



wwPDB EM Validation Summary Report ⓘ

Apr 4, 2024 – 06:16 pm BST

PDB ID : 8RBX
EMDB ID : EMD-19038
Title : Structure of Integrator-PP2A bound to a paused RNA polymerase II-DSIF-N
ELF-nucleosome complex
Authors : Fianu, I.; Ochmann, M.; Walshe, J.L.; Cramer, P.
Deposited on : 2023-12-05
Resolution : 4.10 Å (reported)
Based on initial models : 6SN1, 7PKS, 7OHC, .

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:

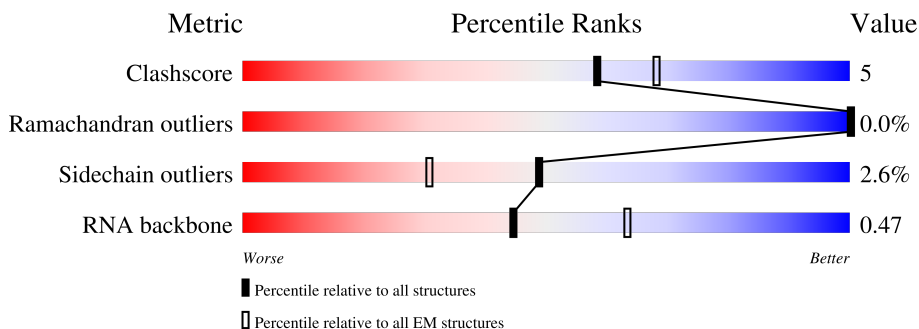
EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

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 4.10 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	1	8	
2	A	1970	
2	Y	1970	
3	B	1174	
4	C	275	
5	D	142	
6	E	210	

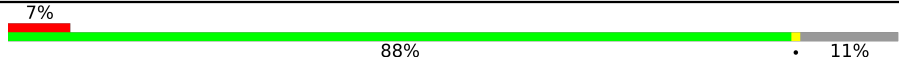
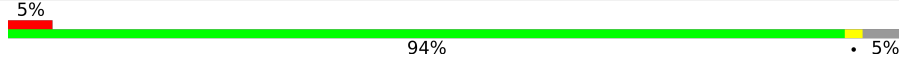
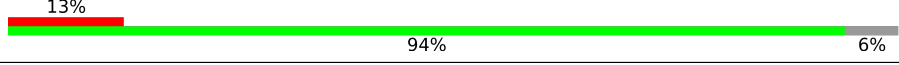
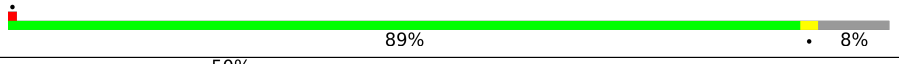
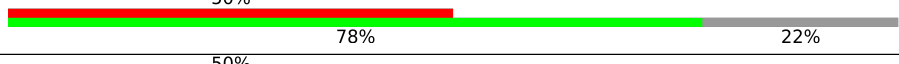
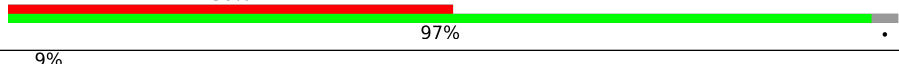
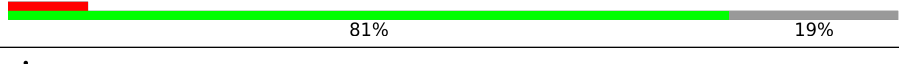
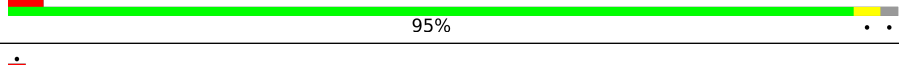
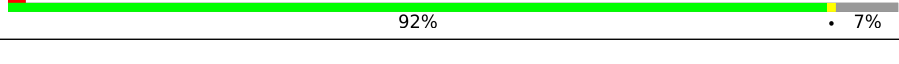
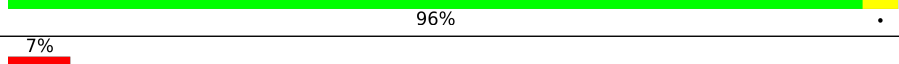

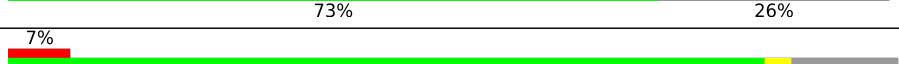

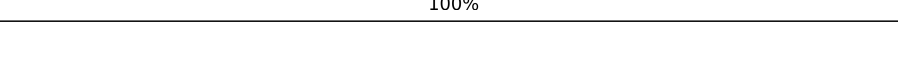
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
7	F	127	
8	G	172	
9	H	150	
10	I	125	
11	J	67	
12	K	117	
13	L	58	
14	M	135	
14	S	135	
15	N	148	
16	O	103	
16	U	103	
17	P	17	
18	Q	130	
18	V	130	
19	R	126	
19	W	126	
20	T	185	
21	Z	1087	
22	a	2192	
23	b	1204	
24	d	963	
25	e	1021	
26	f	889	
27	g	964	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
28	h	995	 7% 88% 11%
29	i	658	 5% 94% 5%
30	j	710	 13% 94% 6%
31	k	602	 89% 8%
32	m	706	 50% 78% 22%
33	n	518	 50% 97%
34	o	451	 9% 81% 19%
35	p	591	 95%
36	q	311	 92% 7%
37	r	28	 96%
38	u	528	 7% 34% 65%
39	v	613	 73% 26%
40	w	583	 7% 85% 12%
41	x	22	 9% 100%

2 Entry composition i

There are 44 unique types of molecules in this entry. The entry contains 129226 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 UNK-UNK-UNK-UNK-UNK-UNK-UNK-UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	1	8	40	24	8	8	0	0

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	1391	11008	6931	1972	2036	69	0	0
2	Y	13	95	60	13	22		0	0

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	TYR	deletion	UNP A0A7M4DUC2
A	?	-	SER	deletion	UNP A0A7M4DUC2
A	?	-	PRO	deletion	UNP A0A7M4DUC2
A	?	-	THR	deletion	UNP A0A7M4DUC2
A	?	-	SER	deletion	UNP A0A7M4DUC2
A	?	-	PRO	deletion	UNP A0A7M4DUC2
A	?	-	SER	deletion	UNP A0A7M4DUC2
A	?	-	TYR	deletion	UNP A0A7M4DUC2
A	?	-	SER	deletion	UNP A0A7M4DUC2
A	?	-	PRO	deletion	UNP A0A7M4DUC2
A	?	-	THR	deletion	UNP A0A7M4DUC2
A	?	-	SER	deletion	UNP A0A7M4DUC2
A	?	-	PRO	deletion	UNP A0A7M4DUC2
A	?	-	SER	deletion	UNP A0A7M4DUC2
Y	?	-	TYR	deletion	UNP A0A7M4DUC2
Y	?	-	SER	deletion	UNP A0A7M4DUC2
Y	?	-	PRO	deletion	UNP A0A7M4DUC2
Y	?	-	THR	deletion	UNP A0A7M4DUC2
Y	?	-	SER	deletion	UNP A0A7M4DUC2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
Y	?	-	PRO	deletion	UNP A0A7M4DUC2
Y	?	-	SER	deletion	UNP A0A7M4DUC2
Y	?	-	TYR	deletion	UNP A0A7M4DUC2
Y	?	-	SER	deletion	UNP A0A7M4DUC2
Y	?	-	PRO	deletion	UNP A0A7M4DUC2
Y	?	-	THR	deletion	UNP A0A7M4DUC2
Y	?	-	SER	deletion	UNP A0A7M4DUC2
Y	?	-	PRO	deletion	UNP A0A7M4DUC2
Y	?	-	SER	deletion	UNP A0A7M4DUC2

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	B	1112	8901	5634	1560	1643	64	0	0

- Molecule 4 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	C	261	2096	1314	360	416	6	0	0

- Molecule 5 is a protein called RNA polymerase II subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	D	126	977	612	169	192	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	E	209	1721	1089	300	324	8	0	0

- Molecule 7 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		
7	F	78	627	401	106	115	5	0	0

- Molecule 8 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	G	171	1316	858	208	242	8	0	0

- Molecule 9 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		
9	H	148	1186	750	194	237	5	0	0

- Molecule 10 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	I	117	944	584	166	183	11	0	0

- Molecule 11 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		
11	J	67	533	345	90	92	6	0	0

- Molecule 12 is a protein called DNA-directed RNA polymerase II subunit RPB11-a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	K	115	917	592	152	171	2	0	0

- Molecule 13 is a protein called RNA polymerase II subunit K.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	L	46	383	238	72	67	6	0	0

- Molecule 14 is a protein called Histone H3.3C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	M	90	729	458	139	130	2	0	0
14	S	91	732	460	140	130	2	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	79	LYS	ASN	conflict	UNP Q6NXT2
M	87	SER	ALA	conflict	UNP Q6NXT2
M	90	MET	GLY	conflict	UNP Q6NXT2
S	79	LYS	ASN	conflict	UNP Q6NXT2
S	87	SER	ALA	conflict	UNP Q6NXT2
S	90	MET	GLY	conflict	UNP Q6NXT2

- Molecule 15 is a DNA chain called non-template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
15	N	148	3050	1446	570	887	147	0	0

- Molecule 16 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	O	82	647	409	124	113	1	0	0
16	U	80	634	398	124	111	1	0	0

- Molecule 17 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
17	P	17	370	163	65	125	17	0	0

- Molecule 18 is a protein called Histone H2A type 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
18	Q	109	839	530	165	144	0	0
18	V	106	814	515	158	141	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	87	VAL	ILE	engineered mutation	UNP P02262
V	87	VAL	ILE	engineered mutation	UNP P02262

- Molecule 19 is a protein called Histone H2B type 1-J.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	85	Total	C	N	O	S	0	0
			656	411	119	124	2		
19	W	95	Total	C	N	O	S	0	0
			746	467	136	141	2		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	1	SER	ALA	conflict	UNP P06899
R	15	ILE	VAL	conflict	UNP P06899
R	121	SER	ALA	conflict	UNP P06899
W	1	SER	ALA	conflict	UNP P06899
W	15	ILE	VAL	conflict	UNP P06899
W	121	SER	ALA	conflict	UNP P06899

- Molecule 20 is a DNA chain called Template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	161	Total	C	N	O	P	0	0
			3277	1556	598	962	161		

- Molecule 21 is a protein called Transcription elongation factor SPT5.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Z	274	Total	C	N	O	S	0	0
			2167	1364	390	403	10		

- Molecule 22 is a protein called Integrator complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	a	1718	Total	C	N	O	S	0	0
			11692	7328	2134	2180	50		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	-1	SER	-	expression tag	UNP Q8N201
a	0	ASN	-	expression tag	UNP Q8N201

- Molecule 23 is a protein called Integrator complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	b	1051	7991	5121	1352	1456	62	0	0

- Molecule 24 is a protein called Integrator complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	d	820	6407	4089	1093	1191	34	0	0

- Molecule 25 is a protein called Integrator complex subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	e	856	6260	3979	1140	1115	26	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
e	-1	SER	-	expression tag	UNP Q6P9B9
e	0	ASN	-	expression tag	UNP Q6P9B9

- Molecule 26 is a protein called Integrator complex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	f	544	4137	2653	701	758	25	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
f	-1	SER	-	expression tag	UNP Q9UL03
f	0	ASN	-	expression tag	UNP Q9UL03

- Molecule 27 is a protein called Integrator complex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	g	886	6722	4259	1166	1257	40	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
g	-1	SER	-	expression tag	UNP Q9NVH2
g	0	ASN	-	expression tag	UNP Q9NVH2

- Molecule 28 is a protein called Integrator complex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	h	887	6751	4334	1156	1223	38	0	0

- Molecule 29 is a protein called Integrator complex subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	i	626	4870	3137	792	908	33	0	0

- Molecule 30 is a protein called Integrator complex subunit 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
30	j	668	3313	1976	668	669	0	0

- Molecule 31 is a protein called Integrator complex subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	k	552	4090	2620	707	735	28	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	-1	SER	-	expression tag	UNP Q5TA45
k	0	ASN	-	expression tag	UNP Q5TA45
k	203	GLN	GLU	engineered mutation	UNP Q5TA45

- Molecule 32 is a protein called Integrator complex subunit 13.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
32	m	552	2864	1714	578	572	0	0

- Molecule 33 is a protein called Integrator complex subunit 14.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
33	n	503	2484	1478	503	503	0	0

- Molecule 34 is a protein called Integrator complex subunit 15.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
34	o	367	1824	1090	367	367	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
o	-1	SER	-	expression tag	UNP Q96N11
o	0	ASN	-	expression tag	UNP Q96N11

- Molecule 35 is a protein called Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	p	580	4431	2821	752	831	27	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
p	-1	SER	-	expression tag	UNP P30153
p	0	ASN	-	expression tag	UNP P30153

- Molecule 36 is a protein called Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	q	290	2322	1467	403	437	15	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
q	-1	SER	-	expression tag	UNP P67775
q	0	ASN	-	expression tag	UNP P67775
q	88	ASN	ASP	engineered mutation	UNP P67775

- Molecule 37 is a protein called DSS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	r	28	250	156	41	52	1	0	0

- Molecule 38 is a protein called Negative elongation factor A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	u	183	1395	887	238	264	6	0	0

- Molecule 39 is a protein called NELF-B,Negative elongation factor B,Negative elongation factor B,Negative elongation factor B,Negative elongation factor B.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
39	v	451	2070	1132	466	472	0	0

- Molecule 40 is a protein called Negative elongation factor C/D.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	w	511	3825	2446	650	710	19	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
w	8	SER	-	expression tag	UNP Q8IXH7
w	9	ASN	-	expression tag	UNP Q8IXH7

- Molecule 41 is a protein called UNK-UNK.

