



Full wwPDB EM Validation Report ⓘ

Jul 28, 2026 – 12:55 PM JST

PDB ID : 9XO1 / pdb_00009xo1
EMDB ID : EMD-67066
Title : PEDV HNXX spike trimer with two D0 down in complex with two N19 Fabs
Authors : Liu, J.; Wang, S.; Wang, J.; Su, M.; Li, Z.; Xiong, X.
Deposited on : 2025-11-13
Resolution : 2.42 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

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 : 1.8.5 (274361), CSD as541be (2020)
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

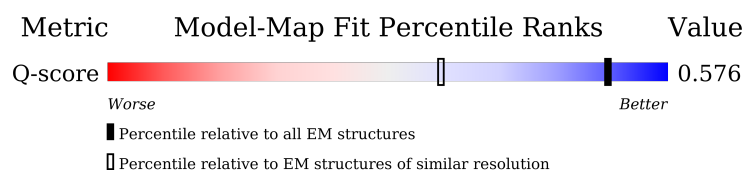
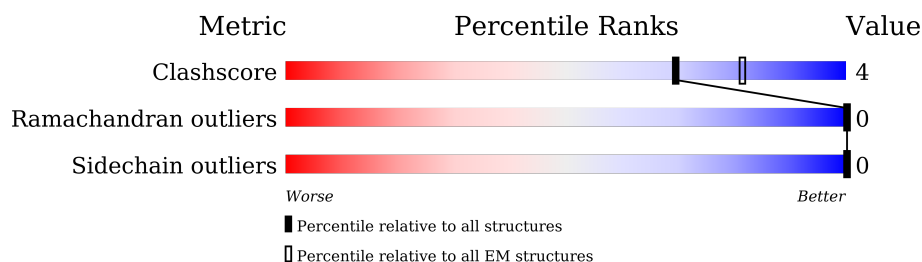
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.42 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	5729 (1.92 - 2.92)

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	A	1327	
1	B	1327	
1	C	1327	
2	D	144	

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Mol	Chain	Length	Quality of chain
2	F	144	
3	E	129	
3	G	129	
4	H	5	
4	P	5	
4	V	5	
5	I	2	
5	J	2	
5	K	2	
5	L	2	
5	M	2	
5	N	2	
5	O	2	
5	Q	2	
5	R	2	
5	S	2	
5	T	2	
5	U	2	

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 29908 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 Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1136	Total	C	N	O	S	0	0
			8719	5553	1426	1696	44		
1	B	1104	Total	C	N	O	S	0	0
			8489	5418	1392	1635	44		
1	C	1104	Total	C	N	O	S	0	0
			8489	5418	1392	1635	44		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	10	SER	PHE	conflict	UNP A0A7G4RNN0
A	888	GLY	ARG	conflict	UNP A0A7G4RNN0
A	908	ASN	SER	conflict	UNP A0A7G4RNN0
A	1010	MET	ILE	conflict	UNP A0A7G4RNN0
B	10	SER	PHE	conflict	UNP A0A7G4RNN0
B	888	GLY	ARG	conflict	UNP A0A7G4RNN0
B	908	ASN	SER	conflict	UNP A0A7G4RNN0
B	1010	MET	ILE	conflict	UNP A0A7G4RNN0
C	10	SER	PHE	conflict	UNP A0A7G4RNN0
C	888	GLY	ARG	conflict	UNP A0A7G4RNN0
C	908	ASN	SER	conflict	UNP A0A7G4RNN0
C	1010	MET	ILE	conflict	UNP A0A7G4RNN0

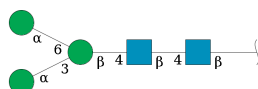
- Molecule 2 is a protein called N19 VH.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	F	117	Total	C	N	O	S	0	0
			881	548	153	176	4		
2	D	117	Total	C	N	O	S	0	0
			881	548	153	176	4		

- Molecule 3 is a protein called N19 VL.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	102	Total	C	N	O	S	0	0
			743	465	131	143	4		
3	E	102	Total	C	N	O	S	0	0
			743	465	131	143	4		

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]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
4	H	5	Total	C	N	O	0	0
			61	34	2	25		
4	P	5	Total	C	N	O	0	0
			61	34	2	25		
4	V	5	Total	C	N	O	0	0
			61	34	2	25		

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



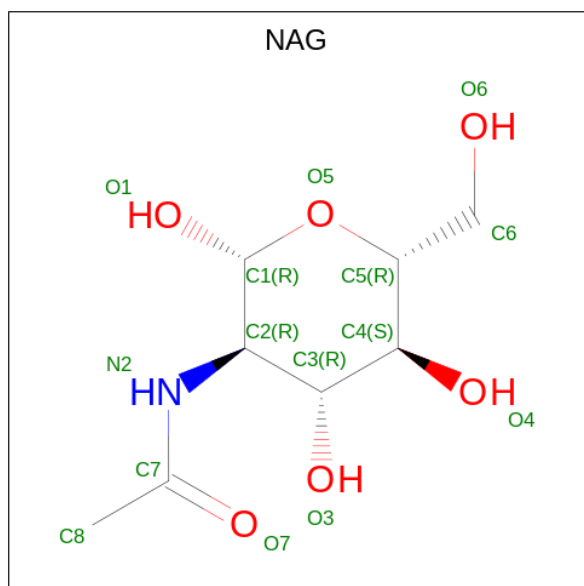
Mol	Chain	Residues	Atoms				AltConf	Trace
5	I	2	Total	C	N	O	0	0
			28	16	2	10		
5	J	2	Total	C	N	O	0	0
			28	16	2	10		
5	K	2	Total	C	N	O	0	0
			28	16	2	10		
5	L	2	Total	C	N	O	0	0
			28	16	2	10		
5	M	2	Total	C	N	O	0	0
			28	16	2	10		
5	N	2	Total	C	N	O	0	0
			28	16	2	10		
5	O	2	Total	C	N	O	0	0
			28	16	2	10		

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Mol	Chain	Residues	Atoms				AltConf	Trace
5	Q	2	Total	C	N	O	0	0
			28	16	2	10		
5	R	2	Total	C	N	O	0	0
			28	16	2	10		
5	S	2	Total	C	N	O	0	0
			28	16	2	10		
5	T	2	Total	C	N	O	0	0
			28	16	2	10		
5	U	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



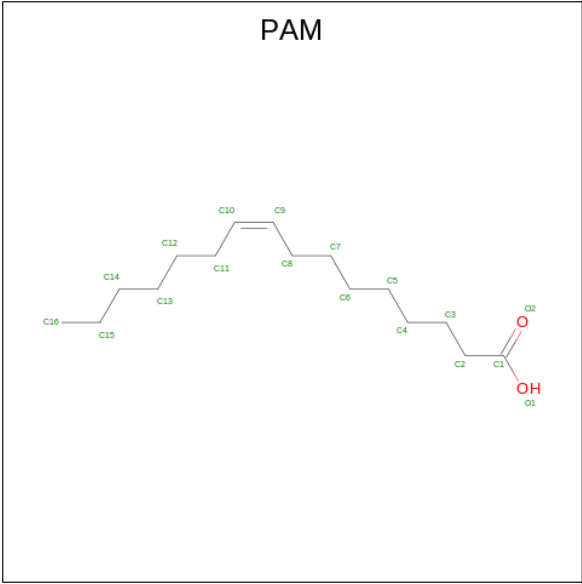
Mol	Chain	Residues	Atoms				AltConf
6	A	1	Total	C	N	O	0
			14	8	1	5	
6	A	1	Total	C	N	O	0
			14	8	1	5	
6	A	1	Total	C	N	O	0
			14	8	1	5	
6	A	1	Total	C	N	O	0
			14	8	1	5	
6	A	1	Total	C	N	O	0
			14	8	1	5	
6	A	1	Total	C	N	O	0
			14	8	1	5	

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

- Molecule 7 is PALMITOLEIC ACID (CCD ID: PAM) (formula: C₁₆H₃₀O₂).

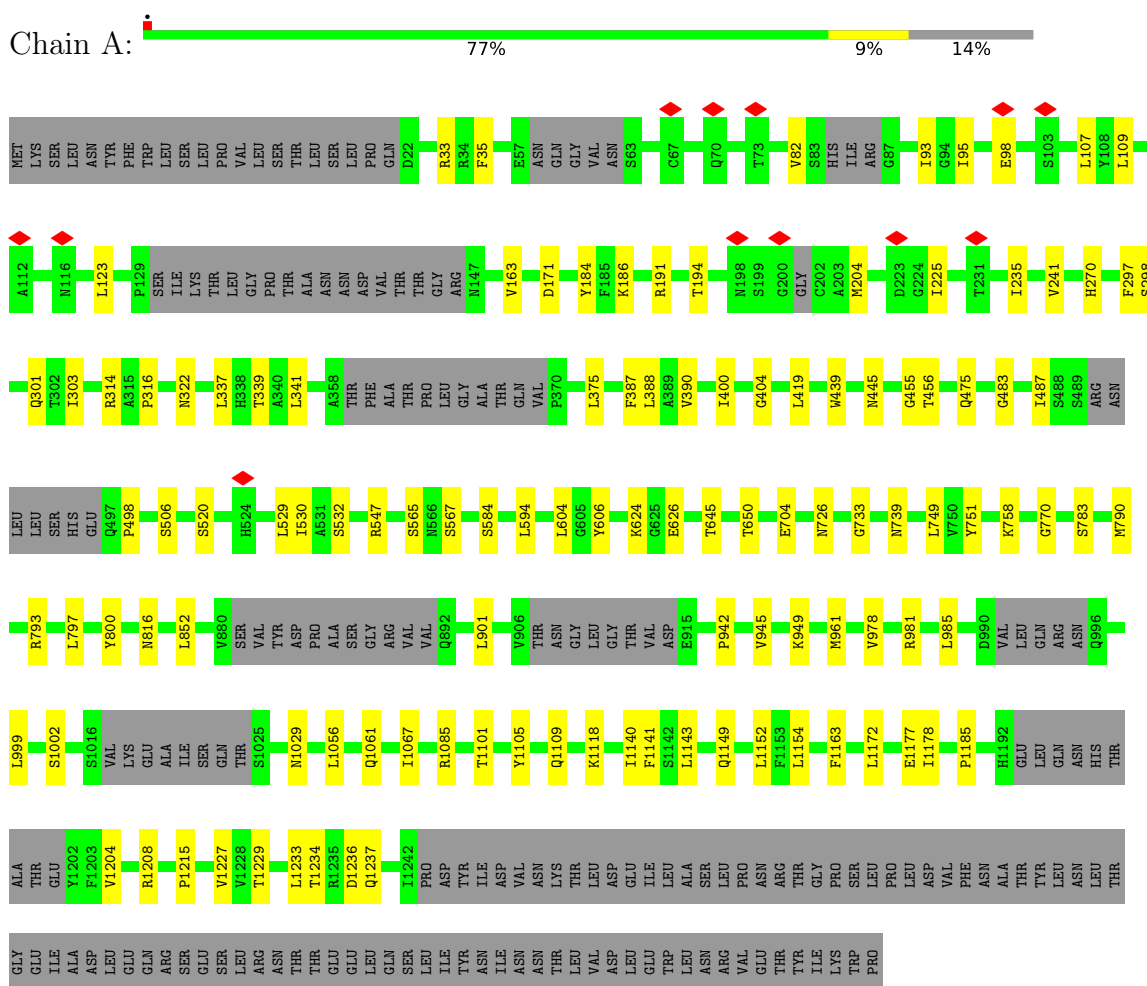


Mol	Chain	Residues	Atoms			AltConf
7	A	1	Total	C	O	0
			18	16	2	
7	A	1	Total	C	O	0
			18	16	2	
7	B	1	Total	C	O	0
			18	16	2	
7	B	1	Total	C	O	0
			18	16	2	
7	C	1	Total	C	O	0
			18	16	2	
7	C	1	Total	C	O	0
			18	16	2	

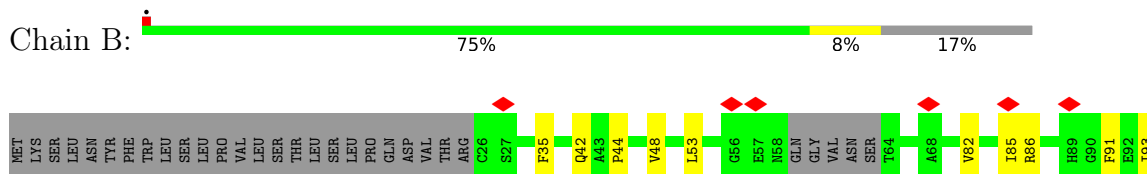
3 Residue-property plots

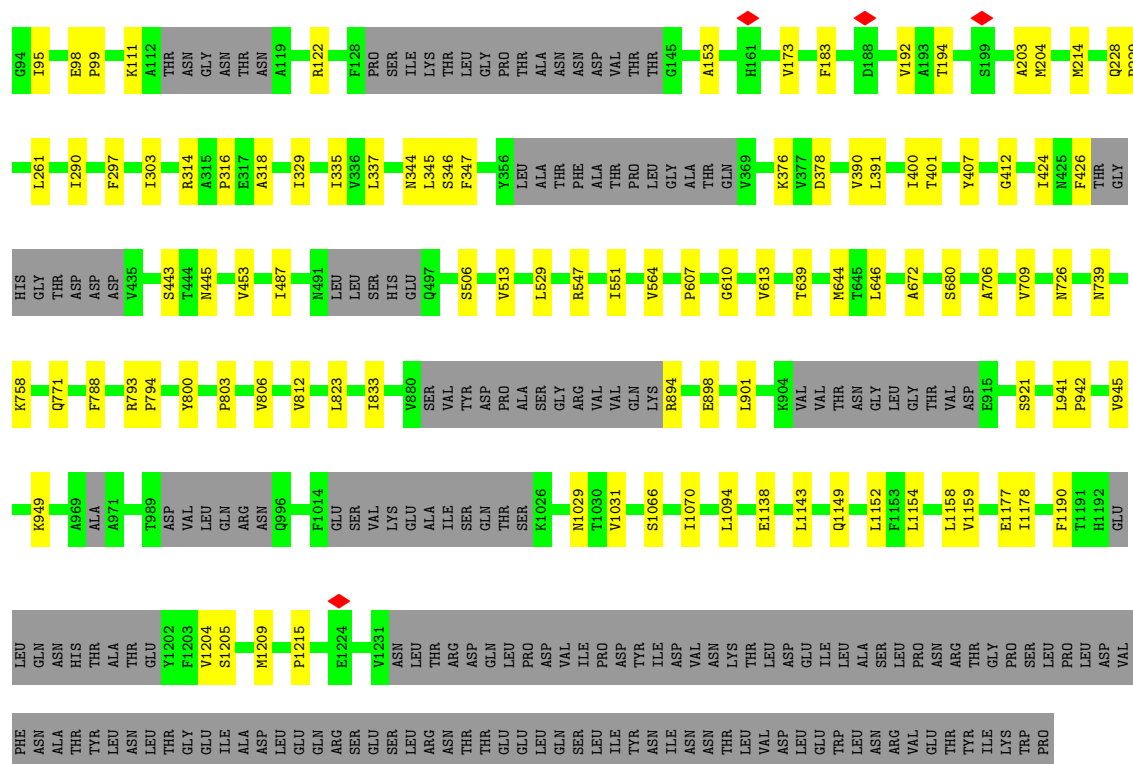
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Spike glycoprotein

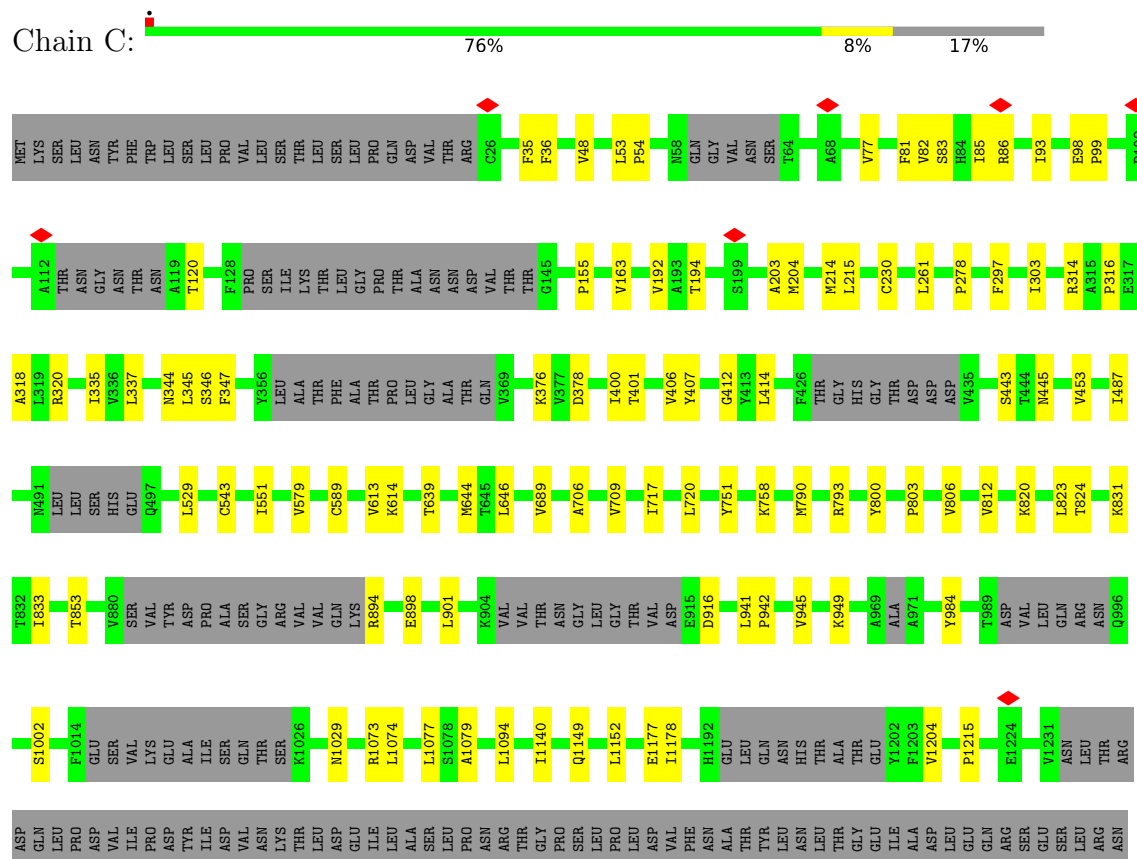


• Molecule 1: Spike glycoprotein



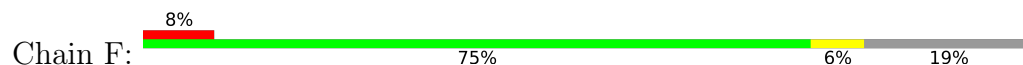


• Molecule 1: Spike glycoprotein



THR THR
GLU GLU
LEU LEU
GLN GLN
SER SER
LEU LEU
ILE ILE
TYR TYR
ASN ASN
ILE ILE
ASN ASN
THR THR
LEU LEU
VAL VAL
ASP ASP
LEU LEU
GLU GLU
TRP TRP
ASN ASN
VAL VAL
ARG ARG
GLU GLU
THR THR
TYR TYR
ILE ILE
LYS LYS
TRP TRP
PRO PRO

• Molecule 2: N19 VH



MET GLU PHE ARG LEU LEU ASN TRP VAL VAL VAL LEU LEU PHE PHE LEU LEU LEU GLN GLY VAL GLN GLY GLU E21
S26 G27 G28 G29 L30 V31 Q32 Q33 P33 Q34 G35 S40 G45 F48 A59 P60 G61 K62 R91 E104 L105 R106 T107 G108 D109 D122 V137 GLU VAL VAL VAL

SER
SER
ALA

• Molecule 2: N19 VH



MET GLU PHE ARG LEU LEU ASN TRP VAL VAL VAL LEU LEU PHE PHE LEU LEU LEU GLN GLY VAL GLN GLY GLU E21
G28 G29 L30 V31 Q32 Q33 P33 Q34 G35 S36 V37 R38 L39 F48 V56 R57 G61 K62 V66 L67 D81 R91 S94 M102 N103 E104 L105 R106 T107 G108 D109

D122 D131 V137 GLU VAL VAL VAL VAL SER SER ALA

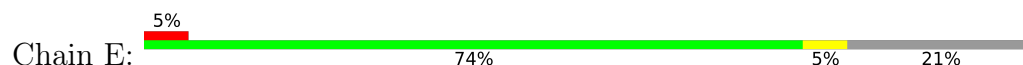
• Molecule 3: N19 VL



MET ALA TRP VAL LEU LEU ILE HIS GLY LEU LEU LEU LEU ALA VAL VAL GLY SER GLY VAL ASP SER SER GLN T21
A27 V30 S31 P32 G33 Q34 T35 V36 T37 L38 S50 P53 Q57 Q61 Q62 L66 L67 M68 Y69 R70 I86 S87 G88 L93 A98 Q99 A100 M101

T113 N116 G121 G122 THR HIS GLY LEU LEU THR VAL VAL LEU LEU GLY

• Molecule 3: N19 VL



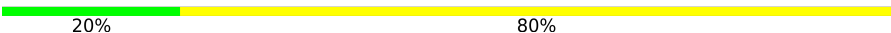
MET ALA TRP THR LEU LEU ILE HIS GLY LEU LEU LEU LEU ALA VAL VAL GLY SER GLY VAL ASP SER SER GLN T21
M28 G33 G34 T35 P53 Q57 L66 L67 M68 Y69 R70 I86 G97 A100 G120 G121 G122 THR HIS LEU LEU THR VAL VAL LEU LEU GLY

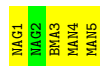
• Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



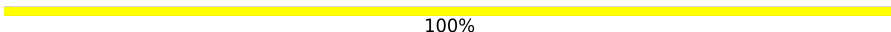
MAG1
MAG2
BKA3
MAN4
MAN5

- Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:  20% 80%

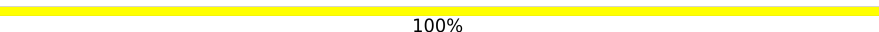


- Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain V:  100%



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

Chain I:  100%



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

Chain J:  50% 50%



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

Chain K:  50% 50%



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

Chain L:  100%



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

Chain M:  100%

NAG1
NAG2

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

Chain N:  100%

NAG1
NAG2

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

Chain O:  50% 50%

NAG1
NAG2

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

Chain Q:  50% 50%

NAG1
NAG2

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

Chain R:  50% 50%

NAG1
NAG2

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

Chain S:  100%

NAG1
NAG2

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

Chain T:  50% 50%

NAG1
NAG2

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

Chain U:  50% 50%

MAG1
MAG2

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	391616	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	4.736	Depositor
Minimum map value	-2.754	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.092	Depositor
Recommended contour level	0.32	Depositor
Map size (Å)	418.5, 418.5, 418.5	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.93, 0.93, 0.93	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, PAM, BMA, MAN

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	0.19	0/8906	0.36	0/12115
1	B	0.20	0/8673	0.38	0/11791
1	C	0.20	0/8673	0.38	0/11791
2	D	0.13	0/902	0.31	0/1222
2	F	0.12	0/902	0.30	0/1222
3	E	0.11	0/761	0.35	0/1035
3	G	0.11	0/761	0.36	0/1035
All	All	0.19	0/29578	0.37	0/40211

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	8719	0	8411	70	0
1	B	8489	0	8206	64	0
1	C	8489	0	8206	62	0
2	D	881	0	812	12	0
2	F	881	0	812	6	0
3	E	743	0	724	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	743	0	724	7	0
4	H	61	0	52	1	0
4	P	61	0	52	0	0
4	V	61	0	52	0	0
5	I	28	0	25	0	0
5	J	28	0	25	1	0
5	K	28	0	25	0	0
5	L	28	0	25	0	0
5	M	28	0	25	0	0
5	N	28	0	25	0	0
5	O	28	0	25	0	0
5	Q	28	0	25	0	0
5	R	28	0	25	0	0
5	S	28	0	25	0	0
5	T	28	0	25	0	0
5	U	28	0	25	0	0
6	A	168	0	156	0	0
6	B	84	0	78	0	0
6	C	84	0	78	0	0
7	A	36	0	58	2	0
7	B	36	0	58	4	0
7	C	36	0	58	1	0
All	All	29908	0	28837	209	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.

