



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 03:17 AM UTC

PDB ID : 8TRH / pdb_00008trh
EMDB ID : EMD-41580
Title : The IDRc bound human core Mediator complex
Authors : Chen, S.F.; Chao, T.C.; Kim, H.J.; Tang, H.C.; Khadka, S.; Li, T.; Murakami, K.; Boyer, T.G.; Tsai, K.L.
Deposited on : 2023-08-09
Resolution : 3.70 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:

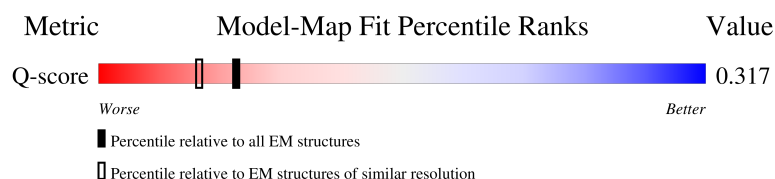
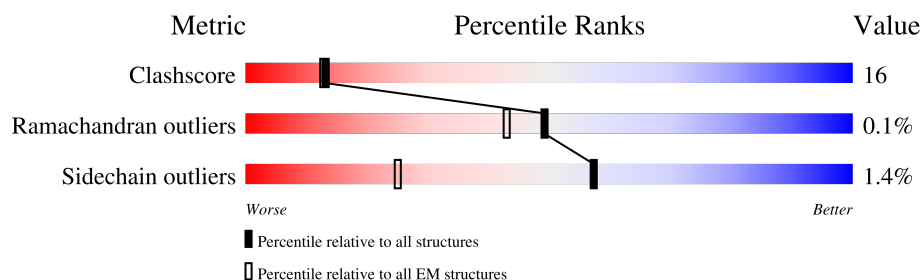
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

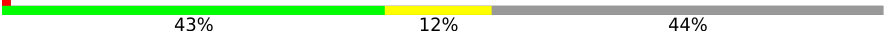
The reported resolution of this entry is 3.70 Å.

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	11569 (3.20 - 4.20)

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	311	 68% 17% 14%
2	1	178	 43% 12% 44%
3	2	200	 48% 9% 42%
4	3	178	 48% 19% 31%

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Mol	Chain	Length	Quality of chain
5	4	131	
6	A	1581	
7	B	20	
8	D	270	
9	F	246	
10	G	233	
11	H	268	
12	I	146	
13	J	135	
14	K	117	
15	N	1454	
16	O	788	
17	P	877	
18	Q	651	
19	R	208	
20	T	212	
21	V	200	
22	W	1368	
23	X	989	
24	d	2174	
25	S	244	
26	U	144	

2 Entry composition

There are 27 unique types of molecules in this entry. The entry contains 59957 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Mediator of RNA polymerase II transcription subunit 27.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	267	Total	C	N	O	S	0	0
			2159	1373	384	390	12		

- Molecule 2 is a protein called Mediator of RNA polymerase II transcription subunit 28.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	99	Total	C	N	O	S	0	0
			817	511	143	160	3		

- Molecule 3 is a protein called Mediator of RNA polymerase II transcription subunit 29.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	115	Total	C	N	O	S	0	0
			899	563	155	172	9		

- Molecule 4 is a protein called Mediator of RNA polymerase II transcription subunit 30.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	122	Total	C	N	O	S	0	0
			1022	639	187	189	7		

- Molecule 5 is a protein called Mediator of RNA polymerase II transcription subunit 31.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	106	Total	C	N	O	S	0	0
			932	610	161	156	5		

- Molecule 6 is a protein called Mediator of RNA polymerase II transcription subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	467	Total	C	N	O	S	0	0
			3578	2278	613	663	24		

- Molecule 7 is a protein called Unknown Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	B	20	Total	C	N	O	0	0
			100	60	20	20		

- Molecule 8 is a protein called Mediator of RNA polymerase II transcription subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	158	Total	C	N	O	S	0	0
			1266	790	228	242	6		

- Molecule 9 is a protein called Mediator of RNA polymerase II transcription subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	167	Total	C	N	O	S	0	0
			1374	888	238	243	5		

- Molecule 10 is a protein called Mediator of RNA polymerase II transcription subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	159	Total	C	N	O	S	0	0
			1284	812	227	235	10		

- Molecule 11 is a protein called Mediator of RNA polymerase II transcription subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	181	Total	C	N	O	S	0	0
			1422	888	250	280	4		

- Molecule 12 is a protein called Mediator of RNA polymerase II transcription subunit 9.

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

- Molecule 13 is a protein called Mediator of RNA polymerase II transcription subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	122	Total	C	N	O	S	0	0
			834	521	151	159	3		

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

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

- Molecule 15 is a protein called Mediator of RNA polymerase II transcription subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	1017	Total	C	N	O	S	0	0
			7768	4955	1364	1407	42		

- Molecule 16 is a protein called Mediator of RNA polymerase II transcription subunit 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	157	Total	C	N	O	S	0	0
			1226	783	213	223	7		

- Molecule 17 is a protein called Mediator of RNA polymerase II transcription subunit 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	753	Total	C	N	O	S	0	0
			5875	3742	1008	1077	48		

- Molecule 18 is a protein called Mediator of RNA polymerase II transcription subunit 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	556	Total	C	N	O	S	0	0
			4387	2774	782	812	19		

- Molecule 19 is a protein called Mediator of RNA polymerase II transcription subunit 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	191	Total	C	N	O	S	0	0
			1532	971	270	276	15		

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

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

- Molecule 21 is a protein called Mediator of RNA polymerase II transcription subunit 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	130	Total	C	N	O	S	0	0
			1063	656	181	222	4		

- Molecule 22 is a protein called Mediator of RNA polymerase II transcription subunit 23.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	1334	Total	C	N	O	S	0	0
			10774	6967	1827	1909	71		

- Molecule 23 is a protein called Mediator of RNA polymerase II transcription subunit 24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	897	Total	C	N	O	S	0	0
			7061	4524	1190	1293	54		

- Molecule 24 is a protein called Mediator of RNA polymerase II transcription subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	d	37	Total	C	N	O	S	0	0
			295	194	46	52	3		

- Molecule 25 is a protein called Mediator of RNA polymerase II transcription subunit 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	74	Total	C	N	O	S	0	0
			435	264	81	89	1		

- Molecule 26 is a protein called Mediator of RNA polymerase II transcription subunit 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	U	116	Total	C	N	O	S	0	0
			869	537	144	183	5		

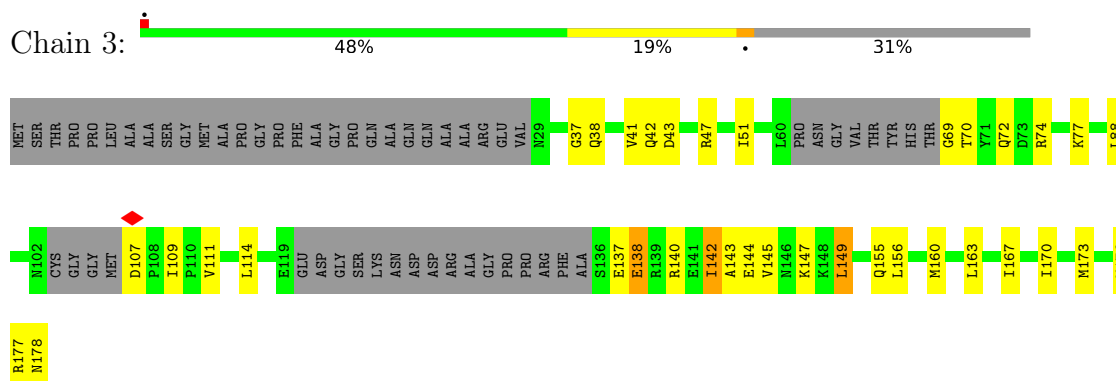
- Molecule 27 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
27	0	1	Total	Zn	0
			1	1	
27	P	1	Total	Zn	0
			1	1	

GLY
THR
LEU

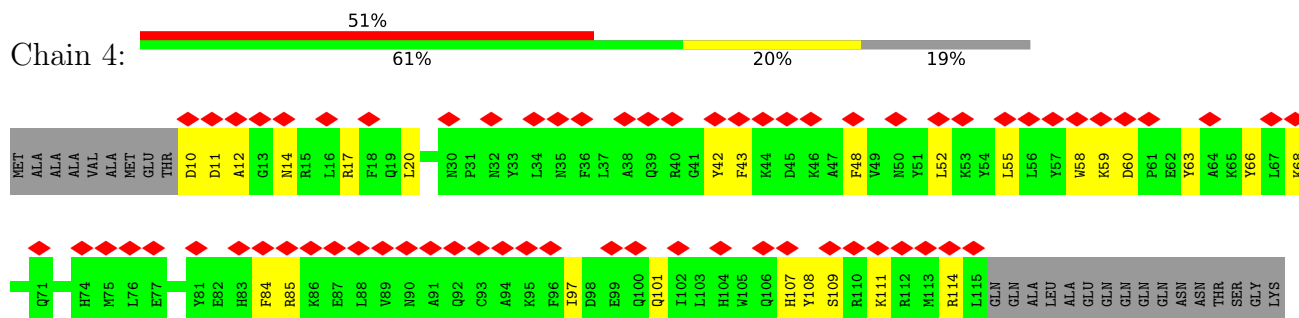
• Molecule 4: Mediator of RNA polymerase II transcription subunit 30

Chain 3:



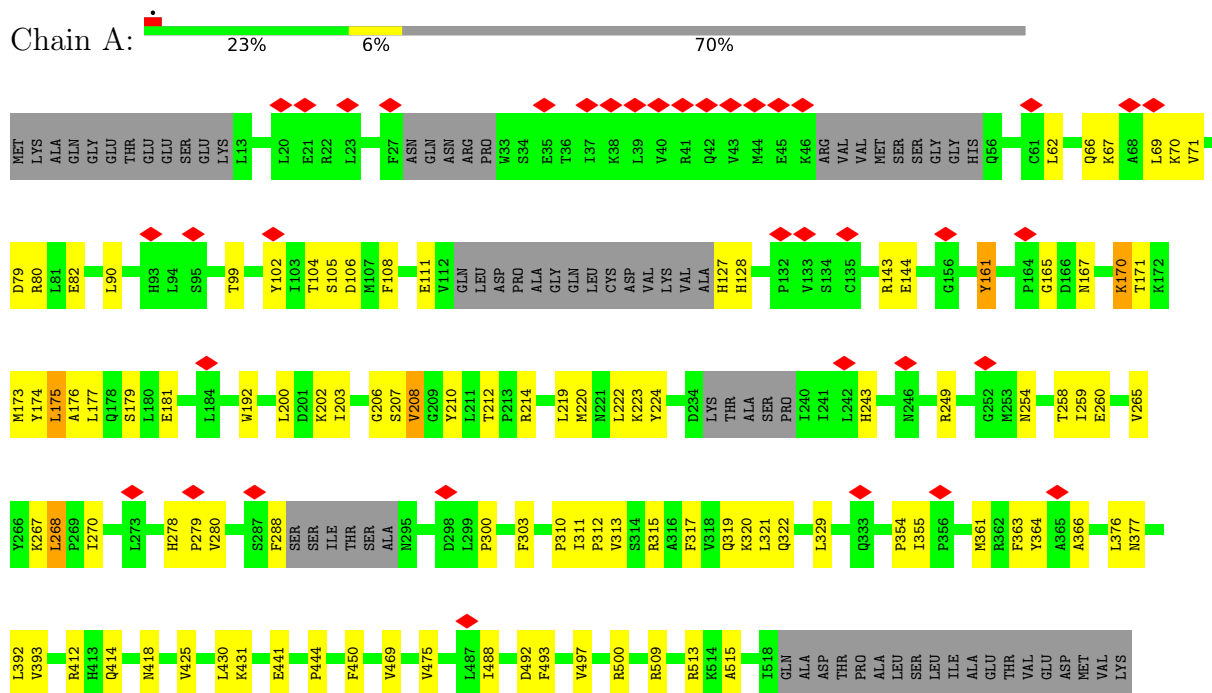
• Molecule 5: Mediator of RNA polymerase II transcription subunit 31