Mol	Chain	Residues	Atoms			AltConf	Trace	
			Total	C	N			O
41	x	22	110	66	22	22	0	0

- Molecule 42 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
42	A	2	Total	Zn	0
			2	2	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
42	B	1	Total 1	Zn 1	0
42	C	1	Total 1	Zn 1	0
42	I	2	Total 2	Zn 2	0
42	J	1	Total 1	Zn 1	0
42	L	1	Total 1	Zn 1	0
42	k	2	Total 2	Zn 2	0

- Molecule 43 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
43	P	1	Total 1	Mg 1	0

- Molecule 44 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		AltConf
44	f	1	Total 1	Mn 1	0
44	q	1	Total 1	Mn 1	0

3 Residue-property plots

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

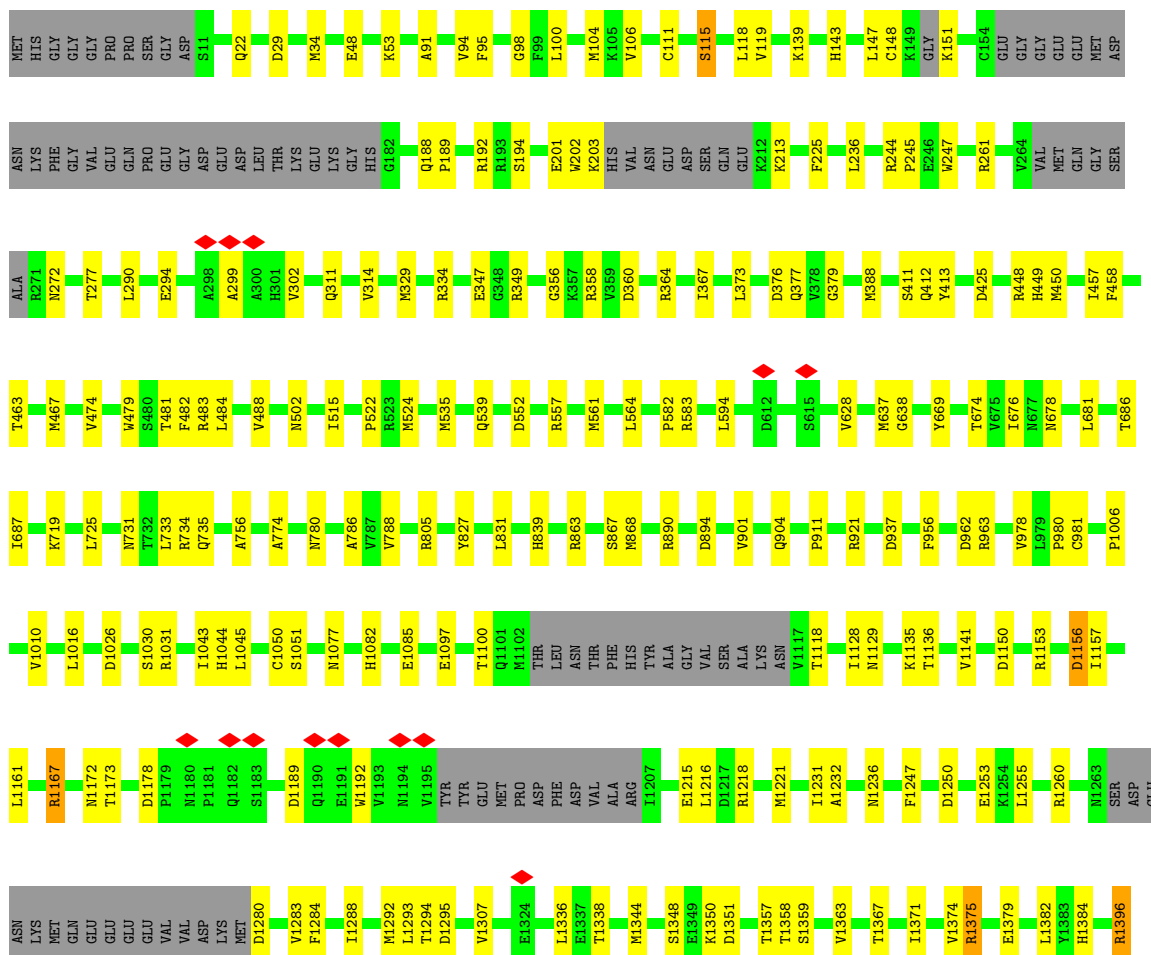
- Molecule 1: UNK-UNK-UNK-UNK-UNK-UNK-UNK-UNK

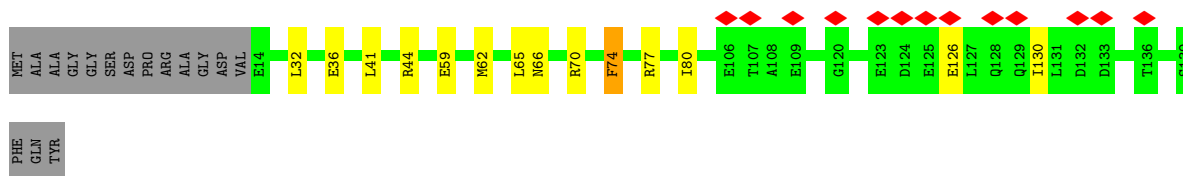
Chain 1:  100%

There are no outlier residues recorded for this chain.

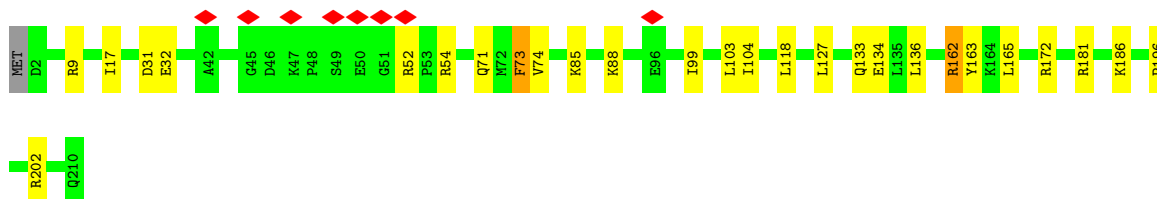
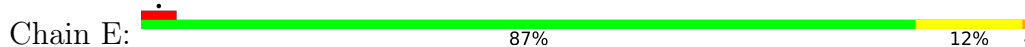
- Molecule 2: DNA-directed RNA polymerase subunit

Chain A:  59% 11% 29%

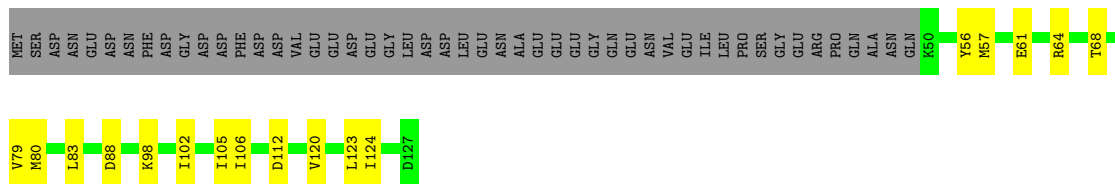




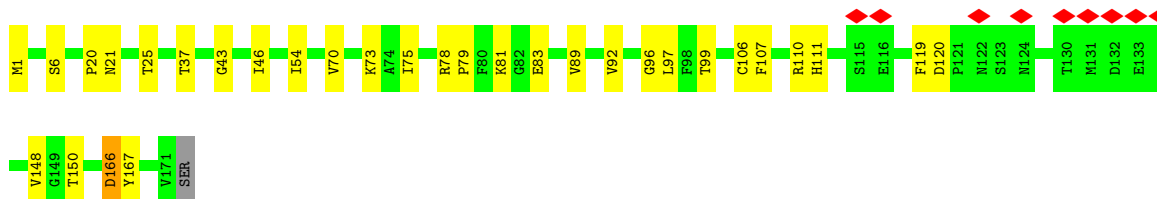
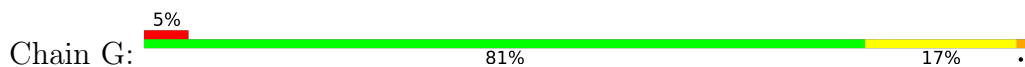
• Molecule 6: DNA-directed RNA polymerase II subunit E



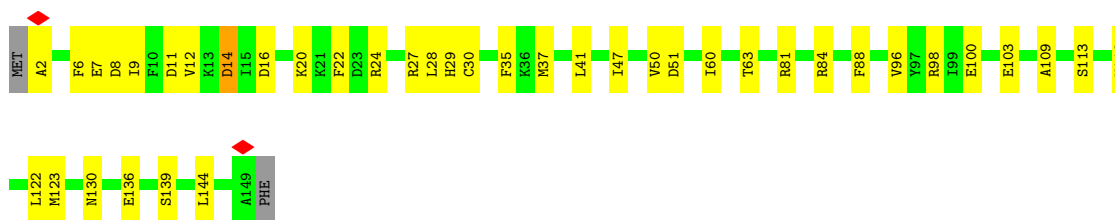
• Molecule 7: DNA-directed RNA polymerases I, II, and III subunit RPABC2



• Molecule 8: DNA-directed RNA polymerase II subunit RPB7

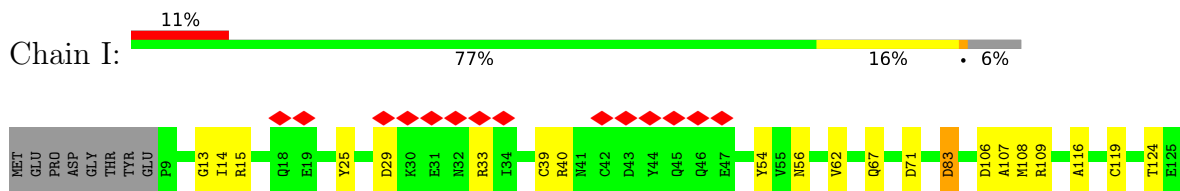


• Molecule 9: DNA-directed RNA polymerases I, II, and III subunit RPABC3

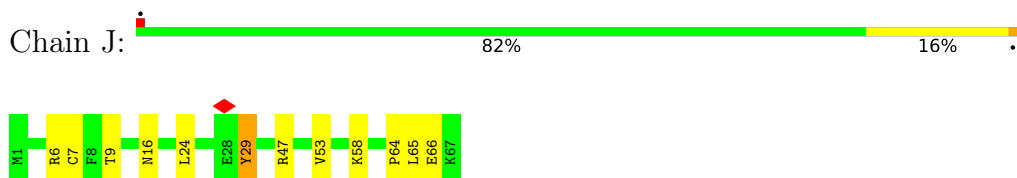


• Molecule 10: DNA-directed RNA polymerase II subunit RPB9

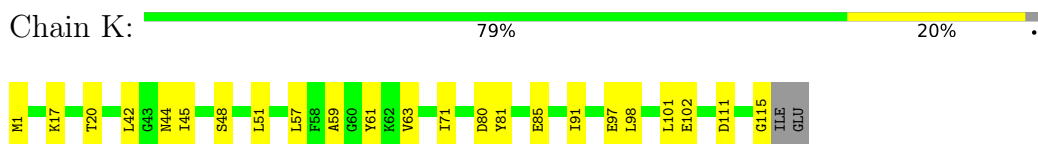




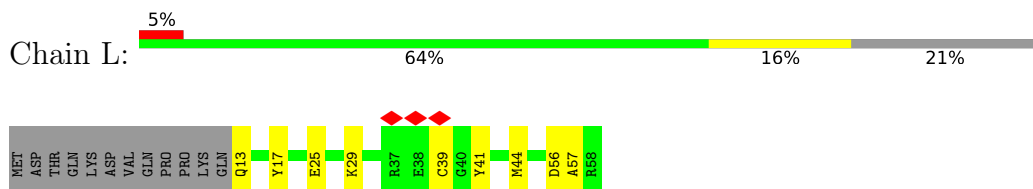
• Molecule 11: DNA-directed RNA polymerases I, II, and III subunit RPABC5



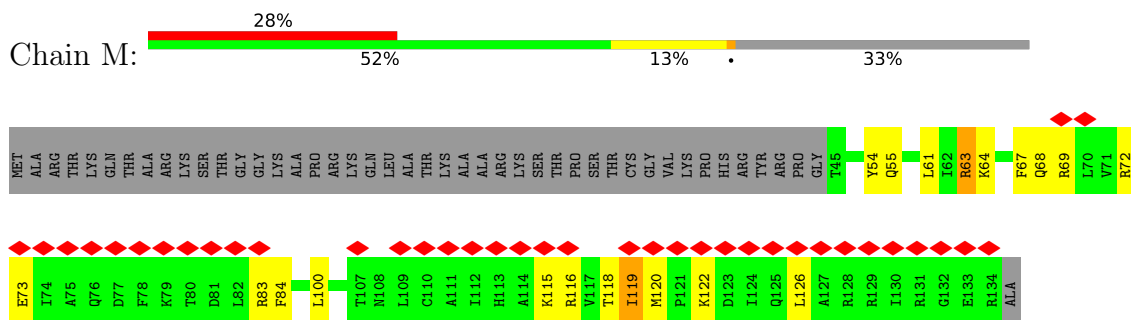
• Molecule 12: DNA-directed RNA polymerase II subunit RPB11-a



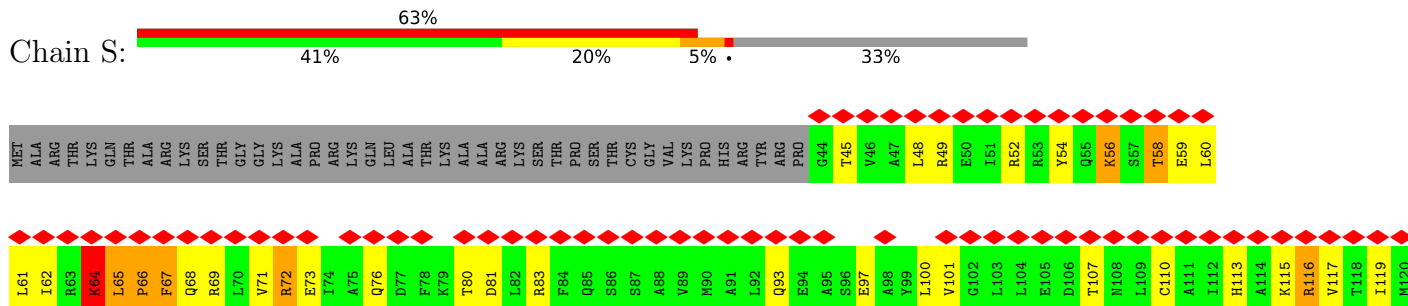
• Molecule 13: RNA polymerase II subunit K

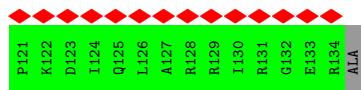


• Molecule 14: Histone H3.3C

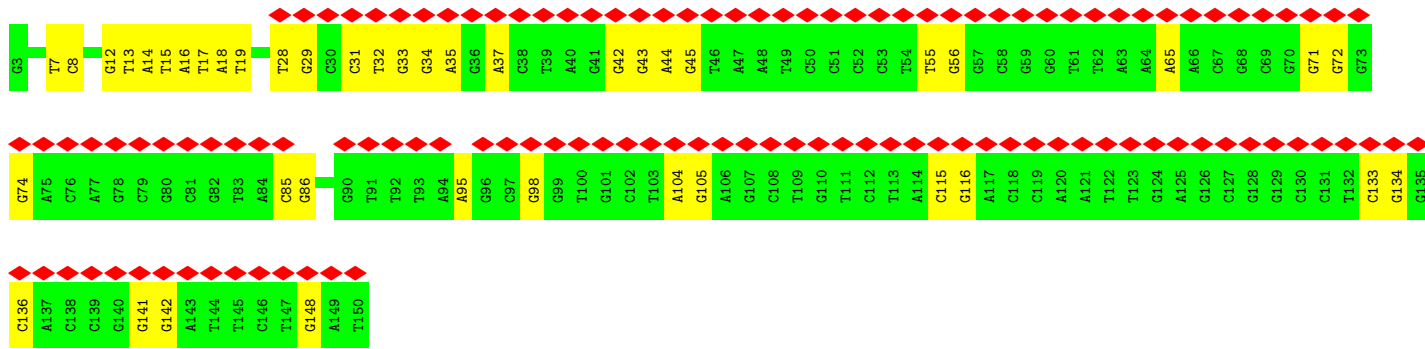
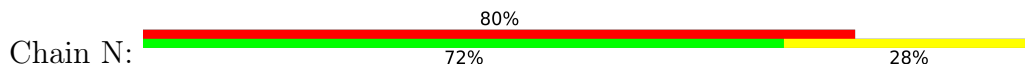


