



## Full wwPDB EM Validation Report ⓘ

Jul 14, 2024 – 09:07 pm BST

PDB ID : 8BQE  
EMDB ID : EMD-16183  
Title : In situ structure of the Caulobacter crescentus S-layer  
Authors : von Kuegelgen, A.; Bharat, T.  
Deposited on : 2022-11-21  
Resolution : 3.50 Å(reported)

This is a Full wwPDB EM Validation 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.dev92  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.37.1

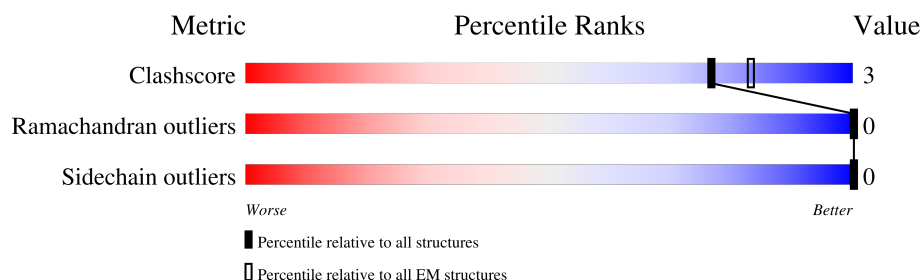
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.50 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	1026	
1	B	1026	
1	C	1026	
1	D	1026	
1	E	1026	
1	F	1026	
2	G	6	
2	H	6	

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Mol	Chain	Length	Quality of chain
2	I	6	<div> <div>33%</div> <div>83%</div> <div>17%</div> </div>
2	J	6	<div> <div>100%</div> <div>100%</div> </div>
2	K	6	<div> <div>33%</div> <div>83%</div> <div>17%</div> </div>
2	L	6	<div> <div>83%</div> <div>100%</div> </div>
2	M	6	<div> <div>50%</div> <div>83%</div> <div>17%</div> </div>
2	N	6	<div> <div>83%</div> <div>100%</div> </div>
2	O	6	<div> <div>33%</div> <div>83%</div> <div>17%</div> </div>
2	P	6	<div> <div>100%</div> <div>100%</div> </div>
2	Q	6	<div> <div>50%</div> <div>83%</div> <div>17%</div> </div>
2	R	6	<div> <div>83%</div> <div>100%</div> </div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 11274 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 S-layer protein rsaA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	242	Total	C	N	O	S	0	0
			1726	1088	281	356	1		
1	C	242	Total	C	N	O	S	0	0
			1726	1088	281	356	1		
1	D	242	Total	C	N	O	S	0	0
			1726	1088	281	356	1		
1	E	242	Total	C	N	O	S	0	0
			1726	1088	281	356	1		
1	F	242	Total	C	N	O	S	0	0
			1726	1088	281	356	1		
1	A	242	Total	C	N	O	S	0	0
			1726	1088	281	356	1		

- Molecule 2 is an oligosaccharide called 4-acetamido-4,6-dideoxy-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-3)-4-acetamido-4,6-dideoxy-alpha-D-mannopyranose-(1-3)-4-acetamido-4,6-dideoxy-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-3)-4-acetamido-4,6-dideoxy-alpha-D-mannopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
2	G	6	Total	C	N	O	0	0
			75	44	4	27		
2	H	6	Total	C	N	O	0	0
			75	44	4	27		
2	I	6	Total	C	N	O	0	0
			75	44	4	27		
2	J	6	Total	C	N	O	0	0
			75	44	4	27		
2	K	6	Total	C	N	O	0	0
			75	44	4	27		

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Mol	Chain	Residues	Atoms				AltConf	Trace
2	L	6	Total 75	C 44	N 4	O 27	0	0
2	M	6	Total 75	C 44	N 4	O 27	0	0
2	N	6	Total 75	C 44	N 4	O 27	0	0
2	O	6	Total 75	C 44	N 4	O 27	0	0
2	P	6	Total 75	C 44	N 4	O 27	0	0
2	Q	6	Total 75	C 44	N 4	O 27	0	0
2	R	6	Total 75	C 44	N 4	O 27	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
3	B	3	Total 3	Ca 3	0
3	C	3	Total 3	Ca 3	0
3	D	3	Total 3	Ca 3	0
3	E	3	Total 3	Ca 3	0
3	F	3	Total 3	Ca 3	0
3	A	3	Total 3	Ca 3	0



ALA THR PHE VAL SER SER GLY ALA ASP ALA VAL ILE LYS LEU THR GLY LEU VAL THR LEU THR THR SER ALA PHE ALA THR GLU VAL LEU THR THR LEU ALA

- Molecule 1: S-layer protein rsaA



MET	A2	L17	A20	P21	D22	Y65	T69	L78	D79	D83	S84	T85	T86	T87	T88	N89	N90	L91	N92	D93	A94	Y95	Y96	S97	S98	N107	G117	A120	A124	T128	L163	S164	R165	Q166	A167	N168	D169	L170	Y171	L172	F175	V176	R177	A178	N179	T180	T182
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P181	F182	T183	A184	A185	A186	D187	L188	D189	A195	T200	D222	D231	M232	M237	T240	P243	SER	SER	GLY	VAL	SER	GLY	SER	THR	THR	LEU	SER	LEU	THR	THR	GLY	THR	ASP	THR	LEU	THR	THR	GLY	THR	ALA	ASN	ALA	ASN	ASP	THR	PHE	THR	VAL	ALA	GLY	GLU	VAL	ALA	GLY	ALA
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ALA	LEU	ASN	THR	THR	SER	GLY	ALA	ALA	ALA	GLN	THR	THR	VAL	VAL	ALA	ALA	GLY	GLN	ASN	ASN	LEU	THR	THR	THR	THR	ALA	ALA	ALA	GLN	ALA	ALA	ASP	ASP	GLY	GLY	GLY	ALA	ALA	ASN	SER	THR	THR	GLY	VAL	THR	THR	SER	GLY	GLY	THR	THR	THR	GLY	VAL	ALA	ALA	ASN	SER	ALA
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ALA	GLY	THR	VAL	SER	SER	ASN	SER	THR	THR	THR	GLY	ALA	ILE	ALA	VAL	THR	GLY	THR	ALA	VAL	VAL	THR	THR	ALA	ASN	ALA	VAL	GLN	THR	THR	THR	THR	THR	LEU	THR	GLN	ALA	ASP	VAL	THR	THR	GLY	THR	ASN	SER	SER	THR	THR	ALA	VAL	VAL	THR	THR	VAL
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GLY THR GLY THR SER SER LEU GLY ILE GLY ARG ALA LEU THR ALA ASN VAL ASN LEU THR THR GLY ILE THR ASP SER GLU ALA ALA ALA ASP ASP GLY PHE THR THR ILE ASN ILE GLY GLY SER THR ALA SER SER SER THR THR

ALA	SER	LEU	VAL	ALA	ALA	ASP	THR	THR	LEU	ASN	ILE	SER	GLY	ASP	ALA	ALA	ARG	VAL	THR	THR	THR	SER	HIS	THR	ALA	ALA	ALA	LEU	THR	THR	GLY	ILE	THR	THR	VAL	THR	THR	ASN	SER	SER	VAL	VAL	GLY	GLY	ALA	ALA	THR	THR	GLY	LEU	VAL	VAL	PHE	THR	GLY	GLY	ALA	ALA	ALA	ASP	SER
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ILE	LEU	LEU	GLY	ALA	THR	THR	LYS	ALA	ALA	ILE	VAL	MET	GLY	GLY	ASP	ASP	THR	VAL	THR	LEU	ALA	ALA	GLY	GLY	SER	SER	THR	LEU	GLY	ASN	VAL	VAL	GLY	GLY	ASP	GLY	THR	ASP	VAL	VAL	VAL	ASN	ALA	LEU	GLY	SER	SER	PHE	SER	ALA	ASP	PRO	PHE	GLY	GLY	PHE	GLU
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THR	ARG	VAL	ALA	GLY	ALA	ALA	GLN	GLY	SER	HIS	ASN	ALA	ALA	ASN	PHE	THR	ALA	GLN	LEU	GLY	LEU	GLY	ALA	THR	THR	PHE	THR	THR	THR	ASN	VAL	VAL	VAL	ASN	GLY	GLY	LEU	THR	VAL	LEU	LEU	ALA	ALA	ALA	PRO	THR	GLY	THR	THR	THR	VAL	THR	LEU	ALA	ASN	ALA	ALA	THR	GLY
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THR	SER	ASP	PHE	ASN	LEU	THR	LEU	SER	SER	ALA	ALA	GLY	THR	VAL	ALA	LEU	ALA	GLY	VAL	GLU	THR	THR	VAL	ASN	ASN	ILE	ALA	ALA	THR	THR	ASP	HIS	VAL	ASP	THR	LEU	THR	LEU	LEU	GLN	ALA	THR	SER	ALA	LYS	SER	ILE	VAL	VAL	THR	GLY	ASN	ALA
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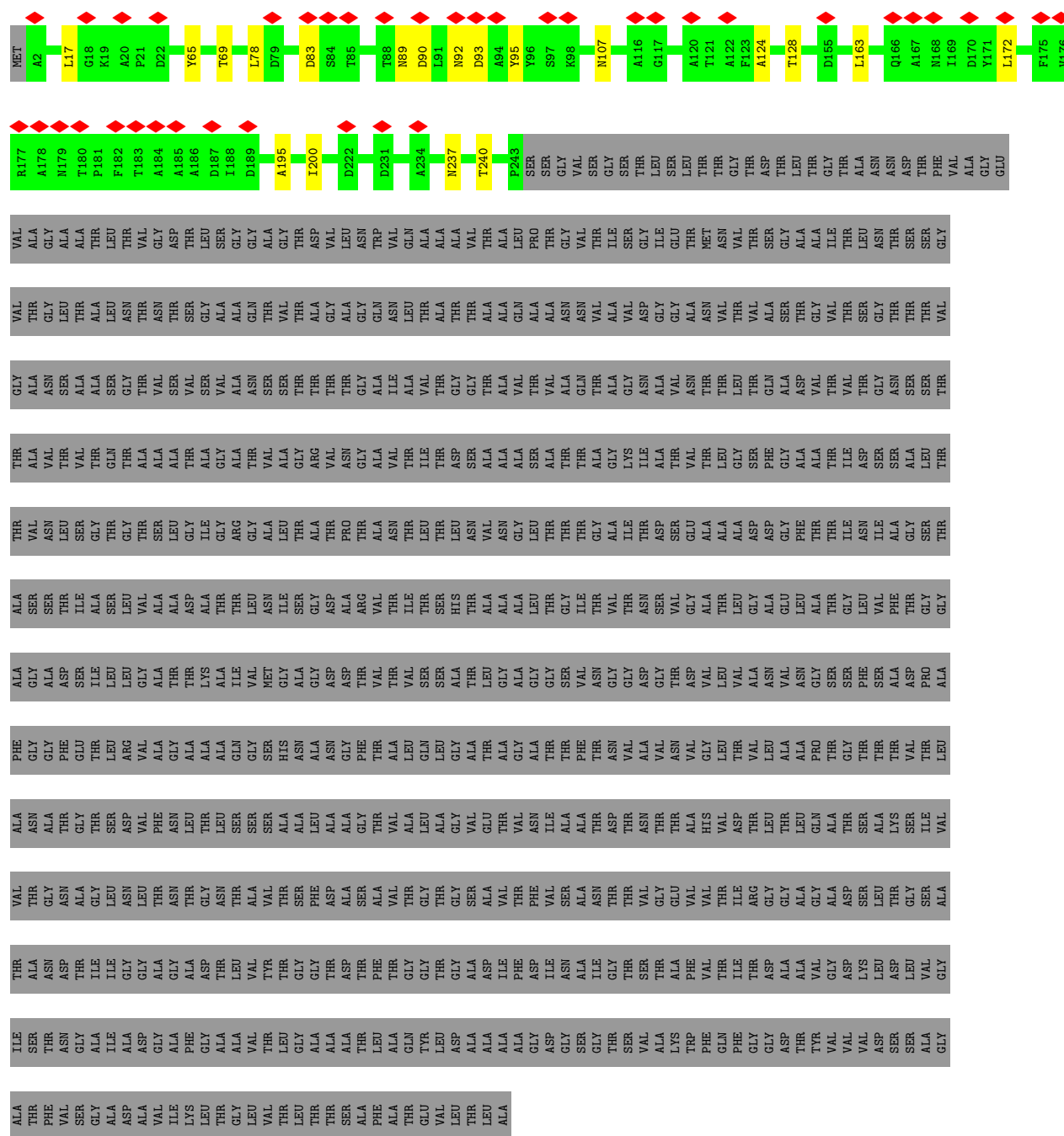
[illegible][illegible]

ALA	ILE	ALA	ALA	ASP	GLY	ALA	PHE	GLY	ALA	ALA	ALA	ALA	VAL	THR	THR	LEU	GLY	ALA	ALA	ALA	ALA	ALA	THR	THR	LEU	LEU	GLN	TYR	LEU	ASP	ASP	GLY	SER	GLY	THR	THR	SER	SER	VAL	VAL	ALA	ALA	LYS	TRP	PHE	PHE	GLN	PHE	GLY	GLY	ASP	THR	THR	TYR	VAL	VAL	ASP	VAL	SER	SER	ALA	ALA	GLY	GLY	PHE	THR	PHE	VAL	SER
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GLY  
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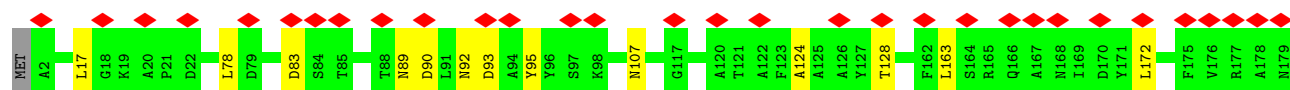
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Chain D:  22% 76%

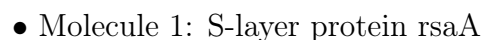


• Molecule 1: S-layer protein rsaA

Chain E:  22% 76%



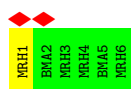
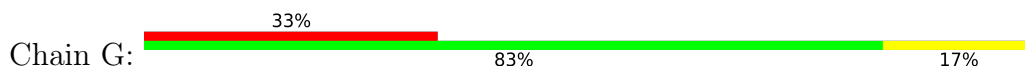


