Full wwPDB X-ray Structure Validation Report (i)

Nov 1, 2023 – 05:11 AM EDT

PDB ID	:	3NIU
Title	:	Crystal structure of the complex of dimeric goat lactoperoxidase with diethylene glycol at 2.9 A resolution
Authors	:	Vikram, G.; Singh, R.P.; Singh, A.K.; Sinha, M.; Kaur, P.; Sharma, S.; Singh, T.P.
Deposited on	:	2010-06-16
Resolution	:	2.94 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:

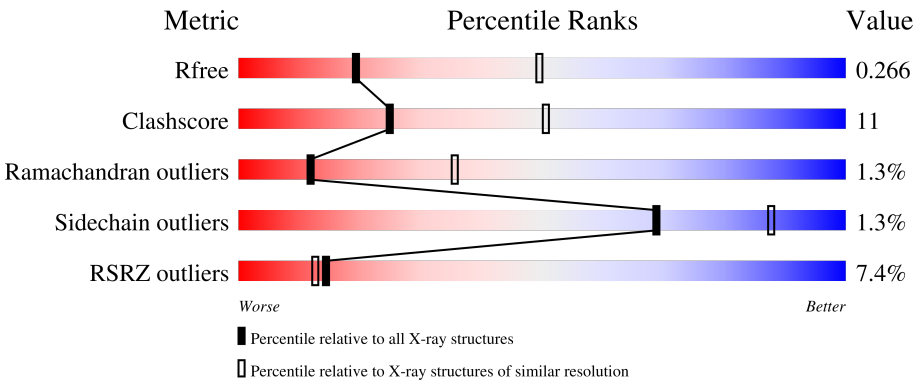
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.94 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}	130704	2969 (2.98-2.90)
Clashscore	141614	3218 (2.98-2.90)
Ramachandran outliers	138981	3122 (2.98-2.90)
Sidechain outliers	138945	3124 (2.98-2.90)
RSRZ outliers	127900	2902 (2.98-2.90)

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	7% 86% 13% •
1	B	595	8% 84% 14% •
2	C	2	50% 50%
2	E	2	100%

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Mol	Chain	Length	Quality of chain
2	F	2	100%
2	G	2	100%
3	D	3	33% 67%
3	H	3	33% 67%

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
1	SEP	B	198	-	-	-	X
2	NAG	C	2	-	-	-	X
2	NAG	E	2	-	-	-	X
2	NAG	F	2	-	-	-	X
2	NAG	G	2	-	-	-	X
3	BMA	D	3	-	-	-	X
3	BMA	H	3	-	-	-	X
4	NAG	B	607	-	-	-	X
5	PO4	A	2001	-	-	X	-
5	PO4	B	2004	-	-	X	-
7	HEM	B	1021	-	-	X	-
8	PEG	A	5001	-	-	X	-
8	PEG	B	5001	-	X	X	X

2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 10318 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.

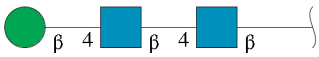
- Molecule 1 is a protein called Lactoperoxidase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	595	4757	3021	844	865	1	26	0	0	0
1	B	595	4757	3021	844	865	1	26	0	0	0

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

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

- Molecule 3 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
			Total	C	N	O			
3	D	3	39	22	2	15	0	0	0

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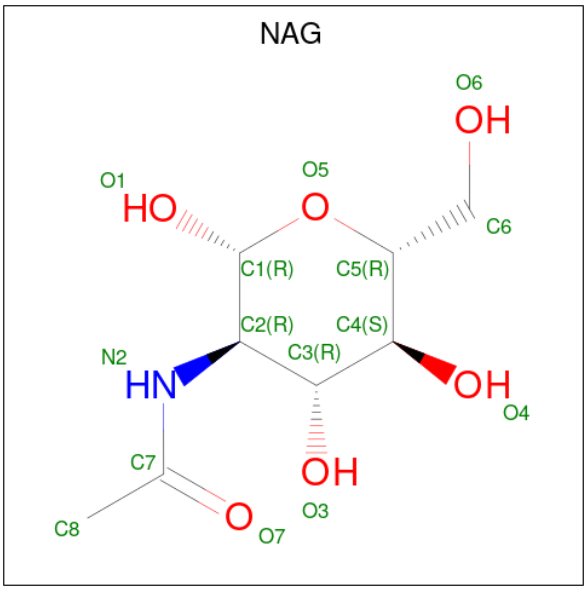
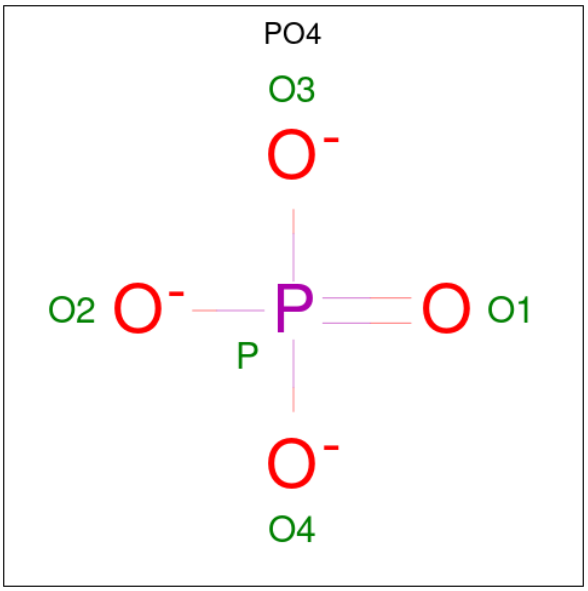
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	H	3	39	22	2	15	0	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	14	8	1	5	0	0
4	B	1	14	8	1	5	0	0

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).

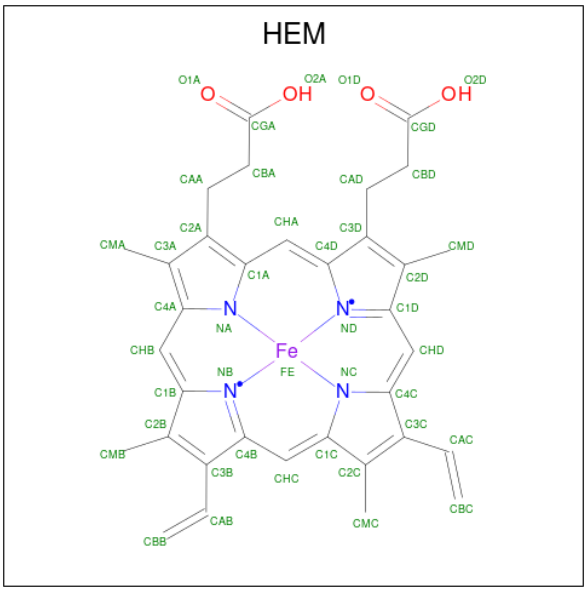


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total O P 5 4 1	0	0
5	A	1	Total O P 5 4 1	0	0
5	B	1	Total O P 5 4 1	0	0
5	B	1	Total O P 5 4 1	0	0

- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

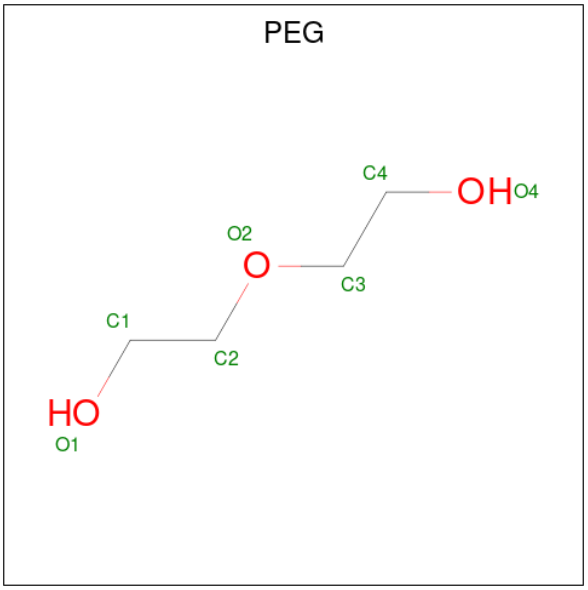
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Ca 1 1	0	0
6	B	1	Total Ca 1 1	0	0

- Molecule 7 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: 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
			Total	C	Fe	N	O		
7	B	1	43	34	1	4	4	0	0

- Molecule 8 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
8	A	1	7	4	3	0	0
			Total	C	O		
8	B	1	7	4	3	0	0

- Molecule 9 is water.

