



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 09:30 PM UTC

PDB ID : 9HED / pdb_00009hed
Title : Unspecific peroxygenase from *Psathyrella aberdarensis* (PabUPO-II) in complex with alpha-damascone
Authors : Fernandez-Garcia, A.; Sanz-Aparicio, J.
Deposited on : 2024-11-13
Resolution : 2.45 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

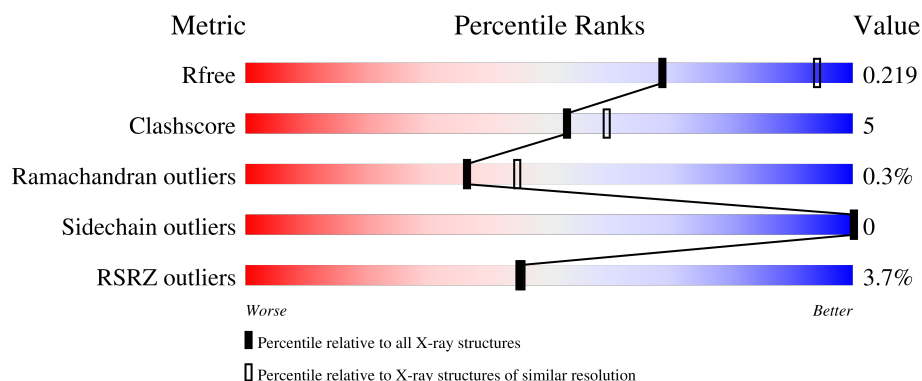
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)

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	2% 93% 7%
1	B	335	3% 95% 5%
1	C	335	6% 92% 8%
2	H	5	20% 80%
2	Y	5	40% 60%

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Mol	Chain	Length	Quality of chain
3	J	7	 71%29%
4	Z	6	 100%
5	m	4	 75%25%
6	n	3	 67%33%

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
8	EPE	A	402	-	-	X	-
8	EPE	A	403	-	-	X	-
8	EPE	C	405	-	-	X	-
9	GOL	C	406	-	-	X	-

2 Entry composition [i](#)

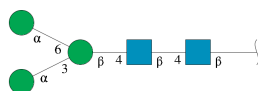
There are 13 unique types of molecules in this entry. The entry contains 8863 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

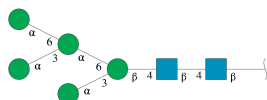
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	335	Total	C	N	O	S	0	7	0
			2629	1671	454	497	7			
1	B	335	Total	C	N	O	S	0	5	0
			2617	1663	451	496	7			
1	C	335	Total	C	N	O	S	0	7	0
			2629	1671	454	497	7			

- 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.



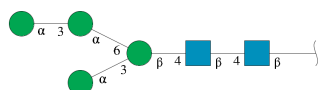
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	H	5	Total	C	N	O	0	0	0
			61	34	2	25			
2	Y	5	Total	C	N	O	0	0	0
			61	34	2	25			

- 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	J	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.



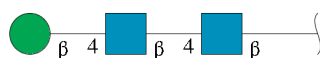
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	Z	6	Total	C	N	O	0	0	0
			72	40	2	30			

- 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.



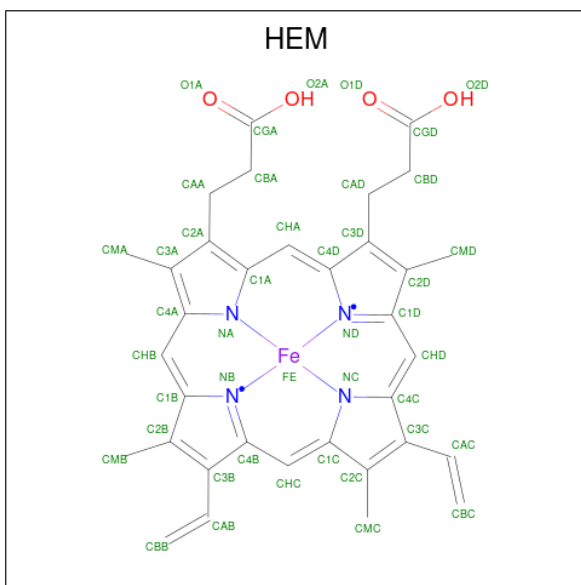
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	m	4	Total	C	N	O	0	0	0
			50	28	2	20			

- 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.



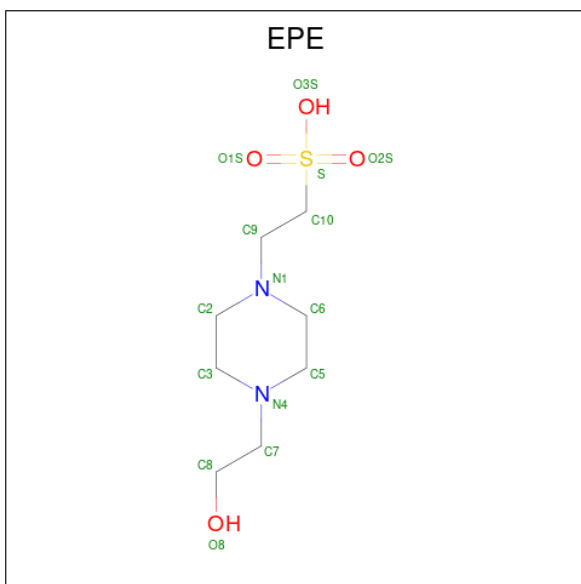
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	n	3	Total	C	N	O	0	0	0
			39	22	2	15			

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



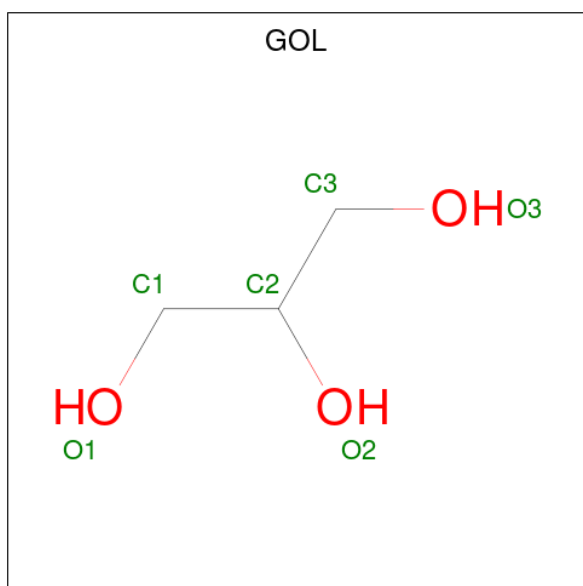
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
7	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
7	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 8 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: $C_8H_{18}N_2O_4S$).



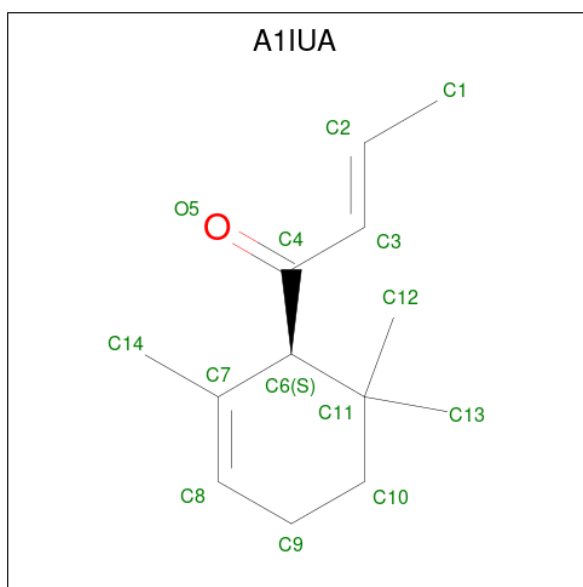
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
8	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
8	C	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
8	C	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
8	C	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 9 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 10 is alpha-damascone (CCD ID: A1IUA) (formula: $C_{13}H_{20}O$) (labeled as "Ligand of Interest" by depositor).

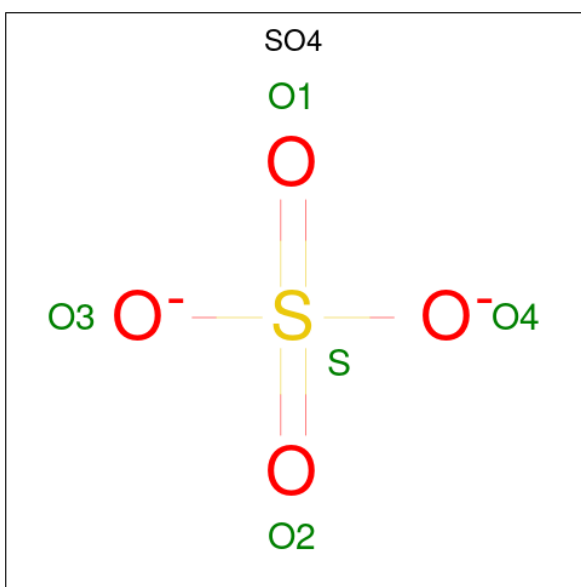


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			14	13	1		
10	B	1	Total	C	O	0	0
			14	13	1		
10	C	1	Total	C	O	0	0
			14	13	1		

- 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	A	1	Total	O	S	0	0
			5	4	1		
12	A	1	Total	O	S	0	0
			5	4	1		
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	B	1	Total	O	S	0	0
			5	4	1		
12	B	1	Total	O	S	0	0
			5	4	1		

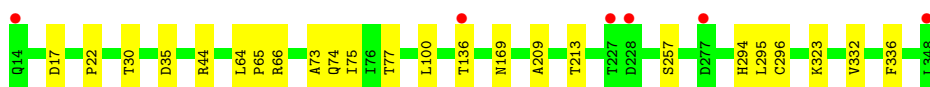
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	134	Total	O	0	0
			134	134		
13	B	93	Total	O	0	0
			93	93		
13	C	83	Total	O	0	0
			83	83		

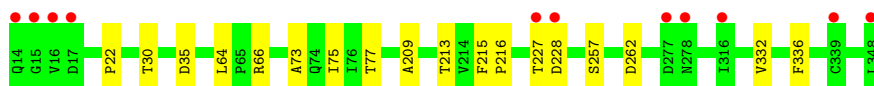
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

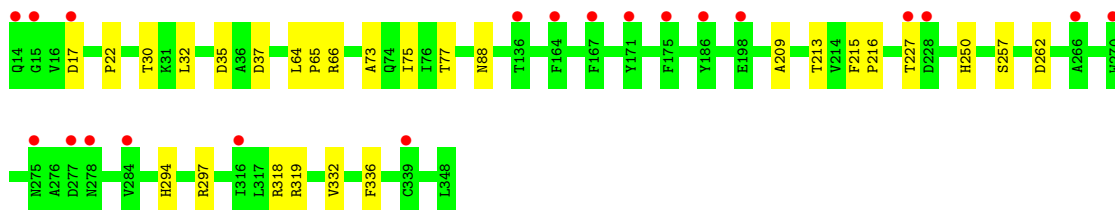
- Molecule 1: Heme-thiolate peroxidase



- Molecule 1: Heme-thiolate peroxidase



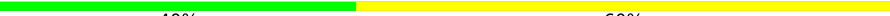
- Molecule 1: Heme-thiolate peroxidase



- 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



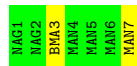
- Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Y:  40% 60%



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

Chain J:  71% 29%



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

Chain Z:  100%



- Molecule 5: α -D-mannopyranose-(1-3)- β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose

Chain m:  75% 25%



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

Chain n:  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	271.39Å 74.36Å 105.60Å 90.00° 111.62° 90.00°	Depositor
Resolution (Å)	49.14 – 2.45 49.14 – 2.45	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.14-2.45) 99.8 (49.14-2.45)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.77 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.8.0419	Depositor
R, R_{free}	0.185 , 0.215 0.191 , 0.219	Depositor DCC
R_{free} test set	3545 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	34.9	Xtriage
Anisotropy	0.784	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 34.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.018 for -h-2*1,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8863	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.86% 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: HEM, MG, SO4, MAN, BMA, EPE, A1IUA, GOL, 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	0.62	0/2731	0.96	2/3732 (0.1%)
1	B	0.59	0/2713	0.95	4/3708 (0.1%)
1	C	0.58	0/2731	0.94	4/3732 (0.1%)
All	All	0.60	0/8175	0.95	10/11172 (0.1%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	30	THR	CA-CB-OG1	-6.35	100.08	109.60
1	C	37	ASP	CA-CB-CG	5.90	118.50	112.60
1	A	30	THR	CA-CB-OG1	-5.77	100.95	109.60
1	B	30	THR	CA-CB-OG1	-5.74	100.98	109.60
1	B	228	ASP	CA-CB-CG	5.71	118.31	112.60
1	B	35	ASP	CA-CB-CG	5.43	118.03	112.60
1	C	35	ASP	CA-CB-CG	5.40	118.00	112.60
1	C	262	ASP	CA-CB-CG	5.40	118.00	112.60
1	A	35	ASP	CA-CB-CG	5.32	117.92	112.60
1	B	262	ASP	CA-CB-CG	5.21	117.81	112.60

