



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 7, 2026 – 03:16 AM UTC

PDB ID : 2PT3 / pdb_00002pt3
Title : Crystal structure of bovine lactoperoxidase at 2.34 Å resolution reveals multiple anion binding sites
Authors : Singh, A.K.; Singh, N.; Sharma, S.; Kaur, P.; Betzel, C.; Singh, T.P.
Deposited on : 2007-05-08
Resolution : 2.34 Å (reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

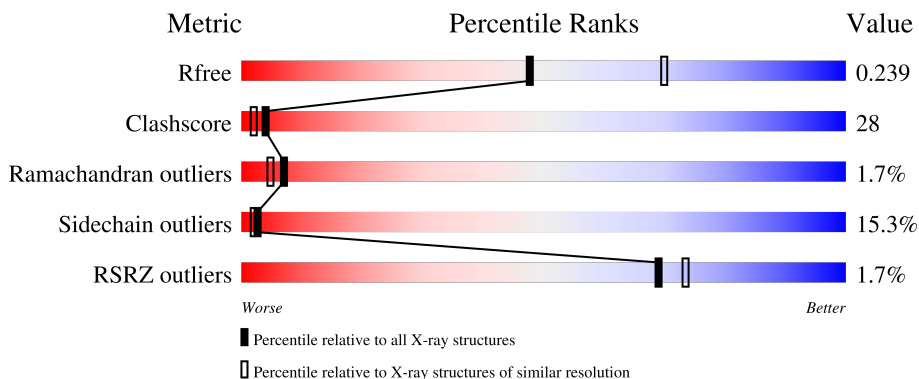
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.34 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	3031 (2.36-2.32)
Clashscore	190562	3127 (2.36-2.32)
Ramachandran outliers	187476	3095 (2.36-2.32)
Sidechain outliers	187428	3095 (2.36-2.32)
RSRZ outliers	180081	3033 (2.36-2.32)

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	595	 2% 50% 39% 9%
2	B	3	 33% 67%
2	D	3	 67% 33%
3	C	2	 50% 50%
3	E	2	 100%

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
2	NAG	B	1	X	-	-	-
5	PO4	A	607	-	-	X	-
5	PO4	A	608	-	X	X	-
5	PO4	A	609	-	X	-	-
5	PO4	A	610	-	X	X	-
5	PO4	A	611	-	X	-	-
5	PO4	A	612	-	X	-	-
5	PO4	A	614	-	X	-	-
5	PO4	A	615	-	X	-	-
5	PO4	A	616	-	-	X	-
5	PO4	A	618	-	X	-	-
5	PO4	A	619	-	X	-	-
5	PO4	A	621	-	X	X	-

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 5281 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.

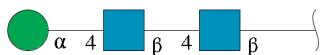
- Molecule 1 is a protein called Lactoperoxidase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	595	4774	3037	847	863	1	26	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	198	SEP	SER	modified residue	UNP P80025

- Molecule 2 is an oligosaccharide called alpha-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
			Total	C	N	O			
2	B	3	39	22	2	15	0	0	0
2	D	3	39	22	2	15	0	0	0

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



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

Continued on next page...

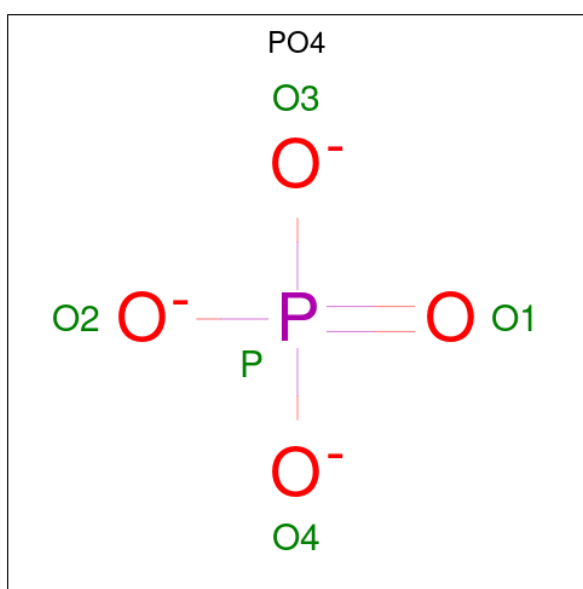
Continued from previous page...

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

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ca	0	0
			1	1		

- Molecule 5 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



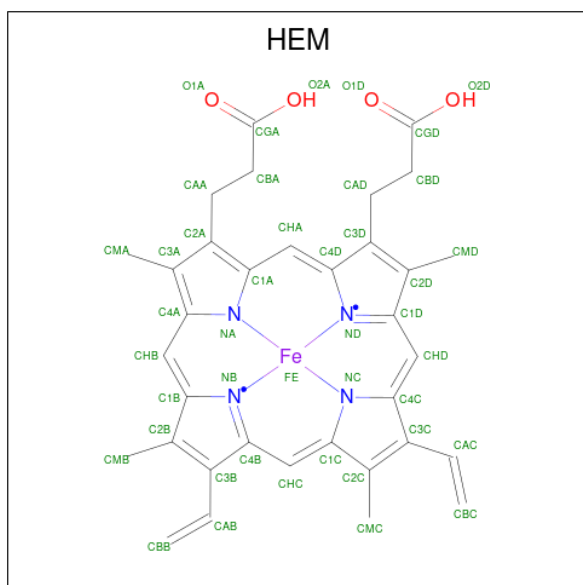
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	P	0	0
			5	4	1		
5	A	1	Total	O	P	0	0
			5	4	1		
5	A	1	Total	O	P	0	0
			5	4	1		
5	A	1	Total	O	P	0	0
			5	4	1		
5	A	1	Total	O	P	0	0
			5	4	1		
5	A	1	Total	O	P	0	0
			5	4	1		
5	A	1	Total	O	P	0	0
			5	4	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	P	0	0
			5	4	1		
5	A	1	Total	O	P	0	0
			5	4	1		
5	A	1	Total	O	P	0	0
			5	4	1		
5	A	1	Total	O	P	0	0
			5	4	1		
5	A	1	Total	O	P	0	0
			5	4	1		
5	A	1	Total	O	P	0	0
			5	4	1		
5	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 6 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

