



wwPDB EM Validation Summary Report ⓘ

Aug 27, 2026 – 10:35 am BST

PDB ID : 9T5H / pdb_00009t5h
EMDB ID : EMD-55583
Title : RNA polymerase II bound to Gdown1 and RPAP2
Authors : Hlavata, A.; Bernecky, C.
Deposited on : 2025-11-05
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:

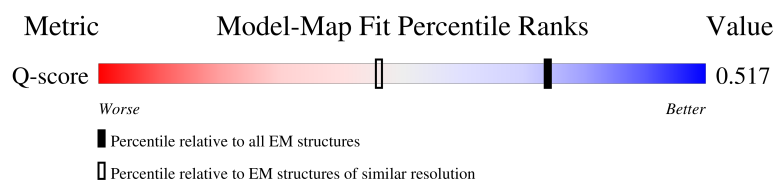
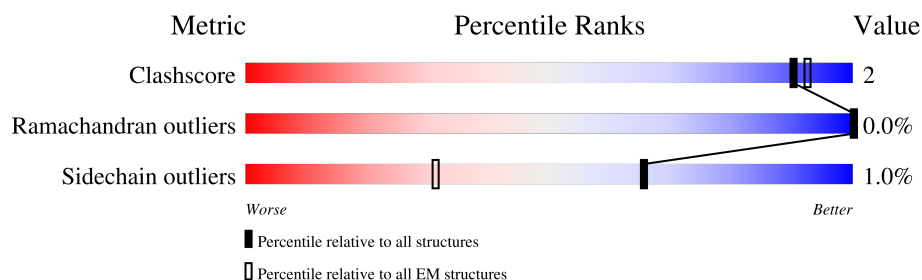
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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.



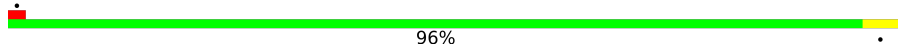
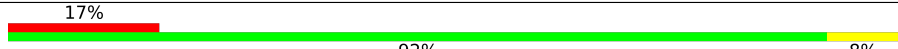
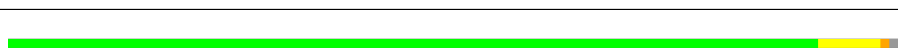
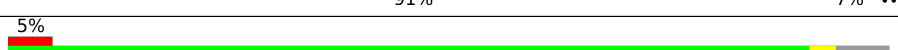
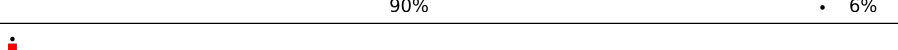
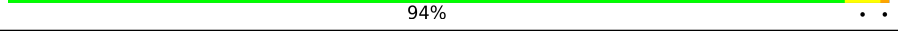
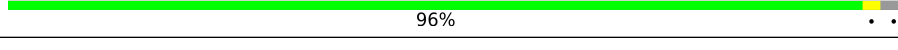
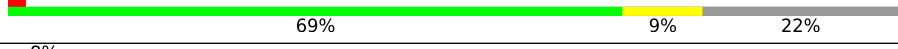
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10327 (2.20 - 3.20)

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	1970	
2	B	1174	
3	C	275	
4	D	142	

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Mol	Chain	Length	Quality of chain
5	E	210	
6	F	127	
7	G	172	
8	H	150	
9	I	125	
10	J	67	
11	K	117	
12	L	58	
13	M	368	
14	N	612	

2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 29315 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1040	Total	C	N	O	S	0	0
			8296	5229	1465	1557	45		

- Molecule 2 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1013	Total	C	N	O	S	0	0
			8111	5150	1411	1500	50		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	258	Total	C	N	O	S	0	0
			2073	1302	356	409	6		

- Molecule 4 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	128	Total	C	N	O	S	0	0
			1013	636	172	201	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	209	Total	C	N	O	S	0	0
			1721	1089	300	324	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	44	PHE	SER	conflict	UNP P19388

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	82	Total	C	N	O	S	0	0
			659	419	113	122	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
			1334	867	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	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	117	Total	C	N	O	S	0	0
			950	587	169	183	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	N	O	S	0	0
			534	345	90	93	6		

- Molecule 11 is a protein called DNA-directed RNA polymerase II subunit RPB11-a.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	114	Total	C	N	O	S	0	0
			912	588	151	172	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	45	Total	C	N	O	S	0	0
			380	236	73	65	6		

- Molecule 13 is a protein called DNA-directed RNA polymerase II subunit GRINL1A.

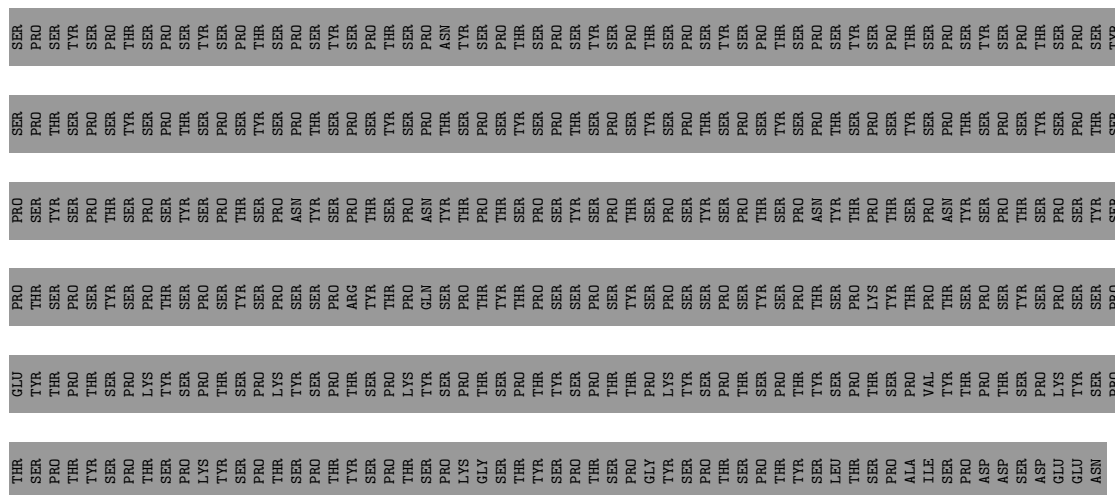
Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	127	Total	C	N	O	S	0	0
			1048	668	188	185	7		

- Molecule 14 is a protein called Putative RNA polymerase II subunit B1 CTD phosphatase RPAP2.

