wwPDB EM Validation Summary Report (i)

Sep 19, 2023 – 10:48 am BST

PDB ID	:	8B3F
EMDB ID	:	EMD-15826
Title	:	Pol II-CSB-CSA-DDB1-ELOF1
Authors	:	Kokic, G.; Cramer, P.
Deposited on	:	2022-09-16
Resolution	:	3.10 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 (i) 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 (i)) were used in the production of this report:

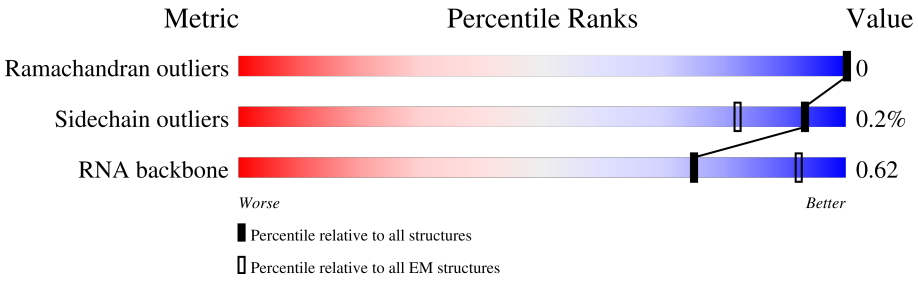
EMDB validation analysis	:	0.0.1.dev50
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 3.10 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.



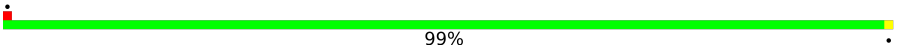
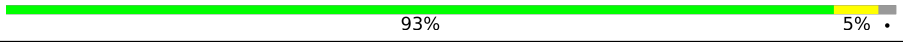
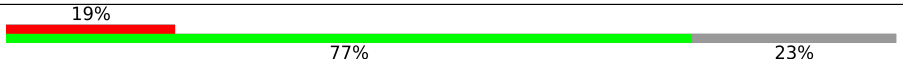
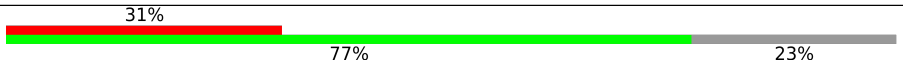
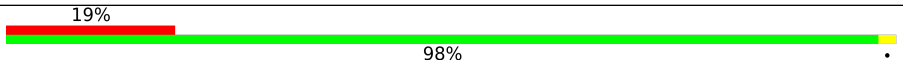
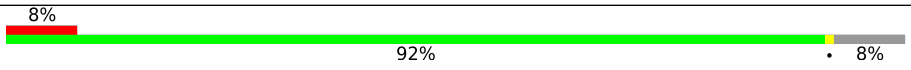
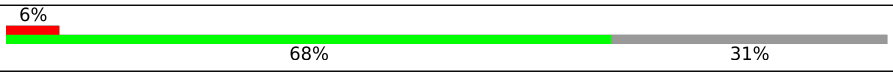
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 >=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 <=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	1970	68% · 28%
2	B	1167	92%
3	C	275	90% · · 5%
4	D	142	79% 85% 5% 10%
5	E	210	90% 10%
6	F	127	61% · · 35%
7	G	172	62% 95% · ·
8	H	150	97% · ·

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	I	125	
10	J	67	
11	K	117	
12	L	58	
13	M	83	
14	N	52	
15	P	10	
16	T	52	
17	a	396	
18	b	1496	
19	d	1140	

2 Entry composition (i)

There are 21 unique types of molecules in this entry. The entry contains 92036 atoms, of which 45119 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.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A	1409	22460	7022	11299	1998	2070	71	0	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	TYR	deletion	UNP A0A7M4DUC2
A	?	-	SER	deletion	UNP A0A7M4DUC2
A	?	-	PRO	deletion	UNP A0A7M4DUC2
A	?	-	THR	deletion	UNP A0A7M4DUC2
A	?	-	SER	deletion	UNP A0A7M4DUC2
A	?	-	PRO	deletion	UNP A0A7M4DUC2
A	?	-	SER	deletion	UNP A0A7M4DUC2
A	?	-	TYR	deletion	UNP A0A7M4DUC2
A	?	-	SER	deletion	UNP A0A7M4DUC2
A	?	-	PRO	deletion	UNP A0A7M4DUC2
A	?	-	THR	deletion	UNP A0A7M4DUC2
A	?	-	SER	deletion	UNP A0A7M4DUC2
A	?	-	PRO	deletion	UNP A0A7M4DUC2
A	?	-	SER	deletion	UNP A0A7M4DUC2

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

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
2	B	1130	18131	5725	9083	1591	1668	64	0	0

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	C	260	4120	1309	2031	359	415	6	0	0

- Molecule 4 is a protein called RNA polymerase II subunit D.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	128	Total	C	H	N	O	S	0	0
			1985	636	972	172	201	4		

- Molecule 5 is a protein called DNA-directed RNA polymerase II subunit E.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	209	Total	C	H	N	O	S	0	0
			3457	1089	1737	300	323	8		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	82	Total	C	H	N	O	S	0	0
			1341	418	684	113	121	5		

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	171	Total	C	H	N	O	S	0	0
			2665	867	1331	216	243	8		

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	H	148	Total	C	H	N	O	S	0	0
			2333	750	1147	194	237	5		

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	I	117	Total	C	H	N	O	S	0	0
			1827	587	878	169	182	11		

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	J	67	Total	C	H	N	O	S	0	0
			1086	345	553	90	92	6		

- Molecule 11 is a protein called RNA_pol_L_2 domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	K	115	Total	C	H	N	O	S	0	0
			1862	593	942	152	173	2		

- Molecule 12 is a protein called RNA polymerase II subunit K.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	L	46	Total	C	H	N	O	S	0	0
			781	241	393	75	66	6		

- Molecule 13 is a protein called Transcription elongation factor 1 homolog.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	M	64	Total	C	H	N	O	S	0	0
			968	312	463	81	105	7		

- Molecule 14 is a DNA chain called NTS.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	N	40	Total	C	H	N	O	P	0	0
			913	393	84	162	234	40		

- Molecule 15 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	P	10	Total	C	H	N	O	P	0	0
			330	98	110	45	67	10		

- Molecule 16 is a DNA chain called TS.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	T	52	Total	C	H	N	O	P	0	0
			1078	476	87	160	303	52		

- Molecule 17 is a protein called DNA excision repair protein ERCC-8.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	a	365	Total	C	H	N	O	S	0	0
			5624	1775	2775	507	548	19		

- Molecule 18 is a protein called DNA excision repair protein ERCC-6.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	b	534	Total	C	H	N	O	S	0	0
			8744	2803	4390	761	769	21		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	-2	SER	-	expression tag	UNP Q03468
b	-1	ASN	-	expression tag	UNP Q03468
b	0	ALA	-	expression tag	UNP Q03468

- Molecule 19 is a protein called DNA damage-binding protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	d	781	Total	C	H	N	O	S	0	0
			12321	3916	6160	1038	1173	34		

- Molecule 20 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
20	A	2	Total	Zn	0
			2	2	
20	B	1	Total	Zn	0
			1	1	
20	C	1	Total	Zn	0
			1	1	
20	I	2	Total	Zn	0
			2	2	
20	J	1	Total	Zn	0
			1	1	
20	L	1	Total	Zn	0
			1	1	
20	M	1	Total	Zn	0
			1	1	

- Molecule 21 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

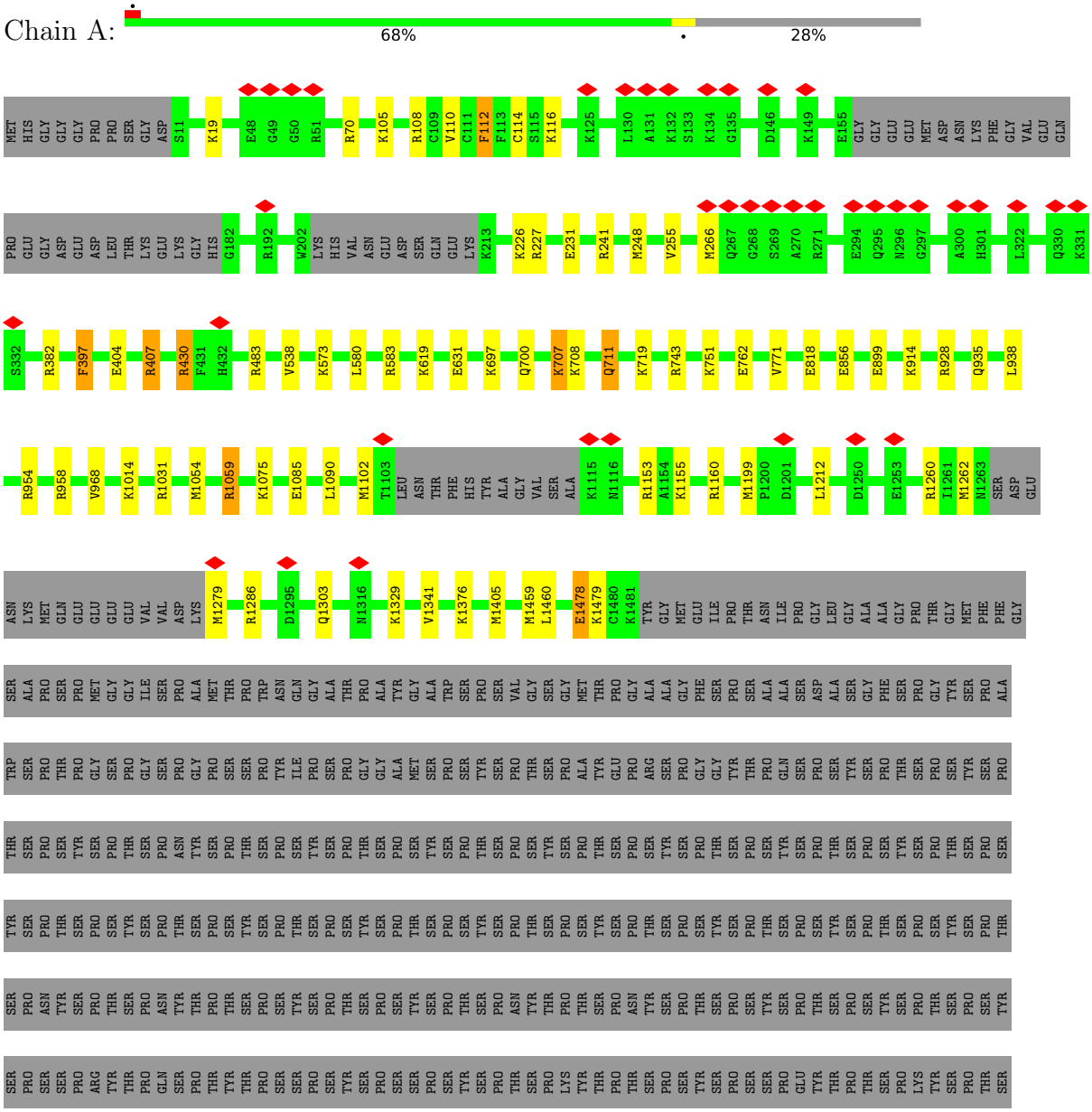
Mol	Chain	Residues	Atoms		AltConf
21	A	1	Total	Mg	0
			1	1	