Chain 4:



• Molecule 6: Mediator of RNA polymerase II transcription subunit 1

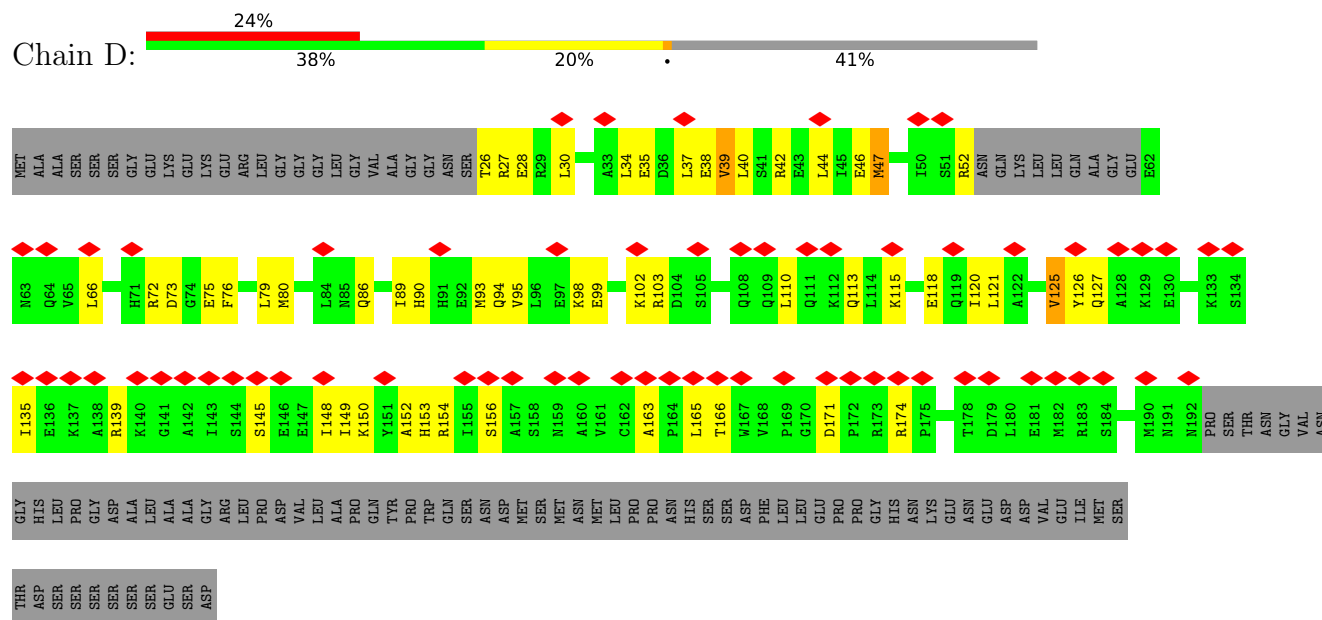
Chain A:



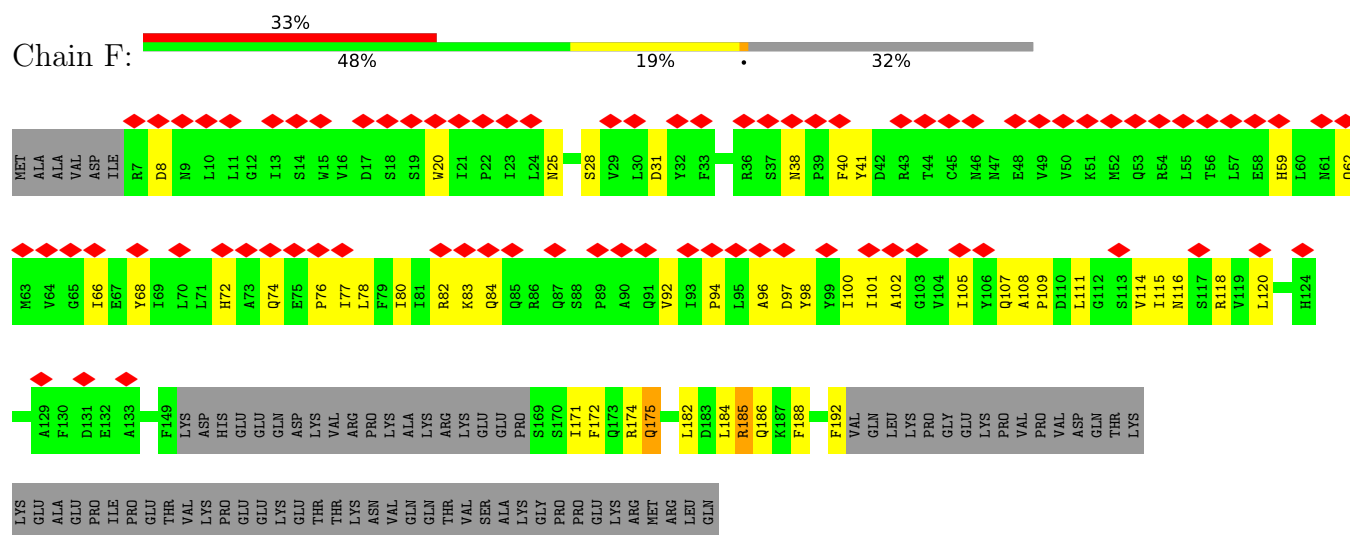
- Molecule 7: Unknown Chain



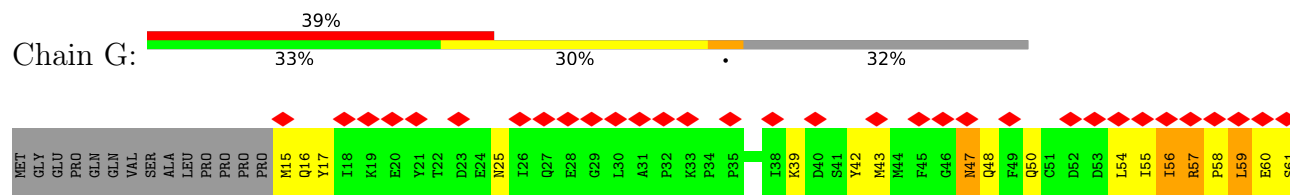
- Molecule 8: Mediator of RNA polymerase II transcription subunit 4



- Molecule 9: Mediator of RNA polymerase II transcription subunit 6

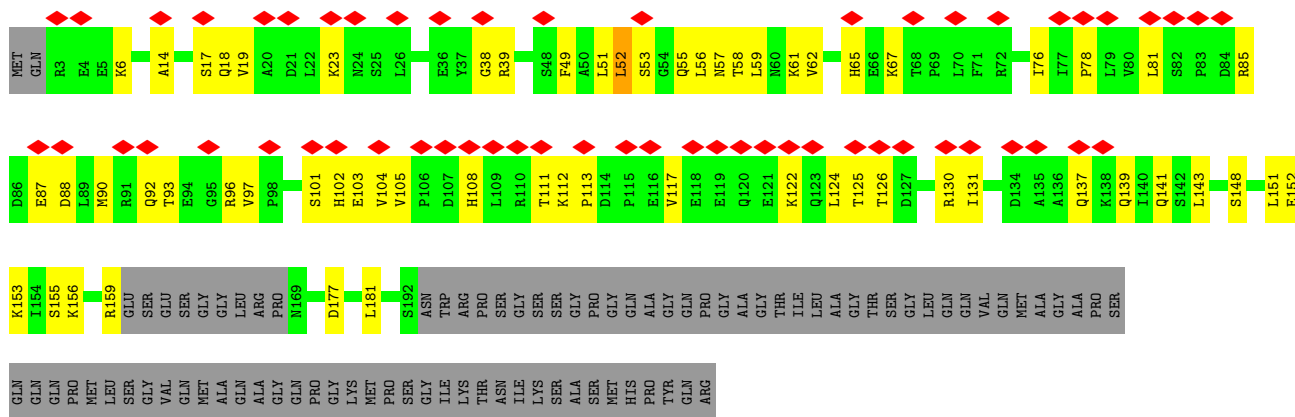


- Molecule 10: Mediator of RNA polymerase II transcription subunit 7

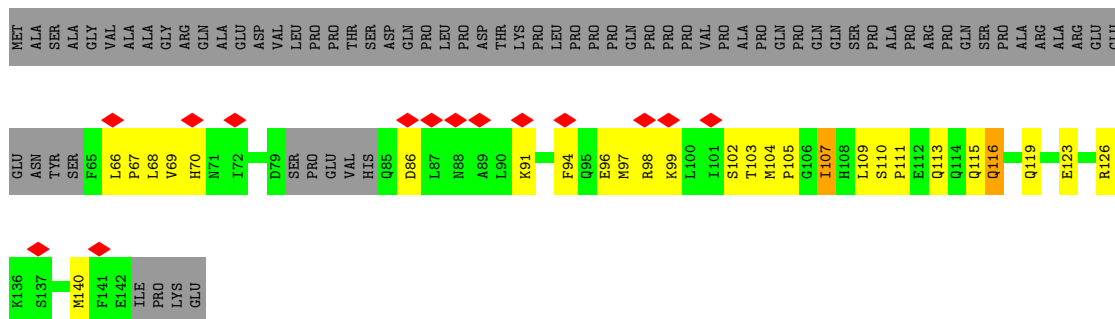
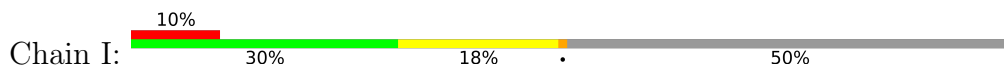




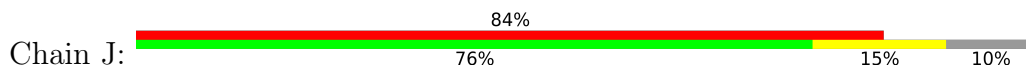
• Molecule 11: Mediator of RNA polymerase II transcription subunit 8



