



Full wwPDB EM Validation Report (i)

Oct 30, 2024 – 02:08 PM JST

PDB ID : 8ZFK
EMDB ID : EMD-60063
Title : *Caenorhabditis elegans ACR-23 in betaine and monepantel bound state*
Authors : Chen, Q.F.; Liu, F.L.; Li, T.Y.; Gong, H.H.; Guo, F.; Liu, S.
Deposited on : 2024-05-08
Resolution : 2.64 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 (i) 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 \(1\)](#)) were used in the production of this report:

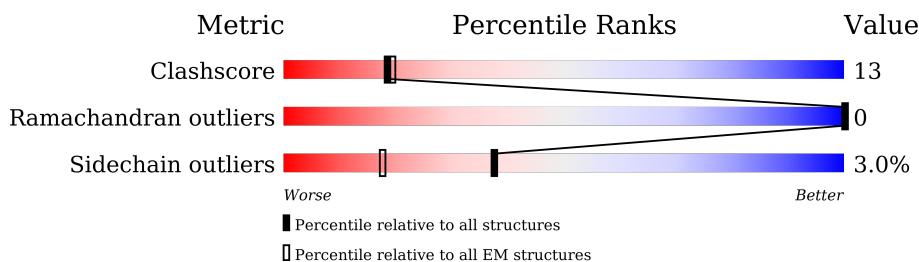
EMDB validation analysis : **FAILED**
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

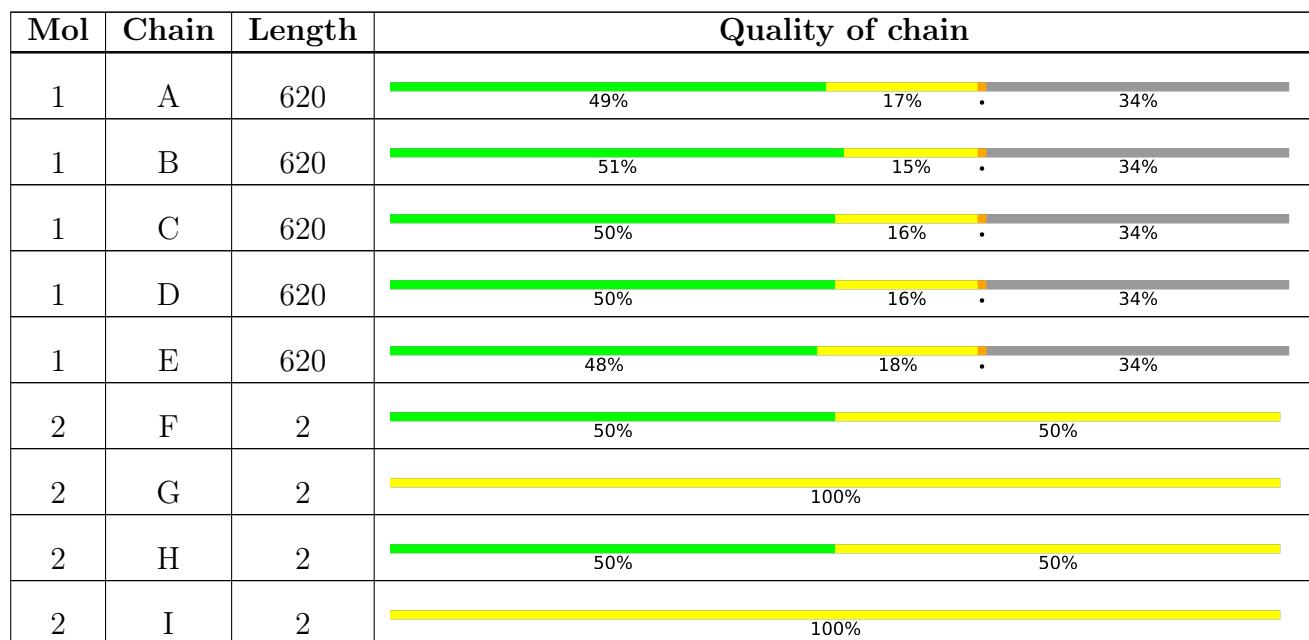
The reported resolution of this entry is 2.64 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%



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The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	H	1	-	-	X	-
2	NAG	L	1	-	-	X	-

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 17345 atoms, of which 60 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 Betaine receptor acr-23,Soluble cytochrome b562.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	412	Total	C	N	O	S	0	0
			3344	2188	538	597	21		
1	A	412	Total	C	N	O	S	0	0
			3344	2188	538	597	21		
1	B	412	Total	C	N	O	S	0	0
			3344	2188	538	597	21		
1	C	412	Total	C	N	O	S	0	0
			3344	2188	538	597	21		
1	E	412	Total	C	N	O	S	0	0
			3344	2188	538	597	21		

There are 220 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	?	-	SER	deletion	UNP G5EG88
D	?	-	VAL	deletion	UNP G5EG88
D	?	-	ASN	deletion	UNP G5EG88
D	?	-	PRO	deletion	UNP G5EG88
D	?	-	PHE	deletion	UNP G5EG88
D	?	-	THR	deletion	UNP G5EG88
D	?	-	ASN	deletion	UNP G5EG88
D	?	-	PHE	deletion	UNP G5EG88
D	?	-	CYS	deletion	UNP G5EG88
D	?	-	ASN	deletion	UNP G5EG88
D	?	-	VAL	deletion	UNP G5EG88
D	385B	MET	-	linker	UNP G5EG88
D	385C	ALA	-	linker	UNP G5EG88
D	385D	GLU	-	linker	UNP G5EG88
D	385E	ALA	-	linker	UNP G5EG88
D	385F	GLY	-	linker	UNP G5EG88
D	385G	ALA	-	linker	UNP G5EG88
D	385H	MET	-	linker	UNP G5EG88
D	385O	TRP	MET	conflict	UNP P0ABE7
D	389F	ILE	HIS	conflict	UNP P0ABE7

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Chain	Residue	Modelled	Actual	Comment	Reference
D	389J	LEU	-	linker	UNP P0ABE7
D	389K	SER	-	linker	UNP P0ABE7
D	535	LEU	-	expression tag	UNP G5EG88
D	536	GLU	-	expression tag	UNP G5EG88
D	537	GLY	-	expression tag	UNP G5EG88
D	538	THR	-	expression tag	UNP G5EG88
D	539	LYS	-	expression tag	UNP G5EG88
D	540	LEU	-	expression tag	UNP G5EG88
D	541	VAL	-	expression tag	UNP G5EG88
D	542	PRO	-	expression tag	UNP G5EG88
D	543	ARG	-	expression tag	UNP G5EG88
D	544	GLY	-	expression tag	UNP G5EG88
D	545	SER	-	expression tag	UNP G5EG88
D	546	SER	-	expression tag	UNP G5EG88
D	547	SER	-	expression tag	UNP G5EG88
D	548	GLY	-	expression tag	UNP G5EG88
D	549	TRP	-	expression tag	UNP G5EG88
D	550	SER	-	expression tag	UNP G5EG88
D	551	HIS	-	expression tag	UNP G5EG88
D	552	PRO	-	expression tag	UNP G5EG88
D	553	GLN	-	expression tag	UNP G5EG88
D	554	PHE	-	expression tag	UNP G5EG88
D	555	GLU	-	expression tag	UNP G5EG88
D	556	LYS	-	expression tag	UNP G5EG88
A	?	-	SER	deletion	UNP G5EG88
A	?	-	VAL	deletion	UNP G5EG88
A	?	-	ASN	deletion	UNP G5EG88
A	?	-	PRO	deletion	UNP G5EG88
A	?	-	PHE	deletion	UNP G5EG88
A	?	-	THR	deletion	UNP G5EG88
A	?	-	ASN	deletion	UNP G5EG88
A	?	-	PHE	deletion	UNP G5EG88
A	?	-	CYS	deletion	UNP G5EG88
A	?	-	ASN	deletion	UNP G5EG88
A	?	-	VAL	deletion	UNP G5EG88
A	385B	MET	-	linker	UNP G5EG88
A	385C	ALA	-	linker	UNP G5EG88
A	385D	GLU	-	linker	UNP G5EG88
A	385E	ALA	-	linker	UNP G5EG88
A	385F	GLY	-	linker	UNP G5EG88
A	385G	ALA	-	linker	UNP G5EG88
A	385H	MET	-	linker	UNP G5EG88

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Chain	Residue	Modelled	Actual	Comment	Reference
A	385O	TRP	MET	conflict	UNP P0ABE7
A	389F	ILE	HIS	conflict	UNP P0ABE7
A	389J	LEU	-	linker	UNP P0ABE7
A	389K	SER	-	linker	UNP P0ABE7
A	535	LEU	-	expression tag	UNP G5EG88
A	536	GLU	-	expression tag	UNP G5EG88
A	537	GLY	-	expression tag	UNP G5EG88
A	538	THR	-	expression tag	UNP G5EG88
A	539	LYS	-	expression tag	UNP G5EG88
A	540	LEU	-	expression tag	UNP G5EG88
A	541	VAL	-	expression tag	UNP G5EG88
A	542	PRO	-	expression tag	UNP G5EG88
A	543	ARG	-	expression tag	UNP G5EG88
A	544	GLY	-	expression tag	UNP G5EG88
A	545	SER	-	expression tag	UNP G5EG88
A	546	SER	-	expression tag	UNP G5EG88
A	547	SER	-	expression tag	UNP G5EG88
A	548	GLY	-	expression tag	UNP G5EG88
A	549	TRP	-	expression tag	UNP G5EG88
A	550	SER	-	expression tag	UNP G5EG88
A	551	HIS	-	expression tag	UNP G5EG88
A	552	PRO	-	expression tag	UNP G5EG88
A	553	GLN	-	expression tag	UNP G5EG88
A	554	PHE	-	expression tag	UNP G5EG88
A	555	GLU	-	expression tag	UNP G5EG88
A	556	LYS	-	expression tag	UNP G5EG88
B	?	-	SER	deletion	UNP G5EG88
B	?	-	VAL	deletion	UNP G5EG88
B	?	-	ASN	deletion	UNP G5EG88
B	?	-	PRO	deletion	UNP G5EG88
B	?	-	PHE	deletion	UNP G5EG88
B	?	-	THR	deletion	UNP G5EG88
B	?	-	ASN	deletion	UNP G5EG88
B	?	-	PHE	deletion	UNP G5EG88
B	?	-	CYS	deletion	UNP G5EG88
B	?	-	ASN	deletion	UNP G5EG88
B	?	-	VAL	deletion	UNP G5EG88
B	385B	MET	-	linker	UNP G5EG88
B	385C	ALA	-	linker	UNP G5EG88
B	385D	GLU	-	linker	UNP G5EG88
B	385E	ALA	-	linker	UNP G5EG88
B	385F	GLY	-	linker	UNP G5EG88

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Chain	Residue	Modelled	Actual	Comment	Reference
B	385G	ALA	-	linker	UNP G5EG88
B	385H	MET	-	linker	UNP G5EG88
B	385O	TRP	MET	conflict	UNP P0ABE7
B	389F	ILE	HIS	conflict	UNP P0ABE7
B	389J	LEU	-	linker	UNP P0ABE7
B	389K	SER	-	linker	UNP P0ABE7
B	535	LEU	-	expression tag	UNP G5EG88
B	536	GLU	-	expression tag	UNP G5EG88
B	537	GLY	-	expression tag	UNP G5EG88
B	538	THR	-	expression tag	UNP G5EG88
B	539	LYS	-	expression tag	UNP G5EG88
B	540	LEU	-	expression tag	UNP G5EG88
B	541	VAL	-	expression tag	UNP G5EG88
B	542	PRO	-	expression tag	UNP G5EG88
B	543	ARG	-	expression tag	UNP G5EG88
B	544	GLY	-	expression tag	UNP G5EG88
B	545	SER	-	expression tag	UNP G5EG88
B	546	SER	-	expression tag	UNP G5EG88
B	547	SER	-	expression tag	UNP G5EG88
B	548	GLY	-	expression tag	UNP G5EG88
B	549	TRP	-	expression tag	UNP G5EG88
B	550	SER	-	expression tag	UNP G5EG88
B	551	HIS	-	expression tag	UNP G5EG88
B	552	PRO	-	expression tag	UNP G5EG88
B	553	GLN	-	expression tag	UNP G5EG88
B	554	PHE	-	expression tag	UNP G5EG88
B	555	GLU	-	expression tag	UNP G5EG88
B	556	LYS	-	expression tag	UNP G5EG88
C	?	-	SER	deletion	UNP G5EG88
C	?	-	VAL	deletion	UNP G5EG88
C	?	-	ASN	deletion	UNP G5EG88
C	?	-	PRO	deletion	UNP G5EG88
C	?	-	PHE	deletion	UNP G5EG88
C	?	-	THR	deletion	UNP G5EG88
C	?	-	ASN	deletion	UNP G5EG88
C	?	-	PHE	deletion	UNP G5EG88
C	?	-	CYS	deletion	UNP G5EG88
C	?	-	ASN	deletion	UNP G5EG88
C	?	-	VAL	deletion	UNP G5EG88
C	385B	MET	-	linker	UNP G5EG88
C	385C	ALA	-	linker	UNP G5EG88
C	385D	GLU	-	linker	UNP G5EG88

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Chain	Residue	Modelled	Actual	Comment	Reference
C	385E	ALA	-	linker	UNP G5EG88
C	385F	GLY	-	linker	UNP G5EG88
C	385G	ALA	-	linker	UNP G5EG88
C	385H	MET	-	linker	UNP G5EG88
C	385O	TRP	MET	conflict	UNP P0ABE7
C	389F	ILE	HIS	conflict	UNP P0ABE7
C	389J	LEU	-	linker	UNP P0ABE7
C	389K	SER	-	linker	UNP P0ABE7
C	535	LEU	-	expression tag	UNP G5EG88
C	536	GLU	-	expression tag	UNP G5EG88
C	537	GLY	-	expression tag	UNP G5EG88
C	538	THR	-	expression tag	UNP G5EG88
C	539	LYS	-	expression tag	UNP G5EG88
C	540	LEU	-	expression tag	UNP G5EG88
C	541	VAL	-	expression tag	UNP G5EG88
C	542	PRO	-	expression tag	UNP G5EG88
C	543	ARG	-	expression tag	UNP G5EG88
C	544	GLY	-	expression tag	UNP G5EG88
C	545	SER	-	expression tag	UNP G5EG88
C	546	SER	-	expression tag	UNP G5EG88
C	547	SER	-	expression tag	UNP G5EG88
C	548	GLY	-	expression tag	UNP G5EG88
C	549	TRP	-	expression tag	UNP G5EG88
C	550	SER	-	expression tag	UNP G5EG88
C	551	HIS	-	expression tag	UNP G5EG88
C	552	PRO	-	expression tag	UNP G5EG88
C	553	GLN	-	expression tag	UNP G5EG88
C	554	PHE	-	expression tag	UNP G5EG88
C	555	GLU	-	expression tag	UNP G5EG88
C	556	LYS	-	expression tag	UNP G5EG88
E	?	-	SER	deletion	UNP G5EG88
E	?	-	VAL	deletion	UNP G5EG88
E	?	-	ASN	deletion	UNP G5EG88
E	?	-	PRO	deletion	UNP G5EG88
E	?	-	PHE	deletion	UNP G5EG88
E	?	-	THR	deletion	UNP G5EG88
E	?	-	ASN	deletion	UNP G5EG88
E	?	-	PHE	deletion	UNP G5EG88
E	?	-	CYS	deletion	UNP G5EG88
E	?	-	ASN	deletion	UNP G5EG88
E	?	-	VAL	deletion	UNP G5EG88
E	385B	MET	-	linker	UNP G5EG88

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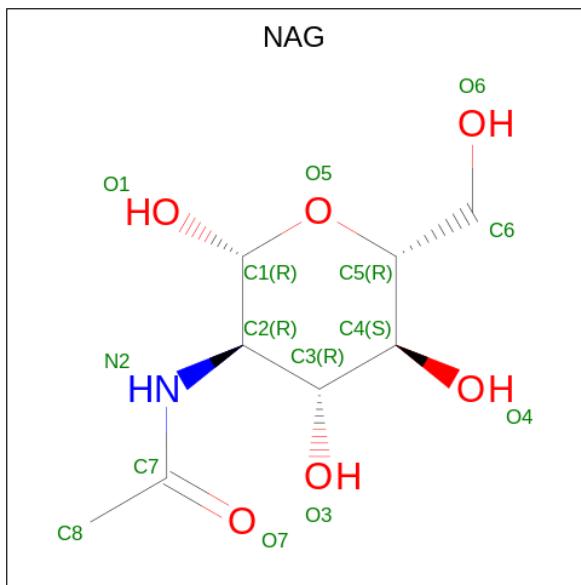
Chain	Residue	Modelled	Actual	Comment	Reference
E	385C	ALA	-	linker	UNP G5EG88
E	385D	GLU	-	linker	UNP G5EG88
E	385E	ALA	-	linker	UNP G5EG88
E	385F	GLY	-	linker	UNP G5EG88
E	385G	ALA	-	linker	UNP G5EG88
E	385H	MET	-	linker	UNP G5EG88
E	385O	TRP	MET	conflict	UNP P0ABE7
E	389F	ILE	HIS	conflict	UNP P0ABE7
E	389J	LEU	-	linker	UNP P0ABE7
E	389K	SER	-	linker	UNP P0ABE7
E	535	LEU	-	expression tag	UNP G5EG88
E	536	GLU	-	expression tag	UNP G5EG88
E	537	GLY	-	expression tag	UNP G5EG88
E	538	THR	-	expression tag	UNP G5EG88
E	539	LYS	-	expression tag	UNP G5EG88
E	540	LEU	-	expression tag	UNP G5EG88
E	541	VAL	-	expression tag	UNP G5EG88
E	542	PRO	-	expression tag	UNP G5EG88
E	543	ARG	-	expression tag	UNP G5EG88
E	544	GLY	-	expression tag	UNP G5EG88
E	545	SER	-	expression tag	UNP G5EG88
E	546	SER	-	expression tag	UNP G5EG88
E	547	SER	-	expression tag	UNP G5EG88
E	548	GLY	-	expression tag	UNP G5EG88
E	549	TRP	-	expression tag	UNP G5EG88
E	550	SER	-	expression tag	UNP G5EG88
E	551	HIS	-	expression tag	UNP G5EG88
E	552	PRO	-	expression tag	UNP G5EG88
E	553	GLN	-	expression tag	UNP G5EG88
E	554	PHE	-	expression tag	UNP G5EG88
E	555	GLU	-	expression tag	UNP G5EG88
E	556	LYS	-	expression tag	UNP G5EG88

