



wwPDB EM Validation Summary Report ⓘ

Dec 11, 2022 – 04:28 am GMT

PDB ID : 6RQL
EMDB ID : EMD-4984
Title : RNA Polymerase I Closed Conformation 2 (CC2)
Authors : Mueller, C.W.; Sadian, Y.; Tafur, L.
Deposited on : 2019-05-16
Resolution : 2.90 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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

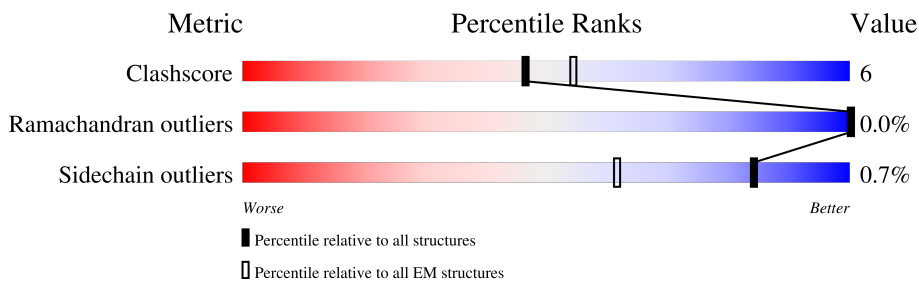
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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.





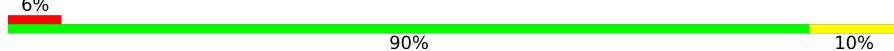

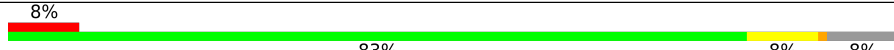

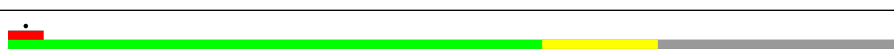



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	M	415	
7	A	1664	
8	B	1203	

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Mol	Chain	Length	Quality of chain
9	C	335	
10	D	137	
11	E	215	
12	F	155	
13	G	326	
14	H	146	
15	I	125	
16	J	70	
17	K	142	
18	L	70	
19	N	233	
20	O	627	

2 Entry composition [i](#)

There are 20 unique types of molecules in this entry. The entry contains 51626 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	42	842	405	141	254	42	0	0

- Molecule 2 is a DNA chain called Nontemplate strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	U	42	877	417	171	248	41	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	476	3931	2526	674	711	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 RPA49.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	M	107	850	540	141	169	0	0

- Molecule 7 is a protein called DNA-directed RNA polymerase I subunit RPA190.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	A	1542	11953	7543	2086	2263	61	0	0

- Molecule 8 is a protein called DNA-directed RNA polymerase I subunit RPA135.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	B	1180	9371	5923	1644	1754	50	0	0

- Molecule 9 is a protein called DNA-directed RNA polymerases I and III subunit RPAC1.

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

- Molecule 10 is a protein called DNA-directed RNA polymerase I subunit RPA14.

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

- Molecule 11 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		
11	E	215	1759	1116	310	321	12	0	0

- Molecule 12 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		
12	F	100	823	522	144	154	3	0	0

- Molecule 13 is a protein called DNA-directed RNA polymerase I subunit RPA43.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	G	199	1576	1012	273	286	5	0	0

- Molecule 14 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

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

- Molecule 15 is a protein called DNA-directed RNA polymerase I subunit RPA12.

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

- Molecule 16 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

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

- Molecule 17 is a protein called DNA-directed RNA polymerases I and III subunit RPAC2.

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

- Molecule 18 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

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

- Molecule 19 is a protein called DNA-directed RNA polymerase I subunit RPA34.

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

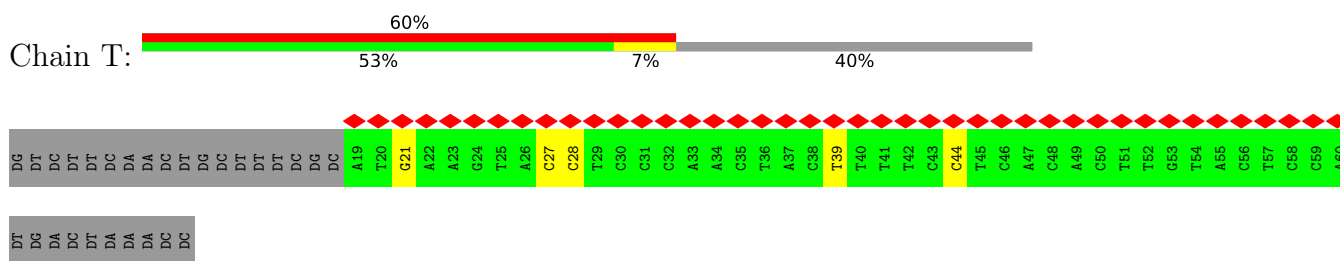
- Molecule 20 is a protein called RNA polymerase I-specific transcription initiation factor RRN3.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	499	Total	C	N	O	S	0	0
			4086	2636	661	767	22		

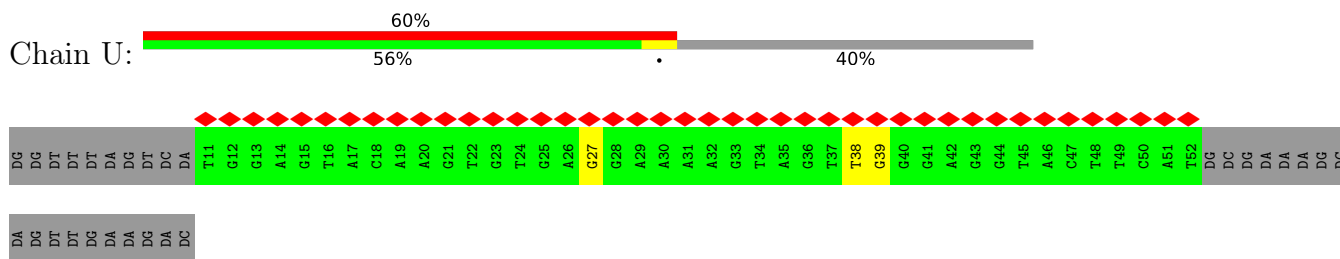
3 Residue-property plots

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 grey connector. Residues present in the sample, but not in the model, are shown in grey.

