



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 08:07 PM UTC

PDB ID : 9MZIP / pdb_00009mzp
EMDB ID : EMD-48764
Title : CryoEM structure of GluK2 bound to glutamate in the shallow desensitized state, composite map
Authors : Chang, P.Z.; Nami, T.
Deposited on : 2025-01-23
Resolution : 3.80 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at
<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	NOT EXECUTED
MapQ	:	FAILED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

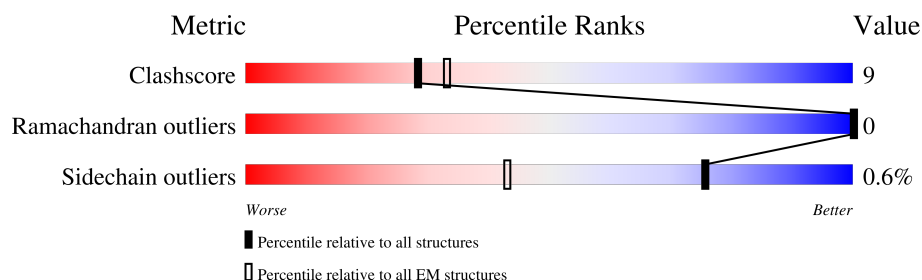
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	908	64% 19% • 15%
1	B	908	65% 19% • 15%
1	C	908	67% 17% • 15%
1	D	908	66% 18% • 15%
2	E	2	100%
2	F	2	50% 50%
2	G	2	100%
2	H	2	50% 50%
2	I	2	50% 50%

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Mol	Chain	Length	Quality of chain
2	J	2	 50%50%
2	K	2	 100%
2	L	2	 50%50%
2	M	2	 100%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 24865 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 Glutamate receptor ionotropic, kainate 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	769	Total	C	N	O	S	0	0
			6085	3907	1011	1133	34		
1	B	772	Total	C	N	O	S	0	0
			6108	3923	1014	1136	35		
1	C	772	Total	C	N	O	S	0	0
			6109	3923	1015	1136	35		
1	D	771	Total	C	N	O	S	0	0
			6103	3920	1014	1134	35		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	676	CYS	LYS	conflict	UNP P42260
A	802	CYS	ASN	conflict	UNP P42260
B	676	CYS	LYS	conflict	UNP P42260
B	802	CYS	ASN	conflict	UNP P42260
C	676	CYS	LYS	conflict	UNP P42260
C	802	CYS	ASN	conflict	UNP P42260
D	676	CYS	LYS	conflict	UNP P42260
D	802	CYS	ASN	conflict	UNP P42260

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

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

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



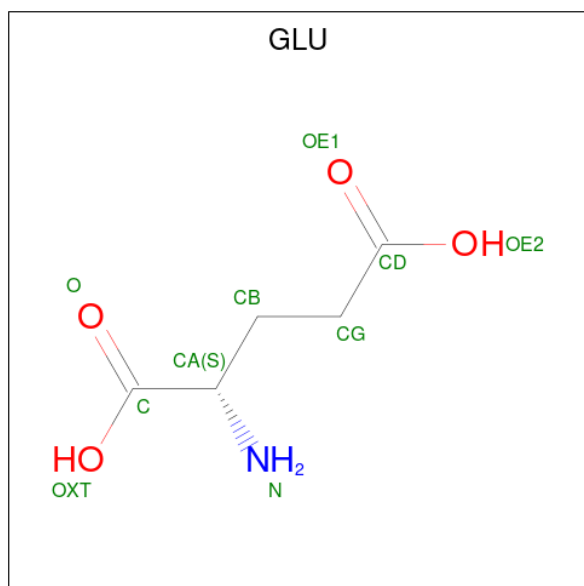
Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	B	1	Total	C	N	O	0
			14	8	1	5	

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

- Molecule 4 is GLUTAMIC ACID (CCD ID: GLU) (formula: $C_5H_9NO_4$).

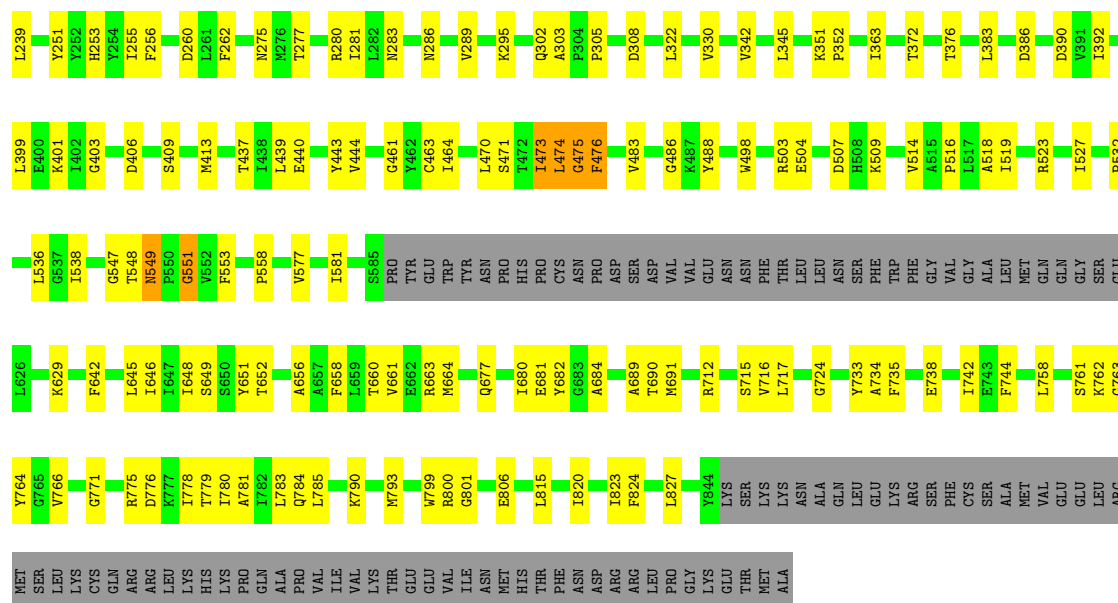


Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	N	O	0
			10	5	1	4	
4	B	1	Total	C	N	O	0
			10	5	1	4	
4	C	1	Total	C	N	O	0
			10	5	1	4	

