Full wwPDB X-ray Structure Validation Report (i)

Aug 5, 2026 – 12:33 PM EDT

PDB ID	:	2PUM / pdb_00002pum
Title	:	Crystal structure of bovine lactoperoxidase complex with catechol and iodide at 2.7 A resolution
Authors	:	Singh, A.K.; Singh, N.; Sharma, S.; Kaur, P.; Singh, T.P.
Deposited on	:	2007-05-09
Resolution	:	2.70 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 (i) 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 (i)) were used in the production of this report:

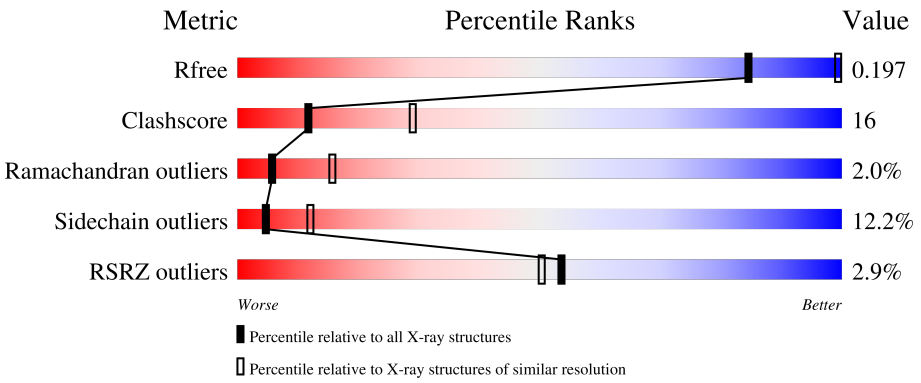
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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 <=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	3%, 64%, 26%, 8%, •
2	B	3	67%, 33%
2	D	3	33%, 67%
3	C	2	100%
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
6	IOD	A	609	-	-	X	-
6	IOD	A	617	-	-	X	-

2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 5260 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.

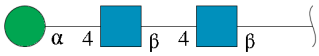
- Molecule 1 is a protein called Lactoperoxidase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	595	4780	3041	847	865	1	26	0	1	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

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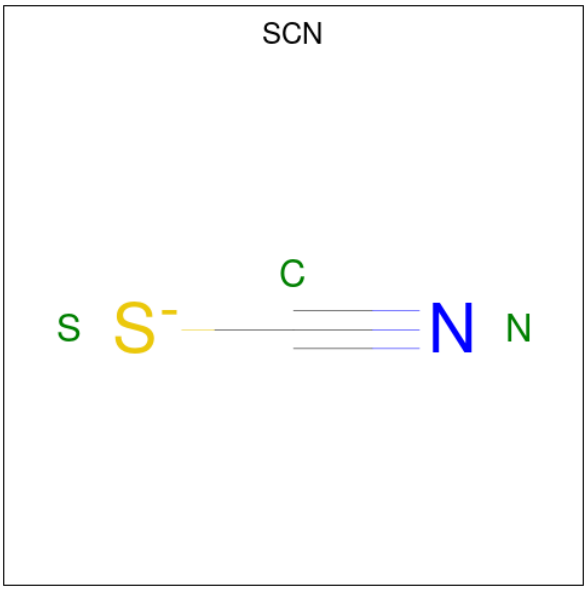
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	E	2	28	16	2	10	0	0	0

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

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

- Molecule 5 is THIOCYANATE ION (CCD ID: SCN) (formula: CNS).

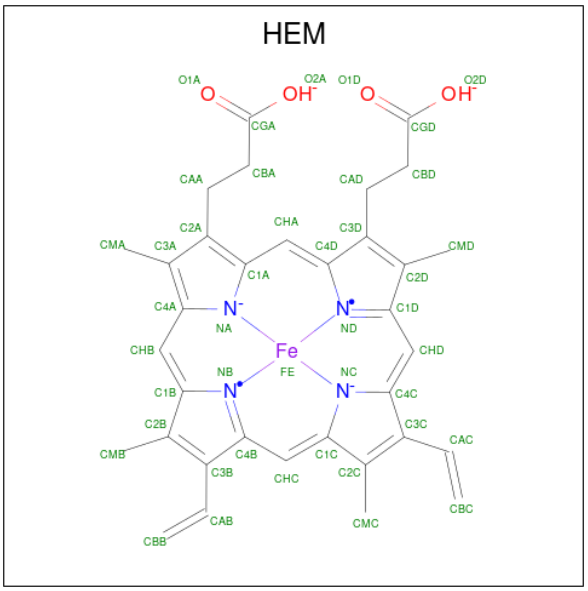


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	S		
5	A	1	3	1	1	1	0	0

- Molecule 6 is IODIDE ION (CCD ID: IOD) (formula: I).

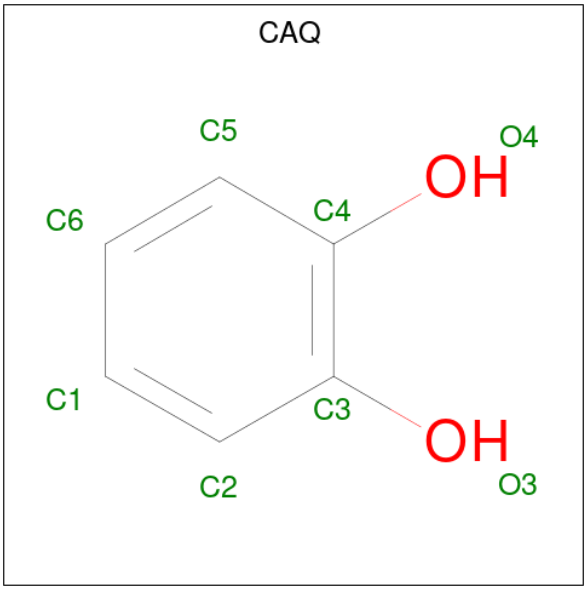
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	I		
6	A	10	10	10	0	0

- Molecule 7 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

- Molecule 8 is CATECHOL (CCD ID: CAQ) (formula: $C_6H_6O_2$).



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

- Molecule 9 is water.

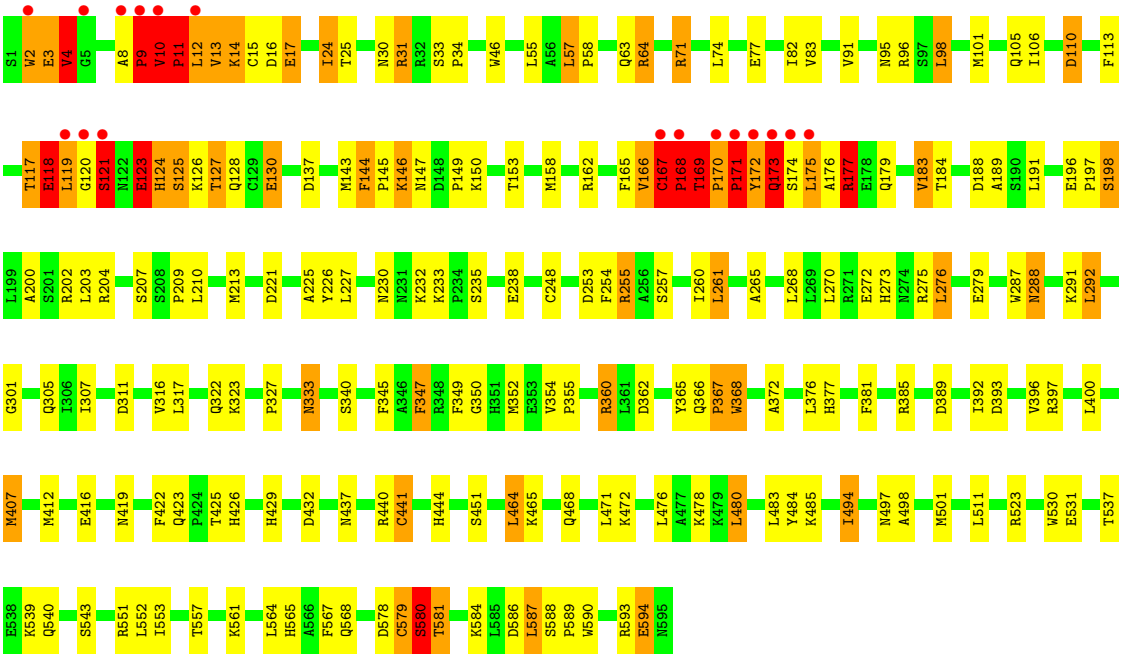
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
9	A	281	281	281	0	0

