



# wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 09:19 AM UTC

PDB ID : 8CEO / pdb\_00008ceo  
EMDB ID : EMD-16611  
Title : Yeast RNA polymerase II transcription pre-initiation complex with core Mediator and the +1 nucleosome  
Authors : Wang, H.; Cramer, P.  
Deposited on : 2023-02-02  
Resolution : 3.60 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](mailto: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>.

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

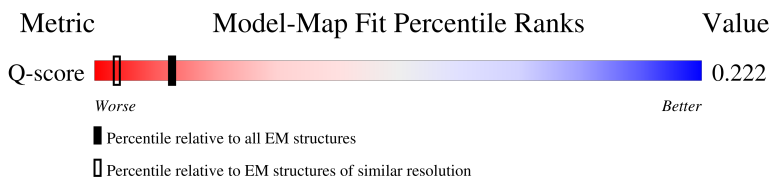
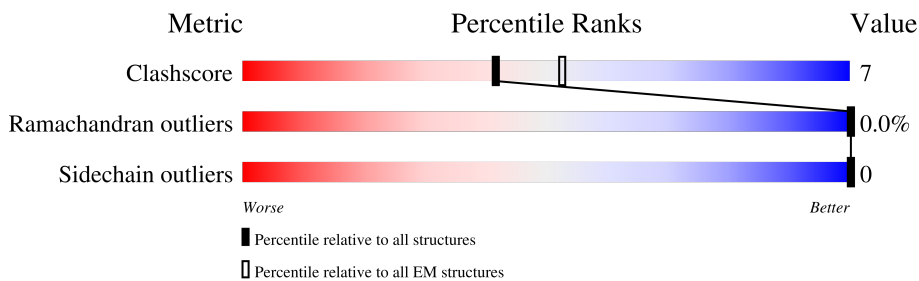
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ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

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

The reported resolution of this entry is 3.60 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	12797 ( 3.10 - 4.10 )

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  $\geq 3$ , 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	778	
2	1	642	
3	2	513	
4	3	321	

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Mol	Chain	Length	Quality of chain
5	4	338	73% 16% 11%
6	5	72	75% 15% 10%
7	6	461	69% 14% 17%
8	7	843	58% 15% 27%
9	A	1733	74% 13% 13%
10	B	1224	83% 14%
11	C	347	67% 10% 23%
12	D	221	63% 12% 24%
13	E	215	89% 10%
14	F	155	59% 17% 24%
15	G	177	76% 20%
16	H	146	70% 26%
17	I	122	75% 20% 5%
18	J	70	86% 13%
19	K	120	88% 8%
20	L	70	51% 13% 36%
21	M	352	74% 14% 12%
22	N	209	33% 84% 16%
23	O	240	62% 14% 25%
24	Q	735	24% 6% 70%
25	R	400	56% 11% 33%
26	T	209	33% 82% 18%
27	U	286	29% 8% 63%
28	V	122	69% 16% 15%
29	W	492	52% 10% 38%

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Mol	Chain	Length	Quality of chain
30	X	328	53% 11% 36%
31	a	295	45% 16% 40%
32	b	223	56% 22% 23%
33	c	115	77% 20%
34	d	687	59% 14% 27%
35	e	307	70% 13% 17%
36	f	210	80% 18%
37	g	121	64% 21% 16%
38	h	284	52% 8% 40%
39	i	222	64% 18% 18%
40	j	149	7% 45% 23% 32%
41	k	157	76% 24%
42	l	1082	39% 10% 51%
43	m	220	48% 11% 41%
44	n	140	71% 26%
45	o	127	68% 19% 13%
46	p	566	18% 35% 5% 60%
47	r	135	14% 54% 18% 28%
47	v	135	58% 15% 27%
48	s	102	12% 54% 26% 20%
48	w	102	62% 17% 22%
49	t	129	17% 75% 9% 16%
49	x	129	5% 64% 19% 18%
50	u	125	19% 65% 13% 22%
50	y	125	62% 14% 24%

## 2 Entry composition [i](#)

There are 53 unique types of molecules in this entry. The entry contains 113584 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 General transcription and DNA repair factor IIIH helicase subunit XPD.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	752	6091	3882	1029	1142	38	0	0

- Molecule 2 is a protein called TFB1 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	522	4214	2660	734	798	22	0	0

- Molecule 3 is a protein called RNA polymerase II transcription factor B subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	452	3647	2354	600	677	16	0	0

- Molecule 4 is a protein called RNA polymerase II transcription factor B subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	3	131	1089	692	180	209	8	0	0

- Molecule 5 is a protein called General transcription and DNA repair factor IIIH subunit TFB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	4	302	2338	1492	390	442	14	0	0

- Molecule 6 is a protein called General transcription and DNA repair factor IIIH subunit TFB5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	5	65	514	326	90	95	3	0	0

- Molecule 7 is a protein called General transcription and DNA repair factor IIIH.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	6	383	3019	1915	523	552	29	0	0

- Molecule 8 is a protein called General transcription and DNA repair factor IIIH helicase subunit XPB.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	7	615	4954	3153	860	914	27	0	0

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	A	1508	11815	7442	2042	2269	62	0	0

- Molecule 10 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	B	1180	9404	5946	1643	1760	55	0	0

- Molecule 11 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	C	266	2092	1315	348	416	13	0	0

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-28	MET	-	initiating methionine	UNP P16370
C	-27	GLY	-	expression tag	UNP P16370
C	-26	SER	-	expression tag	UNP P16370
C	-25	HIS	-	expression tag	UNP P16370
C	-24	HIS	-	expression tag	UNP P16370
C	-23	HIS	-	expression tag	UNP P16370
C	-22	HIS	-	expression tag	UNP P16370
C	-21	HIS	-	expression tag	UNP P16370
C	-20	HIS	-	expression tag	UNP P16370
C	-19	SER	-	expression tag	UNP P16370

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-18	ASN	-	expression tag	UNP P16370
C	-17	SER	-	expression tag	UNP P16370
C	-16	GLY	-	expression tag	UNP P16370
C	-15	LEU	-	expression tag	UNP P16370
C	-14	ASN	-	expression tag	UNP P16370
C	-13	ASP	-	expression tag	UNP P16370
C	-12	ILE	-	expression tag	UNP P16370
C	-11	PHE	-	expression tag	UNP P16370
C	-10	GLU	-	expression tag	UNP P16370
C	-9	ALA	-	expression tag	UNP P16370
C	-8	GLN	-	expression tag	UNP P16370
C	-7	LYS	-	expression tag	UNP P16370
C	-6	ILE	-	expression tag	UNP P16370
C	-5	GLU	-	expression tag	UNP P16370
C	-4	TRP	-	expression tag	UNP P16370
C	-3	HIS	-	expression tag	UNP P16370
C	-2	GLU	-	expression tag	UNP P16370
C	-1	ASP	-	expression tag	UNP P16370
C	0	THR	-	expression tag	UNP P16370
C	1	GLY	-	expression tag	UNP P16370
C	2	SER	-	expression tag	UNP P16370
C	3	SER	-	expression tag	UNP P16370

- Molecule 12 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	D	167	1343	829	242	270	2	0	0

- Molecule 13 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	E	214	1752	1111	309	321	11	0	0

- Molecule 14 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		
14	F	118	983	623	164	193	3	0	0

- Molecule 15 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	G	171	1339	861	222	248	8	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	172	HIS	-	expression tag	UNP P34087
G	173	HIS	-	expression tag	UNP P34087
G	174	HIS	-	expression tag	UNP P34087
G	175	HIS	-	expression tag	UNP P34087
G	176	HIS	-	expression tag	UNP P34087
G	177	HIS	-	expression tag	UNP P34087

- Molecule 16 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		
16	H	140	1120	704	188	224	4	0	0

- Molecule 17 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	I	116	944	581	172	181	10	0	0

- Molecule 18 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	J	69	569	362	101	100	6	0	0

- Molecule 19 is a protein called DNA-directed RNA polymerase II subunit RPB11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	K	115	924	593	157	172	2	0	0

- Molecule 20 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	L	45	359	221	71	63	4	0	0

- Molecule 21 is a protein called Transcription initiation factor IIB.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	M	310	2379	1504	408	449	18	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	346	LYS	-	expression tag	UNP P29055
M	347	HIS	-	expression tag	UNP P29055
M	348	HIS	-	expression tag	UNP P29055
M	349	HIS	-	expression tag	UNP P29055
M	350	HIS	-	expression tag	UNP P29055
M	351	HIS	-	expression tag	UNP P29055
M	352	HIS	-	expression tag	UNP P29055

- Molecule 22 is a DNA chain called Nontemplate DNA (209-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
22	N	209	4263	2035	761	1259	208	0	0

- Molecule 23 is a protein called TATA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	O	181	1422	925	243	248	6	0	0

- Molecule 24 is a protein called Transcription initiation factor IIF subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	Q	221	1871	1179	346	339	7	0	0

- Molecule 25 is a protein called Transcription initiation factor IIF subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	R	268	2230	1409	392	419	10	0	0

- Molecule 26 is a DNA chain called Template DNA (209-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
26	T	209	4300	2045	802	1245	208	0	0

- Molecule 27 is a protein called TOA1 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	U	107	885	559	147	176	3	0	0

- Molecule 28 is a protein called Transcription initiation factor IIA subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	V	104	815	511	136	164	4	0	0

- Molecule 29 is a protein called Transcription initiation factor IIE subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	W	304	2473	1558	431	477	7	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
W	483	ALA	-	expression tag	UNP P36100
W	484	ALA	-	expression tag	UNP P36100
W	485	ALA	-	expression tag	UNP P36100
W	486	LEU	-	expression tag	UNP P36100
W	487	GLU	-	expression tag	UNP P36100
W	488	HIS	-	expression tag	UNP P36100
W	489	HIS	-	expression tag	UNP P36100
W	490	HIS	-	expression tag	UNP P36100
W	491	HIS	-	expression tag	UNP P36100
W	492	HIS	-	expression tag	UNP P36100

- Molecule 30 is a protein called Transcription initiation factor IIE subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	X	211	1708	1089	293	320	6	0	0

- Molecule 31 is a protein called Mediator of RNA polymerase II transcription subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	a	178	1495	970	240	278	7	0	0

- Molecule 32 is a protein called Mediator of RNA polymerase II transcription subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	b	172	1407	895	240	269	3	0	0

- Molecule 33 is a protein called Mediator of RNA polymerase II transcription subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	c	111	902	566	154	178	4	0	0

- Molecule 34 is a protein called Mediator of RNA polymerase II transcription subunit 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	d	501	4063	2613	684	752	14	0	0

- Molecule 35 is a protein called Mediator of RNA polymerase II transcription subunit 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	e	256	2017	1280	336	390	11	0	0

- Molecule 36 is a protein called Mediator of RNA polymerase II transcription subunit 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	f	206	1578	998	266	309	5	0	0

- Molecule 37 is a protein called Mediator of RNA polymerase II transcription subunit 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	g	102	815	512	134	164	5	0	0

- Molecule 38 is a protein called Mediator of RNA polymerase II transcription subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	h	171	1394	884	234	271	5	0	0

- Molecule 39 is a protein called Mediator of RNA polymerase II transcription subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	i	181	1512	973	253	280	6	0	0

- Molecule 40 is a protein called Mediator of RNA polymerase II transcription subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	j	102	852	533	156	162	1	0	0

- Molecule 41 is a protein called Mediator of RNA polymerase II transcription subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	k	157	1259	777	222	257	3	0	0

- Molecule 42 is a protein called Mediator of RNA polymerase II transcription subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	l	535	4385	2846	759	763	17	0	0

- Molecule 43 is a protein called Mediator of RNA polymerase II transcription subunit 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	m	130	1068	672	185	209	2	0	0

- Molecule 44 is a protein called Mediator of RNA polymerase II transcription subunit 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	n	136	1095	685	185	220	5	0	0

- Molecule 45 is a protein called Mediator of RNA polymerase II transcription subunit 31.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	110	Total	C	N	O	S	0	0
			922	607	143	166	6		

- Molecule 46 is a protein called Mediator of RNA polymerase II transcription subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p	225	Total	C	N	O	S	0	0
			1863	1193	298	366	6		

- Molecule 47 is a protein called Histone H3.2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	97	Total	C	N	O	S	0	0
			801	506	155	138	2		
47	v	98	Total	C	N	O	S	0	0
			810	512	157	139	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
r	102	ALA	GLY	conflict	UNP P84233
r	110	ALA	CYS	engineered mutation	UNP P84233
v	102	ALA	GLY	conflict	UNP P84233
v	110	ALA	CYS	engineered mutation	UNP P84233

- Molecule 48 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	s	82	Total	C	N	O	S	0	0
			653	412	127	113	1		
48	w	80	Total	C	N	O	S	0	0
			638	401	125	111	1		

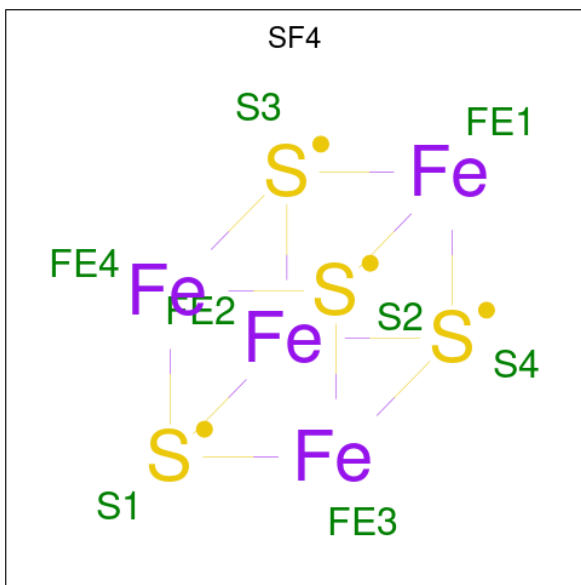
- Molecule 49 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	t	109	Total	C	N	O	0	0
			843	531	167	145		
49	x	106	Total	C	N	O	0	0
			818	516	160	142		

- Molecule 50 is a protein called Histone H2B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	u	97	Total 767	C 481	N 142	O 142	S 2	0	0
50	y	95	Total 745	C 469	N 134	O 140	S 2	0	0

- Molecule 51 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe<sub>4</sub>S<sub>4</sub>).



Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
51	0	1	Total 8	Fe 4	S 4	0

- Molecule 52 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
52	3	2	Total 2	Zn 2	0
52	4	1	Total 1	Zn 1	0
52	6	4	Total 4	Zn 4	0
52	A	2	Total 2	Zn 2	0
52	B	1	Total 1	Zn 1	0
52	C	1	Total 1	Zn 1	0
52	I	2	Total 2	Zn 2	0

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Mol	Chain	Residues	Atoms		AltConf
52	J	1	Total 1	Zn 1	0
52	L	1	Total 1	Zn 1	0
52	M	1	Total 1	Zn 1	0
52	W	1	Total 1	Zn 1	0

- Molecule 53 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
53	A	1	Total 1	Mg 1	0

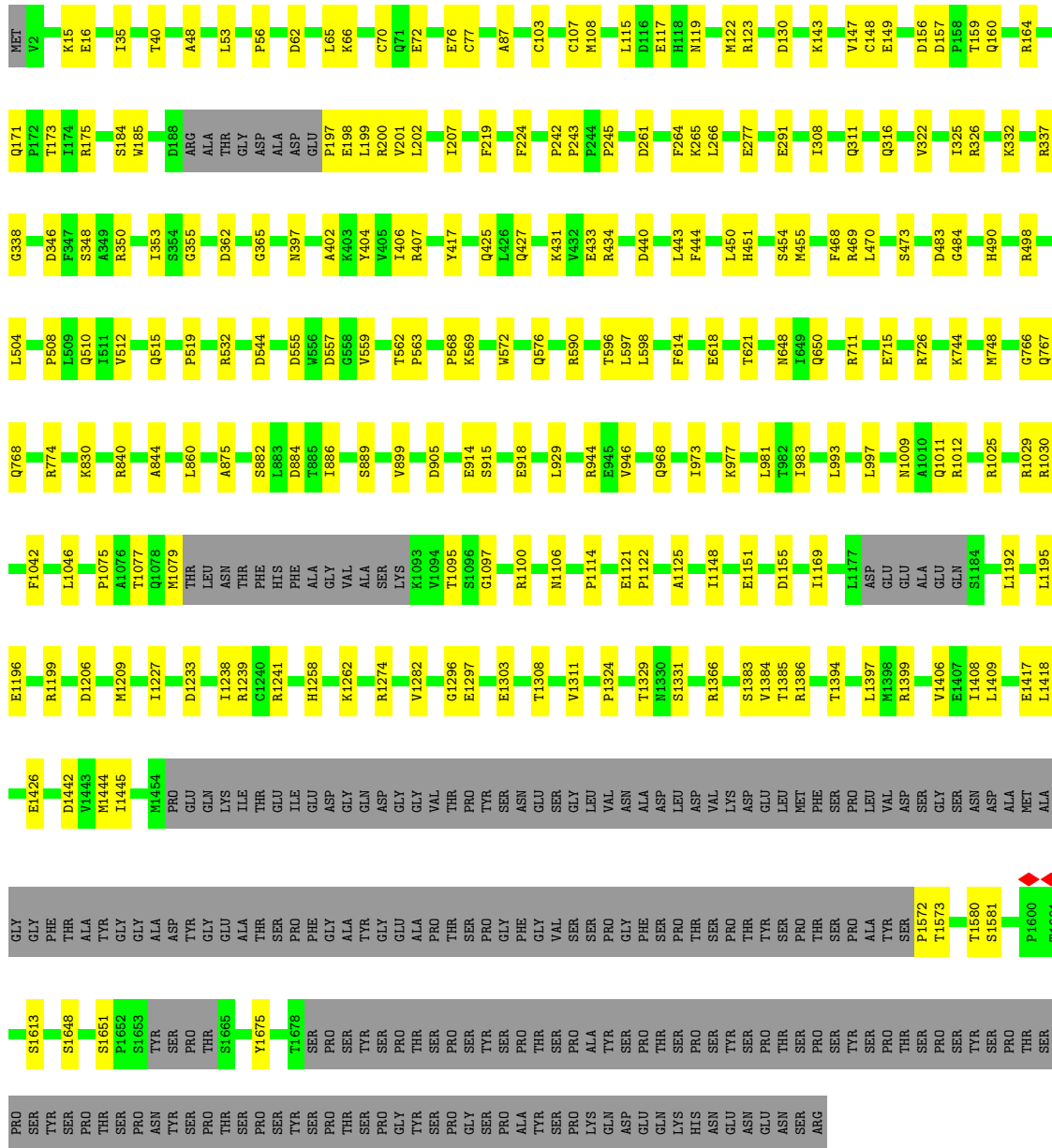






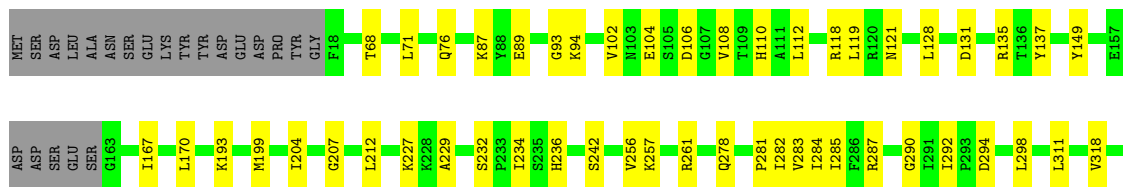
• Molecule 9: DNA-directed RNA polymerase II subunit RPB1

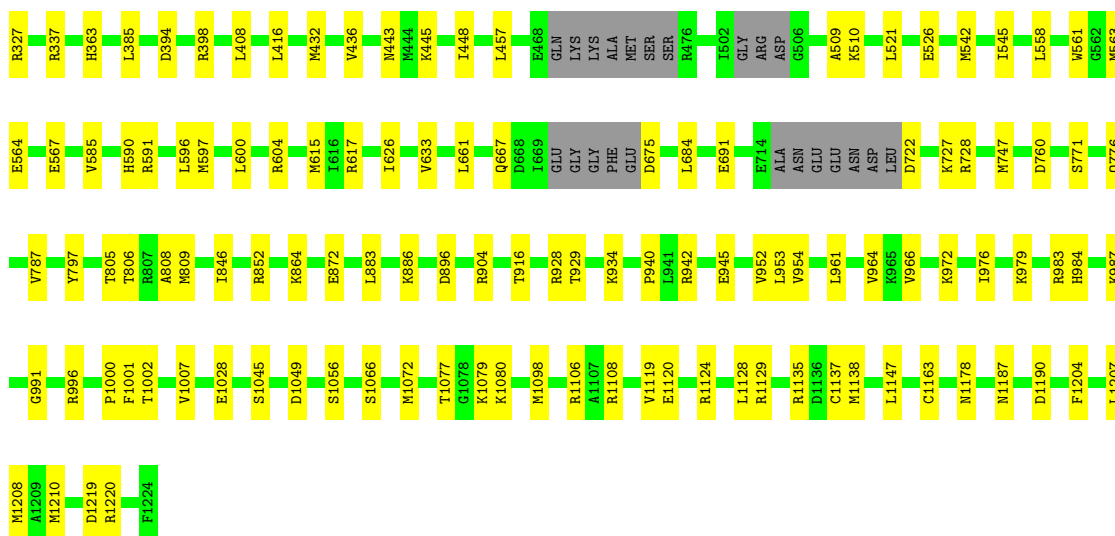
Chain A: 74% 13% 13%



• Molecule 10: DNA-directed RNA polymerase II subunit RPB2

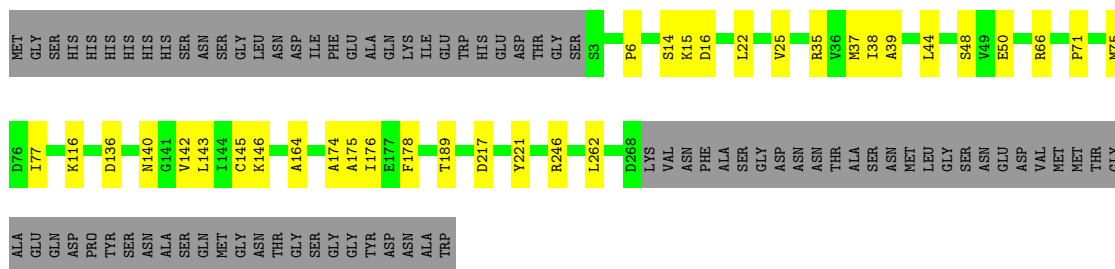
Chain B: 83% 14%





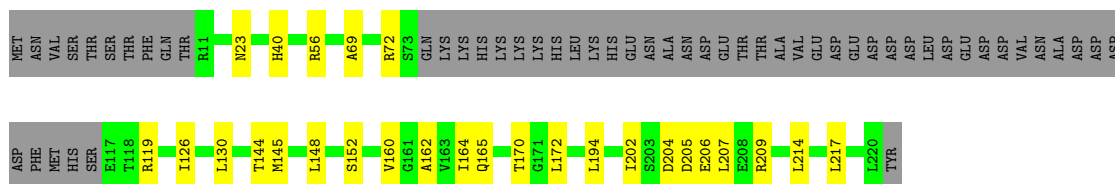
- Molecule 11: DNA-directed RNA polymerase II subunit RPB3

Chain C: 67% 10% 23%



- Molecule 12: DNA-directed RNA polymerase II subunit RPB4

Chain D: 63% 12% 24%



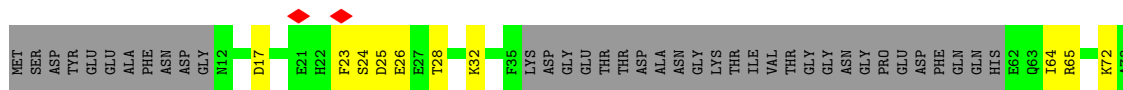
- Molecule 13: DNA-directed RNA polymerases I, II, and III subunit RPABC1

Chain E: 89% 10%



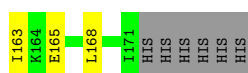
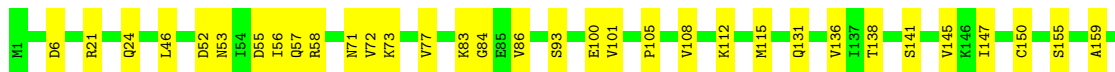
- Molecule 14: DNA-directed RNA polymerases I, II, and III subunit RPABC2

Chain F: 59% 17% 24%



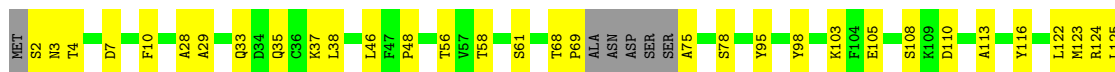
- Molecule 15: DNA-directed RNA polymerase II subunit RPB7

Chain G: 76% 20%



- Molecule 16: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain H: 70% 26%



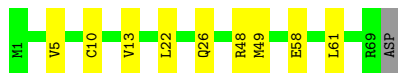
- Molecule 17: DNA-directed RNA polymerase II subunit RPB9

Chain I: 75% 20% 5%



- Molecule 18: DNA-directed RNA polymerases I, II, and III subunit RPABC5

Chain J: 86% 13%

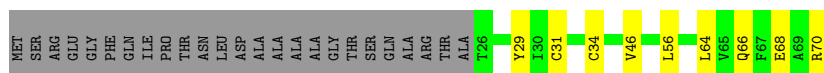


- Molecule 19: DNA-directed RNA polymerase II subunit RPB11

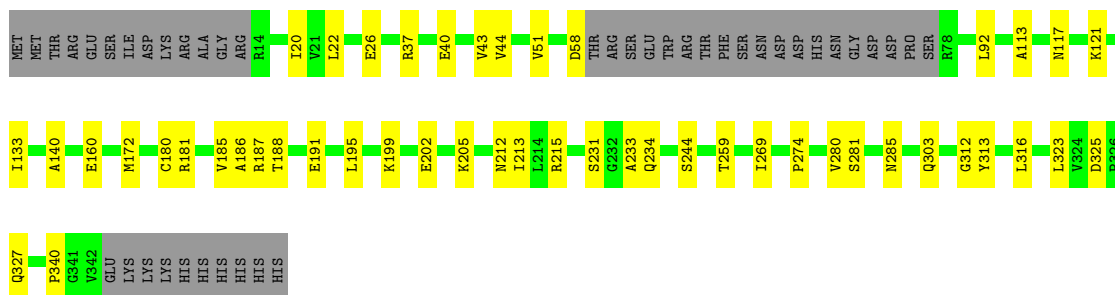
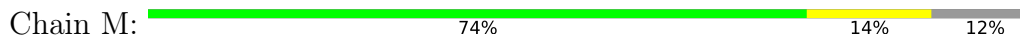
Chain K: 88% 8%