All (209) 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:A:375:LEU:HG	1:A:388:LEU:HD11	1.67	0.76
1:A:726:ASN:HB2	1:A:739:ASN:HA	1.71	0.70
1:A:339:THR:HG22	1:A:341:LEU:H	1.58	0.69
1:A:793:ARG:HB3	1:A:1029:ASN:HB3	1.76	0.68
1:C:85:ILE:HG22	1:C:86:ARG:HG2	1.80	0.63
1:A:93:ILE:HA	1:A:194:THR:HG22	1.79	0.62
1:C:314:ARG:HH11	1:C:445:ASN:HD22	1.47	0.62
1:A:961:MET:HE1	1:A:1143:LEU:HD23	1.81	0.62
1:A:297:PHE:HD1	1:A:303:ILE:HD12	1.64	0.62
1:B:314:ARG:HH11	1:B:445:ASN:HD22	1.45	0.62
7:B:1407:PAM:H22	1:C:689:VAL:HG13	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:26:SER:HB3	2:F:40:SER:HB2	1.82	0.61
1:B:93:ILE:HA	1:B:194:THR:HG22	1.83	0.61
1:B:85:ILE:HG22	1:B:86:ARG:HG2	1.83	0.61
1:C:806:VAL:HG11	1:C:1094:LEU:HD21	1.82	0.60
2:F:122:ASP:HB2	3:G:70:ARG:HH21	1.65	0.60
1:C:644:MET:HE3	1:C:646:LEU:HD21	1.84	0.59
1:B:793:ARG:HB3	1:B:1029:ASN:HB3	1.83	0.59
1:A:95:ILE:HD12	1:A:107:LEU:HD22	1.84	0.59
1:A:1185:PRO:HG3	1:C:984:TYR:HA	1.85	0.58
1:A:1177:GLU:HG3	1:A:1178:ILE:HG13	1.84	0.58
1:A:82:VAL:HG22	1:A:204:MET:HG2	1.85	0.58
1:C:793:ARG:HB3	1:C:1029:ASN:HB3	1.85	0.58
1:B:644:MET:HE3	1:B:646:LEU:HD21	1.86	0.57
1:C:297:PHE:HD1	1:C:303:ILE:HD12	1.67	0.57
1:C:709:VAL:HG11	1:C:758:LYS:HA	1.85	0.57
1:A:1234:THR:HB	1:A:1237:GLN:HG3	1.87	0.57
1:B:297:PHE:HD1	1:B:303:ILE:HD12	1.70	0.57
1:A:790:MET:HG3	1:A:999:LEU:HD22	1.86	0.56
7:B:1408:PAM:H111	1:C:717:ILE:HG21	1.87	0.56
1:B:894:ARG:HD2	1:B:898:GLU:HB3	1.88	0.56
1:A:1143:LEU:HB2	1:A:1154:LEU:HB2	1.87	0.56
1:B:229:PRO:HG2	3:G:50:SER:HB2	1.87	0.56
1:C:120:THR:HG22	1:C:155:PRO:HA	1.88	0.56
1:A:1204:VAL:HG23	1:A:1215:PRO:HG3	1.88	0.55
1:B:806:VAL:HG11	1:B:1094:LEU:HD21	1.87	0.55
3:G:66:LEU:HD21	3:G:69:TYR:HB3	1.88	0.55
1:B:344:ASN:HB2	1:B:378:ASP:HB2	1.87	0.55
1:B:709:VAL:HG11	1:B:758:LYS:HA	1.89	0.55
1:B:91:PHE:H	1:B:111:LYS:HB3	1.72	0.54
1:B:346:SER:HB2	1:B:376:LYS:HB3	1.90	0.54
1:B:1204:VAL:HG23	1:B:1215:PRO:HG3	1.90	0.54
1:C:945:VAL:HG23	1:C:949:LYS:HD3	1.89	0.54
1:B:82:VAL:HG22	1:B:204:MET:HG2	1.88	0.54
1:B:48:VAL:HG22	1:B:214:MET:HA	1.89	0.54
1:B:1177:GLU:HB3	1:B:1178:ILE:HD12	1.90	0.54
1:A:390:VAL:HG11	1:B:639:THR:HG23	1.90	0.53
1:B:35:PHE:HE2	1:B:53:LEU:HG	1.72	0.53
3:G:53:PRO:HG2	3:G:86:ILE:HD11	1.89	0.53
1:C:344:ASN:HB2	1:C:378:ASP:HB2	1.89	0.53
1:A:790:MET:H	1:A:1002:SER:HB3	1.72	0.53
3:G:57:GLN:HB2	3:G:67:LEU:HD11	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:645:THR:HB	1:A:650:THR:HG21	1.91	0.53
1:C:85:ILE:HD11	1:C:203:ALA:HB2	1.91	0.53
1:C:803:PRO:HB2	1:C:941:LEU:HD12	1.90	0.53
1:C:214:MET:HB2	1:C:230:CYS:HB3	1.90	0.53
1:A:456:THR:HG22	1:B:672:ALA:HB3	1.91	0.53
1:B:945:VAL:HG23	1:B:949:LYS:HD3	1.91	0.53
2:F:28:GLY:HA3	2:F:137:VAL:HG11	1.91	0.52
1:B:607:PRO:HG2	1:B:610:GLY:HA3	1.91	0.52
1:A:945:VAL:HG13	1:A:949:LYS:HB3	1.91	0.52
1:B:42:GLN:HG3	1:B:44:PRO:HD2	1.90	0.52
3:E:66:LEU:HD21	3:E:69:TYR:HB3	1.92	0.52
1:C:337:LEU:HD21	1:C:400:ILE:HD13	1.92	0.52
2:D:37:VAL:HG13	2:D:102:MET:HE2	1.92	0.51
1:A:529:LEU:HD22	1:A:532:SER:HB3	1.92	0.51
1:A:733:GLY:HA2	1:C:916:ASP:HA	1.92	0.51
2:F:59:ALA:HB3	2:F:62:LYS:HB2	1.92	0.51
1:B:337:LEU:HD21	1:B:400:ILE:HD13	1.91	0.51
1:A:303:ILE:HD11	1:A:316:PRO:HG3	1.93	0.51
1:B:487:ILE:HD13	1:B:706:ALA:HB2	1.92	0.51
1:B:214:MET:HG2	1:B:228:GLN:HE21	1.77	0.50
1:A:584:SER:HB3	1:A:626:GLU:HA	1.94	0.50
1:A:942:PRO:HD3	7:A:1414:PAM:H122	1.94	0.50
1:C:346:SER:HB2	1:C:376:LYS:HB3	1.93	0.50
1:C:894:ARG:HD2	1:C:898:GLU:HB3	1.93	0.50
1:B:390:VAL:HG11	1:C:639:THR:HG23	1.94	0.50
1:A:567:SER:HB3	1:A:604:LEU:HB2	1.94	0.49
1:C:487:ILE:HD13	1:C:706:ALA:HB2	1.92	0.49
3:E:57:GLN:HB2	3:E:67:LEU:HD11	1.94	0.49
1:B:833:ILE:HD13	1:B:1094:LEU:HB3	1.95	0.49
1:C:35:PHE:HE2	1:C:53:LEU:HG	1.76	0.49
1:C:77:VAL:HG21	1:C:192:VAL:HG12	1.94	0.49
1:A:98:GLU:HG2	1:A:191:ARG:HH21	1.78	0.49
1:C:303:ILE:HG13	1:C:443:SER:HB2	1.95	0.48
1:B:318:ALA:HA	1:B:401:THR:HA	1.96	0.48
1:A:1105:TYR:O	1:A:1109:GLN:HG3	2.14	0.48
1:C:337:LEU:HB2	1:C:345:LEU:HB2	1.96	0.48
1:A:270:HIS:CD2	1:A:455:GLY:H	2.31	0.48
1:B:803:PRO:HB2	1:B:941:LEU:HD12	1.94	0.48
1:A:816:ASN:HD22	1:A:1067:ILE:HG22	1.79	0.48
1:C:82:VAL:HG22	1:C:204:MET:HG2	1.94	0.48
1:B:901:LEU:HD11	1:B:1152:LEU:HD22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:318:ALA:HA	1:C:401:THR:HA	1.96	0.48
1:C:901:LEU:HD11	1:C:1152:LEU:HD22	1.96	0.47
1:B:337:LEU:HB2	1:B:345:LEU:HB2	1.96	0.47
1:C:98:GLU:HB2	1:C:99:PRO:HD3	1.97	0.47
1:C:93:ILE:HA	1:C:194:THR:HG22	1.96	0.47
1:A:483:GLY:HA2	1:A:749:LEU:HD11	1.97	0.47
1:C:406:VAL:HB	1:C:414:LEU:HB2	1.97	0.47
1:C:48:VAL:HG22	1:C:214:MET:HA	1.97	0.47
1:C:407:TYR:HA	1:C:412:GLY:H	1.79	0.47
1:B:1143:LEU:HB2	1:B:1154:LEU:HB2	1.97	0.47
1:B:800:TYR:CZ	1:B:1149:GLN:HA	2.49	0.46
1:A:33:ARG:HA	1:A:225:ILE:HD11	1.97	0.46
1:B:564:VAL:HG22	1:B:607:PRO:HA	1.96	0.46
2:D:56:VAL:HG12	2:D:66:TRP:HA	1.96	0.46
1:A:298:SER:HB3	1:A:301:GLN:HB2	1.98	0.46
1:A:520:SER:HB2	1:A:530:ILE:HB	1.98	0.46
1:A:387:PHE:HE2	1:B:506:SER:HA	1.81	0.46
1:B:921:SER:HB2	1:C:720:LEU:HD23	1.98	0.46
1:A:624:LYS:HE2	1:C:1073:ARG:HH22	1.81	0.46
1:A:985:LEU:HA	1:A:1208:ARG:HH21	1.80	0.46
1:B:95:ILE:HG13	1:B:192:VAL:HG23	1.98	0.46
2:F:48:PHE:HB3	2:F:91:ARG:NH2	2.31	0.46
1:C:36:PHE:HB3	1:C:215:LEU:HD21	1.96	0.46
1:A:1140:ILE:HG12	1:A:1141:PHE:HD1	1.81	0.46
2:D:102:MET:HB3	2:D:105:LEU:HD21	1.97	0.46
1:A:770:GLY:H	1:C:853:THR:HB	1.81	0.46
1:B:303:ILE:HG13	1:B:443:SER:HB2	1.97	0.46
1:B:794:PRO:HG2	1:B:1031:VAL:HG22	1.98	0.45
1:B:85:ILE:HD11	1:B:203:ALA:HB2	1.98	0.45
1:C:83:SER:HB2	1:C:163:VAL:HG12	1.98	0.45
1:A:852:LEU:HD22	1:A:945:VAL:HG21	1.97	0.45
1:A:1234:THR:HG22	1:A:1236:ASP:H	1.81	0.45
1:C:303:ILE:HD11	1:C:316:PRO:HG3	1.99	0.45
1:A:109:LEU:HD12	1:A:123:LEU:HD13	1.99	0.44
1:B:529:LEU:HD21	1:B:613:VAL:HG21	1.99	0.44
2:D:48:PHE:HB3	2:D:91:ARG:HH21	1.83	0.44
1:A:1172:LEU:HD22	1:A:1233:LEU:HD21	1.98	0.44
2:D:48:PHE:HB3	2:D:91:ARG:NH2	2.33	0.44
1:C:942:PRO:HD3	7:C:1401:PAM:H121	2.00	0.44
1:A:35:PHE:HB2	1:A:163:VAL:HB	1.99	0.44
1:C:833:ILE:HD13	1:C:1094:LEU:HB3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:106:ARG:HD3	2:D:109:ASP:HB2	2.00	0.44
1:A:981:ARG:HD3	1:A:1140:ILE:O	2.18	0.44
1:A:901:LEU:HD11	1:A:1152:LEU:HD22	2.00	0.43
2:D:122:ASP:HB2	3:E:70:ARG:HH21	1.83	0.43
1:A:594:LEU:HD23	1:C:614:LYS:HB2	1.99	0.43
1:A:404:GLY:HA2	1:A:419:LEU:HD13	2.00	0.43
1:B:98:GLU:HB2	1:B:99:PRO:HD3	2.01	0.43
1:B:513:VAL:HB	1:B:551:ILE:HG12	1.99	0.43
1:B:942:PRO:HD2	1:C:751:TYR:HE2	1.83	0.43
3:G:113:THR:HB	3:G:116:ASN:HB3	1.99	0.43
1:C:551:ILE:HD12	1:C:579:VAL:HG21	2.00	0.43
1:A:797:LEU:HD11	1:A:1118:LYS:HD2	2.00	0.43
1:B:173:VAL:HG13	1:B:183:PHE:HB2	2.01	0.43
1:B:391:LEU:HD11	7:B:1407:PAM:H142	2.01	0.43
1:B:771:GLN:NE2	1:B:1159:VAL:HG22	2.34	0.43
1:C:529:LEU:HD11	1:C:613:VAL:HG11	2.00	0.43
2:D:39:LEU:HG	2:D:102:MET:HE1	2.01	0.43
1:A:322:ASN:O	1:A:439:TRP:HB2	2.20	0.42
1:A:506:SER:HB2	1:A:547:ARG:NH1	2.34	0.42
2:D:57:ARG:HB2	2:D:67:LEU:HD11	2.00	0.42
1:A:565:SER:HB2	1:A:606:TYR:HB2	2.02	0.42
1:C:278:PRO:HG2	1:C:320:ARG:NH1	2.34	0.42
3:E:53:PRO:HG2	3:E:86:ILE:HD11	2.01	0.42
1:A:235:ILE:HG13	1:A:241:VAL:HG11	2.00	0.42
7:A:1413:PAM:H10	7:A:1413:PAM:H71	1.83	0.42
1:B:303:ILE:HD11	1:B:316:PRO:HG3	2.02	0.42
1:C:790:MET:H	1:C:1002:SER:HB3	1.84	0.42
1:B:942:PRO:HD3	7:B:1408:PAM:H121	2.01	0.42
2:F:48:PHE:HB3	2:F:91:ARG:HH21	1.84	0.42
1:C:1077:LEU:HD12	4:H:5:MAN:H62	2.00	0.42
2:D:28:GLY:HA3	2:D:137:VAL:HG11	1.99	0.42
1:A:751:TYR:HE2	1:C:942:PRO:HD2	1.85	0.42
1:A:337:LEU:HD21	1:A:400:ILE:HD13	2.01	0.42
1:B:1138:GLU:HB2	1:B:1158:LEU:HB2	2.02	0.42
1:C:1204:VAL:HG23	1:C:1215:PRO:HG3	2.01	0.42
1:A:978:VAL:HG13	1:A:1140:ILE:HD11	2.01	0.42
1:C:1074:LEU:HB2	1:C:1079:ALA:HB2	2.02	0.41
1:B:335:ILE:HB	1:B:347:PHE:HD2	1.86	0.41
1:B:407:TYR:HA	1:B:412:GLY:H	1.84	0.41
1:C:800:TYR:CZ	1:C:1149:GLN:HA	2.55	0.41
1:A:487:ILE:HG13	1:A:704:GLU:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:820:LYS:O	1:C:824:THR:HG23	2.20	0.41
1:A:1061:GLN:HB2	1:A:1085:ARG:HH21	1.86	0.41
1:B:329:ILE:HD13	1:B:426:PHE:HZ	1.86	0.41
1:B:1190:PHE:HE1	1:B:1205:SER:HB3	1.85	0.41
1:A:783:SER:OG	1:A:1163:PHE:HB3	2.20	0.41
1:B:812:VAL:HG11	1:B:823:LEU:HD13	2.03	0.41
1:C:1177:GLU:HB3	1:C:1178:ILE:HD12	2.02	0.41
1:A:337:LEU:HB3	1:A:419:LEU:HD21	2.03	0.41
1:A:1056:LEU:HB2	1:B:680:SER:HB2	2.02	0.41
1:B:290:ILE:HG21	1:B:424:ILE:HG22	2.01	0.41
1:B:506:SER:HB2	1:B:547:ARG:HE	1.85	0.41
1:C:335:ILE:HB	1:C:347:PHE:HD2	1.85	0.41
1:C:790:MET:HE2	1:C:1140:ILE:HD13	2.02	0.41
1:C:812:VAL:HG11	1:C:823:LEU:HD13	2.03	0.41
1:A:314:ARG:HD2	1:A:445:ASN:OD1	2.21	0.41
1:A:800:TYR:CZ	1:A:1149:GLN:HA	2.56	0.41
1:B:1066:SER:O	1:B:1070:ILE:HG13	2.21	0.41
1:C:543:CYS:HA	1:C:589:CYS:HA	2.03	0.41
2:D:31:VAL:HG21	2:D:37:VAL:HG11	2.02	0.41
1:A:498:PRO:HD2	1:A:650:THR:HG22	2.03	0.40
1:A:1101:THR:HG22	1:A:1105:TYR:CE2	2.56	0.40
1:B:122:ARG:HA	1:B:153:ALA:HA	2.02	0.40
1:B:726:ASN:OD1	1:B:739:ASN:HA	2.21	0.40
1:A:758:LYS:HE2	1:A:758:LYS:HB2	1.76	0.40
1:B:788:PHE:CE2	1:B:1209:MET:HG2	2.57	0.40
3:G:30:VAL:HG21	3:G:36:VAL:HB	2.02	0.40
1:C:261:LEU:HD22	1:C:453:VAL:HG21	2.02	0.40
1:A:475:GLN:O	1:C:831:LYS:HG3	2.21	0.40
2:D:131:ASP:HA	3:E:66:LEU:HB2	2.04	0.40
1:A:184:TYR:CE2	5:J:1:NAG:H3	2.57	0.40
1:B:261:LEU:HD22	1:B:453:VAL:HG21	2.03	0.40
1:A:171:ASP:OD1	1:A:186:LYS:HA	2.21	0.40
1:A:1227:VAL:HG12	1:A:1229:THR:H	1.86	0.40
1:C:54:PRO:HD3	1:C:81:PHE:CZ	2.57	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	1112/1327 (84%)	1071 (96%)	41 (4%)	0	100	100
1	B	1078/1327 (81%)	1038 (96%)	40 (4%)	0	100	100
1	C	1078/1327 (81%)	1042 (97%)	36 (3%)	0	100	100
2	D	115/144 (80%)	112 (97%)	3 (3%)	0	100	100
2	F	115/144 (80%)	107 (93%)	8 (7%)	0	100	100
3	E	100/129 (78%)	94 (94%)	6 (6%)	0	100	100
3	G	100/129 (78%)	90 (90%)	10 (10%)	0	100	100
All	All	3698/4527 (82%)	3554 (96%)	144 (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	A	977/1149 (85%)	977 (100%)	0	100	100
1	B	948/1149 (82%)	948 (100%)	0	100	100
1	C	948/1149 (82%)	948 (100%)	0	100	100
2	D	90/113 (80%)	90 (100%)	0	100	100
2	F	90/113 (80%)	90 (100%)	0	100	100
3	E	80/101 (79%)	80 (100%)	0	100	100
3	G	80/101 (79%)	80 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	3213/3875 (83%)	3213 (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 (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	ASN
1	A	78	HIS
1	A	1120	ASN
1	B	127	GLN
1	B	228	GLN
1	B	475	GLN
1	B	566	ASN
1	B	636	GLN
1	B	1039	GLN
1	B	1045	GLN
1	B	1095	ASN
1	B	1100	GLN
1	B	1128	GLN
1	B	1149	GLN
2	F	96	ASN
3	G	51	ASN
3	G	111	HIS
1	C	106	GLN
1	C	161	HIS
1	C	228	GLN
1	C	258	ASN
1	C	454	GLN
1	C	988	GLN
1	C	1033	HIS
1	C	1095	ASN
1	C	1139	HIS
2	D	58	GLN
2	D	103	ASN
3	E	58	GLN
3	E	89	ASN
3	E	111	HIS

