



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 09:37 PM UTC

PDB ID : 6X4W / pdb_00006x4w
EMDB ID : EMD-22043
Title : Mfd-bound E.coli RNA polymerase elongation complex - III state
Authors : Llewellyn, E.; Chen, J.; Kang, J.Y.; Darst, S.A.
Deposited on : 2020-05-24
Resolution : 3.80 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:

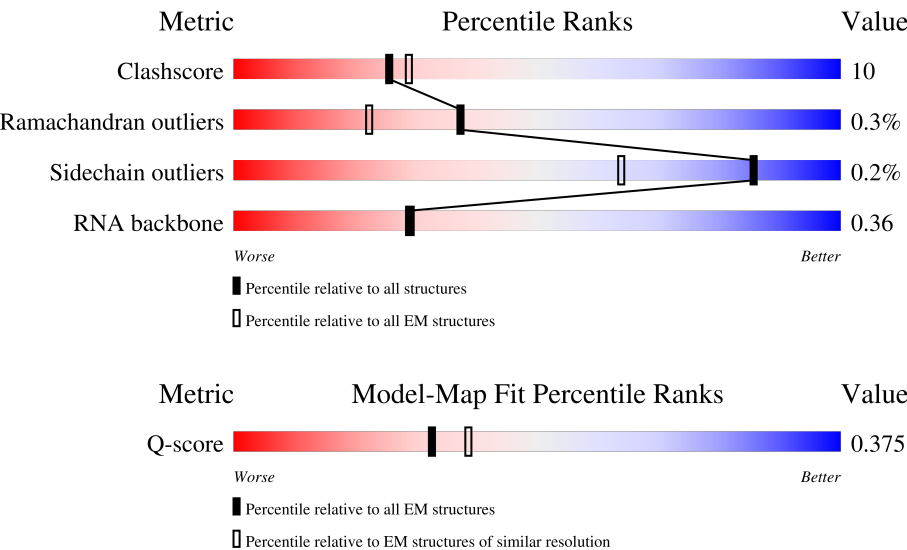
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	1148	72%28%
2	G	329	60%8%32%
2	H	329	50%16%34%

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Mol	Chain	Length	Quality of chain
3	I	1342	
4	J	1407	
5	K	91	
6	R	21	
7	P	64	
8	Q	64	

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 36021 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 Transcription-repair-coupling factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1144	Total	C	N	O	S	0	0
			8955	5669	1595	1655	36		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	224	Total	C	N	O	S	0	0
			1717	1076	302	333	6		
2	H	217	Total	C	N	O	S	0	0
			1667	1043	293	325	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	1316	Total	C	N	O	S	0	0
			10348	6492	1803	2010	43		

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	J	1336	Total	C	N	O	S	0	0
			10373	6519	1849	1955	50		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	1384	VAL	MET	conflict	UNP A0A4S1NBU2

- Molecule 5 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	K	79	Total	C	N	O	S	0	0
			627	382	118	126	1		

- Molecule 6 is a RNA chain called RNA (20-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	R	9	Total	C	N	O	P	0	0
			201	89	42	61	9		

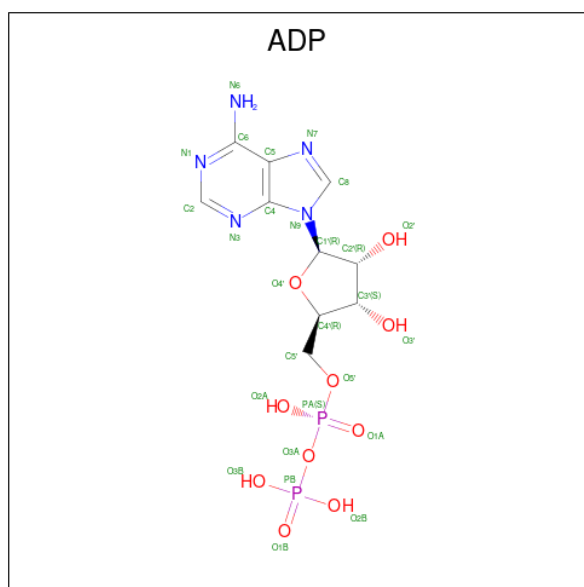
- Molecule 7 is a DNA chain called DNA (64-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	P	55	Total	C	N	O	P	0	0
			1112	531	192	335	54		

- Molecule 8 is a DNA chain called DNA (64-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Q	48	Total	C	N	O	P	0	0
			991	468	192	283	48		

- Molecule 9 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
9	A	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 10 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
10	J	1	Total 1	Mg 1	0

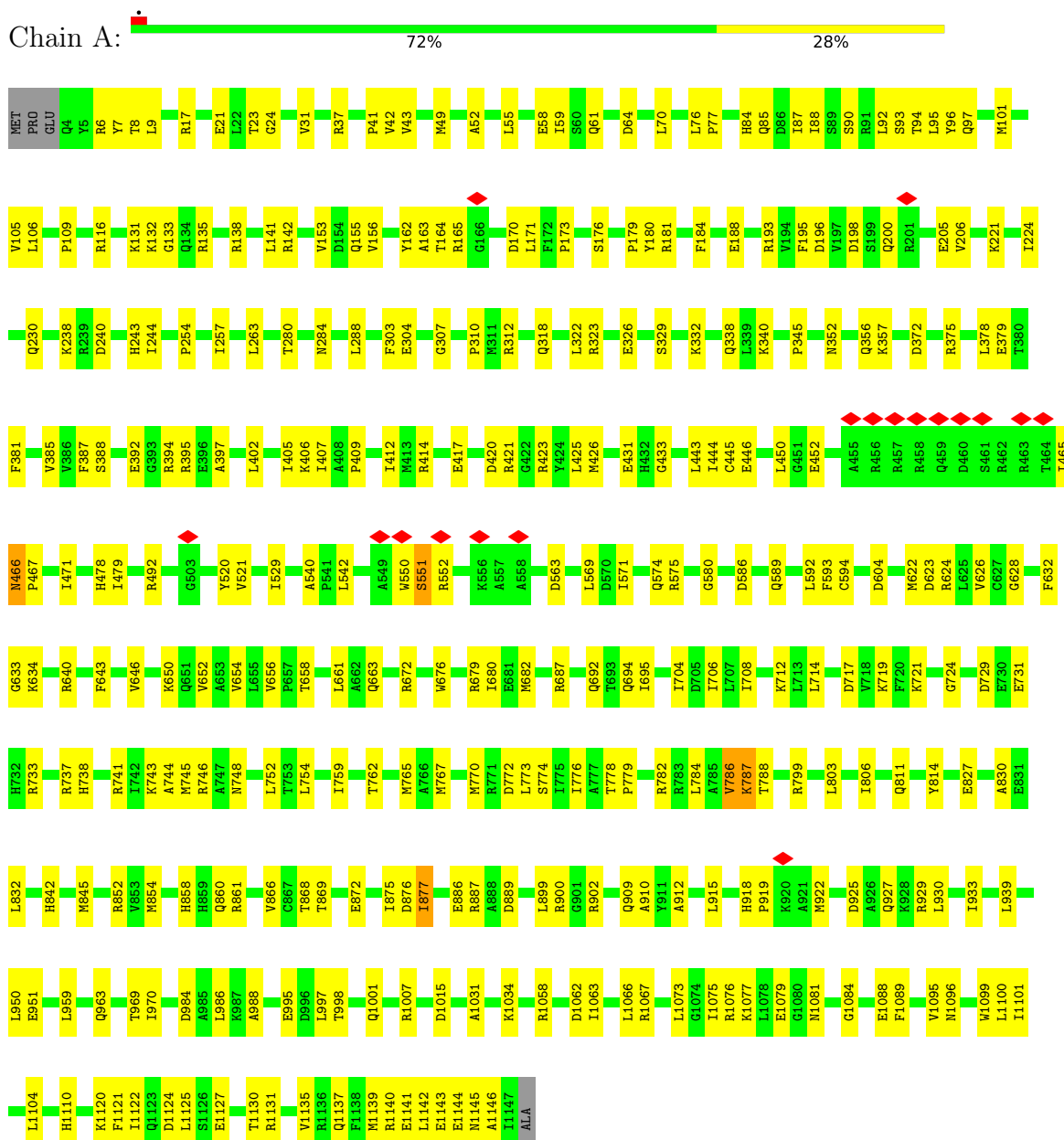
- Molecule 11 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
11	J	2	Total 2	Zn 2	0