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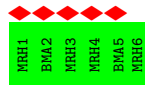
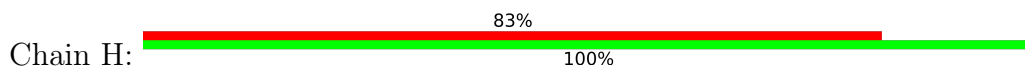


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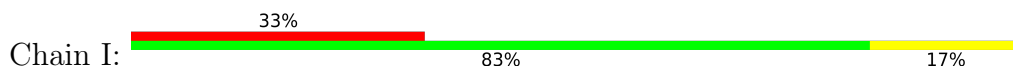
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- Molecule 2: 4-acetamido-4,6-dideoxy-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-3)-4-acetamido-4,6-dideoxy-alpha-D-mannopyranose-(1-3)-4-acetamido-4,6-dideoxy-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-3)-4-acetamido-4,6-dideoxy-alpha-D-mannopyranose

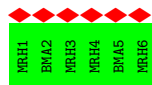


- Molecule 2: 4-acetamido-4,6-dideoxy-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-3)-4-acetamido-4,6-dideoxy-alpha-D-mannopyranose-(1-3)-4-acetamido-4,6-dideoxy-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-3)-4-acetamido-4,6-dideoxy-alpha-D-mannopyranose

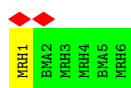
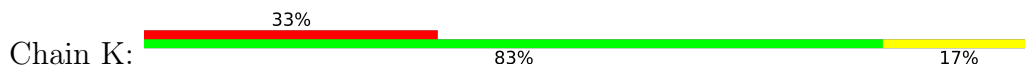




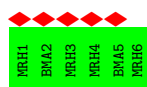
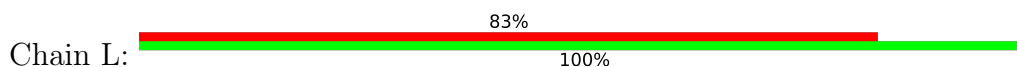
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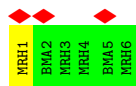
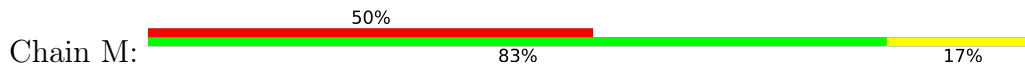
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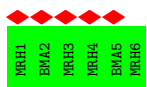
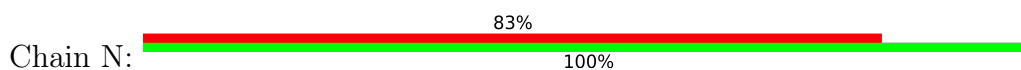
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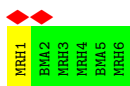
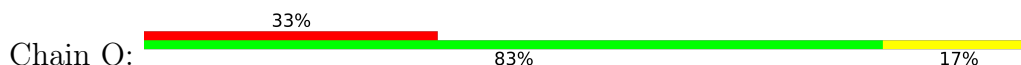
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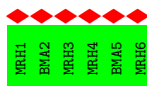
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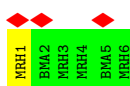
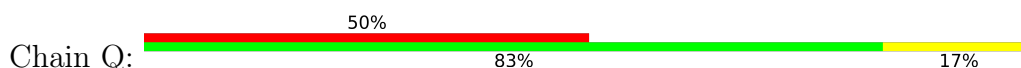
- Molecule 2: 4-acetamido-4,6-dideoxy-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-3)-4-acetamido-4,6-dideoxy-alpha-D-mannopyranose-(1-3)-4-acetamido-4,6-dideoxy-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-3)-4-acetamido-4,6-dideoxy-alpha-D-mannopyranose



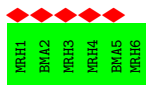
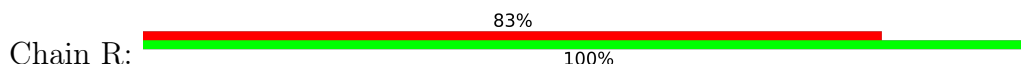
- Molecule 2: 4-acetamido-4,6-dideoxy-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-3)-4-acetamido-4,6-dideoxy-alpha-D-mannopyranose-(1-3)-4-acetamido-4,6-dideoxy-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-3)-4-acetamido-4,6-dideoxy-alpha-D-mannopyranose



- Molecule 2: 4-acetamido-4,6-dideoxy-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-3)-4-acetamido-4,6-dideoxy-alpha-D-mannopyranose-(1-3)-4-acetamido-4,6-dideoxy-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-3)-4-acetamido-4,6-dideoxy-alpha-D-mannopyranose



- Molecule 2: 4-acetamido-4,6-dideoxy-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-3)-4-acetamido-4,6-dideoxy-alpha-D-mannopyranose-(1-3)-4-acetamido-4,6-dideoxy-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-3)-4-acetamido-4,6-dideoxy-alpha-D-mannopyranose



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C6	Depositor
Number of subtomograms used	42990	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; PseudoSubtomograms as described in Zivanov 2022 ( <a href="https://www.biorxiv.org/content/10.1101/2022.02.28.482229v2.abstract">https://www.biorxiv.org/content/10.1101/2022.02.28.482229v2.abstract</a> )	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	140	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.145	Depositor
Minimum map value	-1.449	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.109	Depositor
Recommended contour level	0.54716	Depositor
Map size (Å)	216.0, 216.0, 216.0	wwPDB
Map dimensions	160, 160, 160	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.35, 1.35, 1.35	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: CA, BMA, MRH

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	0.24	0/1752	0.39	0/2407
1	B	0.24	0/1752	0.39	0/2407
1	C	0.24	0/1752	0.39	0/2407
1	D	0.24	0/1752	0.39	0/2407
1	E	0.24	0/1752	0.39	0/2407
1	F	0.24	0/1752	0.39	0/2407
All	All	0.24	0/10512	0.39	0/14442

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	A	1726	0	1684	11	0
1	B	1726	0	1684	11	0
1	C	1726	0	1684	11	0
1	D	1726	0	1684	11	0
1	E	1726	0	1684	10	0
1	F	1726	0	1684	11	0
2	G	75	0	18	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	75	0	18	0	0
2	I	75	0	18	2	0
2	J	75	0	18	0	0
2	K	75	0	18	1	0
2	L	75	0	18	0	0
2	M	75	0	18	1	0
2	N	75	0	18	0	0
2	O	75	0	18	1	0
2	P	75	0	18	0	0
2	Q	75	0	18	1	0
2	R	75	0	18	0	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
3	C	3	0	0	0	0
3	D	3	0	0	0	0
3	E	3	0	0	0	0
3	F	3	0	0	0	0
All	All	11274	0	10320	65	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 3.

All (65) 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)
1:D:83:ASP:HB2	1:D:92:ASN:HD21	1.60	0.67
1:B:83:ASP:HB2	1:B:92:ASN:HD21	1.59	0.67
1:E:83:ASP:HB2	1:E:92:ASN:HD21	1.59	0.67
1:F:83:ASP:HB2	1:F:92:ASN:HD21	1.59	0.66
1:A:83:ASP:HB2	1:A:92:ASN:HD21	1.60	0.66
1:C:83:ASP:HB2	1:C:92:ASN:HD21	1.59	0.66
1:F:124:ALA:O	1:F:128:THR:OG1	2.16	0.63
1:B:124:ALA:O	1:B:128:THR:OG1	2.16	0.63
1:A:124:ALA:O	1:A:128:THR:OG1	2.16	0.63
1:C:124:ALA:O	1:C:128:THR:OG1	2.16	0.61
1:D:124:ALA:O	1:D:128:THR:OG1	2.16	0.59
1:E:124:ALA:O	1:E:128:THR:OG1	2.16	0.57
1:E:172:LEU:HD22	1:E:195:ALA:HB1	1.92	0.52
1:F:172:LEU:HD22	1:F:195:ALA:HB1	1.92	0.51
1:D:172:LEU:HD22	1:D:195:ALA:HB1	1.93	0.51
1:C:172:LEU:HD22	1:C:195:ALA:HB1	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:172:LEU:HD22	1:A:195:ALA:HB1	1.93	0.51
1:B:172:LEU:HD22	1:B:195:ALA:HB1	1.92	0.50
1:B:237:ASN:HB3	1:B:240:THR:HG22	1.94	0.50
1:C:237:ASN:HB3	1:C:240:THR:HG22	1.94	0.49
1:A:237:ASN:HB3	1:A:240:THR:HG22	1.94	0.49
1:E:237:ASN:HB3	1:E:240:THR:HG22	1.94	0.49
1:F:237:ASN:HB3	1:F:240:THR:HG22	1.94	0.49
1:E:107:ASN:ND2	2:K:1:MRH:O7	2.46	0.48
1:F:107:ASN:ND2	2:O:1:MRH:O7	2.46	0.48
1:B:107:ASN:ND2	2:G:1:MRH:O7	2.46	0.48
1:C:107:ASN:ND2	2:I:1:MRH:O7	2.46	0.48
1:D:237:ASN:HB3	1:D:240:THR:HG22	1.94	0.48
1:A:107:ASN:ND2	2:Q:1:MRH:O7	2.46	0.47
1:D:107:ASN:ND2	2:M:1:MRH:O7	2.46	0.47
1:D:90:ASP:OD1	1:D:93:ASP:HB2	2.15	0.46
1:C:90:ASP:OD1	1:C:93:ASP:HB2	2.15	0.46
1:E:90:ASP:OD1	1:E:93:ASP:HB2	2.15	0.46
1:B:65:TYR:O	1:B:69:THR:OG1	2.32	0.46
1:A:90:ASP:OD1	1:A:93:ASP:HB2	2.15	0.46
1:B:90:ASP:OD1	1:B:93:ASP:HB2	2.15	0.45
1:F:90:ASP:OD1	1:F:93:ASP:HB2	2.15	0.45
1:A:83:ASP:HB2	1:A:92:ASN:ND2	2.31	0.44
1:B:163:LEU:HD13	1:B:200:ILE:HG12	2.00	0.44
1:D:65:TYR:O	1:D:69:THR:OG1	2.32	0.44
1:C:89:ASN:HB3	1:C:95:TYR:CD2	2.53	0.44
1:E:17:LEU:HD11	1:E:78:LEU:HB3	2.00	0.43
1:F:163:LEU:HD13	1:F:200:ILE:HG12	2.00	0.43
1:A:163:LEU:HD13	1:A:200:ILE:HG12	2.00	0.43
1:D:89:ASN:HB3	1:D:95:TYR:CD2	2.53	0.43
1:F:17:LEU:HD11	1:F:78:LEU:HB3	2.01	0.43
1:F:89:ASN:HB3	1:F:95:TYR:CD2	2.53	0.43
1:C:95:TYR:OH	2:I:1:MRH:O2	2.24	0.43
1:D:163:LEU:HD13	1:D:200:ILE:HG12	2.00	0.43
1:E:163:LEU:HD13	1:E:200:ILE:HG12	2.00	0.43
1:A:17:LEU:HD11	1:A:78:LEU:HB3	2.00	0.43
1:D:17:LEU:HD11	1:D:78:LEU:HB3	2.00	0.43
1:B:17:LEU:HD11	1:B:78:LEU:HB3	2.00	0.43
1:C:17:LEU:HD11	1:C:78:LEU:HB3	2.01	0.43
1:C:163:LEU:HD13	1:C:200:ILE:HG12	2.00	0.43
1:E:89:ASN:HB3	1:E:95:TYR:CD2	2.53	0.43
1:A:89:ASN:HB3	1:A:95:TYR:CD2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:83:ASP:HB2	1:F:92:ASN:ND2	2.31	0.42
1:B:89:ASN:HB3	1:B:95:TYR:CD2	2.53	0.42
1:C:65:TYR:O	1:C:69:THR:OG1	2.32	0.42
1:D:83:ASP:HB2	1:D:92:ASN:ND2	2.31	0.42
1:B:83:ASP:HB2	1:B:92:ASN:ND2	2.31	0.41
1:F:238:LEU:HD23	1:F:238:LEU:HA	1.89	0.41
1:E:83:ASP:HB2	1:E:92:ASN:ND2	2.31	0.40
1:A:65:TYR:O	1:A:69:THR:OG1	2.32	0.40

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	240/1026 (23%)	237 (99%)	3 (1%)	0	100	100
1	B	240/1026 (23%)	237 (99%)	3 (1%)	0	100	100
1	C	240/1026 (23%)	237 (99%)	3 (1%)	0	100	100
1	D	240/1026 (23%)	237 (99%)	3 (1%)	0	100	100
1	E	240/1026 (23%)	237 (99%)	3 (1%)	0	100	100
1	F	240/1026 (23%)	237 (99%)	3 (1%)	0	100	100
All	All	1440/6156 (23%)	1422 (99%)	18 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 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	168/699 (24%)	168 (100%)	0	100	100
1	B	168/699 (24%)	168 (100%)	0	100	100
1	C	168/699 (24%)	168 (100%)	0	100	100
1	D	168/699 (24%)	168 (100%)	0	100	100
1	E	168/699 (24%)	168 (100%)	0	100	100
1	F	168/699 (24%)	168 (100%)	0	100	100
All	All	1008/4194 (24%)	1008 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	103	ASN
1	C	103	ASN
1	D	103	ASN
1	E	103	ASN
1	F	103	ASN
1	A	103	ASN