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	2629	0	2486	33	0
1	B	2617	0	2466	9	0
1	C	2629	0	2486	29	0
2	H	61	0	52	0	0
2	Y	61	0	52	0	0
3	J	83	0	70	0	0
4	Z	72	0	61	0	0
5	m	50	0	43	1	0
6	n	39	0	34	0	0
7	A	43	0	30	1	0
7	B	43	0	30	1	0
7	C	43	0	30	5	0
8	A	30	0	36	23	0
8	C	45	0	54	15	0
9	A	6	0	8	0	0
9	B	6	0	8	2	0
9	C	6	0	8	6	0
10	A	14	0	0	0	0
10	B	14	0	0	0	0
10	C	14	0	0	0	0
11	A	1	0	0	0	0
11	B	1	0	0	0	0
11	C	1	0	0	0	0
12	A	20	0	0	0	0
12	B	25	0	0	0	0
13	A	134	0	0	3	0
13	B	93	0	0	1	0
13	C	83	0	0	4	0
All	All	8863	0	7954	82	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (82) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:65:PRO:HA	8:A:402:EPE:H62	1.27	1.07
1:A:294:HIS:HA	8:A:403:EPE:C3	1.84	1.06
1:A:295:LEU:H	8:A:403:EPE:H81	1.34	0.92
1:A:294:HIS:HA	8:A:403:EPE:H31	1.48	0.91
1:C:32:LEU:N	8:C:404:EPE:O1S	2.02	0.91
1:B:66:ARG:H	9:B:402:GOL:H12	1.40	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:HIS:HA	8:A:403:EPE:H32	1.57	0.85
1:A:295:LEU:N	8:A:403:EPE:H32	1.92	0.83
9:C:406:GOL:H31	13:C:527:HOH:O	1.78	0.83
1:A:294:HIS:C	8:A:403:EPE:H32	2.04	0.82
1:A:294:HIS:CA	8:A:403:EPE:H32	2.09	0.82
1:B:66:ARG:N	9:B:402:GOL:H12	1.96	0.81
1:A:74:GLN:NE2	8:A:402:EPE:O2S	2.16	0.78
1:A:169:ASN:O	1:C:318[B]:ARG:NH2	2.16	0.77
1:C:250:HIS:NE2	8:C:404:EPE:H51	2.00	0.77
1:B:227:THR:HG22	13:B:570:HOH:O	1.84	0.76
1:A:294:HIS:CA	8:A:403:EPE:C3	2.63	0.76
1:C:66:ARG:H	8:C:405:EPE:H21	1.51	0.76
1:A:73:ALA:O	1:A:77[B]:THR:HG22	1.87	0.74
1:C:294:HIS:HA	8:C:403:EPE:H102	1.69	0.73
7:C:401:HEM:HBB2	7:C:401:HEM:HHC	1.74	0.70
1:A:66:ARG:HB2	8:A:402:EPE:H71	1.75	0.69
1:C:73:ALA:O	1:C:77[B]:THR:HG22	1.94	0.68
1:C:17:ASP:OD1	1:C:319:ARG:NH2	2.27	0.68
1:A:296:CYS:H	8:A:403:EPE:H22	1.59	0.67
1:A:296:CYS:SG	8:A:403:EPE:H52	2.35	0.66
1:C:88:ASN:HD21	9:C:406:GOL:C1	2.10	0.65
1:C:65:PRO:HA	8:C:405:EPE:H31	1.79	0.64
1:C:66:ARG:HG3	8:C:405:EPE:H91	1.83	0.61
1:C:66:ARG:CD	8:C:405:EPE:H91	2.31	0.61
1:C:66:ARG:CG	8:C:405:EPE:H91	2.32	0.60
1:A:296:CYS:HB2	8:A:403:EPE:H22	1.83	0.60
1:A:296:CYS:N	8:A:403:EPE:H22	2.16	0.59
1:C:297:ARG:HE	8:C:403:EPE:H51	1.69	0.58
1:A:295:LEU:H	8:A:403:EPE:H32	1.69	0.58
1:B:73:ALA:O	1:B:77[B]:THR:HG22	2.06	0.56
1:C:65:PRO:HA	8:C:405:EPE:C3	2.36	0.55
1:A:294:HIS:C	8:A:403:EPE:C3	2.82	0.52
1:C:64:LEU:HD21	1:C:75:ILE:HA	1.92	0.52
1:A:17:ASP:OD1	1:A:323:LYS:NZ	2.42	0.51
7:A:401:HEM:HBB2	7:A:401:HEM:HHC	1.94	0.50
7:B:401:HEM:HHC	7:B:401:HEM:HBB2	1.94	0.50
1:B:64:LEU:HD21	1:B:75:ILE:HA	1.93	0.50
1:B:209:ALA:O	1:B:213:THR:HG23	2.12	0.50
1:C:88:ASN:ND2	9:C:406:GOL:H11	2.27	0.49
1:A:100:LEU:HD13	1:A:136[B]:THR:HG23	1.95	0.49
1:A:296:CYS:HB2	8:A:403:EPE:H52	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:66:ARG:HD2	8:C:405:EPE:H91	1.95	0.49
1:A:136[B]:THR:CG2	13:A:504:HOH:O	2.61	0.48
1:C:332:VAL:HG13	1:C:336:PHE:CD2	2.49	0.48
1:C:209:ALA:O	1:C:213:THR:HG23	2.14	0.48
1:A:209:ALA:O	1:A:213:THR:HG23	2.13	0.48
1:C:77[A]:THR:HG22	13:C:579:HOH:O	2.13	0.48
1:C:88:ASN:ND2	9:C:406:GOL:C1	2.77	0.48
1:A:22:PRO:HG2	1:A:77[A]:THR:HG23	1.97	0.47
1:A:44:ARG:NH1	8:A:402:EPE:O8	2.47	0.47
1:A:64:LEU:HD21	1:A:75:ILE:HA	1.96	0.47
1:C:88:ASN:HD21	9:C:406:GOL:H11	1.79	0.47
1:A:332:VAL:HG13	1:A:336:PHE:CD2	2.50	0.47
1:C:22:PRO:HG2	1:C:77[A]:THR:HG23	1.97	0.47
1:A:44:ARG:HH12	8:A:402:EPE:C7	2.28	0.46
1:C:294:HIS:ND1	8:C:403:EPE:H21	2.30	0.46
1:B:22:PRO:HG2	1:B:77[A]:THR:HG23	1.95	0.46
1:C:17:ASP:OD1	1:C:319:ARG:CZ	2.63	0.46
1:A:44:ARG:HH12	8:A:402:EPE:H72	1.80	0.46
1:A:296:CYS:CB	8:A:403:EPE:H52	2.45	0.46
8:C:405:EPE:H62	13:C:572:HOH:O	2.15	0.45
7:C:401:HEM:HHC	7:C:401:HEM:CBB	2.43	0.45
5:m:1:NAG:H83	5:m:1:NAG:H3	1.98	0.45
1:A:136[B]:THR:HG22	13:A:504:HOH:O	2.16	0.45
7:C:401:HEM:CMC	7:C:401:HEM:HBC2	2.46	0.45
1:C:227:THR:HG22	13:C:548:HOH:O	2.18	0.44
1:A:77[B]:THR:HG23	13:A:527:HOH:O	2.17	0.43
1:B:332:VAL:HG13	1:B:336:PHE:CD2	2.53	0.43
7:C:401:HEM:HBB2	7:C:401:HEM:CHC	2.46	0.43
1:C:66:ARG:HD2	8:C:405:EPE:C9	2.49	0.43
1:C:215:PHE:N	1:C:216:PRO:CD	2.83	0.41
8:C:403:EPE:H81	8:C:403:EPE:H52	1.80	0.41
8:A:402:EPE:H22	8:A:402:EPE:H102	1.72	0.41
1:C:88:ASN:HD21	9:C:406:GOL:H12	1.85	0.40
7:C:401:HEM:HBC2	7:C:401:HEM:HMC2	2.03	0.40
1:B:215:PHE:N	1:B:216:PRO:CD	2.84	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	340/335 (102%)	330 (97%)	9 (3%)	1 (0%)	36	45
1	B	338/335 (101%)	326 (96%)	11 (3%)	1 (0%)	36	45
1	C	340/335 (102%)	328 (96%)	11 (3%)	1 (0%)	36	45
All	All	1018/1005 (101%)	984 (97%)	31 (3%)	3 (0%)	36	45

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	257	SER
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	281/274 (103%)	281 (100%)	0	100	100
1	B	279/274 (102%)	279 (100%)	0	100	100
1	C	281/274 (103%)	281 (100%)	0	100	100
All	All	841/822 (102%)	841 (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 (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	200	GLN
1	B	324	ASN
1	C	158	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 ⓘ

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	H	1	1,2	14,14,15	0.48	0	17,19,21	1.05	1 (5%)
2	NAG	H	2	2	14,14,15	0.34	0	17,19,21	1.42	1 (5%)
2	BMA	H	3	2	11,11,12	0.41	0	15,15,17	0.95	0
2	MAN	H	4	2	11,11,12	1.03	1 (9%)	15,15,17	0.98	1 (6%)
2	MAN	H	5	2	11,11,12	0.72	0	15,15,17	0.88	1 (6%)
3	NAG	J	1	1,3	14,14,15	0.32	0	17,19,21	0.65	0
3	NAG	J	2	3	14,14,15	0.37	0	17,19,21	0.85	0
3	BMA	J	3	3	11,11,12	0.32	0	15,15,17	0.75	1 (6%)
3	MAN	J	4	3	11,11,12	0.62	0	15,15,17	0.89	0
3	MAN	J	5	3	11,11,12	0.59	0	15,15,17	0.66	0
3	MAN	J	6	3	11,11,12	0.58	0	15,15,17	0.76	0
3	MAN	J	7	3	11,11,12	0.59	0	15,15,17	0.96	1 (6%)
2	NAG	Y	1	1,2	14,14,15	0.45	0	17,19,21	2.19	4 (23%)
2	NAG	Y	2	2	14,14,15	0.29	0	17,19,21	0.62	0
2	BMA	Y	3	2	11,11,12	0.41	0	15,15,17	0.72	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MAN	Y	4	2	11,11,12	1.31	2 (18%)	15,15,17	0.97	1 (6%)
2	MAN	Y	5	2	11,11,12	1.33	2 (18%)	15,15,17	1.10	2 (13%)
4	NAG	Z	1	1,4	14,14,15	0.31	0	17,19,21	1.09	2 (11%)
4	NAG	Z	2	4	14,14,15	0.36	0	17,19,21	0.91	1 (5%)
4	BMA	Z	3	4	11,11,12	0.39	0	15,15,17	1.25	1 (6%)
4	MAN	Z	4	4	11,11,12	0.58	0	15,15,17	1.09	1 (6%)
4	MAN	Z	5	4	11,11,12	0.59	0	15,15,17	0.63	1 (6%)
4	MAN	Z	6	4	11,11,12	0.67	0	15,15,17	1.24	2 (13%)
5	NAG	m	1	1,5	14,14,15	0.39	0	17,19,21	2.07	4 (23%)
5	NAG	m	2	5	14,14,15	0.41	0	17,19,21	1.01	1 (5%)
5	BMA	m	3	5	11,11,12	1.31	2 (18%)	15,15,17	0.86	1 (6%)
5	MAN	m	4	5	11,11,12	1.18	2 (18%)	15,15,17	1.00	1 (6%)
6	NAG	n	1	1,6	14,14,15	0.27	0	17,19,21	0.66	0
6	NAG	n	2	6	14,14,15	0.41	0	17,19,21	1.36	3 (17%)
6	BMA	n	3	6	11,11,12	0.44	0	15,15,17	0.62	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	H	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	H	2	2	-	0/6/23/26	0/1/1/1
2	BMA	H	3	2	-	0/2/19/22	0/1/1/1
2	MAN	H	4	2	-	0/2/19/22	0/1/1/1
2	MAN	H	5	2	-	2/2/19/22	0/1/1/1
3	NAG	J	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	J	2	3	-	0/6/23/26	0/1/1/1
3	BMA	J	3	3	-	0/2/19/22	0/1/1/1
3	MAN	J	4	3	-	0/2/19/22	0/1/1/1
3	MAN	J	5	3	-	2/2/19/22	0/1/1/1
3	MAN	J	6	3	-	2/2/19/22	0/1/1/1
3	MAN	J	7	3	-	2/2/19/22	0/1/1/1
2	NAG	Y	1	1,2	-	1/6/23/26	0/1/1/1
2	NAG	Y	2	2	-	0/6/23/26	0/1/1/1
2	BMA	Y	3	2	-	0/2/19/22	0/1/1/1
2	MAN	Y	4	2	-	1/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MAN	Y	5	2	-	2/2/19/22	0/1/1/1
4	NAG	Z	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	Z	2	4	-	0/6/23/26	0/1/1/1
4	BMA	Z	3	4	-	0/2/19/22	0/1/1/1
4	MAN	Z	4	4	-	1/2/19/22	0/1/1/1
4	MAN	Z	5	4	-	1/2/19/22	0/1/1/1
4	MAN	Z	6	4	-	2/2/19/22	0/1/1/1
5	NAG	m	1	1,5	-	3/6/23/26	0/1/1/1
5	NAG	m	2	5	-	0/6/23/26	0/1/1/1
5	BMA	m	3	5	-	0/2/19/22	0/1/1/1
5	MAN	m	4	5	-	0/2/19/22	0/1/1/1
6	NAG	n	1	1,6	-	4/6/23/26	0/1/1/1
6	NAG	n	2	6	-	2/6/23/26	0/1/1/1
6	BMA	n	3	6	-	1/2/19/22	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Y	5	MAN	O5-C5	3.28	1.49	1.43
2	Y	4	MAN	O5-C5	3.05	1.49	1.43
5	m	3	BMA	O5-C5	2.91	1.49	1.43
2	H	4	MAN	C2-C3	2.77	1.56	1.52
5	m	3	BMA	C2-C3	2.71	1.56	1.52
5	m	4	MAN	O5-C5	2.62	1.48	1.43
2	Y	5	MAN	C4-C5	2.32	1.58	1.53
5	m	4	MAN	C2-C3	2.27	1.56	1.52
2	Y	4	MAN	C2-C3	2.05	1.55	1.52

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	m	1	NAG	C2-N2-C7	5.68	130.51	122.90
2	Y	1	NAG	C1-C2-N2	5.48	119.07	110.43
5	m	1	NAG	C1-C2-N2	5.00	118.31	110.43
2	H	2	NAG	C1-C2-N2	4.79	117.98	110.43
2	Y	1	NAG	O5-C1-C2	-4.76	103.93	111.29
4	Z	6	MAN	C1-C2-C3	3.85	115.25	109.64
2	Y	1	NAG	C1-O5-C5	3.71	117.16	112.19
4	Z	3	BMA	O2-C2-C3	3.20	116.78	110.15
2	H	4	MAN	O2-C2-C3	3.11	116.58	110.15
6	n	2	NAG	C2-N2-C7	3.00	126.92	122.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Y	4	MAN	C1-O5-C5	2.92	116.09	112.19
5	m	2	NAG	C1-C2-N2	2.88	114.97	110.43
5	m	4	MAN	O2-C2-C3	2.76	115.87	110.15
4	Z	1	NAG	C1-O5-C5	2.74	115.86	112.19
6	n	2	NAG	O5-C5-C4	-2.69	104.28	110.83
2	Y	1	NAG	C4-C3-C2	-2.69	107.08	111.02
2	H	5	MAN	C1-O5-C5	2.66	115.75	112.19
4	Z	4	MAN	C3-C4-C5	2.59	114.93	110.23
4	Z	2	NAG	O5-C5-C4	-2.48	104.79	110.83
4	Z	6	MAN	C1-O5-C5	2.39	115.39	112.19
2	H	1	NAG	C1-O5-C5	-2.34	109.05	112.19
4	Z	1	NAG	C1-C2-N2	2.31	114.08	110.43
5	m	1	NAG	C4-C3-C2	-2.24	107.73	111.02
2	Y	5	MAN	C1-O5-C5	2.20	115.14	112.19
5	m	3	BMA	O3-C3-C4	-2.19	105.20	110.38
2	Y	5	MAN	O4-C4-C5	2.11	114.51	109.32
3	J	7	MAN	C1-C2-C3	2.10	112.70	109.64
6	n	2	NAG	O5-C1-C2	2.08	114.51	111.29
3	J	3	BMA	O2-C2-C3	2.01	114.32	110.15
5	m	1	NAG	C1-O5-C5	2.01	114.88	112.19
4	Z	5	MAN	C1-O5-C5	2.01	114.88	112.19