• Molecule 14: Histone H3.3C

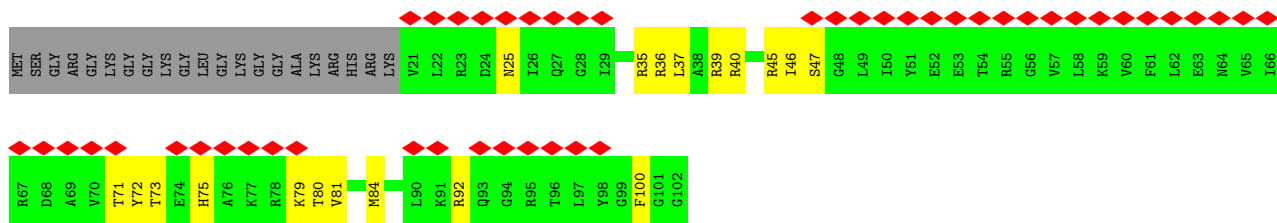




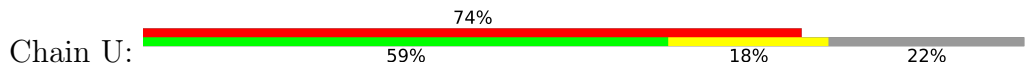
• Molecule 15: non-template DNA



• Molecule 16: Histone H4



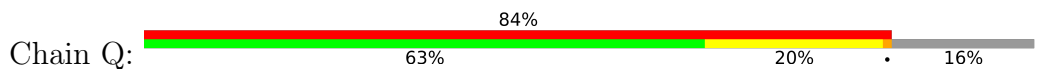
• Molecule 16: Histone H4

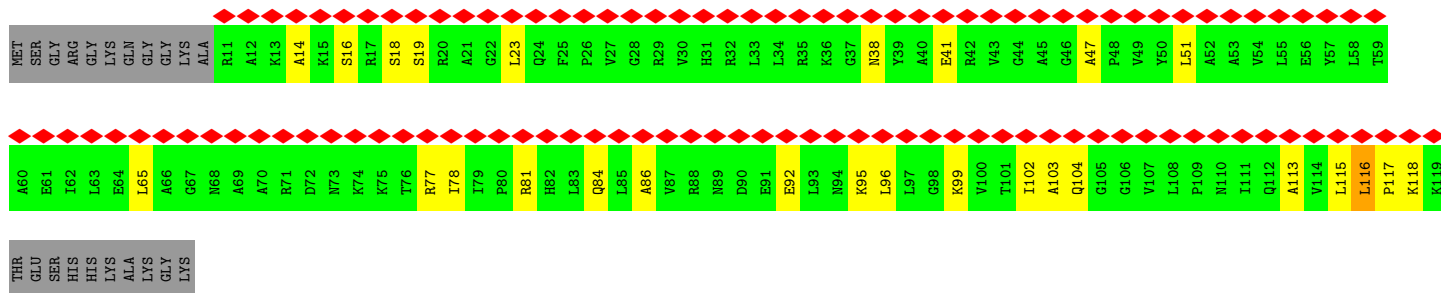


• Molecule 17: RNA

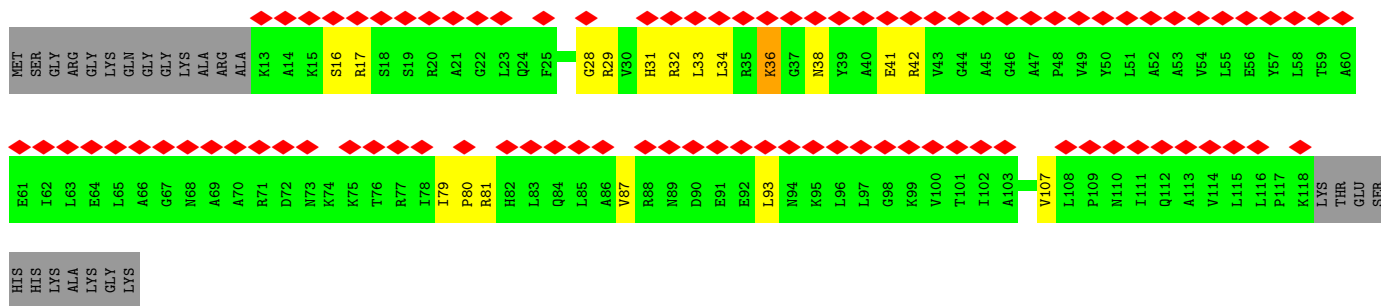


• Molecule 18: Histone H2A type 1

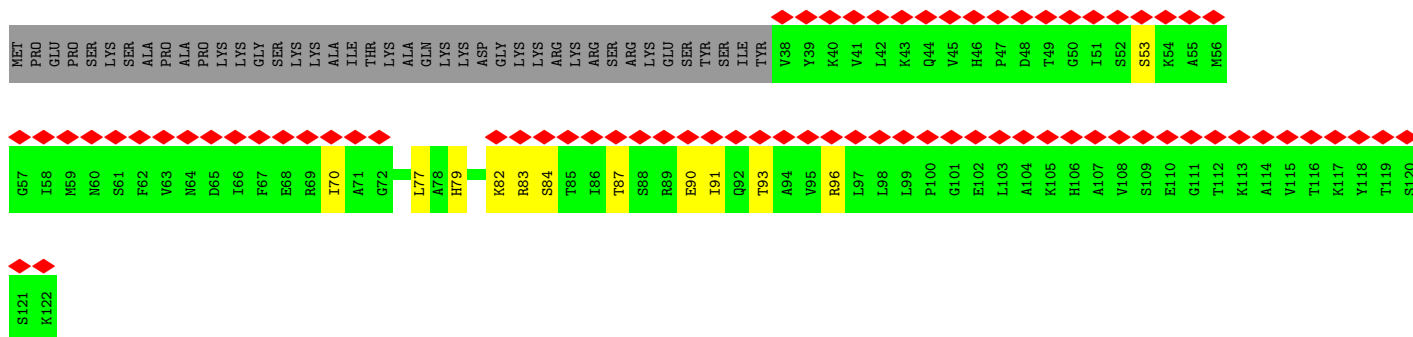




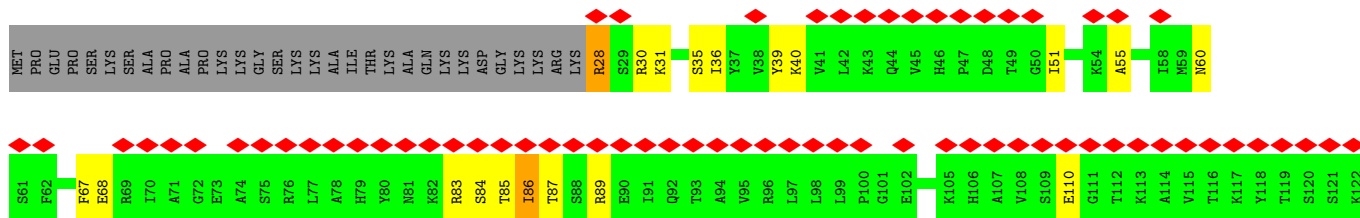
• Molecule 18: Histone H2A type 1



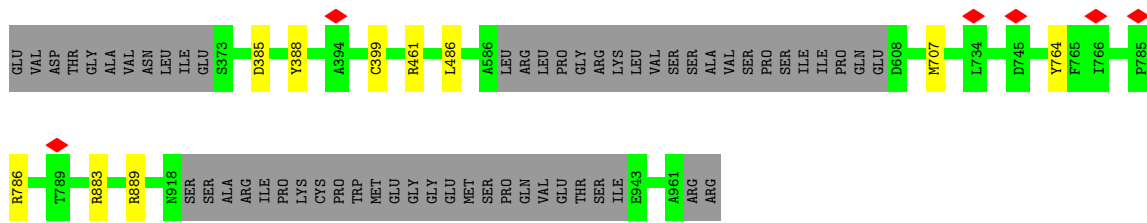
• Molecule 19: Histone H2B type 1-J



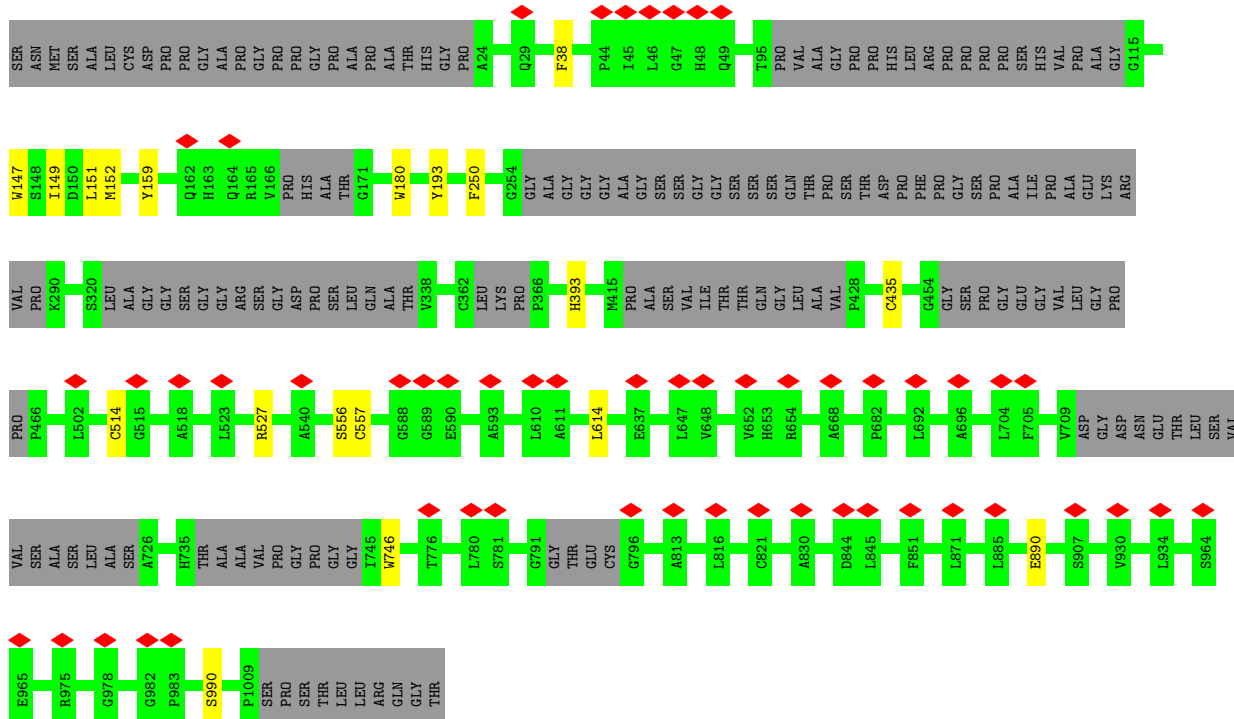
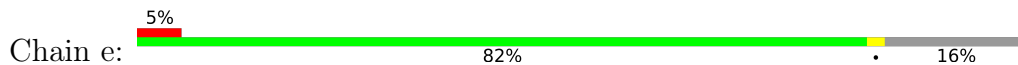
• Molecule 19: Histone H2B type 1-J



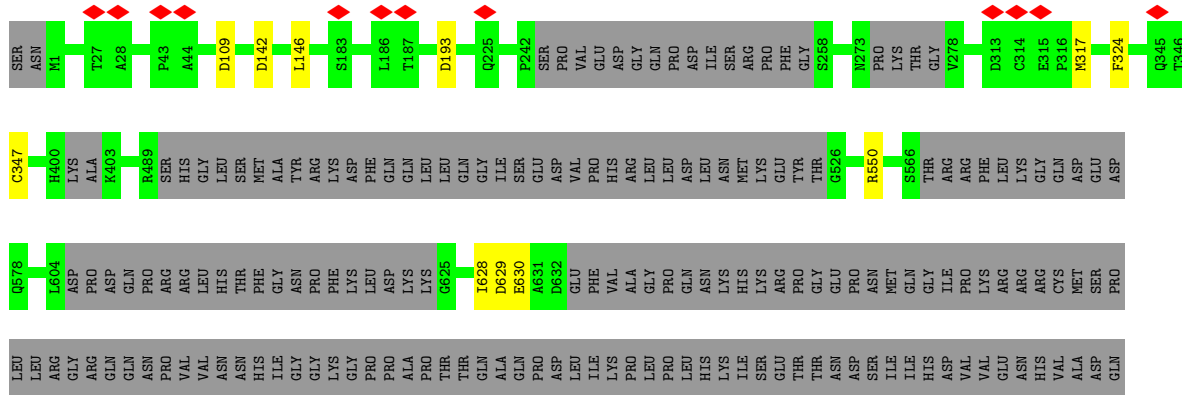
• Molecule 20: Template DNA



• Molecule 25: Integrator complex subunit 5



• Molecule 26: Integrator complex subunit 6



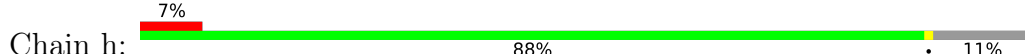
LEU	SER	ASN	ALA	GLU	ASP	SER	ILE	THR	PRO	ASN	ALA	ALA	THR	LEU	ASP	LEU	ASN	GLU	PHE	SER	SER	LYS	ALA	LYS	PRO	HIS	PRO	ALA	SER	LEU	LEU	GLU	ARG	PRO	THR	ASN	ASN	THR	THR	HIS	ASP	HIS	LEU	GLY	THR	THR	ASP	ASN	LEU	VAL	VAL	GLY	GLY	PHE	LEU	GLU	ASN	HIS	GLU	GLY	VAL	ARG	GLN	ASP	LYS	GLU	GLN			
CYS	ALA	GLU	ASP	ASN	ILE	THR	PRO	ASN	ALA	SER	LEU	ASP	LEU	ASN	GLU	LYS	GLY	PHE	SER	SER	LYS	ALA	LYS	PRO	HIS	PRO	ALA	SER	LEU	LEU	GLU	ARG	HIS	LEU	GLU	VAL	ASN	THR	THR	THR	ILE	LEU	GLY	ARG	PRO	LYS	PRO	GLY	ASP	ASN	LEU	VAL	TYR	SER	GLU	ARG	ILE	PHE	THR	LEU	LEU	LYS	HIS	VAL	ARG	GLN	GLY	SER	LEU	GLN
THR	ARG	ILE	PHE	LEU	ASN	THR	GLN	VAL	LYS	ILE	LEU	ASP	ALA	ALA	SER	PHE	LYS	GLY	ARG	MET	GLY	PRO	HIS	THR	ALA	ALA	SER	LEU	LEU	GLN	GLU	ILE	HIS	ARG	ALA	ALA	SER	ILE	GLN	ILE	ILE	THR	ASP	LEU	GLY	HIS	ASN	ASP	ASN	VAL	SER	SER	PRO	GLU	ARG	ILE	PHE	THR	LEU	LEU	LYS	HIS	VAL	ARG	GLN	GLY	SER	LEU	GLN	