### 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 ⓘ

72 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	$\# Z  > 2$
2	MRH	G	1	2	13,14,14	0.21	0	16,20,20	0.27	0
2	BMA	G	2	2	11,11,12	0.60	0	15,15,17	0.78	0
2	MRH	G	3	2	12,13,14	0.17	0	15,18,20	0.39	0
2	MRH	G	4	2	12,13,14	0.17	0	15,18,20	0.39	0
2	BMA	G	5	2	11,11,12	0.61	0	15,15,17	0.78	0
2	MRH	G	6	2	12,13,14	0.17	0	15,18,20	0.37	0
2	MRH	H	1	2	13,14,14	0.23	0	16,20,20	0.27	0
2	BMA	H	2	2	11,11,12	0.61	0	15,15,17	0.77	0
2	MRH	H	3	2	12,13,14	0.16	0	15,18,20	0.38	0
2	MRH	H	4	2	12,13,14	0.17	0	15,18,20	0.37	0
2	BMA	H	5	2	11,11,12	0.63	0	15,15,17	0.77	0
2	MRH	H	6	2	12,13,14	0.17	0	15,18,20	0.41	0
2	MRH	I	1	2	13,14,14	0.21	0	16,20,20	0.26	0
2	BMA	I	2	2	11,11,12	0.60	0	15,15,17	0.79	0
2	MRH	I	3	2	12,13,14	0.16	0	15,18,20	0.37	0
2	MRH	I	4	2	12,13,14	0.17	0	15,18,20	0.39	0
2	BMA	I	5	2	11,11,12	0.60	0	15,15,17	0.78	0
2	MRH	I	6	2	12,13,14	0.16	0	15,18,20	0.38	0
2	MRH	J	1	2	13,14,14	0.22	0	16,20,20	0.27	0
2	BMA	J	2	2	11,11,12	0.60	0	15,15,17	0.77	0
2	MRH	J	3	2	12,13,14	0.17	0	15,18,20	0.39	0
2	MRH	J	4	2	12,13,14	0.16	0	15,18,20	0.38	0
2	BMA	J	5	2	11,11,12	0.62	0	15,15,17	0.78	0
2	MRH	J	6	2	12,13,14	0.16	0	15,18,20	0.40	0
2	MRH	K	1	2	13,14,14	0.21	0	16,20,20	0.27	0
2	BMA	K	2	2	11,11,12	0.61	0	15,15,17	0.79	0
2	MRH	K	3	2	12,13,14	0.16	0	15,18,20	0.38	0
2	MRH	K	4	2	12,13,14	0.17	0	15,18,20	0.39	0
2	BMA	K	5	2	11,11,12	0.60	0	15,15,17	0.78	0
2	MRH	K	6	2	12,13,14	0.18	0	15,18,20	0.38	0
2	MRH	L	1	2	13,14,14	0.22	0	16,20,20	0.27	0
2	BMA	L	2	2	11,11,12	0.60	0	15,15,17	0.78	0
2	MRH	L	3	2	12,13,14	0.17	0	15,18,20	0.38	0
2	MRH	L	4	2	12,13,14	0.16	0	15,18,20	0.37	0
2	BMA	L	5	2	11,11,12	0.63	0	15,15,17	0.77	0
2	MRH	L	6	2	12,13,14	0.17	0	15,18,20	0.41	0
2	MRH	M	1	2	13,14,14	0.21	0	16,20,20	0.27	0
2	BMA	M	2	2	11,11,12	0.61	0	15,15,17	0.79	0
2	MRH	M	3	2	12,13,14	0.17	0	15,18,20	0.38	0
2	MRH	M	4	2	12,13,14	0.17	0	15,18,20	0.37	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	BMA	M	5	2	11,11,12	0.59	0	15,15,17	0.78	0
2	MRH	M	6	2	12,13,14	0.16	0	15,18,20	0.37	0
2	MRH	N	1	2	13,14,14	0.22	0	16,20,20	0.27	0
2	BMA	N	2	2	11,11,12	0.62	0	15,15,17	0.77	0
2	MRH	N	3	2	12,13,14	0.17	0	15,18,20	0.39	0
2	MRH	N	4	2	12,13,14	0.16	0	15,18,20	0.38	0
2	BMA	N	5	2	11,11,12	0.62	0	15,15,17	0.78	0
2	MRH	N	6	2	12,13,14	0.17	0	15,18,20	0.39	0
2	MRH	O	1	2	13,14,14	0.21	0	16,20,20	0.27	0
2	BMA	O	2	2	11,11,12	0.60	0	15,15,17	0.79	0
2	MRH	O	3	2	12,13,14	0.16	0	15,18,20	0.38	0
2	MRH	O	4	2	12,13,14	0.17	0	15,18,20	0.39	0
2	BMA	O	5	2	11,11,12	0.60	0	15,15,17	0.77	0
2	MRH	O	6	2	12,13,14	0.16	0	15,18,20	0.37	0
2	MRH	P	1	2	13,14,14	0.22	0	16,20,20	0.27	0
2	BMA	P	2	2	11,11,12	0.60	0	15,15,17	0.77	0
2	MRH	P	3	2	12,13,14	0.17	0	15,18,20	0.39	0
2	MRH	P	4	2	12,13,14	0.16	0	15,18,20	0.38	0
2	BMA	P	5	2	11,11,12	0.62	0	15,15,17	0.78	0
2	MRH	P	6	2	12,13,14	0.16	0	15,18,20	0.40	0
2	MRH	Q	1	2	13,14,14	0.21	0	16,20,20	0.27	0
2	BMA	Q	2	2	11,11,12	0.61	0	15,15,17	0.79	0
2	MRH	Q	3	2	12,13,14	0.16	0	15,18,20	0.39	0
2	MRH	Q	4	2	12,13,14	0.17	0	15,18,20	0.37	0
2	BMA	Q	5	2	11,11,12	0.60	0	15,15,17	0.79	0
2	MRH	Q	6	2	12,13,14	0.16	0	15,18,20	0.37	0
2	MRH	R	1	2	13,14,14	0.22	0	16,20,20	0.27	0
2	BMA	R	2	2	11,11,12	0.62	0	15,15,17	0.77	0
2	MRH	R	3	2	12,13,14	0.17	0	15,18,20	0.39	0
2	MRH	R	4	2	12,13,14	0.16	0	15,18,20	0.38	0
2	BMA	R	5	2	11,11,12	0.62	0	15,15,17	0.78	0
2	MRH	R	6	2	12,13,14	0.17	0	15,18,20	0.39	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
2	MRH	G	1	2	-	0/4/24/24	0/1/1/1
2	BMA	G	2	2	-	0/2/19/22	0/1/1/1
2	MRH	G	3	2	-	0/4/21/24	0/1/1/1
2	MRH	G	4	2	-	0/4/21/24	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BMA	G	5	2	-	0/2/19/22	0/1/1/1
2	MRH	G	6	2	-	0/4/21/24	0/1/1/1
2	MRH	H	1	2	-	2/4/24/24	0/1/1/1
2	BMA	H	2	2	-	0/2/19/22	0/1/1/1
2	MRH	H	3	2	-	0/4/21/24	0/1/1/1
2	MRH	H	4	2	-	0/4/21/24	0/1/1/1
2	BMA	H	5	2	-	1/2/19/22	0/1/1/1
2	MRH	H	6	2	-	0/4/21/24	0/1/1/1
2	MRH	I	1	2	-	0/4/24/24	0/1/1/1
2	BMA	I	2	2	-	0/2/19/22	0/1/1/1
2	MRH	I	3	2	-	0/4/21/24	0/1/1/1
2	MRH	I	4	2	-	0/4/21/24	0/1/1/1
2	BMA	I	5	2	-	0/2/19/22	0/1/1/1
2	MRH	I	6	2	-	0/4/21/24	0/1/1/1
2	MRH	J	1	2	-	2/4/24/24	0/1/1/1
2	BMA	J	2	2	-	0/2/19/22	0/1/1/1
2	MRH	J	3	2	-	0/4/21/24	0/1/1/1
2	MRH	J	4	2	-	0/4/21/24	0/1/1/1
2	BMA	J	5	2	-	1/2/19/22	0/1/1/1
2	MRH	J	6	2	-	0/4/21/24	0/1/1/1
2	MRH	K	1	2	-	0/4/24/24	0/1/1/1
2	BMA	K	2	2	-	0/2/19/22	0/1/1/1
2	MRH	K	3	2	-	0/4/21/24	0/1/1/1
2	MRH	K	4	2	-	0/4/21/24	0/1/1/1
2	BMA	K	5	2	-	0/2/19/22	0/1/1/1
2	MRH	K	6	2	-	0/4/21/24	0/1/1/1
2	MRH	L	1	2	-	2/4/24/24	0/1/1/1
2	BMA	L	2	2	-	0/2/19/22	0/1/1/1
2	MRH	L	3	2	-	0/4/21/24	0/1/1/1
2	MRH	L	4	2	-	0/4/21/24	0/1/1/1
2	BMA	L	5	2	-	1/2/19/22	0/1/1/1
2	MRH	L	6	2	-	0/4/21/24	0/1/1/1
2	MRH	M	1	2	-	0/4/24/24	0/1/1/1
2	BMA	M	2	2	-	0/2/19/22	0/1/1/1
2	MRH	M	3	2	-	0/4/21/24	0/1/1/1
2	MRH	M	4	2	-	0/4/21/24	0/1/1/1
2	BMA	M	5	2	-	0/2/19/22	0/1/1/1
2	MRH	M	6	2	-	0/4/21/24	0/1/1/1
2	MRH	N	1	2	-	2/4/24/24	0/1/1/1
2	BMA	N	2	2	-	0/2/19/22	0/1/1/1
2	MRH	N	3	2	-	0/4/21/24	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MRH	N	4	2	-	0/4/21/24	0/1/1/1
2	BMA	N	5	2	-	1/2/19/22	0/1/1/1
2	MRH	N	6	2	-	0/4/21/24	0/1/1/1
2	MRH	O	1	2	-	0/4/24/24	0/1/1/1
2	BMA	O	2	2	-	0/2/19/22	0/1/1/1
2	MRH	O	3	2	-	0/4/21/24	0/1/1/1
2	MRH	O	4	2	-	0/4/21/24	0/1/1/1
2	BMA	O	5	2	-	0/2/19/22	0/1/1/1
2	MRH	O	6	2	-	0/4/21/24	0/1/1/1
2	MRH	P	1	2	-	2/4/24/24	0/1/1/1
2	BMA	P	2	2	-	0/2/19/22	0/1/1/1
2	MRH	P	3	2	-	0/4/21/24	0/1/1/1
2	MRH	P	4	2	-	0/4/21/24	0/1/1/1
2	BMA	P	5	2	-	1/2/19/22	0/1/1/1
2	MRH	P	6	2	-	0/4/21/24	0/1/1/1
2	MRH	Q	1	2	-	0/4/24/24	0/1/1/1
2	BMA	Q	2	2	-	0/2/19/22	0/1/1/1
2	MRH	Q	3	2	-	0/4/21/24	0/1/1/1
2	MRH	Q	4	2	-	0/4/21/24	0/1/1/1
2	BMA	Q	5	2	-	0/2/19/22	0/1/1/1
2	MRH	Q	6	2	-	0/4/21/24	0/1/1/1
2	MRH	R	1	2	-	2/4/24/24	0/1/1/1
2	BMA	R	2	2	-	0/2/19/22	0/1/1/1
2	MRH	R	3	2	-	0/4/21/24	0/1/1/1
2	MRH	R	4	2	-	0/4/21/24	0/1/1/1
2	BMA	R	5	2	-	1/2/19/22	0/1/1/1
2	MRH	R	6	2	-	0/4/21/24	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	H	1	MRH	C8-C7-N4-C4
2	H	1	MRH	O7-C7-N4-C4
2	J	1	MRH	C8-C7-N4-C4
2	J	1	MRH	O7-C7-N4-C4
2	L	1	MRH	C8-C7-N4-C4
2	L	1	MRH	O7-C7-N4-C4

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Mol	Chain	Res	Type	Atoms
2	N	1	MRH	C8-C7-N4-C4
2	N	1	MRH	O7-C7-N4-C4
2	P	1	MRH	C8-C7-N4-C4
2	P	1	MRH	O7-C7-N4-C4
2	R	1	MRH	C8-C7-N4-C4
2	R	1	MRH	O7-C7-N4-C4
2	H	5	BMA	O5-C5-C6-O6
2	J	5	BMA	O5-C5-C6-O6
2	L	5	BMA	O5-C5-C6-O6
2	N	5	BMA	O5-C5-C6-O6
2	P	5	BMA	O5-C5-C6-O6
2	R	5	BMA	O5-C5-C6-O6

