



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 07:47 AM UTC

PDB ID : 9TDV / pdb_00009tdv
Title : Structure of D81A-Fructofuranosidase from *Purpureocillum lilacinum* in complex with raffinose
Authors : Ruiz-Nunez, M.; Sanz-Aparicio, J.
Deposited on : 2025-11-24
Resolution : 2.00 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

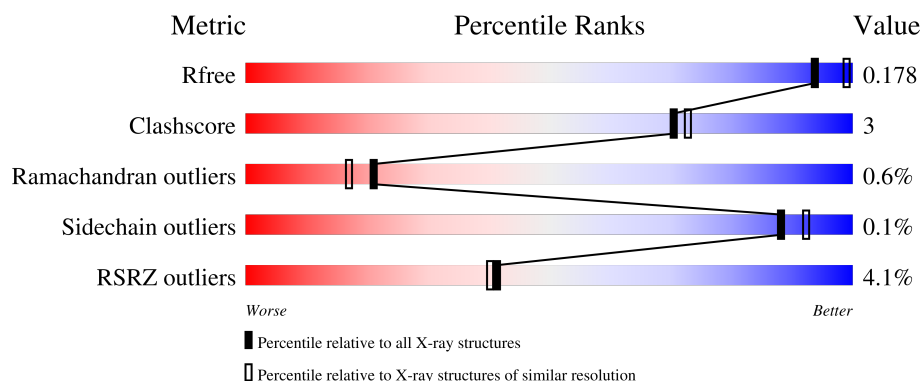
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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.



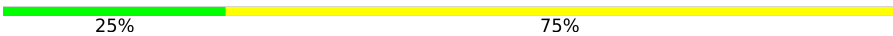
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	576	3% 87% 5% 7%
1	B	576	3% 88% 5% 7%
1	C	576	4% 86% 6% 7%
1	D	576	5% 86% 6% 7%
2	E	2	50% 50%

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Mol	Chain	Length	Quality of chain
2	I	2	 50% 50%
3	F	8	 25% 75%
3	G	8	 75% 25%
3	H	8	 88% 12%
3	J	8	 25% 75%

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
5	TRS	C	604	-	-	-	X
5	TRS	D	602	-	-	-	X

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 18504 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Invertase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	535	Total	C	N	O	S	0	0	0
			4146	2639	703	790	14			
1	B	536	Total	C	N	O	S	0	0	0
			4153	2643	704	792	14			
1	C	537	Total	C	N	O	S	0	0	0
			4159	2646	705	794	14			
1	D	535	Total	C	N	O	S	0	1	0
			4157	2645	707	791	14			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	81	ALA	ASP	engineered mutation	UNP A0A179H0Q0
B	81	ALA	ASP	engineered mutation	UNP A0A179H0Q0
C	81	ALA	ASP	engineered mutation	UNP A0A179H0Q0
D	81	ALA	ASP	engineered mutation	UNP A0A179H0Q0

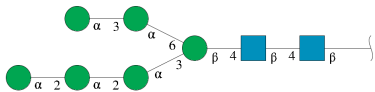
- Molecule 2 is an oligosaccharide called alpha-D-galactopyranose-(1-6)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	E	2	Total	C	O	0	0	0
			22	12	10			
2	I	2	Total	C	O	0	0	0
			22	12	10			

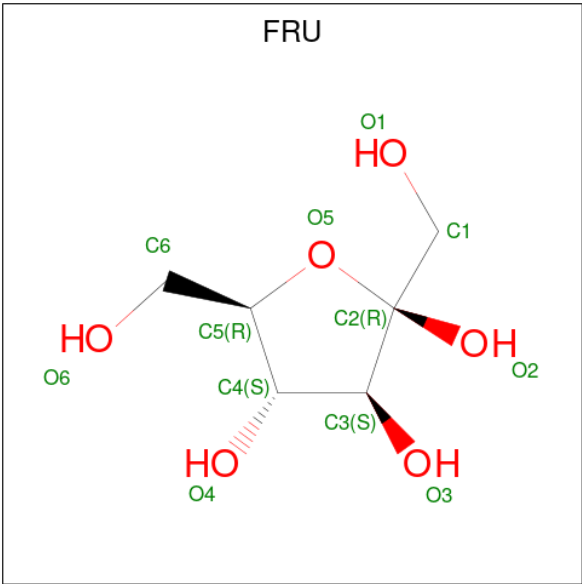
- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-alpha-D-mannopyra

nose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



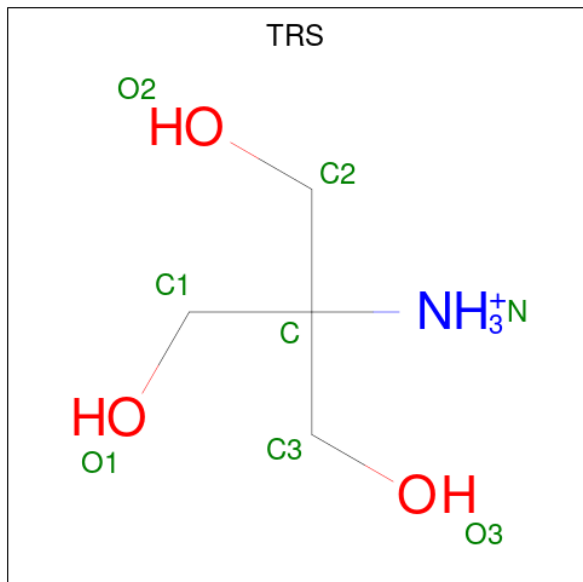
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	F	8	Total	C	N	O	0	0	0
			94	52	2	40			
3	G	8	Total	C	N	O	0	0	0
			94	52	2	40			
3	H	8	Total	C	N	O	0	0	0
			94	52	2	40			
3	J	8	Total	C	N	O	0	0	0
			94	52	2	40			

- Molecule 4 is beta-D-fructofuranose (CCD ID: FRU) (formula: C₆H₁₂O₆) (labeled as "Ligand of Interest" by depositor).



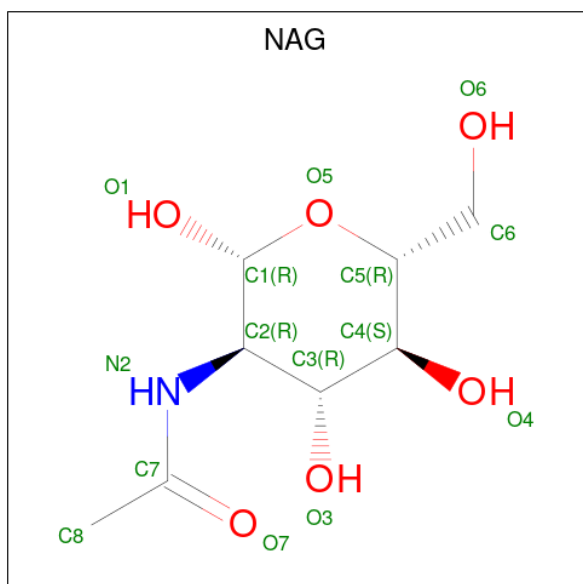
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			12	6	6		
4	B	1	Total	C	O	0	0
			12	6	6		
4	C	1	Total	C	O	0	0
			12	6	6		
4	D	1	Total	C	O	0	0
			12	6	6		

- Molecule 5 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: $C_4H_{12}NO_3$) (labeled as "Ligand of Interest" by depositor).



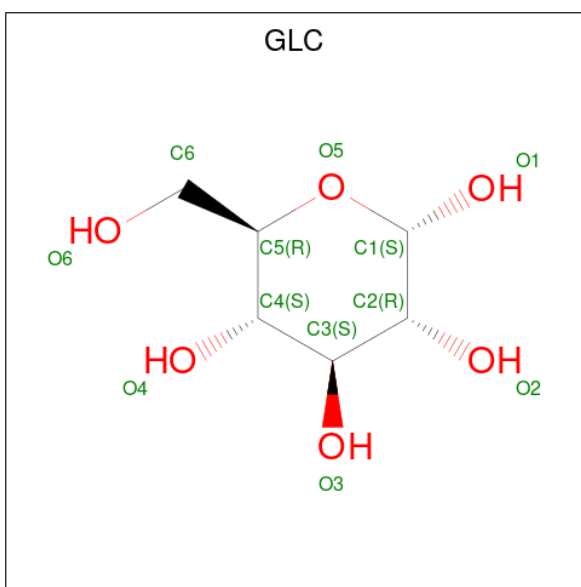
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			8	4	1	3		
5	C	1	Total	C	N	O	0	0
			8	4	1	3		
5	D	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$) (labeled as "Ligand of Interest" by depositor).



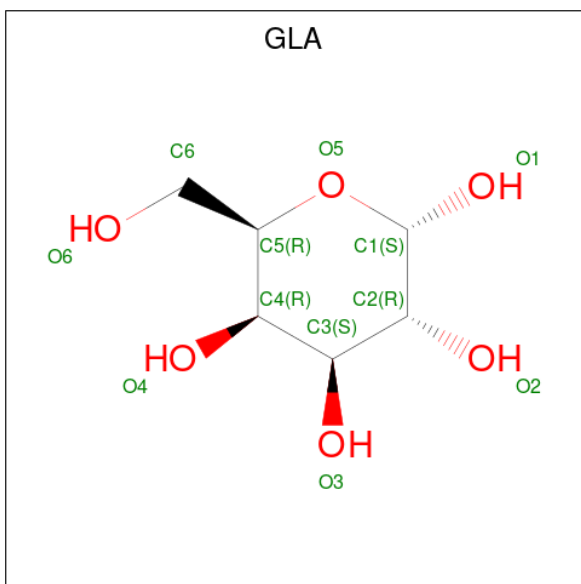
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1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

- Molecule 7 is alpha-D-glucopyranose (CCD ID: GLC) (formula: C₆H₁₂O₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			11	6	5		
7	C	1	Total	C	O	0	0
			11	6	5		

- Molecule 8 is alpha-D-galactopyranose (CCD ID: GLA) (formula: $C_6H_{12}O_6$) (labeled as "Ligand of Interest" by depositor).



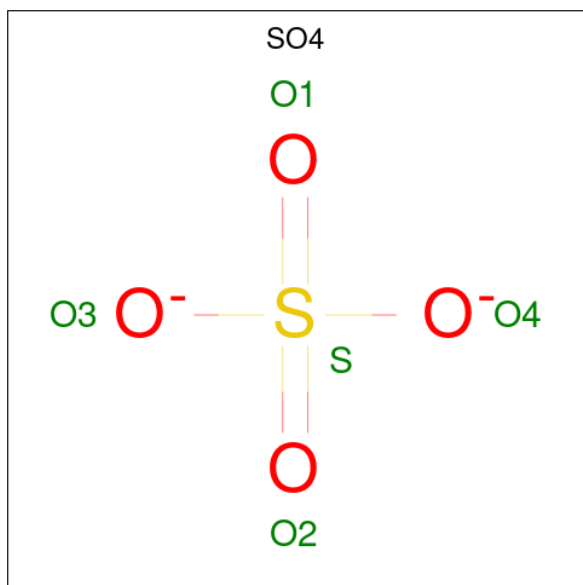
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			11	6	5		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	C	O	0	0
			11	6	5		

- Molecule 9 is SULFATE ION (CCD ID: SO4) (formula: O₄S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	O	S	0	0
			5	4	1		
9	C	1	Total	O	S	0	0
			5	4	1		
9	C	1	Total	O	S	0	0
			5	4	1		
9	D	1	Total	O	S	0	0
			5	4	1		
9	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	293	Total	O	0	0
			293	293		
10	B	272	Total	O	0	0
			272	272		
10	C	304	Total	O	0	0
			304	304		

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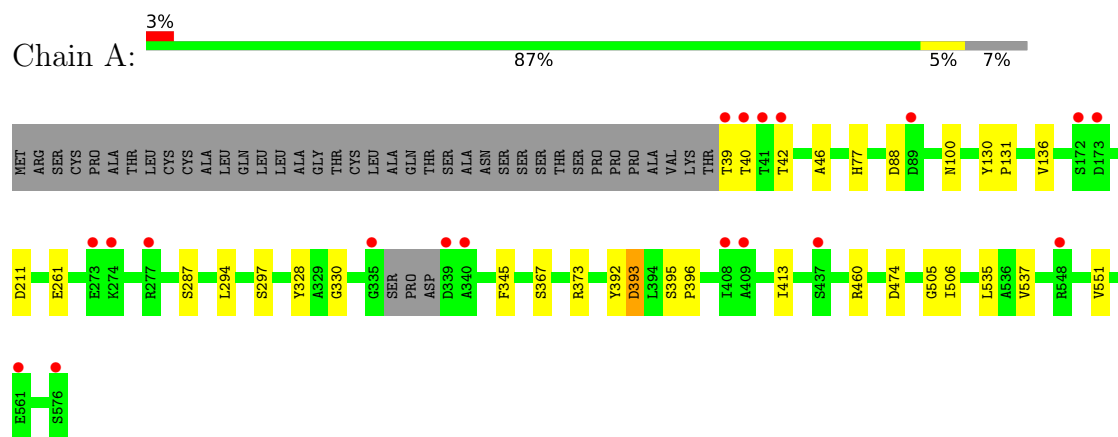
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	D	235	Total 235	O 235	0	0

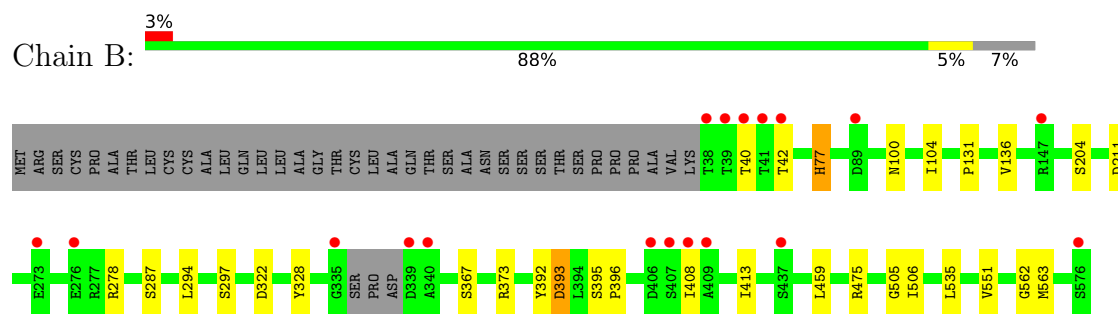
3 Residue-property plots [i](#)

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 and electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

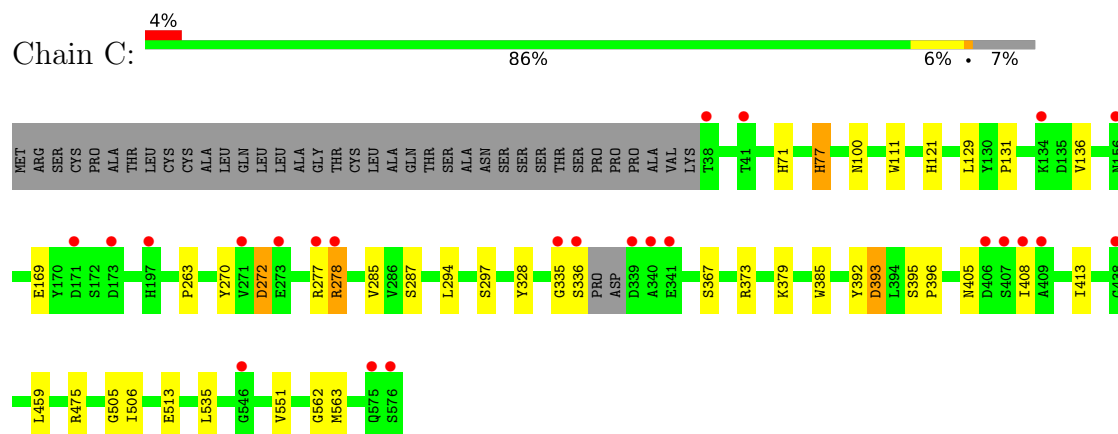
• Molecule 1: Invertase



• Molecule 1: Invertase

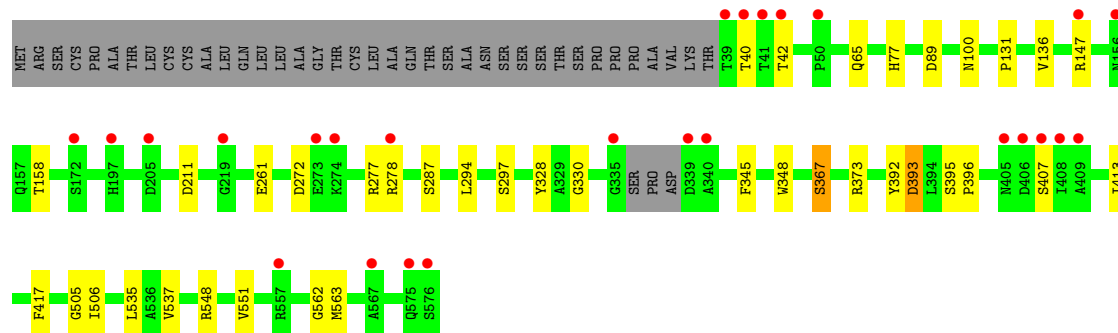


• Molecule 1: Invertase



- Molecule 1: Invertase

Chain D: 



- Molecule 2: alpha-D-galactopyranose-(1-6)-alpha-D-glucopyranose

Chain E: 



- Molecule 2: alpha-D-galactopyranose-(1-6)-alpha-D-glucopyranose

Chain I: 



- Molecule 3: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[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 F: 



- Molecule 3: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[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 G: 



- Molecule 3: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[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

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

Chain H:  88% 12%

MAG1	MAG2	BMA3	MAN4	MAN5	MAN6	MAN7	MAN8
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● Molecule 3: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[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 J:  25% 75%

MAG1	MAG2	BMA3	MAN4	MAN5	MAN6	MAN7	MAN8
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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	79.14Å 141.07Å 252.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.65 – 2.00 48.65 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.65-2.00) 100.0 (48.65-2.00)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.28 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, R_{free}	0.175 , 0.195 (Not available) , 0.178	Depositor DCC
R_{free} test set	9648 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	27.7	Xtriage
Anisotropy	0.015	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 33.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	18504	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.81% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: SO4, BMA, FRU, NAG, TRS, GLA, MAN, GLC

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	0.63	0/4286	0.94	1/5870 (0.0%)
1	B	0.61	0/4293	0.94	1/5880 (0.0%)
1	C	0.62	0/4299	0.94	1/5888 (0.0%)
1	D	0.60	0/4297	0.92	2/5884 (0.0%)
All	All	0.61	0/17175	0.94	5/23522 (0.0%)

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	B	0	1
1	C	0	2
1	D	0	2
All	All	0	5

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	322	ASP	CA-CB-CG	6.57	119.17	112.60
1	C	272	ASP	CA-CB-CG	6.15	118.75	112.60
1	D	272	ASP	CA-CB-CG	5.43	118.03	112.60
1	A	88	ASP	CA-CB-CG	5.11	117.71	112.60
1	D	417	PHE	CA-CB-CG	5.02	118.82	113.80

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	278	ARG	Sidechain
1	C	277	ARG	Sidechain
1	C	278	ARG	Sidechain
1	D	277	ARG	Sidechain
1	D	278	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	4146	0	3844	26	0
1	B	4153	0	3851	29	0
1	C	4159	0	3856	34	0
1	D	4157	0	3856	29	0
2	E	22	0	19	1	0
2	I	22	0	19	1	0
3	F	94	0	79	0	0
3	G	94	0	79	0	0
3	H	94	0	79	0	0
3	J	94	0	79	0	0
4	A	12	0	11	0	0
4	B	12	0	11	3	0
4	C	12	0	11	0	0
4	D	12	0	11	0	0
5	A	8	0	12	0	0
5	C	8	0	12	0	0
5	D	8	0	12	0	0
6	A	56	0	52	0	0
6	B	56	0	52	0	0
6	C	56	0	52	0	0
6	D	56	0	52	0	0
7	B	11	0	9	3	0
7	C	11	0	9	3	0
8	B	11	0	10	0	0
8	C	11	0	10	3	0
9	B	5	0	0	0	0
9	C	10	0	0	0	0
9	D	10	0	0	0	0
10	A	293	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	B	272	0	0	2	0
10	C	304	0	0	3	0
10	D	235	0	0	3	0
All	All	18504	0	16087	114	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (114) 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)
4:B:601:FRU:O2	7:B:602:GLC:C1	1.67	1.43
7:C:602:GLC:O6	8:C:603:GLA:C1	1.66	1.41
1:B:408:ILE:HD11	1:B:551:VAL:CG1	1.77	1.14
1:D:89:ASP:HB3	1:D:147:ARG:HH22	1.05	1.09
1:B:535:LEU:HD21	1:C:535:LEU:HD21	1.35	1.09
1:A:535:LEU:HD21	1:D:535:LEU:HD21	1.40	1.03
1:B:408:ILE:HD11	1:B:551:VAL:HG11	1.39	1.01
1:D:147:ARG:HD3	1:D:158:THR:O	1.65	0.96
1:B:408:ILE:CD1	1:B:551:VAL:CG1	2.48	0.92
1:A:40:THR:HG22	1:A:42:THR:H	1.37	0.90
1:B:408:ILE:HD11	1:B:551:VAL:HG12	1.51	0.89
7:C:602:GLC:C6	8:C:603:GLA:C1	2.54	0.86
1:B:408:ILE:CD1	1:B:551:VAL:HG12	2.06	0.85
1:D:89:ASP:HB3	1:D:147:ARG:NH2	1.91	0.84
4:B:601:FRU:C2	7:B:602:GLC:C1	2.59	0.79
1:D:89:ASP:CB	1:D:147:ARG:HH22	1.93	0.75
1:D:40:THR:HG22	1:D:42:THR:H	1.53	0.74
1:C:270:TYR:OH	1:C:278:ARG:NH1	2.23	0.72
1:A:39:THR:HG21	10:A:763:HOH:O	1.89	0.71
1:B:408:ILE:CD1	1:B:551:VAL:HG11	2.17	0.70
1:C:294:LEU:HD23	1:D:294:LEU:HD23	1.74	0.69
1:B:408:ILE:HG22	1:B:408:ILE:O	1.91	0.68
1:A:294:LEU:HD23	1:B:294:LEU:HD23	1.77	0.66
1:C:272:ASP:HB3	1:C:278:ARG:NE	2.12	0.64
1:D:131:PRO:HB3	1:D:136:VAL:O	1.99	0.62
1:A:131:PRO:HB3	1:A:136:VAL:O	2.00	0.61
1:C:131:PRO:HB3	1:C:136:VAL:O	2.01	0.60
1:C:272:ASP:HB3	1:C:278:ARG:CZ	2.32	0.60
1:B:408:ILE:HD11	1:B:413:ILE:HG13	1.84	0.60
1:C:77:HIS:HE1	10:C:839:HOH:O	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:39:THR:HG22	1:A:40:THR:H	1.67	0.59
1:B:535:LEU:CD2	1:C:535:LEU:HD21	2.22	0.58
1:C:405:ASN:HB3	1:C:408:ILE:HD11	1.84	0.58
1:B:40:THR:HG22	1:B:42:THR:H	1.68	0.58
1:B:408:ILE:O	1:B:408:ILE:CG2	2.51	0.58
1:C:270:TYR:CE2	1:C:278:ARG:HD2	2.39	0.58
1:A:77:HIS:HD2	10:A:967:HOH:O	1.89	0.56
1:D:77:HIS:HE1	10:D:866:HOH:O	1.88	0.56
1:C:287:SER:HB3	1:C:328:TYR:CE1	2.42	0.55
1:D:65:GLN:NE2	10:D:703:HOH:O	2.39	0.54
1:C:272:ASP:CB	1:C:278:ARG:NH1	2.71	0.54
1:C:297:SER:HB2	1:C:328:TYR:CD1	2.43	0.54
1:A:297:SER:HB2	1:A:328:TYR:CD1	2.44	0.53
1:D:297:SER:HB2	1:D:328:TYR:CD1	2.44	0.52
1:C:272:ASP:HB3	1:C:278:ARG:NH1	2.25	0.52
1:B:131:PRO:HB3	1:B:136:VAL:O	2.10	0.52
1:B:297:SER:HB2	1:B:328:TYR:CD1	2.45	0.52
1:C:335:GLY:O	1:C:336:SER:C	2.52	0.51
1:B:287:SER:HB3	1:B:328:TYR:CE1	2.45	0.51
1:A:535:LEU:CD2	1:D:535:LEU:HD21	2.27	0.51
1:D:287:SER:HB3	1:D:328:TYR:CE1	2.46	0.50
7:C:602:GLC:O6	8:C:603:GLA:C2	2.53	0.50
1:A:287:SER:HB3	1:A:328:TYR:CE1	2.47	0.50
1:A:77:HIS:HE1	10:A:958:HOH:O	1.94	0.49
1:A:535:LEU:HD21	1:D:535:LEU:CD2	2.27	0.48
1:A:413:ILE:HG13	1:A:551:VAL:HG11	1.95	0.48
1:B:408:ILE:HD12	1:B:551:VAL:HG12	1.90	0.47
1:D:77:HIS:HD2	10:D:914:HOH:O	1.98	0.47
1:D:562:GLY:C	1:D:563:MET:HE2	2.38	0.47
1:C:562:GLY:C	1:C:563:MET:HE2	2.40	0.46
1:A:261:GLU:OE1	2:E:1:GLC:H3	2.15	0.46
1:C:405:ASN:ND2	10:C:708:HOH:O	2.49	0.46
1:B:77:HIS:HE1	10:B:722:HOH:O	1.97	0.46
1:C:379:LYS:HE2	1:C:385:TRP:CE2	2.49	0.46
1:B:505:GLY:C	1:B:506:ILE:HD12	2.41	0.46
1:C:272:ASP:CB	1:C:278:ARG:CZ	2.94	0.45
1:C:272:ASP:HB2	1:C:278:ARG:NH1	2.31	0.45
1:A:505:GLY:C	1:A:506:ILE:HD12	2.42	0.45
1:D:413:ILE:HG13	1:D:551:VAL:HG11	1.98	0.45
1:B:562:GLY:C	1:B:563:MET:HE2	2.42	0.45
1:D:261:GLU:OE1	2:I:1:GLC:H3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:71:HIS:NE2	1:C:513:GLU:OE1	2.46	0.44
1:B:395:SER:N	1:B:396:PRO:CD	2.80	0.44
1:D:147:ARG:NH1	1:D:158:THR:O	2.51	0.44
1:B:77:HIS:HB3	1:B:100:ASN:O	2.17	0.44
1:C:169:GLU:HG3	10:C:875:HOH:O	2.17	0.44
1:C:505:GLY:C	1:C:506:ILE:HD12	2.43	0.44
4:B:601:FRU:O2	7:B:602:GLC:C2	2.56	0.44
1:C:459:LEU:HD12	1:C:475:ARG:HA	1.99	0.43
1:B:392:TYR:O	1:B:393:ASP:C	2.60	0.43
1:D:392:TYR:O	1:D:393:ASP:C	2.61	0.43
1:D:505:GLY:C	1:D:506:ILE:HD12	2.43	0.43
1:A:373:ARG:HH21	1:A:373:ARG:CG	2.32	0.43
1:A:395:SER:N	1:A:396:PRO:CD	2.82	0.43
1:A:537:VAL:HG21	1:D:535:LEU:HD22	2.00	0.43
1:C:392:TYR:O	1:C:393:ASP:C	2.62	0.43
1:A:535:LEU:HD22	1:D:537:VAL:HG21	2.00	0.42
1:C:413:ILE:HG13	1:C:551:VAL:HG11	2.01	0.42
1:B:459:LEU:HD12	1:B:475:ARG:HA	2.01	0.42
1:A:77:HIS:HB3	1:A:100:ASN:O	2.19	0.42
1:B:373:ARG:HH21	1:B:373:ARG:CG	2.33	0.42
1:A:392:TYR:O	1:A:393:ASP:C	2.63	0.42
1:A:39:THR:HG22	1:A:40:THR:N	2.33	0.42
1:C:77:HIS:HB3	1:C:100:ASN:O	2.18	0.42
1:C:373:ARG:HH21	1:C:373:ARG:HG3	1.85	0.42
1:C:395:SER:N	1:C:396:PRO:CD	2.83	0.41
1:C:121:HIS:HD2	1:C:563:MET:HE3	1.85	0.41
1:C:373:ARG:HH21	1:C:373:ARG:CG	2.33	0.41
1:D:77:HIS:HB3	1:D:100:ASN:O	2.21	0.41
1:B:77:HIS:HD2	10:B:947:HOH:O	2.03	0.41
1:A:460:ARG:HG3	1:A:474:ASP:HB3	2.01	0.41
1:D:395:SER:N	1:D:396:PRO:CD	2.84	0.41
1:B:104:ILE:HD12	1:B:104:ILE:HA	1.94	0.41
1:C:111:TRP:CD2	1:C:129:LEU:HD12	2.56	0.41
1:D:407:SER:OG	1:D:548:ARG:HD2	2.21	0.41
1:A:46:ALA:HB1	1:A:130:TYR:HB2	2.03	0.41
1:A:373:ARG:HH21	1:A:373:ARG:HG3	1.86	0.41
1:D:348:TRP:HE1	1:D:367:SER:HB3	1.86	0.41
1:D:373:ARG:CG	1:D:373:ARG:HH21	2.33	0.41
1:D:330:GLY:HA3	1:D:345:PHE:CZ	2.56	0.40
1:B:535:LEU:HD21	1:C:535:LEU:CD2	2.26	0.40
1:A:330:GLY:HA3	1:A:345:PHE:CZ	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:413:ILE:HG13	1:B:551:VAL:HG11	2.03	0.40
1:C:263:PRO:HA	1:C:285:VAL:O	2.22	0.40

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 X-ray entries followed by that with respect to entries of similar resolution.

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	531/576 (92%)	509 (96%)	19 (4%)	3 (1%)	21	17
1	B	532/576 (92%)	508 (96%)	20 (4%)	4 (1%)	16	11
1	C	533/576 (92%)	511 (96%)	19 (4%)	3 (1%)	21	17
1	D	532/576 (92%)	510 (96%)	19 (4%)	3 (1%)	21	17
All	All	2128/2304 (92%)	2038 (96%)	77 (4%)	13 (1%)	21	17

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	367	SER
1	A	393	ASP
1	B	367	SER
1	B	393	ASP
1	C	367	SER
1	C	393	ASP
1	D	367	SER
1	D	393	ASP
1	B	77	HIS
1	C	77	HIS
1	B	211	ASP
1	A	211	ASP
1	D	211	ASP

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 X-ray entries followed by that with respect to entries of similar resolution.

