



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 08:34 PM UTC

PDB ID : 9GJ5 / pdb_00009gj5
EMDB ID : EMD-51382
Title : Human 80S ribosome in complex with NatA in distal position and Ebp1
Authors : Klein, M.A.; Wild, K.; Sinning, I.
Deposited on : 2024-08-21
Resolution : 4.61 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:

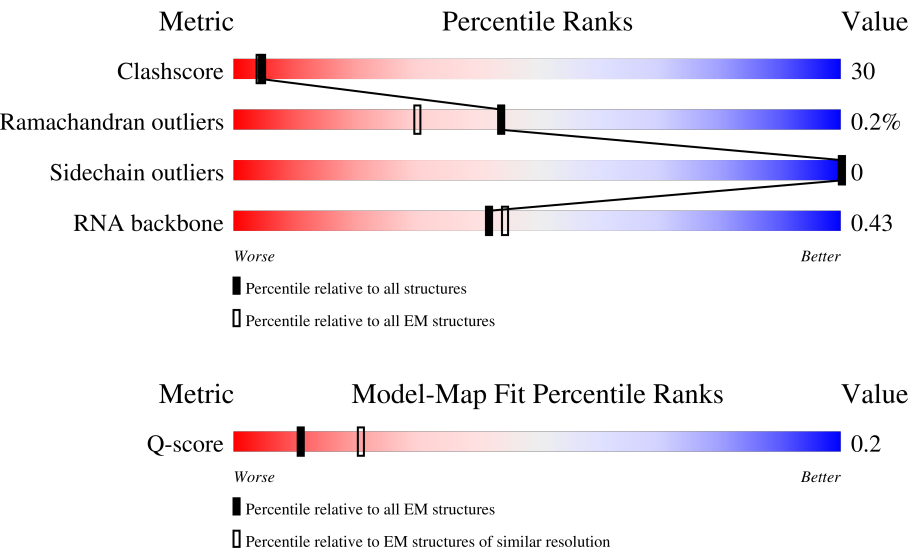
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 4.61 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.



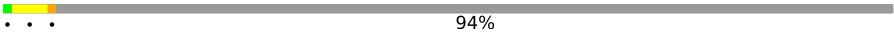



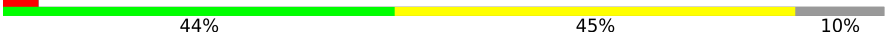


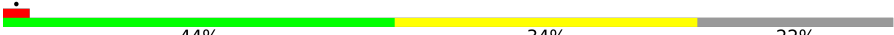

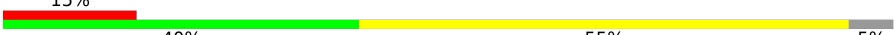
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	2098 (4.11 - 5.11)

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	2	171	<div><div>18%</div><div>32%</div><div>67%</div><div>..</div></div>
2	8	157	<div><div>27%</div><div>5%</div><div>63%</div></div>
3	B	840	<div><div>13%</div><div>40%</div><div>59%</div><div>.</div></div>

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Mol	Chain	Length	Quality of chain
4	1	5070	 94%
5	LC	427	 61% 24% 15%
6	LE	288	 49% 25% 26%
7	Lk	70	 51% 47%
8	LY	144	 44% 45% 10%
9	Lh	122	 52% 48%
10	LX	156	 39% 35% 26%
11	LR	196	 44% 34% 22%
12	Lr	137	 48% 43% 9%
13	A	394	 15% 40% 55% 5%

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 29428 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 N-alpha-acetyltransferase 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	169	Total	C	N	O	S	0	0
			1388	869	253	256	10		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	0	MET	-	initiating methionine	UNP P41227
2	1	GLY	-	expression tag	UNP P41227

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	8	58	Total	C	N	O	P	0	0
			1237	554	224	401	58		

- Molecule 3 is a protein called N-alpha-acetyltransferase 15, NatA auxiliary subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	834	Total	C	N	O	S	0	0
			6880	4379	1189	1271	41		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	ALA	deletion	UNP Q9BXJ9

- Molecule 4 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	1	300	Total	C	N	O	P	0	0
			6425	2859	1169	2097	300		

- Molecule 5 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LC	365	Total	C	N	O	S	0	0
			2908	1829	580	486	13		

- Molecule 6 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LE	214	Total	C	N	O	S	0	0
			1724	1111	327	282	4		

- Molecule 7 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Lk	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 8 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LY	129	Total	C	N	O	S	0	0
			1075	675	218	179	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LY	?	-	LYS	deletion	UNP P61254

- Molecule 9 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 10 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LX	116	Total	C	N	O	S	0	0
			950	606	178	165	1		

- Molecule 11 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LR	153	Total	C	N	O	S	0	0
			1281	799	276	197	9		

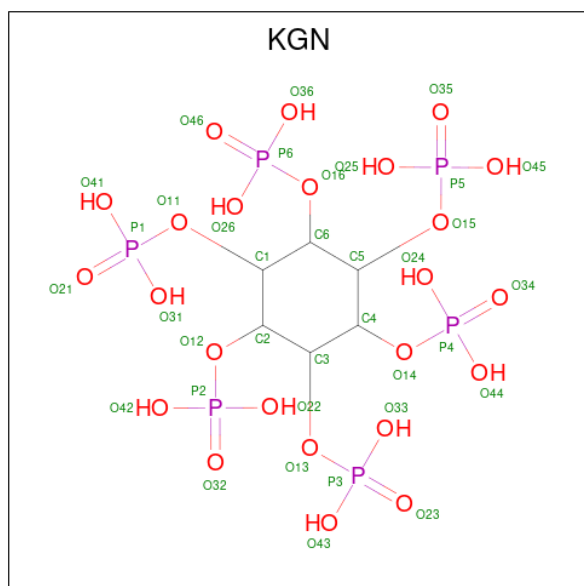
- Molecule 12 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

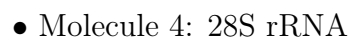
- Molecule 13 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	A	376	Total	C	N	O	S	0	0
			2938	1848	510	563	17		

- Molecule 14 is D-chiro inositol hexakisphosphate (CCD ID: KGN) (formula: $C_6H_{18}O_{24}P_6$).



Mol	Chain	Residues	Atoms				AltConf
14	B	1	Total	C	O	P	0
			36	6	24	6	



94%

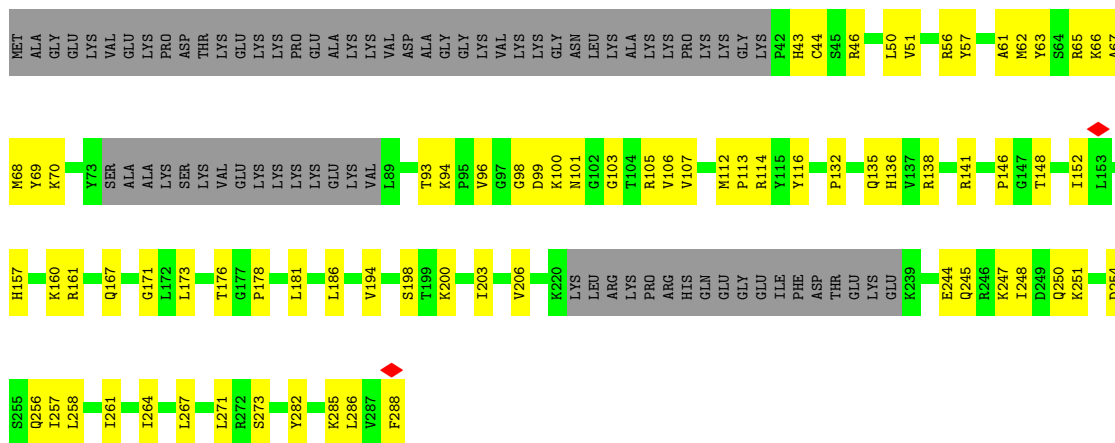
[illegible]



