



wwPDB EM Validation Summary Report ⓘ

Jun 8, 2025 – 04:22 pm BST

PDB ID : 9G1V / pdb_00009g1v
EMDB ID : EMD-50955
Title : Yeast RNA polymerase I elongation complex stalled by an apurinic site
Authors : Santos-Aledo, A.; Plaza-Pegueroles, A.; Ruiz, F.M.; Fernandez-Tornero, C.
Deposited on : 2024-07-10
Resolution : 2.70 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.dev118
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

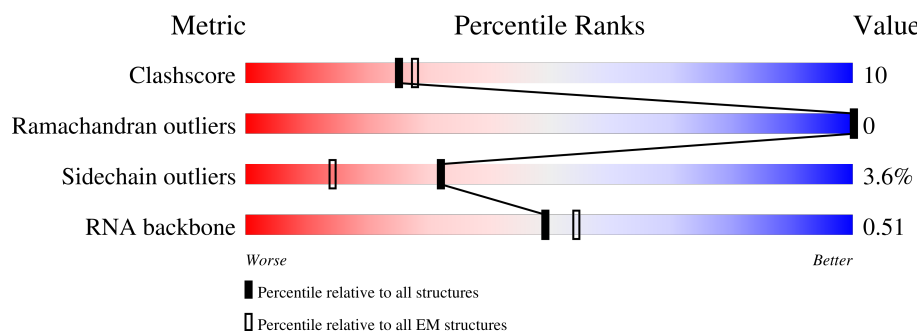
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 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.





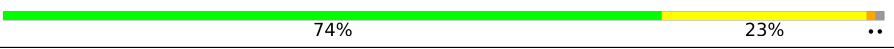
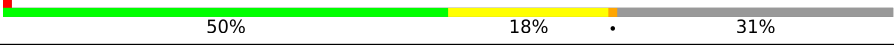



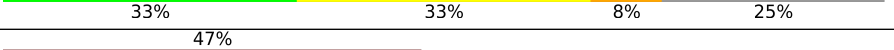
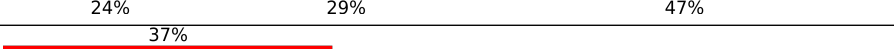
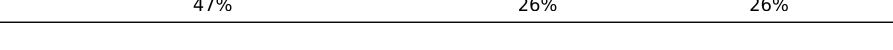
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	A	1664	
2	B	1203	
3	C	335	
4	D	137	
5	E	215	
6	F	155	
7	G	326	

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Mol	Chain	Length	Quality of chain
8	H	146	
9	I	125	
10	J	70	
11	K	142	
12	L	70	
13	M	415	
14	N	233	
15	R	12	
16	S	38	
17	T	38	

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 32718 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called DNA-directed RNA polymerase I subunit RPA190.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1456	Total	C	N	O	S	0	0
			11500	7262	2003	2174	61		

- Molecule 2 is a protein called DNA-directed RNA polymerase I subunit RPA135.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1164	Total	C	N	O	S	0	0
			9254	5852	1626	1725	51		

- Molecule 3 is a protein called DNA-directed RNA polymerases I and III subunit RPAC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	304	Total	C	N	O	S	0	0
			2415	1535	414	458	8		

- Molecule 4 is a protein called DNA-directed RNA polymerase I subunit RPA14.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	19	Total	C	N	O	0	0
			143	91	26	26		

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	214	Total	C	N	O	S	0	0
			1751	1111	309	320	11		

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	101	Total	C	N	O	S	0	0
			827	524	145	155	3		

- Molecule 7 is a protein called DNA-directed RNA polymerase I subunit RPA43.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	90	Total	C	N	O	S	0	0
			716	472	114	126	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	131	Total	C	N	O	S	0	0
			1052	664	176	208	4		

- Molecule 9 is a protein called DNA-directed RNA polymerase I subunit RPA12.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	65	Total	C	N	O	S	0	0
			479	300	79	96	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	69	Total	C	N	O	S	0	0
			569	362	101	100	6		

- Molecule 11 is a protein called DNA-directed RNA polymerases I and III subunit RPAC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	98	Total	C	N	O	S	0	0
			766	481	124	156	5		

- Molecule 12 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	44	Total	C	N	O	S	0	0
			352	217	70	61	4		

- Molecule 13 is a protein called DNA-directed RNA polymerase I subunit RPA49.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	100	Total	C	N	O		0	0
			791	503	131	157			

- Molecule 14 is a protein called DNA-directed RNA polymerase I subunit RPA34.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	117	Total	C	N	O	S	0	0
			933	603	153	173	4		

- Molecule 15 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	R	9	Total	C	N	O	P	0	0
			197	88	40	60	9		

- Molecule 16 is a DNA chain called Non-template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	S	20	Total	C	N	O	P	0	0
			402	193	65	124	20		

- Molecule 17 is a DNA chain called Template DNA.

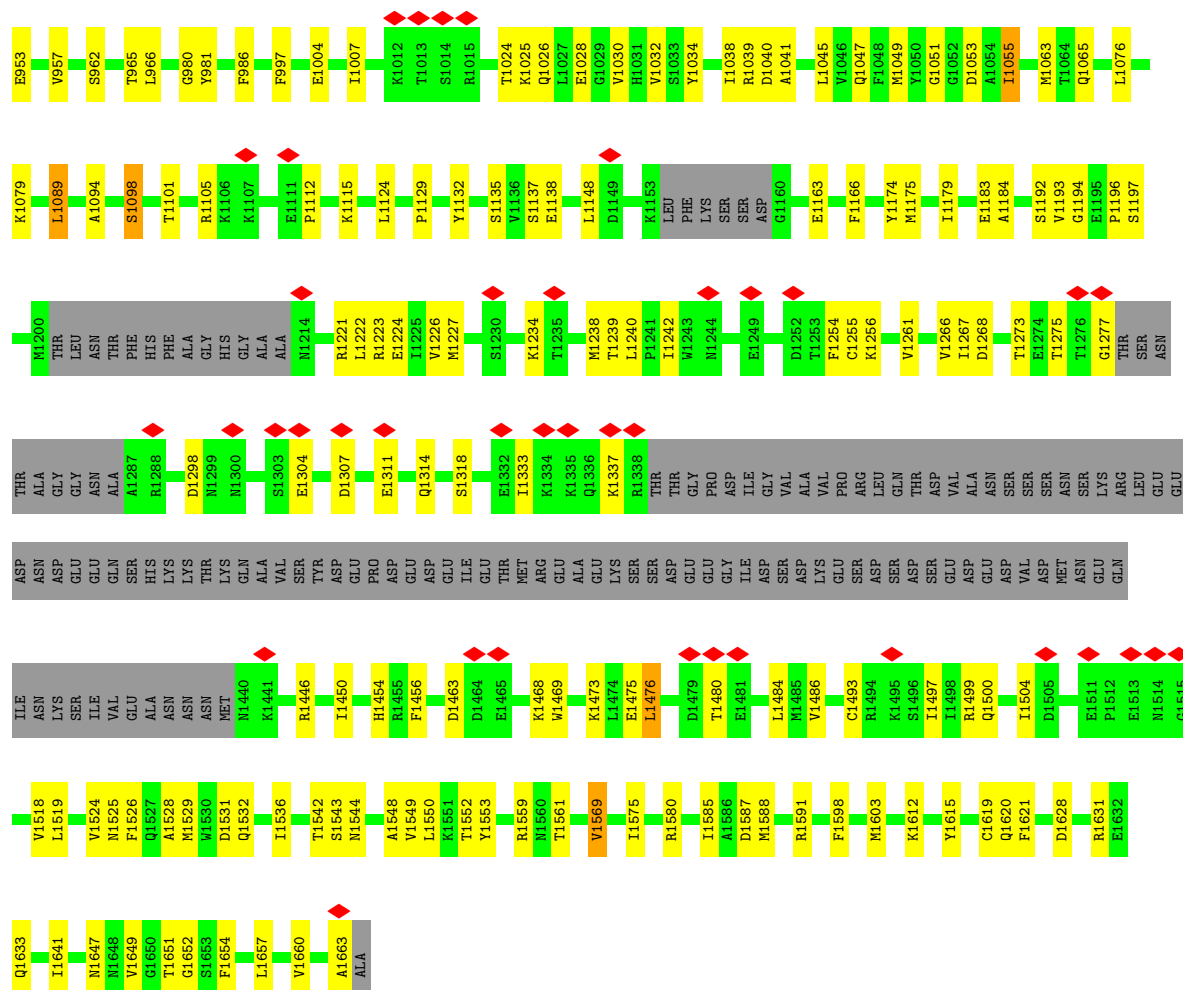
Mol	Chain	Residues	Atoms					AltConf	Trace
17	T	28	Total	C	N	O	P	0	0
			564	269	99	168	28		

