



wwPDB EM Validation Summary Report ⓘ

Aug 2, 2026 – 06:50 PM EDT

PDB ID : 9Y3H / pdb_00009y3h
EMDB ID : EMD-72458
Title : Human SRCAP-CFDP1-nucleosome complex in the unwrapping state of the H2A.Z histone exchange reaction
Authors : Louder, R.K.; Park, G.
Deposited on : 2025-09-02
Resolution : 4.50 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:

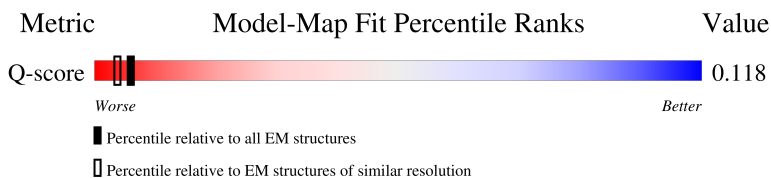
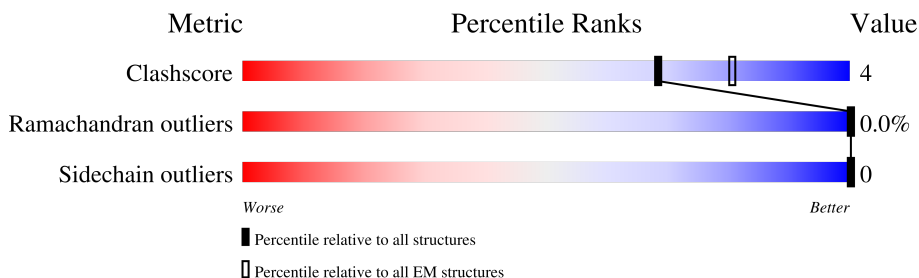
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.50

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 4.50 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.



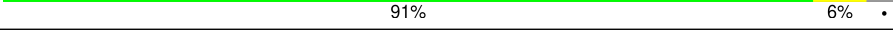
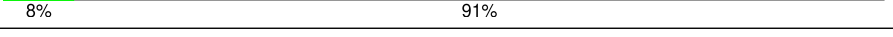
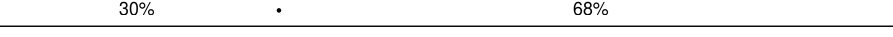
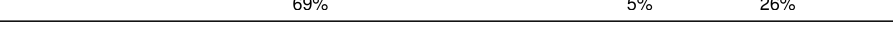
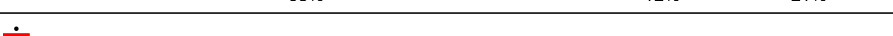
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2937 (4.00 - 5.00)

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	3230	
2	B	364	
3	C	396	
4	D	154	

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Mol	Chain	Length	Quality of chain
5	E	456	
5	G	456	
5	I	456	
6	F	463	
6	H	463	
6	J	463	
7	K	429	
7	M	429	
8	L	375	
9	N	467	
10	P	299	
11	Q	128	
11	S	128	
12	R	125	
12	T	125	
13	U	135	
13	W	135	
14	V	102	
14	X	102	
15	Y	285	
16	Z	285	

2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 55696 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 Helicase SRCAP.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	880	Total	C	N	O	S	0	0
			7255	4612	1329	1274	40		

- Molecule 2 is a protein called Vacuolar protein sorting-associated protein 72 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	166	Total	C	N	O	S	0	0
			1373	860	264	244	5		

- Molecule 3 is a protein called Actin-related protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	396	Total	C	N	O	S	0	0
			3225	2064	528	615	18		

- Molecule 4 is a protein called Zinc finger HIT domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	105	Total	C	N	O	S	0	0
			831	508	164	151	8		

- Molecule 5 is a protein called RuvB-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	433	Total	C	N	O	S	0	0
			3343	2107	574	645	17		
5	G	445	Total	C	N	O	S	0	0
			3429	2159	588	664	18		
5	I	436	Total	C	N	O	S	0	0
			3364	2119	577	651	17		

- Molecule 6 is a protein called RuvB-like 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	438	Total	C	N	O	S	0	0
			3395	2121	596	662	16		
6	H	432	Total	C	N	O	S	0	0
			3361	2101	590	654	16		
6	J	418	Total	C	N	O	S	0	0
			3254	2039	568	632	15		

- Molecule 7 is a protein called Actin-like protein 6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	403	Total	C	N	O	S	0	0
			3143	1987	538	594	24		
7	M	398	Total	C	N	O	S	0	0
			3105	1964	528	589	24		

- Molecule 8 is a protein called Actin, cytoplasmic 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L	361	Total	C	N	O	S	0	0
			2822	1791	473	538	20		

- Molecule 9 is a protein called DNA methyltransferase 1-associated protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	N	41	Total	C	N	O	S	0	0
			360	237	68	53	2		

- Molecule 10 is a protein called Craniofacial development protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	P	97	Total	C	N	O	S	0	0
			793	495	145	150	3		

- Molecule 11 is a protein called Histone H2A type 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Q	96	Total	C	N	O		0	0
			742	465	147	130			
11	S	104	Total	C	N	O		0	0
			800	504	156	140			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	99	ARG	GLY	conflict	UNP P06897
Q	123	SER	-	expression tag	UNP P06897
Q	124	LYS	-	expression tag	UNP P06897
Q	125	SER	-	expression tag	UNP P06897
Q	126	LYS	-	expression tag	UNP P06897
Q	127	SER	-	expression tag	UNP P06897
Q	128	LYS	-	expression tag	UNP P06897
S	99	ARG	GLY	conflict	UNP P06897
S	123	SER	-	expression tag	UNP P06897
S	124	LYS	-	expression tag	UNP P06897
S	125	SER	-	expression tag	UNP P06897
S	126	LYS	-	expression tag	UNP P06897
S	127	SER	-	expression tag	UNP P06897
S	128	LYS	-	expression tag	UNP P06897

- Molecule 12 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	R	92	Total	C	N	O	S	0	0
			719	453	129	135	2		
12	T	95	Total	C	N	O	S	0	0
			744	469	134	139	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	32	THR	SER	conflict	UNP P02281
T	32	THR	SER	conflict	UNP P02281

- Molecule 13 is a protein called Histone H3.2.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	U	90	Total	C	N	O	S	0	0
			740	467	140	130	3		
13	W	96	Total	C	N	O	S	0	0
			795	501	154	137	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	102	ALA	GLY	variant	UNP P84233
W	102	ALA	GLY	variant	UNP P84233

- Molecule 14 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	V	79	Total	C	N	O	S	0	0
			626	395	121	109	1		
14	X	81	Total	C	N	O	S	0	0
			645	407	126	111	1		

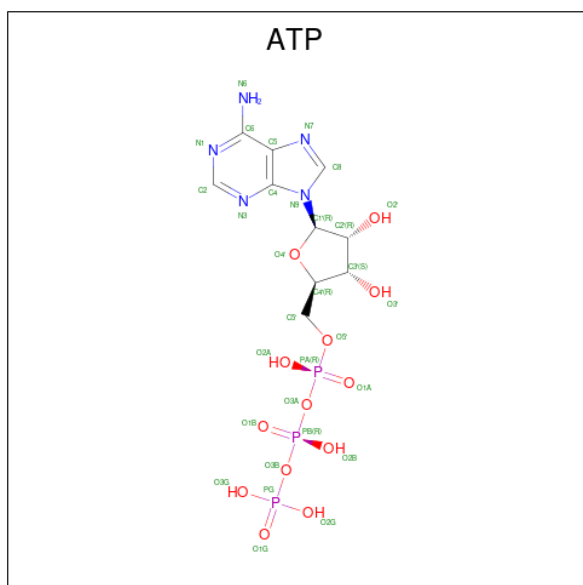
- Molecule 15 is a DNA chain called DNA (285-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Y	161	Total	C	N	O	P	0	0
			3290	1560	600	969	161		

- Molecule 16 is a DNA chain called DNA (285-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Z	161	Total	C	N	O	P	0	0
			3311	1566	621	963	161		

- Molecule 17 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



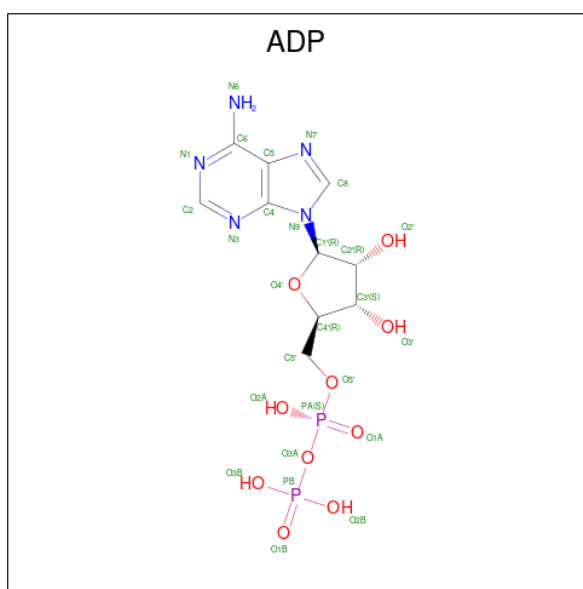
- Molecule 18 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
18	C	1	Total	Mg	0
			1	1	
18	F	1	Total	Mg	0
			1	1	
18	H	1	Total	Mg	0
			1	1	
18	J	1	Total	Mg	0
			1	1	
18	K	1	Total	Mg	0
			1	1	

- Molecule 19 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
19	D	2	Total	Zn	0
			2	2	

- Molecule 20 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



Mol	Chain	Residues	Atoms					AltConf
20	E	1	Total	C	N	O	P	0
			27	10	5	10	2	
20	F	1	Total	C	N	O	P	0
			27	10	5	10	2	
20	G	1	Total	C	N	O	P	0
			27	10	5	10	2	

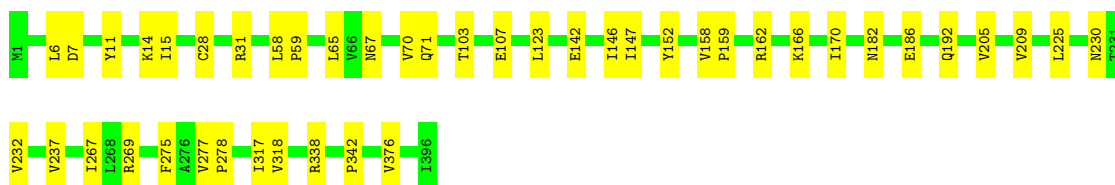
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Mol	Chain	Residues	Atoms					AltConf
20	H	1	Total	C	N	O	P	0
			27	10	5	10	2	
20	I	1	Total	C	N	O	P	0
			27	10	5	10	2	
20	J	1	Total	C	N	O	P	0
			27	10	5	10	2	

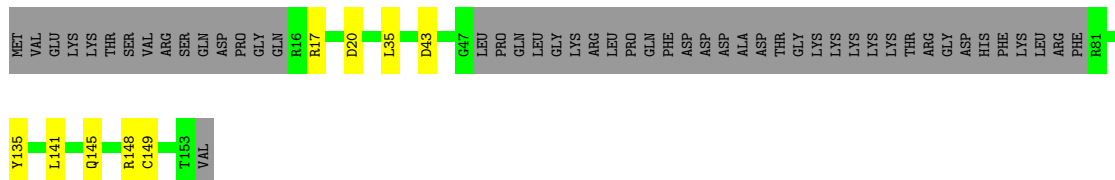






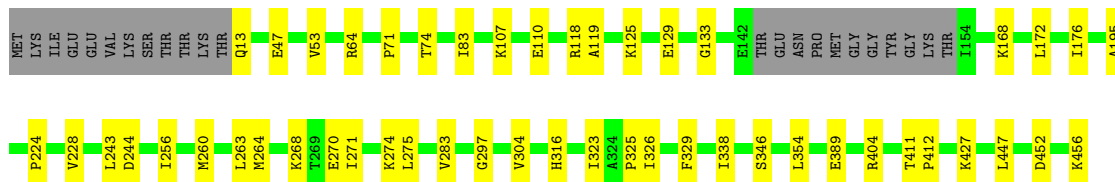
- Molecule 4: Zinc finger HIT domain-containing protein 1

