



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 9, 2020 – 03:56 AM BST

PDB ID : 5MHF
Title : Murine endoplasmic reticulum alpha-glucosidase I with N-9'-methoxynonyl-1-deoxynojirimycin
Authors : Hill, J.C.; Caputo, A.T.; Roversi, P.; Zitzmann, N.
Deposited on : 2016-11-24
Resolution : 2.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

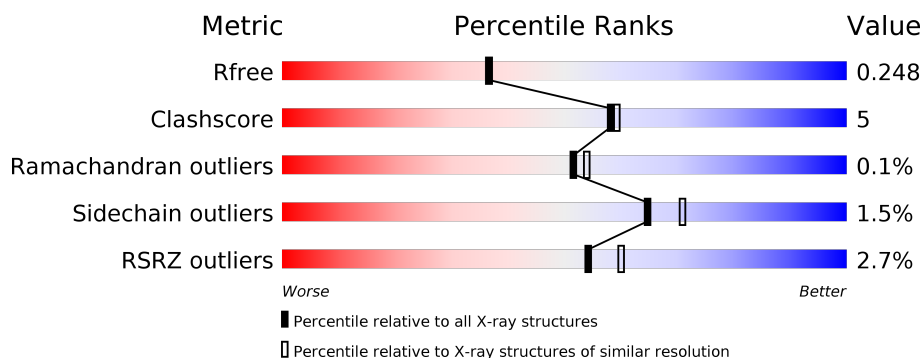
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 on 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	795	<div> <div>3%</div> <div> <div></div> <div>86%</div> <div>8%</div> <div>6%</div> </div> </div>
1	B	795	<div> <div>3%</div> <div> <div></div> <div>85%</div> <div>9%</div> <div>5%</div> </div> </div>
1	C	795	<div> <div>2%</div> <div> <div></div> <div>87%</div> <div>8%</div> <div>...</div> </div> </div>
1	D	795	<div> <div>2%</div> <div> <div></div> <div>87%</div> <div>9%</div> <div>...</div> </div> </div>
2	E	2	<div> <div></div> <div> <div>50%</div> <div>50%</div> </div> </div>
2	F	2	<div> <div></div> <div> <div>50%</div> <div>50%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	G	3	
3	H	3	

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
6	7PG	C	905	-	-	X	-
6	7PG	D	905	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 26145 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 Mannosyl-oligosaccharide glucosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	751	Total	C	N	O	S	0	2	0
			5975	3862	1051	1051	11			
1	B	752	Total	C	N	O	S	0	2	0
			5979	3864	1052	1052	11			
1	C	762	Total	C	N	O	S	0	2	0
			6051	3909	1063	1068	11			
1	D	767	Total	C	N	O	S	0	2	0
			6081	3925	1070	1075	11			

There are 76 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	56	GLU	-	expression tag	UNP Q80UM7
A	57	THR	-	expression tag	UNP Q80UM7
A	58	GLY	-	expression tag	UNP Q80UM7
A	835	ALA	-	expression tag	UNP Q80UM7
A	836	SER	-	expression tag	UNP Q80UM7
A	837	TRP	-	expression tag	UNP Q80UM7
A	838	SER	-	expression tag	UNP Q80UM7
A	839	HIS	-	expression tag	UNP Q80UM7
A	840	PRO	-	expression tag	UNP Q80UM7
A	841	GLN	-	expression tag	UNP Q80UM7
A	842	PHE	-	expression tag	UNP Q80UM7
A	843	GLU	-	expression tag	UNP Q80UM7
A	844	LYS	-	expression tag	UNP Q80UM7
A	845	HIS	-	expression tag	UNP Q80UM7
A	846	HIS	-	expression tag	UNP Q80UM7
A	847	HIS	-	expression tag	UNP Q80UM7
A	848	HIS	-	expression tag	UNP Q80UM7
A	849	HIS	-	expression tag	UNP Q80UM7
A	850	HIS	-	expression tag	UNP Q80UM7
B	56	GLU	-	expression tag	UNP Q80UM7
B	57	THR	-	expression tag	UNP Q80UM7

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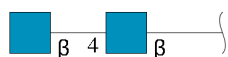
Chain	Residue	Modelled	Actual	Comment	Reference
B	58	GLY	-	expression tag	UNP Q80UM7
B	835	ALA	-	expression tag	UNP Q80UM7
B	836	SER	-	expression tag	UNP Q80UM7
B	837	TRP	-	expression tag	UNP Q80UM7
B	838	SER	-	expression tag	UNP Q80UM7
B	839	HIS	-	expression tag	UNP Q80UM7
B	840	PRO	-	expression tag	UNP Q80UM7
B	841	GLN	-	expression tag	UNP Q80UM7
B	842	PHE	-	expression tag	UNP Q80UM7
B	843	GLU	-	expression tag	UNP Q80UM7
B	844	LYS	-	expression tag	UNP Q80UM7
B	845	HIS	-	expression tag	UNP Q80UM7
B	846	HIS	-	expression tag	UNP Q80UM7
B	847	HIS	-	expression tag	UNP Q80UM7
B	848	HIS	-	expression tag	UNP Q80UM7
B	849	HIS	-	expression tag	UNP Q80UM7
B	850	HIS	-	expression tag	UNP Q80UM7
C	56	GLU	-	expression tag	UNP Q80UM7
C	57	THR	-	expression tag	UNP Q80UM7
C	58	GLY	-	expression tag	UNP Q80UM7
C	835	ALA	-	expression tag	UNP Q80UM7
C	836	SER	-	expression tag	UNP Q80UM7
C	837	TRP	-	expression tag	UNP Q80UM7
C	838	SER	-	expression tag	UNP Q80UM7
C	839	HIS	-	expression tag	UNP Q80UM7
C	840	PRO	-	expression tag	UNP Q80UM7
C	841	GLN	-	expression tag	UNP Q80UM7
C	842	PHE	-	expression tag	UNP Q80UM7
C	843	GLU	-	expression tag	UNP Q80UM7
C	844	LYS	-	expression tag	UNP Q80UM7
C	845	HIS	-	expression tag	UNP Q80UM7
C	846	HIS	-	expression tag	UNP Q80UM7
C	847	HIS	-	expression tag	UNP Q80UM7
C	848	HIS	-	expression tag	UNP Q80UM7
C	849	HIS	-	expression tag	UNP Q80UM7
C	850	HIS	-	expression tag	UNP Q80UM7
D	56	GLU	-	expression tag	UNP Q80UM7
D	57	THR	-	expression tag	UNP Q80UM7
D	58	GLY	-	expression tag	UNP Q80UM7
D	835	ALA	-	expression tag	UNP Q80UM7
D	836	SER	-	expression tag	UNP Q80UM7
D	837	TRP	-	expression tag	UNP Q80UM7

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Chain	Residue	Modelled	Actual	Comment	Reference
D	838	SER	-	expression tag	UNP Q80UM7
D	839	HIS	-	expression tag	UNP Q80UM7
D	840	PRO	-	expression tag	UNP Q80UM7
D	841	GLN	-	expression tag	UNP Q80UM7
D	842	PHE	-	expression tag	UNP Q80UM7
D	843	GLU	-	expression tag	UNP Q80UM7
D	844	LYS	-	expression tag	UNP Q80UM7
D	845	HIS	-	expression tag	UNP Q80UM7
D	846	HIS	-	expression tag	UNP Q80UM7
D	847	HIS	-	expression tag	UNP Q80UM7
D	848	HIS	-	expression tag	UNP Q80UM7
D	849	HIS	-	expression tag	UNP Q80UM7
D	850	HIS	-	expression tag	UNP Q80UM7

- 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				ZeroOcc	AltConf	Trace
2	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	F	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



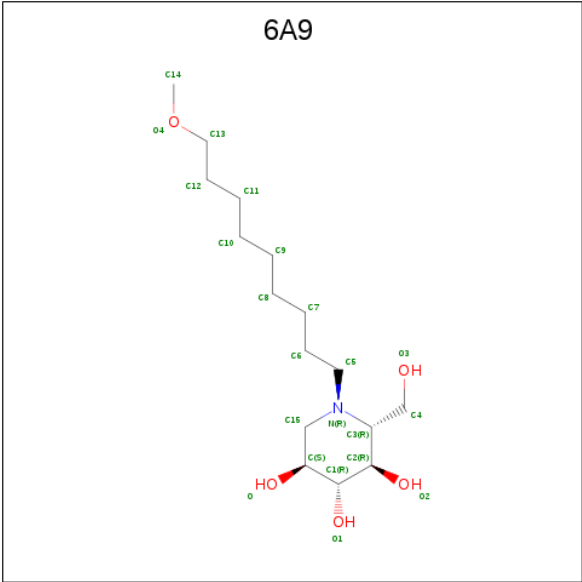
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	G	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	H	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



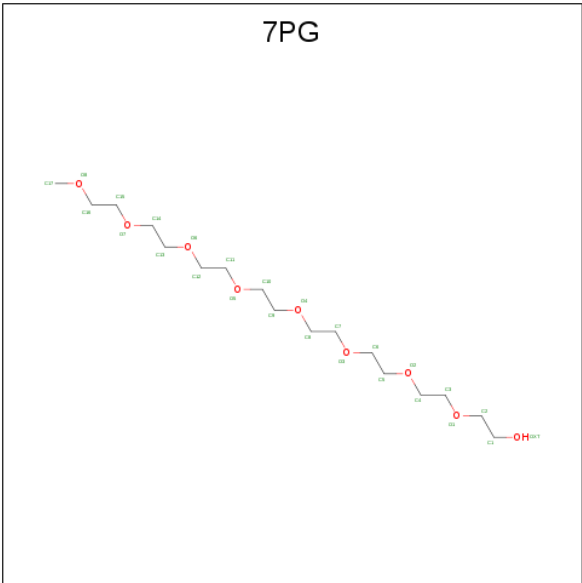
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total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

- Molecule 5 is N-9'-methoxynonyl-1-deoxynojirimycin (three-letter code: 6A9) (formula: C₁₆H₃₃NO₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	1
			88	64	4	20		
5	B	1	Total	C	N	O	0	1
			88	64	4	20		
5	C	1	Total	C	N	O	0	1
			88	64	4	20		
5	D	1	Total	C	N	O	0	1
			88	64	4	20		

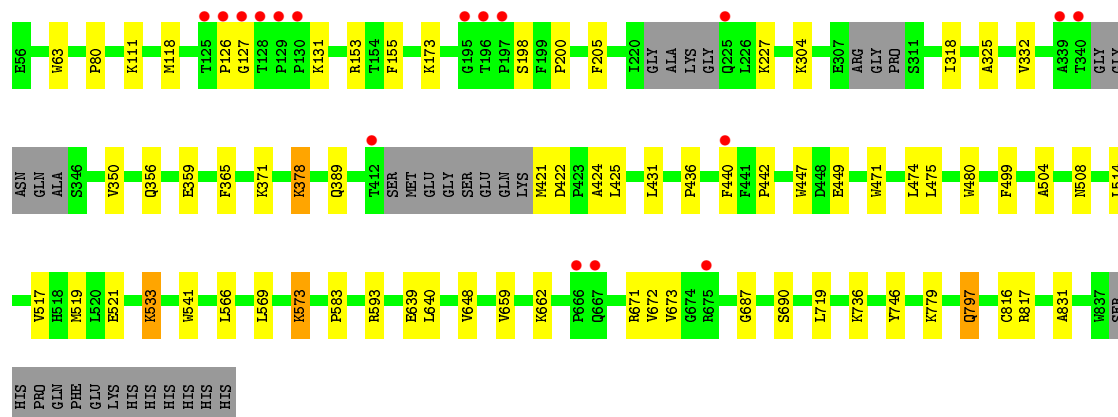
- Molecule 6 is 2,5,8,11,14,17,20,23-OCTAOXAPENTACOSAN-25-OL (three-letter code: 7PG) (formula: C₁₇H₃₆O₉).



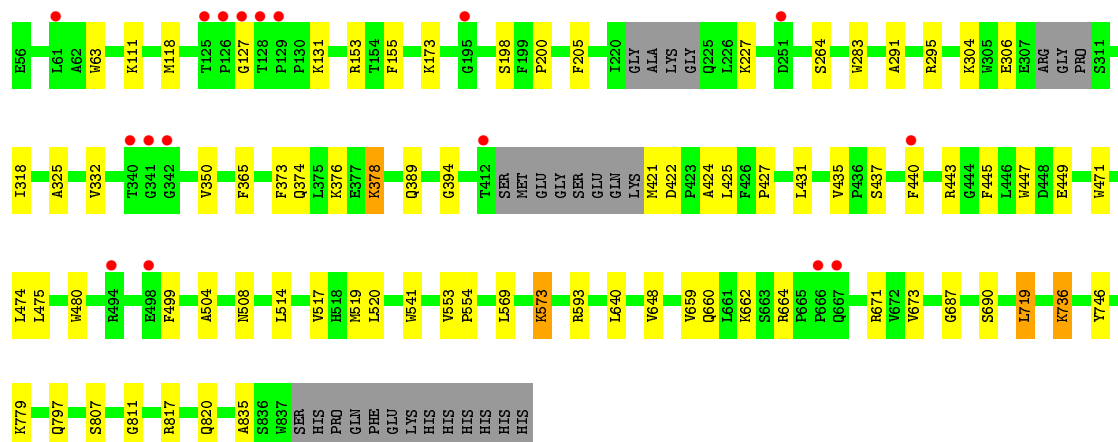
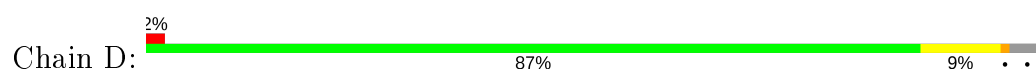
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			24	16	8		
6	B	1	Total	C	O	0	0
			24	16	8		
6	C	1	Total	C	O	0	0
			22	15	7		
6	C	1	Total	C	O	0	0
			17	11	6		
6	D	1	Total	C	O	0	0
			22	15	7		
6	D	1	Total	C	O	0	0
			17	11	6		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	321	Total	O	0	0
			321	321		
7	B	359	Total	O	0	0
			359	359		
7	C	358	Total	O	0	0
			358	358		
7	D	349	Total	O	0	0
			349	349		



● Molecule 1: Mannosyl-oligosaccharide glucosidase



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





- Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:  33% 67%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	108.01Å 130.92Å 135.37Å 90.00° 99.53° 90.00°	Depositor
Resolution (Å)	133.50 – 2.10 133.50 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.4 (133.50-2.10) 99.4 (133.50-2.10)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.66 (at 2.10Å)	Xtrriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.188 , 0.216 0.220 , 0.248	Depositor DCC
R_{free} test set	10477 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	30.1	Xtrriage
Anisotropy	0.522	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 58.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	26145	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 53.95 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.9185e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: BMA, NAG, MLY, 6A9, SO4, SME, 7PG

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	0.52	0/6016	0.65	0/8222
1	B	0.51	0/6020	0.66	1/8227 (0.0%)
1	C	0.51	0/6096	0.65	0/8335
1	D	0.52	0/6127	0.66	0/8378
All	All	0.52	0/24259	0.66	1/33162 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	323	LEU	CB-CA-C	-5.20	100.33	110.20

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	5975	0	5848	49	0
1	B	5979	0	5851	66	0
1	C	6051	0	5916	52	0
1	D	6081	0	5942	64	0
2	E	28	0	25	0	0
2	F	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	39	0	34	0	0
3	H	39	0	34	0	0
4	A	15	0	0	0	0
4	B	15	0	0	0	0
4	C	15	0	0	0	0
4	D	15	0	0	0	0
5	A	88	0	0	1	0
5	B	88	0	0	0	0
5	C	88	0	0	0	0
5	D	88	0	0	0	0
6	A	24	0	31	6	0
6	B	24	0	31	14	0
6	C	39	0	46	31	0
6	D	39	0	46	36	0
7	A	321	0	0	4	0
7	B	359	0	0	2	0
7	C	358	0	0	3	0
7	D	349	0	0	3	0
All	All	26145	0	23829	233	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 5.

The worst 5 of 233 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:C:436:PRO:HD2	1:C:440[B]:PHE:CZ	1.82	1.12
1:C:436:PRO:HD2	1:C:440[B]:PHE:CE2	1.99	0.98
6:A:907:7PG:H132	7:A:1162:HOH:O	1.64	0.98
6:B:906:7PG:H62	6:C:905:7PG:H62	1.46	0.97
1:A:425:LEU:H	6:D:905:7PG:H102	1.29	0.96

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 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	727/795 (91%)	701 (96%)	25 (3%)	1 (0%)	51	54
1	B	728/795 (92%)	707 (97%)	21 (3%)	0	100	100
1	C	740/795 (93%)	719 (97%)	20 (3%)	1 (0%)	51	54
1	D	747/795 (94%)	726 (97%)	21 (3%)	0	100	100
All	All	2942/3180 (92%)	2853 (97%)	87 (3%)	2 (0%)	51	54

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	442	PRO
1	A	442	PRO

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	611/642 (95%)	604 (99%)	7 (1%)	73	79
1	B	611/642 (95%)	599 (98%)	12 (2%)	55	60
1	C	619/642 (96%)	610 (98%)	9 (2%)	65	71
1	D	621/642 (97%)	611 (98%)	10 (2%)	62	69
All	All	2462/2568 (96%)	2424 (98%)	38 (2%)	65	71

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	746	TYR
1	C	198	SER
1	D	746	TYR
1	C	63	TRP
1	C	447	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	405	GLN
1	C	667	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

60 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	MLY	B	131	1	9,10,11	1.00	0	6,11,13	1.85	1 (16%)
1	MLY	C	304	1	9,10,11	1.24	0	6,11,13	1.75	1 (16%)
1	MLY	A	376	1	9,10,11	0.87	0	6,11,13	0.68	0
1	MLY	A	304	1	9,10,11	1.29	1 (11%)	6,11,13	2.10	4 (66%)
1	SME	A	519	1	7,8,9	3.15	2 (28%)	4,9,11	1.10	0
1	MLY	C	779	1	9,10,11	1.06	1 (11%)	6,11,13	1.62	1 (16%)
1	SME	C	519	1	7,8,9	1.78	1 (14%)	4,9,11	2.59	1 (25%)
1	MLY	A	736	1	9,10,11	1.29	1 (11%)	6,11,13	1.79	2 (33%)
1	MLY	C	662	1	9,10,11	1.14	0	6,11,13	1.12	0
1	MLY	C	131	1	9,10,11	0.98	0	6,11,13	2.01	1 (16%)
1	MLY	B	111	1	9,10,11	1.23	2 (22%)	6,11,13	1.96	3 (50%)
1	MLY	B	227	1	9,10,11	0.93	0	6,11,13	0.88	0
1	MLY	A	366	1	9,10,11	0.78	0	6,11,13	1.10	0
1	MLY	A	378	1	9,10,11	0.67	0	6,11,13	5.11	5 (83%)
1	MLY	C	533	1	9,10,11	1.40	2 (22%)	6,11,13	1.84	2 (33%)
1	MLY	C	371	1	9,10,11	1.17	0	6,11,13	1.79	3 (50%)
1	MLY	A	662	1	9,10,11	1.02	0	6,11,13	1.31	1 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	SME	D	421	1	7,8,9	1.62	2 (28%)	4,9,11	1.75	1 (25%)
1	MLY	D	304	1	9,10,11	1.15	1 (11%)	6,11,13	1.47	2 (33%)
1	MLY	B	662	1	9,10,11	1.07	0	6,11,13	1.45	1 (16%)
1	MLY	A	779	1	9,10,11	1.00	0	6,11,13	1.76	2 (33%)
1	MLY	B	378	1	9,10,11	0.69	0	6,11,13	1.58	1 (16%)
1	MLY	D	111	1	9,10,11	1.05	1 (11%)	6,11,13	2.04	3 (50%)
1	MLY	B	533	1	9,10,11	0.69	0	6,11,13	0.85	0
1	SME	C	421	1	7,8,9	1.57	2 (28%)	4,9,11	1.85	2 (50%)
1	MLY	D	376	1	9,10,11	1.17	1 (11%)	6,11,13	0.92	0
1	MLY	B	366	1	9,10,11	0.85	0	6,11,13	1.14	0
1	MLY	A	227	1	9,10,11	1.09	0	6,11,13	0.81	0
1	MLY	D	371	1	9,10,11	0.84	0	6,11,13	1.30	0
1	MLY	B	304	1	9,10,11	1.11	0	6,11,13	0.67	0
1	MLY	D	131	1	9,10,11	1.09	1 (11%)	6,11,13	1.90	2 (33%)
1	MLY	A	533	1	9,10,11	0.80	0	6,11,13	1.53	2 (33%)
1	MLY	B	371	1	9,10,11	1.07	1 (11%)	6,11,13	1.32	1 (16%)
1	MLY	B	573	1	9,10,11	0.95	0	6,11,13	2.18	1 (16%)
1	MLY	A	573	1	9,10,11	1.02	0	6,11,13	2.43	1 (16%)
1	MLY	B	779	1	9,10,11	0.91	0	6,11,13	1.64	2 (33%)
1	SME	B	519	1	7,8,9	1.73	2 (28%)	4,9,11	2.03	1 (25%)
1	MLY	C	736	1	9,10,11	1.95	1 (11%)	6,11,13	0.96	0
1	MLY	D	736	1	9,10,11	1.27	1 (11%)	6,11,13	2.06	4 (66%)
1	MLY	D	533	1	9,10,11	0.70	0	6,11,13	1.17	0
1	MLY	A	371	1	9,10,11	1.06	1 (11%)	6,11,13	2.00	3 (50%)
1	MLY	D	378	1	9,10,11	0.81	0	6,11,13	2.99	1 (16%)
1	MLY	D	227	1	9,10,11	0.94	0	6,11,13	1.32	1 (16%)
1	MLY	C	366	1	9,10,11	0.94	0	6,11,13	1.08	0
1	SME	B	421	1	7,8,9	1.21	1 (14%)	4,9,11	2.15	2 (50%)
1	MLY	A	111	1	9,10,11	0.92	0	6,11,13	1.48	1 (16%)
1	MLY	C	376	1	9,10,11	0.95	0	6,11,13	1.15	0
1	MLY	D	662	1	9,10,11	0.90	0	6,11,13	0.91	0
1	MLY	B	736	1	9,10,11	0.92	0	6,11,13	2.89	3 (50%)
1	MLY	D	573	1	9,10,11	0.96	0	6,11,13	1.81	1 (16%)
1	MLY	C	573	1	9,10,11	1.02	0	6,11,13	1.77	1 (16%)
1	SME	A	421	1	7,8,9	1.17	1 (14%)	4,9,11	2.13	3 (75%)
1	MLY	C	227	1	9,10,11	1.31	2 (22%)	6,11,13	1.86	3 (50%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLY	D	779	1	9,10,11	1.16	1 (11%)	6,11,13	1.51	1 (16%)
1	MLY	B	376	1	9,10,11	0.73	0	6,11,13	1.12	0
1	MLY	A	131	1	9,10,11	0.86	0	6,11,13	1.49	1 (16%)
1	MLY	C	378	1	9,10,11	0.77	0	6,11,13	2.36	3 (50%)
1	MLY	C	111	1	9,10,11	0.90	0	6,11,13	1.83	2 (33%)
1	MLY	D	366	1	9,10,11	0.95	0	6,11,13	1.01	0
1	SME	D	519	1	7,8,9	2.01	1 (14%)	4,9,11	3.24	3 (75%)

