



## wwPDB EM Validation Summary Report ⓘ

Nov 8, 2022 – 07:25 AM EST

PDB ID : 6P18  
EMDB ID : EMD-20233  
Title : Q21 transcription antitermination complex: loading complex  
Authors : Yin, Z.; Ebright, R.H.  
Deposited on : 2019-05-19  
Resolution : 3.50 Å(reported)  
Based on initial models : 5IPL, 4YLN, 4MEY

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

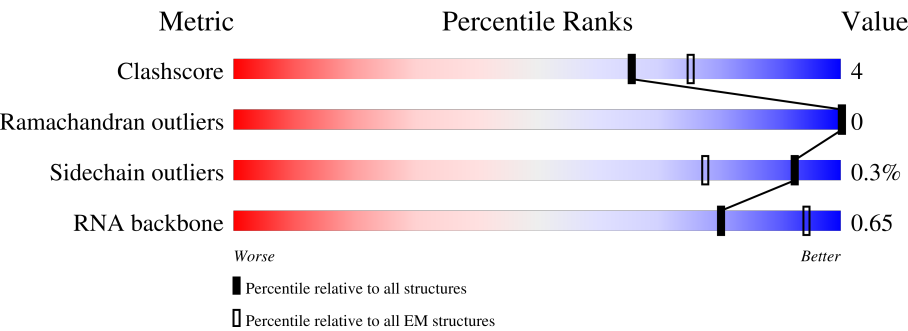
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.50 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
RNA backbone	4643	859

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  $\geq 3$ , 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	1	67	<div><div></div><div>78%6%16%</div></div>
2	2	67	<div><div></div><div>81%16%</div></div>
3	A	329	<div><div></div><div>62%8%30%</div></div>
3	B	329	<div><div>8%</div><div>60%9%31%</div></div>
4	C	1342	<div><div>9%</div><div>87%12%</div></div>
5	D	1430	<div><div>11%</div><div>82%11%7%</div></div>
6	E	91	<div><div>38%</div><div>77%5%18%</div></div>

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Mol	Chain	Length	Quality of chain
7	F	627	<div><div></div><div>24%44%8%48%</div></div>
8	P	162	<div><div></div><div>27%80%9%10%</div></div>
8	Q	162	<div><div></div><div>15%88%8%</div></div>
9	R	11	<div><div></div><div>9%82%9%9%</div></div>

## 2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 32673 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 DNA (67-MER) fragment carrying phage-21 pR' promoter and pause element, nontemplate strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	56	Total	C	N	O	P	0	0
			1153	551	211	335	56		

- Molecule 2 is a DNA chain called DNA (67-MER) fragment carrying phage-21 pR' promoter and pause element, template strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	56	Total	C	N	O	P	0	0
			1142	548	199	339	56		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	230	Total	C	N	O	S	0	0
			1786	1112	317	351	6		
3	B	228	Total	C	N	O	S	0	0
			1767	1100	312	349	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	1340	Total	C	N	O	S	0	0
			10568	6629	1841	2055	43		

- Molecule 5 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	1327	Total	C	N	O	S	0	0
			10319	6484	1839	1947	49		

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1408	LEU	-	expression tag	UNP P0A8T7
D	1409	GLU	-	expression tag	UNP P0A8T7
D	1410	ARG	-	expression tag	UNP P0A8T7
D	1411	ARG	-	expression tag	UNP P0A8T7
D	1412	ALA	-	expression tag	UNP P0A8T7
D	1413	SER	-	expression tag	UNP P0A8T7
D	1414	GLU	-	expression tag	UNP P0A8T7
D	1415	ASN	-	expression tag	UNP P0A8T7
D	1416	LEU	-	expression tag	UNP P0A8T7
D	1417	TYR	-	expression tag	UNP P0A8T7
D	1418	PHE	-	expression tag	UNP P0A8T7
D	1419	GLN	-	expression tag	UNP P0A8T7
D	1420	GLY	-	expression tag	UNP P0A8T7
D	1421	HIS	-	expression tag	UNP P0A8T7
D	1422	HIS	-	expression tag	UNP P0A8T7
D	1423	HIS	-	expression tag	UNP P0A8T7
D	1424	HIS	-	expression tag	UNP P0A8T7
D	1425	HIS	-	expression tag	UNP P0A8T7
D	1426	HIS	-	expression tag	UNP P0A8T7
D	1427	HIS	-	expression tag	UNP P0A8T7
D	1428	HIS	-	expression tag	UNP P0A8T7
D	1429	HIS	-	expression tag	UNP P0A8T7
D	1430	HIS	-	expression tag	UNP P0A8T7

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	75	Total	C	N	O	S	0	0
			600	365	114	120	1		

- Molecule 7 is a protein called RNA polymerase sigma factor RpoD.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	325	Total	C	N	O	S	0	0
			2665	1679	476	494	16		

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-13	MET	-	initiating methionine	UNP P00579
F	-12	GLY	-	expression tag	UNP P00579
F	-11	SER	-	expression tag	UNP P00579
F	-10	SER	-	expression tag	UNP P00579

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-9	HIS	-	expression tag	UNP P00579
F	-8	HIS	-	expression tag	UNP P00579
F	-7	HIS	-	expression tag	UNP P00579
F	-6	HIS	-	expression tag	UNP P00579
F	-5	HIS	-	expression tag	UNP P00579
F	-4	HIS	-	expression tag	UNP P00579
F	-3	SER	-	expression tag	UNP P00579
F	-2	SER	-	expression tag	UNP P00579
F	-1	GLY	-	expression tag	UNP P00579
F	0	HIS	-	expression tag	UNP P00579
F	541	CYS	ARG	engineered mutation	UNP P00579
F	607	PRO	LEU	engineered mutation	UNP P00579

- Molecule 8 is a protein called Q protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	P	145	Total	C	N	O	S	0	0
			1165	743	206	205	11		
8	Q	156	Total	C	N	O	S	0	0
			1261	801	229	220	11		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	1	SER	-	expression tag	UNP Q9XJQ6
P	24	GLY	-	insertion	UNP Q9XJQ6
P	26	TRP	HIS	conflict	UNP Q9XJQ6
P	27	VAL	GLY	conflict	UNP Q9XJQ6
P	28	TYR	LEU	conflict	UNP Q9XJQ6
P	47	VAL	ILE	conflict	UNP Q9XJQ6
Q	1	SER	-	expression tag	UNP Q9XJQ6
Q	24	GLY	-	insertion	UNP Q9XJQ6
Q	26	TRP	HIS	conflict	UNP Q9XJQ6
Q	27	VAL	GLY	conflict	UNP Q9XJQ6
Q	28	TYR	LEU	conflict	UNP Q9XJQ6
Q	47	VAL	ILE	conflict	UNP Q9XJQ6

- Molecule 9 is a RNA chain called RNA (5'-R(P\*UP\*GP\*GP\*GP\*AP\*GP\*AP\*GP\*GP\*UP\*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
9	R	11	Total	C	N	O	P	0	0
			244	108	49	76	11		

- Molecule 10 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

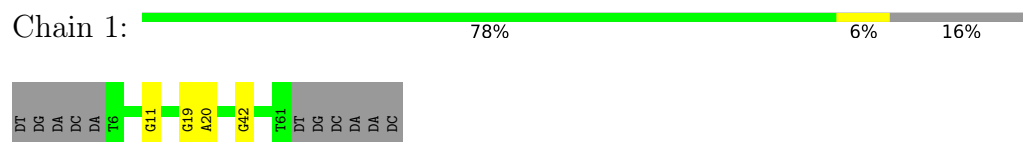
- Molecule 11 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

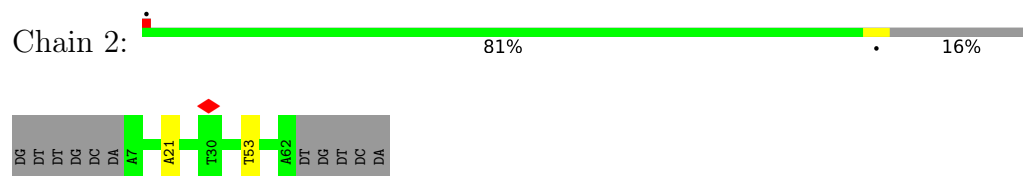
### 3 Residue-property plots

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.