Chain D: 62% 6% 32%



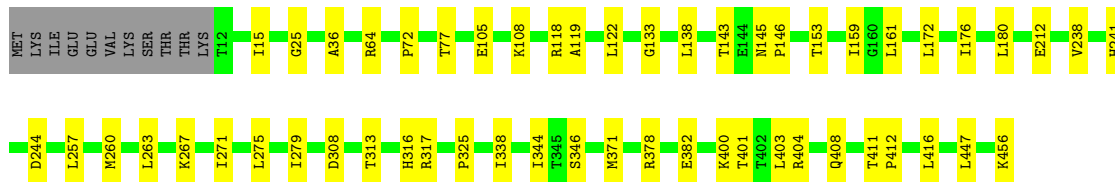
- Molecule 5: RuvB-like 1

Chain E: 84% 11% 5%



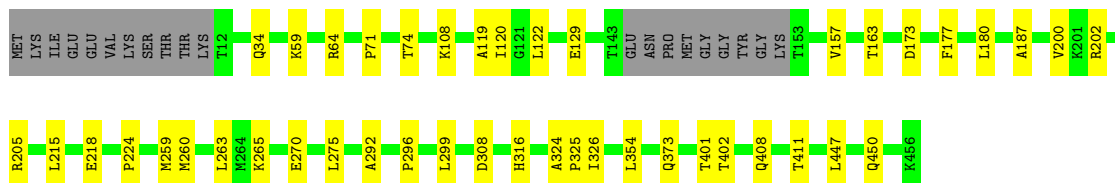
- Molecule 5: RuvB-like 1

Chain G: 86% 12% 2%



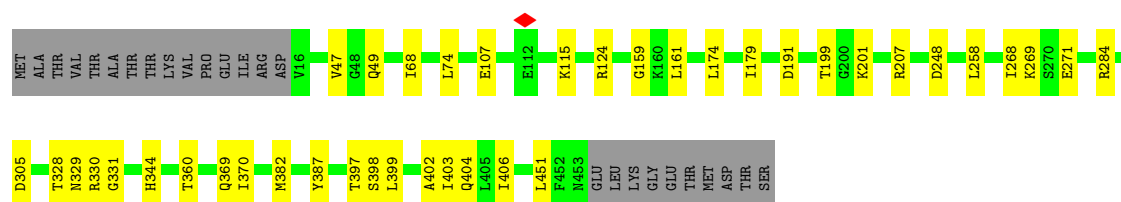
- Molecule 5: RuvB-like 1

Chain I: 86% 10% 4%



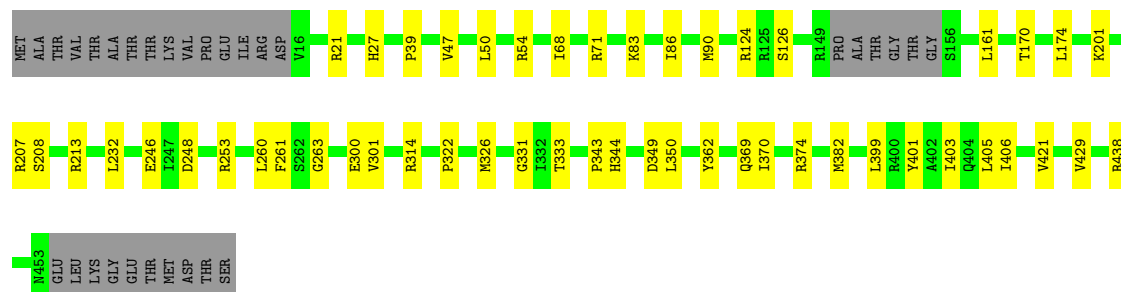
- Molecule 6: RuvB-like 2

Chain F: 86% 9% 5%



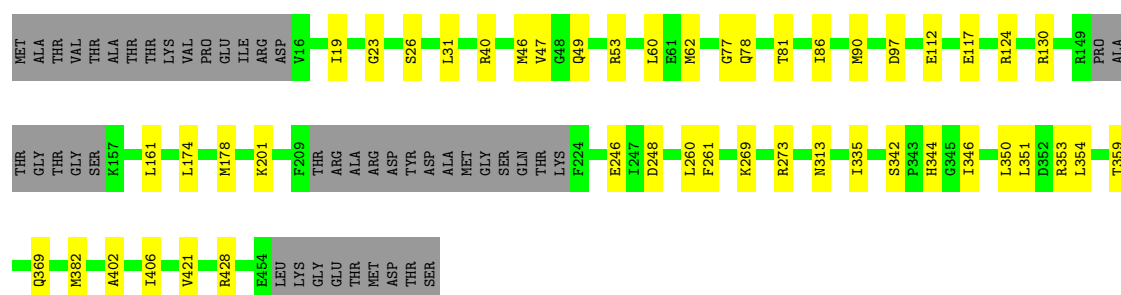
- Molecule 6: RuvB-like 2

Chain H: 82% 11% 7%



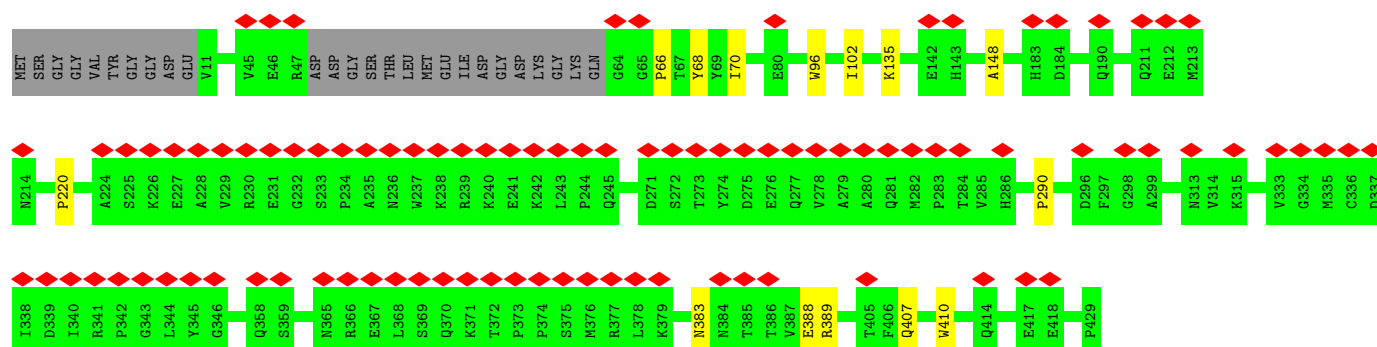
- Molecule 6: RuvB-like 2

Chain J: 80% 10% 10%

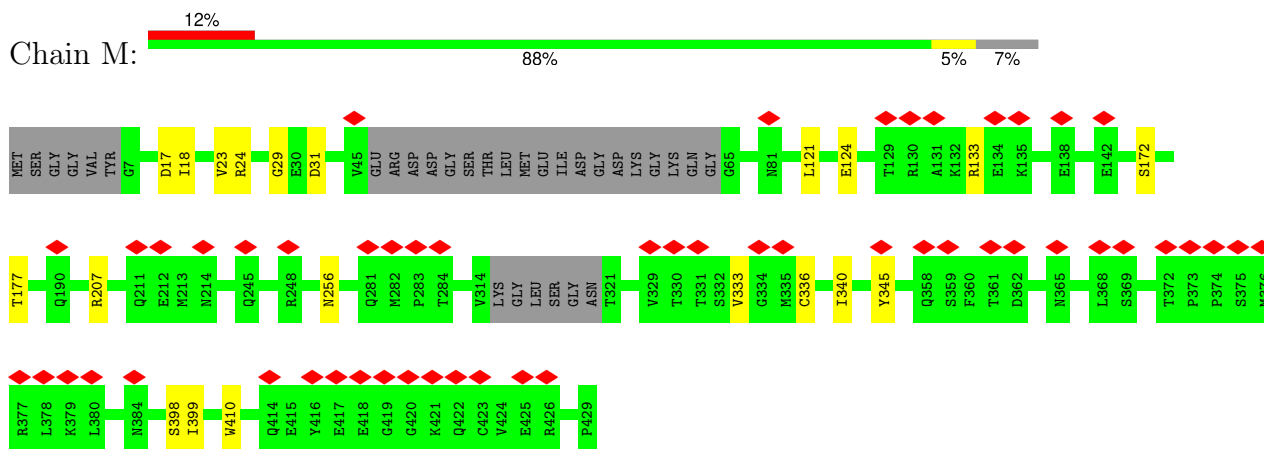


- Molecule 7: Actin-like protein 6A

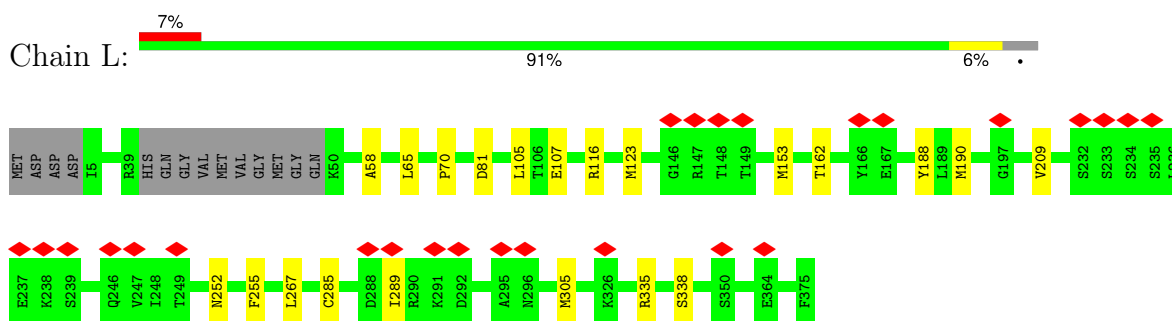
Chain K: 22% 91% 6%



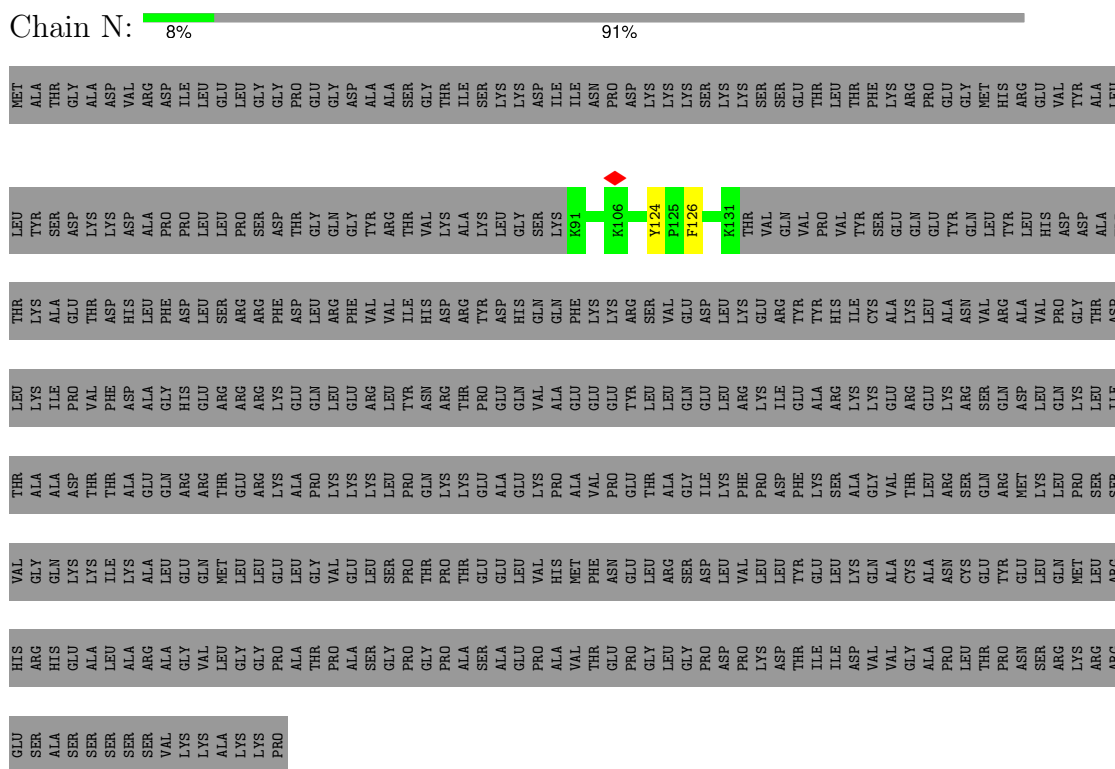
- Molecule 7: Actin-like protein 6A



- Molecule 8: Actin, cytoplasmic 1

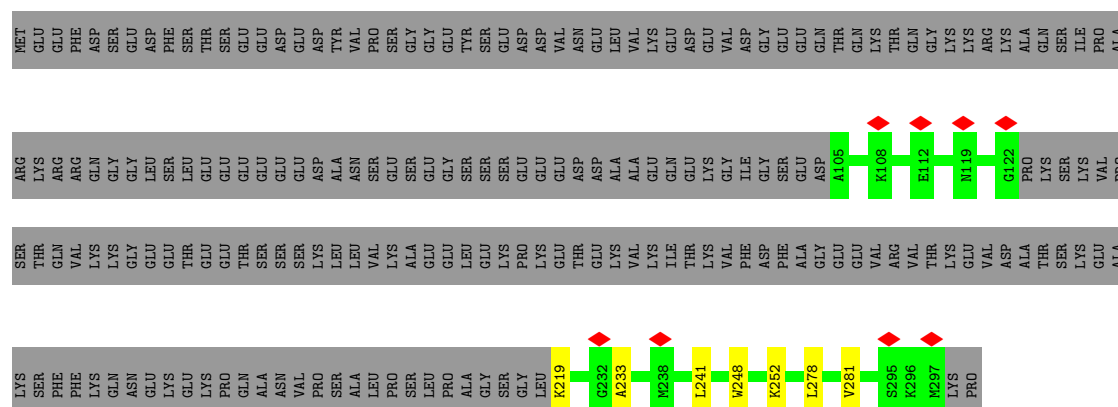


- Molecule 9: DNA methyltransferase 1-associated protein 1



- Molecule 10: Craniofacial development protein 1

Chain P:  30% 68%



- Molecule 11: Histone H2A type 1

Chain Q:  66% 9% 25%



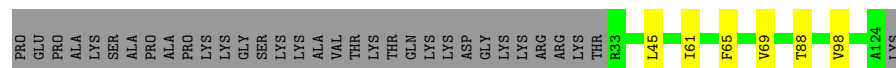
- Molecule 11: Histone H2A type 1

Chain S:  75% 6% 19%



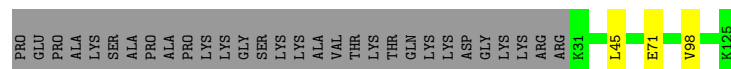
- Molecule 12: Histone H2B 1.1

Chain R:  69% 5% 26%



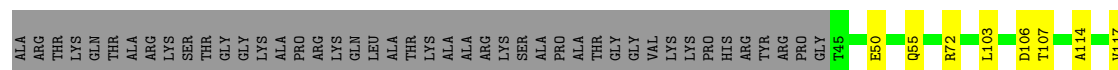
- Molecule 12: Histone H2B 1.1

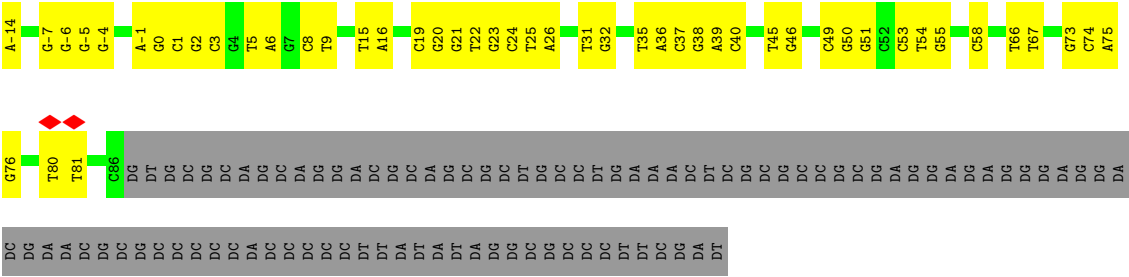
Chain T:  74% 24% 2%



- Molecule 13: Histone H3.2

Chain U:  59% 7% 33%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	22651	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.049	Depositor
Minimum map value	-0.024	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.003	Depositor
Map size (Å)	393.59998, 393.59998, 393.59998	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.025, 1.025, 1.025	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: ADP, MG, ZN, ATP

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	0.12	0/7422	0.32	0/10020
2	B	0.13	0/1404	0.34	0/1892
3	C	0.09	0/3299	0.24	0/4467
4	D	0.07	0/848	0.25	0/1147
5	E	0.09	0/3386	0.25	0/4561
5	G	0.07	0/3475	0.22	0/4683
5	I	0.07	0/3407	0.21	0/4591
6	F	0.07	0/3435	0.22	0/4625
6	H	0.07	0/3399	0.22	0/4573
6	J	0.07	0/3290	0.22	0/4426
7	K	0.12	0/3214	0.37	0/4358
7	M	0.12	0/3175	0.37	0/4306
8	L	0.12	0/2883	0.39	0/3905
9	N	0.10	0/376	0.35	0/505
10	P	0.13	0/802	0.43	0/1058
11	Q	0.07	0/751	0.19	0/1013
11	S	0.08	0/810	0.20	0/1095
12	R	0.07	0/730	0.19	0/983
12	T	0.07	0/755	0.19	0/1015
13	U	0.09	0/748	0.22	0/1003
13	W	0.09	0/806	0.23	0/1081
14	V	0.08	0/633	0.20	0/848
14	X	0.11	0/652	0.26	0/873
15	Y	0.22	0/3687	0.55	0/5686
16	Z	0.22	0/3717	0.53	0/5737
All	All	0.12	0/57104	0.33	0/78451

There are no bond length outliers.

There are no bond angle outliers.

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	7255	0	7330	49	0
2	B	1373	0	1394	10	0
3	C	3225	0	3147	25	0
4	D	831	0	798	9	0
5	E	3343	0	3449	39	0
5	G	3429	0	3530	41	0
5	I	3364	0	3470	34	0
6	F	3395	0	3467	27	0
6	H	3361	0	3434	37	0
6	J	3254	0	3329	34	0
7	K	3143	0	3092	8	0
7	M	3105	0	3044	12	0
8	L	2822	0	2798	11	0
9	N	360	0	345	1	0
10	P	793	0	804	5	0
11	Q	742	0	784	9	0
11	S	800	0	851	7	0
12	R	719	0	740	5	0
12	T	744	0	773	3	0
13	U	740	0	781	8	0
13	W	795	0	833	8	0
14	V	626	0	663	5	0
14	X	645	0	687	9	0
15	Y	3290	0	1807	54	0
16	Z	3311	0	1804	49	0
17	C	31	0	12	0	0
17	K	31	0	12	0	0
18	C	1	0	0	0	0
18	F	1	0	0	0	0
18	H	1	0	0	0	0
18	J	1	0	0	0	0
18	K	1	0	0	0	0
19	D	2	0	0	0	0
20	E	27	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	F	27	0	12	0	0
20	G	27	0	12	1	0
20	H	27	0	12	3	0
20	I	27	0	12	0	0
20	J	27	0	12	0	0
All	All	55696	0	53250	408	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 4.

The worst 5 of 408 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)
16:Z:49:DC:H2'	16:Z:50:DG:C8	2.17	0.79
15:Y:27:DG:H2'	15:Y:28:DG:C8	2.19	0.77
5:E:411:THR:HG21	6:F:68:ILE:HG13	1.71	0.71