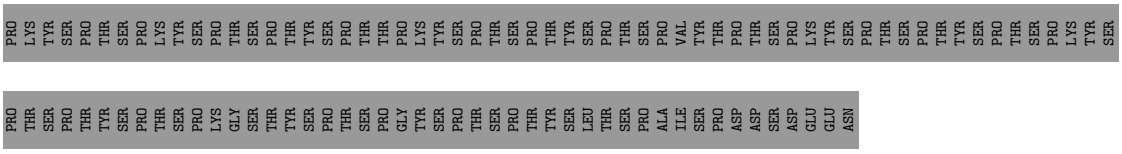
3 Residue-property plots (i)

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

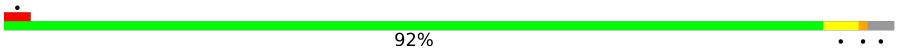
Chain A:

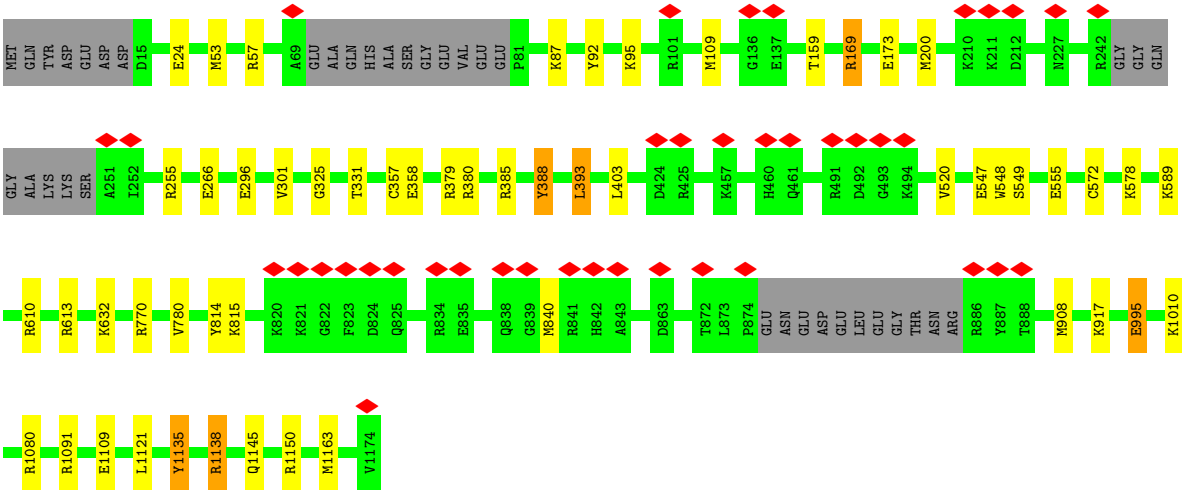




• Molecule 2: DNA-directed RNA polymerase subunit beta

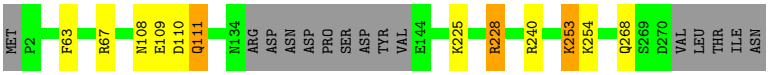
Chain B:





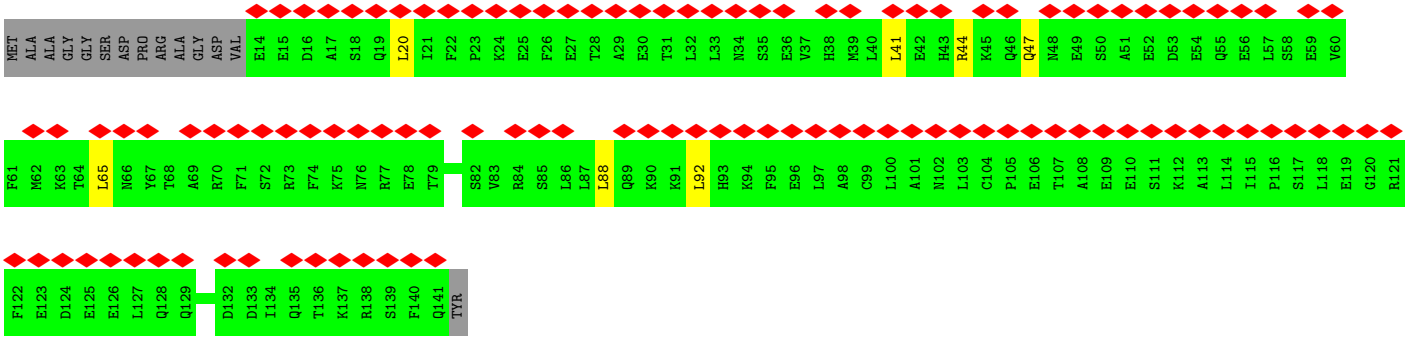
• Molecule 3: DNA-directed RNA polymerase II subunit RPB3

Chain C:



• Molecule 4: RNA polymerase II subunit D

Chain D:

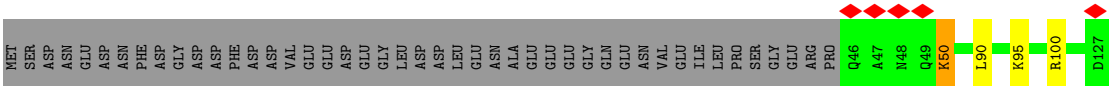


• Molecule 5: DNA-directed RNA polymerase II subunit E

Chain E:

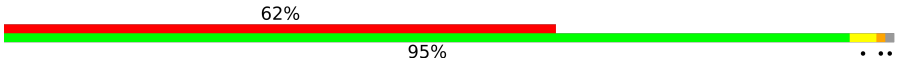
• Molecule 6: DNA-directed RNA polymerase II subunit F

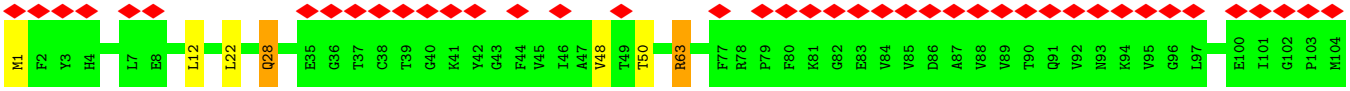
Chain F:

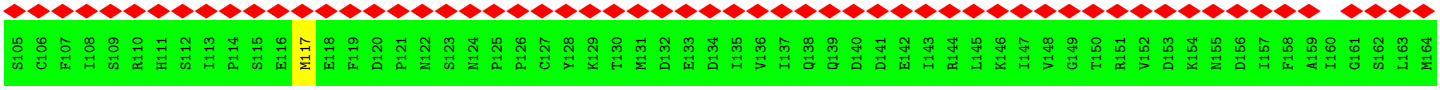


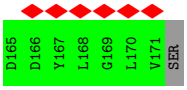
• Molecule 7: DNA-directed RNA polymerase II subunit RPB7

Chain G:



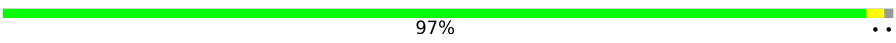






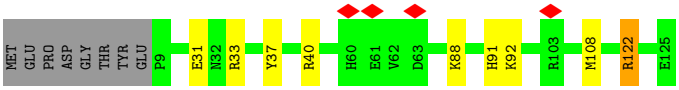
• Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain H:



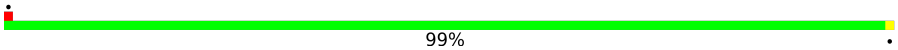
• Molecule 9: DNA-directed RNA polymerase II subunit RPB9