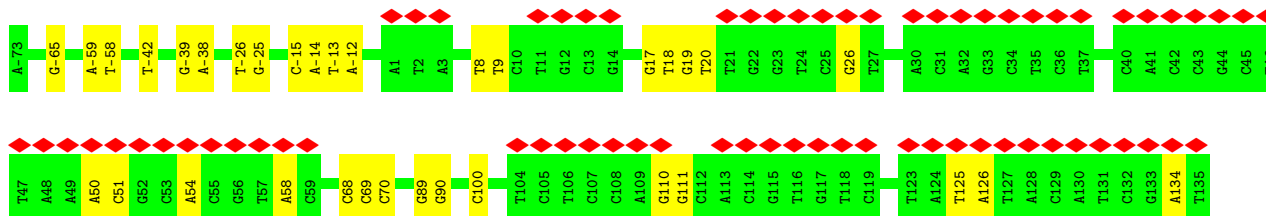
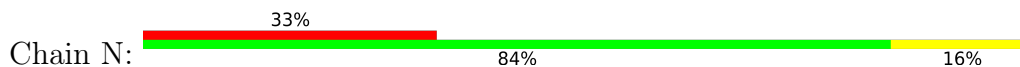
- Molecule 20: DNA-directed RNA polymerases I, II, and III subunit RPABC4



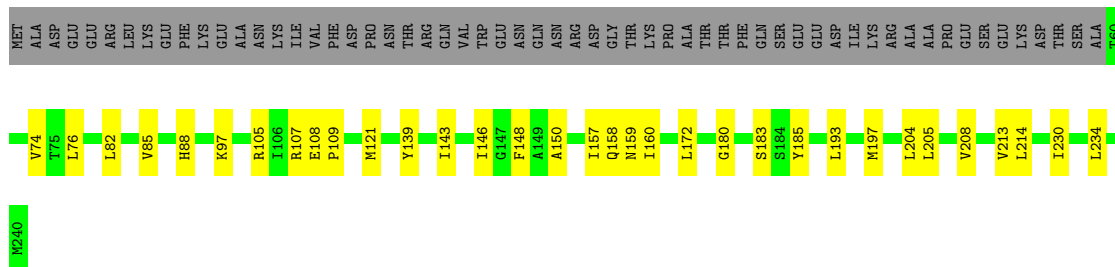
• Molecule 21: Transcription initiation factor IIB



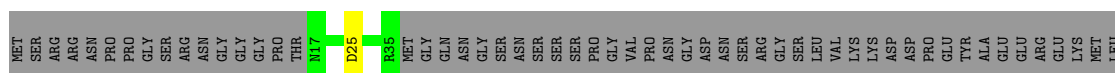
• Molecule 22: Nontemplate DNA (209-MER)

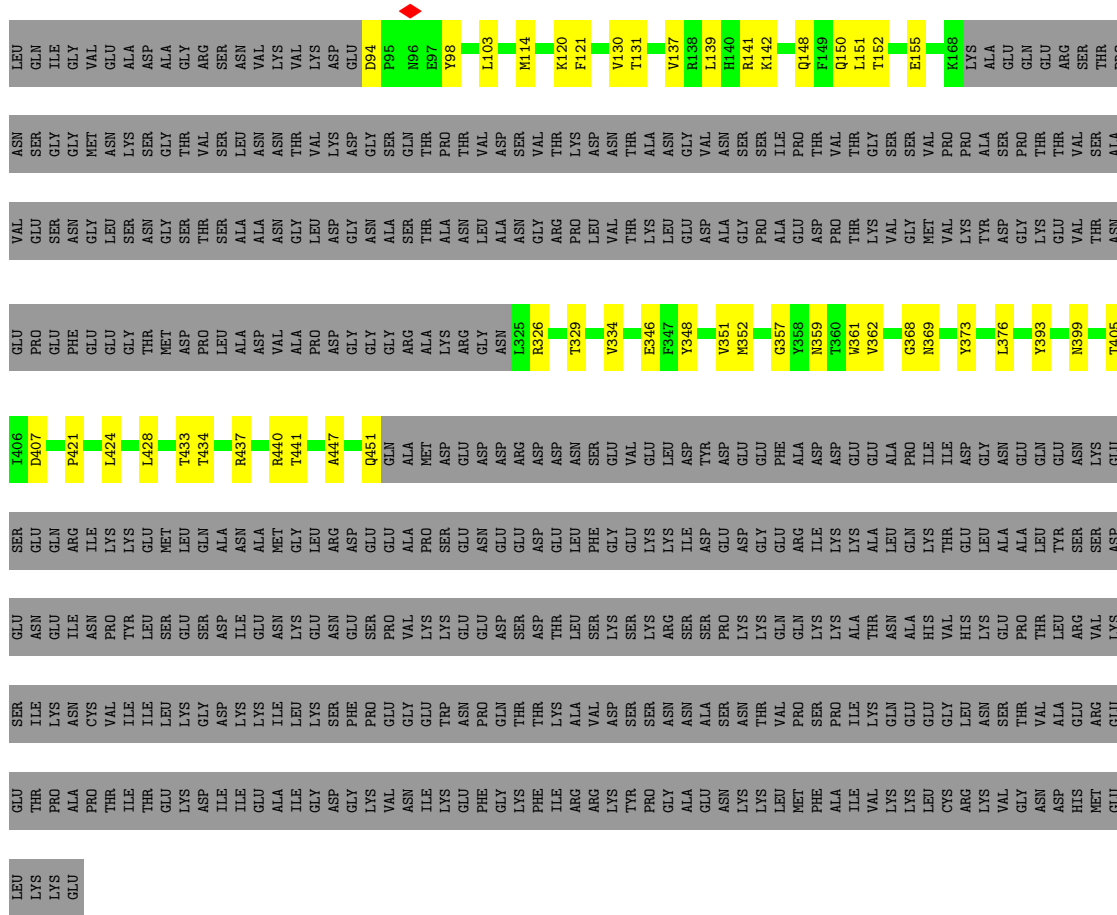


• Molecule 23: TATA-binding protein

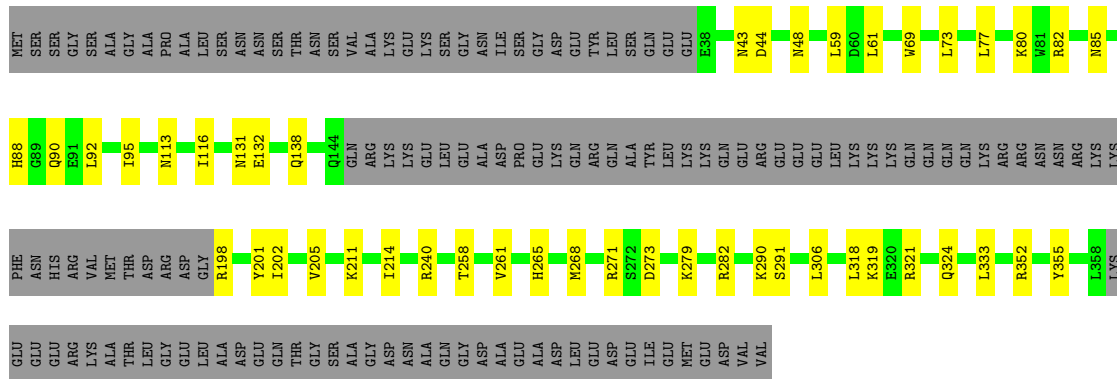


• Molecule 24: Transcription initiation factor IIF subunit alpha

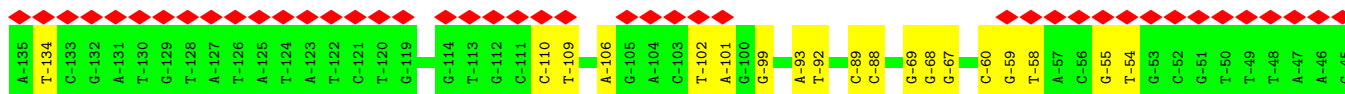
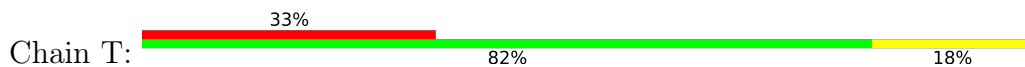


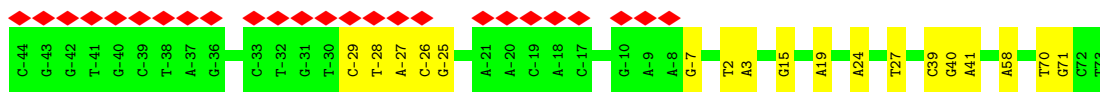


• Molecule 25: Transcription initiation factor IIF subunit beta

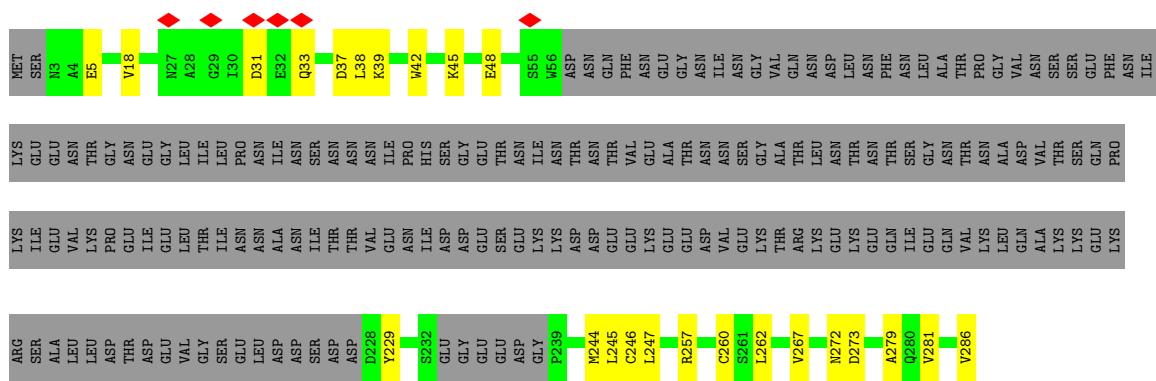


• Molecule 26: Template DNA (209-MER)





