



wwPDB EM Validation Summary Report ⓘ

Nov 13, 2022 – 01:53 PM EST

PDB ID : 6WMR
EMDB ID : EMD-21851
Title : F. tularensis RNAPs70-(MglA-SspA)-iglA DNA complex
Authors : Travis, B.A.; Brennan, R.G.; Schumacher, M.A.
Deposited on : 2020-04-21
Resolution : 3.46 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) : 2.31.2

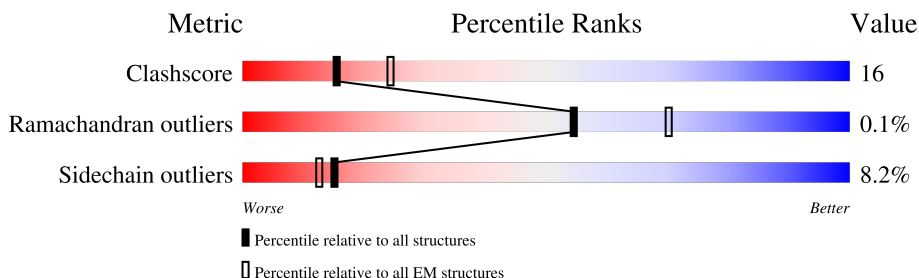
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.46 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.



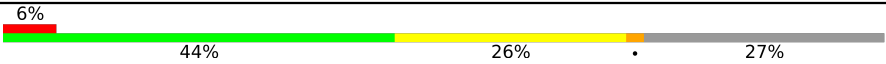

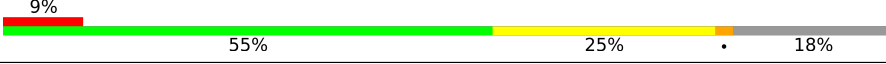

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	G	35	
2	H	24	
3	X	11	
4	J	11	
5	S	210	
6	M	205	
7	Z	577	
8	A	323	

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Mol	Chain	Length	Quality of chain
9	B	317	
10	C	1358	
11	D	1417	
12	E	72	

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 30440 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 NT-strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	G	35	Total	C	N	O	P	0	0
			720	347	118	220	35		

- Molecule 2 is a DNA chain called DNA T-strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	24	Total	C	N	O	P	0	0
			487	233	94	136	24		

- Molecule 3 is a DNA chain called DNA NT-strand downstream.

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

- Molecule 4 is a DNA chain called DNA T-strand downstream.

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

- Molecule 5 is a protein called Stringent starvation protein A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	S	202	Total	C	N	O	S	0	0
			1583	1024	265	287	7		

- Molecule 6 is a protein called Macrophage growth locus, subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	M	201	Total	C	N	O	S	0	0
			1598	1042	258	293	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Z	470	Total	C	N	O	S	0	0
			3772	2392	666	698	16		

- Molecule 8 is a protein called DNA-directed RNA polymerase subunit alpha 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	223	Total	C	N	O	S	0	0
			1688	1075	280	331	2		

- Molecule 9 is a protein called DNA-directed RNA polymerase subunit alpha 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	230	Total	C	N	O	S	0	0
			1769	1116	289	358	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C	1186	Total	C	N	O	S	0	0
			8922	5616	1560	1709	37		

- Molecule 11 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	D	1159	Total	C	N	O	S	0	0
			8880	5589	1568	1681	42		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	E	72	Total	C	N	O	S	0	0
			567	349	98	116	4		

- Molecule 13 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

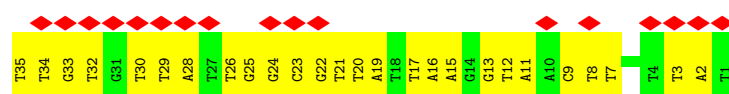
- Molecule 14 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

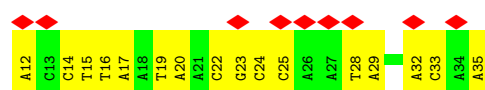
3 Residue-property plots [i](#)

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 NT-strand



- Molecule 2: DNA T-strand



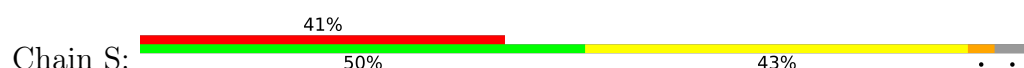
- Molecule 3: DNA NT-strand downstream



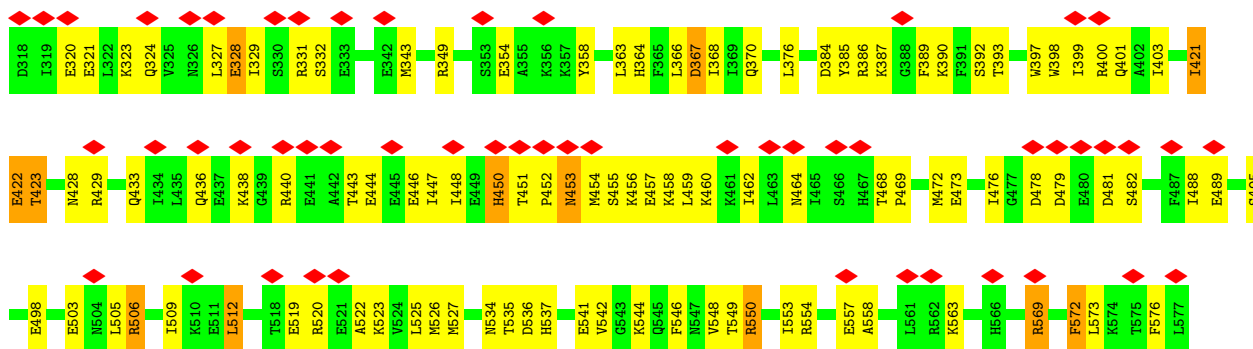
- Molecule 4: DNA T-strand downstream



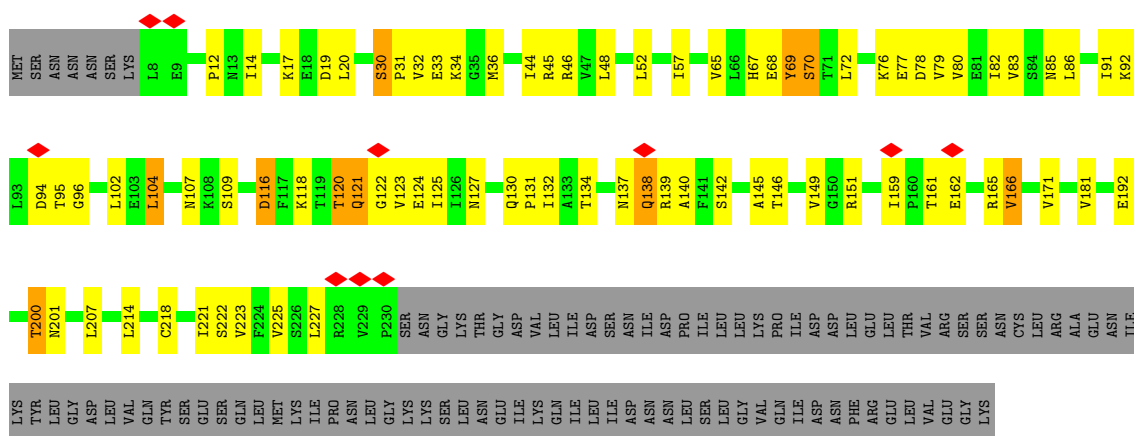
- Molecule 5: Stringent starvation protein A