• Molecule 27: Integrator complex subunit 7



SER	ASN	MET	ALA	LEU	ASP	SER	THR	LYS	PHE	LEU	ALA	ASP	ALA	GLY	TYR	GLY	GLU	GLN	D21	H140	S181	L235	L246	L315	F328	SER	ILE	VAL	PRO	GLY	ASN	VAL	SER	SER	PRO	R340	E350	K377	L409	L419	E432	C450
L453	A454	D465	D470	R503	A504	I529	D540	Q573	A591	A602	T609	L611	L614	A650	THR	THR	ILE	MET	THR	LEU	GLY	ASN	ASP	L661	A695	I713	L722	S809	P810	SER	PRO	ARG	ASN	PRO	PRO	ALA	ALA	P816	S860	LYS	SER	GLY
GLN	ASP	TYR	LYS	ILE	PRO	ILE	ASP	R872	K919	A945	ALA	GLN	ARG	GLN	PRO	LEU	GLN	GLN	GLN	ARG	ASN	ALA	ALA	THR	ARG	PHE																

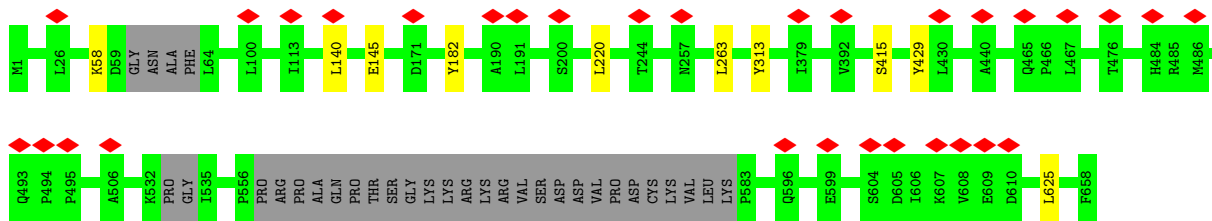
• Molecule 28: Integrator complex subunit 8



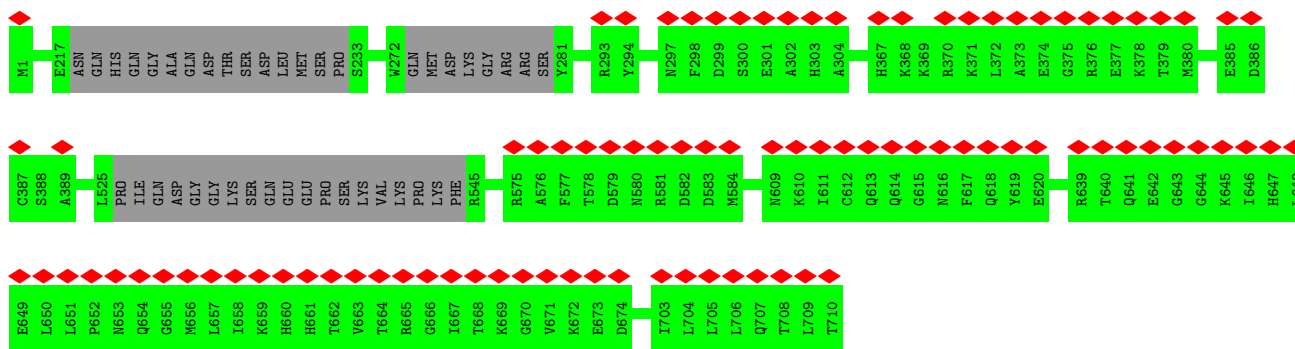
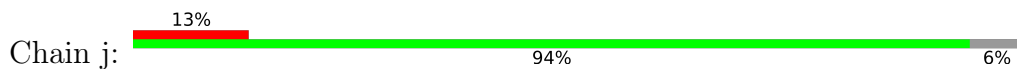
MET	SER	ALA	GLU	ALA	ALA	ASP	ARG	GLY	LEU	ALA	THR	SER	SER	ARG	PRO	CYS	THR	PRO	PRO	GLN	T22	L38	ARG	LYS	PRO	CYS	PRO	ASP	PRO	ALA	F47	P61	SER	VAL	ASN	GLU	GLN	ASN	GLN	VAL	GLN	PRO	PRO	PRO	ASP	N75	K101	V121	PRO	PRO	GLY	THR	K126	D129
M130	D131	L132	A133	T134	L135	P168	GLY	PRO	PRO	GLN	LEU	SER	VAL	MET	ASN	Q176	E193	A204	K207	L208	M209	K210	D211	LYR	VAL	HIS	THR	MET	THR	THR	THR	LEU	LEU	LEU	ALA	ALA	GLU	GLU	PRO	PRO	GLY	MET	VAL	ASN	GLY	THR	THR	SER	SER	THR	THR	ALA	L241	C250
L266	M267	S268	A269	S292	LEU	HIS	C295	S315	SER	ASP	SER	SER	SER	THR	SER	GLN	L323	S335	G336	M337	Y338	Q339	V362	M374	E375	A376	D392	E413	D416	F442	V446	F465	R487	K493	F499	ASP	ILE	P502	I530	G534	S537													
E538	A562	D563	T601	E602	F603	S604	F605	S636	D637	S640	R641	Y642	R643	G644	E647	M648	R649	L650	P651	D652	V664	L678	A679	V680	F681	A682	F683	K708	E709	D716	E719	S729	GLN	HIS	LYS	ARG	GLY	ASN	ASP	GLY	R738	I773	L776	K784	GLU									
ASP	ILE	VAL	ASN	D790	T817	T825	I842	T856	F873	D874	A924	F925	D926	D934	I961	E972	M990	A991	T994	F995																																		

• Molecule 29: Integrator complex subunit 9

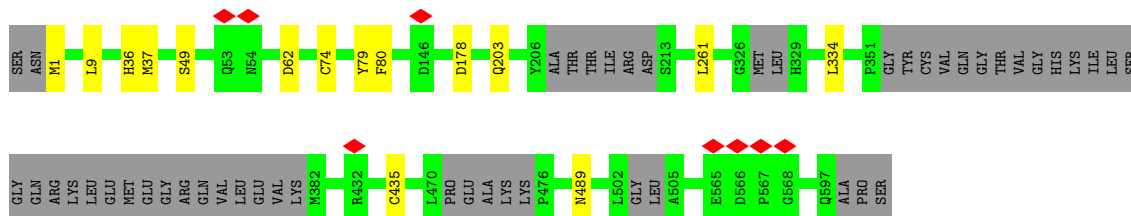
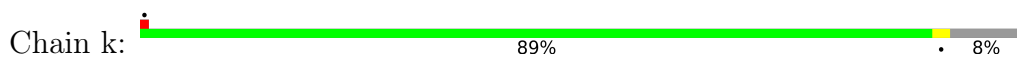




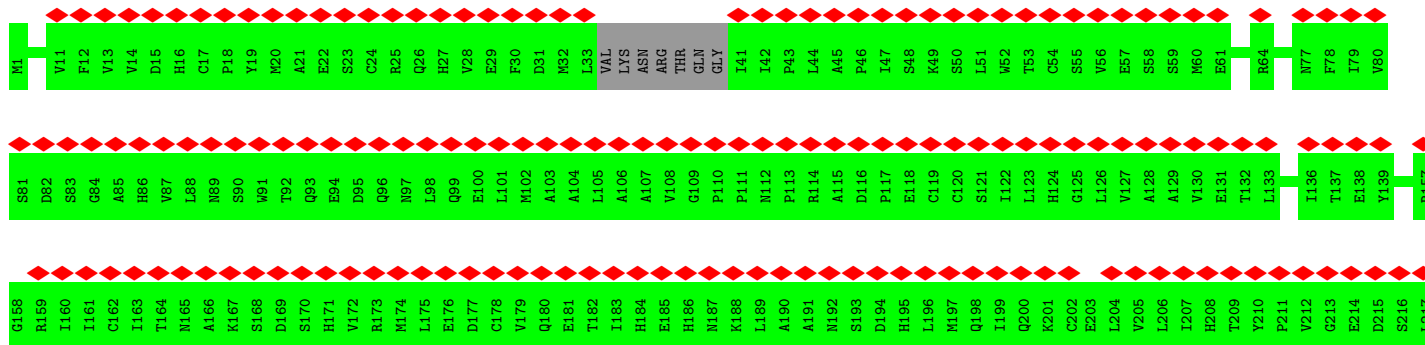
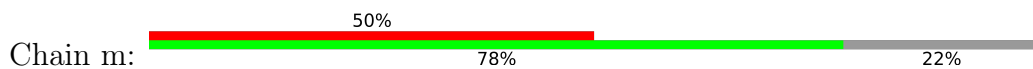
• Molecule 30: Integrator complex subunit 10

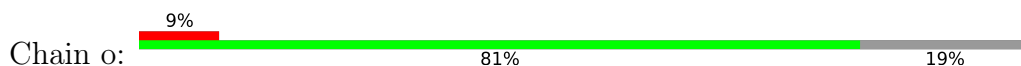
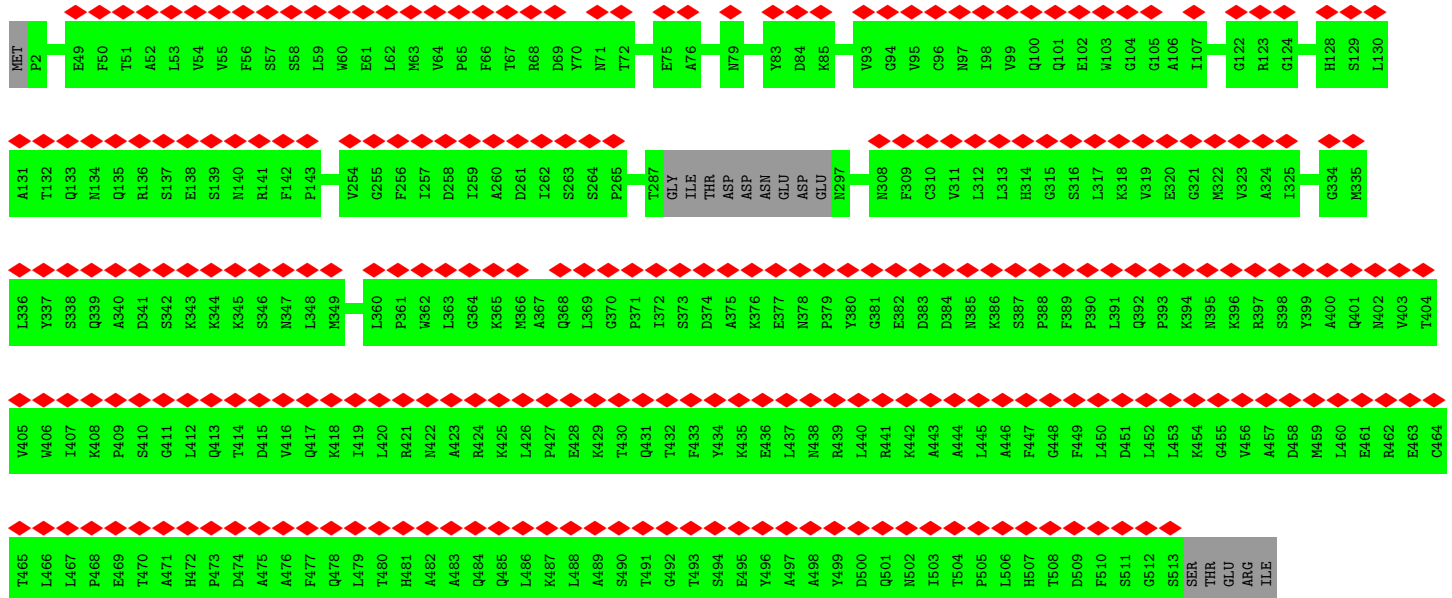
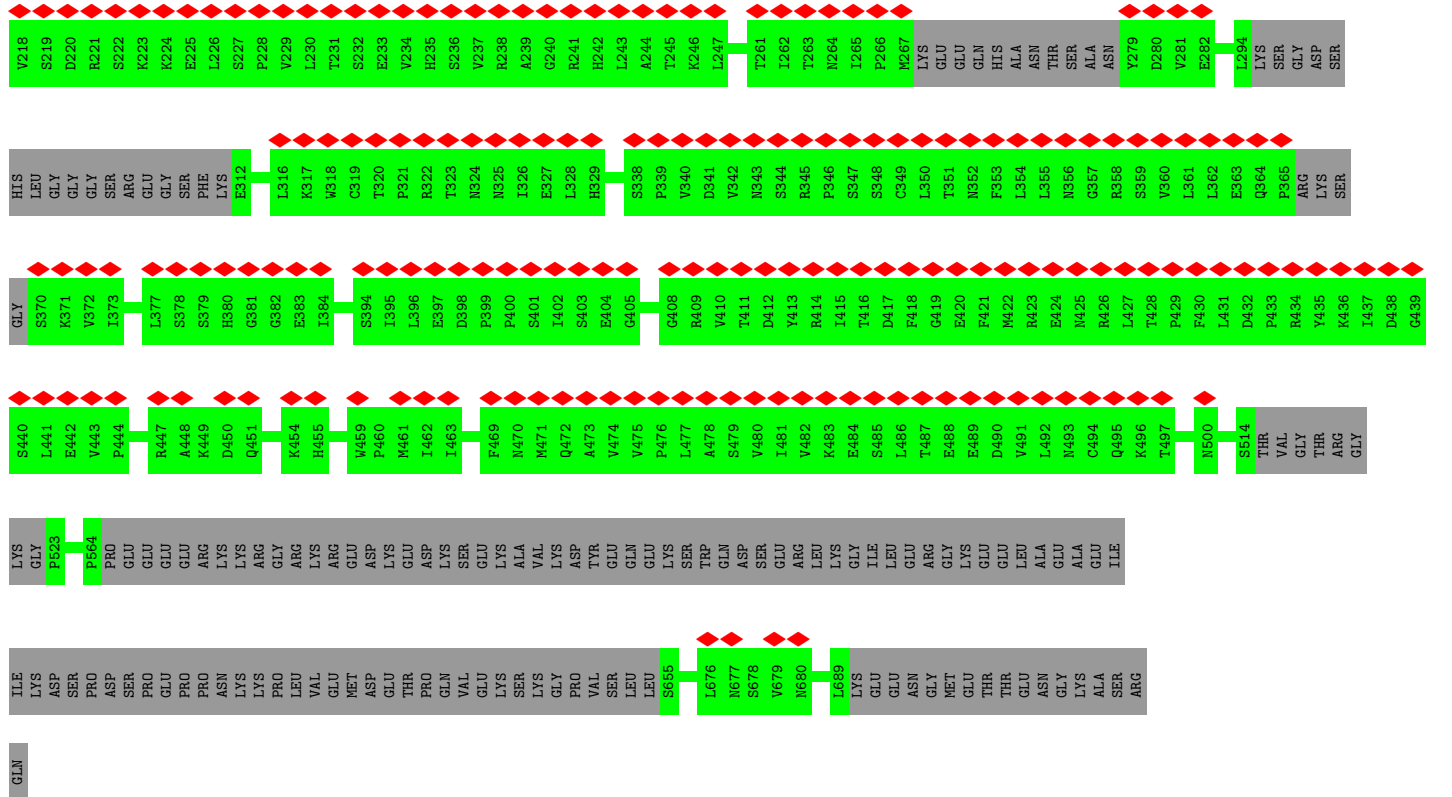


