



wwPDB EM Validation Summary Report ⓘ

Nov 5, 2024 – 03:43 AM EST

PDB ID : 9BRZ
EMDB ID : EMD-44846
Title : V0-only V-ATPase and synaptophysin complex in mouse brain isolated synaptic vesicles
Authors : Wang, C.; Jiang, W.; Yang, K.; Wang, X.; Guo, Q.; Brunger, A.T.
Deposited on : 2024-05-12
Resolution : 3.80 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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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.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

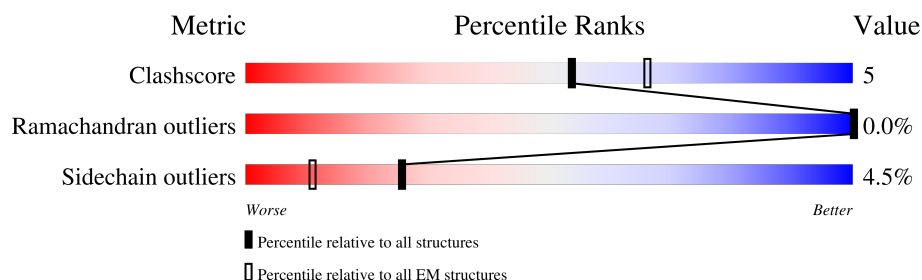
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 Å.

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



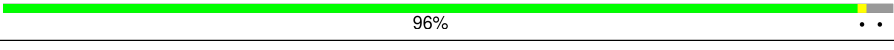
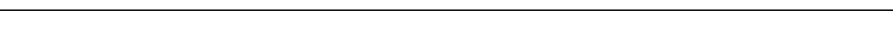
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	c	463	
2	b	205	
3	d	351	
4	f	98	
5	g	155	
5	h	155	
5	i	155	
5	j	155	

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Mol	Chain	Length	Quality of chain
5	k	155	
5	l	155	
5	m	155	
5	n	155	
5	o	155	
6	p	350	
7	s	314	
8	e	81	
9	a	838	
10	A	3	
11	B	2	
11	C	2	
11	D	2	

2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 25204 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 V-type proton ATPase subunit S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	c	203	Total	C	N	O	S	0	0
			1642	1079	259	295	9		

- Molecule 2 is a protein called V-type proton ATPase 21 kDa proteolipid subunit c”.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	203	Total	C	N	O	S	0	0
			1503	996	237	259	11		

- Molecule 3 is a protein called V-type proton ATPase subunit d 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	d	350	Total	C	N	O	S	0	0
			2833	1829	460	530	14		

- Molecule 4 is a protein called Ribonuclease kappa.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	f	86	Total	C	N	O	S	0	0
			666	440	103	116	7		

- Molecule 5 is a protein called V-type proton ATPase 16 kDa proteolipid subunit c.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	g	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
5	h	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
5	i	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
5	j	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	k	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
5	l	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
5	m	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
5	n	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
5	o	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		

- Molecule 6 is a protein called Renin receptor cytoplasmic fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	p	52	Total	C	N	O	S	0	0
			433	292	63	75	3		

- Molecule 7 is a protein called Synaptophysin.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	s	211	Total	C	N	O	S	0	0
			1671	1097	263	299	12		

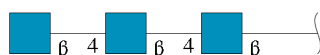
- Molecule 8 is a protein called V-type proton ATPase subunit e 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	e	79	Total	C	N	O	S	0	0
			637	439	99	96	3		

- Molecule 9 is a protein called V-type proton ATPase 116 kDa subunit a 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	a	743	Total	C	N	O	S	0	0
			6039	3943	1009	1046	41		

- Molecule 10 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



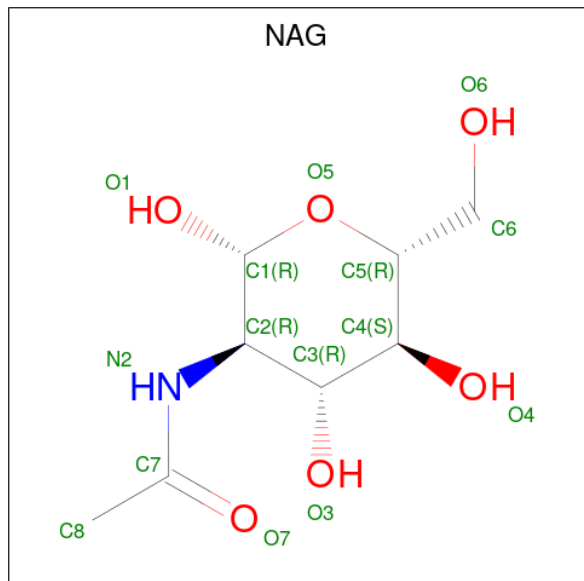
Mol	Chain	Residues	Atoms				AltConf	Trace
10	A	3	Total	C	N	O	0	0
			42	24	3	15		

- Molecule 11 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
11	B	2	Total	C	N	O	0	0
			28	16	2	10		
11	C	2	Total	C	N	O	0	0
			28	16	2	10		
11	D	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 12 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				AltConf
12	c	1	Total	C	N	O	0
			14	8	1	5	
12	c	1	Total	C	N	O	0
			14	8	1	5	

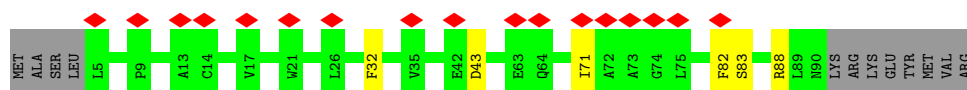
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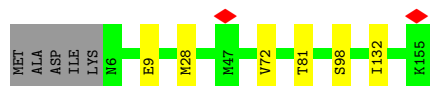
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
12	c	1	14	8	1	5	0

- Molecule 1: V-type proton ATPase subunit S1

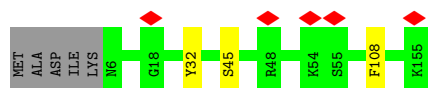




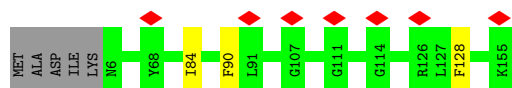
- Molecule 5: V-type proton ATPase 16 kDa proteolipid subunit c



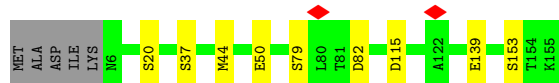
- Molecule 5: V-type proton ATPase 16 kDa proteolipid subunit c



- Molecule 5: V-type proton ATPase 16 kDa proteolipid subunit c



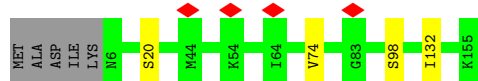
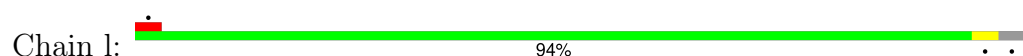
- Molecule 5: V-type proton ATPase 16 kDa proteolipid subunit c



- Molecule 5: V-type proton ATPase 16 kDa proteolipid subunit c



- Molecule 5: V-type proton ATPase 16 kDa proteolipid subunit c



- Molecule 5: V-type proton ATPase 16 kDa proteolipid subunit c

MET
ALA
ASP
ILE
LYS
N6
Y32
I67
V74
S98
R119
Q123
F137
K155

- Chain n:  91% 6%

Sequence logo for the R126 position. The y-axis represents information content in bits, ranging from 0 to 1.5. The x-axis lists amino acids: MET, ALA, ASP, ILE, LYS, N6, S12, V16, S20, S37, S79, Y87, S98, D115, R126, L127, F128, and K155. The R126 position shows a strong preference for Arginine (R), indicated by a red diamond above the bar.

- Chain 0: 96% ..