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: Transcription-repair-coupling factor



[illegible]

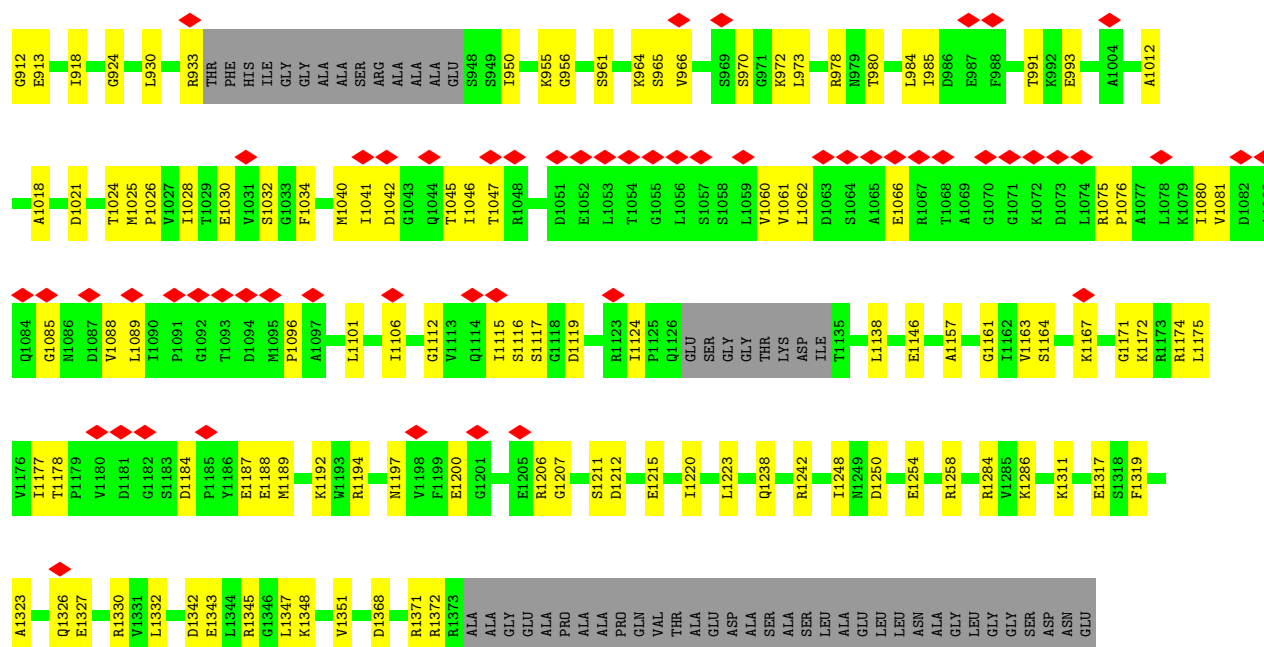
Chain H:

Category	Percentage
MET	50%
V5	16%
E7	34%

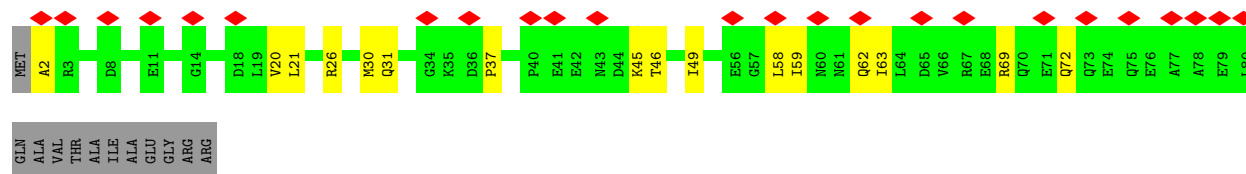
Chain I:

75% 23%

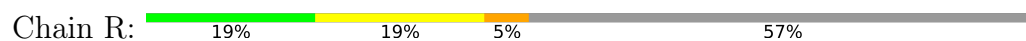
Item	Category
A543	Green
G544	Green
F545	Green
V550	Yellow
R557	Green
P560	Green
I561	Green
P564	Green
N568	Green
I572	Green
N573	Green
S576	Green
V577	Green
R592	Green
K593	Green
V594	Green
T595	Green
D596	Green
V599	Green
L606	Green
S607	Green
A608	Green
E611	Green
F629	Green
V630	Green
E631	Green
D632	Green
L633	Green
C636	Green
L644	Green
F645	Green
R647	Green
M653	Green
D654	Green
Q659	Green
V660	Green
V661	Green
S666	Green
G682	Green
A683	Green
N684	Green
D393	Green
R403	Green
K404	Green
I419	Green
L420	Green
S421	Green
K422	Green
D423	Green
D424	Green
I425	Green
I426	Green
M429	Green
R436	Green
M437	Green
R465	Green
L468	Green
E472	Green
V475	Green
K476	Green
E477	Green
R478	Green
L481	Green
M488	Green
P489	Green
Q490	Green
D491	Green
S508	Green
L511	Green
F514	Green
N519	Green
P520	Green
L521	Green
S522	Green
E523	Green
I524	Green
T525	Green
R528	Green
R529	Green
L538	Green
T539	Green
R540	Green
G259	Green
K260	Green
V261	Green
V263	Green
R267	Green
R268	Green
R275	Green
Q276	Green
L277	Green
E278	Green
K279	Green
V282	Green
V283	Green
L284	Green
E290	Green
V291	Green
A293	Green
V297	Green
D300	Green
Y301	Green
I302	Green
S305	Green
L309	Green
A312	Green
A313	Green
L317	Green
S318	Green
L319	Green
D342	Green
I347	Green
S348	Green
S349	Green
T350	Green
L351	Green
R352	Green
I354	Green
V355	Green
D354	Green
P375	Green
P376	Green
R378	Green
S383	Green
V387	Green
L129	Green
M130	Green
G134	Green
I138	Green
V155	Green
D158	Green
S159	Green
D160	Green
K161	Green
G162	Green
M163	Green
L171	Green
R175	Green
R180	Green
P190	Green
K191	Green
D192	Green
N193	Green
L194	Green
F195	Green
V196	Green
R197	Green
K203	Green
L204	Green
T207	Green
L208	Green
F224	Green
F230	Green
R233	Green
D234	Green
N235	Green
K236	Green
L237	Green
Q238	Green
M239	Green
E240	Green
L241	Green
R247	Green
T250	Green
A251	Green
T255	Green
E256	Green
A257	Green
N258	Green
E111	Yellow
G112	Yellow
K115	Yellow
D116	Yellow
I117	Yellow
Q120	Yellow
E121	Yellow
V122	Yellow
Y123	Yellow
M124	Yellow
I127	Yellow
P128	Yellow



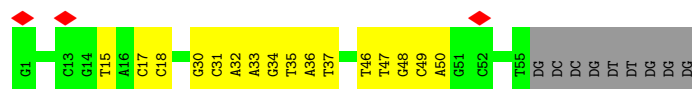
- Molecule 5: DNA-directed RNA polymerase subunit omega



- Molecule 6: RNA (20-mer)

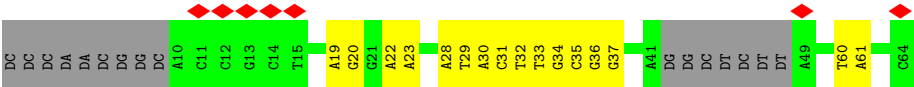


- Molecule 7: DNA (64-MER)



- Molecule 8: DNA (64-MER)





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	47000	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	30.442	Depositor
Minimum map value	-17.295	Depositor
Average map value	0.010	Depositor
Map value standard deviation	1.075	Depositor
Recommended contour level	4.5	Depositor
Map size (Å)	390.0, 390.0, 390.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3, 1.3, 1.3	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ADP, MG, 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	0.39	0/9134	0.75	2/12387 (0.0%)
2	G	0.41	0/1737	0.70	0/2356
2	H	0.36	0/1686	0.71	0/2286
3	I	0.45	0/10511	0.70	4/14186 (0.0%)
4	J	0.40	0/10530	0.70	2/14219 (0.0%)
5	K	0.30	0/629	0.72	0/847
6	R	0.42	0/226	0.45	0/352
7	P	0.40	0/1242	0.58	0/1913
8	Q	0.36	0/1113	0.50	0/1714
All	All	0.41	0/36808	0.70	8/50260 (0.0%)

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	877	ILE	CA-CB-CG2	5.77	120.31	110.50
3	I	1079	ILE	CA-C-N	5.56	131.51	120.94
3	I	1079	ILE	C-N-CA	5.56	131.51	120.94
4	J	212	THR	N-CA-C	-5.50	107.57	114.56
3	I	112	GLY	CA-C-N	5.40	131.04	121.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	8955	0	8859	219	0
2	G	1717	0	1753	20	0
2	H	1667	0	1699	36	0
3	I	10348	0	10347	206	0
4	J	10373	0	10583	244	0
5	K	627	0	634	11	0
6	R	201	0	98	4	0
7	P	1112	0	622	15	0
8	Q	991	0	538	14	0
9	A	27	0	12	2	0
10	J	1	0	0	0	0
11	J	2	0	0	0	0
All	All	36021	0	35145	732	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 732 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)
4:J:850:LYS:HD2	4:J:875:ASN:ND2	1.58	1.17
4:J:850:LYS:HG2	4:J:851:PRO:CD	1.75	1.17
4:J:850:LYS:HG2	4:J:851:PRO:HD2	1.15	1.10
4:J:850:LYS:HG3	4:J:857:LEU:HD22	1.18	1.09
4:J:850:LYS:HE2	4:J:851:PRO:HD2	1.28	1.08

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	1142/1148 (100%)	1023 (90%)	112 (10%)	7 (1%)	21	54
2	G	220/329 (67%)	199 (90%)	21 (10%)	0	100	100
2	H	213/329 (65%)	196 (92%)	17 (8%)	0	100	100
3	I	1312/1342 (98%)	1219 (93%)	93 (7%)	0	100	100
4	J	1330/1407 (94%)	1231 (93%)	95 (7%)	4 (0%)	36	67
5	K	77/91 (85%)	70 (91%)	7 (9%)	0	100	100
All	All	4294/4646 (92%)	3938 (92%)	345 (8%)	11 (0%)	37	67

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	471	ILE
1	A	551	SER
1	A	786	VAL
1	A	787	LYS
4	J	209	ASN

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	930/973 (96%)	930 (100%)	0	100	100
2	G	189/286 (66%)	189 (100%)	0	100	100
2	H	184/286 (64%)	184 (100%)	0	100	100
3	I	1128/1157 (98%)	1126 (100%)	2 (0%)	87	87
4	J	1116/1168 (96%)	1111 (100%)	5 (0%)	84	83
5	K	67/75 (89%)	67 (100%)	0	100	100
All	All	3614/3945 (92%)	3607 (100%)	7 (0%)	85	87

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	J	777	HIS

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Mol	Chain	Res	Type
4	J	850	LYS
4	J	1326	GLN
4	J	853	THR
4	J	207	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
3	I	1017	GLN
4	J	1238	GLN
4	J	232	ASN
5	K	72	GLN
4	J	1044	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
6	R	8/21 (38%)	1 (12%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	R	14	A

There are no RNA pucker outliers to report.