- 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	F	2	Total 28	C 16	N 2	O 10	0	0
2	G	2	Total 28	C 16	N 2	O 10	0	0
2	H	2	Total 28	C 16	N 2	O 10	0	0
2	I	2	Total 28	C 16	N 2	O 10	0	0
2	J	2	Total 28	C 16	N 2	O 10	0	0
2	K	2	Total 28	C 16	N 2	O 10	0	0
2	L	2	Total 28	C 16	N 2	O 10	0	0
2	M	2	Total 28	C 16	N 2	O 10	0	0
2	N	2	Total 28	C 16	N 2	O 10	0	0
2	O	2	Total 28	C 16	N 2	O 10	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



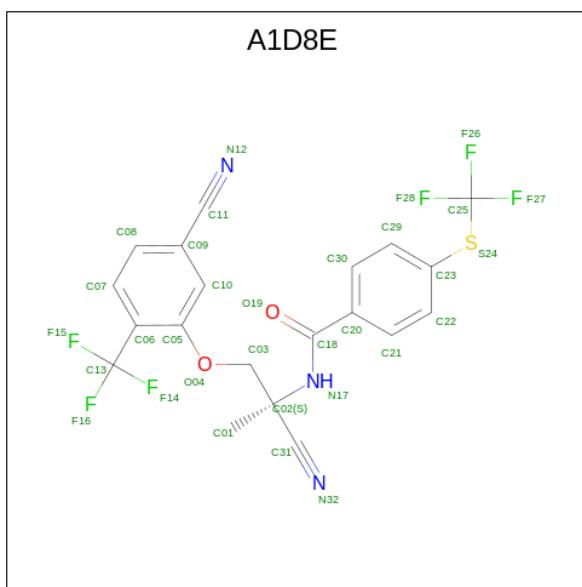
Mol	Chain	Residues	Atoms				AltConf
3	D	1	Total 14	C 8	N 1	O 5	0

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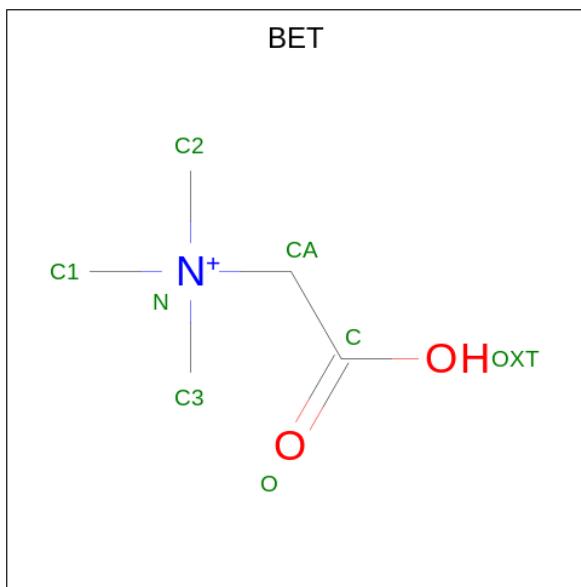
Mol	Chain	Residues	Atoms	AltConf
3	A	1	Total C N O 14 8 1 5	0
3	B	1	Total C N O 14 8 1 5	0
3	C	1	Total C N O 14 8 1 5	0
3	E	1	Total C N O 14 8 1 5	0

- Molecule 4 is {N}-[(2 {S})-2-cyano-1-[5-cyano-2-(trifluoromethyl)phenoxy]propan-2-yl]-4-(t trifluoromethylsulfanyl)benzamide (three-letter code: A1D8E) (formula: C₂₀H₁₃F₆N₃O₂S).



Mol	Chain	Residues	Atoms	AltConf
4	D	1	Total C F H N O S 44 20 6 12 3 2 1	0
4	A	1	Total C F H N O S 44 20 6 12 3 2 1	0
4	B	1	Total C F H N O S 44 20 6 12 3 2 1	0
4	C	1	Total C F H N O S 44 20 6 12 3 2 1	0
4	E	1	Total C F H N O S 44 20 6 12 3 2 1	0

- Molecule 5 is TRIMETHYL GLYCINE (three-letter code: BET) (formula: C₅H₁₂NO₂).



Mol	Chain	Residues	Atoms			AltConf
5	D	1	Total	C	N	O
			8	5	1	2
5	A	1	Total	C	N	O
			8	5	1	2
5	B	1	Total	C	N	O
			8	5	1	2
5	C	1	Total	C	N	O
			8	5	1	2
5	E	1	Total	C	N	O
			8	5	1	2

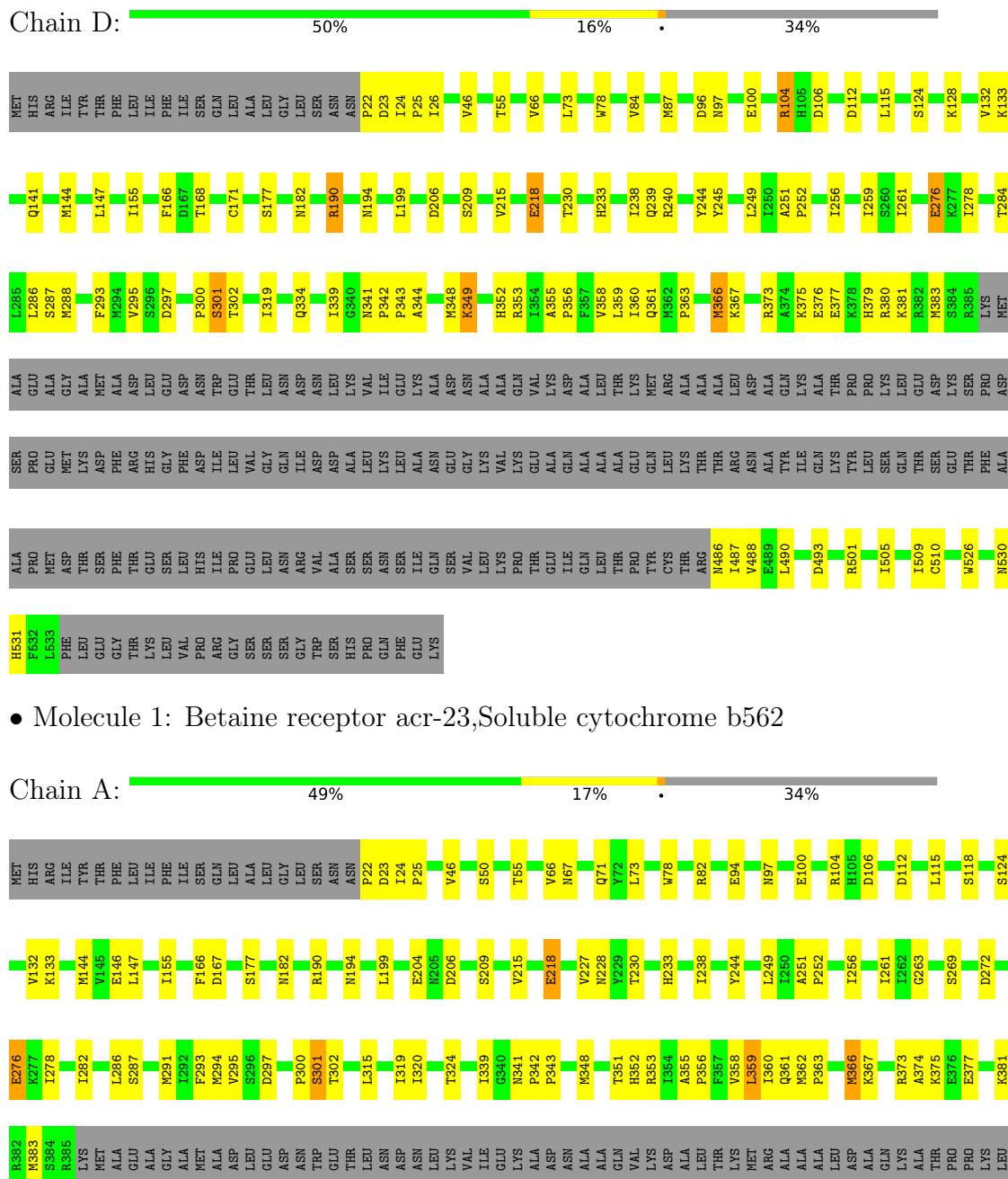
- Molecule 6 is water.

Mol	Chain	Residues	Atoms			AltConf
6	D	3	Total	O		
			3	3		0
6	A	3	Total	O		
			3	3		0
6	B	3	Total	O		
			3	3		0
6	C	3	Total	O		
			3	3		0
6	E	3	Total	O		
			3	3		0

3 Residue-property plots i

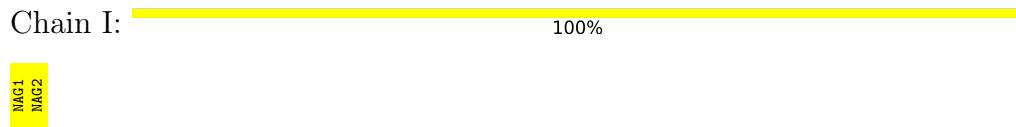
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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: Betaine receptor acr-23, Soluble cytochrome b562





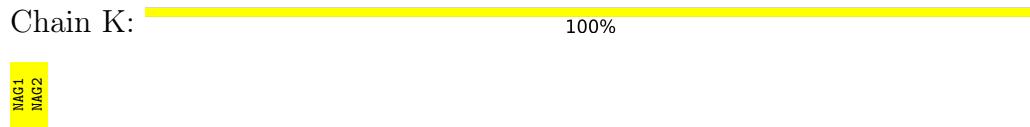
- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



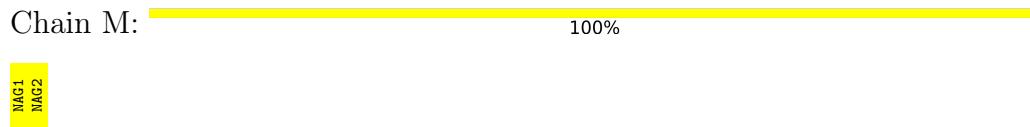
- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



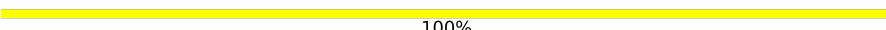
- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



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

Chain O:  100%

MAG1
MAG2

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	219723	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)	1200	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K2 BASE (4k 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, A1D8E, BET

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	0.25	0/3431	0.45	0/4668
1	B	0.25	0/3431	0.44	0/4668
1	C	0.25	0/3431	0.44	0/4668
1	D	0.25	0/3431	0.44	0/4668
1	E	0.25	0/3431	0.44	0/4668
All	All	0.25	0/17155	0.44	0/23340

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	3344	0	3381	96	0
1	B	3344	0	3381	81	0
1	C	3344	0	3381	90	0
1	D	3344	0	3381	92	0
1	E	3344	0	3381	92	0
2	F	28	0	25	3	0
2	G	28	0	25	4	0
2	H	28	0	25	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	I	28	0	25	5	0
2	J	28	0	25	6	0
2	K	28	0	25	4	0
2	L	28	0	25	7	0
2	M	28	0	25	4	0
2	N	28	0	25	4	0
2	O	28	0	25	5	0
3	A	14	0	13	1	0
3	B	14	0	13	1	0
3	C	14	0	13	1	0
3	D	14	0	13	1	0
3	E	14	0	13	1	0
4	A	32	12	0	1	0
4	B	32	12	0	1	0
4	C	32	12	0	2	0
4	D	32	12	0	1	0
4	E	32	12	0	1	0
5	A	8	0	11	2	0
5	B	8	0	11	2	0
5	C	8	0	11	2	0
5	D	8	0	11	1	0
5	E	8	0	11	1	0
6	A	3	0	0	1	0
6	B	3	0	0	1	0
6	C	3	0	0	1	0
6	D	3	0	0	1	0
6	E	3	0	0	1	0
All	All	17285	60	17275	441	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 13.

