



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:43 AM UTC

PDB ID : 9IFQ / pdb_00009ifq
Title : Unspecific peroxygenase from *Psathyrella aberdarensis* (PabUPO-II) in complex with 5-hydroxymethylfurfural
Authors : Fernandez-Garcia, A.; Sanz-Aparicio, J.
Deposited on : 2025-02-18
Resolution : 2.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

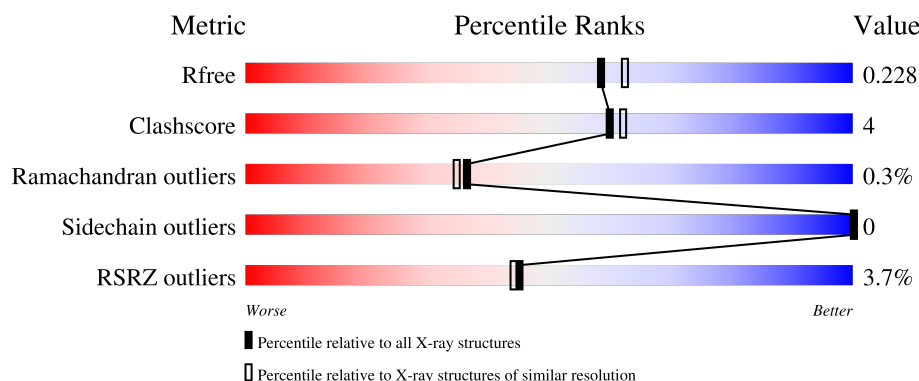
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 Å.

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







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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	335	<div> <div>2%</div> <div>93%</div> <div>7%</div> </div>
1	B	335	<div> <div>3%</div> <div>95%</div> <div>5%</div> </div>
1	C	335	<div> <div>6%</div> <div>93%</div> <div>7%</div> </div>
2	D	5	<div> <div>100%</div> </div>
2	F	5	<div> <div>20%</div> <div>80%</div> </div>

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Mol	Chain	Length	Quality of chain
3	E	7	 57% 43%
4	G	6	 50% 17% 33%
5	H	4	 75% 25%
6	I	3	 67% 33%

2 Entry composition [i](#)

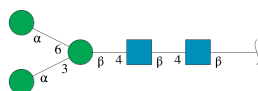
There are 13 unique types of molecules in this entry. The entry contains 9217 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Heme-thiolate peroxidase.

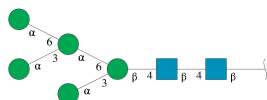
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	335	Total	C	N	O	S	0	6	0
			2623	1666	453	498	6			
1	B	335	Total	C	N	O	S	0	4	0
			2612	1659	451	496	6			
1	C	335	Total	C	N	O	S	0	4	0
			2609	1658	448	496	7			

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



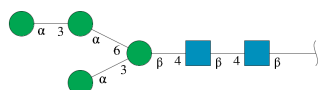
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	5	Total	C	N	O	0	0	0
			61	34	2	25			
2	F	5	Total	C	N	O	0	0	0
			61	34	2	25			

- 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	E	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.



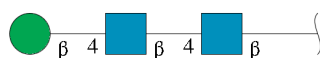
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	G	6	Total	C	N	O	0	0	0
			72	40	2	30			

- Molecule 5 is an oligosaccharide called 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.



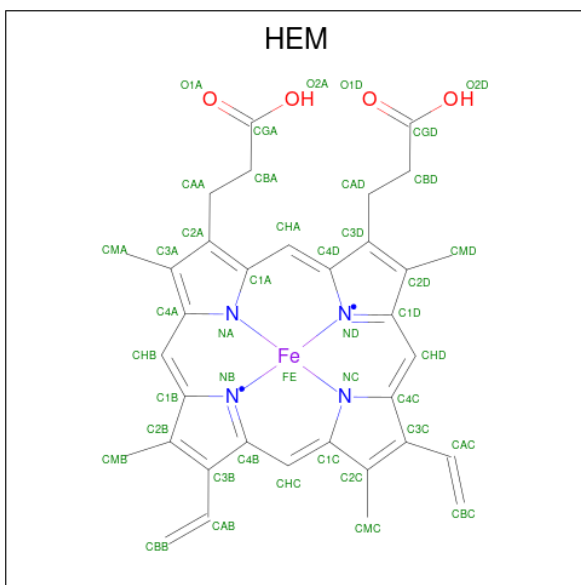
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	H	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 6 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.



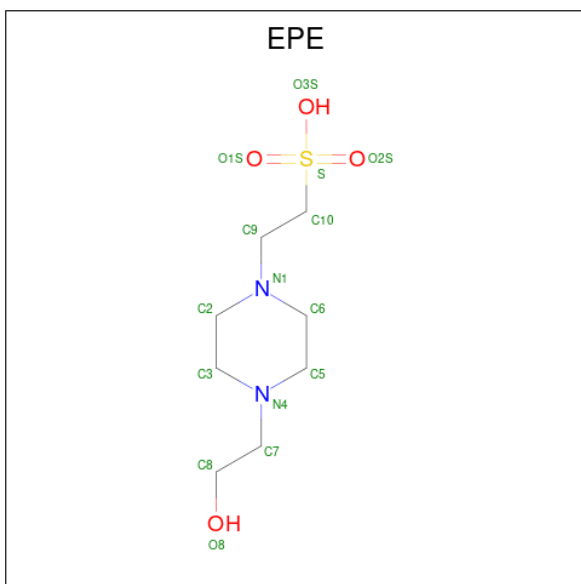
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	I	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 7 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: C₃₄H₃₂FeN₄O₄) (labeled as "Ligand of Interest" by depositor).



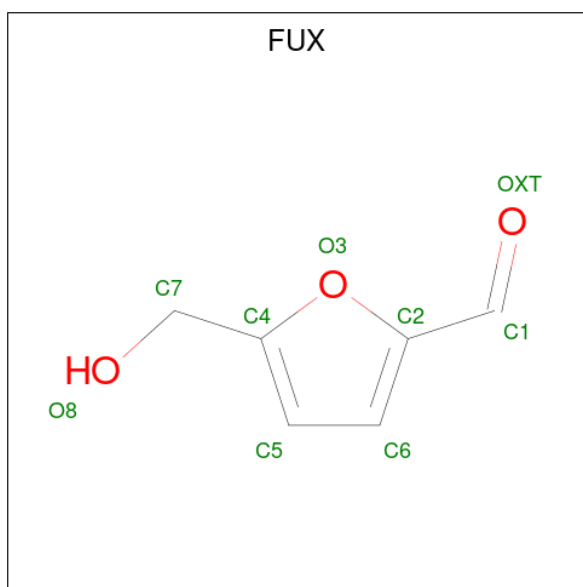
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
7	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
7	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 8 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: $\text{C}_8\text{H}_{18}\text{N}_2\text{O}_4\text{S}$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
8	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
8	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 9 is 5-HYDROXYMETHYL-FURFURAL (CCD ID: FUX) (formula: $C_6H_6O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			9	6	3		
9	A	1	Total	C	O	0	0
			9	6	3		
9	B	1	Total	C	O	0	0
			9	6	3		
9	B	1	Total	C	O	0	0
			9	6	3		
9	C	1	Total	C	O	0	0
			9	6	3		
9	C	1	Total	C	O	0	0
			9	6	3		

- Molecule 10 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			6	3	3		
10	B	1	Total	C	O	0	0
			6	3	3		
10	B	1	Total	C	O	0	0
			6	3	3		
10	C	1	Total	C	O	0	0
			6	3	3		
10	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 11 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	1	Total	Mg	0	0
			1	1		
11	B	1	Total	Mg	0	0
			1	1		
11	C	1	Total	Mg	0	0
			1	1		

- Molecule 12 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

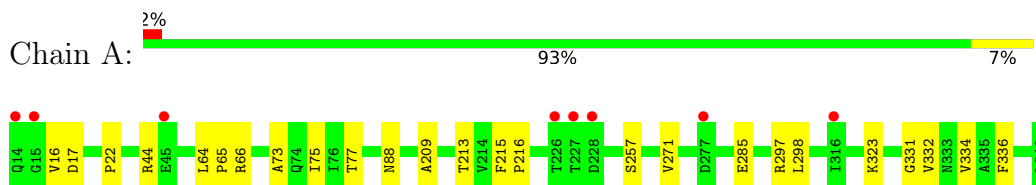
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	301	Total	O	0	0
			301	301		
13	B	240	Total	O	0	0
			240	240		
13	C	180	Total	O	0	0
			180	180		

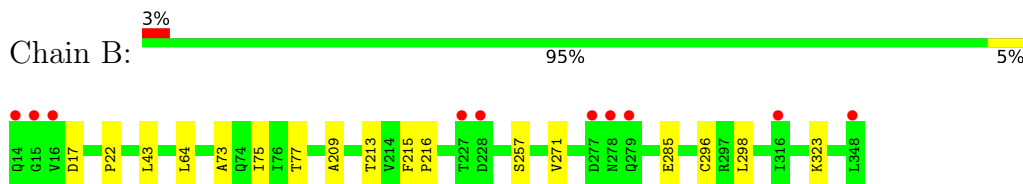
3 Residue-property plots

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.

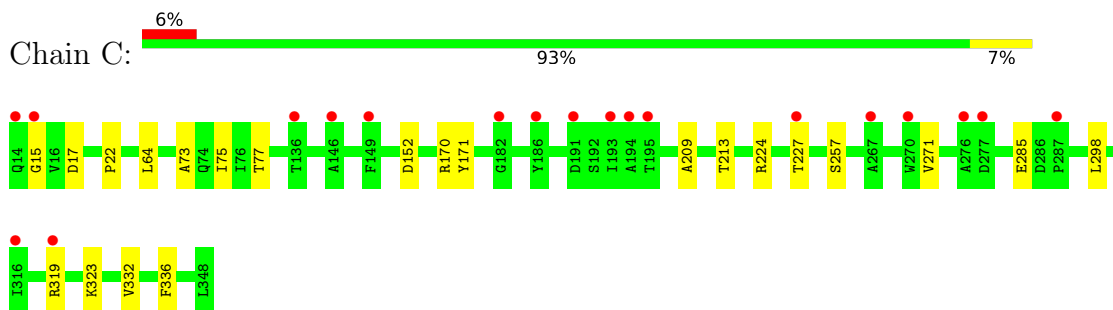
- Molecule 1: Heme-thiolate peroxidase



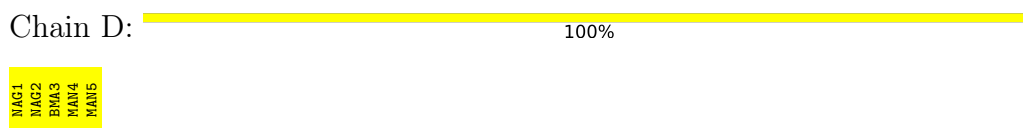
- Molecule 1: Heme-thiolate peroxidase



- Molecule 1: Heme-thiolate peroxidase



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



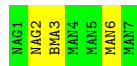
- Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  20% 80%



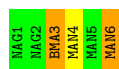
- Molecule 3: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:  57% 43%

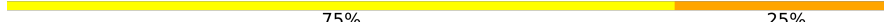


- Molecule 4: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  50% 17% 33%



- Molecule 5: 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 H:  75% 25%



- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  67% 33%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	272.21Å 75.11Å 105.39Å 90.00° 111.68° 90.00°	Depositor
Resolution (Å)	48.35 – 2.00 48.35 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.35-2.00) 99.4 (48.35-2.00)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.07 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0419	Depositor
R, R_{free}	0.195 , 0.221 0.203 , 0.228	Depositor DCC
R_{free} test set	6758 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	32.5	Xtriage
Anisotropy	0.767	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 30.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.012 for -h-2*1,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9217	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EPE, SO4, GOL, FUX, NAG, MG, BMA, HEM, MAN

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	0.62	0/2722	0.92	0/3721
1	B	0.58	0/2705	0.92	0/3698
1	C	0.58	0/2702	0.91	0/3694
All	All	0.59	0/8129	0.92	0/11113

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2623	0	2471	23	0
1	B	2612	0	2457	14	0
1	C	2609	0	2453	17	0
2	D	61	0	52	1	0
2	F	61	0	52	0	0
3	E	83	0	70	0	0
4	G	72	0	61	1	0
5	H	50	0	43	1	0
6	I	39	0	34	0	0
7	A	43	0	30	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	43	0	30	0	0
7	C	43	0	30	3	0
8	A	30	0	36	8	0
8	B	15	0	18	3	0
9	A	18	0	12	1	0
9	B	18	0	12	0	0
9	C	18	0	12	0	0
10	A	6	0	8	0	0
10	B	12	0	16	4	0
10	C	12	0	16	2	0
11	A	1	0	0	0	0
11	B	1	0	0	0	0
11	C	1	0	0	0	0
12	A	5	0	0	0	0
12	B	10	0	0	0	0
12	C	10	0	0	0	0
13	A	301	0	0	9	0
13	B	240	0	0	6	0
13	C	180	0	0	5	0
All	All	9217	0	7913	71	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 4.