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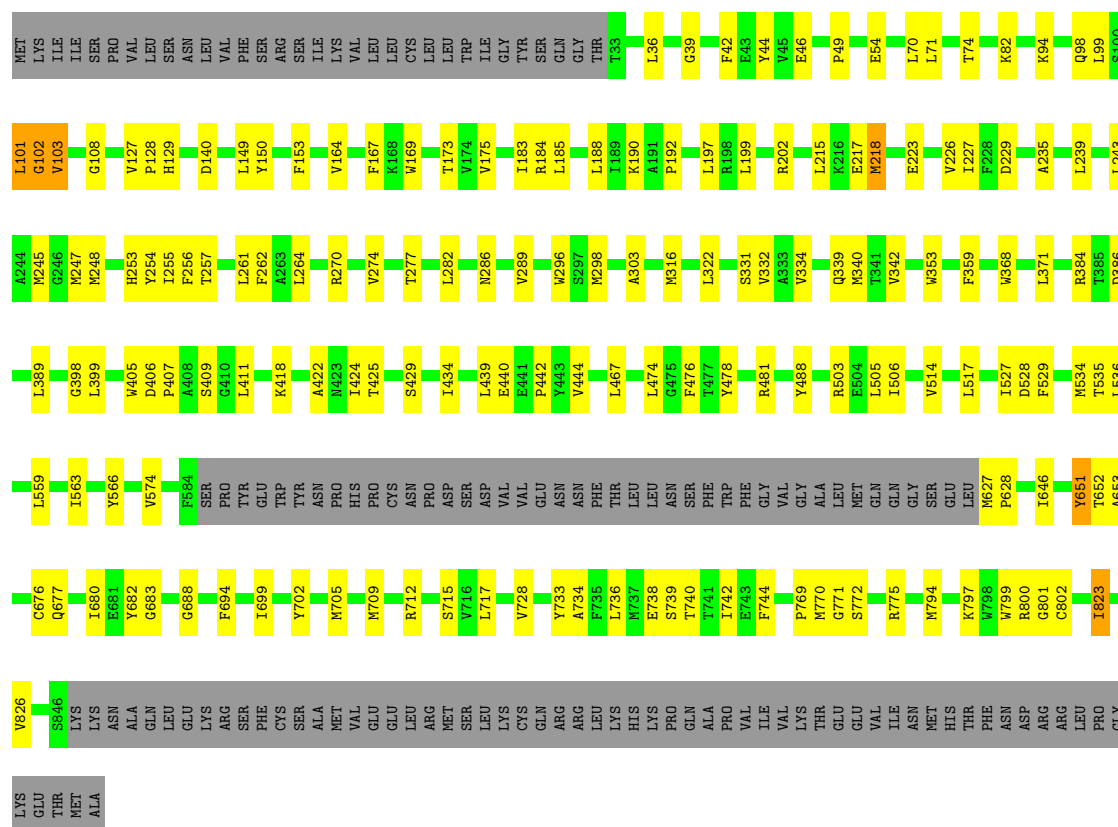
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Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
4	D	1	10	5	1	4	0



- Molecule 1: Glutamate receptor ionotropic, kainate 2

Chain C: 67% 17% 15%



- Molecule 1: Glutamate receptor ionotropic, kainate 2

Chain D: 66% 18% 15%

Chain H:  50% 50%

MAG1
MAG2

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

Chain I:  50% 50%

MAG1
MAG2

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

Chain J:  50% 50%

MAG1
MAG2

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

Chain K:  100%

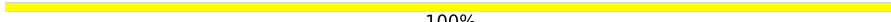
MAG1
MAG2

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

Chain L:  50% 50%

MAG1
MAG2

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

Chain M:  100%

MAG1
MAG2

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	81654	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.16	0/6219	0.60	15/8419 (0.2%)
1	B	0.15	0/6243	0.68	16/8452 (0.2%)
1	C	0.12	0/6244	0.47	8/8452 (0.1%)
1	D	0.13	0/6238	0.60	11/8444 (0.1%)
All	All	0.14	0/24944	0.59	50/33767 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	474	LEU	N-CA-C	-24.62	72.06	109.24
1	D	788	GLU	N-CA-C	-24.54	75.01	110.59
1	B	474	LEU	N-CA-C	-23.65	69.86	108.41
1	C	101	LEU	N-CA-C	-23.63	75.55	110.52
1	B	475	GLY	N-CA-C	22.03	151.57	115.66

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	800	ARG	Sidechain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6085	0	6076	138	0
1	B	6108	0	6104	127	0
1	C	6109	0	6104	114	0
1	D	6103	0	6099	119	0
2	E	28	0	25	0	0
2	F	28	0	25	1	0
2	G	28	0	25	0	0
2	H	28	0	25	0	0
2	I	28	0	25	0	0
2	J	28	0	25	1	0
2	K	28	0	25	0	0
2	L	28	0	25	0	0
2	M	28	0	25	0	0
3	A	42	0	39	0	0
3	B	28	0	26	1	0
3	C	42	0	39	0	0
3	D	56	0	52	1	0
4	A	10	0	5	1	0
4	B	10	0	5	2	0
4	C	10	0	5	0	0
4	D	10	0	5	1	0
All	All	24865	0	24784	471	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 9.

The worst 5 of 471 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:B:470:LEU:O	1:B:474:LEU:O	1.57	1.22
1:B:102:GLY:O	1:B:342:VAL:HG21	1.45	1.15
1:B:102:GLY:O	1:B:342:VAL:CG2	1.98	1.12
1:A:804:CYS:H	1:A:805:PRO:HD2	1.17	1.10
1:D:98:GLN:O	1:D:101:LEU:O	1.73	1.06

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	A	765/908 (84%)	729 (95%)	36 (5%)	0	100	100
1	B	768/908 (85%)	723 (94%)	45 (6%)	0	100	100
1	C	768/908 (85%)	736 (96%)	32 (4%)	0	100	100
1	D	767/908 (84%)	740 (96%)	27 (4%)	0	100	100
All	All	3068/3632 (84%)	2928 (95%)	140 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	666/794 (84%)	661 (99%)	5 (1%)	73	76
1	B	669/794 (84%)	664 (99%)	5 (1%)	76	77
1	C	669/794 (84%)	667 (100%)	2 (0%)	86	84
1	D	668/794 (84%)	663 (99%)	5 (1%)	76	77
All	All	2672/3176 (84%)	2655 (99%)	17 (1%)	76	79

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	750	CYS
1	D	807	GLU
1	B	691	MET
1	B	742	ILE
1	B	827	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	73	ASN
1	D	129	HIS
1	D	123	ASN
1	D	131	GLN
1	A	747	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 ⓘ