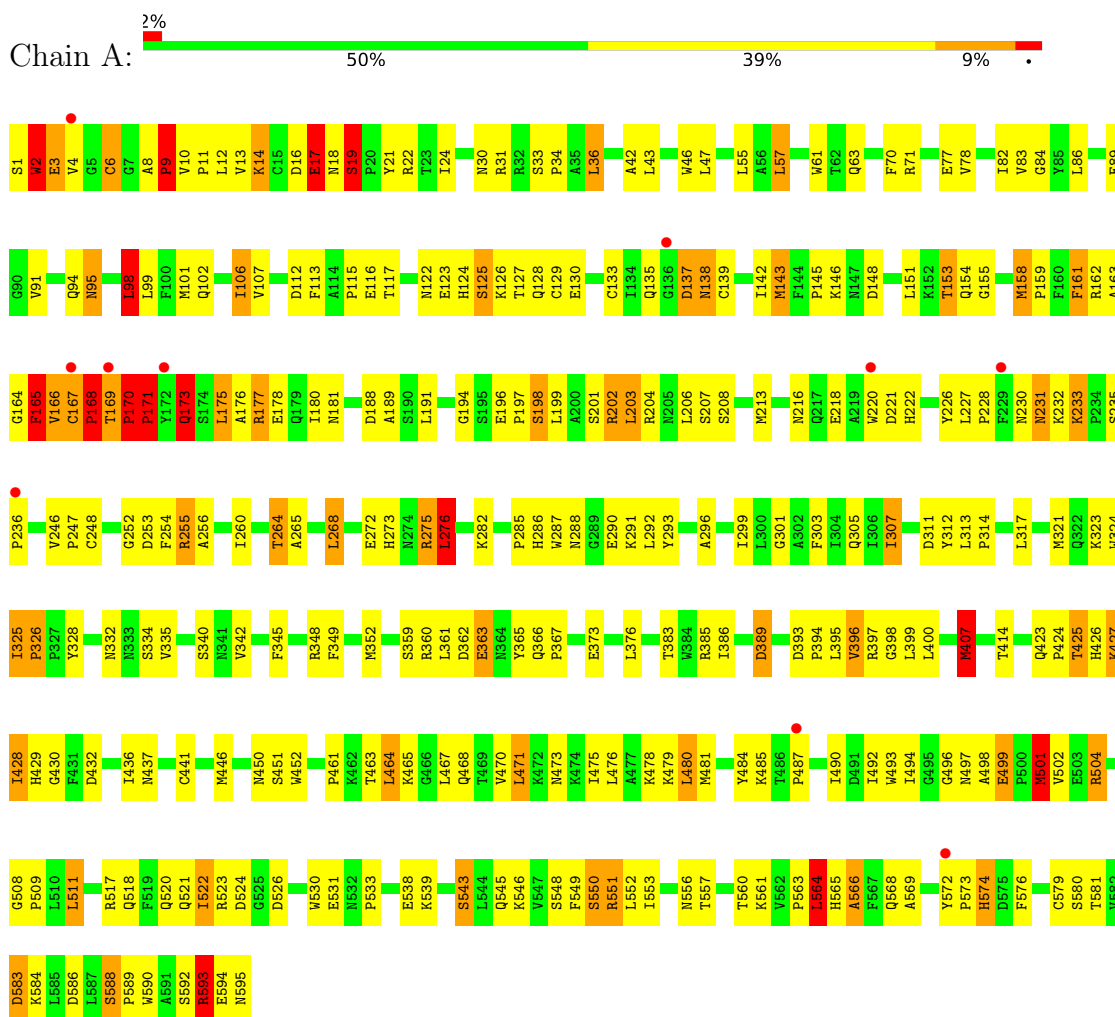
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	249	Total 249	O 249	0	0

3 Residue-property plots i

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

- Molecule 1: Lactoperoxidase



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

Chain D:  67% 33%

MAG1
MAG2
MAG3

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

Chain C:  50% 50%

MAG1
MAG2

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

Chain E:  100%

MAG1
MAG2

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	53.91Å 80.05Å 75.67Å 90.00° 103.23° 90.00°	Depositor
Resolution (Å)	19.38 – 2.34 19.38 – 2.34	Depositor EDS
% Data completeness (in resolution range)	96.8 (19.38-2.34) 96.7 (19.38-2.34)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.08 (at 2.30Å)	Xtrriage
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.231 , 0.247 0.236 , 0.239	Depositor DCC
R_{free} test set	834 reflections (3.03%)	wwPDB-VP
Wilson B-factor (Å ²)	49.6	Xtrriage
Anisotropy	0.690	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 52.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5281	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.37% 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: SEP, HEM, MAN, NAG, PO4, CA

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	1.04	9/4891 (0.2%)	1.36	47/6634 (0.7%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	158	MET	SD-CE	11.08	2.07	1.79
1	A	407	MET	SD-CE	6.54	1.96	1.79
1	A	170	PRO	CA-C	6.21	1.57	1.52
1	A	396	VAL	CA-CB	-5.63	1.46	1.54
1	A	264	THR	CA-C	-5.52	1.45	1.52

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	17	GLU	N-CA-C	-15.73	93.73	113.23
1	A	10	VAL	N-CA-C	10.14	117.59	107.55
1	A	564	LEU	N-CA-C	-9.41	101.69	113.55
1	A	170	PRO	N-CA-C	8.12	120.60	110.70
1	A	254	PHE	N-CA-C	6.81	120.84	112.54

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	135	GLN	Peptide
1	A	231	ASN	Peptide
1	A	233	LYS	Peptide

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	4774	0	4688	266	0
2	B	39	0	34	6	0
2	D	39	0	34	1	0
3	C	28	0	25	0	0
3	E	28	0	25	2	0
4	A	1	0	0	0	0
5	A	80	0	0	17	0
6	A	43	0	30	7	0
7	A	249	0	0	20	0
All	All	5281	0	4836	276	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 28.

The worst 5 of 276 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:158:MET:CE	1:A:158:MET:SD	2.07	1.42
1:A:478:LYS:HB3	7:A:701:HOH:O	1.36	1.20
1:A:169:THR:HG22	1:A:170:PRO:HD3	1.34	1.06
1:A:561:LYS:HG3	7:A:638:HOH:O	1.57	1.04
1:A:504:ARG:HG2	1:A:504:ARG:HH11	1.19	1.03

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	592/595 (100%)	539 (91%)	43 (7%)	10 (2%)	7 5

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	167	CYS
1	A	593	ARG
1	A	2	TRP
1	A	3	GLU
1	A	138	ASN

5.3.2 Protein sidechains [i](#)

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	517/517 (100%)	438 (85%)	79 (15%)	3 2

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	407	MET
1	A	550	SER
1	A	464	LEU
1	A	501	MET
1	A	583	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	468	GLN
1	A	521	GLN
1	A	574	HIS
1	A	366	GLN
1	A	423	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	SEP	A	198	1	8,9,10	1.54	1 (12%)	7,12,14	3.49	5 (71%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	SEP	A	198	1	-	2/6/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	198	SEP	CA-N	-2.87	1.40	1.48

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	198	SEP	OG-P-O1P	6.26	123.37	106.44
1	A	198	SEP	O2P-P-OG	4.14	117.47	106.67
1	A	198	SEP	OG-CB-CA	-3.51	104.73	108.14
1	A	198	SEP	O3P-P-O1P	-3.34	97.81	110.83
1	A	198	SEP	O3P-P-OG	-2.01	101.44	106.67

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	198	SEP	N-CA-CB-OG
1	A	198	SEP	C-CA-CB-OG

