



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 07:13 PM UTC

PDB ID : 8W7M / pdb_00008w7m
EMDB ID : EMD-37343
Title : Yeast replisome in state V
Authors : Dang, S.; Zhai, Y.; Feng, J.; Yu, D.; Xu, Z.
Deposited on : 2023-08-30
Resolution : 4.12 Å (reported)
Based on initial model : 6SKL

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:

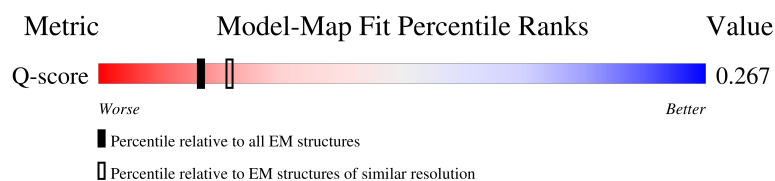
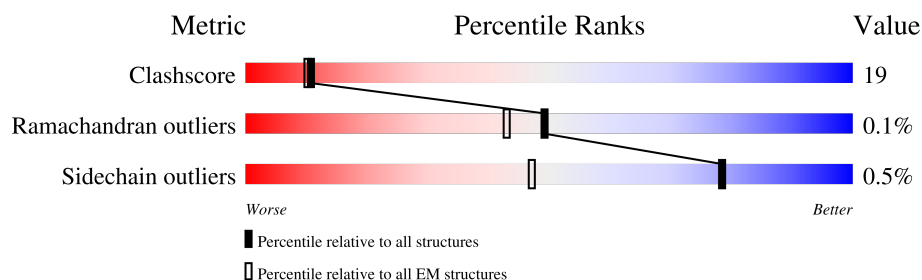
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.49

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 4.12 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.



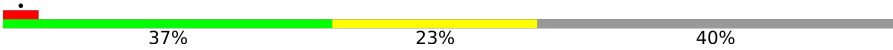
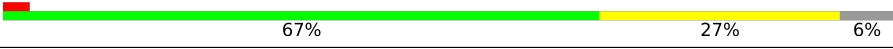
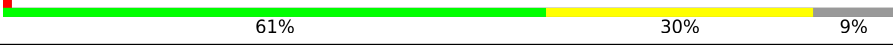
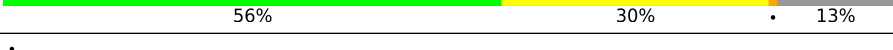
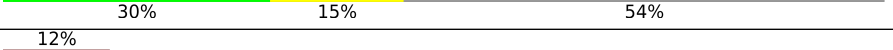
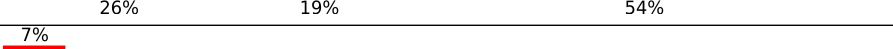
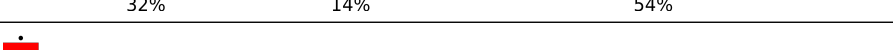
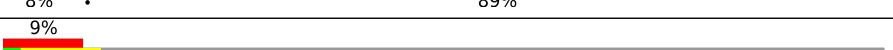
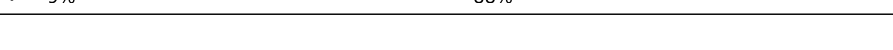
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5662 (3.62 - 4.62)

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	2	868	6% 45% 28% 28%
2	3	971	38% 26% 36%
3	4	933	7% 39% 28% 33%
4	5	775	44% 25% 32%

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Mol	Chain	Length	Quality of chain
5	6	1017	
6	7	845	
7	A	208	
8	B	213	
9	C	194	
10	D	294	
11	E	650	
12	F	927	
12	G	927	
12	H	927	
13	I	71	
14	N	689	

2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 51196 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 DNA replication licensing factor MCM2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	627	Total	C	N	O	S	0	0
			4955	3124	885	928	18		

- Molecule 2 is a protein called DNA replication licensing factor MCM3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	619	Total	C	N	O	S	0	0
			4835	3046	860	916	13		

- Molecule 3 is a protein called DNA replication licensing factor MCM4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	623	Total	C	N	O	S	0	0
			4947	3118	852	948	29		

- Molecule 4 is a protein called Minichromosome maintenance protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	5	529	Total	C	N	O	S	0	0
			4176	2644	714	796	22		

- Molecule 5 is a protein called DNA replication licensing factor MCM6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	6	613	Total	C	N	O	S	0	0
			4837	3051	839	923	24		

- Molecule 6 is a protein called DNA replication licensing factor MCM7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	7	657	Total	C	N	O	S	0	0
			5124	3238	888	970	28		

- Molecule 7 is a protein called DNA replication complex GINS protein PSF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	196	Total	C	N	O	S	0	0
			1602	1006	276	311	9		

- Molecule 8 is a protein called DNA replication complex GINS protein PSF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	193	Total	C	N	O	S	0	0
			1617	1039	286	287	5		

- Molecule 9 is a protein called DNA replication complex GINS protein PSF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	172	Total	C	N	O	S	0	0
			1387	904	223	253	7		

- Molecule 10 is a protein called DNA replication complex GINS protein SLD5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	243	Total	C	N	O	S	0	0
			2004	1276	327	389	12		

- Molecule 11 is a protein called Cell division control protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	568	Total	C	N	O	S	0	0
			4591	2930	774	873	14		

- Molecule 12 is a protein called DNA polymerase alpha-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	424	Total	C	N	O	S	0	0
			3404	2188	564	637	15		
12	G	422	Total	C	N	O	S	0	0
			3380	2172	557	636	15		
12	H	425	Total	C	N	O	S	0	0
			3411	2193	565	638	15		

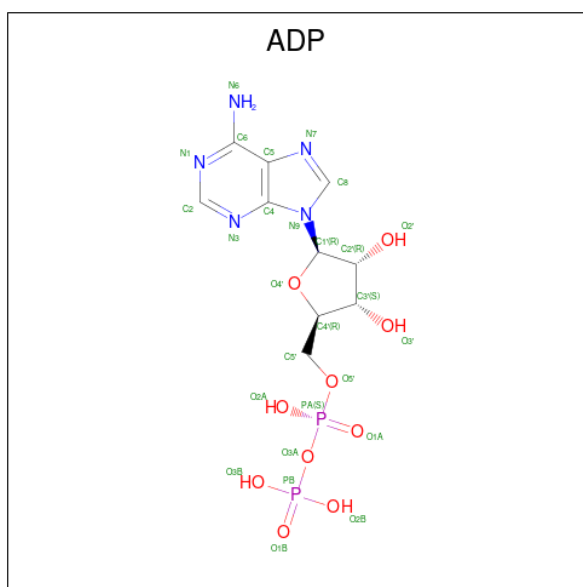
- Molecule 13 is a DNA chain called DNA (71-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	8	Total	C	N	O	P	0	0
			160	80	16	56	8		

- Molecule 14 is a protein called DNA polymerase epsilon subunit B.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	83	Total	C	N	O	S	0	0
			641	410	111	119	1		

- Molecule 15 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
15	2	1	Total	C	N	O	P	0
			27	10	5	10	2	
15	3	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 16 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
16	2	1	Total	Mg	0
			1	1	
16	3	1	Total	Mg	0
			1	1	

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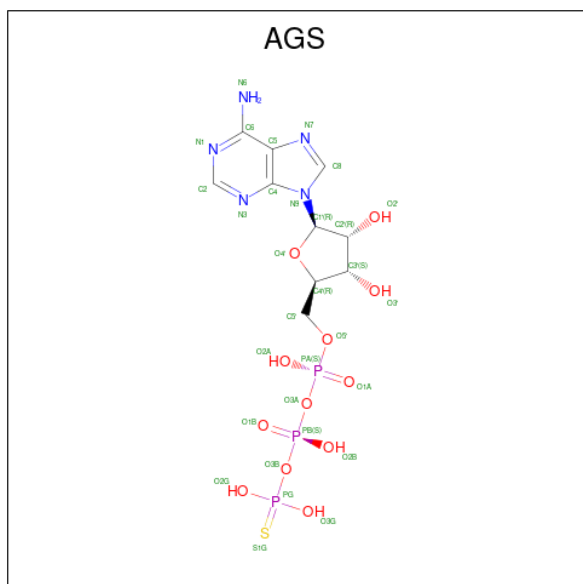
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Mol	Chain	Residues	Atoms		AltConf
16	4	1	Total	Mg	0
			1	1	
16	7	1	Total	Mg	0
			1	1	

- Molecule 17 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
17	2	1	Total	Zn	0
			1	1	
17	4	1	Total	Zn	0
			1	1	
17	5	1	Total	Zn	0
			1	1	
17	6	1	Total	Zn	0
			1	1	
17	7	1	Total	Zn	0
			1	1	

- Molecule 18 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (CCD ID: AGS) (formula: C₁₀H₁₆N₅O₁₂P₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf	
18	4	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	

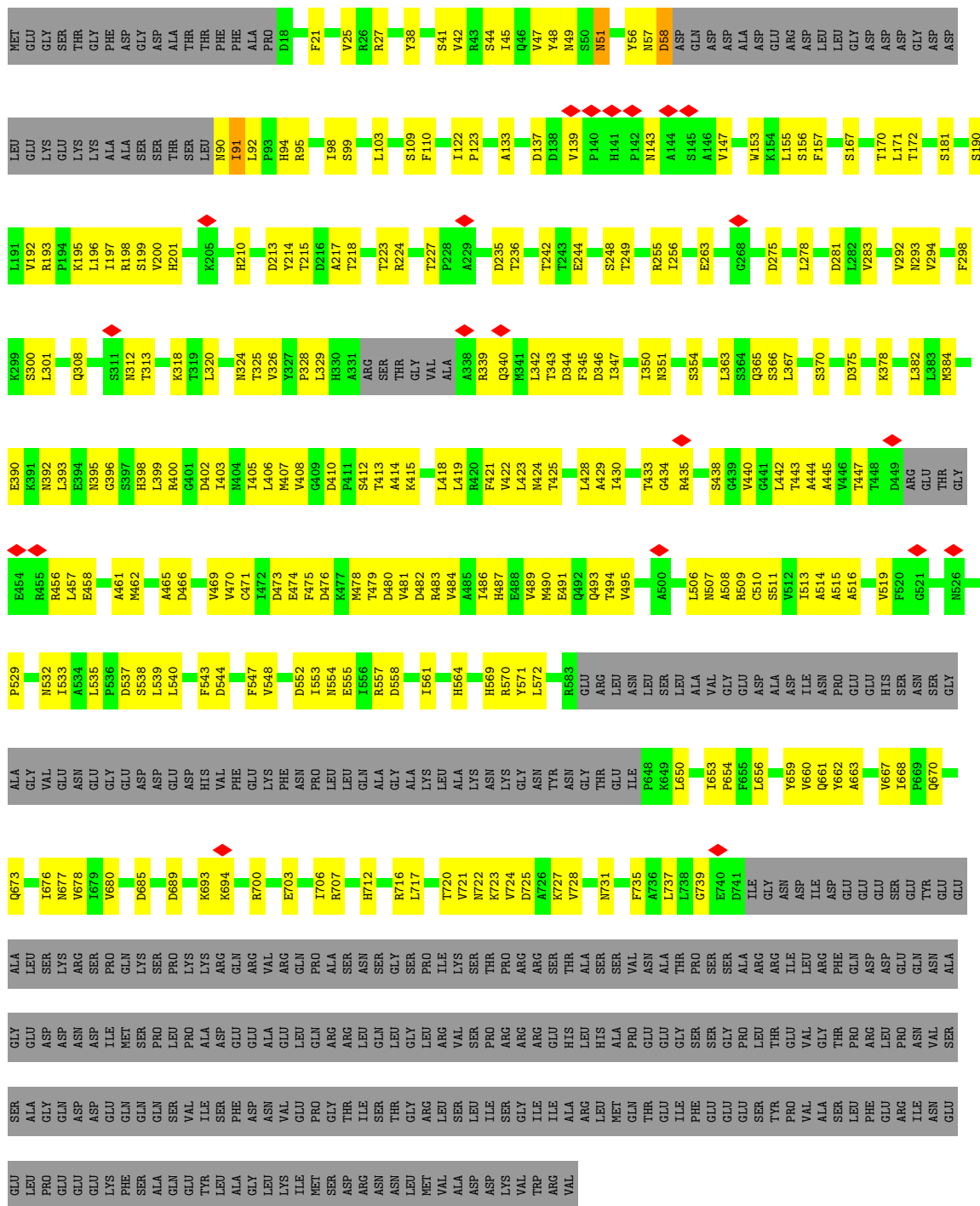
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Mol	Chain	Residues	Atoms						AltConf
			Total	C	N	O	P	S	
18	7	1	31	10	5	12	3	1	0

