



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 03:37 PM UTC

PDB ID : 3SIO / pdb_00003sio
Title : Ac-AChBP ligand binding domain (not including beta 9-10 linker) mutated to human alpha-7 nAChR
Authors : Nemecz, A.; Taylor, P.W.
Deposited on : 2011-06-19
Resolution : 2.32 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 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

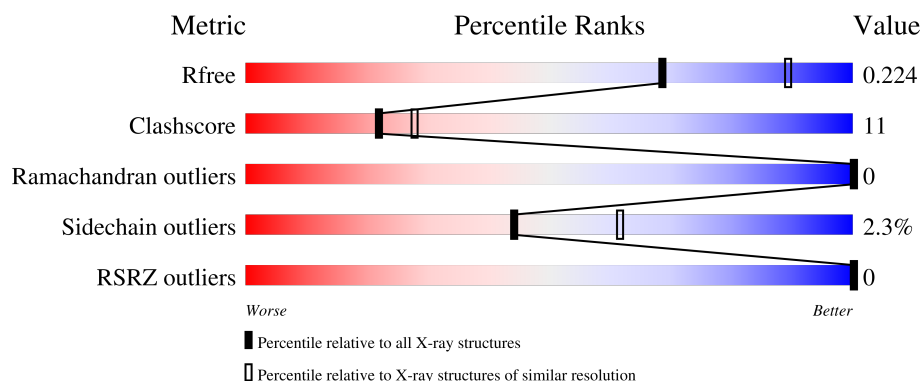
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

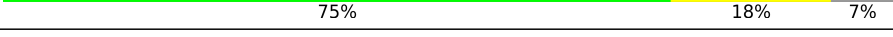
The reported resolution of this entry is 2.32 Å.

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.



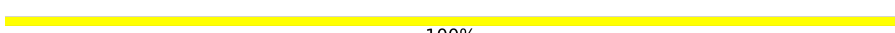
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7754 (2.34-2.30)
Clashscore	190562	8383 (2.34-2.30)
Ramachandran outliers	187476	8303 (2.34-2.30)
Sidechain outliers	187428	8303 (2.34-2.30)
RSRZ outliers	180081	7760 (2.34-2.30)

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	230	
1	B	230	
1	C	230	
1	D	230	
1	E	230	

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Mol	Chain	Length	Quality of chain
1	F	230	 77% 15% 7%
1	G	230	 75% 19% 6%
1	H	230	 76% 19% 5%
1	I	230	 79% 13% 7%
1	J	230	 71% 22% 6%
2	K	2	 100%
2	M	2	 50% 50%
2	O	2	 100%
3	L	7	 57% 43%
3	P	7	 86% 14%
4	N	6	 33% 50% 17%
4	Q	6	 50% 33% 17%

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	NAG	A	225	-	-	X	-
7	MRD	D	251	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 19701 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 Soluble acetylcholine receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	214	Total	C	N	O	S	0	7	0
			1752	1106	289	349	8			
1	B	216	Total	C	N	O	S	0	8	0
			1781	1124	289	360	8			
1	C	221	Total	C	N	O	S	0	9	0
			1815	1147	299	361	8			
1	D	214	Total	C	N	O	S	0	9	0
			1764	1113	288	355	8			
1	E	216	Total	C	N	O	S	0	9	0
			1789	1130	291	360	8			
1	F	214	Total	C	N	O	S	0	9	0
			1762	1112	292	350	8			
1	G	216	Total	C	N	O	S	0	10	0
			1793	1132	291	362	8			
1	H	221	Total	C	N	O	S	0	7	0
			1810	1143	302	357	8			
1	I	214	Total	C	N	O	S	0	6	0
			1753	1105	285	355	8			
1	J	216	Total	C	N	O	S	0	11	0
			1796	1135	294	358	9			

There are 290 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	ASP	-	expression tag	UNP Q8WSF8
A	-7	TYR	-	expression tag	UNP Q8WSF8
A	-6	LYS	-	expression tag	UNP Q8WSF8
A	-5	ASP	-	expression tag	UNP Q8WSF8
A	-4	ASP	-	expression tag	UNP Q8WSF8
A	-3	ASP	-	expression tag	UNP Q8WSF8
A	-2	ASP	-	expression tag	UNP Q8WSF8
A	-1	LYS	-	expression tag	UNP Q8WSF8
A	0	LEU	-	expression tag	UNP Q8WSF8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	32	TYR	THR	engineered mutation	UNP Q8WSF8
A	34	SER	GLY	engineered mutation	UNP Q8WSF8
A	36	SER	THR	engineered mutation	UNP Q8WSF8
A	38	LEU	GLN	engineered mutation	UNP Q8WSF8
A	55	TRP	TYR	engineered mutation	UNP Q8WSF8
A	59	SER	ARG	engineered mutation	UNP Q8WSF8
A	106	ASN	ILE	engineered mutation	UNP Q8WSF8
A	108	LEU	VAL	engineered mutation	UNP Q8WSF8
A	110	ASN	THR	engineered mutation	UNP Q8WSF8
A	111	SER	HIS	engineered mutation	UNP Q8WSF8
A	112	SER	ASP	engineered mutation	UNP Q8WSF8
A	114	HIS	SER	engineered mutation	UNP Q8WSF8
A	116	GLN	MET	engineered mutation	UNP Q8WSF8
A	117	TYR	PHE	engineered mutation	UNP Q8WSF8
A	118	LEU	ILE	engineered mutation	UNP Q8WSF8
A	148	SER	VAL	engineered mutation	UNP Q8WSF8
A	150	GLY	SER	engineered mutation	UNP Q8WSF8
A	152	TRP	PHE	engineered mutation	UNP Q8WSF8
A	220	SER	-	expression tag	UNP Q8WSF8
A	221	ARG	-	expression tag	UNP Q8WSF8
B	-8	ASP	-	expression tag	UNP Q8WSF8
B	-7	TYR	-	expression tag	UNP Q8WSF8
B	-6	LYS	-	expression tag	UNP Q8WSF8
B	-5	ASP	-	expression tag	UNP Q8WSF8
B	-4	ASP	-	expression tag	UNP Q8WSF8
B	-3	ASP	-	expression tag	UNP Q8WSF8
B	-2	ASP	-	expression tag	UNP Q8WSF8
B	-1	LYS	-	expression tag	UNP Q8WSF8
B	0	LEU	-	expression tag	UNP Q8WSF8
B	32	TYR	THR	engineered mutation	UNP Q8WSF8
B	34	SER	GLY	engineered mutation	UNP Q8WSF8
B	36	SER	THR	engineered mutation	UNP Q8WSF8
B	38	LEU	GLN	engineered mutation	UNP Q8WSF8
B	55	TRP	TYR	engineered mutation	UNP Q8WSF8
B	59	SER	ARG	engineered mutation	UNP Q8WSF8
B	106	ASN	ILE	engineered mutation	UNP Q8WSF8
B	108	LEU	VAL	engineered mutation	UNP Q8WSF8
B	110	ASN	THR	engineered mutation	UNP Q8WSF8
B	111	SER	HIS	engineered mutation	UNP Q8WSF8
B	112	SER	ASP	engineered mutation	UNP Q8WSF8
B	114	HIS	SER	engineered mutation	UNP Q8WSF8
B	116	GLN	MET	engineered mutation	UNP Q8WSF8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	117	TYR	PHE	engineered mutation	UNP Q8WSF8
B	118	LEU	ILE	engineered mutation	UNP Q8WSF8
B	148	SER	VAL	engineered mutation	UNP Q8WSF8
B	150	GLY	SER	engineered mutation	UNP Q8WSF8
B	152	TRP	PHE	engineered mutation	UNP Q8WSF8
B	220	SER	-	expression tag	UNP Q8WSF8
B	221	ARG	-	expression tag	UNP Q8WSF8
C	-8	ASP	-	expression tag	UNP Q8WSF8
C	-7	TYR	-	expression tag	UNP Q8WSF8
C	-6	LYS	-	expression tag	UNP Q8WSF8
C	-5	ASP	-	expression tag	UNP Q8WSF8
C	-4	ASP	-	expression tag	UNP Q8WSF8
C	-3	ASP	-	expression tag	UNP Q8WSF8
C	-2	ASP	-	expression tag	UNP Q8WSF8
C	-1	LYS	-	expression tag	UNP Q8WSF8
C	0	LEU	-	expression tag	UNP Q8WSF8
C	32	TYR	THR	engineered mutation	UNP Q8WSF8
C	34	SER	GLY	engineered mutation	UNP Q8WSF8
C	36	SER	THR	engineered mutation	UNP Q8WSF8
C	38	LEU	GLN	engineered mutation	UNP Q8WSF8
C	55	TRP	TYR	engineered mutation	UNP Q8WSF8
C	59	SER	ARG	engineered mutation	UNP Q8WSF8
C	106	ASN	ILE	engineered mutation	UNP Q8WSF8
C	108	LEU	VAL	engineered mutation	UNP Q8WSF8
C	110	ASN	THR	engineered mutation	UNP Q8WSF8
C	111	SER	HIS	engineered mutation	UNP Q8WSF8
C	112	SER	ASP	engineered mutation	UNP Q8WSF8
C	114	HIS	SER	engineered mutation	UNP Q8WSF8
C	116	GLN	MET	engineered mutation	UNP Q8WSF8
C	117	TYR	PHE	engineered mutation	UNP Q8WSF8
C	118	LEU	ILE	engineered mutation	UNP Q8WSF8
C	148	SER	VAL	engineered mutation	UNP Q8WSF8
C	150	GLY	SER	engineered mutation	UNP Q8WSF8
C	152	TRP	PHE	engineered mutation	UNP Q8WSF8
C	220	SER	-	expression tag	UNP Q8WSF8
C	221	ARG	-	expression tag	UNP Q8WSF8
D	-8	ASP	-	expression tag	UNP Q8WSF8
D	-7	TYR	-	expression tag	UNP Q8WSF8
D	-6	LYS	-	expression tag	UNP Q8WSF8
D	-5	ASP	-	expression tag	UNP Q8WSF8
D	-4	ASP	-	expression tag	UNP Q8WSF8
D	-3	ASP	-	expression tag	UNP Q8WSF8

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-2	ASP	-	expression tag	UNP Q8WSF8
D	-1	LYS	-	expression tag	UNP Q8WSF8
D	0	LEU	-	expression tag	UNP Q8WSF8
D	32	TYR	THR	engineered mutation	UNP Q8WSF8
D	34	SER	GLY	engineered mutation	UNP Q8WSF8
D	36	SER	THR	engineered mutation	UNP Q8WSF8
D	38	LEU	GLN	engineered mutation	UNP Q8WSF8
D	55	TRP	TYR	engineered mutation	UNP Q8WSF8
D	59	SER	ARG	engineered mutation	UNP Q8WSF8
D	106	ASN	ILE	engineered mutation	UNP Q8WSF8
D	108	LEU	VAL	engineered mutation	UNP Q8WSF8
D	110	ASN	THR	engineered mutation	UNP Q8WSF8
D	111	SER	HIS	engineered mutation	UNP Q8WSF8
D	112	SER	ASP	engineered mutation	UNP Q8WSF8
D	114	HIS	SER	engineered mutation	UNP Q8WSF8
D	116	GLN	MET	engineered mutation	UNP Q8WSF8
D	117	TYR	PHE	engineered mutation	UNP Q8WSF8
D	118	LEU	ILE	engineered mutation	UNP Q8WSF8
D	148	SER	VAL	engineered mutation	UNP Q8WSF8
D	150	GLY	SER	engineered mutation	UNP Q8WSF8
D	152	TRP	PHE	engineered mutation	UNP Q8WSF8
D	220	SER	-	expression tag	UNP Q8WSF8
D	221	ARG	-	expression tag	UNP Q8WSF8
E	-8	ASP	-	expression tag	UNP Q8WSF8
E	-7	TYR	-	expression tag	UNP Q8WSF8
E	-6	LYS	-	expression tag	UNP Q8WSF8
E	-5	ASP	-	expression tag	UNP Q8WSF8
E	-4	ASP	-	expression tag	UNP Q8WSF8
E	-3	ASP	-	expression tag	UNP Q8WSF8
E	-2	ASP	-	expression tag	UNP Q8WSF8
E	-1	LYS	-	expression tag	UNP Q8WSF8
E	0	LEU	-	expression tag	UNP Q8WSF8
E	32	TYR	THR	engineered mutation	UNP Q8WSF8
E	34	SER	GLY	engineered mutation	UNP Q8WSF8
E	36	SER	THR	engineered mutation	UNP Q8WSF8
E	38	LEU	GLN	engineered mutation	UNP Q8WSF8
E	55	TRP	TYR	engineered mutation	UNP Q8WSF8
E	59	SER	ARG	engineered mutation	UNP Q8WSF8
E	106	ASN	ILE	engineered mutation	UNP Q8WSF8
E	108	LEU	VAL	engineered mutation	UNP Q8WSF8
E	110	ASN	THR	engineered mutation	UNP Q8WSF8
E	111	SER	HIS	engineered mutation	UNP Q8WSF8

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Chain	Residue	Modelled	Actual	Comment	Reference
E	112	SER	ASP	engineered mutation	UNP Q8WSF8
E	114	HIS	SER	engineered mutation	UNP Q8WSF8
E	116	GLN	MET	engineered mutation	UNP Q8WSF8
E	117	TYR	PHE	engineered mutation	UNP Q8WSF8
E	118	LEU	ILE	engineered mutation	UNP Q8WSF8
E	148	SER	VAL	engineered mutation	UNP Q8WSF8
E	150	GLY	SER	engineered mutation	UNP Q8WSF8
E	152	TRP	PHE	engineered mutation	UNP Q8WSF8
E	220	SER	-	expression tag	UNP Q8WSF8
E	221	ARG	-	expression tag	UNP Q8WSF8
F	-8	ASP	-	expression tag	UNP Q8WSF8
F	-7	TYR	-	expression tag	UNP Q8WSF8
F	-6	LYS	-	expression tag	UNP Q8WSF8
F	-5	ASP	-	expression tag	UNP Q8WSF8
F	-4	ASP	-	expression tag	UNP Q8WSF8
F	-3	ASP	-	expression tag	UNP Q8WSF8
F	-2	ASP	-	expression tag	UNP Q8WSF8
F	-1	LYS	-	expression tag	UNP Q8WSF8
F	0	LEU	-	expression tag	UNP Q8WSF8
F	32	TYR	THR	engineered mutation	UNP Q8WSF8
F	34	SER	GLY	engineered mutation	UNP Q8WSF8
F	36	SER	THR	engineered mutation	UNP Q8WSF8
F	38	LEU	GLN	engineered mutation	UNP Q8WSF8
F	55	TRP	TYR	engineered mutation	UNP Q8WSF8
F	59	SER	ARG	engineered mutation	UNP Q8WSF8
F	106	ASN	ILE	engineered mutation	UNP Q8WSF8
F	108	LEU	VAL	engineered mutation	UNP Q8WSF8
F	110	ASN	THR	engineered mutation	UNP Q8WSF8
F	111	SER	HIS	engineered mutation	UNP Q8WSF8
F	112	SER	ASP	engineered mutation	UNP Q8WSF8
F	114	HIS	SER	engineered mutation	UNP Q8WSF8
F	116	GLN	MET	engineered mutation	UNP Q8WSF8
F	117	TYR	PHE	engineered mutation	UNP Q8WSF8
F	118	LEU	ILE	engineered mutation	UNP Q8WSF8
F	148	SER	VAL	engineered mutation	UNP Q8WSF8
F	150	GLY	SER	engineered mutation	UNP Q8WSF8
F	152	TRP	PHE	engineered mutation	UNP Q8WSF8
F	220	SER	-	expression tag	UNP Q8WSF8
F	221	ARG	-	expression tag	UNP Q8WSF8
G	-8	ASP	-	expression tag	UNP Q8WSF8
G	-7	TYR	-	expression tag	UNP Q8WSF8
G	-6	LYS	-	expression tag	UNP Q8WSF8

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-5	ASP	-	expression tag	UNP Q8WSF8
G	-4	ASP	-	expression tag	UNP Q8WSF8
G	-3	ASP	-	expression tag	UNP Q8WSF8
G	-2	ASP	-	expression tag	UNP Q8WSF8
G	-1	LYS	-	expression tag	UNP Q8WSF8
G	0	LEU	-	expression tag	UNP Q8WSF8
G	32	TYR	THR	engineered mutation	UNP Q8WSF8
G	34	SER	GLY	engineered mutation	UNP Q8WSF8
G	36	SER	THR	engineered mutation	UNP Q8WSF8
G	38	LEU	GLN	engineered mutation	UNP Q8WSF8
G	55	TRP	TYR	engineered mutation	UNP Q8WSF8
G	59	SER	ARG	engineered mutation	UNP Q8WSF8
G	106	ASN	ILE	engineered mutation	UNP Q8WSF8
G	108	LEU	VAL	engineered mutation	UNP Q8WSF8
G	110	ASN	THR	engineered mutation	UNP Q8WSF8
G	111	SER	HIS	engineered mutation	UNP Q8WSF8
G	112	SER	ASP	engineered mutation	UNP Q8WSF8
G	114	HIS	SER	engineered mutation	UNP Q8WSF8
G	116	GLN	MET	engineered mutation	UNP Q8WSF8
G	117	TYR	PHE	engineered mutation	UNP Q8WSF8
G	118	LEU	ILE	engineered mutation	UNP Q8WSF8
G	148	SER	VAL	engineered mutation	UNP Q8WSF8
G	150	GLY	SER	engineered mutation	UNP Q8WSF8
G	152	TRP	PHE	engineered mutation	UNP Q8WSF8
G	220	SER	-	expression tag	UNP Q8WSF8
G	221	ARG	-	expression tag	UNP Q8WSF8
H	-8	ASP	-	expression tag	UNP Q8WSF8
H	-7	TYR	-	expression tag	UNP Q8WSF8
H	-6	LYS	-	expression tag	UNP Q8WSF8
H	-5	ASP	-	expression tag	UNP Q8WSF8
H	-4	ASP	-	expression tag	UNP Q8WSF8
H	-3	ASP	-	expression tag	UNP Q8WSF8
H	-2	ASP	-	expression tag	UNP Q8WSF8
H	-1	LYS	-	expression tag	UNP Q8WSF8
H	0	LEU	-	expression tag	UNP Q8WSF8
H	32	TYR	THR	engineered mutation	UNP Q8WSF8
H	34	SER	GLY	engineered mutation	UNP Q8WSF8
H	36	SER	THR	engineered mutation	UNP Q8WSF8
H	38	LEU	GLN	engineered mutation	UNP Q8WSF8
H	55	TRP	TYR	engineered mutation	UNP Q8WSF8
H	59	SER	ARG	engineered mutation	UNP Q8WSF8
H	106	ASN	ILE	engineered mutation	UNP Q8WSF8