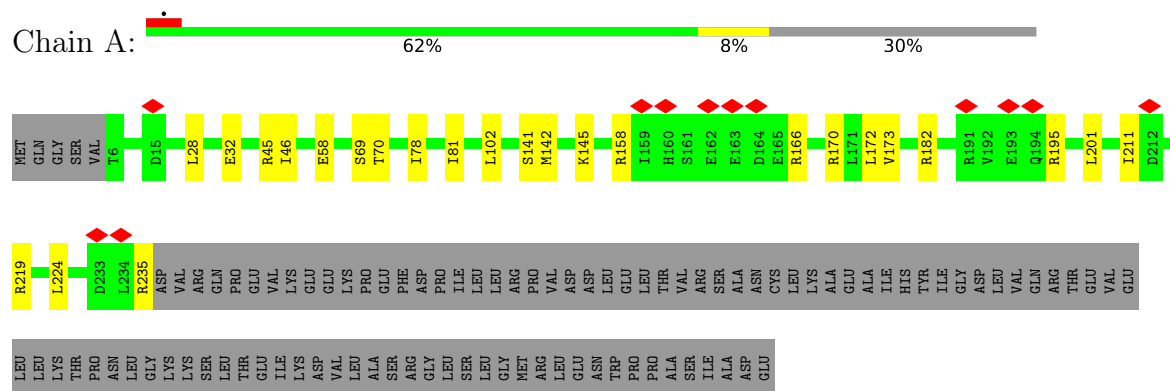
- Molecule 1: DNA (67-MER) fragment carrying phage-21 pR' promoter and pause element, nontemplate strand



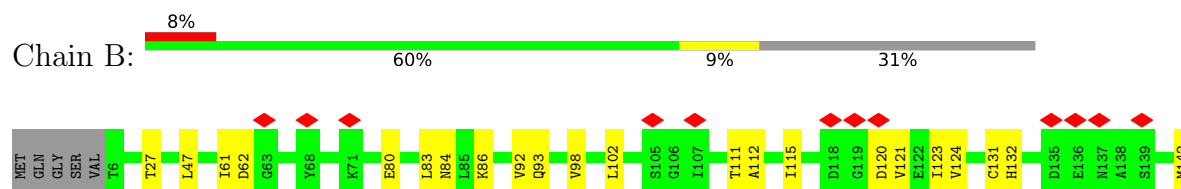
- Molecule 2: DNA (67-MER) fragment carrying phage-21 pR' promoter and pause element, template strand



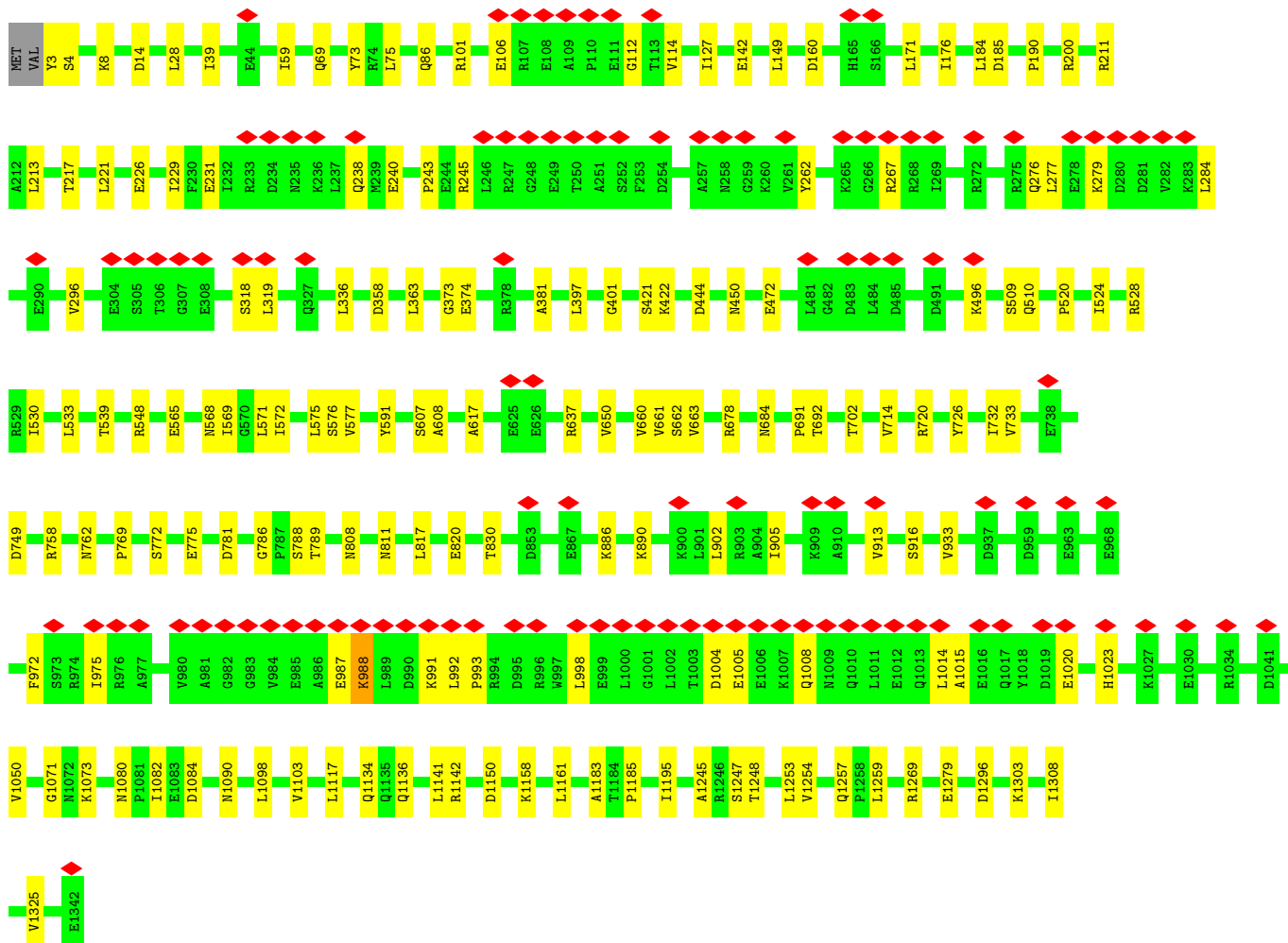
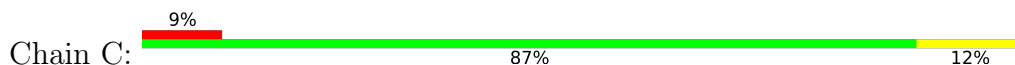
- Molecule 3: DNA-directed RNA polymerase subunit alpha



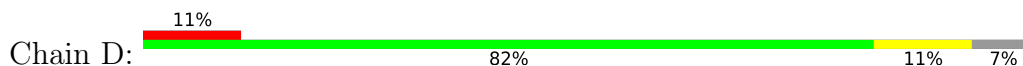
- Molecule 3: DNA-directed RNA polymerase subunit alpha