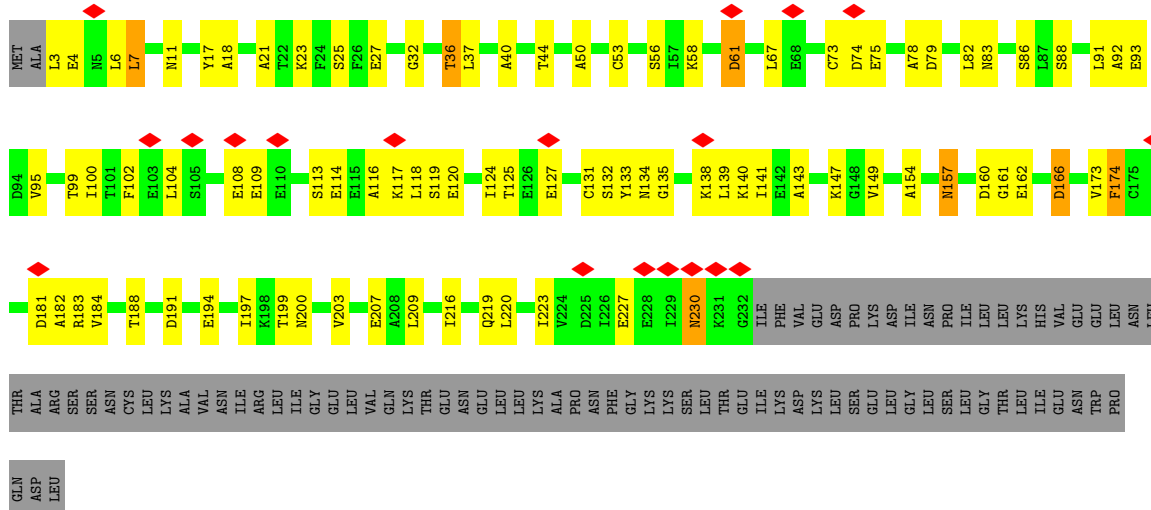
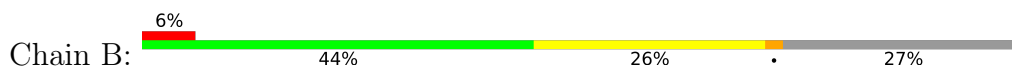




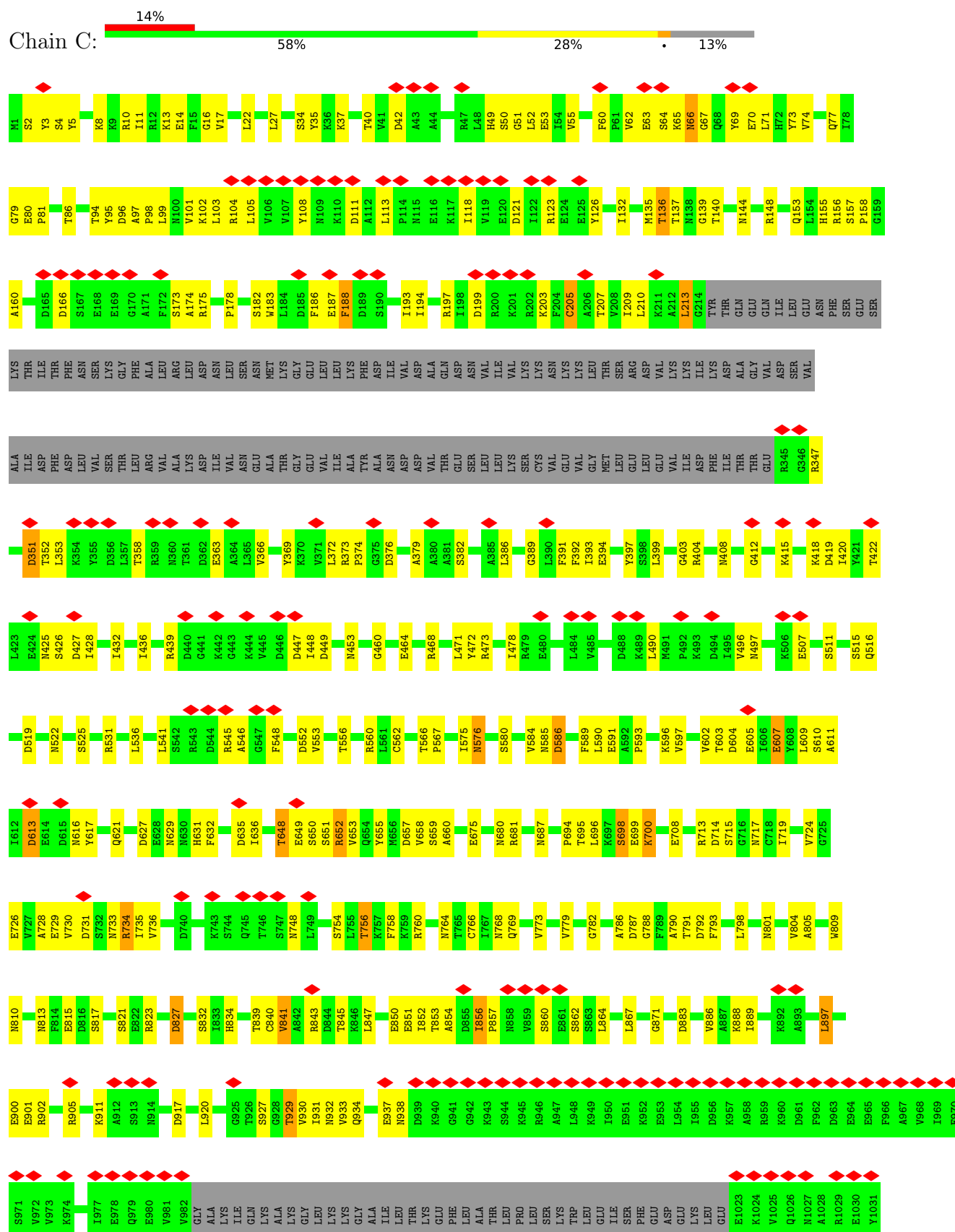
• Molecule 8: DNA-directed RNA polymerase subunit alpha 1