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 ⓘ

39 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	$\# Z > 2$
4	NAG	H	1	1,4	14,14,15	0.86	1 (7%)	17,19,21	1.37	2 (11%)
4	NAG	H	2	4	14,14,15	0.77	0	17,19,21	0.88	0
4	BMA	H	3	4	11,11,12	1.05	0	15,15,17	2.36	5 (33%)
4	MAN	H	4	4	11,11,12	0.71	0	15,15,17	1.44	1 (6%)
4	MAN	H	5	4	11,11,12	0.70	0	15,15,17	1.97	2 (13%)
5	NAG	I	1	1,5	14,14,15	0.79	0	17,19,21	0.97	1 (5%)
5	NAG	I	2	5	14,14,15	0.73	0	17,19,21	1.05	2 (11%)
5	NAG	J	1	1,5	14,14,15	0.74	0	17,19,21	1.10	2 (11%)
5	NAG	J	2	5	14,14,15	0.72	0	17,19,21	0.94	1 (5%)
5	NAG	K	1	1,5	14,14,15	0.72	0	17,19,21	1.02	1 (5%)
5	NAG	K	2	5	14,14,15	0.71	0	17,19,21	0.80	0
5	NAG	L	1	1,5	14,14,15	0.77	0	17,19,21	1.06	0
5	NAG	L	2	5	14,14,15	0.76	0	17,19,21	0.86	0
5	NAG	M	1	1,5	14,14,15	0.83	1 (7%)	17,19,21	1.19	2 (11%)
5	NAG	M	2	5	14,14,15	0.71	0	17,19,21	1.38	1 (5%)
5	NAG	N	1	1,5	14,14,15	0.77	0	17,19,21	0.92	0
5	NAG	N	2	5	14,14,15	0.73	0	17,19,21	0.91	0
5	NAG	O	1	1,5	14,14,15	0.72	0	17,19,21	0.97	1 (5%)
5	NAG	O	2	5	14,14,15	0.72	0	17,19,21	0.88	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	P	1	1,4	14,14,15	0.82	0	17,19,21	1.31	2 (11%)
4	NAG	P	2	4	14,14,15	0.82	0	17,19,21	0.92	0
4	BMA	P	3	4	11,11,12	1.02	0	15,15,17	2.61	7 (46%)
4	MAN	P	4	4	11,11,12	0.68	0	15,15,17	1.53	1 (6%)
4	MAN	P	5	4	11,11,12	0.69	0	15,15,17	1.38	1 (6%)
5	NAG	Q	1	1,5	14,14,15	0.76	0	17,19,21	1.01	1 (5%)
5	NAG	Q	2	5	14,14,15	0.69	0	17,19,21	0.88	0
5	NAG	R	1	1,5	14,14,15	0.75	0	17,19,21	0.96	1 (5%)
5	NAG	R	2	5	14,14,15	0.75	0	17,19,21	0.96	0
5	NAG	S	1	1,5	14,14,15	0.83	0	17,19,21	1.21	2 (11%)
5	NAG	S	2	5	14,14,15	0.72	0	17,19,21	1.48	1 (5%)
5	NAG	T	1	1,5	14,14,15	0.73	0	17,19,21	0.86	0
5	NAG	T	2	5	14,14,15	0.71	0	17,19,21	0.89	2 (11%)
5	NAG	U	1	1,5	14,14,15	0.79	0	17,19,21	1.00	1 (5%)
5	NAG	U	2	5	14,14,15	0.71	0	17,19,21	0.83	0
4	NAG	V	1	1,4	14,14,15	0.82	0	17,19,21	1.24	2 (11%)
4	NAG	V	2	4	14,14,15	0.83	0	17,19,21	1.01	1 (5%)
4	BMA	V	3	4	11,11,12	0.94	0	15,15,17	2.82	6 (40%)
4	MAN	V	4	4	11,11,12	0.69	0	15,15,17	1.36	1 (6%)
4	MAN	V	5	4	11,11,12	0.73	0	15,15,17	1.58	2 (13%)

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
4	NAG	H	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	H	2	4	-	0/6/23/26	0/1/1/1
4	BMA	H	3	4	-	2/2/19/22	0/1/1/1
4	MAN	H	4	4	-	0/2/19/22	0/1/1/1
4	MAN	H	5	4	-	2/2/19/22	0/1/1/1
5	NAG	I	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	I	2	5	-	3/6/23/26	0/1/1/1
5	NAG	J	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	J	2	5	-	0/6/23/26	0/1/1/1
5	NAG	K	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	K	2	5	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	L	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	L	2	5	-	1/6/23/26	0/1/1/1
5	NAG	M	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	M	2	5	-	1/6/23/26	0/1/1/1
5	NAG	N	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	N	2	5	-	0/6/23/26	0/1/1/1
5	NAG	O	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	O	2	5	-	0/6/23/26	0/1/1/1
4	NAG	P	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	P	2	4	-	0/6/23/26	0/1/1/1
4	BMA	P	3	4	-	0/2/19/22	0/1/1/1
4	MAN	P	4	4	-	0/2/19/22	0/1/1/1
4	MAN	P	5	4	-	0/2/19/22	0/1/1/1
5	NAG	Q	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	Q	2	5	-	0/6/23/26	0/1/1/1
5	NAG	R	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	R	2	5	-	1/6/23/26	0/1/1/1
5	NAG	S	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	S	2	5	-	1/6/23/26	0/1/1/1
5	NAG	T	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	T	2	5	-	2/6/23/26	0/1/1/1
5	NAG	U	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	U	2	5	-	0/6/23/26	0/1/1/1
4	NAG	V	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	V	2	4	-	0/6/23/26	0/1/1/1
4	BMA	V	3	4	-	0/2/19/22	0/1/1/1
4	MAN	V	4	4	-	2/2/19/22	0/1/1/1
4	MAN	V	5	4	-	0/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	1	NAG	O5-C1	-2.09	1.40	1.43
5	M	1	NAG	O5-C1	-2.00	1.40	1.43

All (52) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	V	3	BMA	C1-O5-C5	7.88	122.87	112.19
4	P	3	BMA	C1-O5-C5	6.75	121.34	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	5	MAN	C1-O5-C5	6.12	120.48	112.19
4	H	3	BMA	C1-O5-C5	5.10	119.11	112.19
4	P	4	MAN	C1-O5-C5	4.88	118.80	112.19
4	H	4	MAN	C1-O5-C5	4.59	118.41	112.19
5	S	2	NAG	C2-N2-C7	4.25	128.96	122.90
4	P	5	MAN	C1-O5-C5	4.17	117.84	112.19
4	V	4	MAN	C1-O5-C5	4.14	117.81	112.19
4	V	5	MAN	C1-O5-C5	4.04	117.66	112.19
5	M	2	NAG	C2-N2-C7	4.03	128.64	122.90
4	P	3	BMA	C2-C3-C4	3.87	117.59	110.89
4	H	3	BMA	C2-C3-C4	3.87	117.59	110.89
4	V	3	BMA	C3-C4-C5	3.76	116.95	110.24
4	H	3	BMA	C3-C4-C5	3.70	116.84	110.24
4	V	3	BMA	C2-C3-C4	3.62	117.17	110.89
4	P	3	BMA	C3-C4-C5	3.60	116.66	110.24
4	P	1	NAG	C2-N2-C7	3.55	127.95	122.90
4	H	1	NAG	C2-N2-C7	3.22	127.49	122.90
4	V	1	NAG	C2-N2-C7	3.19	127.45	122.90
4	V	5	MAN	C1-C2-C3	3.01	113.37	109.67
4	H	5	MAN	C1-C2-C3	2.91	113.25	109.67
4	H	3	BMA	O4-C4-C3	-2.90	103.65	110.35
4	V	3	BMA	O5-C5-C4	2.74	117.48	110.83
5	S	1	NAG	C2-N2-C7	2.70	126.75	122.90
4	V	3	BMA	O4-C4-C3	-2.67	104.17	110.35
5	M	1	NAG	C2-N2-C7	2.54	126.53	122.90
5	R	1	NAG	C1-O5-C5	2.50	115.58	112.19
5	M	1	NAG	O4-C4-C3	-2.48	104.61	110.35
4	P	3	BMA	O5-C5-C4	2.48	116.86	110.83
4	P	3	BMA	O4-C4-C3	-2.48	104.62	110.35
5	S	1	NAG	O4-C4-C3	-2.47	104.65	110.35
4	H	1	NAG	O3-C3-C2	-2.45	104.40	109.47
5	Q	1	NAG	C2-N2-C7	2.36	126.26	122.90
5	K	1	NAG	C2-N2-C7	2.36	126.26	122.90
4	V	3	BMA	O3-C3-C2	-2.34	105.52	109.99
5	O	1	NAG	C2-N2-C7	2.29	126.16	122.90
5	J	1	NAG	C1-O5-C5	2.28	115.28	112.19
4	V	1	NAG	O3-C3-C2	-2.23	104.86	109.47
5	I	2	NAG	C2-N2-C7	2.16	125.98	122.90
4	H	3	BMA	O3-C3-C2	-2.14	105.90	109.99
5	U	1	NAG	C2-N2-C7	2.10	125.89	122.90
5	T	2	NAG	C1-O5-C5	2.09	115.02	112.19
5	I	1	NAG	C1-O5-C5	2.09	115.02	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	P	3	BMA	O3-C3-C2	-2.08	106.02	109.99
4	V	2	NAG	C1-O5-C5	2.07	115.00	112.19
4	P	1	NAG	O3-C3-C2	-2.06	105.20	109.47
5	J	1	NAG	C2-N2-C7	2.04	125.80	122.90
5	I	2	NAG	C1-O5-C5	2.02	114.94	112.19
4	P	3	BMA	O2-C2-C3	2.02	114.19	110.14
5	J	2	NAG	C1-O5-C5	2.02	114.93	112.19
5	T	2	NAG	O5-C1-C2	-2.02	108.10	111.29

There are no chirality outliers.

All (35) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	H	3	BMA	O5-C5-C6-O6
4	H	3	BMA	C4-C5-C6-O6
4	P	1	NAG	C8-C7-N2-C2
4	P	1	NAG	O7-C7-N2-C2
4	V	1	NAG	C8-C7-N2-C2
4	V	1	NAG	O7-C7-N2-C2
5	I	2	NAG	C8-C7-N2-C2
5	I	2	NAG	O7-C7-N2-C2
5	J	1	NAG	C8-C7-N2-C2
5	J	1	NAG	O7-C7-N2-C2
5	K	1	NAG	C8-C7-N2-C2
5	K	1	NAG	O7-C7-N2-C2
5	M	1	NAG	C8-C7-N2-C2
5	M	1	NAG	O7-C7-N2-C2
5	O	1	NAG	C8-C7-N2-C2
5	O	1	NAG	O7-C7-N2-C2
5	Q	1	NAG	C8-C7-N2-C2
5	Q	1	NAG	O7-C7-N2-C2
5	S	1	NAG	C8-C7-N2-C2
5	S	1	NAG	O7-C7-N2-C2
5	U	1	NAG	C8-C7-N2-C2
5	U	1	NAG	O7-C7-N2-C2
4	H	5	MAN	O5-C5-C6-O6
5	T	2	NAG	O5-C5-C6-O6
4	V	4	MAN	C4-C5-C6-O6
4	H	1	NAG	O5-C5-C6-O6
4	H	1	NAG	C4-C5-C6-O6
5	I	2	NAG	O5-C5-C6-O6
5	L	2	NAG	O5-C5-C6-O6

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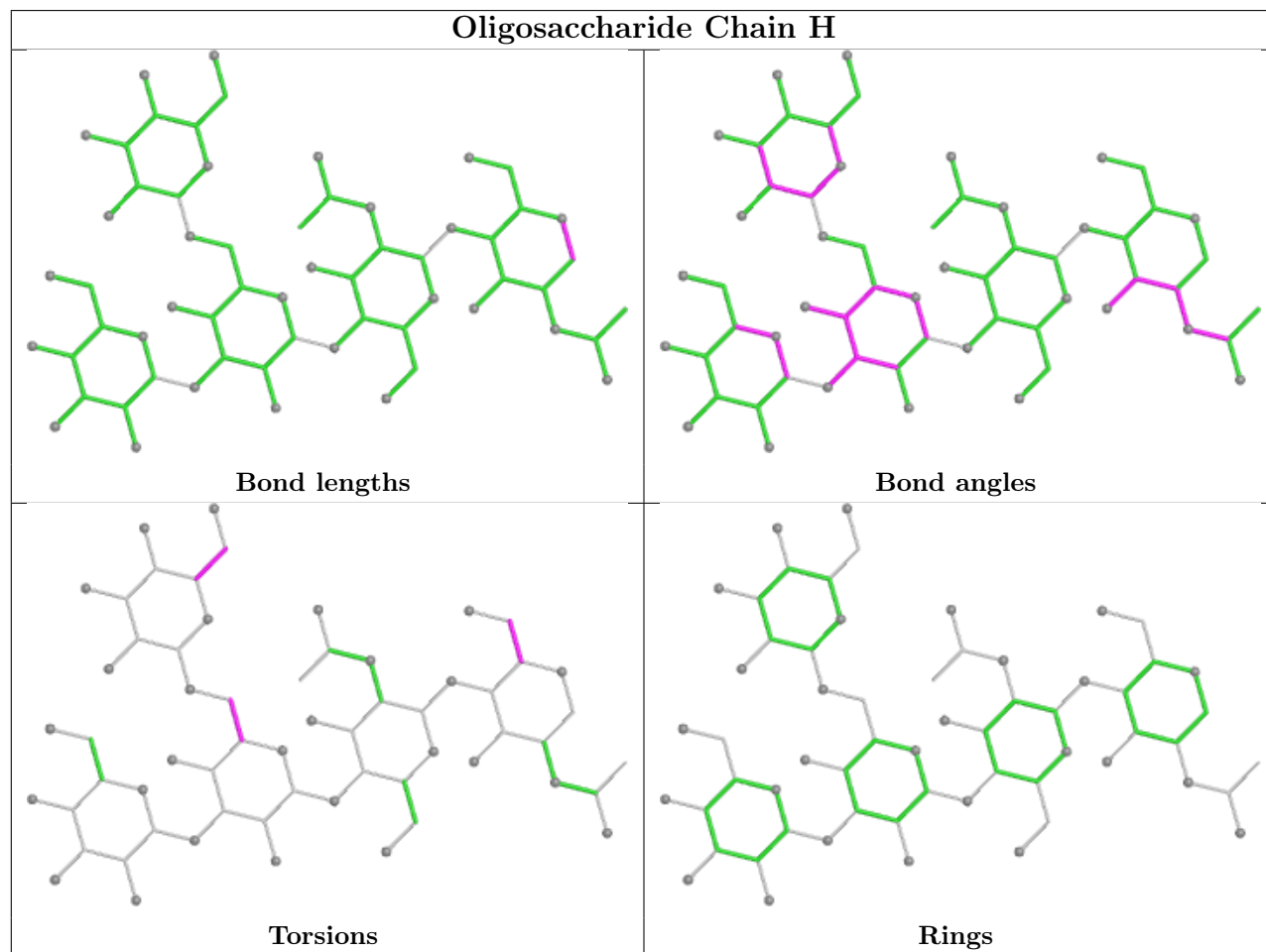
Mol	Chain	Res	Type	Atoms
5	R	2	NAG	O5-C5-C6-O6
4	V	4	MAN	O5-C5-C6-O6
5	T	2	NAG	C4-C5-C6-O6
4	H	5	MAN	C4-C5-C6-O6
5	M	2	NAG	C3-C2-N2-C7
5	S	2	NAG	C3-C2-N2-C7

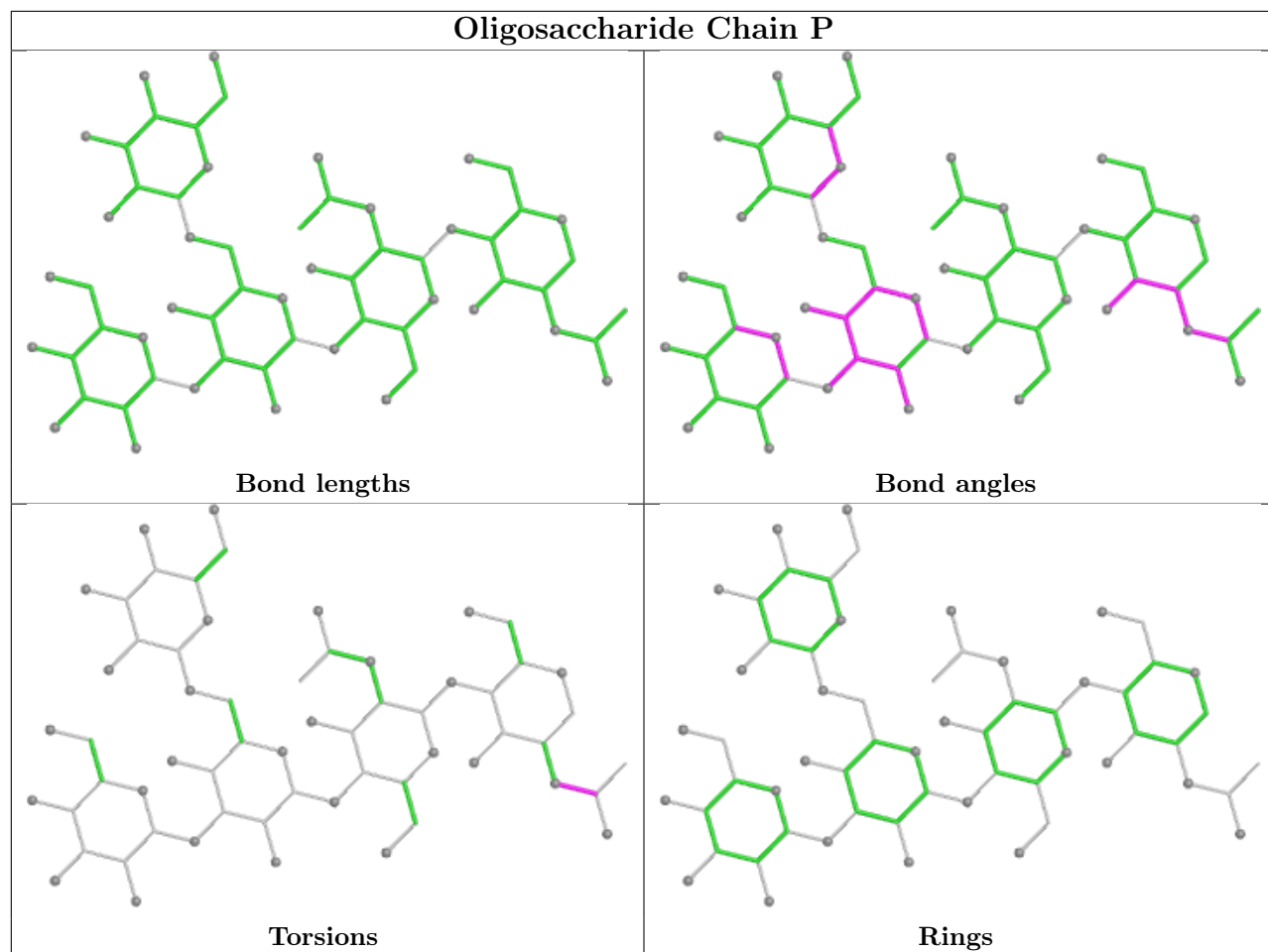
There are no ring outliers.