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
1	MLY	B	131	1	-	1/8/9/11	-
1	MLY	C	304	1	-	3/8/9/11	-
1	MLY	A	376	1	-	6/8/9/11	-
1	MLY	A	304	1	-	4/8/9/11	-
1	SME	A	519	1	-	2/6/7/9	-
1	MLY	C	779	1	-	5/8/9/11	-
1	SME	C	519	1	-	2/6/7/9	-
1	MLY	A	736	1	-	2/8/9/11	-
1	MLY	C	662	1	-	1/8/9/11	-
1	MLY	C	131	1	-	1/8/9/11	-
1	MLY	B	111	1	-	2/8/9/11	-
1	MLY	B	227	1	-	1/8/9/11	-
1	MLY	A	366	1	-	3/8/9/11	-
1	MLY	A	378	1	-	2/8/9/11	-
1	MLY	C	533	1	-	6/8/9/11	-
1	MLY	C	371	1	-	3/8/9/11	-
1	MLY	A	662	1	-	2/8/9/11	-
1	SME	D	421	1	-	2/6/7/9	-
1	MLY	D	304	1	-	5/8/9/11	-
1	MLY	B	662	1	-	3/8/9/11	-
1	MLY	A	779	1	-	3/8/9/11	-
1	MLY	B	378	1	-	4/8/9/11	-
1	MLY	D	111	1	-	2/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	B	533	1	-	5/8/9/11	-
1	SME	C	421	1	-	2/6/7/9	-
1	MLY	D	376	1	-	3/8/9/11	-
1	MLY	B	366	1	-	3/8/9/11	-
1	MLY	A	227	1	-	2/8/9/11	-
1	MLY	D	371	1	-	3/8/9/11	-
1	MLY	B	304	1	-	4/8/9/11	-
1	MLY	D	131	1	-	3/8/9/11	-
1	MLY	A	533	1	-	4/8/9/11	-
1	MLY	B	371	1	-	4/8/9/11	-
1	MLY	B	573	1	-	0/8/9/11	-
1	MLY	A	573	1	-	0/8/9/11	-
1	MLY	B	779	1	-	2/8/9/11	-
1	SME	B	519	1	-	0/6/7/9	-
1	MLY	C	736	1	-	4/8/9/11	-
1	MLY	D	736	1	-	5/8/9/11	-
1	MLY	D	533	1	-	5/8/9/11	-
1	MLY	A	371	1	-	3/8/9/11	-
1	MLY	D	378	1	-	2/8/9/11	-
1	MLY	D	227	1	-	4/8/9/11	-
1	MLY	C	366	1	-	3/8/9/11	-
1	SME	B	421	1	-	3/6/7/9	-
1	MLY	A	111	1	-	1/8/9/11	-
1	MLY	C	376	1	-	2/8/9/11	-
1	MLY	D	662	1	-	5/8/9/11	-
1	MLY	B	736	1	-	2/8/9/11	-
1	MLY	D	573	1	-	0/8/9/11	-
1	MLY	C	573	1	-	0/8/9/11	-
1	SME	A	421	1	-	3/6/7/9	-
1	MLY	C	227	1	-	3/8/9/11	-
1	MLY	D	779	1	-	3/8/9/11	-
1	MLY	B	376	1	-	3/8/9/11	-
1	MLY	A	131	1	-	3/8/9/11	-
1	MLY	C	378	1	-	2/8/9/11	-
1	MLY	C	111	1	-	2/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	D	366	1	-	3/8/9/11	-
1	SME	D	519	1	-	1/6/7/9	-

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	519	SME	OE-S	-6.64	1.32	1.50
1	C	736	MLY	CB-CA	5.07	1.60	1.53
1	A	519	SME	CB-CA	-4.90	1.47	1.53
1	D	519	SME	OE-S	-4.79	1.37	1.50
1	C	519	SME	OE-S	-4.11	1.39	1.50

The worst 5 of 80 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	378	MLY	CH2-NZ-CH1	-10.65	82.20	109.73
1	D	378	MLY	CH2-NZ-CH1	-6.86	92.00	109.73
1	A	573	MLY	CH2-NZ-CH1	-5.55	95.39	109.73
1	B	736	MLY	CH2-NZ-CH1	-5.14	96.44	109.73
1	B	573	MLY	CH2-NZ-CH1	-5.06	96.66	109.73

There are no chirality outliers.

5 of 162 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	376	MLY	N-CA-CB-CG
1	A	376	MLY	C-CA-CB-CG
1	A	304	MLY	N-CA-CB-CG
1	A	519	SME	CB-CG-S-OE
1	C	779	MLY	N-CA-CB-CG

There are no ring outliers.

14 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	376	MLY	1	0
1	C	662	MLY	1	0
1	A	378	MLY	2	0
1	C	533	MLY	1	0
1	B	662	MLY	1	0
1	B	573	MLY	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	573	MLY	1	0
1	D	736	MLY	1	0
1	D	378	MLY	3	0
1	D	662	MLY	1	0
1	B	736	MLY	2	0
1	D	573	MLY	1	0
1	C	573	MLY	1	0
1	C	378	MLY	3	0

5.5 Carbohydrates

10 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	E	1	1,2	14,14,15	0.30	0	17,19,21	0.54	0
2	NAG	E	2	2	14,14,15	0.29	0	17,19,21	0.87	1 (5%)
2	NAG	F	1	1,2	14,14,15	0.30	0	17,19,21	0.51	0
2	NAG	F	2	2	14,14,15	0.31	0	17,19,21	0.80	1 (5%)
3	NAG	G	1	1,3	14,14,15	0.29	0	17,19,21	0.57	0
3	NAG	G	2	3	14,14,15	0.39	0	17,19,21	1.25	1 (5%)
3	BMA	G	3	3	11,11,12	0.61	0	15,15,17	1.25	1 (6%)
3	NAG	H	1	1,3	14,14,15	0.31	0	17,19,21	0.50	0
3	NAG	H	2	3	14,14,15	0.41	0	17,19,21	1.55	3 (17%)
3	BMA	H	3	3	11,11,12	0.63	0	15,15,17	1.28	2 (13%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	E	1	1,2	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	E	2	2	-	0/6/23/26	0/1/1/1
2	NAG	F	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	F	2	2	-	0/6/23/26	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	-	2/2/19/22	0/1/1/1
3	NAG	H	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	H	2	3	-	2/6/23/26	0/1/1/1
3	BMA	H	3	3	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	2	NAG	O5-C1-C2	-4.55	104.11	111.29
3	G	2	NAG	O5-C1-C2	-3.91	105.11	111.29
3	G	3	BMA	C1-C2-C3	3.58	114.07	109.67
3	H	3	BMA	C1-C2-C3	3.27	113.68	109.67
2	E	2	NAG	O5-C1-C2	-2.79	106.88	111.29

There are no chirality outliers.

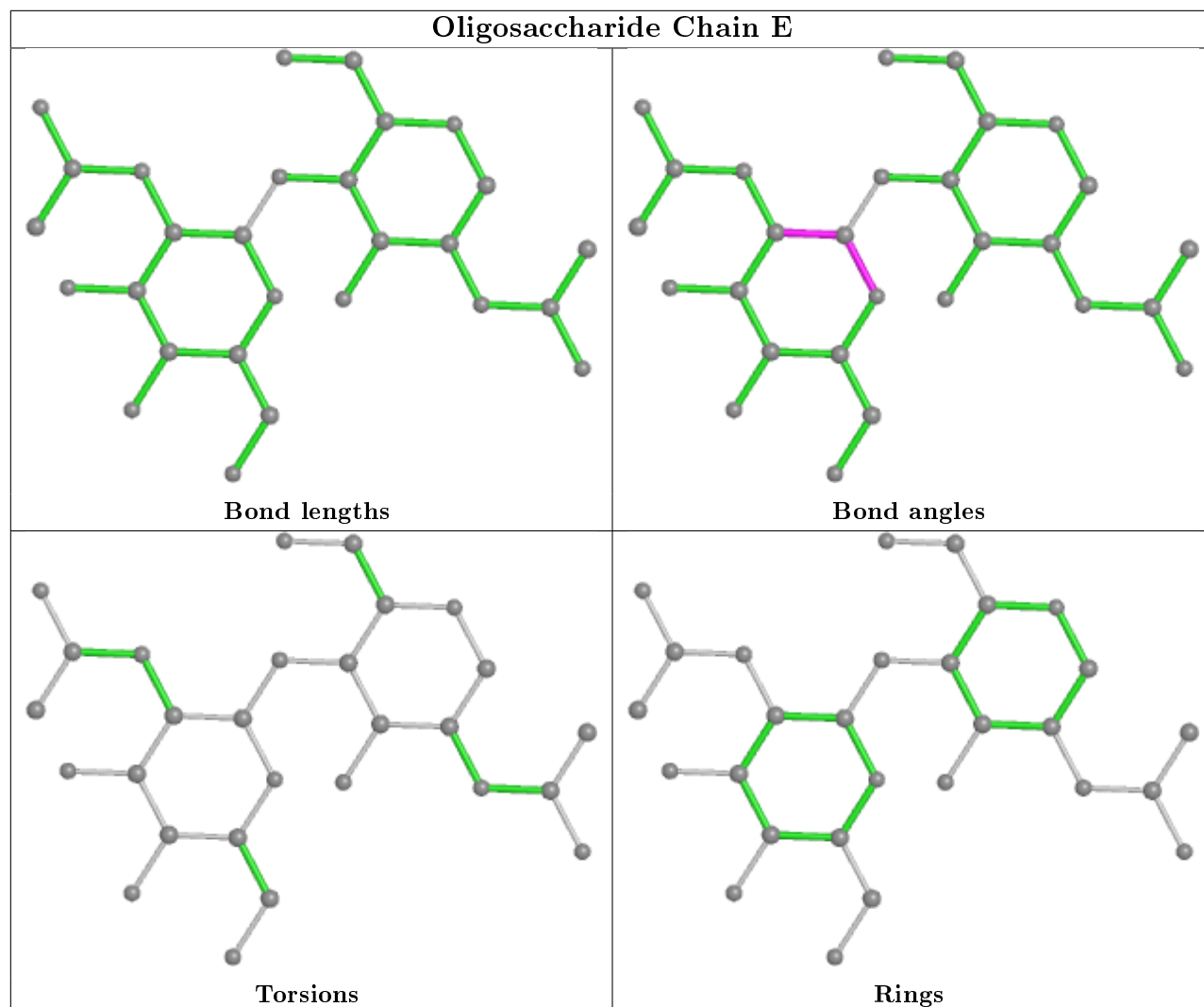
5 of 6 torsion outliers are listed below:

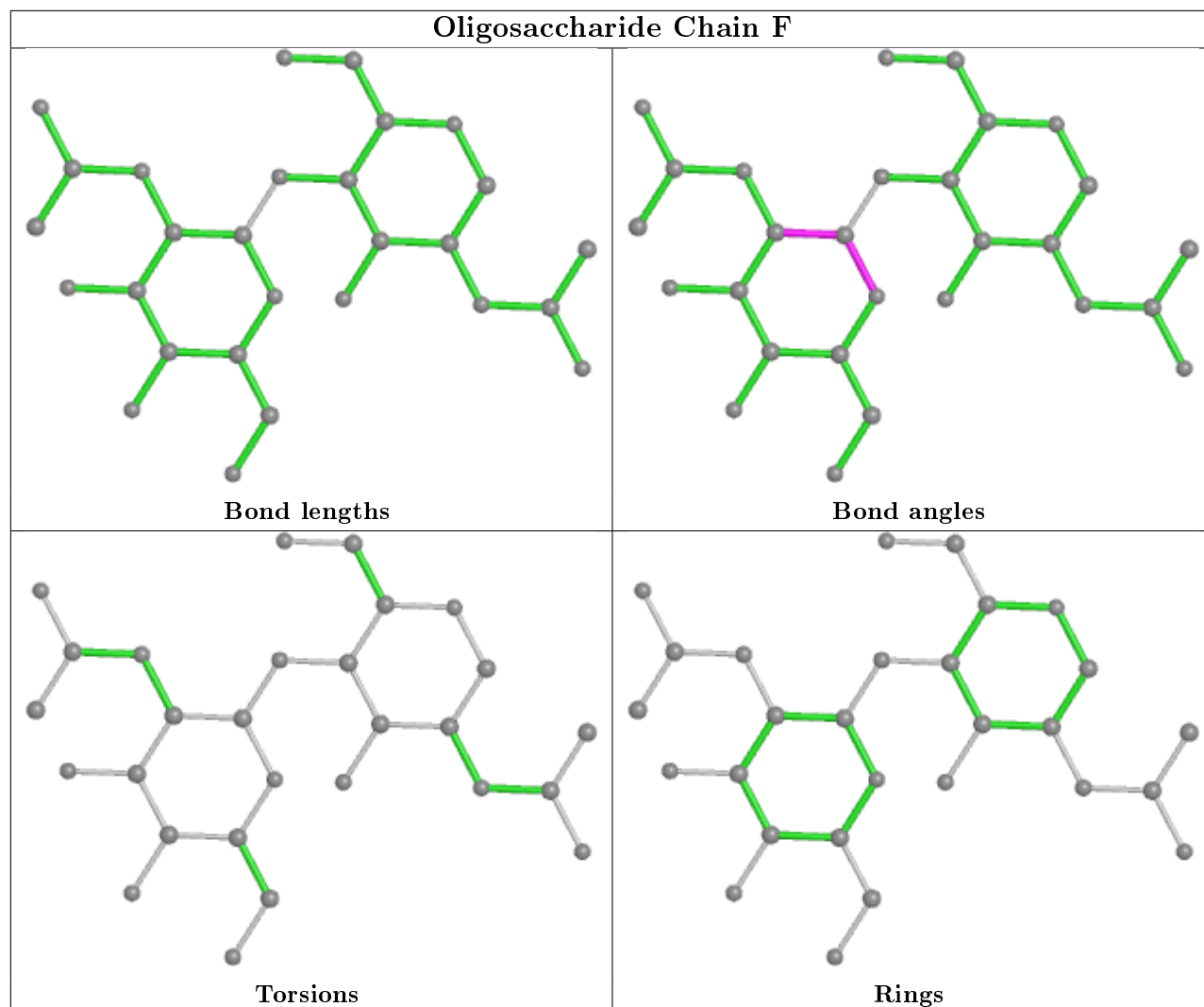
Mol	Chain	Res	Type	Atoms
3	H	3	BMA	C4-C5-C6-O6
3	H	3	BMA	O5-C5-C6-O6
3	H	2	NAG	C4-C5-C6-O6
3	G	3	BMA	C4-C5-C6-O6
3	H	2	NAG	O5-C5-C6-O6

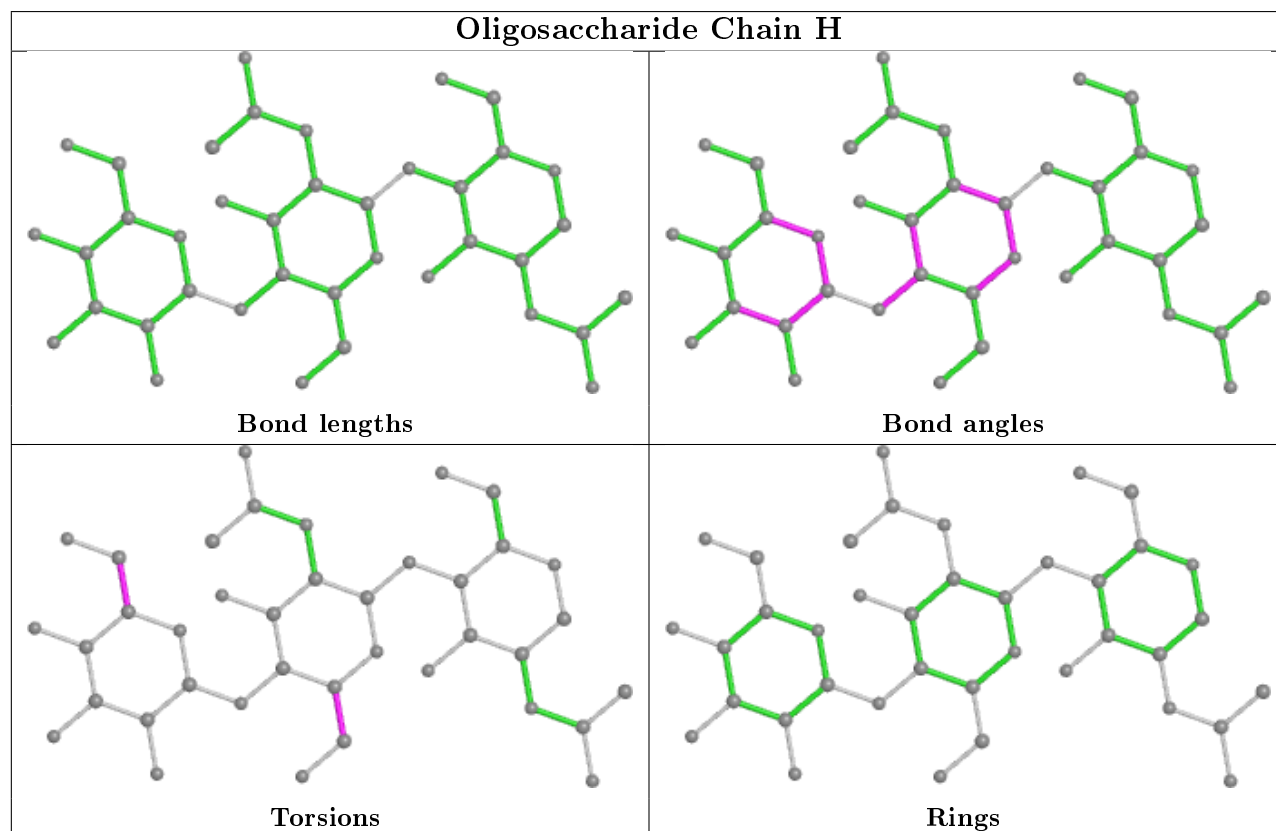
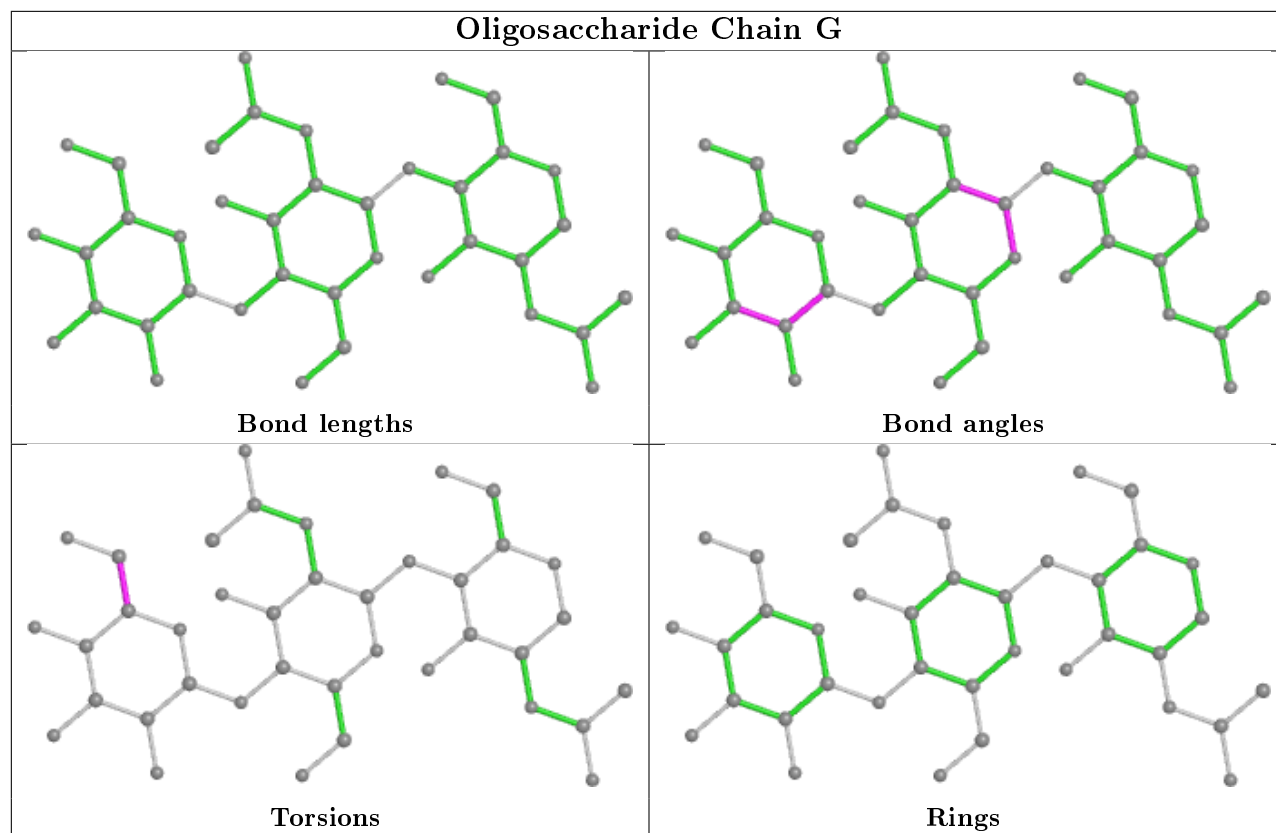
There are no ring outliers.

