



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 04:18 PM UTC

PDB ID : 6WJV / pdb_00006wjv
EMDB ID : EMD-21701
Title : Structure of the *Saccharomyces cerevisiae* polymerase epsilon holoenzyme
Authors : Yuan, Z.; Georgescu, R.; Schauer, G.D.; O'Donnell, M.; Li, H.
Deposited on : 2020-04-14
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

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

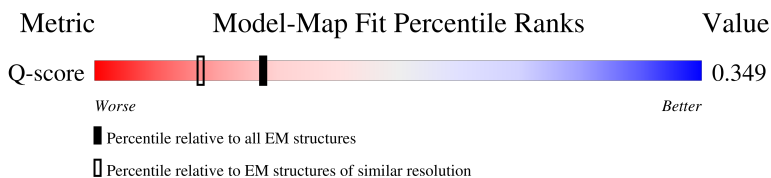
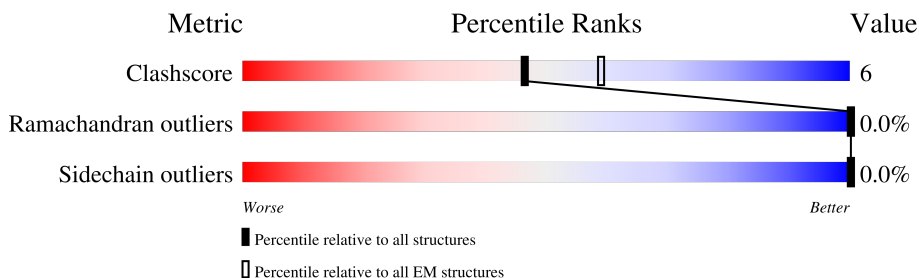
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	2222	55% 74% 14% 12%
2	2	689	50% 11% 38%
3	3	201	15% 37% 5% 58%
4	4	196	23% 44% 10% 45%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 19593 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 epsilon catalytic subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1951	Total	C	N	O	S	0	0
			14886	9527	2476	2813	70		

- Molecule 2 is a protein called DNA polymerase epsilon subunit B.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	424	Total	C	N	O	S	0	0
			3225	2055	545	610	15		

- Molecule 3 is a protein called DNA polymerase epsilon subunit C.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	85	Total	C	N	O	S	0	0
			652	417	107	126	2		

- Molecule 4 is a protein called DNA polymerase epsilon subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	107	Total	C	N	O	S	0	0
			829	521	146	161	1		

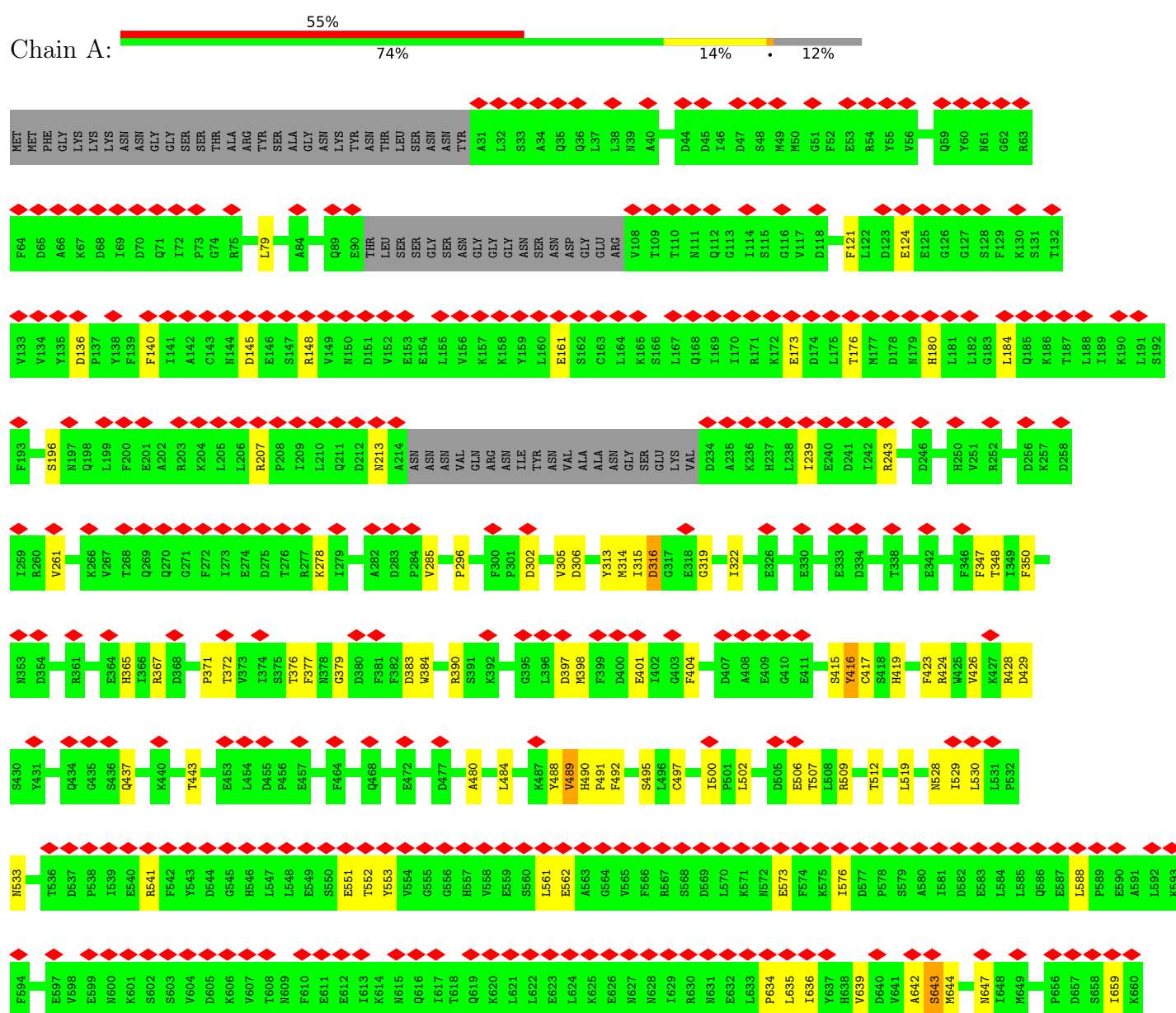
- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
5	A	1	Total	Zn	0
			1	1	