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 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
9	ADP	A	2000	-	28,29,29	1.34	4 (14%)	43,45,45	1.86	9 (20%)

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
9	ADP	A	2000	-	-	4/16/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	2000	ADP	C5-C4	4.29	1.46	1.39
9	A	2000	ADP	C5-N7	-2.66	1.34	1.39
9	A	2000	ADP	C5-C6	2.34	1.47	1.41
9	A	2000	ADP	C4-N9	-2.25	1.33	1.37

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	2000	ADP	C5-C4-N3	-5.96	118.50	126.72
9	A	2000	ADP	N3-C4-N9	4.90	135.51	127.17
9	A	2000	ADP	C2-N3-C4	3.60	120.61	111.83
9	A	2000	ADP	C4-C5-N7	-3.00	107.15	110.58
9	A	2000	ADP	N3-C2-N1	-2.88	124.22	128.58

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	A	2000	ADP	C5'-O5'-PA-O1A
9	A	2000	ADP	O4'-C4'-C5'-O5'

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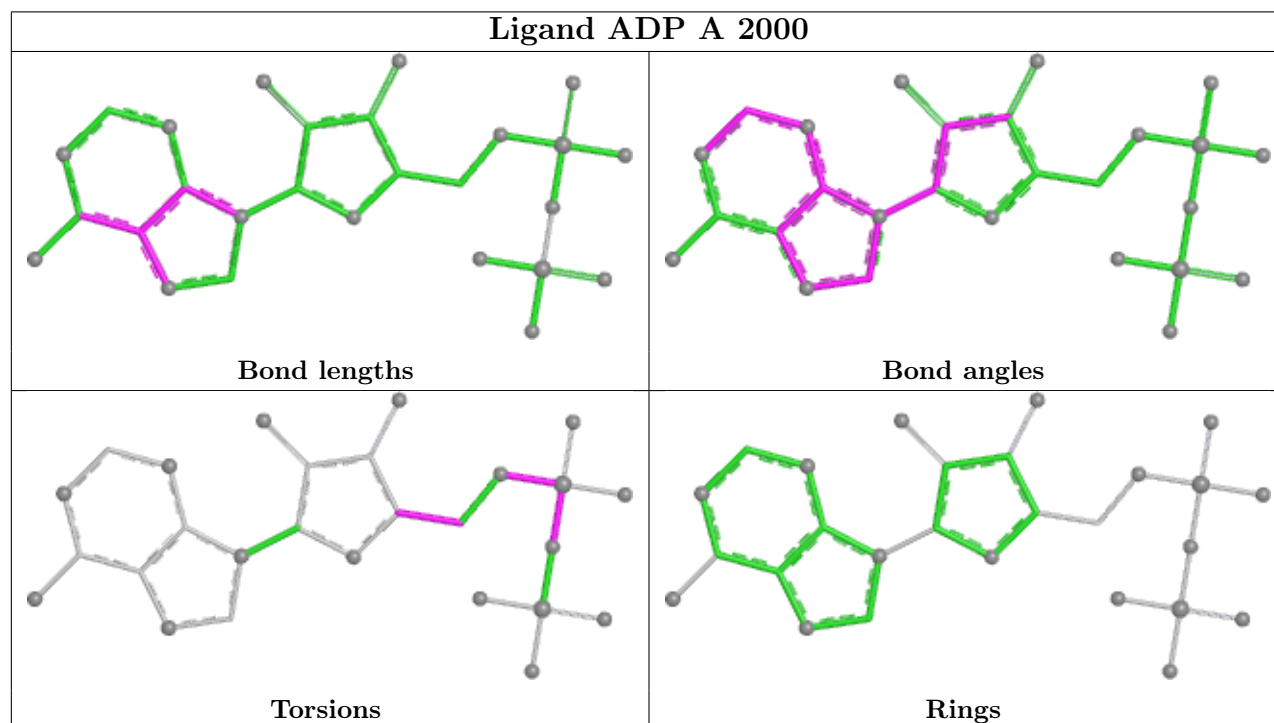
Mol	Chain	Res	Type	Atoms
9	A	2000	ADP	C3'-C4'-C5'-O5'
9	A	2000	ADP	PB-O3A-PA-O5'

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	2000	ADP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

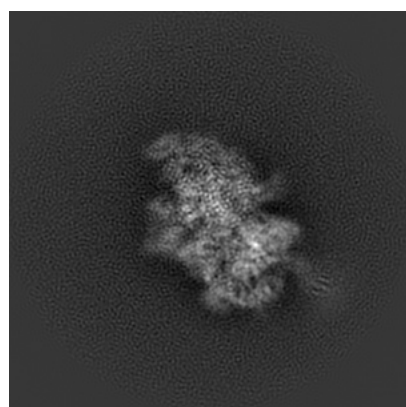
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22043. These allow visual inspection of the internal detail of the map and identification of artifacts.

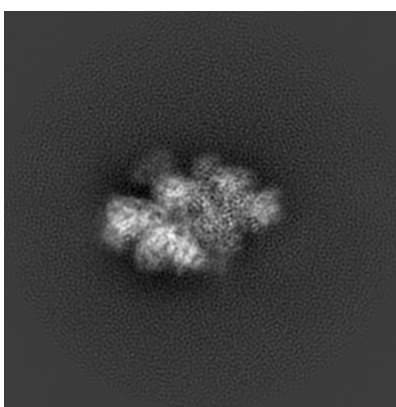
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

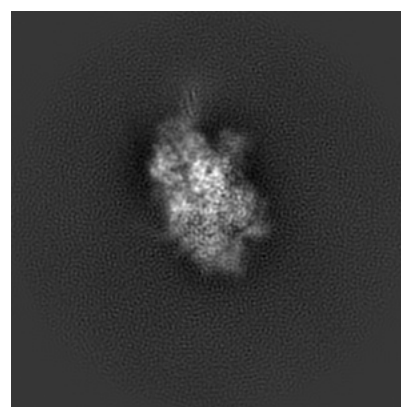
6.1.1 Primary map



X



Y

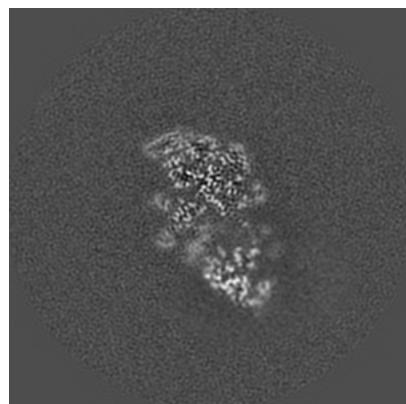


Z

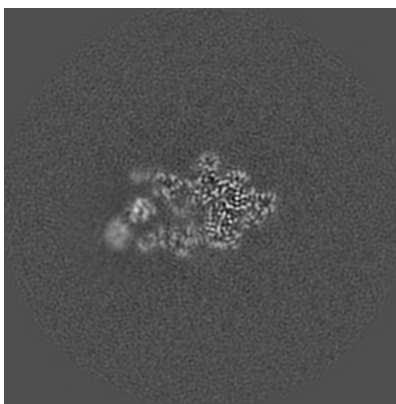
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

