



## wwPDB EM Validation Summary Report ⓘ

Jul 7, 2024 – 05:02 pm BST

PDB ID : 7OZN  
EMDB ID : EMD-13129  
Title : RNA Polymerase II dimer (Class 1)  
Authors : Aibara, S.; Dienemann, C.; Cramer, P.  
Deposited on : 2021-06-28  
Resolution : 3.50 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.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

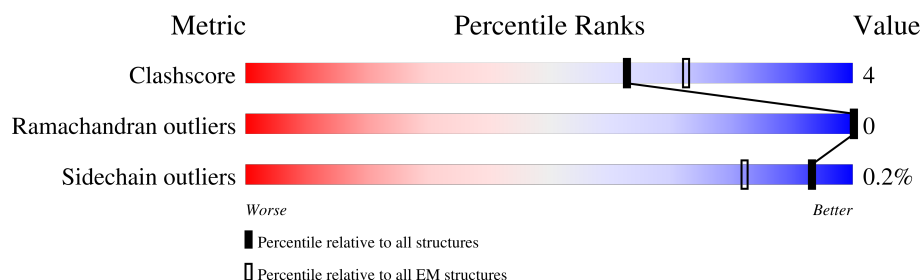
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



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

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	1970	<div> <div>5%</div> <div>46%</div> <div>6%</div> <div>48%</div> </div>
1	M	1970	<div> <div>5%</div> <div>46%</div> <div>6%</div> <div>48%</div> </div>
2	B	1174	<div> <div>9%</div> <div>77%</div> <div>10%</div> <div>13%</div> </div>
2	N	1174	<div> <div>10%</div> <div>77%</div> <div>10%</div> <div>13%</div> </div>
3	C	275	<div> <div>7%</div> <div>80%</div> <div>13%</div> <div>7%</div> </div>
3	O	275	<div> <div>8%</div> <div>81%</div> <div>13%</div> <div>7%</div> </div>
4	D	142	<div> <div>10%</div> <div>80%</div> <div>11%</div> <div>9%</div> </div>
4	P	142	<div> <div>10%</div> <div>82%</div> <div>9%</div> <div>9%</div> </div>

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Mol	Chain	Length	Quality of chain
5	E	210	
5	Q	210	
6	F	127	
6	R	127	
7	G	172	
7	S	172	
8	H	150	
8	T	150	
9	I	125	
9	U	125	
10	J	67	
10	V	67	
11	K	117	
11	W	117	
12	L	58	
12	X	58	

## 2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 54330 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 RPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1033	Total	C	N	O	S	0	0
			8233	5186	1452	1550	45		
1	M	1033	Total	C	N	O	S	0	0
			8233	5186	1452	1550	45		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1023	Total	C	N	O	S	0	0
			8179	5188	1423	1518	50		
2	N	1023	Total	C	N	O	S	0	0
			8179	5188	1423	1518	50		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	257	Total	C	N	O	S	0	0
			2059	1294	351	408	6		
3	O	257	Total	C	N	O	S	0	0
			2059	1294	351	408	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	129	Total	C	N	O	S	0	0
			1063	665	179	215	4		
4	P	129	Total	C	N	O	S	0	0
			1063	665	179	215	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	N	O	S	0	0
			1720	1089	300	323	8		
5	Q	209	Total	C	N	O	S	0	0
			1720	1089	300	323	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	79	Total	C	N	O	S	0	0
			635	406	108	116	5		
6	R	79	Total	C	N	O	S	0	0
			635	406	108	116	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	N	O	S	0	0
			1351	875	219	249	8		
7	S	171	Total	C	N	O	S	0	0
			1351	875	219	249	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	N	O	S	0	0
			1186	750	194	237	5		
8	T	148	Total	C	N	O	S	0	0
			1186	750	194	237	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	114	Total	C	N	O	S	0	0
			927	571	166	179	11		
9	U	114	Total	C	N	O	S	0	0
			927	571	166	179	11		

- Molecule 10 is a protein called RPB10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	65	Total	C	N	O	S	0	0
			515	334	87	88	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	V	65	Total	C	N	O	S	0	0
			515	334	87	88	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	N	O	S	0	0
			920	593	152	173	2		
11	W	115	Total	C	N	O	S	0	0
			920	593	152	173	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	44	Total	C	N	O	S	0	0
			372	231	72	63	6		
12	X	44	Total	C	N	O	S	0	0
			372	231	72	63	6		

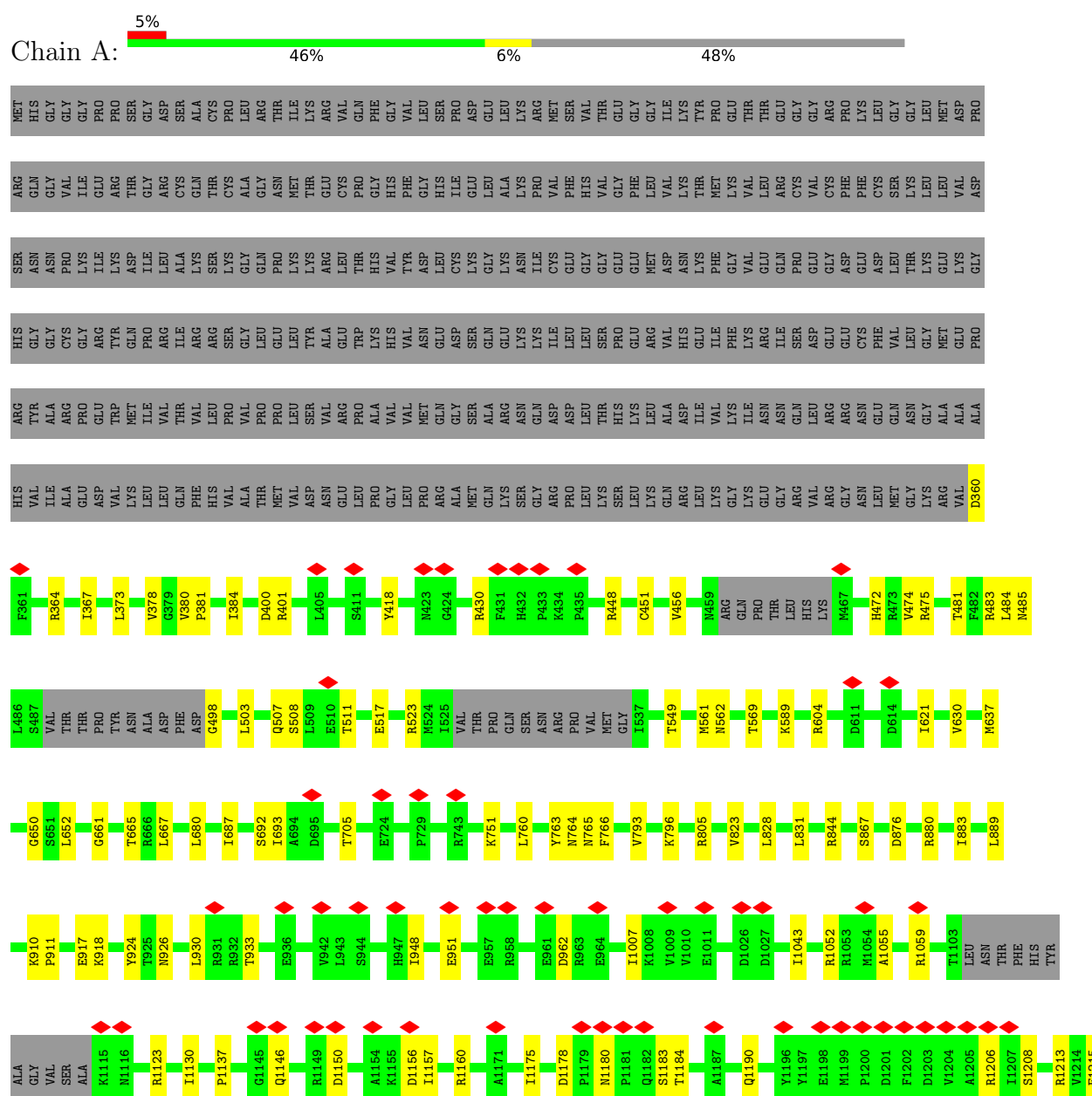
- Molecule 13 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
13	C	1	Total	Zn	0
			1	1	
13	I	2	Total	Zn	0
			2	2	
13	J	1	Total	Zn	0
			1	1	
13	L	1	Total	Zn	0
			1	1	
13	O	1	Total	Zn	0
			1	1	
13	U	2	Total	Zn	0
			2	2	
13	V	1	Total	Zn	0
			1	1	
13	X	1	Total	Zn	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: RPB1









Chain B:

9%

77%

10%

13%

ARG  
SER  
GLY  
ASP  
ASN  
LYS  
THR  
GLN  
PHE  
SER  
GLY  
LEU  
LEU  
VAL  
ARG  
MET  
PRO  
ALA  
CYS  
LEU  
PHE  
GLN  
GLY  
PHE  
LEU  
MET  
SER  
ILE  
ALA  
PHE  
GLY  
SER  
MET  
SER  
VAL

D905  
Q913  
E914  
I921  
R924  
R927  
Q941  
G946  
I947  
Y949  
I967  
I972  
R975  
M976  
C984  
N992  
K993  
R1035  
T1046  
R1050  
M1054  
D1087  
S1061  
ARG  
ALA  
MET  
GLY  
ILE  
MET  
ALA  
GLY  
PRO  
ILE  
GLN  
ASN  
ILE  
THR  
ARG  
LEU  
ASN  
THR  
HIS  
THR  
GLY  
MET  
GLY  
CYS

H577  
K578  
Q582  
L583  
R608  
R613  
R623  
K630  
L635  
I640  
E647  
Y648  
N649  
N650  
E670  
E697  
C707  
A732  
M733  
G734  
W735  
Y736  
I737  
T738  
N739  
R743  
L751  
Y752  
L767  
I776  
T782  
A783  
S784  
Y785  
T786  
D792  
S793  
V794  
R798  
R803

