



## wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 07:12 PM UTC

PDB ID : 9GJ6 / pdb\_00009gj6  
EMDB ID : EMD-51383  
Title : Human 80S ribosome in complex with NatA in proximal and distal position  
Authors : Klein, M.A.; Wild, K.; Sinning, I.  
Deposited on : 2024-08-21  
Resolution : 3.91 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

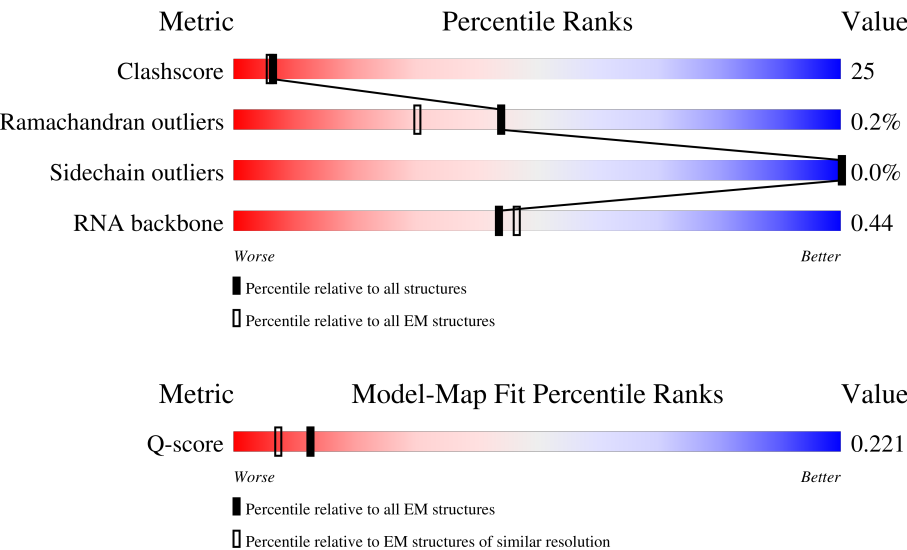
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (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 3.91 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	7920 ( 3.41 - 4.41 )

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  $\geq 3$ , 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	235	<div><div>77%</div><div><div></div><div>39%</div><div>39%</div><div>22%</div></div></div>
1	C	235	<div><div>75%</div><div><div></div><div>33%</div><div>43%</div><div>25%</div></div></div>
2	B	840	<div><div>96%</div><div><div></div><div>49%</div><div>50%</div></div></div>

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Mol	Chain	Length	Quality of chain
2	D	840	
3	1	5070	
4	8	157	
5	LC	427	
6	LE	288	
7	Lk	70	
8	LY	145	
9	Lh	122	
10	LX	156	
11	LR	196	
12	Lr	137	
13	LU	127	
14	Ld	125	
15	LP	184	

## 2 Entry composition [i](#)

There are 16 unique types of molecules in this entry. The entry contains 43288 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	A	184	Total	C	N	O	S	0	0
			1496	936	272	278	10		
1	C	177	Total	C	N	O	S	0	0
			1444	905	262	267	10		

- Molecule 2 is a protein called N-alpha-acetyltransferase 15, NatA auxiliary subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	833	Total	C	N	O	S	0	0
			6874	4374	1188	1271	41		
2	B	839	Total	C	N	O	S	0	0
			6914	4401	1194	1278	41		

There are 2 discrepancies between the modelled and reference sequences:

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

- Molecule 3 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1	552	Total	C	N	O	P	0	0
			11798	5251	2127	3868	552		

- Molecule 4 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	8	58	Total	C	N	O	P	0	0
			1237	554	224	401	58		

- 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		

- 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 Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LU	98	Total	C	N	O	S	0	0
			799	513	139	145	2		

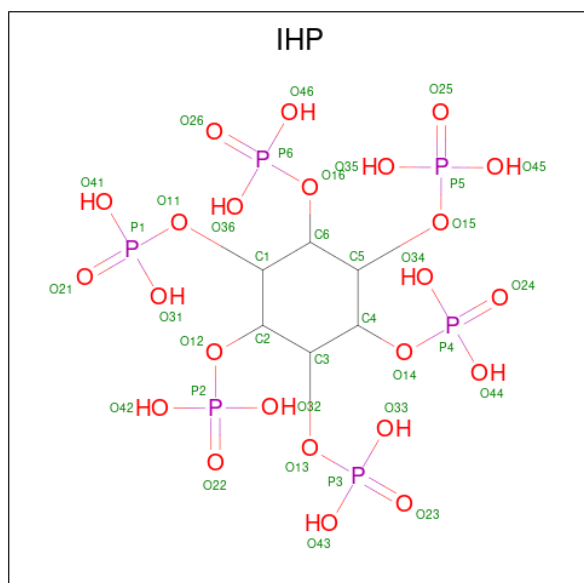
- Molecule 14 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Ld	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 15 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 16 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula:  $C_6H_{18}O_{24}P_6$ ).



Mol	Chain	Residues	Atoms				AltConf
16	D	1	Total	C	O	P	0
			36	6	24	6	

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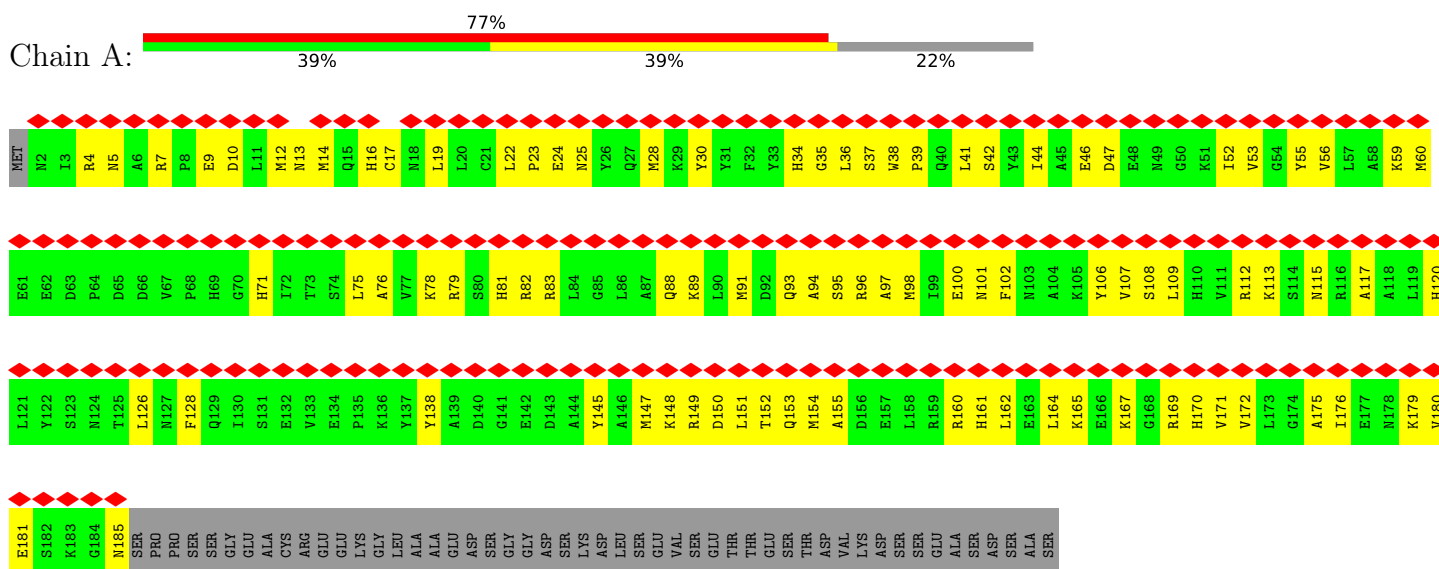
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Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
16	B	1	36	6	24	6	0

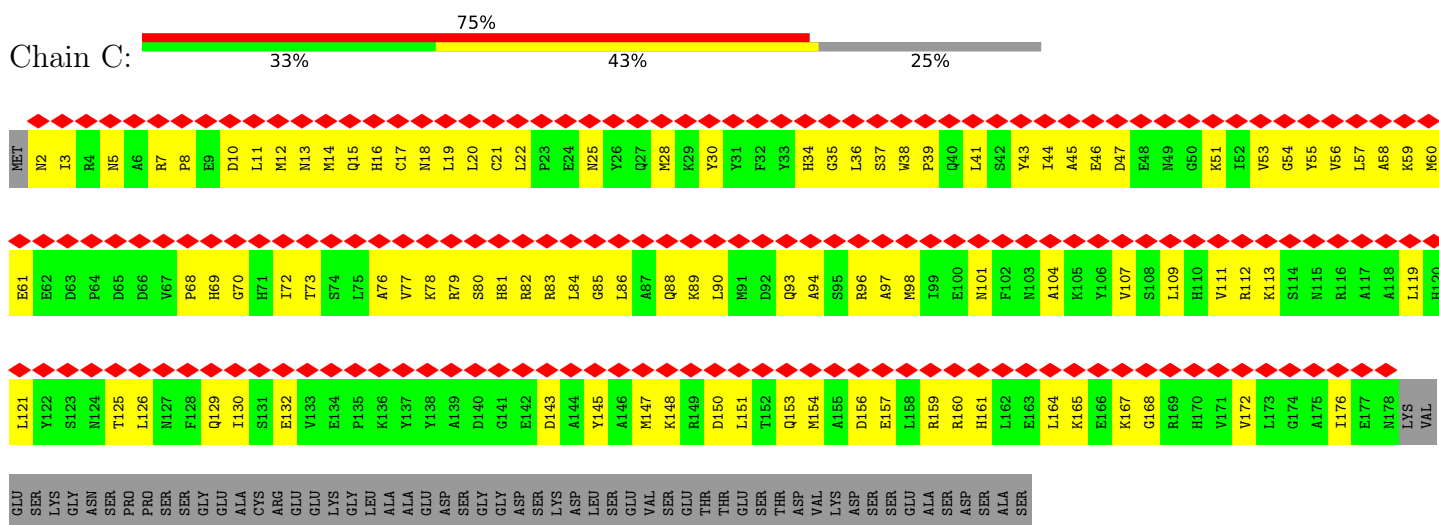
### 3 Residue-property plots

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: N-alpha-acetyltransferase 10