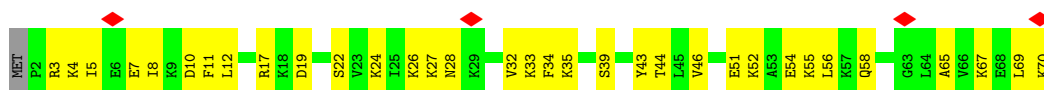




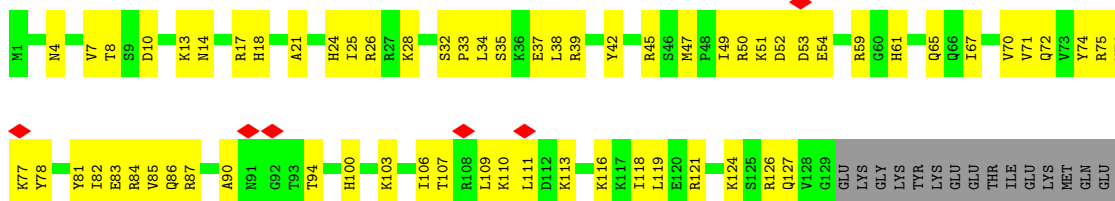




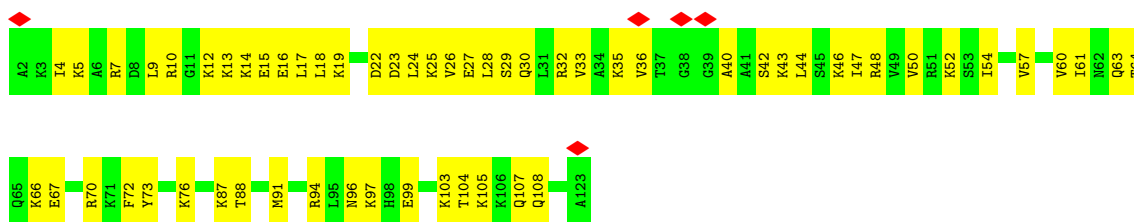
• Molecule 7: 60S ribosomal protein L38



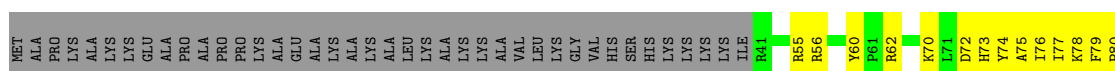
• Molecule 8: Large ribosomal subunit protein uL24

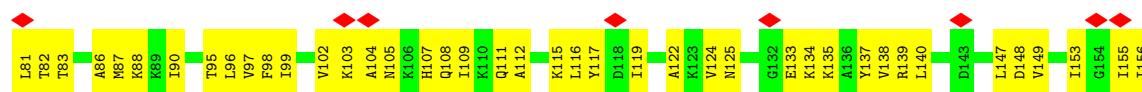


• Molecule 9: 60S ribosomal protein L35

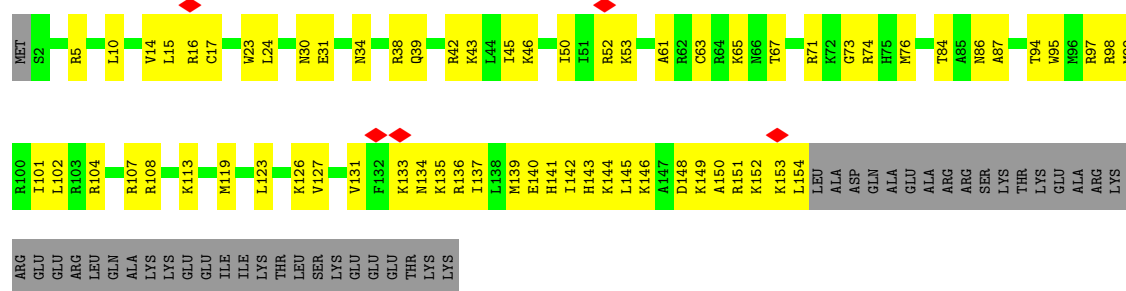


• Molecule 10: 60S ribosomal protein L23a

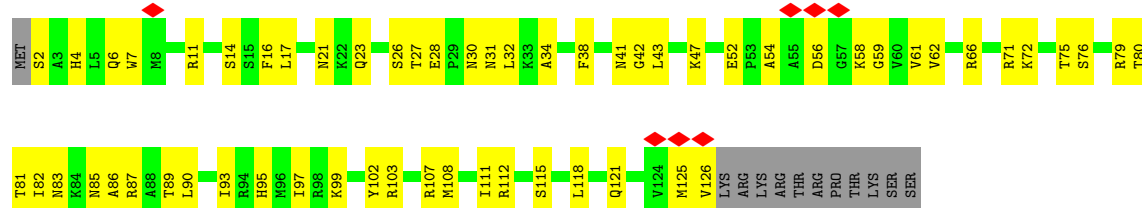




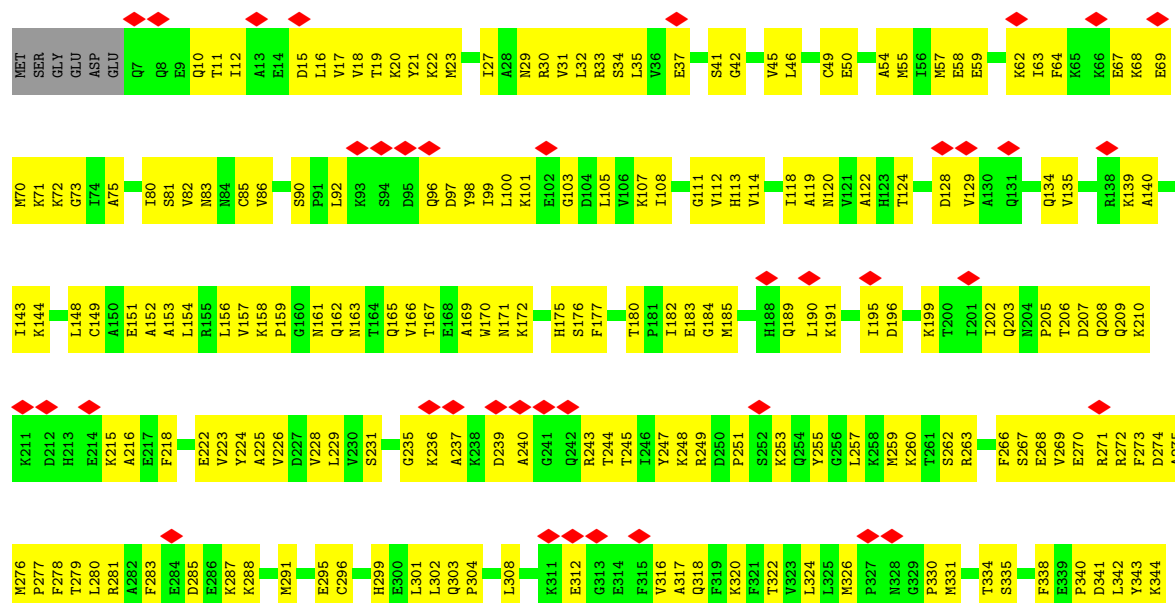
• Molecule 11: 60S ribosomal protein L19



• Molecule 12: 60S ribosomal protein L28



• Molecule 13: Proliferation-associated protein 2G4



S345	E346	M347	E348	V349	Q350	D351	A352	E353	L354	K355	A356	L357	L358	Q359	S360	S361	A362	S363	R364	K365	T366	Q367	K368	K369	K370	K371	K372	K373	A374	S375	K376	T377	A378	E379	N380	A381	T382	SER	GLY	GLU	THR	LEU	GLU	ASN	GLU	ALA	GLY	ASP
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	17235	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	51.65	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	2.693	Depositor
Minimum map value	-1.123	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.114	Depositor
Recommended contour level	0.6	Depositor
Map size (\AA)	782.72003, 782.72003, 782.72003	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.223, 1.223, 1.223	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: KGN