MET
ALA
ASP
ILE
LYS
N6
S21
K155

- Chain p:  13% 85%

NET	ALA	ALA	VAL	VAL	LEU	VAL	VAL	VAL	LEU	LEU	LEU	PHE	PHE	LEU	VAL	VAL	ASN	GLU	PHE	SER	SER	ILE	LEU	ARG	SER	PRO	PRO	GLY	SER	SER	VAL	VAL	PHE	ARG	ASN	ASN	GLY	TRP	PRO	PRO	ILE	PRO	ASP	VAL	ALA	ALA	LEU	SER	NET	GLY	PHE	SER	VAL	LYS	GLU	ASP	LEU	SER
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TRP	PRO	PRO	GLY	LEU	ALA	VAL	GLY	ASN	LEU	PHE	HIS	ARG	PRO	ARG	ALA	THR	ILE	MET	VAL	MET	LYS	VAL	GLY	ASP	LYS	LEU	ALA	PRO	GLY	ALA	GLY	SER	VAL	ILE	SER	TYR	PRO	LEU	GLU	ASN	ALA	VAL	PRO	PHE	SER	SER	LEU	ASP	SER	VAL	ALA	ASN	ILE	HIS	SER	PHE	LEU	PHE	SER	ILE	TRP
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GLU	THR	PRO	VAL	VAL	LEU	GLN	LEU	LEU	ALA	ALA	SER	SER	GLU	GLU	GLU	ARG	VAL	TYR	MET	VAL	GLY	LYS	ALA	ALA	ASN	SER	VAL	PHE	GLU	ASP	LEU	VAL	SER	VAL	THR	LEU	ARG	GLN	LEU	ARG	ASN	ASN	LEU	PHE	LEU	ASN	GLN	GLU	ASN	SER	SER	LEU	LEU	LEU	ASN	SER	LEU	PRO	ARG	ASN	ASN	ASN	GLU	VAL
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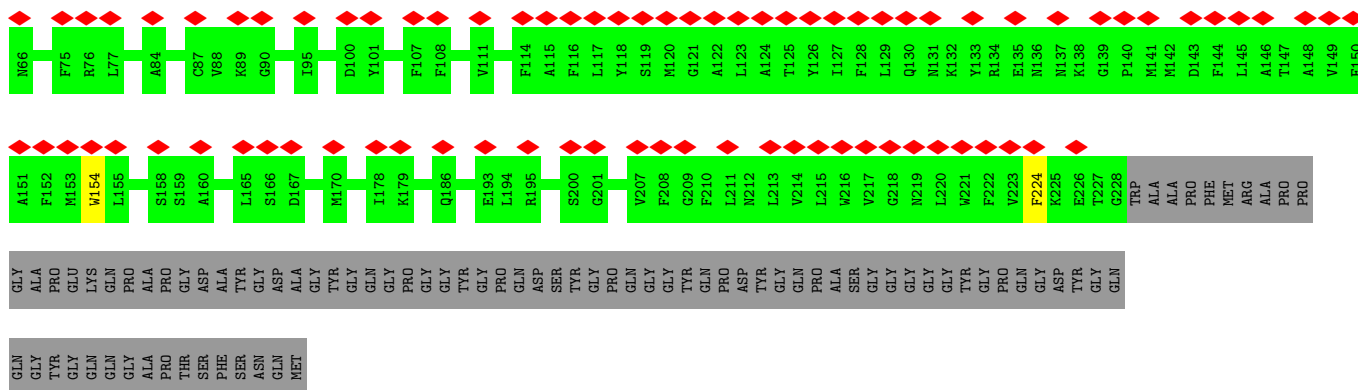
ASP	LEU	LEU	PHE	LEU	SER	GLU	LEU	GLN	VAL	LEU	HIS	ASP	ILE	SER	LEU	LEU	SER	ARG	HIS	LYS	HIS	LEU	ALA	LYS	ASP	HIS	SER	TYR	LEU	PRO	ASP	LEU	GLU	LEU	GLU	ASP	GLY	GLY	LEU	ASP	TYR	GLY	GLY	GLN	GLN	PHE	ARG	ASP	ALA	ALA	LYS	THR
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LEU	VAL	ASP	ALA	LEU	GLN	PHE	LYS	ALA	ASP	ASP	MET	TYR	SER	LEU	GLY	GLY	ASN	ALA	VAL	VAL	GLU	LEU	VAL	THR	VAL	LYS	SER	PHE	ASP	THR	SER	SER	LEU	VAL	VAL	ARG	LYS	SER	SER	ARG	THR	THR	ILE	LEU	LEU	GLU	ALA	LYS	GLN	GLU	ASN	THR	GLN	SER	SER	P590	Y591	N592	N606	V619	V621
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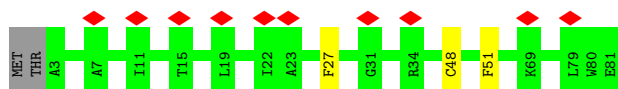
Y638 R639 M640 T641 ASN GLN LYS ILE ARG ILE ASP

- Chain s:  36% 66% 33%

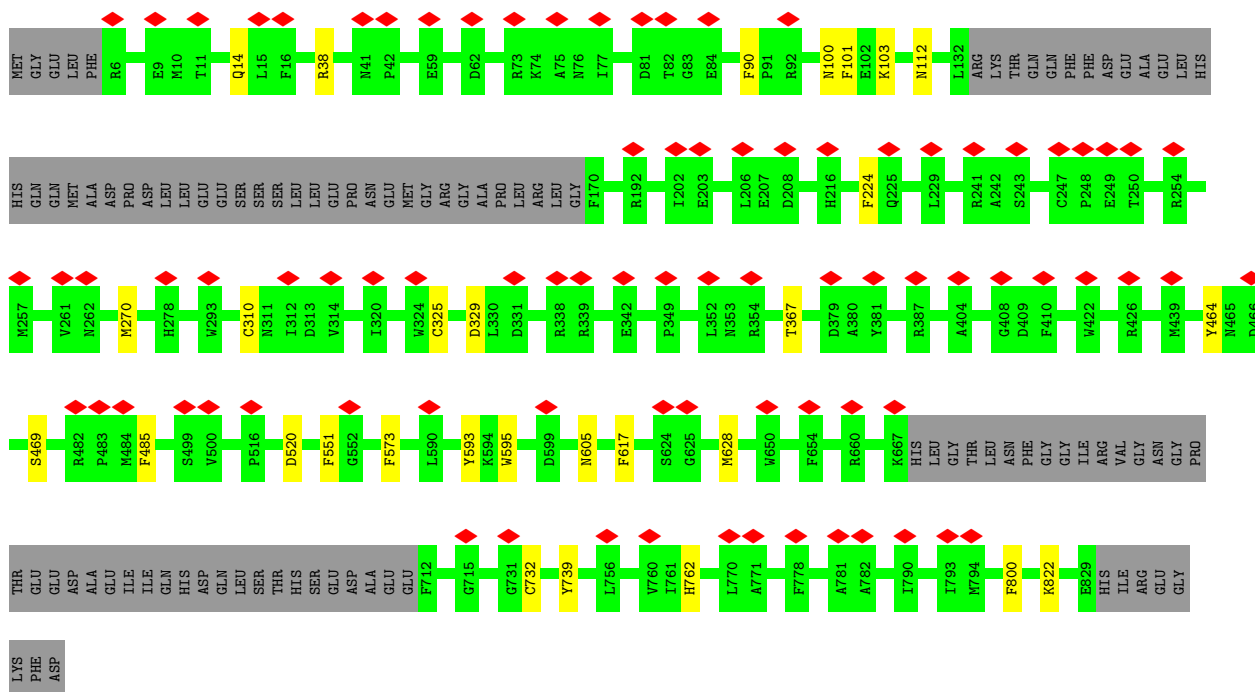
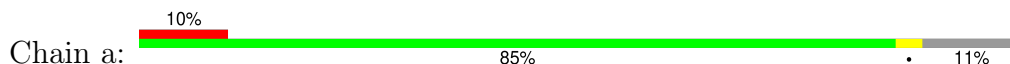
[illegible]



- Molecule 8: V-type proton ATPase subunit e 2



- Molecule 9: V-type proton ATPase 116 kDa subunit a 1



- Molecule 10: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose





- Molecule 11: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:  100%



- Molecule 11: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:  50% 100%



- Molecule 11: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:  100%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	42137	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.960	Depositor
Minimum map value	-1.514	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.087	Depositor
Recommended contour level	0.35	Depositor
Map size (Å)	319.968, 319.968, 319.968	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.111, 1.111, 1.111	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: NAG

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	c	0.33	0/1697	0.63	0/2311
2	b	0.33	0/1537	0.55	0/2088
3	d	0.33	0/2899	0.58	0/3927
4	f	0.46	0/682	0.65	0/926
5	g	0.33	0/1083	0.59	0/1466
5	h	0.35	0/1083	0.60	0/1466
5	i	0.35	0/1083	0.60	0/1466
5	j	0.32	0/1083	0.60	0/1466
5	k	0.32	0/1083	0.60	0/1466
5	l	0.33	0/1083	0.60	0/1466
5	m	0.35	0/1083	0.60	0/1466
5	n	0.35	0/1083	0.60	0/1466
5	o	0.34	0/1083	0.61	0/1466
6	p	0.50	0/446	0.64	0/610
7	s	0.30	0/1716	0.55	0/2327
8	e	0.31	0/662	0.57	0/910
9	a	0.32	0/6195	0.61	0/8382
All	All	0.33	0/25581	0.60	0/34675

There are no bond length outliers.

There are no bond angle outliers.

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	c	1642	0	1561	0	0
2	b	1503	0	1551	0	0
3	d	2833	0	2770	0	0
4	f	666	0	663	0	0
5	g	1068	0	1136	0	0
5	h	1068	0	1136	0	0
5	i	1068	0	1136	0	0
5	j	1068	0	1136	0	0
5	k	1068	0	1136	0	0
5	l	1068	0	1136	0	0
5	m	1068	0	1136	0	0
5	n	1068	0	1136	0	0
5	o	1068	0	1136	0	0
6	p	433	0	432	0	0
7	s	1671	0	1649	0	0
8	e	637	0	652	0	0
9	a	6039	0	6068	0	0
10	A	42	0	37	0	0
11	B	28	0	25	0	0
11	C	28	0	25	0	0
11	D	28	0	25	0	0
12	c	42	0	39	0	0
All	All	25204	0	25721	0	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 5.

There are no clashes within the asymmetric unit.

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	c	201/463 (43%)	174 (87%)	27 (13%)	0	100	100
2	b	201/205 (98%)	195 (97%)	6 (3%)	0	100	100
3	d	348/351 (99%)	330 (95%)	18 (5%)	0	100	100
4	f	84/98 (86%)	73 (87%)	11 (13%)	0	100	100
5	g	148/155 (96%)	142 (96%)	6 (4%)	0	100	100
5	h	148/155 (96%)	144 (97%)	4 (3%)	0	100	100
5	i	148/155 (96%)	146 (99%)	2 (1%)	0	100	100
5	j	148/155 (96%)	146 (99%)	2 (1%)	0	100	100
5	k	148/155 (96%)	144 (97%)	4 (3%)	0	100	100
5	l	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
5	m	148/155 (96%)	146 (99%)	2 (1%)	0	100	100
5	n	148/155 (96%)	144 (97%)	4 (3%)	0	100	100
5	o	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
6	p	50/350 (14%)	44 (88%)	5 (10%)	1 (2%)	6	32
7	s	209/314 (67%)	203 (97%)	6 (3%)	0	100	100
8	e	77/81 (95%)	76 (99%)	1 (1%)	0	100	100
9	a	737/838 (88%)	689 (94%)	48 (6%)	0	100	100
All	All	3239/4095 (79%)	3086 (95%)	152 (5%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	p	631	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	c	180/395 (46%)	169 (94%)	11 (6%)	15	41
2	b	156/158 (99%)	150 (96%)	6 (4%)	28	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	d	305/306 (100%)	296 (97%)	9 (3%)	36	58
4	f	72/83 (87%)	66 (92%)	6 (8%)	9	32
5	g	109/113 (96%)	103 (94%)	6 (6%)	18	43
5	h	109/113 (96%)	106 (97%)	3 (3%)	38	59
5	i	109/113 (96%)	106 (97%)	3 (3%)	38	59
5	j	109/113 (96%)	100 (92%)	9 (8%)	9	32
5	k	109/113 (96%)	104 (95%)	5 (5%)	23	47
5	l	109/113 (96%)	105 (96%)	4 (4%)	29	53
5	m	109/113 (96%)	102 (94%)	7 (6%)	14	39
5	n	109/113 (96%)	100 (92%)	9 (8%)	9	32
5	o	109/113 (96%)	108 (99%)	1 (1%)	75	82
6	p	47/309 (15%)	43 (92%)	4 (8%)	8	31
7	s	180/246 (73%)	175 (97%)	5 (3%)	38	59
8	e	66/68 (97%)	63 (96%)	3 (4%)	23	47
9	a	661/741 (89%)	632 (96%)	29 (4%)	24	48
All	All	2648/3323 (80%)	2528 (96%)	120 (4%)	26	47