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

Chain A: 3% 64% 26% 8%



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

Chain B: 67% 33%

• 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: 33% 67%

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

Chain C: 100%

NAG1
NAG2

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

Chain E: 100%

NAG1
NAG2

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	54.42Å 80.49Å 77.32Å 90.00° 102.60° 90.00°	Depositor
Resolution (Å)	24.93 – 2.70 24.93 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.2 (24.93-2.70) 99.2 (24.93-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.98 (at 2.72Å)	Xtriage
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.165 , 0.203 0.168 , 0.197	Depositor DCC
R_{free} test set	912 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	30.7	Xtriage
Anisotropy	0.152	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 62.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	5260	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.39% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: MAN, SCN, SEP, NAG, IOD, CA, HEM, CAQ

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	11/4900 (0.2%)	1.35	66/6646 (1.0%)

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	2

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	412	MET	SD-CE	-11.21	1.51	1.79
1	A	9	PRO	C-N	-10.34	1.21	1.33
1	A	10	VAL	N-CA	-9.32	1.35	1.46
1	A	169	THR	C-N	7.28	1.42	1.33
1	A	167	CYS	N-CA	-6.68	1.36	1.46
1	A	2	TRP	CA-C	6.28	1.61	1.52
1	A	580	SER	CA-C	-6.22	1.44	1.52
1	A	9	PRO	CA-C	-5.79	1.43	1.52
1	A	3	GLU	N-CA	5.66	1.53	1.46
1	A	169	THR	CA-C	5.55	1.59	1.52
1	A	170	PRO	CA-C	5.33	1.57	1.52

All (66) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	118[A]	GLU	O-C-N	-12.35	106.17	122.59
1	A	118[B]	GLU	O-C-N	-12.35	106.17	122.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	3	GLU	CA-C-N	10.96	141.69	121.97
1	A	3	GLU	C-N-CA	10.96	141.69	121.97
1	A	125	SER	N-CA-C	-10.51	101.51	114.75
1	A	173	GLN	OE1-CD-NE2	-10.11	112.49	122.60
1	A	123	GLU	N-CA-C	10.01	124.75	110.23
1	A	232	LYS	N-CA-C	9.97	123.51	109.15
1	A	174	SER	N-CA-C	9.80	125.50	108.75
1	A	366	GLN	OE1-CD-NE2	-9.05	113.55	122.60
1	A	3	GLU	N-CA-C	-8.67	92.32	110.80
1	A	173	GLN	CA-C-N	-8.35	107.25	121.94
1	A	173	GLN	C-N-CA	-8.35	107.25	121.94
1	A	126	LYS	N-CA-C	-8.33	102.83	113.16
1	A	316	VAL	N-CA-C	-8.22	103.86	111.67
1	A	2	TRP	CA-C-N	8.04	136.90	121.54
1	A	2	TRP	C-N-CA	8.04	136.90	121.54
1	A	3	GLU	N-CA-CB	7.33	122.88	110.49
1	A	83	VAL	N-CA-C	7.24	118.90	111.00
1	A	14	LYS	N-CA-C	7.22	121.80	110.17
1	A	3	GLU	O-C-N	7.22	132.19	122.59
1	A	170	PRO	CA-N-CD	-6.94	102.28	112.00
1	A	4	VAL	N-CA-C	6.84	123.58	109.34
1	A	594	GLU	N-CA-C	6.82	121.43	113.18
1	A	124	HIS	N-CA-C	-6.77	98.62	109.39
1	A	144	PHE	CA-C-N	6.77	126.75	119.78
1	A	144	PHE	C-N-CA	6.77	126.75	119.78
1	A	366	GLN	CG-CD-NE2	6.75	126.53	116.40
1	A	166	VAL	N-CA-C	6.62	117.69	110.21
1	A	171	PRO	CA-N-CD	-6.52	102.88	112.00
1	A	3	GLU	CA-C-O	6.49	129.78	120.51
1	A	207	SER	N-CA-C	-6.33	104.27	112.68
1	A	367	PRO	CB-CA-C	6.26	121.88	111.56
1	A	121	SER	N-CA-C	-6.16	102.89	110.65
1	A	173	GLN	CG-CD-NE2	6.13	125.60	116.40
1	A	233	LYS	N-CA-C	-6.02	102.00	110.31
1	A	254	PHE	N-CA-C	5.88	118.48	111.71
1	A	172	TYR	N-CA-C	5.87	119.17	110.48
1	A	288	ASN	N-CA-CB	-5.86	101.55	110.45
1	A	225	ALA	N-CA-C	5.85	118.31	110.35
1	A	168	PRO	N-CA-C	5.84	124.49	112.47
1	A	31	ARG	CA-C-N	-5.79	111.30	122.06
1	A	31	ARG	C-N-CA	-5.79	111.30	122.06
1	A	168	PRO	CA-C-N	5.74	135.81	121.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	168	PRO	C-N-CA	5.74	135.81	121.80
1	A	437	ASN	CA-CB-CG	5.72	118.32	112.60
1	A	311	ASP	N-CA-C	5.67	120.33	113.41
1	A	441	CYS	N-CA-C	-5.67	105.18	111.36
1	A	9	PRO	O-C-N	5.65	128.74	122.24
1	A	230	ASN	CA-C-N	5.64	128.16	120.54
1	A	230	ASN	C-N-CA	5.64	128.16	120.54
1	A	110	ASP	N-CA-C	-5.63	105.91	112.89
1	A	12	LEU	N-CA-C	5.33	117.34	108.02
1	A	171	PRO	CA-C-N	-5.29	112.61	121.39
1	A	171	PRO	C-N-CA	-5.29	112.61	121.39
1	A	173	GLN	O-C-N	-5.27	115.58	122.59
1	A	407	MET	N-CA-C	-5.22	102.65	110.23
1	A	177	ARG	N-CA-C	5.19	117.74	109.96
1	A	345	PHE	N-CA-C	-5.17	107.52	113.88
1	A	368	TRP	N-CA-C	5.17	117.55	108.56
1	A	11	PRO	CB-CA-C	5.15	118.10	111.46
1	A	423	GLN	CA-C-N	5.11	124.83	119.82
1	A	423	GLN	C-N-CA	5.11	124.83	119.82
1	A	137	ASP	CB-CA-C	-5.08	110.70	116.54
1	A	170	PRO	CB-CA-C	5.07	117.11	110.92
1	A	197	PRO	CA-N-CD	-5.02	104.97	112.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	118[A]	GLU	Mainchain
1	A	118[B]	GLU	Mainchain

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	4780	0	4692	149	0
2	B	39	0	34	1	0
2	D	39	0	34	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	28	0	25	0	0
3	E	28	0	25	0	0
4	A	1	0	0	0	0
5	A	3	0	0	0	0
6	A	10	0	0	6	0
7	A	43	0	30	8	0
8	A	8	0	4	0	0
9	A	281	0	0	17	0
All	All	5260	0	4844	156	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 16.

