



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 02:41 AM UTC

PDB ID : 6V92 / pdb_00006v92
EMDB ID : EMD-21114
Title : RSC-NCP
Authors : Patel, A.B.; Moore, C.M.; Greber, B.J.; Nogales, E.
Deposited on : 2019-12-13
Resolution : 20.00 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

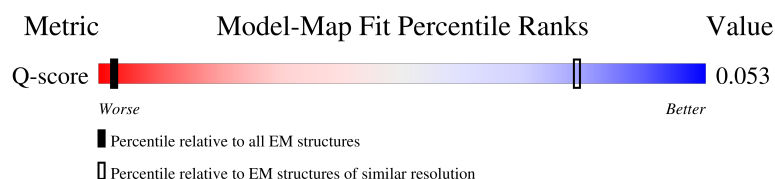
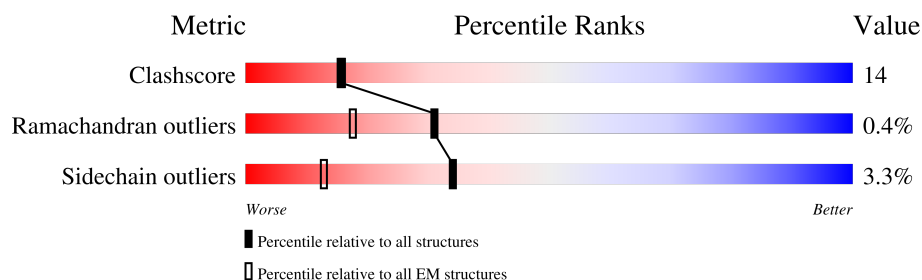
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 20.00 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	28 (19.50 - 20.50)

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	A	477	23% 52% 27% 16%
2	R	1359	18% 6% 76%
3	B	467	20% 61% 22% 15%
4	P	157	11% 19% 14% 66%

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Mol	Chain	Length	Quality of chain
5	C	78	
6	D	180	
7	E	435	
8	F	889	
9	G	885	
10	H	625	
11	I	557	
11	J	557	
11	K	557	
11	L	557	
12	M	483	
13	N	581	
14	O	502	
15	Q	426	
16	S	883	
17	2	28	
18	3	19	
18	4	19	
19	5	14	
20	6	15	
21	7	49	
22	i	146	
22	j	146	
23	a	136	
23	e	136	

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Mol	Chain	Length	Quality of chain
24	b	103	
24	f	103	
25	c	130	
25	g	130	
26	d	126	
26	h	126	

2 Entry composition

There are 27 unique types of molecules in this entry. The entry contains 44583 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 Actin-related protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	399	Total	C	N	O	S	3	0
			3227	2081	528	603	15		

- Molecule 2 is a protein called Nuclear protein STH1/NPS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	R	325	Total	C	N	O	S	0	0
			2663	1668	487	504	4		

- Molecule 3 is a protein called Actin-like protein ARP9.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	396	Total	C	N	O	S	1	0
			3198	2053	523	615	7		

- Molecule 4 is a protein called Regulator of Ty1 transposition protein 102.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	P	54	Total	C	N	O	S	0	0
			490	313	84	92	1		

- Molecule 5 is a protein called High temperature lethal protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	60	Total	C	N	O	S	0	0
			493	301	92	96	4		

- Molecule 6 is a protein called Chromatin structure-remodeling complex protein RSC14.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	100	Total	C	N	O	S	0	0
			772	490	132	148	2		

- Molecule 7 is a protein called Chromatin structure-remodeling complex subunit RSC7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	120	Total	C	N	O	S	0	0
			978	610	166	200	2		

- Molecule 8 is a protein called Chromatin structure-remodeling complex subunit RSC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	67	Total	C	N	O	S	0	0
			536	346	94	95	1		

- Molecule 9 is a protein called Chromatin structure-remodeling complex protein RSC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	53	Total	C	N	O	S	0	0
			422	270	71	79	2		

- Molecule 10 is a protein called Chromatin structure-remodeling complex subunit RSC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	131	Total	C	N	O	S	0	0
			1083	696	175	205	7		

- Molecule 11 is a protein called Chromatin structure-remodeling complex protein RSC8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	293	Total	C	N	O	S	0	0
			2416	1537	423	448	8		
11	J	115	Total	C	N	O	S	0	0
			924	579	149	190	6		
11	K	109	Total	C	N	O	S	0	0
			878	554	139	179	6		
11	L	298	Total	C	N	O	S	0	0
			2445	1557	428	452	8		

- Molecule 12 is a protein called Chromatin structure-remodeling complex protein RSC6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	310	Total	C	N	O	S	0	0
			2474	1558	414	496	6		

- Molecule 13 is a protein called Chromatin structure-remodeling complex subunit RSC9.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	412	Total	C	N	O	S	0	0
			3275	2105	540	612	18		

- Molecule 14 is a protein called Chromatin structure-remodeling complex protein RSC58.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	384	Total	C	N	O	S	0	0
			3145	2025	529	581	10		

- Molecule 15 is a protein called Chromatin structure-remodeling complex subunit SFH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Q	264	Total	C	N	O	S	0	0
			2137	1349	362	418	8		

- Molecule 16 is a protein called Chromatin structure-remodeling complex protein RSC30.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	S	34	Total	C	N	O	S	0	0
			278	182	41	54	1		

- Molecule 17 is a protein called Unknown Protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	2	28	Total	C	N	O	0	0
			140	84	28	28		

- Molecule 18 is a protein called Unknown Protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	3	19	Total	C	N	O	0	0
			95	57	19	19		
18	4	19	Total	C	N	O	0	0
			95	57	19	19		

- Molecule 19 is a protein called Unknown Protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	5	14	Total	C	N	O	0	0
			70	42	14	14		

- Molecule 20 is a protein called Unknown Protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	6	15	Total	C	N	O	0	0
			75	45	15	15		

- Molecule 21 is a protein called Unknown Protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	7	49	Total	C	N	O	0	0
			245	147	49	49		

- Molecule 22 is a DNA chain called DNA (146-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
22	i	146	Total	C	N	O	P	0	0
			2990	1431	540	874	145		
22	j	146	Total	C	N	O	P	0	0
			2990	1431	540	874	145		

- Molecule 23 is a protein called Histone H3.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	a	97	Total	C	N	O	S	0	0
			801	505	155	137	4		
23	e	99	Total	C	N	O	S	0	0
			816	514	158	140	4		

- Molecule 24 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	b	78	Total	C	N	O	S	0	0
			619	391	120	107	1		
24	f	85	Total	C	N	O	S	0	0
			683	430	136	116	1		

- Molecule 25 is a protein called Histone H2A type 1-B/E.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	c	108	Total	C	N	O	0	0
			835	526	165	144		
25	g	104	Total	C	N	O	0	0
			805	508	157	140		

- Molecule 26 is a protein called Histone H2B type 1-K.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	d	96	Total	C	N	O	S	0	0
			754	473	138	141	2		
26	h	94	Total	C	N	O	S	0	0
			735	461	134	138	2		

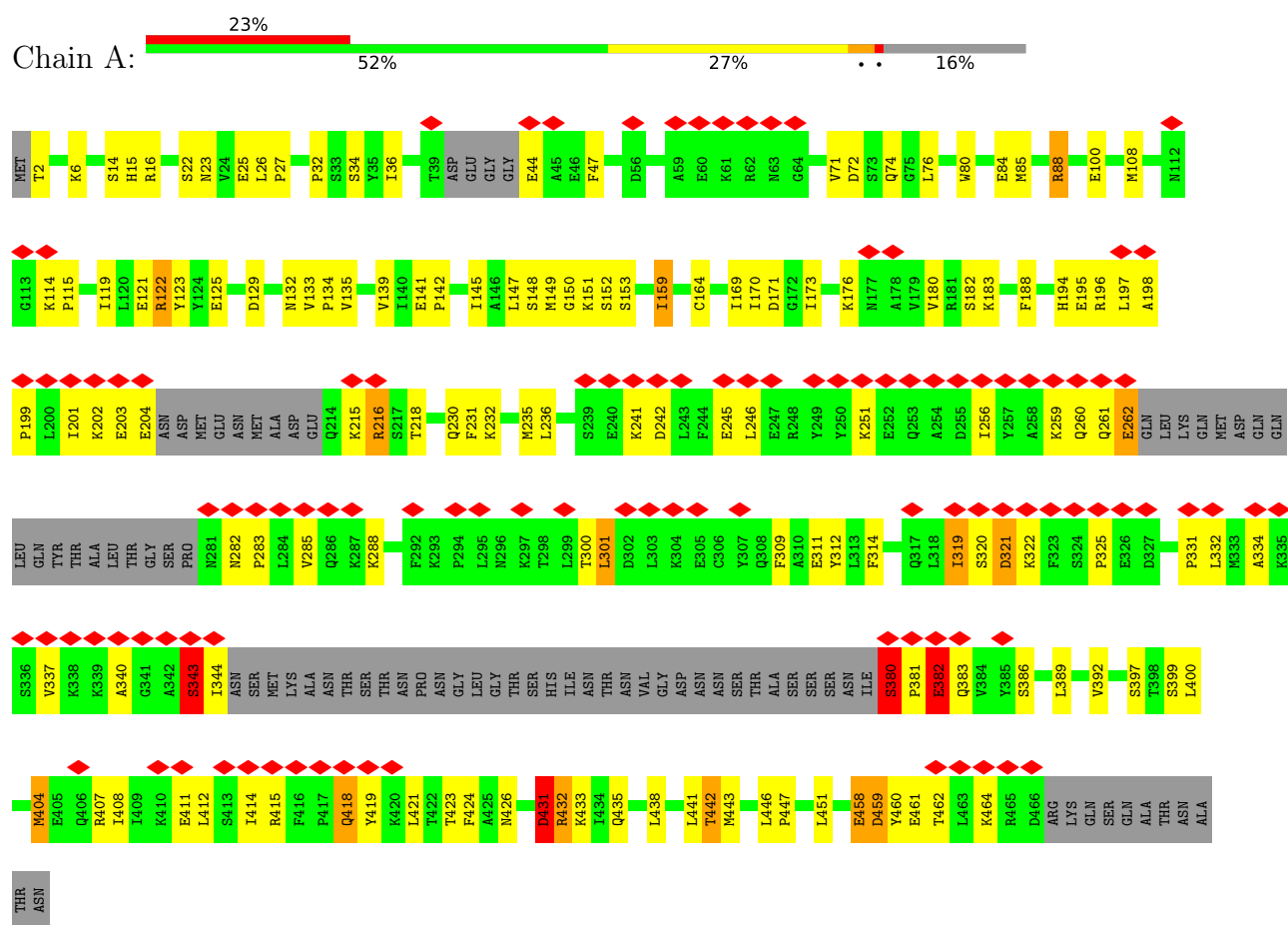
- Molecule 27 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

