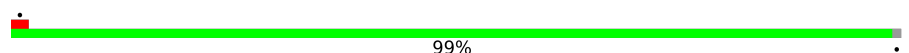
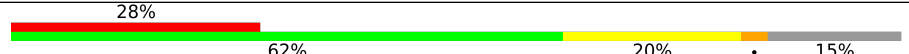
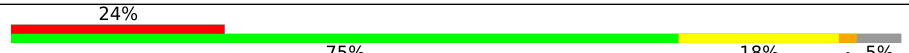
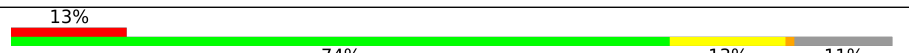

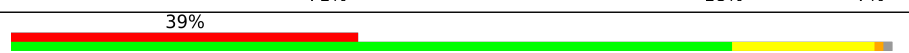


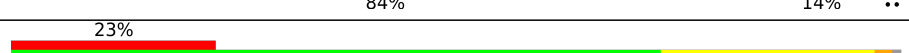

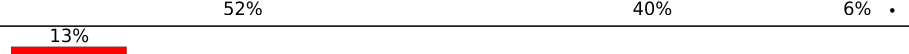
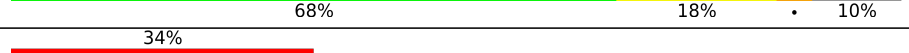

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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

Mol	Chain	Length	Quality of chain
1	F	216	
2	H	200	
3	Q	545	
4	R	207	
5	T	193	
6	K	116	
7	V	136	
8	N	931	
9	D	239	

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Mol	Chain	Length	Quality of chain
10	G	376	
11	U	138	
12	3	139	
13	2	273	
14	I	121	
15	S	139	
16	J	132	
17	a	1752	
18	b	1210	
19	c	297	
20	d	135	
21	e	210	
22	f	142	
23	g	172	
24	h	125	
25	i	113	
26	j	71	
27	k	123	
28	l	63	

2 Entry composition [i](#)

There are 28 unique types of molecules in this entry. The entry contains 51548 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Mediator complex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	F	188	1534	979	258	288	9	0	0

- Molecule 2 is a protein called Mediator complex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	H	182	1493	941	257	292	3	0	0

- Molecule 3 is a protein called Mediator complex subunit 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	Q	500	3787	2393	651	725	18	0	0

- Molecule 4 is a protein called Mediator complex subunit 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	R	207	1694	1082	288	316	8	0	0

- Molecule 5 is a protein called Mediator complex subunit 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	T	176	1435	938	234	258	5	0	0

- Molecule 6 is a protein called Mediator complex subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	K	98	769	486	128	154	1	0	0

- Molecule 7 is a protein called Mediator complex subunit 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	V	118	949	599	161	187	2	0	0

- Molecule 8 is a protein called Mediator complex subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	N	520	3887	2498	683	698	8	0	0

- Molecule 9 is a protein called Mediator complex subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	D	96	480	288	96	96	0	0

- Molecule 10 is a protein called Mediator complex subunit 7.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	G	194	965	577	194	194	0	0

- Molecule 11 is a protein called Mediator complex subunit 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	U	122	608	364	122	122	0	0

- Molecule 12 is a protein called Mediator complex subunit 31.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	3	103	515	309	103	103	0	0

- Molecule 13 is a protein called Mediator complex subunit 27.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	2	78	388	232	78	78	0	0

- Molecule 14 is a protein called Mediator complex subunit 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	I	75	374	224	75	75	0	0

- Molecule 15 is a protein called Mediator complex subunit 19.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	S	122	610	366	122	122	0	0

- Molecule 16 is a protein called Mediator complex subunit 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	J	131	655	393	131	131	0	0

- Molecule 17 is a protein called RNA polymerase II subunit Rpb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	a	1490	11761	7388	2065	2238	70	0	0

- Molecule 18 is a protein called RNA polymerase II subunit Rpb2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	b	1150	9180	5772	1630	1716	62	0	0

- Molecule 19 is a protein called RNA polymerase II subunit Rpb3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	c	263	2088	1315	355	406	12	0	0

- Molecule 20 is a protein called RNA polymerase II subunit Rpb4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	d	125	988	619	166	197	6	0	0

- Molecule 21 is a protein called RNA polymerase II subunit Rpb5.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	e	207	Total	C	N	O	S	0	0
			1663	1050	301	306	6		

- Molecule 22 is a protein called RNA polymerase II subunit Rpb6.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	f	83	Total	C	N	O	S	0	0
			656	416	112	125	3		

- Molecule 23 is a protein called RNA polymerase II subunit Rpb7.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	g	170	Total	C	N	O	S	0	0
			1330	860	217	247	6		

- Molecule 24 is a protein called RNA polymerase II subunit Rpb8.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	h	124	Total	C	N	O	S	0	0
			996	631	167	195	3		

- Molecule 25 is a protein called RNA polymerase II subunit Rpb9.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	i	111	Total	C	N	O	S	0	0
			902	551	164	176	11		

- Molecule 26 is a protein called RNA polymerase II subunit Rpb10.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	j	64	Total	C	N	O	S	0	0
			518	330	87	94	7		

- Molecule 27 is a protein called RNA polymerase II subunit Rpb11.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	k	119	Total	C	N	O	S	0	0
			955	608	159	182	6		

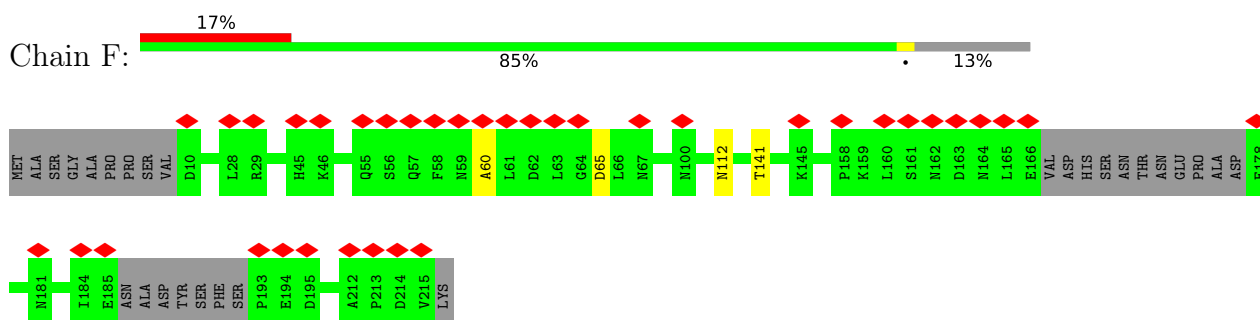
- Molecule 28 is a protein called RNA polymerase II subunit Rpb12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	1	45	368	225	74	61	8	0	0

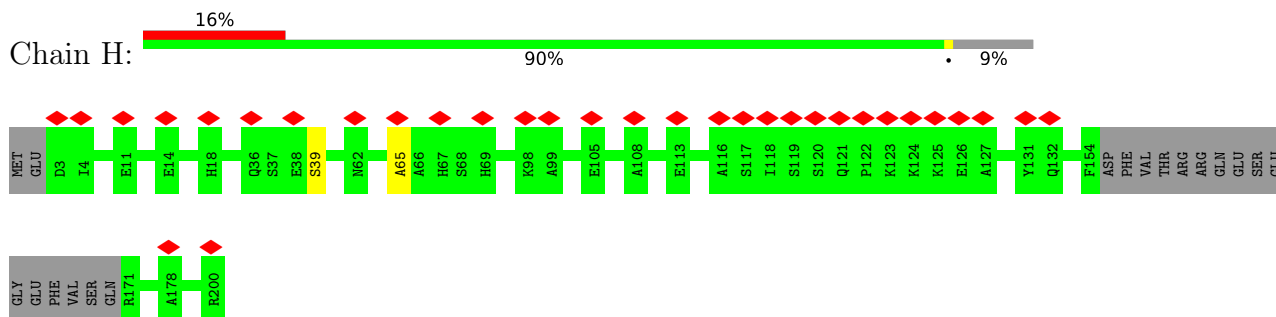
3 Residue-property plots [i](#)

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

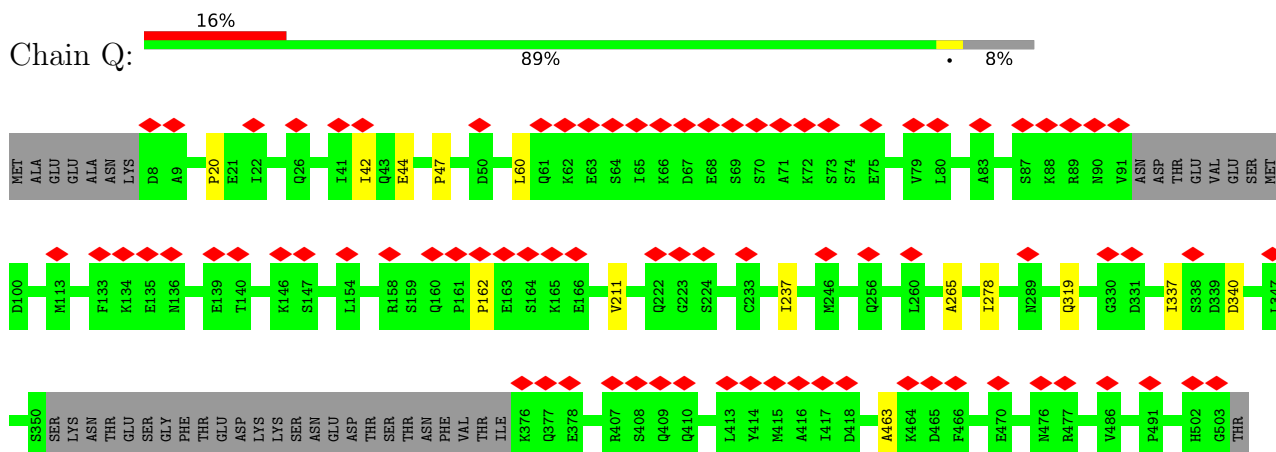
- Molecule 1: Mediator complex subunit 6