All (156) 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)
7:A:618:HEM:HMB1	7:A:618:HEM:HBB2	1.29	1.15
1:A:578:ASP:OD1	1:A:580:SER:HB2	1.53	1.05
1:A:227:LEU:HD23	1:A:270:LEU:HD22	1.37	1.03
1:A:31:ARG:HD2	6:A:609:IOD:I	2.29	1.02
1:A:33:SER:HB2	9:A:896:HOH:O	1.62	1.00
1:A:118[A]:GLU:HG3	1:A:119:LEU:N	1.75	0.92
1:A:118[A]:GLU:HG3	1:A:119:LEU:H	1.09	0.88
1:A:106:ILE:HD11	1:A:265:ALA:HB1	1.59	0.84
1:A:167:CYS:CB	1:A:168:PRO:HD2	2.12	0.80
1:A:551:ARG:HD3	1:A:584:LYS:HA	1.62	0.80
7:A:618:HEM:HBB2	7:A:618:HEM:CMB	2.12	0.76
1:A:130:GLU:CD	1:A:426:HIS:HD2	1.95	0.74
1:A:8:ALA:N	1:A:9:PRO:HD2	2.02	0.73
1:A:9:PRO:O	1:A:11:PRO:HD3	1.89	0.73
1:A:71:ARG:HH11	1:A:71:ARG:HG3	1.52	0.73
1:A:537:THR:OG1	1:A:540:GLN:HG3	1.89	0.72
1:A:167:CYS:CB	1:A:168:PRO:CD	2.67	0.72
1:A:196:GLU:HB3	1:A:198:SEP:O3P	1.88	0.72
1:A:578:ASP:C	1:A:580:SER:H	1.98	0.72
1:A:167:CYS:HB3	1:A:168:PRO:HD2	1.72	0.72
1:A:407:MET:HB3	1:A:501:MET:HE3	1.72	0.71
6:A:609:IOD:I	9:A:723:HOH:O	2.78	0.71
1:A:275:ARG:NH1	9:A:800:HOH:O	2.26	0.69
1:A:2:TRP:HA	1:A:4:VAL:HG13	1.75	0.69
1:A:327:PRO:HD2	9:A:799:HOH:O	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:147:ASN:O	1:A:149:PRO:HD3	1.93	0.67
1:A:8:ALA:N	1:A:9:PRO:CD	2.58	0.67
1:A:167:CYS:HB3	1:A:168:PRO:CD	2.25	0.67
1:A:464:LEU:O	1:A:468:GLN:HG3	1.96	0.66
1:A:360:ARG:NH1	1:A:372:ALA:HA	2.13	0.64
1:A:144:PHE:HE2	1:A:158:MET:HE2	1.64	0.63
1:A:213:MET:HG2	1:A:273:HIS:CD2	2.33	0.63
1:A:71:ARG:HH11	1:A:71:ARG:CG	2.10	0.63
1:A:150:LYS:NZ	1:A:419:ASN:O	2.30	0.63
1:A:17:GLU:HG3	9:A:894:HOH:O	1.98	0.63
1:A:167:CYS:HB2	1:A:168:PRO:HD2	1.81	0.62
7:A:618:HEM:HMB1	7:A:618:HEM:CBB	2.15	0.59
1:A:8:ALA:H	1:A:9:PRO:HD2	1.65	0.59
1:A:578:ASP:C	1:A:580:SER:N	2.61	0.59
1:A:587:LEU:HD23	1:A:587:LEU:O	2.02	0.59
1:A:347:PHE:HB3	7:A:618:HEM:HMD2	1.83	0.59
9:A:861:HOH:O	2:B:3:MAN:H2	2.02	0.59
1:A:82:ILE:HG21	1:A:494:ILE:HD11	1.84	0.58
1:A:121:SER:HB2	9:A:827:HOH:O	2.04	0.58
1:A:98:LEU:HD22	1:A:101:MET:HE3	1.85	0.58
1:A:530:TRP:CE2	1:A:531:GLU:HG3	2.39	0.58
1:A:10:VAL:CG2	1:A:10:VAL:O	2.51	0.57
1:A:10:VAL:O	1:A:10:VAL:HG23	2.03	0.57
1:A:95:ASN:O	1:A:96:ARG:HD3	2.05	0.57
1:A:64:ARG:HD3	1:A:64:ARG:C	2.30	0.56
1:A:476:LEU:HD21	1:A:498:ALA:HB1	1.87	0.56
1:A:365:TYR:CE1	1:A:397:ARG:HB3	2.41	0.56
1:A:117:THR:OG1	1:A:162:ARG:O	2.23	0.55
1:A:191:LEU:H	1:A:191:LEU:HD23	1.71	0.55
1:A:16:ASP:OD1	1:A:16:ASP:C	2.48	0.55
1:A:272:GLU:O	1:A:276:LEU:HB2	2.06	0.55
1:A:71:ARG:CG	1:A:71:ARG:NH1	2.68	0.54
1:A:333:ASN:C	1:A:333:ASN:HD22	2.15	0.54
1:A:362:ASP:OD1	1:A:362:ASP:C	2.51	0.54
1:A:272:GLU:HG3	1:A:276:LEU:HD22	1.89	0.54
1:A:451:SER:HA	9:A:696:HOH:O	2.08	0.53
1:A:14:LYS:HG3	1:A:15:CYS:N	2.23	0.53
1:A:169:THR:OG1	1:A:170:PRO:CD	2.57	0.53
1:A:484:TYR:O	1:A:485:LYS:HB2	2.08	0.53
1:A:588:SER:C	1:A:590:TRP:H	2.16	0.53
1:A:422:PHE:HB2	1:A:429:HIS:CD2	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:400:LEU:HD11	1:A:553:ILE:HD13	1.91	0.52
1:A:288:ASN:O	1:A:292:LEU:HD23	2.10	0.52
1:A:567:PHE:HD2	6:A:617:IOD:I	2.63	0.52
1:A:127:THR:HA	1:A:130:GLU:HB2	1.91	0.52
1:A:123:GLU:HG2	1:A:125:SER:HB2	1.92	0.52
1:A:16:ASP:HB2	9:A:816:HOH:O	2.09	0.51
1:A:33:SER:CB	9:A:896:HOH:O	2.36	0.51
1:A:110:ASP:OD2	1:A:189:ALA:N	2.43	0.51
1:A:9:PRO:HG3	9:A:708:HOH:O	2.11	0.51
1:A:128:GLN:NE2	9:A:820:HOH:O	2.43	0.51
1:A:360:ARG:HH12	1:A:372:ALA:HA	1.76	0.51
1:A:106:ILE:HD11	1:A:265:ALA:CB	2.36	0.51
1:A:146:LYS:HE3	1:A:147:ASN:HD21	1.76	0.51
1:A:166:VAL:O	1:A:167:CYS:HB2	2.10	0.50
1:A:578:ASP:O	1:A:580:SER:N	2.45	0.50
1:A:9:PRO:O	1:A:11:PRO:CD	2.57	0.50
1:A:106:ILE:HG23	1:A:191:LEU:HD11	1.93	0.50
1:A:172:TYR:CD1	1:A:173:GLN:N	2.80	0.49
1:A:16:ASP:OD1	1:A:16:ASP:O	2.31	0.49
1:A:143:MET:HE3	9:A:675:HOH:O	2.13	0.49
1:A:385:ARG:O	1:A:389:ASP:HB2	2.13	0.49
1:A:235:SER:HB3	1:A:238:GLU:HB2	1.94	0.48
1:A:565:HIS:HB3	6:A:617:IOD:I	2.83	0.48
1:A:118[A]:GLU:OE2	1:A:120:GLY:N	2.38	0.48
1:A:347:PHE:HB3	7:A:618:HEM:CMD	2.43	0.48
1:A:268:LEU:CD1	1:A:392:ILE:HD12	2.42	0.48
1:A:165:PHE:CB	1:A:177:ARG:HD2	2.44	0.48
1:A:368:TRP:O	1:A:368:TRP:CE3	2.66	0.48
1:A:392:ILE:O	1:A:396:VAL:HG23	2.13	0.48
1:A:82:ILE:CG2	1:A:494:ILE:HD11	2.44	0.48
1:A:169:THR:OG1	1:A:170:PRO:HD3	2.14	0.48
1:A:98:LEU:CD2	1:A:101:MET:HE3	2.43	0.47
1:A:257:SER:O	1:A:381:PHE:HA	2.14	0.47
1:A:188:ASP:O	1:A:189:ALA:HB3	2.14	0.47
1:A:165:PHE:CG	1:A:177:ARG:HD2	2.50	0.47
1:A:301:GLY:O	1:A:305:GLN:HG3	2.15	0.47
1:A:287:TRP:CE2	1:A:291:LYS:HD3	2.49	0.47
1:A:354:VAL:HA	1:A:355:PRO:HD3	1.79	0.47
1:A:255:ARG:HG2	6:A:608:IOD:I	2.85	0.47
1:A:567:PHE:HB2	6:A:617:IOD:I	2.85	0.47
1:A:30:ASN:O	1:A:34:PRO:HA	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:ILE:HD11	1:A:483:LEU:HD12	1.96	0.46
1:A:248:CYS:HB3	1:A:257:SER:OG	2.16	0.46
1:A:221:ASP:HB2	1:A:226:TYR:CZ	2.51	0.46
1:A:288:ASN:O	1:A:292:LEU:CD2	2.64	0.46
1:A:407:MET:HB3	1:A:501:MET:CE	2.40	0.45
1:A:46:TRP:CE2	1:A:340:SER:HB3	2.51	0.45
1:A:58:PRO:HG3	1:A:162:ARG:NH2	2.31	0.45
1:A:105:GLN:NE2	7:A:618:HEM:C4B	2.84	0.45
1:A:543:SER:OG	1:A:586:ASP:O	2.25	0.45
1:A:123:GLU:C	1:A:125:SER:N	2.75	0.45
1:A:578:ASP:O	1:A:581:THR:HB	2.17	0.45
2:D:2:NAG:H4	2:D:3:MAN:H2	1.61	0.45
1:A:200:ALA:O	1:A:204:ARG:HG3	2.18	0.44
1:A:130:GLU:CD	1:A:426:HIS:CD2	2.86	0.44
1:A:349:PHE:CB	1:A:497:ASN:HD21	2.29	0.44
1:A:594:GLU:CD	1:A:594:GLU:H	2.25	0.44
1:A:169:THR:HA	9:A:874:HOH:O	2.18	0.44
1:A:77:GLU:HB2	1:A:145:PRO:HG3	2.00	0.43
1:A:124:HIS:HA	1:A:127:THR:HB	1.99	0.43
1:A:468:GLN:O	1:A:472:LYS:N	2.51	0.43
1:A:333:ASN:C	1:A:333:ASN:ND2	2.75	0.43
1:A:63:GLN:HB2	9:A:805:HOH:O	2.18	0.43
1:A:57:LEU:HA	1:A:58:PRO:HD3	1.84	0.43
1:A:440:ARG:O	1:A:440:ARG:HG3	2.18	0.43
1:A:432:ASP:OD1	1:A:432:ASP:C	2.62	0.43
1:A:580:SER:C	1:A:581:THR:OG1	2.61	0.43
1:A:82:ILE:CD1	1:A:483:LEU:HD12	2.48	0.42
1:A:253:ASP:OD2	1:A:255:ARG:HD3	2.19	0.42
1:A:480:LEU:HD12	1:A:480:LEU:HA	1.76	0.42
7:A:618:HEM:CMB	7:A:618:HEM:CBB	2.82	0.42
1:A:276:LEU:HD12	1:A:587:LEU:HD11	2.01	0.42
1:A:393:ASP:OD1	1:A:557:THR:HB	2.20	0.42
1:A:113:PHE:HB3	1:A:183:VAL:HG13	2.02	0.42
1:A:292:LEU:HD13	1:A:292:LEU:HA	1.88	0.42
1:A:478:LYS:HB3	1:A:478:LYS:HE2	1.82	0.41
1:A:15:CYS:HA	9:A:684:HOH:O	2.21	0.41
1:A:63:GLN:O	1:A:71:ARG:NH1	2.53	0.41
1:A:441:CYS:HB3	9:A:672:HOH:O	2.19	0.41
1:A:425:THR:HB	1:A:426:HIS:ND1	2.35	0.41
1:A:25:THR:O	1:A:184:THR:HG22	2.21	0.41
1:A:179:GLN:HG2	1:A:444:HIS:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:377:HIS:HB3	1:A:416:GLU:OE2	2.21	0.41
1:A:588:SER:C	1:A:590:TRP:N	2.77	0.41
1:A:24:ILE:HD13	1:A:24:ILE:HA	1.83	0.41
1:A:260:ILE:HG23	1:A:261:LEU:N	2.36	0.41
1:A:350:GLY:HA3	7:A:618:HEM:CBC	2.50	0.41
1:A:261:LEU:HD12	1:A:261:LEU:HA	1.90	0.40
1:A:12:LEU:O	1:A:13:VAL:HG13	2.22	0.40
1:A:287:TRP:CD2	1:A:291:LYS:HD3	2.56	0.40