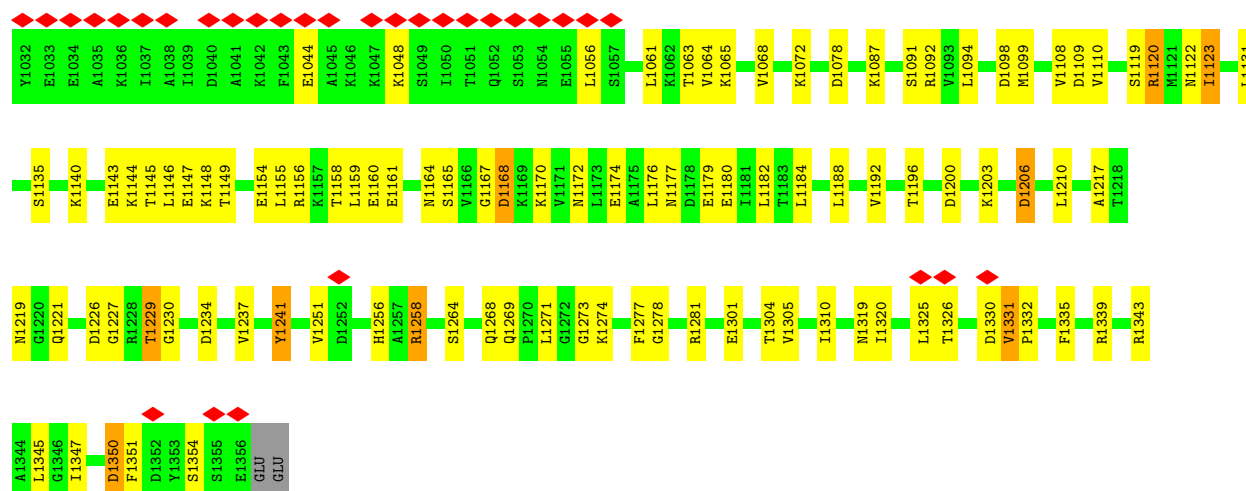


• Molecule 9: DNA-directed RNA polymerase subunit alpha 2

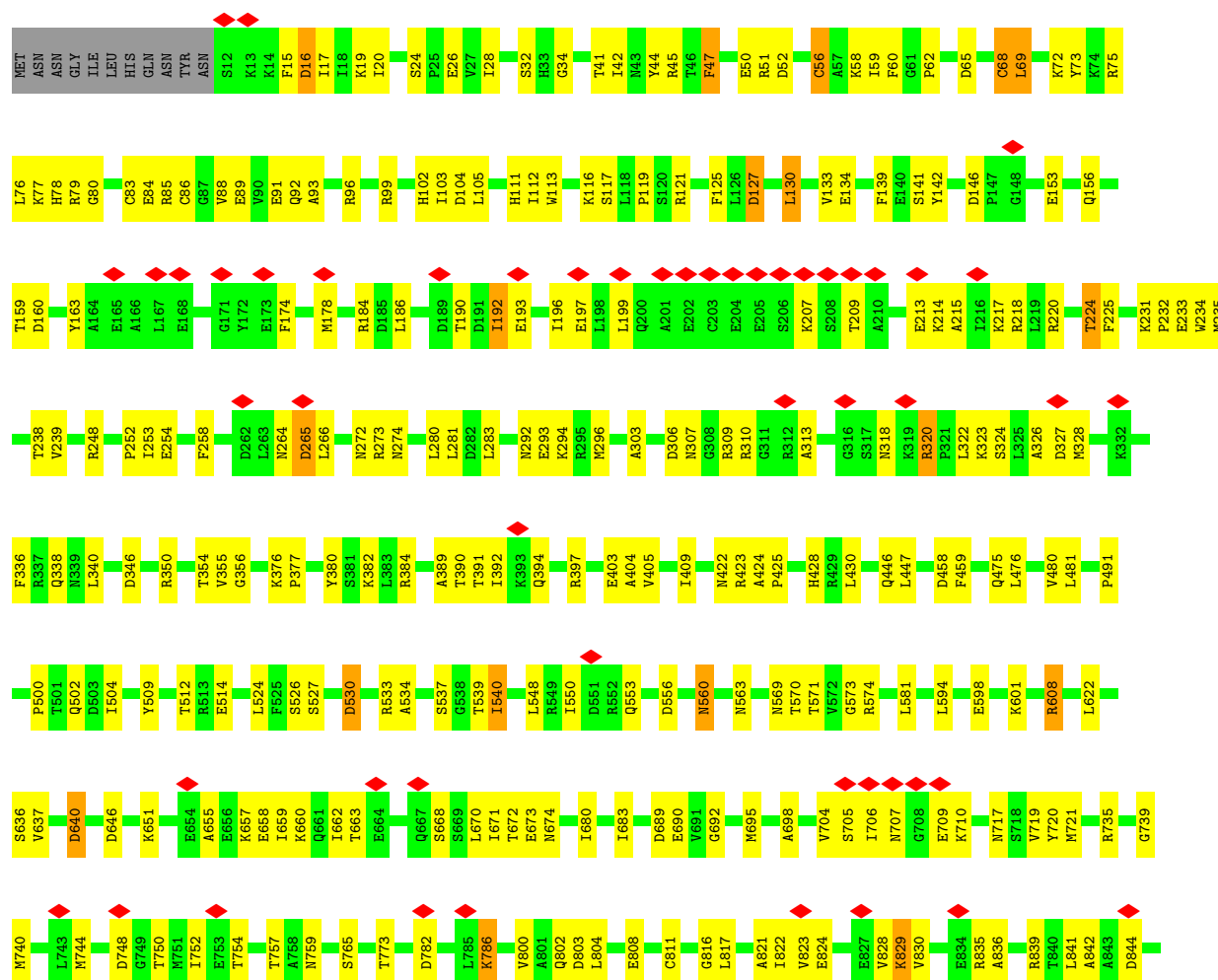


• Molecule 10: DNA-directed RNA polymerase subunit beta





• Molecule 11: DNA-directed RNA polymerase subunit beta'



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21457	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 ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	36.668	Depositor
Minimum map value	-21.358	Depositor
Average map value	0.006	Depositor
Map value standard deviation	1.641	Depositor
Recommended contour level	6.5	Depositor
Map size (\AA)	379.47998, 379.47998, 379.47998	wwPDB
Map dimensions	358, 358, 358	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.06, 1.06, 1.06	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: MG, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	G	0.70	0/804	1.07	0/1241
2	H	0.72	0/547	0.89	0/839
3	X	0.66	0/251	0.96	0/385
4	J	0.65	0/253	0.81	0/388
5	S	0.34	0/1611	0.47	0/2173
6	M	0.34	0/1626	0.46	0/2208
7	Z	0.33	0/3825	0.47	0/5138
8	A	0.43	0/1708	0.53	0/2318
9	B	0.39	0/1789	0.49	0/2414
10	C	0.47	0/9064	0.51	0/12264
11	D	0.46	1/9000 (0.0%)	0.51	0/12149
12	E	0.35	0/568	0.49	0/760
All	All	0.45	1/31046 (0.0%)	0.55	0/42277

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
7	Z	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	D	47	PHE	C-N	-5.02	1.22	1.34

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	Z	213	LYS	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	G	720	0	403	26	0
2	H	487	0	269	15	0
3	X	225	0	124	13	0
4	J	226	0	123	9	0
5	S	1583	0	1600	79	0
6	M	1598	0	1650	78	0
7	Z	3772	0	3813	166	0
8	A	1688	0	1726	60	0
9	B	1769	0	1767	57	0
10	C	8922	0	8667	263	0
11	D	8880	0	8947	274	0
12	E	567	0	581	23	0
13	D	1	0	0	0	0
14	D	2	0	0	0	0
All	All	30440	0	29670	983	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 16.