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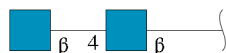
Chain	Residue	Modelled	Actual	Comment	Reference
H	108	LEU	VAL	engineered mutation	UNP Q8WSF8
H	110	ASN	THR	engineered mutation	UNP Q8WSF8
H	111	SER	HIS	engineered mutation	UNP Q8WSF8
H	112	SER	ASP	engineered mutation	UNP Q8WSF8
H	114	HIS	SER	engineered mutation	UNP Q8WSF8
H	116	GLN	MET	engineered mutation	UNP Q8WSF8
H	117	TYR	PHE	engineered mutation	UNP Q8WSF8
H	118	LEU	ILE	engineered mutation	UNP Q8WSF8
H	148	SER	VAL	engineered mutation	UNP Q8WSF8
H	150	GLY	SER	engineered mutation	UNP Q8WSF8
H	152	TRP	PHE	engineered mutation	UNP Q8WSF8
H	220	SER	-	expression tag	UNP Q8WSF8
H	221	ARG	-	expression tag	UNP Q8WSF8
I	-8	ASP	-	expression tag	UNP Q8WSF8
I	-7	TYR	-	expression tag	UNP Q8WSF8
I	-6	LYS	-	expression tag	UNP Q8WSF8
I	-5	ASP	-	expression tag	UNP Q8WSF8
I	-4	ASP	-	expression tag	UNP Q8WSF8
I	-3	ASP	-	expression tag	UNP Q8WSF8
I	-2	ASP	-	expression tag	UNP Q8WSF8
I	-1	LYS	-	expression tag	UNP Q8WSF8
I	0	LEU	-	expression tag	UNP Q8WSF8
I	32	TYR	THR	engineered mutation	UNP Q8WSF8
I	34	SER	GLY	engineered mutation	UNP Q8WSF8
I	36	SER	THR	engineered mutation	UNP Q8WSF8
I	38	LEU	GLN	engineered mutation	UNP Q8WSF8
I	55	TRP	TYR	engineered mutation	UNP Q8WSF8
I	59	SER	ARG	engineered mutation	UNP Q8WSF8
I	106	ASN	ILE	engineered mutation	UNP Q8WSF8
I	108	LEU	VAL	engineered mutation	UNP Q8WSF8
I	110	ASN	THR	engineered mutation	UNP Q8WSF8
I	111	SER	HIS	engineered mutation	UNP Q8WSF8
I	112	SER	ASP	engineered mutation	UNP Q8WSF8
I	114	HIS	SER	engineered mutation	UNP Q8WSF8
I	116	GLN	MET	engineered mutation	UNP Q8WSF8
I	117	TYR	PHE	engineered mutation	UNP Q8WSF8
I	118	LEU	ILE	engineered mutation	UNP Q8WSF8
I	148	SER	VAL	engineered mutation	UNP Q8WSF8
I	150	GLY	SER	engineered mutation	UNP Q8WSF8
I	152	TRP	PHE	engineered mutation	UNP Q8WSF8
I	220	SER	-	expression tag	UNP Q8WSF8
I	221	ARG	-	expression tag	UNP Q8WSF8

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Chain	Residue	Modelled	Actual	Comment	Reference
J	-8	ASP	-	expression tag	UNP Q8WSF8
J	-7	TYR	-	expression tag	UNP Q8WSF8
J	-6	LYS	-	expression tag	UNP Q8WSF8
J	-5	ASP	-	expression tag	UNP Q8WSF8
J	-4	ASP	-	expression tag	UNP Q8WSF8
J	-3	ASP	-	expression tag	UNP Q8WSF8
J	-2	ASP	-	expression tag	UNP Q8WSF8
J	-1	LYS	-	expression tag	UNP Q8WSF8
J	0	LEU	-	expression tag	UNP Q8WSF8
J	32	TYR	THR	engineered mutation	UNP Q8WSF8
J	34	SER	GLY	engineered mutation	UNP Q8WSF8
J	36	SER	THR	engineered mutation	UNP Q8WSF8
J	38	LEU	GLN	engineered mutation	UNP Q8WSF8
J	55	TRP	TYR	engineered mutation	UNP Q8WSF8
J	59	SER	ARG	engineered mutation	UNP Q8WSF8
J	106	ASN	ILE	engineered mutation	UNP Q8WSF8
J	108	LEU	VAL	engineered mutation	UNP Q8WSF8
J	110	ASN	THR	engineered mutation	UNP Q8WSF8
J	111	SER	HIS	engineered mutation	UNP Q8WSF8
J	112	SER	ASP	engineered mutation	UNP Q8WSF8
J	114	HIS	SER	engineered mutation	UNP Q8WSF8
J	116	GLN	MET	engineered mutation	UNP Q8WSF8
J	117	TYR	PHE	engineered mutation	UNP Q8WSF8
J	118	LEU	ILE	engineered mutation	UNP Q8WSF8
J	148	SER	VAL	engineered mutation	UNP Q8WSF8
J	150	GLY	SER	engineered mutation	UNP Q8WSF8
J	152	TRP	PHE	engineered mutation	UNP Q8WSF8
J	220	SER	-	expression tag	UNP Q8WSF8
J	221	ARG	-	expression tag	UNP Q8WSF8

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



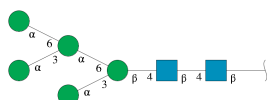
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	K	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	M	2	Total	C	N	O	0	0	0
			28	16	2	10			

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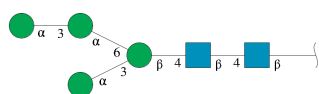
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	O	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



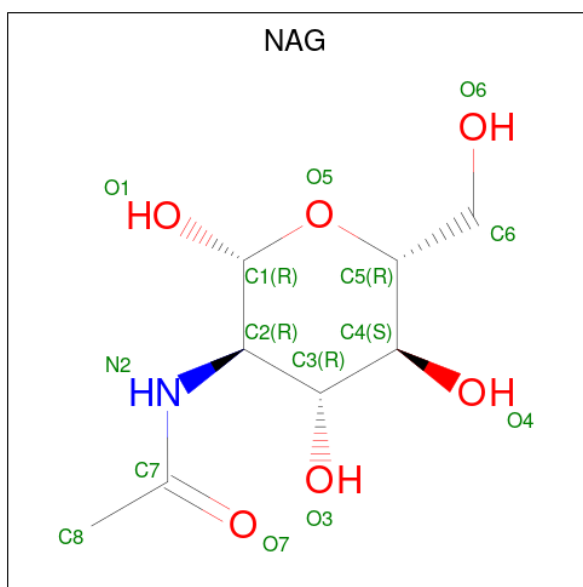
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	L	7	Total	C	N	O	0	0	0
			83	46	2	35			
3	P	7	Total	C	N	O	0	0	0
			83	46	2	35			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



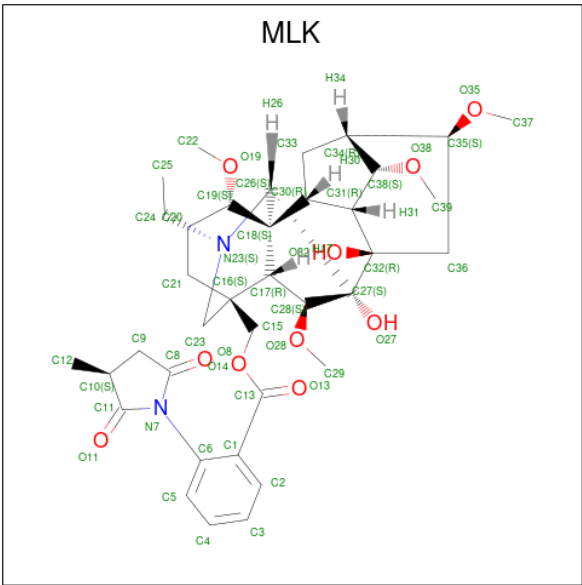
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	N	6	Total	C	N	O	0	0	0
			72	40	2	30			
4	Q	6	Total	C	N	O	0	0	0
			72	40	2	30			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



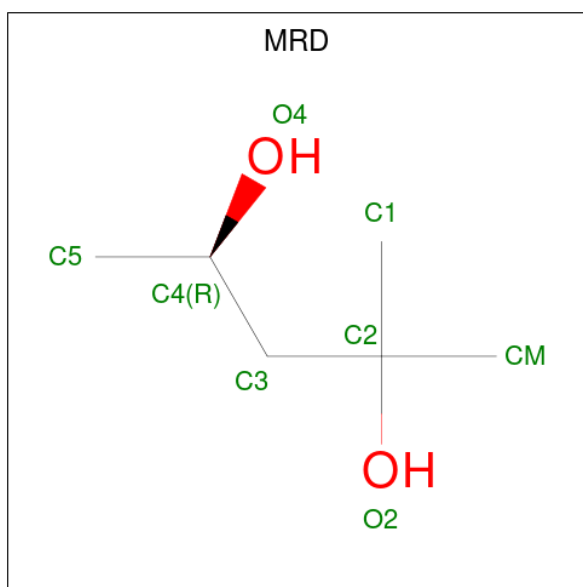
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	C	1	Total	C	N	O	0	0
			14	8	1	5		
5	E	1	Total	C	N	O	0	0
			14	8	1	5		
5	F	1	Total	C	N	O	0	0
			14	8	1	5		
5	H	1	Total	C	N	O	0	0
			14	8	1	5		
5	I	1	Total	C	N	O	0	0
			14	8	1	5		
5	J	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 6 is METHYLLYCACONITINE (CCD ID: MLK) (formula: $C_{37}H_{50}N_2O_{10}$).



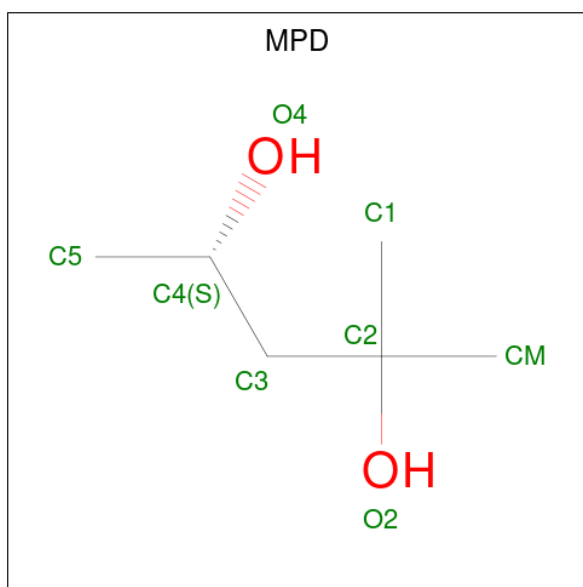
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			49	37	2	10		
6	B	1	Total	C	N	O	0	0
			49	37	2	10		
6	C	1	Total	C	N	O	0	0
			49	37	2	10		
6	D	1	Total	C	N	O	0	0
			49	37	2	10		
6	E	1	Total	C	N	O	0	0
			49	37	2	10		
6	F	1	Total	C	N	O	0	0
			49	37	2	10		
6	G	1	Total	C	N	O	0	0
			49	37	2	10		
6	H	1	Total	C	N	O	0	0
			49	37	2	10		
6	I	1	Total	C	N	O	0	0
			49	37	2	10		
6	J	1	Total	C	N	O	0	0
			49	37	2	10		

- Molecule 7 is (4R)-2-METHYLPENTANE-2,4-DIOL (CCD ID: MRD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			8	6	2		
7	C	1	Total	C	O	0	0
			8	6	2		
7	D	1	Total	C	O	0	0
			8	6	2		
7	D	1	Total	C	O	0	0
			8	6	2		
7	G	1	Total	C	O	0	0
			8	6	2		
7	H	1	Total	C	O	0	0
			8	6	2		
7	I	1	Total	C	O	0	0
			8	6	2		

- Molecule 8 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	C	O	0	0
			8	6	2		
8	I	1	Total	C	O	0	0
			8	6	2		

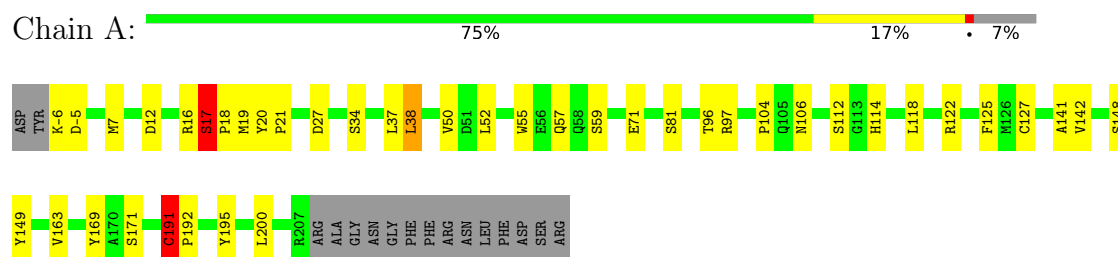
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	98	Total	O	0	0
			98	98		
9	B	100	Total	O	0	0
			100	100		
9	C	87	Total	O	0	0
			87	87		
9	D	62	Total	O	0	0
			62	62		
9	E	67	Total	O	0	0
			67	67		
9	F	92	Total	O	0	0
			92	92		
9	G	100	Total	O	0	0
			100	100		
9	H	84	Total	O	0	0
			84	84		
9	I	59	Total	O	0	0
			59	59		
9	J	83	Total	O	0	0
			83	83		

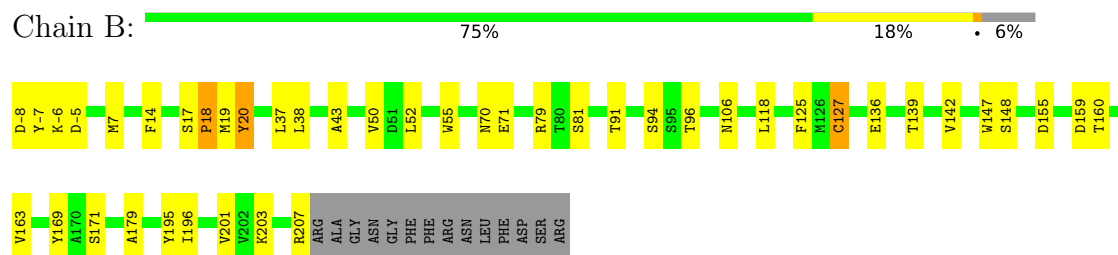
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and 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.

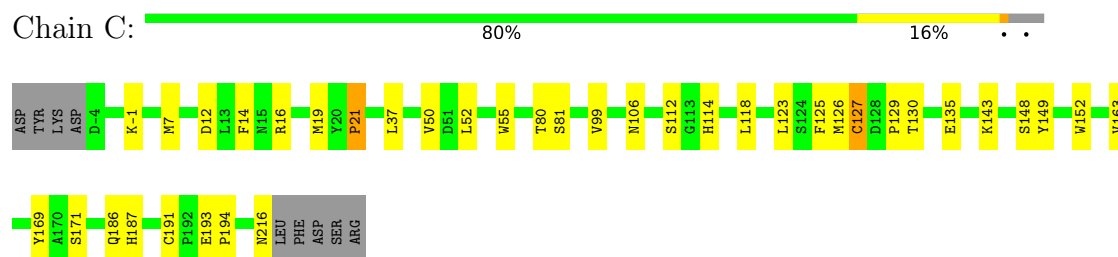
• Molecule 1: Soluble acetylcholine receptor



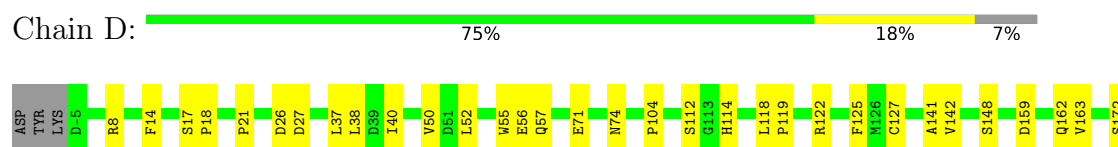
• Molecule 1: Soluble acetylcholine receptor



• Molecule 1: Soluble acetylcholine receptor



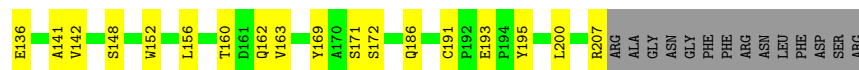
• Molecule 1: Soluble acetylcholine receptor





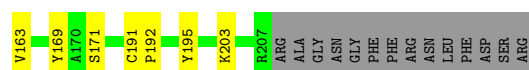
- Molecule 1: Soluble acetylcholine receptor

Chain E: 71% 22% 6%



- Molecule 1: Soluble acetylcholine receptor

Chain F: 77% 15% 7%



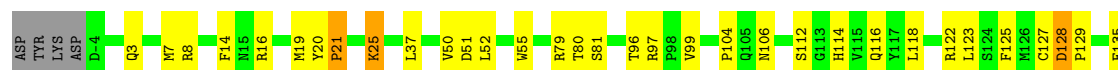
- Molecule 1: Soluble acetylcholine receptor

Chain G: 75% 19% 6%



- Molecule 1: Soluble acetylcholine receptor

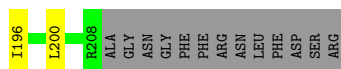
Chain H: 76% 19% 5%



- Molecule 1: Soluble acetylcholine receptor

Chain I: 79% 13% 7%





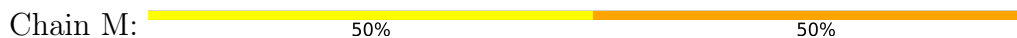
- Molecule 1: Soluble acetylcholine receptor



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



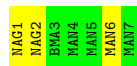
- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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

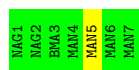


- Molecule 3: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



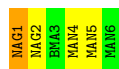
- Molecule 3: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:  86% 14%



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

Chain N:  33% 50% 17%



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

Chain Q:  50% 33% 17%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	143.22Å 142.37Å 144.48Å 90.00° 90.02° 90.00°	Depositor
Resolution (Å)	48.16 – 2.32 48.16 – 2.32	Depositor EDS
% Data completeness (in resolution range)	95.9 (48.16-2.32) 99.5 (48.16-2.32)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.63 (at 2.29Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, R_{free}	0.182 , 0.230 0.178 , 0.224	Depositor DCC
R_{free} test set	6374 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	36.7	Xtriage
Anisotropy	0.355	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 25.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.017 for k,h,-l 0.017 for -k,-h,-l 0.467 for -h,-k,l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	19701	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.95% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MLK, MAN, MPD, BMA, MRD, NAG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.59	0/1817	0.93	9/2476 (0.4%)
1	B	0.69	0/1852	0.90	4/2524 (0.2%)
1	C	0.62	2/1888 (0.1%)	0.88	2/2573 (0.1%)
1	D	0.51	0/1835	0.85	4/2501 (0.2%)
1	E	0.53	0/1864	0.91	8/2540 (0.3%)
1	F	0.55	2/1833 (0.1%)	0.90	6/2497 (0.2%)
1	G	0.64	3/1871 (0.2%)	0.93	6/2550 (0.2%)
1	H	0.53	0/1877	0.95	9/2556 (0.4%)
1	I	0.50	0/1818	0.94	8/2479 (0.3%)
1	J	0.49	0/1874	0.88	8/2552 (0.3%)
All	All	0.57	7/18529 (0.0%)	0.91	64/25248 (0.3%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	203	LYS	C-O	-5.83	1.17	1.24
1	G	97[A]	ARG	C-O	-5.69	1.18	1.24
1	G	97[B]	ARG	C-O	-5.69	1.18	1.24
1	C	21	PRO	C-O	-5.50	1.17	1.23
1	F	97[A]	ARG	C-O	-5.23	1.18	1.24

The worst 5 of 64 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	17	SER	N-CA-C	10.97	118.09	108.22
1	I	128	ASP	CA-C-N	-10.54	111.00	121.65
1	I	128	ASP	C-N-CA	-10.54	111.00	121.65
1	H	20	TYR	CA-C-N	-10.20	111.35	121.65
1	H	20	TYR	C-N-CA	-10.20	111.35	121.65

There are no chirality outliers.

