



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 06:21 PM UTC

PDB ID : 7NZ4 / pdb_00007nz4
EMDB ID : EMD-12664
Title : Cryo-EM structure of the MukBEF dimer
Authors : Buermann, F.; Lowe, J.
Deposited on : 2021-03-23
Resolution : 13.00 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:

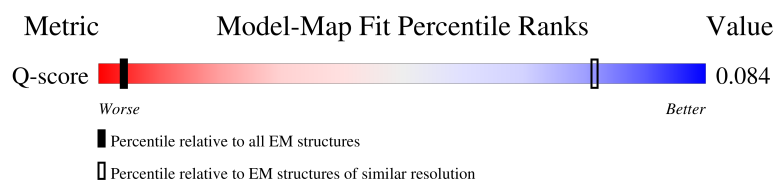
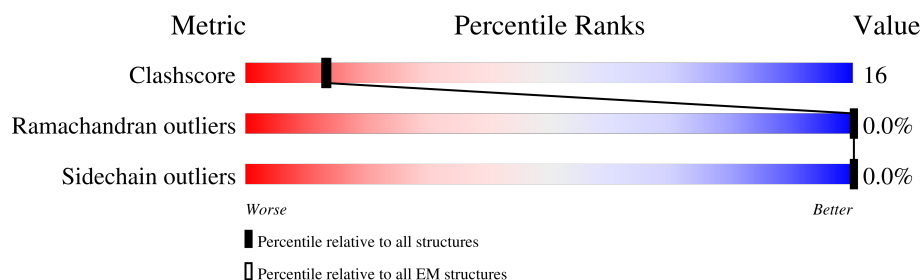
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

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

The reported resolution of this entry is 13.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	65 (12.50 - 13.50)

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	A1	1482	
1	A2	1482	
1	B1	1482	
1	B2	1482	

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Mol	Chain	Length	Quality of chain
2	C1	440	 71%27%.
2	D1	440	 71%26%..
3	E1	240	 56%29%15%
3	E2	240	 56%29%15%
3	F1	240	 72%11%18%
3	F2	240	 70%12%18%
4	G1	78	 65%27%8%
4	G2	78	 64%28%8%
4	H1	78	 67%26%8%
4	H2	78	 67%26%8%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 125656 atoms, of which 62472 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 Chromosome partition protein MukB.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A1	1467	Total	C	H	N	O	S	0	0
			23553	7298	11713	2189	2313	40		
1	A2	1467	Total	C	H	N	O	S	0	0
			23553	7298	11713	2189	2313	40		
1	B1	1467	Total	C	H	N	O	S	0	0
			23552	7298	11712	2189	2313	40		
1	B2	1467	Total	C	H	N	O	S	0	0
			23552	7298	11712	2189	2313	40		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A1	1407	GLN	GLU	engineered mutation	UNP A0A0F7LRY2
A2	1407	GLN	GLU	engineered mutation	UNP A0A0F7LRY2
B1	1407	GLN	GLU	engineered mutation	UNP A0A0F7LRY2
B2	1407	GLN	GLU	engineered mutation	UNP A0A0F7LRY2

- Molecule 2 is a protein called Chromosome partition protein MukF.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	C1	431	Total	C	H	N	O	S	0	0
			6845	2174	3385	604	670	12		
2	D1	431	Total	C	H	N	O	S	0	0
			6845	2174	3385	604	670	12		

- Molecule 3 is a protein called Chromosome partition protein MukE.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	E1	205	Total	C	H	N	O	S	0	0
			3338	1058	1671	291	309	9		
3	E2	205	Total	C	H	N	O	S	0	0
			3338	1058	1671	291	309	9		

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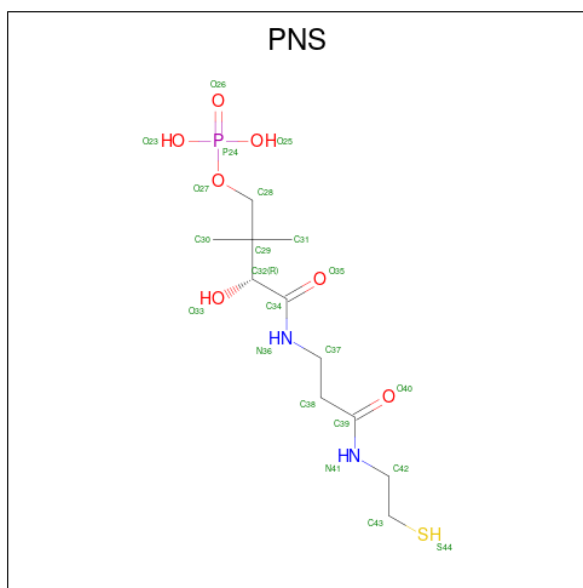
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Mol	Chain	Residues	Atoms						AltConf	Trace
3	F1	198	Total	C	H	N	O	S	0	0
			3246	1029	1627	284	298	8		
3	F2	198	Total	C	H	N	O	S	0	0
			3246	1029	1627	284	298	8		

- Molecule 4 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	G1	72	Total	C	H	N	O	S	0	0
			1105	349	543	85	127	1		
4	G2	72	Total	C	H	N	O	S	0	0
			1105	349	543	85	127	1		
4	H1	72	Total	C	H	N	O	S	0	0
			1105	349	543	85	127	1		
4	H2	72	Total	C	H	N	O	S	0	0
			1105	349	543	85	127	1		

- Molecule 5 is 4'-PHOSPHOPANTETHEINE (CCD ID: PNS) (formula: C₁₁H₂₃N₂O₇PS).



Mol	Chain	Residues	Atoms							AltConf
5	G1	1	Total	C	H	N	O	P	S	0
			42	11	21	2	6	1	1	
5	G2	1	Total	C	H	N	O	P	S	0
			42	11	21	2	6	1	1	
5	H1	1	Total	C	H	N	O	P	S	0
			42	11	21	2	6	1	1	

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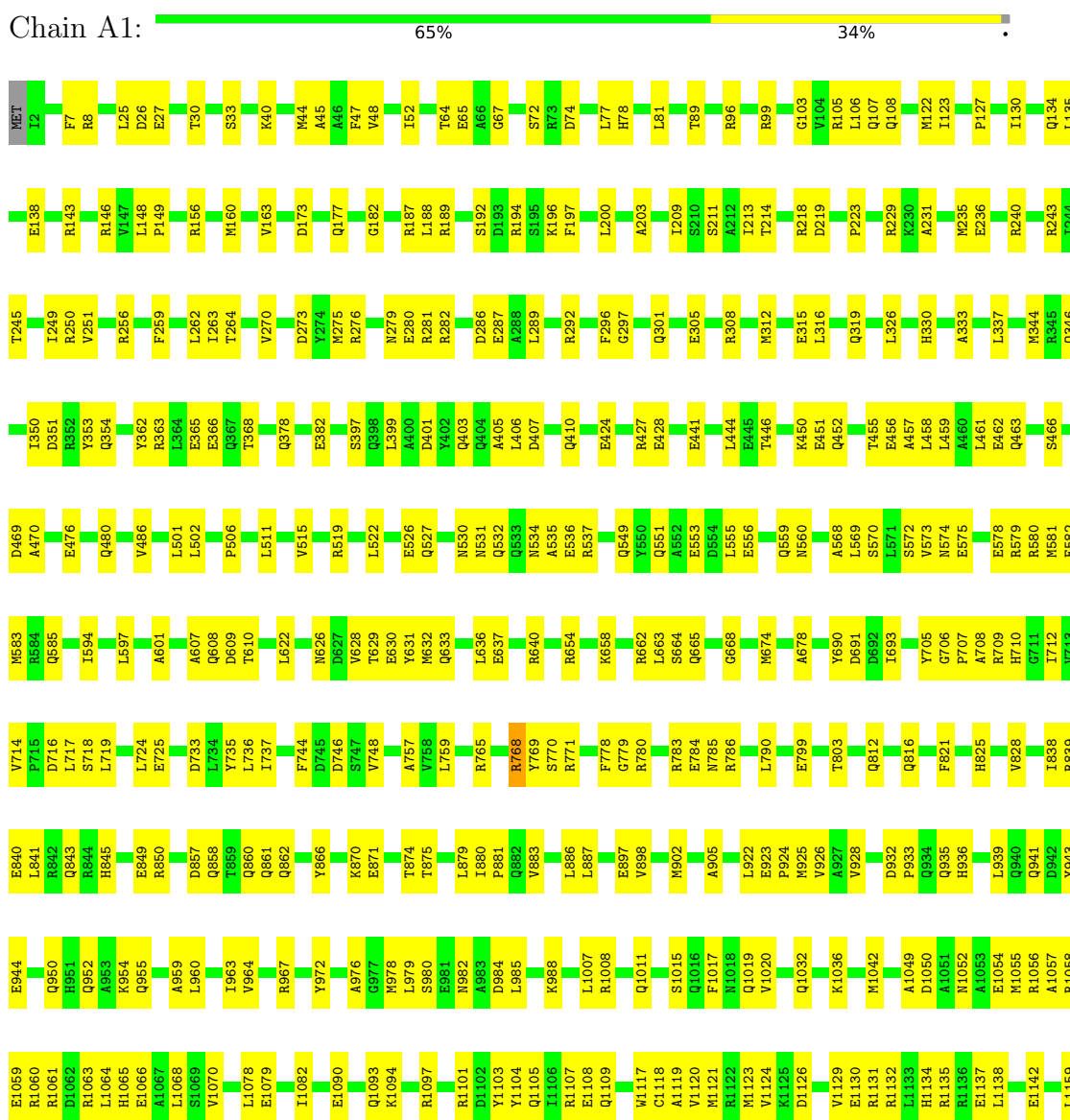
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Mol	Chain	Residues	Atoms							AltConf
			Total	C	H	N	O	P	S	
5	H2	1	42	11	21	2	6	1	1	0