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	2	0.20	0/1418	0.57	0/1909
2	8	0.25	0/1384	0.35	0/2154
3	B	0.23	0/7018	0.52	0/9440
4	1	0.28	0/7175	0.44	0/11173
5	LC	0.18	0/2962	0.43	0/3977
6	LE	0.16	0/1758	0.42	0/2359
7	Lk	0.21	0/575	0.41	0/761
8	LY	0.21	0/1092	0.49	0/1454
9	Lh	0.24	0/1023	0.54	0/1351
10	LX	0.23	0/967	0.48	0/1301
11	LR	0.22	0/1297	0.50	0/1716
12	Lr	0.19	0/1017	0.41	0/1364
13	A	0.25	0/2985	0.54	1/4010 (0.0%)
All	All	0.23	0/30671	0.48	1/42969 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
13	A	367	GLN	CA-CB-CG	5.20	124.51	114.10

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	2	1388	0	1356	145	0
2	8	1237	0	625	61	0
3	B	6880	0	6921	563	0
4	1	6425	0	3260	336	0
5	LC	2908	0	3082	83	0
6	LE	1724	0	1874	62	0
7	Lk	569	0	637	29	0
8	LY	1075	0	1157	70	0
9	Lh	1015	0	1148	63	0
10	LX	950	0	1016	62	0
11	LR	1281	0	1418	70	0
12	Lr	1002	0	1068	48	0
13	A	2938	0	2974	251	0
14	B	36	0	0	4	0
All	All	29428	0	26536	1686	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 30.

The worst 5 of 1686 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)
4:1:512:U:H3	4:1:647:G:H1	1.09	0.97
3:B:771:VAL:HG11	3:B:779:GLN:HB2	1.45	0.97
11:LR:151:ARG:NH1	11:LR:151:ARG:O	1.97	0.96
3:B:93:ASP:HB2	3:B:95:LYS:HE2	1.49	0.95
10:LX:86:ALA:HB1	10:LX:97:VAL:HG21	1.48	0.95

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	2	167/171 (98%)	155 (93%)	10 (6%)	2 (1%)	10	42
3	B	832/840 (99%)	785 (94%)	43 (5%)	4 (0%)	24	63
5	LC	363/427 (85%)	344 (95%)	19 (5%)	0	100	100
6	LE	208/288 (72%)	196 (94%)	12 (6%)	0	100	100
7	Lk	67/70 (96%)	67 (100%)	0	0	100	100
8	LY	127/144 (88%)	124 (98%)	3 (2%)	0	100	100
9	Lh	120/122 (98%)	119 (99%)	1 (1%)	0	100	100
10	LX	114/156 (73%)	109 (96%)	5 (4%)	0	100	100
11	LR	151/196 (77%)	151 (100%)	0	0	100	100
12	Lr	123/137 (90%)	115 (94%)	8 (6%)	0	100	100
13	A	374/394 (95%)	349 (93%)	25 (7%)	0	100	100
All	All	2646/2945 (90%)	2514 (95%)	126 (5%)	6 (0%)	44	77

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	B	292	VAL
3	B	726	SER
1	2	8	PRO
3	B	778	SER
1	2	141	GLY

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	2	148/149 (99%)	148 (100%)	0	100	100
3	B	743/749 (99%)	743 (100%)	0	100	100
5	LC	304/348 (87%)	304 (100%)	0	100	100
6	LE	190/252 (75%)	190 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	Lk	64/65 (98%)	64 (100%)	0	100	100
8	LY	120/134 (90%)	120 (100%)	0	100	100
9	Lh	109/109 (100%)	109 (100%)	0	100	100
10	LX	104/133 (78%)	104 (100%)	0	100	100
11	LR	137/175 (78%)	137 (100%)	0	100	100
12	Lr	109/121 (90%)	109 (100%)	0	100	100
13	A	322/336 (96%)	322 (100%)	0	100	100
All	All	2350/2571 (91%)	2350 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
5	LC	223	ASN
12	Lr	6	GLN
5	LC	245	HIS
8	LY	14	ASN
12	Lr	83	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	8	57/157 (36%)	12 (21%)	0
4	1	291/5070 (5%)	82 (28%)	4 (1%)
All	All	348/5227 (6%)	94 (27%)	4 (1%)

5 of 94 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	8	52	A
2	8	59	A
2	8	62	A
2	8	63	U
2	8	80	A

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	1	412	G
4	1	685	C
4	1	2711	G
4	1	2713	C

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](#)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
14	KGN	B	901	-	36,36,36	1.47	6 (16%)	60,60,60	1.16	4 (6%)

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
14	KGN	B	901	-	-	5/30/54/54	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	B	901	KGN	P2-O12	3.63	1.65	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	B	901	KGN	P3-O13	3.26	1.65	1.59
14	B	901	KGN	P6-O16	3.17	1.65	1.59
14	B	901	KGN	P5-O15	2.61	1.64	1.59
14	B	901	KGN	P1-O11	2.58	1.64	1.59

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	B	901	KGN	O13-C3-C4	4.51	118.36	108.76
14	B	901	KGN	C5-C4-C3	3.28	117.63	110.43
14	B	901	KGN	C4-C3-C2	2.53	115.99	110.43
14	B	901	KGN	O22-P2-O12	2.14	114.18	105.85

There are no chirality outliers.

All (5) torsion outliers are listed below:

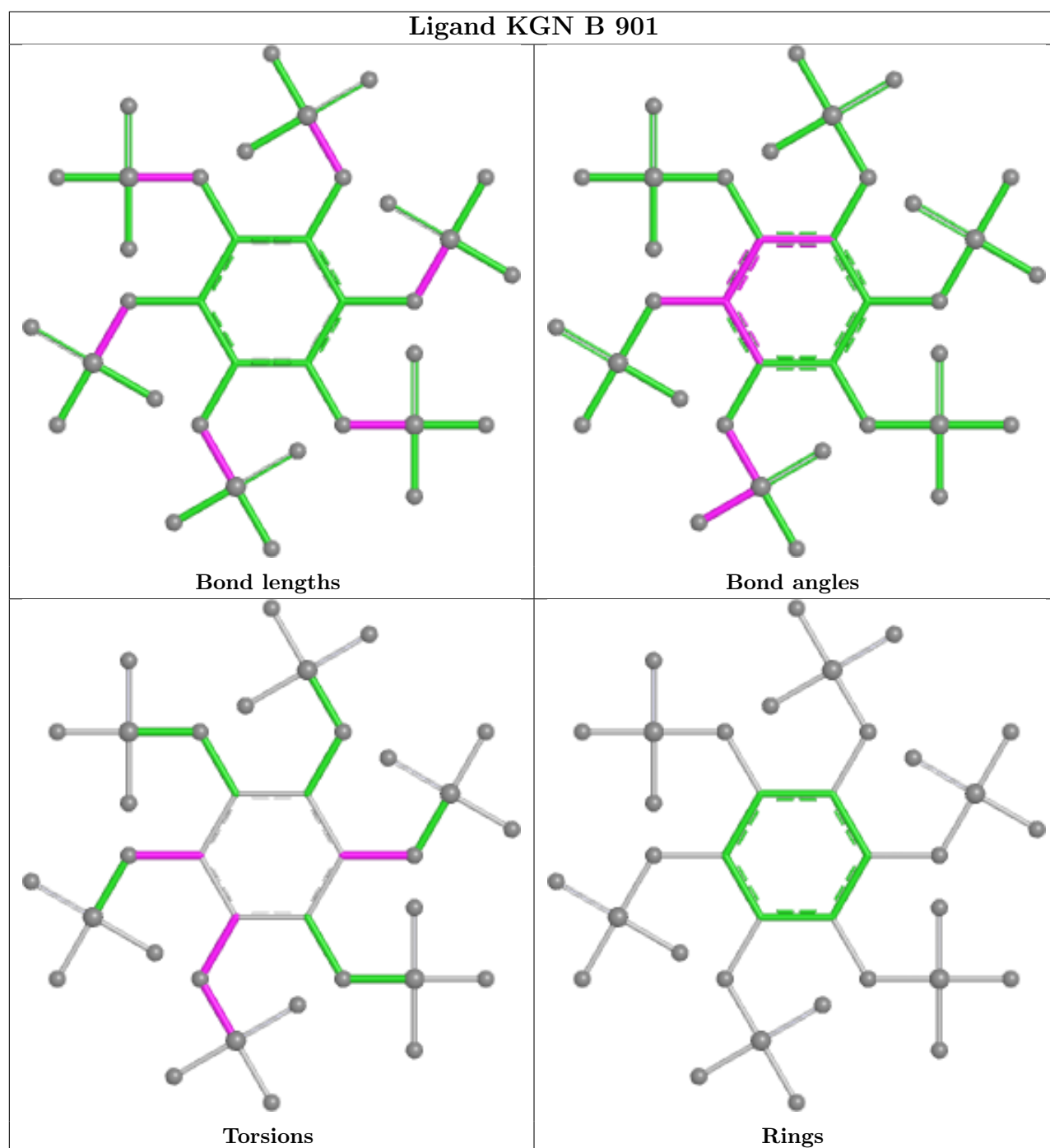
Mol	Chain	Res	Type	Atoms
14	B	901	KGN	C1-C2-O12-P2
14	B	901	KGN	C3-C2-O12-P2
14	B	901	KGN	C4-C3-O13-P3
14	B	901	KGN	C1-C6-O16-P6
14	B	901	KGN	C2-O12-P2-O32