There are no planarity outliers.

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	1752	0	1678	39	0
1	B	1781	0	1697	40	0
1	C	1815	0	1737	35	0
1	D	1764	0	1688	29	0
1	E	1789	0	1706	55	0
1	F	1762	0	1694	32	0
1	G	1793	0	1708	44	0
1	H	1810	0	1735	37	0
1	I	1753	0	1667	24	0
1	J	1796	0	1722	57	0
2	K	28	0	25	0	0
2	M	28	0	25	1	0
2	O	28	0	25	2	0
3	L	83	0	70	0	0
3	P	83	0	70	0	0
4	N	72	0	61	2	0
4	Q	72	0	61	2	0
5	A	14	0	13	7	0
5	C	14	0	13	0	0
5	E	14	0	13	0	0
5	F	14	0	13	0	0
5	H	14	0	13	0	0
5	I	14	0	13	0	0
5	J	14	0	13	0	0
6	A	49	0	50	7	0
6	B	49	0	50	4	0
6	C	49	0	50	7	0
6	D	49	0	50	8	0
6	E	49	0	50	12	0
6	F	49	0	50	8	0
6	G	49	0	50	5	0
6	H	49	0	50	9	0
6	I	49	0	50	7	0
6	J	49	0	50	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	8	0	14	1	0
7	C	8	0	14	1	0
7	D	16	0	28	10	0
7	G	8	0	14	5	0
7	H	8	0	14	1	0
7	I	8	0	14	0	0
8	C	8	0	14	0	0
8	I	8	0	14	5	0
9	A	98	0	0	3	0
9	B	100	0	0	1	0
9	C	87	0	0	3	0
9	D	62	0	0	5	0
9	E	67	0	0	4	0
9	F	92	0	0	2	0
9	G	100	0	0	1	0
9	H	84	0	0	8	0
9	I	59	0	0	1	0
9	J	83	0	0	8	0
All	All	19701	0	18086	397	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 11.

The worst 5 of 397 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:37[B]:LEU:HD11	1:B:52:LEU:HD11	1.18	1.11
1:J:160:THR:HG22	1:J:162:GLN:H	1.09	1.09
1:G:86:TRP:HE1	7:G:250:MRD:HMC1	1.18	1.08
5:A:225:NAG:H3	5:A:225:NAG:H83	1.43	1.00
1:G:52:LEU:HD22	1:G:54:TYR:HD2	1.26	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	218/230 (95%)	217 (100%)	1 (0%)	0	100	100
1	B	222/230 (96%)	220 (99%)	2 (1%)	0	100	100
1	C	228/230 (99%)	226 (99%)	2 (1%)	0	100	100
1	D	221/230 (96%)	218 (99%)	3 (1%)	0	100	100
1	E	223/230 (97%)	220 (99%)	3 (1%)	0	100	100
1	F	220/230 (96%)	216 (98%)	4 (2%)	0	100	100
1	G	224/230 (97%)	223 (100%)	1 (0%)	0	100	100
1	H	226/230 (98%)	224 (99%)	2 (1%)	0	100	100
1	I	219/230 (95%)	216 (99%)	3 (1%)	0	100	100
1	J	224/230 (97%)	220 (98%)	4 (2%)	0	100	100
All	All	2225/2300 (97%)	2200 (99%)	25 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	202/208 (97%)	198 (98%)	4 (2%)	48	66
1	B	206/208 (99%)	200 (97%)	6 (3%)	37	53
1	C	208/208 (100%)	203 (98%)	5 (2%)	43	60
1	D	204/208 (98%)	198 (97%)	6 (3%)	37	53
1	E	207/208 (100%)	205 (99%)	2 (1%)	68	81
1	F	204/208 (98%)	198 (97%)	6 (3%)	37	53
1	G	208/208 (100%)	203 (98%)	5 (2%)	43	60
1	H	206/208 (99%)	200 (97%)	6 (3%)	37	53
1	I	202/208 (97%)	196 (97%)	6 (3%)	36	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	J	208/208 (100%)	203 (98%)	5 (2%)	43 60
All	All	2055/2080 (99%)	2004 (98%)	51 (2%)	44 59

5 of 51 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	160	THR
1	H	25[B]	LYS
1	J	159[B]	ASP
1	G	17	SER
1	G	135[B]	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	187	HIS
1	H	162	GLN
1	H	57	GLN
1	H	114	HIS
1	I	3	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

32 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	K	1	2,1	14,14,15	0.65	0	17,19,21	1.46	2 (11%)
2	NAG	K	2	2	14,14,15	0.60	0	17,19,21	1.17	2 (11%)
3	NAG	L	1	3,1	14,14,15	0.55	0	17,19,21	0.82	1 (5%)
3	NAG	L	2	3	14,14,15	0.44	0	17,19,21	1.79	5 (29%)
3	BMA	L	3	3	11,11,12	0.36	0	15,15,17	0.90	0
3	MAN	L	4	3	11,11,12	0.72	0	15,15,17	0.73	0
3	MAN	L	5	3	11,11,12	0.52	0	15,15,17	0.74	0
3	MAN	L	6	3	11,11,12	0.47	0	15,15,17	0.81	1 (6%)
3	MAN	L	7	3	11,11,12	0.65	0	15,15,17	0.77	0
2	NAG	M	1	2,1	14,14,15	0.38	0	17,19,21	1.70	2 (11%)
2	NAG	M	2	2	14,14,15	0.58	0	17,19,21	1.67	4 (23%)
4	NAG	N	1	4,1	14,14,15	0.45	0	17,19,21	1.27	1 (5%)
4	NAG	N	2	4	14,14,15	0.51	0	17,19,21	0.73	0
4	BMA	N	3	4	11,11,12	0.26	0	15,15,17	0.60	0
4	MAN	N	4	4	11,11,12	0.79	0	15,15,17	1.46	2 (13%)
4	MAN	N	5	4	11,11,12	0.46	0	15,15,17	1.37	1 (6%)
4	MAN	N	6	4	11,11,12	0.57	0	15,15,17	0.57	0
2	NAG	O	1	2,1	14,14,15	0.59	0	17,19,21	1.25	2 (11%)
2	NAG	O	2	2	14,14,15	0.51	0	17,19,21	1.18	1 (5%)
3	NAG	P	1	3,1	14,14,15	0.61	0	17,19,21	0.69	0
3	NAG	P	2	3	14,14,15	0.57	0	17,19,21	0.91	0
3	BMA	P	3	3	11,11,12	0.42	0	15,15,17	0.66	0
3	MAN	P	4	3	11,11,12	0.73	0	15,15,17	0.84	0
3	MAN	P	5	3	11,11,12	0.67	0	15,15,17	1.12	1 (6%)
3	MAN	P	6	3	11,11,12	0.61	0	15,15,17	0.64	0
3	MAN	P	7	3	11,11,12	0.56	0	15,15,17	0.79	0
4	NAG	Q	1	4,1	14,14,15	0.45	0	17,19,21	1.43	1 (5%)
4	NAG	Q	2	4	14,14,15	0.55	0	17,19,21	0.66	0
4	BMA	Q	3	4	11,11,12	0.40	0	15,15,17	0.75	0
4	MAN	Q	4	4	11,11,12	0.48	0	15,15,17	1.64	2 (13%)
4	MAN	Q	5	4	11,11,12	0.64	0	15,15,17	0.90	1 (6%)
4	MAN	Q	6	4	11,11,12	0.64	0	15,15,17	1.05	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	K	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	K	2	2	-	0/6/23/26	0/1/1/1
3	NAG	L	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	L	2	3	-	2/6/23/26	0/1/1/1
3	BMA	L	3	3	-	0/2/19/22	0/1/1/1
3	MAN	L	4	3	-	0/2/19/22	0/1/1/1
3	MAN	L	5	3	-	2/2/19/22	0/1/1/1
3	MAN	L	6	3	-	0/2/19/22	0/1/1/1
3	MAN	L	7	3	-	0/2/19/22	0/1/1/1
2	NAG	M	1	2,1	-	3/6/23/26	0/1/1/1
2	NAG	M	2	2	-	2/6/23/26	0/1/1/1
4	NAG	N	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	N	2	4	-	3/6/23/26	0/1/1/1
4	BMA	N	3	4	-	0/2/19/22	0/1/1/1
4	MAN	N	4	4	-	2/2/19/22	0/1/1/1
4	MAN	N	5	4	-	0/2/19/22	0/1/1/1
4	MAN	N	6	4	-	0/2/19/22	0/1/1/1
2	NAG	O	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	O	2	2	-	2/6/23/26	0/1/1/1
3	NAG	P	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	P	2	3	-	4/6/23/26	0/1/1/1
3	BMA	P	3	3	-	2/2/19/22	0/1/1/1
3	MAN	P	4	3	-	2/2/19/22	0/1/1/1
3	MAN	P	5	3	-	1/2/19/22	0/1/1/1
3	MAN	P	6	3	-	0/2/19/22	0/1/1/1
3	MAN	P	7	3	-	0/2/19/22	0/1/1/1
4	NAG	Q	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	Q	2	4	-	2/6/23/26	0/1/1/1
4	BMA	Q	3	4	-	0/2/19/22	0/1/1/1
4	MAN	Q	4	4	-	0/2/19/22	1/1/1/1
4	MAN	Q	5	4	-	0/2/19/22	0/1/1/1
4	MAN	Q	6	4	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	Q	4	MAN	C1-O5-C5	5.13	119.06	112.19
2	M	1	NAG	C1-O5-C5	4.64	118.41	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	Q	1	NAG	C1-O5-C5	4.49	118.20	112.19
4	N	5	MAN	C1-O5-C5	4.36	118.02	112.19
2	K	1	NAG	C4-C3-C2	4.09	117.02	111.02

There are no chirality outliers.

5 of 35 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	M	1	NAG	C8-C7-N2-C2
2	M	1	NAG	O7-C7-N2-C2
2	O	2	NAG	C3-C2-N2-C7
4	N	4	MAN	O5-C5-C6-O6
3	P	2	NAG	C4-C5-C6-O6

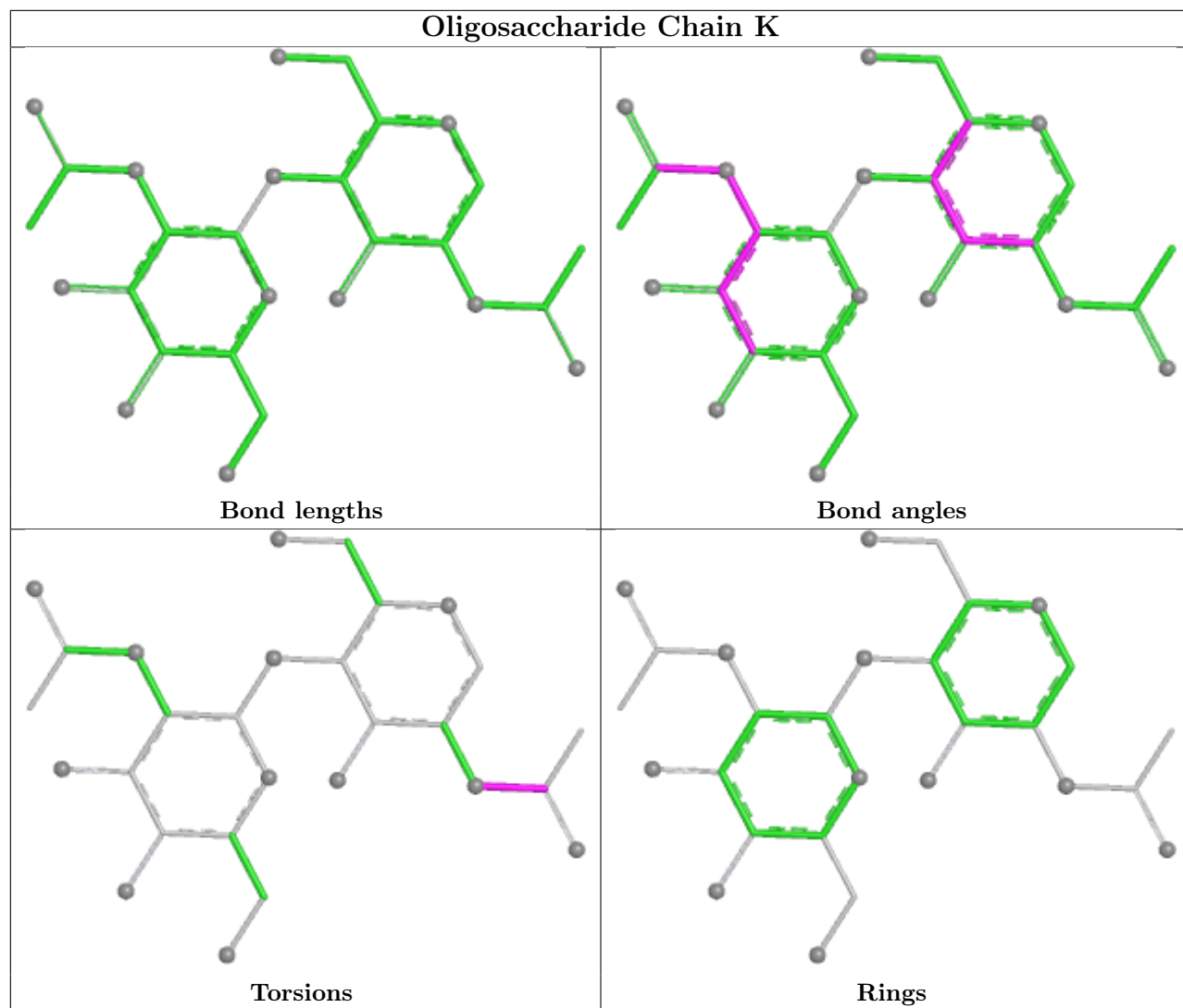
All (1) ring outliers are listed below:

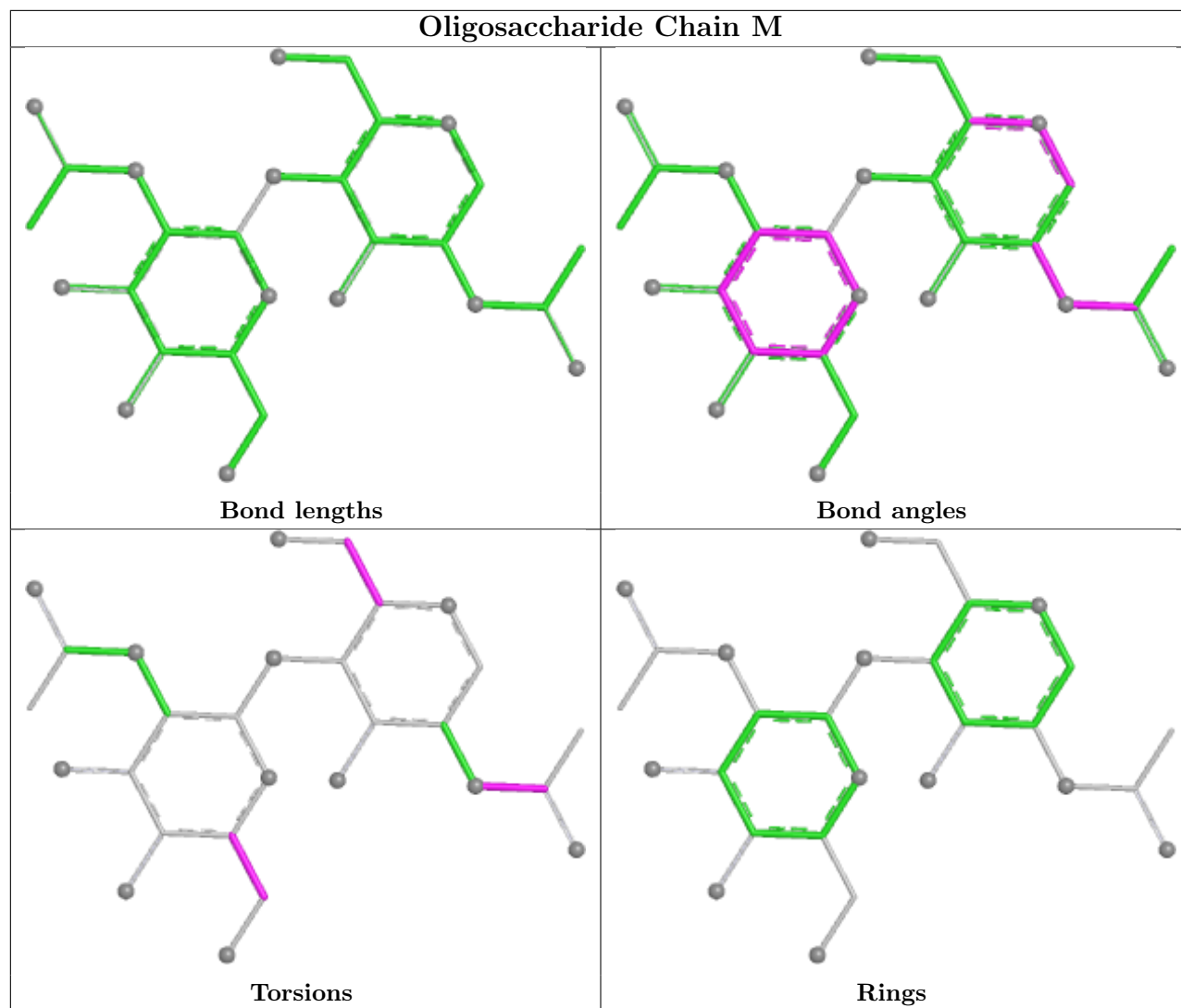
Mol	Chain	Res	Type	Atoms
4	Q	4	MAN	C1-C2-C3-C4-C5-O5