3 Residue-property plots

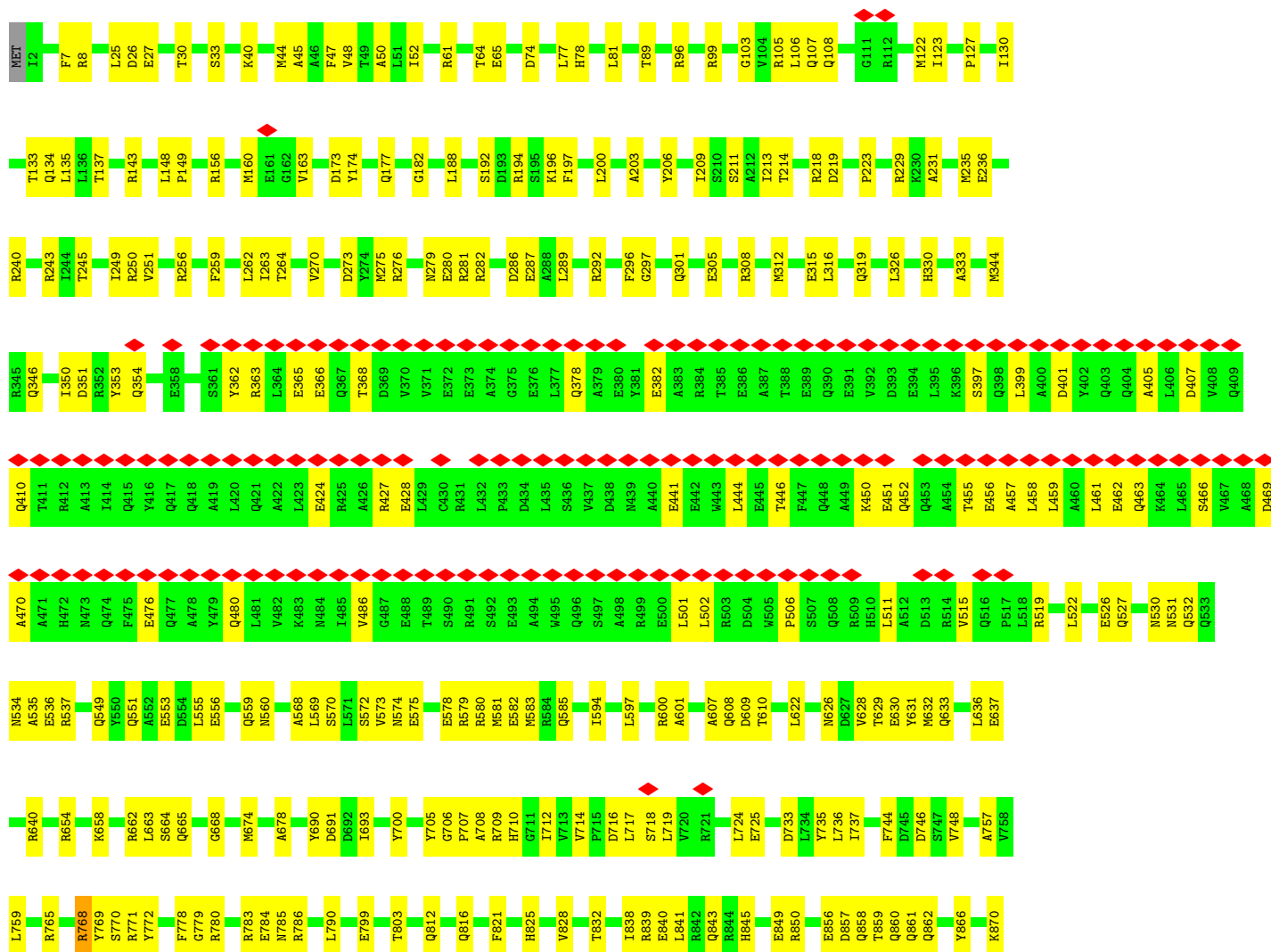
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

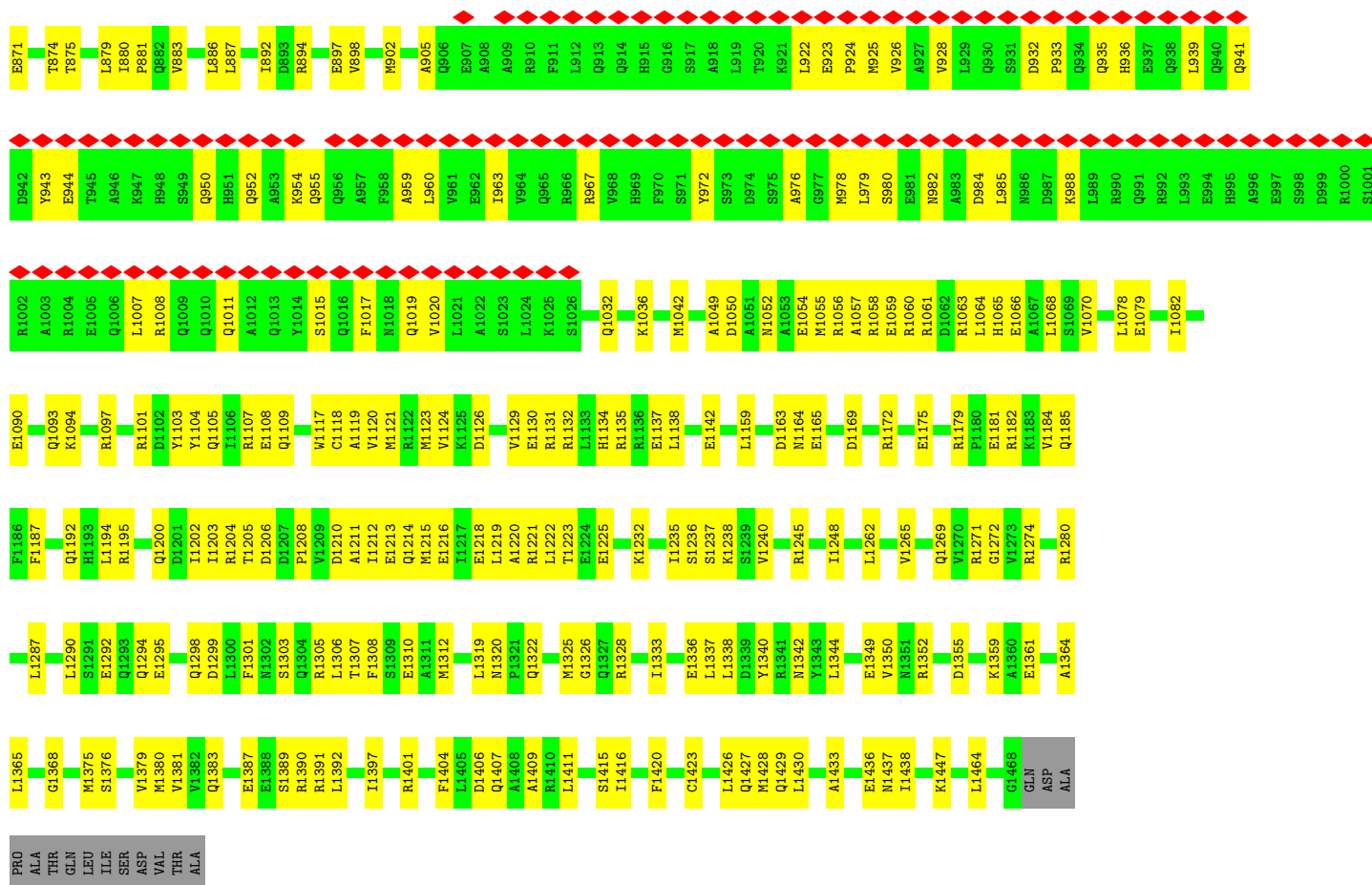
• Molecule 1: Chromosome partition protein MukB



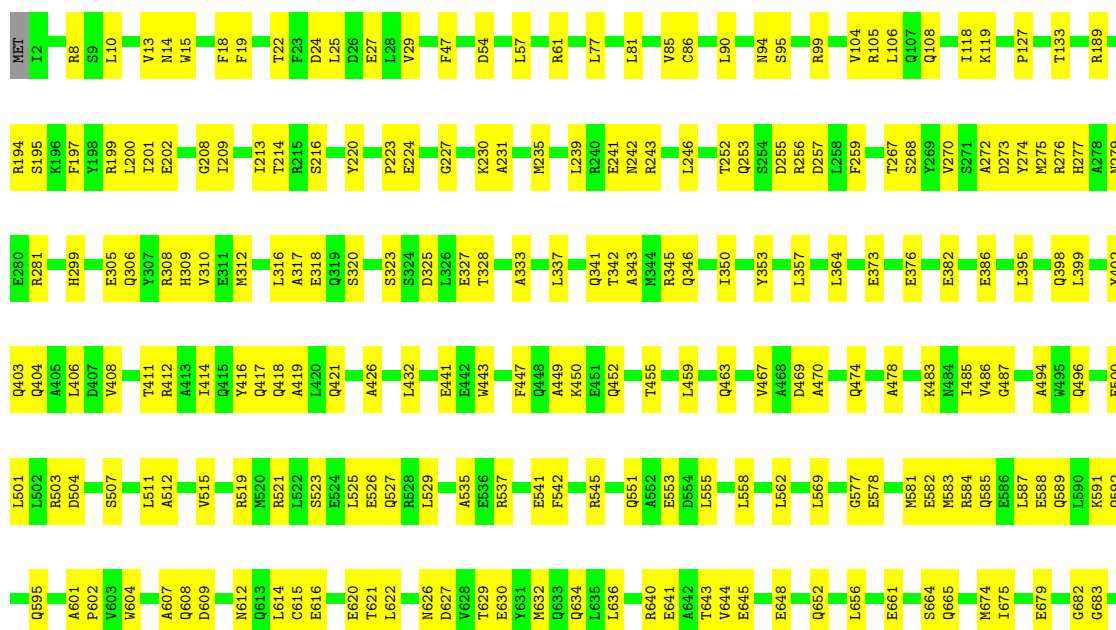


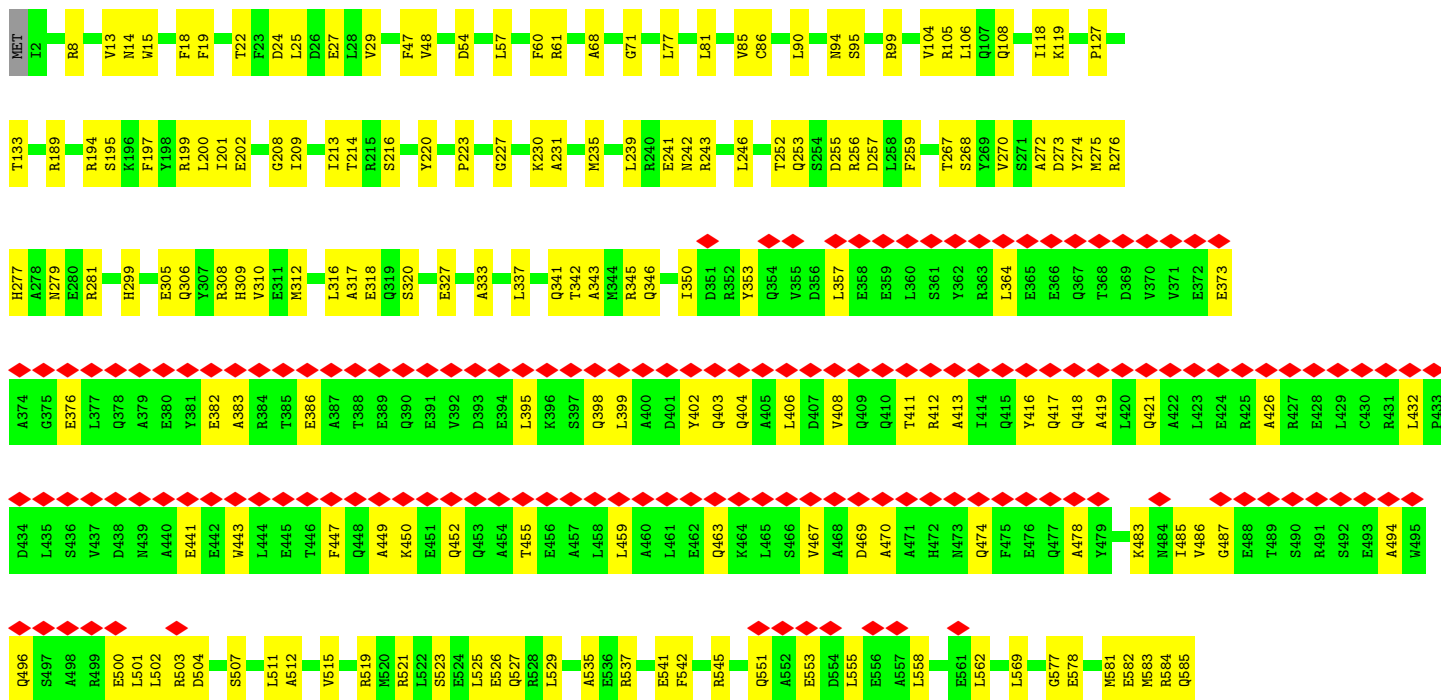
• Molecule 1: Chromosome partition protein MukB