5 of 120 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	k	133	LEU
9	a	593	TYR
5	n	20	SER
9	a	573	PHE
9	a	800	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	b	169	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

9 monosaccharides 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
10	NAG	A	1	1,10	14,14,15	1.03	1 (7%)	17,19,21	2.28	9 (52%)
10	NAG	A	2	10	14,14,15	0.65	0	17,19,21	1.53	3 (17%)
10	NAG	A	3	10	14,14,15	0.72	0	17,19,21	1.45	2 (11%)
11	NAG	B	1	1,11	14,14,15	0.74	0	17,19,21	2.03	3 (17%)
11	NAG	B	2	11	14,14,15	0.80	0	17,19,21	1.04	1 (5%)
11	NAG	C	1	1,11	14,14,15	0.71	0	17,19,21	0.96	0
11	NAG	C	2	11	14,14,15	0.75	0	17,19,21	0.85	0
11	NAG	D	1	1,11	14,14,15	1.32	1 (7%)	17,19,21	2.27	7 (41%)
11	NAG	D	2	11	14,14,15	0.73	0	17,19,21	1.12	1 (5%)

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
10	NAG	A	1	1,10	-	1/6/23/26	0/1/1/1
10	NAG	A	2	10	-	0/6/23/26	0/1/1/1
10	NAG	A	3	10	-	3/6/23/26	0/1/1/1
11	NAG	B	1	1,11	-	2/6/23/26	0/1/1/1
11	NAG	B	2	11	-	2/6/23/26	0/1/1/1
11	NAG	C	1	1,11	-	0/6/23/26	0/1/1/1
11	NAG	C	2	11	-	0/6/23/26	0/1/1/1
11	NAG	D	1	1,11	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	NAG	D	2	11	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	D	1	NAG	C1-C2	4.36	1.58	1.52
10	A	1	NAG	C1-C2	3.37	1.56	1.52

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	D	1	NAG	C1-C2-N2	5.54	119.16	110.43
11	B	1	NAG	C2-N2-C7	4.55	129.00	122.90
11	B	1	NAG	O5-C1-C2	-4.47	104.38	111.29
10	A	2	NAG	C1-O5-C5	4.16	117.76	112.19
10	A	3	NAG	C2-N2-C7	4.13	128.44	122.90

There are no chirality outliers.

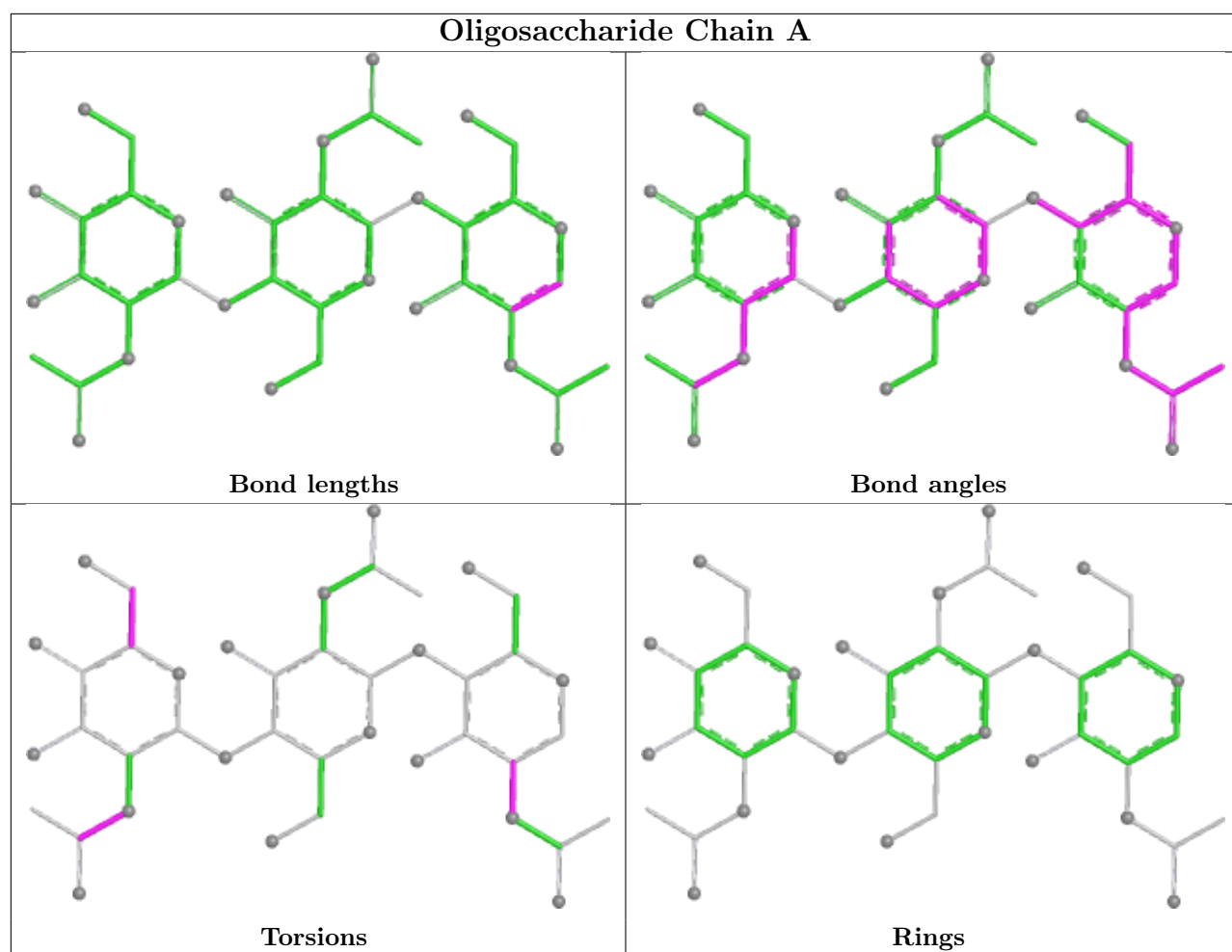
5 of 8 torsion outliers are listed below:

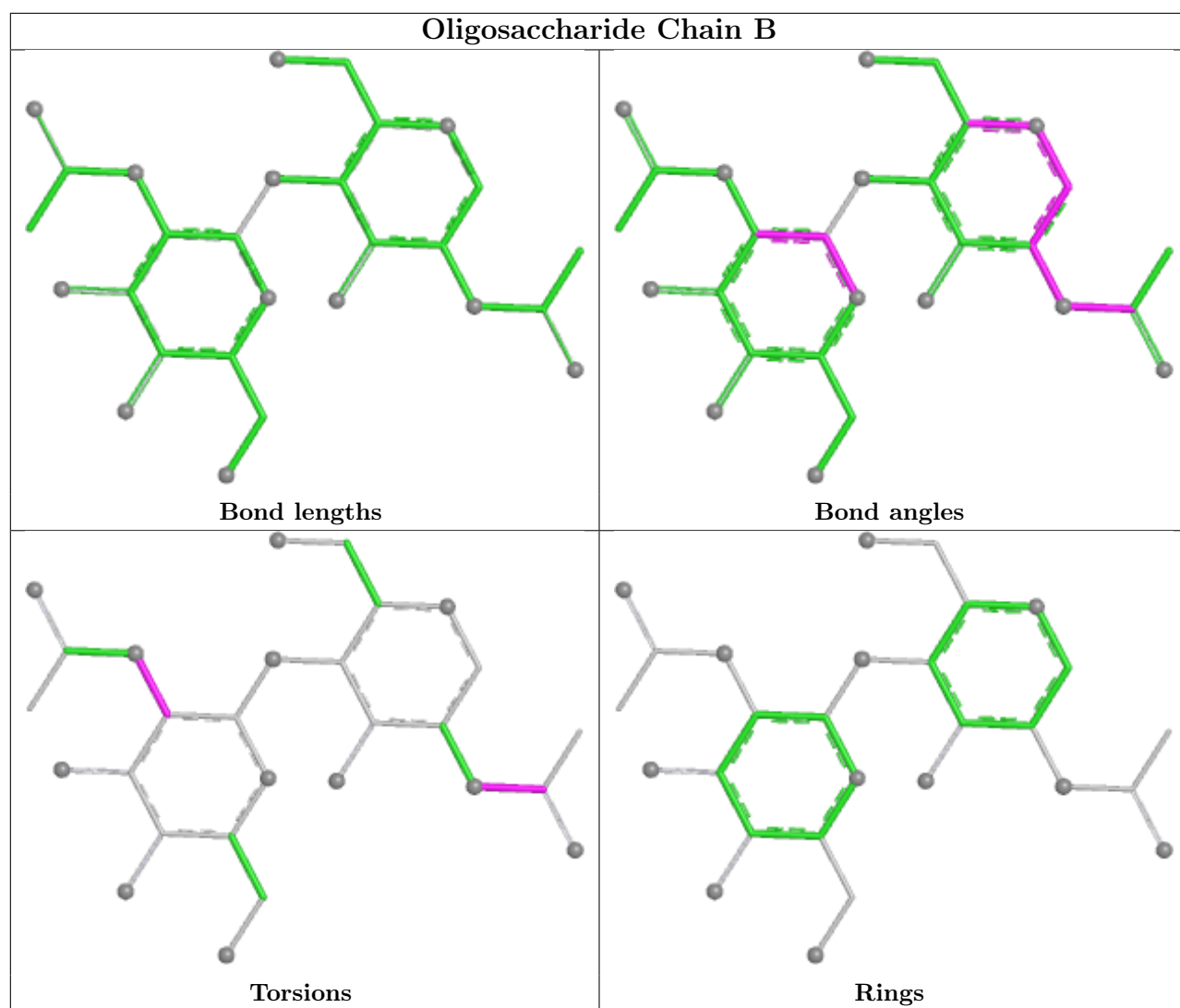
Mol	Chain	Res	Type	Atoms
11	B	2	NAG	C1-C2-N2-C7
10	A	3	NAG	C8-C7-N2-C2
10	A	3	NAG	O7-C7-N2-C2
11	B	1	NAG	C8-C7-N2-C2
11	B	1	NAG	O7-C7-N2-C2