18 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	E	1	1,2	14,14,15	0.73	0	17,19,21	0.91	1 (5%)
2	NAG	E	2	2	14,14,15	0.75	0	17,19,21	1.26	1 (5%)
2	NAG	F	1	1,2	14,14,15	0.74	0	17,19,21	2.48	4 (23%)
2	NAG	F	2	2	14,14,15	0.76	0	17,19,21	0.92	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	G	1	1,2	14,14,15	0.71	0	17,19,21	0.81	0
2	NAG	G	2	2	14,14,15	0.73	0	17,19,21	0.85	0
2	NAG	H	1	1,2	14,14,15	0.73	0	17,19,21	0.76	0
2	NAG	H	2	2	14,14,15	0.71	0	17,19,21	0.89	1 (5%)
2	NAG	I	1	1,2	14,14,15	0.88	0	17,19,21	1.49	2 (11%)
2	NAG	I	2	2	14,14,15	0.72	0	17,19,21	0.83	0
2	NAG	J	1	1,2	14,14,15	0.80	0	17,19,21	1.72	4 (23%)
2	NAG	J	2	2	14,14,15	0.78	0	17,19,21	0.86	1 (5%)
2	NAG	K	1	1,2	14,14,15	0.71	0	17,19,21	0.81	0
2	NAG	K	2	2	14,14,15	0.72	0	17,19,21	0.87	0
2	NAG	L	1	1,2	14,14,15	0.72	0	17,19,21	0.80	0
2	NAG	L	2	2	14,14,15	0.76	0	17,19,21	1.02	1 (5%)
2	NAG	M	1	1,2	14,14,15	0.74	0	17,19,21	1.24	1 (5%)
2	NAG	M	2	2	14,14,15	0.72	0	17,19,21	0.92	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
2	NAG	E	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	E	2	2	-	2/6/23/26	0/1/1/1
2	NAG	F	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	F	2	2	-	2/6/23/26	0/1/1/1
2	NAG	G	1	1,2	-	1/6/23/26	0/1/1/1
2	NAG	G	2	2	-	0/6/23/26	0/1/1/1
2	NAG	H	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	H	2	2	-	2/6/23/26	0/1/1/1
2	NAG	I	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	I	2	2	-	0/6/23/26	0/1/1/1
2	NAG	J	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	J	2	2	-	0/6/23/26	0/1/1/1
2	NAG	K	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	K	2	2	-	2/6/23/26	0/1/1/1
2	NAG	L	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	L	2	2	-	2/6/23/26	0/1/1/1
2	NAG	M	1	1,2	-	1/6/23/26	0/1/1/1
2	NAG	M	2	2	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	1	NAG	C2-N2-C7	8.29	134.01	122.90
2	J	1	NAG	C4-C3-C2	5.00	118.34	111.02
2	I	1	NAG	C4-C3-C2	4.31	117.34	111.02
2	M	1	NAG	C1-O5-C5	4.12	117.71	112.19
2	F	1	NAG	O5-C1-C2	-3.18	106.37	111.29

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

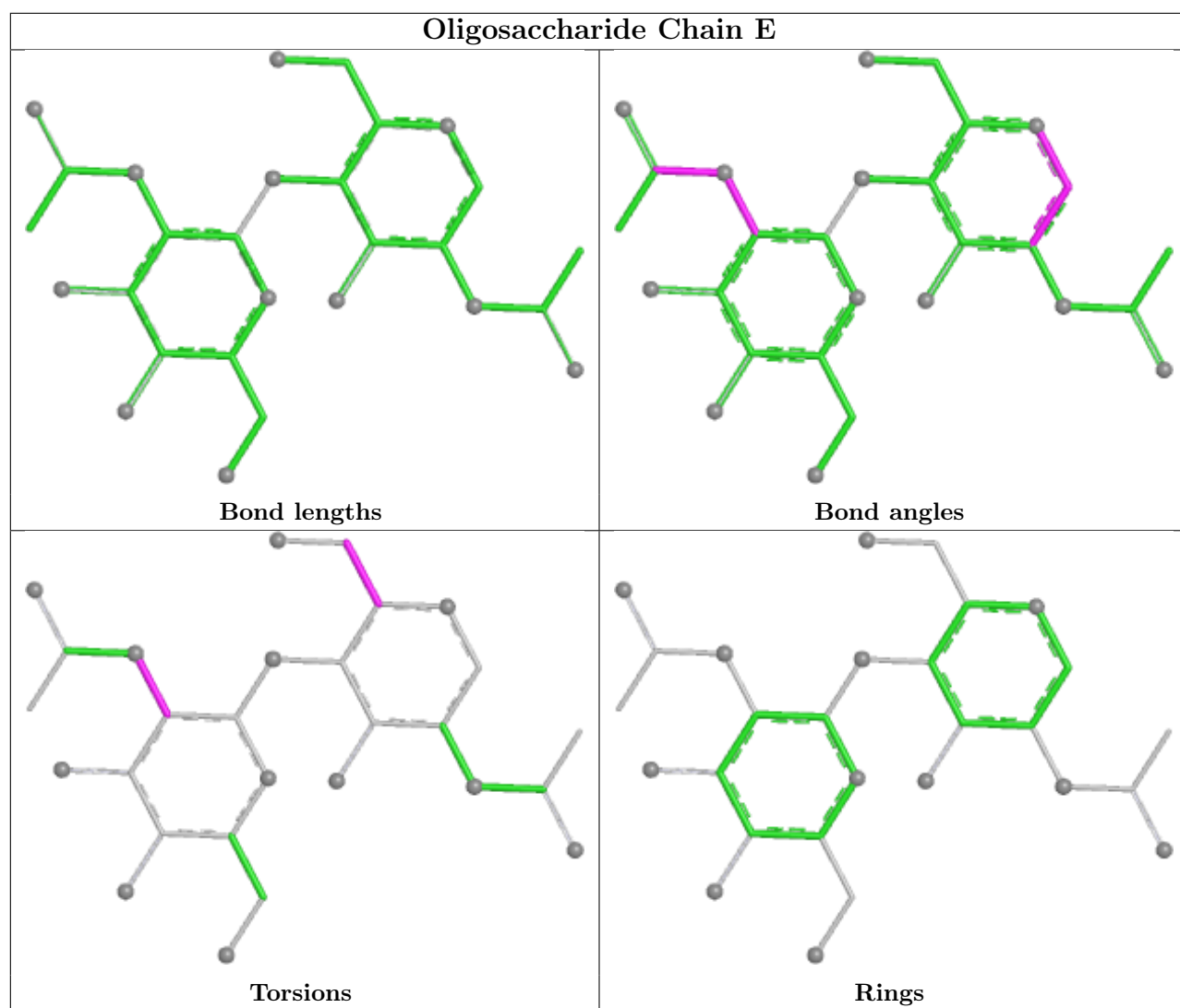
Mol	Chain	Res	Type	Atoms
2	E	1	NAG	O5-C5-C6-O6
2	F	1	NAG	C8-C7-N2-C2
2	F	1	NAG	O7-C7-N2-C2
2	H	2	NAG	C8-C7-N2-C2
2	H	2	NAG	O7-C7-N2-C2