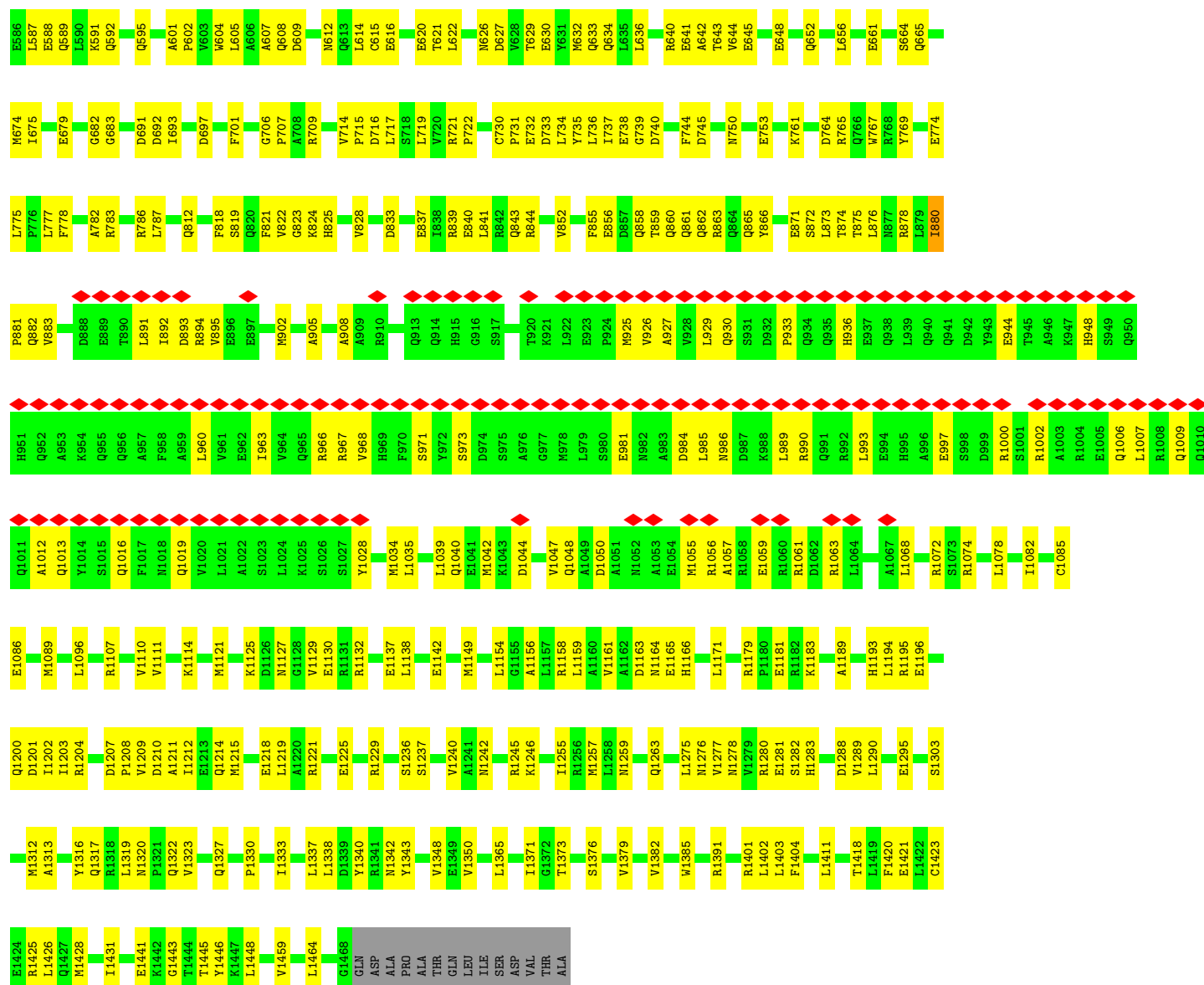




Chain B1: 66% 33%







• Molecule 2: Chromosome partition protein MukF

Chain C1: 71% 27%



Chain D1: 71% 26% ..



PRO VAL GLU SER GLY THR HIS LEU SER LEU ASP ASP SER GLU ASN ASP ASP GLU THR PRO ASP ASP ASN SER SER ALA ALA GLY GLY ALA GLY ASP GLU GLN PRO

• Molecule 3: Chromosome partition protein MukE

Chain F2:  70% 12% 18%

MET SER THR THR ILE LEU GLN F9 M10 E25 R31 A32 D42 M43 Q61 E55 I66 R76 I83 P84 E90 L91 D92 C100 Y103 L104 E107 R108 I114 M134 V137 N138 L151 V155 T158 M167 A189 M204

I205 R206 ASP GLU ALA MET PRO VAL GLU SER LEU SER LEU ASP THR PRO ASN SER ALA GLY ALA GLY ASP GLN PRO

• Molecule 4: Acyl carrier protein

Chain G1:  65% 27% 8%

MET SER T2 E5 R6 V7 I10 I11 G12 E13 Q14 Q19 V22 F28 E41 M44 A45 E48 E53 I54 E57 E58 I62 V65 Q66 D70 N73 GLY HIS GLN ALA

• Molecule 4: Acyl carrier protein

Chain G2:  64% 28% 8%

MET SER T2 E5 R6 V7 I10 I11 G12 E13 Q14 Q19 V22 F28 E41 L42 M44 A45 E48 E53 I54 E57 E58 I62 V65 Q66 D70 N73 GLY HIS GLN ALA

• Molecule 4: Acyl carrier protein

Chain H1:  67% 26% 8%

MET SER T2 E5 R6 V7 K8 G12 G16 N24 D38 T39 V40 E41 M44 E47 E48 E49 F50 D51 I54 E57 Q66 N73 GLY HIS GLN ALA

• Molecule 4: Acyl carrier protein

Chain H2:  67% 26% 8%

MET SER T2 E5 R6 V7 K8 G12 G16 N24 D38 T39 V40 E41 M44 E47 E48 E49 F50 D51 I54 E57 Q66 N73 GLY HIS GLN ALA

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	4197	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.217	Depositor
Minimum map value	-0.041	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.017	Depositor
Map size ($\text{\AA}$)	924.48004, 924.48004, 924.48004	wwPDB
Map dimensions	216, 216, 216	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	4.28, 4.28, 4.28	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: PNS

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	A1	0.21	0/11999	0.40	0/16166
1	A2	0.21	0/11999	0.40	0/16166
1	B1	0.21	0/11999	0.39	0/16166
1	B2	0.21	0/11999	0.39	0/16166
2	C1	0.21	0/3519	0.43	4/4762 (0.1%)
2	D1	0.30	2/3519 (0.1%)	0.51	7/4762 (0.1%)
3	E1	0.15	0/1697	0.39	0/2285
3	E2	0.15	0/1697	0.39	0/2285
3	F1	0.13	0/1648	0.35	0/2218
3	F2	0.13	0/1648	0.35	0/2218
4	G1	0.19	0/565	0.36	0/765
4	G2	0.19	0/565	0.36	0/765
4	H1	0.17	0/565	0.39	0/765
4	H2	0.17	0/565	0.39	0/765
All	All	0.21	2/63984 (0.0%)	0.40	11/86254 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A1	0	2
1	A2	0	2
1	B1	0	1
1	B2	0	1
All	All	0	6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D1	23	SER	C-N	8.66	1.44	1.33
2	D1	23	SER	N-CA	6.52	1.54	1.46

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D1	23	SER	CA-C-N	-10.18	108.65	123.30
2	D1	23	SER	C-N-CA	-10.18	108.65	123.30
2	D1	118	ARG	N-CA-C	-7.98	103.49	113.23
2	D1	116	ARG	N-CA-C	-7.80	100.23	110.53
2	C1	118	ARG	N-CA-C	-7.16	95.92	108.23

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A1	768	ARG	Sidechain
1	A1	886	LEU	Peptide
1	A2	768	ARG	Sidechain
1	A2	886	LEU	Peptide
1	B1	880	ILE	Peptide

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	A1	11840	11713	11708	428	0
1	A2	11840	11713	11708	423	0
1	B1	11840	11712	11708	419	0
1	B2	11840	11712	11708	423	0
2	C1	3460	3385	3382	170	0
2	D1	3460	3385	3381	170	0
3	E1	1667	1671	1669	76	0
3	E2	1667	1671	1669	73	0
3	F1	1619	1627	1626	27	0
3	F2	1619	1627	1626	28	0
4	G1	562	543	542	17	0
4	G2	562	543	542	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H1	562	543	542	20	0
4	H2	562	543	542	20	0
5	G1	21	21	21	1	0
5	G2	21	21	21	1	0
5	H1	21	21	21	2	0
5	H2	21	21	21	2	0
All	All	63184	62472	62437	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 16.