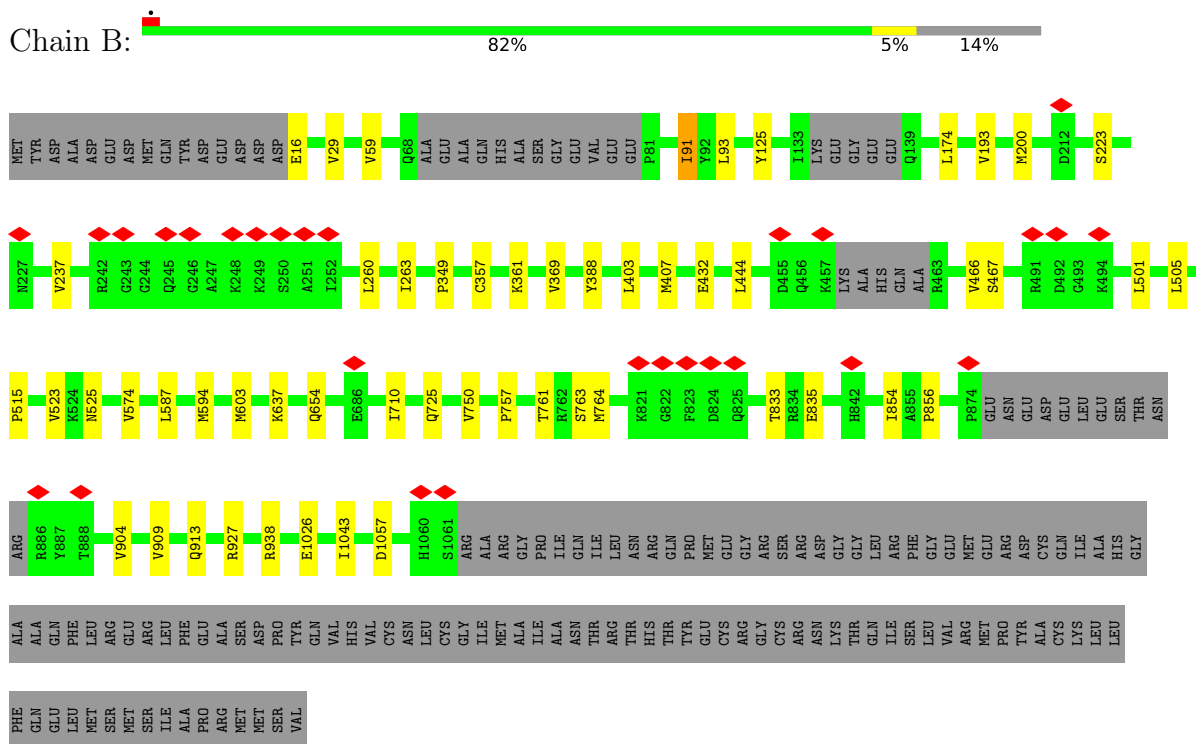
Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	132	Total	C	N	O	S	0	0
			1092	703	184	199	6		

- Molecule 15 is ZINC ION (CCD ID: ZN) (formula: Zn).

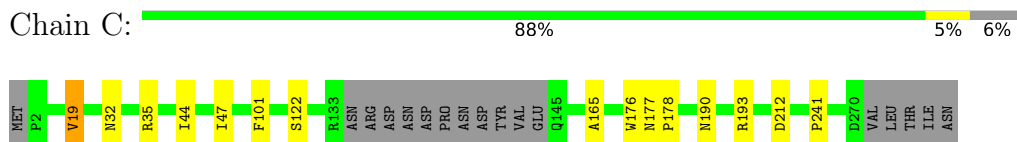
Mol	Chain	Residues	Atoms		AltConf
15	C	1	Total	Zn	0
			1	1	
15	I	2	Total	Zn	0
			2	2	
15	J	1	Total	Zn	0
			1	1	
15	L	1	Total	Zn	0
			1	1	
15	N	1	Total	Zn	0
			1	1	



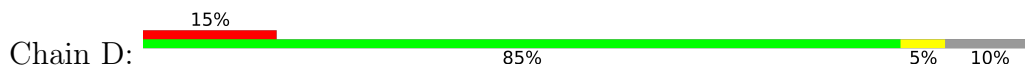
- Molecule 2: DNA-directed RNA polymerase II subunit RPB2

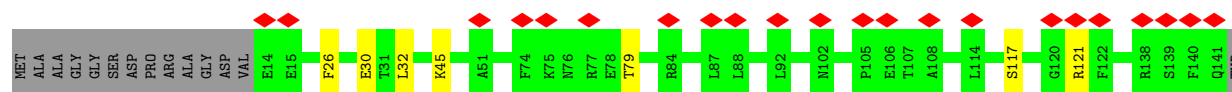


- Molecule 3: DNA-directed RNA polymerase II subunit RPB3

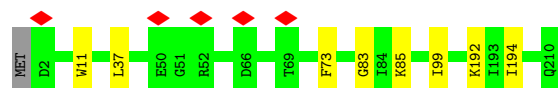


- Molecule 4: DNA-directed RNA polymerase II subunit RPB4

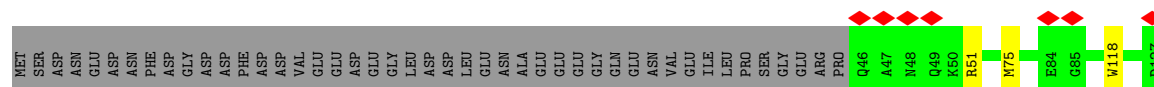




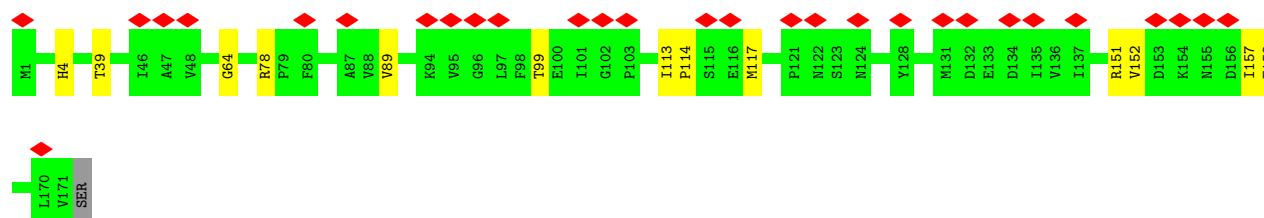
- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1



