



wwPDB EM Validation Summary Report ⓘ

May 19, 2024 – 03:59 am BST

PDB ID : 6RRD
EMDB ID : EMD-4987
Title : RNA Polymerase I Pre-initiation complex DNA opening intermediate 1
Authors : Mueller, C.W.; Sadian, Y.; Tafur, L.
Deposited on : 2019-05-17
Resolution : 3.10 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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

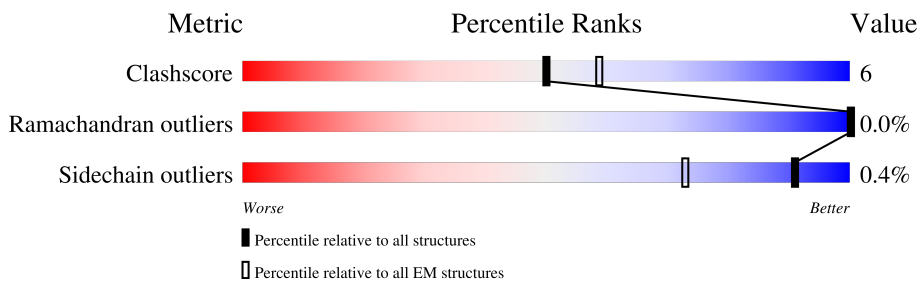
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.





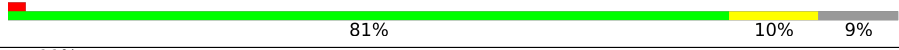
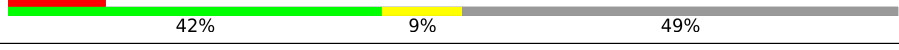



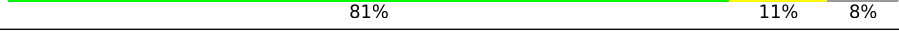
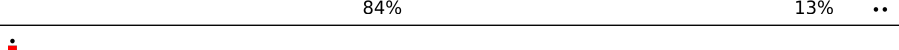
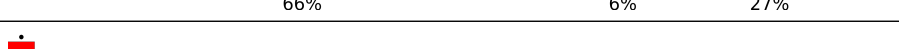

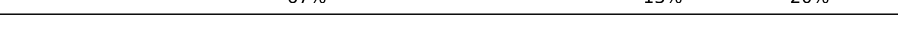
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	
2	U	70	
3	Q	514	
4	S	894	
5	R	507	
6	I	125	
7	N	233	
8	M	415	

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Mol	Chain	Length	Quality of chain
9	A	1664	 77% 11% 12%
10	B	1203	 85% 13%
11	C	335	 81% 10% 9%
12	D	137	 11% 42% 9% 49%
13	E	215	 89% 11%
14	F	155	 59% 5% 35%
15	G	326	 5% 50% 12% 38%
16	H	146	 81% 11% 8%
17	J	70	 84% 13%
18	K	142	 66% 6% 27%
19	L	70	 57% 7% 36%
20	O	627	 20% 67% 13% 20%

2 Entry composition [i](#)

There are 21 unique types of molecules in this entry. The entry contains 51631 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
			Total	C	N	O	P		
1	T	51	1019	491	163	314	51	0	0

- Molecule 2 is a DNA chain called Nontemplate strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	U	48	1010	478	206	279	47	0	0

- Molecule 3 is a protein called RNA polymerase I-specific transcription initiation factor RRN7.

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

- Molecule 4 is a protein called RNA polymerase I-specific transcription initiation factor RRN6.

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

- Molecule 5 is a protein called RNA polymerase I-specific transcription initiation factor RRN11.

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

- Molecule 6 is a protein called DNA-directed RNA polymerase I subunit RPA12.

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

- Molecule 7 is a protein called DNA-directed RNA polymerase I subunit RPA34.

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

- Molecule 8 is a protein called DNA-directed RNA polymerase I subunit RPA49.

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

- Molecule 9 is a protein called DNA-directed RNA polymerase I subunit RPA190.

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

- Molecule 10 is a protein called DNA-directed RNA polymerase I subunit RPA135.

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

- Molecule 11 is a protein called DNA-directed RNA polymerases I and III subunit RPAC1.

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

- Molecule 12 is a protein called DNA-directed RNA polymerase I subunit RPA14.

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

- Molecule 13 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

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

- Molecule 14 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

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

- Molecule 15 is a protein called DNA-directed RNA polymerase I subunit RPA43.

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

- Molecule 16 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

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

- Molecule 17 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

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

- Molecule 18 is a protein called DNA-directed RNA polymerases I and III subunit RPAC2.

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

- Molecule 19 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

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

- Molecule 20 is a protein called RNA polymerase I-specific transcription initiation factor RRN3.

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

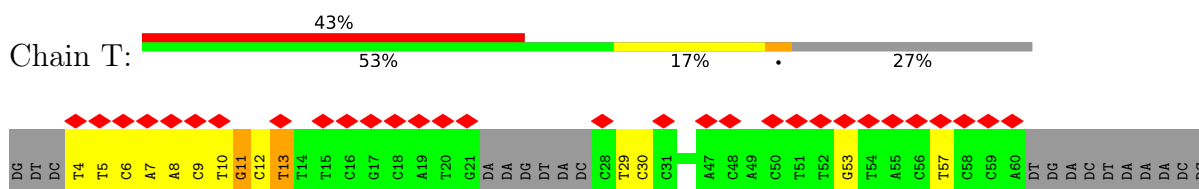
- Molecule 21 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

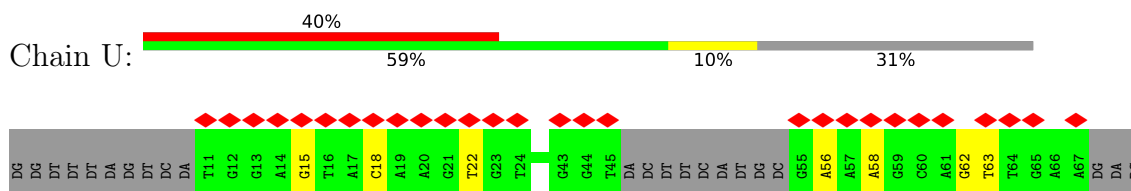
3 Residue-property plots [i](#)

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.

