



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 01:34 PM UTC

PDB ID : 6RUI / pdb_00006rui
EMDB ID : EMD-10006
Title : RNA Polymerase I Pre-initiation complex DNA opening intermediate 2
Authors : Mueller, C.W.; Sadian, Y.; Tafur, L.
Deposited on : 2019-05-28
Resolution : 2.70 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:

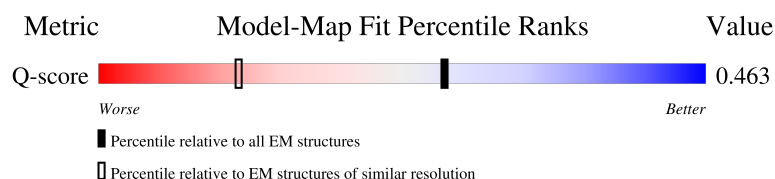
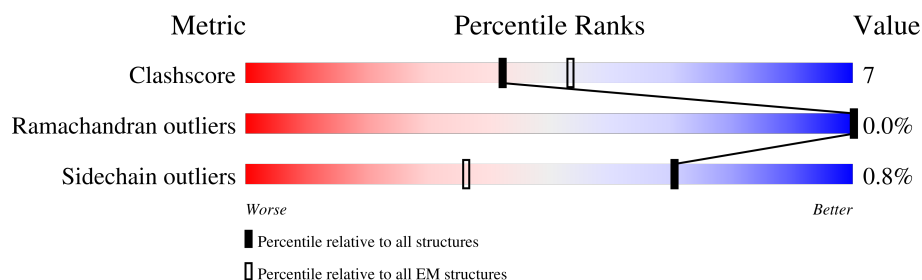
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.70 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	10327 (2.20 - 3.20)

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	T	70	50% 46% 23% 31%
2	U	70	53% 44% 21% 34%
3	I	125	35% 80% 19%
4	N	233	35% 52% 8% 40%

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Mol	Chain	Length	Quality of chain
5	M	415	
6	A	1664	
7	B	1203	
8	C	335	
9	D	137	
10	E	215	
11	F	155	
12	G	326	
13	H	146	
14	J	70	
15	K	142	
16	L	70	
17	O	627	
18	Q	514	
19	S	894	
20	R	507	

2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 51525 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 DNA chain called Template strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	T	48	Total	C	N	O	P	0	0
			958	462	153	295	48		

- Molecule 2 is a DNA chain called Nontemplate strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	U	46	Total	C	N	O	P	0	0
			965	457	197	266	45		

- Molecule 3 is a protein called DNA-directed RNA polymerase I subunit RPA12.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	124	Total	C	N	O	S	0	0
			942	584	160	189	9		

- Molecule 4 is a protein called DNA-directed RNA polymerase I subunit RPA34.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	139	Total	C	N	O	S	0	0
			1103	706	179	214	4		

- Molecule 5 is a protein called DNA-directed RNA polymerase I subunit RPA49.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	M	108	Total	C	N	O	0	0
			856	543	142	171		

- Molecule 6 is a protein called DNA-directed RNA polymerase I subunit RPA190.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	1465	Total	C	N	O	S	0	0
			11565	7306	2011	2186	62		

- Molecule 7 is a protein called DNA-directed RNA polymerase I subunit RPA135.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	1180	Total	C	N	O	S	0	0
			9365	5920	1641	1754	50		

- Molecule 8 is a protein called DNA-directed RNA polymerases I and III subunit RPAC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	304	Total	C	N	O	S	0	0
			2418	1536	414	460	8		

- Molecule 9 is a protein called DNA-directed RNA polymerase I subunit RPA14.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	70	Total	C	N	O	S	0	0
			551	340	100	109	2		

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	215	Total	C	N	O	S	0	0
			1759	1116	310	321	12		

- Molecule 11 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	100	Total	C	N	O	S	0	0
			823	522	144	154	3		

- Molecule 12 is a protein called DNA-directed RNA polymerase I subunit RPA43.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	202	Total	C	N	O	S	0	0
			1600	1026	276	293	5		

- Molecule 13 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	134	Total	C	N	O	S	0	0
			1072	676	181	211	4		

- Molecule 14 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

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

- Molecule 15 is a protein called DNA-directed RNA polymerases I and III subunit RPAC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	103	Total	C	N	O	S	0	0
			810	506	132	167	5		

- Molecule 16 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

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

- Molecule 17 is a protein called RNA polymerase I-specific transcription initiation factor RRN3.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	504	Total	C	N	O	S	0	0
			4139	2663	666	788	22		

- Molecule 18 is a protein called RNA polymerase I-specific transcription initiation factor RRN7.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	477	Total	C	N	O	S	0	0
			3936	2529	675	712	20		

- Molecule 19 is a protein called RNA polymerase I-specific transcription initiation factor RRN6.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	610	Total	C	N	O	S	0	0
			4963	3160	842	950	11		

- Molecule 20 is a protein called RNA polymerase I-specific transcription initiation factor RRN11.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R	330	Total	C	N	O	S	0	0
			2771	1791	489	480	11		

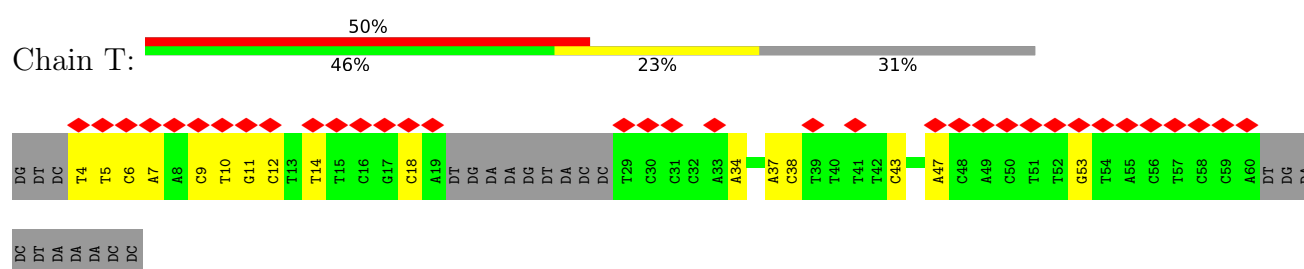
- Molecule 21 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
21	Q	1	Total	Zn	0
			1	1	

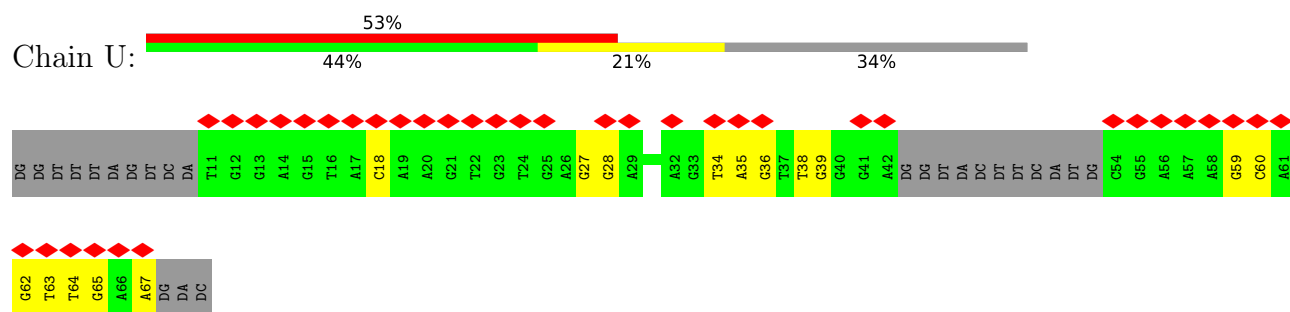
3 Residue-property plots [i](#)

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.

