



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 01:00 AM UTC

PDB ID : 6JNX / pdb_00006jnx
EMDB ID : EMD-9852
Title : Cryo-EM structure of a Q-engaged arrested complex
Authors : Feng, Y.; Shi, J.
Deposited on : 2019-03-18
Resolution : 4.08 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:

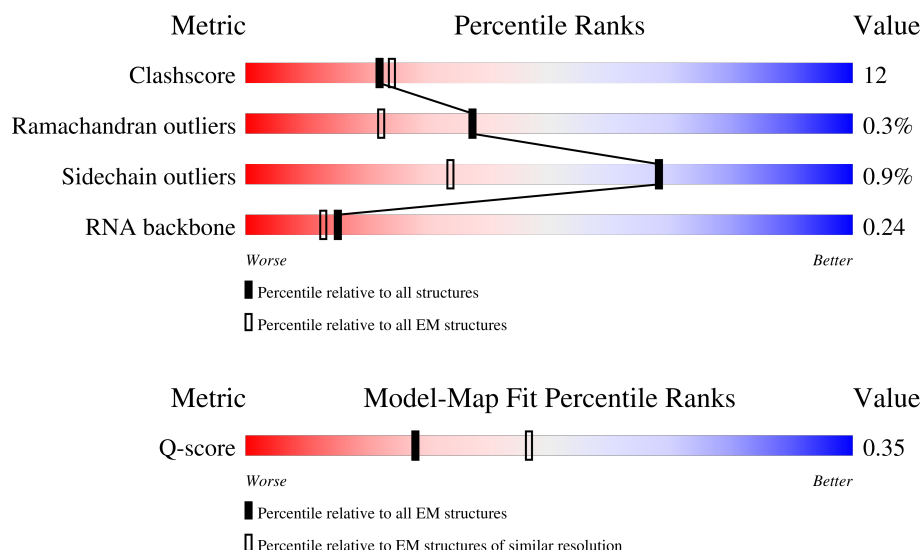
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.08 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	6428 (3.58 - 4.58)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	329	
1	B	329	
2	C	1342	

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Mol	Chain	Length	Quality of chain
3	D	1407	
4	E	91	
5	F	613	
6	N	63	
7	R	18	
8	T	63	
9	P	162	
9	Q	162	

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 32639 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-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	219	Total	C	N	O	S	0	0
			1686	1056	298	326	6		
1	B	218	Total	C	N	O	S	0	0
			1681	1050	297	328	6		

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	1340	Total	C	N	O	S	0	0
			10567	6631	1841	2052	43		

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	1335	Total	C	N	O	S	0	0
			10388	6526	1854	1958	50		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	79	Total	C	N	O	S	0	0
			627	382	118	126	1		

- Molecule 5 is a protein called RNA polymerase sigma factor RpoD.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	307	Total	C	N	O	S	0	0
			2513	1583	442	473	15		

- Molecule 6 is a DNA chain called DNA (63-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	63	Total	C	N	O	P	0	0
			1303	620	247	373	63		

- Molecule 7 is a RNA chain called RNA (5'-R(P*AP*UP*AP*AP*GP*GP*UP*GP*GP*GP*GP*UP*UP*AP*GP*UP*GP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
7	R	18	Total	C	N	O	P	0	0
			394	175	75	126	18		

- Molecule 8 is a DNA chain called DNA (63-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	T	63	Total	C	N	O	P	0	0
			1281	614	223	381	63		

- Molecule 9 is a protein called Antiterminator Q protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	P	147	Total	C	N	O	S	0	0
			1179	750	210	208	11		
9	Q	126	Total	C	N	O	S	0	0
			1017	651	179	179	8		

- Molecule 10 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
10	D	1	Total	Mg	0
			1	1	

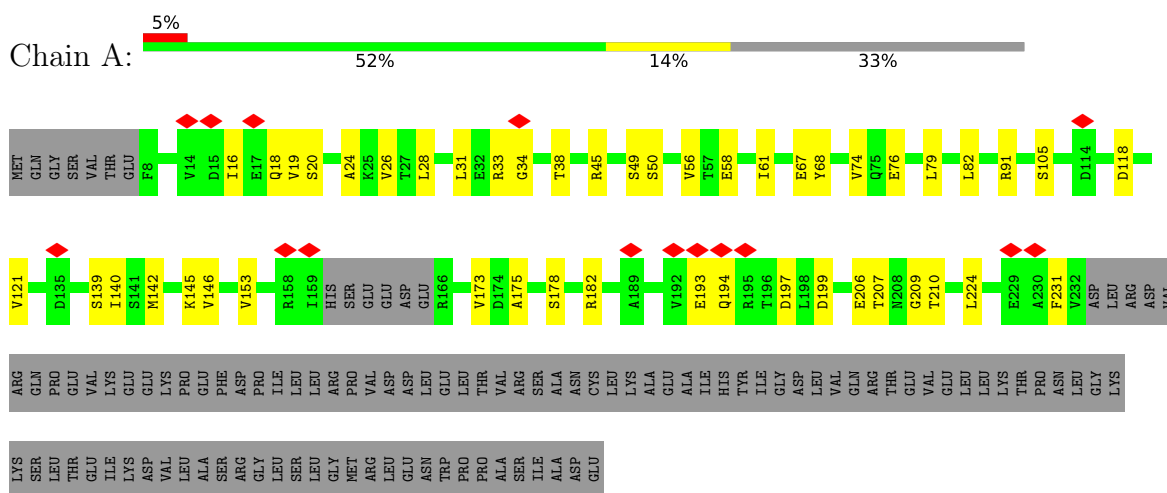
- Molecule 11 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

