



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 04:41 PM UTC

PDB ID : 6KNB / pdb_00006knb
EMDB ID : EMD-0723
Title : PolD-PCNA-DNA (form A)
Authors : Mayanagi, K.; Oki, K.; Miyazaki, N.; Ishino, S.; Yamagami, T.; Iwasaki, K.;
Kohda, D.; Morikawa, K.; Shirai, T.; Ishino, Y.
Deposited on : 2019-08-05
Resolution : 6.90 Å (reported)
Based on initial models : 3LX1, 5IJL, 5IHE

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.dev132
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) : 2.49

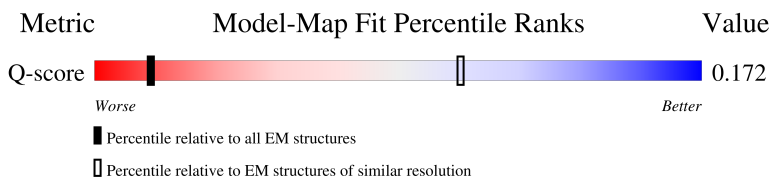
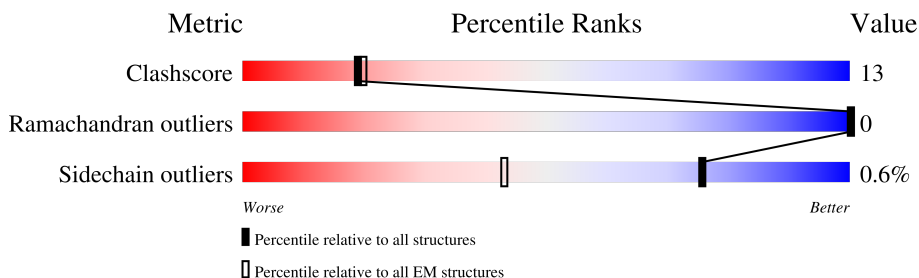
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.90 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.



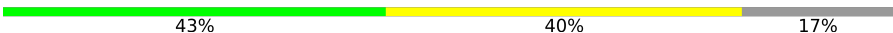
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	479 (6.40 - 7.40)

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	537	 5% 57% 26% 16%
2	B	1324	 1% 61% 24% 15%
3	C	249	 1% 73% 27%
3	D	249	 1% 66% 34%

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Mol	Chain	Length	Quality of chain
3	E	249	 72% 27%
4	F	30	 53% 30% 17%
5	G	30	 43% 40% 17%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 19581 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 polymerase II small subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	450	Total	C	N	O	S	0	0
			3604	2325	612	659	8		

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	199	MET	-	initiating methionine	UNP Q5JET1
A	200	LEU	-	expression tag	UNP Q5JET1
A	201	VAL	-	expression tag	UNP Q5JET1
A	202	GLU	-	expression tag	UNP Q5JET1
A	203	ASP	-	expression tag	UNP Q5JET1
A	204	LEU	-	expression tag	UNP Q5JET1
A	205	LEU	-	expression tag	UNP Q5JET1
A	206	LYS	-	expression tag	UNP Q5JET1
A	207	ASN	-	expression tag	UNP Q5JET1
A	208	ASN	-	expression tag	UNP Q5JET1
A	209	TYR	-	expression tag	UNP Q5JET1
A	210	LEU	-	expression tag	UNP Q5JET1
A	211	ILE	-	expression tag	UNP Q5JET1
A	212	THR	-	expression tag	UNP Q5JET1
A	213	PRO	-	expression tag	UNP Q5JET1
A	214	SER	-	expression tag	UNP Q5JET1
A	215	ALA	-	expression tag	UNP Q5JET1
A	216	TYR	-	expression tag	UNP Q5JET1
A	217	TYR	-	expression tag	UNP Q5JET1
A	218	LEU	-	expression tag	UNP Q5JET1
A	219	LEU	-	expression tag	UNP Q5JET1
A	220	SER	-	expression tag	UNP Q5JET1
A	221	ASP	-	expression tag	UNP Q5JET1
A	222	HIS	-	expression tag	UNP Q5JET1
A	223	TYR	-	expression tag	UNP Q5JET1
A	224	LYS	-	expression tag	UNP Q5JET1
A	225	LYS	-	expression tag	UNP Q5JET1
A	226	ALA	-	expression tag	UNP Q5JET1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	227	PHE	-	expression tag	UNP Q5JET1
A	228	THR	-	expression tag	UNP Q5JET1
A	229	LEU	-	expression tag	UNP Q5JET1
A	230	ALA	-	expression tag	UNP Q5JET1
A	231	GLU	-	expression tag	UNP Q5JET1
A	232	LEU	-	expression tag	UNP Q5JET1
A	233	ILE	-	expression tag	UNP Q5JET1
A	234	LYS	-	expression tag	UNP Q5JET1
A	235	PHE	-	expression tag	UNP Q5JET1
A	236	ALA	-	expression tag	UNP Q5JET1
A	237	LYS	-	expression tag	UNP Q5JET1
A	238	ASN	-	expression tag	UNP Q5JET1
A	239	ARG	-	expression tag	UNP Q5JET1
A	240	GLY	-	expression tag	UNP Q5JET1
A	241	THR	-	expression tag	UNP Q5JET1
A	242	PHE	-	expression tag	UNP Q5JET1
A	243	VAL	-	expression tag	UNP Q5JET1
A	244	VAL	-	expression tag	UNP Q5JET1
A	245	ASP	-	expression tag	UNP Q5JET1
A	246	SER	-	expression tag	UNP Q5JET1
A	247	ASN	-	expression tag	UNP Q5JET1
A	248	LEU	-	expression tag	UNP Q5JET1
A	249	ALA	-	expression tag	UNP Q5JET1
A	250	ARG	-	expression tag	UNP Q5JET1
A	251	GLU	-	expression tag	UNP Q5JET1
A	252	PHE	-	expression tag	UNP Q5JET1
A	253	LEU	-	expression tag	UNP Q5JET1
A	254	ALA	-	expression tag	UNP Q5JET1
A	255	GLU	-	expression tag	UNP Q5JET1
A	256	LYS	-	expression tag	UNP Q5JET1
A	257	GLY	-	expression tag	UNP Q5JET1
A	258	ILE	-	expression tag	UNP Q5JET1
A	259	ILE	-	expression tag	UNP Q5JET1
A	260	SER	-	expression tag	UNP Q5JET1
A	261	SER	-	expression tag	UNP Q5JET1
A	262	GLY	-	expression tag	UNP Q5JET1

- Molecule 2 is a protein called DNA polymerase D DP2 (DNA polymerase II large) subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1120	Total	C	N	O	S	0	0
			8998	5753	1554	1658	33		

- Molecule 3 is a protein called DNA polymerase sliding clamp 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	249	Total	C	N	O	S	0	0
			1983	1268	313	393	9		
3	D	249	Total	C	N	O	S	0	0
			1983	1268	313	393	9		
3	E	249	Total	C	N	O	S	0	0
			1983	1268	313	393	9		