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
14	B	901	KGN	4	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.

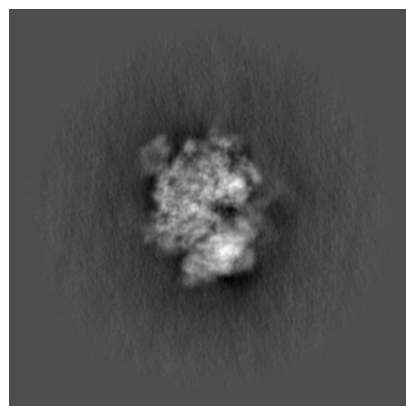
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51382. These allow visual inspection of the internal detail of the map and identification of artifacts.

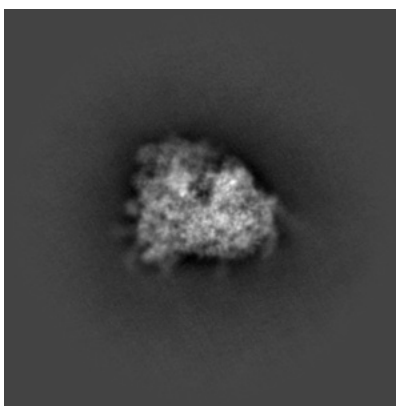
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

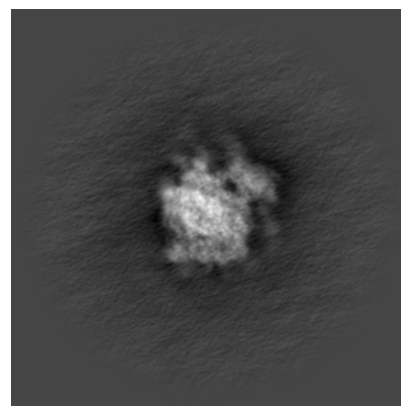
6.1.1 Primary map



X

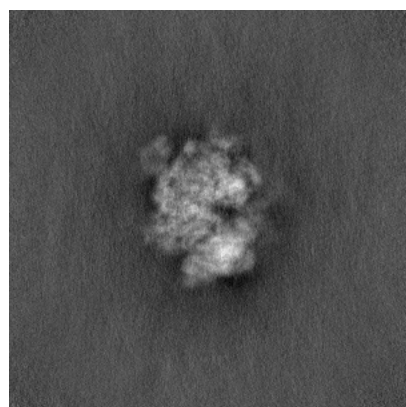


Y

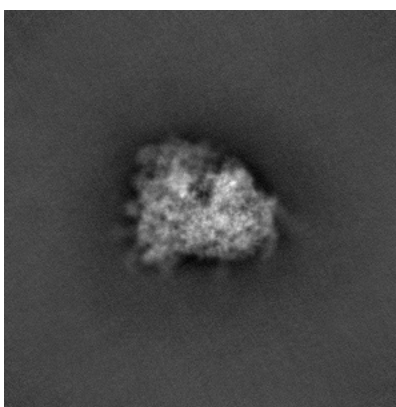


Z

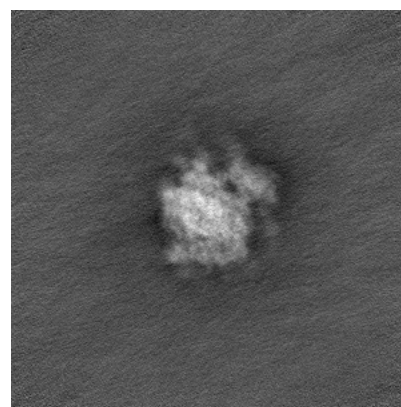
6.1.2 Raw map



X



Y

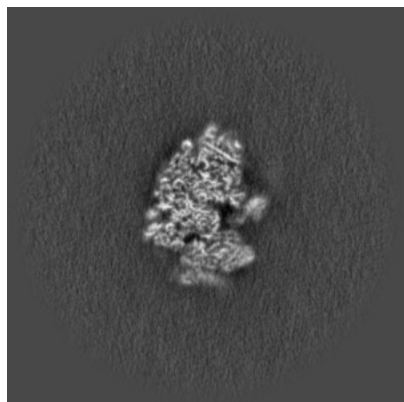


Z

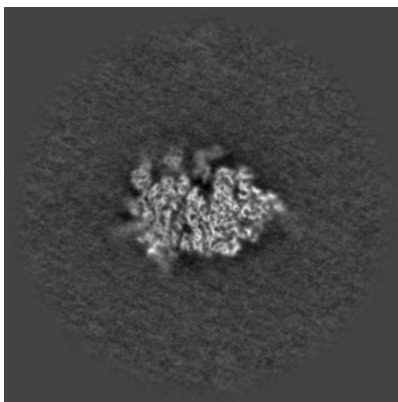
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