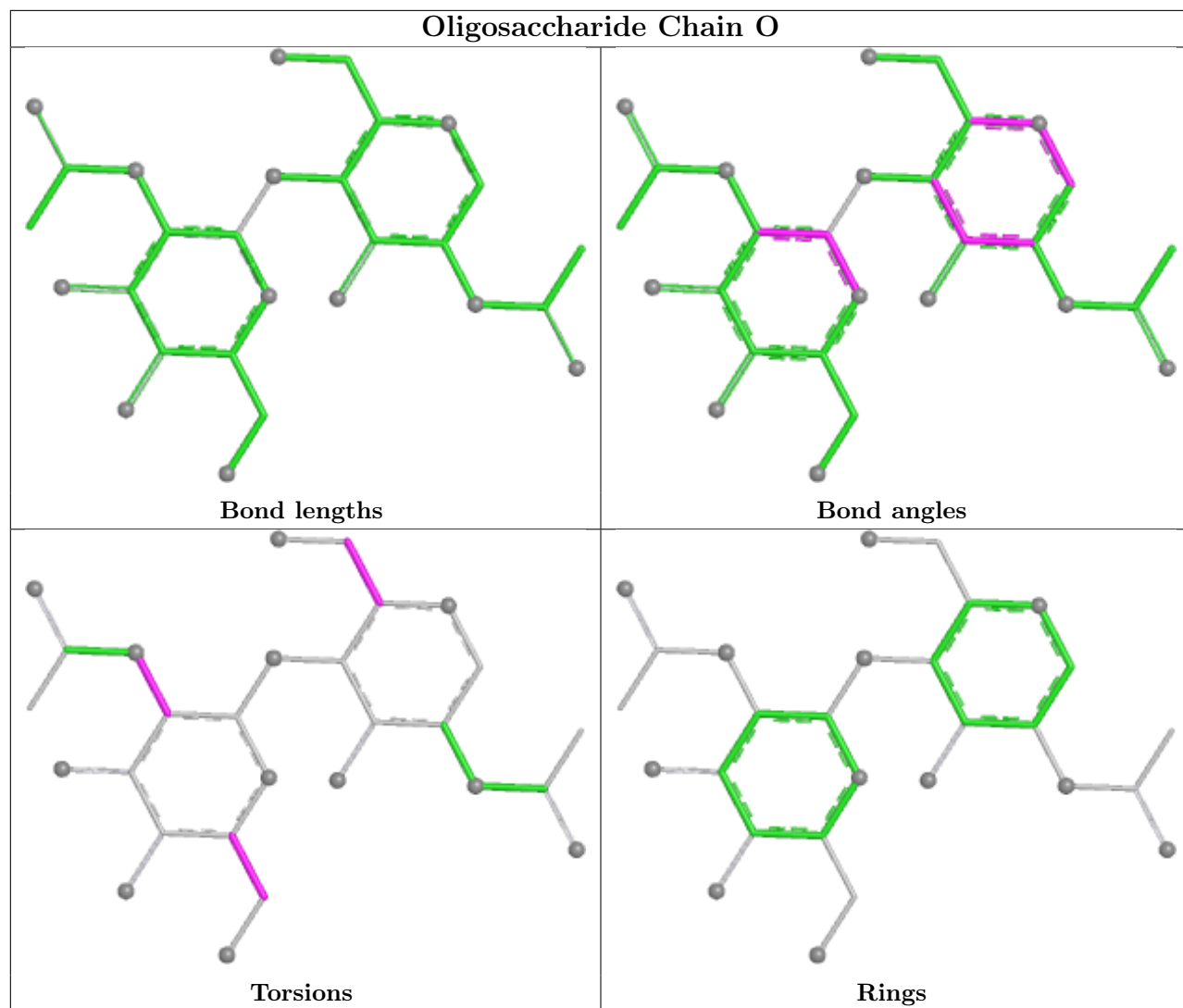
6 monomers are involved in 7 short contacts:

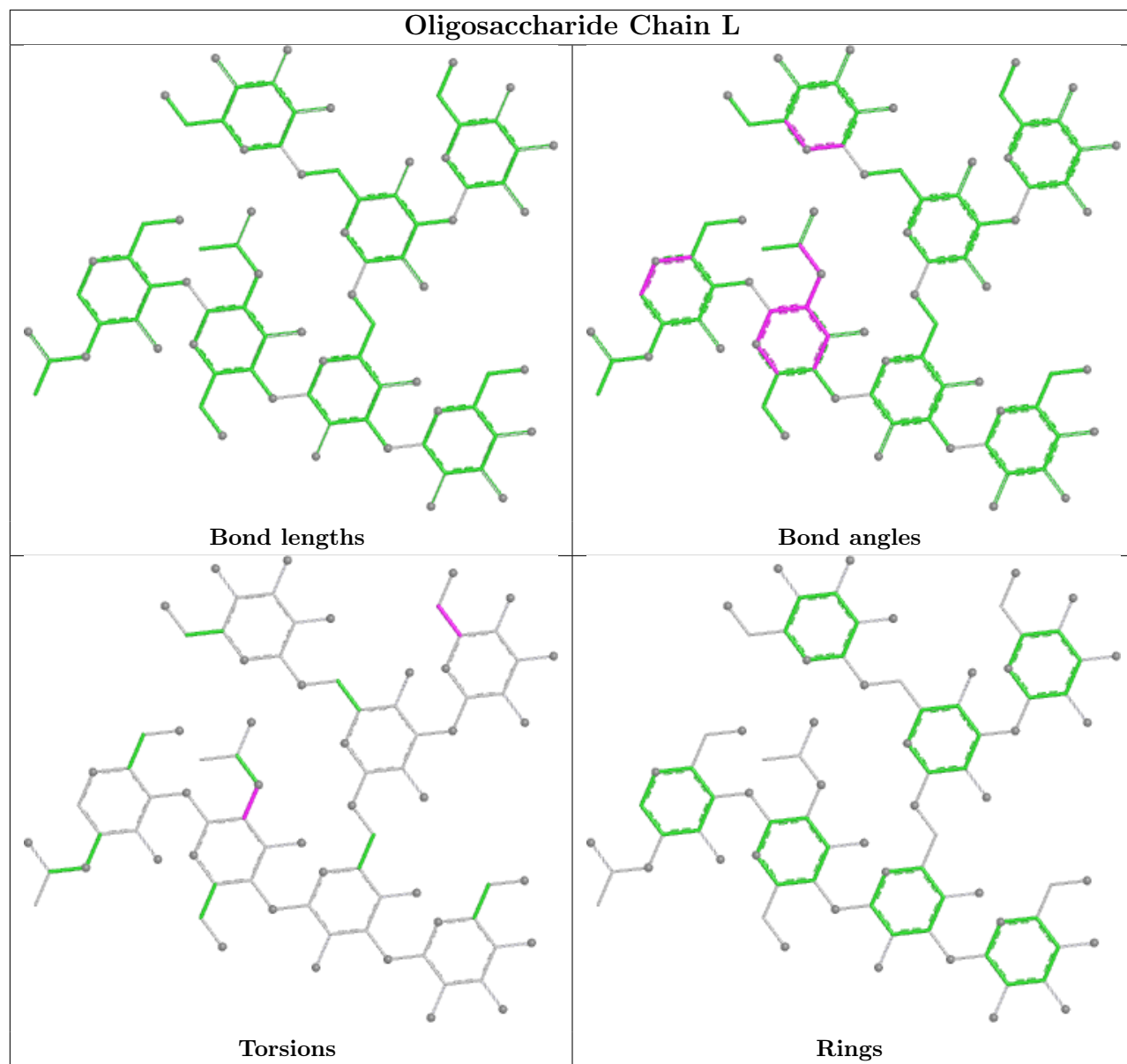
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	O	1	NAG	1	0
4	Q	1	NAG	2	0
2	M	1	NAG	1	0
4	N	2	NAG	1	0
2	O	2	NAG	1	0
4	N	1	NAG	1	0

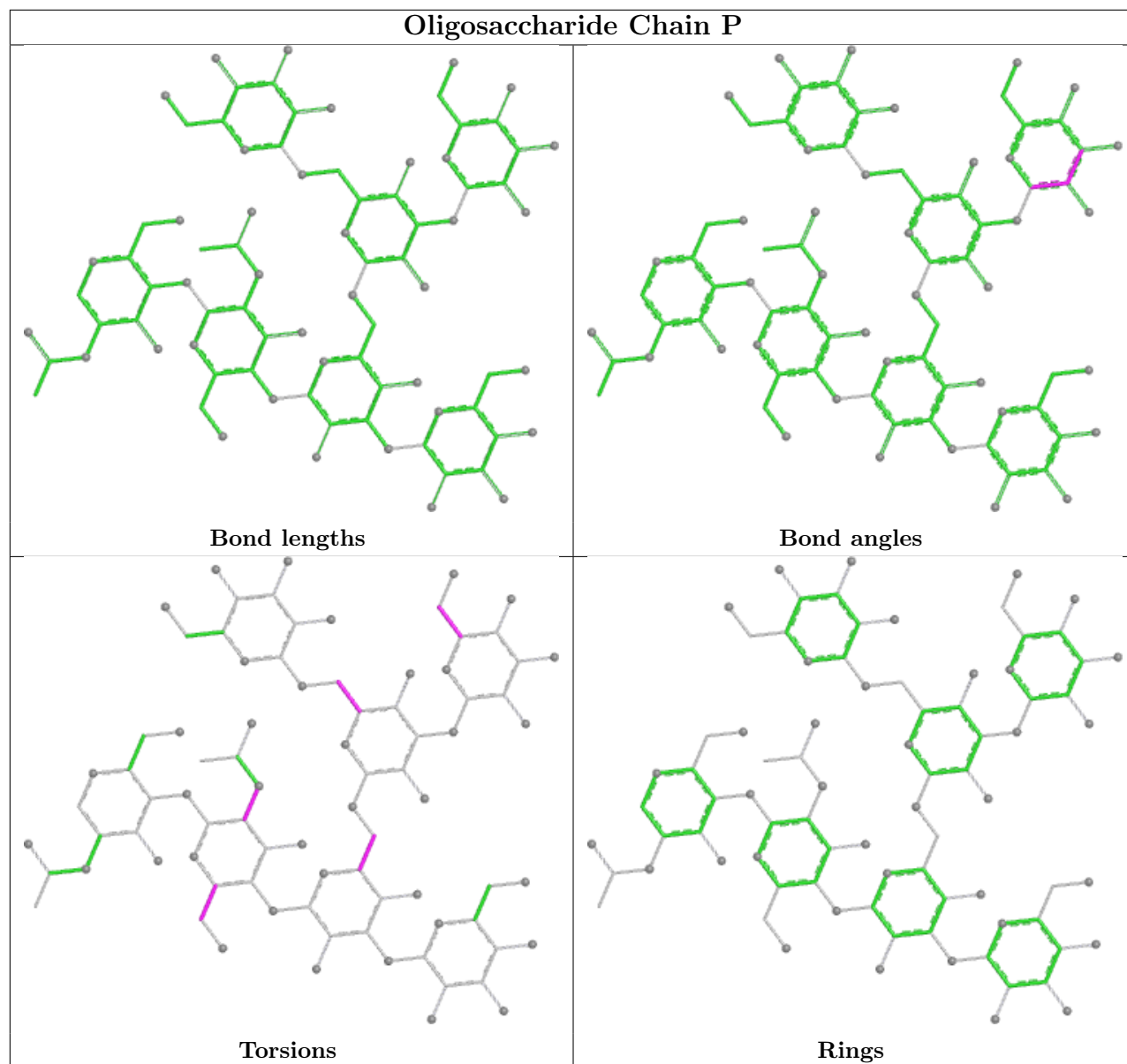
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