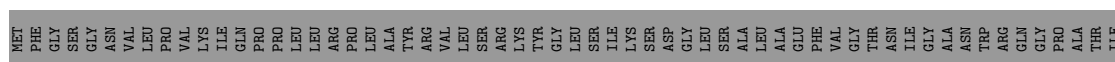
3 Residue-property plots

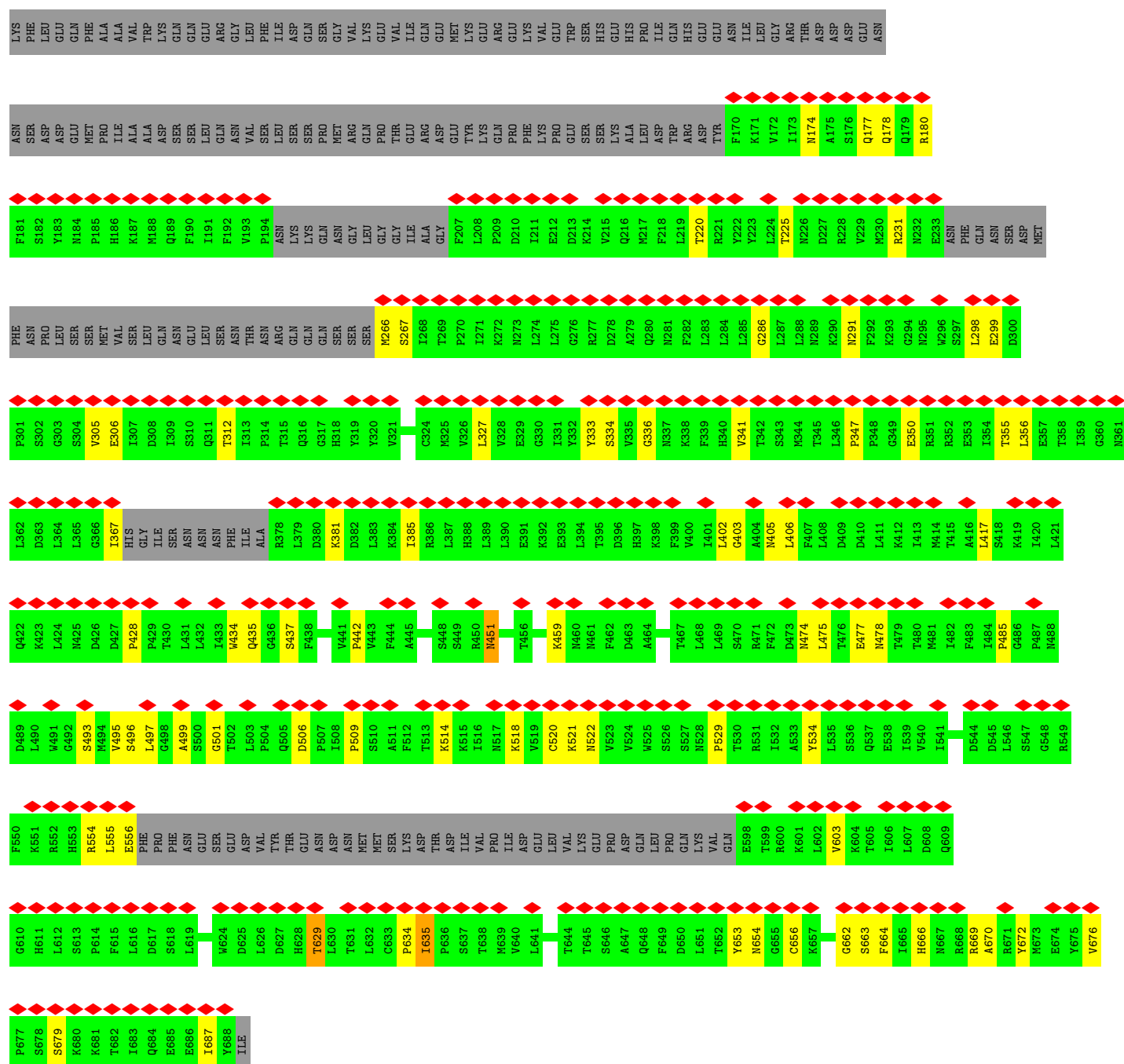
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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 epsilon catalytic subunit A

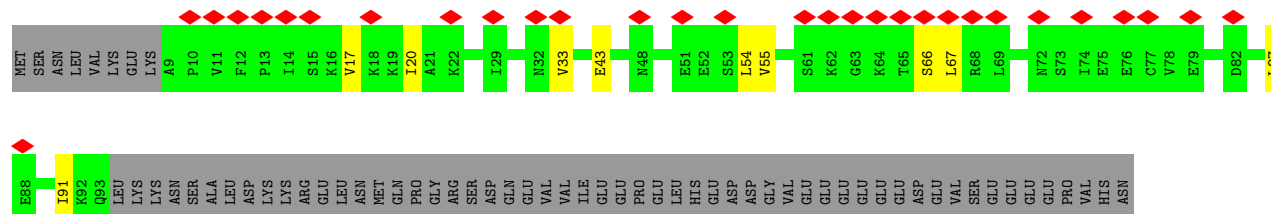
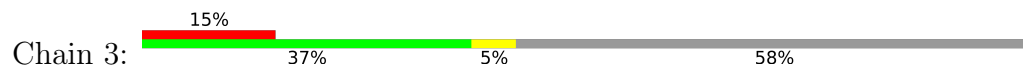