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)
2:C1:105:PRO:HB2	2:D1:113:TYR:CE1	1.27	1.63
2:C1:113:TYR:HE1	2:D1:105:PRO:CB	1.06	1.61
2:C1:105:PRO:CB	2:D1:113:TYR:CE1	1.78	1.58
2:C1:105:PRO:HB2	2:D1:113:TYR:CD1	1.27	1.57
2:C1:113:TYR:CE1	2:D1:105:PRO:HB2	1.08	1.56

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	A1	1465/1482 (99%)	1388 (95%)	77 (5%)	0	100	100
1	A2	1465/1482 (99%)	1388 (95%)	77 (5%)	0	100	100
1	B1	1465/1482 (99%)	1403 (96%)	62 (4%)	0	100	100
1	B2	1465/1482 (99%)	1402 (96%)	63 (4%)	0	100	100
2	C1	429/440 (98%)	405 (94%)	24 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D1	429/440 (98%)	404 (94%)	24 (6%)	1 (0%)	43	78
3	E1	203/240 (85%)	200 (98%)	3 (2%)	0	100	100
3	E2	203/240 (85%)	200 (98%)	3 (2%)	0	100	100
3	F1	196/240 (82%)	191 (97%)	5 (3%)	0	100	100
3	F2	196/240 (82%)	191 (97%)	5 (3%)	0	100	100
4	G1	70/78 (90%)	64 (91%)	6 (9%)	0	100	100
4	G2	70/78 (90%)	64 (91%)	6 (9%)	0	100	100
4	H1	70/78 (90%)	65 (93%)	5 (7%)	0	100	100
4	H2	70/78 (90%)	65 (93%)	5 (7%)	0	100	100
All	All	7796/8080 (96%)	7430 (95%)	365 (5%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D1	119	GLU

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	A1	1269/1281 (99%)	1269 (100%)	0	100	100
1	A2	1269/1281 (99%)	1269 (100%)	0	100	100
1	B1	1269/1281 (99%)	1269 (100%)	0	100	100
1	B2	1269/1281 (99%)	1269 (100%)	0	100	100
2	C1	367/376 (98%)	367 (100%)	0	100	100
2	D1	367/376 (98%)	365 (100%)	2 (0%)	81	83
3	E1	182/212 (86%)	182 (100%)	0	100	100
3	E2	182/212 (86%)	182 (100%)	0	100	100
3	F1	177/212 (84%)	177 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	F2	177/212 (84%)	177 (100%)	0	100	100
4	G1	63/67 (94%)	63 (100%)	0	100	100
4	G2	63/67 (94%)	63 (100%)	0	100	100
4	H1	63/67 (94%)	63 (100%)	0	100	100
4	H2	63/67 (94%)	63 (100%)	0	100	100
All	All	6780/6992 (97%)	6778 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D1	115	ILE
2	D1	119	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 100 such sidechains are listed below:

Mol	Chain	Res	Type
1	B1	1253	ASN
1	B2	936	HIS
4	H2	19	GLN
1	B1	1278	ASN
1	B2	532	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	$\# Z > 2$
5	PNS	H2	101	4	14,20,21	0.24	0	18,26,29	0.53	0
5	PNS	G2	101	4	14,20,21	0.22	0	18,26,29	0.47	0
5	PNS	G1	101	4	14,20,21	0.22	0	18,26,29	0.47	0
5	PNS	H1	101	4	14,20,21	0.24	0	18,26,29	0.52	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
5	PNS	H2	101	4	-	5/24/26/27	-
5	PNS	G2	101	4	-	3/24/26/27	-
5	PNS	G1	101	4	-	3/24/26/27	-
5	PNS	H1	101	4	-	5/24/26/27	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

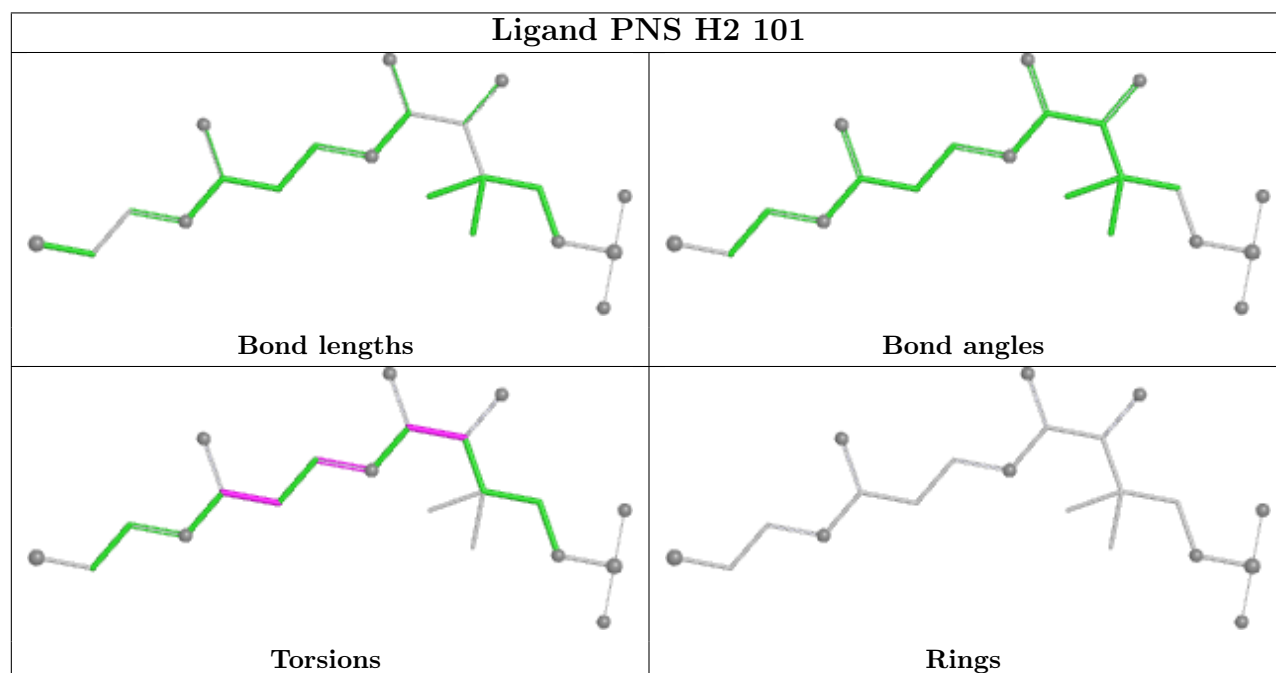
Mol	Chain	Res	Type	Atoms
5	H1	101	PNS	C37-C38-C39-N41
5	H2	101	PNS	C37-C38-C39-N41
5	H1	101	PNS	O33-C32-C34-O35
5	H2	101	PNS	O33-C32-C34-O35
5	H1	101	PNS	C37-C38-C39-O40

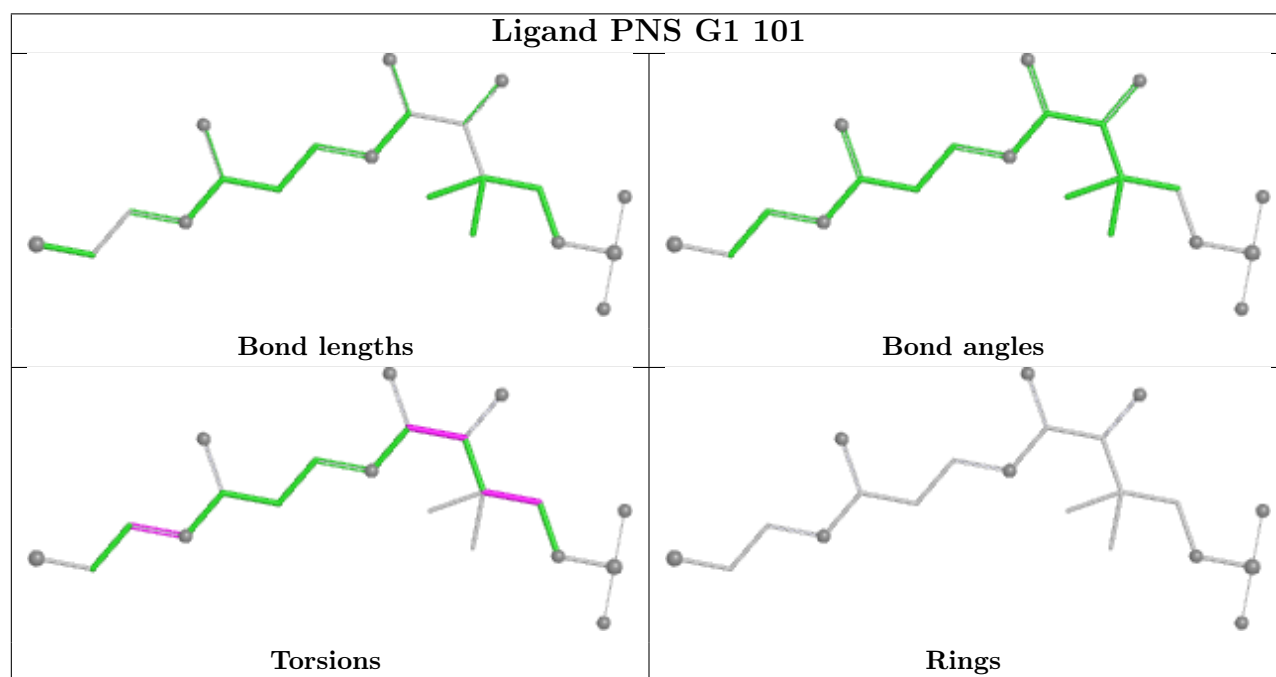
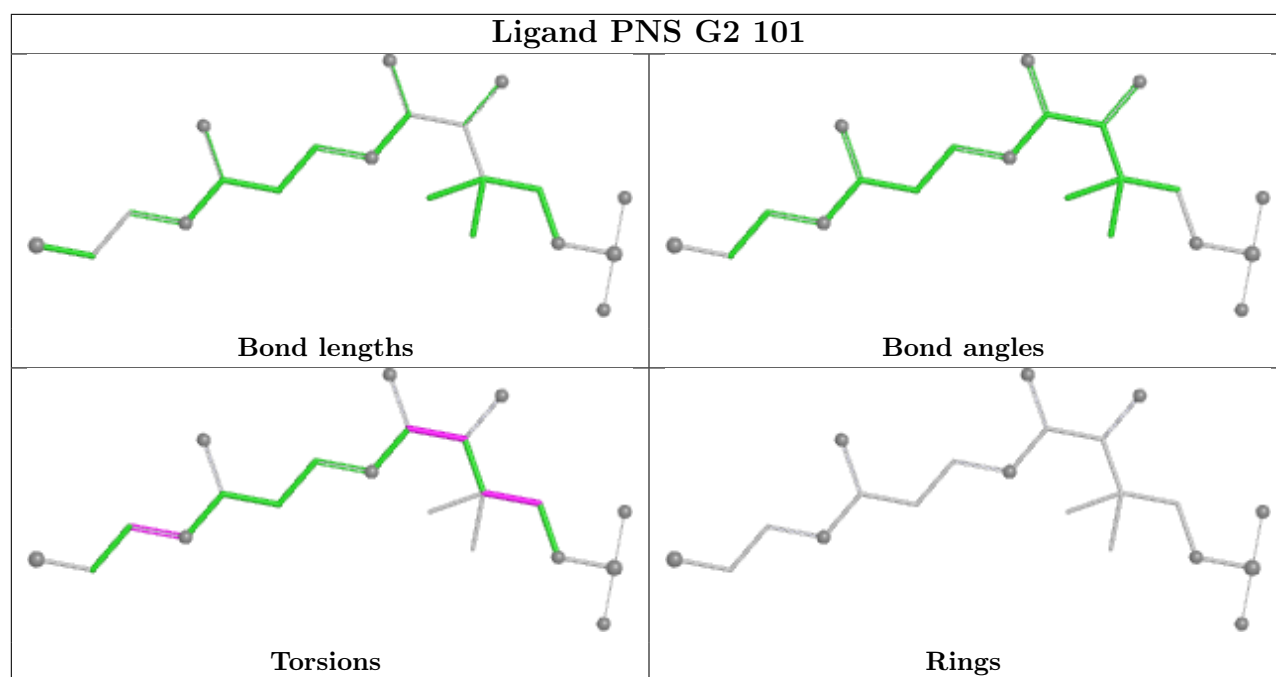
There are no ring outliers.