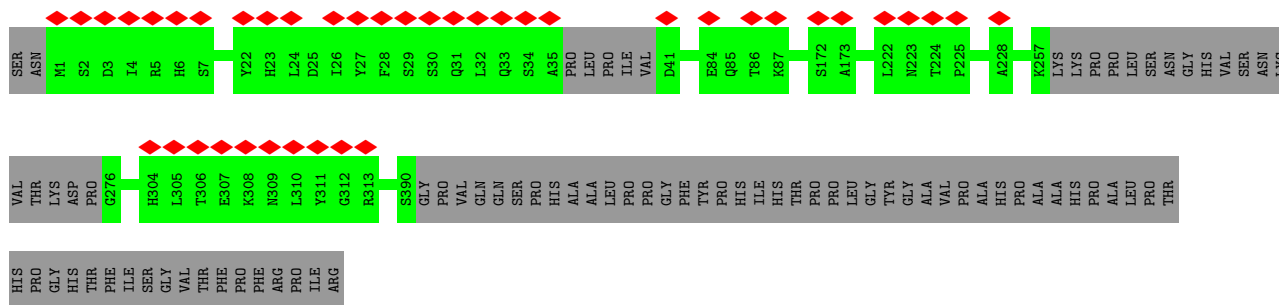
• Molecule 31: Integrator complex subunit 11



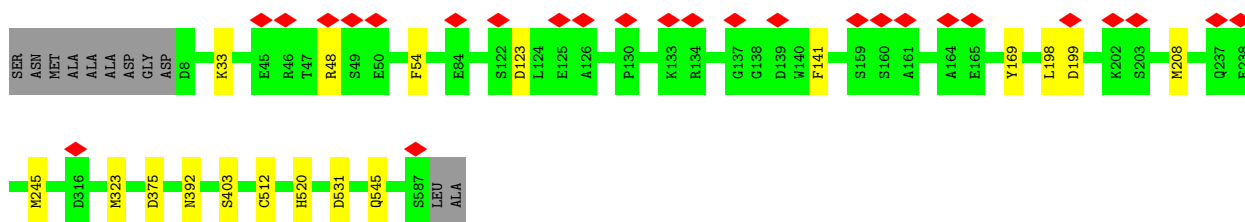
• Molecule 32: Integrator complex subunit 13



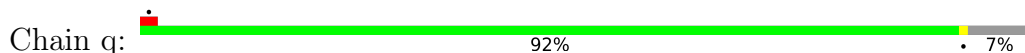




- Molecule 35: Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform



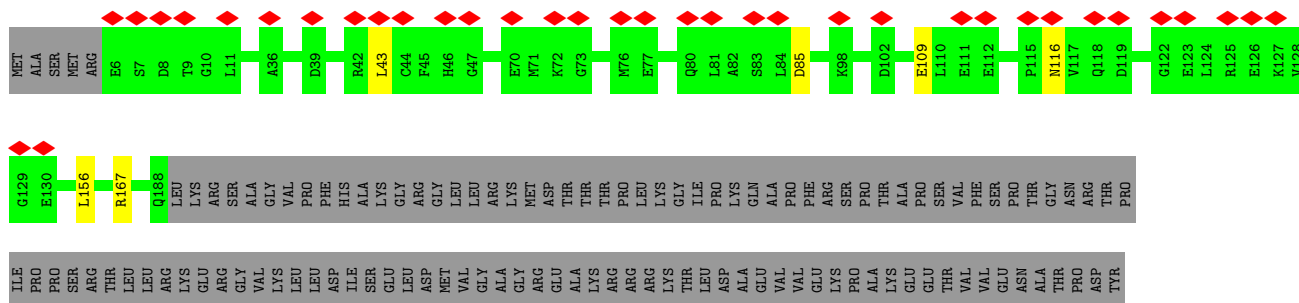
- Molecule 36: Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform



- Molecule 37: DSS1



- Molecule 38: Negative elongation factor A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	80717	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.44	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.105	Depositor
Minimum map value	-0.046	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.00453	Depositor
Map size (\AA)	525.0, 525.0, 525.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	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, MG, MN

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
2	A	0.35	0/11205	0.60	0/15122
2	Y	0.50	0/100	0.49	0/139
3	B	0.36	1/9076 (0.0%)	0.60	0/12250
4	C	0.38	0/2139	0.58	0/2906
5	D	0.28	0/990	0.54	0/1335
6	E	0.37	0/1752	0.61	0/2366
7	F	0.38	0/637	0.67	0/859
8	G	0.31	0/1347	0.59	0/1833
9	H	0.41	0/1207	0.73	0/1628
10	I	0.40	0/967	0.70	0/1309
11	J	0.42	0/542	0.59	0/730
12	K	0.37	0/936	0.58	0/1267
13	L	0.44	0/389	0.71	0/517
14	M	0.30	0/736	0.67	0/989
14	S	0.44	0/739	0.86	1/993 (0.1%)
15	N	0.59	0/3425	0.96	0/5290
16	O	0.32	0/654	0.69	0/876
16	U	0.38	0/641	0.69	0/858
17	P	0.46	0/413	1.06	3/644 (0.5%)
18	Q	0.28	0/849	0.65	1/1143 (0.1%)
18	V	0.32	0/824	0.67	0/1111
19	R	0.26	0/665	0.54	0/893
19	W	0.32	0/757	0.58	0/1015
20	T	0.65	1/3672 (0.0%)	0.98	5/5658 (0.1%)
21	Z	0.29	0/2200	0.59	0/2964
22	a	0.32	0/11854	0.57	0/16192
23	b	0.43	0/8131	0.63	0/11076
24	d	0.40	0/6532	0.62	0/8873
25	e	0.35	0/6398	0.60	0/8718
26	f	0.37	0/4240	0.61	0/5784
27	g	0.40	0/6832	0.61	0/9268
28	h	0.38	0/6870	0.56	0/9334

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
29	i	0.39	0/4989	0.60	0/6802
30	j	0.24	0/3309	0.38	0/4608
31	k	0.31	0/4179	0.59	0/5679
32	m	0.25	0/2863	0.44	0/3972
33	n	0.24	0/2482	0.46	0/3453
34	o	0.24	0/1821	0.38	0/2538
35	p	0.33	0/4505	0.62	0/6129
36	q	0.44	0/2378	0.61	0/3228
37	r	0.45	0/255	0.71	0/345
38	u	0.32	0/1419	0.63	0/1930
39	v	0.25	0/1952	0.45	0/2522
40	w	0.30	0/3900	0.57	0/5310
All	All	0.37	2/131771 (0.0%)	0.62	10/180456 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
19	R	1	0
19	W	1	0
All	All	2	0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	953	ASP	C-N	-5.27	1.22	1.34
20	T	161	DG	C5-C4	-5.07	1.34	1.38

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	T	9	DC	O5'-P-OP2	10.31	123.07	110.70
17	P	-10	U	N3-C2-O2	-8.96	115.93	122.20
20	T	9	DC	OP1-P-OP2	-8.50	106.85	119.60
17	P	-10	U	N1-C2-O2	8.38	128.67	122.80
20	T	9	DC	O5'-P-OP1	-8.16	98.36	105.70

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
19	R	66	ILE	CB
19	W	66	ILE	CB

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	1	40	0	12	0	0
2	A	11008	0	11156	130	0
2	Y	95	0	82	0	0
3	B	8901	0	8923	94	0
4	C	2096	0	2040	21	0
5	D	977	0	929	7	0
6	E	1721	0	1737	15	0
7	F	627	0	657	10	0
8	G	1316	0	1288	16	0
9	H	1186	0	1147	24	0
10	I	944	0	868	16	0
11	J	533	0	553	8	0
12	K	917	0	940	14	0
13	L	383	0	382	6	0
14	M	729	0	763	19	0
14	S	732	0	763	35	0
15	N	3050	0	1664	35	0
16	O	647	0	685	17	0
16	U	634	0	665	19	0
17	P	370	0	182	2	0
18	Q	839	0	906	20	0
18	V	814	0	875	15	0
19	R	656	0	677	13	0
19	W	746	0	766	12	0
20	T	3277	0	1805	45	0
21	Z	2167	0	2180	12	0
22	a	11692	0	10122	0	0
23	b	7991	0	8034	0	0
24	d	6407	0	6432	0	0
25	e	6260	0	6070	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	f	4137	0	3989	0	0
27	g	6722	0	6685	0	0
28	h	6751	0	6615	0	0
29	i	4870	0	4849	0	0
30	j	3313	0	1464	0	0
31	k	4090	0	3891	0	0
32	m	2864	0	1380	0	0
33	n	2484	0	1104	0	0
34	o	1824	0	802	0	0
35	p	4431	0	4483	0	0
36	q	2322	0	2215	0	0
37	r	250	0	217	0	0
38	u	1395	0	1434	0	0
39	v	2070	0	921	0	0
40	w	3825	0	3650	0	0
41	x	110	0	24	0	0
42	A	2	0	0	0	0
42	B	1	0	0	0	0
42	C	1	0	0	0	0
42	I	2	0	0	0	0
42	J	1	0	0	0	0
42	L	1	0	0	0	0
42	k	2	0	0	0	0
43	P	1	0	0	0	0
44	f	1	0	0	0	0
44	q	1	0	0	0	0
All	All	129226	0	117026	482	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 5.

The worst 5 of 482 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)
18:Q:84:GLN:HE21	18:Q:102:ILE:HG22	1.41	0.84
15:N:55:DT:H5'	14:S:83:ARG:HD3	1.64	0.78
20:T:111:DT:H4'	18:V:42:ARG:HA	1.66	0.78
15:N:35:DA:H4'	18:V:16:SER:HA	1.68	0.76
3:B:927:ARG:NH1	3:B:1054:MET:SD	2.64	0.71

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	
2	A	1375/1970 (70%)	1322 (96%)	53 (4%)	0	100	100
2	Y	11/1970 (1%)	11 (100%)	0	0	100	100
3	B	1096/1174 (93%)	1063 (97%)	33 (3%)	0	100	100
4	C	257/275 (94%)	249 (97%)	8 (3%)	0	100	100
5	D	124/142 (87%)	120 (97%)	4 (3%)	0	100	100
6	E	207/210 (99%)	201 (97%)	6 (3%)	0	100	100
7	F	76/127 (60%)	73 (96%)	3 (4%)	0	100	100
8	G	169/172 (98%)	158 (94%)	11 (6%)	0	100	100
9	H	146/150 (97%)	139 (95%)	7 (5%)	0	100	100
10	I	115/125 (92%)	111 (96%)	4 (4%)	0	100	100
11	J	65/67 (97%)	64 (98%)	1 (2%)	0	100	100
12	K	113/117 (97%)	109 (96%)	4 (4%)	0	100	100
13	L	44/58 (76%)	40 (91%)	4 (9%)	0	100	100
14	M	88/135 (65%)	83 (94%)	5 (6%)	0	100	100
14	S	89/135 (66%)	77 (86%)	8 (9%)	4 (4%)	2	23
16	O	80/103 (78%)	78 (98%)	2 (2%)	0	100	100
16	U	78/103 (76%)	77 (99%)	1 (1%)	0	100	100
18	Q	107/130 (82%)	105 (98%)	2 (2%)	0	100	100
18	V	104/130 (80%)	99 (95%)	5 (5%)	0	100	100
19	R	83/126 (66%)	80 (96%)	3 (4%)	0	100	100
19	W	93/126 (74%)	85 (91%)	7 (8%)	1 (1%)	14	50
21	Z	268/1087 (25%)	248 (92%)	20 (8%)	0	100	100
22	a	1676/2192 (76%)	1612 (96%)	64 (4%)	0	100	100
23	b	1033/1204 (86%)	979 (95%)	54 (5%)	0	100	100
24	d	810/963 (84%)	778 (96%)	32 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	e	834/1021 (82%)	799 (96%)	35 (4%)	0	100	100
26	f	530/889 (60%)	507 (96%)	23 (4%)	0	100	100
27	g	876/964 (91%)	835 (95%)	41 (5%)	0	100	100
28	h	865/995 (87%)	840 (97%)	25 (3%)	0	100	100
29	i	618/658 (94%)	581 (94%)	37 (6%)	0	100	100
30	j	660/710 (93%)	627 (95%)	33 (5%)	0	100	100
31	k	540/602 (90%)	488 (90%)	52 (10%)	0	100	100
32	m	538/706 (76%)	505 (94%)	33 (6%)	0	100	100
33	n	499/518 (96%)	448 (90%)	51 (10%)	0	100	100
34	o	361/451 (80%)	337 (93%)	24 (7%)	0	100	100
35	p	578/591 (98%)	554 (96%)	24 (4%)	0	100	100
36	q	288/311 (93%)	275 (96%)	13 (4%)	0	100	100
37	r	26/28 (93%)	24 (92%)	2 (8%)	0	100	100
38	u	181/528 (34%)	174 (96%)	7 (4%)	0	100	100
39	v	400/613 (65%)	371 (93%)	29 (7%)	0	100	100
40	w	501/583 (86%)	479 (96%)	22 (4%)	0	100	100
All	All	16602/23159 (72%)	15805 (95%)	792 (5%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	S	64	LYS
14	S	66	PRO
14	S	67	PHE
19	W	86	ILE
14	S	116	ARG

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	
2	A	1223/1749 (70%)	1197 (98%)	26 (2%)	53	72
2	Y	13/1749 (1%)	12 (92%)	1 (8%)	13	40
3	B	978/1027 (95%)	963 (98%)	15 (2%)	65	79
4	C	238/252 (94%)	236 (99%)	2 (1%)	81	88
5	D	101/126 (80%)	98 (97%)	3 (3%)	41	64
6	E	191/192 (100%)	187 (98%)	4 (2%)	53	72
7	F	68/111 (61%)	66 (97%)	2 (3%)	42	64
8	G	141/153 (92%)	136 (96%)	5 (4%)	36	61
9	H	129/131 (98%)	123 (95%)	6 (5%)	26	53
10	I	104/112 (93%)	98 (94%)	6 (6%)	20	48
11	J	56/56 (100%)	53 (95%)	3 (5%)	22	50
12	K	103/106 (97%)	99 (96%)	4 (4%)	32	58
13	L	42/55 (76%)	42 (100%)	0	100	100
14	M	77/113 (68%)	70 (91%)	7 (9%)	9	33
14	S	76/113 (67%)	68 (90%)	8 (10%)	7	27
16	O	66/79 (84%)	63 (96%)	3 (4%)	27	54
16	U	64/79 (81%)	61 (95%)	3 (5%)	26	53
18	Q	85/99 (86%)	85 (100%)	0	100	100
18	V	83/99 (84%)	81 (98%)	2 (2%)	49	69
19	R	71/107 (66%)	71 (100%)	0	100	100
19	W	81/107 (76%)	73 (90%)	8 (10%)	8	29
21	Z	240/940 (26%)	237 (99%)	3 (1%)	69	81
22	a	955/1909 (50%)	924 (97%)	31 (3%)	39	62
23	b	870/1072 (81%)	849 (98%)	21 (2%)	49	69
24	d	703/845 (83%)	683 (97%)	20 (3%)	43	65
25	e	617/814 (76%)	598 (97%)	19 (3%)	40	63
26	f	438/798 (55%)	427 (98%)	11 (2%)	47	68
27	g	723/842 (86%)	713 (99%)	10 (1%)	67	80
28	h	701/896 (78%)	689 (98%)	12 (2%)	60	78
29	i	555/600 (92%)	545 (98%)	10 (2%)	59	77
31	k	405/522 (78%)	390 (96%)	15 (4%)	34	59
32	m	32/639 (5%)	32 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	p	485/514 (94%)	467 (96%)	18 (4%)	34	59
36	q	251/276 (91%)	247 (98%)	4 (2%)	62	78
37	r	28/28 (100%)	27 (96%)	1 (4%)	35	60
38	u	154/451 (34%)	148 (96%)	6 (4%)	32	58
39	v	59/515 (12%)	57 (97%)	2 (3%)	37	61
40	w	387/511 (76%)	372 (96%)	15 (4%)	32	58
All	All	11593/18787 (62%)	11287 (97%)	306 (3%)	49	67

5 of 306 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	h	643	ARG
38	u	116	ASN
29	i	182	TYR
35	p	33	LYS
40	w	425	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
24	d	120	ASN
24	d	689	GLN
40	w	394	HIS
26	f	116	ASN
27	g	707	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
17	P	16/17 (94%)	4 (25%)	0

All (4) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
17	P	-16	U
17	P	-15	G
17	P	-14	U
17	P	-11	C

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 13 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.