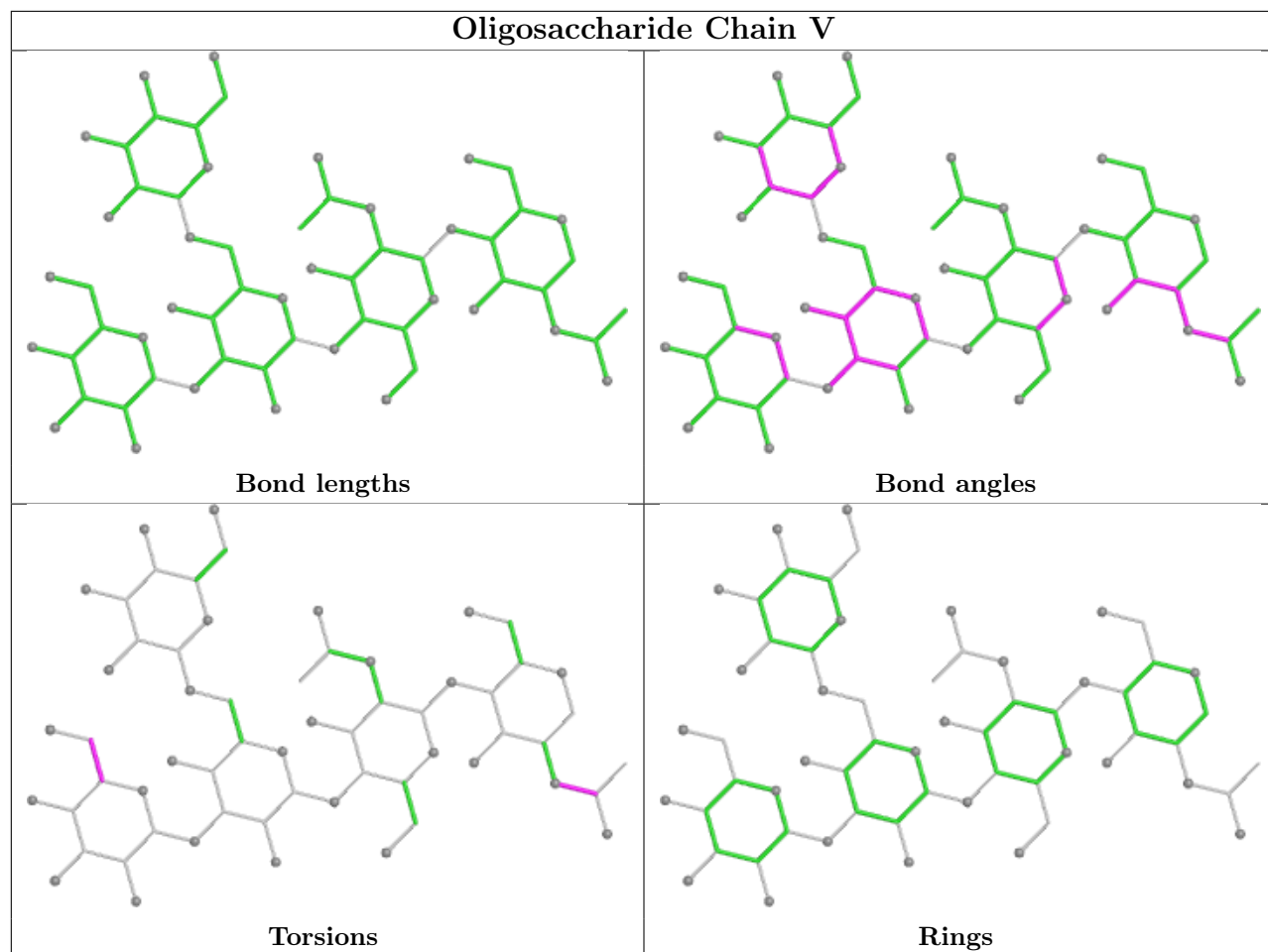
2 monomers are involved in 2 short contacts:

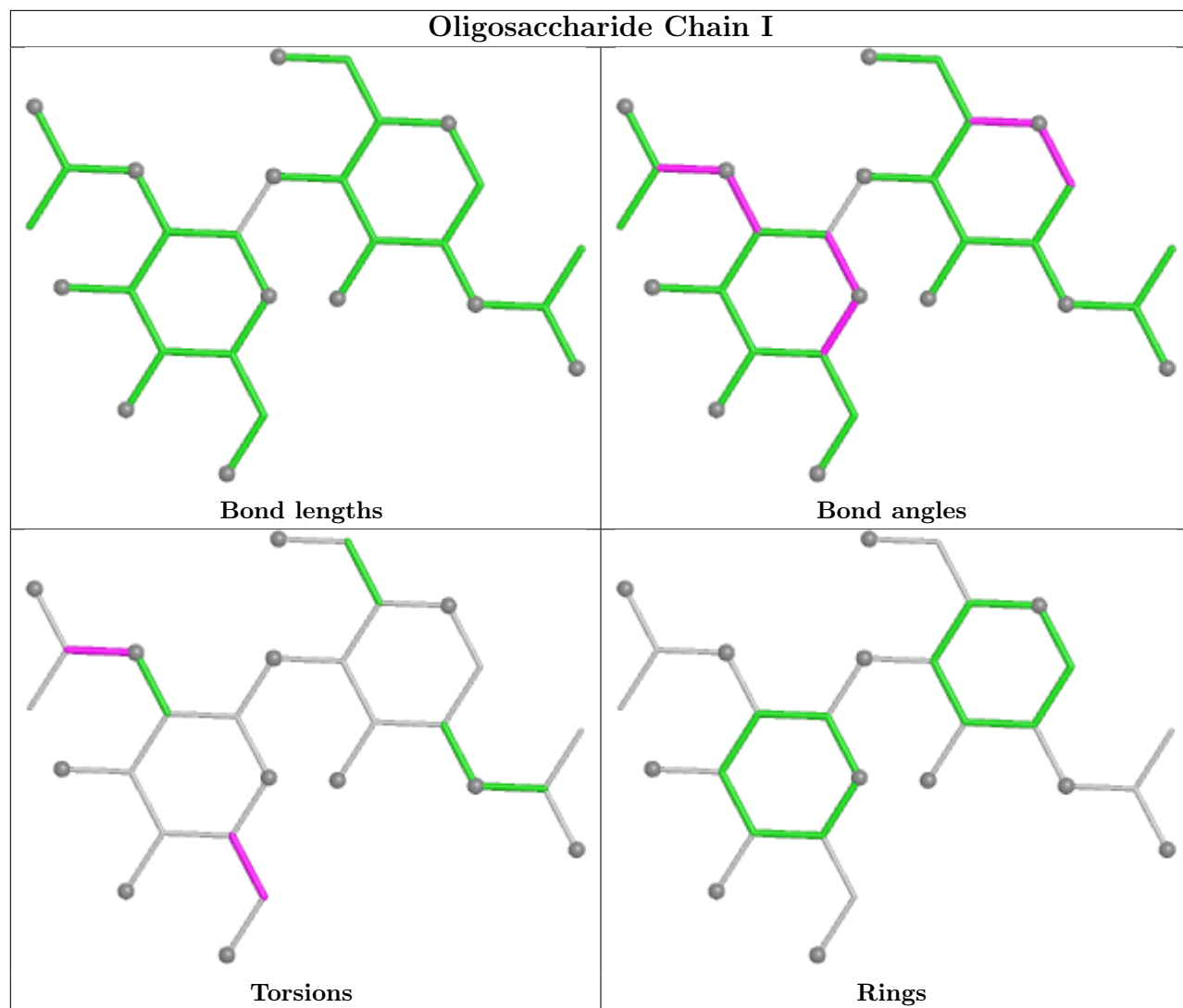
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	J	1	NAG	1	0
4	H	5	MAN	1	0

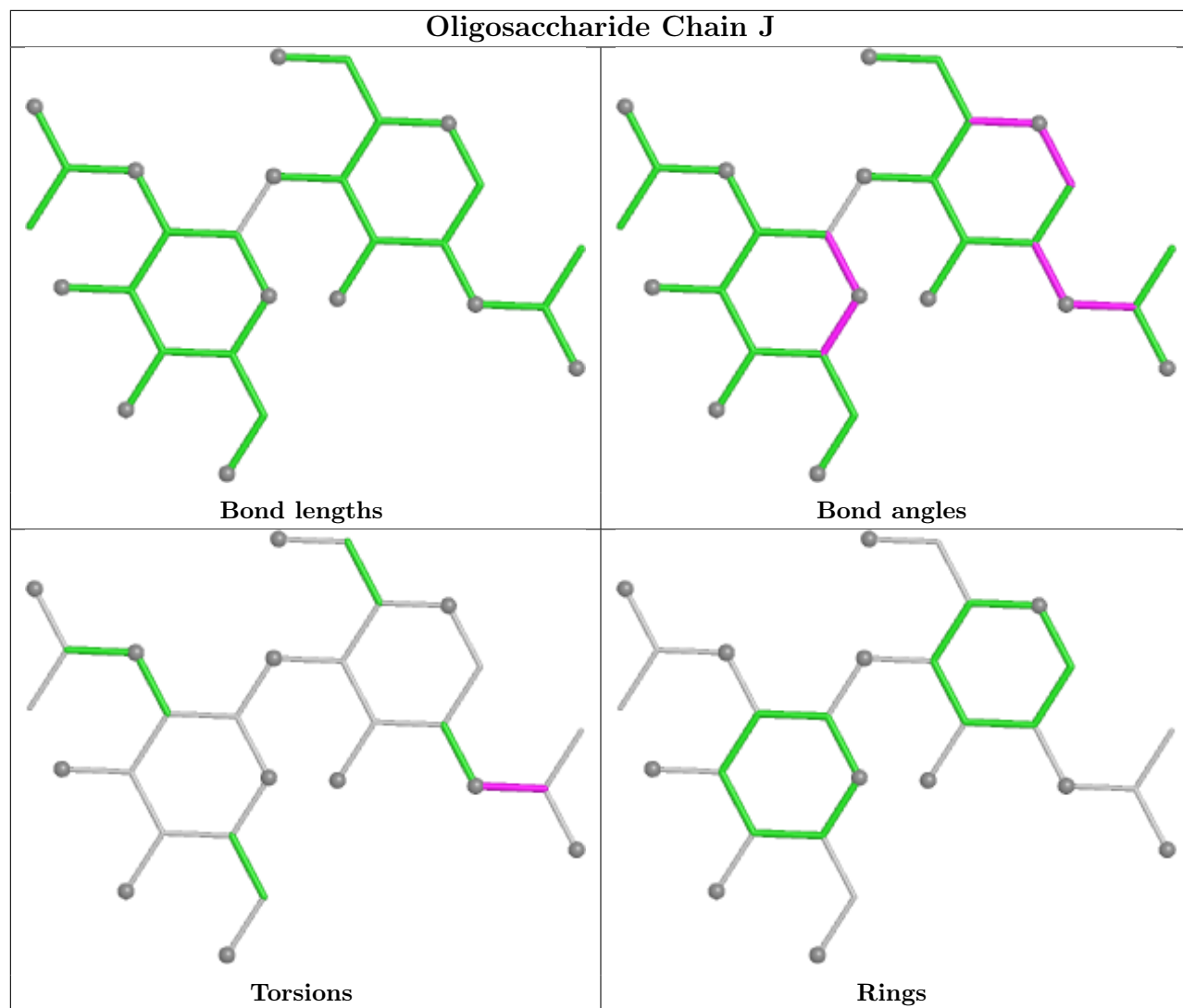
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