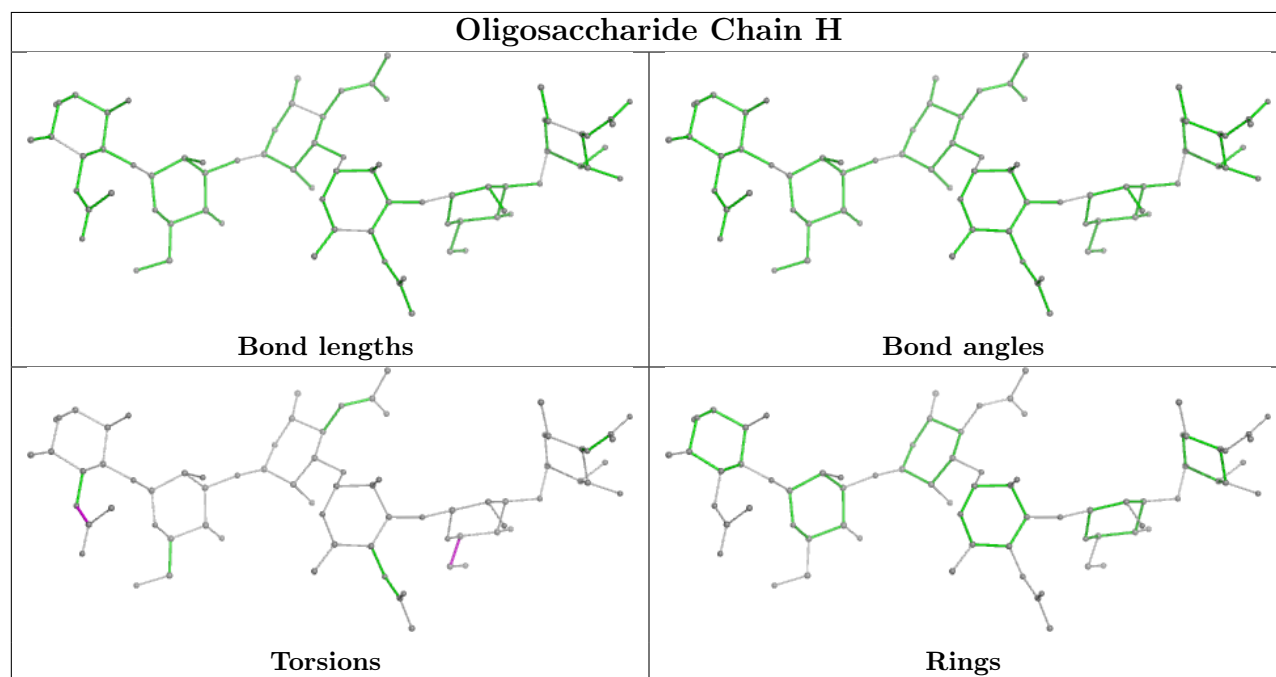
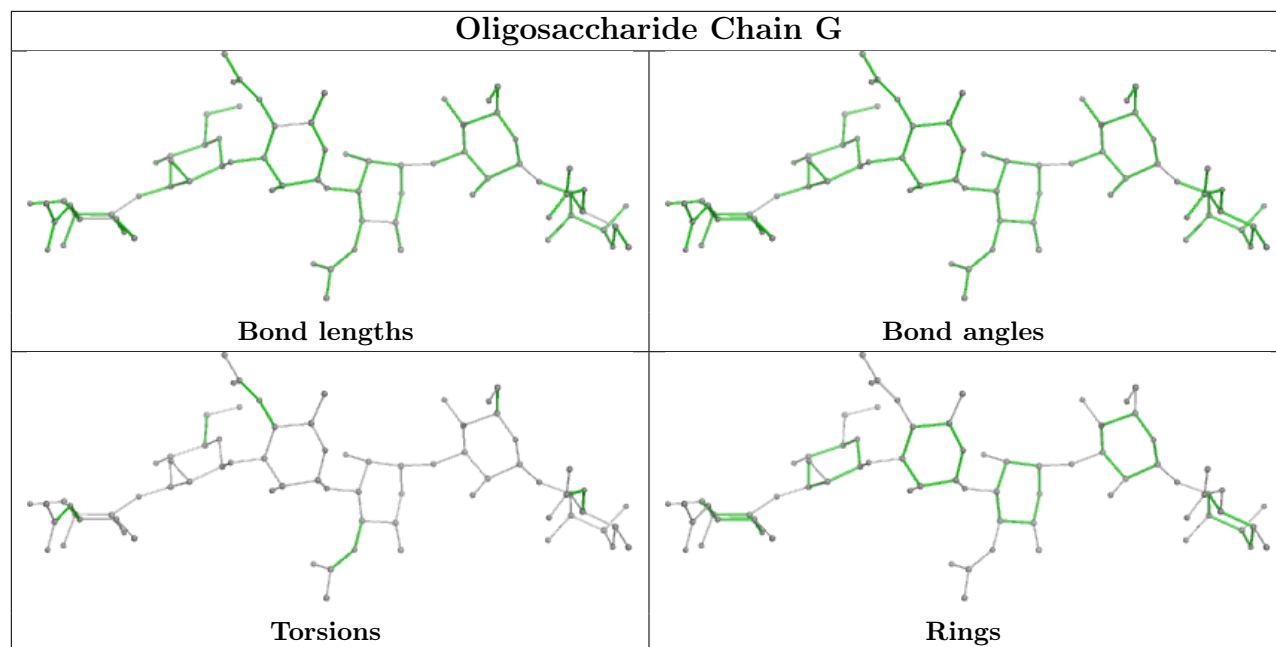
There are no ring outliers.

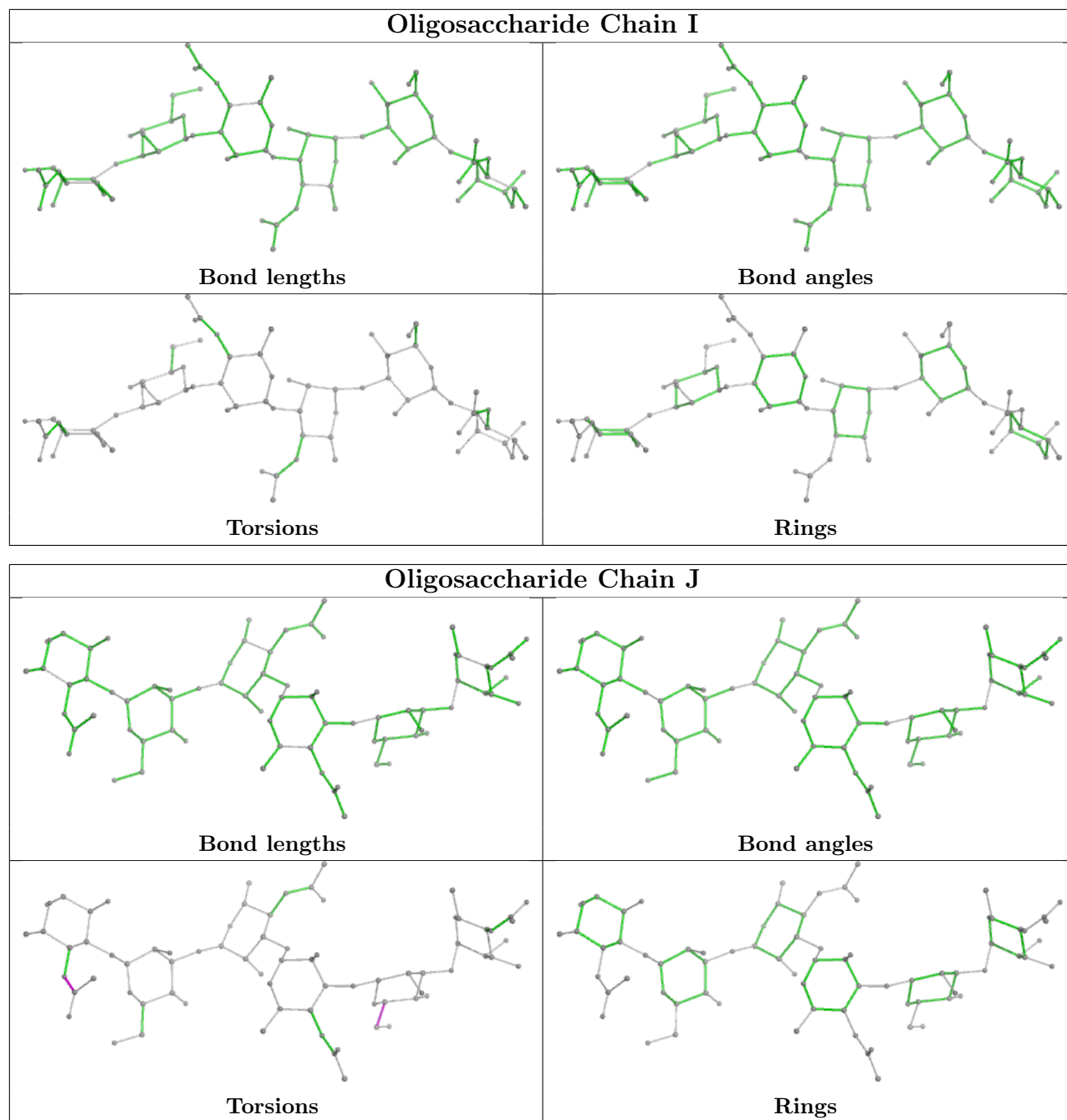
6 monomers are involved in 7 short contacts:

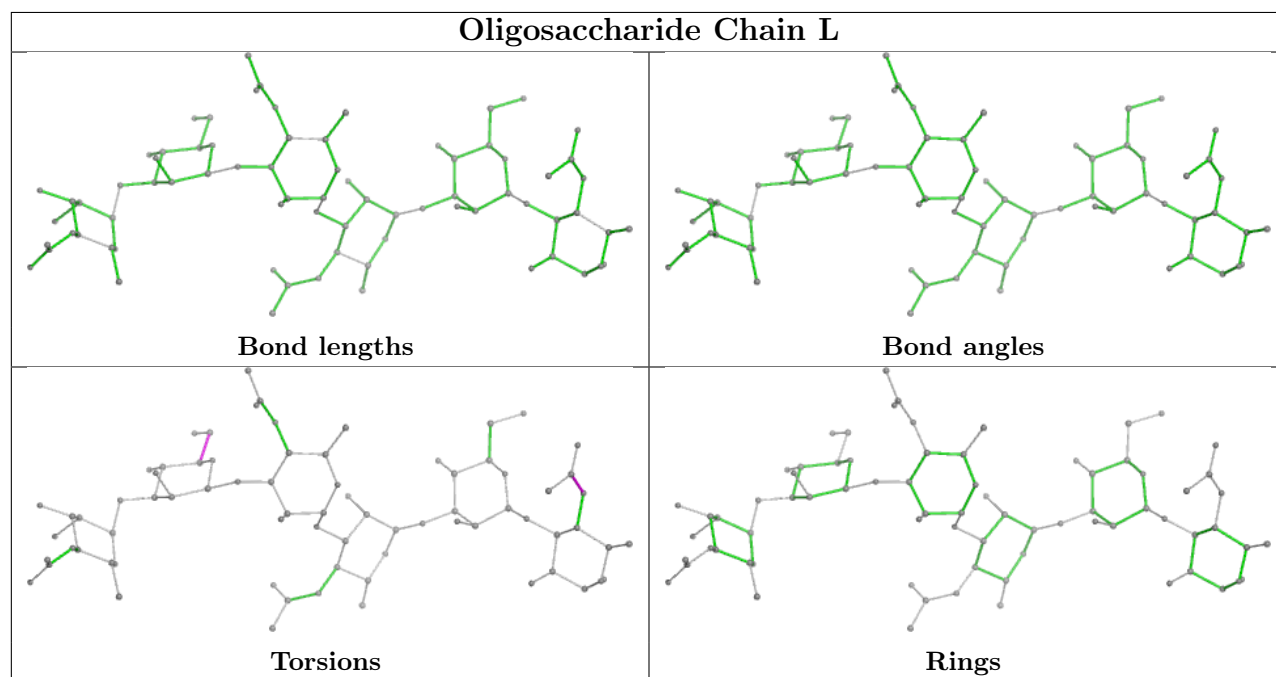
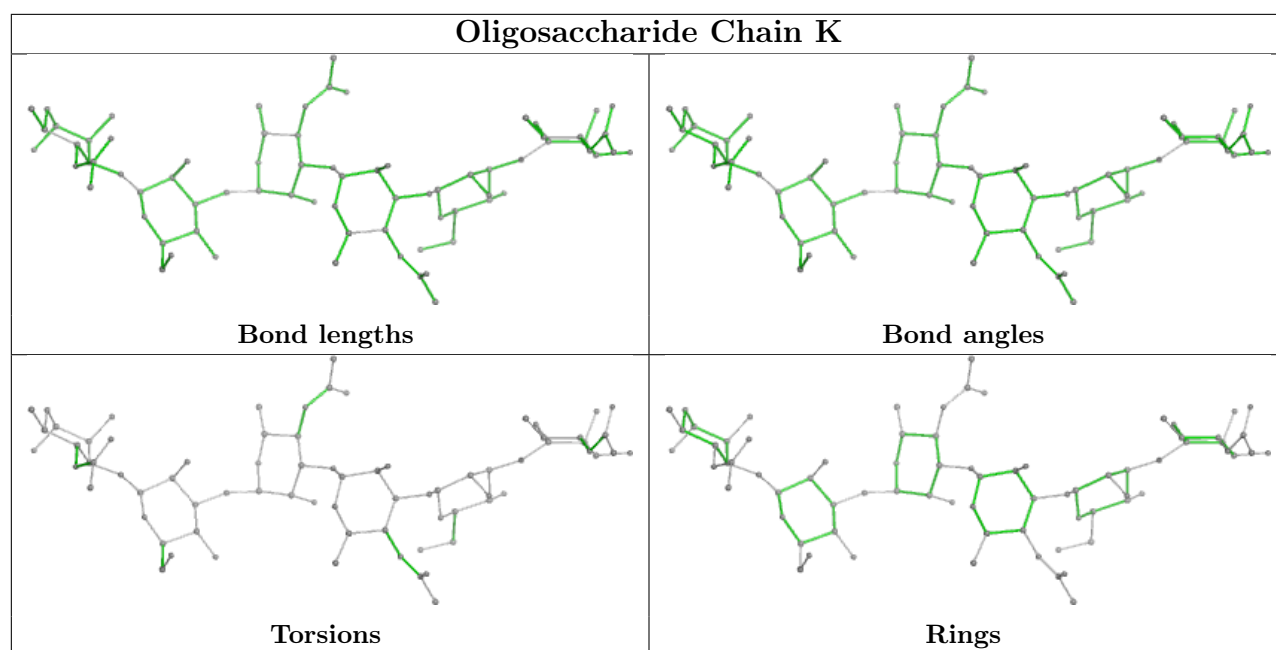
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	K	1	MRH	1	0
2	O	1	MRH	1	0
2	I	1	MRH	2	0
2	Q	1	MRH	1	0
2	G	1	MRH	1	0
2	M	1	MRH	1	0