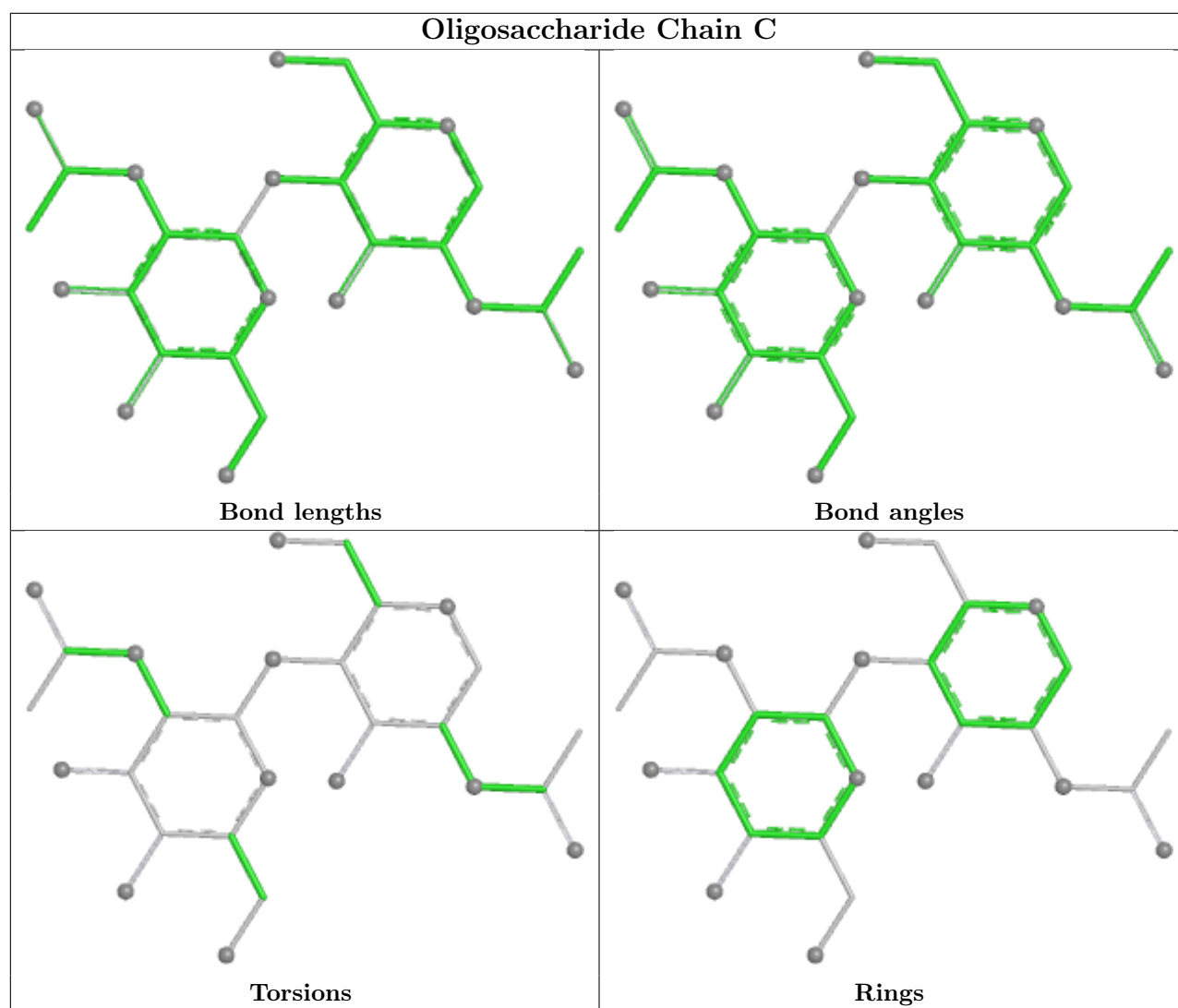
There are no ring outliers.

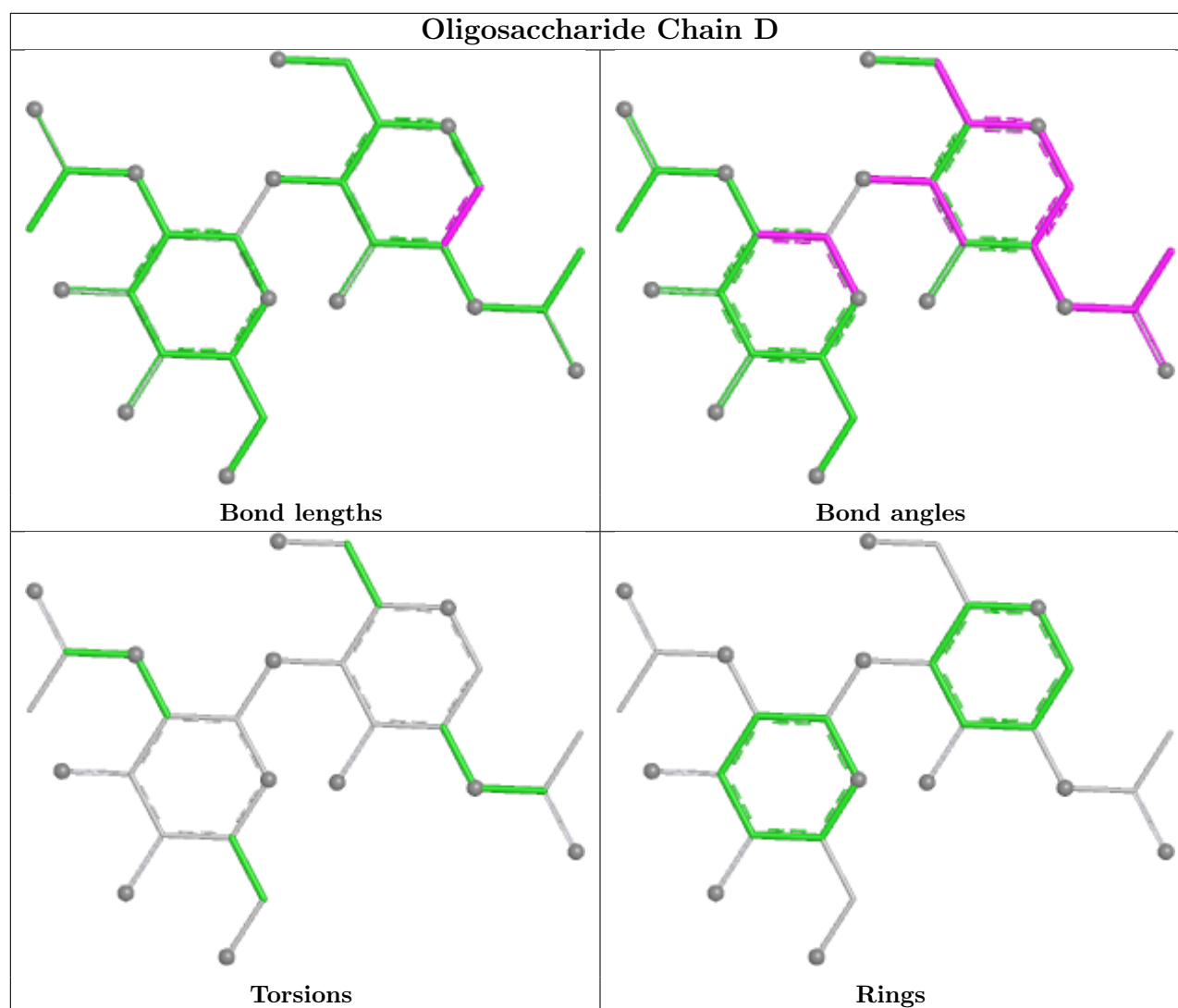
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.









5.6 Ligand geometry [i](#)

3 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	$\# Z > 2$
12	NAG	c	502	1	14,14,15	0.92	1 (7%)	17,19,21	1.51	2 (11%)
12	NAG	c	501	1	14,14,15	0.74	0	17,19,21	0.98	0
12	NAG	c	503	1	14,14,15	0.76	0	17,19,21	1.22	1 (5%)

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
12	NAG	c	502	1	-	0/6/23/26	0/1/1/1
12	NAG	c	501	1	-	0/6/23/26	0/1/1/1
12	NAG	c	503	1	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	c	502	NAG	C1-C2	2.40	1.55	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	c	502	NAG	C1-O5-C5	4.79	118.61	112.19
12	c	503	NAG	O5-C1-C2	-3.21	106.32	111.29
12	c	502	NAG	O5-C1-C2	-2.42	107.54	111.29

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	c	503	NAG	C1-C2-N2-C7
12	c	503	NAG	C3-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

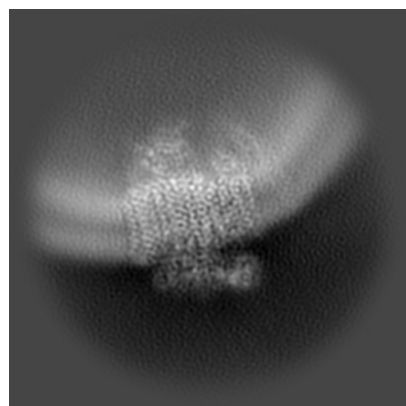
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44846. These allow visual inspection of the internal detail of the map and identification of artifacts.