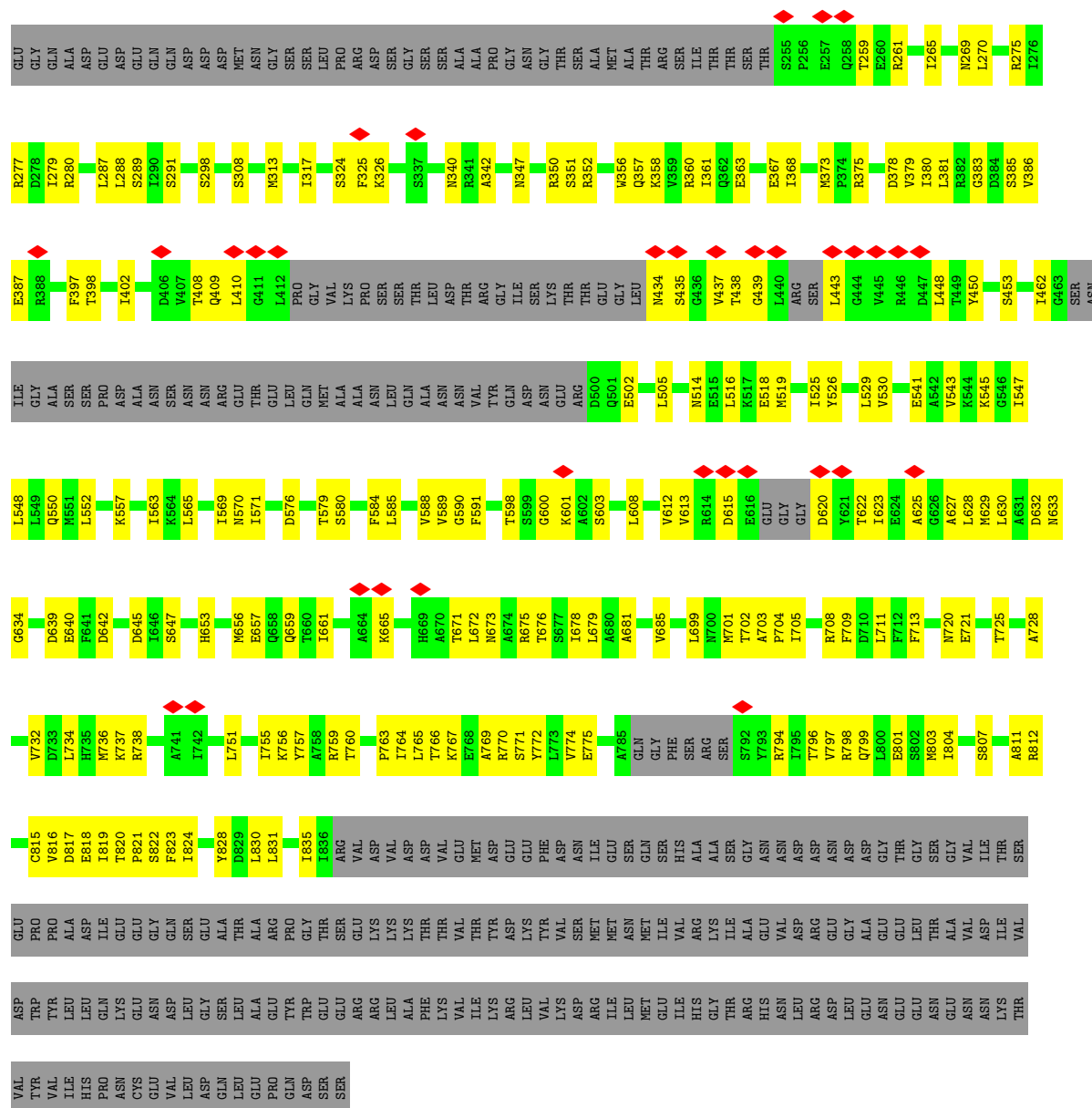
- Molecule 2: DNA replication licensing factor MCM3

Chain 3: 38% 26% 36%

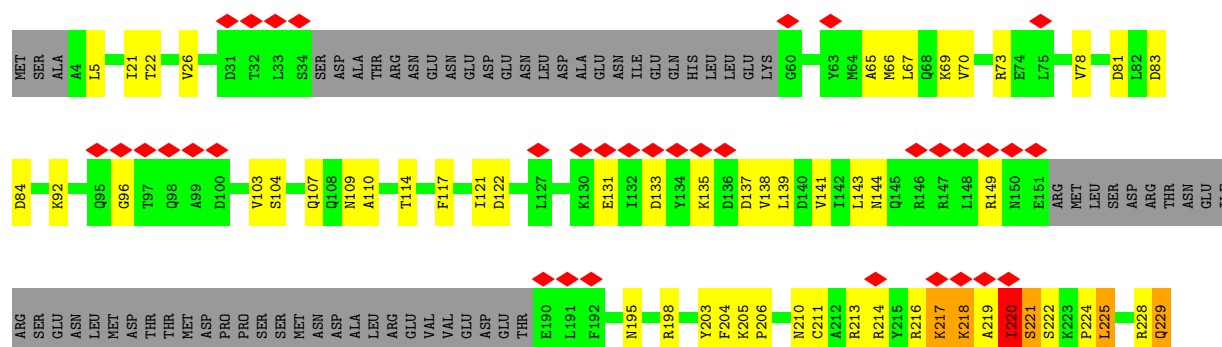


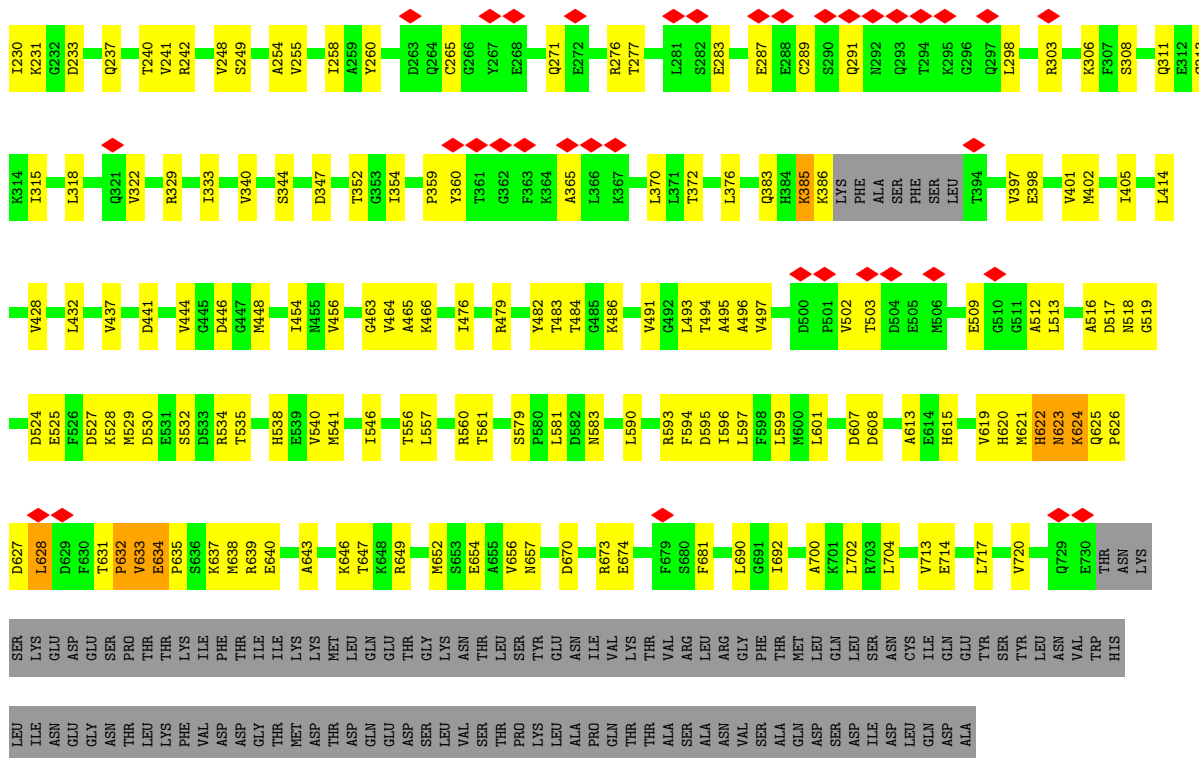
- Molecule 3: DNA replication licensing factor MCM4