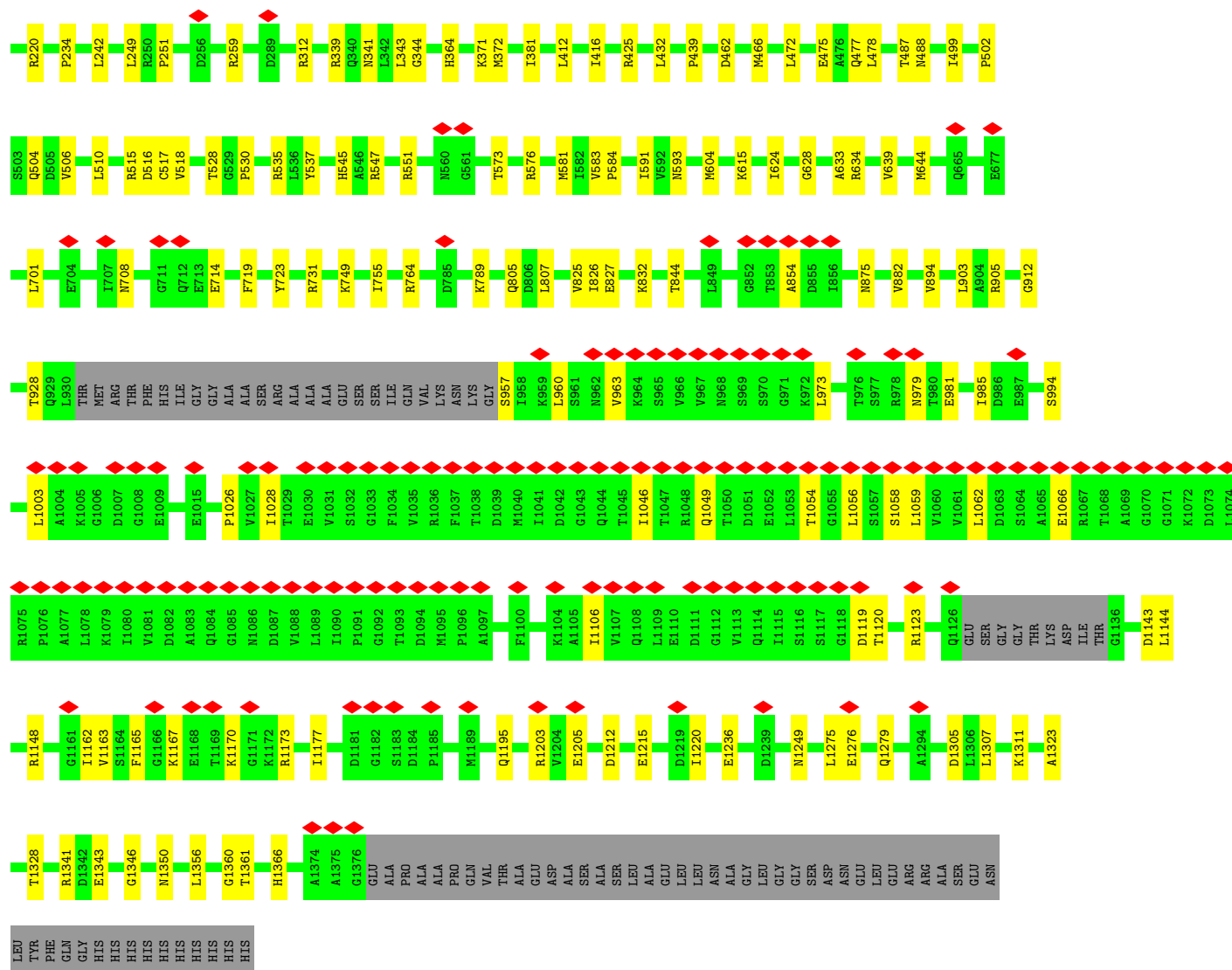


- Molecule 4: DNA-directed RNA polymerase subunit beta

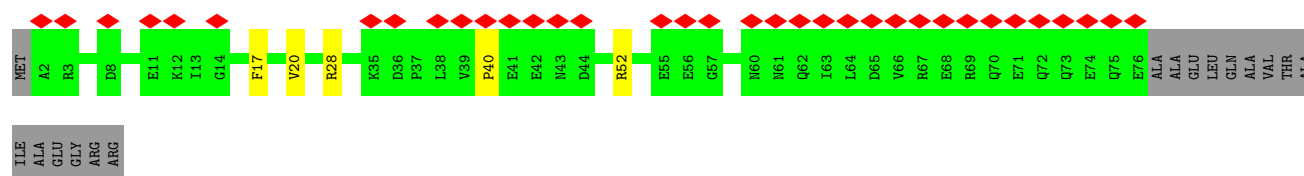
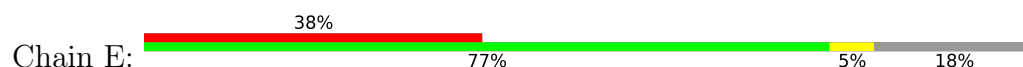


- Molecule 5: DNA-directed RNA polymerase subunit beta'

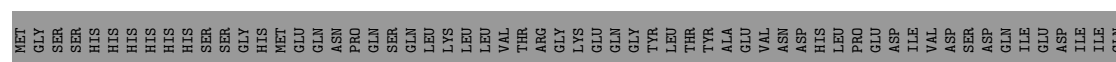
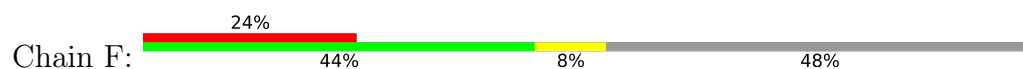