- Molecule 4 is a DNA chain called pri25DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	25	Total	C	N	O	P	0	0
			511	242	97	147	25		

- Molecule 5 is a DNA chain called temp35DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	25	Total	C	N	O	P	0	0
			514	244	92	153	25		

- Molecule 6 is FE (III) ION (CCD ID: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		AltConf
6	A	1	Total	Fe	0
			1	1	

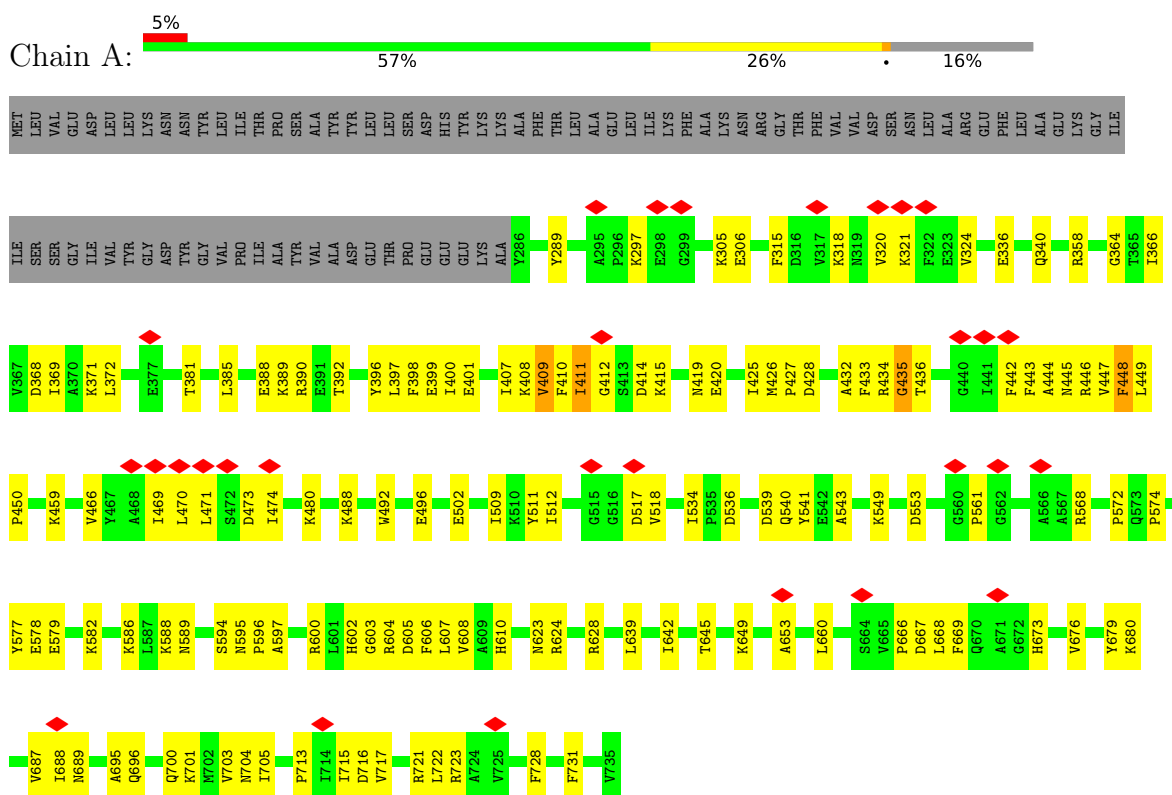
- Molecule 7 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
7	A	1	Total	Zn	0
			1	1	
7	B	3	Total	Zn	0
			3	3	

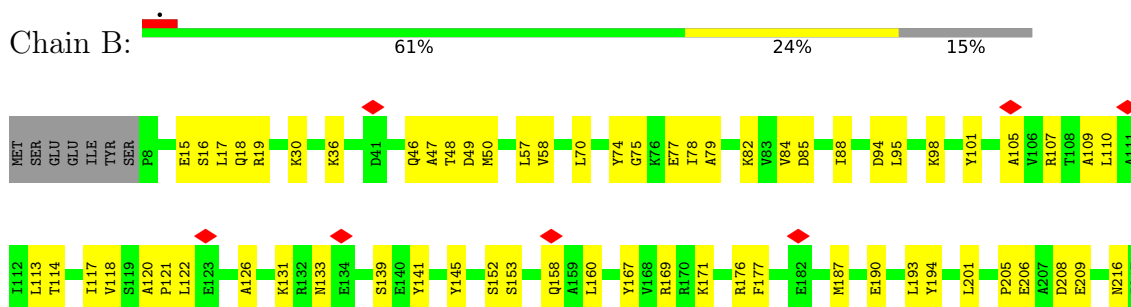
3 Residue-property plots

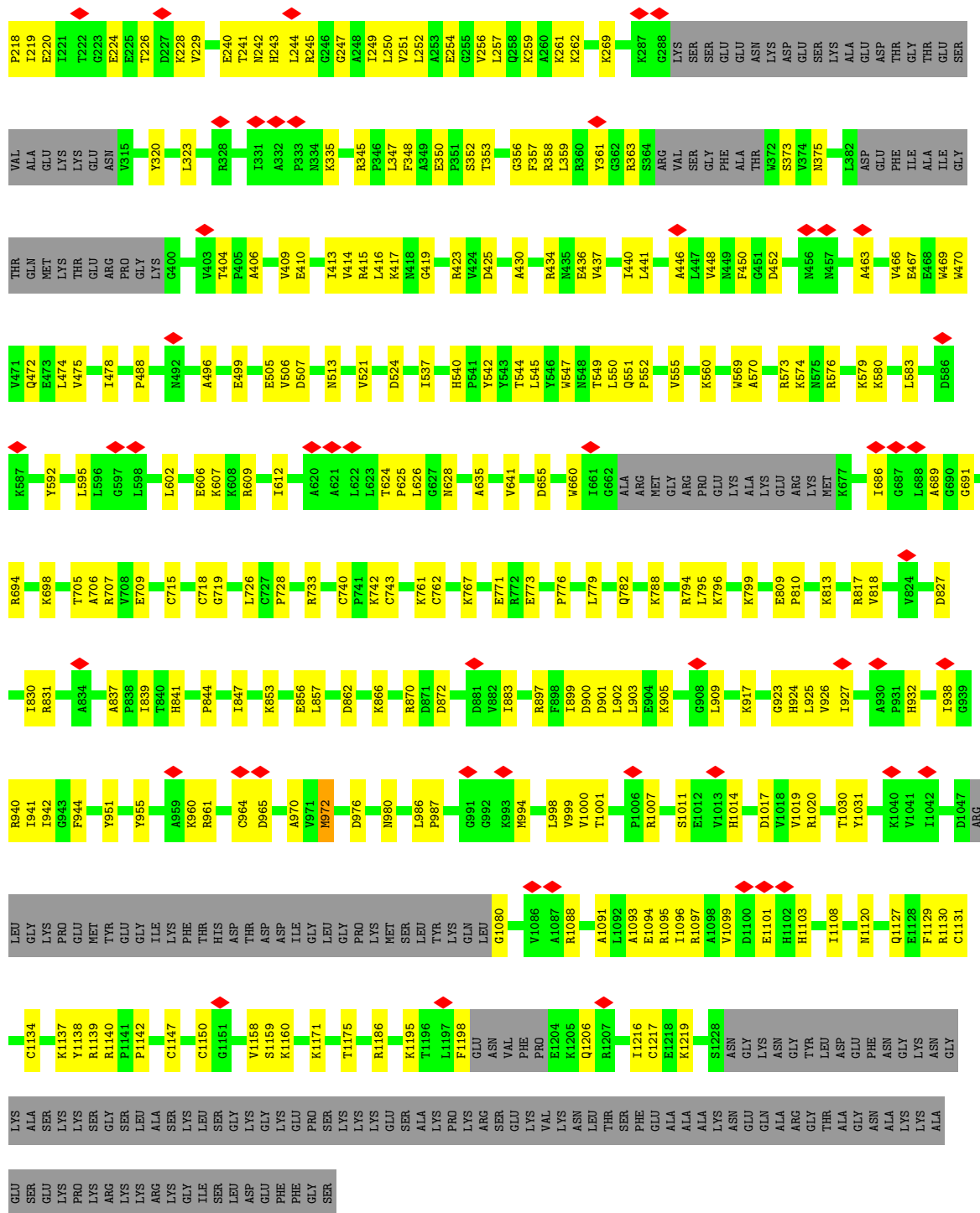
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: DNA polymerase II small subunit