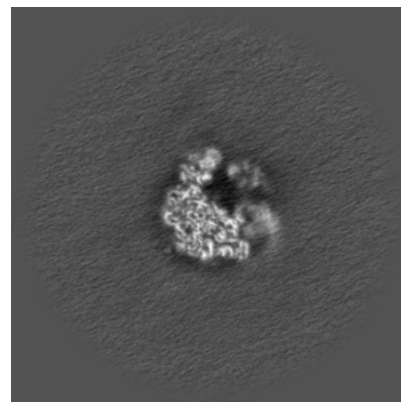
6.2.1 Primary map



X Index: 320

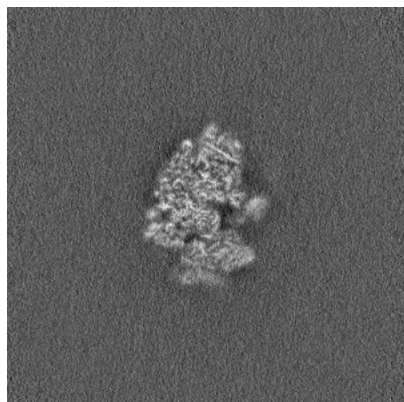


Y Index: 320

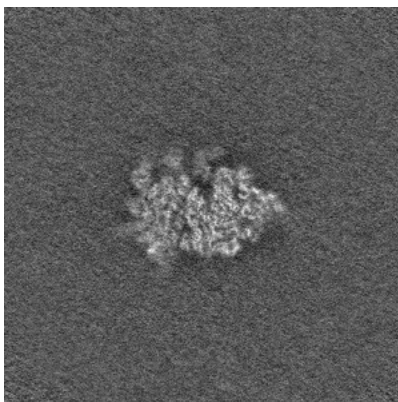


Z Index: 320

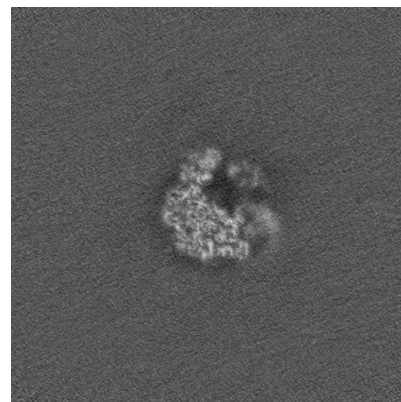
6.2.2 Raw map



X Index: 320



Y Index: 320

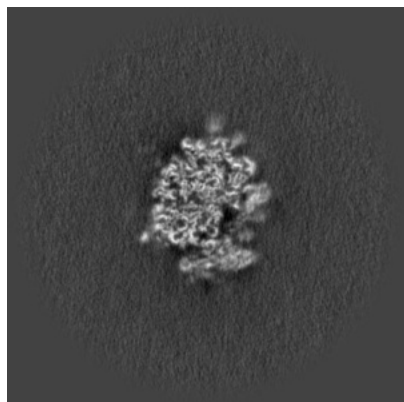


Z Index: 320

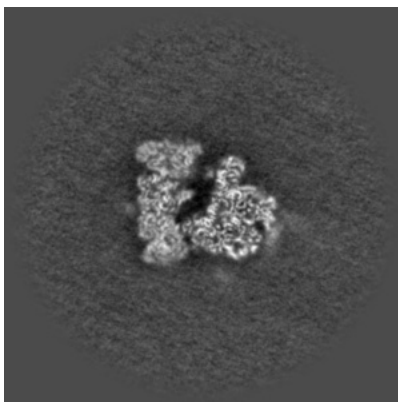
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

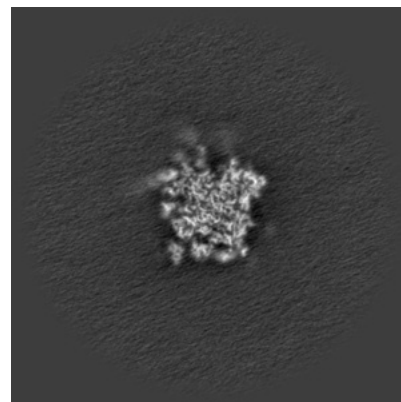
6.3.1 Primary map



X Index: 307

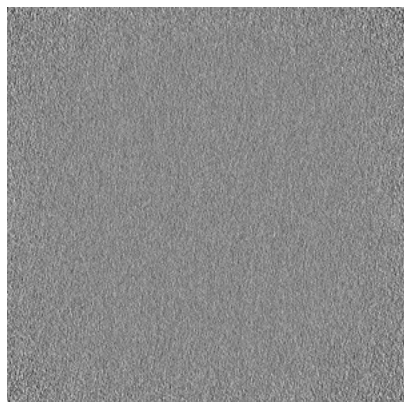


Y Index: 345

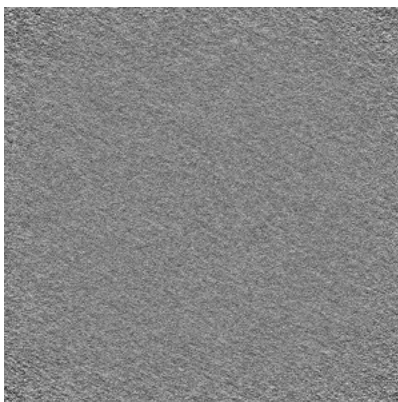


Z Index: 356

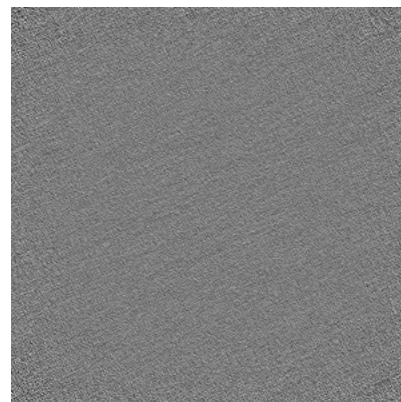
6.3.2 Raw map



X Index: 0



Y Index: 0

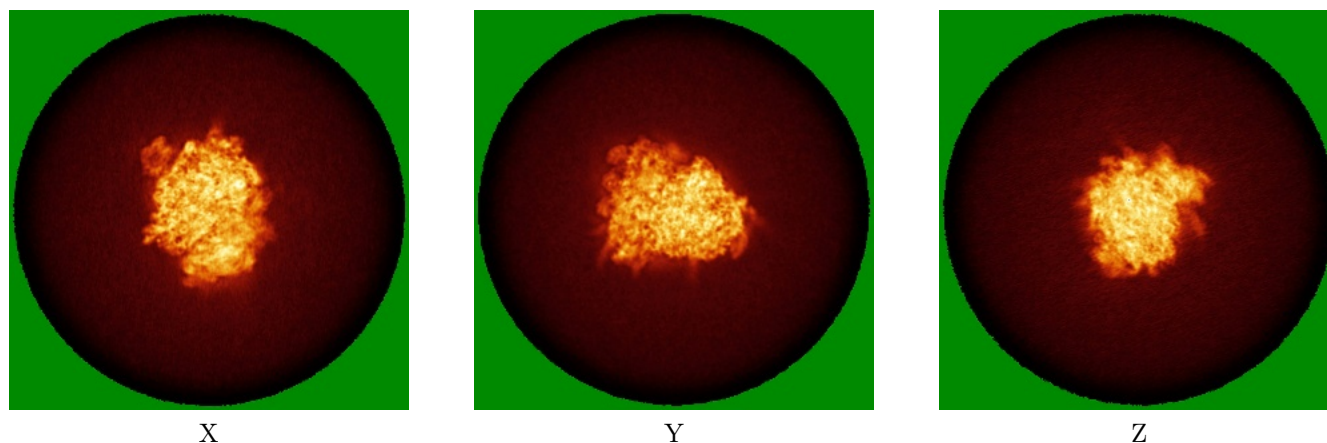


Z Index: 639

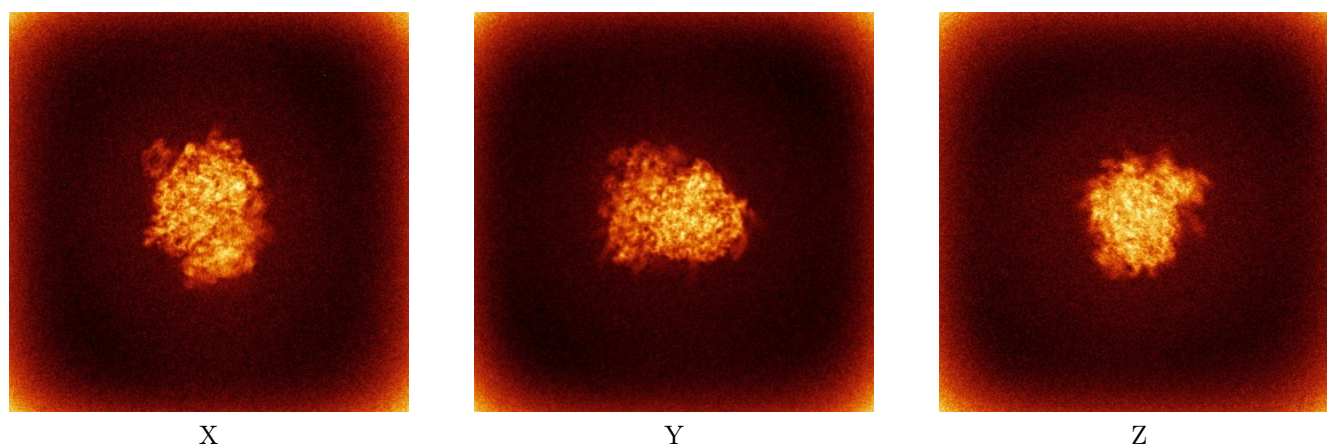
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