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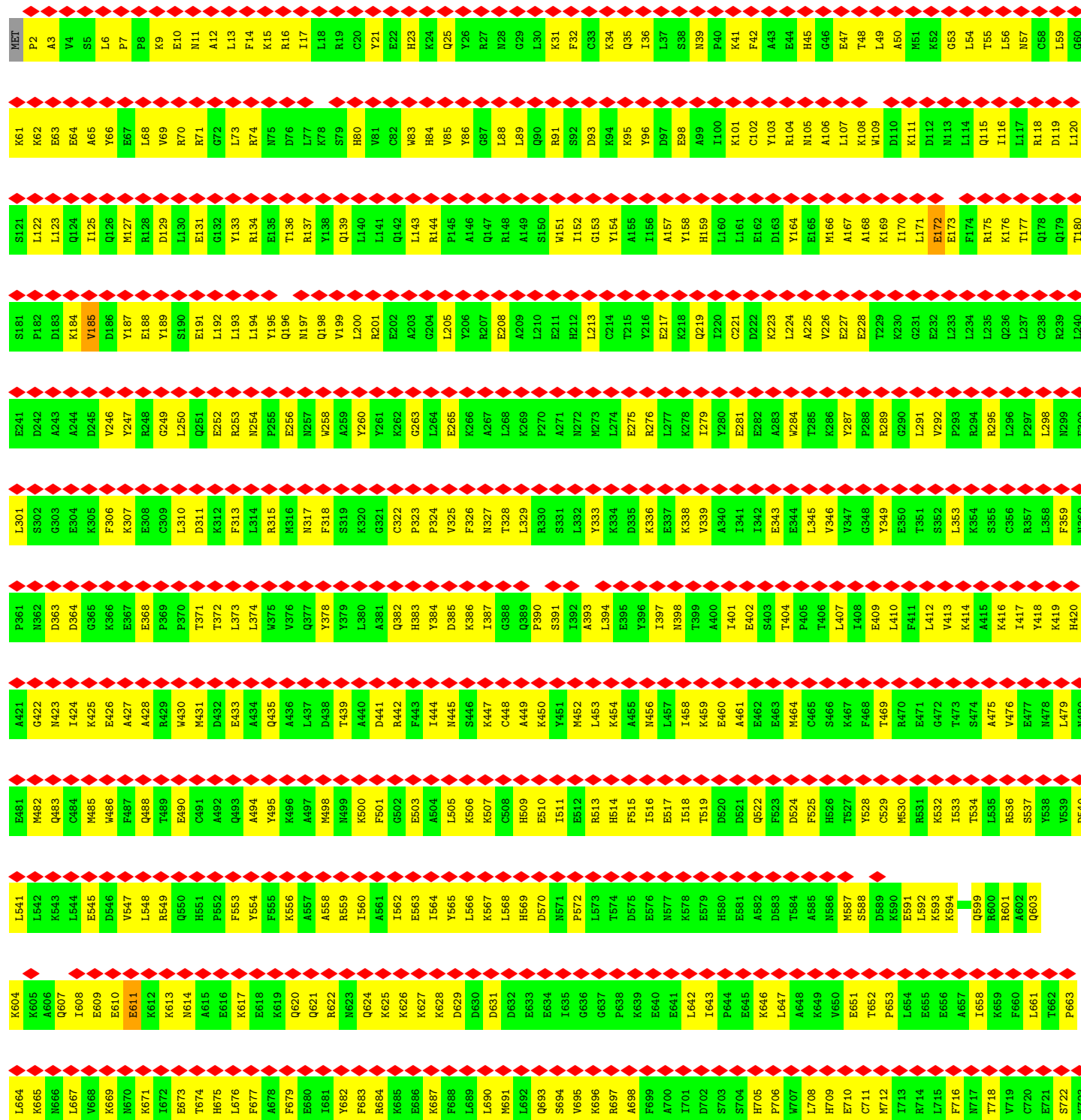
#### • Molecule 2: N-alpha-acetyltransferase 15, NatA auxiliary subunit

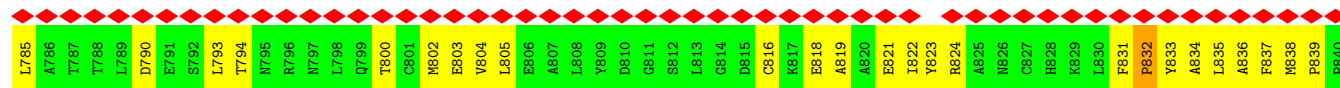






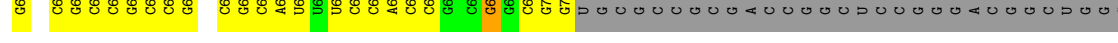
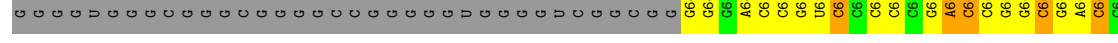
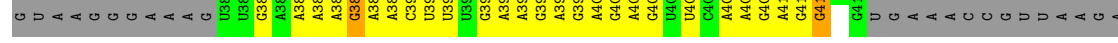
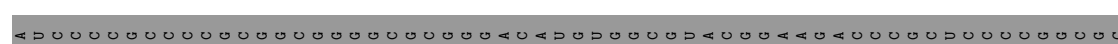
• Molecule 2: N-alpha-acetyltransferase 15, NatA auxiliary subunit





### • Molecule 3: 28S rRNA

Chain 1: 6% 89%









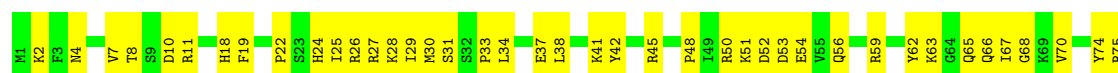


Chain Lk: 



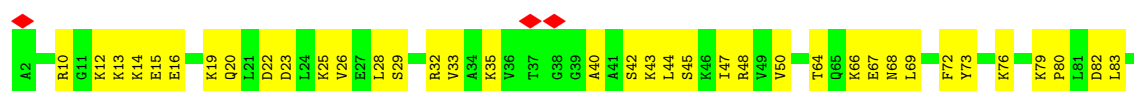
- Molecule 8: Large ribosomal subunit protein uL24

Chain LY: 



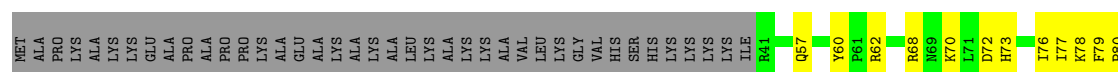
- Molecule 9: 60S ribosomal protein L35

Chain Lh: 



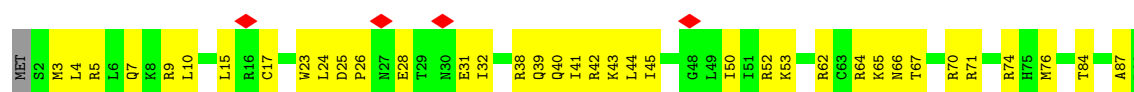
- Molecule 10: 60S ribosomal protein L23a

Chain LX: 



- Molecule 11: 60S ribosomal protein L19

Chain LR: 







## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	17765	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 ( $e^-/\text{\AA}^2$ )	27.51	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	2.758	Depositor
Minimum map value	-1.148	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.115	Depositor
Recommended contour level	0.6	Depositor
Map size ( $\text{\AA}$ )	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 ( $\text{\AA}$ )	1.223, 1.223, 1.223	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: IHP

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	0.20	0/1526	0.50	0/2054
1	C	0.19	0/1474	0.51	0/1986
2	B	0.20	0/7053	0.52	2/9489 (0.0%)
2	D	0.23	0/7011	0.55	1/9429 (0.0%)
3	1	0.23	0/13174	0.43	0/20523
4	8	0.21	0/1384	0.33	0/2154
5	LC	0.20	0/2962	0.47	0/3977
6	LE	0.17	0/1758	0.45	0/2359
7	Lk	0.20	0/575	0.50	0/761
8	LY	0.23	0/1092	0.54	0/1454
9	Lh	0.22	0/1023	0.56	0/1351
10	LX	0.23	0/967	0.57	0/1301
11	LR	0.24	0/1297	0.64	0/1716
12	Lr	0.24	0/1017	0.61	0/1364
13	LU	0.26	0/813	0.66	1/1091 (0.1%)
14	Ld	0.26	0/903	0.66	0/1216
15	LP	0.24	0/1268	0.65	0/1701
All	All	0.22	0/45297	0.50	4/63926 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	LU	34	MET	CB-CG-SD	8.18	137.23	112.70
2	B	172	GLU	N-CA-CB	6.76	120.06	110.12
2	D	691	MET	CA-CB-CG	5.33	124.77	114.10
2	B	611	GLU	N-CA-CB	5.29	117.90	110.12

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	1496	0	1471	103	0
1	C	1444	0	1416	102	0
2	B	6914	0	6961	401	0
2	D	6874	0	6917	395	0
3	1	11798	0	5988	456	0
4	8	1237	0	625	47	0
5	LC	2908	0	3082	101	0
6	LE	1724	0	1874	71	0
7	Lk	569	0	637	28	0
8	LY	1075	0	1157	77	0
9	Lh	1015	0	1148	52	0
10	LX	950	0	1016	51	0
11	LR	1281	0	1418	76	0
12	Lr	1002	0	1068	45	0
13	LU	799	0	823	57	0
14	Ld	888	0	930	72	0
15	LP	1242	0	1269	77	0
16	B	36	0	6	1	0
16	D	36	0	6	1	0
All	All	43288	0	37812	2023	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 25.