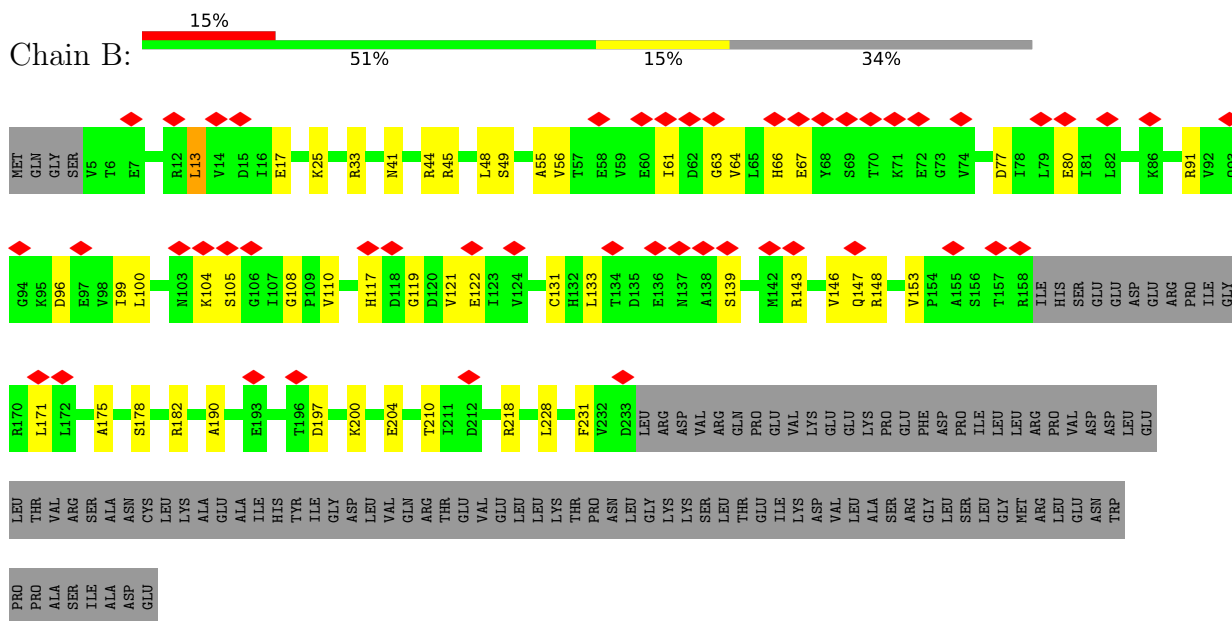
3 Residue-property plots

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

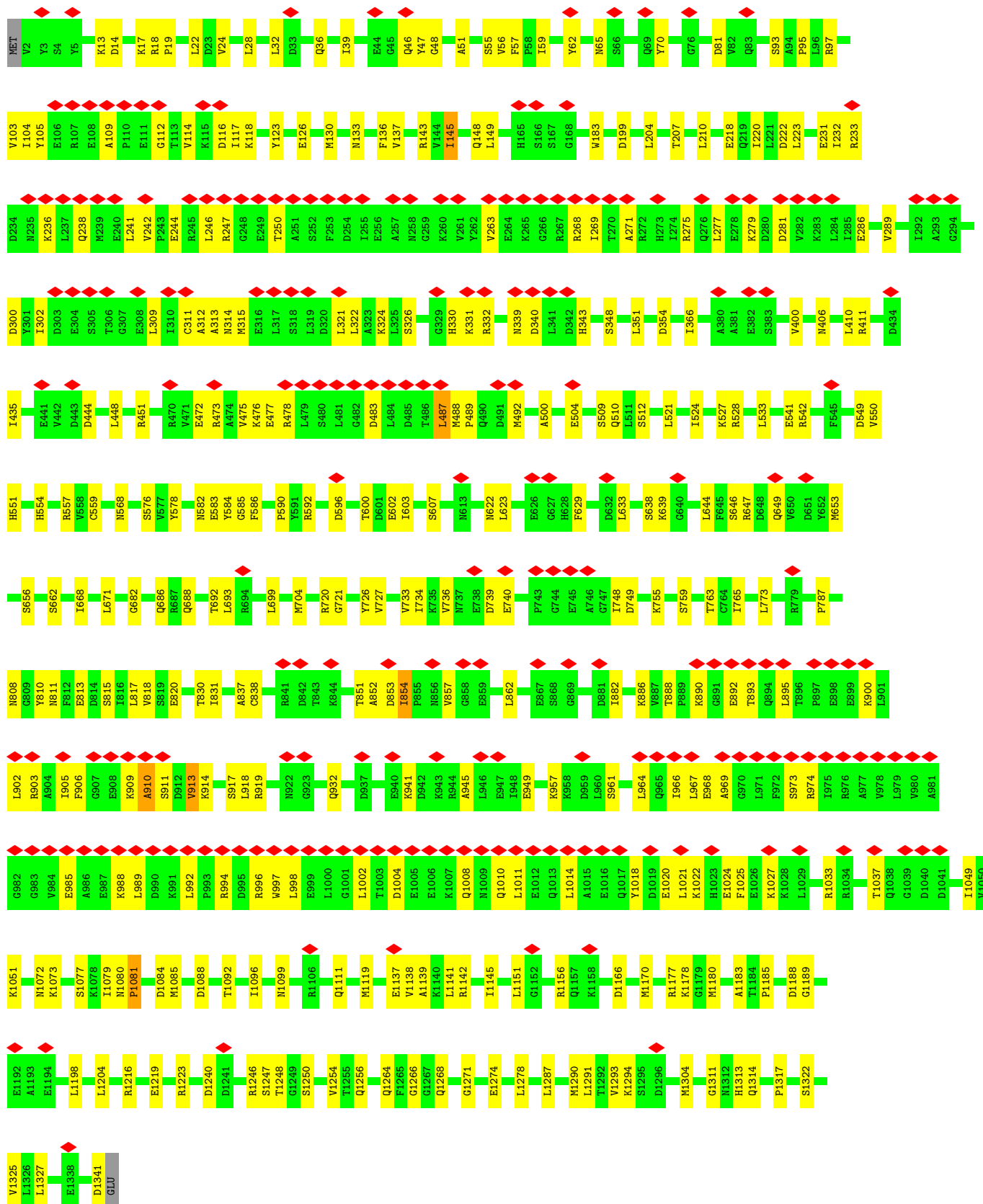
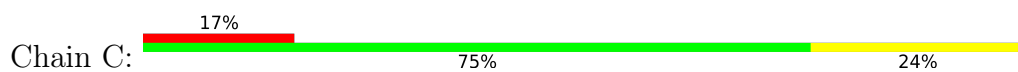
- Molecule 1: DNA-directed RNA polymerase subunit alpha



- Molecule 1: DNA-directed RNA polymerase subunit alpha

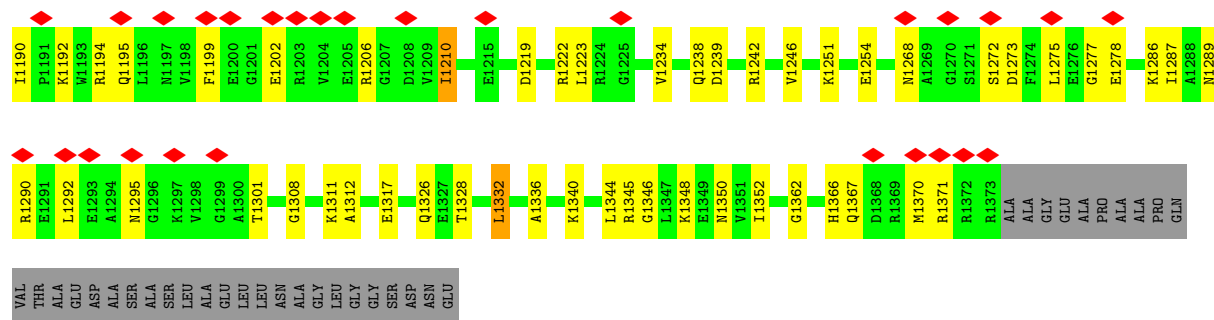


- Molecule 2: DNA-directed RNA polymerase subunit beta



Chain D:

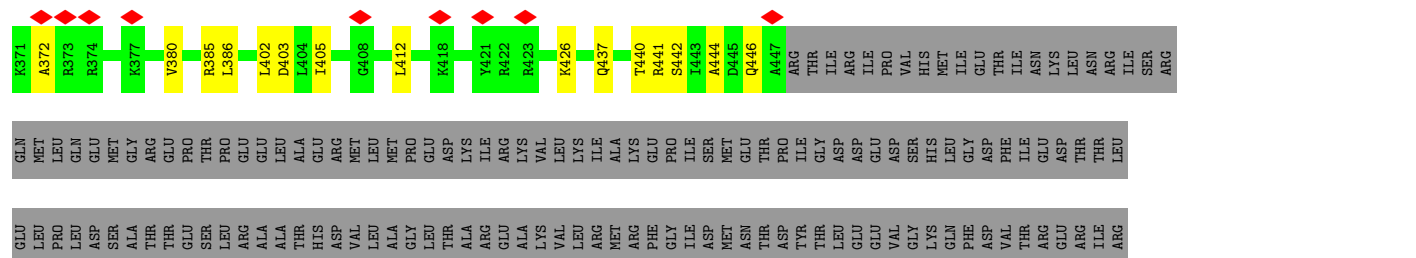
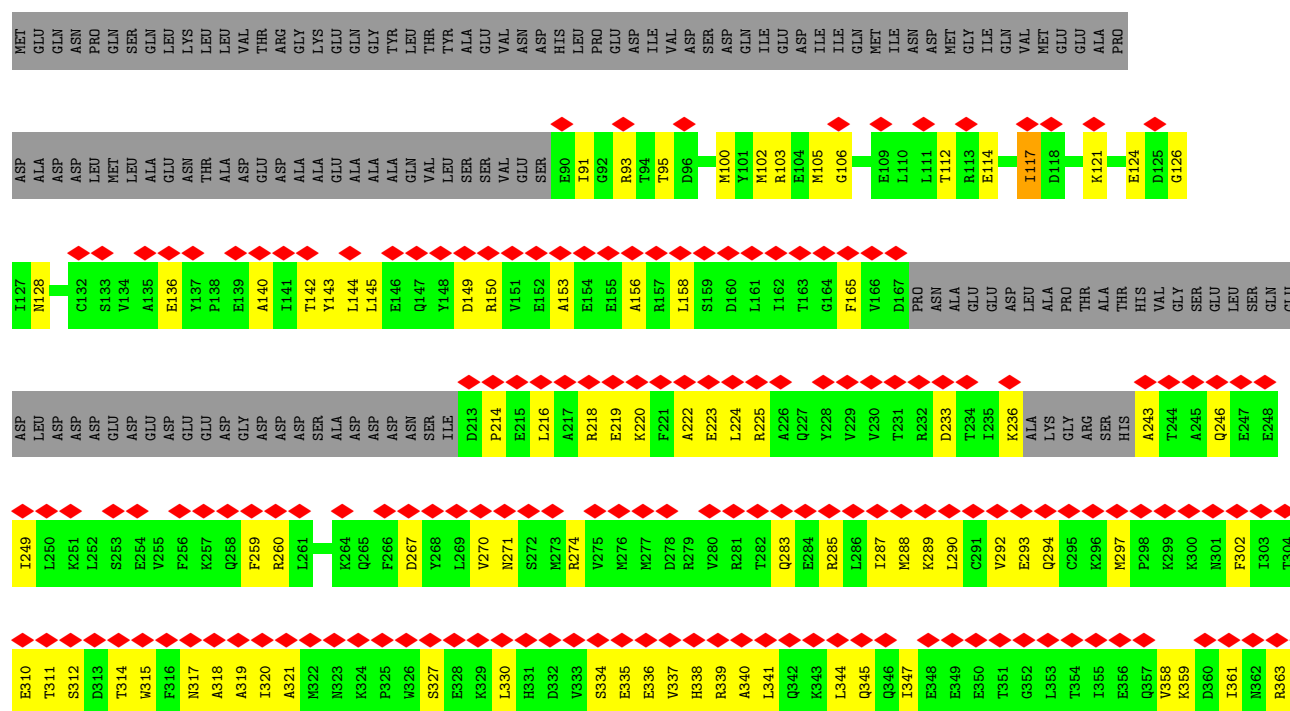
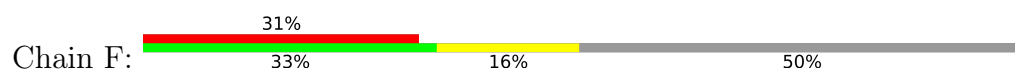




• Molecule 4: DNA-directed RNA polymerase subunit omega



• Molecule 5: RNA polymerase sigma factor RpoD

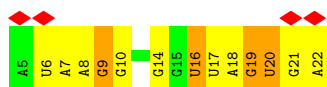


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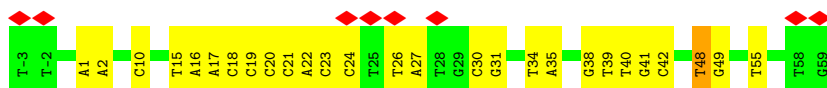
• Molecule 6: DNA (63-MER)



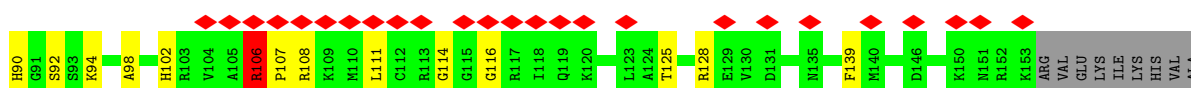
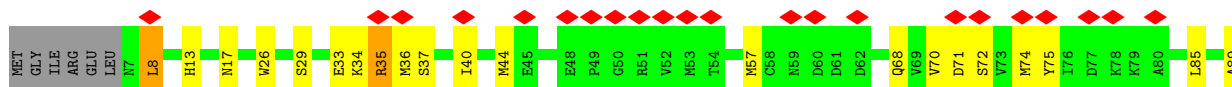
• Molecule 7: RNA (5'-R(P*AP*UP*AP*AP*GP*GP*UP*GP*GP*GP*GP*UP*UP*AP*GP*UP*GP*A)-3')