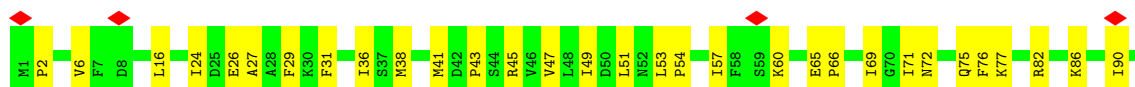
• Molecule 2: DNA polymerase D DP2 (DNA polymerase II large) subunit

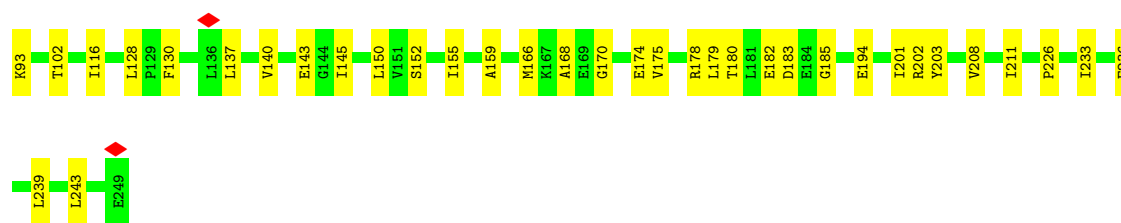




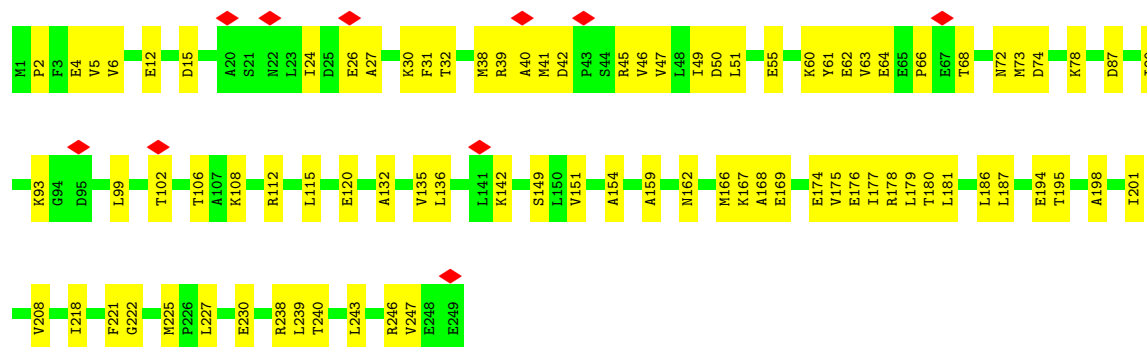
• Molecule 3: DNA polymerase sliding clamp 1

Chain C: 73% 27%

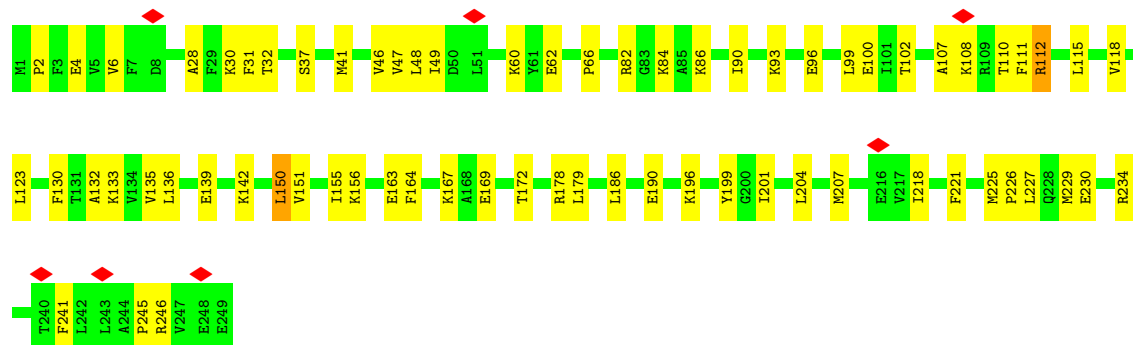




• Molecule 3: DNA polymerase sliding clamp 1



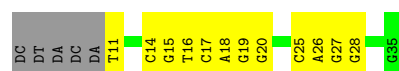
• Molecule 3: DNA polymerase sliding clamp 1



• Molecule 4: pri25DNA



• Molecule 5: temp35DNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	41073	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.078	Depositor
Minimum map value	-0.047	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0069	Depositor
Map size (Å)	179.2, 179.2, 179.2	wwPDB
Map dimensions	160, 160, 160	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.12, 1.12, 1.12	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, FE

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	0/3692	0.37	2/5006 (0.0%)
2	B	0.10	0/9184	0.29	0/12404
3	C	0.09	0/2010	0.27	0/2702
3	D	0.11	0/2010	0.32	0/2702
3	E	0.09	0/2010	0.27	0/2702
4	F	0.15	0/573	0.33	0/881
5	G	0.12	0/575	0.28	0/886
All	All	0.11	0/20054	0.31	2/27283 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	435	GLY	CA-C-N	-5.04	106.29	121.98
1	A	435	GLY	C-N-CA	-5.04	106.29	121.98

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	3604	0	3609	110	0
2	B	8998	0	9080	219	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	1983	0	2010	44	0
3	D	1983	0	2010	71	0
3	E	1983	0	2010	52	0
4	F	511	0	280	7	0
5	G	514	0	283	12	0
6	A	1	0	0	0	0
7	A	1	0	0	0	0
7	B	3	0	0	0	0
All	All	19581	0	19282	499	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 13.