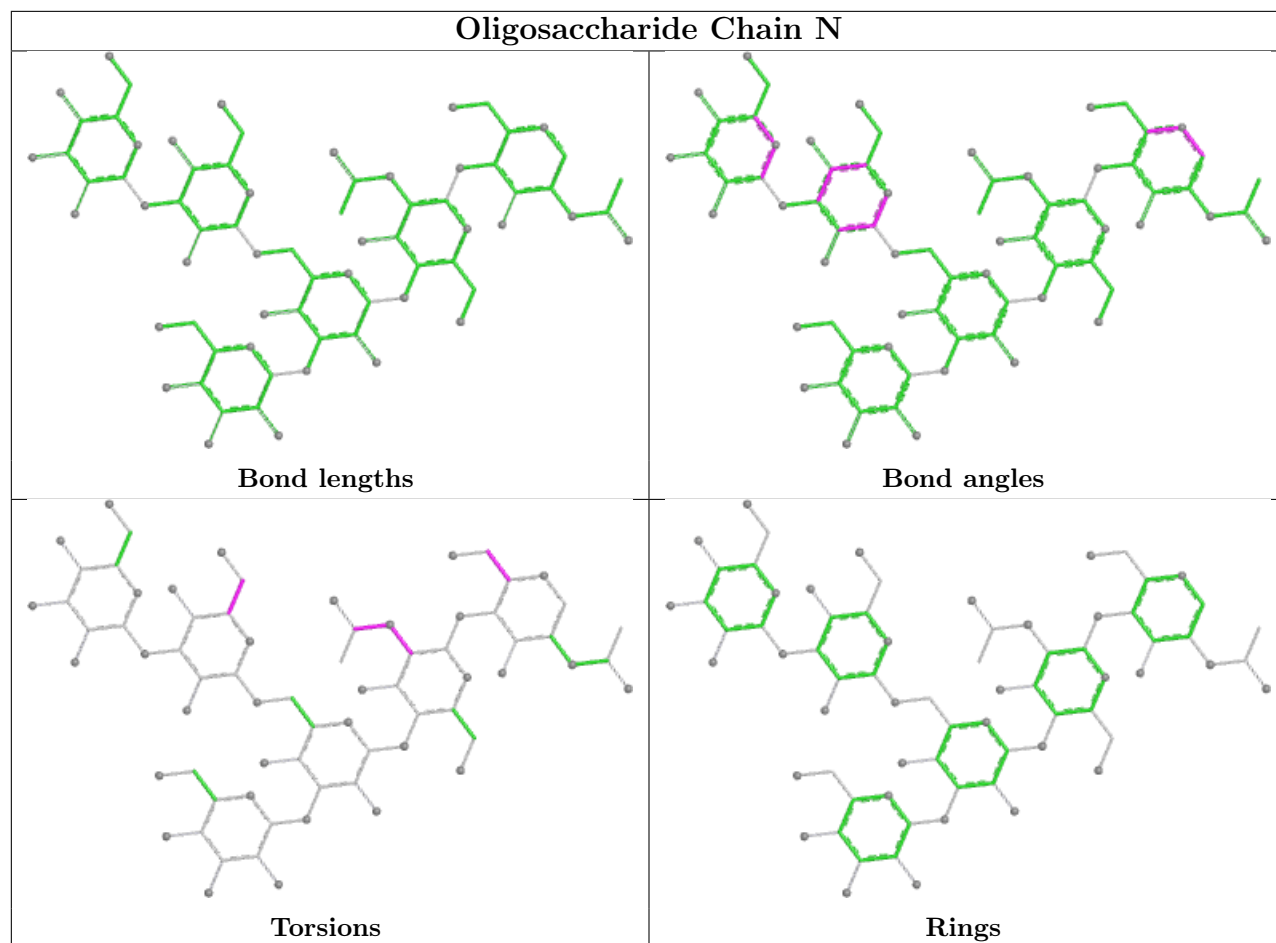


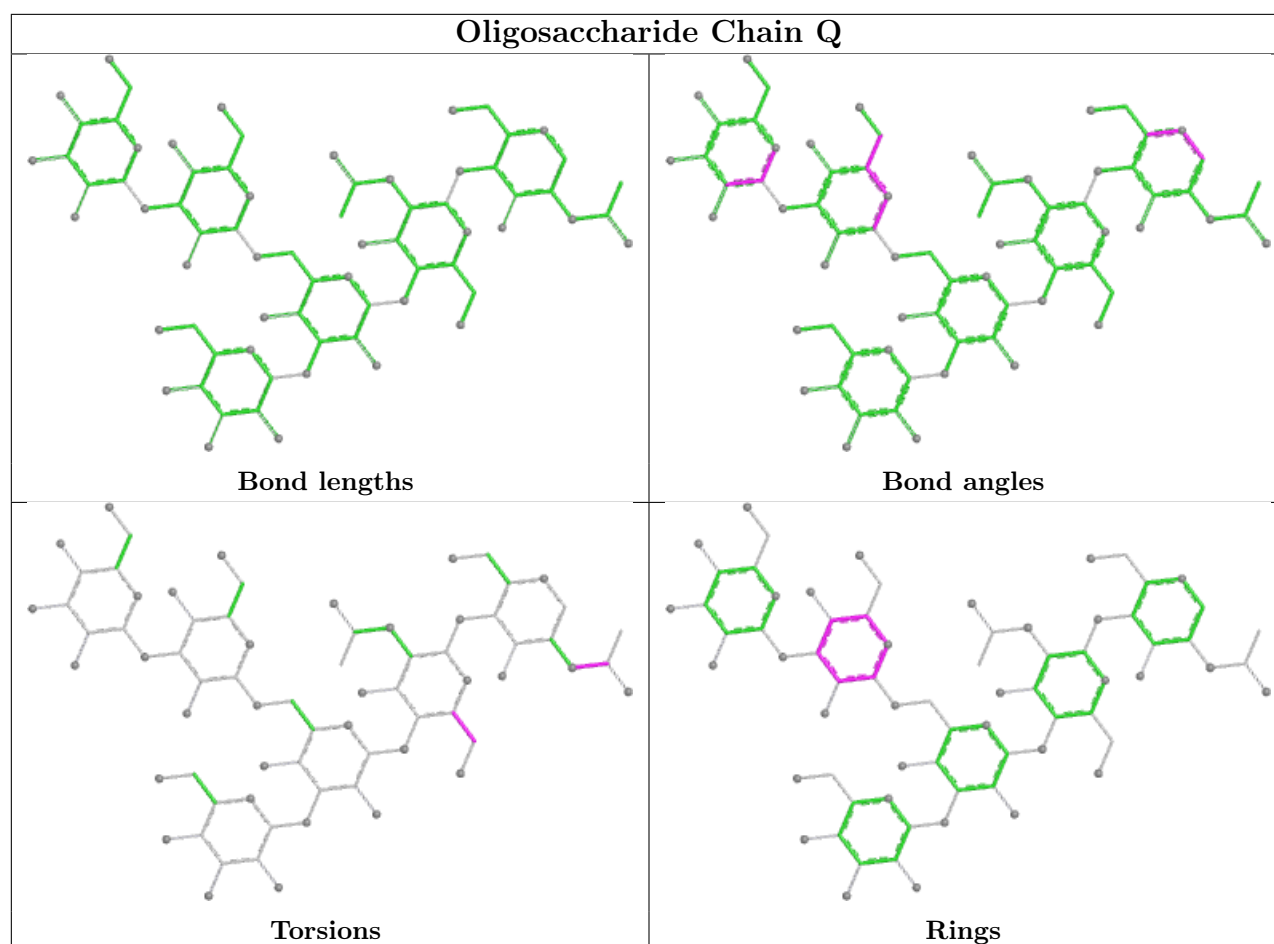












5.6 Ligand geometry [i](#)

26 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	MLK	G	260	-	56,56,56	1.08	3 (5%)	82,92,92	1.65	15 (18%)
7	MRD	B	250	-	7,7,7	0.37	0	9,10,10	0.52	0
6	MLK	E	260	-	56,56,56	1.05	3 (5%)	82,92,92	1.65	18 (21%)
6	MLK	J	260	-	56,56,56	1.06	3 (5%)	82,92,92	1.63	16 (19%)
6	MLK	A	260	-	56,56,56	1.09	4 (7%)	82,92,92	1.59	14 (17%)
5	NAG	H	225	1	14,14,15	0.53	0	17,19,21	0.75	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	MRD	I	222	-	7,7,7	0.43	0	9,10,10	0.65	0
8	MPD	I	250	-	7,7,7	0.28	0	9,10,10	0.41	0
6	MLK	H	260	-	56,56,56	1.07	4 (7%)	82,92,92	1.60	14 (17%)
5	NAG	I	225	1	14,14,15	0.40	0	17,19,21	1.35	1 (5%)
6	MLK	B	260	-	56,56,56	1.04	5 (8%)	82,92,92	1.69	13 (15%)
7	MRD	H	250	-	7,7,7	0.33	0	9,10,10	0.24	0
6	MLK	D	260	-	56,56,56	1.03	4 (7%)	82,92,92	1.55	14 (17%)
7	MRD	C	250	-	7,7,7	0.32	0	9,10,10	0.20	0
5	NAG	E	240	1	14,14,15	0.49	0	17,19,21	1.01	1 (5%)
5	NAG	J	240	1	14,14,15	0.50	0	17,19,21	0.86	1 (5%)
5	NAG	F	225	1	14,14,15	0.43	0	17,19,21	1.10	1 (5%)
7	MRD	D	250	-	7,7,7	0.39	0	9,10,10	0.43	0
5	NAG	A	225	1	14,14,15	0.57	0	17,19,21	1.84	4 (23%)
6	MLK	F	260	-	56,56,56	1.07	4 (7%)	82,92,92	1.57	16 (19%)
7	MRD	G	250	-	7,7,7	0.40	0	9,10,10	0.35	0
6	MLK	C	260	-	56,56,56	1.10	3 (5%)	82,92,92	1.62	11 (13%)
8	MPD	C	222	-	7,7,7	0.36	0	9,10,10	0.40	0
5	NAG	C	225	1	14,14,15	0.47	0	17,19,21	1.04	1 (5%)
7	MRD	D	251	-	7,7,7	0.31	0	9,10,10	0.51	0
6	MLK	I	260	-	56,56,56	1.01	3 (5%)	82,92,92	1.68	14 (17%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	MLK	G	260	-	-	1/24/141/141	0/2/8/8
7	MRD	B	250	-	-	3/5/5/5	-
6	MLK	E	260	-	-	0/24/141/141	0/2/8/8
6	MLK	J	260	-	-	2/24/141/141	0/2/8/8
6	MLK	A	260	-	-	2/24/141/141	0/2/8/8
5	NAG	H	225	1	-	0/6/23/26	0/1/1/1
7	MRD	I	222	-	-	1/5/5/5	-
8	MPD	I	250	-	-	2/5/5/5	-
6	MLK	H	260	-	-	0/24/141/141	0/2/8/8
5	NAG	I	225	1	-	1/6/23/26	0/1/1/1
6	MLK	B	260	-	-	1/24/141/141	0/2/8/8
7	MRD	H	250	-	-	1/5/5/5	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	MLK	D	260	-	-	1/24/141/141	0/2/8/8
7	MRD	C	250	-	-	1/5/5/5	-
5	NAG	E	240	1	-	0/6/23/26	0/1/1/1
5	NAG	J	240	1	-	2/6/23/26	0/1/1/1
5	NAG	F	225	1	-	4/6/23/26	0/1/1/1
7	MRD	D	250	-	-	3/5/5/5	-
5	NAG	A	225	1	-	3/6/23/26	0/1/1/1
6	MLK	F	260	-	-	3/24/141/141	0/2/8/8
7	MRD	G	250	-	-	1/5/5/5	-
6	MLK	C	260	-	-	1/24/141/141	0/2/8/8
8	MPD	C	222	-	-	4/5/5/5	-
5	NAG	C	225	1	-	0/6/23/26	0/1/1/1
7	MRD	D	251	-	-	4/5/5/5	-
6	MLK	I	260	-	-	1/24/141/141	0/2/8/8

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	260	MLK	C8-N7	-4.45	1.34	1.40
6	C	260	MLK	C8-N7	-4.22	1.34	1.40
6	G	260	MLK	C8-N7	-4.21	1.34	1.40
6	F	260	MLK	C8-N7	-4.12	1.34	1.40
6	H	260	MLK	C8-N7	-4.09	1.34	1.40

The worst 5 of 154 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	260	MLK	C23-C16-C17	6.34	112.96	108.22
6	C	260	MLK	C23-C16-C17	6.21	112.86	108.22
6	B	260	MLK	O27-C27-C26	5.81	115.80	110.45
6	I	260	MLK	O27-C27-C26	5.78	115.77	110.45
6	G	260	MLK	C23-C16-C17	5.44	112.28	108.22

There are no chirality outliers.

5 of 42 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	225	NAG	C3-C2-N2-C7
5	A	225	NAG	C8-C7-N2-C2
5	A	225	NAG	O7-C7-N2-C2

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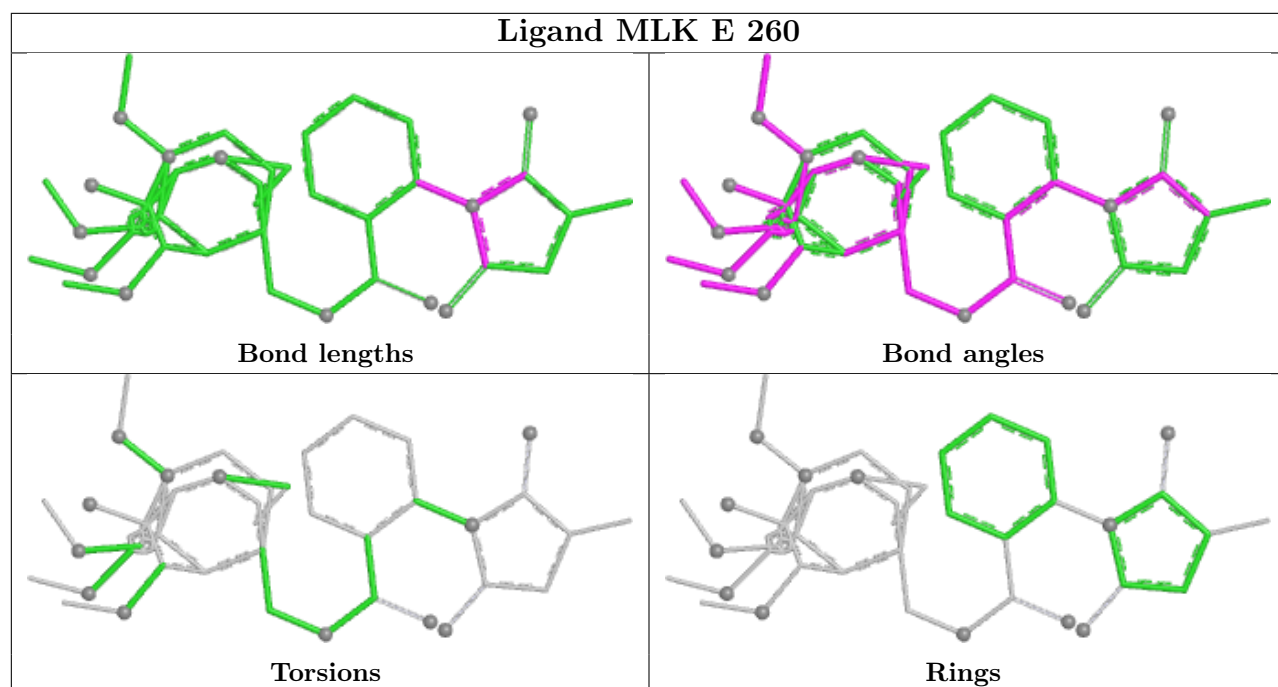
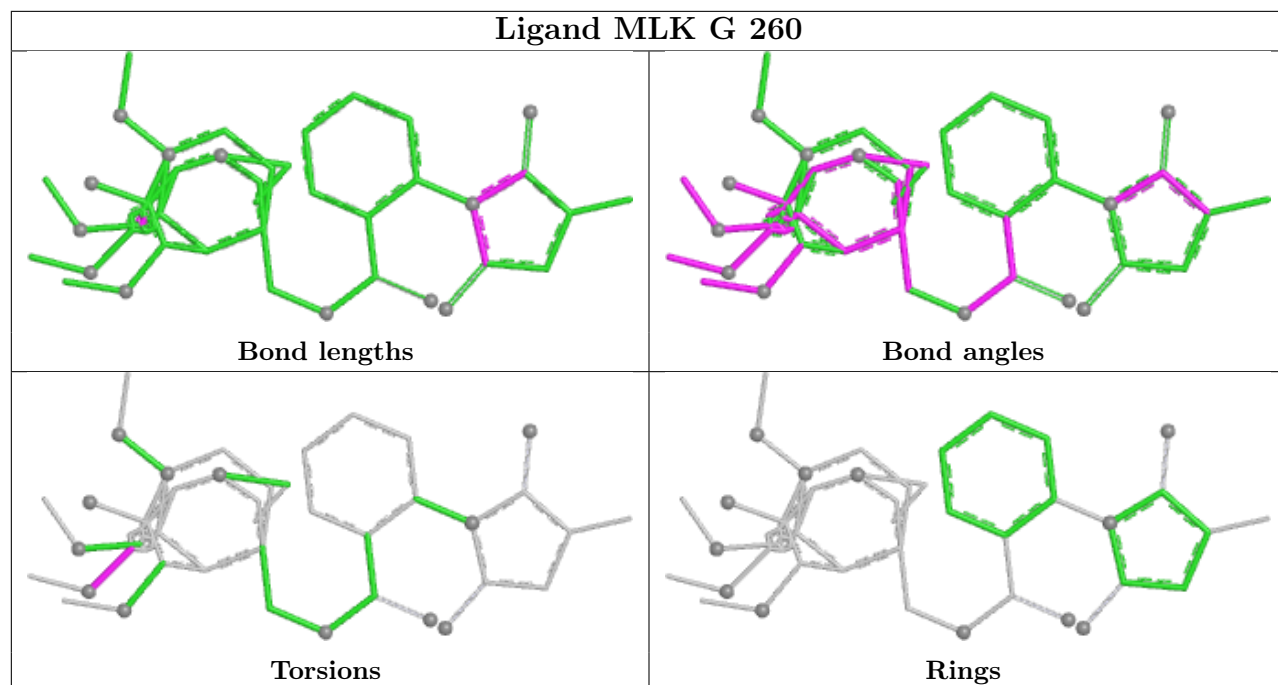
Mol	Chain	Res	Type	Atoms
7	B	250	MRD	C1-C2-C3-C4
7	B	250	MRD	O2-C2-C3-C4

There are no ring outliers.

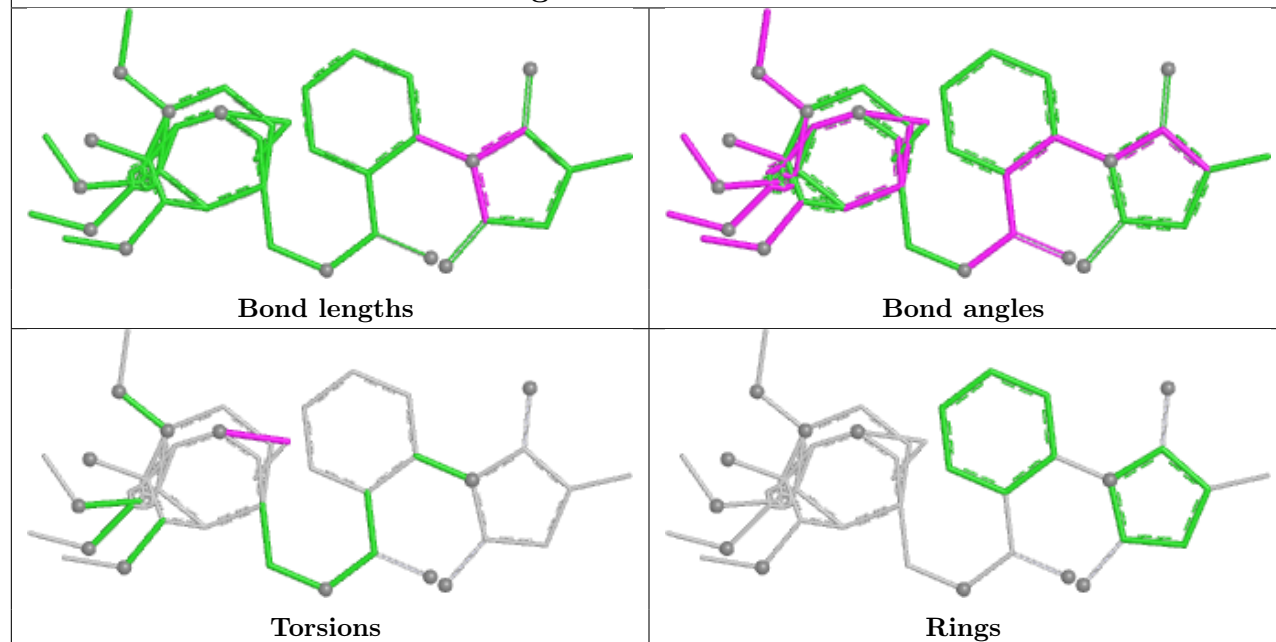
18 monomers are involved in 112 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	G	260	MLK	5	0
7	B	250	MRD	1	0
6	E	260	MLK	12	0
6	J	260	MLK	15	0
6	A	260	MLK	7	0
8	I	250	MPD	5	0
6	H	260	MLK	9	0
6	B	260	MLK	4	0
7	H	250	MRD	1	0
6	D	260	MLK	8	0
7	C	250	MRD	1	0
7	D	250	MRD	1	0
5	A	225	NAG	7	0
6	F	260	MLK	8	0
7	G	250	MRD	5	0
6	C	260	MLK	7	0
7	D	251	MRD	9	0
6	I	260	MLK	7	0

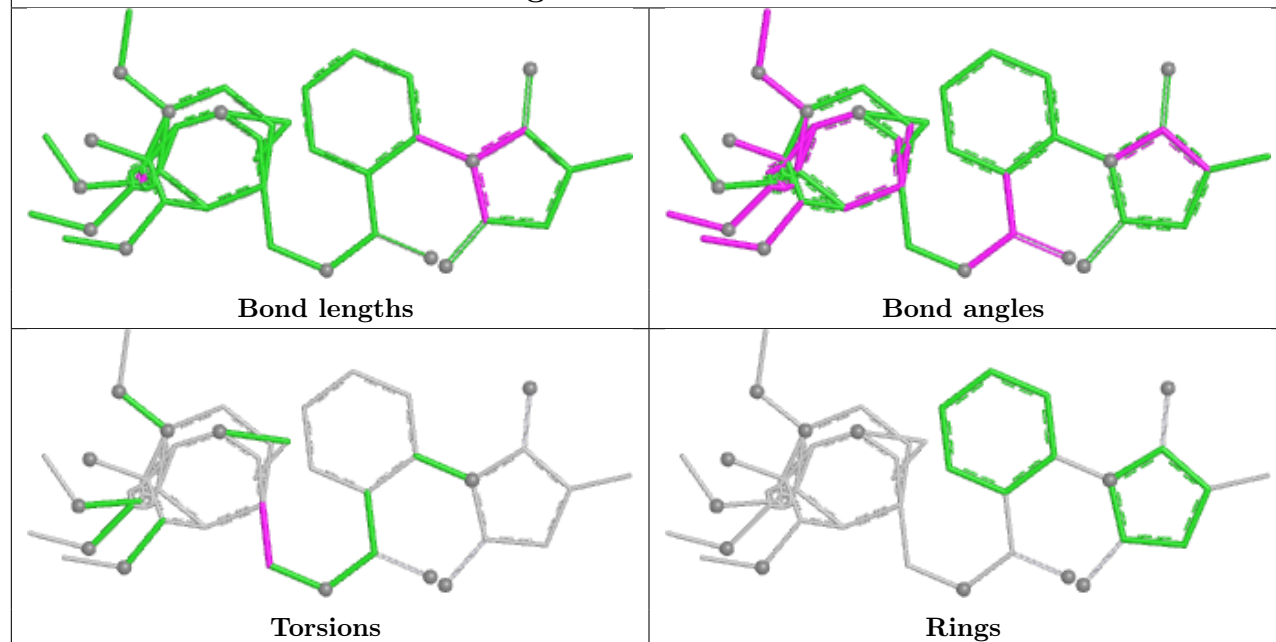
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