The worst 5 of 983 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)
8:A:12:PRO:HA	8:A:31:PRO:HD2	1.52	0.92
6:M:81:MET:HB3	6:M:157:VAL:HB	1.55	0.87
10:C:447:ASP:O	10:C:453:ASN:ND2	2.14	0.80
7:Z:109:ILE:HA	7:Z:112:ARG:HD3	1.65	0.79
10:C:94:THR:HG22	10:C:144:ASN:H	1.47	0.78

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	
5	S	198/210 (94%)	164 (83%)	33 (17%)	1 (0%)	29	66
6	M	199/205 (97%)	176 (88%)	22 (11%)	1 (0%)	29	66
7	Z	464/577 (80%)	398 (86%)	65 (14%)	1 (0%)	47	80
8	A	221/323 (68%)	188 (85%)	33 (15%)	0	100	100
9	B	228/317 (72%)	199 (87%)	29 (13%)	0	100	100
10	C	1180/1358 (87%)	988 (84%)	192 (16%)	0	100	100
11	D	1155/1417 (82%)	996 (86%)	158 (14%)	1 (0%)	51	84
12	E	70/72 (97%)	56 (80%)	13 (19%)	1 (1%)	11	44
All	All	3715/4479 (83%)	3165 (85%)	545 (15%)	5 (0%)	54	84

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	M	65	LEU
12	E	62	SER
5	S	54	LEU
7	Z	479	ASP
11	D	1263	VAL

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	
5	S	165/184 (90%)	151 (92%)	14 (8%)	10	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	M	179/191 (94%)	157 (88%)	22 (12%)	4	22
7	Z	401/527 (76%)	360 (90%)	41 (10%)	7	30
8	A	189/287 (66%)	173 (92%)	16 (8%)	10	38
9	B	194/276 (70%)	177 (91%)	17 (9%)	10	36
10	C	911/1169 (78%)	831 (91%)	80 (9%)	10	36
11	D	937/1219 (77%)	885 (94%)	52 (6%)	21	53
12	E	63/64 (98%)	56 (89%)	7 (11%)	6	26
All	All	3039/3917 (78%)	2790 (92%)	249 (8%)	15	39

5 of 249 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	C	42	ASP
11	D	748	ASP
10	C	613	ASP
11	D	646	ASP
11	D	1256	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
10	C	1319	ASN
11	D	433	GLN
10	C	1336	ASN
11	D	362	HIS
11	D	487	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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 [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.

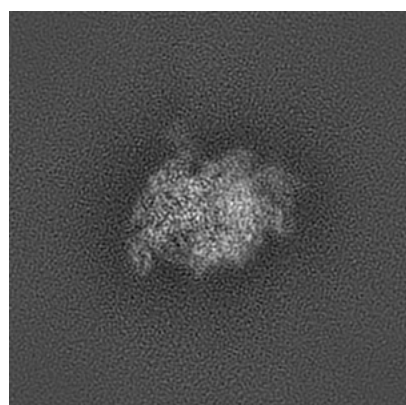
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21851. These allow visual inspection of the internal detail of the map and identification of artifacts.

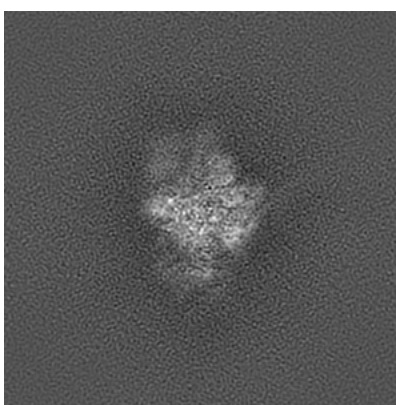
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

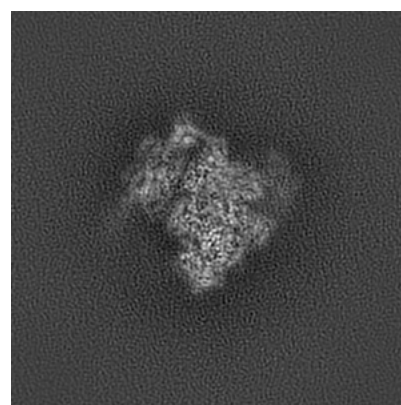
6.1.1 Primary map



X



Y

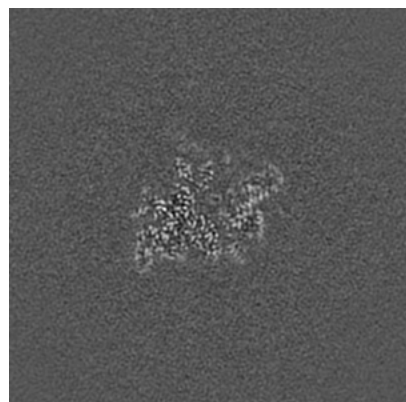


Z

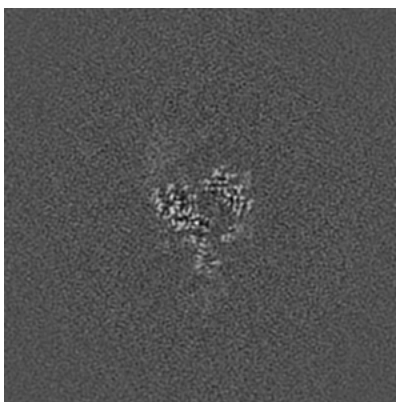
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