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	440/474 (93%)	440 (100%)	0	100	100
1	B	441/474 (93%)	440 (100%)	1 (0%)	87	92
1	C	442/474 (93%)	442 (100%)	0	100	100
1	D	441/474 (93%)	441 (100%)	0	100	100
All	All	1764/1896 (93%)	1763 (100%)	1 (0%)	88	92

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	204	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	65	GLN
1	A	69	GLN
1	A	77	HIS
1	A	80	ASN
1	A	98	GLN
1	A	197	HIS
1	A	220	HIS
1	A	253	HIS
1	B	65	GLN
1	B	77	HIS
1	B	80	ASN
1	B	98	GLN
1	B	197	HIS
1	B	220	HIS
1	B	423	ASN
1	B	531	GLN
1	C	77	HIS
1	C	98	GLN

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Mol	Chain	Res	Type
1	C	156	ASN
1	C	423	ASN
1	C	575	GLN
1	D	65	GLN
1	D	77	HIS
1	D	80	ASN
1	D	98	GLN
1	D	289	ASN
1	D	423	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

36 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	GLC	E	1	2	11,11,12	0.67	0	15,15,17	0.81	1 (6%)
2	GLA	E	2	2	11,11,12	0.69	0	15,15,17	0.88	1 (6%)
3	NAG	F	1	1,3	14,14,15	0.52	0	17,19,21	0.86	1 (5%)
3	NAG	F	2	3	14,14,15	0.43	0	17,19,21	0.65	0
3	BMA	F	3	3	11,11,12	0.95	1 (9%)	15,15,17	0.71	0
3	MAN	F	4	3	11,11,12	0.54	0	15,15,17	1.08	3 (20%)
3	MAN	F	5	3	11,11,12	1.09	1 (9%)	15,15,17	0.69	0
3	MAN	F	6	3	11,11,12	1.09	0	15,15,17	1.05	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	MAN	F	7	3	11,11,12	1.14	1 (9%)	15,15,17	0.83	0
3	MAN	F	8	3	11,11,12	0.62	0	15,15,17	0.58	0
3	NAG	G	1	1,3	14,14,15	0.47	0	17,19,21	0.95	0
3	NAG	G	2	3	14,14,15	0.33	0	17,19,21	0.63	0
3	BMA	G	3	3	11,11,12	1.09	1 (9%)	15,15,17	0.72	0
3	MAN	G	4	3	11,11,12	0.59	0	15,15,17	0.79	0
3	MAN	G	5	3	11,11,12	0.72	0	15,15,17	0.76	0
3	MAN	G	6	3	11,11,12	0.87	0	15,15,17	0.62	0
3	MAN	G	7	3	11,11,12	1.08	1 (9%)	15,15,17	0.67	0
3	MAN	G	8	3	11,11,12	0.71	0	15,15,17	0.66	0
3	NAG	H	1	1,3	14,14,15	0.36	0	17,19,21	0.63	0
3	NAG	H	2	3	14,14,15	0.48	0	17,19,21	0.69	0
3	BMA	H	3	3	11,11,12	0.61	0	15,15,17	0.81	0
3	MAN	H	4	3	11,11,12	0.78	0	15,15,17	0.89	0
3	MAN	H	5	3	11,11,12	0.88	0	15,15,17	0.75	0
3	MAN	H	6	3	11,11,12	0.72	0	15,15,17	0.88	0
3	MAN	H	7	3	11,11,12	0.88	1 (9%)	15,15,17	0.75	0
3	MAN	H	8	3	11,11,12	0.74	0	15,15,17	0.62	0
2	GLC	I	1	2	11,11,12	0.62	0	15,15,17	0.89	1 (6%)
2	GLA	I	2	2	11,11,12	0.62	0	15,15,17	0.92	1 (6%)
3	NAG	J	1	1,3	14,14,15	0.38	0	17,19,21	0.84	1 (5%)
3	NAG	J	2	3	14,14,15	0.41	0	17,19,21	0.67	0
3	BMA	J	3	3	11,11,12	0.84	0	15,15,17	0.93	1 (6%)
3	MAN	J	4	3	11,11,12	0.64	0	15,15,17	1.08	2 (13%)
3	MAN	J	5	3	11,11,12	0.92	1 (9%)	15,15,17	0.98	1 (6%)
3	MAN	J	6	3	11,11,12	1.22	1 (9%)	15,15,17	0.56	0
3	MAN	J	7	3	11,11,12	0.69	1 (9%)	15,15,17	0.68	0
3	MAN	J	8	3	11,11,12	0.87	0	15,15,17	0.74	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	GLC	E	1	2	-	0/2/19/22	0/1/1/1
2	GLA	E	2	2	-	0/2/19/22	0/1/1/1
3	NAG	F	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	F	2	3	-	0/6/23/26	0/1/1/1
3	BMA	F	3	3	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MAN	F	4	3	-	0/2/19/22	0/1/1/1
3	MAN	F	5	3	-	0/2/19/22	0/1/1/1
3	MAN	F	6	3	-	0/2/19/22	0/1/1/1
3	MAN	F	7	3	-	0/2/19/22	0/1/1/1
3	MAN	F	8	3	-	0/2/19/22	0/1/1/1
3	NAG	G	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	G	2	3	-	0/6/23/26	0/1/1/1
3	BMA	G	3	3	-	0/2/19/22	0/1/1/1
3	MAN	G	4	3	-	1/2/19/22	0/1/1/1
3	MAN	G	5	3	-	0/2/19/22	0/1/1/1
3	MAN	G	6	3	-	0/2/19/22	0/1/1/1
3	MAN	G	7	3	-	0/2/19/22	0/1/1/1
3	MAN	G	8	3	-	0/2/19/22	0/1/1/1
3	NAG	H	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	H	2	3	-	0/6/23/26	0/1/1/1
3	BMA	H	3	3	-	0/2/19/22	0/1/1/1
3	MAN	H	4	3	-	0/2/19/22	0/1/1/1
3	MAN	H	5	3	-	0/2/19/22	0/1/1/1
3	MAN	H	6	3	-	0/2/19/22	0/1/1/1
3	MAN	H	7	3	-	0/2/19/22	0/1/1/1
3	MAN	H	8	3	-	0/2/19/22	0/1/1/1
2	GLC	I	1	2	-	0/2/19/22	0/1/1/1
2	GLA	I	2	2	-	0/2/19/22	0/1/1/1
3	NAG	J	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	J	2	3	-	0/6/23/26	0/1/1/1
3	BMA	J	3	3	-	0/2/19/22	0/1/1/1
3	MAN	J	4	3	-	0/2/19/22	0/1/1/1
3	MAN	J	5	3	-	1/2/19/22	0/1/1/1
3	MAN	J	6	3	-	0/2/19/22	0/1/1/1
3	MAN	J	7	3	-	0/2/19/22	0/1/1/1
3	MAN	J	8	3	-	0/2/19/22	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	J	6	MAN	C2-C3	-3.39	1.47	1.52
3	G	7	MAN	O5-C5	3.32	1.49	1.43
3	F	7	MAN	O5-C5	3.10	1.49	1.43
3	F	5	MAN	O5-C5	2.67	1.48	1.43
3	H	7	MAN	O5-C5	2.58	1.48	1.43
3	G	3	BMA	C2-C3	-2.56	1.48	1.52
3	F	3	BMA	O5-C5	2.52	1.48	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	J	5	MAN	C2-C3	-2.09	1.49	1.52
3	J	7	MAN	O5-C5	2.01	1.47	1.43

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	3	BMA	O2-C2-C3	2.98	116.33	110.15
2	I	1	GLC	C1-C2-C3	2.56	113.37	109.64
3	F	6	MAN	C1-O5-C5	-2.54	108.78	112.19
2	E	2	GLA	C1-O5-C5	2.54	115.59	112.19
3	F	1	NAG	C2-N2-C7	2.47	126.22	122.90
3	J	4	MAN	C1-C2-C3	2.44	113.20	109.64
2	E	1	GLC	C1-C2-C3	2.43	113.18	109.64
2	I	2	GLA	C1-O5-C5	2.28	115.24	112.19
3	F	4	MAN	C1-O5-C5	2.25	115.20	112.19
3	J	5	MAN	C1-O5-C5	2.18	115.11	112.19
3	J	4	MAN	C1-O5-C5	2.10	115.01	112.19
3	J	1	NAG	C1-O5-C5	2.08	114.97	112.19
3	F	4	MAN	C1-C2-C3	2.04	112.62	109.64
3	F	6	MAN	O5-C5-C4	-2.04	105.86	110.83
3	F	4	MAN	O3-C3-C2	-2.02	105.93	110.05

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	G	4	MAN	O5-C5-C6-O6
3	J	5	MAN	O5-C5-C6-O6

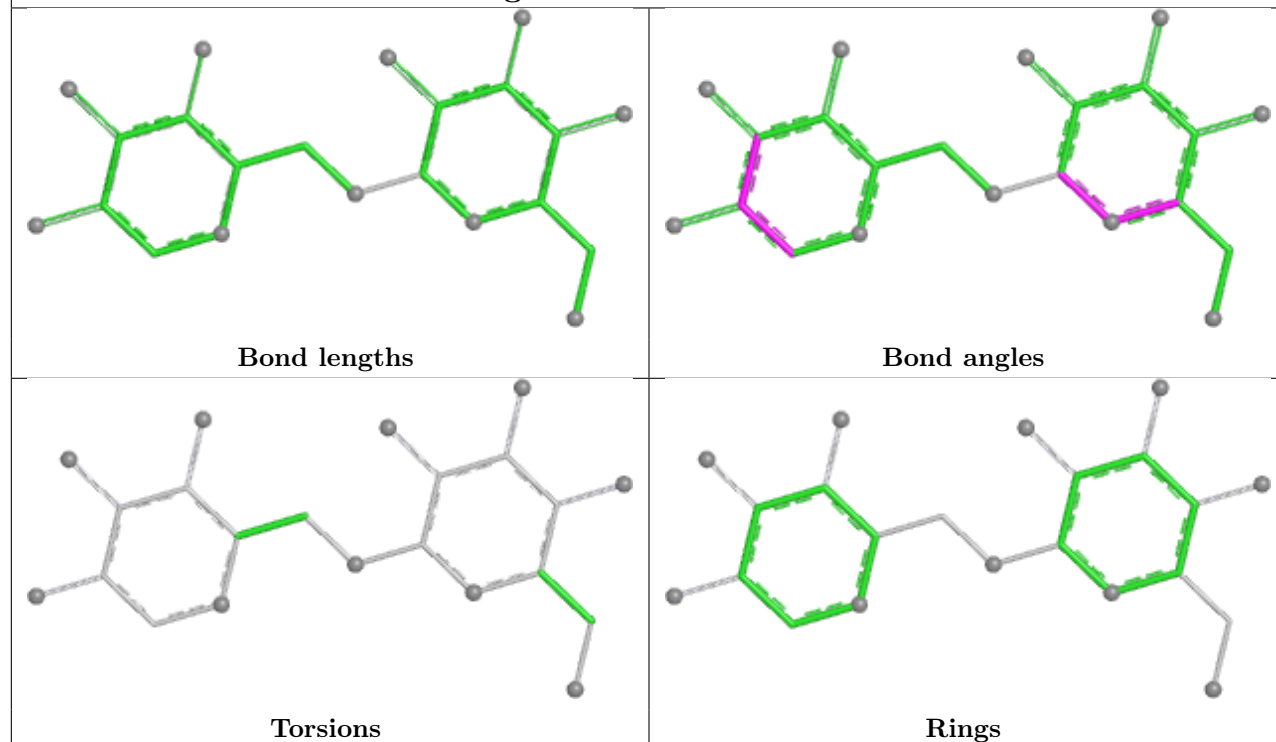
There are no ring outliers.

2 monomers are involved in 2 short contacts:

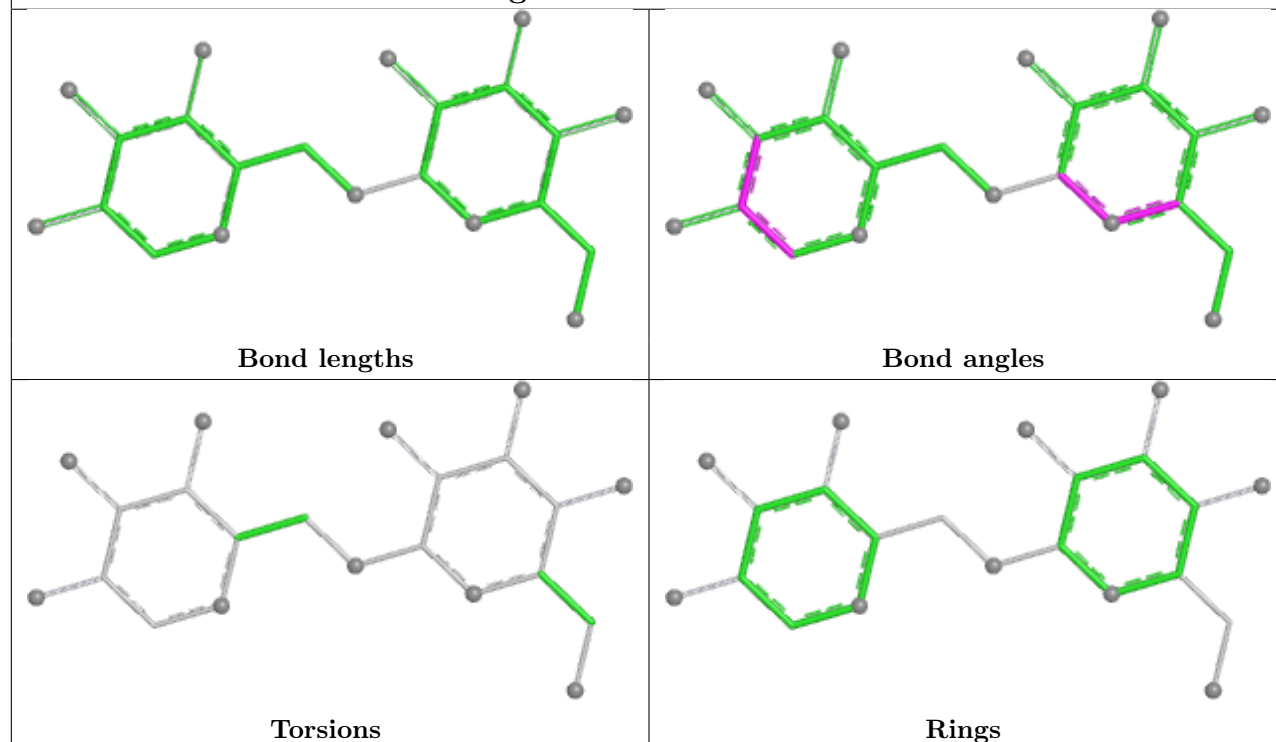
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	I	1	GLC	1	0
2	E	1	GLC	1	0

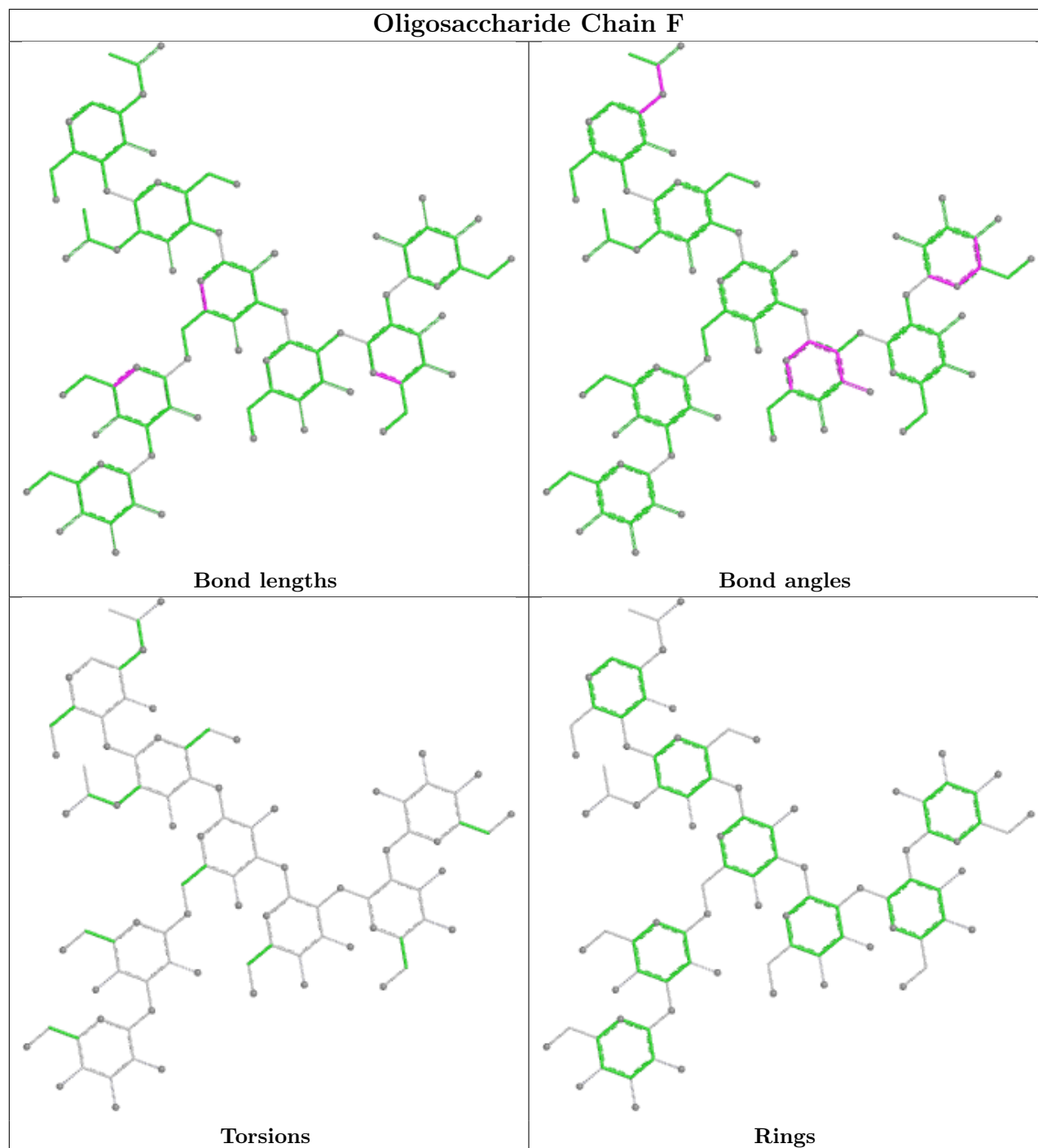
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

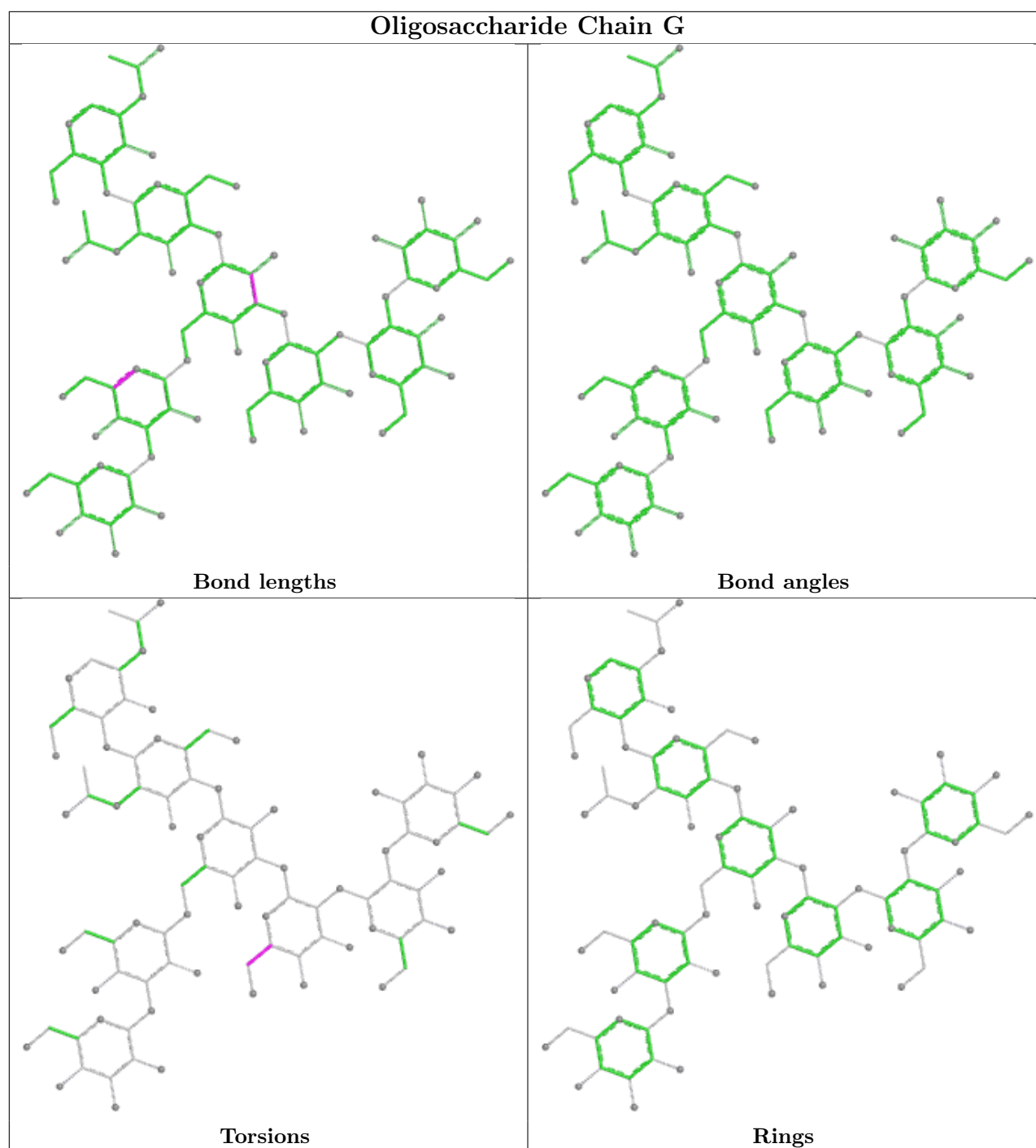
Oligosaccharide Chain E



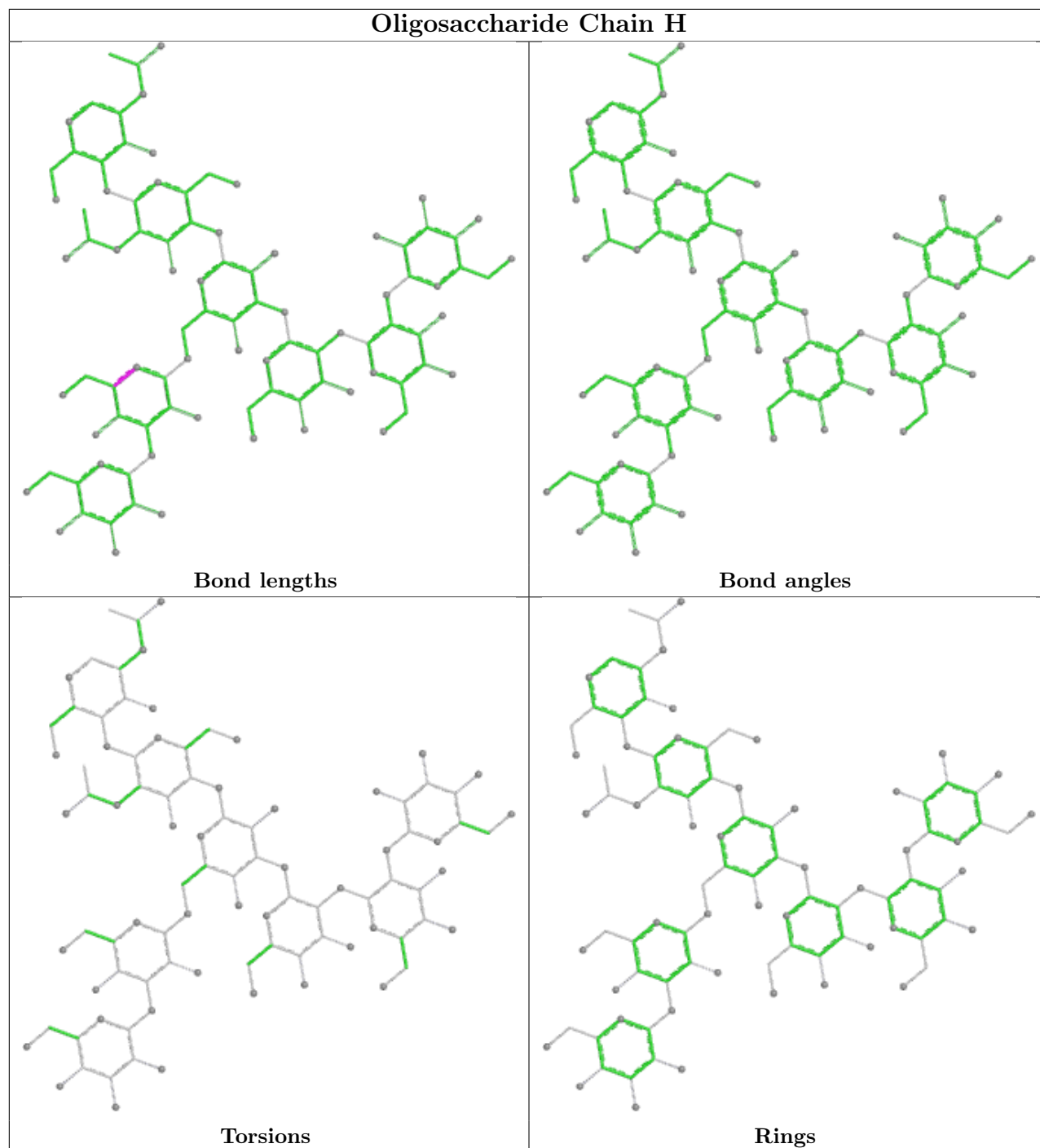
Oligosaccharide Chain I

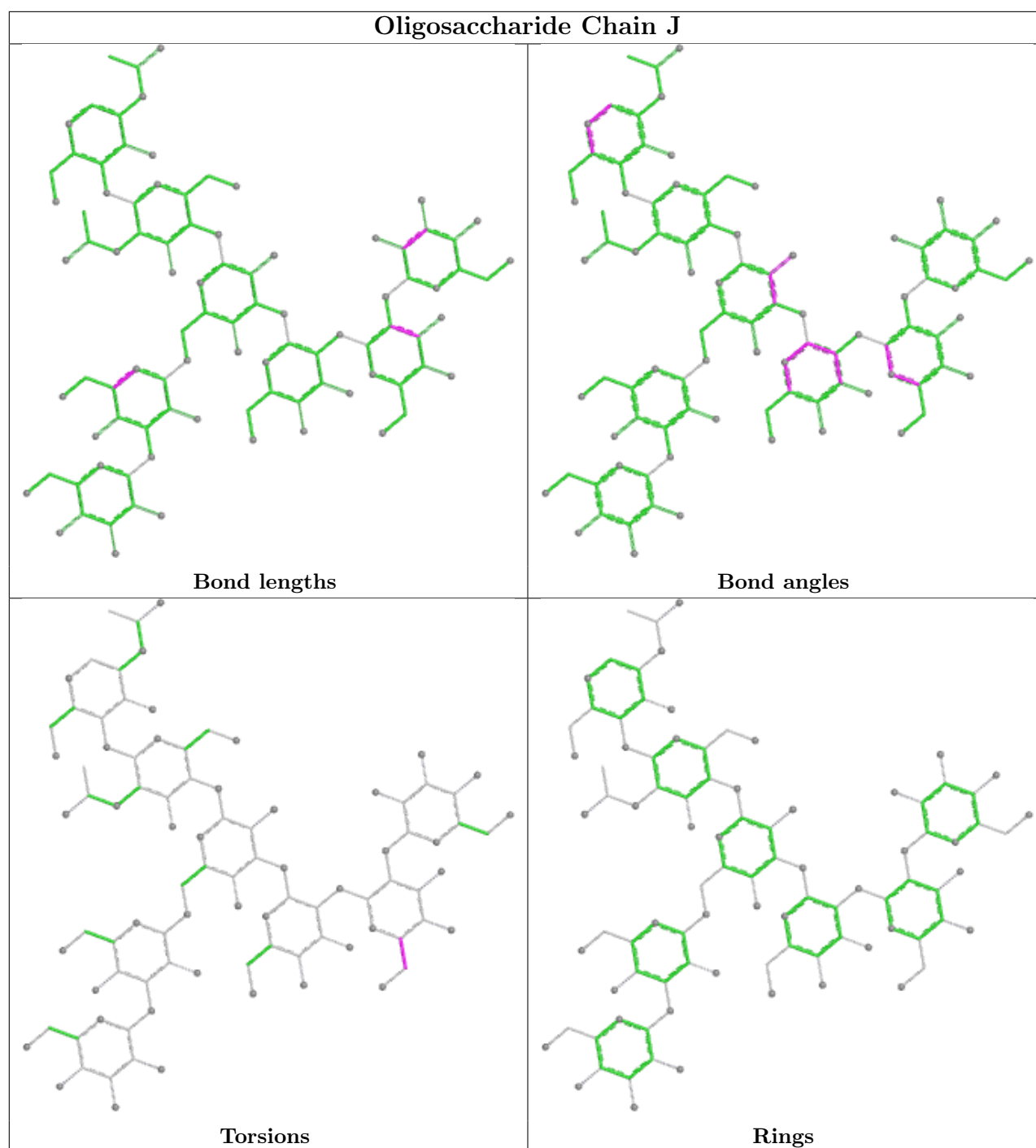






Oligosaccharide Chain H





5.6 Ligand geometry [i](#)

32 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	$\# Z > 2$
7	GLC	B	602	-	11,11,12	0.73	0	15,15,17	0.69	0
6	NAG	A	605	1	14,14,15	0.56	0	17,19,21	0.93	1 (5%)
6	NAG	C	609	1	14,14,15	0.46	0	17,19,21	1.28	2 (11%)
6	NAG	A	603	1	14,14,15	0.51	0	17,19,21	0.82	0
6	NAG	B	608	1	14,14,15	0.42	0	17,19,21	0.90	1 (5%)
9	SO4	B	604	-	4,4,4	0.54	0	6,6,6	0.25	0
9	SO4	C	605	-	4,4,4	0.41	0	6,6,6	0.32	0
7	GLC	C	602	-	11,11,12	0.57	0	15,15,17	0.89	1 (6%)
6	NAG	A	606	1	14,14,15	0.47	0	17,19,21	0.98	1 (5%)
6	NAG	C	607	1	14,14,15	0.43	0	17,19,21	0.79	0
6	NAG	C	610	1	14,14,15	0.62	1 (7%)	17,19,21	1.02	1 (5%)
6	NAG	C	608	1	14,14,15	0.45	0	17,19,21	1.06	1 (5%)
6	NAG	B	606	1	14,14,15	0.54	0	17,19,21	1.01	1 (5%)
9	SO4	D	604	-	4,4,4	0.47	0	6,6,6	0.25	0
6	NAG	D	608	1	14,14,15	0.44	0	17,19,21	1.16	2 (11%)
6	NAG	A	604	1	14,14,15	0.49	0	17,19,21	0.80	0
4	FRU	A	601	-	11,12,12	0.41	0	10,18,18	0.52	0
8	GLA	C	603	-	11,11,12	0.41	0	15,15,17	0.83	0
6	NAG	B	607	1	14,14,15	0.55	0	17,19,21	1.31	1 (5%)
6	NAG	B	605	1	14,14,15	0.48	0	17,19,21	1.00	2 (11%)
9	SO4	D	603	-	4,4,4	0.33	0	6,6,6	0.35	0
4	FRU	B	601	-	11,12,12	0.55	0	10,18,18	0.53	0
4	FRU	D	601	-	11,12,12	0.63	0	10,18,18	0.52	0
6	NAG	D	607	1	14,14,15	0.36	0	17,19,21	1.37	3 (17%)
8	GLA	B	603	-	11,11,12	0.55	0	15,15,17	0.98	1 (6%)
5	TRS	C	604	-	7,7,7	0.28	0	9,9,9	0.82	0
6	NAG	D	605	1	14,14,15	0.47	0	17,19,21	0.80	1 (5%)
4	FRU	C	601	-	11,12,12	0.49	0	10,18,18	0.67	0
6	NAG	D	606	1	14,14,15	0.49	0	17,19,21	0.99	1 (5%)
5	TRS	A	602	-	7,7,7	0.23	0	9,9,9	0.73	0
5	TRS	D	602	-	7,7,7	0.35	0	9,9,9	0.76	0
9	SO4	C	606	-	4,4,4	0.34	0	6,6,6	0.55	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
7	GLC	B	602	-	-	0/2/19/22	0/1/1/1
6	NAG	A	605	1	-	0/6/23/26	0/1/1/1
6	NAG	C	609	1	-	2/6/23/26	0/1/1/1
6	NAG	A	603	1	-	0/6/23/26	0/1/1/1
6	NAG	B	608	1	-	0/6/23/26	0/1/1/1
7	GLC	C	602	-	-	0/2/19/22	0/1/1/1
6	NAG	A	606	1	-	0/6/23/26	0/1/1/1
6	NAG	C	607	1	-	0/6/23/26	0/1/1/1
6	NAG	C	610	1	-	0/6/23/26	0/1/1/1
6	NAG	C	608	1	-	0/6/23/26	0/1/1/1
6	NAG	B	606	1	-	0/6/23/26	0/1/1/1
6	NAG	D	608	1	-	0/6/23/26	0/1/1/1
6	NAG	A	604	1	-	0/6/23/26	0/1/1/1
4	FRU	A	601	-	-	1/5/24/24	0/1/1/1
8	GLA	C	603	-	-	0/2/19/22	0/1/1/1
6	NAG	B	607	1	-	2/6/23/26	0/1/1/1
6	NAG	B	605	1	-	0/6/23/26	0/1/1/1
4	FRU	B	601	-	-	1/5/24/24	0/1/1/1
4	FRU	D	601	-	-	1/5/24/24	0/1/1/1
6	NAG	D	607	1	-	0/6/23/26	0/1/1/1
8	GLA	B	603	-	-	0/2/19/22	0/1/1/1
5	TRS	C	604	-	-	0/9/9/9	-
6	NAG	D	605	1	-	0/6/23/26	0/1/1/1
4	FRU	C	601	-	-	1/5/24/24	0/1/1/1
6	NAG	D	606	1	-	0/6/23/26	0/1/1/1
5	TRS	A	602	-	-	6/9/9/9	-
5	TRS	D	602	-	-	3/9/9/9	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	610	NAG	C1-C2	2.02	1.55	1.52

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	607	NAG	C2-N2-C7	3.87	128.09	122.90
6	D	607	NAG	C2-N2-C7	3.45	127.53	122.90
6	A	606	NAG	C2-N2-C7	3.24	127.25	122.90
8	B	603	GLA	C1-O5-C5	3.02	116.24	112.19
6	C	608	NAG	C1-O5-C5	2.98	116.18	112.19
6	D	608	NAG	C1-C2-N2	2.98	115.13	110.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	609	NAG	C2-N2-C7	2.74	126.57	122.90
6	D	608	NAG	C1-O5-C5	2.68	115.77	112.19
6	B	605	NAG	O3-C3-C2	-2.63	103.95	109.40
6	D	607	NAG	C1-O5-C5	2.54	115.59	112.19
6	B	606	NAG	O3-C3-C2	-2.51	104.18	109.40
6	C	610	NAG	C1-C2-N2	2.49	114.36	110.43
6	D	607	NAG	O3-C3-C2	-2.44	104.33	109.40
6	C	609	NAG	C1-O5-C5	2.34	115.33	112.19
6	A	605	NAG	O4-C4-C3	-2.31	104.93	110.38
6	B	605	NAG	C1-O5-C5	2.28	115.24	112.19
6	D	606	NAG	C1-C2-N2	2.22	113.93	110.43
6	D	605	NAG	C1-O5-C5	2.20	115.14	112.19
7	C	602	GLC	C1-O5-C5	2.14	115.05	112.19
6	B	608	NAG	C2-N2-C7	2.01	125.60	122.90

There are no chirality outliers.