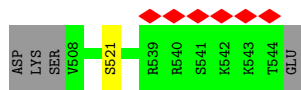


- Molecule 2: Mediator complex subunit 8

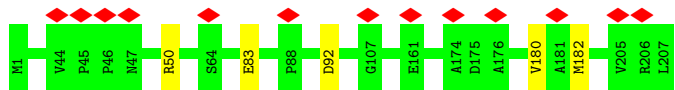


- Molecule 3: Mediator complex subunit 17

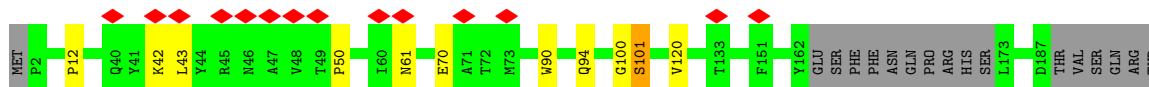
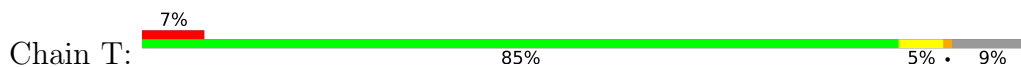




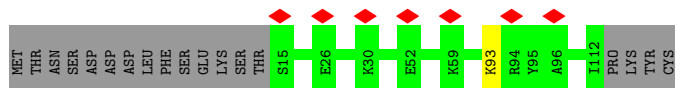
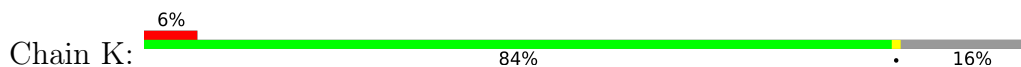
• Molecule 4: Mediator complex subunit 18



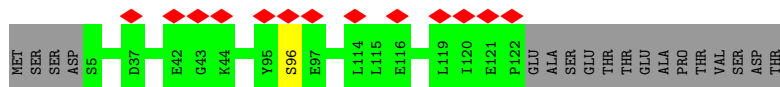
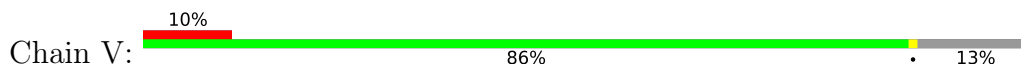
• Molecule 5: Mediator complex subunit 20



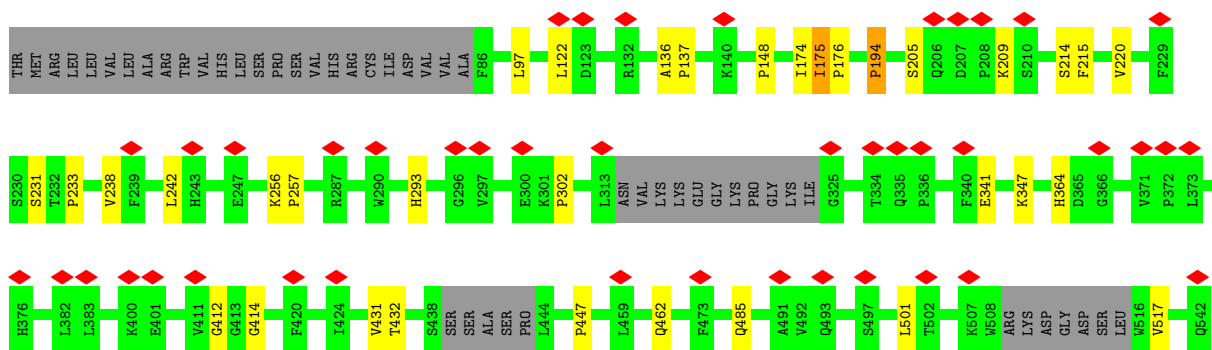
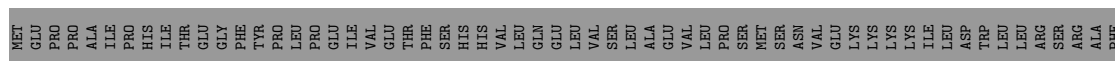
• Molecule 6: Mediator complex subunit 11

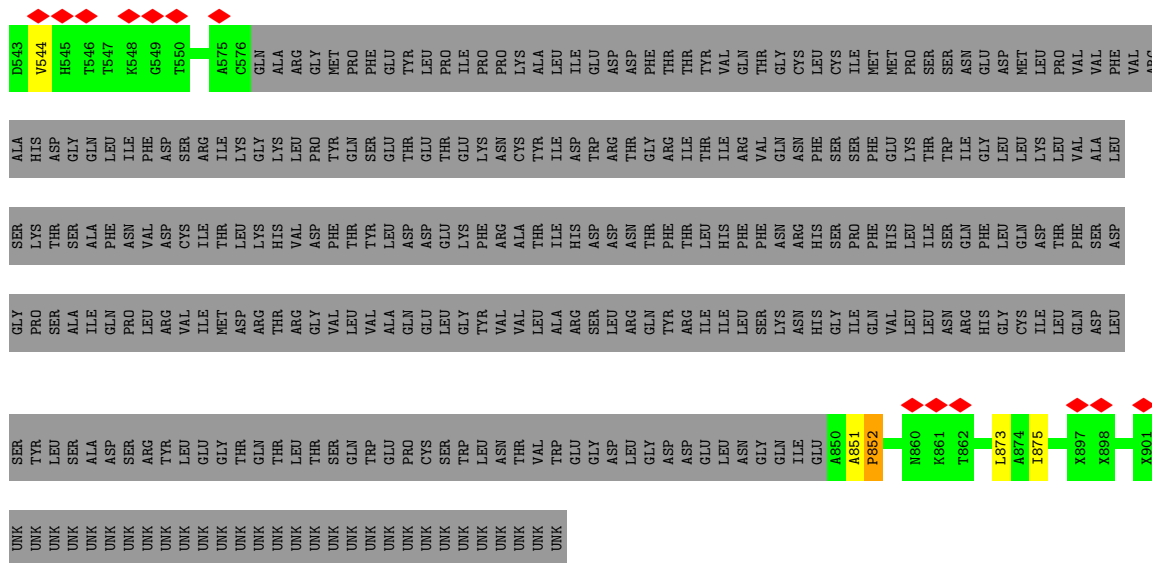


• Molecule 7: Mediator complex subunit 22

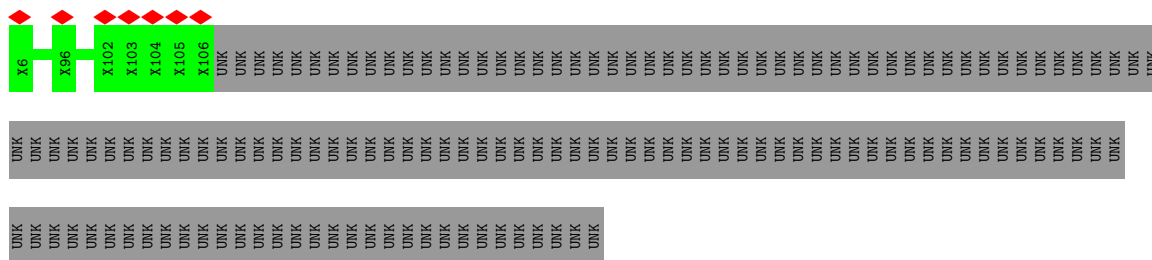


• Molecule 8: Mediator complex subunit 14

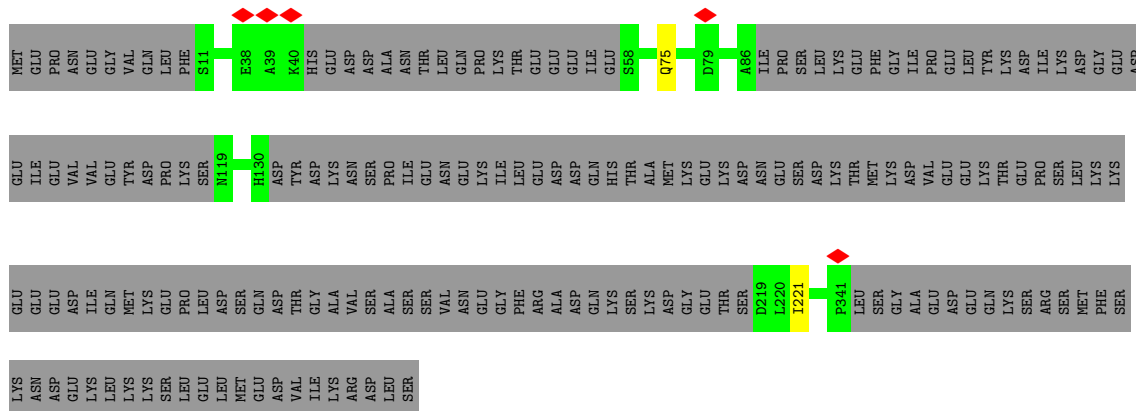




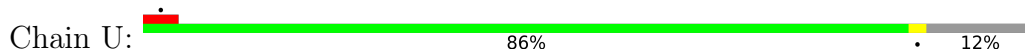
• Molecule 9: Mediator complex subunit 4