M1470	PHE	E1315	GLU	LYS	P1130	L1045	L981	K917	I857	A788	L721	A661
A1471	LYS	A1318	GLU	GLN	S1131	L1046	K982	H921	I858	K789	T722	E662
E1472	THR	A1319	ASP	THR	L1132	C1047	G983	Q922	Q859	T790	F723	R663
M1473	LEU	W1322	LEU	SER	E1133	E1048	F984	Y923	M860	K791	D724	ASP
E1474	PRO		VAL	THR	L1134	N1049	E985	Q924	R862	K792	E725	ALA
R1475	LEU		LEU	LYS	D1135	R1050	L986	E925	A963	G793	L726	SER
Y1476	SER		PRO	PHE	D1136	R1051	K987	L926	A964	N794	S727	CYS
L1477	GLU		GLU	SER	I1137	M1052	R988	L864	V965	L795	A728	ASP
S1478	ILE		ILE	LYS	R1138	S1053	R989	K927	E966	S796	Y729	PHE
G1479	THR		THR	LYS	R1139	K1054	G990	D928	E967	K797	D730	ASN
F1480	SER		SER	ASN	I1140	T1055	E991	P929	V968	I798	A731	ARG
S1481	PRO		PRO	VAL	I1141	L1056	L982	L930	G969	D799	V732	PRO
S1482	GLU		GLU	THR	D1142	E1058	Q993	N931	R870	P800	I733	GLY
D1483	ASP		ASP	THR	W1143	Y1059	L994	Y932	P871	S801	H734	LYS
I1484	TYR		TYR	MET			L995	I933	L872	D802	I735	THR
G1485			GLY	GLY	R1147	E1060	K996	I934	L873	D802	I735	A678
Y1486			ILE	LYS	E1148	G1061	N997	Y935	E973	K903	K736	R679
F1490			LYS	LYS	R1149	R1071	Q998	E936	L874	H904	K737	K680
F1491			ASP	ASP	L1150	L1072	Q999	T936	D875	A805	R738	L681
T1492			ILE	ILE	G1151	L1073	S1000	H937	T876	R906	L739	K682
S1493			GLU	ASP	S1152	D1075	I1002	S938	D877	D807	T740	W683
I1494			ASP	PHE	A1153	D1076	I1003	E939	G978	E908	E741	A684
V1423			LEU	LEU	I1154		F1003	N940	I879	A809	Y742	W685
L1424			GLU	GLU	Q1155	D1080	K1004	T941	W880	K310	S743	R686
G1425			PRO	PRO	K1156	V1082	V1005	I942	C881	K811	R744	G687
V1426			THR	THR	I1157	V1082	F1006	F943	I882	M812	K745	E688
F1427			VAL	VAL	I1158	K1083	L1007	E945	L883	F690	V746	F689
E1428			GLU	GLU	I1159	D1084	L1008	Y946	K885	P691	Y747	F691
R1285			GLU	ASP	T1159	S1094	G1009	D947	S886	S692	H748	S692
D1286			ASP	ALA	P1161	S1095	D1010	G948	F887	K693	R749	K693
K1288			ASN	LYS	A1162	K1096	T1011	P949	P888	M694	V750	M694
R1289			LYS	ILE	A1163	P1097	L1012	Y950	E889	D695	K751	D695
R1290			LYS	ILE	L1164	F1098	E1013	K951	T890	E696	V752	E696
D1291			ALA	ALA	L1165	N1099	G1014	A952	Y891	Y697	S753	Y697
Q1292			ARG	ARG	G1166	A1100	C1015	N953	F992	N628	E754	N698
L1293			THR	THR	V1167	P1101	Y1016	I954	F993	S929	I755	M699
G1295			LYS	LYS	S1168	A1106	S1017	I955	T894	F830	V756	I700
N1296			LYS	LYS	M1169		A1018	P956	L895	Y831	E757	K701
T1297			ALA	ALA	P1170		V1019	S957	E996	G832	R758	R702
N1298			VAL	VAL	V1171		A1020	S958	N997	Y833	E759	A703
S1299			SER	SER	P1172		A1021	K959	G998	V834	A760	L704
R1301			LYS	ARG	R1173		K960	E961	K999	M835	I761	Q705
E1302			LYS	LYS	V1174		E961	E961	K900	R836	R765	N706
R1303			ARG	ARG	E1175		M1025	G962	L901	K937	E766	E707
R1304			ASN	ASN	H1176		W1026	K963	Y902	G838	E767	T708
A1305			GLN	GLN	P1177		L1027	G964	L903	S839	E768	F709
P1384			LEU	LEU	D1178		D1028	I965	Y905	Y842	Y770	F710
L1306			THR	ASN	W1179		V1029	K966	Y906	S943	V771	N711
G1307			THR		L1180		L1030	K967	S904	M844	D772	N712
S1308					K1181		D1031	R968	S943	E845	K713	K714
M1309					R1182		S1032	F972	M909	T850	F715	F715
R1311					K1183		H1033	N973	L910	C951	S776	S776
R1312					L1184		G1034	E974	N911	L852	D779	K717
Q1313					A1185		M1036	D975	Y912	A855	Y782	K718
A1314					T1186		L1037	G976	R913	T856	Y782	K719
					LYS		E1038	S977	H915		G786	V720
					GLU		D1039	L978				
					ASP		E1040	A979				
					PHE		D1041	E980				





• Molecule 3: DNA polymerase epsilon subunit C



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

● Molecule 4: DNA polymerase epsilon subunit D



MET
PRO
PRO
LYS
GLY
TRP
ARG
LYS
ASP
ASP
ALA
GLN
GLY
ASN
TYR
PRO
THR
THR
S18
Y19
I20
K21
E22
Q23
E24
N25
I26
T27
I28
Q29
D30
L31
L32
F33
R43
E44
V45
P46
Q47
Q48
S49
G50
K51
K52
L53
L54
I55
N56
K57
D58
L61
R65
G66
V71
L75
L76

F77
A78
R79
E80
I81
A82
K83
S84
Q85
D86
K87
K88
S91
V92
D93
D94
V95
D100
L107
P110
D113
D116
E117
Y118
Q119
Q124
ARG
LYS
LYS
GLU
LYS
LEU
LEU
ASP
SER
GLY
GLU
VAL
ASP
ALA
ASP
GLY
ASP
ILE
ASP
MET
GLY
GLU
ASP
LYS
GLU
ASN
VAL
PRO

VAL
GLU
LYS
VAL
LYS
GLU
HIS
ASP
GLU
ILE
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GLY
ASP
ALA
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ASP
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ASP
VAL
GLU
THR
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VAL
GLN
ASN
LEU
GLU
GLN
THR

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	187298	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.223	Depositor
Minimum map value	-0.112	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	263.424, 263.424, 263.424	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.029, 1.029, 1.029	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