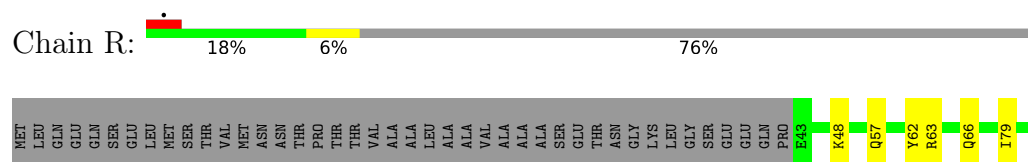
3 Residue-property plots [i](#)

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

• Molecule 1: Actin-related protein 7

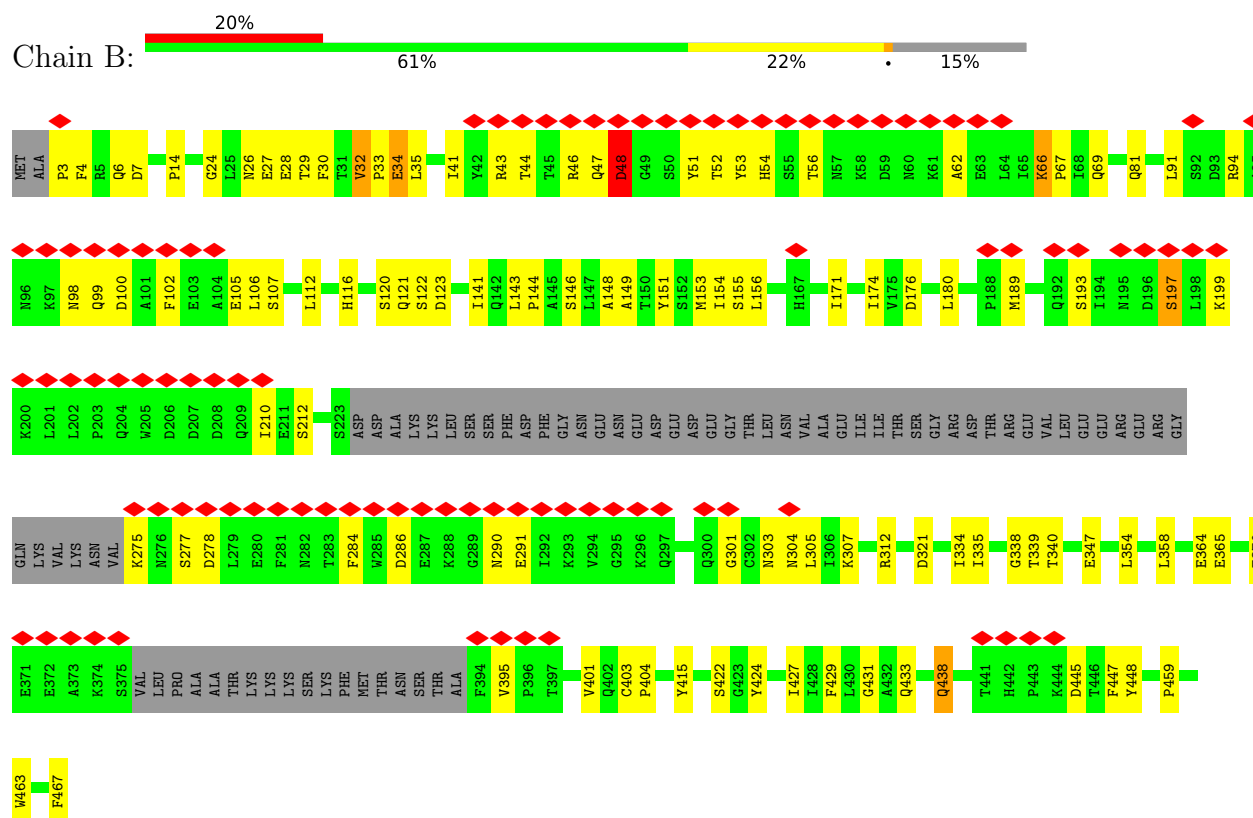


• Molecule 2: Nuclear protein STH1/NPS1

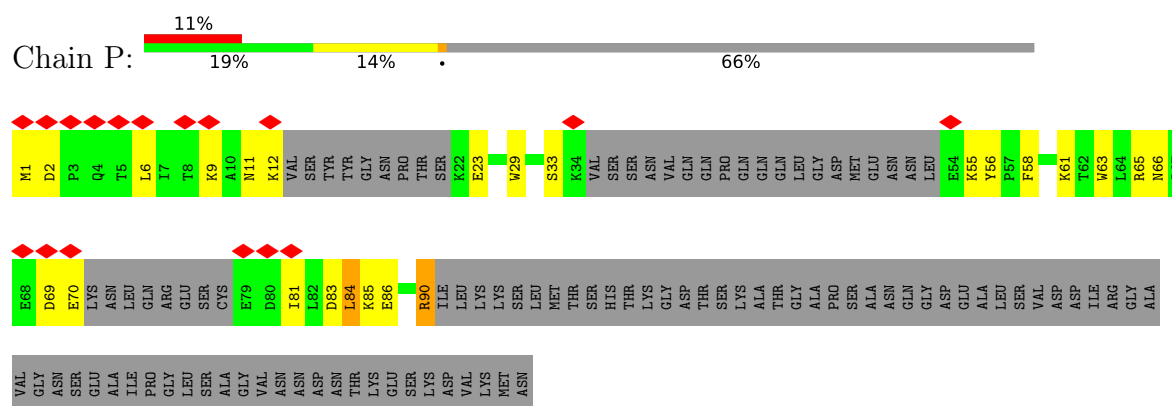




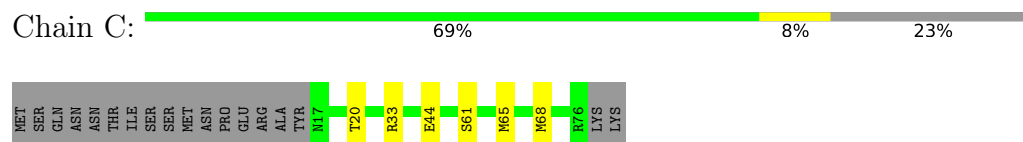
- Molecule 3: Actin-like protein ARP9



- Molecule 4: Regulator of Ty1 transposition protein 102

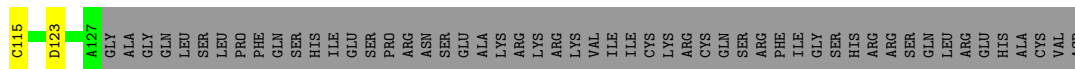


- Molecule 5: High temperature lethal protein 1

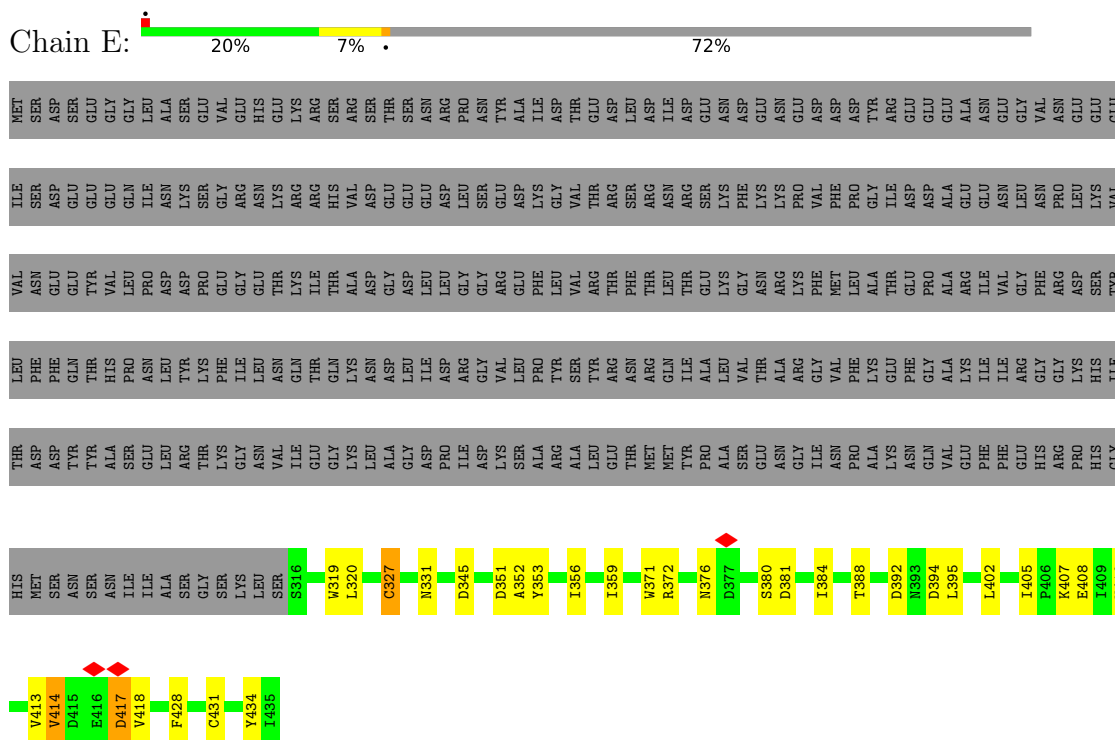


- Molecule 6: Chromatin structure-remodeling complex protein RSC14

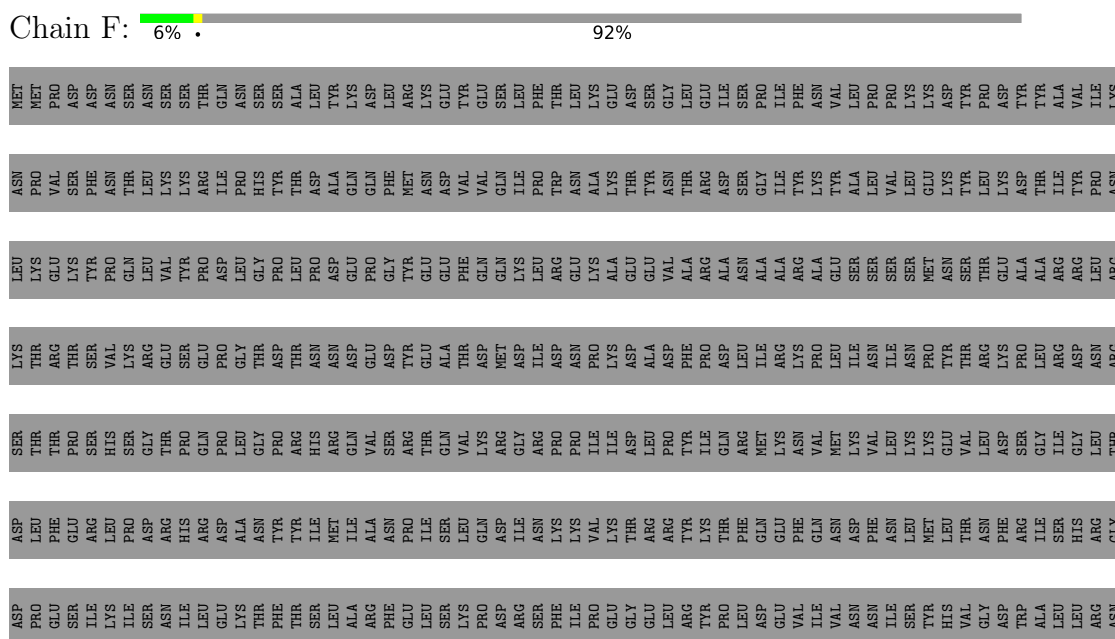




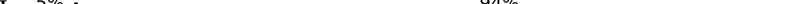
- Molecule 7: Chromatin structure-remodeling complex subunit RSC7