No monomer is involved in short contacts.

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







5.6 Ligand geometry

34 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	$\# Z > 2$
5	6A9	B	903[D]	-	22,22,22	0.29	0	25,27,27	0.95	3 (12%)
6	7PG	C	906	-	16,16,25	0.27	0	15,15,24	0.45	0
4	SO4	C	903	-	4,4,4	0.14	0	6,6,6	0.07	0
5	6A9	D	904[D]	-	22,22,22	0.30	0	25,27,27	0.94	3 (12%)
4	SO4	D	903	-	4,4,4	0.12	0	6,6,6	0.10	0
4	SO4	C	901	-	4,4,4	0.28	0	6,6,6	0.28	0
6	7PG	D	905	-	21,21,25	0.26	0	20,20,24	0.49	0
4	SO4	A	906	-	4,4,4	0.19	0	6,6,6	0.11	0
4	SO4	D	902	-	4,4,4	0.28	0	6,6,6	0.19	0
4	SO4	D	901	-	4,4,4	0.36	0	6,6,6	0.31	0
4	SO4	A	901	-	4,4,4	0.26	0	6,6,6	0.18	0
5	6A9	D	904[B]	-	22,22,22	0.34	0	25,27,27	1.09	3 (12%)
6	7PG	B	906	-	23,23,25	0.18	0	22,22,24	0.43	0
5	6A9	C	904[A]	-	22,22,22	0.31	0	25,27,27	0.93	3 (12%)
5	6A9	D	904[C]	-	22,22,22	0.29	0	25,27,27	0.95	2 (8%)
5	6A9	D	904[A]	-	22,22,22	0.32	0	25,27,27	0.93	2 (8%)
5	6A9	C	904[C]	-	22,22,22	0.30	0	25,27,27	0.94	2 (8%)
5	6A9	C	904[B]	-	22,22,22	0.34	0	25,27,27	1.07	3 (12%)
5	6A9	C	904[D]	-	22,22,22	0.28	0	25,27,27	0.92	3 (12%)
6	7PG	D	906	-	16,16,25	0.31	0	15,15,24	0.64	0
6	7PG	C	905	-	21,21,25	0.35	0	20,20,24	0.51	0
5	6A9	A	903[A]	-	22,22,22	0.33	0	25,27,27	0.94	2 (8%)
4	SO4	B	907	-	4,4,4	0.27	0	6,6,6	0.14	0
5	6A9	A	903[B]	-	22,22,22	0.35	0	25,27,27	1.09	3 (12%)
5	6A9	B	903[C]	-	22,22,22	0.31	0	25,27,27	0.95	2 (8%)
5	6A9	A	903[C]	-	22,22,22	0.30	0	25,27,27	0.95	2 (8%)
5	6A9	B	903[B]	-	22,22,22	0.34	0	25,27,27	1.09	3 (12%)
5	6A9	A	903[D]	-	22,22,22	0.32	0	25,27,27	0.96	2 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	6A9	B	903[A]	-	22,22,22	0.33	0	25,27,27	0.95	3 (12%)
4	SO4	B	901	-	4,4,4	0.24	0	6,6,6	0.09	0
4	SO4	C	902	-	4,4,4	0.25	0	6,6,6	0.18	0
6	7PG	A	907	-	23,23,25	0.23	0	22,22,24	0.41	0
4	SO4	B	902	-	4,4,4	0.27	0	6,6,6	0.22	0
4	SO4	A	902	-	4,4,4	0.33	0	6,6,6	0.17	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	6A9	B	903[D]	-	-	6/13/33/33	0/1/1/1
6	7PG	C	906	-	-	8/14/14/23	-
6	7PG	B	906	-	-	13/21/21/23	-
6	7PG	D	905	-	-	12/19/19/23	-
5	6A9	D	904[D]	-	-	6/13/33/33	0/1/1/1
5	6A9	D	904[B]	-	-	5/13/33/33	0/1/1/1
5	6A9	D	904[C]	-	-	5/13/33/33	0/1/1/1
5	6A9	C	904[A]	-	-	4/13/33/33	0/1/1/1
5	6A9	D	904[A]	-	-	4/13/33/33	0/1/1/1
5	6A9	C	904[C]	-	-	5/13/33/33	0/1/1/1
5	6A9	C	904[B]	-	-	5/13/33/33	0/1/1/1
5	6A9	C	904[D]	-	-	6/13/33/33	0/1/1/1
6	7PG	D	906	-	-	10/14/14/23	-
5	6A9	A	903[A]	-	-	4/13/33/33	0/1/1/1
5	6A9	A	903[B]	-	-	5/13/33/33	0/1/1/1
5	6A9	B	903[C]	-	-	5/13/33/33	0/1/1/1
5	6A9	A	903[C]	-	-	5/13/33/33	0/1/1/1
5	6A9	B	903[B]	-	-	5/13/33/33	0/1/1/1
5	6A9	A	903[D]	-	-	6/13/33/33	0/1/1/1
5	6A9	B	903[A]	-	-	4/13/33/33	0/1/1/1
6	7PG	A	907	-	-	16/21/21/23	-
6	7PG	C	905	-	-	13/19/19/23	-

There are no bond length outliers.

The worst 5 of 41 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	904[B]	6A9	C4-C3-C2	-3.71	107.21	112.90
5	B	903[B]	6A9	C4-C3-C2	-3.70	107.23	112.90
5	A	903[B]	6A9	C4-C3-C2	-3.70	107.23	112.90
5	C	904[B]	6A9	C4-C3-C2	-3.63	107.34	112.90
5	B	903[C]	6A9	C4-C3-C2	-3.59	107.40	112.90

There are no chirality outliers.

5 of 152 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	903[D]	6A9	C6-C5-N-C3
5	D	904[D]	6A9	C6-C5-N-C3
5	D	904[B]	6A9	C6-C5-N-C3
5	C	904[A]	6A9	C6-C5-N-C3
5	D	904[A]	6A9	C6-C5-N-C3

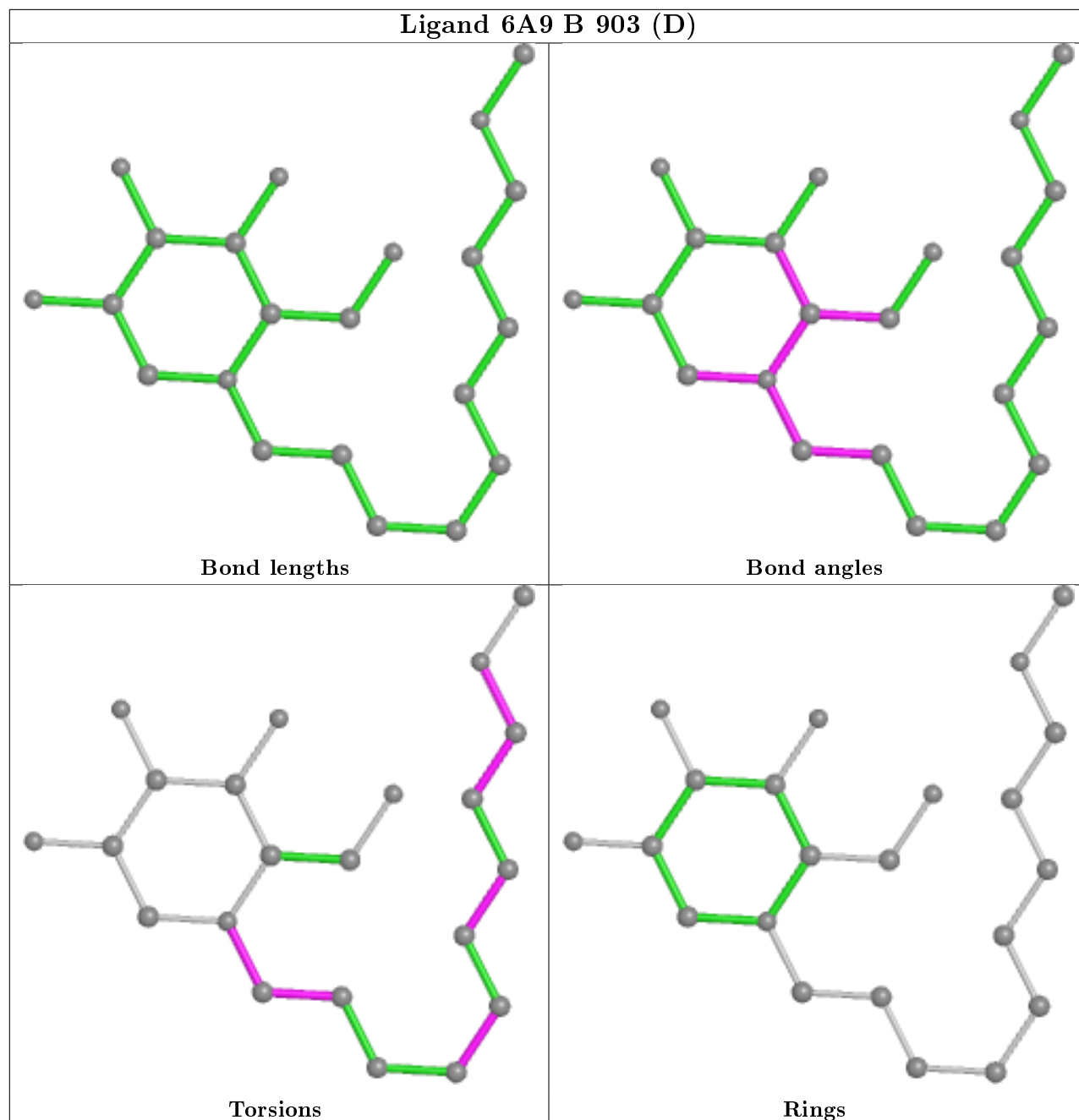
There are no ring outliers.

7 monomers are involved in 80 short contacts:

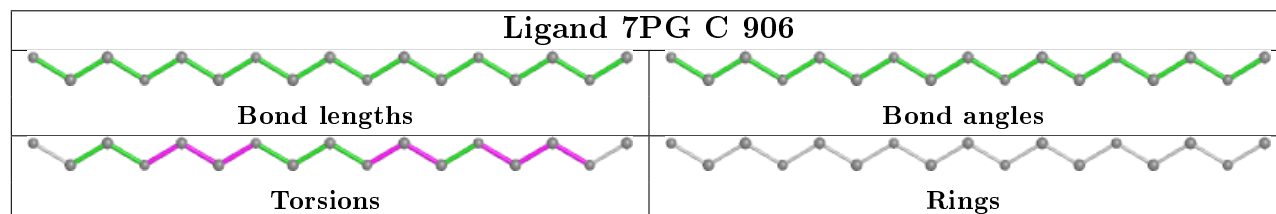
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	906	7PG	4	0
6	D	905	7PG	30	0
6	B	906	7PG	14	0
6	D	906	7PG	6	0
6	C	905	7PG	27	0
5	A	903[D]	6A9	1	0
6	A	907	7PG	6	0

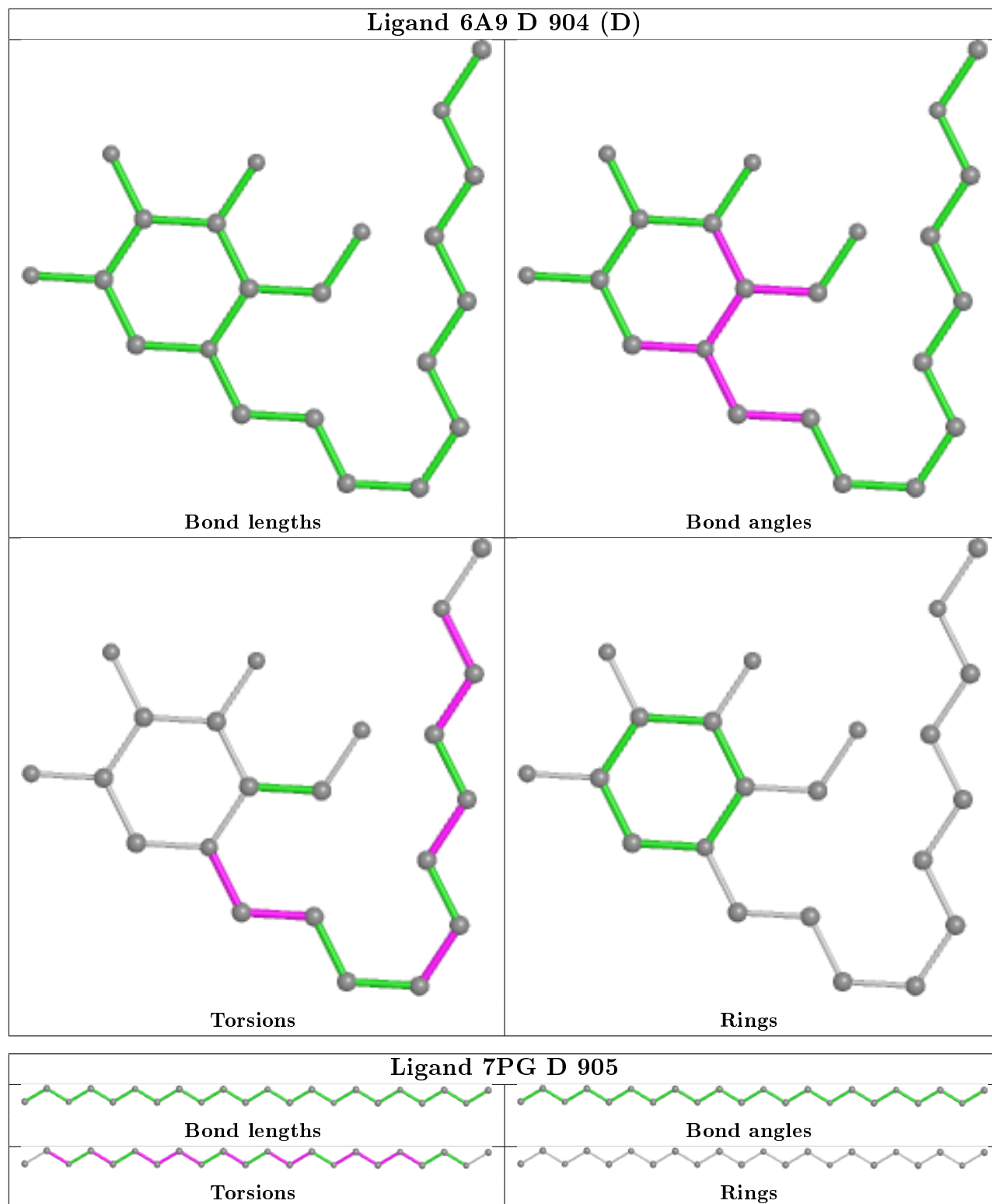
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

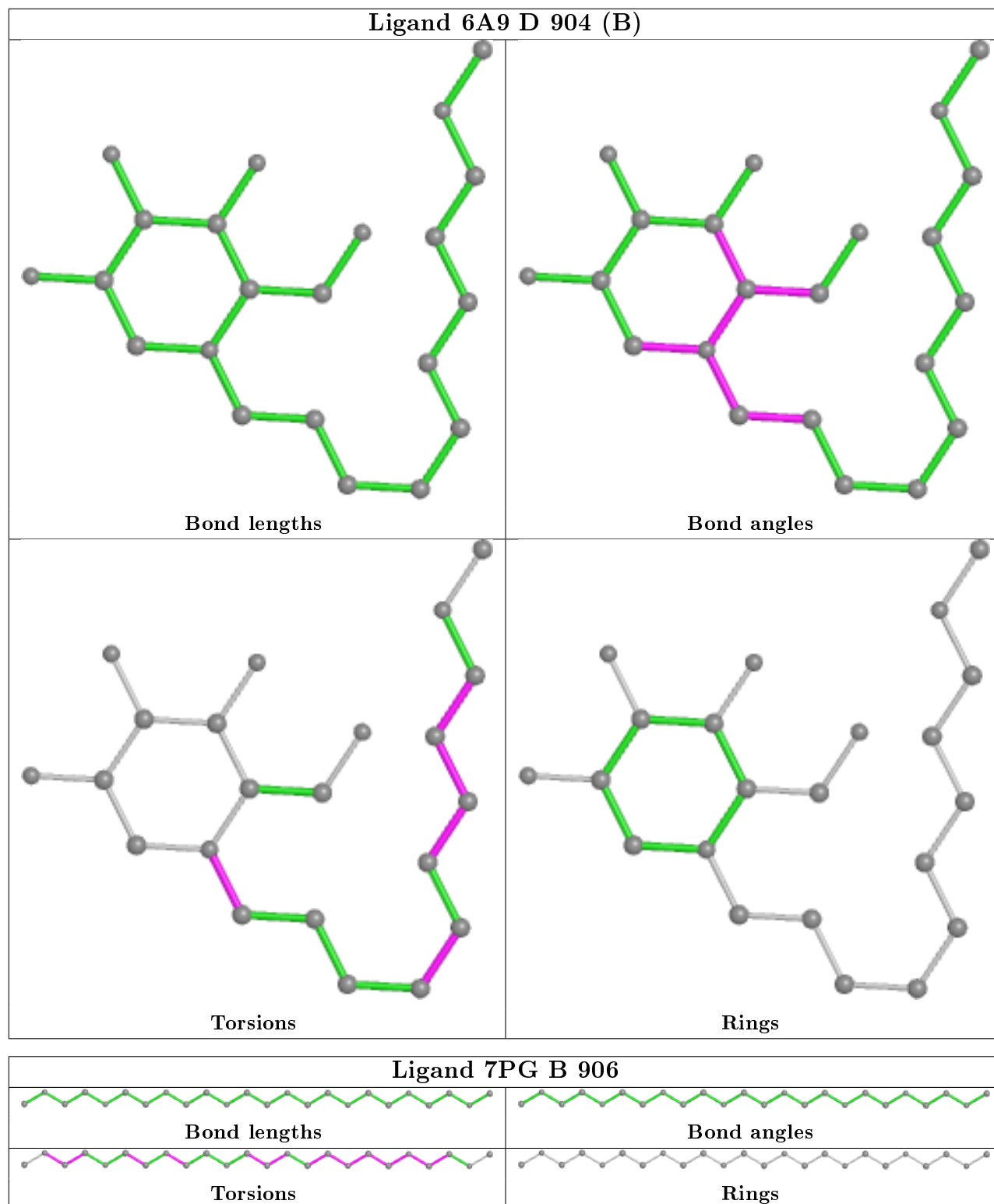
Ligand 6A9 B 903 (D)