All (71) 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)
8:A:402:EPE:H31	13:A:513:HOH:O	1.68	0.94
1:A:65:PRO:HA	8:A:402:EPE:H62	1.54	0.90
8:A:402:EPE:C3	13:A:513:HOH:O	2.29	0.78
1:C:77[B]:THR:HG21	13:C:649:HOH:O	1.85	0.77
1:B:77[A]:THR:HG22	13:B:657:HOH:O	1.85	0.77
1:A:88[B]:ASN:HD21	1:A:334:VAL:HB	1.54	0.73
1:C:224:ARG:HH11	10:C:419:GOL:H12	1.56	0.71
1:A:88[B]:ASN:ND2	1:A:334:VAL:HB	2.06	0.70
1:A:297:ARG:HE	8:A:410:EPE:H32	1.59	0.68
1:A:73:ALA:O	1:A:77[B]:THR:HG22	1.94	0.66
1:A:66:ARG:HB2	8:A:402:EPE:H71	1.78	0.64
1:B:17:ASP:OD1	1:B:323:LYS:NZ	2.30	0.64
1:C:17:ASP:OD1	1:C:323:LYS:NZ	2.31	0.64
1:A:17:ASP:OD1	1:A:323:LYS:NZ	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:402:EPE:H62	13:B:713:HOH:O	1.98	0.62
1:A:88[B]:ASN:ND2	1:A:331:GLY:O	2.34	0.60
7:C:414:HEM:HHC	7:C:414:HEM:HBB2	1.84	0.60
1:A:77[B]:THR:HG21	13:A:739:HOH:O	2.00	0.59
1:B:209:ALA:O	1:B:213:THR:HG23	2.03	0.59
1:C:73:ALA:O	1:C:77[B]:THR:HG22	2.04	0.58
1:C:209:ALA:O	1:C:213:THR:HG23	2.04	0.58
1:A:209:ALA:O	1:A:213:THR:HG23	2.02	0.58
1:C:77[A]:THR:HG22	13:C:655:HOH:O	2.04	0.57
1:B:271:VAL:HG11	1:B:285[B]:GLU:CD	2.31	0.55
1:B:296:CYS:SG	10:B:420:GOL:H11	2.46	0.55
9:A:409:FUX:H72	13:A:507:HOH:O	2.07	0.53
1:A:22:PRO:HG2	1:A:77[A]:THR:HG23	1.91	0.53
1:C:15:GLY:HA2	13:C:644:HOH:O	2.09	0.52
1:B:22:PRO:HG2	1:B:77[A]:THR:HG23	1.92	0.52
8:B:402:EPE:H51	13:B:708:HOH:O	2.11	0.51
1:A:77[B]:THR:HG23	13:A:547:HOH:O	2.11	0.51
7:C:414:HEM:CMC	7:C:414:HEM:HBC2	2.42	0.50
1:C:22:PRO:HG2	1:C:77[A]:THR:HG23	1.92	0.50
10:B:419:GOL:H12	13:B:595:HOH:O	2.10	0.50
1:A:297:ARG:HG3	8:A:410:EPE:H92	1.94	0.50
1:B:43:LEU:N	8:B:402:EPE:O3S	2.35	0.49
1:A:271:VAL:HG11	1:A:285[B]:GLU:CD	2.37	0.49
1:A:16:VAL:HG13	13:A:673:HOH:O	2.13	0.49
1:B:73:ALA:O	1:B:77[B]:THR:HG22	2.13	0.48
1:C:64:LEU:HD21	1:C:75:ILE:HA	1.95	0.48
13:A:674:HOH:O	2:D:3:BMA:H5	2.13	0.48
1:B:77[B]:THR:HG21	13:B:695:HOH:O	2.14	0.47
7:C:414:HEM:HBC2	7:C:414:HEM:HMC2	1.96	0.47
7:A:401:HEM:CMC	7:A:401:HEM:HBC2	2.45	0.46
1:B:64:LEU:HD21	1:B:75:ILE:HA	1.97	0.46
10:B:419:GOL:H32	13:B:639:HOH:O	2.17	0.45
7:A:401:HEM:HBB2	7:A:401:HEM:HHC	1.99	0.45
4:G:3:BMA:H2	4:G:6:MAN:H2	1.98	0.45
1:B:22:PRO:HG2	1:B:77[A]:THR:CG2	2.48	0.44
1:A:65:PRO:HB3	8:A:402:EPE:H21	1.99	0.44
1:B:298:LEU:C	1:B:298:LEU:HD23	2.44	0.43
1:C:227:THR:HG22	13:C:640:HOH:O	2.19	0.43
1:A:22:PRO:HG2	1:A:77[A]:THR:CG2	2.49	0.43
1:C:298:LEU:C	1:C:298:LEU:HD23	2.44	0.43
13:A:628:HOH:O	10:C:420:GOL:H31	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77[A]:THR:HG21	13:A:739:HOH:O	2.19	0.42
5:H:1:NAG:C1	5:H:1:NAG:H82	2.50	0.42
1:C:170:ARG:HD2	1:C:171:TYR:CZ	2.54	0.42
1:C:22:PRO:HG2	1:C:77[A]:THR:CG2	2.48	0.42
1:A:64:LEU:HD21	1:A:75:ILE:HA	2.00	0.42
1:A:298:LEU:HD23	1:A:298:LEU:C	2.44	0.42
1:A:44:ARG:HH12	8:A:402:EPE:H72	1.84	0.41
1:B:296:CYS:HB2	10:B:420:GOL:C1	2.50	0.41
1:B:215:PHE:N	1:B:216:PRO:CD	2.83	0.41
1:C:319:ARG:HD2	13:C:661:HOH:O	2.20	0.41
1:A:332:VAL:HG13	1:A:336:PHE:CD2	2.55	0.41
1:A:215:PHE:N	1:A:216:PRO:CD	2.83	0.41
7:A:401:HEM:HBC2	7:A:401:HEM:HMC2	2.03	0.41
1:C:152:ASP:OD1	1:C:152:ASP:C	2.64	0.40
1:C:271:VAL:HG11	1:C:285[B]:GLU:CD	2.46	0.40
1:C:332:VAL:HG13	1:C:336:PHE:CD2	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	339/335 (101%)	331 (98%)	7 (2%)	1 (0%)	36	35
1	B	337/335 (101%)	329 (98%)	7 (2%)	1 (0%)	36	35
1	C	337/335 (101%)	328 (97%)	8 (2%)	1 (0%)	36	35
All	All	1013/1005 (101%)	988 (98%)	22 (2%)	3 (0%)	36	35

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	257	SER

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Mol	Chain	Res	Type
1	B	257	SER
1	C	257	SER

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	280/274 (102%)	280 (100%)	0	100	100
1	B	278/274 (102%)	278 (100%)	0	100	100
1	C	278/274 (102%)	278 (100%)	0	100	100
All	All	836/822 (102%)	836 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	200	GLN
1	B	200	GLN
1	B	281	ASN
1	C	263	GLN
1	C	281	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

30 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	D	1	1,2	14,14,15	0.40	0	17,19,21	1.10	1 (5%)
2	NAG	D	2	2	14,14,15	0.28	0	17,19,21	0.94	1 (5%)
2	BMA	D	3	2	11,11,12	0.47	0	15,15,17	0.76	0
2	MAN	D	4	2	11,11,12	1.01	1 (9%)	15,15,17	1.06	1 (6%)
2	MAN	D	5	2	11,11,12	0.77	0	15,15,17	1.12	2 (13%)
3	NAG	E	1	3,1	14,14,15	0.39	0	17,19,21	0.74	0
3	NAG	E	2	3	14,14,15	0.37	0	17,19,21	0.94	2 (11%)
3	BMA	E	3	3	11,11,12	0.27	0	15,15,17	1.07	1 (6%)
3	MAN	E	4	3	11,11,12	0.71	0	15,15,17	0.96	0
3	MAN	E	5	3	11,11,12	0.55	0	15,15,17	0.50	0
3	MAN	E	6	3	11,11,12	0.65	0	15,15,17	0.96	2 (13%)
3	MAN	E	7	3	11,11,12	0.46	0	15,15,17	0.78	0
2	NAG	F	1	1,2	14,14,15	0.43	0	17,19,21	2.36	5 (29%)
2	NAG	F	2	2	14,14,15	0.30	0	17,19,21	0.77	1 (5%)
2	BMA	F	3	2	11,11,12	0.80	0	15,15,17	0.62	0
2	MAN	F	4	2	11,11,12	1.25	2 (18%)	15,15,17	1.25	2 (13%)
2	MAN	F	5	2	11,11,12	1.23	1 (9%)	15,15,17	1.51	2 (13%)
4	NAG	G	1	1,4	14,14,15	0.34	0	17,19,21	0.73	0
4	NAG	G	2	4	14,14,15	0.34	0	17,19,21	0.72	0
4	BMA	G	3	4	11,11,12	0.50	0	15,15,17	1.31	3 (20%)
4	MAN	G	4	4	11,11,12	0.73	0	15,15,17	1.68	2 (13%)
4	MAN	G	5	4	11,11,12	0.54	0	15,15,17	0.77	0
4	MAN	G	6	4	11,11,12	0.69	0	15,15,17	1.35	1 (6%)
5	NAG	H	1	5,1	14,14,15	0.45	0	17,19,21	1.72	3 (17%)
5	NAG	H	2	5	14,14,15	0.42	0	17,19,21	0.88	1 (5%)
5	BMA	H	3	5	11,11,12	1.00	1 (9%)	15,15,17	0.99	1 (6%)
5	MAN	H	4	5	11,11,12	1.19	1 (9%)	15,15,17	0.87	1 (6%)
6	NAG	I	1	6,1	14,14,15	0.29	0	17,19,21	0.60	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	I	2	6	14,14,15	0.44	0	17,19,21	1.32	2 (11%)
6	BMA	I	3	6	11,11,12	0.38	0	15,15,17	0.69	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	D	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	0/6/23/26	0/1/1/1
2	BMA	D	3	2	-	0/2/19/22	0/1/1/1
2	MAN	D	4	2	-	0/2/19/22	0/1/1/1
2	MAN	D	5	2	-	0/2/19/22	0/1/1/1
3	NAG	E	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	1/6/23/26	0/1/1/1
3	BMA	E	3	3	-	0/2/19/22	0/1/1/1
3	MAN	E	4	3	-	2/2/19/22	0/1/1/1
3	MAN	E	5	3	-	2/2/19/22	0/1/1/1
3	MAN	E	6	3	-	2/2/19/22	0/1/1/1
3	MAN	E	7	3	-	2/2/19/22	0/1/1/1
2	NAG	F	1	1,2	-	1/6/23/26	0/1/1/1
2	NAG	F	2	2	-	0/6/23/26	0/1/1/1
2	BMA	F	3	2	-	0/2/19/22	0/1/1/1
2	MAN	F	4	2	-	0/2/19/22	0/1/1/1
2	MAN	F	5	2	-	0/2/19/22	0/1/1/1
4	NAG	G	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	G	2	4	-	0/6/23/26	0/1/1/1
4	BMA	G	3	4	-	0/2/19/22	0/1/1/1
4	MAN	G	4	4	-	1/2/19/22	0/1/1/1
4	MAN	G	5	4	-	2/2/19/22	0/1/1/1
4	MAN	G	6	4	-	2/2/19/22	0/1/1/1
5	NAG	H	1	5,1	-	3/6/23/26	0/1/1/1
5	NAG	H	2	5	-	3/6/23/26	0/1/1/1
5	BMA	H	3	5	-	2/2/19/22	0/1/1/1
5	MAN	H	4	5	-	0/2/19/22	0/1/1/1
6	NAG	I	1	6,1	-	2/6/23/26	0/1/1/1
6	NAG	I	2	6	-	0/6/23/26	0/1/1/1
6	BMA	I	3	6	-	2/2/19/22	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	4	MAN	C2-C3	2.97	1.57	1.52
5	H	4	MAN	O5-C5	2.94	1.49	1.43
2	F	5	MAN	O5-C5	2.85	1.49	1.43
2	F	4	MAN	O5-C5	2.60	1.48	1.43
2	D	4	MAN	C2-C3	2.40	1.56	1.52
5	H	3	BMA	C2-C3	2.26	1.55	1.52

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	1	NAG	C1-C2-N2	7.78	122.69	110.43
5	H	1	NAG	C1-C2-N2	4.45	117.45	110.43
4	G	6	MAN	C1-C2-C3	4.29	115.89	109.64
2	F	5	MAN	C1-C2-C3	4.16	115.70	109.64
2	F	1	NAG	O5-C1-C2	-3.93	105.22	111.29
2	F	5	MAN	C1-O5-C5	3.85	117.34	112.19
4	G	4	MAN	C3-C4-C5	3.81	117.14	110.23
4	G	4	MAN	C1-O5-C5	3.44	116.80	112.19
2	F	4	MAN	C1-O5-C5	3.39	116.73	112.19
6	I	2	NAG	C4-C3-C2	3.19	115.69	111.02
2	D	4	MAN	O2-C2-C3	3.15	116.69	110.15
3	E	3	BMA	O2-C2-C3	3.14	116.66	110.15
2	D	2	NAG	C1-C2-N2	3.11	115.33	110.43
5	H	1	NAG	C2-N2-C7	3.08	127.02	122.90
4	G	3	BMA	O2-C2-C3	2.98	116.32	110.15
5	H	3	BMA	C1-O5-C5	2.93	116.12	112.19
2	D	5	MAN	C1-C2-C3	2.82	113.75	109.64
5	H	1	NAG	C1-O5-C5	2.80	115.94	112.19
2	F	4	MAN	O2-C2-C3	2.61	115.56	110.15
3	E	2	NAG	C1-O5-C5	2.58	115.65	112.19
6	I	2	NAG	O5-C5-C4	-2.58	104.56	110.83
2	D	5	MAN	C1-O5-C5	2.56	115.62	112.19
3	E	6	MAN	C1-C2-C3	2.50	113.28	109.64
3	E	6	MAN	C1-O5-C5	2.47	115.50	112.19
2	F	2	NAG	C2-N2-C7	2.35	126.05	122.90
2	F	1	NAG	C1-O5-C5	2.32	115.30	112.19
2	D	1	NAG	C1-C2-N2	-2.25	106.88	110.43
5	H	2	NAG	O5-C1-C2	-2.23	107.83	111.29
4	G	3	BMA	O3-C3-C2	2.23	114.61	110.05
4	G	3	BMA	C1-O5-C5	2.23	115.17	112.19
2	F	1	NAG	C4-C3-C2	-2.19	107.81	111.02
3	E	2	NAG	C1-C2-N2	2.10	113.74	110.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	H	4	MAN	C1-O5-C5	2.05	114.94	112.19
2	F	1	NAG	C2-N2-C7	2.04	125.63	122.90

There are no chirality outliers.

All (29) torsion outliers are listed below:

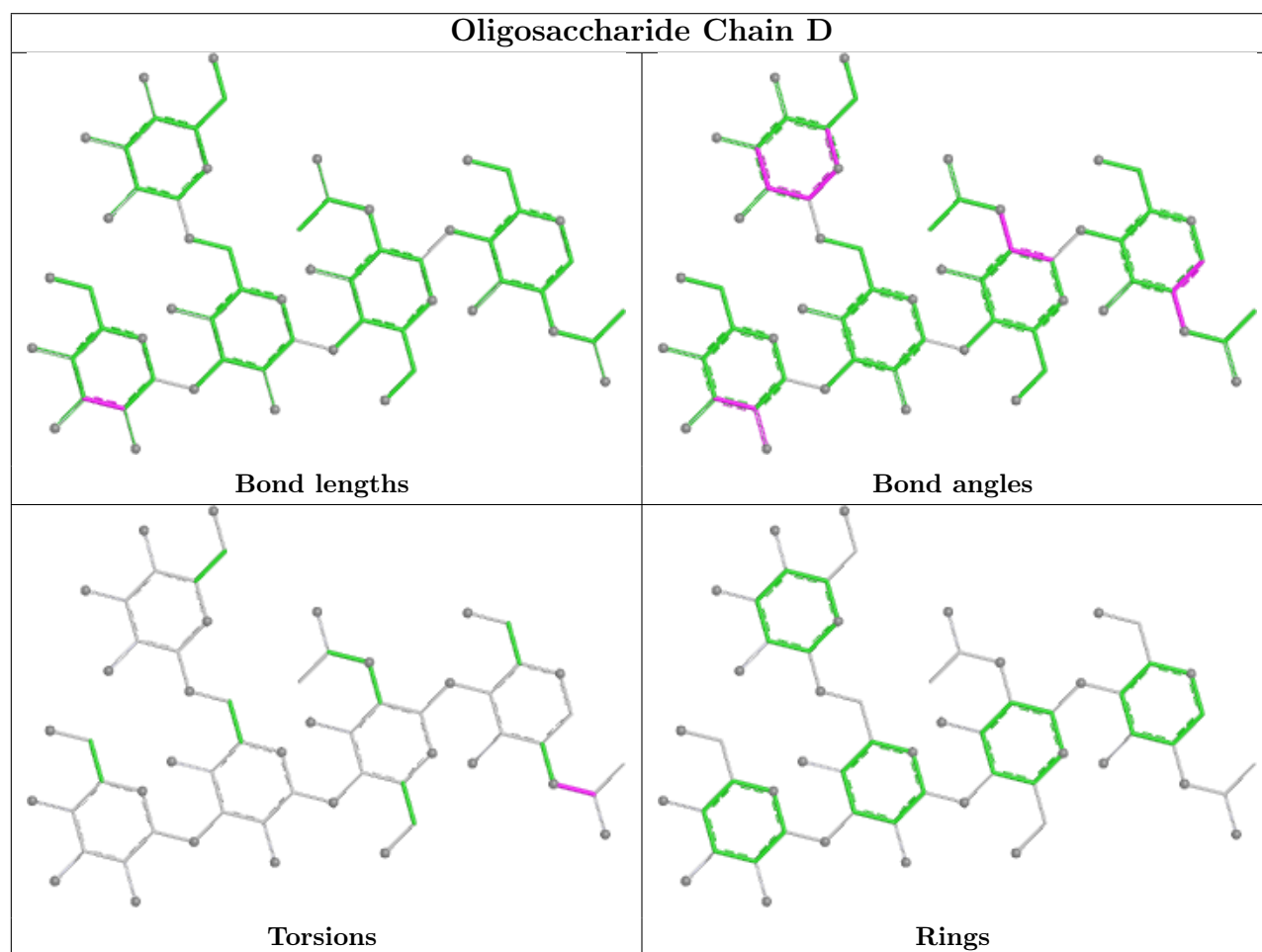
Mol	Chain	Res	Type	Atoms
2	F	1	NAG	C1-C2-N2-C7
5	H	1	NAG	C1-C2-N2-C7
5	H	1	NAG	C8-C7-N2-C2
5	H	1	NAG	O7-C7-N2-C2
4	G	6	MAN	O5-C5-C6-O6
3	E	7	MAN	O5-C5-C6-O6
4	G	6	MAN	C4-C5-C6-O6
5	H	3	BMA	O5-C5-C6-O6
6	I	1	NAG	C8-C7-N2-C2
3	E	5	MAN	C4-C5-C6-O6
3	E	7	MAN	C4-C5-C6-O6
3	E	5	MAN	O5-C5-C6-O6
5	H	3	BMA	C4-C5-C6-O6
2	D	1	NAG	C8-C7-N2-C2
6	I	1	NAG	O7-C7-N2-C2
4	G	5	MAN	C4-C5-C6-O6
6	I	3	BMA	O5-C5-C6-O6
2	D	1	NAG	O7-C7-N2-C2
5	H	2	NAG	C8-C7-N2-C2
4	G	5	MAN	O5-C5-C6-O6
3	E	6	MAN	C4-C5-C6-O6
4	G	4	MAN	O5-C5-C6-O6
5	H	2	NAG	O7-C7-N2-C2
6	I	3	BMA	C4-C5-C6-O6
3	E	6	MAN	O5-C5-C6-O6
3	E	4	MAN	C4-C5-C6-O6
3	E	2	NAG	O5-C5-C6-O6
5	H	2	NAG	C4-C5-C6-O6
3	E	4	MAN	O5-C5-C6-O6

