



## wwPDB EM Validation Summary Report ⓘ

Nov 14, 2022 – 06:03 AM EST

PDB ID : 6WMU  
EMDB ID : EMD-21853  
Title : E. coli RNAPs70-SspA-gadA DNA complex  
Authors : Travis, B.A.; Brennan, R.G.; Schumacher, M.A.  
Deposited on : 2020-04-21  
Resolution : 3.18 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](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

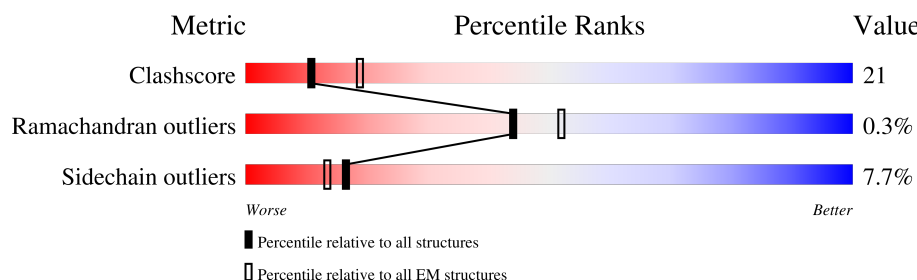
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.18 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  $\geq 3$ , 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	A	329	
1	B	329	
2	C	1342	
3	D	1430	
4	E	91	
5	F	613	
6	G	37	
7	H	27	

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Mol	Chain	Length	Quality of chain
8	I	11	<div><div></div><div>36%64%</div></div>
9	J	11	<div><div></div><div>27%73%</div></div>
10	K	232	<div><div></div><div>50%34%14%</div></div>
10	L	232	<div><div></div><div>47%36%5%12%</div></div>

## 2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 34094 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	230	Total	C	N	O	S	0	0
			1787	1112	317	352	6		
1	B	228	Total	C	N	O	S	0	0
			1767	1100	312	349	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	1339	Total	C	N	O	S	0	0
			10556	6624	1840	2049	43		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	1363	Total	C	N	O	S	0	0
			10504	6594	1872	1988	50		

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

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Chain	Residue	Modelled	Actual	Comment	Reference
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 4 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	87	Total	C	N	O	S	0	0
			660	401	126	132	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	471	Total	C	N	O	S	0	0
			3836	2403	684	726	23		

- Molecule 6 is a DNA chain called DNA NT-strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	37	Total	C	N	O	P	0	0
			746	361	116	232	37		

- Molecule 7 is a DNA chain called DNA T-strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	27	Total	C	N	O	P	0	0
			561	266	109	159	27		

- Molecule 8 is a DNA chain called DNA NT-strand downstream.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	11	Total	C	N	O	P	0	0
			225	106	41	67	11		

- Molecule 9 is a DNA chain called DNA T-strand downstream.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	11	Total	C	N	O	P	0	0
			226	106	44	65	11		

- Molecule 10 is a protein called Stringent starvation protein A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	199	Total	C	N	O	S	0	0
			1592	1024	262	298	8		
10	L	204	Total	C	N	O	S	0	0
			1631	1049	274	300	8		

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	-19	MET	-	initiating methionine	UNP A0A1X3LEF3
K	-18	GLY	-	expression tag	UNP A0A1X3LEF3
K	-17	SER	-	expression tag	UNP A0A1X3LEF3
K	-16	SER	-	expression tag	UNP A0A1X3LEF3
K	-15	HIS	-	expression tag	UNP A0A1X3LEF3
K	-14	HIS	-	expression tag	UNP A0A1X3LEF3
K	-13	HIS	-	expression tag	UNP A0A1X3LEF3
K	-12	HIS	-	expression tag	UNP A0A1X3LEF3
K	-11	HIS	-	expression tag	UNP A0A1X3LEF3
K	-10	HIS	-	expression tag	UNP A0A1X3LEF3
K	-9	SER	-	expression tag	UNP A0A1X3LEF3
K	-8	SER	-	expression tag	UNP A0A1X3LEF3
K	-7	GLY	-	expression tag	UNP A0A1X3LEF3
K	-6	LEU	-	expression tag	UNP A0A1X3LEF3
K	-5	VAL	-	expression tag	UNP A0A1X3LEF3
K	-4	PRO	-	expression tag	UNP A0A1X3LEF3
K	-3	ARG	-	expression tag	UNP A0A1X3LEF3
K	-2	GLY	-	expression tag	UNP A0A1X3LEF3
K	-1	SER	-	expression tag	UNP A0A1X3LEF3
K	0	HIS	-	expression tag	UNP A0A1X3LEF3
L	-19	MET	-	initiating methionine	UNP A0A1X3LEF3
L	-18	GLY	-	expression tag	UNP A0A1X3LEF3
L	-17	SER	-	expression tag	UNP A0A1X3LEF3
L	-16	SER	-	expression tag	UNP A0A1X3LEF3
L	-15	HIS	-	expression tag	UNP A0A1X3LEF3
L	-14	HIS	-	expression tag	UNP A0A1X3LEF3
L	-13	HIS	-	expression tag	UNP A0A1X3LEF3
L	-12	HIS	-	expression tag	UNP A0A1X3LEF3
L	-11	HIS	-	expression tag	UNP A0A1X3LEF3

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Chain	Residue	Modelled	Actual	Comment	Reference
L	-10	HIS	-	expression tag	UNP A0A1X3LEF3
L	-9	SER	-	expression tag	UNP A0A1X3LEF3
L	-8	SER	-	expression tag	UNP A0A1X3LEF3
L	-7	GLY	-	expression tag	UNP A0A1X3LEF3
L	-6	LEU	-	expression tag	UNP A0A1X3LEF3
L	-5	VAL	-	expression tag	UNP A0A1X3LEF3
L	-4	PRO	-	expression tag	UNP A0A1X3LEF3
L	-3	ARG	-	expression tag	UNP A0A1X3LEF3
L	-2	GLY	-	expression tag	UNP A0A1X3LEF3
L	-1	SER	-	expression tag	UNP A0A1X3LEF3
L	0	HIS	-	expression tag	UNP A0A1X3LEF3

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

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

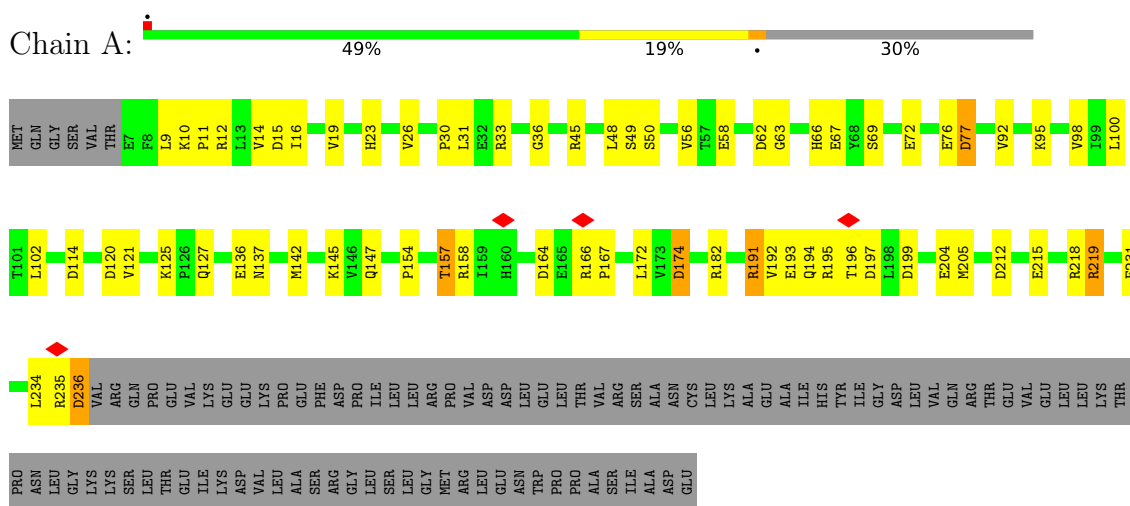
- Molecule 12 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