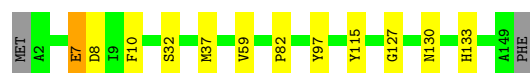
- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2



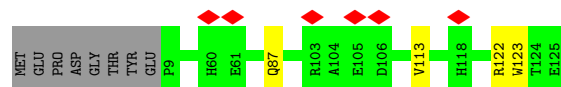
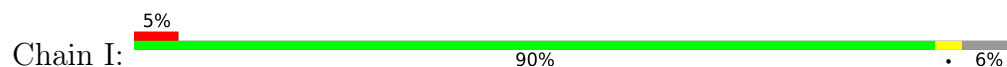
- Molecule 7: DNA-directed RNA polymerase II subunit RPB7



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



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



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





- Molecule 11: DNA-directed RNA polymerase II subunit RPB11-a

Chain K: 96%



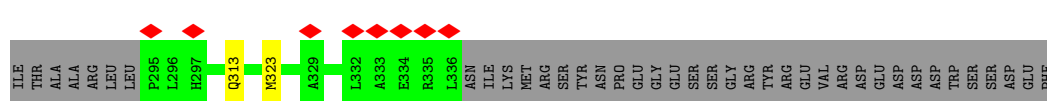
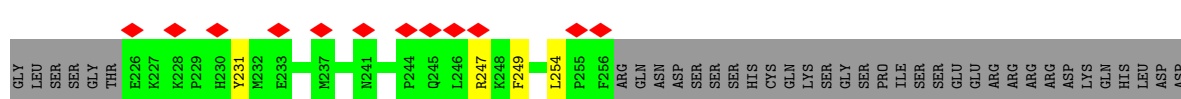
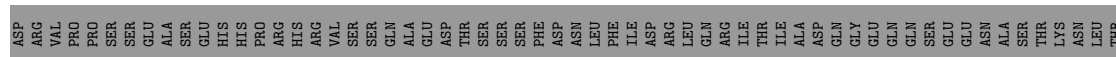
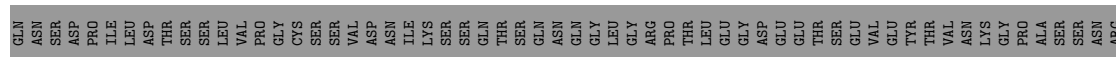
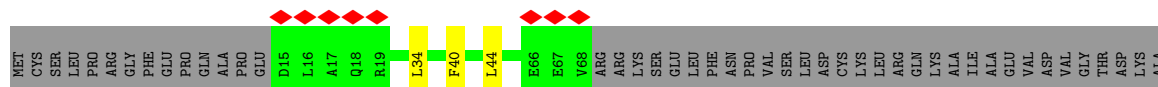
- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4

Chain L: 69% 9% 22%



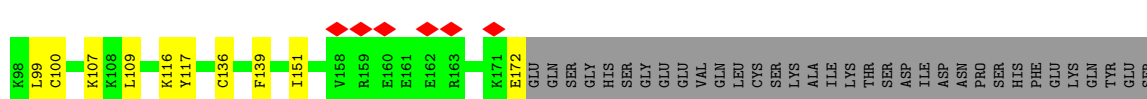
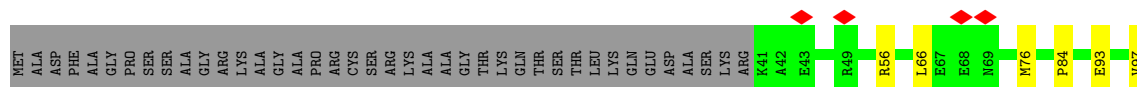
- Molecule 13: DNA-directed RNA polymerase II subunit GRINL1A

Chain M: 8% 32% 65%



- Molecule 14: Putative RNA polymerase II subunit B1 CTD phosphatase RPAP2

Chain N: 19% 78%



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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	886711	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	75	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.248	Depositor
Minimum map value	0.000	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.026	Depositor
Map size (Å)	503.808, 503.808, 503.808	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.312, 1.312, 1.312	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	0.13	0/8447	0.43	0/11416
2	B	0.15	0/8275	0.44	0/11176
3	C	0.16	0/2116	0.46	0/2874
4	D	0.11	0/1027	0.41	0/1384
5	E	0.13	0/1752	0.41	0/2366
6	F	0.13	0/669	0.38	0/903
7	G	0.12	0/1365	0.41	0/1853
8	H	0.14	0/1207	0.43	0/1628
9	I	0.14	0/973	0.43	0/1316
10	J	0.16	0/543	0.44	0/730
11	K	0.15	0/931	0.44	0/1261
12	L	0.16	0/386	0.45	0/511
13	M	0.11	0/1062	0.41	0/1414
14	N	0.14	0/1115	0.48	0/1498
All	All	0.14	0/29868	0.43	0/40330

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	1
10	J	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	483	ARG	Sidechain
10	J	47	ARG	Sidechain

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	8296	0	8351	18	0
2	B	8111	0	8157	32	0
3	C	2073	0	2023	8	0
4	D	1013	0	972	4	0
5	E	1721	0	1737	9	0
6	F	659	0	686	2	0
7	G	1334	0	1333	8	0
8	H	1186	0	1147	7	0
9	I	950	0	879	2	0
10	J	534	0	553	3	0
11	K	912	0	930	0	0
12	L	380	0	386	3	0
13	M	1048	0	1107	15	0
14	N	1092	0	1102	13	0
15	C	1	0	0	0	0
15	I	2	0	0	0	0
15	J	1	0	0	0	0
15	L	1	0	0	0	0
15	N	1	0	0	0	0
All	All	29315	0	29363	99	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 2.