All (441) 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:339:ILE:HD12	1:A:339:ILE:O	1.65	0.96
1:B:50:SER:HB2	2:J:1:NAG:H81	1.45	0.93
1:C:339:ILE:HD12	1:C:339:ILE:O	1.70	0.91
1:C:115:LEU:HD21	1:C:155:ILE:HG22	1.53	0.90
2:I:1:NAG:H83	2:I:1:NAG:H3	1.54	0.90
2:G:1:NAG:H3	2:G:1:NAG:H83	1.53	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:1:NAG:H83	2:K:1:NAG:H3	1.54	0.89
2:M:1:NAG:H83	2:M:1:NAG:H3	1.55	0.89
2:O:1:NAG:H3	2:O:1:NAG:H83	1.54	0.89
1:D:115:LEU:HD21	1:D:155:ILE:HG22	1.55	0.88
1:B:206:ASP:HB3	1:C:302:THR:HB	1.56	0.87
1:C:206:ASP:HB3	1:E:302:THR:HB	1.58	0.86
2:J:1:NAG:H3	2:J:1:NAG:H83	1.58	0.85
1:A:115:LEU:HD21	1:A:155:ILE:HG22	1.56	0.85
2:H:1:NAG:H83	2:H:1:NAG:H3	1.58	0.84
2:L:1:NAG:H3	2:L:1:NAG:H83	1.59	0.84
1:B:115:LEU:HD21	1:B:155:ILE:HG22	1.59	0.83
1:E:115:LEU:HD21	1:E:155:ILE:HG22	1.59	0.82
1:B:363:PRO:HA	1:C:339:ILE:HA	1.62	0.80
1:D:287:SER:CB	1:A:286:LEU:HD22	2.12	0.80
1:A:100:GLU:HG2	1:A:133:LYS:HE2	1.63	0.78
1:B:100:GLU:HG2	1:B:133:LYS:HE2	1.65	0.78
1:E:100:GLU:HG2	1:E:133:LYS:HE2	1.65	0.77
1:C:361:GLN:HG3	1:E:339:ILE:HG21	1.66	0.77
1:C:287:SER:CB	1:E:286:LEU:HD22	2.15	0.76
2:N:1:NAG:H3	2:N:1:NAG:H83	1.68	0.76
1:B:287:SER:CB	1:C:286:LEU:HD22	2.16	0.76
1:C:100:GLU:HG2	1:C:133:LYS:HE2	1.68	0.75
1:B:50:SER:HB2	2:J:1:NAG:C8	2.16	0.75
1:A:261:ILE:HD11	1:A:319:ILE:HG21	1.68	0.74
1:D:286:LEU:HD23	1:E:256:ILE:HD13	1.68	0.74
1:D:100:GLU:HG2	1:D:133:LYS:HE2	1.70	0.73
1:D:363:PRO:HA	1:A:339:ILE:HA	1.70	0.73
2:F:1:NAG:H83	2:F:1:NAG:H3	1.69	0.73
1:A:182:ASN:OD1	1:A:230:THR:OG1	2.04	0.72
1:C:182:ASN:OD1	1:C:230:THR:OG1	2.05	0.72
5:B:603:BET:O	6:B:701:HOH:O	2.08	0.72
1:B:256:ILE:HD13	1:C:286:LEU:HD23	1.71	0.72
1:D:302:THR:HB	1:E:206:ASP:HB3	1.73	0.70
1:A:94:GLU:N	1:A:94:GLU:OE1	2.25	0.70
1:D:286:LEU:HD22	1:E:287:SER:CB	2.22	0.70
1:A:25:PRO:HG3	1:B:46:VAL:HG22	1.73	0.70
1:A:206:ASP:HB3	1:B:302:THR:HB	1.72	0.70
1:E:182:ASN:OD1	1:E:230:THR:OG1	2.07	0.70
1:D:206:ASP:HB3	1:A:302:THR:HB	1.73	0.69
1:A:256:ILE:HD13	1:B:286:LEU:HD23	1.74	0.69
5:D:603:BET:O	6:D:701:HOH:O	2.11	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:287:SER:CB	1:B:286:LEU:HD22	2.22	0.69
1:C:300:PRO:HB2	1:C:302:THR:HG23	1.74	0.69
5:E:603:BET:O	6:E:701:HOH:O	2.12	0.68
5:A:603:BET:O	6:A:701:HOH:O	2.11	0.67
1:E:300:PRO:HB2	1:E:302:THR:HG23	1.75	0.67
1:D:182:ASN:OD1	1:D:230:THR:OG1	2.06	0.67
1:A:300:PRO:HB2	1:A:302:THR:HG23	1.77	0.67
1:B:94:GLU:N	1:B:94:GLU:OE1	2.27	0.67
1:B:300:PRO:HB2	1:B:302:THR:HG23	1.77	0.67
1:C:287:SER:HB2	1:E:286:LEU:HD22	1.77	0.66
1:C:166:PHE:HB3	1:C:526:TRP:HB2	1.77	0.66
1:C:256:ILE:HD13	1:E:286:LEU:HD23	1.77	0.66
1:D:287:SER:HB2	1:A:286:LEU:HD22	1.77	0.66
1:B:182:ASN:OD1	1:B:230:THR:OG1	2.08	0.66
1:D:300:PRO:HB2	1:D:302:THR:HG23	1.78	0.65
5:C:603:BET:O	6:C:701:HOH:O	2.14	0.65
1:A:166:PHE:HB3	1:A:526:TRP:HB2	1.79	0.64
1:C:348:MET:O	1:C:352:HIS:ND1	2.31	0.64
1:B:166:PHE:HB3	1:B:526:TRP:HB2	1.78	0.64
1:A:50:SER:HB3	2:H:1:NAG:H81	1.79	0.64
1:D:339:ILE:HG22	1:D:339:ILE:O	1.97	0.63
1:D:344:ALA:HB3	1:D:348:MET:HG2	1.78	0.63
1:C:50:SER:HB3	2:L:1:NAG:H81	1.80	0.63
1:C:361:GLN:HG3	1:E:339:ILE:CG2	2.29	0.63
1:D:286:LEU:HD22	1:E:287:SER:HB2	1.81	0.63
1:E:300:PRO:HD2	4:E:602:A1D8E:N12	2.14	0.63
1:A:348:MET:O	1:A:352:HIS:ND1	2.31	0.62
1:B:300:PRO:HD2	4:B:602:A1D8E:N12	2.14	0.62
1:B:287:SER:HB2	1:C:286:LEU:HD22	1.81	0.62
2:F:1:NAG:C1	2:F:1:NAG:H82	2.30	0.62
1:B:339:ILE:HG22	1:B:339:ILE:O	1.97	0.62
1:D:256:ILE:HD13	1:A:286:LEU:HD23	1.82	0.61
1:B:269:SER:OG	1:B:272:ASP:HB2	1.99	0.61
1:D:339:ILE:HG21	1:E:361:GLN:HG3	1.83	0.61
1:E:348:MET:O	1:E:352:HIS:ND1	2.32	0.61
1:D:300:PRO:HD2	4:D:602:A1D8E:N12	2.16	0.61
2:N:1:NAG:H82	2:N:1:NAG:C1	2.31	0.61
2:O:1:NAG:H3	2:O:1:NAG:C8	2.30	0.61
1:A:300:PRO:HD2	4:A:602:A1D8E:N12	2.15	0.61
1:A:287:SER:HB2	1:B:286:LEU:HD22	1.82	0.61
1:E:166:PHE:HB3	1:E:526:TRP:HB2	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:300:PRO:HD2	4:C:602:A1D8E:N12	2.16	0.60
2:I:1:NAG:H3	2:I:1:NAG:C8	2.30	0.60
1:D:194:ASN:HD21	1:D:199:LEU:H	1.49	0.60
2:K:2:NAG:O7	2:K:2:NAG:O3	2.18	0.60
1:D:84:VAL:HG22	1:D:144:MET:HE2	1.84	0.60
1:A:194:ASN:HD21	1:A:199:LEU:H	1.50	0.60
1:D:25:PRO:HG3	1:A:46:VAL:HG22	1.84	0.60
1:A:301:SER:OG	1:A:301:SER:O	2.17	0.60
1:A:525:ILE:O	1:A:529:GLU:HG3	2.02	0.60
1:E:249:LEU:HD22	1:E:295:VAL:HG22	1.84	0.60
1:D:73:LEU:HD22	1:D:171:CYS:SG	2.42	0.59
1:B:348:MET:O	1:B:352:HIS:ND1	2.32	0.59
1:B:525:ILE:O	1:B:529:GLU:HG3	2.02	0.59
1:B:362:MET:SD	1:B:366:MET:HG2	2.42	0.59
1:A:50:SER:CB	2:H:1:NAG:H81	2.31	0.59
1:D:377:GLU:O	1:D:381:LYS:HB2	2.02	0.59
1:B:249:LEU:HD22	1:B:295:VAL:HG22	1.83	0.59
2:K:1:NAG:H3	2:K:1:NAG:C8	2.30	0.59
1:A:300:PRO:HB2	1:A:302:THR:CG2	2.33	0.59
1:D:353:ARG:O	1:D:356:PRO:HD2	2.03	0.59
1:C:249:LEU:HD22	1:C:295:VAL:HG22	1.85	0.58
1:D:249:LEU:HD22	1:D:295:VAL:HG22	1.85	0.58
1:B:25:PRO:HG3	1:C:46:VAL:HG22	1.85	0.58
1:E:377:GLU:O	1:E:381:LYS:HB2	2.03	0.58
2:G:1:NAG:H3	2:G:1:NAG:C8	2.29	0.58
1:D:348:MET:O	1:D:352:HIS:ND1	2.34	0.58
1:C:300:PRO:O	1:C:301:SER:HB3	2.03	0.58
1:E:363:PRO:HD2	1:E:366:MET:HE2	1.85	0.58
1:B:300:PRO:HB2	1:B:302:THR:CG2	2.33	0.58
1:C:276:GLU:OE1	1:C:278:ILE:HB	2.04	0.58
1:B:300:PRO:O	1:B:301:SER:HB3	2.02	0.58
1:D:166:PHE:HB3	1:D:526:TRP:HB2	1.86	0.58
1:C:525:ILE:O	1:C:529:GLU:HG3	2.04	0.58
1:C:50:SER:HB3	2:L:1:NAG:C8	2.34	0.57
1:C:363:PRO:HA	1:E:339:ILE:HA	1.87	0.57
1:E:97:ASN:HB2	3:E:601:NAG:O5	2.03	0.57
1:E:339:ILE:HG22	1:E:339:ILE:O	2.03	0.57
1:A:300:PRO:O	1:A:301:SER:HB3	2.03	0.57
1:E:300:PRO:O	1:E:301:SER:HB3	2.03	0.57
2:M:1:NAG:H3	2:M:1:NAG:C8	2.30	0.57
1:D:300:PRO:HB2	1:D:302:THR:CG2	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:SER:HB3	2:H:1:NAG:C8	2.34	0.57
1:C:50:SER:CB	2:L:1:NAG:H81	2.35	0.57
2:L:1:NAG:H82	2:L:1:NAG:C1	2.35	0.57
1:D:112:ASP:OD1	1:D:177:SER:OG	2.17	0.56
1:E:301:SER:O	1:E:301:SER:OG	2.16	0.56
2:H:1:NAG:C1	2:H:1:NAG:H82	2.35	0.56
1:D:300:PRO:O	1:D:301:SER:HB3	2.03	0.56
1:A:276:GLU:OE2	1:A:278:ILE:HB	2.06	0.56
1:B:194:ASN:HD21	1:B:199:LEU:H	1.52	0.56
1:B:353:ARG:O	1:B:356:PRO:HD2	2.05	0.56
1:D:97:ASN:HB2	3:D:601:NAG:O5	2.04	0.56
1:C:25:PRO:HG3	1:E:46:VAL:HG22	1.86	0.56
2:G:2:NAG:O7	2:G:2:NAG:O3	2.22	0.56
2:J:1:NAG:H3	2:J:1:NAG:C8	2.34	0.56
1:D:46:VAL:HG22	1:E:25:PRO:HG3	1.87	0.56
1:C:353:ARG:O	1:C:356:PRO:HD2	2.06	0.56
1:A:375:LYS:HA	1:A:375:LYS:HE2	1.87	0.56
1:E:194:ASN:HD21	1:E:199:LEU:H	1.53	0.56
1:E:73:LEU:HD22	1:E:171:CYS:SG	2.46	0.56
1:D:276:GLU:OE2	1:D:278:ILE:HB	2.07	0.55
1:B:301:SER:O	1:B:301:SER:OG	2.17	0.55
1:C:341:ASN:N	1:C:342:PRO:CD	2.70	0.55
2:I:2:NAG:O7	2:I:2:NAG:O3	2.20	0.55
2:J:1:NAG:H82	2:J:1:NAG:C1	2.35	0.55
1:A:363:PRO:HA	1:B:339:ILE:HA	1.88	0.55
1:D:375:LYS:HA	1:D:375:LYS:HE2	1.87	0.55
1:B:377:GLU:O	1:B:381:LYS:HB2	2.07	0.55
1:A:341:ASN:N	1:A:342:PRO:CD	2.70	0.55
1:C:301:SER:O	1:C:301:SER:OG	2.16	0.55
1:D:339:ILE:CG2	1:E:361:GLN:HG3	2.36	0.54
1:D:209:SER:O	1:D:238:ILE:HA	2.07	0.54
1:B:276:GLU:OE2	1:B:278:ILE:HB	2.06	0.54
1:A:341:ASN:HB2	1:A:488:VAL:HG21	1.89	0.54
1:A:353:ARG:O	1:A:356:PRO:HD2	2.07	0.54
1:A:377:GLU:O	1:A:381:LYS:HB2	2.07	0.54
1:C:300:PRO:HB2	1:C:302:THR:CG2	2.36	0.54
1:C:358:VAL:HB	1:C:501:ARG:HG3	1.89	0.54
2:M:2:NAG:O7	2:M:2:NAG:O3	2.21	0.54
1:C:194:ASN:HD21	1:C:199:LEU:H	1.54	0.54
1:A:361:GLN:HG3	1:B:339:ILE:HG21	1.88	0.54
1:D:141:GLN:OE1	1:D:141:GLN:N	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:276:GLU:OE1	1:E:278:ILE:HB	2.07	0.54
1:A:486:ASN:O	1:A:490:LEU:HG	2.08	0.54
2:H:1:NAG:H3	2:H:1:NAG:C8	2.34	0.54
1:B:341:ASN:N	1:B:342:PRO:CD	2.71	0.54
1:C:377:GLU:O	1:C:381:LYS:HB2	2.07	0.54
1:C:66:VAL:HG22	1:C:73:LEU:CD1	2.38	0.53
1:D:341:ASN:N	1:D:342:PRO:CD	2.71	0.53
1:B:97:ASN:HB2	3:B:601:NAG:O5	2.07	0.53
1:E:341:ASN:N	1:E:342:PRO:CD	2.71	0.53
1:E:300:PRO:HB2	1:E:302:THR:CG2	2.37	0.53
1:D:259:ILE:HG22	1:A:282:ILE:HD11	1.90	0.53
1:E:209:SER:O	1:E:238:ILE:HA	2.08	0.53
1:A:97:ASN:HB2	3:A:601:NAG:O5	2.07	0.52
1:D:132:VAL:HG12	1:D:147:LEU:HD13	1.92	0.52
1:E:269:SER:OG	1:E:272:ASP:HB2	2.09	0.52
1:E:486:ASN:O	1:E:490:LEU:HG	2.10	0.52
1:B:244:TYR:CE1	1:C:301:SER:HA	2.44	0.52
1:C:97:ASN:HB2	3:C:601:NAG:O5	2.10	0.52
1:A:112:ASP:OD1	1:A:177:SER:OG	2.18	0.52
1:A:209:SER:O	1:A:238:ILE:HA	2.09	0.52
1:C:244:TYR:CE1	1:E:301:SER:HA	2.45	0.52
1:C:486:ASN:O	1:C:490:LEU:HG	2.10	0.52
1:C:209:SER:O	1:C:238:ILE:HA	2.10	0.52
1:E:66:VAL:HG22	1:E:73:LEU:CD1	2.39	0.52
1:B:209:SER:O	1:B:238:ILE:HA	2.11	0.51
1:D:26:ILE:HG12	1:D:96:ASP:HB2	1.92	0.51
1:C:341:ASN:HB2	1:C:488:VAL:HG21	1.90	0.51
1:A:194:ASN:HD21	1:A:199:LEU:N	2.08	0.51
1:D:358:VAL:HB	1:D:501:ARG:HG3	1.92	0.51
2:F:1:NAG:C1	2:F:1:NAG:C8	2.88	0.51
1:D:286:LEU:CD2	1:E:256:ILE:HD13	2.39	0.51
1:D:358:VAL:HG12	1:D:505:ILE:CD1	2.40	0.51
1:E:376:GLU:O	1:E:380:ARG:HB2	2.11	0.51
1:C:104:ARG:HH11	1:C:104:ARG:HB3	1.76	0.51
1:D:486:ASN:O	1:D:490:LEU:HG	2.11	0.51
1:E:84:VAL:HG22	1:E:144:MET:HE2	1.92	0.51
1:D:339:ILE:HA	1:E:363:PRO:HA	1.93	0.51
1:B:486:ASN:O	1:B:490:LEU:HG	2.11	0.51
1:D:66:VAL:HG22	1:D:73:LEU:CD1	2.41	0.51
1:D:376:GLU:O	1:D:380:ARG:HB2	2.11	0.51
2:M:1:NAG:C1	2:M:1:NAG:H82	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:358:VAL:HB	1:A:501:ARG:HG3	1.93	0.50
1:E:353:ARG:O	1:E:356:PRO:HD2	2.11	0.50
1:A:132:VAL:HG12	1:A:147:LEU:HD13	1.94	0.50
2:N:1:NAG:C1	2:N:1:NAG:C8	2.89	0.50
1:B:82:ARG:HG2	1:B:146:GLU:HG3	1.93	0.50
2:L:1:NAG:H3	2:L:1:NAG:C8	2.35	0.50
1:E:132:VAL:HG12	1:E:147:LEU:HD13	1.94	0.50
2:K:1:NAG:C1	2:K:1:NAG:H82	2.42	0.50
2:G:1:NAG:H82	2:G:1:NAG:C1	2.42	0.50
1:D:104:ARG:HB3	1:D:104:ARG:HH11	1.77	0.49
1:B:288:MET:HE1	1:B:316:MET:HB2	1.94	0.49
1:A:82:ARG:HG2	1:A:146:GLU:HG3	1.93	0.49
1:A:218:GLU:HG2	1:A:233:HIS:NE2	2.27	0.49
1:A:358:VAL:HG12	1:A:505:ILE:CD1	2.42	0.49
1:D:240:ARG:HD3	1:D:245:TYR:CE1	2.47	0.49
2:O:1:NAG:H82	2:O:1:NAG:C1	2.42	0.49
1:C:240:ARG:HD3	1:C:245:TYR:CE1	2.47	0.49
1:D:244:TYR:CE1	1:A:301:SER:HA	2.47	0.49
1:B:341:ASN:O	1:B:343:PRO:HD3	2.13	0.49
1:E:358:VAL:HG12	1:E:505:ILE:CD1	2.43	0.49
1:B:358:VAL:HB	1:B:501:ARG:HG3	1.95	0.49
1:E:512:LEU:O	1:E:516:ILE:HB	2.13	0.49
1:D:334:GLN:NE2	1:D:493:ASP:OD1	2.33	0.49
1:D:301:SER:HA	1:E:244:TYR:CE1	2.47	0.49
1:B:73:LEU:HD22	1:B:171:CYS:SG	2.53	0.49
1:E:358:VAL:HB	1:E:501:ARG:HG3	1.95	0.48
1:E:380:ARG:HD3	1:E:383:MET:CE	2.43	0.48
1:B:218:GLU:HG2	1:B:233:HIS:NE2	2.28	0.48
1:B:358:VAL:HG12	1:B:505:ILE:CD1	2.43	0.48
1:C:358:VAL:HG12	1:C:505:ILE:CD1	2.43	0.48
2:I:1:NAG:C1	2:I:1:NAG:H82	2.42	0.48
1:A:341:ASN:O	1:A:343:PRO:HD3	2.13	0.48
1:C:132:VAL:HG12	1:C:147:LEU:HD13	1.96	0.48
1:B:256:ILE:HD13	1:C:286:LEU:CD2	2.43	0.48
1:C:359:LEU:O	1:C:501:ARG:NH1	2.46	0.48
1:D:380:ARG:HD3	1:D:383:MET:CE	2.43	0.47
1:C:383:MET:HA	1:C:383:MET:CE	2.43	0.47
1:C:256:ILE:HD13	1:E:286:LEU:CD2	2.44	0.47
1:A:249:LEU:HD22	1:A:295:VAL:HG22	1.97	0.47
1:A:341:ASN:HA	1:A:488:VAL:HG11	1.96	0.47
1:B:66:VAL:HG22	1:B:73:LEU:CD1	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:22:PRO:HD2	1:D:24:ILE:HG22	1.97	0.47
1:D:215:VAL:HA	1:D:233:HIS:O	2.15	0.47
1:A:339:ILE:O	1:A:339:ILE:CD1	2.51	0.47
1:B:240:ARG:HD3	1:B:245:TYR:CE1	2.49	0.47
1:C:104:ARG:HB3	1:C:104:ARG:NH1	2.29	0.47
1:C:341:ASN:O	1:C:343:PRO:HD3	2.14	0.47
1:D:301:SER:O	1:D:301:SER:OG	2.17	0.47
1:B:344:ALA:HB3	1:B:348:MET:HG2	1.96	0.47
1:E:22:PRO:HD2	1:E:24:ILE:HG22	1.97	0.47
1:C:351:THR:HG23	1:C:498:VAL:HG21	1.96	0.47
1:D:361:GLN:HG3	1:A:339:ILE:HD13	1.95	0.47
1:E:341:ASN:O	1:E:343:PRO:HD3	2.14	0.47
1:B:287:SER:OG	1:C:286:LEU:HD22	2.14	0.46
1:E:137:LEU:HB2	1:E:142:GLY:O	2.15	0.46
1:D:104:ARG:HB3	1:D:104:ARG:NH1	2.30	0.46
1:D:373:ARG:HD3	1:D:487:ILE:HD13	1.97	0.46
1:A:269:SER:OG	1:A:272:ASP:OD1	2.27	0.46
1:D:218:GLU:HG2	1:D:233:HIS:NE2	2.30	0.46
1:C:215:VAL:HA	1:C:233:HIS:O	2.14	0.46
1:C:375:LYS:HZ3	1:C:375:LYS:HB2	1.81	0.46
1:E:358:VAL:O	1:E:360:ILE:N	2.48	0.46
2:L:1:NAG:C8	2:L:1:NAG:C1	2.93	0.46
1:D:194:ASN:HD21	1:D:199:LEU:N	2.12	0.46
1:C:284:THR:O	1:C:288:MET:HG3	2.16	0.46
2:H:1:NAG:C8	2:H:1:NAG:C1	2.93	0.46
2:O:1:NAG:H83	2:O:1:NAG:C3	2.37	0.46
1:C:22:PRO:HD2	1:C:24:ILE:HG22	1.97	0.46
1:C:516:ILE:O	1:C:520:LEU:HB2	2.16	0.46
1:A:244:TYR:CE1	1:B:301:SER:HA	2.51	0.46
1:B:350:TRP:HZ3	1:B:353:ARG:HH12	1.62	0.46
1:C:91:ASP:HB3	1:C:94:GLU:HG2	1.97	0.46
1:A:359:LEU:O	1:A:501:ARG:NH1	2.49	0.46
1:A:530:ASN:OD1	1:A:531:HIS:N	2.49	0.46
1:E:55:THR:CG2	1:E:190:ARG:HB2	2.46	0.46
1:E:101:ILE:HG22	1:E:134:LEU:HB2	1.98	0.46
1:E:240:ARG:HD3	1:E:245:TYR:CE1	2.50	0.46
1:E:341:ASN:HB2	1:E:488:VAL:HG21	1.98	0.46
1:D:341:ASN:HA	1:D:488:VAL:HG11	1.99	0.46
1:C:66:VAL:HG22	1:C:73:LEU:HD11	1.97	0.46
1:C:67:ASN:O	1:C:71:GLN:N	2.48	0.46
2:J:1:NAG:C8	2:J:1:NAG:C1	2.94	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:375:LYS:HB2	1:C:375:LYS:NZ	2.30	0.45
1:E:194:ASN:HD21	1:E:199:LEU:N	2.12	0.45
1:A:282:ILE:HG22	1:A:286:LEU:CD1	2.46	0.45
1:E:516:ILE:O	1:E:520:LEU:HB2	2.16	0.45
1:D:284:THR:O	1:D:288:MET:HG3	2.16	0.45
1:B:194:ASN:HD21	1:B:199:LEU:N	2.12	0.45
1:B:22:PRO:HD2	1:B:24:ILE:HG22	1.98	0.45
1:B:215:VAL:HA	1:B:233:HIS:O	2.16	0.45
1:C:383:MET:HA	1:C:383:MET:HE2	1.97	0.45
1:A:351:THR:HG23	1:A:498:VAL:HG21	1.99	0.45
1:D:341:ASN:HB2	1:D:488:VAL:HG21	1.99	0.45
1:C:82:ARG:HG2	1:C:146:GLU:HG3	1.98	0.45
1:C:168:THR:OG1	1:C:239:GLN:HG3	2.16	0.45
1:E:341:ASN:HA	1:E:488:VAL:HG11	1.99	0.45
2:N:1:NAG:H3	2:N:1:NAG:C8	2.44	0.45
1:C:341:ASN:HA	1:C:488:VAL:HG11	1.99	0.45
1:D:349:LYS:HE3	1:D:353:ARG:HH11	1.82	0.45
1:D:530:ASN:OD1	1:D:531:HIS:N	2.50	0.45
1:A:22:PRO:HD2	1:A:24:ILE:HG22	1.99	0.45
1:A:256:ILE:HD13	1:B:286:LEU:CD2	2.46	0.45
1:A:373:ARG:HD3	1:A:487:ILE:HD13	1.99	0.45
1:B:168:THR:OG1	1:B:239:GLN:HG3	2.17	0.45
1:E:373:ARG:HD3	1:E:487:ILE:HD13	1.99	0.45
1:E:215:VAL:HA	1:E:233:HIS:O	2.18	0.44
1:D:84:VAL:CG2	1:D:144:MET:HE2	2.45	0.44
1:D:128:LYS:HB2	1:D:128:LYS:HE3	1.81	0.44
1:A:282:ILE:HG22	1:A:286:LEU:HD11	1.99	0.44
1:B:358:VAL:O	1:B:360:ILE:N	2.50	0.44
1:D:358:VAL:O	1:D:360:ILE:N	2.50	0.44
1:A:367:LYS:HB2	1:A:367:LYS:HE2	1.87	0.44
1:E:261:ILE:HD11	1:E:319:ILE:HG21	2.00	0.44
1:D:168:THR:OG1	1:D:239:GLN:HG3	2.18	0.44
1:C:259:ILE:HG22	1:E:282:ILE:HD11	1.99	0.44
1:E:218:GLU:HG2	1:E:233:HIS:NE2	2.33	0.44
1:D:341:ASN:O	1:D:343:PRO:HD3	2.17	0.44
1:A:261:ILE:HD11	1:A:319:ILE:CG2	2.43	0.44
1:C:358:VAL:HG23	1:C:358:VAL:O	2.18	0.44
1:D:358:VAL:O	1:D:358:VAL:HG23	2.18	0.44
1:A:263:GLY:HA3	1:B:278:ILE:HG21	1.98	0.44
1:A:294:MET:CE	1:B:293:PHE:HB3	2.48	0.44
1:A:67:ASN:O	1:A:71:GLN:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:358:VAL:O	1:C:360:ILE:N	2.50	0.44
1:D:376:GLU:HG3	1:D:380:ARG:HG3	2.00	0.43
1:A:66:VAL:HG22	1:A:73:LEU:CD1	2.48	0.43
1:A:358:VAL:O	1:A:360:ILE:N	2.51	0.43
1:B:358:VAL:O	1:B:358:VAL:HG23	2.18	0.43
1:E:350:TRP:HA	1:E:350:TRP:CE3	2.54	0.43
1:E:358:VAL:O	1:E:358:VAL:HG23	2.19	0.43
2:O:2:NAG:O7	2:O:2:NAG:O3	2.32	0.43
1:E:374:ALA:O	1:E:377:GLU:HB3	2.19	0.43
1:A:509:ILE:HG13	1:A:510:CYS:N	2.33	0.43
1:E:315:LEU:HD13	1:E:514:SER:HB3	2.00	0.43
1:E:380:ARG:HD3	1:E:383:MET:SD	2.58	0.43
1:E:530:ASN:OD1	1:E:531:HIS:N	2.51	0.43
1:B:359:LEU:O	1:B:501:ARG:NH1	2.47	0.43
1:E:67:ASN:O	1:E:71:GLN:N	2.52	0.43
1:E:284:THR:O	1:E:288:MET:HG3	2.19	0.43
1:E:374:ALA:HA	1:E:377:GLU:HB3	2.01	0.43
1:C:261:ILE:HD11	1:C:319:ILE:HG21	2.01	0.42
1:E:66:VAL:HG22	1:E:73:LEU:HD11	2.00	0.42
1:D:359:LEU:O	1:D:501:ARG:NH1	2.46	0.42
1:A:22:PRO:HB2	1:A:23:ASP:H	1.66	0.42
1:B:509:ILE:HG13	1:B:510:CYS:N	2.34	0.42
1:C:90:TRP:CE2	1:C:136:THR:HB	2.54	0.42
1:D:251:ALA:HB3	1:D:252:PRO:HD3	2.01	0.42
1:A:227:VAL:HG12	1:A:228:ASN:N	2.34	0.42
1:C:227:VAL:HG12	1:C:228:ASN:N	2.35	0.42
1:A:358:VAL:O	1:A:358:VAL:HG23	2.18	0.42
1:B:261:ILE:HD11	1:B:319:ILE:HG21	2.01	0.42
1:C:194:ASN:HD21	1:C:199:LEU:N	2.15	0.42
1:A:282:ILE:CG2	1:A:286:LEU:HD11	2.50	0.42
1:A:362:MET:SD	1:A:366:MET:HG2	2.60	0.42
1:B:132:VAL:HG12	1:B:147:LEU:HD13	2.01	0.42
1:C:530:ASN:OD1	1:C:531:HIS:N	2.53	0.42
1:D:509:ILE:HG13	1:D:510:CYS:N	2.35	0.42
1:A:218:GLU:HG2	1:A:233:HIS:CD2	2.54	0.42
1:B:144:MET:HE2	1:B:144:MET:HB2	1.92	0.42
1:D:380:ARG:HD3	1:D:383:MET:SD	2.60	0.42
1:A:251:ALA:HB3	1:A:252:PRO:HD3	2.01	0.42
1:A:355:ALA:O	1:A:358:VAL:O	2.37	0.42
1:D:66:VAL:HG22	1:D:73:LEU:HD11	2.02	0.42
1:E:355:ALA:O	1:E:358:VAL:O	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:287:SER:OG	1:A:286:LEU:HD22	2.19	0.42
1:D:355:ALA:O	1:D:358:VAL:O	2.37	0.42
1:A:78:TRP:CE3	5:B:603:BET:HA2	2.55	0.42
1:D:55:THR:CG2	1:D:190:ARG:HB2	2.50	0.42
1:A:55:THR:CG2	1:A:190:ARG:HB2	2.50	0.42
1:A:315:LEU:HD13	1:A:514:SER:HB3	2.01	0.42
1:B:25:PRO:HD3	1:C:87:MET:SD	2.60	0.42
1:C:66:VAL:HG22	1:C:73:LEU:HD12	2.02	0.42
1:D:256:ILE:HD13	1:A:286:LEU:CD2	2.48	0.41
1:B:315:LEU:HD13	1:B:514:SER:HB3	2.02	0.41
1:C:339:ILE:O	1:C:339:ILE:CD1	2.56	0.41
1:D:366:MET:HE2	1:D:366:MET:HB2	1.72	0.41
1:A:155:ILE:O	1:A:155:ILE:HG13	2.20	0.41
1:A:366:MET:HE2	1:A:366:MET:HB2	1.57	0.41
1:B:366:MET:HE2	1:B:366:MET:HB2	1.70	0.41
1:C:509:ILE:HG13	1:C:510:CYS:N	2.35	0.41
1:E:90:TRP:CE2	1:E:136:THR:HB	2.55	0.41
1:D:22:PRO:HB2	1:D:23:ASP:H	1.66	0.41
1:D:78:TRP:CE3	5:A:603:BET:HA2	2.56	0.41
1:B:346:LYS:O	1:B:346:LYS:HG2	2.20	0.41
1:B:355:ALA:O	1:B:358:VAL:O	2.38	0.41
1:D:261:ILE:HD11	1:D:319:ILE:HG21	2.02	0.41
1:A:50:SER:HB2	2:H:1:NAG:H81	2.03	0.41
1:C:287:SER:OG	1:E:286:LEU:HD22	2.19	0.41
1:E:128:LYS:HB2	1:E:128:LYS:HE3	1.81	0.41
1:D:218:GLU:HG2	1:D:233:HIS:CD2	2.55	0.41
1:A:144:MET:HE2	1:A:144:MET:HB2	1.93	0.41
1:B:341:ASN:HA	1:B:488:VAL:HG11	2.02	0.41
1:B:530:ASN:OD1	1:B:531:HIS:N	2.53	0.41
1:C:55:THR:CG2	1:C:190:ARG:HB2	2.51	0.41
1:C:355:ALA:O	1:C:358:VAL:O	2.38	0.41
1:E:251:ALA:HB3	1:E:252:PRO:HD3	2.02	0.41
2:I:1:NAG:C8	2:I:1:NAG:C3	2.95	0.41
1:D:144:MET:HE2	1:D:144:MET:HB2	1.93	0.41
1:A:320:ILE:O	1:A:324:THR:OG1	2.38	0.41
1:E:181:ASP:OD2	1:E:227:VAL:HB	2.21	0.41
1:B:251:ALA:HB3	1:B:252:PRO:HD3	2.02	0.41
1:B:288:MET:HE2	1:B:288:MET:HB3	1.97	0.41
1:C:73:LEU:HD22	1:C:171:CYS:SG	2.61	0.41
1:A:167:ASP:OD1	1:A:167:ASP:N	2.46	0.41
1:C:59:GLN:HG3	1:C:192:PHE:CZ	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:66:VAL:HG22	1:E:73:LEU:HD12	2.02	0.41
1:E:84:VAL:CG2	1:E:144:MET:HE2	2.51	0.41
1:E:196:PRO:HB3	1:E:215:VAL:HB	2.03	0.41
1:E:362:MET:HE3	1:E:367:LYS:HG3	2.03	0.41
1:D:87:MET:SD	1:E:25:PRO:HD3	2.61	0.41
1:A:374:ALA:HA	1:A:377:GLU:HB3	2.02	0.41
1:C:115:LEU:HD21	1:C:155:ILE:CG2	2.38	0.41
1:A:215:VAL:HA	1:A:233:HIS:O	2.21	0.41
1:C:312:PHE:O	1:C:316:MET:HG2	2.21	0.41
1:E:509:ILE:HG13	1:E:510:CYS:N	2.35	0.41
1:A:115:LEU:HD21	1:A:155:ILE:CG2	2.40	0.40
1:C:310:ALA:HB2	4:C:602:A1D8E:N32	2.37	0.40
1:C:374:ALA:HA	1:C:377:GLU:HB3	2.02	0.40
1:D:367:LYS:HB2	1:D:367:LYS:HE2	1.81	0.40
1:A:294:MET:HE1	1:B:293:PHE:HB3	2.03	0.40
1:C:346:LYS:HG2	1:C:346:LYS:O	2.22	0.40
1:E:227:VAL:HG12	1:E:228:ASN:N	2.37	0.40
1:B:78:TRP:CE3	5:C:603:BET:HA2	2.57	0.40
1:D:375:LYS:O	1:D:379:HIS:HB3	2.22	0.40
1:A:115:LEU:HD23	1:A:118:SER:HB2	2.04	0.40
1:B:239:GLN:NE2	1:B:529:GLU:HB2	2.37	0.40
1:B:374:ALA:HA	1:B:377:GLU:HB3	2.03	0.40
1:E:29:GLU:H	1:E:29:GLU:HG2	1.72	0.40
1:E:218:GLU:HG2	1:E:233:HIS:CD2	2.56	0.40
1:D:66:VAL:HG22	1:D:73:LEU:HD12	2.04	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	408/620 (66%)	398 (98%)	10 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	408/620 (66%)	396 (97%)	12 (3%)	0	100 100
1	C	408/620 (66%)	397 (97%)	11 (3%)	0	100 100
1	D	408/620 (66%)	396 (97%)	12 (3%)	0	100 100
1	E	408/620 (66%)	396 (97%)	12 (3%)	0	100 100
All	All	2040/3100 (66%)	1983 (97%)	57 (3%)	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	375/551 (68%)	362 (96%)	13 (4%)	31 48
1	B	375/551 (68%)	363 (97%)	12 (3%)	34 52
1	C	375/551 (68%)	366 (98%)	9 (2%)	44 64
1	D	375/551 (68%)	364 (97%)	11 (3%)	37 57
1	E	375/551 (68%)	363 (97%)	12 (3%)	34 52
All	All	1875/2755 (68%)	1818 (97%)	57 (3%)	37 55

