



wwPDB EM Validation Summary Report ⓘ

Jul 28, 2026 – 04:50 PM EDT

PDB ID : 9DZJ / pdb_00009dzj
EMDB ID : EMD-47331
Title : Human GC-A bound to ANP and 2xREGN5308
Authors : Liu, S.; Huang, X.-Y.
Deposited on : 2024-10-16
Resolution : 2.70 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.dev133
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) : 2.50

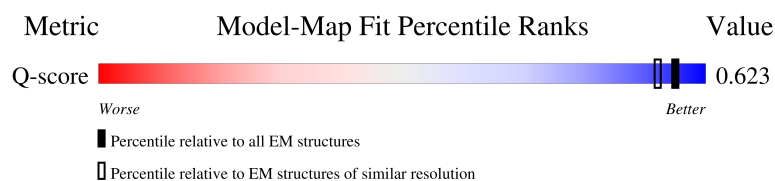
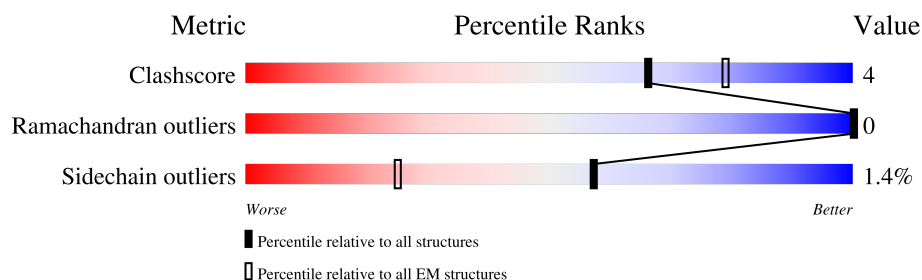
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 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.



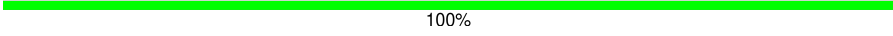
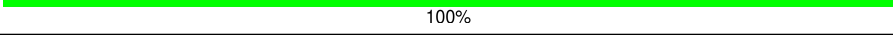
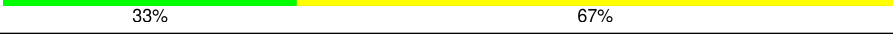
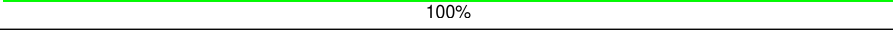
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10327 (2.20 - 3.20)

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	G	227	
1	H	227	
2	K	213	
2	L	213	

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Mol	Chain	Length	Quality of chain
3	A	1031	
3	B	1031	
4	C	28	
5	D	3	
5	E	3	
5	I	3	
5	M	3	
6	F	2	
6	J	2	

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 10145 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 REGN5308 - Heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	H	124	Total	C	N	O	S	0	0
			935	599	162	167	7		
1	G	124	Total	C	N	O	S	0	0
			937	600	162	168	7		

- Molecule 2 is a protein called REGN5308 - Light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	106	Total	C	N	O	S	0	0
			762	491	132	136	3		
2	K	106	Total	C	N	O	S	0	0
			759	490	132	134	3		

- Molecule 3 is a protein called Atrial natriuretic peptide receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	427	Total	C	N	O	S	0	0
			3188	2070	563	543	12		
3	B	427	Total	C	N	O	S	0	0
			3185	2067	563	543	12		

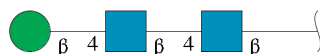
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	ALA	-	expression tag	UNP P16066
B	-1	ALA	-	expression tag	UNP P16066

- Molecule 4 is a protein called Atrial natriuretic peptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	20	Total	C	N	O	S	0	0
			135	82	27	23	3		

- Molecule 5 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
5	E	3	Total	C	N	O	0	0
			39	22	2	15		
5	D	3	Total	C	N	O	0	0
			39	22	2	15		
5	I	3	Total	C	N	O	0	0
			39	22	2	15		
5	M	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 6 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
6	F	2	Total	C	N	O	0	0
			28	16	2	10		
6	J	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
7	A	1	Total	Cl	0
			1	1	
7	B	1	Total	Cl	0
			1	1	

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
8	A	1	Total	C	N	O	0
			14	8	1	5	
8	B	1	Total	C	N	O	0
			14	8	1	5	

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		AltConf
9	H	1	Total	O	0
			1	1	
9	G	1	Total	O	0
			1	1	

THR	VAL	#1
LYS	GLN	
SER	TRP	\$9
PHE	LYS	\$10
ASN	VAL	L11
ARG	ASP	
GLY	ASN	L33
GLU	ALA	
CYS	LEU	Q37
	GLN	
	SER	V50
	GLY	
	ASN	L78
	SER	Q79
	GLN	
	GLU	D82
	SER	
	VAL	T101
	THR	R102
	GLU	L103
	GLN	
	ASP	K108
	SER	ARG
	LYS	THR
	ASP	VAL
	SER	ALA
	THR	ALA
	TVR	PRO
	SER	SER
	LEU	VAL
	SER	PHE
	SER	ILE
	THR	PHE
	LEU	PRO
	THR	PRO
	LEU	SER
	SER	ASP
	LYS	GLU
	ALA	GLN
	ASP	LEU
	TVR	LYS
	GLU	SER
	LYS	GLY
	HIS	THR
	LYS	ALA
	VAL	SER
	TVR	VAL
	ALA	VAL
	CYS	CYS
	GLU	LEU
	VAL	LEU
	THR	ASN
	HIS	ASN
	GLN	PHE
	GLY	TYR
	LEU	PRO
	SER	ARG
	SER	GLU
	PRO	ALA
	VAL	LYS

LEU	ARG	GLY	ILE	ASN	PRO	PHE	LEU	LEU	TYR	ALA	TYR	Q304	A-1
ARG	GLY	ILE	HIS	PHE	HIS	GLN	ARG	ARG	CYS	LYS	ARG	Q304	A-1
GLY	ASP	HIS	SER	ASP	SER	GLN	SER	ILE	PRO	THR	LYS	M309	A6
VAL	VAL	THR	VAL	VAL	VAL	ILE	GLY	THR	ARG	ALA	MET	Q304	A6
GLU	LYS	PRO	GLU	LYS	ARG	LEU	PHE	ASP	GLY	TYR	GLN	T317	L11
MET	VAL	VAL	GLN	VAL	THR	LEU	GLU	GLY	LEU	TYR	LEU	P318	L11
LYS	GLY	ALA	LEU	THR	LEU	ARG	VAL	GLU	GLN	GLY	LYS	L327	M20
LYS	GLY	ALA	ARG	ILE	ARG	LYS	GLY	GLU	ASP	ASN	GLU	L327	M20
LYS	VAL	VAL	GLY	GLY	GLY	PHE	LEU	PHE	ILE	LEU	LEU	T341	L50
LYS	VAL	VAL	GLU	ASP	ASN	PHE	ASP	ARG	GLU	VAL	ALA	T341	L50
VAL	VAL	VAL	THR	ALA	ARG	ASN	LEU	ARG	LEU	ALA	SER	V342	A65
VAL	VAL	VAL	THR	ALA	ARG	ASN	ASP	ARG	GLU	VAL	SER	V342	A65
ARG	THR	LYS	VAL	THR	GLU	GLU	LEU	LEU	ASN	VAL	GLU	T343	P66
THR	ARG	LYS	VAL	THR	VAL	GLU	LEU	LEU	ASN	VAL	GLU	T343	P66
THR	LYS	LYS	VAL	MET	VAL	ASN	PRO	LEU	SER	ARG	TRP	T348	L72
TYR	MET	VAL	ALA	VAL	ALA	SER	LYS	PRO	ILE	VAL	VAL	M352	V60
TRP	VAL	PRO	GLU	VAL	GLU	SER	GLU	GLU	THR	ASN	VAL	M352	V60
LEU	LEU	ARG	ALA	SER	ALA	ASN	ILE	GLN	LEU	ARG	ARG	R355	F81
LEU	GLY	TYR	PHE	GLY	ILE	ILE	ILE	GLY	ASP	LYS	TRP	R355	F81
GLY	GLY	LEU	LEU	LEU	LEU	LEU	GLU	HIS	TRP	ARG	GLU	L364	L52
GLU	GLU	LEU	SER	ASP	ARG	ASP	VAL	THR	MET	ILE	ASP	L364	L52
ARG	VAL	PHE	VAL	VAL	VAL	ASN	ARG	VAL	PHE	GLU	VAL	R389	Q83
GLY	ARG	GLY	THR	ARG	THR	LEU	THR	TYR	ARG	LEU	GLU	R389	Q83
SER	SER	ASP	ILE	ASN	ILE	LEU	ARG	ALA	TYR	THR	PRO	F425	A91
SER	SER	THR	TYR	GLY	TYR	SER	GLY	ARG	LYS	ARG	ASP	F425	A91
THR	THR	VAL	PHE	ARG	PHE	ARG	GLN	GLU	SER	LYS	SER	ASP	P92
ARG	ARG	ASN	SER	LEU	SER	MET	GLU	THR	LEU	VAL	LEU	ASP	P92
GLY	GLY	THR	ILE	HIS	ASP	GLU	PRO	THR	ASN	LEU	GLU	ASP	P92
ALA	ALA	ALA	ILE	ALA	GLN	GLN	PRO	THR	ASP	PHE	ARG	ALA	L104
SER	CYS	VAL	VAL	VAL	TYR	TYR	PHE	ALA	ILE	GLU	HIS	ALA	L104
ARG	GLU	ARG	GLY	GLU	ALA	ALA	ARG	PRO	VAL	LEU	GLY	CYS	L105
MET	VAL	MET	PHE	VAL	GLY	ASN	ARG	GLU	LYS	LEU	ARG	ASN	L105
GLU	ALA	GLU	THR	ALA	VAL	VAL	SER	LEU	GLY	VAL	GLN	GLU	L153
SER	ALA	THR	ALA	ASN	GLU	GLU	ASN	LEU	LYS	VAL	ASN	LEU	L153
ASN	ARG	GLU	ALA	HIS	ASP	GLU	PRO	THR	ASN	LEU	GLU	ASP	Y154
ALA	ALA	ALA	ILE	ALA	ILE	GLN	PRO	THR	ASP	PHE	ARG	PRO	Y154
SER	GLY	SER	VAL	CYS	VAL	TYR	PHE	ALA	ILE	GLU	HIS	ALA	A155
GLY	GLY	SER	VAL	VAL	LEU	GLU	ALA	ALA	LEU	ARG	GLY	LEU	A155
GLY	GLY	ASN	LEU	MET	SER	GLU	LEU	LEU	PHE	ASP	SER	SER	V169
GLY	GLY	GLY	LEU	ALA	LEU	LEU	LEU	MET	LEU	ARG	GLY	LEU	V169
ALA	ALA	ALA	ALA	VAL	ALA	GLN	GLN	ALA	LEU	VAL	ARG	ARG	E190
MET	VAL	MET	PHE	VAL	GLY	ASN	ARG	PRO	VAL	LEU	LEU	THR	E190
GLU	VAL	GLU	THR	VAL	VAL	VAL	SER	PRO	LYS	HIS	GLN	THR	E190
S													

Chain B: 36% 5% 59%



● Molecule 4: Atrial natriuretic peptide



● Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



● Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose





- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  100%



- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:  33% 67%



- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  50% 50%



- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  100%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	211000	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 (6k x 4k)	Depositor
Maximum map value	6.770	Depositor
Minimum map value	-4.347	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.164	Depositor
Recommended contour level	0.6	Depositor
Map size (Å)	273.92, 273.92, 273.92	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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: BMA, CL, 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	G	0.25	0/964	0.35	0/1314
1	H	0.25	0/962	0.36	0/1311
2	K	0.25	0/776	0.40	0/1059
2	L	0.26	0/779	0.43	0/1063
3	A	0.23	0/3281	0.31	0/4489
3	B	0.24	0/3278	0.33	1/4485 (0.0%)
4	C	0.16	0/136	0.27	0/178
All	All	0.24	0/10176	0.34	1/13899 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	70	VAL	CG1-CB-CG2	5.20	122.24	110.80

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	G	937	0	856	5	0
1	H	935	0	851	5	0
2	K	759	0	691	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	L	762	0	699	8	0
3	A	3188	0	3061	24	0
3	B	3185	0	3052	27	0
4	C	135	0	122	0	0
5	D	39	0	34	0	0
5	E	39	0	34	1	0
5	I	39	0	34	0	0
5	M	39	0	34	1	0
6	F	28	0	25	1	0
6	J	28	0	25	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
8	A	14	0	13	0	0
8	B	14	0	13	0	0
9	G	1	0	0	0	0
9	H	1	0	0	0	0
All	All	10145	0	9544	76	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 4.