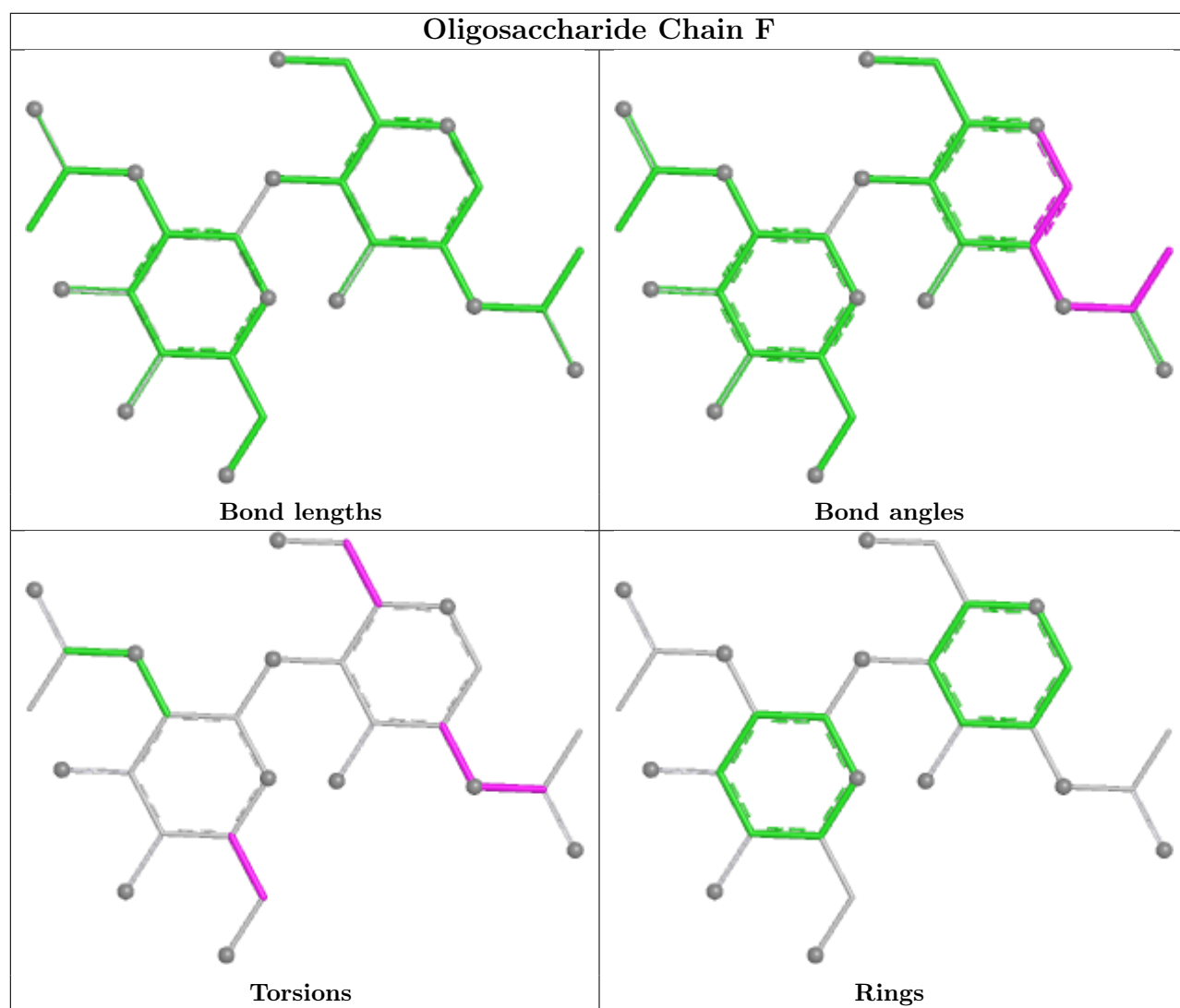
There are no ring outliers.

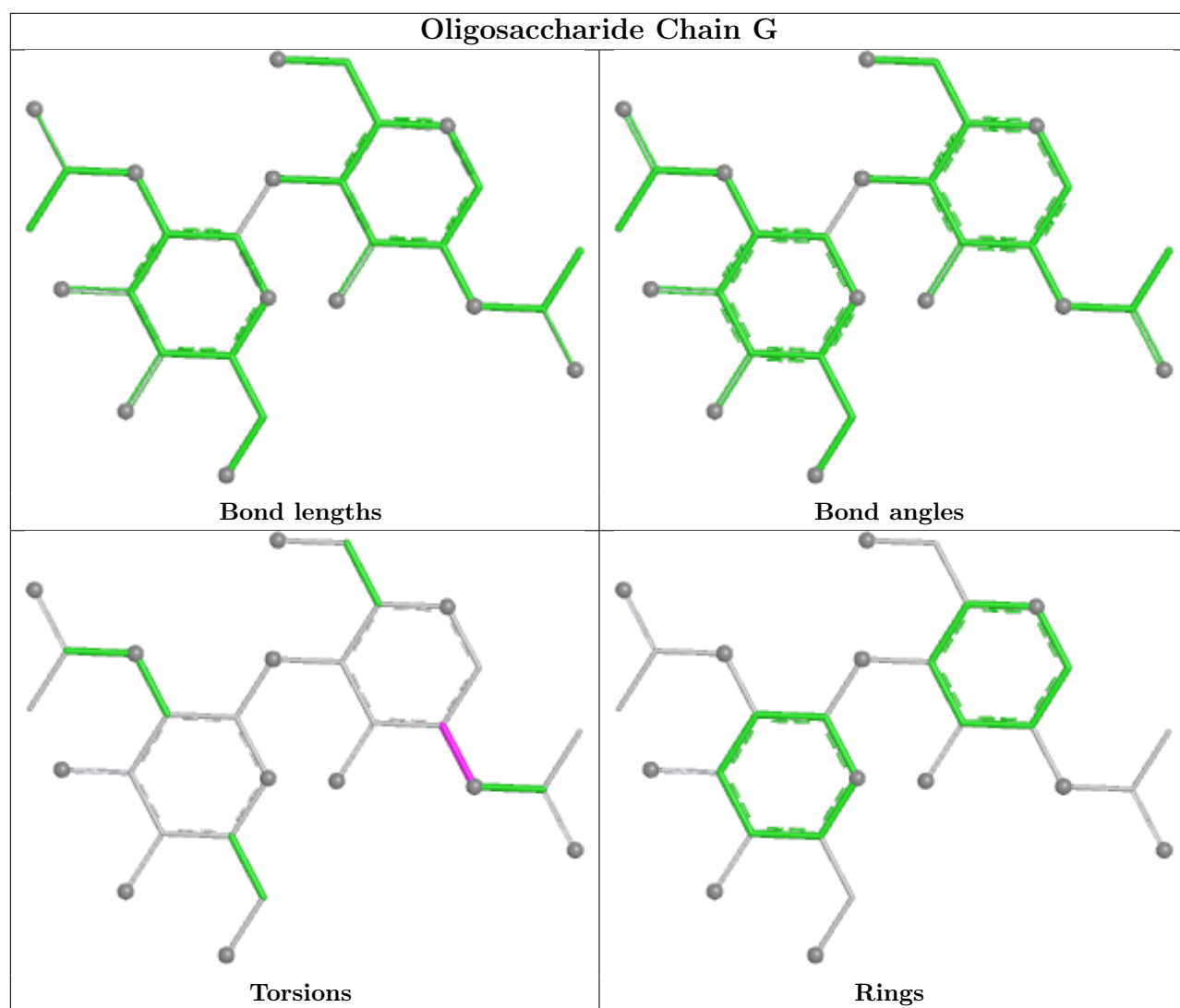
2 monomers are involved in 2 short contacts:

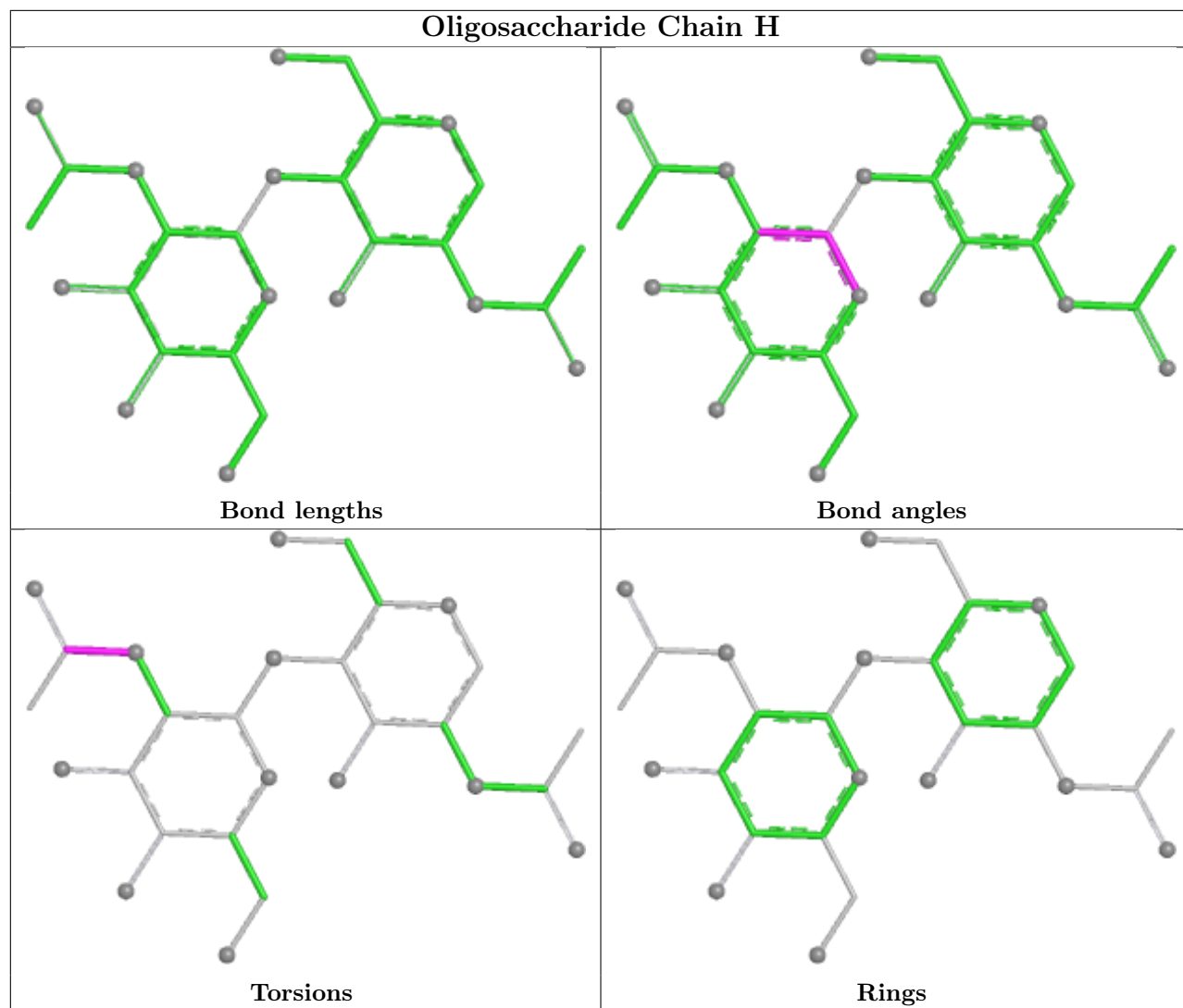
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	1	NAG	1	0
2	J	2	NAG	1	0

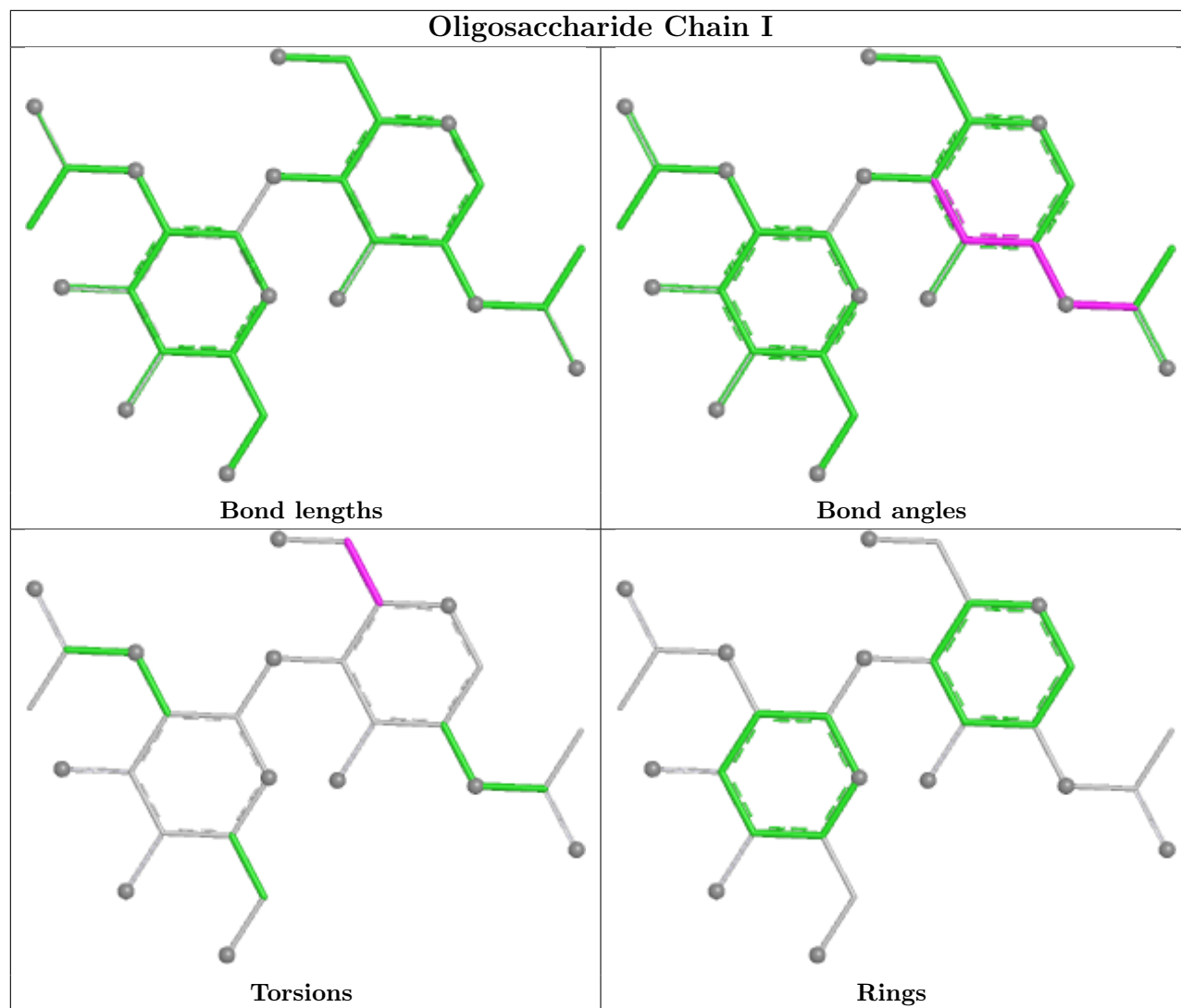
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