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	Y	1	NAG	C1-C2-N2-C7
6	n	1	NAG	O7-C7-N2-C2
6	n	1	NAG	C8-C7-N2-C2
6	n	2	NAG	O5-C5-C6-O6
3	J	7	MAN	O5-C5-C6-O6
4	Z	6	MAN	C4-C5-C6-O6
6	n	2	NAG	C4-C5-C6-O6
4	Z	6	MAN	O5-C5-C6-O6
3	J	7	MAN	C4-C5-C6-O6
5	m	1	NAG	C8-C7-N2-C2
5	m	1	NAG	O7-C7-N2-C2
2	Y	5	MAN	O5-C5-C6-O6
3	J	5	MAN	C4-C5-C6-O6
2	H	5	MAN	O5-C5-C6-O6
4	Z	4	MAN	O5-C5-C6-O6
2	Y	4	MAN	O5-C5-C6-O6

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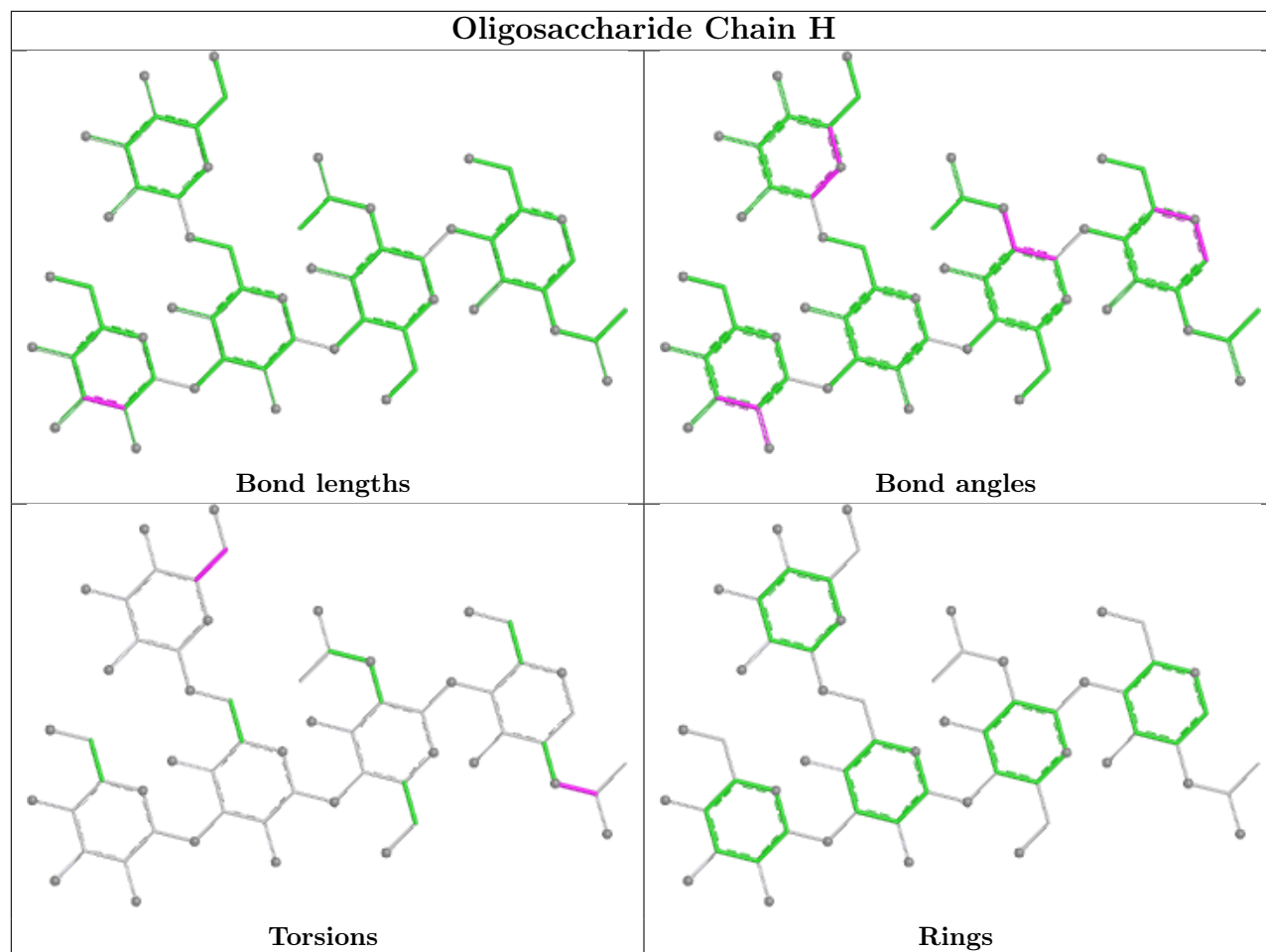
Mol	Chain	Res	Type	Atoms
3	J	6	MAN	C4-C5-C6-O6
6	n	3	BMA	O5-C5-C6-O6
2	H	1	NAG	C8-C7-N2-C2
3	J	5	MAN	O5-C5-C6-O6
3	J	6	MAN	O5-C5-C6-O6
6	n	1	NAG	O5-C5-C6-O6
5	m	1	NAG	C3-C2-N2-C7
6	n	1	NAG	C4-C5-C6-O6
2	Y	5	MAN	C4-C5-C6-O6
2	H	1	NAG	O7-C7-N2-C2
4	Z	5	MAN	C4-C5-C6-O6
2	H	5	MAN	C4-C5-C6-O6

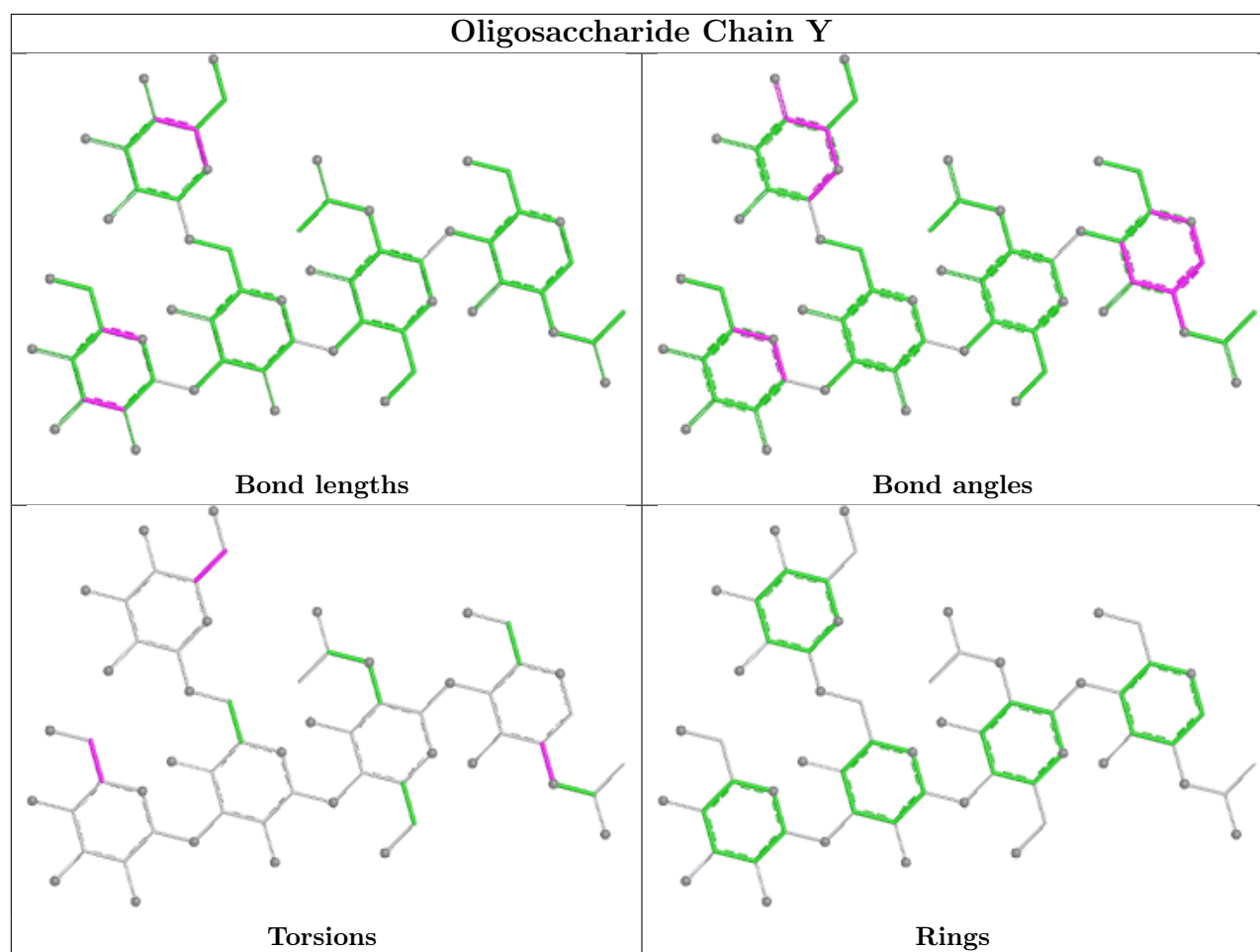
There are no ring outliers.

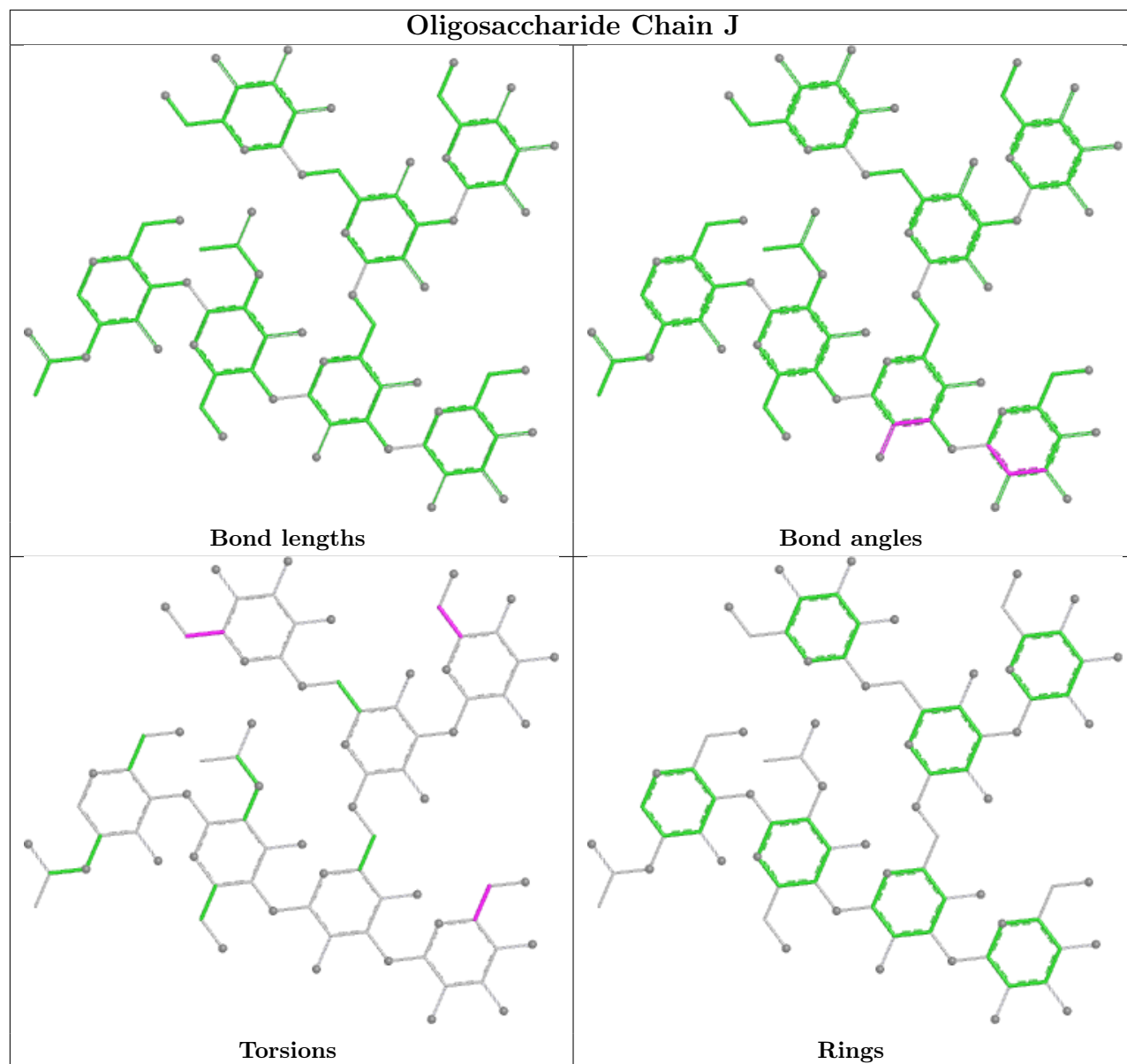
1 monomer is involved in 1 short contact:

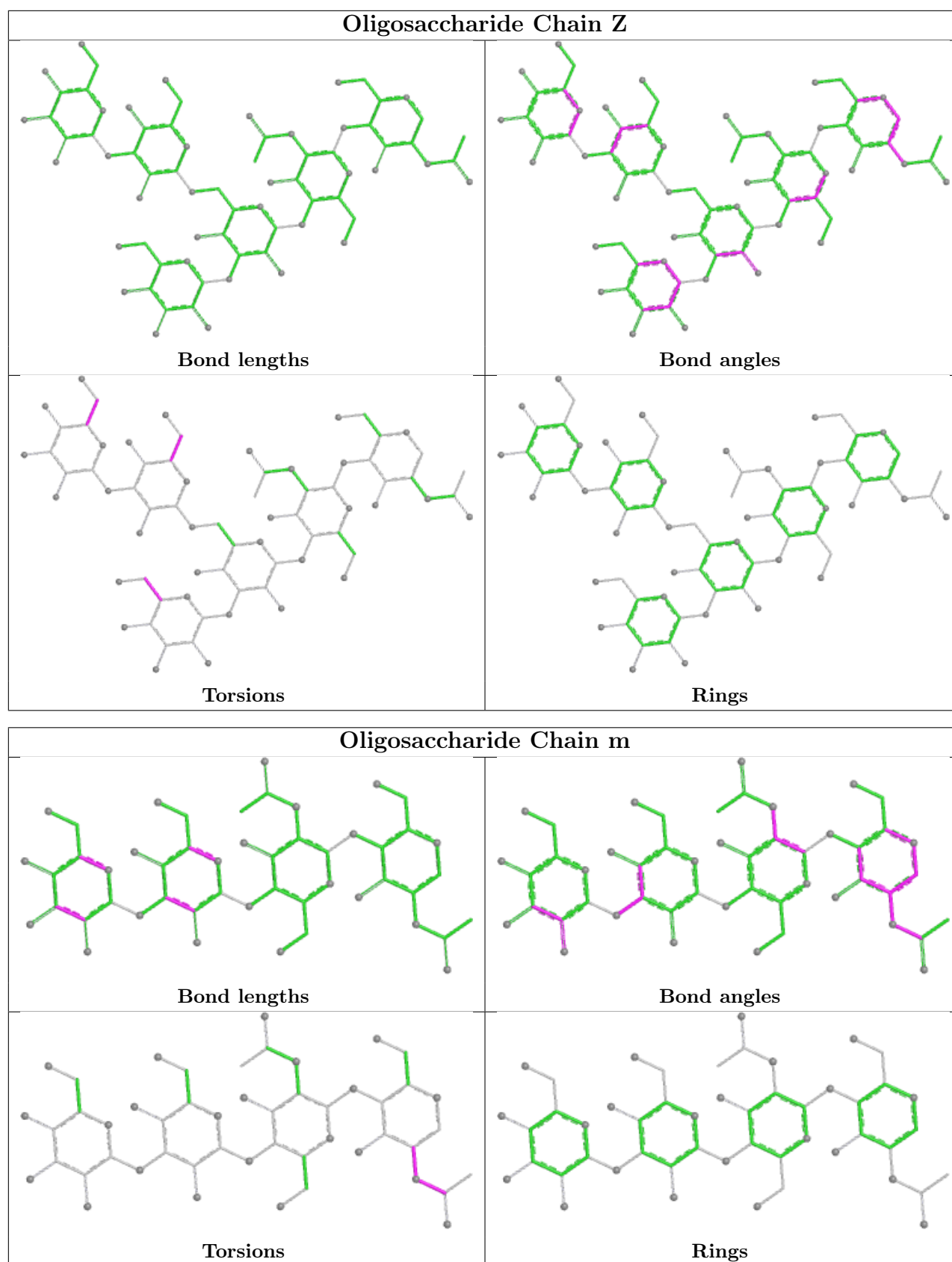
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	m	1	NAG	1	0

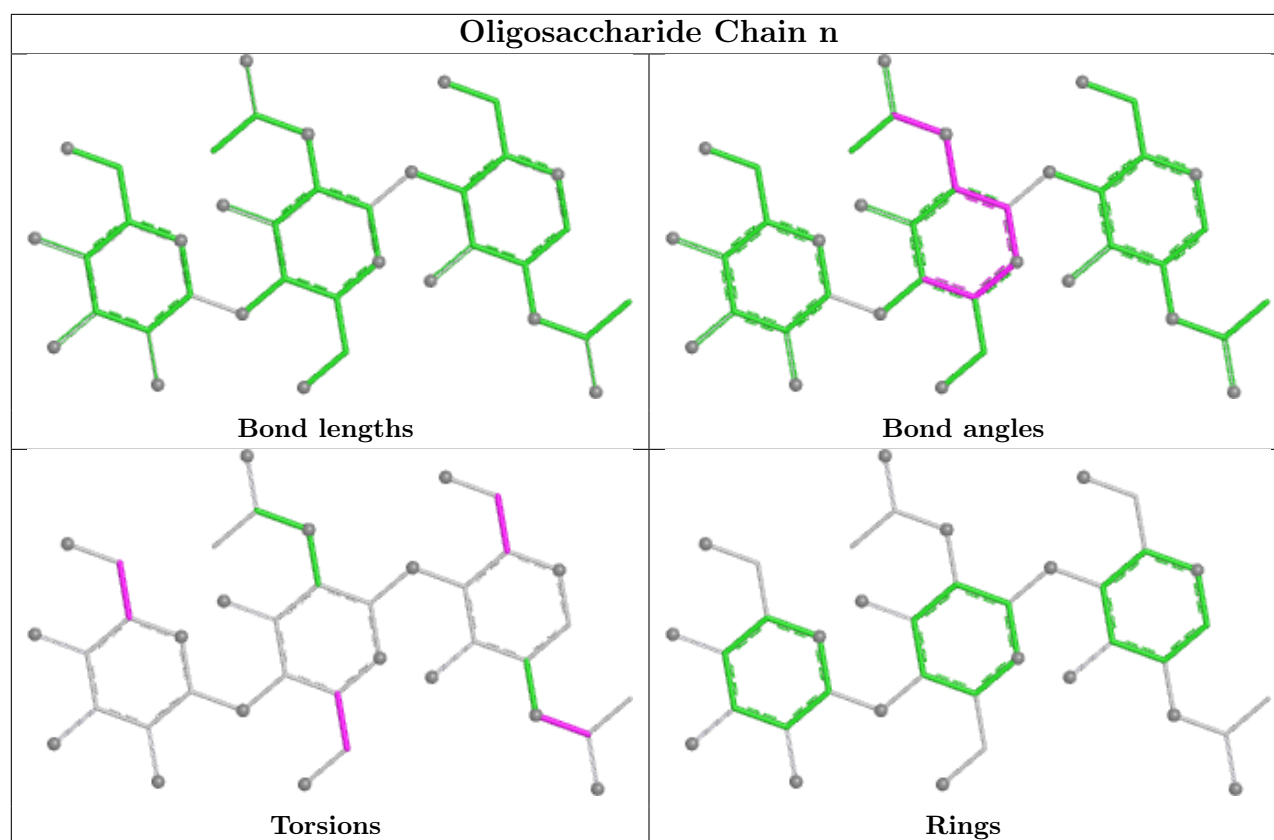
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

Of 26 ligands modelled in this entry, 3 are monoatomic - leaving 23 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$
8	EPE	C	405	-	15,15,15	1.12	1 (6%)	19,20,20	0.80	1 (5%)
10	A1IUA	B	403	-	13,14,14	1.11	1 (7%)	13,20,20	1.09	1 (7%)
12	SO4	A	410	-	4,4,4	0.33	0	6,6,6	0.35	0
7	HEM	B	401	1,11	50,50,50	1.54	10 (20%)	67,82,82	1.71	11 (16%)
10	A1IUA	C	402	-	13,14,14	0.71	0	13,20,20	0.39	0
8	EPE	C	403	-	15,15,15	1.14	1 (6%)	19,20,20	0.77	1 (5%)
9	GOL	C	406	-	5,5,5	0.42	0	5,5,5	0.78	0
12	SO4	B	405	-	4,4,4	0.27	0	6,6,6	0.40	0
12	SO4	B	406	-	4,4,4	0.60	0	6,6,6	0.13	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	SO4	A	407	-	4,4,4	0.31	0	6,6,6	0.47	0
7	HEM	A	401	1,11	50,50,50	1.65	8 (16%)	67,82,82	1.77	17 (25%)
12	SO4	B	407	-	4,4,4	0.34	0	6,6,6	0.22	0
8	EPE	C	404	-	15,15,15	1.12	1 (6%)	19,20,20	1.25	2 (10%)
12	SO4	B	408	-	4,4,4	0.35	0	6,6,6	0.07	0
9	GOL	A	404	-	5,5,5	0.29	0	5,5,5	0.43	0
12	SO4	A	409	-	4,4,4	0.39	0	6,6,6	0.30	0
12	SO4	A	408	-	4,4,4	0.67	0	6,6,6	0.23	0
8	EPE	A	403	-	15,15,15	1.02	1 (6%)	19,20,20	1.57	4 (21%)
10	A1IUA	A	405	-	13,14,14	0.92	1 (7%)	13,20,20	0.72	0
7	HEM	C	401	1,11	50,50,50	1.69	10 (20%)	67,82,82	1.63	14 (20%)
8	EPE	A	402	-	15,15,15	1.19	1 (6%)	19,20,20	1.02	2 (10%)
9	GOL	B	402	-	5,5,5	0.26	0	5,5,5	0.48	0
12	SO4	B	409	-	4,4,4	0.45	0	6,6,6	0.18	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
8	EPE	A	403	-	-	1/9/19/19	0/1/1/1
8	EPE	C	404	-	-	2/9/19/19	0/1/1/1
10	A1IUA	A	405	-	-	0/6/24/24	0/1/1/1
10	A1IUA	C	402	-	-	0/6/24/24	0/1/1/1
9	GOL	C	406	-	-	4/4/4/4	-
7	HEM	C	401	1,11	-	4/14/54/54	-
8	EPE	C	405	-	-	3/9/19/19	0/1/1/1
8	EPE	A	402	-	-	7/9/19/19	0/1/1/1
7	HEM	A	401	1,11	-	3/14/54/54	-
10	A1IUA	B	403	-	-	0/6/24/24	0/1/1/1
9	GOL	A	404	-	-	3/4/4/4	-
7	HEM	B	401	1,11	-	2/14/54/54	-
9	GOL	B	402	-	-	2/4/4/4	-
8	EPE	C	403	-	-	1/9/19/19	0/1/1/1

All (35) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	401	HEM	FE-NC	5.25	2.12	1.95
7	C	401	HEM	FE-NB	4.95	2.10	1.94
7	B	401	HEM	FE-NB	4.38	2.08	1.94
7	C	401	HEM	FE-NC	4.30	2.09	1.95
7	A	401	HEM	C1B-NB	-4.28	1.32	1.40
7	A	401	HEM	FE-NB	4.02	2.07	1.94
8	A	402	EPE	O3S-S	4.01	1.62	1.47
8	C	405	EPE	O3S-S	3.81	1.61	1.47
7	B	401	HEM	C1B-NB	-3.73	1.33	1.40
8	C	404	EPE	O3S-S	3.69	1.61	1.47
8	C	403	EPE	O3S-S	3.68	1.61	1.47
7	C	401	HEM	C1B-NB	-3.37	1.34	1.40
7	C	401	HEM	C4D-ND	-3.36	1.34	1.40
10	B	403	A1IUA	C3-C4	3.07	1.71	1.50
7	A	401	HEM	C4D-ND	-3.06	1.34	1.40
7	B	401	HEM	C4D-ND	-3.04	1.35	1.40
7	B	401	HEM	C1D-ND	-2.98	1.33	1.38
7	C	401	HEM	C4B-NB	-2.90	1.33	1.38
7	C	401	HEM	C1D-ND	-2.88	1.33	1.38
7	B	401	HEM	FE-NC	2.74	2.04	1.95
8	A	403	EPE	O3S-S	2.72	1.57	1.47
7	A	401	HEM	C1C-C2C	-2.55	1.40	1.45
7	B	401	HEM	C4B-NB	-2.44	1.34	1.38
7	A	401	HEM	C4C-NC	-2.36	1.35	1.39
7	A	401	HEM	C3C-C4C	-2.32	1.42	1.46
10	A	405	A1IUA	C1-C2	2.32	1.59	1.49
7	C	401	HEM	C4C-NC	-2.18	1.35	1.39
7	C	401	HEM	FE-ND	-2.17	1.88	1.94
7	B	401	HEM	O2D-CGD	-2.15	1.23	1.30
7	B	401	HEM	C1A-C2A	-2.10	1.40	1.44
7	C	401	HEM	C3C-C4C	-2.08	1.42	1.46
7	B	401	HEM	C3D-C2D	-2.07	1.32	1.36
7	A	401	HEM	C1A-C2A	-2.02	1.40	1.44
7	C	401	HEM	C1C-C2C	-2.01	1.41	1.45
7	B	401	HEM	C3C-C4C	-2.01	1.42	1.46