The worst 5 of 99 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:85:LYS:NZ	14:N:66:LEU:HD22	2.02	0.74
2:B:654:GLN:HB2	13:M:249:PHE:CD1	2.27	0.69
2:B:432:GLU:HG3	13:M:323:MET:HE1	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:89:VAL:HA	7:G:99:THR:HG22	1.79	0.65
10:J:29:TYR:OH	13:M:44:LEU:HD13	1.96	0.65

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	1030/1970 (52%)	1000 (97%)	30 (3%)	0	100	100
2	B	1003/1174 (85%)	974 (97%)	29 (3%)	0	100	100
3	C	254/275 (92%)	247 (97%)	7 (3%)	0	100	100
4	D	126/142 (89%)	120 (95%)	6 (5%)	0	100	100
5	E	207/210 (99%)	205 (99%)	2 (1%)	0	100	100
6	F	80/127 (63%)	75 (94%)	5 (6%)	0	100	100
7	G	169/172 (98%)	163 (96%)	6 (4%)	0	100	100
8	H	146/150 (97%)	141 (97%)	4 (3%)	1 (1%)	18	41
9	I	115/125 (92%)	111 (96%)	4 (4%)	0	100	100
10	J	65/67 (97%)	64 (98%)	1 (2%)	0	100	100
11	K	112/117 (96%)	109 (97%)	3 (3%)	0	100	100
12	L	43/58 (74%)	41 (95%)	2 (5%)	0	100	100
13	M	121/368 (33%)	120 (99%)	1 (1%)	0	100	100
14	N	130/612 (21%)	124 (95%)	6 (5%)	0	100	100
All	All	3601/5567 (65%)	3494 (97%)	106 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	H	82	PRO

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	927/1749 (53%)	919 (99%)	8 (1%)	70	87
2	B	892/1028 (87%)	879 (98%)	13 (2%)	57	81
3	C	235/252 (93%)	233 (99%)	2 (1%)	70	87
4	D	108/126 (86%)	106 (98%)	2 (2%)	50	77
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%)	146 (99%)	1 (1%)	76	90
8	H	129/131 (98%)	128 (99%)	1 (1%)	73	88
9	I	105/112 (94%)	105 (100%)	0	100	100
10	J	56/56 (100%)	55 (98%)	1 (2%)	51	78
11	K	103/106 (97%)	101 (98%)	2 (2%)	50	77
12	L	42/55 (76%)	42 (100%)	0	100	100
13	M	115/332 (35%)	115 (100%)	0	100	100
14	N	121/561 (22%)	119 (98%)	2 (2%)	53	79
All	All	3242/4964 (65%)	3210 (99%)	32 (1%)	65	86

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	K	42	LEU
11	K	82	SER
2	B	388	TYR
2	B	200	MET
14	N	56	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
5	E	35	GLN
7	G	122	ASN
13	M	297	HIS
1	A	1163	HIS
1	A	1116	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 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.

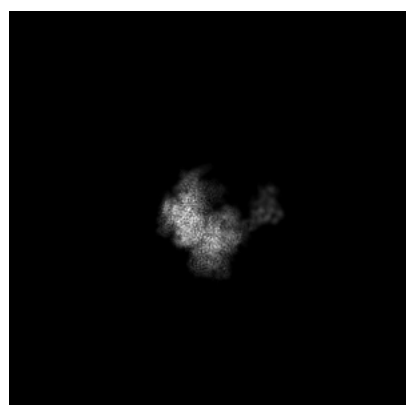
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55583. These allow visual inspection of the internal detail of the map and identification of artifacts.

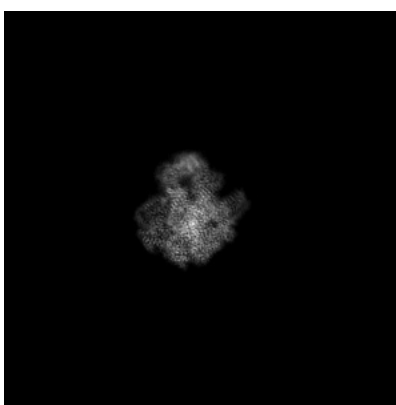
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

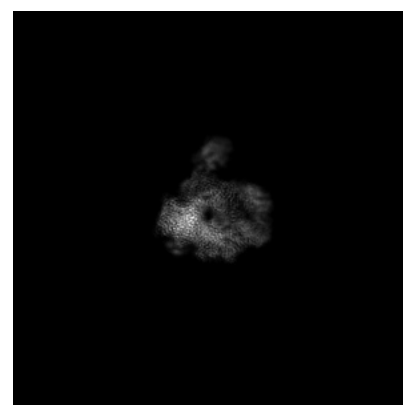
6.1.1 Primary map



X



Y

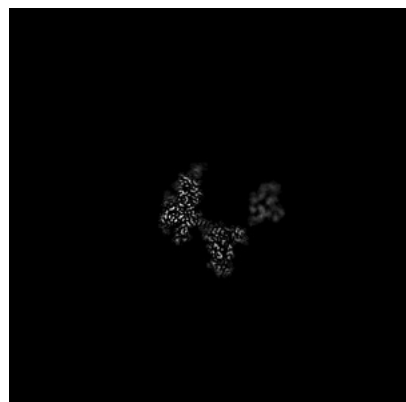


Z

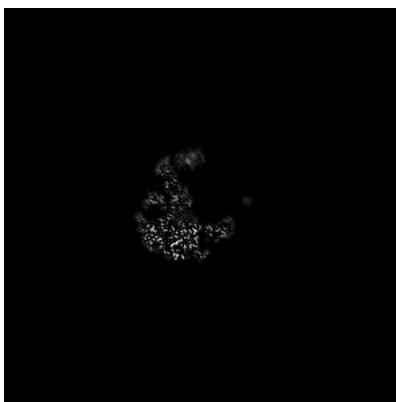
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 192



Y Index: 192

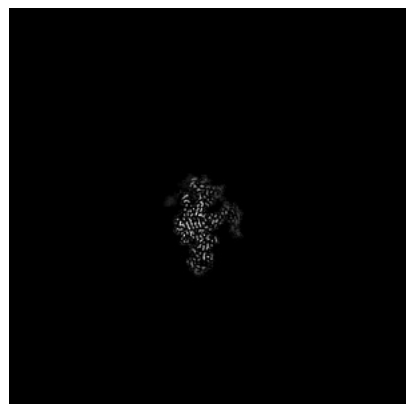


Z Index: 192

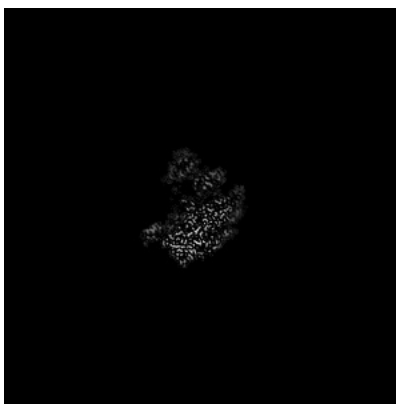
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