R807  
S808  
W809  
E818  
S819  
K820  
K821  
G822  
F823  
D824  
E826  
F829  
E835  
T836  
C837  
Q838  
A843  
T844  
D850  
P856  
W860  
D863  
T866  
W871  
P874  
GLU  
ASN  
GLU  
ASP  
GLU  
LEU  
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TYR  
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L896  
E900  
V904

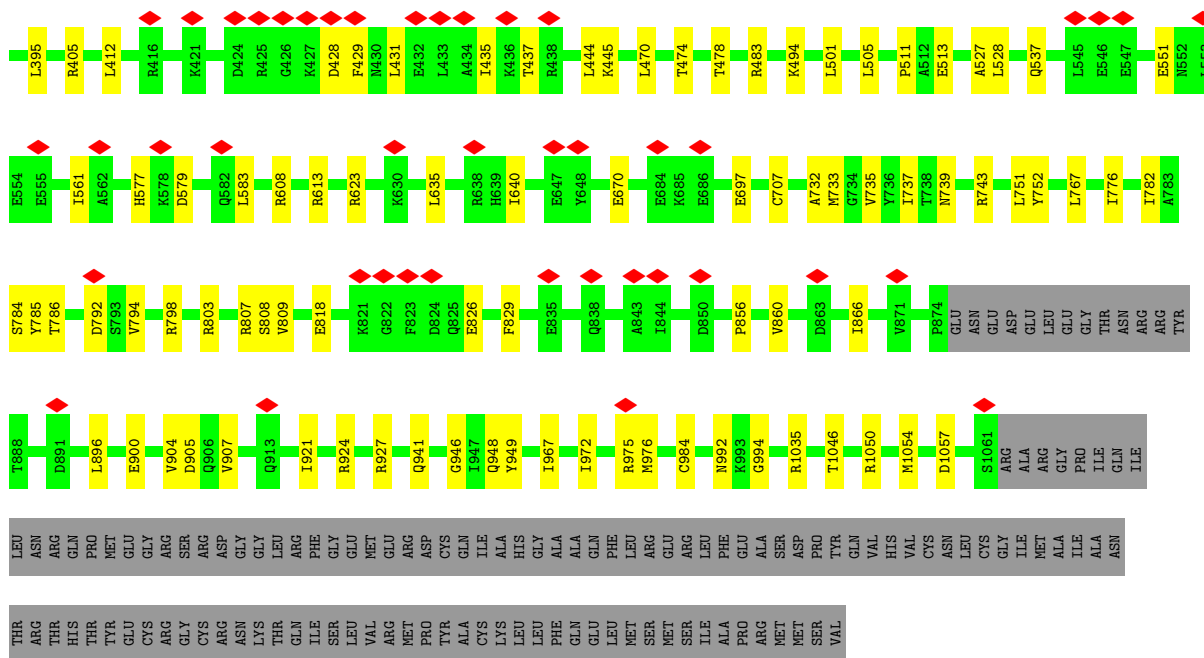
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D424  
R425  
G426  
K427  
D428  
F429  
N430  
L431  
E432  
L433  
A434  
I435  
K436  
T437  
R438  
D442  
G443  
L444  
L470  
T474  
T478  
R483  
K494  
L501  
L505  
P511  
A512  
E513  
A527  
L528  
Q537  
L545  
E546  
E551  
N552  
L553  
E554  
E555  
I561  
A562

A251  
I252  
G253  
Q254  
R255  
T259  
E266  
F273  
R282  
D283  
I284  
K285  
E286  
D291  
F292  
E293  
D294  
V310  
I311  
Q312  
E313  
A317  
F320  
R324  
G325  
A326  
K327  
P328  
G329  
K332  
Q344  
K345  
E346  
F356  
C357  
E358  
K361  
Y367  
R371  
L396  
R405  
L412

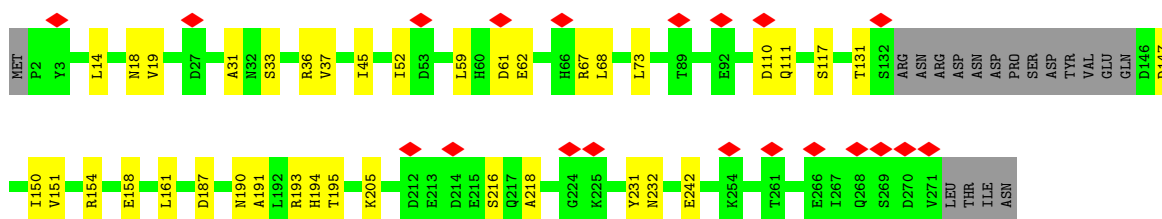
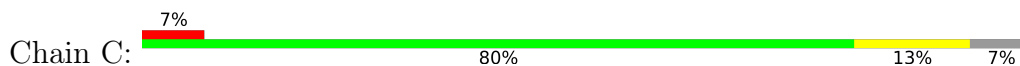
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E137  
E138  
Q139  
L140  
Q141  
T142  
Q143  
H144  
Q145  
F148  
I149  
G150  
K151  
I152  
T159  
M164  
G165  
D168  
R169  
Q170  
L171  
P178  
E191  
K192  
V193  
V205  
K210  
K211  
D212  
S213  
K214  
Y215  
T218  
L225  
E226  
N227  
S228  
S229  
R230  
R242  
G243  
G244  
Q245  
G246  
A247  
K248  
S249

MET  
TYR  
ASP  
ALA  
ASP  
GLU  
ASP  
MET  
GLN  
TYR  
ASP  
GLU  
ASP  
ASP  
D15  
L39  
Q42  
Q43  
R57  
I65  
D66  
L67  
Q68  
A69  
GLU  
ALA  
GLN  
HIS  
ALA  
SER  
GLY  
GLU  
VAL  
GLU  
GLU  
P81  
P82  
R83  
Y84  
E89  
E100  
H101  
D102  
G103  
A104  
P105  
R114  
T131  
V132  
I133  
K134  
E135

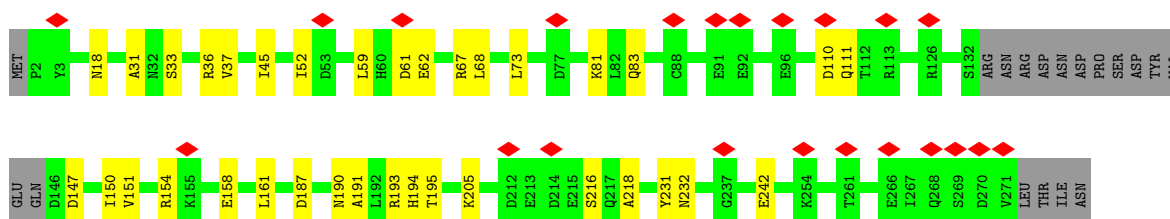
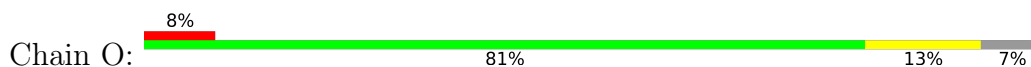
Chain N:



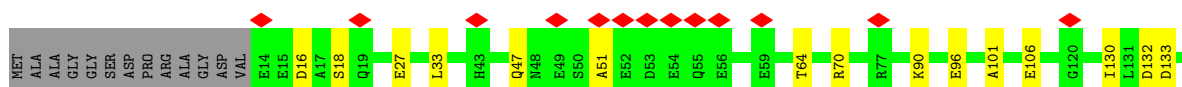
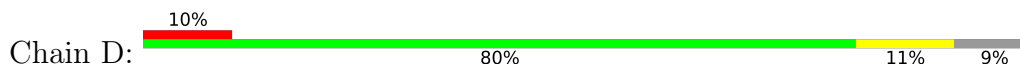
- Molecule 3: DNA-directed RNA polymerase II subunit RPB3



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

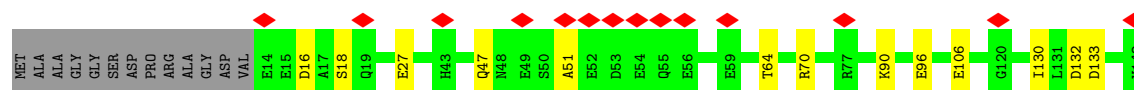
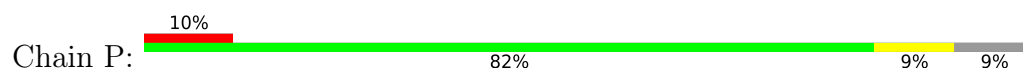


- Molecule 4: RNA polymerase II subunit D

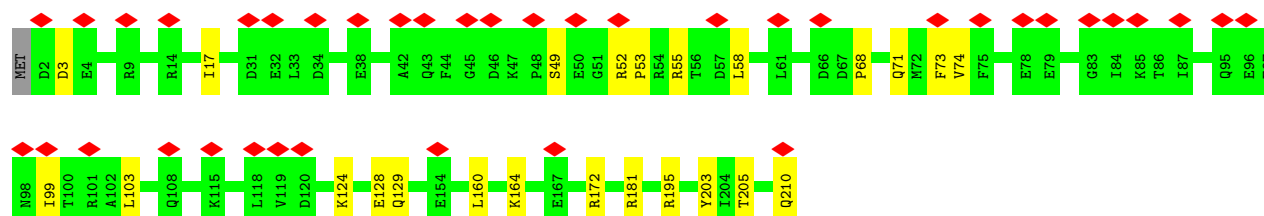




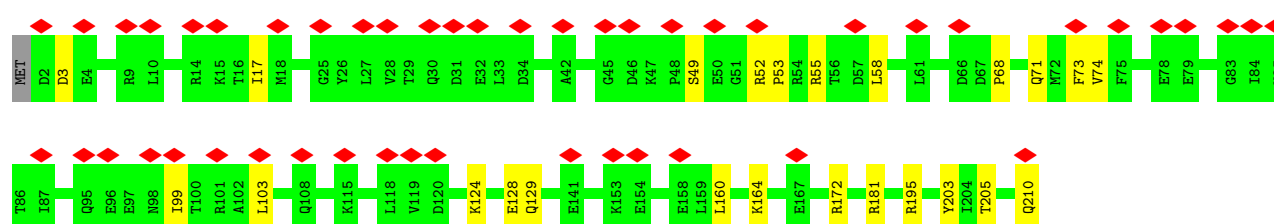
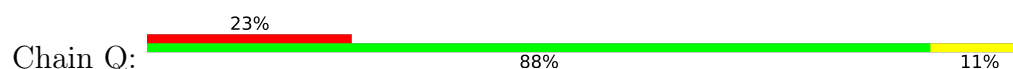
• Molecule 4: RNA polymerase II subunit D