The worst 5 of 2023 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)
13:LU:100:LEU:HD12	13:LU:112:LEU:HB3	1.39	1.04
2:D:691:MET:HB3	2:D:715:LEU:HD12	1.40	1.00
3:1:2701:U:H3	3:1:2715:G:H1	1.06	0.95
14:Ld:67:ARG:NH2	14:Ld:107:THR:HA	1.82	0.94
3:1:4740:G:H1	3:1:4959:U:H3	0.95	0.93

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	182/235 (77%)	177 (97%)	5 (3%)	0	100	100
1	C	175/235 (74%)	171 (98%)	4 (2%)	0	100	100
2	B	837/840 (100%)	806 (96%)	28 (3%)	3 (0%)	30	65
2	D	831/840 (99%)	790 (95%)	37 (4%)	4 (0%)	24	59
5	LC	363/427 (85%)	346 (95%)	17 (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	127/145 (88%)	126 (99%)	1 (1%)	0	100	100
9	Lh	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
10	LX	114/156 (73%)	112 (98%)	2 (2%)	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	LU	96/127 (76%)	91 (95%)	5 (5%)	0	100	100
14	Ld	105/125 (84%)	97 (92%)	8 (8%)	0	100	100
15	LP	151/184 (82%)	144 (95%)	7 (5%)	0	100	100
All	All	3650/4127 (88%)	3506 (96%)	137 (4%)	7 (0%)	44	75

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	363	ASP
2	B	62	LYS
2	D	360	ASN
2	B	832	PRO
2	D	405	PRO

### 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	160/202 (79%)	160 (100%)	0	100	100
1	C	154/202 (76%)	154 (100%)	0	100	100
2	B	748/749 (100%)	748 (100%)	0	100	100
2	D	743/749 (99%)	742 (100%)	1 (0%)	88	89
5	LC	304/348 (87%)	304 (100%)	0	100	100
6	LE	190/252 (75%)	190 (100%)	0	100	100
7	Lk	64/65 (98%)	64 (100%)	0	100	100
8	LY	120/135 (89%)	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	LU	88/114 (77%)	88 (100%)	0	100	100
14	Ld	98/110 (89%)	98 (100%)	0	100	100
15	LP	134/163 (82%)	134 (100%)	0	100	100
All	All	3262/3627 (90%)	3261 (100%)	1 (0%)	100	100

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

Mol	Chain	Res	Type
2	D	715	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	569	HIS
1	C	16	HIS
2	B	603	GLN

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Mol	Chain	Res	Type
2	B	693	GLN
1	C	81	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	1	541/5070 (10%)	157 (29%)	4 (0%)
4	8	57/157 (36%)	9 (15%)	2 (3%)
All	All	598/5227 (11%)	166 (27%)	6 (1%)

5 of 166 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	1	200	U
3	1	210	C
3	1	216	C
3	1	218	A
3	1	233	U

5 of 6 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	1	4949	G
4	8	84	A
4	8	85	U
3	1	4870	G
3	1	4740	G

## 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](#)

2 ligands are 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	$\# Z  > 2$
16	IHP	D	900	-	36,36,36	1.50	6 (16%)	60,60,60	0.79	0
16	IHP	B	901	-	36,36,36	1.60	6 (16%)	60,60,60	0.74	0

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
16	IHP	D	900	-	-	3/30/54/54	0/1/1/1
16	IHP	B	901	-	-	7/30/54/54	0/1/1/1

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	B	901	IHP	P3-O13	3.72	1.66	1.59
16	B	901	IHP	P5-O15	3.47	1.65	1.59
16	B	901	IHP	P6-O16	3.43	1.65	1.59
16	B	901	IHP	P4-O14	3.38	1.65	1.59
16	B	901	IHP	P1-O11	3.34	1.65	1.59

There are no bond angle outliers.

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
16	B	901	IHP	C4-C3-O13-P3
16	B	901	IHP	C2-C3-O13-P3
16	B	901	IHP	C1-O11-P1-O21
16	D	900	IHP	C1-O11-P1-O41
16	D	900	IHP	C1-C2-O12-P2

There are no ring outliers.

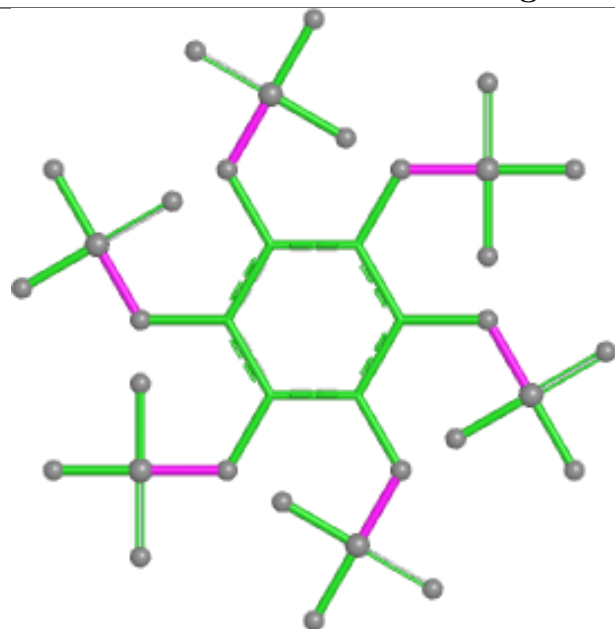


2 monomers are involved in 2 short contacts:

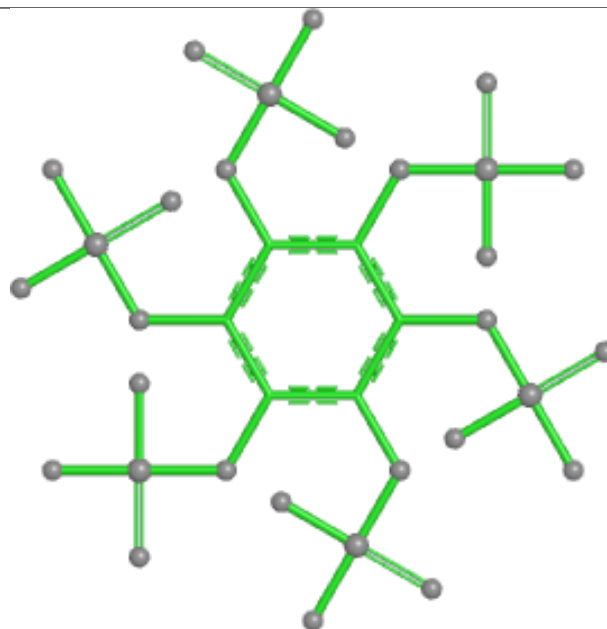
Mol	Chain	Res	Type	Clashes	Symm-Clashes
16	D	900	IHP	1	0
16	B	901	IHP	1	0

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.