All (17) torsion outliers are listed below:

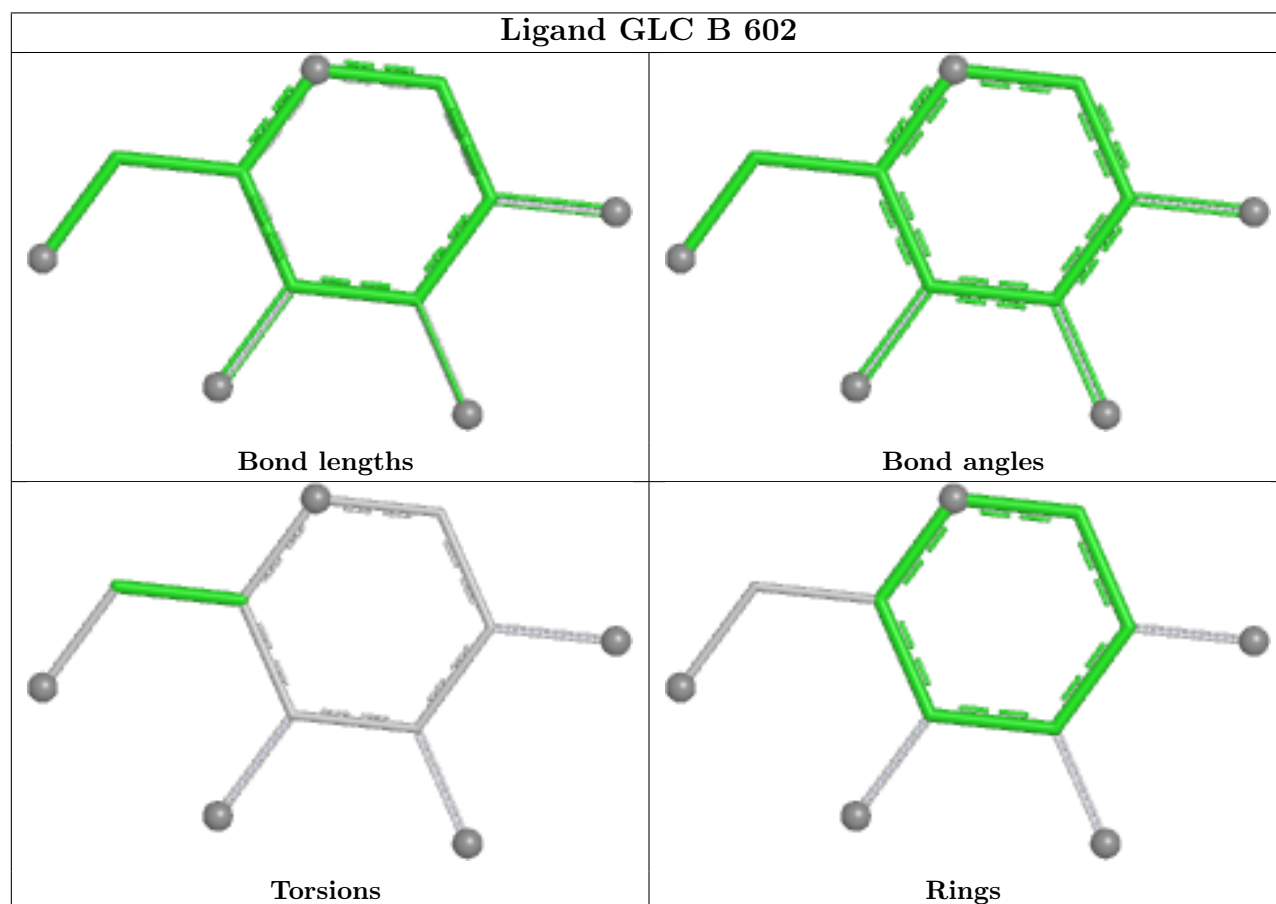
Mol	Chain	Res	Type	Atoms
5	A	602	TRS	N-C-C1-O1
5	D	602	TRS	N-C-C2-O2
6	B	607	NAG	C8-C7-N2-C2
6	B	607	NAG	O7-C7-N2-C2
6	C	609	NAG	C8-C7-N2-C2
6	C	609	NAG	O7-C7-N2-C2
5	A	602	TRS	C3-C-C1-O1
5	D	602	TRS	C1-C-C2-O2
4	D	601	FRU	O1-C1-C2-C3
5	A	602	TRS	N-C-C3-O3
5	A	602	TRS	C2-C-C1-O1
5	A	602	TRS	C3-C-C2-O2
5	D	602	TRS	C3-C-C2-O2
4	A	601	FRU	O1-C1-C2-C3
4	C	601	FRU	O1-C1-C2-C3
5	A	602	TRS	N-C-C2-O2
4	B	601	FRU	O1-C1-C2-C3

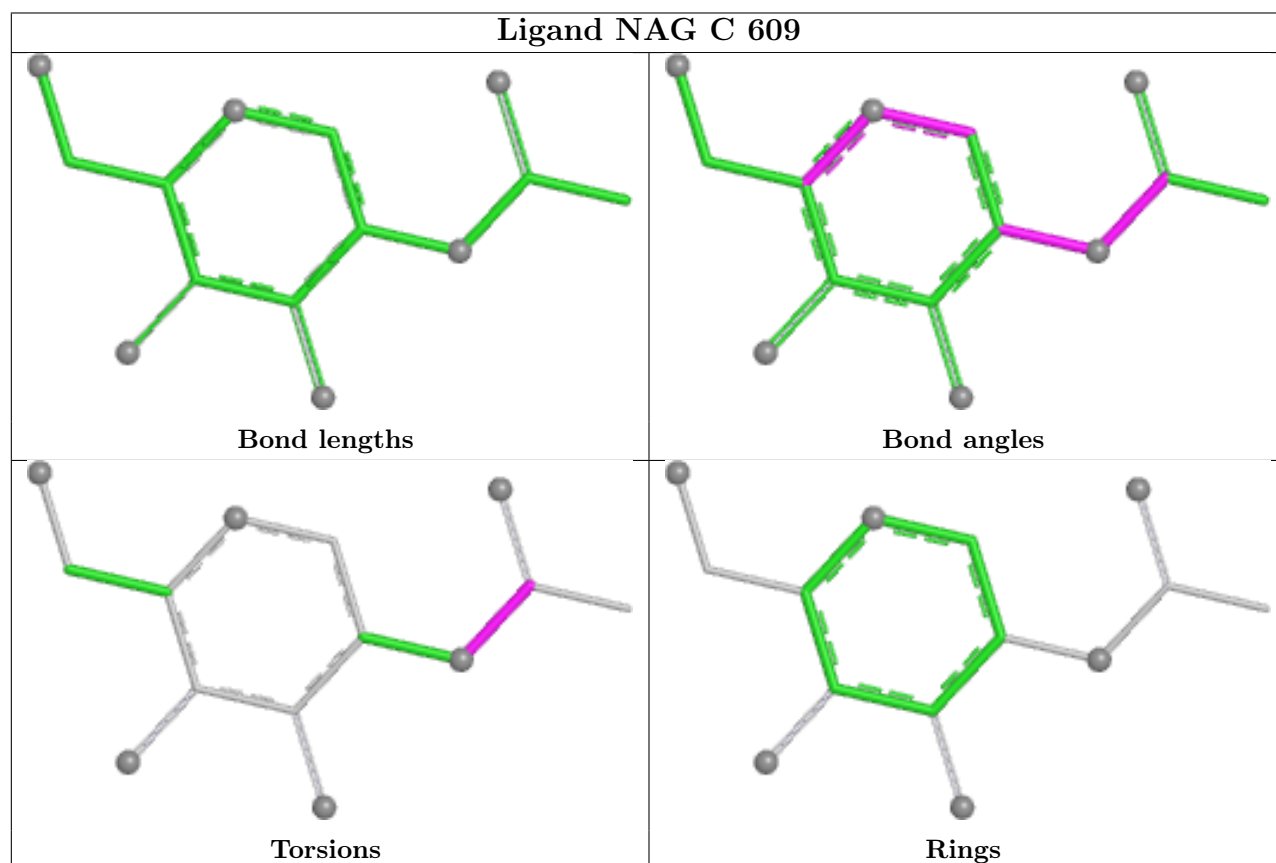
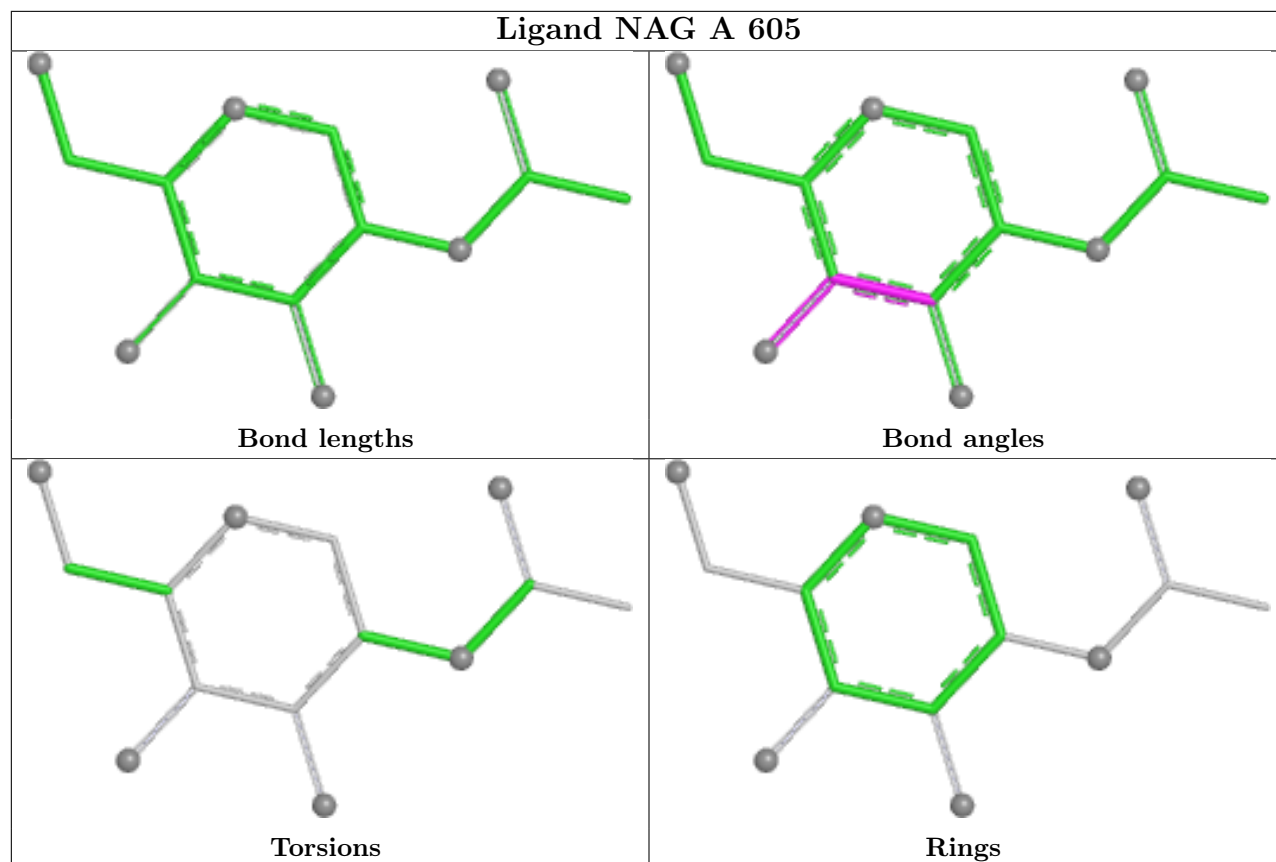
There are no ring outliers.

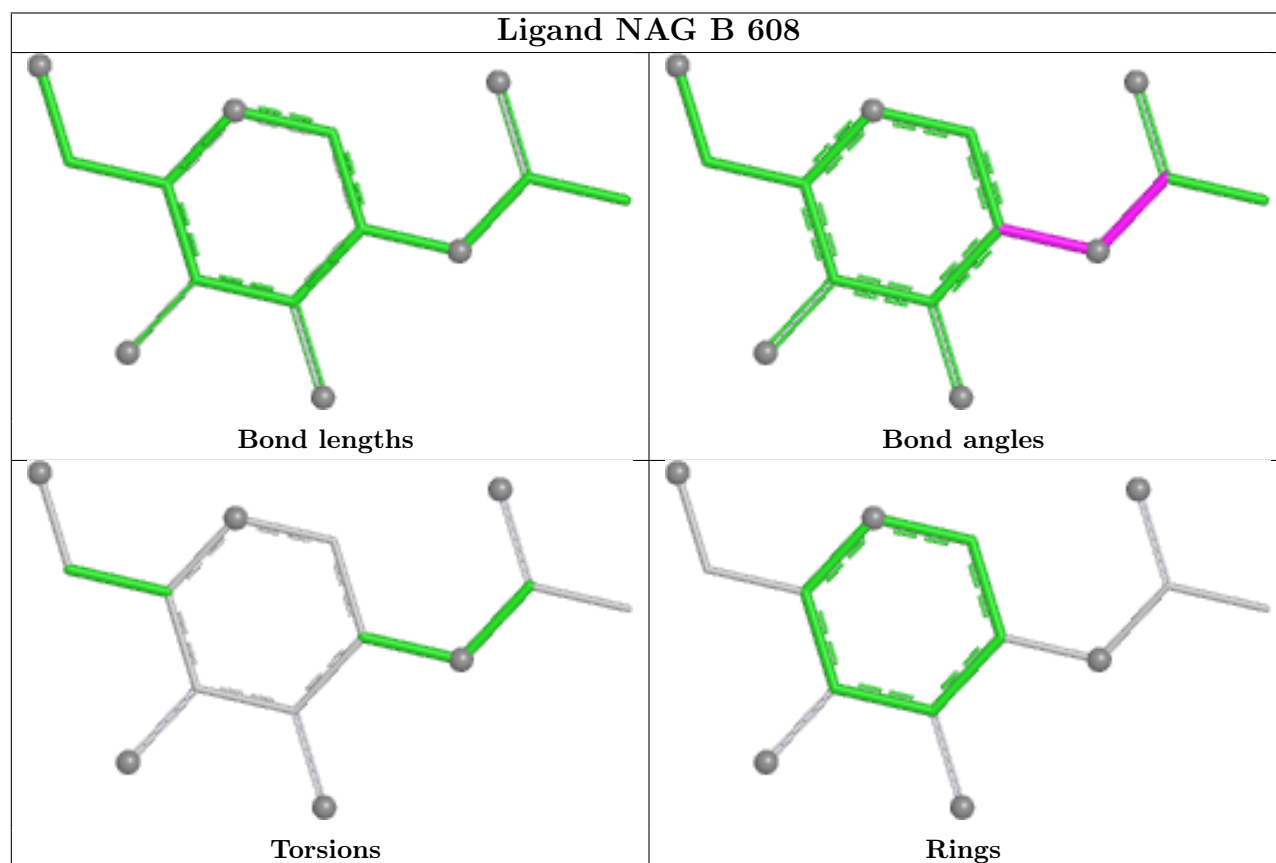
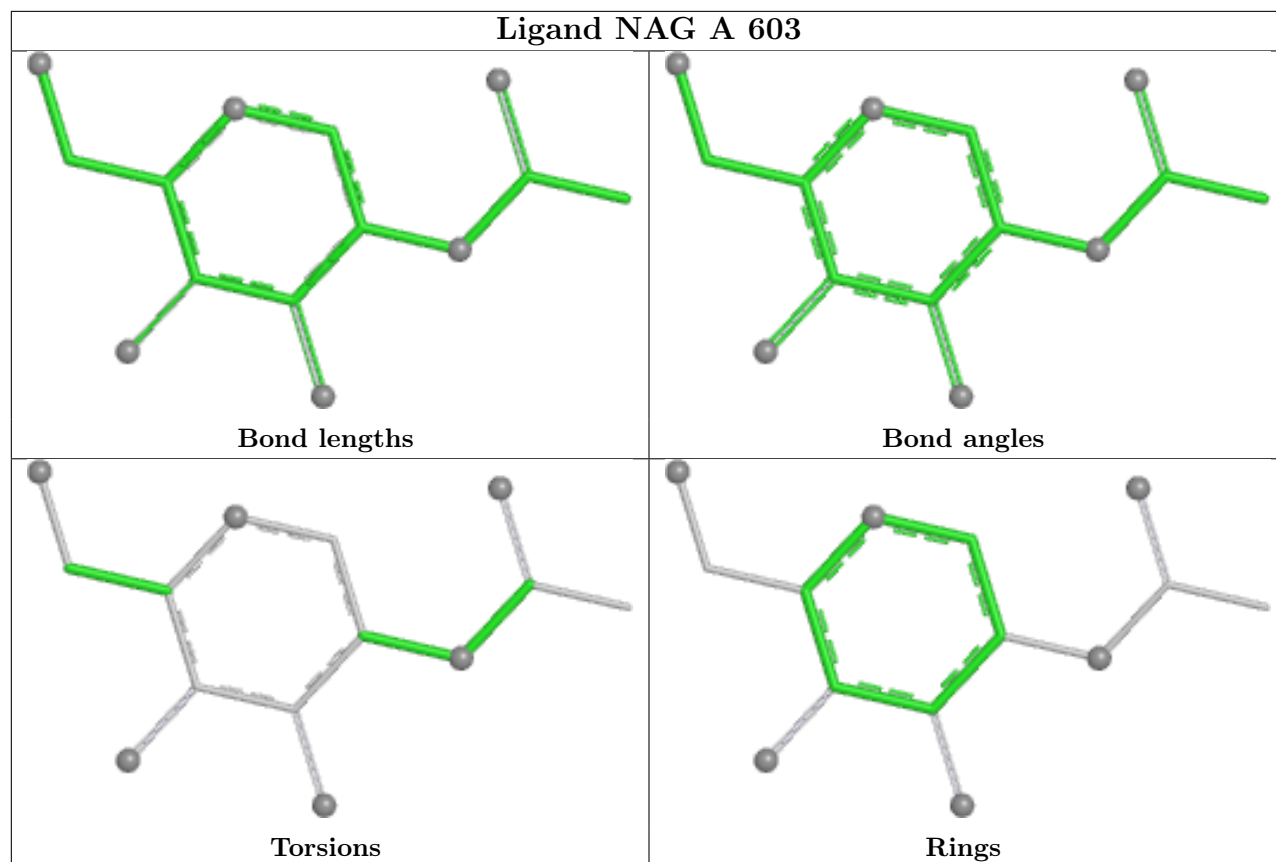
4 monomers are involved in 6 short contacts:

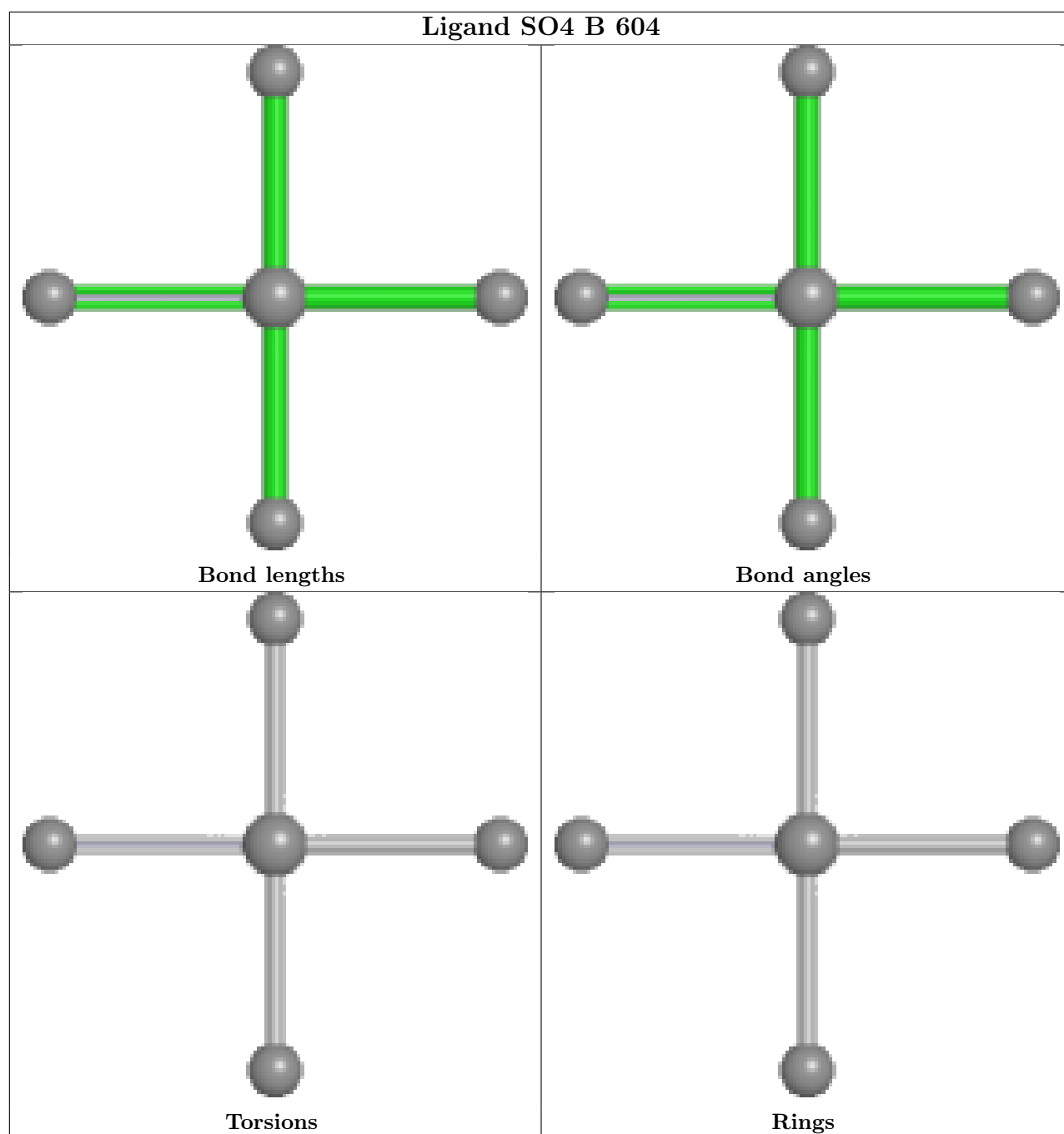
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	602	GLC	3	0
7	C	602	GLC	3	0
8	C	603	GLA	3	0
4	B	601	FRU	3	0

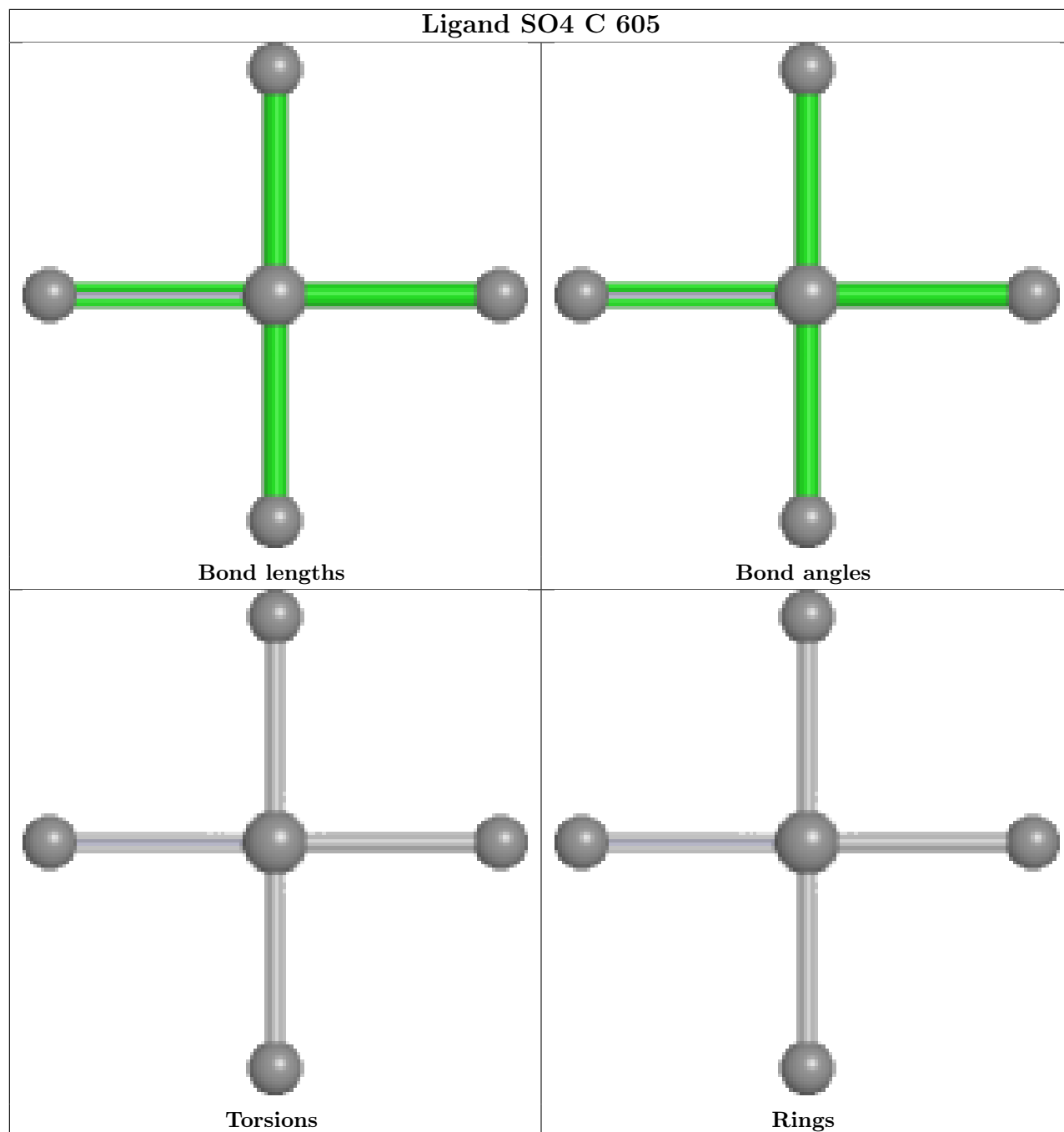
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



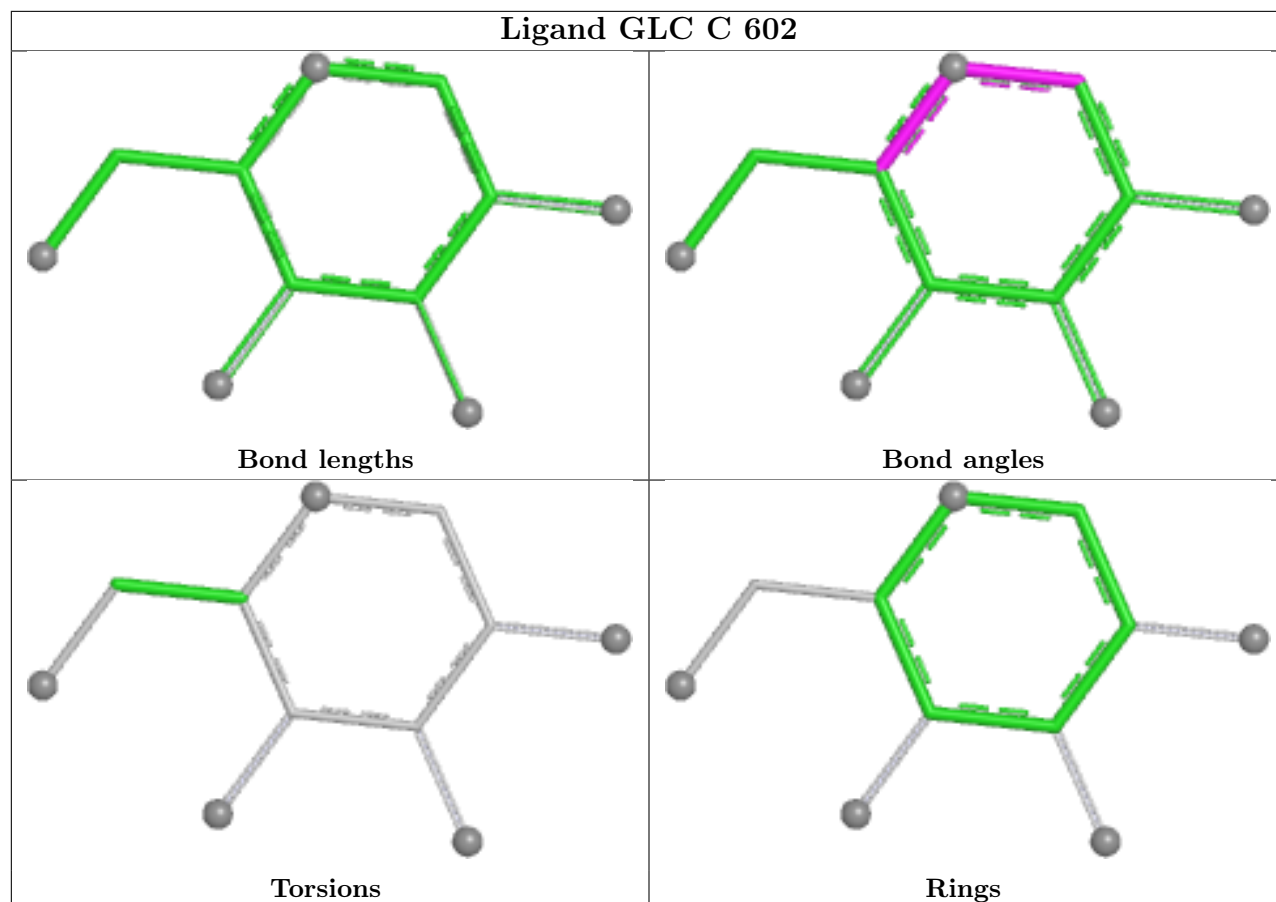




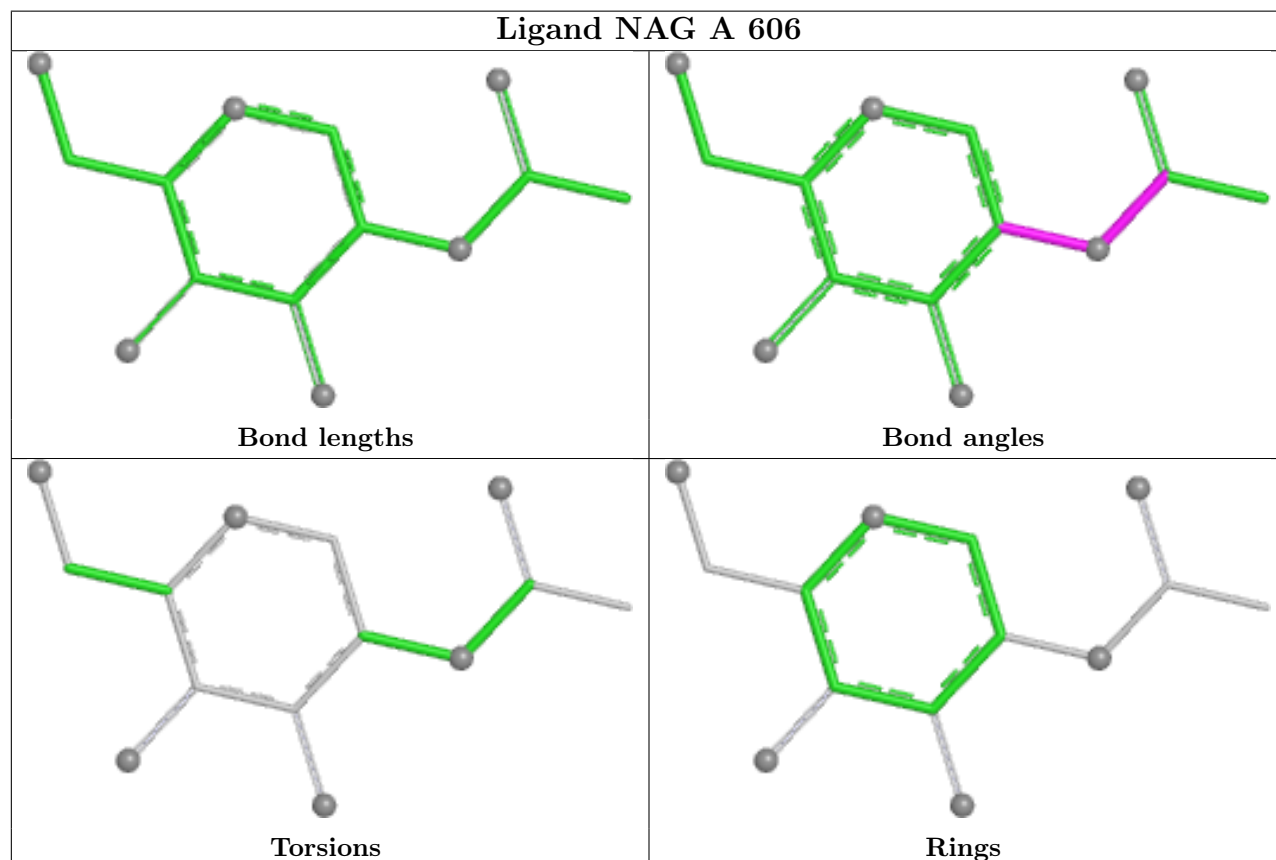


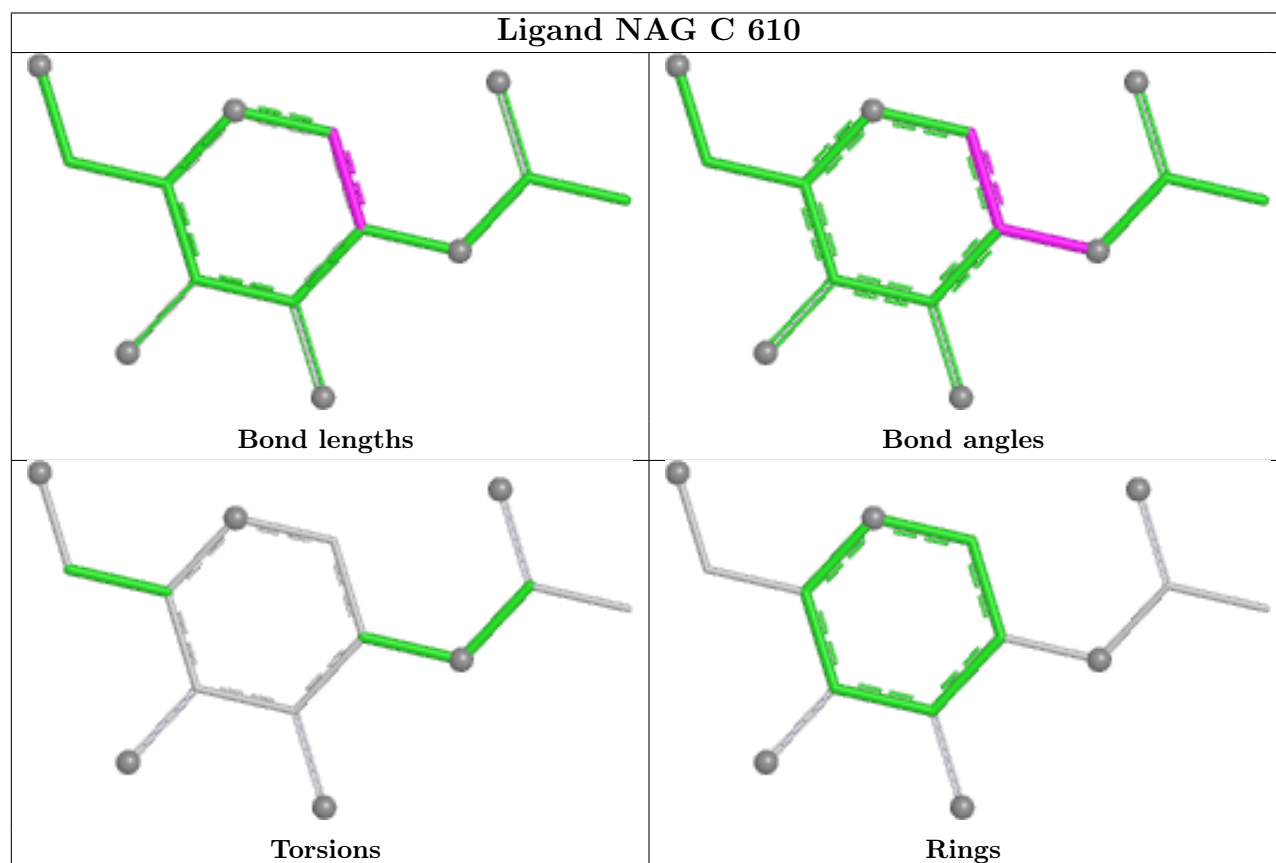
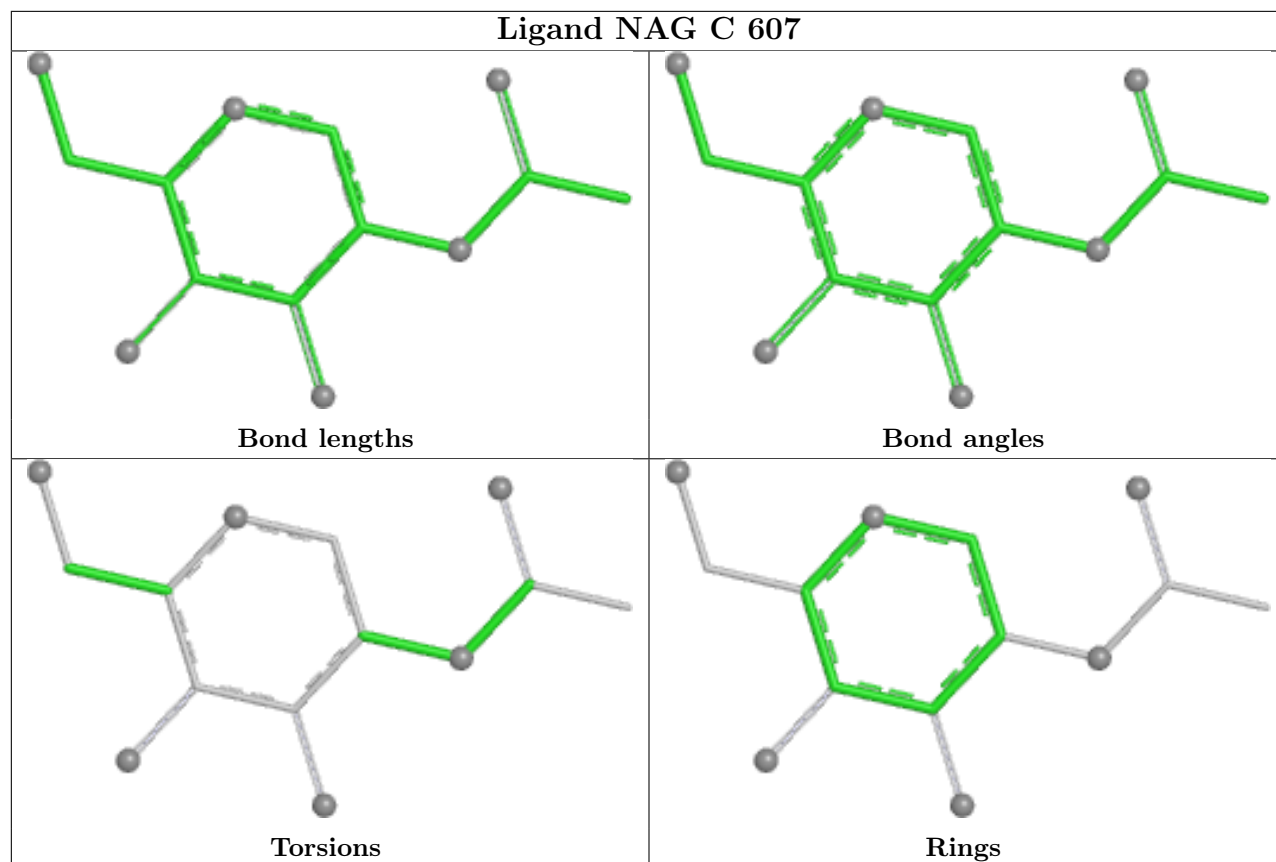