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	593/595 (100%)	541 (91%)	40 (7%)	12 (2%)	6 16

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	VAL
1	A	167	CYS
1	A	168	PRO
1	A	176	ALA
1	A	169	THR
1	A	175	LEU
1	A	581	THR
1	A	3	GLU
1	A	589	PRO
1	A	579	CYS
1	A	209	PRO
1	A	171	PRO

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	518/517 (100%)	454 (88%)	64 (12%)	4 11

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	VAL
1	A	9	PRO
1	A	10	VAL
1	A	11	PRO
1	A	13	VAL
1	A	17	GLU
1	A	24	ILE
1	A	55	LEU
1	A	57	LEU
1	A	64	ARG
1	A	71	ARG
1	A	74	LEU
1	A	91	VAL
1	A	98	LEU
1	A	117	THR
1	A	118[A]	GLU
1	A	118[B]	GLU
1	A	119	LEU
1	A	121	SER
1	A	123	GLU
1	A	127	THR
1	A	130	GLU
1	A	146	LYS
1	A	153	THR
1	A	169	THR
1	A	171	PRO
1	A	173	GLN
1	A	175	LEU
1	A	177	ARG
1	A	183	VAL

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Mol	Chain	Res	Type
1	A	202	ARG
1	A	203	LEU
1	A	210	LEU
1	A	255	ARG
1	A	261	LEU
1	A	276	LEU
1	A	279	GLU
1	A	292	LEU
1	A	307	ILE
1	A	317	LEU
1	A	322	GLN
1	A	323	LYS
1	A	333	ASN
1	A	347	PHE
1	A	352	MET
1	A	360	ARG
1	A	367	PRO
1	A	376	LEU
1	A	464	LEU
1	A	465	LYS
1	A	471	LEU
1	A	480	LEU
1	A	494	ILE
1	A	511	LEU
1	A	523	ARG
1	A	539	LYS
1	A	552	LEU
1	A	561	LYS
1	A	564	LEU
1	A	568	GLN
1	A	579	CYS
1	A	580	SER
1	A	587	LEU
1	A	593	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	ASN
1	A	138	ASN
1	A	322	GLN
1	A	329	GLN

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Mol	Chain	Res	Type
1	A	333	ASN
1	A	364	ASN
1	A	423	GLN
1	A	426	HIS
1	A	437	ASN
1	A	460	GLN
1	A	497	ASN
1	A	520	GLN
1	A	545	GLN
1	A	568	GLN
1	A	570	ASN
1	A	574	HIS

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	1.20	0	7,12,14	1.79	3 (42%)

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	-	4/6/8/10	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	198	SEP	OG-CB-CA	2.13	110.22	108.14
1	A	198	SEP	O2P-P-OG	2.05	112.02	106.67
1	A	198	SEP	O2P-P-O1P	-2.00	103.04	110.83

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	198	SEP	CB-OG-P-O2P
1	A	198	SEP	CB-OG-P-O3P
1	A	198	SEP	CB-OG-P-O1P
1	A	198	SEP	CA-CB-OG-P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	198	SEP	1	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	2,1	14,14,15	0.57	0	17,19,21	1.80	5 (29%)
2	NAG	B	2	2	14,14,15	0.64	0	17,19,21	1.36	2 (11%)
2	MAN	B	3	2	11,11,12	0.54	0	15,15,17	1.25	1 (6%)
3	NAG	C	1	1,3	14,14,15	0.66	0	17,19,21	1.35	3 (17%)
3	NAG	C	2	3	14,14,15	0.65	0	17,19,21	1.77	3 (17%)
2	NAG	D	1	2,1	14,14,15	0.66	0	17,19,21	1.57	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NAG	D	2	2	14,14,15	0.58	0	17,19,21	1.64	1 (5%)
2	MAN	D	3	2	11,11,12	0.50	0	15,15,17	1.94	4 (26%)
3	NAG	E	1	1,3	14,14,15	0.84	0	17,19,21	1.98	4 (23%)
3	NAG	E	2	3	14,14,15	0.64	0	17,19,21	1.45	2 (11%)

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	2,1	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	4/6/23/26	0/1/1/1
2	MAN	B	3	2	-	2/2/19/22	1/1/1/1
3	NAG	C	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	4/6/23/26	0/1/1/1
2	NAG	D	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
2	MAN	D	3	2	-	2/2/19/22	0/1/1/1
3	NAG	E	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	E	2	3	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	2	NAG	C1-O5-C5	5.83	120.00	112.19
2	D	3	MAN	C1-O5-C5	5.71	119.84	112.19
3	E	1	NAG	C4-C3-C2	5.25	118.72	111.02
2	B	1	NAG	O5-C1-C2	-3.85	105.33	111.29
2	B	3	MAN	C1-O5-C5	3.81	117.29	112.19
2	D	1	NAG	O5-C1-C2	-3.66	105.63	111.29
3	C	2	NAG	C1-O5-C5	3.62	117.04	112.19
3	E	2	NAG	O5-C1-C2	-3.49	105.89	111.29
3	C	2	NAG	C2-N2-C7	-3.48	118.24	122.90
2	B	1	NAG	C3-C4-C5	-3.33	104.19	110.23
3	C	2	NAG	O5-C1-C2	3.32	116.43	111.29
2	B	2	NAG	C4-C3-C2	3.29	115.84	111.02
3	E	2	NAG	C1-O5-C5	-3.13	107.99	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	2	NAG	C1-O5-C5	2.98	116.19	112.19
3	E	1	NAG	O5-C1-C2	-2.96	106.71	111.29
3	C	1	NAG	O5-C1-C2	-2.86	106.86	111.29
2	D	1	NAG	O4-C4-C3	-2.84	103.68	110.38
3	E	1	NAG	C1-O5-C5	2.82	115.97	112.19
2	B	1	NAG	O4-C4-C5	2.81	116.23	109.32
3	C	1	NAG	C4-C3-C2	2.64	114.89	111.02
2	D	1	NAG	C2-N2-C7	-2.52	119.53	122.90
2	B	1	NAG	O5-C5-C6	2.44	112.40	107.66
2	D	3	MAN	C3-C4-C5	-2.31	106.05	110.23
3	C	1	NAG	C1-O5-C5	2.18	115.11	112.19
2	D	3	MAN	C1-C2-C3	2.16	112.79	109.64
3	E	1	NAG	O3-C3-C2	-2.09	105.07	109.40
2	B	1	NAG	C1-O5-C5	2.09	114.98	112.19
2	D	3	MAN	C2-C3-C4	-2.00	107.34	110.86