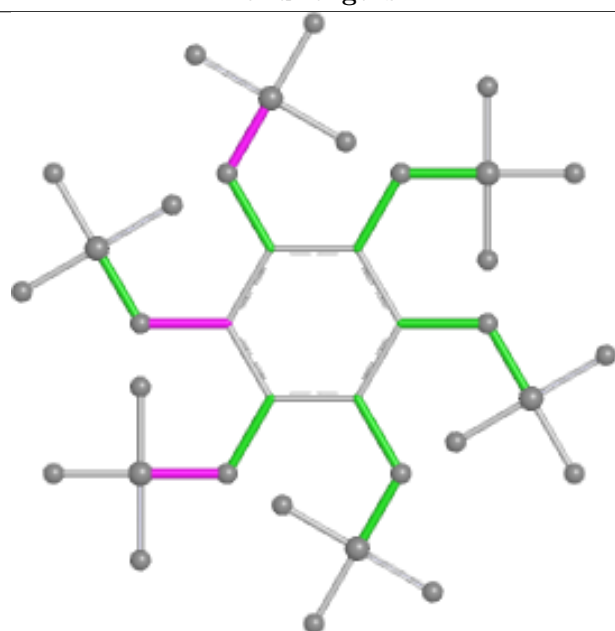
## Ligand IHP D 900



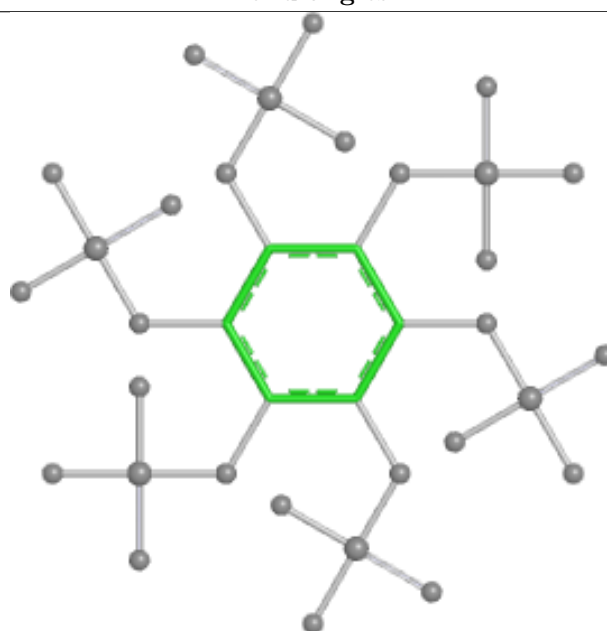
Bond lengths



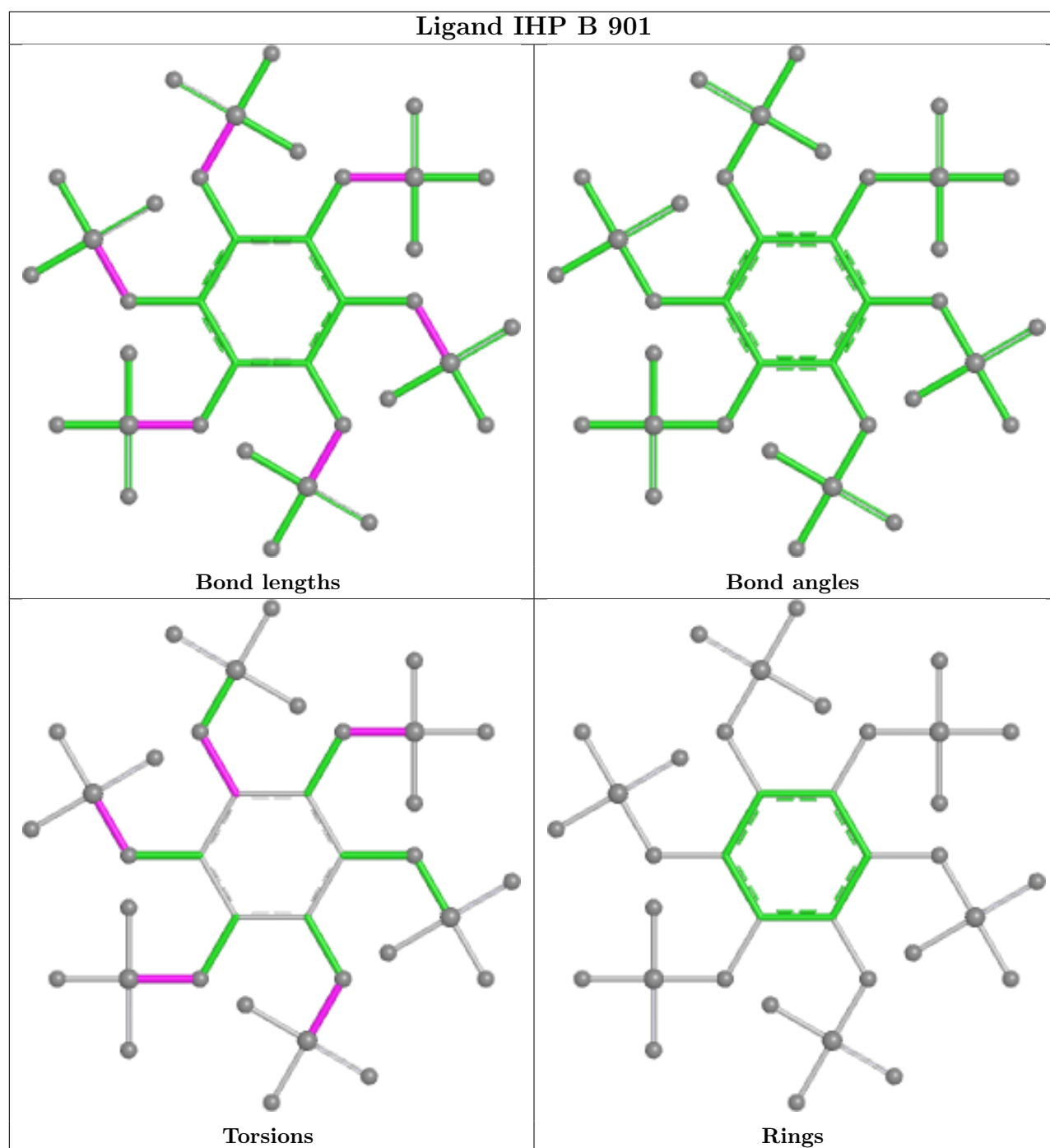
Bond angles



Torsions



Rings



## 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.

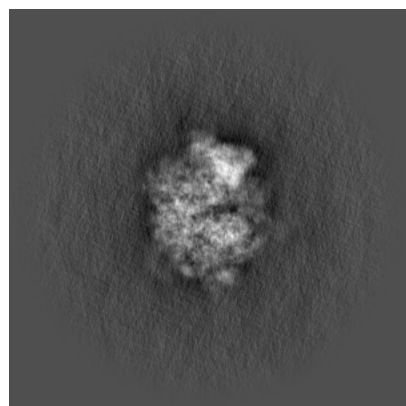
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51383. These allow visual inspection of the internal detail of the map and identification of artifacts.

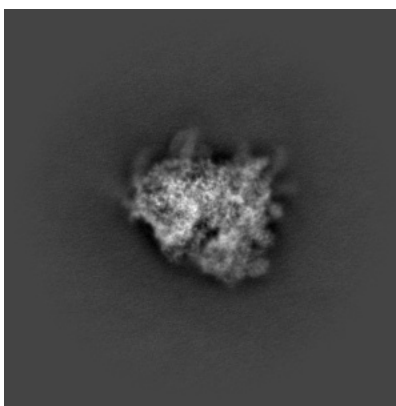
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

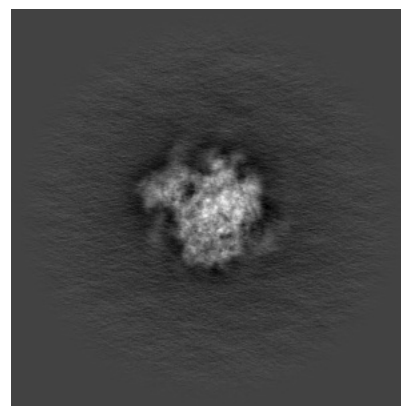
#### 6.1.1 Primary map



X

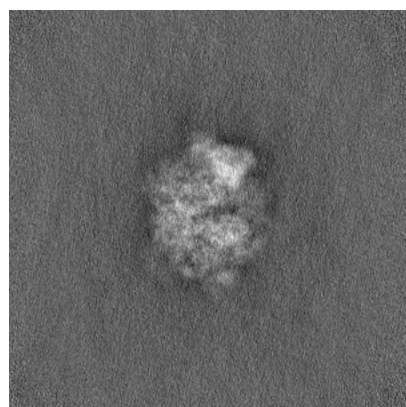


Y

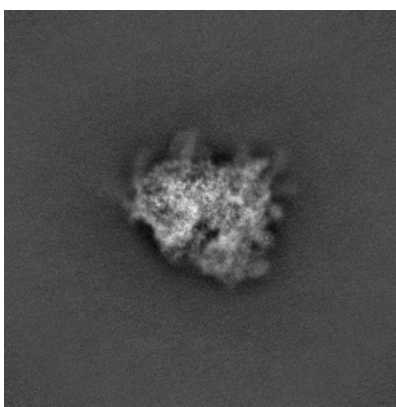


Z

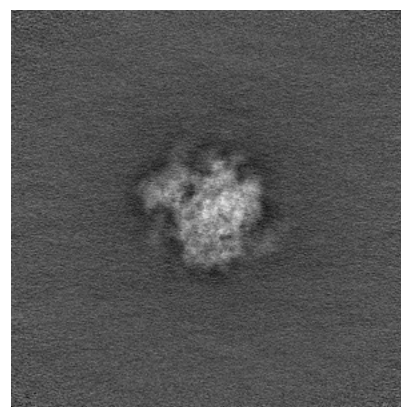
#### 6.1.2 Raw map



X



Y

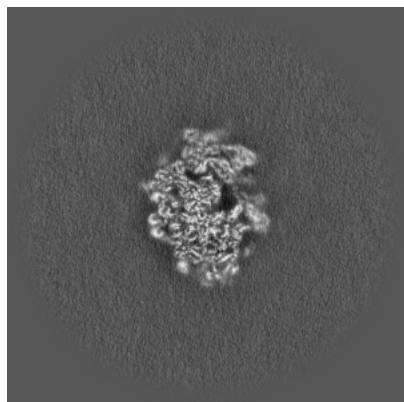


Z

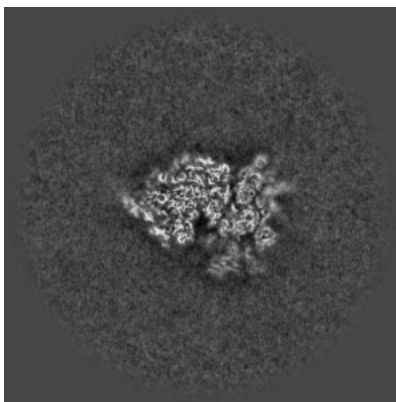
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