The worst 5 of 76 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:L:50:VAL:O	2:L:50:VAL:HG12	1.87	0.75
2:L:46:LEU:HD23	2:L:55:GLN:OE1	1.90	0.71
1:H:46:GLU:OE1	1:H:63:ARG:NH1	2.25	0.69
3:B:83:GLY:HA3	3:B:104:LEU:HD11	1.75	0.69
2:L:78:LEU:HD11	2:L:103:LEU:HD21	1.76	0.68

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	G	122/227 (54%)	119 (98%)	3 (2%)	0	100	100
1	H	122/227 (54%)	120 (98%)	2 (2%)	0	100	100
2	K	104/213 (49%)	93 (89%)	11 (11%)	0	100	100
2	L	104/213 (49%)	89 (86%)	15 (14%)	0	100	100
3	A	425/1031 (41%)	411 (97%)	14 (3%)	0	100	100
3	B	425/1031 (41%)	416 (98%)	9 (2%)	0	100	100
4	C	18/28 (64%)	17 (94%)	1 (6%)	0	100	100
All	All	1320/2970 (44%)	1265 (96%)	55 (4%)	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	G	87/192 (45%)	86 (99%)	1 (1%)	65	85
1	H	86/192 (45%)	83 (96%)	3 (4%)	32	61
2	K	66/189 (35%)	63 (96%)	3 (4%)	24	52
2	L	68/189 (36%)	68 (100%)	0	100	100
3	A	300/871 (34%)	297 (99%)	3 (1%)	68	86
3	B	299/871 (34%)	296 (99%)	3 (1%)	68	86
4	C	12/22 (54%)	12 (100%)	0	100	100
All	All	918/2526 (36%)	905 (99%)	13 (1%)	57	82

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	304	GLN
3	A	364	LEU

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Mol	Chain	Res	Type
3	B	389	ARG
3	B	175	VAL
3	B	342	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
2	L	89	GLN
3	A	76	HIS
3	A	296	GLN
3	B	296	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 ⓘ

16 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	$\# Z > 2$
5	NAG	D	1	3,5	14,14,15	0.32	0	17,19,21	0.48	0
5	NAG	D	2	5	14,14,15	0.34	0	17,19,21	0.53	0
5	BMA	D	3	5	11,11,12	0.52	0	15,15,17	0.70	0
5	NAG	E	1	3,5	14,14,15	0.33	0	17,19,21	0.45	0
5	NAG	E	2	5	14,14,15	0.21	0	17,19,21	0.41	0
5	BMA	E	3	5	11,11,12	0.52	0	15,15,17	0.72	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	F	1	6,3	14,14,15	0.28	0	17,19,21	0.54	0
6	NAG	F	2	6	14,14,15	0.21	0	17,19,21	0.45	0
5	NAG	I	1	3,5	14,14,15	0.31	0	17,19,21	0.49	0
5	NAG	I	2	5	14,14,15	0.35	0	17,19,21	0.53	0
5	BMA	I	3	5	11,11,12	0.52	0	15,15,17	0.69	0
6	NAG	J	1	6,3	14,14,15	0.27	0	17,19,21	0.48	0
6	NAG	J	2	6	14,14,15	0.23	0	17,19,21	0.45	0
5	NAG	M	1	3,5	14,14,15	0.32	0	17,19,21	0.45	0
5	NAG	M	2	5	14,14,15	0.21	0	17,19,21	0.40	0
5	BMA	M	3	5	11,11,12	0.49	0	15,15,17	0.72	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	NAG	D	1	3,5	-	0/6/23/26	0/1/1/1
5	NAG	D	2	5	-	2/6/23/26	0/1/1/1
5	BMA	D	3	5	-	1/2/19/22	0/1/1/1
5	NAG	E	1	3,5	-	2/6/23/26	0/1/1/1
5	NAG	E	2	5	-	2/6/23/26	0/1/1/1
5	BMA	E	3	5	-	0/2/19/22	0/1/1/1
6	NAG	F	1	6,3	-	2/6/23/26	0/1/1/1
6	NAG	F	2	6	-	2/6/23/26	0/1/1/1
5	NAG	I	1	3,5	-	0/6/23/26	0/1/1/1
5	NAG	I	2	5	-	2/6/23/26	0/1/1/1
5	BMA	I	3	5	-	1/2/19/22	0/1/1/1
6	NAG	J	1	6,3	-	2/6/23/26	0/1/1/1
6	NAG	J	2	6	-	2/6/23/26	0/1/1/1
5	NAG	M	1	3,5	-	2/6/23/26	0/1/1/1
5	NAG	M	2	5	-	2/6/23/26	0/1/1/1
5	BMA	M	3	5	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

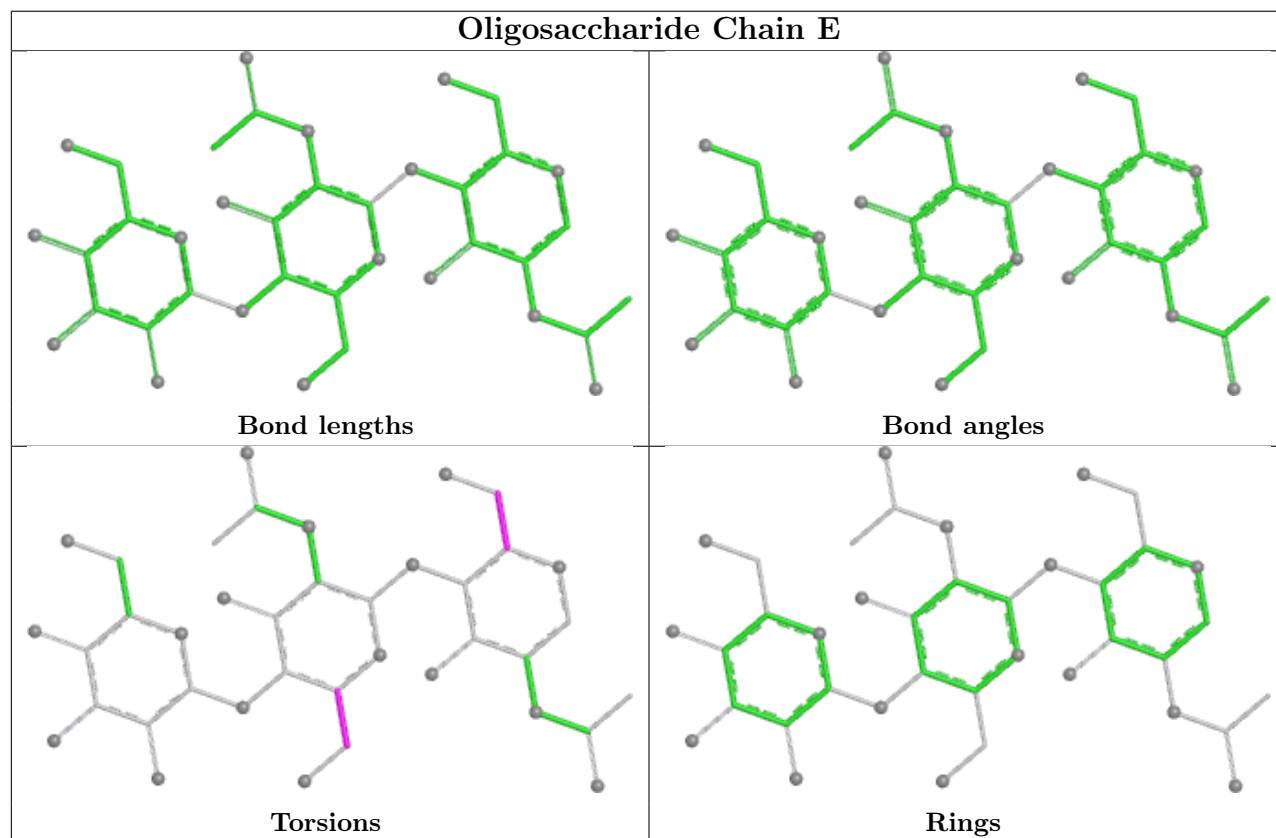
Mol	Chain	Res	Type	Atoms
5	E	2	NAG	O5-C5-C6-O6
5	M	2	NAG	O5-C5-C6-O6
6	J	1	NAG	O5-C5-C6-O6
6	F	1	NAG	O5-C5-C6-O6
5	E	2	NAG	C4-C5-C6-O6