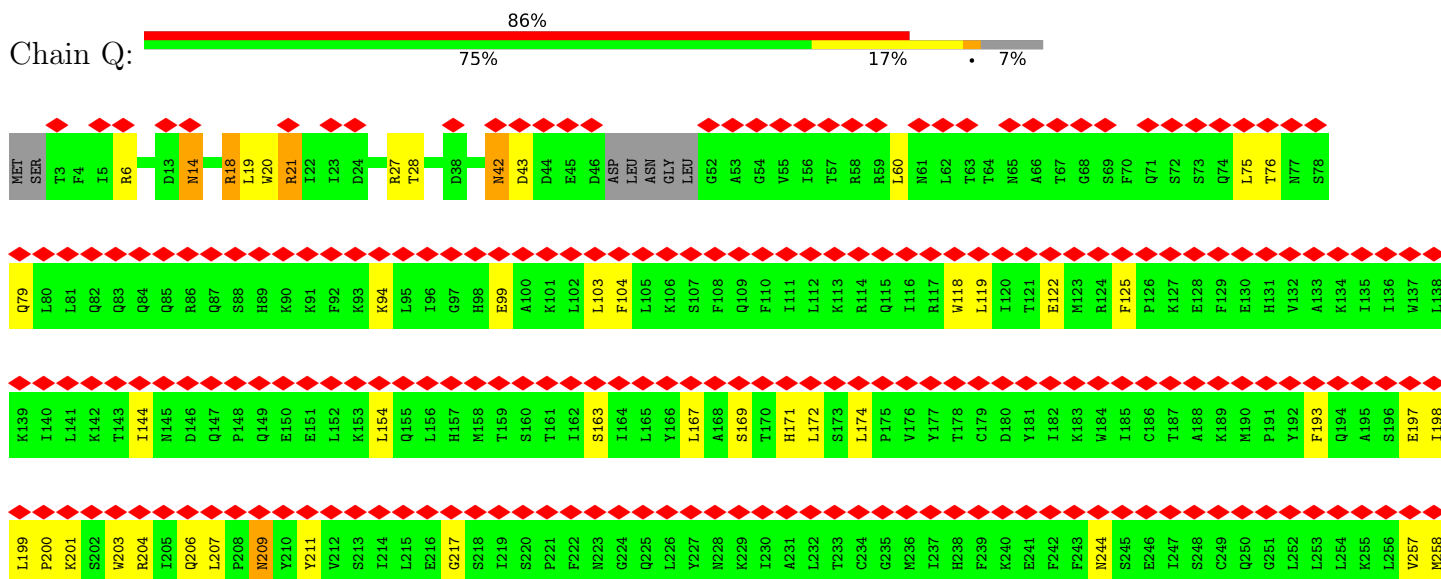
- Molecule 1: Template strand

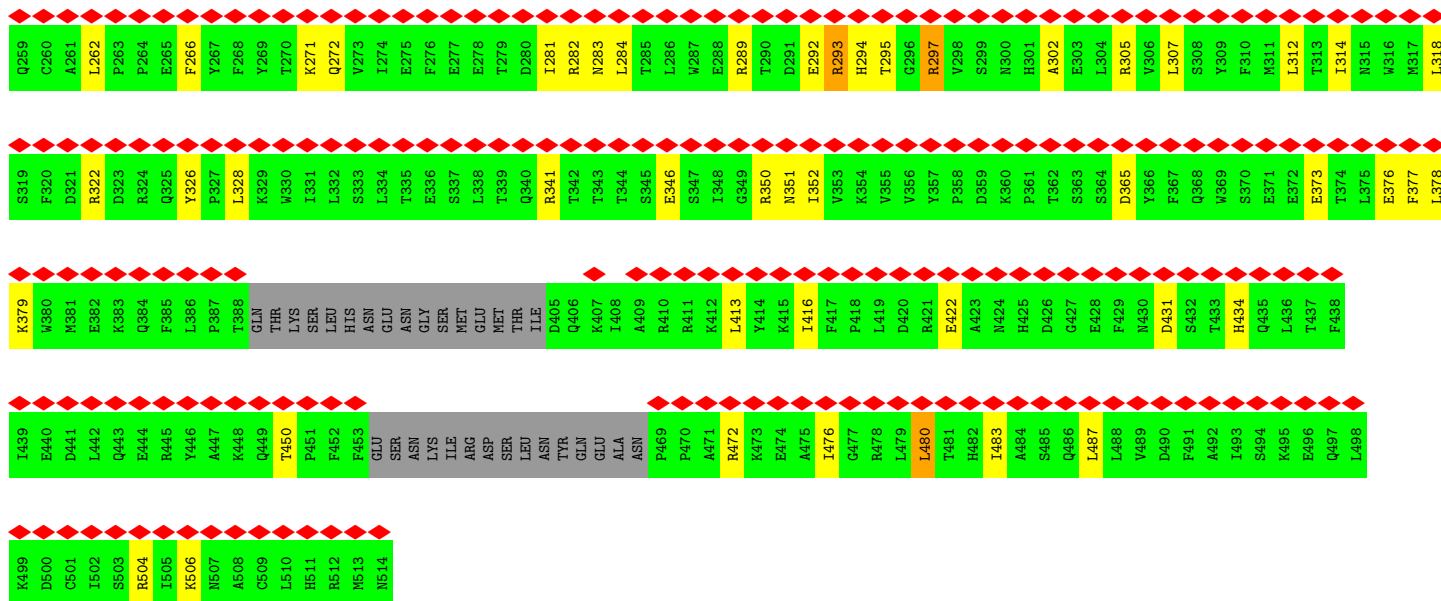


- Molecule 2: Nontemplate strand

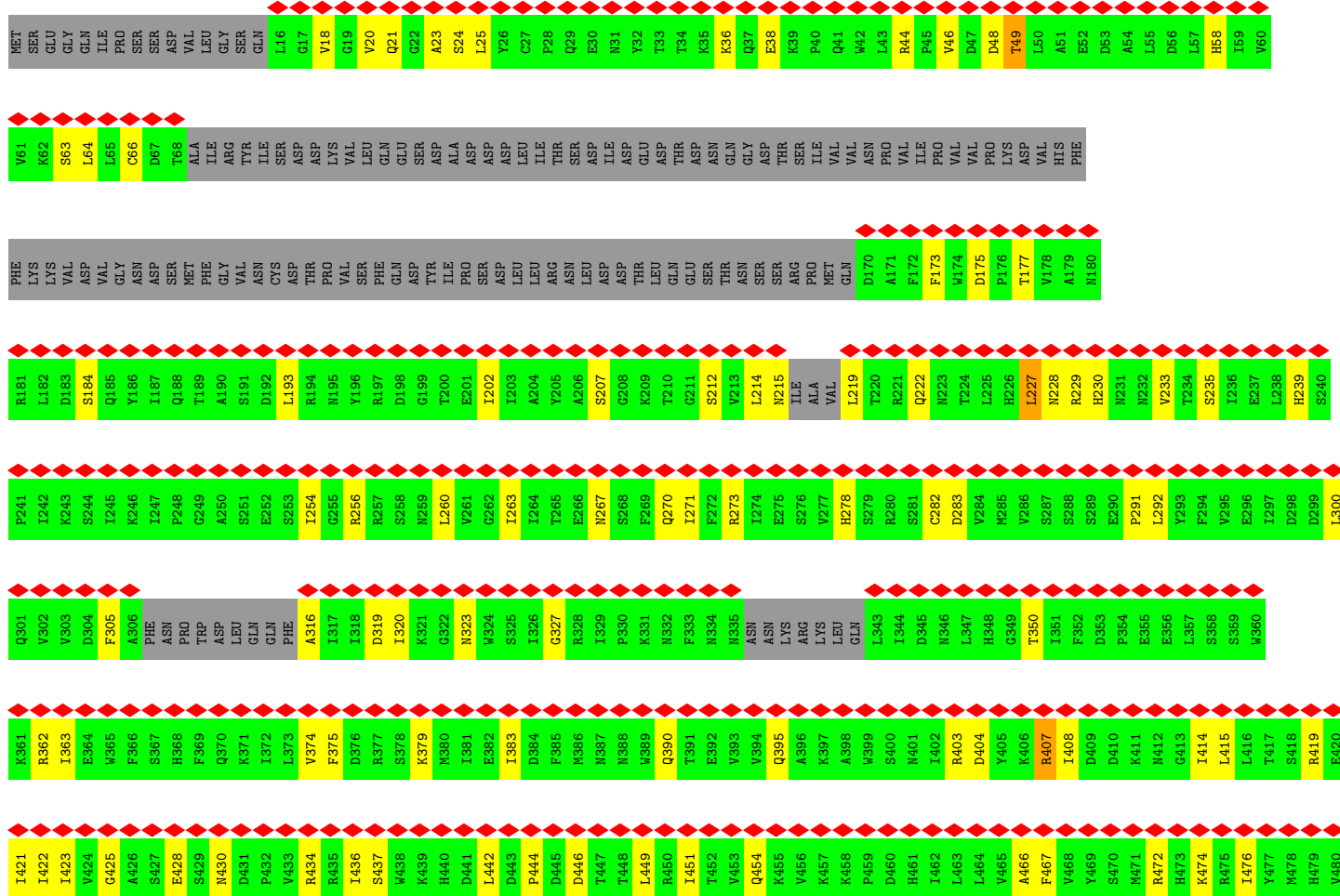


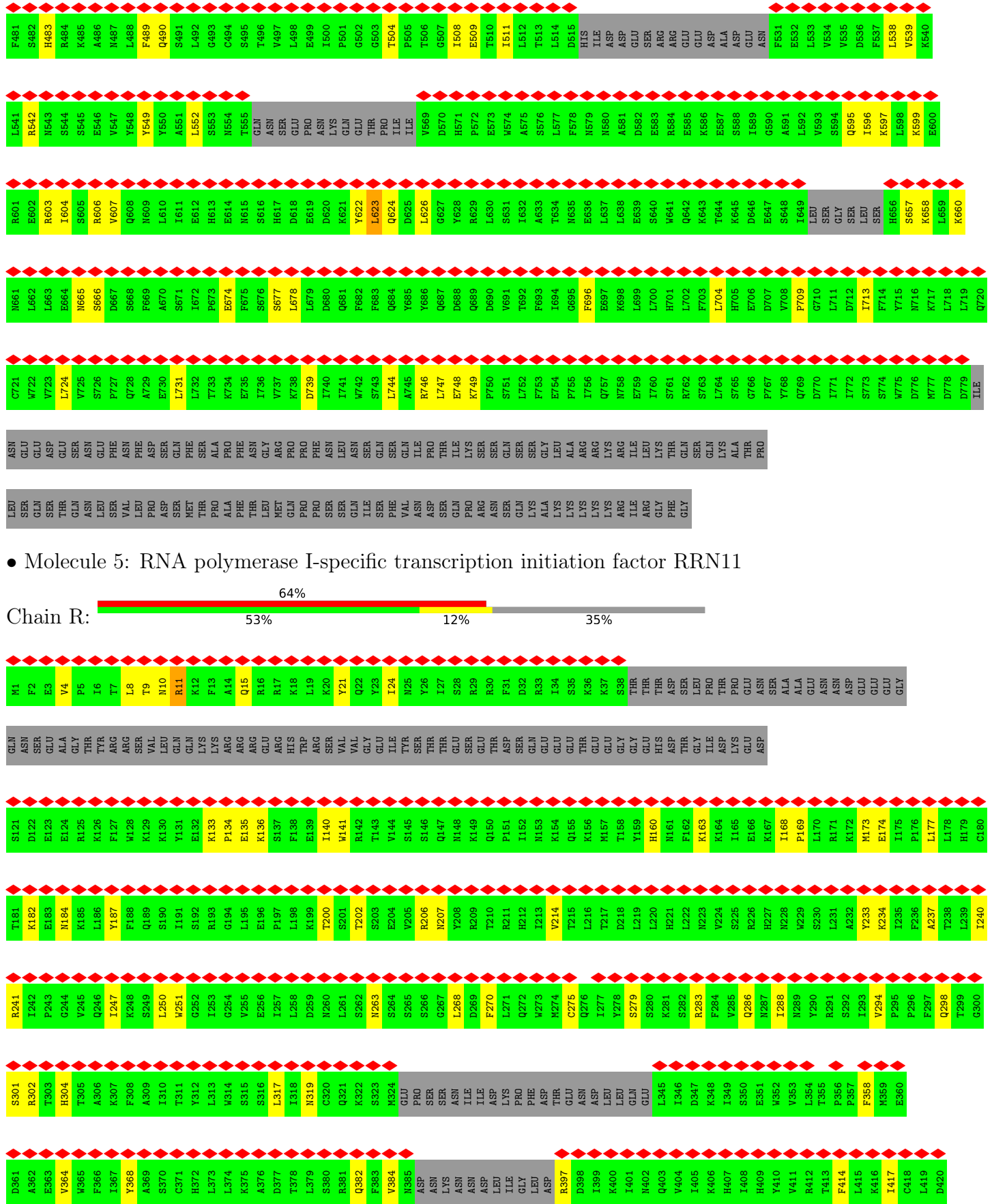
- Molecule 3: RNA polymerase I-specific transcription initiation factor RRN7