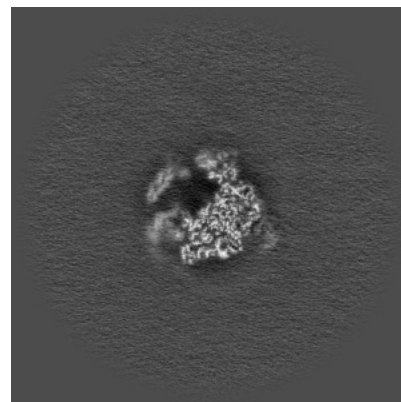
### 6.2.1 Primary map



X Index: 320

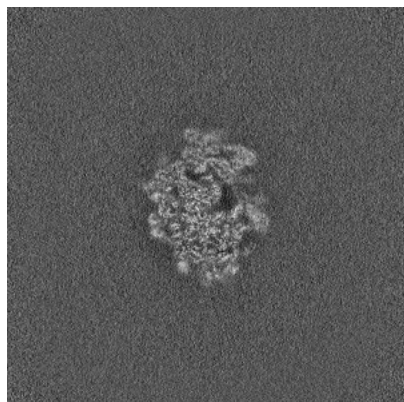


Y Index: 320

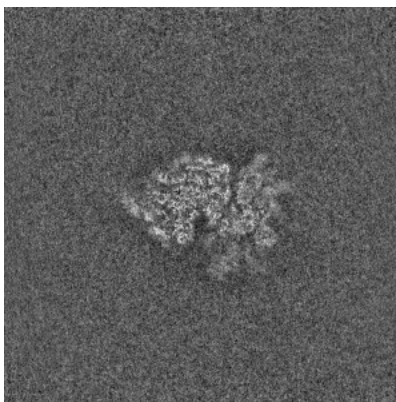


Z Index: 320

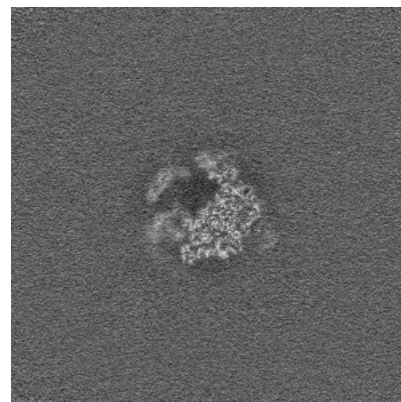
### 6.2.2 Raw map



X Index: 320



Y Index: 320



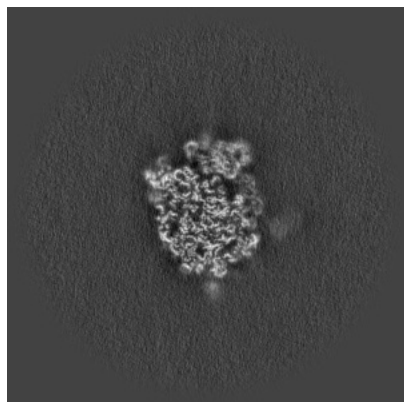
Z Index: 320

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

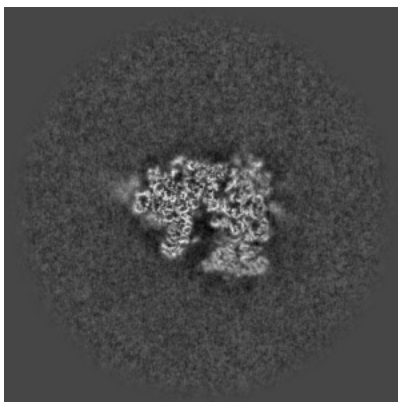


## 6.3 Largest variance slices [i](#)

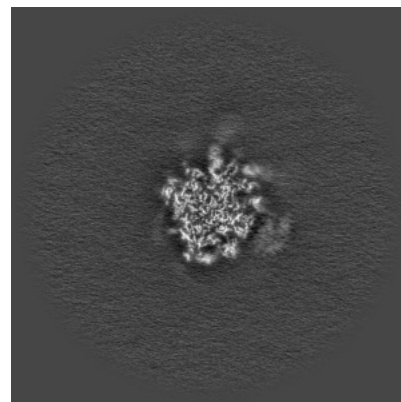
### 6.3.1 Primary map



X Index: 339

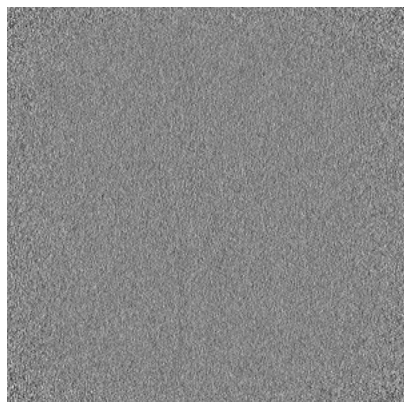


Y Index: 334

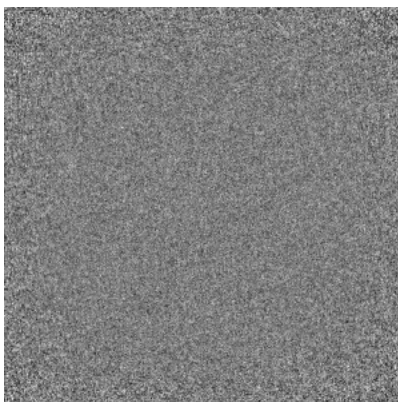


Z Index: 285

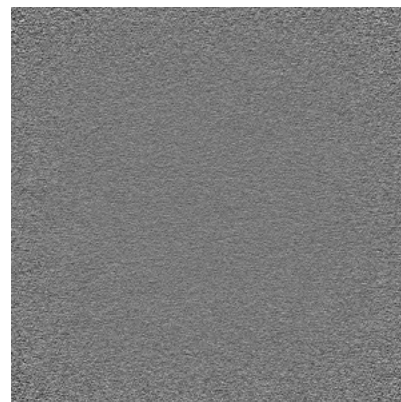
### 6.3.2 Raw map



X Index: 0



Y Index: 0

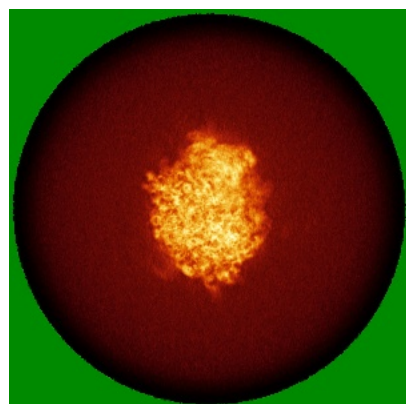


Z Index: 639

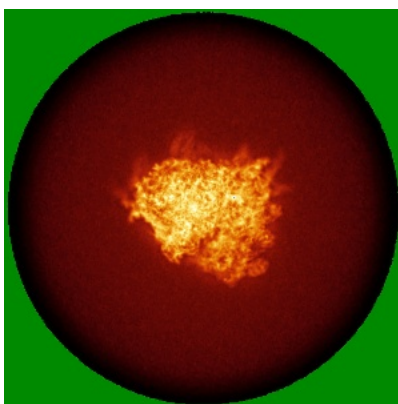
The images above show the largest variance slices of the map in three orthogonal directions.