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	104	ARG
1	D	106	ASP
1	D	124	SER
1	D	190	ARG
1	D	218	GLU
1	D	276	GLU
1	D	293	PHE
1	D	297	ASP
1	D	301	SER
1	D	349	LYS

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Mol	Chain	Res	Type
1	D	366	MET
1	A	104	ARG
1	A	106	ASP
1	A	124	SER
1	A	204	GLU
1	A	218	GLU
1	A	276	GLU
1	A	291	MET
1	A	293	PHE
1	A	297	ASP
1	A	301	SER
1	A	359	LEU
1	A	366	MET
1	A	383	MET
1	B	47	ARG
1	B	104	ARG
1	B	106	ASP
1	B	124	SER
1	B	181	ASP
1	B	204	GLU
1	B	218	GLU
1	B	276	GLU
1	B	291	MET
1	B	297	ASP
1	B	301	SER
1	B	366	MET
1	C	104	ARG
1	C	106	ASP
1	C	124	SER
1	C	276	GLU
1	C	293	PHE
1	C	297	ASP
1	C	301	SER
1	C	366	MET
1	C	375	LYS
1	E	47	ARG
1	E	50	SER
1	E	106	ASP
1	E	190	ARG
1	E	218	GLU
1	E	276	GLU
1	E	291	MET

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Mol	Chain	Res	Type
1	E	293	PHE
1	E	297	ASP
1	E	301	SER
1	E	349	LYS
1	E	375	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [\(i\)](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [\(i\)](#)

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

5.5 Carbohydrates [\(i\)](#)

20 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	F	1	2,1	14,14,15	0.30	0	17,19,21	0.66	0
2	NAG	F	2	2	14,14,15	0.24	0	17,19,21	0.44	0
2	NAG	G	1	2,1	14,14,15	0.24	0	17,19,21	0.65	0
2	NAG	G	2	2	14,14,15	0.23	0	17,19,21	0.40	0
2	NAG	H	1	2,1	14,14,15	0.23	0	17,19,21	0.56	0
2	NAG	H	2	2	14,14,15	0.21	0	17,19,21	0.41	0
2	NAG	I	1	2,1	14,14,15	0.24	0	17,19,21	0.65	0
2	NAG	I	2	2	14,14,15	0.25	0	17,19,21	0.41	0
2	NAG	J	1	2,1	14,14,15	0.25	0	17,19,21	0.58	0
2	NAG	J	2	2	14,14,15	0.22	0	17,19,21	0.41	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	K	1	2,1	14,14,15	0.23	0	17,19,21	0.63	0
2	NAG	K	2	2	14,14,15	0.23	0	17,19,21	0.40	0
2	NAG	L	1	2,1	14,14,15	0.23	0	17,19,21	0.58	0
2	NAG	L	2	2	14,14,15	0.22	0	17,19,21	0.41	0
2	NAG	M	1	2,1	14,14,15	0.22	0	17,19,21	0.66	0
2	NAG	M	2	2	14,14,15	0.24	0	17,19,21	0.39	0
2	NAG	N	1	2,1	14,14,15	0.30	0	17,19,21	0.65	0
2	NAG	N	2	2	14,14,15	0.28	0	17,19,21	0.44	0
2	NAG	O	1	2,1	14,14,15	0.21	0	17,19,21	0.64	0
2	NAG	O	2	2	14,14,15	0.22	0	17,19,21	0.40	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	F	1	2,1	-	6/6/23/26	0/1/1/1
2	NAG	F	2	2	-	0/6/23/26	0/1/1/1
2	NAG	G	1	2,1	-	4/6/23/26	0/1/1/1
2	NAG	G	2	2	-	2/6/23/26	0/1/1/1
2	NAG	H	1	2,1	-	5/6/23/26	0/1/1/1
2	NAG	H	2	2	-	0/6/23/26	0/1/1/1
2	NAG	I	1	2,1	-	4/6/23/26	0/1/1/1
2	NAG	I	2	2	-	2/6/23/26	0/1/1/1
2	NAG	J	1	2,1	-	5/6/23/26	0/1/1/1
2	NAG	J	2	2	-	0/6/23/26	0/1/1/1
2	NAG	K	1	2,1	-	4/6/23/26	0/1/1/1
2	NAG	K	2	2	-	2/6/23/26	0/1/1/1
2	NAG	L	1	2,1	-	5/6/23/26	0/1/1/1
2	NAG	L	2	2	-	0/6/23/26	0/1/1/1
2	NAG	M	1	2,1	-	4/6/23/26	0/1/1/1
2	NAG	M	2	2	-	2/6/23/26	0/1/1/1
2	NAG	N	1	2,1	-	6/6/23/26	0/1/1/1
2	NAG	N	2	2	-	0/6/23/26	0/1/1/1
2	NAG	O	1	2,1	-	4/6/23/26	0/1/1/1
2	NAG	O	2	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (57) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	K	2	NAG	C1-C2-N2-C7
2	G	2	NAG	C1-C2-N2-C7
2	I	2	NAG	C1-C2-N2-C7
2	M	2	NAG	C1-C2-N2-C7
2	F	1	NAG	C8-C7-N2-C2
2	F	1	NAG	O7-C7-N2-C2
2	G	1	NAG	C8-C7-N2-C2
2	G	1	NAG	O7-C7-N2-C2
2	H	1	NAG	C8-C7-N2-C2
2	H	1	NAG	O7-C7-N2-C2
2	I	1	NAG	C8-C7-N2-C2
2	I	1	NAG	O7-C7-N2-C2
2	J	1	NAG	C8-C7-N2-C2
2	J	1	NAG	O7-C7-N2-C2
2	K	1	NAG	C8-C7-N2-C2
2	K	1	NAG	O7-C7-N2-C2
2	L	1	NAG	C8-C7-N2-C2
2	L	1	NAG	O7-C7-N2-C2
2	M	1	NAG	C8-C7-N2-C2
2	M	1	NAG	O7-C7-N2-C2
2	N	1	NAG	C8-C7-N2-C2
2	N	1	NAG	O7-C7-N2-C2
2	O	1	NAG	C8-C7-N2-C2
2	O	1	NAG	O7-C7-N2-C2
2	H	1	NAG	C4-C5-C6-O6
2	F	1	NAG	C4-C5-C6-O6
2	L	1	NAG	C4-C5-C6-O6
2	J	1	NAG	C4-C5-C6-O6
2	H	1	NAG	O5-C5-C6-O6
2	N	1	NAG	C4-C5-C6-O6
2	L	1	NAG	O5-C5-C6-O6
2	F	1	NAG	O5-C5-C6-O6
2	O	2	NAG	C1-C2-N2-C7
2	J	1	NAG	O5-C5-C6-O6
2	N	1	NAG	O5-C5-C6-O6
2	I	1	NAG	O5-C5-C6-O6
2	O	1	NAG	O5-C5-C6-O6
2	G	1	NAG	O5-C5-C6-O6
2	M	1	NAG	O5-C5-C6-O6