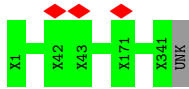


• Molecule 10: Mediator complex subunit 7

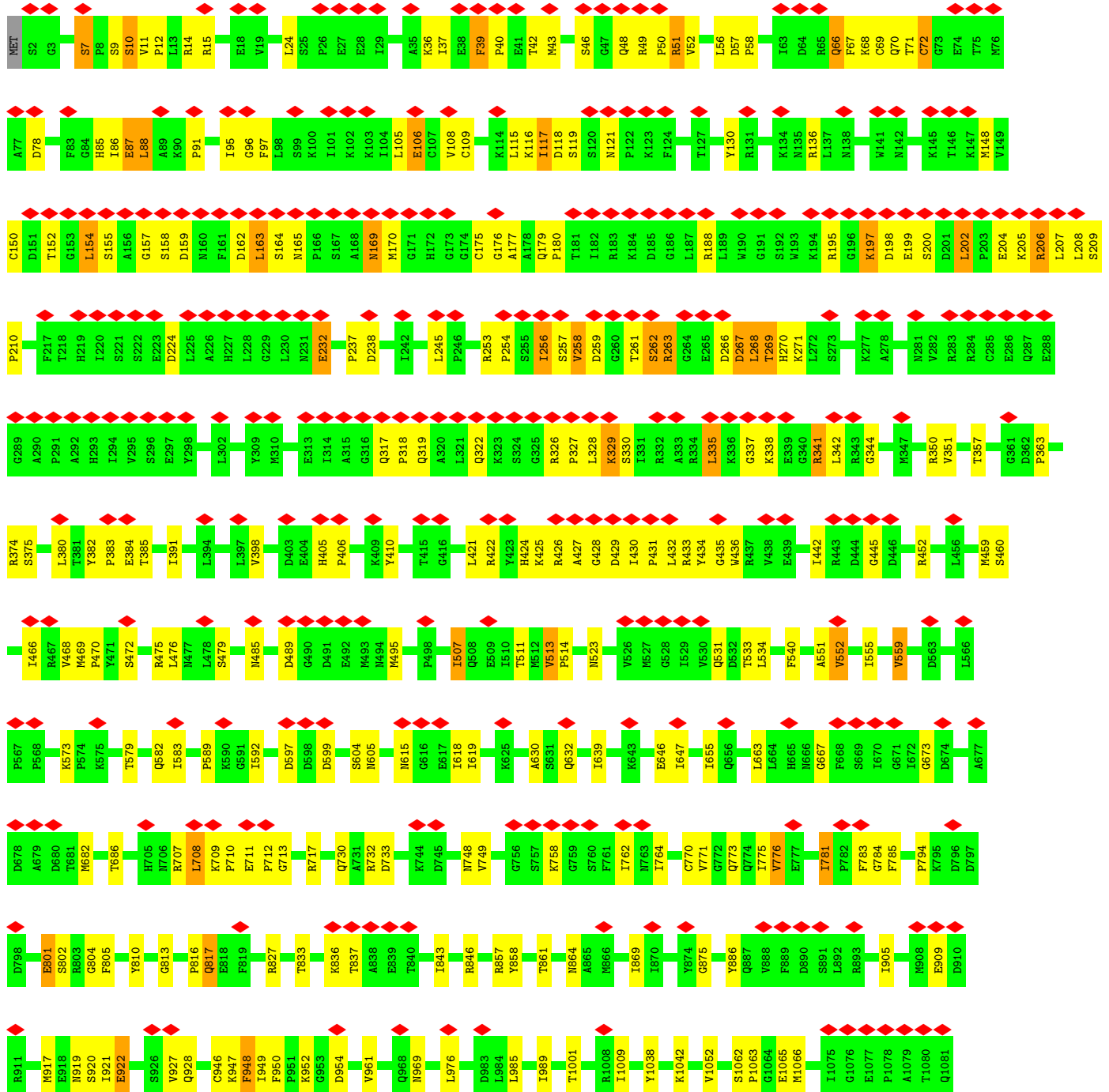


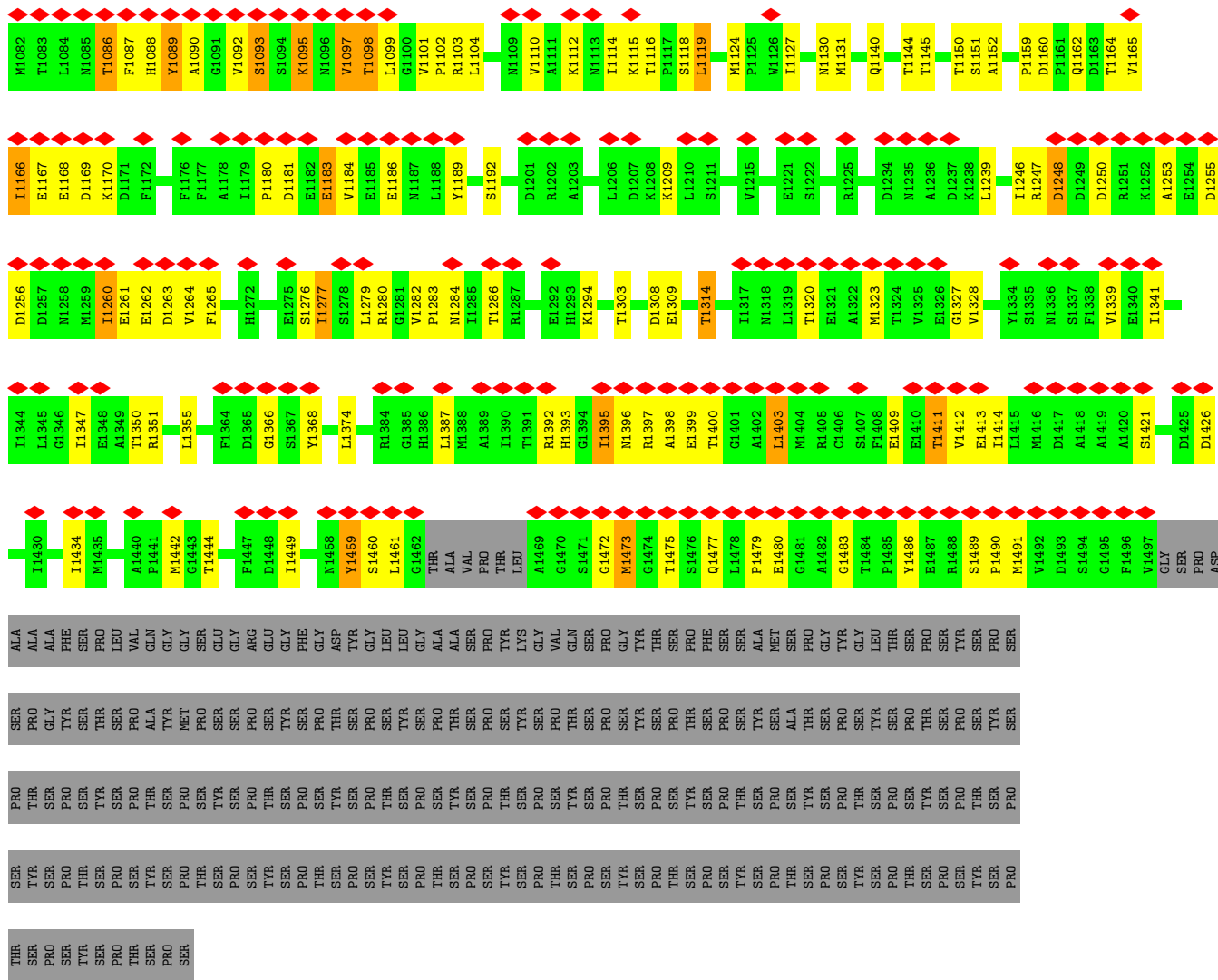
• Molecule 11: Mediator complex subunit 21



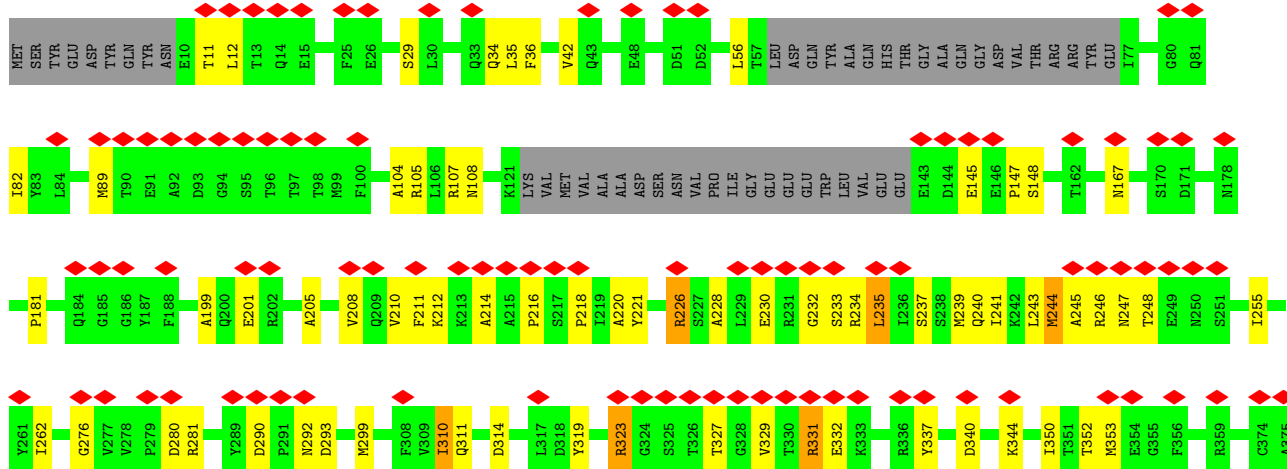
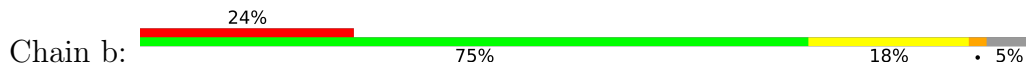