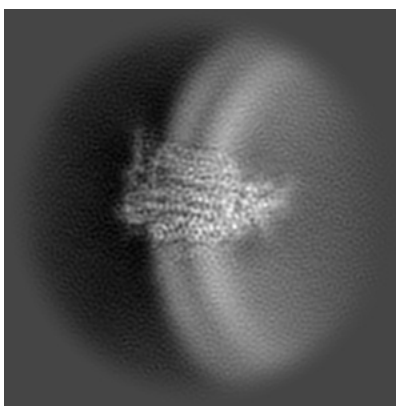
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

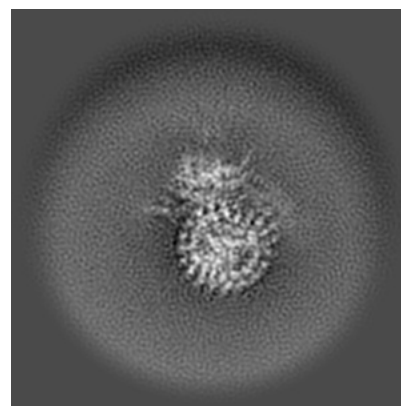
6.1.1 Primary map



X

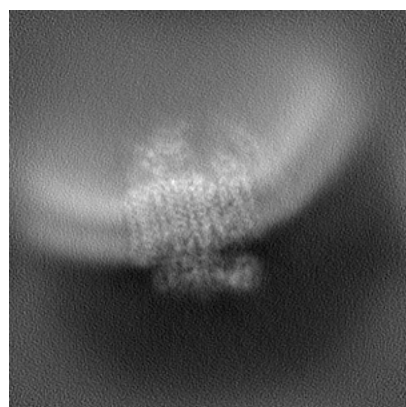


Y

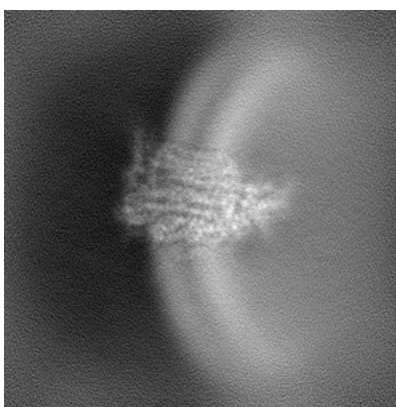


Z

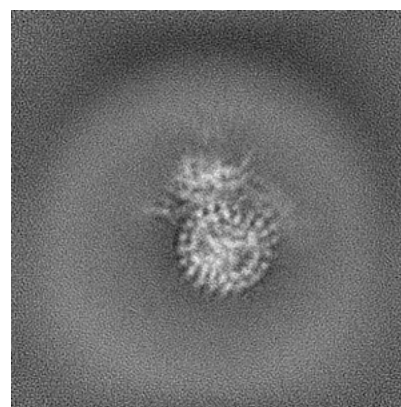
6.1.2 Raw map



X



Y

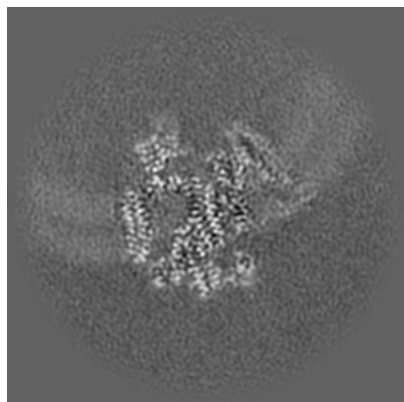


Z

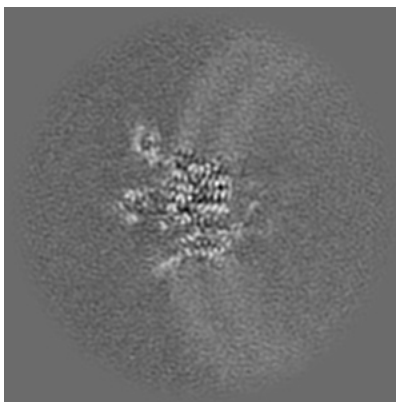
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

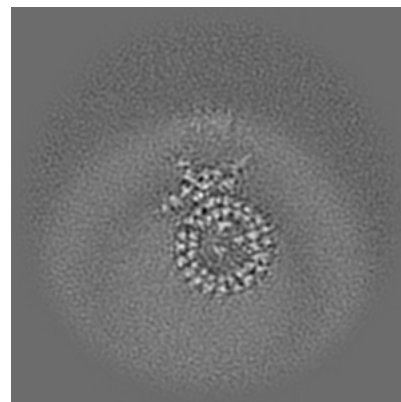
6.2.1 Primary map



X Index: 144

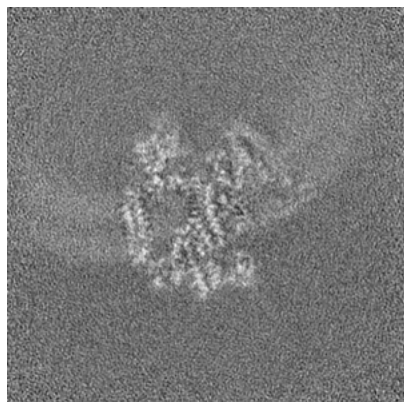


Y Index: 144

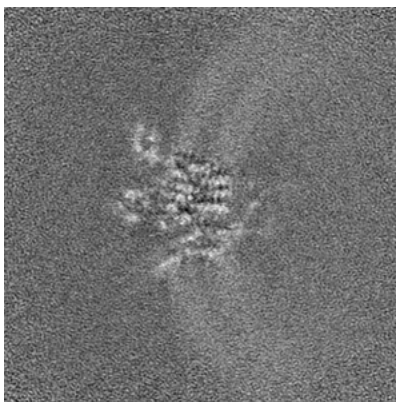


Z Index: 144

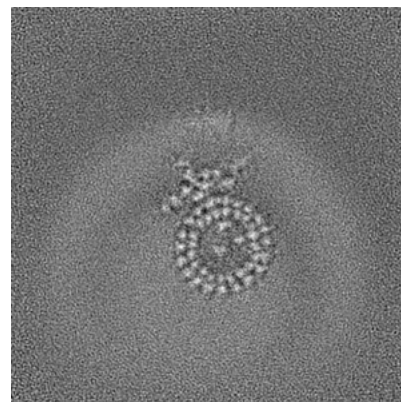
6.2.2 Raw map



X Index: 144



Y Index: 144

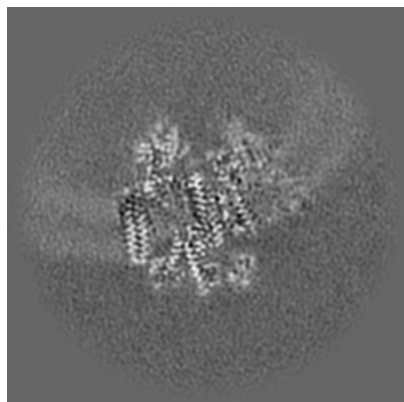


Z Index: 144

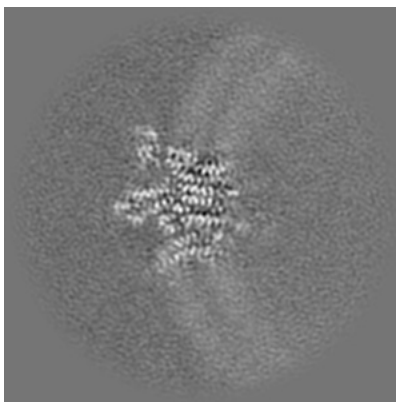
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

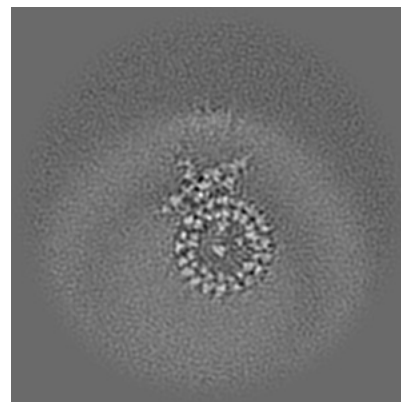
6.3.1 Primary map



X Index: 146

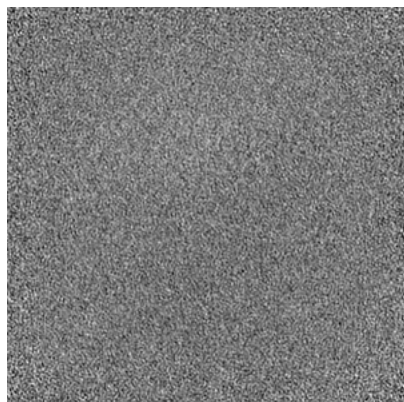


Y Index: 141

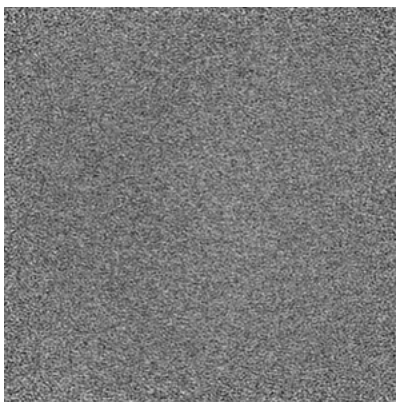


Z Index: 145

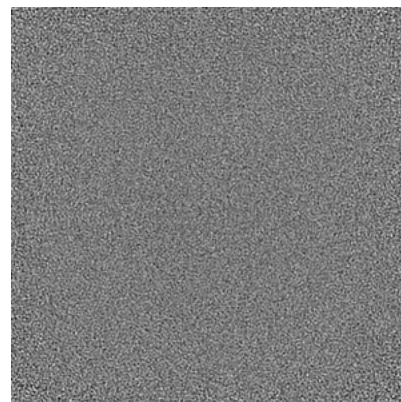
6.3.2 Raw map



X Index: 0



Y Index: 0

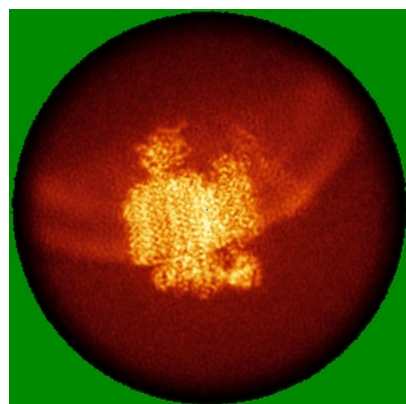


Z Index: 0

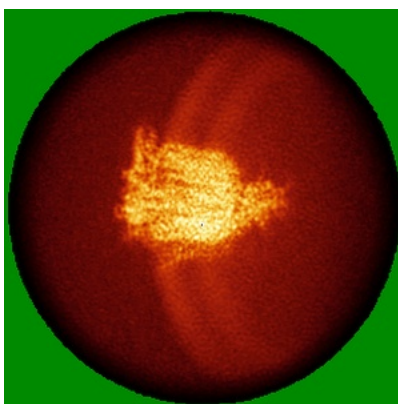
The images above show the largest variance slices of the map in three orthogonal directions.