5:G:263:LEU:O	6:H:253:ARG:NH2	2.25	0.69
5:G:411:THR:HG21	6:H:68:ILE:HG13	1.75	0.69

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	870/3230 (27%)	859 (99%)	11 (1%)	0	100	100
2	B	162/364 (44%)	160 (99%)	2 (1%)	0	100	100
3	C	394/396 (100%)	379 (96%)	15 (4%)	0	100	100
4	D	101/154 (66%)	99 (98%)	2 (2%)	0	100	100
5	E	429/456 (94%)	424 (99%)	5 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	G	443/456 (97%)	440 (99%)	3 (1%)	0	100	100
5	I	432/456 (95%)	424 (98%)	8 (2%)	0	100	100
6	F	436/463 (94%)	429 (98%)	7 (2%)	0	100	100
6	H	428/463 (92%)	419 (98%)	9 (2%)	0	100	100
6	J	412/463 (89%)	404 (98%)	8 (2%)	0	100	100
7	K	399/429 (93%)	393 (98%)	6 (2%)	0	100	100
7	M	392/429 (91%)	388 (99%)	4 (1%)	0	100	100
8	L	357/375 (95%)	351 (98%)	6 (2%)	0	100	100
9	N	39/467 (8%)	38 (97%)	1 (3%)	0	100	100
10	P	93/299 (31%)	90 (97%)	2 (2%)	1 (1%)	11	45
11	Q	94/128 (73%)	91 (97%)	3 (3%)	0	100	100
11	S	102/128 (80%)	101 (99%)	1 (1%)	0	100	100
12	R	90/125 (72%)	88 (98%)	2 (2%)	0	100	100
12	T	93/125 (74%)	91 (98%)	2 (2%)	0	100	100
13	U	88/135 (65%)	88 (100%)	0	0	100	100
13	W	94/135 (70%)	91 (97%)	3 (3%)	0	100	100
14	V	77/102 (76%)	76 (99%)	1 (1%)	0	100	100
14	X	79/102 (78%)	78 (99%)	1 (1%)	0	100	100
All	All	6104/9880 (62%)	6001 (98%)	102 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	P	233	ALA

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	790/2721 (29%)	790 (100%)	0	100	100
2	B	150/312 (48%)	150 (100%)	0	100	100
3	C	361/361 (100%)	361 (100%)	0	100	100
4	D	89/133 (67%)	89 (100%)	0	100	100
5	E	367/387 (95%)	367 (100%)	0	100	100
5	G	376/387 (97%)	376 (100%)	0	100	100
5	I	370/387 (96%)	370 (100%)	0	100	100
6	F	368/390 (94%)	368 (100%)	0	100	100
6	H	365/390 (94%)	365 (100%)	0	100	100
6	J	354/390 (91%)	354 (100%)	0	100	100
7	K	345/364 (95%)	345 (100%)	0	100	100
7	M	341/364 (94%)	341 (100%)	0	100	100
8	L	307/318 (96%)	307 (100%)	0	100	100
9	N	34/400 (8%)	34 (100%)	0	100	100
10	P	84/261 (32%)	84 (100%)	0	100	100
11	Q	75/101 (74%)	75 (100%)	0	100	100
11	S	82/101 (81%)	82 (100%)	0	100	100
12	R	78/105 (74%)	78 (100%)	0	100	100
12	T	81/105 (77%)	81 (100%)	0	100	100
13	U	79/110 (72%)	79 (100%)	0	100	100
13	W	84/110 (76%)	84 (100%)	0	100	100
14	V	64/78 (82%)	64 (100%)	0	100	100
14	X	66/78 (85%)	66 (100%)	0	100	100
All	All	5310/8353 (64%)	5310 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
8	L	12	ASN
13	U	68	GLN
7	M	105	HIS
12	R	47	GLN
14	V	93	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 7 are monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
20	ADP	H	501	18	28,29,29	1.41	4 (14%)	43,45,45	1.79	9 (20%)
17	ATP	C	401	18	32,33,33	0.28	0	48,52,52	0.44	0
20	ADP	J	501	18	28,29,29	1.42	4 (14%)	43,45,45	1.77	9 (20%)
17	ATP	K	501	18	32,33,33	0.30	0	48,52,52	0.45	0
20	ADP	E	501	-	28,29,29	1.42	4 (14%)	43,45,45	1.76	8 (18%)
20	ADP	F	501	18	28,29,29	1.42	4 (14%)	43,45,45	1.76	8 (18%)
20	ADP	G	501	-	28,29,29	1.42	4 (14%)	43,45,45	1.77	8 (18%)
20	ADP	I	501	-	28,29,29	1.42	4 (14%)	43,45,45	1.77	8 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
20	ADP	H	501	18	-	0/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
17	ATP	C	401	18	-	0/22/38/38	0/3/3/3
20	ADP	J	501	18	-	7/16/32/32	0/3/3/3
17	ATP	K	501	18	-	2/22/38/38	0/3/3/3
20	ADP	E	501	-	-	3/16/32/32	0/3/3/3
20	ADP	F	501	18	-	4/16/32/32	0/3/3/3
20	ADP	G	501	-	-	5/16/32/32	0/3/3/3
20	ADP	I	501	-	-	3/16/32/32	0/3/3/3

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	E	501	ADP	C5-C4	4.75	1.47	1.39
20	I	501	ADP	C5-C4	4.73	1.47	1.39
20	F	501	ADP	C5-C4	4.72	1.47	1.39
20	G	501	ADP	C5-C4	4.71	1.47	1.39
20	J	501	ADP	C5-C4	4.70	1.47	1.39

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	H	501	ADP	C5-C4-N3	-5.92	118.56	126.72
20	I	501	ADP	C5-C4-N3	-5.87	118.64	126.72
20	E	501	ADP	C5-C4-N3	-5.87	118.64	126.72
20	G	501	ADP	C5-C4-N3	-5.86	118.64	126.72
20	J	501	ADP	C5-C4-N3	-5.85	118.66	126.72