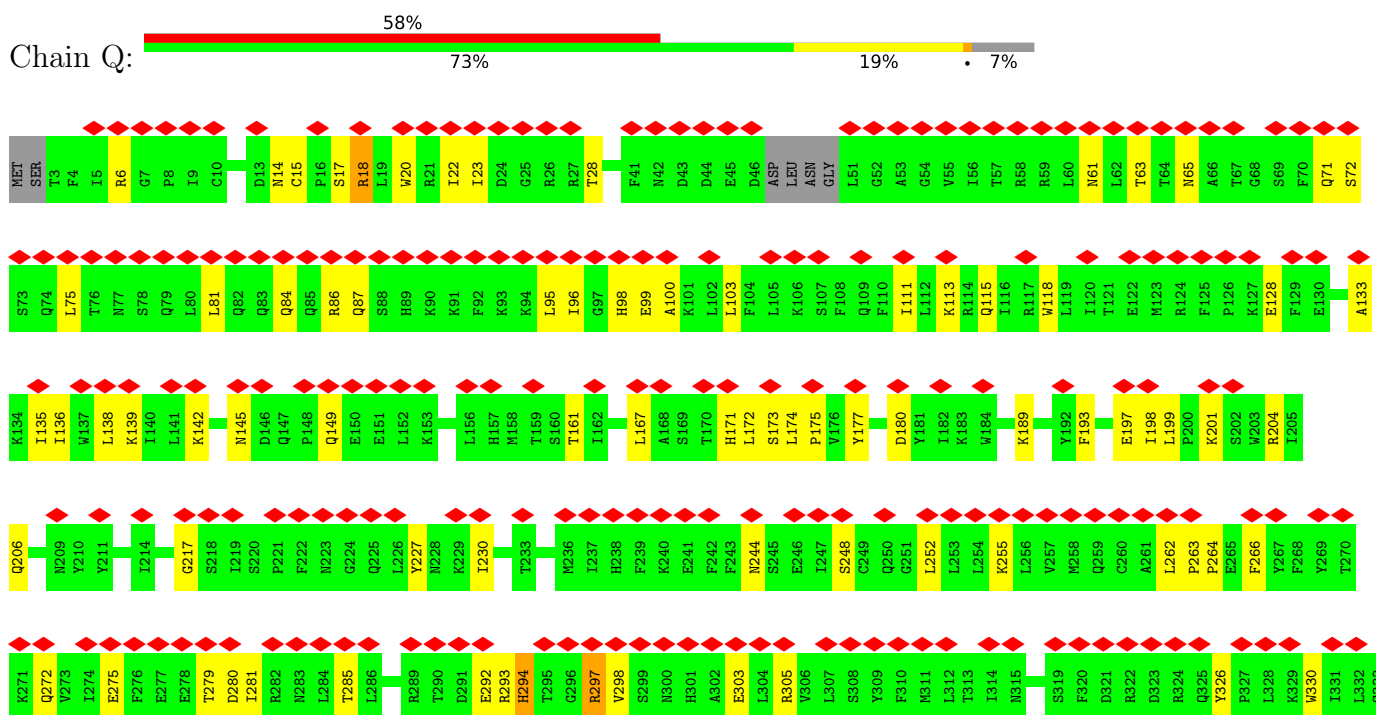
- Molecule 1: Template strand

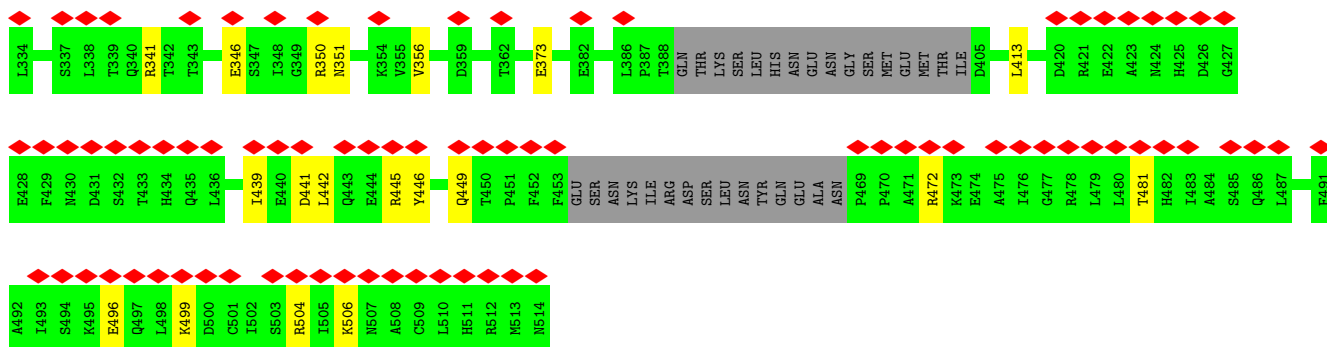


- Molecule 2: Nontemplate strand

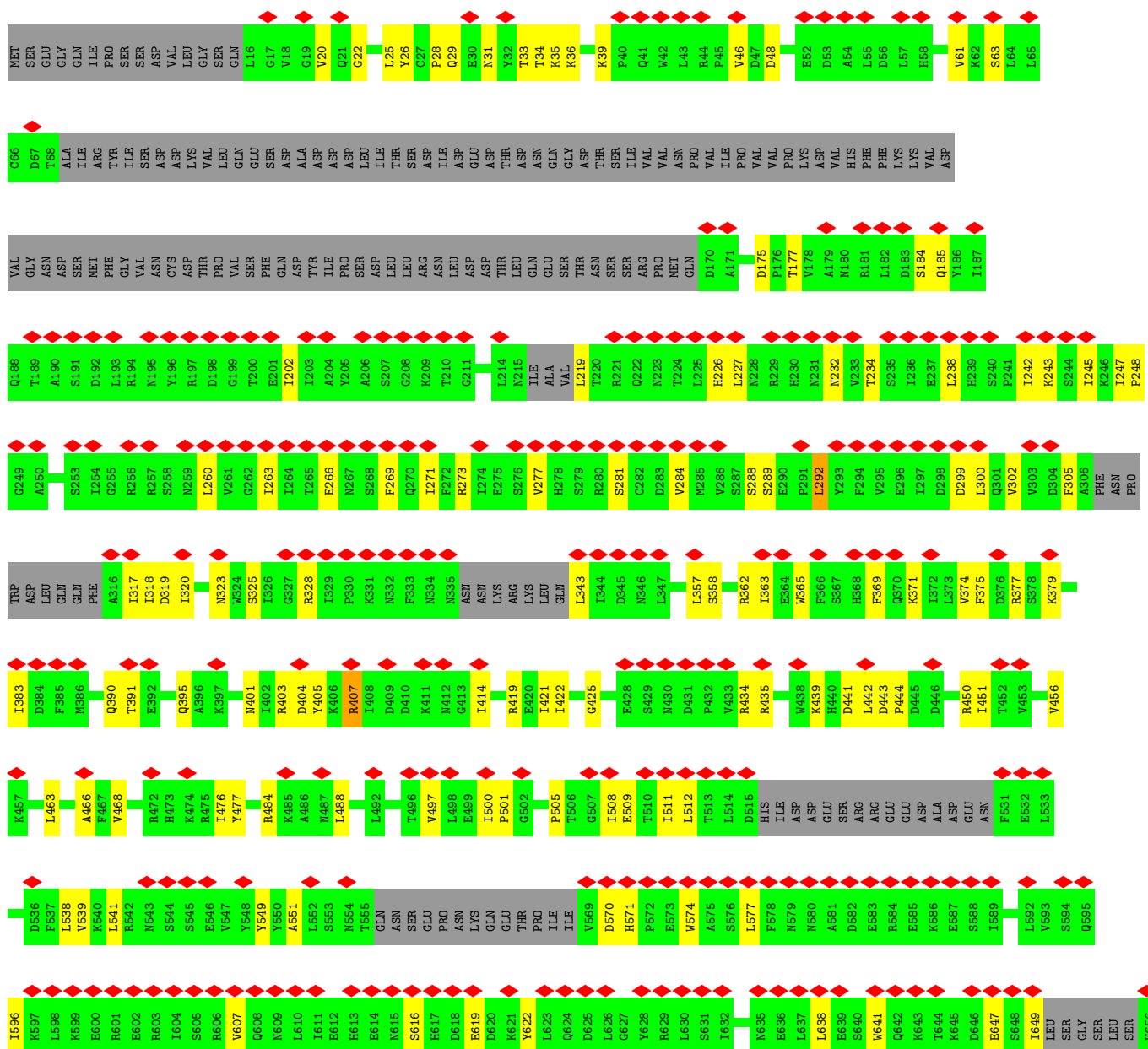
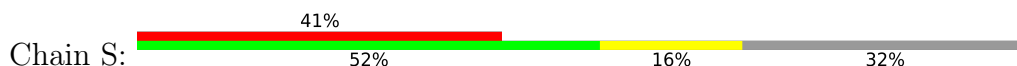


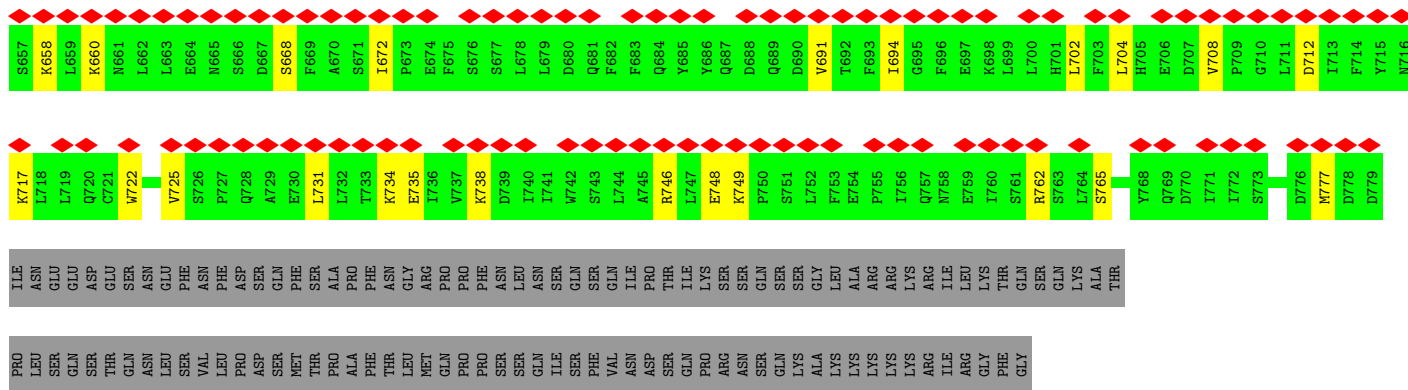
- Molecule 3: RNA polymerase I-specific transcription initiation factor RRN7