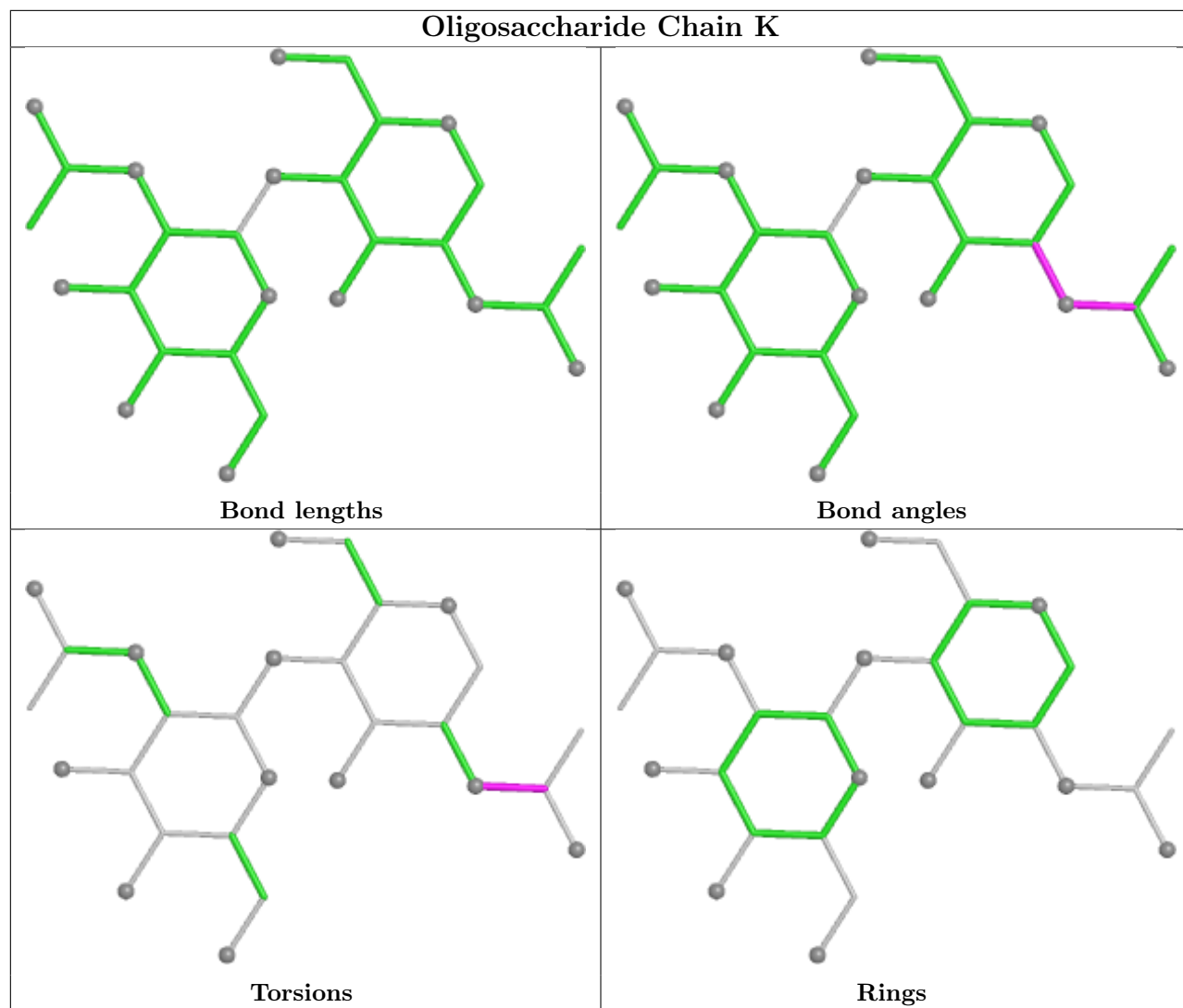


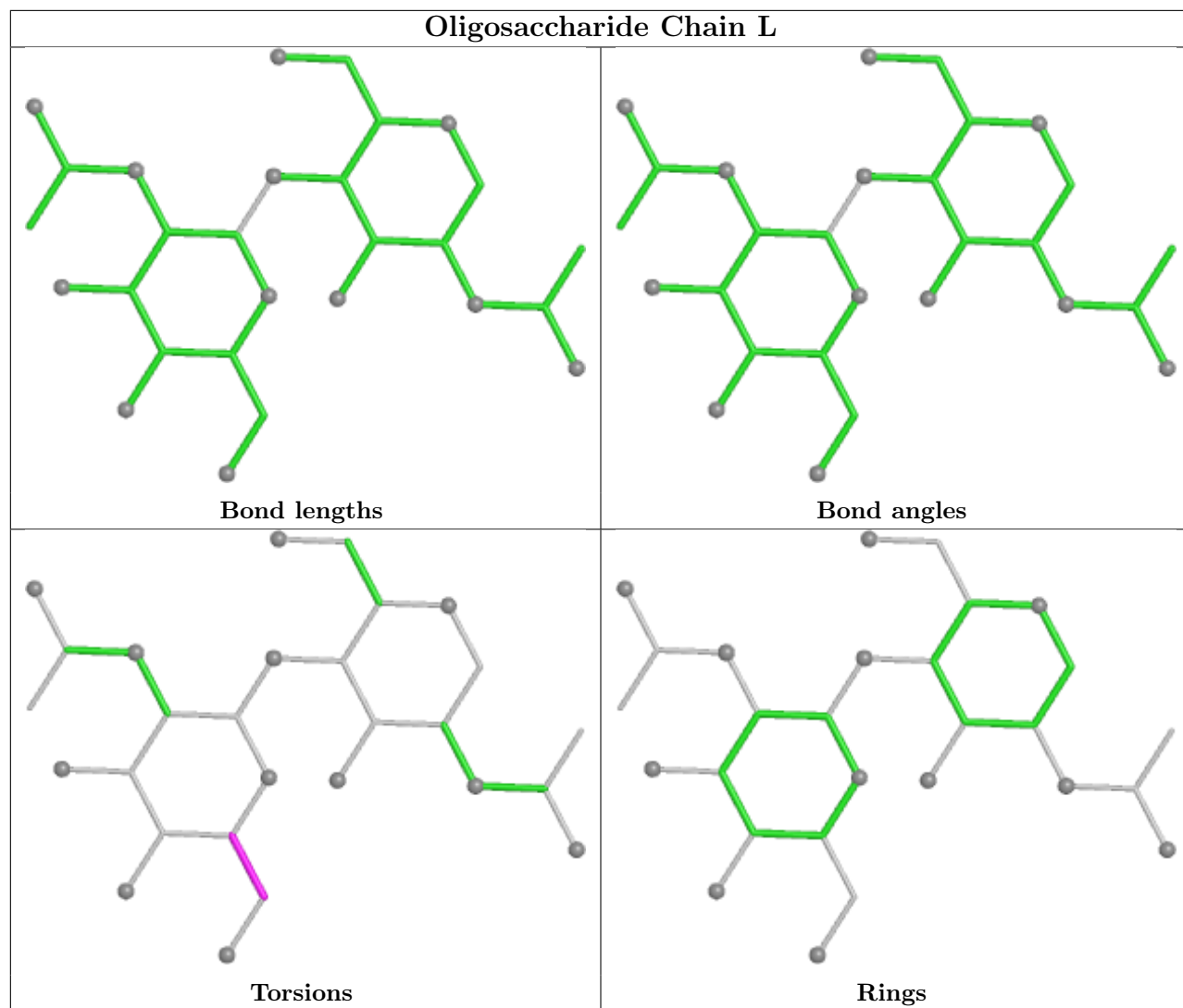


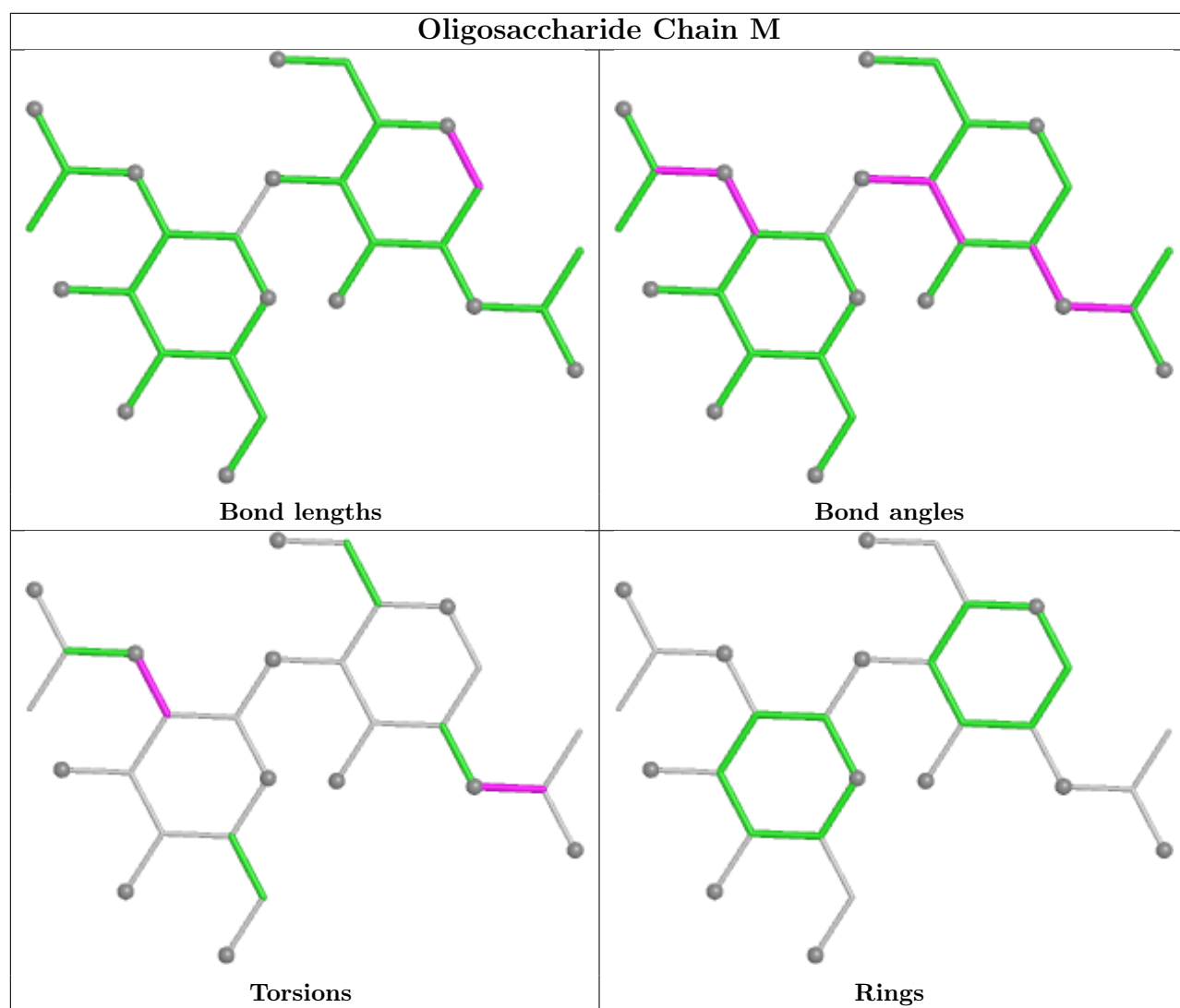


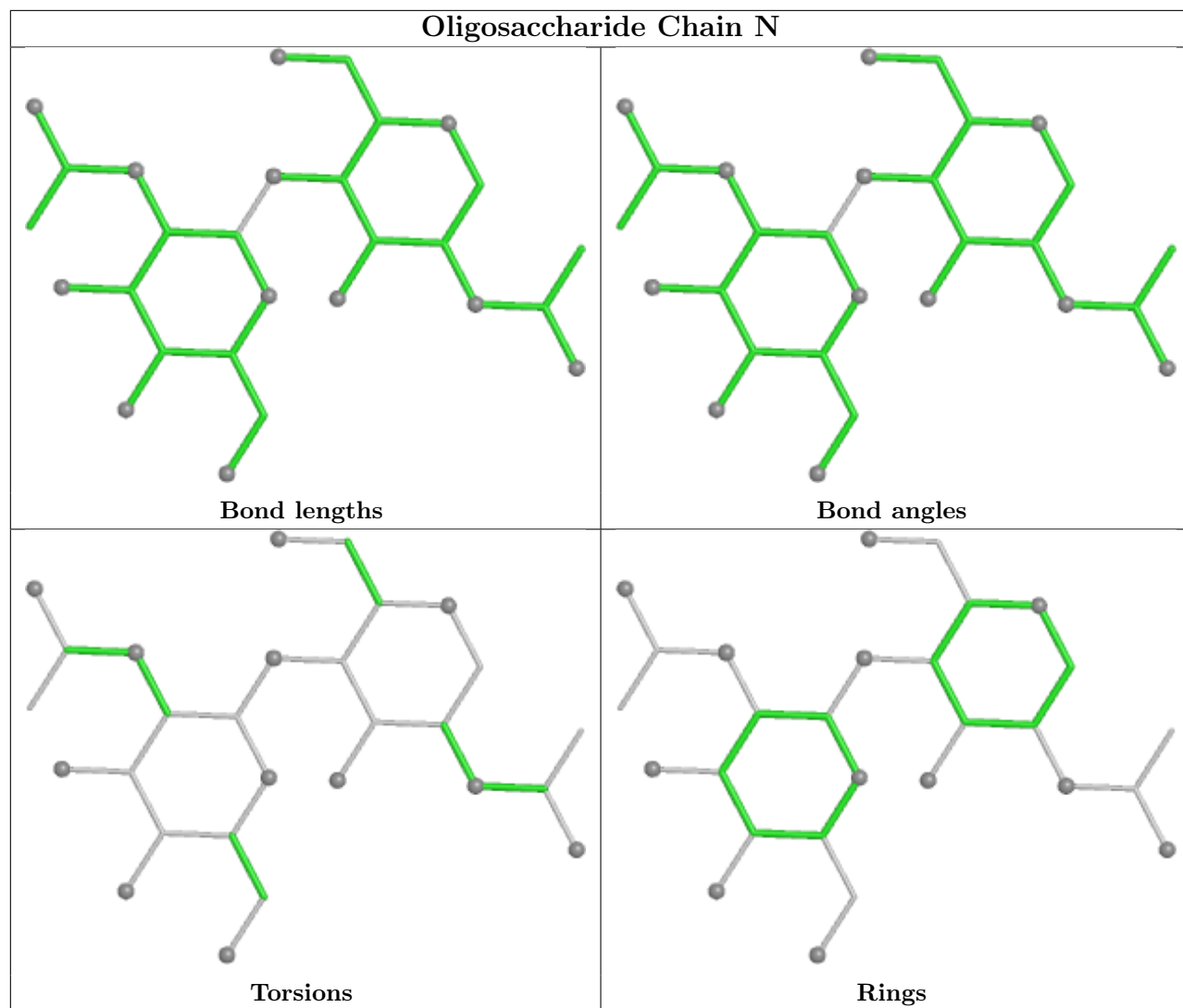


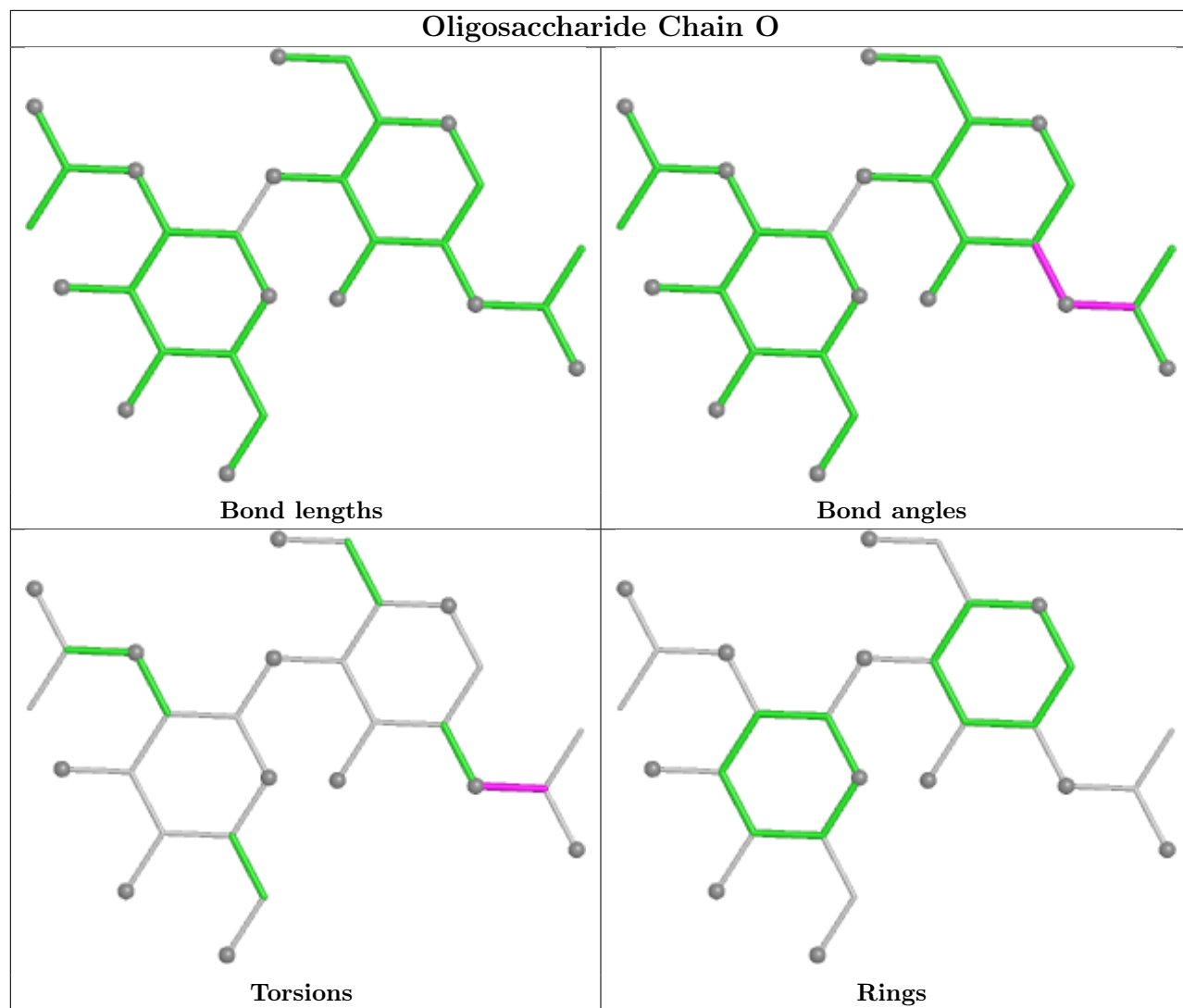


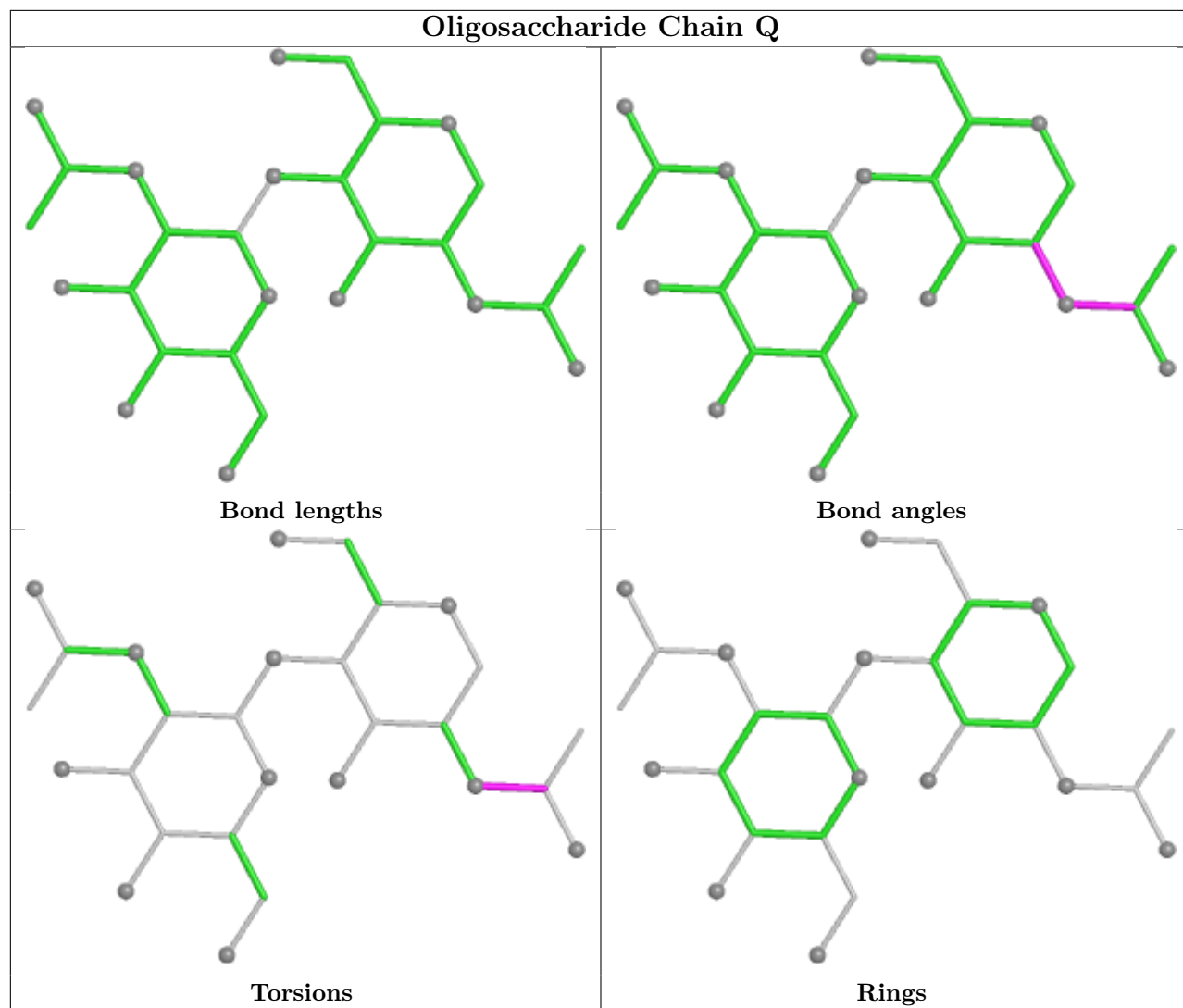


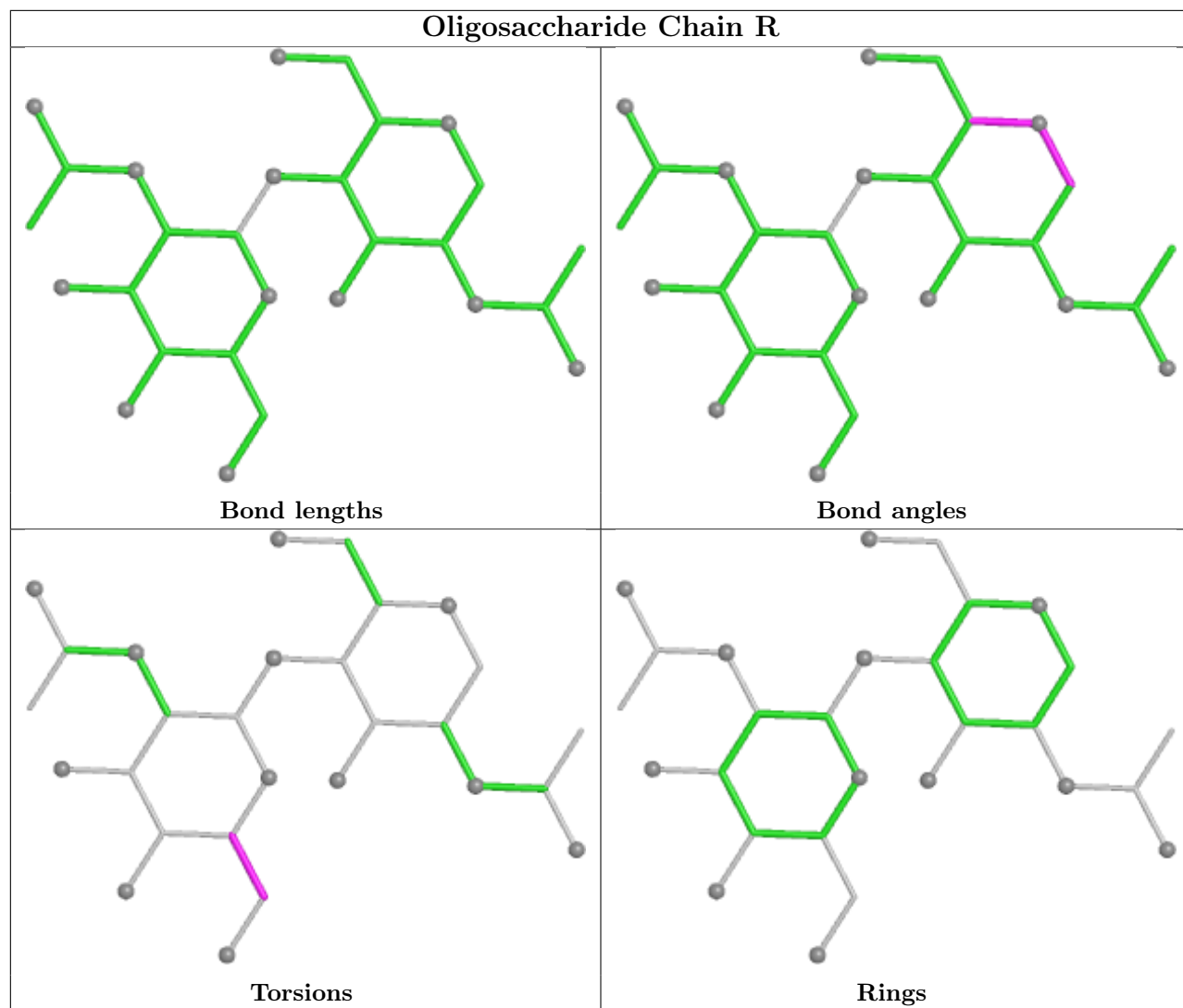


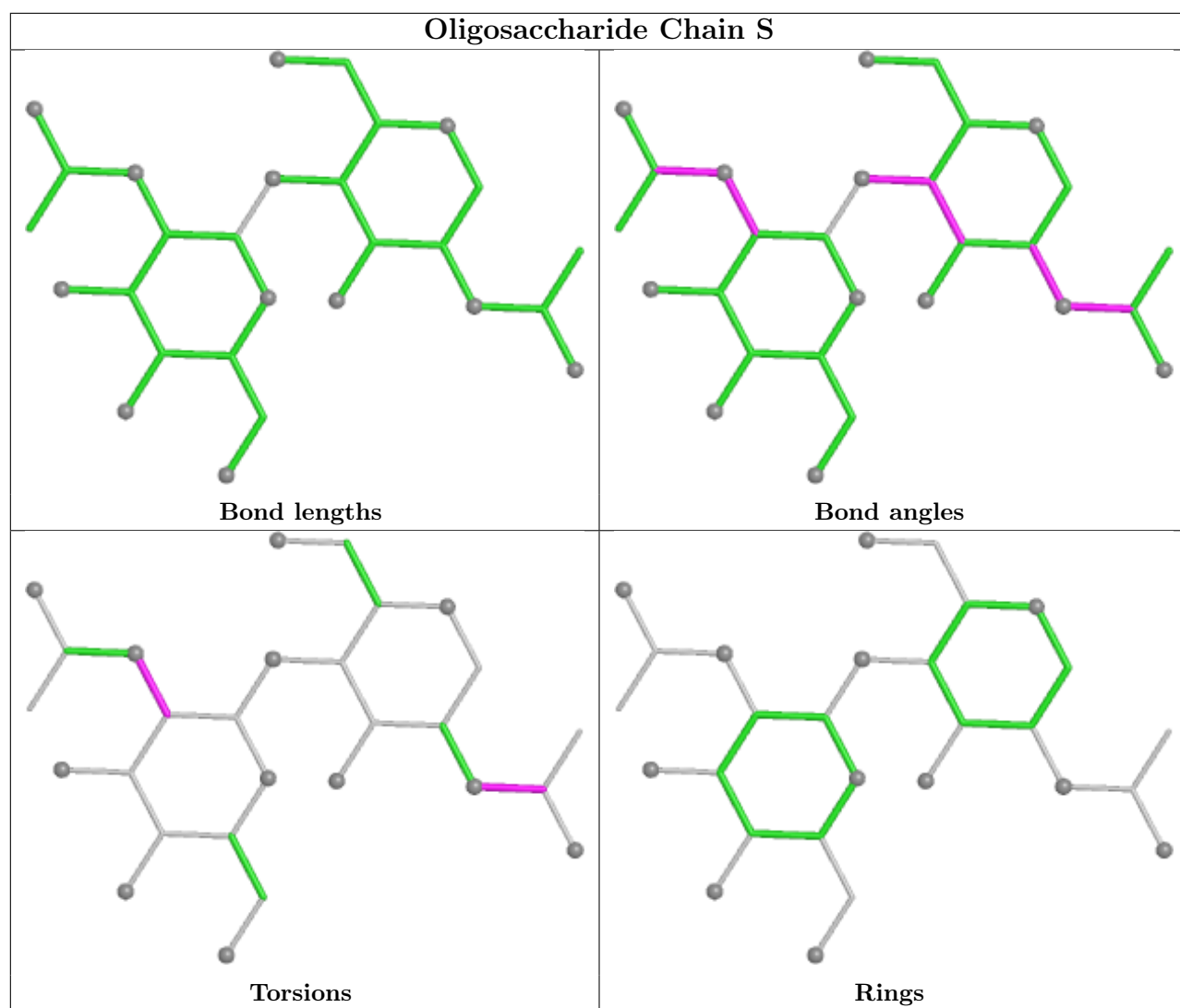


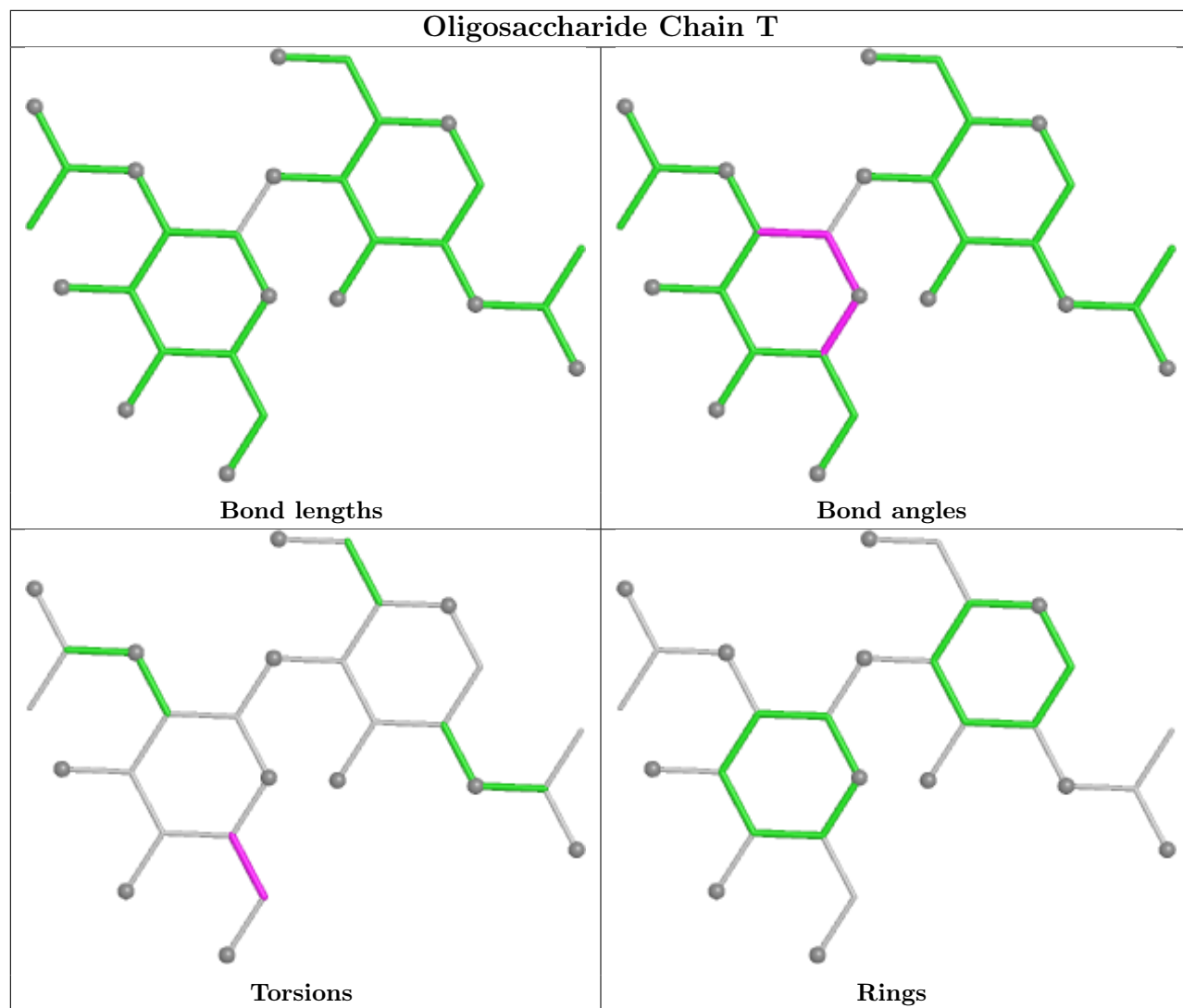


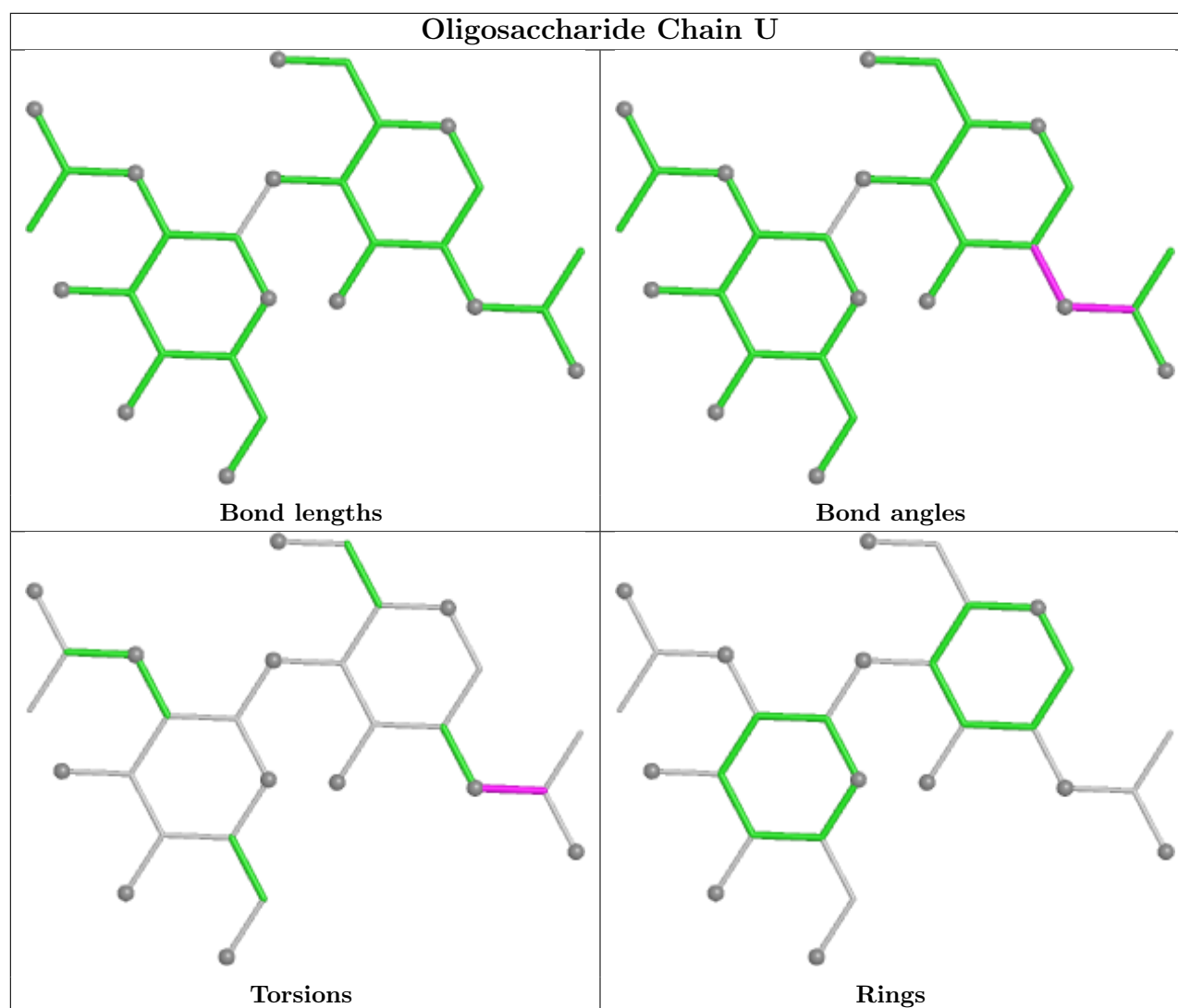












5.6 Ligand geometry [i](#)

30 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	$\# Z > 2$
6	NAG	A	1412	1	14,14,15	0.72	0	17,19,21	0.86	0
6	NAG	B	1403	1	14,14,15	0.74	0	17,19,21	0.82	0
6	NAG	A	1404	1	14,14,15	0.70	0	17,19,21	1.33	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	A	1409	1	14,14,15	0.72	0	17,19,21	0.96	1 (5%)
6	NAG	A	1408	1	14,14,15	0.76	0	17,19,21	1.01	0
6	NAG	B	1402	1	14,14,15	0.76	0	17,19,21	1.42	2 (11%)
6	NAG	B	1406	1	14,14,15	0.75	0	17,19,21	1.07	1 (5%)
6	NAG	A	1403	1	14,14,15	0.75	0	17,19,21	0.95	0
6	NAG	C	1407	1	14,14,15	0.74	0	17,19,21	1.07	1 (5%)
6	NAG	A	1402	1	14,14,15	0.71	0	17,19,21	0.79	0
6	NAG	A	1401	1	14,14,15	0.78	0	17,19,21	1.38	1 (5%)
6	NAG	B	1401	1	14,14,15	0.74	0	17,19,21	0.88	0
7	PAM	B	1407	-	17,17,17	0.62	0	17,17,17	0.59	0
7	PAM	A	1414	-	17,17,17	0.61	0	17,17,17	0.54	0
6	NAG	B	1404	1	14,14,15	0.75	0	17,19,21	0.77	0
6	NAG	A	1411	1	14,14,15	0.71	0	17,19,21	0.80	0
6	NAG	A	1406	1	14,14,15	0.74	0	17,19,21	0.80	0
6	NAG	A	1407	1	14,14,15	0.78	0	17,19,21	1.42	2 (11%)
6	NAG	C	1405	1	14,14,15	0.72	0	17,19,21	0.89	0
6	NAG	C	1403	1	14,14,15	0.76	0	17,19,21	1.50	2 (11%)
6	NAG	A	1405	1	14,14,15	0.74	0	17,19,21	0.87	1 (5%)
6	NAG	B	1405	1	14,14,15	0.74	0	17,19,21	1.08	2 (11%)
7	PAM	B	1408	-	17,17,17	0.64	0	17,17,17	0.52	0
7	PAM	C	1401	-	17,17,17	0.62	0	17,17,17	0.54	0
6	NAG	C	1402	1	14,14,15	0.74	0	17,19,21	0.92	1 (5%)
6	NAG	C	1406	1	14,14,15	0.71	0	17,19,21	1.01	1 (5%)
6	NAG	A	1410	1	14,14,15	0.76	0	17,19,21	2.61	3 (17%)
7	PAM	A	1413	-	17,17,17	0.64	0	17,17,17	0.54	0
7	PAM	C	1408	-	17,17,17	0.64	0	17,17,17	0.51	0
6	NAG	C	1404	1	14,14,15	0.73	0	17,19,21	1.02	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
6	NAG	A	1412	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1403	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1404	1	-	2/6/23/26	0/1/1/1
6	NAG	A	1409	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1408	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	B	1402	1	-	1/6/23/26	0/1/1/1
6	NAG	B	1406	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1403	1	-	0/6/23/26	0/1/1/1
6	NAG	C	1407	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1402	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1401	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1401	1	-	0/6/23/26	0/1/1/1
7	PAM	B	1407	-	-	6/15/15/15	-
7	PAM	A	1414	-	-	2/15/15/15	-
6	NAG	B	1404	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1411	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1406	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1407	1	-	2/6/23/26	0/1/1/1