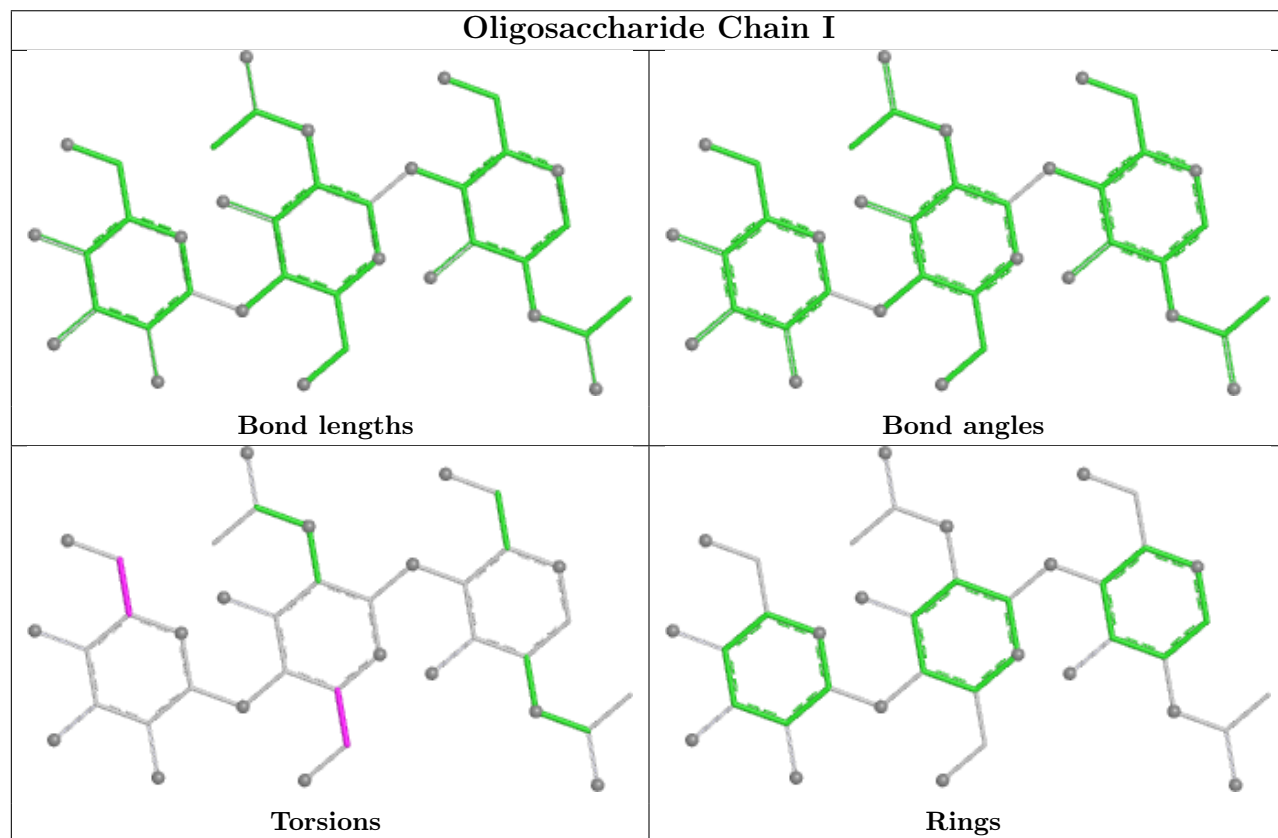
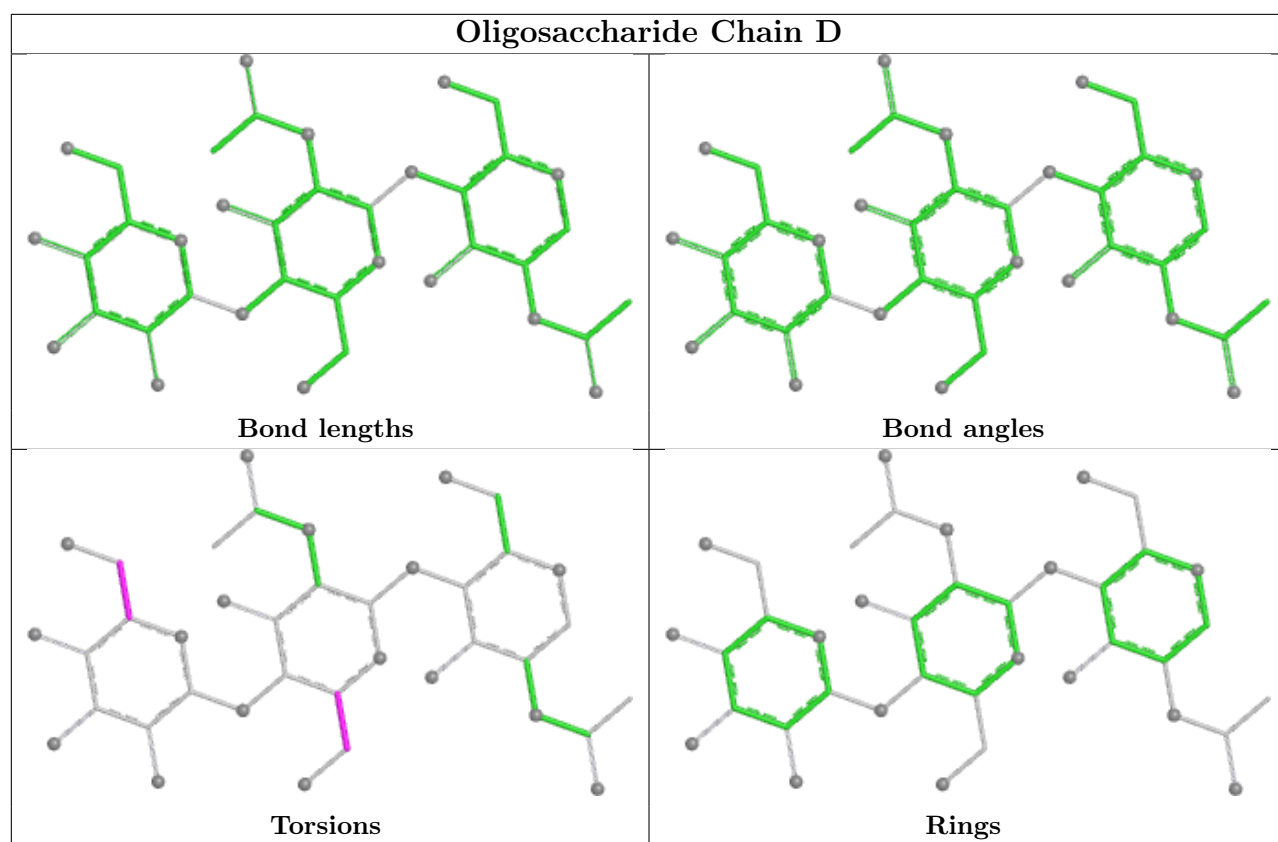
There are no ring outliers.

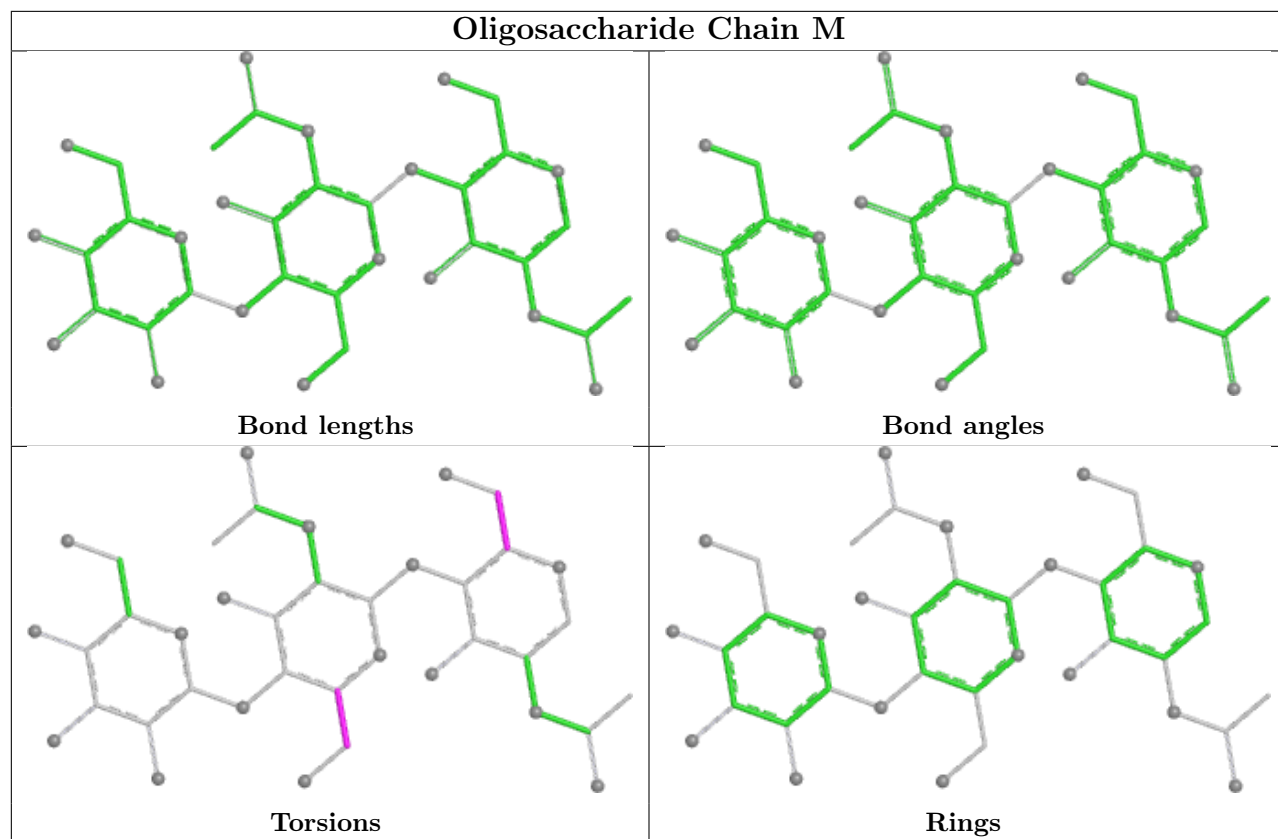
5 monomers are involved in 3 short contacts:

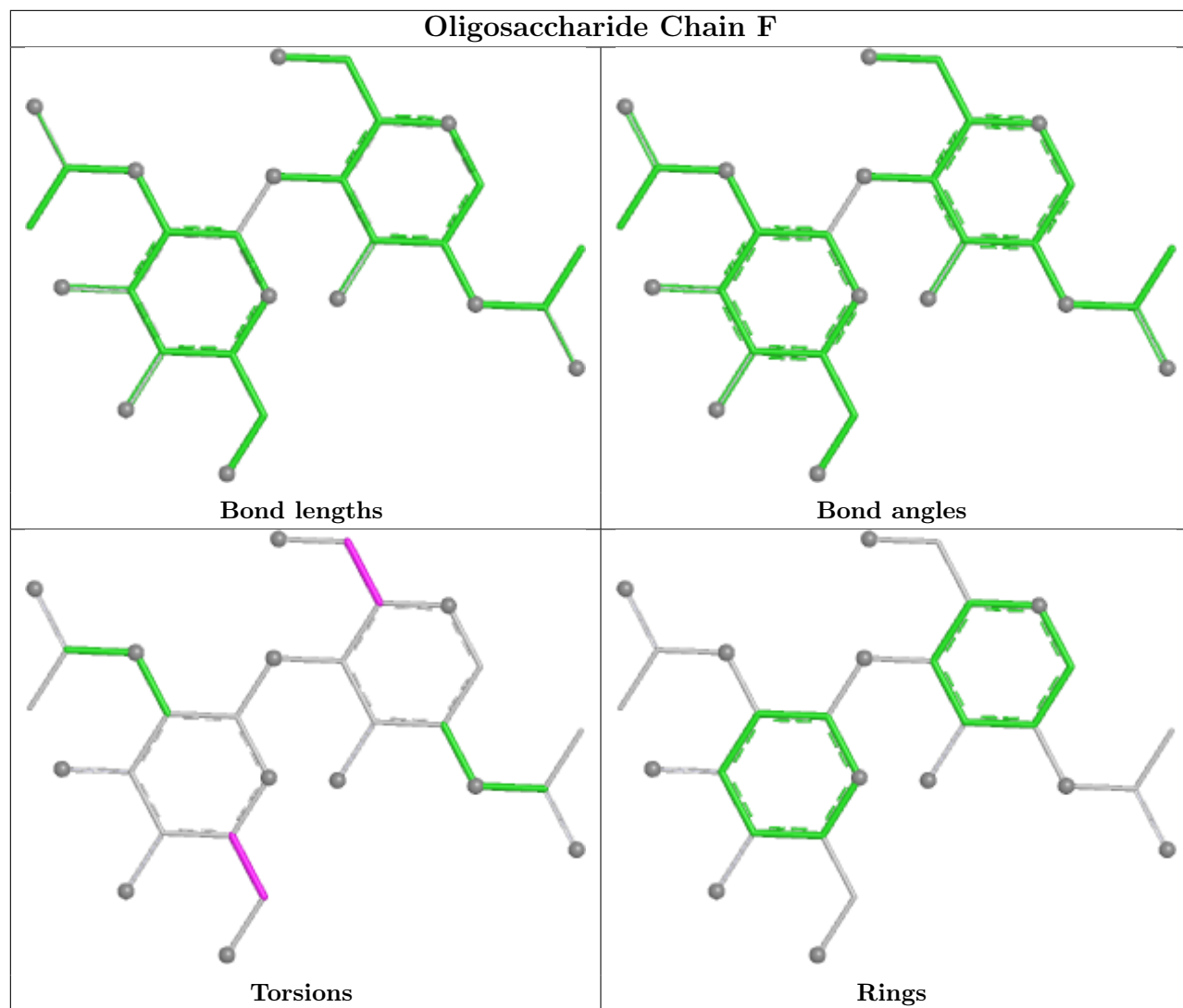
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	2	NAG	1	0
5	M	2	NAG	1	0
5	M	1	NAG	1	0
6	F	1	NAG	1	0
5	E	1	NAG	1	0