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

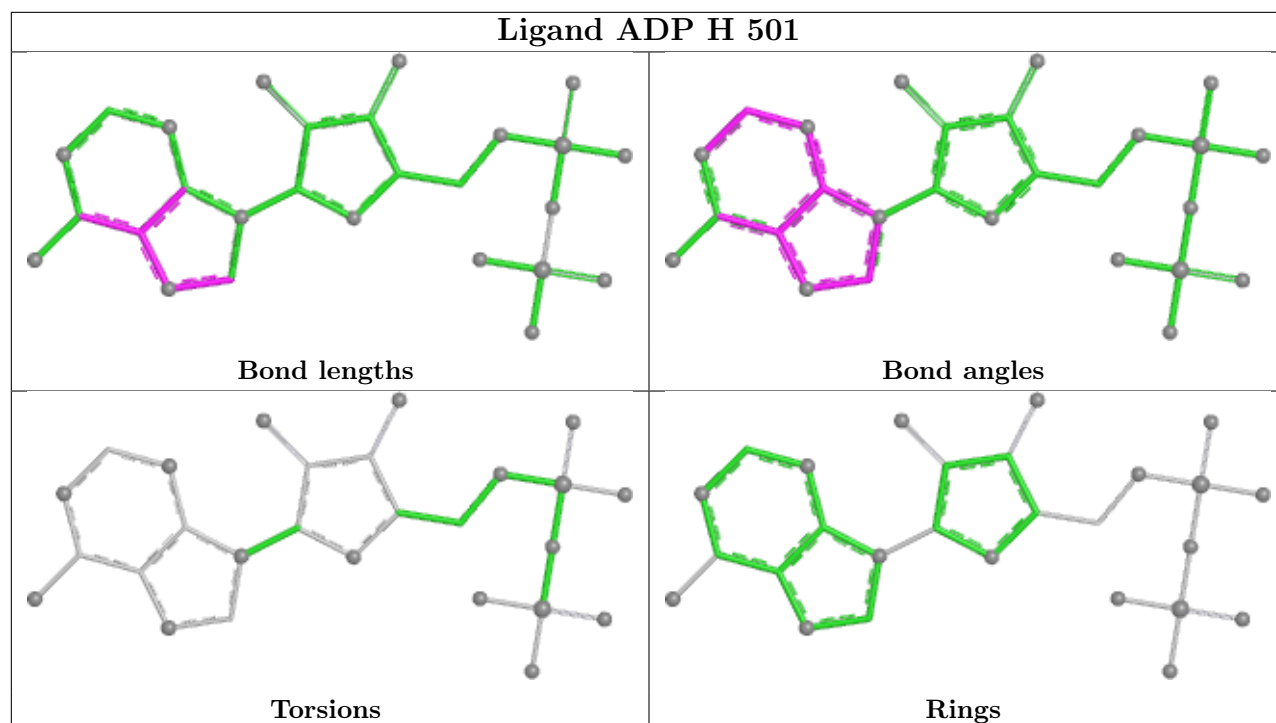
Mol	Chain	Res	Type	Atoms
17	K	501	ATP	PB-O3B-PG-O2G
17	K	501	ATP	PB-O3B-PG-O3G
20	F	501	ADP	PA-O3A-PB-O2B
20	G	501	ADP	C5'-O5'-PA-O1A
20	G	501	ADP	C5'-O5'-PA-O3A

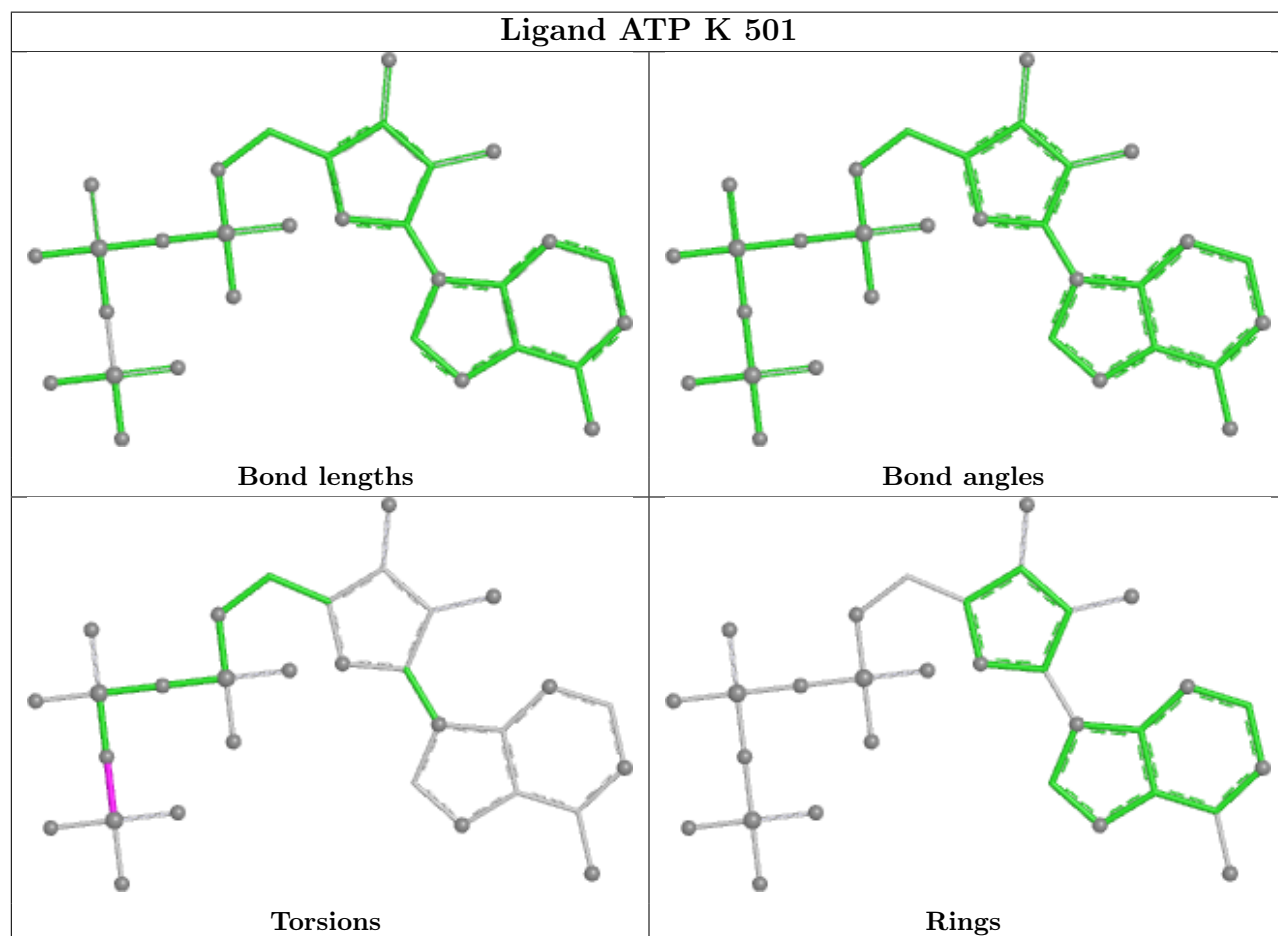
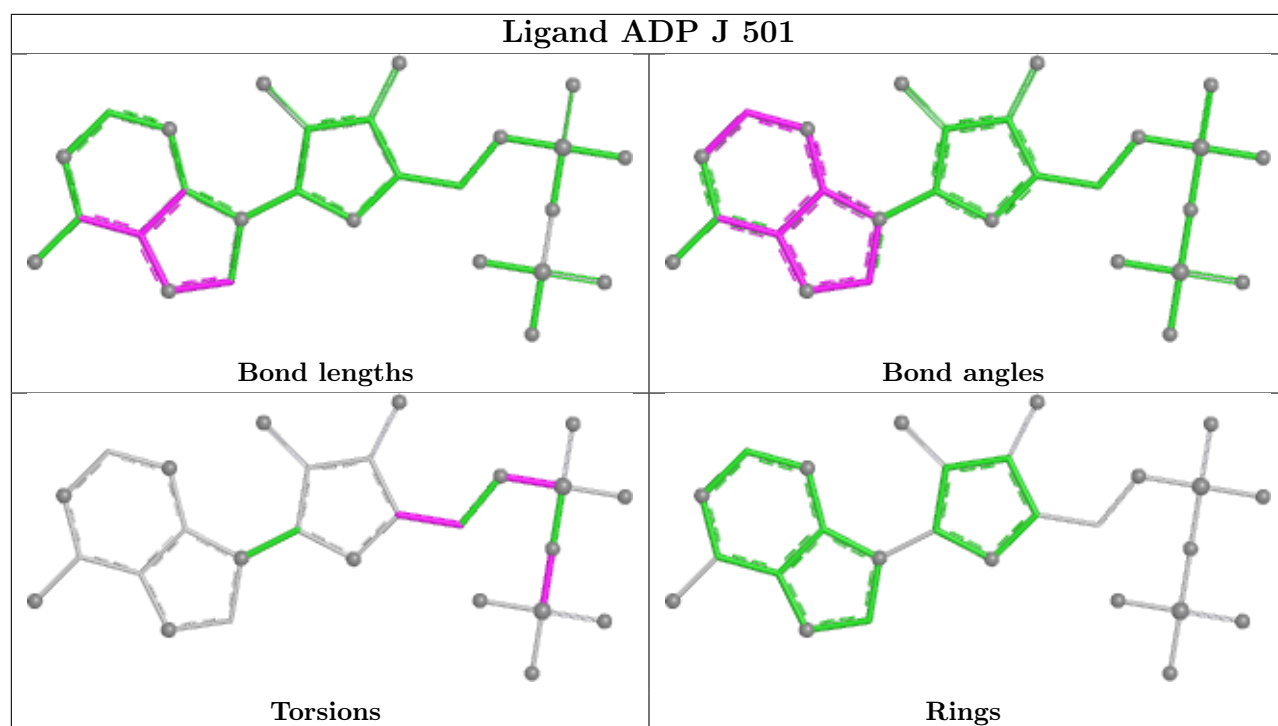
There are no ring outliers.