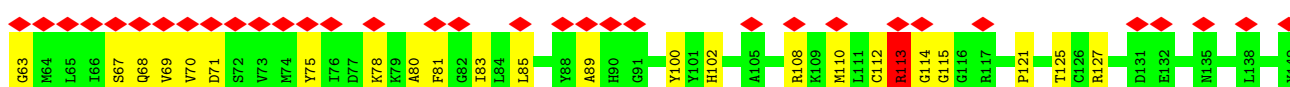
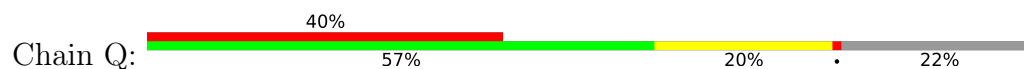
• Molecule 8: DNA (63-MER)



• Molecule 9: Antiterminator Q protein



• Molecule 9: Antiterminator Q protein



P143	
V144	
LEU	ASP
	SER
	ALA
	PHE
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	ARG
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	HIS
	VAL
	ALA

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	64497	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 ($e^-/\text{\AA}^2$)	56	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	0.151	Depositor
Minimum map value	-0.093	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.026	Depositor
Map size (Å)	261.4, 261.4, 261.4	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3069999, 1.3069999, 1.3069999	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, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.56	1/1706 (0.1%)	0.72	0/2312
1	B	0.51	0/1700	0.71	0/2304
2	C	0.59	0/10736	0.76	3/14487 (0.0%)
3	D	0.57	0/10545	0.80	9/14236 (0.1%)
4	E	0.48	0/629	0.75	0/847
5	F	0.40	0/2547	0.70	0/3421
6	N	0.63	0/1465	0.62	0/2261
7	R	0.58	0/442	0.69	1/689 (0.1%)
8	T	0.66	0/1433	0.64	1/2207 (0.0%)
9	P	0.54	0/1206	0.80	2/1623 (0.1%)
9	Q	0.39	0/1040	0.75	1/1399 (0.1%)
All	All	0.56	1/33449 (0.0%)	0.75	17/45786 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	178	SER	C-N	-5.49	1.27	1.34

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	Q	113	ARG	N-CA-C	-9.15	101.38	111.36
3	D	710	ASP	N-CA-C	-7.79	104.26	113.38
3	D	1210	ILE	N-CA-C	-6.43	106.72	112.12
8	T	48	DT	C2'-C3'-O3'	-6.29	102.06	111.50
3	D	1171	GLY	N-CA-C	-5.97	107.97	115.08

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1686	0	1726	25	0
1	B	1681	0	1714	34	0
2	C	10567	0	10585	244	0
3	D	10388	0	10611	280	0
4	E	627	0	634	16	0
5	F	2513	0	2546	74	0
6	N	1303	0	710	19	0
7	R	394	0	194	7	0
8	T	1281	0	714	23	0
9	P	1179	0	1180	37	0
9	Q	1017	0	1017	37	0
10	D	1	0	0	0	0
11	D	2	0	0	0	0
All	All	32639	0	31631	735	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 12.

The worst 5 of 735 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)
2:C:890:LYS:CD	2:C:914:LYS:HE3	1.58	1.30
2:C:890:LYS:HD2	2:C:914:LYS:CE	1.61	1.28
3:D:1171:GLY:O	3:D:1172:LYS:HD3	1.05	1.20
3:D:146:VAL:HG12	3:D:178:ALA:CB	1.79	1.11
8:T:26:DT:H2''	8:T:27:DA:OP1	1.45	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	
1	A	215/329 (65%)	196 (91%)	19 (9%)	0	100	100
1	B	214/329 (65%)	198 (92%)	16 (8%)	0	100	100
2	C	1338/1342 (100%)	1224 (92%)	111 (8%)	3 (0%)	43	75
3	D	1329/1407 (94%)	1209 (91%)	114 (9%)	6 (0%)	24	61
4	E	77/91 (85%)	72 (94%)	5 (6%)	0	100	100
5	F	301/613 (49%)	293 (97%)	8 (3%)	0	100	100
9	P	145/162 (90%)	133 (92%)	9 (6%)	3 (2%)	5	32
9	Q	122/162 (75%)	117 (96%)	5 (4%)	0	100	100
All	All	3741/4435 (84%)	3442 (92%)	287 (8%)	12 (0%)	37	70

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	910	ALA
3	D	1345	ARG
3	D	1169	THR
9	P	107	PRO
2	C	1081	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	
1	A	186/286 (65%)	184 (99%)	2 (1%)	65	74
1	B	186/286 (65%)	185 (100%)	1 (0%)	81	82
2	C	1155/1157 (100%)	1145 (99%)	10 (1%)	70	77
3	D	1120/1168 (96%)	1109 (99%)	11 (1%)	68	76
4	E	67/75 (89%)	66 (98%)	1 (2%)	57	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	F	271/540 (50%)	270 (100%)	1 (0%)	84	83
9	P	126/140 (90%)	124 (98%)	2 (2%)	55	70
9	Q	108/140 (77%)	107 (99%)	1 (1%)	70	77
All	All	3219/3792 (85%)	3190 (99%)	29 (1%)	68	77

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	47	ARG
9	P	106	ARG
3	D	268	LEU
4	E	63	ILE
3	D	114	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
4	E	62	GLN
9	Q	95	HIS
5	F	271	ASN
5	F	409	ASN
3	D	157	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
7	R	17/18 (94%)	9 (52%)	0

5 of 9 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	R	6	U
7	R	7	A
7	R	8	A
7	R	9	G
7	R	10	G

There are no RNA pucker outliers to report.

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 3 ligands modelled in this entry, 3 are 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.

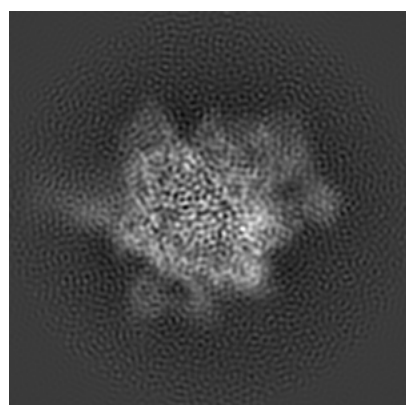
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9852. These allow visual inspection of the internal detail of the map and identification of artifacts.