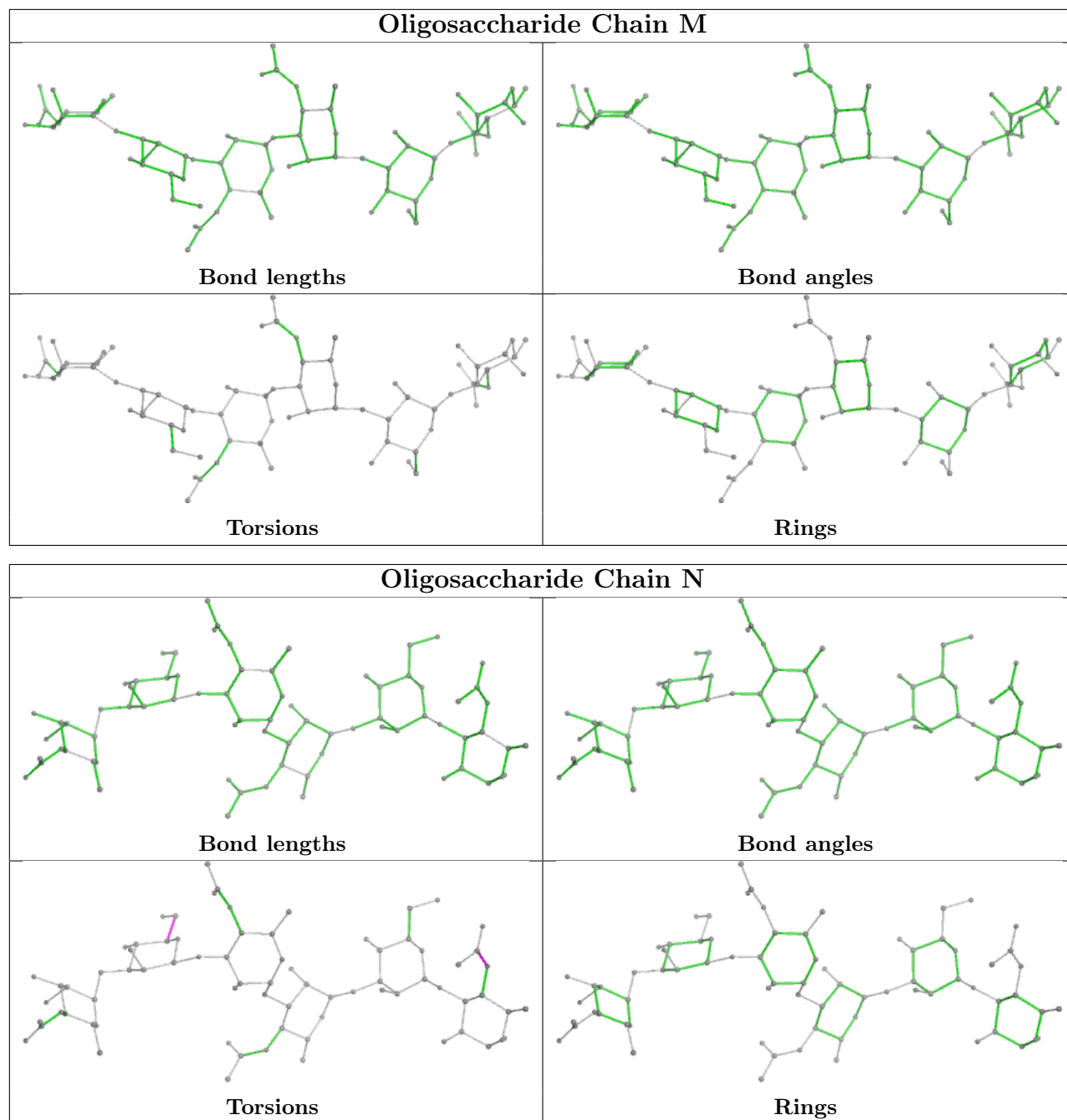
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

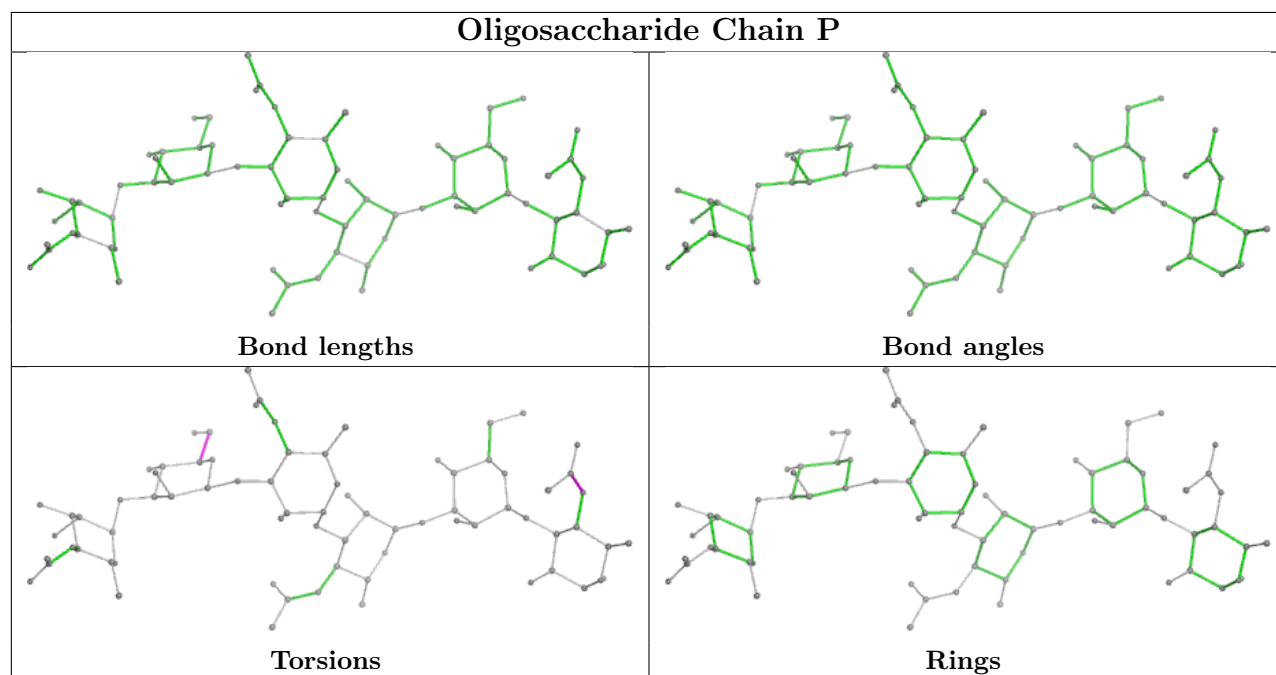
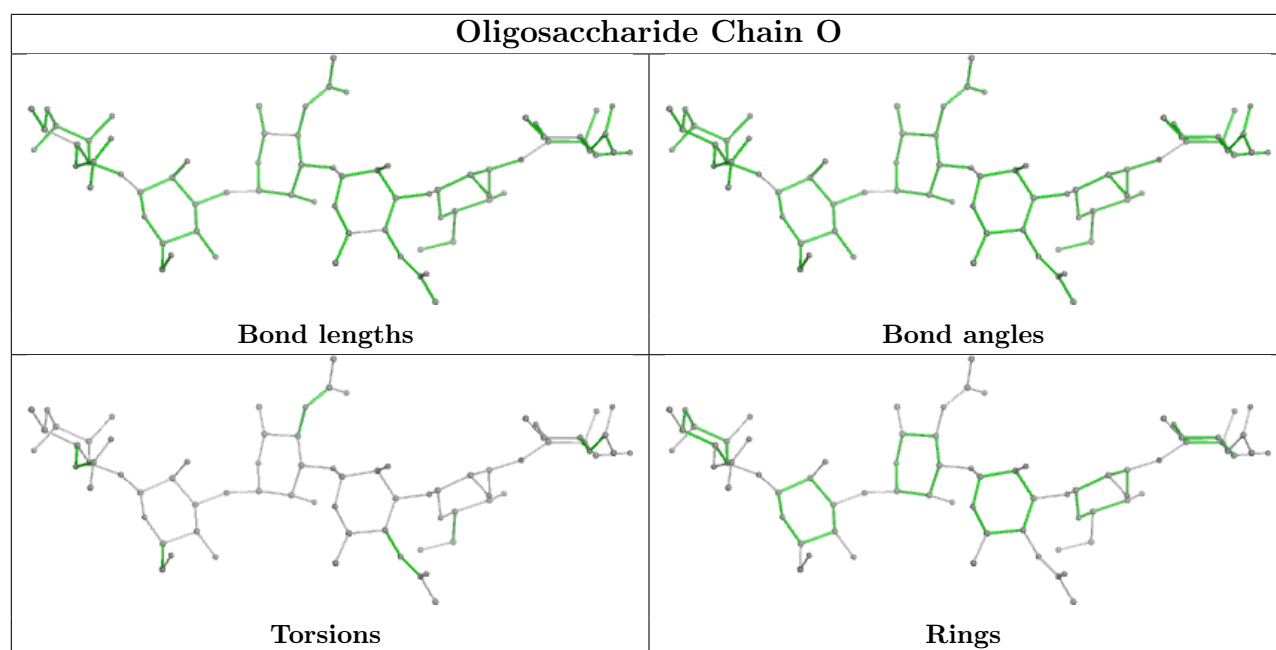


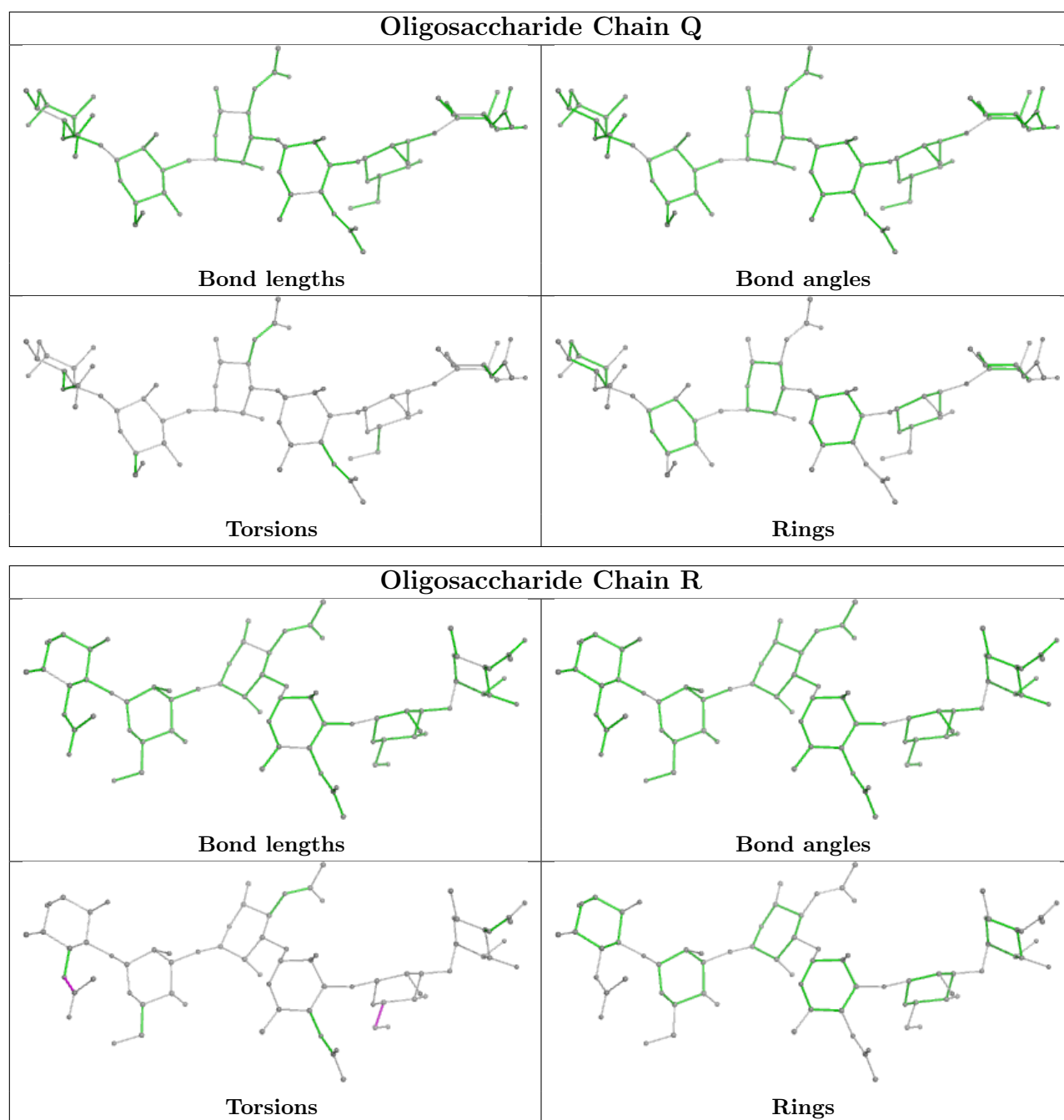












## 5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 18 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

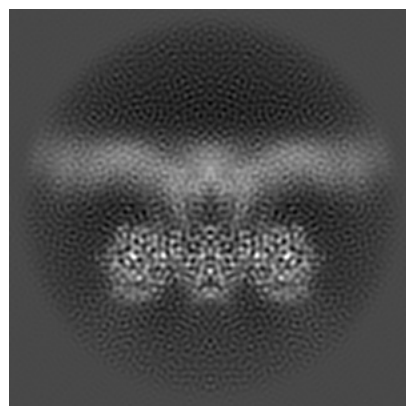
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16183. These allow visual inspection of the internal detail of the map and identification of artifacts.