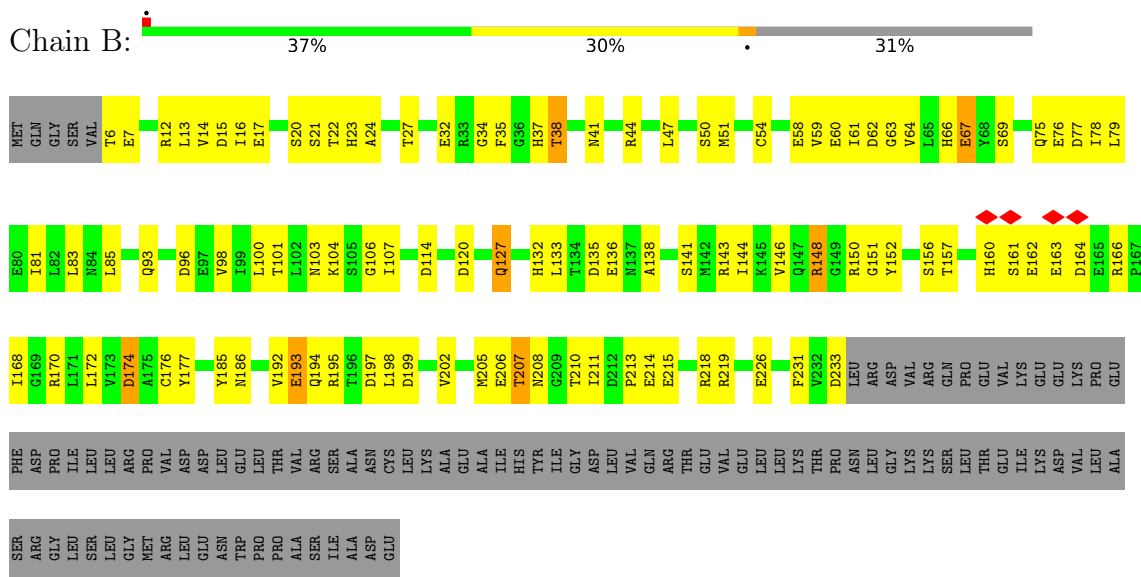
### 3 Residue-property plots [i](#)

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: DNA-directed RNA polymerase subunit alpha