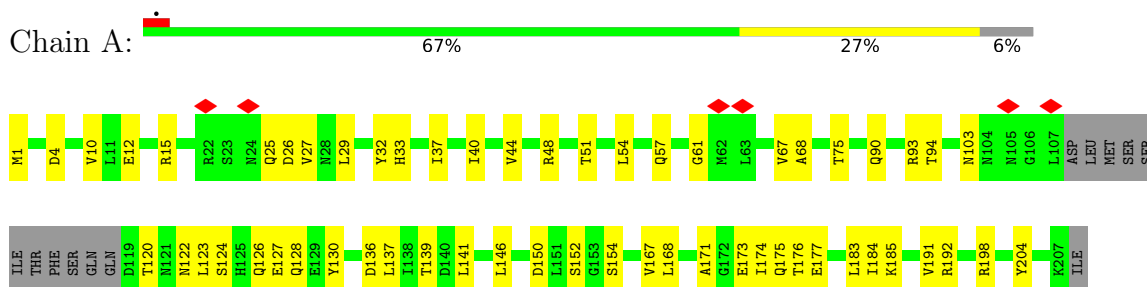


● Molecule 6: DNA replication licensing factor MCM7

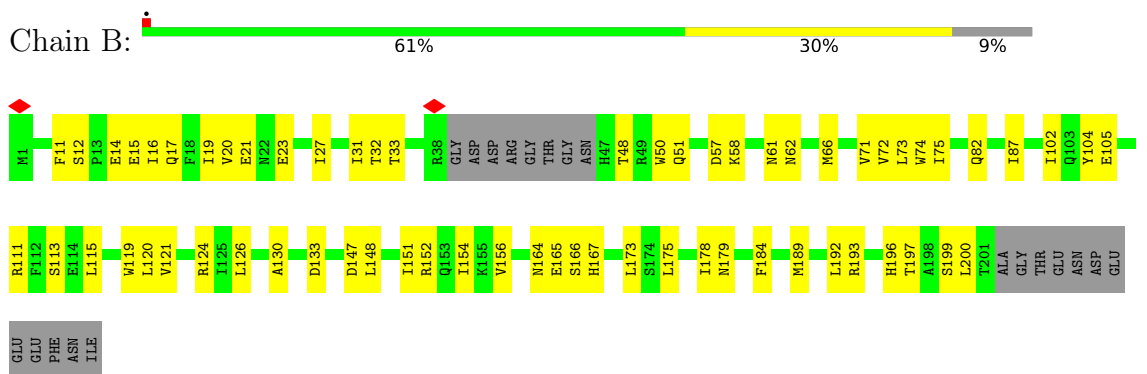




- Molecule 7: DNA replication complex GINS protein PSF1

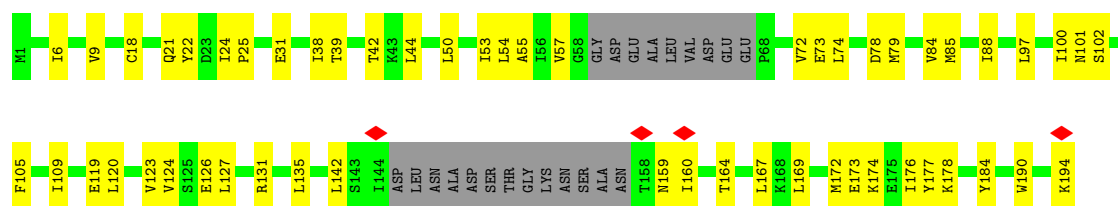


- Molecule 8: DNA replication complex GINS protein PSF2

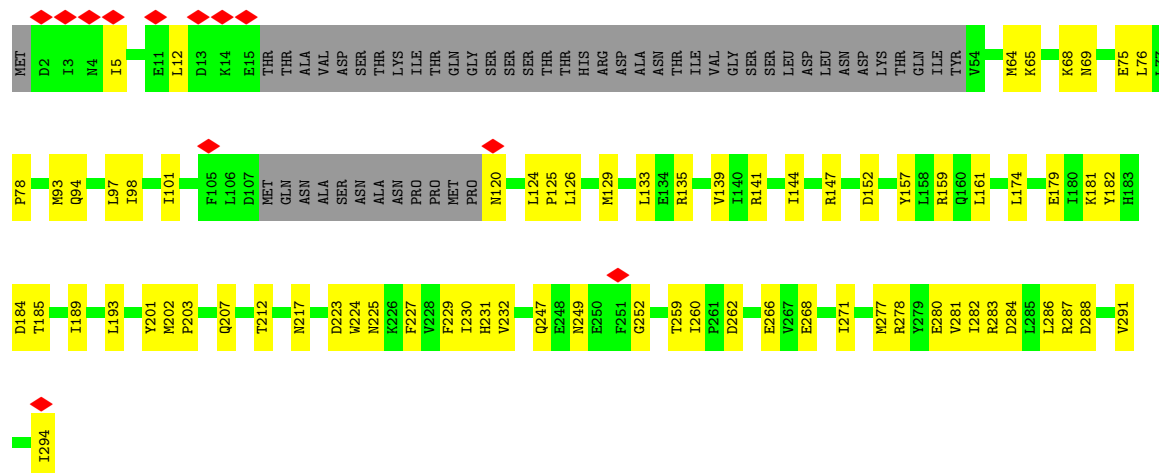


- Molecule 9: DNA replication complex GINS protein PSF3

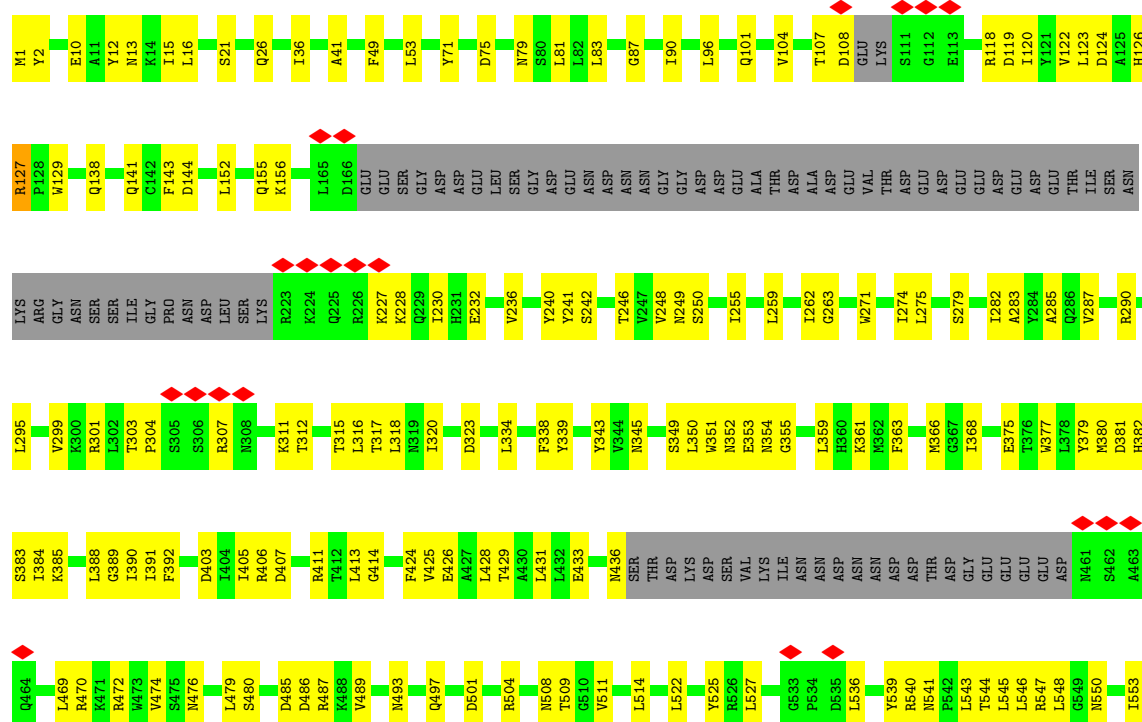


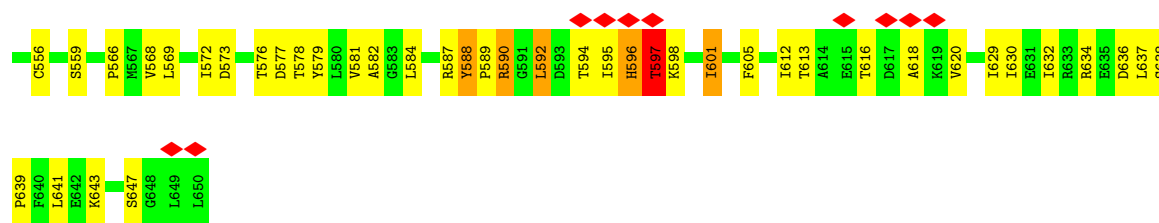


• Molecule 10: DNA replication complex GINS protein SLD5

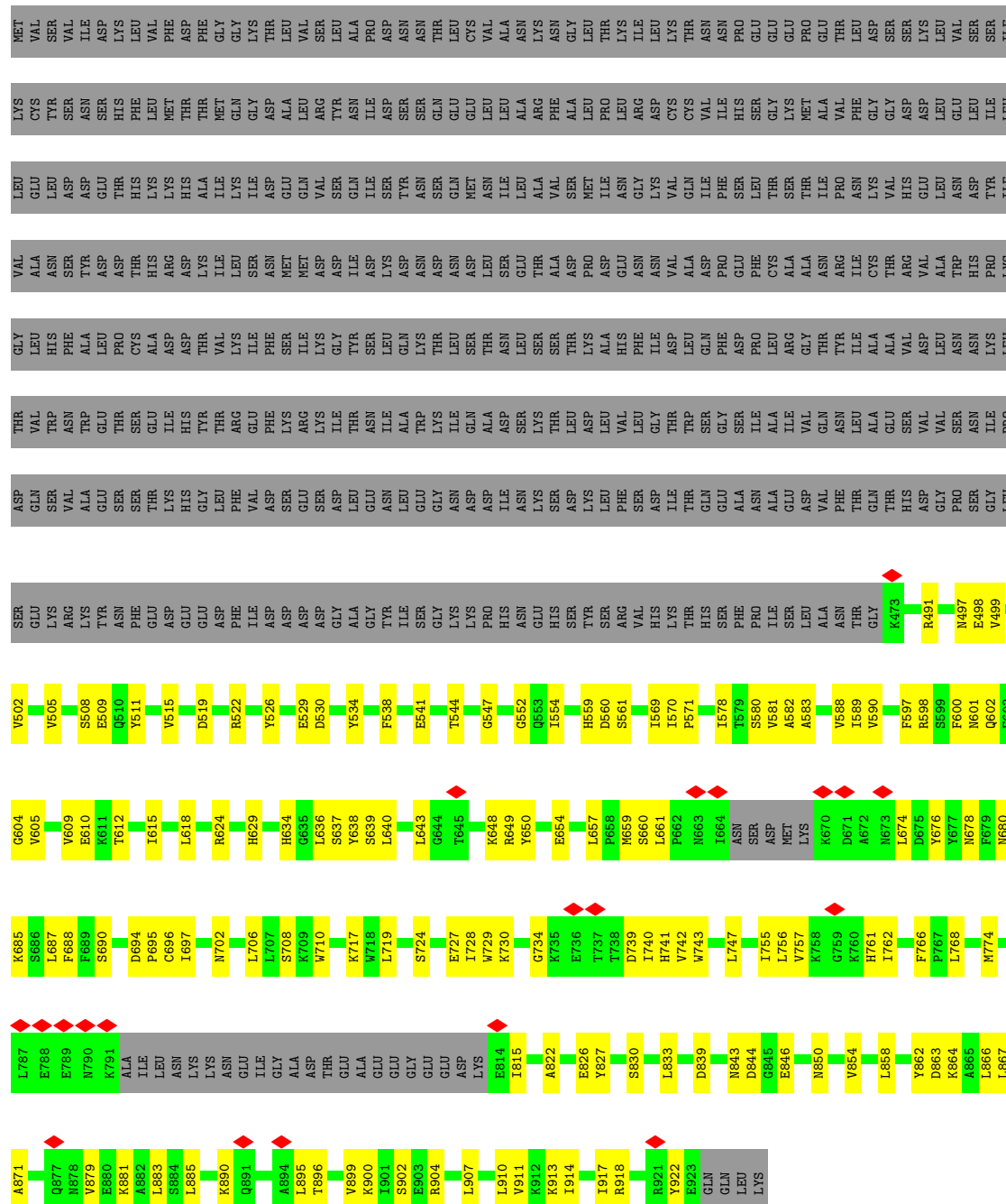
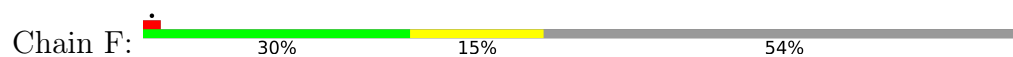


• Molecule 11: Cell division control protein 45

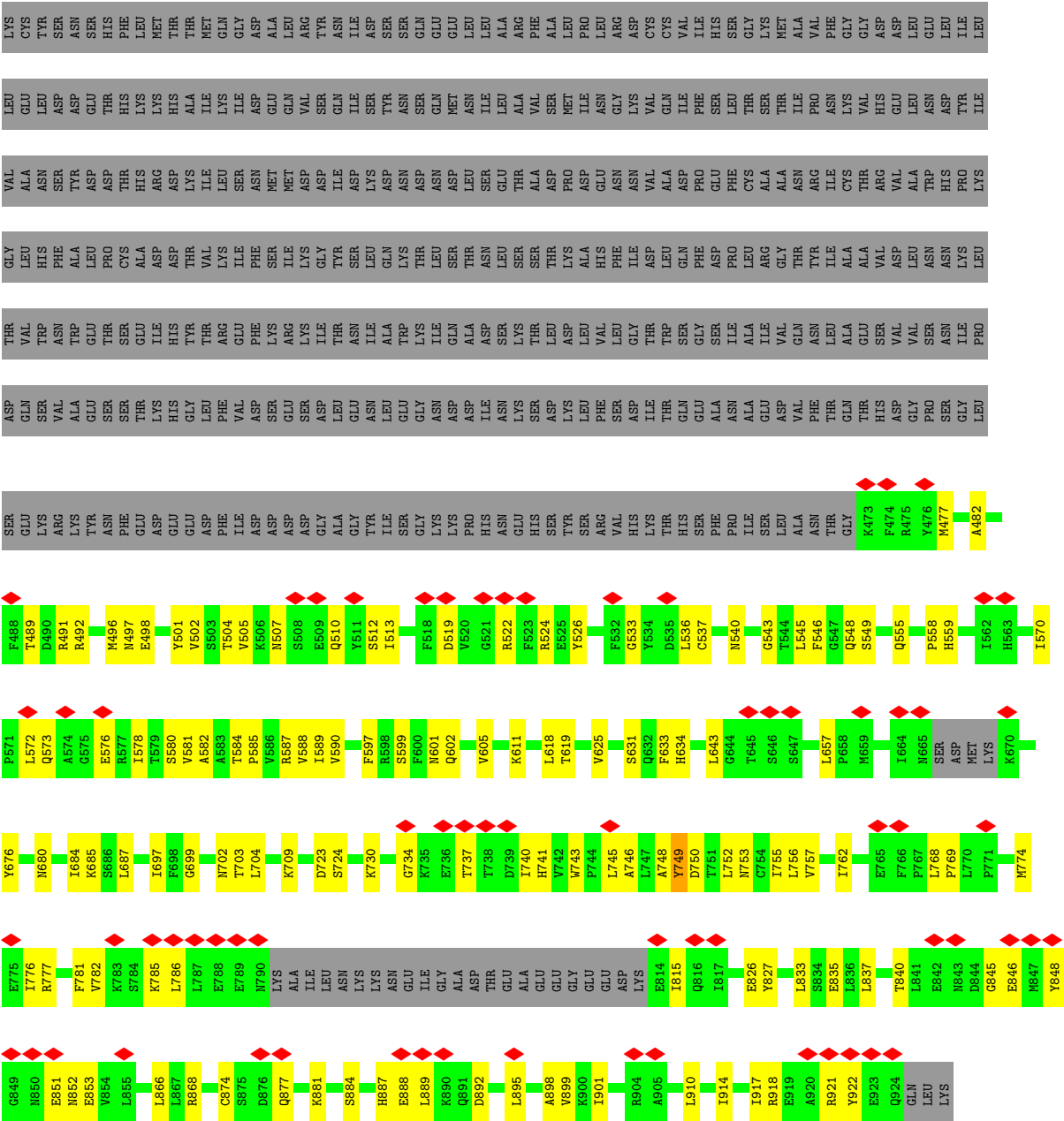




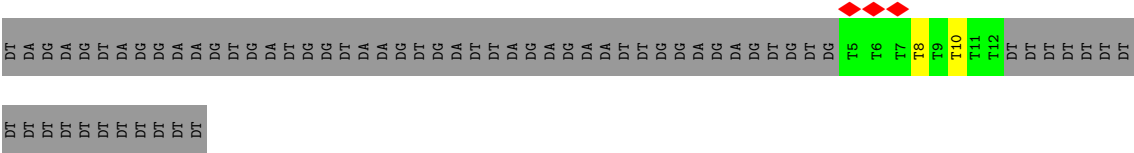
• Molecule 12: DNA polymerase alpha-binding protein