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	0.47	3/15201 (0.0%)	1.10	125/20663 (0.6%)
2	2	0.44	0/3286	1.19	34/4467 (0.8%)
3	3	0.37	0/660	1.01	5/891 (0.6%)
4	4	0.55	1/839 (0.1%)	1.24	12/1132 (1.1%)
All	All	0.46	4/19986 (0.0%)	1.12	176/27153 (0.6%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1161	PRO	N-CD	-8.78	1.35	1.47
1	A	1515	LYS	C-N	8.25	1.41	1.33
4	4	110	PRO	N-CD	-7.32	1.37	1.47
1	A	490	HIS	C-N	6.62	1.42	1.34

The worst 5 of 176 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1310	ILE	N-CA-C	-11.10	102.91	111.90
4	4	28	ILE	N-CA-C	-10.89	103.08	111.90
1	A	1552	ILE	N-CA-C	-10.35	102.97	112.90
1	A	1721	ILE	N-CA-C	-10.01	103.29	112.90
2	2	385	ILE	N-CA-C	-9.61	103.32	112.83

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	14886	0	13968	185	0
2	2	3225	0	3134	42	0
3	3	652	0	664	4	0
4	4	829	0	842	10	0
5	A	1	0	0	0	0
All	All	19593	0	18608	231	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 6.

The worst 5 of 231 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:305:VAL:HG13	1:A:1301:ARG:NH1	1.48	1.26
1:A:1115:ASP:OD1	1:A:1118:ILE:CG1	1.99	1.08
1:A:1540:LYS:HA	1:A:1543:ILE:HG22	1.32	1.05
1:A:306:ASP:OD1	1:A:1301:ARG:NH1	1.93	1.00
1:A:1115:ASP:OD1	1:A:1118:ILE:HG12	1.60	0.98

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	1929/2222 (87%)	1802 (93%)	127 (7%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	2	414/689 (60%)	370 (89%)	43 (10%)	1 (0%)	43	74
3	3	83/201 (41%)	80 (96%)	3 (4%)	0	100	100
4	4	105/196 (54%)	96 (91%)	9 (9%)	0	100	100
All	All	2531/3308 (76%)	2348 (93%)	182 (7%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	2	434	TRP

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	1522/2014 (76%)	1522 (100%)	0	100	100
2	2	351/629 (56%)	351 (100%)	0	100	100
3	3	72/185 (39%)	71 (99%)	1 (1%)	59	71
4	4	91/173 (53%)	91 (100%)	0	100	100
All	All	2036/3001 (68%)	2035 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	3	43	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
1	A	1916	ASN
2	2	289	ASN
1	A	1930	ASN
2	2	184	ASN

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Mol	Chain	Res	Type
2	2	451	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 1 ligands modelled in this entry, 1 is 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.

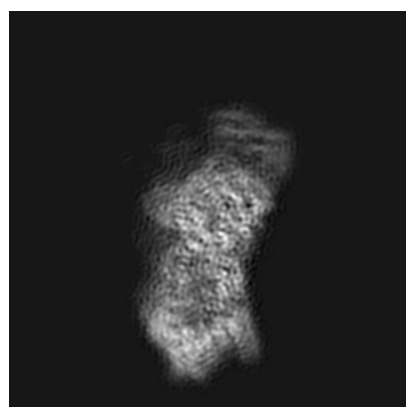
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21701. These allow visual inspection of the internal detail of the map and identification of artifacts.

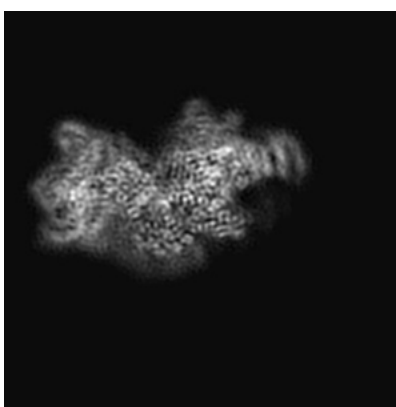
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

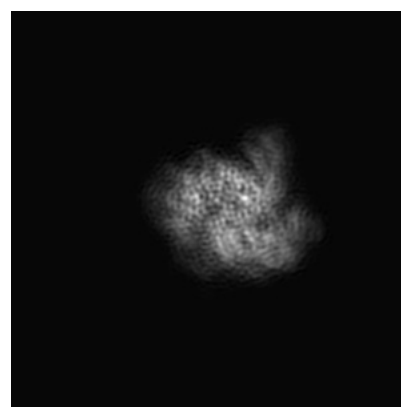
6.1.1 Primary map



X



Y



Z

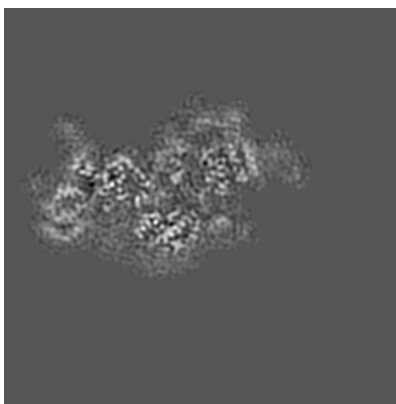
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

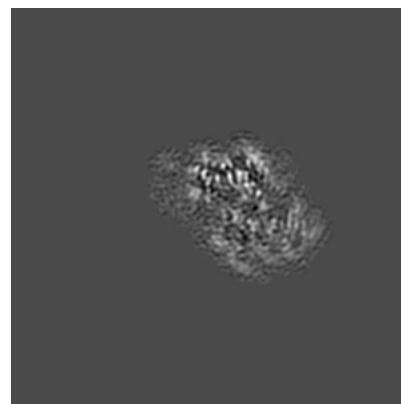
6.2.1 Primary map



X Index: 128



Y Index: 128



Z Index: 128

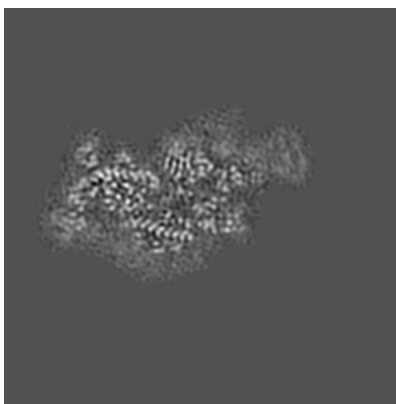
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