The worst 5 of 499 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)
1:A:435:GLY:HA3	1:A:445:ASN:H	1.18	1.09
1:A:408:LYS:O	1:A:443:PHE:HA	1.67	0.95
1:A:434:ARG:O	1:A:446:ARG:HB3	1.67	0.95
3:D:230:GLU:CB	3:D:240:THR:HG22	1.98	0.93
1:A:434:ARG:O	1:A:446:ARG:CB	2.16	0.93

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	448/537 (83%)	416 (93%)	32 (7%)	0	100	100
2	B	1106/1324 (84%)	1052 (95%)	54 (5%)	0	100	100
3	C	247/249 (99%)	236 (96%)	11 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	D	247/249 (99%)	238 (96%)	9 (4%)	0	100	100
3	E	247/249 (99%)	240 (97%)	7 (3%)	0	100	100
All	All	2295/2608 (88%)	2182 (95%)	113 (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	389/462 (84%)	383 (98%)	6 (2%)	57	72
2	B	961/1129 (85%)	958 (100%)	3 (0%)	86	86
3	C	217/217 (100%)	217 (100%)	0	100	100
3	D	217/217 (100%)	216 (100%)	1 (0%)	81	83
3	E	217/217 (100%)	214 (99%)	3 (1%)	59	72
All	All	2001/2242 (89%)	1988 (99%)	13 (1%)	76	83

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	972	MET
2	B	994	MET
3	E	150	LEU
3	E	111	PHE
3	E	112	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	914	ASN
3	C	72	ASN
2	B	1120	ASN

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Mol	Chain	Res	Type
3	D	72	ASN
1	A	704	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 5 ligands modelled in this entry, 5 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.

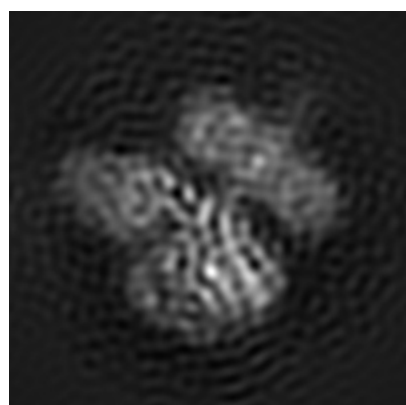
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0723. These allow visual inspection of the internal detail of the map and identification of artifacts.

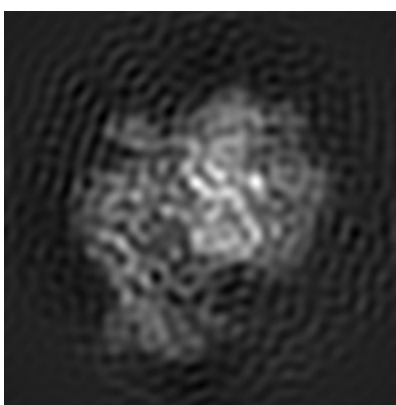
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

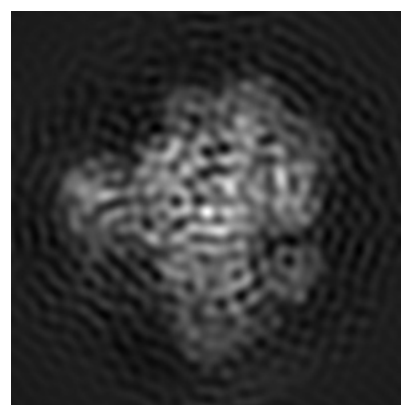
6.1.1 Primary map



X



Y

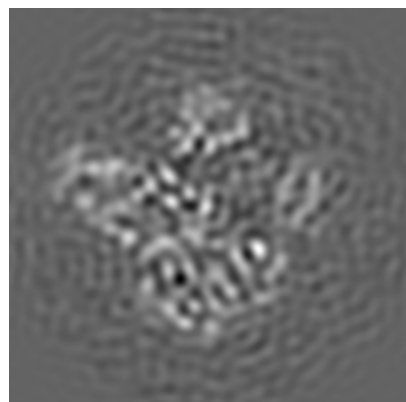


Z

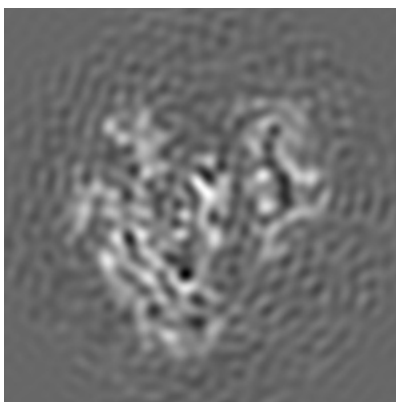
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

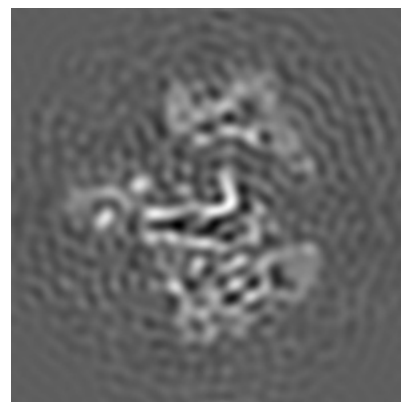
6.2.1 Primary map



X Index: 80



Y Index: 80

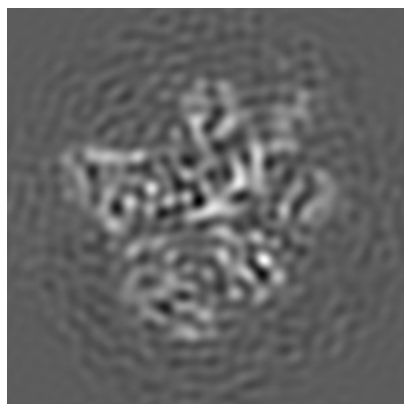


Z Index: 80

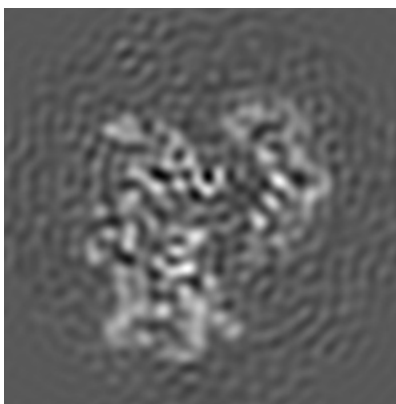
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