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	401	HEM	CHC-C4B-NB	4.86	129.65	124.42
7	B	401	HEM	C1B-NB-C4B	4.51	110.55	105.21
7	C	401	HEM	CHC-C4B-NB	4.34	129.09	124.42
7	B	401	HEM	O2A-CGA-CBA	4.22	127.34	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	401	HEM	CHC-C4B-NB	3.92	128.64	124.42
7	B	401	HEM	C3B-C4B-NB	-3.84	106.71	109.47
8	A	403	EPE	O3S-S-O1S	-3.84	101.80	111.40
7	A	401	HEM	O2A-CGA-CBA	3.82	126.07	114.00
8	C	404	EPE	O3S-S-O1S	-3.69	102.17	111.40
7	A	401	HEM	C1B-NB-C4B	3.66	109.54	105.21
7	C	401	HEM	CHD-C1D-ND	3.65	128.35	124.42
7	C	401	HEM	CHA-C4D-ND	3.49	128.69	124.37
7	A	401	HEM	CHB-C1B-NB	3.39	128.56	124.37
7	B	401	HEM	O1A-CGA-CBA	-3.27	112.71	123.09
7	C	401	HEM	C1B-NB-C4B	3.26	109.06	105.21
7	C	401	HEM	O2D-CGD-CBD	3.24	124.24	114.00
7	B	401	HEM	CHB-C1B-NB	3.19	128.32	124.37
7	A	401	HEM	O1A-CGA-CBA	-3.13	113.18	123.09
8	A	403	EPE	O3S-S-C10	3.08	112.04	106.00
7	C	401	HEM	CAD-CBD-CGD	-2.94	105.87	113.67
7	A	401	HEM	C3B-C4B-NB	-2.91	107.38	109.47
8	A	403	EPE	O2S-S-O1S	2.91	123.29	113.82
7	C	401	HEM	CHD-C1D-C2D	-2.84	120.55	125.03
7	A	401	HEM	CHD-C4C-NC	2.83	127.53	124.45
7	A	401	HEM	CHD-C1D-ND	2.82	127.46	124.42
7	B	401	HEM	CHD-C4C-NC	2.80	127.50	124.45
7	C	401	HEM	CHA-C4D-C3D	-2.70	120.26	125.23
7	C	401	HEM	CHB-C1B-NB	2.66	127.66	124.37
7	B	401	HEM	CHD-C1D-ND	2.66	127.29	124.42
7	B	401	HEM	CHA-C4D-ND	2.64	127.64	124.37
7	A	401	HEM	CHA-C4D-ND	2.62	127.61	124.37
7	C	401	HEM	C3B-C4B-NB	-2.62	107.59	109.47
7	A	401	HEM	C3C-C2C-C1C	-2.52	104.66	107.05
7	C	401	HEM	CHD-C4C-NC	2.52	127.19	124.45
7	A	401	HEM	CHA-C4D-C3D	-2.51	120.60	125.23
8	C	404	EPE	O3S-S-O2S	2.40	117.40	111.40
7	A	401	HEM	C2A-C1A-NA	-2.39	107.50	110.15
7	C	401	HEM	O1D-CGD-CBD	-2.36	115.62	123.09
7	A	401	HEM	O2D-CGD-CBD	2.33	121.37	114.00
8	A	402	EPE	O2S-S-C10	-2.33	103.20	106.73
7	C	401	HEM	CMD-C2D-C1D	2.24	128.53	125.03
10	B	403	A1IUA	C10-C9-C8	-2.23	108.32	112.07
7	A	401	HEM	CMD-C2D-C1D	2.23	128.51	125.03
8	C	403	EPE	O2S-S-O1S	2.19	120.95	113.82
7	A	401	HEM	CHA-C1A-NA	2.17	127.80	123.86
8	A	403	EPE	C2-C3-N4	2.16	115.01	110.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	401	HEM	CHD-C1D-C2D	-2.12	121.68	125.03
7	C	401	HEM	C1A-CHA-C4D	-2.10	121.30	126.25
8	C	405	EPE	O2S-S-O1S	2.05	120.50	113.82
7	A	401	HEM	CMB-C2B-C1B	2.05	128.24	125.03
7	B	401	HEM	CAB-C3B-C2B	-2.05	121.78	128.43
7	A	401	HEM	CHD-C1D-C2D	-2.02	121.83	125.03
8	A	402	EPE	O2S-S-O1S	2.01	120.34	113.82

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	402	EPE	C10-C9-N1-C2
8	A	402	EPE	C8-C7-N4-C5
9	A	404	GOL	O1-C1-C2-C3
9	C	406	GOL	O1-C1-C2-C3
9	C	406	GOL	C1-C2-C3-O3
9	A	404	GOL	O1-C1-C2-O2
8	A	402	EPE	C9-C10-S-O3S
9	B	402	GOL	C1-C2-C3-O3
9	C	406	GOL	O1-C1-C2-O2
9	C	406	GOL	O2-C2-C3-O3
8	C	405	EPE	N4-C7-C8-O8
8	A	402	EPE	S-C10-C9-N1
8	A	402	EPE	N4-C7-C8-O8
8	C	404	EPE	N4-C7-C8-O8
9	A	404	GOL	O2-C2-C3-O3
9	B	402	GOL	O2-C2-C3-O3
8	A	402	EPE	C9-C10-S-O1S
8	A	402	EPE	C9-C10-S-O2S
8	A	403	EPE	S-C10-C9-N1
8	C	403	EPE	S-C10-C9-N1
8	C	404	EPE	S-C10-C9-N1
8	C	405	EPE	C10-C9-N1-C2
8	C	405	EPE	C10-C9-N1-C6
7	A	401	HEM	CAA-CBA-CGA-O2A
7	A	401	HEM	CAA-CBA-CGA-O1A
7	C	401	HEM	CAA-CBA-CGA-O2A
7	C	401	HEM	CAA-CBA-CGA-O1A
7	B	401	HEM	CAA-CBA-CGA-O1A
7	B	401	HEM	CAA-CBA-CGA-O2A
7	C	401	HEM	CAD-CBD-CGD-O2D

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Mol	Chain	Res	Type	Atoms
7	A	401	HEM	CAD-CBD-CGD-O1D
7	C	401	HEM	CAD-CBD-CGD-O1D

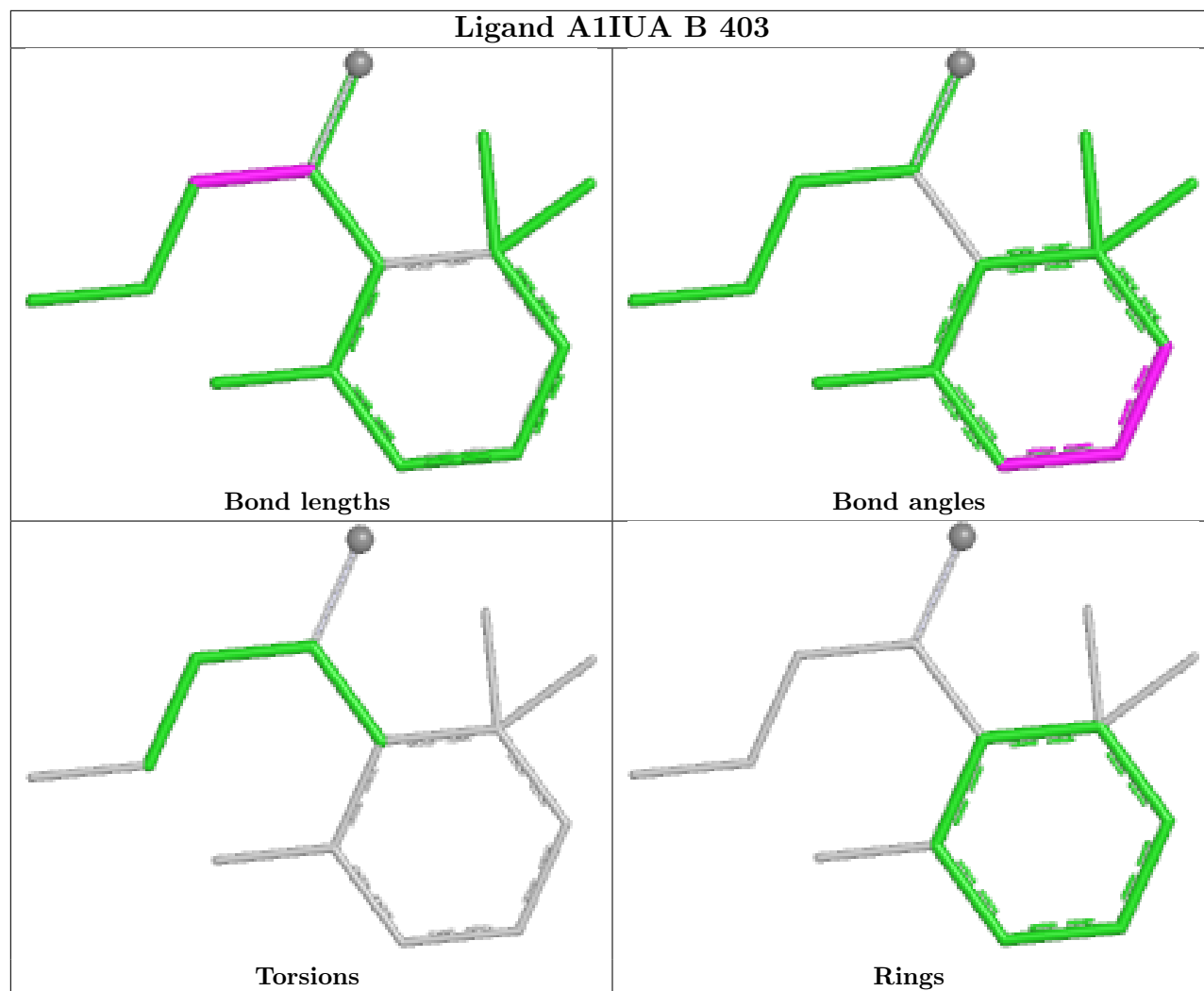
There are no ring outliers.

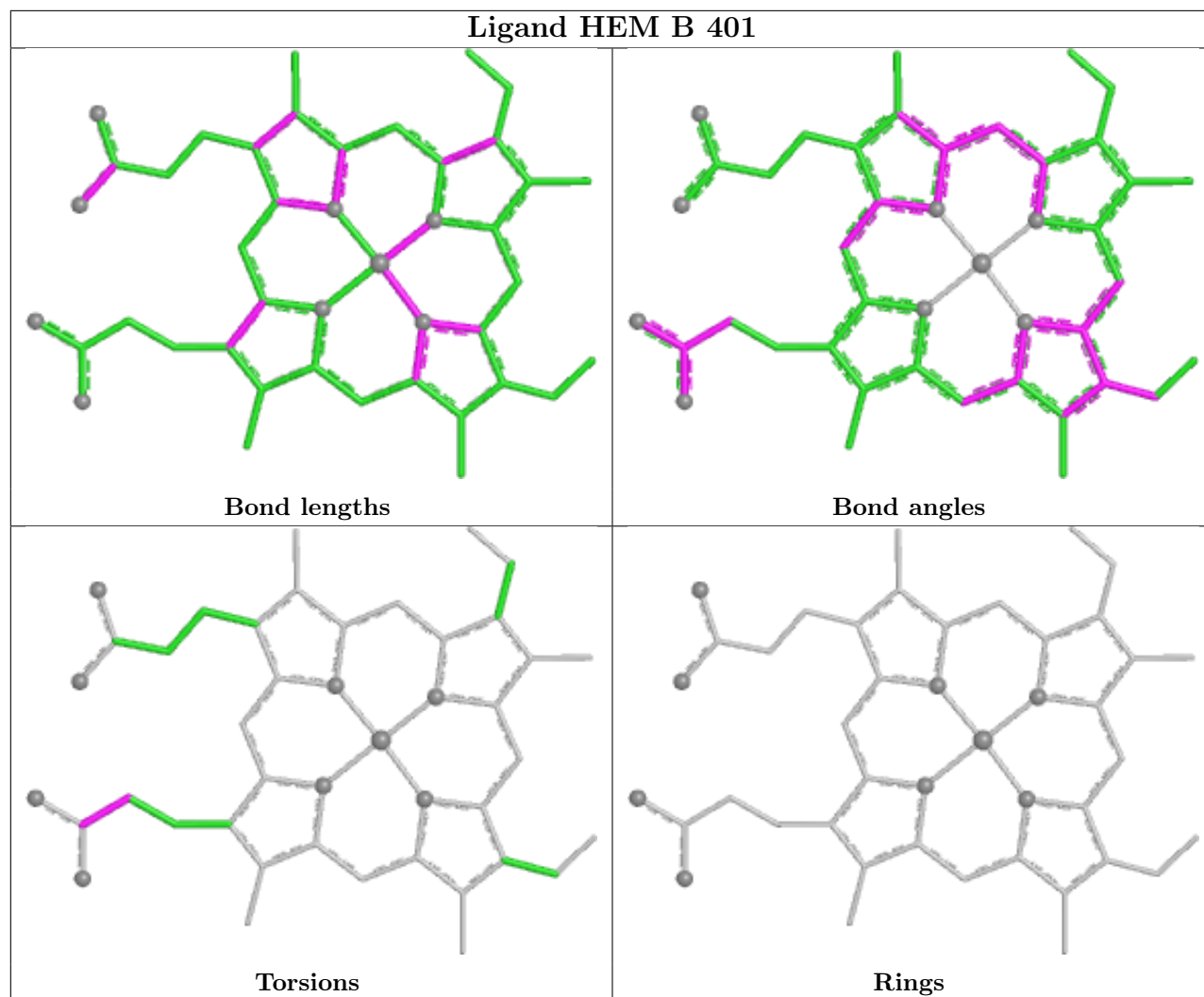
10 monomers are involved in 53 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	C	405	EPE	9	0
7	B	401	HEM	1	0
8	C	403	EPE	4	0
9	C	406	GOL	6	0
7	A	401	HEM	1	0
8	C	404	EPE	2	0
8	A	403	EPE	16	0
7	C	401	HEM	5	0
8	A	402	EPE	7	0
9	B	402	GOL	2	0