• Molecule 12: Mediator of RNA polymerase II transcription subunit 9

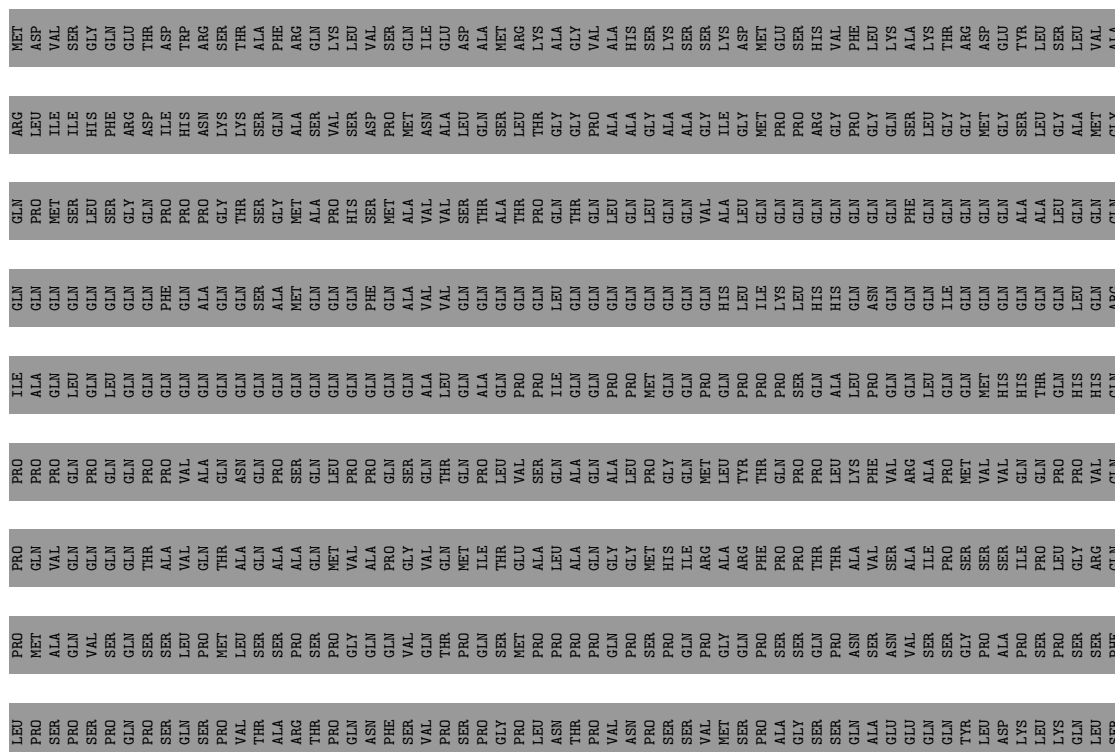


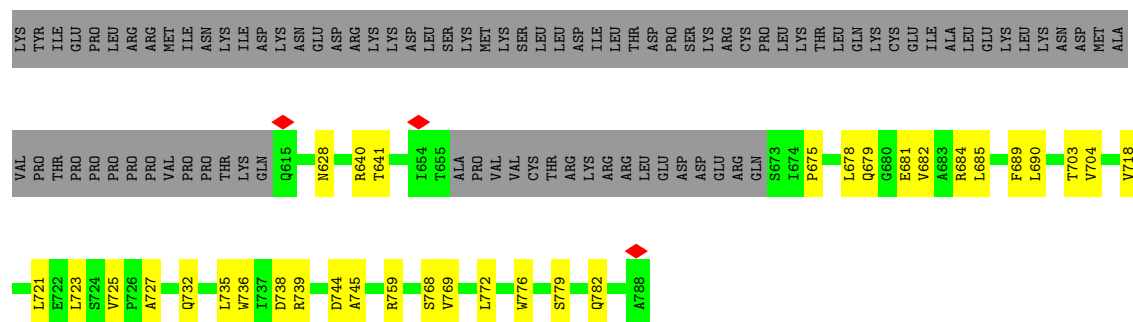
• Molecule 13: Mediator of RNA polymerase II transcription subunit 10



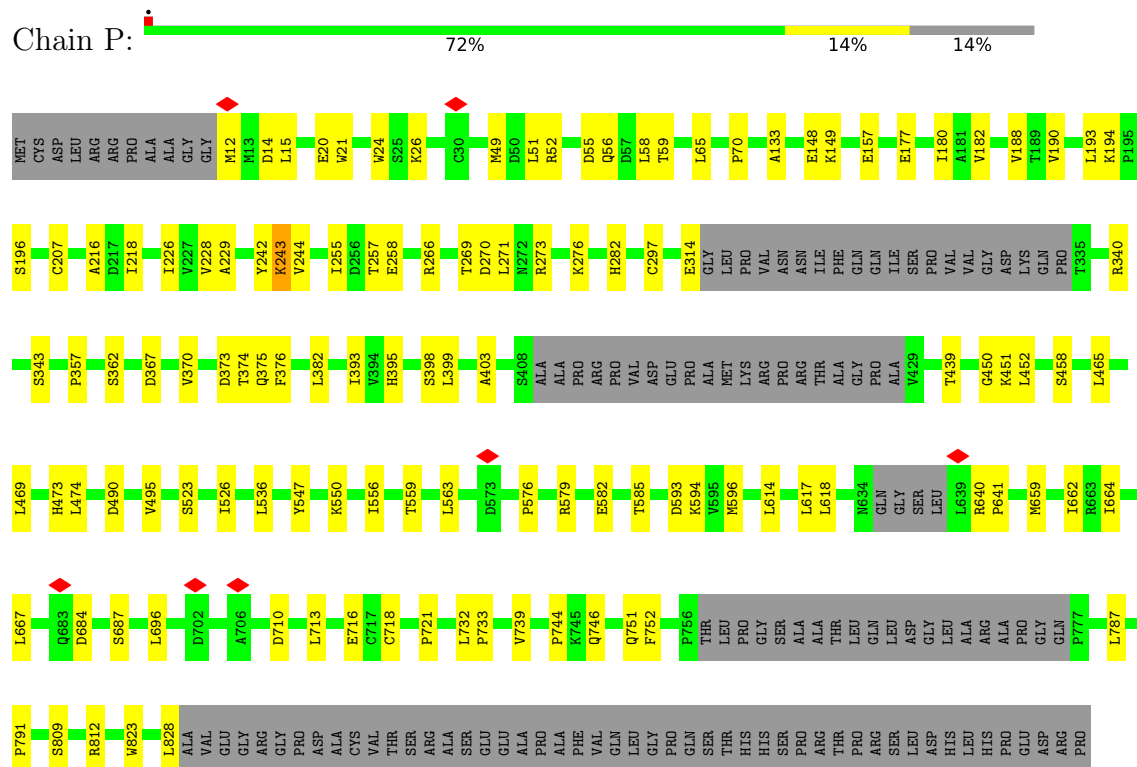


Chain 0: 16% . 80%

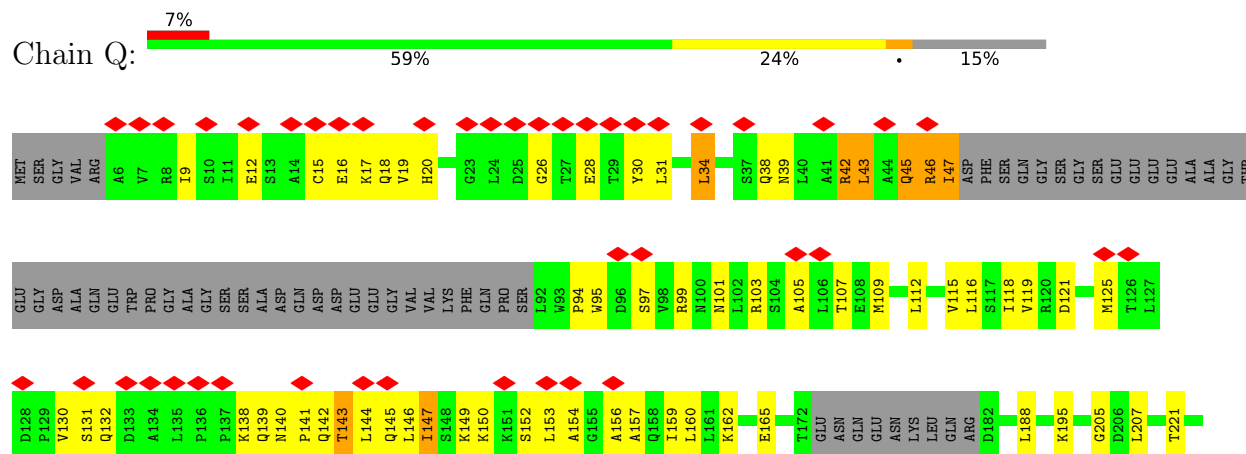


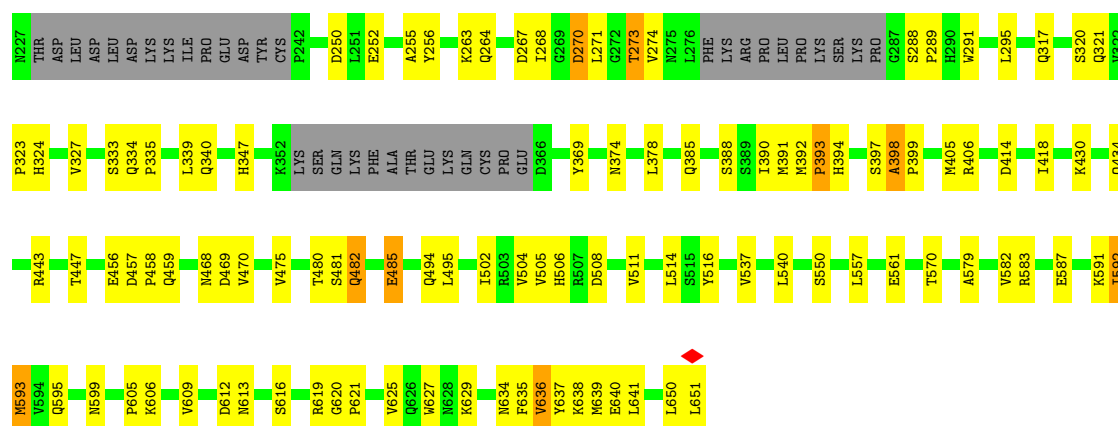


• Molecule 17: Mediator of RNA polymerase II transcription subunit 16

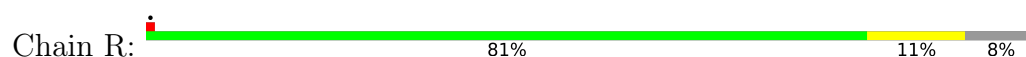


• Molecule 18: Mediator of RNA polymerase II transcription subunit 17

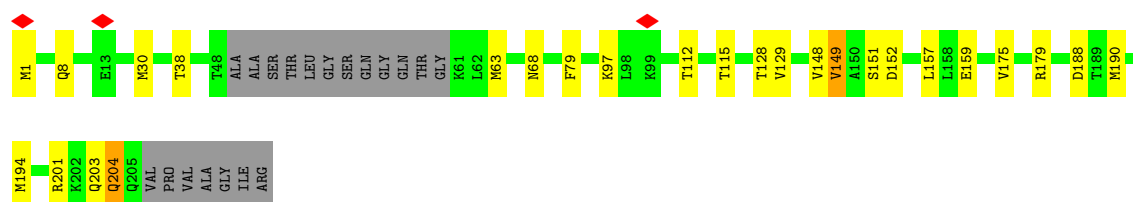
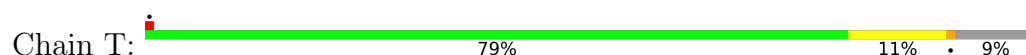




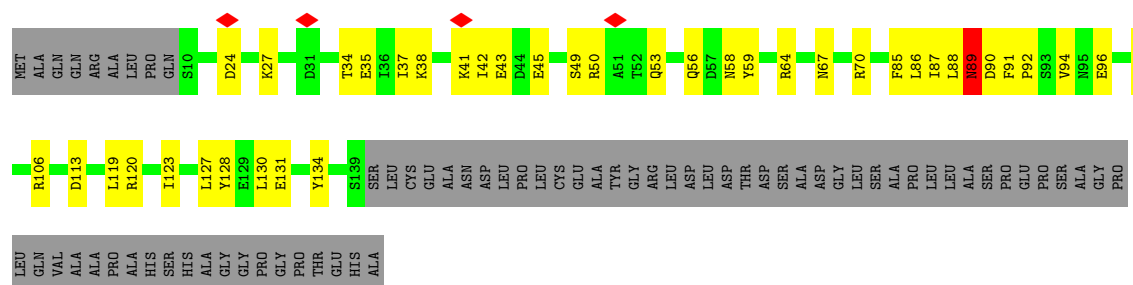
- Molecule 19: Mediator of RNA polymerase II transcription subunit 18



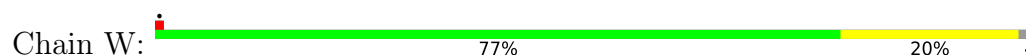
- Molecule 20: Mediator of RNA polymerase II transcription subunit 20