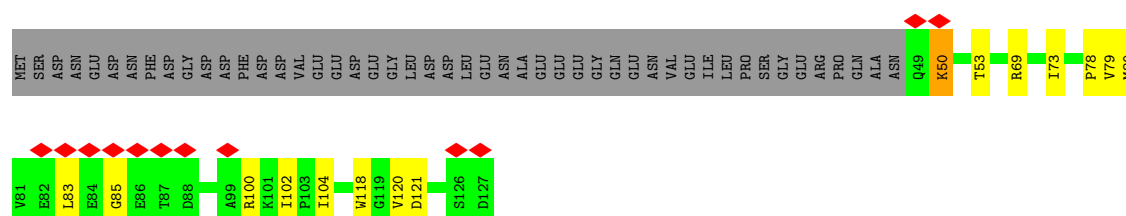
• Molecule 5: DNA-directed RNA polymerase II subunit E



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

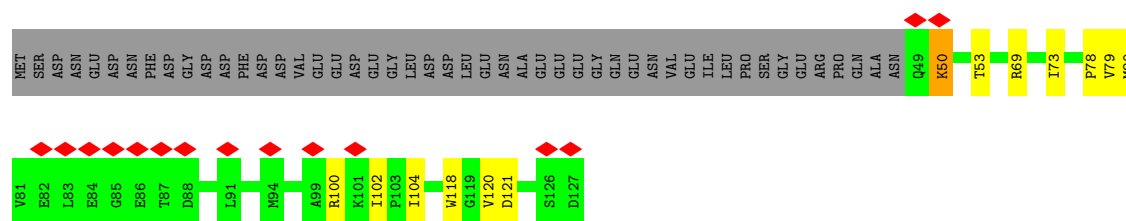


• Molecule 6: DNA-directed RNA polymerase II subunit F

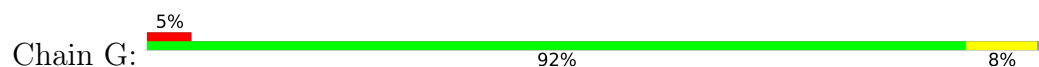


• Molecule 6: DNA-directed RNA polymerase II subunit F

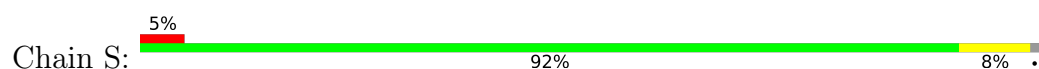




- Molecule 7: DNA-directed RNA polymerase II subunit RPB7



- Molecule 8: DNA-directed RNA polymerase II subunit RPB7



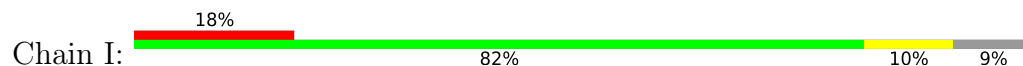
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3

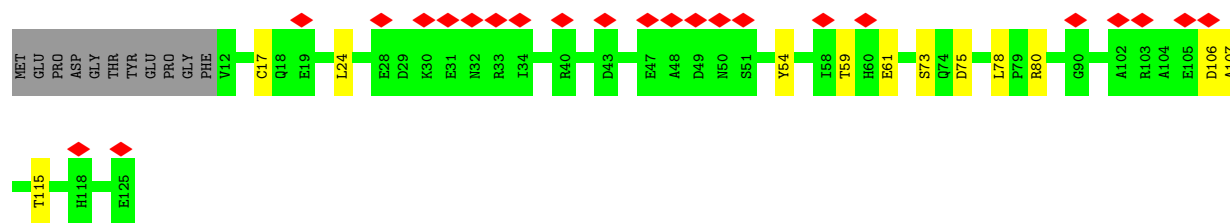


- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3

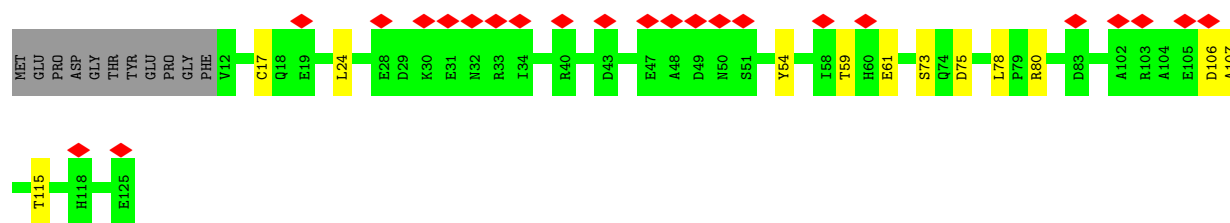
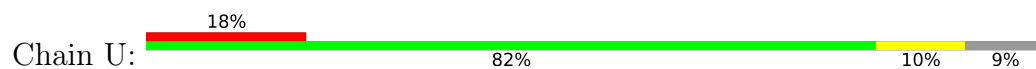


- Molecule 9: DNA-directed RNA polymerase II subunit RPB9

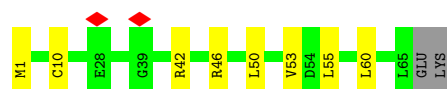
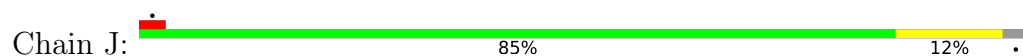




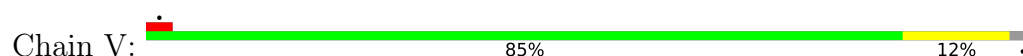
- Molecule 9: DNA-directed RNA polymerase II subunit RPB9



- Molecule 10: RPB10



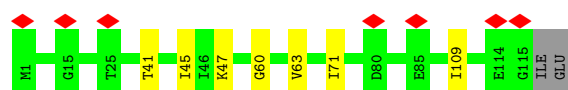
- Molecule 10: RPB10



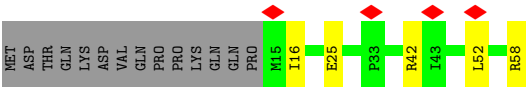
- Molecule 11: RNA\_pol\_L\_2 domain-containing protein



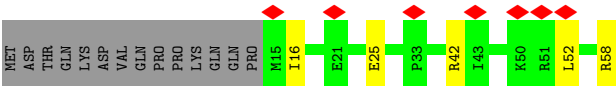
- Molecule 11: RNA\_pol\_L\_2 domain-containing protein



- Molecule 12: RNA polymerase II subunit K



● Molecule 12: RNA polymerase II subunit K



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	71781	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	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	37.307	Depositor
Minimum map value	-25.680	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.924	Depositor
Recommended contour level	5.0	Depositor
Map size (Å)	367.65, 367.65, 367.65	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.817, 0.817, 0.817	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

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	0.23	0/8378	0.38	0/11315
1	M	0.23	0/8378	0.39	0/11315
2	B	0.24	0/8345	0.40	0/11272
2	N	0.24	0/8345	0.40	0/11272
3	C	0.23	0/2102	0.40	0/2857
3	O	0.23	0/2102	0.40	0/2857
4	D	0.23	0/1078	0.35	0/1446
4	P	0.23	0/1078	0.36	0/1446
5	E	0.23	0/1751	0.39	0/2366
5	Q	0.23	0/1751	0.39	0/2366
6	F	0.23	0/645	0.39	0/871
6	R	0.23	0/645	0.39	0/871
7	G	0.25	0/1382	0.41	0/1874
7	S	0.25	0/1382	0.41	0/1874
8	H	0.24	0/1207	0.41	0/1628
8	T	0.24	0/1207	0.41	0/1628
9	I	0.23	0/948	0.39	0/1284
9	U	0.23	0/948	0.39	0/1284
10	J	0.24	0/524	0.38	0/707
10	V	0.24	0/524	0.37	0/707
11	K	0.24	0/939	0.37	0/1271
11	W	0.24	0/939	0.37	0/1271
12	L	0.23	0/377	0.41	0/500
12	X	0.23	0/377	0.41	0/500
All	All	0.24	0/55352	0.39	0/74782

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

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	8233	0	8273	82	0
1	M	8233	0	8273	80	0
2	B	8179	0	8218	83	0
2	N	8179	0	8218	84	0
3	C	2059	0	2007	23	0
3	O	2059	0	2007	22	0
4	D	1063	0	1042	10	0
4	P	1063	0	1042	9	0
5	E	1720	0	1737	14	0
5	Q	1720	0	1737	14	0
6	F	635	0	665	10	0
6	R	635	0	665	9	0
7	G	1351	0	1358	8	0
7	S	1351	0	1358	8	0
8	H	1186	0	1147	16	0
8	T	1186	0	1147	16	0
9	I	927	0	859	7	0
9	U	927	0	859	7	0
10	J	515	0	534	8	0
10	V	515	0	534	8	0
11	K	920	0	942	9	0
11	W	920	0	942	9	0
12	L	372	0	378	4	0
12	X	372	0	378	4	0
13	C	1	0	0	0	0
13	I	2	0	0	0	0
13	J	1	0	0	0	0
13	L	1	0	0	0	0
13	O	1	0	0	0	0
13	U	2	0	0	0	0
13	V	1	0	0	0	0
13	X	1	0	0	0	0
All	All	54330	0	54320	482	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 482 close contacts within the same asymmetric unit are listed below, sorted by

their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:984:CYS:SG	2:N:1046:THR:OG1	2.32	0.88
2:B:984:CYS:SG	2:B:1046:THR:OG1	2.32	0.87
3:C:67:ARG:NH1	3:C:150:ILE:O	2.11	0.83
3:O:67:ARG:NH1	3:O:150:ILE:O	2.11	0.82
2:B:733:MET:SD	2:B:1050:ARG:NH1	2.55	0.78