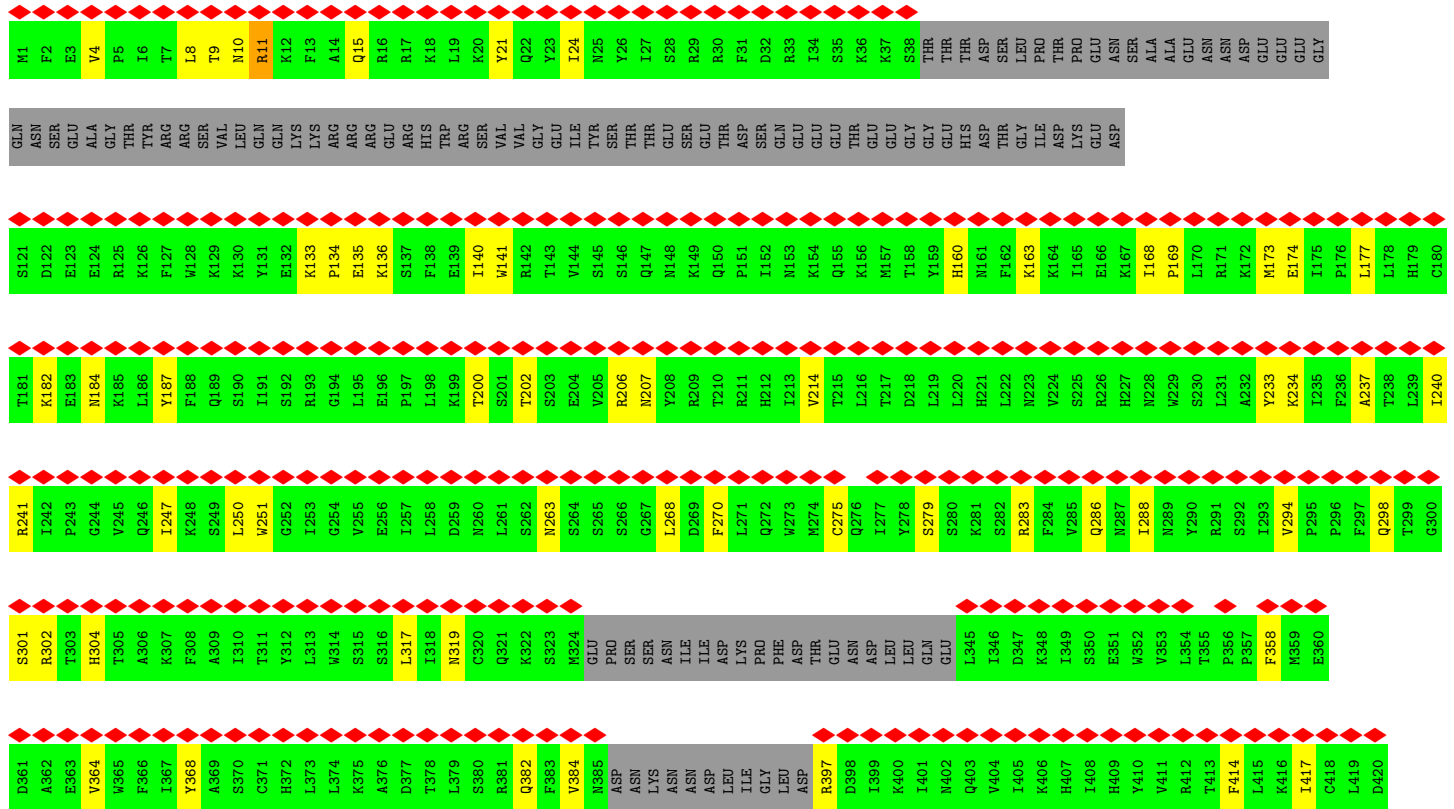


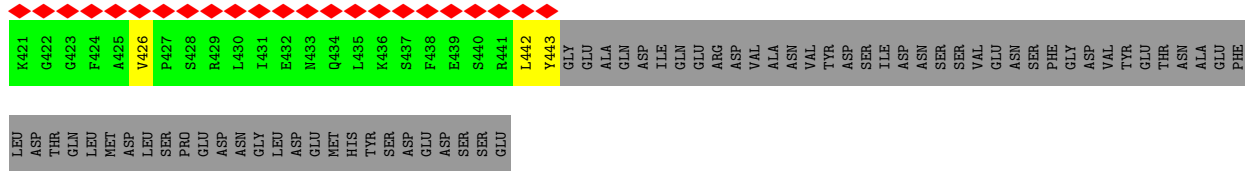
● Molecule 4: RNA polymerase I-specific transcription initiation factor RRN6



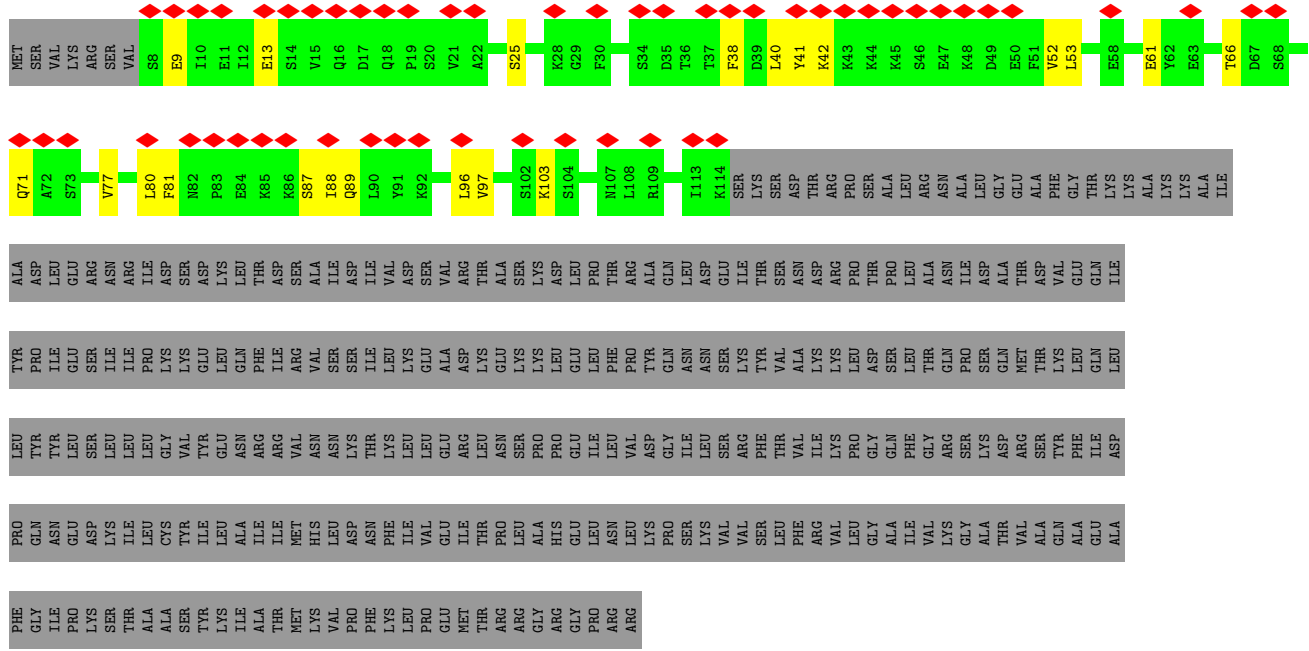


● Molecule 5: RNA polymerase I-specific transcription initiation factor RRN11

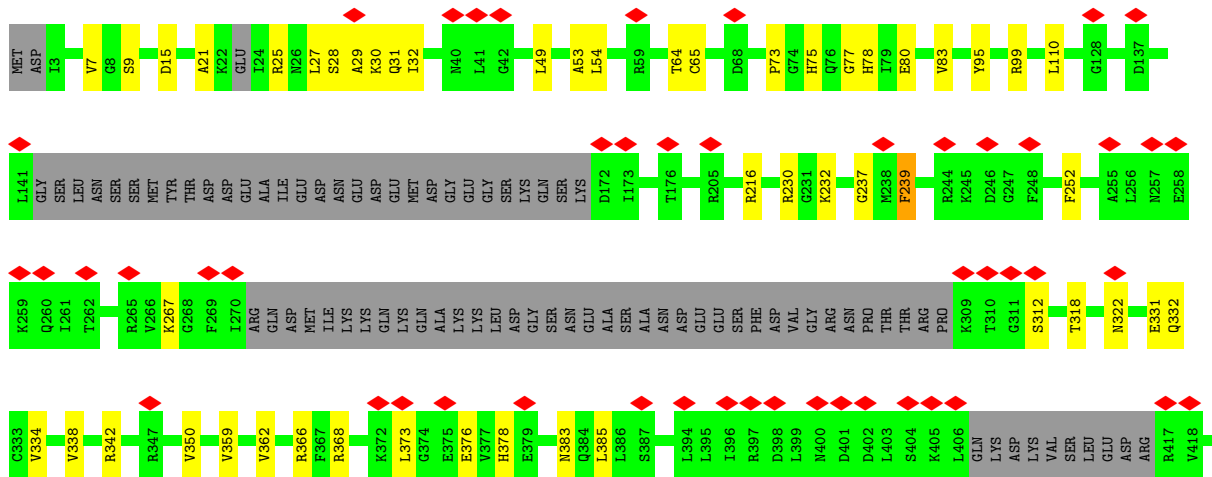
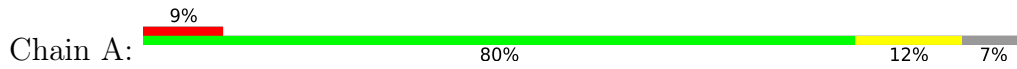