- Molecule 8: Chromatin structure-remodeling complex subunit RSC2



- Molecule 9: Chromatin structure-remodeling complex protein RSC3

Chain G:  5% 94%

[illegible]

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

- Molecule 10: Chromatin structure-remodeling complex subunit RSC4

Chain H: 16% 5% 79%

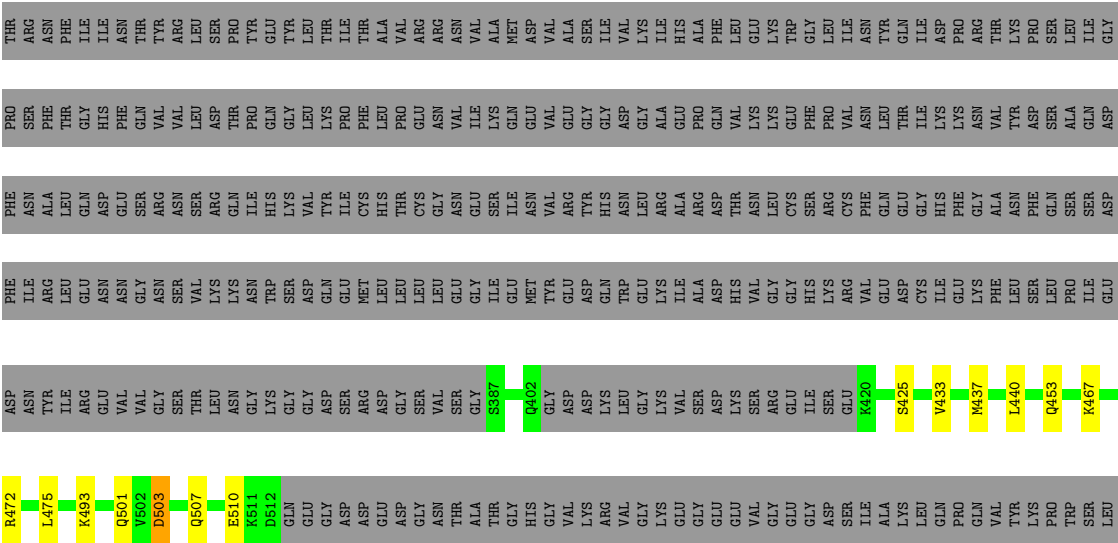
[illegible]

- Molecule 11: Chromatin structure-remodeling complex protein RSC8

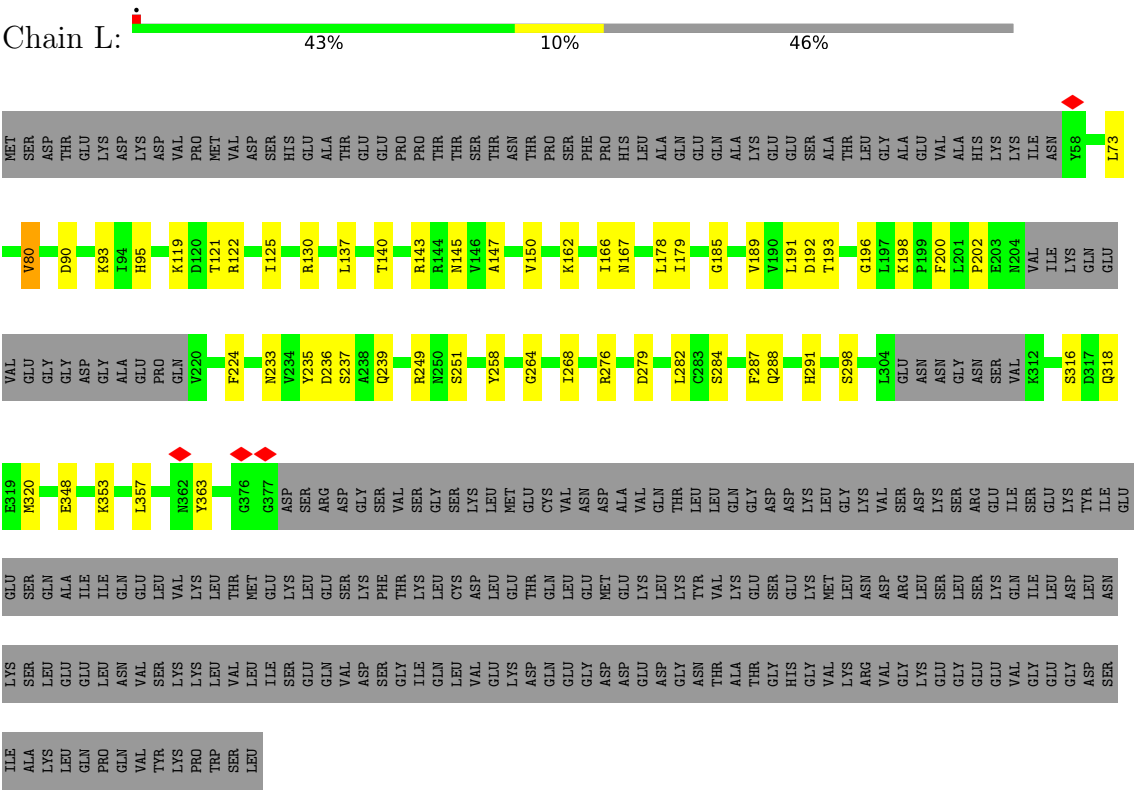
Chain I: 43% 9% 47%

MET	ASP	THR	GLU	LYS	ASP	LYS	ASP	VAL	PRO	MET	VAL	ASP	HIS	GLU	ALA	THR	GLU	GLY	PRO	THR	THR	SER	ASN	PRO	SER	PHE	PRO	HIS	LEU	ALA	GLN	GLN	ALA	LVS	GLY	GLY	SER	ALA	THR	LEU	GLY	ALA	VAL	ALA	HIS	LVS	LVS	LVS	ILE	N57	E69
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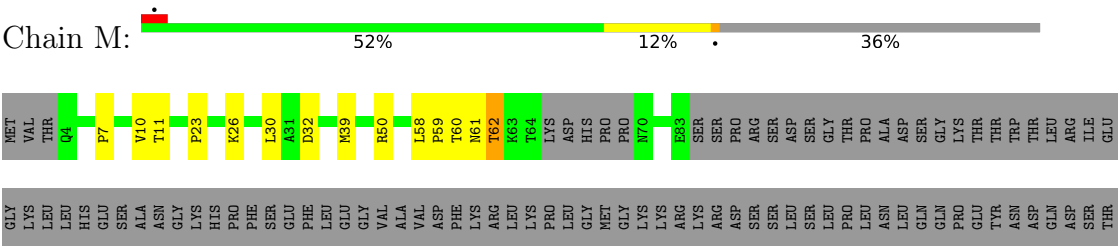