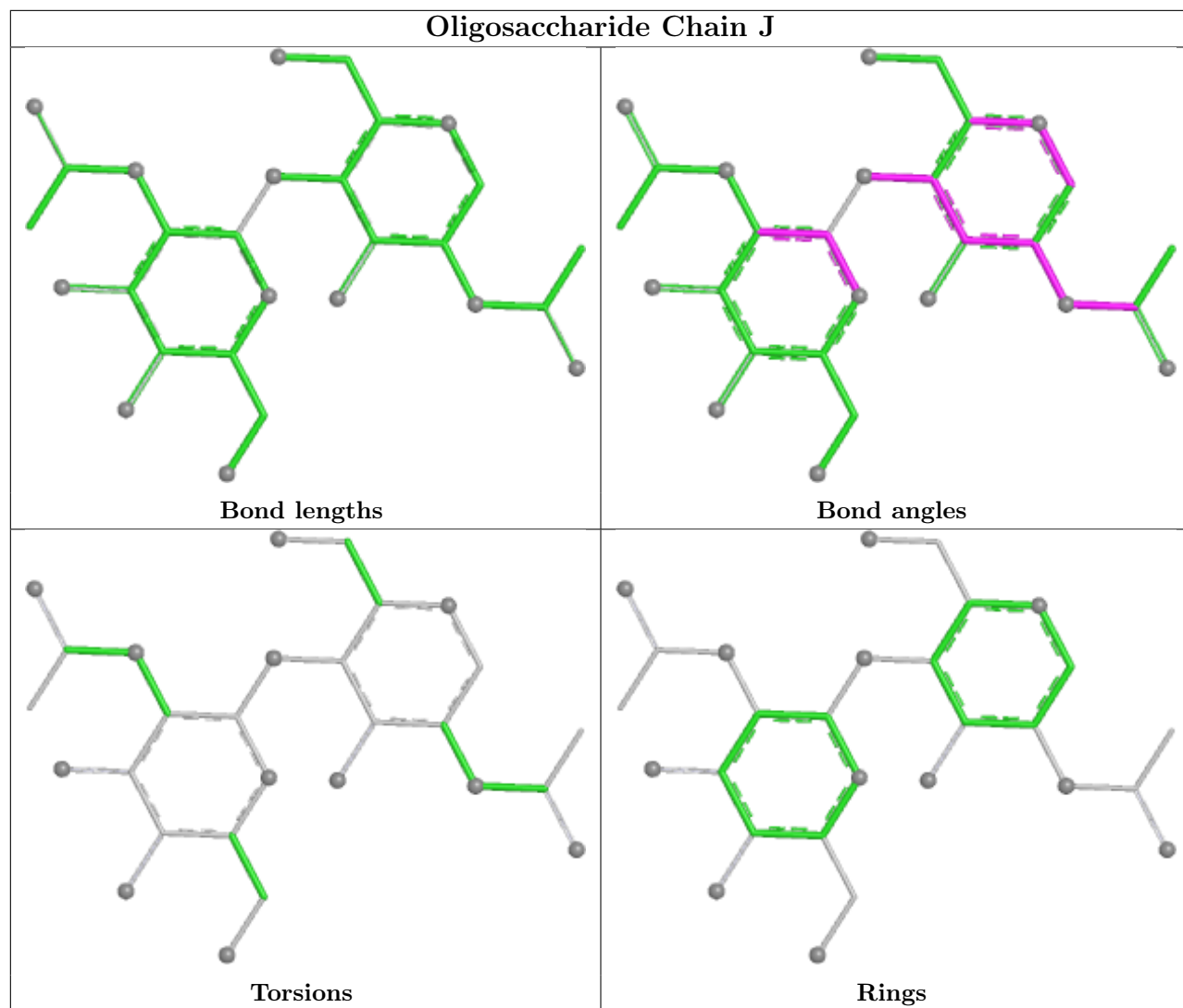


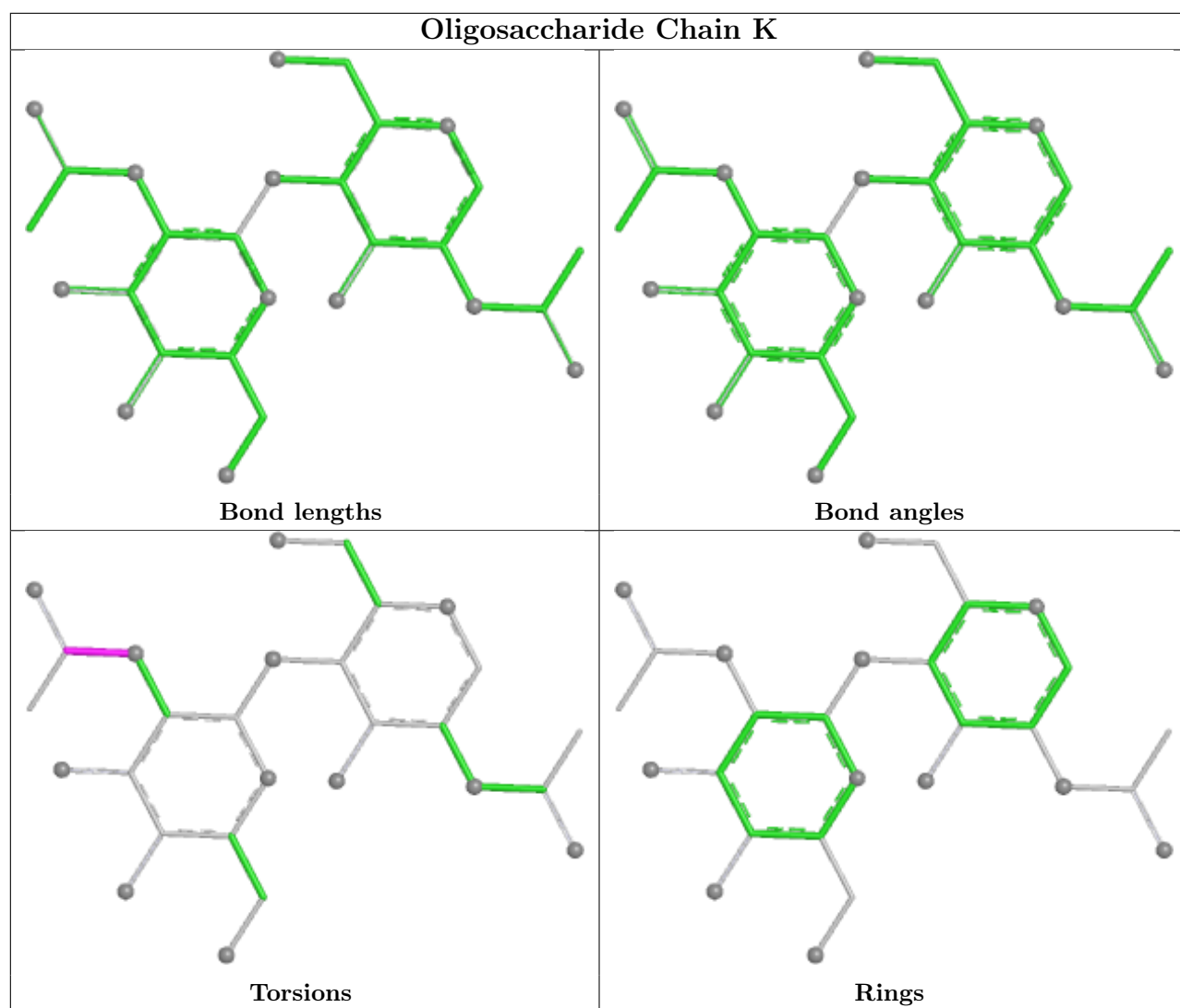


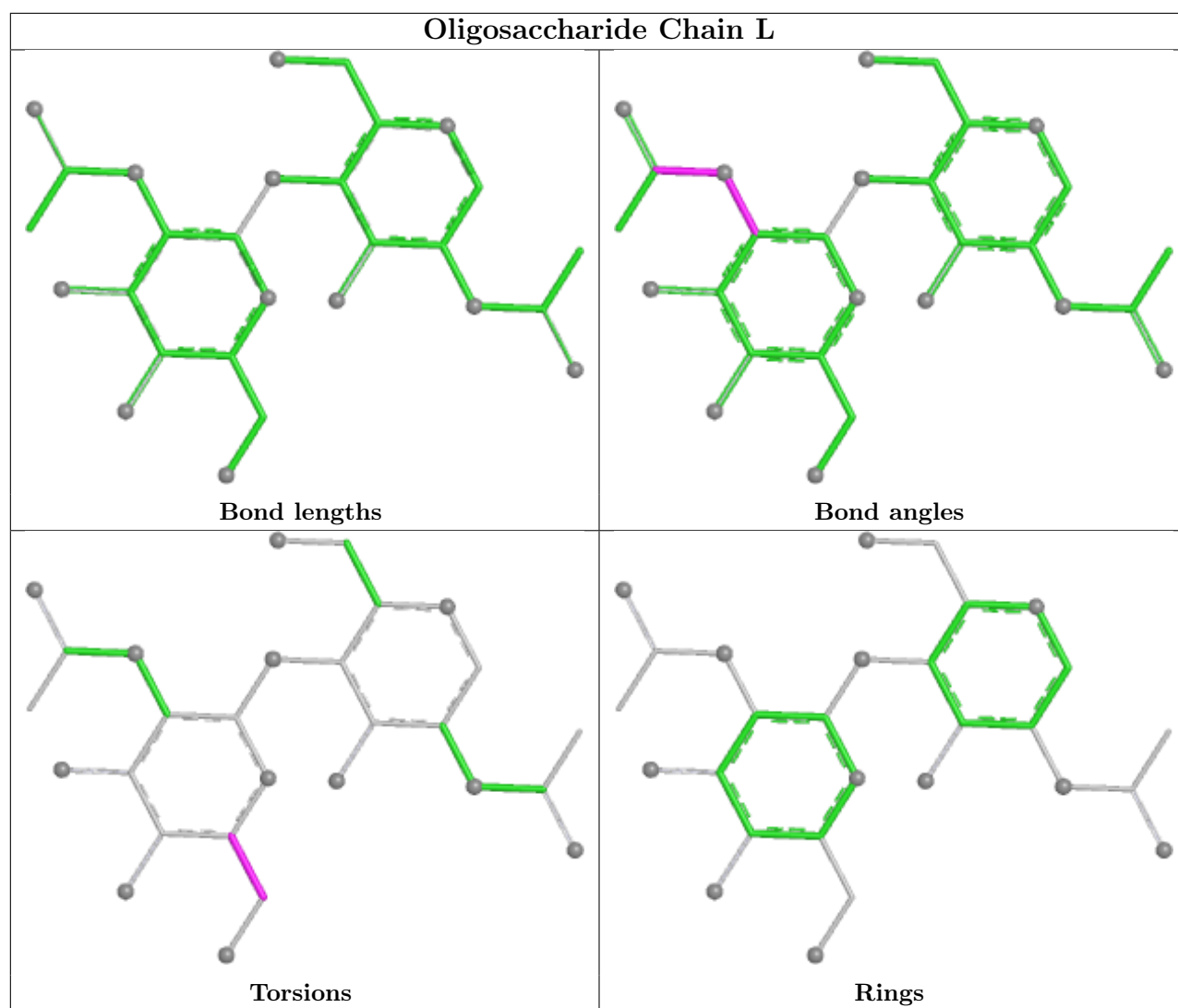


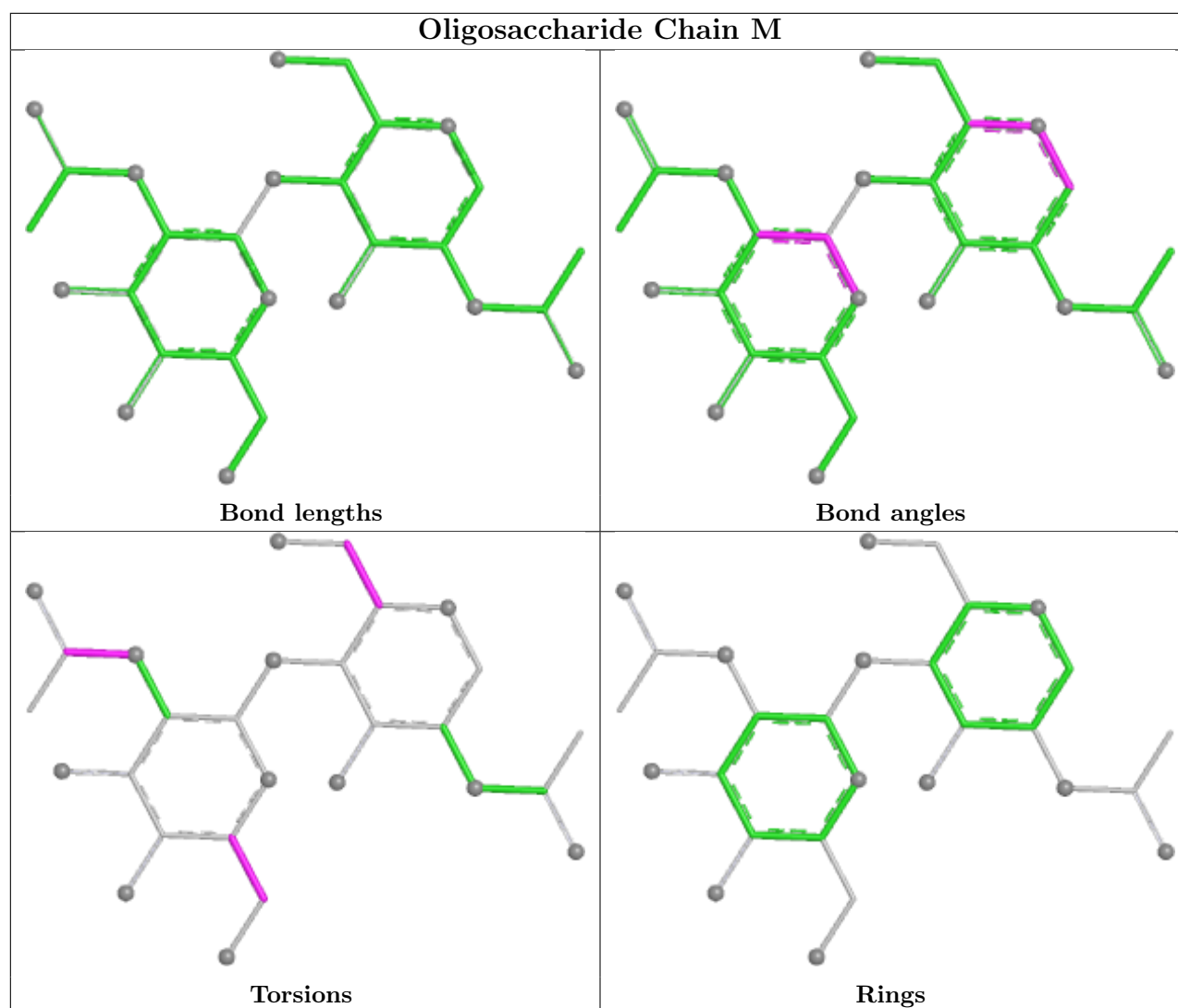












5.6 Ligand geometry [i](#)

16 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	$\# Z > 2$
3	NAG	D	1003	1	14,14,15	0.71	0	17,19,21	0.74	0
3	NAG	C	1001	1	14,14,15	0.70	0	17,19,21	0.80	0
3	NAG	C	1003	1	14,14,15	0.70	0	17,19,21	0.88	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	A	1002	1	14,14,15	0.75	0	17,19,21	0.98	1 (5%)
4	GLU	B	1003	-	8,9,9	1.12	1 (12%)	8,11,11	1.20	1 (12%)
3	NAG	B	1002	1	14,14,15	0.72	0	17,19,21	0.87	0
4	GLU	A	1004	-	8,9,9	1.10	1 (12%)	8,11,11	1.11	1 (12%)
4	GLU	D	1005	-	8,9,9	1.11	1 (12%)	8,11,11	1.07	1 (12%)
3	NAG	B	1001	1	14,14,15	0.87	0	17,19,21	1.44	3 (17%)
3	NAG	A	1003	1	14,14,15	0.75	0	17,19,21	1.02	1 (5%)
3	NAG	D	1004	1	14,14,15	0.69	0	17,19,21	0.85	0