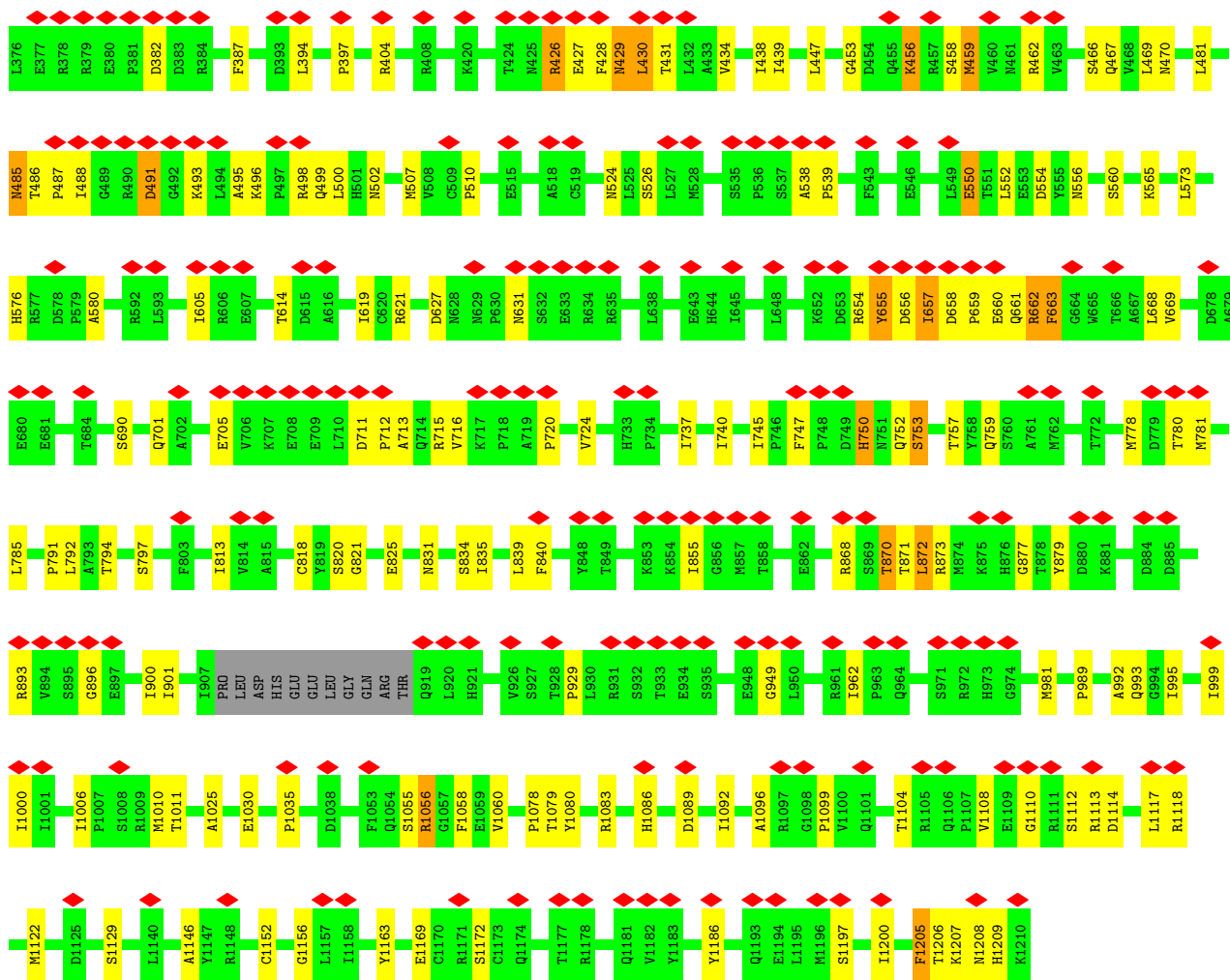
• Molecule 17: RNA polymerase II subunit Rpb1



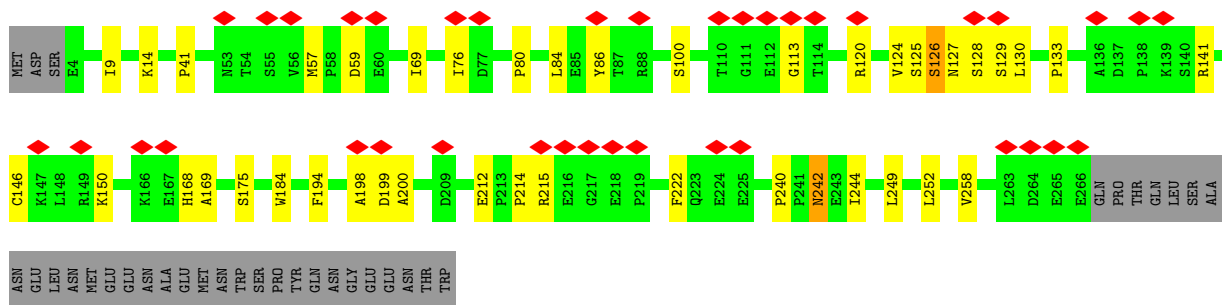
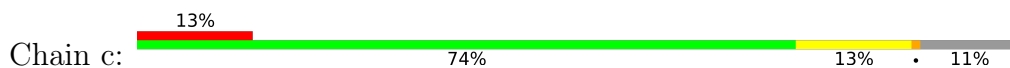


● Molecule 18: RNA polymerase II subunit Rpb2

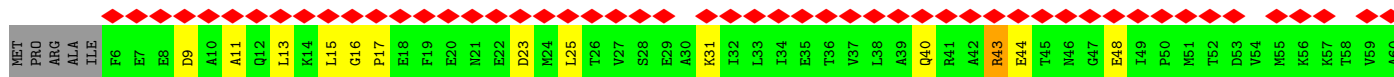


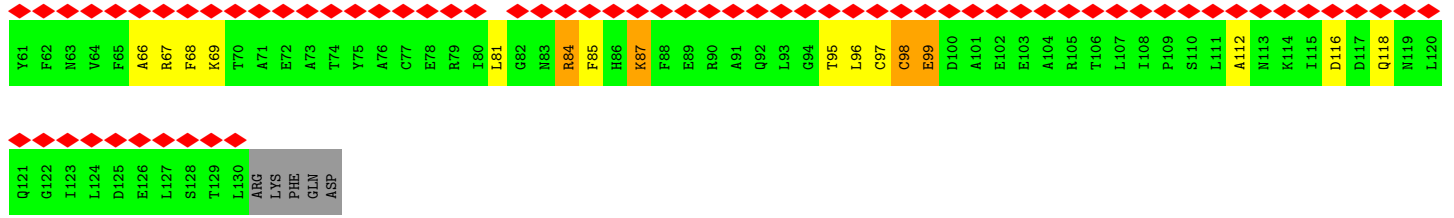


• Molecule 19: RNA polymerase II subunit Rpb3

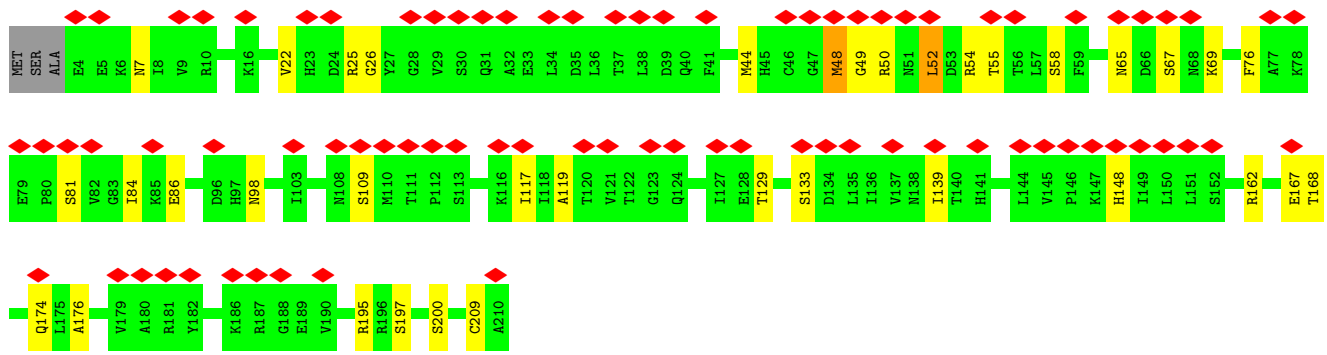
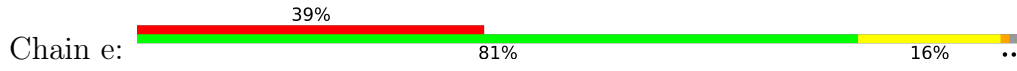


• Molecule 20: RNA polymerase II subunit Rpb4

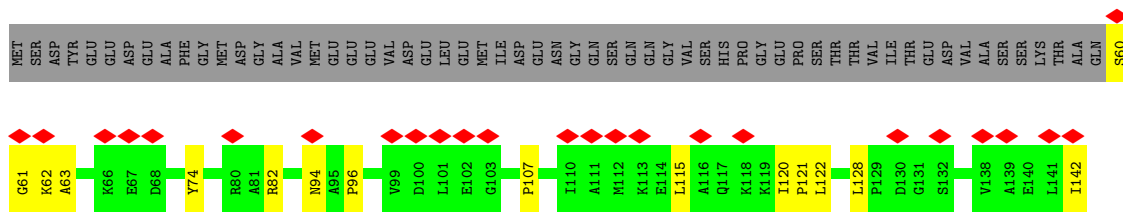




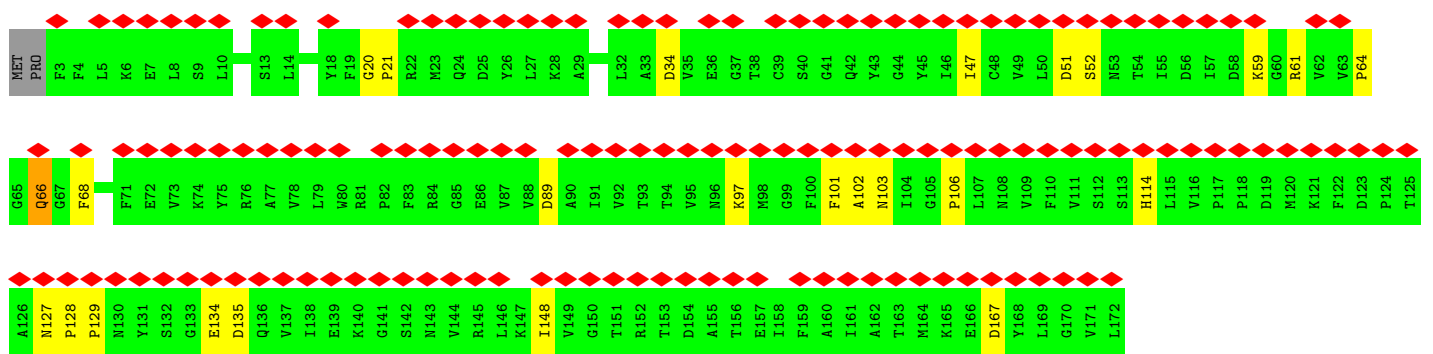
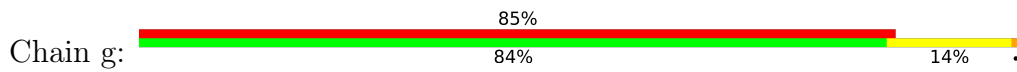
• Molecule 21: RNA polymerase II subunit Rpb5