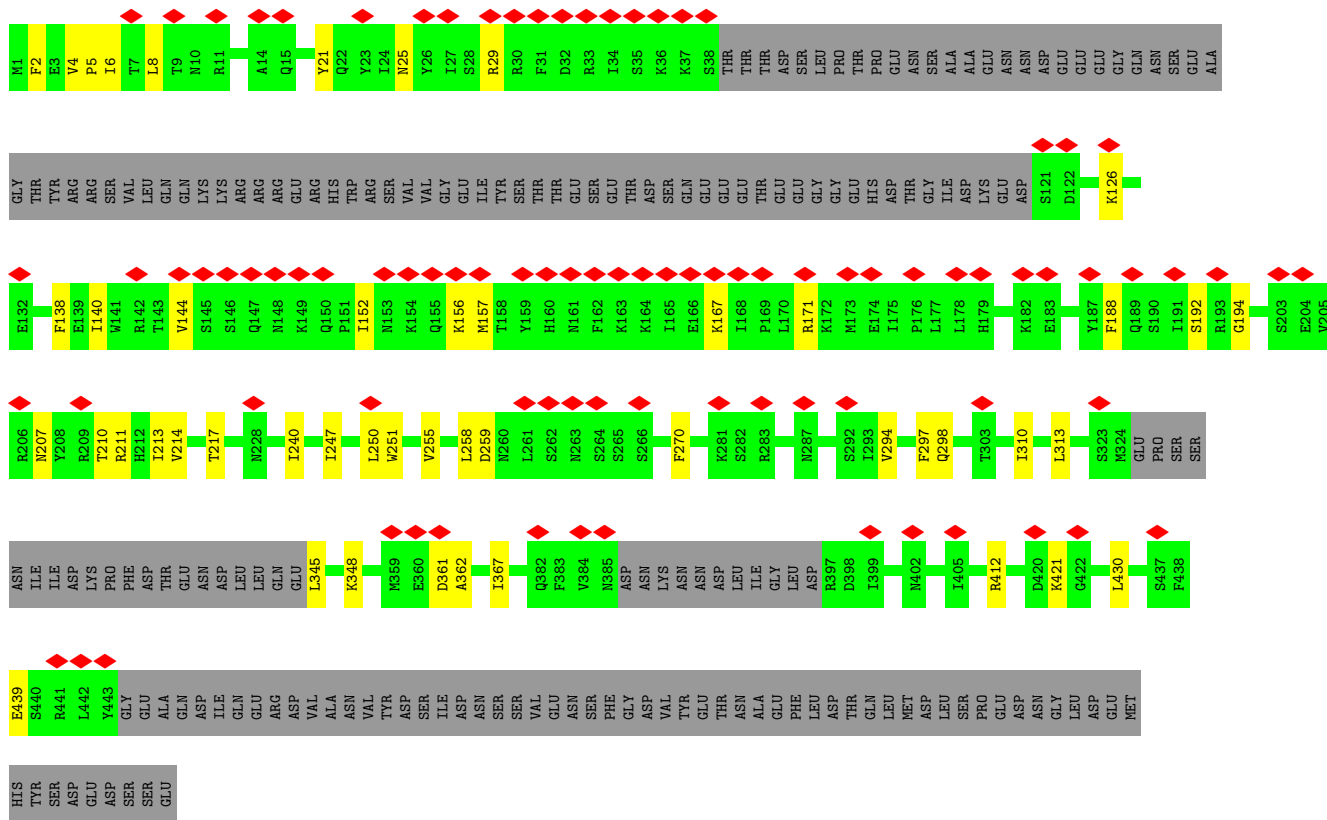


● Molecule 4: RNA polymerase I-specific transcription initiation factor RRN6

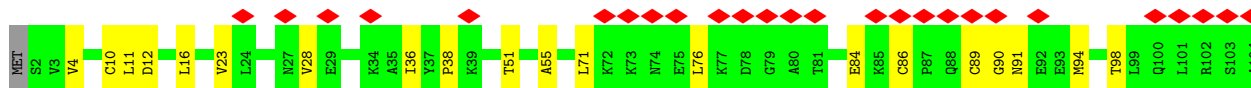
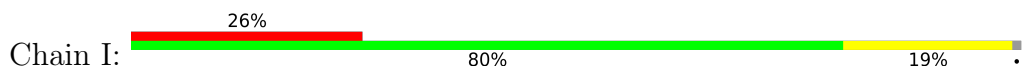


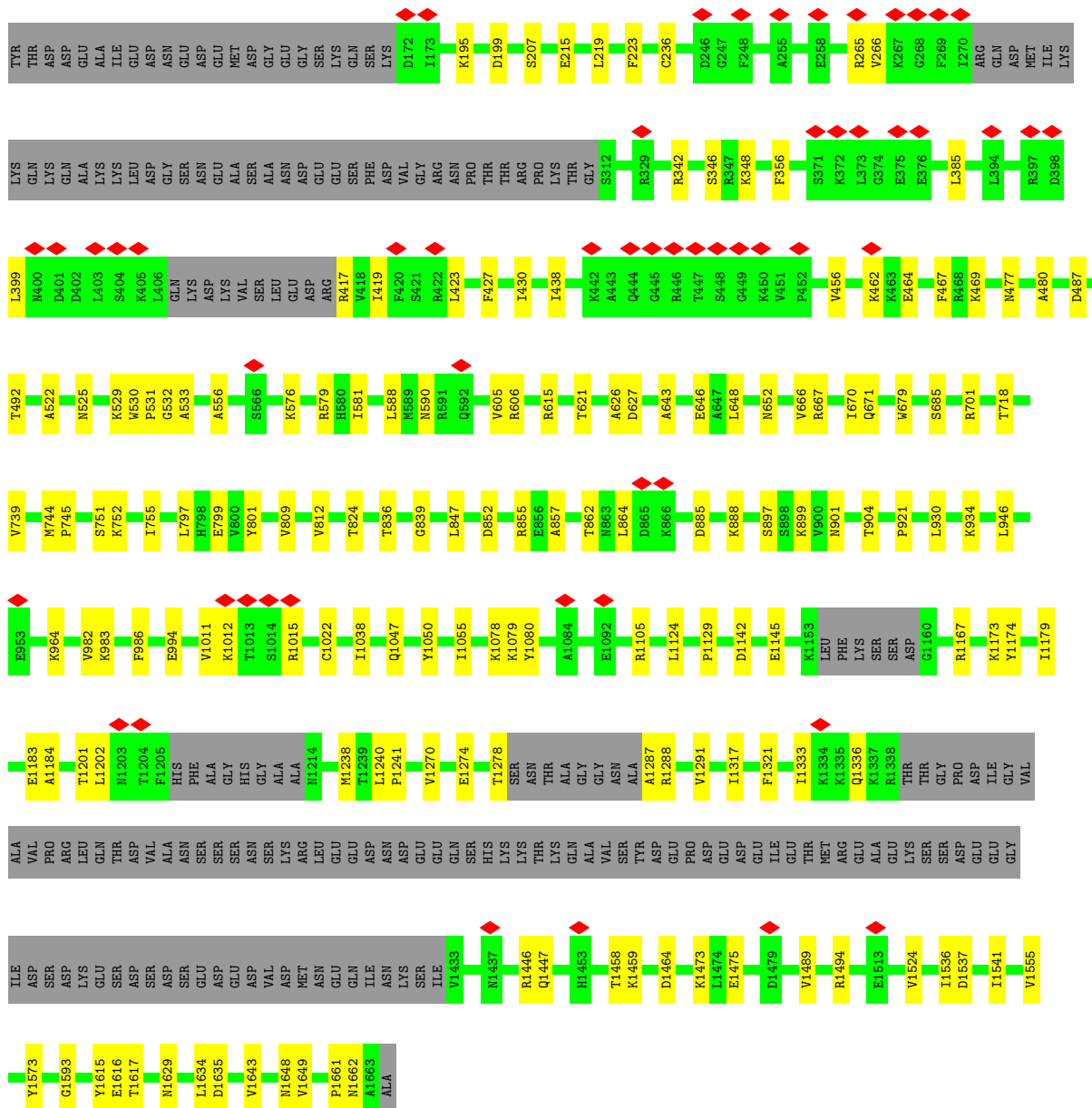


● Molecule 5: RNA polymerase I-specific transcription initiation factor RRN1

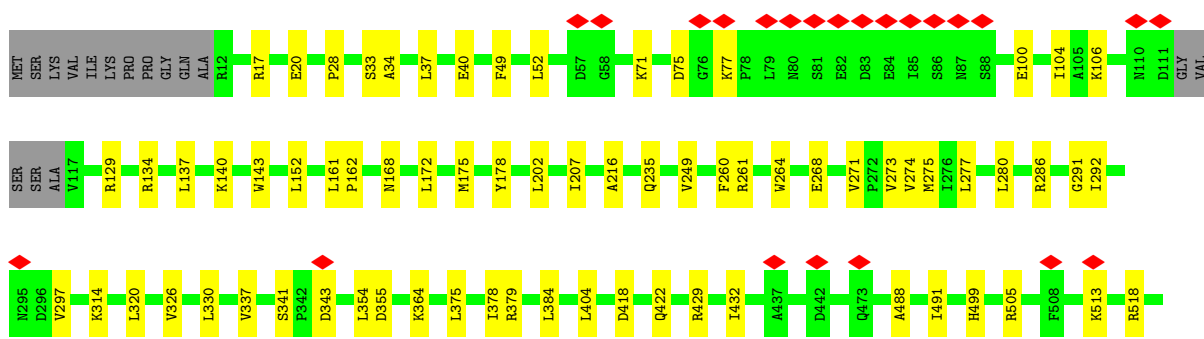
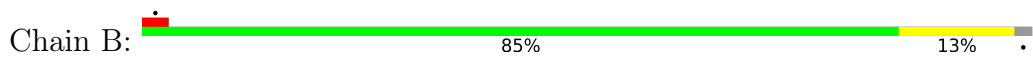