6	NAG	C	1405	1	-	0/6/23/26	0/1/1/1
6	NAG	C	1403	1	-	1/6/23/26	0/1/1/1
6	NAG	A	1405	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1405	1	-	4/6/23/26	0/1/1/1
7	PAM	B	1408	-	-	1/15/15/15	-
7	PAM	C	1401	-	-	4/15/15/15	-
6	NAG	C	1402	1	-	0/6/23/26	0/1/1/1
6	NAG	C	1406	1	-	4/6/23/26	0/1/1/1
6	NAG	A	1410	1	-	4/6/23/26	0/1/1/1
7	PAM	A	1413	-	-	2/15/15/15	-
7	PAM	C	1408	-	-	4/15/15/15	-
6	NAG	C	1404	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1410	NAG	C2-N2-C7	9.21	136.02	122.90
6	A	1404	NAG	C2-N2-C7	4.08	128.71	122.90
6	C	1403	NAG	C2-N2-C7	3.93	128.49	122.90
6	B	1402	NAG	C2-N2-C7	3.62	128.06	122.90
6	A	1407	NAG	C2-N2-C7	3.48	127.86	122.90
6	C	1403	NAG	C1-O5-C5	3.28	116.64	112.19
6	A	1401	NAG	C2-N2-C7	3.24	127.52	122.90
6	A	1410	NAG	C8-C7-N2	3.16	121.45	116.10
6	B	1402	NAG	C1-O5-C5	2.80	115.99	112.19
6	B	1406	NAG	C1-O5-C5	2.74	115.90	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	1406	NAG	C2-N2-C7	2.61	126.61	122.90
6	C	1404	NAG	C1-O5-C5	2.61	115.72	112.19
6	A	1407	NAG	C1-O5-C5	2.55	115.65	112.19
6	A	1410	NAG	C1-C2-N2	2.47	114.71	110.49
6	A	1409	NAG	O5-C1-C2	-2.28	107.69	111.29
6	C	1402	NAG	C1-O5-C5	2.14	115.09	112.19
6	C	1407	NAG	C1-O5-C5	2.14	115.09	112.19
6	A	1405	NAG	C1-O5-C5	2.14	115.08	112.19
6	B	1405	NAG	C2-N2-C7	2.05	125.82	122.90
6	B	1405	NAG	C1-O5-C5	2.04	114.96	112.19

There are no chirality outliers.

All (37) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	1410	NAG	C8-C7-N2-C2
6	A	1410	NAG	O7-C7-N2-C2
6	B	1405	NAG	C8-C7-N2-C2
6	B	1405	NAG	O7-C7-N2-C2
6	C	1406	NAG	C8-C7-N2-C2
6	C	1406	NAG	O7-C7-N2-C2
6	C	1406	NAG	O5-C5-C6-O6
6	B	1405	NAG	O5-C5-C6-O6
7	C	1408	PAM	C4-C5-C6-C7
6	A	1410	NAG	O5-C5-C6-O6
7	B	1407	PAM	C5-C6-C7-C8
7	A	1413	PAM	C6-C7-C8-C9
7	C	1408	PAM	C7-C8-C9-C10
7	C	1408	PAM	C5-C6-C7-C8
7	B	1407	PAM	C1-C2-C3-C4
7	A	1414	PAM	C11-C12-C13-C14
6	C	1406	NAG	C4-C5-C6-O6
7	A	1413	PAM	C7-C8-C9-C10
6	B	1405	NAG	C4-C5-C6-O6
7	C	1401	PAM	C2-C3-C4-C5
6	A	1404	NAG	C3-C2-N2-C7
6	A	1407	NAG	C3-C2-N2-C7
6	C	1403	NAG	C3-C2-N2-C7
7	B	1408	PAM	C2-C3-C4-C5
7	B	1407	PAM	C6-C7-C8-C9
7	C	1401	PAM	C4-C5-C6-C7
6	A	1404	NAG	C1-C2-N2-C7

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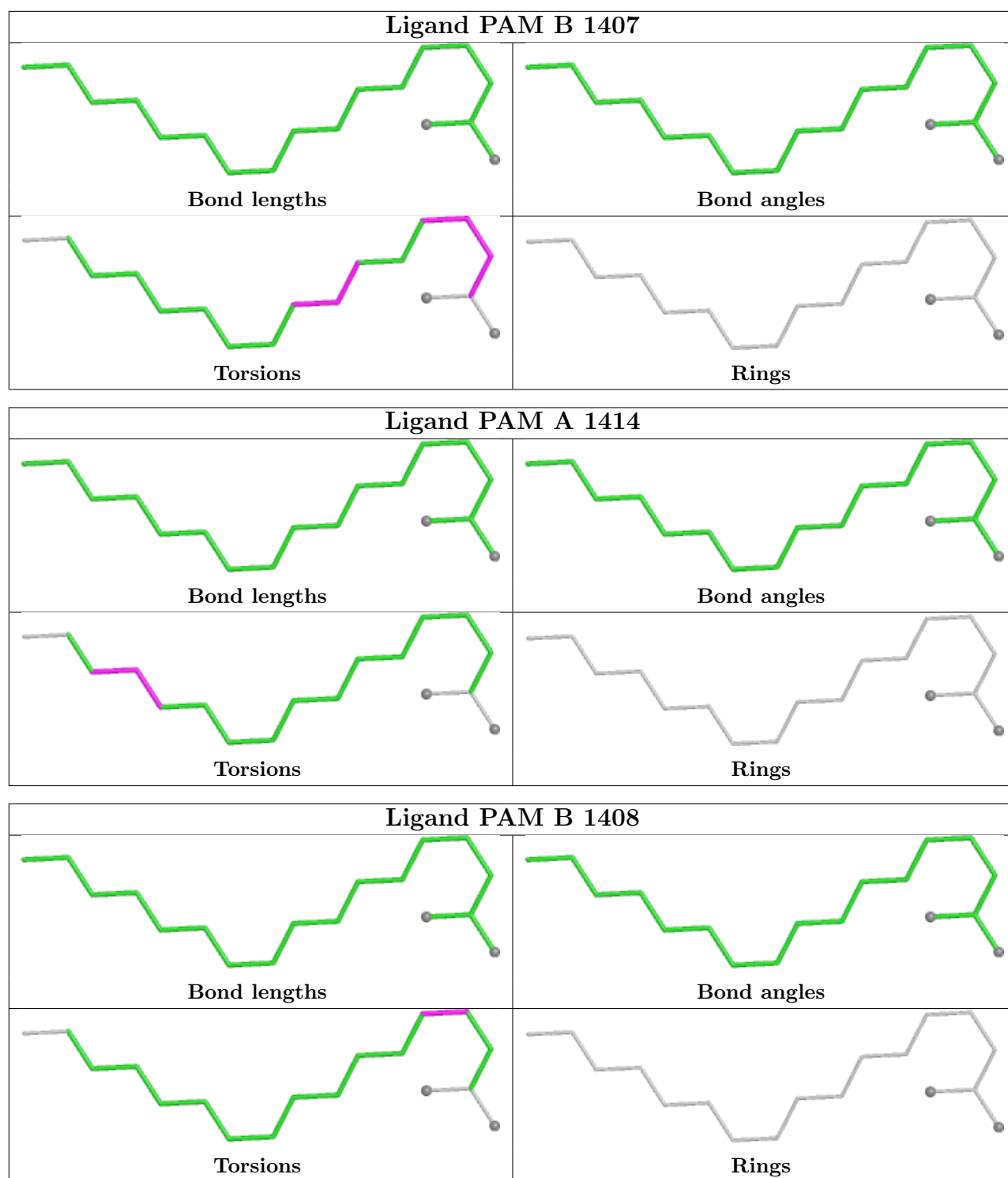
Mol	Chain	Res	Type	Atoms
7	A	1414	PAM	C12-C13-C14-C15
7	C	1401	PAM	C11-C12-C13-C14
7	B	1407	PAM	O2-C1-C2-C3
6	A	1407	NAG	O5-C5-C6-O6
7	B	1407	PAM	O1-C1-C2-C3
7	C	1401	PAM	C9-C10-C11-C12
6	A	1410	NAG	C3-C2-N2-C7
6	B	1402	NAG	C3-C2-N2-C7
7	C	1408	PAM	C3-C4-C5-C6
7	B	1407	PAM	C2-C3-C4-C5

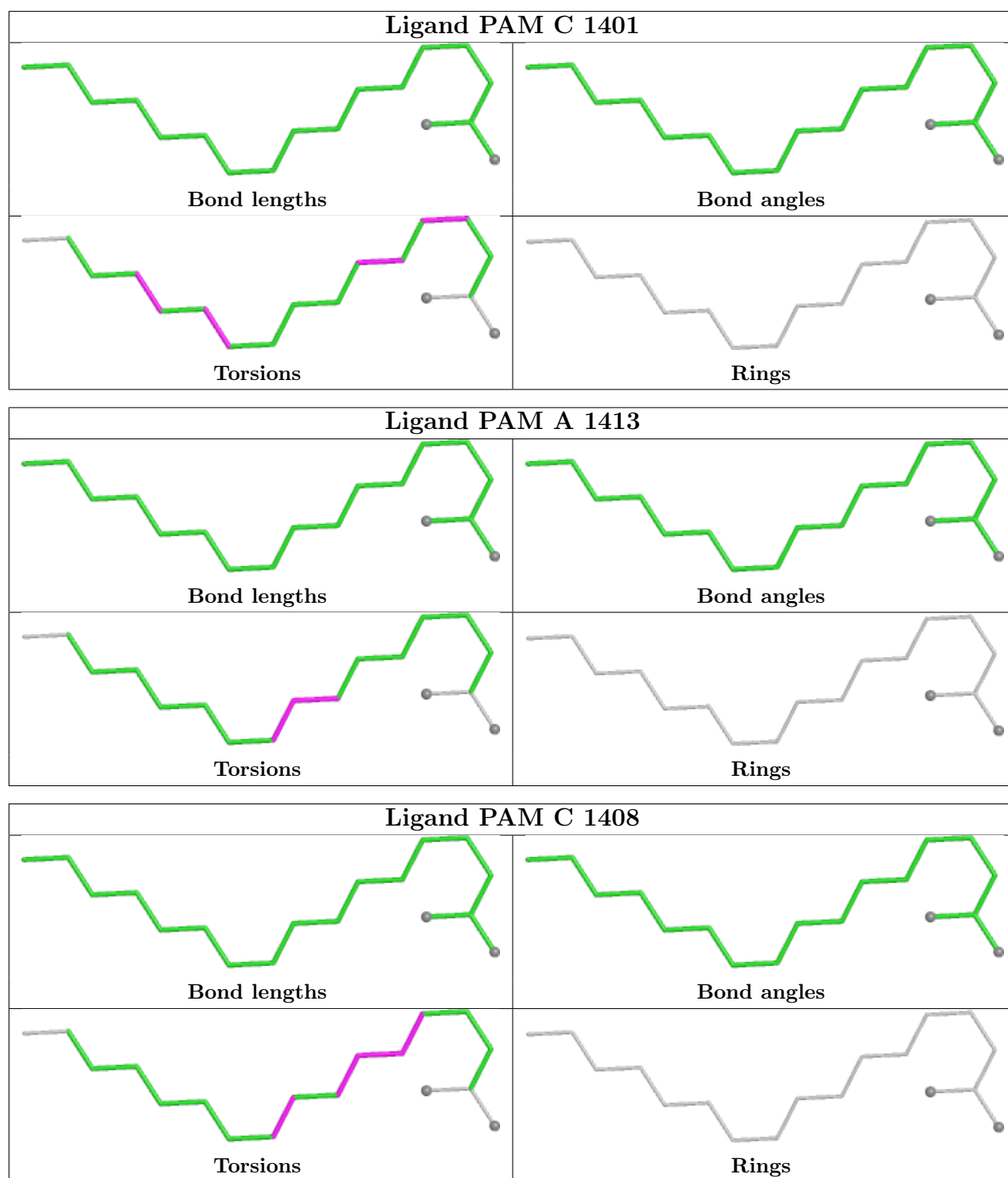
There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	1407	PAM	2	0
7	A	1414	PAM	1	0
7	B	1408	PAM	2	0
7	C	1401	PAM	1	0
7	A	1413	PAM	1	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

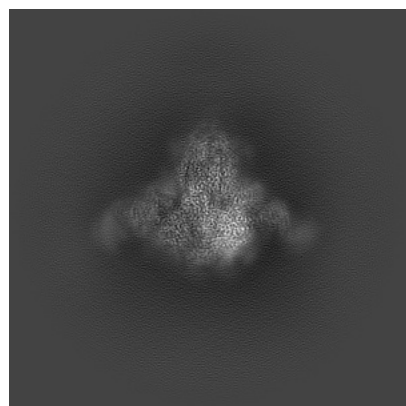
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-67066. These allow visual inspection of the internal detail of the map and identification of artifacts.