- Molecule 18 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

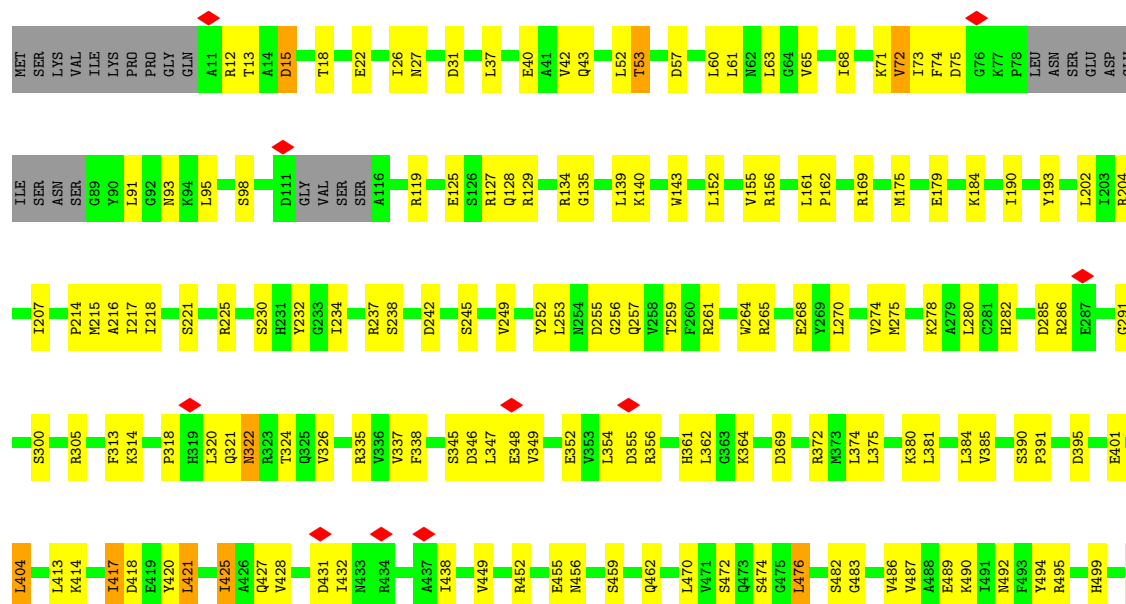
Mol	Chain	Residues	Atoms		AltConf
18	A	1	Total	Mg	0
			1	1	

- Molecule 19 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
19	A	2	Total	Zn	0
			2	2	
19	B	1	Total	Zn	0
			1	1	
19	I	1	Total	Zn	0
			1	1	
19	J	1	Total	Zn	0
			1	1	
19	L	1	Total	Zn	0
			1	1	



• Molecule 2: DNA-directed RNA polymerase I subunit RPA135

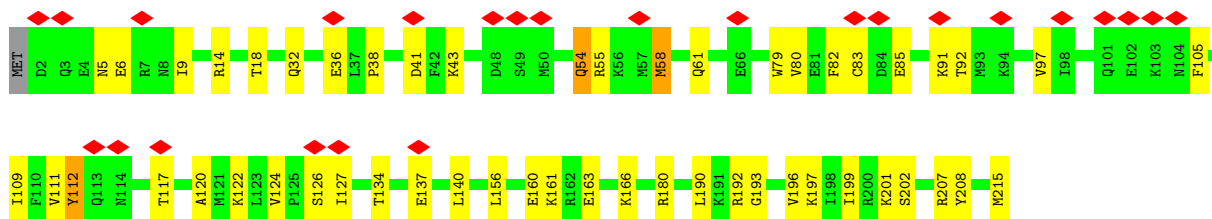




ALA
THR
GLY
GLY
LYS
LYS
THR
THR
PHE
ALA
ASP
GLU

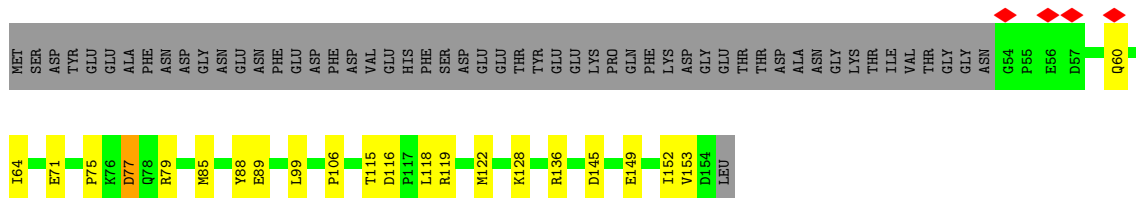
- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1

Chain E: 12% 75% 23%



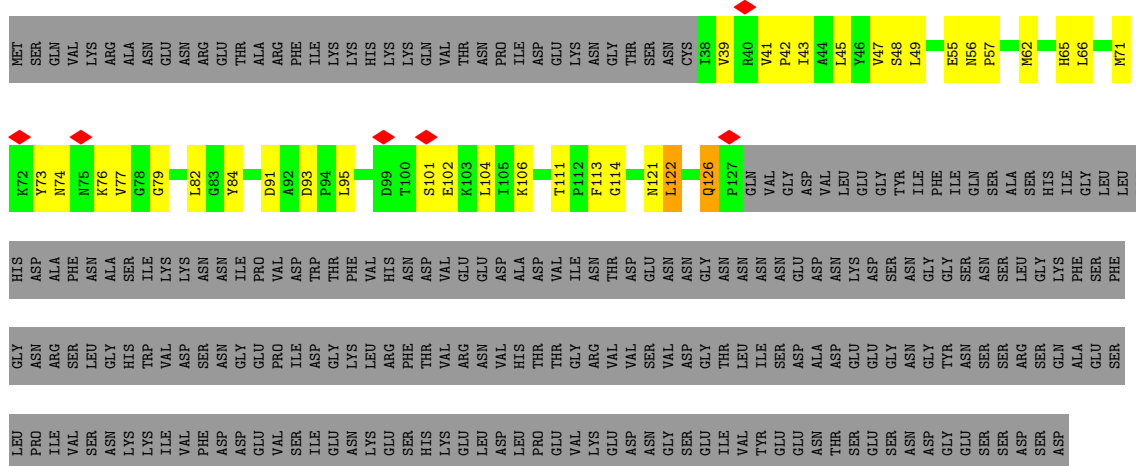
- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2

Chain F: 51% 14% 35%



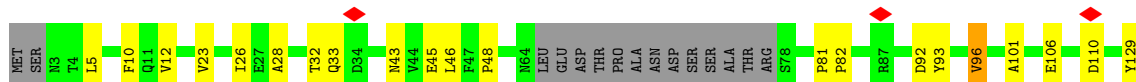
- Molecule 7: DNA-directed RNA polymerase I subunit RPA43

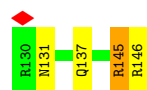
Chain G: 17% 10% 72%



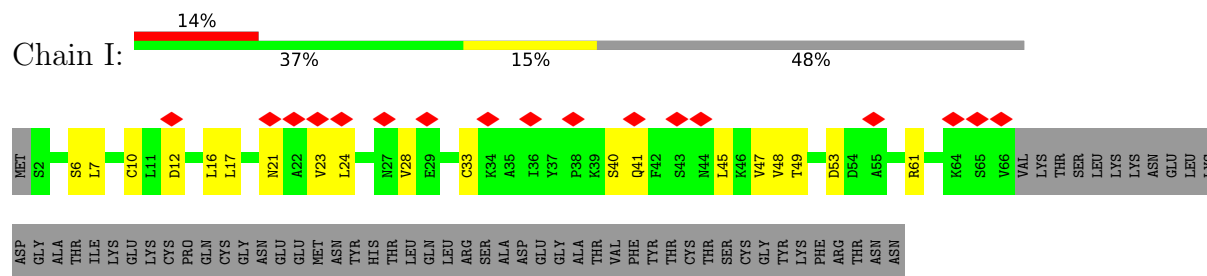
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain H: 73% 16% 10%

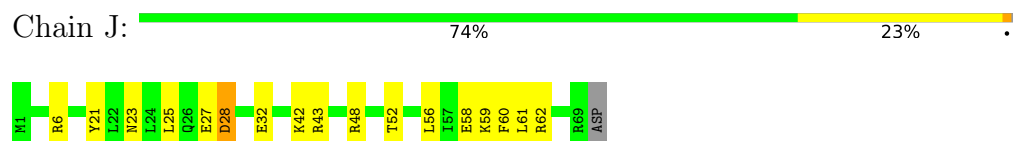




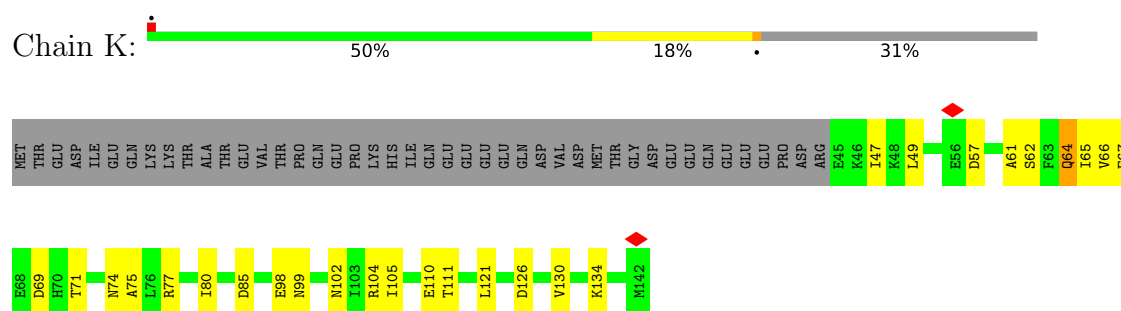
- Molecule 9: DNA-directed RNA polymerase I subunit RPA12