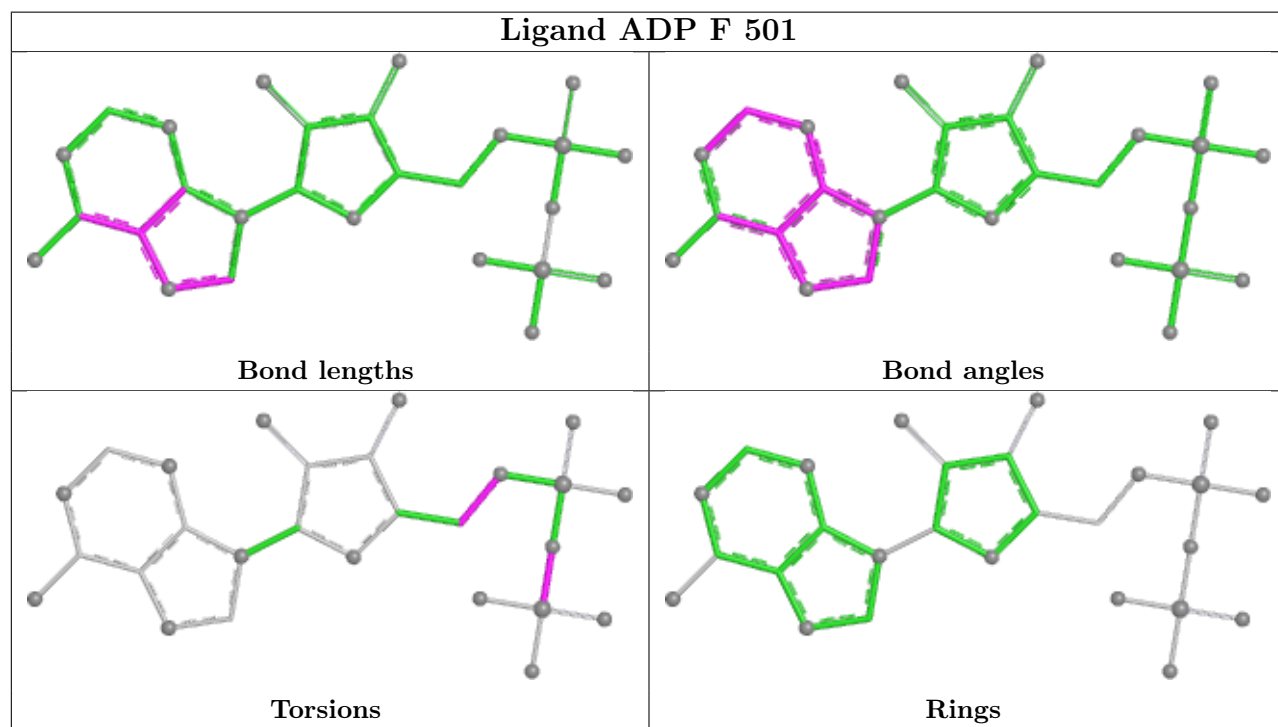
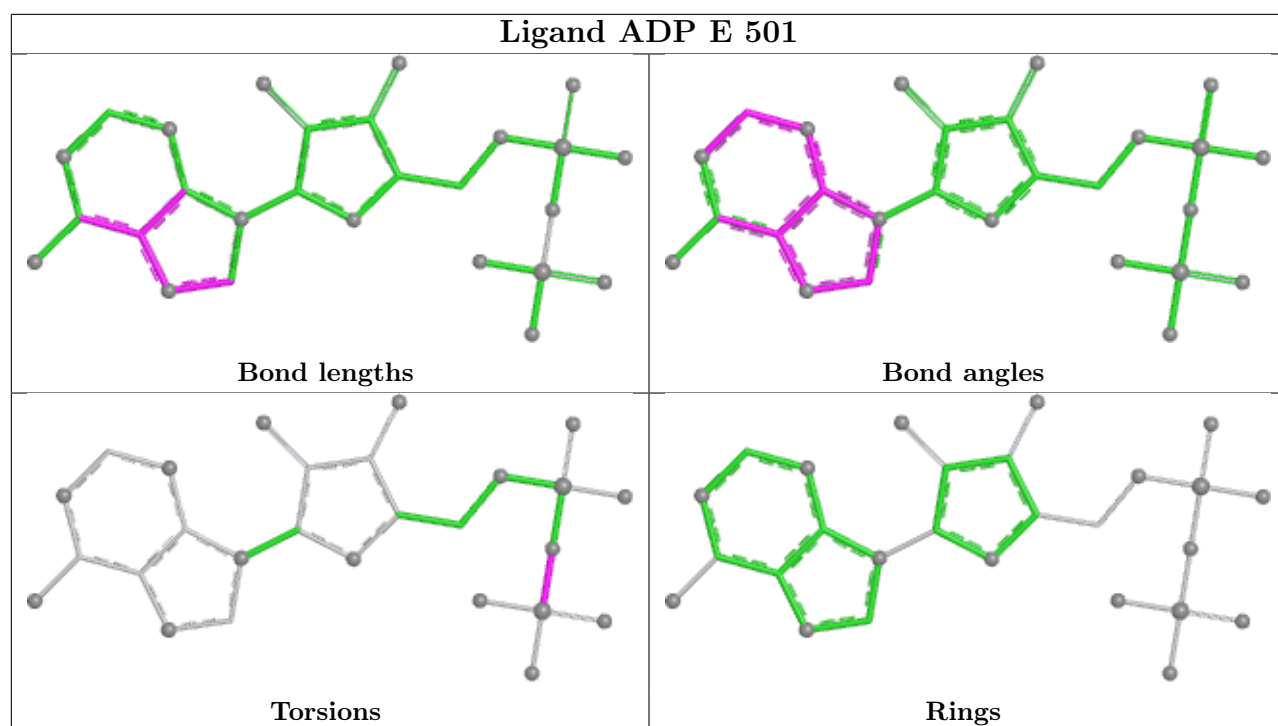
3 monomers are involved in 5 short contacts:

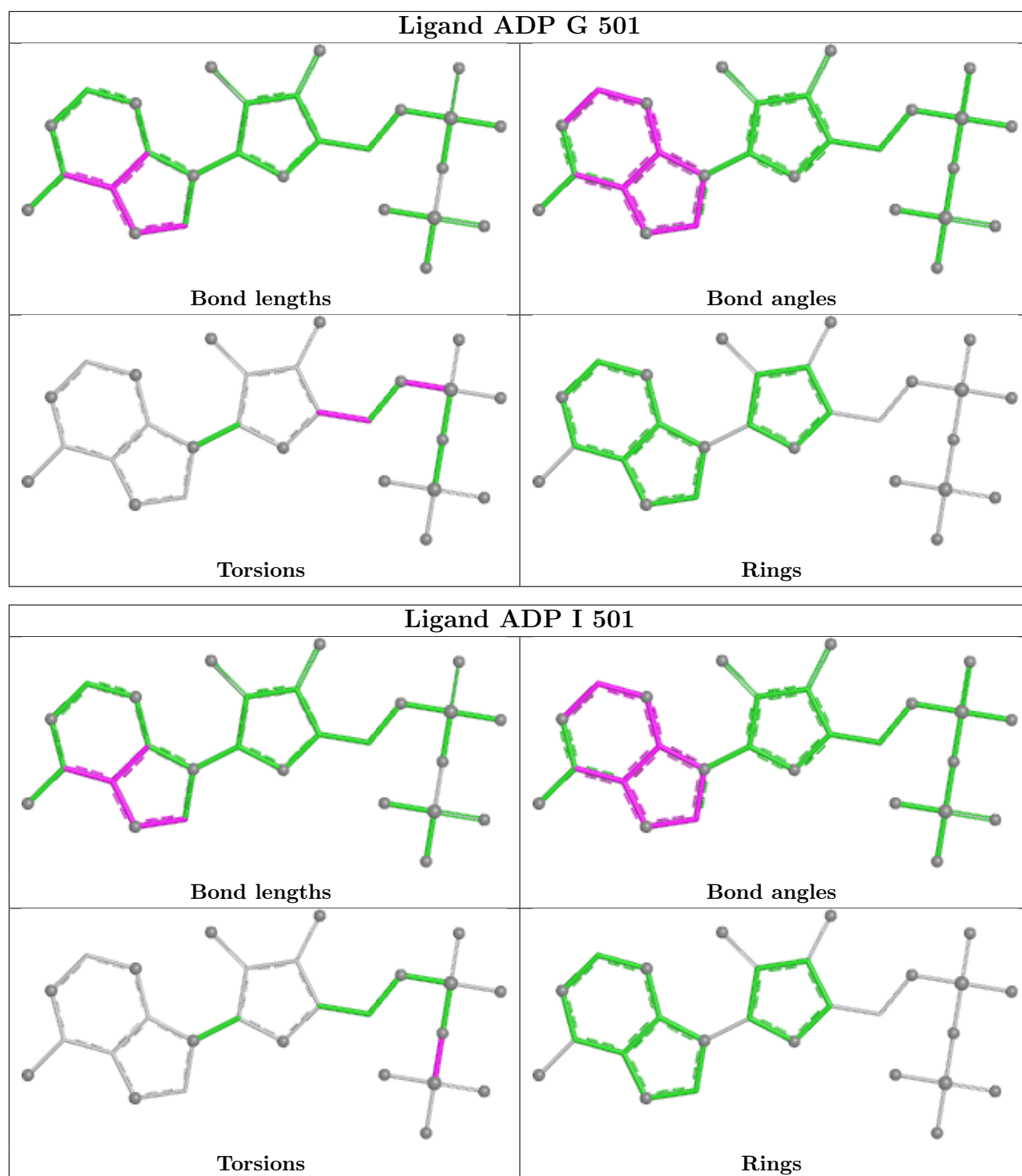
Mol	Chain	Res	Type	Clashes	Symm-Clashes
20	H	501	ADP	3	0
20	E	501	ADP	1	0
20	G	501	ADP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

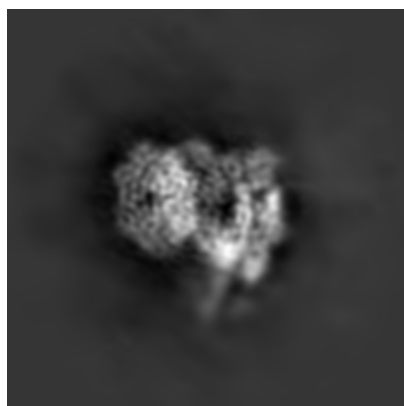
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72458. These allow visual inspection of the internal detail of the map and identification of artifacts.

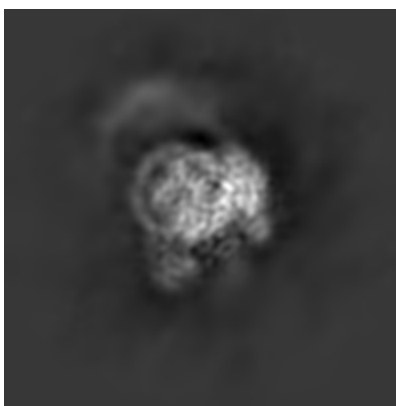
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

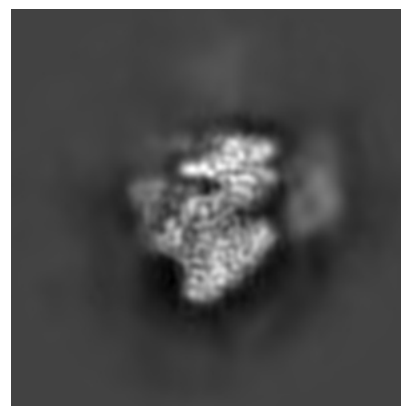
6.1.1 Primary map



X

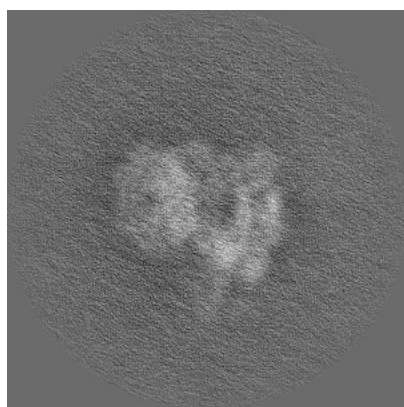


Y

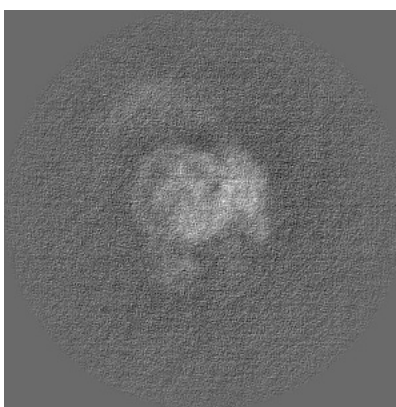


Z

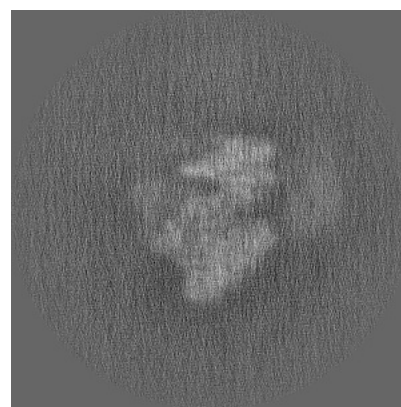
6.1.2 Raw map



X



Y

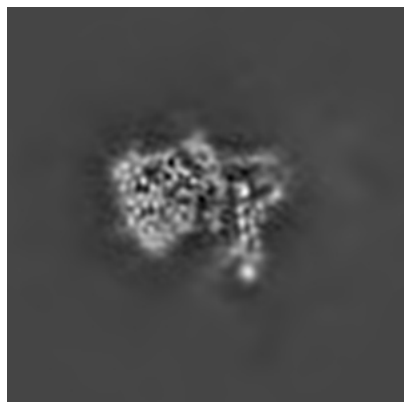


Z

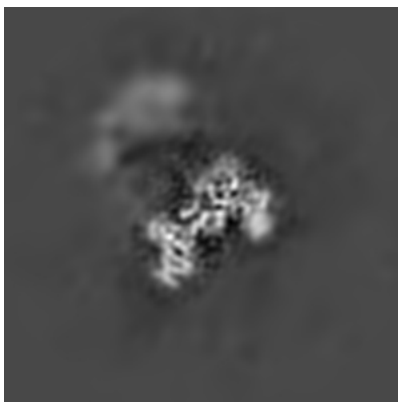
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