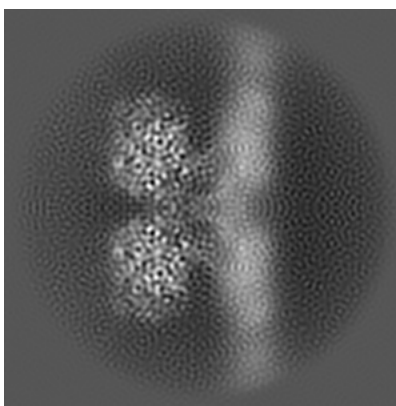
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

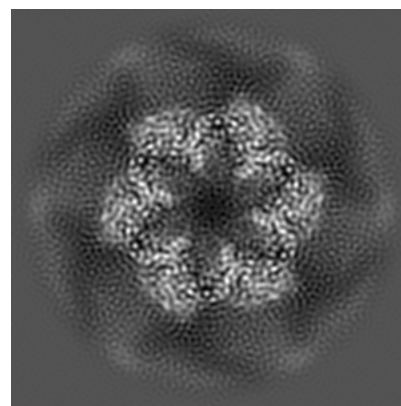
#### 6.1.1 Primary map



X

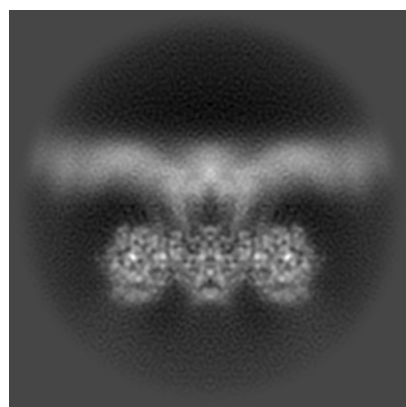


Y

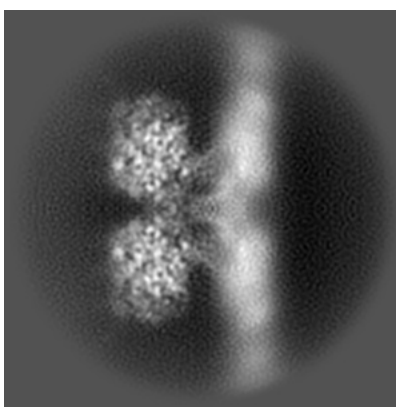


Z

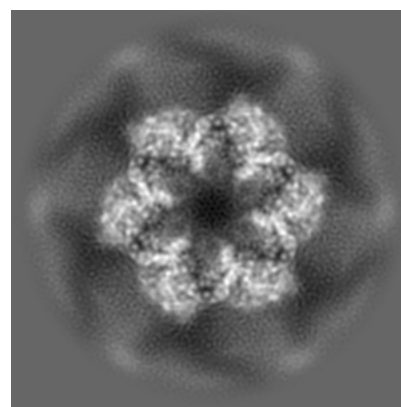
#### 6.1.2 Raw map



X



Y



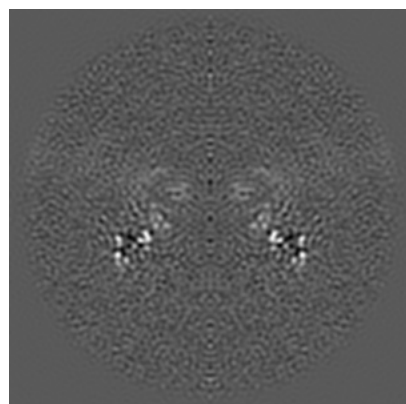
Z

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

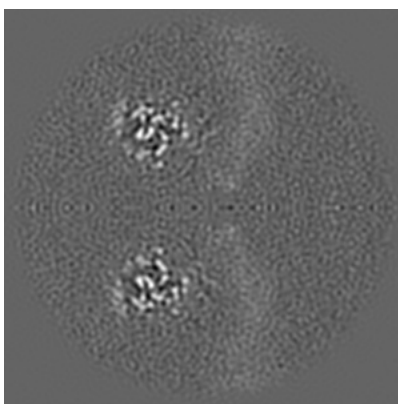


## 6.2 Central slices [i](#)

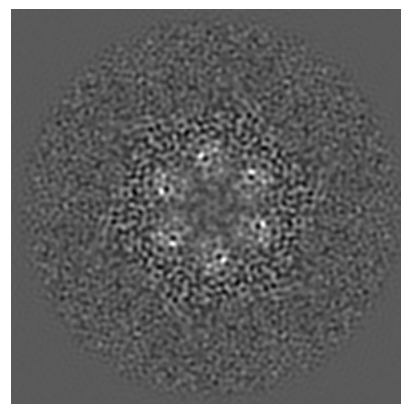
### 6.2.1 Primary map



X Index: 80

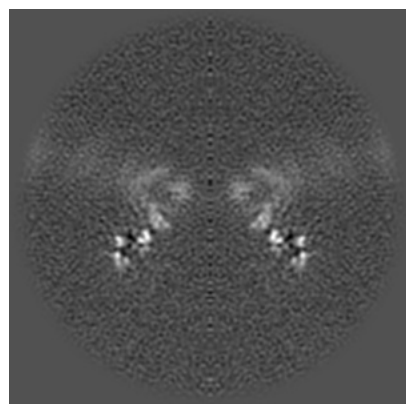


Y Index: 80

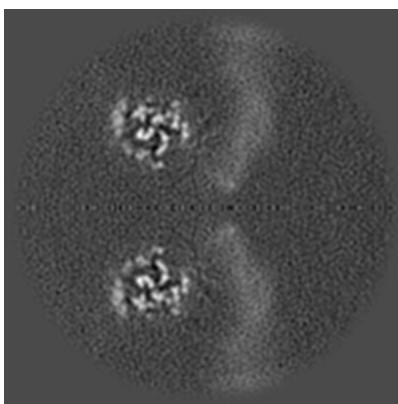


Z Index: 80

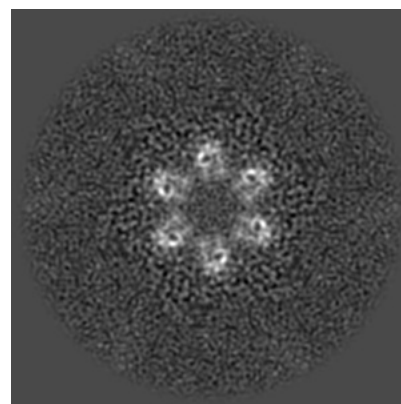
### 6.2.2 Raw map



X Index: 80



Y Index: 80

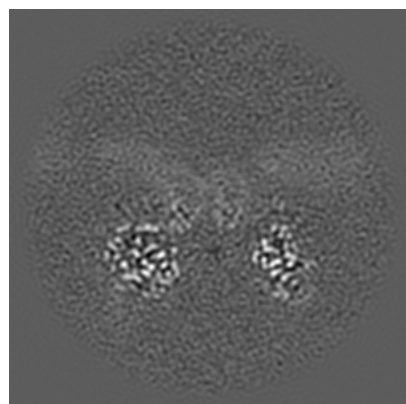


Z Index: 80

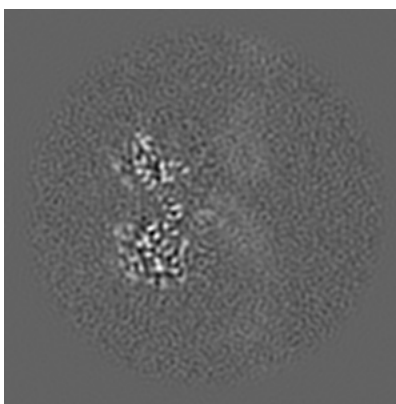
The images above show central slices of the map in three orthogonal directions.

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

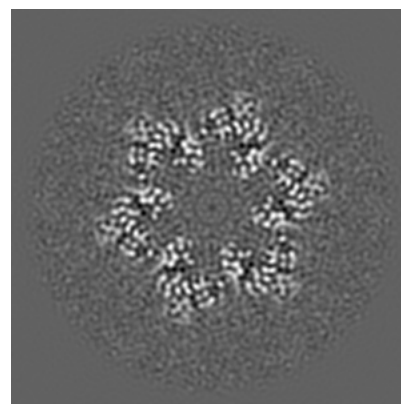
### 6.3.1 Primary map



X Index: 65

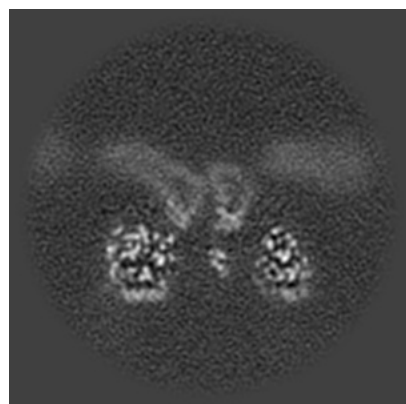


Y Index: 105

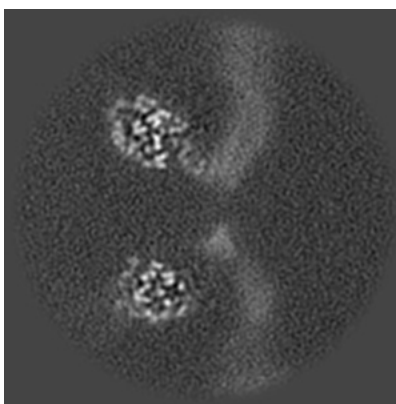


Z Index: 61

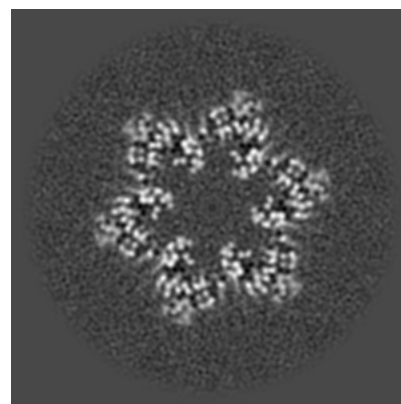
### 6.3.2 Raw map



X Index: 62



Y Index: 77

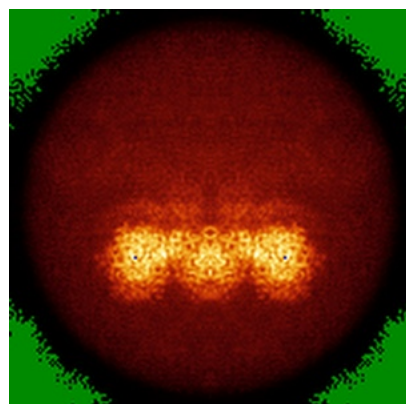


Z Index: 61

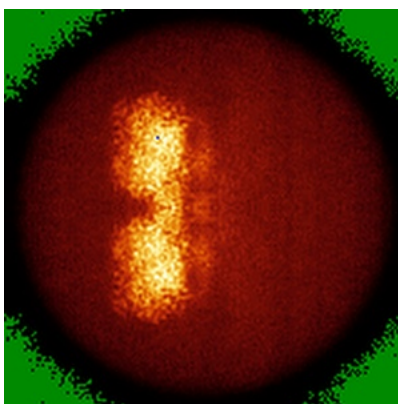
The images above show the largest variance slices of the map in three orthogonal directions.

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

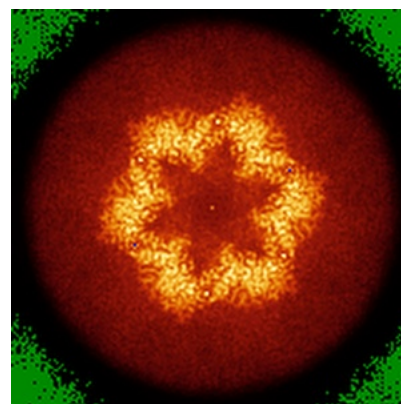
### 6.4.1 Primary map



X

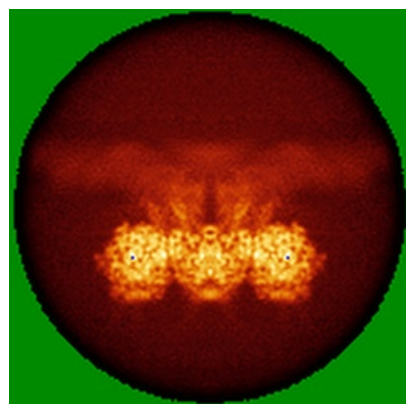


Y

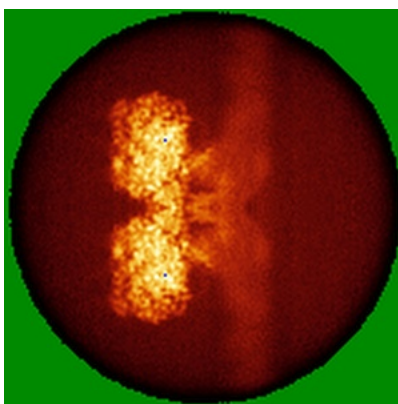


Z

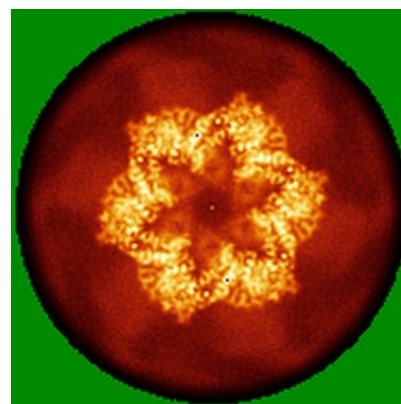
### 6.4.2 Raw map



X



Y

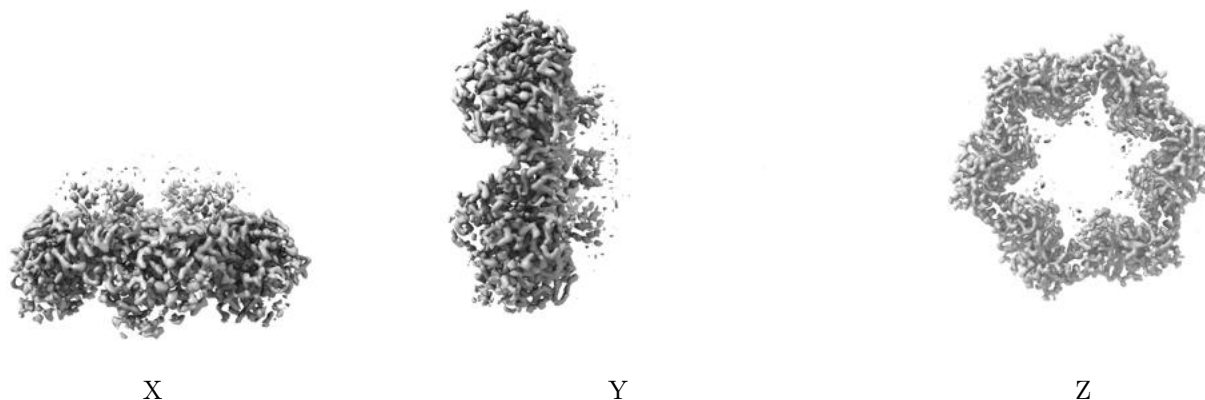


Z

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.