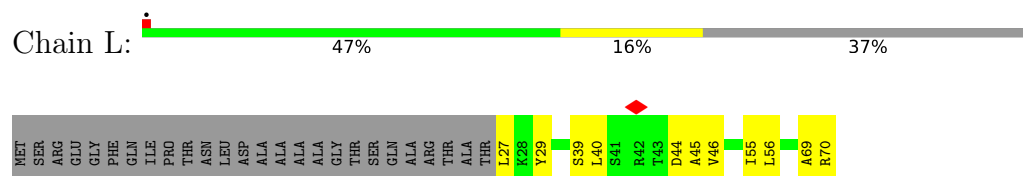
- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5



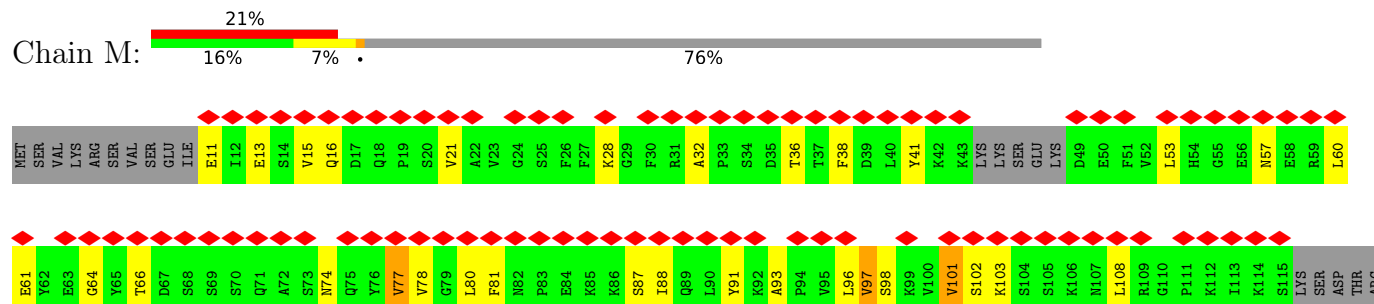
- Molecule 11: DNA-directed RNA polymerases I and III subunit RPAC2



- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4

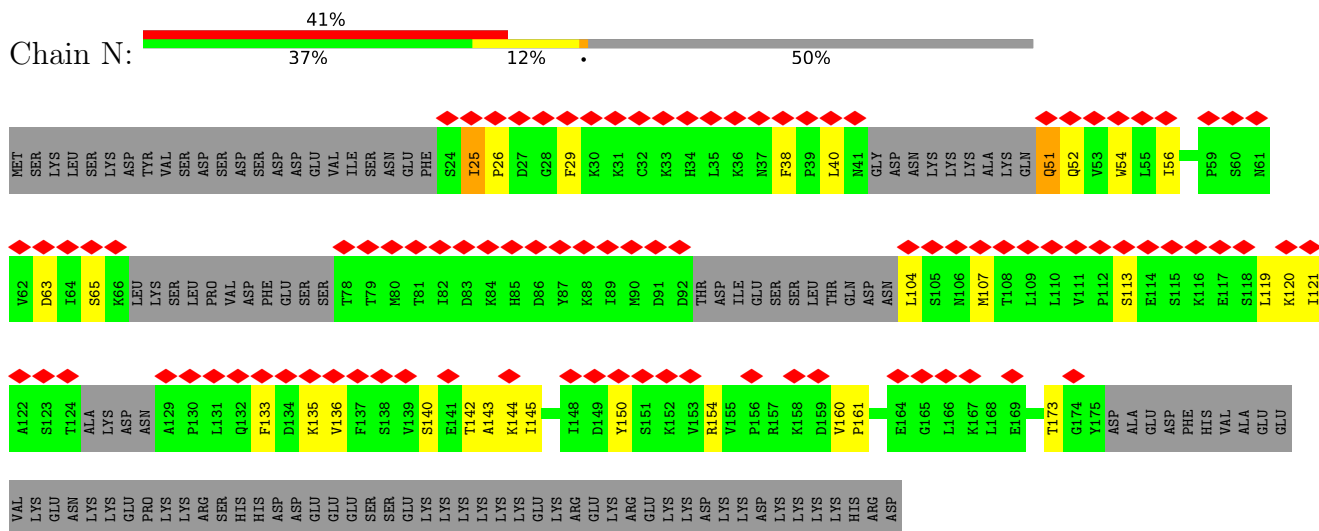


- Molecule 13: DNA-directed RNA polymerase I subunit RPA49

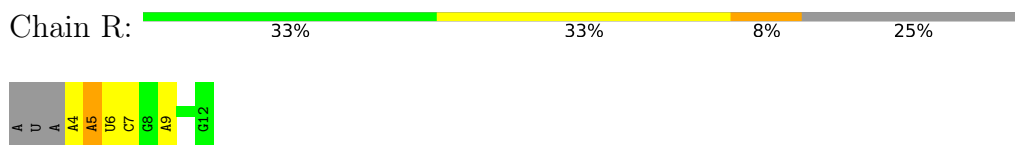


VAL	SER	VAL	ARG	LYS	ILE	PRO
SER	LEU	THR	PHE	THR	VAL	SER
LEU	PHE	VAL	VAL	ALA	SER	ALA
ARG	ARG	ILE	LYS	LYS	ASN	ARG
VAL	VAL	VAL	LYS	LEU	ARG	ASN
LEU	LEU	PRO	PRO	ASP	PRO	ALA
GLY	GLY	GLY	GLY	ASP	THR	LEU
ALA	ALA	GLN	GLN	SER	PRO	GLY
ILE	ILE	PHE	PHE	LEU	LEU	ALA
VAL	VAL	GLY	GLY	THR	ALA	ALA
LYS	LYS	ARG	ARG	GLN	ASN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

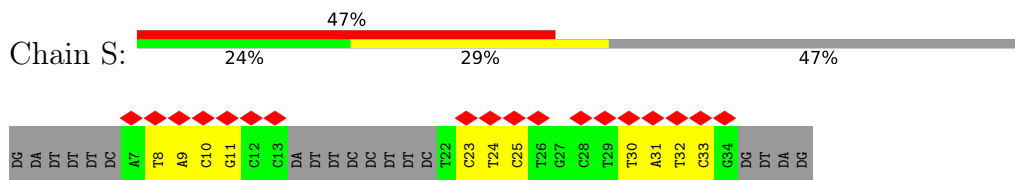
- Molecule 14: DNA-directed RNA polymerase I subunit RPA34



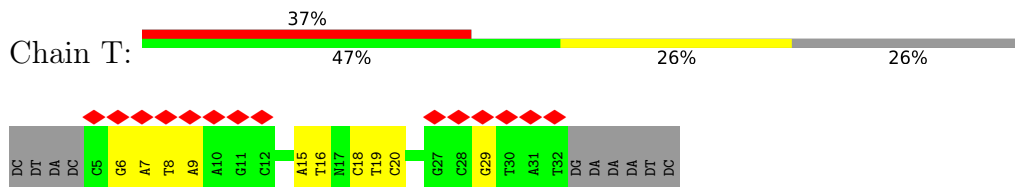
- Molecule 15: RNA



- Molecule 16: Non-template DNA



- Molecule 17: Template DNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	834570	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.1	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.157	Depositor
Minimum map value	-0.086	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0203	Depositor
Map size (\AA)	301.536, 301.536, 301.536	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.047, 1.047, 1.047	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, 3DR, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.22	0/11709	0.33	0/15811
2	B	0.24	0/9459	0.33	0/12785
3	C	0.24	0/2467	0.29	0/3344
4	D	0.14	0/146	0.23	0/203
5	E	0.18	0/1787	0.29	0/2406
6	F	0.22	0/842	0.29	0/1135
7	G	0.18	0/736	0.30	0/1005
8	H	0.22	0/1070	0.30	0/1449
9	I	0.15	0/485	0.34	0/657
10	J	0.28	0/578	0.33	0/775
11	K	0.23	0/776	0.28	0/1047
12	L	0.23	0/354	0.32	0/468
13	M	0.11	0/806	0.29	0/1083
14	N	0.11	0/950	0.27	0/1276
15	R	0.23	0/221	0.31	0/343
16	S	0.18	0/446	0.40	0/682
17	T	0.25	0/618	0.37	0/949
All	All	0.22	0/33450	0.32	0/45418

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	11500	0	11589	249	0
2	B	9254	0	9145	238	0
3	C	2415	0	2403	46	0
4	D	143	0	147	6	0
5	E	1751	0	1776	35	0
6	F	827	0	843	14	0
7	G	716	0	735	25	0
8	H	1052	0	1021	14	0
9	I	479	0	481	10	0
10	J	569	0	585	14	0
11	K	766	0	765	20	0
12	L	352	0	374	11	0
13	M	791	0	782	27	0
14	N	933	0	960	24	0
15	R	197	0	98	5	0
16	S	402	0	229	10	0
17	T	564	0	314	7	0
18	A	1	0	0	0	0
19	A	2	0	0	0	0
19	B	1	0	0	0	0
19	I	1	0	0	0	0
19	J	1	0	0	0	0
19	L	1	0	0	0	0
All	All	32718	0	32247	660	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 10.