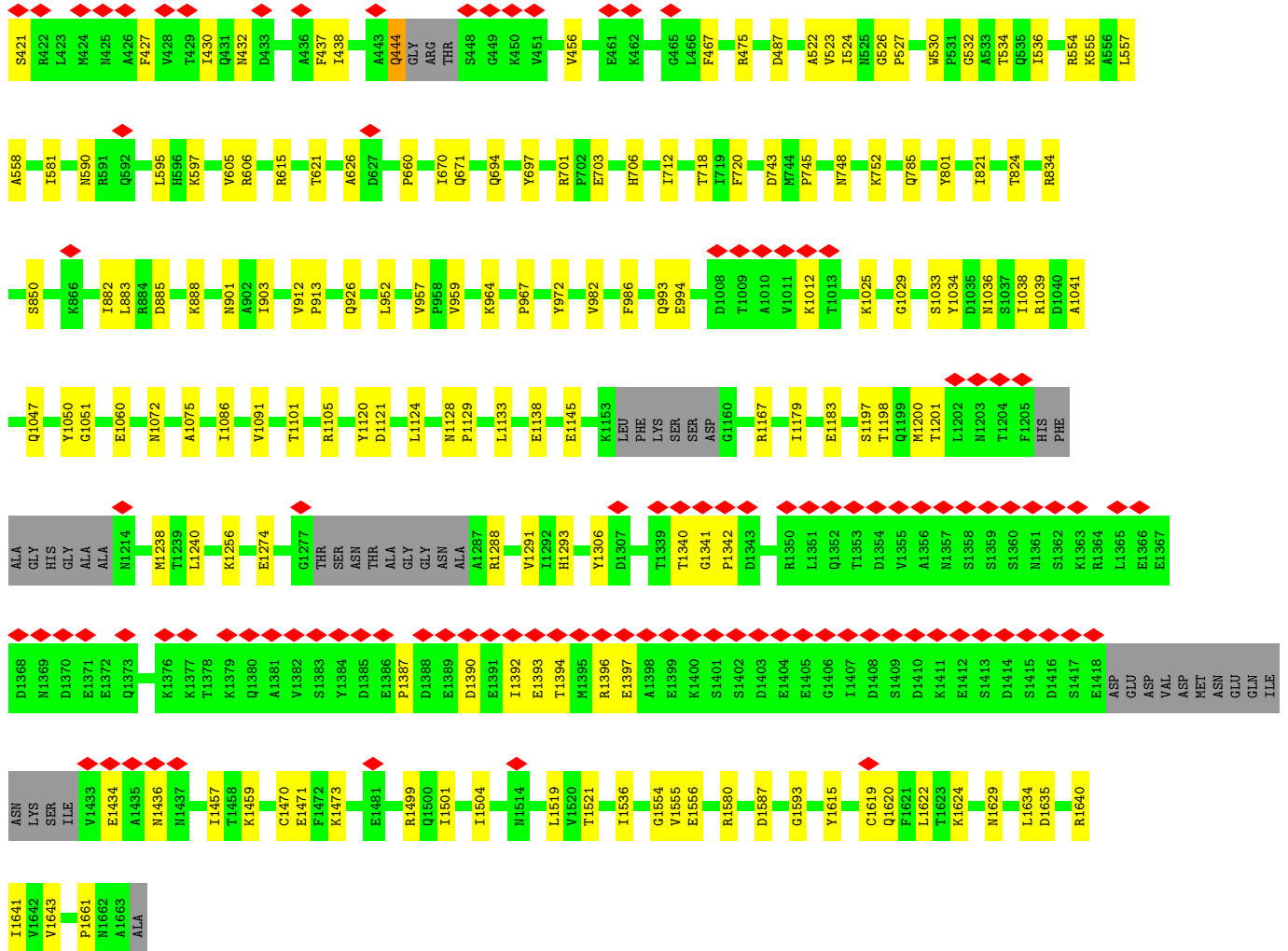


• Molecule 6: DNA-directed RNA polymerase I subunit RPA49

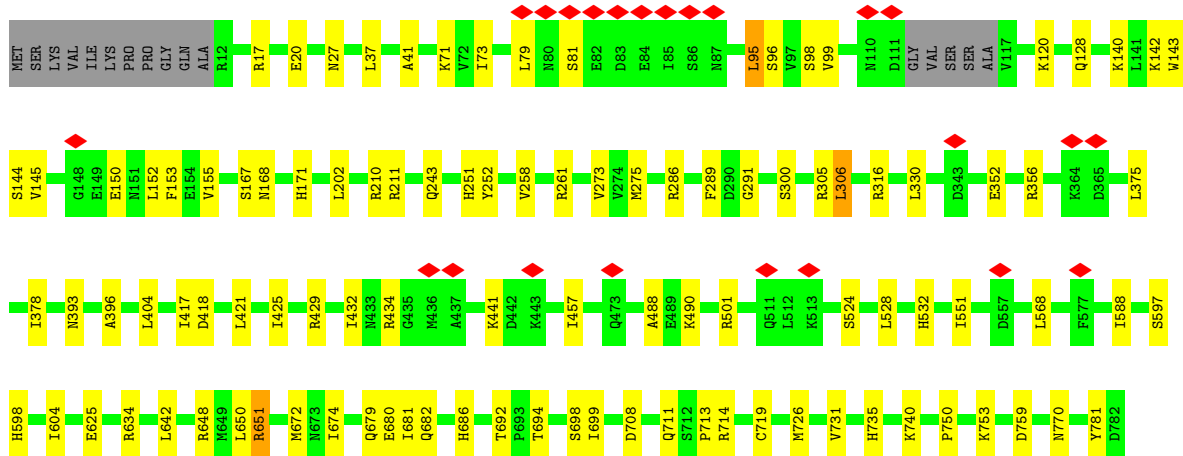
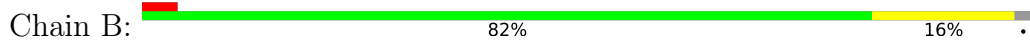


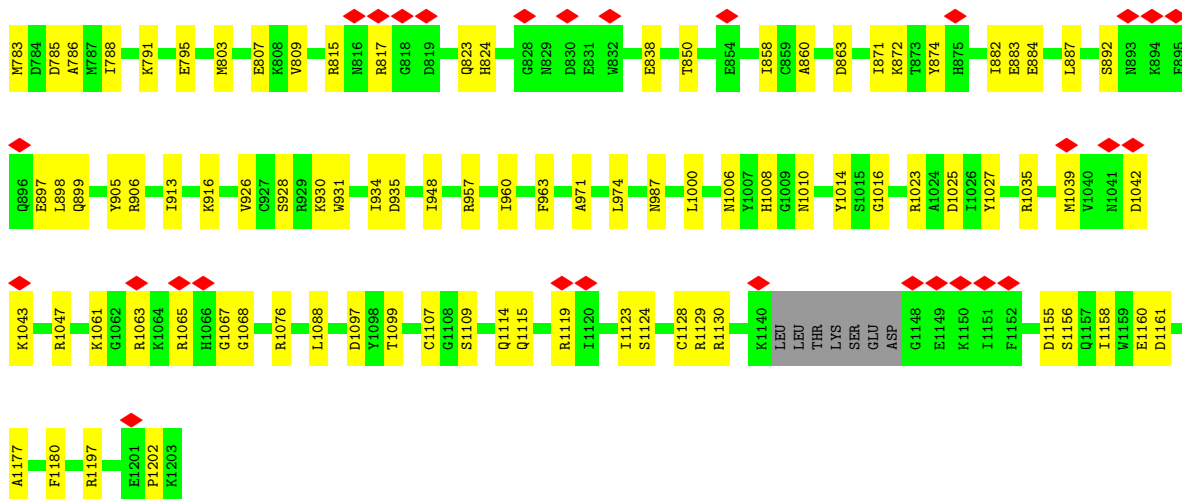
• Molecule 7: DNA-directed RNA polymerase I subunit RPA190



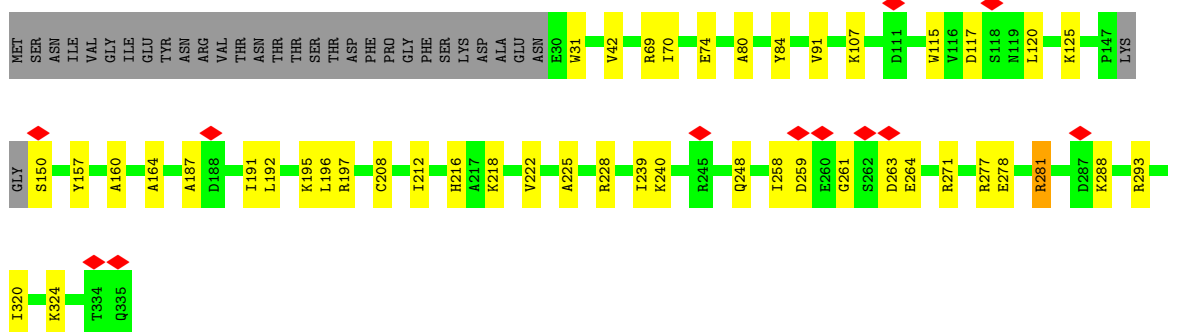
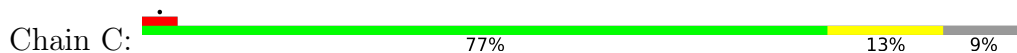


• Molecule 8: DNA-directed RNA polymerase I subunit RPA135

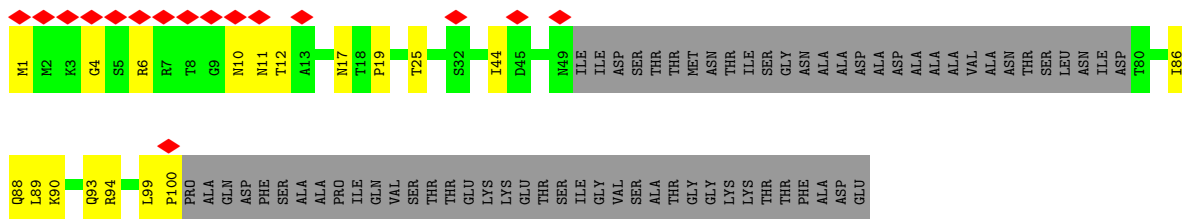
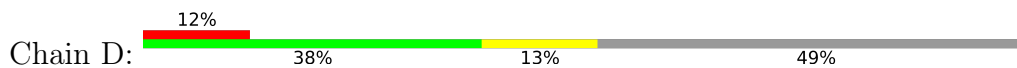




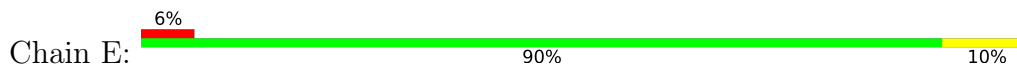
• Molecule 9: DNA-directed RNA polymerases I and III subunit RPAC1




• Molecule 10: DNA-directed RNA polymerase I subunit RPA14

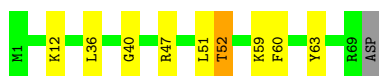


• Molecule 11: DNA-directed RNA polymerases I, II, and III subunit RPABC1



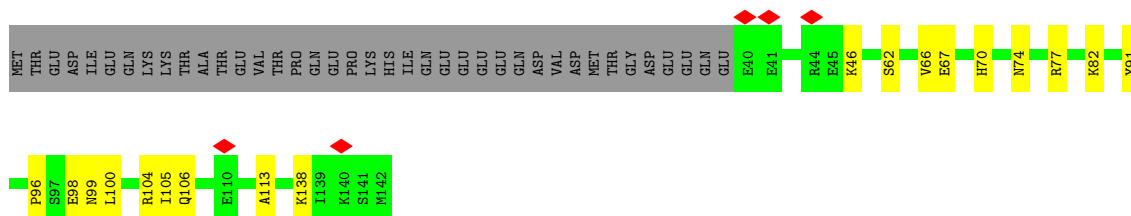
- Molecule 16: DNA-directed RNA polymerases I, II, and III subunit RPABC5

Chain J:  86% 11% ..