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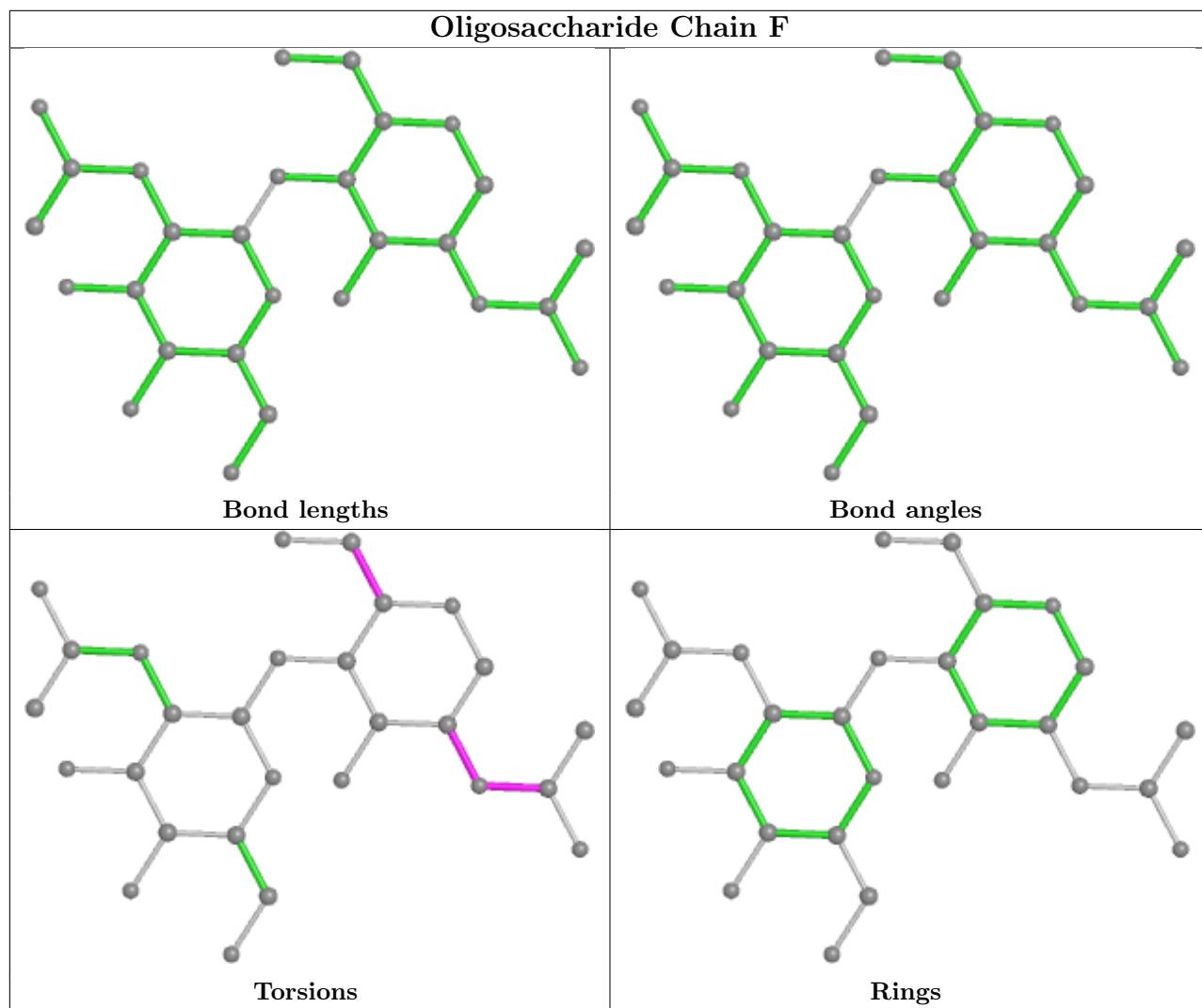
Mol	Chain	Res	Type	Atoms
2	K	1	NAG	O5-C5-C6-O6
2	F	1	NAG	C3-C2-N2-C7
2	G	1	NAG	C3-C2-N2-C7
2	G	2	NAG	C3-C2-N2-C7
2	I	1	NAG	C3-C2-N2-C7
2	I	2	NAG	C3-C2-N2-C7
2	K	1	NAG	C3-C2-N2-C7
2	K	2	NAG	C3-C2-N2-C7
2	M	1	NAG	C3-C2-N2-C7
2	M	2	NAG	C3-C2-N2-C7
2	N	1	NAG	C3-C2-N2-C7
2	O	1	NAG	C3-C2-N2-C7
2	O	2	NAG	C3-C2-N2-C7
2	F	1	NAG	C1-C2-N2-C7
2	N	1	NAG	C1-C2-N2-C7
2	H	1	NAG	C3-C2-N2-C7
2	J	1	NAG	C3-C2-N2-C7
2	L	1	NAG	C3-C2-N2-C7

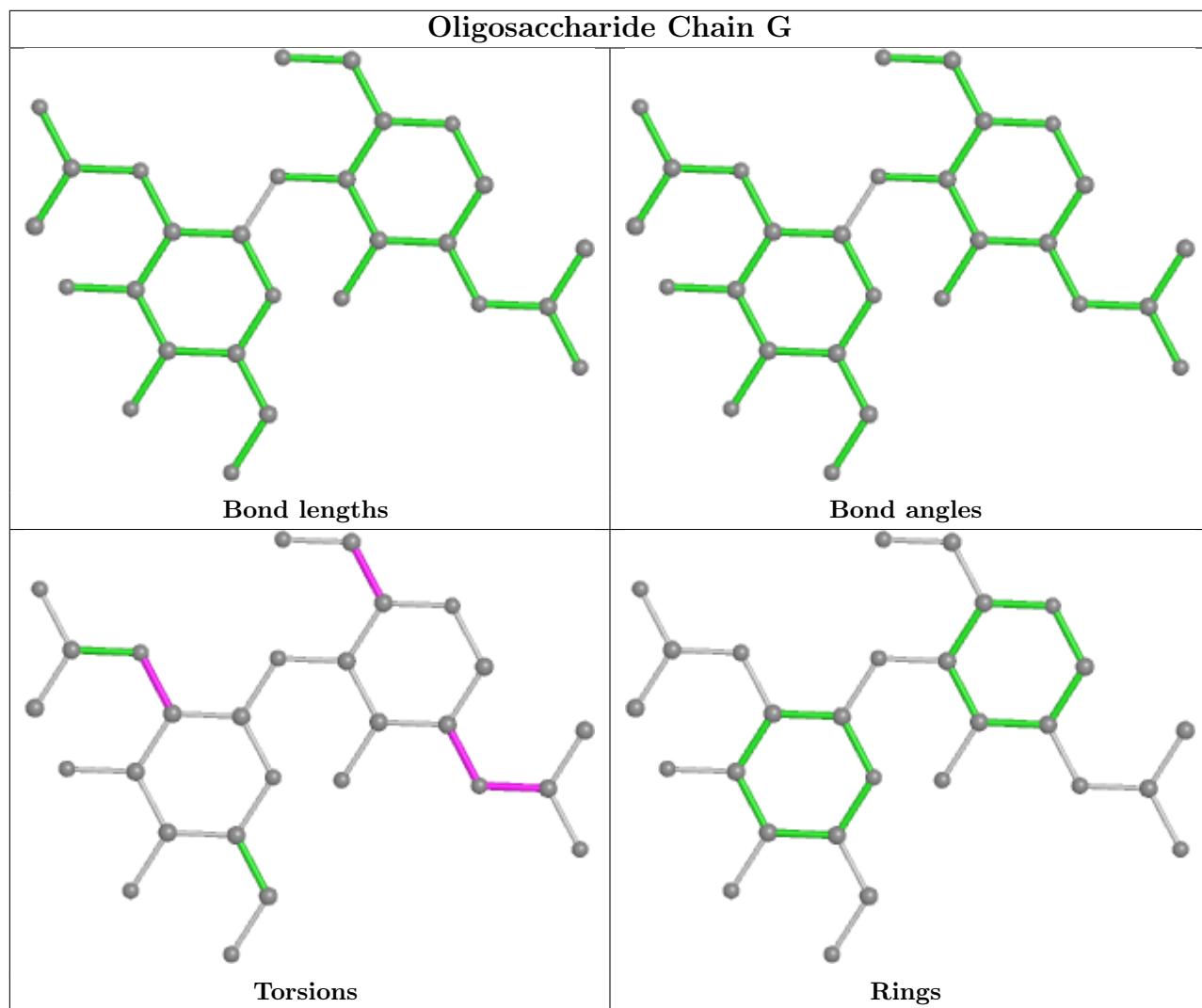
There are no ring outliers.

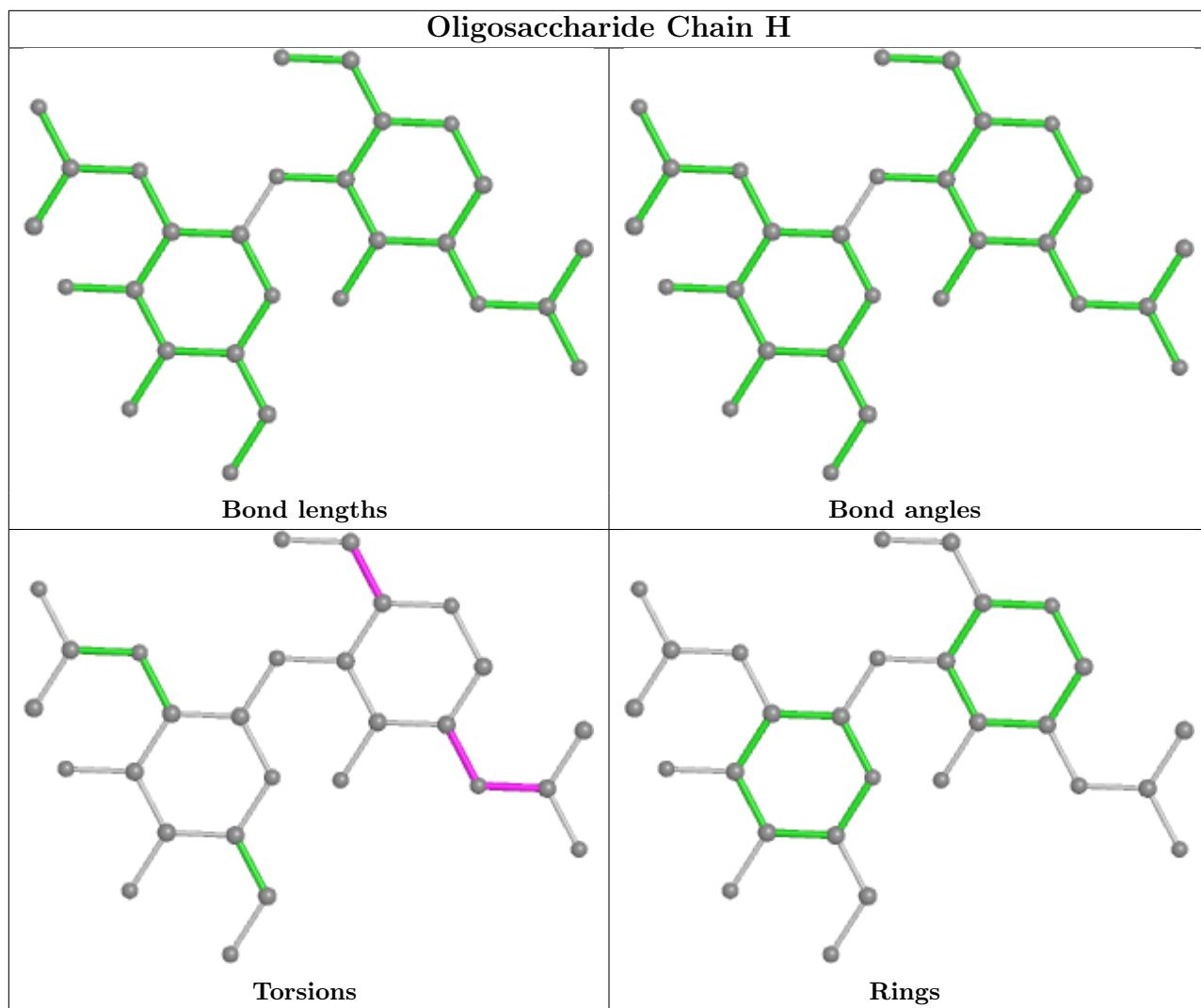
15 monomers are involved in 50 short contacts:

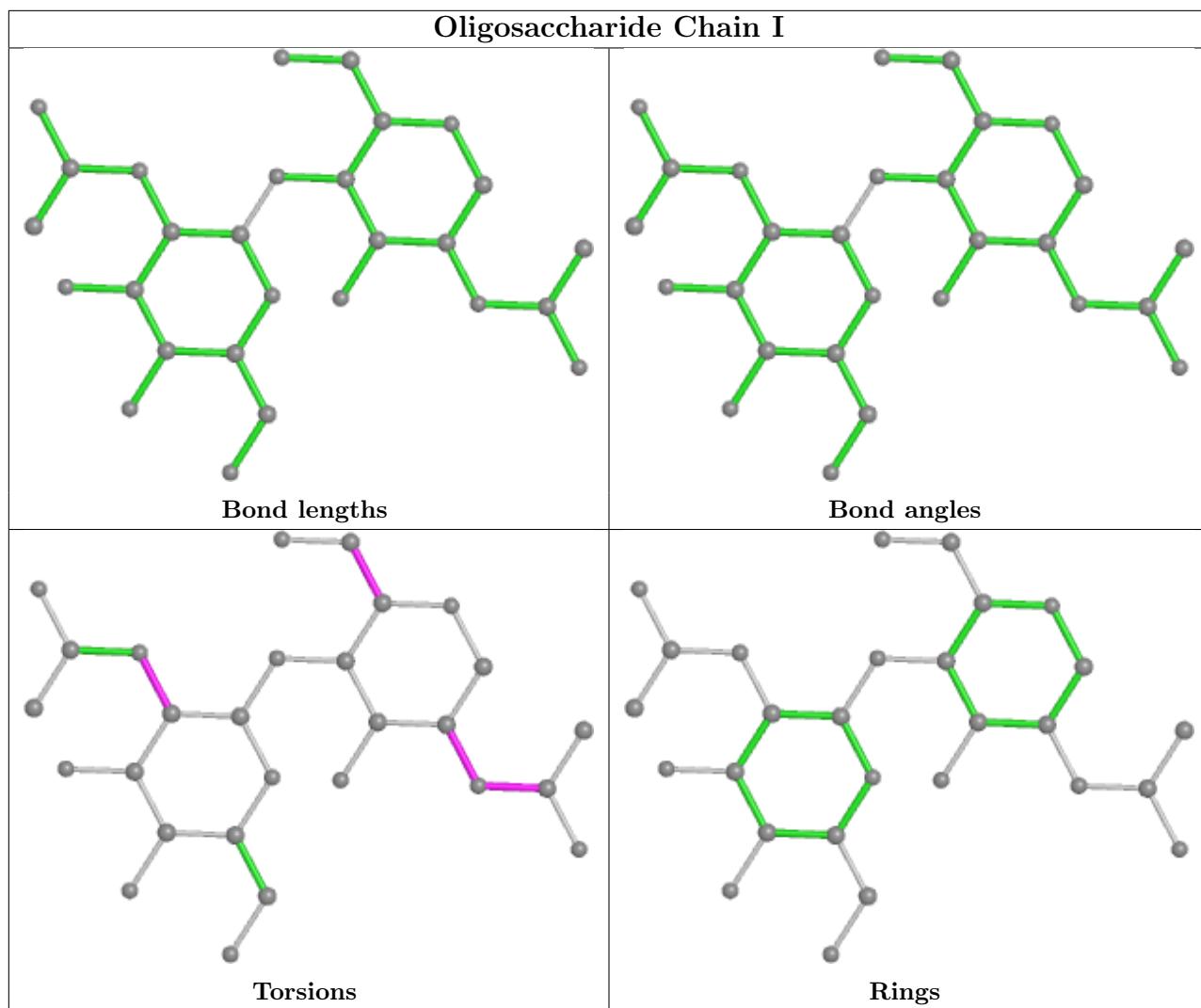
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	1	NAG	3	0
2	M	2	NAG	1	0
2	H	1	NAG	8	0
2	I	1	NAG	4	0
2	O	2	NAG	1	0
2	I	2	NAG	1	0
2	K	1	NAG	3	0
2	M	1	NAG	3	0
2	L	1	NAG	7	0
2	N	1	NAG	4	0
2	K	2	NAG	1	0
2	O	1	NAG	4	0
2	G	2	NAG	1	0
2	J	1	NAG	6	0
2	F	1	NAG	3	0