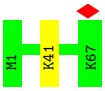
Chain I:



• Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5

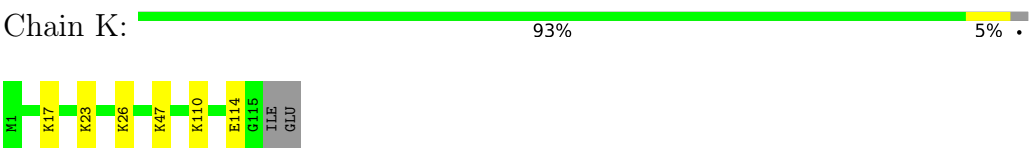
Chain J:





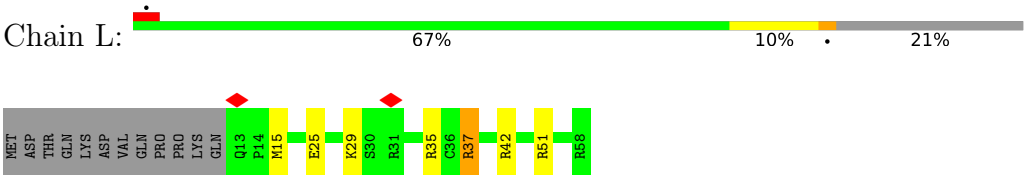
• Molecule 11: RNA_pol_L_2 domain-containing protein

Chain K:



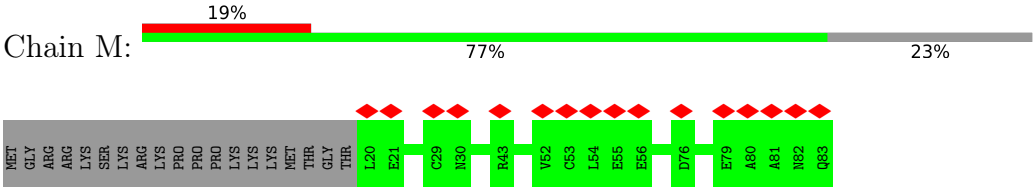
• Molecule 12: RNA polymerase II subunit K

Chain L:



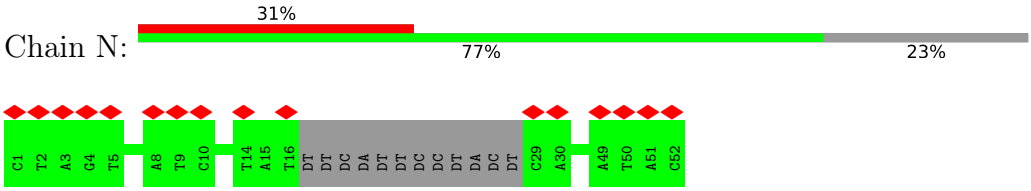
• Molecule 13: Transcription elongation factor 1 homolog

Chain M:



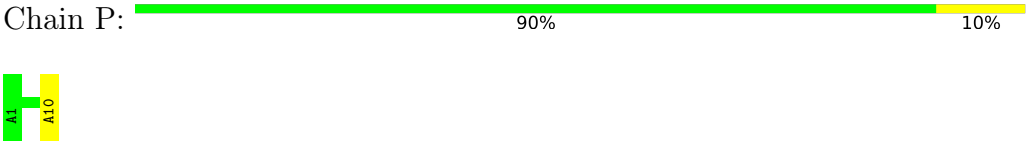
• Molecule 14: NTS

Chain N:



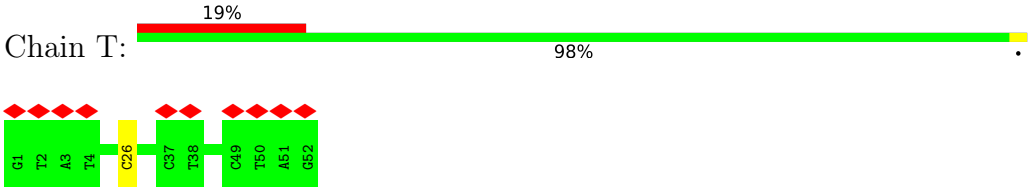
• Molecule 15: RNA

Chain P:



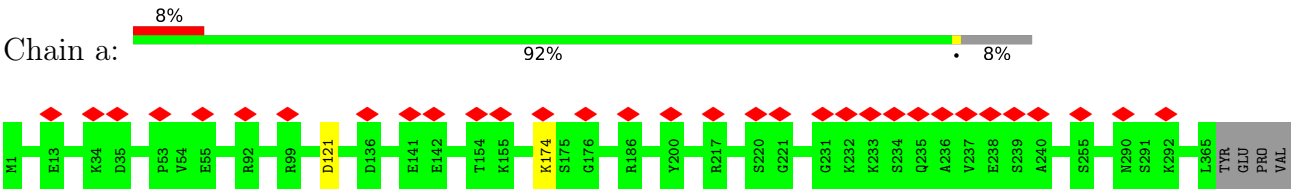
• Molecule 16: TS

Chain T:



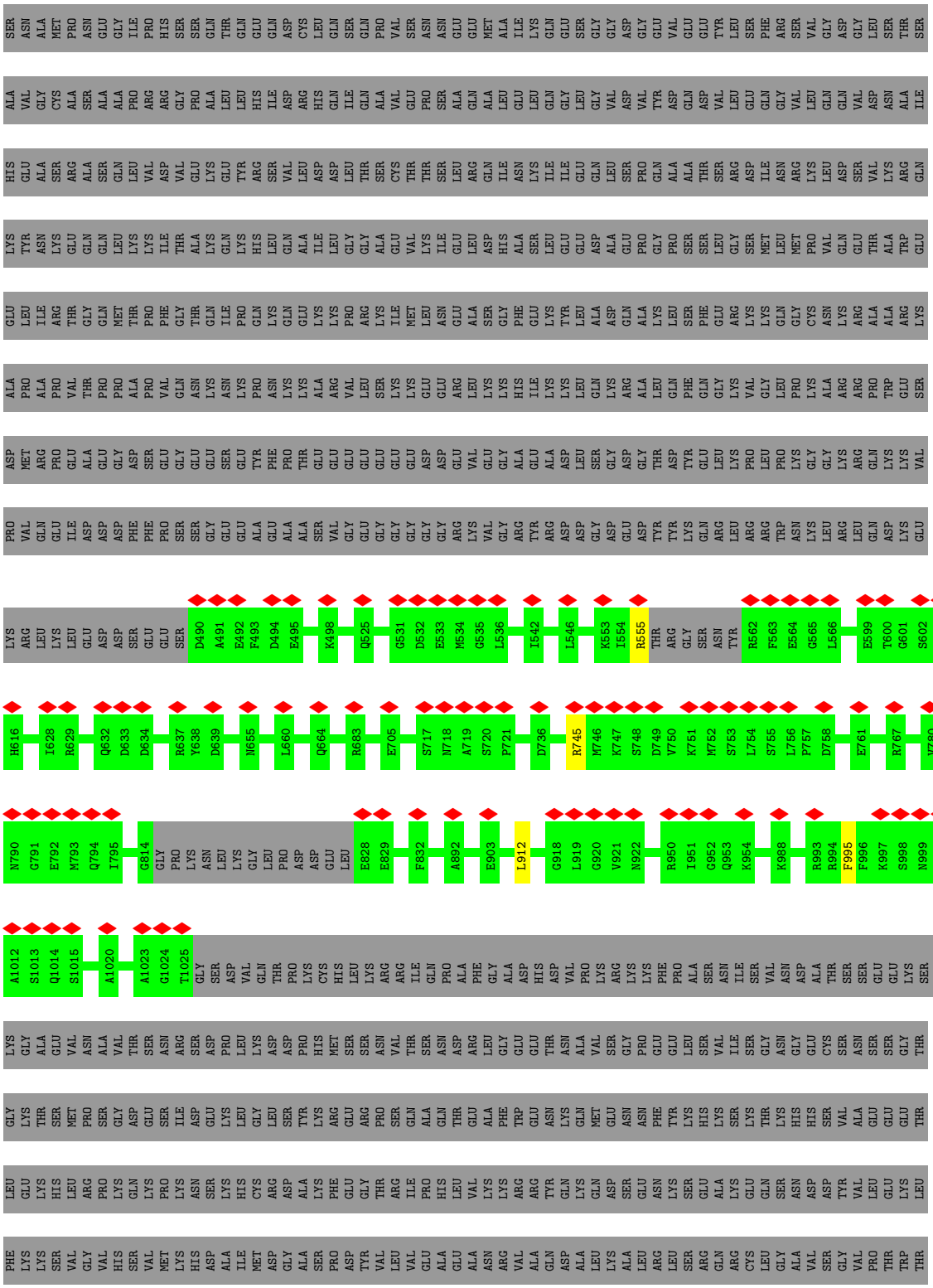
• Molecule 17: DNA excision repair protein ERCC-8

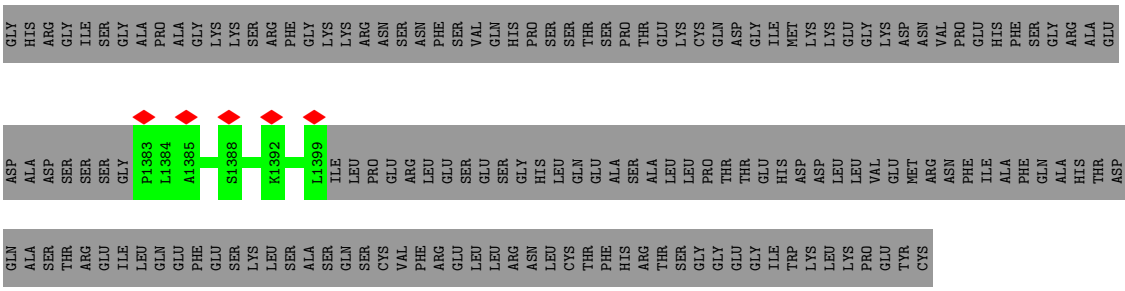
Chain a:



• Molecule 18: DNA excision repair protein ERCC-6

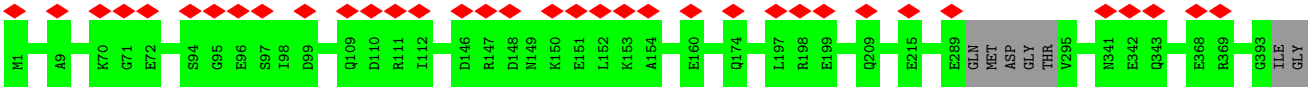
Chain b:

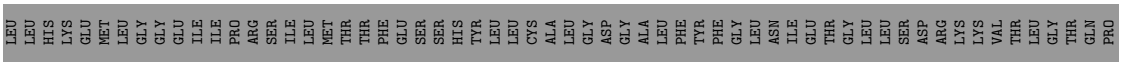


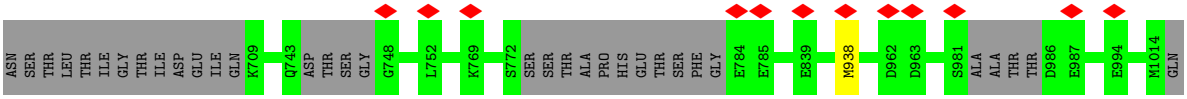


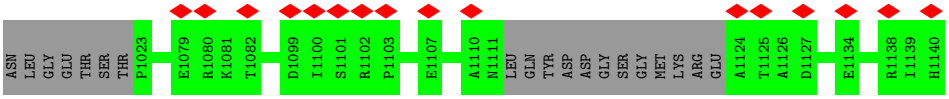
• Molecule 19: DNA damage-binding protein 1

Chain d:









4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	220655	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 ($e^-/Å^2$)	42	Depositor
Minimum defocus (nm)	140	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.181	Depositor
Minimum map value	-0.112	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.00762	Depositor
Map size (Å)	398.99997, 398.99997, 398.99997	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	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	A	0.57	22/11364 (0.2%)	1.08	127/15342 (0.8%)
2	B	0.59	18/9229 (0.2%)	0.90	70/12458 (0.6%)
3	C	0.60	4/2132 (0.2%)	0.99	19/2896 (0.7%)
4	D	0.62	0/1027	1.45	19/1384 (1.4%)
5	E	0.76	9/1751 (0.5%)	1.18	27/2366 (1.1%)
6	F	0.51	0/667	1.00	8/901 (0.9%)
7	G	0.57	1/1365 (0.1%)	1.26	18/1853 (1.0%)
8	H	0.48	1/1207 (0.1%)	0.81	6/1628 (0.4%)
9	I	0.63	3/972 (0.3%)	1.03	12/1316 (0.9%)
10	J	0.47	0/542	0.96	3/730 (0.4%)
11	K	0.61	2/939 (0.2%)	1.04	11/1271 (0.9%)
12	L	0.91	3/394 (0.8%)	1.54	14/524 (2.7%)
13	M	0.30	0/515	0.46	0/700
14	N	0.54	0/932	0.85	0/1435
15	P	0.81	0/247	0.92	0/384
16	T	0.65	0/1102	0.97	1/1682 (0.1%)
17	a	0.29	0/2908	0.56	1/3939 (0.0%)
18	b	0.30	0/4458	0.55	0/6021
19	d	0.29	0/6268	0.54	0/8466
All	All	0.53	63/48019 (0.1%)	0.92	336/65296 (0.5%)

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
1	A	0	9
2	B	0	6
3	C	0	5
5	E	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
6	F	0	1
7	G	0	2
9	I	0	2
12	L	0	1
17	a	0	1
18	b	0	2
All	All	0	30

The worst 5 of 63 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	91	CYS	CB-SG	-9.74	1.65	1.82
1	A	771	VAL	CB-CG1	-8.79	1.34	1.52
2	B	301	VAL	CB-CG2	-8.74	1.34	1.52
5	E	39	GLU	CB-CG	-7.46	1.38	1.52
7	G	1	MET	CB-CG	-7.34	1.27	1.51

The worst 5 of 336 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1286	ARG	CG-CD-NE	23.33	160.79	111.80
4	D	41	LEU	CB-CG-CD1	22.81	149.78	111.00
1	A	958	ARG	CG-CD-NE	22.54	159.13	111.80
4	D	65	LEU	CB-CG-CD2	-19.10	78.53	111.00
1	A	266	MET	CA-CB-CG	18.50	144.74	113.30

There are no chirality outliers.

5 of 30 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	112	PHE	Sidechain
1	A	397	PHE	Sidechain
1	A	407	ARG	Sidechain
1	A	430	ARG	Sidechain
1	A	538	VAL	Peptide

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	1399/1970 (71%)	1348 (96%)	51 (4%)	0	100	100
2	B	1122/1167 (96%)	1072 (96%)	50 (4%)	0	100	100
3	C	256/275 (93%)	248 (97%)	8 (3%)	0	100	100
4	D	126/142 (89%)	117 (93%)	9 (7%)	0	100	100
5	E	207/210 (99%)	196 (95%)	11 (5%)	0	100	100
6	F	80/127 (63%)	75 (94%)	5 (6%)	0	100	100
7	G	169/172 (98%)	159 (94%)	10 (6%)	0	100	100
8	H	146/150 (97%)	141 (97%)	5 (3%)	0	100	100
9	I	115/125 (92%)	106 (92%)	9 (8%)	0	100	100
10	J	65/67 (97%)	64 (98%)	1 (2%)	0	100	100
11	K	113/117 (97%)	109 (96%)	4 (4%)	0	100	100
12	L	44/58 (76%)	40 (91%)	4 (9%)	0	100	100
13	M	62/83 (75%)	61 (98%)	1 (2%)	0	100	100
17	a	363/396 (92%)	343 (94%)	20 (6%)	0	100	100
18	b	526/1496 (35%)	507 (96%)	19 (4%)	0	100	100
19	d	765/1140 (67%)	730 (95%)	35 (5%)	0	100	100
All	All	5558/7695 (72%)	5316 (96%)	242 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	1241/1749 (71%)	1239 (100%)	2 (0%)	93 97
2	B	992/1021 (97%)	988 (100%)	4 (0%)	91 96
3	C	237/252 (94%)	237 (100%)	0	100 100
4	D	108/126 (86%)	108 (100%)	0	100 100
5	E	191/192 (100%)	191 (100%)	0	100 100
6	F	71/111 (64%)	71 (100%)	0	100 100
7	G	147/153 (96%)	147 (100%)	0	100 100
8	H	129/131 (98%)	129 (100%)	0	100 100
9	I	105/112 (94%)	105 (100%)	0	100 100
10	J	56/56 (100%)	56 (100%)	0	100 100
11	K	104/106 (98%)	103 (99%)	1 (1%)	76 90
12	L	43/55 (78%)	43 (100%)	0	100 100
13	M	59/76 (78%)	59 (100%)	0	100 100
17	a	320/348 (92%)	320 (100%)	0	100 100
18	b	476/1299 (37%)	474 (100%)	2 (0%)	91 96
19	d	685/999 (69%)	684 (100%)	1 (0%)	93 98
All	All	4964/6786 (73%)	4954 (100%)	10 (0%)	93 97

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

Mol	Chain	Res	Type
18	b	555	ARG
18	b	745	ARG
19	d	938	MET
2	B	393	LEU
2	B	1072	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	350	HIS
2	B	790	GLN
13	M	31	HIS
17	a	33	ASN

5.3.3 RNA

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

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
15	P	10	A

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 monosaccharides in this entry.

5.6 Ligand geometry

Of 10 ligands modelled in this entry, 10 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.

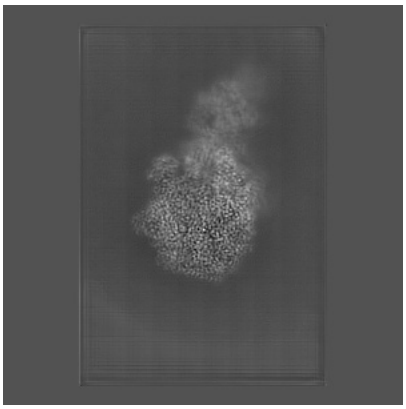
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-15826. These allow visual inspection of the internal detail of the map and identification of artifacts.