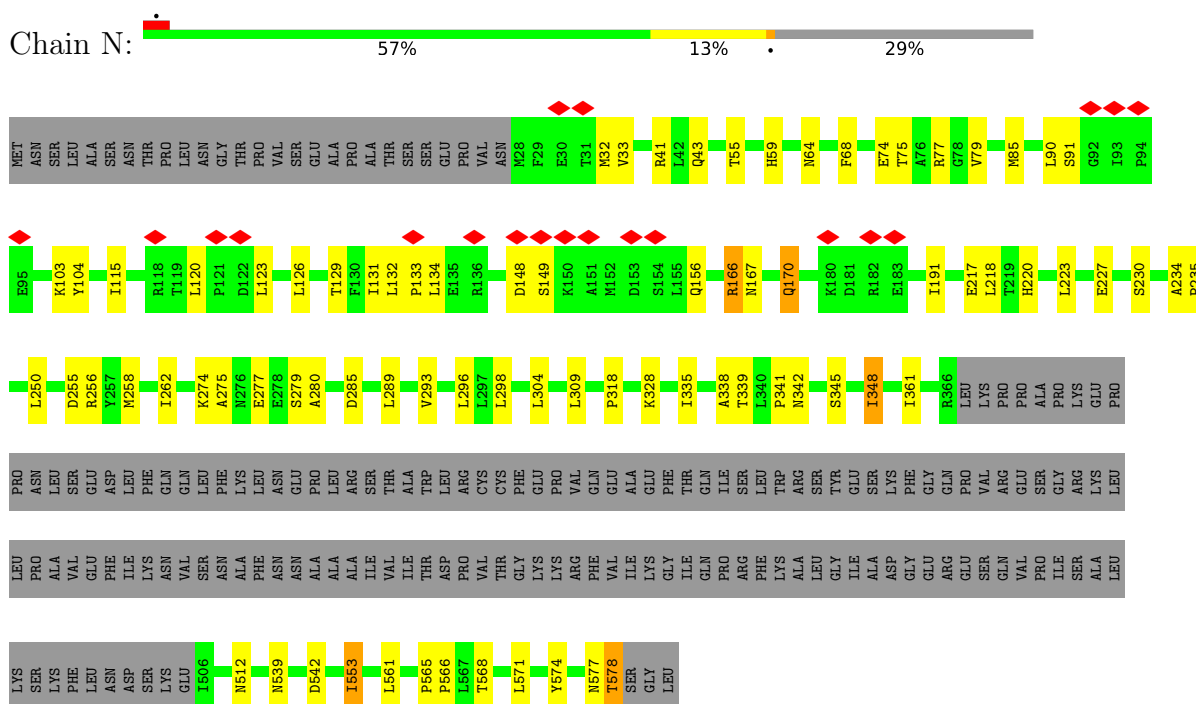
● Molecule 11: Chromatin structure-remodeling complex protein RSC8



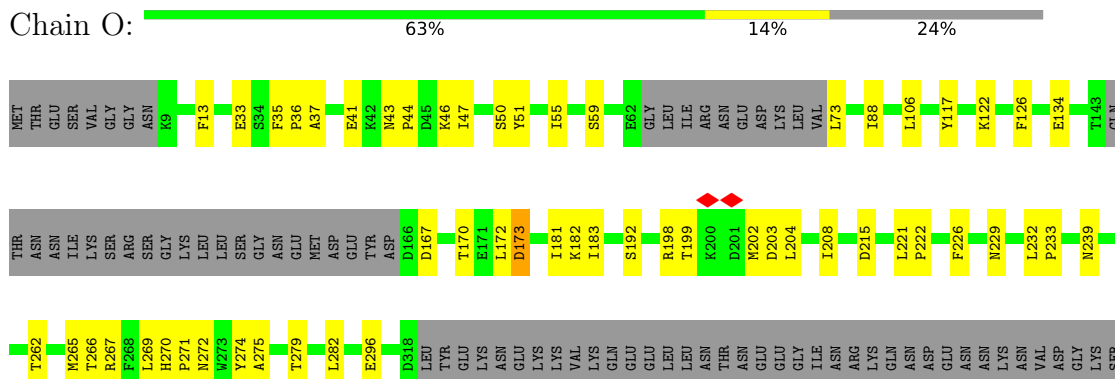
● Molecule 12: Chromatin structure-remodeling complex protein RSC6



- Molecule 13: Chromatin structure-remodeling complex subunit RSC9



- Molecule 14: Chromatin structure-remodeling complex protein RSC58





[illegible]

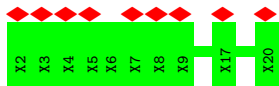
- Molecule 17: Unknown Protein

Chain 2: 93% 7%



- Molecule 18: Unknown Protein

Chain 3:  47% 100%



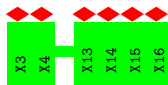
- Molecule 18: Unknown Protein

Chain 4: 95% 5%

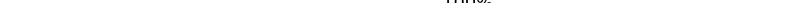


- Molecule 19: Unknown Protein

Chain 5:  43% 100%

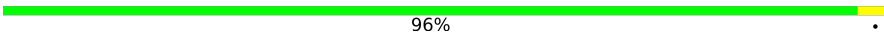


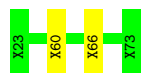
- Molecule 20: Unknown Protein

Chain 6:  100%

There are no outlier residues recorded for this chain.

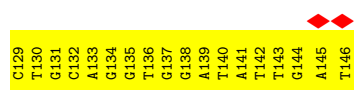
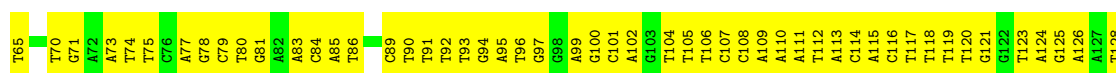
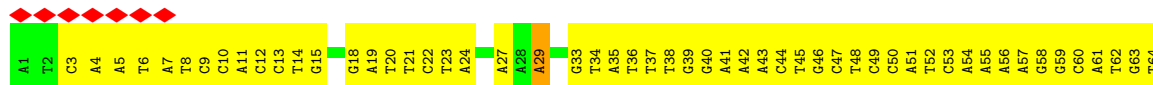
- Molecule 21: Unknown Protein

Chain 7:  96%



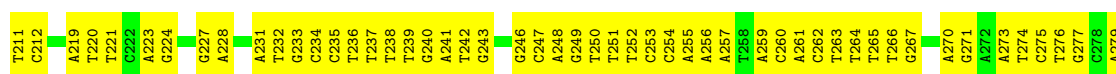
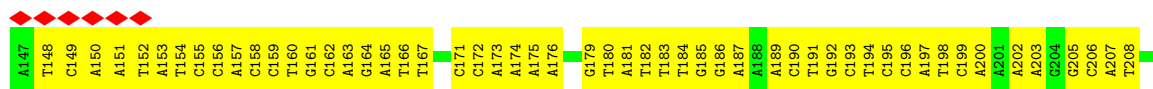
- Molecule 22: DNA (146-MER)

Chain i:  6% 16% 84%



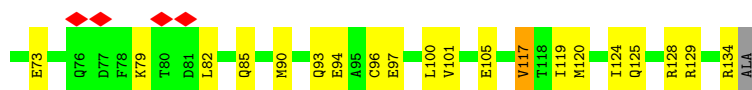
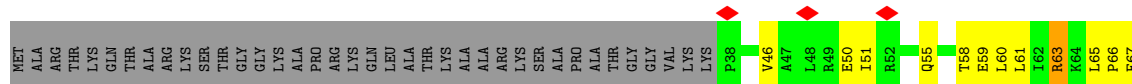
- Molecule 22: DNA (146-MER)