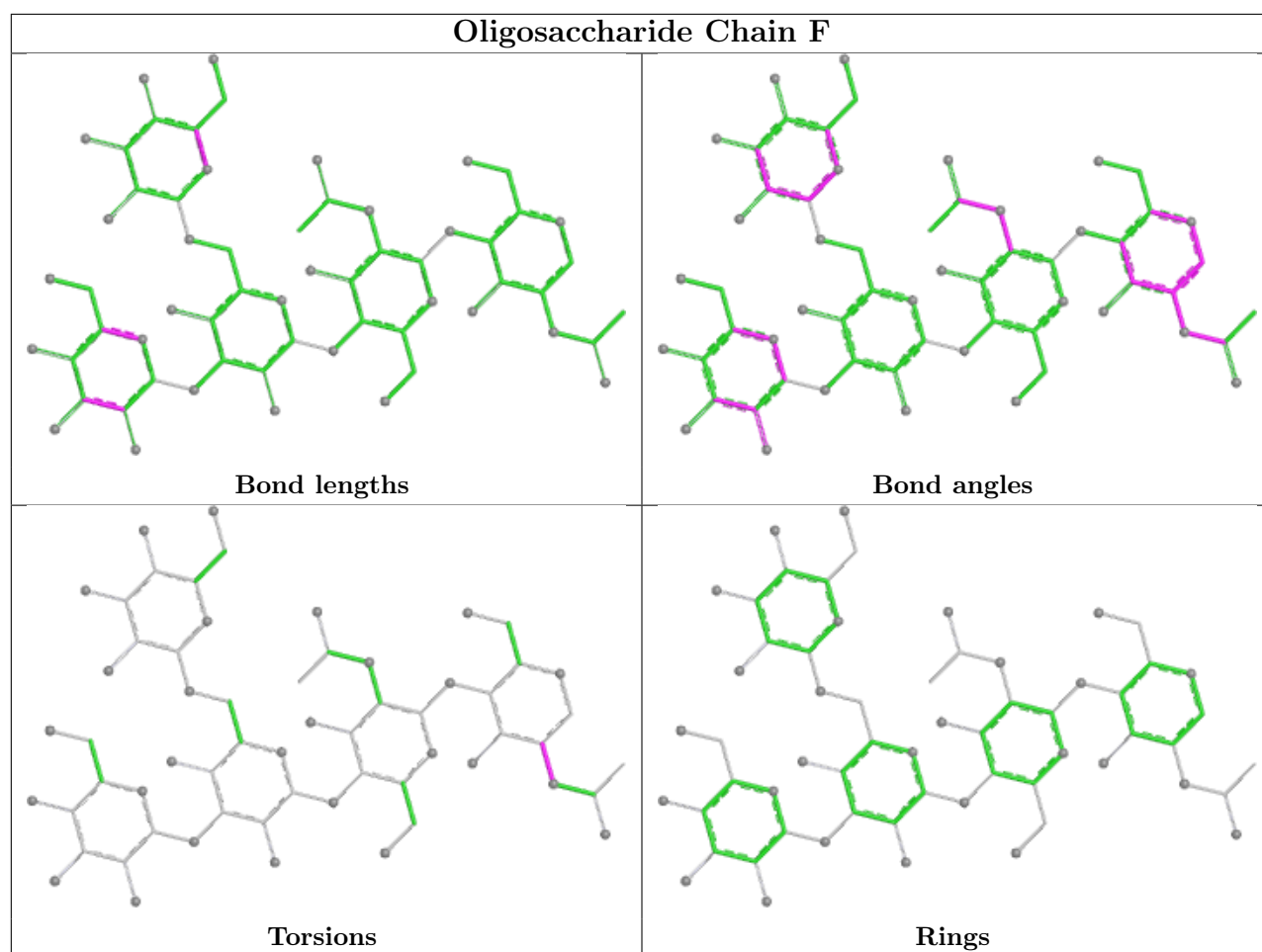
There are no ring outliers.

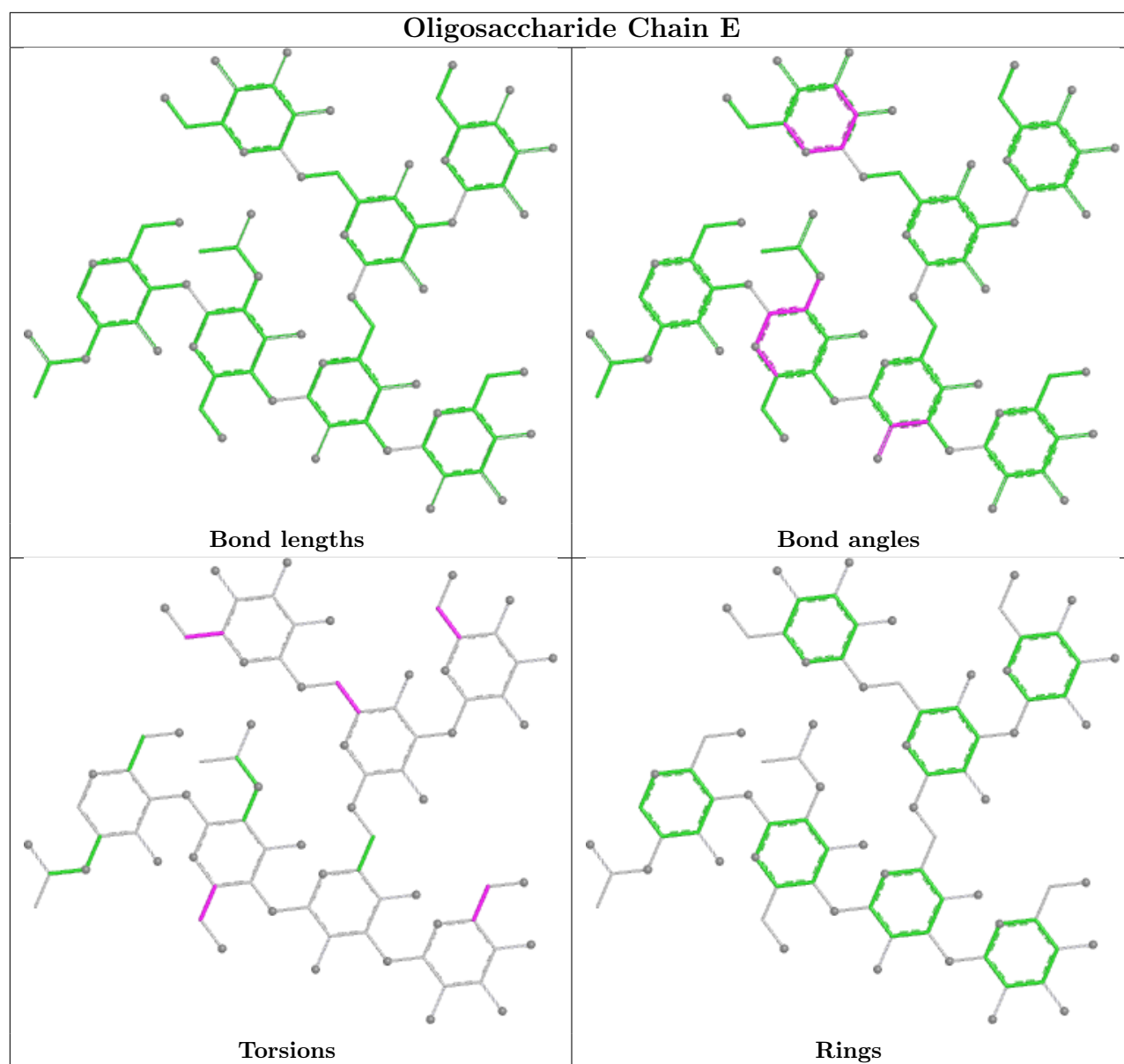
4 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	6	MAN	1	0
5	H	1	NAG	1	0
4	G	3	BMA	1	0
2	D	3	BMA	1	0

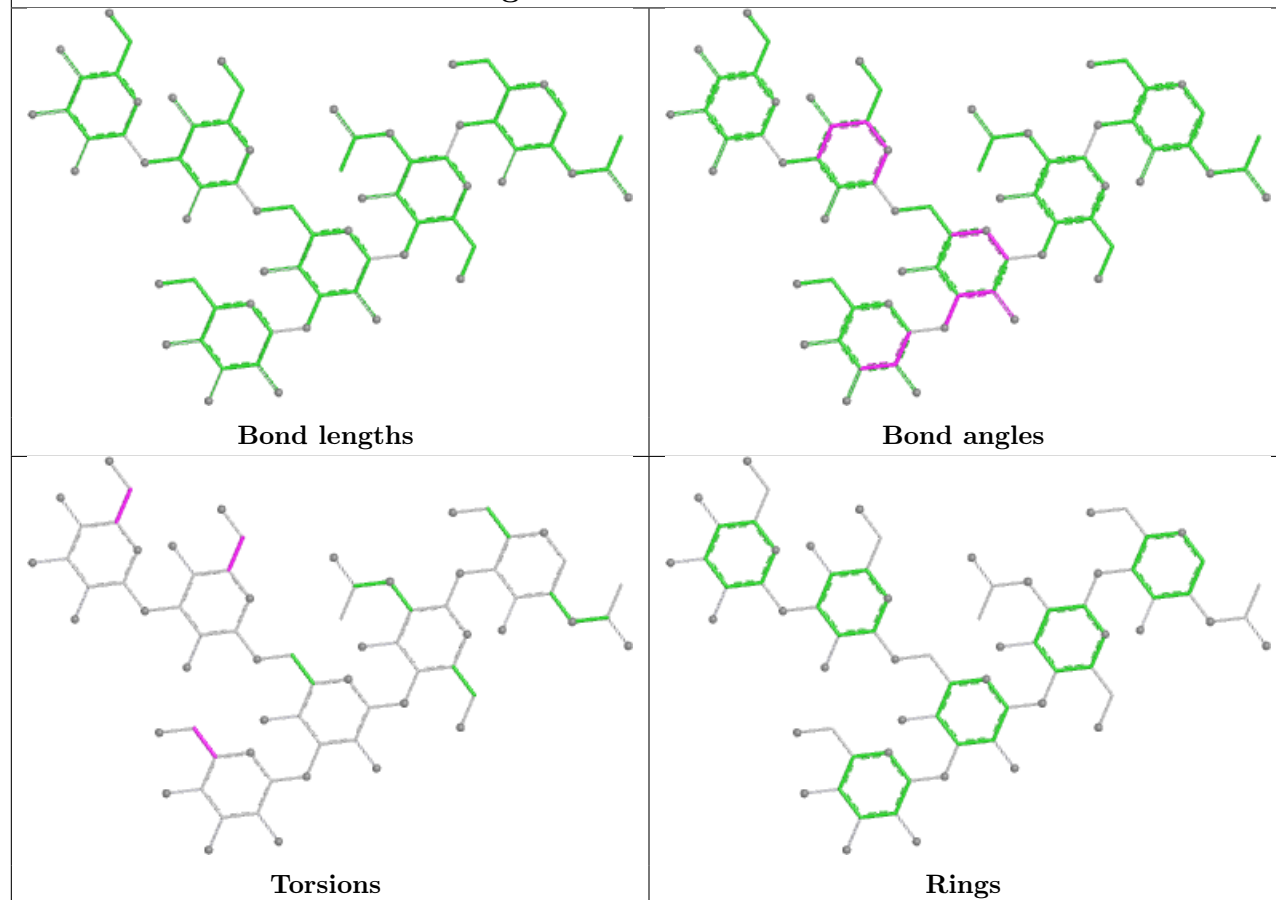
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