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	198	SEP	2	0

5.5 Carbohydrates i

10 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	B	1	1,2	14,14,15	0.75	0	17,19,21	2.08	6 (35%)
2	NAG	B	2	2	14,14,15	0.73	1 (7%)	17,19,21	1.72	5 (29%)
2	MAN	B	3	2	11,11,12	0.77	0	15,15,17	1.34	3 (20%)
3	NAG	C	1	1,3	14,14,15	0.56	0	17,19,21	2.31	3 (17%)
3	NAG	C	2	3	14,14,15	0.64	0	17,19,21	0.99	0
2	NAG	D	1	1,2	14,14,15	0.74	0	17,19,21	1.66	2 (11%)
2	NAG	D	2	2	14,14,15	0.73	1 (7%)	17,19,21	1.21	2 (11%)
2	MAN	D	3	2	11,11,12	0.62	0	15,15,17	1.68	3 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	E	1	1,3	14,14,15	0.70	1 (7%)	17,19,21	1.28	2 (11%)
3	NAG	E	2	3	14,14,15	0.61	0	17,19,21	1.09	1 (5%)

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	B	1	1,2	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	B	2	2	-	1/6/23/26	0/1/1/1
2	MAN	B	3	2	-	2/2/19/22	1/1/1/1
3	NAG	C	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	C	2	3	-	2/6/23/26	0/1/1/1
2	NAG	D	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	0/6/23/26	0/1/1/1
2	MAN	D	3	2	-	2/2/19/22	0/1/1/1
3	NAG	E	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	2	NAG	O5-C1	-2.25	1.39	1.43
2	B	2	NAG	O5-C1	-2.06	1.40	1.43
3	E	1	NAG	O5-C1	-2.04	1.40	1.43

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1	NAG	C1-O5-C5	7.81	122.65	112.19
2	B	1	NAG	C1-O5-C5	5.59	119.68	112.19
2	D	3	MAN	C1-C2-C3	4.41	116.06	109.64
2	D	1	NAG	O5-C1-C2	-4.25	104.71	111.29
2	D	1	NAG	C2-N2-C7	-3.98	117.56	122.90

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	1	NAG	C1

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2	NAG	C3-C2-N2-C7
3	E	1	NAG	O5-C5-C6-O6
3	E	2	NAG	O5-C5-C6-O6
2	D	3	MAN	O5-C5-C6-O6
3	E	1	NAG	C4-C5-C6-O6

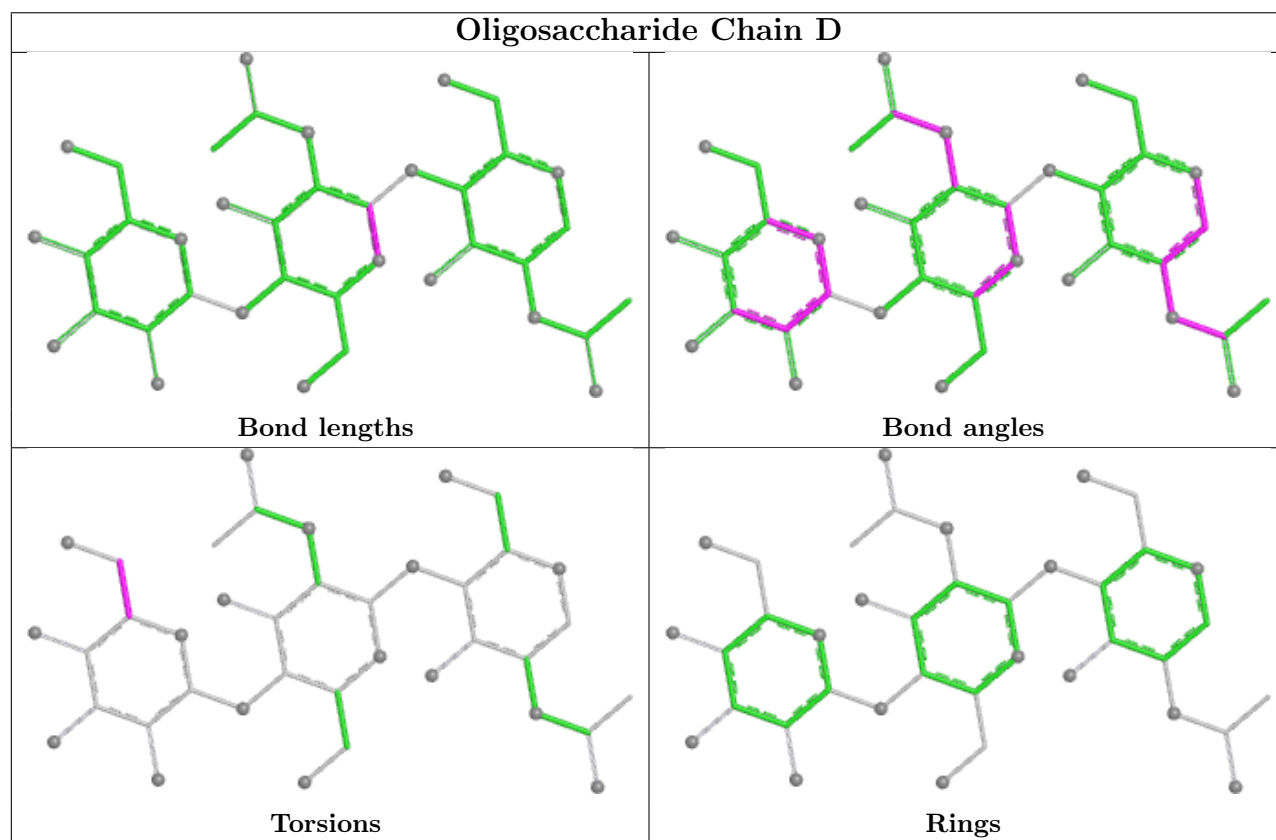
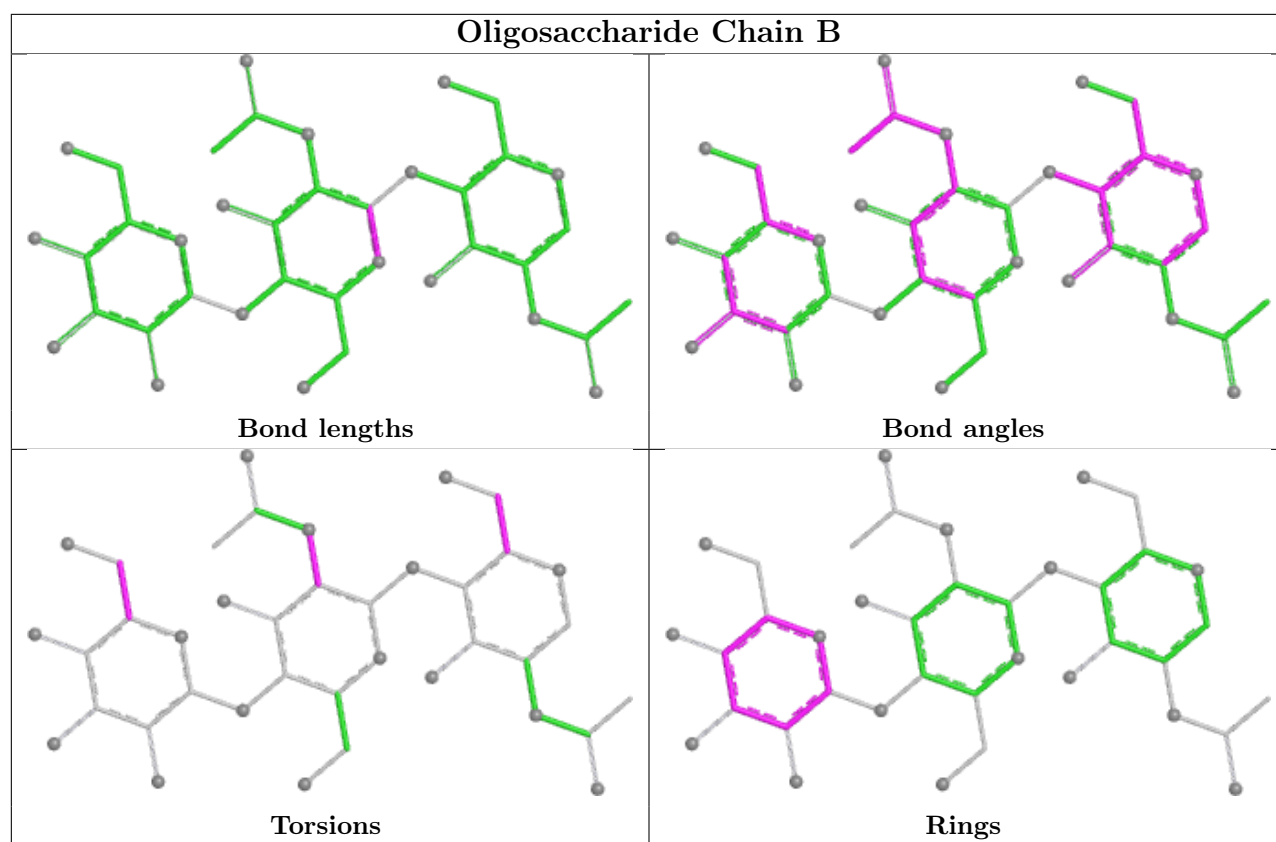
All (1) ring outliers are listed below:

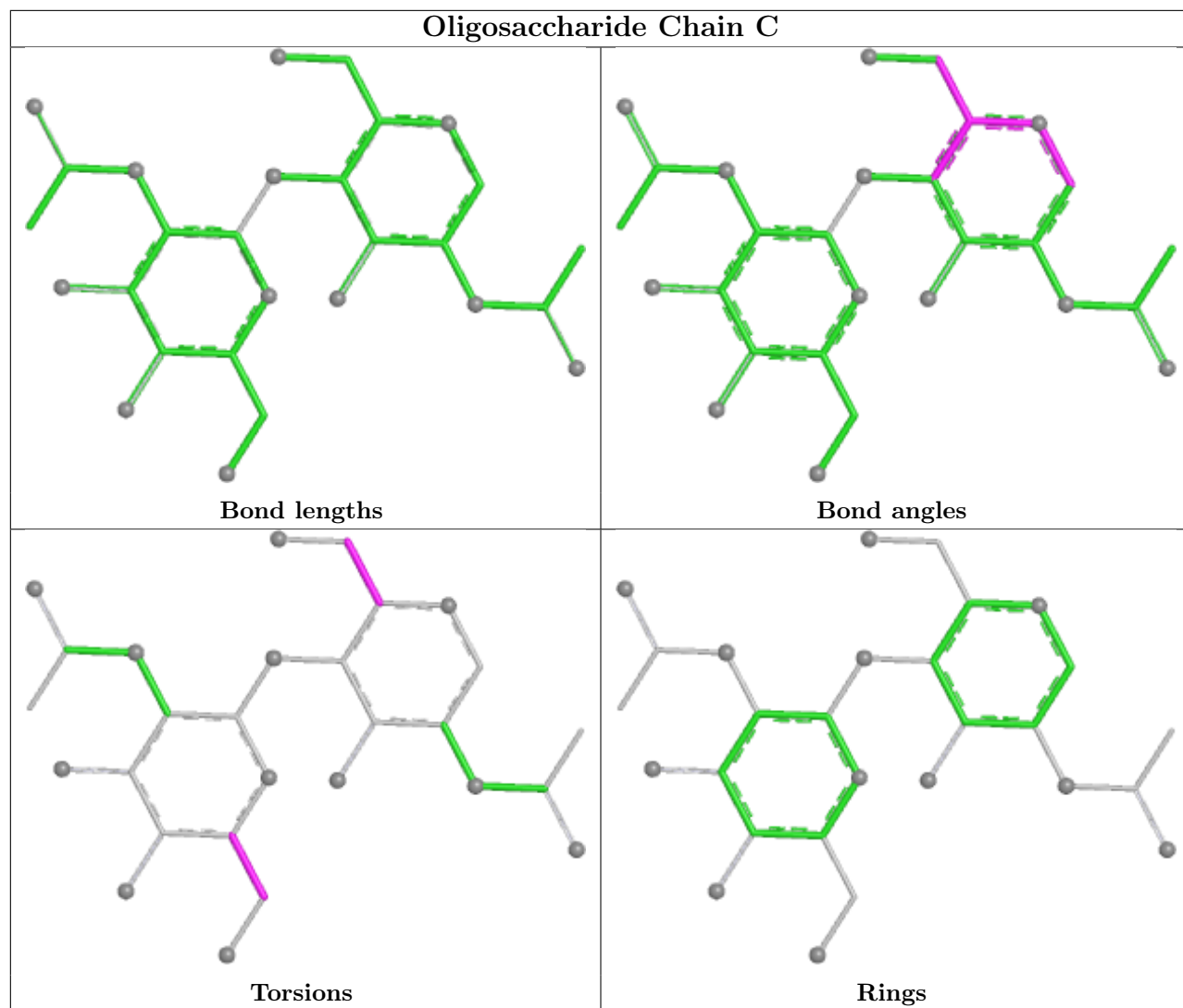
Mol	Chain	Res	Type	Atoms
2	B	3	MAN	C1-C2-C3-C4-C5-O5