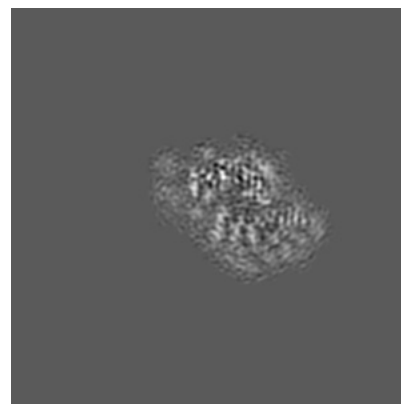
6.3.1 Primary map



X Index: 150



Y Index: 136

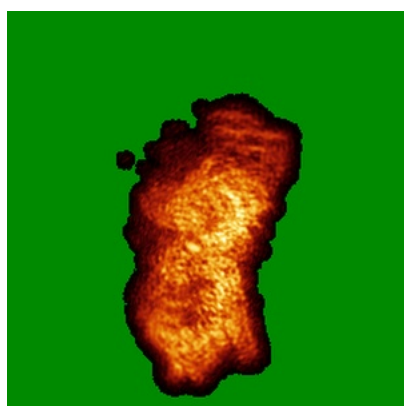


Z Index: 125

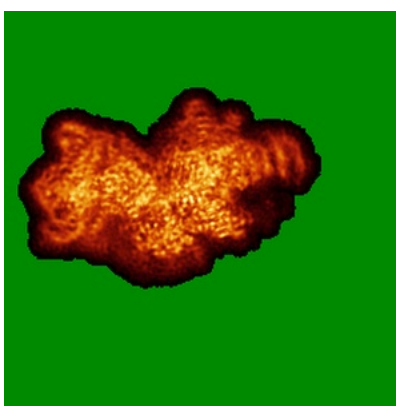
The images above show the largest variance slices of the map in three orthogonal directions.

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

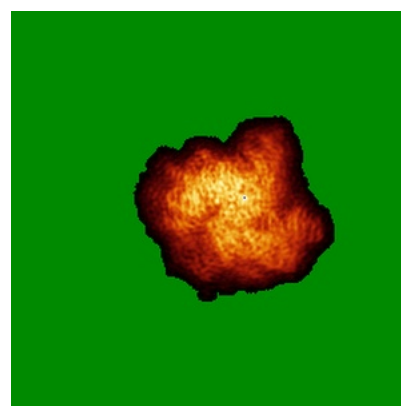
6.4.1 Primary map



X



Y

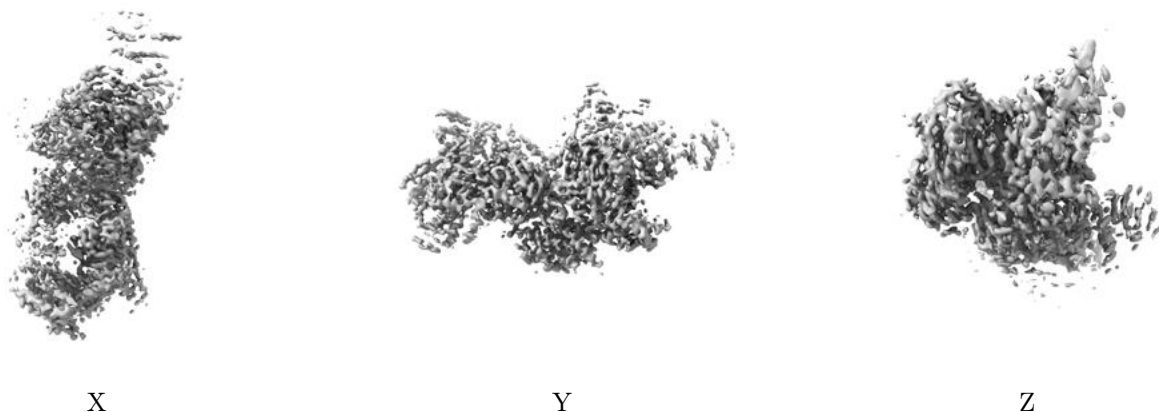


Z

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

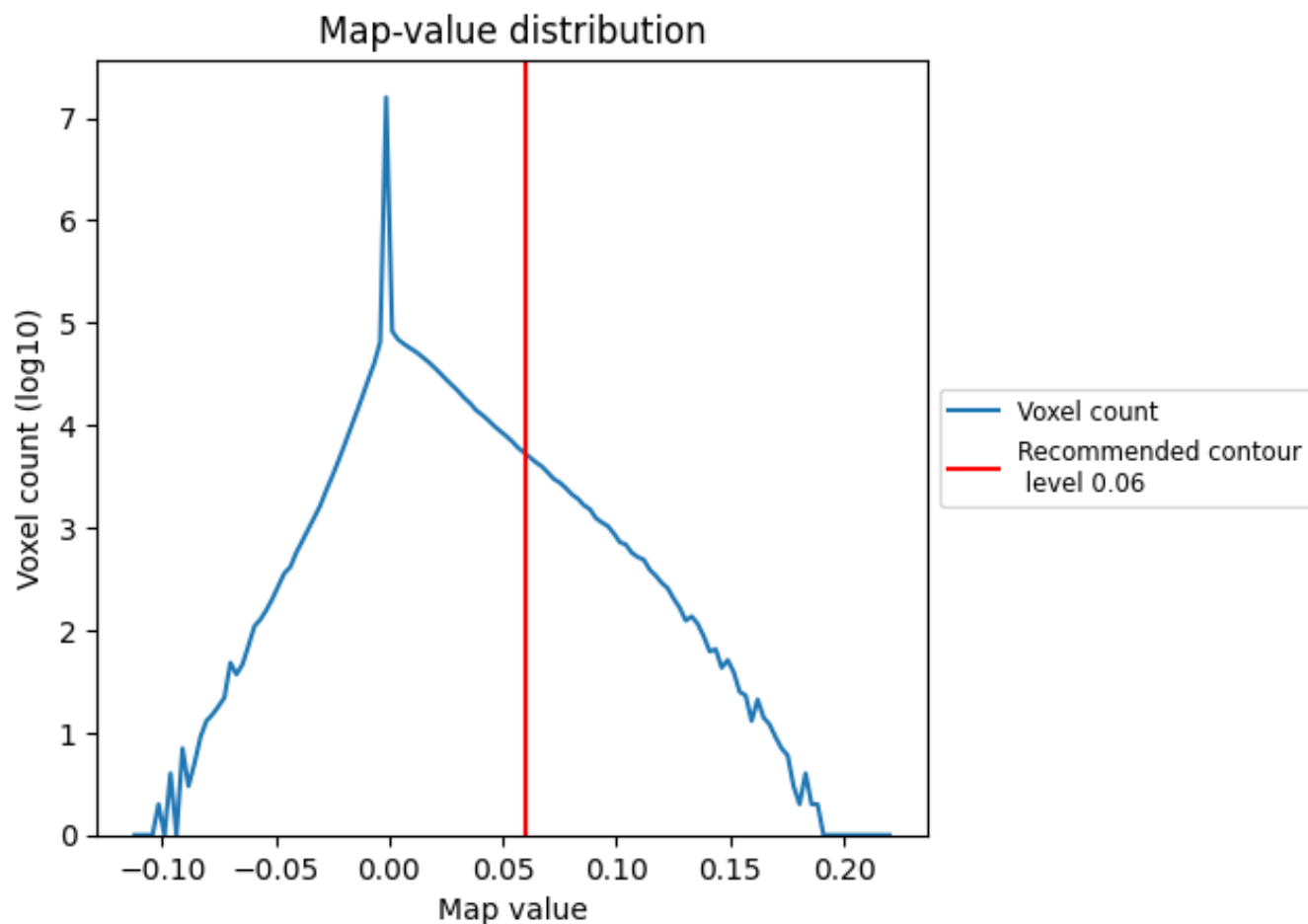
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