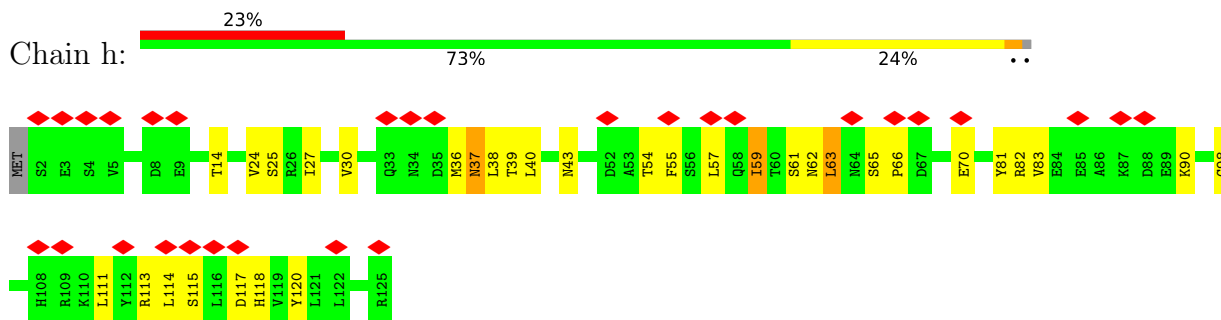
• Molecule 22: RNA polymerase II subunit Rpb6



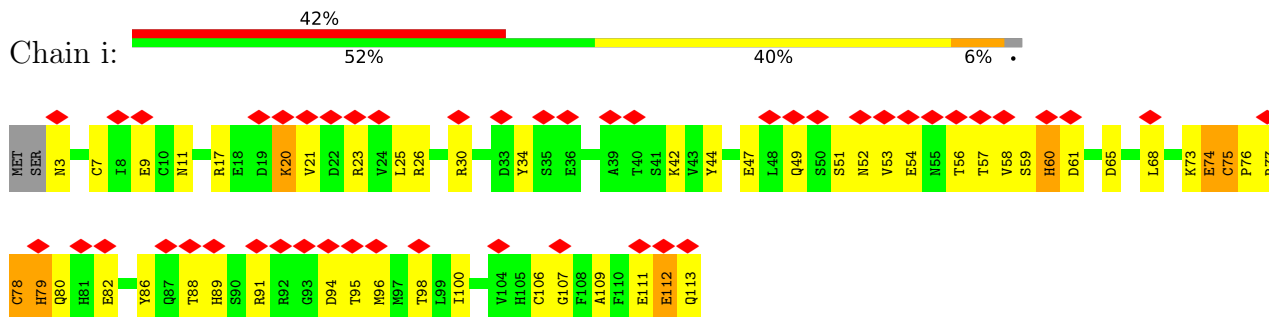
• Molecule 23: RNA polymerase II subunit Rpb7



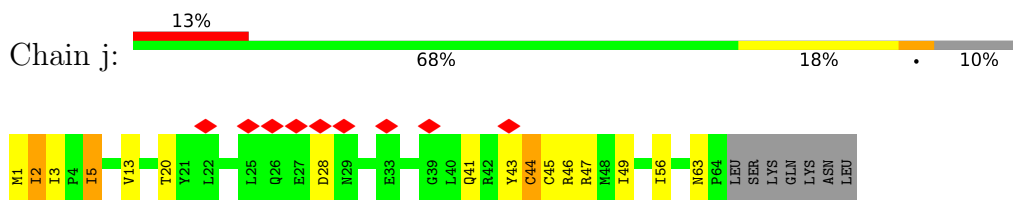
• Molecule 24: RNA polymerase II subunit Rpb8



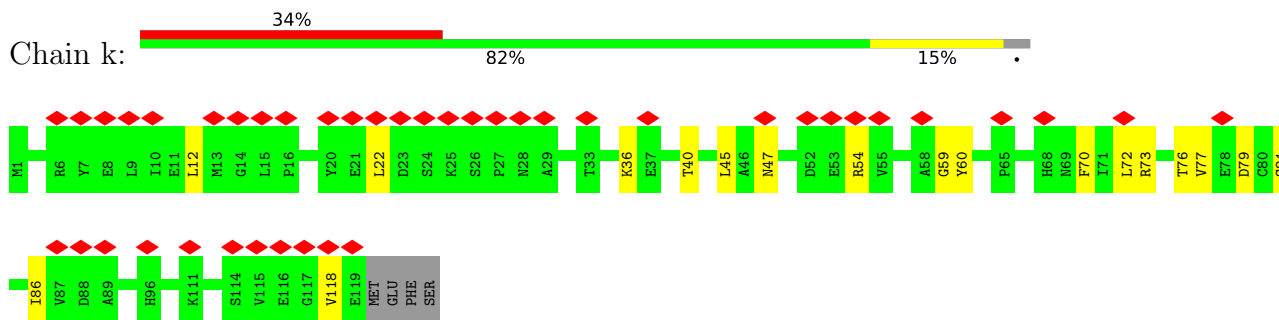
• Molecule 25: RNA polymerase II subunit Rpb9



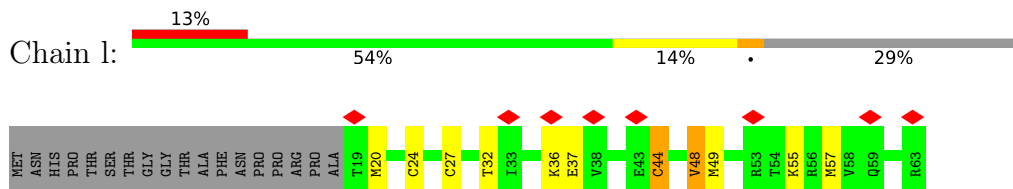
• Molecule 26: RNA polymerase II subunit Rpb10



• Molecule 27: RNA polymerase II subunit Rpb11



• Molecule 28: RNA polymerase II subunit Rpb12



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	3862	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 ($e^-/\text{\AA}^2$)	9.6	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.229	Depositor
Minimum map value	-0.114	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.08	Depositor
Map size (\AA)	461.12, 461.12, 461.12	wwPDB
Map dimensions	176, 176, 176	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	2.62, 2.62, 2.62	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	F	0.28	0/1570	0.49	0/2126
2	H	0.27	0/1523	0.48	0/2063
3	Q	0.29	0/3856	0.49	2/5223 (0.0%)
4	R	0.28	0/1739	0.51	0/2362
5	T	0.31	0/1469	0.74	5/1992 (0.3%)
6	K	0.30	0/778	0.50	0/1049
7	V	0.27	0/963	0.46	0/1309
8	N	0.30	0/3865	0.61	6/5275 (0.1%)
10	G	0.30	0/961	0.50	0/1336
11	U	0.27	0/606	0.47	0/844
12	3	0.26	0/514	0.52	1/718 (0.1%)
13	2	0.23	0/382	0.40	0/524
14	I	0.25	0/373	0.45	0/520
17	a	0.42	0/11983	0.57	1/16197 (0.0%)
18	b	0.44	0/9360	0.60	5/12643 (0.0%)
19	c	0.45	0/2135	0.60	0/2904
20	d	0.25	0/1000	0.38	0/1348
21	e	0.39	0/1695	0.60	0/2287
22	f	0.50	0/666	0.67	0/901
23	g	0.27	0/1361	0.57	3/1847 (0.2%)
24	h	0.42	0/1010	0.65	0/1363
25	i	0.23	0/921	0.37	0/1246
26	j	0.57	0/526	0.77	0/709
27	k	0.47	0/972	0.62	0/1317
28	l	0.37	0/371	0.57	0/491
All	All	0.37	0/50599	0.57	23/68594 (0.0%)

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.

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Mol	Chain	#Chirality outliers	#Planarity outliers
-----	-------	---------------------	---------------------

Mol	Chain	#Chirality outliers	#Planarity outliers
8	N	0	2

There are no bond length outliers.

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	T	100	GLY	C-N-CA	12.78	153.64	121.70
5	T	101	SER	O-C-N	-9.55	107.42	122.70
8	N	175	ILE	C-N-CD	-9.20	100.37	120.60
8	N	194	PRO	CA-N-CD	-8.83	99.14	111.50
5	T	100	GLY	CA-C-N	7.08	132.76	117.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	N	256	LYS	Peptide
8	N	302	PRO	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	182/216 (84%)	154 (85%)	24 (13%)	4 (2%)	6	35
2	H	178/200 (89%)	161 (90%)	15 (8%)	2 (1%)	14	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	Q	492/545 (90%)	424 (86%)	55 (11%)	13 (3%)	5	31
4	R	205/207 (99%)	177 (86%)	23 (11%)	5 (2%)	6	33
5	T	172/193 (89%)	141 (82%)	21 (12%)	10 (6%)	1	18
6	K	96/116 (83%)	88 (92%)	7 (7%)	1 (1%)	15	55
7	V	116/136 (85%)	107 (92%)	8 (7%)	1 (1%)	17	57
8	N	489/931 (52%)	382 (78%)	72 (15%)	35 (7%)	1	14
10	G	186/376 (50%)	166 (89%)	18 (10%)	2 (1%)	14	52
11	U	118/138 (86%)	110 (93%)	5 (4%)	3 (2%)	5	32
12	3	101/139 (73%)	76 (75%)	9 (9%)	16 (16%)	0	3
13	2	66/273 (24%)	62 (94%)	3 (4%)	1 (2%)	10	46
14	I	73/121 (60%)	67 (92%)	3 (4%)	3 (4%)	3	23
17	a	1486/1752 (85%)	937 (63%)	276 (19%)	273 (18%)	0	2
18	b	1142/1210 (94%)	735 (64%)	244 (21%)	163 (14%)	0	4
19	c	261/297 (88%)	178 (68%)	56 (22%)	27 (10%)	0	8
20	d	123/135 (91%)	85 (69%)	20 (16%)	18 (15%)	0	4
21	e	205/210 (98%)	137 (67%)	43 (21%)	25 (12%)	0	6
22	f	81/142 (57%)	57 (70%)	16 (20%)	8 (10%)	0	9
23	g	168/172 (98%)	128 (76%)	24 (14%)	16 (10%)	0	10
24	h	122/125 (98%)	73 (60%)	27 (22%)	22 (18%)	0	3
25	i	109/113 (96%)	46 (42%)	27 (25%)	36 (33%)	0	0
26	j	62/71 (87%)	41 (66%)	15 (24%)	6 (10%)	0	10
27	k	117/123 (95%)	80 (68%)	24 (20%)	13 (11%)	0	7
28	l	43/63 (68%)	23 (54%)	12 (28%)	8 (19%)	0	2
All	All	6393/8004 (80%)	4635 (72%)	1047 (16%)	711 (11%)	1	7