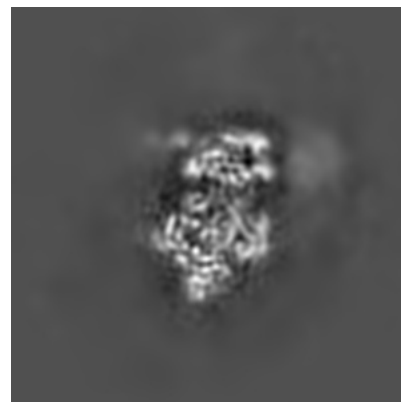
6.2.1 Primary map



X Index: 192

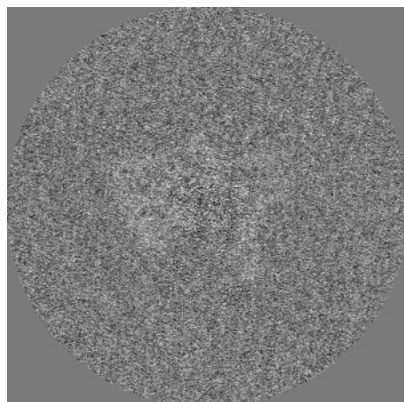


Y Index: 192

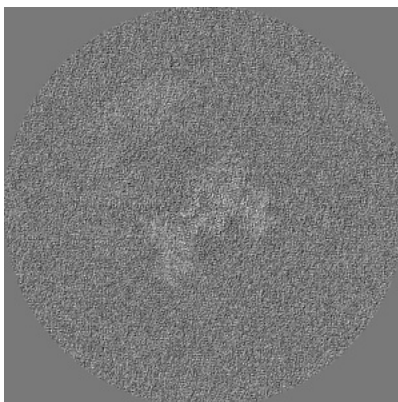


Z Index: 192

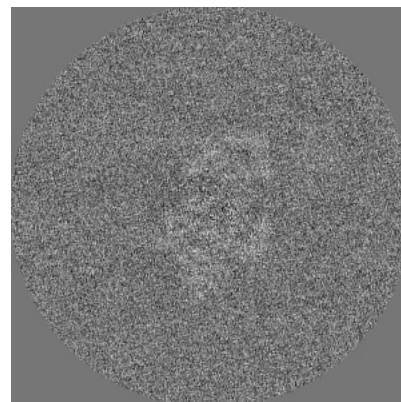
6.2.2 Raw map



X Index: 192



Y Index: 192

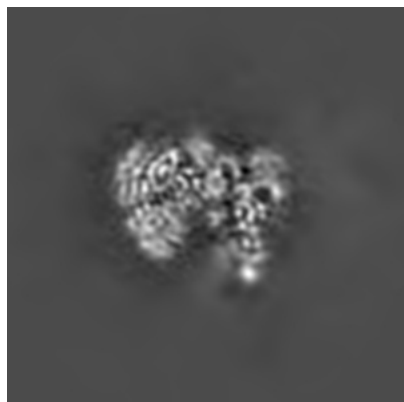


Z Index: 192

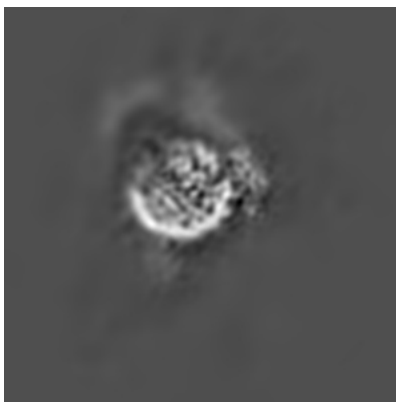
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

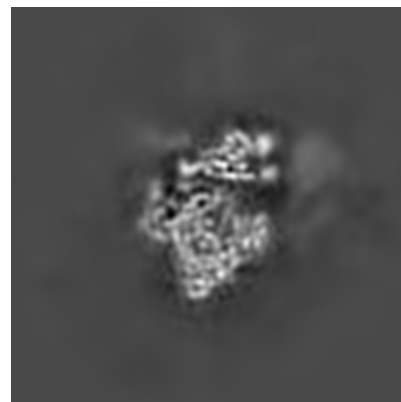
6.3.1 Primary map



X Index: 198

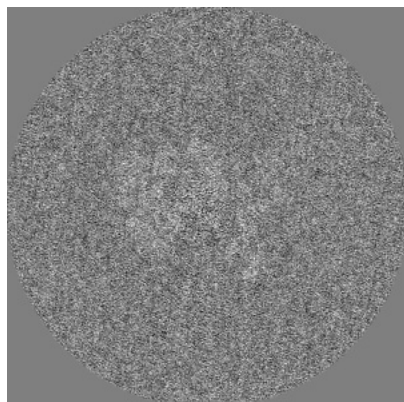


Y Index: 229

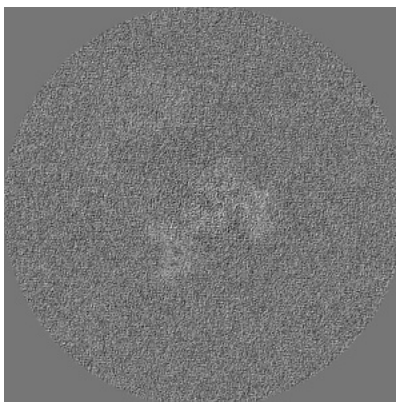


Z Index: 182

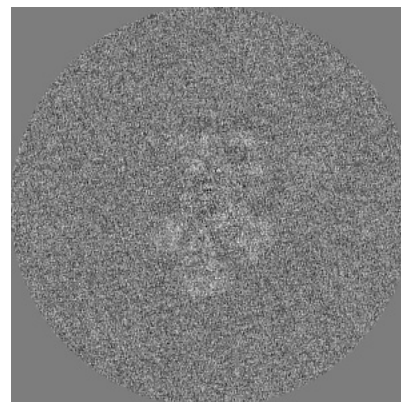
6.3.2 Raw map



X Index: 195



Y Index: 191

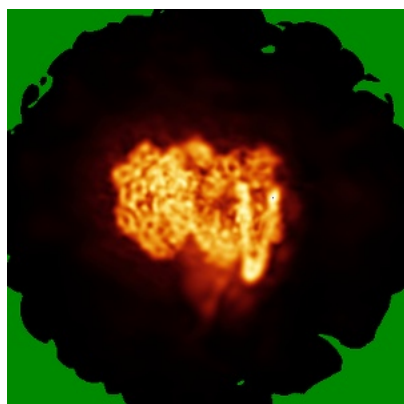


Z Index: 198

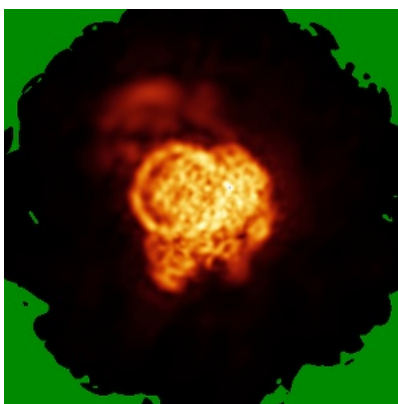
The images above show the largest variance slices of the map in three orthogonal directions.

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

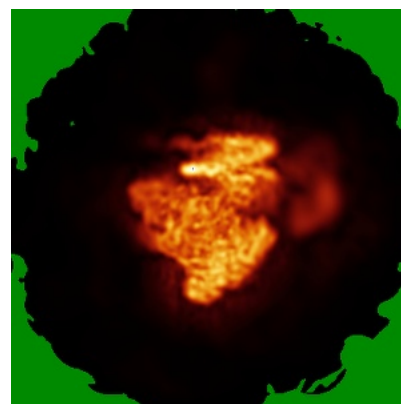
6.4.1 Primary map



X

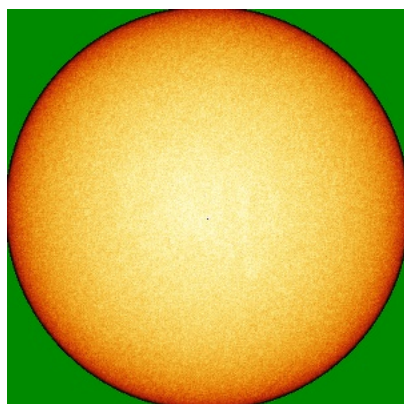


Y

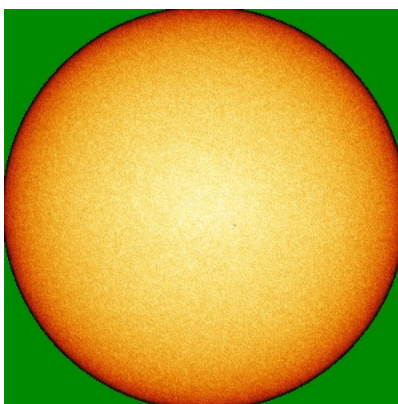


Z

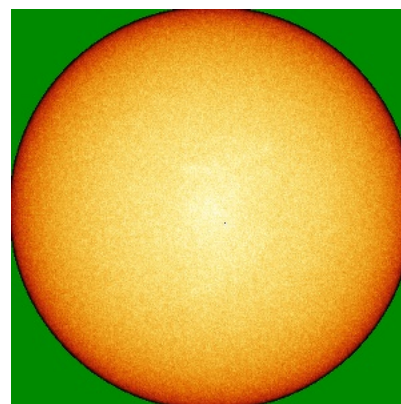
6.4.2 Raw map



X



Y

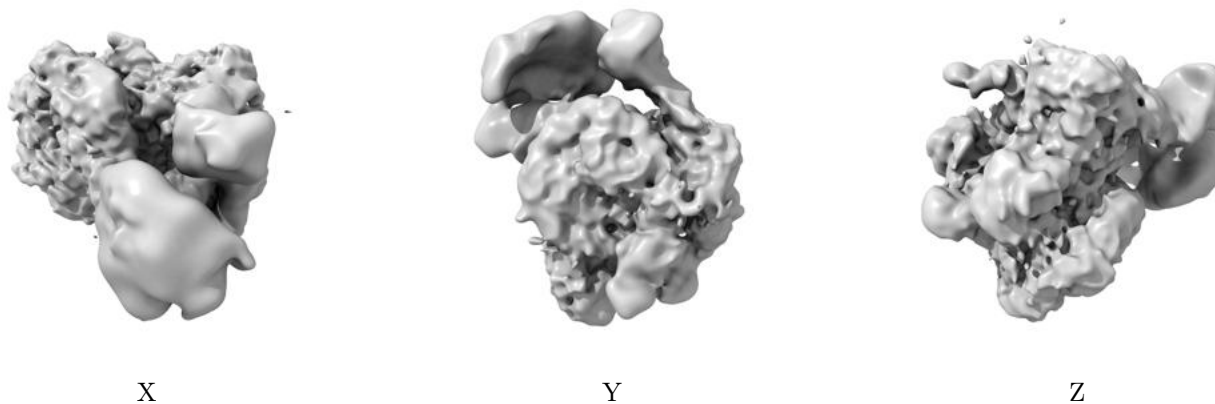


Z

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.

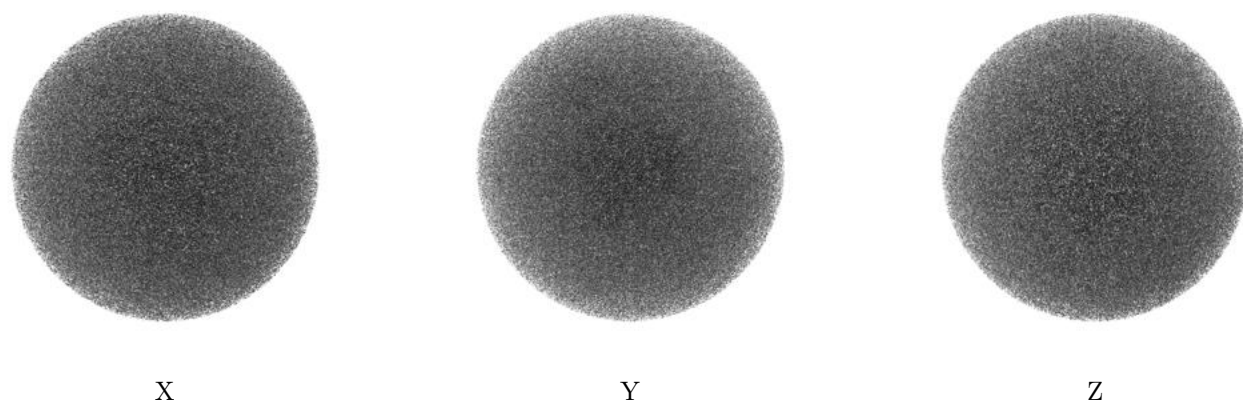
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.003. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