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2	NAG	C8-C7-N2-C2
2	B	2	NAG	O7-C7-N2-C2
3	E	2	NAG	C8-C7-N2-C2
3	E	2	NAG	O7-C7-N2-C2
2	D	1	NAG	O5-C5-C6-O6
2	B	2	NAG	C4-C5-C6-O6
2	D	1	NAG	C4-C5-C6-O6
3	C	2	NAG	C4-C5-C6-O6
3	C	2	NAG	O5-C5-C6-O6
2	B	2	NAG	O5-C5-C6-O6
3	E	2	NAG	C4-C5-C6-O6
2	D	3	MAN	C4-C5-C6-O6
2	D	2	NAG	C4-C5-C6-O6
3	E	2	NAG	O5-C5-C6-O6
2	D	3	MAN	O5-C5-C6-O6
2	B	3	MAN	C4-C5-C6-O6
3	E	1	NAG	O5-C5-C6-O6
2	D	2	NAG	O5-C5-C6-O6
2	B	3	MAN	O5-C5-C6-O6
3	C	2	NAG	C8-C7-N2-C2
3	C	2	NAG	O7-C7-N2-C2

All (1) ring outliers are listed below:

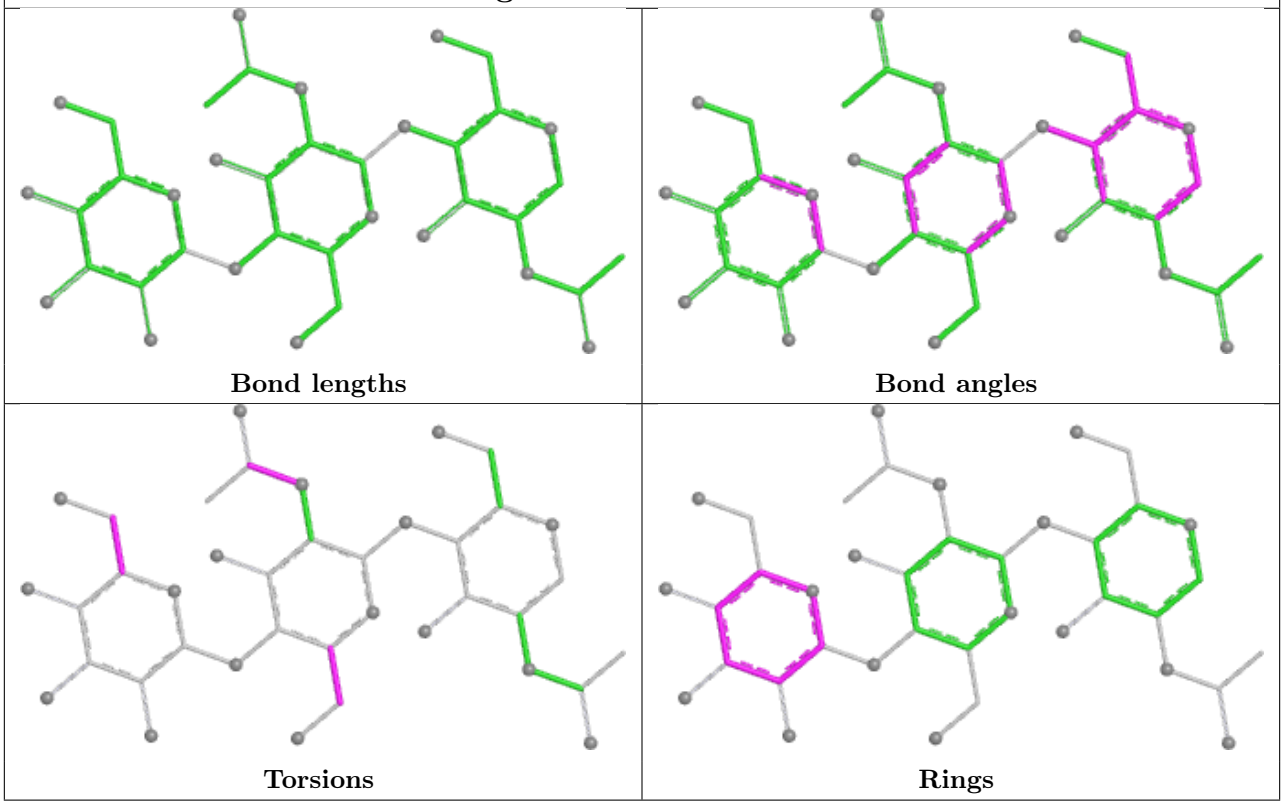
Mol	Chain	Res	Type	Atoms
2	B	3	MAN	C1-C2-C3-C4-C5-O5

3 monomers are involved in 2 short contacts:

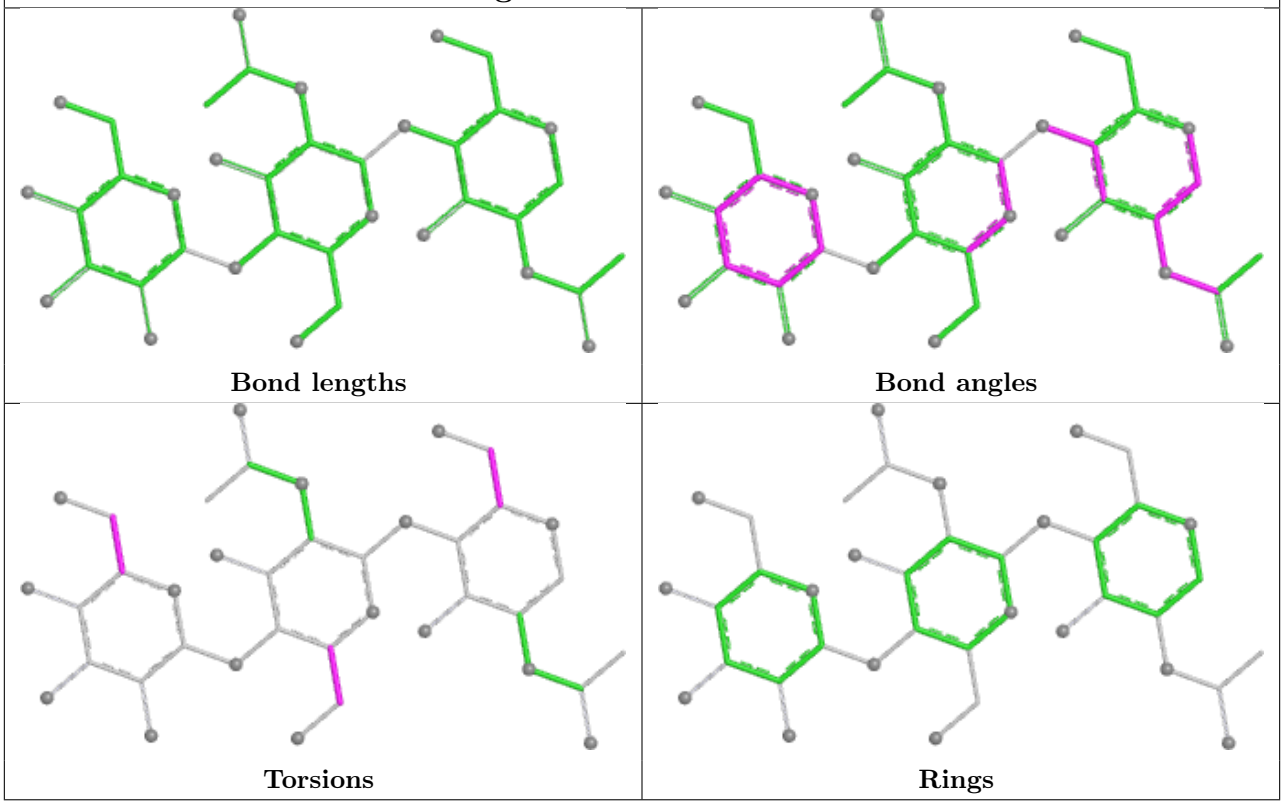
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	3	MAN	1	0
2	D	3	MAN	1	0
2	D	2	NAG	1	0