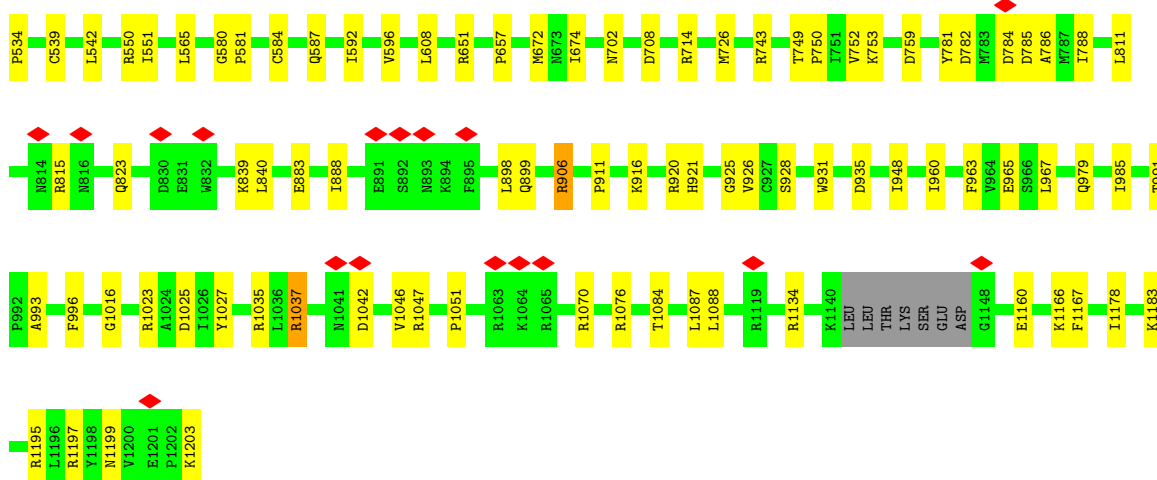
● Molecule 6: DNA-directed RNA polymerase I subunit RPA12



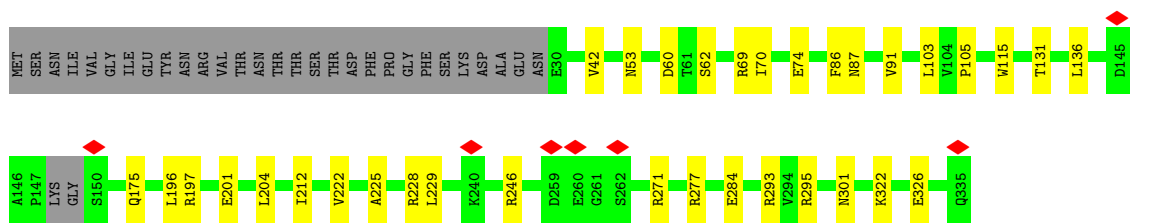
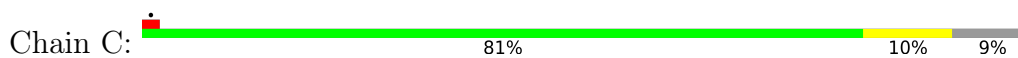


● Molecule 10: DNA-directed RNA polymerase I subunit RPA135

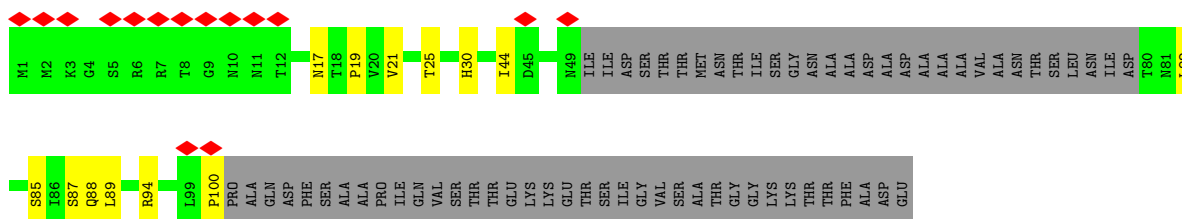




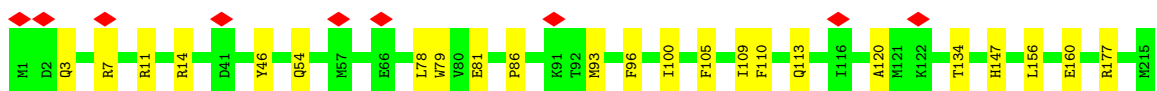
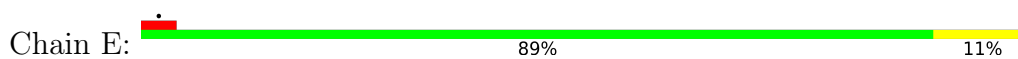
• Molecule 11: DNA-directed RNA polymerases I and III subunit RPAC1



• Molecule 12: DNA-directed RNA polymerase I subunit RPA14

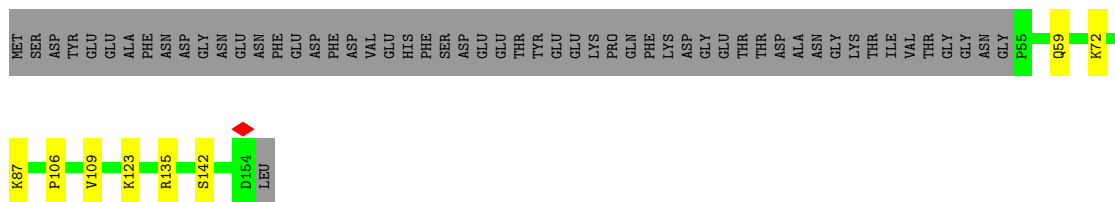


• Molecule 13: DNA-directed RNA polymerases I, II, and III subunit RPABC1

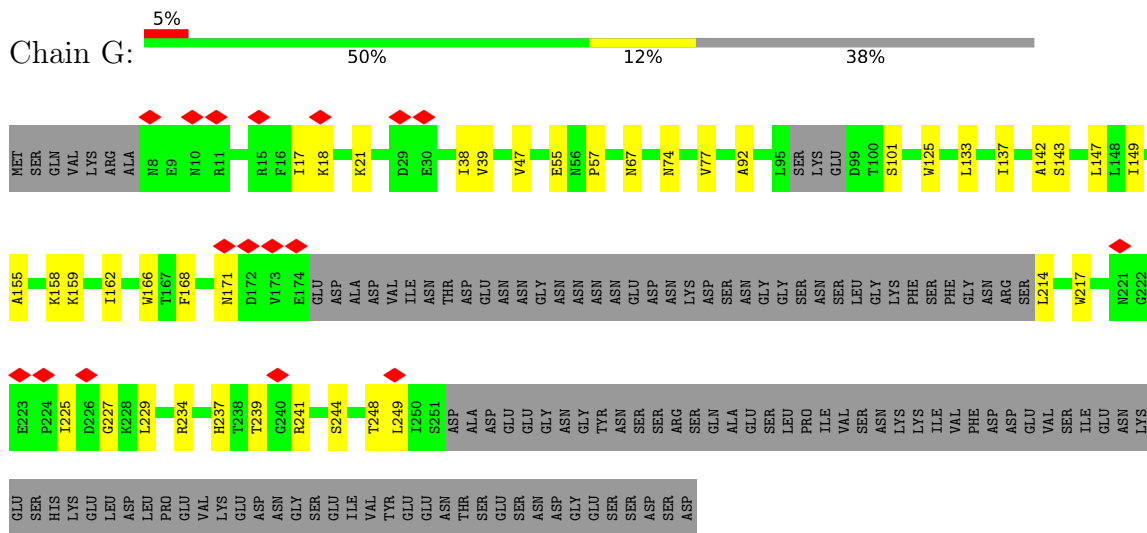


• Molecule 14: DNA-directed RNA polymerases I, II, and III subunit RPABC2

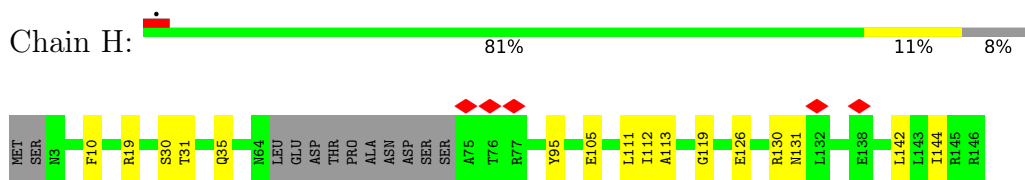




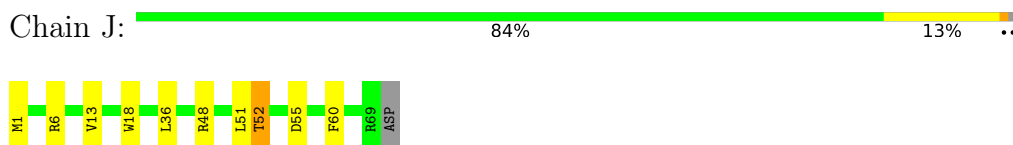
• Molecule 15: DNA-directed RNA polymerase I subunit RPA43