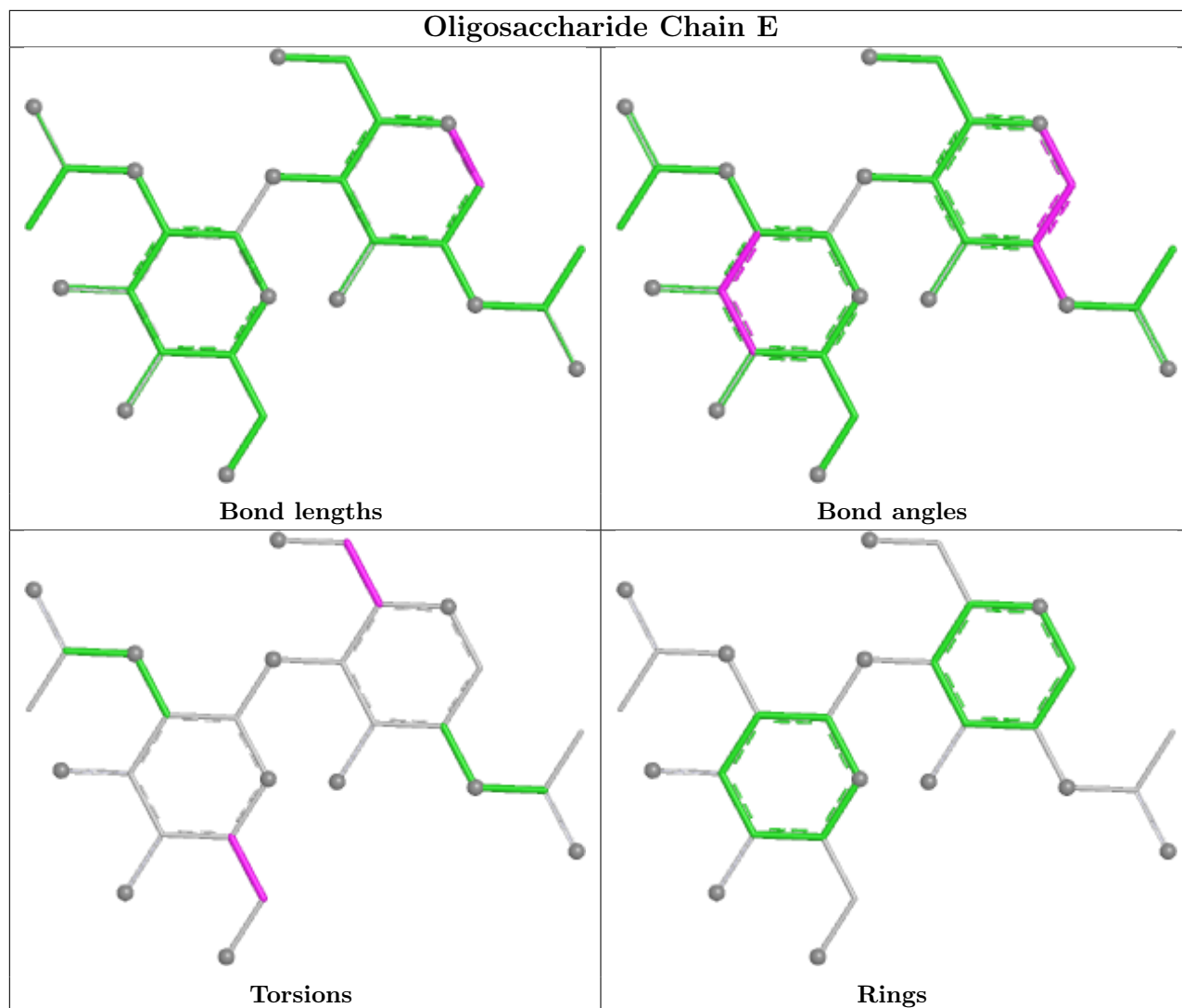
5 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1	NAG	4	0
3	E	2	NAG	2	0
2	B	2	NAG	2	0
3	E	1	NAG	2	0
2	D	2	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 18 ligands modelled in this entry, 1 is monoatomic - leaving 17 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	$\# Z > 2$
5	PO4	A	607	-	4,4,4	1.26	0	6,6,6	1.22	1 (16%)
5	PO4	A	620	-	4,4,4	1.12	0	6,6,6	0.48	0
5	PO4	A	618	-	4,4,4	2.43	2 (50%)	6,6,6	2.14	3 (50%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	PO4	A	617	-	4,4,4	1.42	1 (25%)	6,6,6	1.09	0
5	PO4	A	621	-	4,4,4	2.38	2 (50%)	6,6,6	3.25	4 (66%)
5	PO4	A	613	-	4,4,4	0.90	0	6,6,6	0.92	0
5	PO4	A	612	-	4,4,4	1.93	2 (50%)	6,6,6	2.30	3 (50%)
5	PO4	A	609	-	4,4,4	2.73	3 (75%)	6,6,6	1.44	2 (33%)
5	PO4	A	614	-	4,4,4	2.14	2 (50%)	6,6,6	3.04	4 (66%)
5	PO4	A	619	-	4,4,4	1.70	2 (50%)	6,6,6	1.71	2 (33%)
5	PO4	A	616	-	4,4,4	1.68	1 (25%)	6,6,6	1.67	1 (16%)
6	HEM	A	623	1,7	50,50,50	1.96	13 (26%)	67,82,82	1.46	12 (17%)
5	PO4	A	615	-	4,4,4	4.75	4 (100%)	6,6,6	3.27	4 (66%)
5	PO4	A	610	-	4,4,4	1.93	2 (50%)	6,6,6	3.66	4 (66%)
5	PO4	A	611	-	4,4,4	2.56	2 (50%)	6,6,6	1.68	3 (50%)
5	PO4	A	622	-	4,4,4	0.79	0	6,6,6	0.39	0
5	PO4	A	608	-	4,4,4	3.06	4 (100%)	6,6,6	0.46	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
6	HEM	A	623	1,7	-	4/14/54/54	-

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	615	PO4	P-O1	-7.09	1.34	1.50
6	A	623	HEM	FE-NA	6.10	2.15	1.95
6	A	623	HEM	C3D-C2D	5.93	1.49	1.36
5	A	608	PO4	P-O1	4.68	1.61	1.50
5	A	615	PO4	P-O4	-3.90	1.43	1.54

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	610	PO4	O4-P-O3	-7.23	85.43	107.91
5	A	621	PO4	O3-P-O2	6.42	127.88	107.91
5	A	615	PO4	O4-P-O1	-5.27	92.33	110.95
5	A	614	PO4	O3-P-O1	4.66	127.43	110.95

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	614	PO4	O3-P-O2	-4.35	94.38	107.91

There are no chirality outliers.