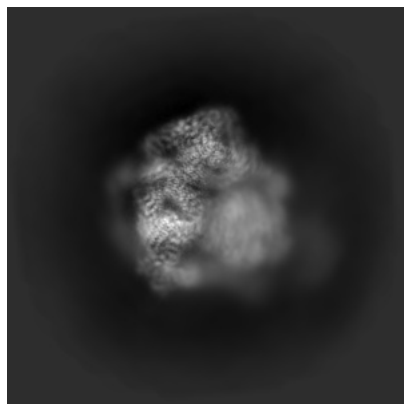
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19038. These allow visual inspection of the internal detail of the map and identification of artifacts.

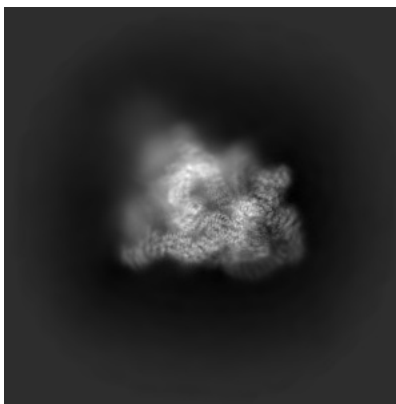
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

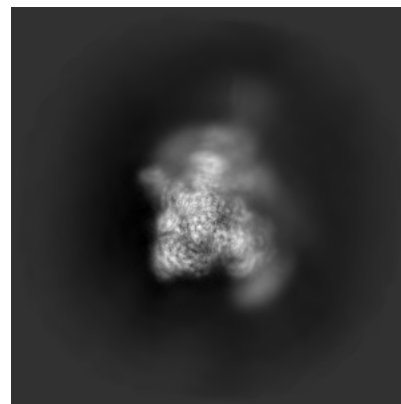
6.1.1 Primary map



X

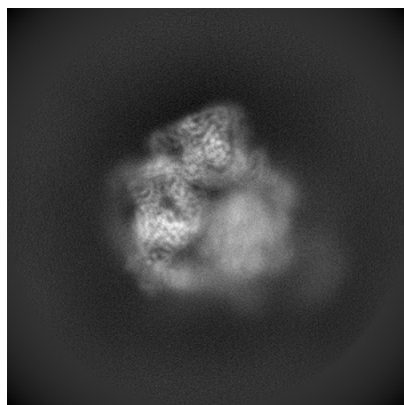


Y

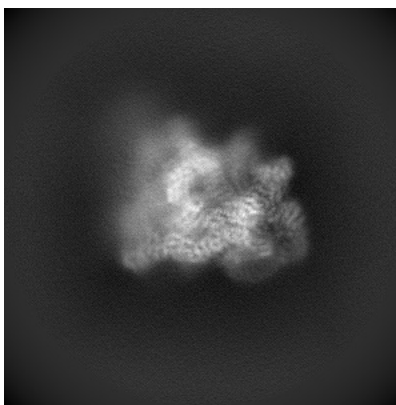


Z

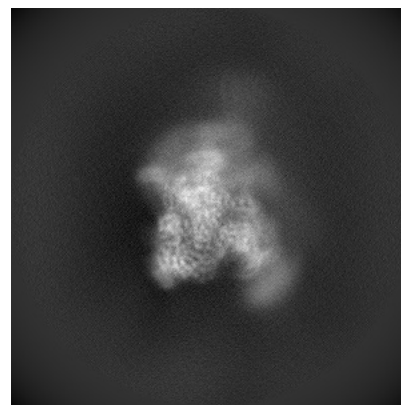
6.1.2 Raw map



X



Y

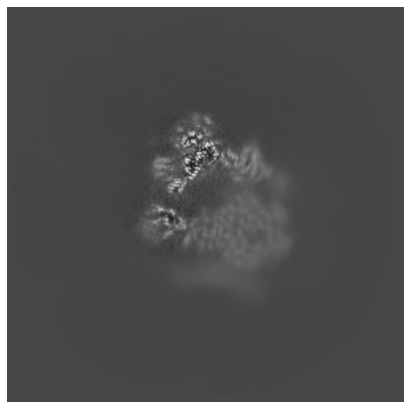


Z

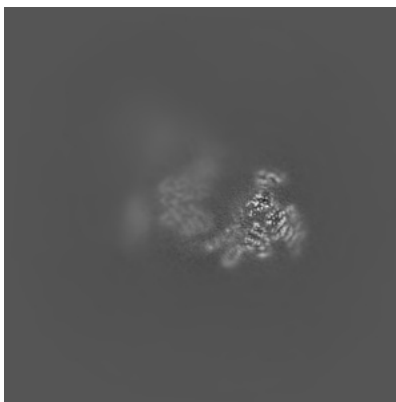
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

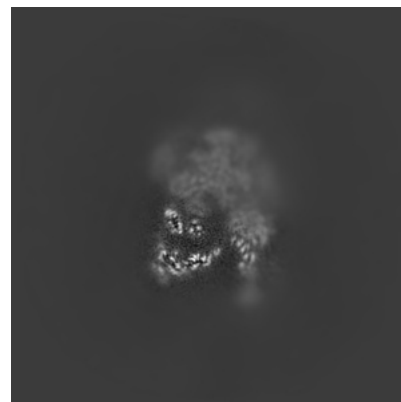
6.2.1 Primary map



X Index: 250

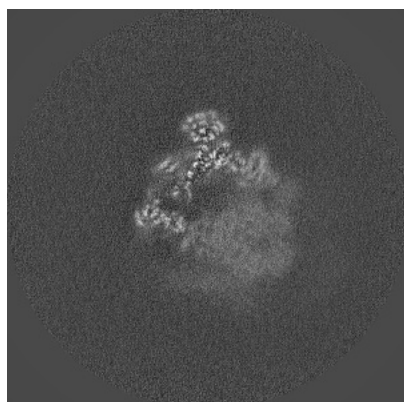


Y Index: 250

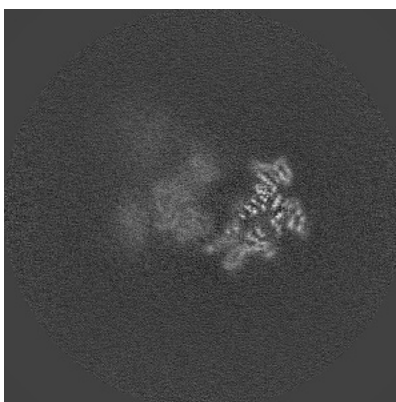


Z Index: 250

6.2.2 Raw map



X Index: 250



Y Index: 250

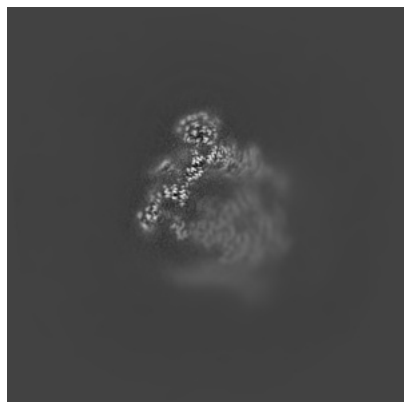


Z Index: 250

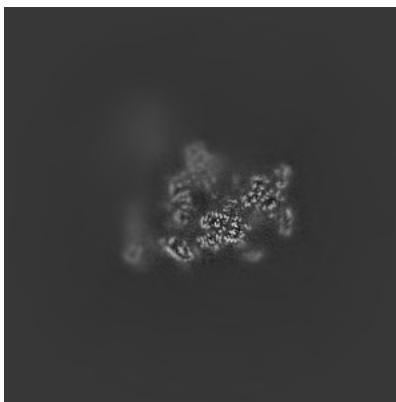
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

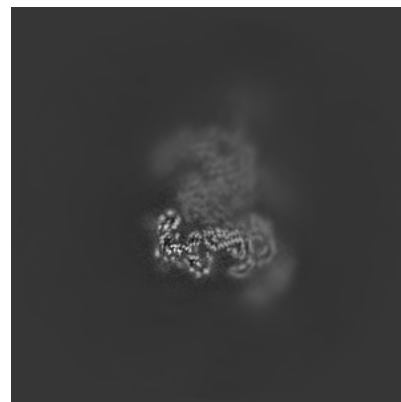
6.3.1 Primary map



X Index: 240

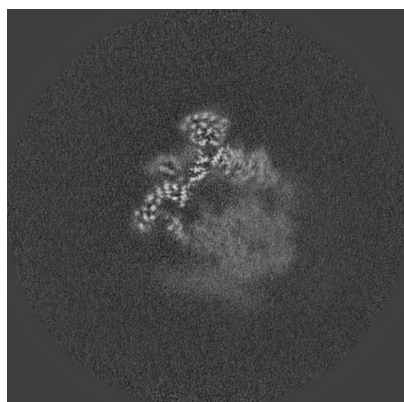


Y Index: 221

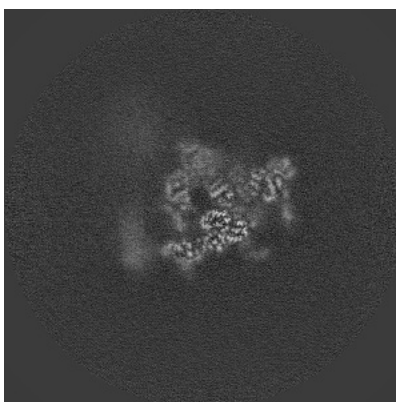


Z Index: 230

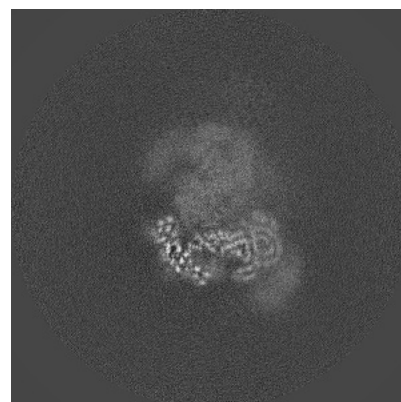
6.3.2 Raw map



X Index: 244



Y Index: 220

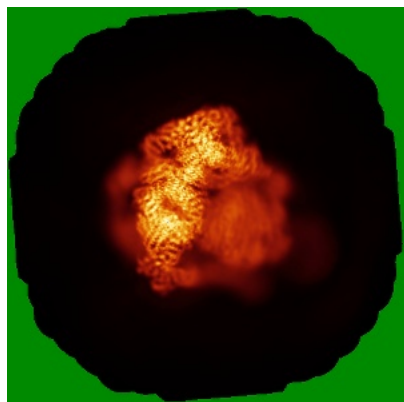


Z Index: 228

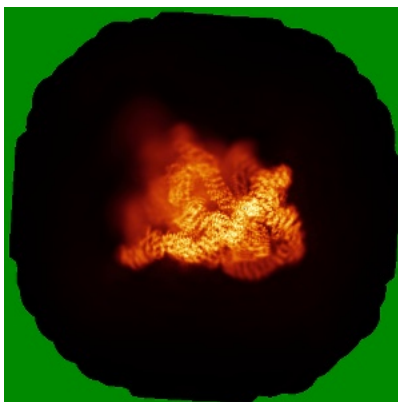
The images above show the largest variance slices of the map in three orthogonal directions.

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

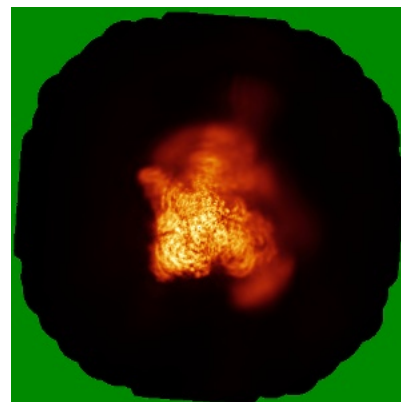
6.4.1 Primary map



X

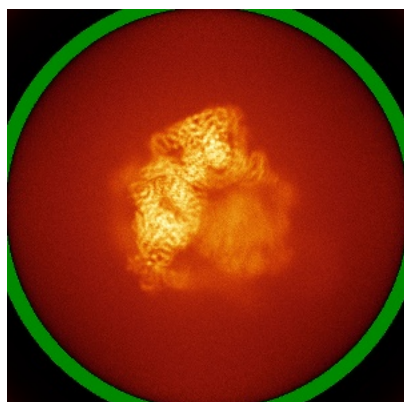


Y

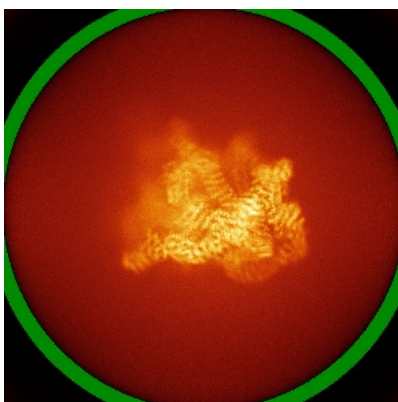


Z

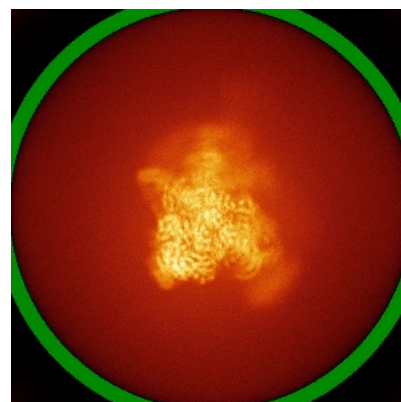
6.4.2 Raw map



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.