5 of 711 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	Q	319	GLN
4	R	50	ARG
5	T	101	SER
8	N	175	ILE
8	N	194	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	F	171/198 (86%)	171 (100%)	0	100	100
2	H	168/185 (91%)	168 (100%)	0	100	100
3	Q	389/509 (76%)	389 (100%)	0	100	100
4	R	191/191 (100%)	191 (100%)	0	100	100
5	T	161/178 (90%)	161 (100%)	0	100	100
6	K	88/108 (82%)	88 (100%)	0	100	100
7	V	112/129 (87%)	112 (100%)	0	100	100
8	N	369/799 (46%)	369 (100%)	0	100	100
17	a	1296/1536 (84%)	1109 (86%)	187 (14%)	3	16
18	b	1012/1064 (95%)	912 (90%)	100 (10%)	8	26
19	c	236/267 (88%)	219 (93%)	17 (7%)	14	39
20	d	106/115 (92%)	90 (85%)	16 (15%)	3	14
21	e	182/184 (99%)	169 (93%)	13 (7%)	14	39
22	f	71/121 (59%)	64 (90%)	7 (10%)	8	26
23	g	146/148 (99%)	139 (95%)	7 (5%)	25	51
24	h	113/114 (99%)	99 (88%)	14 (12%)	4	19
25	i	103/105 (98%)	80 (78%)	23 (22%)	1	5
26	j	59/66 (89%)	46 (78%)	13 (22%)	1	5
27	k	109/113 (96%)	104 (95%)	5 (5%)	27	52
28	l	39/53 (74%)	34 (87%)	5 (13%)	4	18
All	All	5121/6183 (83%)	4714 (92%)	407 (8%)	16	35

5 of 407 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	b	655	TYR
18	b	1205	PHE
27	k	72	LEU

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Mol	Chain	Res	Type
18	b	715	ARG
18	b	873	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 154 such sidechains are listed below:

Mol	Chain	Res	Type
18	b	1093	HIS
25	i	49	GLN
18	b	1209	HIS
21	e	19	HIS
27	k	39	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
15	S	6
16	J	3
9	D	1

The worst 5 of 10 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	J	56:UNK	C	160:UNK	N	39.54
1	J	204:UNK	C	310:UNK	N	28.97
1	S	265:UNK	C	271:UNK	N	28.24
1	S	366:UNK	C	381:UNK	N	25.63
1	S	287:UNK	C	301:UNK	N	18.84

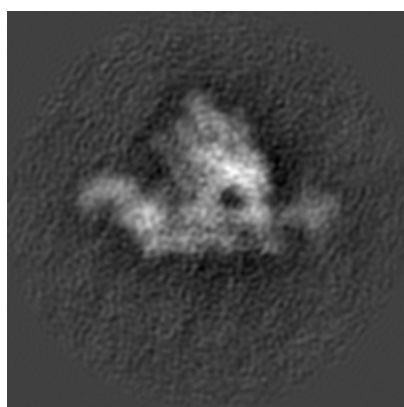
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8480. These allow visual inspection of the internal detail of the map and identification of artifacts.

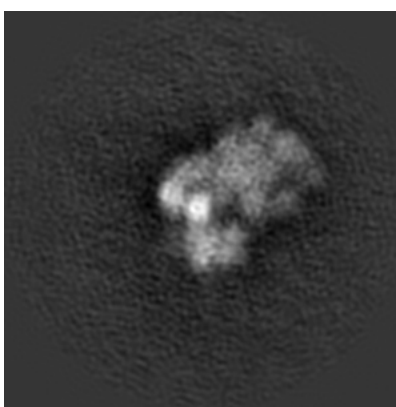
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

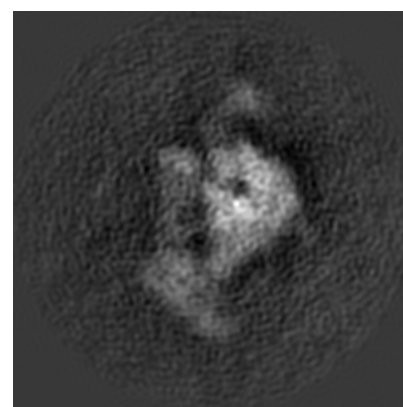
6.1.1 Primary map



X



Y

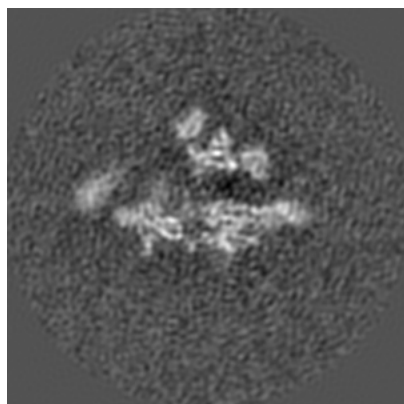


Z

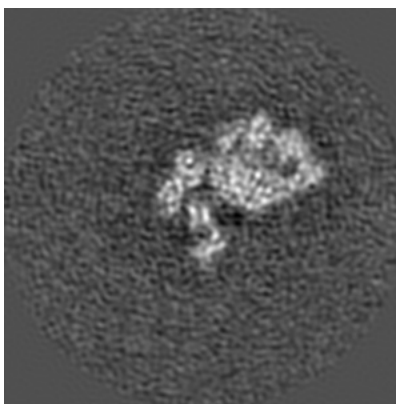
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

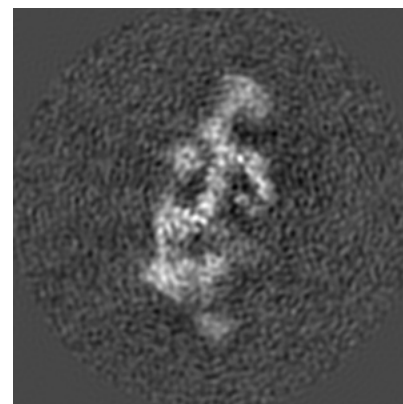
6.2.1 Primary map



X Index: 88



Y Index: 88

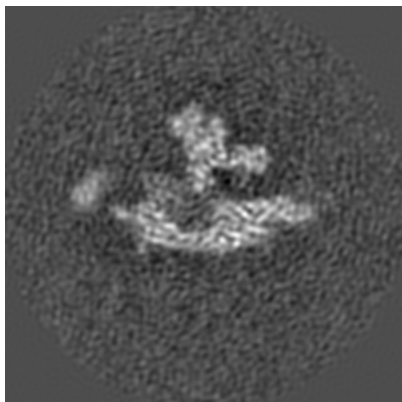


Z Index: 88

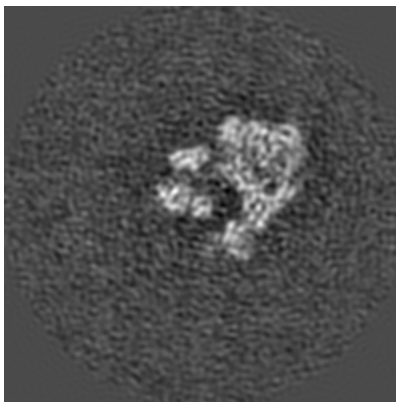
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

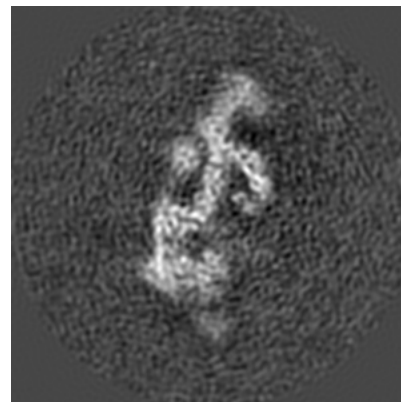
6.3.1 Primary map



X Index: 91



Y Index: 94

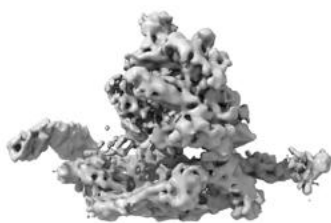


Z Index: 87

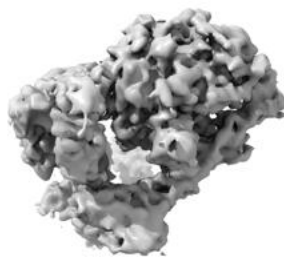
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