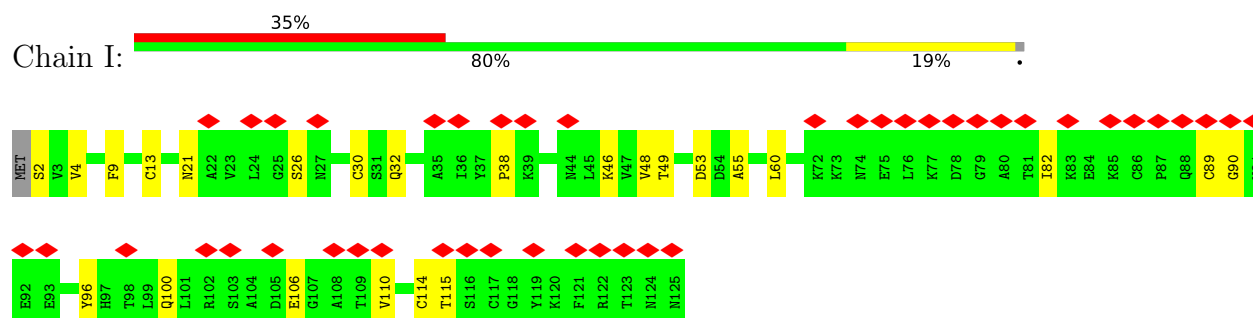
- Molecule 1: Template strand



- Molecule 2: Nontemplate strand

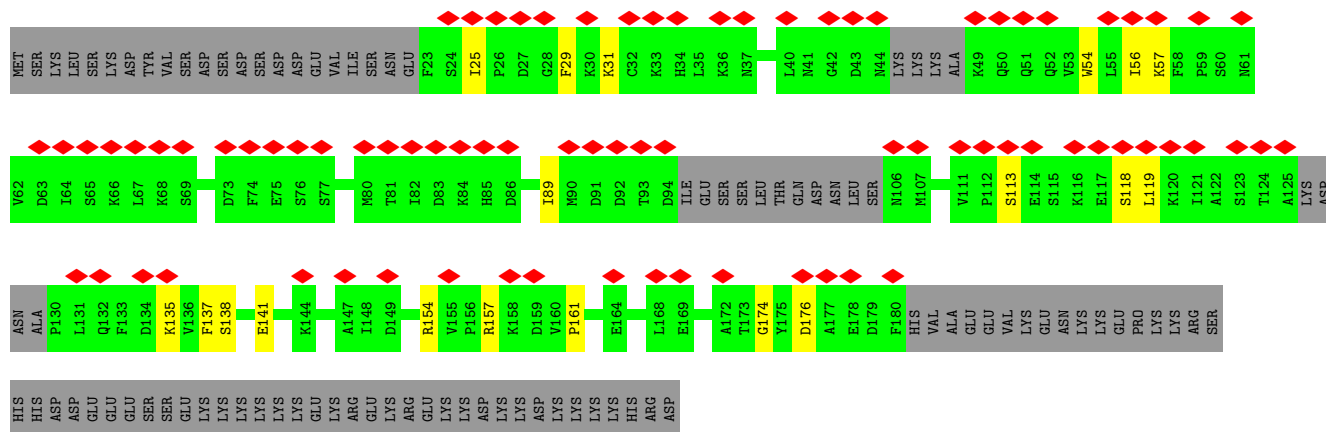


- Molecule 3: DNA-directed RNA polymerase I subunit RPA12

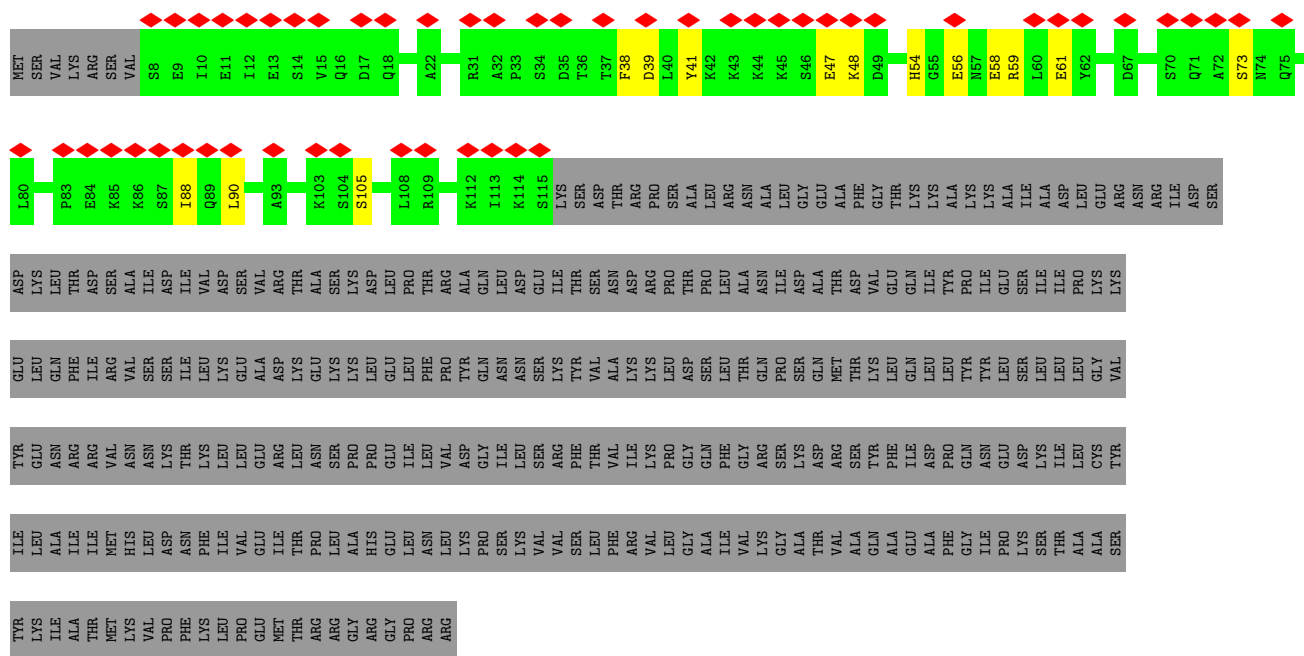


- Molecule 4: DNA-directed RNA polymerase I subunit RPA34

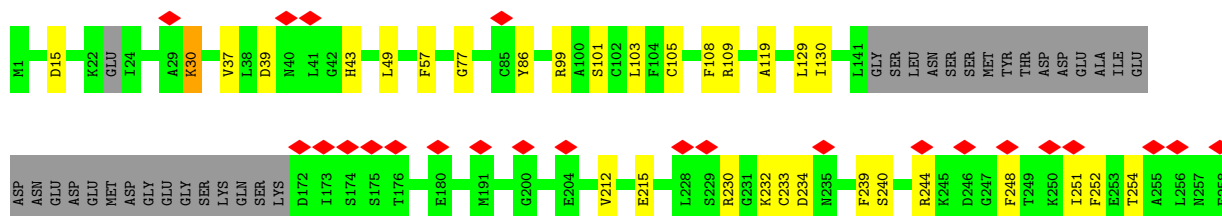
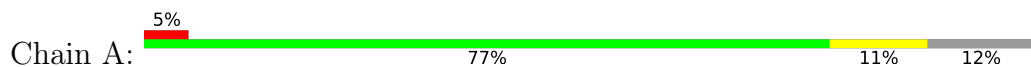