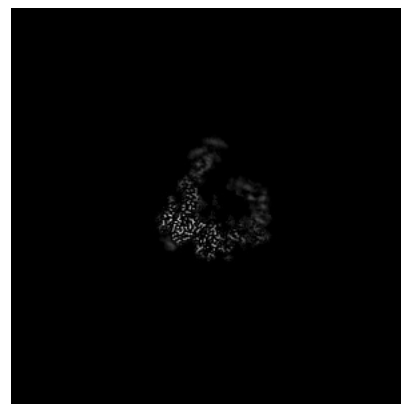
6.3.1 Primary map



X Index: 167



Y Index: 174

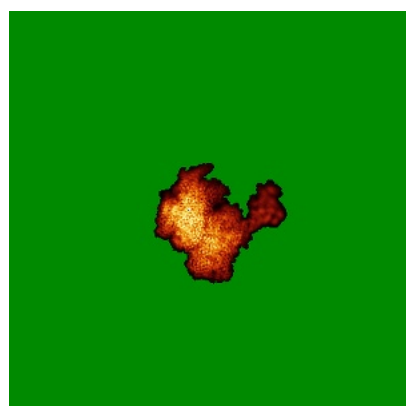


Z Index: 181

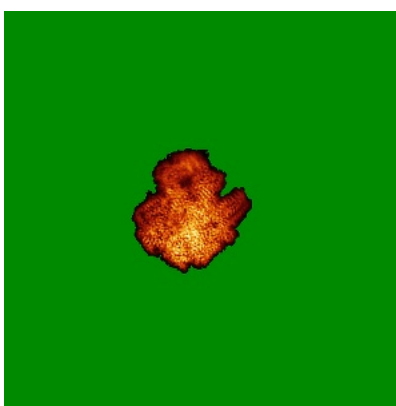
The images above show the largest variance slices of the map in three orthogonal directions.

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

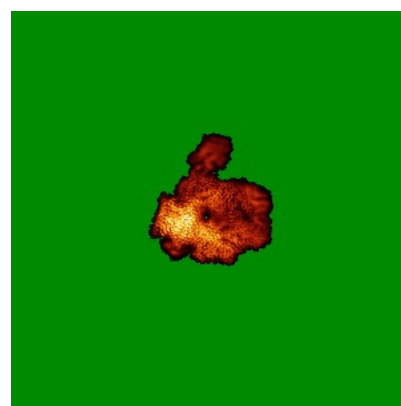
6.4.1 Primary map



X



Y

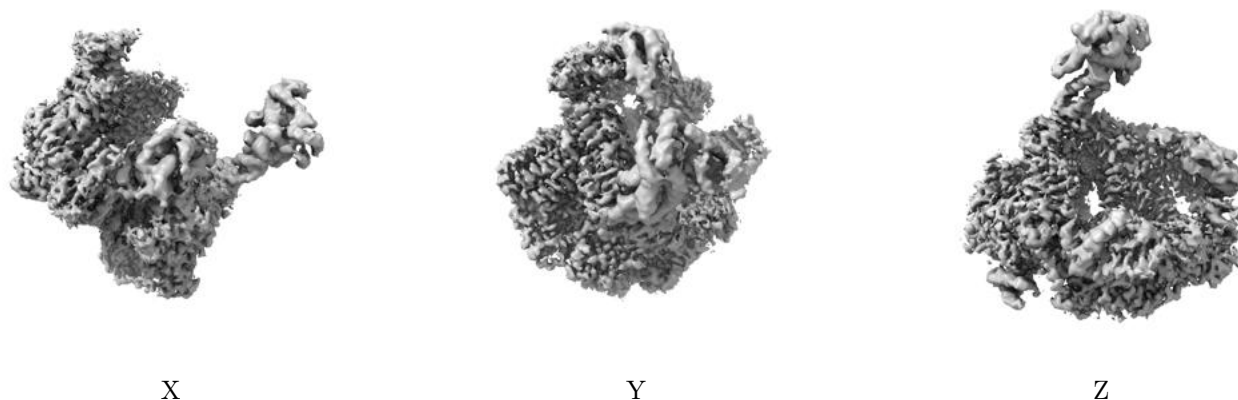


Z

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

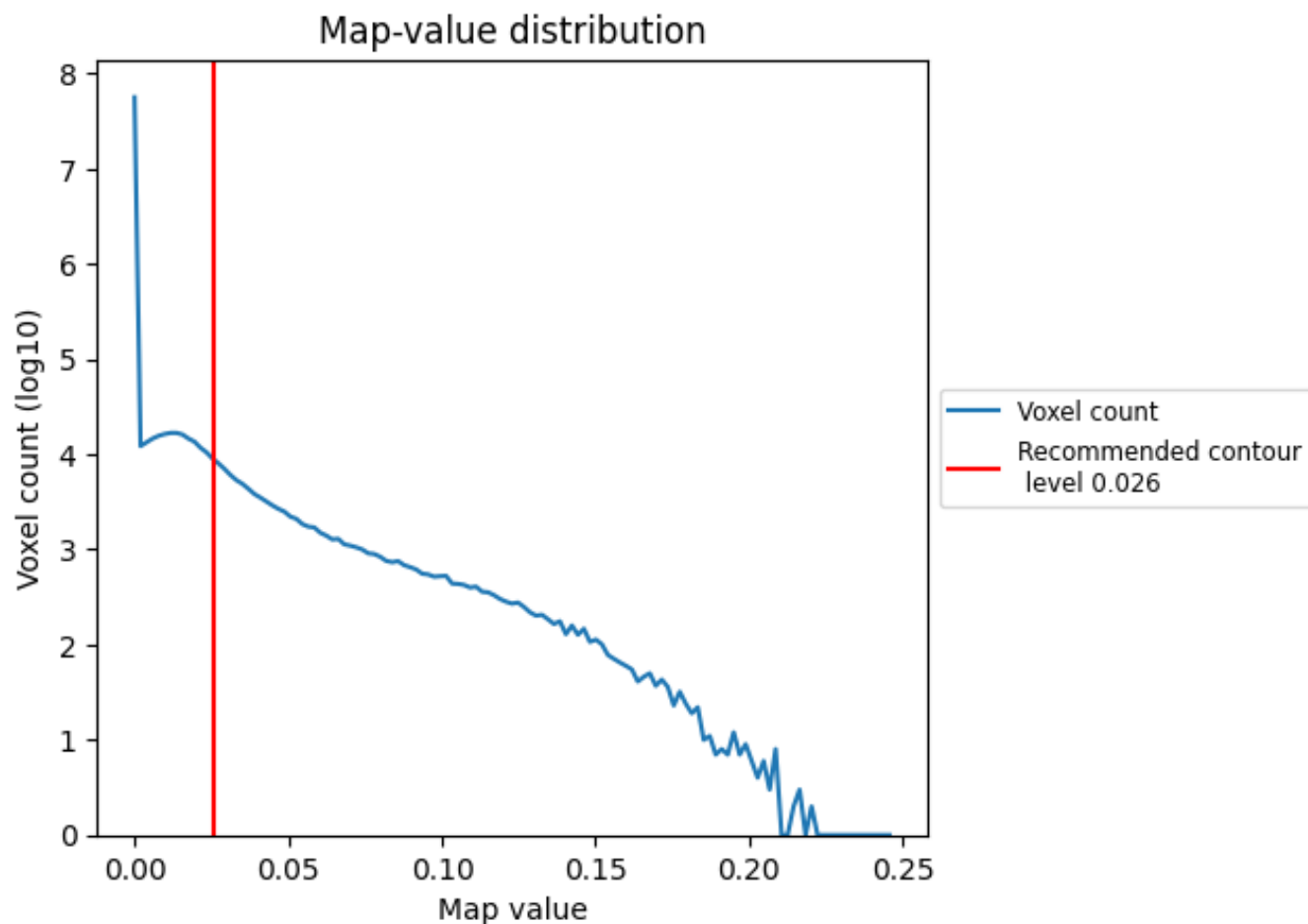
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