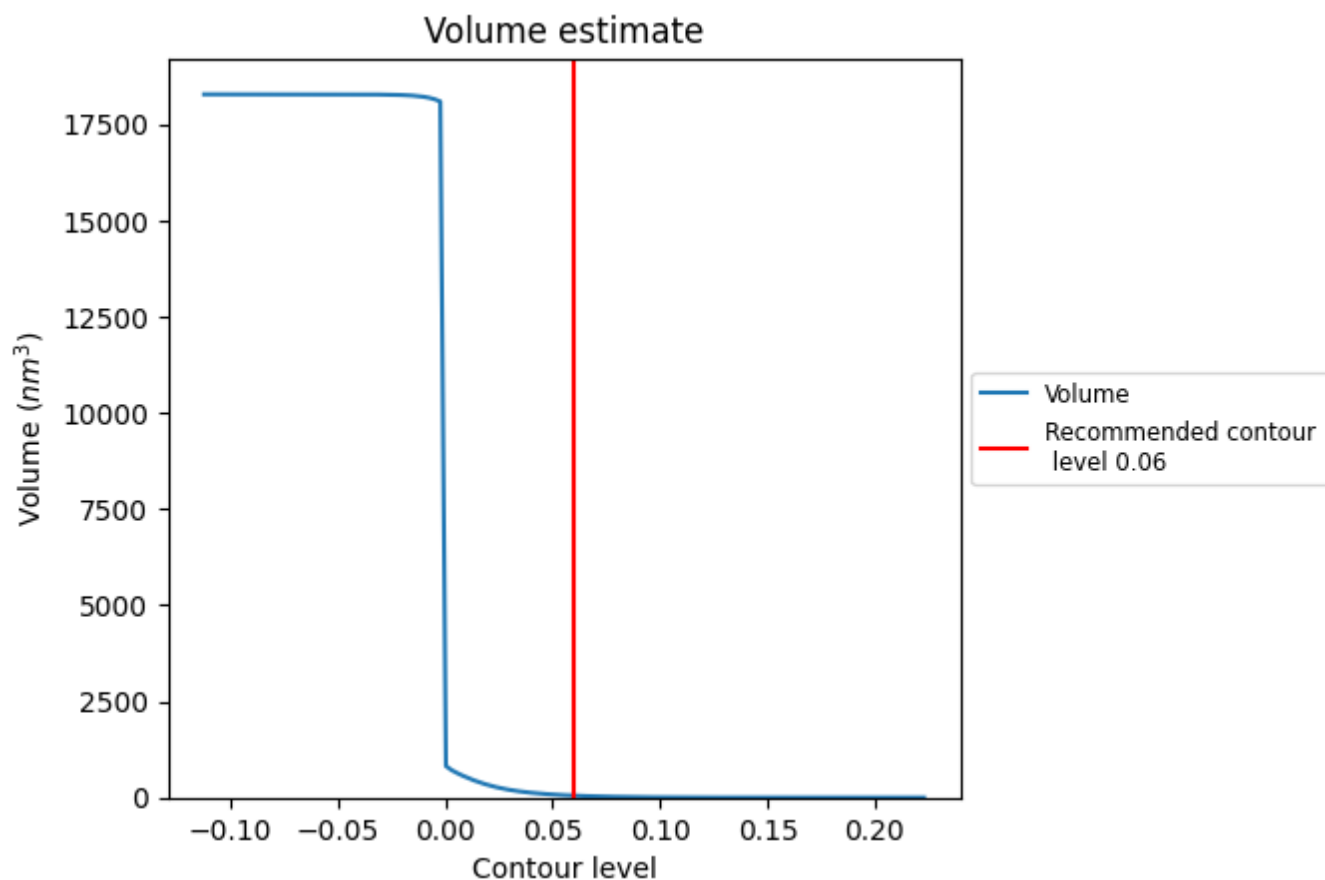
This section contains the results of statistical analysis of the map.

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.