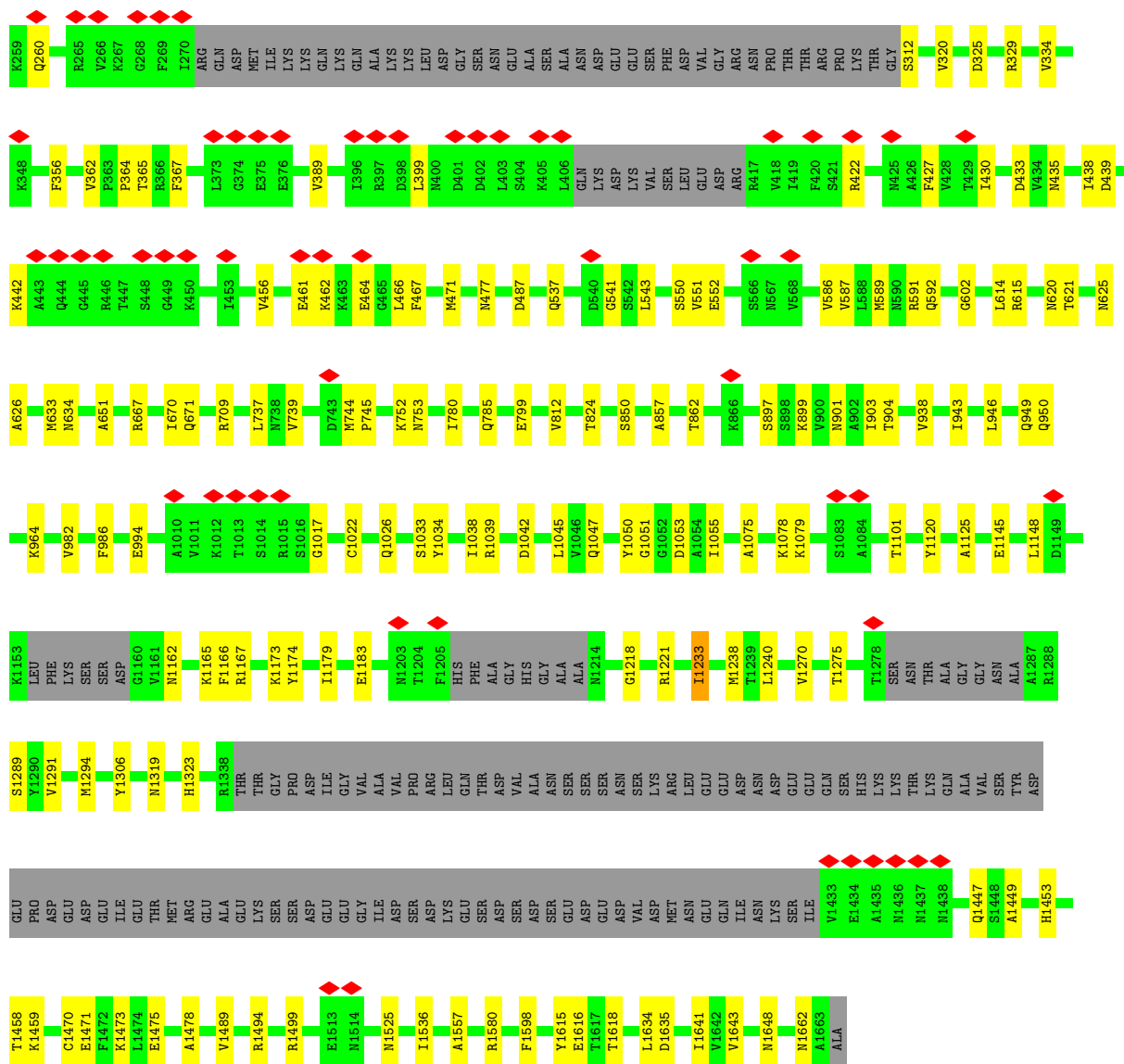


• Molecule 5: DNA-directed RNA polymerase I subunit RPA49



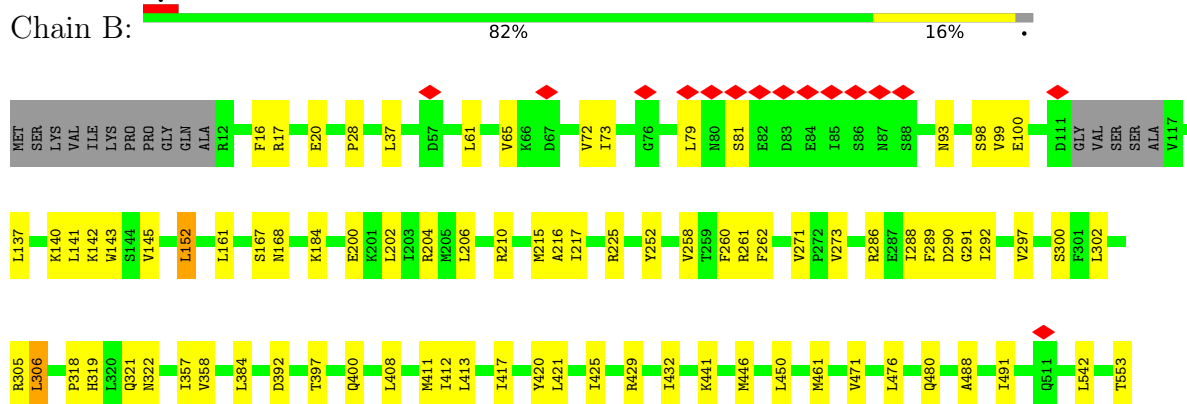
• Molecule 6: DNA-directed RNA polymerase I subunit RPA190

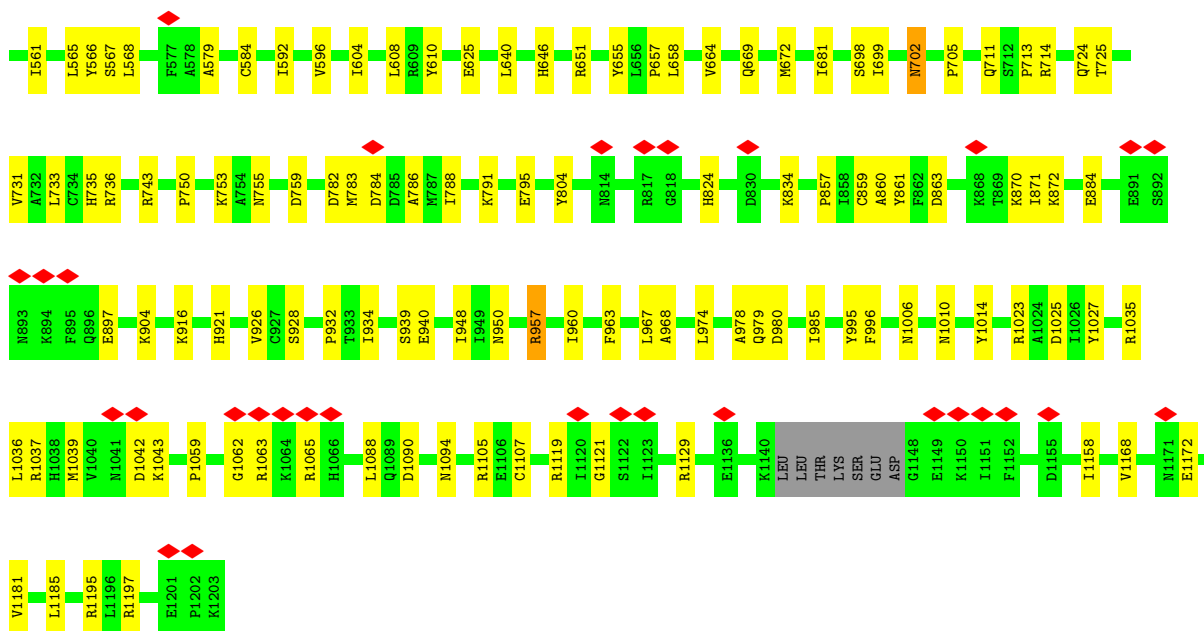




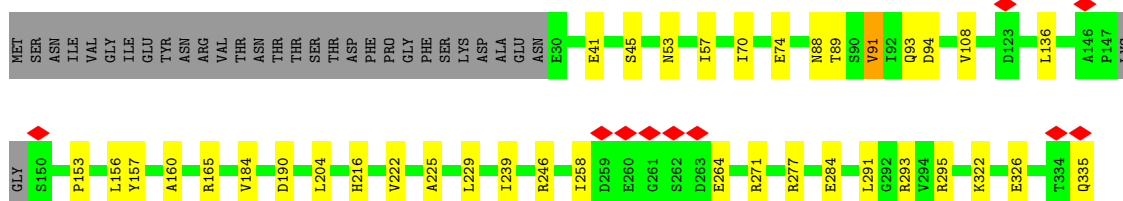
• Molecule 7: DNA-directed RNA polymerase I subunit RPA135

Chain B:

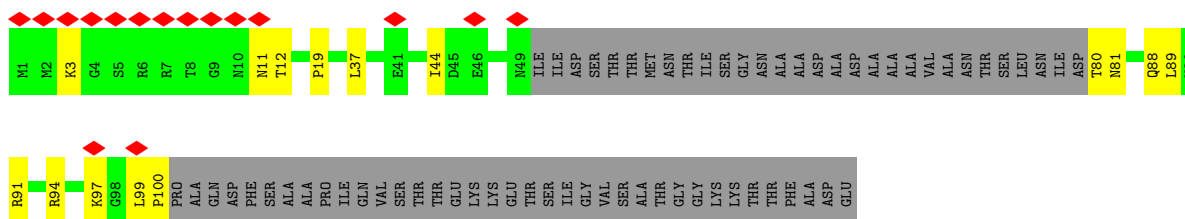
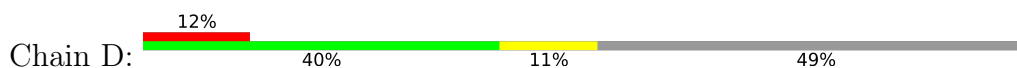