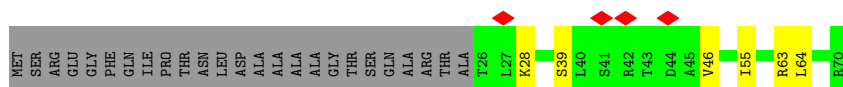
- Molecule 17: DNA-directed RNA polymerases I and III subunit RPAC2

Chain K:  60% 13% 27%




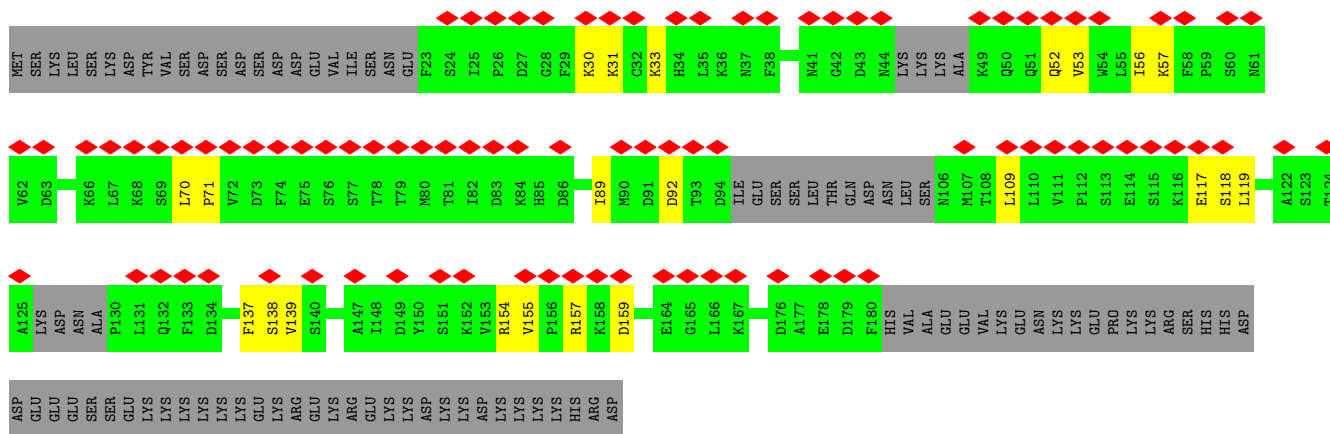
- Molecule 18: DNA-directed RNA polymerases I, II, and III subunit RPABC4

Chain L:  6% 56% 9% 36%



- Molecule 19: DNA-directed RNA polymerase I subunit RPA34

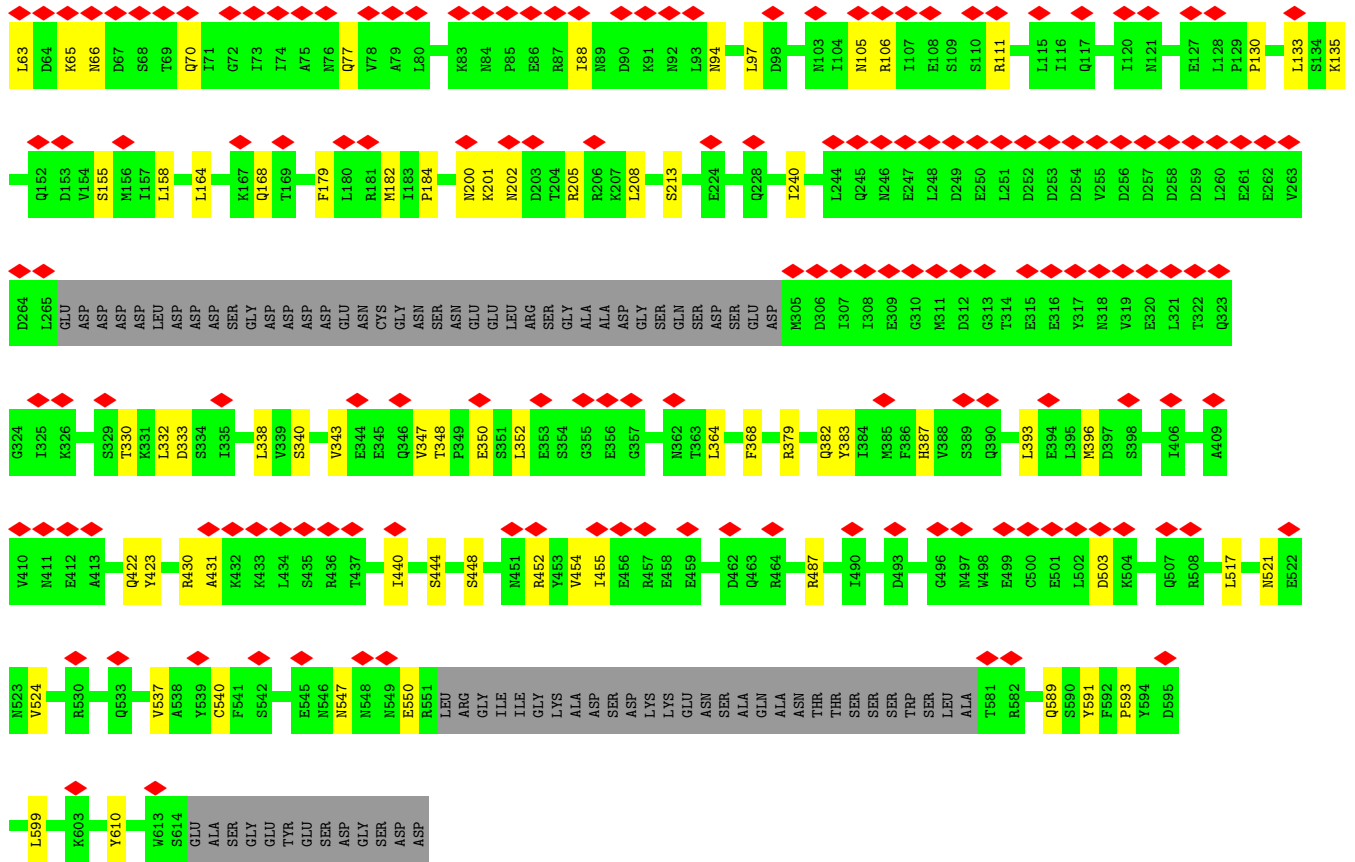
Chain N:  39% 50% 9% 40%



- Molecule 20: RNA polymerase I-specific transcription initiation factor RRN3

Chain O:  26% 68% 12% 20%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24482	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	0.274	Depositor
Minimum map value	-0.175	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 [i](#)

5.1 Standard geometry [i](#)

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	0.75	0/939	1.05	0/1442
2	U	0.64	0/988	0.92	0/1528
3	Q	0.36	0/4023	0.64	1/5434 (0.0%)
4	S	0.35	0/5065	0.63	0/6859
5	R	0.41	0/2836	0.65	0/3817
6	M	0.35	0/866	0.61	0/1162
7	A	0.47	0/12165	0.60	1/16450 (0.0%)
8	B	0.53	0/9578	0.65	0/12948
9	C	0.48	0/2469	0.61	0/3347
10	D	0.35	0/557	0.59	0/750
11	E	0.41	0/1795	0.54	0/2416
12	F	0.52	0/838	0.60	0/1129
13	G	0.40	0/1613	0.59	0/2193
14	H	0.49	0/1090	0.61	0/1476
15	I	0.37	0/955	0.61	0/1288
16	J	0.58	0/578	0.71	0/775
17	K	0.48	0/821	0.61	0/1108
18	L	0.49	0/361	0.77	0/478
19	N	0.32	0/1124	0.58	0/1512
20	O	0.36	0/4173	0.57	0/5645
All	All	0.46	0/52834	0.64	2/71757 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Q	60	LEU	CA-CB-CG	5.55	128.07	115.30
7	A	1387	PRO	N-CA-CB	5.17	109.50	103.30

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	842	0	476	9	0
2	U	877	0	475	2	0
3	Q	3931	0	3918	67	0
4	S	4963	0	4890	99	0
5	R	2771	0	2844	42	0
6	M	850	0	850	15	0
7	A	11953	0	11848	152	0
8	B	9371	0	9243	141	0
9	C	2418	0	2401	41	0
10	D	551	0	558	14	0
11	E	1759	0	1788	13	0
12	F	823	0	841	7	0
13	G	1576	0	1581	24	0
14	H	1072	0	1042	8	0
15	I	942	0	937	17	0
16	J	569	0	589	8	0
17	K	810	0	801	15	0
18	L	359	0	385	5	0
19	N	1103	0	1106	18	0
20	O	4086	0	4024	43	0
All	All	51626	0	50597	644	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 644 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)
7:A:232:LYS:HG2	7:A:239:PHE:CD1	1.59	1.36
4:S:442:LEU:HD21	4:S:444:PRO:CG	1.63	1.27
4:S:623:LEU:HD12	4:S:624:GLN:N	1.56	1.19
7:A:30:LYS:HD2	7:A:53:ALA:HB1	1.29	1.15
4:S:442:LEU:HD23	4:S:444:PRO:HD2	1.32	1.11