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	1019/1970 (52%)	1001 (98%)	18 (2%)	0	100	100
1	M	1019/1970 (52%)	1000 (98%)	19 (2%)	0	100	100
2	B	1017/1174 (87%)	990 (97%)	27 (3%)	0	100	100
2	N	1017/1174 (87%)	990 (97%)	27 (3%)	0	100	100
3	C	253/275 (92%)	248 (98%)	5 (2%)	0	100	100
3	O	253/275 (92%)	248 (98%)	5 (2%)	0	100	100
4	D	127/142 (89%)	125 (98%)	2 (2%)	0	100	100
4	P	127/142 (89%)	125 (98%)	2 (2%)	0	100	100
5	E	207/210 (99%)	202 (98%)	5 (2%)	0	100	100
5	Q	207/210 (99%)	202 (98%)	5 (2%)	0	100	100
6	F	77/127 (61%)	76 (99%)	1 (1%)	0	100	100
6	R	77/127 (61%)	76 (99%)	1 (1%)	0	100	100
7	G	169/172 (98%)	167 (99%)	2 (1%)	0	100	100
7	S	169/172 (98%)	167 (99%)	2 (1%)	0	100	100
8	H	146/150 (97%)	146 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	T	146/150 (97%)	146 (100%)	0	0	100	100
9	I	112/125 (90%)	109 (97%)	3 (3%)	0	100	100
9	U	112/125 (90%)	109 (97%)	3 (3%)	0	100	100
10	J	63/67 (94%)	61 (97%)	2 (3%)	0	100	100
10	V	63/67 (94%)	61 (97%)	2 (3%)	0	100	100
11	K	113/117 (97%)	113 (100%)	0	0	100	100
11	W	113/117 (97%)	113 (100%)	0	0	100	100
12	L	42/58 (72%)	41 (98%)	1 (2%)	0	100	100
12	X	42/58 (72%)	41 (98%)	1 (2%)	0	100	100
All	All	6690/9174 (73%)	6557 (98%)	133 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	918/1749 (52%)	918 (100%)	0	100	100
1	M	918/1749 (52%)	918 (100%)	0	100	100
2	B	898/1027 (87%)	896 (100%)	2 (0%)	93	98
2	N	898/1027 (87%)	896 (100%)	2 (0%)	93	98
3	C	234/252 (93%)	234 (100%)	0	100	100
3	O	234/252 (93%)	234 (100%)	0	100	100
4	D	119/126 (94%)	119 (100%)	0	100	100
4	P	119/126 (94%)	119 (100%)	0	100	100
5	E	191/192 (100%)	190 (100%)	1 (0%)	88	94
5	Q	191/192 (100%)	190 (100%)	1 (0%)	88	94
6	F	69/111 (62%)	68 (99%)	1 (1%)	67	85
6	R	69/111 (62%)	68 (99%)	1 (1%)	67	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	G	152/153 (99%)	152 (100%)	0	100	100
7	S	152/153 (99%)	152 (100%)	0	100	100
8	H	129/131 (98%)	128 (99%)	1 (1%)	81	91
8	T	129/131 (98%)	128 (99%)	1 (1%)	81	91
9	I	103/112 (92%)	103 (100%)	0	100	100
9	U	103/112 (92%)	103 (100%)	0	100	100
10	J	54/56 (96%)	53 (98%)	1 (2%)	57	80
10	V	54/56 (96%)	53 (98%)	1 (2%)	57	80
11	K	104/106 (98%)	104 (100%)	0	100	100
11	W	104/106 (98%)	104 (100%)	0	100	100
12	L	41/55 (74%)	41 (100%)	0	100	100
12	X	41/55 (74%)	41 (100%)	0	100	100
All	All	6024/8140 (74%)	6012 (100%)	12 (0%)	93	98

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	N	608	ARG
5	Q	124	LYS
10	V	42	ARG
6	R	50	LYS
6	F	50	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	485	ASN
1	M	485	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 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 [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

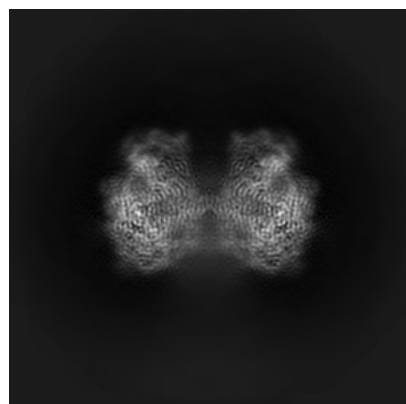
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13129. These allow visual inspection of the internal detail of the map and identification of artifacts.

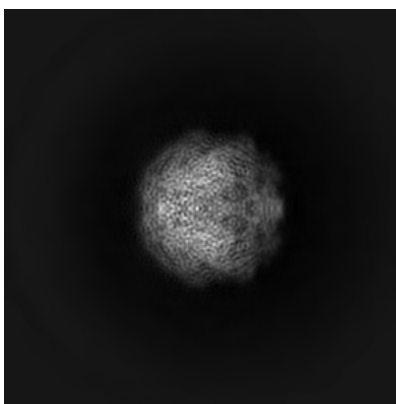
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

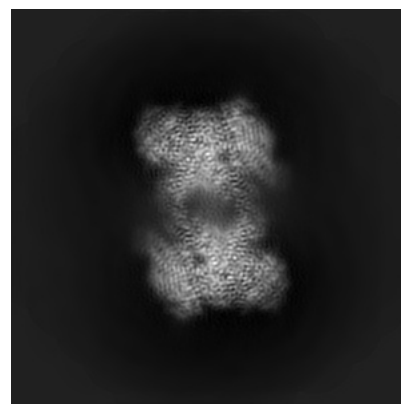
#### 6.1.1 Primary map



X

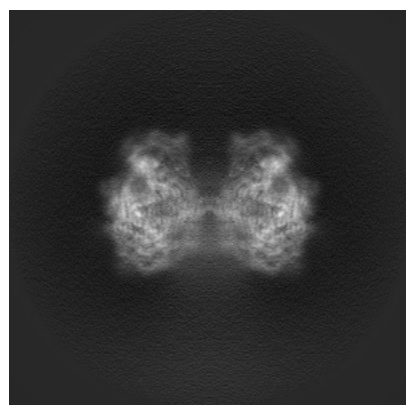


Y

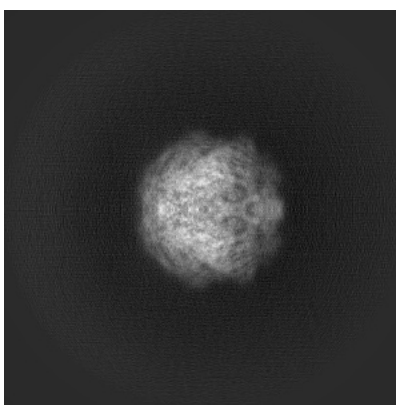


Z

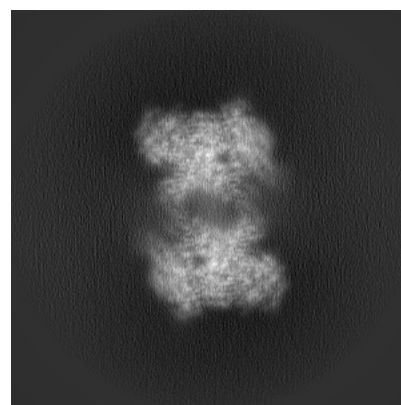
#### 6.1.2 Raw map



X



Y

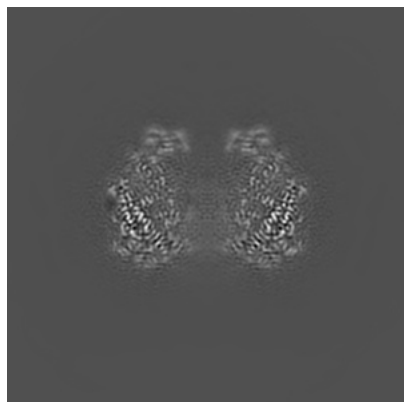


Z

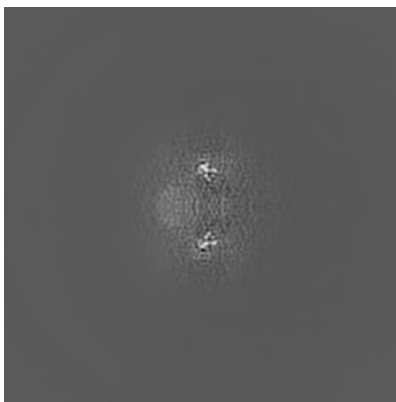
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