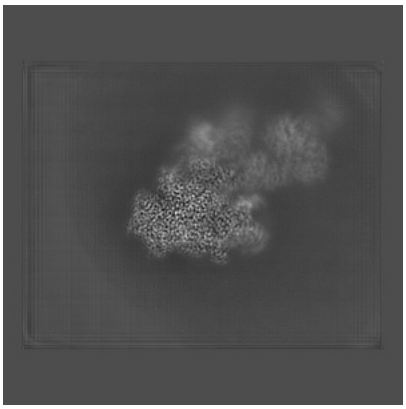
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

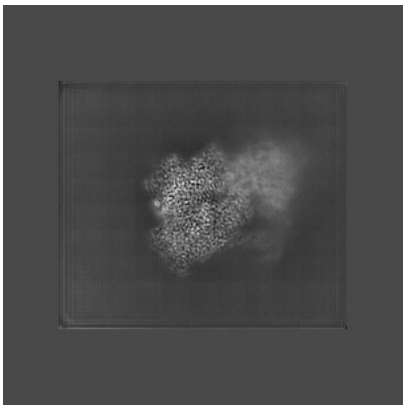
6.1.1 Primary map



X

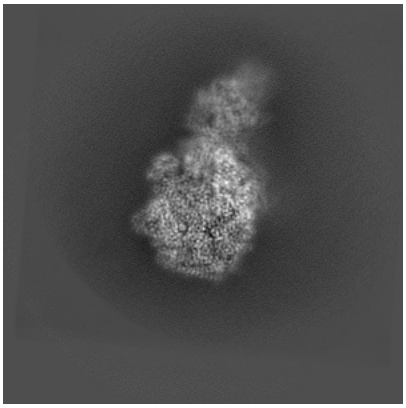


Y

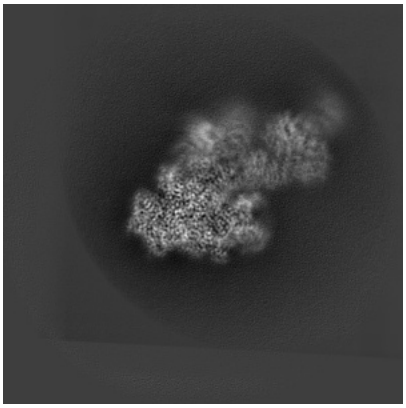


Z

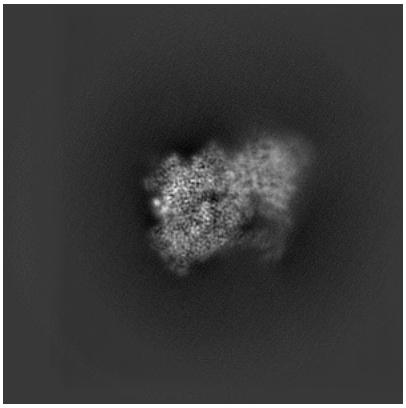
6.1.2 Raw map



X



Y

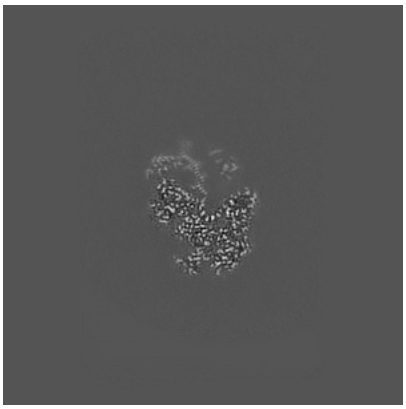


Z

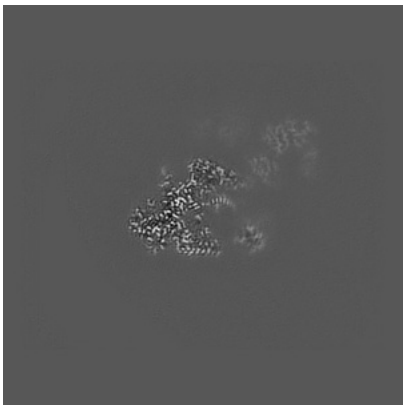
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

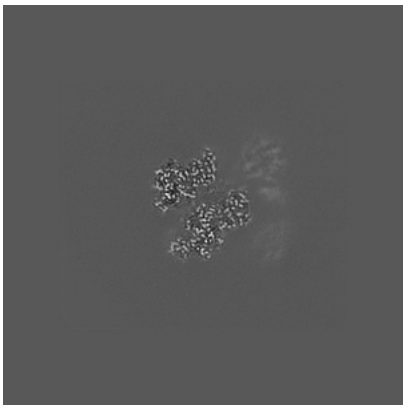
6.2.1 Primary map



X Index: 190

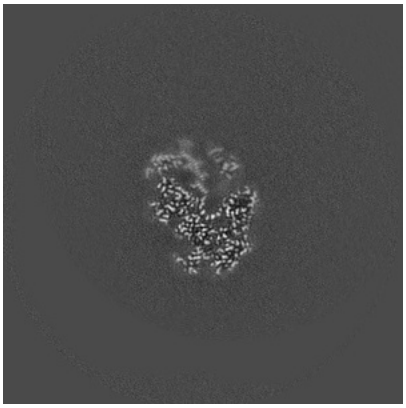


Y Index: 190

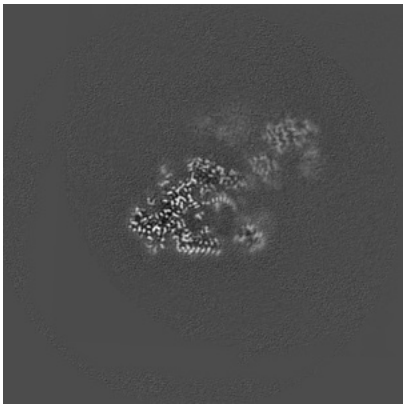


Z Index: 190

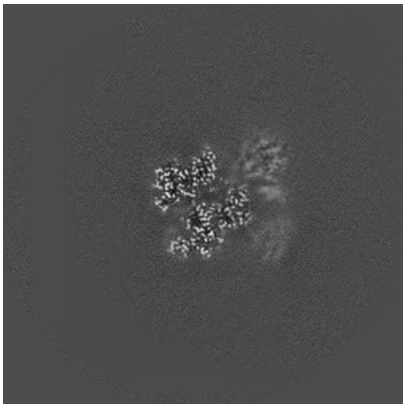
6.2.2 Raw map



X Index: 190



Y Index: 190

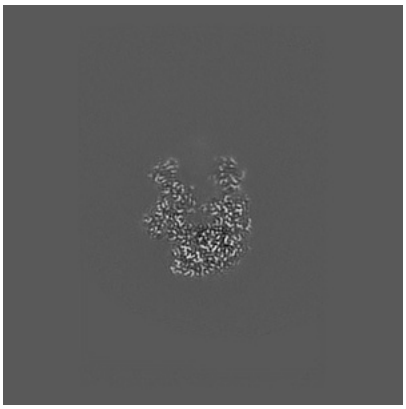


Z Index: 190

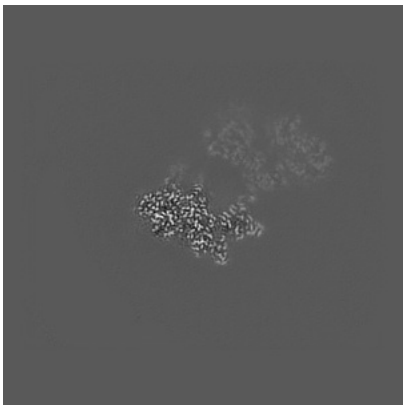
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

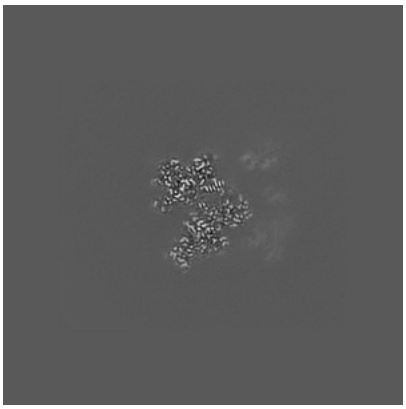
6.3.1 Primary map



X Index: 180

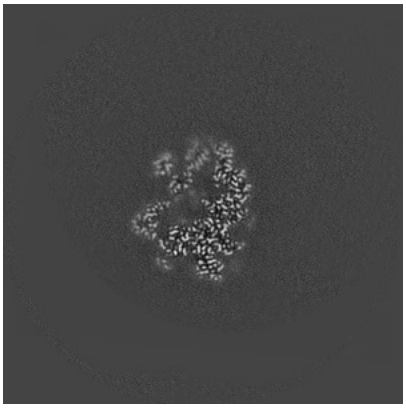


Y Index: 212

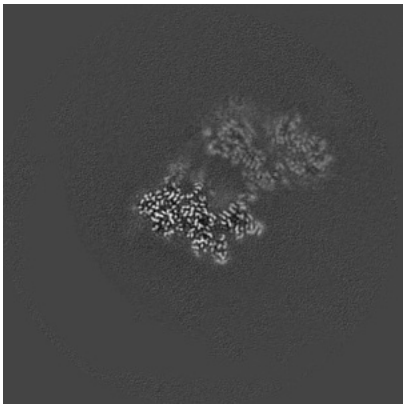


Z Index: 183

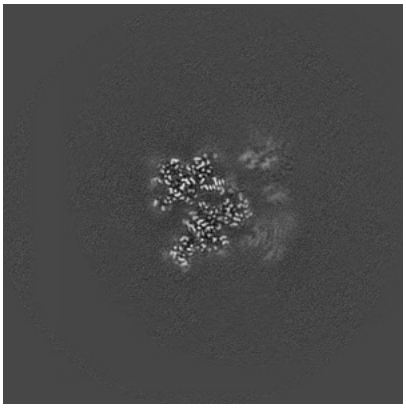
6.3.2 Raw map



X Index: 166



Y Index: 212

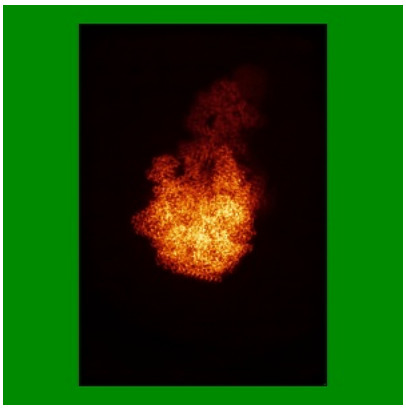


Z Index: 183

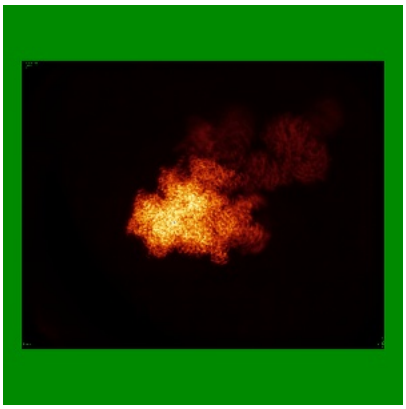
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