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	Q	468/514 (91%)	409 (87%)	58 (12%)	1 (0%)	47	78
4	S	594/894 (66%)	509 (86%)	85 (14%)	0	100	100
5	R	322/507 (64%)	292 (91%)	30 (9%)	0	100	100
6	M	105/415 (25%)	98 (93%)	7 (7%)	0	100	100
7	A	1524/1664 (92%)	1416 (93%)	108 (7%)	0	100	100
8	B	1174/1203 (98%)	1095 (93%)	79 (7%)	0	100	100
9	C	300/335 (90%)	283 (94%)	17 (6%)	0	100	100
10	D	66/137 (48%)	62 (94%)	4 (6%)	0	100	100
11	E	213/215 (99%)	208 (98%)	5 (2%)	0	100	100
12	F	98/155 (63%)	93 (95%)	5 (5%)	0	100	100
13	G	193/326 (59%)	178 (92%)	15 (8%)	0	100	100
14	H	130/146 (89%)	118 (91%)	12 (9%)	0	100	100
15	I	122/125 (98%)	104 (85%)	18 (15%)	0	100	100
16	J	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
17	K	101/142 (71%)	95 (94%)	6 (6%)	0	100	100
18	L	43/70 (61%)	41 (95%)	2 (5%)	0	100	100
19	N	131/233 (56%)	115 (88%)	16 (12%)	0	100	100
20	O	493/627 (79%)	453 (92%)	40 (8%)	0	100	100
All	All	6144/7778 (79%)	5633 (92%)	510 (8%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	Q	281	ILE

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%)	427 (98%)	9 (2%)	53	81
4	S	563/828 (68%)	555 (99%)	8 (1%)	67	89
5	R	313/474 (66%)	305 (97%)	8 (3%)	46	77
6	M	97/371 (26%)	97 (100%)	0	100	100
7	A	1297/1465 (88%)	1293 (100%)	4 (0%)	92	98
8	B	1030/1053 (98%)	1026 (100%)	4 (0%)	91	97
9	C	269/296 (91%)	268 (100%)	1 (0%)	91	97
10	D	65/116 (56%)	65 (100%)	0	100	100
11	E	197/197 (100%)	195 (99%)	2 (1%)	76	92
12	F	90/137 (66%)	89 (99%)	1 (1%)	73	92
13	G	177/291 (61%)	177 (100%)	0	100	100
14	H	116/128 (91%)	115 (99%)	1 (1%)	78	93
15	I	109/110 (99%)	108 (99%)	1 (1%)	78	93
16	J	64/65 (98%)	63 (98%)	1 (2%)	62	86
17	K	93/130 (72%)	93 (100%)	0	100	100
18	L	40/57 (70%)	40 (100%)	0	100	100
19	N	128/220 (58%)	128 (100%)	0	100	100
20	O	457/576 (79%)	457 (100%)	0	100	100
All	All	5541/6990 (79%)	5501 (99%)	40 (1%)	84	95

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	A	590	ASN
11	E	200	ARG
8	B	95	LEU
8	B	783	MET
14	H	142	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 65 such sidechains are listed below:

Mol	Chain	Res	Type
15	I	95	ASN
20	O	66	ASN
7	A	592	GLN
7	A	431	GLN
20	O	94	ASN

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](#)

There are no ligands in this entry.

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.

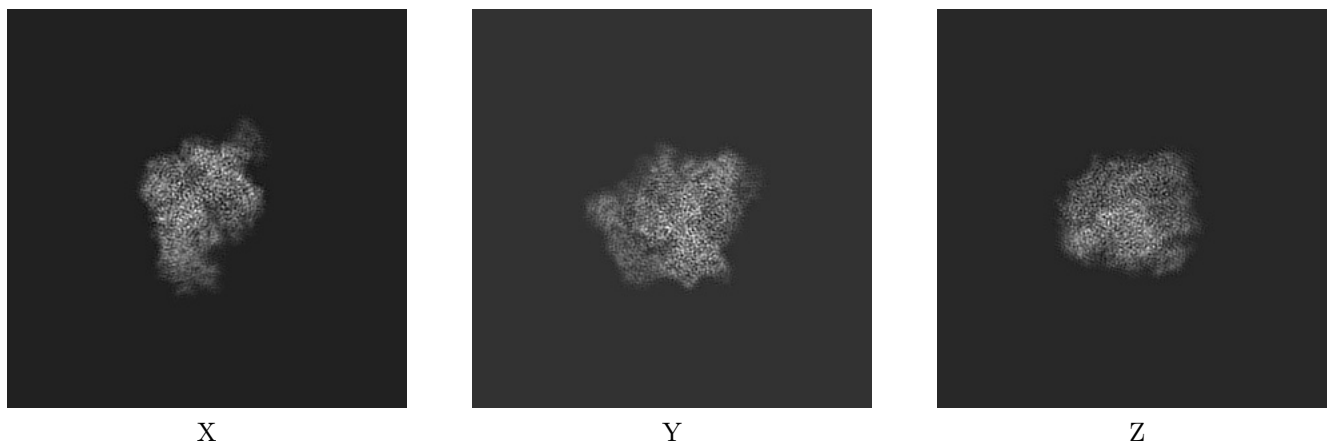
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4984. 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](#)

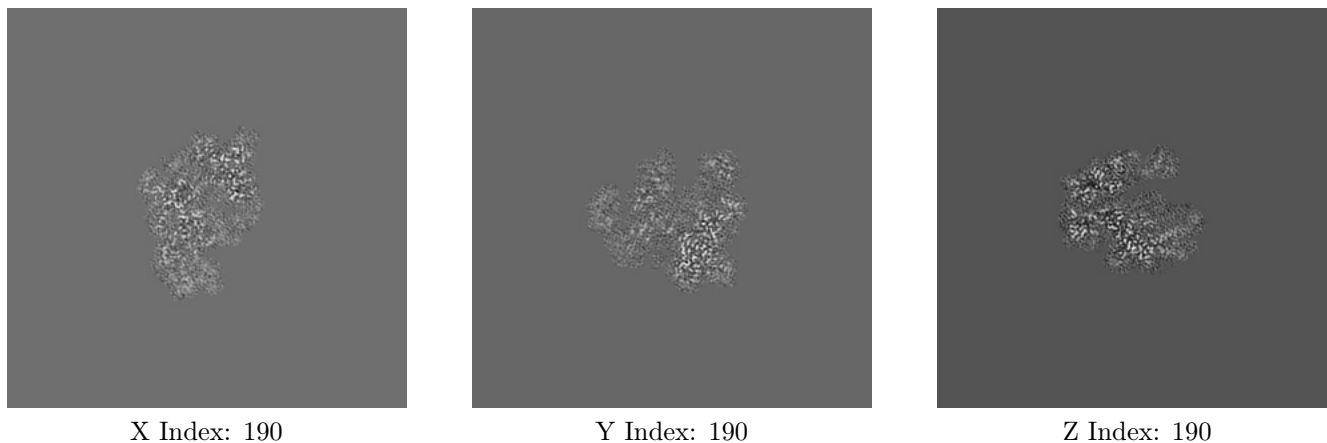
6.1.1 Primary map



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

6.2 Central slices [i](#)

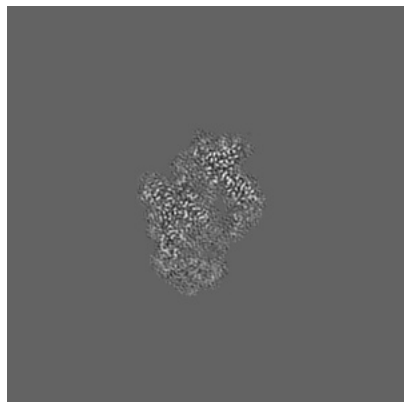
6.2.1 Primary map



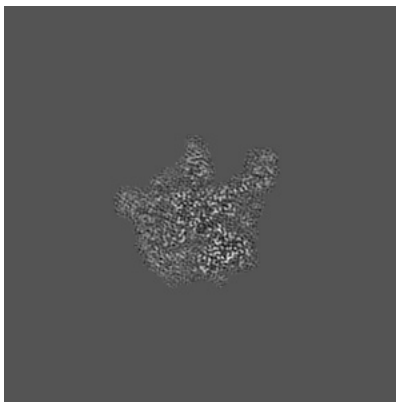
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

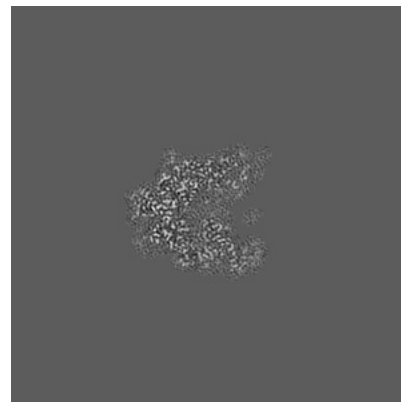
6.3.1 Primary map



X Index: 181



Y Index: 168



Z Index: 209

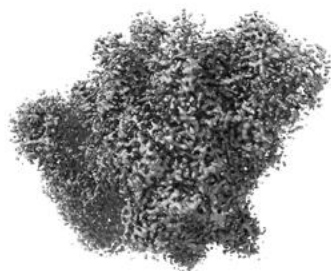
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