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

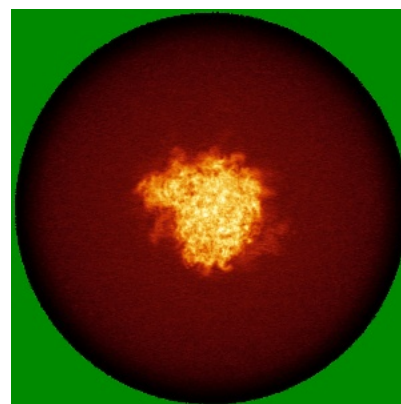
### 6.4.1 Primary map



X

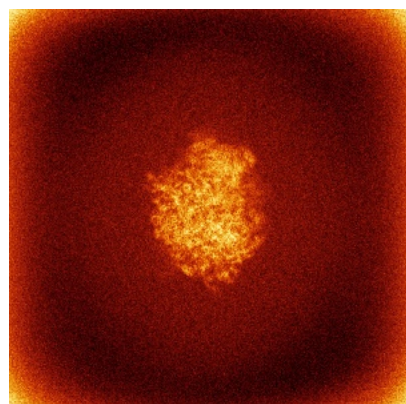


Y

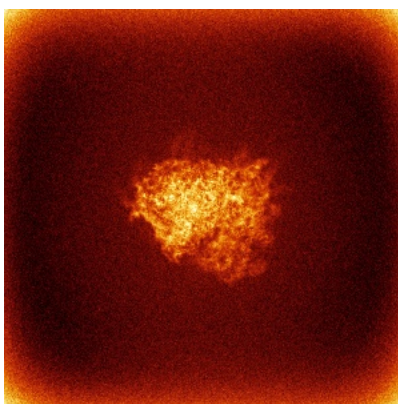


Z

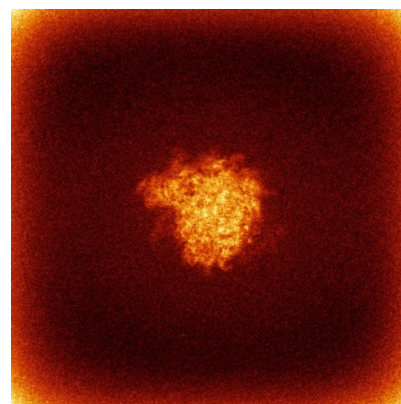
### 6.4.2 Raw map



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



X



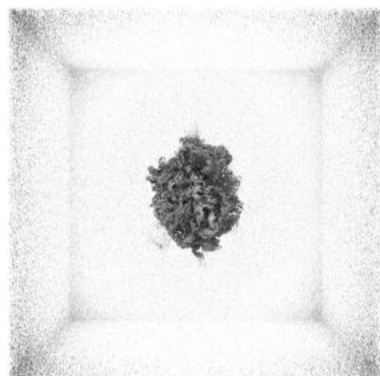
Y



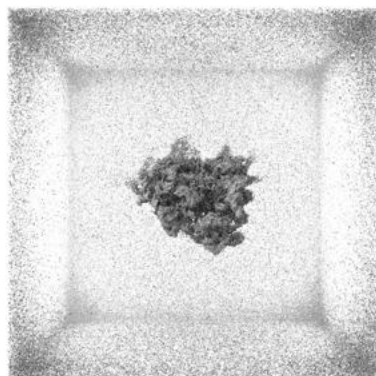
Z

The images above show the 3D surface view of the map at the recommended contour level 0.6. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

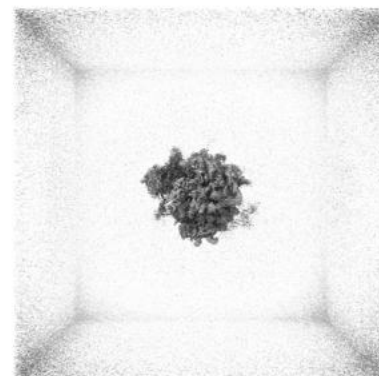
### 6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

## 6.6 Mask visualisation [i](#)

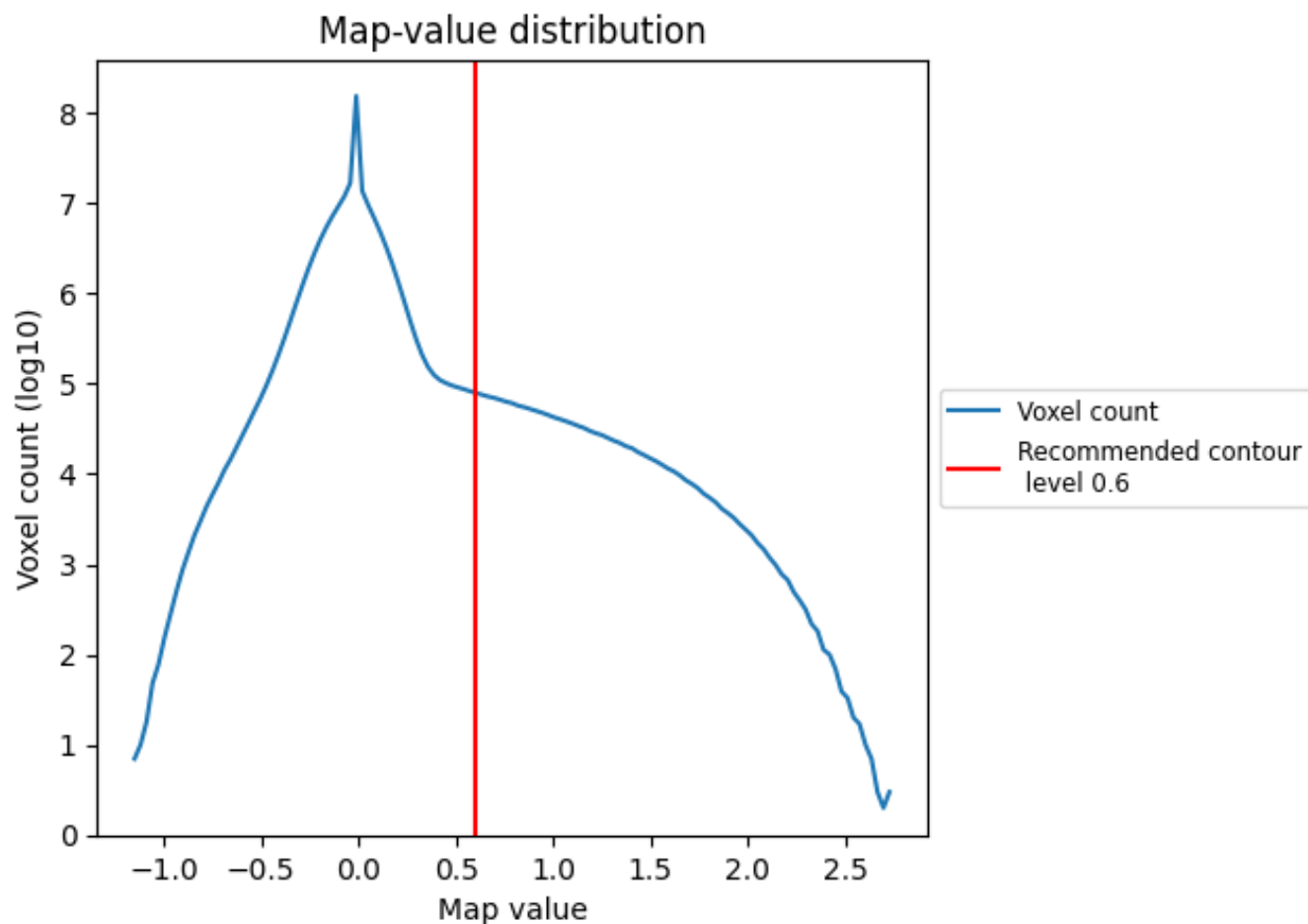
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

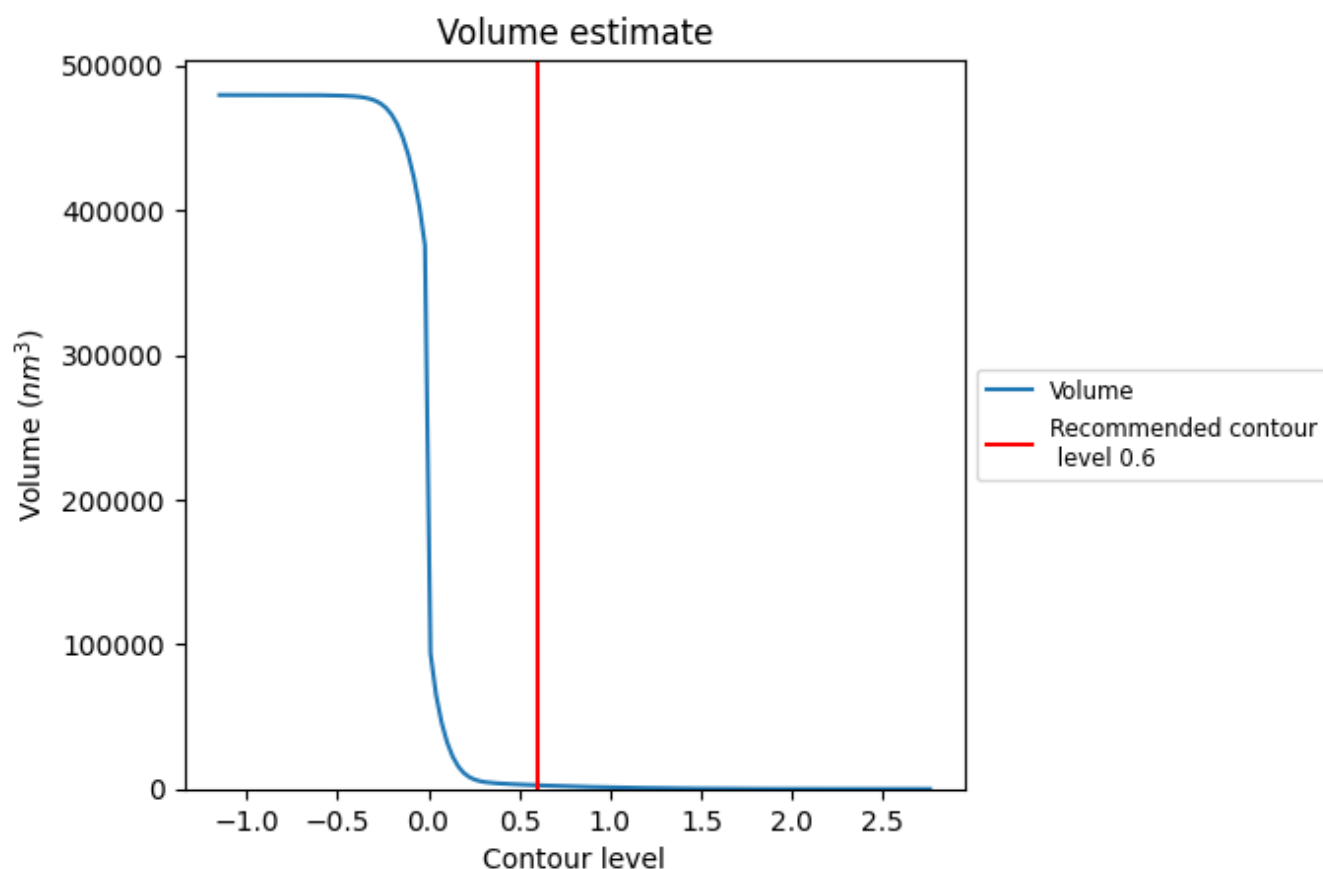
This section contains the results of statistical analysis of the map.