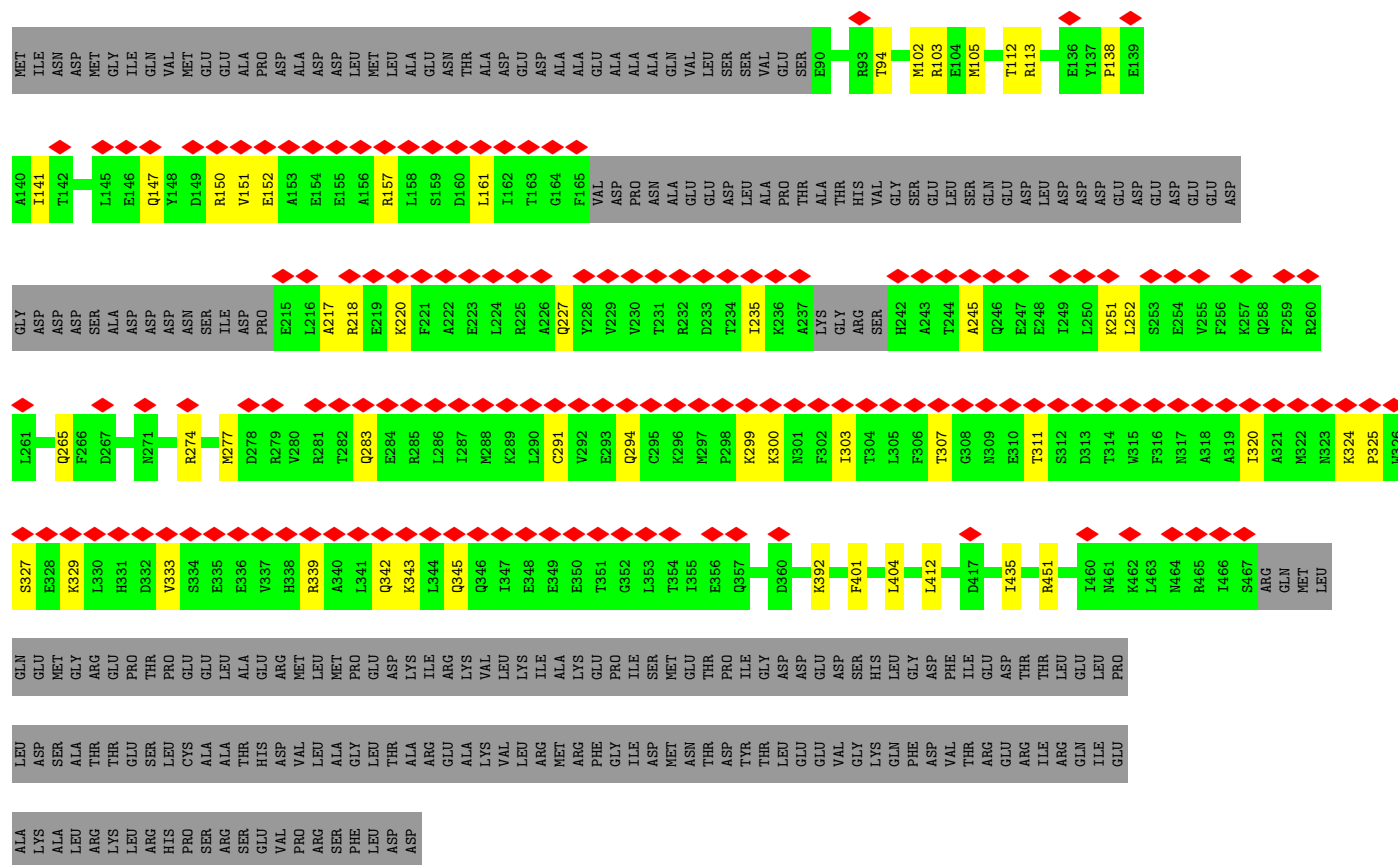


• Molecule 6: DNA-directed RNA polymerase subunit omega

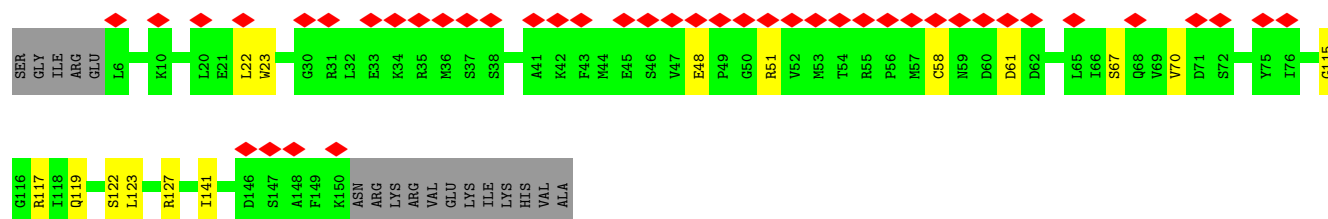
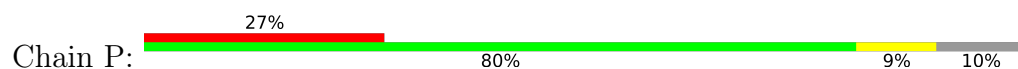


• Molecule 7: RNA polymerase sigma factor RpoD

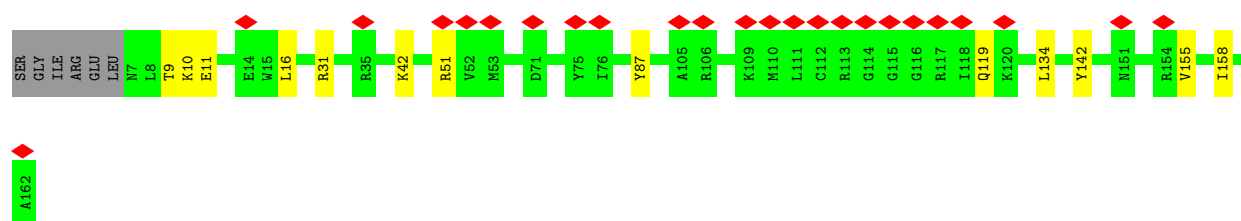
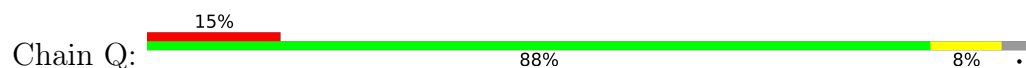




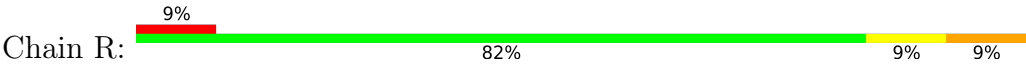
### • Molecule 8: Q protein



### • Molecule 8: Q protein



### • Molecule 9: RNA (5'-R(P\*UP\*GP\*GP\*GP\*AP\*GP\*AP\*GP\*GP\*UP\*A)-3')



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	150310	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 ( $e^-/\text{\AA}^2$ )	1.4	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	47608	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.324	Depositor
Minimum map value	-0.205	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.0286	Depositor
Map size (Å)	272.896, 272.896, 272.896	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.066, 1.066, 1.066	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	1	0.49	0/1294	0.97	0/1996
2	2	0.50	0/1278	0.98	0/1969
3	A	0.24	0/1808	0.45	0/2450
3	B	0.26	0/1789	0.51	0/2425
4	C	0.26	0/10737	0.50	0/14486
5	D	0.26	0/10476	0.50	0/14146
6	E	0.27	0/602	0.49	0/810
7	F	0.27	0/2701	0.57	0/3627
8	P	0.25	0/1192	0.53	0/1605
8	Q	0.27	0/1289	0.47	0/1731
9	R	0.21	0/274	0.73	0/427
All	All	0.29	0/33440	0.56	0/45672

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	1153	0	634	4	0
2	2	1142	0	636	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	1786	0	1813	16	0
3	B	1767	0	1789	21	0
4	C	10568	0	10575	103	0
5	D	10319	0	10527	98	0
6	E	600	0	607	4	0
7	F	2665	0	2721	27	0
8	P	1165	0	1170	10	0
8	Q	1261	0	1277	8	0
9	R	244	0	119	2	0
10	D	2	0	0	0	0
11	D	1	0	0	0	0
All	All	32673	0	31868	265	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 4.

The worst 5 of 265 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)
4:C:992:LEU:HD12	4:C:993:PRO:HD2	1.33	1.06
4:C:992:LEU:HD12	4:C:993:PRO:CD	2.01	0.91
4:C:992:LEU:CD1	4:C:993:PRO:HD2	2.12	0.78
4:C:238:GLN:HB3	4:C:284:LEU:HD11	1.76	0.67
4:C:975:ILE:HG22	4:C:1014:LEU:HD13	1.79	0.64

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	A	228/329 (69%)	225 (99%)	3 (1%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	B	226/329 (69%)	217 (96%)	9 (4%)	0	100	100
4	C	1338/1342 (100%)	1278 (96%)	60 (4%)	0	100	100
5	D	1321/1430 (92%)	1251 (95%)	70 (5%)	0	100	100
6	E	73/91 (80%)	71 (97%)	2 (3%)	0	100	100
7	F	319/627 (51%)	302 (95%)	17 (5%)	0	100	100
8	P	143/162 (88%)	137 (96%)	6 (4%)	0	100	100
8	Q	154/162 (95%)	152 (99%)	2 (1%)	0	100	100
All	All	3802/4472 (85%)	3633 (96%)	169 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	A	198/286 (69%)	198 (100%)	0	100	100
3	B	196/286 (68%)	196 (100%)	0	100	100
4	C	1154/1157 (100%)	1151 (100%)	3 (0%)	92	97
5	D	1110/1189 (93%)	1110 (100%)	0	100	100
6	E	65/75 (87%)	65 (100%)	0	100	100
7	F	288/552 (52%)	284 (99%)	4 (1%)	67	85
8	P	125/140 (89%)	125 (100%)	0	100	100
8	Q	135/140 (96%)	132 (98%)	3 (2%)	52	78
All	All	3271/3825 (86%)	3261 (100%)	10 (0%)	92	97

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	Q	11	GLU
8	Q	31	ARG

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Mol	Chain	Res	Type
8	Q	155	VAL
7	F	150	ARG
7	F	277	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
5	D	1238	GLN
7	F	258	GLN
7	F	128	ASN
7	F	283	GLN
4	C	1237	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
9	R	10/11 (90%)	1 (10%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	R	2	G

There are no RNA pucker outliers to report.