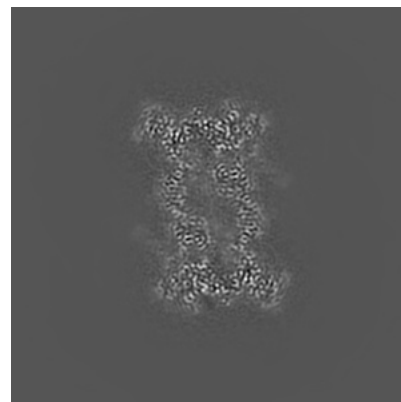
### 6.2.1 Primary map



X Index: 225

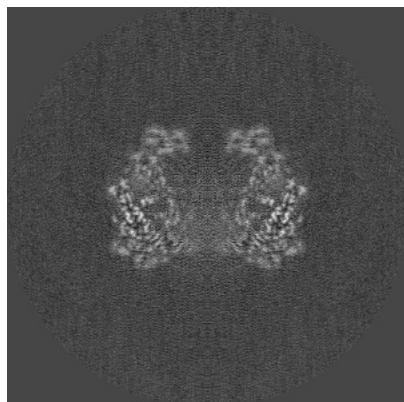


Y Index: 225

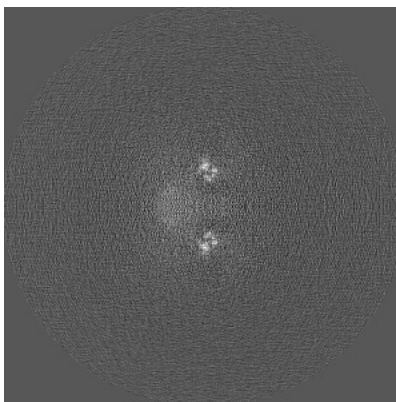


Z Index: 225

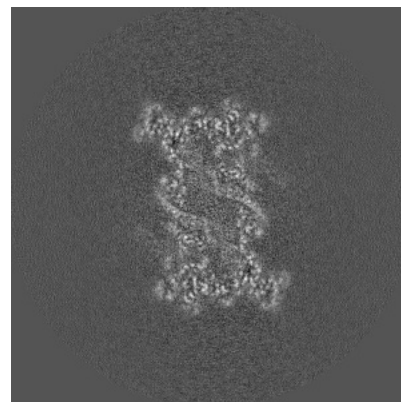
### 6.2.2 Raw map



X Index: 225



Y Index: 225



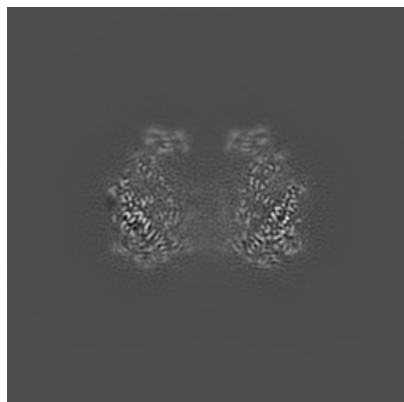
Z Index: 225

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

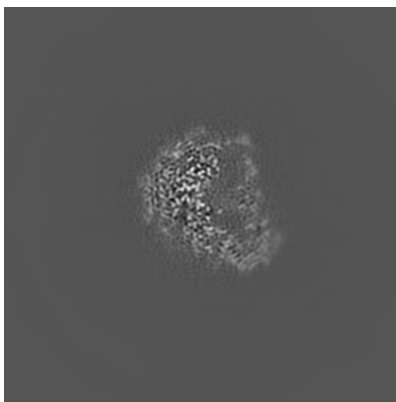


## 6.3 Largest variance slices [i](#)

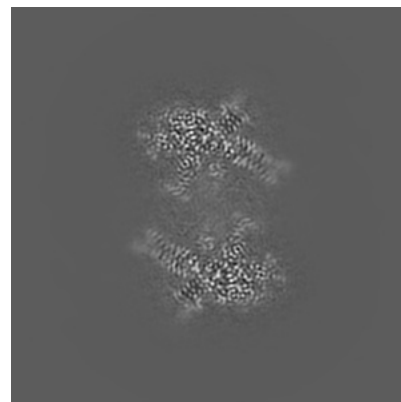
### 6.3.1 Primary map



X Index: 224

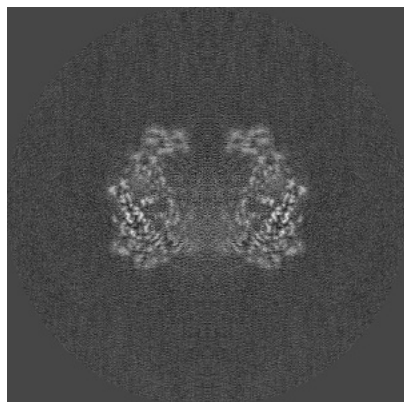


Y Index: 147

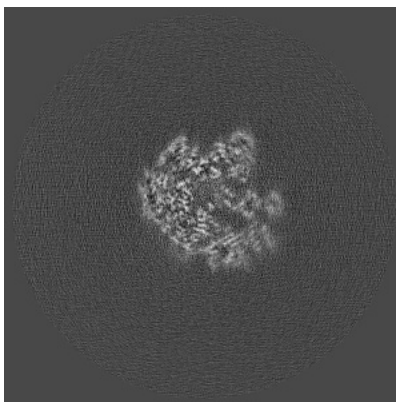


Z Index: 207

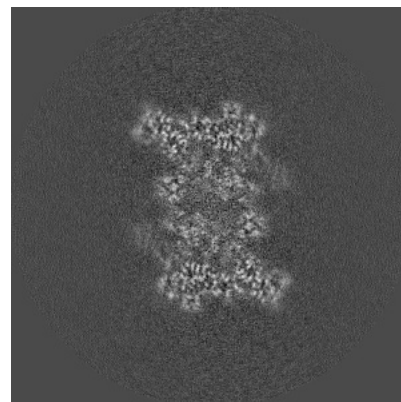
### 6.3.2 Raw map



X Index: 225



Y Index: 158

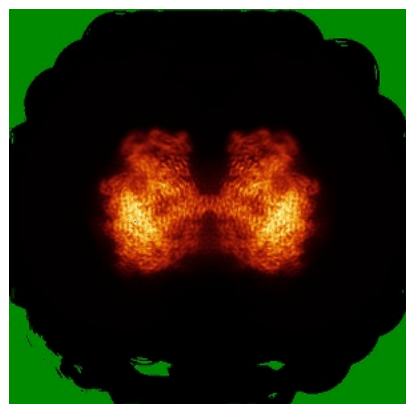


Z Index: 220

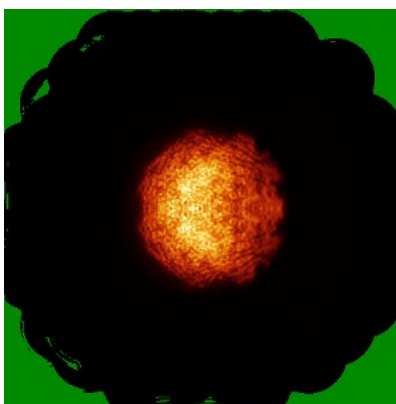
The images above show the largest variance slices of the map in three orthogonal directions.

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

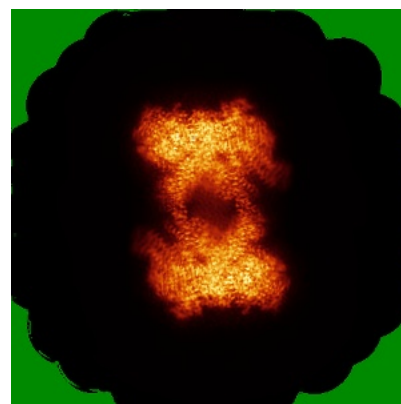
### 6.4.1 Primary map



X

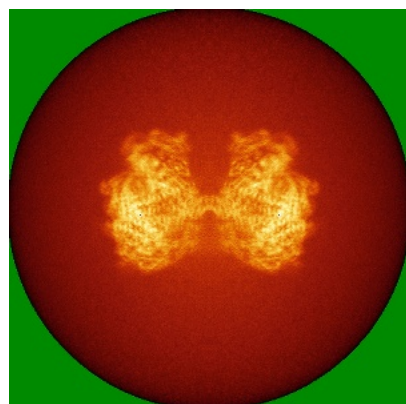


Y

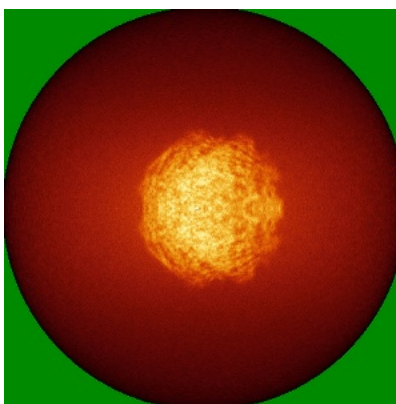


Z

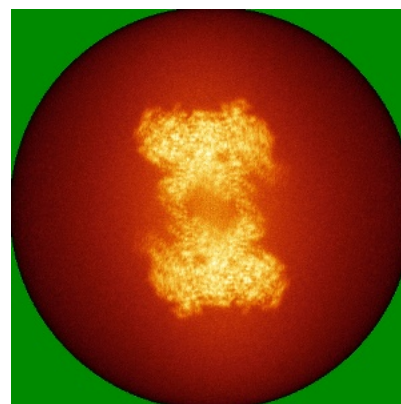
### 6.4.2 Raw map



X



Y

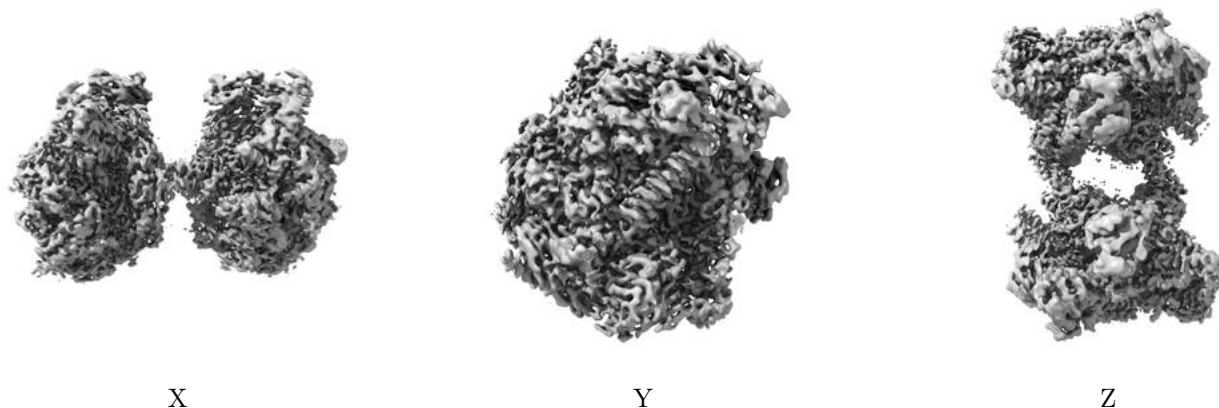


Z

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.