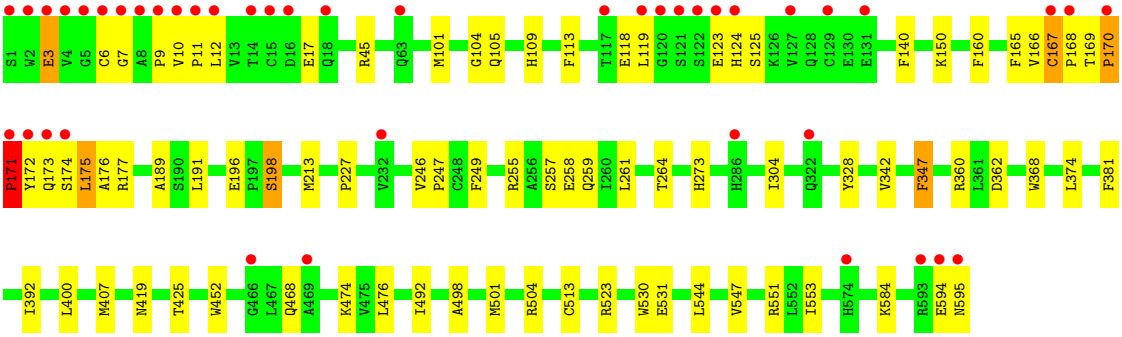
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
9	A	224	224	224	0	0
			Total	O		
9	B	240	240	240	0	0

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.

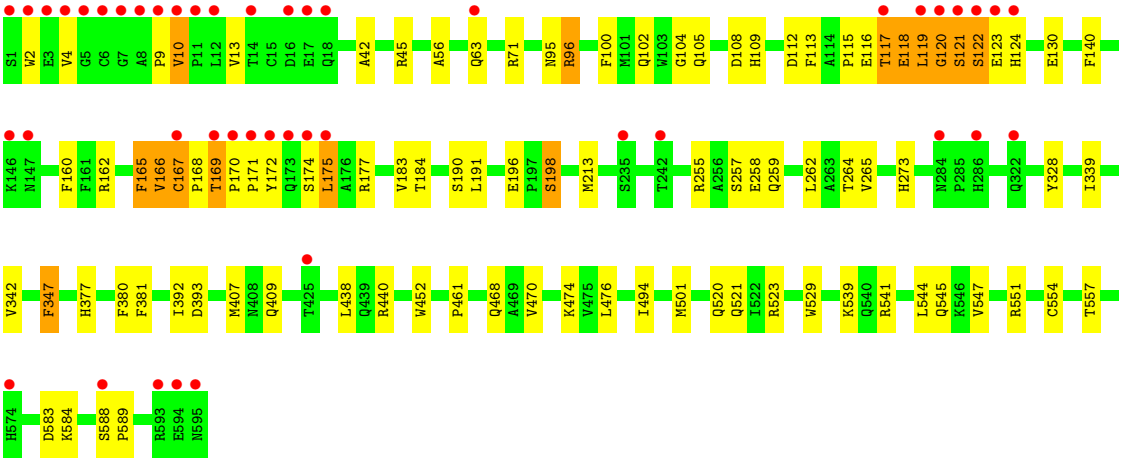
• Molecule 1: Lactoperoxidase

Chain A:



• Molecule 1: Lactoperoxidase

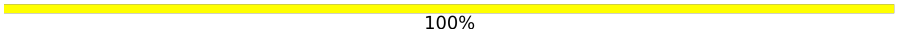
Chain B:



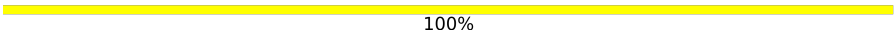
• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:

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

Chain E: 

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

Chain F: 

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

Chain G:

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

Chain D:

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

Chain H:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	59.20Å 75.59Å 83.81Å 79.93° 77.86° 72.50°	Depositor
Resolution (Å)	25.00 – 2.94 24.51 – 2.94	Depositor EDS
% Data completeness (in resolution range)	95.0 (25.00-2.94) 95.1 (24.51-2.94)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.81 (at 2.94Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.197 , 0.232 0.202 , 0.266	Depositor DCC
R_{free} test set	1366 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	28.6	Xtriage
Anisotropy	0.375	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 51.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	10318	wwPDB-VP
Average B, all atoms (Å^2)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.82% 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: CA, HEM, NAG, BMA, SEP, PO4, PEG