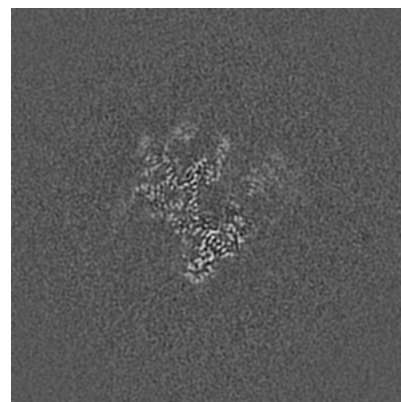
6.2.1 Primary map



X Index: 179



Y Index: 179

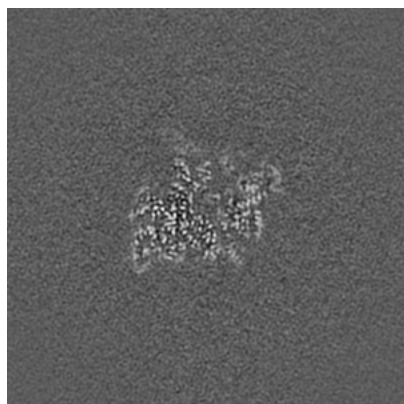


Z Index: 179

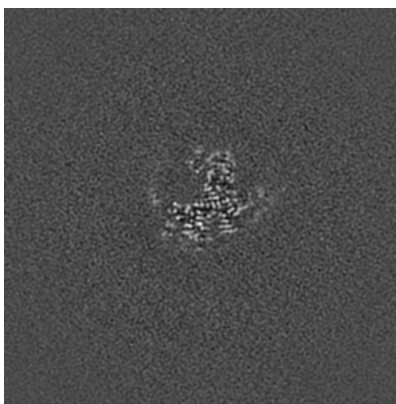
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

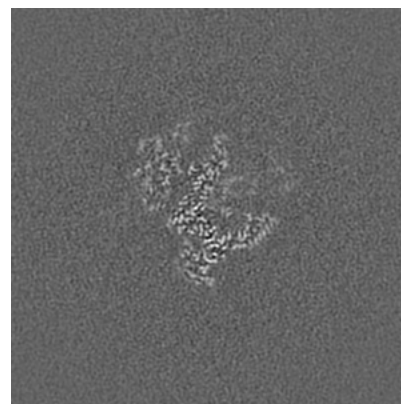
6.3.1 Primary map



X Index: 178



Y Index: 161



Z Index: 172

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 6.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