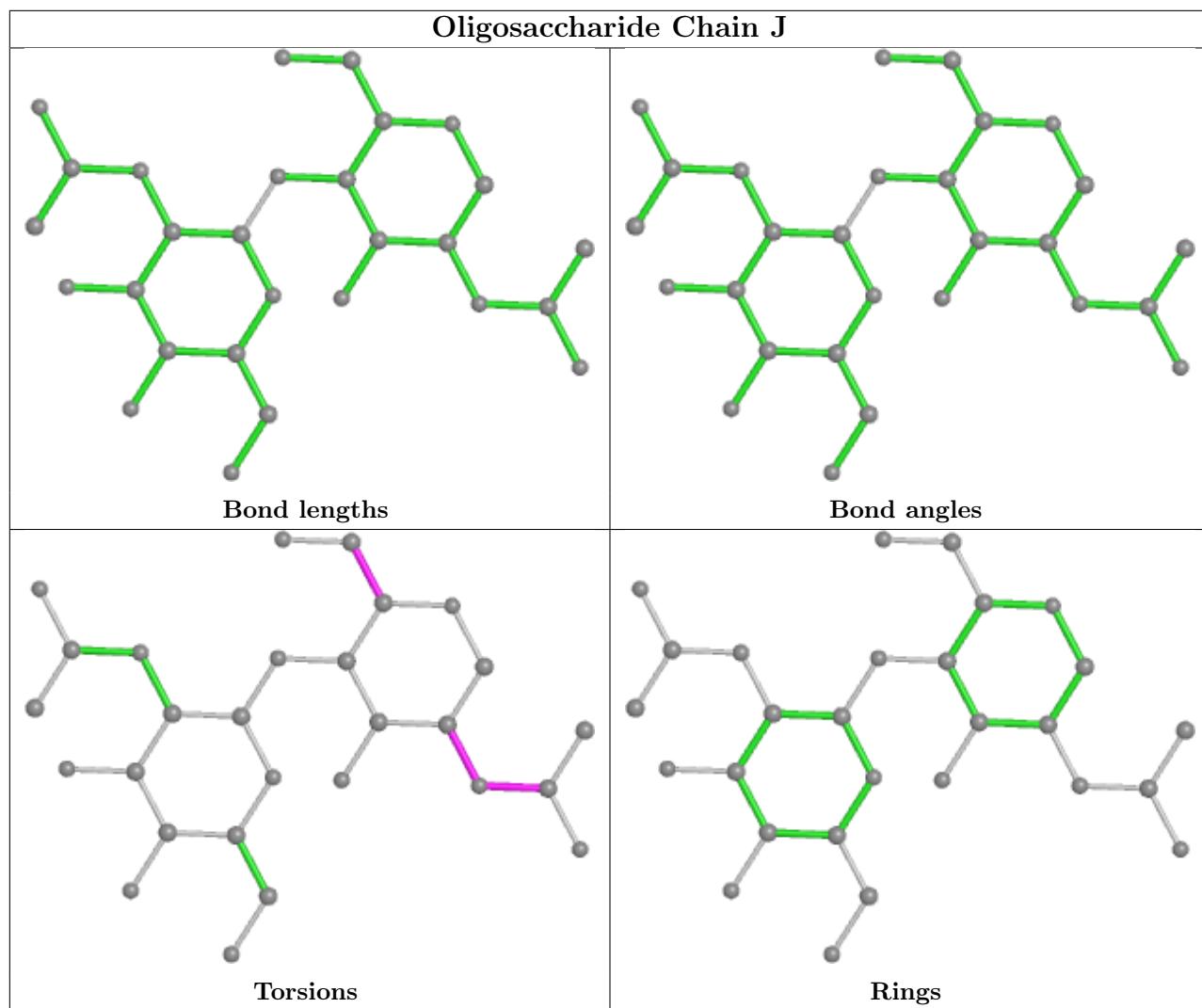
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