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

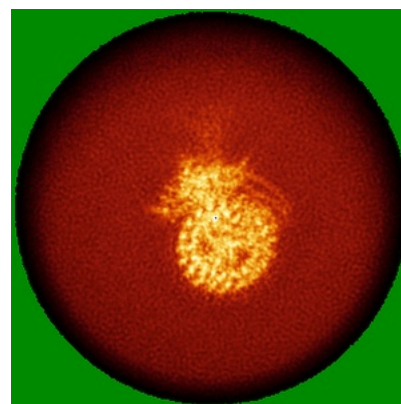
6.4.1 Primary map



X

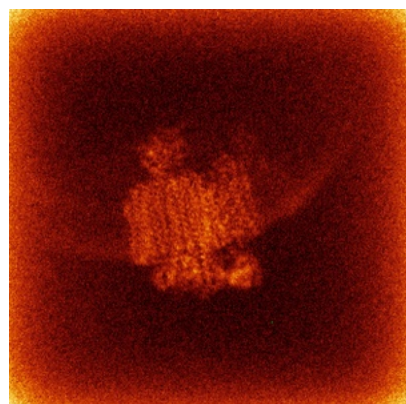


Y

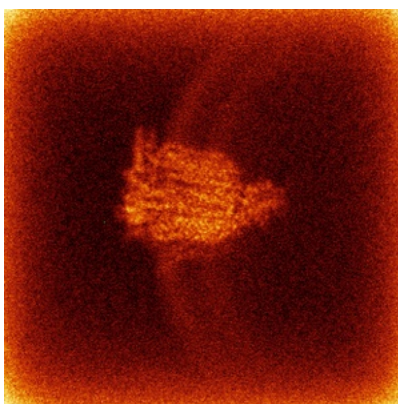


Z

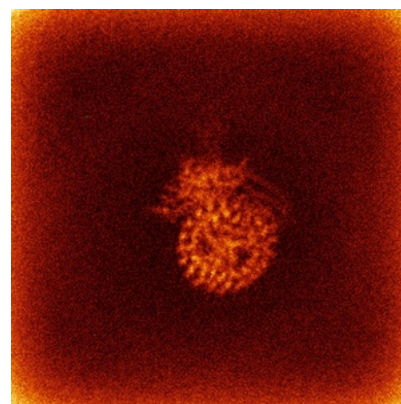
6.4.2 Raw map



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.

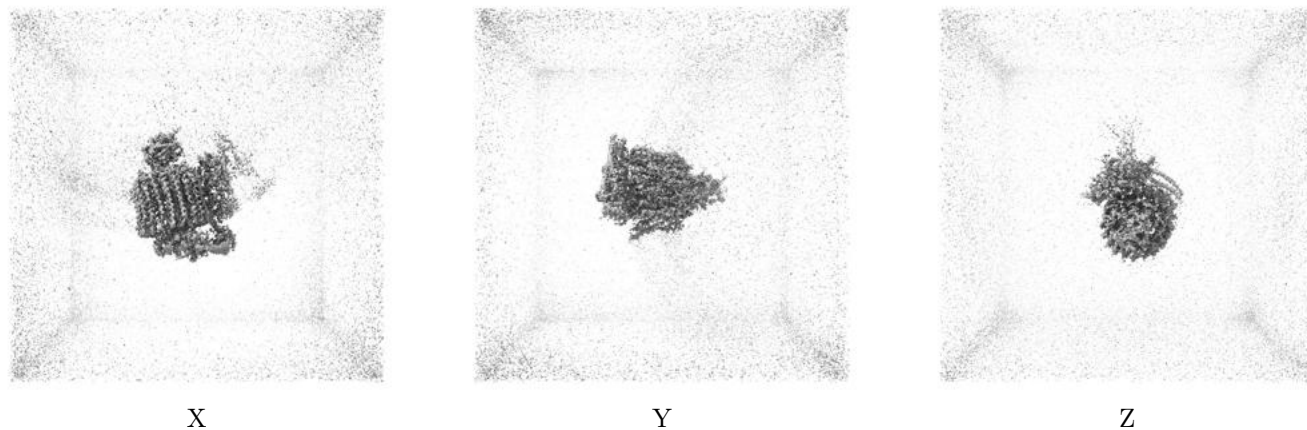
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.35. 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.

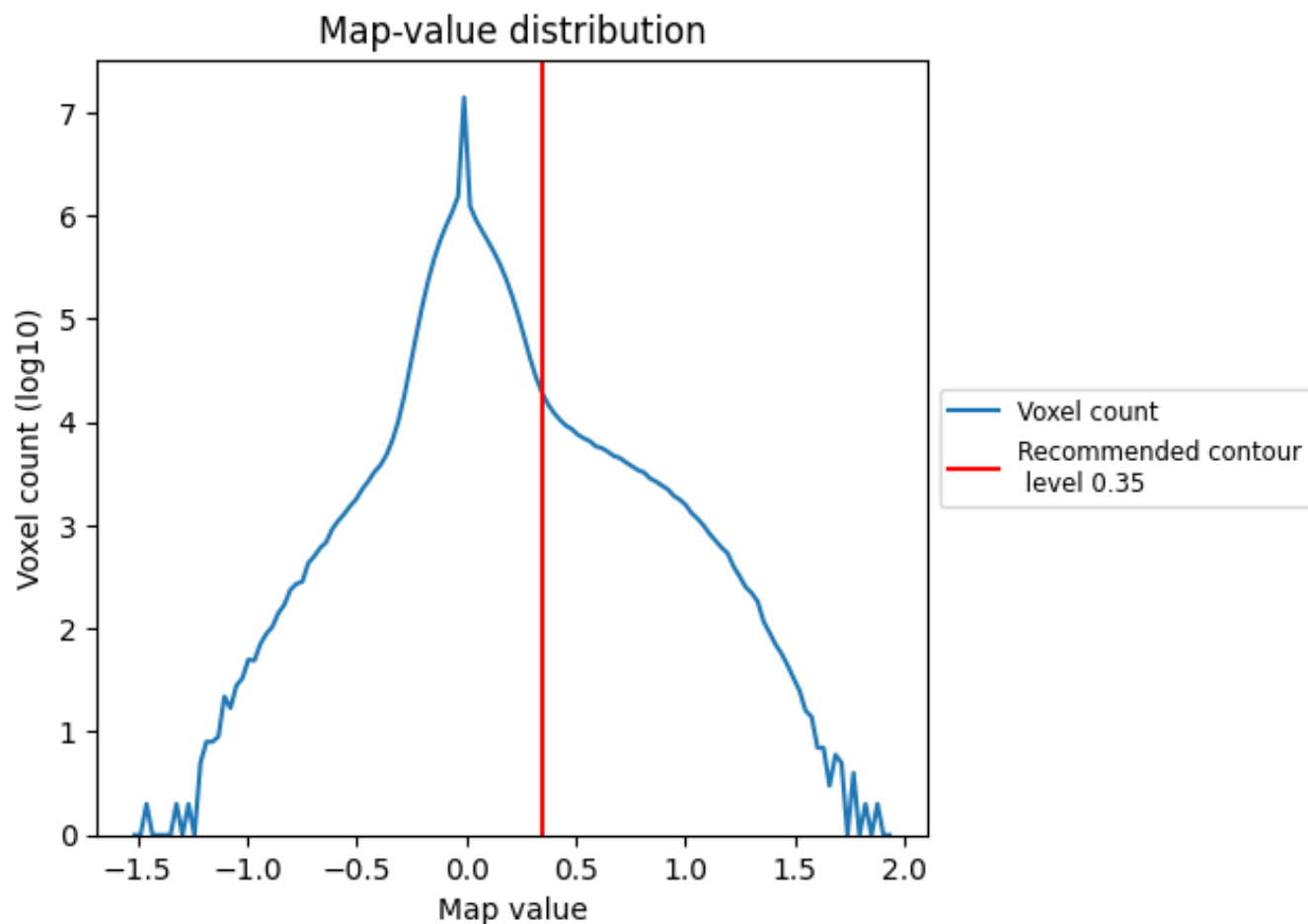
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