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

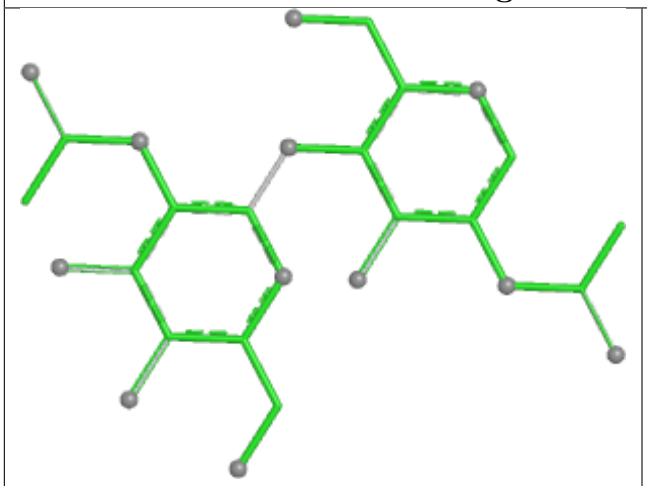
Oligosaccharide Chain B



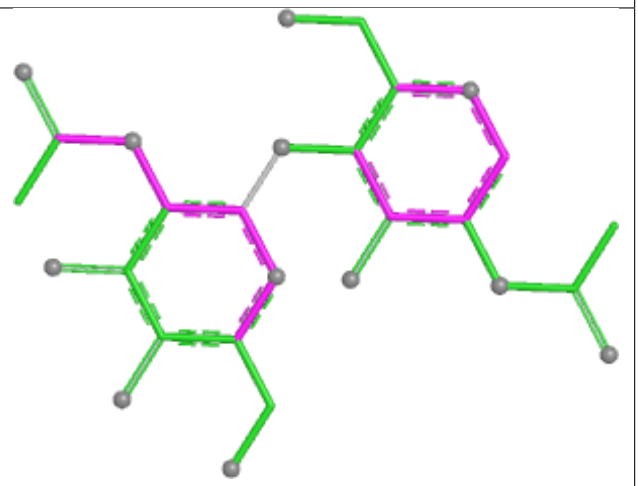
Oligosaccharide Chain D



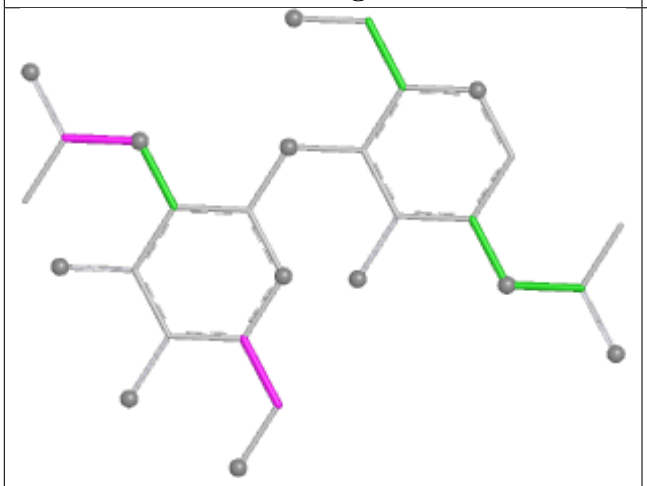
Oligosaccharide Chain C



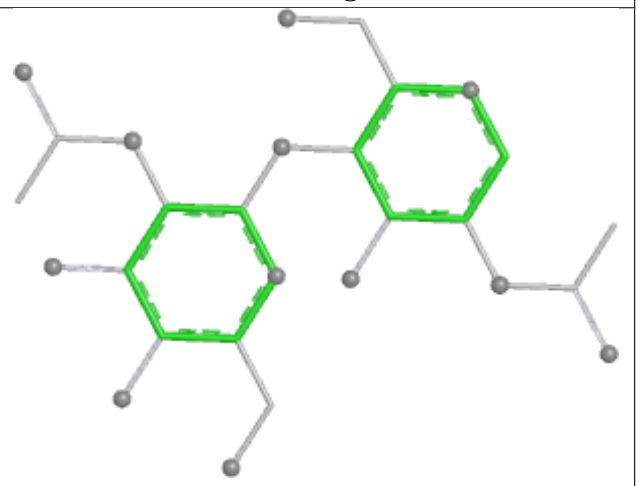
Bond lengths



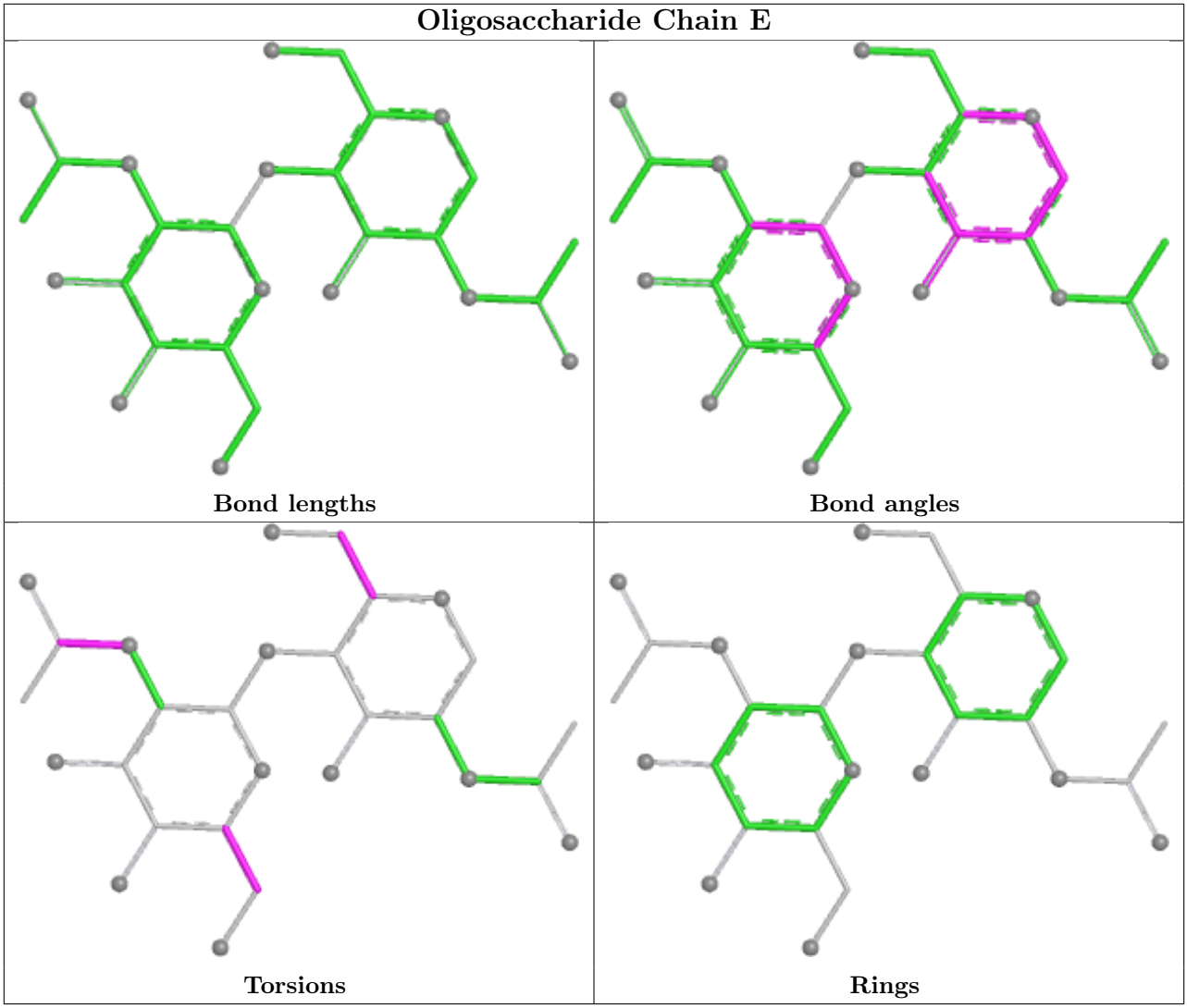
Bond angles



Torsions



Rings



5.6 Ligand geometry (i)

Of 14 ligands modelled in this entry, 11 are monoatomic - leaving 3 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	$\#\|Z\| > 2$
7	HEM	A	618	9,1	50,50,50	1.84	8 (16%)	67,82,82	1.11	4 (5%)
5	SCN	A	607	-	1,2,2	0.21	0	0,1,1	-	-
8	CAQ	A	619	-	8,8,8	2.19	1 (12%)	10,10,10	2.34	4 (40%)