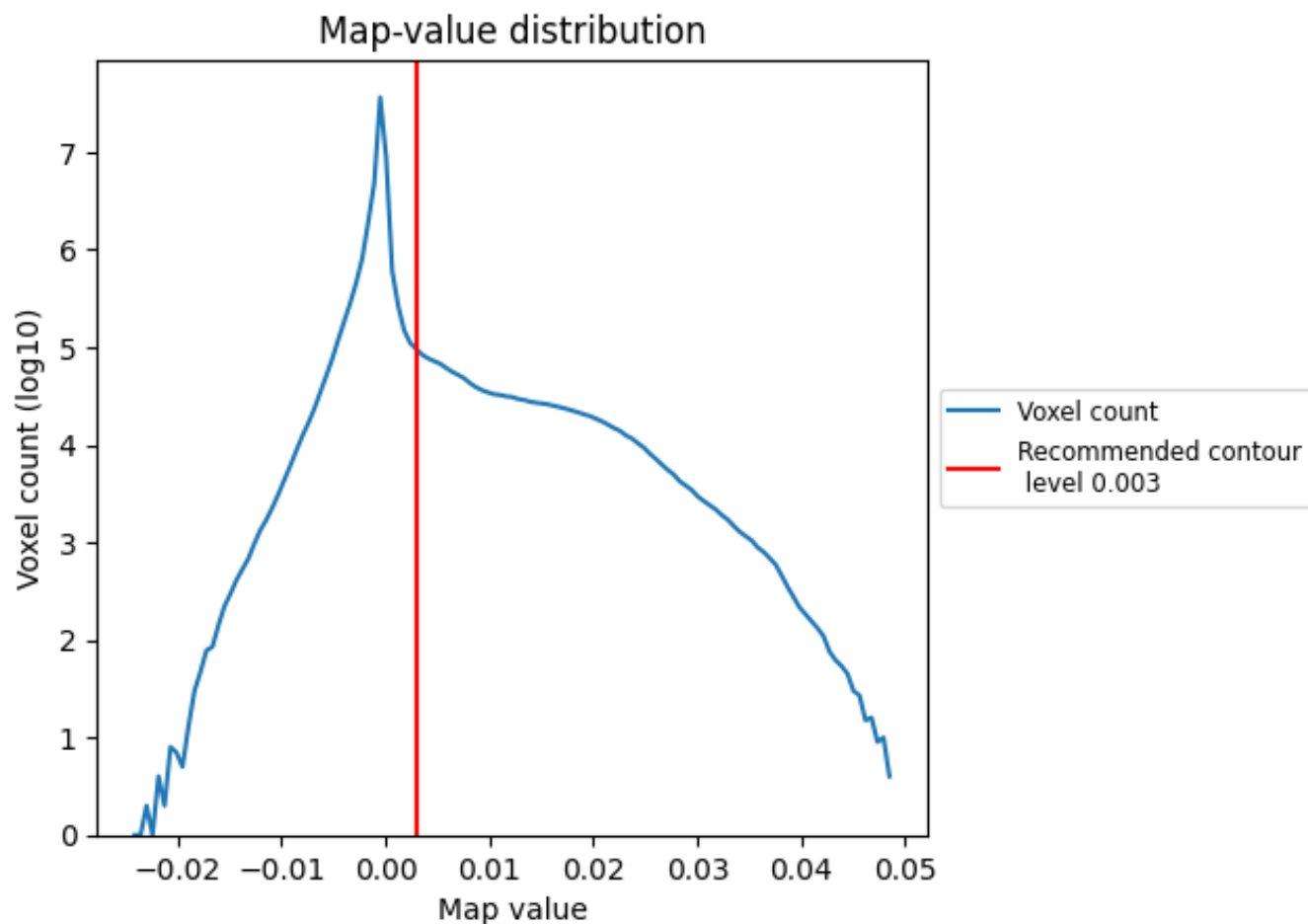
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

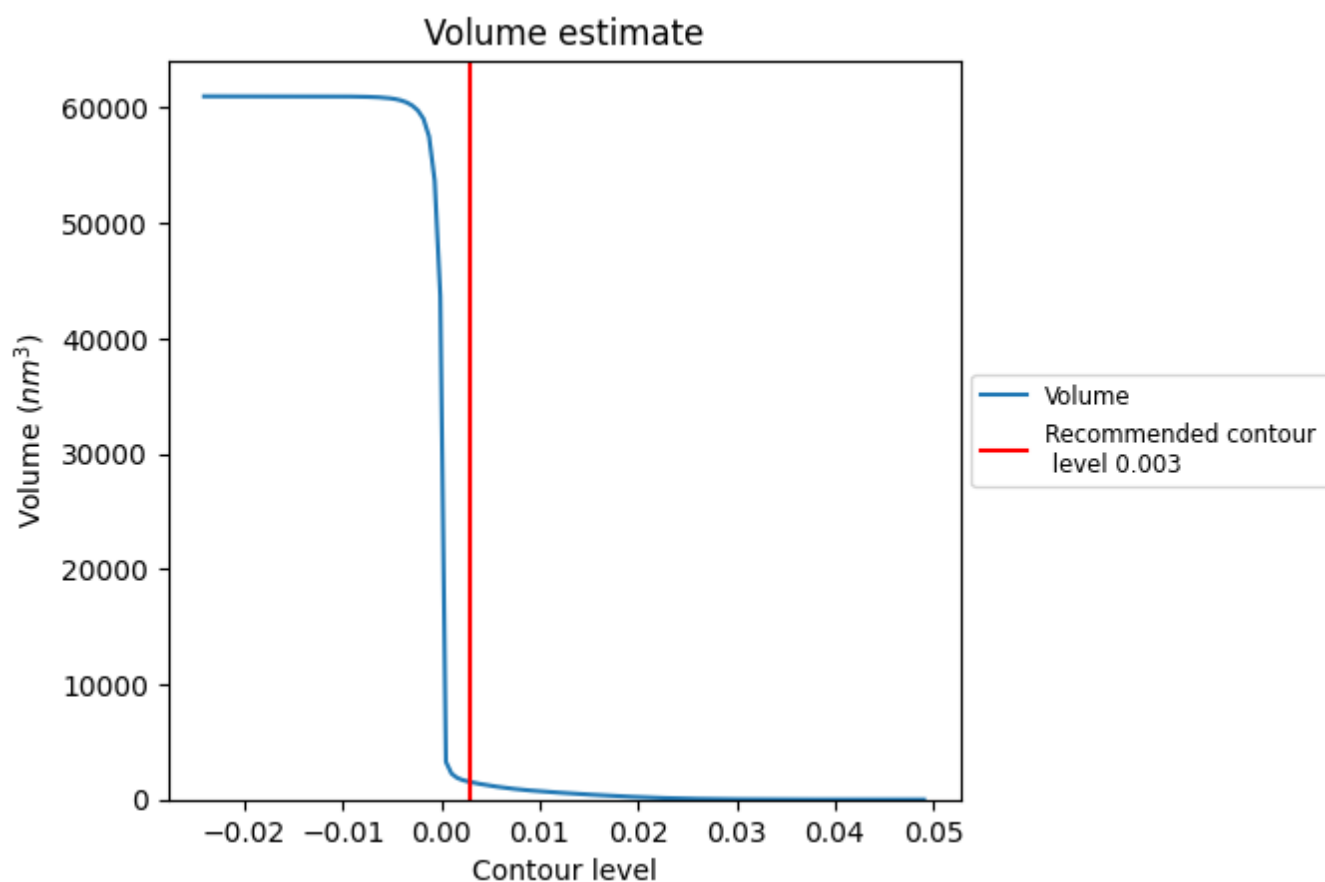
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

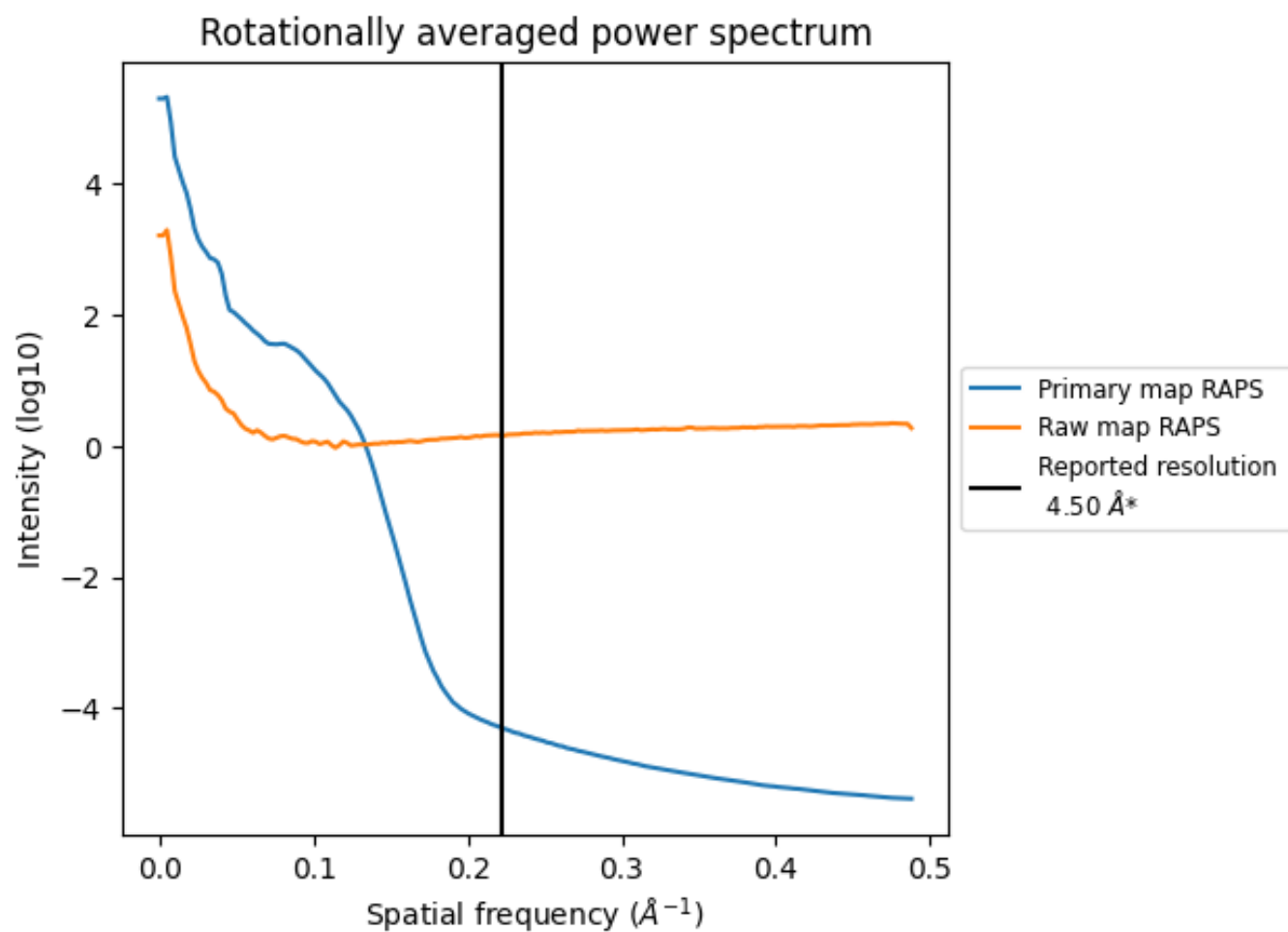
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1512 nm³; this corresponds to an approximate mass of 1366 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 ⓘ