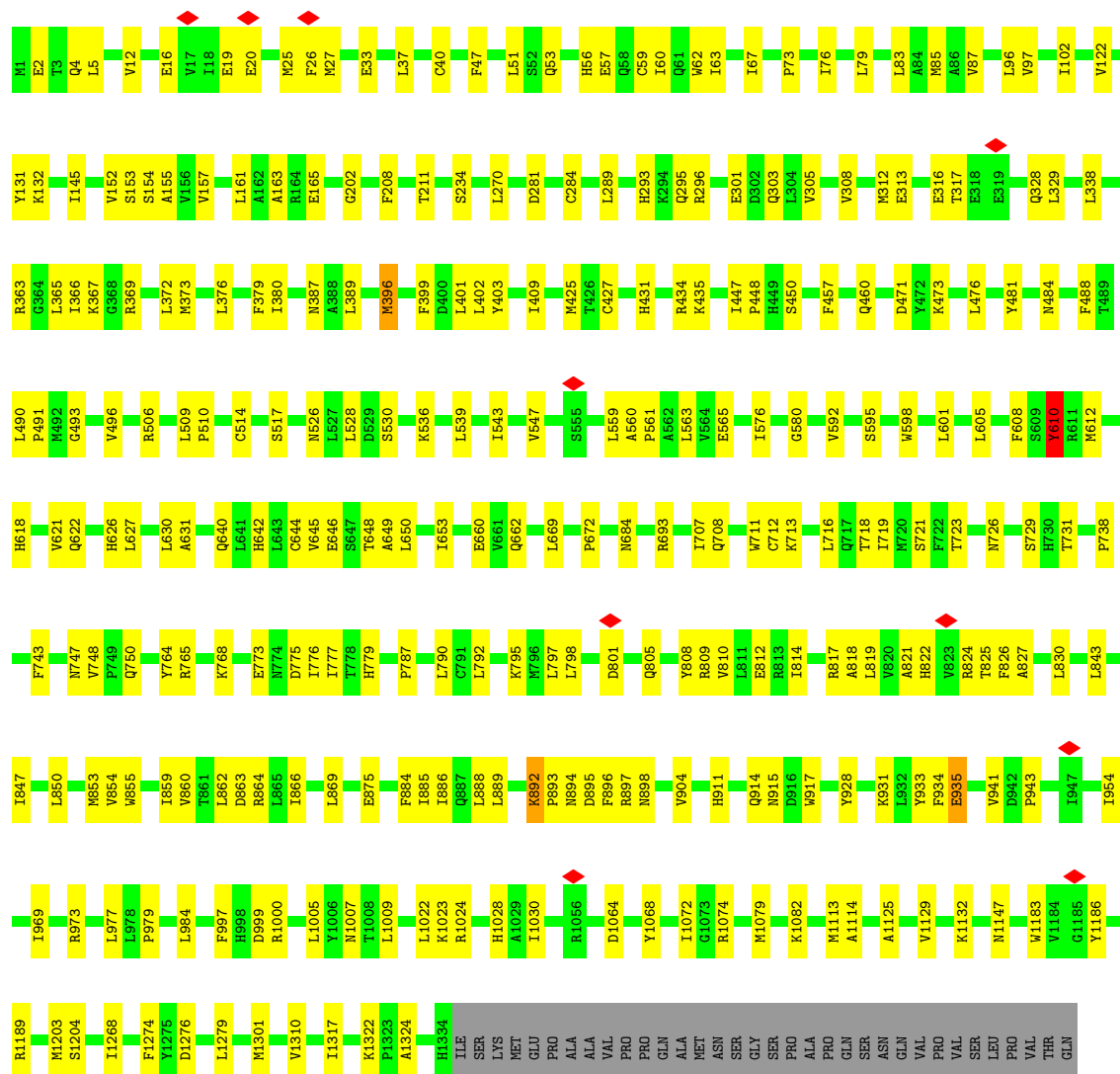


- Molecule 21: Mediator of RNA polymerase II transcription subunit 22



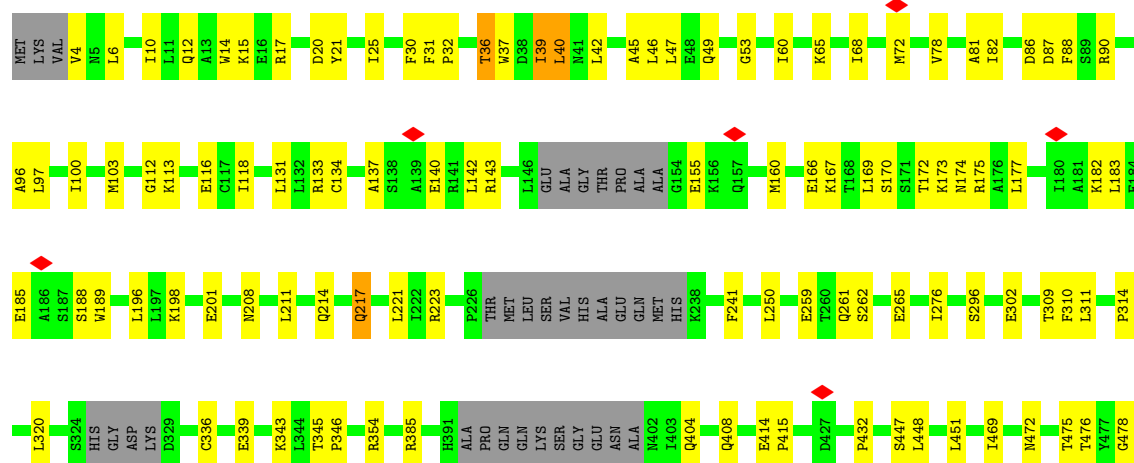
- Molecule 22: Mediator of RNA polymerase II transcription subunit 23



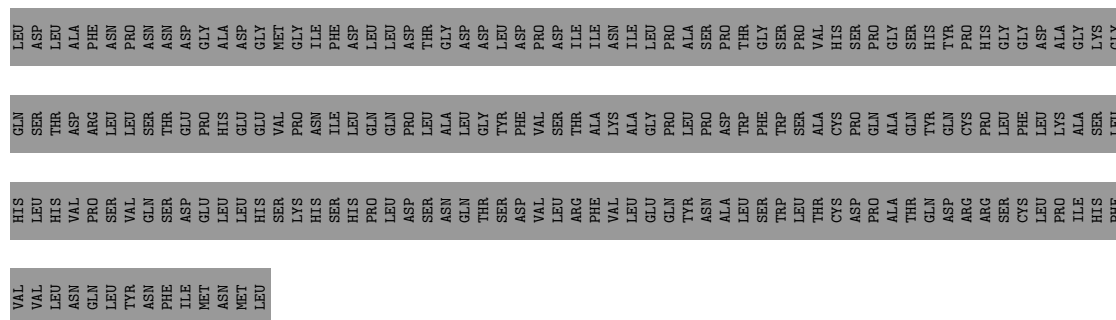


• Molecule 23: Mediator of RNA polymerase II transcription subunit 24

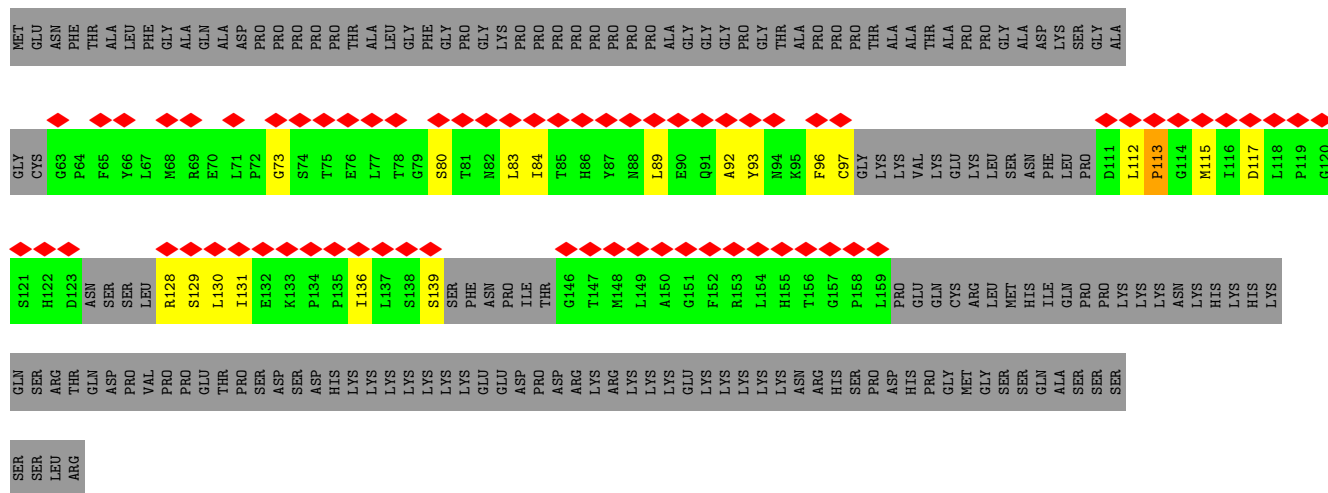
Chain X: 70% 20% 9%



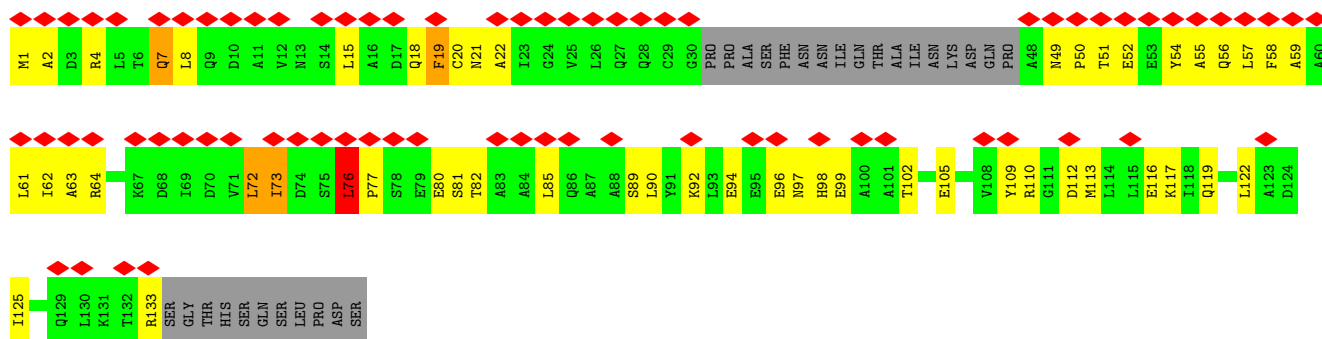




- Molecule 25: Mediator of RNA polymerase II transcription subunit 19



- Molecule 26: Mediator of RNA polymerase II transcription subunit 21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	97904	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	52	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.187	Depositor
Minimum map value	-0.103	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	549.3488, 549.3488, 549.3488	wwPDB
Map dimensions	392, 392, 392	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.4014001, 1.4014001, 1.4014001	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	0	0.20	0/2201	0.41	0/2972
2	1	0.28	0/825	0.55	0/1107
3	2	0.18	0/911	0.37	0/1229
4	3	0.21	0/1029	0.45	0/1378
5	4	0.19	0/959	0.44	0/1291
6	A	0.21	0/3653	0.53	2/4961 (0.0%)
8	D	0.24	0/1279	0.60	0/1715
9	F	0.22	0/1411	0.51	0/1916
10	G	0.29	0/1310	0.83	4/1769 (0.2%)
11	H	0.24	0/1441	0.63	0/1946
12	I	0.28	0/612	0.78	1/815 (0.1%)
13	J	0.16	0/842	0.34	0/1141
14	K	0.34	0/885	0.71	0/1190
15	N	0.28	0/7919	0.75	31/10757 (0.3%)
16	O	0.18	0/1261	0.40	0/1731
17	P	0.15	0/6001	0.36	0/8151
18	Q	0.33	0/4469	0.76	3/6038 (0.0%)
19	R	0.19	0/1562	0.41	0/2101
20	T	0.20	0/1530	0.45	1/2066 (0.0%)
21	V	0.27	0/1072	0.57	2/1440 (0.1%)
22	W	0.27	0/11056	0.55	4/15023 (0.0%)
23	X	0.17	0/7191	0.39	0/9728
24	d	0.29	0/304	1.47	8/413 (1.9%)
25	S	0.49	1/436 (0.2%)	1.21	7/594 (1.2%)
26	U	0.32	0/875	0.81	4/1186 (0.3%)
All	All	0.24	1/61034 (0.0%)	0.58	67/82658 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	S	129	SER	CA-C	5.75	1.60	1.52

The worst 5 of 67 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	N	204	VAL	N-CA-C	11.60	121.44	110.53
25	S	129	SER	N-CA-C	-11.08	98.96	111.71
24	d	929	PRO	CA-C-N	10.54	130.87	119.28
24	d	929	PRO	C-N-CA	10.54	130.87	119.28
10	G	68	HIS	CA-C-N	9.14	129.07	120.03

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	2159	0	2176	49	0
2	1	817	0	818	30	0
3	2	899	0	908	14	0
4	3	1022	0	1054	40	0
5	4	932	0	914	35	0
6	A	3578	0	3522	94	0
7	B	100	0	23	0	0
8	D	1266	0	1300	94	0
9	F	1374	0	1357	77	0
10	G	1284	0	1248	174	0
11	H	1422	0	1440	67	0
12	I	605	0	628	68	0
13	J	834	0	711	80	0
14	K	879	0	886	63	0
15	N	7768	0	7546	385	0
16	O	1226	0	1217	27	0
17	P	5875	0	5969	73	0
18	Q	4387	0	4461	236	0
19	R	1532	0	1542	19	0
20	T	1499	0	1484	26	0
21	V	1063	0	1051	84	0
22	W	10774	0	10838	232	0
23	X	7061	0	7223	179	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	d	295	0	302	102	0
25	S	435	0	293	49	0
26	U	869	0	846	140	0
27	0	1	0	0	0	0
27	P	1	0	0	0	0
All	All	59957	0	59757	1956	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 16.