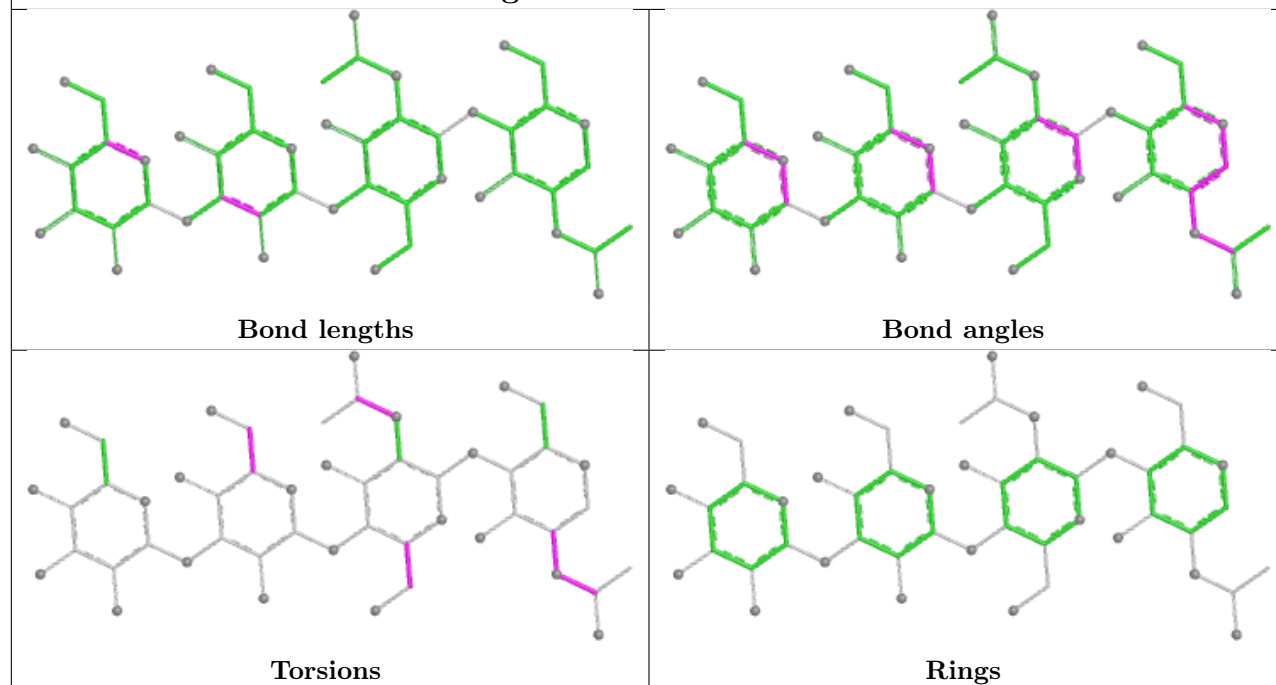


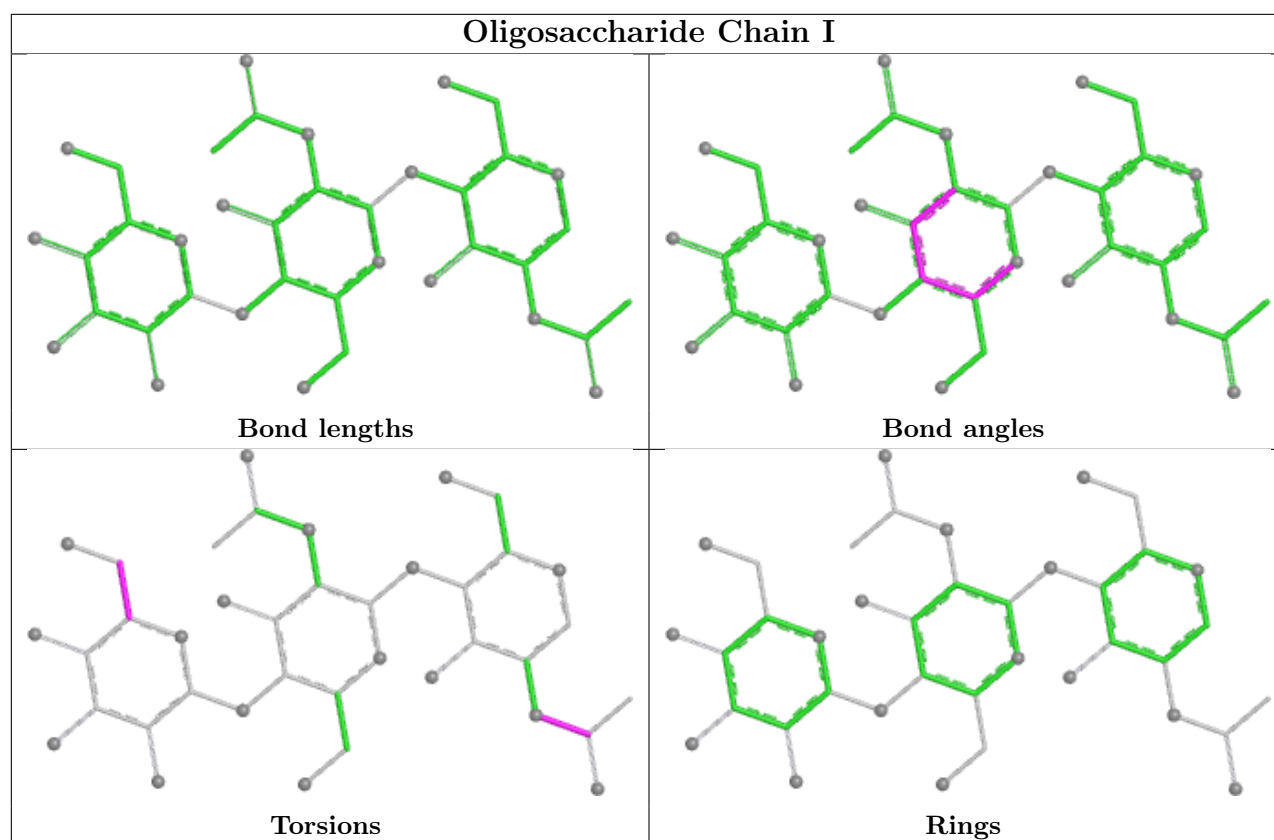


Oligosaccharide Chain G



Oligosaccharide Chain H





5.6 Ligand geometry [i](#)

Of 25 ligands modelled in this entry, 3 are monoatomic - leaving 22 for Mogul analysis.

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$
9	FUX	B	413	-	9,9,9	0.38	0	11,11,11	0.72	0
8	EPE	A	410	-	15,15,15	1.32	1 (6%)	19,20,20	0.95	1 (5%)
10	GOL	A	411	-	5,5,5	0.24	0	5,5,5	0.40	0
10	GOL	C	420	-	5,5,5	0.20	0	5,5,5	0.28	0
12	SO4	B	417	-	4,4,4	0.32	0	6,6,6	0.19	0
12	SO4	B	418	-	4,4,4	0.18	0	6,6,6	0.33	0
8	EPE	B	402	-	15,15,15	1.06	1 (6%)	19,20,20	1.07	2 (10%)
10	GOL	B	419	-	5,5,5	0.24	0	5,5,5	0.39	0
12	SO4	C	417	-	4,4,4	0.21	0	6,6,6	0.06	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	FUX	C	412	7	9,9,9	0.90	1 (11%)	11,11,11	0.42	0
12	SO4	C	418	-	4,4,4	0.32	0	6,6,6	0.15	0
9	FUX	A	408	-	9,9,9	0.43	0	11,11,11	0.26	0
9	FUX	B	412	7	9,9,9	0.54	0	11,11,11	0.49	0
7	HEM	C	414	11,1,9	50,50,50	1.51	10 (20%)	67,82,82	1.77	17 (25%)
10	GOL	C	419	-	5,5,5	0.26	0	5,5,5	0.44	0
7	HEM	B	414	11,1,9	50,50,50	1.49	12 (24%)	67,82,82	1.91	20 (29%)
9	FUX	A	409	7	9,9,9	0.99	1 (11%)	11,11,11	0.48	0
12	SO4	A	413	-	4,4,4	0.28	0	6,6,6	0.26	0
7	HEM	A	401	11,1,9	50,50,50	1.57	13 (26%)	67,82,82	1.85	16 (23%)
10	GOL	B	420	-	5,5,5	0.09	0	5,5,5	0.30	0
9	FUX	C	413	-	9,9,9	0.62	0	11,11,11	0.66	0
8	EPE	A	402	-	15,15,15	1.26	1 (6%)	19,20,20	1.45	3 (15%)

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
9	FUX	B	413	-	-	2/4/4/4	0/1/1/1
8	EPE	A	410	-	-	7/9/19/19	0/1/1/1
10	GOL	A	411	-	-	2/4/4/4	-
10	GOL	C	420	-	-	1/4/4/4	-
9	FUX	B	412	7	-	2/4/4/4	0/1/1/1
7	HEM	C	414	11,1,9	-	2/14/54/54	-
8	EPE	B	402	-	-	6/9/19/19	0/1/1/1
7	HEM	A	401	11,1,9	-	2/14/54/54	-
9	FUX	C	412	7	-	2/4/4/4	0/1/1/1
10	GOL	B	420	-	-	4/4/4/4	-
7	HEM	B	414	11,1,9	-	2/14/54/54	-
10	GOL	C	419	-	-	0/4/4/4	-
9	FUX	A	409	7	-	2/4/4/4	0/1/1/1
10	GOL	B	419	-	-	1/4/4/4	-
9	FUX	C	413	-	-	0/4/4/4	0/1/1/1
9	FUX	A	408	-	-	2/4/4/4	0/1/1/1
8	EPE	A	402	-	-	5/9/19/19	0/1/1/1

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	402	EPE	O3S-S	4.60	1.64	1.47
8	A	410	EPE	O3S-S	4.56	1.64	1.47
7	C	414	HEM	FE-NC	4.36	2.09	1.95
7	B	414	HEM	FE-NB	4.21	2.07	1.94
7	A	401	HEM	FE-NC	3.93	2.08	1.95
7	A	401	HEM	C1B-NB	-3.56	1.34	1.40
7	B	414	HEM	C1B-NB	-3.54	1.34	1.40
8	B	402	EPE	O3S-S	3.43	1.60	1.47
7	C	414	HEM	C1B-NB	-3.24	1.34	1.40
7	C	414	HEM	FE-NB	3.15	2.04	1.94
7	A	401	HEM	O1A-CGA	3.11	1.32	1.22
7	B	414	HEM	FE-NC	2.98	2.05	1.95
7	B	414	HEM	C1D-ND	-2.89	1.33	1.38
7	A	401	HEM	FE-NB	2.62	2.03	1.94
7	A	401	HEM	C4D-ND	-2.53	1.35	1.40
7	A	401	HEM	C3C-C4C	-2.51	1.41	1.46
7	B	414	HEM	C3C-C4C	-2.49	1.41	1.46
7	A	401	HEM	C1C-NC	-2.44	1.35	1.39
9	A	409	FUX	OXT-C1	2.43	1.27	1.22
7	C	414	HEM	C4D-ND	-2.40	1.36	1.40
7	B	414	HEM	C1A-C2A	-2.32	1.39	1.44
7	B	414	HEM	C4B-NB	-2.32	1.34	1.38
9	C	412	FUX	OXT-C1	2.28	1.27	1.22
7	B	414	HEM	C1C-C2C	-2.28	1.40	1.45
7	A	401	HEM	C4B-NB	-2.27	1.34	1.38
7	A	401	HEM	C1D-ND	-2.26	1.34	1.38
7	C	414	HEM	C1C-C2C	-2.24	1.40	1.45
7	C	414	HEM	C2A-C3A	-2.24	1.33	1.38
7	B	414	HEM	C1C-NC	-2.21	1.35	1.39
7	A	401	HEM	C3B-C4B	2.19	1.49	1.44
7	C	414	HEM	CBD-CGD	2.19	1.55	1.50
7	B	414	HEM	C3B-C4B	2.18	1.49	1.44
7	C	414	HEM	C3B-C4B	2.17	1.49	1.44
7	A	401	HEM	C1C-C2C	-2.14	1.41	1.45
7	B	414	HEM	O1A-CGA	2.07	1.28	1.22
7	A	401	HEM	C1A-NA	-2.06	1.35	1.39
7	C	414	HEM	FE-ND	-2.02	1.88	1.94
7	A	401	HEM	C4A-NA	-2.02	1.35	1.39
7	B	414	HEM	C4D-ND	-2.02	1.36	1.40
7	C	414	HEM	C1A-NA	-2.00	1.35	1.39

All (59) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	401	HEM	CHC-C4B-NB	5.21	130.03	124.42
7	A	401	HEM	C3B-C4B-NB	-4.87	105.97	109.47
7	B	414	HEM	CHC-C4B-NB	4.29	129.04	124.42
7	B	414	HEM	CHD-C4C-NC	4.22	129.05	124.45
7	C	414	HEM	CHB-C1B-NB	4.21	129.58	124.37
7	C	414	HEM	CHC-C4B-NB	4.12	128.86	124.42
7	B	414	HEM	CAA-CBA-CGA	-4.08	102.85	113.67
7	A	401	HEM	CHB-C1B-NB	4.06	129.38	124.37
7	C	414	HEM	CHD-C4C-NC	4.02	128.84	124.45
8	A	402	EPE	O3S-S-O1S	-3.90	101.63	111.40
7	A	401	HEM	CHD-C4C-NC	3.89	128.69	124.45
7	C	414	HEM	CHD-C1D-ND	3.77	128.48	124.42
7	A	401	HEM	C1B-NB-C4B	3.63	109.51	105.21
7	B	414	HEM	CHB-C1B-NB	3.57	128.79	124.37
7	C	414	HEM	CAA-CBA-CGA	-3.43	104.58	113.67
7	B	414	HEM	C1B-NB-C4B	3.30	109.11	105.21
7	B	414	HEM	CHD-C1D-ND	3.29	127.96	124.42
7	B	414	HEM	C3B-C4B-NB	-3.26	107.12	109.47
8	A	410	EPE	O3S-S-C10	-3.25	99.65	106.00
7	B	414	HEM	CHA-C4D-ND	3.20	128.33	124.37
7	A	401	HEM	CHD-C1D-ND	3.09	127.75	124.42
7	C	414	HEM	C3B-C4B-NB	-3.05	107.28	109.47
7	B	414	HEM	CHA-C4D-C3D	-3.02	119.65	125.23
8	B	402	EPE	O2S-S-O1S	2.99	123.54	113.82
7	C	414	HEM	C1B-NB-C4B	2.93	108.68	105.21
7	A	401	HEM	CAA-CBA-CGA	-2.86	106.07	113.67
7	B	414	HEM	O2D-CGD-CBD	2.85	123.02	114.00
8	A	402	EPE	O2S-S-O1S	2.85	123.09	113.82
7	B	414	HEM	CAD-CBD-CGD	-2.83	106.17	113.67
7	A	401	HEM	CHA-C4D-C3D	-2.77	120.12	125.23
7	C	414	HEM	C4C-CHD-C1D	-2.75	120.17	126.02
7	B	414	HEM	O2D-CGD-O1D	-2.75	116.26	123.33
7	C	414	HEM	CHD-C1D-C2D	-2.75	120.69	125.03
7	B	414	HEM	CMB-C2B-C1B	2.74	129.31	125.03
7	A	401	HEM	CHB-C1B-C2B	-2.72	119.22	126.95
7	C	414	HEM	CHB-C1B-C2B	-2.68	119.33	126.95
7	A	401	HEM	CHA-C4D-ND	2.65	127.65	124.37
7	B	414	HEM	C4C-CHD-C1D	-2.61	120.48	126.02
7	C	414	HEM	CHA-C4D-ND	2.57	127.55	124.37
7	A	401	HEM	CMB-C2B-C1B	2.57	129.04	125.03
7	C	414	HEM	O2A-CGA-CBA	2.46	121.77	114.00
7	B	414	HEM	CHD-C1D-C2D	-2.46	121.15	125.03
7	C	414	HEM	C4C-NC-C1C	2.45	109.81	105.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	C	414	HEM	CHA-C4D-C3D	-2.44	120.73	125.23
7	A	401	HEM	C4C-C3C-C2C	2.42	108.91	106.81
7	B	414	HEM	C1A-CHA-C4D	-2.41	120.58	126.25
7	B	414	HEM	O2A-CGA-CBA	2.33	121.36	114.00
7	C	414	HEM	CAD-CBD-CGD	-2.32	107.50	113.67
7	B	414	HEM	CHA-C1A-NA	2.31	128.05	123.86
7	A	401	HEM	CHA-C1A-NA	2.30	128.02	123.86
7	A	401	HEM	CHD-C1D-C2D	-2.28	121.43	125.03
7	B	414	HEM	CHB-C1B-C2B	-2.25	120.56	126.95
7	A	401	HEM	CMD-C2D-C1D	2.15	128.39	125.03
7	B	414	HEM	CAB-C3B-C2B	-2.14	121.46	128.43
8	A	402	EPE	O2S-S-C10	-2.13	103.51	106.73
7	C	414	HEM	CMB-C2B-C1B	2.08	128.29	125.03
7	C	414	HEM	CHA-C1A-NA	2.05	127.59	123.86
7	A	401	HEM	C4C-CHD-C1D	-2.02	121.73	126.02
8	B	402	EPE	O3S-S-O2S	-2.00	106.39	111.40

There are no chirality outliers.