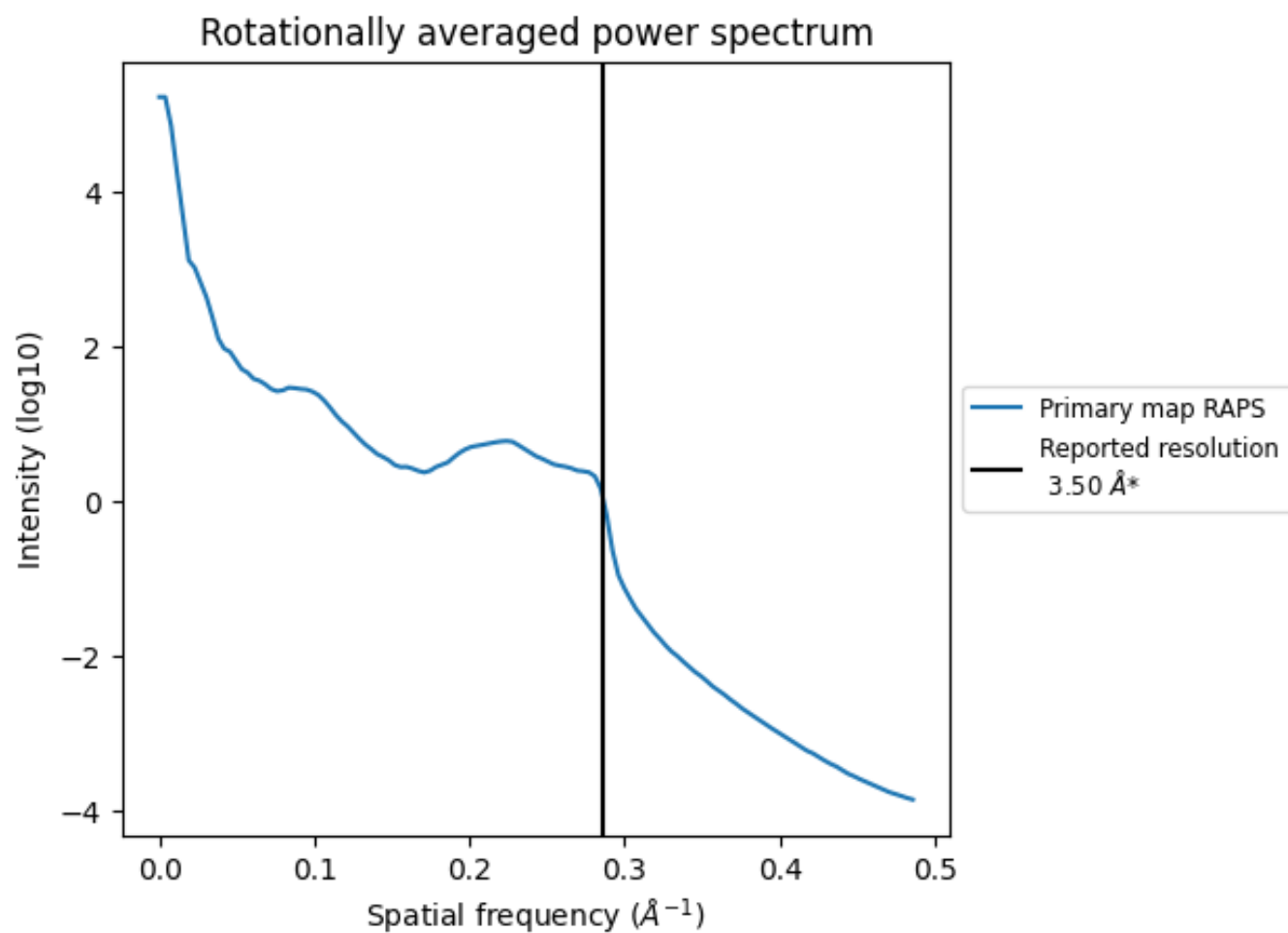
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 50 nm³; this corresponds to an approximate mass of 45 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⁻¹

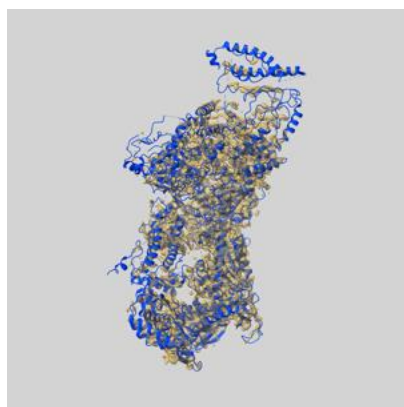
8 Fourier-Shell correlation

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

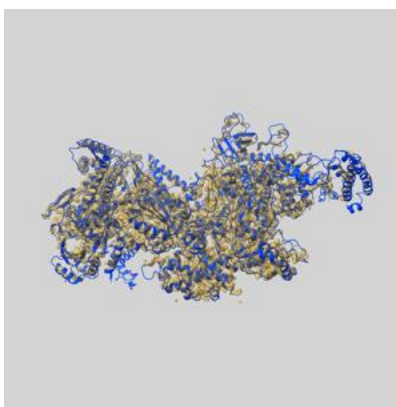
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21701 and PDB model 6WJV. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

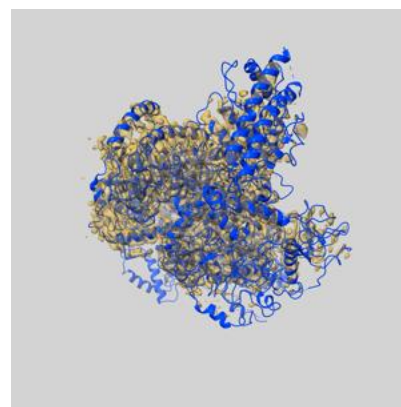
9.1 Map-model overlay [i](#)