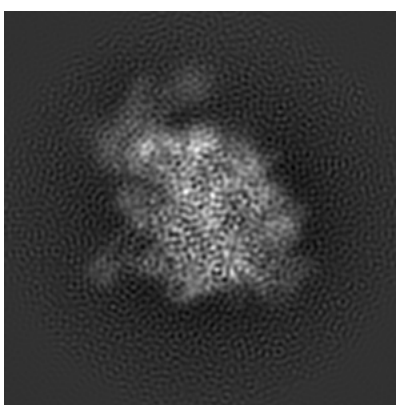
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

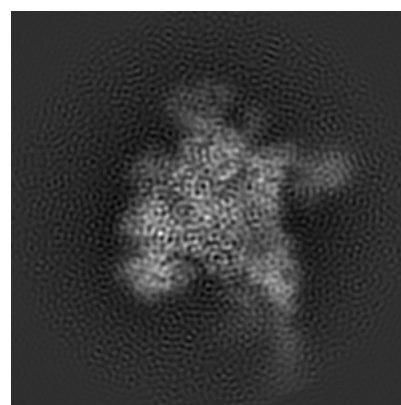
6.1.1 Primary map



X



Y

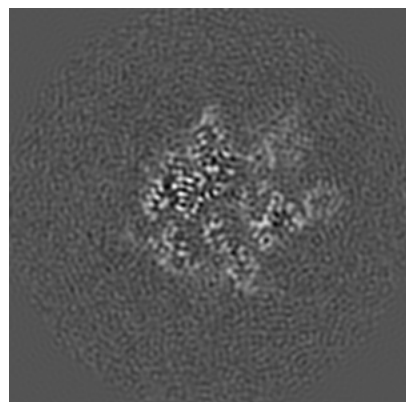


Z

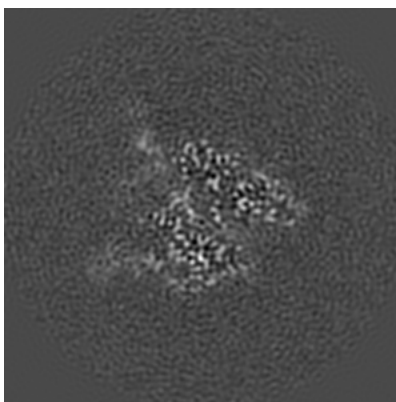
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

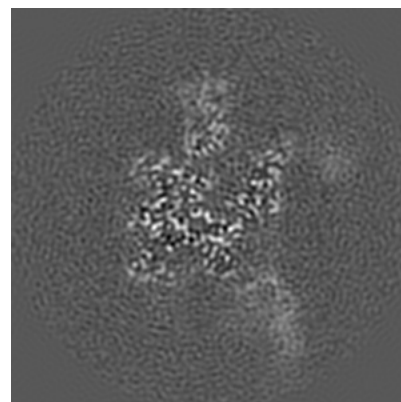
6.2.1 Primary map



X Index: 100



Y Index: 100

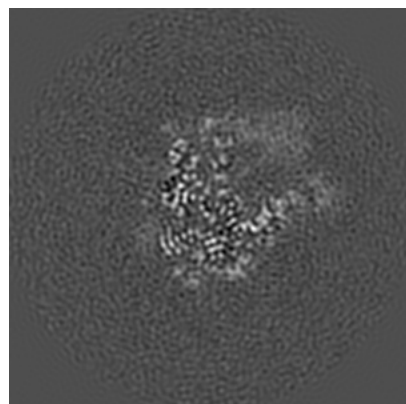


Z Index: 100

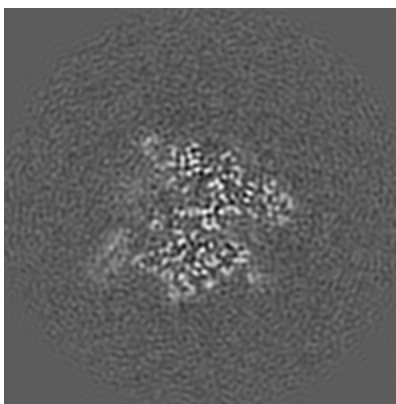
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

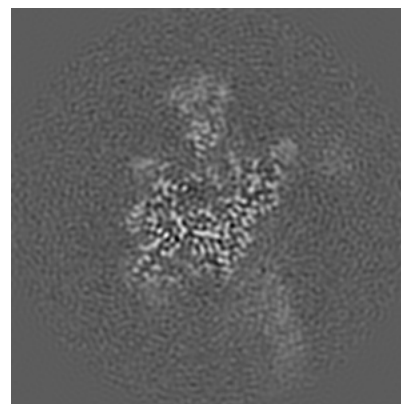
6.3.1 Primary map



X Index: 92



Y Index: 96

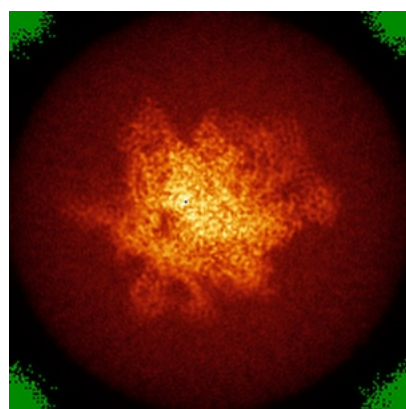


Z Index: 103

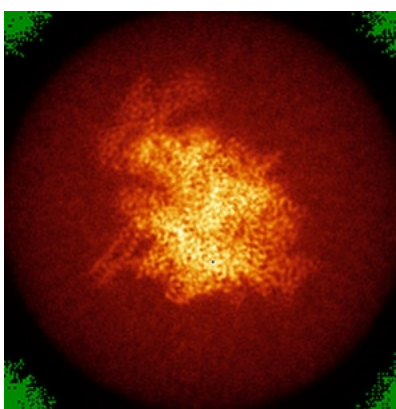
The images above show the largest variance slices of the map in three orthogonal directions.

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

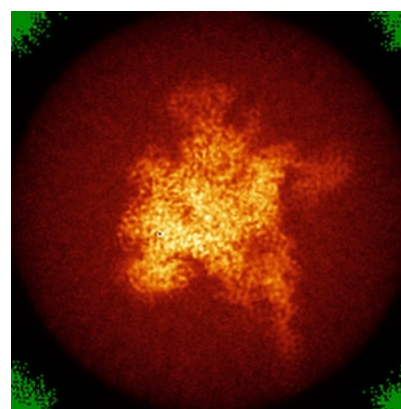
6.4.1 Primary map



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.