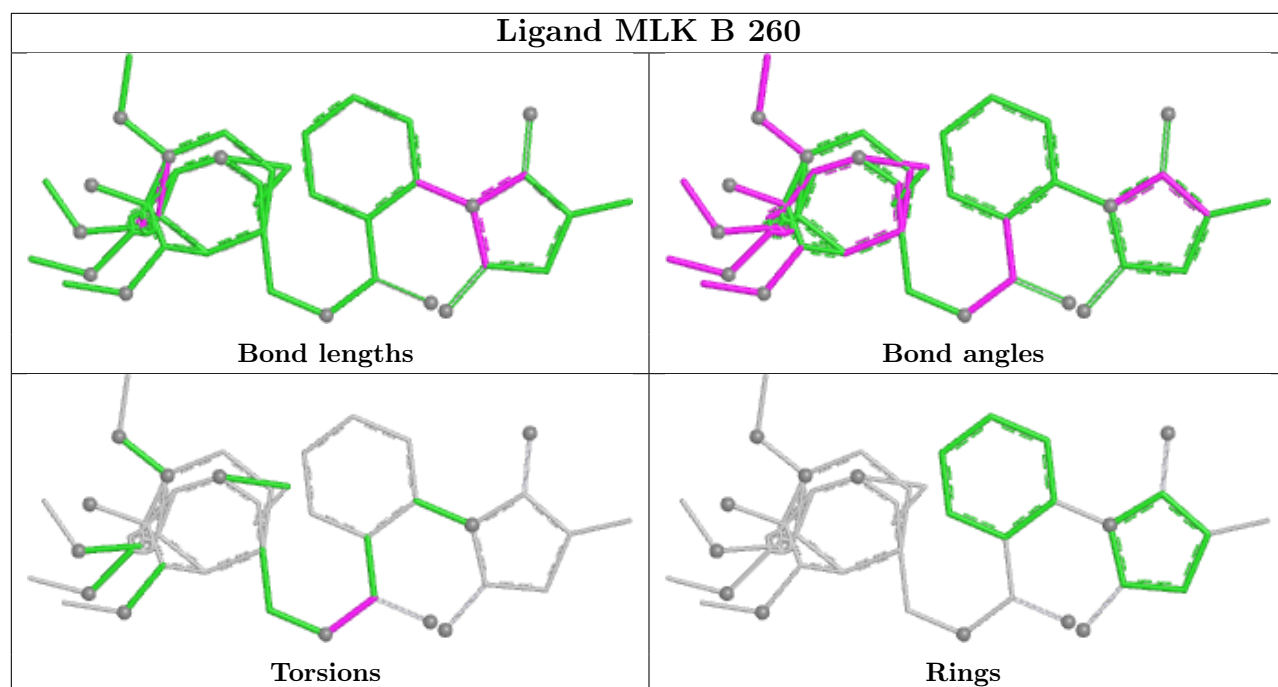
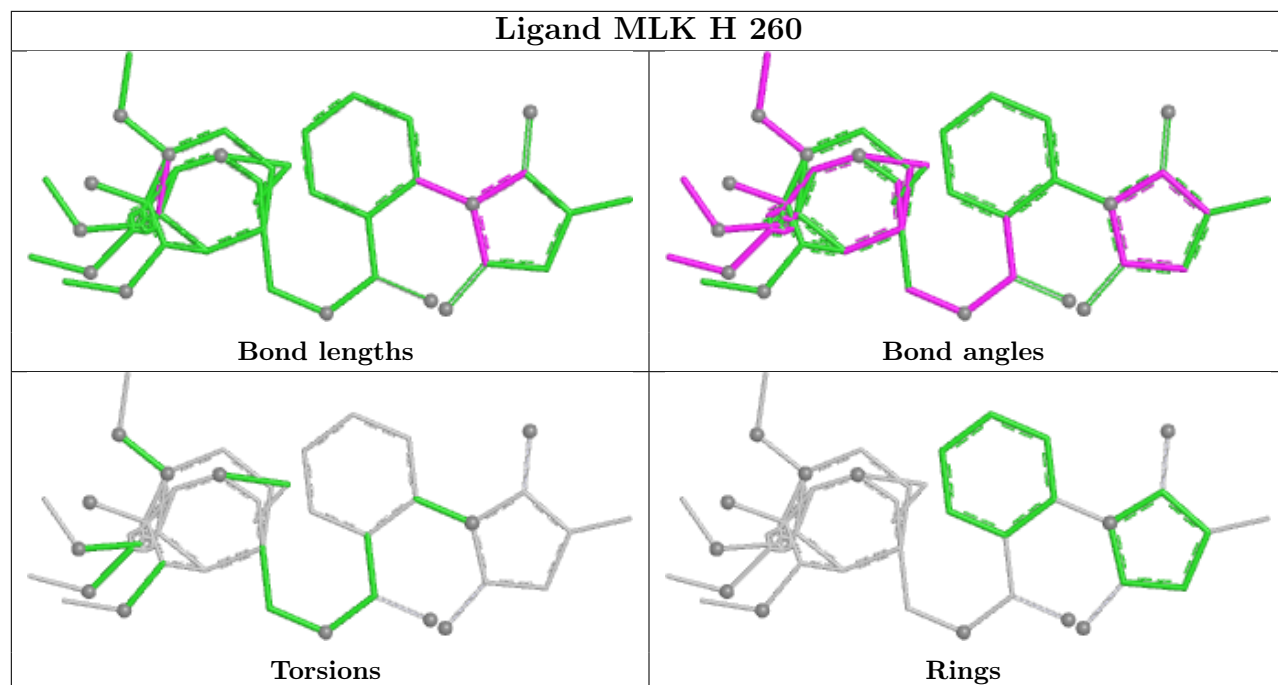


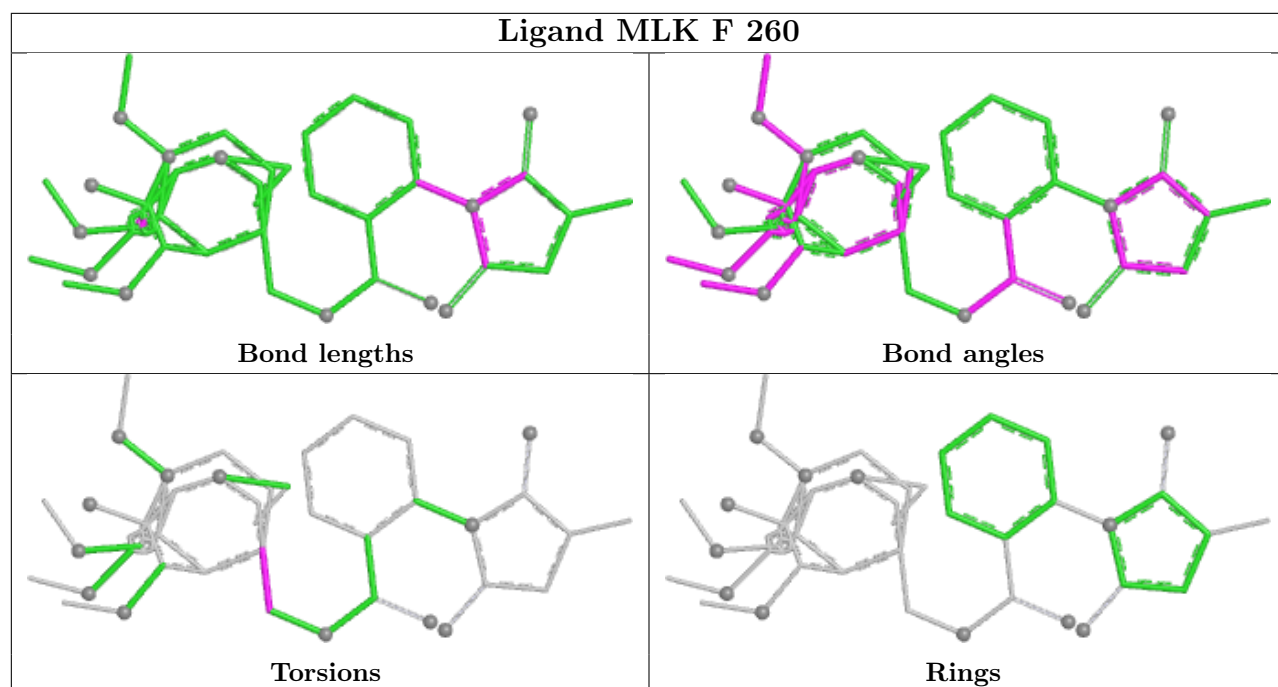
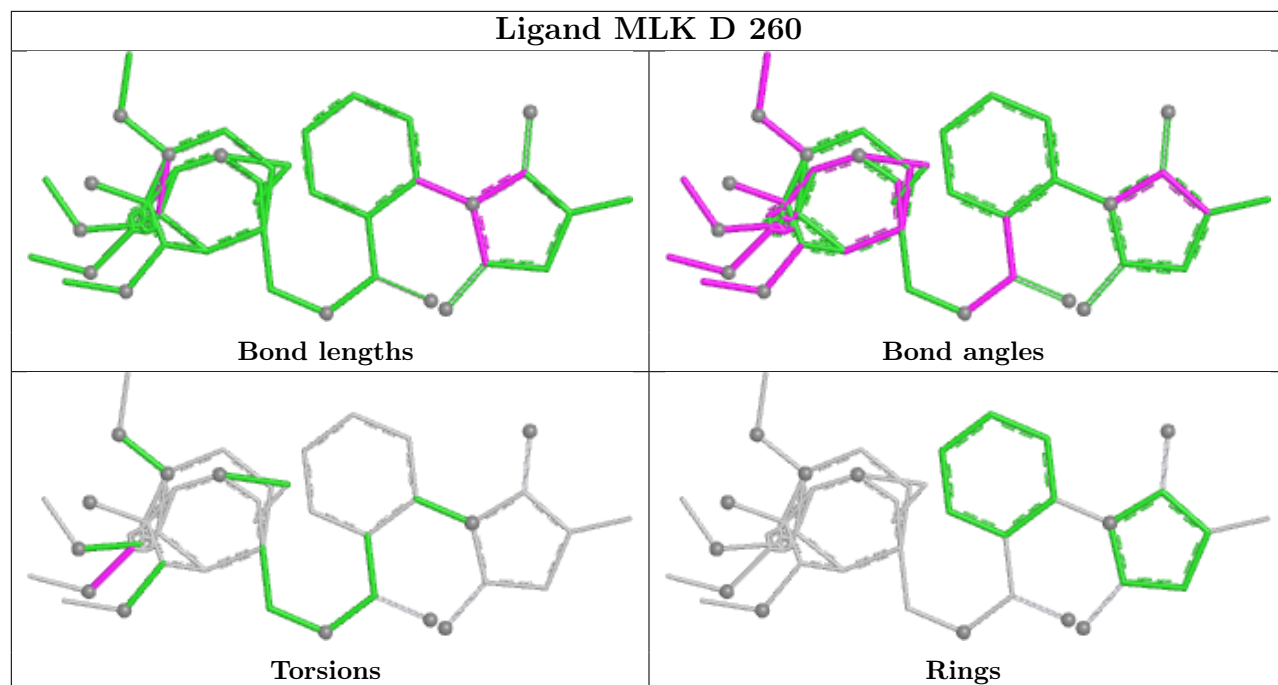
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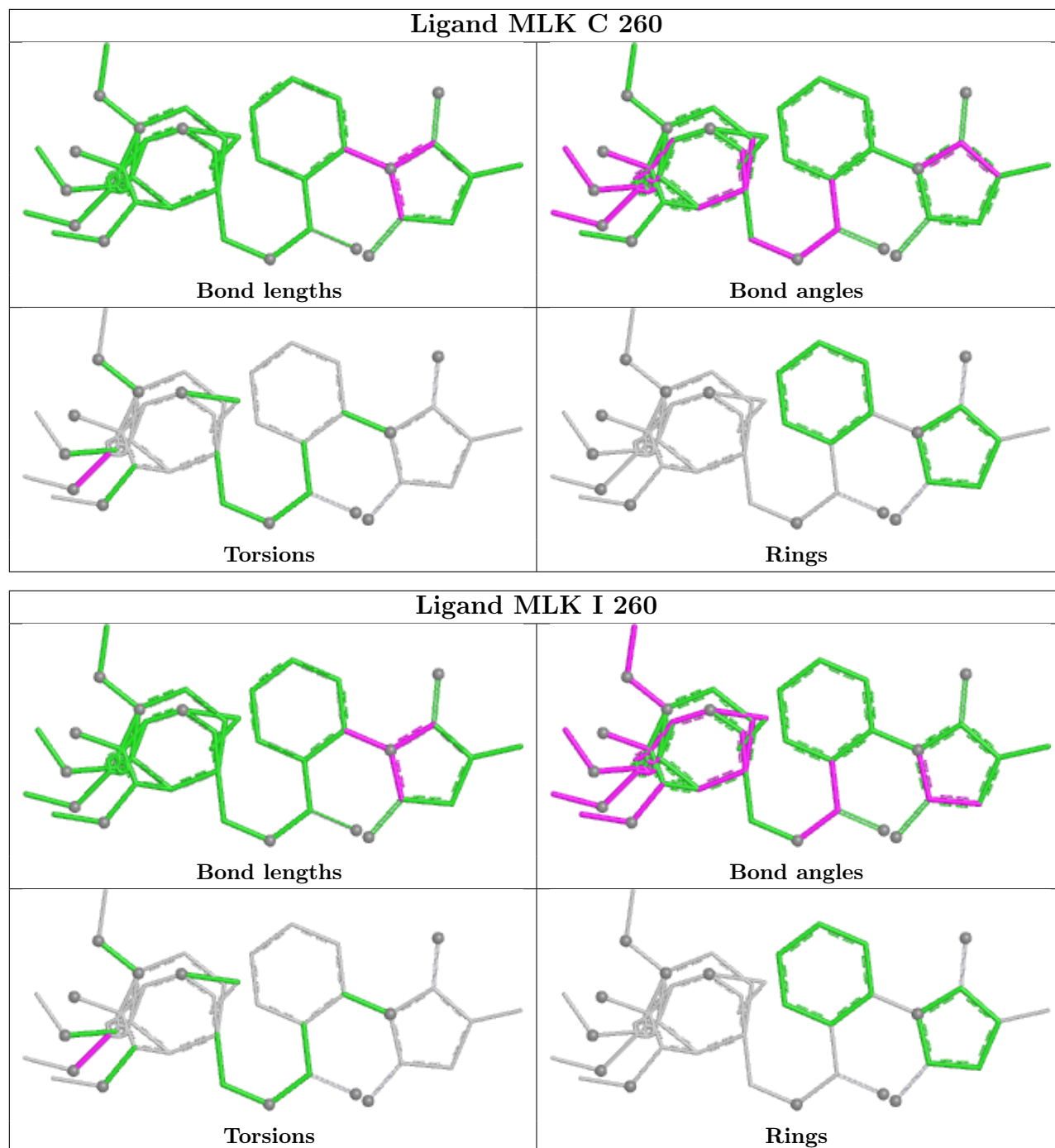


Ligand MLK A 260









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 [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	214/230 (93%)	-1.36	0 100 100	15, 32, 63, 93	7 (3%)
1	B	216/230 (93%)	-1.36	0 100 100	16, 31, 65, 97	8 (3%)
1	C	221/230 (96%)	-1.28	0 100 100	14, 32, 78, 109	9 (4%)
1	D	214/230 (93%)	-1.30	0 100 100	15, 34, 76, 107	9 (4%)
1	E	216/230 (93%)	-1.31	0 100 100	16, 31, 64, 98	9 (4%)
1	F	214/230 (93%)	-1.37	0 100 100	14, 32, 61, 90	9 (4%)
1	G	216/230 (93%)	-1.35	0 100 100	15, 31, 62, 97	10 (4%)
1	H	221/230 (96%)	-1.28	0 100 100	14, 32, 78, 114	7 (3%)
1	I	214/230 (93%)	-1.26	0 100 100	16, 35, 78, 119	6 (2%)
1	J	216/230 (93%)	-1.34	0 100 100	16, 31, 60, 98	11 (5%)
All	All	2162/2300 (94%)	-1.32	0 100 100	14, 32, 70, 119	85 (3%)

There are no RSRZ outliers to report.

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	P	5	11/12	0.93	0.07	80,97,109,111	0

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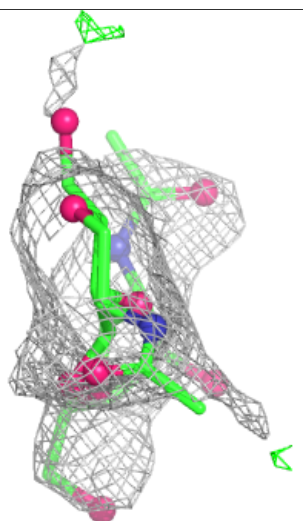
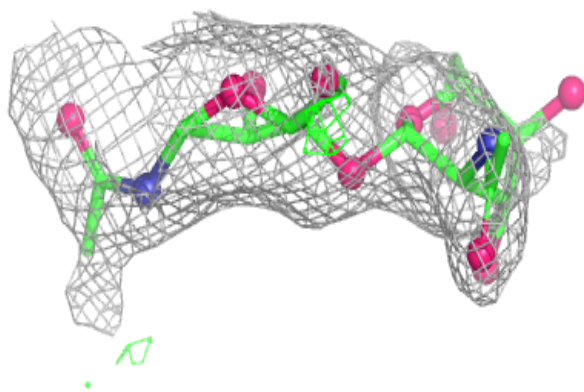
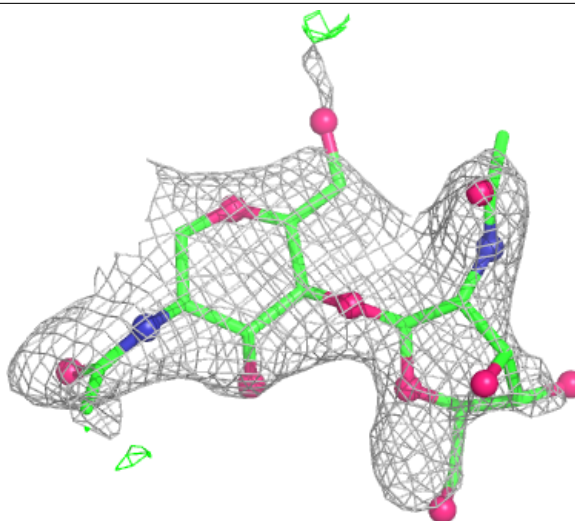
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	MAN	N	4	11/12	0.94	0.07	91,102,109,112	0
2	NAG	M	2	14/15	0.95	0.06	98,102,109,110	0
4	MAN	Q	4	11/12	0.95	0.07	100,103,109,115	0
4	MAN	Q	6	11/12	0.95	0.08	82,102,114,115	0
3	MAN	L	5	11/12	0.96	0.06	87,92,99,101	0
4	BMA	Q	3	11/12	0.96	0.06	95,101,112,114	0
2	NAG	O	2	14/15	0.97	0.07	70,93,104,105	0
3	MAN	P	6	11/12	0.97	0.05	73,85,89,92	0
4	NAG	N	2	14/15	0.97	0.04	57,71,82,85	0
3	NAG	L	2	14/15	0.97	0.05	73,90,96,97	0
4	MAN	N	6	11/12	0.97	0.07	65,78,90,94	0
2	NAG	K	2	14/15	0.97	0.06	84,91,102,104	0
3	MAN	L	6	11/12	0.97	0.06	70,76,84,87	0
3	NAG	P	2	14/15	0.97	0.05	79,90,95,99	0
4	NAG	N	1	14/15	0.98	0.05	42,50,70,73	0
3	NAG	L	1	14/15	0.98	0.05	69,75,82,91	0
4	BMA	N	3	11/12	0.98	0.04	81,87,99,100	0
3	MAN	L	7	11/12	0.98	0.06	65,76,87,88	0
4	MAN	N	5	11/12	0.98	0.05	60,73,83,83	0
3	NAG	P	1	14/15	0.98	0.04	68,76,83,95	0
4	NAG	Q	2	14/15	0.98	0.05	66,73,80,91	0
2	NAG	O	1	14/15	0.98	0.05	54,68,79,82	0
3	MAN	L	4	11/12	0.98	0.06	70,73,84,94	0
4	MAN	Q	5	11/12	0.98	0.07	61,70,91,91	0
2	NAG	M	1	14/15	0.98	0.05	68,74,86,97	0
4	NAG	Q	1	14/15	0.99	0.04	45,54,69,74	0
3	MAN	P	4	11/12	0.99	0.04	71,79,84,99	0
2	NAG	K	1	14/15	0.99	0.04	57,65,78,79	0
3	BMA	L	3	11/12	0.99	0.04	63,81,88,95	0
3	MAN	P	7	11/12	0.99	0.05	61,76,87,88	0
3	BMA	P	3	11/12	0.99	0.03	61,77,87,91	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.