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
7	HEM	A	618	9,1	-	2/14/54/54	-
8	CAQ	A	619	-	-	-	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	618	HEM	C3D-C2D	7.27	1.52	1.36
8	A	619	CAQ	C4-C3	5.93	1.50	1.40
7	A	618	HEM	FE-NC	4.78	2.10	1.95
7	A	618	HEM	FE-NB	3.75	2.06	1.94
7	A	618	HEM	CAC-C3C	3.05	1.55	1.47
7	A	618	HEM	CAB-C3B	2.55	1.54	1.47
7	A	618	HEM	C3B-C2B	-2.53	1.32	1.37
7	A	618	HEM	CMC-C2C	2.30	1.55	1.50
7	A	618	HEM	CAA-C2A	2.04	1.56	1.51

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	A	619	CAQ	C5-C4-C3	-4.49	114.87	119.66
8	A	619	CAQ	C1-C6-C5	3.70	124.81	120.24
7	A	618	HEM	C4D-ND-C1D	3.47	109.32	105.21
7	A	618	HEM	CAD-C3D-C4D	2.79	129.56	124.70
8	A	619	CAQ	C6-C1-C2	-2.52	117.13	120.24
7	A	618	HEM	O2A-CGA-CBA	2.46	121.78	114.00
7	A	618	HEM	O1A-CGA-CBA	-2.39	115.50	123.09
8	A	619	CAQ	O3-C3-C4	2.09	124.00	118.42

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	618	HEM	CAD-CBD-CGD-O2D
7	A	618	HEM	CAD-CBD-CGD-O1D

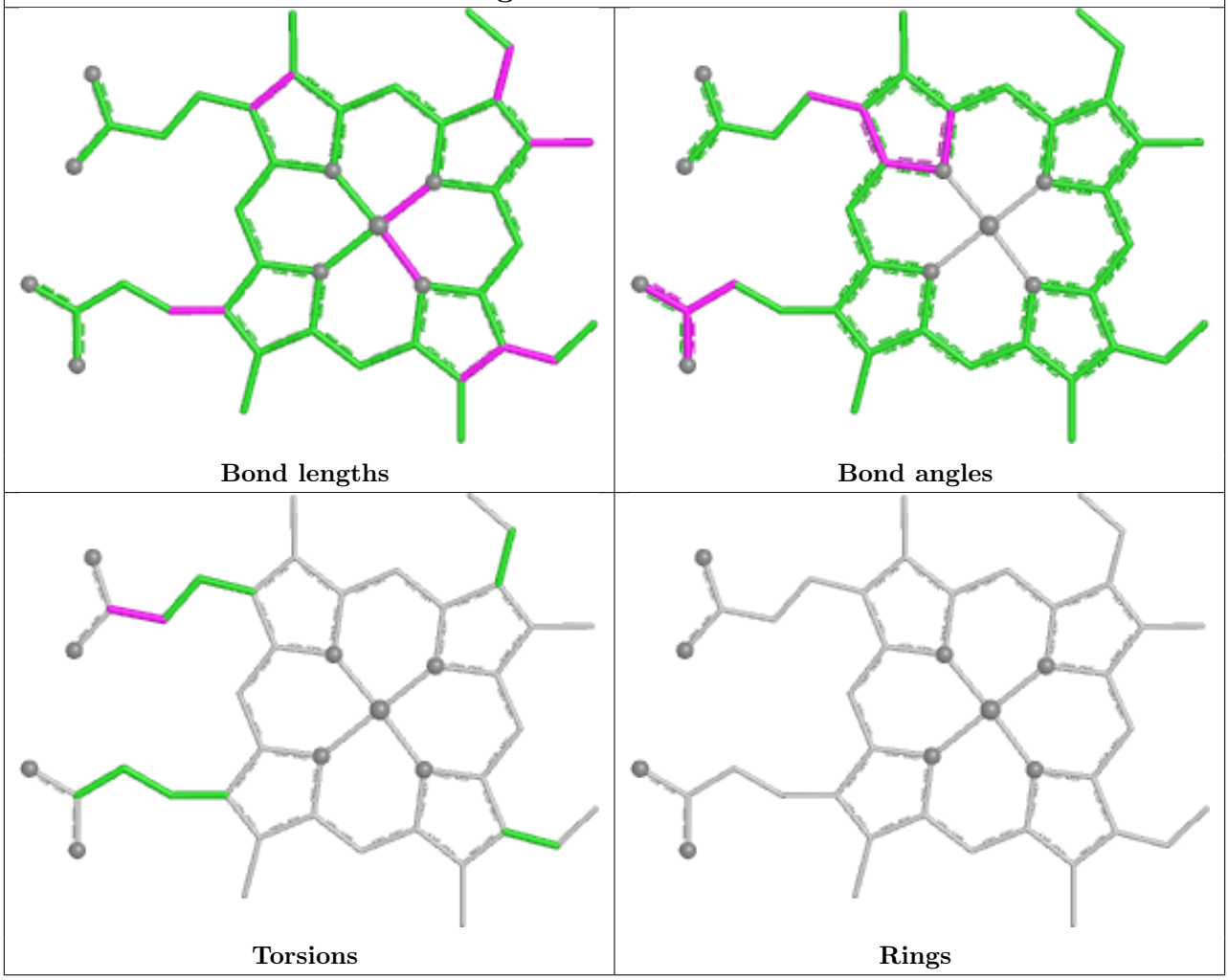
There are no ring outliers.

1 monomer is involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	618	HEM	8	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 then 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 HEM A 618



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%)	-0.46	17 (2%) 53 50	12, 27, 69, 106	1 (0%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	174	SER	3.9
1	A	2	TRP	3.7
1	A	170	PRO	3.5
1	A	8	ALA	3.4
1	A	120	GLY	2.9
1	A	12	LEU	2.8
1	A	175	LEU	2.8
1	A	168	PRO	2.7
1	A	119	LEU	2.7
1	A	171	PRO	2.6
1	A	172	TYR	2.6
1	A	9	PRO	2.4
1	A	167	CYS	2.3
1	A	5	GLY	2.2
1	A	121	SER	2.2
1	A	173	GLN	2.1
1	A	10	VAL	2.0

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	0.92	0.12	20,27,28,30	0

6.3 Carbohydrates (i)

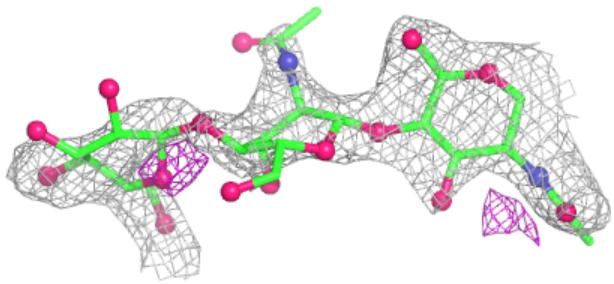
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

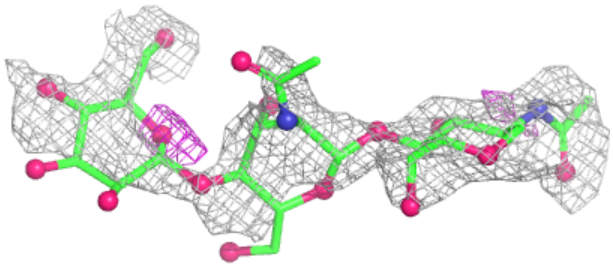
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	MAN	B	3	11/12	0.29	0.16	91,92,93,94	0
2	MAN	D	3	11/12	0.45	0.13	86,89,91,92	0
3	NAG	E	2	14/15	0.68	0.12	70,73,75,77	0
2	NAG	D	2	14/15	0.78	0.12	67,73,76,82	0
3	NAG	E	1	14/15	0.79	0.12	51,60,63,67	0
2	NAG	B	1	14/15	0.80	0.13	47,53,61,68	0
3	NAG	C	2	14/15	0.82	0.10	53,58,61,61	0
2	NAG	B	2	14/15	0.84	0.11	76,82,84,87	0
3	NAG	C	1	14/15	0.92	0.07	42,44,47,49	0
2	NAG	D	1	14/15	0.94	0.08	44,47,54,59	0

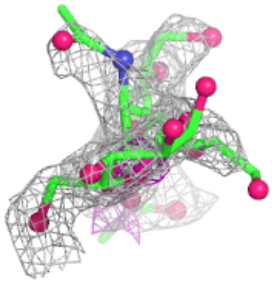
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain B:

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

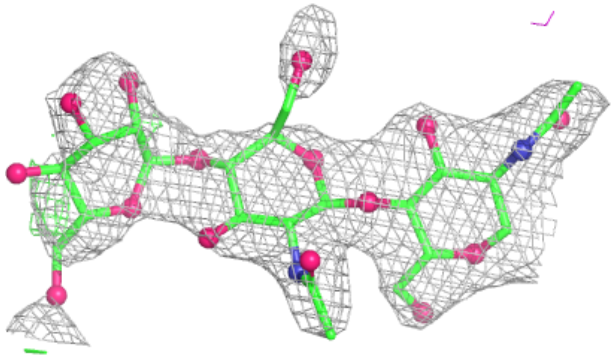


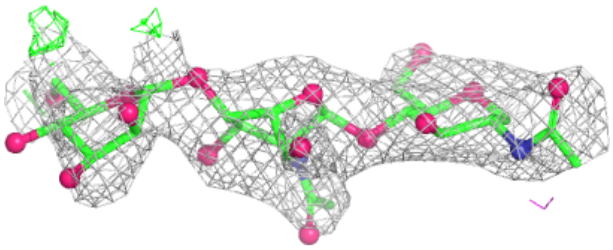


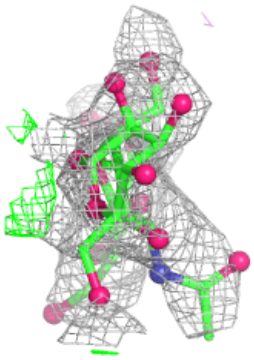


Electron density around Chain D:

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

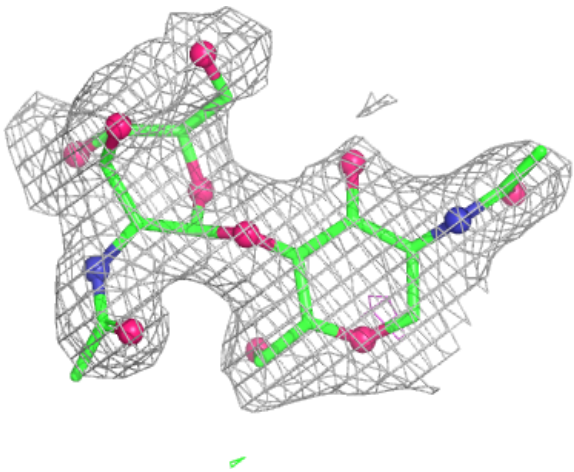


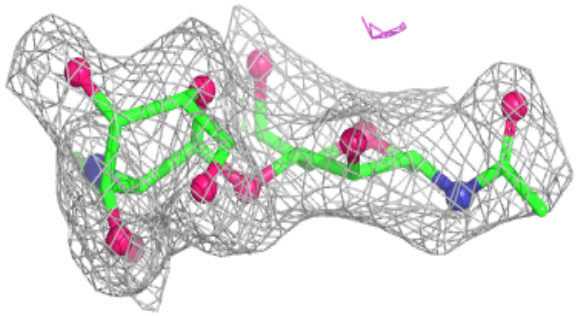


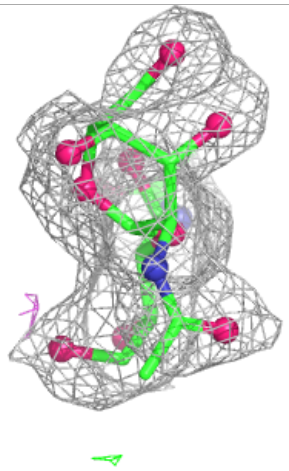


Electron density around Chain C:

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

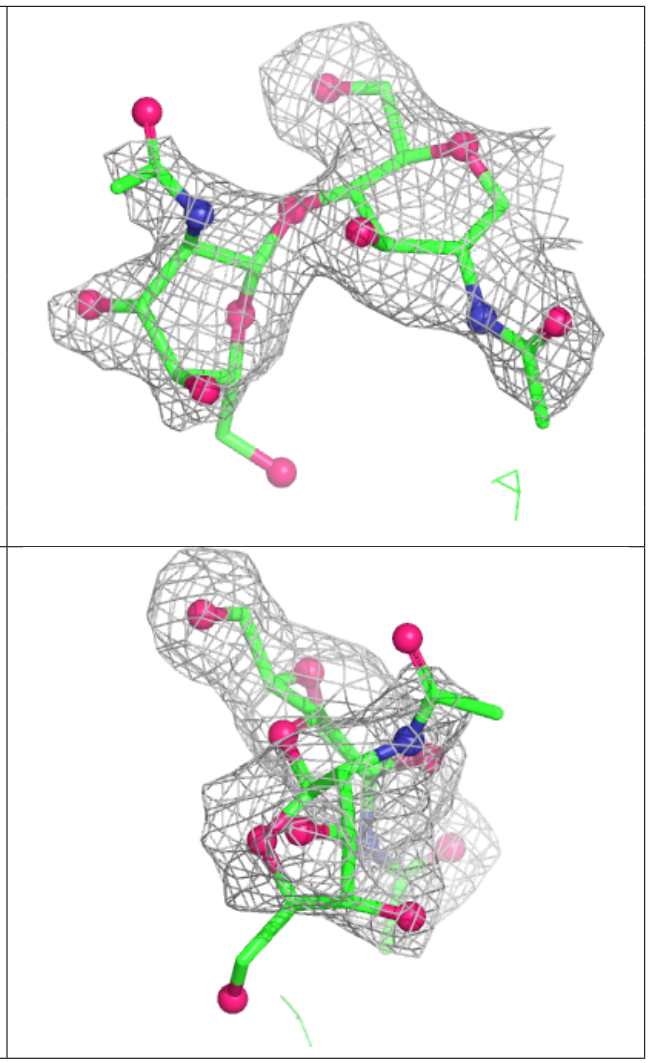






Electron density around Chain E:

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



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
8	CAQ	A	619	8/8	0.59	0.17	36,37,39,41	0
6	IOD	A	609	1/1	0.94	0.19	98,98,98,98	0
6	IOD	A	617	1/1	0.95	0.20	99,99,99,99	0
6	IOD	A	612	1/1	0.96	0.08	99,99,99,99	0
4	CA	A	606	1/1	0.97	0.03	17,17,17,17	0
7	HEM	A	618	43/43	0.97	0.06	8,16,18,25	0
5	SCN	A	607	3/3	0.97	0.13	18,18,18,20	0
6	IOD	A	614	1/1	0.98	0.08	77,77,77,77	0
6	IOD	A	611	1/1	0.98	0.08	86,86,86,86	0

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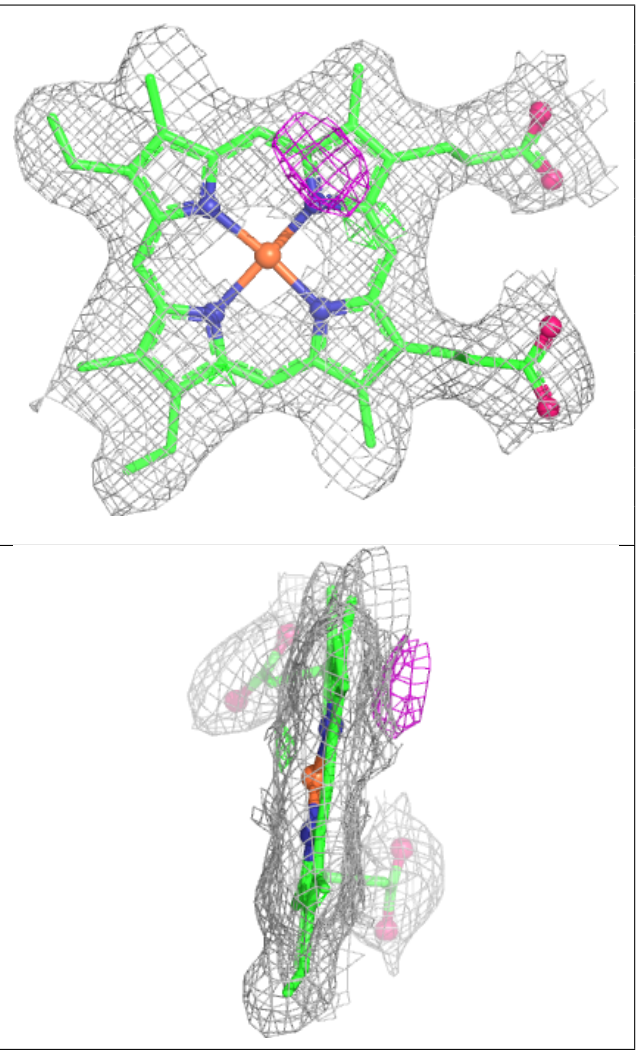
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	IOD	A	616	1/1	0.99	0.06	54,54,54,54	0
6	IOD	A	613	1/1	0.99	0.05	59,59,59,59	0
6	IOD	A	608	1/1	0.99	0.08	65,65,65,65	0
6	IOD	A	615	1/1	0.99	0.06	58,58,58,58	0
6	IOD	A	610	1/1	1.00	0.00	21,21,21,21	0

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 HEM A 618:

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.