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	0.40	0/4875	0.58	3/6621 (0.0%)
1	B	0.48	2/4875 (0.0%)	0.58	2/6621 (0.0%)
All	All	0.44	2/9750 (0.0%)	0.58	5/13242 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	165	PHE	CD2-CE2	-5.17	1.28	1.39
1	B	166	VAL	CB-CG1	-5.05	1.42	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	171	PRO	CA-N-CD	-9.73	97.87	111.50
1	B	124	HIS	CA-CB-CG	5.73	123.34	113.60
1	B	120	GLY	N-CA-C	-5.29	99.87	113.10
1	A	191	LEU	CA-CB-CG	5.23	127.33	115.30
1	A	119	LEU	N-CA-C	5.17	124.96	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4757	0	4644	87	0
1	B	4757	0	4644	109	0
2	C	28	0	25	1	0
2	E	28	0	25	0	0
2	F	28	0	25	0	0
2	G	28	0	25	2	0
3	D	39	0	34	0	0
3	H	39	0	34	0	0
4	A	14	0	13	0	0
4	B	14	0	13	0	0
5	A	10	0	0	3	0
5	B	10	0	0	3	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
7	A	43	0	30	15	0
7	B	43	0	30	21	0
8	A	7	0	10	4	0
8	B	7	0	10	9	0
9	A	224	0	0	1	0
9	B	240	0	0	0	0
All	All	10318	0	9562	209	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (209) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:108:ASP:OD1	7:B:1021:HEM:CMD	1.66	1.43
1:B:167:CYS:HB3	1:B:168:PRO:HD3	1.25	1.17
1:B:108:ASP:OD1	7:B:1021:HEM:HMD1	0.99	1.15
1:A:170:PRO:HB2	1:A:171:PRO:HD3	1.17	1.10
1:B:167:CYS:CB	1:B:168:PRO:CD	2.30	1.09
1:B:167:CYS:CB	1:B:168:PRO:HD3	1.80	1.09
1:B:117:THR:HG23	1:B:118:GLU:N	1.47	1.08
1:A:196:GLU:HB3	1:A:198:SEP:O2P	1.60	1.01
1:B:117:THR:CG2	1:B:118:GLU:N	2.21	0.99
1:B:169:THR:H	1:B:170:PRO:HD3	1.26	0.98
1:A:167:CYS:HB3	1:A:168:PRO:CD	1.97	0.94
1:A:170:PRO:HB2	1:A:171:PRO:CD	1.96	0.94
1:A:167:CYS:HB3	1:A:168:PRO:HD3	1.50	0.93
1:B:196:GLU:HB3	1:B:198:SEP:O2P	1.69	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:10:VAL:HG12	1:B:10:VAL:O	1.68	0.93
1:A:170:PRO:CB	1:A:171:PRO:HD3	1.99	0.92
1:B:117:THR:HG23	1:B:118:GLU:H	1.12	0.91
1:A:167:CYS:CB	1:A:168:PRO:CD	2.49	0.90
1:B:167:CYS:HB2	1:B:168:PRO:CD	2.01	0.88
1:B:116:GLU:O	1:B:117:THR:HG22	1.73	0.88
1:B:259:GLN:OE1	7:B:1021:HEM:CBB	2.23	0.86
1:B:167:CYS:HB2	1:B:168:PRO:HD2	1.59	0.84
1:A:169:THR:N	1:A:170:PRO:CD	2.39	0.84
1:A:360:ARG:HH12	1:A:374:LEU:HD11	1.43	0.83
1:A:166:VAL:CG1	1:A:167:CYS:N	2.40	0.83
1:B:169:THR:N	1:B:170:PRO:HD3	1.92	0.82
1:B:259:GLN:OE1	7:B:1021:HEM:CAB	2.26	0.82
1:B:258:GLU:HG3	8:B:5001:PEG:H21	1.60	0.82
1:A:166:VAL:HG13	1:A:167:CYS:H	1.44	0.81
1:B:108:ASP:OD1	7:B:1021:HEM:C2D	2.33	0.80
1:B:117:THR:HB	1:B:162:ARG:O	1.81	0.79
1:B:169:THR:N	1:B:170:PRO:CD	2.46	0.79
1:B:120:GLY:O	1:B:121:SER:HB3	1.80	0.78
1:B:2:TRP:O	1:B:4:VAL:HG23	1.84	0.76
1:B:258:GLU:HG3	8:B:5001:PEG:C2	2.15	0.76
1:A:167:CYS:HB2	1:A:168:PRO:HD2	1.69	0.75
1:A:167:CYS:CB	1:A:168:PRO:HD2	2.16	0.74
1:A:166:VAL:HG13	1:A:167:CYS:N	2.01	0.74
1:A:258:GLU:OE1	7:A:1001:HEM:C2B	2.36	0.74
1:A:258:GLU:HG3	8:A:5001:PEG:H21	1.69	0.74
1:B:2:TRP:CZ3	1:B:174:SER:HB2	2.24	0.73
7:A:1001:HEM:C3A	8:A:5001:PEG:H22	2.24	0.73
1:B:10:VAL:HG12	1:B:13:VAL:CG1	2.19	0.72
1:A:105:GLN:NE2	7:A:1001:HEM:C4B	2.58	0.72
1:A:45:ARG:HD3	5:A:2001:PO4:O4	1.90	0.71
1:B:10:VAL:HG12	1:B:13:VAL:HG13	1.71	0.70
1:B:342:VAL:HB	5:B:2004:PO4:O3	1.93	0.69
7:A:1001:HEM:HMC2	7:A:1001:HEM:HBC2	1.75	0.68
1:B:117:THR:CG2	1:B:118:GLU:H	1.87	0.68
1:A:407:MET:HB3	1:A:501:MET:CE	2.24	0.68
1:B:167:CYS:HB3	1:B:168:PRO:CD	2.04	0.68
1:A:551:ARG:HD3	1:A:584:LYS:HA	1.77	0.67
1:A:169:THR:N	1:A:170:PRO:HD3	2.08	0.67
1:A:109:HIS:HA	1:A:255:ARG:NH2	2.11	0.65
1:A:173:GLN:CG	1:A:174:SER:H	2.10	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:259:GLN:OE1	7:B:1021:HEM:HBB1	1.98	0.64
1:A:407:MET:HB3	1:A:501:MET:HE1	1.81	0.63
1:A:7:GLY:HA2	1:A:166:VAL:HG13	1.78	0.63
1:A:381:PHE:HZ	8:A:5001:PEG:H41	1.64	0.63
1:B:121:SER:O	1:B:122:SER:HB3	1.98	0.63
7:B:1021:HEM:C2A	8:B:5001:PEG:H41	2.33	0.63
1:B:168:PRO:CB	1:B:170:PRO:HD2	2.30	0.62
1:A:360:ARG:HH12	1:A:374:LEU:CD1	2.12	0.62
1:B:407:MET:HB3	1:B:501:MET:CE	2.30	0.62
1:A:166:VAL:HG12	1:A:167:CYS:N	2.14	0.61
1:A:105:GLN:HG3	7:A:1001:HEM:C1C	2.36	0.61
1:A:259:GLN:NE2	1:A:261:LEU:HB2	2.16	0.61
1:A:175:LEU:HD12	1:A:176:ALA:H	1.65	0.60
1:A:173:GLN:HG2	1:A:174:SER:H	1.66	0.60
1:B:117:THR:CB	1:B:162:ARG:O	2.49	0.60
1:B:108:ASP:OD1	7:B:1021:HEM:HMD2	1.92	0.60
1:A:166:VAL:O	1:A:167:CYS:HB2	2.01	0.59
1:B:13:VAL:HG23	1:B:13:VAL:O	2.02	0.59
1:A:342:VAL:HB	5:A:2001:PO4:O3	2.02	0.59
1:B:168:PRO:HB2	1:B:170:PRO:HD2	1.84	0.58
1:A:113:PHE:CG	1:A:255:ARG:NH1	2.71	0.58
1:B:117:THR:CG2	1:B:162:ARG:O	2.52	0.57
1:A:109:HIS:HA	1:A:255:ARG:HH21	1.67	0.57
1:B:4:VAL:HG12	1:B:4:VAL:O	2.03	0.57
1:B:407:MET:HB3	1:B:501:MET:HE1	1.87	0.57
1:B:174:SER:O	1:B:175:LEU:O	2.22	0.57
1:B:539:LYS:HB3	1:B:589:PRO:HB3	1.85	0.57
1:B:56:ALA:HB1	1:B:177:ARG:HD2	1.86	0.57
1:A:113:PHE:CD1	1:A:255:ARG:NH1	2.73	0.57
1:B:259:GLN:OE1	7:B:1021:HEM:HAB	2.03	0.56
1:A:259:GLN:OE1	7:A:1001:HEM:HBB1	2.05	0.56
1:B:116:GLU:O	1:B:117:THR:C	2.41	0.56
1:B:113:PHE:CD1	1:B:255:ARG:NH1	2.73	0.56
1:B:468:GLN:HG2	1:B:474:LYS:HA	1.88	0.55
1:B:258:GLU:OE1	7:B:1021:HEM:C2B	2.56	0.55
1:B:257:SER:O	1:B:381:PHE:HA	2.06	0.55
7:A:1001:HEM:HBC2	7:A:1001:HEM:CMC	2.37	0.54
1:B:118:GLU:OE2	1:B:119:LEU:HG	2.07	0.54
7:B:1021:HEM:HAA1	8:B:5001:PEG:H41	1.88	0.54
1:B:328:TYR:HA	1:B:523:ARG:HH12	1.72	0.54