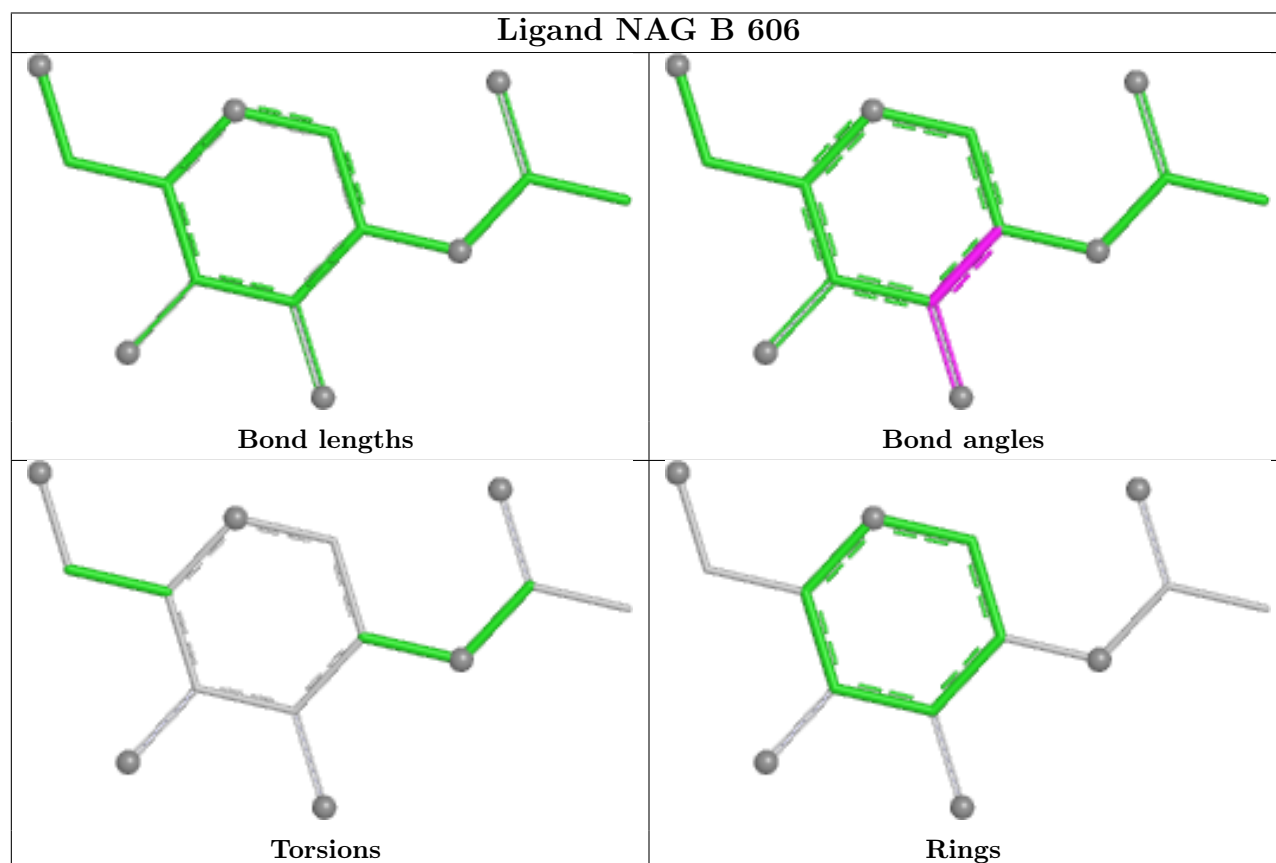
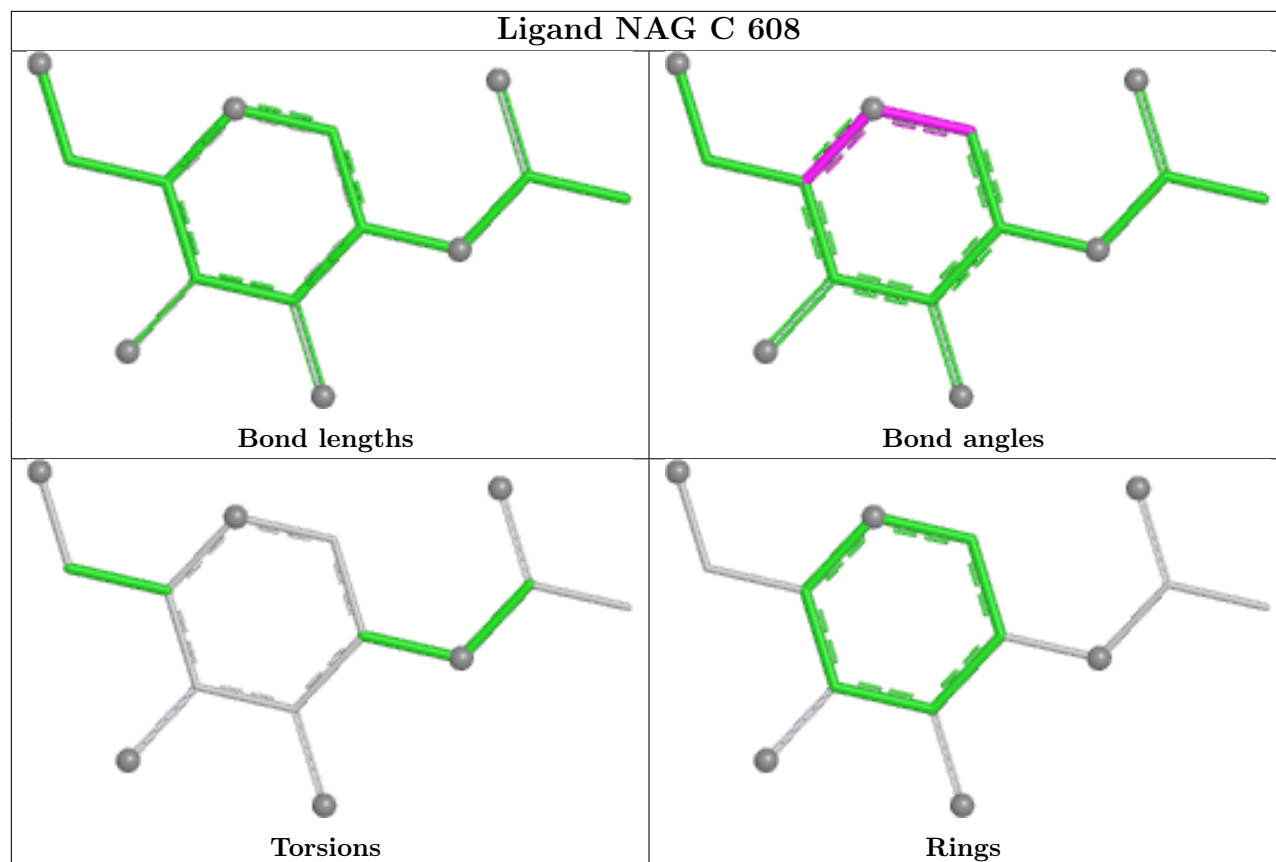
Ligand GLC C 602

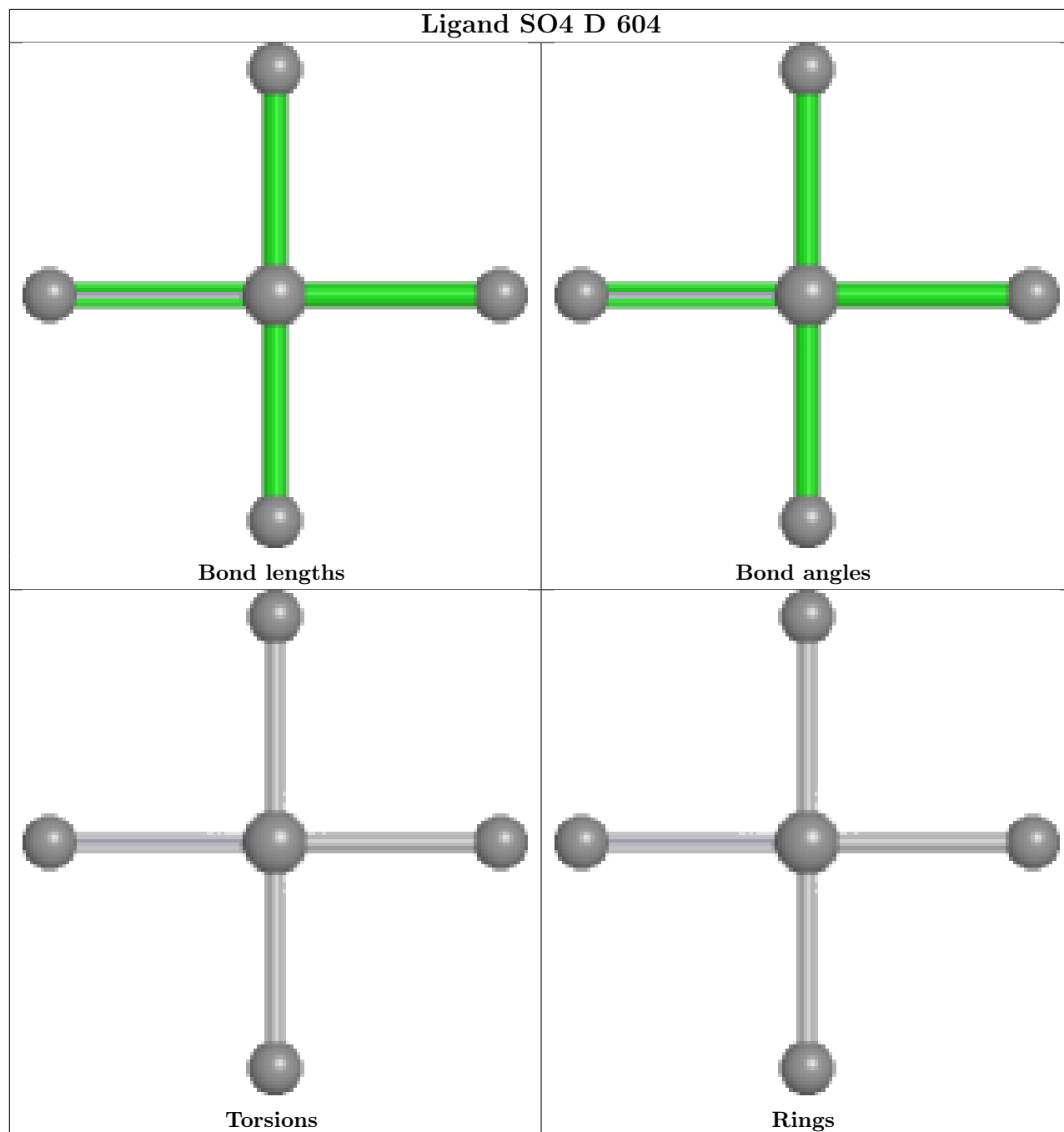


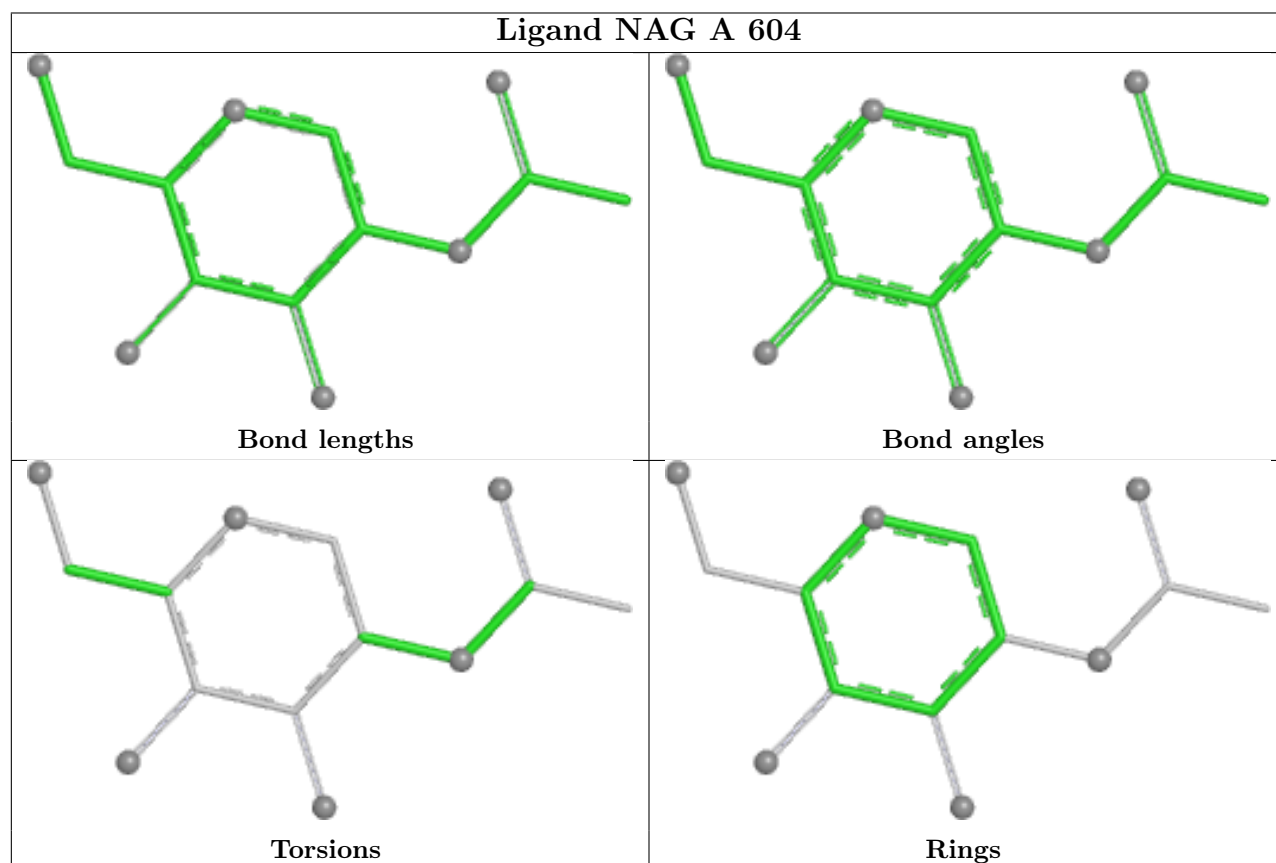
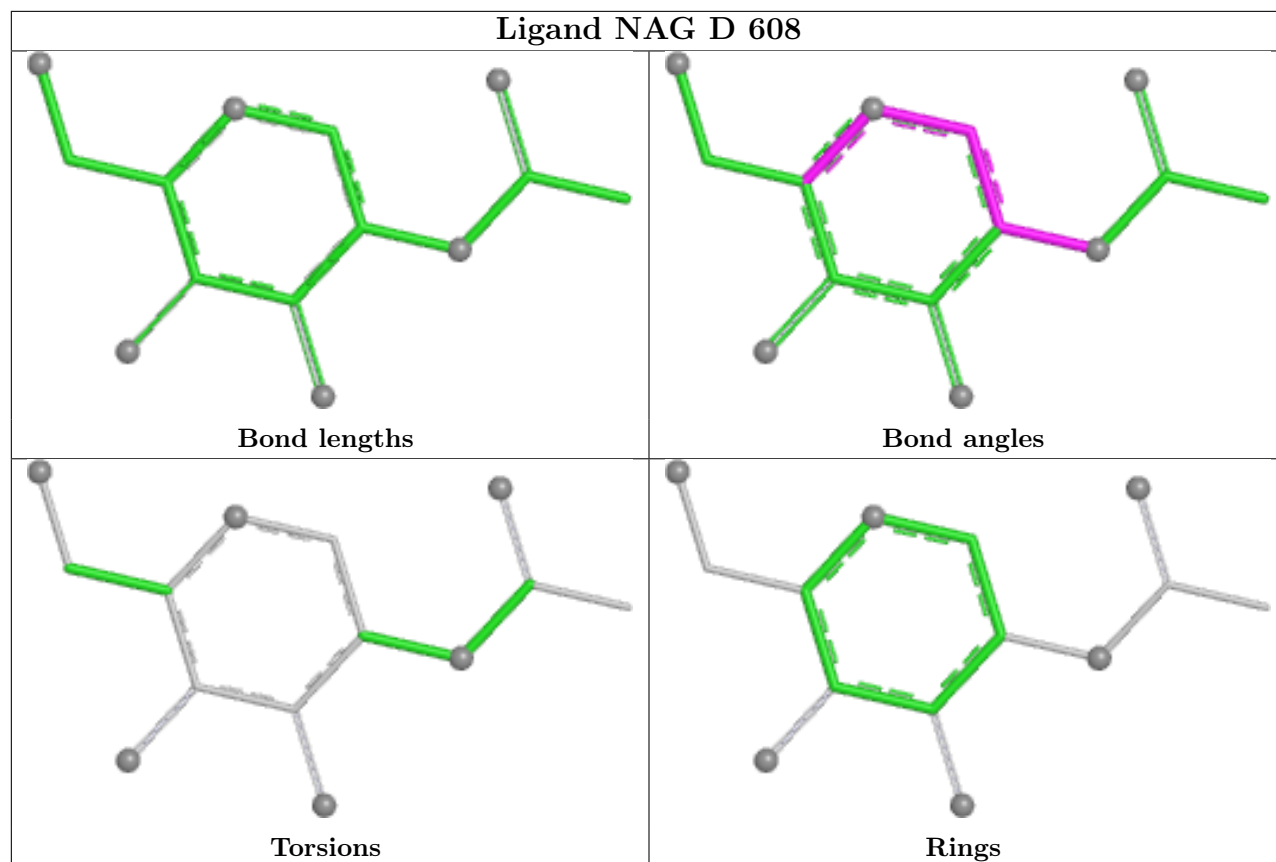
Ligand NAG A 606