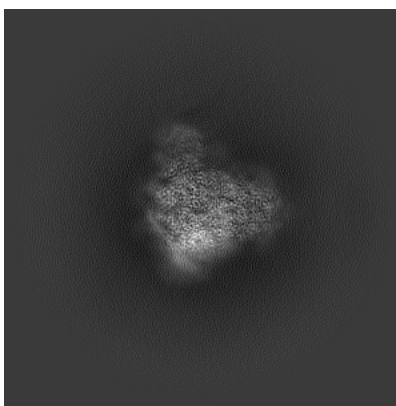
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

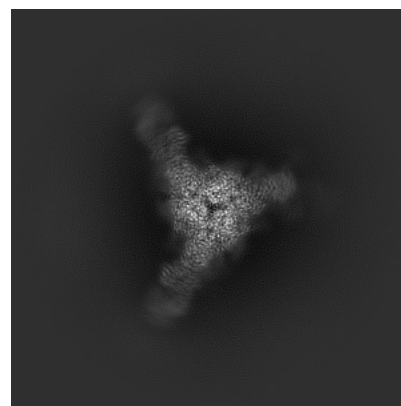
6.1.1 Primary map



X

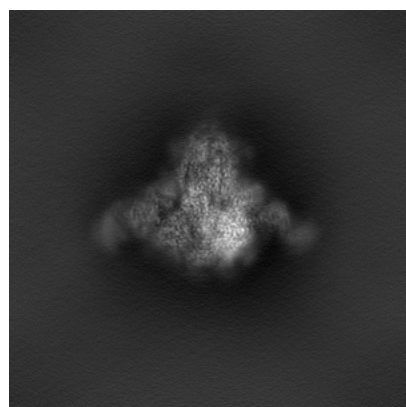


Y

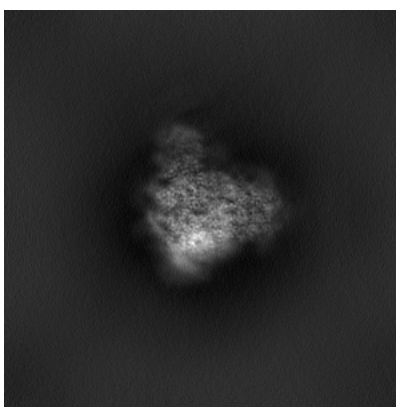


Z

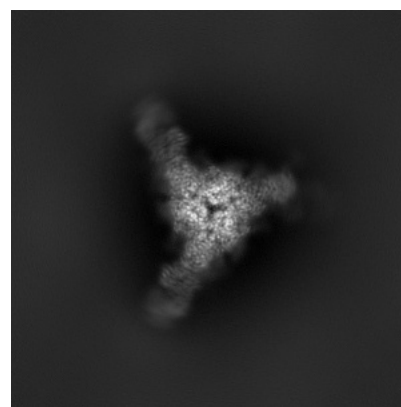
6.1.2 Raw map



X



Y

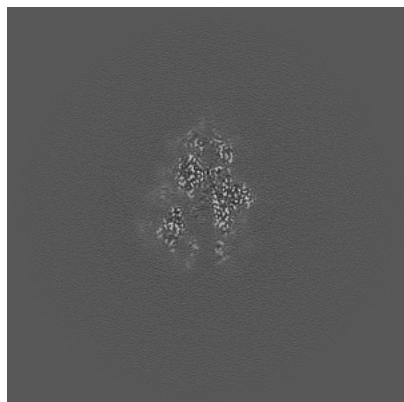


Z

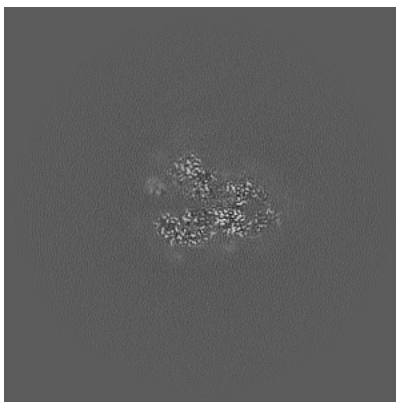
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

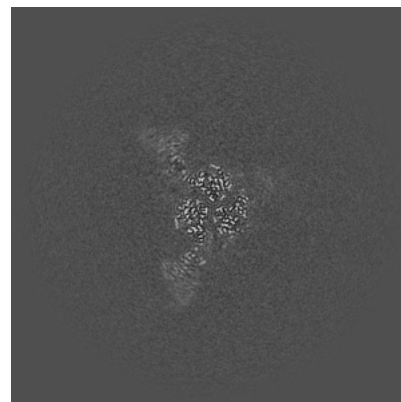
6.2.1 Primary map



X Index: 225

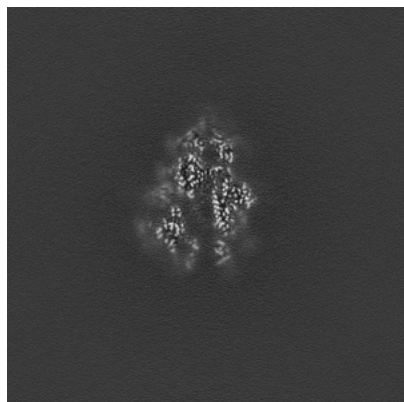


Y Index: 225

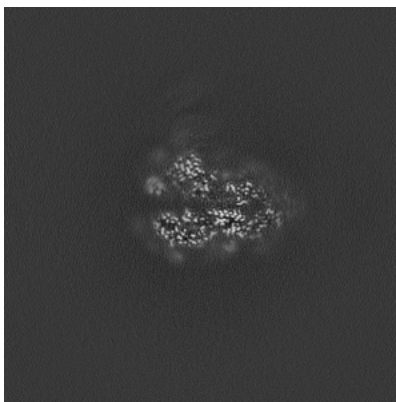


Z Index: 225

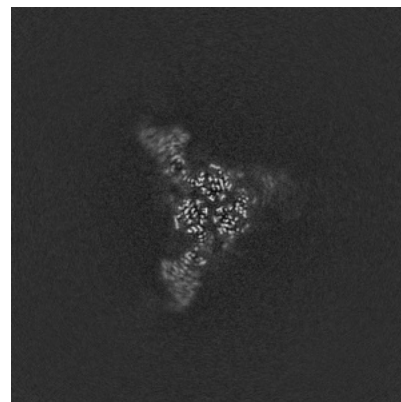
6.2.2 Raw map



X Index: 225



Y Index: 225

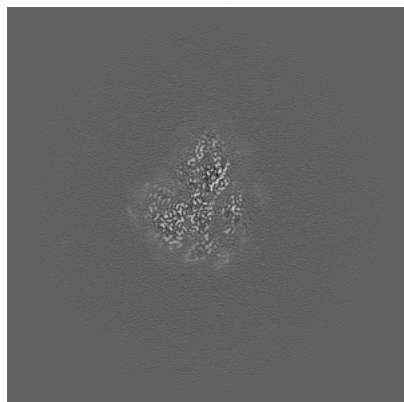


Z Index: 225

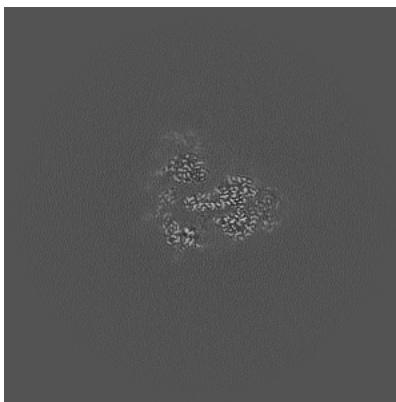
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

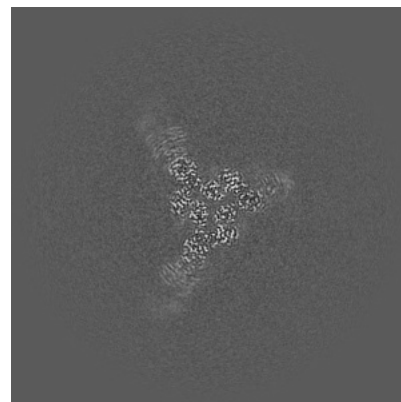
6.3.1 Primary map



X Index: 212

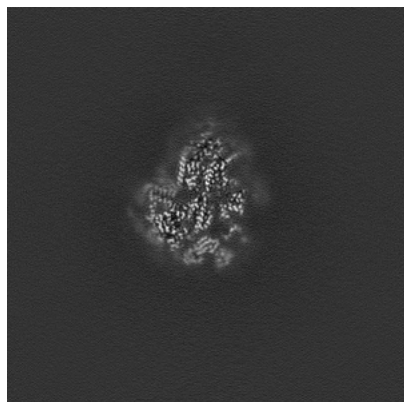


Y Index: 235

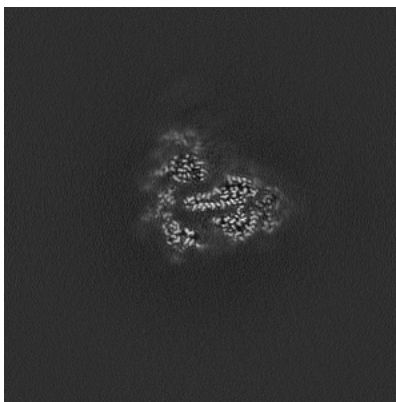


Z Index: 213

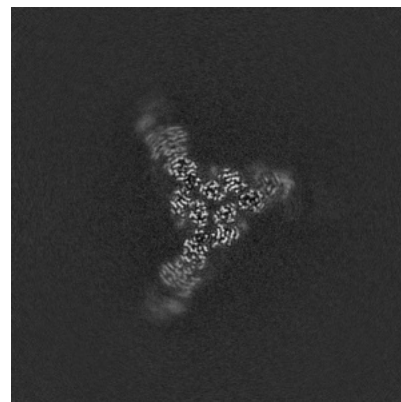
6.3.2 Raw map



X Index: 215



Y Index: 235

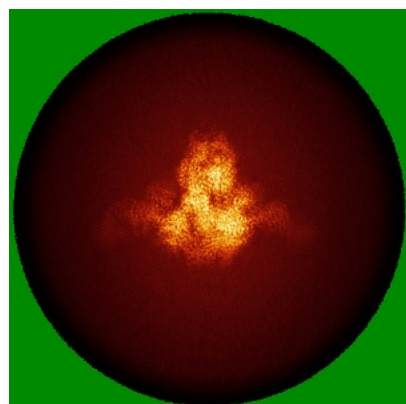


Z Index: 213

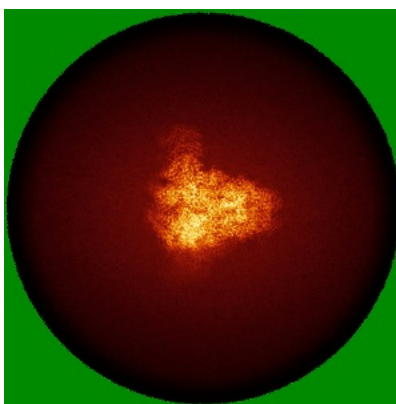
The images above show the largest variance slices of the map in three orthogonal directions.

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

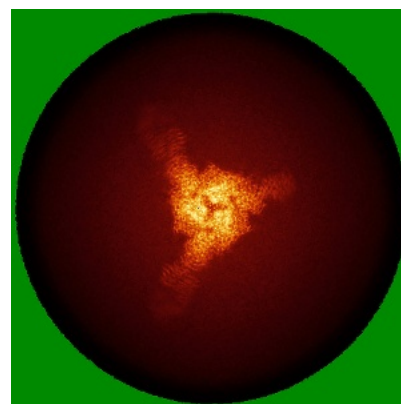
6.4.1 Primary map



X

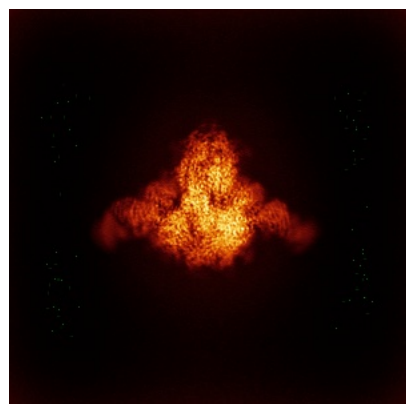


Y

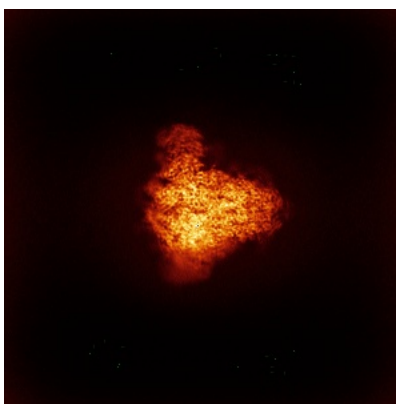


Z

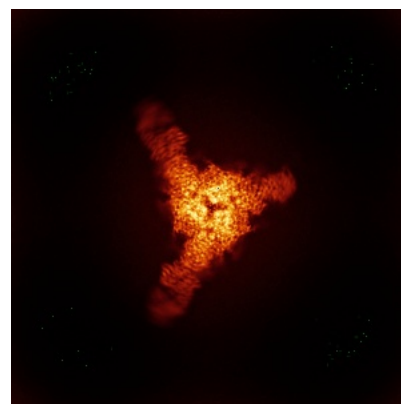
6.4.2 Raw map



X



Y

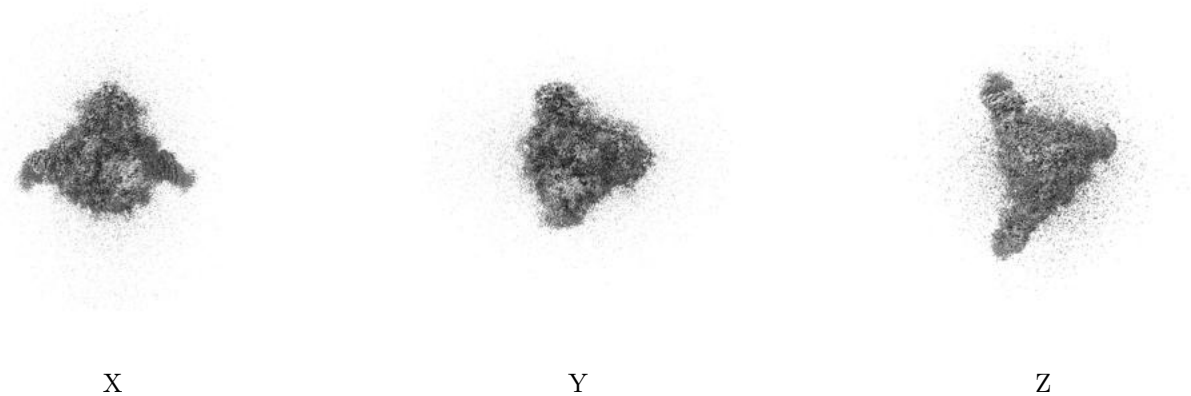


Z

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.

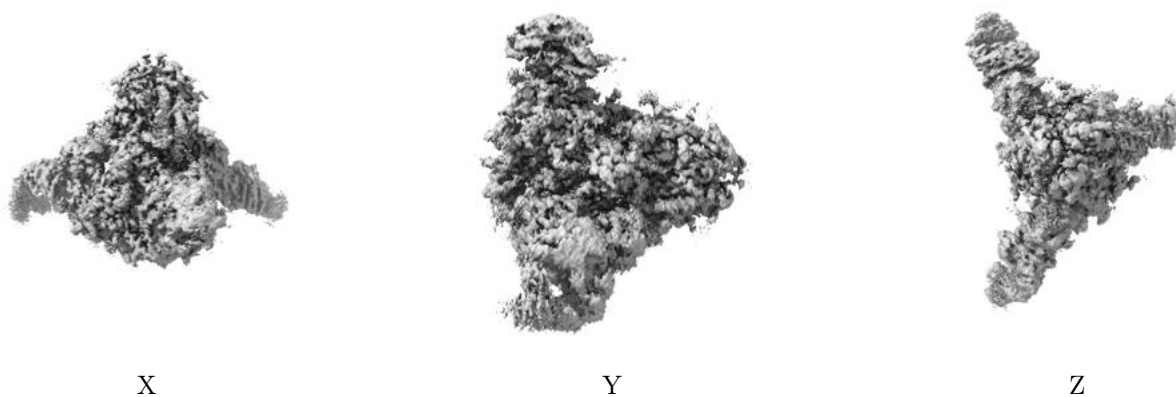
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.32. 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.

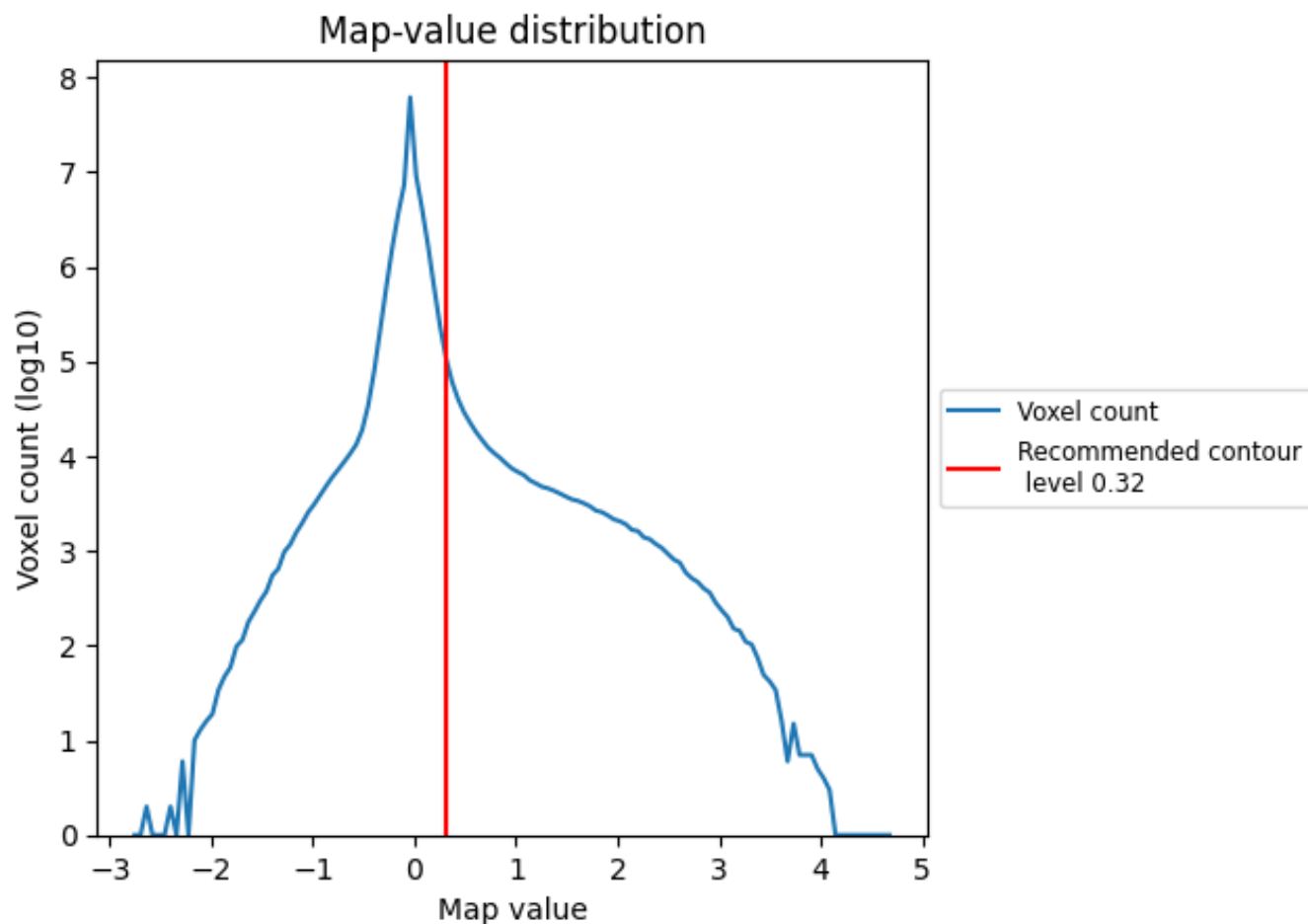
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