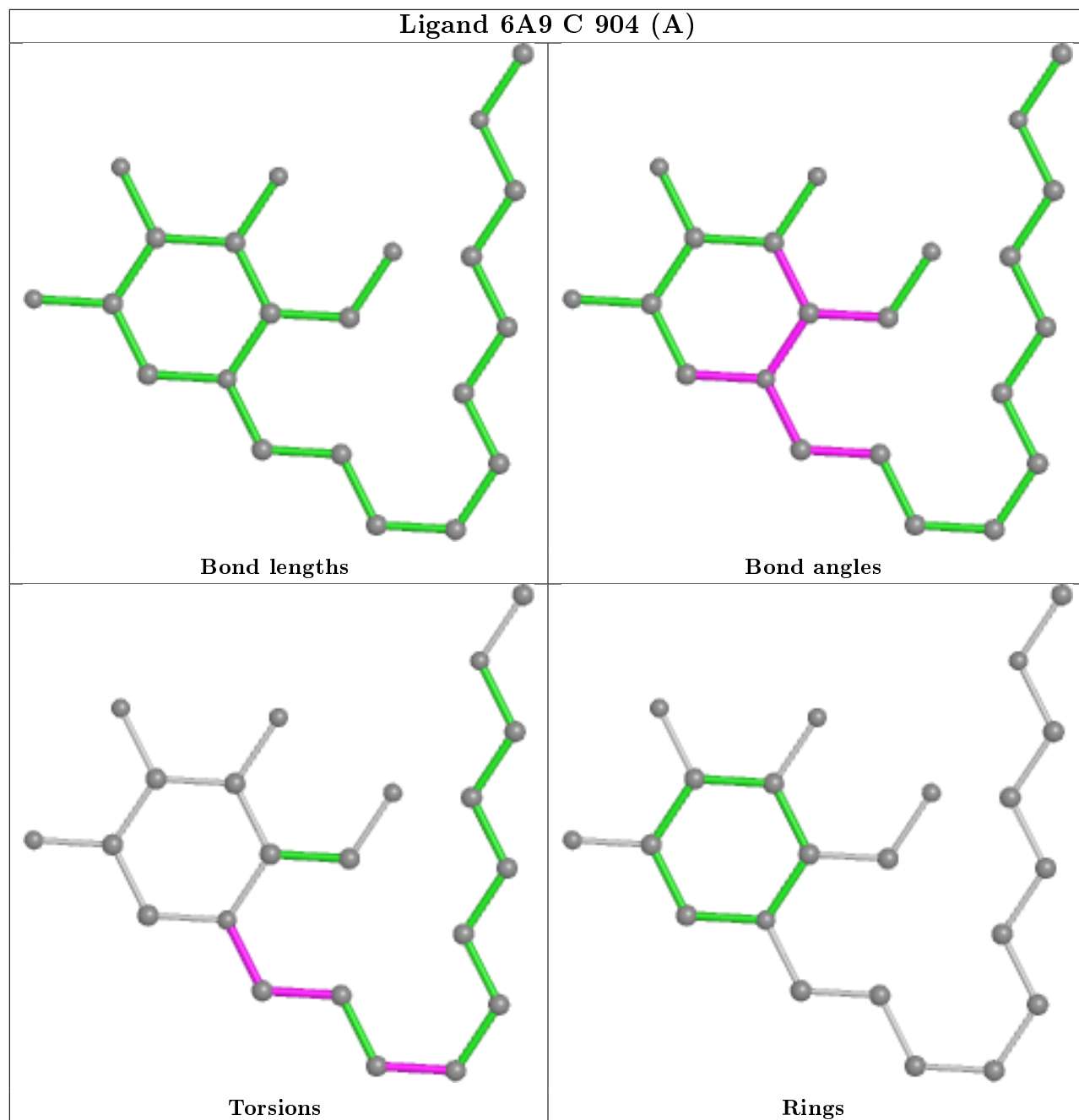
Ligand 7PG C 906



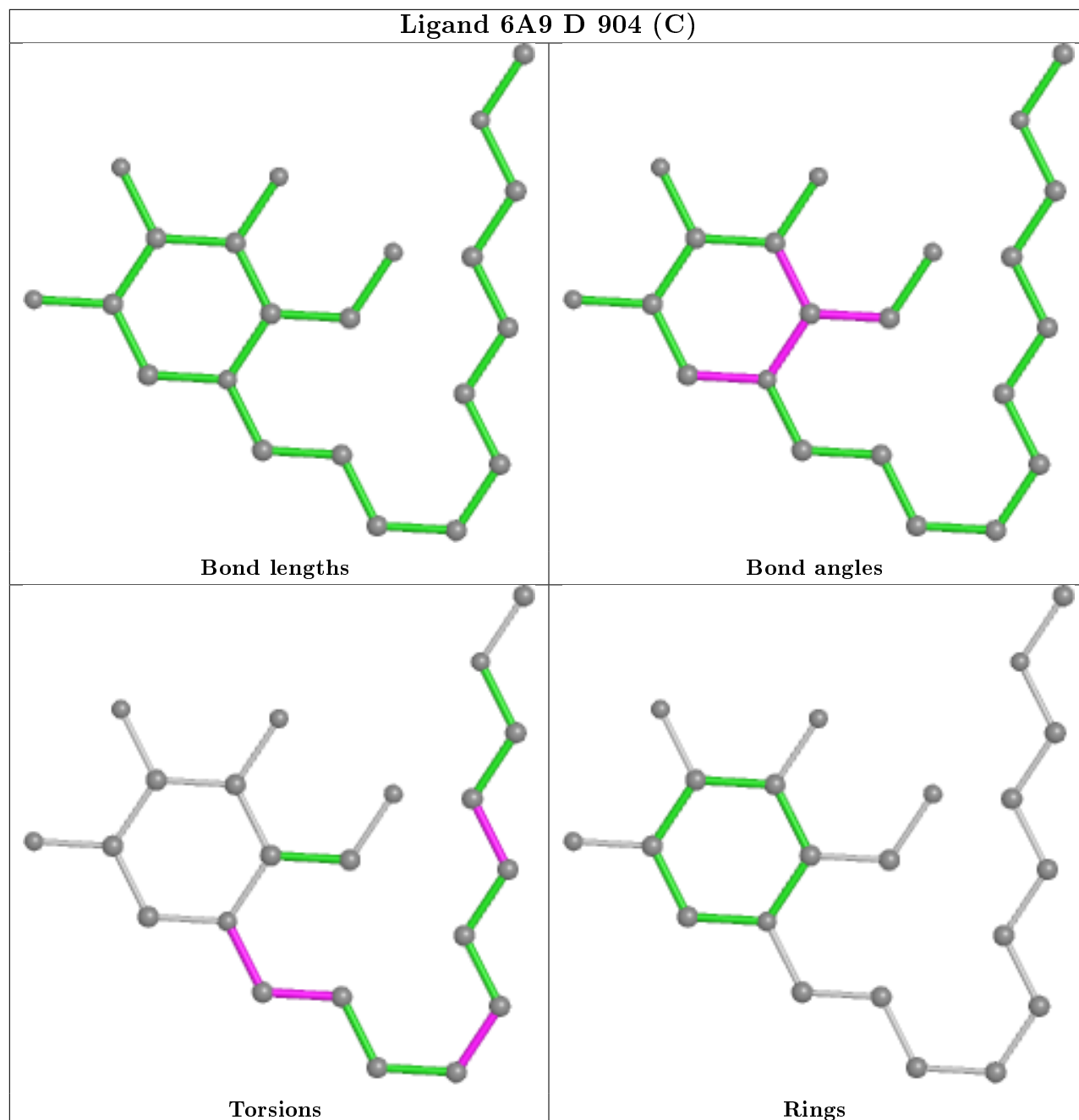




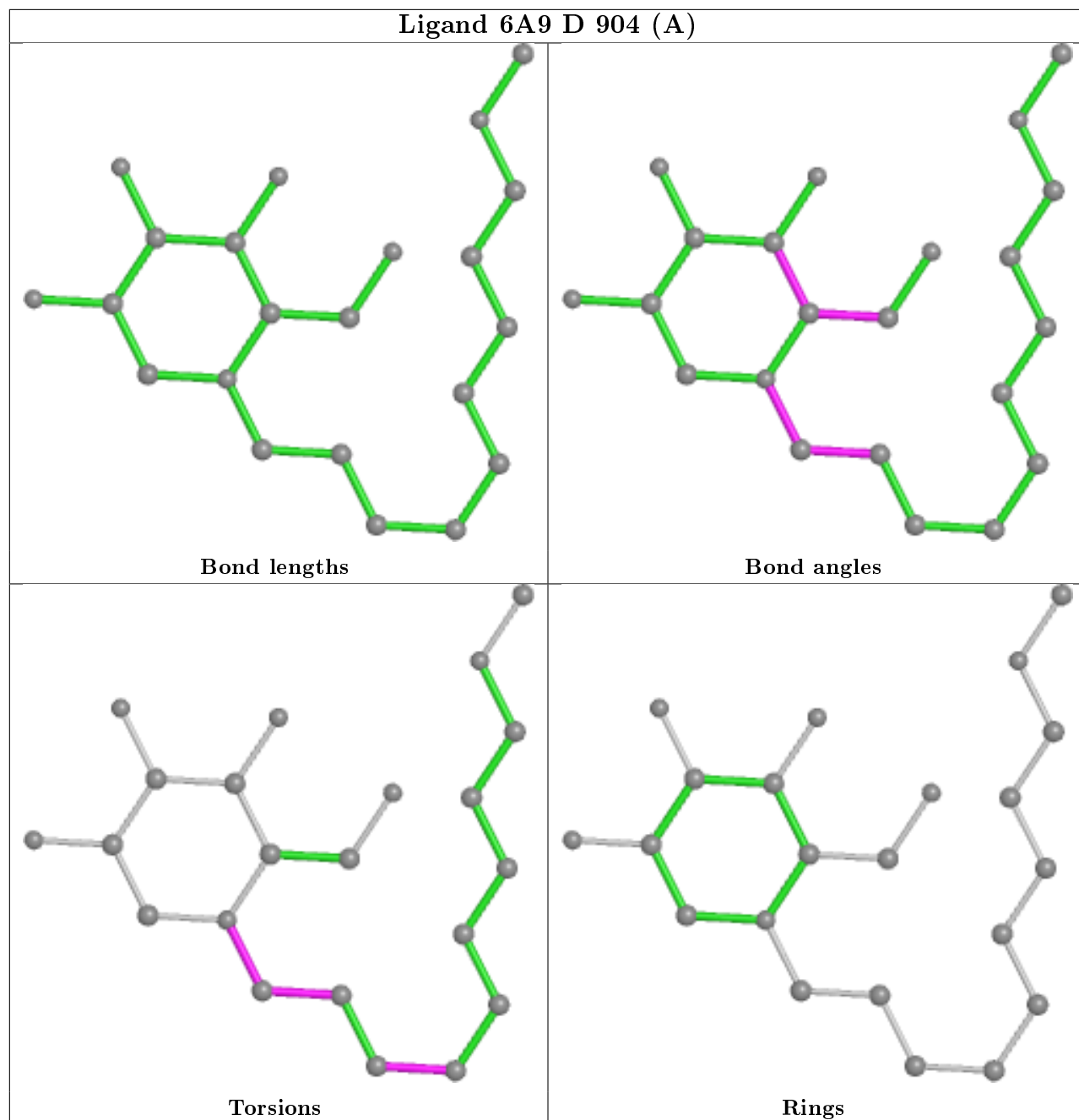
Ligand 6A9 C 904 (A)



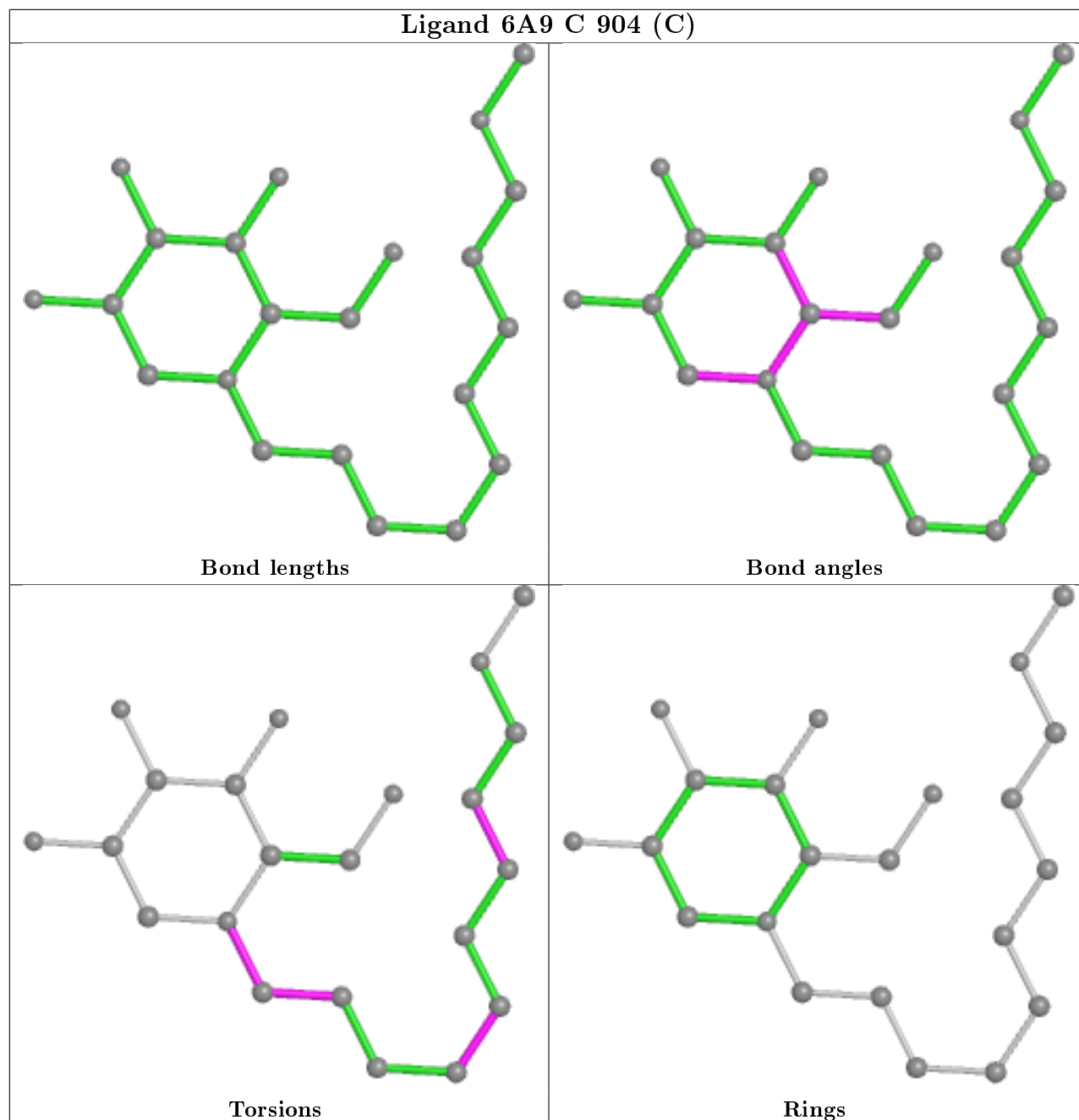
Ligand 6A9 D 904 (C)



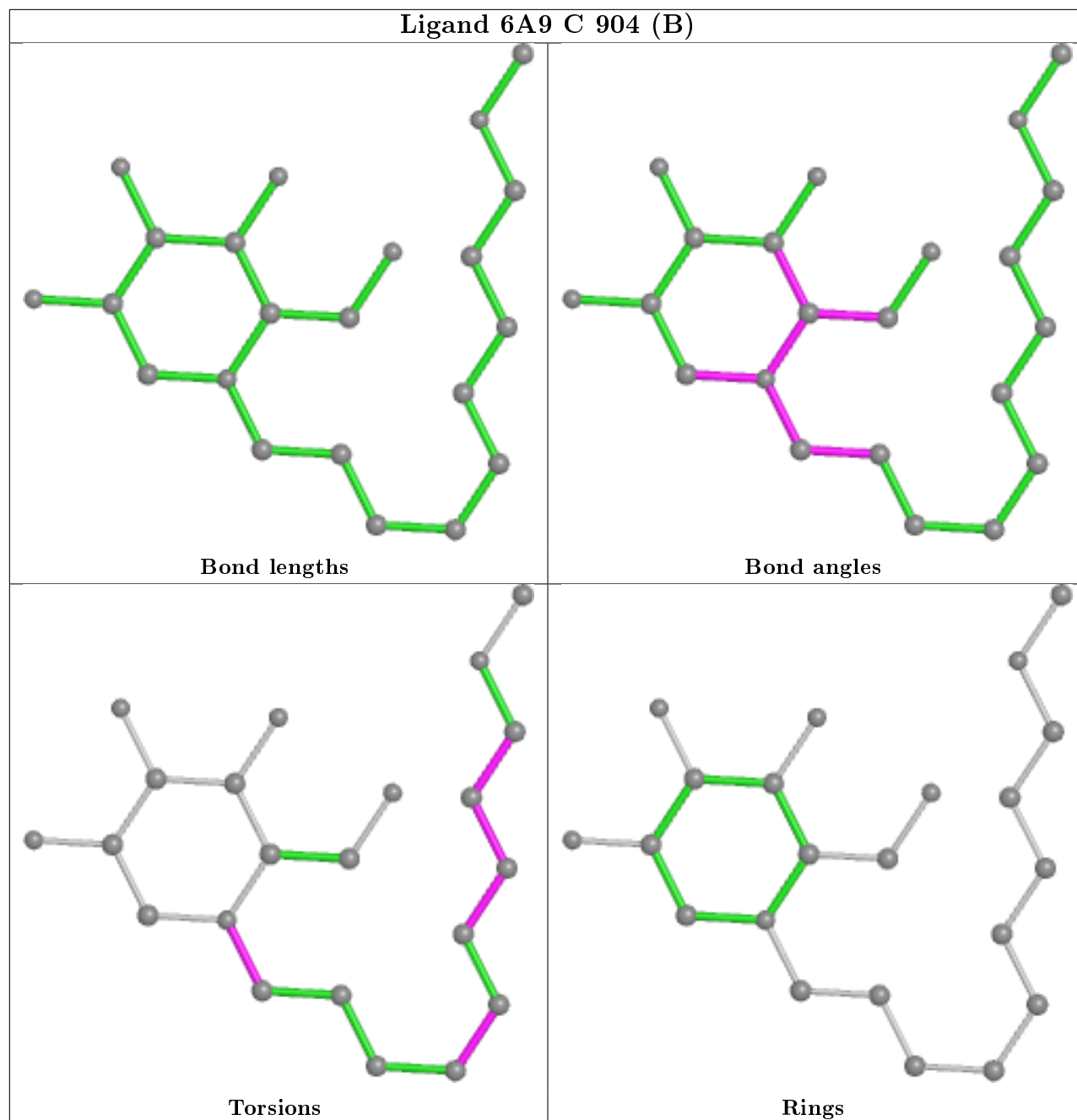
Ligand 6A9 D 904 (A)



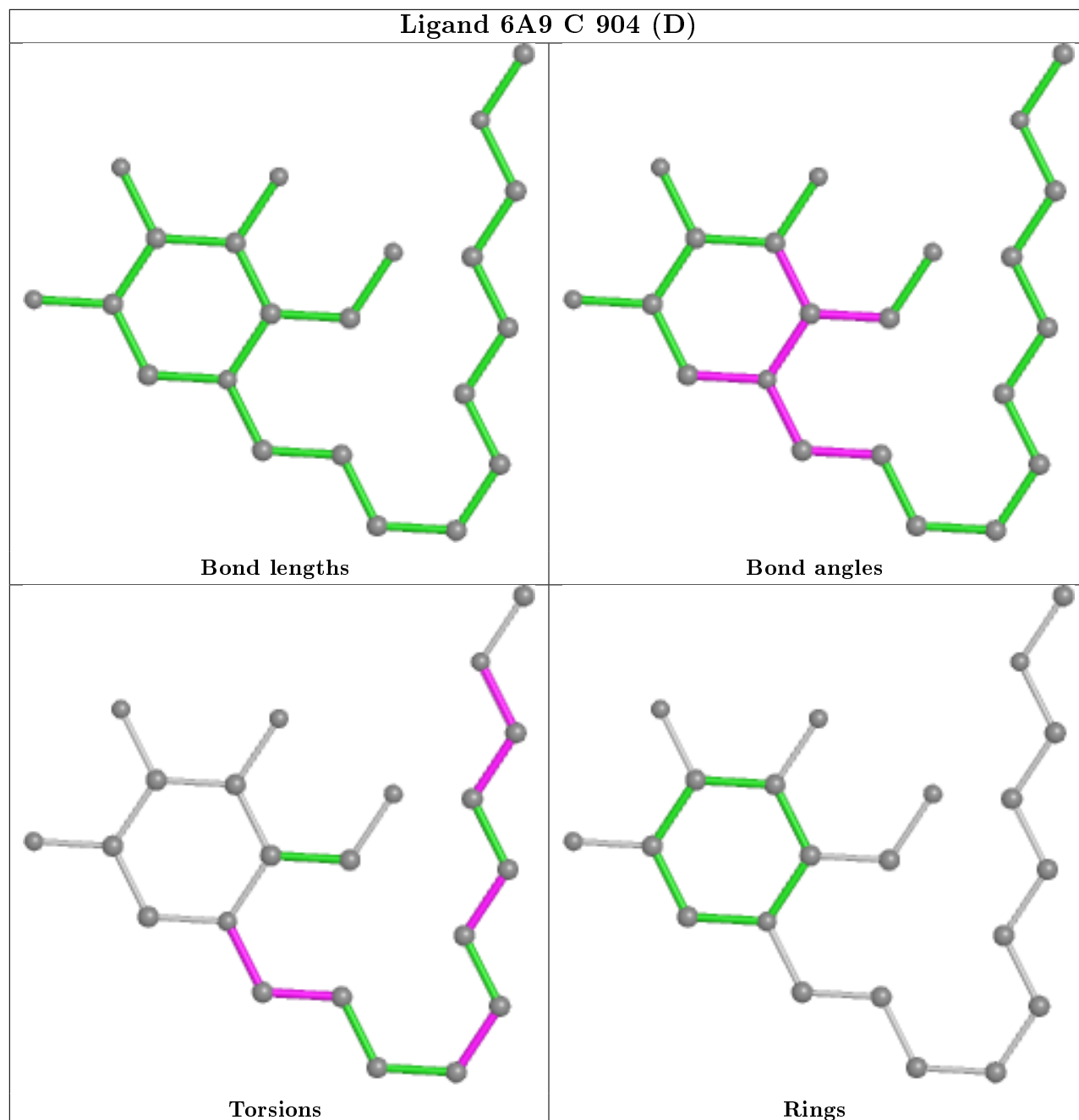
Ligand 6A9 C 904 (C)