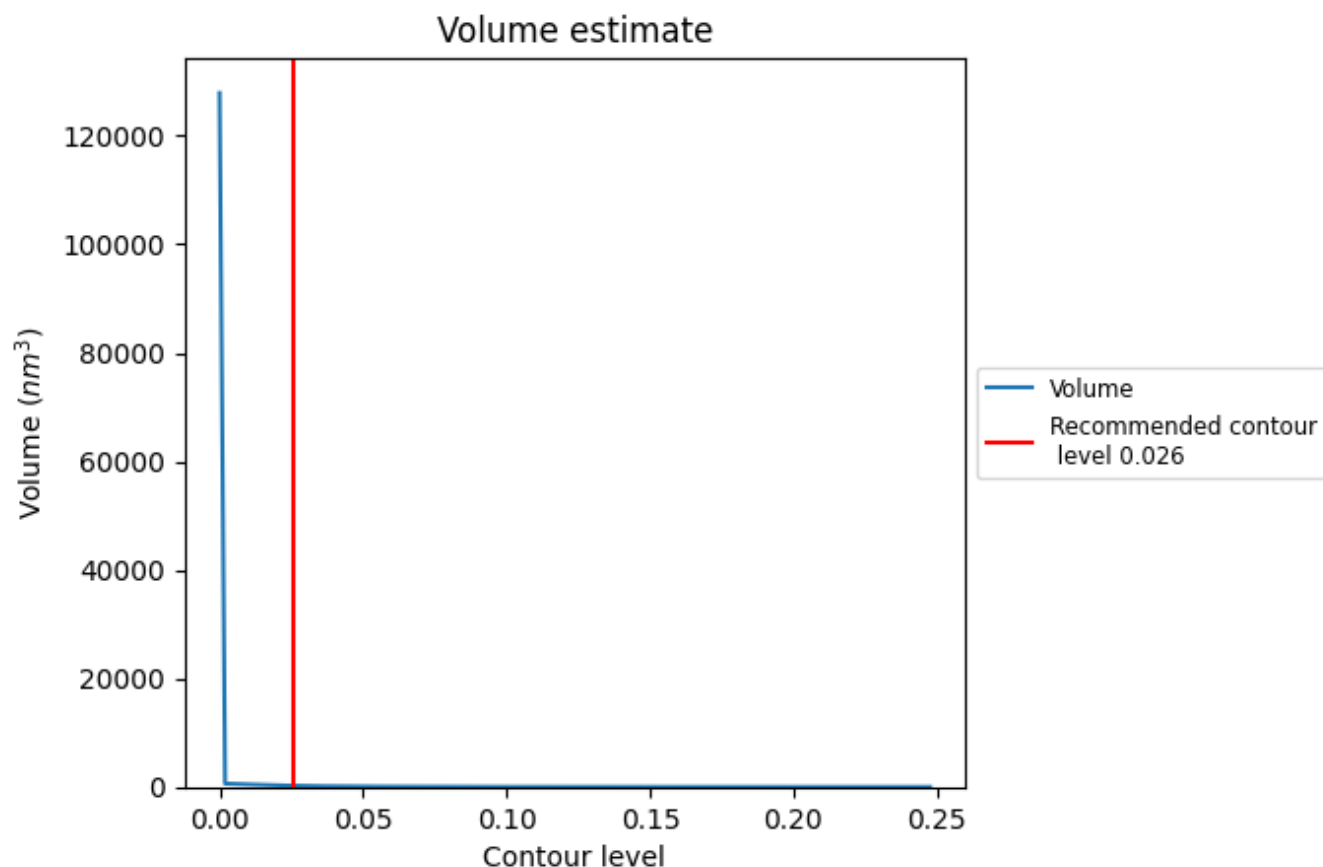
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