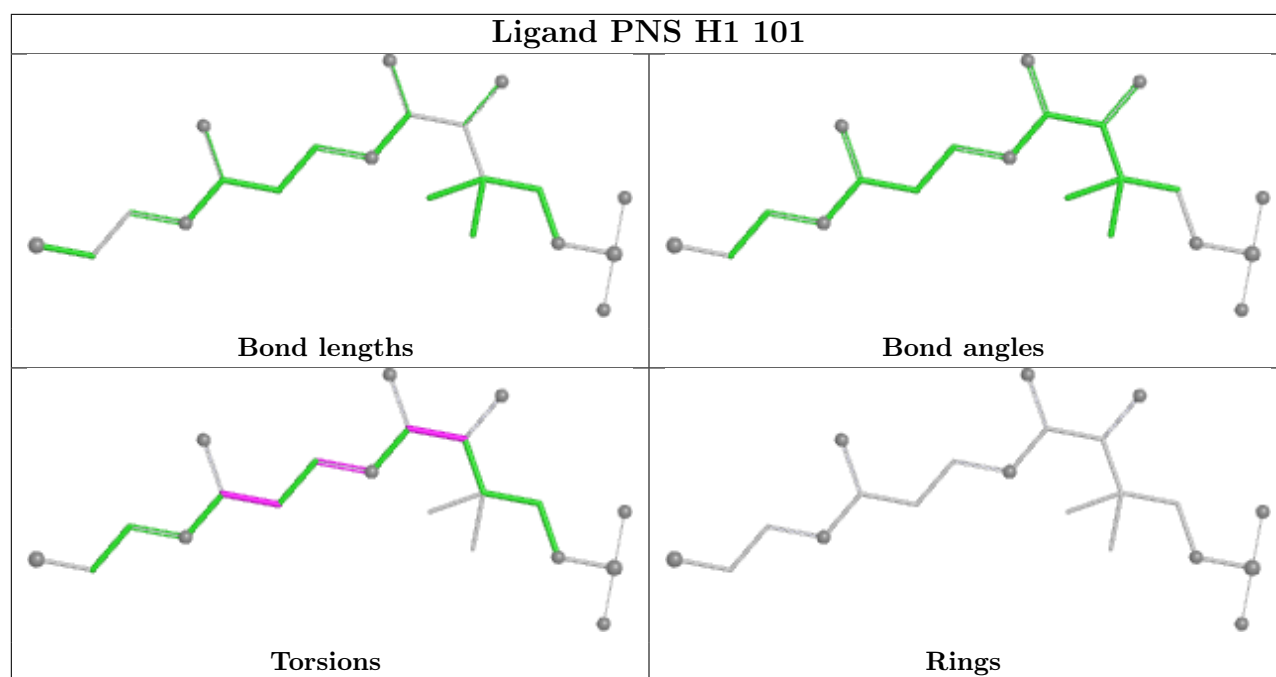
4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	H2	101	PNS	2	0
5	G2	101	PNS	1	0
5	G1	101	PNS	1	0
5	H1	101	PNS	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.

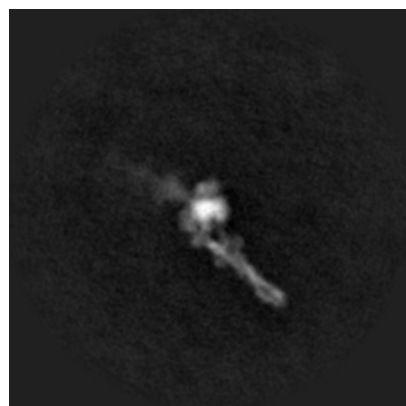
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12664. These allow visual inspection of the internal detail of the map and identification of artifacts.

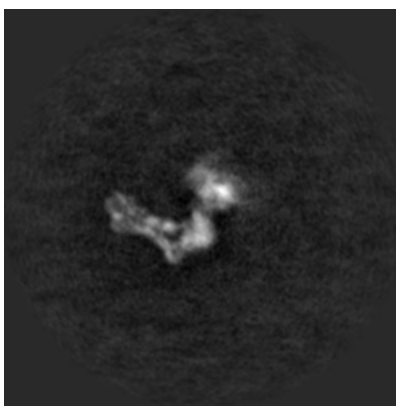
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

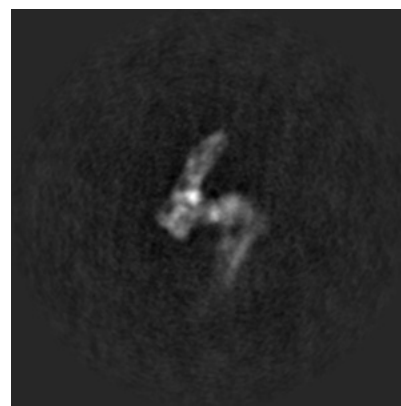
6.1.1 Primary map



X

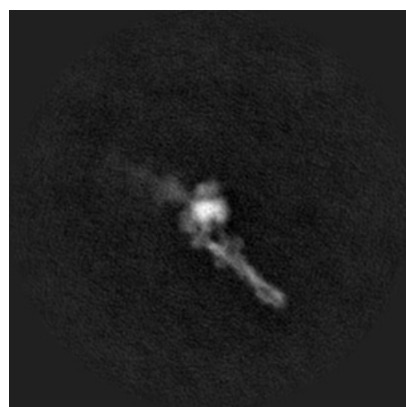


Y

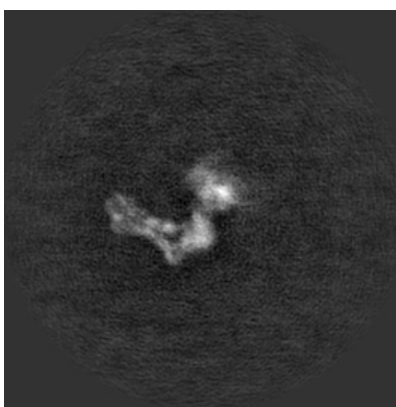


Z

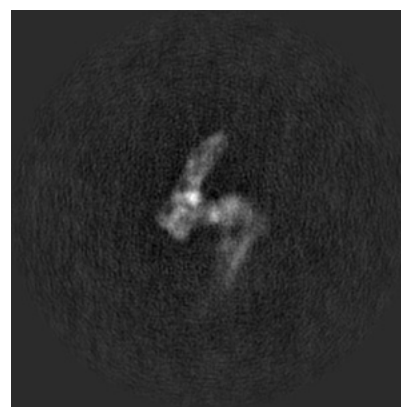
6.1.2 Raw map



X



Y



Z

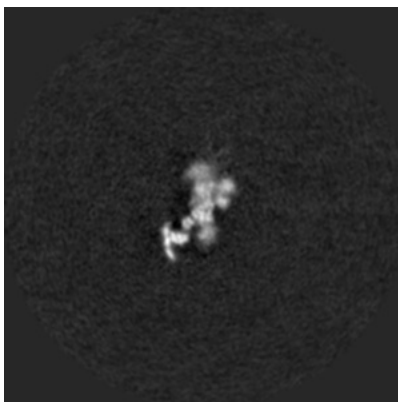
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

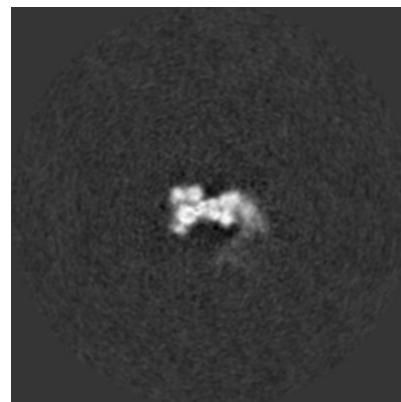
6.2.1 Primary map



X Index: 108



Y Index: 108

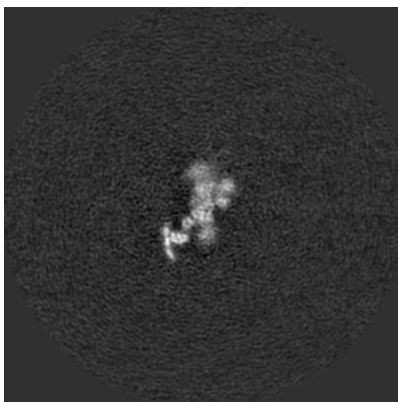


Z Index: 108

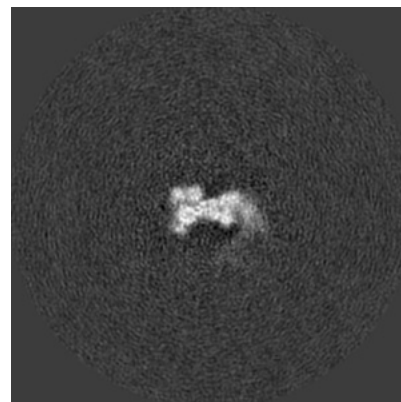
6.2.2 Raw map



X Index: 108



Y Index: 108

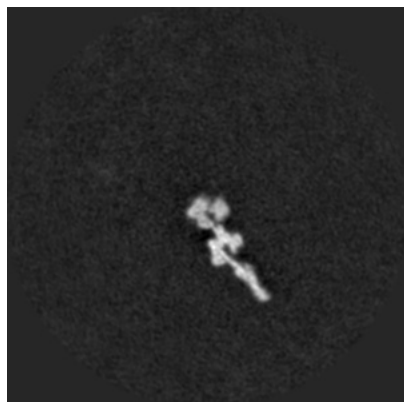


Z Index: 108

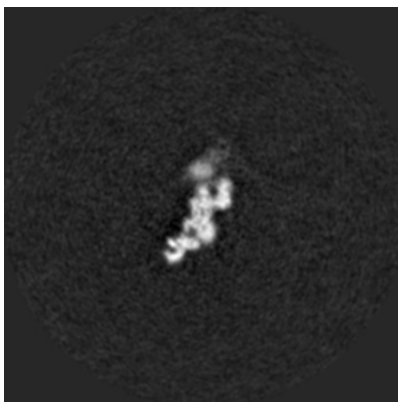
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