1:B:10:VAL:O	1:B:10:VAL:CG1	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:123:GLU:HG2	1:A:125:SER:H	1.72	0.54
1:A:452:TRP:HH2	5:A:2001:PO4:O2	1.91	0.53
1:B:264:THR:HG23	1:B:392:ILE:HB	1.90	0.53
1:A:104:GLY:HA3	7:A:1001:HEM:CBC	2.38	0.53
1:B:520:GLN:HG3	1:B:521:GLN:N	2.22	0.53
2:G:1:NAG:H62	2:G:2:NAG:HN2	1.73	0.53
1:B:213:MET:HG2	1:B:273:HIS:CD2	2.44	0.53
1:A:347:PHE:HB3	7:A:1001:HEM:CMD	2.39	0.52
1:A:173:GLN:CG	1:A:174:SER:N	2.72	0.52
1:A:168:PRO:C	1:A:170:PRO:CD	2.78	0.52
1:A:213:MET:HG2	1:A:273:HIS:CD2	2.44	0.52
1:A:407:MET:HB3	1:A:501:MET:HE3	1.91	0.52
1:B:116:GLU:O	1:B:117:THR:CG2	2.52	0.52
1:A:109:HIS:CD2	1:A:255:ARG:HH21	2.28	0.52
1:B:63:GLN:HB3	1:B:71:ARG:HH12	1.75	0.51
1:B:123:GLU:OE2	1:B:123:GLU:HA	2.09	0.51
1:A:105:GLN:HB2	7:A:1001:HEM:CMC	2.41	0.51
1:B:170:PRO:O	1:B:171:PRO:C	2.44	0.51
1:B:258:GLU:HG3	8:B:5001:PEG:H22	1.92	0.51
1:B:42:ALA:HB2	1:B:166:VAL:HG11	1.93	0.50
1:A:113:PHE:HB2	1:A:255:ARG:HH12	1.76	0.50
1:B:2:TRP:CE3	1:B:174:SER:HB2	2.45	0.50
1:B:45:ARG:HD3	5:B:2004:PO4:O4	2.11	0.50
1:B:117:THR:O	1:B:118:GLU:HB3	2.11	0.50
1:A:140:PHE:O	1:A:160:PHE:HB3	2.11	0.50
1:A:150:LYS:NZ	1:A:419:ASN:O	2.39	0.50
1:B:541:ARG:O	1:B:545:GLN:HG3	2.11	0.50
1:B:102:GLN:HE22	1:B:262:LEU:HA	1.77	0.50
7:B:1021:HEM:CAA	8:B:5001:PEG:H41	2.42	0.50
1:A:257:SER:O	1:A:381:PHE:HA	2.11	0.50
1:A:175:LEU:CD1	1:A:176:ALA:H	2.25	0.49
1:B:117:THR:HG23	1:B:118:GLU:CA	2.37	0.49
1:A:12:LEU:HD12	1:A:12:LEU:O	2.13	0.49
1:B:102:GLN:CG	1:B:265:VAL:HG21	2.42	0.49
1:B:113:PHE:O	1:B:115:PRO:HD3	2.12	0.49
7:B:1021:HEM:C4A	8:B:5001:PEG:H22	2.47	0.49
1:A:172:TYR:CD1	1:A:172:TYR:C	2.85	0.49
1:A:530:TRP:CE2	1:A:531:GLU:HG3	2.48	0.49
1:B:117:THR:O	1:B:118:GLU:CB	2.60	0.49
1:A:168:PRO:C	1:A:170:PRO:HD2	2.33	0.49
1:B:10:VAL:CG1	1:B:13:VAL:CG1	2.89	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:113:PHE:CE2	1:B:115:PRO:HG3	2.48	0.48
1:A:165:PHE:N	1:A:165:PHE:CD2	2.81	0.48
1:B:452:TRP:HH2	5:B:2004:PO4:O2	1.97	0.48
1:B:104:GLY:HA3	7:B:1021:HEM:CBC	2.44	0.48
1:B:393:ASP:OD1	1:B:557:THR:HB	2.13	0.48
1:B:102:GLN:HG2	1:B:265:VAL:HG21	1.94	0.48
1:A:3:GLU:HG3	1:A:6:CYS:HB2	1.96	0.47
7:B:1021:HEM:C1A	8:B:5001:PEG:H41	2.49	0.47
1:B:102:GLN:NE2	1:B:262:LEU:HA	2.30	0.47
1:A:105:GLN:CD	7:A:1001:HEM:CHC	2.83	0.47
1:B:588:SER:N	1:B:589:PRO:HD2	2.29	0.47
1:B:544:LEU:O	1:B:547:VAL:HG22	2.14	0.47
7:B:1021:HEM:HMC2	7:B:1021:HEM:HBC2	1.97	0.47
1:A:400:LEU:HD11	1:A:553:ILE:HD13	1.96	0.47
1:B:4:VAL:O	1:B:4:VAL:CG1	2.61	0.47
1:B:95:ASN:O	1:B:96:ARG:HD3	2.16	0.46
1:B:551:ARG:HD3	1:B:583:ASP:O	2.14	0.46
1:A:362:ASP:HB3	1:A:368:TRP:HD1	1.80	0.46
1:B:10:VAL:CG1	1:B:13:VAL:HG11	2.46	0.46
1:A:544:LEU:O	1:A:547:VAL:HG22	2.16	0.45
1:B:347:PHE:HB3	7:B:1021:HEM:CMD	2.46	0.45
1:A:118:GLU:OE1	1:A:425:THR:HG21	2.16	0.45
1:A:264:THR:HG23	1:A:392:ILE:HB	1.99	0.45
1:B:121:SER:O	1:B:122:SER:CB	2.62	0.45
1:A:476:LEU:HD21	1:A:498:ALA:HB1	1.99	0.45
1:B:109:HIS:CE1	1:B:255:ARG:HB2	2.51	0.45
7:B:1021:HEM:HBC2	7:B:1021:HEM:CMC	2.47	0.45
1:B:409:GLN:HB3	1:B:476:LEU:HD22	1.99	0.45
1:B:551:ARG:HD3	1:B:584:LYS:HA	1.98	0.45
1:A:468:GLN:HG2	1:A:474:LYS:HA	2.00	0.44
1:B:119:LEU:CD2	1:B:121:SER:HA	2.47	0.44
1:B:120:GLY:O	1:B:121:SER:CB	2.56	0.44
1:B:461:PRO:HG3	1:B:470:VAL:HG21	1.98	0.44
1:B:10:VAL:HG12	1:B:13:VAL:HG11	1.96	0.44
1:B:407:MET:HB3	1:B:501:MET:HE3	1.99	0.44
7:B:1021:HEM:HAA1	8:B:5001:PEG:C4	2.47	0.44
1:B:183:VAL:HG12	1:B:184:THR:N	2.33	0.44
1:A:168:PRO:HB2	1:A:171:PRO:HD2	1.98	0.43
1:B:169:THR:O	1:B:169:THR:OG1	2.30	0.43
1:B:168:PRO:HB3	1:B:170:PRO:HD2	1.99	0.43
1:B:118:GLU:HG2	1:B:119:LEU:H	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10:VAL:HA	1:A:11:PRO:HD3	1.88	0.43
1:A:227:PRO:HG2	1:A:249:PHE:CG	2.53	0.43
1:B:523:ARG:HG3	1:B:529:TRP:CE2	2.54	0.43
1:A:259:GLN:HE22	1:A:261:LEU:HB2	1.84	0.43
1:A:594:GLU:HG3	1:A:595:ASN:H	1.84	0.43
1:A:105:GLN:HB2	7:A:1001:HEM:HMC1	2.00	0.43
1:A:175:LEU:CG	1:A:176:ALA:H	2.32	0.42
1:A:255:ARG:HB3	8:A:5001:PEG:H31	2.00	0.42
1:B:105:GLN:HB2	7:B:1021:HEM:CMC	2.48	0.42
1:B:113:PHE:HD1	1:B:255:ARG:NH1	2.15	0.42
2:G:1:NAG:H62	2:G:2:NAG:N2	2.34	0.42
1:B:140:PHE:O	1:B:160:PHE:HB3	2.19	0.42
1:A:189:ALA:HB2	1:A:304:ILE:HD12	2.02	0.42
1:A:101:MET:O	7:A:1001:HEM:HMC2	2.20	0.41
1:A:113:PHE:CB	1:A:255:ARG:HH12	2.33	0.41
1:B:165:PHE:CD1	1:B:165:PHE:N	2.87	0.41
1:A:452:TRP:CD1	1:A:492:ILE:HD13	2.55	0.41
1:A:176:ALA:HB3	9:A:664:HOH:O	2.20	0.41
1:A:347:PHE:HB3	7:A:1001:HEM:HMD3	2.01	0.41
1:A:360:ARG:NH1	1:A:374:LEU:HD11	2.24	0.41
1:B:438:LEU:HD21	1:B:494:ILE:HB	2.03	0.41
1:A:170:PRO:CB	1:A:171:PRO:CD	2.75	0.41
1:A:246:VAL:HA	1:A:247:PRO:HD3	1.85	0.41
1:B:377:HIS:HA	1:B:380:PHE:CE2	2.56	0.41
1:B:440:ARG:NH2	7:B:1021:HEM:O1A	2.50	0.41
1:A:504:ARG:HH22	2:C:2:NAG:H3	1.85	0.41
1:A:328:TYR:CD1	1:A:523:ARG:HD3	2.56	0.40
1:A:347:PHE:HB3	7:A:1001:HEM:HMD1	2.03	0.40
1:B:96:ARG:HG3	1:B:100:PHE:CG	2.56	0.40
1:B:112:ASP:HB3	1:B:339:ILE:HG21	2.03	0.40
1:B:165:PHE:CE1	1:B:177:ARG:NH2	2.89	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	592/595 (100%)	568 (96%)	17 (3%)	7 (1%)	13	38
1	B	592/595 (100%)	561 (95%)	23 (4%)	8 (1%)	11	34
All	All	1184/1190 (100%)	1129 (95%)	40 (3%)	15 (1%)	12	35