Chain j:  10% 20% 80%



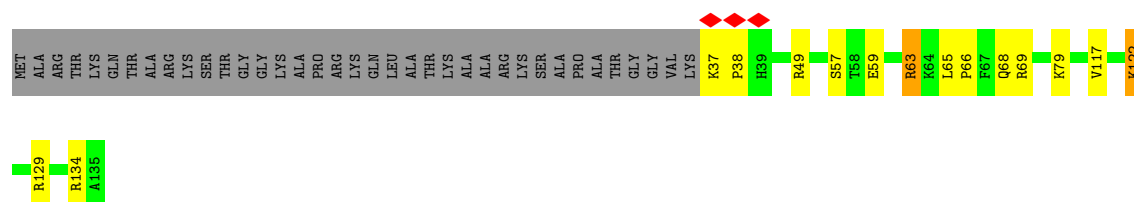
- Molecule 23: Histone H3.1

Chain a:  5% 48% 22% 29%

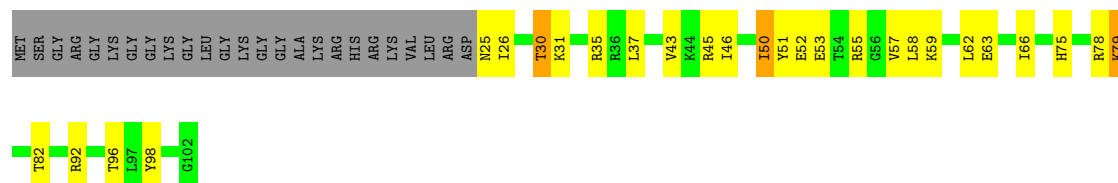


- Molecule 23: Histone H3.1

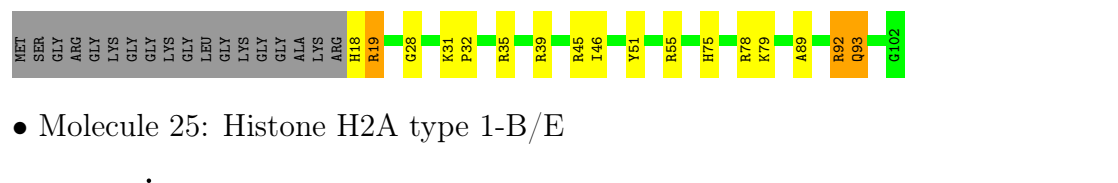
Chain e:  62% 10% 27%



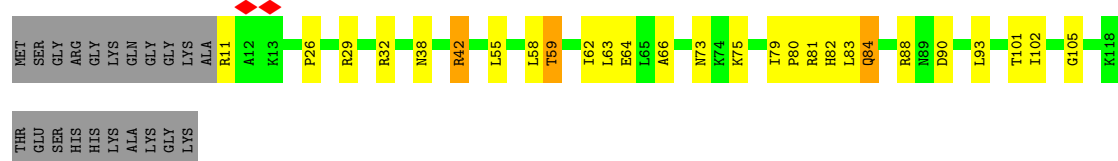
- Molecule 24: Histone H4



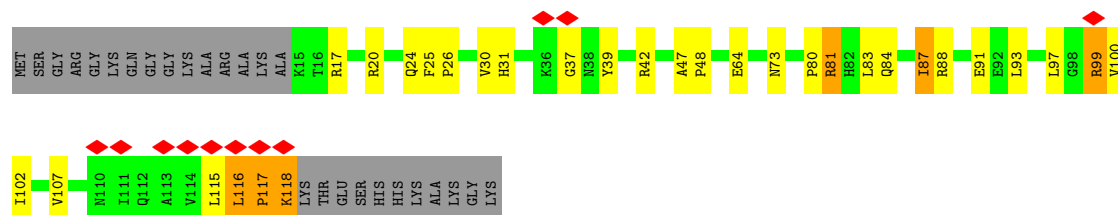
- Molecule 24: Histone H4



- Molecule 25: Histone H2A type 1-B/E

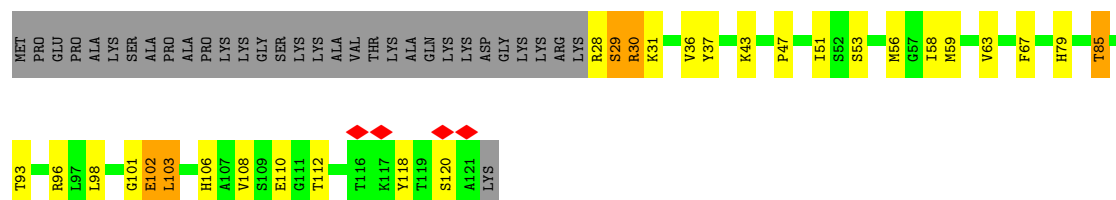


- Molecule 25: Histone H2A type 1-B/E



- Molecule 26: Histone H2B type 1-K





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	13337	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.110	Depositor
Minimum map value	-0.064	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.03	Depositor
Map size ($\text{\AA}$)	437.76, 437.76, 437.76	wwPDB
Map dimensions	128, 128, 128	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	3.42, 3.42, 3.42	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

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	A	0.56	1/3303 (0.0%)	0.90	6/4465 (0.1%)
2	R	0.44	2/2697 (0.1%)	0.67	7/3616 (0.2%)
3	B	0.58	0/3269	0.88	2/4432 (0.0%)
4	P	0.46	0/501	0.82	0/669
5	C	0.17	0/495	0.27	0/662
6	D	0.14	0/786	0.25	0/1062
7	E	0.17	0/997	0.31	0/1356
8	F	0.18	0/551	0.27	0/748
9	G	0.14	0/431	0.24	0/584
10	H	0.18	0/1108	0.35	0/1497
11	I	0.22	0/2474	0.31	0/3343
11	J	0.21	0/926	0.31	0/1233
11	K	0.17	0/879	0.25	0/1172
11	L	0.18	0/2502	0.29	0/3376
12	M	0.18	0/2515	0.29	0/3423
13	N	0.21	0/3334	0.34	0/4515
14	O	0.19	0/3216	0.32	0/4358
15	Q	0.18	0/2181	0.36	0/2964
16	S	0.10	0/281	0.17	0/378
22	i	0.30	0/3354	0.76	1/5175 (0.0%)
22	j	0.30	0/3354	0.76	0/5175
23	a	0.47	0/813	0.89	1/1090 (0.1%)
23	e	0.55	0/828	0.86	1/1109 (0.1%)
24	b	0.49	0/626	0.99	4/837 (0.5%)
24	f	0.58	0/691	0.94	2/923 (0.2%)
25	c	0.51	0/845	0.91	1/1139 (0.1%)
25	g	0.48	0/815	0.99	8/1100 (0.7%)
26	d	0.51	0/765	0.94	2/1025 (0.2%)
26	h	0.51	0/746	0.87	0/1003
All	All	0.36	3/45283 (0.0%)	0.63	35/62429 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	R	328	LYS	C-O	9.02	1.34	1.24
2	R	333	ILE	C-O	8.93	1.34	1.24
1	A	380	SER	C-N	5.22	1.40	1.34

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	R	333	ILE	N-CA-C	10.80	121.63	110.62
2	R	328	LYS	N-CA-C	9.98	122.16	111.28
2	R	333	ILE	CA-C-O	9.85	131.19	120.95
2	R	328	LYS	CA-C-O	9.68	130.81	120.55
24	b	50	ILE	N-CA-C	7.14	117.90	110.62

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	A	3227	0	3251	154	0
2	R	2663	0	2746	164	0
3	B	3198	0	3187	138	0
4	P	490	0	467	19	0
5	C	493	0	507	5	0
6	D	772	0	754	11	0
7	E	978	0	935	27	0
8	F	536	0	533	13	0
9	G	422	0	423	9	0
10	H	1083	0	1062	22	0
11	I	2416	0	2358	40	0
11	J	924	0	976	12	0
11	K	878	0	930	12	0
11	L	2445	0	2402	49	0
12	M	2474	0	2465	48	0
13	N	3275	0	3373	50	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	O	3145	0	3168	53	0
15	Q	2137	0	2069	44	0
16	S	278	0	287	6	0
17	2	140	0	34	2	0
18	3	95	0	21	0	0
18	4	95	0	21	1	0
19	5	70	0	16	0	0
20	6	75	0	17	0	0
21	7	245	0	63	2	0
22	i	2990	0	1652	217	0
22	j	2990	0	1652	184	0
23	a	801	0	839	39	0
23	e	816	0	856	19	0
24	b	619	0	659	34	0
24	f	683	0	729	22	0
25	c	835	0	897	26	0
25	g	805	0	861	32	0
26	d	754	0	782	39	0
26	h	735	0	756	38	0
27	I	1	0	0	0	0
All	All	44583	0	41748	1250	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 14.

The worst 5 of 1250 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)
2:R:353:PHE:CZ	3:B:447:PHE:CE2	2.05	1.45
2:R:353:PHE:CZ	3:B:447:PHE:HE2	1.34	1.41
2:R:353:PHE:CE1	3:B:447:PHE:HE2	1.47	1.33
2:R:365:GLU:HG2	3:B:415:TYR:CD2	1.65	1.32
2:R:353:PHE:CE2	3:B:447:PHE:CE2	2.21	1.29

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	A	392/477 (82%)	369 (94%)	18 (5%)	5 (1%)	9	42
2	R	319/1359 (24%)	296 (93%)	23 (7%)	0	100	100
3	B	391/467 (84%)	368 (94%)	21 (5%)	2 (0%)	24	63
4	P	46/157 (29%)	43 (94%)	2 (4%)	1 (2%)	5	29
5	C	58/78 (74%)	56 (97%)	2 (3%)	0	100	100
6	D	96/180 (53%)	90 (94%)	6 (6%)	0	100	100
7	E	118/435 (27%)	108 (92%)	10 (8%)	0	100	100
8	F	63/889 (7%)	56 (89%)	7 (11%)	0	100	100
9	G	51/885 (6%)	49 (96%)	2 (4%)	0	100	100
10	H	127/625 (20%)	114 (90%)	10 (8%)	3 (2%)	4	27
11	I	289/557 (52%)	274 (95%)	15 (5%)	0	100	100
11	J	113/557 (20%)	109 (96%)	4 (4%)	0	100	100
11	K	105/557 (19%)	101 (96%)	4 (4%)	0	100	100
11	L	292/557 (52%)	277 (95%)	15 (5%)	0	100	100
12	M	302/483 (62%)	281 (93%)	21 (7%)	0	100	100
13	N	408/581 (70%)	380 (93%)	28 (7%)	0	100	100
14	O	376/502 (75%)	352 (94%)	24 (6%)	0	100	100
15	Q	258/426 (61%)	224 (87%)	34 (13%)	0	100	100
16	S	32/883 (4%)	32 (100%)	0	0	100	100
23	a	95/136 (70%)	92 (97%)	3 (3%)	0	100	100
23	e	97/136 (71%)	95 (98%)	2 (2%)	0	100	100
24	b	76/103 (74%)	75 (99%)	1 (1%)	0	100	100
24	f	83/103 (81%)	80 (96%)	3 (4%)	0	100	100
25	c	106/130 (82%)	101 (95%)	5 (5%)	0	100	100
25	g	102/130 (78%)	98 (96%)	3 (3%)	1 (1%)	12	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	d	94/126 (75%)	89 (95%)	4 (4%)	1 (1%)	11	46
26	h	92/126 (73%)	88 (96%)	0	4 (4%)	2	17
All	All	4581/11645 (39%)	4297 (94%)	267 (6%)	17 (0%)	31	67