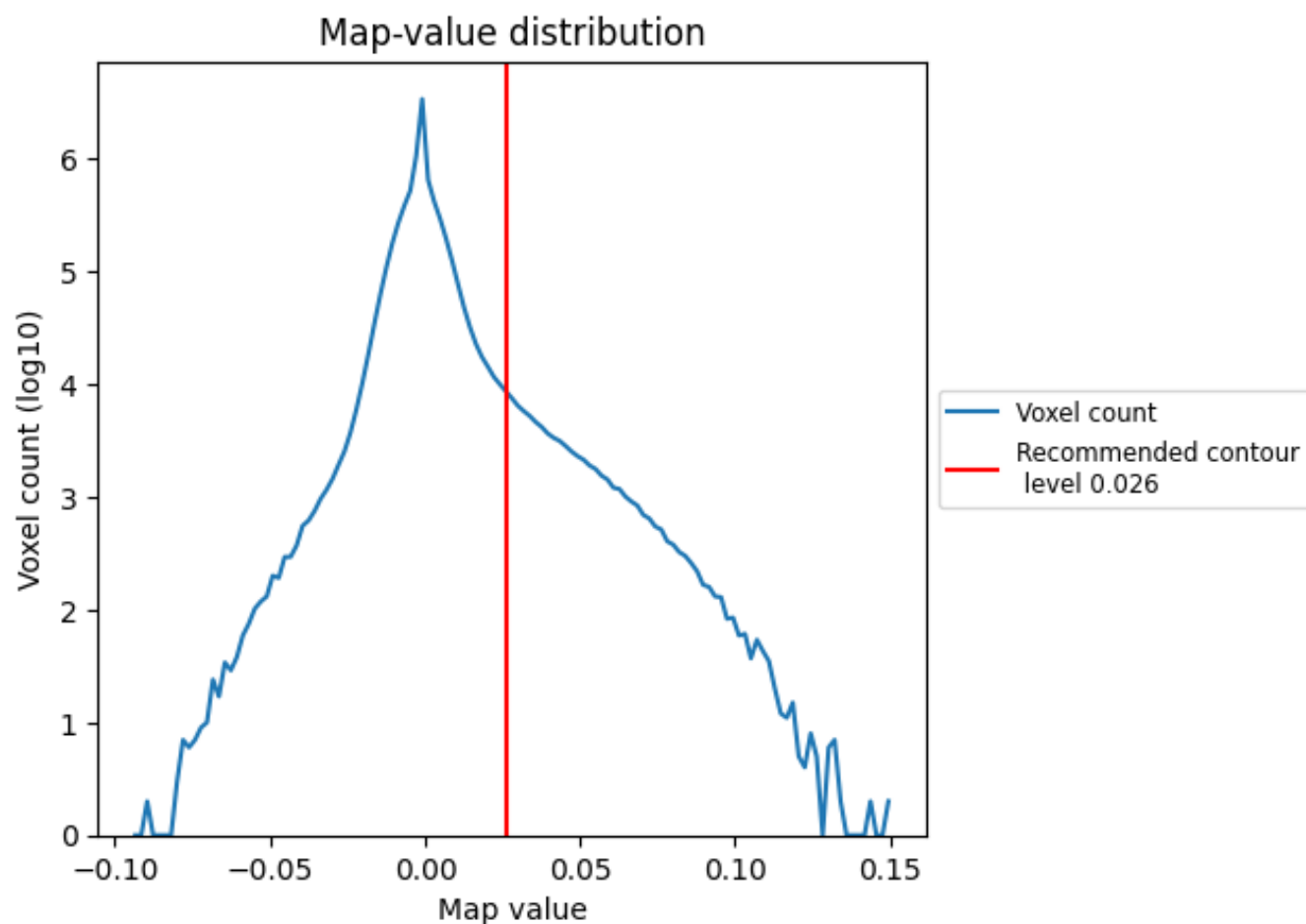
6.6 Mask visualisation

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

7 Map analysis [i](#)

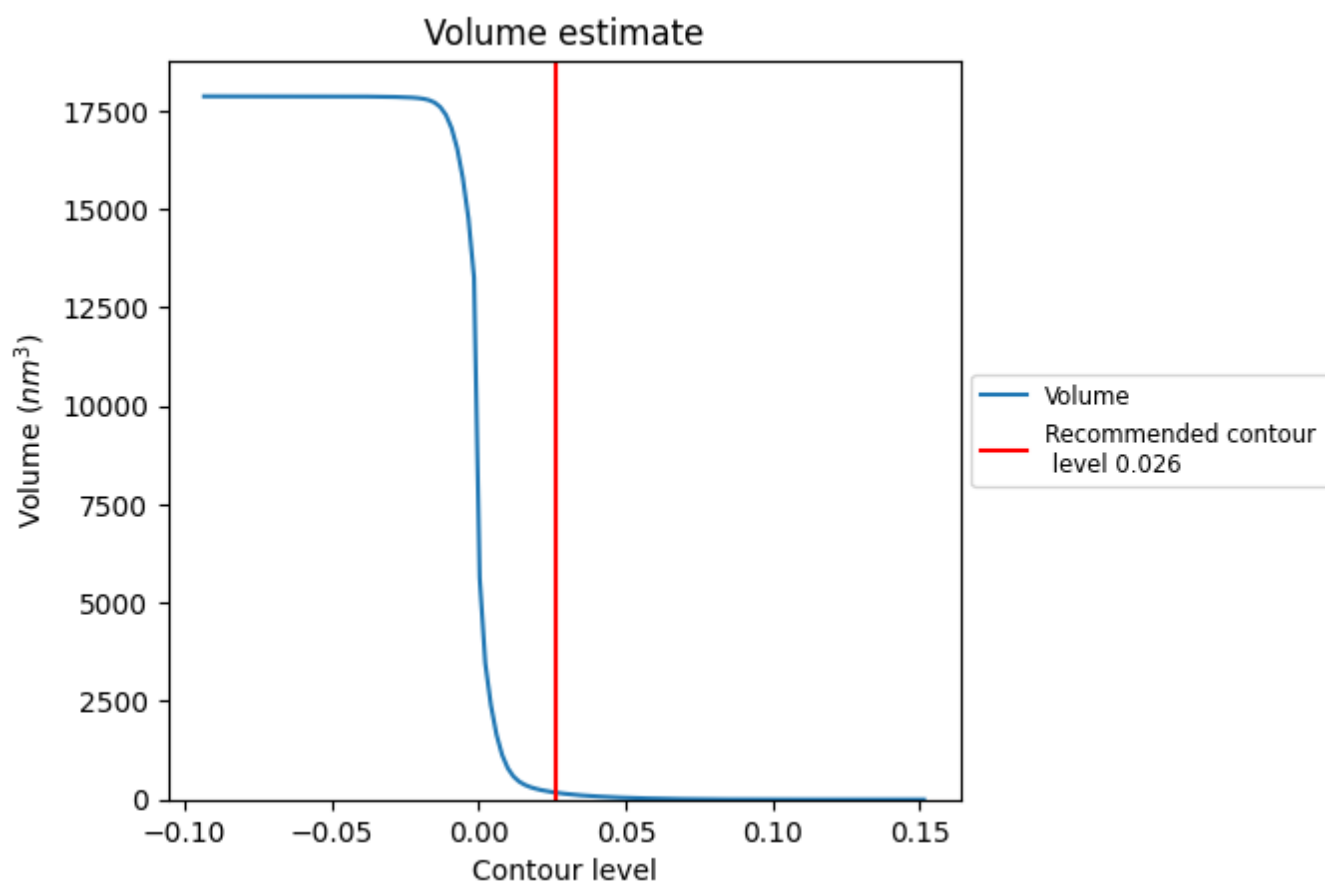
This section contains the results of statistical analysis of the map.