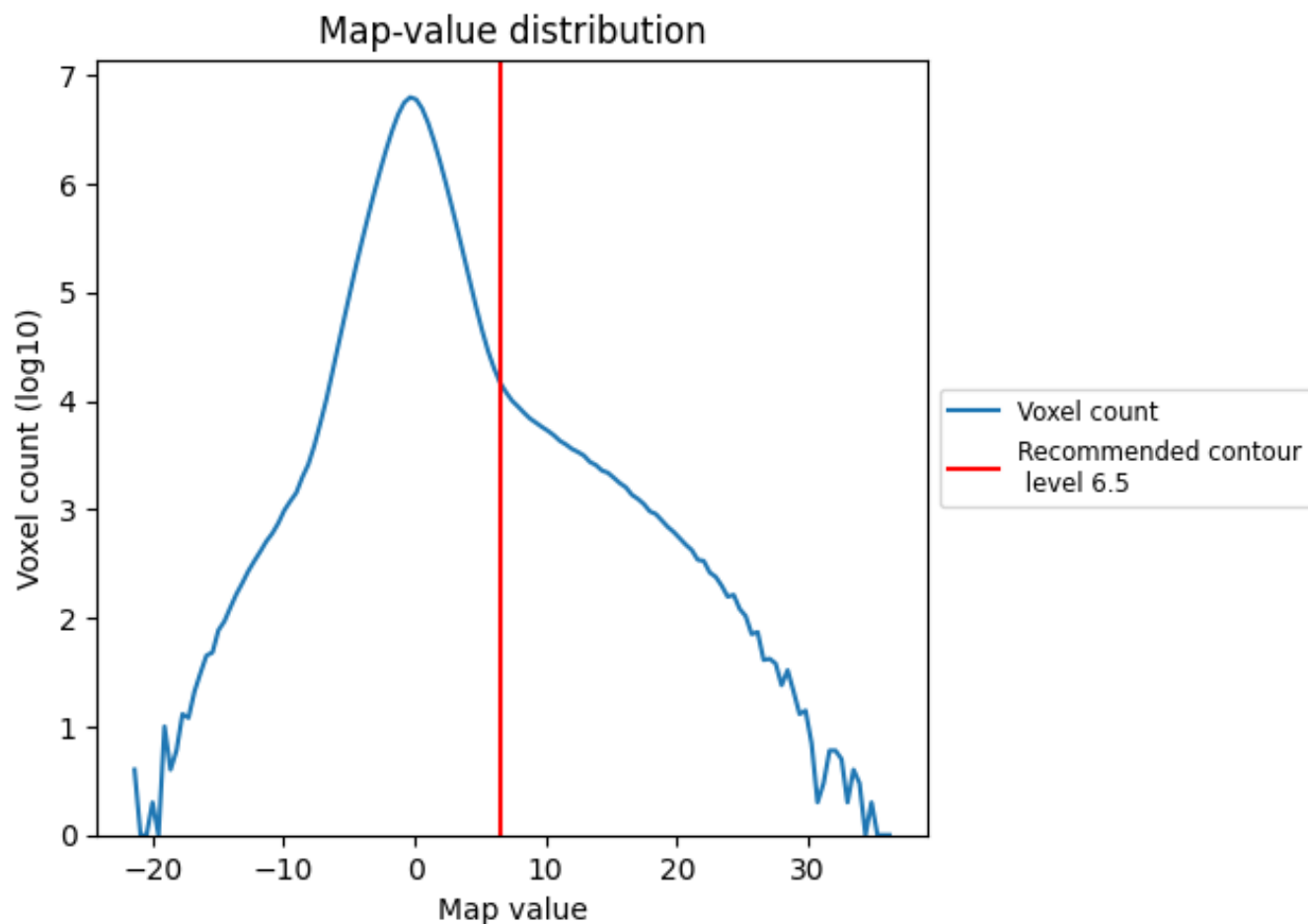
6.5 Mask visualisation

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

7 Map analysis [i](#)

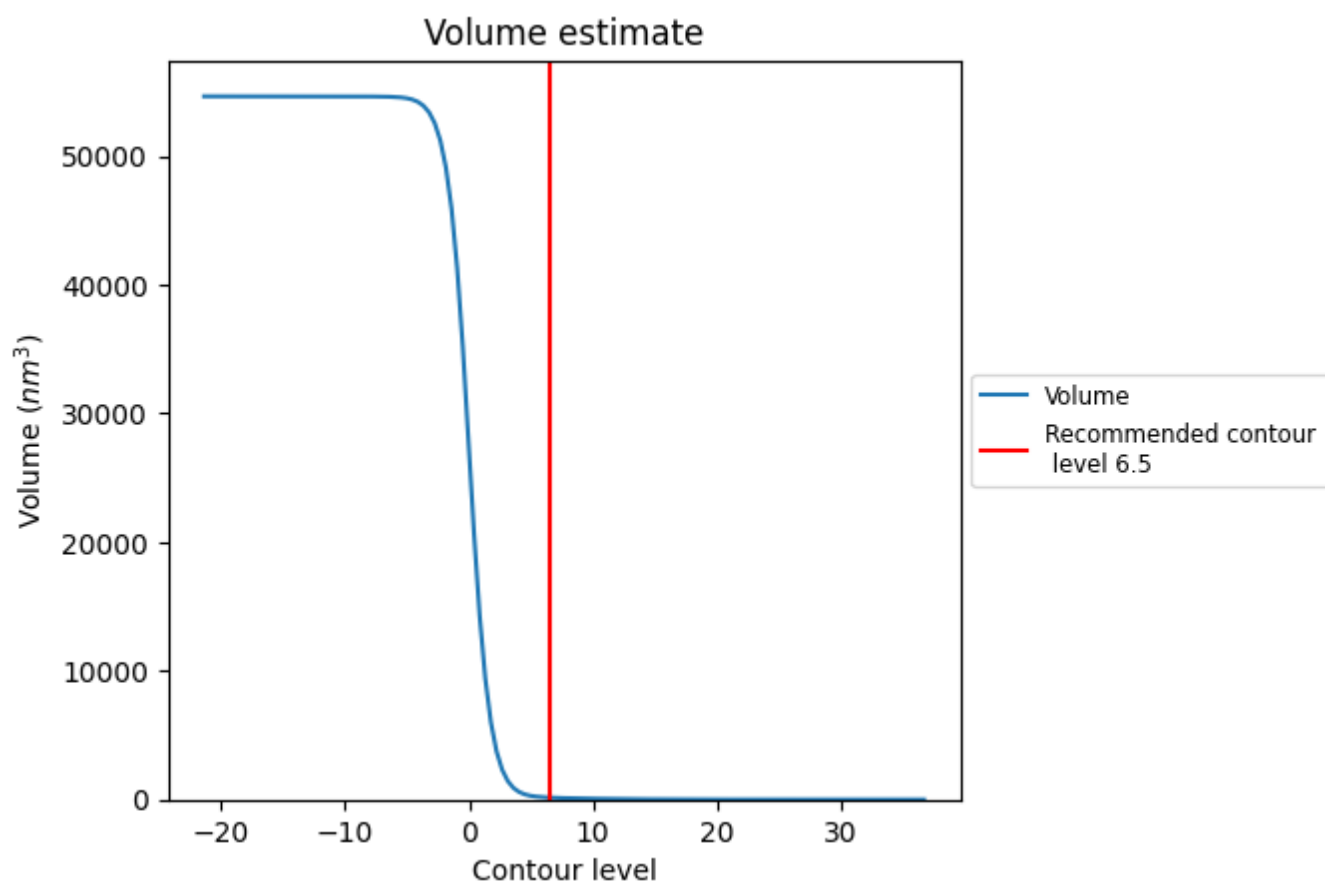
This section contains the results of statistical analysis of the map.

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.

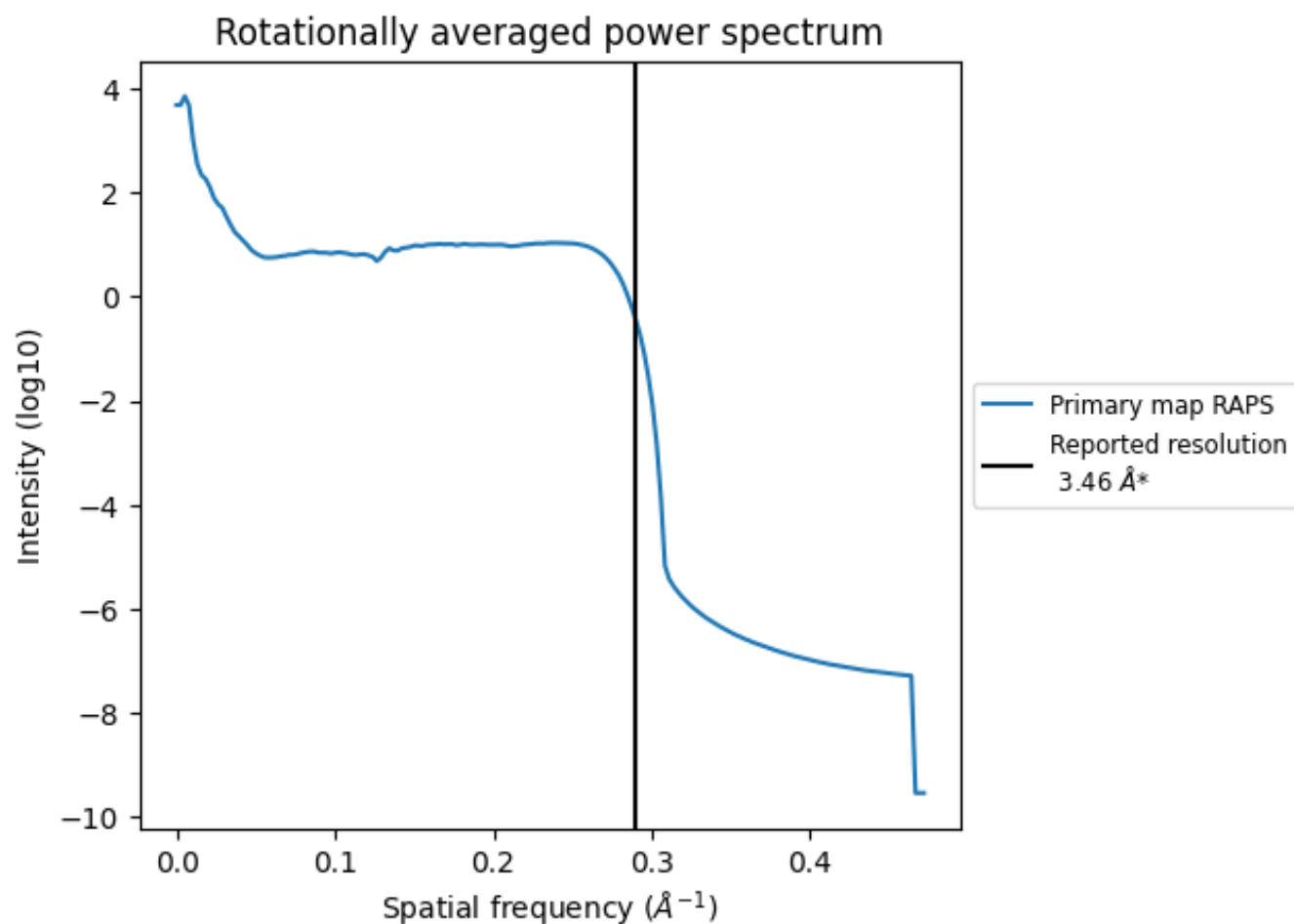
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 153 nm³; this corresponds to an approximate mass of 138 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 ⓘ