The worst 5 of 660 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:B:1107:CYS:HB3	2:B:1131:CYS:SG	2.08	0.93
2:B:1010:ASN:HB3	2:B:1025:ASP:HB3	1.60	0.83
2:B:225:ARG:NH2	2:B:268:GLU:OE2	2.16	0.78
7:G:111:THR:HG22	7:G:113:PHE:H	1.50	0.76
1:A:239:PHE:HB2	1:A:264:ASN:HD21	1.51	0.76

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	
1	A	1440/1664 (86%)	1377 (96%)	63 (4%)	0	100	100
2	B	1156/1203 (96%)	1102 (95%)	54 (5%)	0	100	100
3	C	302/335 (90%)	288 (95%)	14 (5%)	0	100	100
4	D	17/137 (12%)	15 (88%)	2 (12%)	0	100	100
5	E	212/215 (99%)	204 (96%)	8 (4%)	0	100	100
6	F	99/155 (64%)	95 (96%)	4 (4%)	0	100	100
7	G	88/326 (27%)	87 (99%)	1 (1%)	0	100	100
8	H	127/146 (87%)	119 (94%)	8 (6%)	0	100	100
9	I	63/125 (50%)	53 (84%)	10 (16%)	0	100	100
10	J	67/70 (96%)	62 (92%)	5 (8%)	0	100	100
11	K	96/142 (68%)	92 (96%)	4 (4%)	0	100	100
12	L	42/70 (60%)	39 (93%)	3 (7%)	0	100	100
13	M	96/415 (23%)	91 (95%)	5 (5%)	0	100	100
14	N	107/233 (46%)	101 (94%)	6 (6%)	0	100	100
All	All	3912/5236 (75%)	3725 (95%)	187 (5%)	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	1285/1465 (88%)	1245 (97%)	40 (3%)	35	64
2	B	1017/1053 (97%)	976 (96%)	41 (4%)	27	55
3	C	268/296 (90%)	259 (97%)	9 (3%)	32	61
4	D	17/116 (15%)	17 (100%)	0	100	100
5	E	196/197 (100%)	190 (97%)	6 (3%)	35	64
6	F	90/137 (66%)	86 (96%)	4 (4%)	24	51
7	G	81/291 (28%)	77 (95%)	4 (5%)	21	47
8	H	115/128 (90%)	110 (96%)	5 (4%)	25	52
9	I	57/110 (52%)	52 (91%)	5 (9%)	8	20
10	J	64/65 (98%)	62 (97%)	2 (3%)	35	64
11	K	88/130 (68%)	85 (97%)	3 (3%)	32	61
12	L	39/57 (68%)	39 (100%)	0	100	100
13	M	90/371 (24%)	85 (94%)	5 (6%)	17	41
14	N	109/220 (50%)	106 (97%)	3 (3%)	38	68
All	All	3516/4636 (76%)	3389 (96%)	127 (4%)	32	59

5 of 127 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	604	ILE
9	I	21	ASN
2	B	1030	VAL
9	I	7	LEU
11	K	110	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	1114	GLN
5	E	115	ASN
2	B	1171	ASN
3	C	301	ASN
8	H	137	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
15	R	8/12 (66%)	1 (12%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
15	R	5	A

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
17	3DR	T	17	17	8,11,12	0.53	0	9,14,17	0.53	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
17	3DR	T	17	17	-	2/3/15/16	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	T	17	3DR	C3'-C4'-C5'-O5'
17	T	17	3DR	O4'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 7 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.

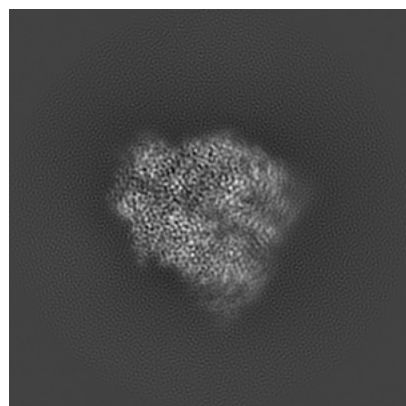
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-50955. These allow visual inspection of the internal detail of the map and identification of artifacts.

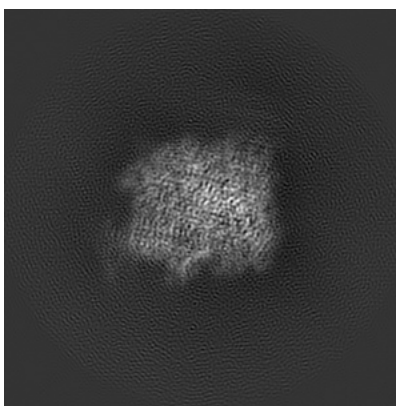
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

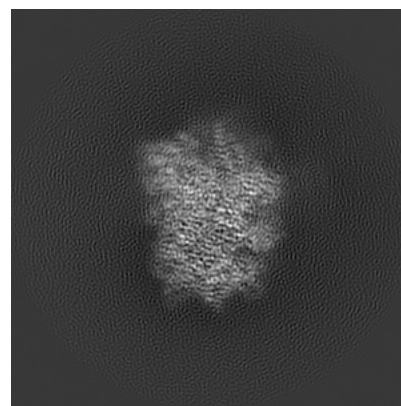
6.1.1 Primary map



X

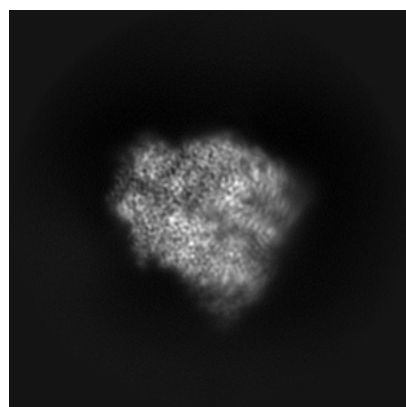


Y

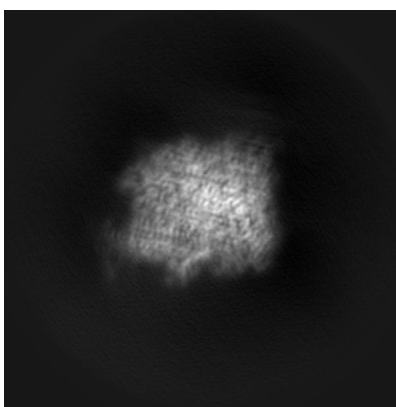


Z

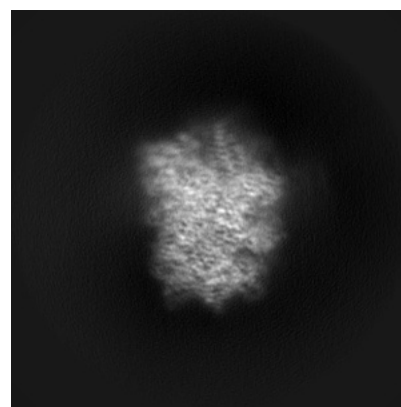
6.1.2 Raw map



X



Y

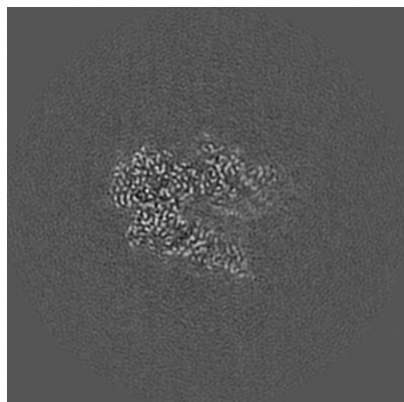


Z

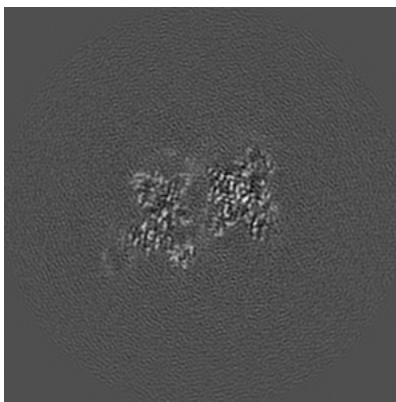
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