All (42) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	402	EPE	C10-C9-N1-C2
8	A	402	EPE	C9-C10-S-O1S
8	A	402	EPE	C9-C10-S-O3S
8	A	410	EPE	C9-C10-S-O1S
8	A	410	EPE	C9-C10-S-O3S
8	B	402	EPE	C10-C9-N1-C2
9	A	409	FUX	O3-C4-C7-O8
9	B	413	FUX	OXT-C1-C2-C6
10	B	420	GOL	C1-C2-C3-O3
8	B	402	EPE	N4-C7-C8-O8
8	B	402	EPE	C9-C10-S-O3S
10	B	420	GOL	O1-C1-C2-C3
10	C	420	GOL	O1-C1-C2-C3
10	B	420	GOL	O2-C2-C3-O3
8	B	402	EPE	S-C10-C9-N1
8	A	402	EPE	N4-C7-C8-O8
10	B	420	GOL	O1-C1-C2-O2
8	A	410	EPE	C8-C7-N4-C3
8	A	410	EPE	C8-C7-N4-C5
9	A	408	FUX	C5-C4-C7-O8
10	A	411	GOL	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
10	B	419	GOL	O2-C2-C3-O3
8	A	402	EPE	C9-C10-S-O2S
8	A	410	EPE	C9-C10-S-O2S
8	B	402	EPE	C9-C10-S-O1S
8	B	402	EPE	C9-C10-S-O2S
9	A	408	FUX	O3-C4-C7-O8
8	A	410	EPE	C10-C9-N1-C2
8	A	410	EPE	C10-C9-N1-C6
7	A	401	HEM	CAA-CBA-CGA-O2A
7	A	401	HEM	CAA-CBA-CGA-O1A
7	B	414	HEM	CAA-CBA-CGA-O2A
7	B	414	HEM	CAA-CBA-CGA-O1A
7	C	414	HEM	CAA-CBA-CGA-O2A
9	A	409	FUX	C5-C4-C7-O8
9	B	412	FUX	C5-C4-C7-O8
9	C	412	FUX	C5-C4-C7-O8
9	B	412	FUX	O3-C4-C7-O8
9	B	413	FUX	O3-C4-C7-O8
9	C	412	FUX	O3-C4-C7-O8
10	A	411	GOL	O1-C1-C2-C3
7	C	414	HEM	CAA-CBA-CGA-O1A

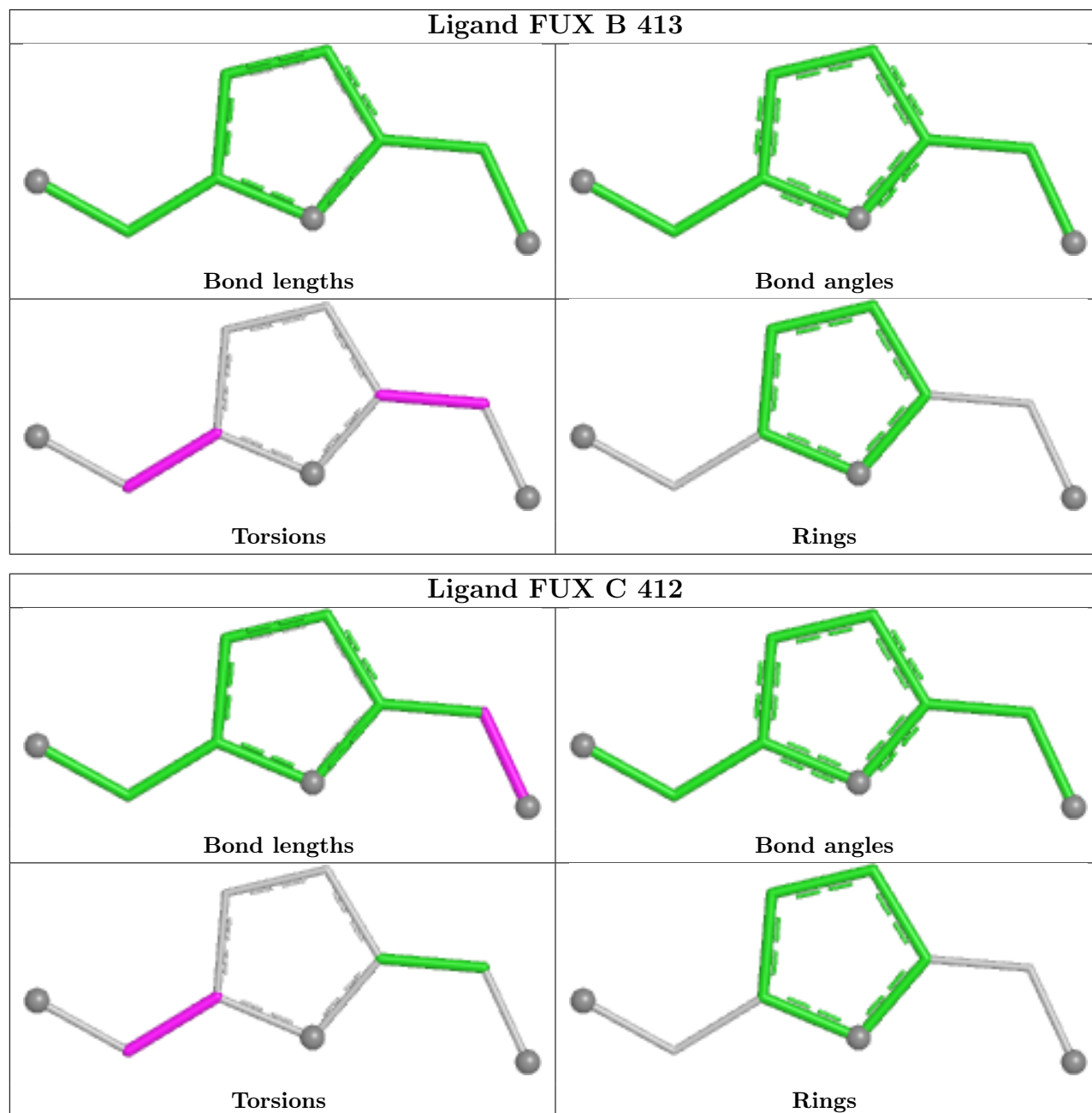
There are no ring outliers.

10 monomers are involved in 24 short contacts:

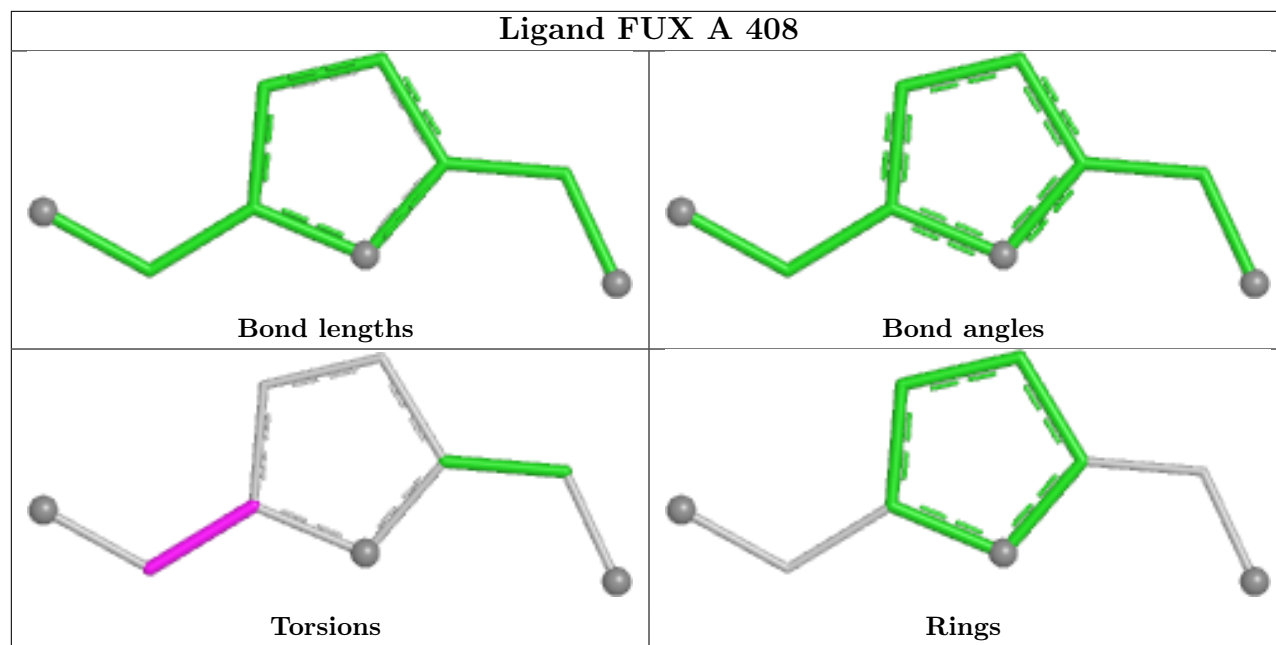
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	410	EPE	2	0
10	C	420	GOL	1	0
8	B	402	EPE	3	0
10	B	419	GOL	2	0
7	C	414	HEM	3	0
10	C	419	GOL	1	0
9	A	409	FUX	1	0
7	A	401	HEM	3	0
10	B	420	GOL	2	0
8	A	402	EPE	6	0

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.

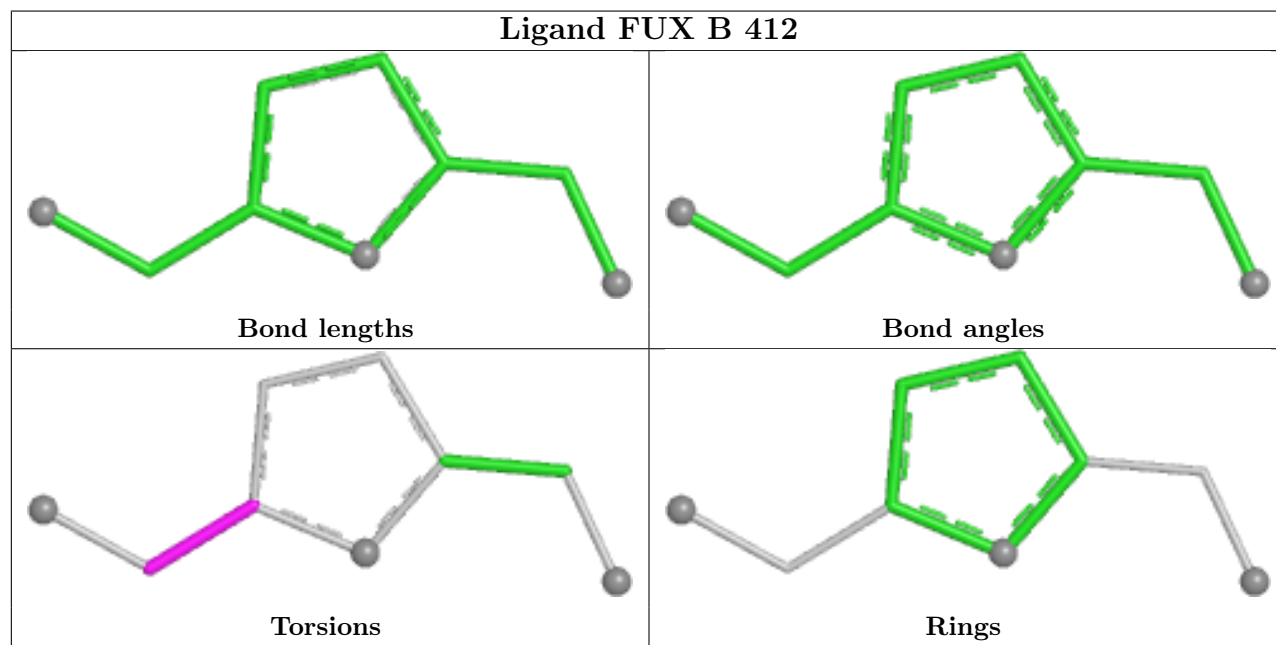
Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD 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.