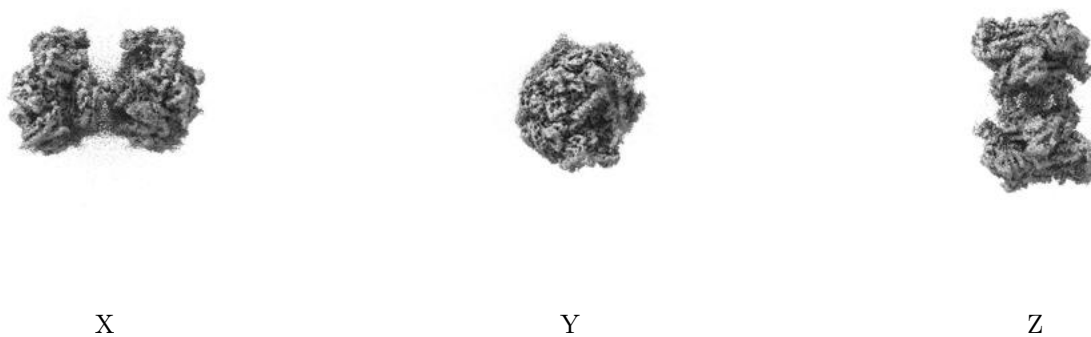
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 5.0. 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



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.

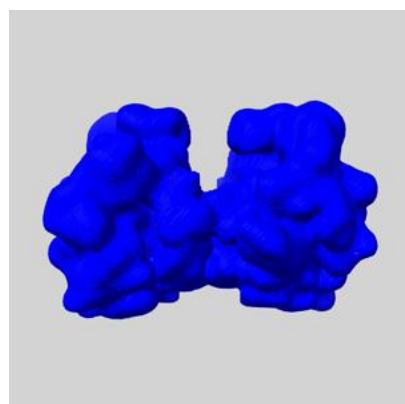
## 6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

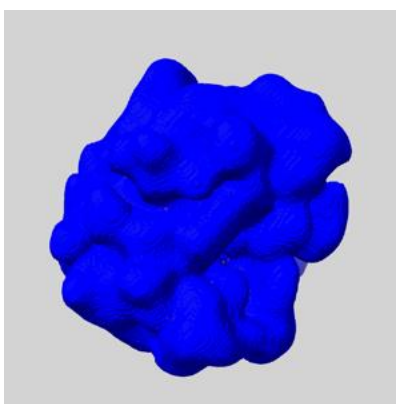
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

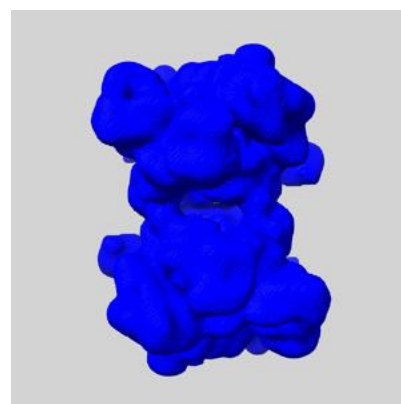
### 6.6.1 emd\_13129\_msk\_1.map [i](#)



X



Y

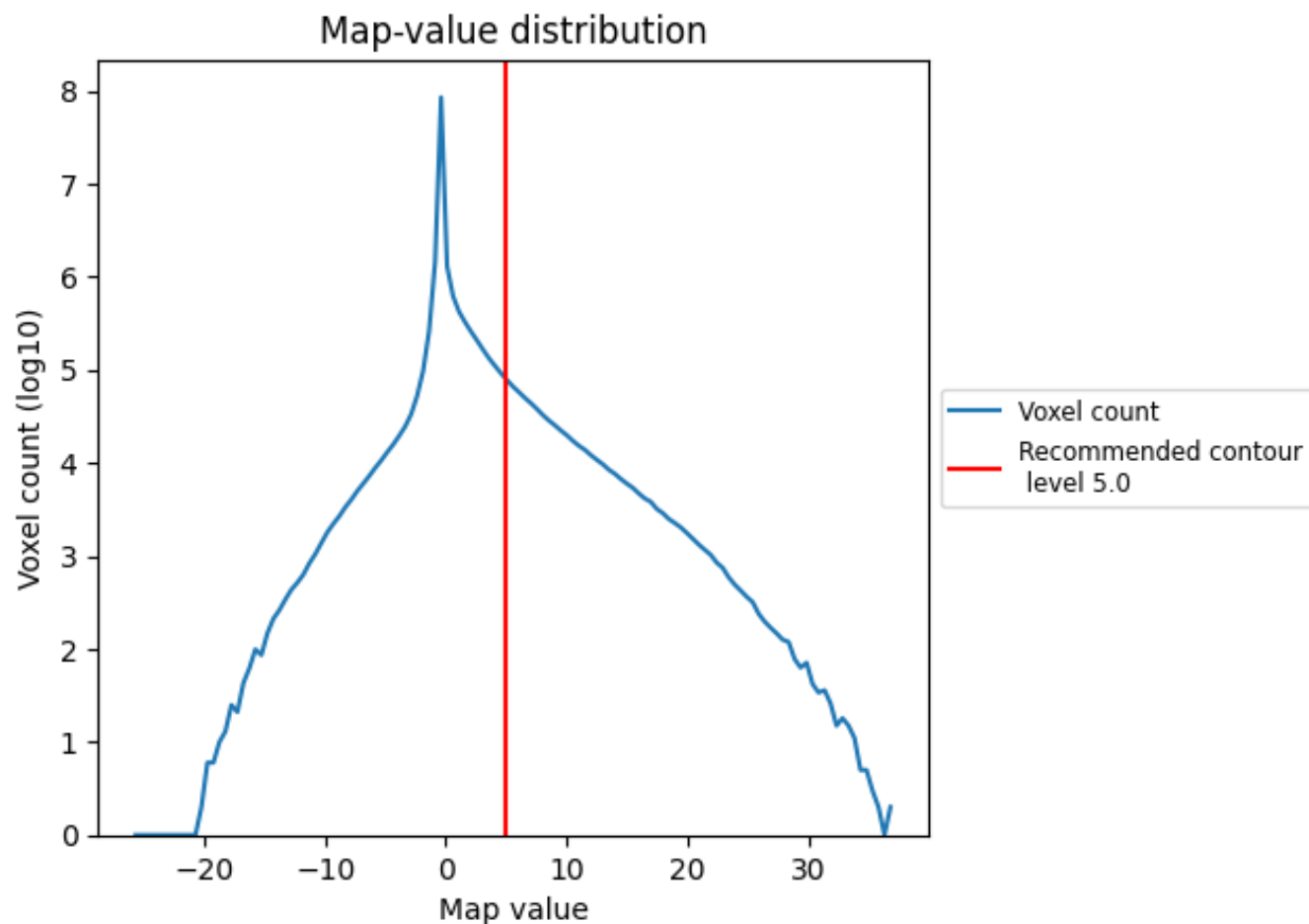


Z

## 7 Map analysis [i](#)

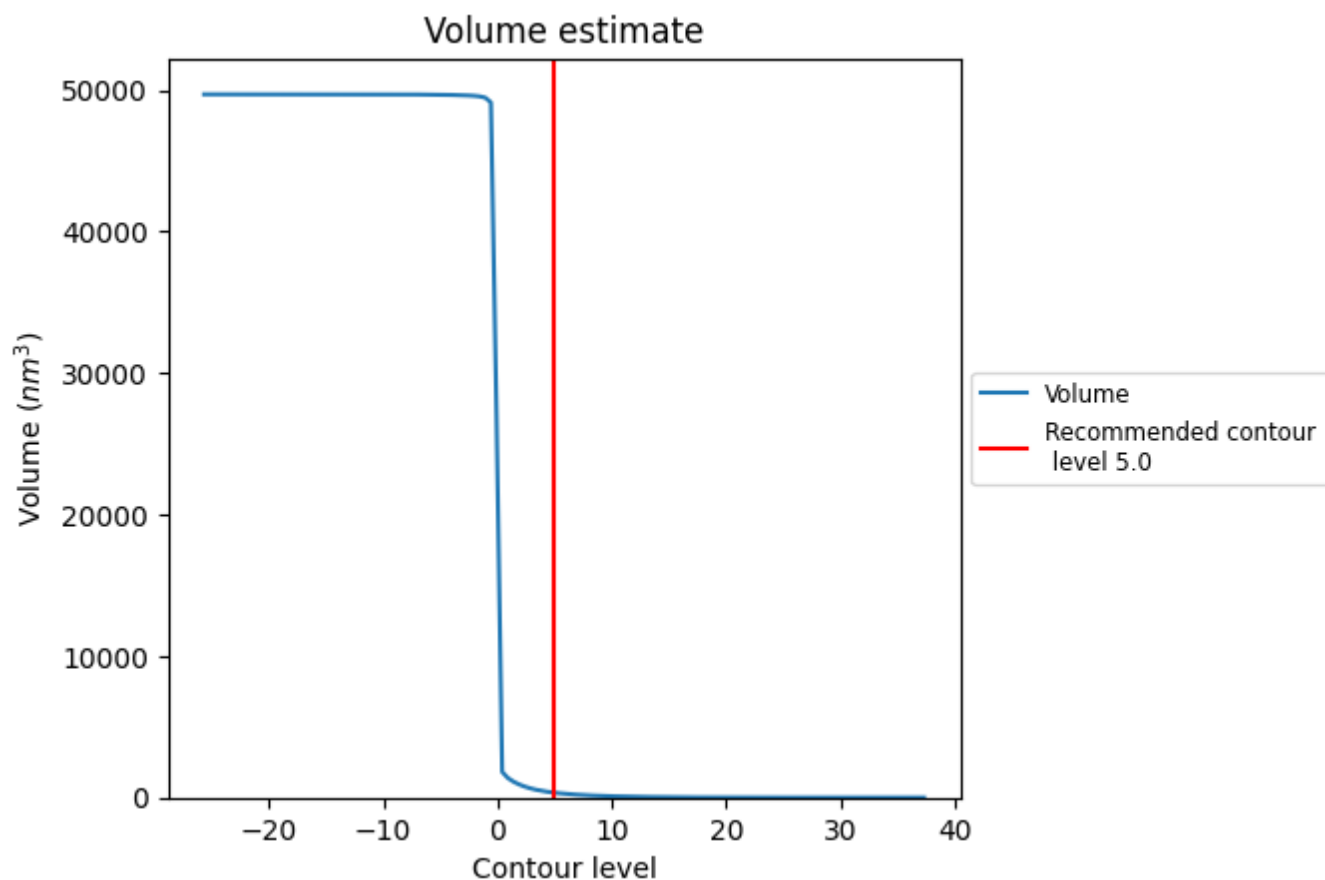
This section contains the results of statistical analysis of the map.