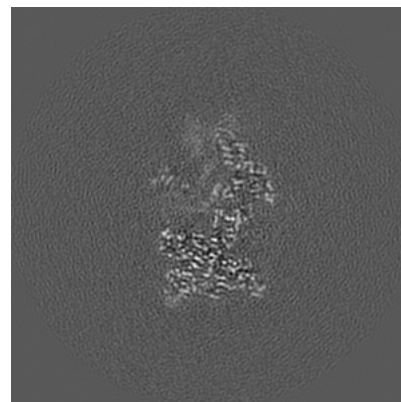
6.2.1 Primary map



X Index: 144

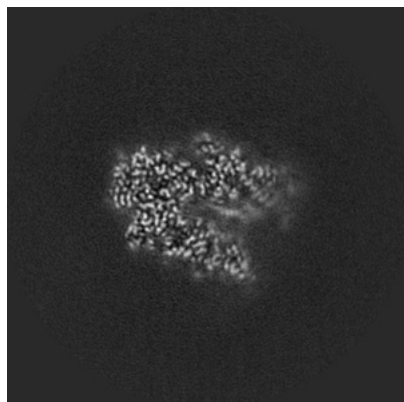


Y Index: 144

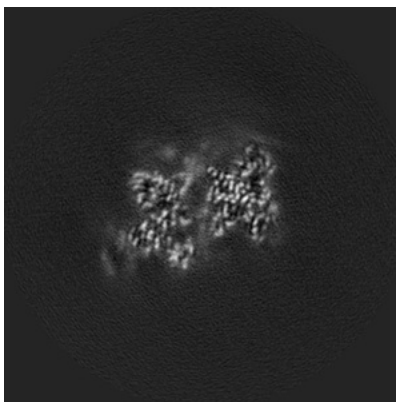


Z Index: 144

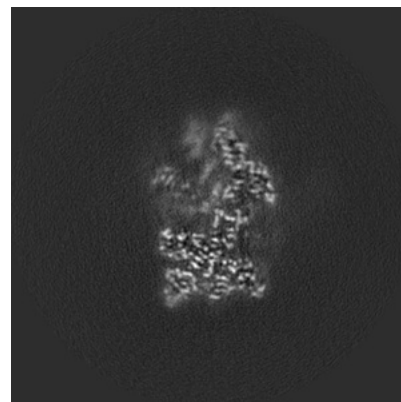
6.2.2 Raw map



X Index: 144



Y Index: 144

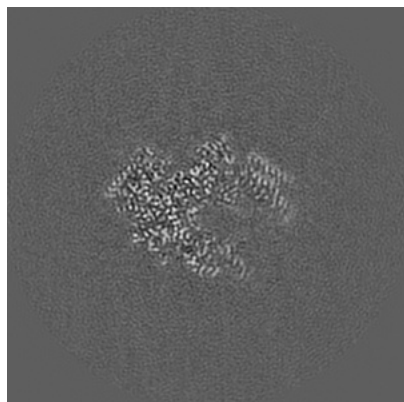


Z Index: 144

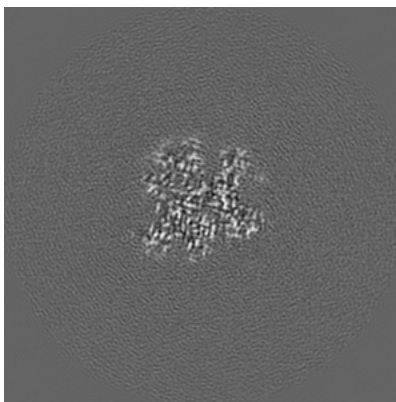
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

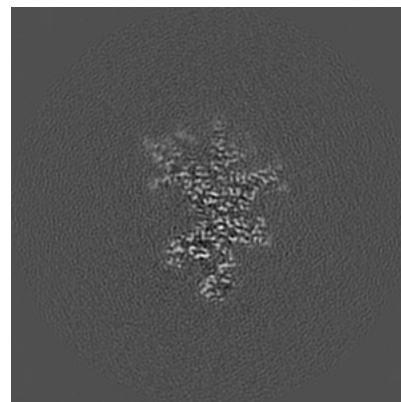
6.3.1 Primary map



X Index: 150

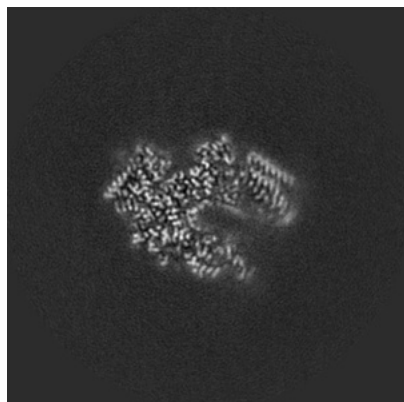


Y Index: 123

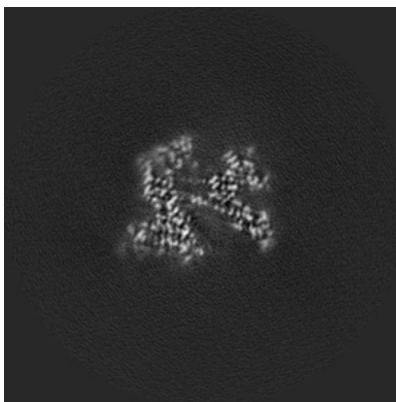


Z Index: 162

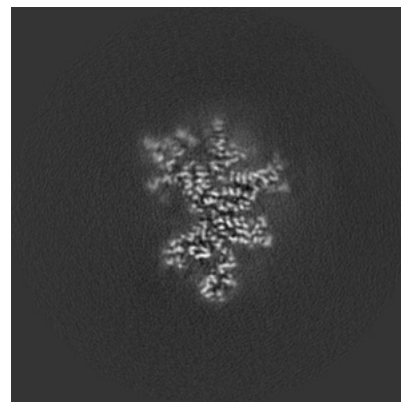
6.3.2 Raw map



X Index: 150



Y Index: 130

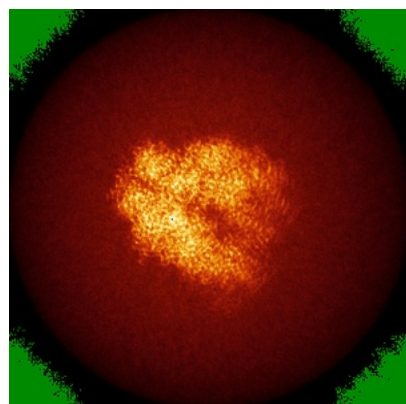


Z Index: 162

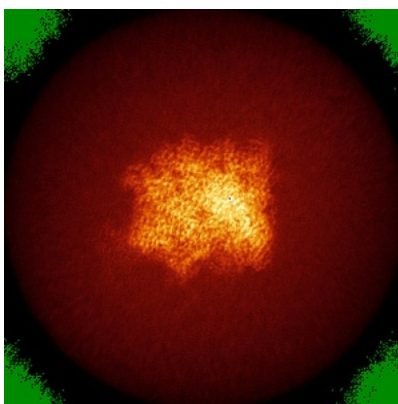
The images above show the largest variance slices of the map in three orthogonal directions.

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

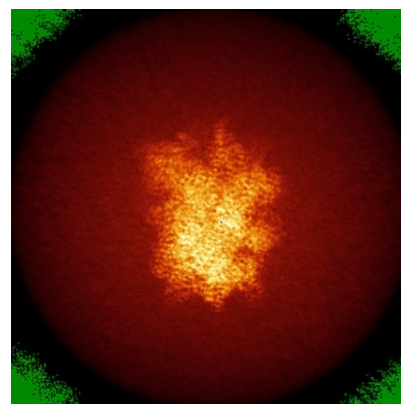
6.4.1 Primary map



X

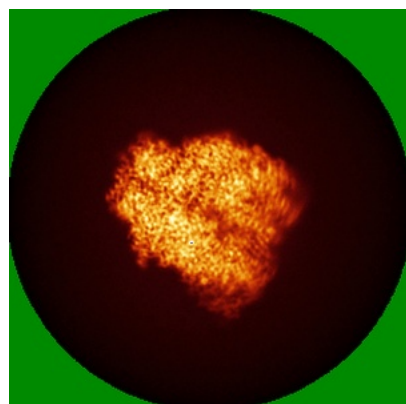


Y

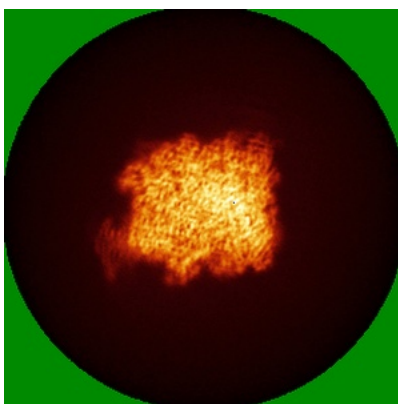


Z

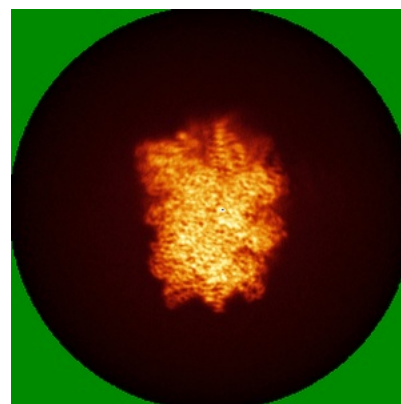
6.4.2 Raw map



X



Y

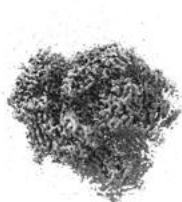


Z

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



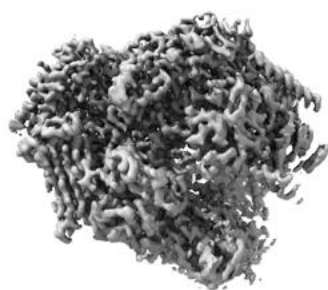
Y



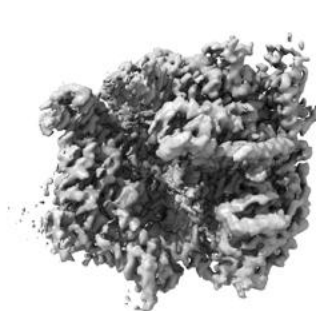
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0203. 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.