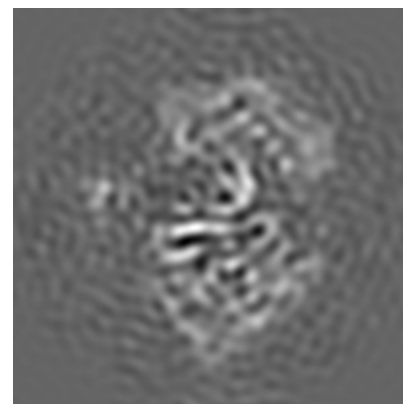
6.3.1 Primary map



X Index: 88



Y Index: 86

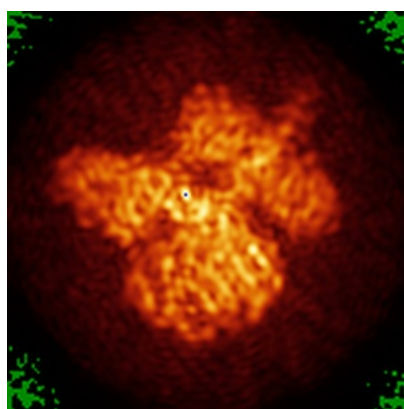


Z Index: 86

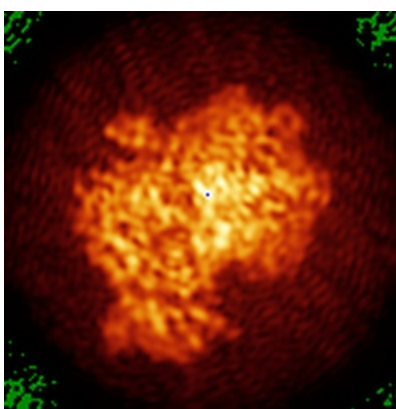
The images above show the largest variance slices of the map in three orthogonal directions.

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

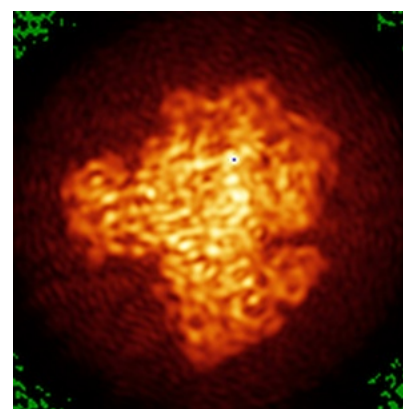
6.4.1 Primary map



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 0.0069. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

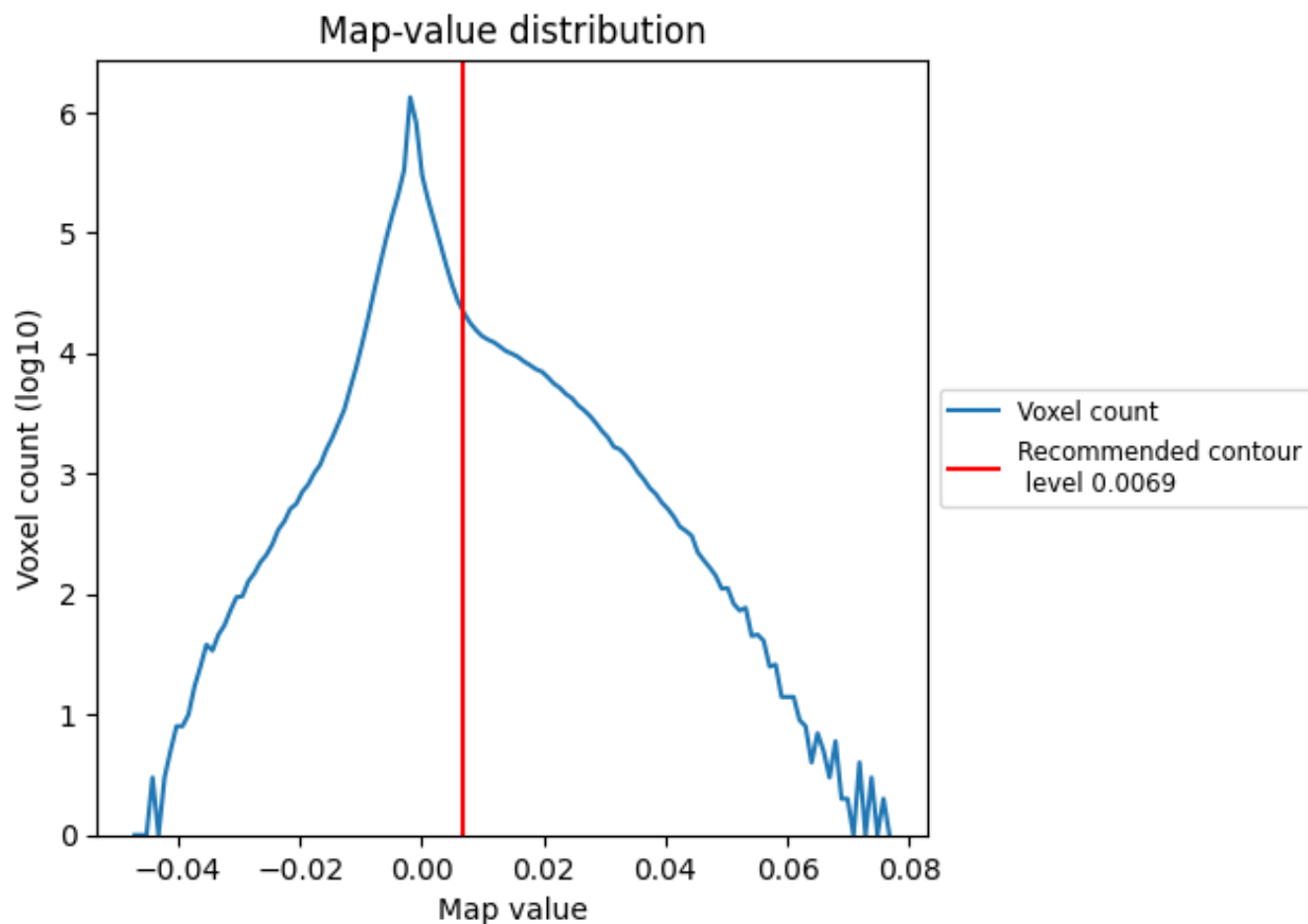
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