## 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 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.

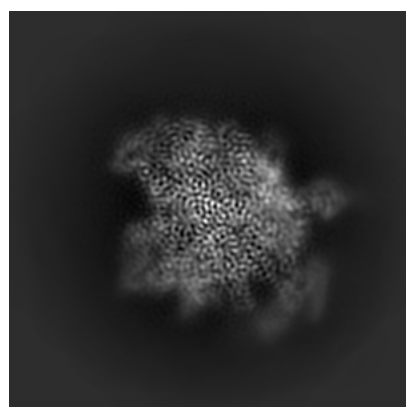
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20233. These allow visual inspection of the internal detail of the map and identification of artifacts.

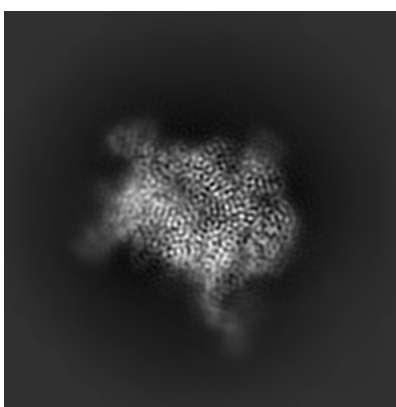
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

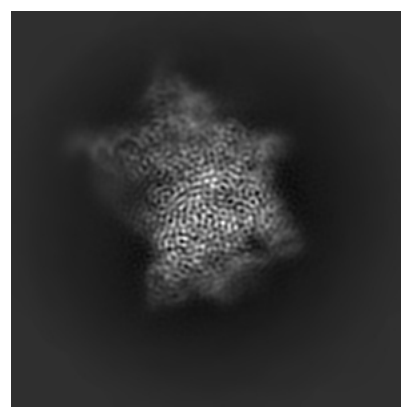
#### 6.1.1 Primary map



X



Y

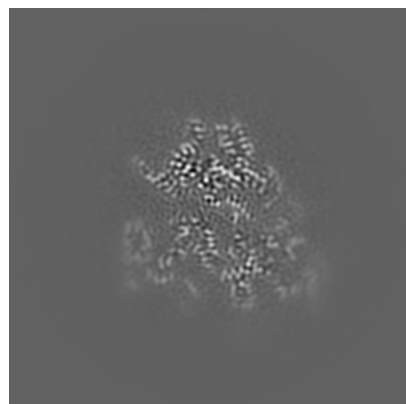


Z

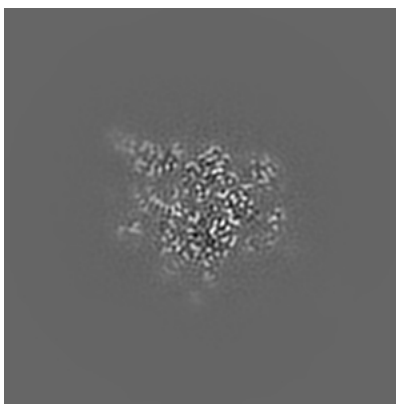
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

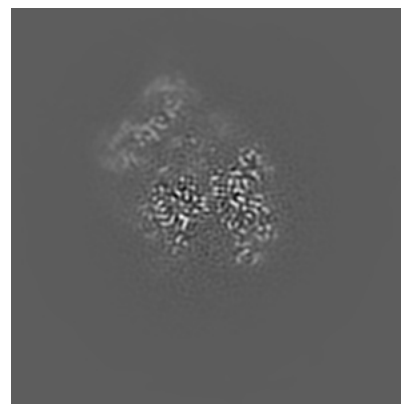
#### 6.2.1 Primary map



X Index: 128



Y Index: 128

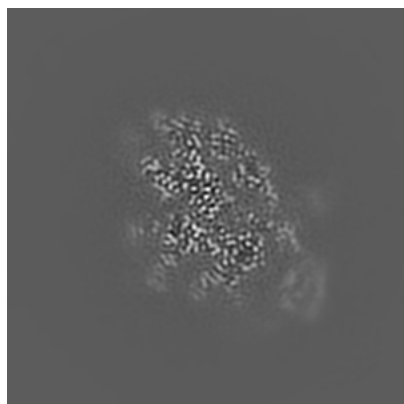


Z Index: 128

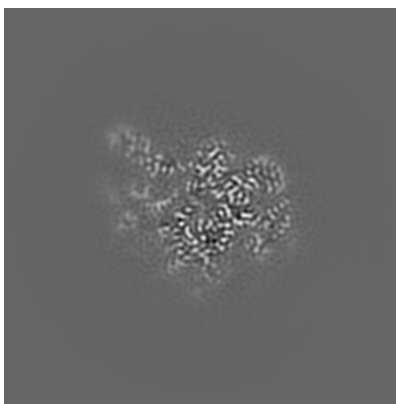
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

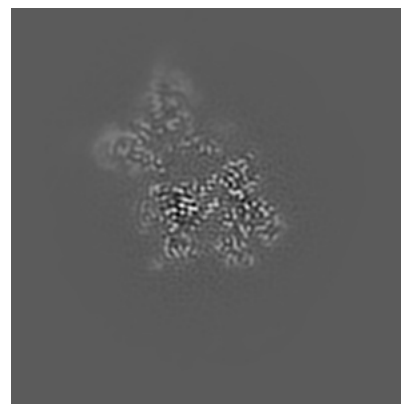
### 6.3.1 Primary map



X Index: 118



Y Index: 123

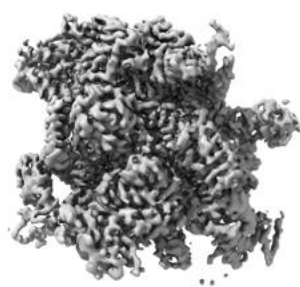


Z Index: 134

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

## 6.4 Orthogonal surface views [i](#)

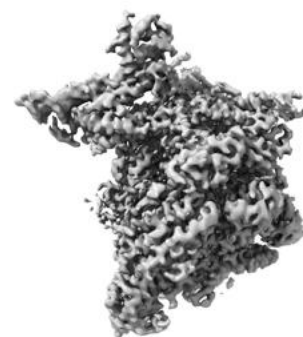
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0286. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

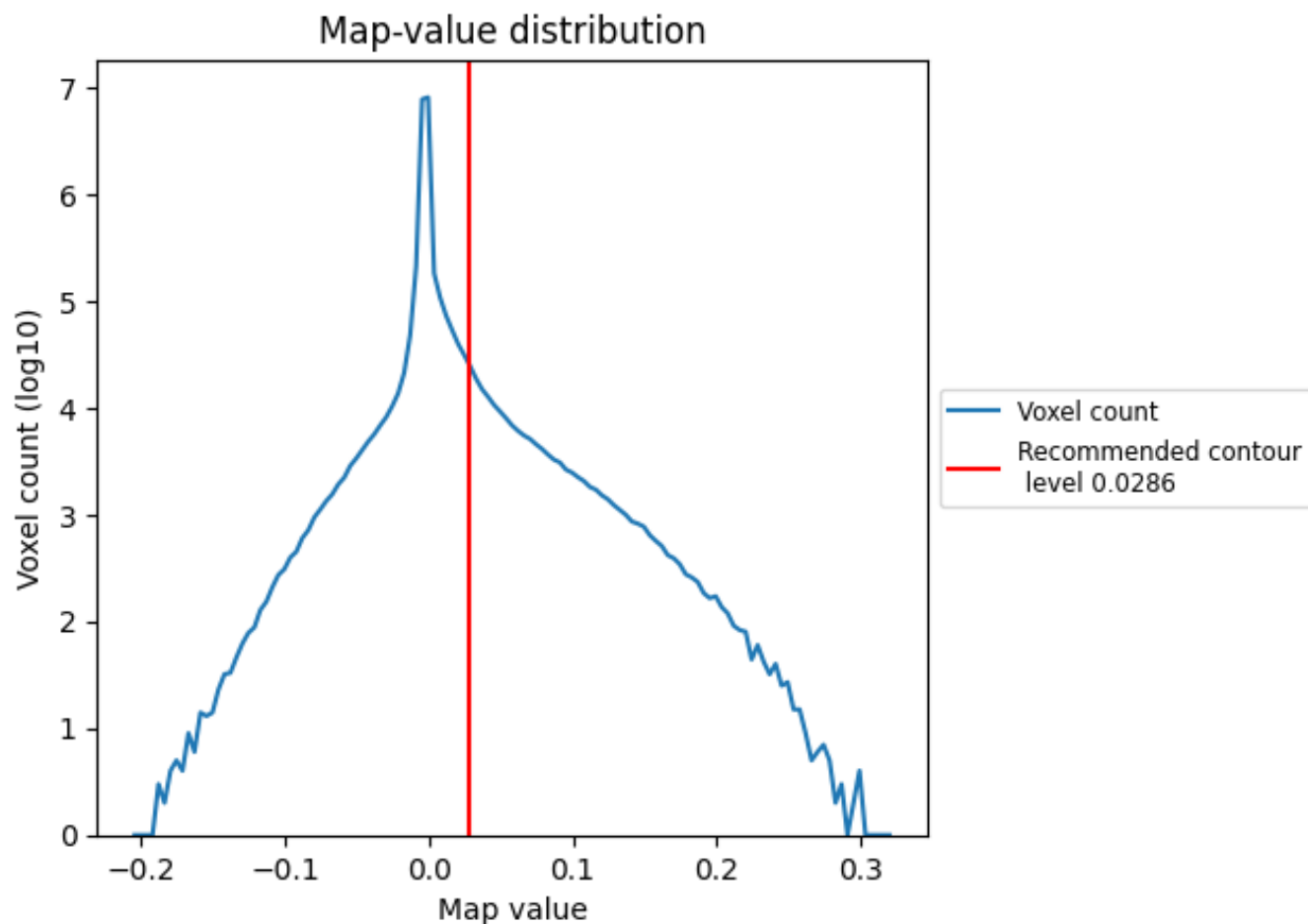
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