• Molecule 12: DNA polymerase alpha-binding protein



• Molecule 13: DNA (71-mer)



• Molecule 14: DNA polymerase epsilon subunit B



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	28871	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	53	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.261	Depositor
Minimum map value	-0.265	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.056	Depositor
Recommended contour level	0.45	Depositor
Map size (Å)	466.39996, 466.39996, 466.39996	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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, AGS, 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	2	0.15	0/5036	0.32	0/6796
2	3	0.21	0/4920	0.37	0/6675
3	4	0.14	0/5020	0.33	0/6785
4	5	0.18	0/4227	0.33	0/5701
5	6	0.15	0/4913	0.34	0/6631
6	7	0.27	0/5204	0.42	0/7039
7	A	0.16	0/1622	0.29	0/2183
8	B	0.18	0/1650	0.32	0/2231
9	C	0.16	0/1420	0.30	0/1918
10	D	0.17	0/2040	0.32	0/2755
11	E	0.22	0/4677	0.36	0/6335
12	F	0.14	0/3489	0.31	0/4724
12	G	0.14	0/3465	0.32	0/4696
12	H	0.14	0/3496	0.33	0/4735
13	I	0.20	0/175	0.53	0/268
14	N	0.32	0/654	0.53	0/883
All	All	0.18	0/52008	0.35	0/70355

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 [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	2	4955	0	5000	187	0
2	3	4835	0	4881	202	0
3	4	4947	0	5020	208	0
4	5	4176	0	4261	173	0
5	6	4837	0	4830	185	0
6	7	5124	0	5175	169	0
7	A	1602	0	1604	51	0
8	B	1617	0	1674	57	0
9	C	1387	0	1405	41	0
10	D	2004	0	2001	62	0
11	E	4591	0	4567	153	0
12	F	3404	0	3352	114	0
12	G	3380	0	3310	153	0
12	H	3411	0	3355	104	0
13	I	160	0	97	2	0
14	N	641	0	622	151	0
15	2	27	0	12	8	0
15	3	27	0	12	6	0
16	2	1	0	0	0	0
16	3	1	0	0	0	0
16	4	1	0	0	0	0
16	7	1	0	0	0	0
17	2	1	0	0	0	0
17	4	1	0	0	0	0
17	5	1	0	0	0	0
17	6	1	0	0	0	0
17	7	1	0	0	0	0
18	4	31	0	12	6	0
18	7	31	0	12	7	0
All	All	51196	0	51202	1905	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 19.

The worst 5 of 1905 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)
6:7:622:HIS:HB2	6:7:624:LYS:NZ	1.58	1.17
6:7:622:HIS:CB	6:7:624:LYS:NZ	2.08	1.17
14:N:25:LEU:HD13	14:N:63:LEU:HD12	1.42	1.01
11:E:589:PRO:HD2	11:E:592:LEU:HD12	1.44	1.00
6:7:622:HIS:CB	6:7:624:LYS:HZ3	1.73	0.99

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	2	613/868 (71%)	581 (95%)	32 (5%)	0	100	100
2	3	609/971 (63%)	579 (95%)	30 (5%)	0	100	100
3	4	613/933 (66%)	583 (95%)	30 (5%)	0	100	100
4	5	503/775 (65%)	484 (96%)	19 (4%)	0	100	100
5	6	599/1017 (59%)	567 (95%)	32 (5%)	0	100	100
6	7	649/845 (77%)	626 (96%)	21 (3%)	2 (0%)	36	70
7	A	192/208 (92%)	191 (100%)	1 (0%)	0	100	100
8	B	189/213 (89%)	180 (95%)	9 (5%)	0	100	100
9	C	166/194 (86%)	161 (97%)	5 (3%)	0	100	100
10	D	237/294 (81%)	228 (96%)	9 (4%)	0	100	100
11	E	560/650 (86%)	529 (94%)	28 (5%)	3 (0%)	24	61
12	F	418/927 (45%)	407 (97%)	11 (3%)	0	100	100
12	G	416/927 (45%)	398 (96%)	18 (4%)	0	100	100
12	H	419/927 (45%)	399 (95%)	19 (4%)	1 (0%)	43	76
14	N	81/689 (12%)	71 (88%)	10 (12%)	0	100	100
All	All	6264/10438 (60%)	5984 (96%)	274 (4%)	6 (0%)	49	81

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	7	220	ILE
11	E	127	ARG
11	E	597	THR
12	H	749	TYR
11	E	596	HIS

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	2	544/770 (71%)	544 (100%)	0	100	100
2	3	534/835 (64%)	529 (99%)	5 (1%)	70	76
3	4	561/848 (66%)	561 (100%)	0	100	100
4	5	478/688 (70%)	478 (100%)	0	100	100
5	6	531/886 (60%)	531 (100%)	0	100	100
6	7	566/753 (75%)	549 (97%)	17 (3%)	36	57
7	A	181/193 (94%)	181 (100%)	0	100	100
8	B	183/198 (92%)	183 (100%)	0	100	100
9	C	155/173 (90%)	155 (100%)	0	100	100
10	D	234/279 (84%)	234 (100%)	0	100	100
11	E	509/586 (87%)	503 (99%)	6 (1%)	63	73
12	F	375/825 (46%)	375 (100%)	0	100	100
12	G	372/825 (45%)	372 (100%)	0	100	100
12	H	375/825 (46%)	375 (100%)	0	100	100
14	N	63/629 (10%)	60 (95%)	3 (5%)	23	46
All	All	5661/9313 (61%)	5630 (100%)	31 (0%)	78	82

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	7	385	LYS
11	E	601	ILE
6	7	623	ASN
14	N	92	LYS
11	E	592	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

Mol	Chain	Res	Type
9	C	103	HIS
11	E	130	ASN
14	N	72	GLN
12	G	634	HIS
9	C	130	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 13 ligands modelled in this entry, 9 are monoatomic - leaving 4 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	$\# Z > 2$
15	ADP	3	1001	16	28,29,29	1.38	4 (14%)	43,45,45	1.85	9 (20%)
15	ADP	2	901	16	28,29,29	1.40	4 (14%)	43,45,45	1.86	10 (23%)
18	AGS	7	902	16	32,33,33	0.61	1 (3%)	45,52,52	0.73	1 (2%)
18	AGS	4	1001	16	32,33,33	0.64	1 (3%)	45,52,52	0.74	1 (2%)

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
15	ADP	3	1001	16	-	3/16/32/32	0/3/3/3
15	ADP	2	901	16	-	3/16/32/32	0/3/3/3
18	AGS	7	902	16	-	5/21/38/38	0/3/3/3
18	AGS	4	1001	16	-	8/21/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	2	901	ADP	C5-C4	4.66	1.47	1.39
15	3	1001	ADP	C5-C4	4.61	1.47	1.39
15	3	1001	ADP	C5-C6	2.77	1.48	1.41
15	2	901	ADP	C5-C6	2.76	1.48	1.41
15	2	901	ADP	C8-N7	2.40	1.36	1.31

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	3	1001	ADP	C5-C4-N3	-5.93	118.56	126.72
15	2	901	ADP	C5-C4-N3	-5.70	118.86	126.72
15	3	1001	ADP	N3-C4-N9	4.52	134.85	127.17
15	2	901	ADP	N3-C4-N9	4.44	134.72	127.17
18	4	1001	AGS	PB-O3B-PG	-4.22	117.74	133.17

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

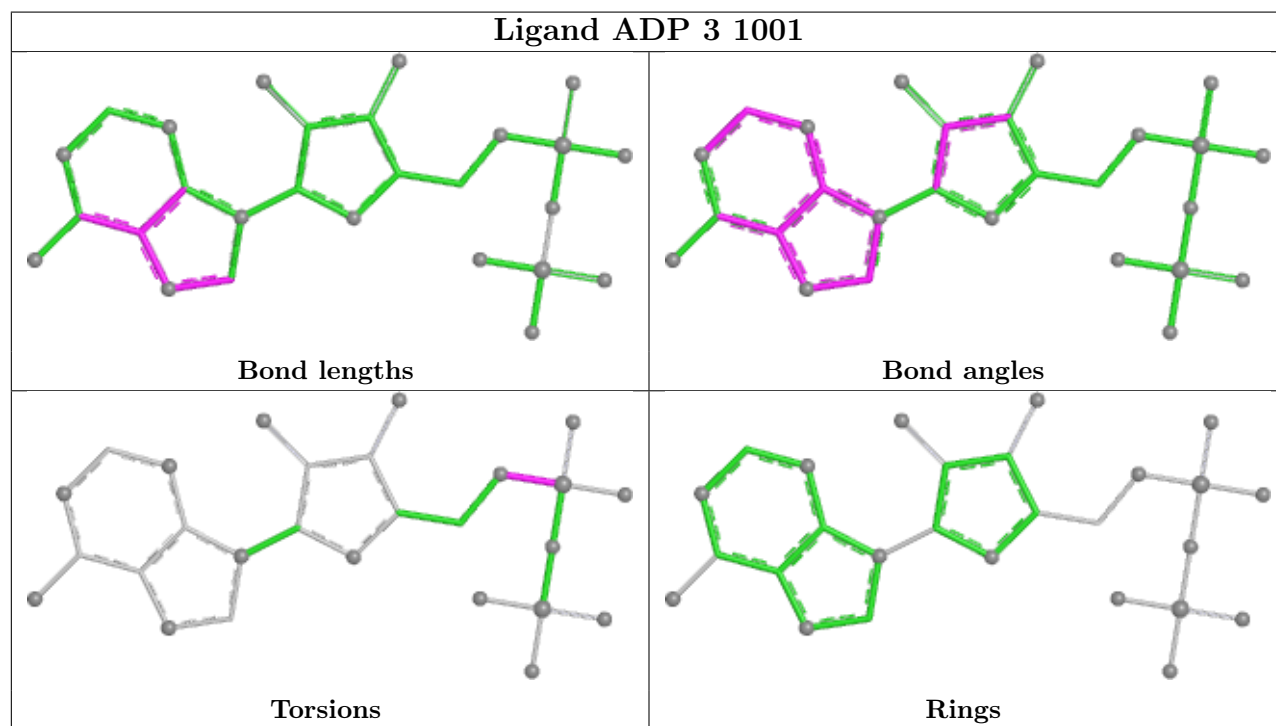
Mol	Chain	Res	Type	Atoms
15	2	901	ADP	C5'-O5'-PA-O1A
15	2	901	ADP	C5'-O5'-PA-O2A
15	2	901	ADP	C5'-O5'-PA-O3A
15	3	1001	ADP	C5'-O5'-PA-O1A
15	3	1001	ADP	C5'-O5'-PA-O2A

There are no ring outliers.