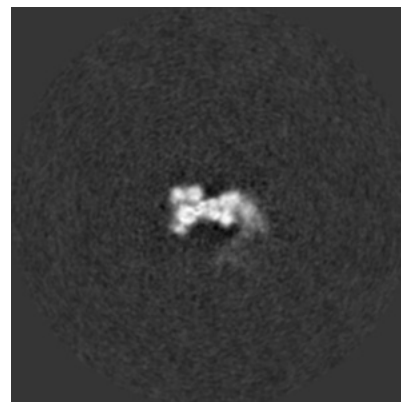
6.3.1 Primary map



X Index: 98

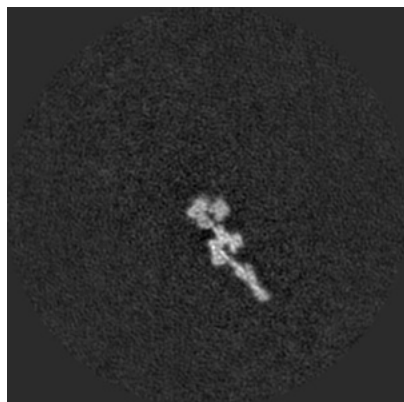


Y Index: 104

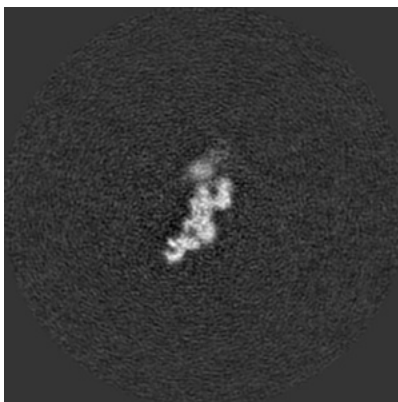


Z Index: 108

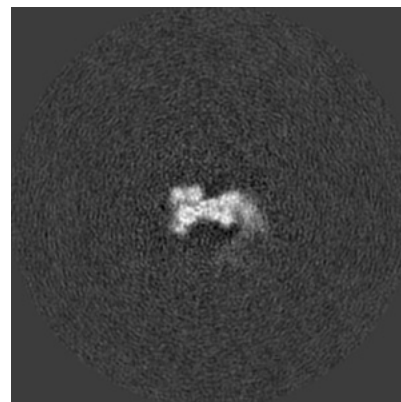
6.3.2 Raw map



X Index: 98



Y Index: 104



Z Index: 108

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

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

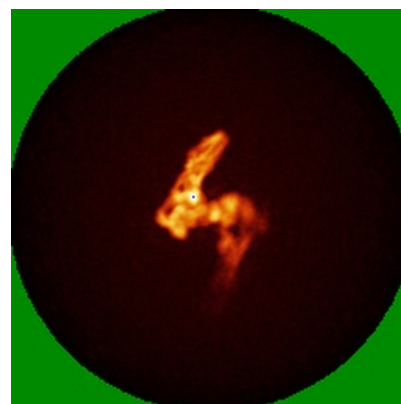
6.4.1 Primary map



X

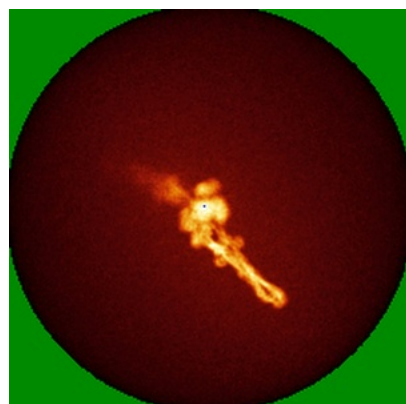


Y

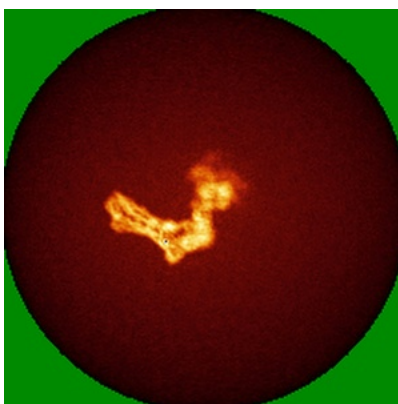


Z

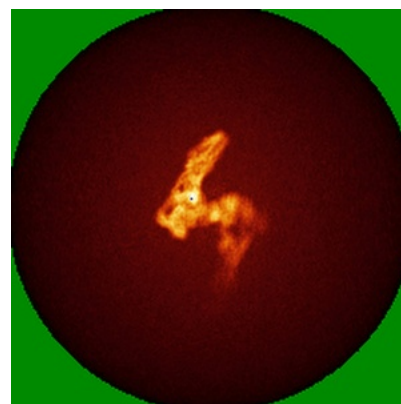
6.4.2 Raw map



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.

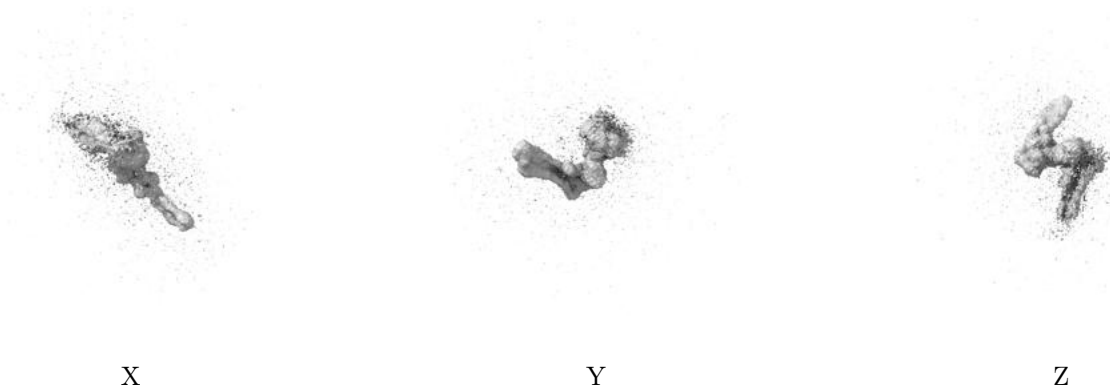
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.017. 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



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.

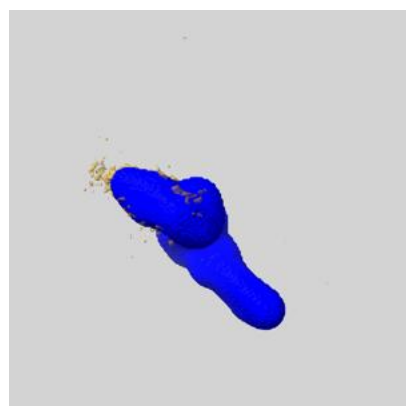
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

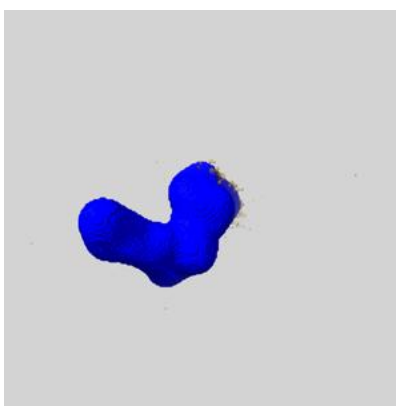
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

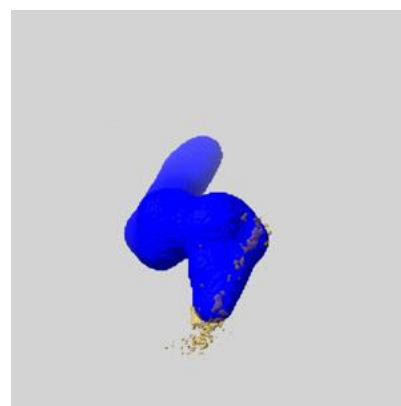
6.6.1 emd_12664_msk_1.map [i](#)