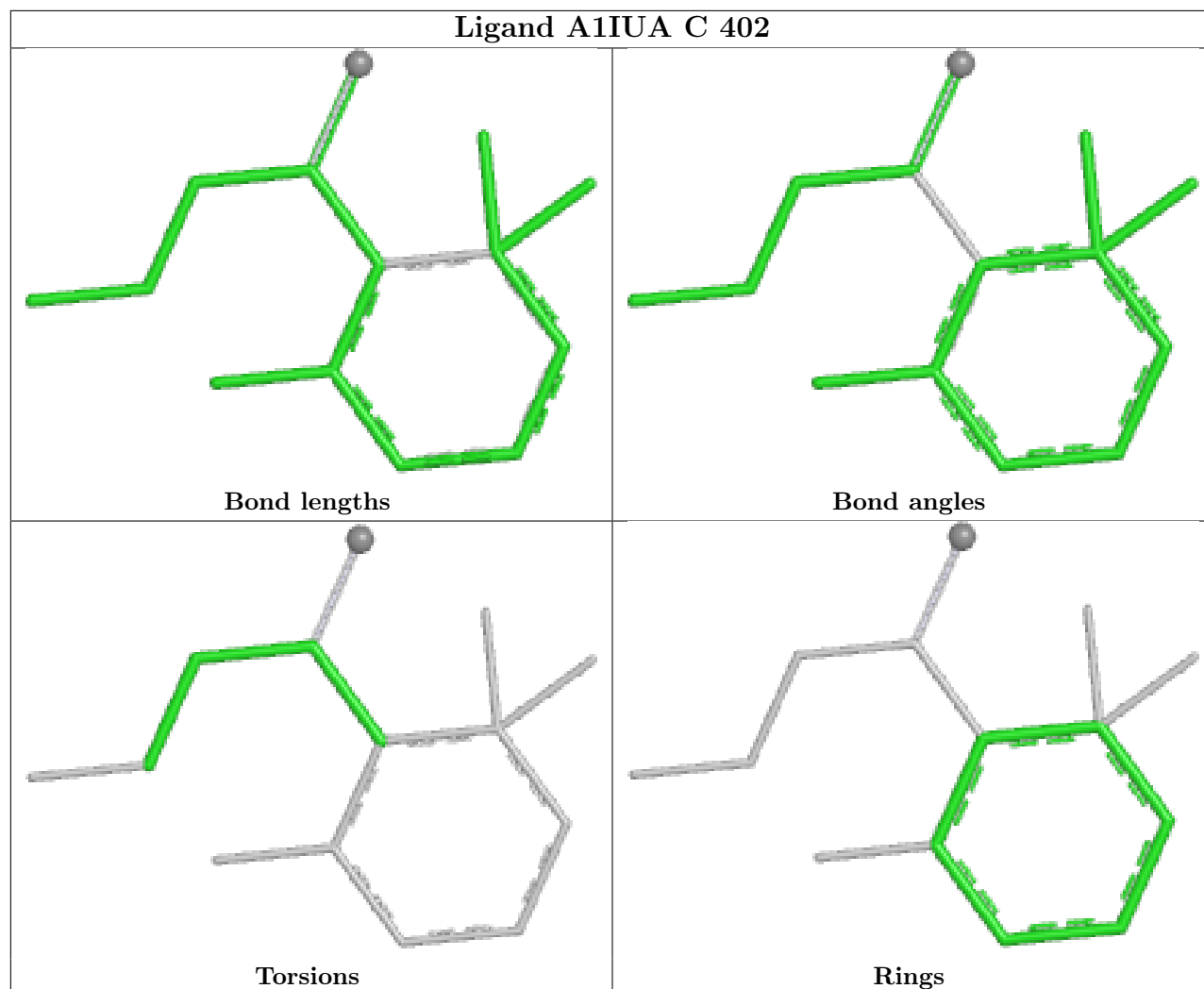
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

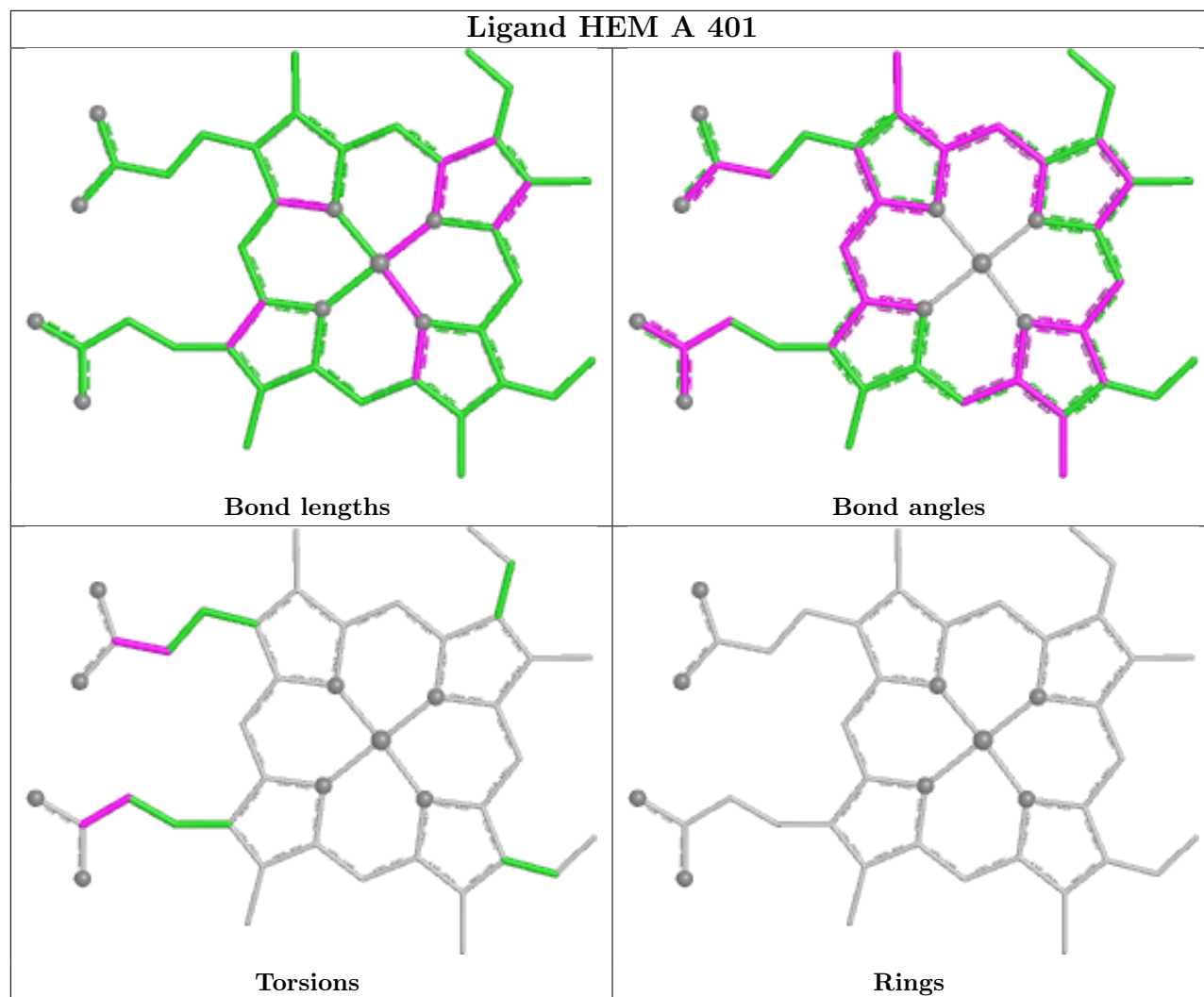
Ligand A1IUA B 403



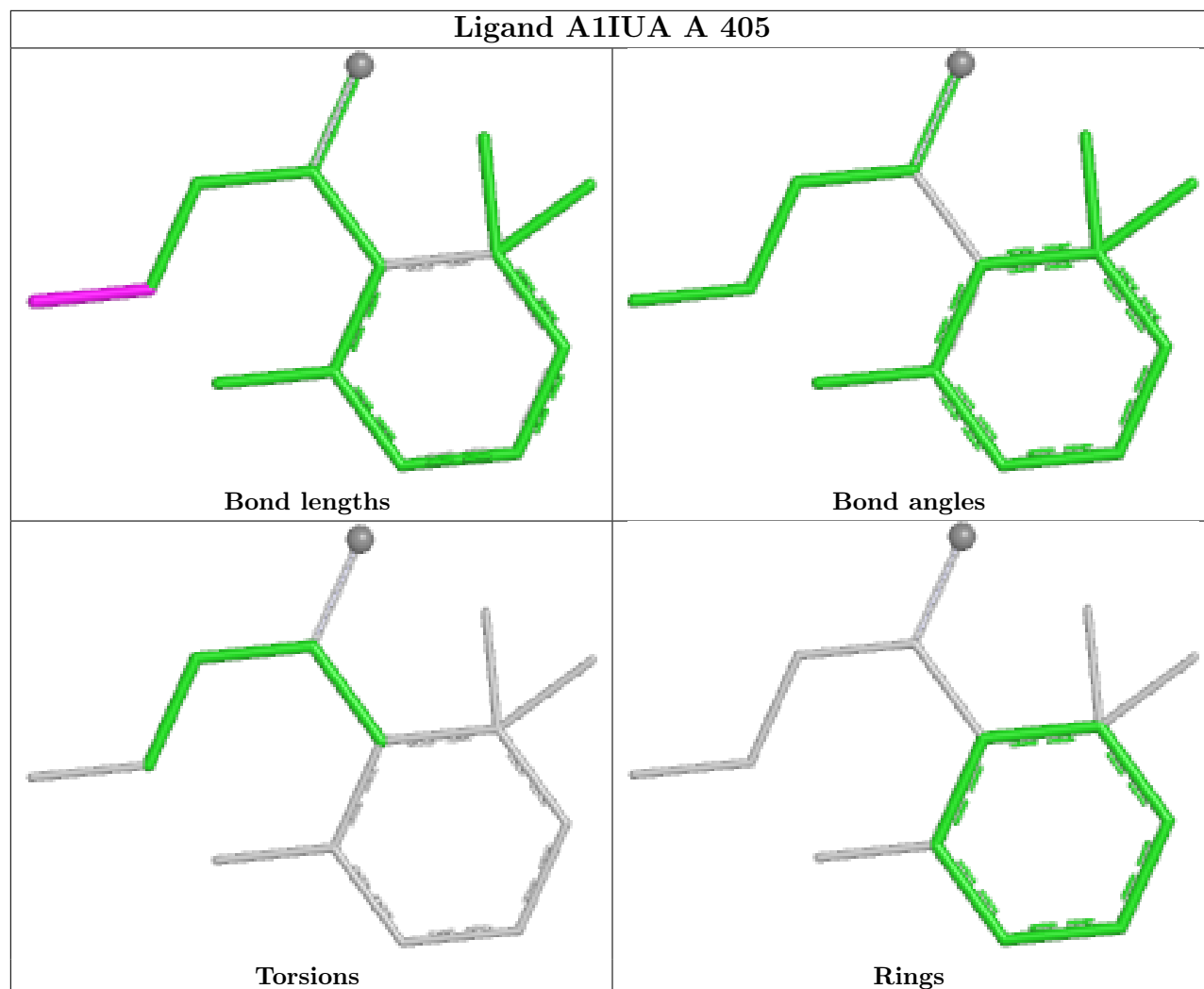


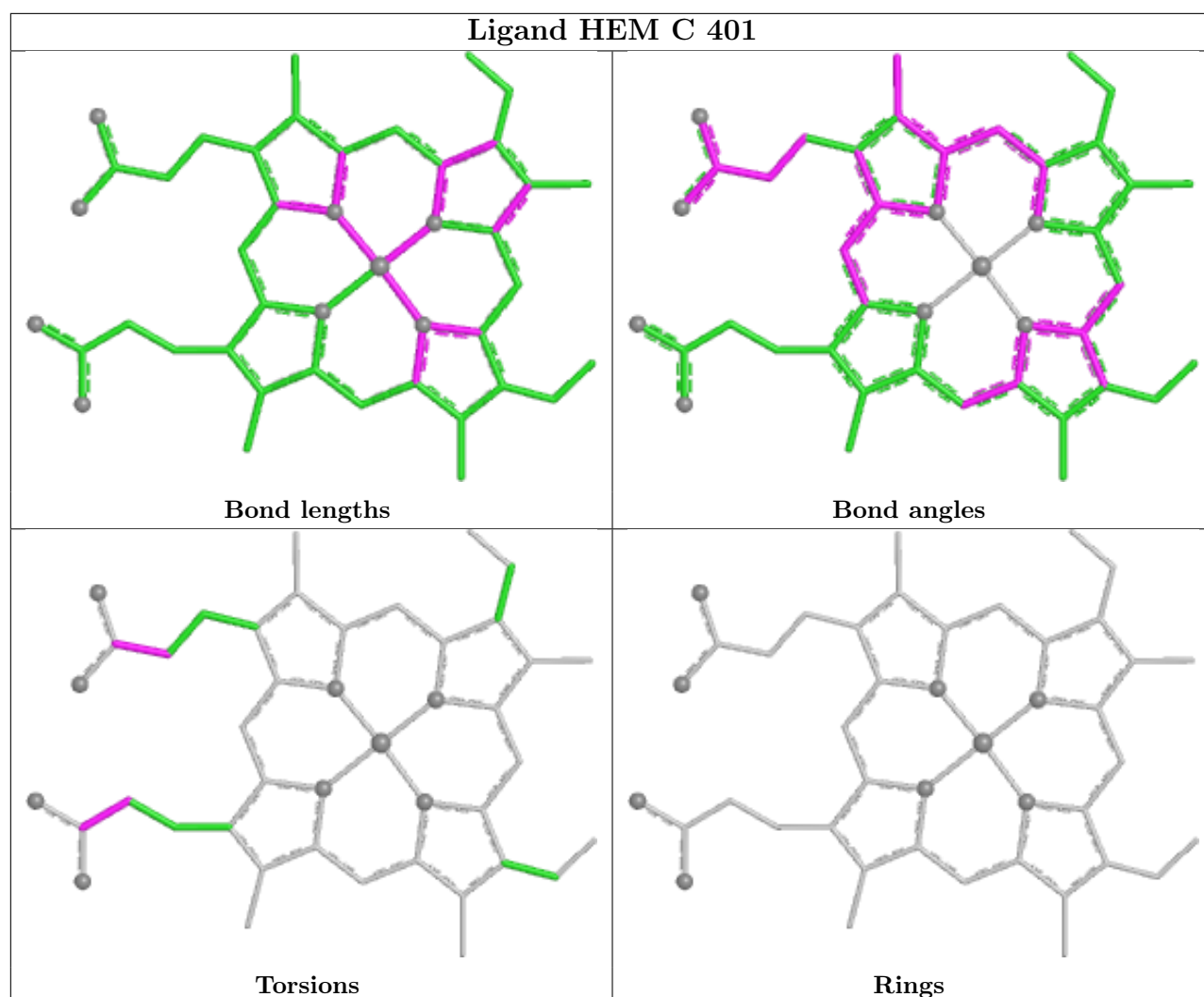
Ligand A1IUA C 402





Ligand A1IUA A 405





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%)	-0.17	6 (1%) 67 69	16, 36, 59, 116	7 (2%)
1	B	335/335 (100%)	-0.03	11 (3%) 49 50	18, 40, 68, 119	5 (1%)
1	C	335/335 (100%)	0.39	20 (5%) 27 24	17, 48, 80, 121	7 (2%)
All	All	1005/1005 (100%)	0.06	37 (3%) 45 45	16, 40, 75, 121	19 (1%)