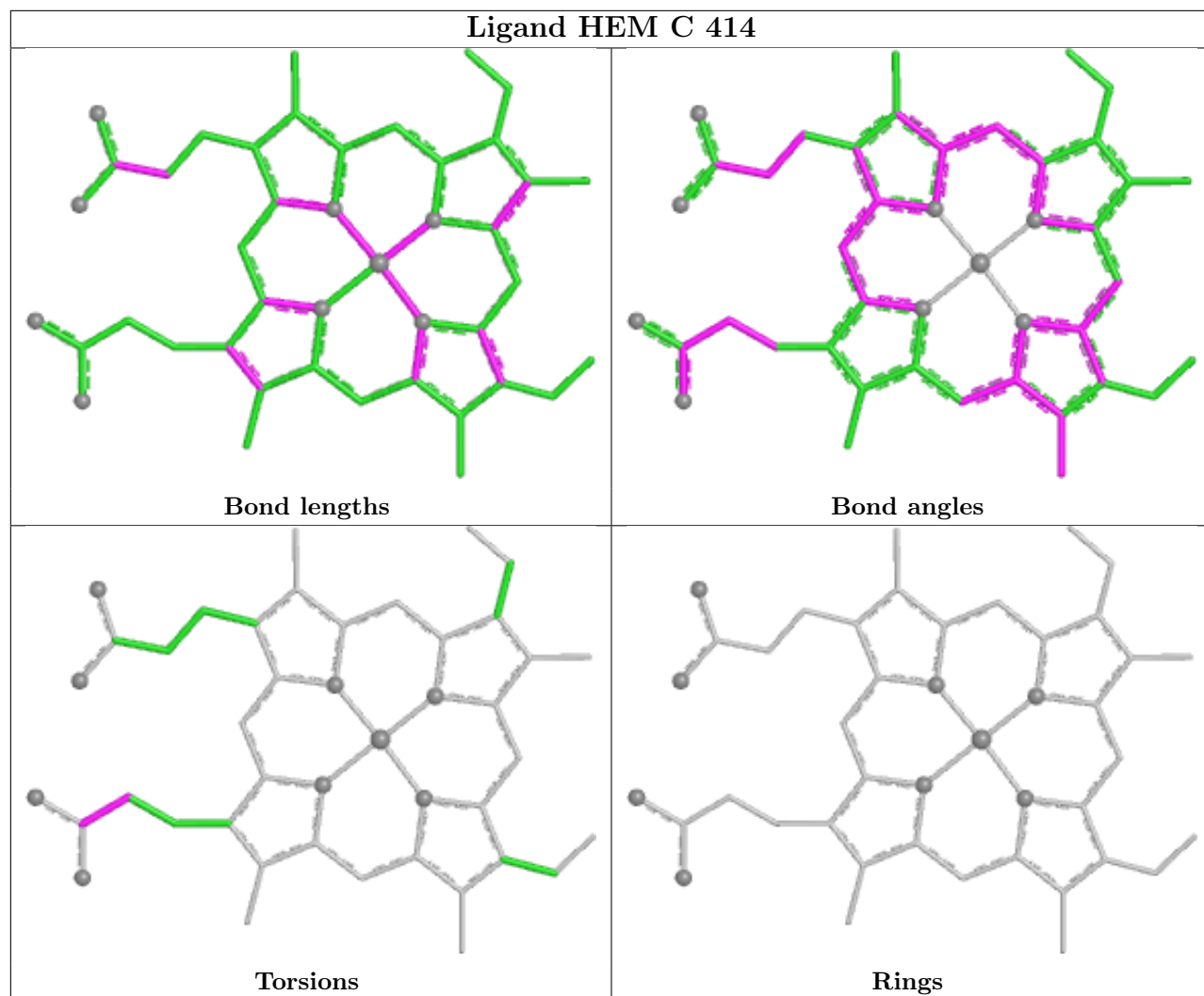


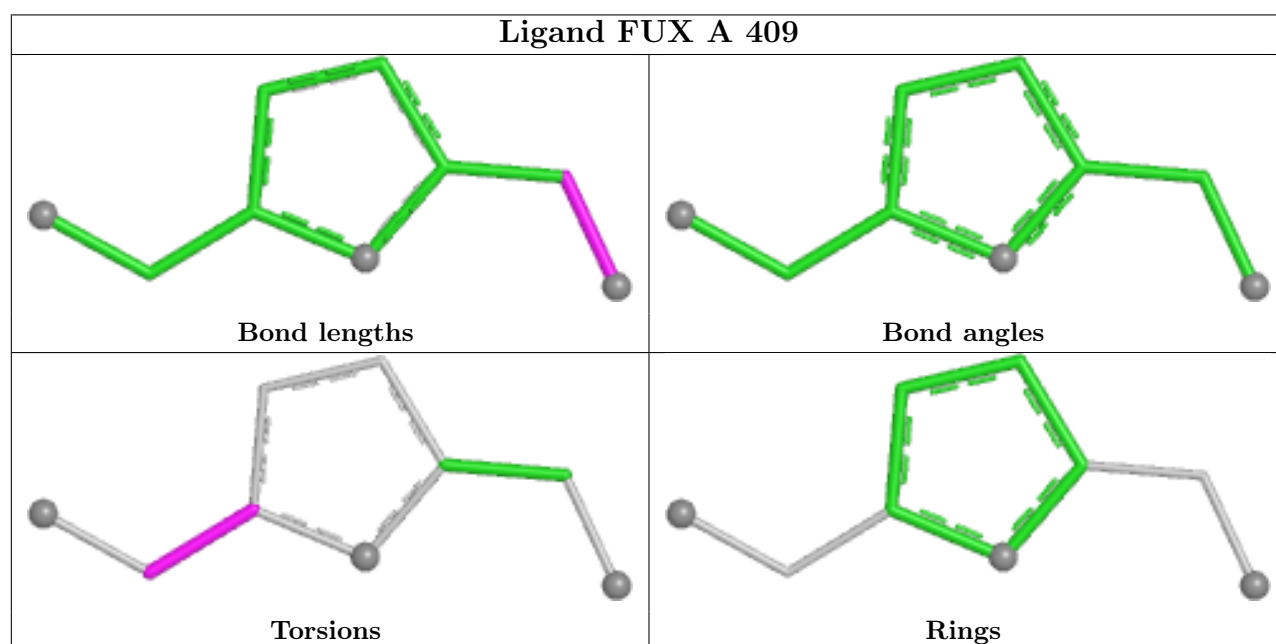
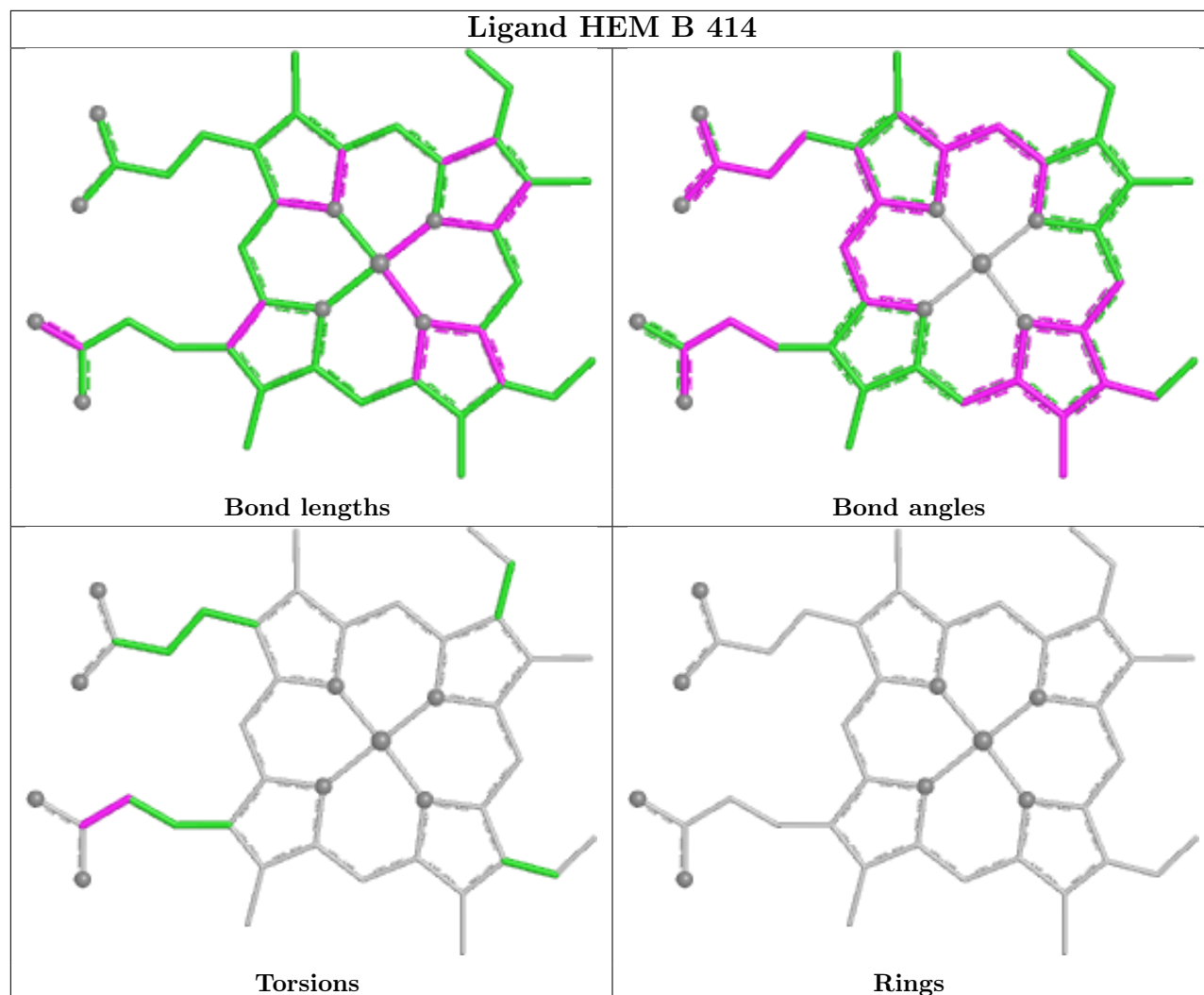
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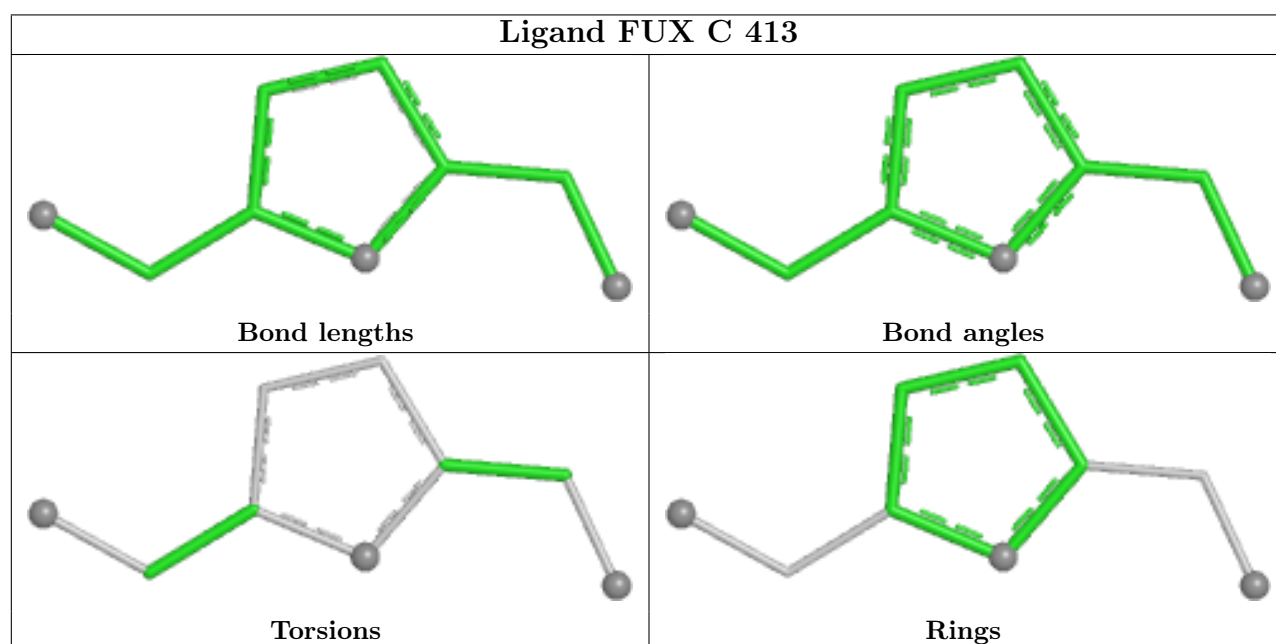
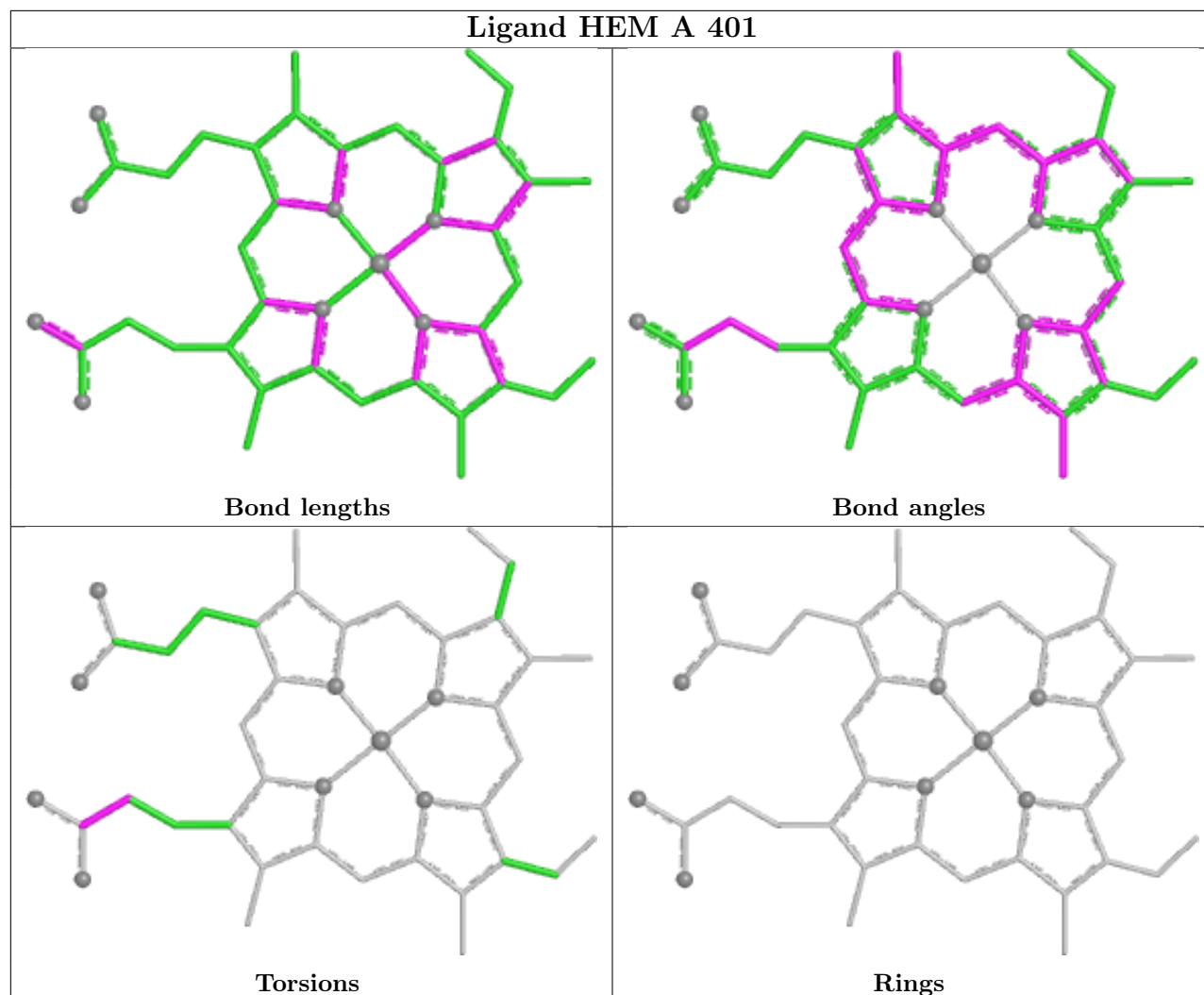


Ligand FUX B 412









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	335/335 (100%)	-0.04	8 (2%) 59 59	18, 34, 51, 114	6 (1%)
1	B	335/335 (100%)	0.31	10 (2%) 52 51	18, 40, 62, 127	4 (1%)
1	C	335/335 (100%)	0.56	19 (5%) 29 28	18, 43, 70, 142	4 (1%)
All	All	1005/1005 (100%)	0.27	37 (3%) 45 44	18, 38, 65, 142	14 (1%)

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	14	GLN	5.2
1	B	277	ASP	3.8
1	C	227	THR	3.7
1	B	348	LEU	3.6
1	B	227	THR	3.6
1	B	14	GLN	3.6
1	C	316	ILE	3.5
1	C	149	PHE	3.5
1	A	316	ILE	3.4
1	C	186	TYR	3.2
1	A	14	GLN	3.2
1	B	316	ILE	3.1
1	B	228	ASP	3.0
1	A	227	THR	3.0
1	B	15	GLY	3.0
1	C	276	ALA	2.7
1	B	278	ASN	2.7
1	A	15	GLY	2.6
1	A	45	GLU	2.4
1	B	16	VAL	2.3
1	C	287	PRO	2.3
1	A	228	ASP	2.2
1	C	146	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	136	THR	2.2
1	B	279	GLN	2.2
1	C	270	TRP	2.2
1	C	319	ARG	2.2
1	C	191	ASP	2.1
1	C	195	THR	2.1
1	C	15	GLY	2.1
1	A	226	THR	2.1
1	C	193	ILE	2.1
1	C	277	ASP	2.0
1	C	194	ALA	2.0
1	C	267	ALA	2.0
1	A	277	ASP	2.0
1	C	182	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	BMA	I	3	11/12	0.20	0.18	133,157,166,170	0
6	NAG	I	2	14/15	0.32	0.22	106,133,148,167	0
3	MAN	E	6	11/12	0.35	0.19	115,144,159,161	0
5	BMA	H	3	11/12	0.37	0.20	71,91,99,103	0
3	MAN	E	7	11/12	0.39	0.17	103,114,123,124	0
2	MAN	F	5	11/12	0.41	0.23	70,86,101,101	0
4	MAN	G	6	11/12	0.52	0.16	114,127,140,141	0
4	MAN	G	4	11/12	0.58	0.15	87,98,104,116	0
2	BMA	F	3	11/12	0.63	0.17	82,95,102,105	0
3	MAN	E	5	11/12	0.64	0.21	80,95,102,103	0
2	MAN	D	5	11/12	0.64	0.18	81,98,117,120	0
5	MAN	H	4	11/12	0.69	0.17	64,77,86,87	0
3	MAN	E	4	11/12	0.70	0.16	85,96,122,145	0
2	MAN	D	4	11/12	0.71	0.18	74,88,98,101	0

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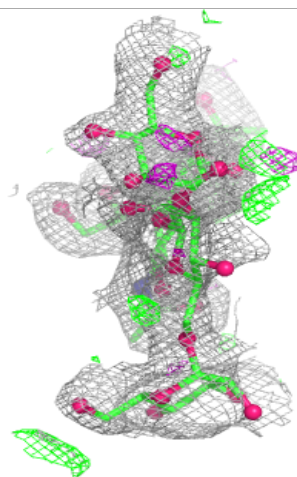
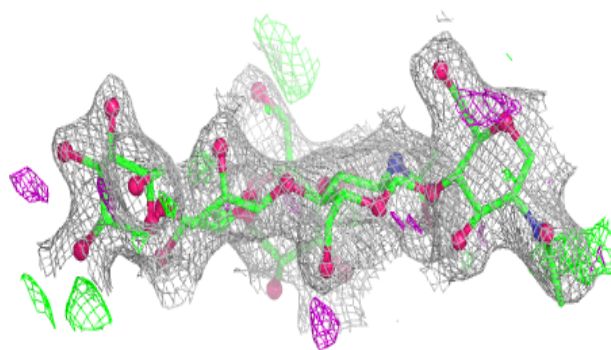
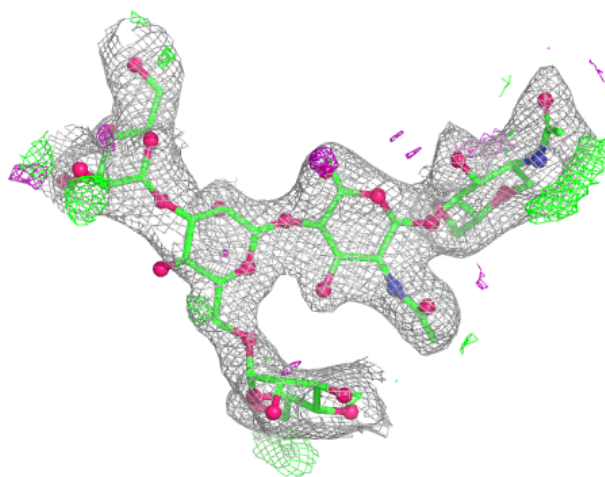
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	BMA	G	3	11/12	0.71	0.14	81,95,107,122	0
4	MAN	G	5	11/12	0.73	0.15	81,93,98,99	0
2	BMA	D	3	11/12	0.76	0.15	70,104,114,119	0
5	NAG	H	1	14/15	0.76	0.16	56,69,76,78	0
2	MAN	F	4	11/12	0.76	0.18	63,74,87,93	0
3	BMA	E	3	11/12	0.78	0.14	63,88,105,106	0
2	NAG	F	1	14/15	0.79	0.17	51,61,70,75	0
5	NAG	H	2	14/15	0.83	0.14	65,73,78,80	0
6	NAG	I	1	14/15	0.85	0.13	69,77,86,104	0
4	NAG	G	2	14/15	0.86	0.12	42,56,73,78	0
3	NAG	E	2	14/15	0.89	0.12	38,50,67,73	0
2	NAG	F	2	14/15	0.89	0.12	64,71,78,81	0
2	NAG	D	1	14/15	0.90	0.12	46,54,66,69	0
2	NAG	D	2	14/15	0.92	0.11	52,60,70,85	0
3	NAG	E	1	14/15	0.93	0.09	37,40,44,45	0
4	NAG	G	1	14/15	0.94	0.08	38,41,46,48	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.