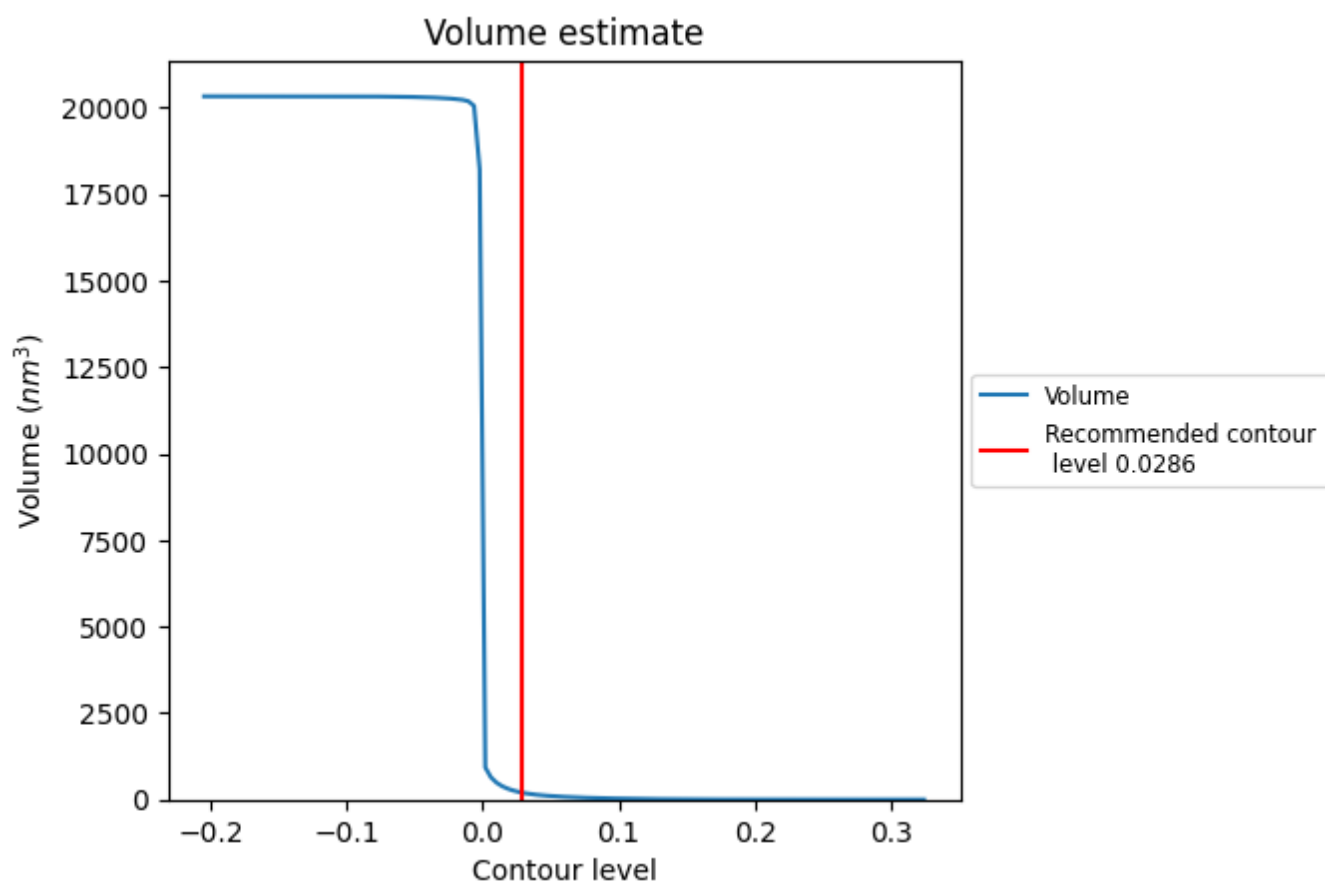
This section contains the results of statistical analysis of the map.

### 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.

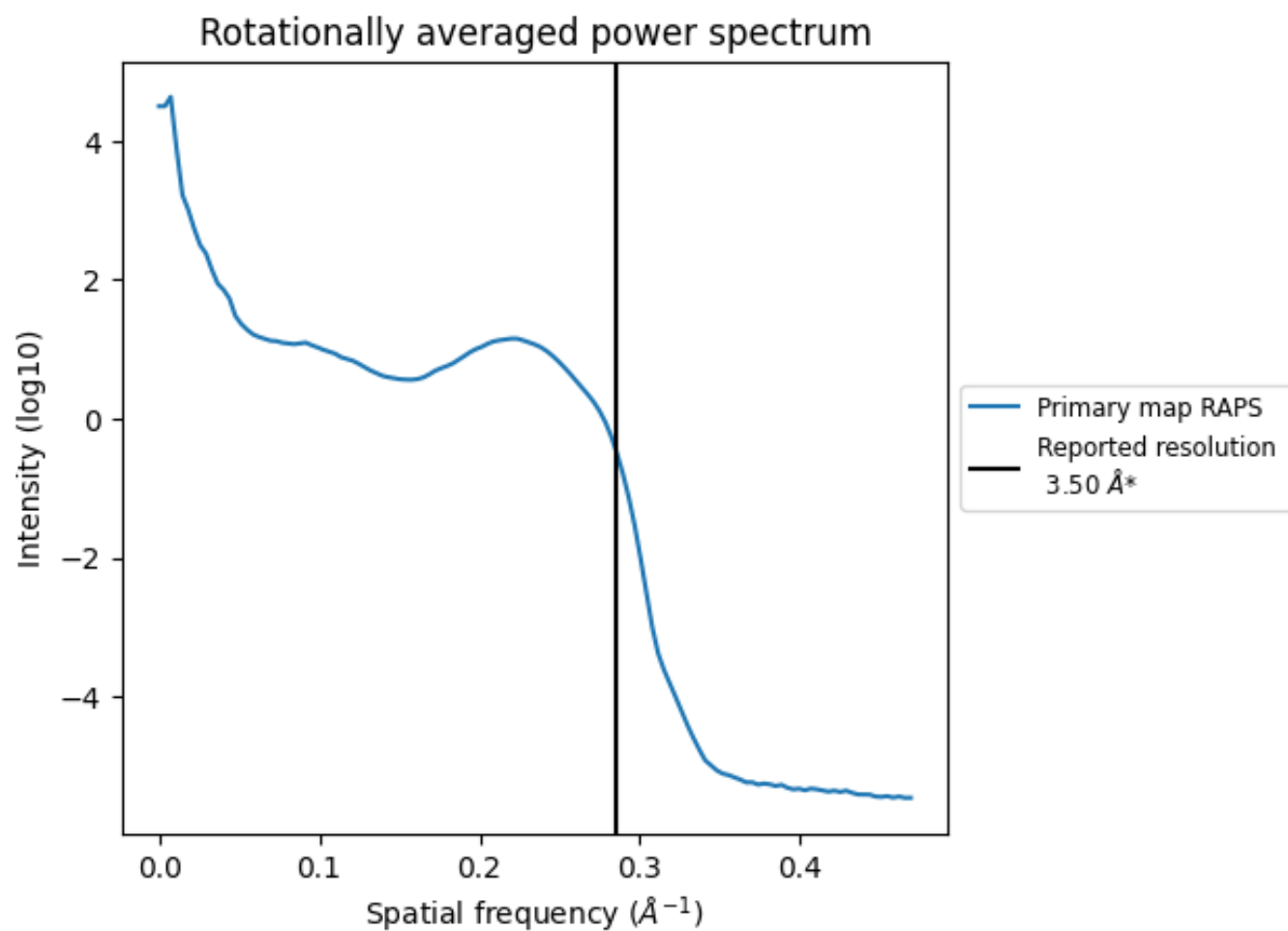
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 204 nm<sup>3</sup>; this corresponds to an approximate mass of 185 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 ⓘ