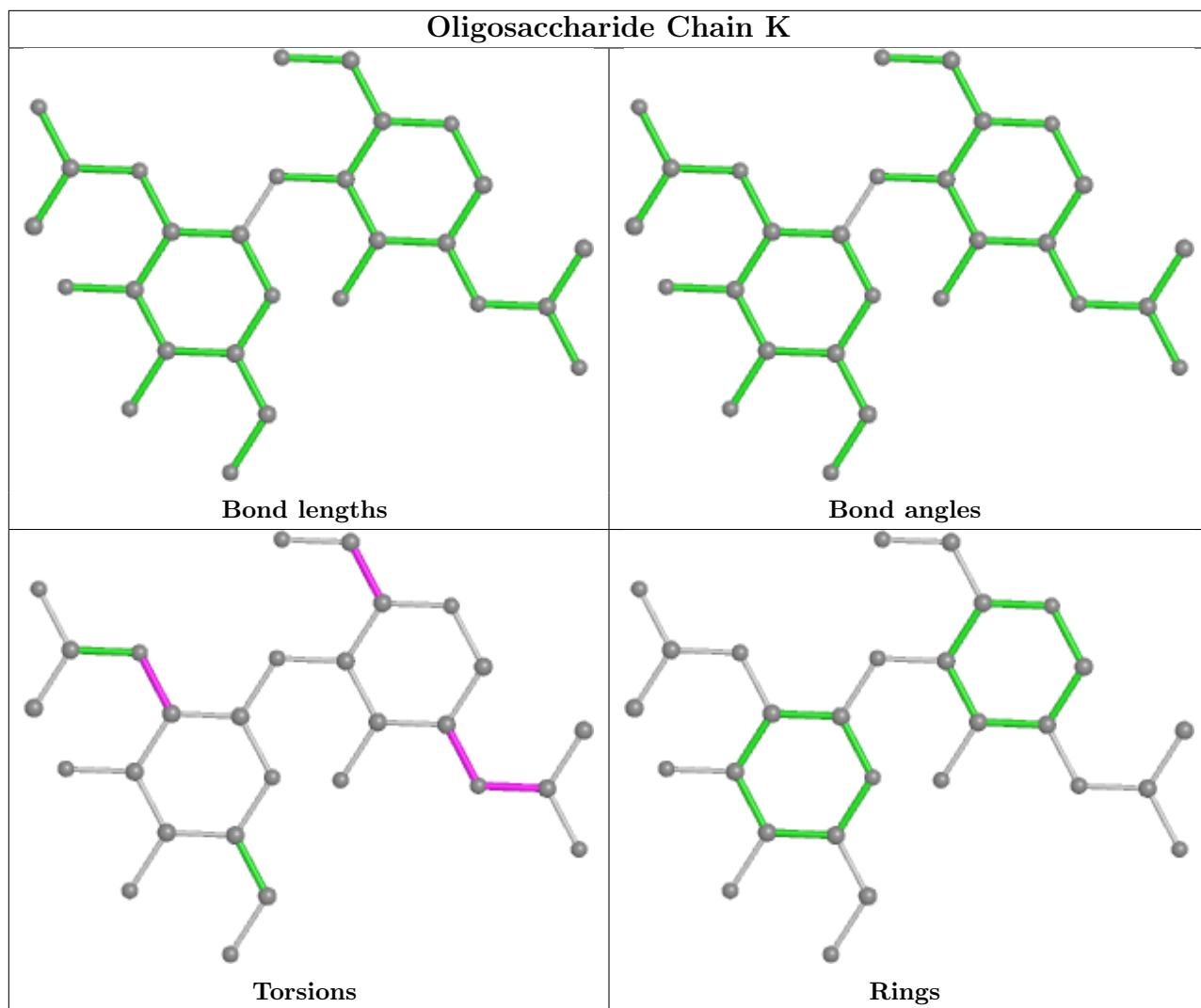


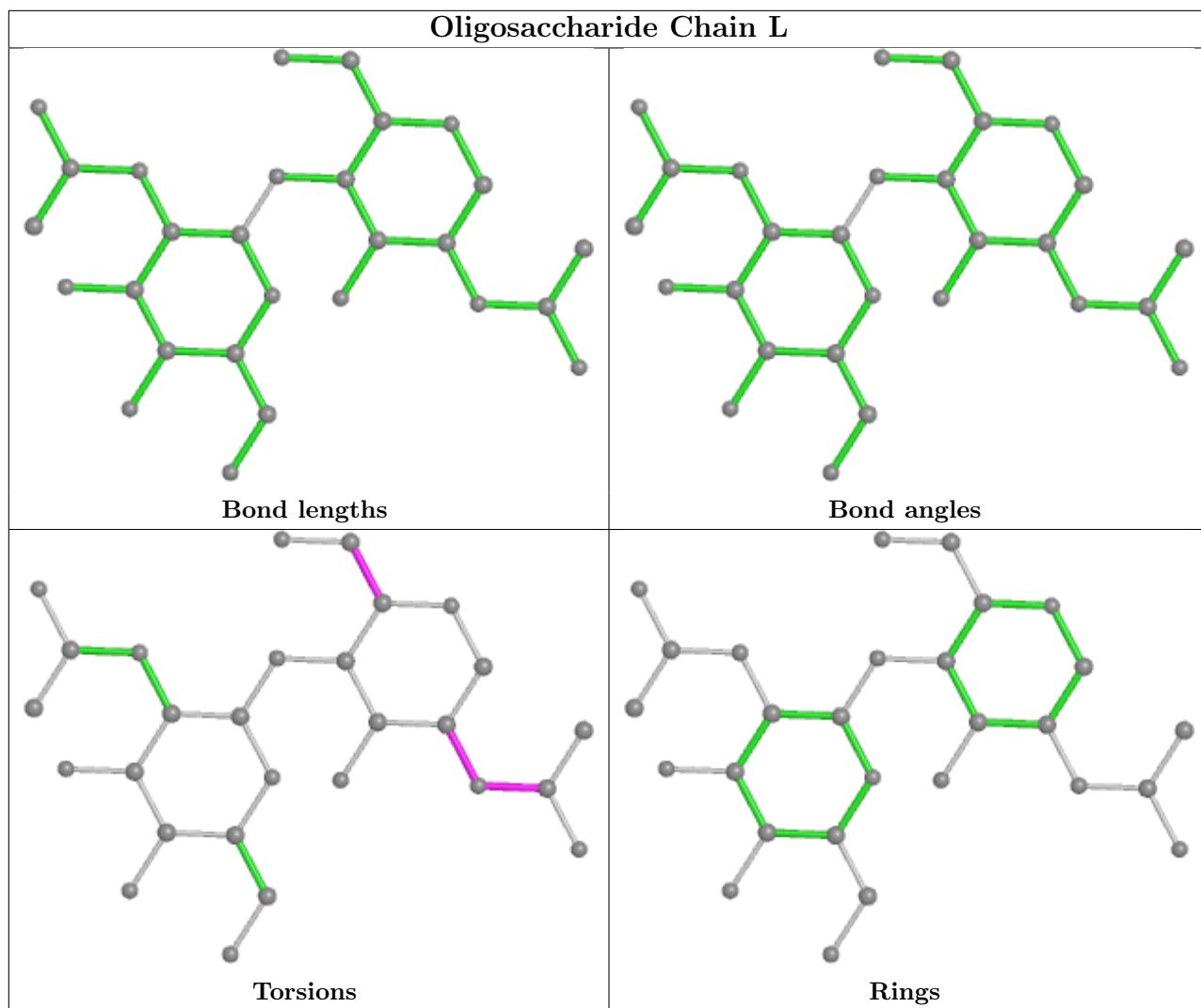


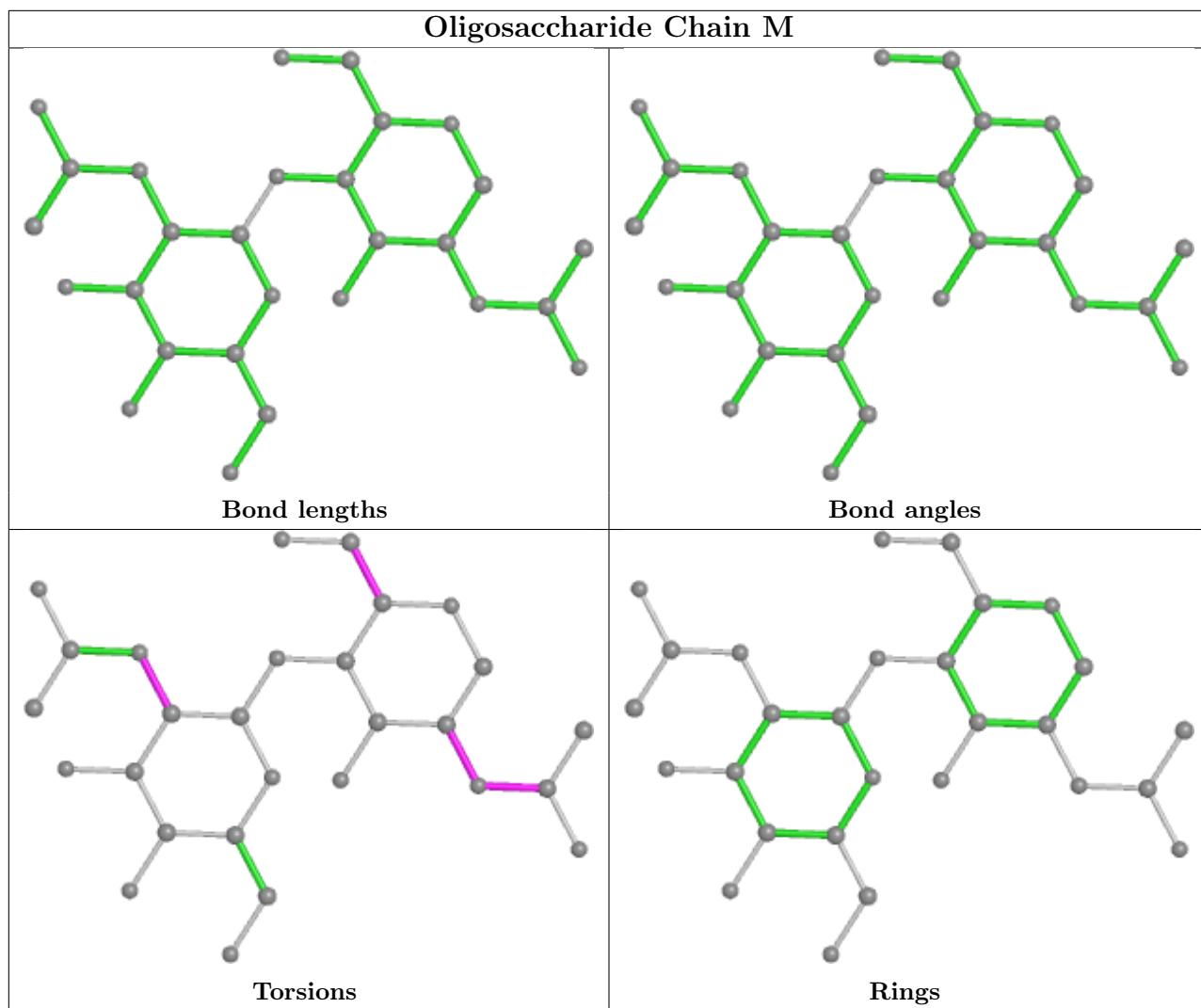


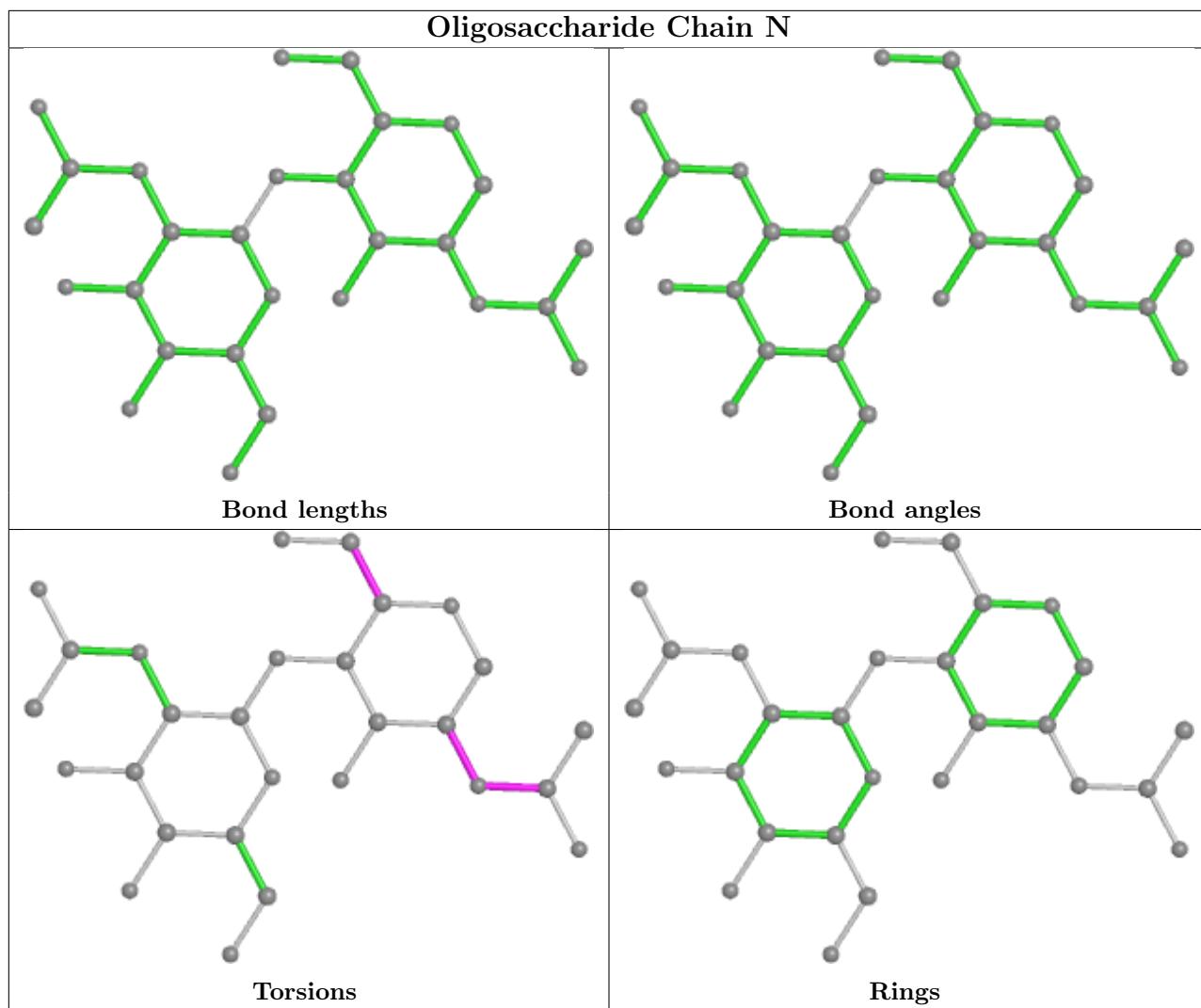


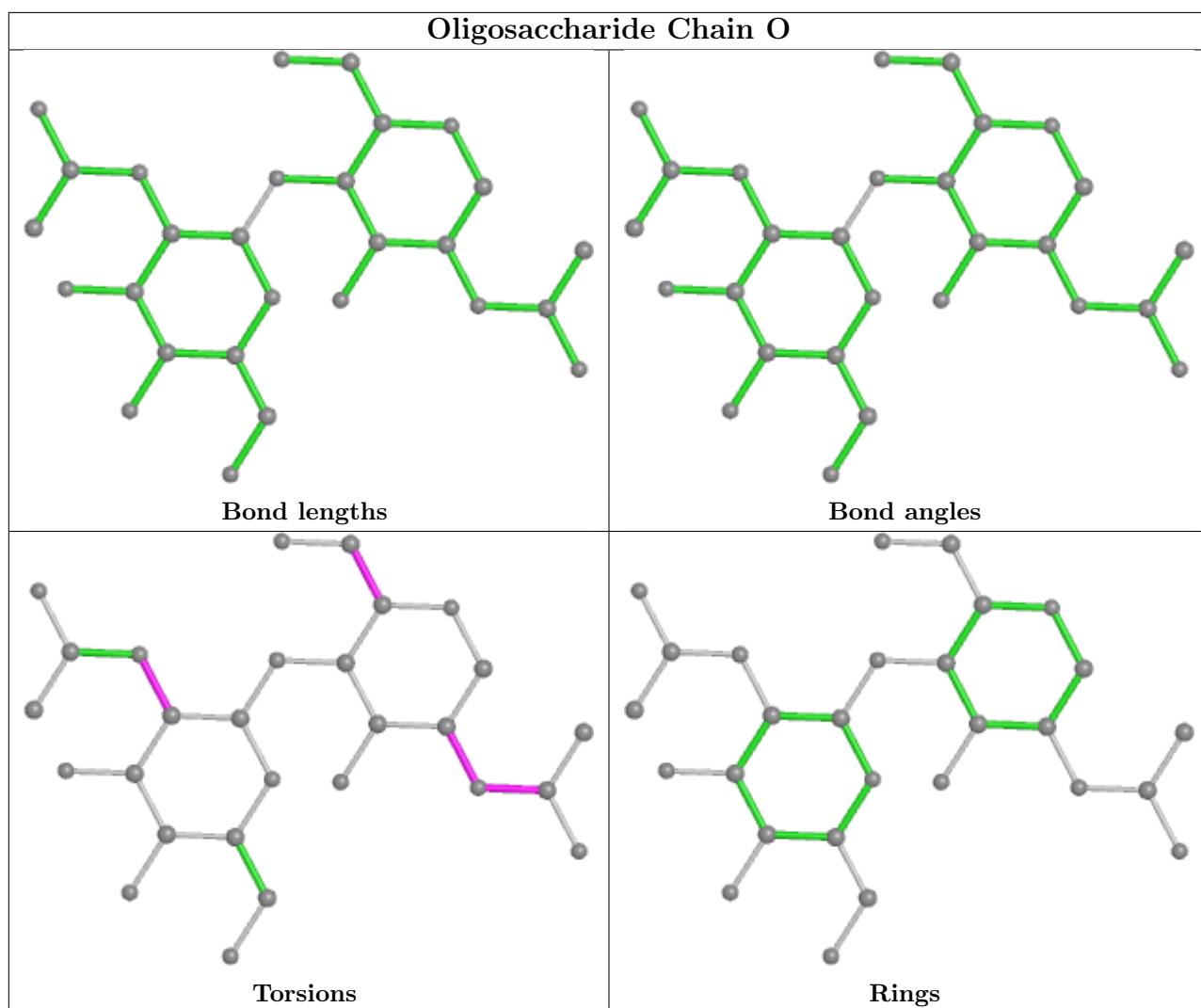












5.6 Ligand geometry (i)

15 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	C	601	1	14,14,15	0.22	0	17,19,21	0.33	0
4	A1D8E	A	602	-	32,33,33	3.17	7 (21%)	46,49,49	3.06	11 (23%)
4	A1D8E	E	602	-	32,33,33	3.17	7 (21%)	46,49,49	3.05	12 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	BET	D	603	-	7,7,7	1.08	0	10,10,10	1.58	1 (10%)
3	NAG	E	601	1	14,14,15	0.25	0	17,19,21	0.34	0
3	NAG	D	601	1	14,14,15	0.25	0	17,19,21	0.33	0
5	BET	A	603	-	7,7,7	1.07	0	10,10,10	1.59	1 (10%)
5	BET	E	603	-	7,7,7	1.08	0	10,10,10	1.57	1 (10%)
3	NAG	A	601	1	14,14,15	0.24	0	17,19,21	0.34	0
4	A1D8E	B	602	-	32,33,33	3.17	7 (21%)	46,49,49	3.06	12 (26%)
5	BET	B	603	-	7,7,7	1.05	0	10,10,10	1.61	1 (10%)
3	NAG	B	601	1	14,14,15	0.23	0	17,19,21	0.32	0
4	A1D8E	C	602	-	32,33,33	3.16	7 (21%)	46,49,49	3.06	12 (26%)
5	BET	C	603	-	7,7,7	1.07	0	10,10,10	1.60	1 (10%)
4	A1D8E	D	602	-	32,33,33	3.16	7 (21%)	46,49,49	3.06	12 (26%)

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	C	601	1	-	0/6/23/26	0/1/1/1
4	A1D8E	A	602	-	-	5/28/31/31	0/2/2/2
4	A1D8E	E	602	-	-	5/28/31/31	0/2/2/2
5	BET	D	603	-	-	5/5/5/5	-
3	NAG	E	601	1	-	2/6/23/26	0/1/1/1
3	NAG	D	601	1	-	0/6/23/26	0/1/1/1
5	BET	A	603	-	-	5/5/5/5	-
5	BET	E	603	-	-	5/5/5/5	-
3	NAG	A	601	1	-	0/6/23/26	0/1/1/1
4	A1D8E	B	602	-	-	5/28/31/31	0/2/2/2
5	BET	B	603	-	-	5/5/5/5	-
3	NAG	B	601	1	-	0/6/23/26	0/1/1/1
4	A1D8E	C	602	-	-	5/28/31/31	0/2/2/2
5	BET	C	603	-	-	5/5/5/5	-
4	A1D8E	D	602	-	-	5/28/31/31	0/2/2/2

All (35) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	602	A1D8E	C02-N17	-14.45	1.25	1.46
4	E	602	A1D8E	C02-N17	-14.43	1.25	1.46
4	B	602	A1D8E	C02-N17	-14.39	1.26	1.46
4	C	602	A1D8E	C02-N17	-14.35	1.26	1.46
4	D	602	A1D8E	C02-N17	-14.34	1.26	1.46
4	C	602	A1D8E	C18-N17	6.19	1.46	1.34
4	E	602	A1D8E	C18-N17	6.18	1.46	1.34
4	D	602	A1D8E	C18-N17	6.17	1.46	1.34
4	A	602	A1D8E	C18-N17	6.16	1.46	1.34
4	B	602	A1D8E	C18-N17	6.15	1.46	1.34
4	C	602	A1D8E	C02-C31	5.00	1.53	1.49
4	D	602	A1D8E	C02-C31	4.99	1.53	1.49
4	B	602	A1D8E	C02-C31	4.96	1.53	1.49
4	A	602	A1D8E	C02-C31	4.95	1.53	1.49
4	E	602	A1D8E	C02-C31	4.94	1.53	1.49
4	D	602	A1D8E	C09-C11	3.82	1.53	1.44
4	E	602	A1D8E	C09-C11	3.82	1.53	1.44
4	B	602	A1D8E	C09-C11	3.80	1.53	1.44
4	A	602	A1D8E	C09-C11	3.80	1.53	1.44
4	C	602	A1D8E	C09-C11	3.79	1.53	1.44
4	B	602	A1D8E	C23-S24	3.62	1.82	1.78
4	A	602	A1D8E	C23-S24	3.53	1.82	1.78
4	E	602	A1D8E	C23-S24	3.53	1.82	1.78
4	D	602	A1D8E	C23-S24	3.50	1.82	1.78
4	C	602	A1D8E	C23-S24	3.50	1.82	1.78
4	E	602	A1D8E	O19-C18	-2.28	1.18	1.23
4	B	602	A1D8E	O19-C18	-2.25	1.18	1.23
4	C	602	A1D8E	O19-C18	-2.25	1.18	1.23
4	A	602	A1D8E	O19-C18	-2.23	1.18	1.23
4	D	602	A1D8E	O19-C18	-2.19	1.18	1.23
4	A	602	A1D8E	O04-C05	2.10	1.41	1.37
4	D	602	A1D8E	O04-C05	2.09	1.41	1.37
4	B	602	A1D8E	O04-C05	2.08	1.41	1.37
4	E	602	A1D8E	O04-C05	2.08	1.41	1.37
4	C	602	A1D8E	O04-C05	2.07	1.41	1.37

All (64) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	602	A1D8E	C01-C02-C31	-11.34	97.50	108.06
4	E	602	A1D8E	C01-C02-C31	-11.30	97.54	108.06
4	A	602	A1D8E	C01-C02-C31	-11.29	97.56	108.06
4	C	602	A1D8E	C01-C02-C31	-11.24	97.60	108.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	602	A1D8E	C01-C02-C31	-11.17	97.67	108.06
4	D	602	A1D8E	C01-C02-C03	10.54	120.13	110.96
4	A	602	A1D8E	C01-C02-C03	10.47	120.08	110.96
4	C	602	A1D8E	C01-C02-C03	10.34	119.96	110.96
4	E	602	A1D8E	C01-C02-C03	10.32	119.94	110.96
4	B	602	A1D8E	C01-C02-C03	10.31	119.94	110.96
4	B	602	A1D8E	C03-C02-C31	-7.89	96.00	108.68
4	E	602	A1D8E	C03-C02-C31	-7.80	96.15	108.68
4	A	602	A1D8E	C03-C02-C31	-7.76	96.20	108.68
4	C	602	A1D8E	C03-C02-C31	-7.76	96.21	108.68
4	D	602	A1D8E	C03-C02-C31	-7.75	96.23	108.68
4	B	602	A1D8E	C01-C02-N17	5.84	115.69	109.52
4	E	602	A1D8E	C01-C02-N17	5.73	115.58	109.52
4	D	602	A1D8E	C01-C02-N17	5.67	115.52	109.52
4	C	602	A1D8E	C01-C02-N17	5.67	115.51	109.52
4	A	602	A1D8E	C01-C02-N17	5.62	115.47	109.52
4	C	602	A1D8E	C25-S24-C23	4.15	110.05	99.21
4	D	602	A1D8E	C25-S24-C23	4.08	109.86	99.21
4	E	602	A1D8E	C25-S24-C23	4.07	109.83	99.21
4	B	602	A1D8E	C25-S24-C23	3.97	109.59	99.21
4	A	602	A1D8E	C25-S24-C23	3.95	109.53	99.21
5	B	603	BET	C-CA-N	3.71	121.44	116.34
5	C	603	BET	C-CA-N	3.70	121.42	116.34
4	C	602	A1D8E	C10-C05-C06	-3.66	118.83	122.20
5	A	603	BET	C-CA-N	3.61	121.30	116.34
5	D	603	BET	C-CA-N	3.57	121.25	116.34
5	E	603	BET	C-CA-N	3.56	121.23	116.34
4	B	602	A1D8E	C10-C05-C06	-3.55	118.94	122.20
4	A	602	A1D8E	C10-C05-C06	-3.52	118.96	122.20
4	D	602	A1D8E	C10-C05-C06	-3.48	119.00	122.20
4	C	602	A1D8E	C07-C06-C05	3.47	120.53	116.52
4	E	602	A1D8E	C10-C05-C06	-3.46	119.01	122.20
4	B	602	A1D8E	C07-C06-C05	3.46	120.52	116.52
4	B	602	A1D8E	C31-C02-N17	-3.44	106.49	109.74
4	D	602	A1D8E	C07-C06-C05	3.44	120.49	116.52
4	E	602	A1D8E	C07-C06-C05	3.36	120.41	116.52
4	A	602	A1D8E	C07-C06-C05	3.35	120.39	116.52
4	B	602	A1D8E	C03-C02-N17	3.35	115.54	109.98
4	C	602	A1D8E	C03-C02-N17	3.34	115.52	109.98
4	E	602	A1D8E	C03-C02-N17	3.33	115.51	109.98
4	A	602	A1D8E	C03-C02-N17	3.30	115.46	109.98
4	C	602	A1D8E	C31-C02-N17	-3.25	106.67	109.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	602	A1D8E	C31-C02-N17	-3.22	106.70	109.74
4	A	602	A1D8E	C31-C02-N17	-3.22	106.70	109.74
4	D	602	A1D8E	C03-C02-N17	3.19	115.28	109.98
4	D	602	A1D8E	C31-C02-N17	-3.04	106.88	109.74
4	A	602	A1D8E	C02-C31-N32	2.70	179.87	175.17
4	B	602	A1D8E	C02-C31-N32	2.69	179.85	175.17
4	E	602	A1D8E	C02-C31-N32	2.68	179.84	175.17
4	C	602	A1D8E	C02-C31-N32	2.66	179.80	175.17
4	D	602	A1D8E	C02-C31-N32	2.64	179.76	175.17
4	B	602	A1D8E	F16-C13-C06	-2.11	109.03	112.70
4	B	602	A1D8E	O04-C05-C06	2.09	119.55	116.65
4	C	602	A1D8E	O04-C05-C06	2.08	119.54	116.65
4	C	602	A1D8E	F16-C13-C06	-2.03	109.17	112.70
4	D	602	A1D8E	O04-C05-C06	2.01	119.45	116.65
4	D	602	A1D8E	F16-C13-C06	-2.01	109.20	112.70
4	E	602	A1D8E	F16-C13-C06	-2.01	109.20	112.70
4	E	602	A1D8E	O04-C05-C06	2.00	119.43	116.65
4	A	602	A1D8E	O04-C05-C06	2.00	119.43	116.65

There are no chirality outliers.

All (52) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	603	BET	O-C-CA-N
5	D	603	BET	OXT-C-CA-N
5	A	603	BET	C-CA-N-C3
5	A	603	BET	O-C-CA-N
5	A	603	BET	OXT-C-CA-N
5	B	603	BET	C-CA-N-C1
5	B	603	BET	C-CA-N-C3
5	B	603	BET	O-C-CA-N
5	B	603	BET	OXT-C-CA-N
5	C	603	BET	C-CA-N-C3
5	C	603	BET	O-C-CA-N
5	C	603	BET	OXT-C-CA-N
5	E	603	BET	O-C-CA-N
5	E	603	BET	OXT-C-CA-N
5	D	603	BET	C-CA-N-C1
5	D	603	BET	C-CA-N-C3
5	A	603	BET	C-CA-N-C1
5	C	603	BET	C-CA-N-C1
5	B	603	BET	C-CA-N-C2

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Mol	Chain	Res	Type	Atoms
5	E	603	BET	C-CA-N-C3
5	A	603	BET	C-CA-N-C2
5	C	603	BET	C-CA-N-C2
3	E	601	NAG	C4-C5-C6-O6
5	D	603	BET	C-CA-N-C2
5	E	603	BET	C-CA-N-C1
5	E	603	BET	C-CA-N-C2
3	E	601	NAG	O5-C5-C6-O6
4	D	602	A1D8E	C22-C23-S24-C25
4	A	602	A1D8E	C22-C23-S24-C25
4	C	602	A1D8E	C22-C23-S24-C25
4	D	602	A1D8E	N17-C02-C03-O04
4	A	602	A1D8E	N17-C02-C03-O04
4	B	602	A1D8E	N17-C02-C03-O04
4	C	602	A1D8E	N17-C02-C03-O04
4	E	602	A1D8E	N17-C02-C03-O04
4	D	602	A1D8E	F26-C25-S24-C23
4	D	602	A1D8E	F27-C25-S24-C23
4	A	602	A1D8E	F26-C25-S24-C23
4	B	602	A1D8E	F26-C25-S24-C23
4	E	602	A1D8E	F26-C25-S24-C23
4	E	602	A1D8E	F27-C25-S24-C23
4	D	602	A1D8E	F28-C25-S24-C23
4	A	602	A1D8E	F27-C25-S24-C23
4	A	602	A1D8E	F28-C25-S24-C23
4	B	602	A1D8E	F27-C25-S24-C23
4	B	602	A1D8E	F28-C25-S24-C23
4	E	602	A1D8E	F28-C25-S24-C23
4	B	602	A1D8E	C22-C23-S24-C25
4	C	602	A1D8E	C29-C23-S24-C25
4	E	602	A1D8E	C22-C23-S24-C25
4	C	602	A1D8E	F26-C25-S24-C23
4	C	602	A1D8E	F28-C25-S24-C23

There are no ring outliers.