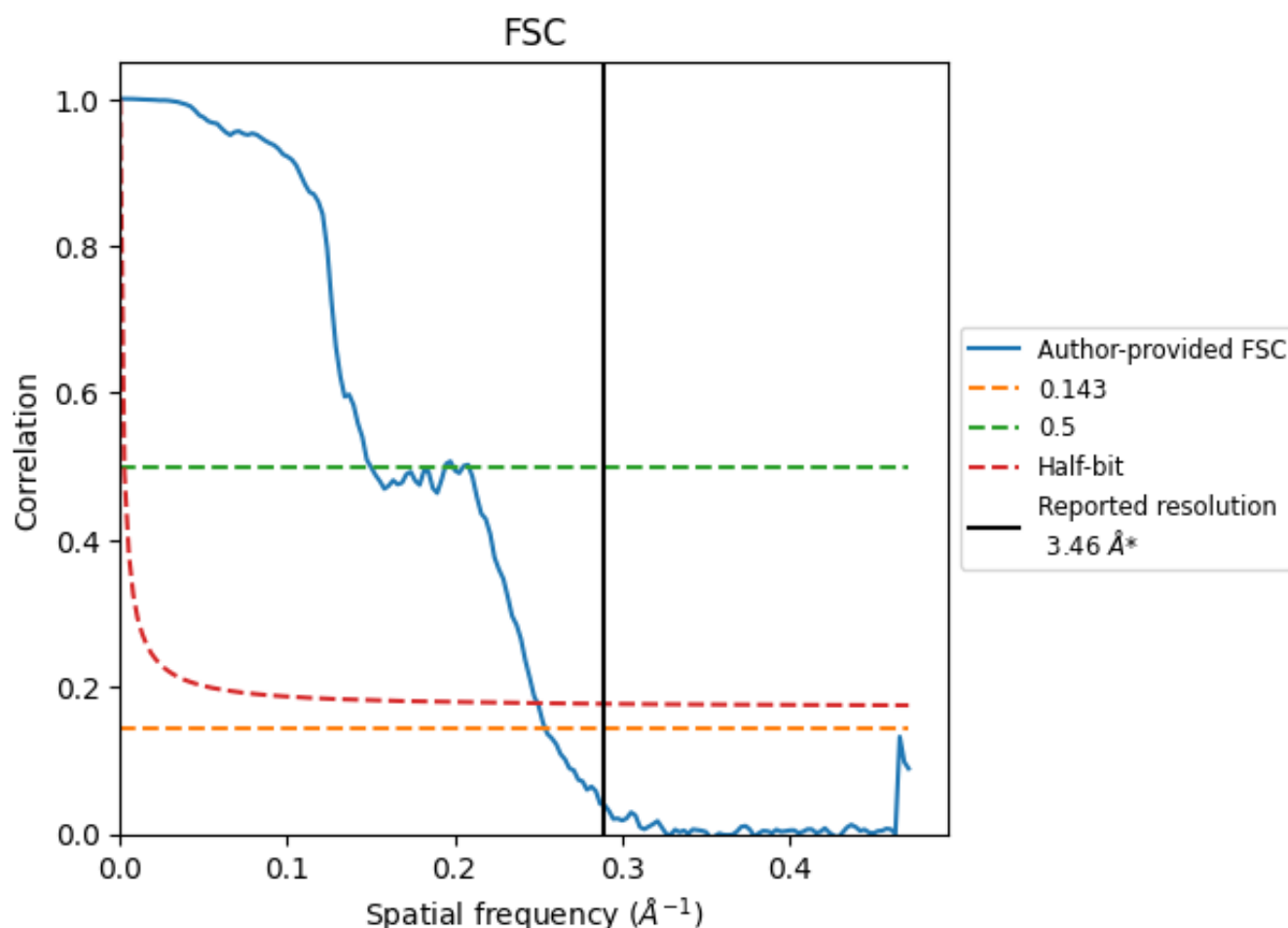


*Reported resolution corresponds to spatial frequency of 0.289 Å⁻¹

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 0.289 Å⁻¹

8.2 Resolution estimates [i](#)

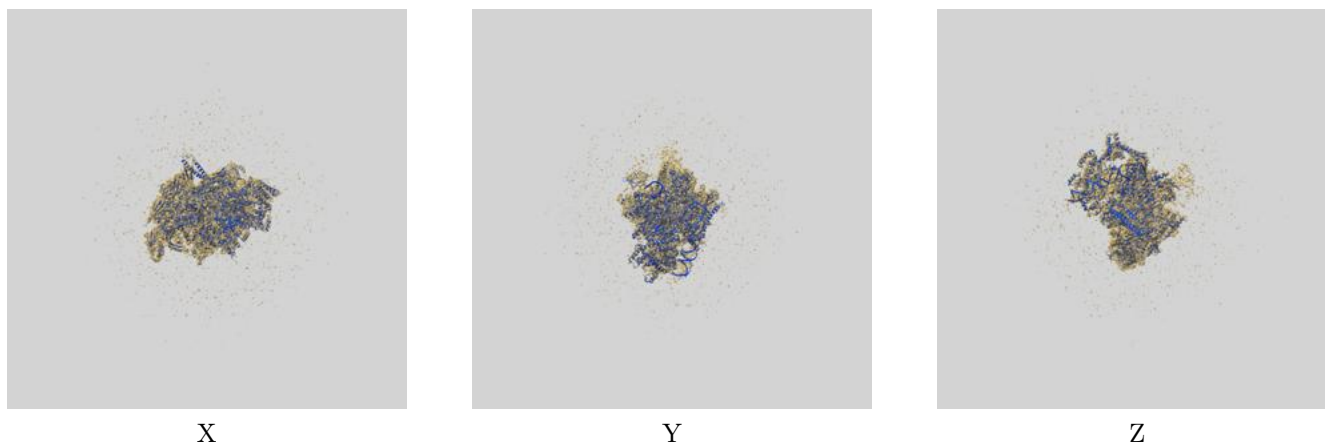
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.46	-	-
Author-provided FSC curve	3.93	6.67	4.00
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.93 differs from the reported value 3.46 by more than 10 %

9 Map-model fit [i](#)

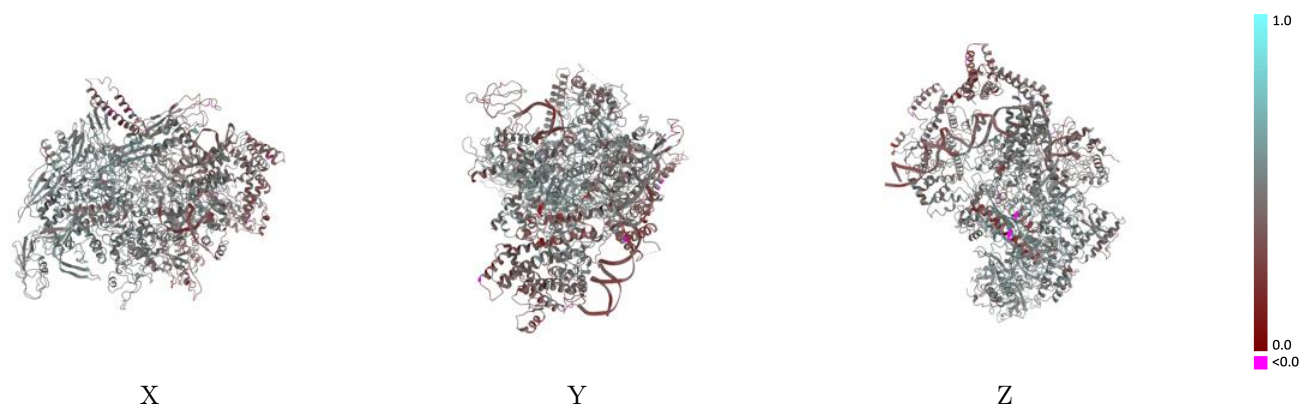
This section contains information regarding the fit between EMDB map EMD-21851 and PDB model 6WMR. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