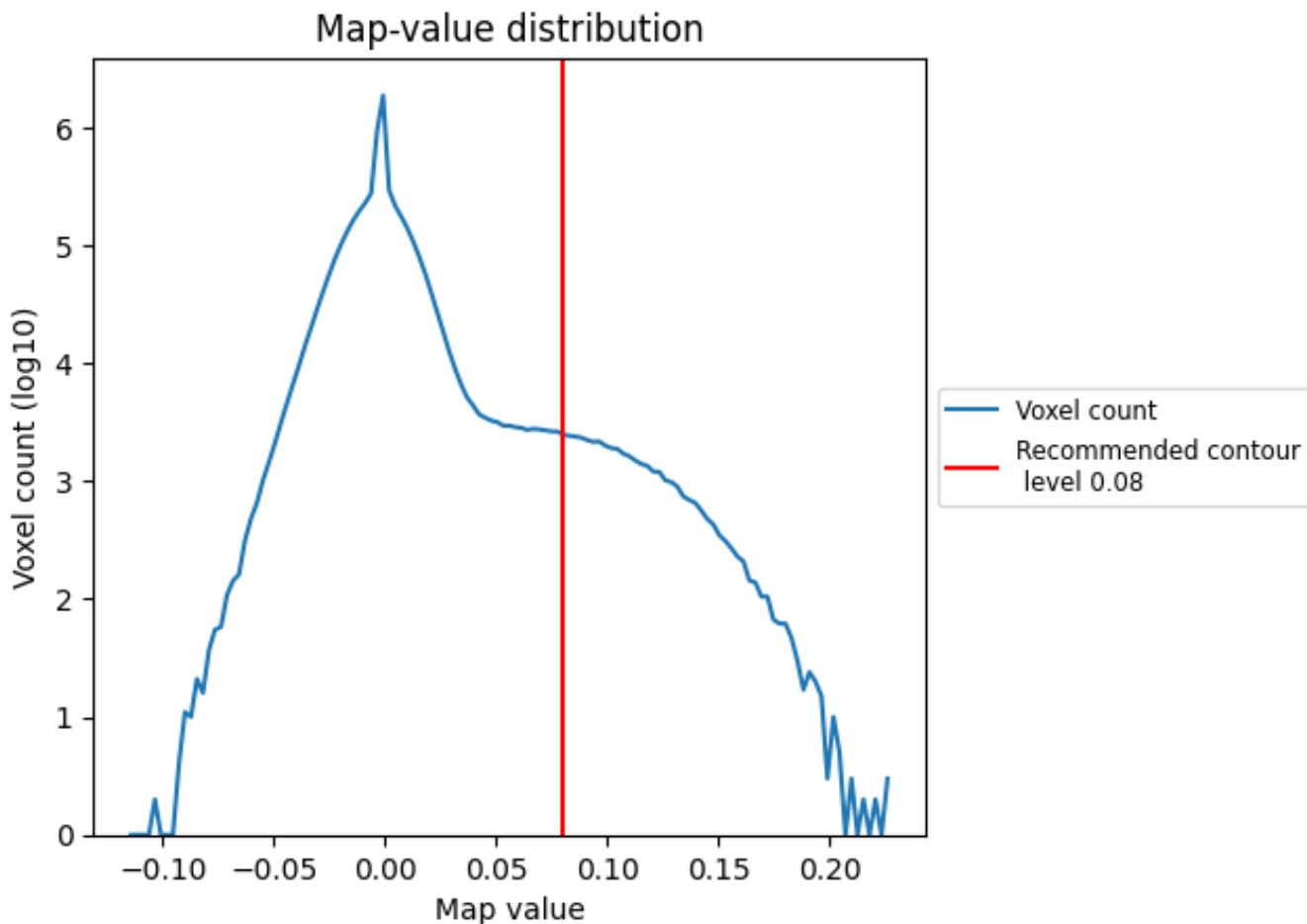
6.5 Mask visualisation

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

7 Map analysis [i](#)

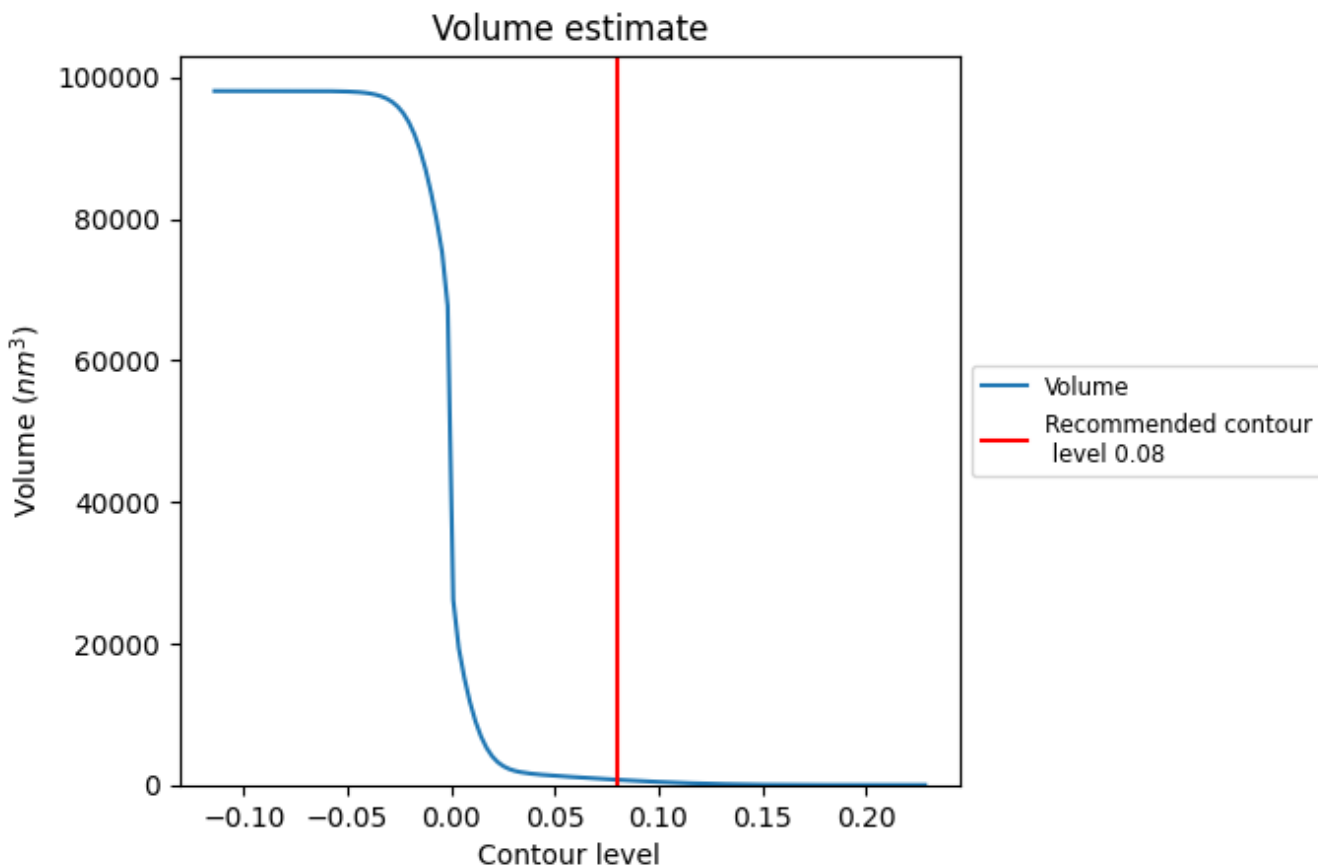
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

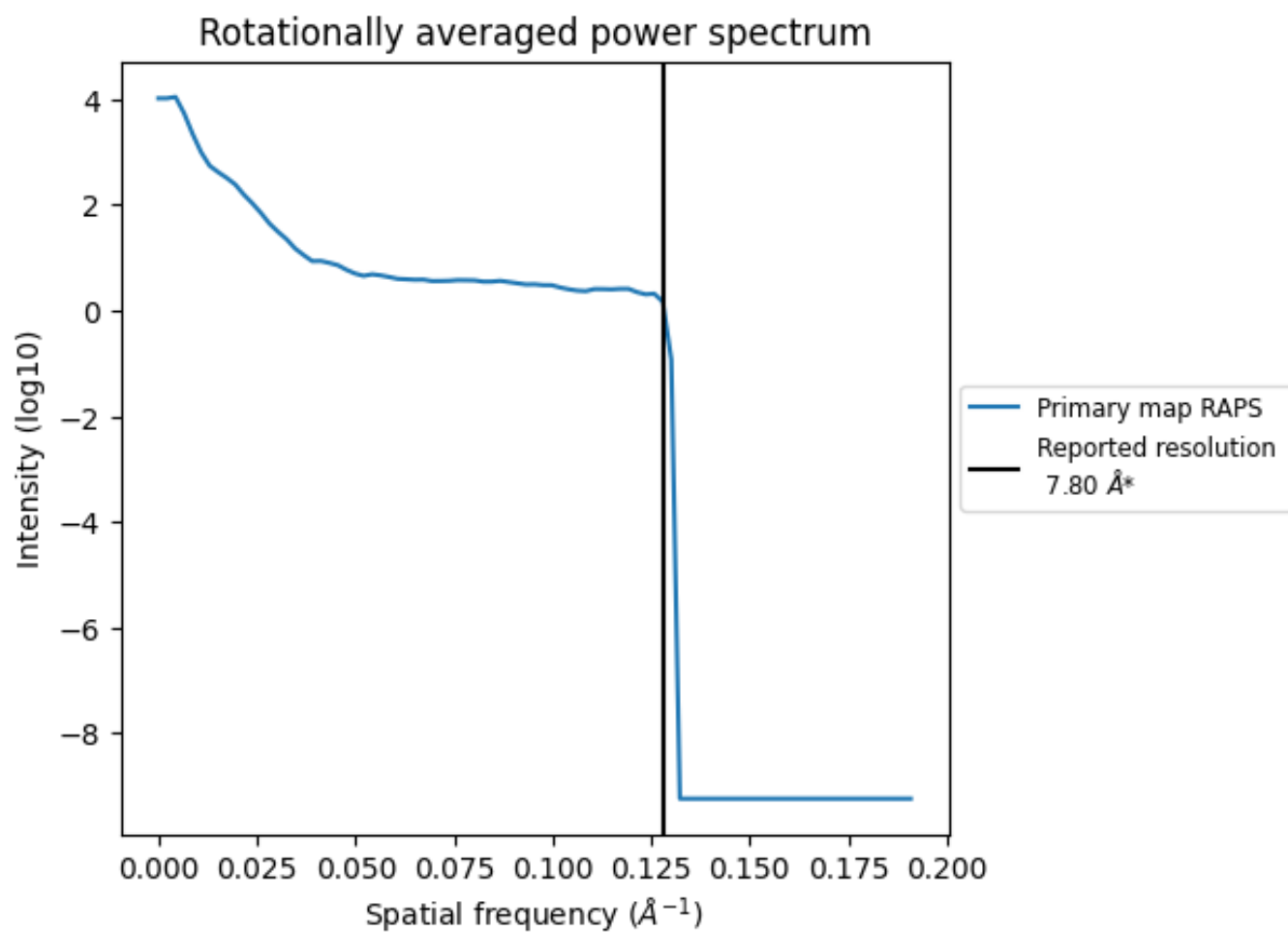
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 735 nm³; this corresponds to an approximate mass of 664 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 0.128 Å⁻¹