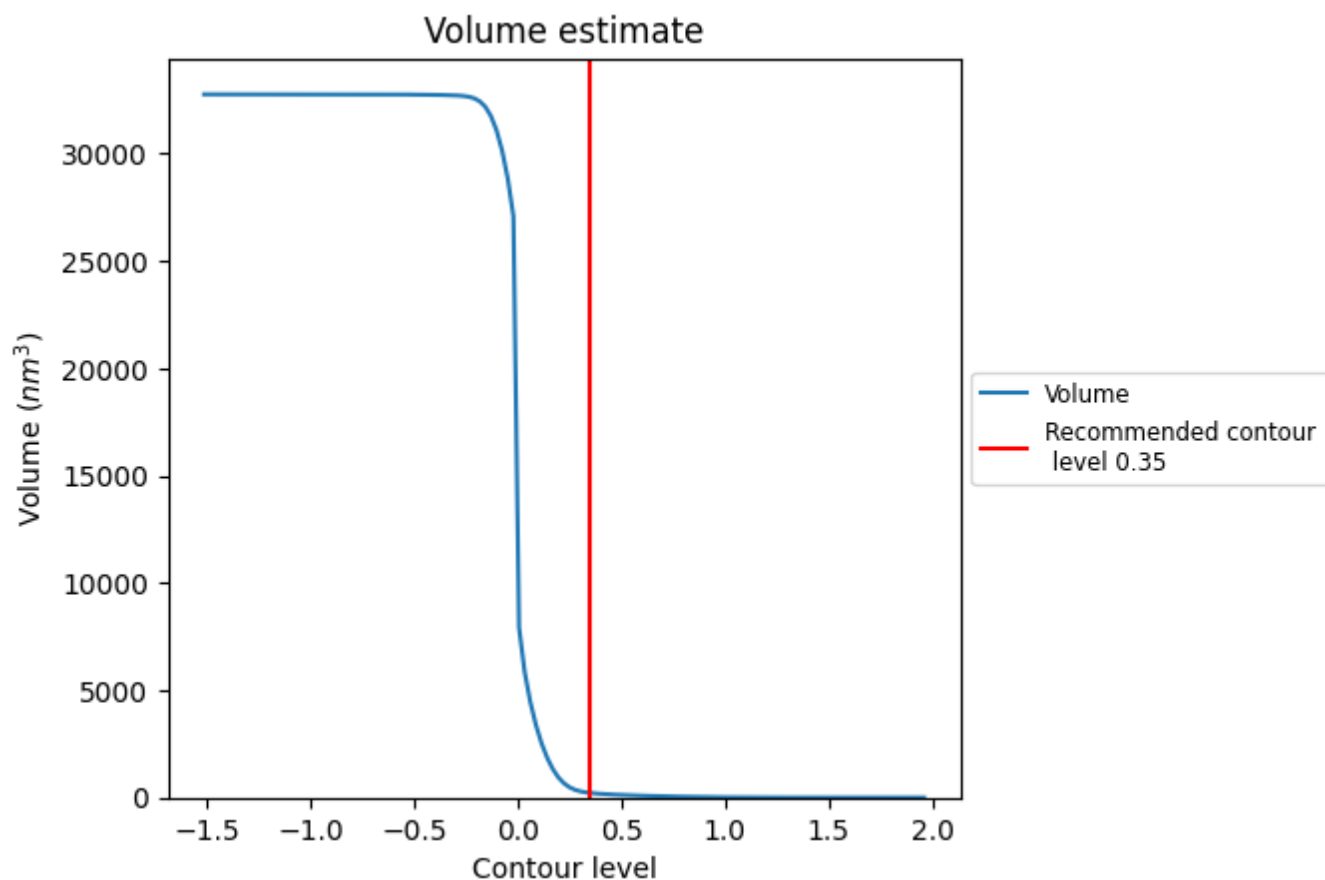
This section contains the results of statistical analysis of the map.

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.

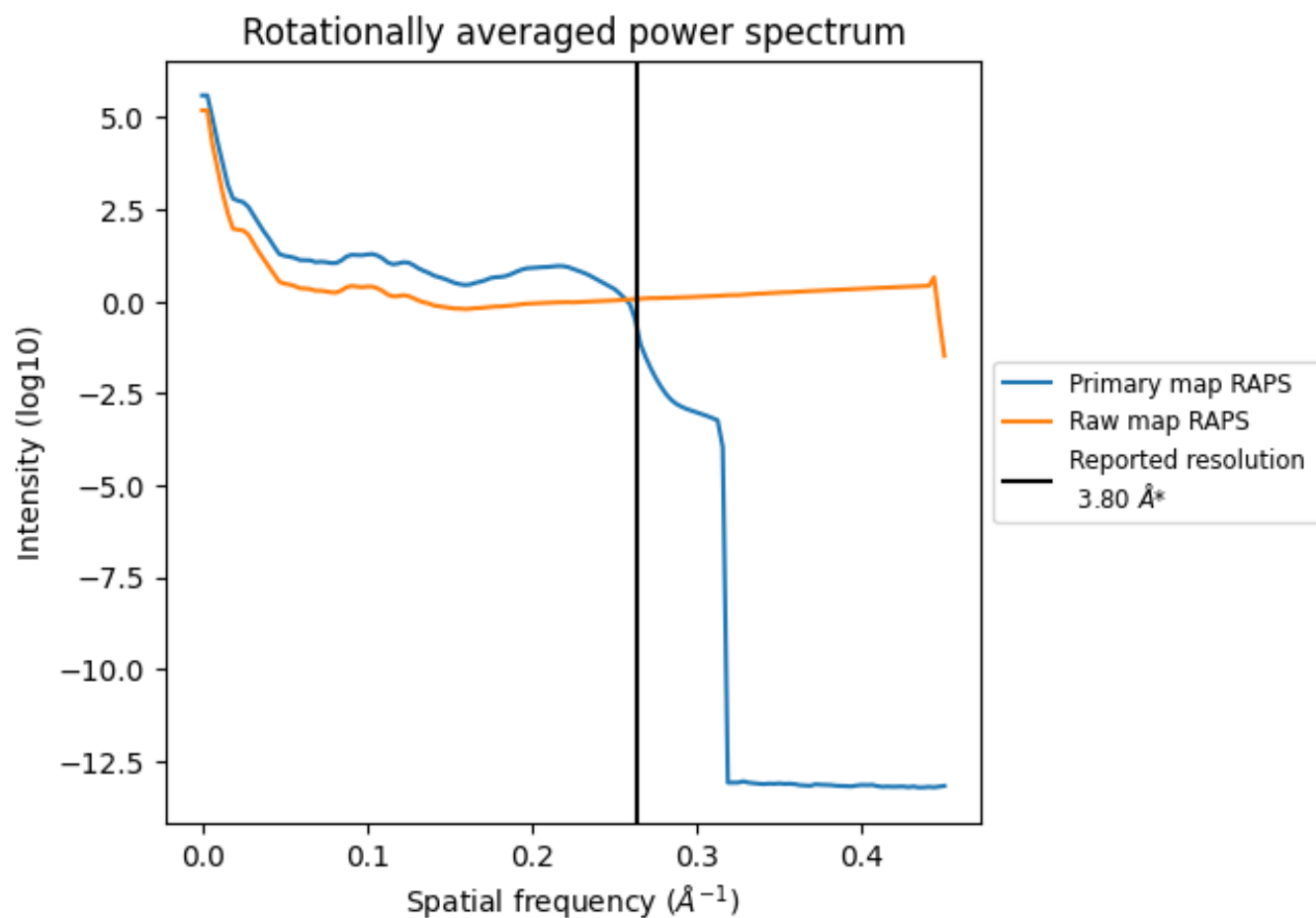
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 216 nm³; this corresponds to an approximate mass of 195 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