### 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.

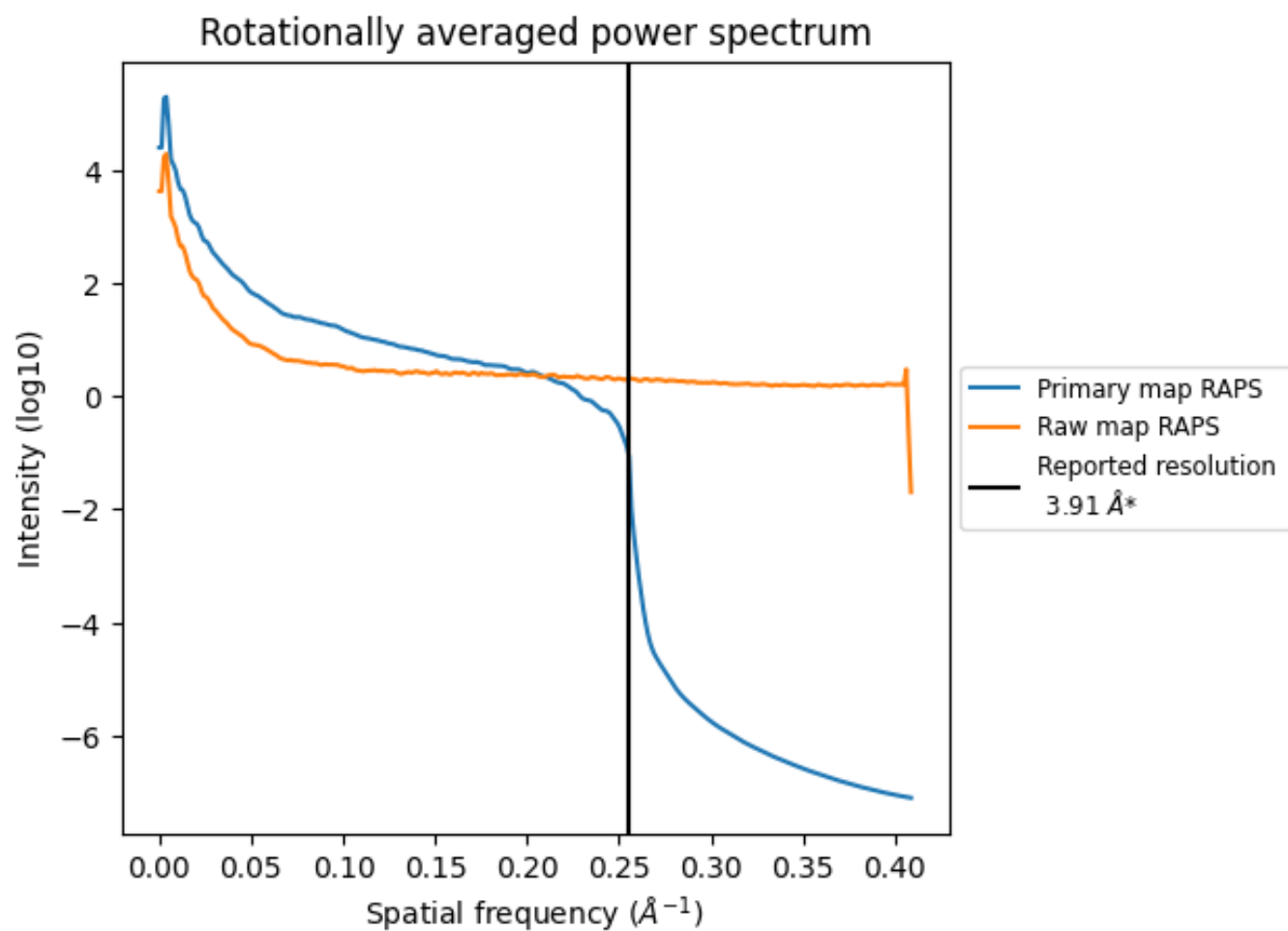
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2567  $\text{nm}^3$ ; this corresponds to an approximate mass of 2318 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 ⓘ

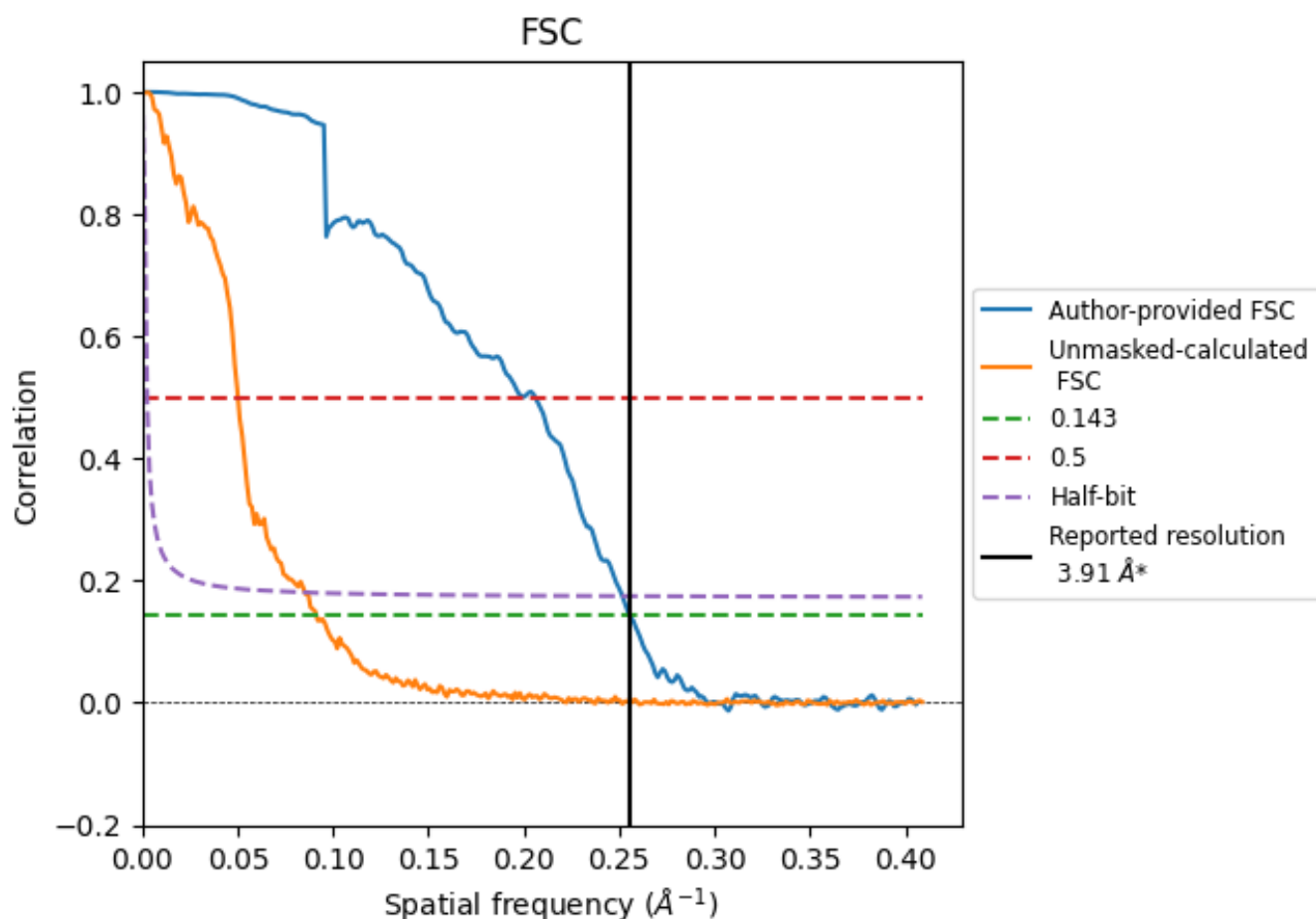


\*Reported resolution corresponds to spatial frequency of 0.256 Å<sup>-1</sup>

## 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 0.256  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

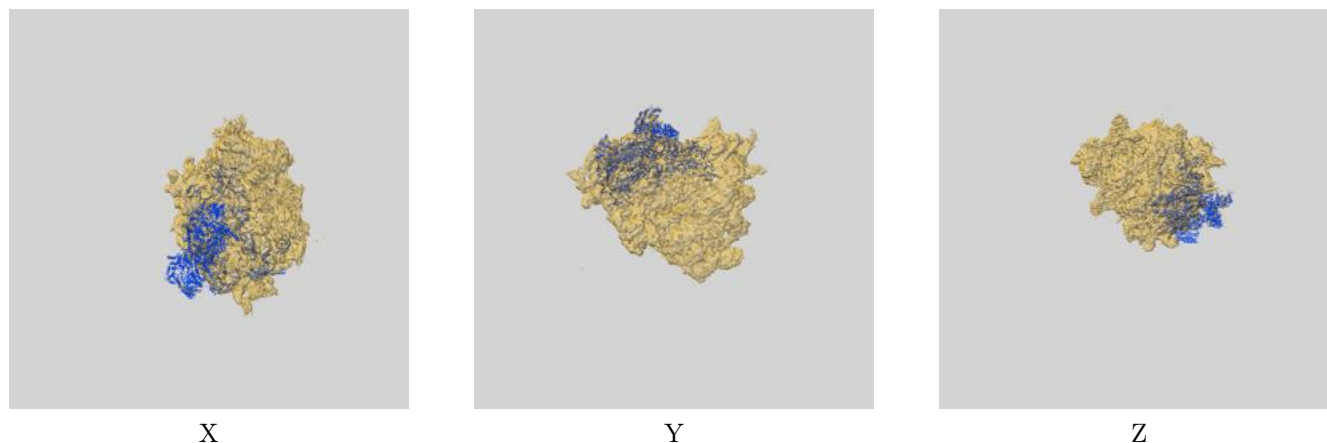
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.91	-	-
Author-provided FSC curve	3.92	4.85	3.97
Unmasked-calculated*	10.95	19.92	11.72