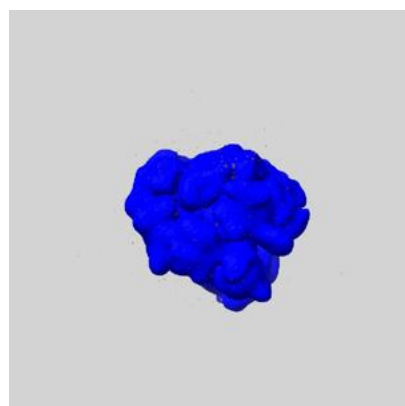
6.6 Mask visualisation [i](#)

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

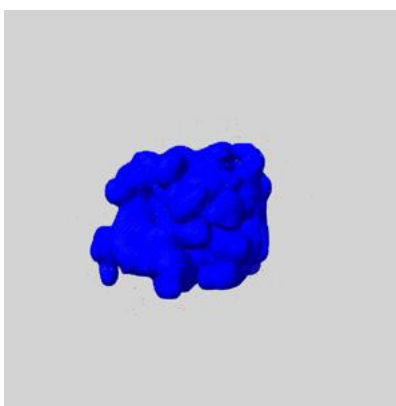
A mask typically either:

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

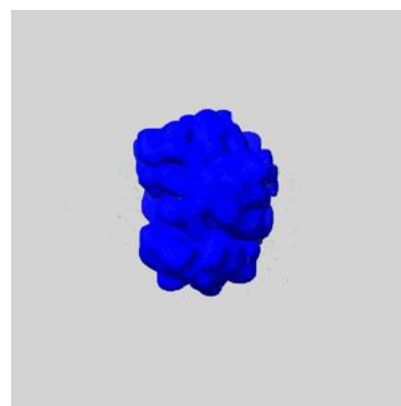
6.6.1 emd_50955_msk_1.map [i](#)



X



Y

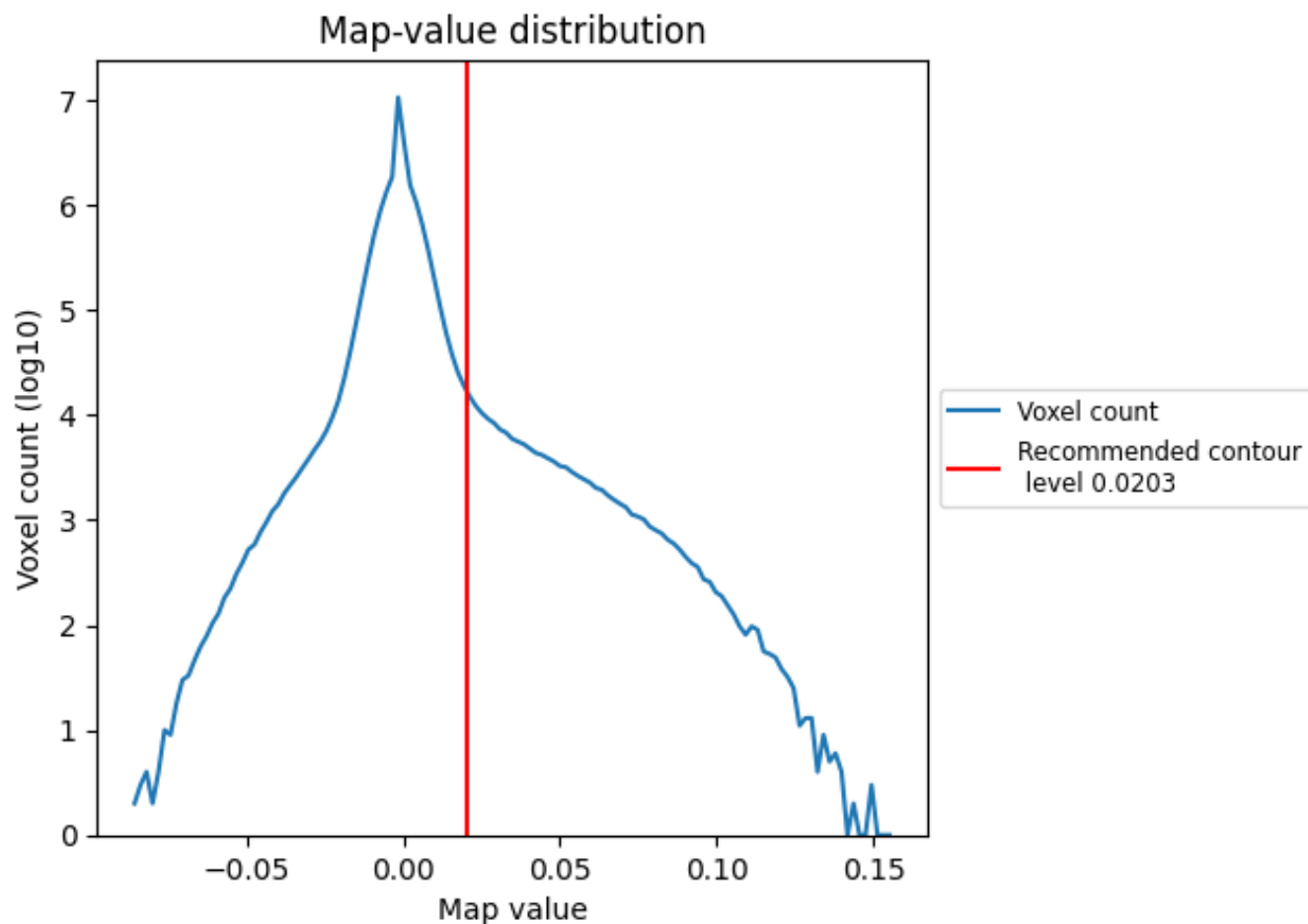


Z

7 Map analysis [i](#)

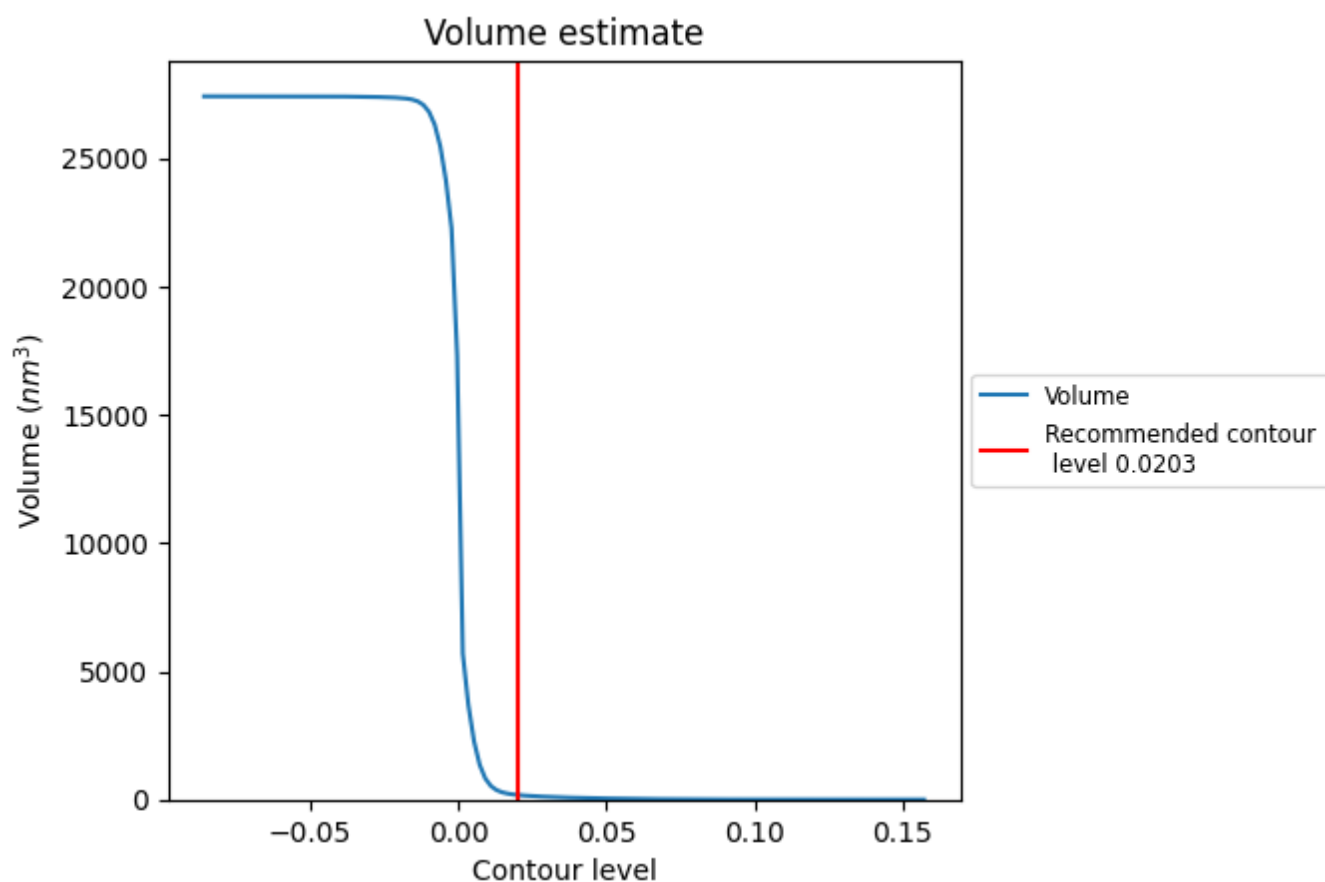
This section contains the results of statistical analysis of the map.