15 monomers are involved in 19 short contacts:

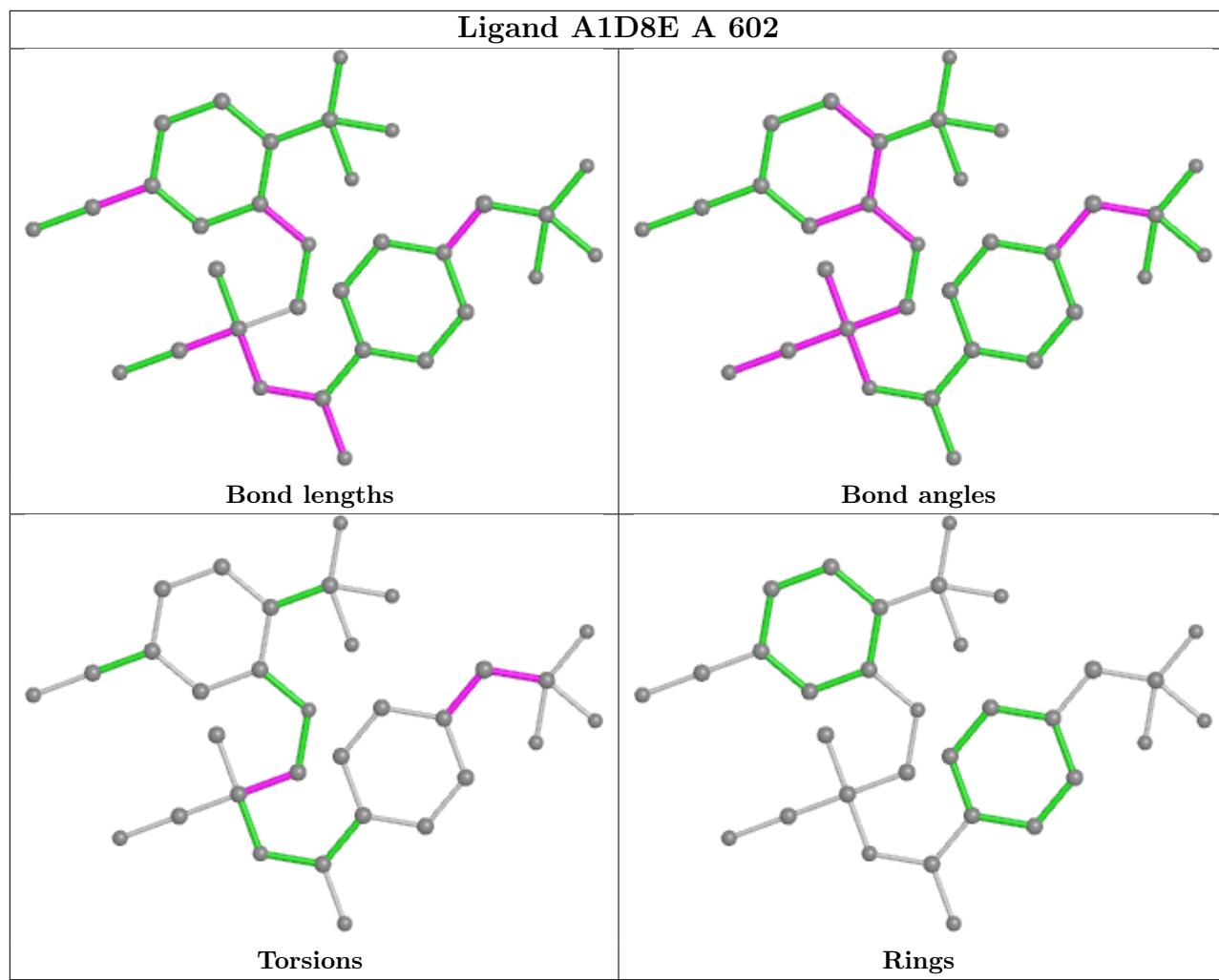
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	601	NAG	1	0
4	A	602	A1D8E	1	0
4	E	602	A1D8E	1	0
5	D	603	BET	1	0

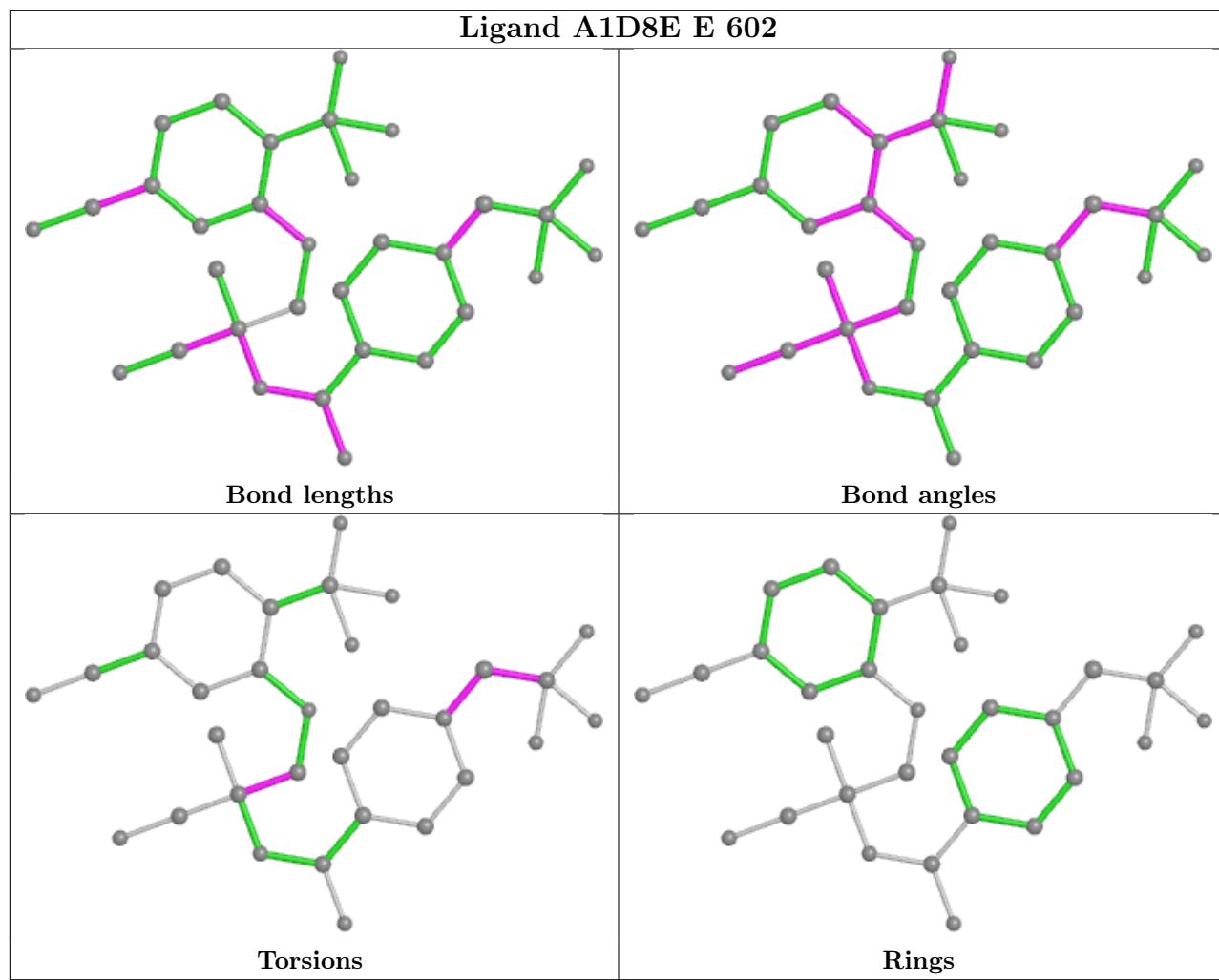
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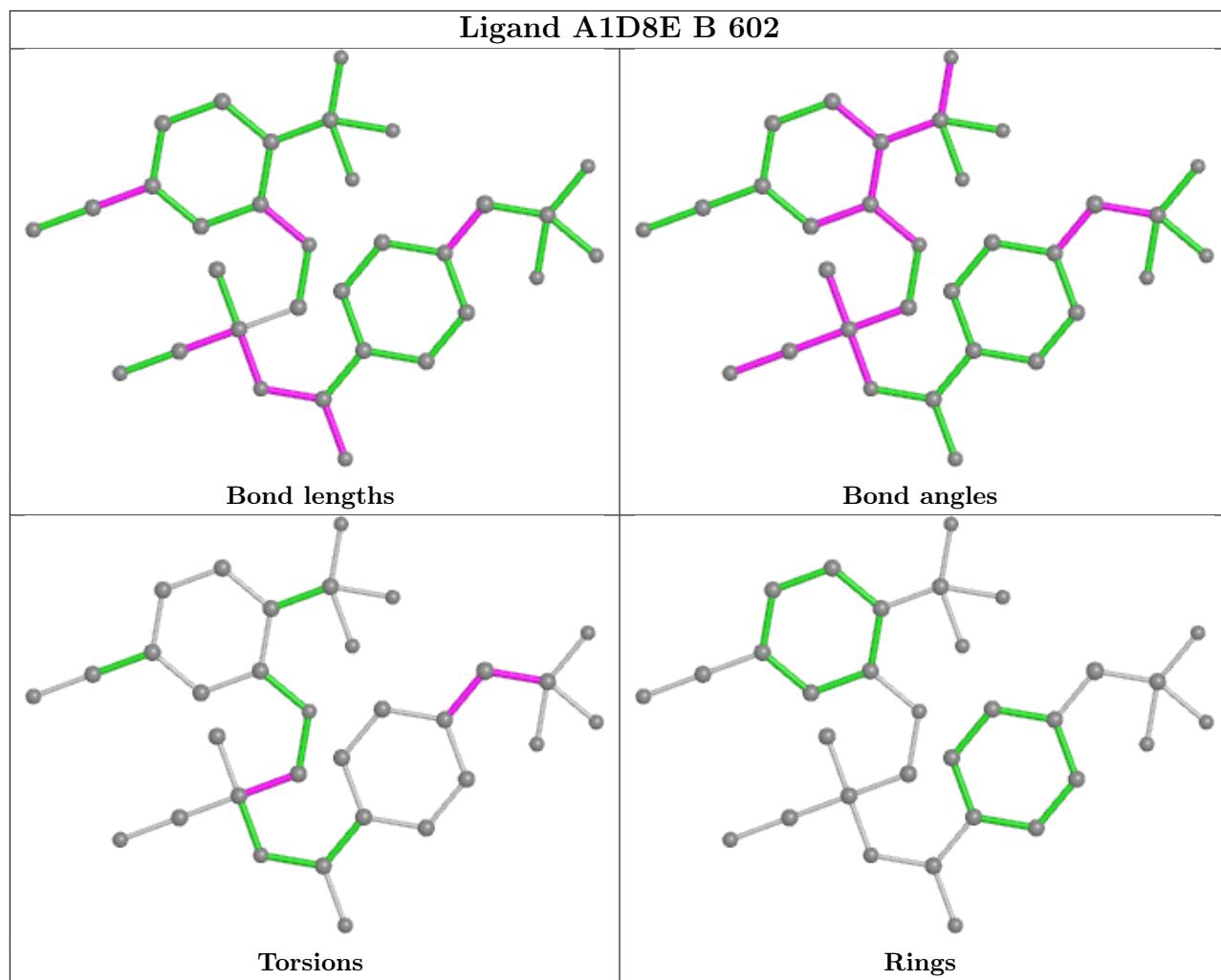
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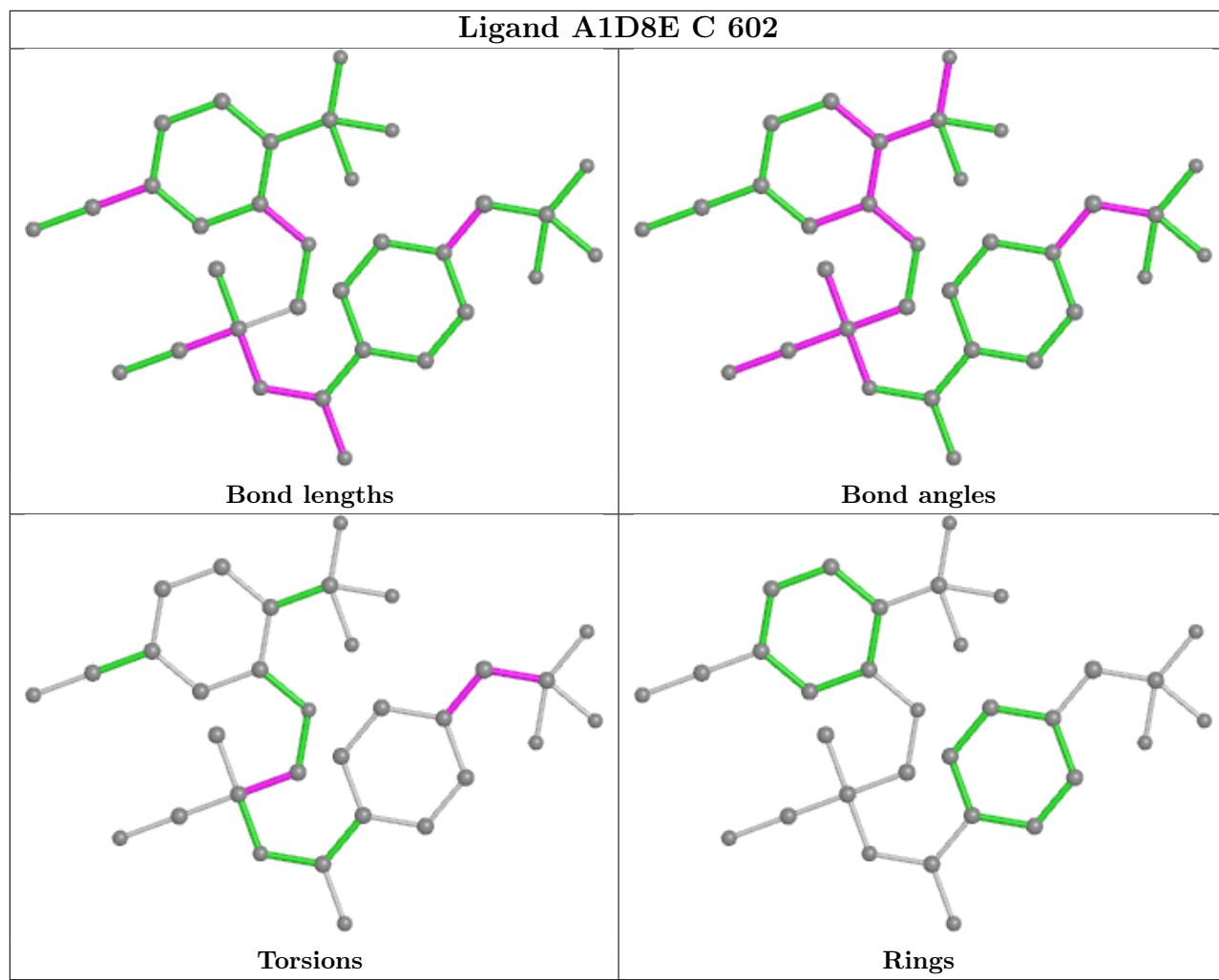
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	601	NAG	1	0
3	D	601	NAG	1	0
5	A	603	BET	2	0
5	E	603	BET	1	0
3	A	601	NAG	1	0
4	B	602	A1D8E	1	0
5	B	603	BET	2	0
3	B	601	NAG	1	0
4	C	602	A1D8E	2	0
5	C	603	BET	2	0
4	D	602	A1D8E	1	0

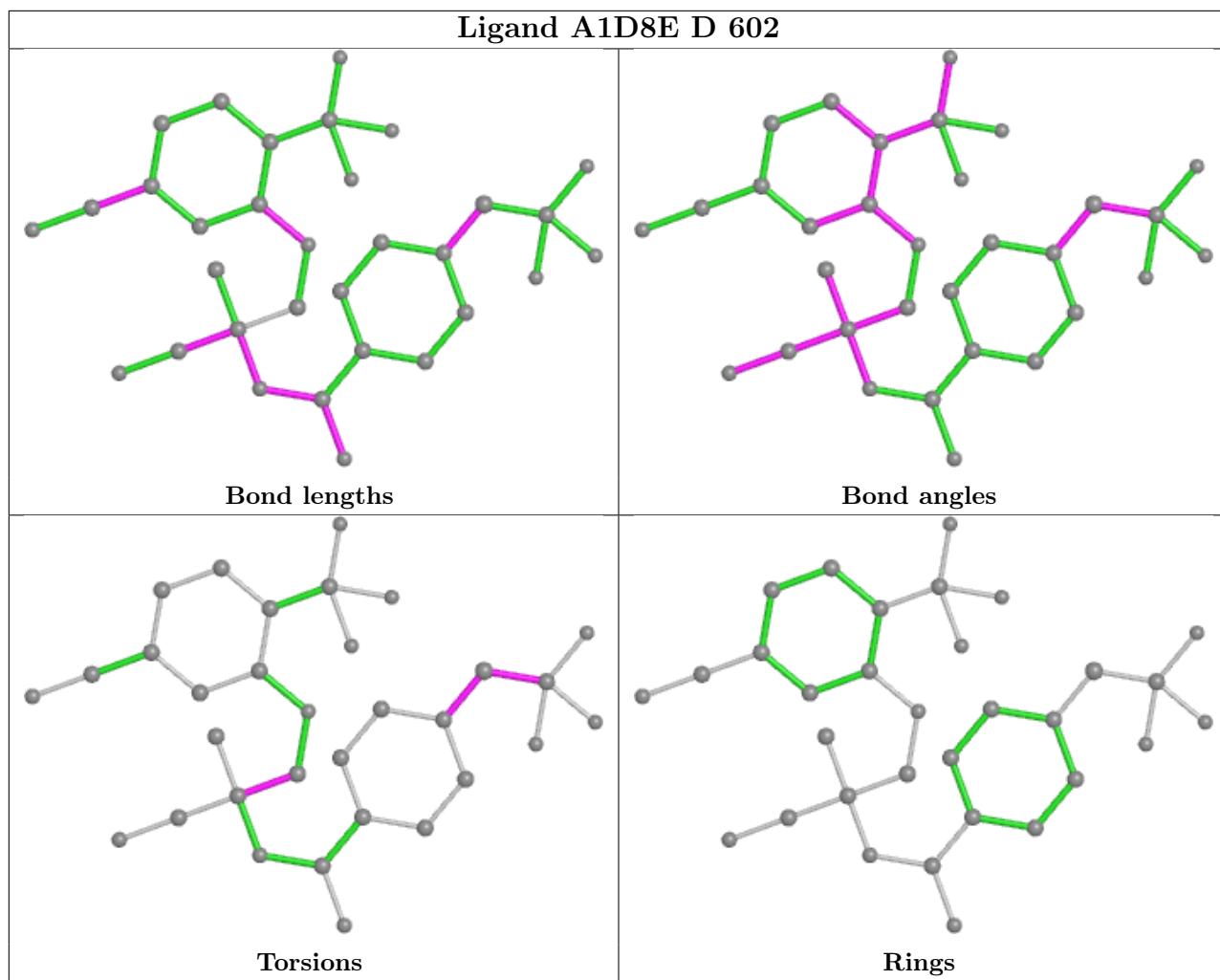
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 [\(i\)](#)

There are no chain breaks in this entry.