### 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.

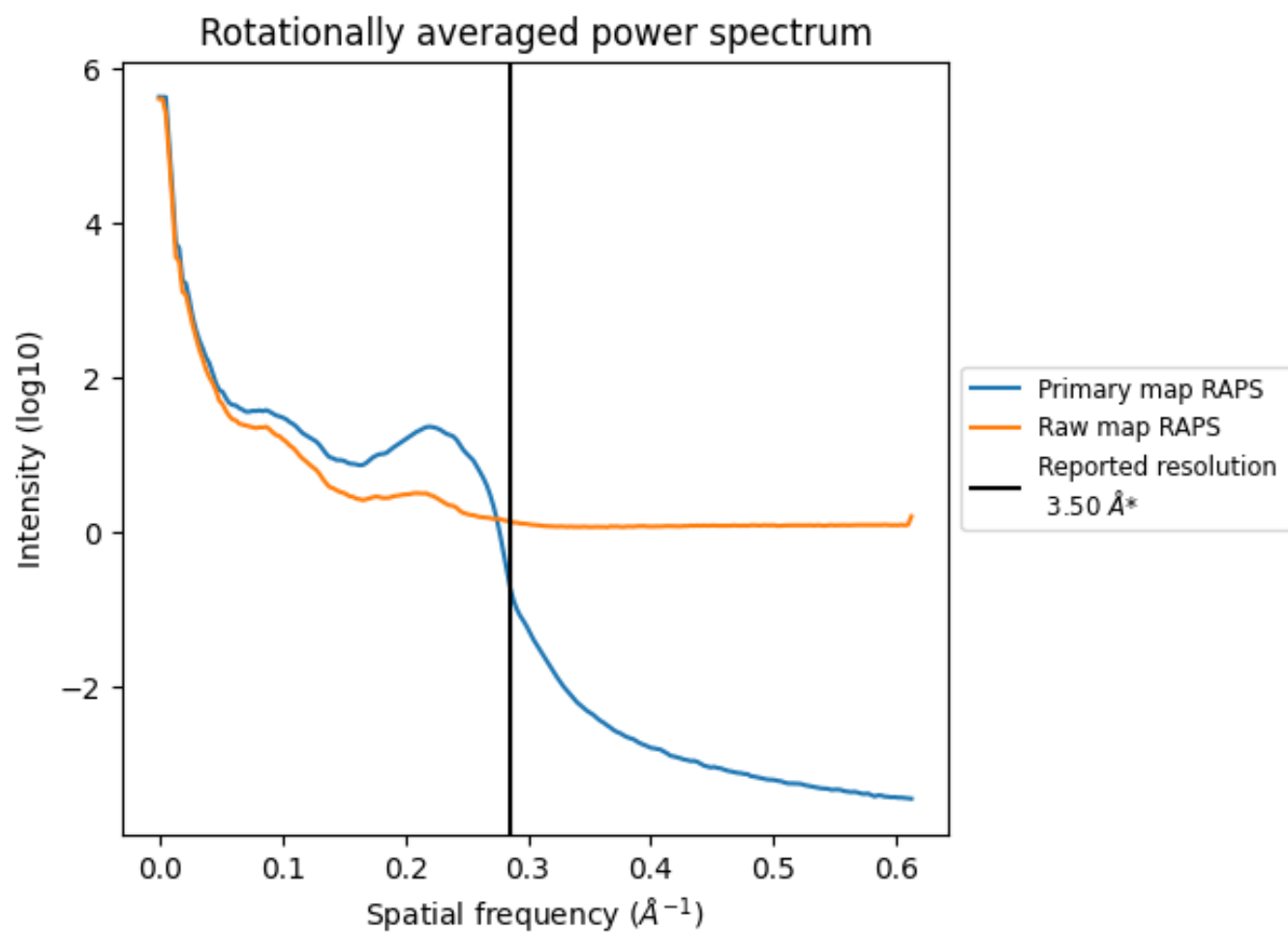
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 341  $\text{nm}^3$ ; this corresponds to an approximate mass of 308 kDa.

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

### 7.3 Rotationally averaged power spectrum ⓘ

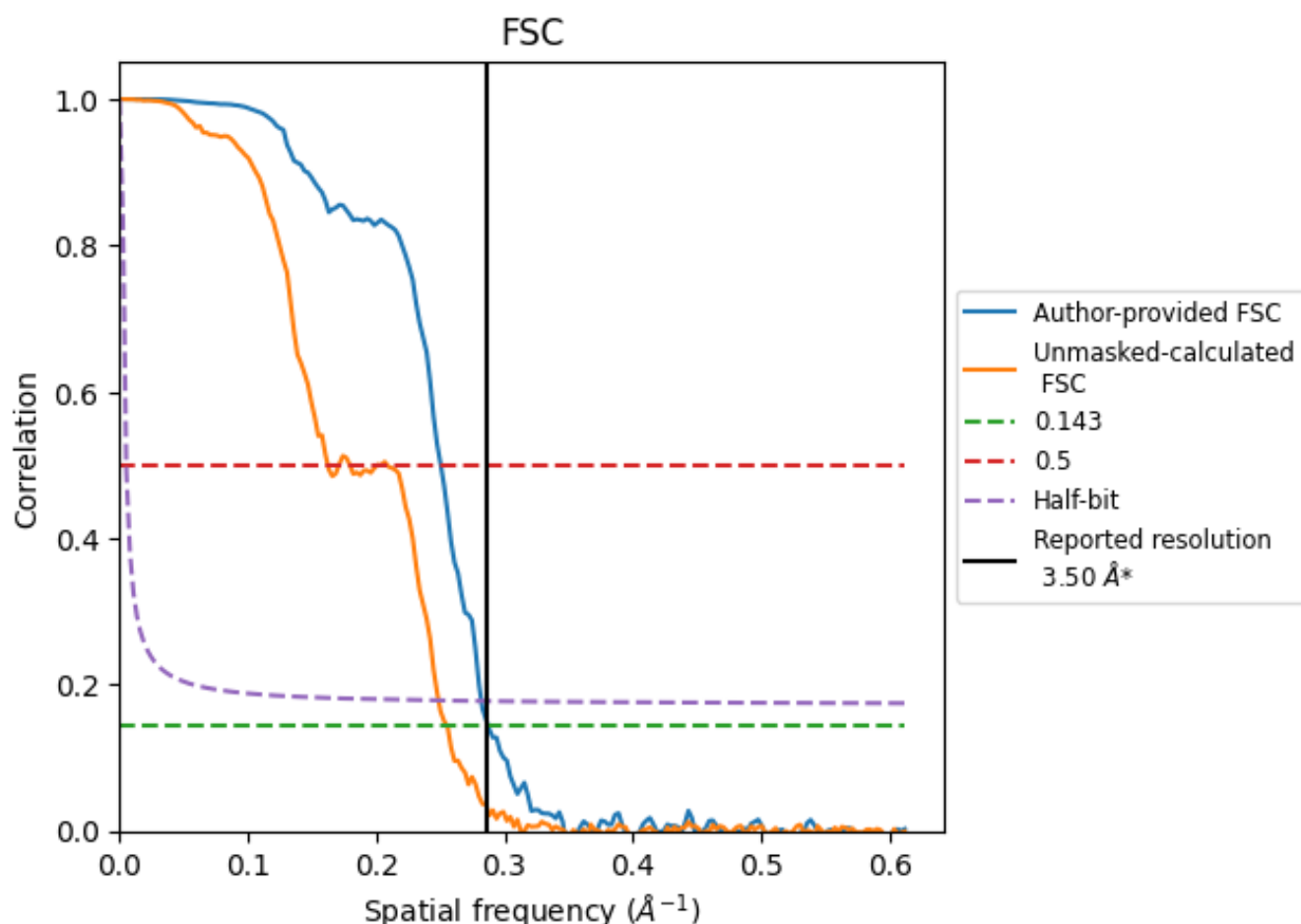


\*Reported resolution corresponds to spatial frequency of 0.286 Å<sup>-1</sup>

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

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.286  $\text{\AA}^{-1}$



## 8.2 Resolution estimates [i](#)

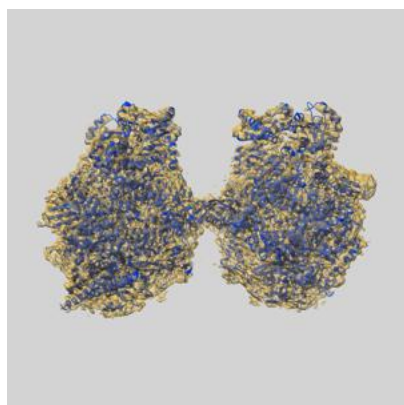
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.48	3.99	3.55
Unmasked-calculated*	3.92	6.16	4.02

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.92 differs from the reported value 3.5 by more than 10 %

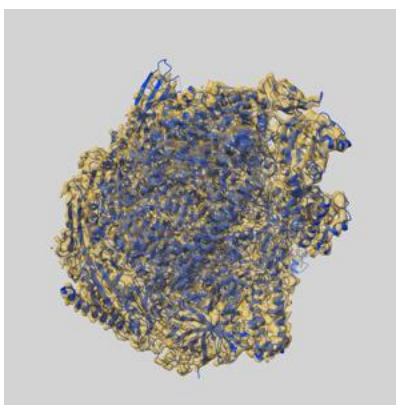
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13129 and PDB model 7OZN. Per-residue inclusion information can be found in section 3 on page 7.