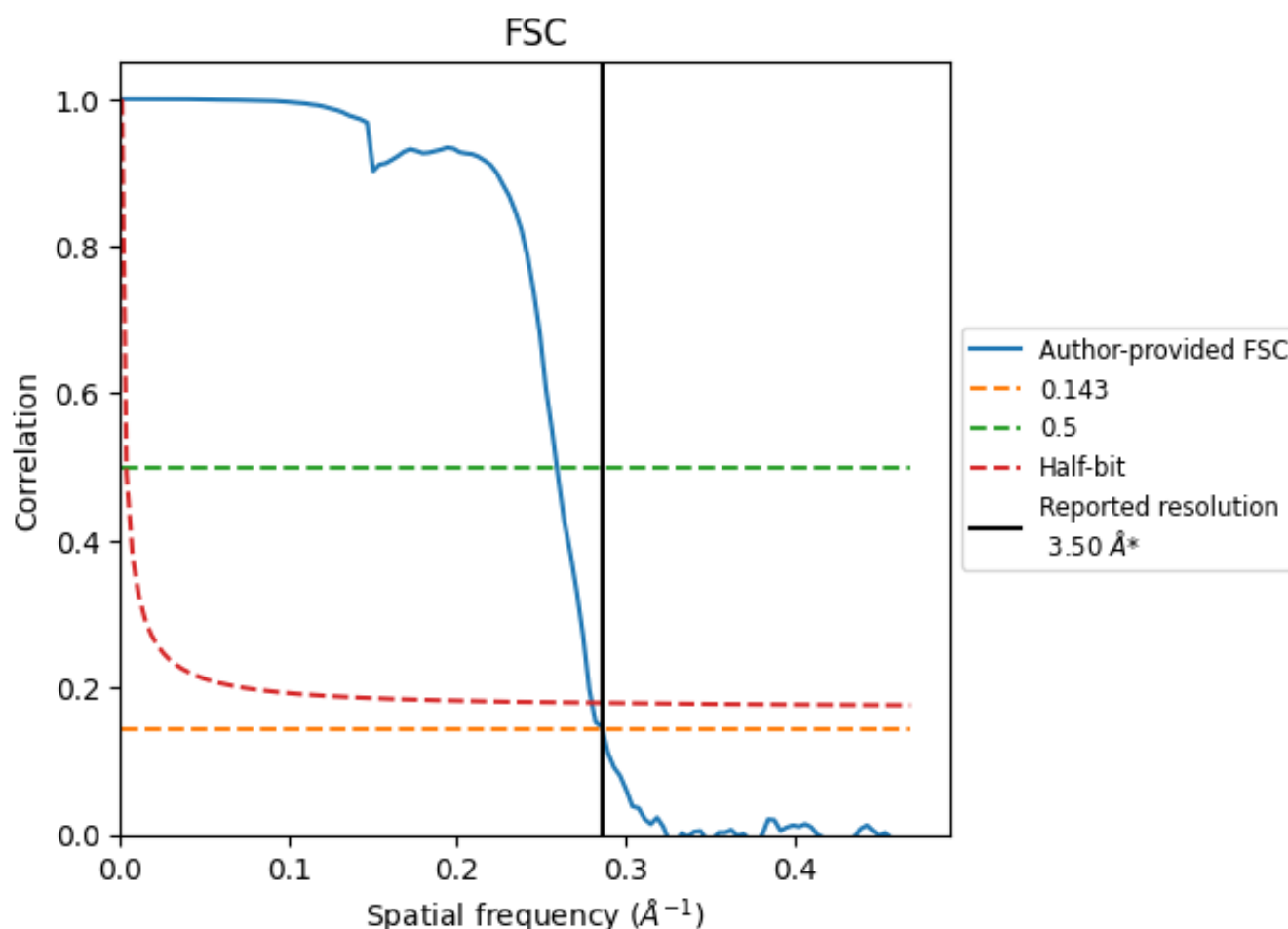


\*Reported resolution corresponds to spatial frequency of 0.286 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.286 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

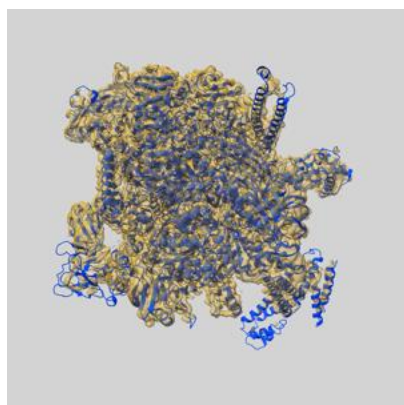
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.49	3.86	3.57
Unmasked-calculated*	-	-	-

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

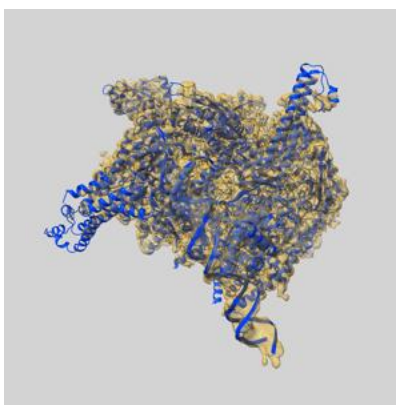
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20233 and PDB model 6P18. Per-residue inclusion information can be found in section [3](#) on page [8](#).