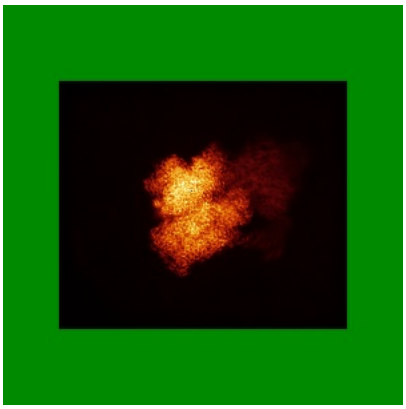
6.4.1 Primary map



X

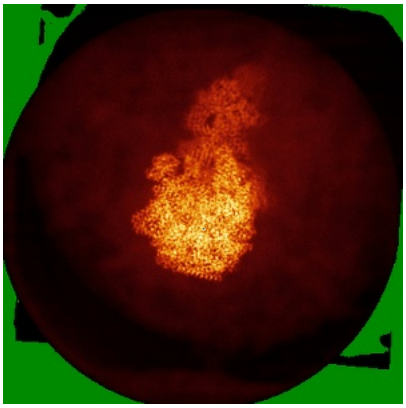


Y

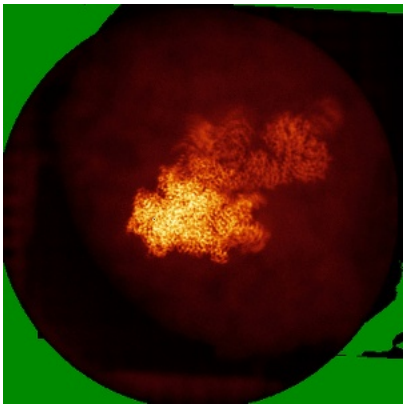


Z

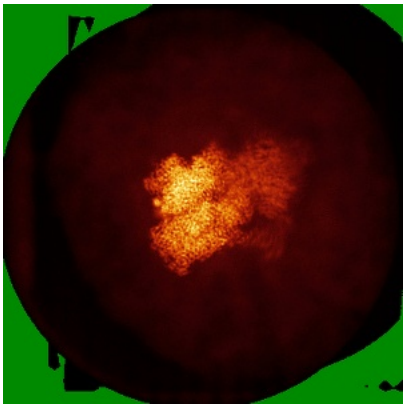
6.4.2 Raw map



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 (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.00762. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map

X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

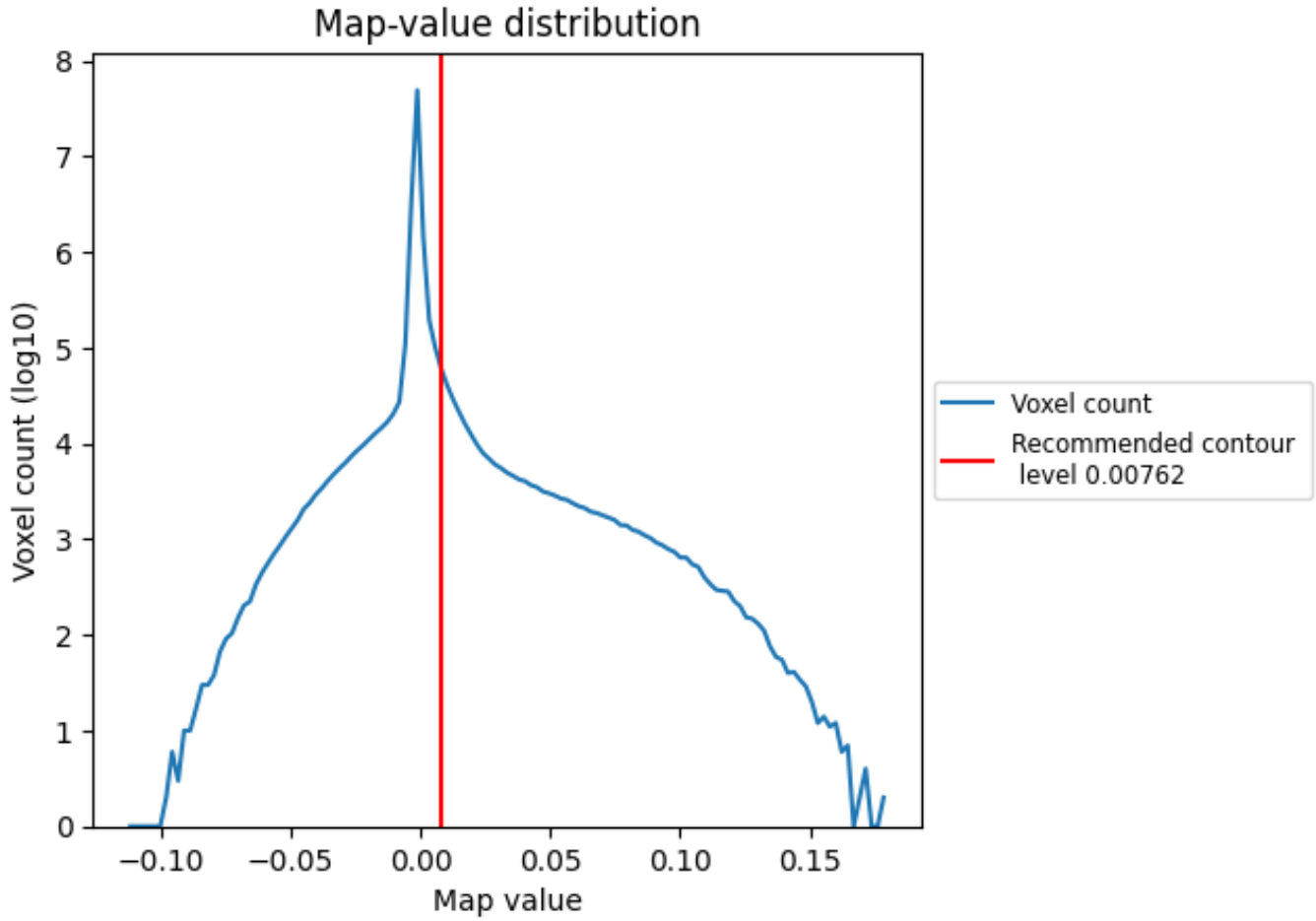
6.6 Mask visualisation (i)

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

7 Map analysis

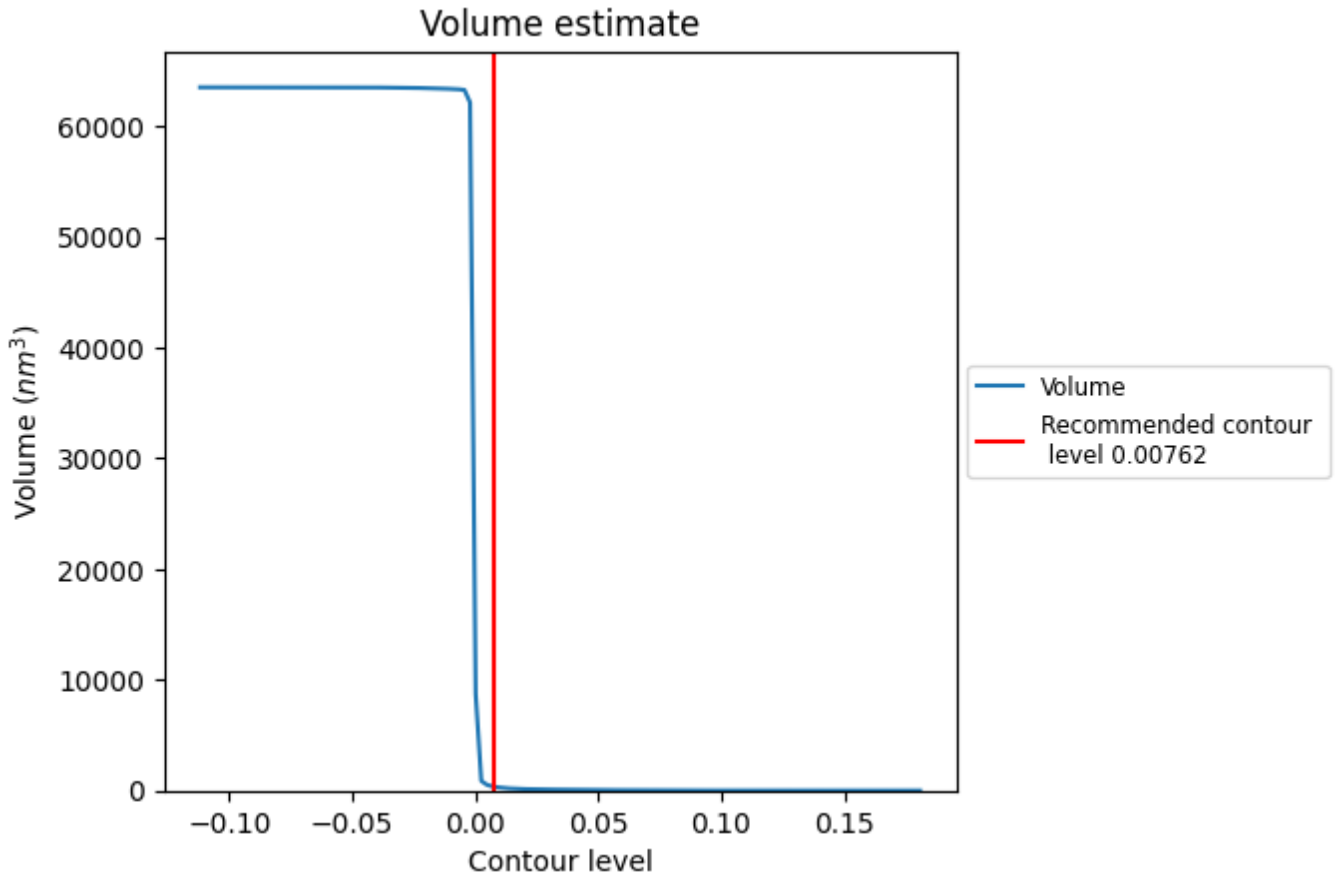
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