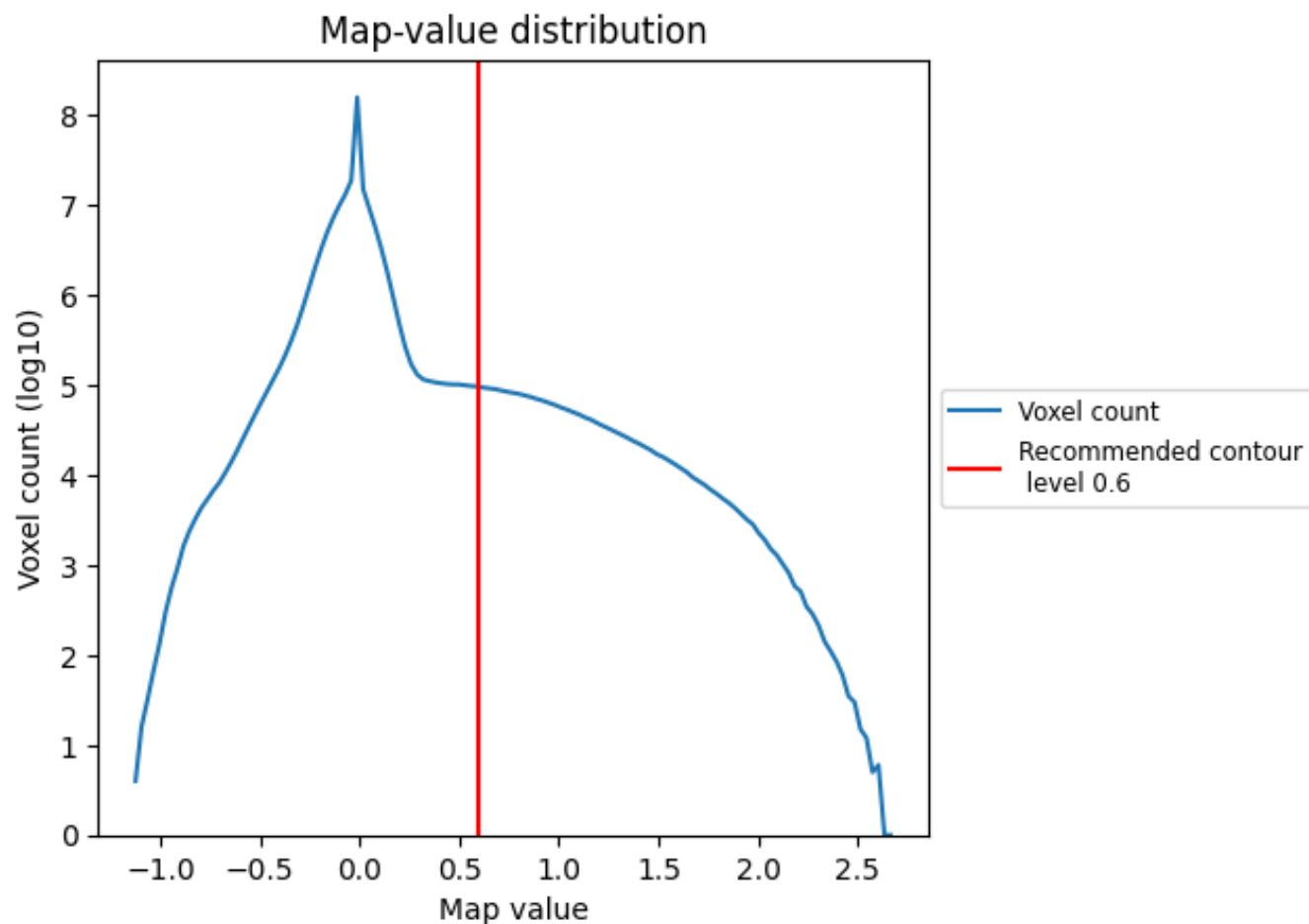
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

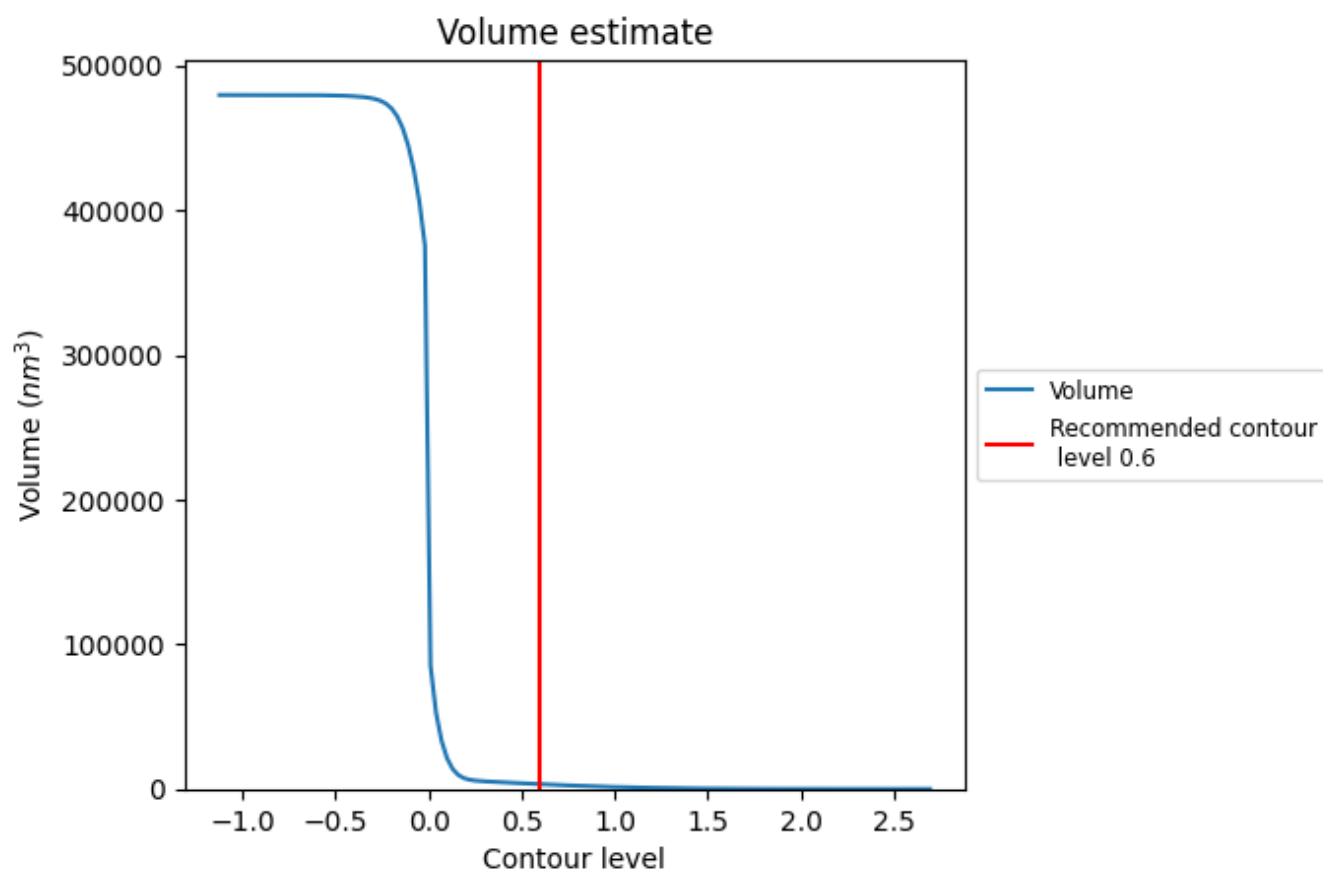
This section contains the results of statistical analysis of the map.

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.