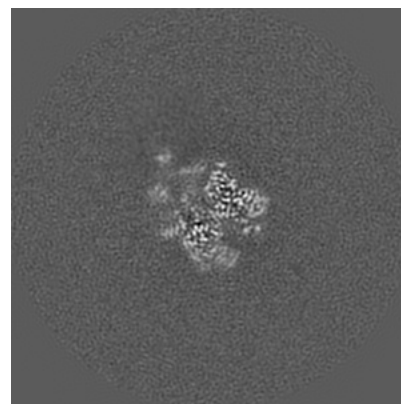
6.2.1 Primary map



X Index: 150



Y Index: 150

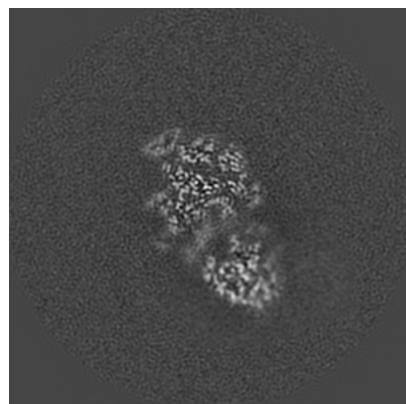


Z Index: 150

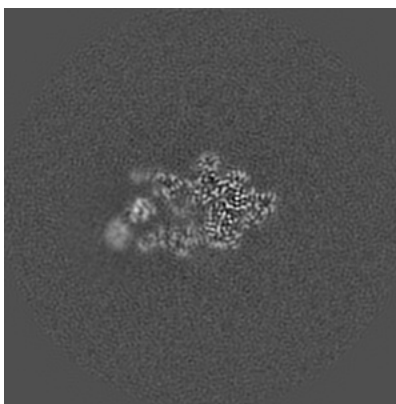
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

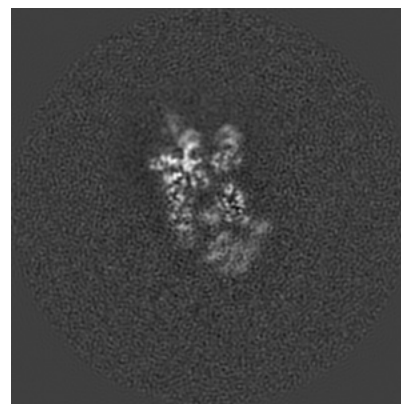
6.3.1 Primary map



X Index: 146



Y Index: 150

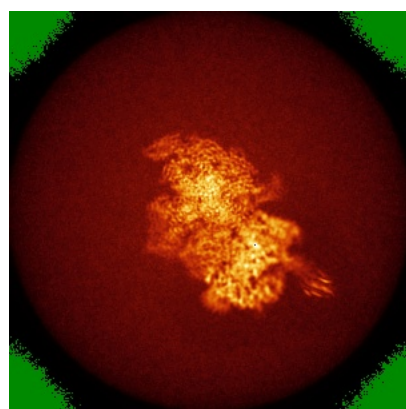


Z Index: 124

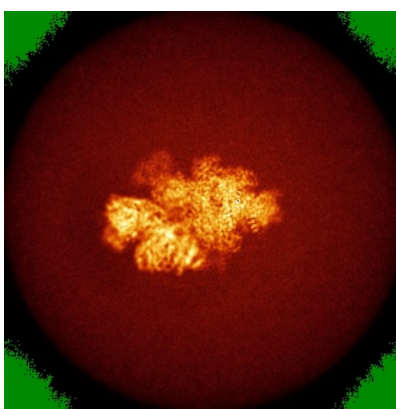
The images above show the largest variance slices of the map in three orthogonal directions.