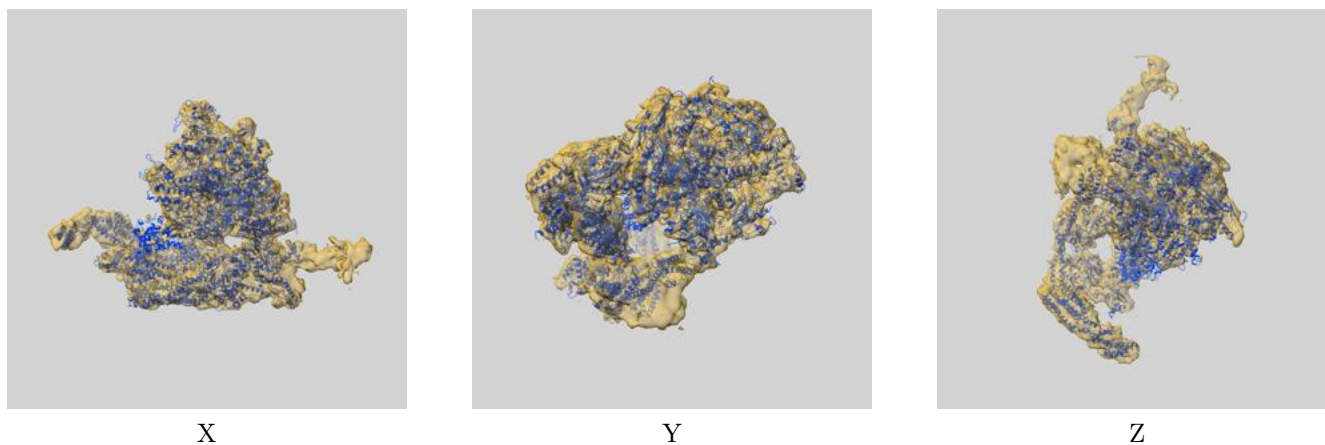
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

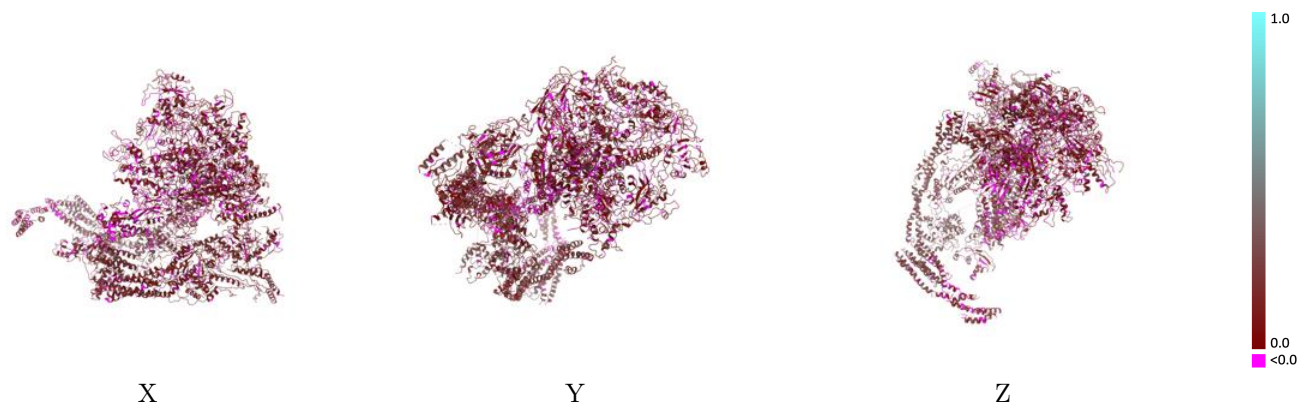
This section contains information regarding the fit between EMDB map EMD-8480 and PDB model 5U0S. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)



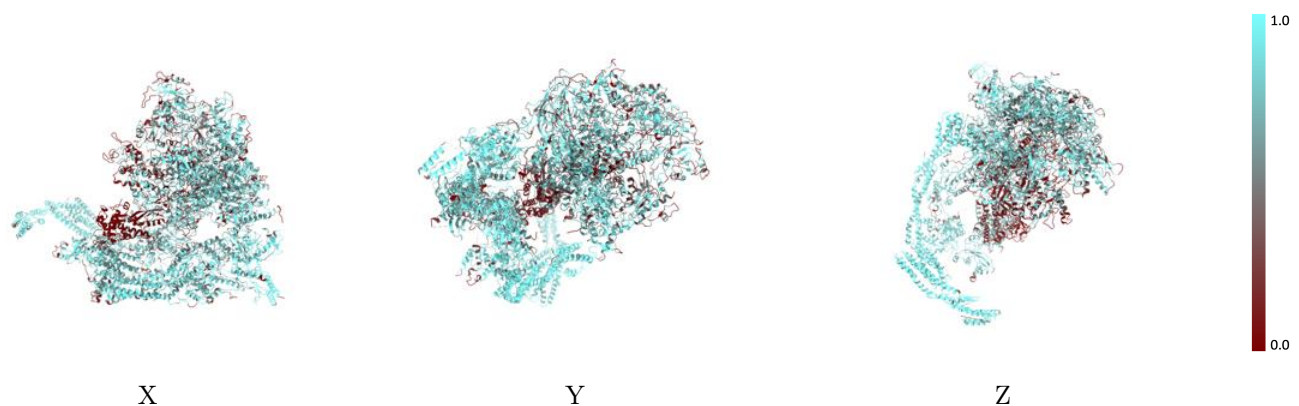
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



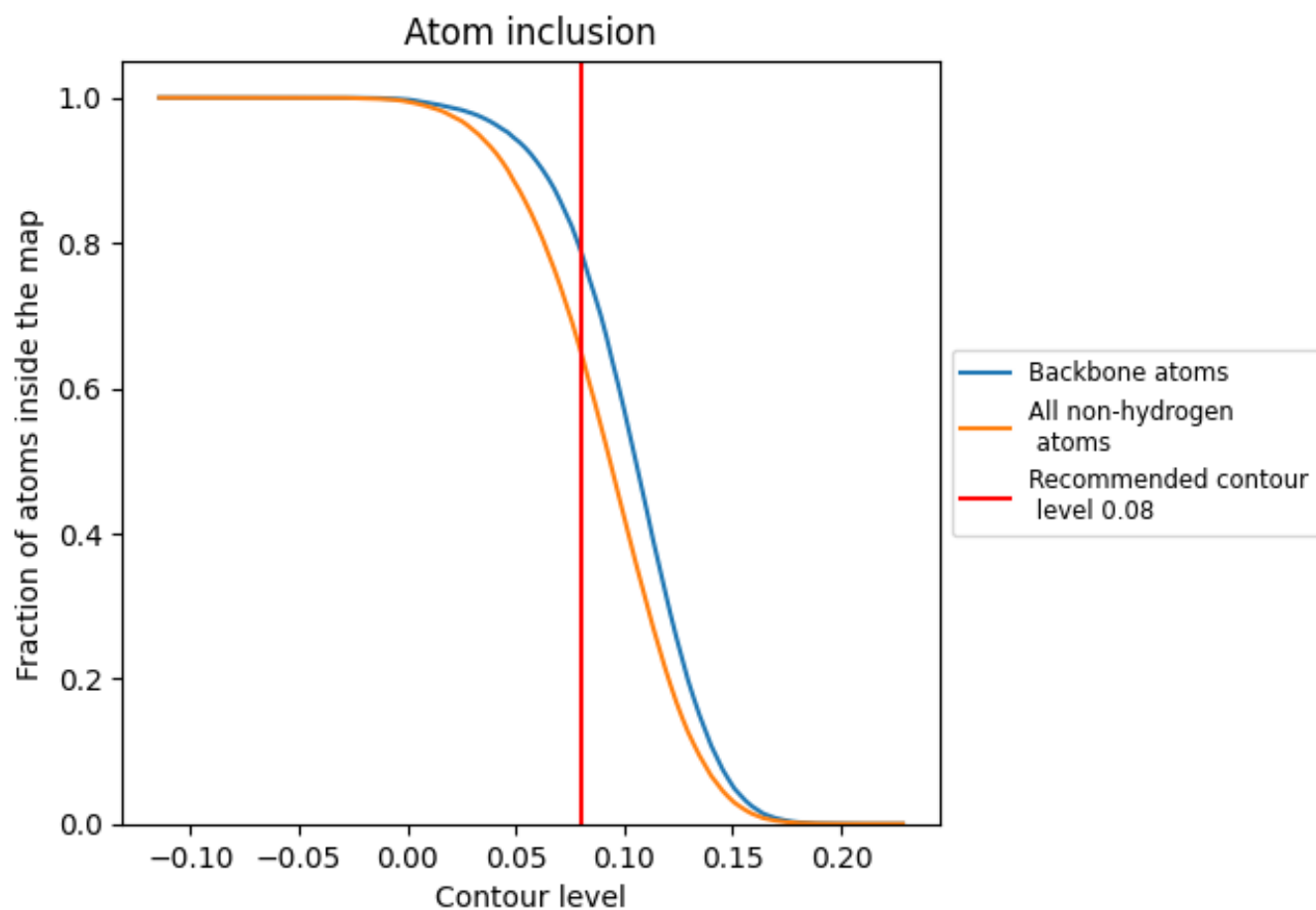
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).



























































9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 65% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6510	 0.1230
2	 0.9433	 0.2260
3	 0.9437	 0.2070
D	 0.9042	 0.2350
F	 0.7215	 0.1270
G	 0.9513	 0.2160
H	 0.6984	 0.1620
I	 0.9465	 0.2090
J	 0.9649	 0.1540
K	 0.8314	 0.1410
N	 0.7832	 0.1550
Q	 0.7089	 0.1510
R	 0.7782	 0.1390
S	 0.8951	 0.1070
T	 0.8173	 0.1470
U	 0.9293	 0.1950
V	 0.7994	 0.1510
a	 0.5629	 0.1050
b	 0.6172	 0.1000
c	 0.7057	 0.1160
d	 0.0247	 0.0450
e	 0.5413	 0.1010
f	 0.5837	 0.1210
g	 0.1185	 0.0370
h	 0.6745	 0.1180
i	 0.4989	 0.0900
j	 0.7095	 0.0990
k	 0.5408	 0.1320
l	 0.6193	 0.0870