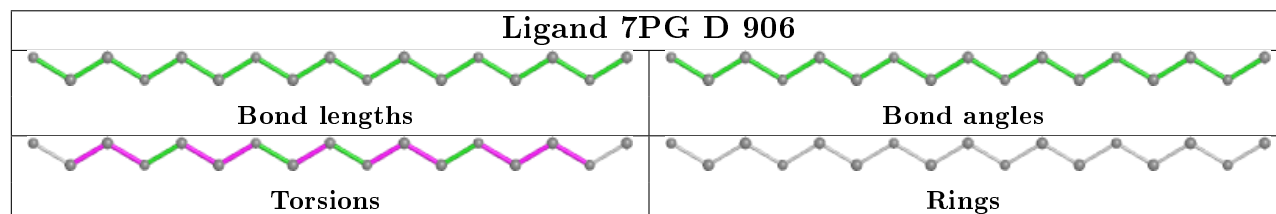
Ligand 6A9 C 904 (B)



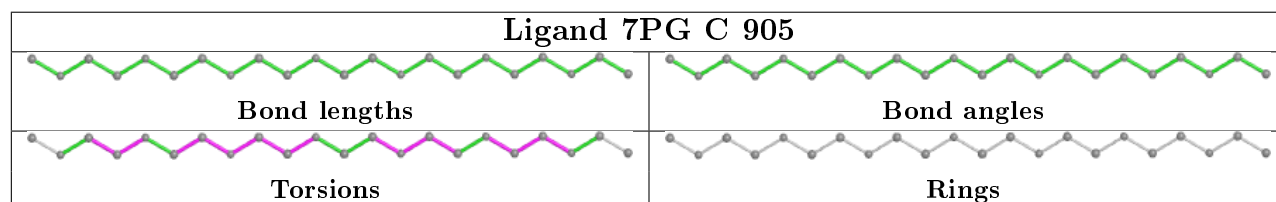
Ligand 6A9 C 904 (D)



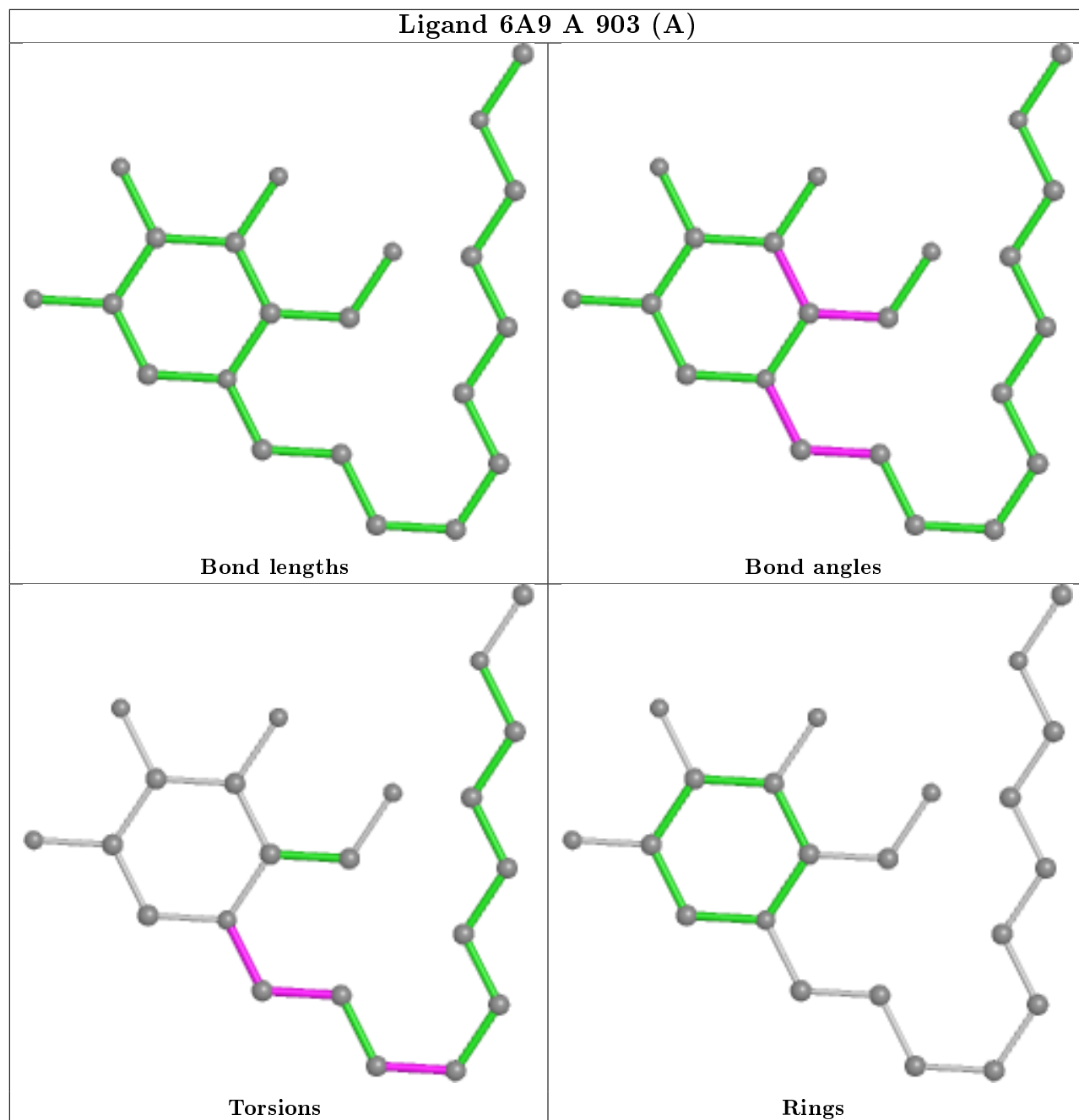
Ligand 7PG D 906



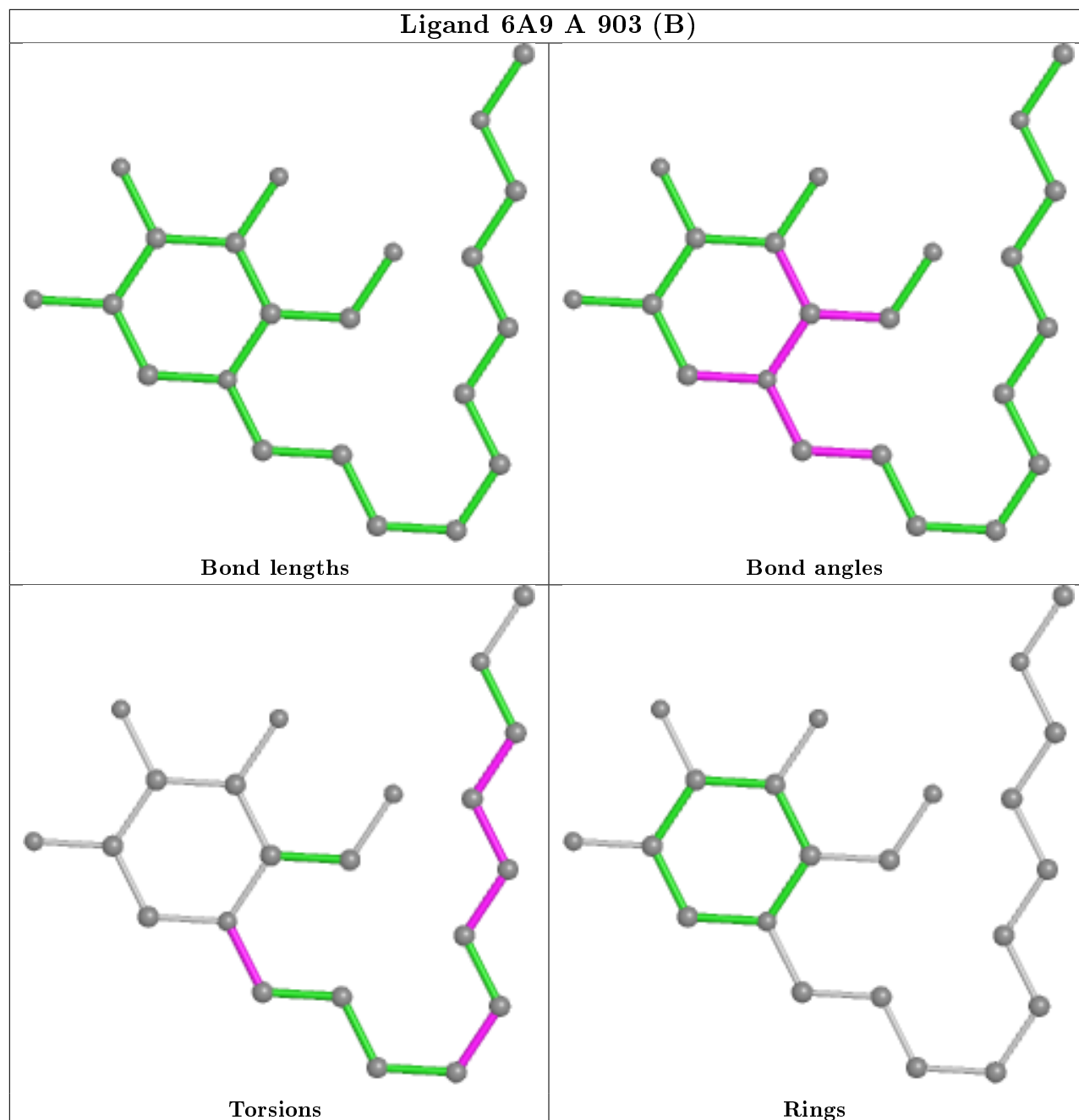
Ligand 7PG C 905



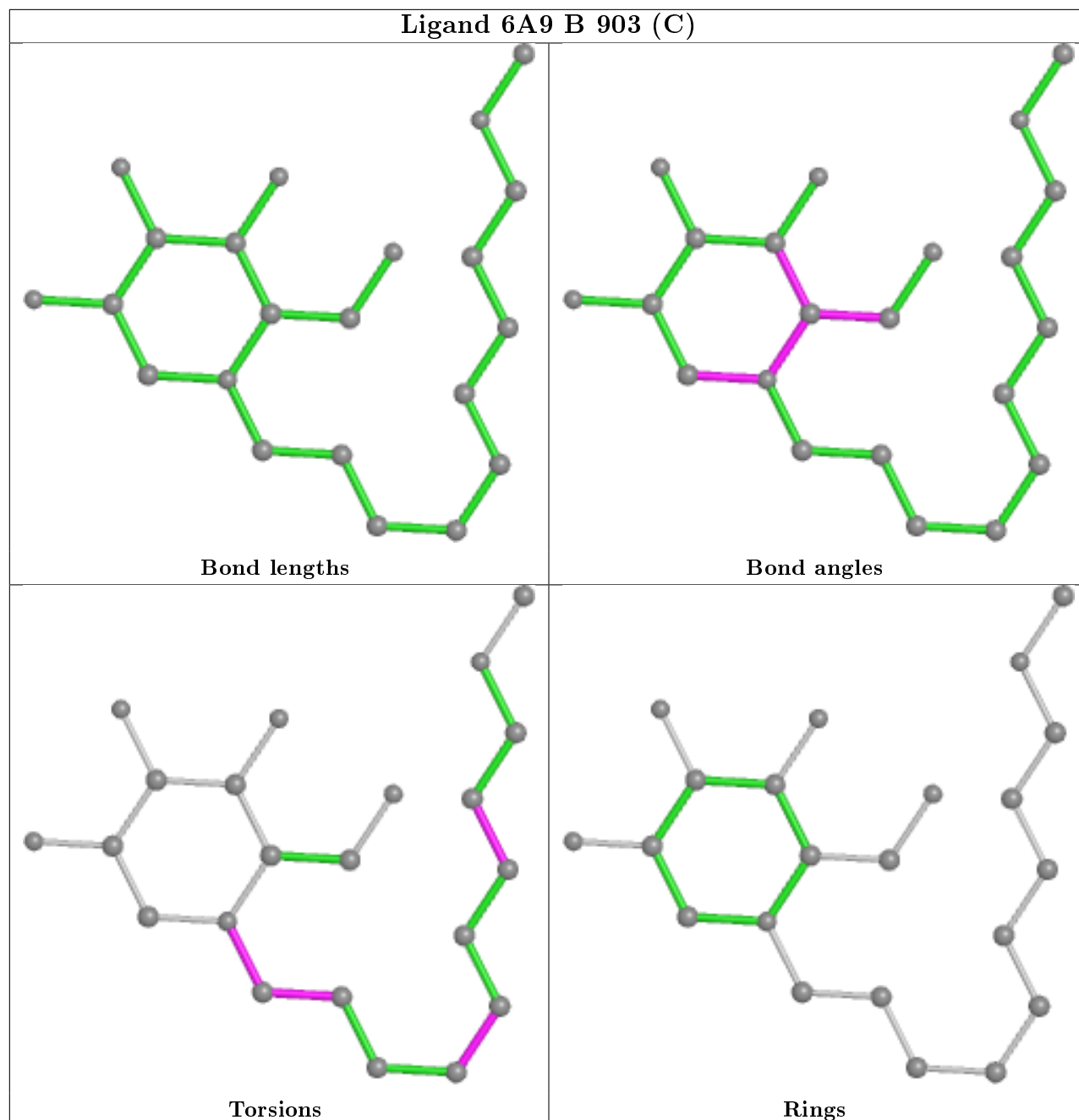
Ligand 6A9 A 903 (A)



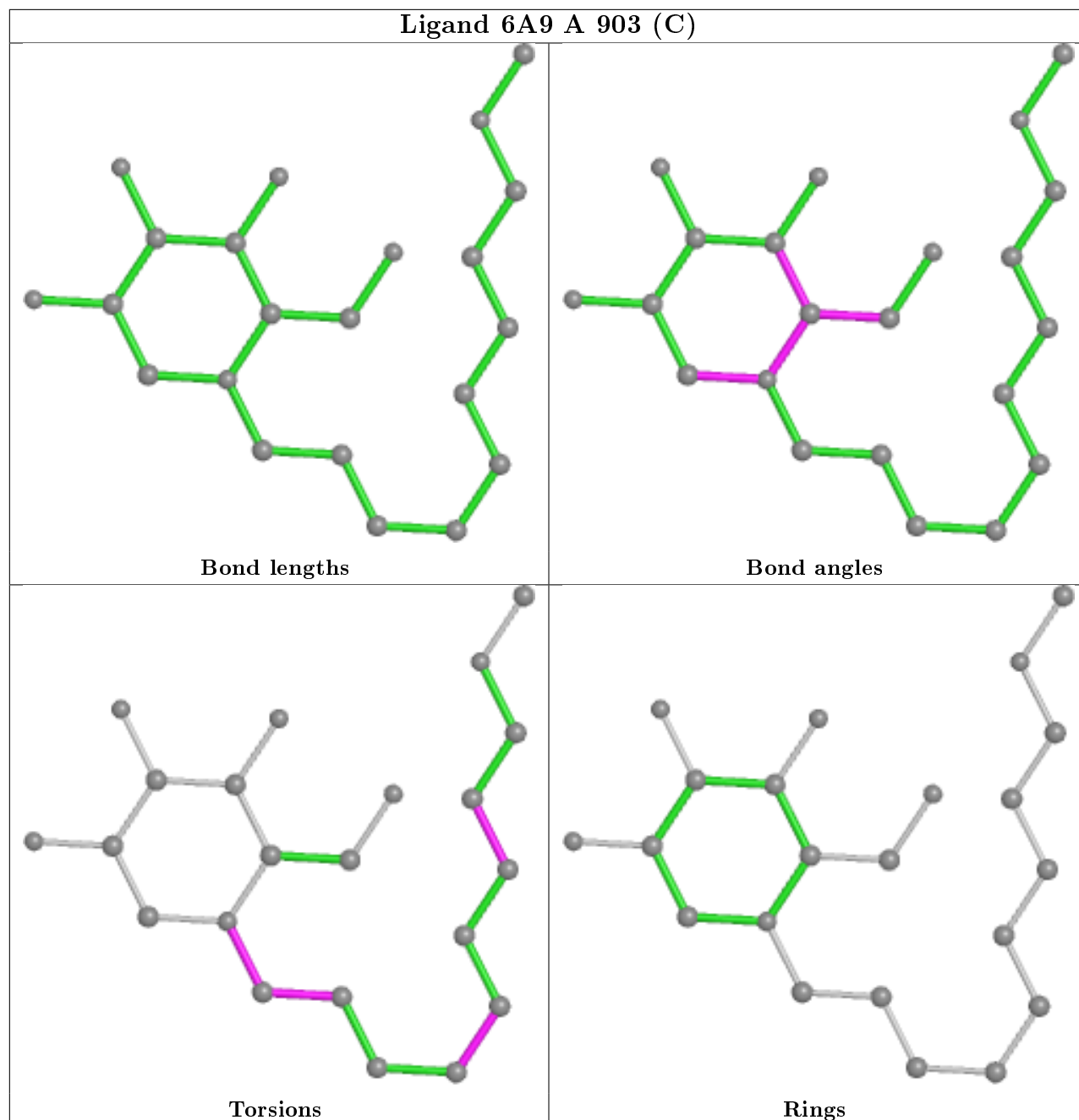
Ligand 6A9 A 903 (B)



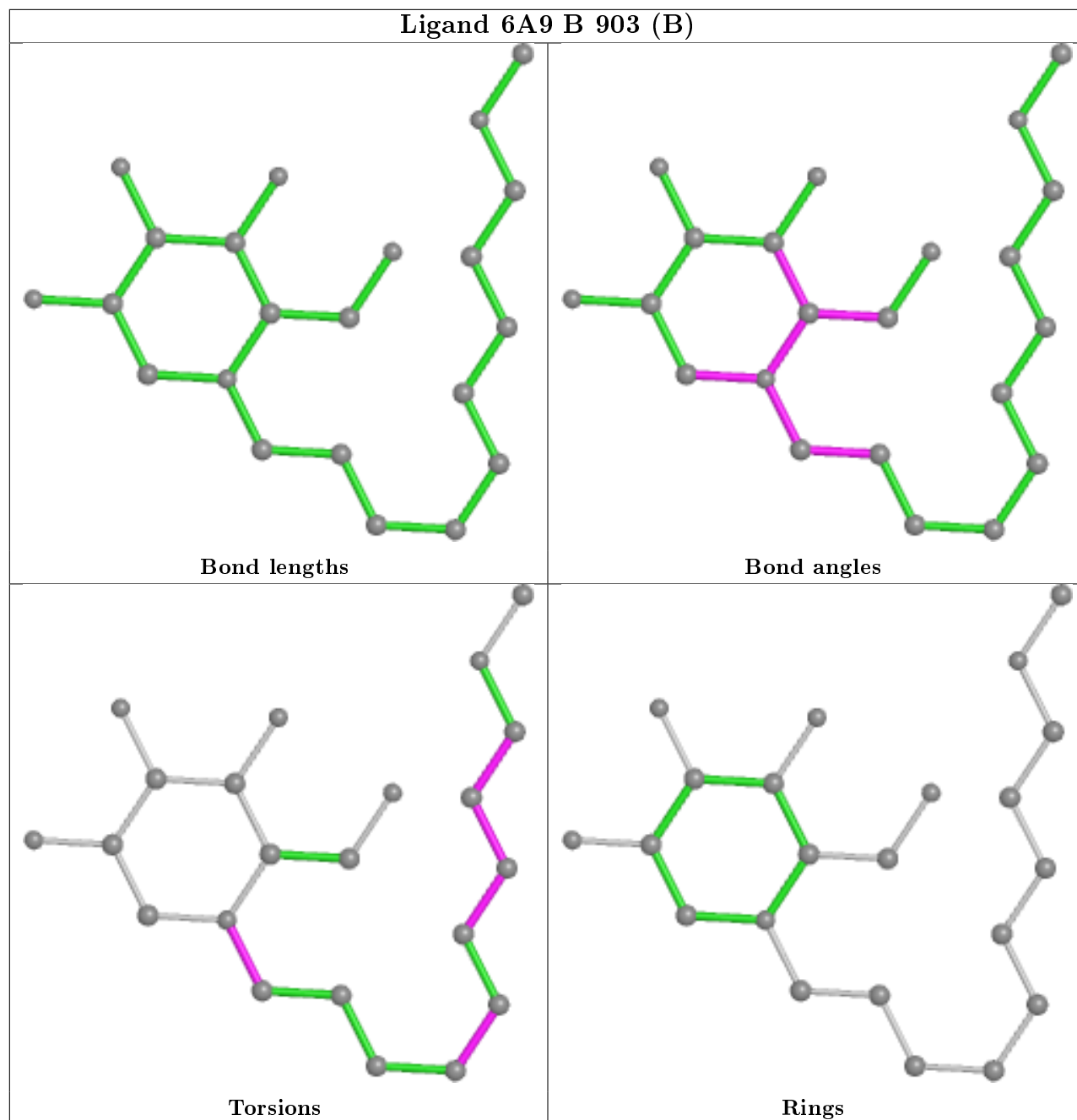
Ligand 6A9 B 903 (C)