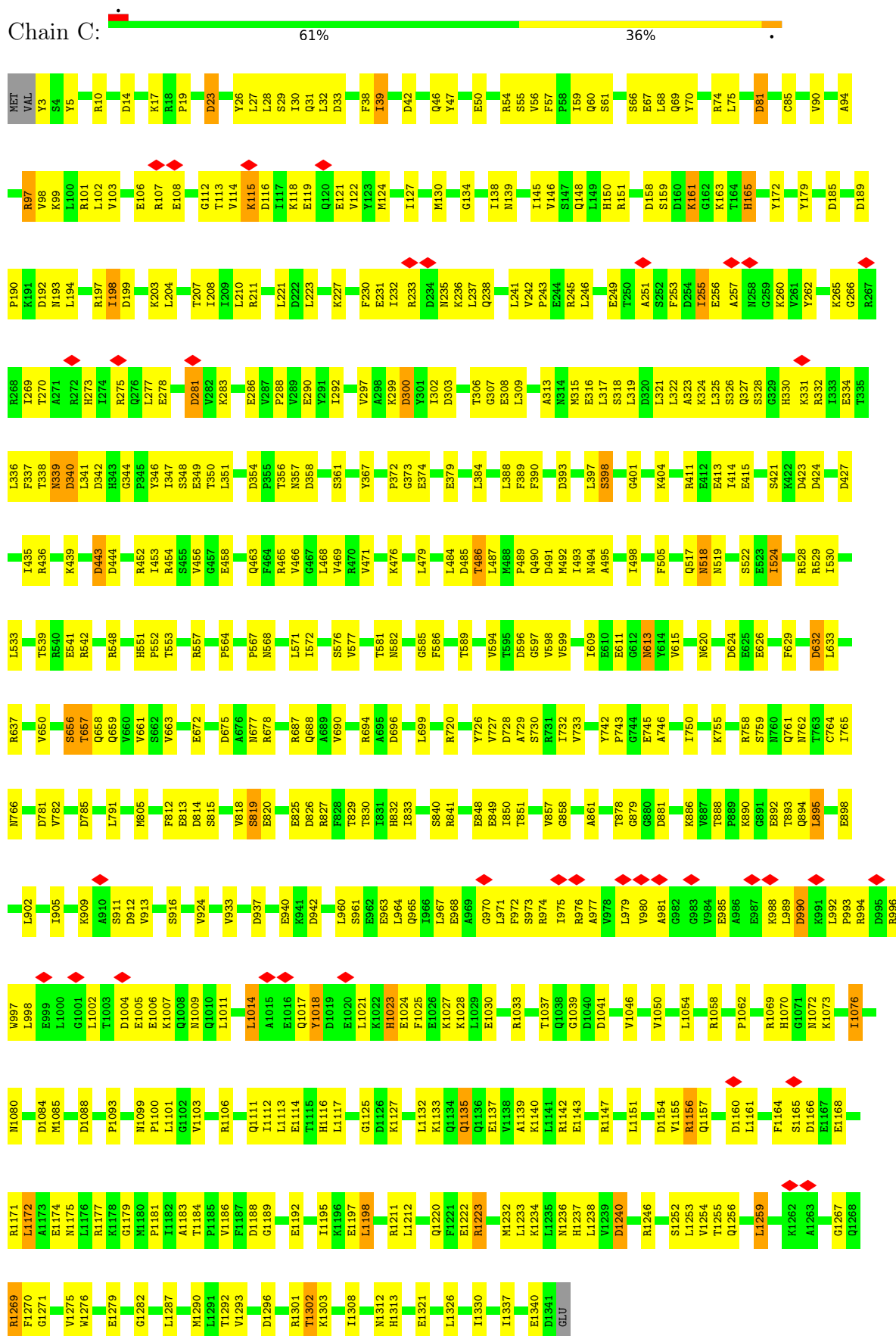


- Molecule 1: DNA-directed RNA polymerase subunit alpha

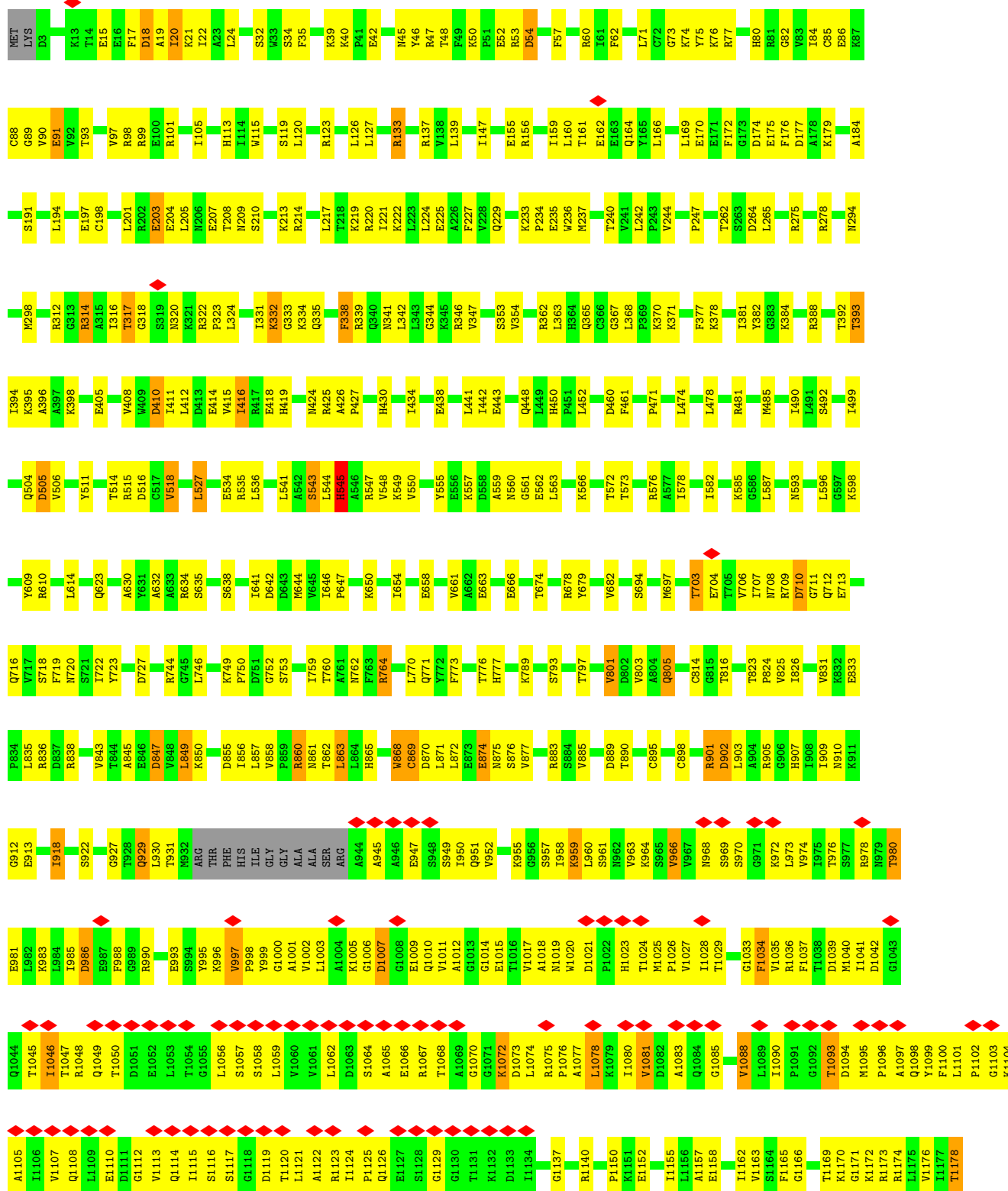


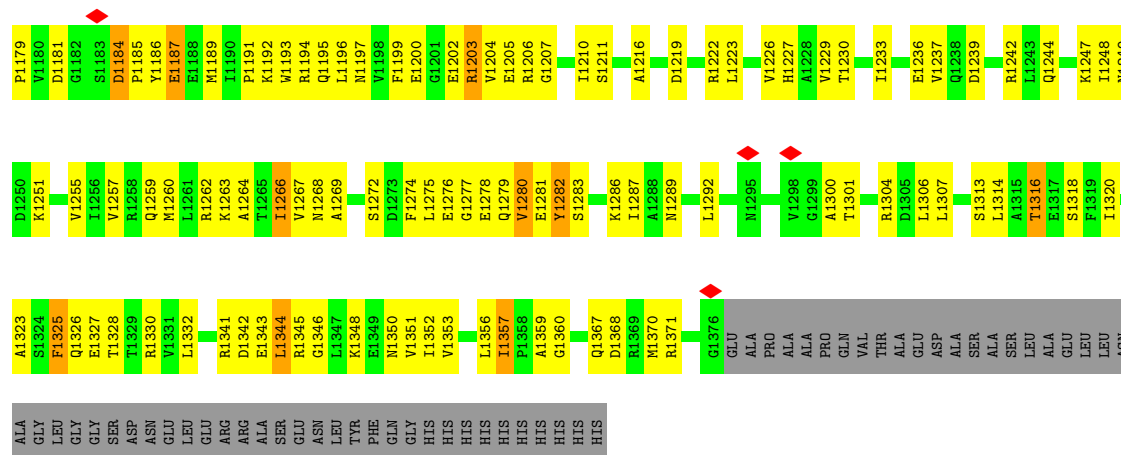
- Molecule 2: DNA-directed RNA polymerase subunit beta



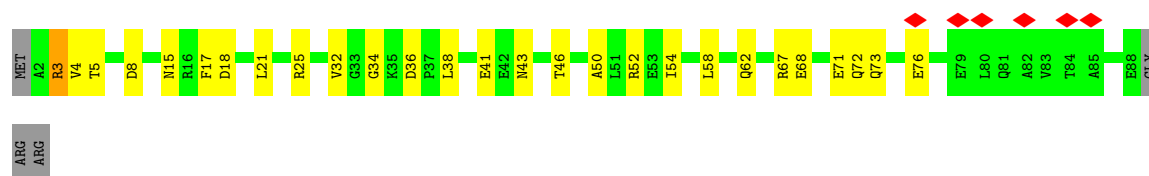


● Molecule 3: DNA-directed RNA polymerase subunit beta'

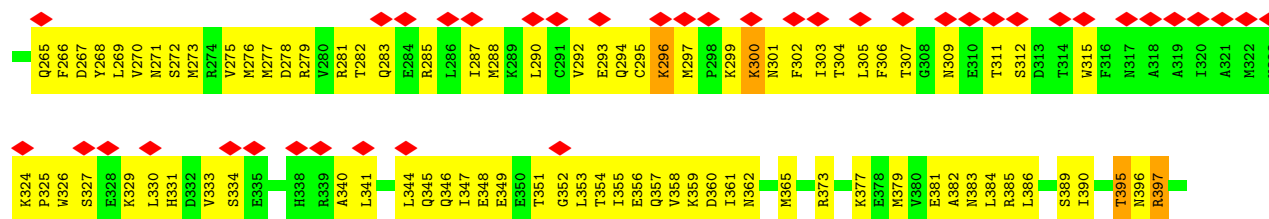
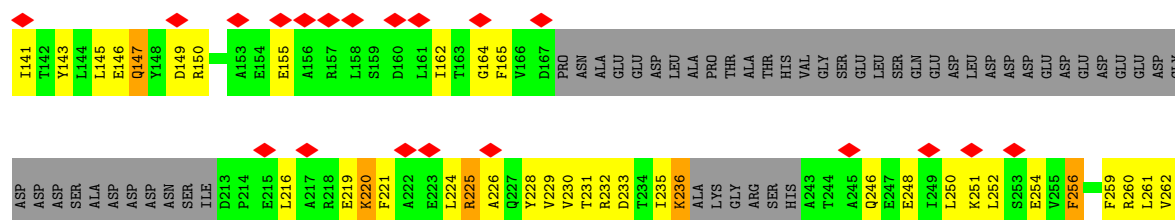
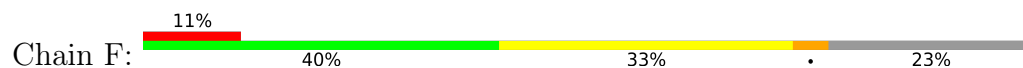


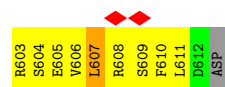
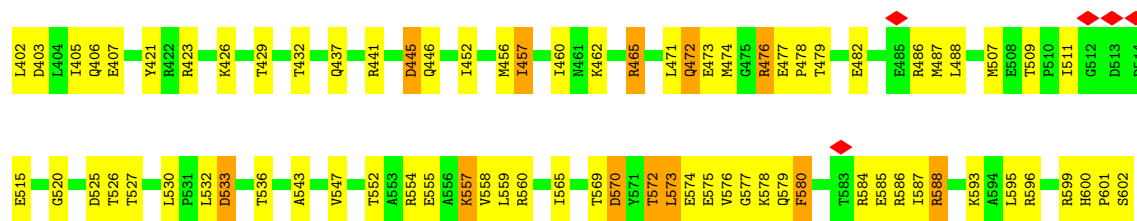