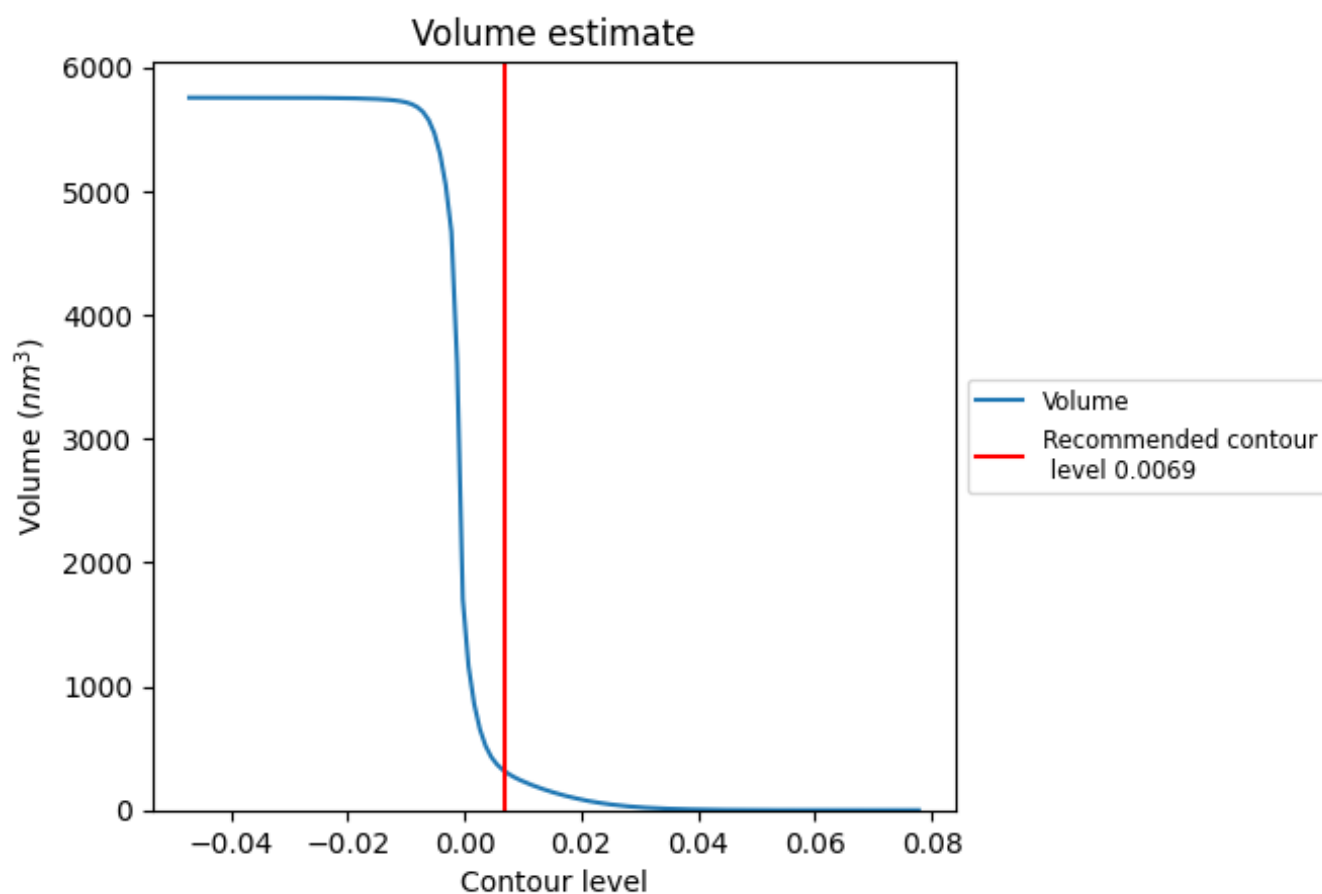
This section contains the results of statistical analysis of the map.

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.

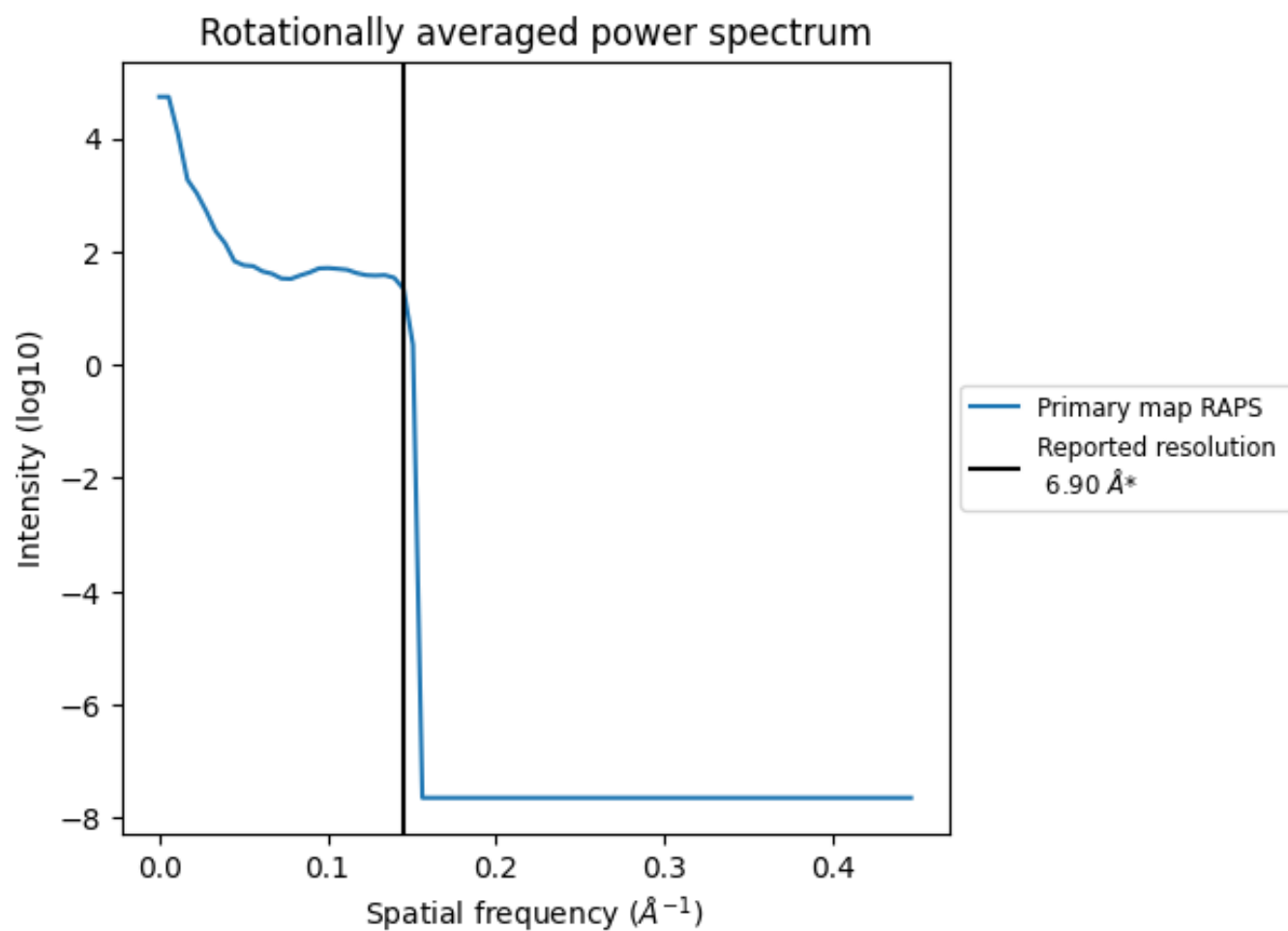
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 315 nm³; this corresponds to an approximate mass of 284 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 ⓘ