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.

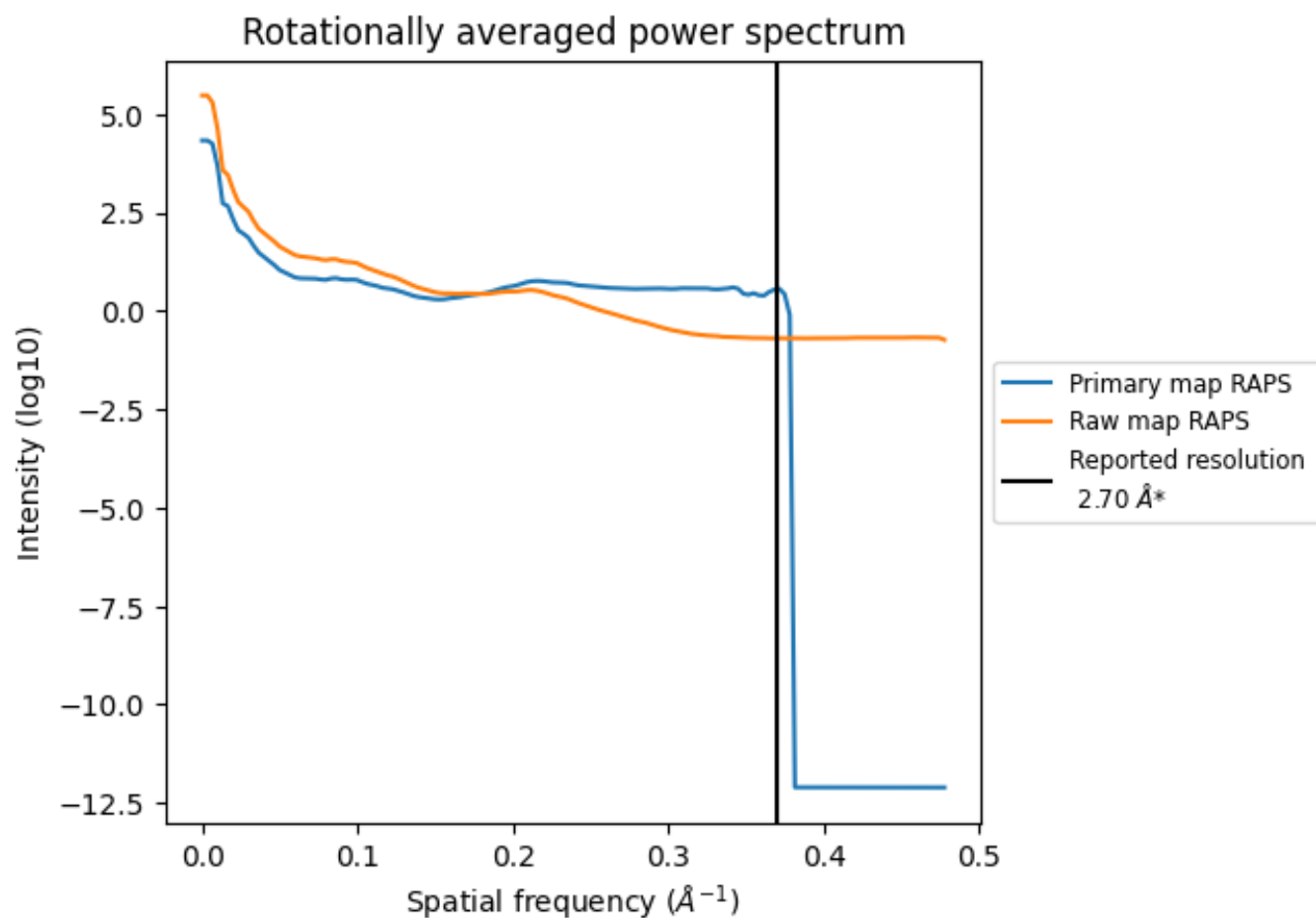
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 177 nm³; this corresponds to an approximate mass of 160 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 ⓘ

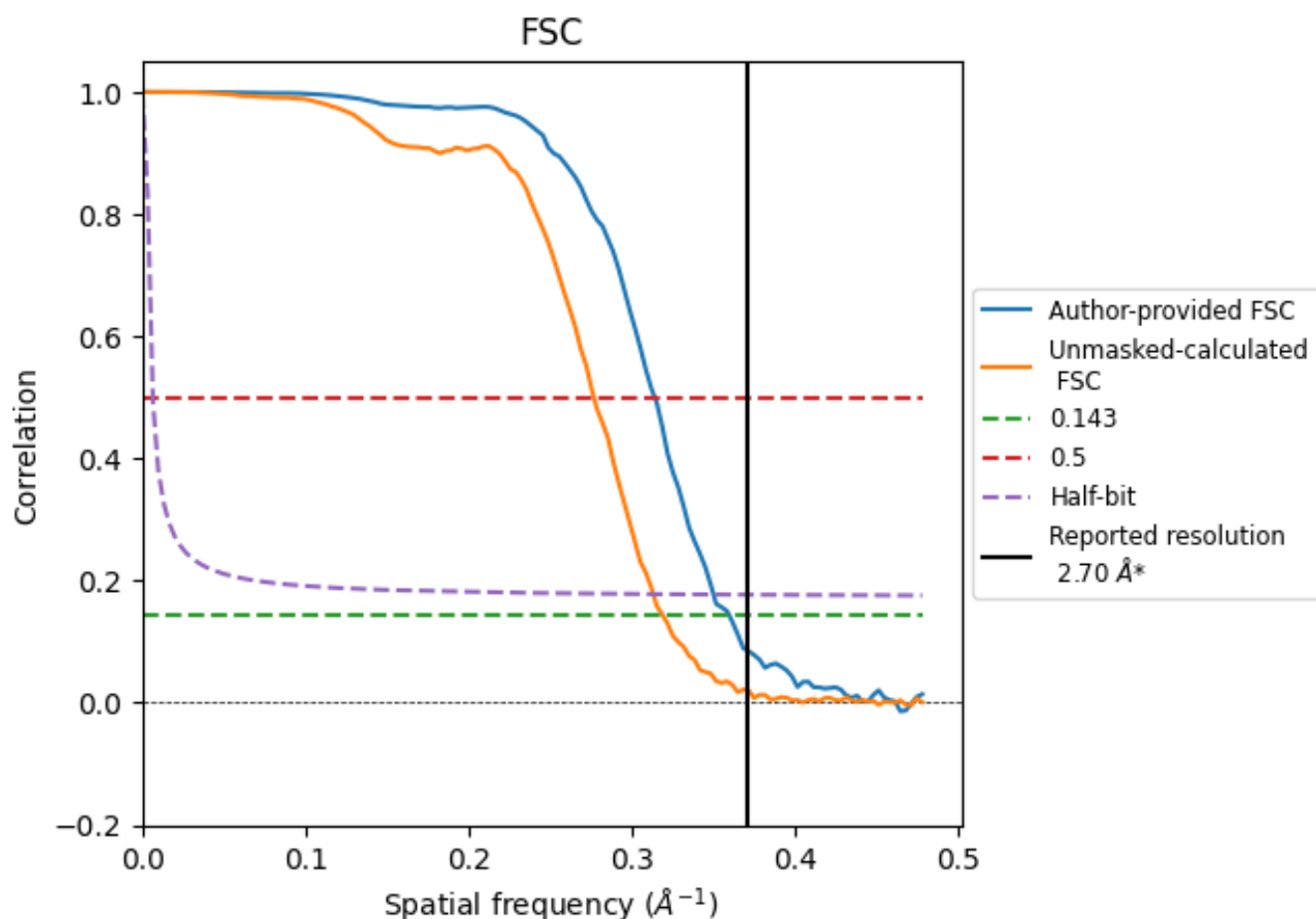


*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

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 0.370 \AA^{-1}

8.2 Resolution estimates [i](#)

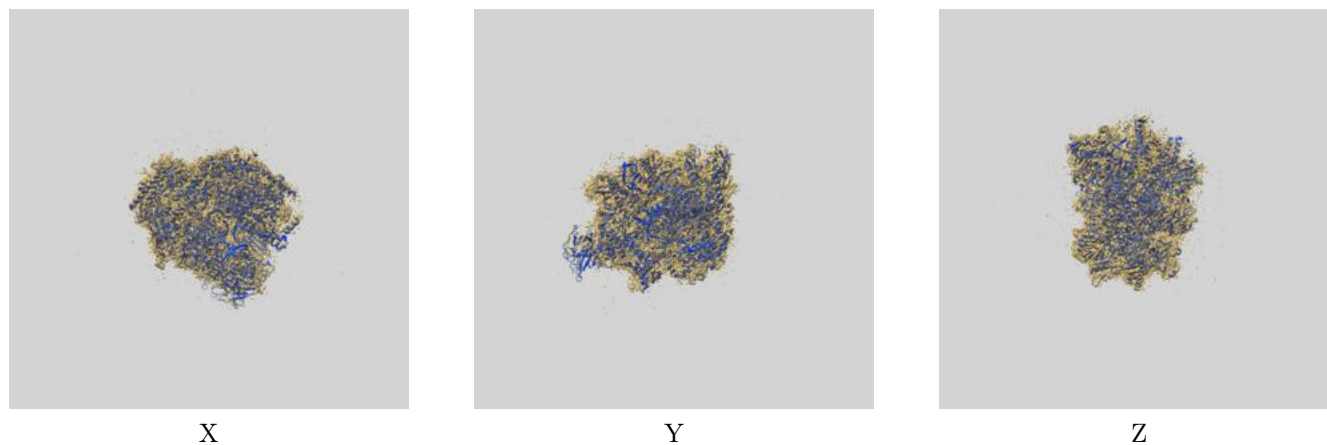
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.78	3.19	2.86
Unmasked-calculated*	3.14	3.62	3.19