The worst 5 of 1956 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)
13:J:108:LEU:HD21	26:U:55:ALA:CB	1.37	1.52
14:K:70:LEU:HD21	21:V:86:LEU:CD1	1.40	1.51
24:d:923:LEU:HG	24:d:924:PRO:CD	1.52	1.40
24:d:923:LEU:CG	24:d:924:PRO:HD3	1.52	1.39
10:G:68:HIS:ND1	10:G:69:PRO:HD2	1.41	1.35

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	261/311 (84%)	254 (97%)	7 (3%)	0	100	100
2	1	95/178 (53%)	95 (100%)	0	0	100	100
3	2	111/200 (56%)	107 (96%)	4 (4%)	0	100	100
4	3	114/178 (64%)	112 (98%)	2 (2%)	0	100	100
5	4	104/131 (79%)	100 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	A	455/1581 (29%)	435 (96%)	19 (4%)	1 (0%)	43	72
8	D	154/270 (57%)	149 (97%)	5 (3%)	0	100	100
9	F	163/246 (66%)	145 (89%)	18 (11%)	0	100	100
10	G	157/233 (67%)	153 (98%)	4 (2%)	0	100	100
11	H	177/268 (66%)	160 (90%)	17 (10%)	0	100	100
12	I	69/146 (47%)	67 (97%)	2 (3%)	0	100	100
13	J	120/135 (89%)	116 (97%)	4 (3%)	0	100	100
14	K	110/117 (94%)	104 (94%)	6 (6%)	0	100	100
15	N	995/1454 (68%)	925 (93%)	66 (7%)	4 (0%)	30	60
16	O	153/788 (19%)	142 (93%)	11 (7%)	0	100	100
17	P	743/877 (85%)	695 (94%)	48 (6%)	0	100	100
18	Q	544/651 (84%)	496 (91%)	46 (8%)	2 (0%)	30	60
19	R	189/208 (91%)	181 (96%)	8 (4%)	0	100	100
20	T	189/212 (89%)	173 (92%)	16 (8%)	0	100	100
21	V	128/200 (64%)	126 (98%)	2 (2%)	0	100	100
22	W	1332/1368 (97%)	1277 (96%)	55 (4%)	0	100	100
23	X	877/989 (89%)	844 (96%)	33 (4%)	0	100	100
24	d	35/2174 (2%)	27 (77%)	6 (17%)	2 (6%)	1	15
25	S	66/244 (27%)	63 (96%)	3 (4%)	0	100	100
26	U	112/144 (78%)	107 (96%)	5 (4%)	0	100	100
All	All	7453/13303 (56%)	7053 (95%)	391 (5%)	9 (0%)	49	78

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	N	1355	PRO
18	Q	34	LEU
24	d	928	LEU
15	N	209	PRO
24	d	934	PRO

5.3.2 Protein sidechains ⓘ

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	241/280 (86%)	239 (99%)	2 (1%)	73	76
2	1	94/152 (62%)	93 (99%)	1 (1%)	65	73
3	2	102/163 (63%)	102 (100%)	0	100	100
4	3	116/155 (75%)	112 (97%)	4 (3%)	32	55
5	4	97/115 (84%)	97 (100%)	0	100	100
6	A	394/1391 (28%)	388 (98%)	6 (2%)	57	68
8	D	138/230 (60%)	132 (96%)	6 (4%)	26	50
9	F	151/223 (68%)	148 (98%)	3 (2%)	48	64
10	G	139/216 (64%)	127 (91%)	12 (9%)	10	34
11	H	161/225 (72%)	160 (99%)	1 (1%)	78	79
12	I	71/133 (53%)	68 (96%)	3 (4%)	26	51
13	J	65/124 (52%)	65 (100%)	0	100	100
14	K	94/98 (96%)	93 (99%)	1 (1%)	65	73
15	N	809/1271 (64%)	791 (98%)	18 (2%)	45	63
16	O	141/697 (20%)	141 (100%)	0	100	100
17	P	670/766 (88%)	669 (100%)	1 (0%)	88	88
18	Q	496/577 (86%)	481 (97%)	15 (3%)	36	57
19	R	169/183 (92%)	169 (100%)	0	100	100
20	T	166/178 (93%)	165 (99%)	1 (1%)	78	79
21	V	122/173 (70%)	121 (99%)	1 (1%)	73	76
22	W	1203/1232 (98%)	1192 (99%)	11 (1%)	70	75
23	X	789/864 (91%)	785 (100%)	4 (0%)	81	80
24	d	34/1918 (2%)	33 (97%)	1 (3%)	37	57
25	S	24/208 (12%)	24 (100%)	0	100	100
26	U	91/119 (76%)	87 (96%)	4 (4%)	25	50
All	All	6577/11691 (56%)	6482 (99%)	95 (1%)	57	70

5 of 95 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	P	243	LYS
18	Q	636	VAL
18	Q	43	LEU
18	Q	270	ASP
22	W	33	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 83 such sidechains are listed below:

Mol	Chain	Res	Type
20	T	8	GLN
23	X	12	GLN
20	T	47	HIS
22	W	783	GLN
23	X	799	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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-41580. These allow visual inspection of the internal detail of the map and identification of artifacts.

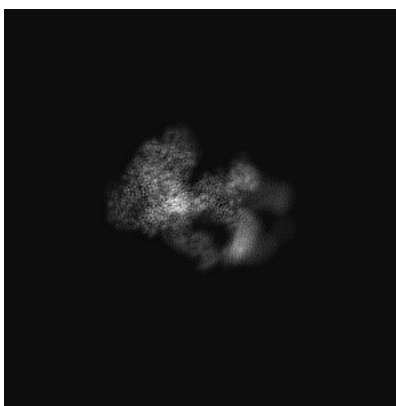
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

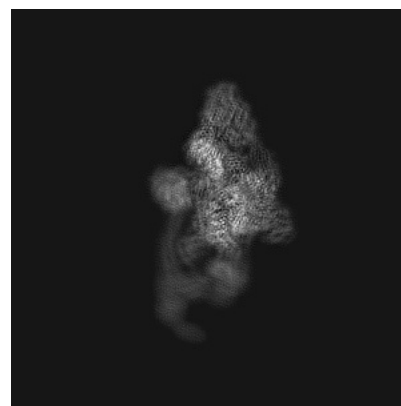
6.1.1 Primary map



X

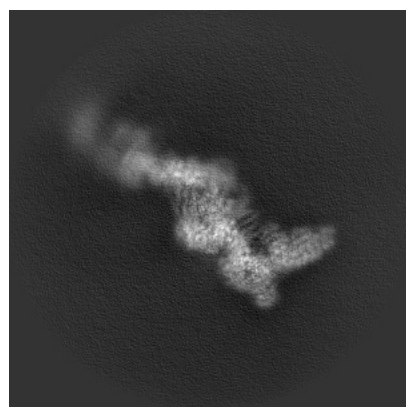


Y

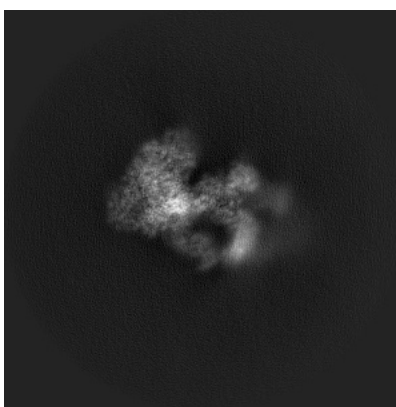


Z

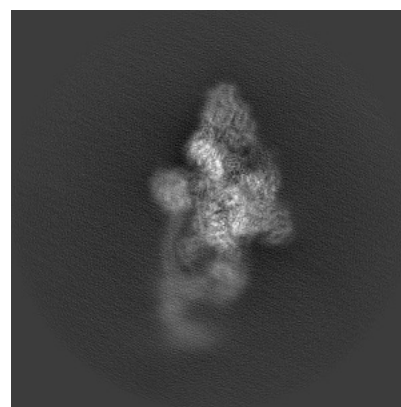
6.1.2 Raw map



X



Y

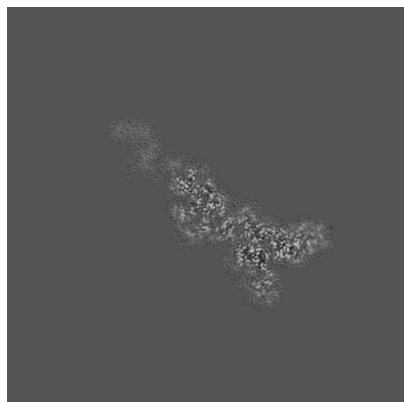


Z

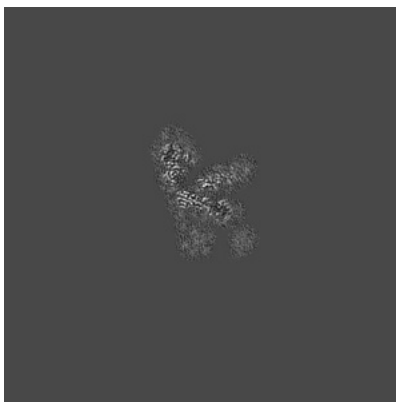
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

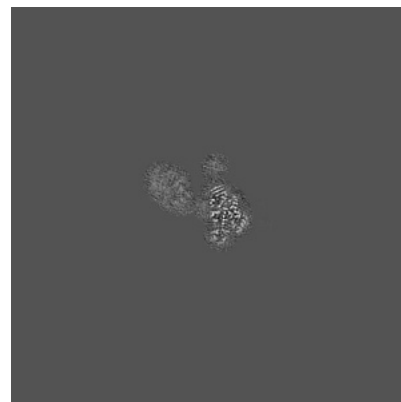
6.2.1 Primary map



X Index: 196

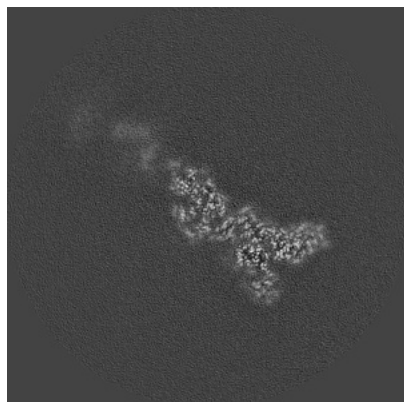


Y Index: 196

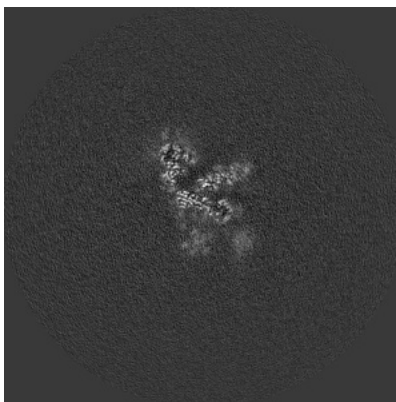


Z Index: 196

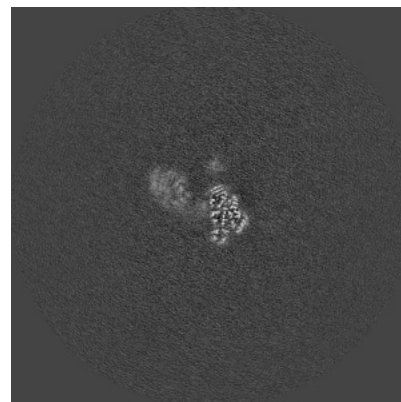
6.2.2 Raw map



X Index: 196



Y Index: 196

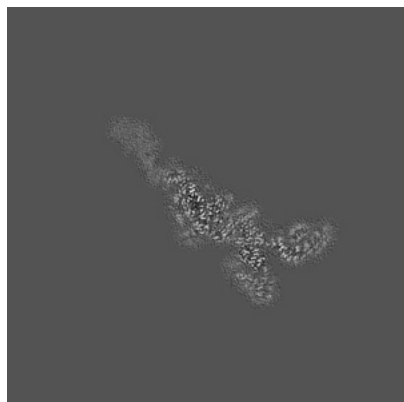


Z Index: 196

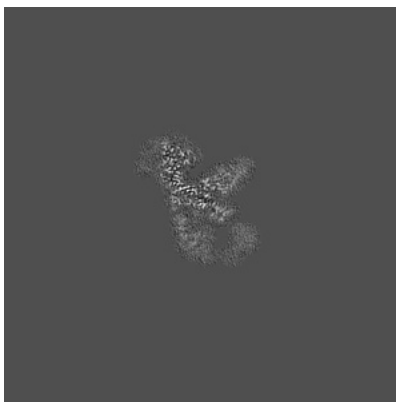
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