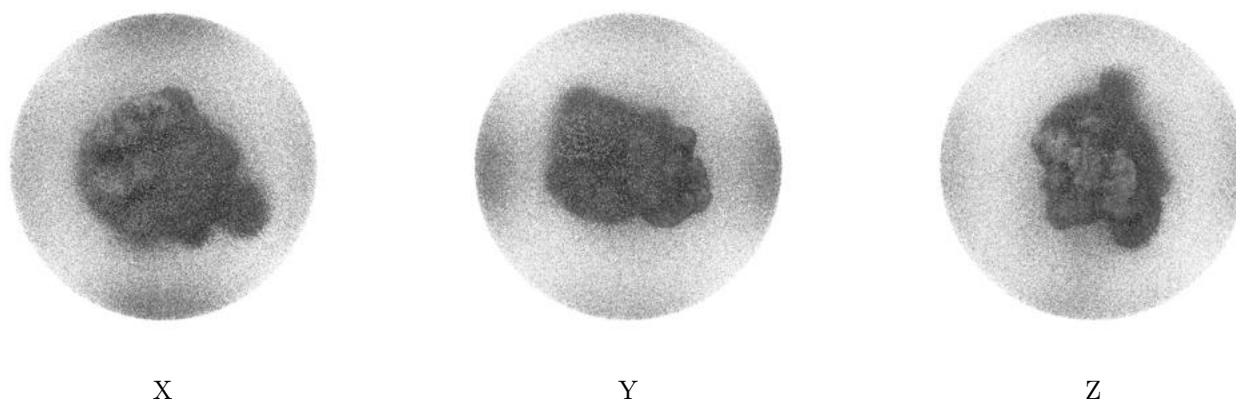
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00453. 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.

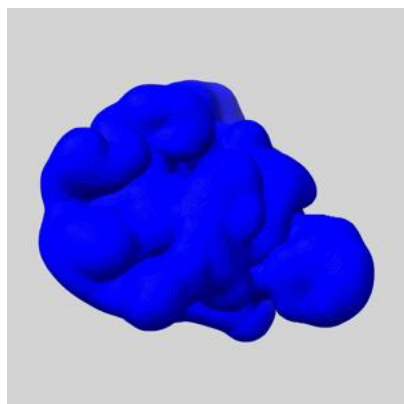
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

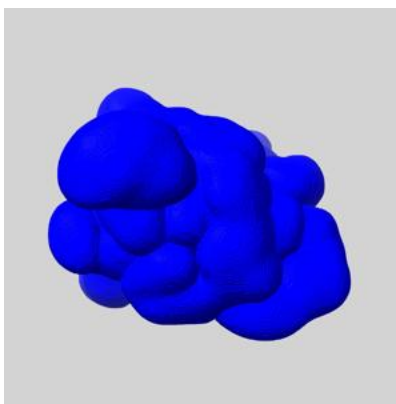
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

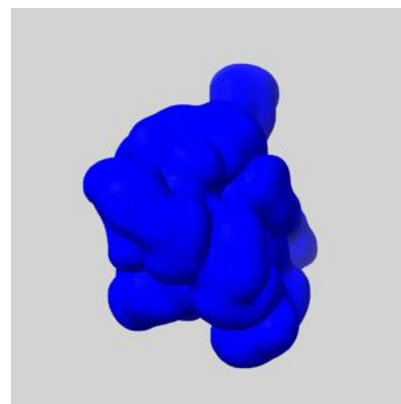
6.6.1 emd_19038_msk_1.map [i](#)



X



Y

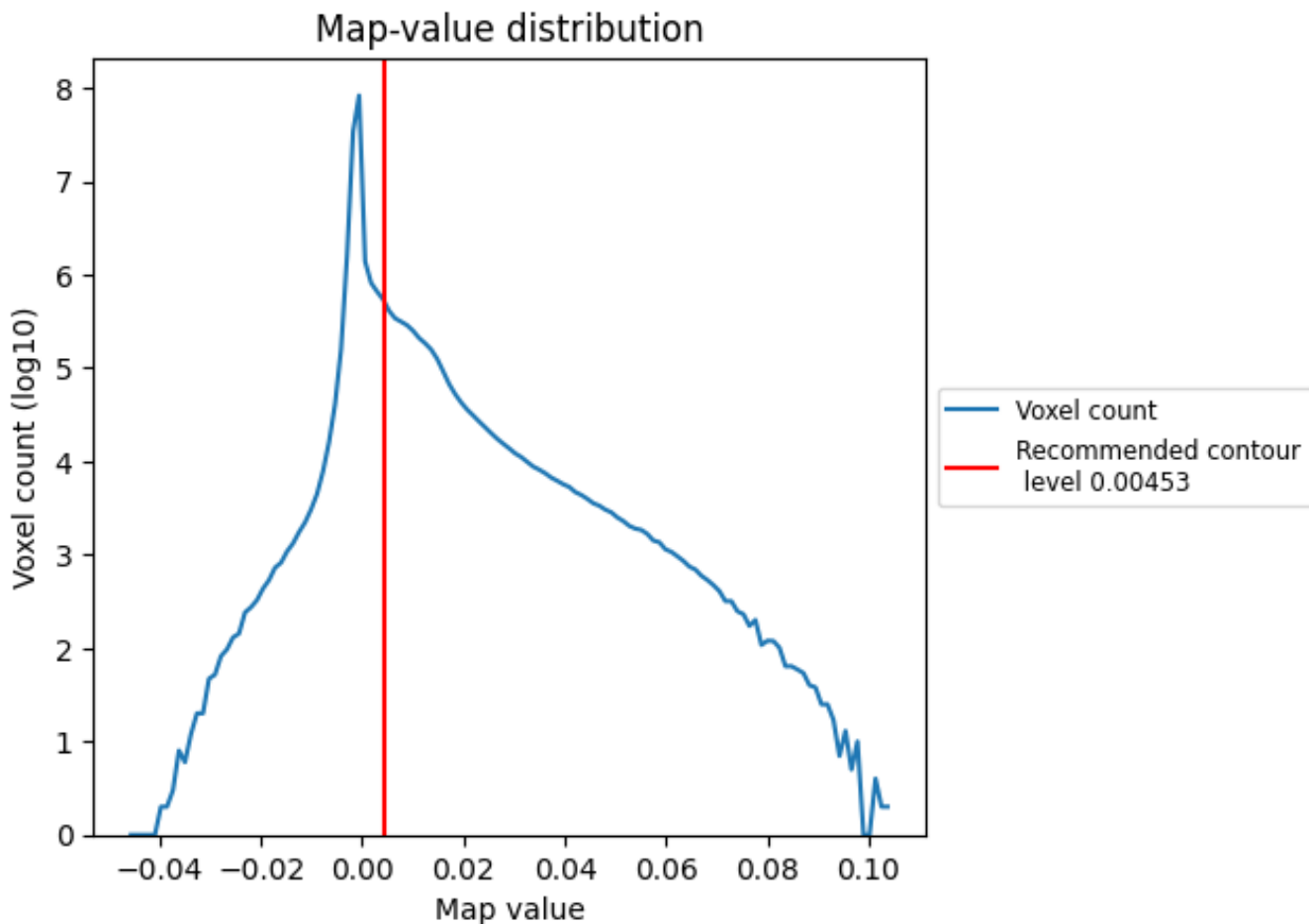


Z

7 Map analysis [i](#)

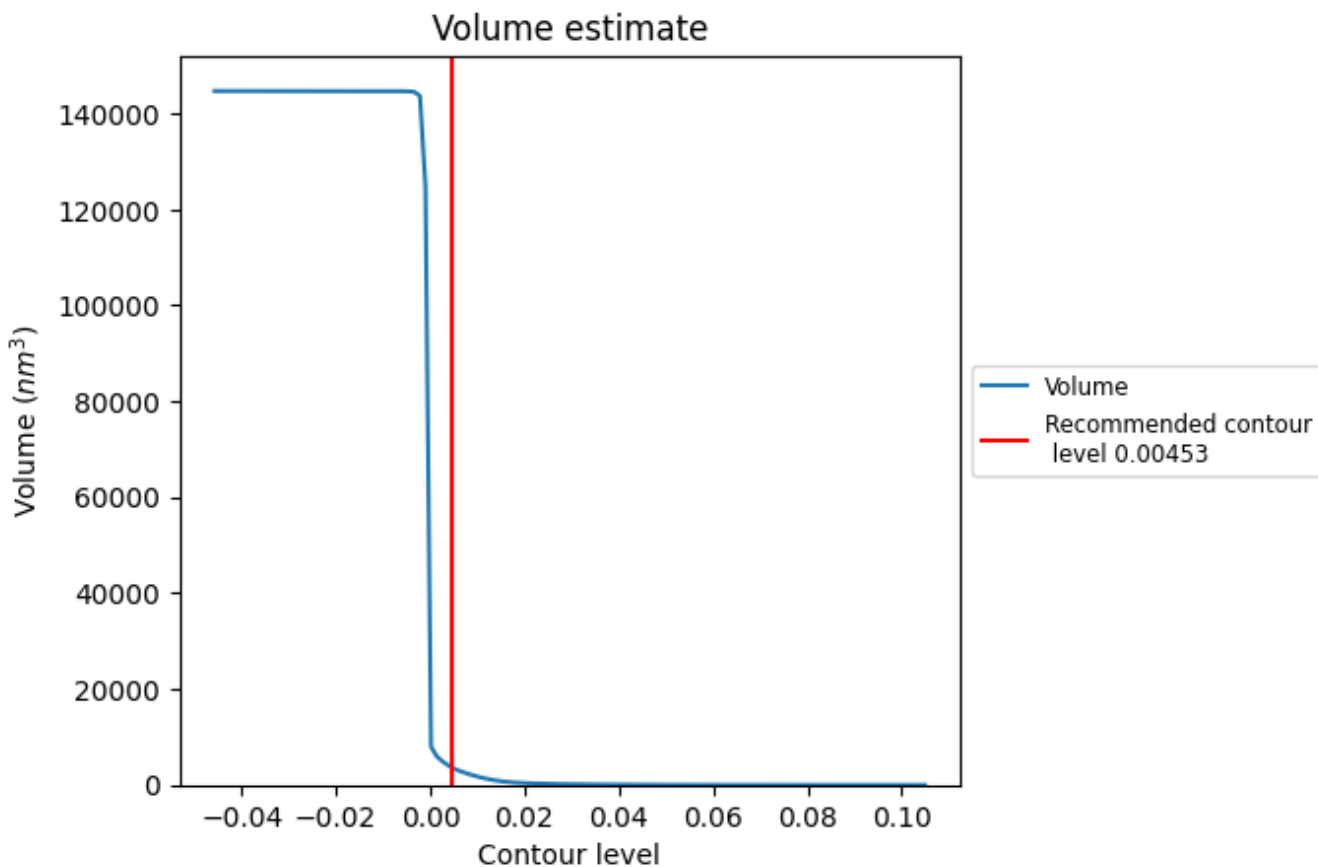
This section contains the results of statistical analysis of the map.

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.

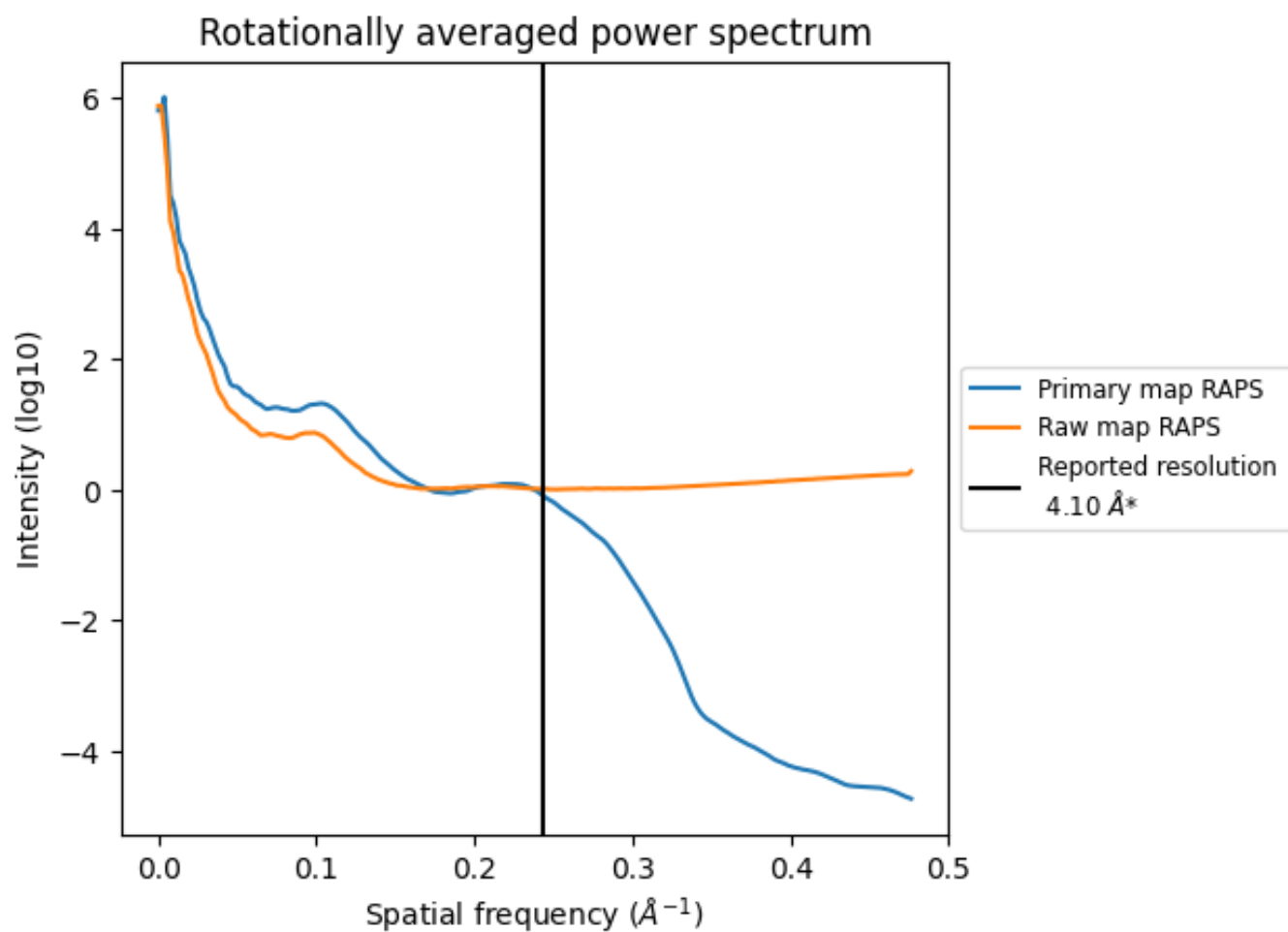
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 3701 nm^3 ; this corresponds to an approximate mass of 3343 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](#)