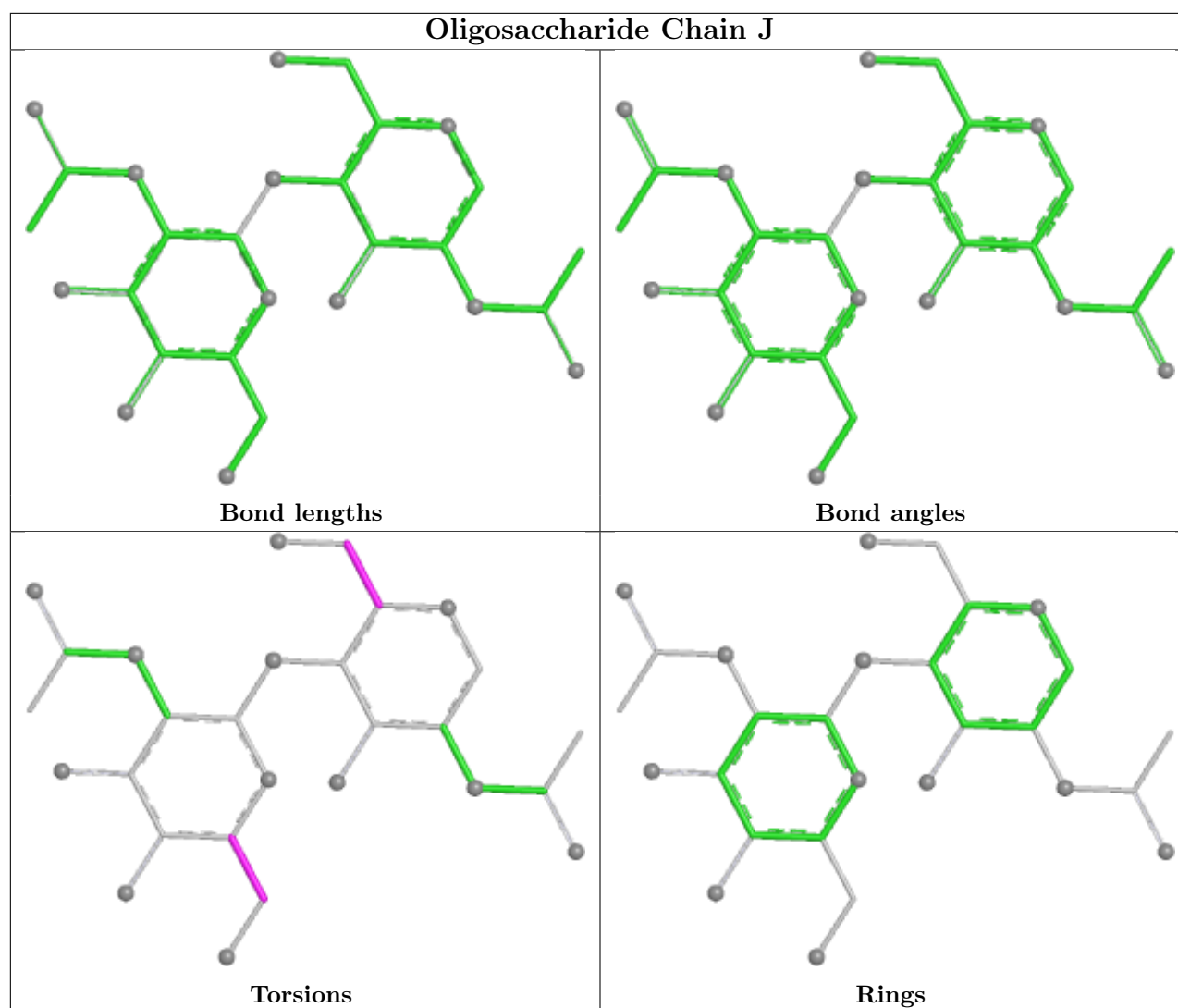
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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	$\# Z > 2$
8	NAG	B	1102	3	14,14,15	0.21	0	17,19,21	0.46	0
8	NAG	A	1102	3	14,14,15	0.20	0	17,19,21	0.47	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
8	NAG	B	1102	3	-	0/6/23/26	0/1/1/1
8	NAG	A	1102	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

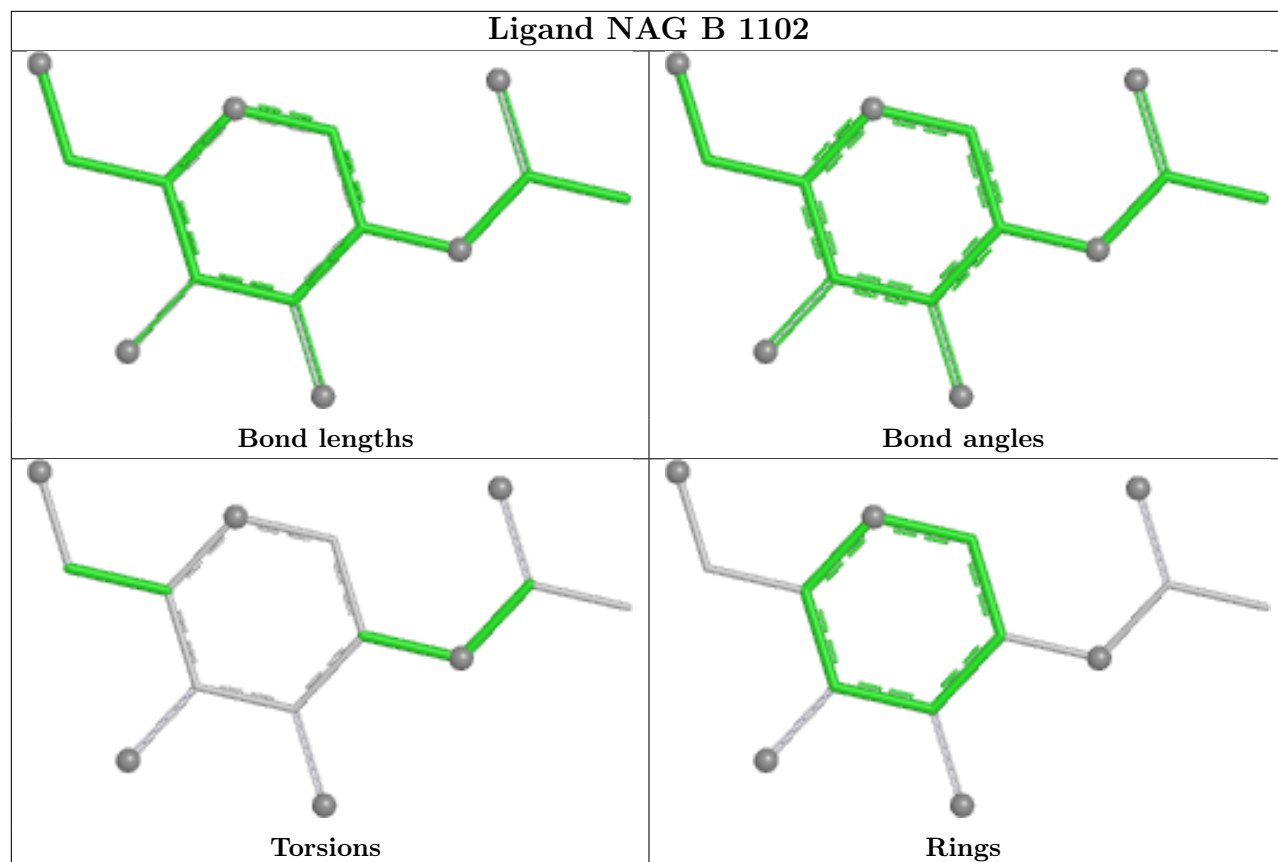
There are no torsion outliers.

There are no ring outliers.