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	167	CYS
1	A	171	PRO
1	B	9	PRO
1	B	121	SER
1	B	167	CYS
1	B	175	LEU
1	A	3	GLU
1	B	10	VAL
1	B	119	LEU
1	B	122	SER
1	A	175	LEU
1	A	9	PRO
1	A	17	GLU
1	B	169	THR
1	A	170	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	516/516 (100%)	512 (99%)	4 (1%)	81	93
1	B	516/516 (100%)	507 (98%)	9 (2%)	60	83
All	All	1032/1032 (100%)	1019 (99%)	13 (1%)	69	88

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	124	HIS
1	A	177	ARG
1	A	347	PHE
1	A	513	CYS
1	B	96	ARG
1	B	117	THR
1	B	118	GLU
1	B	130	GLU
1	B	172	TYR
1	B	190	SER
1	B	191	LEU
1	B	347	PHE
1	B	554	CYS

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	94	GLN
1	A	102	GLN
1	A	105	GLN
1	A	147	ASN
1	A	259	GLN
1	A	426	HIS
1	A	468	GLN
1	A	497	ASN
1	A	520	GLN
1	A	570	ASN
1	B	105	GLN
1	B	147	ASN
1	B	423	GLN
1	B	437	ASN
1	B	460	GLN
1	B	468	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)

2 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	SEP	A	198	1	8,9,10	1.71	1 (12%)	8,12,14	1.43	1 (12%)
1	SEP	B	198	1	8,9,10	1.72	1 (12%)	8,12,14	1.24	1 (12%)

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	-	4/5/8/10	-
1	SEP	B	198	1	-	4/5/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	198	SEP	P-O1P	3.70	1.62	1.50
1	A	198	SEP	P-O1P	3.61	1.62	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	198	SEP	OG-CB-CA	2.93	110.99	108.14
1	B	198	SEP	OG-CB-CA	2.42	110.50	108.14

There are no chirality outliers.