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	17	ASP	4.6
1	A	14	GLN	4.2
1	B	227	THR	4.2
1	C	227	THR	3.8
1	B	316	ILE	3.8
1	C	186	TYR	3.1
1	B	277	ASP	3.0
1	B	339	CYS	3.0
1	C	316	ILE	2.9
1	C	278	ASN	2.8
1	A	227	THR	2.8
1	B	15	GLY	2.7
1	B	14	GLN	2.7
1	C	164	PHE	2.7
1	B	348	LEU	2.7
1	C	270	TRP	2.7
1	A	277	ASP	2.6
1	B	278	ASN	2.6
1	C	14	GLN	2.5
1	B	228	ASP	2.5
1	A	348	LEU	2.5
1	C	167	PHE	2.4
1	C	277	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	136[A]	THR	2.3
1	C	171	TYR	2.3
1	C	339	CYS	2.3
1	A	228	ASP	2.2
1	C	266	ALA	2.2
1	C	228	ASP	2.2
1	B	16	VAL	2.2
1	C	284	VAL	2.2
1	C	175	PHE	2.2
1	C	15	GLY	2.1
1	C	198	GLU	2.1
1	C	275	ASN	2.1
1	A	136[A]	THR	2.1
1	B	17	ASP	2.1

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
2	BMA	H	3	11/12	0.47	0.23	80,98,110,112	0
2	MAN	H	4	11/12	0.65	0.17	59,77,88,91	0
2	NAG	H	1	14/15	0.75	0.19	45,56,70,75	0
2	NAG	H	2	14/15	0.83	0.15	48,63,77,86	0
2	MAN	H	5	11/12	-	-	77,96,107,111	0
2	NAG	Y	1	14/15	-	-	53,62,71,72	0
2	NAG	Y	2	14/15	-	-	66,77,85,91	0
2	BMA	Y	3	11/12	-	-	86,98,104,105	0
2	MAN	Y	4	11/12	-	-	49,69,76,81	0
2	MAN	Y	5	11/12	-	-	61,77,84,92	0
3	NAG	J	1	14/15	-	-	38,43,50,53	0
3	NAG	J	2	14/15	-	-	42,56,72,73	0
3	BMA	J	3	11/12	-	-	66,92,102,102	0
3	MAN	J	4	11/12	-	-	86,108,135,155	0

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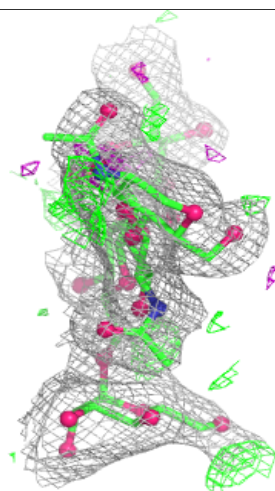
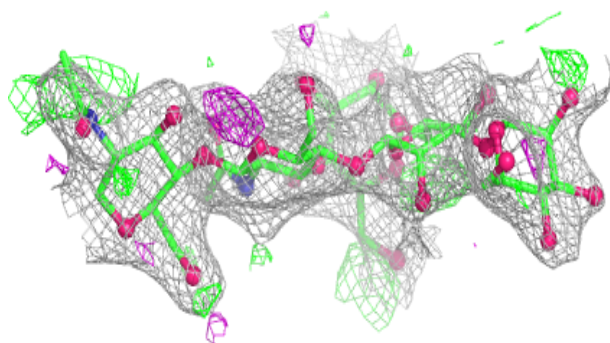
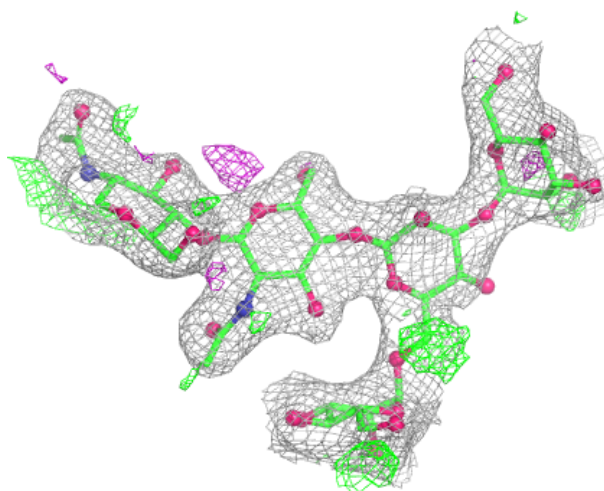
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MAN	J	5	11/12	-	-	95,111,116,116	0
3	MAN	J	6	11/12	-	-	108,137,147,150	0
3	MAN	J	7	11/12	-	-	98,115,130,133	0
4	NAG	Z	1	14/15	-	-	38,46,54,56	0
4	NAG	Z	2	14/15	-	-	43,58,79,92	0
4	BMA	Z	3	11/12	-	-	75,97,105,122	0
4	MAN	Z	4	11/12	-	-	97,103,107,107	0
4	MAN	Z	5	11/12	-	-	88,106,114,115	0
4	MAN	Z	6	11/12	-	-	116,139,146,148	0
5	NAG	m	1	14/15	-	-	71,80,91,92	0
5	NAG	m	2	14/15	-	-	61,67,71,74	0
5	BMA	m	3	11/12	-	-	64,78,82,82	0
5	MAN	m	4	11/12	-	-	59,65,76,78	0
6	NAG	n	1	14/15	-	-	72,91,100,114	0
6	NAG	n	2	14/15	-	-	91,131,147,157	0
6	BMA	n	3	11/12	-	-	124,150,164,168	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.

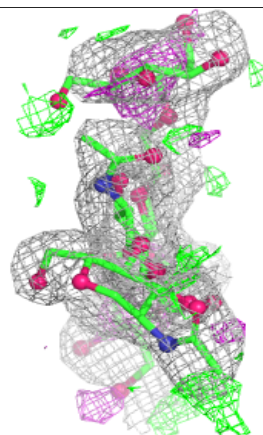
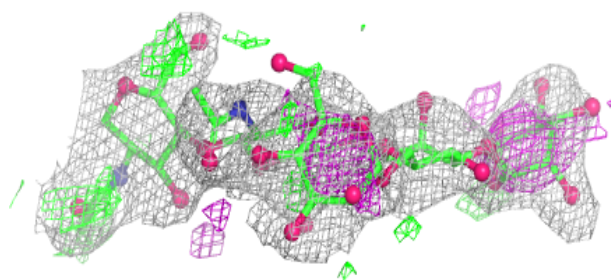
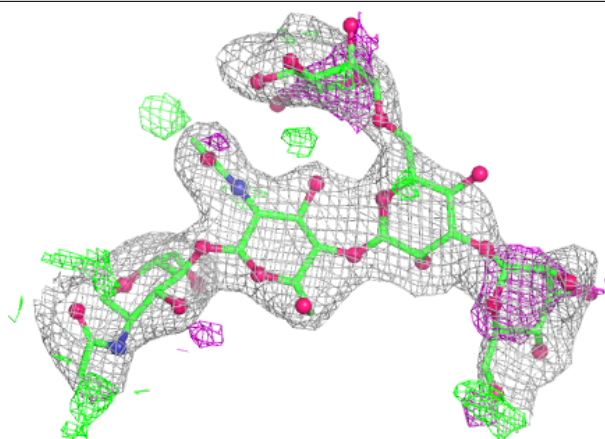
Electron density around Chain H:

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

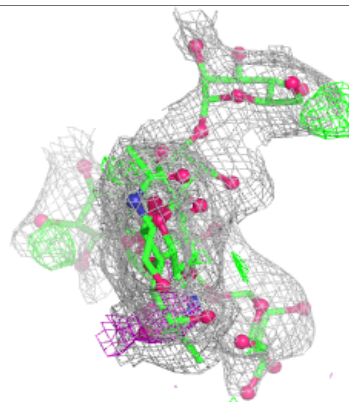
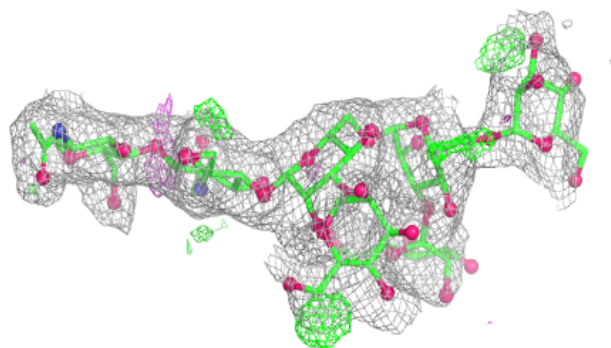
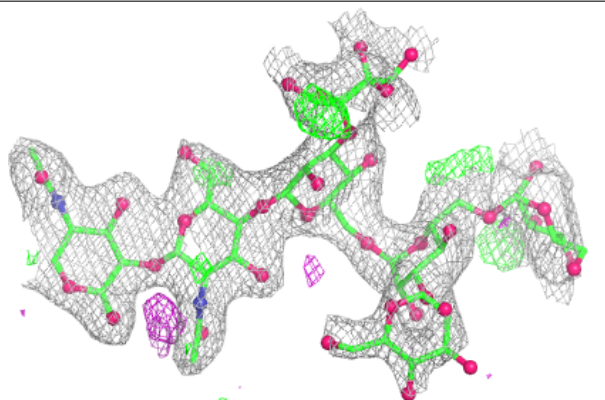


Electron density around Chain Y:

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

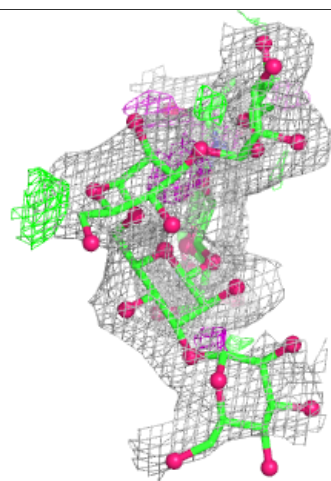
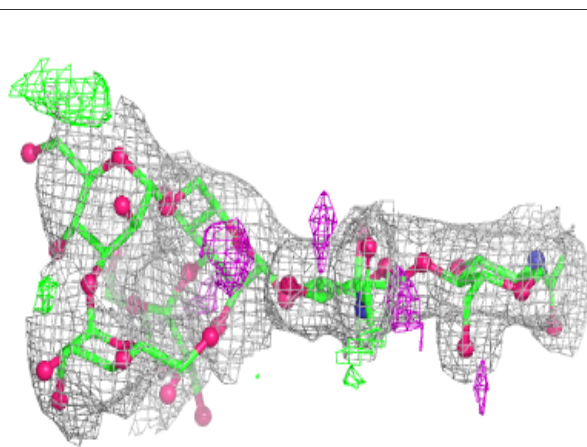
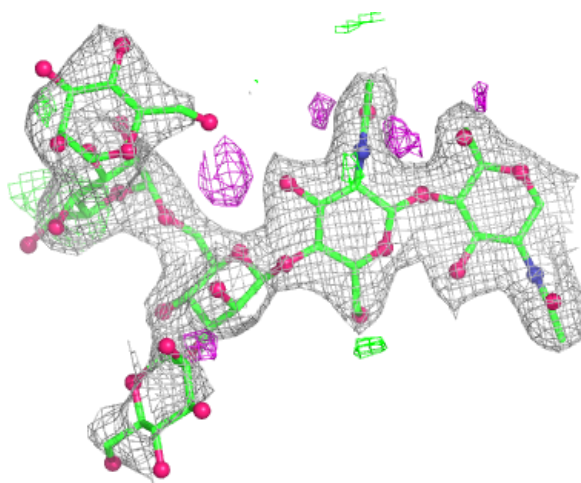
**Electron density around Chain J:**

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



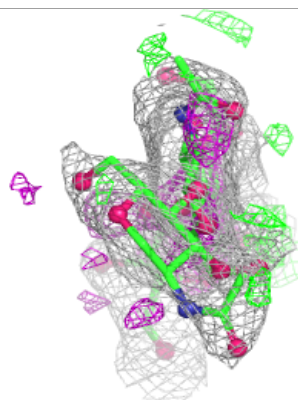
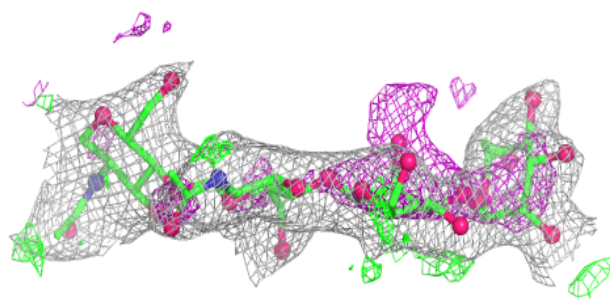
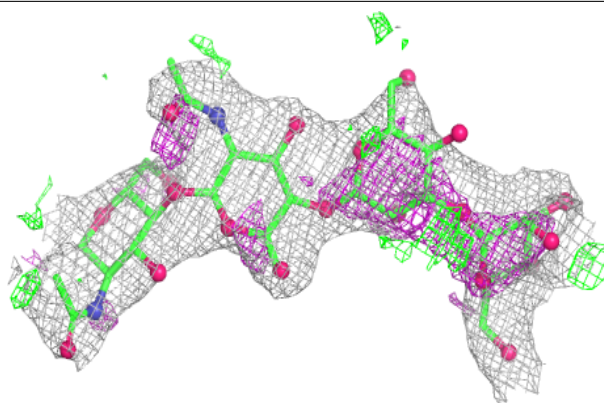
Electron density around Chain Z:

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

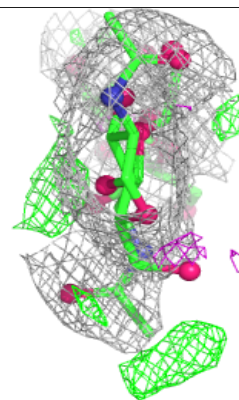
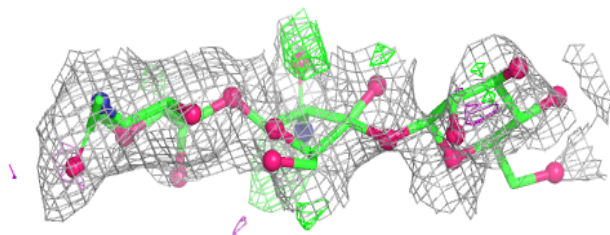
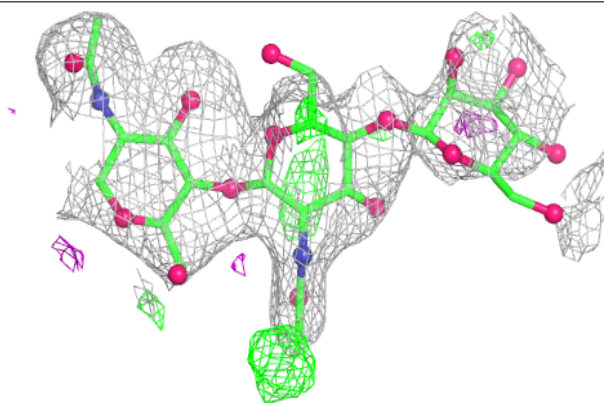


Electron density around Chain m:

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

**Electron density around Chain 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 ⓘ

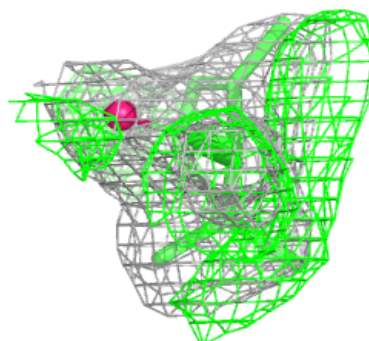
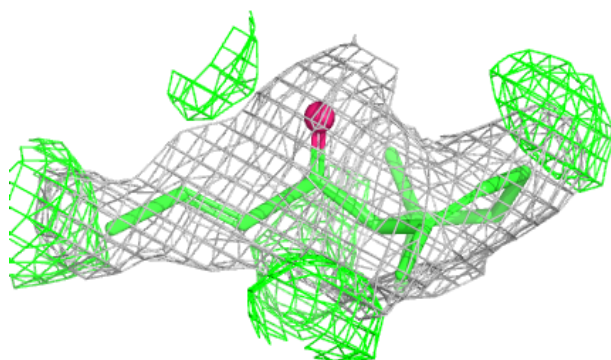
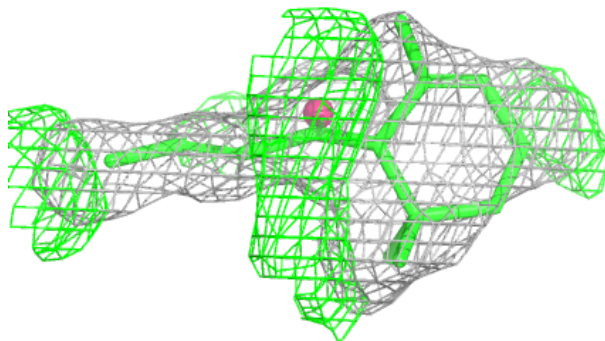
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
8	EPE	A	402	15/15	0.58	0.31	46,51,62,63	15
8	EPE	C	405	15/15	0.60	0.33	48,59,63,69	15
8	EPE	C	404	15/15	0.66	0.32	48,59,63,65	15
8	EPE	C	403	15/15	0.71	0.29	52,57,62,67	15
8	EPE	A	403	15/15	0.76	0.22	47,55,59,59	15
12	SO4	B	407	5/5	0.78	0.24	63,64,65,75	0
12	SO4	A	408	5/5	0.79	0.29	51,51,69,75	0
10	A1IUA	B	403	14/14	0.79	0.25	49,54,57,57	0
9	GOL	A	404	6/6	0.80	0.19	47,53,57,62	0
12	SO4	B	406	5/5	0.81	0.34	59,60,61,75	0
10	A1IUA	A	405	14/14	0.82	0.22	43,48,54,55	0
11	MG	B	404	1/1	0.83	0.28	49,49,49,49	0
12	SO4	A	410	5/5	0.83	0.31	56,62,66,66	0
10	A1IUA	C	402	14/14	0.84	0.22	46,54,55,60	0
9	GOL	C	406	6/6	0.85	0.28	41,47,48,52	0
12	SO4	B	408	5/5	0.85	0.36	61,63,71,72	0
12	SO4	B	405	5/5	0.87	0.17	55,58,66,70	0
12	SO4	A	407	5/5	0.88	0.16	52,53,60,63	0
11	MG	C	407	1/1	0.89	0.22	58,58,58,58	0
9	GOL	B	402	6/6	0.89	0.15	43,48,52,54	0
11	MG	A	406	1/1	0.90	0.16	41,41,41,41	0
12	SO4	A	409	5/5	0.91	0.26	48,51,57,61	0
12	SO4	B	409	5/5	0.92	0.26	46,53,57,59	0
7	HEM	C	401	43/43	0.98	0.09	31,40,57,69	0
7	HEM	A	401	43/43	0.98	0.08	27,31,41,46	0
7	HEM	B	401	43/43	0.98	0.07	27,30,40,54	0

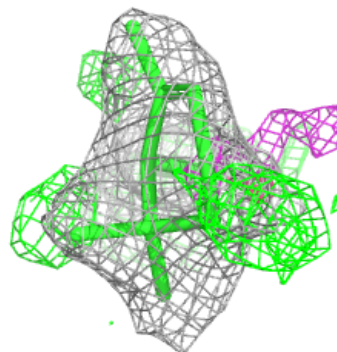
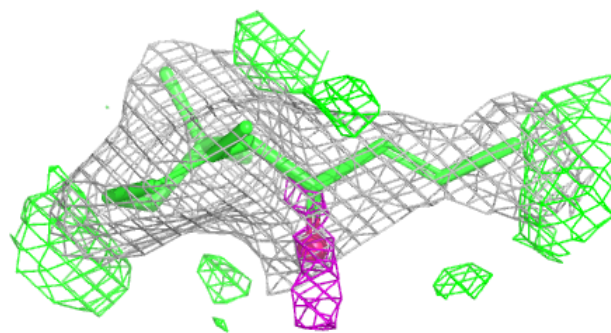
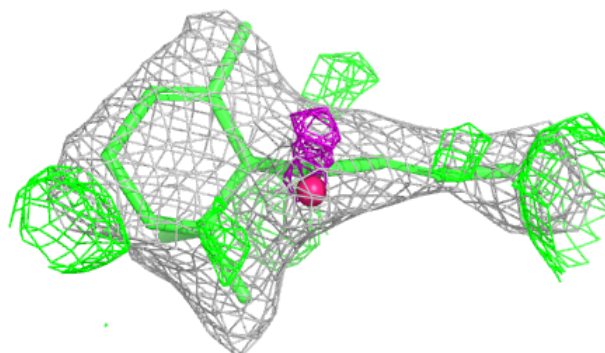
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around A1IUA B 403:

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

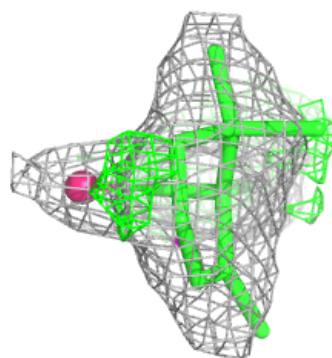
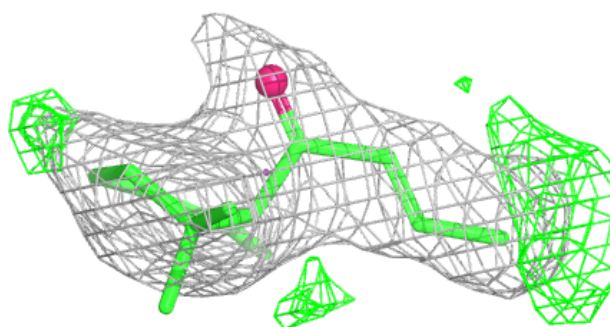
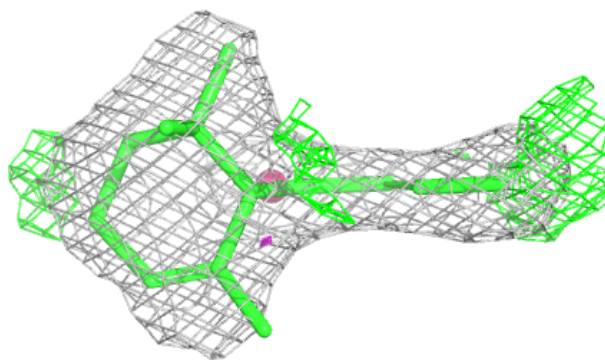
**Electron density around A1IUA A 405:**

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

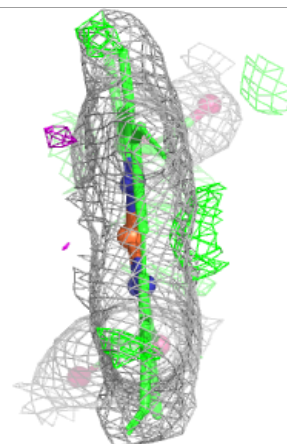
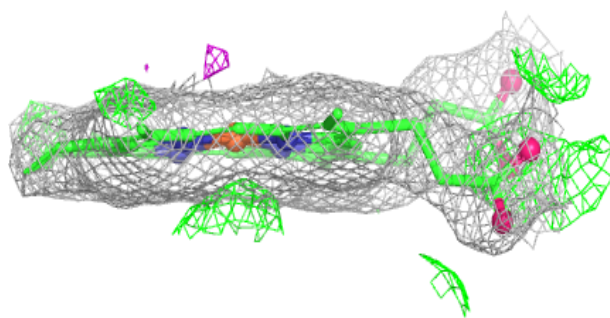
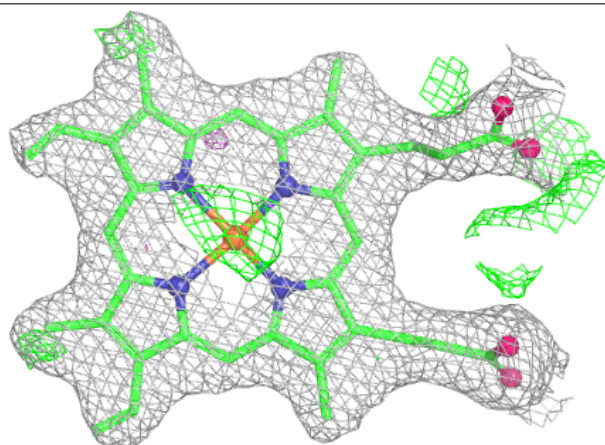


Electron density around A1IUA C 402:

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

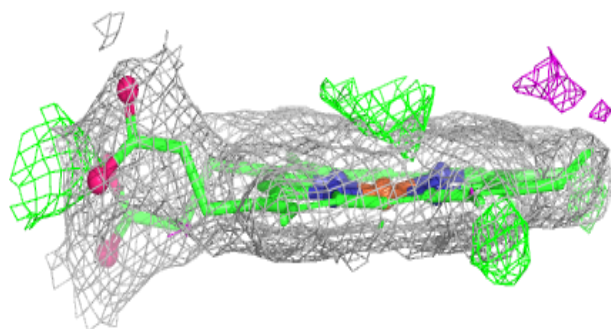
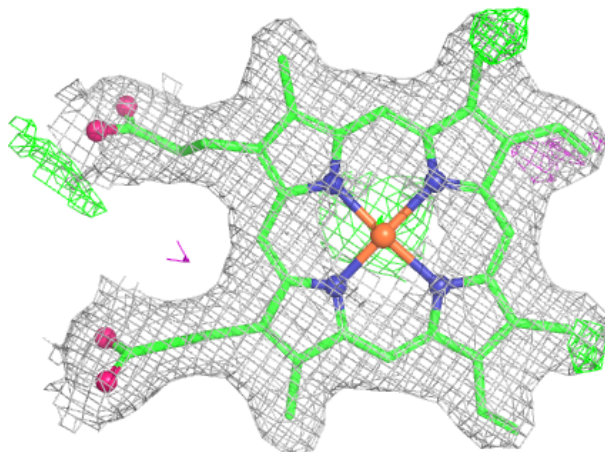
**Electron density around HEM C 401:**

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



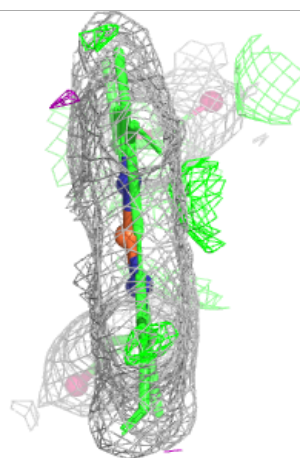
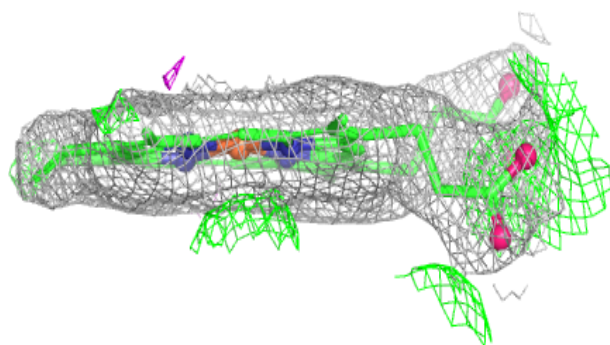
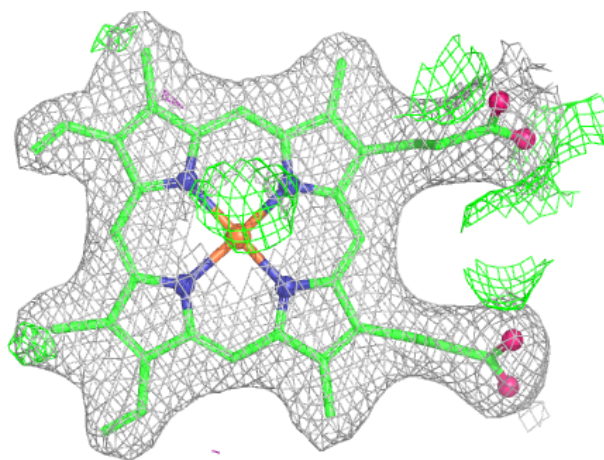
Electron density around HEM A 401:

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



Electron density around HEM B 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.