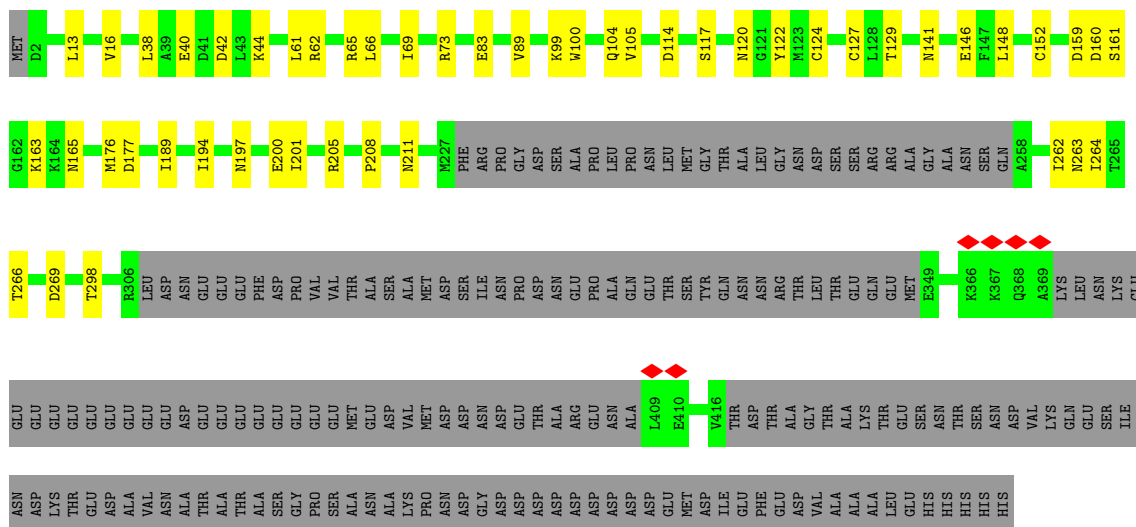
• Molecule 27: TOA1 isoform 1



• Molecule 28: Transcription initiation factor IIA subunit 2



• Molecule 29: Transcription initiation factor IIE subunit alpha



• Molecule 30: Transcription initiation factor IIE subunit beta



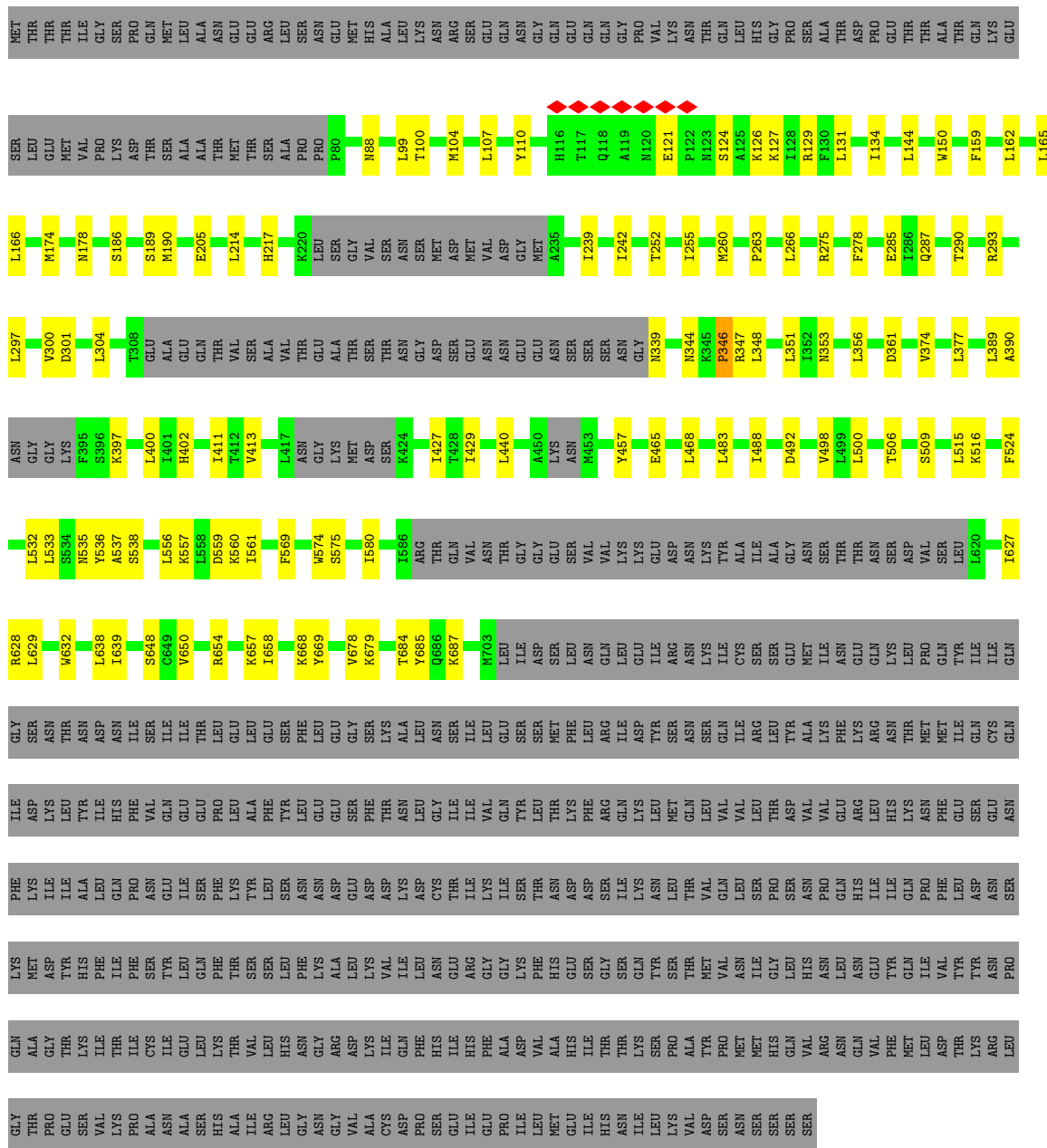
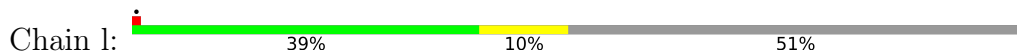




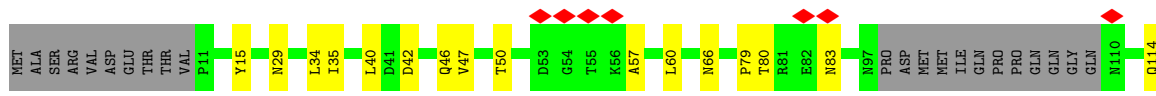


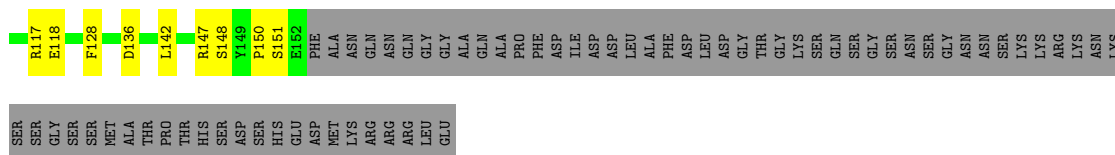


• Molecule 42: Mediator of RNA polymerase II transcription subunit 14

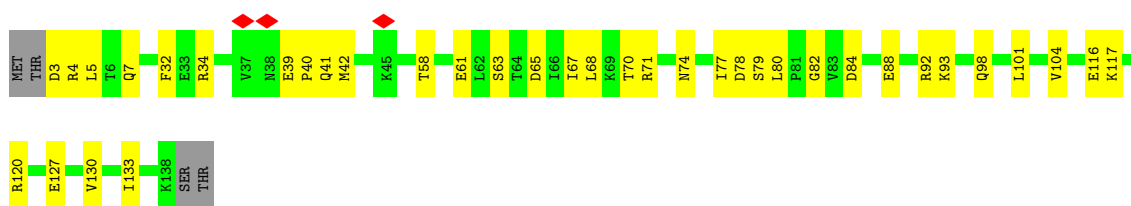


• Molecule 43: Mediator of RNA polymerase II transcription subunit 19





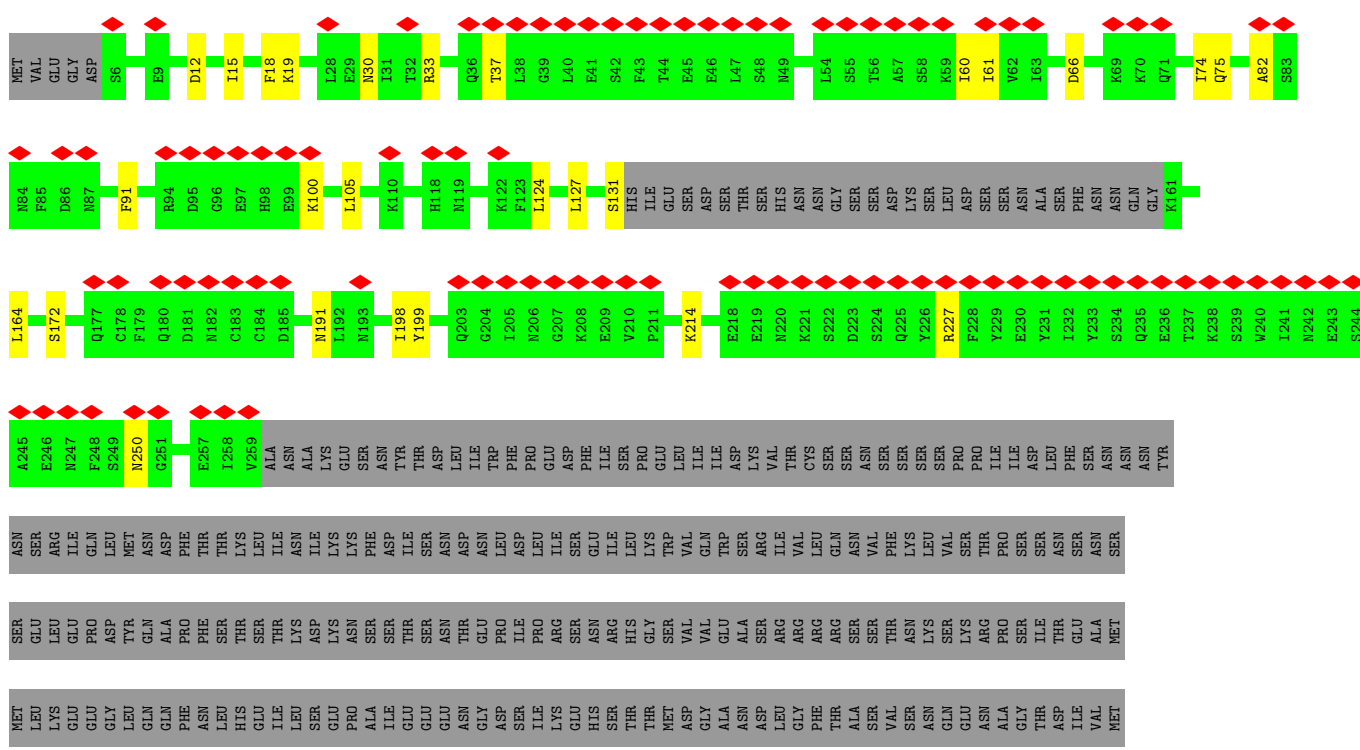
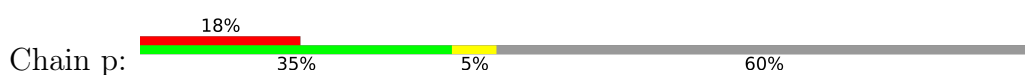
• Molecule 44: Mediator of RNA polymerase II transcription subunit 21



• Molecule 45: Mediator of RNA polymerase II transcription subunit 31



• Molecule 46: Mediator of RNA polymerase II transcription subunit 1





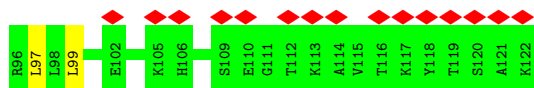
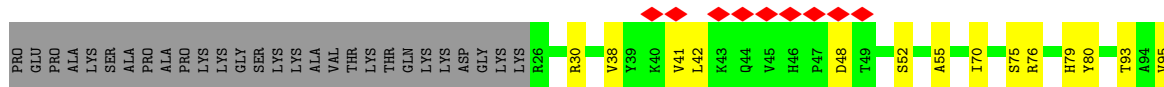
SER  
SER  
LYS  
SER  
ALA  
LYS  
SER  
LYS

• Molecule 49: Histone H2A

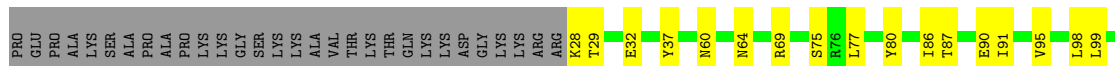


LYS  
THR  
GLU  
SER  
SER  
LYS  
SER  
ALA  
LYS  
LYS

• Molecule 50: Histone H2B



• Molecule 50: Histone H2B



K122

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	50715	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 ( $e^-/\text{\AA}^2$ )	42	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.234	Depositor
Minimum map value	-0.121	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.006	Depositor
Map size (Å)	419.99997, 419.99997, 419.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	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	0.16	0/6209	0.34	0/8384
2	1	0.14	0/4277	0.33	0/5755
3	2	0.17	0/3717	0.42	0/5028
4	3	0.13	0/1109	0.36	0/1492
5	4	0.16	0/2377	0.35	0/3216
6	5	0.20	0/520	0.51	0/701
7	6	0.16	0/3082	0.39	0/4165
8	7	0.16	0/5059	0.35	0/6841
9	A	0.20	0/12048	0.37	0/16321
10	B	0.22	0/9589	0.36	0/12934
11	C	0.23	0/2130	0.36	0/2887
12	D	0.14	0/1351	0.37	0/1811
13	E	0.19	0/1788	0.45	2/2406 (0.1%)
14	F	0.22	0/1001	0.44	0/1347
15	G	0.18	0/1367	0.44	0/1844
16	H	0.20	0/1139	0.40	0/1544
17	I	0.19	0/962	0.43	0/1295
18	J	0.25	0/578	0.43	0/775
19	K	0.23	0/942	0.44	0/1272
20	L	0.23	0/361	0.49	0/478
21	M	0.17	0/2408	0.42	0/3241
22	N	0.23	0/4776	0.41	0/7366
23	O	0.21	0/1449	0.45	0/1952
24	Q	0.17	0/1907	0.37	0/2556
25	R	0.15	0/2270	0.37	0/3052
26	T	0.22	0/4830	0.37	0/7457
27	U	0.17	0/898	0.47	0/1212
28	V	0.17	0/822	0.45	0/1109
29	W	0.13	0/2513	0.34	0/3388
30	X	0.13	0/1739	0.37	0/2339
31	a	0.16	0/1531	0.45	0/2072
32	b	0.18	0/1436	0.50	0/1947

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	c	0.20	0/913	0.46	0/1228
34	d	0.17	0/4118	0.42	0/5532
35	e	0.17	0/2054	0.41	1/2782 (0.0%)
36	f	0.18	0/1602	0.36	0/2169
37	g	0.20	0/818	0.48	0/1104
38	h	0.23	0/1415	0.62	0/1907
39	i	0.17	0/1543	0.45	1/2084 (0.0%)
40	j	0.24	0/865	0.71	0/1166
41	k	0.19	0/1277	0.48	0/1727
42	l	0.18	0/4468	0.49	3/6048 (0.0%)
43	m	0.15	0/1093	0.40	0/1481
44	n	0.21	0/1106	0.61	0/1488
45	o	0.19	0/949	0.48	0/1294
46	p	0.15	0/1898	0.40	0/2559
47	r	0.20	0/813	0.51	0/1091
47	v	0.18	0/822	0.44	0/1103
48	s	0.23	0/660	0.59	0/883
48	w	0.21	0/645	0.53	0/862
49	t	0.22	0/853	0.53	0/1149
49	x	0.18	0/828	0.45	0/1117
50	u	0.20	0/778	0.50	0/1043
50	y	0.20	0/756	0.54	0/1015
All	All	0.19	0/116459	0.41	7/159019 (0.0%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	l	346	PRO	CA-N-CD	-11.55	95.84	112.00
42	l	346	PRO	N-CA-C	6.33	122.98	114.18
35	e	55	ARG	CA-CB-CG	6.29	126.69	114.10
42	l	346	PRO	N-CD-CG	-5.39	95.11	103.20
39	i	190	ARG	CB-CG-CD	5.21	123.28	111.30

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	6091	0	6155	90	0
2	1	4214	0	4288	52	0
3	2	3647	0	3732	38	0
4	3	1089	0	1069	19	0
5	4	2338	0	2404	40	0
6	5	514	0	541	10	0
7	6	3019	0	3040	47	0
8	7	4954	0	4946	81	0
9	A	11815	0	11816	156	0
10	B	9404	0	9398	112	0
11	C	2092	0	2050	28	0
12	D	1343	0	1366	18	0
13	E	1752	0	1776	12	0
14	F	983	0	968	22	0
15	G	1339	0	1357	23	0
16	H	1120	0	1086	27	0
17	I	944	0	899	15	0
18	J	569	0	585	6	0
19	K	924	0	934	7	0
20	L	359	0	381	7	0
21	M	2379	0	2488	38	0
22	N	4263	0	2359	37	0
23	O	1422	0	1500	25	0
24	Q	1871	0	1883	36	0
25	R	2230	0	2254	35	0
26	T	4300	0	2352	29	0
27	U	885	0	866	23	0
28	V	815	0	822	18	0
29	W	2473	0	2476	35	0
30	X	1708	0	1761	25	0
31	a	1495	0	1476	29	0
32	b	1407	0	1404	42	0
33	c	902	0	918	18	0
34	d	4063	0	4247	71	0
35	e	2017	0	2024	31	0
36	f	1578	0	1595	23	0
37	g	815	0	839	21	0
38	h	1394	0	1420	18	0
39	i	1512	0	1544	34	0
40	j	852	0	857	23	0
41	k	1259	0	1241	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	l	4385	0	4612	76	0
43	m	1068	0	1021	25	0
44	n	1095	0	1116	31	0
45	o	922	0	907	18	0
46	p	1863	0	1819	17	0
47	r	801	0	841	23	0
47	v	810	0	853	16	0
48	s	653	0	696	27	0
48	w	638	0	676	13	0
49	t	843	0	908	12	0
49	x	818	0	877	16	0
50	u	767	0	799	15	0
50	y	745	0	773	15	0
51	0	8	0	0	0	0
52	3	2	0	0	0	0
52	4	1	0	0	0	0
52	6	4	0	0	0	0
52	A	2	0	0	0	0
52	B	1	0	0	0	0
52	C	1	0	0	0	0
52	I	2	0	0	0	0
52	J	1	0	0	0	0
52	L	1	0	0	0	0
52	M	1	0	0	0	0
52	W	1	0	0	0	0
53	A	1	0	0	0	0
All	All	113584	0	111015	1429	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 7.