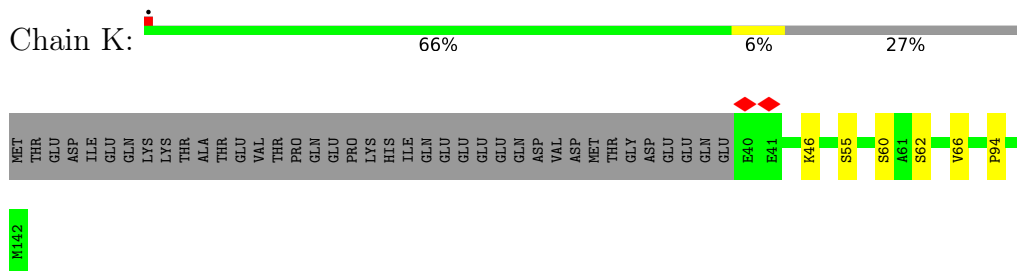
• Molecule 16: DNA-directed RNA polymerases I, II, and III subunit RPABC3



• Molecule 17: DNA-directed RNA polymerases I, II, and III subunit RPABC5



• Molecule 18: DNA-directed RNA polymerases I and III subunit RPAC2



• Molecule 19: DNA-directed RNA polymerases I, II, and III subunit RPABC4

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24848	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 ($e^-/\text{\AA}^2$)	1.054	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	0.265	Depositor
Minimum map value	-0.145	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	395.58002, 395.58002, 395.58002	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.041, 1.041, 1.041	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section:
ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	T	0.69	1/1133 (0.1%)	1.10	1/1738 (0.1%)
2	U	0.59	0/1140	1.01	0/1762
3	Q	0.33	0/4028	0.64	0/5441
4	S	0.32	0/5065	0.62	0/6859
5	R	0.36	0/2836	0.62	0/3817
6	I	0.35	0/955	0.61	0/1288
7	N	0.32	0/1124	0.63	0/1512
8	M	0.35	0/872	0.62	0/1170
9	A	0.43	0/11776	0.60	0/15906
10	B	0.47	0/9572	0.64	0/12941
11	C	0.44	0/2469	0.62	0/3347
12	D	0.32	0/557	0.58	0/750
13	E	0.38	0/1795	0.54	0/2416
14	F	0.47	0/838	0.58	0/1129
15	G	0.37	0/1637	0.58	0/2226
16	H	0.45	0/1090	0.65	0/1476
17	J	0.51	0/578	0.70	0/775
18	K	0.43	0/821	0.62	0/1108
19	L	0.42	0/361	0.72	0/478
20	O	0.34	0/4226	0.59	0/5717
All	All	0.42	1/52873 (0.0%)	0.64	1/71856 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	T	11	DG	O3'-P	6.26	1.68	1.61

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	13	DT	C2'-C3'-O3'	-5.14	95.63	112.60

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	T	1019	0	581	23	0
2	U	1010	0	541	15	0
3	Q	3936	0	3920	67	0
4	S	4963	0	4890	109	0
5	R	2771	0	2844	38	0
6	I	942	0	937	18	0
7	N	1103	0	1106	17	0
8	M	856	0	855	17	0
9	A	11565	0	11657	130	0
10	B	9365	0	9232	111	0
11	C	2418	0	2401	24	0
12	D	551	0	558	10	0
13	E	1759	0	1788	14	0
14	F	823	0	841	5	0
15	G	1600	0	1600	28	0
16	H	1072	0	1042	9	0
17	J	569	0	589	8	0
18	K	810	0	801	6	0
19	L	359	0	385	4	0
20	O	4139	0	4061	55	0
21	Q	1	0	0	0	0
All	All	51631	0	50629	599	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 6.

The worst 5 of 599 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)
9:A:1012:LYS:HD2	9:A:1201:THR:CG2	1.68	1.23
9:A:1012:LYS:CD	9:A:1201:THR:HG21	1.69	1.22
2:U:22:DT:H72	3:Q:294:HIS:CD2	1.78	1.19
2:U:22:DT:H72	3:Q:294:HIS:NE2	1.68	1.08
4:S:269:PHE:HD2	4:S:292:LEU:HD21	1.13	1.06

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	Q	469/514 (91%)	409 (87%)	60 (13%)	0	100	100
4	S	594/894 (66%)	509 (86%)	85 (14%)	0	100	100
5	R	322/507 (64%)	286 (89%)	36 (11%)	0	100	100
6	I	122/125 (98%)	103 (84%)	19 (16%)	0	100	100
7	N	131/233 (56%)	118 (90%)	12 (9%)	1 (1%)	19	54
8	M	106/415 (26%)	94 (89%)	11 (10%)	1 (1%)	17	52
9	A	1449/1664 (87%)	1362 (94%)	87 (6%)	0	100	100
10	B	1174/1203 (98%)	1096 (93%)	78 (7%)	0	100	100
11	C	300/335 (90%)	284 (95%)	16 (5%)	0	100	100
12	D	66/137 (48%)	60 (91%)	6 (9%)	0	100	100
13	E	213/215 (99%)	205 (96%)	8 (4%)	0	100	100
14	F	98/155 (63%)	94 (96%)	3 (3%)	1 (1%)	15	49
15	G	196/326 (60%)	179 (91%)	17 (9%)	0	100	100
16	H	130/146 (89%)	125 (96%)	5 (4%)	0	100	100
17	J	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
18	K	101/142 (71%)	94 (93%)	7 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	L	43/70 (61%)	36 (84%)	7 (16%)	0	100	100
20	O	498/627 (79%)	464 (93%)	34 (7%)	0	100	100
All	All	6079/7778 (78%)	5582 (92%)	494 (8%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	N	113	SER
14	F	87	LYS
8	M	46	SER

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	Q	436/476 (92%)	430 (99%)	6 (1%)	67	86
4	S	563/828 (68%)	560 (100%)	3 (0%)	88	94
5	R	313/474 (66%)	312 (100%)	1 (0%)	92	96
6	I	109/110 (99%)	109 (100%)	0	100	100
7	N	128/220 (58%)	127 (99%)	1 (1%)	81	92
8	M	98/371 (26%)	97 (99%)	1 (1%)	76	90
9	A	1293/1465 (88%)	1291 (100%)	2 (0%)	93	97
10	B	1029/1053 (98%)	1025 (100%)	4 (0%)	91	96
11	C	269/296 (91%)	269 (100%)	0	100	100
12	D	65/116 (56%)	64 (98%)	1 (2%)	65	85
13	E	197/197 (100%)	197 (100%)	0	100	100
14	F	90/137 (66%)	90 (100%)	0	100	100
15	G	180/291 (62%)	180 (100%)	0	100	100
16	H	116/128 (91%)	115 (99%)	1 (1%)	78	91
17	J	64/65 (98%)	63 (98%)	1 (2%)	62	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	K	93/130 (72%)	93 (100%)	0	100	100
19	L	40/57 (70%)	40 (100%)	0	100	100
20	O	466/576 (81%)	464 (100%)	2 (0%)	91	96
All	All	5549/6990 (79%)	5526 (100%)	23 (0%)	91	96

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	B	651	ARG
10	B	1037	ARG
10	B	906	ARG
12	D	17	ASN
4	S	292	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
9	A	221	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