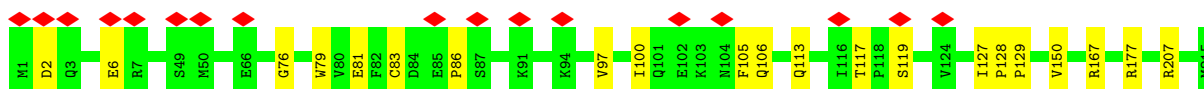
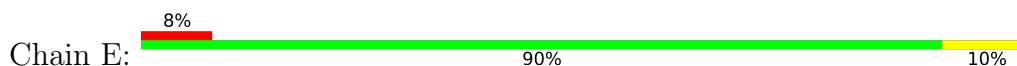
- Molecule 8: DNA-directed RNA polymerases I and III subunit RPAC1



- Molecule 9: DNA-directed RNA polymerase I subunit RPA14

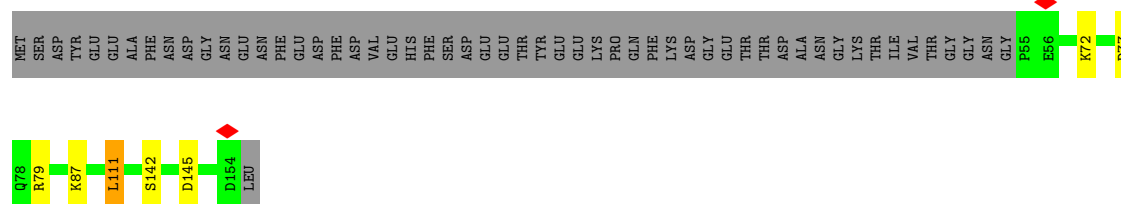


- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC1



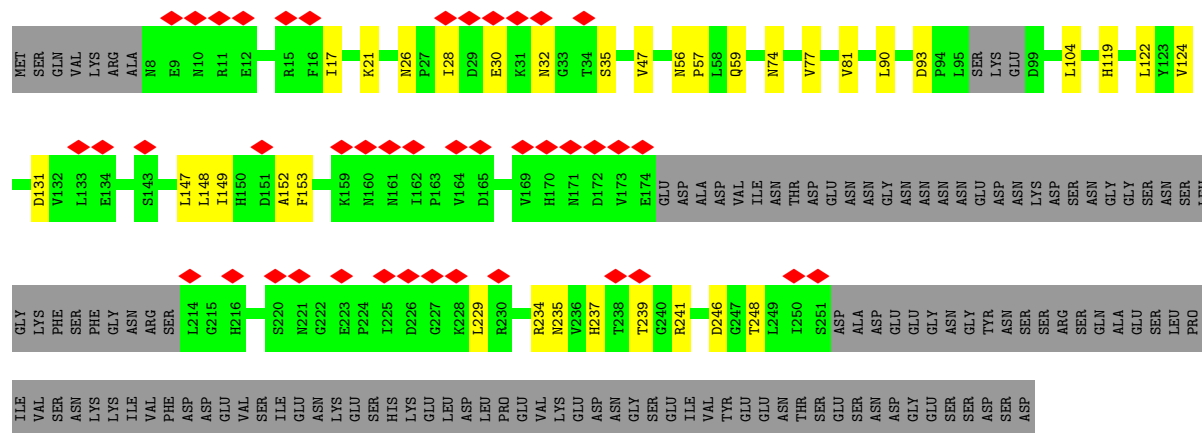
- Molecule 11: DNA-directed RNA polymerases I, II, and III subunit RPABC2

Chain F: 



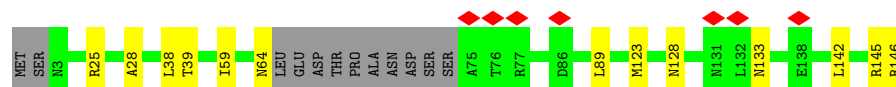
- Molecule 12: DNA-directed RNA polymerase I subunit RPA43

Chain G: 



- Molecule 13: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain H: 



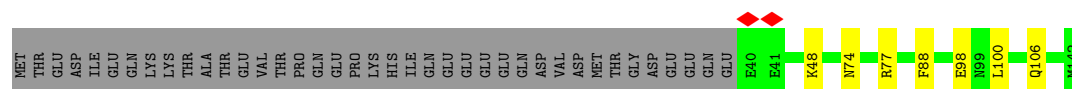
- Molecule 14: DNA-directed RNA polymerases I, II, and III subunit RPABC5

Chain J: 

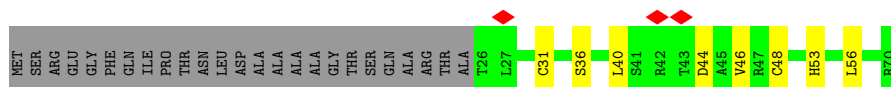


- Molecule 15: DNA-directed RNA polymerases I and III subunit RPAC2

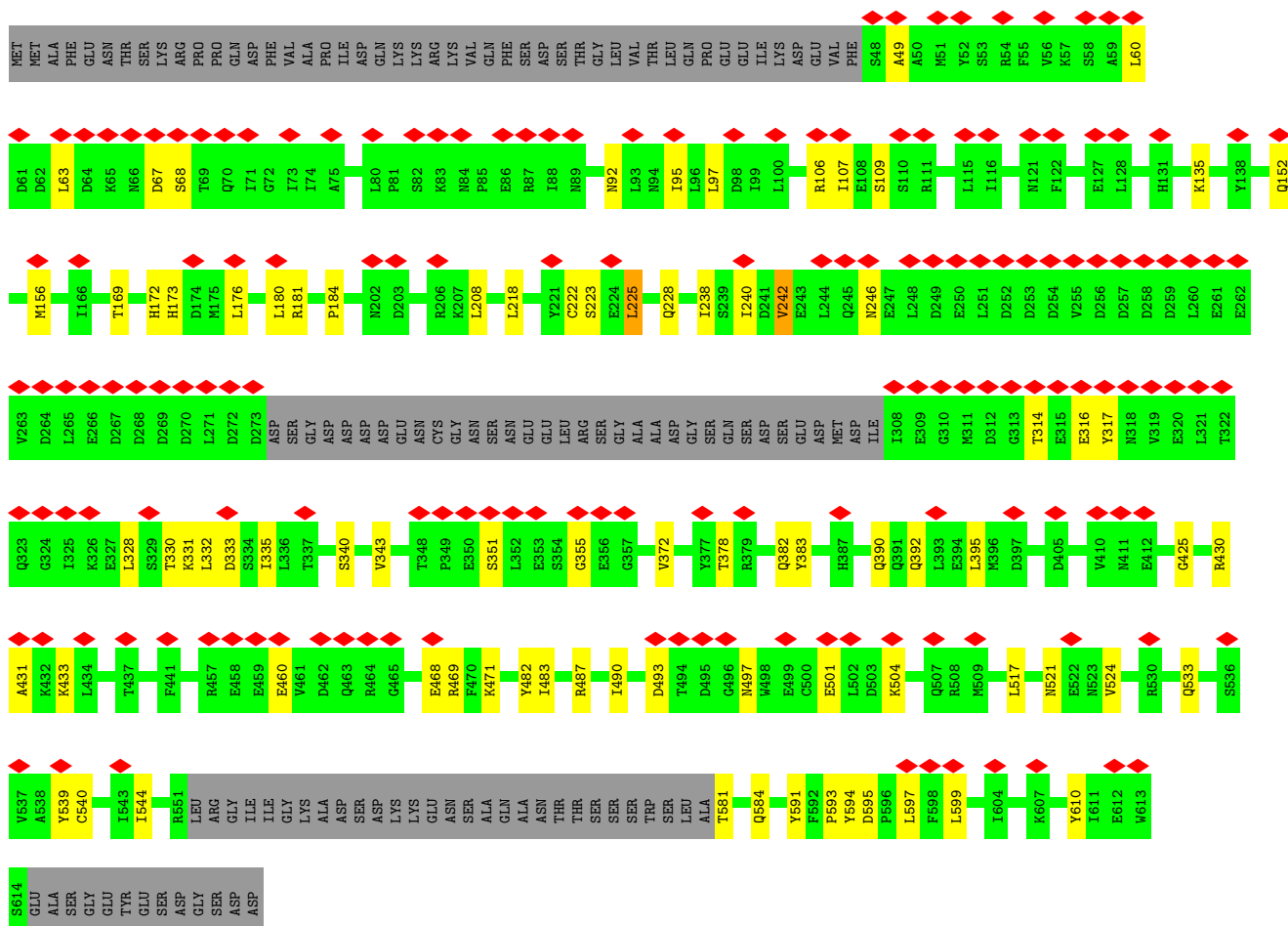
Chain K: 