• Molecule 4: DNA-directed RNA polymerase subunit omega

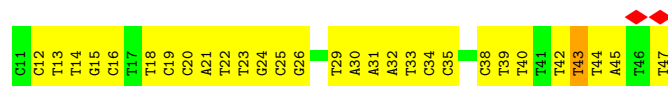


• Molecule 5: RNA polymerase sigma factor RpoD

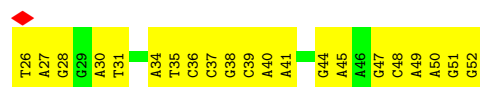




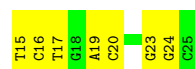
• Molecule 6: DNA NT-strand



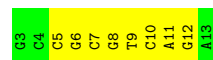
• Molecule 7: DNA T-strand



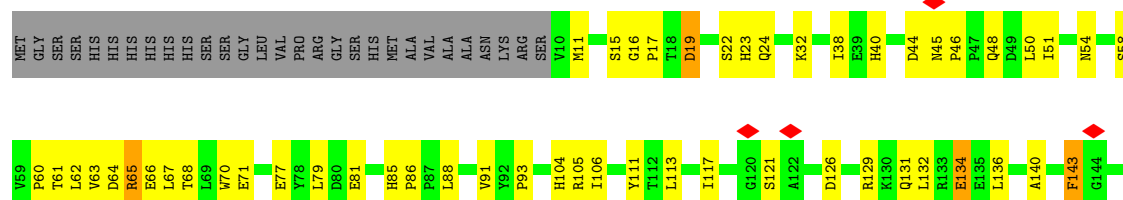
• Molecule 8: DNA NT-strand downstream

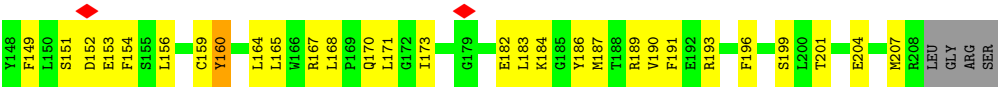


• Molecule 9: DNA T-strand downstream

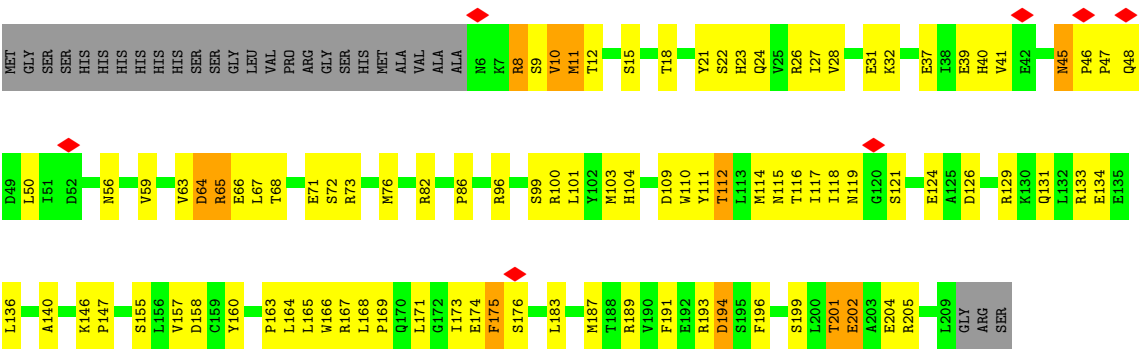


• Molecule 10: Stringent starvation protein A





• Molecule 10: Stringent starvation protein A



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	49560	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 ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.151	Depositor
Minimum map value	-0.089	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	317.99997, 317.99997, 317.99997	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, 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	0.79	1/1809 (0.1%)	0.63	0/2451
1	B	0.64	0/1789	0.60	0/2425
2	C	0.83	1/10725 (0.0%)	0.60	0/14472
3	D	0.77	1/10662 (0.0%)	0.62	0/14404
4	E	0.57	0/662	0.53	0/894
5	F	0.53	0/3887	0.51	0/5224
6	G	1.10	0/830	1.13	1/1277 (0.1%)
7	H	0.99	0/631	0.96	0/973
8	I	1.44	0/251	0.99	0/385
9	J	1.23	0/253	0.88	0/388
10	K	0.54	0/1633	0.50	0/2222
10	L	0.58	0/1672	0.53	0/2272
All	All	0.77	3/34804 (0.0%)	0.63	1/47387 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	C	0	1
3	D	0	4
10	L	0	1
All	All	0	6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	50	SER	C-N	-5.80	1.20	1.34
3	D	545	HIS	CA-CB	-5.61	1.41	1.53
2	C	517	GLN	CA-CB	-5.03	1.42	1.53

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	G	43	DT	O4'-C4'-C3'	-5.00	102.50	104.50

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	198	ILE	Peptide
3	D	1184	ASP	Peptide
3	D	119	SER	Peptide
3	D	1344	LEU	Peptide
3	D	860	ARG	Peptide

## 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	1787	0	1810	52	0
1	B	1767	0	1789	85	0
2	C	10556	0	10572	382	0
3	D	10504	0	10644	481	0
4	E	660	0	646	15	0
5	F	3836	0	3907	226	0
6	G	746	0	425	51	0
7	H	561	0	304	28	0
8	I	225	0	124	11	0
9	J	226	0	123	13	0
10	K	1592	0	1550	60	0
10	L	1631	0	1601	74	0
11	D	1	0	0	0	0
12	D	2	0	0	0	0
All	All	34094	0	33495	1393	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 21.

The worst 5 of 1393 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)
5:F:607:LEU:HA	5:F:610:PHE:HB2	1.51	0.89
8:I:23:DG:N1	9:J:5:DC:N3	2.21	0.89
6:G:12:DC:H2''	6:G:13:DT:H5'	1.55	0.89
5:F:604:SER:O	5:F:607:LEU:N	2.07	0.87
10:L:41:VAL:HG11	10:L:59:VAL:HG11	1.58	0.86

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	
1	A	228/329 (69%)	208 (91%)	20 (9%)	0	100	100
1	B	226/329 (69%)	199 (88%)	25 (11%)	2 (1%)	17	54
2	C	1337/1342 (100%)	1167 (87%)	168 (13%)	2 (0%)	51	83
3	D	1359/1430 (95%)	1188 (87%)	168 (12%)	3 (0%)	47	78
4	E	85/91 (93%)	74 (87%)	11 (13%)	0	100	100
5	F	465/613 (76%)	426 (92%)	39 (8%)	0	100	100
10	K	197/232 (85%)	171 (87%)	25 (13%)	1 (0%)	29	66
10	L	202/232 (87%)	175 (87%)	23 (11%)	4 (2%)	7	35
All	All	4099/4598 (89%)	3608 (88%)	479 (12%)	12 (0%)	44	73

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	710	ASP
3	D	1345	ARG
1	B	21	SER
10	L	10	VAL
2	C	398	SER

### 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	198/286 (69%)	184 (93%)	14 (7%)	14	45
1	B	196/286 (68%)	179 (91%)	17 (9%)	10	35
2	C	1153/1157 (100%)	1078 (94%)	75 (6%)	17	48
3	D	1116/1189 (94%)	1016 (91%)	100 (9%)	9	33
4	E	65/75 (87%)	62 (95%)	3 (5%)	27	61
5	F	419/540 (78%)	383 (91%)	36 (9%)	10	36
10	K	172/204 (84%)	162 (94%)	10 (6%)	20	53
10	L	175/204 (86%)	160 (91%)	15 (9%)	10	36
All	All	3494/3941 (89%)	3224 (92%)	270 (8%)	16	42

5 of 270 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	F	509	THR
5	F	572	THR
10	L	112	THR
2	C	1233	LEU
2	C	1198	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
3	D	1218	HIS
5	F	309	ASN
3	D	1235	ASN
4	E	70	GLN
5	F	406	GLN

### 5.3.3 RNA ⓘ

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 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 [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

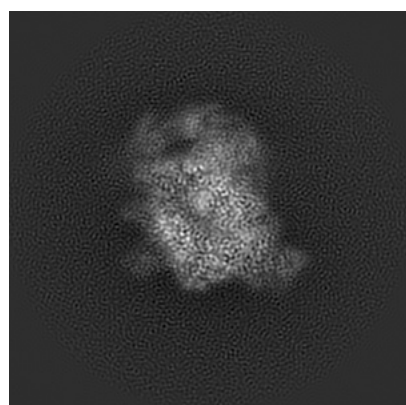
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21853. These allow visual inspection of the internal detail of the map and identification of artifacts.