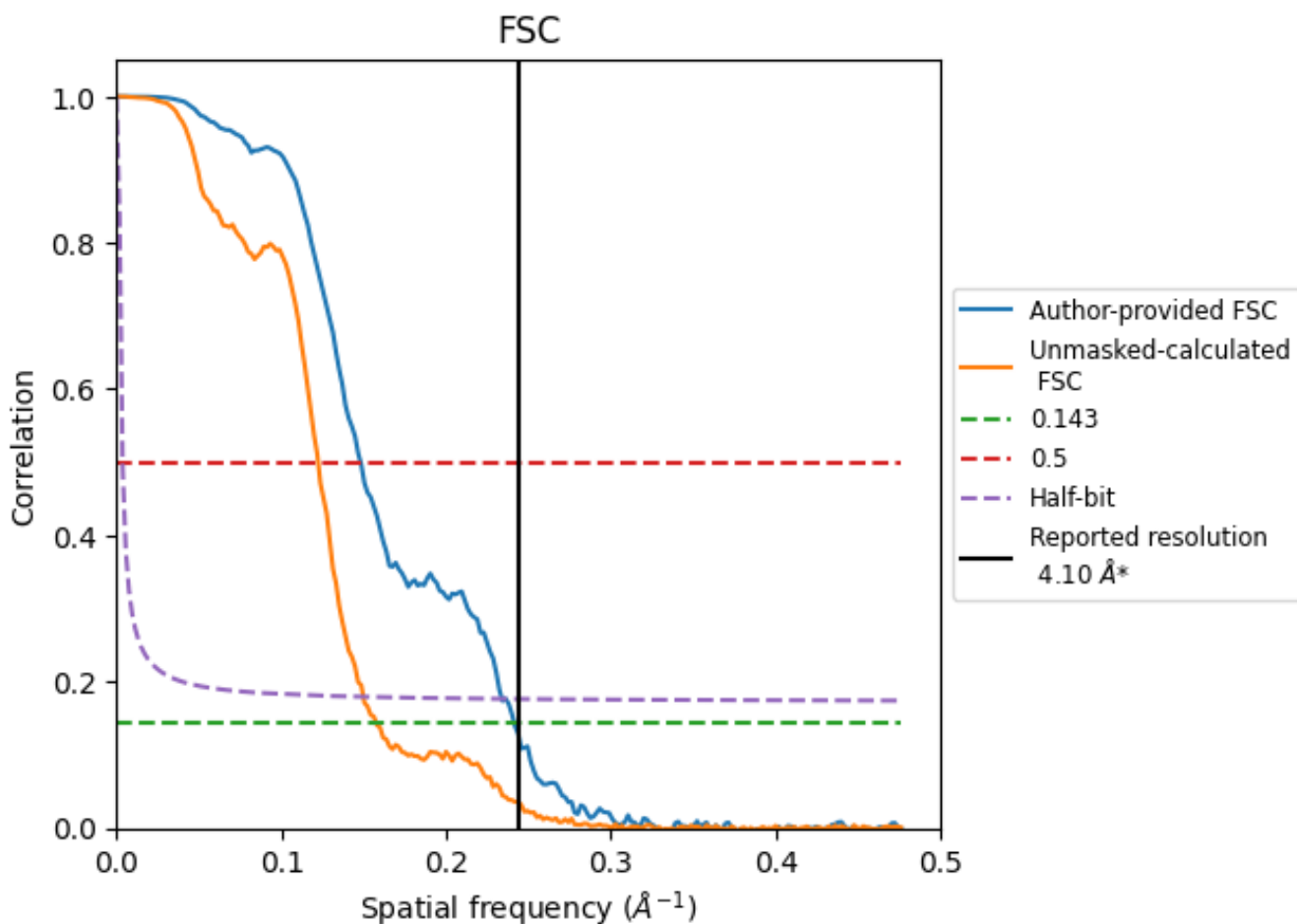


*Reported resolution corresponds to spatial frequency of 0.244 \AA^{-1}

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 0.244 Å⁻¹

8.2 Resolution estimates

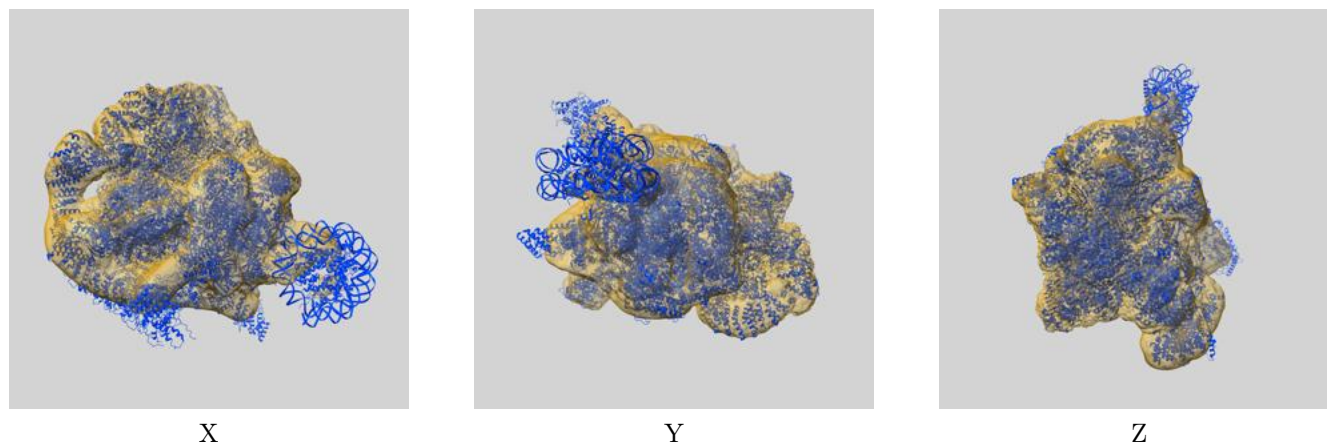
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.14	6.75	4.28
Unmasked-calculated*	6.34	8.17	6.68

*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 6.34 differs from the reported value 4.1 by more than 10 %

9 Map-model fit [i](#)

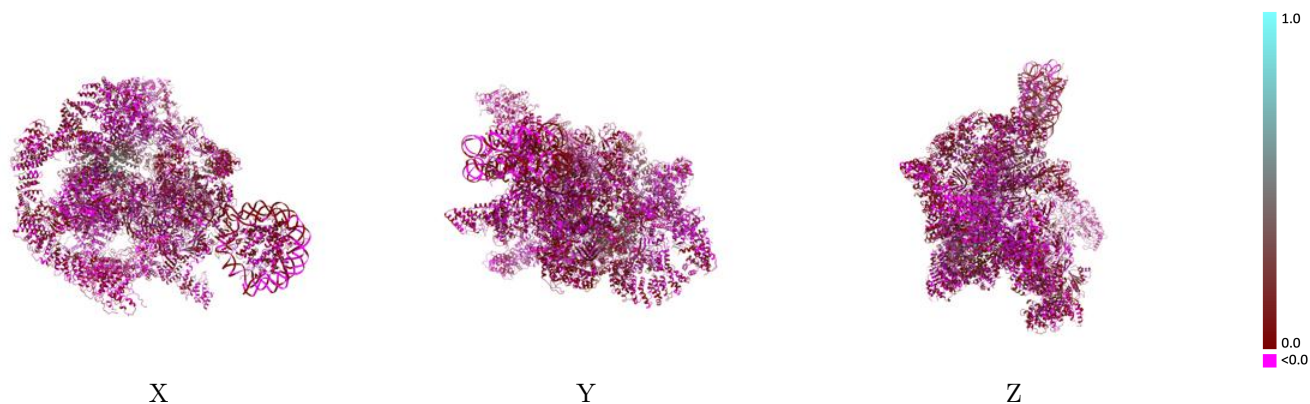
This section contains information regarding the fit between EMDB map EMD-19038 and PDB model 8RBX. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



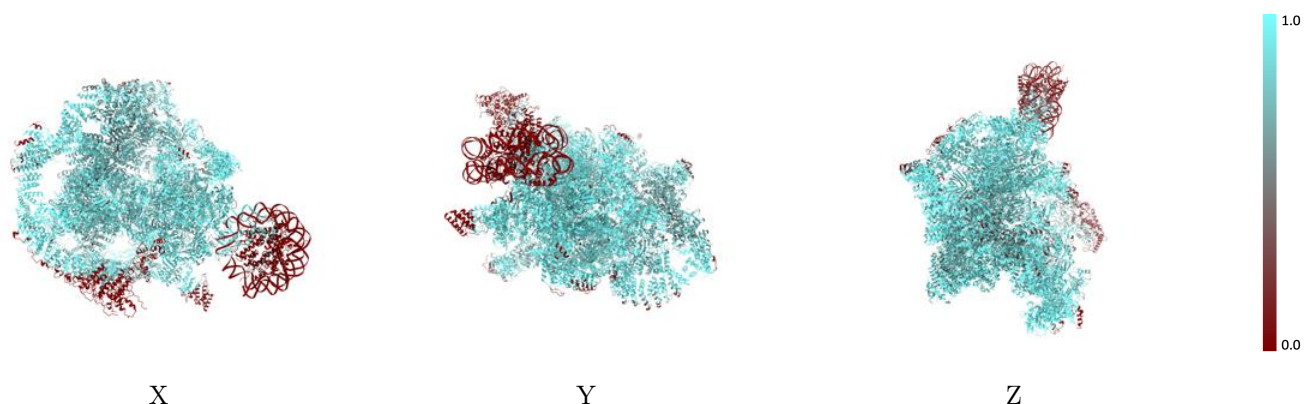
The images above show the 3D surface view of the map at the recommended contour level 0.00453 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



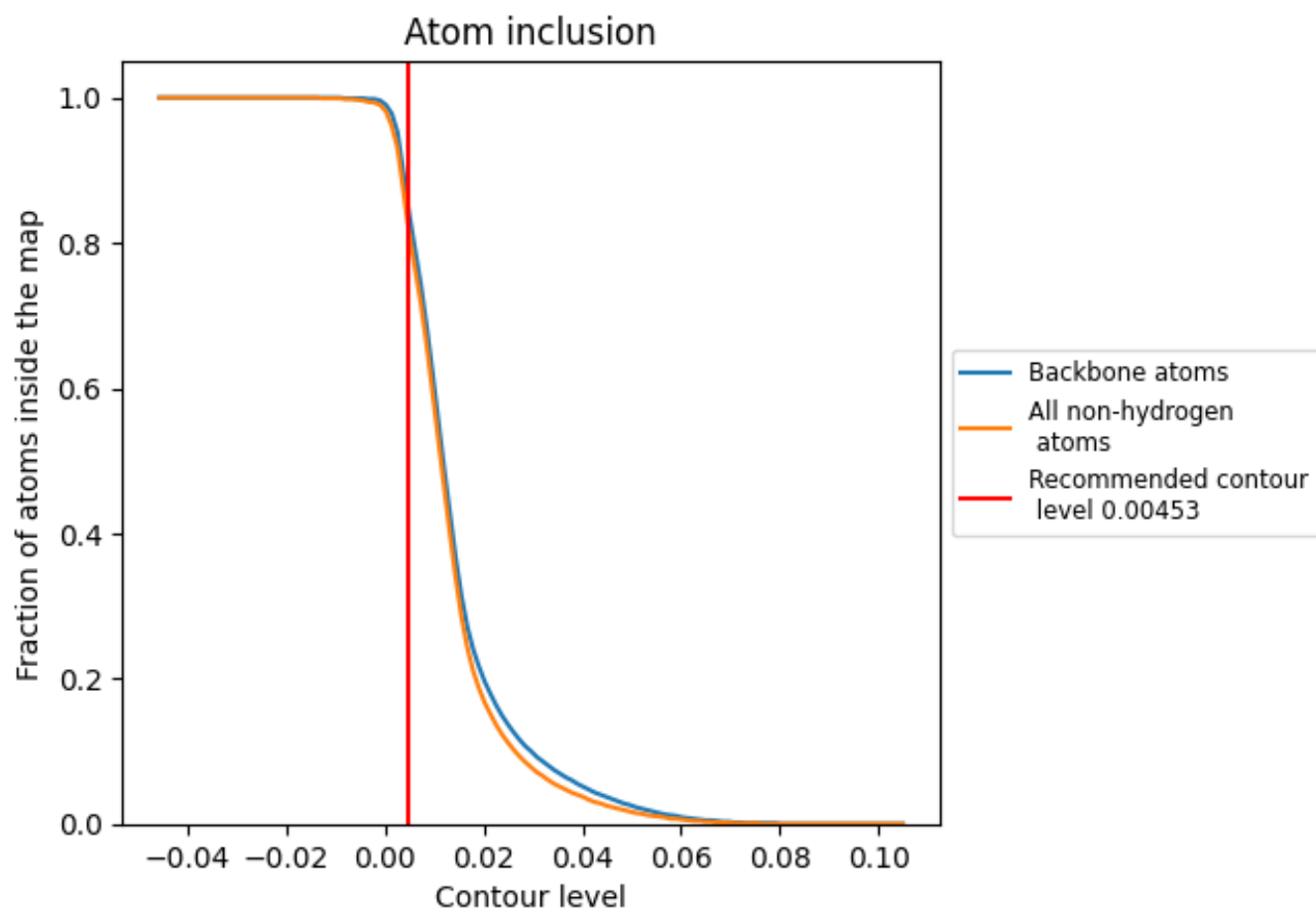
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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 (0.00453).







































































9.4 Atom inclusion [i](#)

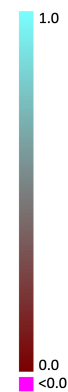


At the recommended contour level, 86% of all backbone atoms, 83% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

























The table lists the average atom inclusion at the recommended contour level (0.00453) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8330	 0.0370
1	 1.0000	 0.1450
A	 0.9910	 0.0430
B	 0.9940	 0.0130
C	 0.9620	 0.0280
D	 0.8820	 0.0530
E	 0.9570	 0.0570
F	 0.9980	 0.0880
G	 0.9380	 0.0570
H	 0.9780	 0.0640
I	 0.8810	 0.0390
J	 0.9620	 0.0310
K	 0.9780	 0.0280
L	 0.9160	 0.0240
M	 0.5350	 0.0490
N	 0.2030	 0.0260
O	 0.3660	 0.0120
P	 1.0000	 0.0260
Q	 0.0000	 0.0270
R	 0.1090	 0.0500
S	 0.0740	 0.0420
T	 0.3020	 0.0350
U	 0.0590	 -0.0090
V	 0.1290	 0.0070
W	 0.2780	 0.0300
Y	 0.9680	 0.3810
Z	 0.9830	 0.0240
a	 0.8430	 0.0360
b	 0.8860	 0.0940
d	 0.9250	 0.0240
e	 0.8810	 0.0130
f	 0.9450	 0.0270
g	 0.8950	 0.0990
h	 0.8590	 0.0010
i	 0.9110	 -0.0080



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
j	 0.8610	 0.0450
k	 0.9750	 0.0380
m	 0.3720	 0.0090
n	 0.4800	 0.0090
o	 0.8850	 0.0530
p	 0.9320	 0.0720
q	 0.9130	 -0.0130
r	 0.8650	 0.0140
u	 0.7800	 0.0340
v	 0.9490	 0.0730
w	 0.9240	 0.0540
x	 0.9180	 0.0330