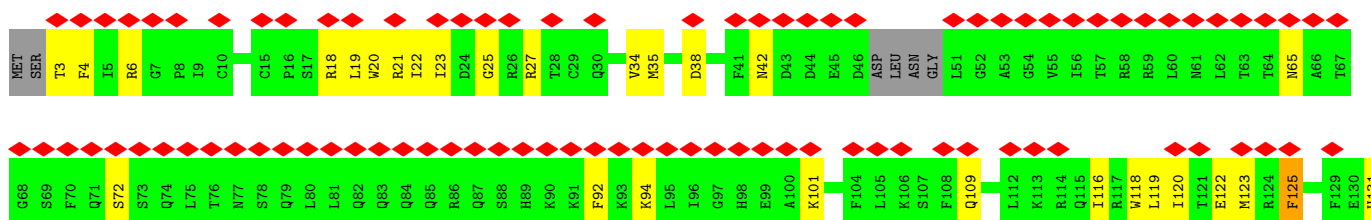
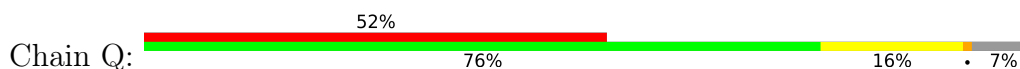
- Molecule 16: DNA-directed RNA polymerases I, II, and III subunit RPABC4



- Molecule 17: RNA polymerase I-specific transcription initiation factor RRN3



- Molecule 18: RNA polymerase I-specific transcription initiation factor RRN7



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	42727	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 ($e^-/\text{\AA}^2$)	1.1075	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.317	Depositor
Minimum map value	-0.171	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	395.19998, 395.19998, 395.19998	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	Depositor

5 Model quality

5.1 Standard geometry

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	T	0.31	0/1065	0.57	0/1633
2	U	0.27	0/1089	0.49	0/1682
3	I	0.34	0/955	0.58	0/1288
4	N	0.27	0/1124	0.53	0/1512
5	M	0.28	0/872	0.59	0/1170
6	A	0.49	0/11776	0.62	2/15906 (0.0%)
7	B	0.57	1/9572 (0.0%)	0.69	4/12941 (0.0%)
8	C	0.53	0/2469	0.63	0/3347
9	D	0.35	0/557	0.61	0/750
10	E	0.42	0/1795	0.54	0/2416
11	F	0.51	0/838	0.62	0/1129
12	G	0.38	0/1637	0.54	0/2226
13	H	0.49	0/1090	0.63	0/1476
14	J	0.66	0/578	0.78	2/775 (0.3%)
15	K	0.55	0/821	0.61	0/1108
16	L	0.52	0/361	0.78	0/478
17	O	0.34	0/4226	0.63	0/5717
18	Q	0.34	0/4028	0.69	1/5441 (0.0%)
19	S	0.30	0/5065	0.65	0/6859
20	R	0.40	0/2836	0.74	3/3817 (0.1%)
All	All	0.45	1/52754 (0.0%)	0.64	12/71671 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	28	PRO	CA-C	-5.01	1.49	1.51

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	Q	125	PHE	N-CA-C	-7.34	98.55	109.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	J	14	VAL	N-CA-C	-5.78	108.22	113.71
6	A	1218	GLY	CA-C-N	5.73	123.85	120.24
6	A	1218	GLY	C-N-CA	5.73	123.85	120.24
7	B	783	MET	CA-C-N	5.71	132.44	121.54

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	T	958	0	547	34	0
2	U	965	0	518	27	0
3	I	942	0	937	21	0
4	N	1103	0	1106	15	0
5	M	856	0	855	10	0
6	A	11565	0	11657	120	0
7	B	9365	0	9232	160	0
8	C	2418	0	2401	26	0
9	D	551	0	558	13	0
10	E	1759	0	1788	15	0
11	F	823	0	841	4	0
12	G	1600	0	1600	21	0
13	H	1072	0	1042	8	0
14	J	569	0	589	12	0
15	K	810	0	801	4	0
16	L	359	0	385	5	0
17	O	4139	0	4061	54	0
18	Q	3936	0	3918	73	0
19	S	4963	0	4890	94	0
20	R	2771	0	2844	63	0
21	Q	1	0	0	0	0
All	All	51525	0	50570	667	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 667 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)
3:I:13:CYS:SG	3:I:32:GLN:HB2	1.68	1.33
7:B:860:ALA:CB	7:B:871:ILE:HG22	1.70	1.20
6:A:986:PHE:HB3	7:B:960:ILE:HD12	1.21	1.11
3:I:13:CYS:SG	3:I:32:GLN:CB	2.38	1.09
18:Q:101:LYS:HD2	18:Q:152:LEU:HD21	1.35	1.07

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	
3	I	122/125 (98%)	103 (84%)	19 (16%)	0	100	100
4	N	131/233 (56%)	119 (91%)	12 (9%)	0	100	100
5	M	106/415 (26%)	93 (88%)	13 (12%)	0	100	100
6	A	1449/1664 (87%)	1366 (94%)	83 (6%)	0	100	100
7	B	1174/1203 (98%)	1106 (94%)	68 (6%)	0	100	100
8	C	300/335 (90%)	287 (96%)	13 (4%)	0	100	100
9	D	66/137 (48%)	63 (96%)	3 (4%)	0	100	100
10	E	213/215 (99%)	204 (96%)	9 (4%)	0	100	100
11	F	98/155 (63%)	93 (95%)	4 (4%)	1 (1%)	12	32
12	G	196/326 (60%)	185 (94%)	11 (6%)	0	100	100
13	H	130/146 (89%)	121 (93%)	9 (7%)	0	100	100
14	J	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
15	K	101/142 (71%)	96 (95%)	5 (5%)	0	100	100
16	L	43/70 (61%)	38 (88%)	5 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	O	498/627 (79%)	465 (93%)	33 (7%)	0	100	100
18	Q	469/514 (91%)	414 (88%)	54 (12%)	1 (0%)	43	68
19	S	594/894 (66%)	524 (88%)	70 (12%)	0	100	100
20	R	322/507 (64%)	290 (90%)	31 (10%)	1 (0%)	36	60
All	All	6079/7778 (78%)	5632 (93%)	444 (7%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	Q	281	ILE
11	F	87	LYS
20	R	356	PRO

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	
3	I	109/110 (99%)	107 (98%)	2 (2%)	51	78
4	N	128/220 (58%)	127 (99%)	1 (1%)	73	88
5	M	98/371 (26%)	98 (100%)	0	100	100
6	A	1293/1465 (88%)	1288 (100%)	5 (0%)	84	93
7	B	1029/1053 (98%)	1017 (99%)	12 (1%)	63	84
8	C	269/296 (91%)	265 (98%)	4 (2%)	57	81
9	D	65/116 (56%)	65 (100%)	0	100	100
10	E	197/197 (100%)	197 (100%)	0	100	100
11	F	90/137 (66%)	89 (99%)	1 (1%)	65	85
12	G	180/291 (62%)	180 (100%)	0	100	100
13	H	116/128 (91%)	116 (100%)	0	100	100
14	J	64/65 (98%)	61 (95%)	3 (5%)	23	51
15	K	93/130 (72%)	93 (100%)	0	100	100

Continued on next page...

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	L	40/57 (70%)	40 (100%)	0	100	100
17	O	466/576 (81%)	461 (99%)	5 (1%)	65	85
18	Q	436/476 (92%)	435 (100%)	1 (0%)	87	95
19	S	563/828 (68%)	558 (99%)	5 (1%)	70	87
20	R	313/474 (66%)	307 (98%)	6 (2%)	50	77
All	All	5549/6990 (79%)	5504 (99%)	45 (1%)	70	88

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	O	223	SER
19	S	363	ILE
17	O	225	LEU
17	O	490	ILE
19	S	415	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 61 such sidechains are listed below:

Mol	Chain	Res	Type
7	B	735	HIS
19	S	595	GLN
11	F	59	GLN
19	S	580	ASN
20	R	319	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

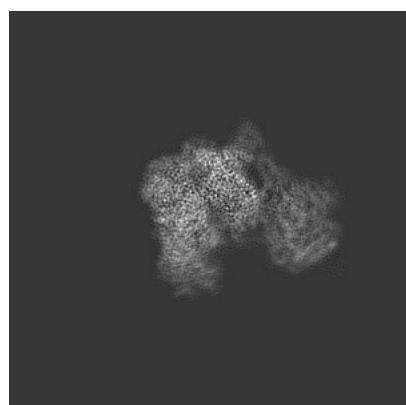
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10006. These allow visual inspection of the internal detail of the map and identification of artifacts.