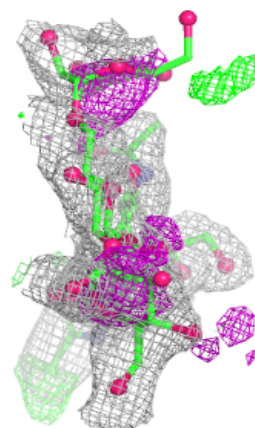
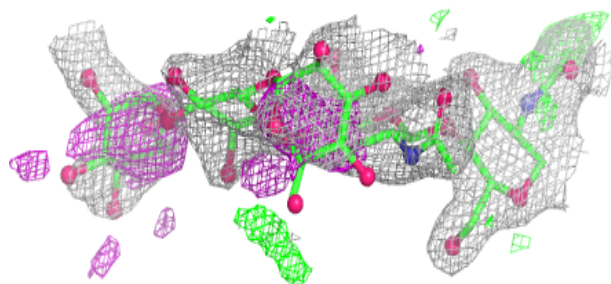
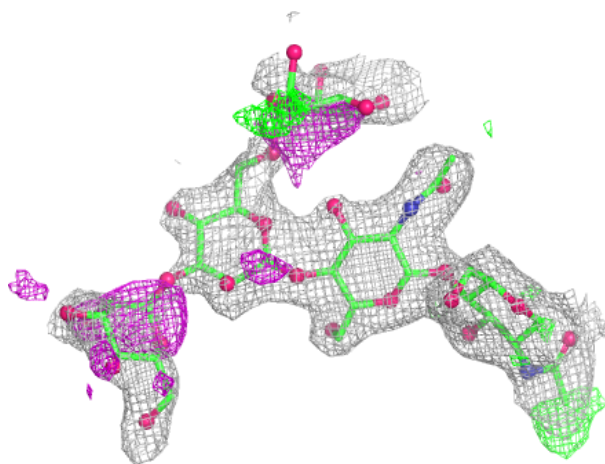
Electron density around Chain D:

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



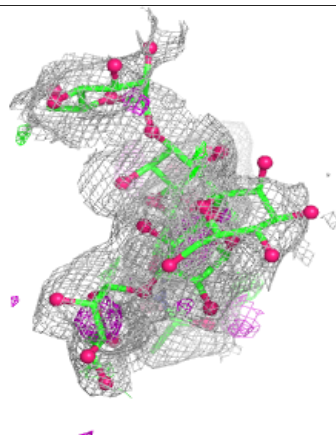
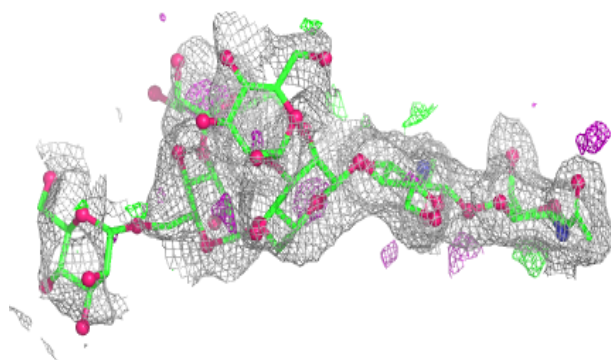
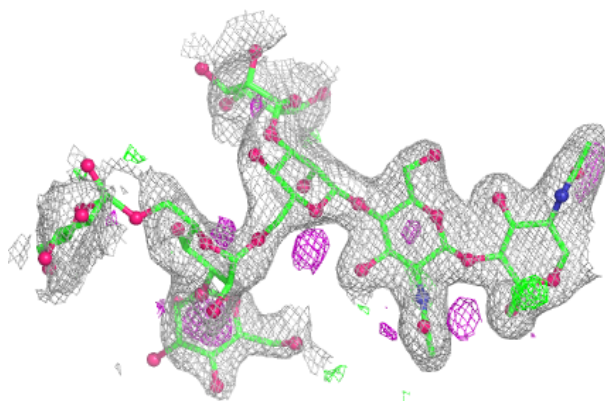
Electron density around Chain F:

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



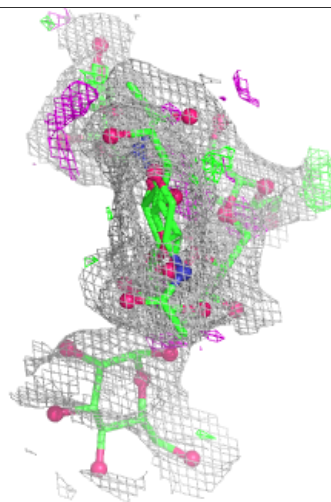
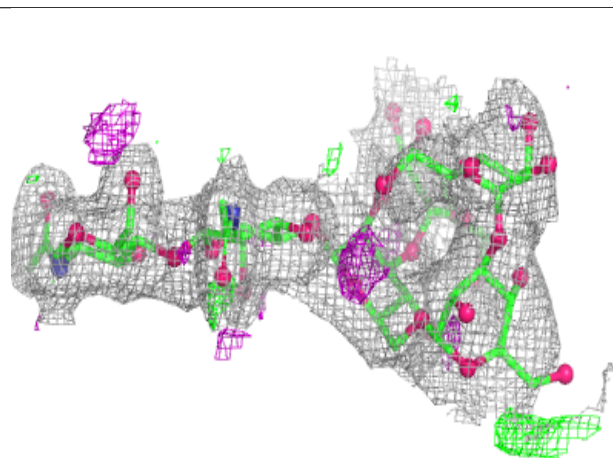
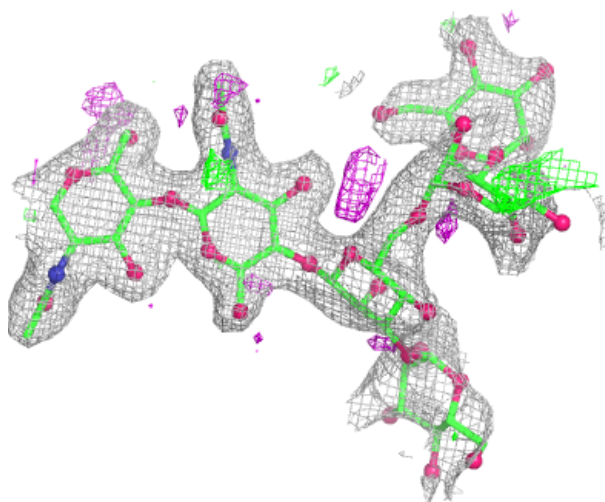
Electron density around Chain E:

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



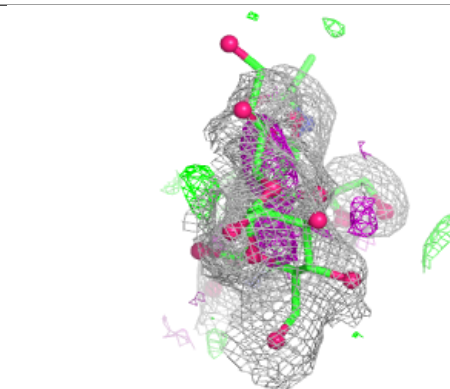
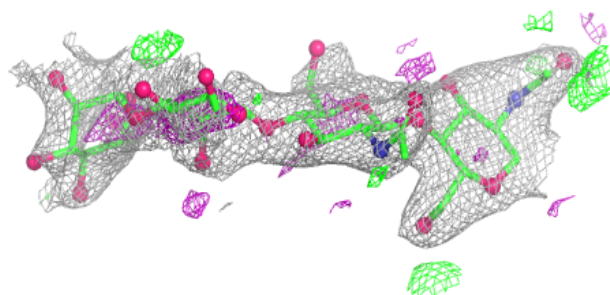
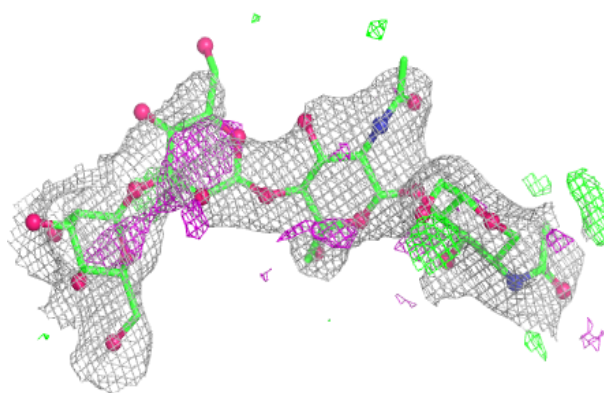
Electron density around Chain G:

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

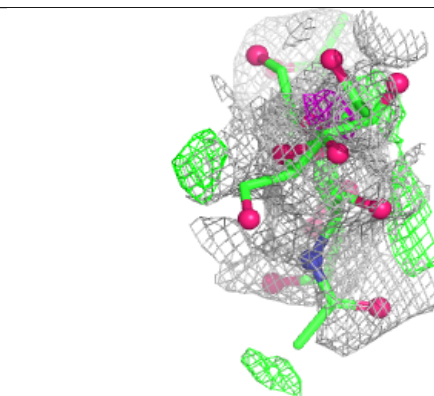
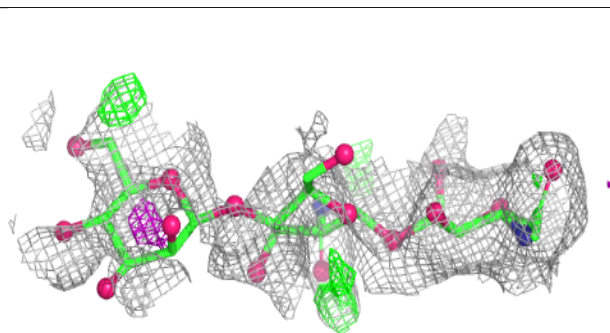
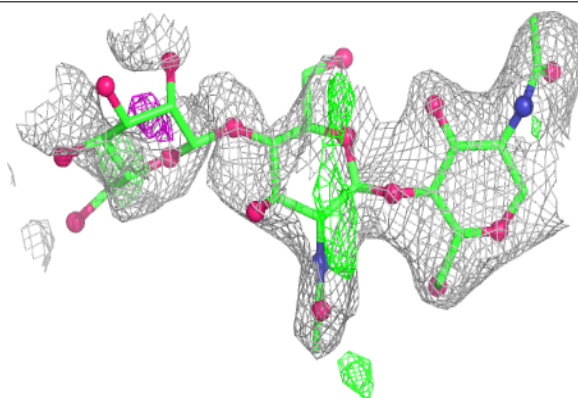


Electron density around Chain H:

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

**Electron density around Chain I:**

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



6.4 Ligands ⓘ

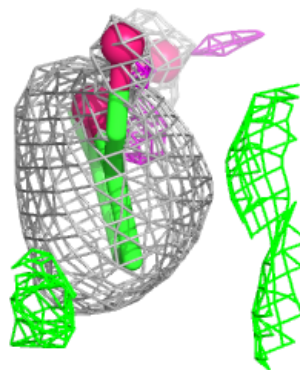
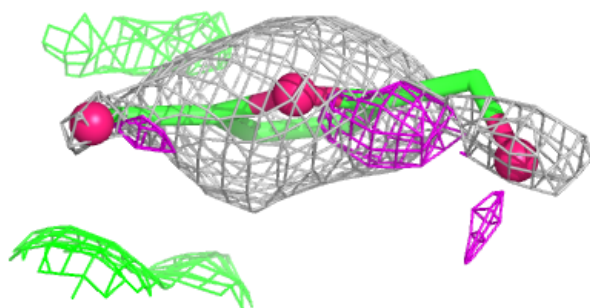
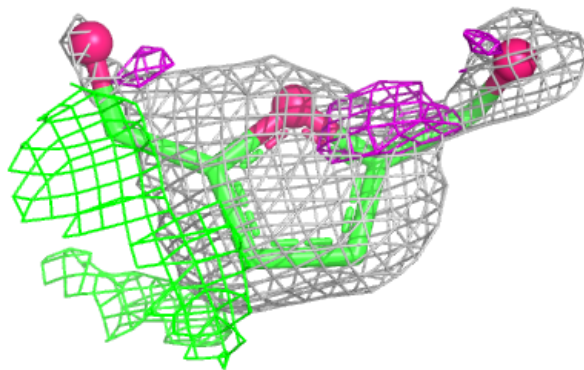
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
8	EPE	A	402	15/15	0.57	0.26	52,60,67,72	0
12	SO4	A	413	5/5	0.58	0.15	69,73,76,86	0
12	SO4	C	417	5/5	0.62	0.13	72,74,84,85	0
8	EPE	A	410	15/15	0.68	0.25	47,63,76,77	0
12	SO4	C	418	5/5	0.68	0.14	65,75,78,88	0
12	SO4	B	418	5/5	0.69	0.13	68,75,81,84	0
10	GOL	C	420	6/6	0.71	0.23	54,55,56,57	0
10	GOL	A	411	6/6	0.76	0.21	44,49,51,52	0
10	GOL	C	419	6/6	0.77	0.15	61,61,62,63	0
10	GOL	B	420	6/6	0.80	0.16	51,59,64,64	0
9	FUX	C	413	9/9	0.82	0.22	59,69,73,79	0
10	GOL	B	419	6/6	0.83	0.20	50,55,58,61	0
9	FUX	A	408	9/9	0.85	0.24	64,65,70,70	9
9	FUX	B	413	9/9	0.85	0.23	55,58,63,65	9
8	EPE	B	402	15/15	0.85	0.24	40,65,73,73	0
12	SO4	B	417	5/5	0.87	0.10	58,61,67,75	0
11	MG	C	416	1/1	0.91	0.11	50,50,50,50	0
9	FUX	C	412	9/9	0.91	0.14	40,44,48,50	0
9	FUX	B	412	9/9	0.92	0.12	35,41,47,49	0
9	FUX	A	409	9/9	0.93	0.12	31,40,47,48	0
7	HEM	C	414	43/43	0.98	0.08	30,35,41,45	0
7	HEM	A	401	43/43	0.98	0.07	23,27,34,46	0
7	HEM	B	414	43/43	0.98	0.07	28,32,38,42	0
11	MG	B	416	1/1	0.99	0.03	37,37,37,37	0
11	MG	A	412	1/1	1.00	0.02	35,35,35,35	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.