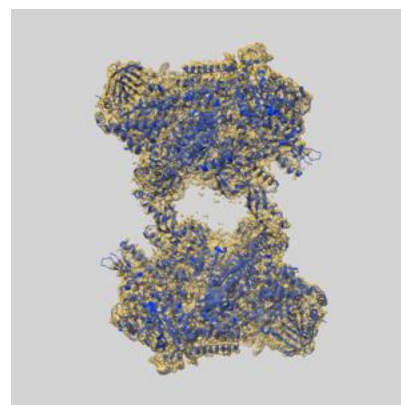
### 9.1 Map-model overlay [i](#)



X



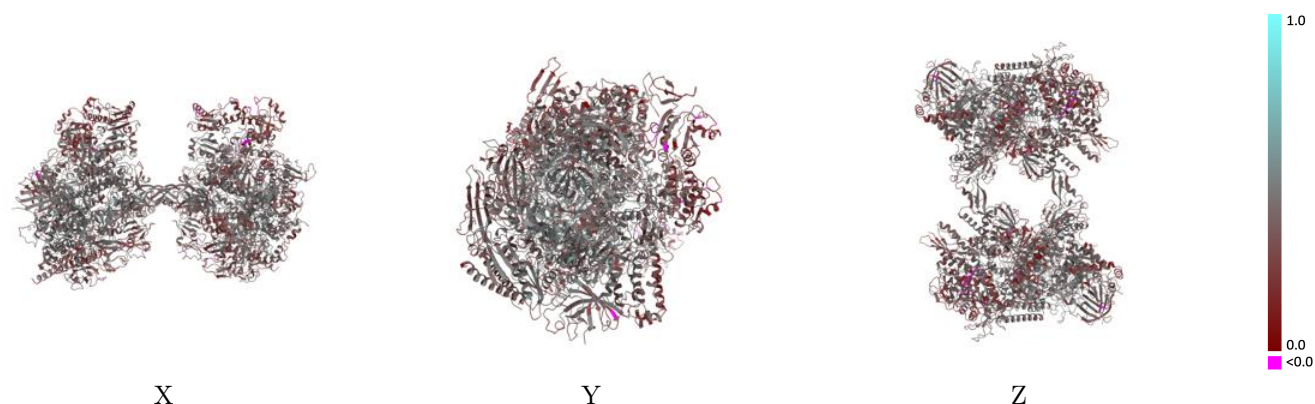
Y



Z

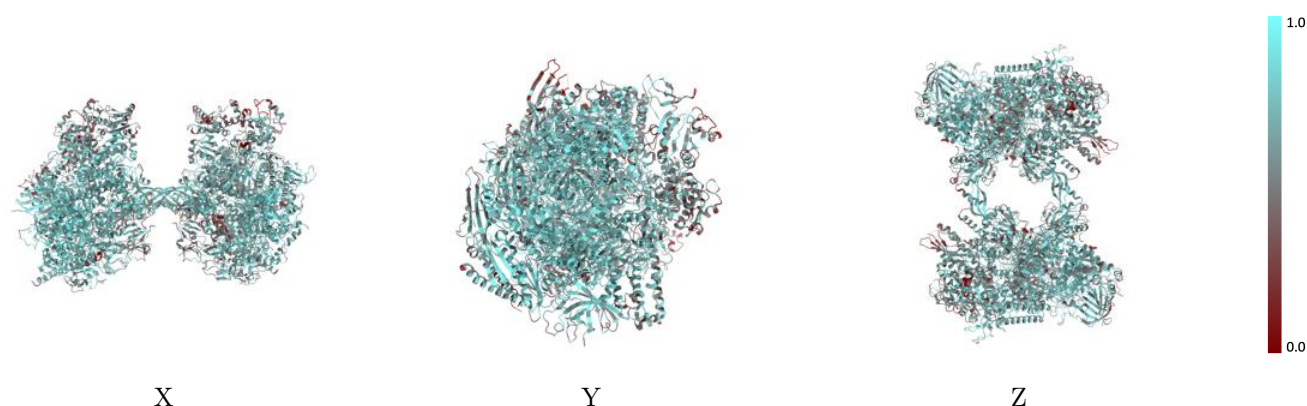
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



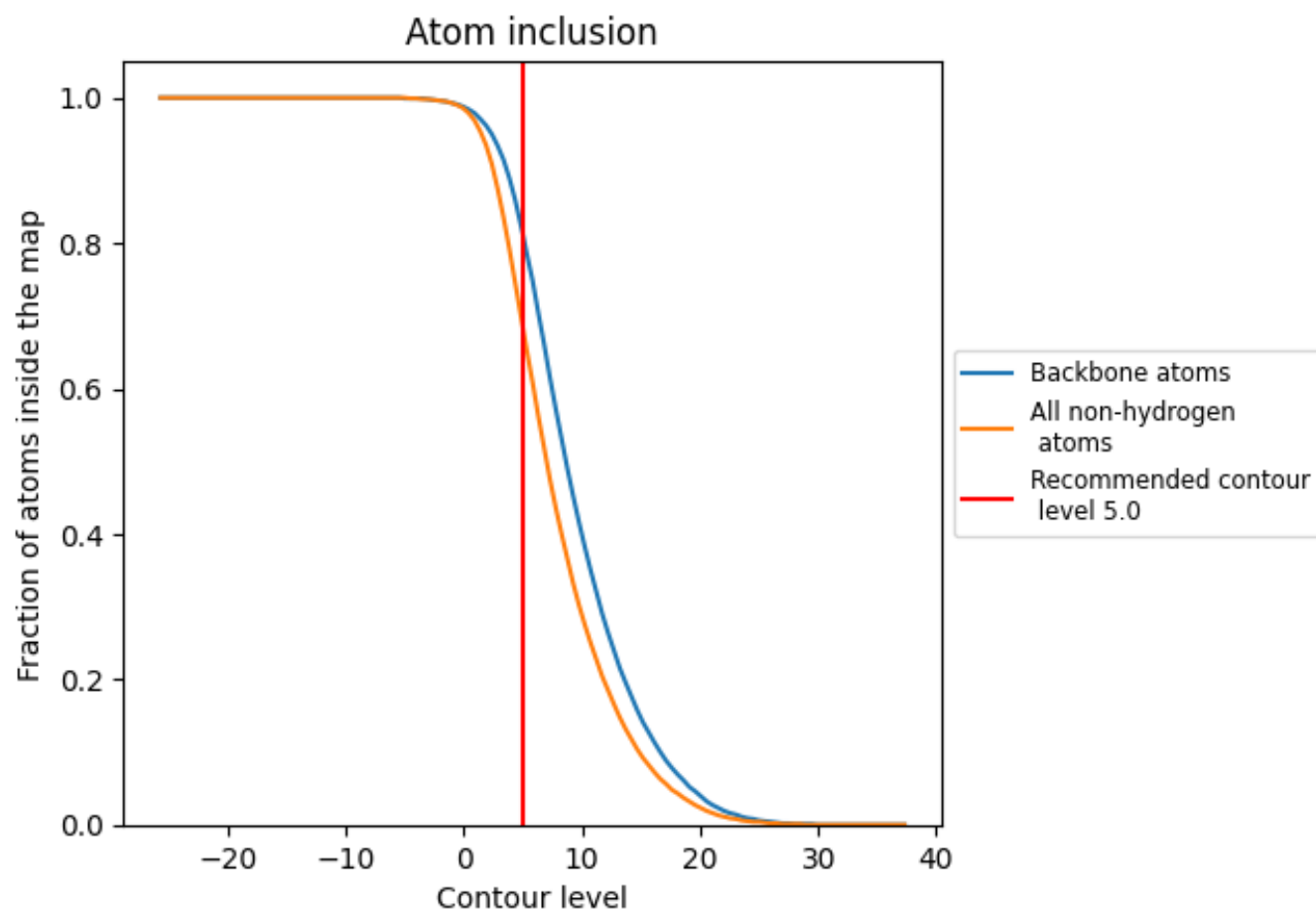
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (5.0).



















































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 68% 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 (5.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6840	 0.3870
A	 0.6940	 0.3980
B	 0.7000	 0.3920
C	 0.6970	 0.3760
D	 0.6470	 0.3870
E	 0.5880	 0.3220
F	 0.6660	 0.4120
G	 0.7190	 0.4130
H	 0.6510	 0.3820
I	 0.6130	 0.3350
J	 0.7570	 0.3990
K	 0.7200	 0.3940
L	 0.6400	 0.3420
M	 0.6970	 0.3990
N	 0.6970	 0.3900
O	 0.6840	 0.3780
P	 0.6570	 0.3920
Q	 0.5660	 0.3230
R	 0.6400	 0.4050
S	 0.7290	 0.4140
T	 0.6600	 0.3880
U	 0.6130	 0.3320
V	 0.7810	 0.4010
W	 0.7160	 0.4010
X	 0.6260	 0.3360