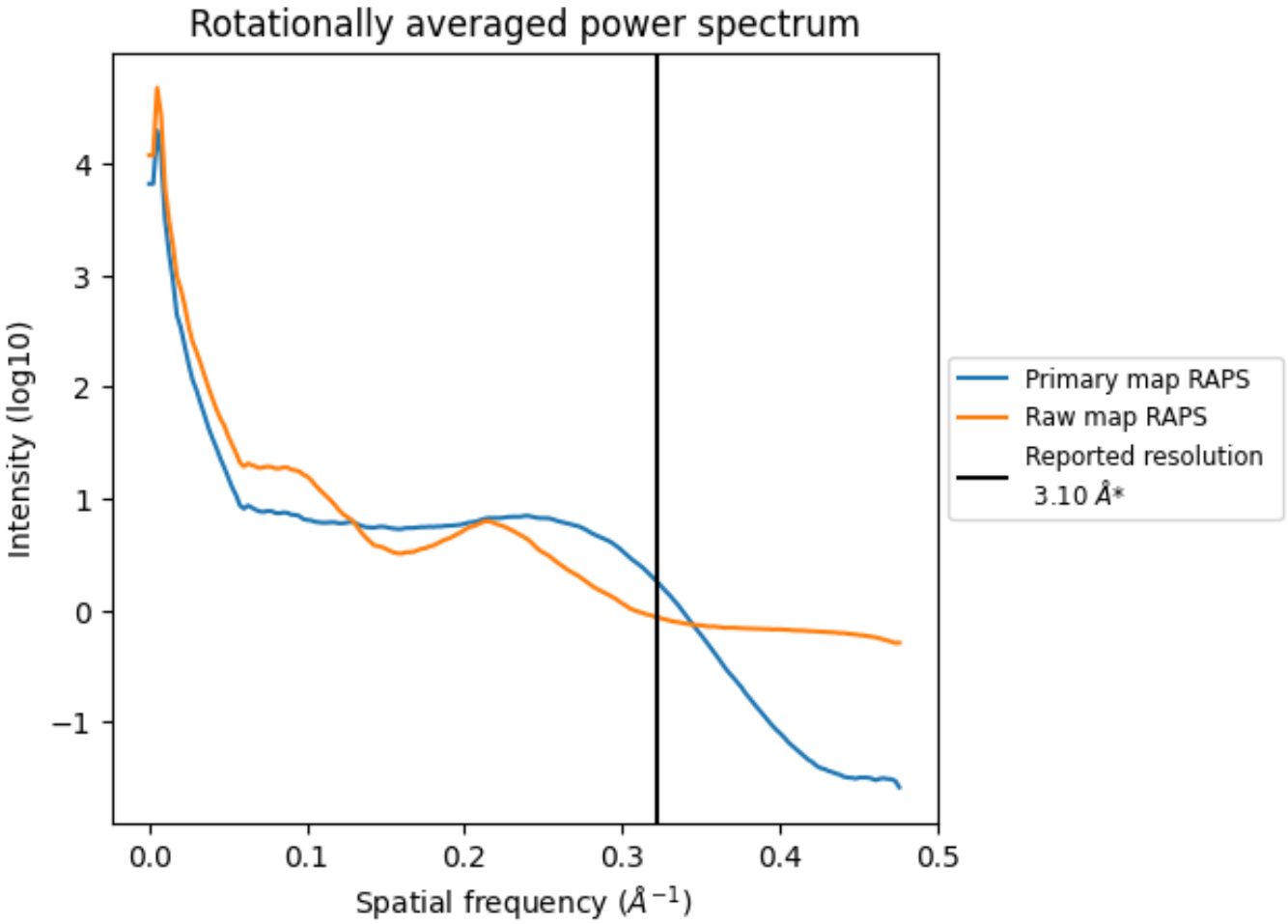
7.2 Volume estimate (i)



The volume at the recommended contour level is 348 nm^3; this corresponds to an approximate mass of 314 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

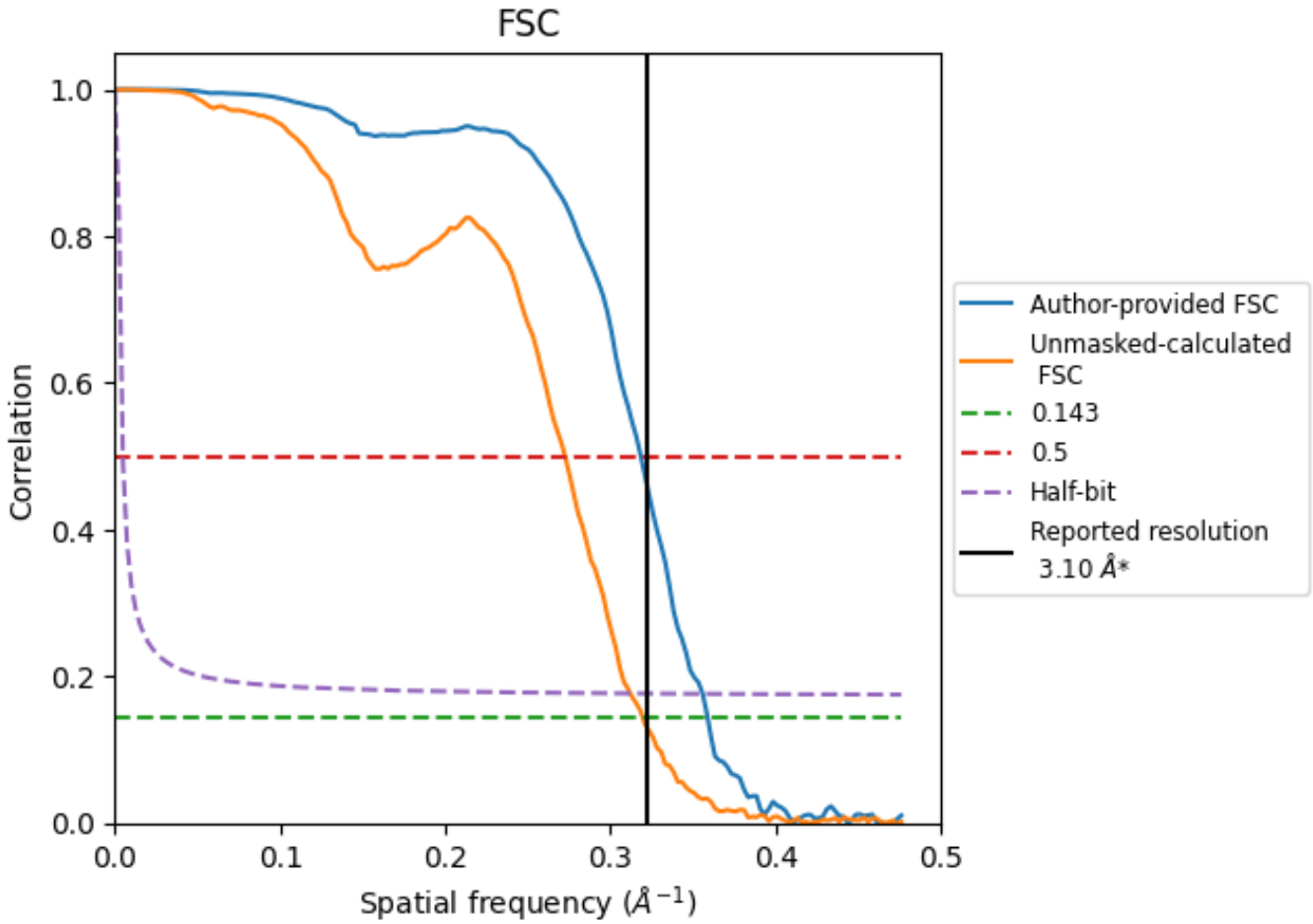


*Reported resolution corresponds to spatial frequency of 0.323 $Å^{-1}$

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.323 Å^{-1}

8.2 Resolution estimates (i)

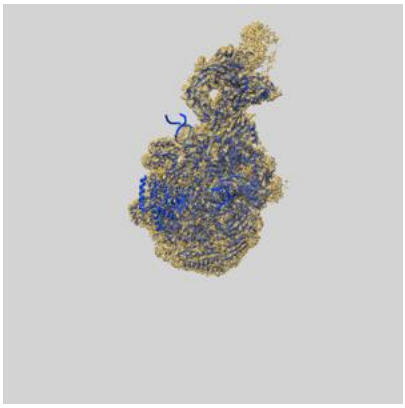
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	2.79	3.14	2.81
Unmasked-calculated*	3.13	3.67	3.20

*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 2.79 differs from the reported value 3.1 by more than 10 %

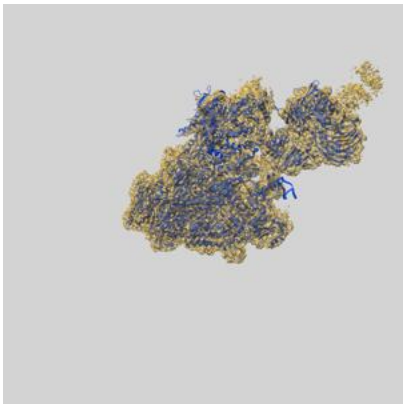
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-15826 and PDB model 8B3F. Per-residue inclusion information can be found in section 3 on page 8.