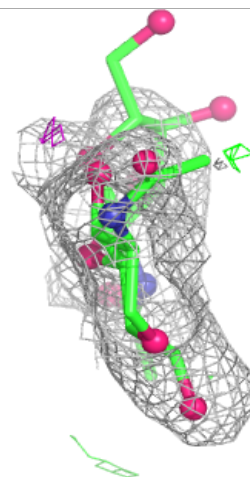
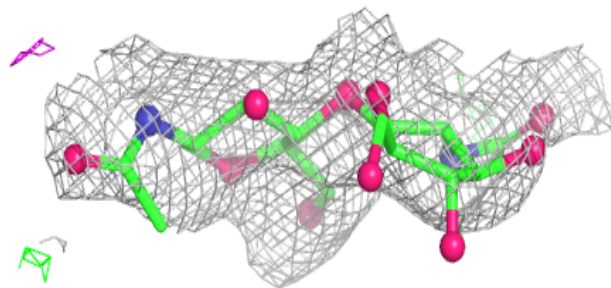
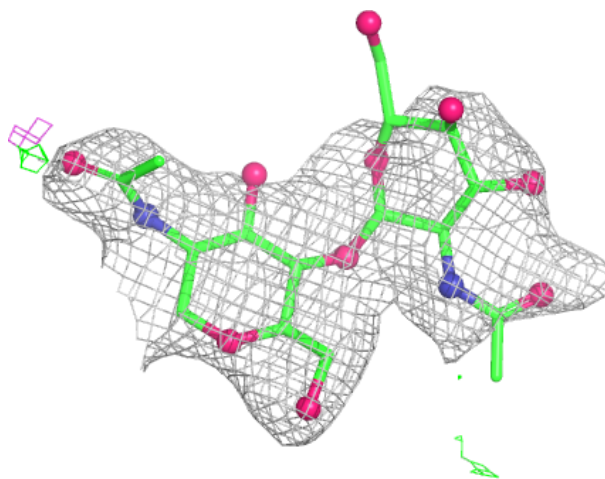
Electron density around Chain K:

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



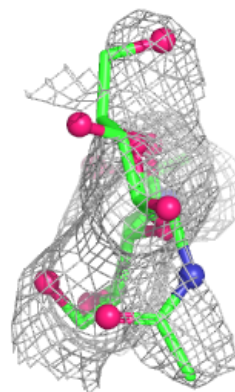
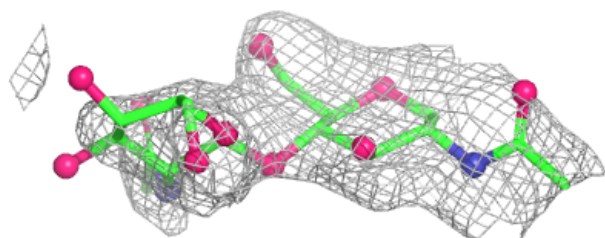
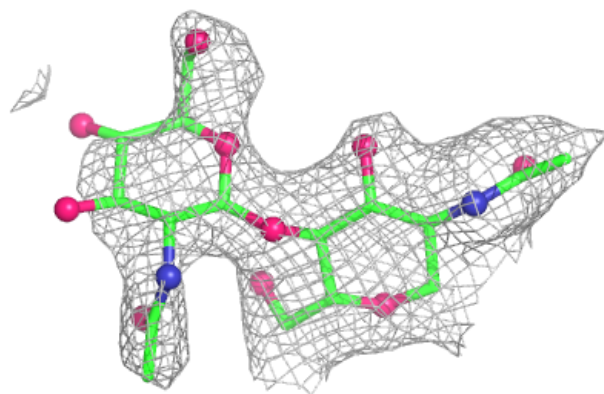
Electron density around Chain M:

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



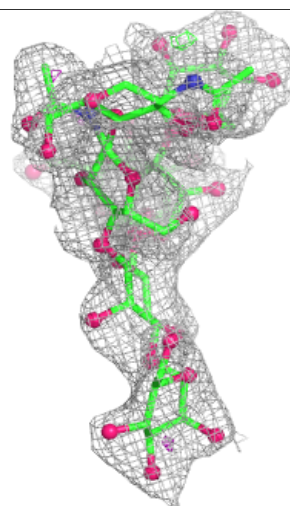
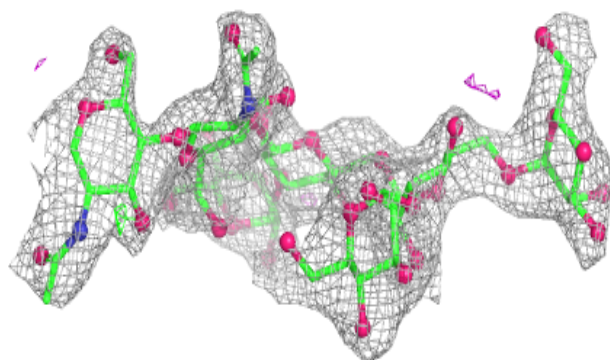
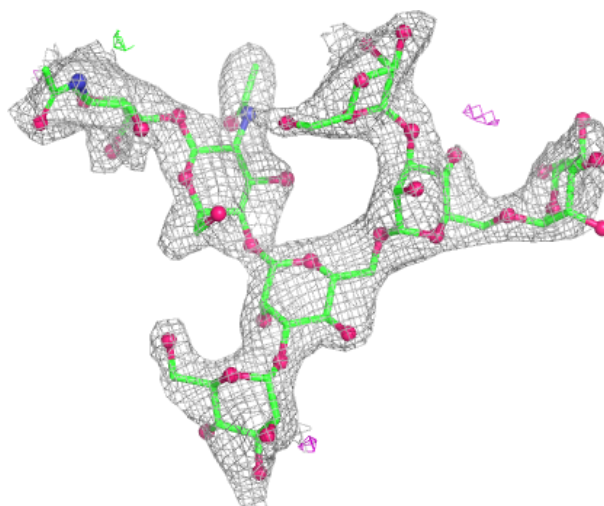
Electron density around Chain O:

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



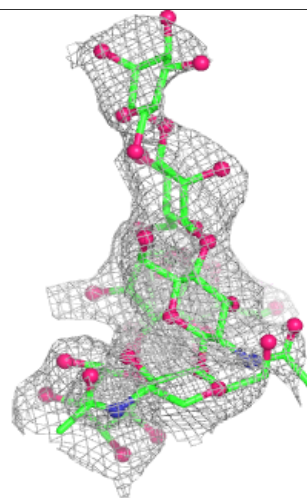
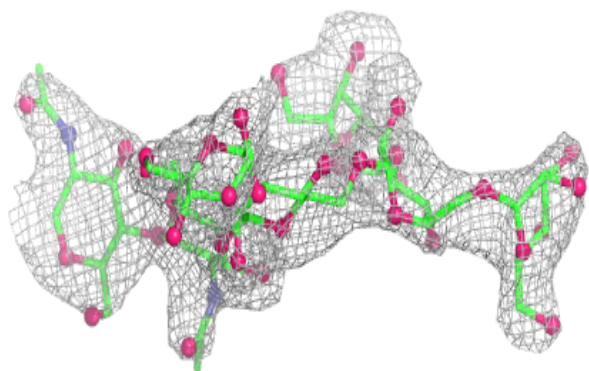
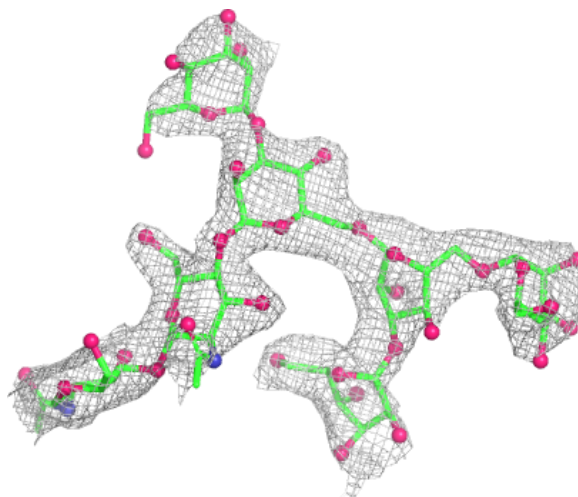
Electron density around Chain L:

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



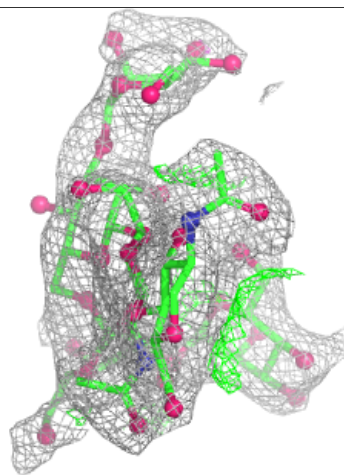
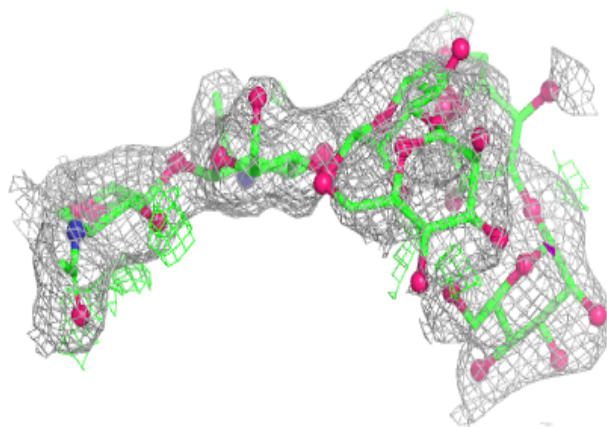
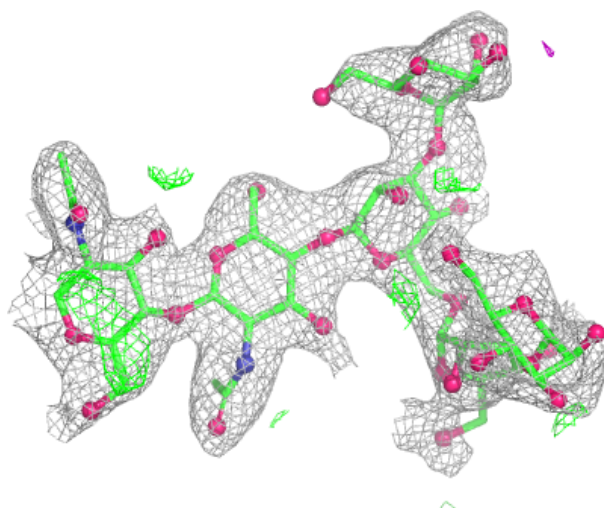
Electron density around Chain P:

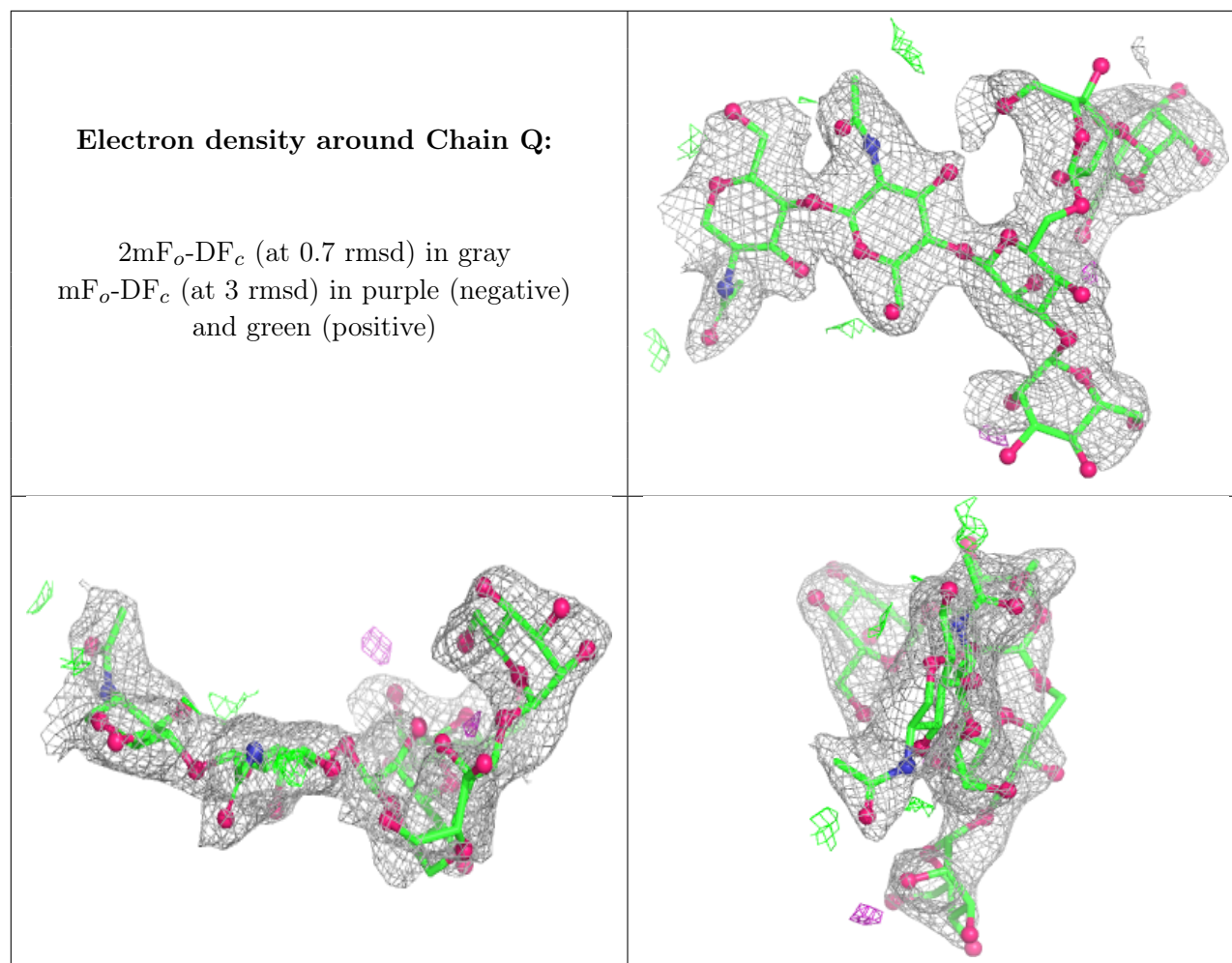
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain N:

$2mF_o-DF_c$ (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.

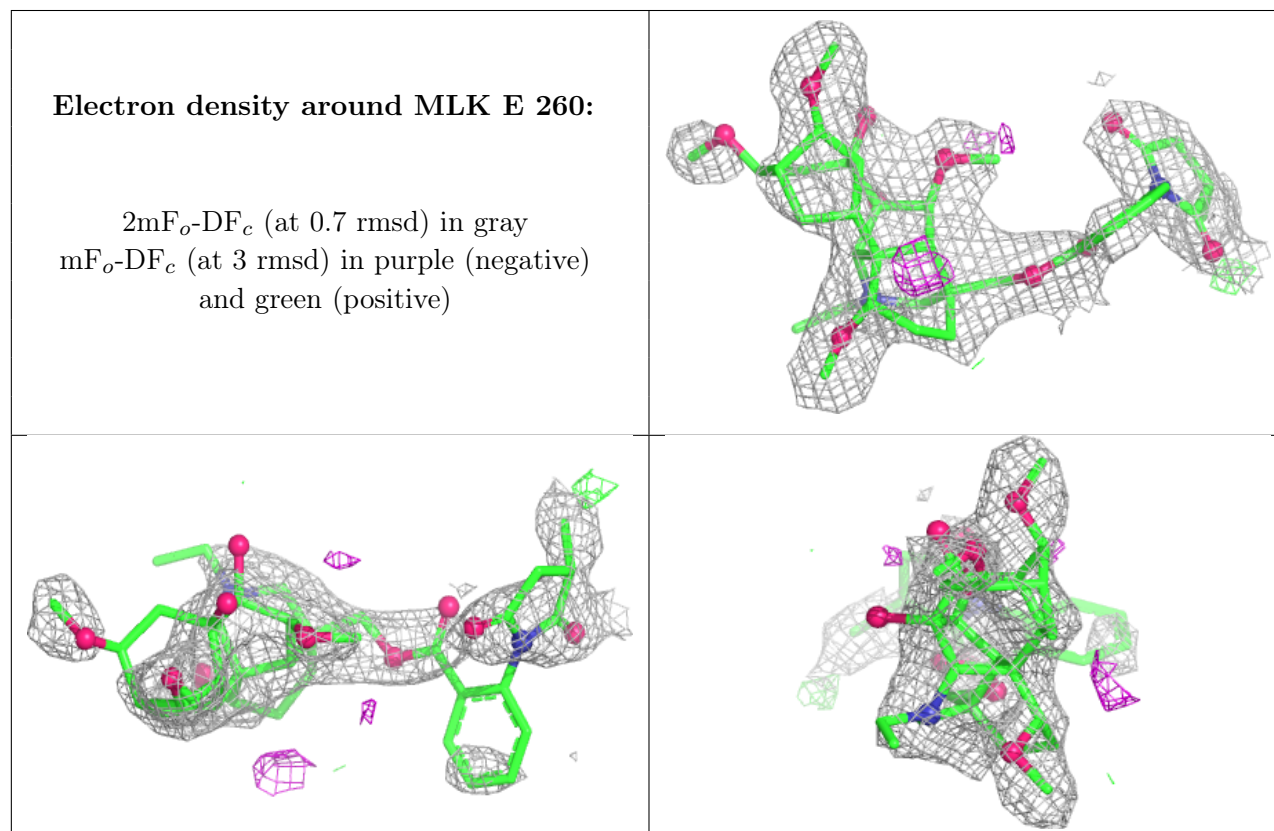
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	NAG	A	225	14/15	0.97	0.07	59,66,78,80	0
5	NAG	C	225	14/15	0.97	0.04	60,67,76,84	0
5	NAG	F	225	14/15	0.97	0.05	56,70,79,83	0
5	NAG	J	240	14/15	0.97	0.06	67,78,87,87	0
7	MRD	G	250	8/8	0.97	0.07	31,47,57,58	0
8	MPD	I	250	8/8	0.97	0.08	44,57,65,72	0
5	NAG	E	240	14/15	0.98	0.06	69,81,89,98	0
6	MLK	E	260	49/49	0.98	0.06	40,64,84,91	0
6	MLK	J	260	49/49	0.98	0.06	46,66,81,92	0
7	MRD	B	250	8/8	0.98	0.06	37,50,67,68	0

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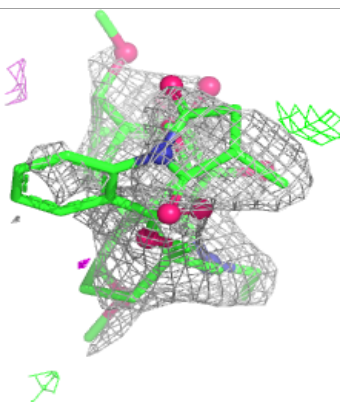
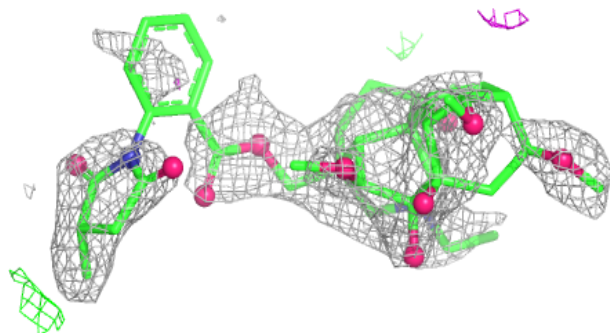
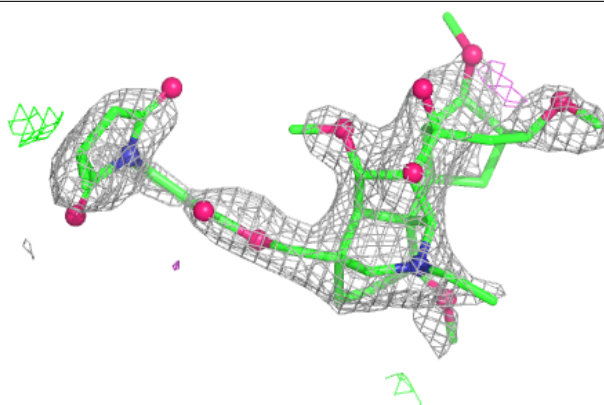
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	MRD	C	250	8/8	0.98	0.06	40,53,61,71	0
7	MRD	D	251	8/8	0.98	0.06	52,63,71,74	0
7	MRD	D	250	8/8	0.98	0.08	48,58,73,73	0
5	NAG	H	225	14/15	0.98	0.04	61,68,77,84	0
7	MRD	H	250	8/8	0.98	0.05	42,54,62,73	0
7	MRD	I	222	8/8	0.98	0.07	51,61,73,74	0
8	MPD	C	222	8/8	0.98	0.07	43,61,73,87	0
5	NAG	I	225	14/15	0.98	0.06	58,71,77,78	0
6	MLK	D	260	49/49	0.99	0.04	35,46,55,62	0
6	MLK	A	260	49/49	0.99	0.04	29,42,52,69	0
6	MLK	F	260	49/49	0.99	0.03	33,42,54,70	0
6	MLK	G	260	49/49	0.99	0.04	31,42,51,60	0
6	MLK	H	260	49/49	0.99	0.03	31,42,52,61	0
6	MLK	I	260	49/49	0.99	0.04	35,45,52,58	0
6	MLK	B	260	49/49	0.99	0.04	31,42,52,63	0
6	MLK	C	260	49/49	0.99	0.03	31,43,52,62	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.