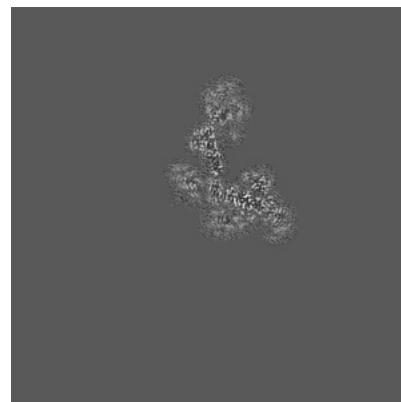
6.3.1 Primary map



X Index: 203

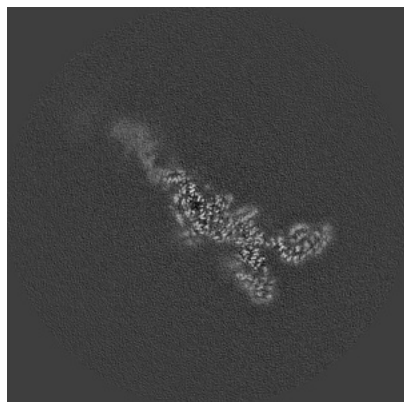


Y Index: 202

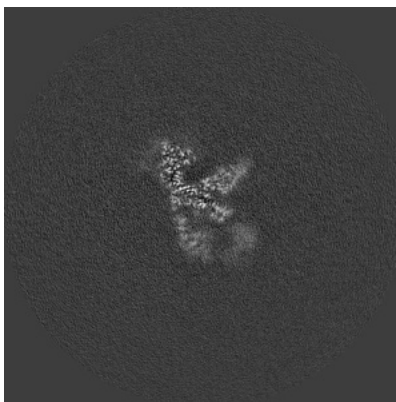


Z Index: 167

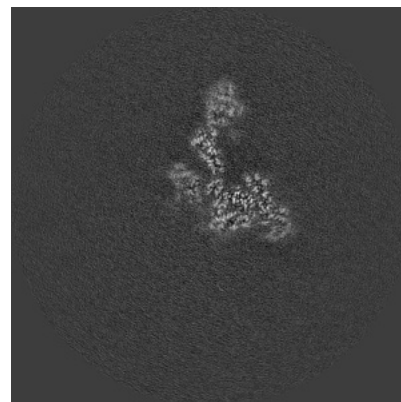
6.3.2 Raw map



X Index: 203



Y Index: 202

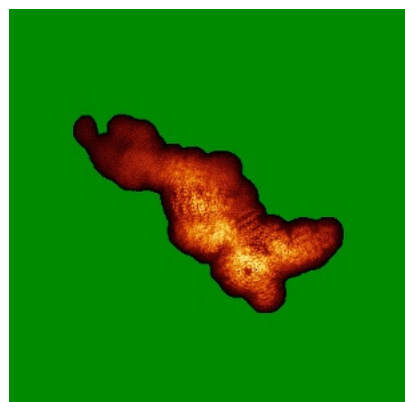


Z Index: 170

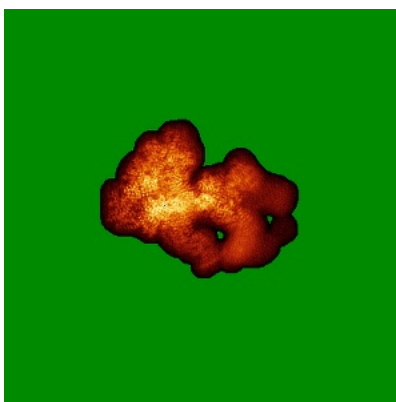
The images above show the largest variance slices of the map in three orthogonal directions.

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

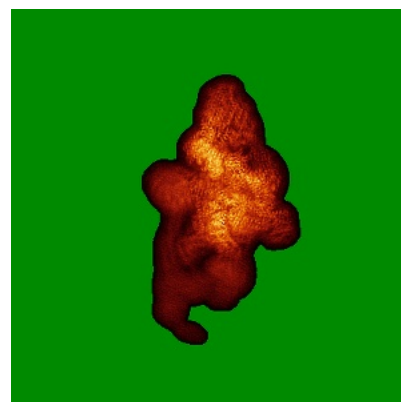
6.4.1 Primary map



X

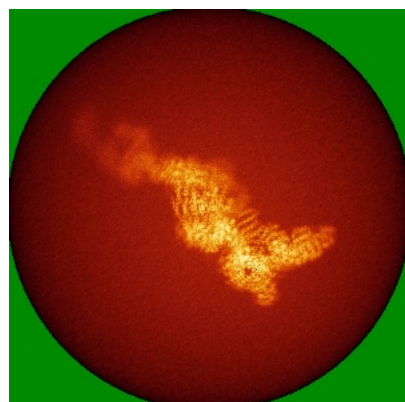


Y

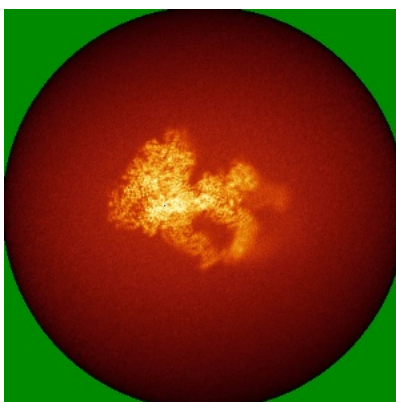


Z

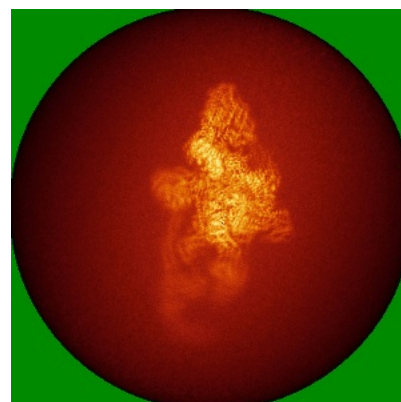
6.4.2 Raw map



X



Y

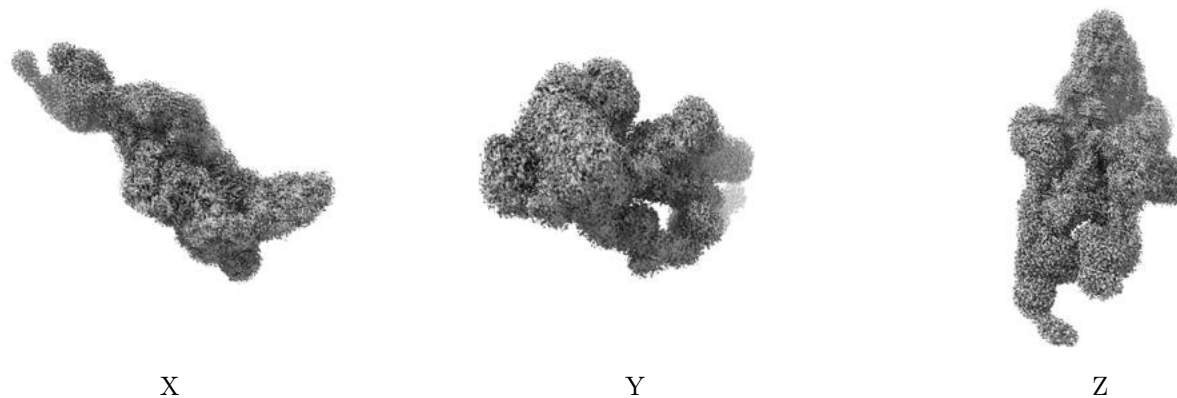


Z

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.

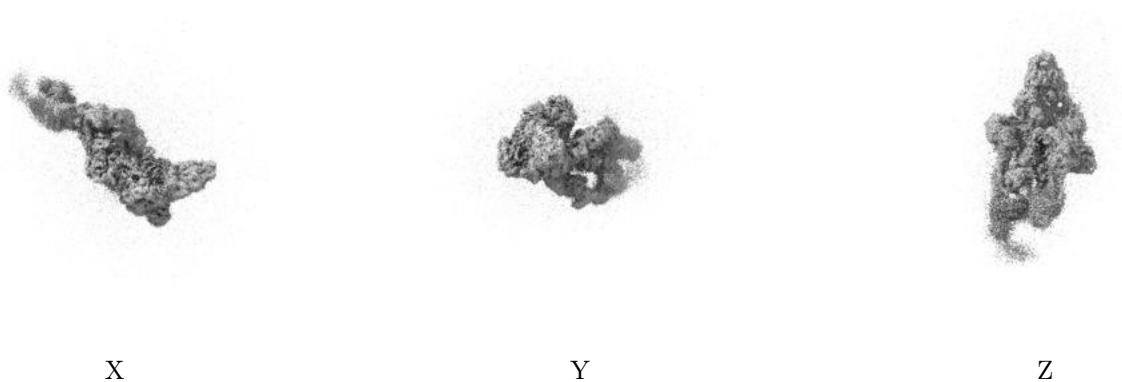
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