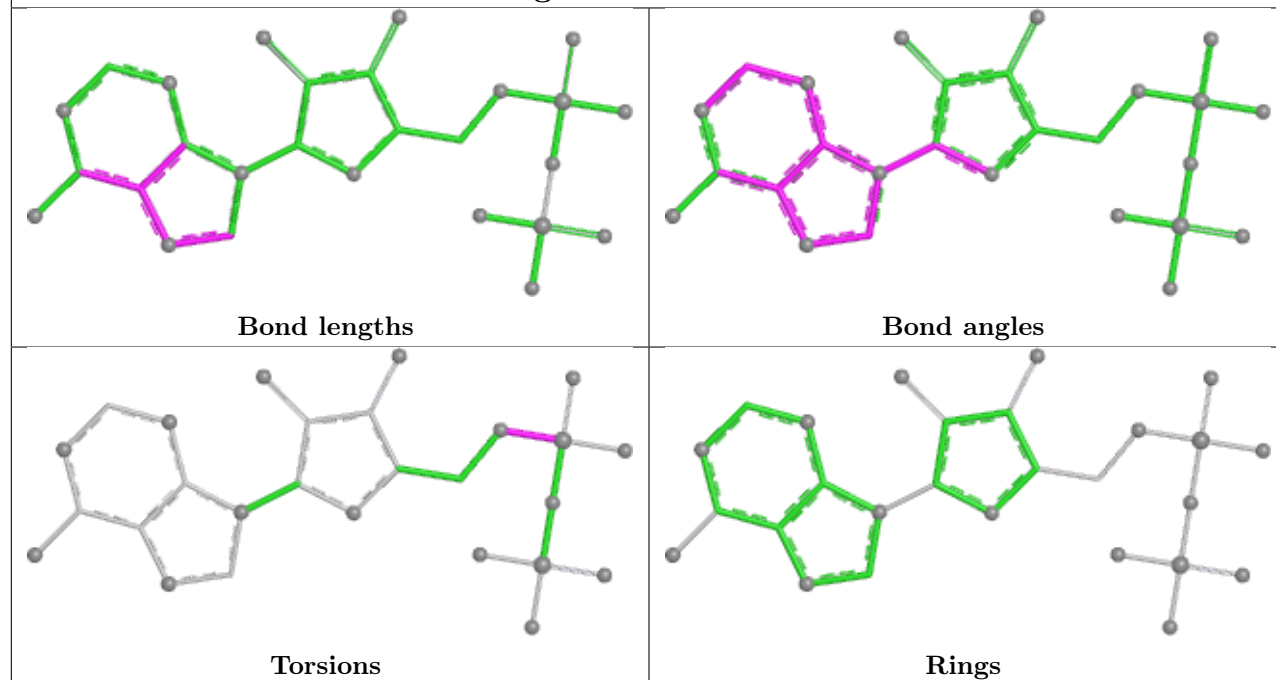
4 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	3	1001	ADP	6	0
15	2	901	ADP	8	0
18	7	902	AGS	7	0
18	4	1001	AGS	6	0

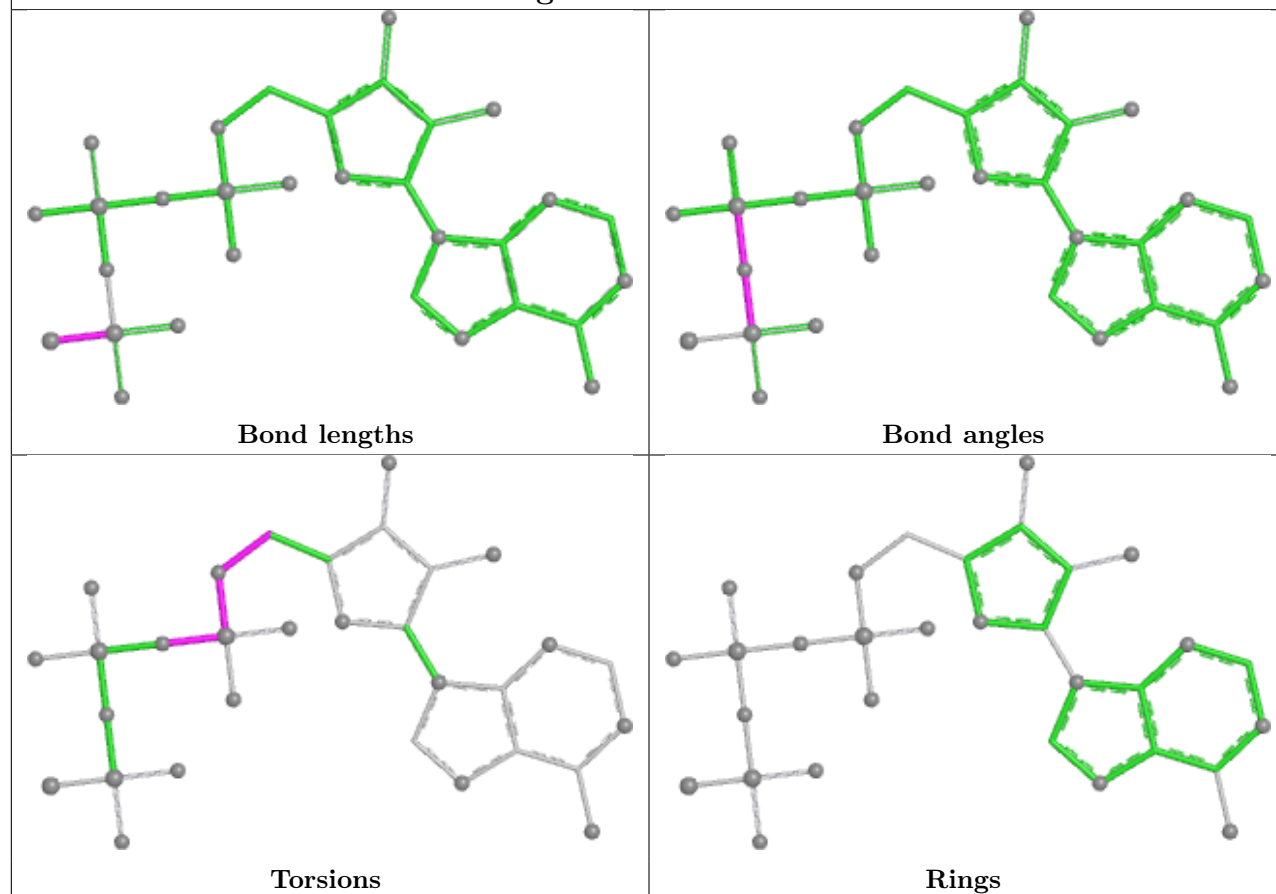
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

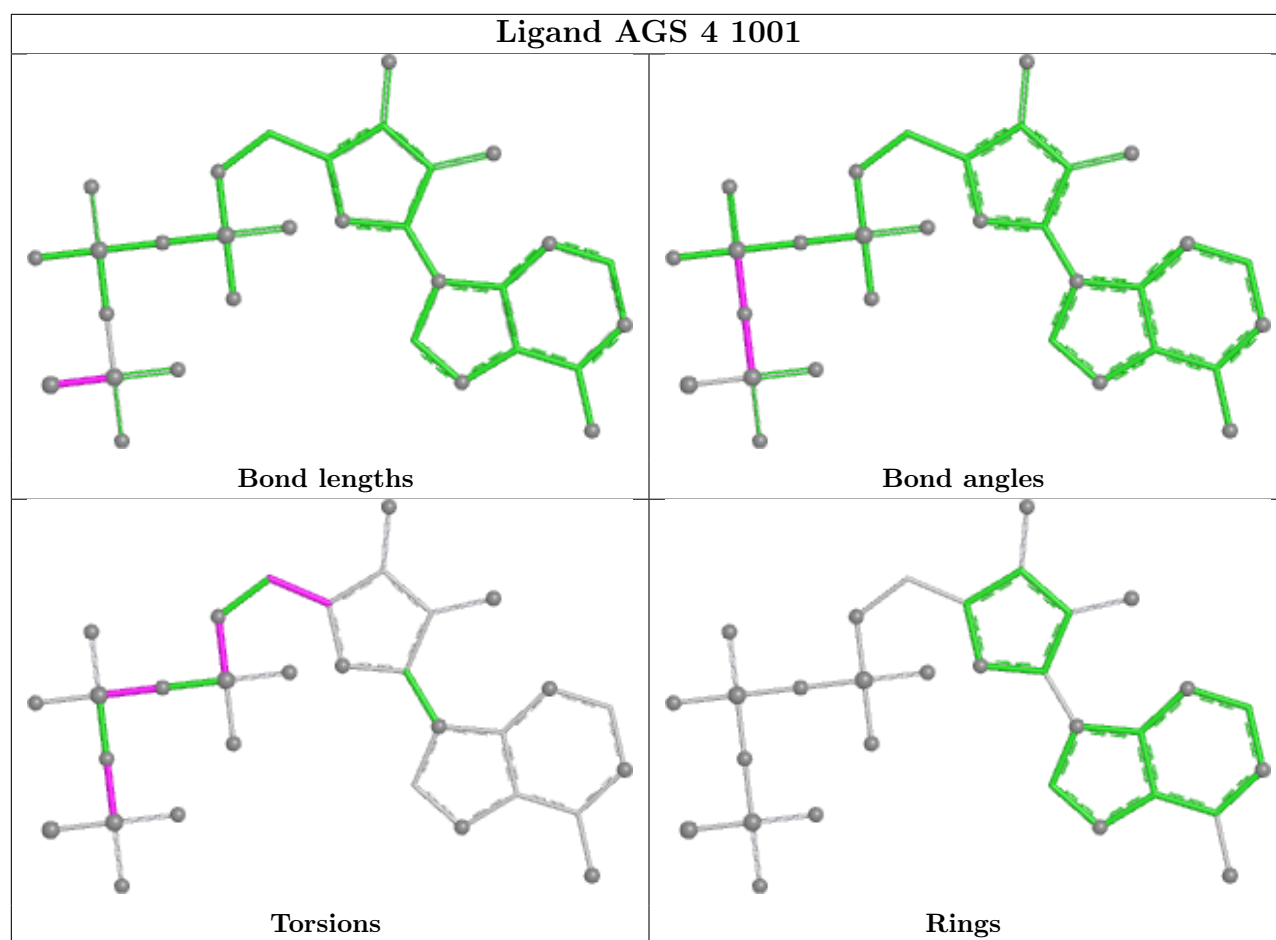


Ligand ADP 2 901



Ligand AGS 7 902





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.

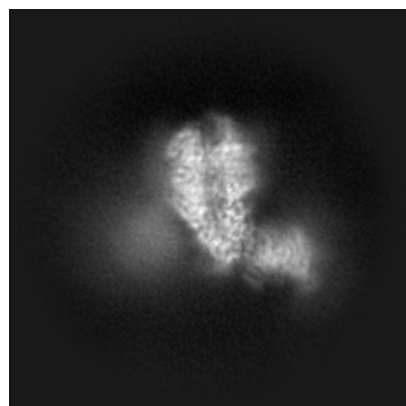
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37343. These allow visual inspection of the internal detail of the map and identification of artifacts.

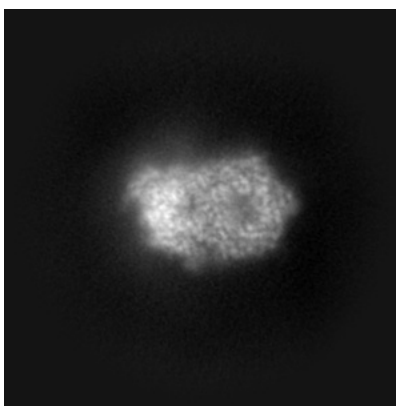
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

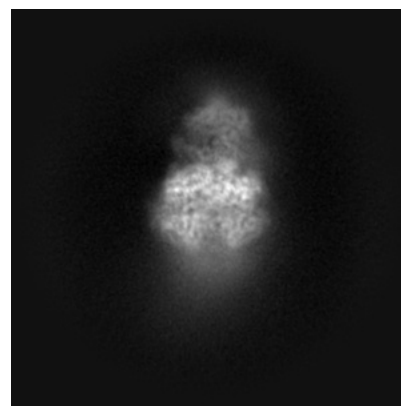
6.1.1 Primary map



X

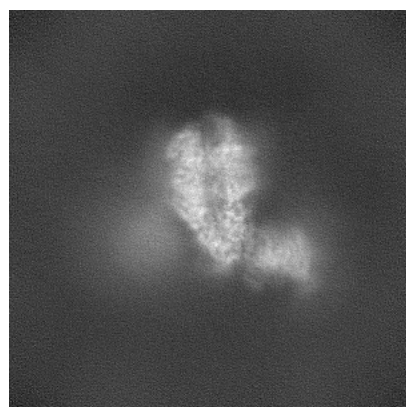


Y

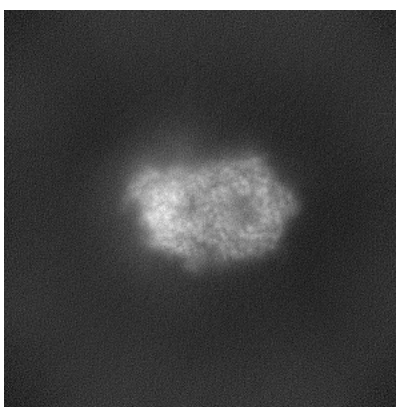


Z

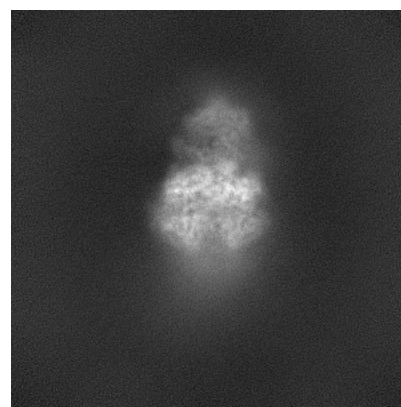
6.1.2 Raw map



X



Y

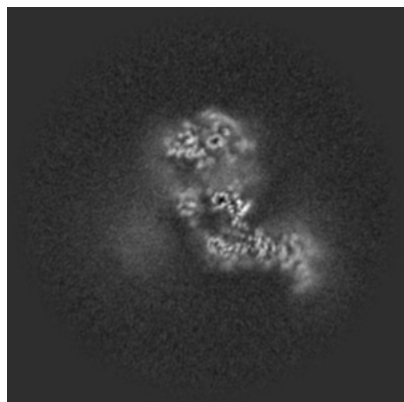


Z

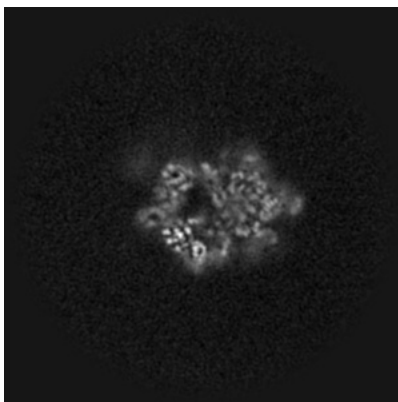
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