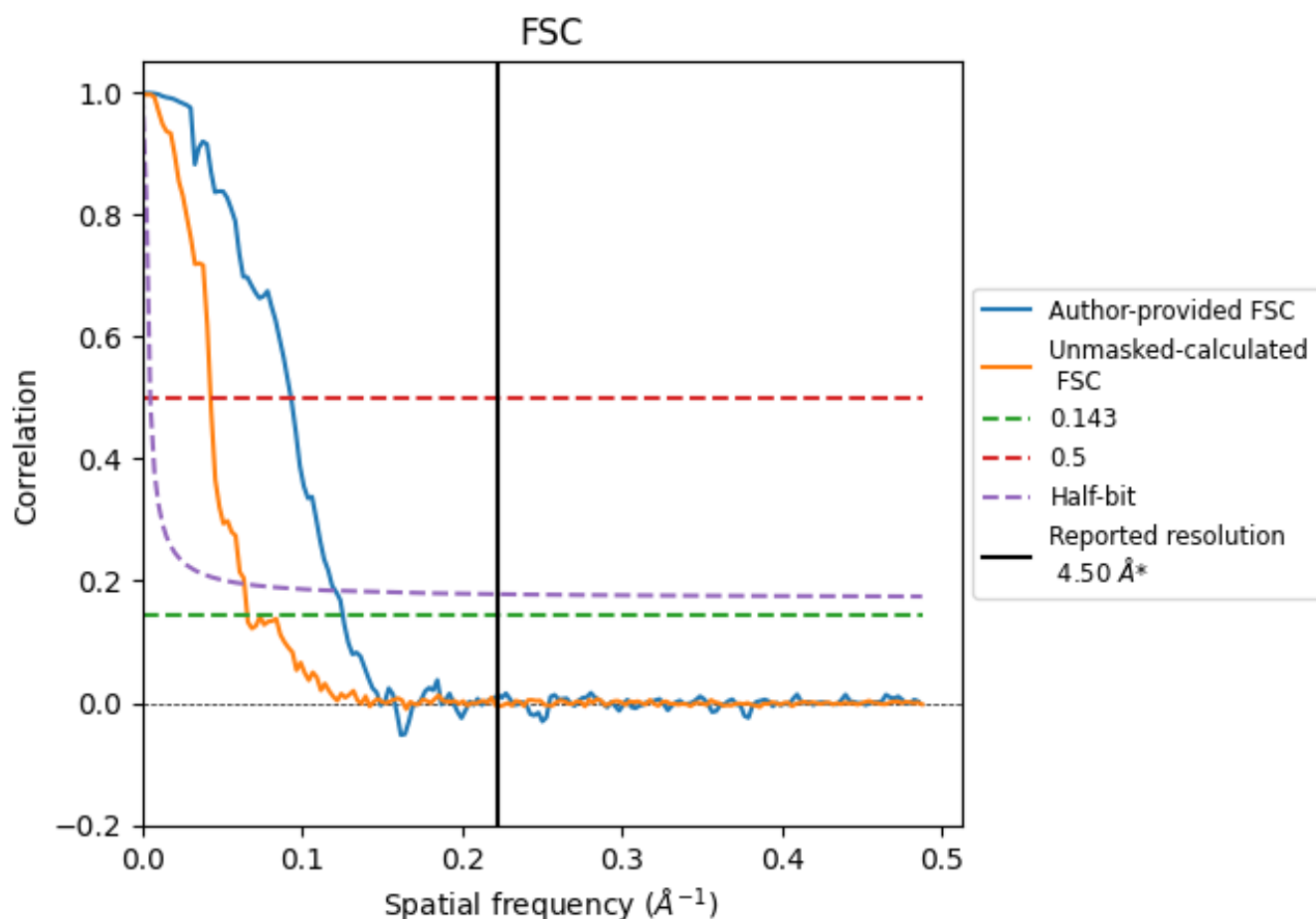


*Reported resolution corresponds to spatial frequency of 0.222 $\text{\AA}^{-1}$

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 0.222 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	7.97	10.74	8.28
Unmasked-calculated*	15.22	23.36	15.65

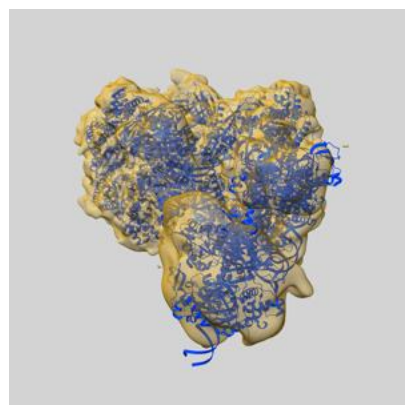
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 7.97 differs from the reported value 4.5 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 15.22 differs from the reported value 4.5 by more than 10 %

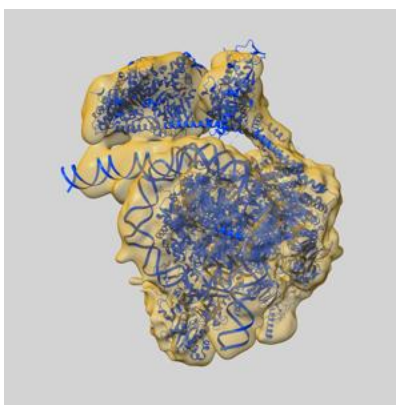
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-72458 and PDB model 9Y3H. Per-residue inclusion information can be found in section [3](#) on page [10](#).

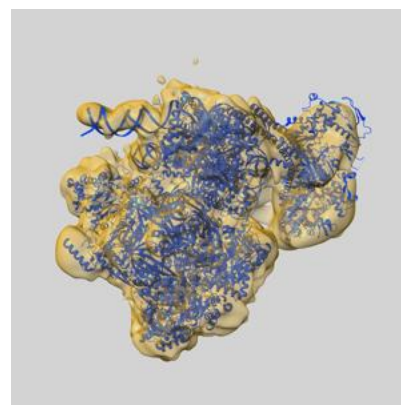
9.1 Map-model overlay [i](#)



X



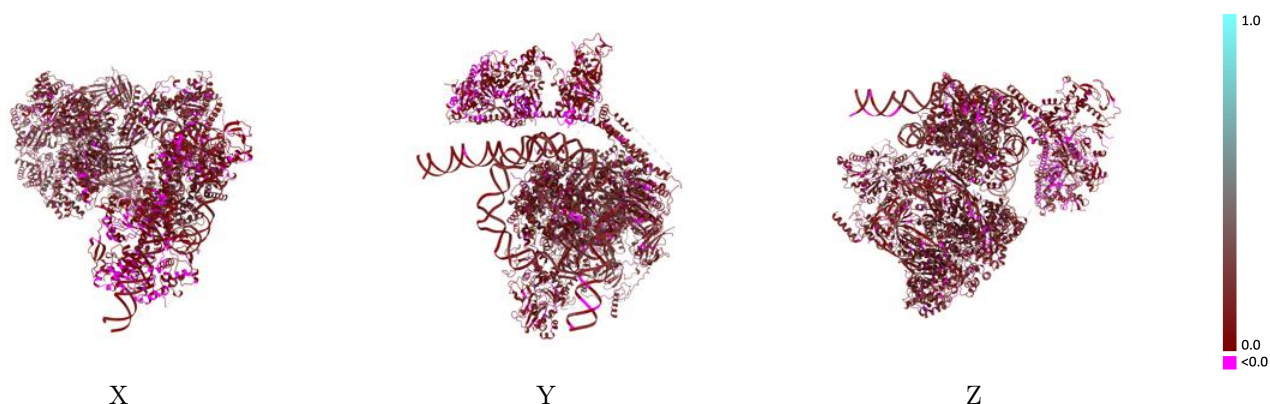
Y



Z

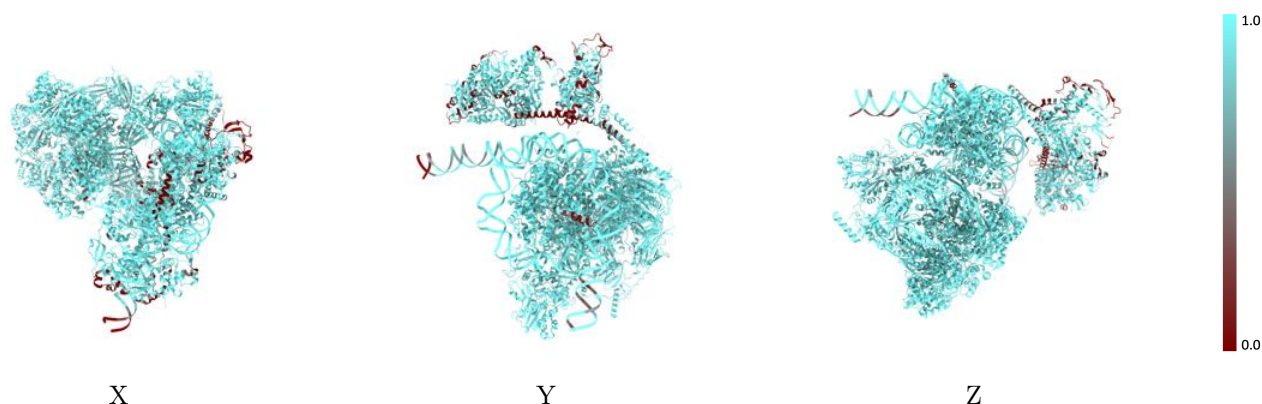
The images above show the 3D surface view of the map at the recommended contour level 0.003 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



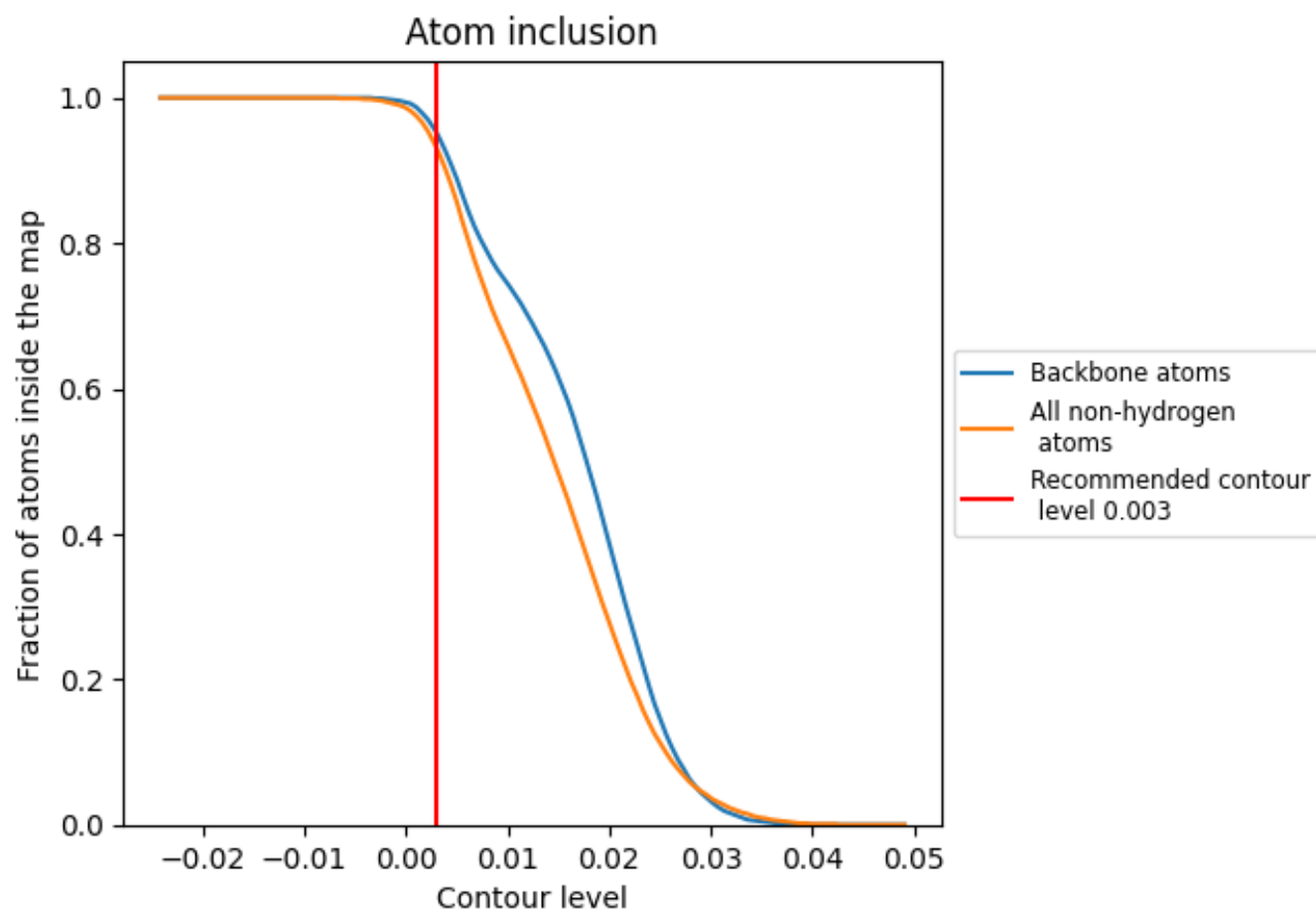
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.003).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 93% 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 (0.003) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9320	 0.1180
A	 0.9230	 0.1240
B	 0.8860	 0.1180
C	 0.9880	 0.1180
D	 0.9590	 0.1440
E	 0.9740	 0.1400
F	 0.9810	 0.1370
G	 0.9700	 0.1340
H	 0.9770	 0.1370
I	 0.9790	 0.1410
J	 0.9710	 0.1350
K	 0.7310	 0.0510
L	 0.9100	 0.0430
M	 0.8330	 0.0310
N	 0.9600	 0.0670
P	 0.8460	 0.0940
Q	 0.9710	 0.1140
R	 0.9670	 0.1490
S	 0.9770	 0.1560
T	 0.9740	 0.1470
U	 0.9940	 0.1250
V	 0.9880	 0.1280
W	 0.9320	 0.1250
X	 0.9030	 0.1210
Y	 0.9150	 0.1430
Z	 0.9270	 0.1450