X



Y

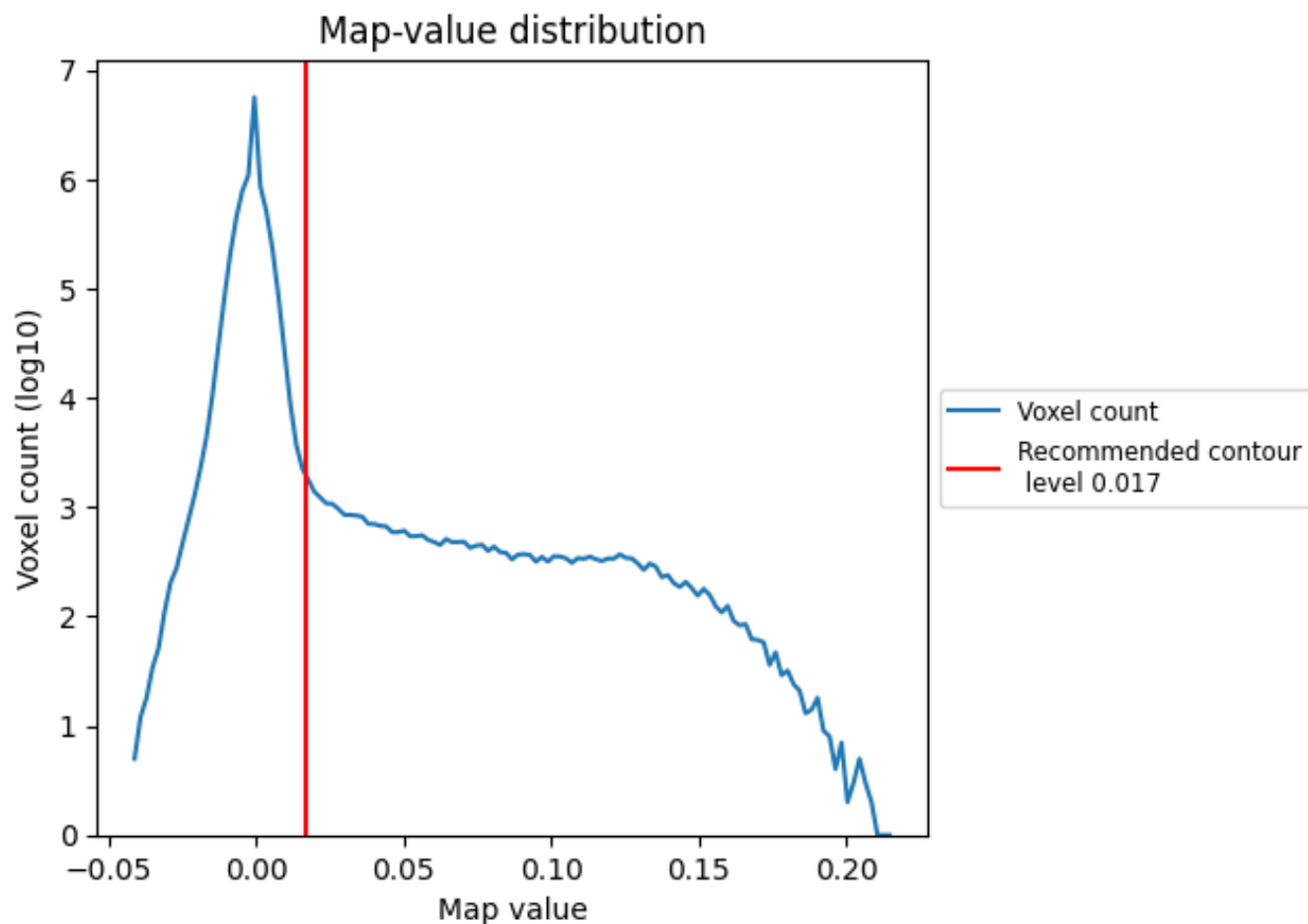


Z

7 Map analysis [i](#)

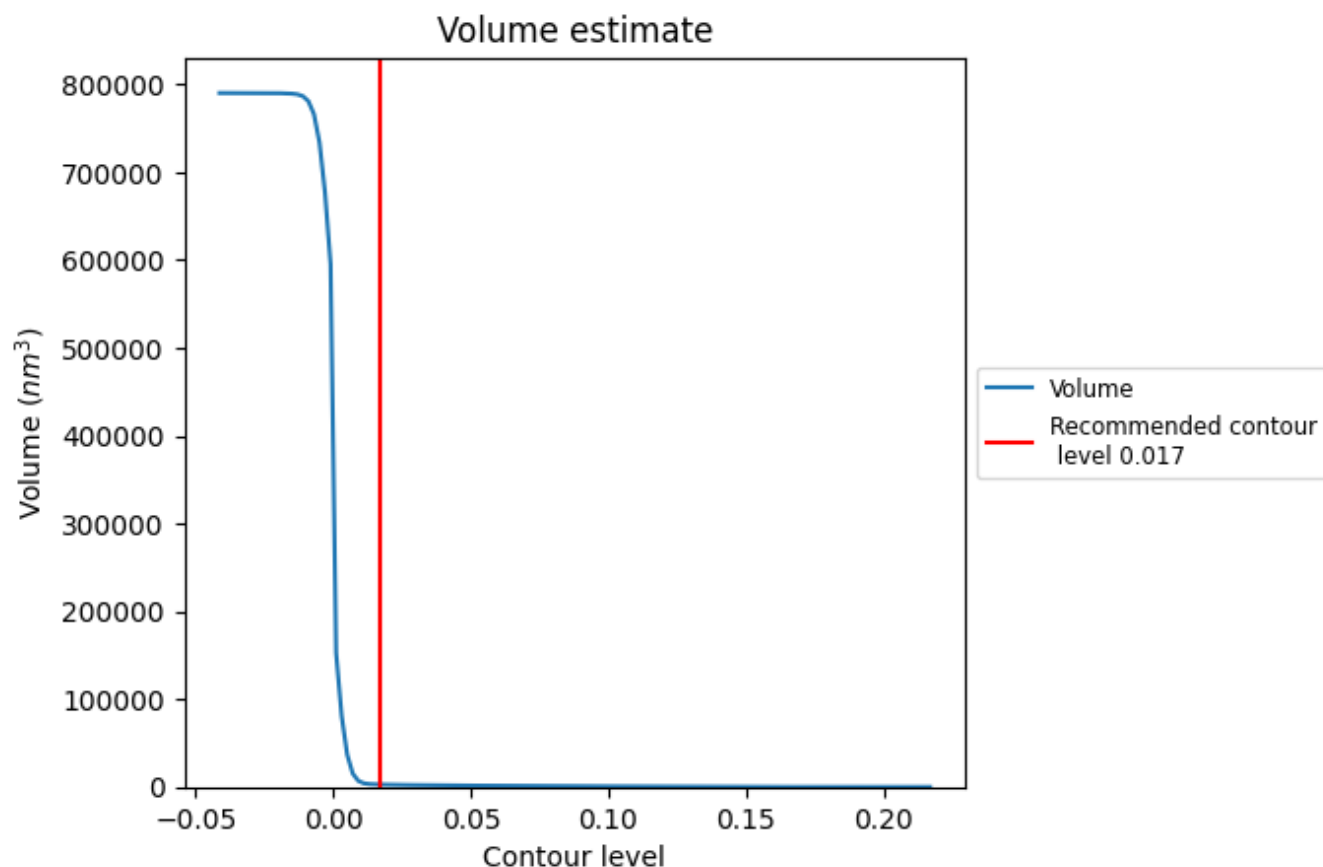
This section contains the results of statistical analysis of the map.

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.

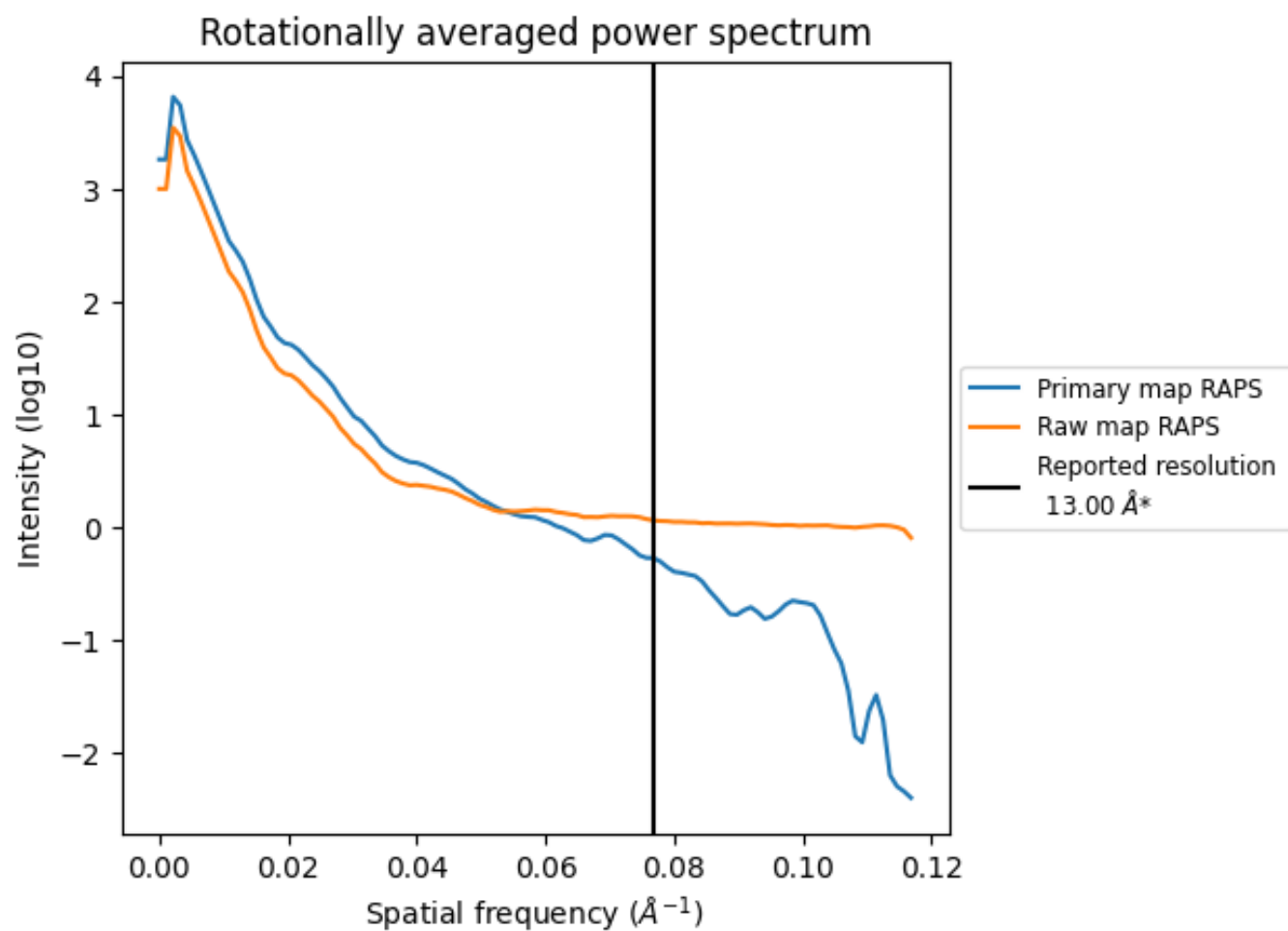
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2767 nm³; this corresponds to an approximate mass of 2499 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 ⓘ