4	GLU	C	1004	-	8,9,9	1.10	1 (12%)	8,11,11	1.21	1 (12%)
3	NAG	D	1001	1	14,14,15	0.71	0	17,19,21	0.85	0
3	NAG	D	1002	1	14,14,15	0.72	0	17,19,21	0.81	0
3	NAG	A	1001	1	14,14,15	0.71	0	17,19,21	0.82	0
3	NAG	C	1002	1	14,14,15	0.72	0	17,19,21	0.80	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
3	NAG	D	1003	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1001	1	-	1/6/23/26	0/1/1/1
3	NAG	C	1003	1	-	1/6/23/26	0/1/1/1
3	NAG	A	1002	1	-	4/6/23/26	0/1/1/1
4	GLU	B	1003	-	-	3/9/9/9	-
3	NAG	B	1002	1	-	2/6/23/26	0/1/1/1
4	GLU	A	1004	-	-	0/9/9/9	-
4	GLU	D	1005	-	-	1/9/9/9	-
3	NAG	B	1001	1	-	2/6/23/26	0/1/1/1
3	NAG	A	1003	1	-	2/6/23/26	0/1/1/1
3	NAG	D	1004	1	-	3/6/23/26	0/1/1/1
4	GLU	C	1004	-	-	1/9/9/9	-
3	NAG	D	1001	1	-	0/6/23/26	0/1/1/1
3	NAG	D	1002	1	-	1/6/23/26	0/1/1/1
3	NAG	A	1001	1	-	1/6/23/26	0/1/1/1
3	NAG	C	1002	1	-	0/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1003	GLU	OXT-C	-2.29	1.23	1.30
4	A	1004	GLU	OXT-C	-2.27	1.23	1.30
4	D	1005	GLU	OXT-C	-2.25	1.23	1.30
4	C	1004	GLU	OXT-C	-2.22	1.23	1.30

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1001	NAG	C2-N2-C7	3.60	127.73	122.90
4	C	1004	GLU	OXT-C-O	-2.71	117.93	124.08
4	B	1003	GLU	OXT-C-O	-2.69	117.98	124.08
3	B	1001	NAG	O5-C5-C4	-2.50	104.75	110.83
3	A	1002	NAG	C2-N2-C7	2.46	126.20	122.90

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1002	NAG	C8-C7-N2-C2
3	A	1002	NAG	O7-C7-N2-C2
3	A	1003	NAG	C8-C7-N2-C2
3	A	1003	NAG	O7-C7-N2-C2
3	B	1001	NAG	C8-C7-N2-C2

There are no ring outliers.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1003	GLU	2	0
4	A	1004	GLU	1	0
4	D	1005	GLU	1	0
3	B	1001	NAG	1	0
3	D	1001	NAG	1	0

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

This section contains visualisations of the EMDB entry EMD-48764. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.