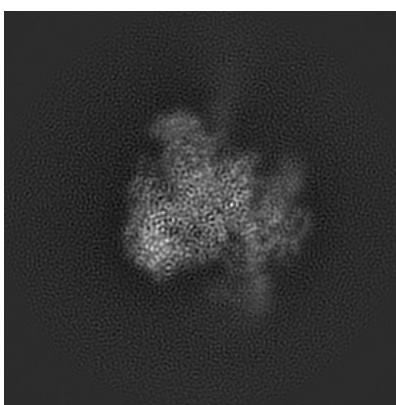
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

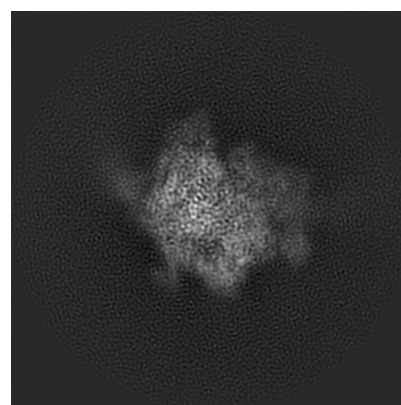
#### 6.1.1 Primary map



X



Y

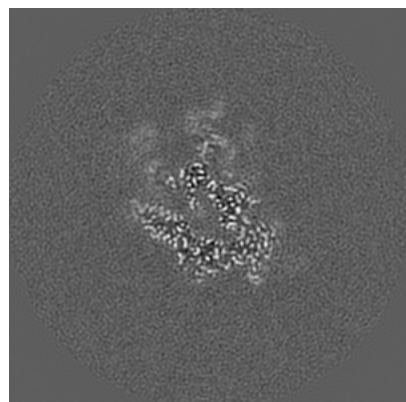


Z

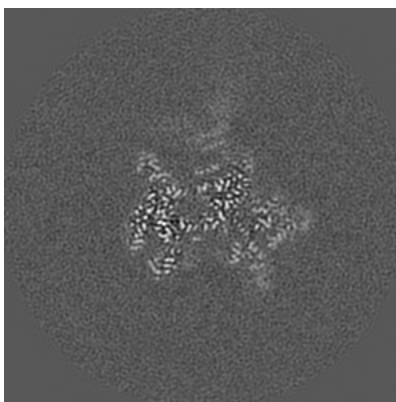
The images above show the map projected in three orthogonal directions.

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

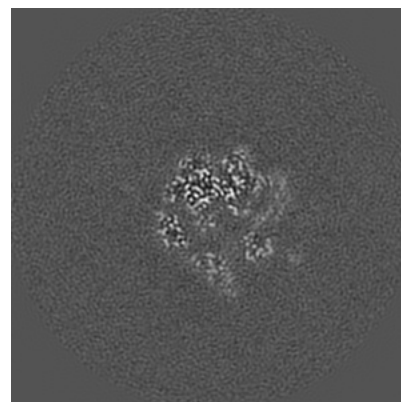
#### 6.2.1 Primary map



X Index: 150



Y Index: 150

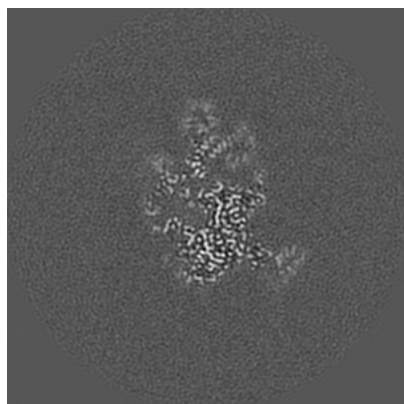


Z Index: 150

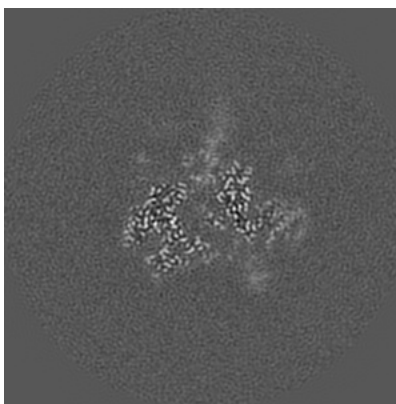
The images above show central slices of the map in three orthogonal directions.

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

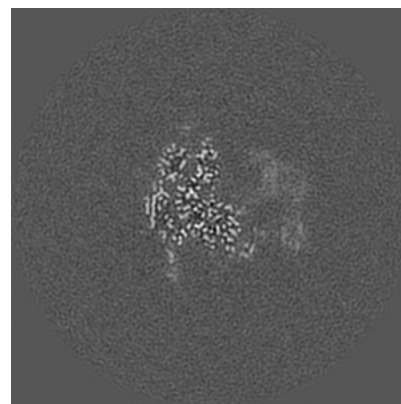
### 6.3.1 Primary map



X Index: 138



Y Index: 144



Z Index: 123

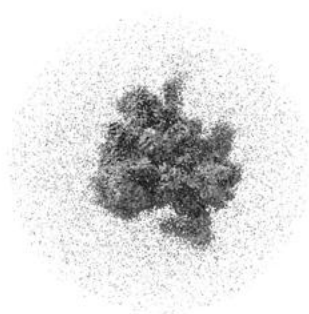
The images above show the largest variance slices of the map in three orthogonal directions.

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

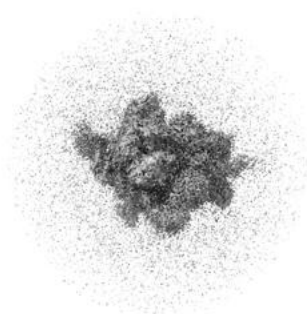
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

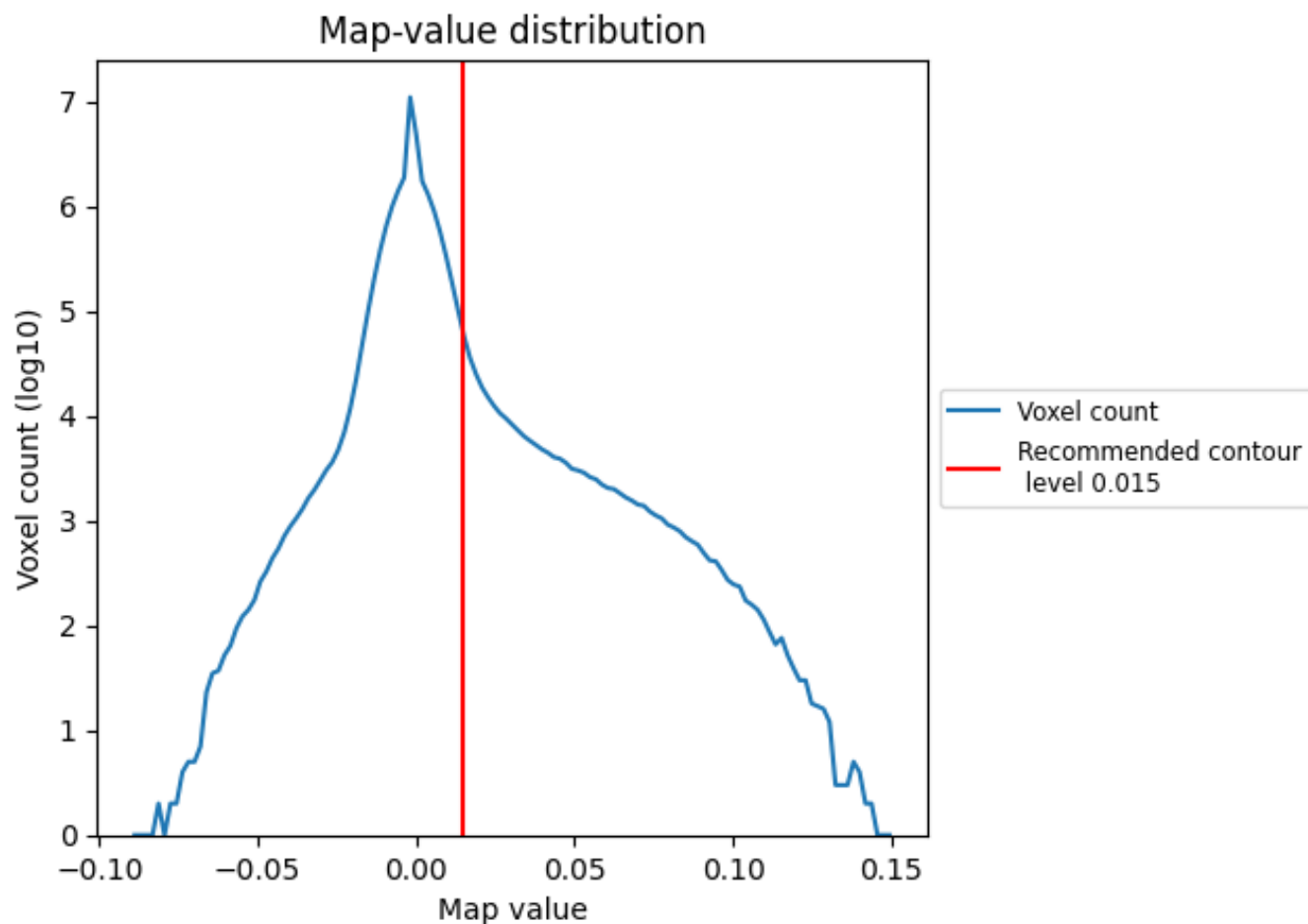
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