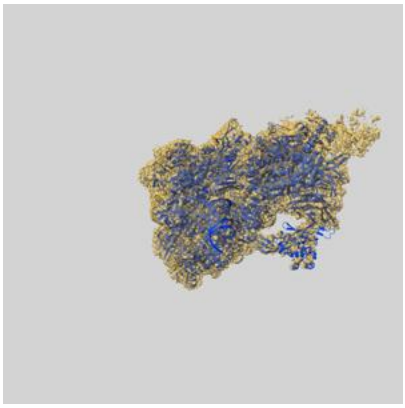
9.1 Map-model overlay



X



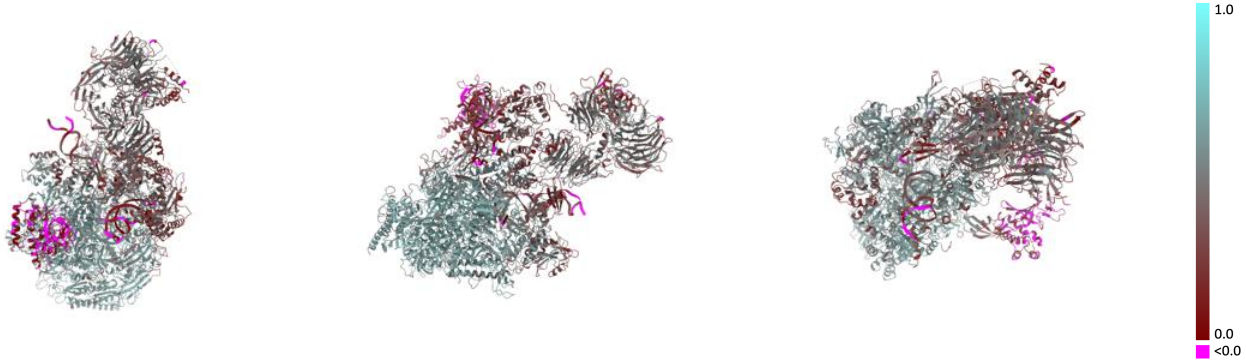
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.00762 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.

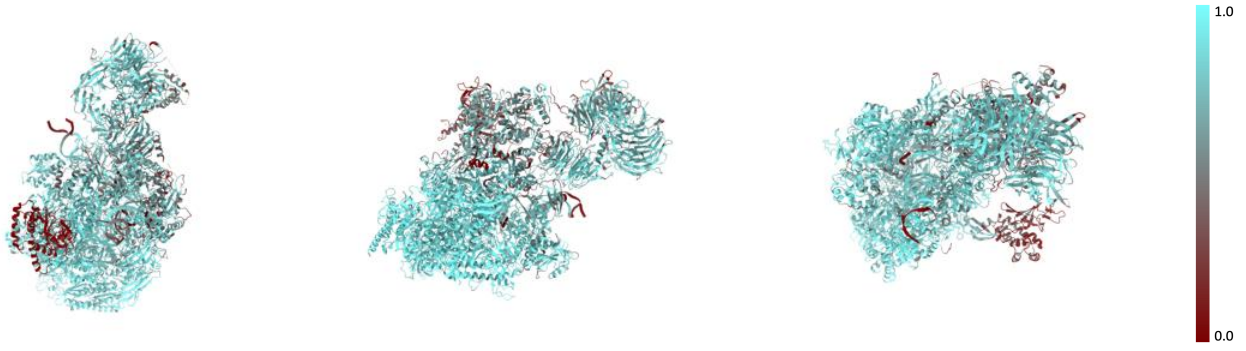
9.2 Q-score mapped to coordinate model



X Y Z

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.

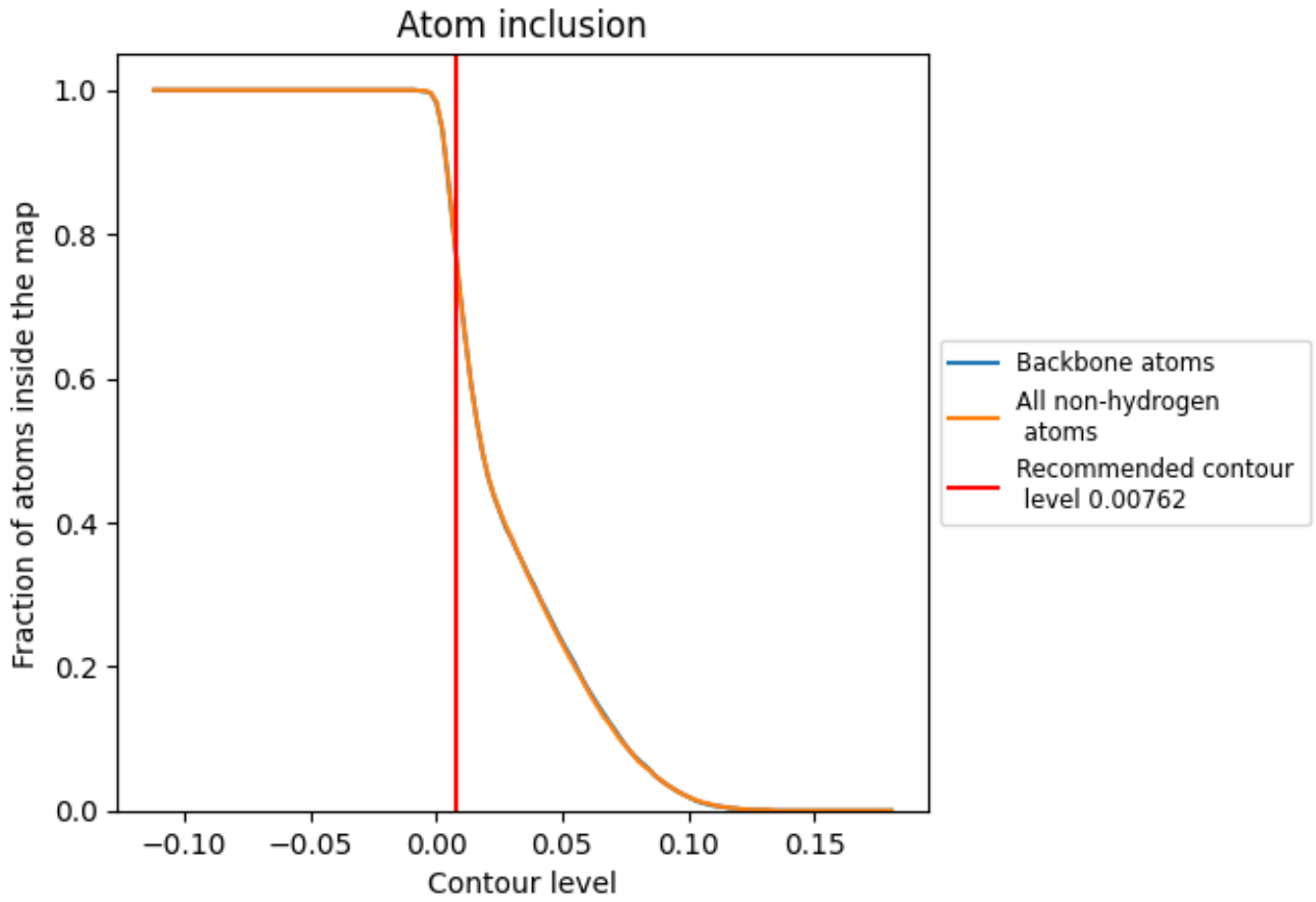
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.00762).

9.4 Atom inclusion (i)



At the recommended contour level, 78% of all backbone atoms, 78% 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 (0.00762) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7800	0.4560
A	0.8880	0.5410
B	0.8900	0.5450
C	0.9330	0.5850
D	0.1420	0.0370
E	0.9150	0.5250
F	0.8930	0.5620
G	0.3160	0.1480
H	0.9430	0.5770
I	0.8510	0.4610
J	0.9540	0.6050
K	0.9350	0.5880
L	0.8550	0.4770
M	0.5730	0.2010
N	0.5370	0.1810
P	0.9320	0.5860
T	0.7230	0.2880
a	0.7340	0.4200
b	0.5830	0.3010
d	0.7170	0.3830