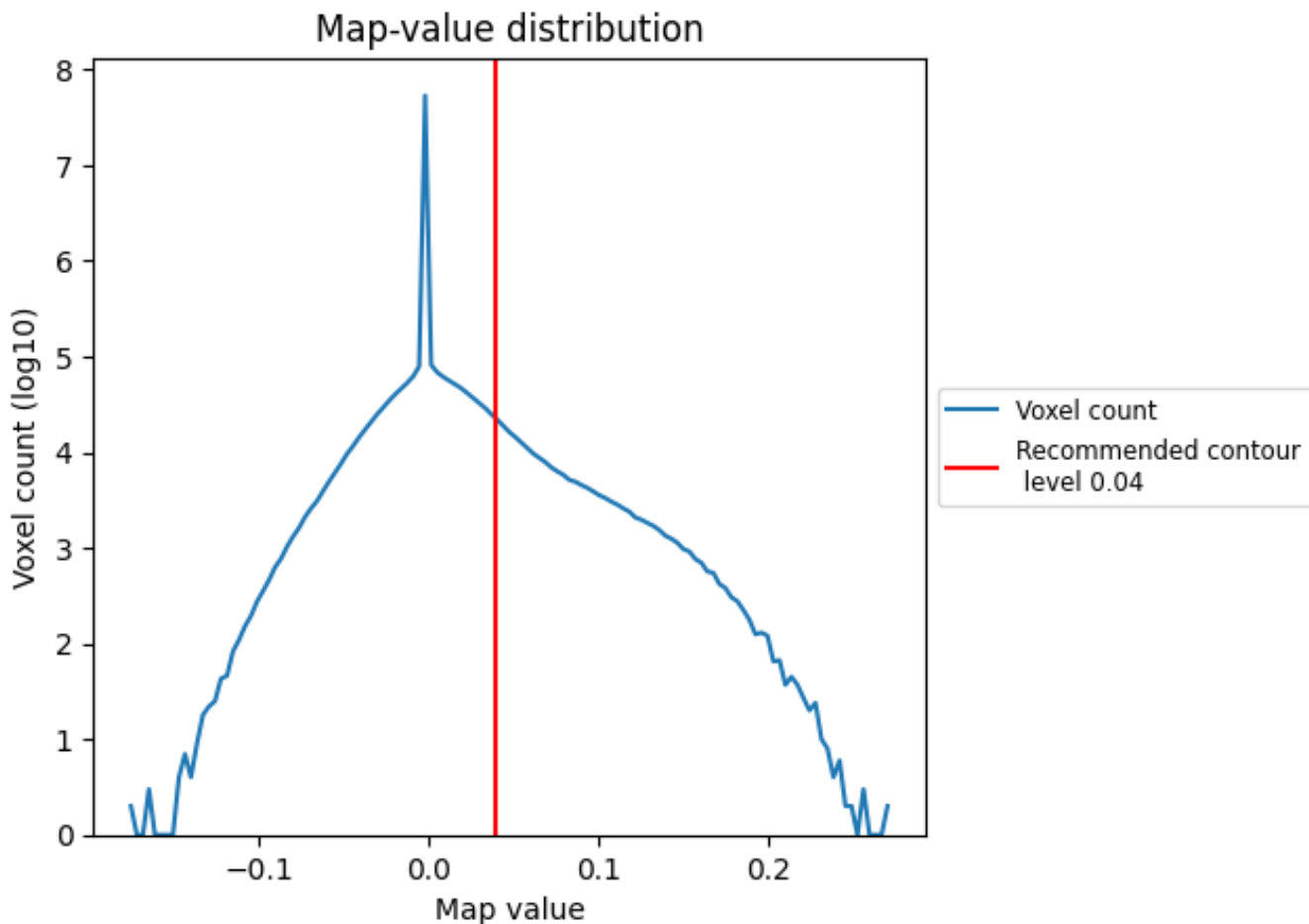
6.5 Mask visualisation

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

7 Map analysis [i](#)

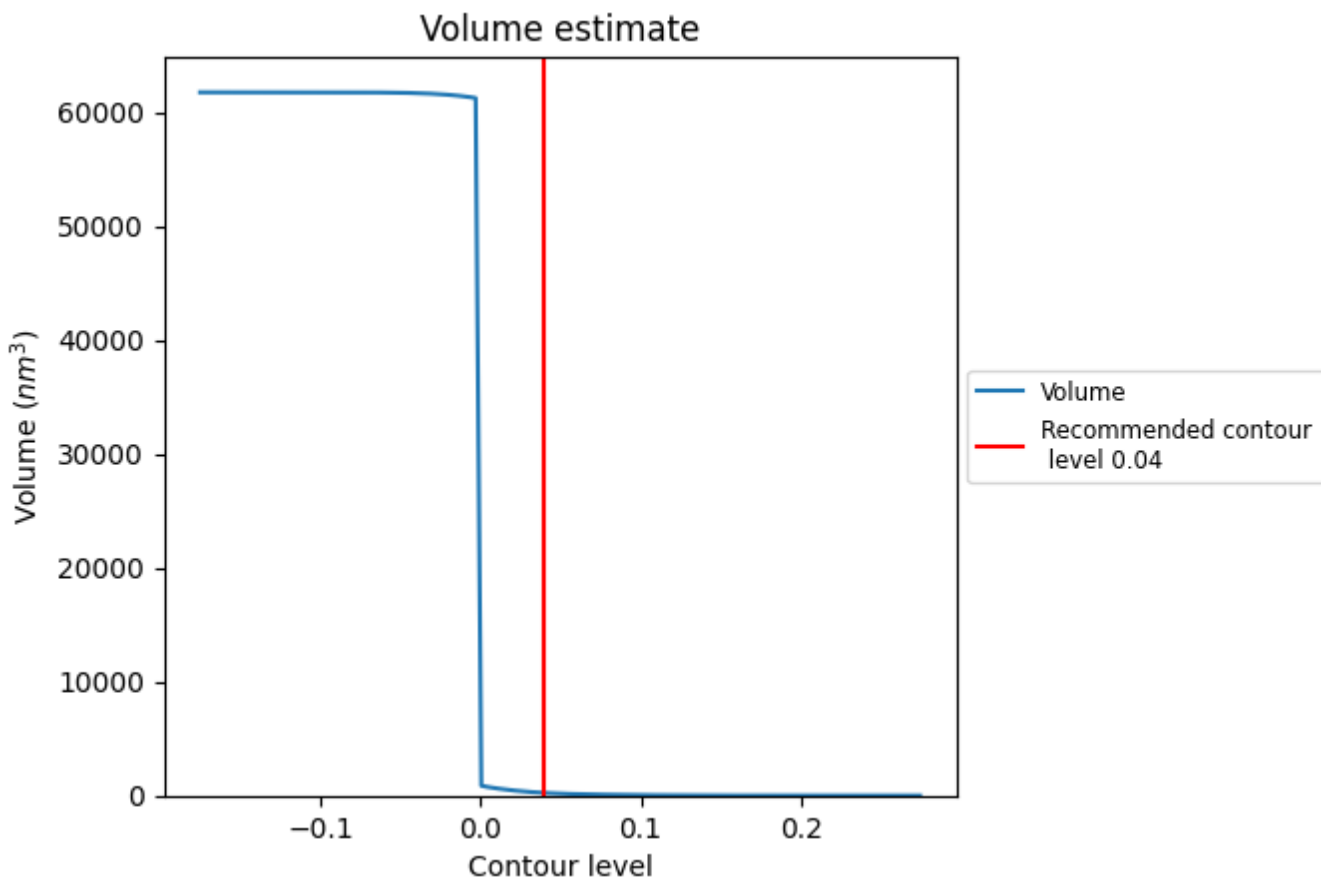
This section contains the results of statistical analysis of the map.

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.

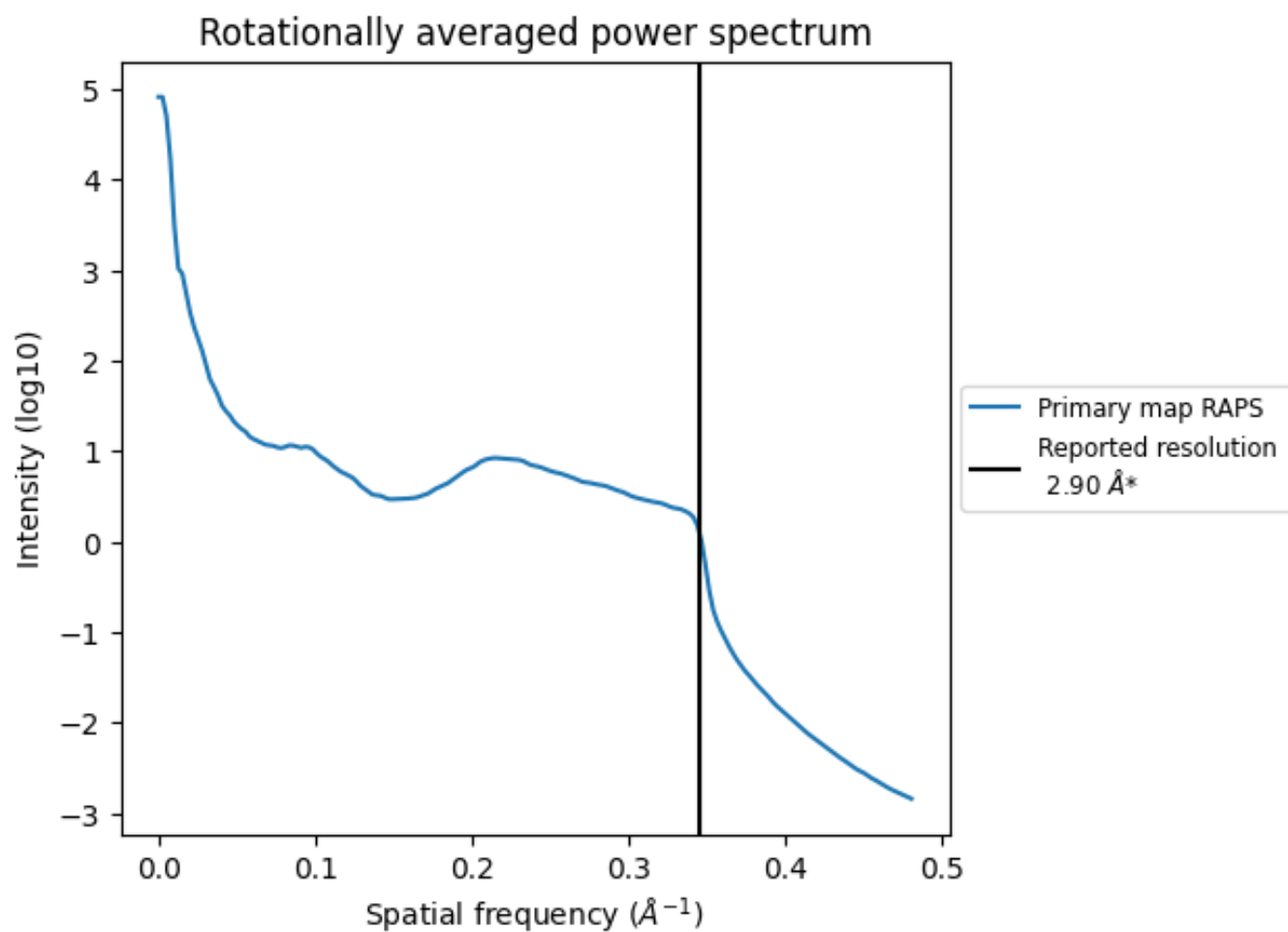
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 233 nm³; this corresponds to an approximate mass of 210 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 0.345\AA^{-1}