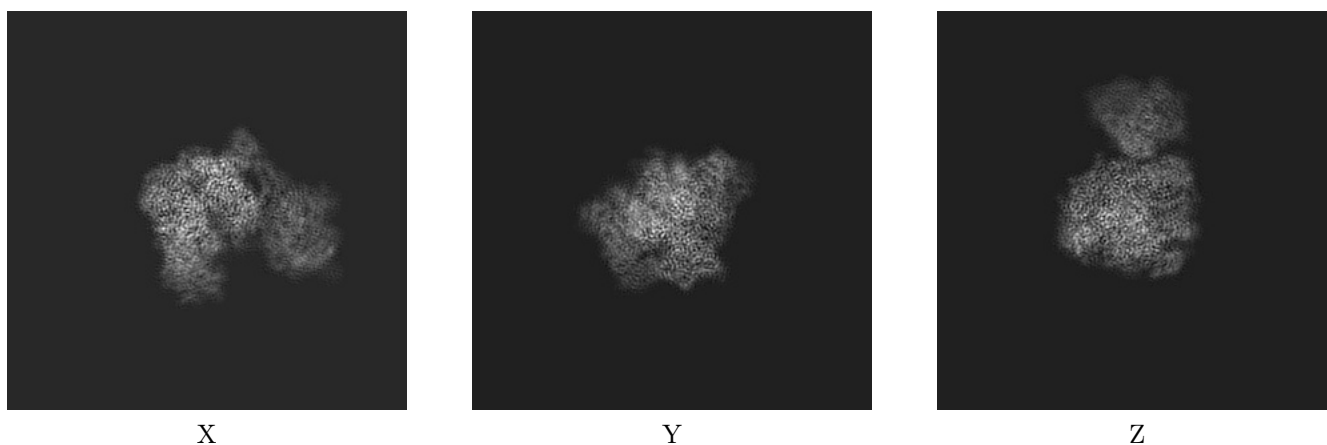
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4987. 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](#)

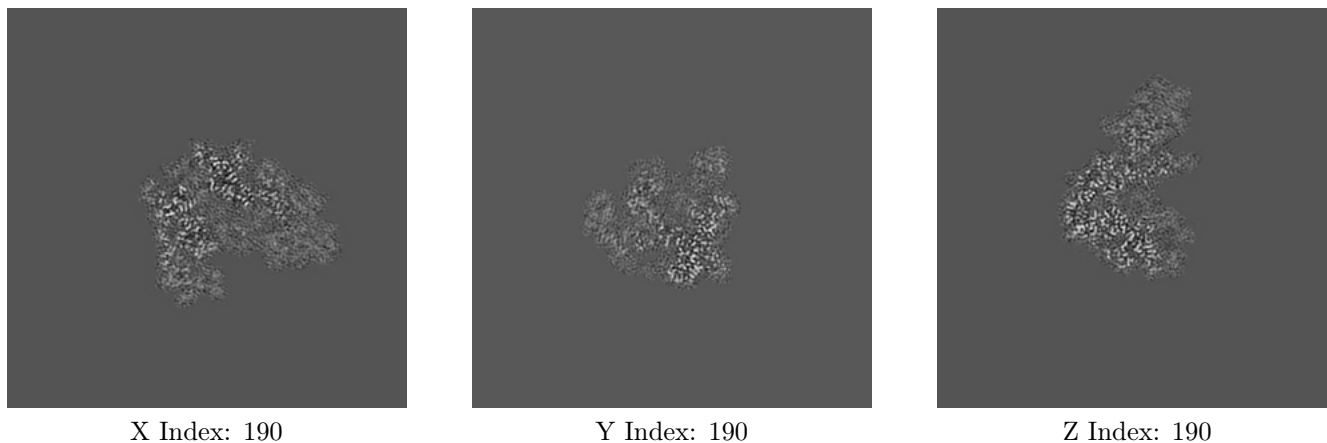
6.1.1 Primary map



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

6.2 Central slices [i](#)

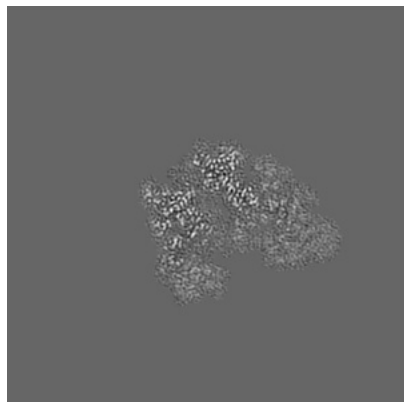
6.2.1 Primary map



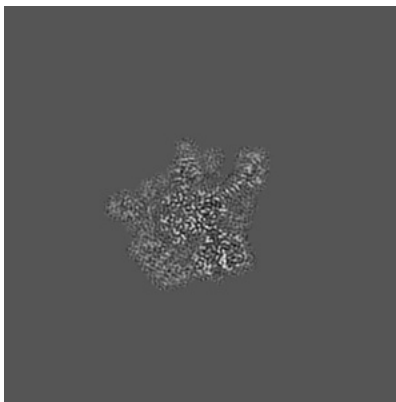
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 183



Y Index: 167

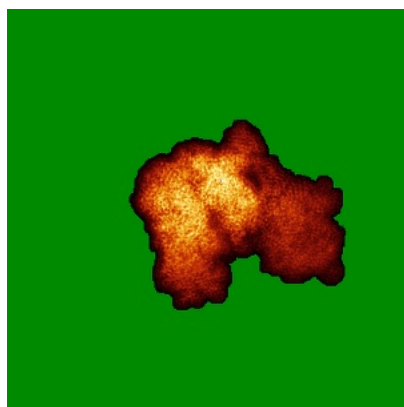


Z Index: 195

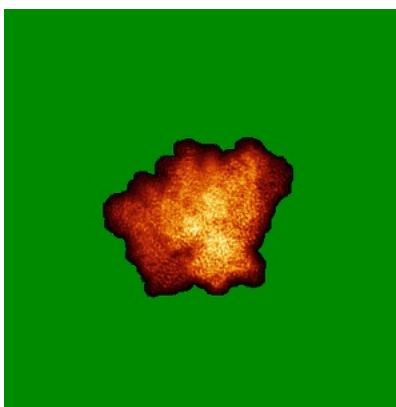
The images above show the largest variance slices of the map in three orthogonal directions.

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

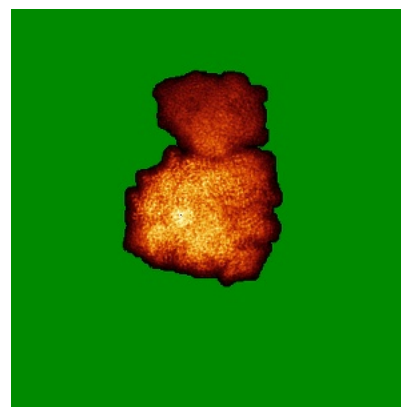
6.4.1 Primary map



X



Y

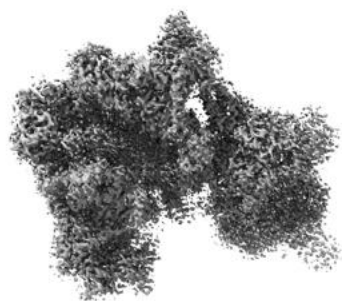


Z

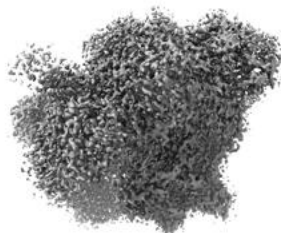
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

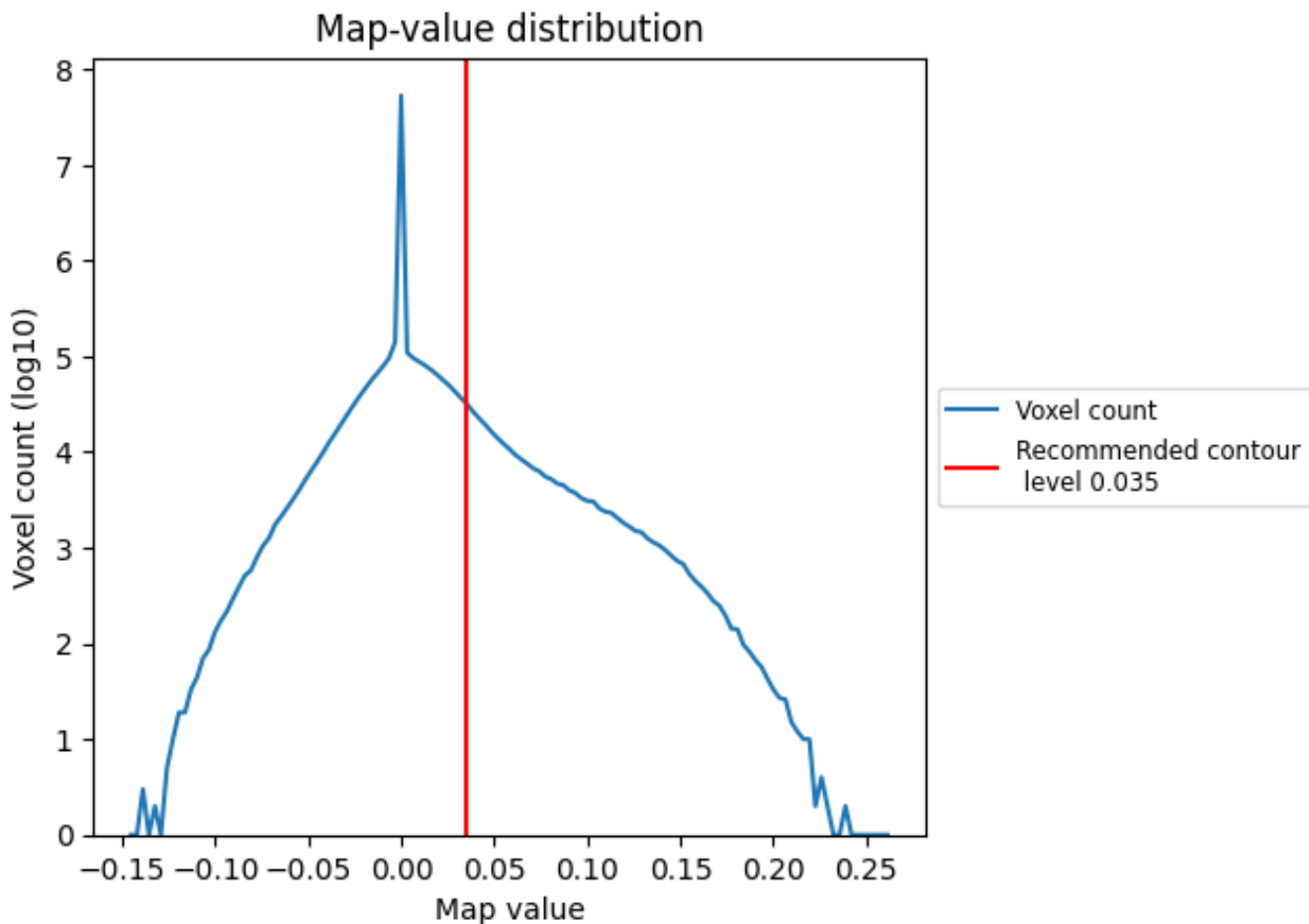
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