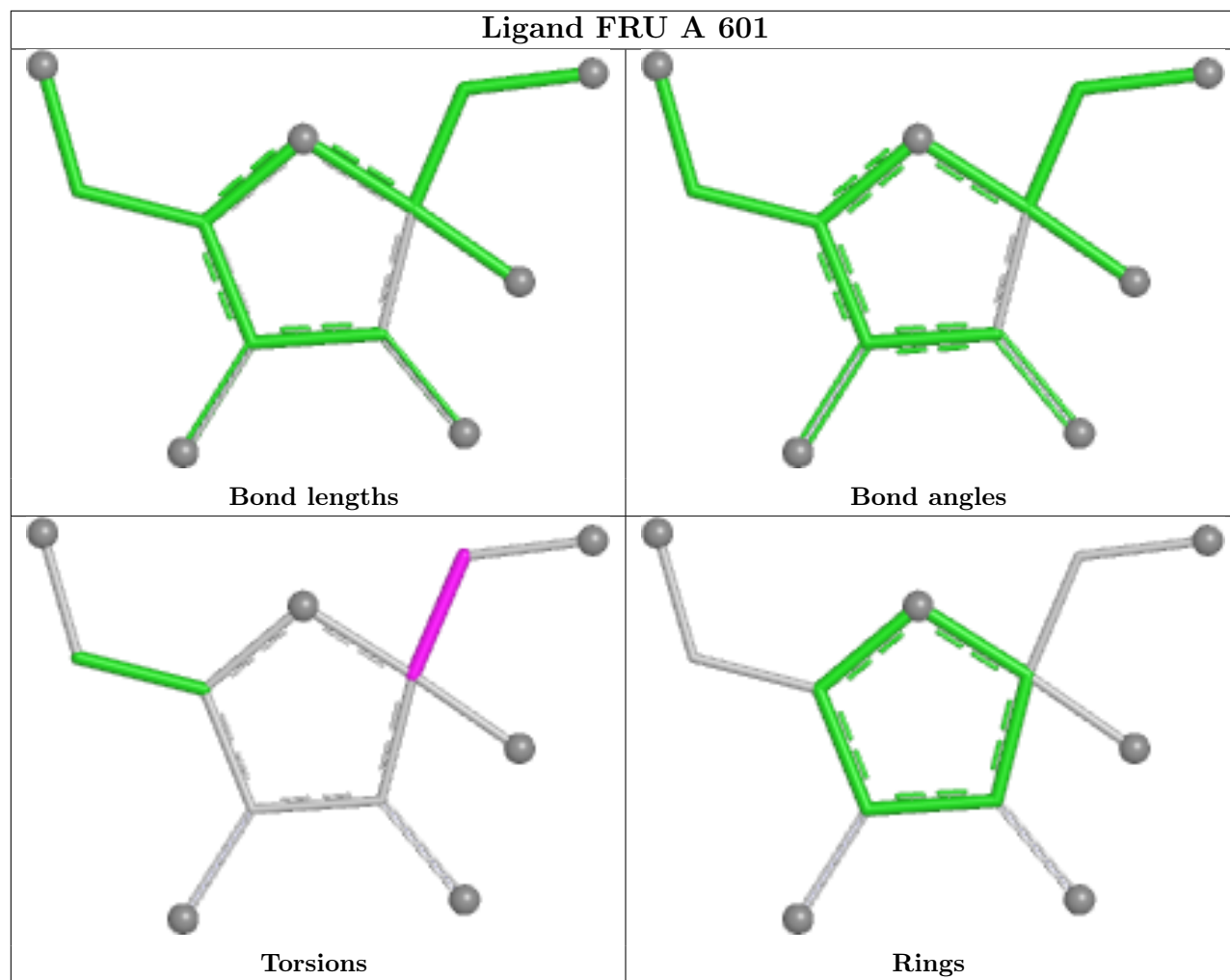




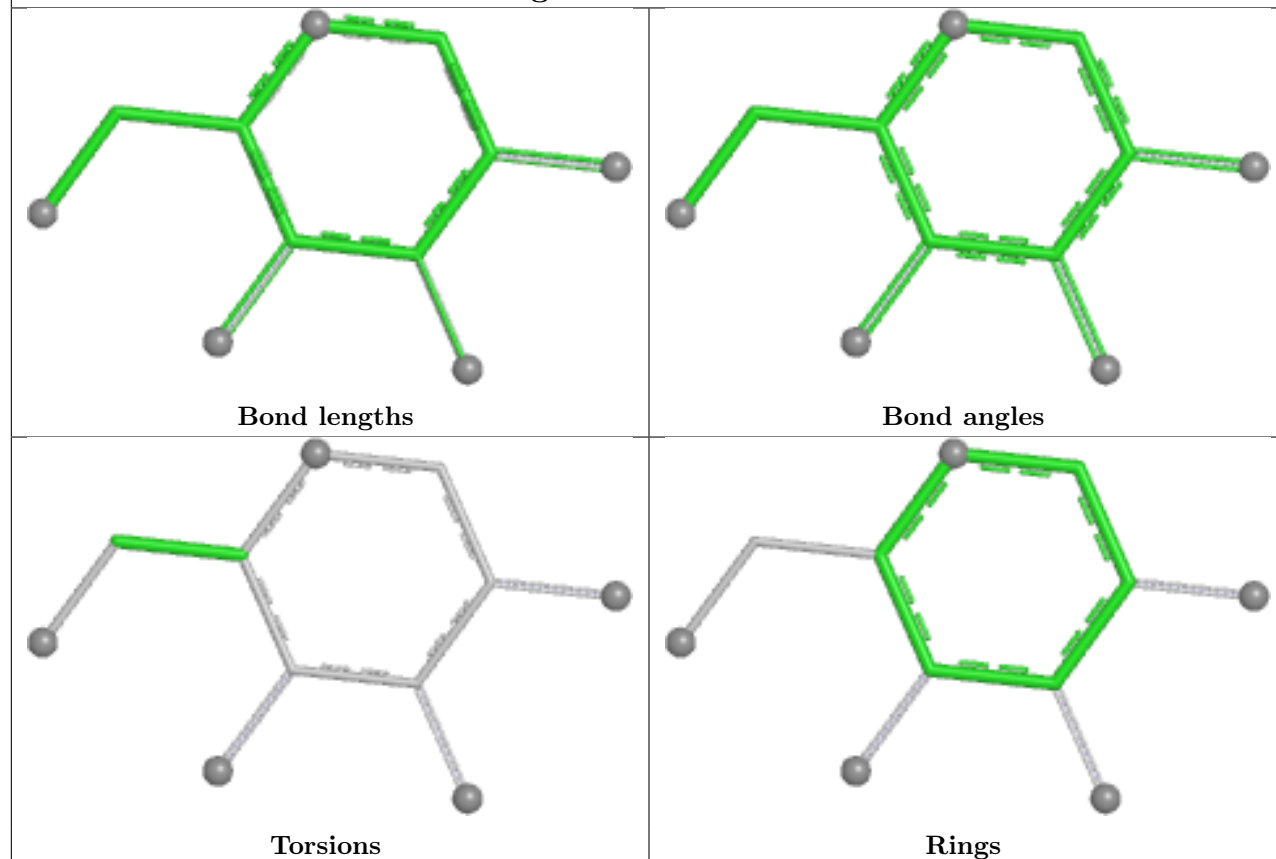




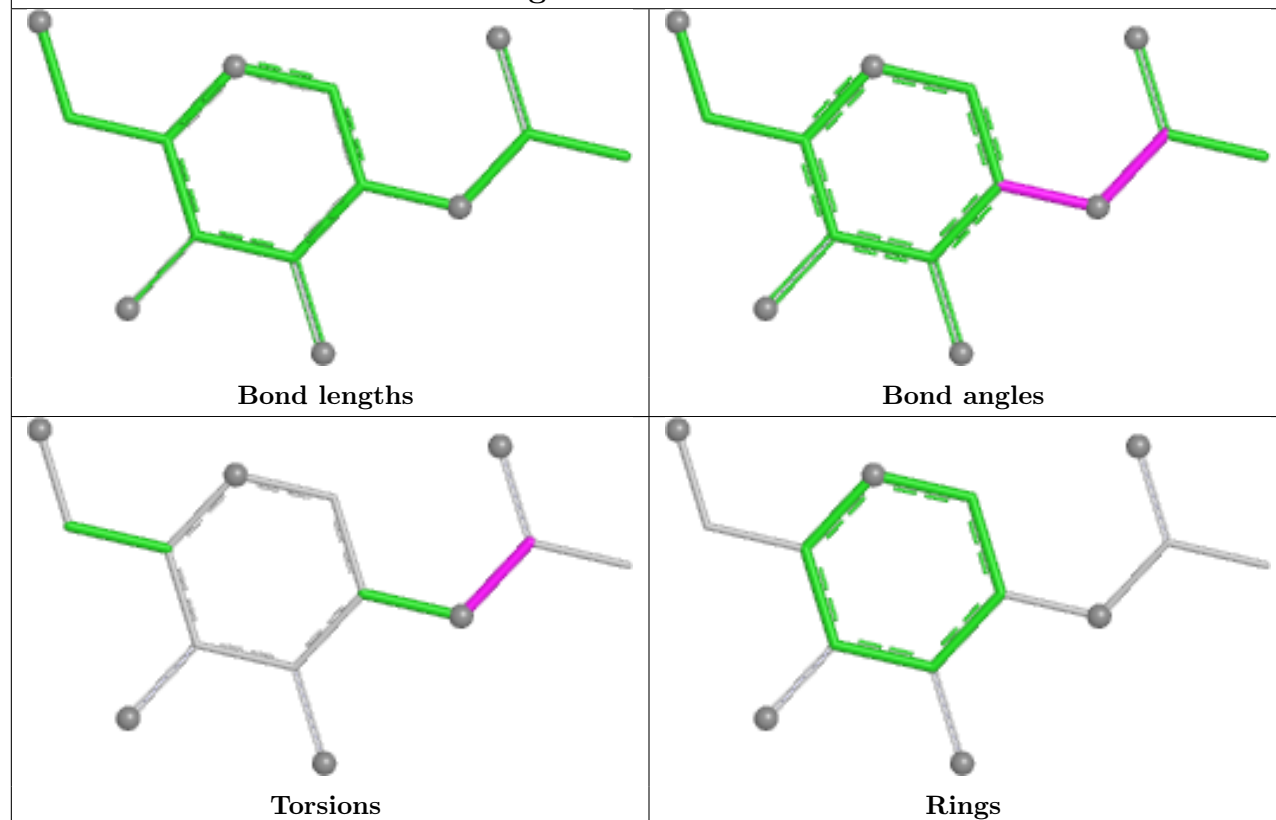


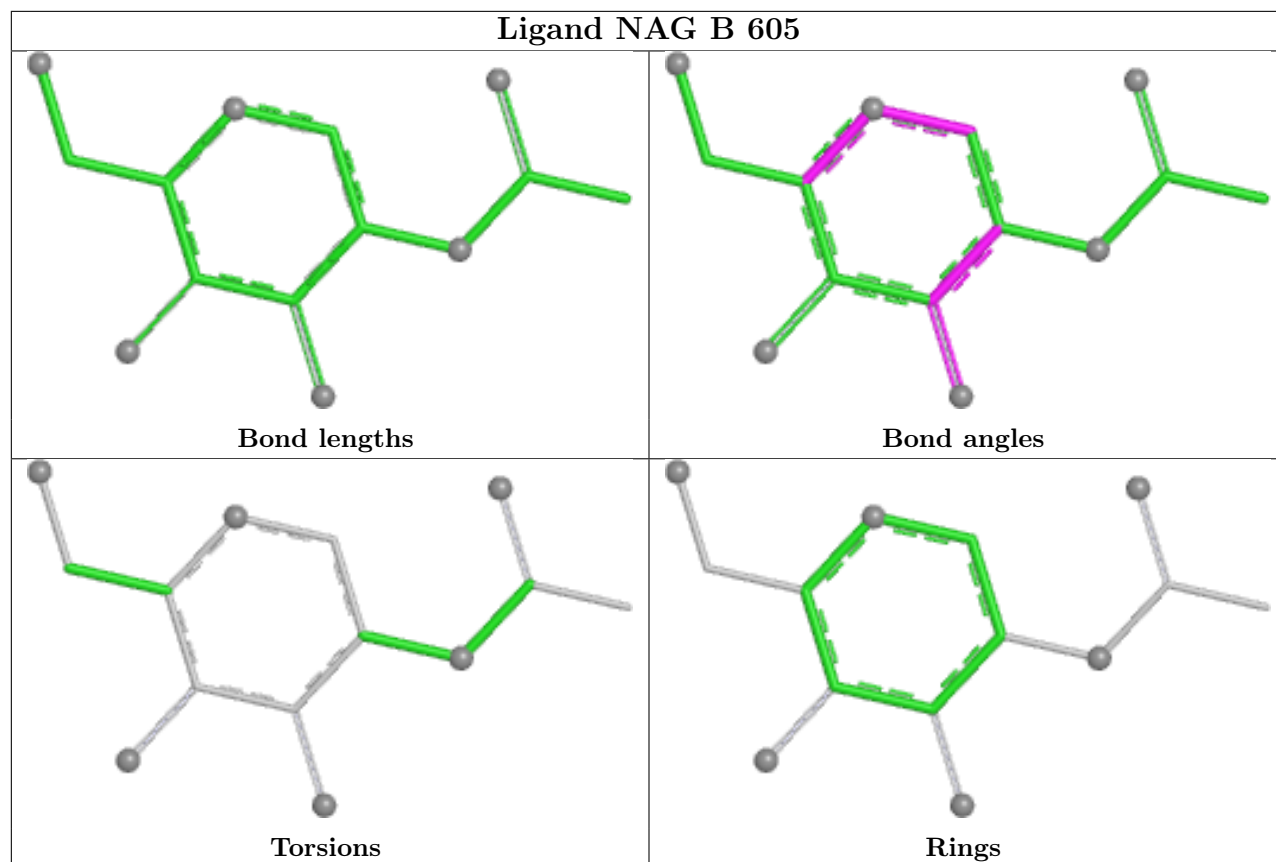


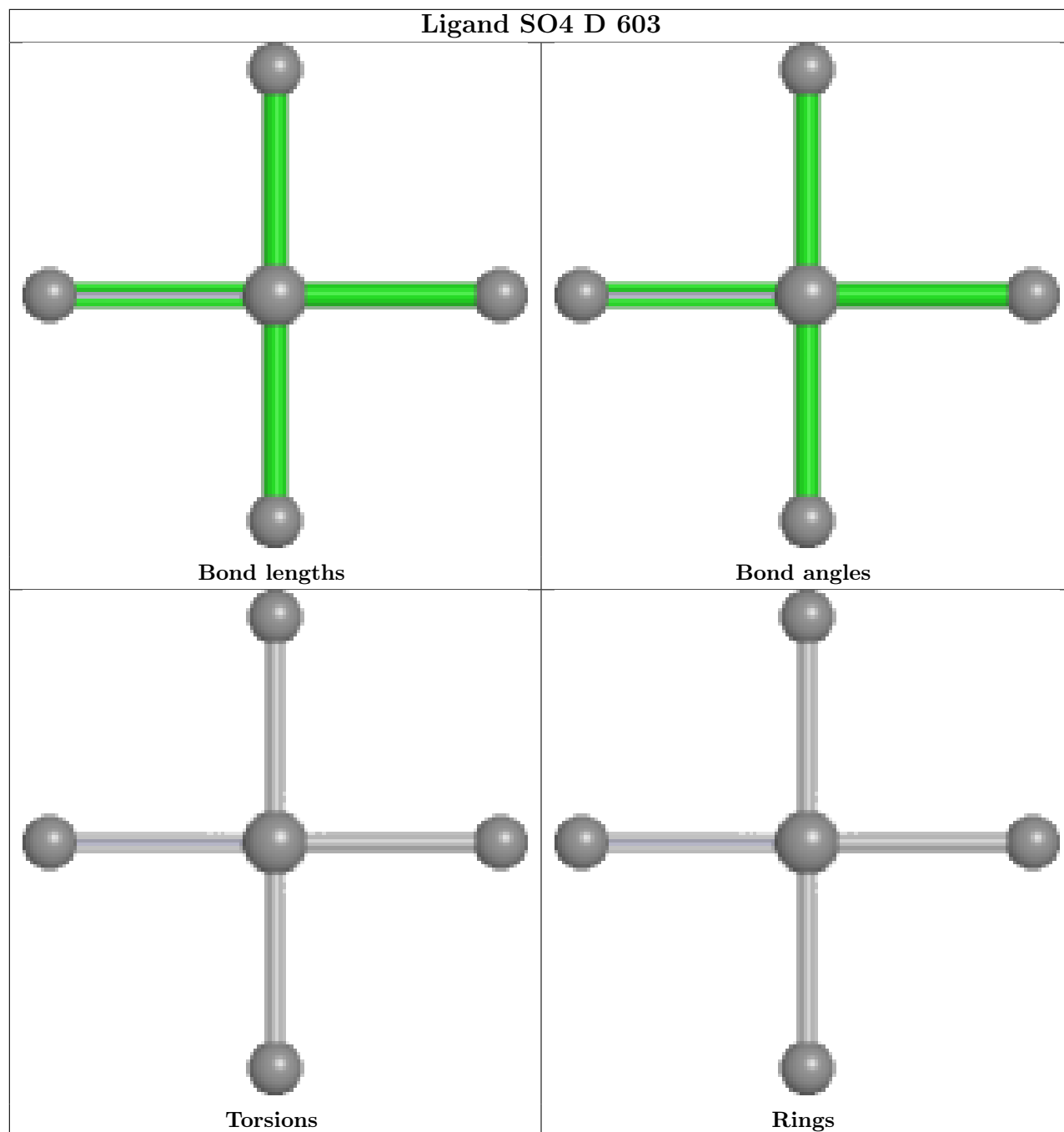
Ligand GLA C 603

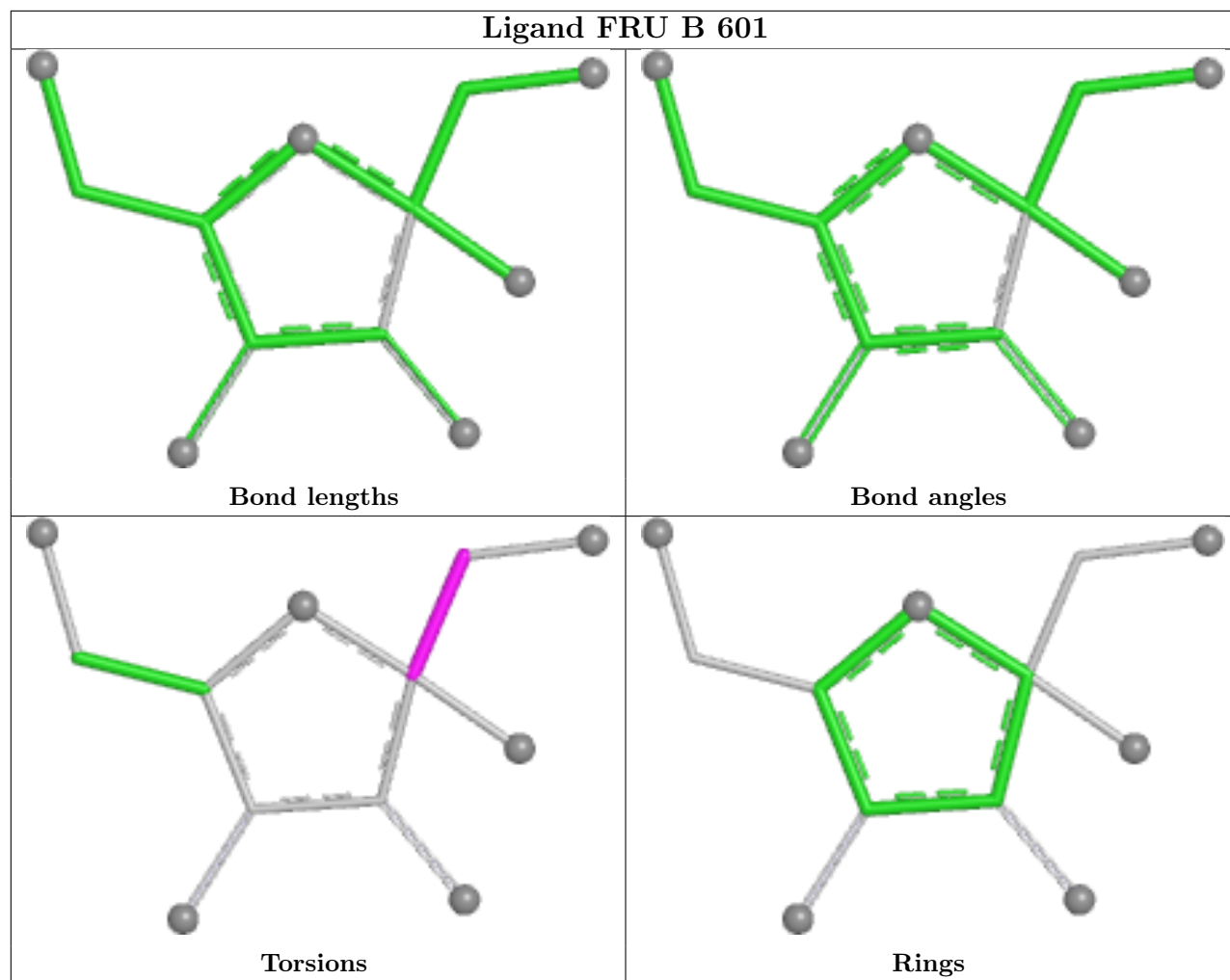


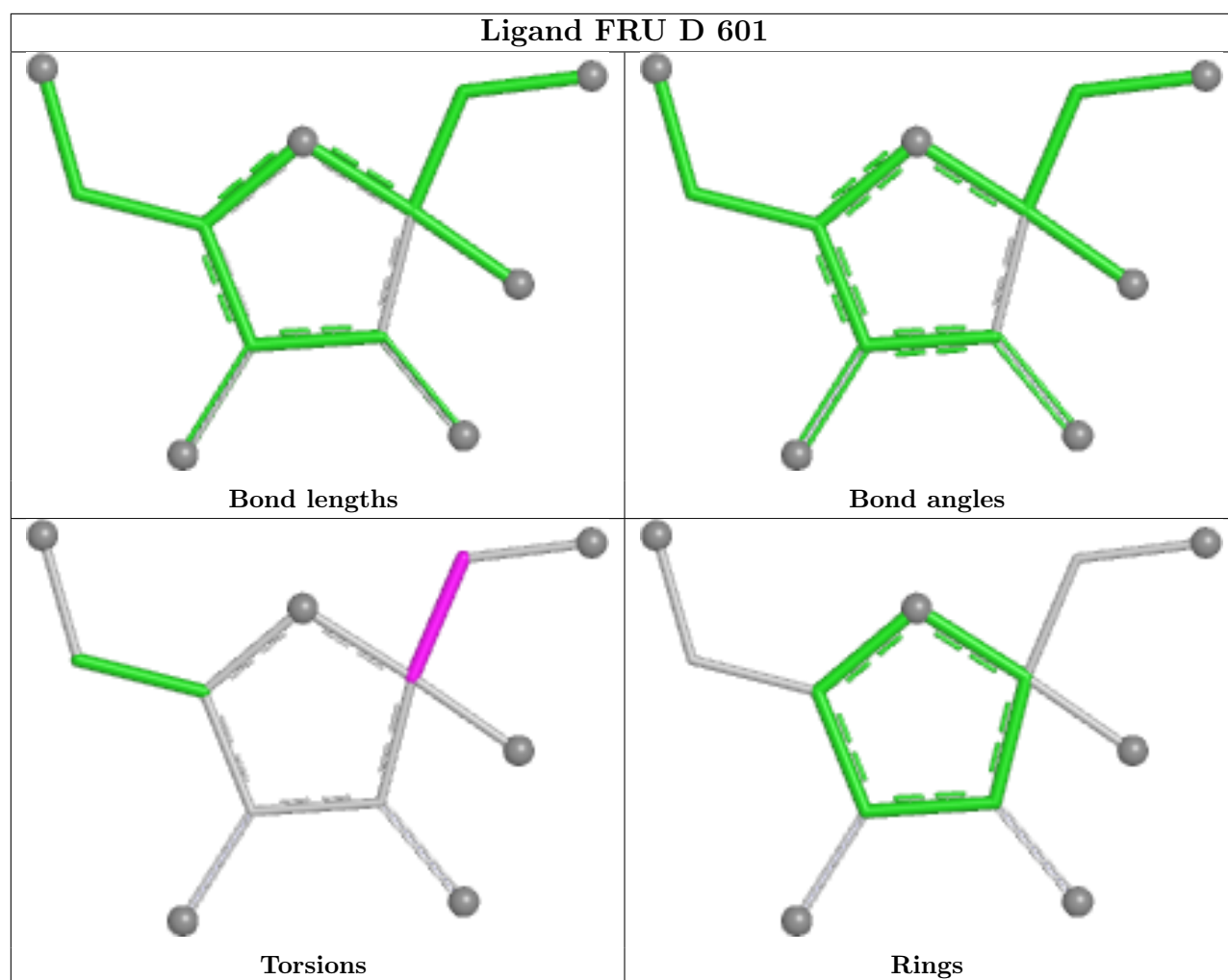
Ligand NAG B 607

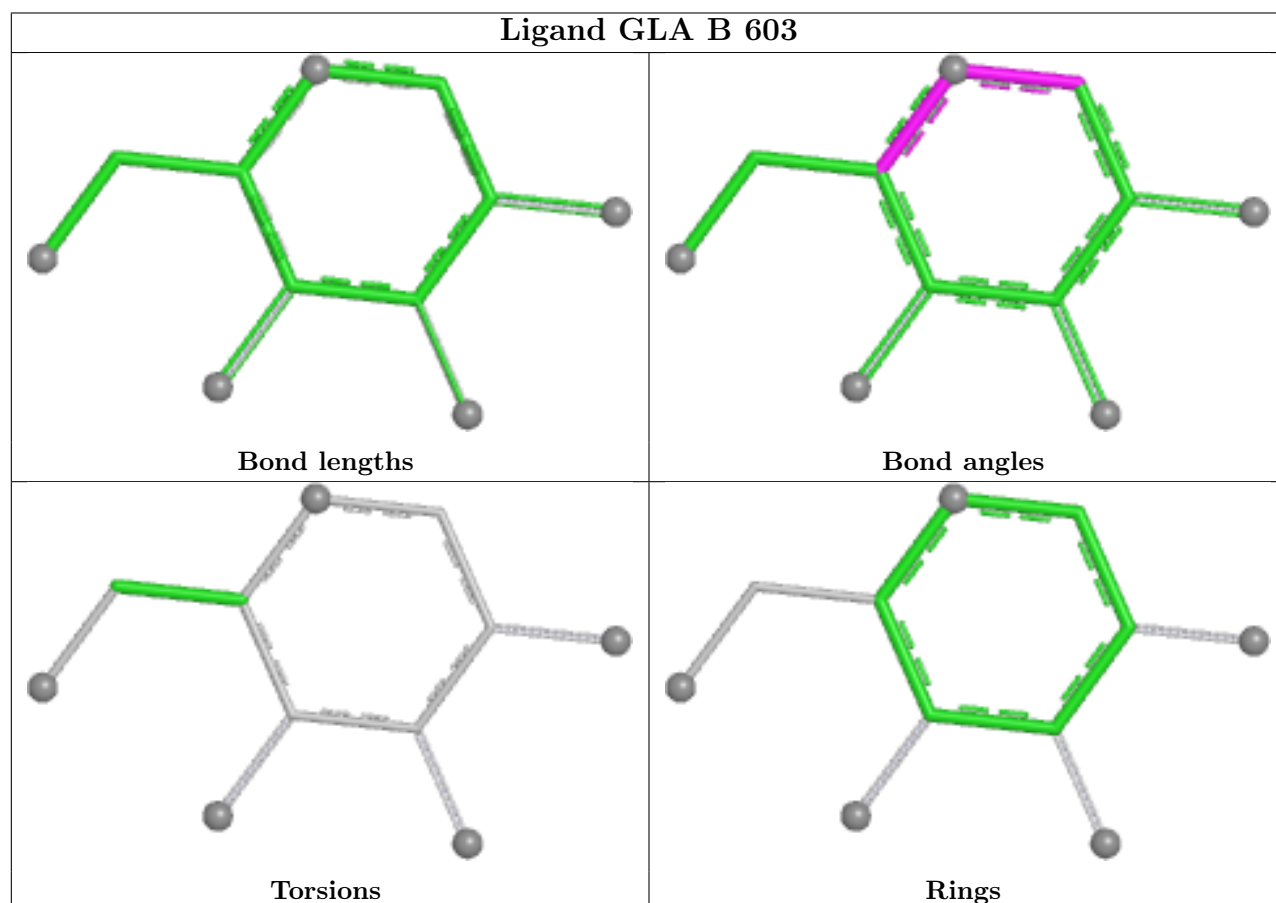
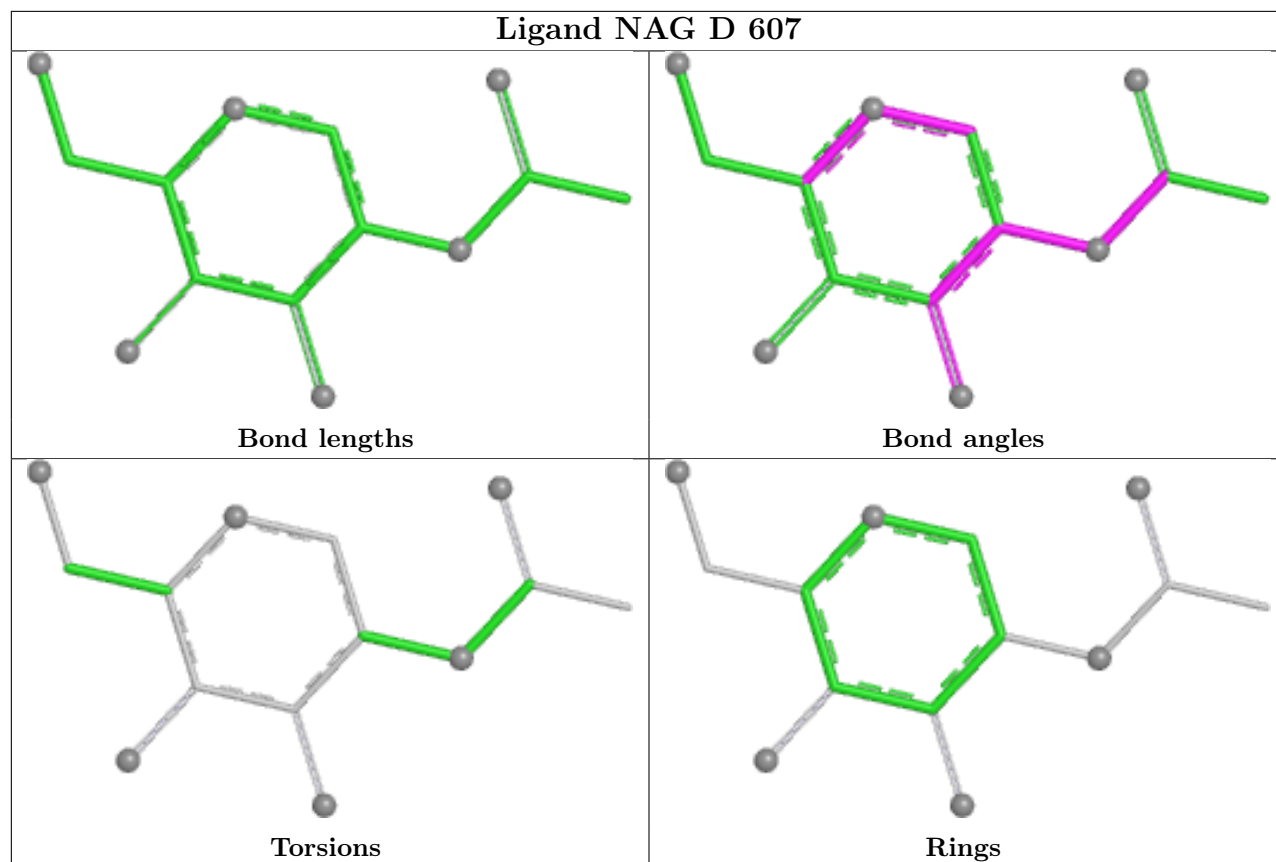