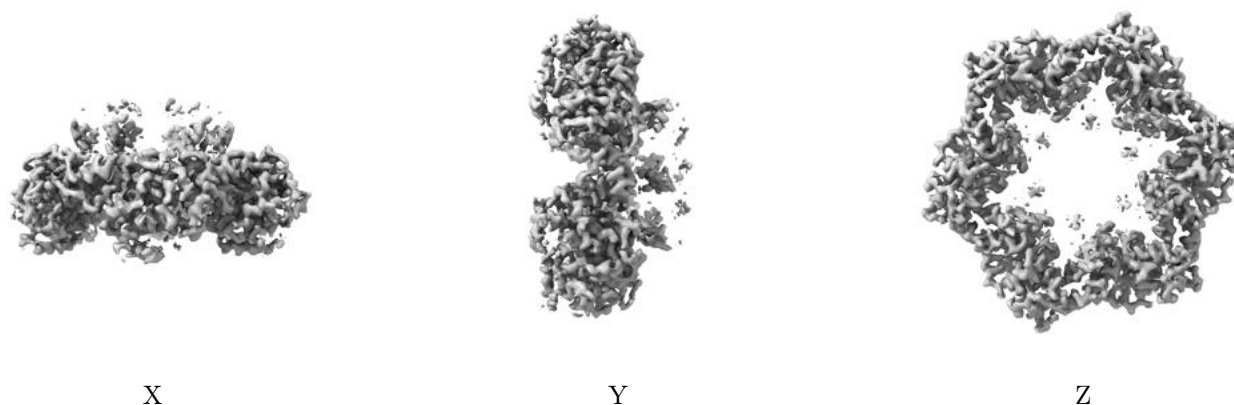
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.54716. 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.

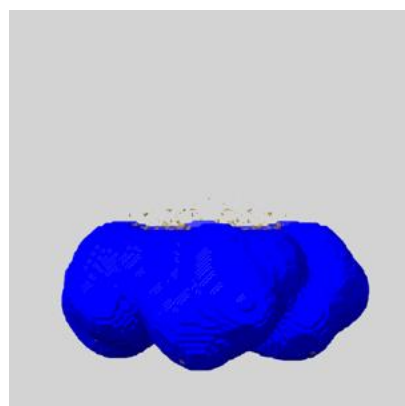
## 6.6 Mask visualisation [i](#)

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

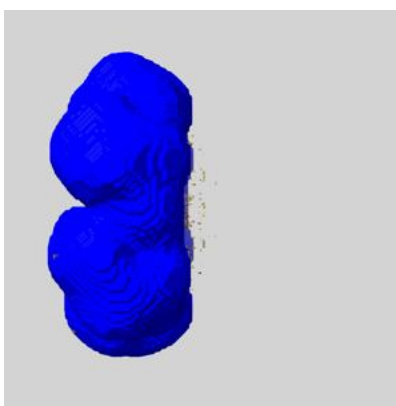
A mask typically either:

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

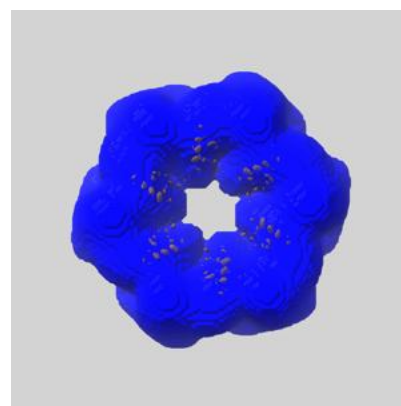
### 6.6.1 emd\_16183\_msk\_1.map [i](#)



X



Y

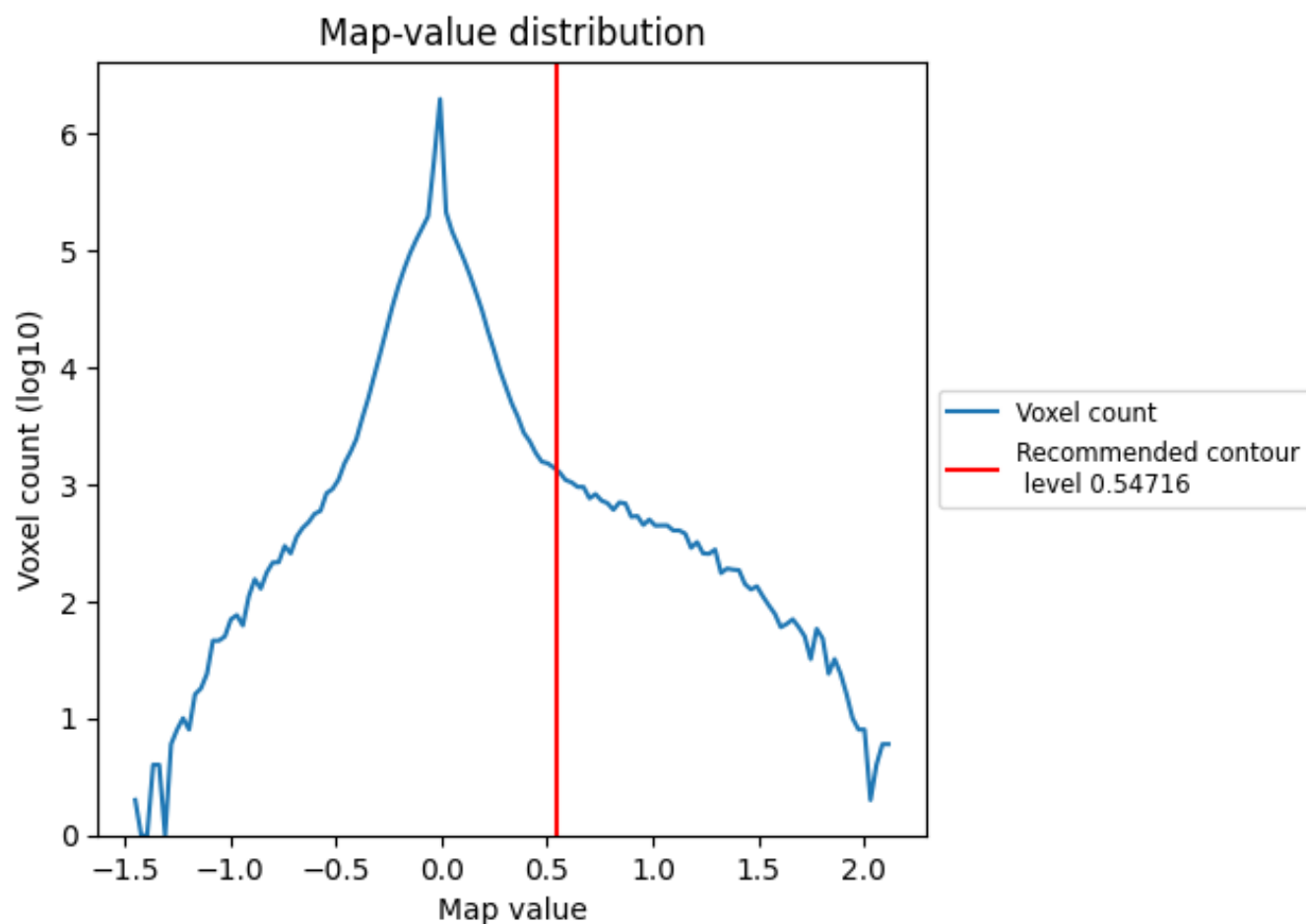


Z

## 7 Map analysis [i](#)

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

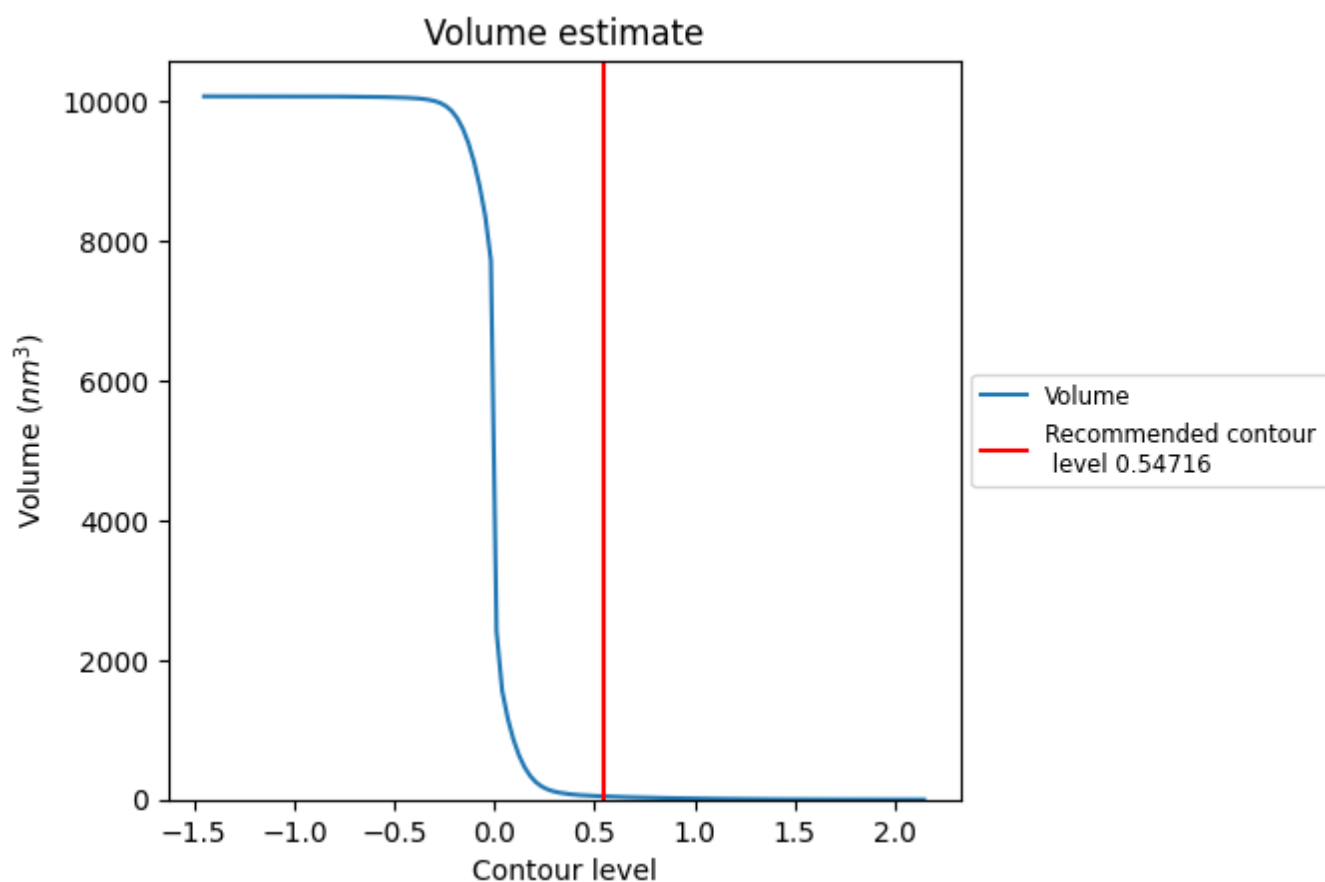
### 7.1 Map-value distribution [i](#)



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.



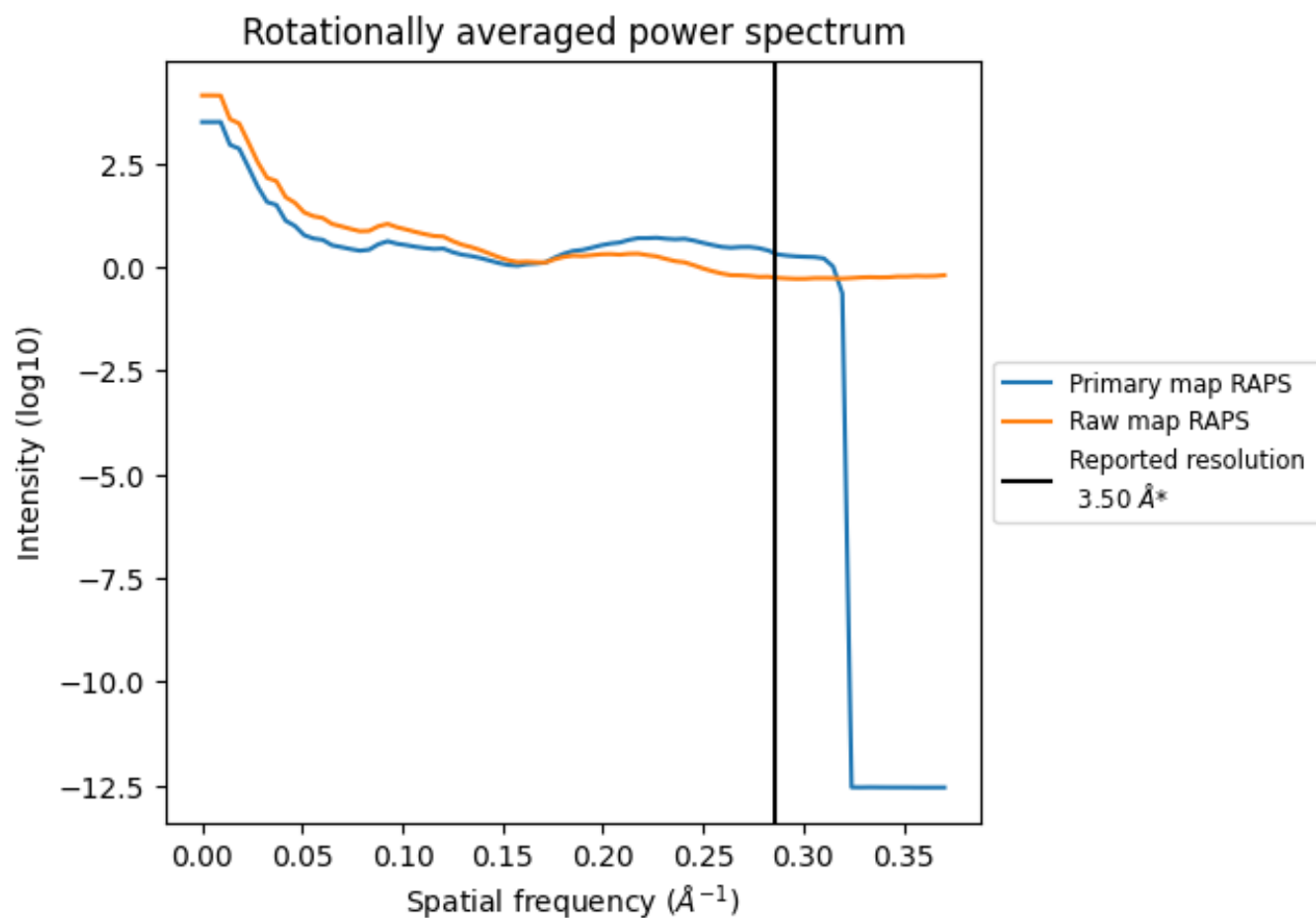
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 46 nm<sup>3</sup>; this corresponds to an approximate mass of 42 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 ⓘ