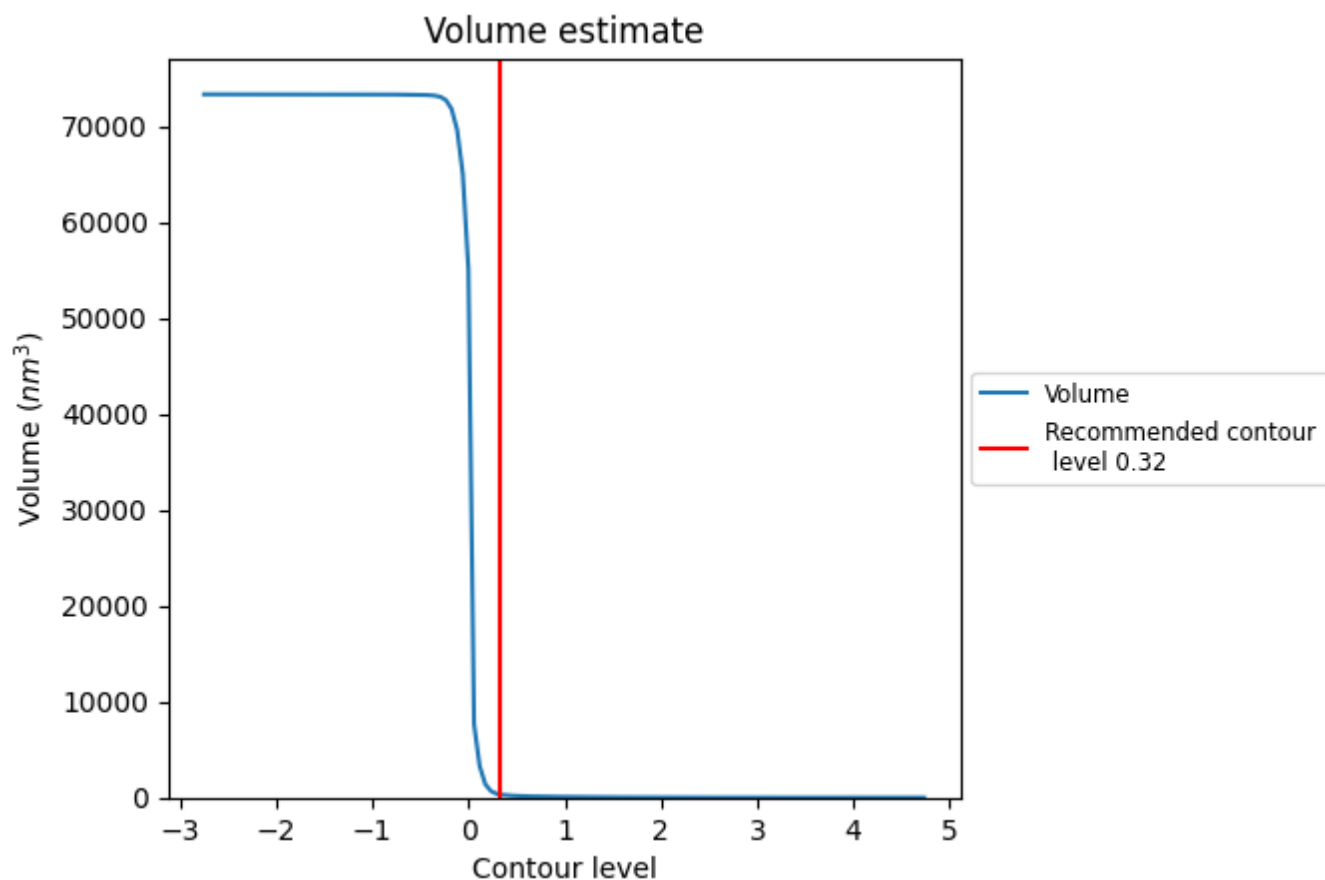
This section contains the results of statistical analysis of the map.

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.

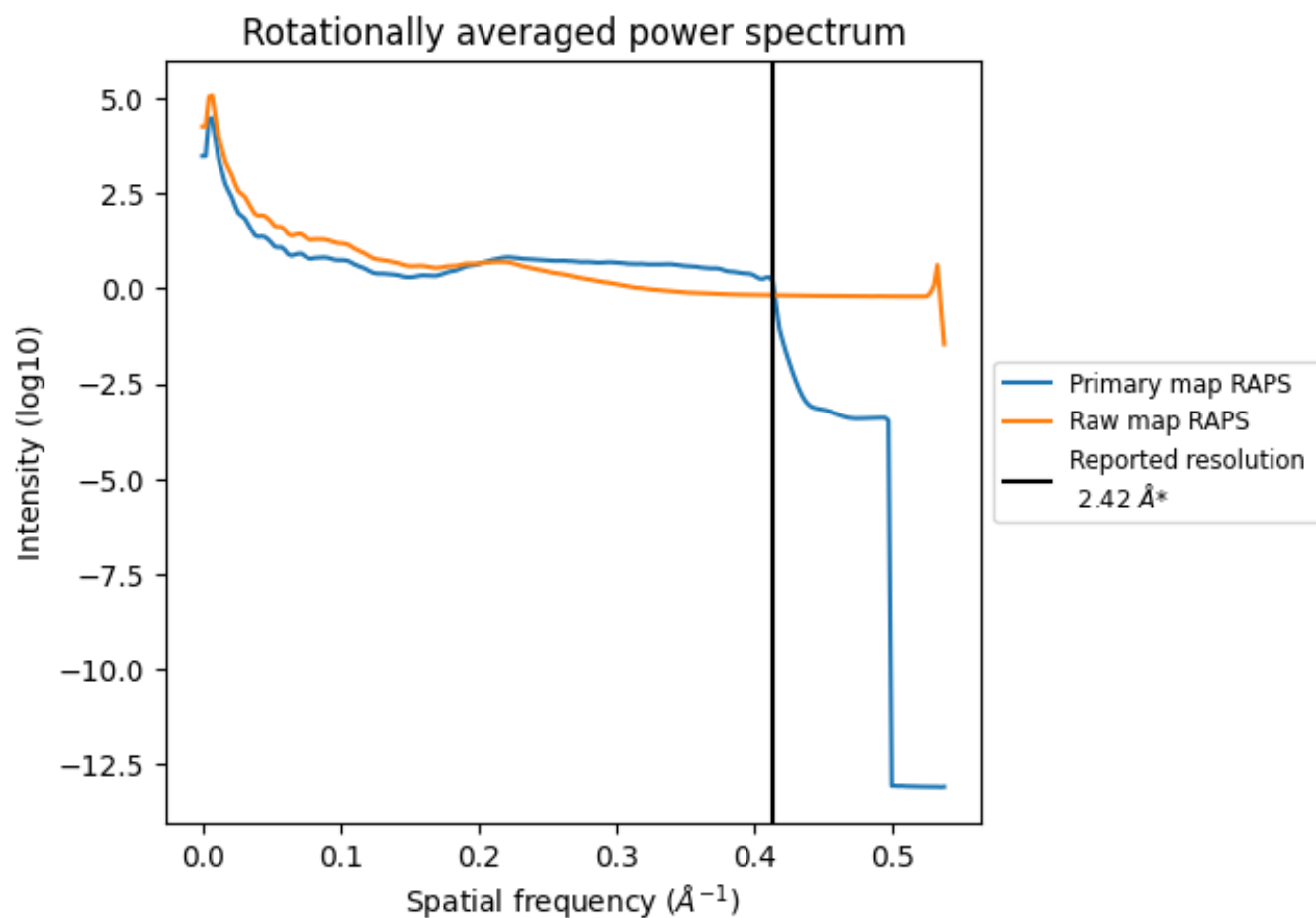
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 341 nm³; this corresponds to an approximate mass of 308 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 ⓘ

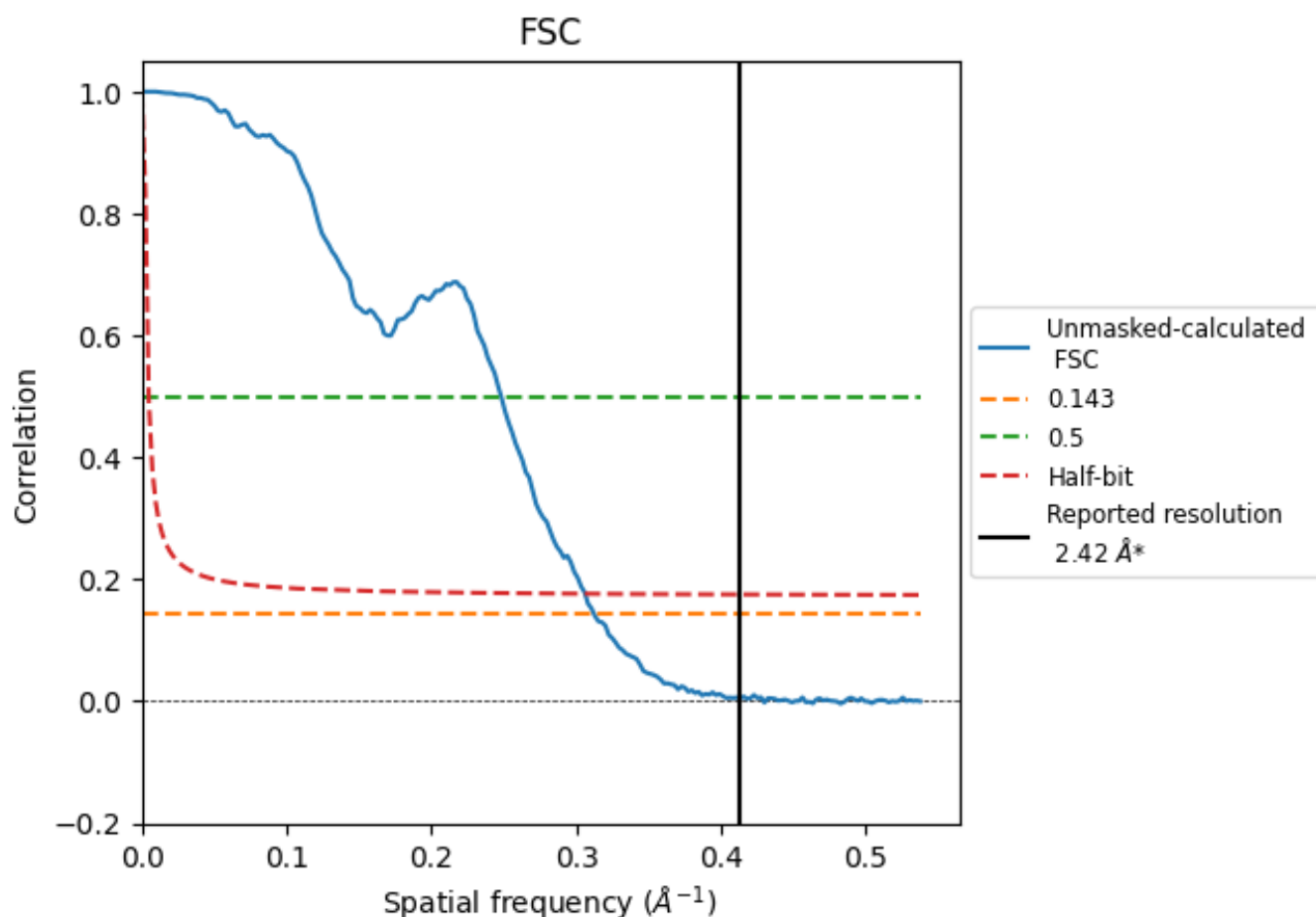


*Reported resolution corresponds to spatial frequency of 0.413 $\text{\AA}^{-1}$

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 0.413 Å⁻¹

8.2 Resolution estimates [i](#)

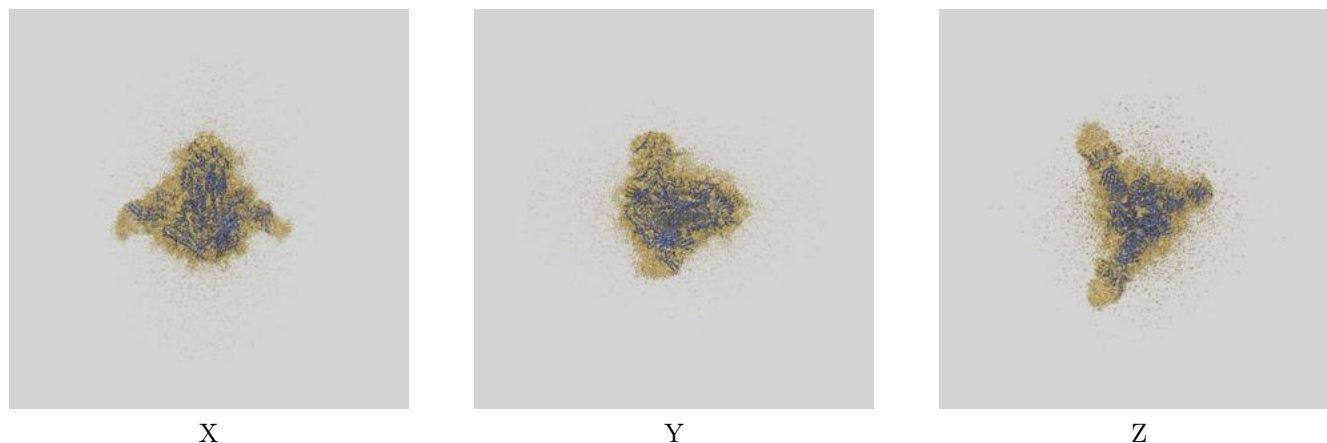
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.42	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.20	4.03	3.27

*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 3.20 differs from the reported value 2.42 by more than 10 %

9 Map-model fit [i](#)

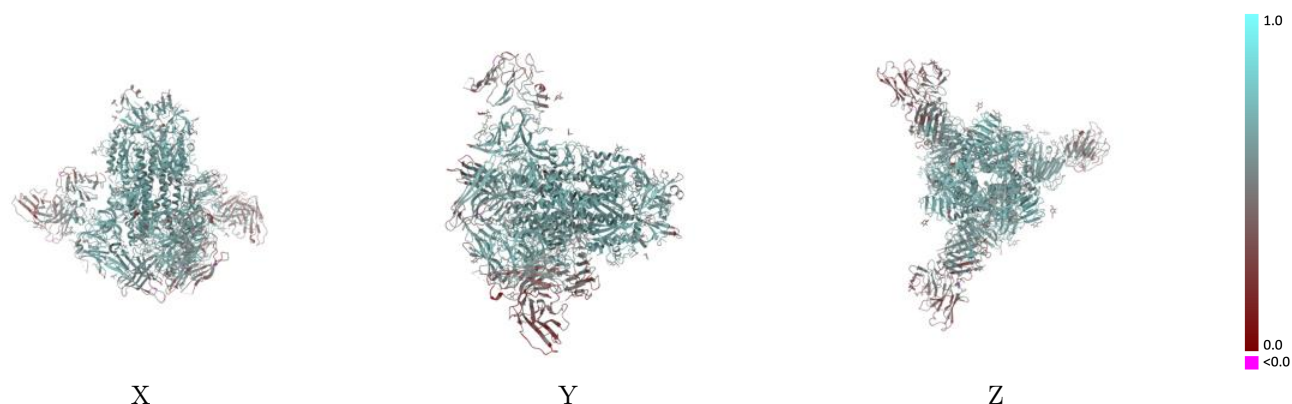
This section contains information regarding the fit between EMDB map EMD-67066 and PDB model 9XO1. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)



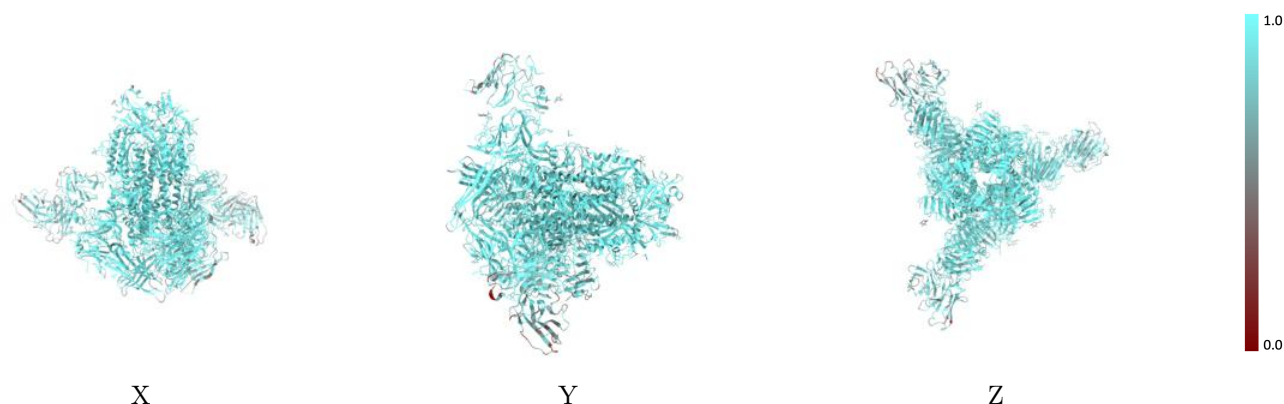
The images above show the 3D surface view of the map at the recommended contour level 0.32 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



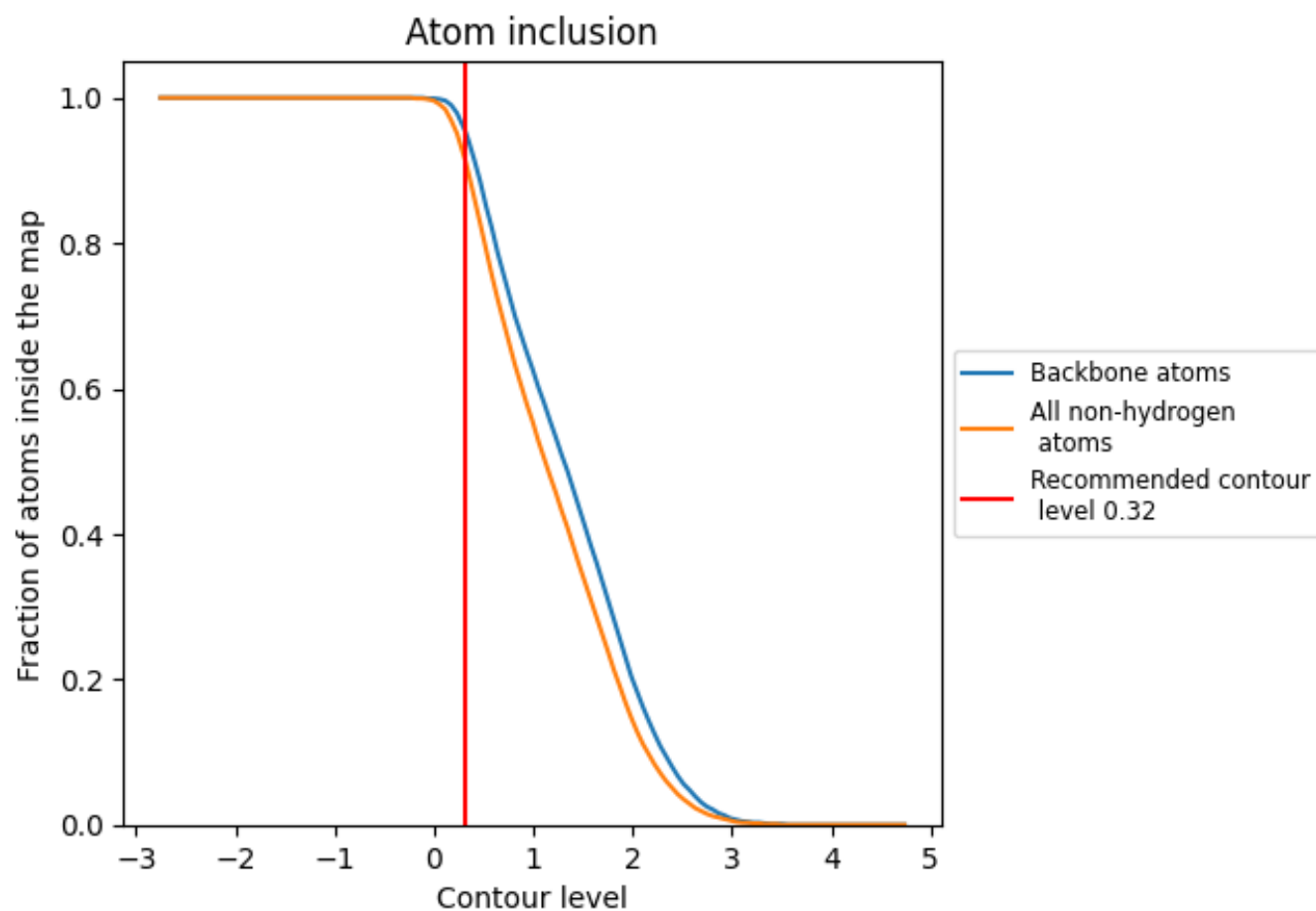
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.32).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 91% 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 (0.32) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9110	 0.5760
A	 0.9210	 0.5910
B	 0.9390	 0.6050
C	 0.9430	 0.6070
D	 0.7540	 0.4050
E	 0.7690	 0.3940
F	 0.7090	 0.3720
G	 0.6590	 0.3490
H	 0.9840	 0.5800
I	 0.8570	 0.5470
J	 0.7140	 0.3950
K	 0.8210	 0.4760
L	 0.8930	 0.5360
M	 0.9640	 0.5580
N	 0.9640	 0.5170
O	 0.8570	 0.5330
P	 0.9840	 0.6030
Q	 0.7500	 0.4280
R	 0.8930	 0.5720
S	 1.0000	 0.6450
T	 0.8570	 0.4570
U	 0.8570	 0.4930
V	 0.9840	 0.6190