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

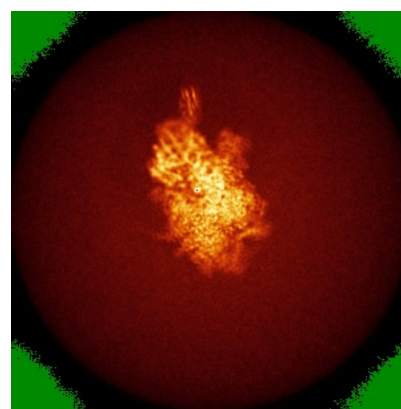
6.4.1 Primary map



X



Y

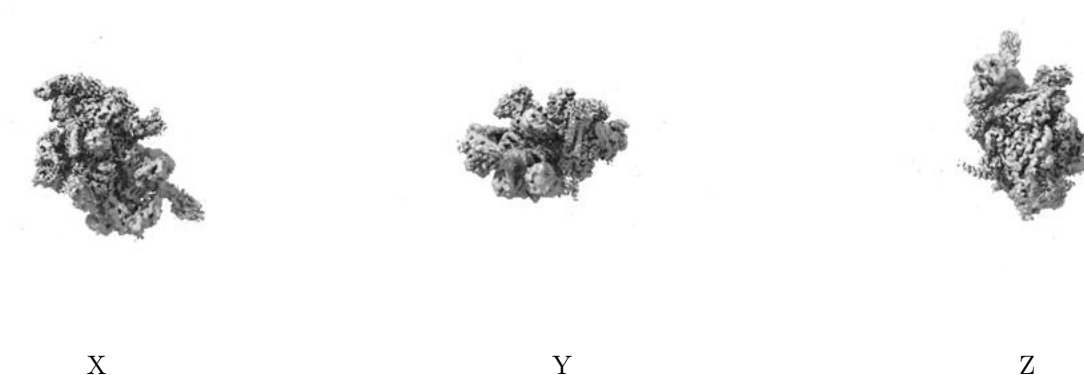


Z

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

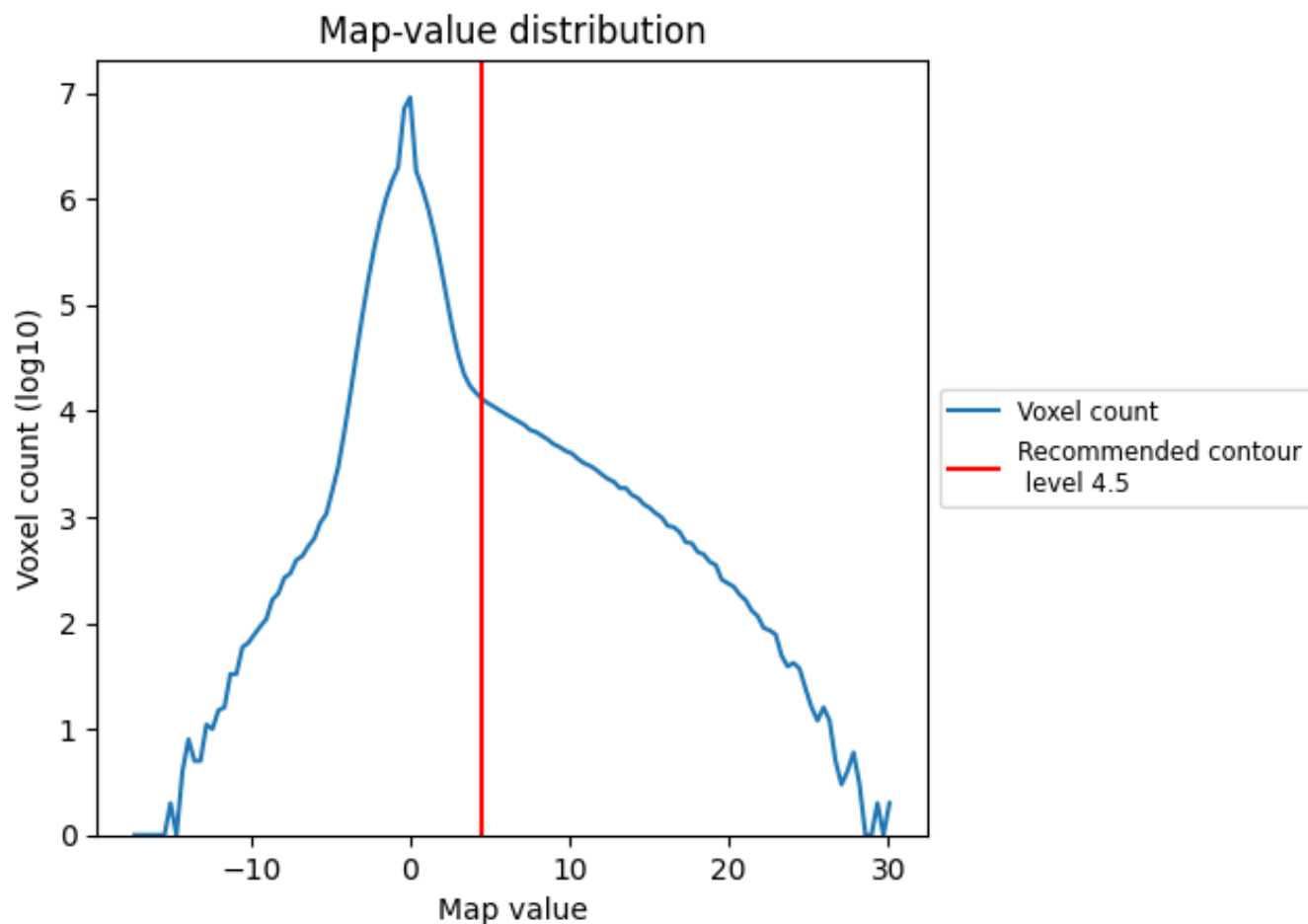
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

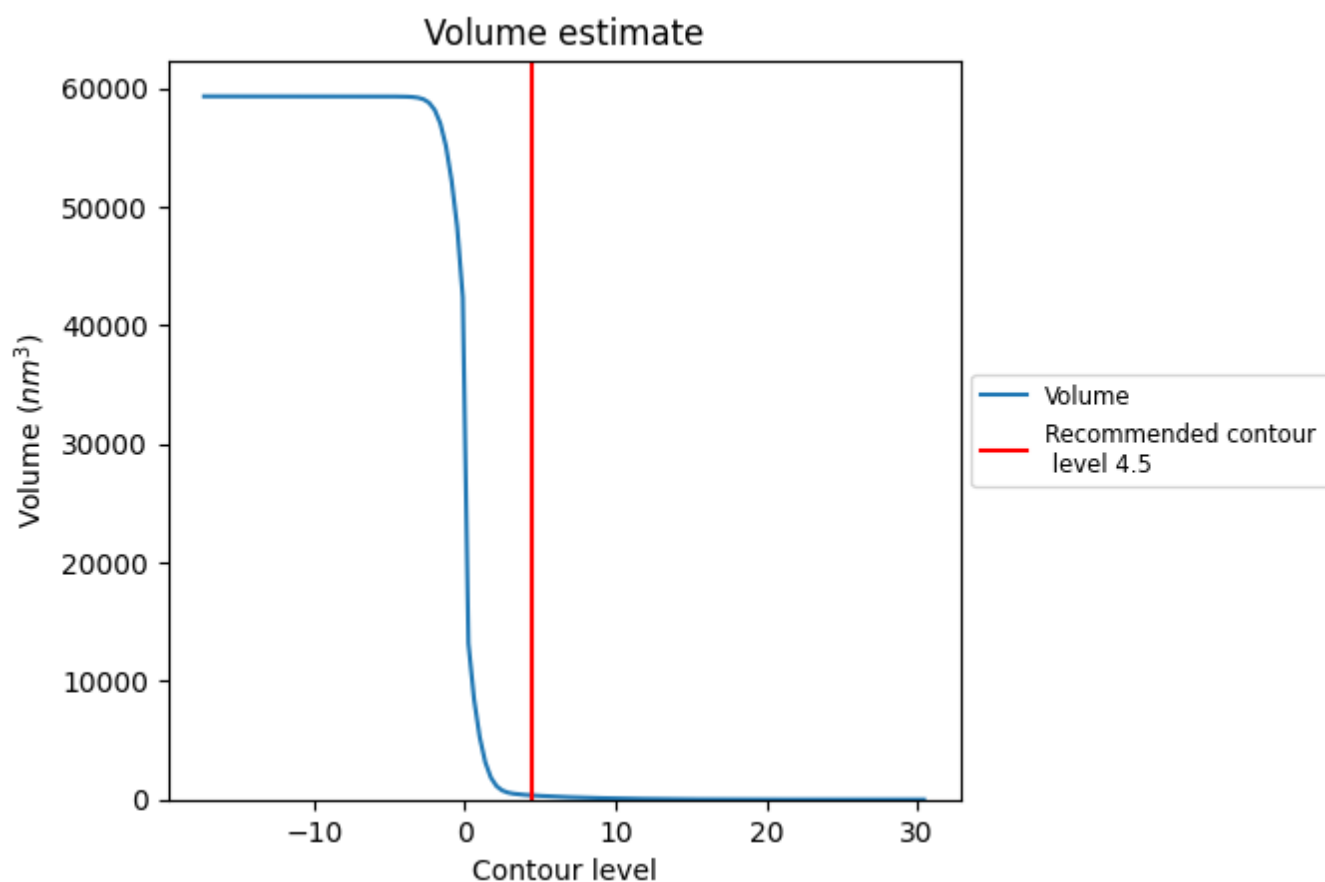
This section contains the results of statistical analysis of the map.

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.