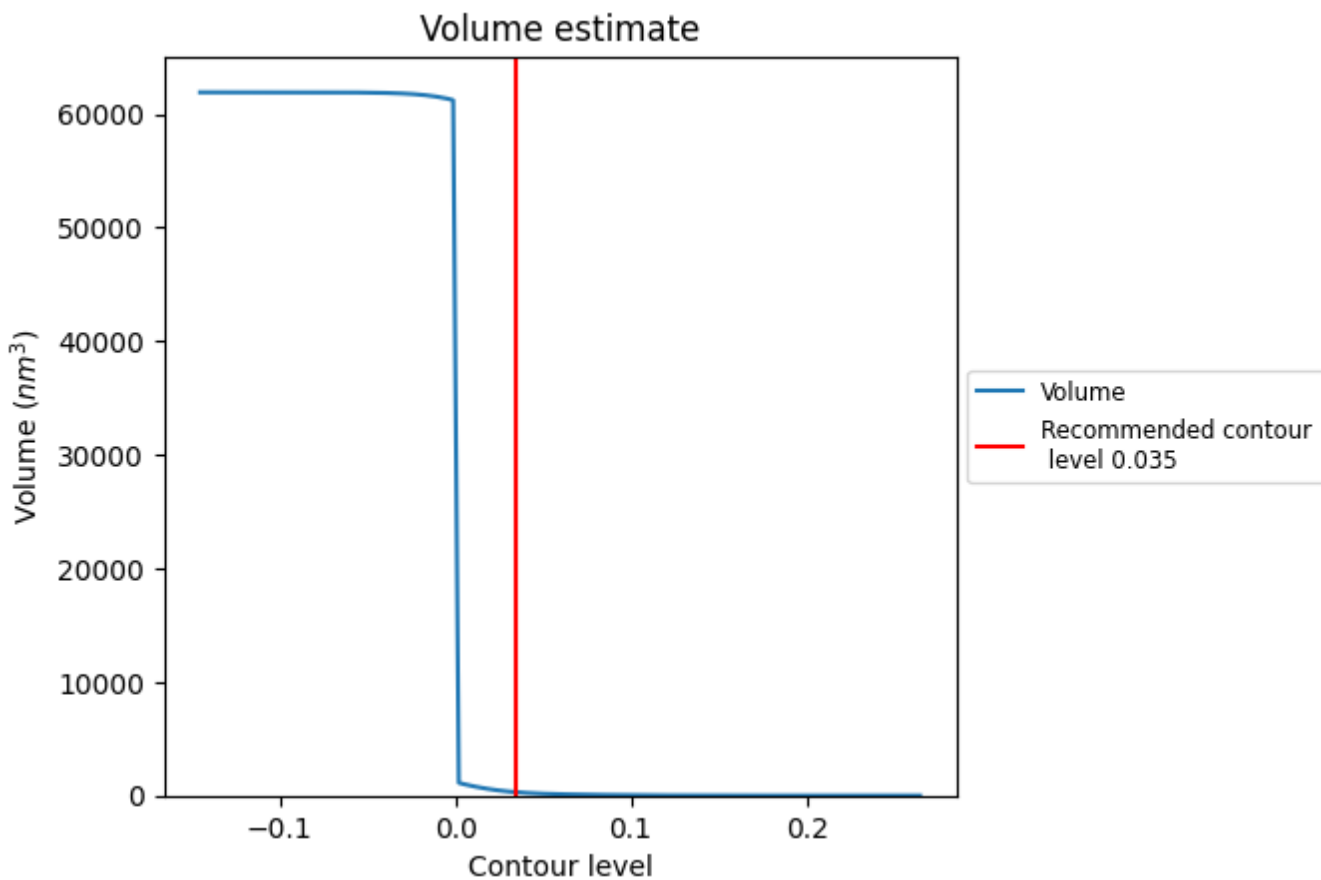
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

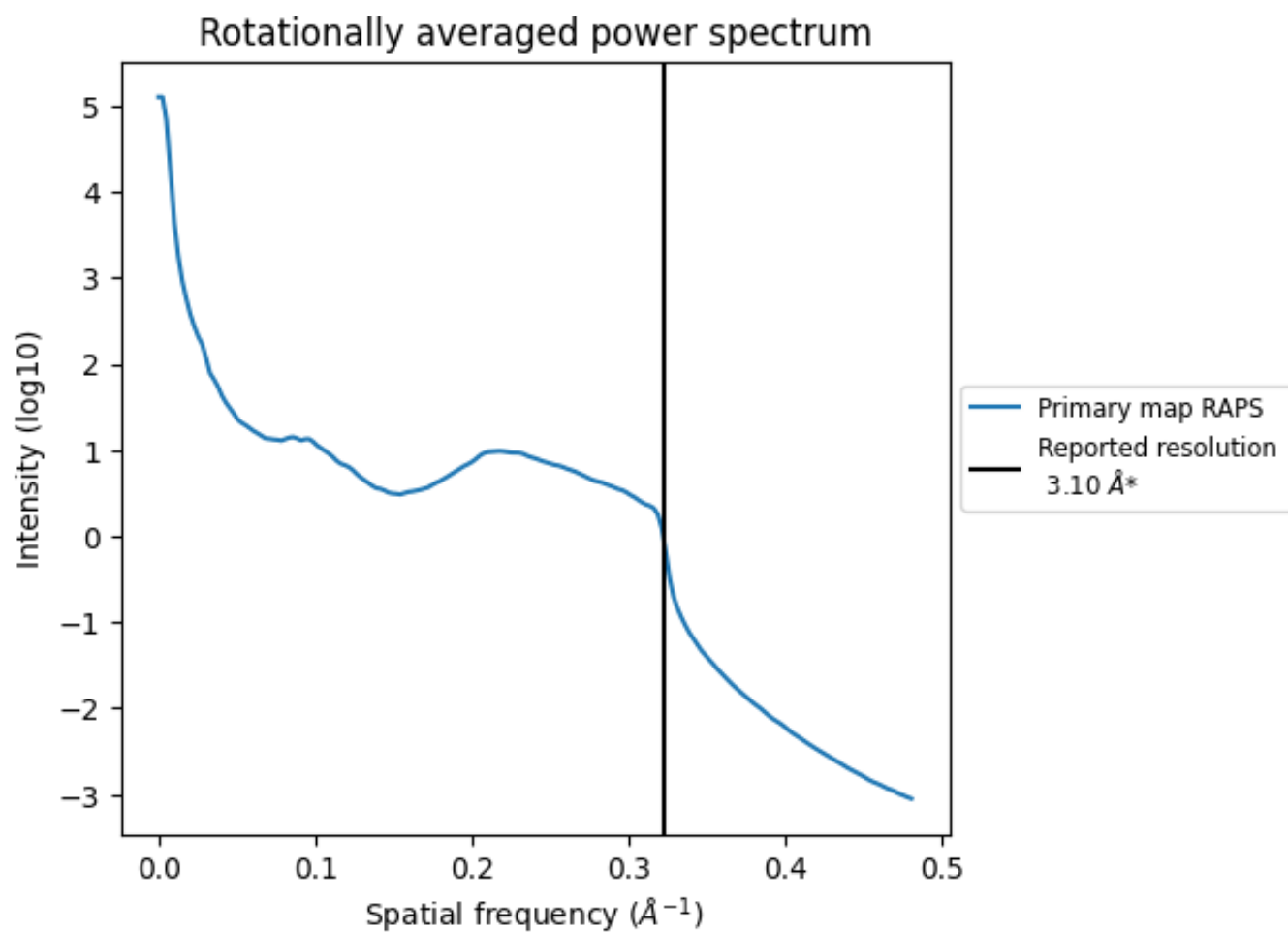
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 293 nm³; this corresponds to an approximate mass of 265 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.323\AA^{-1}