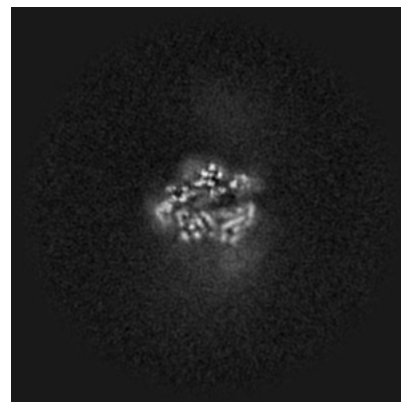
6.2.1 Primary map



X Index: 220

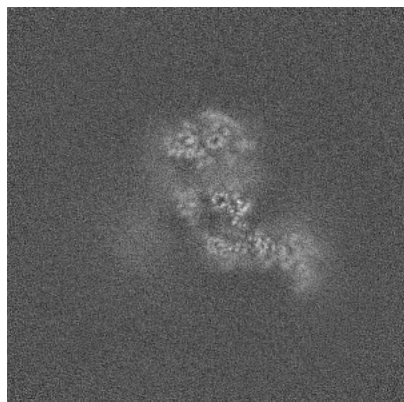


Y Index: 220

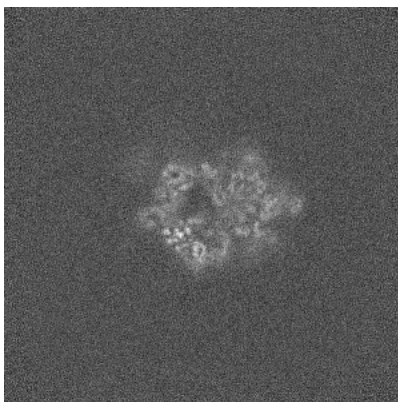


Z Index: 220

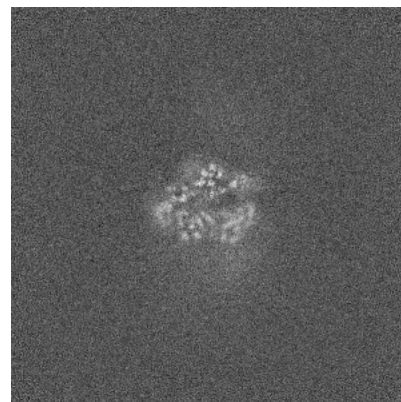
6.2.2 Raw map



X Index: 220



Y Index: 220

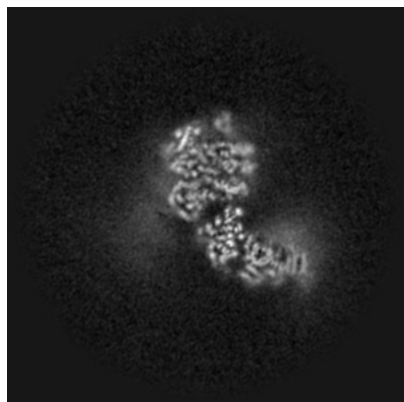


Z Index: 220

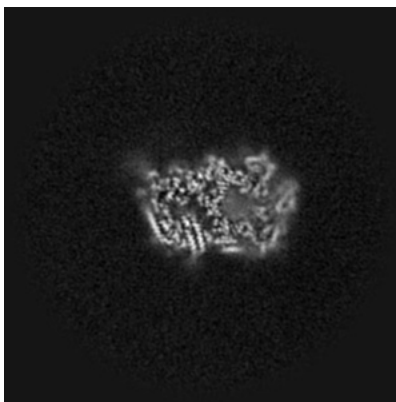
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

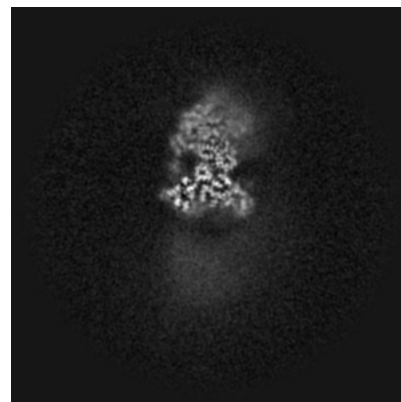
6.3.1 Primary map



X Index: 240

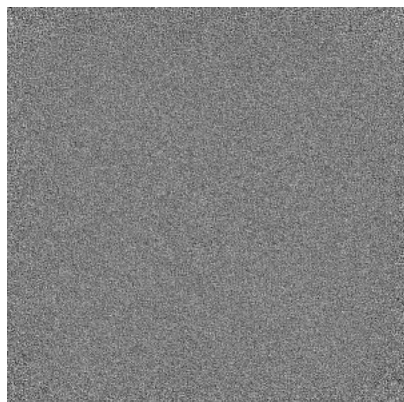


Y Index: 241

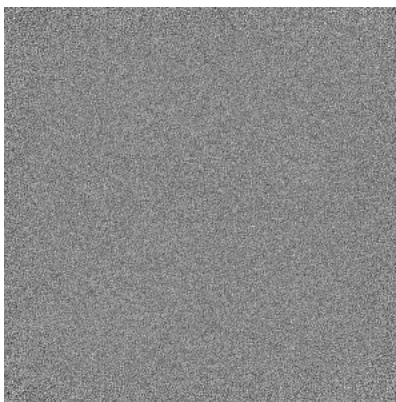


Z Index: 178

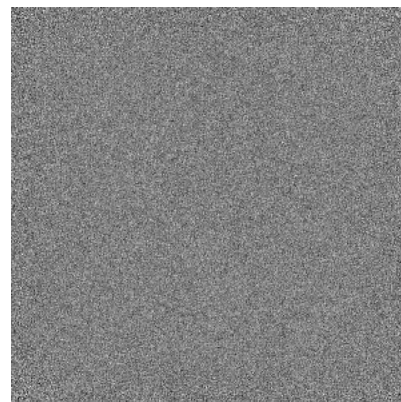
6.3.2 Raw map



X Index: 0



Y Index: 0

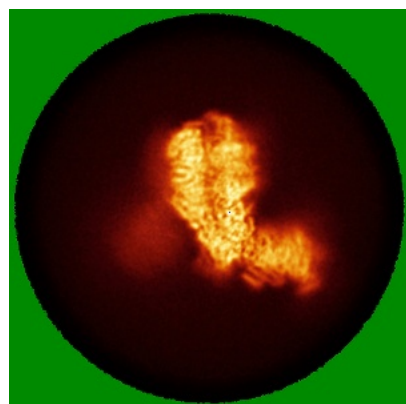


Z Index: 0

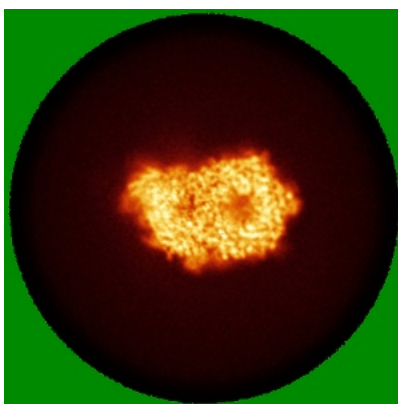
The images above show the largest variance slices of the map in three orthogonal directions.

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

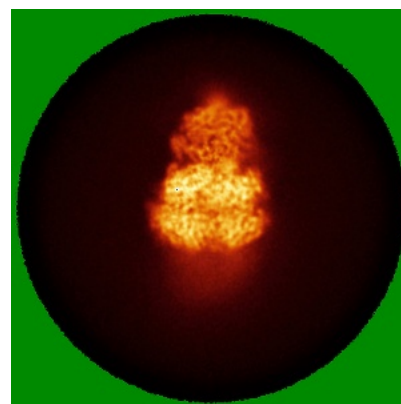
6.4.1 Primary map



X

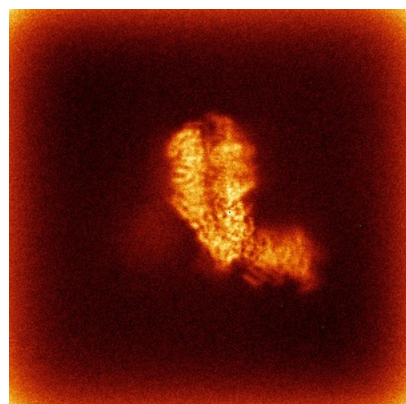


Y

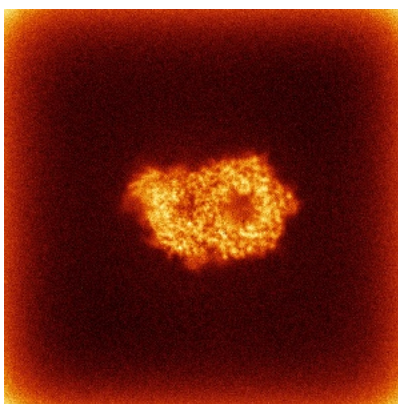


Z

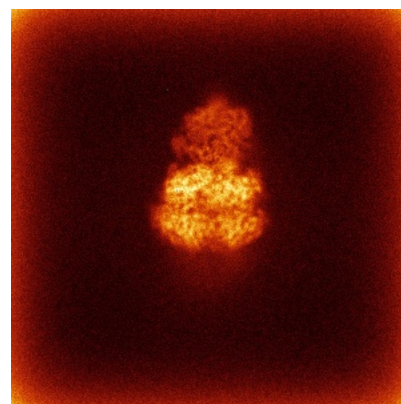
6.4.2 Raw map



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](#)

This section was not generated.