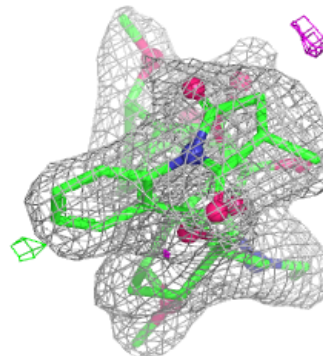
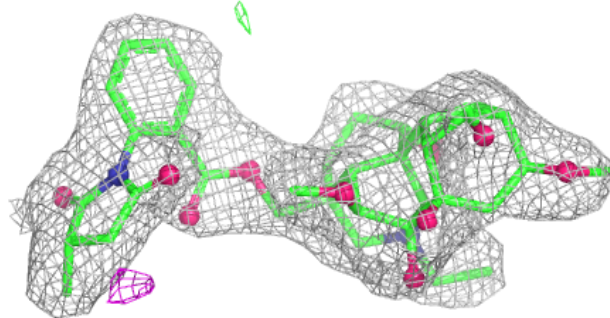
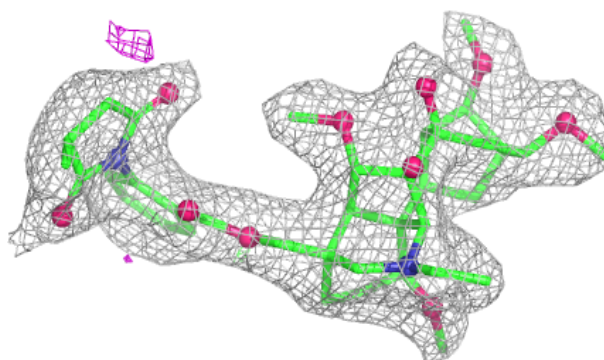


Electron density around MLK J 260:

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

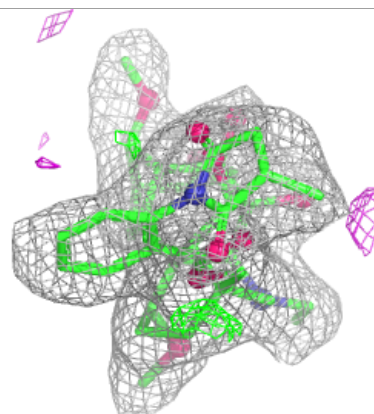
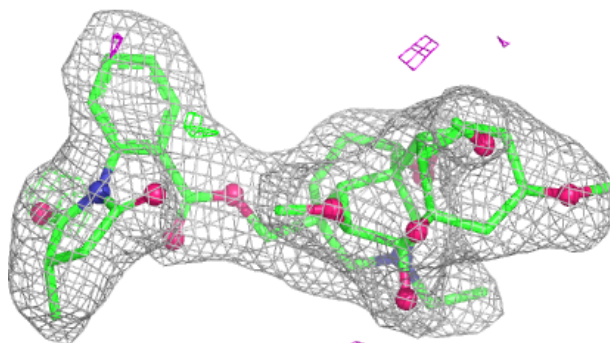
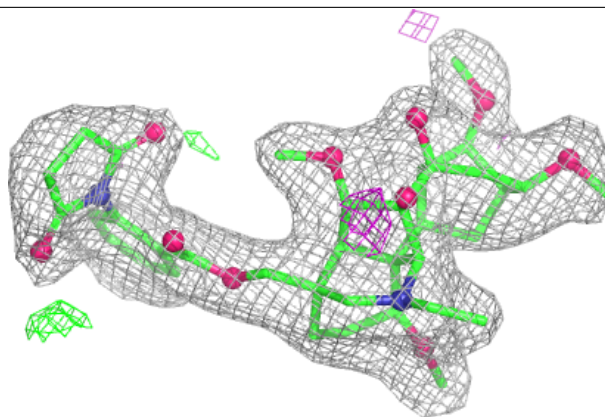
**Electron density around MLK D 260:**

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

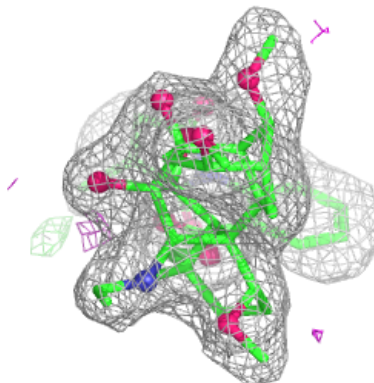
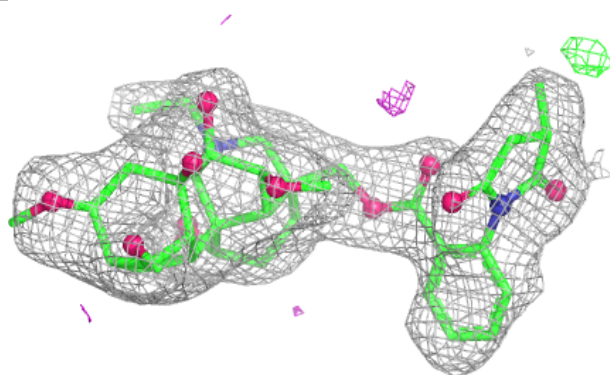
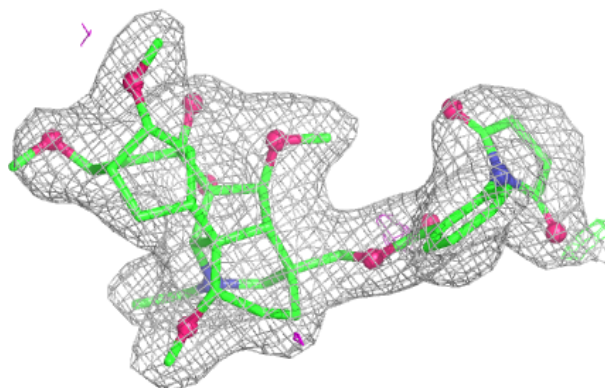


Electron density around MLK A 260:

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

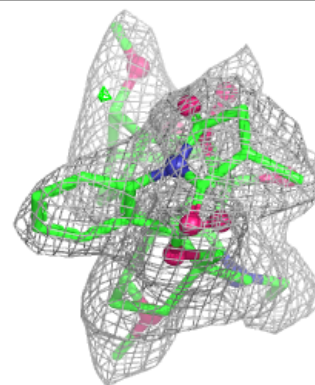
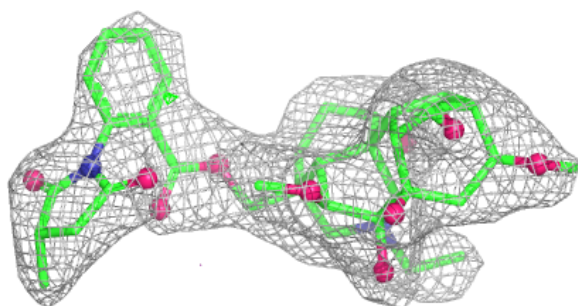
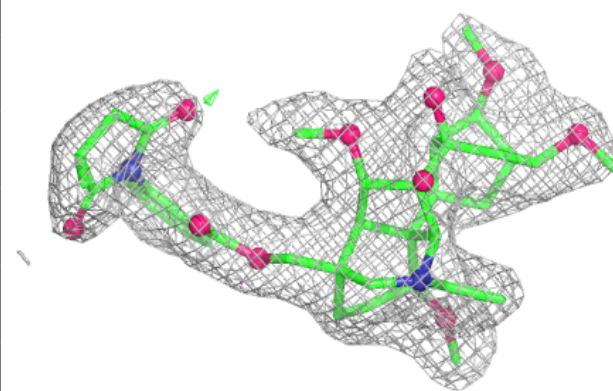
**Electron density around MLK F 260:**

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

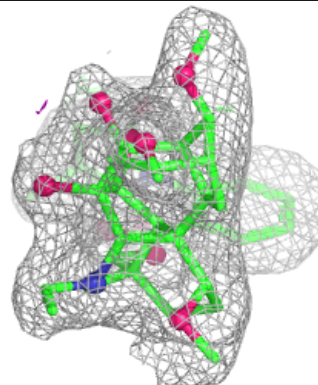
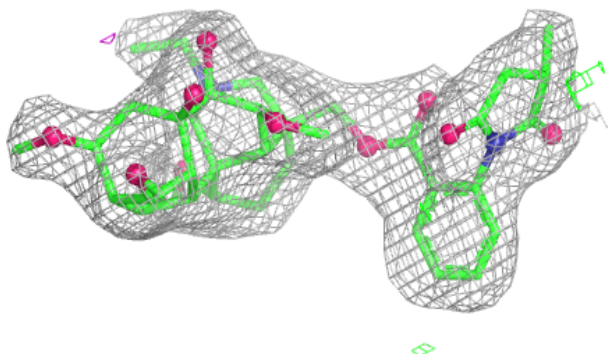
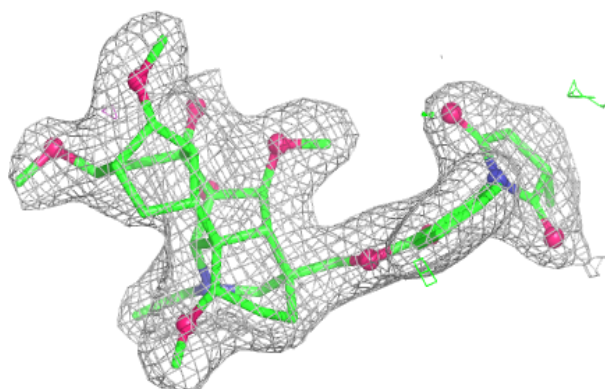


Electron density around MLK G 260:

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

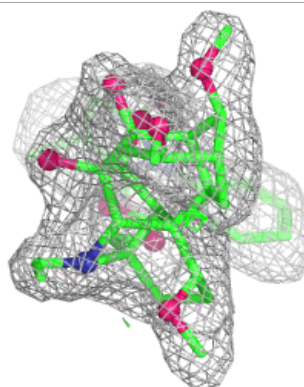
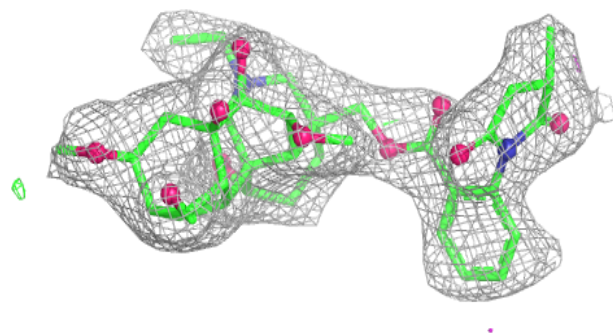
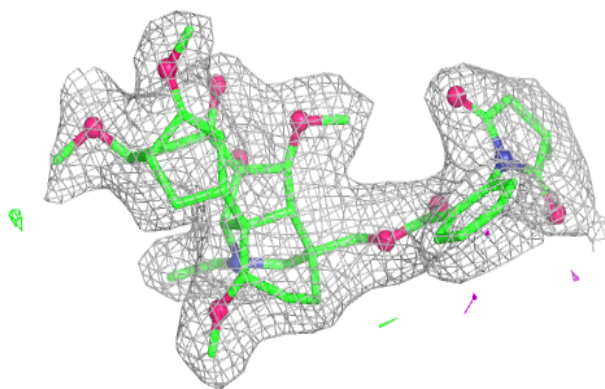
**Electron density around MLK H 260:**

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

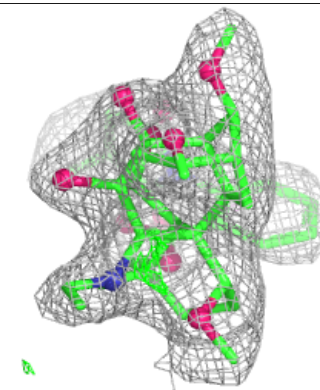
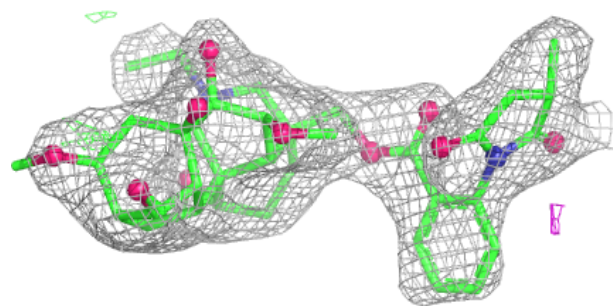
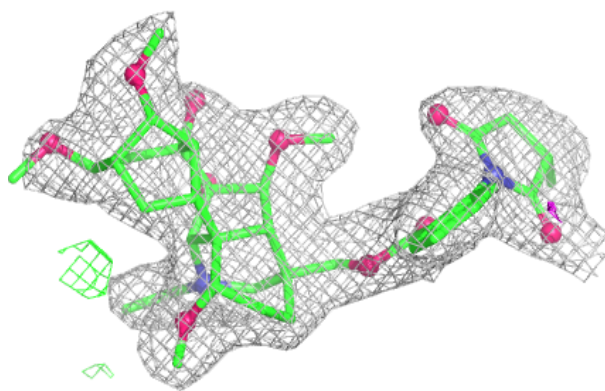


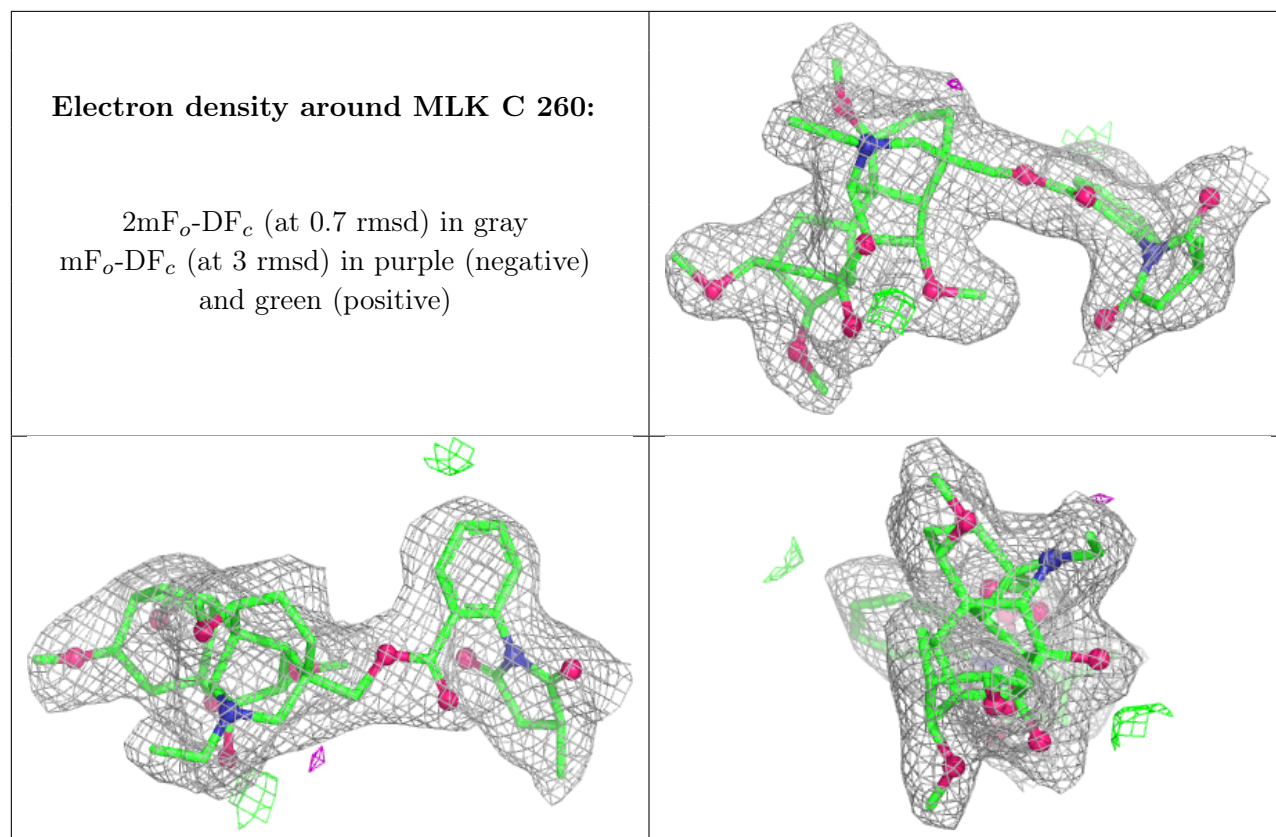
Electron density around MLK I 260:

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

**Electron density around MLK B 260:**

$2mF_o-DF_c$ (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.