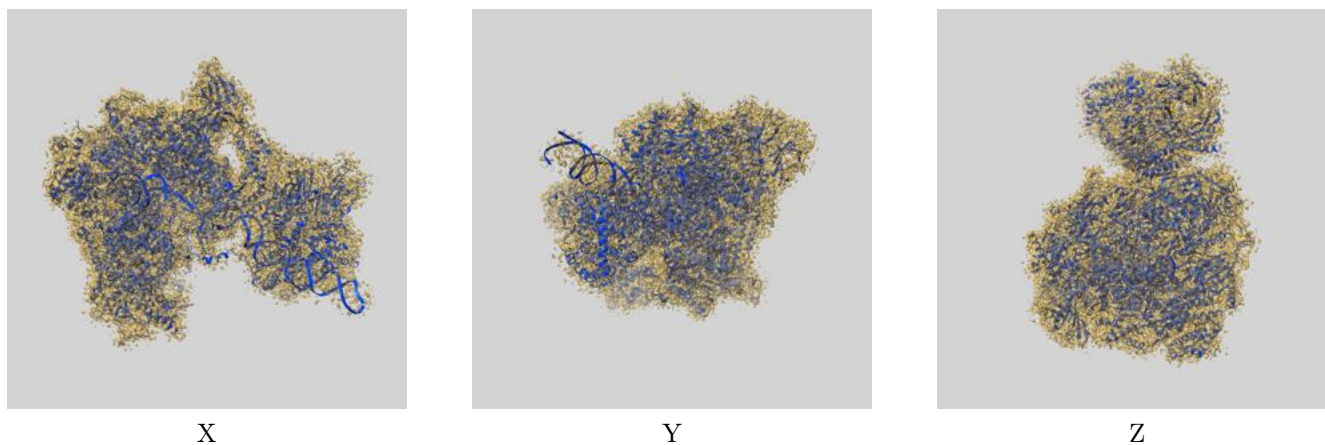
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4987 and PDB model 6RRD. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



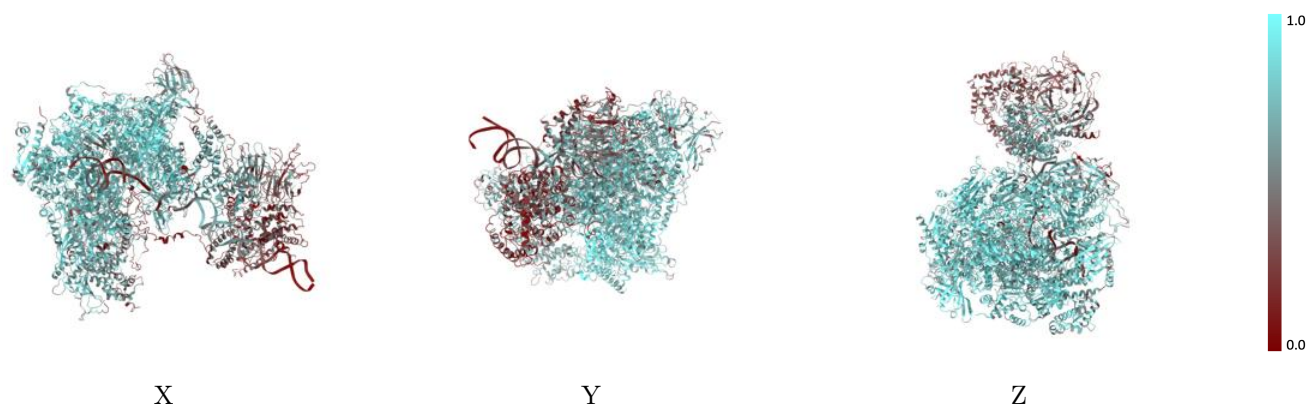
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



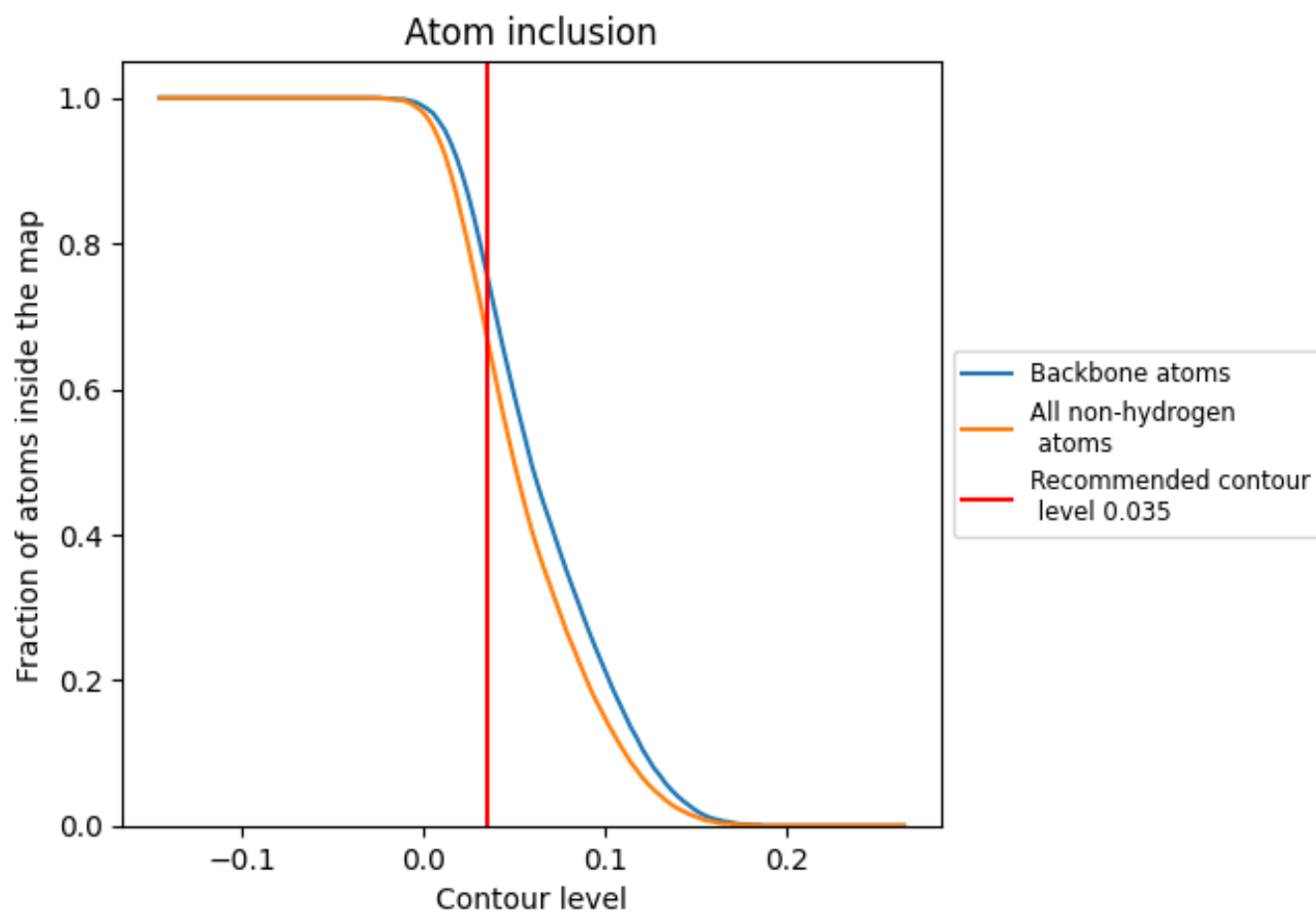
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.035).











































9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 67% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6700	 0.4520
A	 0.8070	 0.5240
B	 0.8310	 0.5400
C	 0.8430	 0.5400
D	 0.6430	 0.4530
E	 0.7610	 0.5020
F	 0.8410	 0.5580
G	 0.7320	 0.4710
H	 0.8390	 0.5360
I	 0.5460	 0.4220
J	 0.8970	 0.5740
K	 0.8330	 0.5480
L	 0.7860	 0.5130
M	 0.5780	 0.3950
N	 0.5950	 0.4110
O	 0.5700	 0.3850
Q	 0.3580	 0.2890
R	 0.5700	 0.4050
S	 0.3660	 0.2970
T	 0.3260	 0.2570
U	 0.3740	 0.2740