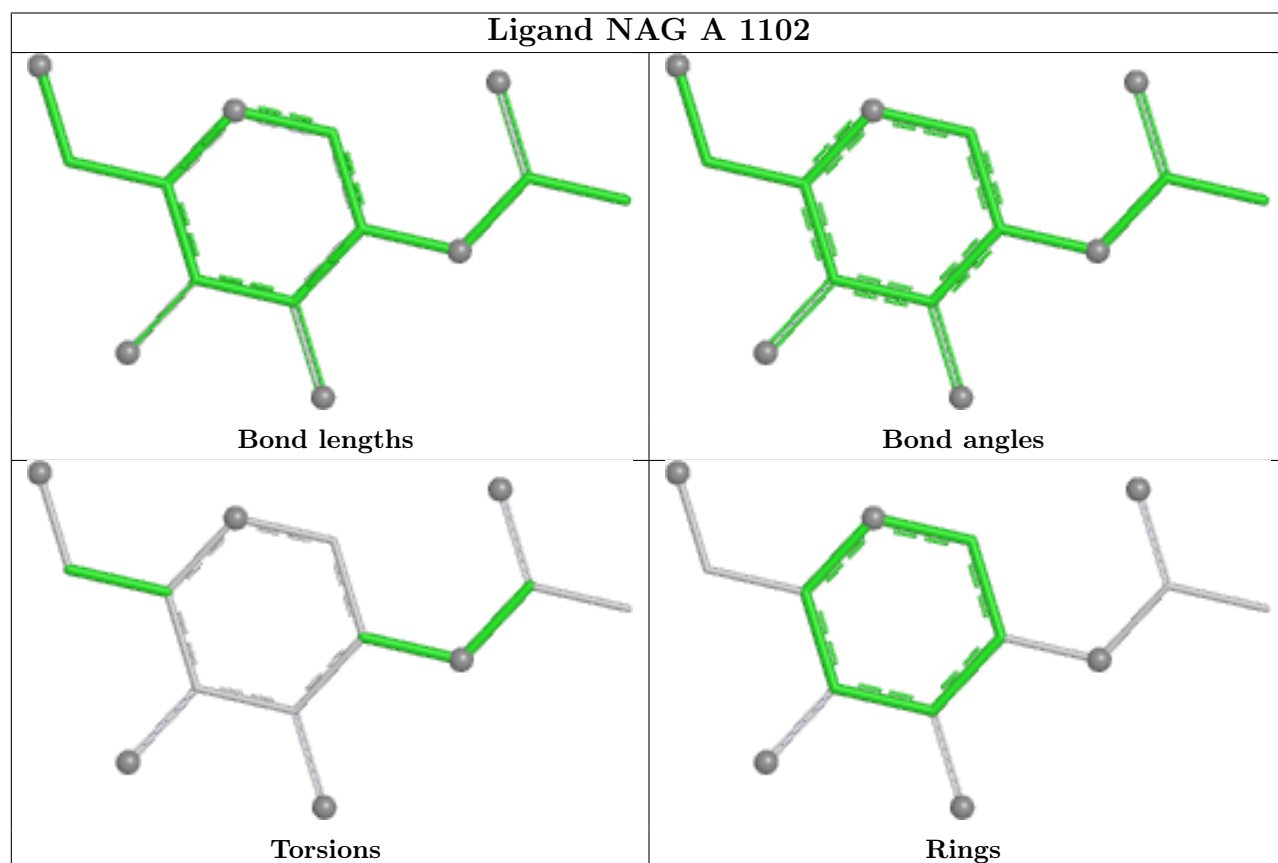
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand NAG B 1102



Ligand NAG A 1102



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.

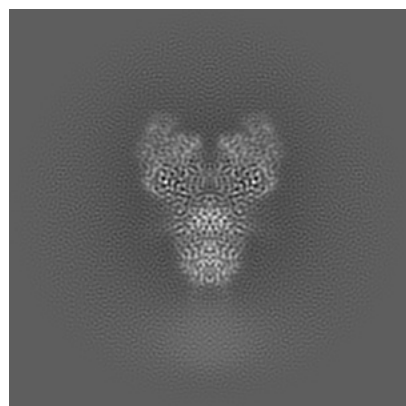
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47331. These allow visual inspection of the internal detail of the map and identification of artifacts.

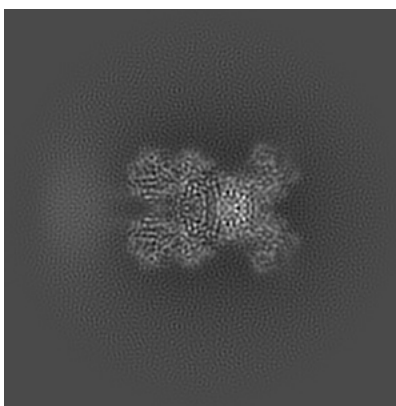
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

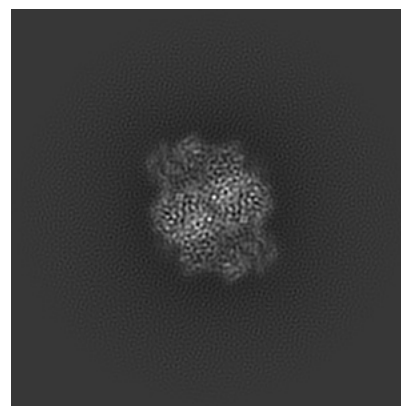
6.1.1 Primary map



X

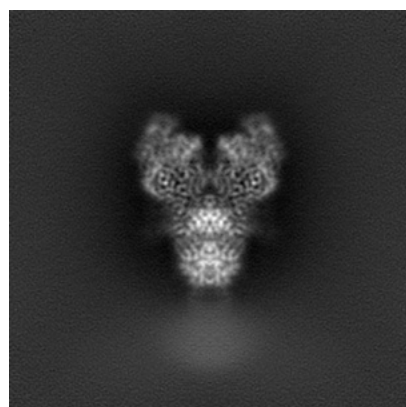


Y

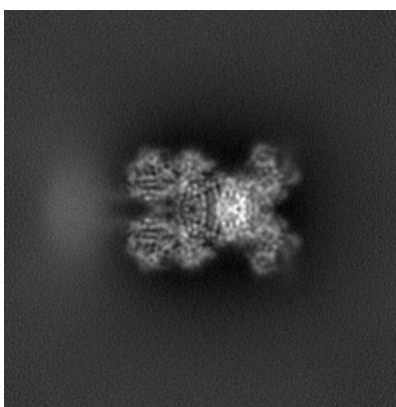


Z

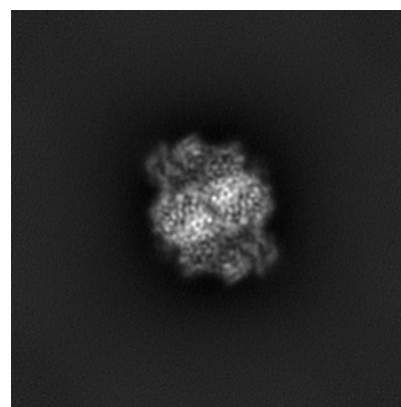
6.1.2 Raw map



X



Y

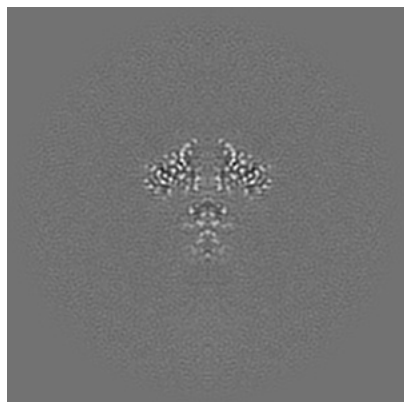


Z

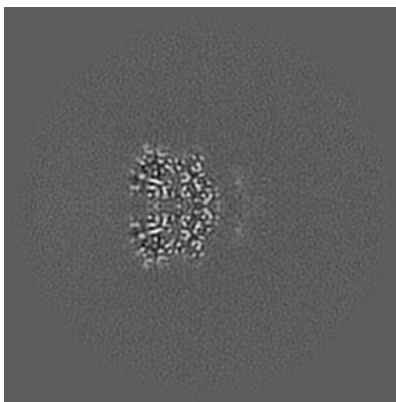
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

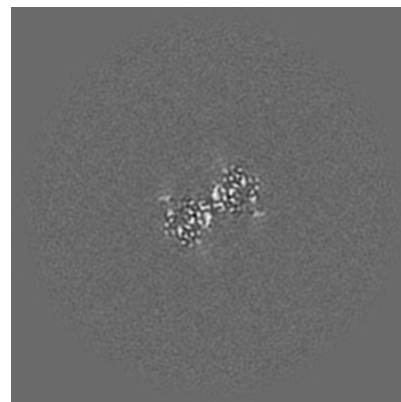
6.2.1 Primary map



X Index: 128

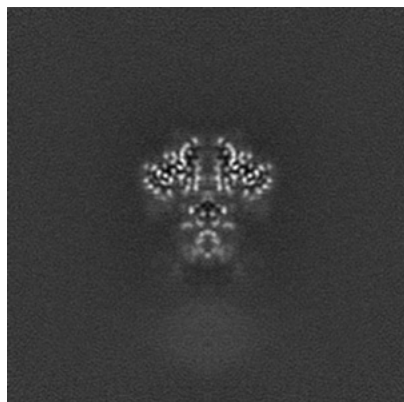


Y Index: 128

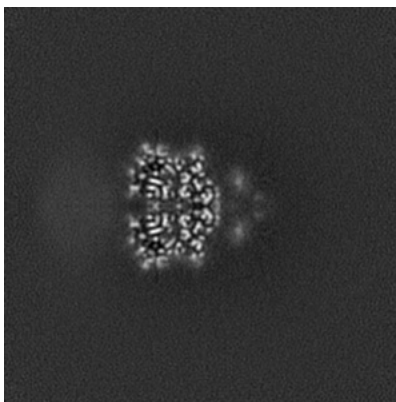


Z Index: 128

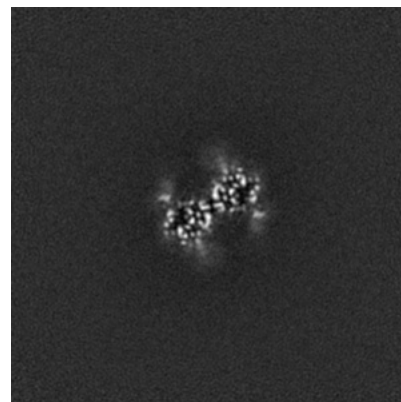
6.2.2 Raw map



X Index: 128



Y Index: 128

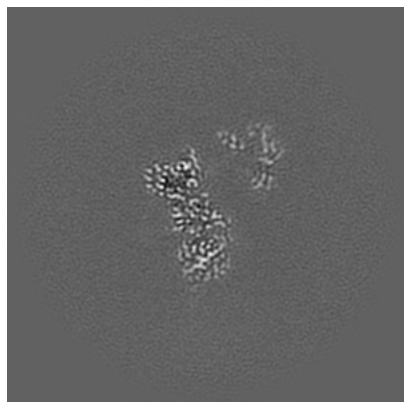


Z Index: 128

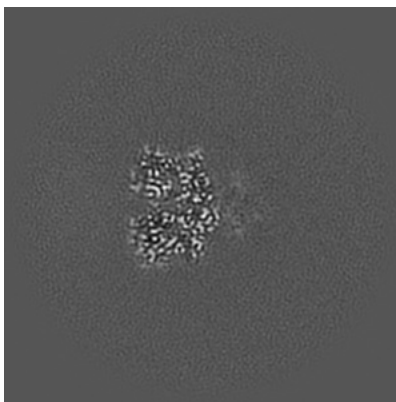
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