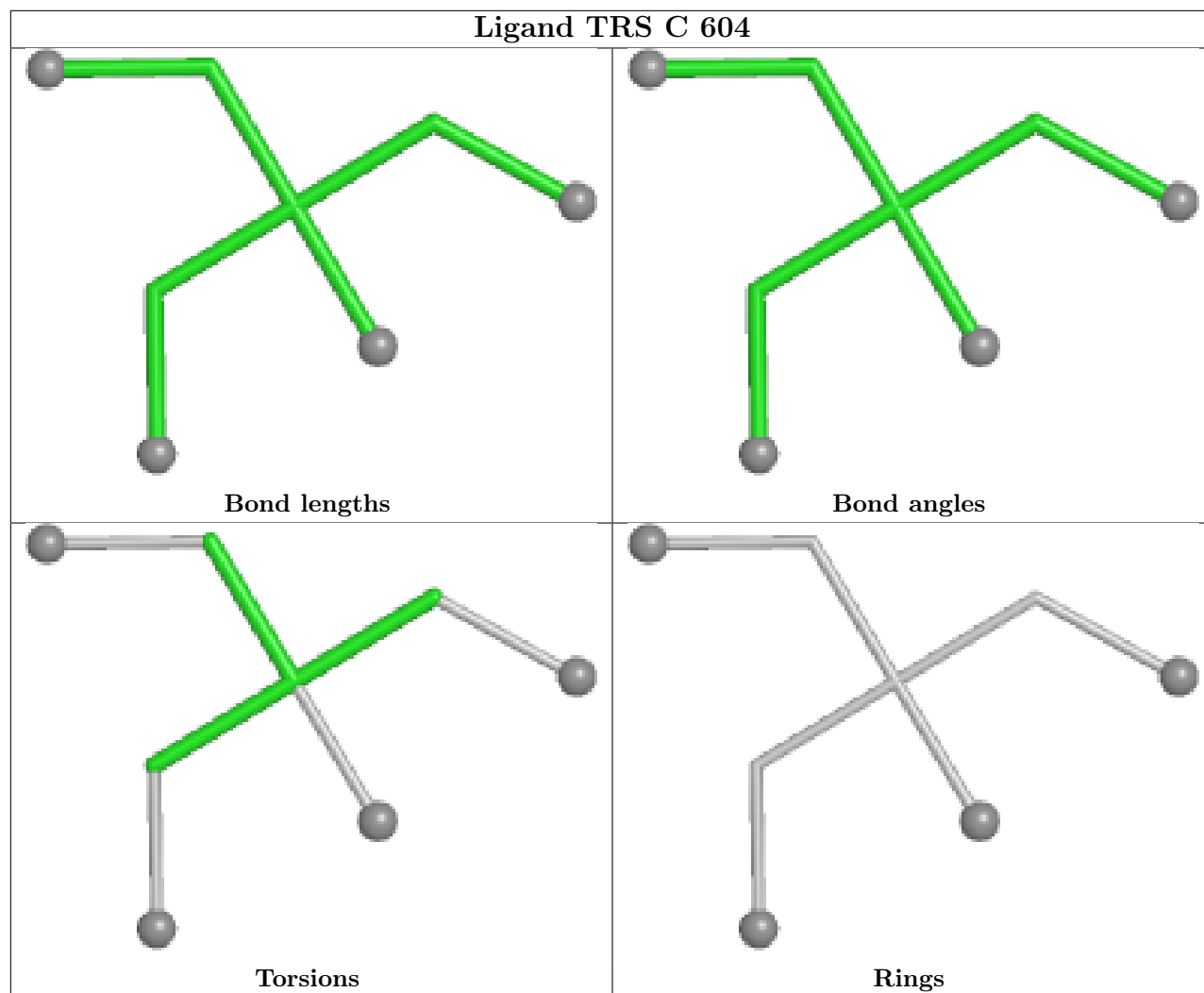


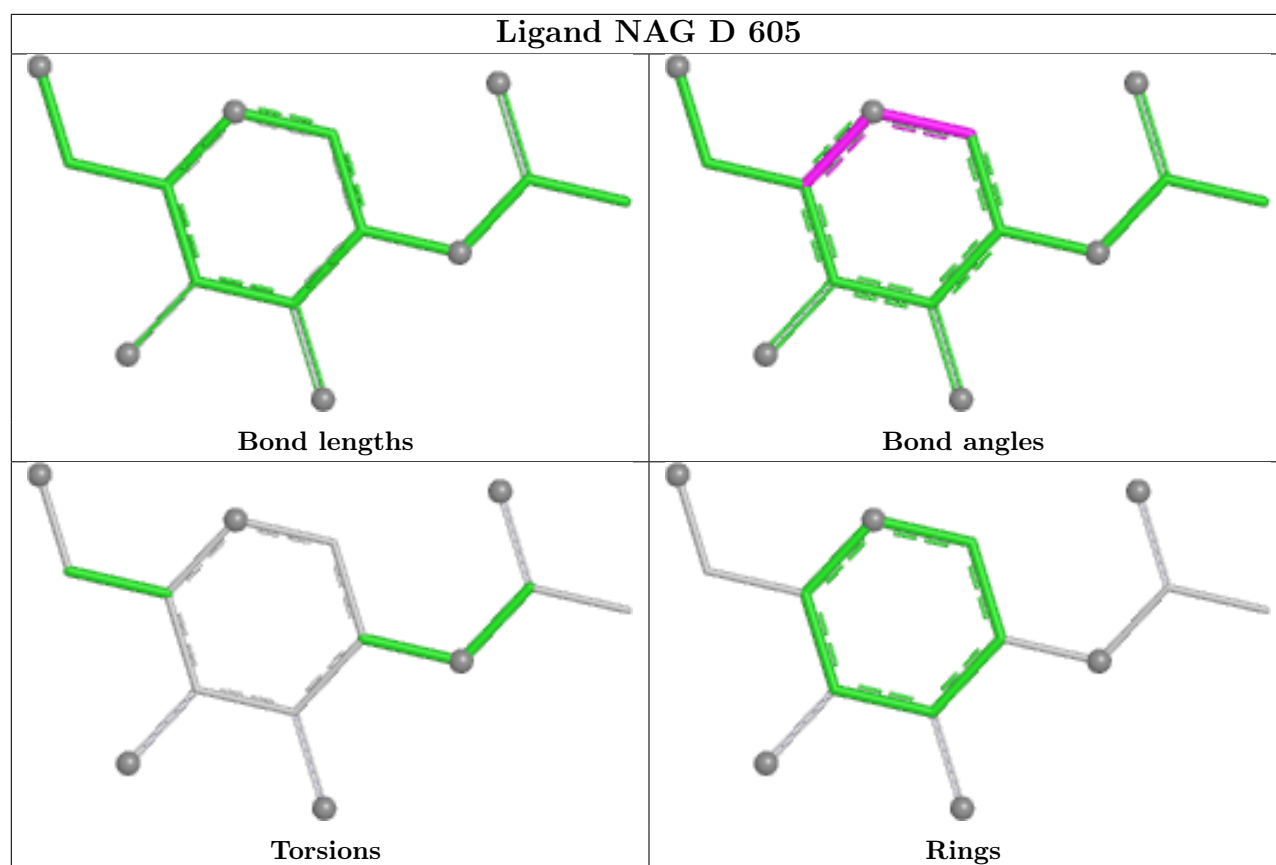


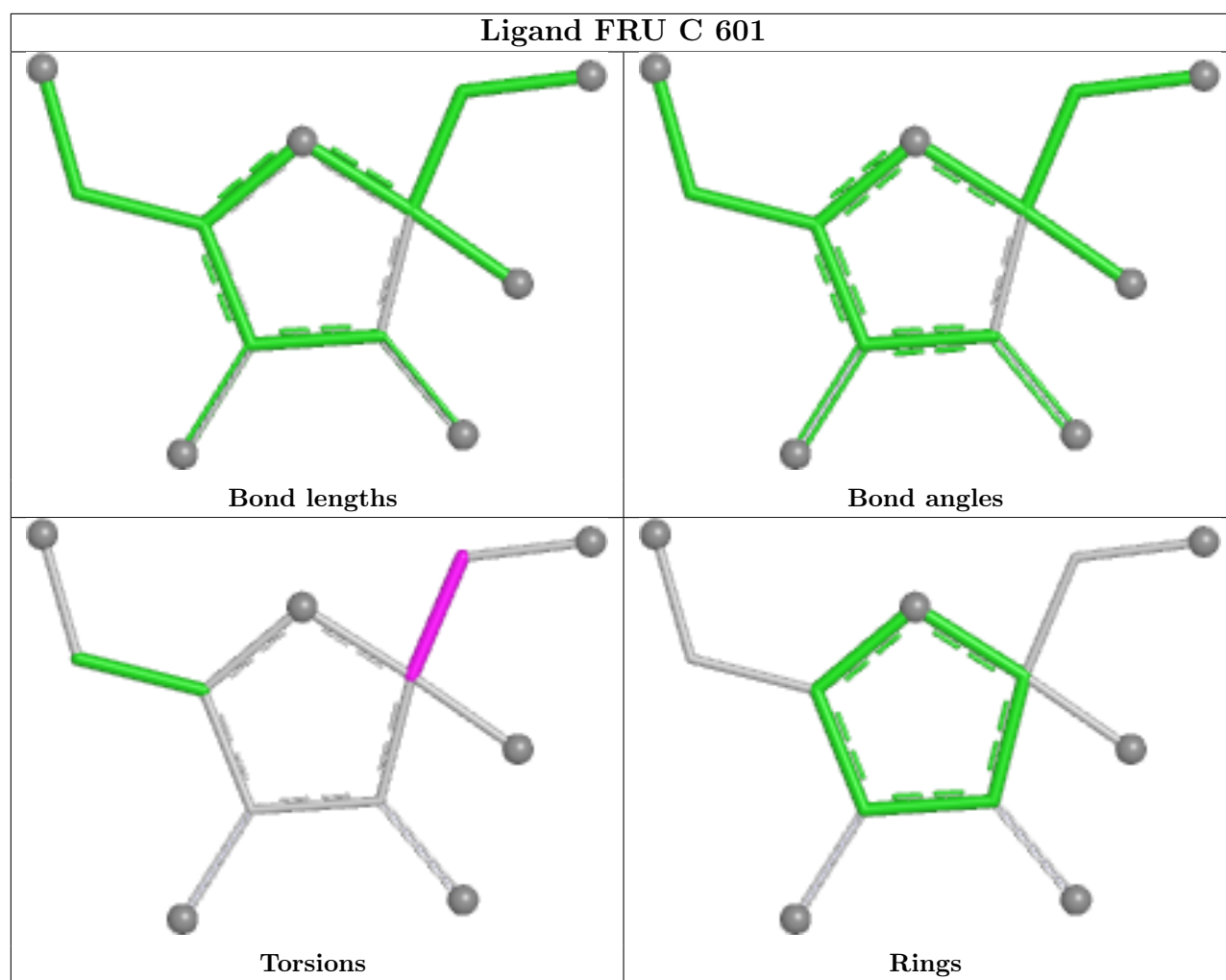


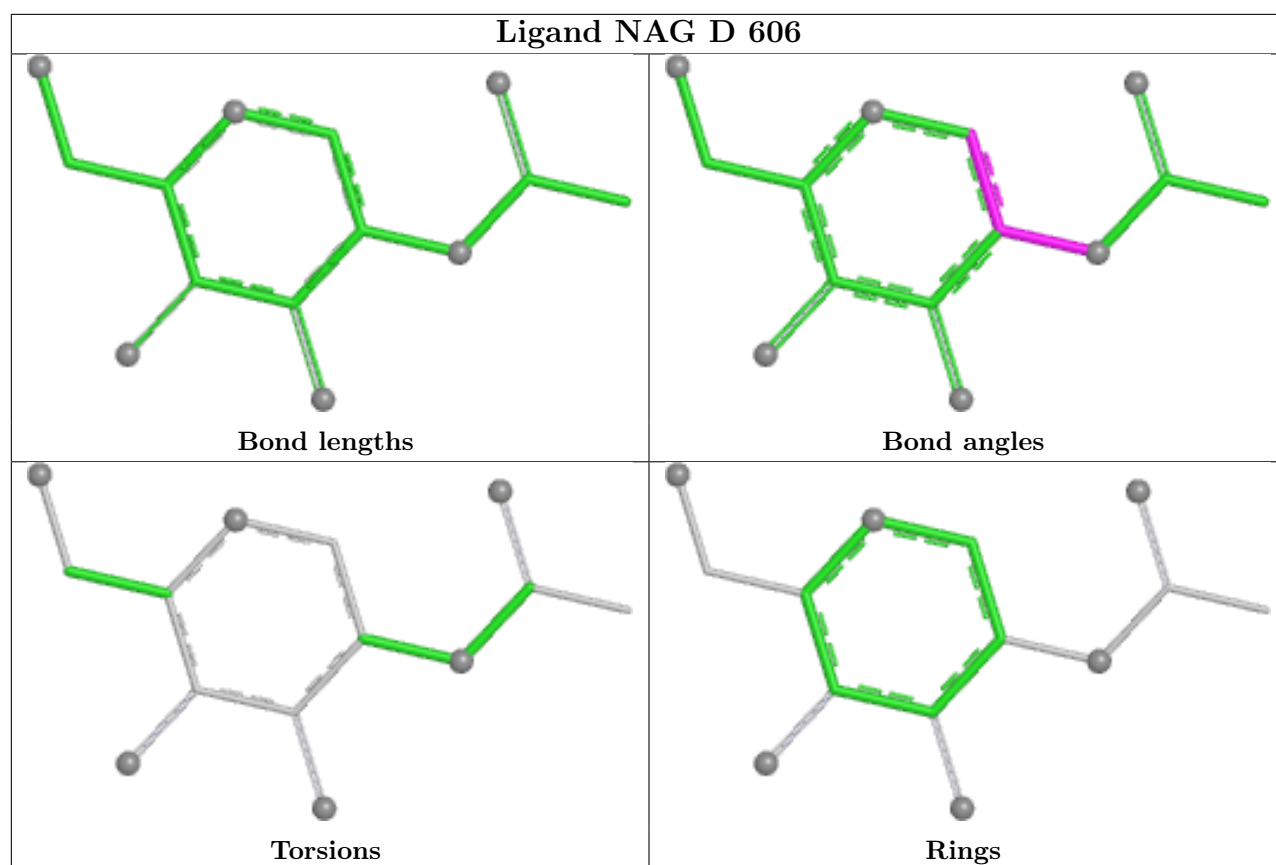


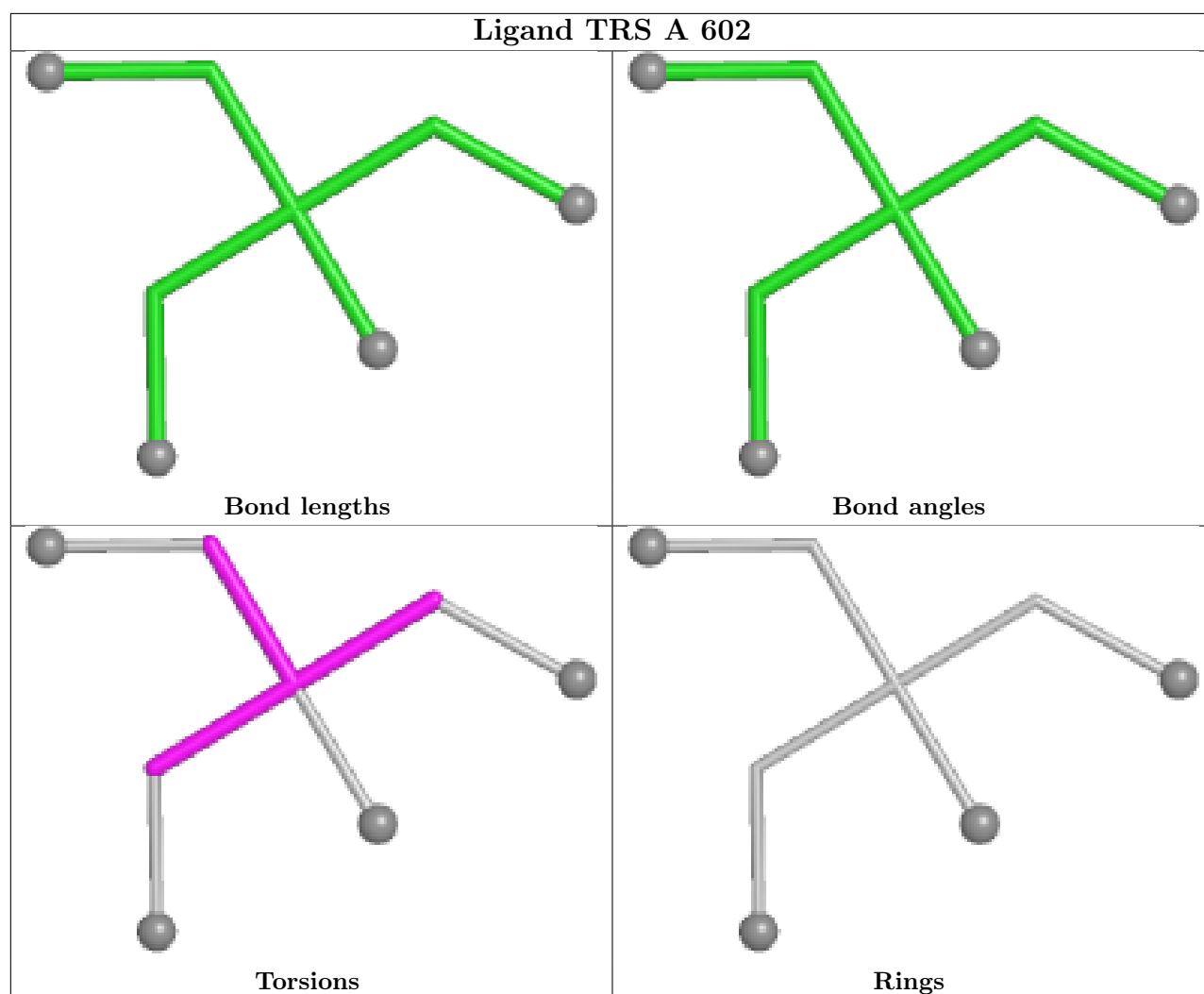


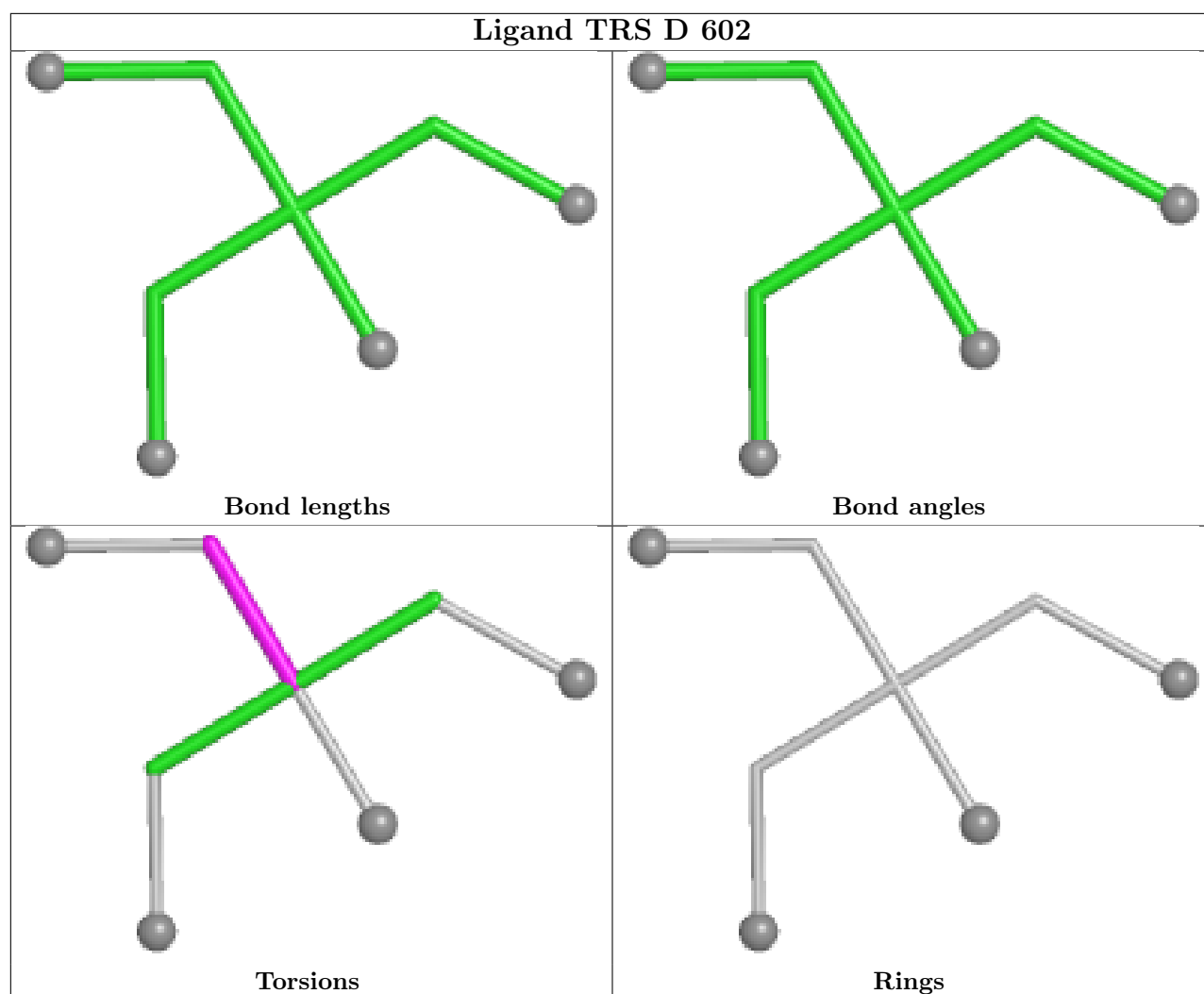


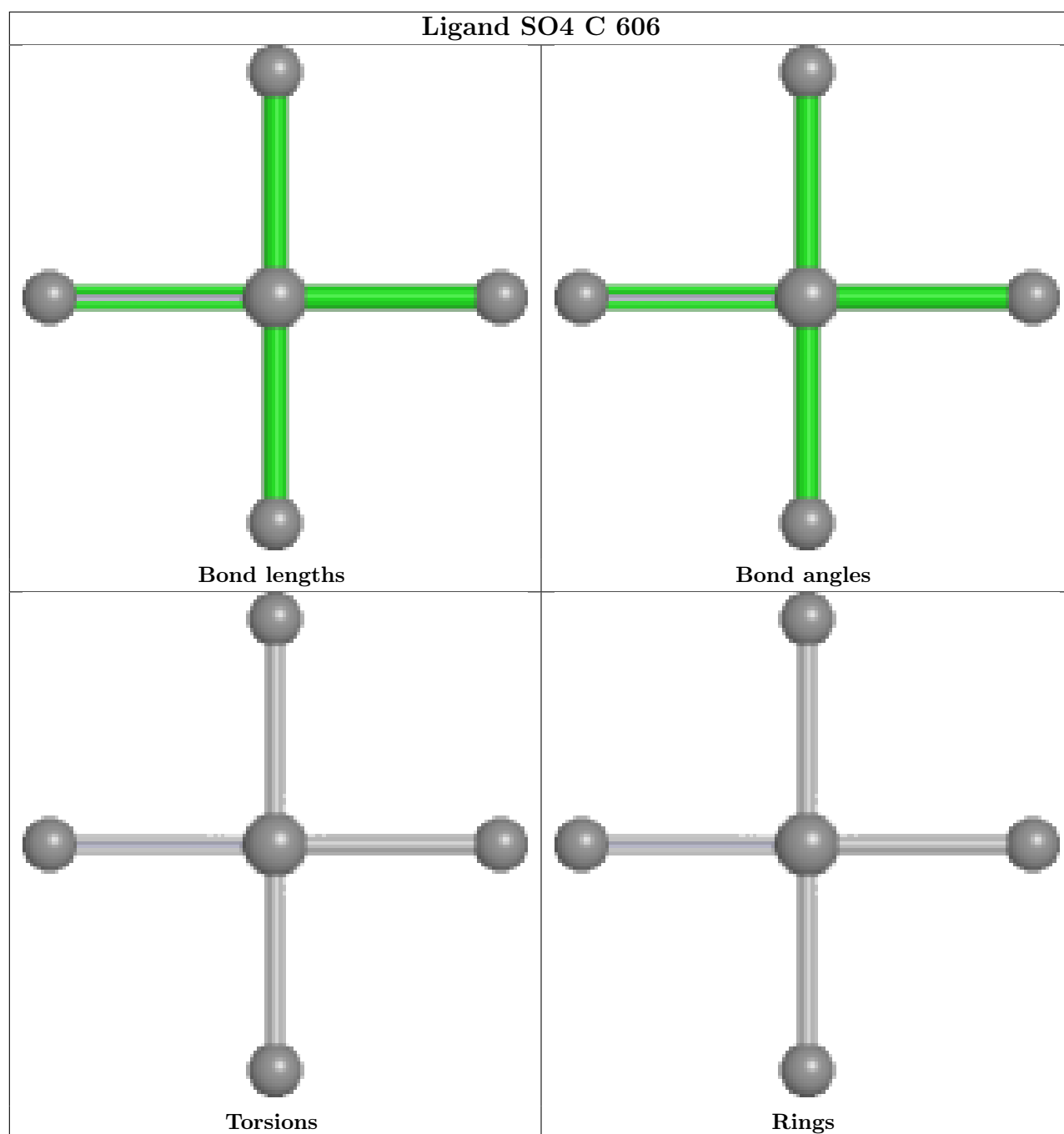












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	535/576 (92%)	-0.16	19 (3%) 46 45	17, 25, 53, 101	0
1	B	536/576 (93%)	0.04	18 (3%) 48 47	19, 29, 56, 90	0
1	C	537/576 (93%)	-0.09	24 (4%) 38 37	18, 27, 54, 90	1 (0%)
1	D	535/576 (92%)	0.22	26 (4%) 35 34	17, 32, 60, 93	1 (0%)
All	All	2143/2304 (93%)	0.00	87 (4%) 41 40	17, 28, 57, 101	2 (0%)

All (87) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	408	ILE	6.2
1	C	340	ALA	6.0
1	B	408	ILE	5.5
1	A	39	THR	5.4
1	D	408	ILE	5.4
1	B	38	THR	5.4
1	A	40	THR	4.8
1	A	576	SER	4.5
1	D	40	THR	4.3
1	B	39	THR	4.3
1	C	278	ARG	4.2
1	A	41	THR	4.1
1	A	339	ASP	4.1
1	B	40	THR	4.1
1	D	407	SER	3.9
1	D	147	ARG	3.9
1	D	335	GLY	3.8
1	D	41	THR	3.8
1	C	336	SER	3.7
1	C	576	SER	3.7
1	B	409	ALA	3.7

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Mol	Chain	Res	Type	RSRZ
1	D	409	ALA	3.7
1	C	339	ASP	3.7
1	D	39	THR	3.6
1	A	409	ALA	3.6
1	C	408	ILE	3.4
1	D	340	ALA	3.4
1	C	335	GLY	3.4
1	C	38	THR	3.3
1	A	173	ASP	3.3
1	B	576	SER	3.2
1	B	340	ALA	3.1
1	C	173	ASP	3.1
1	D	557[A]	ARG	3.1
1	D	406	ASP	3.1
1	D	42	THR	3.1
1	B	147	ARG	3.1
1	A	335	GLY	3.0
1	C	156	ASN	3.0
1	D	405	ASN	3.0
1	C	406	ASP	3.0
1	A	548	ARG	2.9
1	D	274	LYS	2.9
1	D	172	SER	2.9
1	A	340	ALA	2.9
1	A	274	LYS	2.8
1	B	335	GLY	2.8
1	C	407	SER	2.7
1	D	197	HIS	2.7
1	B	406	ASP	2.7
1	B	41	THR	2.7
1	B	42	THR	2.7
1	B	339	ASP	2.6
1	D	205	ASP	2.6
1	B	407	SER	2.6
1	D	575	GLN	2.6
1	C	273	GLU	2.6
1	C	409	ALA	2.5
1	B	89	ASP	2.5
1	A	172	SER	2.5
1	B	437	SER	2.5
1	C	438	GLY	2.4
1	D	219	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	561	GLU	2.4
1	A	437	SER	2.4
1	D	567	ALA	2.4
1	A	273	GLU	2.4
1	D	156	ASN	2.4
1	A	89	ASP	2.4
1	D	576	SER	2.3
1	D	339	ASP	2.3
1	A	277	ARG	2.3
1	B	273	GLU	2.3
1	C	277	ARG	2.3
1	D	278	ARG	2.3
1	A	42	THR	2.2
1	C	171	ASP	2.2
1	D	273	GLU	2.2
1	C	575	GLN	2.2
1	C	271	VAL	2.2
1	C	341	GLU	2.2
1	C	134	LYS	2.2
1	D	50	PRO	2.1
1	C	41	THR	2.1
1	C	197	HIS	2.1
1	C	546	GLY	2.0
1	B	276	GLU	2.0

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

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

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MAN	J	8	11/12	0.64	0.19	43,45,47,52	0
3	MAN	G	8	11/12	0.72	0.20	42,45,49,49	0
3	MAN	J	7	11/12	0.73	0.14	41,43,46,46	0
3	MAN	F	8	11/12	0.74	0.17	40,45,49,49	0

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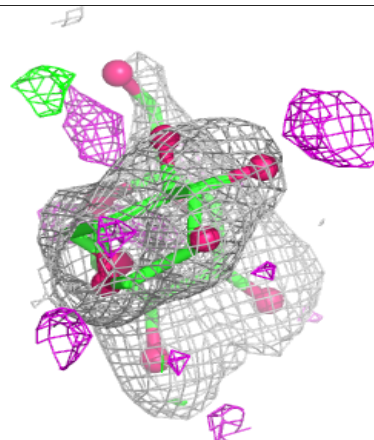
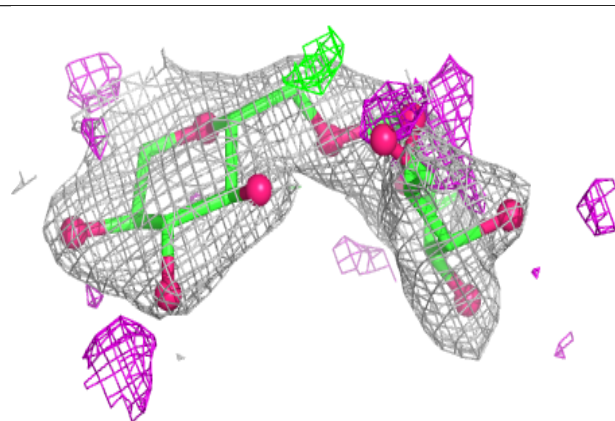
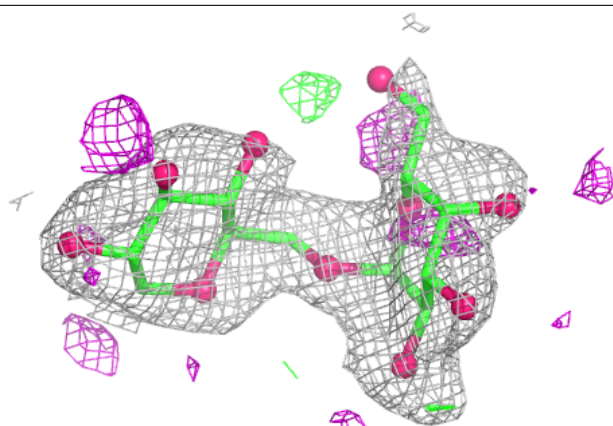
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MAN	H	8	11/12	0.77	0.16	44,45,48,48	0
3	MAN	G	7	11/12	0.77	0.12	41,44,48,49	0
3	MAN	F	7	11/12	0.77	0.14	39,42,45,48	0
3	MAN	H	7	11/12	0.79	0.13	39,43,45,46	0
2	GLA	E	2	11/12	0.79	0.18	51,62,70,74	0
2	GLA	I	2	11/12	0.82	0.17	51,66,76,76	0
3	MAN	F	6	11/12	0.84	0.12	35,37,43,45	0
3	MAN	J	6	11/12	0.84	0.12	32,35,42,43	0
3	MAN	H	6	11/12	0.85	0.12	33,36,43,44	0
3	BMA	F	3	11/12	0.85	0.10	32,36,39,40	0
3	BMA	H	3	11/12	0.86	0.10	31,36,40,43	0
3	MAN	J	5	11/12	0.87	0.10	31,34,42,47	0
3	BMA	G	3	11/12	0.88	0.10	28,33,38,41	0
3	MAN	G	6	11/12	0.88	0.10	31,37,41,44	0
3	MAN	H	5	11/12	0.89	0.10	33,36,40,45	0
3	MAN	J	4	11/12	0.89	0.09	30,32,36,40	0
3	BMA	J	3	11/12	0.90	0.10	27,35,42,44	0
2	GLC	I	1	11/12	0.91	0.11	40,47,53,54	0
3	MAN	F	5	11/12	0.91	0.09	32,36,42,43	0
3	MAN	G	4	11/12	0.92	0.09	31,33,39,49	0
3	MAN	H	4	11/12	0.92	0.08	33,35,39,47	0
2	GLC	E	1	11/12	0.92	0.10	37,41,50,55	0
3	MAN	G	5	11/12	0.93	0.08	32,34,40,43	0
3	MAN	F	4	11/12	0.93	0.07	31,35,39,45	0
3	NAG	J	2	14/15	0.94	0.08	24,27,30,33	0
3	NAG	G	2	14/15	0.95	0.07	25,27,29,31	0
3	NAG	H	2	14/15	0.95	0.07	26,29,32,34	0
3	NAG	F	2	14/15	0.95	0.07	27,30,33,34	0
3	NAG	F	1	14/15	0.96	0.09	23,26,27,29	0
3	NAG	G	1	14/15	0.97	0.07	23,26,29,33	0
3	NAG	J	1	14/15	0.97	0.07	24,25,26,27	0
3	NAG	H	1	14/15	0.97	0.08	24,26,29,31	0

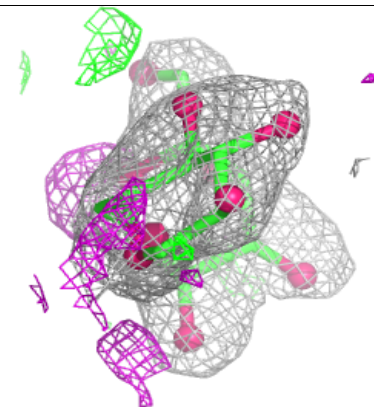
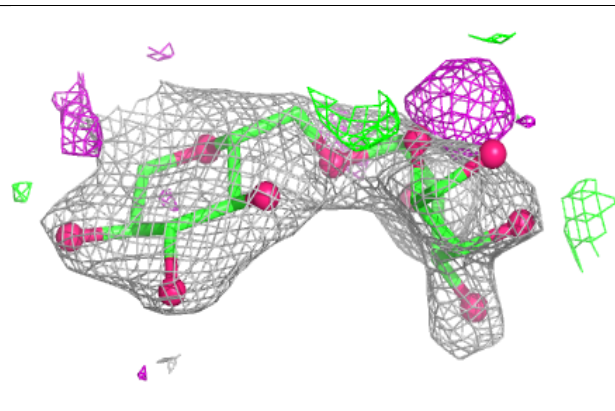
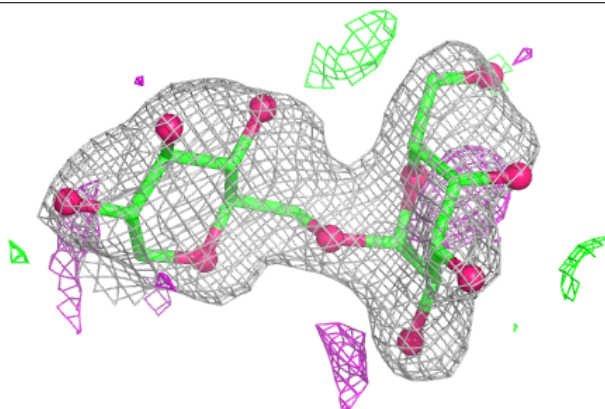
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain E:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

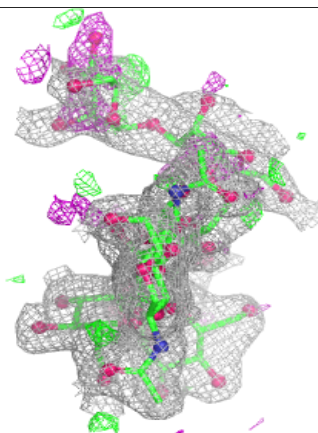
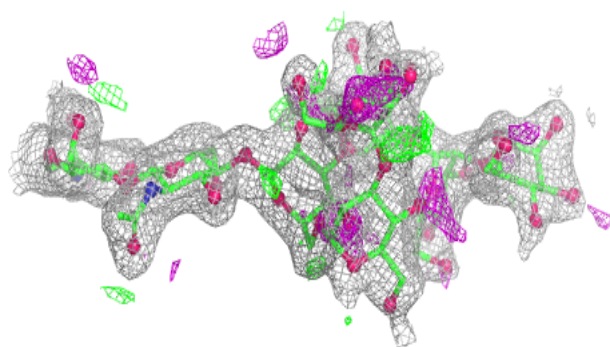
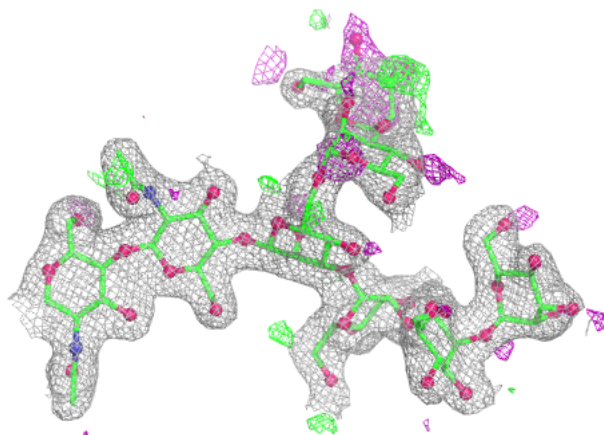
**Electron density around Chain I:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

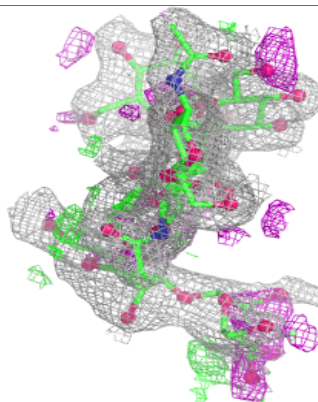
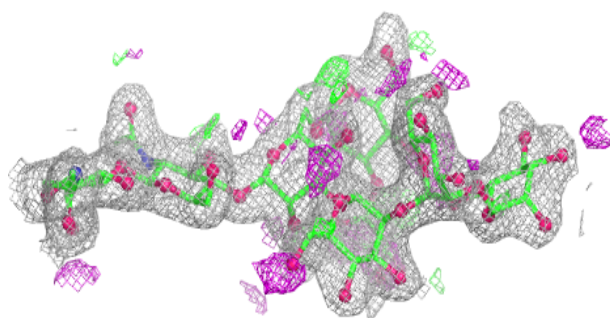
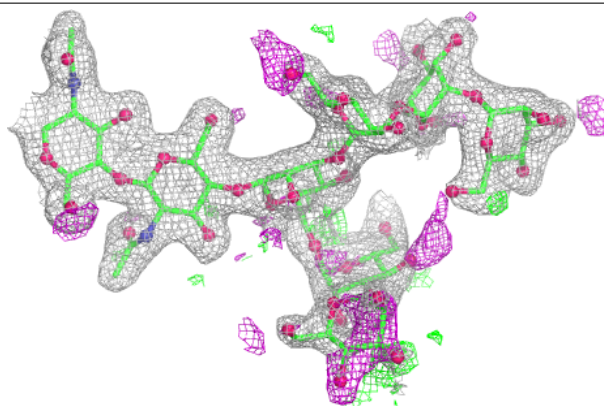


Electron density around Chain F:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

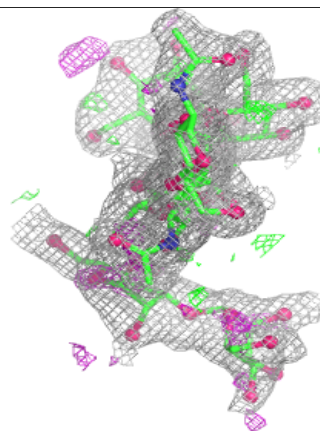
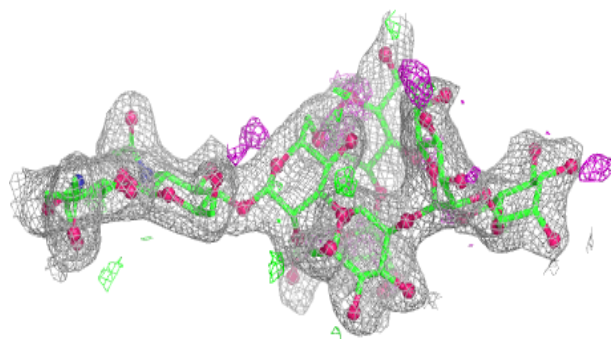
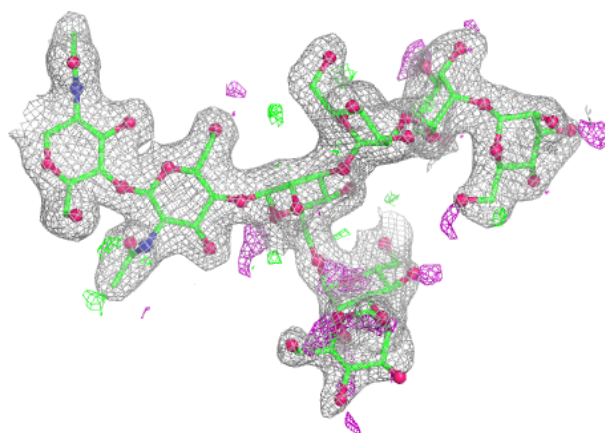
**Electron density around Chain G:**

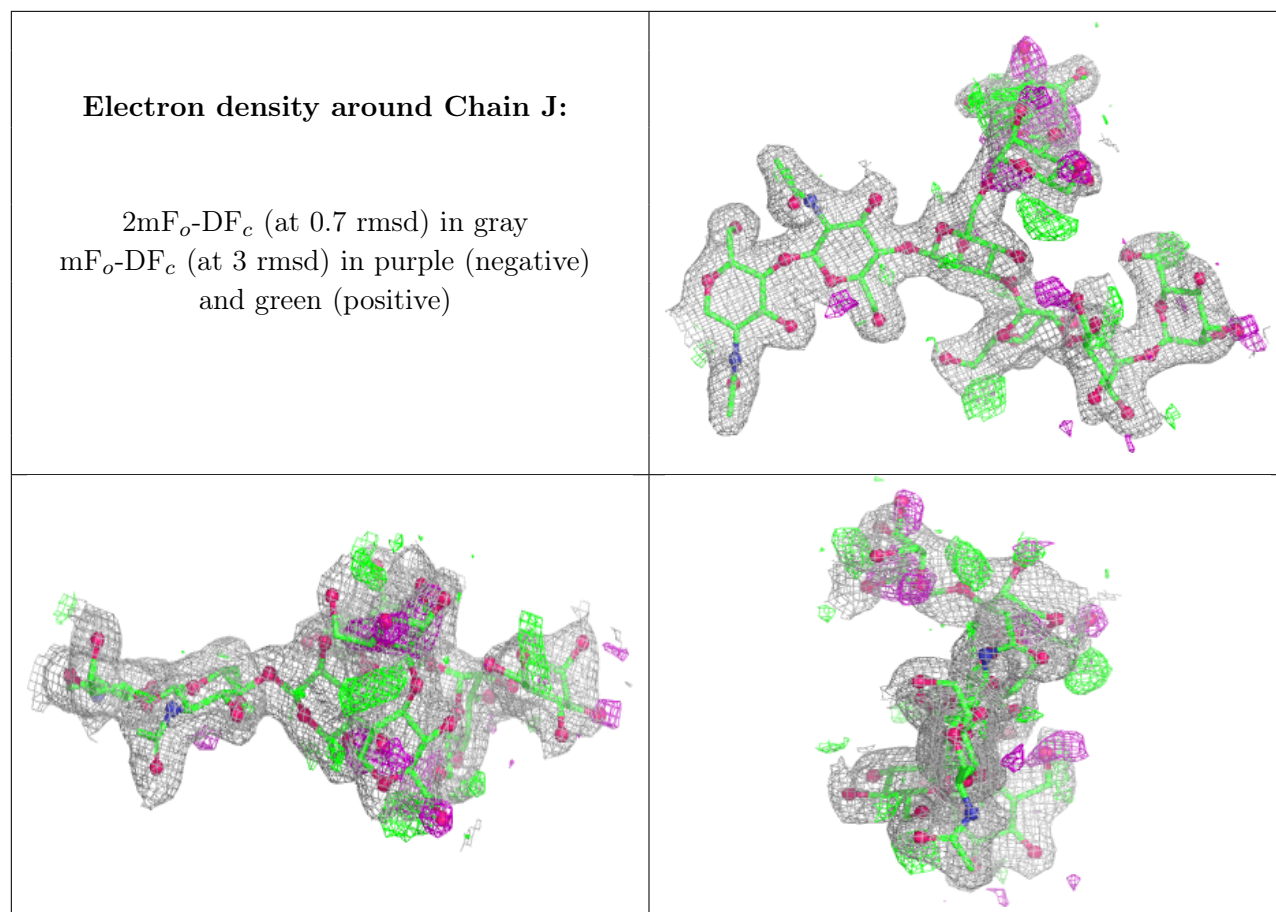
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain H:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	TRS	C	604	8/8	0.55	0.41	24,28,30,33	8
5	TRS	D	602	8/8	0.60	0.45	30,34,39,42	8
5	TRS	A	602	8/8	0.68	0.37	22,27,31,31	8
8	GLA	C	603	11/12	0.73	0.22	59,75,81,96	0
8	GLA	B	603	11/12	0.77	0.18	46,69,76,78	0
6	NAG	A	604	14/15	0.77	0.12	38,42,46,46	0
6	NAG	B	607	14/15	0.80	0.12	37,40,47,47	0
6	NAG	C	608	14/15	0.80	0.13	39,42,48,49	0
6	NAG	D	608	14/15	0.81	0.12	39,42,45,45	0
6	NAG	B	606	14/15	0.81	0.12	37,42,46,50	0
6	NAG	D	606	14/15	0.81	0.12	39,43,46,48	0
6	NAG	C	609	14/15	0.83	0.12	35,38,42,42	0

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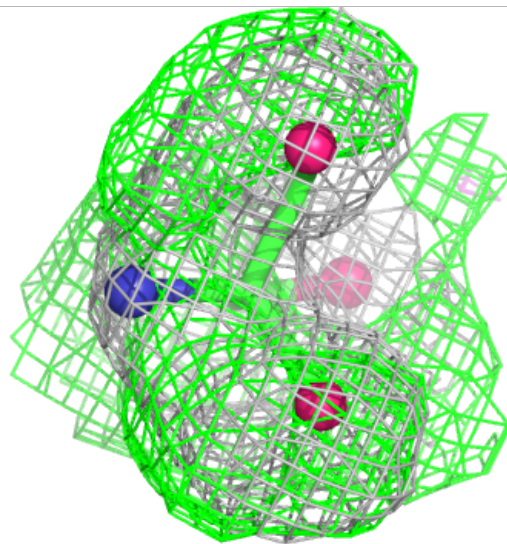
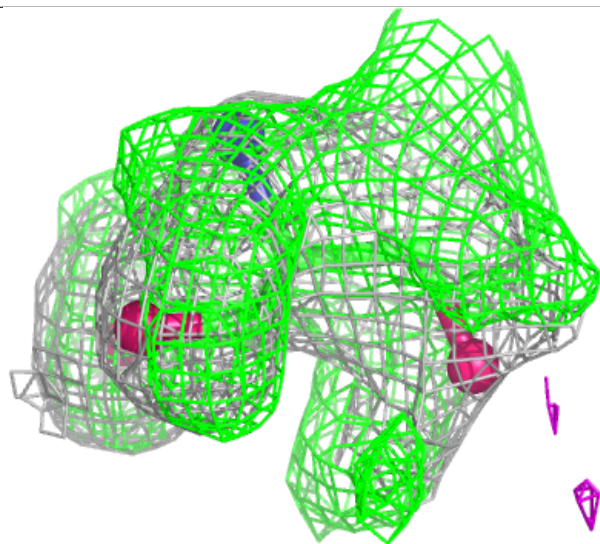
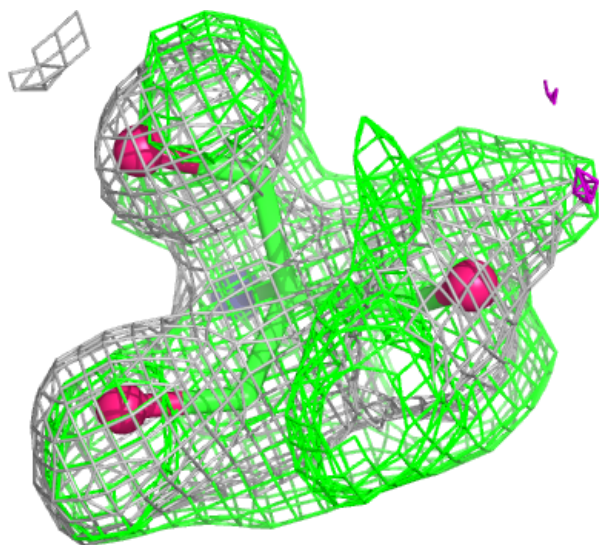
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	NAG	C	610	14/15	0.85	0.12	36,40,41,43	0
6	NAG	D	607	14/15	0.86	0.10	35,39,42,46	0
6	NAG	B	608	14/15	0.87	0.10	38,41,42,44	0
6	NAG	D	605	14/15	0.88	0.10	35,37,40,40	0
7	GLC	C	602	11/12	0.88	0.12	33,43,55,55	0
7	GLC	B	602	11/12	0.90	0.10	30,40,46,48	0
6	NAG	A	605	14/15	0.90	0.09	34,37,43,45	0
9	SO4	C	606	5/5	0.90	0.22	19,20,22,23	5
9	SO4	D	603	5/5	0.90	0.12	28,29,31,32	5
6	NAG	A	603	14/15	0.91	0.08	30,33,35,37	0
4	FRU	D	601	12/12	0.91	0.10	26,33,42,42	0
4	FRU	B	601	12/12	0.91	0.09	24,31,36,42	0
6	NAG	A	606	14/15	0.91	0.09	33,37,39,40	0
6	NAG	C	607	14/15	0.92	0.08	30,35,37,38	0
6	NAG	B	605	14/15	0.93	0.08	29,33,37,38	0
4	FRU	A	601	12/12	0.94	0.08	25,29,32,35	0
4	FRU	C	601	12/12	0.95	0.08	22,28,35,47	0
9	SO4	C	605	5/5	0.95	0.16	22,23,26,26	5
9	SO4	B	604	5/5	0.97	0.16	16,18,20,20	5
9	SO4	D	604	5/5	0.97	0.17	22,22,27,27	5