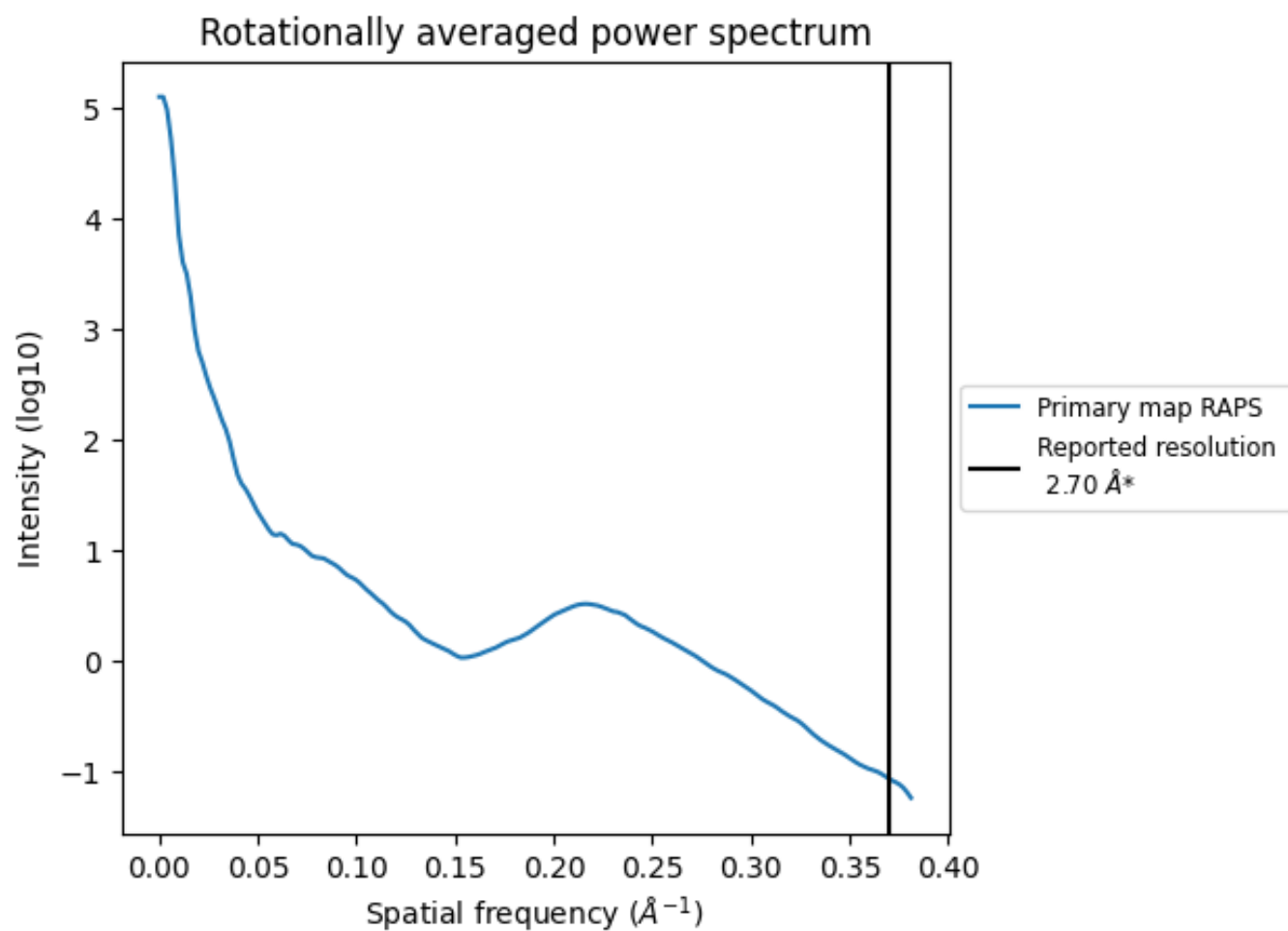
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 218 nm^3 ; this corresponds to an approximate mass of 197 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

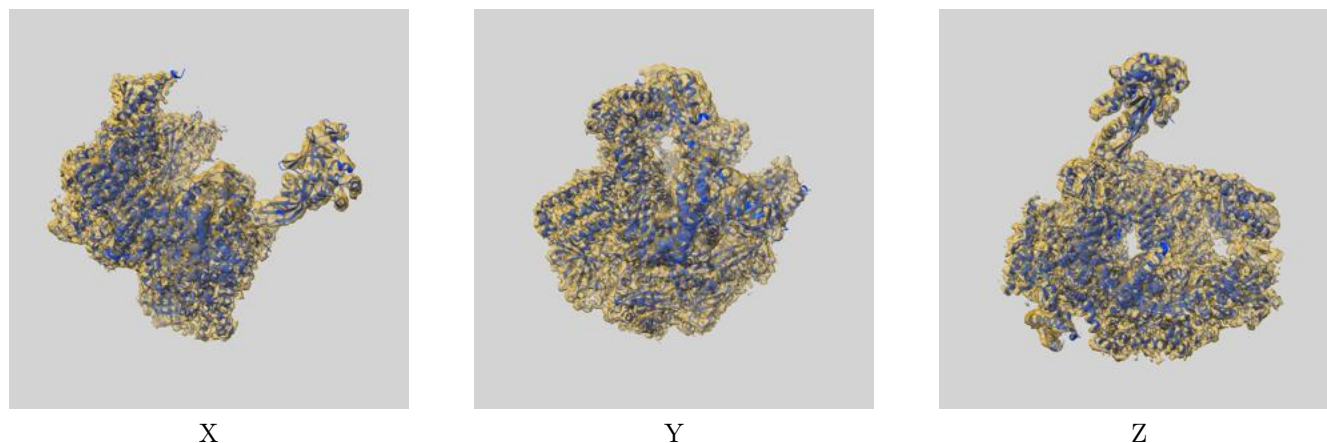
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

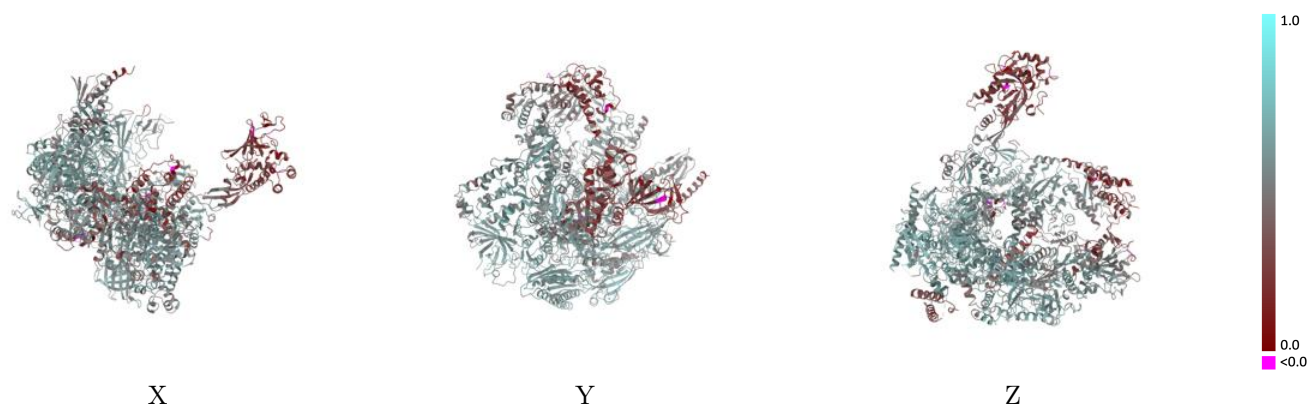
This section contains information regarding the fit between EMDB map EMD-55583 and PDB model 9T5H. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