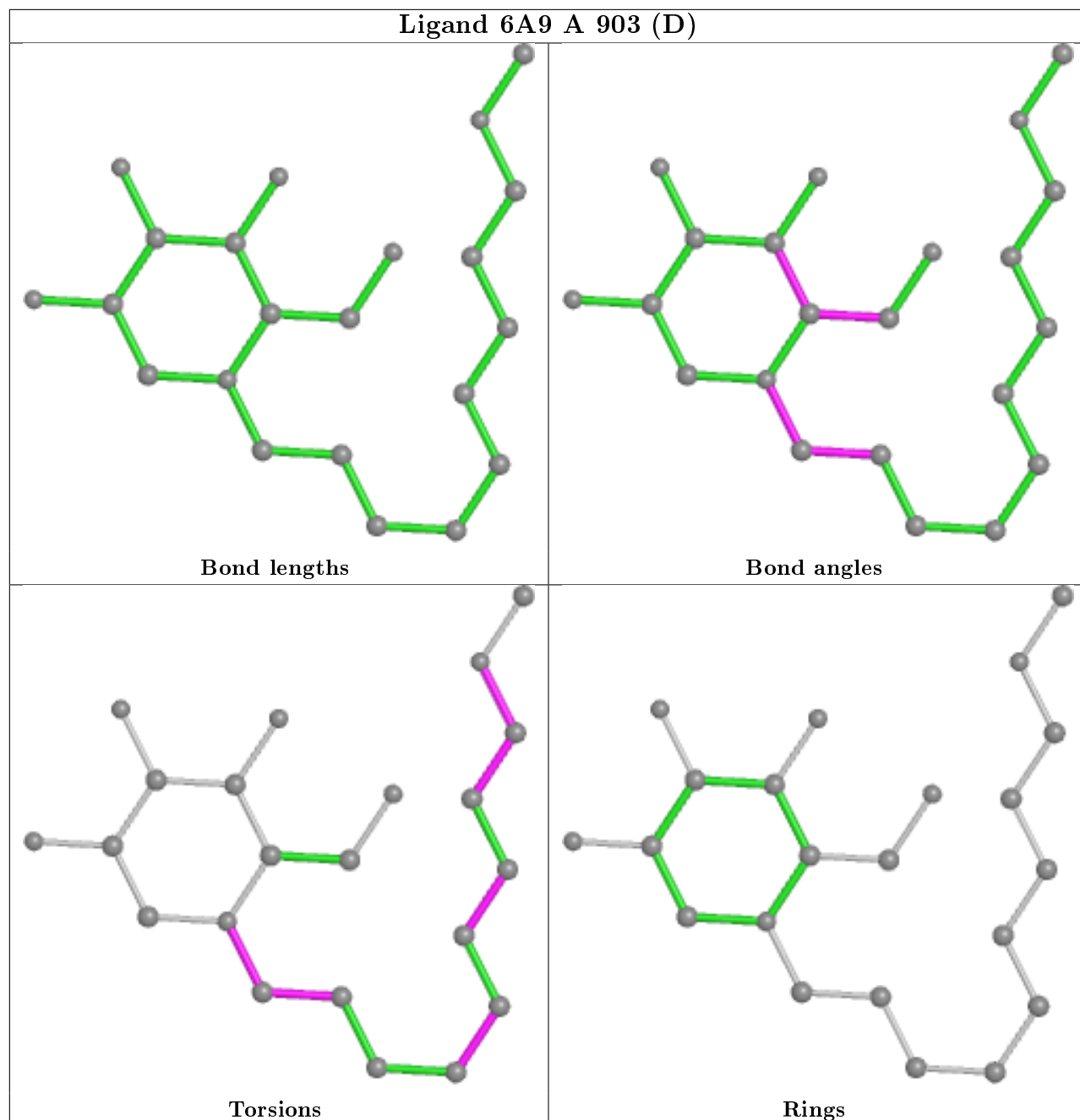
Ligand 6A9 A 903 (C)

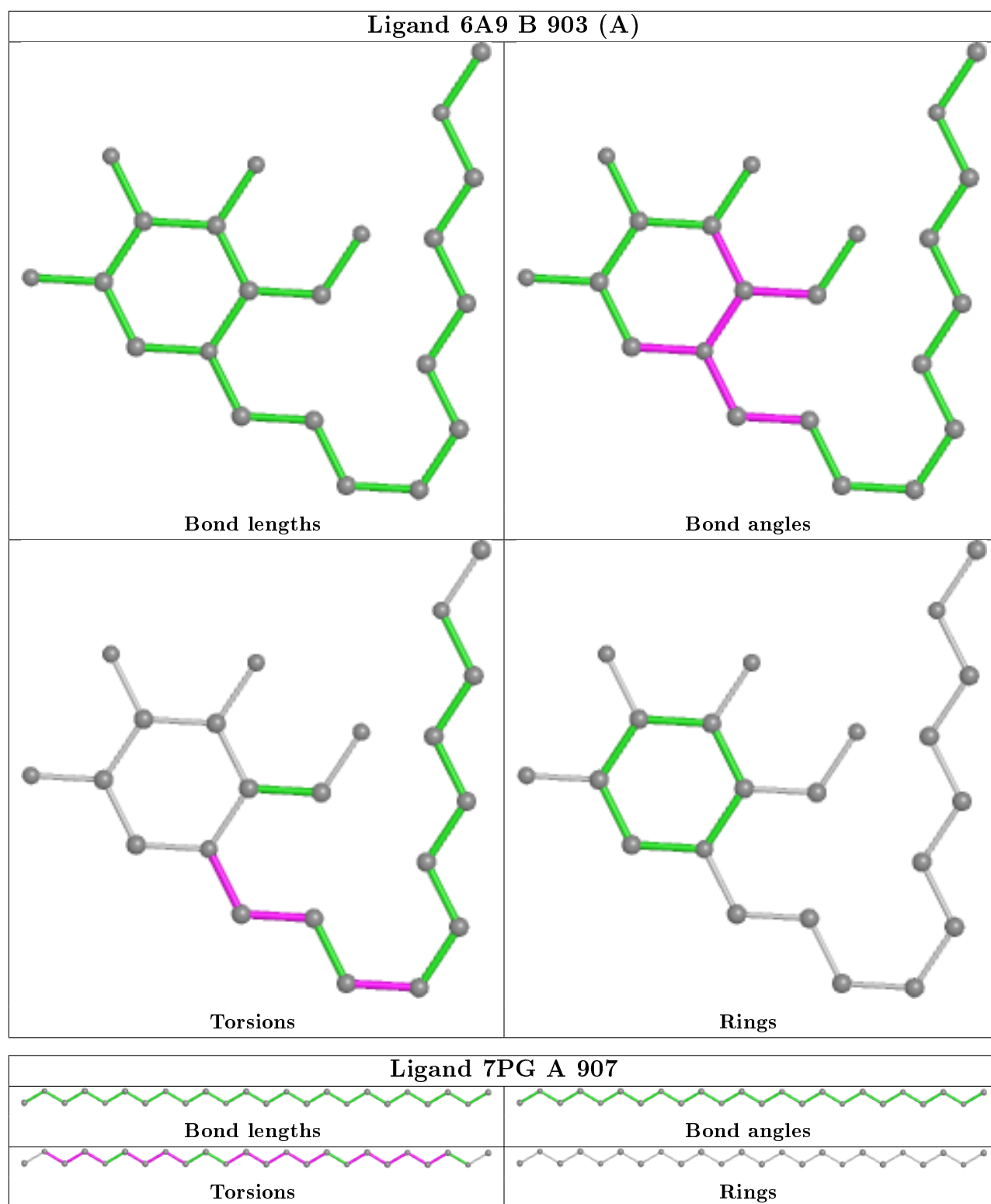


Ligand 6A9 B 903 (B)



Ligand 6A9 A 903 (D)





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	736/795 (92%)	-0.03	20 (2%) 54 60	19, 37, 75, 109	0
1	B	737/795 (92%)	0.04	27 (3%) 41 48	22, 41, 73, 105	0
1	C	747/795 (93%)	-0.04	17 (2%) 60 65	24, 41, 73, 113	0
1	D	752/795 (94%)	-0.02	17 (2%) 60 65	22, 40, 74, 107	0
All	All	2972/3180 (93%)	-0.01	81 (2%) 54 60	19, 40, 74, 113	0

The worst 5 of 81 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	127	GLY	6.1
1	B	125	THR	6.0
1	D	129	PRO	5.8
1	A	128	THR	5.4
1	C	197	PRO	5.1

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	MLY	B	662	11/12	0.79	0.22	66,77,81,82	0
1	MLY	C	662	11/12	0.80	0.24	72,82,85,86	0
1	MLY	B	227	11/12	0.81	0.22	58,63,73,74	0
1	MLY	D	662	11/12	0.81	0.13	60,69,72,72	0
1	SME	D	421	9/10	0.84	0.19	41,44,61,64	0
1	SME	B	421	9/10	0.85	0.20	56,62,75,80	0
1	MLY	C	304	11/12	0.86	0.23	52,59,68,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	MLY	B	304	11/12	0.86	0.20	57,61,70,71	0
1	MLY	C	227	11/12	0.86	0.21	49,53,64,66	0
1	MLY	C	366	11/12	0.87	0.25	57,63,71,72	0
1	SME	C	421	9/10	0.87	0.20	42,49,66,70	0
1	MLY	C	376	11/12	0.87	0.32	65,73,77,80	0
1	MLY	A	227	11/12	0.87	0.20	66,68,78,79	0
1	MLY	A	304	11/12	0.87	0.23	64,69,78,80	0
1	MLY	A	131	11/12	0.87	0.24	54,65,70,71	0
1	MLY	C	371	11/12	0.88	0.18	57,61,73,76	0
1	MLY	B	371	11/12	0.88	0.23	50,55,72,75	0
1	MLY	C	131	11/12	0.88	0.26	42,58,69,70	0
1	MLY	D	304	11/12	0.88	0.20	52,59,69,70	0
1	MLY	A	376	11/12	0.89	0.20	44,53,67,68	0
1	SME	A	421	9/10	0.89	0.19	53,59,71,76	0
1	MLY	A	662	11/12	0.89	0.18	55,65,71,73	0
1	MLY	D	376	11/12	0.89	0.24	52,57,62,62	0
1	MLY	C	736	11/12	0.90	0.16	37,45,56,59	0
1	MLY	B	111	11/12	0.90	0.18	38,40,57,58	0
1	MLY	C	378	11/12	0.90	0.22	70,71,74,74	0
1	MLY	B	378	11/12	0.91	0.17	54,55,59,61	0
1	MLY	D	533	11/12	0.91	0.20	40,45,60,61	0
1	MLY	D	378	11/12	0.91	0.16	57,59,63,64	0
1	MLY	D	227	11/12	0.91	0.17	53,58,69,70	0
1	MLY	B	736	11/12	0.92	0.13	39,44,55,55	0
1	MLY	D	371	11/12	0.92	0.19	57,61,76,76	0
1	MLY	C	533	11/12	0.92	0.18	42,45,57,58	0
1	MLY	B	376	11/12	0.92	0.20	55,62,71,71	0
1	MLY	D	131	11/12	0.92	0.25	51,64,73,75	0
1	MLY	A	366	11/12	0.92	0.16	41,46,58,60	0
1	MLY	A	371	11/12	0.93	0.18	40,46,63,64	0
1	MLY	A	573	11/12	0.93	0.17	25,29,44,45	0
1	MLY	B	779	11/12	0.93	0.12	47,52,65,66	0
1	SME	A	519	9/10	0.93	0.15	37,45,51,55	0
1	MLY	D	736	11/12	0.93	0.18	34,43,58,60	0
1	MLY	A	111	11/12	0.93	0.17	35,39,53,54	0
1	MLY	A	378	11/12	0.93	0.18	47,49,52,55	0
1	MLY	D	366	11/12	0.93	0.17	46,51,57,58	0
1	MLY	D	111	11/12	0.94	0.12	35,39,48,49	0
1	MLY	B	533	11/12	0.94	0.14	40,45,61,62	0
1	MLY	A	533	11/12	0.94	0.16	36,40,59,60	0
1	MLY	B	131	11/12	0.94	0.20	47,56,66,67	0
1	MLY	D	779	11/12	0.95	0.17	41,47,59,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	MLY	C	779	11/12	0.95	0.13	49,55,66,68	0
1	MLY	C	573	11/12	0.95	0.15	28,31,43,44	0
1	MLY	B	573	11/12	0.95	0.20	31,34,50,50	0
1	MLY	C	111	11/12	0.95	0.19	34,39,52,54	0
1	MLY	A	736	11/12	0.95	0.12	28,35,46,47	0
1	SME	D	519	9/10	0.95	0.12	46,53,58,61	0
1	MLY	B	366	11/12	0.96	0.14	45,50,63,65	0
1	SME	B	519	9/10	0.96	0.13	39,48,53,56	0
1	MLY	A	779	11/12	0.96	0.10	37,42,54,55	0
1	SME	C	519	9/10	0.96	0.10	47,53,58,61	0
1	MLY	D	573	11/12	0.97	0.15	27,29,40,42	0

6.3 Carbohydrates

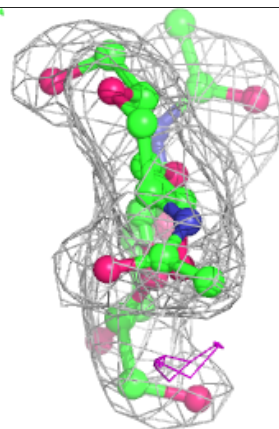
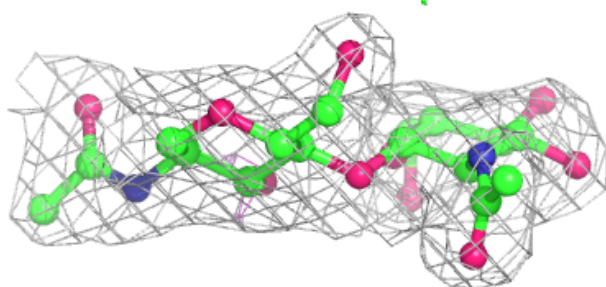
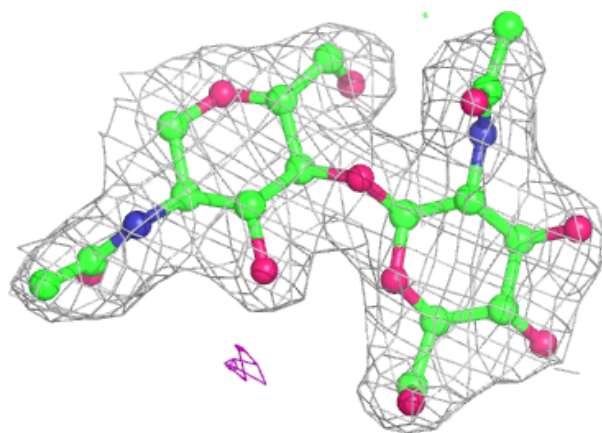
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	BMA	H	3	11/12	0.72	0.23	99,103,107,107	0
2	NAG	F	2	14/15	0.83	0.21	81,87,92,92	0
3	NAG	H	2	14/15	0.83	0.17	72,77,87,93	0
3	BMA	G	3	11/12	0.83	0.15	104,109,112,112	0
3	NAG	G	2	14/15	0.86	0.15	78,84,93,98	0
2	NAG	E	2	14/15	0.93	0.14	57,62,67,70	0
3	NAG	G	1	14/15	0.95	0.10	48,54,60,70	0
2	NAG	F	1	14/15	0.96	0.08	48,55,64,73	0
3	NAG	H	1	14/15	0.97	0.09	41,47,56,65	0
2	NAG	E	1	14/15	0.97	0.09	35,39,45,51	0

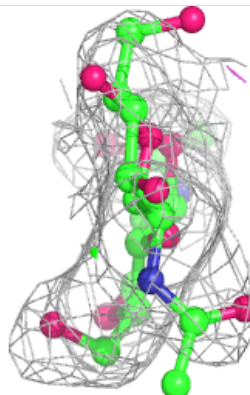
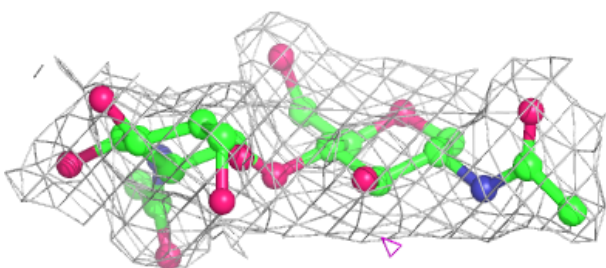
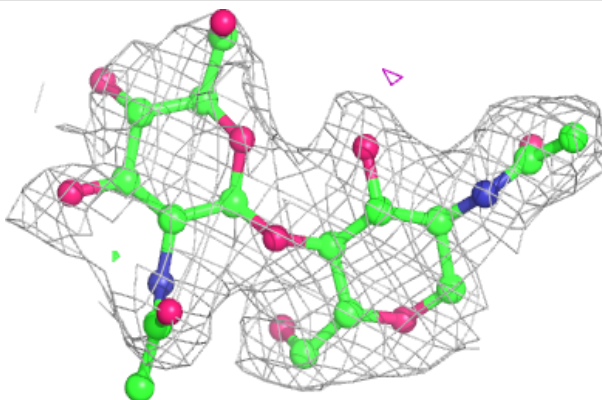
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

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)

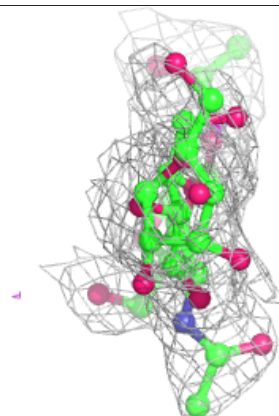
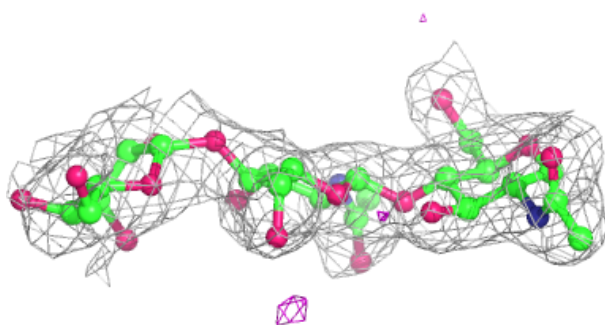
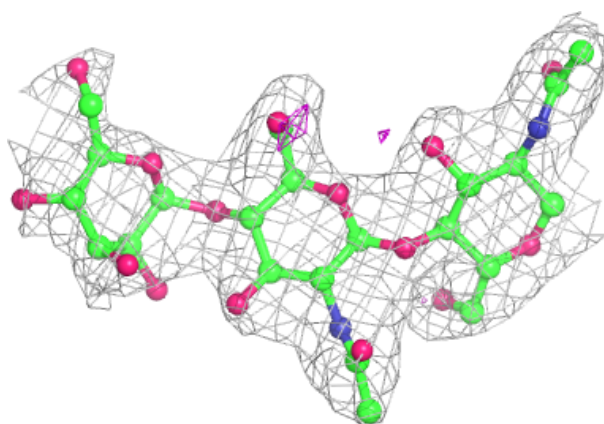
**Electron density around Chain F:**

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

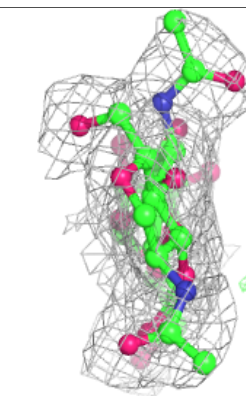
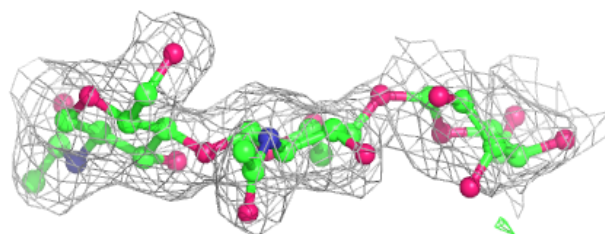
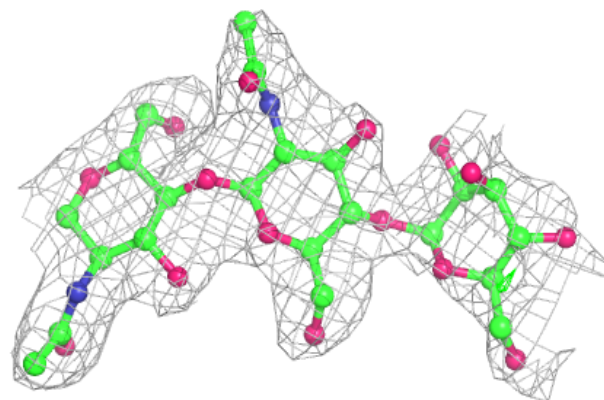


Electron density around Chain G:

$2mF_o-DF_c$ (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 ⓘ

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.