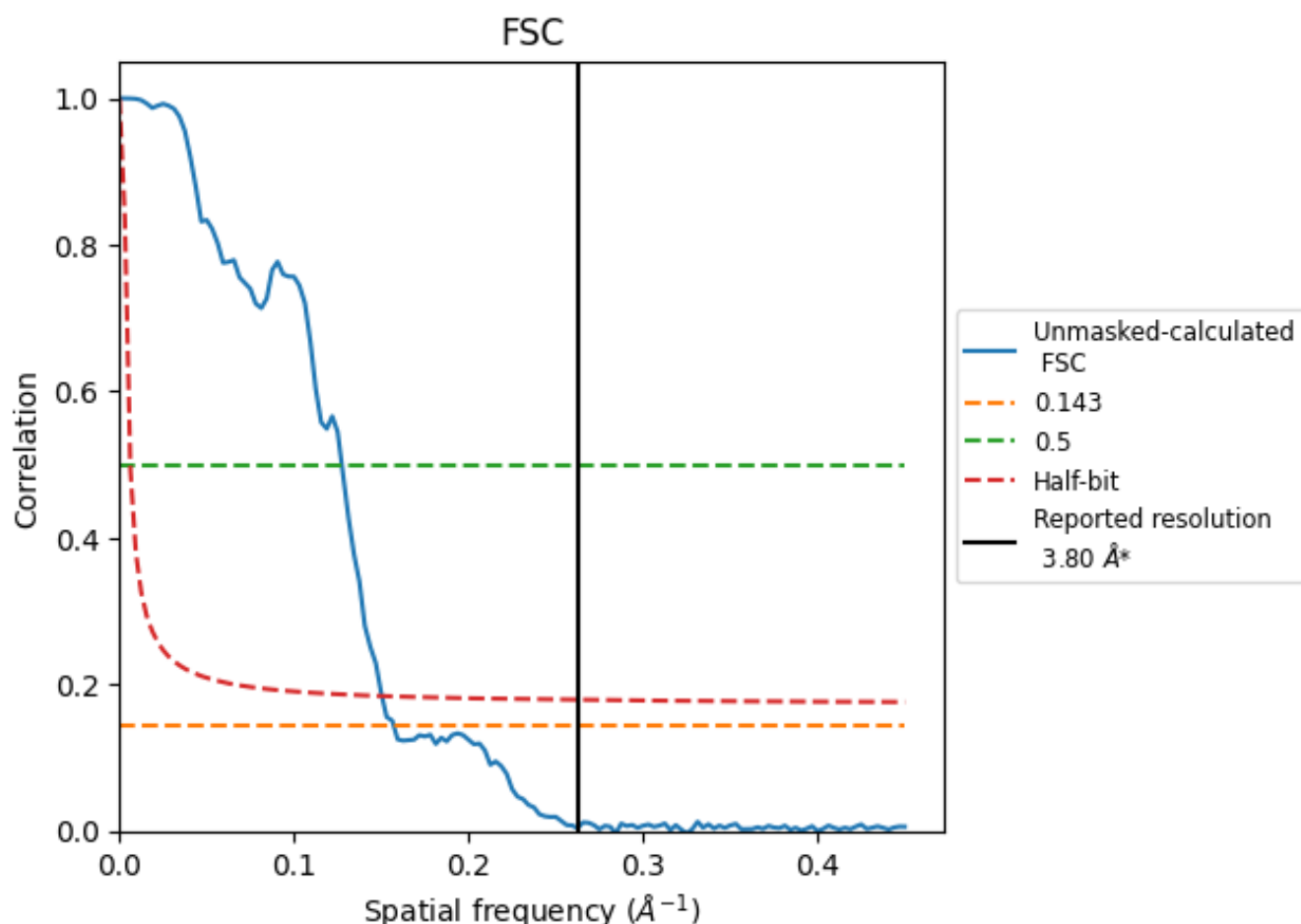


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

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 0.263 \AA^{-1}

8.2 Resolution estimates [i](#)

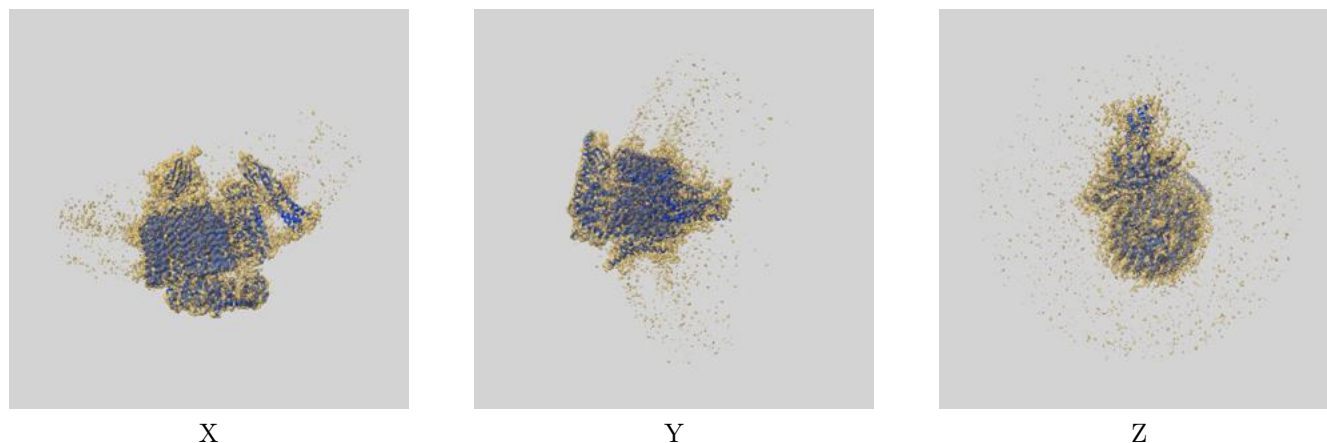
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.37	7.85	6.65

*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 6.37 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

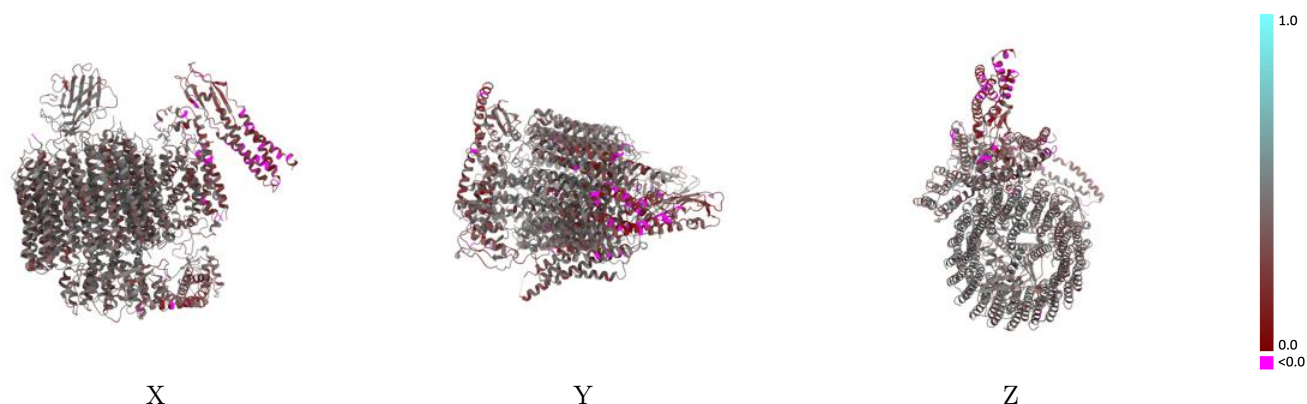
This section contains information regarding the fit between EMDB map EMD-44846 and PDB model 9BRZ. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



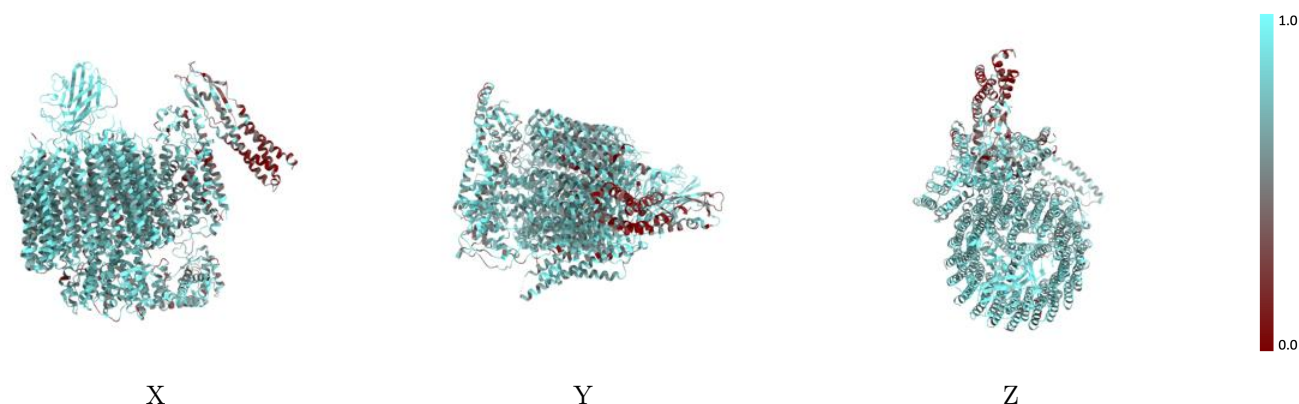
The images above show the 3D surface view of the map at the recommended contour level 0.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



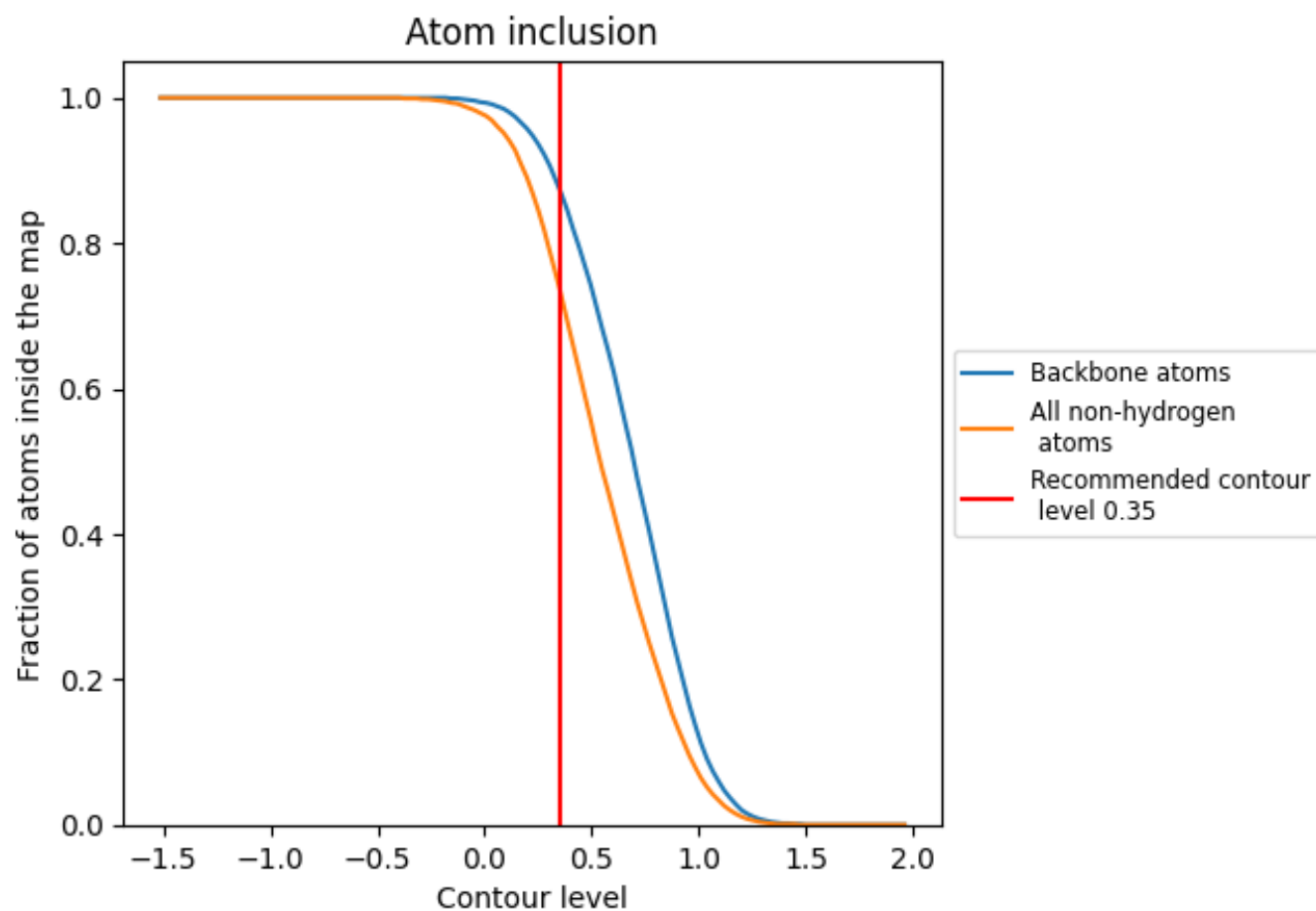
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.35).













































9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 74% 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 (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7370	 0.3850
A	 0.6430	 0.3300
B	 0.6790	 0.3030
C	 0.6070	 0.3510
D	 0.7860	 0.4750
a	 0.6970	 0.3490
b	 0.8190	 0.4520
c	 0.8630	 0.4330
d	 0.7700	 0.4290
e	 0.7110	 0.3430
f	 0.6480	 0.2990
g	 0.8030	 0.4380
h	 0.7740	 0.3950
i	 0.7540	 0.3980
j	 0.7770	 0.3970
k	 0.7900	 0.4150
l	 0.7550	 0.4080
m	 0.7700	 0.4250
n	 0.8190	 0.4440
o	 0.8050	 0.4510
p	 0.8030	 0.4370
s	 0.3860	 0.1760