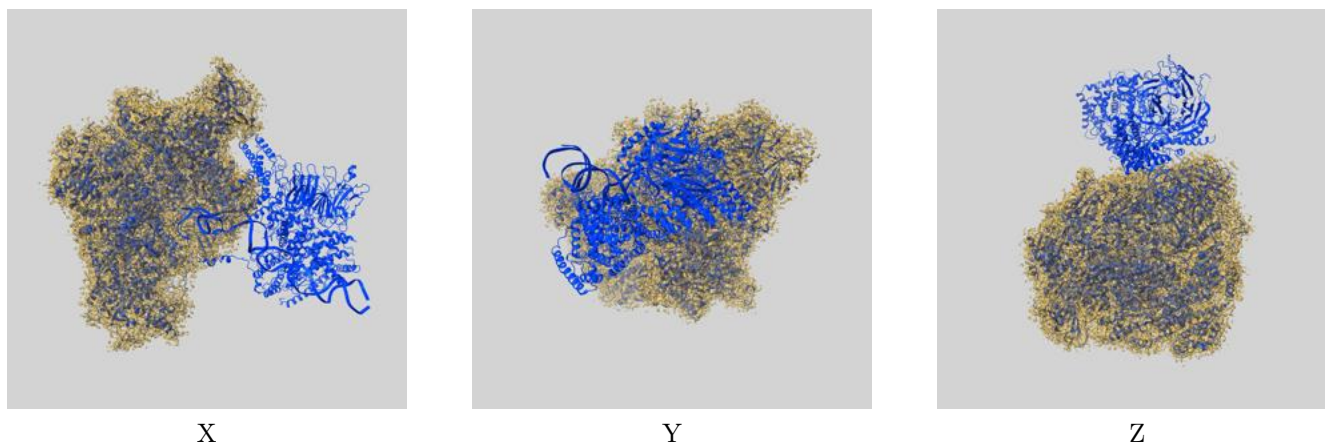
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

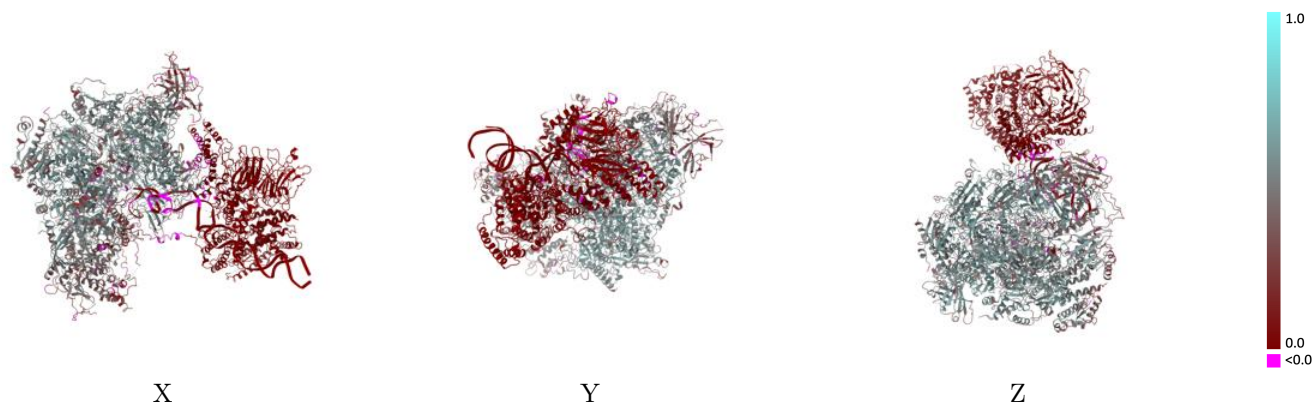
This section contains information regarding the fit between EMDB map EMD-4984 and PDB model 6RQL. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



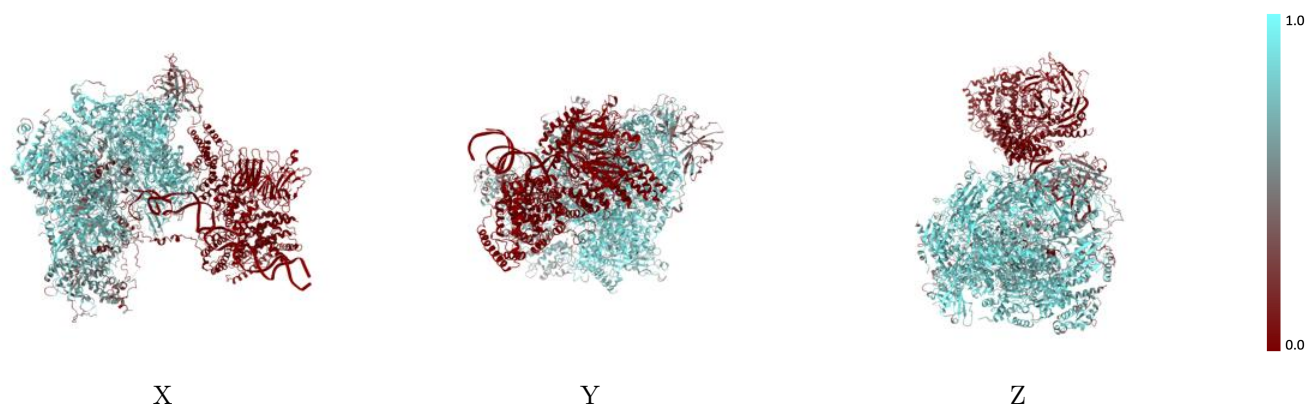
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



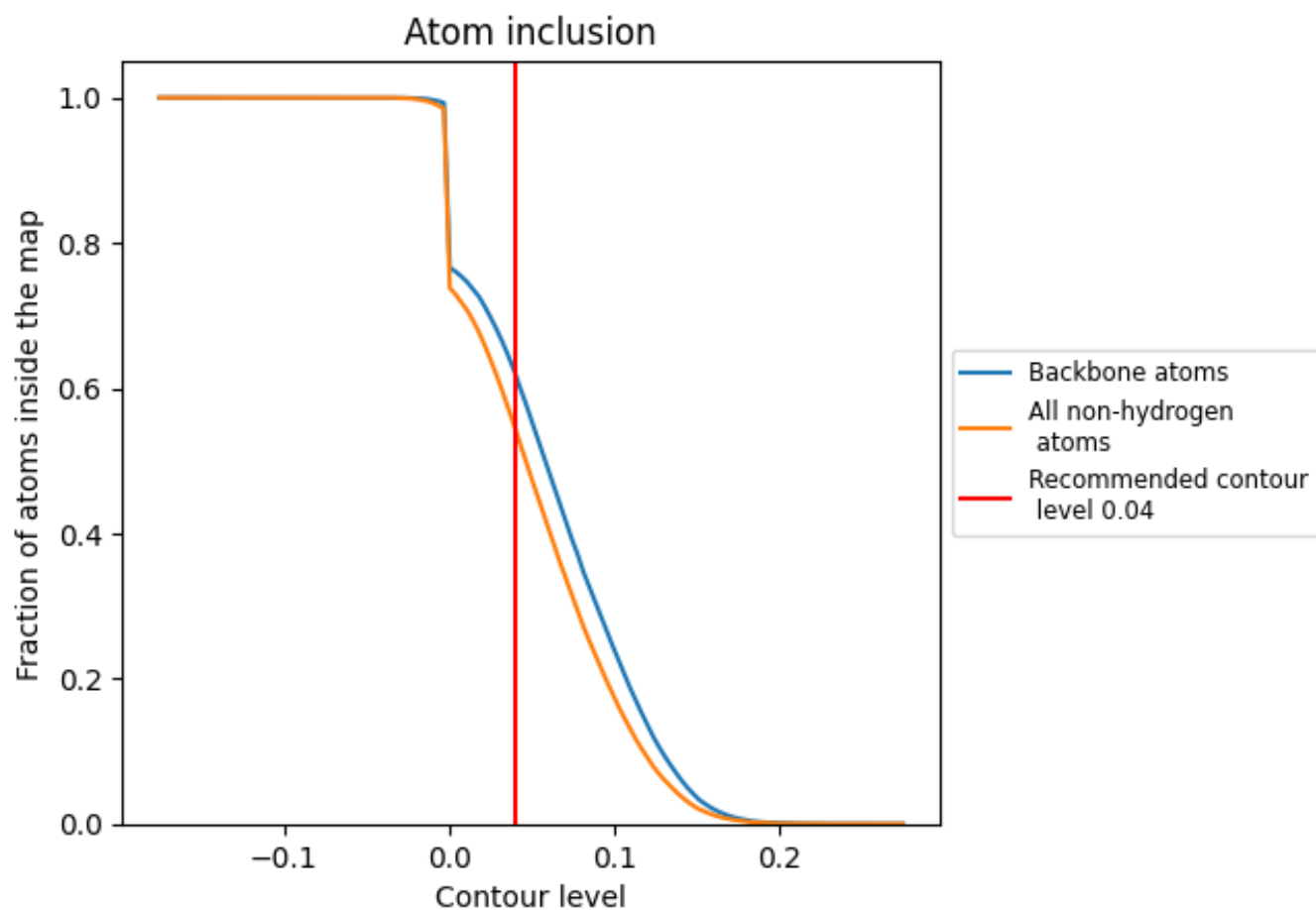
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.04).











































9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 54% 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	 0.5443	 0.3550
A	 0.7696	 0.5030
B	 0.8188	 0.5260
C	 0.7957	 0.5050
D	 0.5893	 0.3940
E	 0.7564	 0.4740
F	 0.8190	 0.5470
G	 0.6686	 0.4190
H	 0.7720	 0.4890
I	 0.5494	 0.3860
J	 0.8947	 0.5630
K	 0.7953	 0.5230
L	 0.7775	 0.4850
M	 0.3957	 0.3260
N	 0.3498	 0.3050
O	 0.5298	 0.3390
Q	 0.0618	 0.0400
R	 0.0070	 0.0080
S	 0.0000	 0.0000
T	 0.0095	 0.0080
U	 0.0034	 0.0100