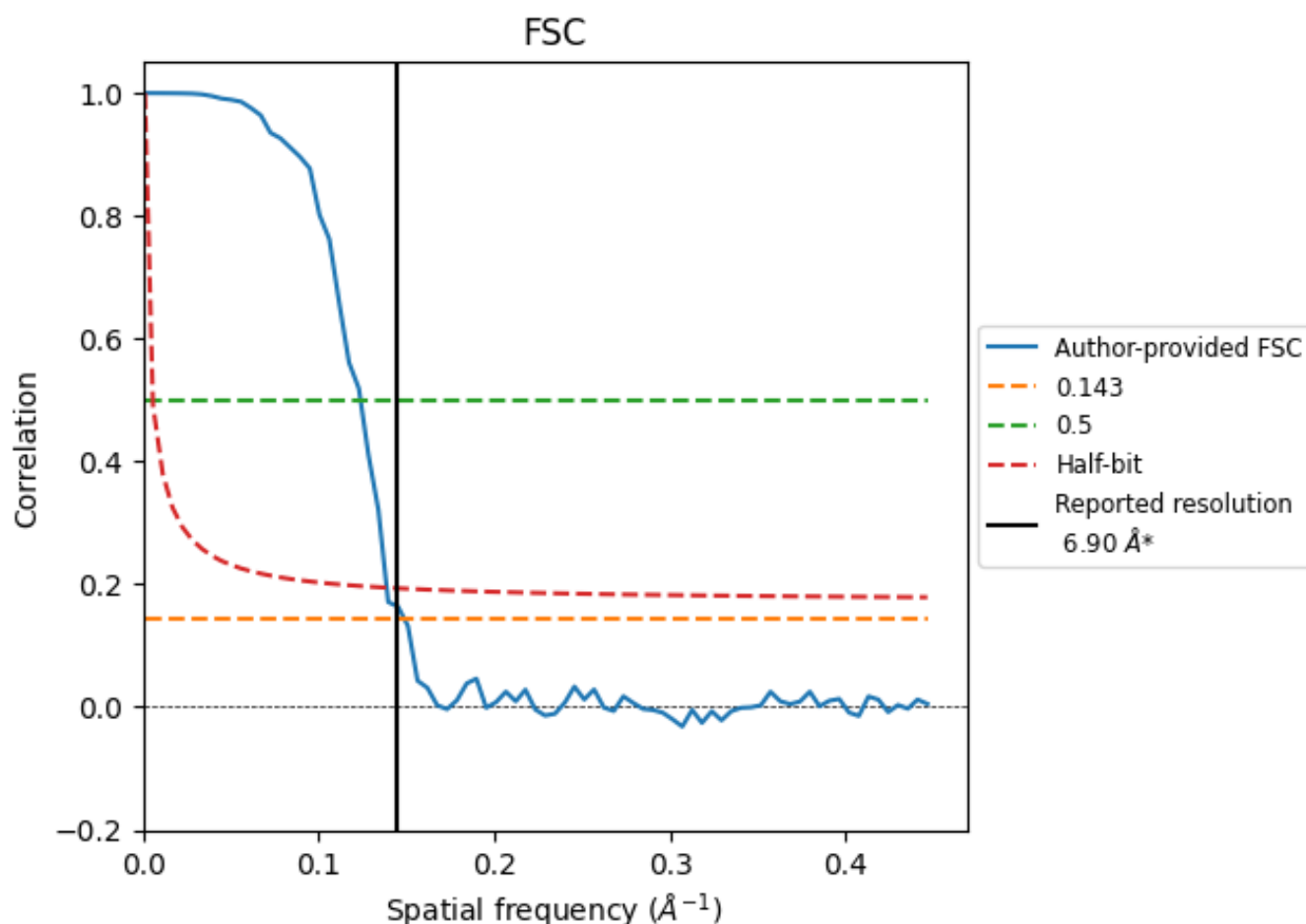


*Reported resolution corresponds to spatial frequency of 0.145 Å⁻¹

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 0.145 Å⁻¹

8.2 Resolution estimates [i](#)

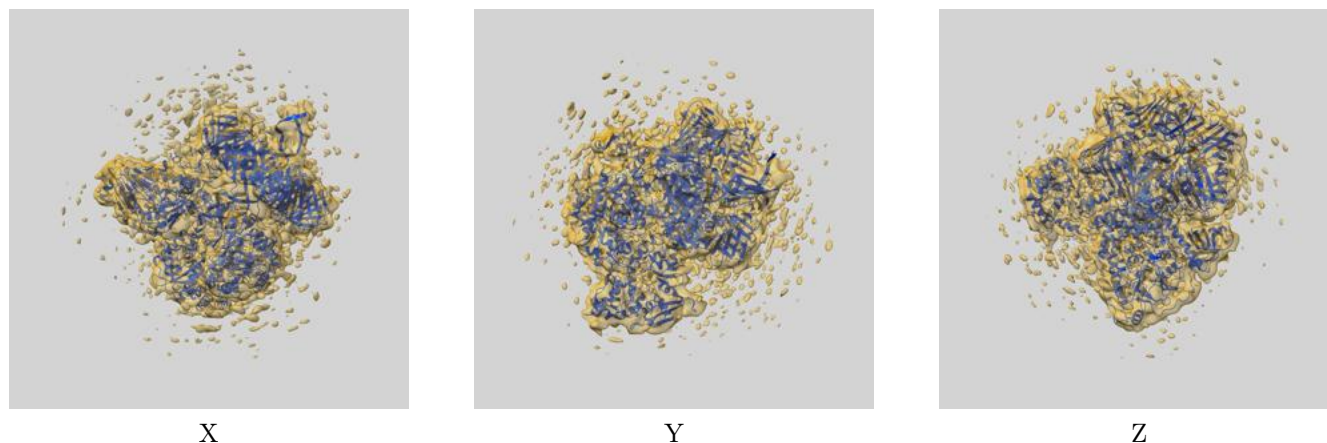
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.90	-	-
Author-provided FSC curve	6.72	8.08	7.22
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