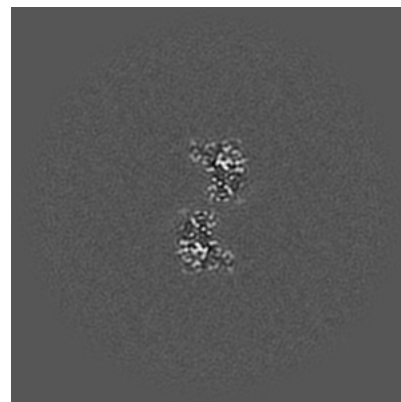
6.3.1 Primary map



X Index: 117

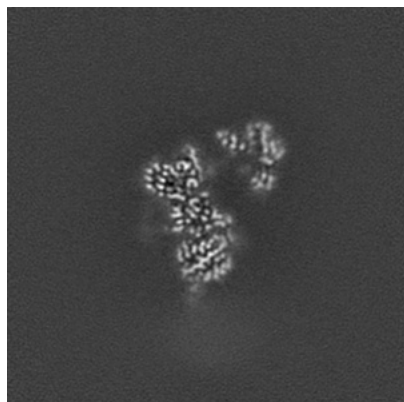


Y Index: 127

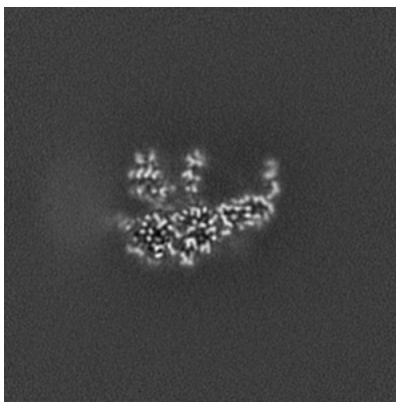


Z Index: 145

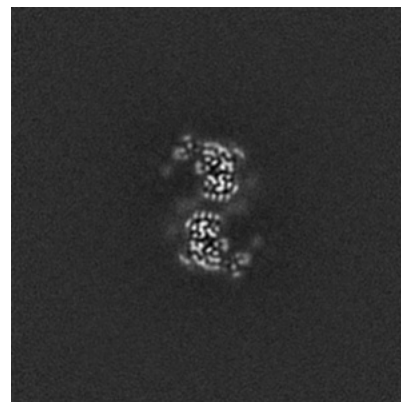
6.3.2 Raw map



X Index: 117



Y Index: 120

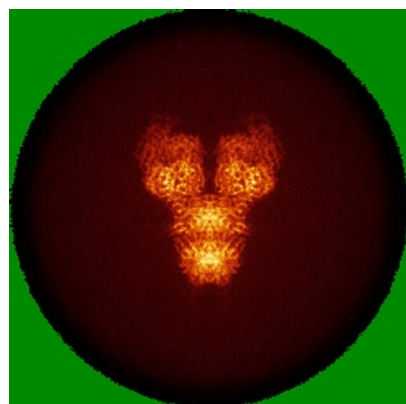


Z Index: 153

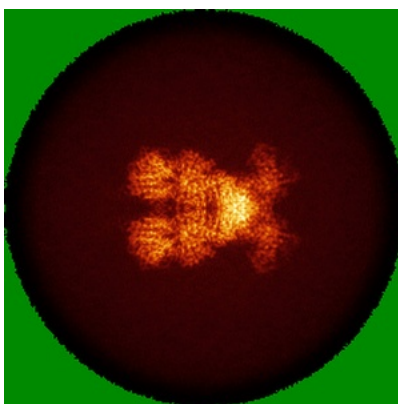
The images above show the largest variance slices of the map in three orthogonal directions.

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

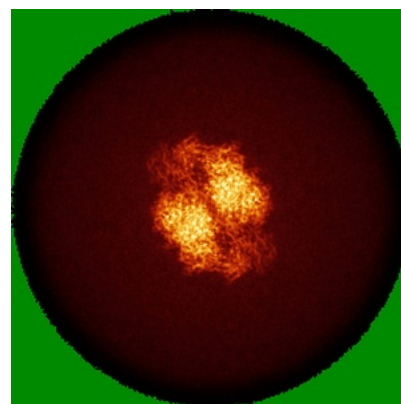
6.4.1 Primary map



X

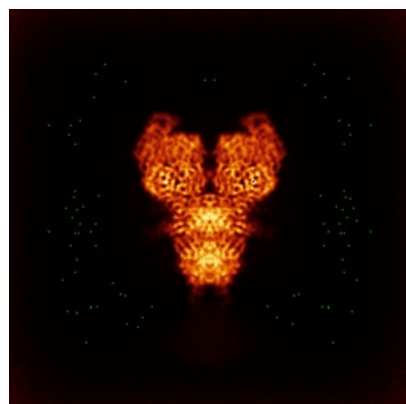


Y

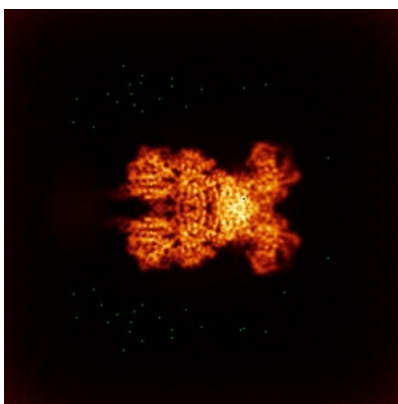


Z

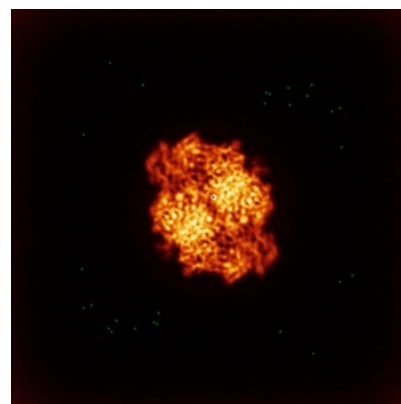
6.4.2 Raw map



X



Y

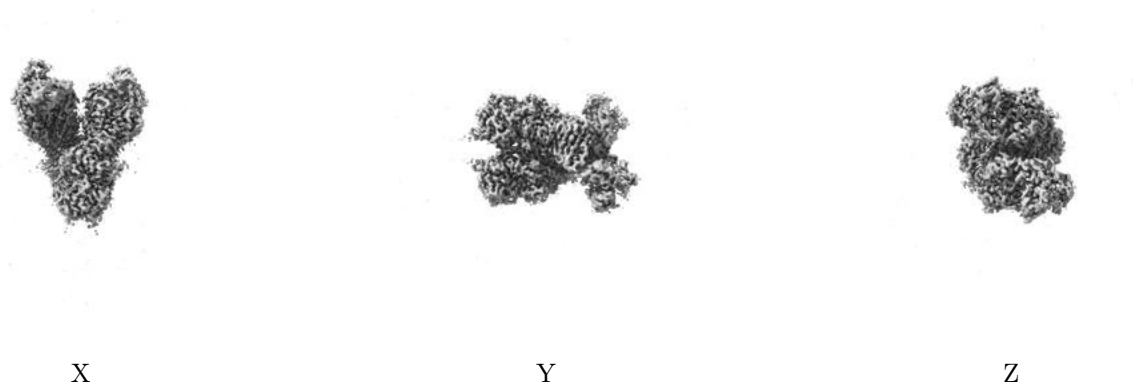


Z

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.

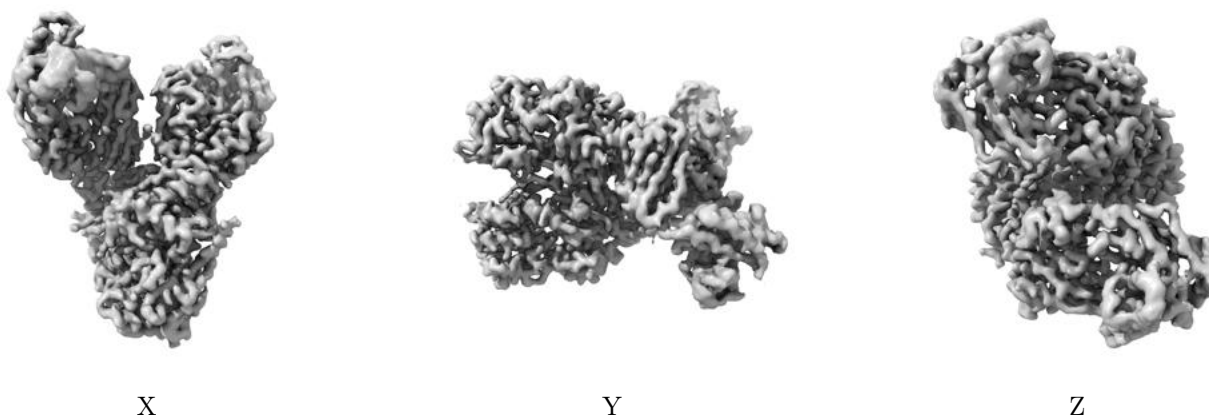
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

6.5.2 Raw map



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.

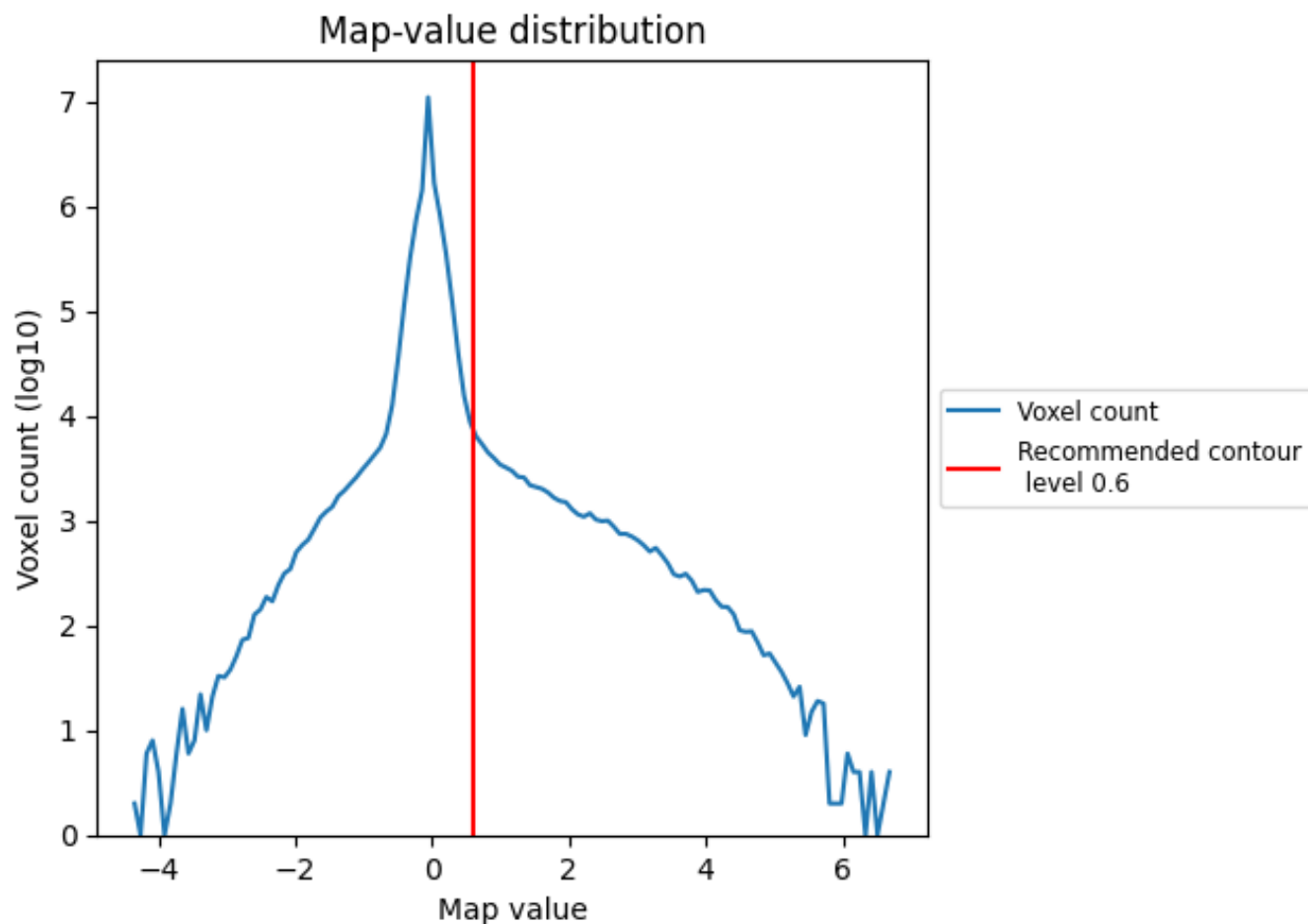
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