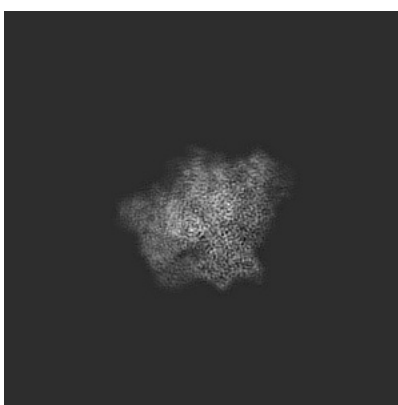
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

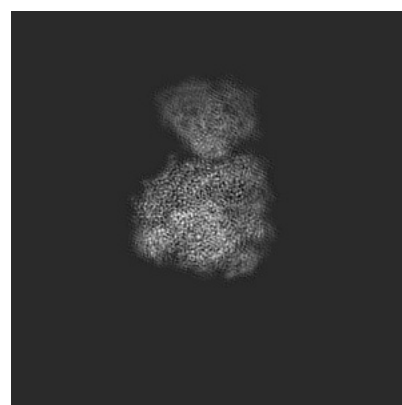
6.1.1 Primary map



X



Y

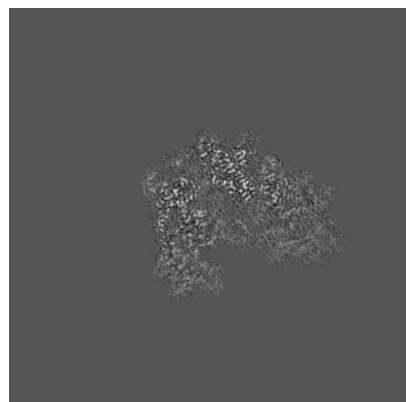


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 190



Y Index: 190

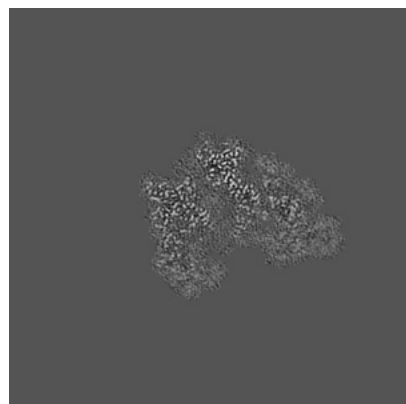


Z Index: 190

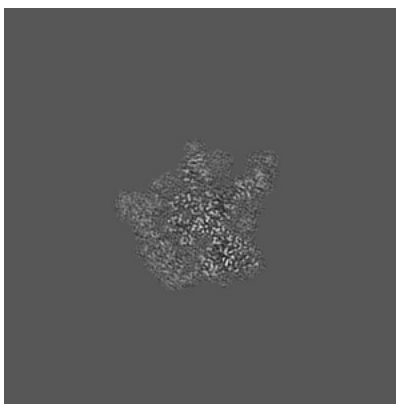
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

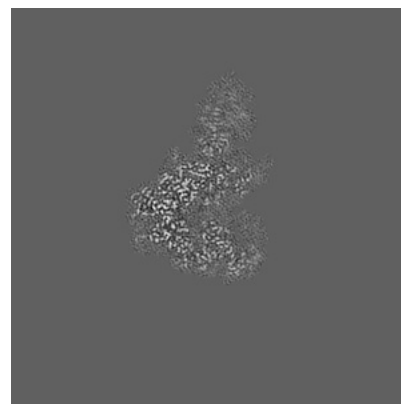
6.3.1 Primary map



X Index: 182



Y Index: 165

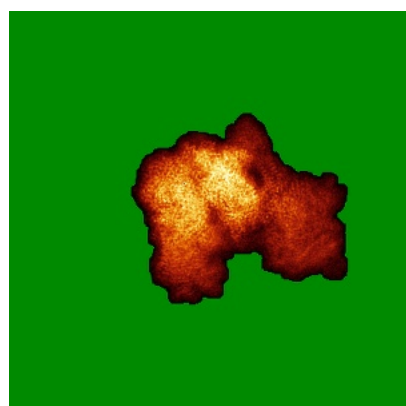


Z Index: 210

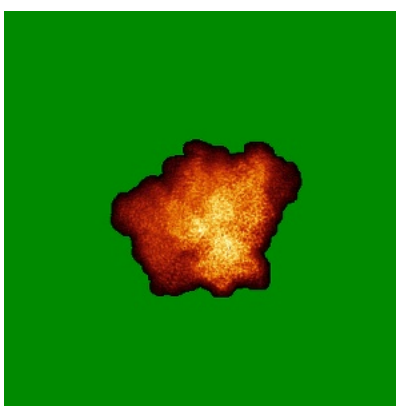
The images above show the largest variance slices of the map in three orthogonal directions.

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

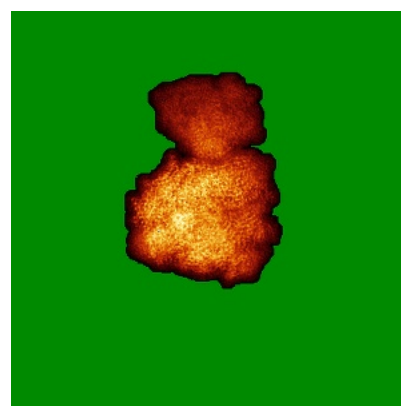
6.4.1 Primary map



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

This section was not generated.