All (4) torsion outliers are listed below:

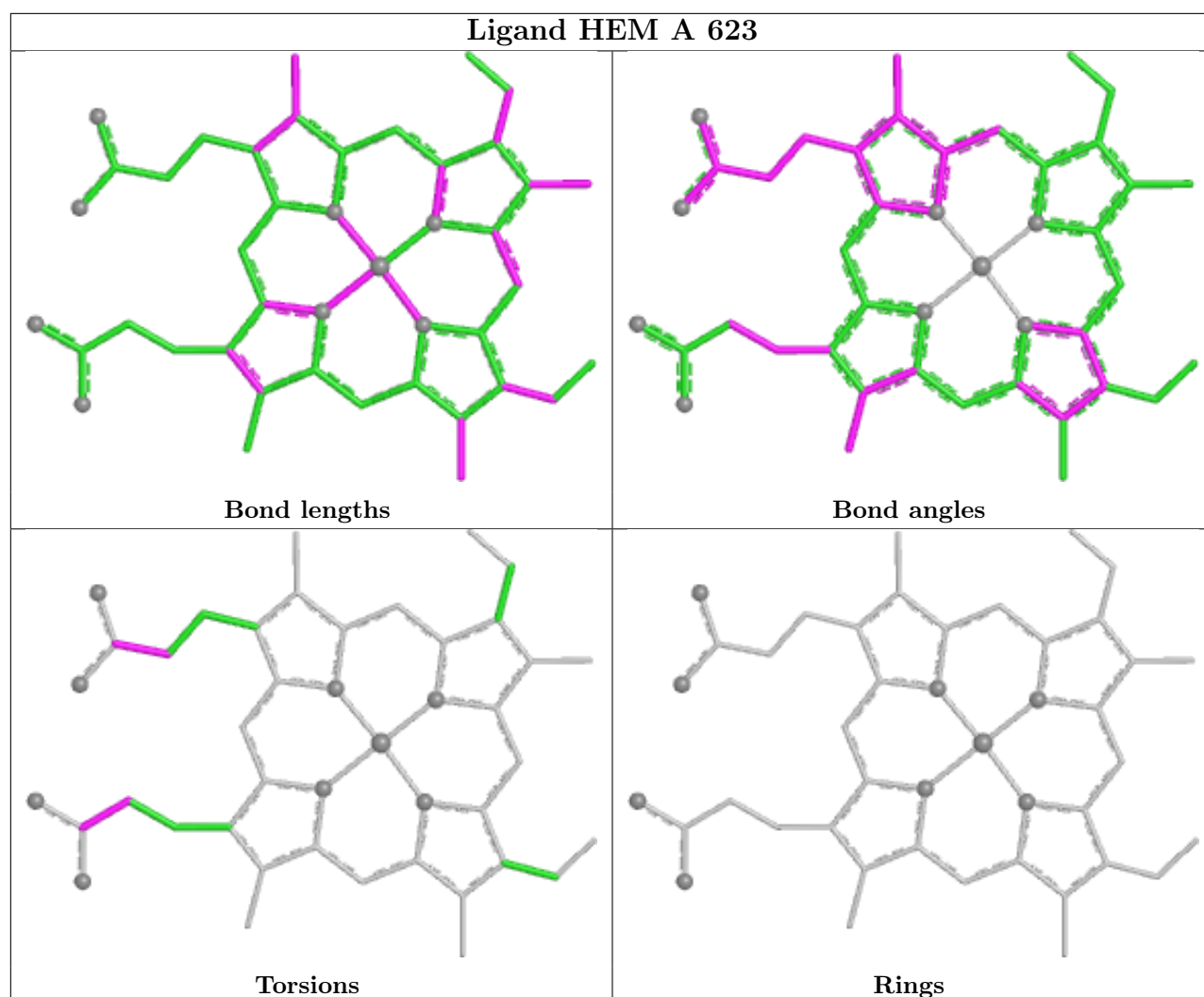
Mol	Chain	Res	Type	Atoms
6	A	623	HEM	CAA-CBA-CGA-O2A
6	A	623	HEM	CAD-CBD-CGD-O1D
6	A	623	HEM	CAD-CBD-CGD-O2D
6	A	623	HEM	CAA-CBA-CGA-O1A

There are no ring outliers.

10 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	607	PO4	2	0
5	A	620	PO4	1	0
5	A	621	PO4	2	0
5	A	609	PO4	1	0
5	A	616	PO4	4	0
6	A	623	HEM	7	0
5	A	610	PO4	2	0
5	A	611	PO4	1	0
5	A	622	PO4	1	0
5	A	608	PO4	3	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	594/595 (99%)	0.17	10 (1%) 69 73	36, 58, 92, 100	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	236	PRO	3.1
1	A	4	VAL	3.0
1	A	229	PHE	2.7
1	A	487	PRO	2.6
1	A	169	THR	2.3

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	SEP	A	198	10/11	0.88	0.12	43,55,57,61	0

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.

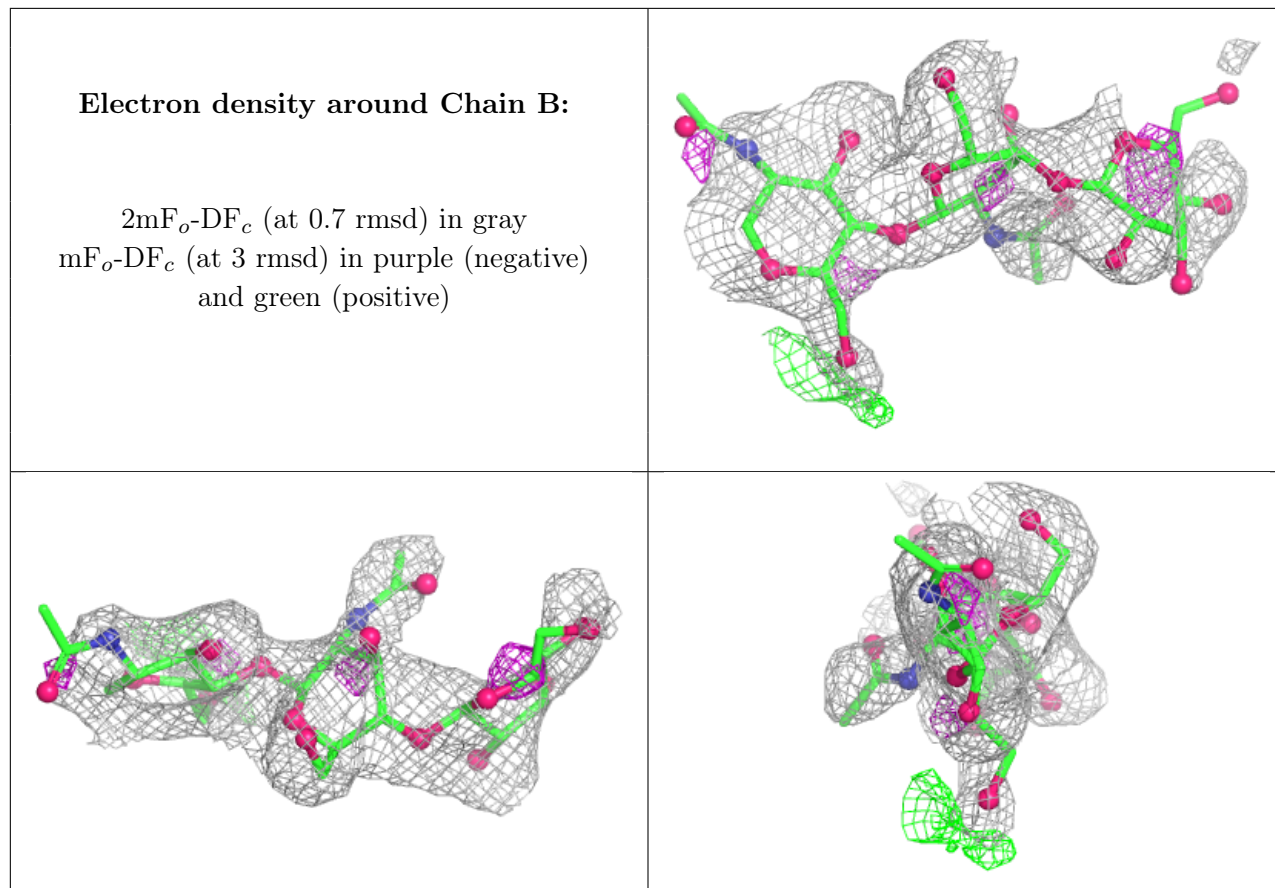
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NAG	B	2	14/15	0.34	0.13	91,94,97,97	0

Continued on next page...