The worst 5 of 1429 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)
20:L:31:CYS:HB3	20:L:34:CYS:SG	2.08	0.93
16:H:75:ALA:N	16:H:98:TYR:HH	1.70	0.89
29:W:127:CYS:HB3	29:W:152:CYS:SG	2.13	0.88
41:k:82:GLU:O	41:k:86:TYR:HB2	1.84	0.78
32:b:80:THR:HG21	37:g:52:THR:HG21	1.67	0.76

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	750/778 (96%)	735 (98%)	15 (2%)	0	100	100
2	1	508/642 (79%)	504 (99%)	4 (1%)	0	100	100
3	2	448/513 (87%)	434 (97%)	14 (3%)	0	100	100
4	3	129/321 (40%)	127 (98%)	2 (2%)	0	100	100
5	4	298/338 (88%)	288 (97%)	10 (3%)	0	100	100
6	5	63/72 (88%)	61 (97%)	2 (3%)	0	100	100
7	6	379/461 (82%)	367 (97%)	12 (3%)	0	100	100
8	7	609/843 (72%)	584 (96%)	25 (4%)	0	100	100
9	A	1494/1733 (86%)	1449 (97%)	45 (3%)	0	100	100
10	B	1168/1224 (95%)	1131 (97%)	37 (3%)	0	100	100
11	C	264/347 (76%)	258 (98%)	6 (2%)	0	100	100
12	D	163/221 (74%)	160 (98%)	3 (2%)	0	100	100
13	E	212/215 (99%)	205 (97%)	7 (3%)	0	100	100
14	F	114/155 (74%)	111 (97%)	3 (3%)	0	100	100
15	G	169/177 (96%)	161 (95%)	8 (5%)	0	100	100
16	H	136/146 (93%)	134 (98%)	2 (2%)	0	100	100
17	I	114/122 (93%)	109 (96%)	5 (4%)	0	100	100
18	J	67/70 (96%)	67 (100%)	0	0	100	100
19	K	113/120 (94%)	110 (97%)	3 (3%)	0	100	100
20	L	43/70 (61%)	42 (98%)	1 (2%)	0	100	100
21	M	306/352 (87%)	295 (96%)	11 (4%)	0	100	100
23	O	179/240 (75%)	170 (95%)	9 (5%)	0	100	100
24	Q	215/735 (29%)	205 (95%)	10 (5%)	0	100	100
25	R	264/400 (66%)	255 (97%)	9 (3%)	0	100	100
27	U	101/286 (35%)	96 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	V	100/122 (82%)	99 (99%)	1 (1%)	0	100	100
29	W	296/492 (60%)	290 (98%)	6 (2%)	0	100	100
30	X	207/328 (63%)	200 (97%)	7 (3%)	0	100	100
31	a	170/295 (58%)	161 (95%)	9 (5%)	0	100	100
32	b	168/223 (75%)	162 (96%)	6 (4%)	0	100	100
33	c	109/115 (95%)	108 (99%)	1 (1%)	0	100	100
34	d	481/687 (70%)	468 (97%)	13 (3%)	0	100	100
35	e	252/307 (82%)	244 (97%)	8 (3%)	0	100	100
36	f	202/210 (96%)	194 (96%)	8 (4%)	0	100	100
37	g	96/121 (79%)	93 (97%)	3 (3%)	0	100	100
38	h	169/284 (60%)	166 (98%)	3 (2%)	0	100	100
39	i	175/222 (79%)	173 (99%)	2 (1%)	0	100	100
40	j	98/149 (66%)	93 (95%)	5 (5%)	0	100	100
41	k	155/157 (99%)	154 (99%)	1 (1%)	0	100	100
42	l	521/1082 (48%)	503 (96%)	17 (3%)	1 (0%)	43	72
43	m	126/220 (57%)	120 (95%)	6 (5%)	0	100	100
44	n	134/140 (96%)	132 (98%)	2 (2%)	0	100	100
45	o	108/127 (85%)	108 (100%)	0	0	100	100
46	p	221/566 (39%)	207 (94%)	14 (6%)	0	100	100
47	r	95/135 (70%)	94 (99%)	1 (1%)	0	100	100
47	v	96/135 (71%)	95 (99%)	1 (1%)	0	100	100
48	s	80/102 (78%)	78 (98%)	2 (2%)	0	100	100
48	w	78/102 (76%)	76 (97%)	2 (3%)	0	100	100
49	t	107/129 (83%)	103 (96%)	4 (4%)	0	100	100
49	x	104/129 (81%)	104 (100%)	0	0	100	100
50	u	95/125 (76%)	91 (96%)	4 (4%)	0	100	100
50	y	93/125 (74%)	90 (97%)	3 (3%)	0	100	100
All	All	12842/17410 (74%)	12464 (97%)	377 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
42	l	648	SER

### 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	684/707 (97%)	684 (100%)	0	100	100
2	1	483/589 (82%)	483 (100%)	0	100	100
3	2	414/468 (88%)	414 (100%)	0	100	100
4	3	125/303 (41%)	125 (100%)	0	100	100
5	4	267/300 (89%)	267 (100%)	0	100	100
6	5	59/66 (89%)	59 (100%)	0	100	100
7	6	346/418 (83%)	346 (100%)	0	100	100
8	7	547/737 (74%)	547 (100%)	0	100	100
9	A	1330/1520 (88%)	1330 (100%)	0	100	100
10	B	1024/1061 (96%)	1024 (100%)	0	100	100
11	C	234/299 (78%)	234 (100%)	0	100	100
12	D	149/200 (74%)	149 (100%)	0	100	100
13	E	196/197 (100%)	196 (100%)	0	100	100
14	F	108/137 (79%)	108 (100%)	0	100	100
15	G	152/158 (96%)	152 (100%)	0	100	100
16	H	123/128 (96%)	123 (100%)	0	100	100
17	I	110/116 (95%)	110 (100%)	0	100	100
18	J	64/65 (98%)	64 (100%)	0	100	100
19	K	99/102 (97%)	99 (100%)	0	100	100
20	L	40/57 (70%)	40 (100%)	0	100	100
21	M	267/306 (87%)	267 (100%)	0	100	100
23	O	153/205 (75%)	153 (100%)	0	100	100
24	Q	204/641 (32%)	204 (100%)	0	100	100
25	R	252/363 (69%)	252 (100%)	0	100	100
27	U	99/260 (38%)	99 (100%)	0	100	100
28	V	94/108 (87%)	94 (100%)	0	100	100

*Continued on next page...*

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	W	275/436 (63%)	275 (100%)	0	100	100
30	X	193/295 (65%)	193 (100%)	0	100	100
31	a	170/259 (66%)	170 (100%)	0	100	100
32	b	161/207 (78%)	161 (100%)	0	100	100
33	c	104/108 (96%)	104 (100%)	0	100	100
34	d	469/642 (73%)	469 (100%)	0	100	100
35	e	232/280 (83%)	232 (100%)	0	100	100
36	f	174/178 (98%)	174 (100%)	0	100	100
37	g	95/113 (84%)	95 (100%)	0	100	100
38	h	158/258 (61%)	158 (100%)	0	100	100
39	i	174/208 (84%)	174 (100%)	0	100	100
40	j	100/144 (69%)	100 (100%)	0	100	100
41	k	145/145 (100%)	145 (100%)	0	100	100
42	l	505/1001 (50%)	505 (100%)	0	100	100
43	m	119/195 (61%)	119 (100%)	0	100	100
44	n	128/132 (97%)	128 (100%)	0	100	100
45	o	103/117 (88%)	103 (100%)	0	100	100
46	p	212/528 (40%)	212 (100%)	0	100	100
47	r	84/109 (77%)	84 (100%)	0	100	100
47	v	85/109 (78%)	85 (100%)	0	100	100
48	s	67/78 (86%)	67 (100%)	0	100	100
48	w	65/78 (83%)	65 (100%)	0	100	100
49	t	86/101 (85%)	86 (100%)	0	100	100
49	x	84/101 (83%)	84 (100%)	0	100	100
50	u	83/105 (79%)	83 (100%)	0	100	100
50	y	81/105 (77%)	81 (100%)	0	100	100
All	All	11775/15543 (76%)	11775 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 116 such sidechains are listed below:

Mol	Chain	Res	Type
27	U	40	ASN
46	p	203	GLN
32	b	165	ASN
46	p	177	GLN
42	l	403	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 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	$\# Z  > 2$
51	SF4	0	801	1	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
51	SF4	0	801	1	-	-	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
9	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1614:PRO	C	1629:THR	N	22.84

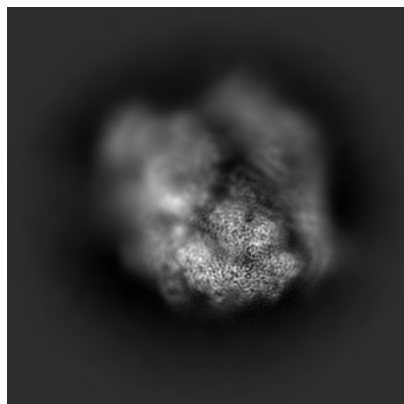
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16611. These allow visual inspection of the internal detail of the map and identification of artifacts.

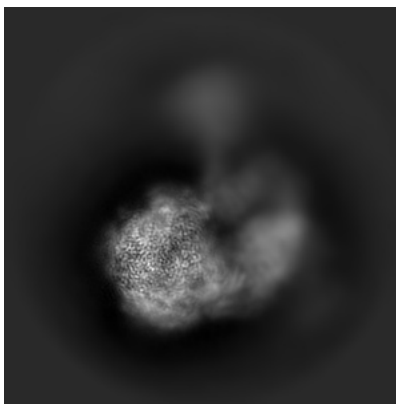
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

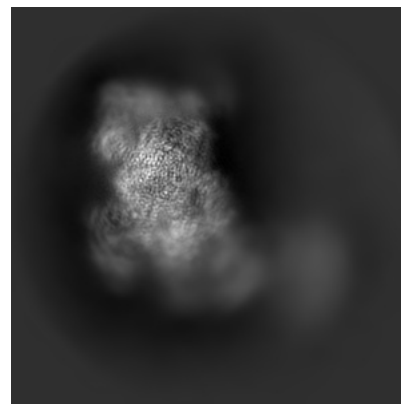
#### 6.1.1 Primary map



X

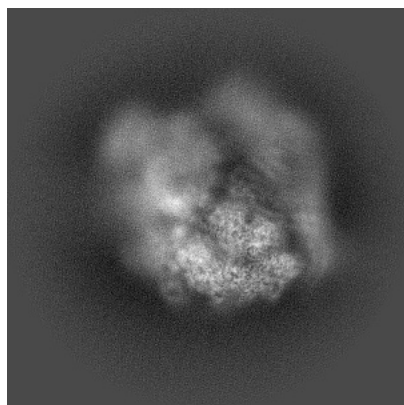


Y

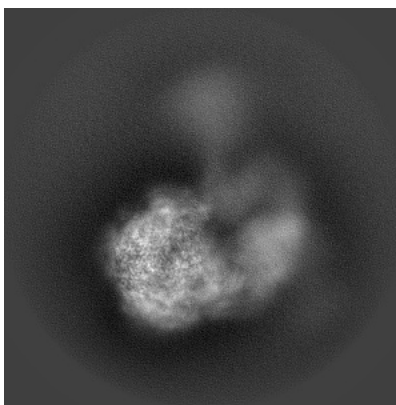


Z

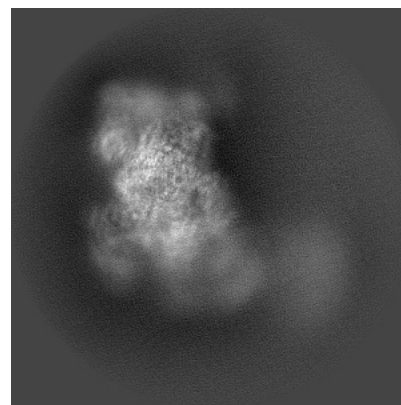
#### 6.1.2 Raw map



X



Y

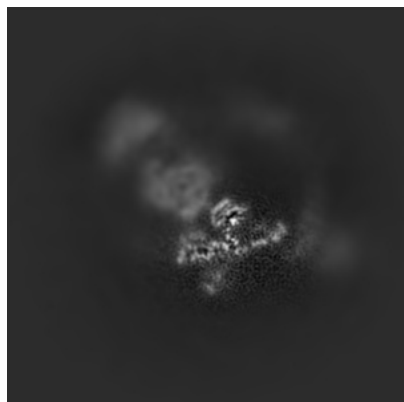


Z

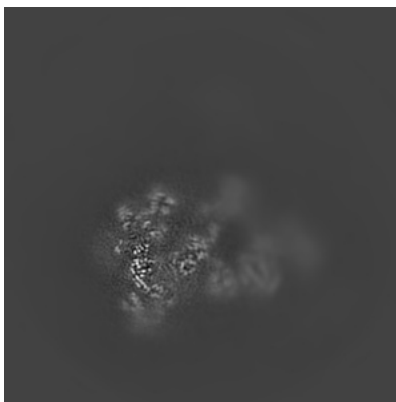
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