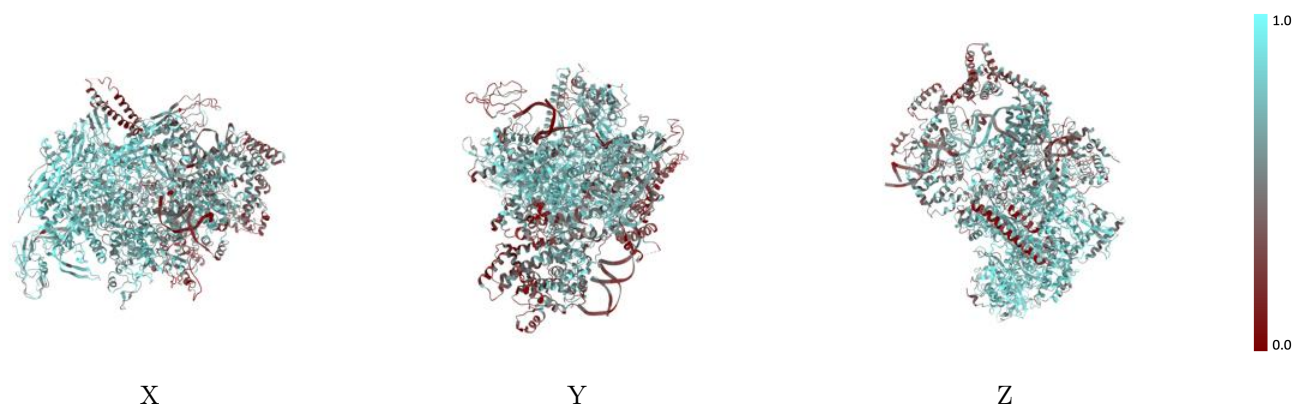
The images above show the 3D surface view of the map at the recommended contour level 6.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



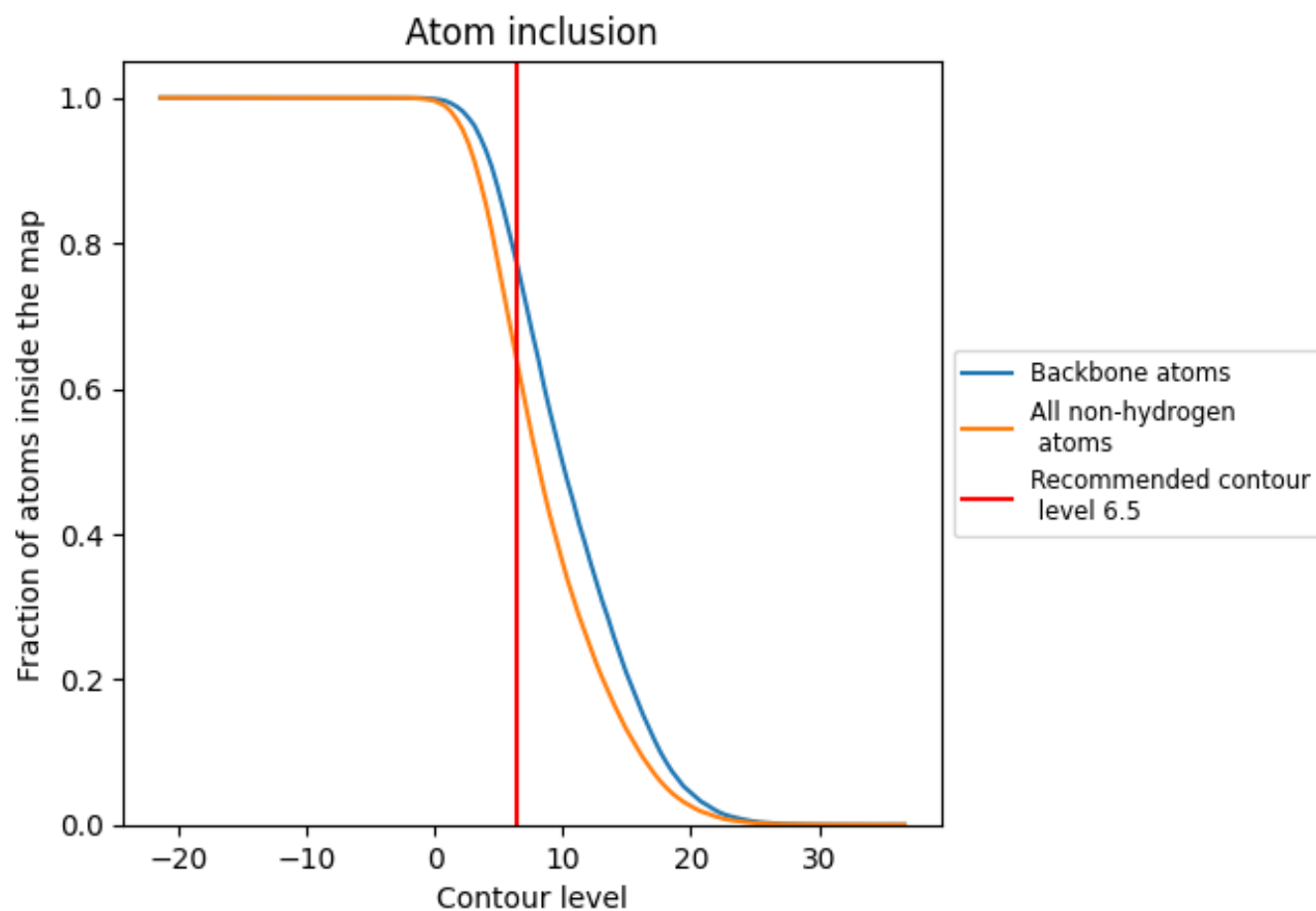
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (6.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 63% 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 (6.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6319	<div></div> 0.4660
A	<div></div> 0.7678	<div></div> 0.4990
B	<div></div> 0.7047	<div></div> 0.4850
C	<div></div> 0.6855	<div></div> 0.4920
D	<div></div> 0.7083	<div></div> 0.4960
E	<div></div> 0.5054	<div></div> 0.4550
G	<div></div> 0.4569	<div></div> 0.3820
H	<div></div> 0.4743	<div></div> 0.3540
J	<div></div> 0.3142	<div></div> 0.3640
M	<div></div> 0.4423	<div></div> 0.3980
S	<div></div> 0.4746	<div></div> 0.4170
X	<div></div> 0.1111	<div></div> 0.2730
Z	<div></div> 0.5008	<div></div> 0.4110

1.0

0.0

<0.0