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	B	48	ASP
10	H	528	ILE
26	h	120	SER
1	A	343	SER
26	d	101	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	357/420 (85%)	331 (93%)	26 (7%)	13	34
2	R	297/1228 (24%)	292 (98%)	5 (2%)	53	69
3	B	363/423 (86%)	344 (95%)	19 (5%)	21	42
4	P	53/140 (38%)	51 (96%)	2 (4%)	29	50
5	C	58/75 (77%)	58 (100%)	0	100	100
6	D	82/151 (54%)	82 (100%)	0	100	100
7	E	113/388 (29%)	105 (93%)	8 (7%)	13	35
8	F	60/810 (7%)	60 (100%)	0	100	100
9	G	48/832 (6%)	47 (98%)	1 (2%)	47	65
10	H	126/578 (22%)	123 (98%)	3 (2%)	43	64
11	I	268/500 (54%)	259 (97%)	9 (3%)	32	54
11	J	111/500 (22%)	110 (99%)	1 (1%)	70	79
11	K	106/500 (21%)	105 (99%)	1 (1%)	70	79
11	L	270/500 (54%)	267 (99%)	3 (1%)	65	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	M	286/435 (66%)	281 (98%)	5 (2%)	53	69
13	N	374/521 (72%)	364 (97%)	10 (3%)	39	61
14	O	358/462 (78%)	351 (98%)	7 (2%)	48	66
15	Q	243/384 (63%)	233 (96%)	10 (4%)	27	49
16	S	33/824 (4%)	32 (97%)	1 (3%)	36	57
23	a	85/111 (77%)	82 (96%)	3 (4%)	32	53
23	e	86/111 (78%)	82 (95%)	4 (5%)	23	45
24	b	63/79 (80%)	63 (100%)	0	100	100
24	f	70/79 (89%)	67 (96%)	3 (4%)	26	47
25	c	85/100 (85%)	80 (94%)	5 (6%)	18	39
25	g	83/100 (83%)	78 (94%)	5 (6%)	17	39
26	d	82/105 (78%)	76 (93%)	6 (7%)	13	34
26	h	80/105 (76%)	77 (96%)	3 (4%)	29	50
All	All	4240/10461 (40%)	4100 (97%)	140 (3%)	34	55

5 of 140 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
25	c	59	THR
26	d	28	ARG
24	f	92	ARG
3	B	422	SER
3	B	347	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 81 such sidechains are listed below:

Mol	Chain	Res	Type
14	O	391	GLN
25	c	112	GLN
15	Q	3	HIS
23	a	113	HIS
25	g	24	GLN

5.3.3 RNA ⓘ

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 1 ligands modelled in this entry, 1 is 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
21	7	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	7	57:UNK	C	60:UNK	N	4.98

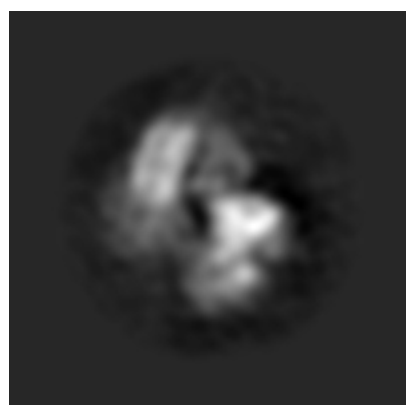
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21114. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

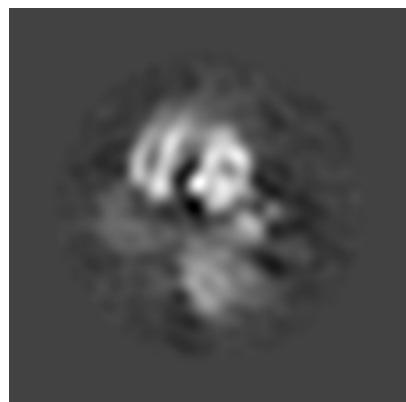


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 64



Y Index: 64



Z Index: 64

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

6.3 Largest variance slices [i](#)

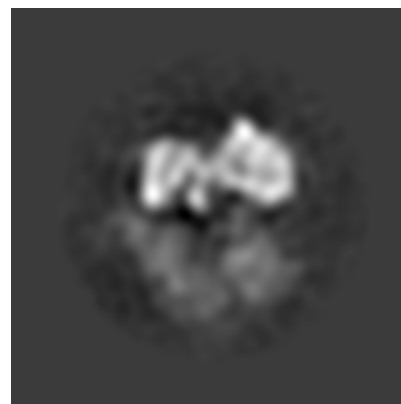
6.3.1 Primary map



X Index: 68



Y Index: 71

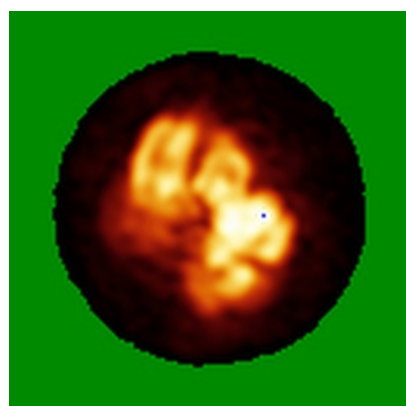


Z Index: 59

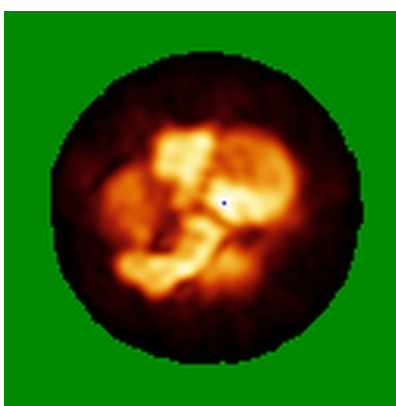
The images above show the largest variance slices of the map in three orthogonal directions.

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

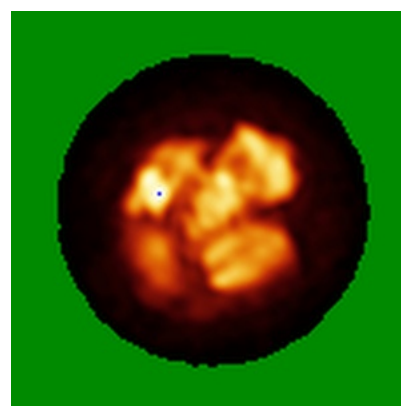
6.4.1 Primary map



X



Y

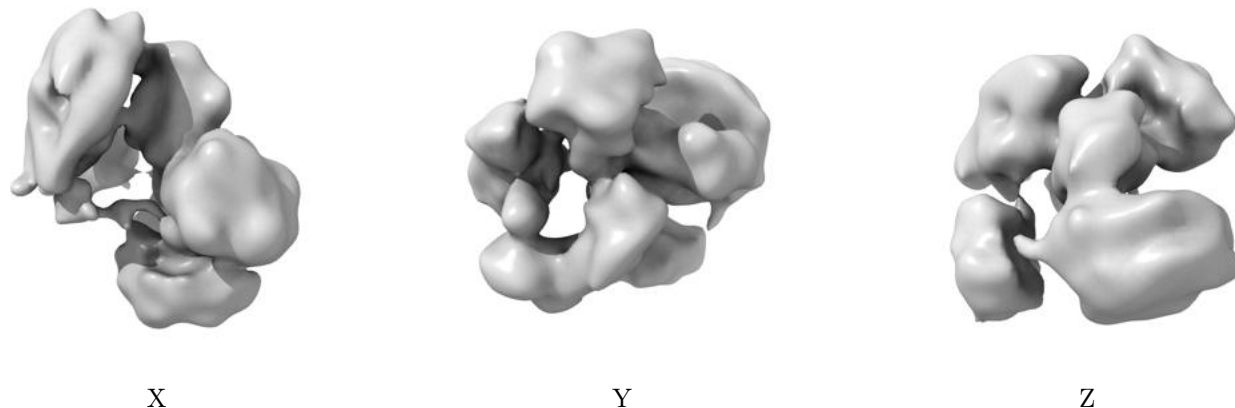


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

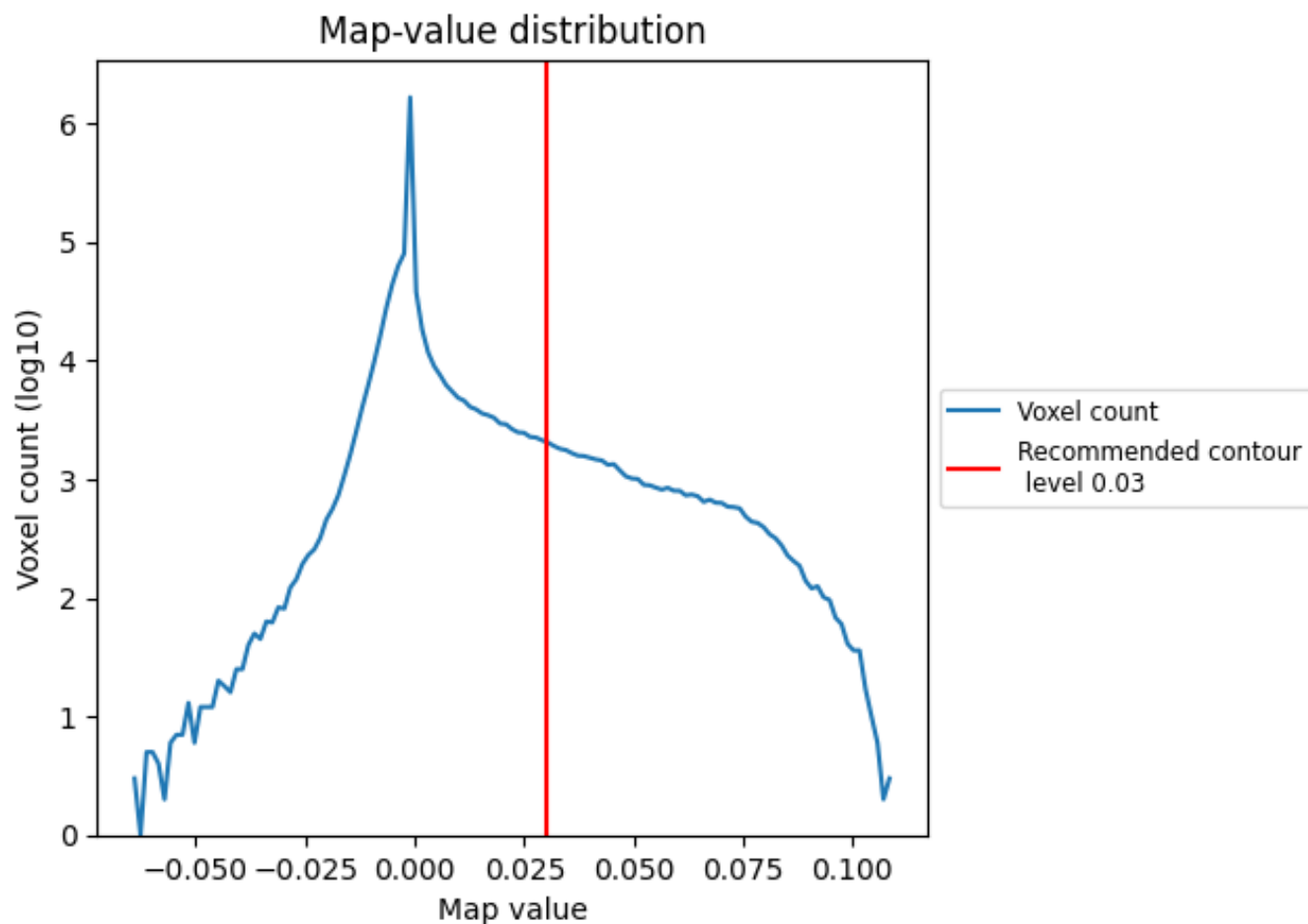
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