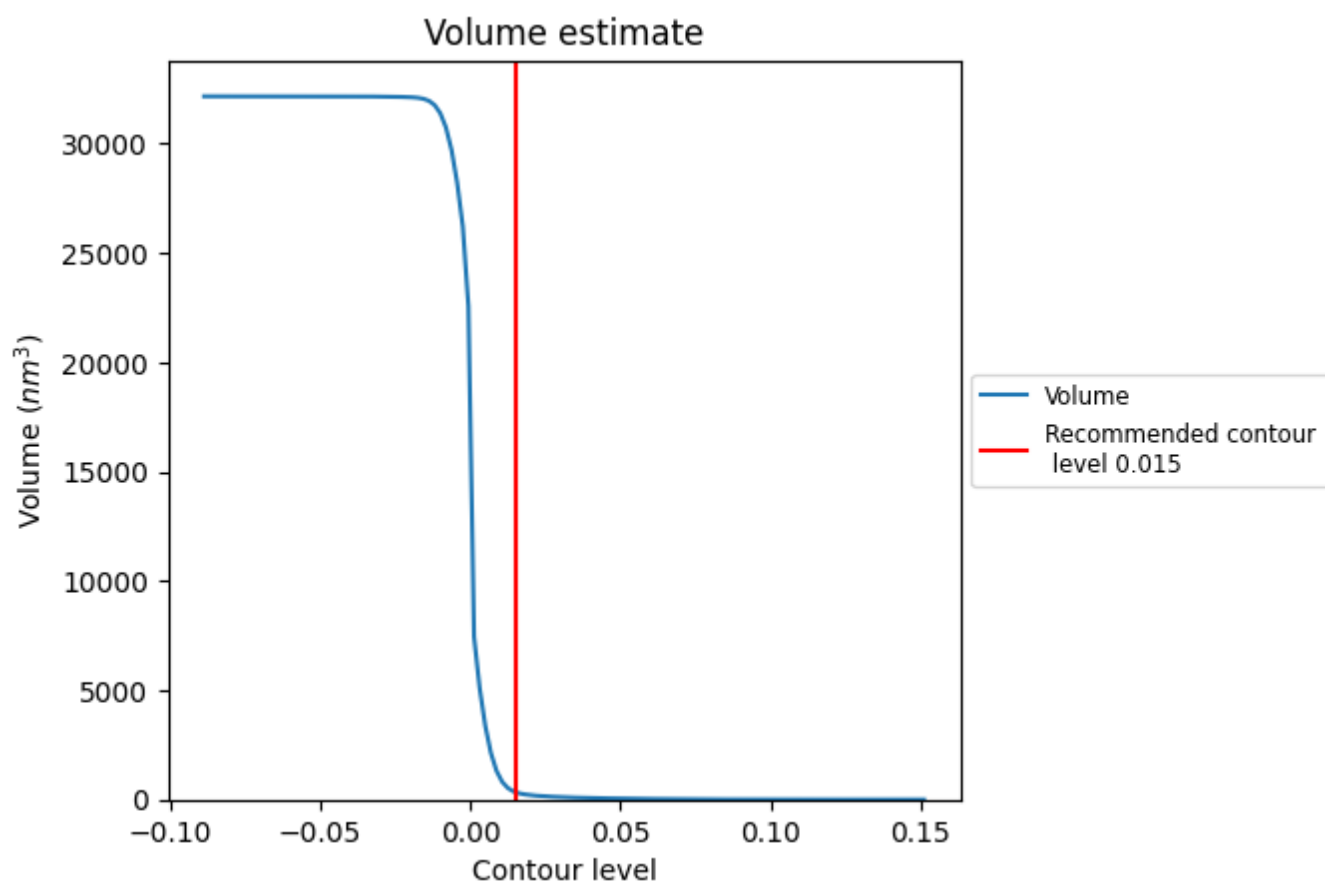
This section contains the results of statistical analysis of the map.