All (8) 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	B	198	SEP	CB-OG-P-O1P
1	B	198	SEP	CB-OG-P-O2P
1	B	198	SEP	CB-OG-P-O3P

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

There are no ring outliers.

2 monomers are involved in 2 short contacts:

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

5.5 Carbohydrates (i)

14 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	C	1	1,2	14,14,15	0.59	0	17,19,21	1.26	1 (5%)
2	NAG	C	2	2	14,14,15	0.50	0	17,19,21	0.78	1 (5%)
3	NAG	D	1	1,3	14,14,15	0.55	0	17,19,21	0.81	1 (5%)
3	NAG	D	2	3	14,14,15	0.65	0	17,19,21	1.40	1 (5%)
3	BMA	D	3	3	11,11,12	0.62	0	15,15,17	1.11	0
2	NAG	E	1	1,2	14,14,15	0.54	0	17,19,21	1.25	2 (11%)
2	NAG	E	2	2	14,14,15	0.42	0	17,19,21	1.45	1 (5%)
2	NAG	F	1	1,2	14,14,15	0.56	0	17,19,21	0.99	1 (5%)
2	NAG	F	2	2	14,14,15	0.59	0	17,19,21	1.12	1 (5%)
2	NAG	G	1	1,2	14,14,15	0.55	0	17,19,21	1.14	2 (11%)
2	NAG	G	2	2	14,14,15	0.44	0	17,19,21	1.43	2 (11%)
3	NAG	H	1	1,3	14,14,15	0.57	0	17,19,21	1.11	2 (11%)
3	NAG	H	2	3	14,14,15	0.46	0	17,19,21	1.14	1 (5%)
3	BMA	H	3	3	11,11,12	0.59	0	15,15,17	1.10	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	C	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1
3	NAG	D	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1
3	BMA	D	3	3	-	2/2/19/22	0/1/1/1
2	NAG	E	1	1,2	-	1/6/23/26	0/1/1/1
2	NAG	E	2	2	-	2/6/23/26	0/1/1/1
2	NAG	F	1	1,2	-	3/6/23/26	0/1/1/1
2	NAG	F	2	2	-	4/6/23/26	0/1/1/1
2	NAG	G	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	G	2	2	-	3/6/23/26	0/1/1/1
3	NAG	H	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	H	2	3	-	2/6/23/26	0/1/1/1
3	BMA	H	3	3	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	2	NAG	C1-O5-C5	5.10	119.10	112.19
3	D	2	NAG	C4-C3-C2	4.64	117.83	111.02
2	C	1	NAG	C4-C3-C2	4.02	116.91	111.02
2	G	2	NAG	C1-O5-C5	3.73	117.24	112.19
2	F	2	NAG	C1-O5-C5	3.67	117.16	112.19
2	G	1	NAG	C1-O5-C5	3.33	116.70	112.19
2	F	1	NAG	C4-C3-C2	3.05	115.49	111.02
3	H	2	NAG	C1-O5-C5	2.90	116.12	112.19
3	H	1	NAG	C4-C3-C2	2.81	115.14	111.02
2	E	1	NAG	C4-C3-C2	2.63	114.87	111.02
2	E	1	NAG	C1-O5-C5	2.59	115.71	112.19
2	C	2	NAG	C1-O5-C5	2.27	115.27	112.19
2	G	1	NAG	C4-C3-C2	2.17	114.20	111.02
3	H	1	NAG	C1-O5-C5	2.13	115.08	112.19
3	D	1	NAG	C4-C3-C2	2.12	114.13	111.02
2	G	2	NAG	O5-C1-C2	-2.08	108.01	111.29

There are no chirality outliers.

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	2	NAG	C8-C7-N2-C2
2	C	2	NAG	O7-C7-N2-C2
2	F	2	NAG	C8-C7-N2-C2
2	F	2	NAG	O7-C7-N2-C2
2	G	2	NAG	C8-C7-N2-C2
2	G	2	NAG	O7-C7-N2-C2
3	H	2	NAG	O5-C5-C6-O6
2	E	2	NAG	C8-C7-N2-C2
2	E	2	NAG	O7-C7-N2-C2
2	F	1	NAG	C8-C7-N2-C2
2	F	1	NAG	O7-C7-N2-C2
2	F	2	NAG	C4-C5-C6-O6
3	H	2	NAG	C4-C5-C6-O6
2	G	1	NAG	C8-C7-N2-C2
2	F	2	NAG	O5-C5-C6-O6
2	G	1	NAG	O7-C7-N2-C2
2	C	1	NAG	C4-C5-C6-O6
2	C	1	NAG	O5-C5-C6-O6
2	G	2	NAG	C4-C5-C6-O6
2	F	1	NAG	O5-C5-C6-O6
3	D	2	NAG	C8-C7-N2-C2
3	D	2	NAG	O7-C7-N2-C2
3	D	3	BMA	C4-C5-C6-O6
3	H	3	BMA	C4-C5-C6-O6
2	E	1	NAG	C4-C5-C6-O6
3	H	3	BMA	O5-C5-C6-O6
3	D	3	BMA	O5-C5-C6-O6

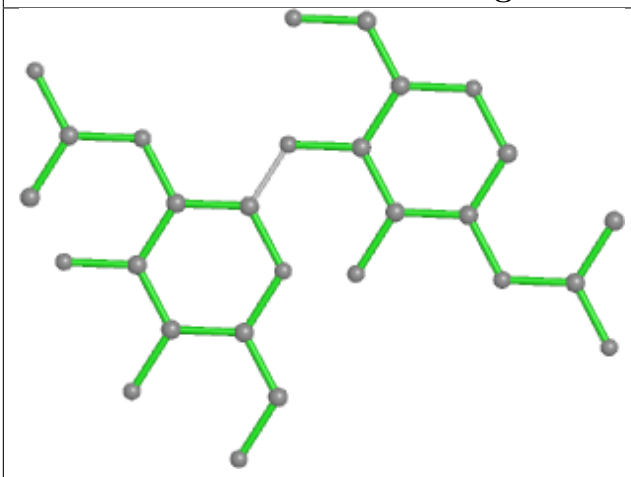
There are no ring outliers.

3 monomers are involved in 3 short contacts:

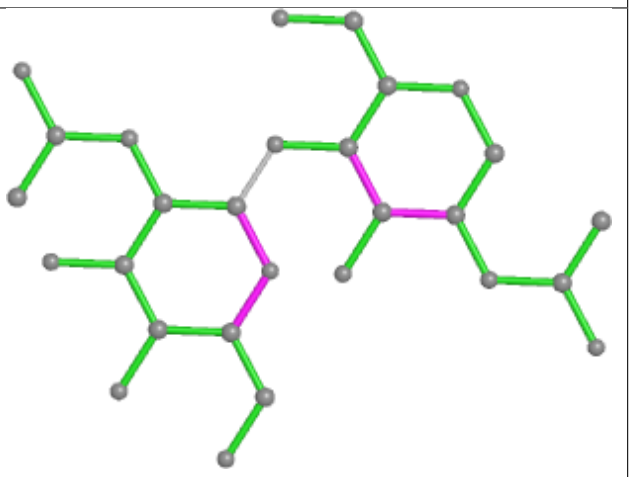
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	2	NAG	2	0
2	C	2	NAG	1	0
2	G	1	NAG	2	0