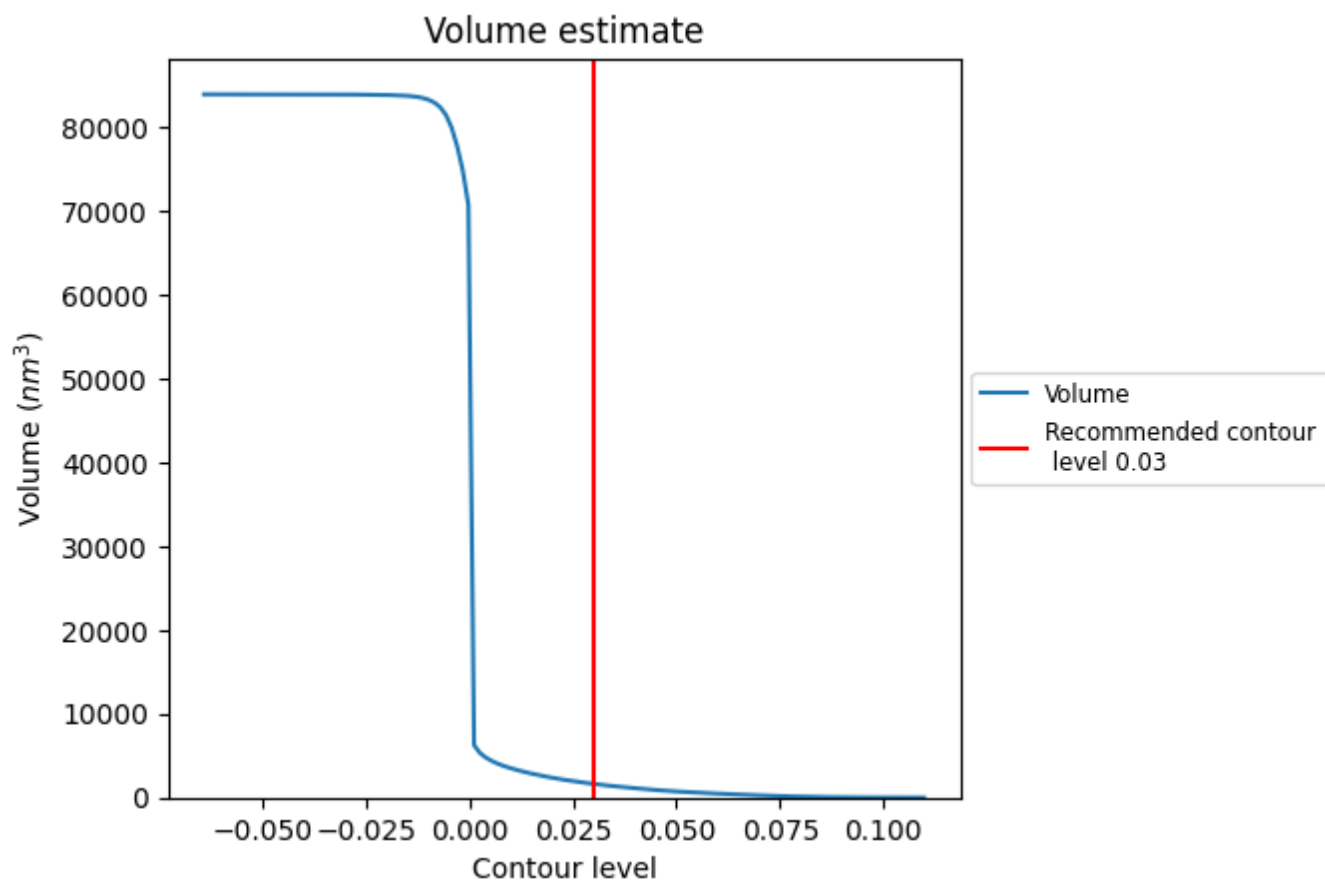
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

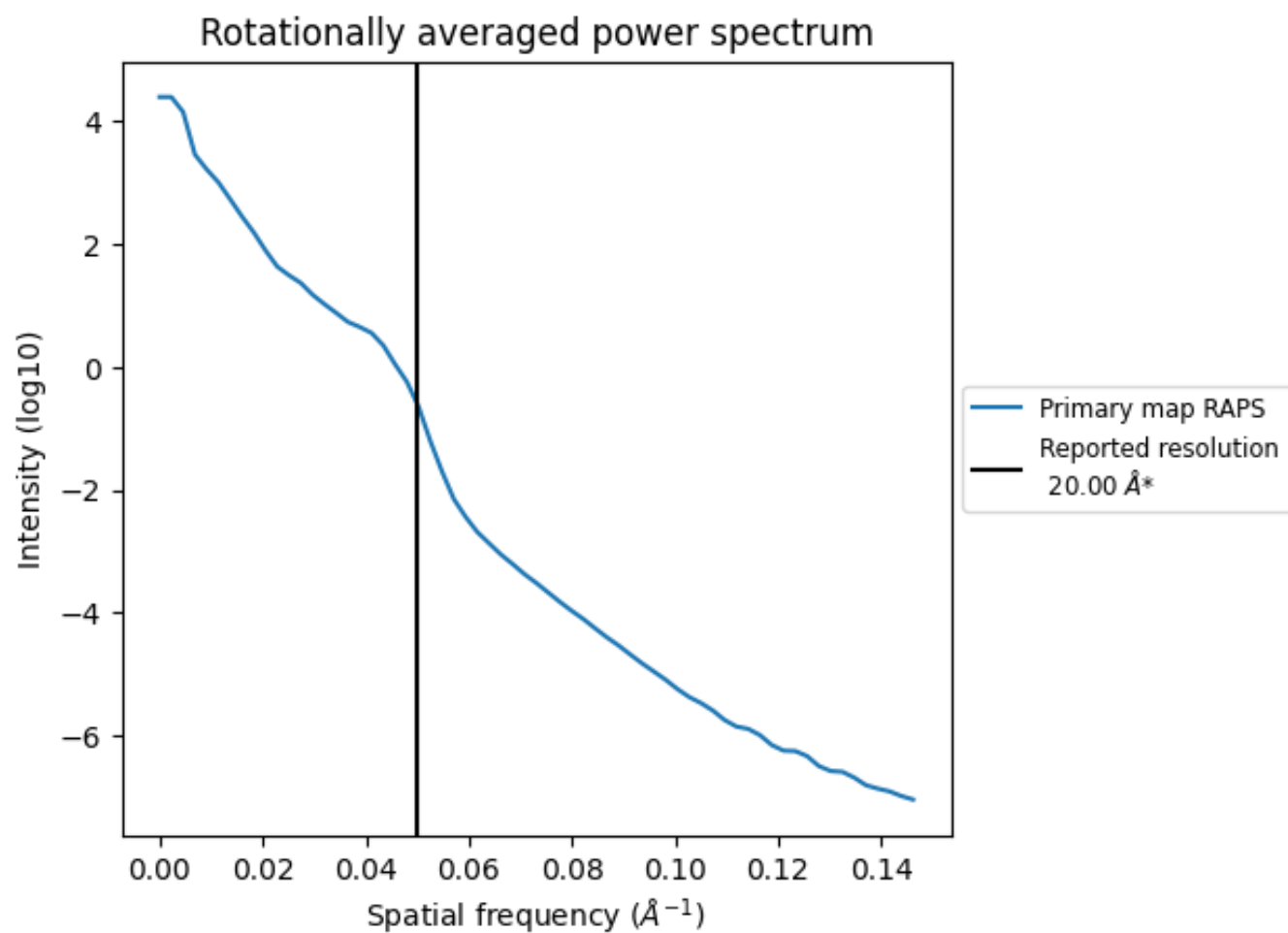
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1633 nm^3 ; this corresponds to an approximate mass of 1475 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.050 Å⁻¹

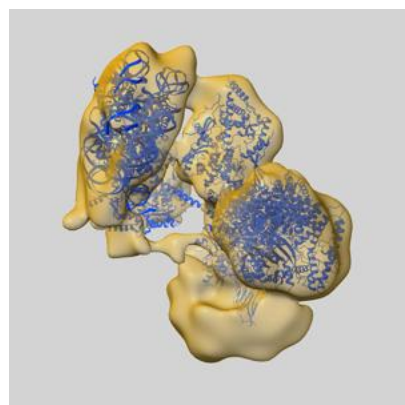
8 Fourier-Shell correlation ⓘ

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

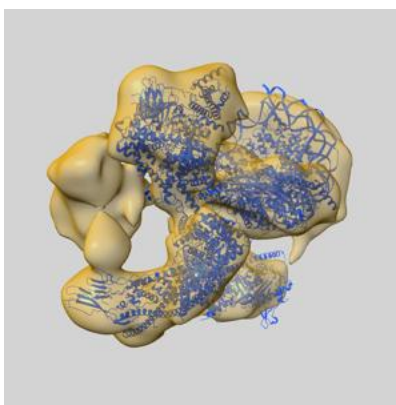
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21114 and PDB model 6V92. Per-residue inclusion information can be found in section [3](#) on page [10](#).