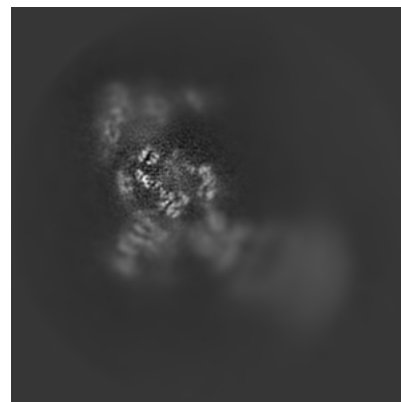
### 6.2.1 Primary map



X Index: 200

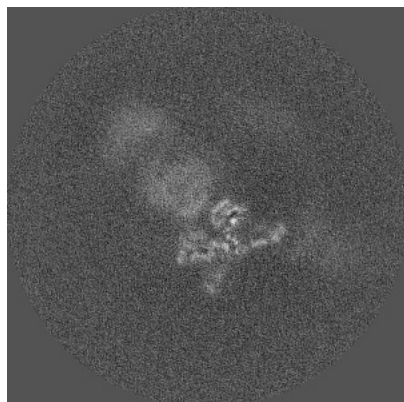


Y Index: 200

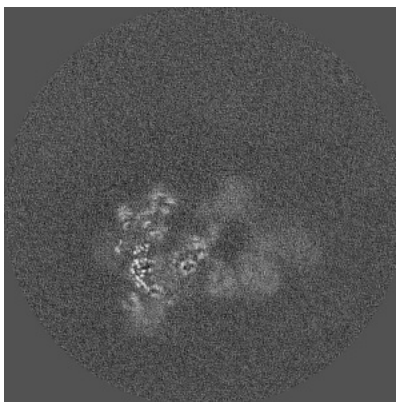


Z Index: 200

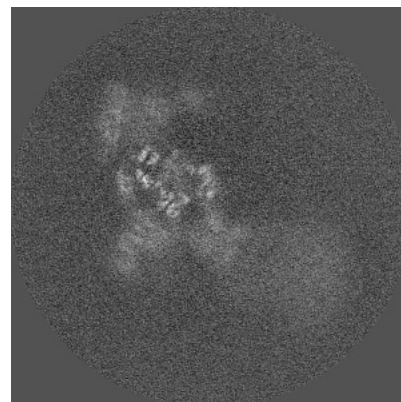
### 6.2.2 Raw map



X Index: 200



Y Index: 200

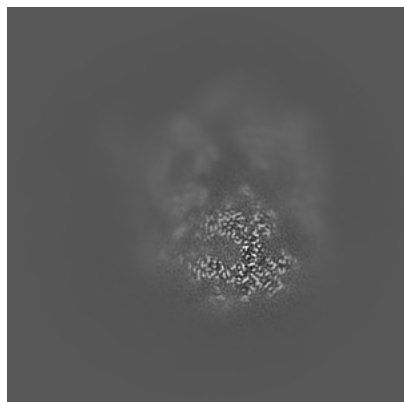


Z Index: 200

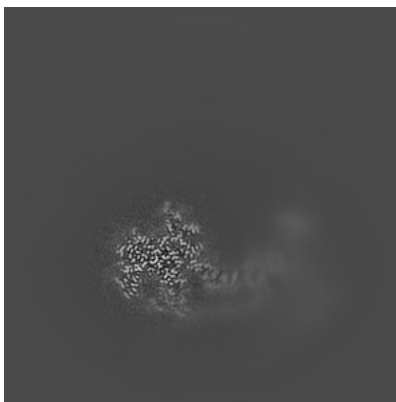
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

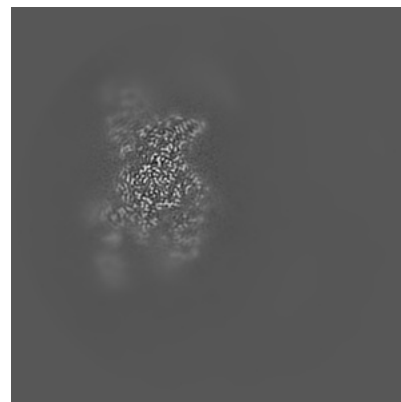
### 6.3.1 Primary map



X Index: 145

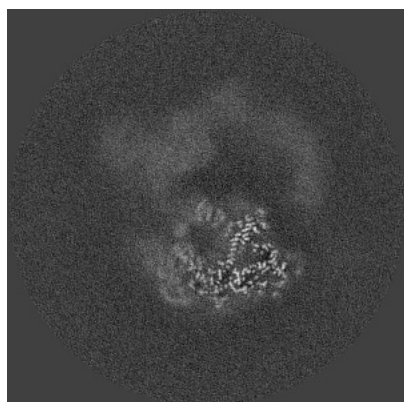


Y Index: 248

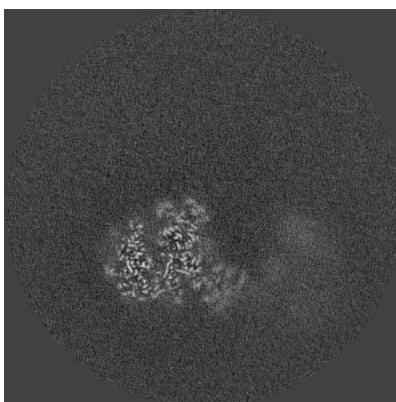


Z Index: 138

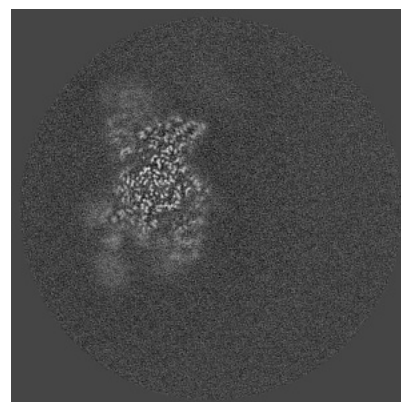
### 6.3.2 Raw map



X Index: 163



Y Index: 232

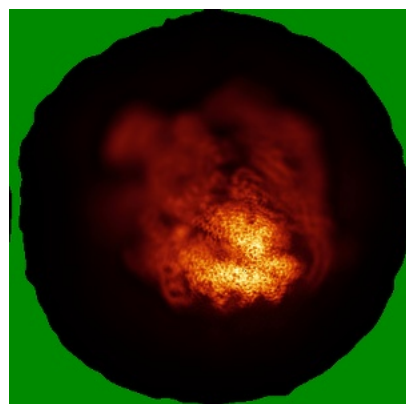


Z Index: 138

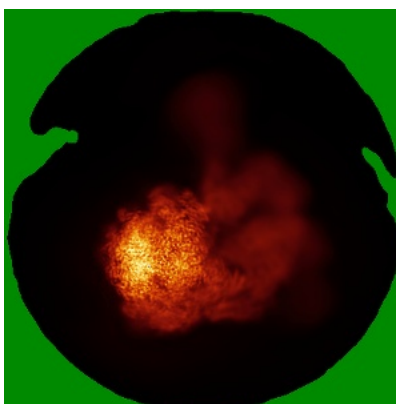
The images above show the largest variance slices of the map in three orthogonal directions.

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

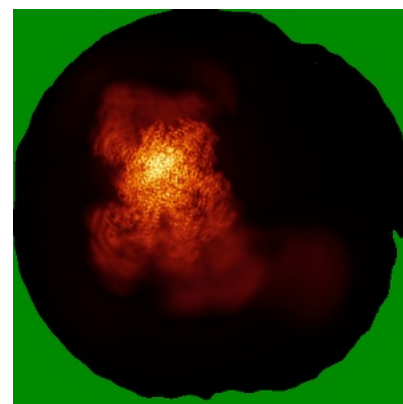
### 6.4.1 Primary map



X

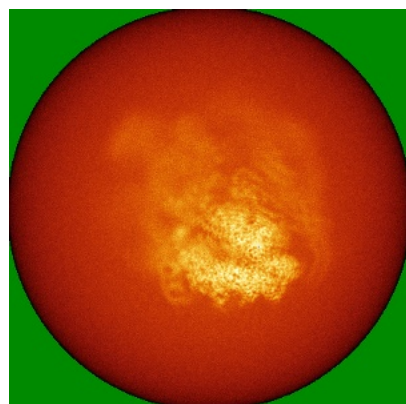


Y

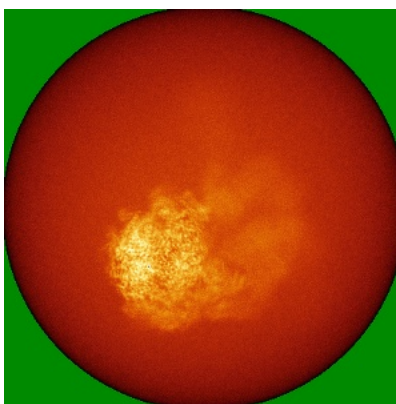


Z

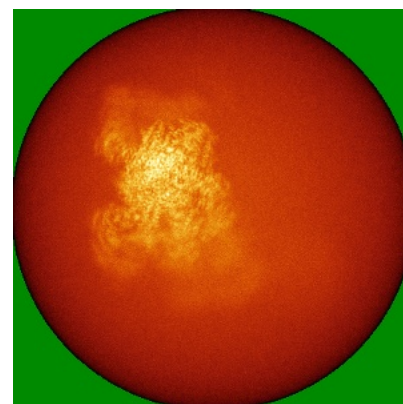
### 6.4.2 Raw map



X



Y

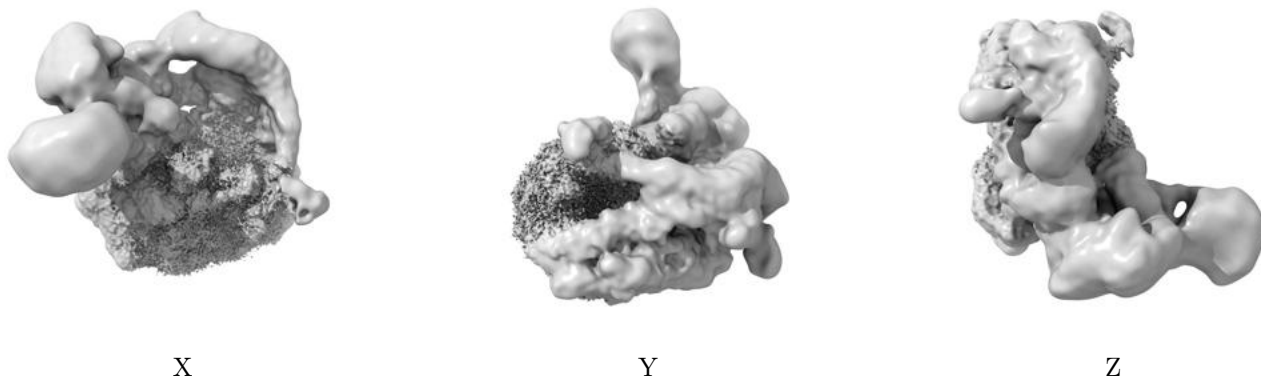


Z

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.

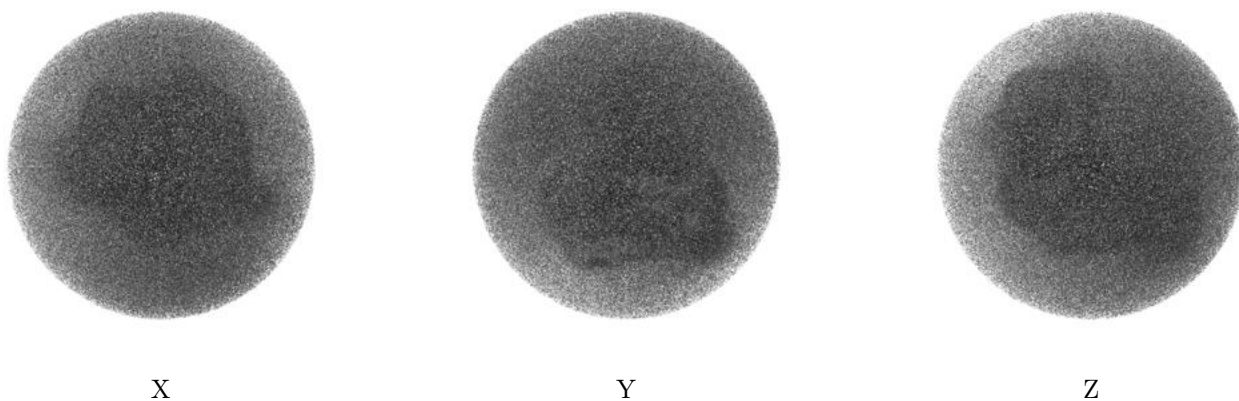
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.006. 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.