### 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](#)

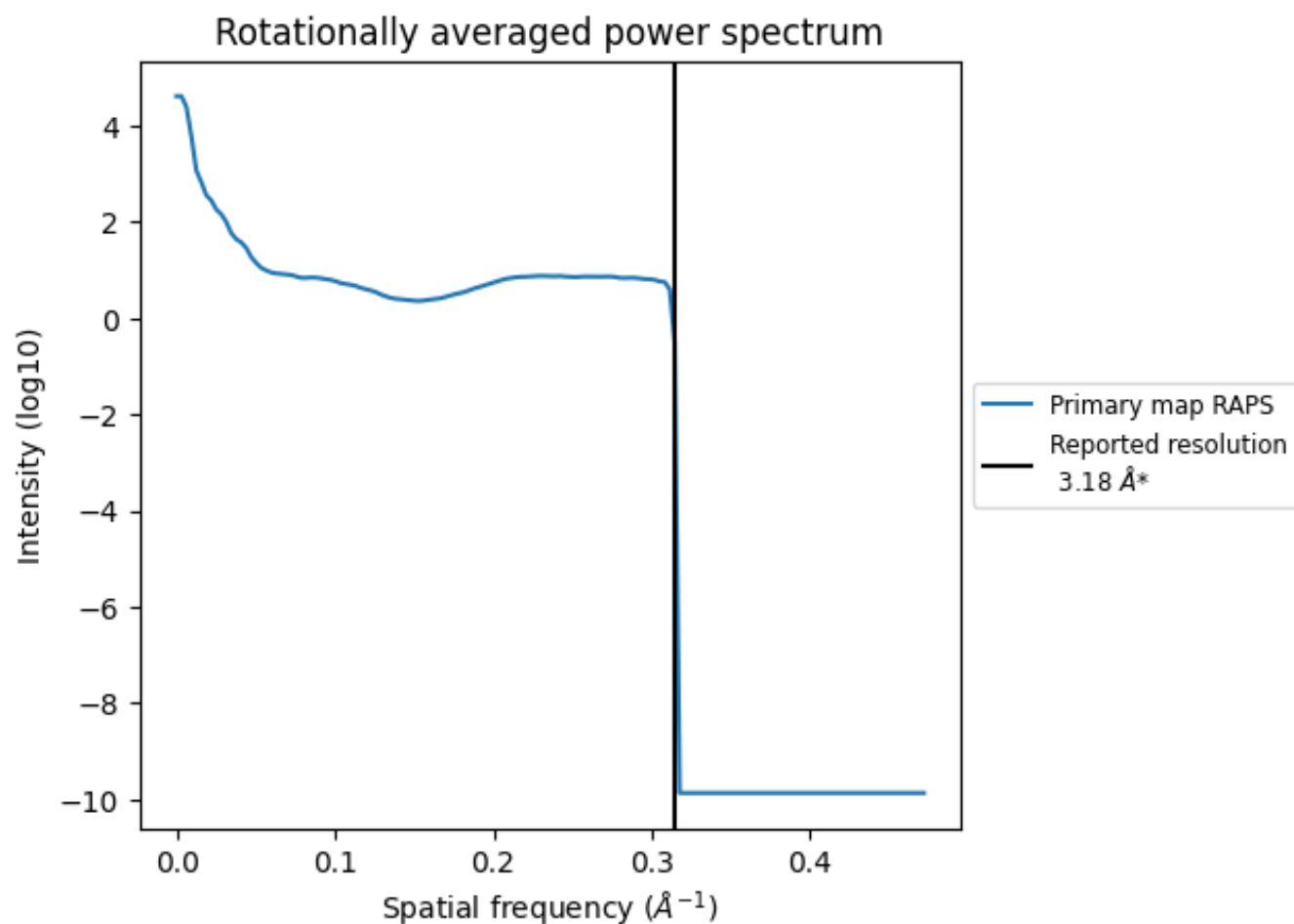


The volume at the recommended contour level is 343  $\text{nm}^3$ ; this corresponds to an approximate mass of 310 kDa.

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 ⓘ

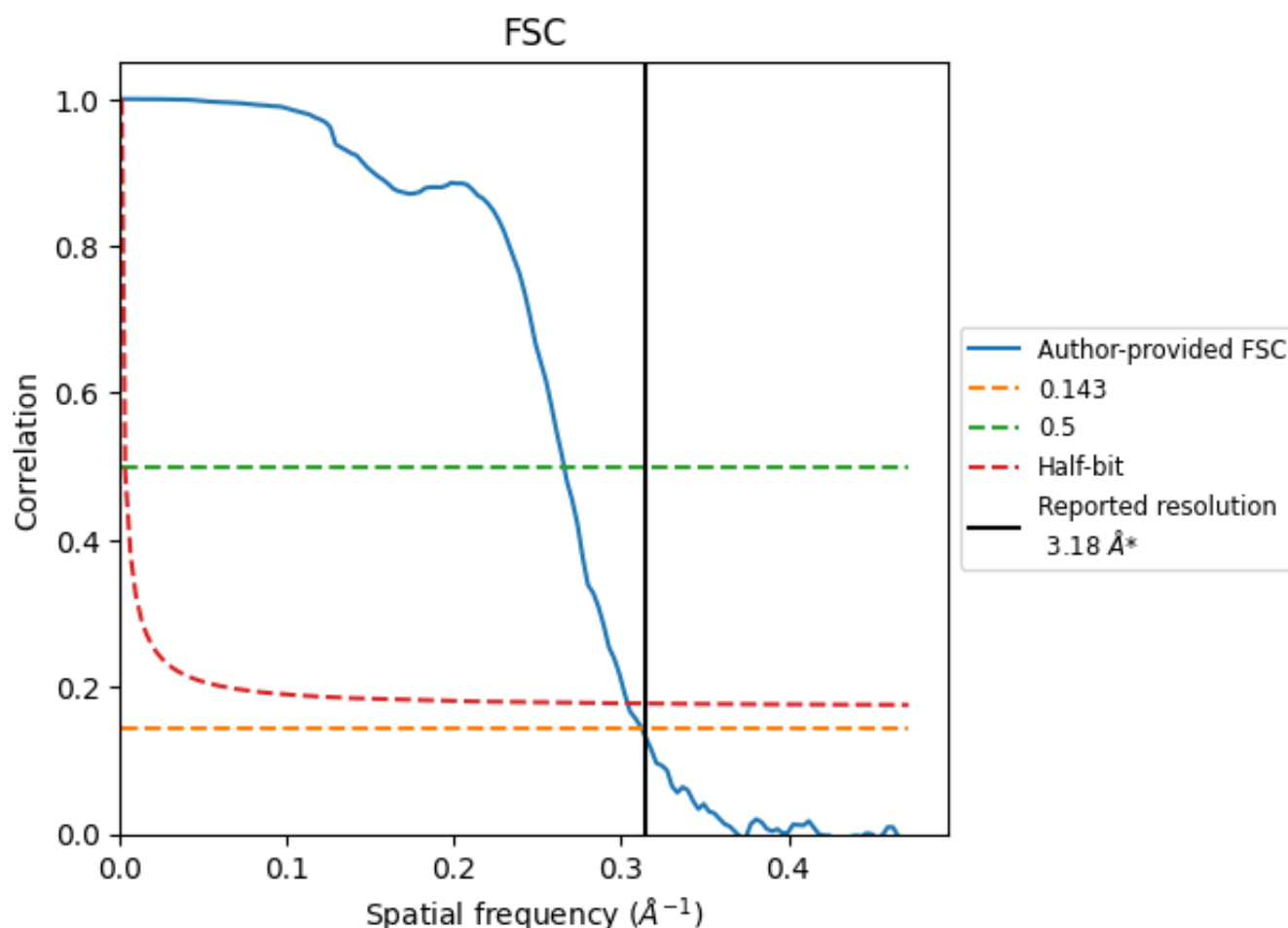


\*Reported resolution corresponds to spatial frequency of 0.314 Å<sup>-1</sup>

## 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 0.314 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

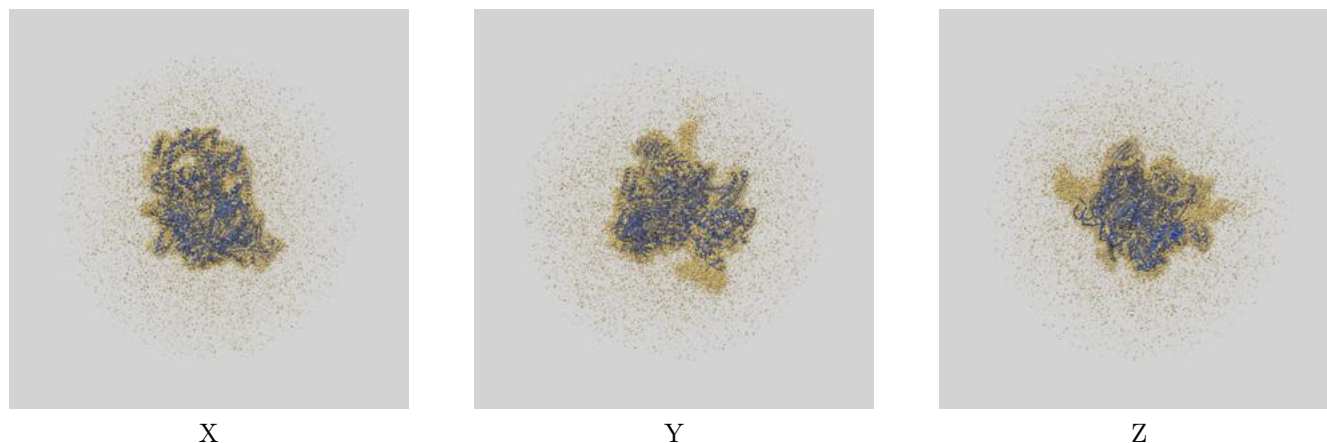
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.18	-	-
Author-provided FSC curve	3.20	3.76	3.29
Unmasked-calculated*	-	-	-