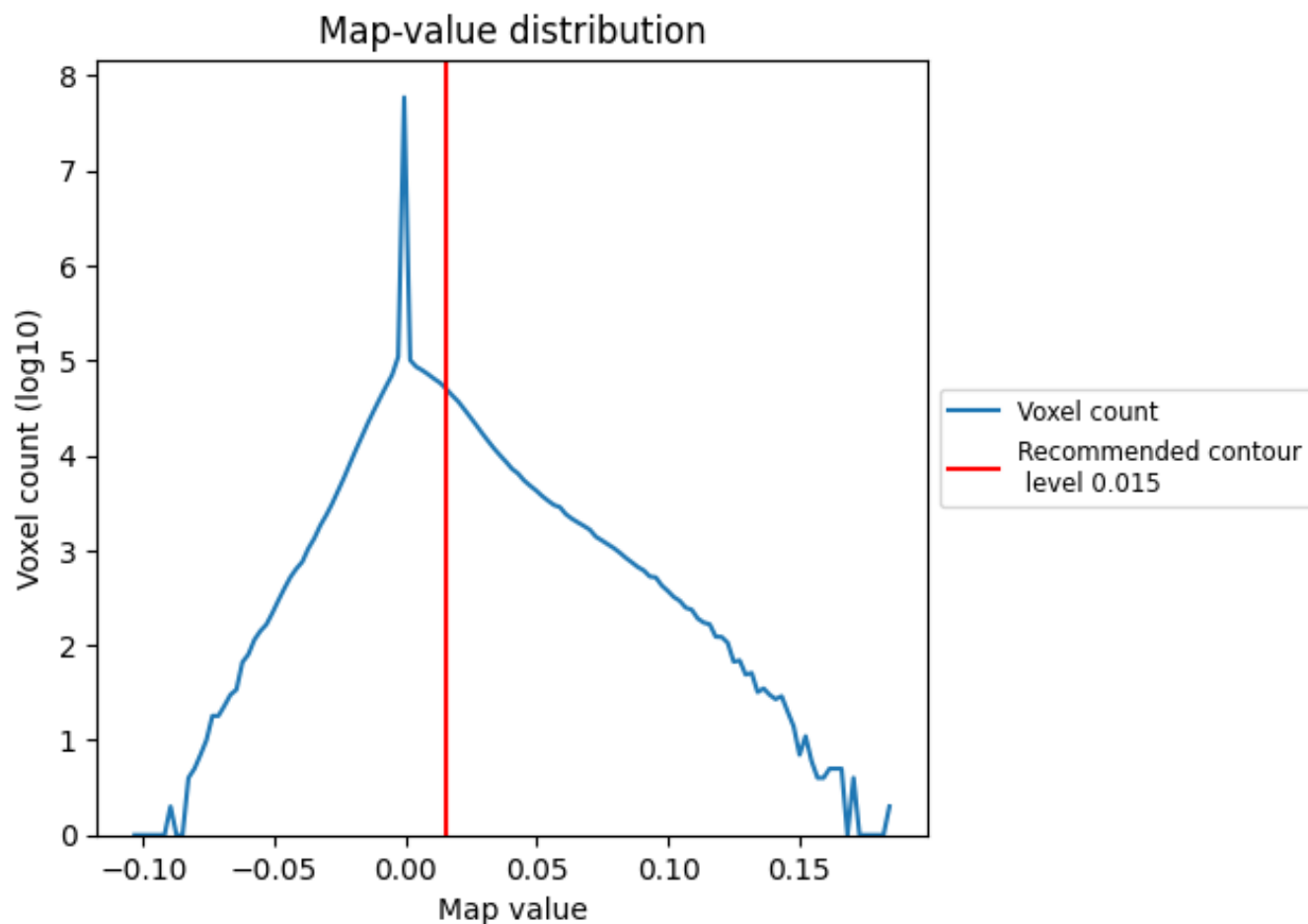
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

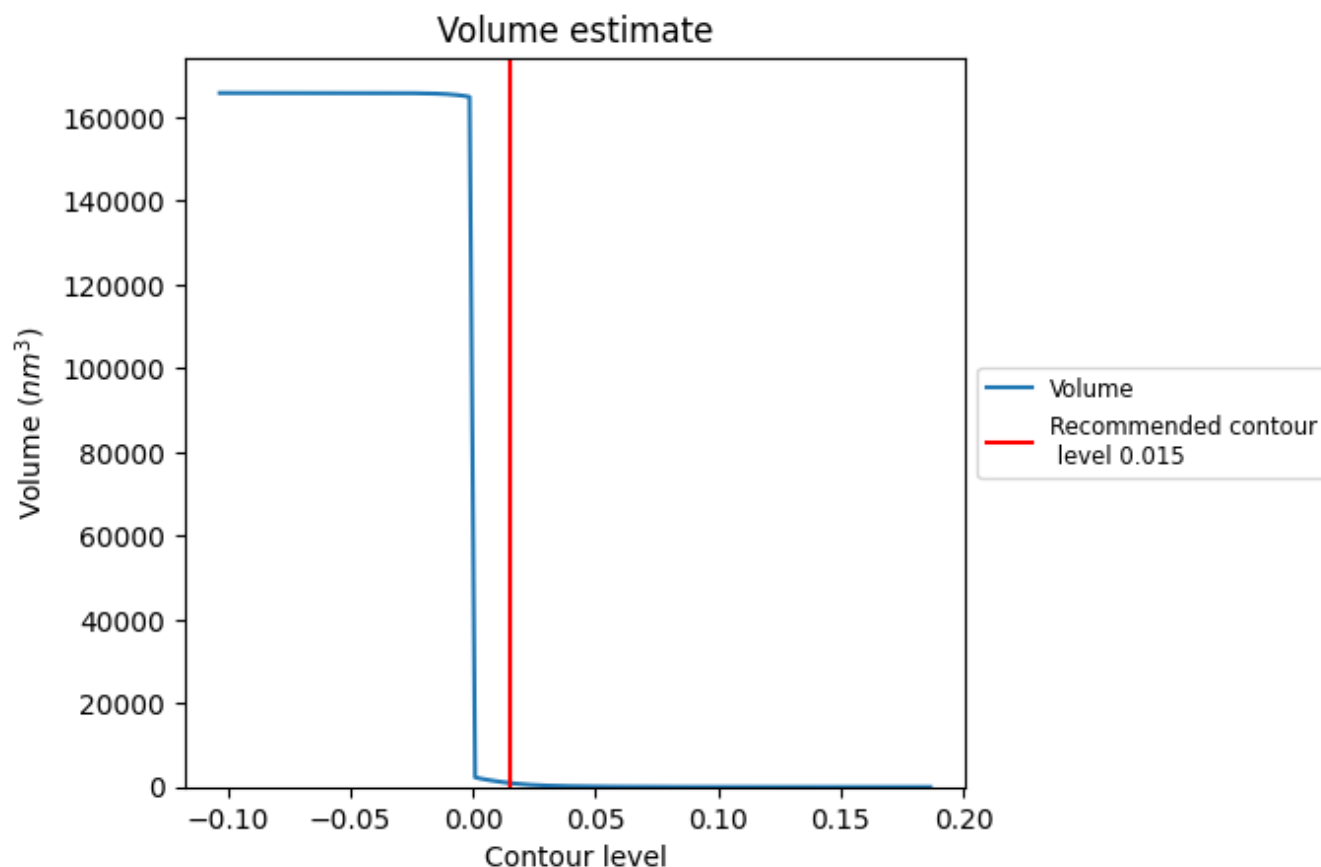
This section contains the results of statistical analysis of the map.

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.

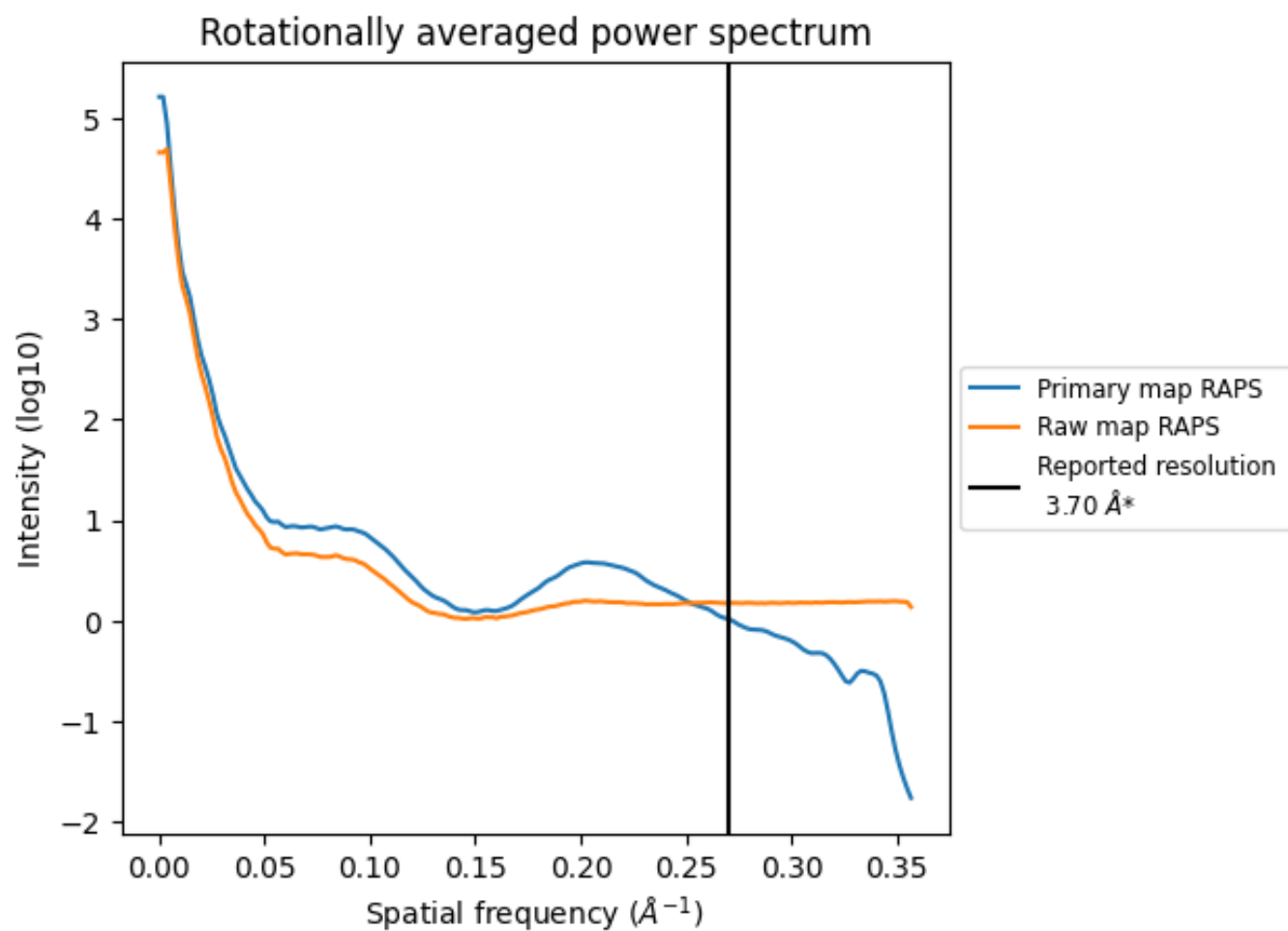
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 945 nm^3 ; this corresponds to an approximate mass of 853 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