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

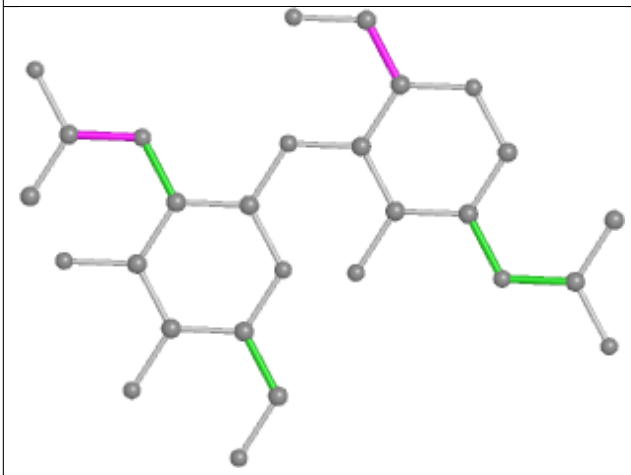
Oligosaccharide Chain C



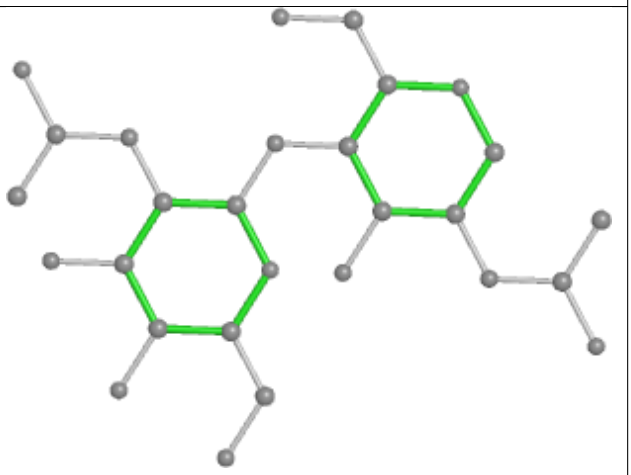
Bond lengths



Bond angles

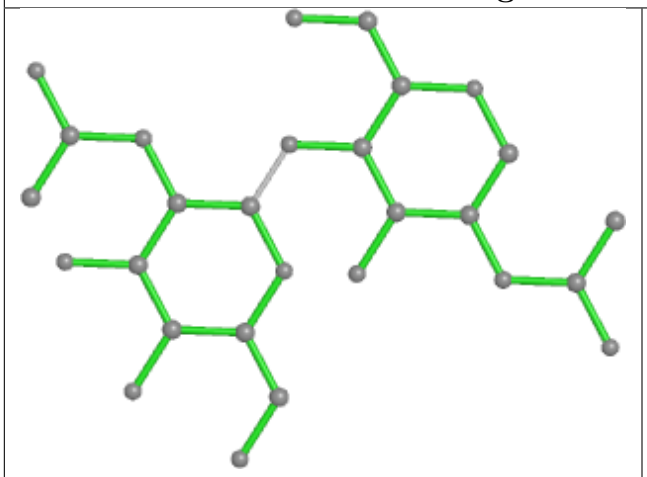


Torsions

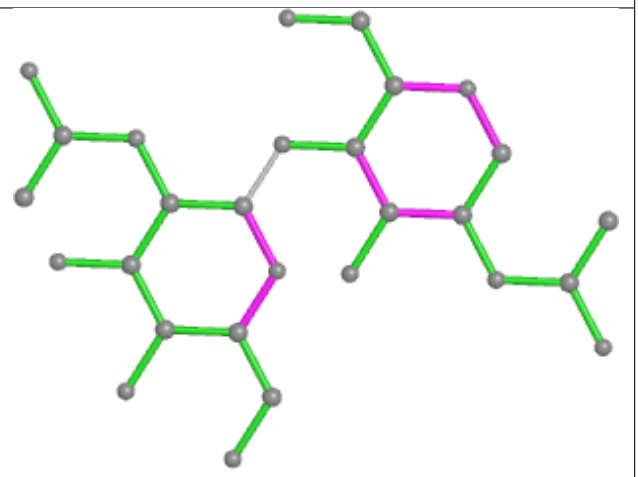


Rings

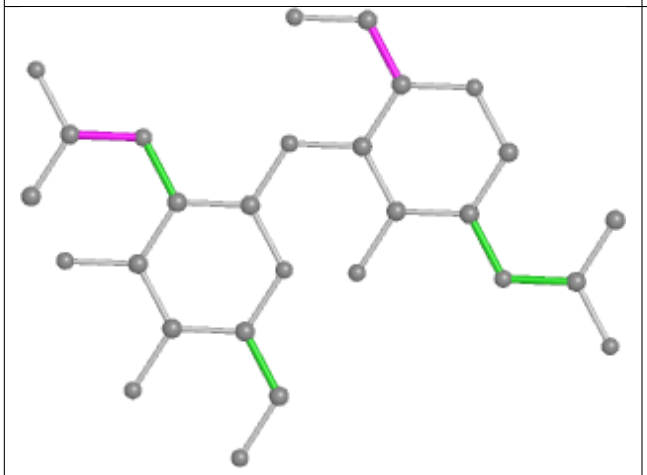
Oligosaccharide Chain E



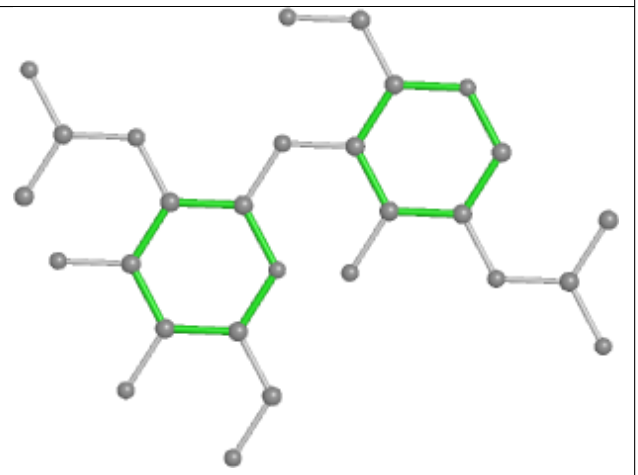
Bond lengths



Bond angles

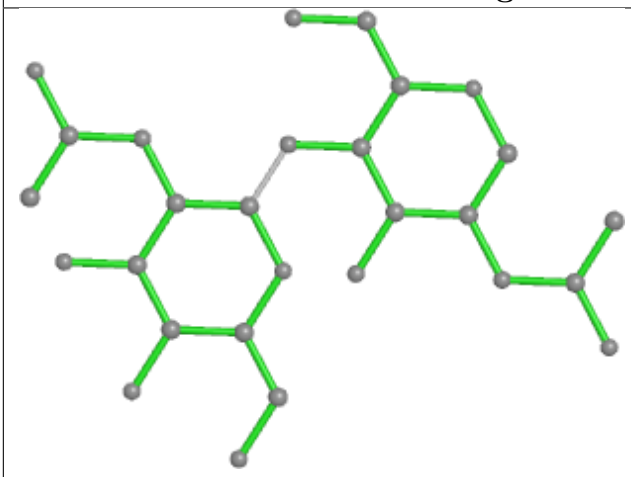


Torsions

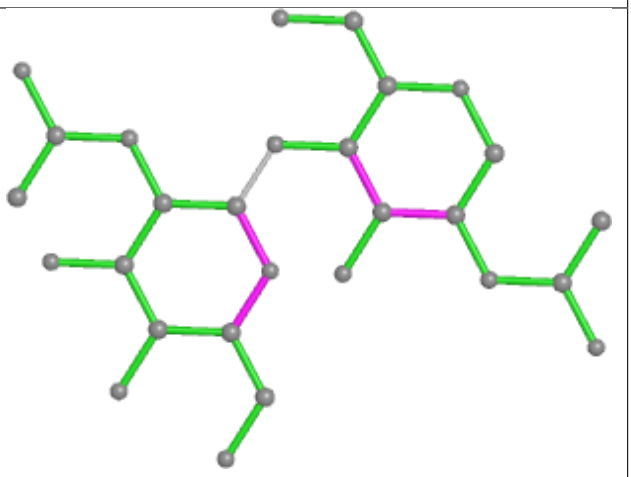


Rings

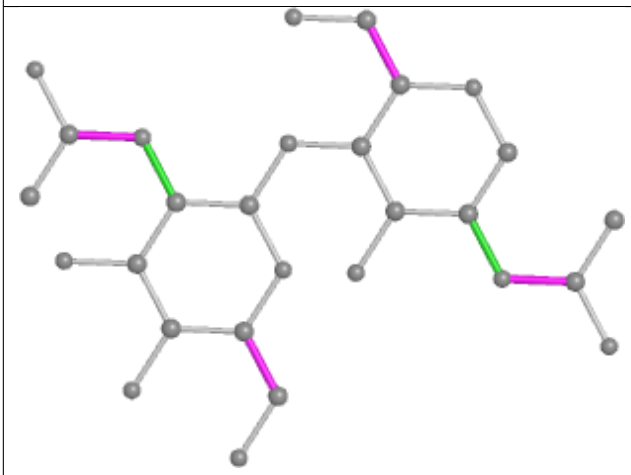
Oligosaccharide Chain F



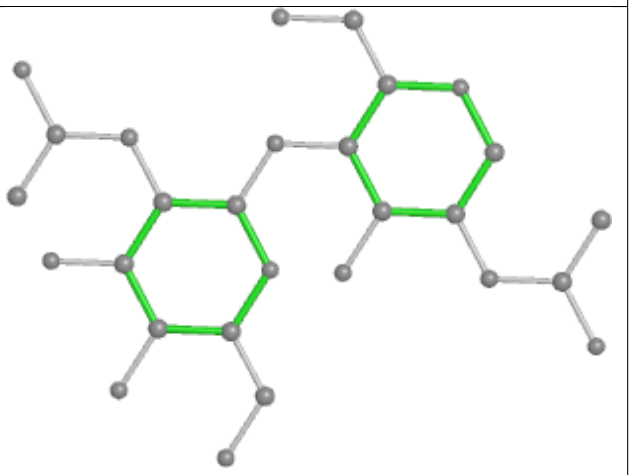
Bond lengths



Bond angles

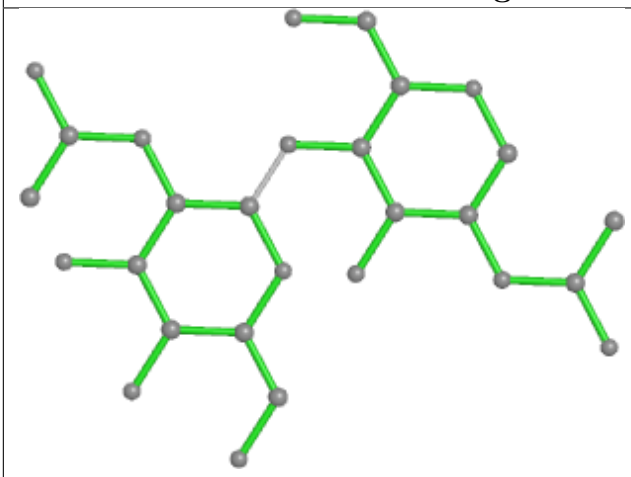


Torsions

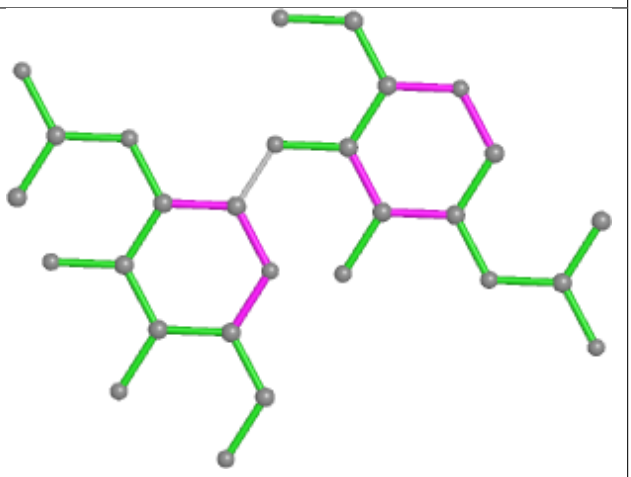


Rings

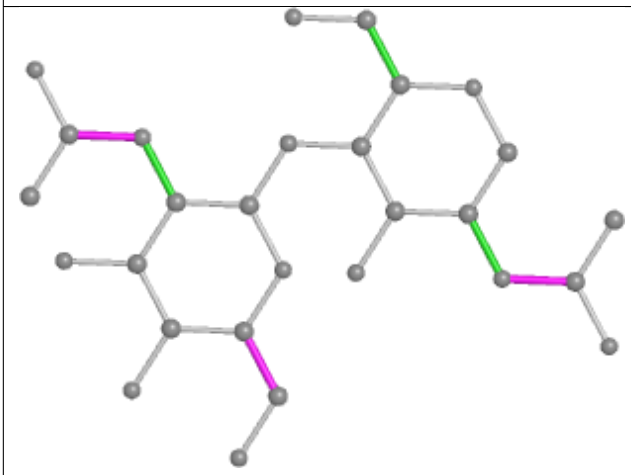
Oligosaccharide Chain G



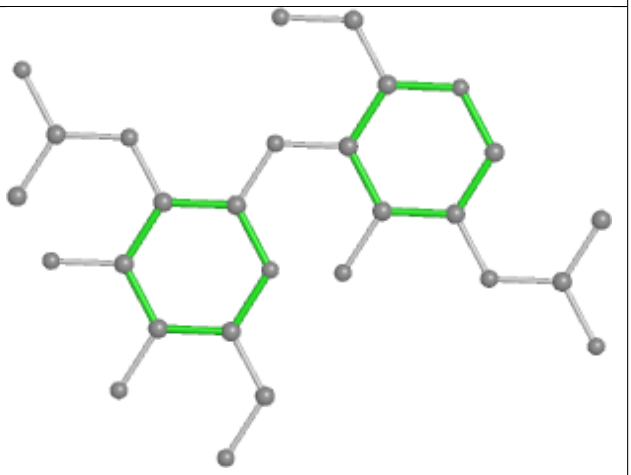
Bond lengths



Bond angles

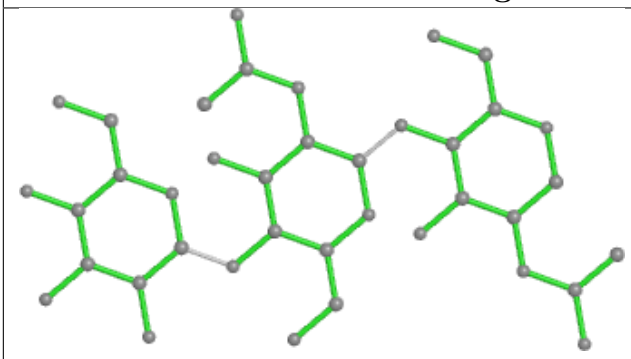


Torsions

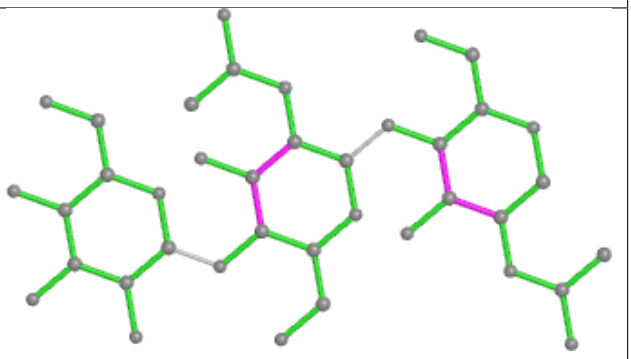


Rings

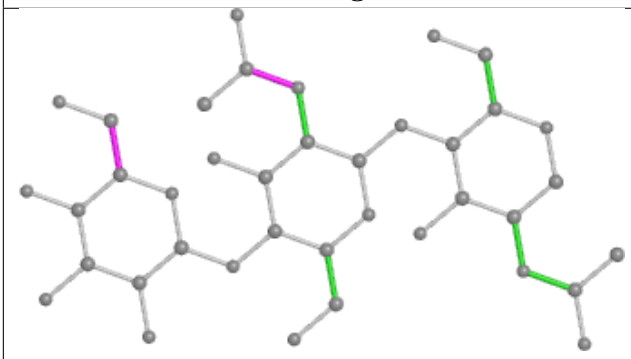
Oligosaccharide Chain D



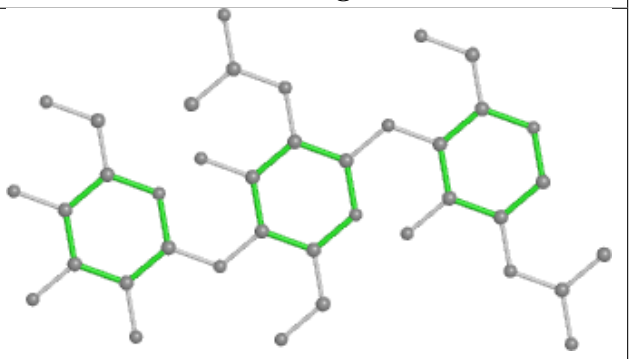
Bond lengths



Bond angles

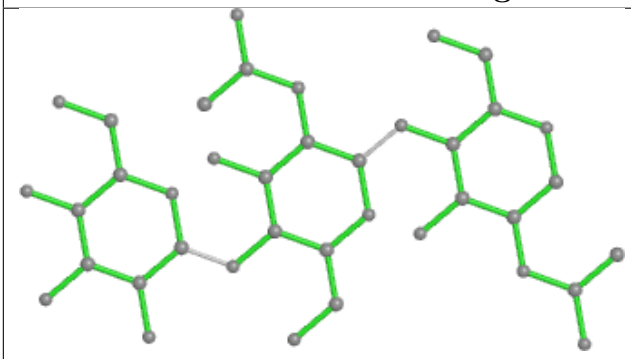


Torsions

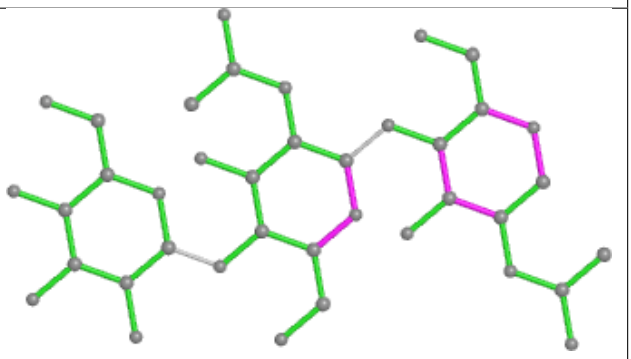


Rings

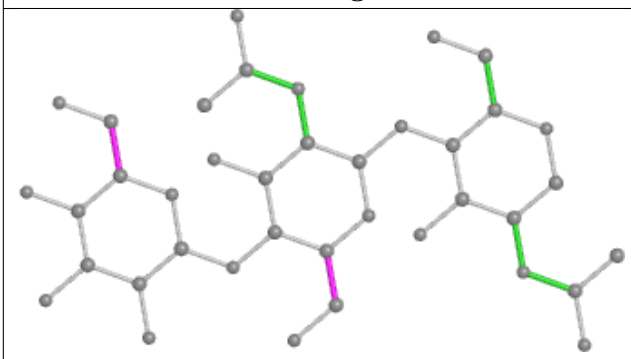
Oligosaccharide Chain H



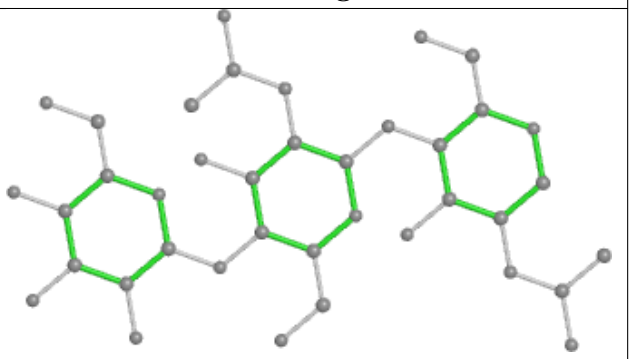
Bond lengths



Bond angles



Torsions



Rings

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 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	B	2004	-	4,4,4	1.00	0	6,6,6	0.50	0
5	PO4	A	2002	-	4,4,4	0.80	0	6,6,6	0.42	0
8	PEG	B	5001	-	6,6,6	0.69	0	5,5,5	5.22	3 (60%)
4	NAG	A	604	1	14,14,15	0.49	0	17,19,21	0.92	0
7	HEM	A	1001	1	41,50,50	1.92	6 (14%)	45,82,82	1.81	8 (17%)
5	PO4	A	2001	-	4,4,4	1.02	0	6,6,6	0.49	0
8	PEG	A	5001	-	6,6,6	0.66	0	5,5,5	3.20	2 (40%)
5	PO4	B	2003	-	4,4,4	0.90	0	6,6,6	0.43	0
7	HEM	B	1021	1	41,50,50	1.90	7 (17%)	45,82,82	1.85	7 (15%)
4	NAG	B	607	1	14,14,15	0.61	0	17,19,21	1.08	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