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

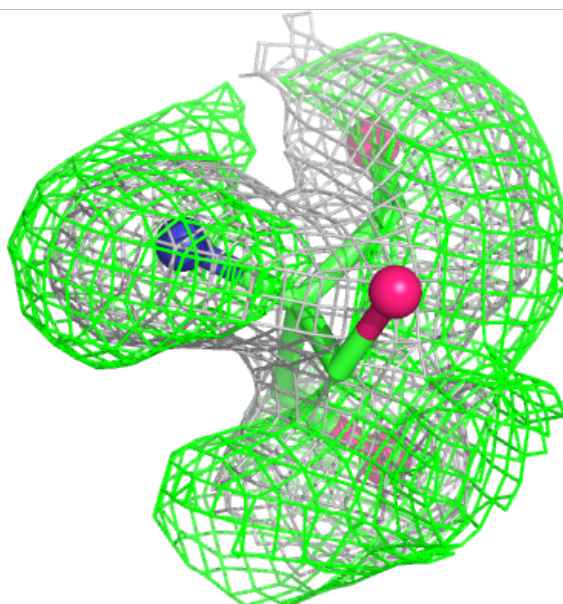
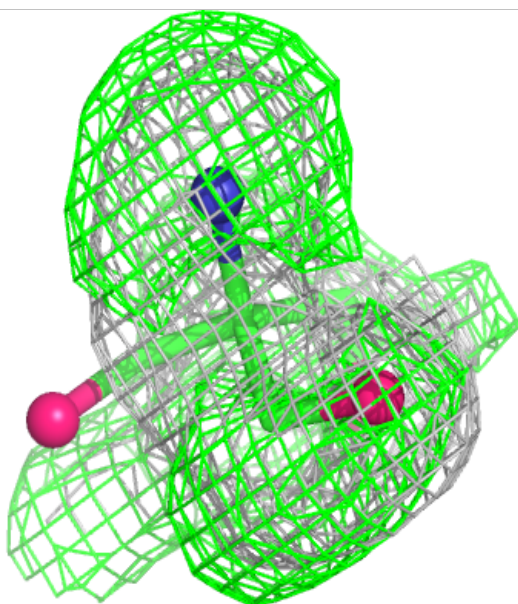
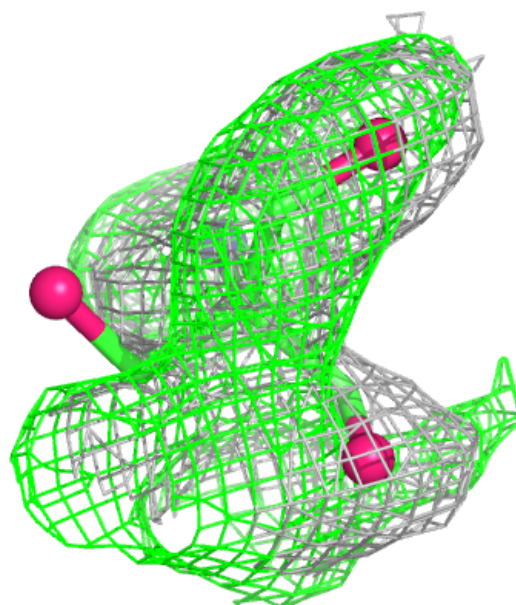
Electron density around TRS C 604:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



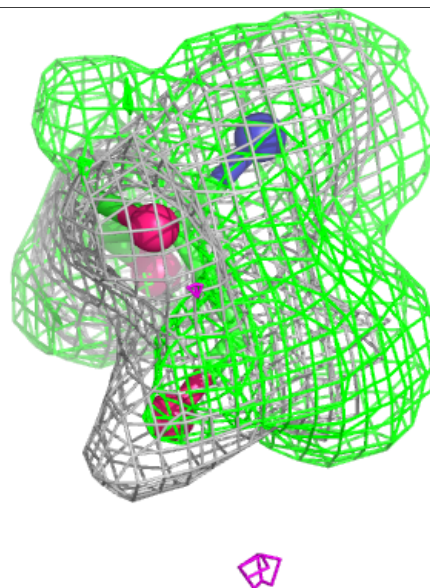
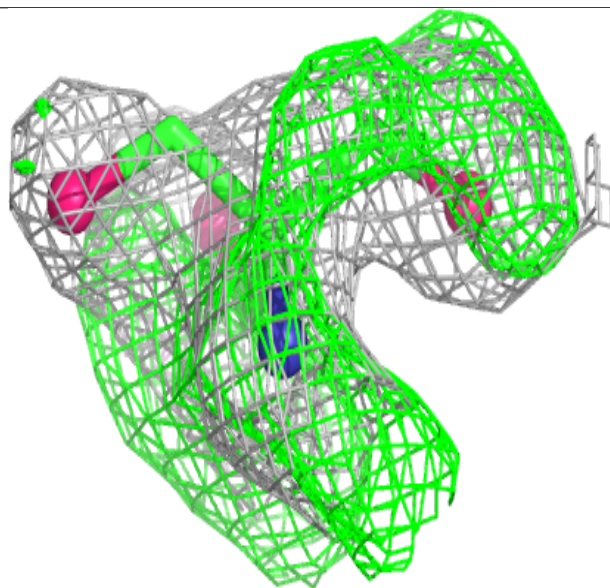
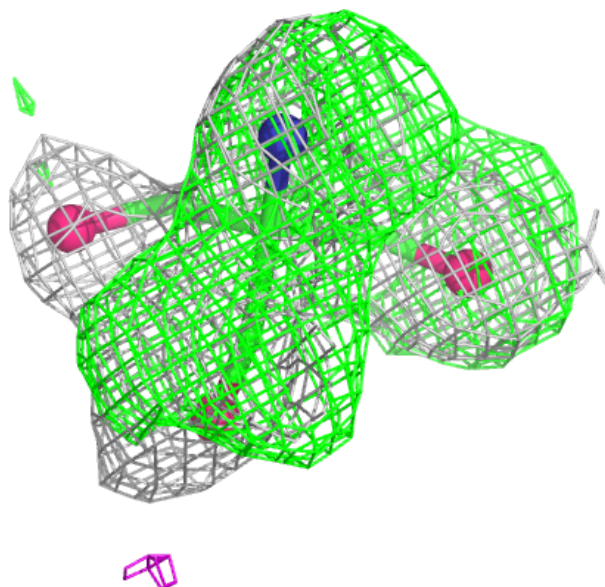
Electron density around TRS D 602:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



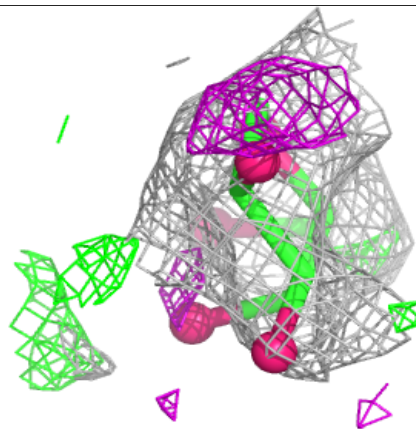
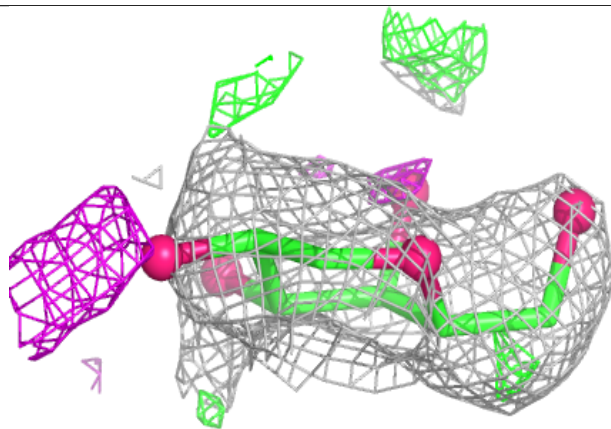
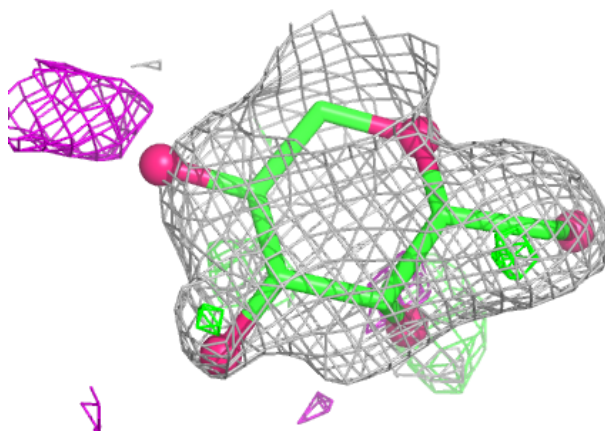
Electron density around TRS A 602:

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and green (positive)



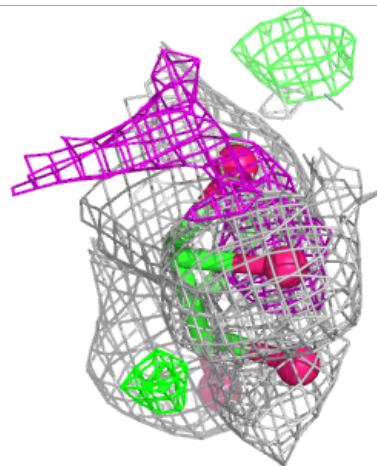
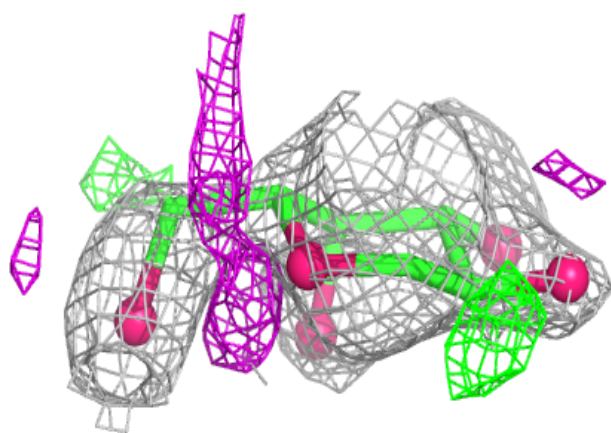
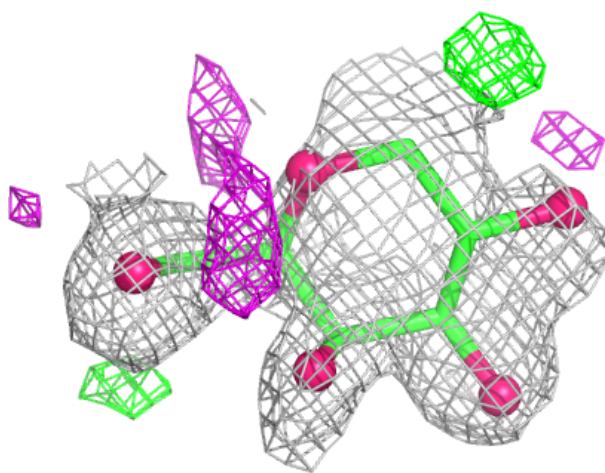
Electron density around GLA C 603:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



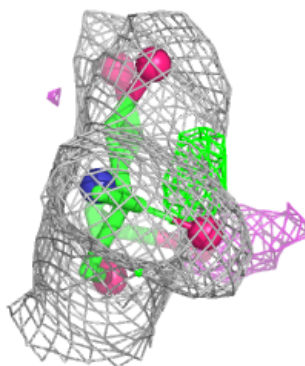
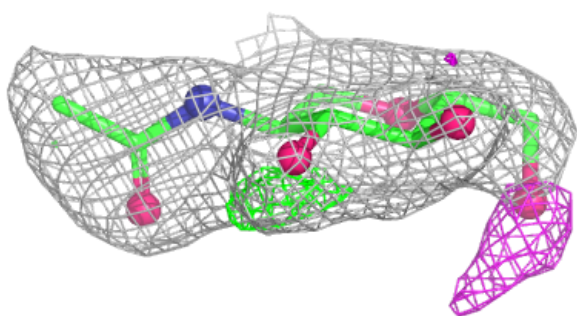
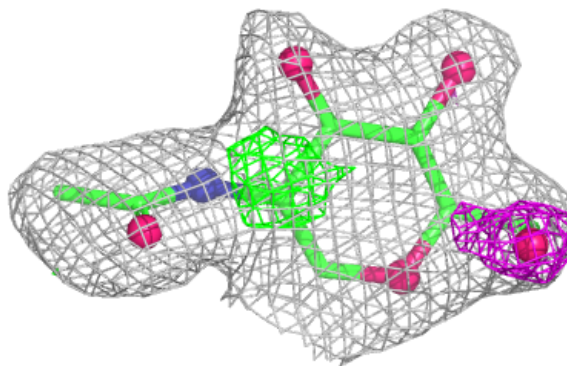
Electron density around GLA B 603:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

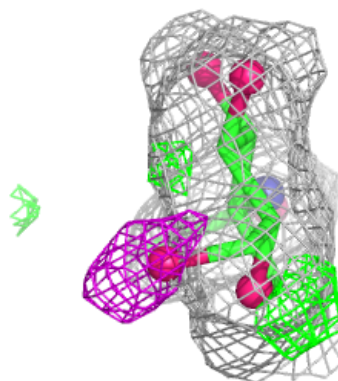
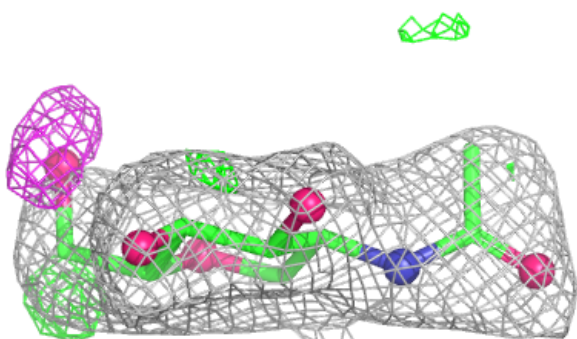
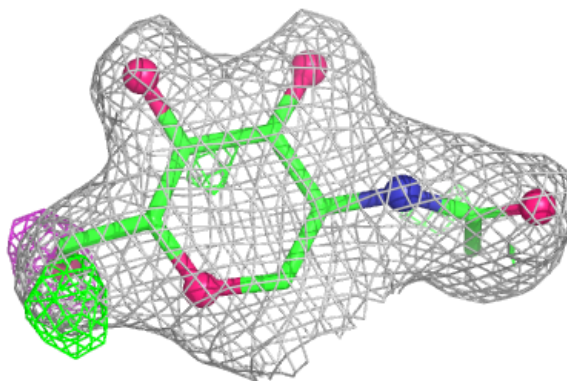


Electron density around NAG A 604:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

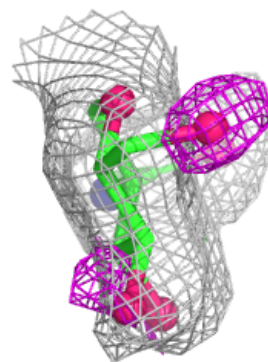
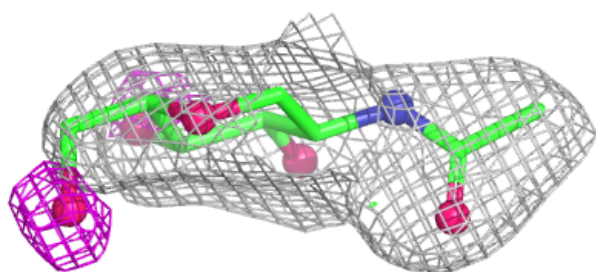
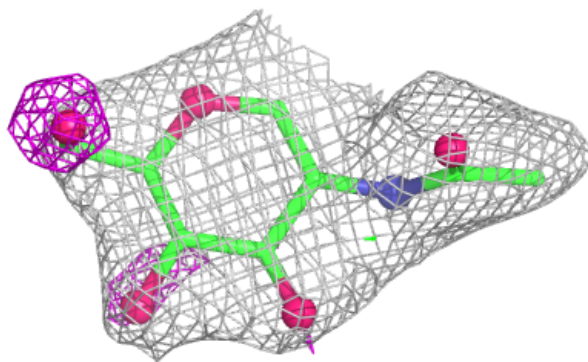
**Electron density around NAG B 607:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



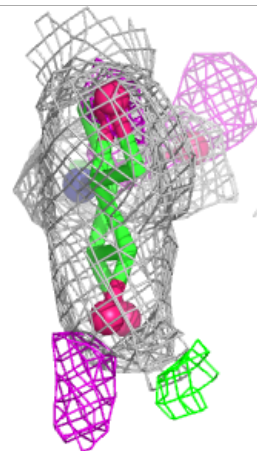
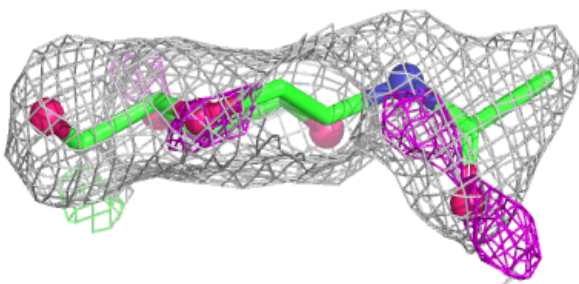
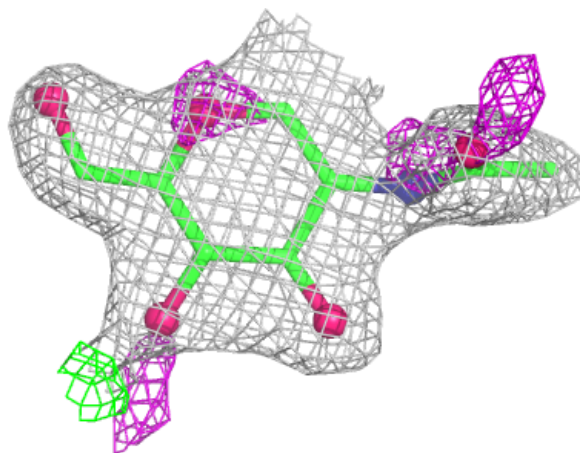
Electron density around NAG C 608:

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 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



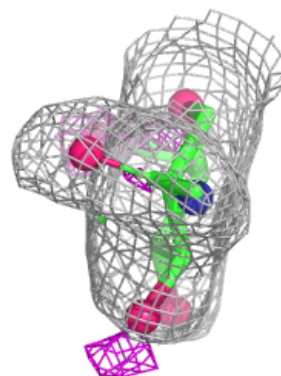
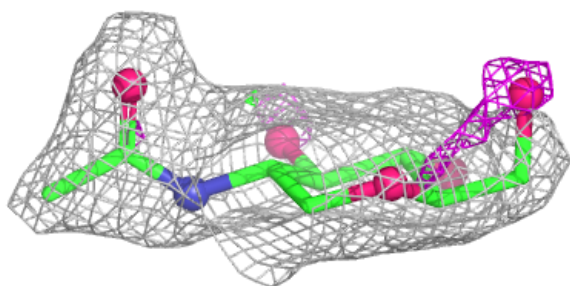
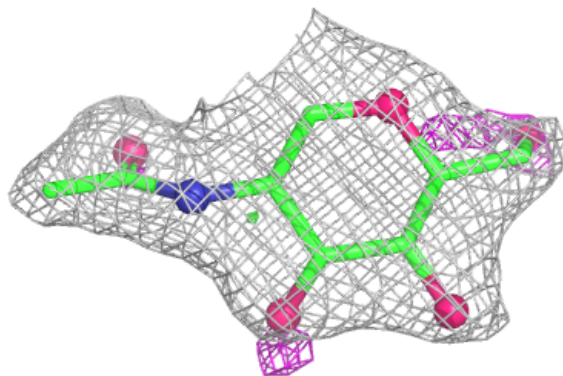
Electron density around NAG D 608:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

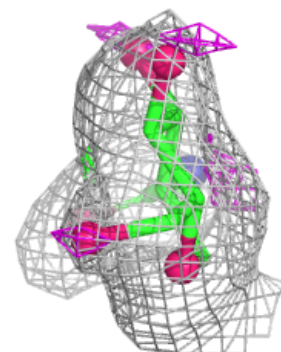
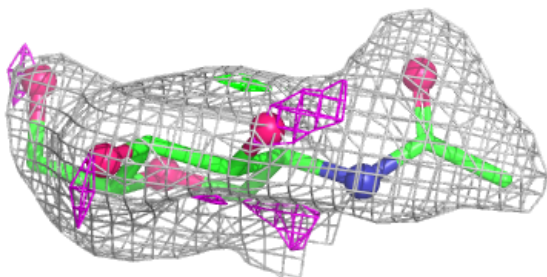
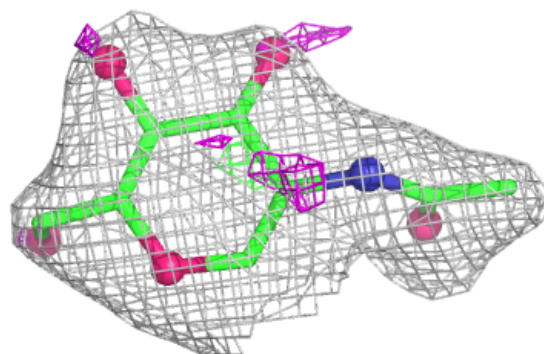


Electron density around NAG B 606:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

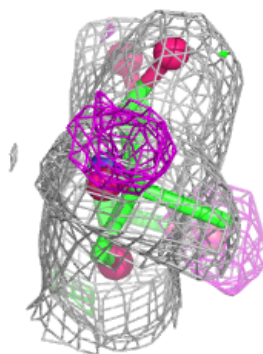
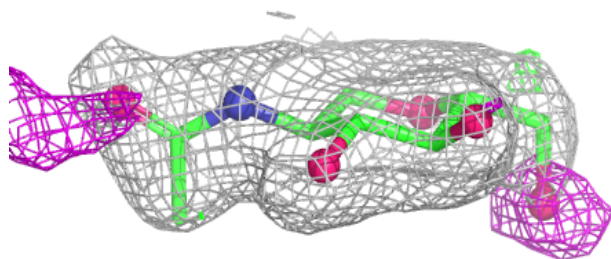
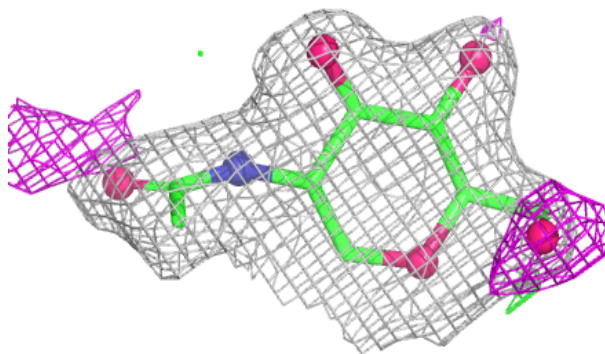
**Electron density around NAG D 606:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



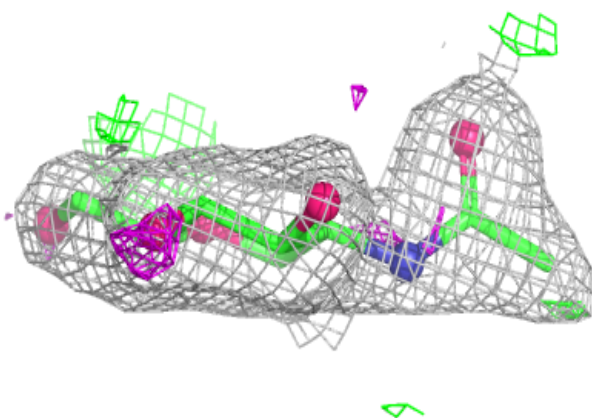
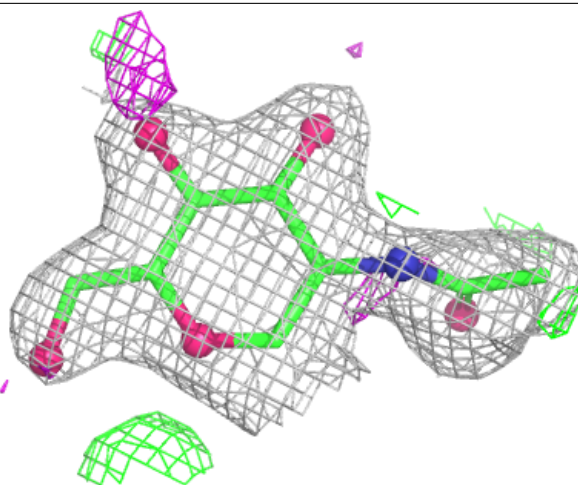
Electron density around NAG C 609:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



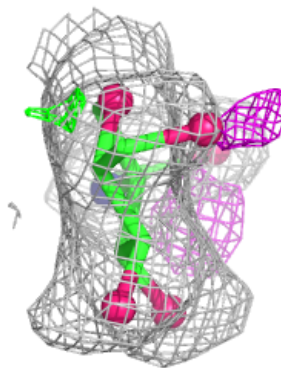
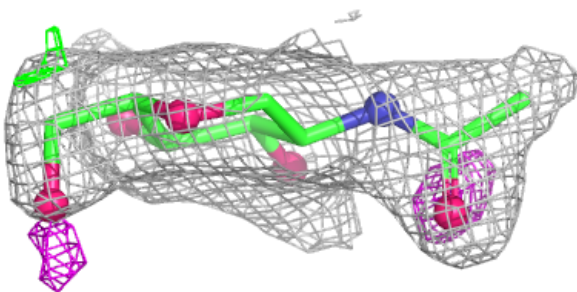
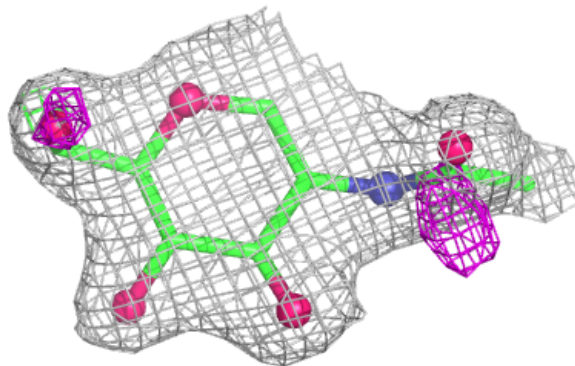
Electron density around NAG C 610:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



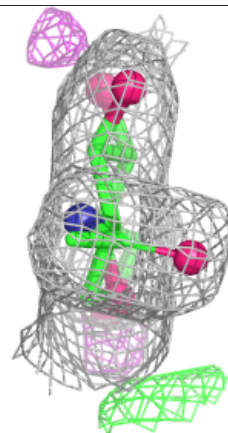
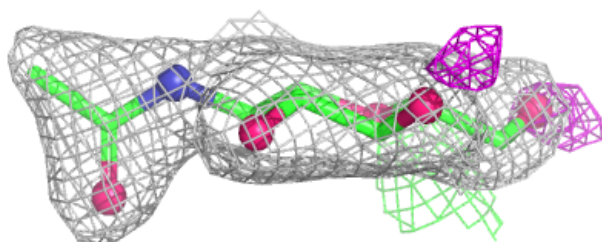
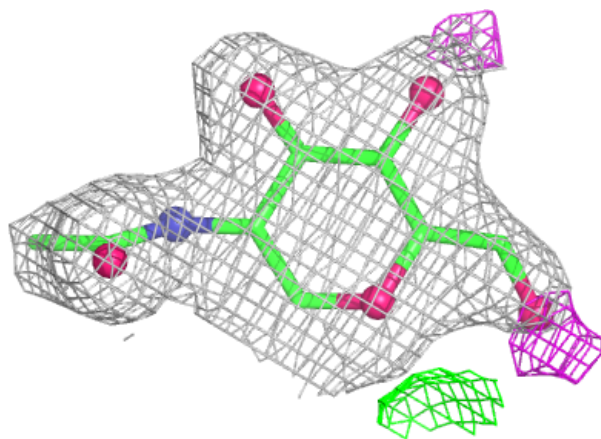
Electron density around NAG D 607:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



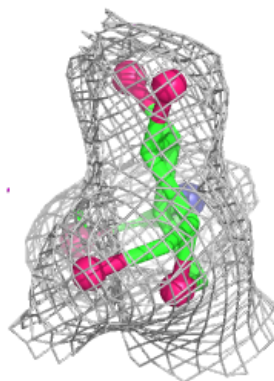
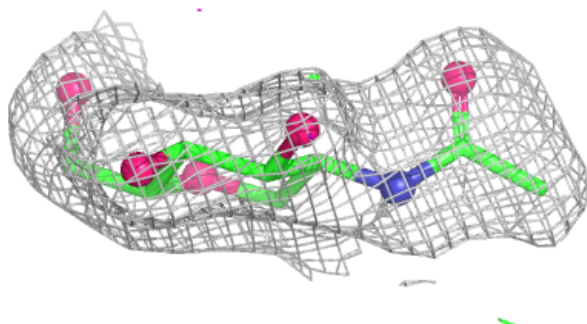
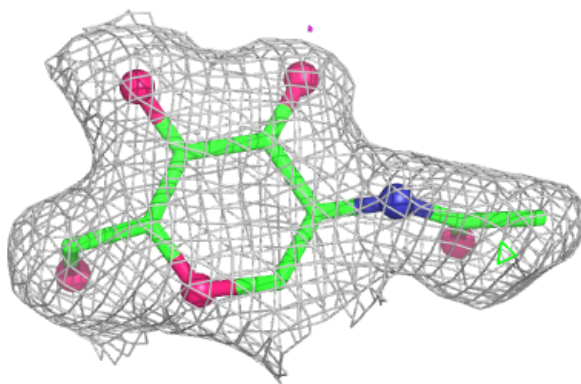
Electron density around NAG B 608:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



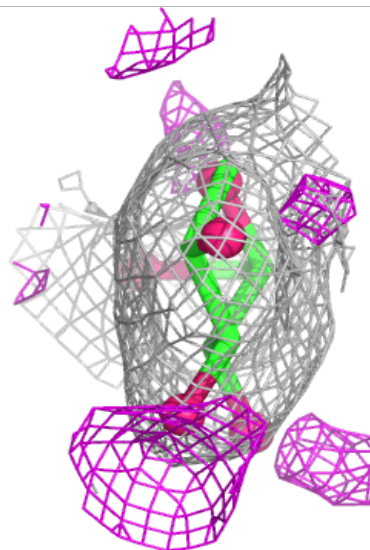
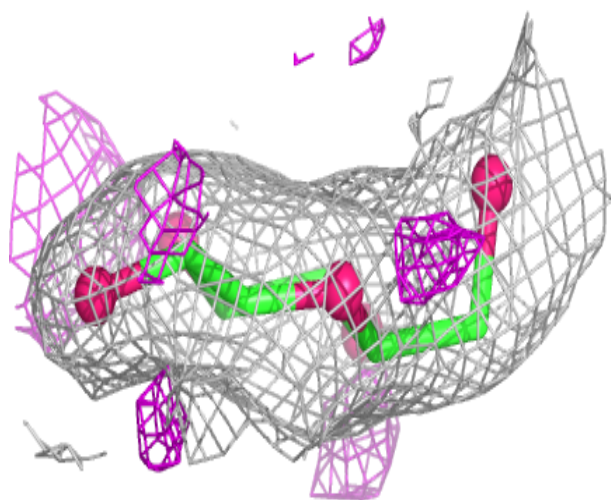
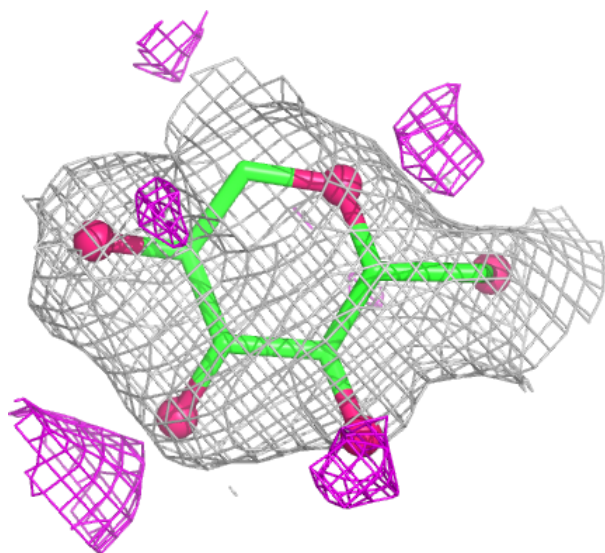
Electron density around NAG D 605:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