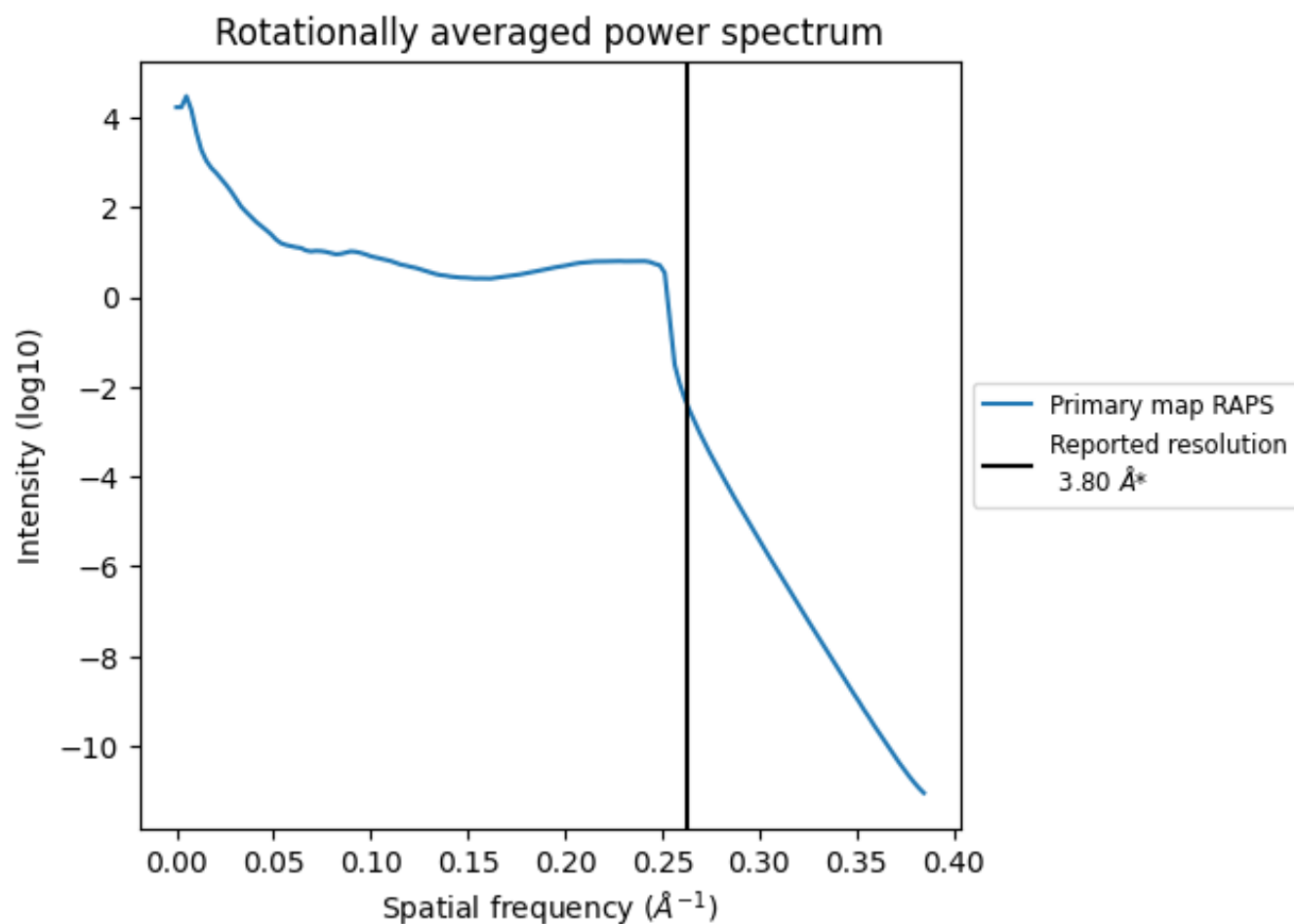
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 350 nm^3 ; this corresponds to an approximate mass of 316 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 0.263 $\text{\AA}^{-1}$

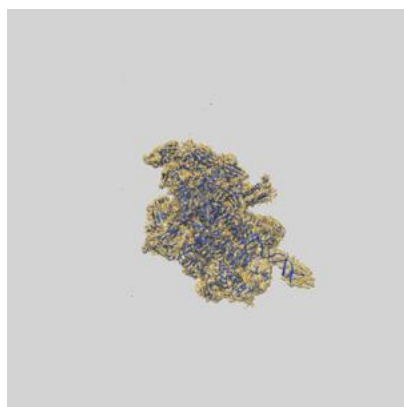
8 Fourier-Shell correlation ⓘ

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

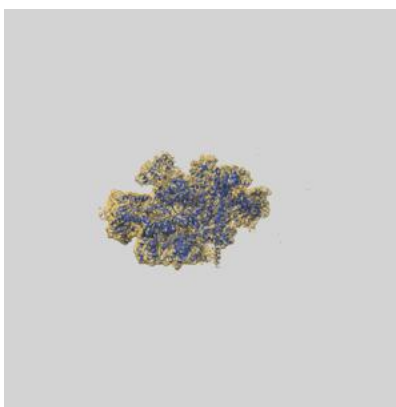
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-22043 and PDB model 6X4W. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

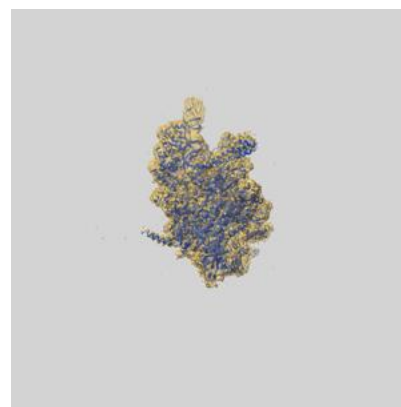
9.1 Map-model overlay [i](#)