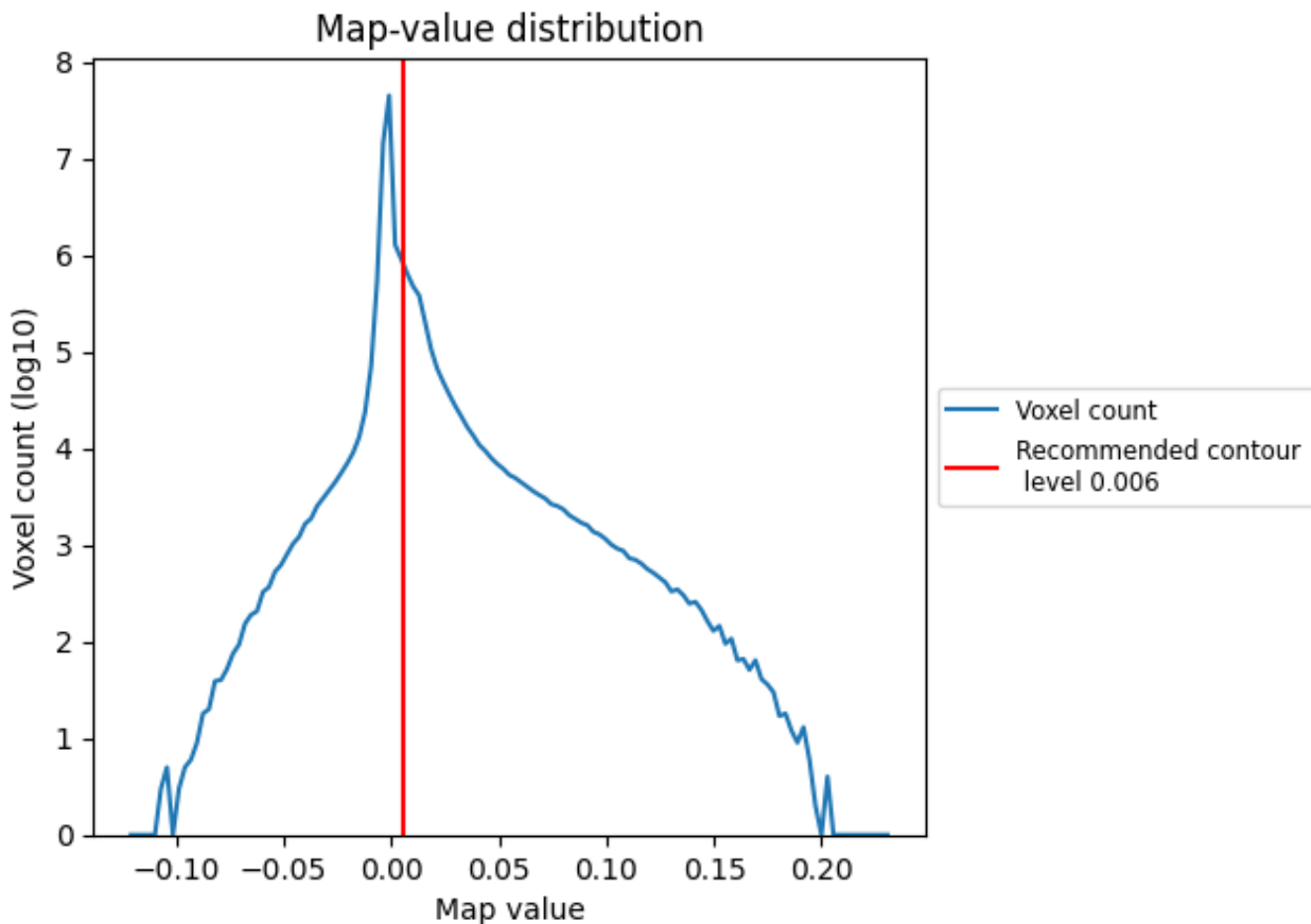
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

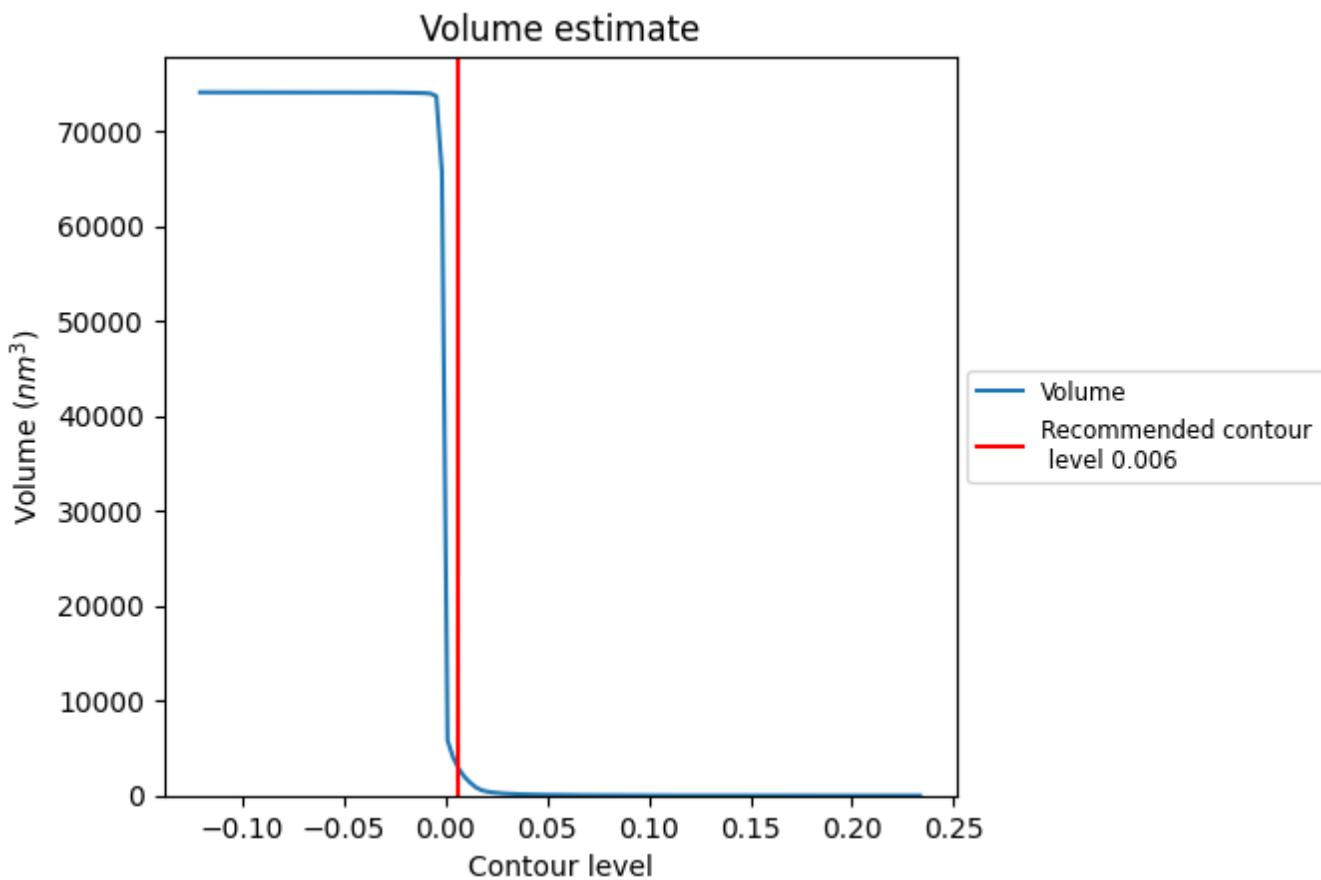
This section contains the results of statistical analysis of the map.

### 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.

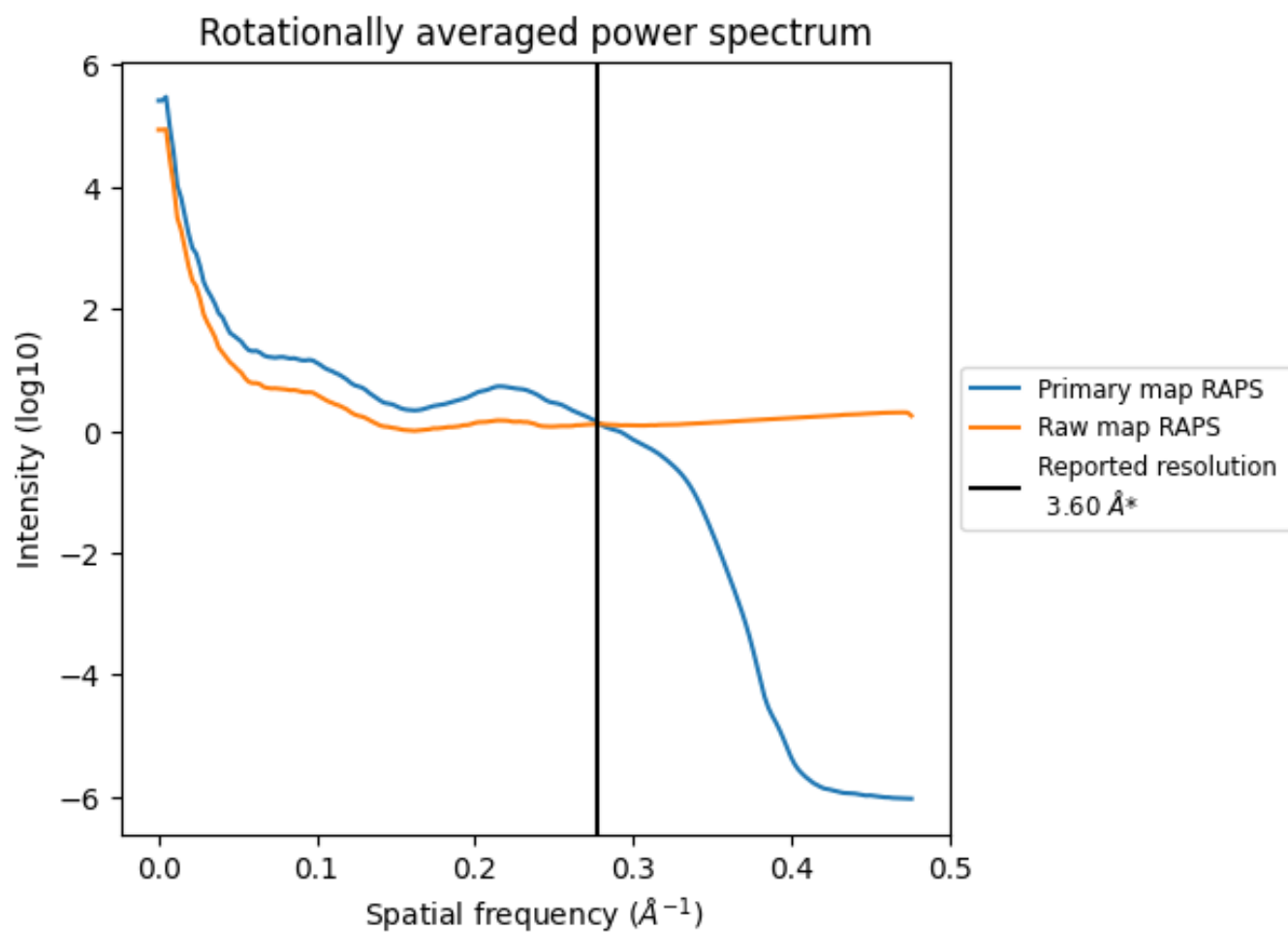
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2978  $\text{nm}^3$ ; this corresponds to an approximate mass of 2690 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