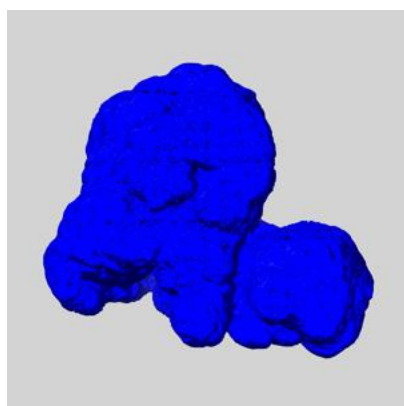
6.6 Mask visualisation [i](#)

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

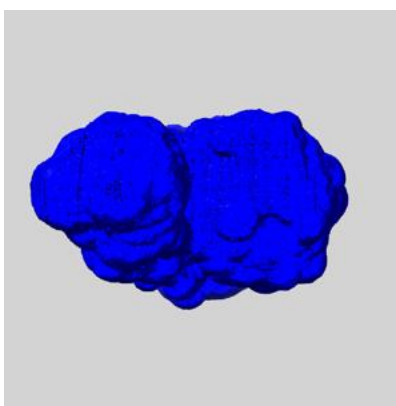
A mask typically either:

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

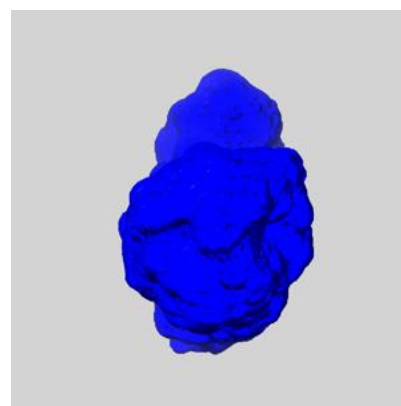
6.6.1 emd_37343_msk_1.map [i](#)



X



Y

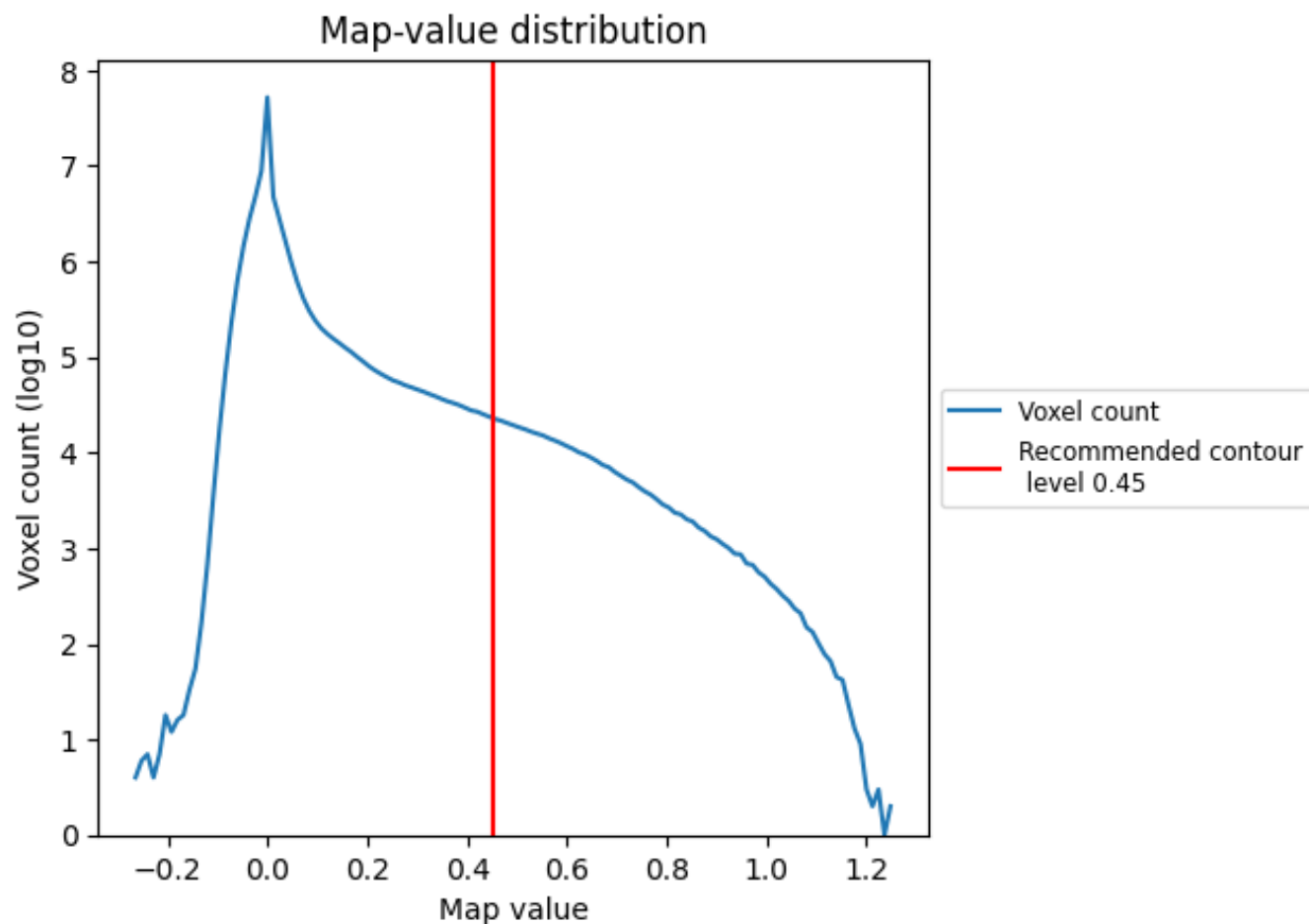


Z

7 Map analysis [i](#)

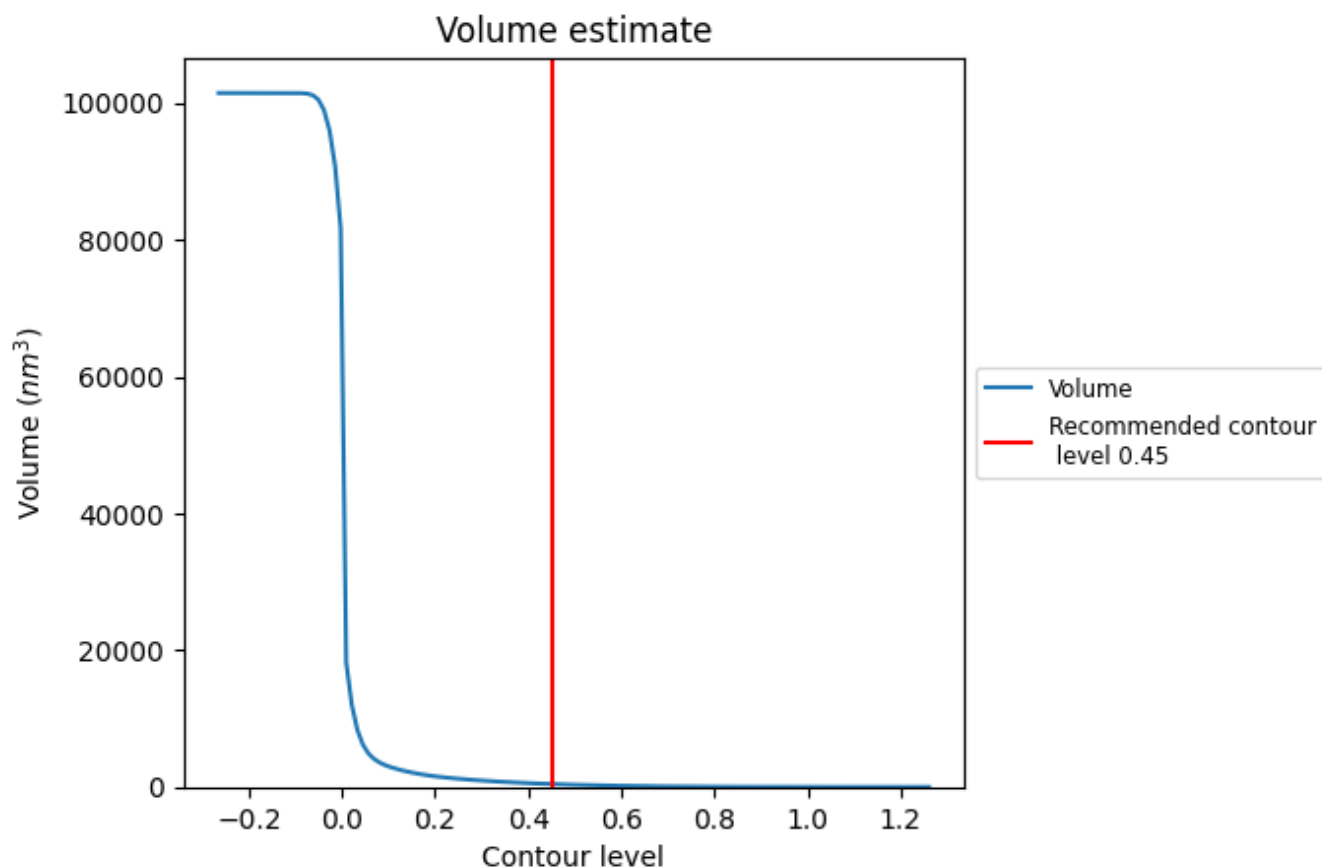
This section contains the results of statistical analysis of the map.

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.

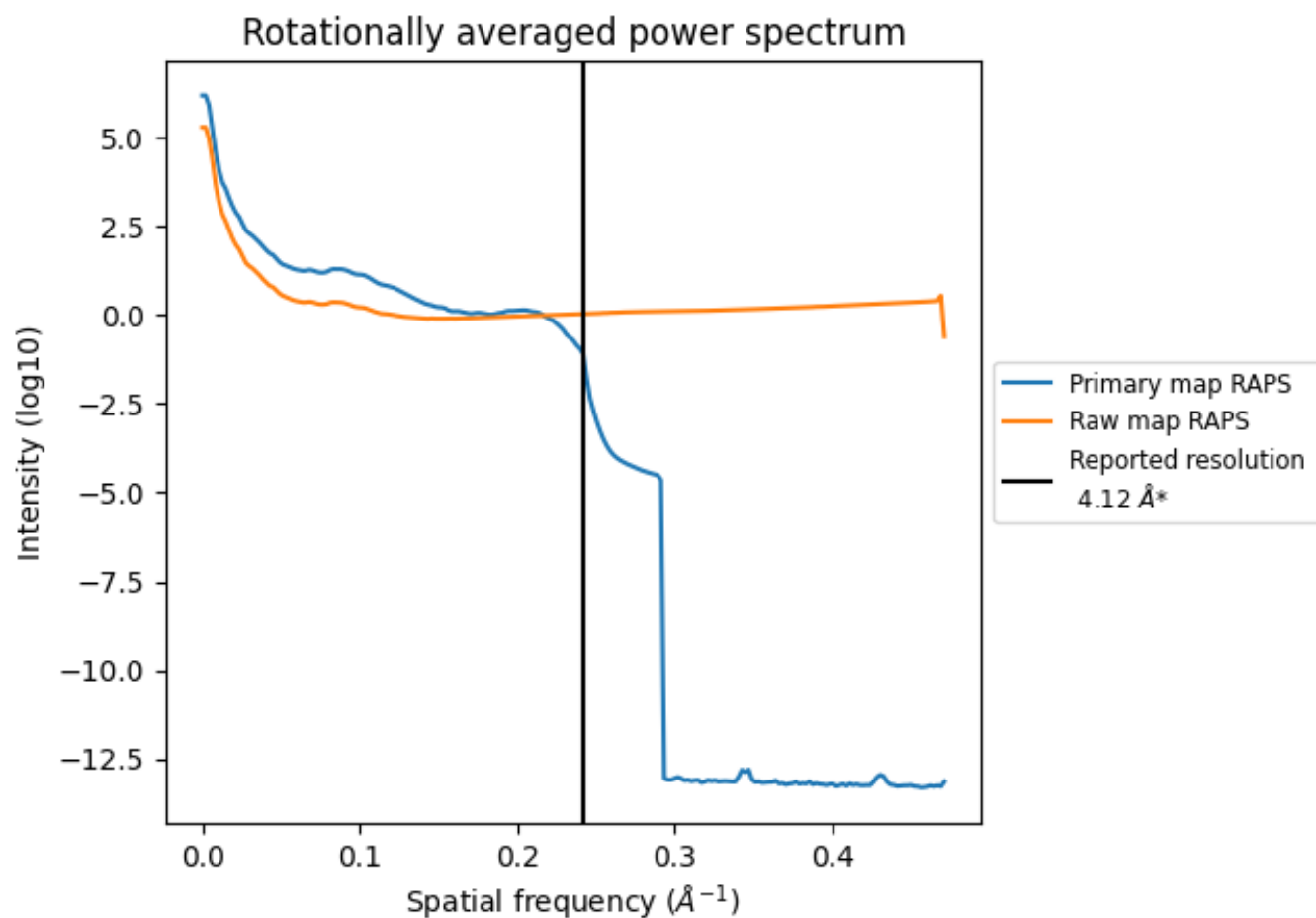
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 427 nm³; this corresponds to an approximate mass of 386 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 ⓘ