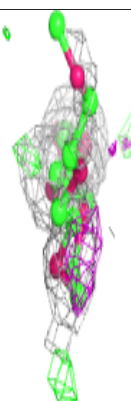
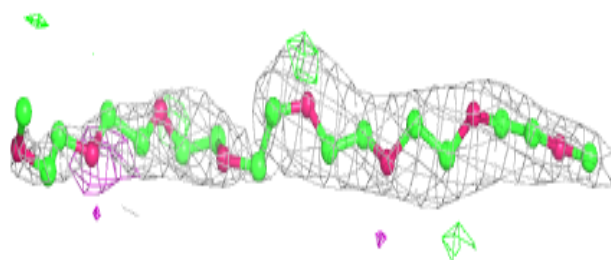
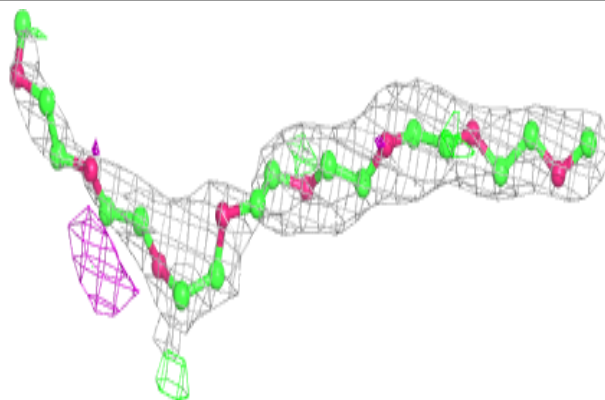
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	7PG	B	906	24/26	0.74	0.27	88,97,105,107	0
6	7PG	C	906	17/26	0.76	0.39	59,64,80,80	0
6	7PG	A	907	24/26	0.79	0.28	74,82,88,90	0
4	SO4	C	903	5/5	0.82	0.22	166,167,168,170	0
4	SO4	D	903	5/5	0.84	0.20	143,145,145,146	0
6	7PG	C	905	22/26	0.85	0.38	23,28,36,40	22
6	7PG	D	905	22/26	0.86	0.33	16,24,31,36	22
6	7PG	D	906	17/26	0.87	0.31	45,54,67,68	0
5	6A9	B	903[D]	22/22	0.90	0.29	12,14,21,24	22
5	6A9	B	903[C]	22/22	0.90	0.29	14,17,29,32	22
5	6A9	B	903[B]	22/22	0.90	0.29	36,41,45,46	22
5	6A9	B	903[A]	22/22	0.90	0.29	24,30,43,43	22
5	6A9	C	904[C]	22/22	0.91	0.26	27,28,30,30	22
5	6A9	C	904[B]	22/22	0.91	0.26	38,40,41,41	22
5	6A9	C	904[D]	22/22	0.91	0.26	13,16,25,26	22
5	6A9	C	904[A]	22/22	0.91	0.26	24,30,35,36	22
5	6A9	A	903[C]	22/22	0.92	0.28	25,27,35,37	22
5	6A9	A	903[B]	22/22	0.92	0.28	40,42,48,49	22
5	6A9	A	903[D]	22/22	0.92	0.28	9,11,15,17	22
5	6A9	A	903[A]	22/22	0.92	0.28	15,22,45,46	22
5	6A9	D	904[B]	22/22	0.93	0.24	33,38,41,42	22
5	6A9	D	904[C]	22/22	0.93	0.24	24,29,30,31	22
5	6A9	D	904[D]	22/22	0.93	0.24	11,15,27,31	22
5	6A9	D	904[A]	22/22	0.93	0.24	13,25,34,35	22
4	SO4	A	901	5/5	0.94	0.14	83,84,86,86	0
4	SO4	B	907	5/5	0.94	0.13	99,100,101,102	0
4	SO4	A	906	5/5	0.94	0.12	93,94,95,96	0
4	SO4	C	902	5/5	0.95	0.15	83,84,85,85	0
4	SO4	B	901	5/5	0.95	0.13	77,80,80,82	0
4	SO4	D	902	5/5	0.96	0.12	77,78,79,80	0
4	SO4	B	902	5/5	0.97	0.12	71,71,73,75	0
4	SO4	A	902	5/5	0.97	0.16	60,62,66,67	0
4	SO4	D	901	5/5	0.98	0.09	47,48,54,56	0
4	SO4	C	901	5/5	0.98	0.09	49,49,52,52	0

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.

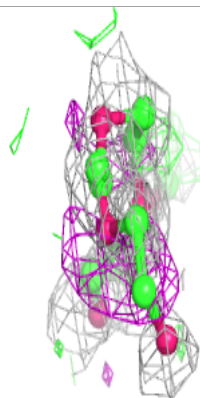
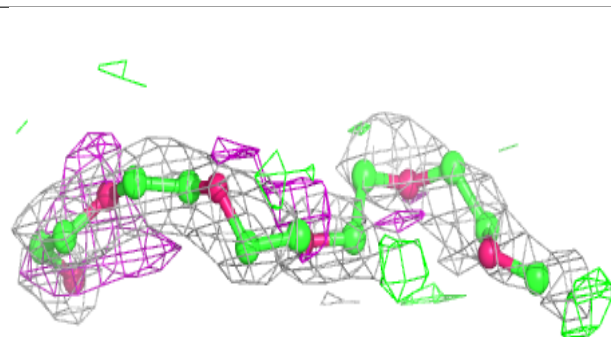
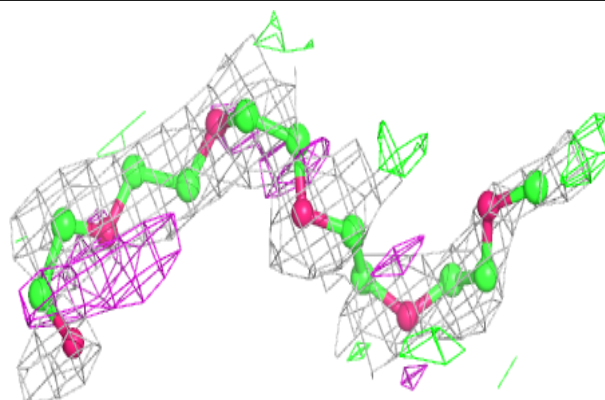
Electron density around 7PG B 906:

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



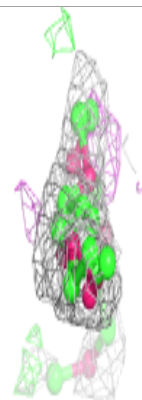
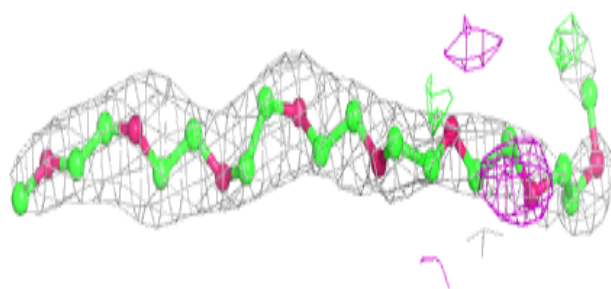
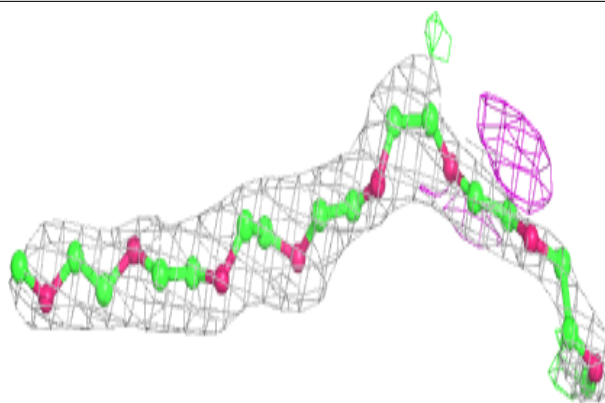
Electron density around 7PG C 906:

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

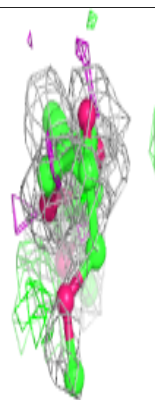
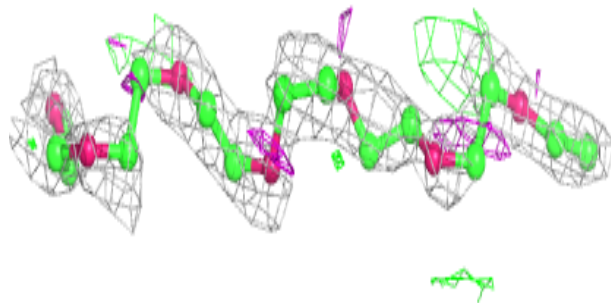
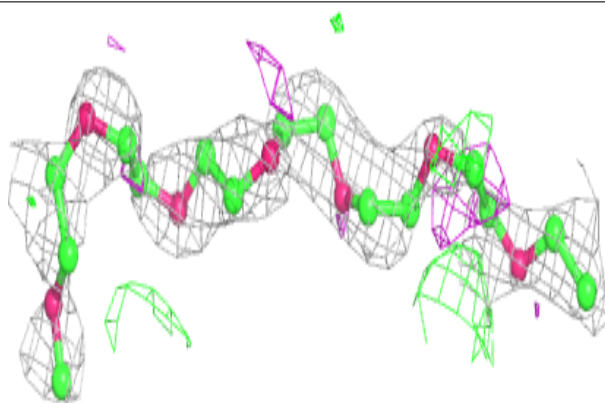


Electron density around 7PG A 907:

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

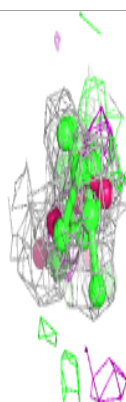
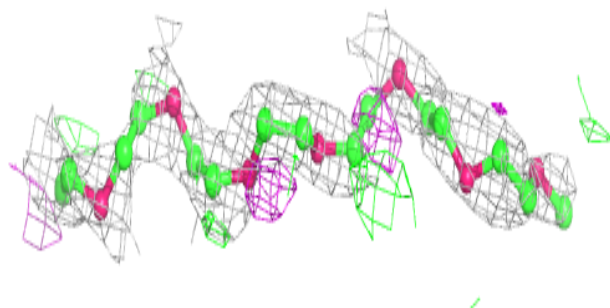
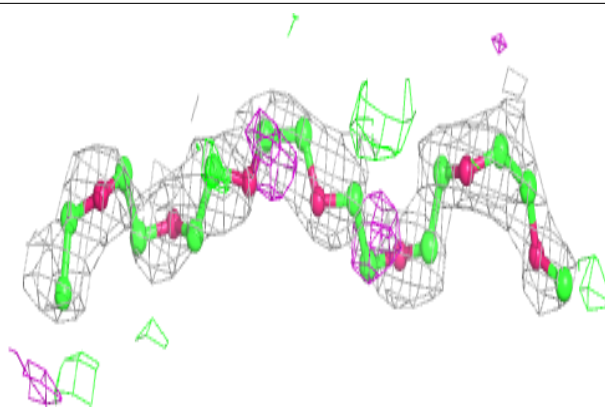
**Electron density around 7PG C 905:**

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

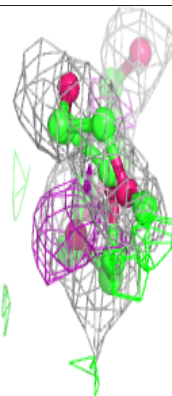
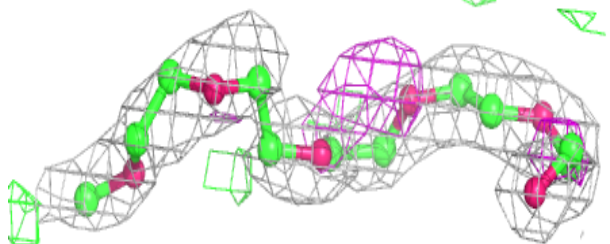
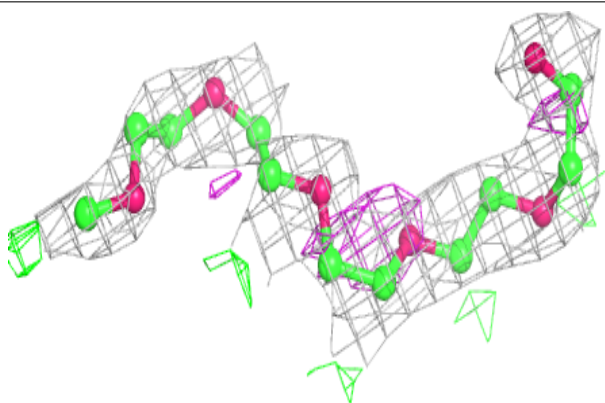


Electron density around 7PG D 905:

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

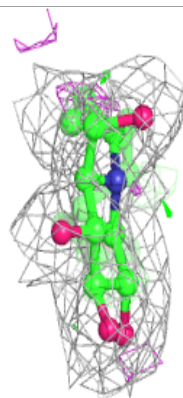
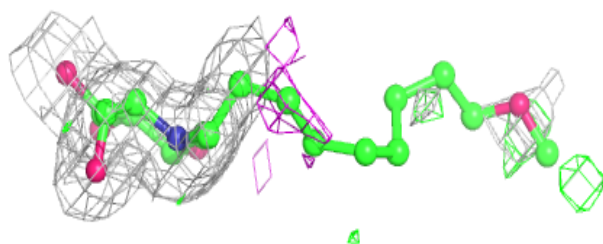
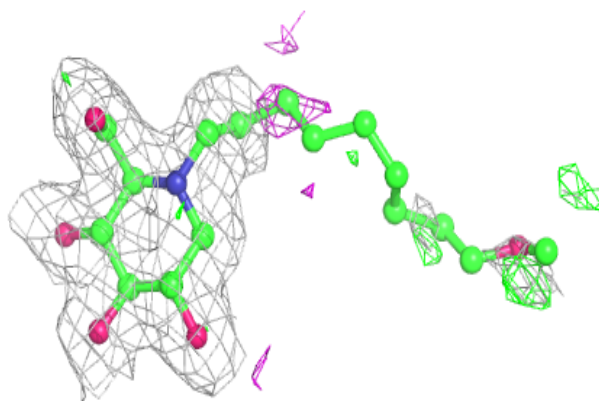
**Electron density around 7PG D 906:**

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

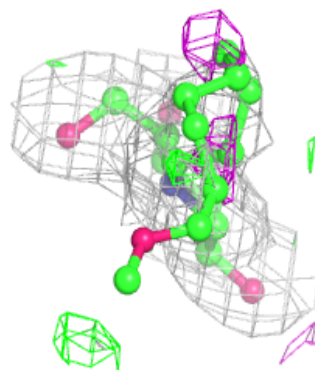
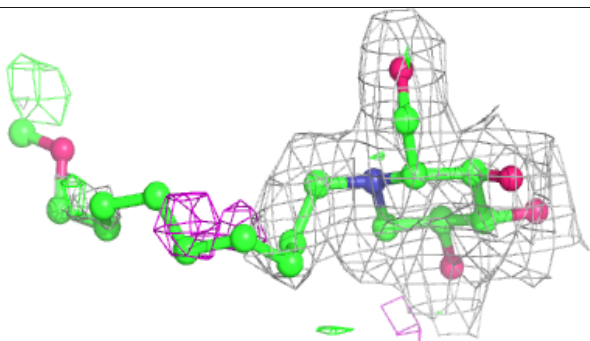
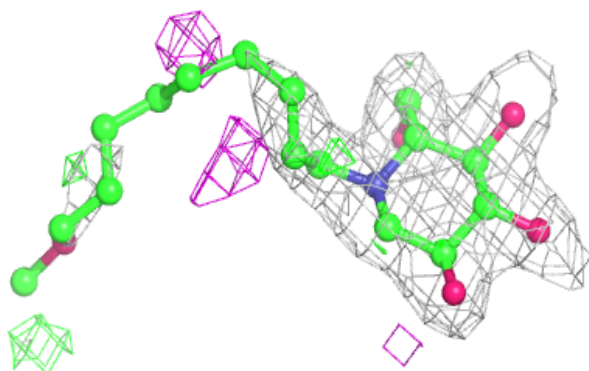


Electron density around 6A9 B 903 (D):

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

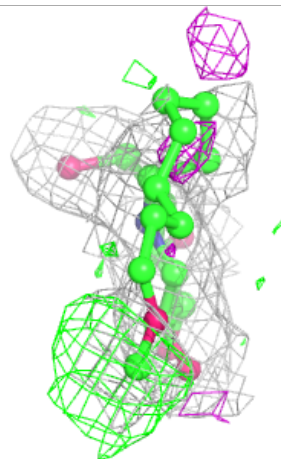
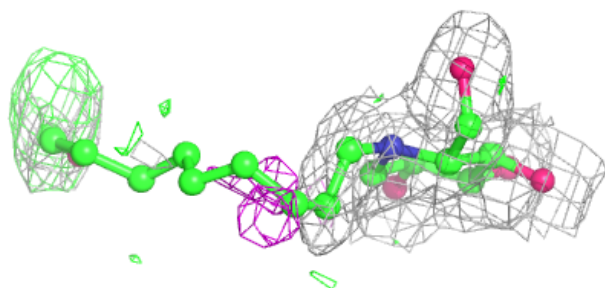
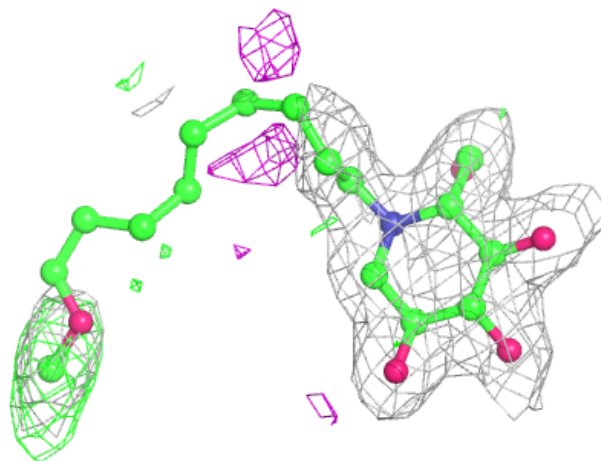
**Electron density around 6A9 B 903 (C):**

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



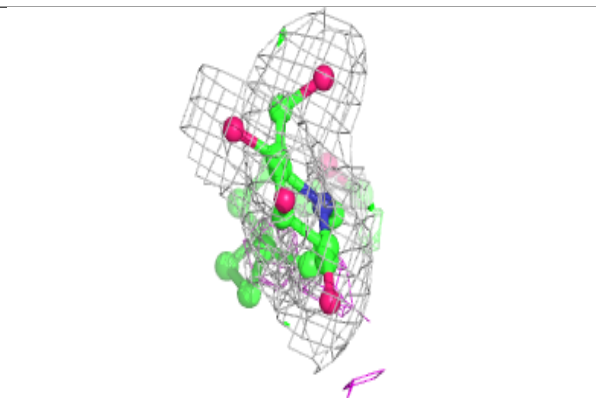
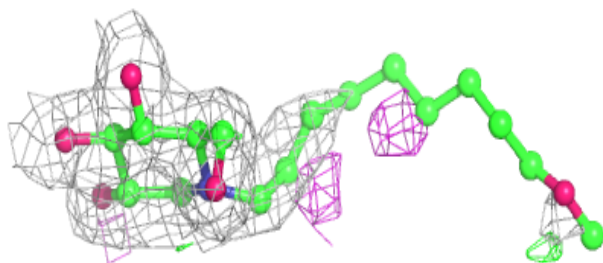
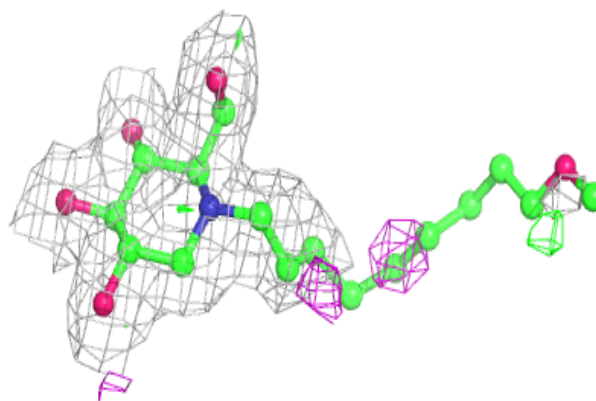
Electron density around 6A9 B 903 (B):

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

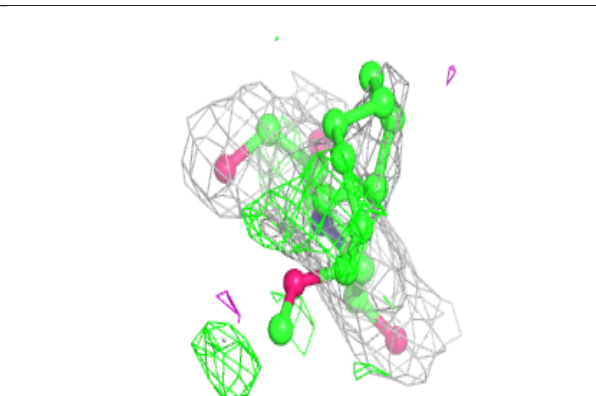
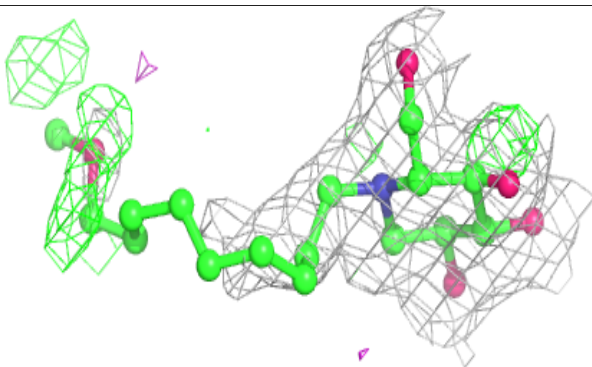
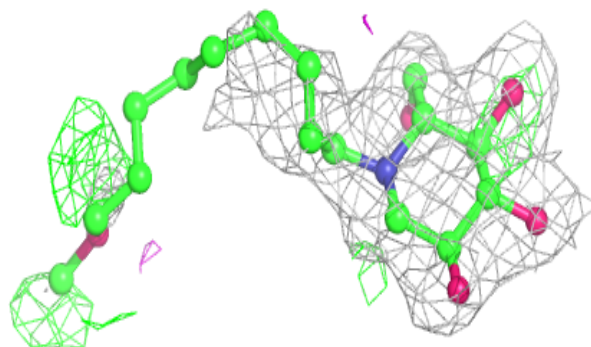