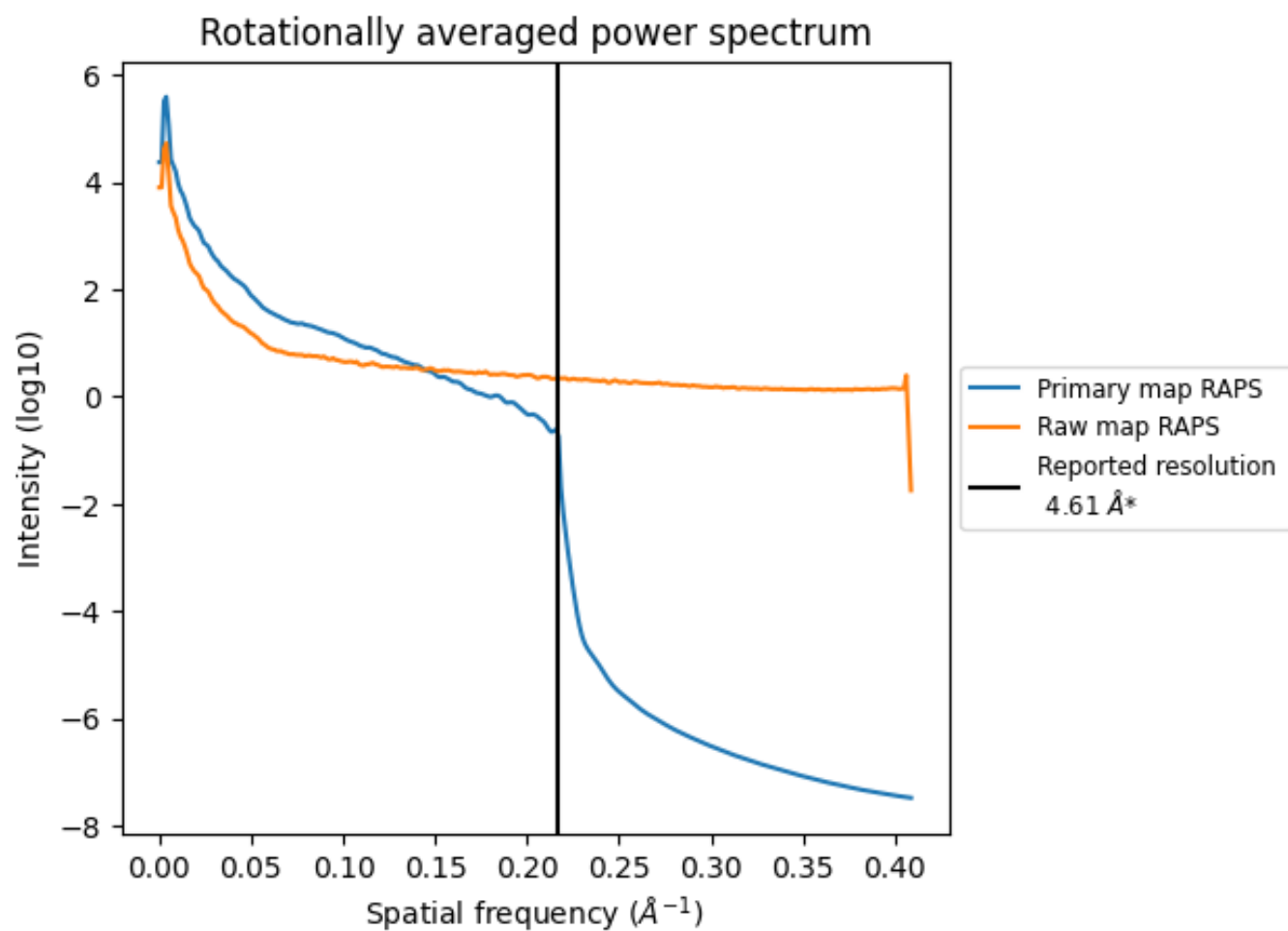
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3326 nm³; this corresponds to an approximate mass of 3005 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 ⓘ

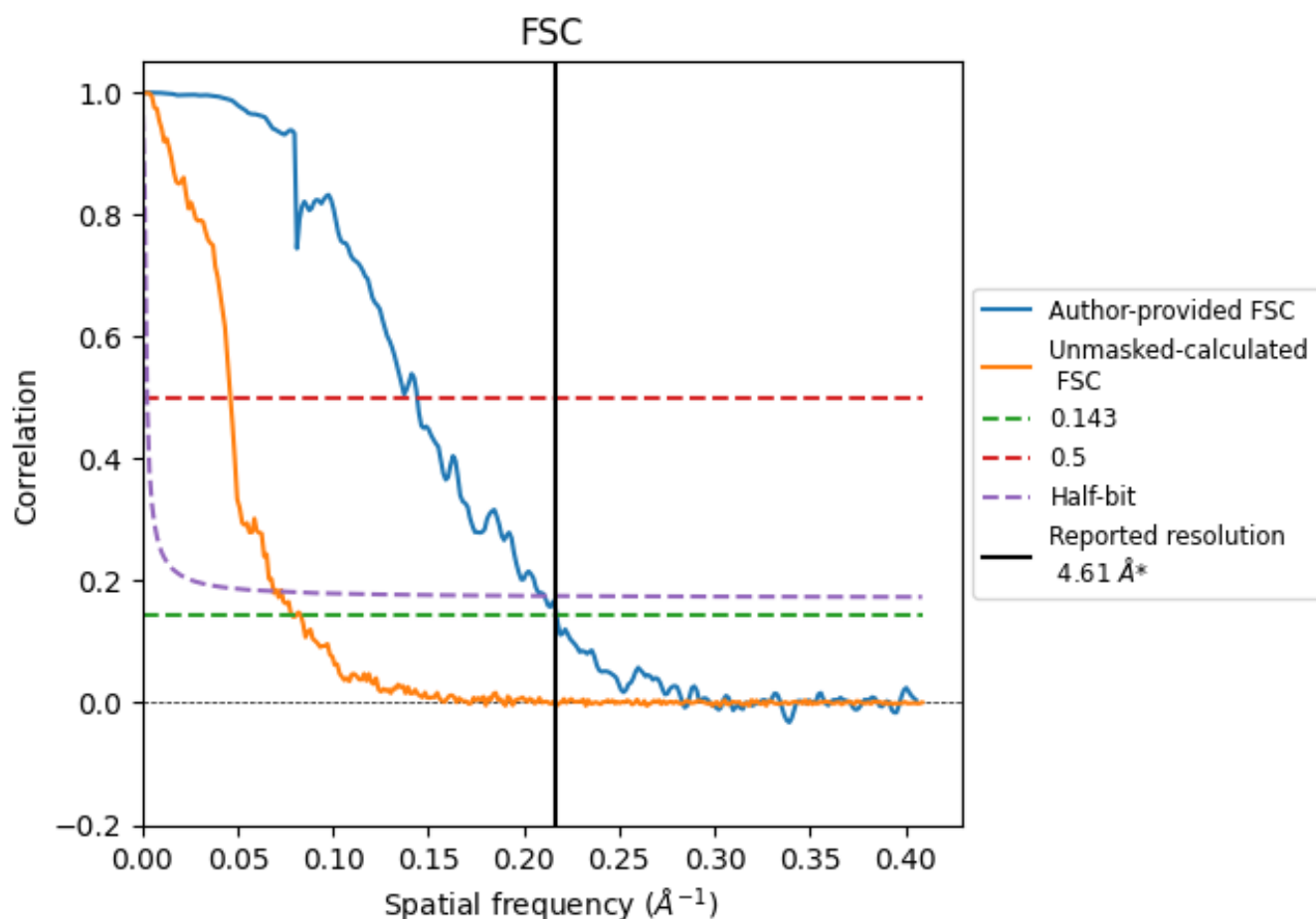


*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

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 0.217 \AA^{-1}

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.61	-	-
Author-provided FSC curve	4.60	6.94	4.75
Unmasked-calculated*	12.69	21.60	14.53

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 12.69 differs from the reported value 4.61 by more than 10 %