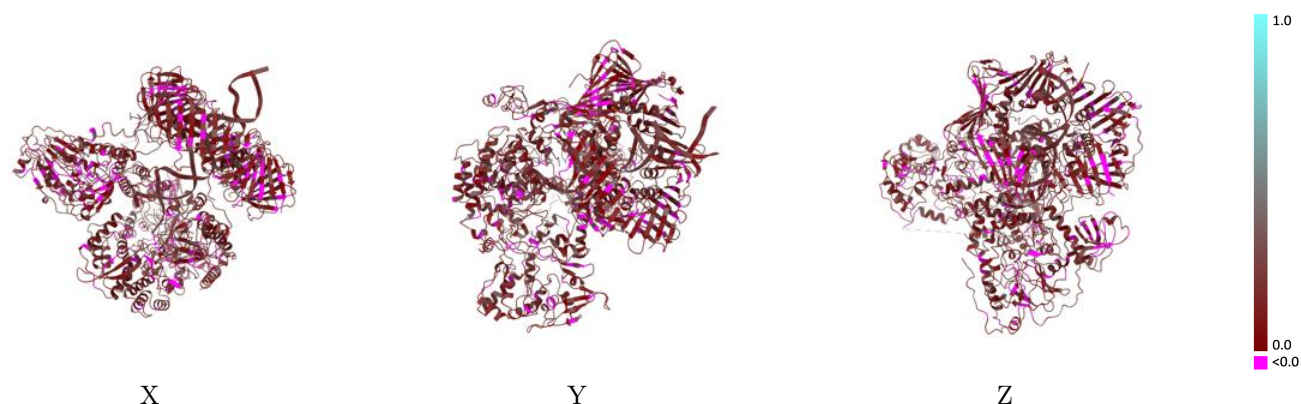
This section contains information regarding the fit between EMDB map EMD-0723 and PDB model 6KNB. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



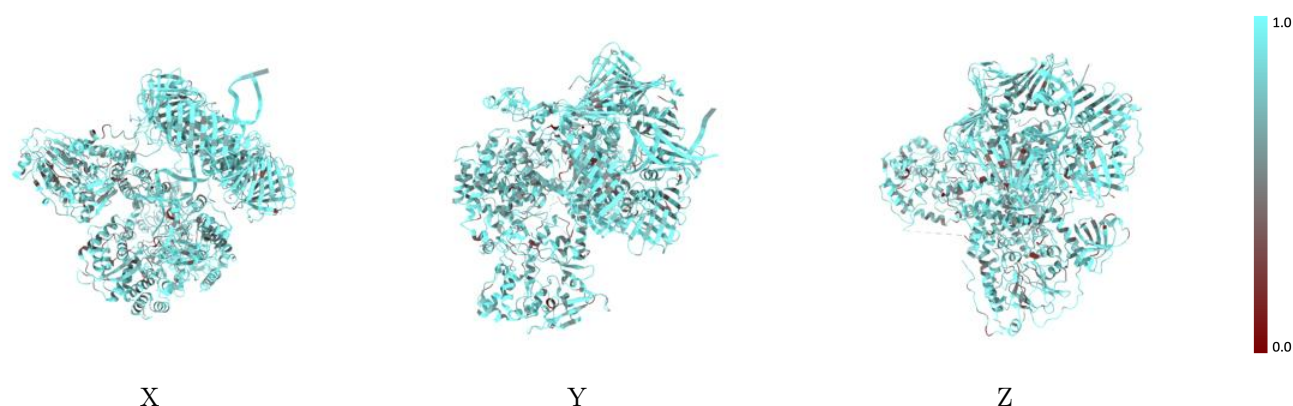
The images above show the 3D surface view of the map at the recommended contour level 0.0069 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



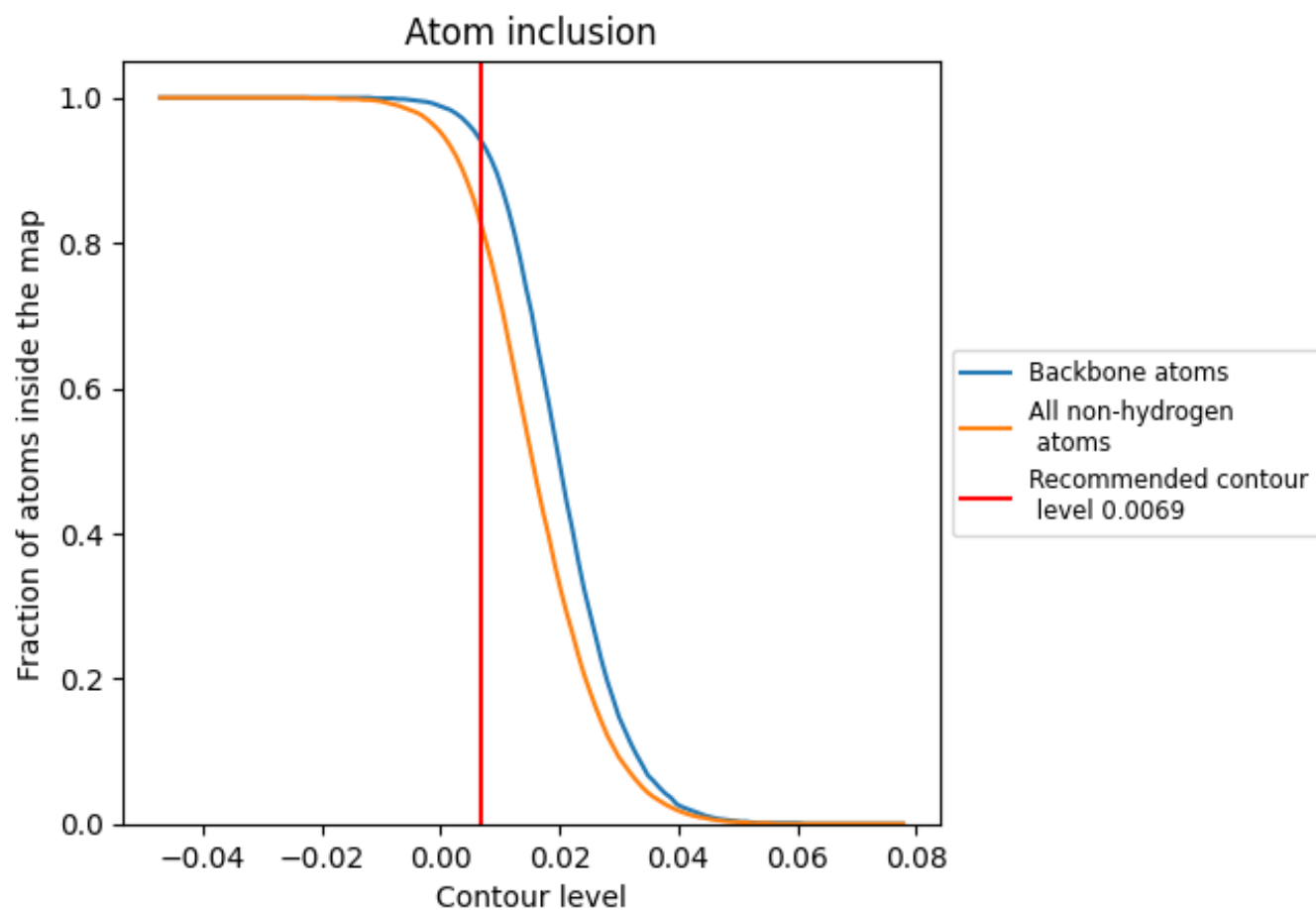
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0069).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 82% 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 (0.0069) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8220	0.1720
A	0.8060	0.1620
B	0.8080	0.1790
C	0.8440	0.1560
D	0.8250	0.1570
E	0.8350	0.1630
F	0.9140	0.2220
G	0.9420	0.2420

1.0

0.0

<0.0