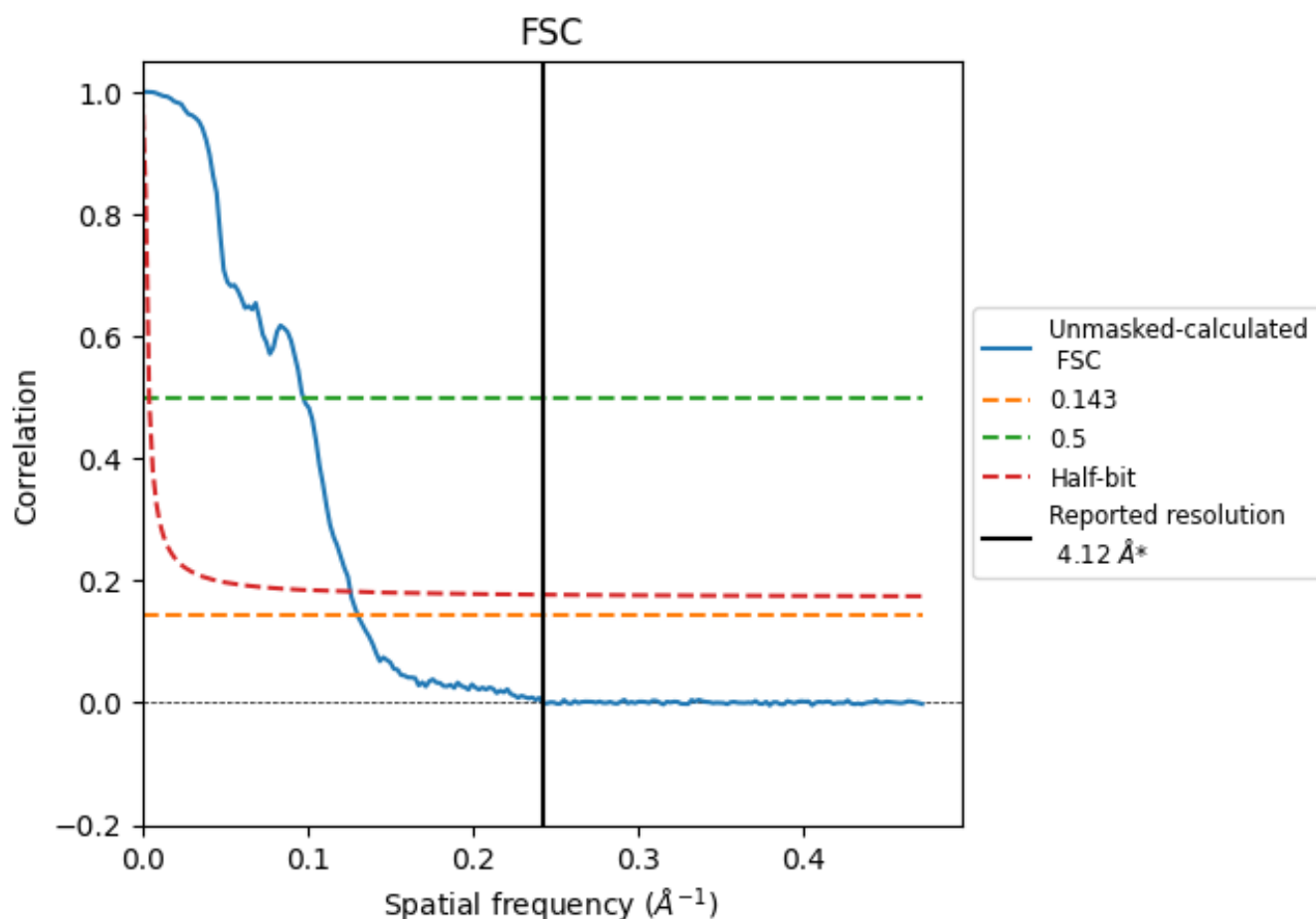


*Reported resolution corresponds to spatial frequency of 0.243 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.243 Å⁻¹

8.2 Resolution estimates [i](#)

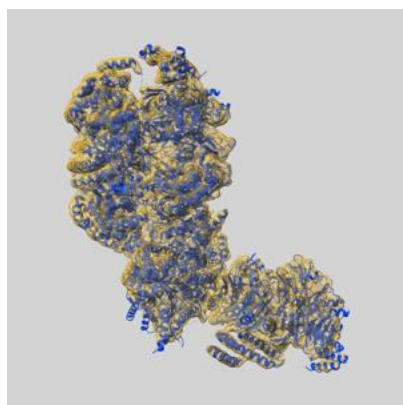
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.12	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.67	10.27	7.94

*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 7.67 differs from the reported value 4.12 by more than 10 %

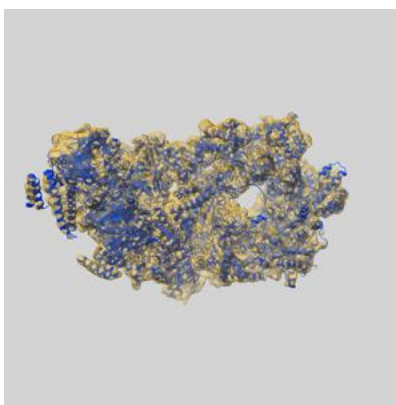
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37343 and PDB model 8W7M. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

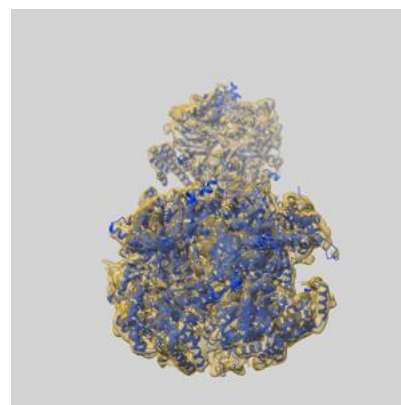
9.1 Map-model overlay [i](#)



X



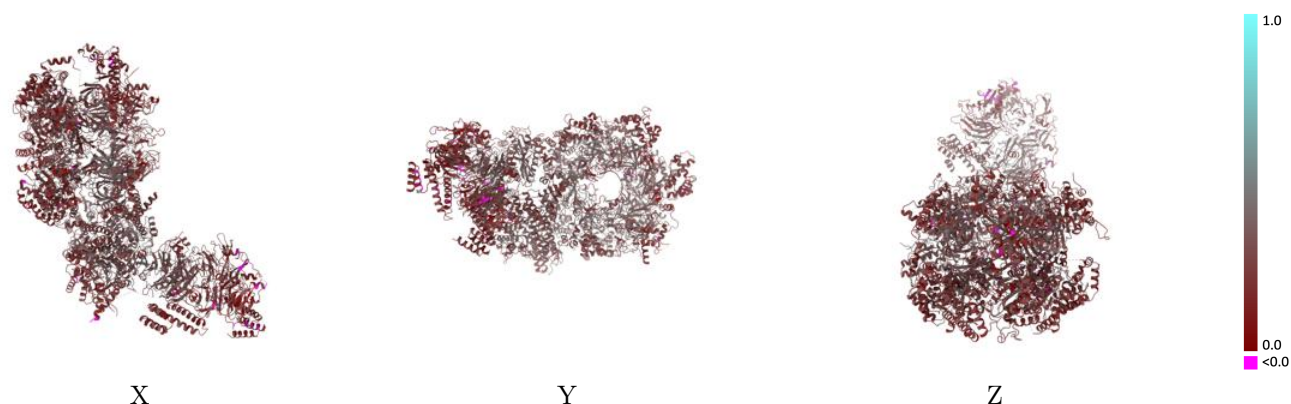
Y



Z

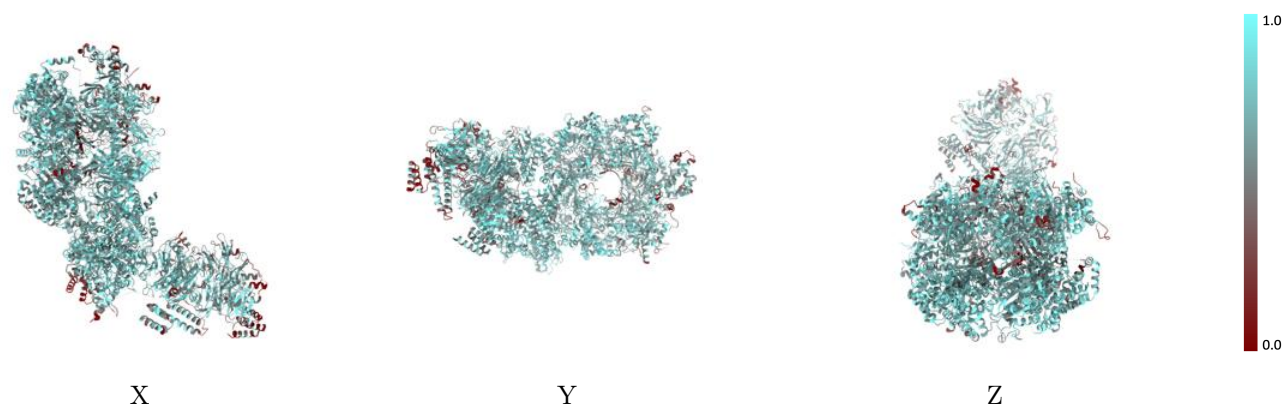
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



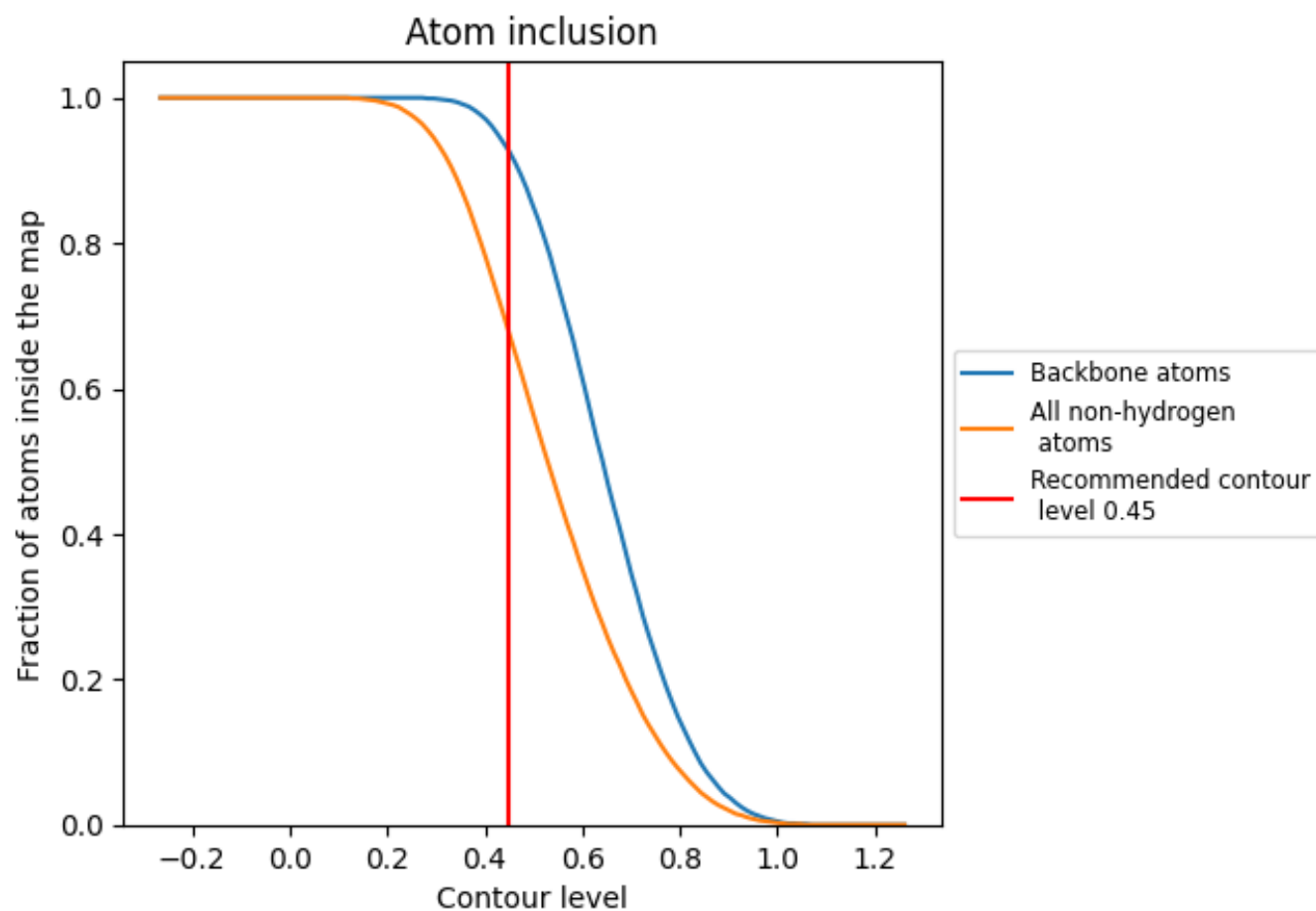
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.45).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 68% 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 (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6760	 0.2670
2	 0.6790	 0.2610
3	 0.7350	 0.2910
4	 0.6630	 0.2440
5	 0.7140	 0.2920
6	 0.6790	 0.2490
7	 0.6590	 0.2580
A	 0.7130	 0.2750
B	 0.7520	 0.3310
C	 0.7550	 0.2980
D	 0.7450	 0.3110
E	 0.7050	 0.2900
F	 0.6880	 0.2980
G	 0.5560	 0.2050
H	 0.6160	 0.2210
I	 0.4560	 0.2750
N	 0.2230	 0.2120