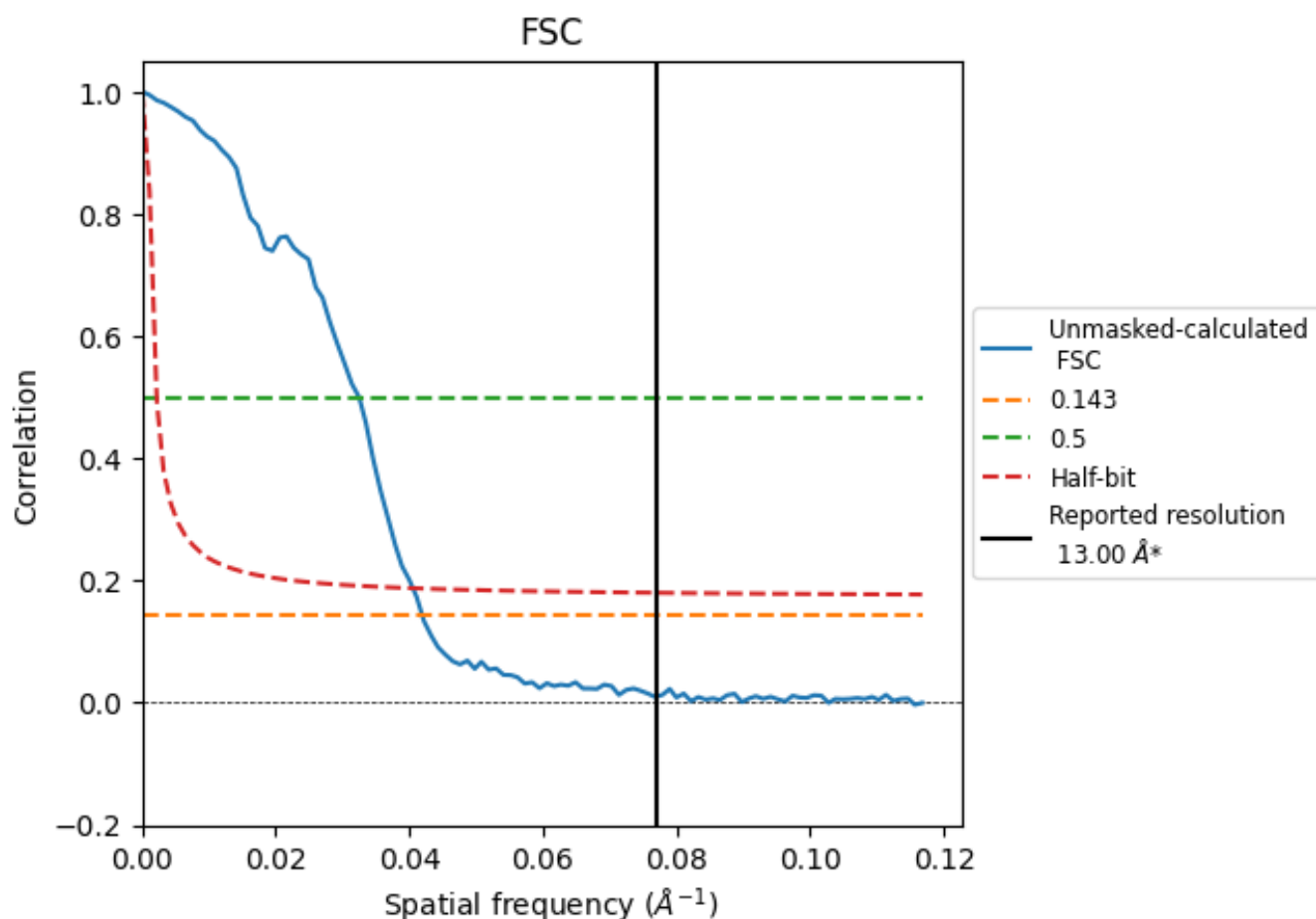


*Reported resolution corresponds to spatial frequency of 0.077 Å⁻¹

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 0.077 Å⁻¹

8.2 Resolution estimates [i](#)

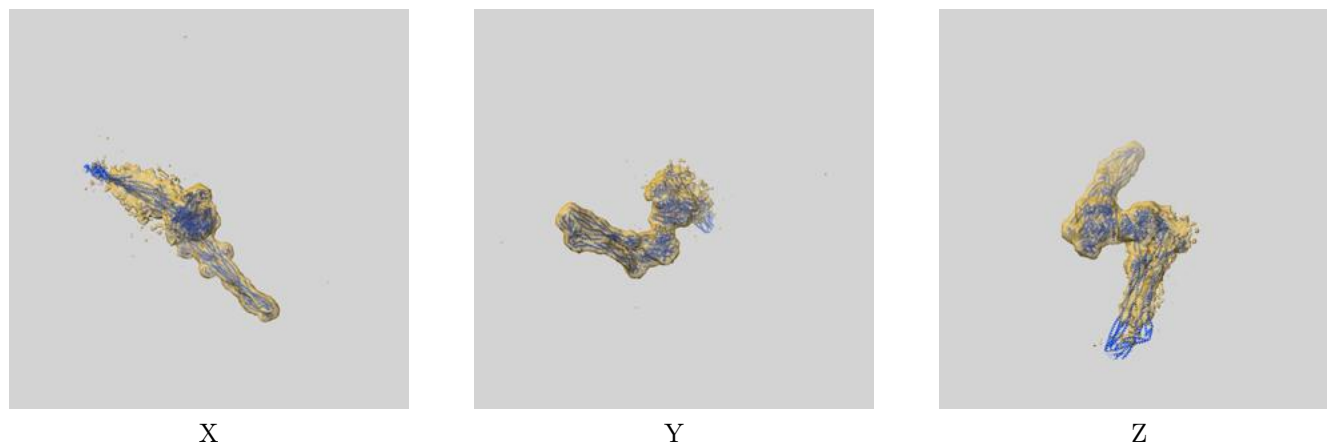
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	13.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	23.87	30.86	24.69

*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 23.87 differs from the reported value 13.0 by more than 10 %

9 Map-model fit [i](#)

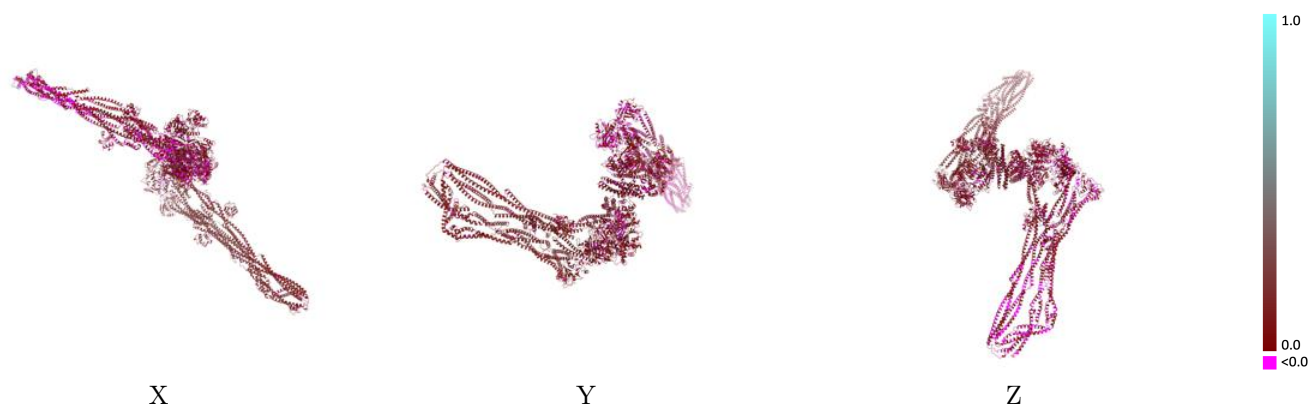
This section contains information regarding the fit between EMDB map EMD-12664 and PDB model 7NZ4. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



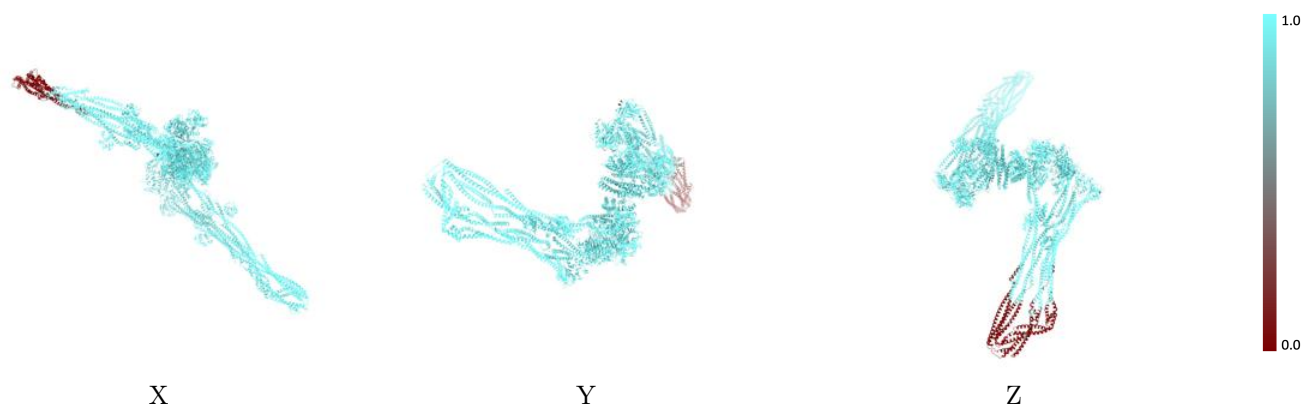
The images above show the 3D surface view of the map at the recommended contour level 0.017 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



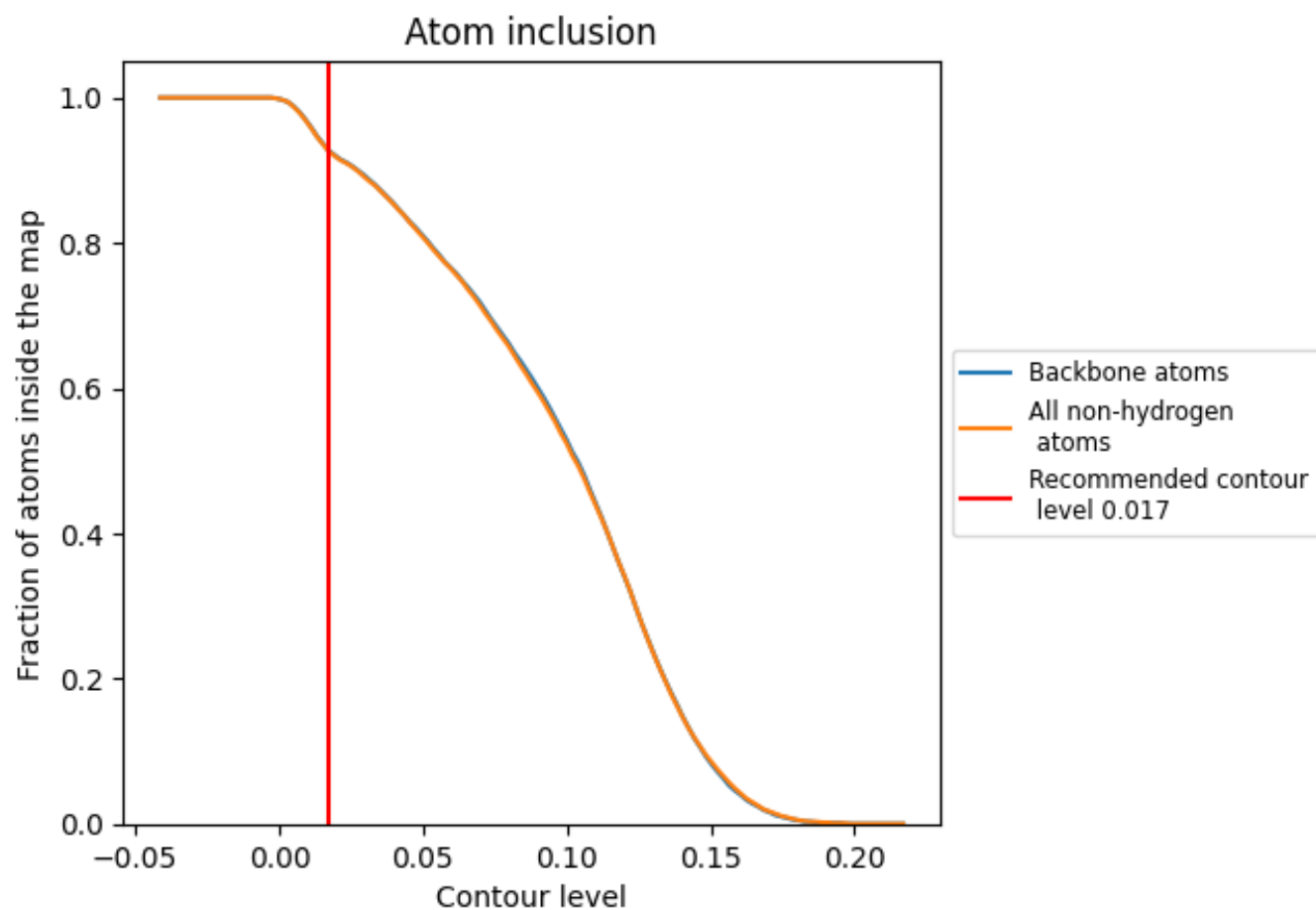
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.017).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 93% 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 (0.017) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9270	0.0840
A1	1.0000	0.1240
A2	0.8080	0.0490
B1	1.0000	0.1200
B2	0.8000	0.0490
C1	1.0000	0.0980
D1	1.0000	0.0780
E1	1.0000	0.0720
E2	1.0000	0.0650
F1	1.0000	0.0790
F2	1.0000	0.0730
G1	1.0000	0.1140
G2	1.0000	0.0400
H1	1.0000	0.1100
H2	1.0000	0.0820