\*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 10.95 differs from the reported value 3.91 by more than 10 %

## 9 Map-model fit [i](#)

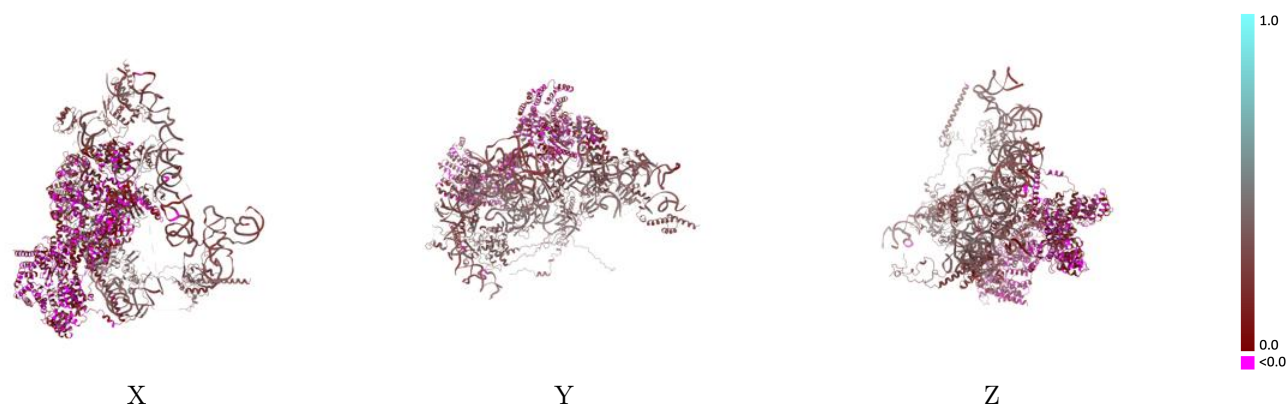
This section contains information regarding the fit between EMDB map EMD-51383 and PDB model 9GJ6. Per-residue inclusion information can be found in section [3](#) on page [8](#).

### 9.1 Map-model overlay [i](#)



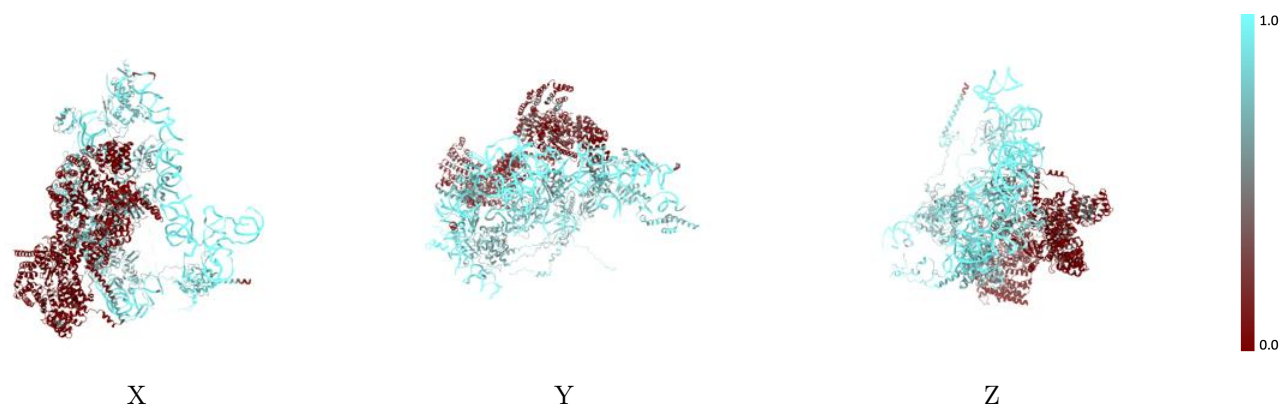
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



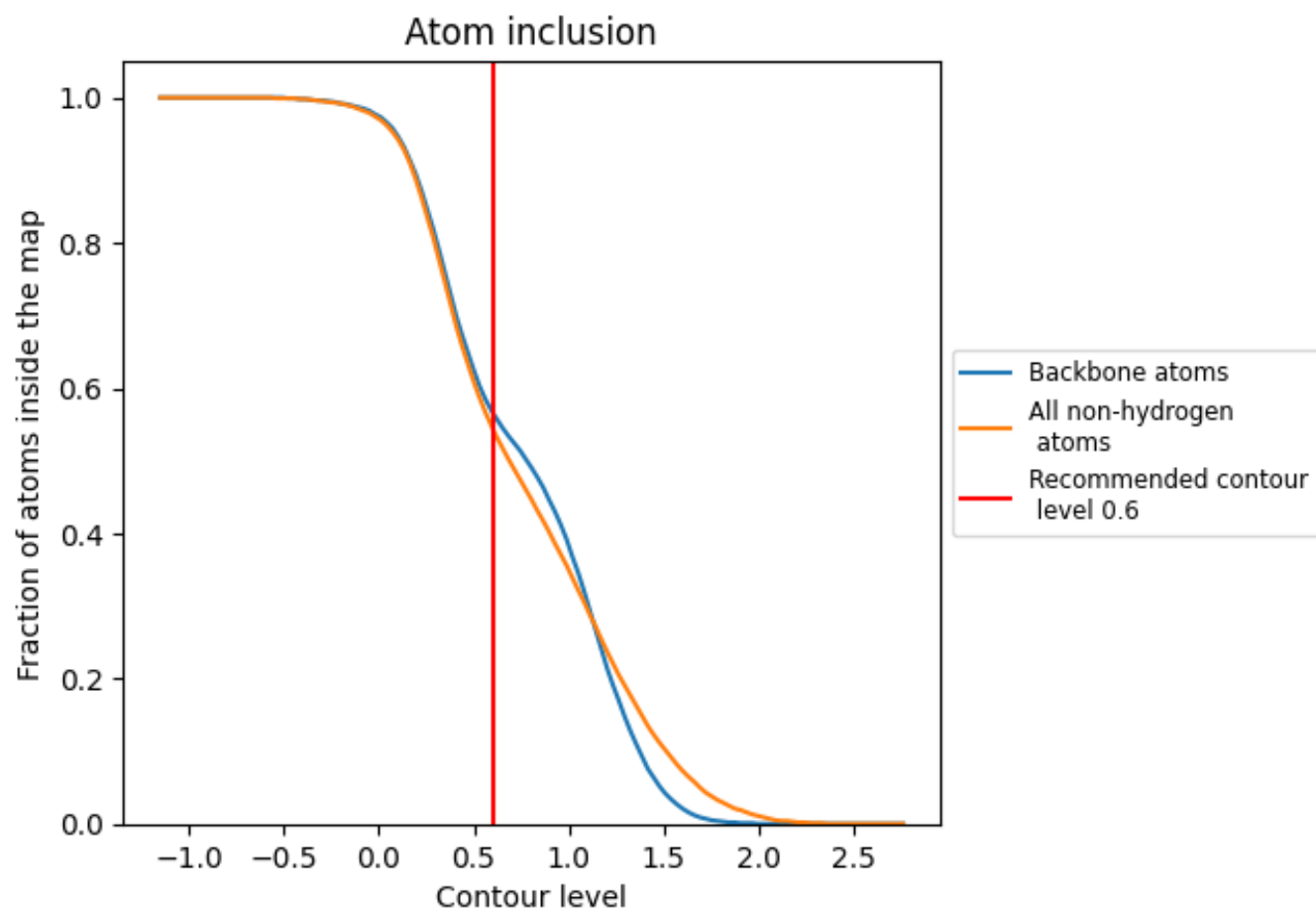
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 57% of all backbone atoms, 54% 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	 0.5440	 0.2210
1	 0.9560	 0.3050
8	 0.9450	 0.3390
A	 0.0250	 0.0620
B	 0.0450	 0.0770
C	 0.0060	 0.0750
D	 0.0940	 0.0860
LC	 0.7070	 0.3330
LE	 0.8460	 0.3290
LP	 0.6870	 0.3210
LR	 0.7390	 0.2910
LU	 0.7530	 0.2830
LX	 0.7290	 0.3080
LY	 0.7850	 0.3190
Ld	 0.6620	 0.2930
Lh	 0.7830	 0.2820
Lk	 0.7810	 0.3050
Lr	 0.7300	 0.3350