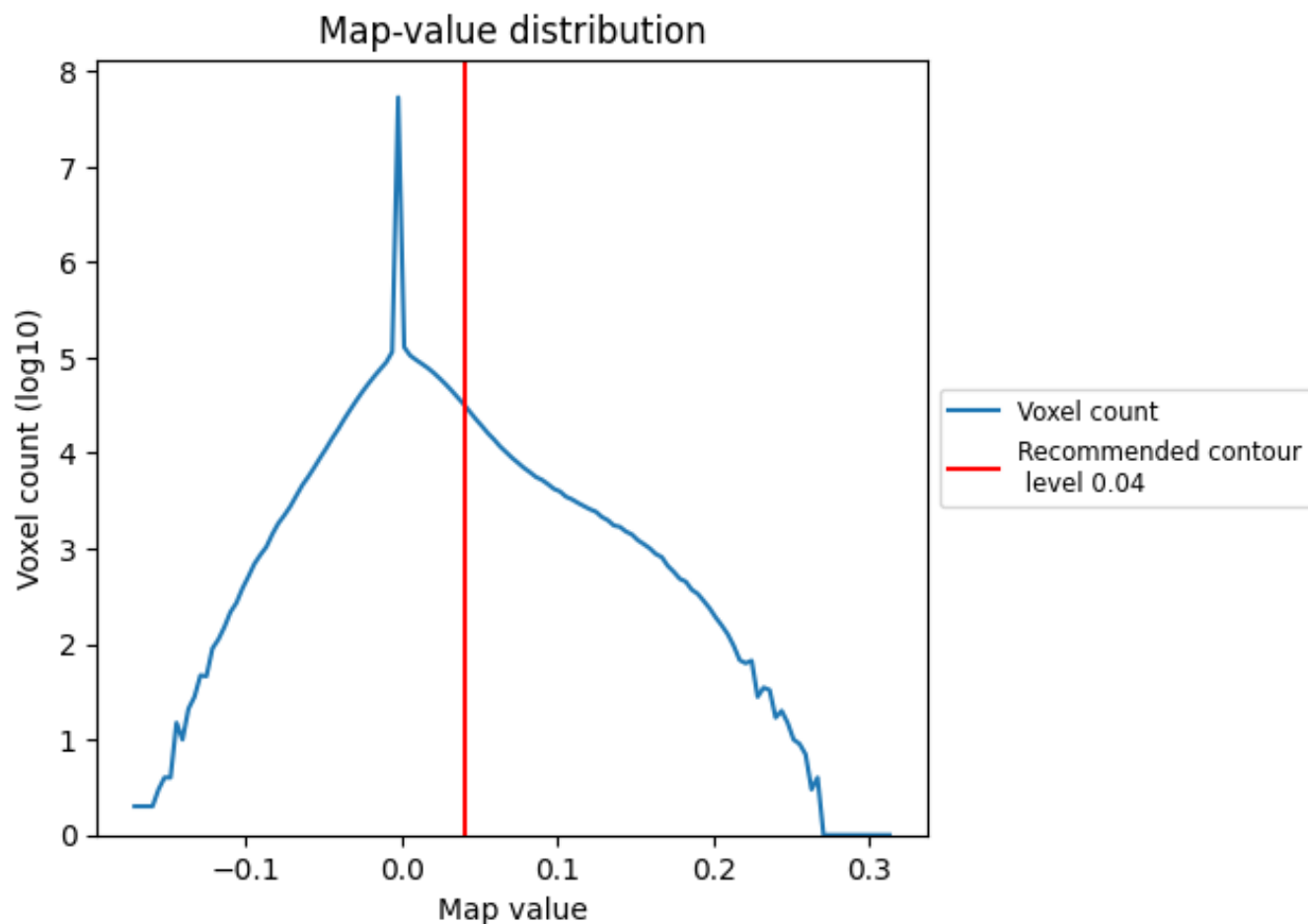
6.6 Mask visualisation

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

7 Map analysis [i](#)

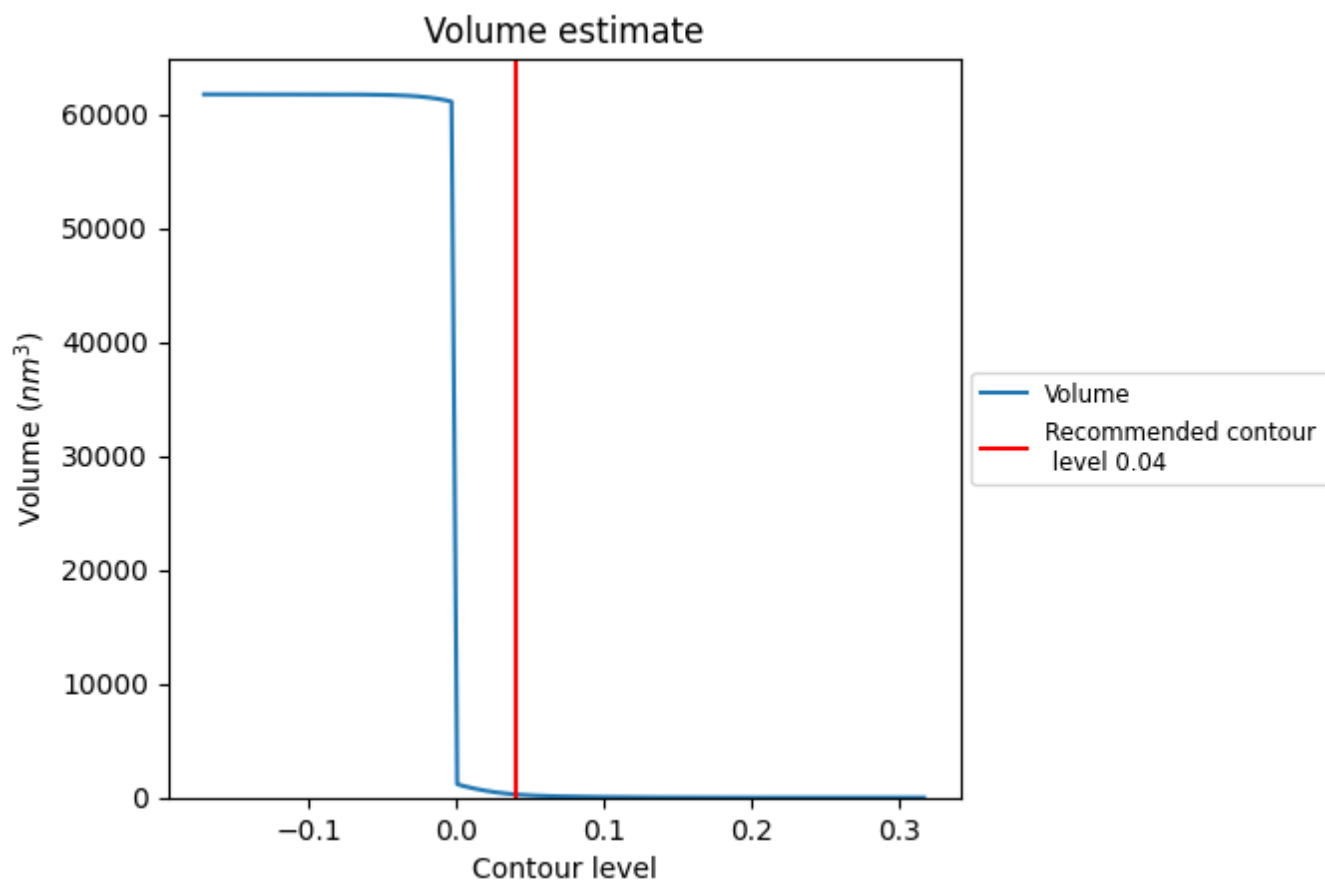
This section contains the results of statistical analysis of the map.

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.

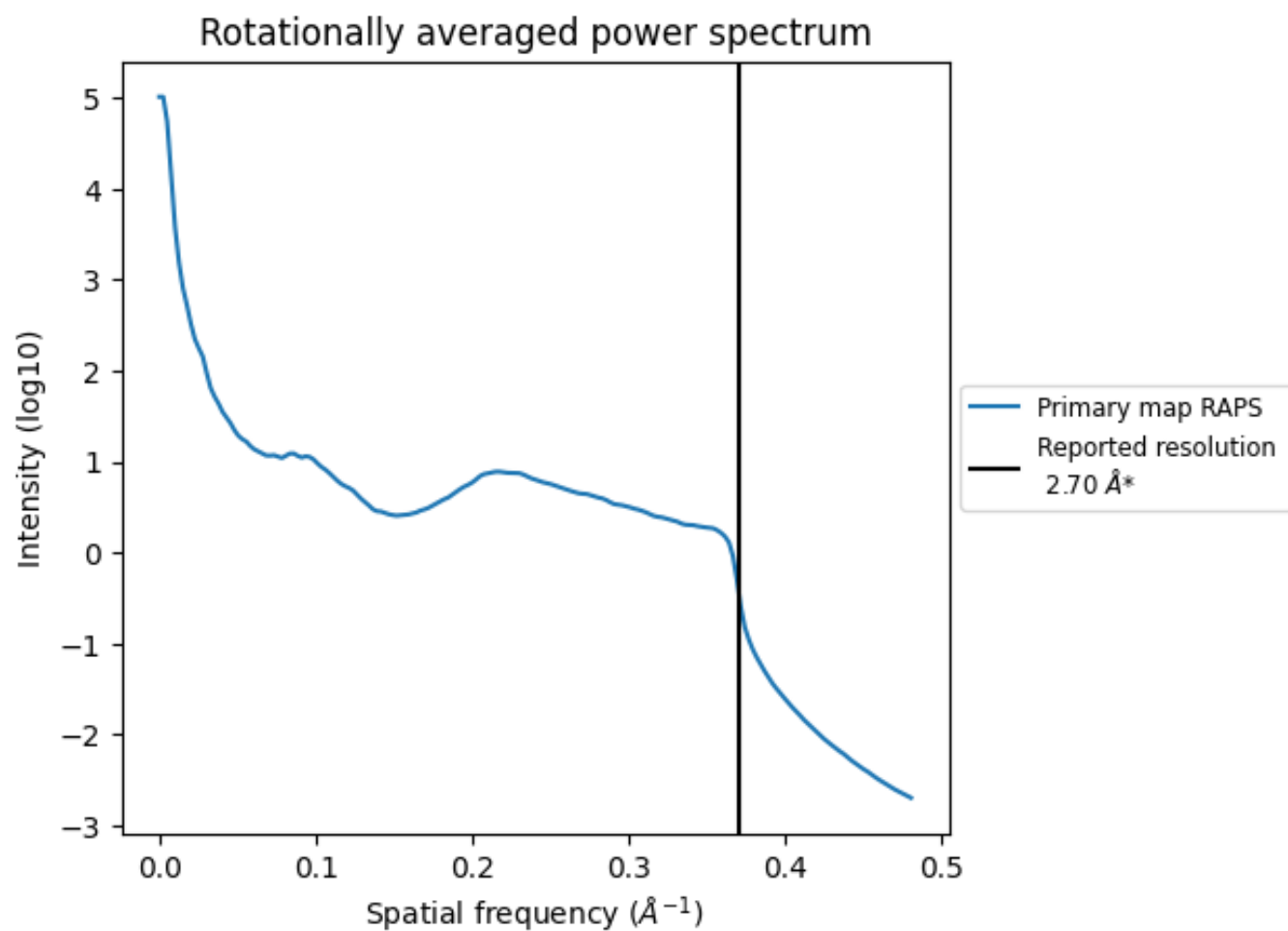
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 275 nm³; this corresponds to an approximate mass of 249 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 0.370 Å⁻¹