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.

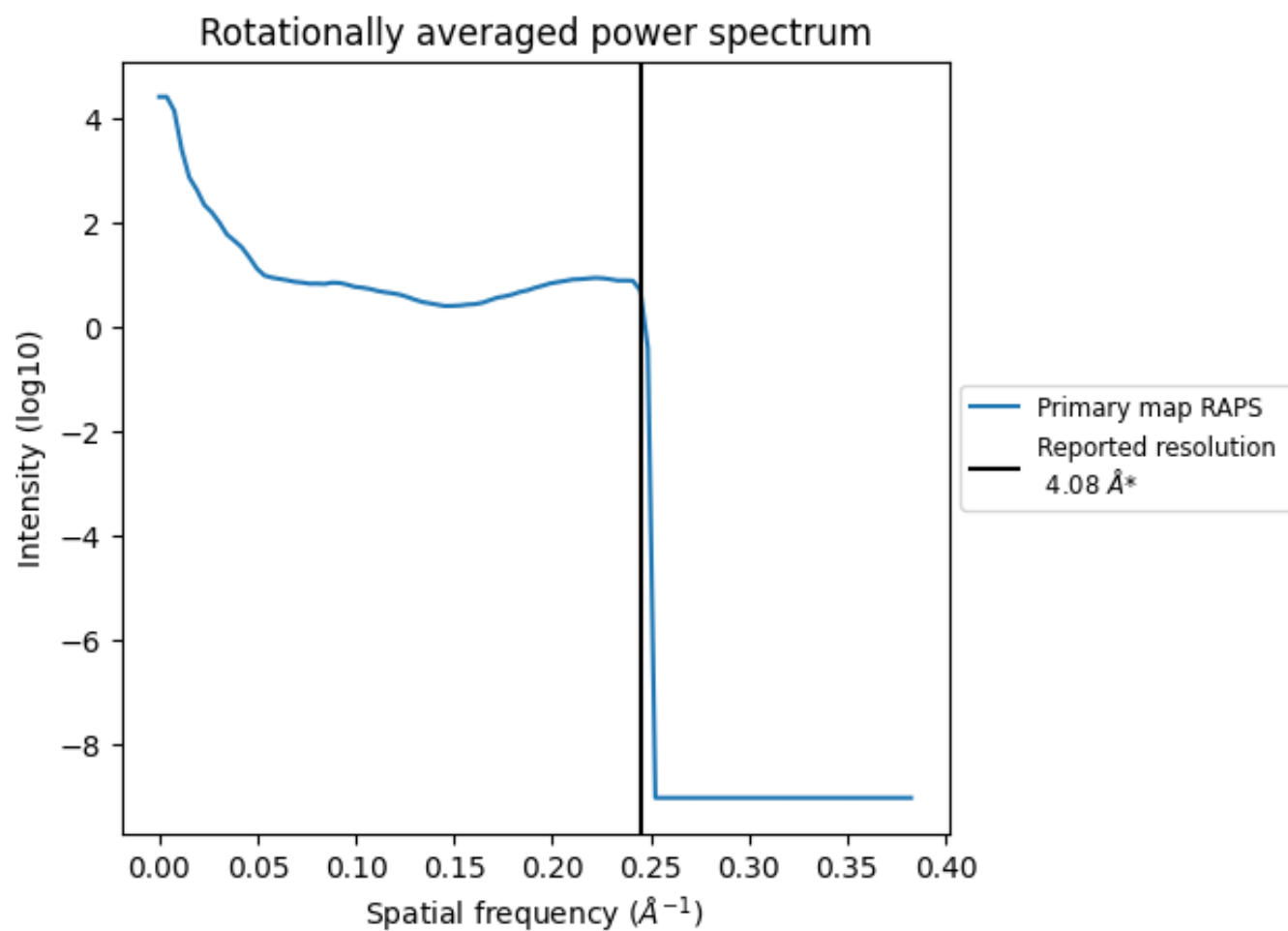
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 179 nm³; this corresponds to an approximate mass of 161 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 0.245 Å⁻¹

8 Fourier-Shell correlation

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

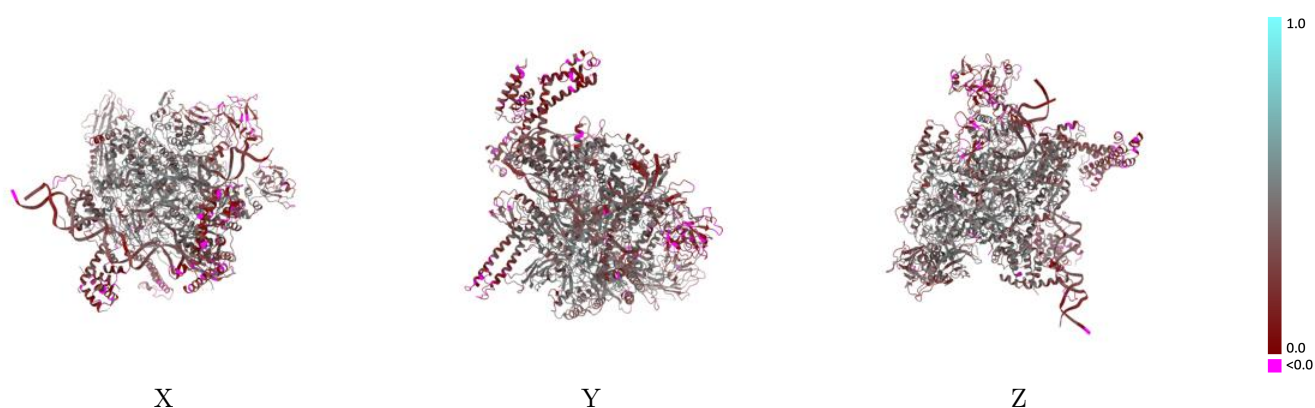
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-9852 and PDB model 6JNX. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)