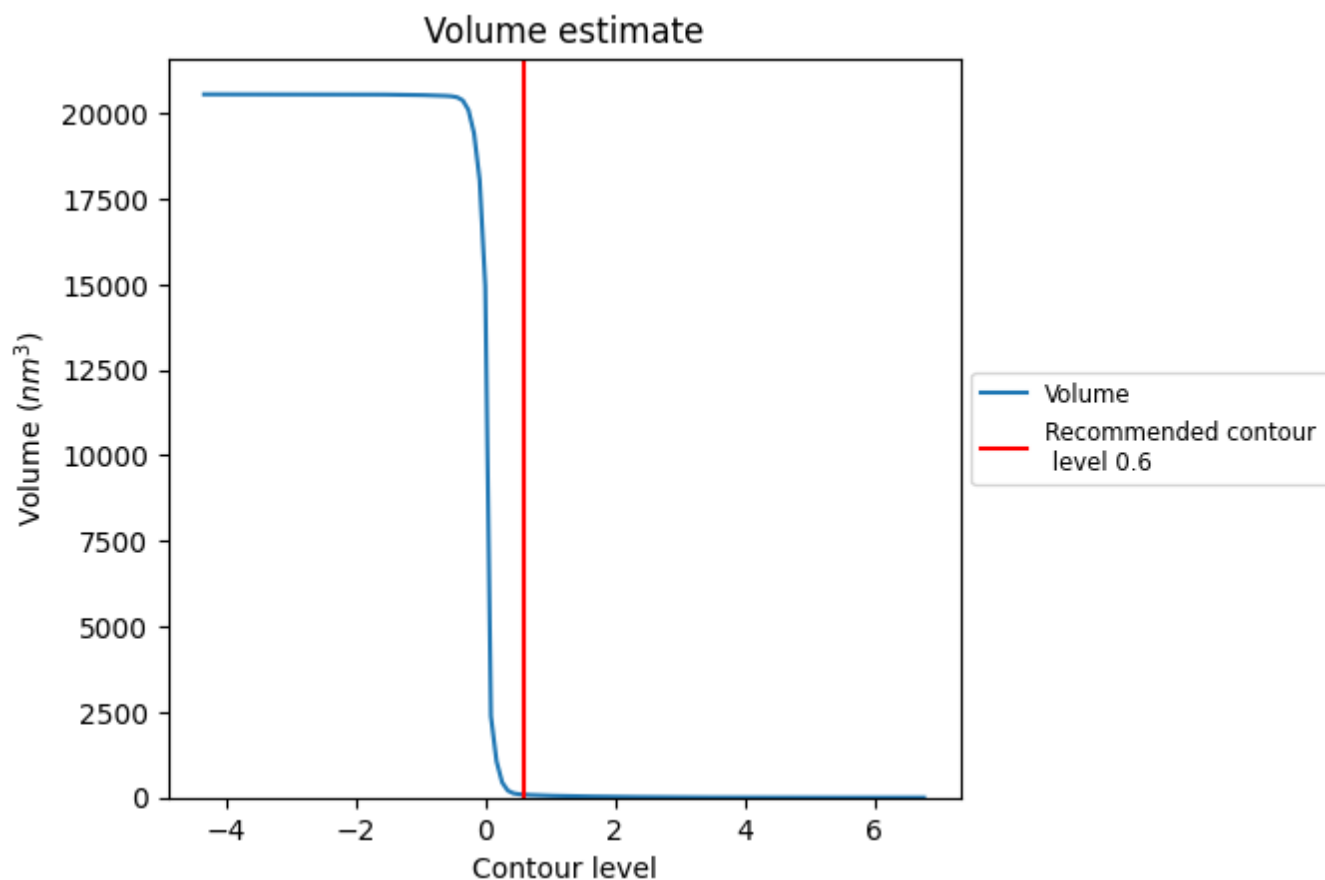
This section contains the results of statistical analysis of the map.

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.

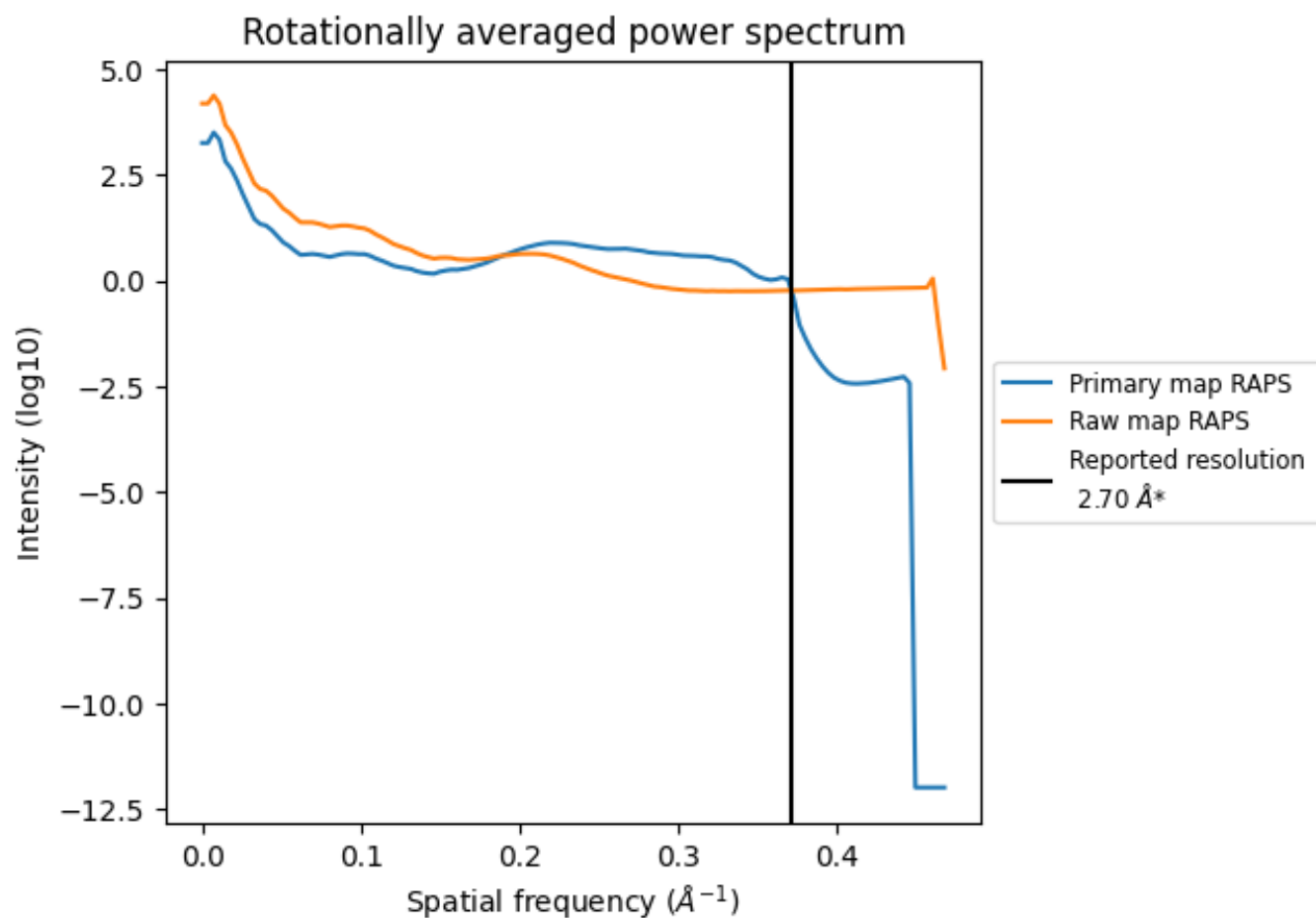
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 84 nm^3 ; this corresponds to an approximate mass of 76 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 ⓘ