Continued from previous page...

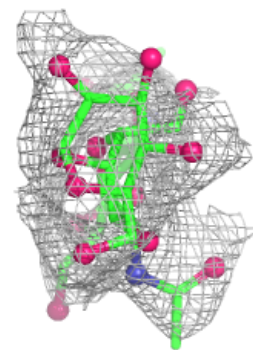
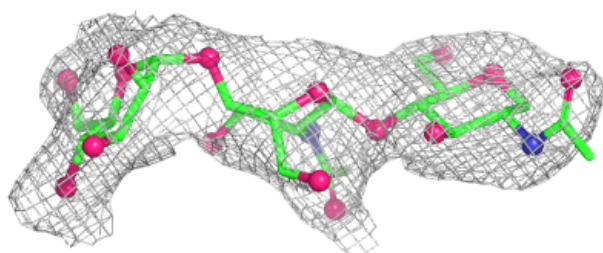
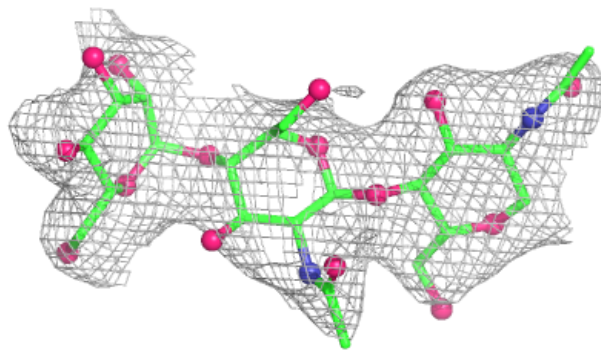
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	MAN	B	3	11/12	0.39	0.13	90,94,95,95	0
2	NAG	B	1	14/15	0.62	0.13	73,80,84,86	0
2	MAN	D	3	11/12	0.70	0.08	93,94,97,99	0
3	NAG	C	2	14/15	0.74	0.11	95,96,98,100	0
3	NAG	E	1	14/15	0.75	0.09	82,90,92,96	0
3	NAG	E	2	14/15	0.76	0.08	98,100,102,103	0
2	NAG	D	2	14/15	0.81	0.09	81,85,90,91	0
3	NAG	C	1	14/15	0.82	0.10	78,83,87,91	0
2	NAG	D	1	14/15	0.91	0.09	64,67,72,76	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.



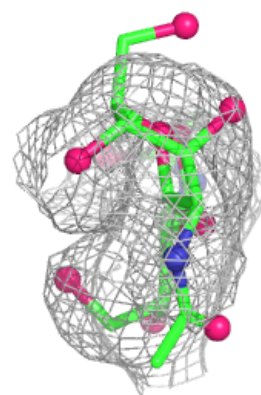
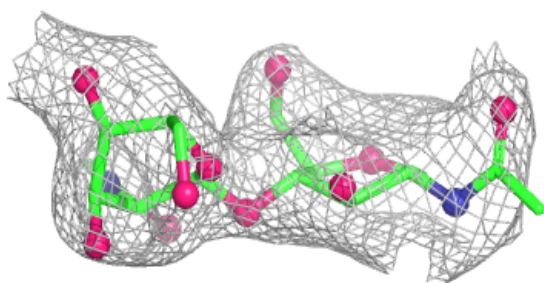
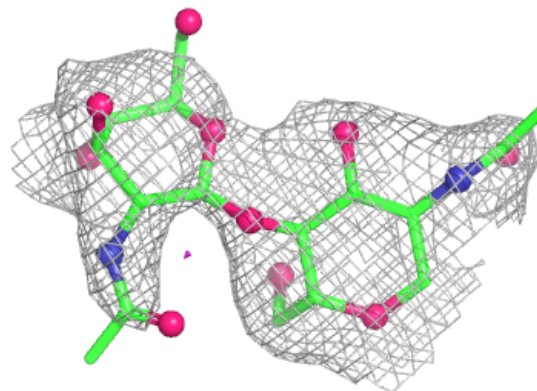
Electron density around Chain D:

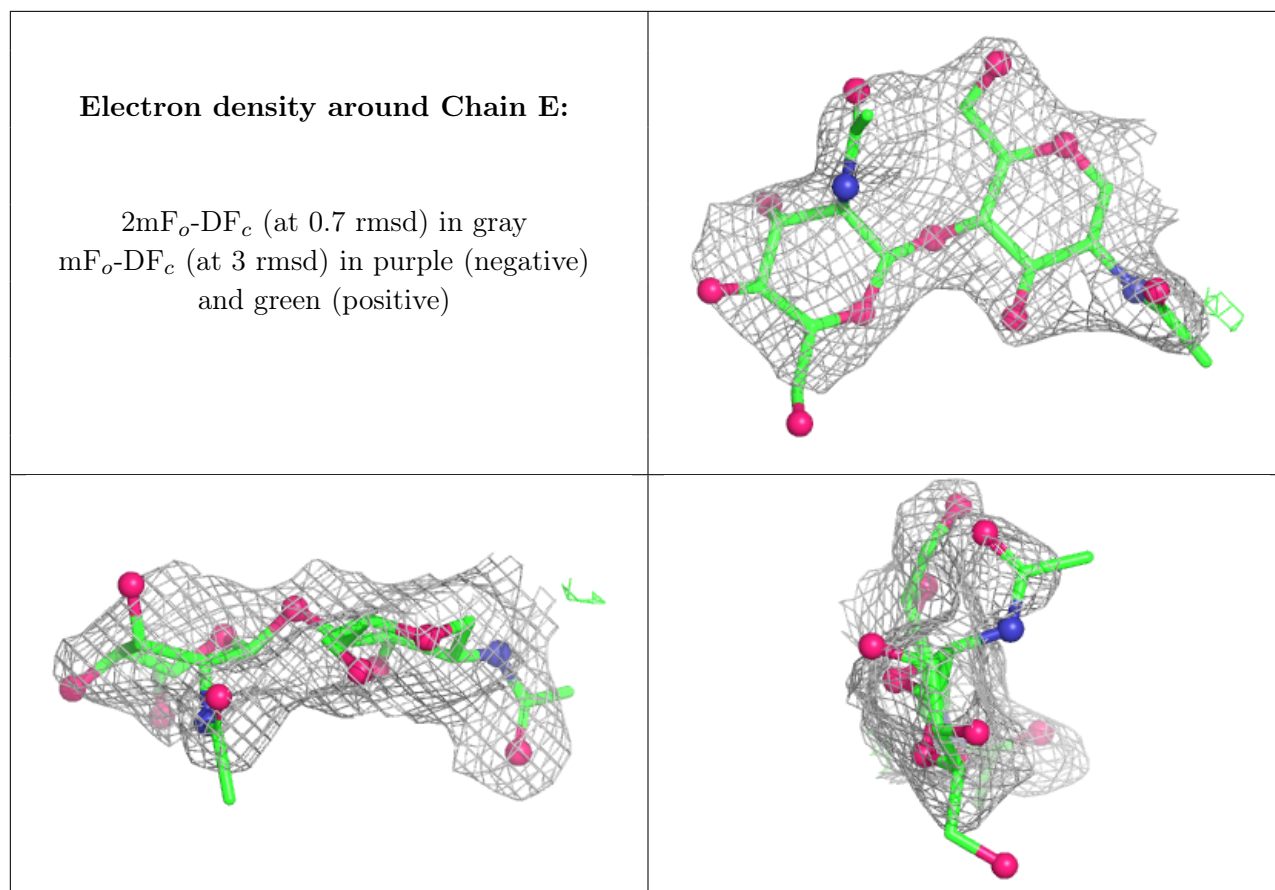
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain C:

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





6.4 Ligands [i](#)

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

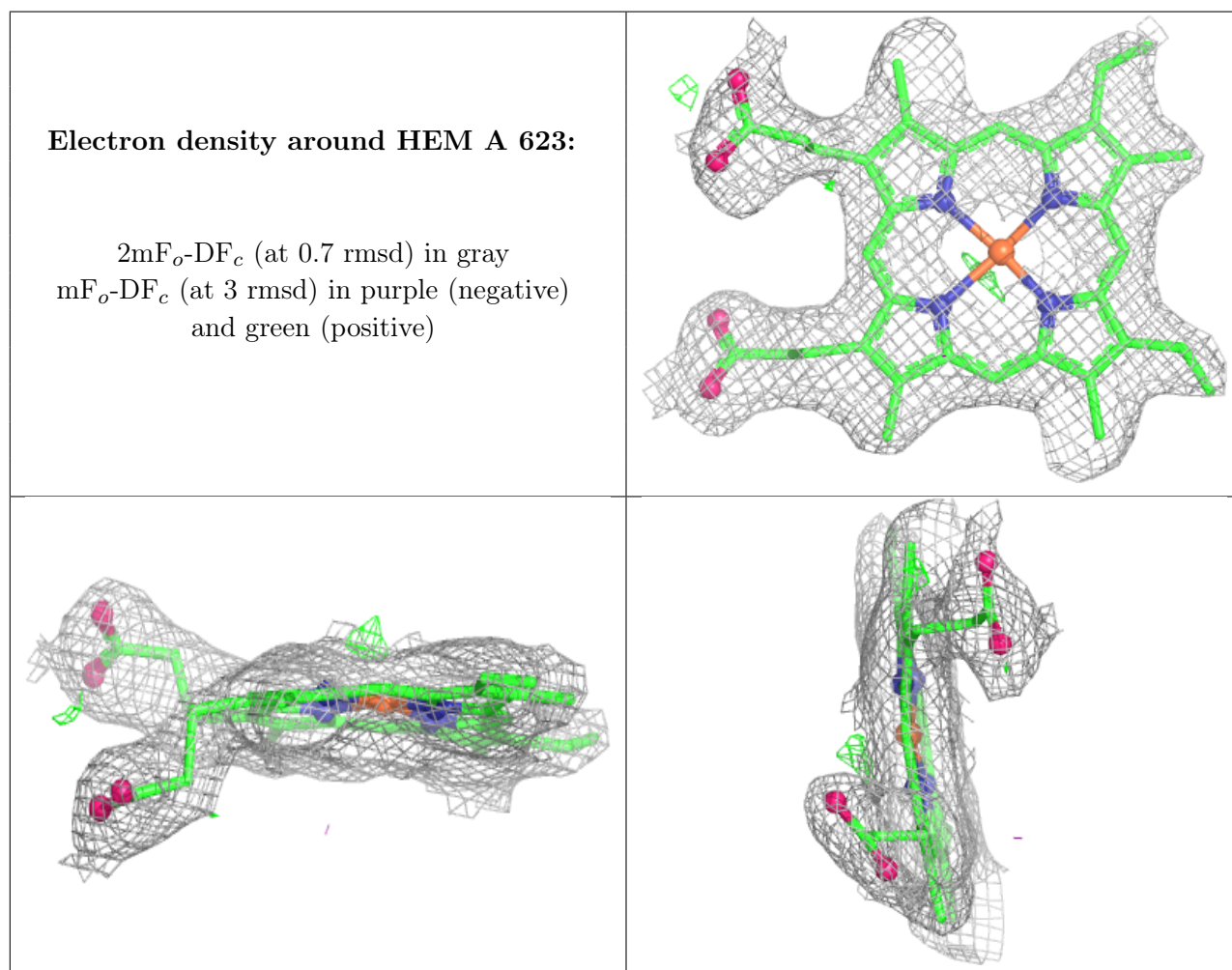
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	PO4	A	622	5/5	0.66	0.14	97,98,99,100	0
5	PO4	A	620	5/5	0.72	0.14	95,95,97,97	0
5	PO4	A	613	5/5	0.83	0.17	69,70,71,72	0
5	PO4	A	621	5/5	0.85	0.14	45,49,60,63	0
5	PO4	A	619	5/5	0.87	0.15	49,54,61,64	0
5	PO4	A	610	5/5	0.88	0.14	52,54,58,62	0
5	PO4	A	617	5/5	0.89	0.09	55,58,63,67	0
5	PO4	A	616	5/5	0.90	0.18	54,60,61,65	0
5	PO4	A	607	5/5	0.92	0.18	47,49,53,55	0
5	PO4	A	618	5/5	0.94	0.10	35,40,50,57	0
5	PO4	A	611	5/5	0.95	0.06	33,33,48,49	0
5	PO4	A	609	5/5	0.95	0.09	31,43,47,51	0
5	PO4	A	608	5/5	0.95	0.18	14,23,33,40	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	PO4	A	612	5/5	0.96	0.07	40,45,51,56	0
5	PO4	A	614	5/5	0.97	0.11	27,40,54,54	0
6	HEM	A	623	43/43	0.97	0.07	29,36,47,50	0
4	CA	A	606	1/1	0.98	0.03	44,44,44,44	0
5	PO4	A	615	5/5	0.98	0.12	29,31,45,53	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.



6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.