*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 3.14 differs from the reported value 2.7 by more than 10 %

9 Map-model fit [i](#)

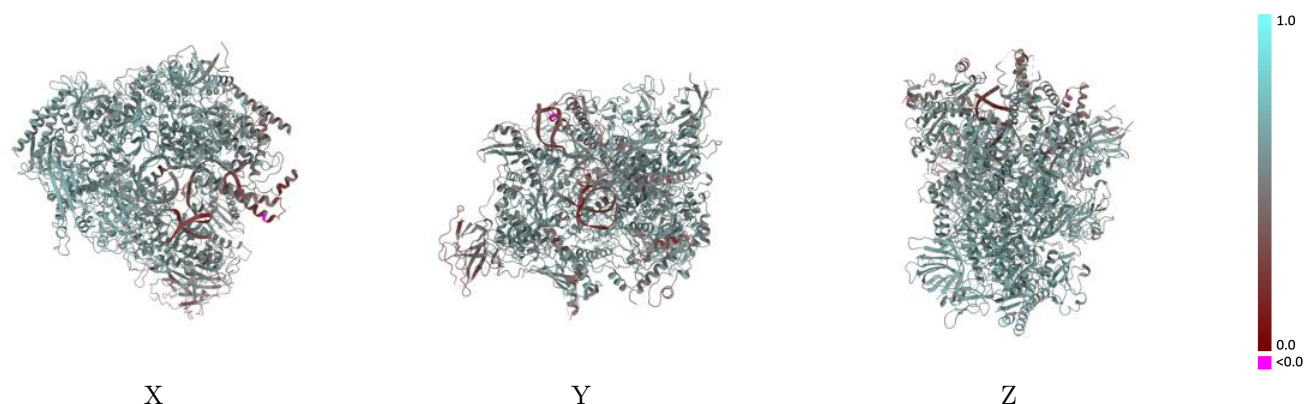
This section contains information regarding the fit between EMDB map EMD-50955 and PDB model 9G1V. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



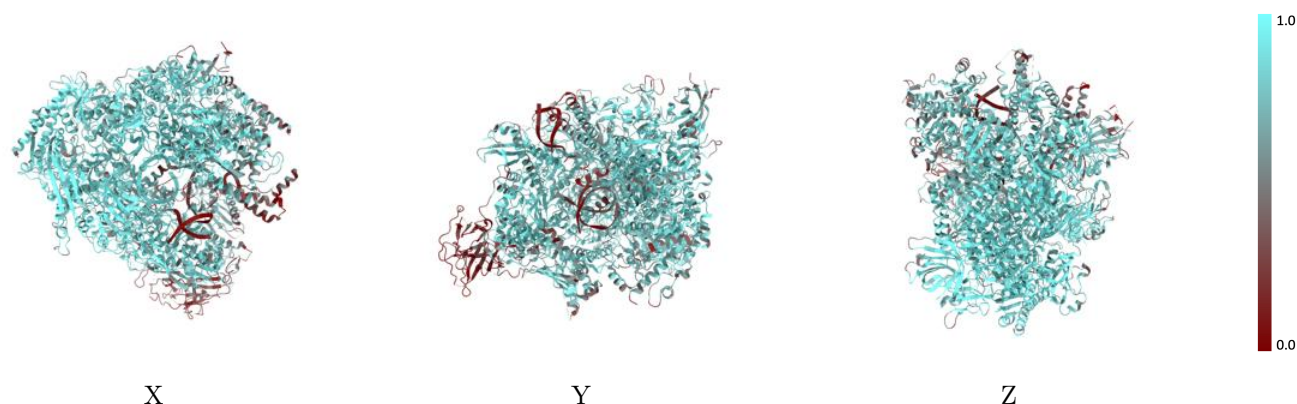
The images above show the 3D surface view of the map at the recommended contour level 0.0203 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



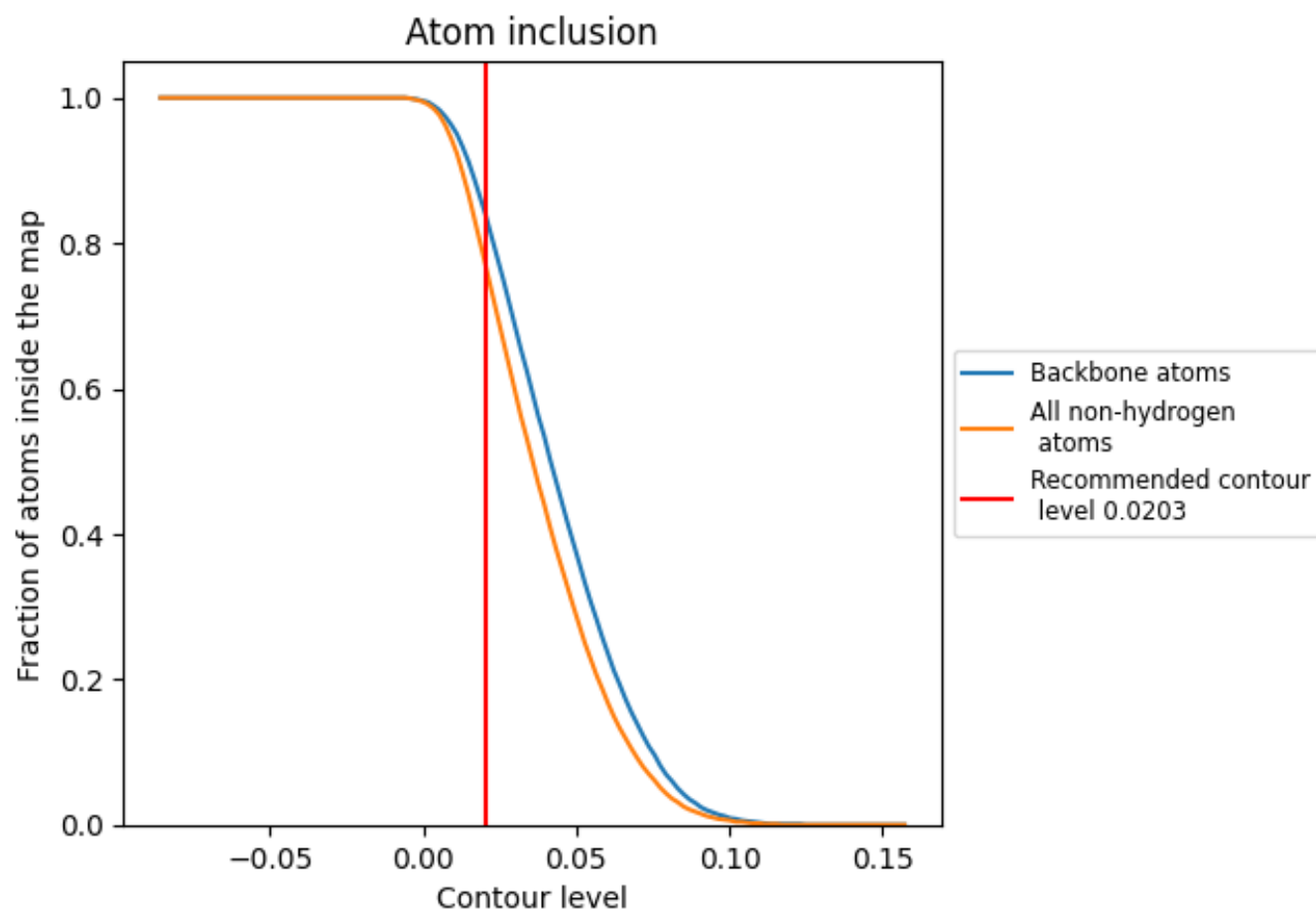
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0203).





































9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 77% 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 (0.0203) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7720	 0.5490
A	 0.7930	 0.5540
B	 0.8580	 0.5780
C	 0.8620	 0.5850
D	 0.7060	 0.5460
E	 0.7230	 0.5090
F	 0.8520	 0.5760
G	 0.7090	 0.5430
H	 0.8490	 0.5840
I	 0.5660	 0.4880
J	 0.9200	 0.6160
K	 0.8740	 0.5840
L	 0.8500	 0.5740
M	 0.1870	 0.4090
N	 0.2260	 0.4250
R	 0.8880	 0.5540
S	 0.1990	 0.2640
T	 0.4680	 0.3890