X



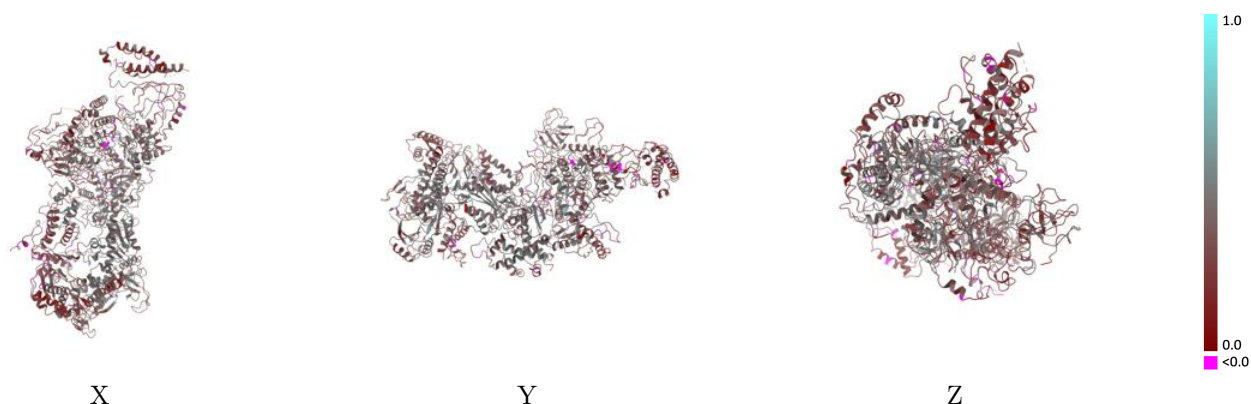
Y



Z

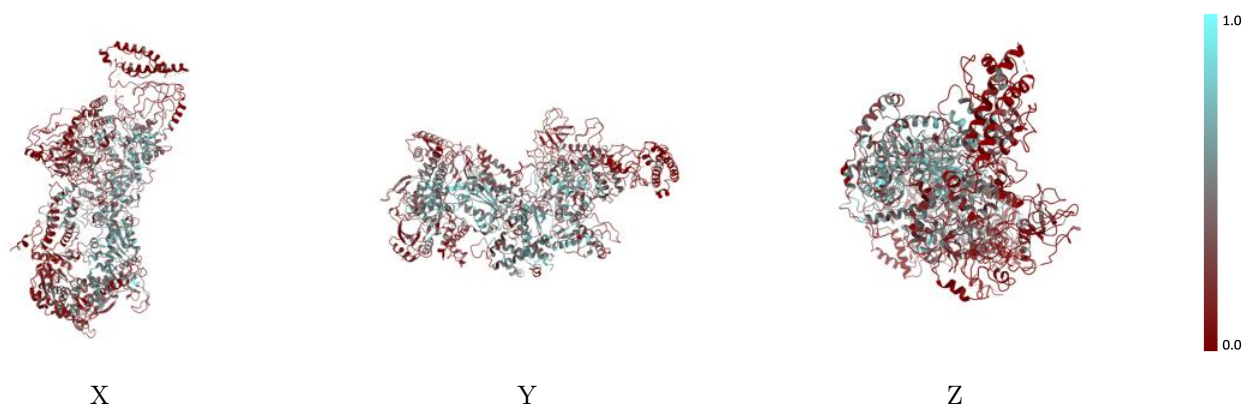
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



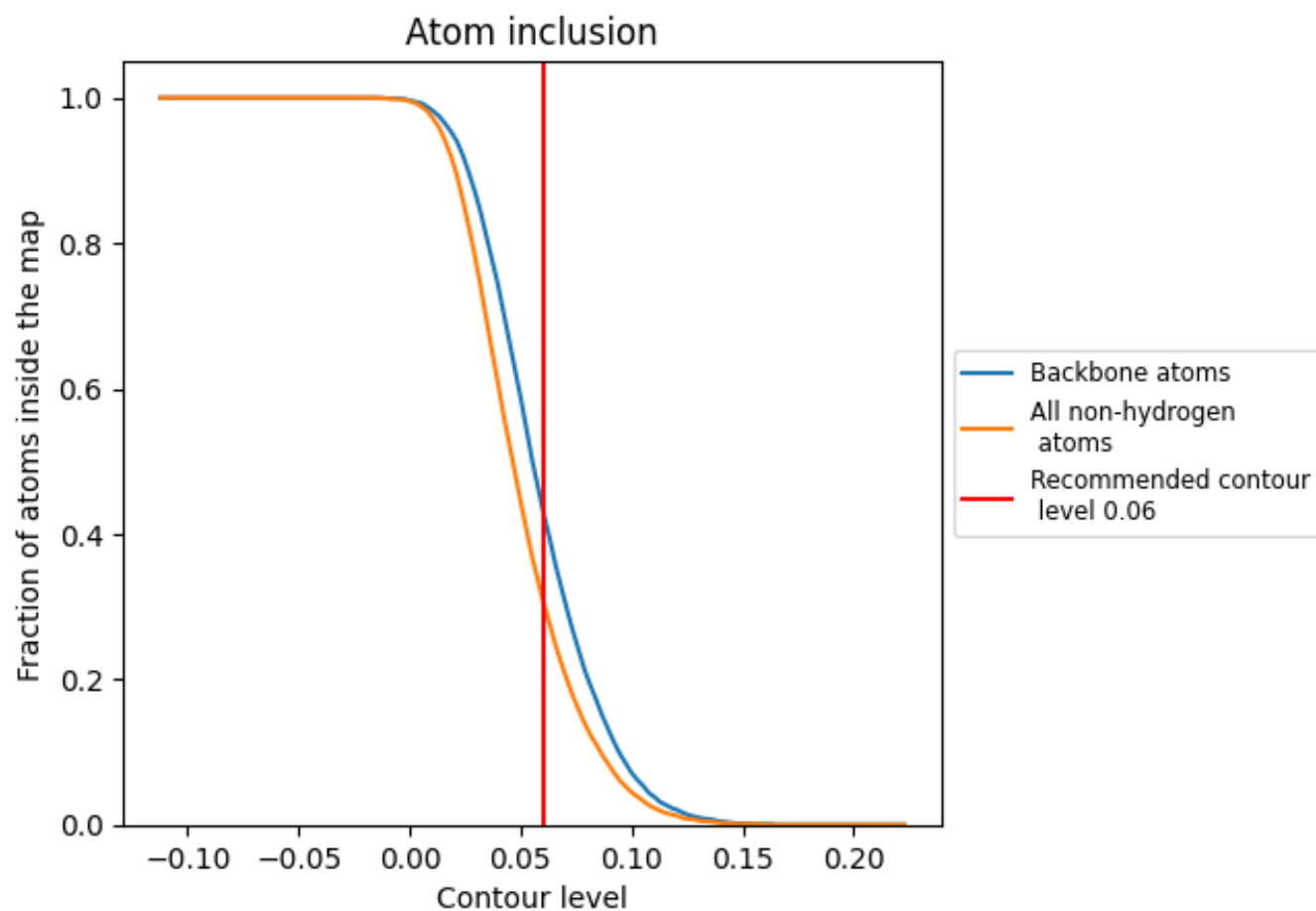
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).

9.4 Atom inclusion [i](#)



At the recommended contour level, 43% of all backbone atoms, 31% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3090	0.3490
2	0.2000	0.3340
3	0.4410	0.3700
4	0.4350	0.3910
A	0.3190	0.3490