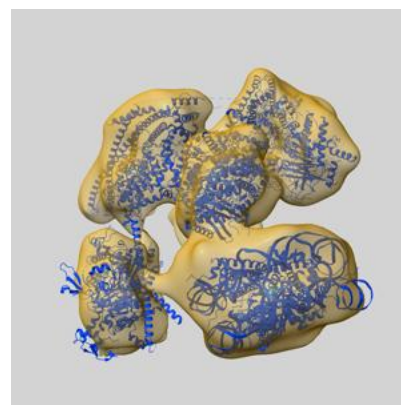
9.1 Map-model overlay [i](#)



X



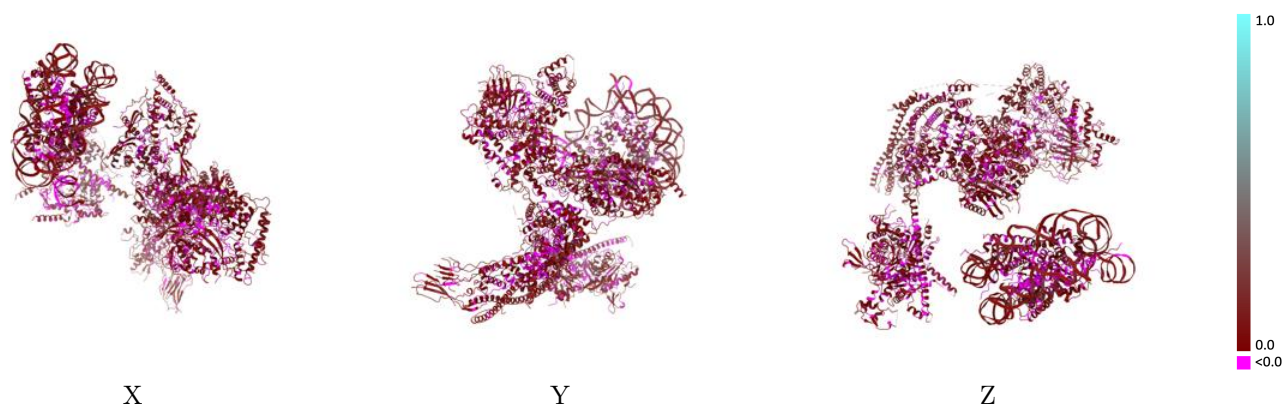
Y



Z

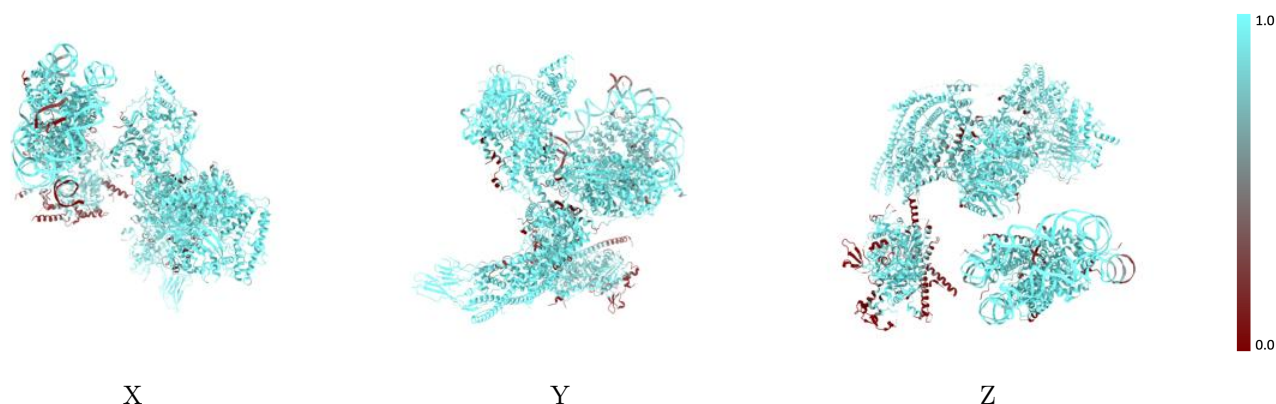
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



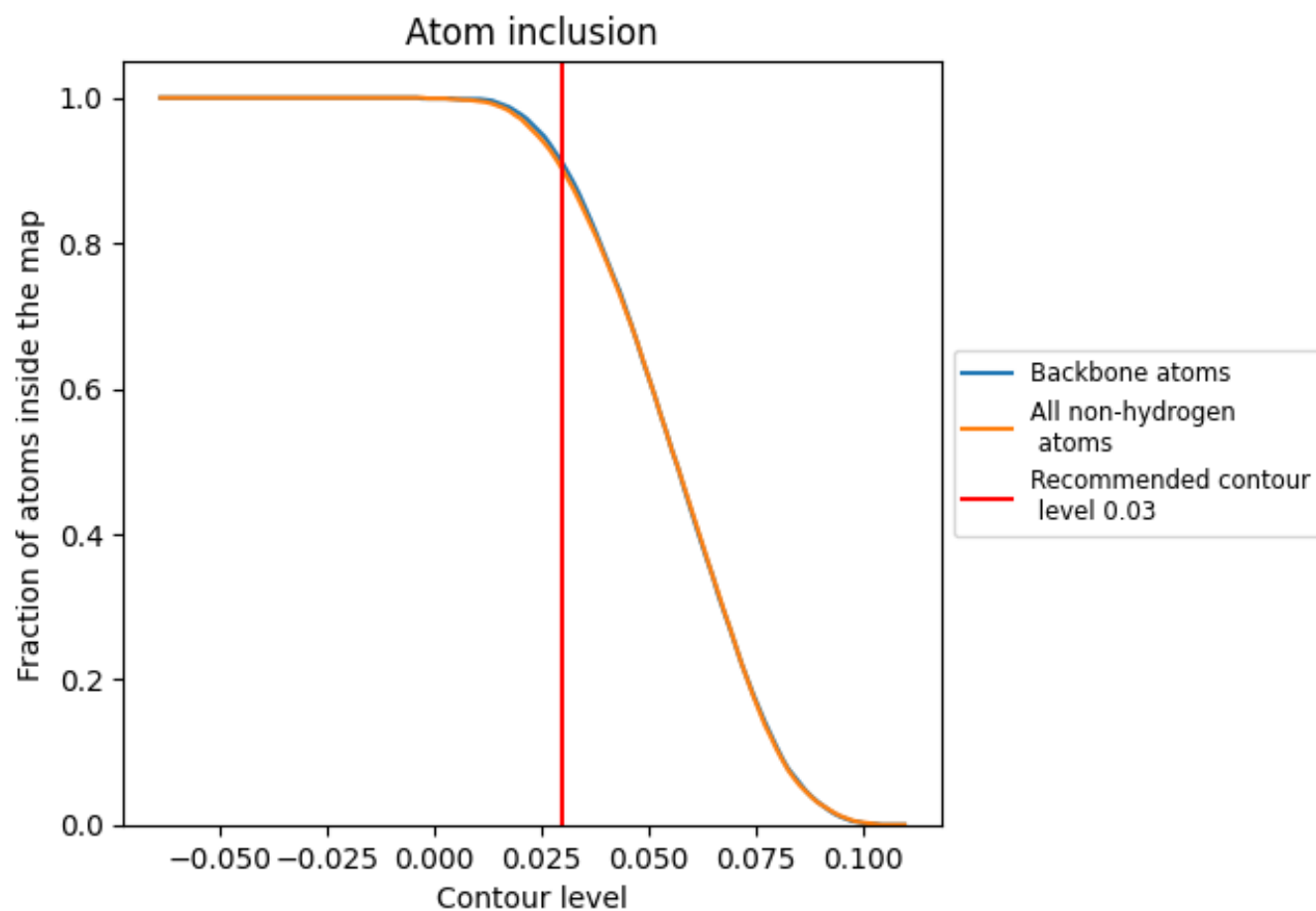
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 90% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9000	 0.0530
2	 1.0000	 0.0480
3	 0.5790	 0.0250
4	 0.9900	 0.0580
5	 0.5710	 0.0050
6	 1.0000	 0.0500
7	 0.9880	 0.0500
A	 0.6960	 0.0330
B	 0.7390	 0.0370
C	 0.9920	 0.0650
D	 0.8760	 0.0380
E	 0.9690	 0.0740
F	 1.0000	 0.0290
G	 0.8230	 0.0470
H	 0.9570	 0.0530
I	 0.9710	 0.0510
J	 0.9720	 0.0800
K	 0.9690	 0.0810
L	 0.9720	 0.0510
M	 0.9430	 0.0480
N	 0.9370	 0.0490
O	 0.9940	 0.0650
P	 0.6980	 0.0590
Q	 0.9560	 0.0660
R	 0.8230	 0.0410
S	 0.7630	 0.0680
a	 0.9360	 0.0280
b	 0.9900	 0.0440
c	 0.9580	 0.0380
d	 0.8560	 0.0200
e	 0.9550	 0.0430
f	 0.9950	 0.0050
g	 0.8830	 0.0110
h	 0.9370	 0.0120
i	 0.8990	 0.0860
j	 0.8970	 0.0930