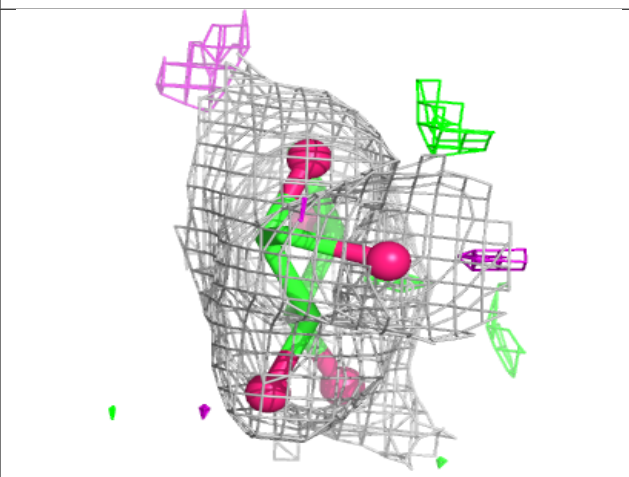
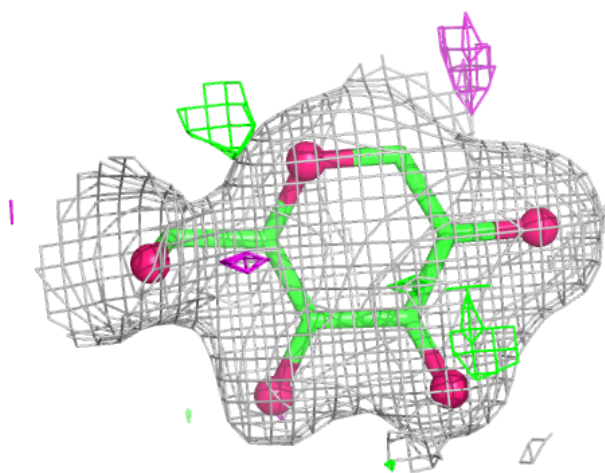
Electron density around GLC C 602:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



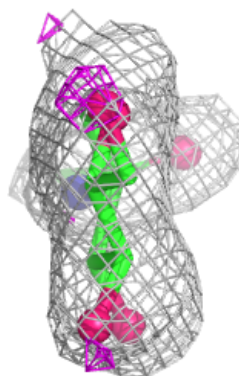
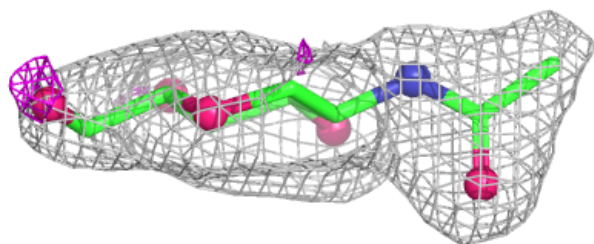
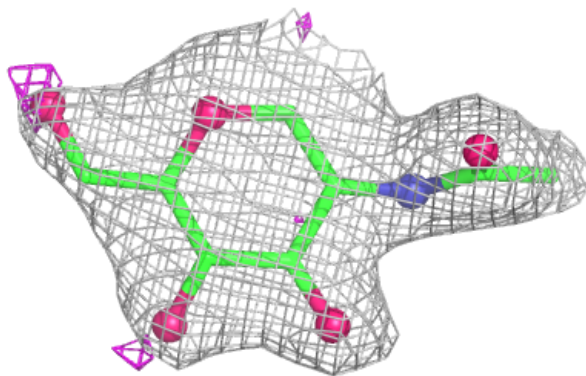
Electron density around GLC B 602:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



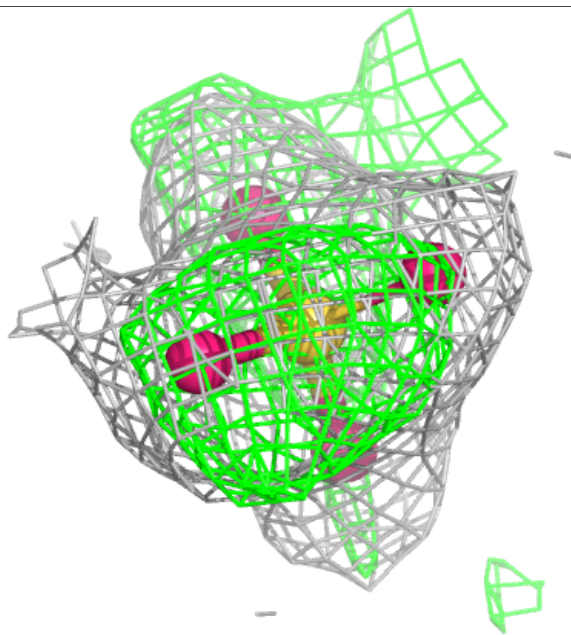
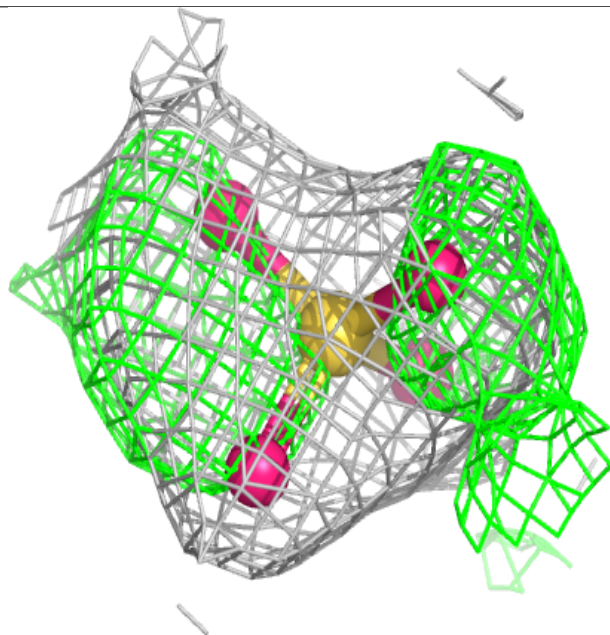
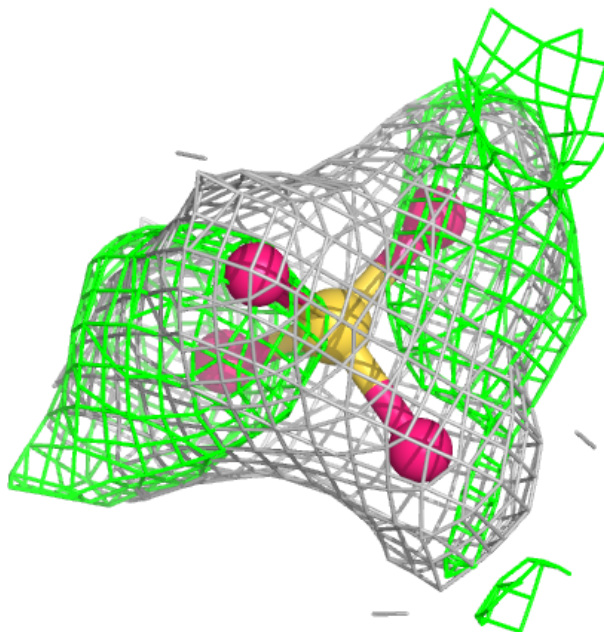
Electron density around NAG A 605:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



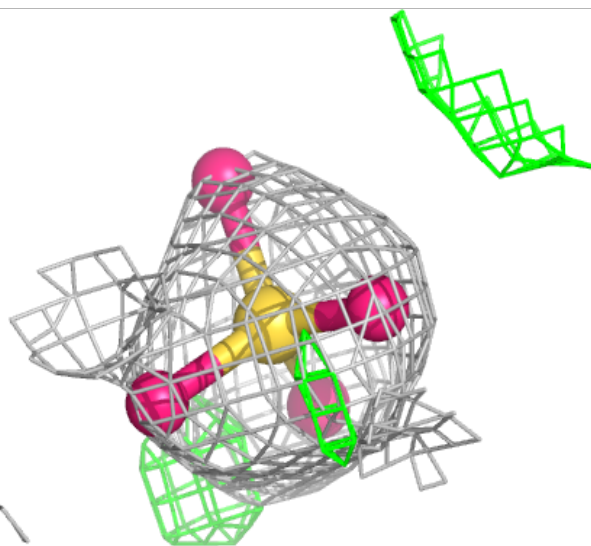
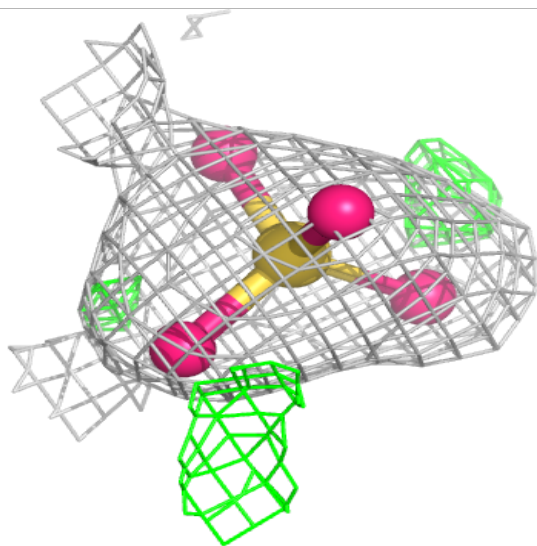
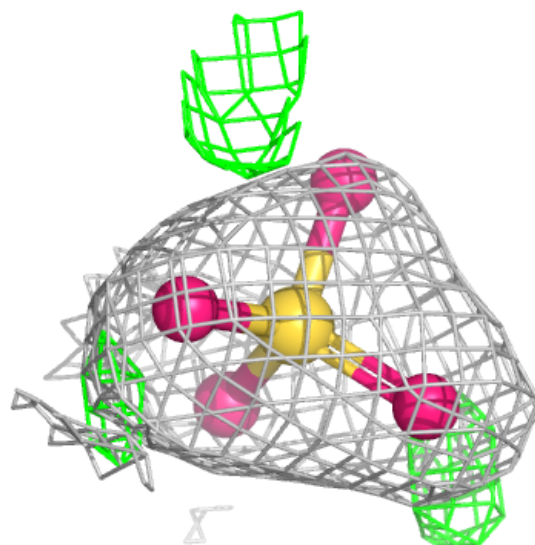
Electron density around SO4 C 606:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



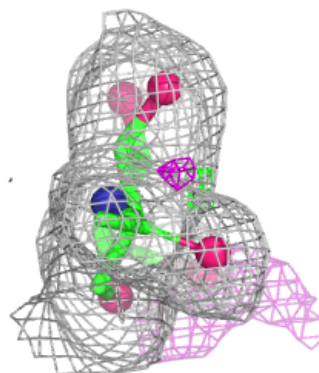
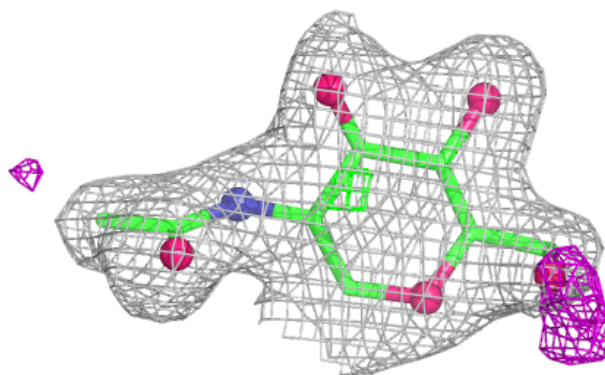
Electron density around SO4 D 603:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



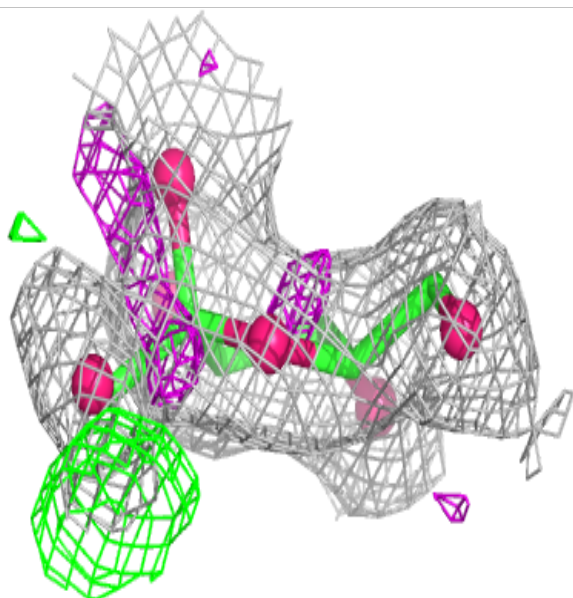
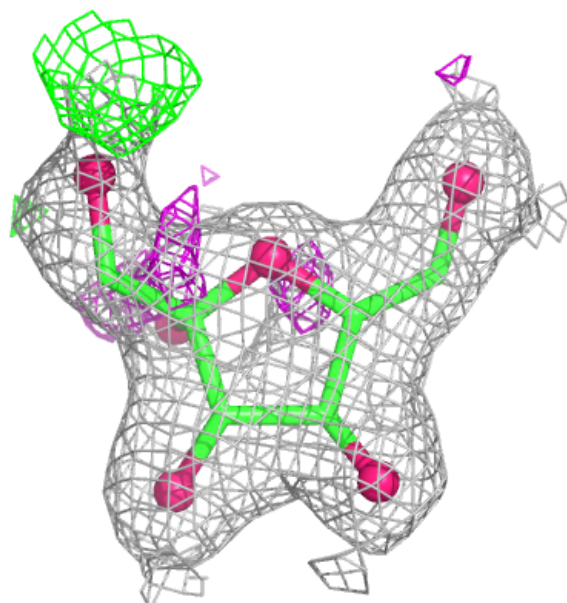
Electron density around NAG A 603:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



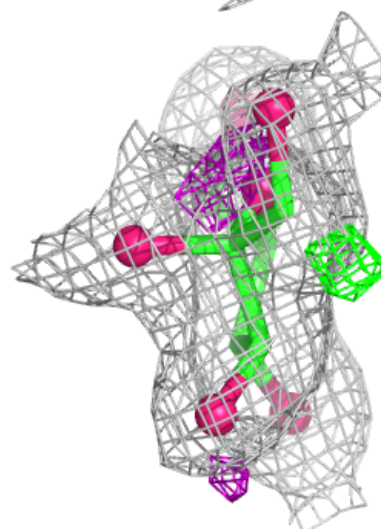
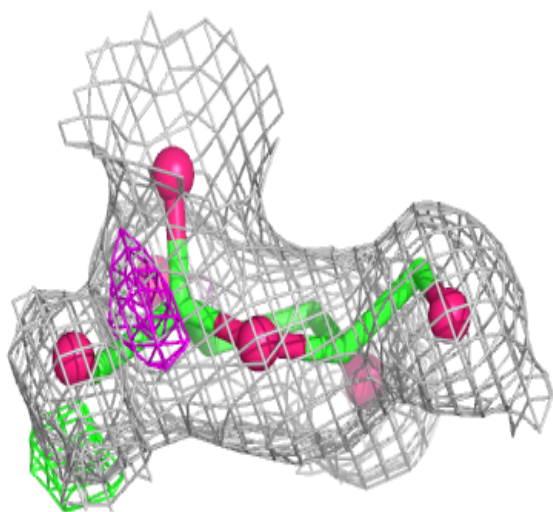
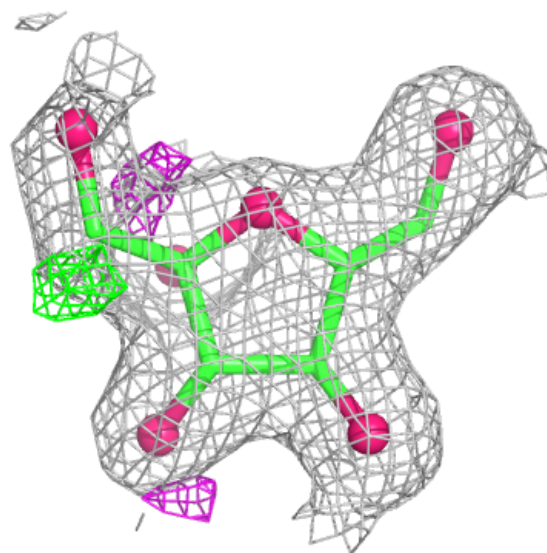
Electron density around FRU D 601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



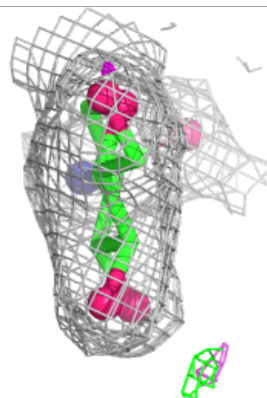
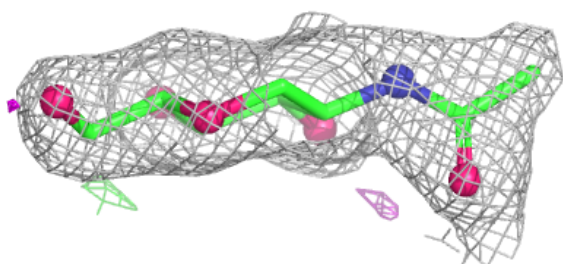
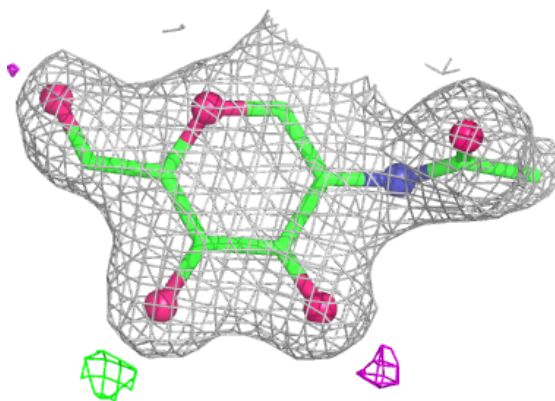
Electron density around FRU B 601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

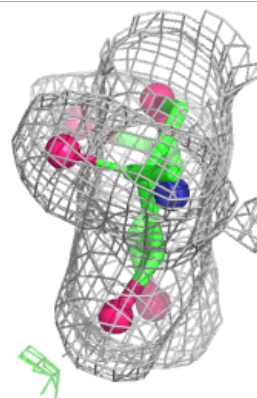
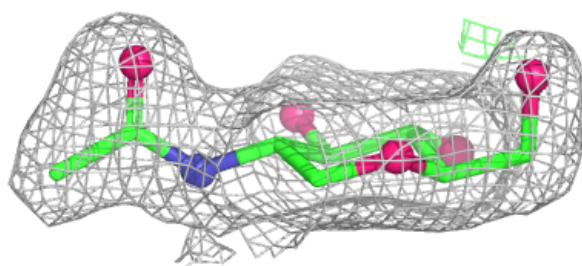
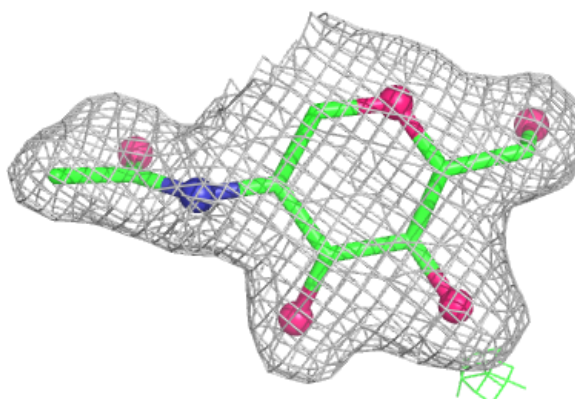


Electron density around NAG A 606:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

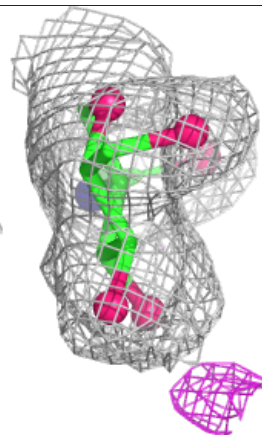
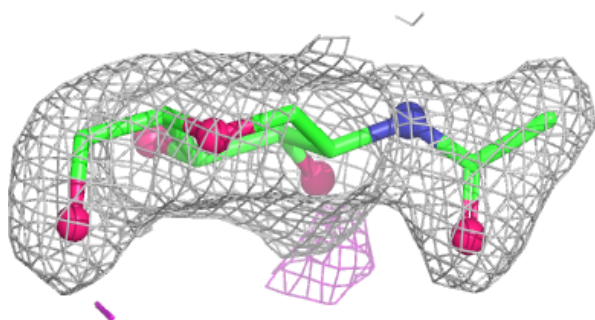
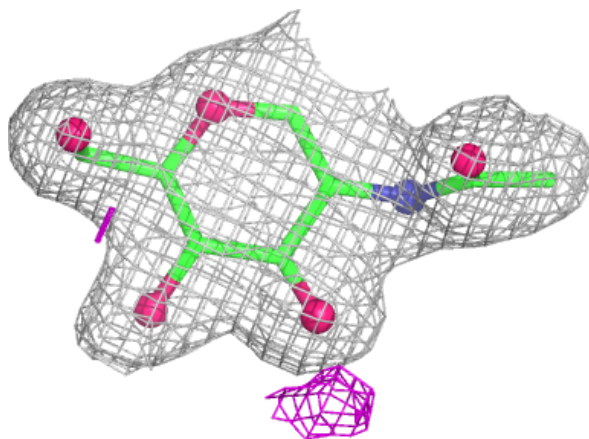
**Electron density around NAG C 607:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



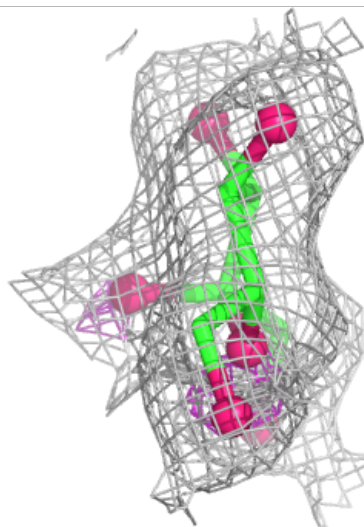
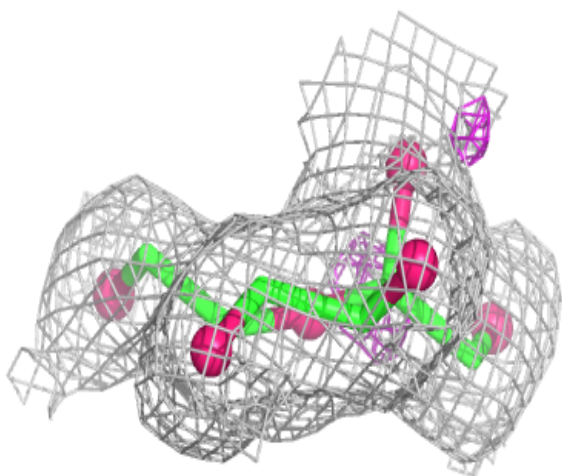
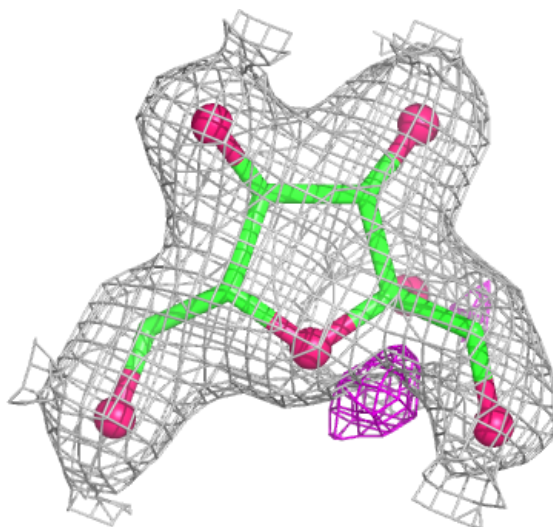
Electron density around NAG B 605:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



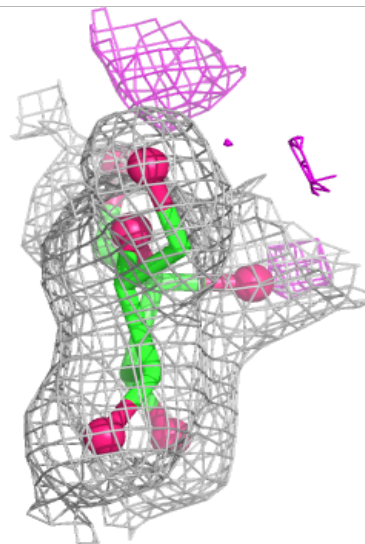
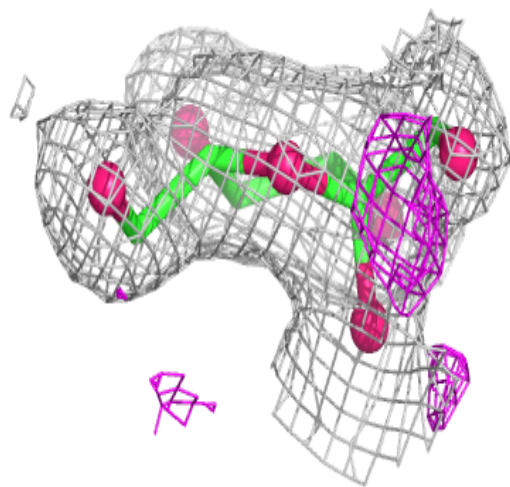
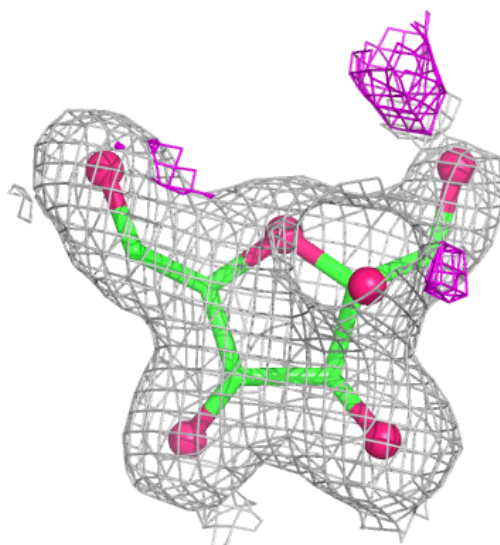
Electron density around FRU A 601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



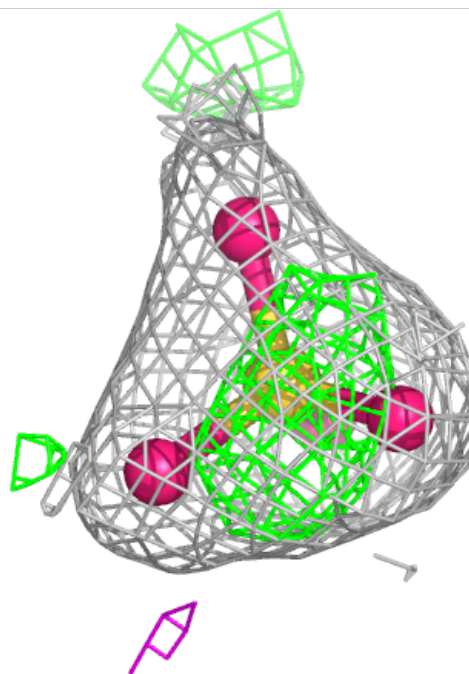
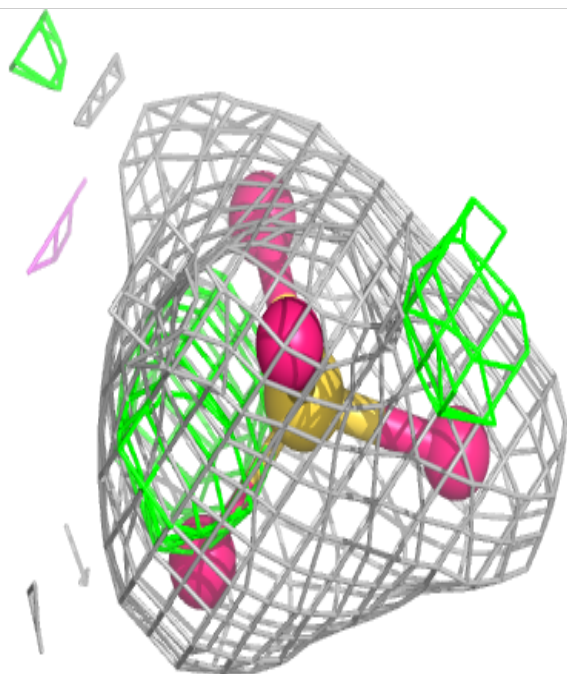
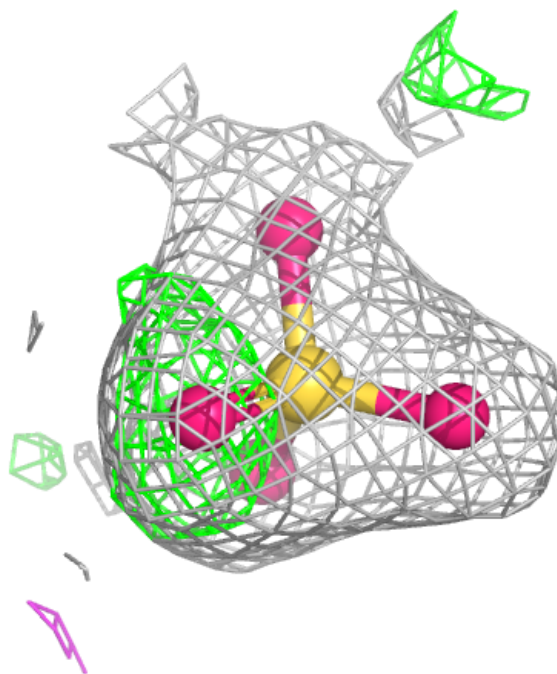
Electron density around FRU C 601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



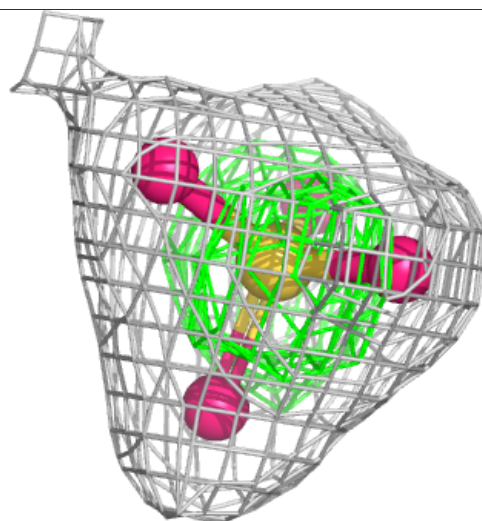
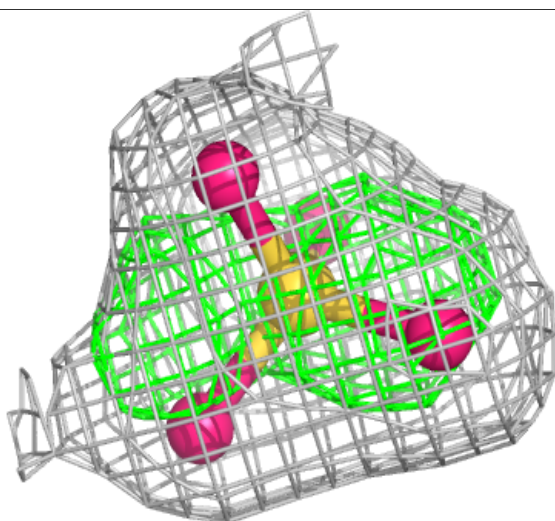
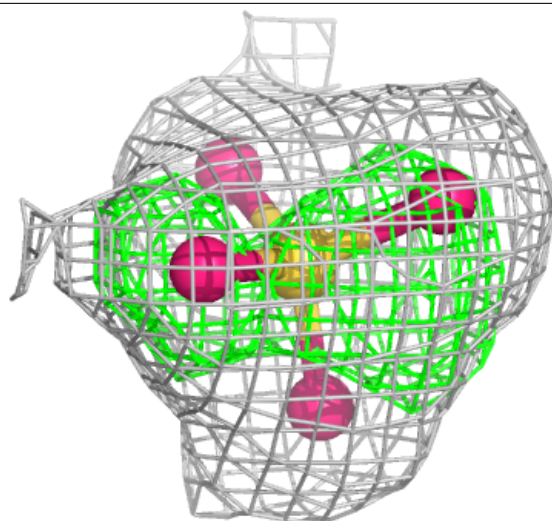
Electron density around SO4 C 605:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



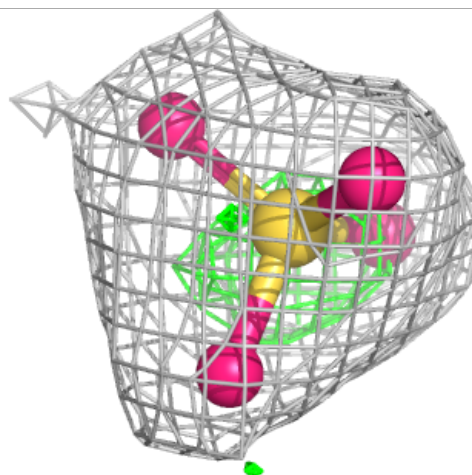
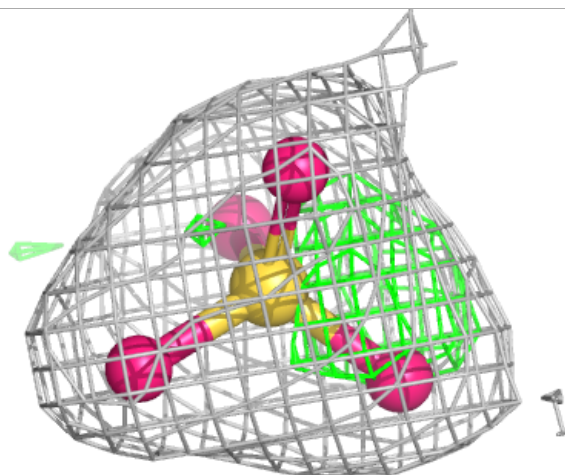
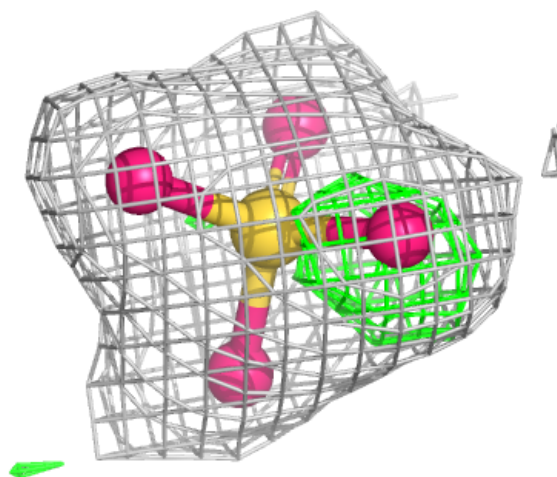
Electron density around SO4 B 604:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around SO4 D 604:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.