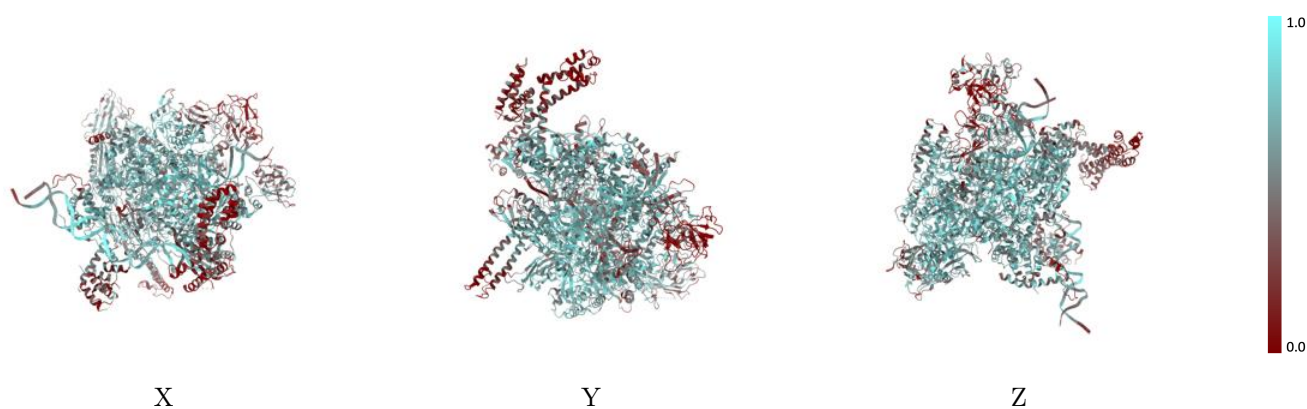
This section was not generated.

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



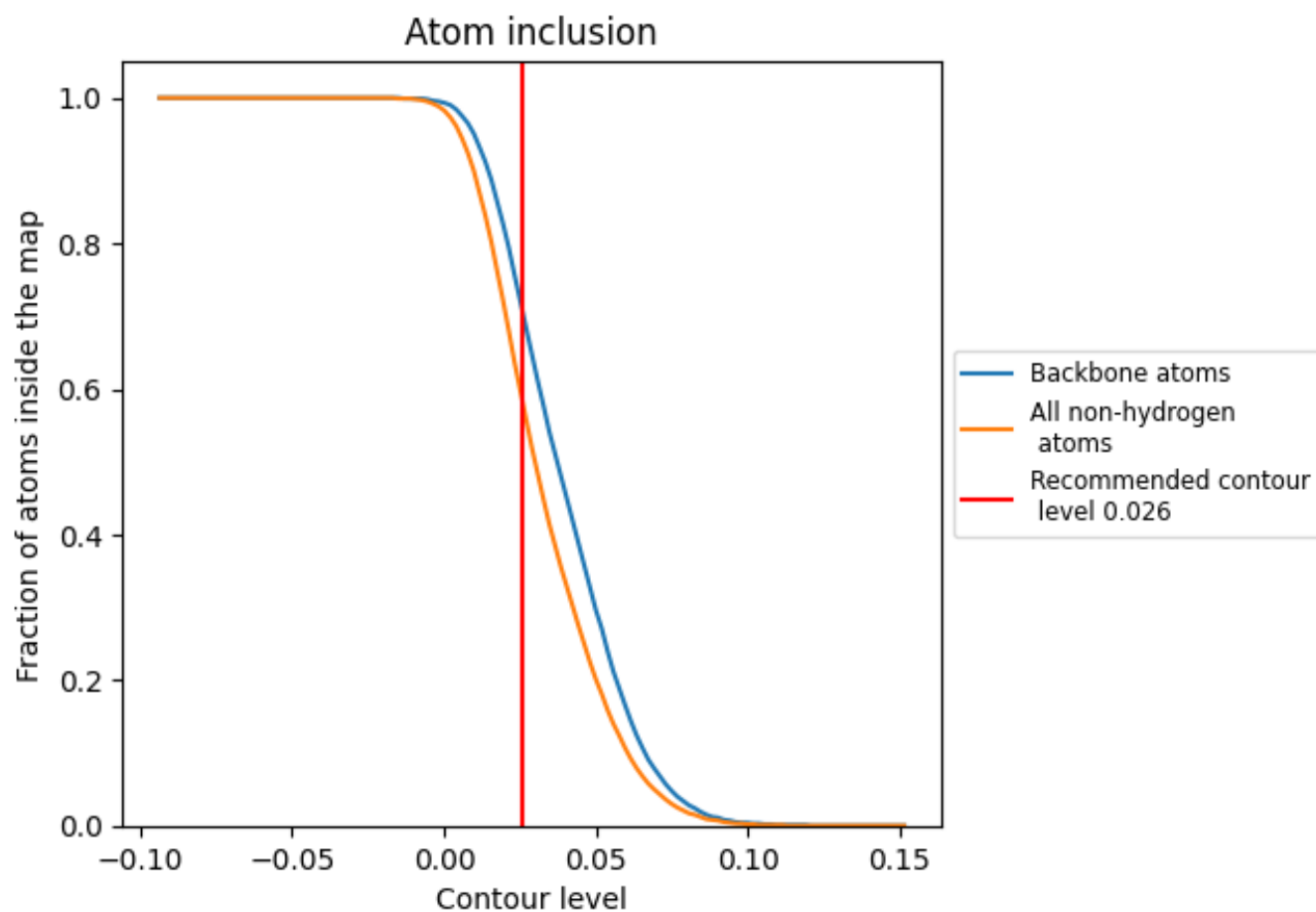
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.026).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 58% 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 (0.026) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5800	 0.3500
A	 0.6600	 0.4130
B	 0.5540	 0.3490
C	 0.6220	 0.3800
D	 0.5860	 0.3650
E	 0.5370	 0.3550
F	 0.3210	 0.2220
N	 0.6950	 0.2920
P	 0.5350	 0.3160
Q	 0.4080	 0.2260
R	 0.6240	 0.3830
T	 0.6710	 0.3130