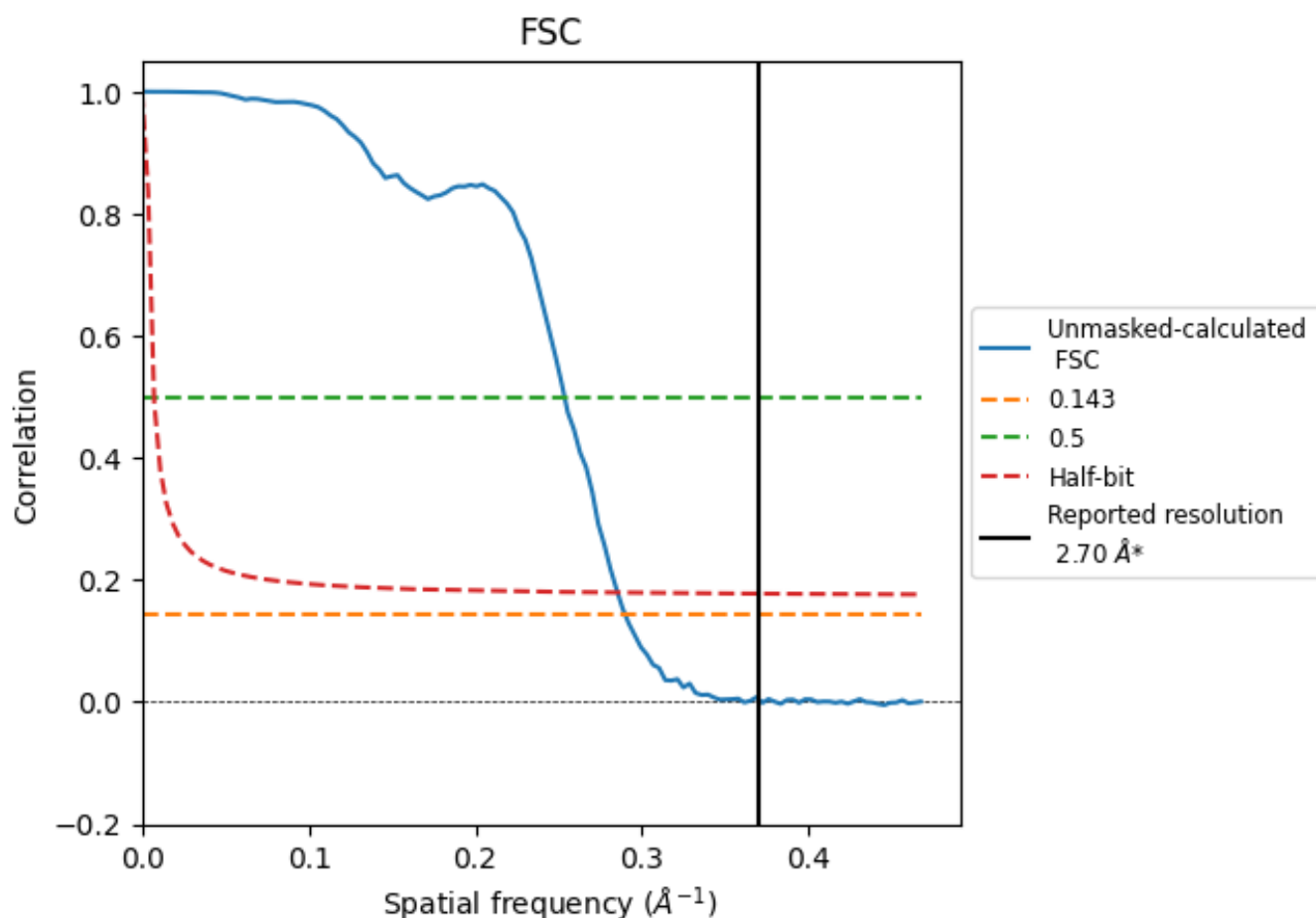


*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

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 0.370 Å⁻¹

8.2 Resolution estimates [i](#)

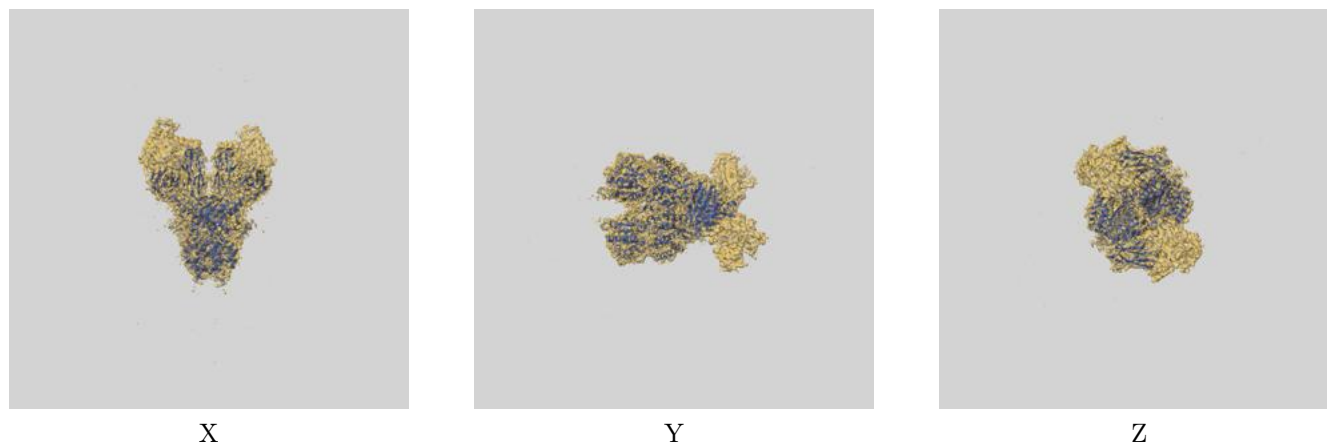
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.45	3.94	3.51

*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 3.45 differs from the reported value 2.7 by more than 10 %

9 Map-model fit [i](#)

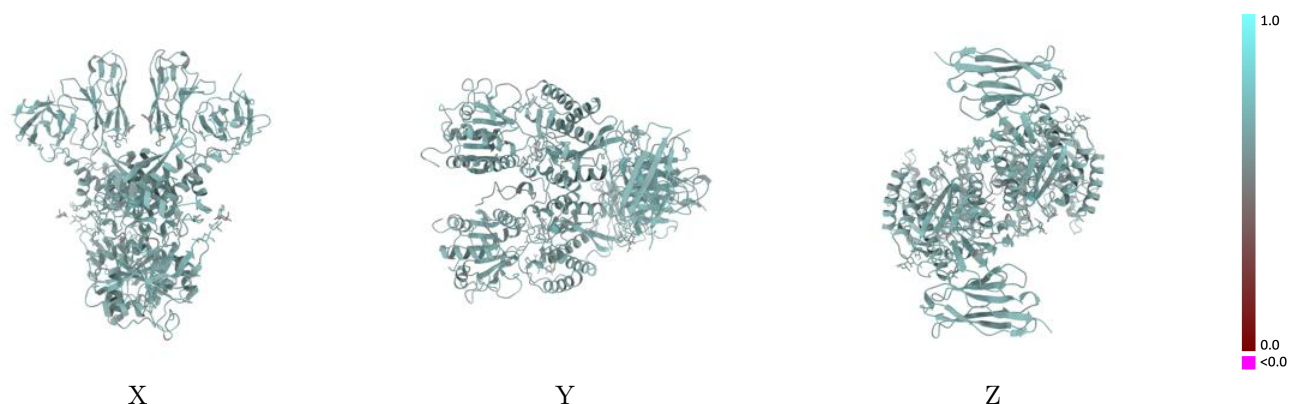
This section contains information regarding the fit between EMDB map EMD-47331 and PDB model 9DZJ. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



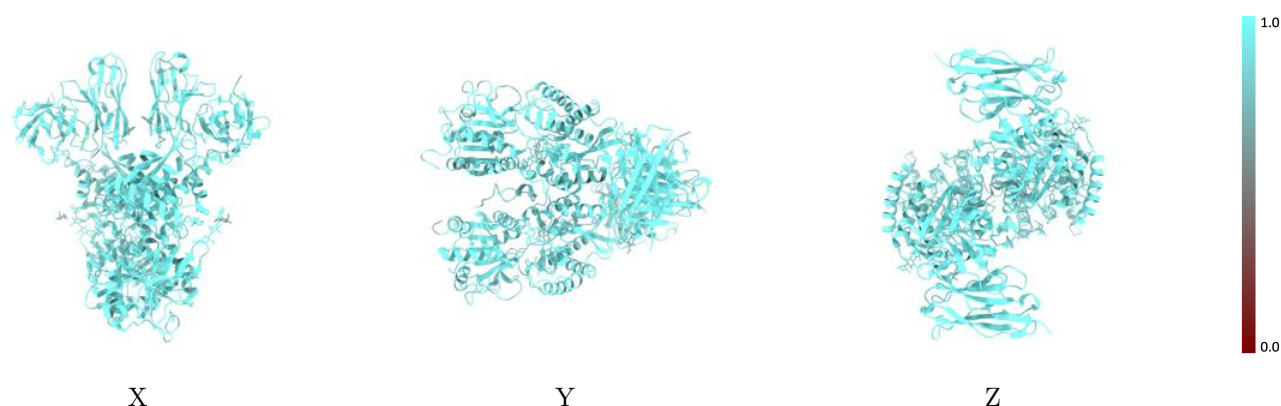
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



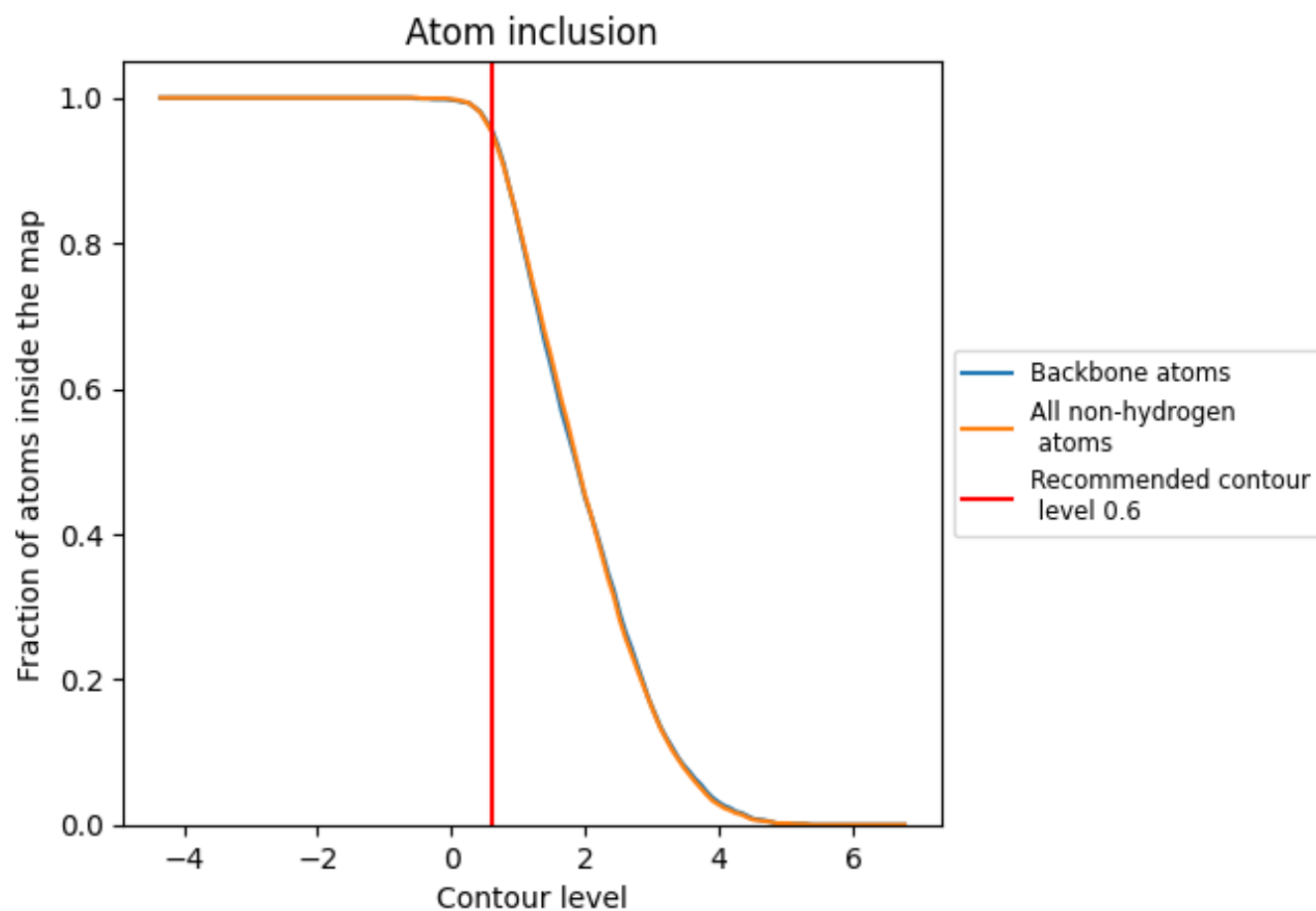
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.6).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 95% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9530	0.6230
A	0.9560	0.6240
B	0.9570	0.6220
C	0.8550	0.5670
D	0.9740	0.6130
E	0.8970	0.5940
F	0.7860	0.5580
G	0.9700	0.6280
H	0.9690	0.6320
I	0.9740	0.6040
J	0.7500	0.5630
K	0.9610	0.6240
L	0.9630	0.6210
M	0.8970	0.5900

1.0

0.0

<0.0