X



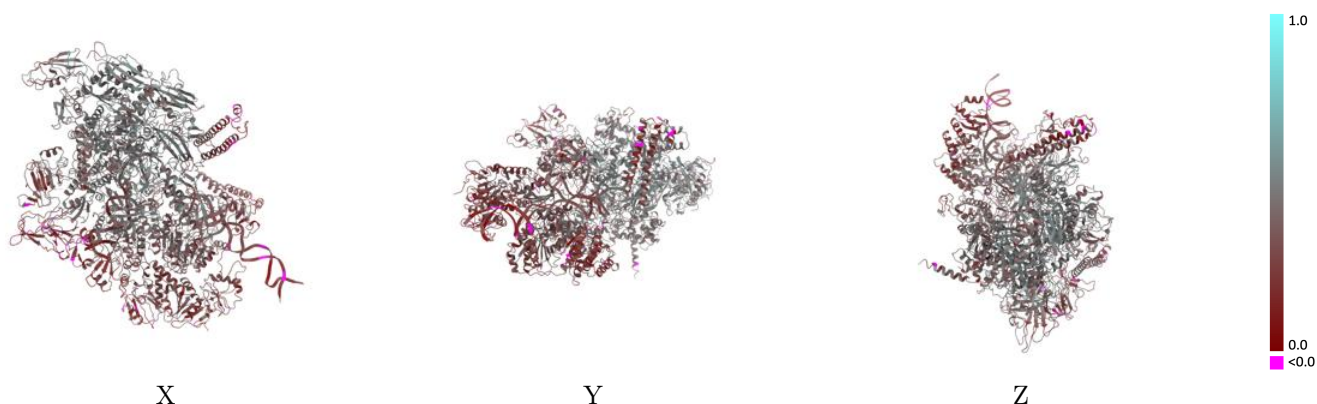
Y



Z

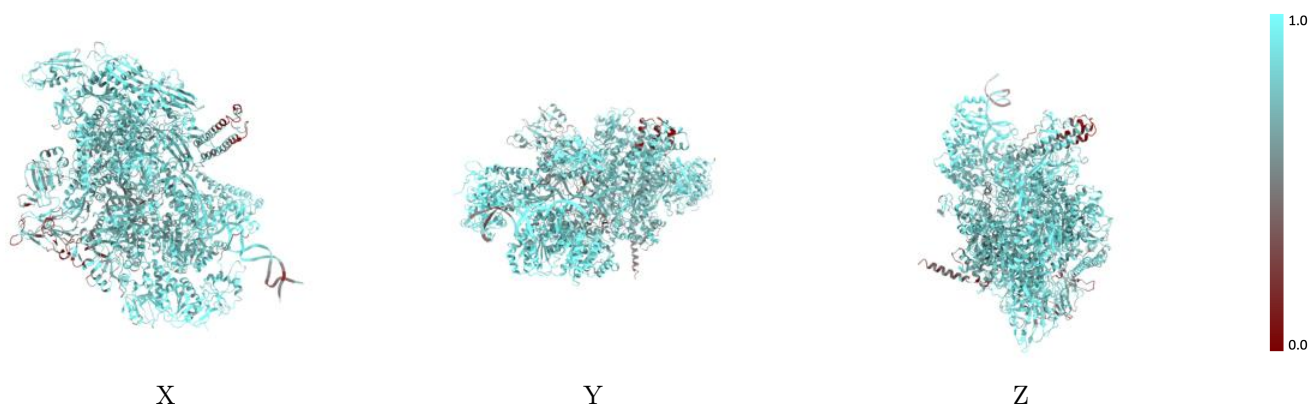
The images above show the 3D surface view of the map at the recommended contour level 4.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



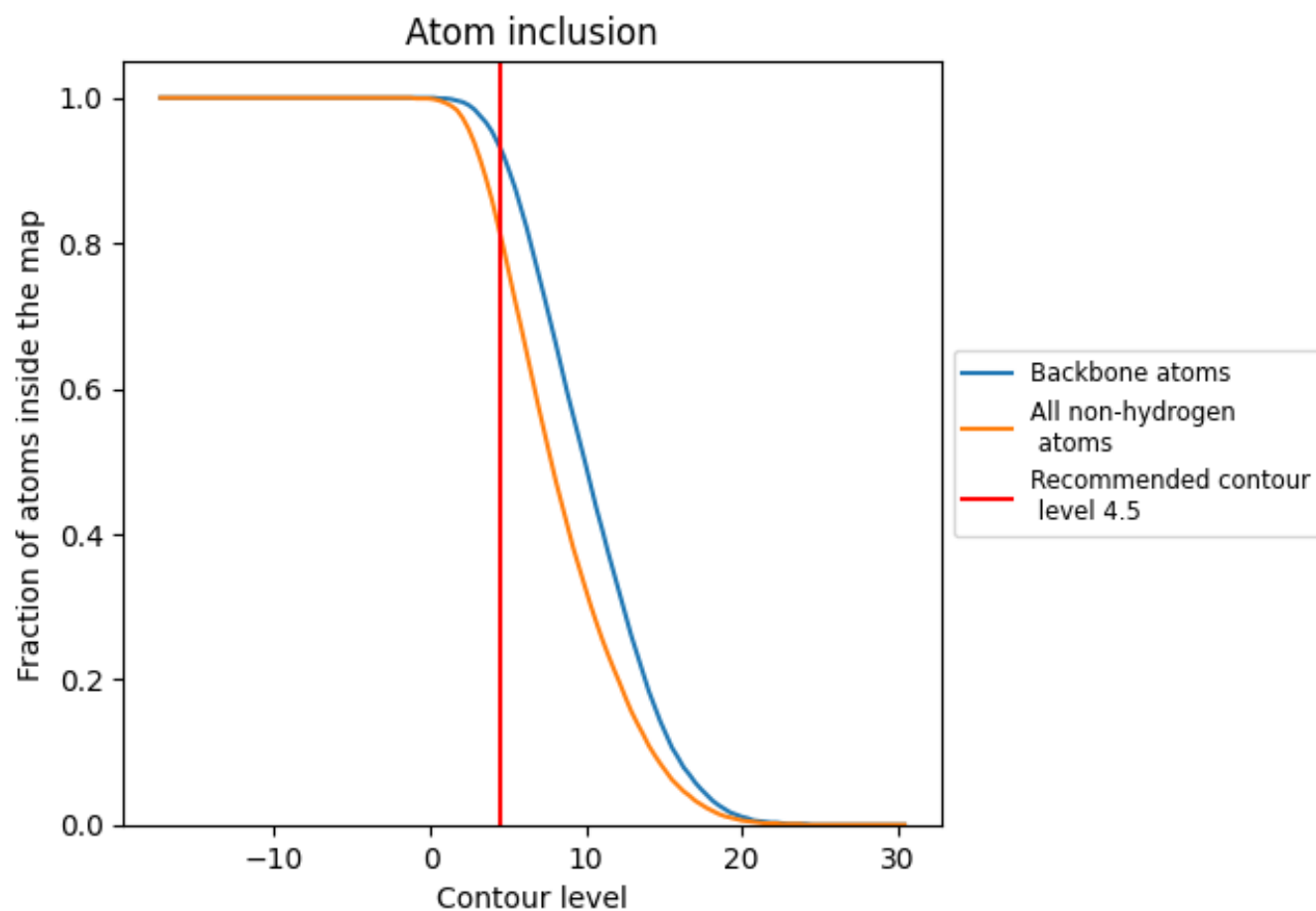
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 81% 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 (4.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8120	0.3750
A	0.8880	0.2970
G	0.8560	0.4620
H	0.8420	0.4220
I	0.8040	0.4220
J	0.7670	0.3930
K	0.5200	0.3790
P	0.8050	0.2890
Q	0.7460	0.2440
R	0.8860	0.4130

1.0

0.0

<0.0