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

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

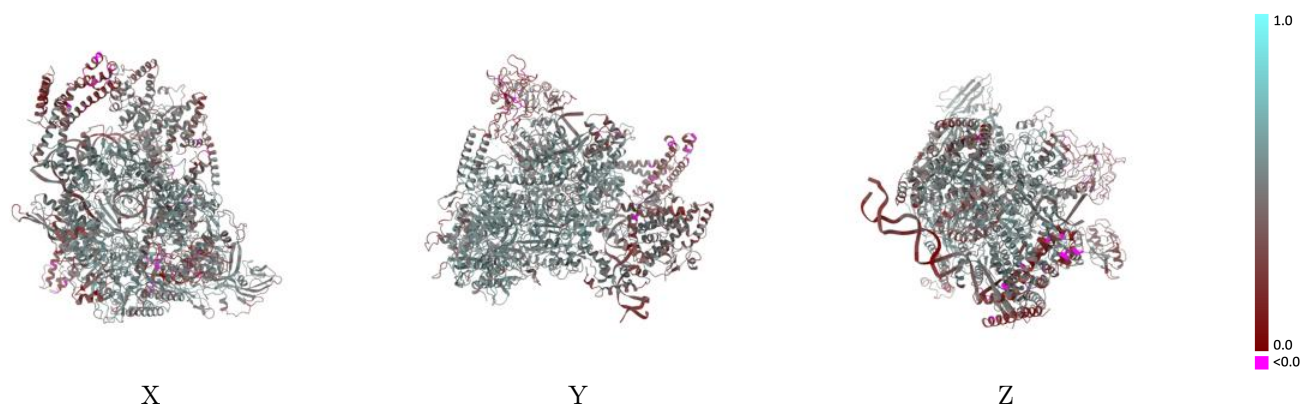
This section contains information regarding the fit between EMDB map EMD-21853 and PDB model 6WMU. Per-residue inclusion information can be found in section [3](#) on page [8](#).

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



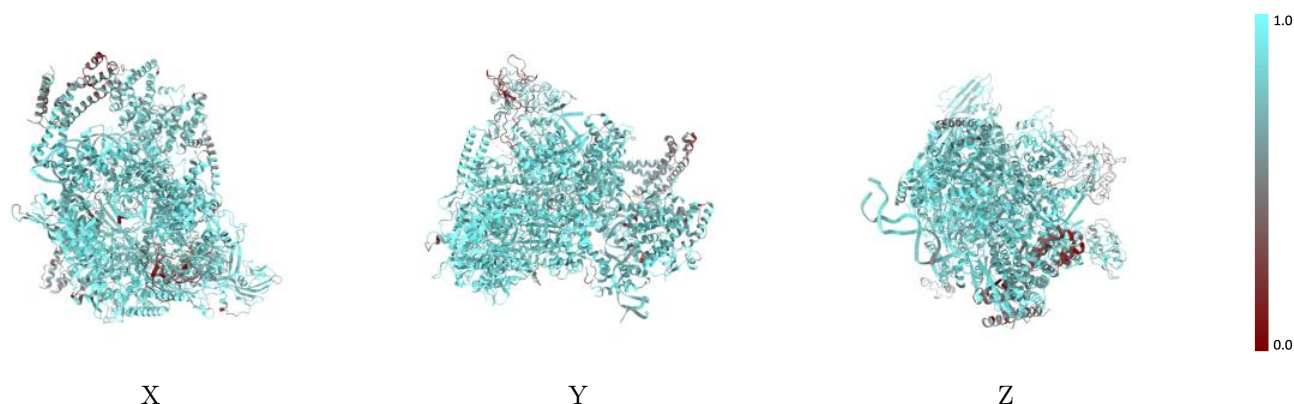
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



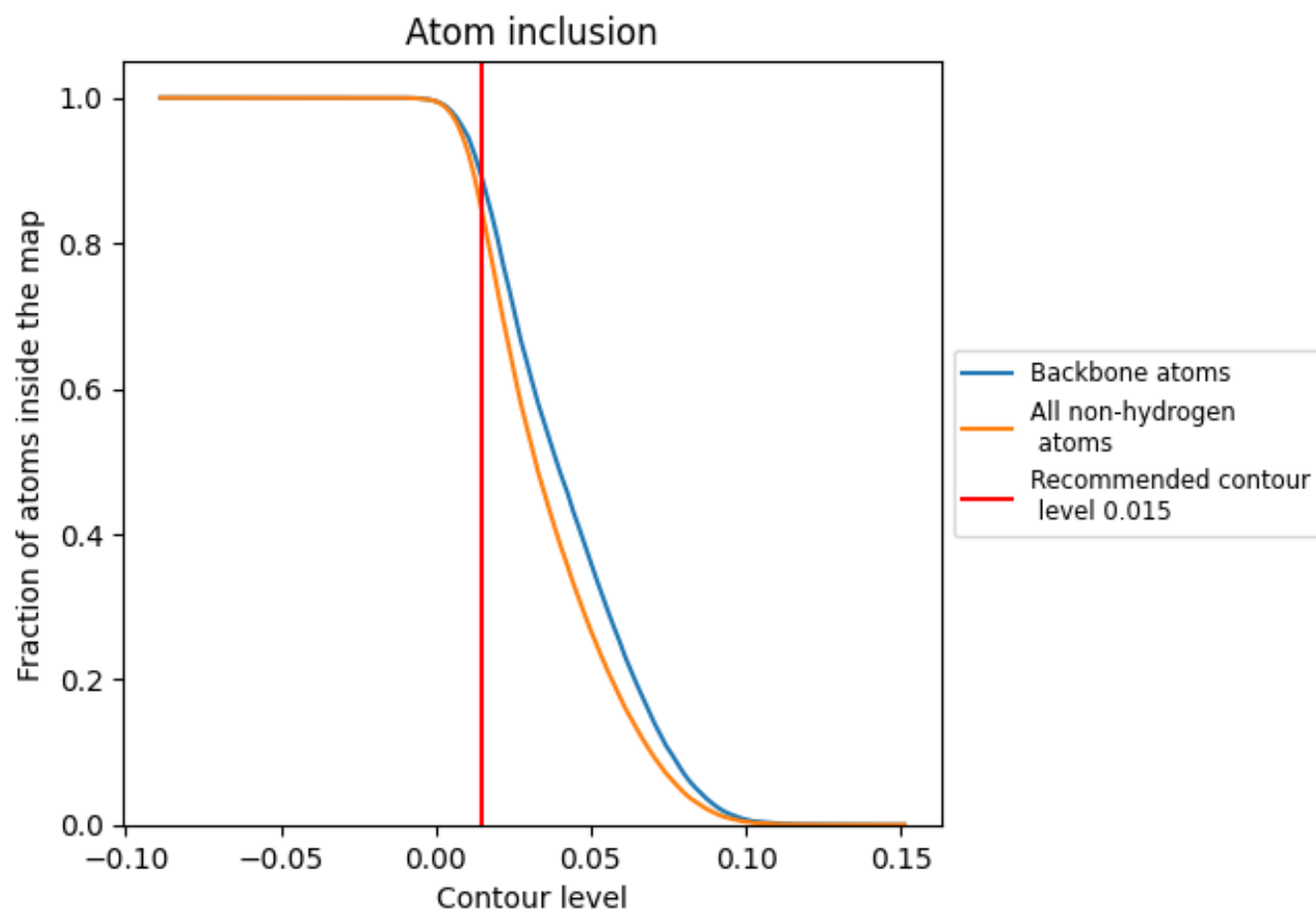
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 84% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.8415</div>	<div><div></div>0.4710</div>
A	<div><div></div>0.9137</div>	<div><div></div>0.5390</div>
B	<div><div></div>0.8608</div>	<div><div></div>0.4980</div>
C	<div><div></div>0.8805</div>	<div><div></div>0.5090</div>
D	<div><div></div>0.8354</div>	<div><div></div>0.4830</div>
E	<div><div></div>0.8276</div>	<div><div></div>0.4980</div>
F	<div><div></div>0.7292</div>	<div><div></div>0.3820</div>
G	<div><div></div>0.7882</div>	<div><div></div>0.3160</div>
H	<div><div></div>0.7540</div>	<div><div></div>0.2780</div>
I	<div><div></div>0.9333</div>	<div><div></div>0.4220</div>
J	<div><div></div>0.9381</div>	<div><div></div>0.4280</div>
K	<div><div></div>0.8328</div>	<div><div></div>0.4270</div>
L	<div><div></div>0.8333</div>	<div><div></div>0.4340</div>

1.0

0.0

<0.0