Electron density around 6A9 B 903 (A):

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

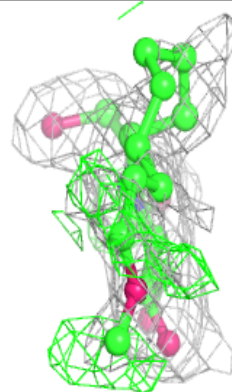
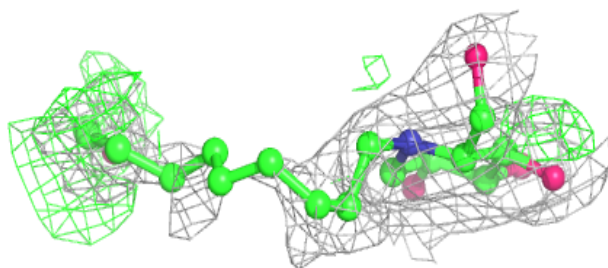
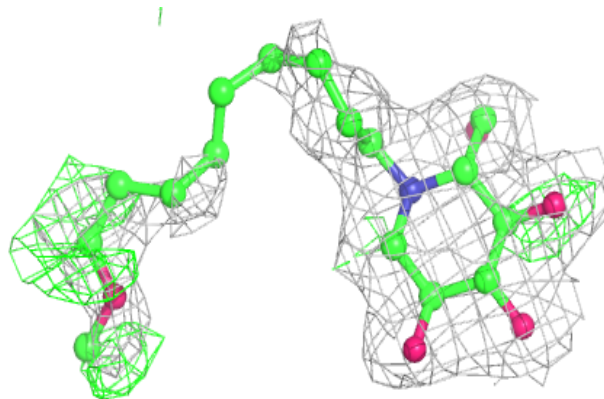
**Electron density around 6A9 C 904 (C):**

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

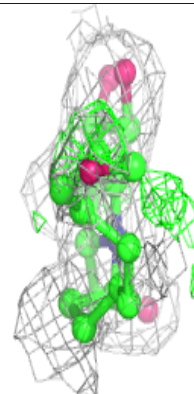
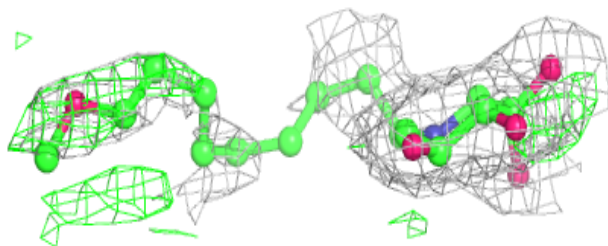
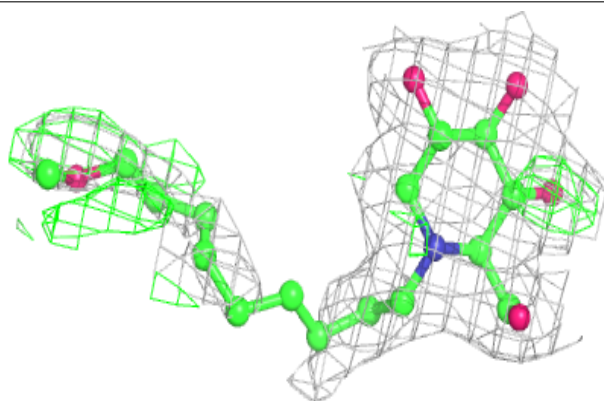


Electron density around 6A9 C 904 (B):

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

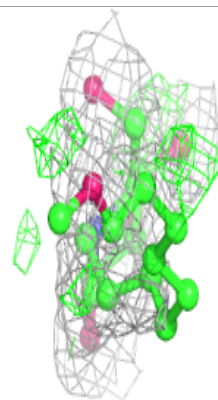
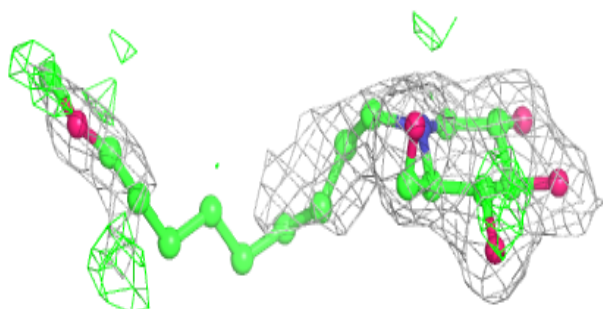
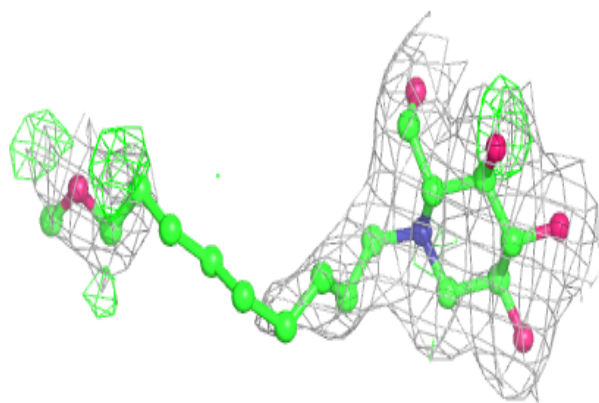
**Electron density around 6A9 C 904 (D):**

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

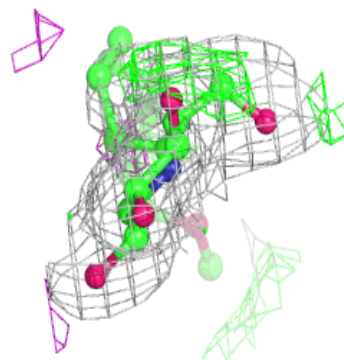
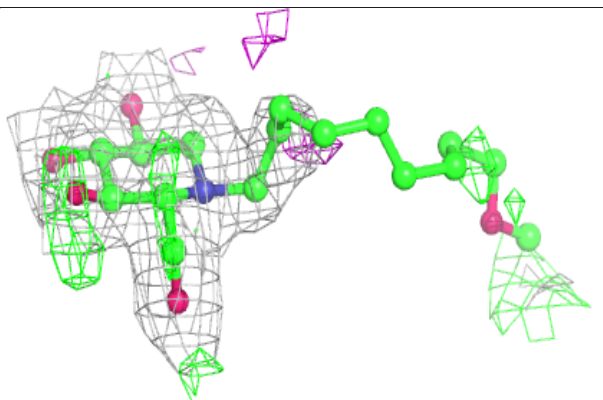
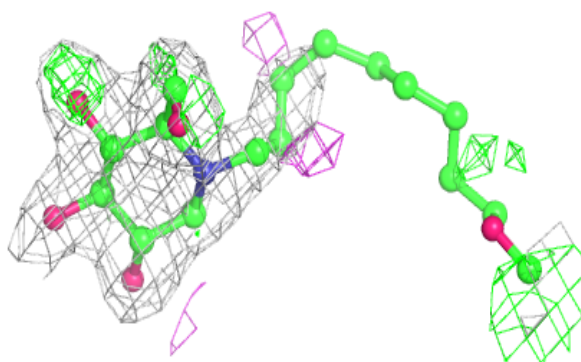


Electron density around 6A9 C 904 (A):

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

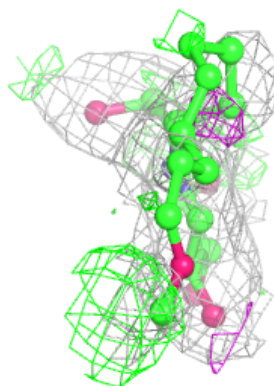
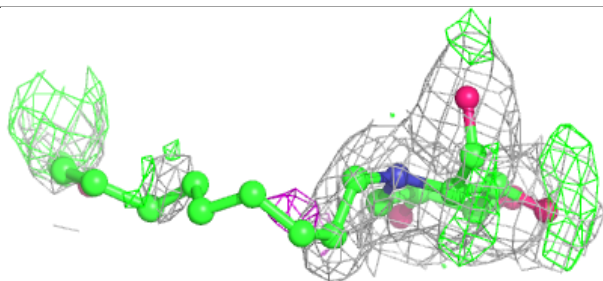
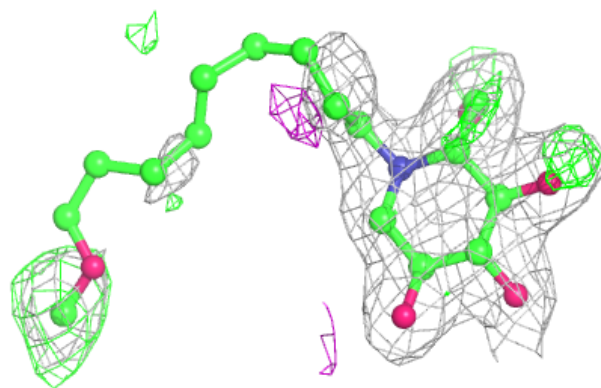
**Electron density around 6A9 A 903 (C):**

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

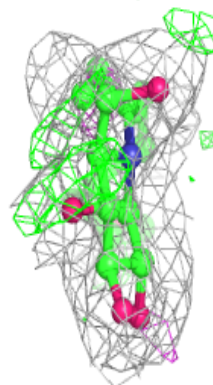
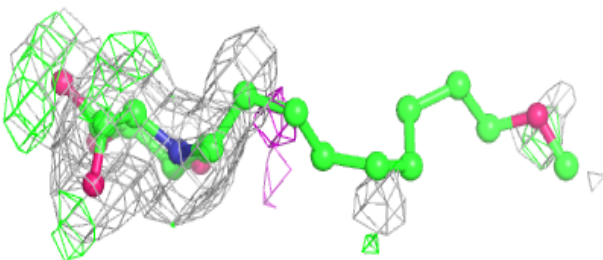
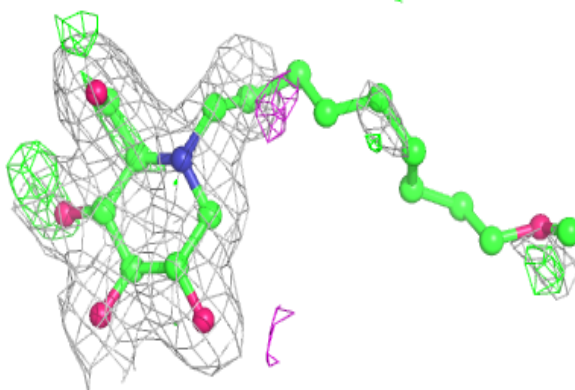


Electron density around 6A9 A 903 (B):

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

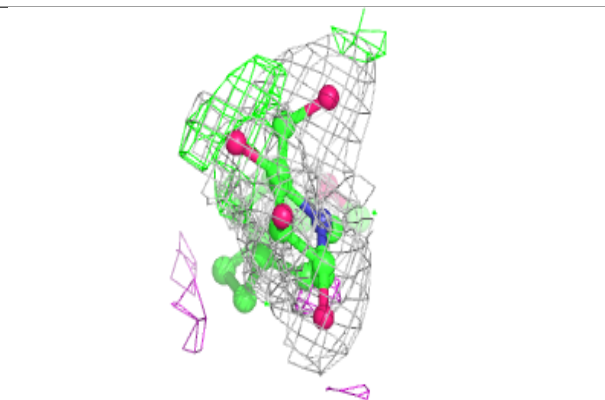
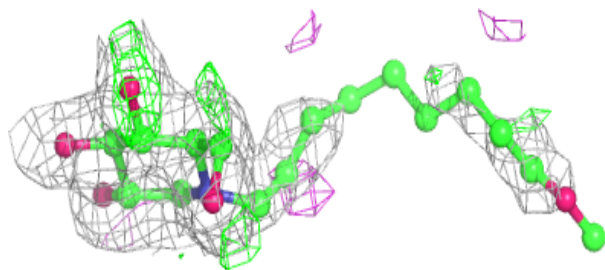
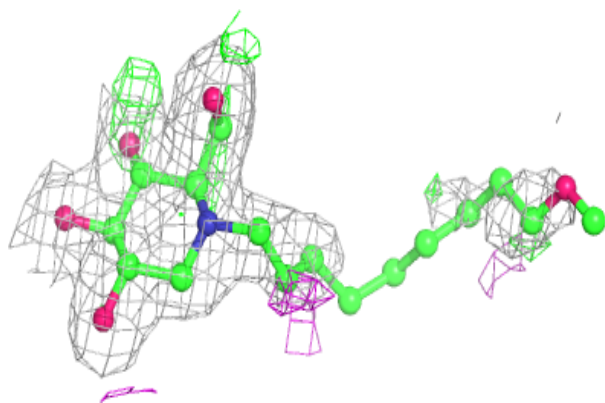
**Electron density around 6A9 A 903 (D):**

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

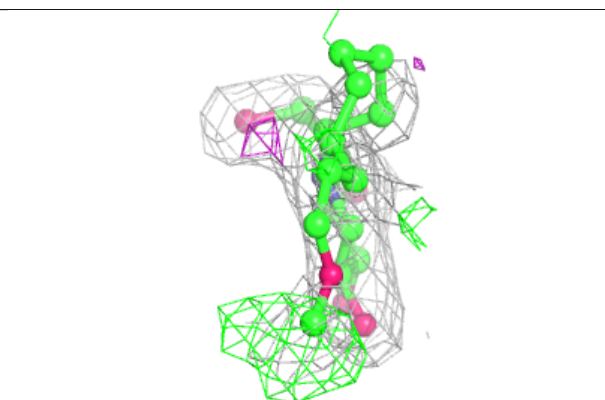
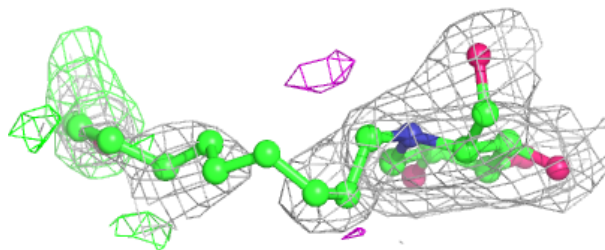
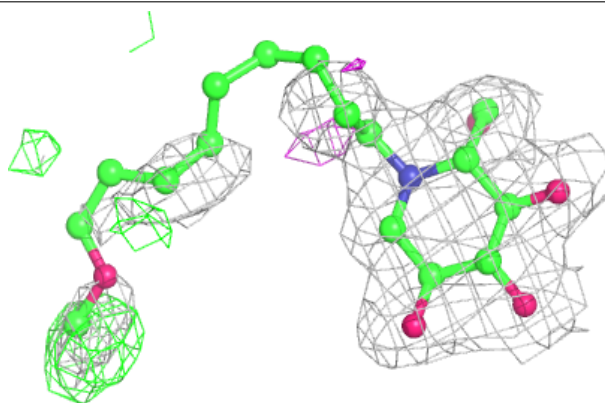


Electron density around 6A9 A 903 (A):

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

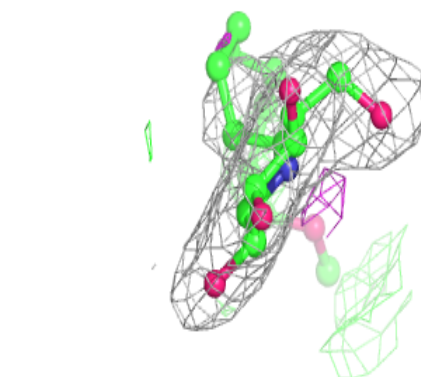
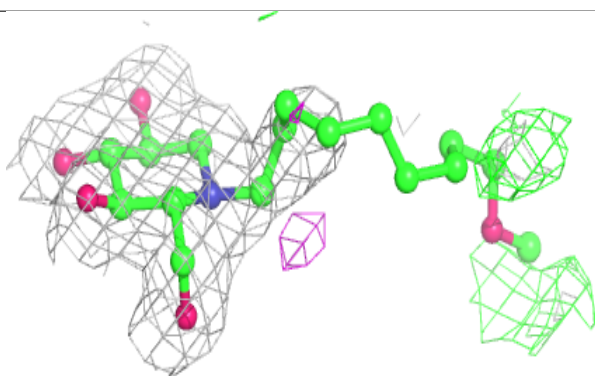
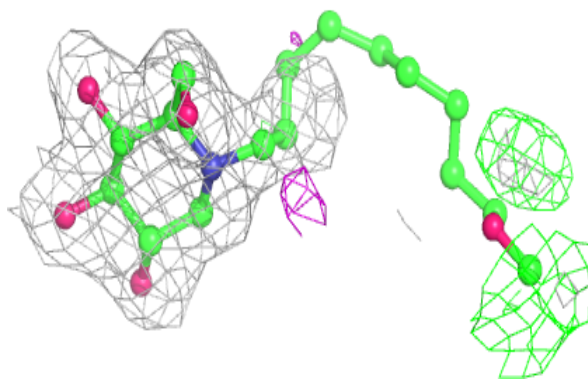
**Electron density around 6A9 D 904 (B):**

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

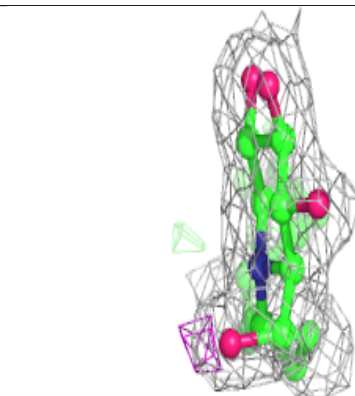
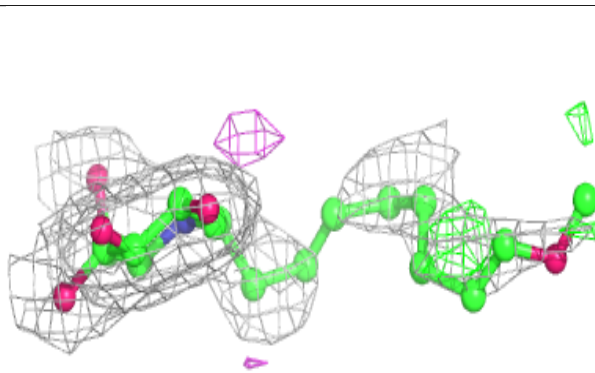
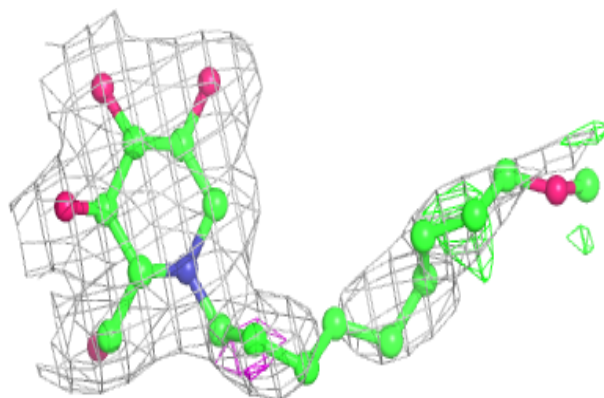


Electron density around 6A9 D 904 (C):

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

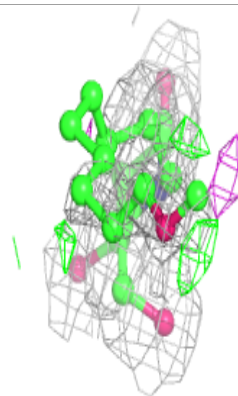
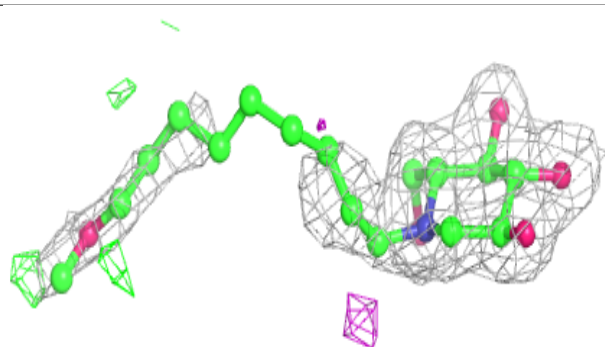
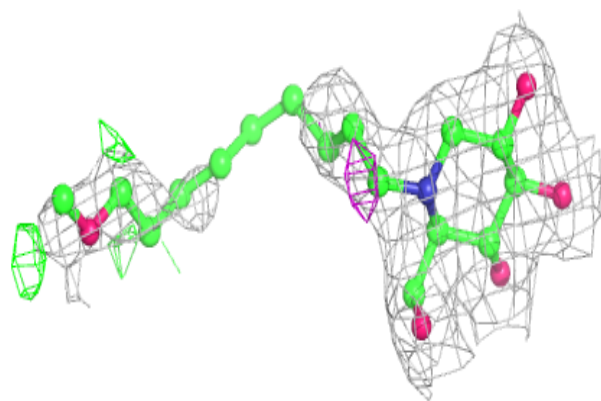
**Electron density around 6A9 D 904 (D):**

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



Electron density around 6A9 D 904 (A):

$2mF_o-DF_c$ (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.