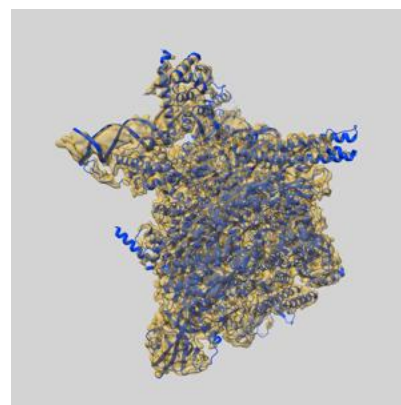
### 9.1 Map-model overlay [i](#)



X



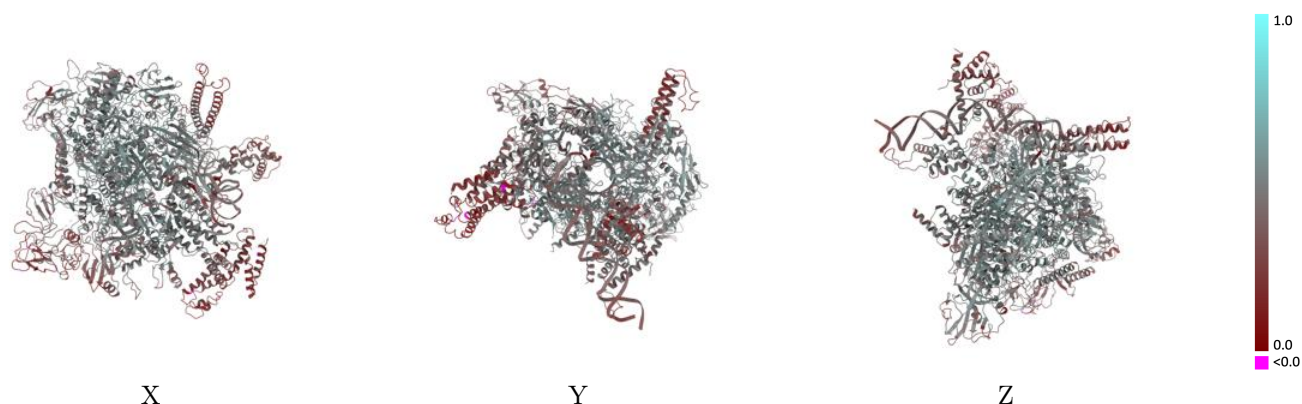
Y



Z

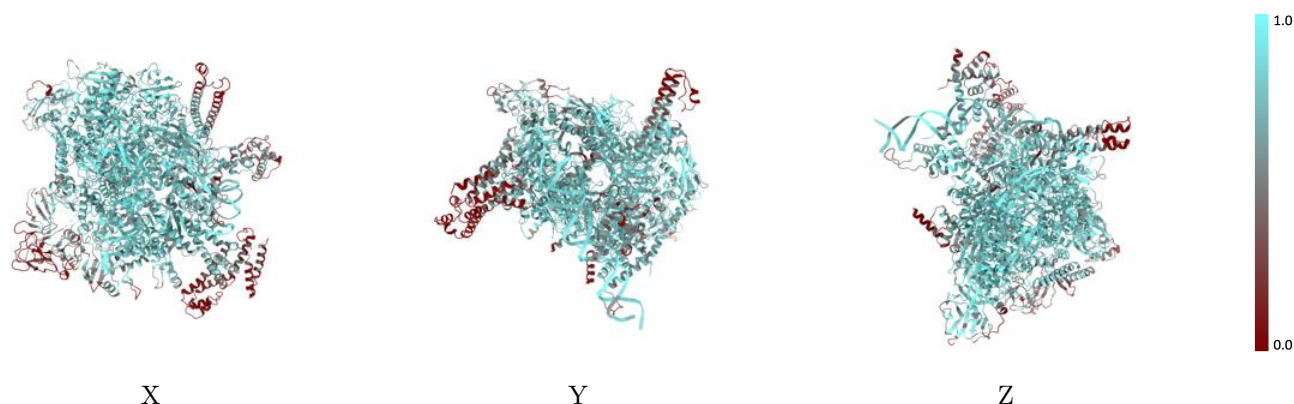
The images above show the 3D surface view of the map at the recommended contour level 0.0286 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



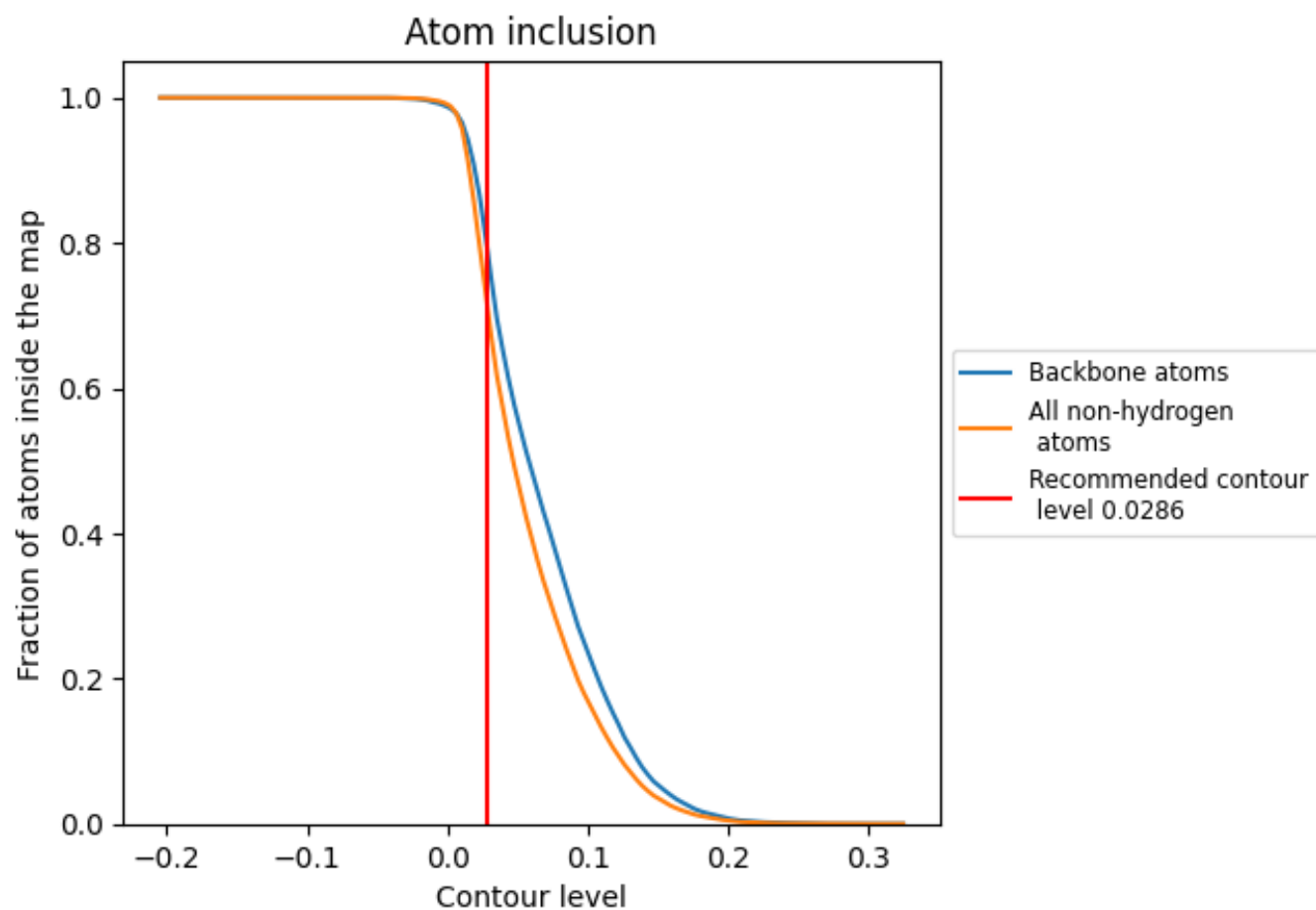
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0286).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 71% 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 (0.0286) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7069	<div></div> 0.4470
1	<div></div> 0.8448	<div></div> 0.4070
2	<div></div> 0.8301	<div></div> 0.4010
A	<div></div> 0.7740	<div></div> 0.4940
B	<div></div> 0.7071	<div></div> 0.4510
C	<div></div> 0.7502	<div></div> 0.4730
D	<div></div> 0.7315	<div></div> 0.4650
E	<div></div> 0.3870	<div></div> 0.4280
F	<div></div> 0.4188	<div></div> 0.3220
P	<div></div> 0.5389	<div></div> 0.3520
Q	<div></div> 0.6855	<div></div> 0.4390
R	<div></div> 0.8648	<div></div> 0.5020

1.0  
0.0  
<0.0