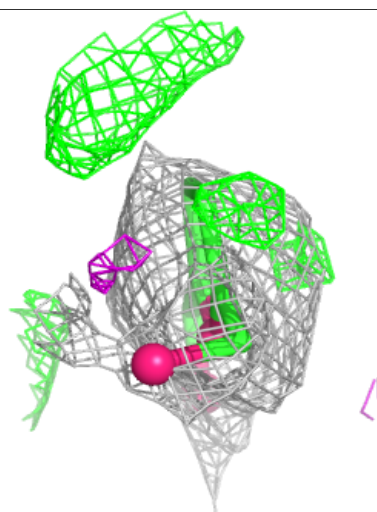
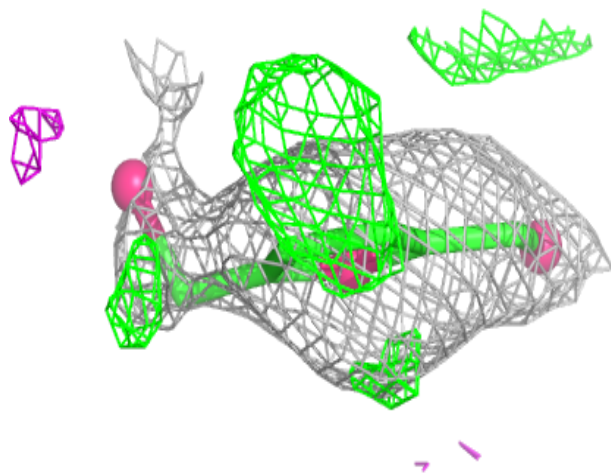
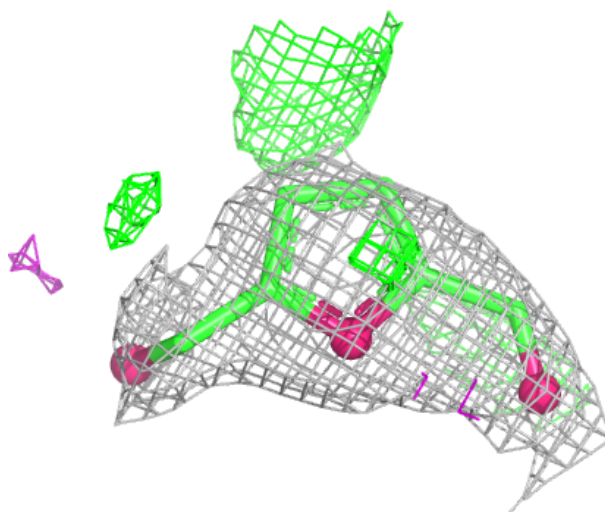
Electron density around FUX C 413:

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



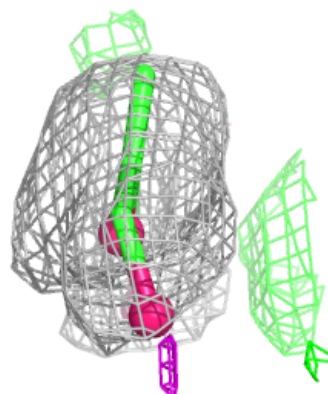
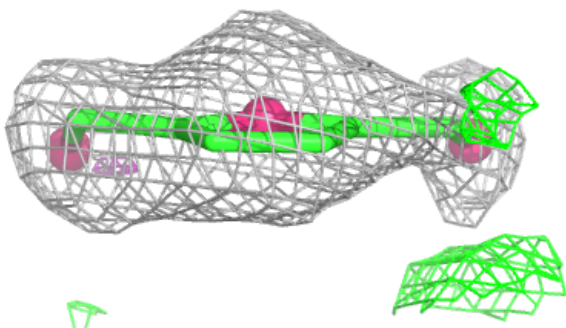
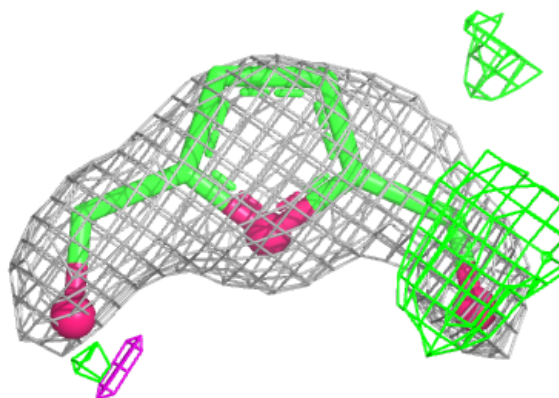
Electron density around FUX A 408:

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

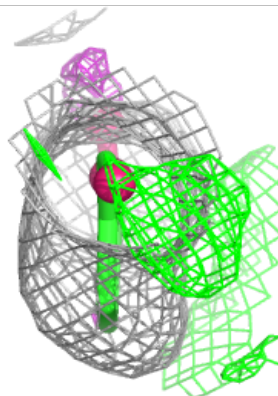
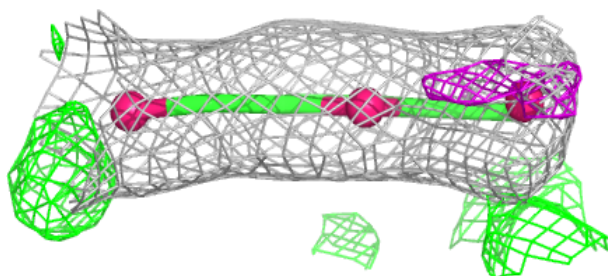
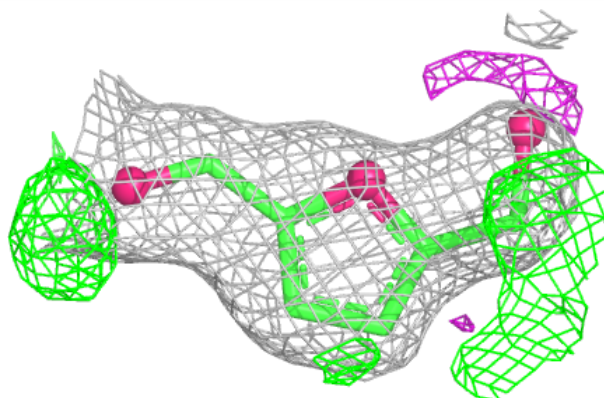


Electron density around FUX B 413:

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

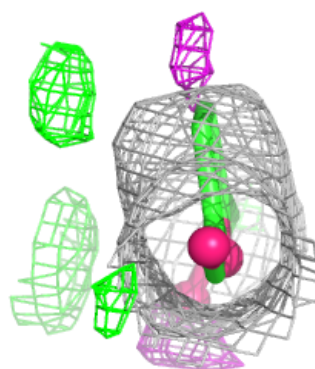
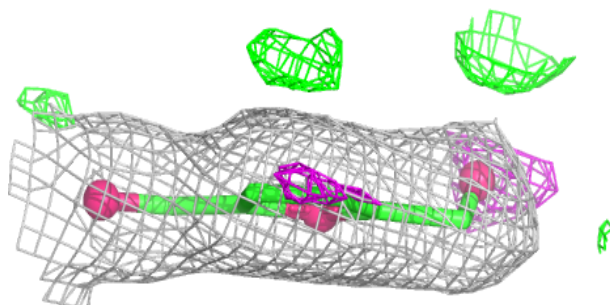
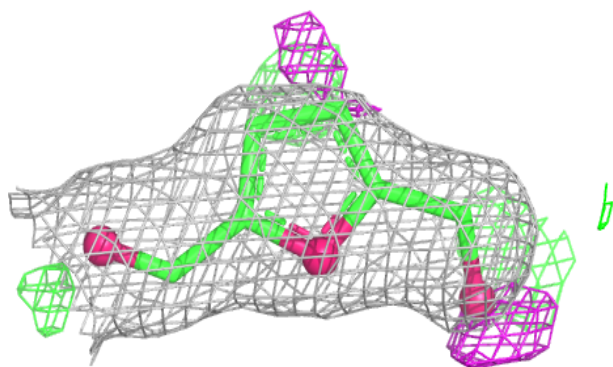
**Electron density around FUX C 412:**

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

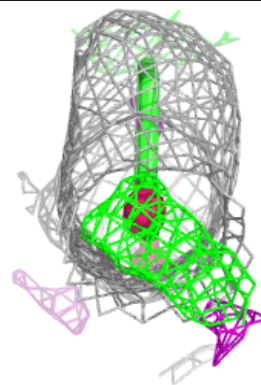
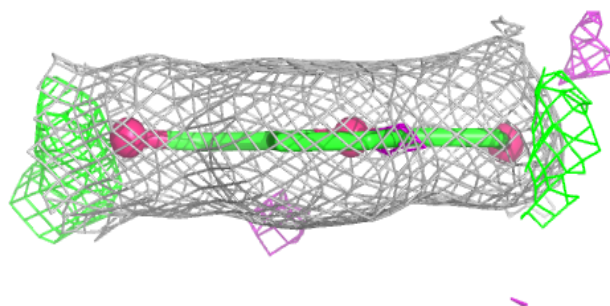
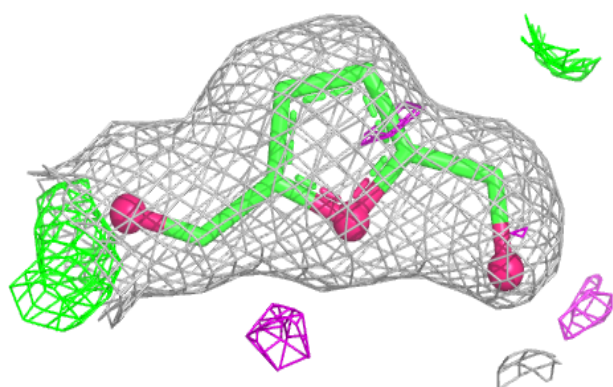


Electron density around FUX B 412:

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

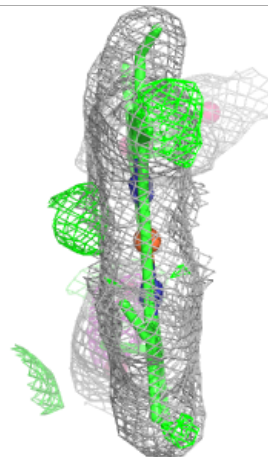
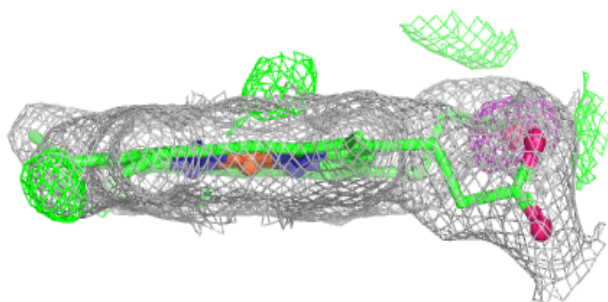
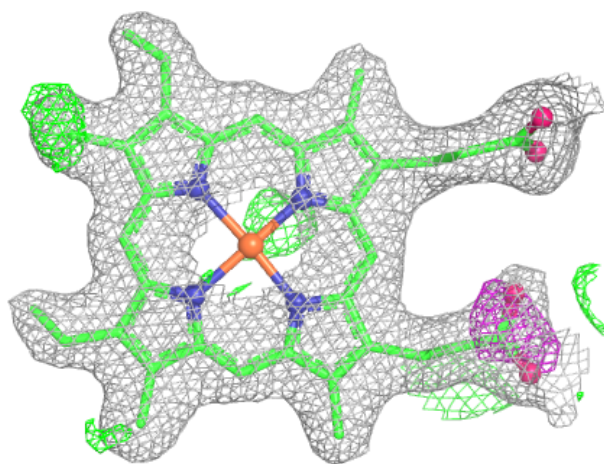
**Electron density around FUX A 409:**

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



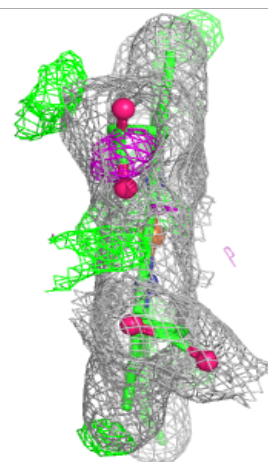
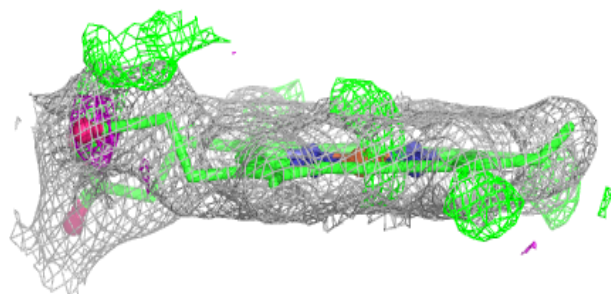
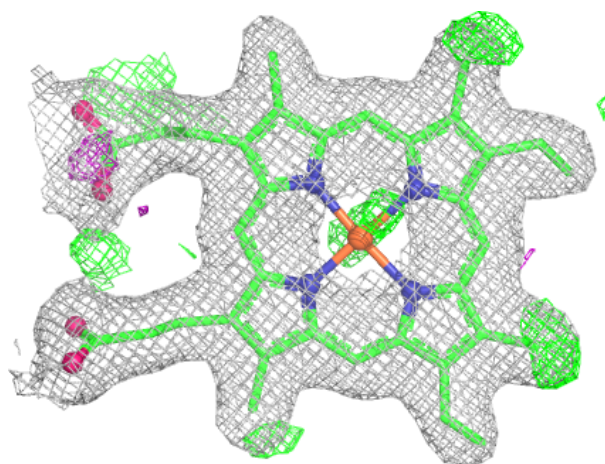
Electron density around HEM C 414:

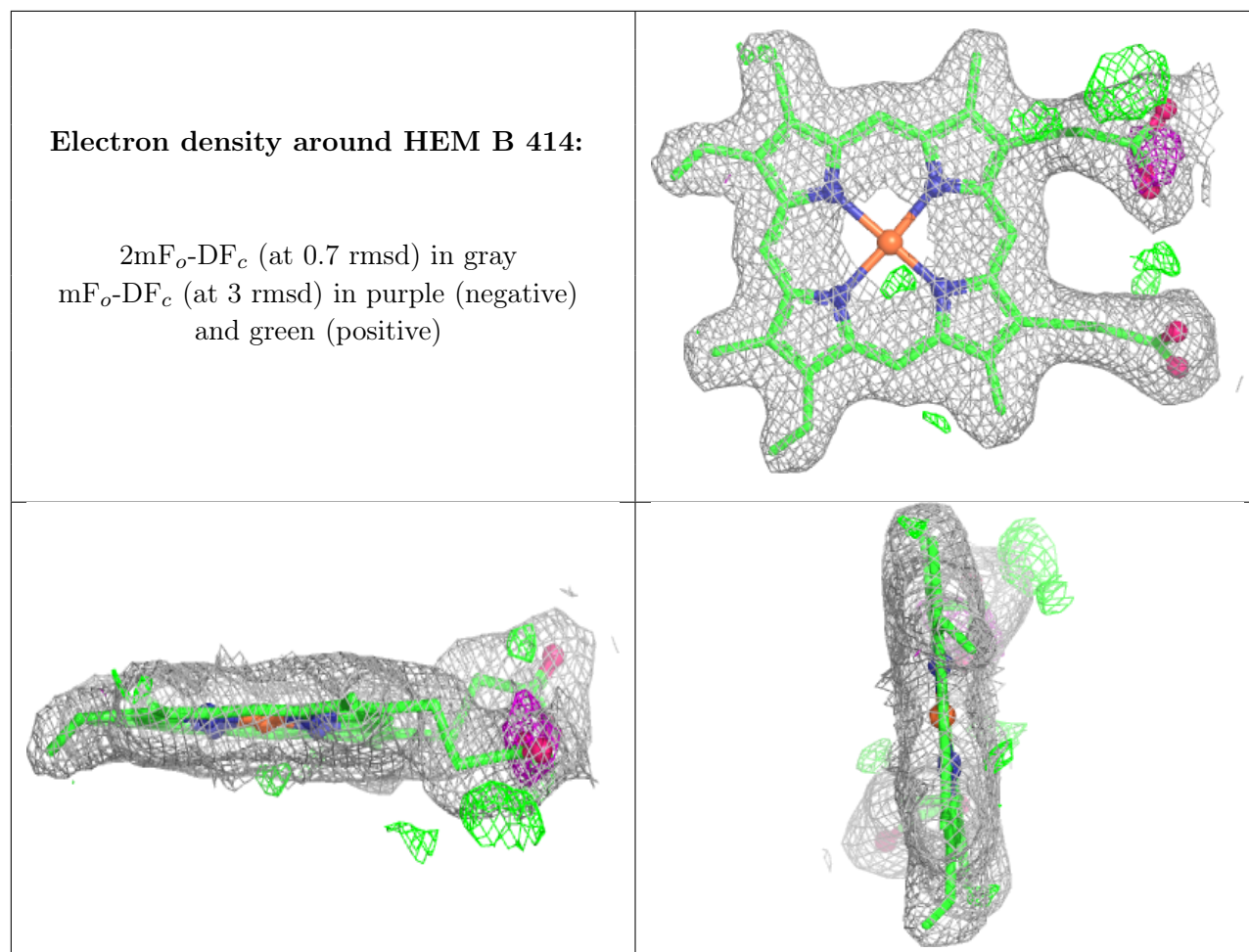
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM A 401:

$2mF_o-DF_c$ (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.