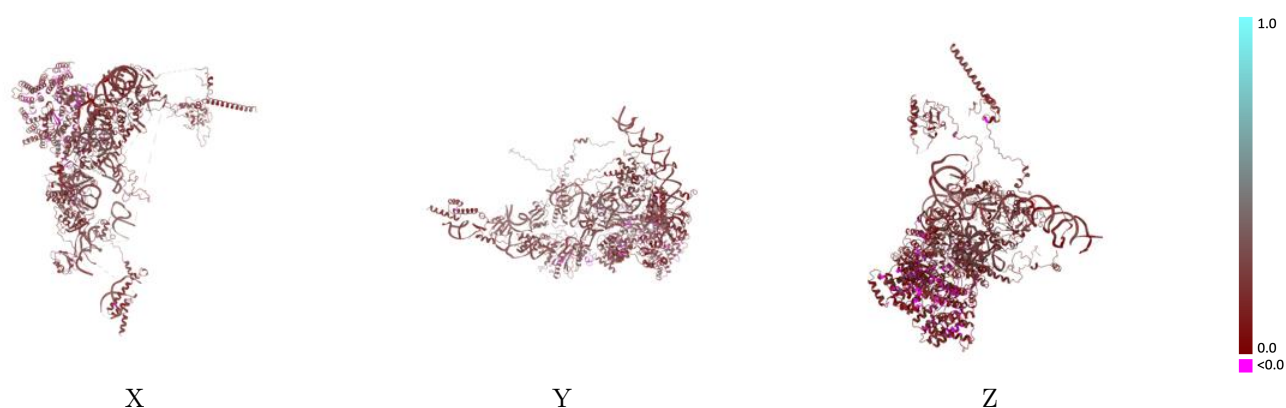
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-51382 and PDB model 9GJ5. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)

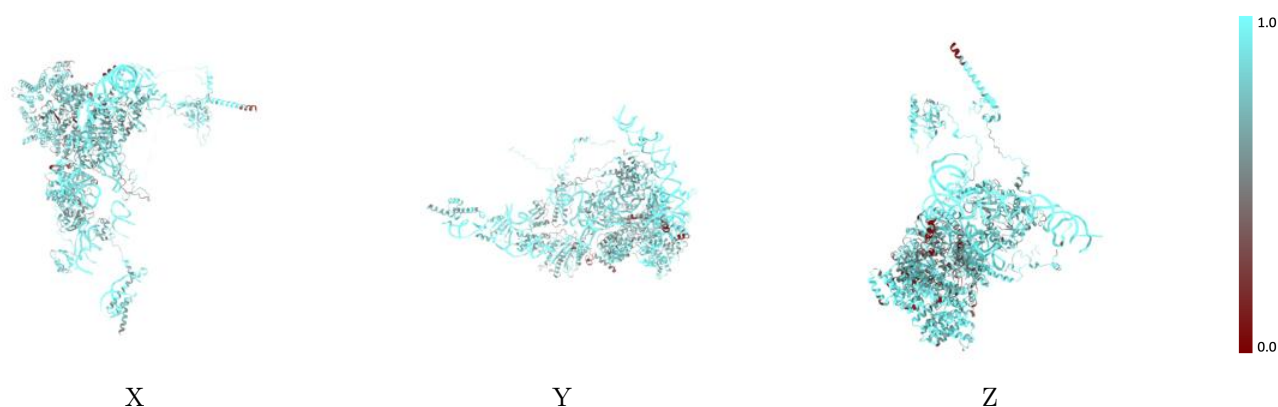
This section was not generated.

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



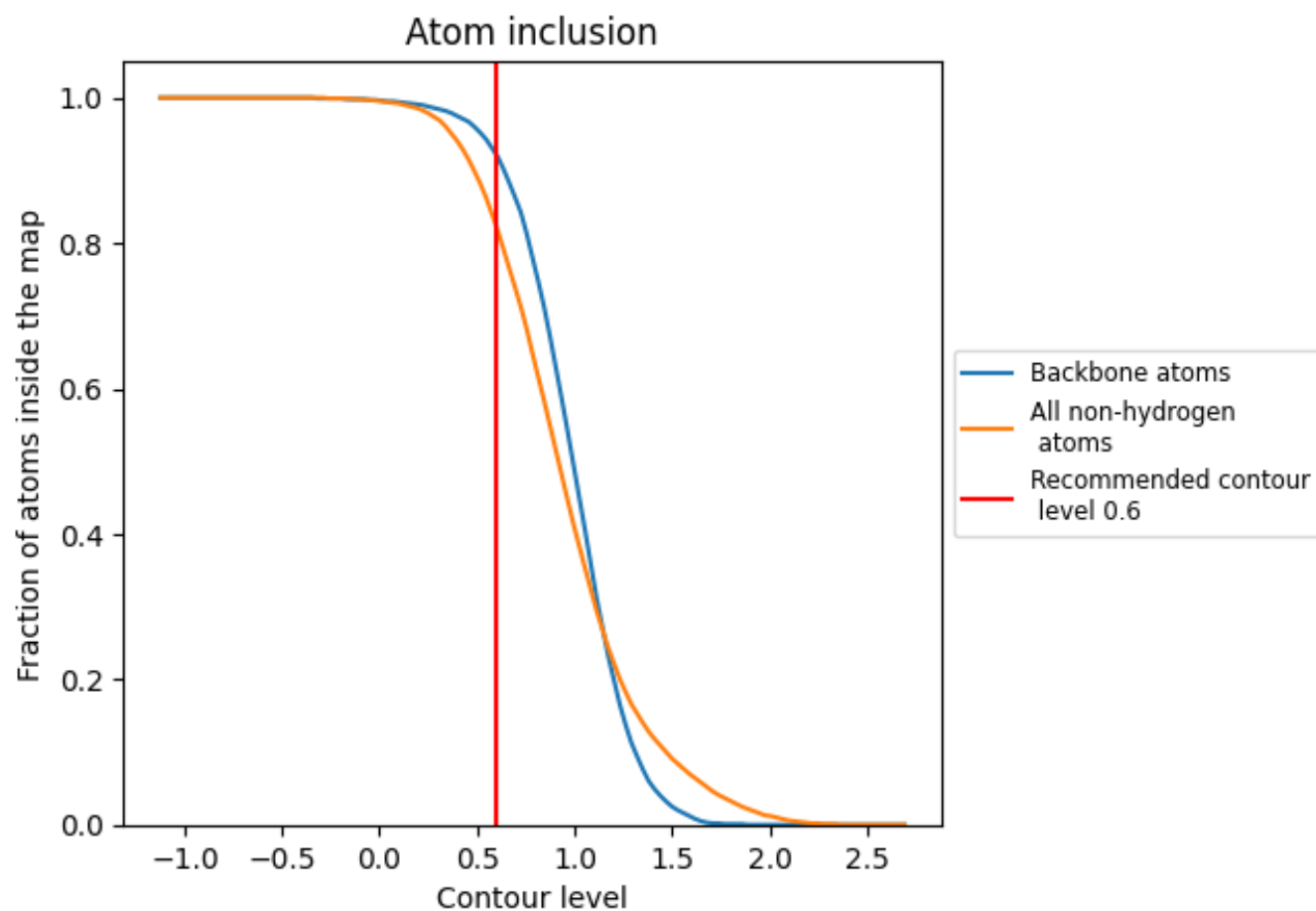
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.6).





























9.4 Atom inclusion [i](#)



At the recommended contour level, 92% 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 (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8230	 0.2000
1	 0.9730	 0.2410
2	 0.7440	 0.1520
8	 0.9530	 0.2720
A	 0.7100	 0.1650
B	 0.7740	 0.1410
LC	 0.7140	 0.2290
LE	 0.8810	 0.2220
LR	 0.7840	 0.2100
LX	 0.7500	 0.2260
LY	 0.7570	 0.2130
Lh	 0.8410	 0.2130
Lk	 0.8460	 0.2040
Lr	 0.8190	 0.2470