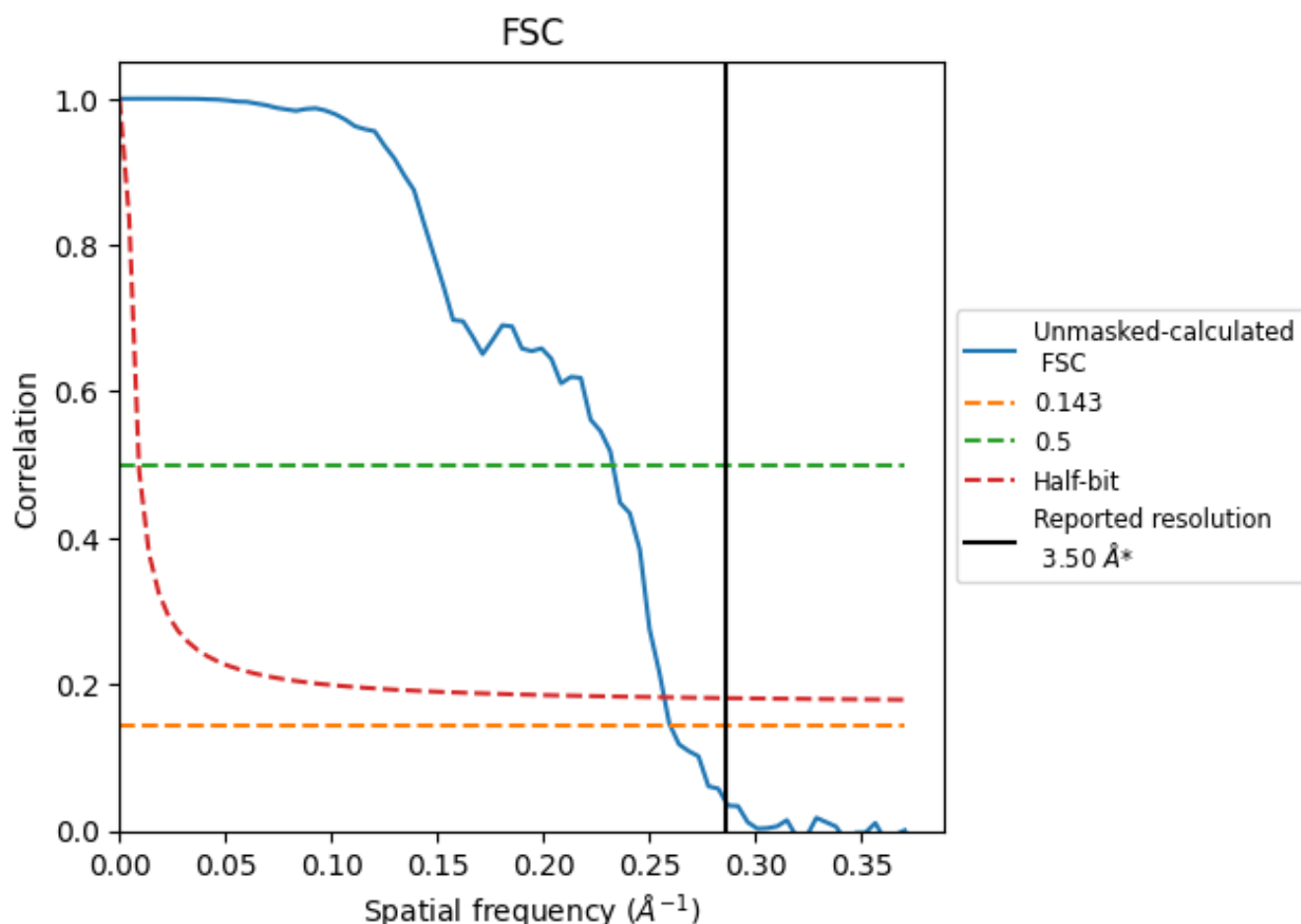
\*Reported resolution corresponds to spatial frequency of  $0.286 \text{ \AA}^{-1}$



## 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 0.286 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

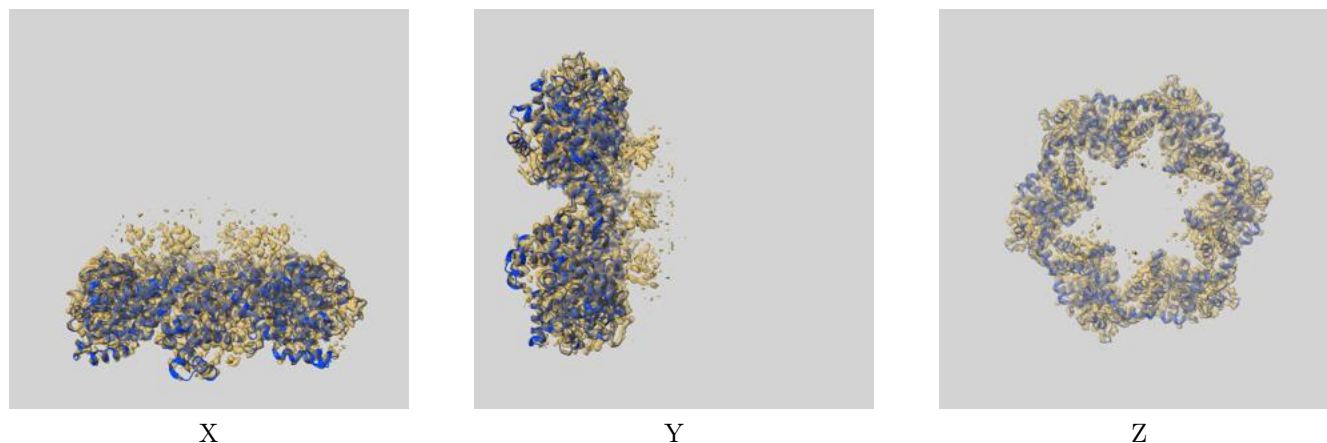
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.85	4.30	3.89

\*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 3.85 differs from the reported value 3.5 by more than 10 %

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

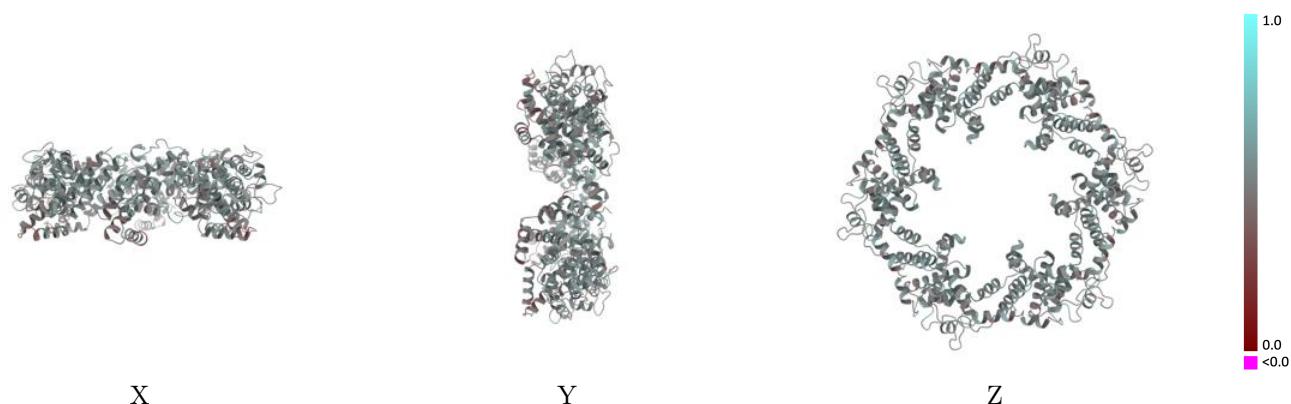
This section contains information regarding the fit between EMDB map EMD-16183 and PDB model 8BQE. Per-residue inclusion information can be found in section [3](#) on page [6](#).

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



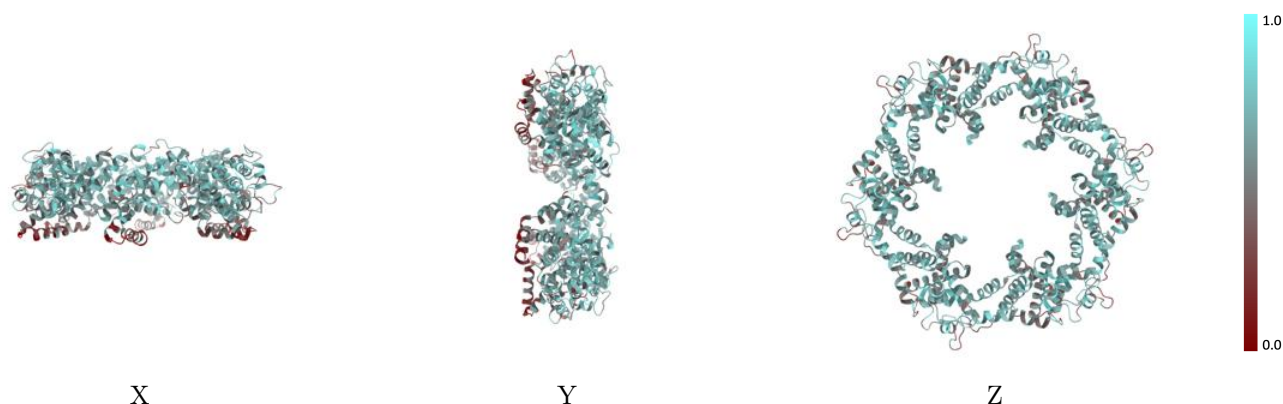
The images above show the 3D surface view of the map at the recommended contour level 0.54716 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



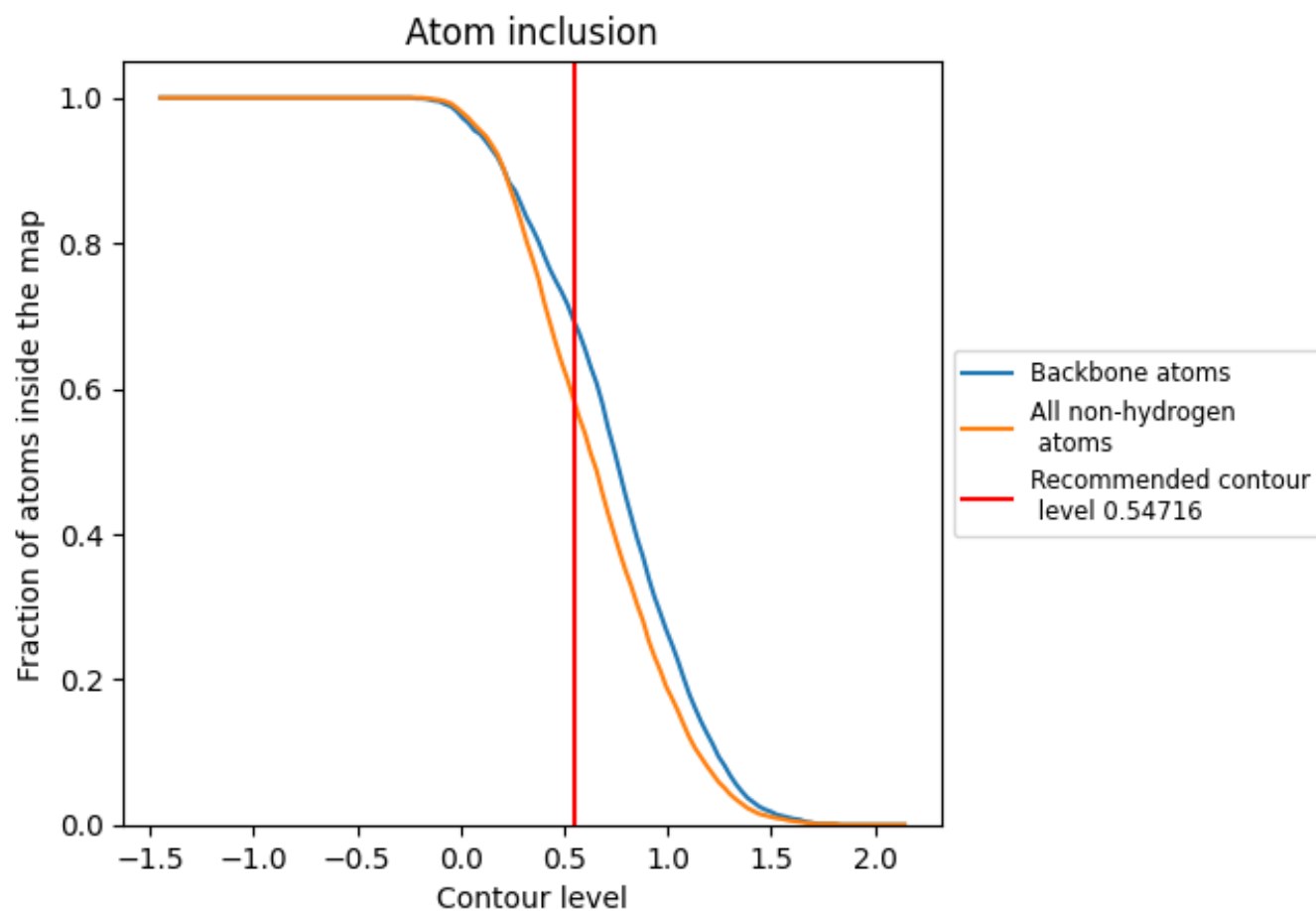
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.54716).







































## 9.4 Atom inclusion ⓘ



At the recommended contour level, 69% of all backbone atoms, 58% 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 (0.54716) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5840	 0.5050
A	 0.6080	 0.5050
B	 0.6070	 0.5080
C	 0.6130	 0.5100
D	 0.6080	 0.5070
E	 0.6070	 0.5080
F	 0.6130	 0.5060
G	 0.4000	 0.4910
H	 0.2000	 0.4800
I	 0.4130	 0.4840
J	 0.1730	 0.4670
K	 0.4000	 0.4850
L	 0.2000	 0.4730
M	 0.4000	 0.4790
N	 0.1600	 0.4810
O	 0.4130	 0.4830
P	 0.1730	 0.4710
Q	 0.4000	 0.4750
R	 0.1600	 0.4830