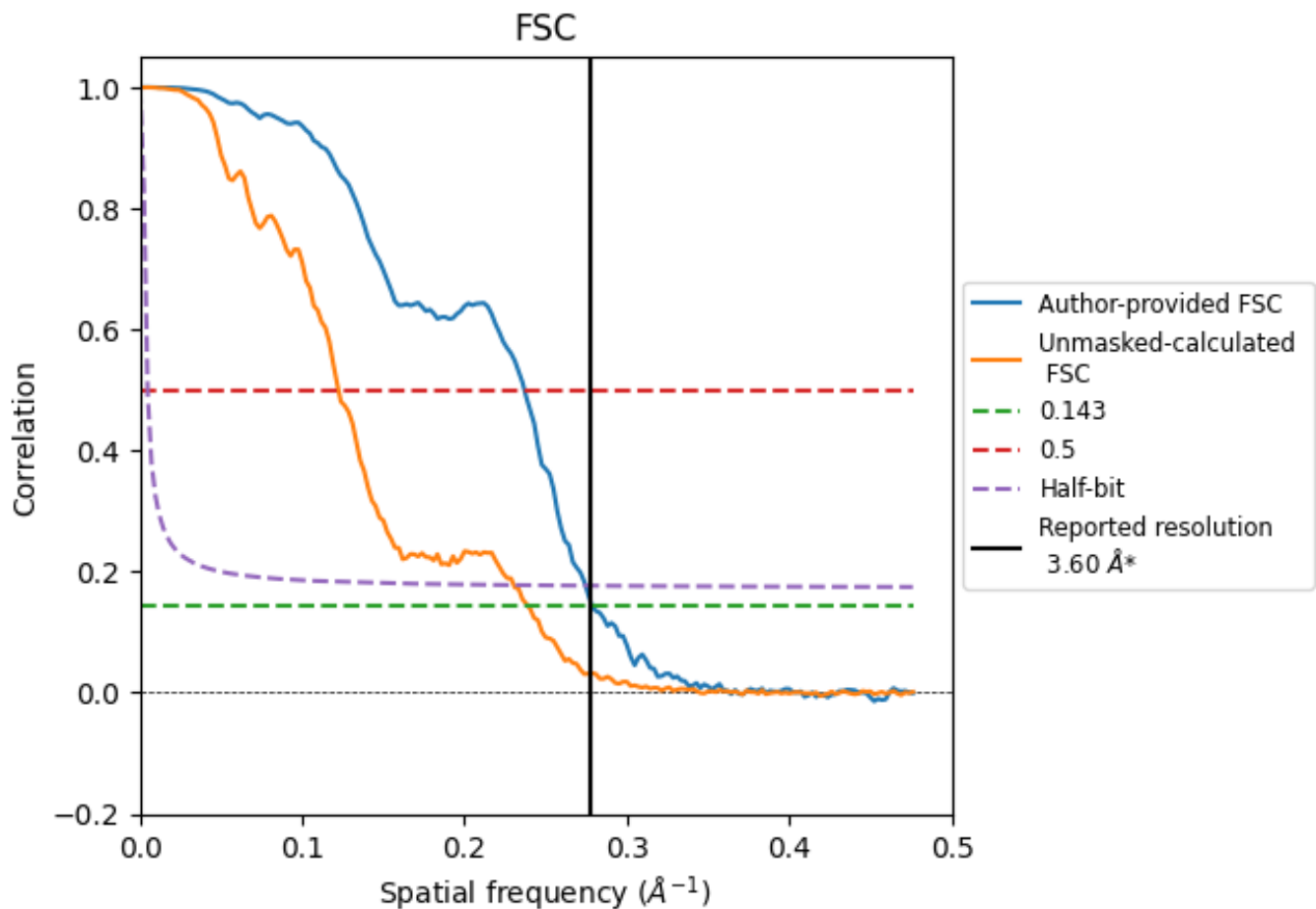


\*Reported resolution corresponds to spatial frequency of 0.278 Å<sup>-1</sup>

## 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 0.278 Å<sup>-1</sup>

## 8.2 Resolution estimates

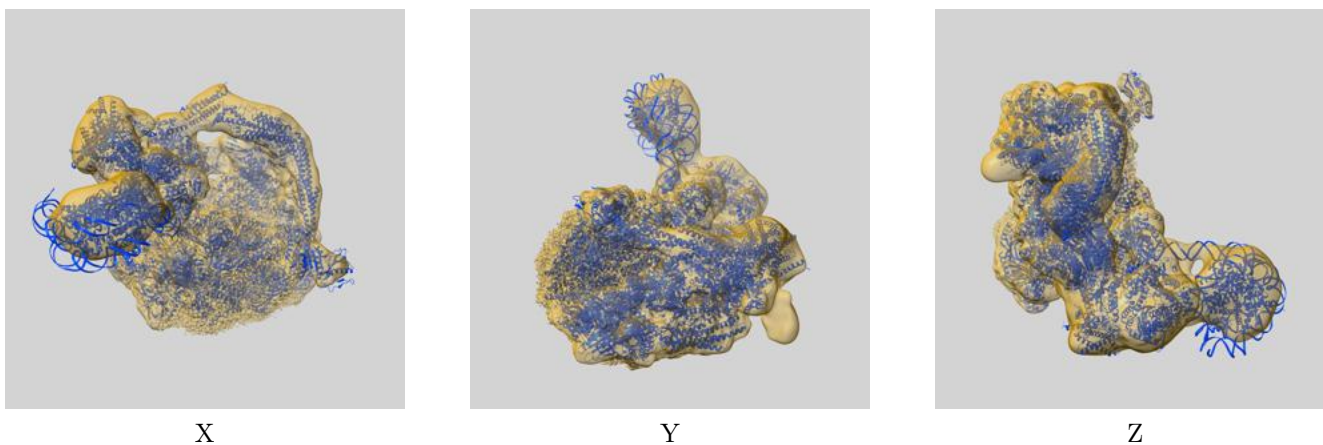
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.59	4.22	3.64
Unmasked-calculated*	4.18	8.18	4.34

\*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 4.18 differs from the reported value 3.6 by more than 10 %

## 9 Map-model fit [i](#)

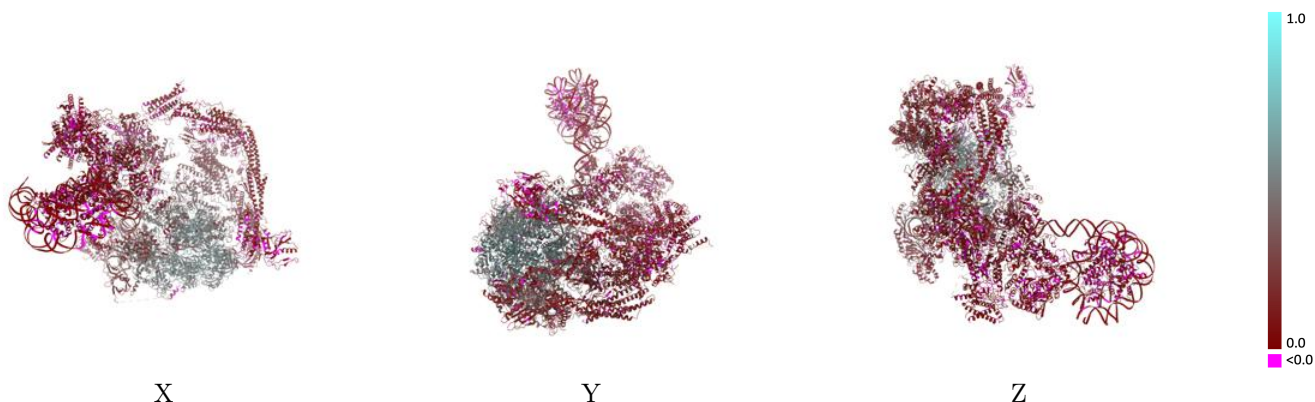
This section contains information regarding the fit between EMDB map EMD-16611 and PDB model 8CEO. Per-residue inclusion information can be found in section 3 on page 16.

### 9.1 Map-model overlay [i](#)



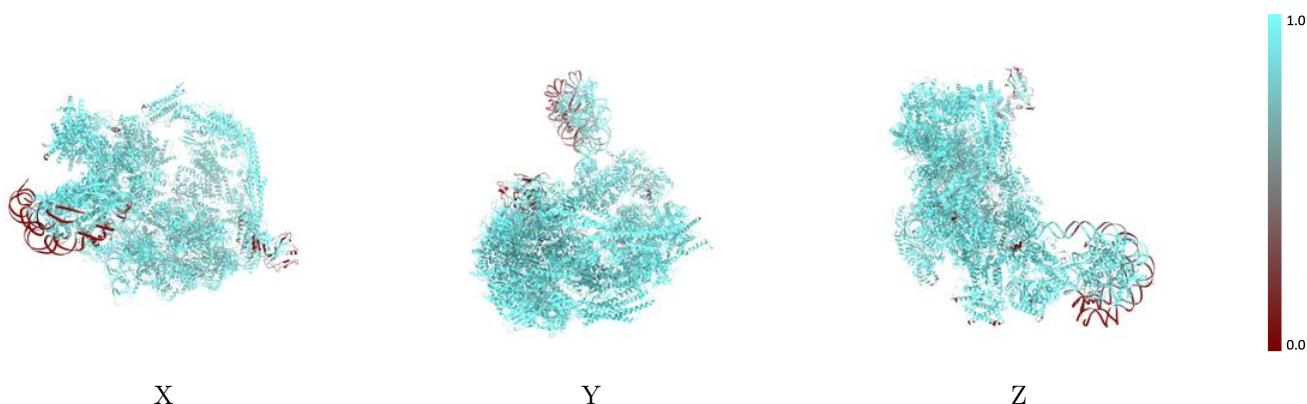
The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



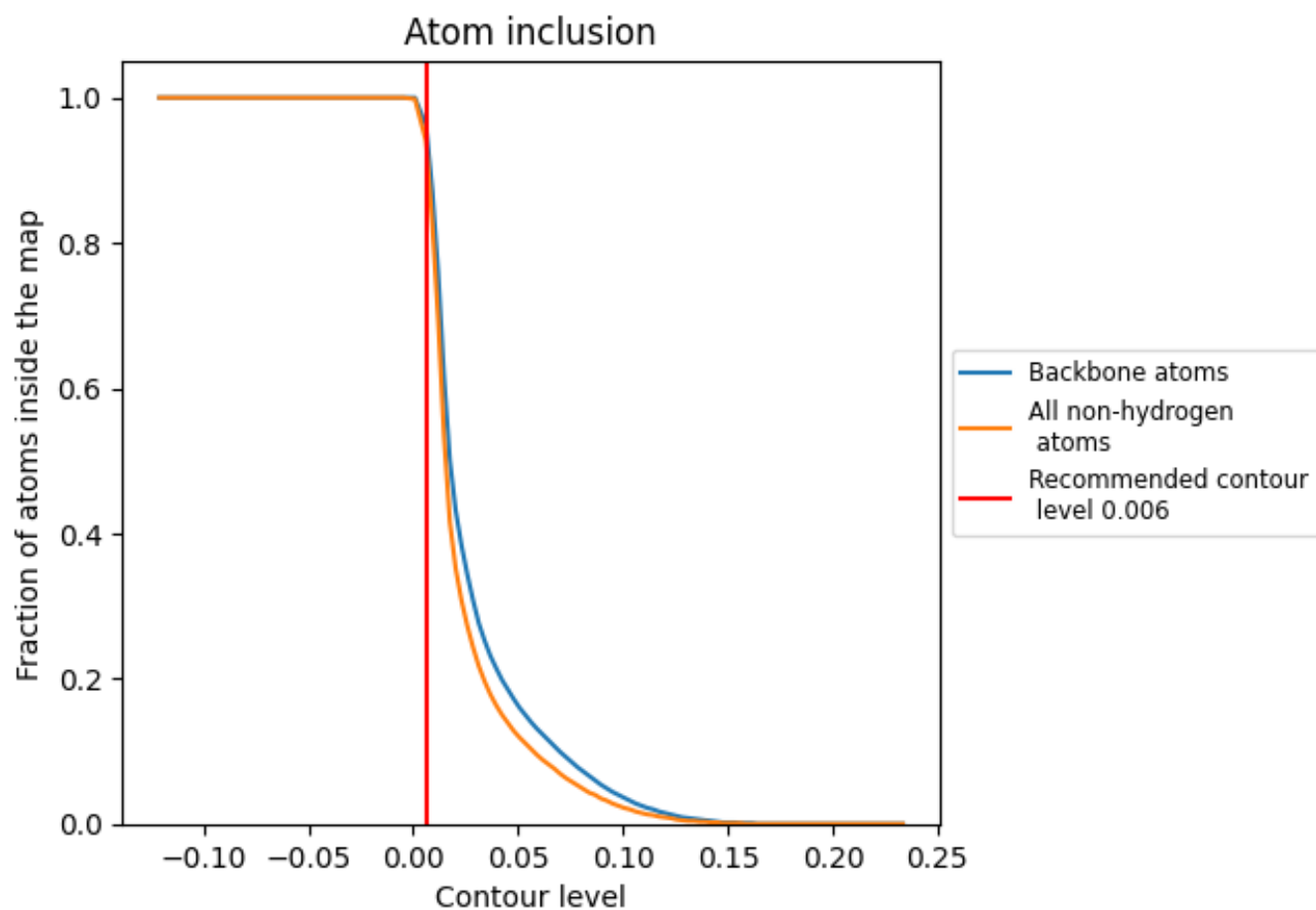
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.006).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 94% 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 (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9410	 0.2220
0	 0.9880	 0.1100
1	 0.9590	 0.0830
2	 0.9790	 0.0750
3	 0.9880	 0.1710
4	 0.9970	 0.0610
5	 1.0000	 0.0720
6	 0.9640	 0.0820
7	 0.9890	 0.1030
A	 0.9860	 0.4510
B	 0.9850	 0.5000
C	 0.9890	 0.5120
D	 0.9670	 0.1990
E	 0.9900	 0.3850
F	 0.9220	 0.3790
G	 0.9840	 0.3480
H	 0.9780	 0.4460
I	 0.9910	 0.3480
J	 0.9910	 0.5340
K	 0.9770	 0.5050
L	 0.9860	 0.4710
M	 0.9770	 0.3570
N	 0.6520	 0.0940
O	 0.9940	 0.2260
Q	 0.9790	 0.2350
R	 0.9950	 0.2040
T	 0.6500	 0.0970
U	 0.9270	 0.1280
V	 0.9930	 0.1340
W	 0.9690	 0.1600
X	 0.9910	 0.1520
a	 0.9970	 0.1340
b	 0.9870	 0.1620
c	 0.9970	 0.1800
d	 0.9940	 0.1620



*Continued on next page...*

*Continued from previous page...*

Chain	Atom inclusion	Q-score
e	 0.9620	 0.3730
f	 0.9630	 0.3520
g	 0.9960	 0.1630
h	 0.9550	 0.1030
i	 0.9980	 0.1290
j	 0.8210	 0.1120
k	 0.9450	 0.0840
l	 0.9750	 0.1270
m	 0.9210	 0.0650
n	 0.9680	 0.0960
o	 0.9790	 0.1190
p	 0.5320	 0.0620
r	 0.7950	 0.0260
s	 0.7970	 0.0360
t	 0.7720	 0.0170
u	 0.7470	 0.0230
v	 0.9740	 0.0510
w	 1.0000	 0.0850
x	 0.9280	 0.0490
y	 0.9930	 0.0530