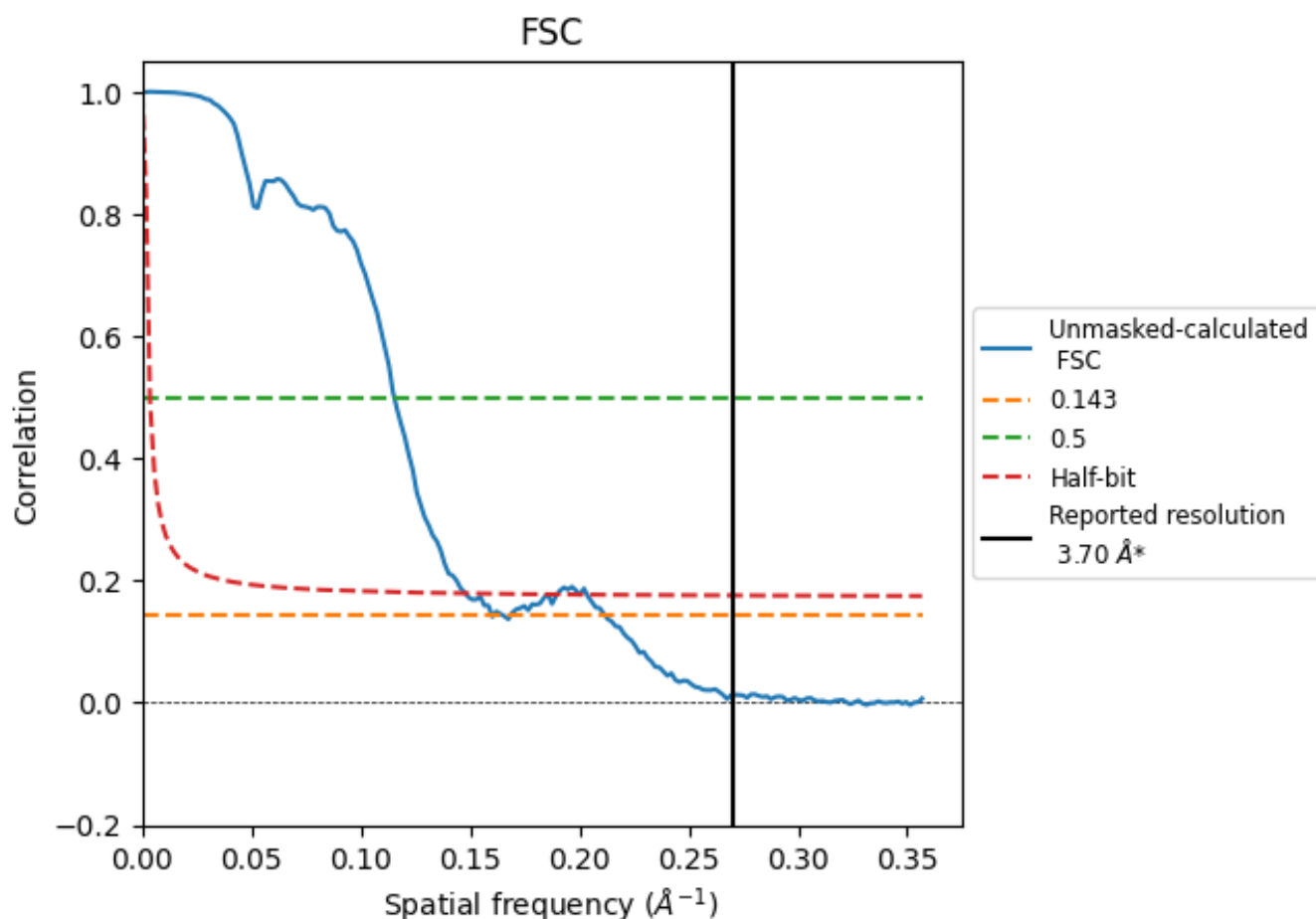


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

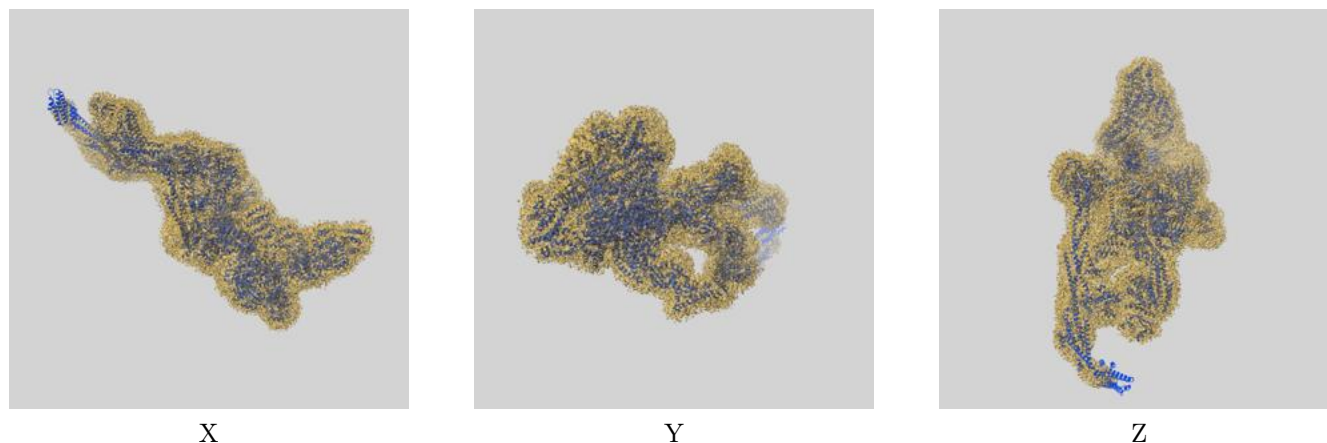
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.25	8.67	6.76

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.25 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

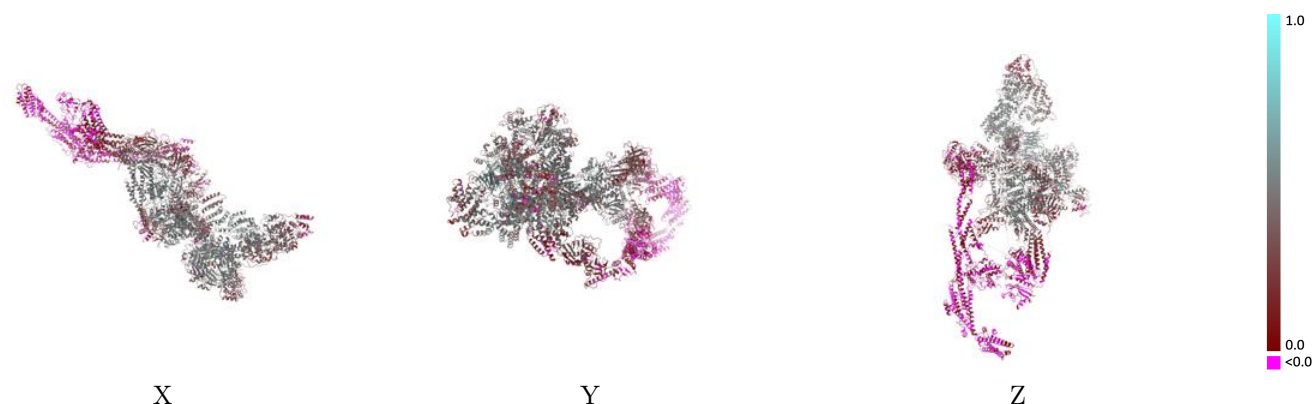
This section contains information regarding the fit between EMDB map EMD-41580 and PDB model 8TRH. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



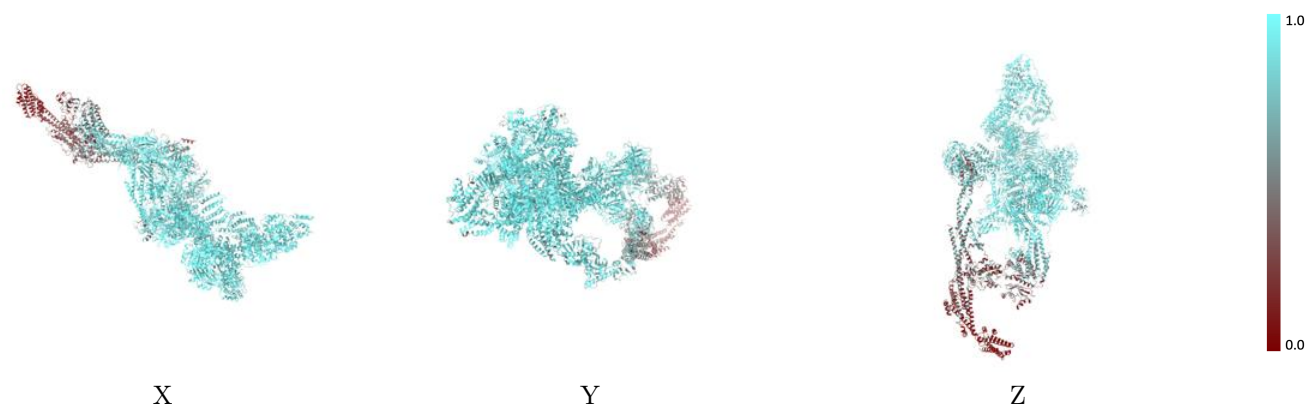
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



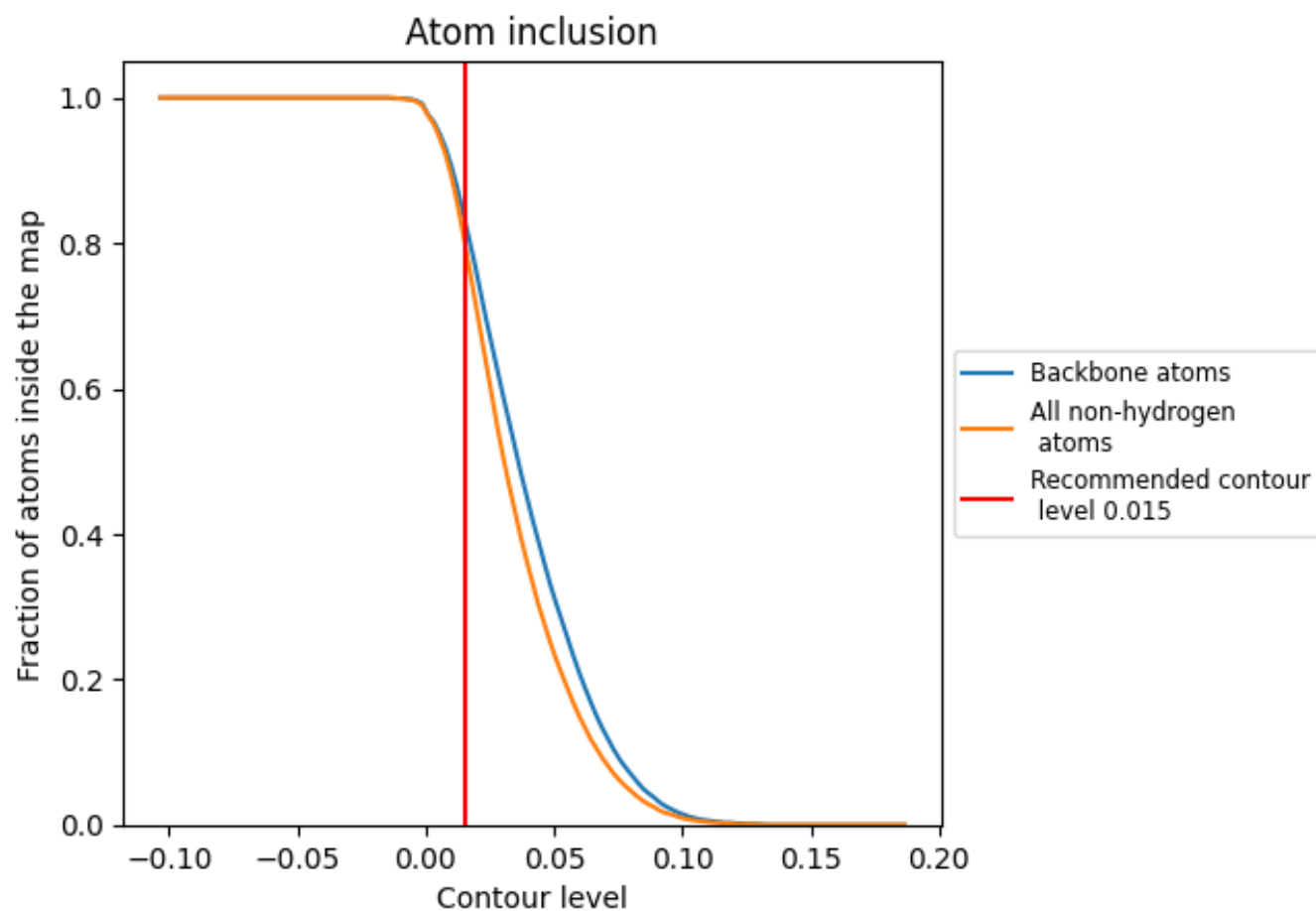
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 81% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8060	 0.3170
0	 0.9430	 0.4670
1	 0.9520	 0.4210
2	 0.9100	 0.4040
3	 0.9250	 0.4000
4	 0.3490	 0.0150
A	 0.7810	 0.2080
B	 0.8700	 0.2510
D	 0.4710	 0.0200
F	 0.4680	 0.0590
G	 0.3670	 0.0150
H	 0.5390	 0.0480
I	 0.5850	 0.0570
J	 0.1130	 0.0170
K	 0.8070	 0.2610
N	 0.8090	 0.3390
O	 0.9240	 0.4100
P	 0.9350	 0.4470
Q	 0.8410	 0.3620
R	 0.8850	 0.2980
S	 0.1010	 -0.0070
T	 0.8890	 0.3230
U	 0.3500	 0.0010
V	 0.8340	 0.2780
W	 0.9300	 0.4070
X	 0.9000	 0.3810
d	 0.1450	 -0.0340