8 Fourier-Shell correlation

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

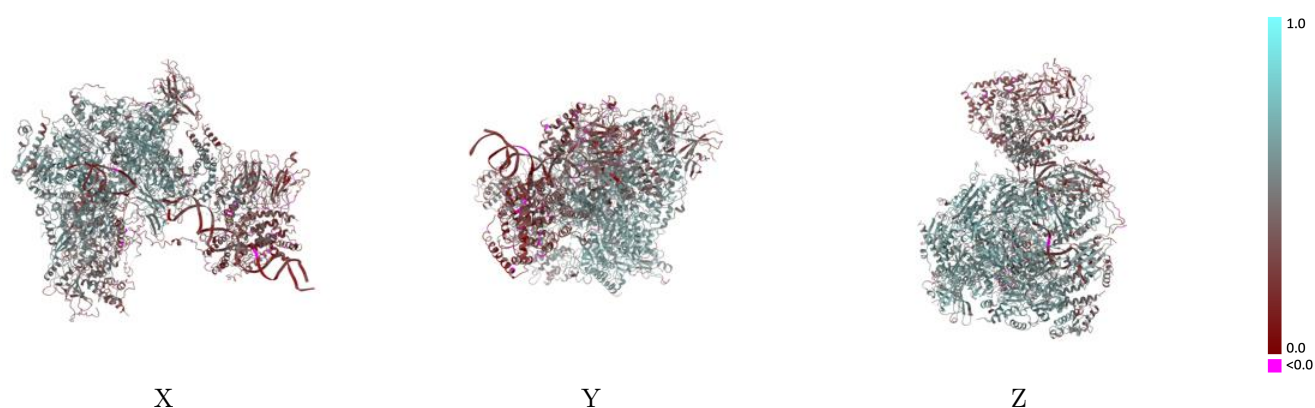
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-10006 and PDB model 6RUI. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)

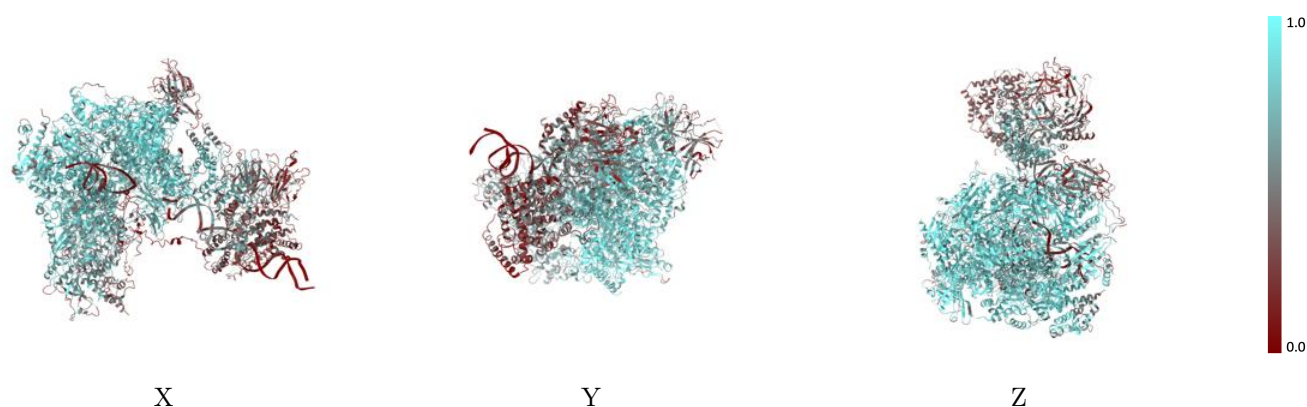
This section was not generated.

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



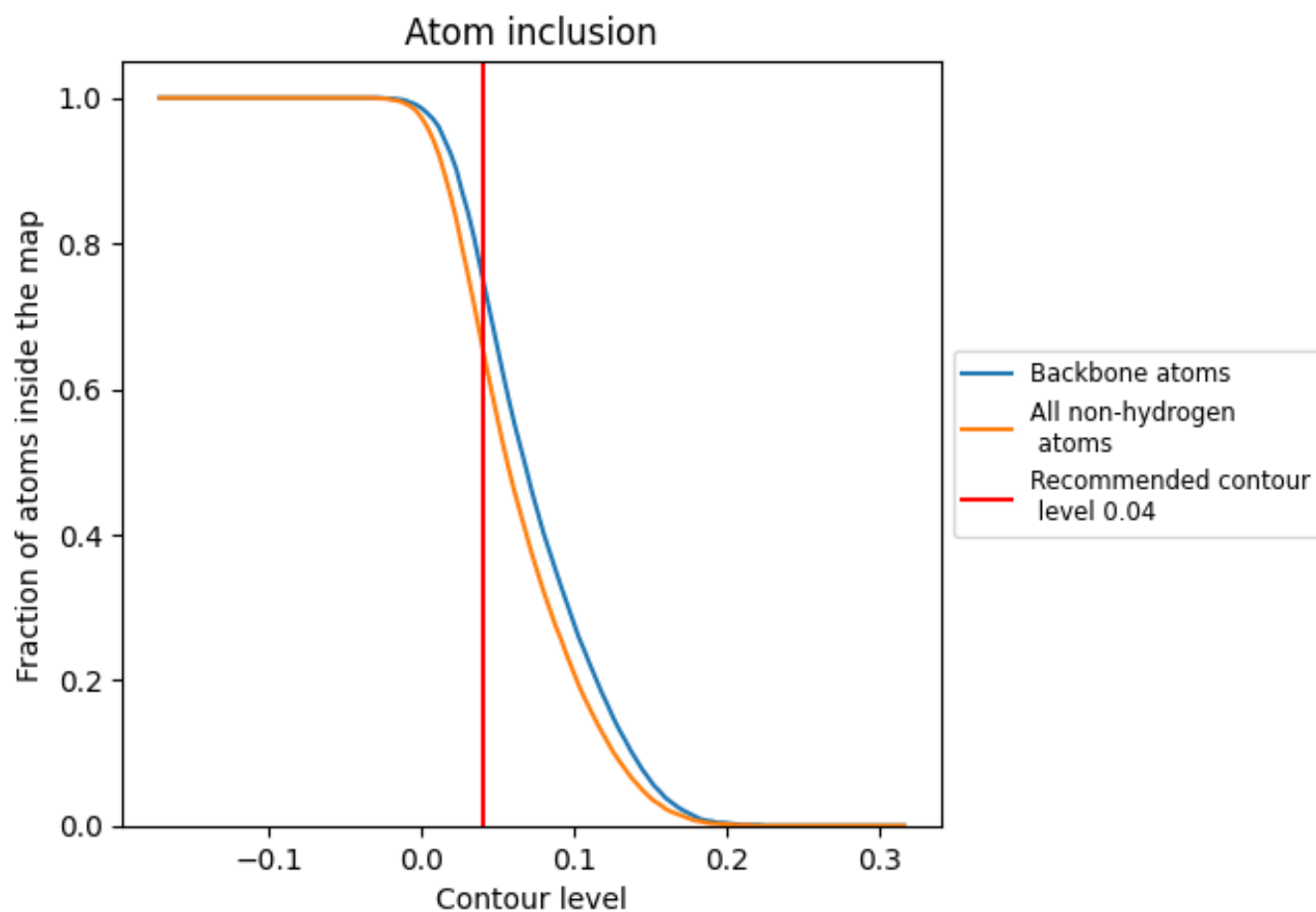
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 66% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6600	 0.4630
A	 0.8150	 0.5450
B	 0.8560	 0.5700
C	 0.8580	 0.5710
D	 0.5840	 0.4270
E	 0.7830	 0.5280
F	 0.8660	 0.5880
G	 0.6540	 0.4550
H	 0.8240	 0.5500
I	 0.5150	 0.3850
J	 0.9180	 0.6120
K	 0.8610	 0.5820
L	 0.8010	 0.5330
M	 0.3950	 0.3650
N	 0.3750	 0.3680
O	 0.5240	 0.3870
Q	 0.3740	 0.3030
R	 0.5910	 0.4070
S	 0.3510	 0.2910
T	 0.2300	 0.2240
U	 0.2250	 0.2190