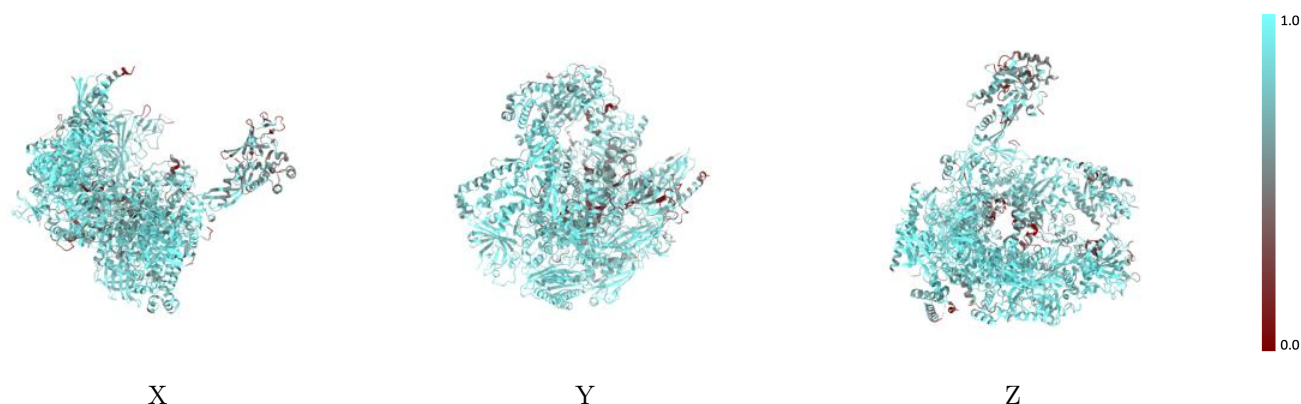
The images above show the 3D surface view of the map at the recommended contour level 0.026 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



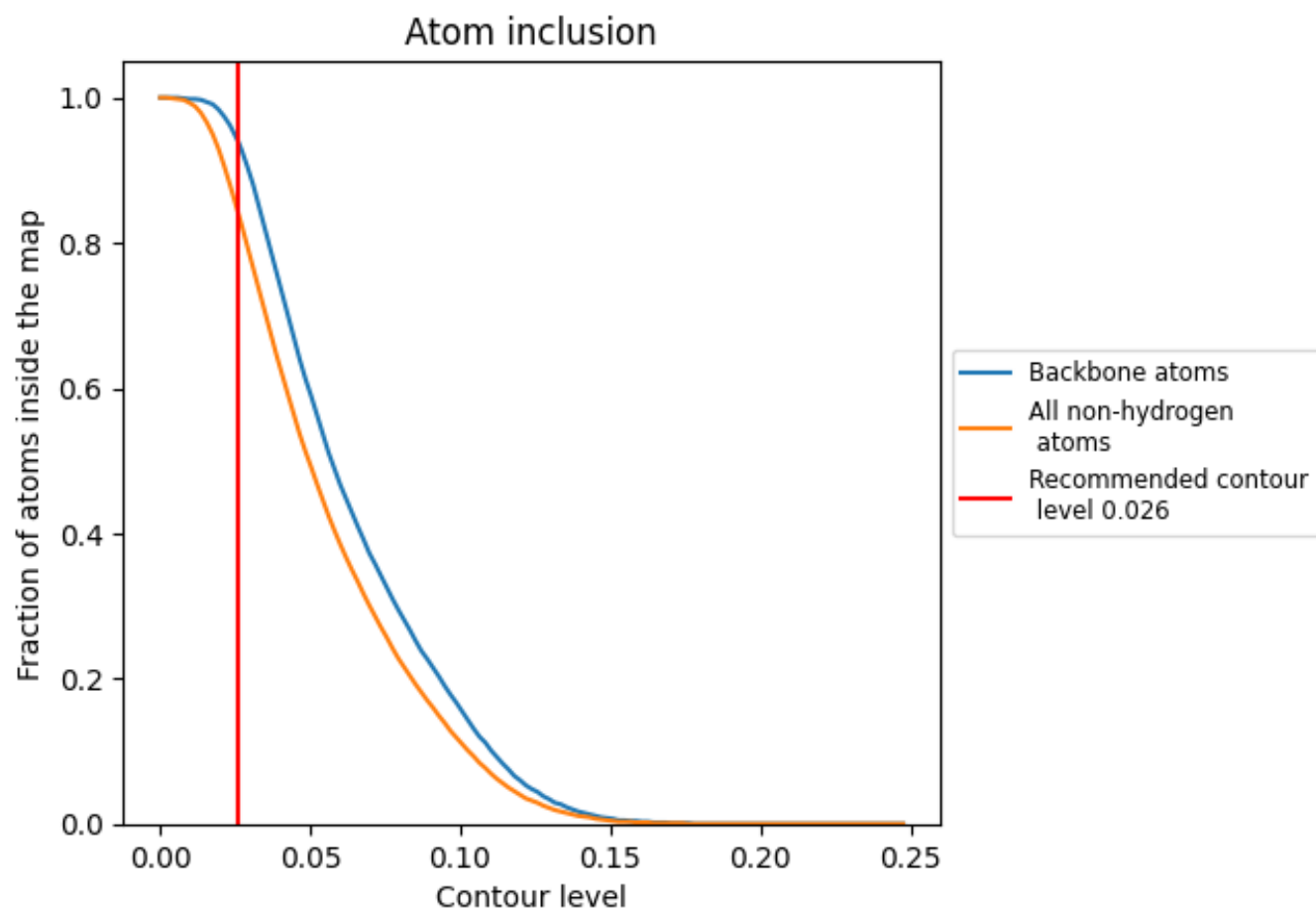
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.026).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.026) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8400	 0.5170
A	 0.8390	 0.5340
B	 0.9040	 0.5770
C	 0.9450	 0.6080
D	 0.5680	 0.2370
E	 0.8370	 0.4980
F	 0.8410	 0.5240
G	 0.6380	 0.2940
H	 0.9100	 0.5830
I	 0.8190	 0.5270
J	 0.9410	 0.6120
K	 0.9350	 0.6090
L	 0.8980	 0.5530
M	 0.6010	 0.3600
N	 0.7150	 0.2550