8	PEG	B	5001	-	-	4/4/4/4	-
4	NAG	A	604	1	-	0/6/23/26	0/1/1/1
7	HEM	A	1001	1	-	4/12/54/54	-
8	PEG	A	5001	-	-	2/4/4/4	-
7	HEM	B	1021	1	-	4/12/54/54	-
4	NAG	B	607	1	-	0/6/23/26	0/1/1/1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	1001	HEM	C3D-C2D	7.73	1.53	1.36
7	B	1021	HEM	C3D-C2D	7.72	1.53	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	1021	HEM	C3C-C2C	-3.83	1.35	1.40
7	A	1001	HEM	C3C-C2C	-3.76	1.35	1.40
7	A	1001	HEM	C3C-CAC	3.74	1.55	1.47
7	B	1021	HEM	C3C-CAC	3.48	1.54	1.47
7	A	1001	HEM	CAB-C3B	2.86	1.55	1.47
7	B	1021	HEM	CAB-C3B	2.74	1.54	1.47
7	B	1021	HEM	FE-NB	2.58	2.09	1.96
7	A	1001	HEM	FE-NB	2.57	2.09	1.96
7	B	1021	HEM	CAA-C2A	2.28	1.55	1.52
7	A	1001	HEM	FE-ND	2.21	2.07	1.96
7	B	1021	HEM	FE-ND	2.17	2.07	1.96

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	B	5001	PEG	C3-O2-C2	8.47	150.00	113.29
8	B	5001	PEG	O2-C2-C1	7.29	142.09	110.07
7	B	1021	HEM	C4D-ND-C1D	6.81	112.11	105.07
7	A	1001	HEM	C4D-ND-C1D	6.63	111.92	105.07
8	A	5001	PEG	O2-C2-C1	5.81	135.59	110.07
8	A	5001	PEG	O2-C3-C4	4.15	128.31	110.07
7	B	1021	HEM	C4B-CHC-C1C	3.74	127.49	122.56
7	A	1001	HEM	C4B-CHC-C1C	3.41	127.06	122.56
4	B	607	NAG	C4-C3-C2	3.20	115.71	111.02
7	A	1001	HEM	C4C-CHD-C1D	3.10	126.65	122.56
7	B	1021	HEM	C1B-NB-C4B	2.96	108.13	105.07
7	A	1001	HEM	CMD-C2D-C1D	2.94	129.52	125.04
7	A	1001	HEM	C1B-NB-C4B	2.86	108.02	105.07
7	B	1021	HEM	CMD-C2D-C1D	2.75	129.23	125.04
7	B	1021	HEM	C4C-CHD-C1D	2.73	126.17	122.56
8	B	5001	PEG	O2-C3-C4	2.57	121.35	110.07
7	A	1001	HEM	CBA-CAA-C2A	-2.53	108.31	112.62
7	A	1001	HEM	C3B-C2B-C1B	2.22	108.13	106.49
7	A	1001	HEM	CAD-C3D-C4D	2.10	128.33	124.66
7	B	1021	HEM	C3B-C2B-C1B	2.10	108.04	106.49
7	B	1021	HEM	CAD-C3D-C4D	2.07	128.28	124.66

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	B	5001	PEG	C4-C3-O2-C2

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Mol	Chain	Res	Type	Atoms
8	B	5001	PEG	C1-C2-O2-C3
8	A	5001	PEG	O2-C3-C4-O4
8	A	5001	PEG	O1-C1-C2-O2
8	B	5001	PEG	O1-C1-C2-O2
8	B	5001	PEG	O2-C3-C4-O4
7	A	1001	HEM	CAD-CBD-CGD-O2D
7	A	1001	HEM	CAD-CBD-CGD-O1D
7	B	1021	HEM	CAD-CBD-CGD-O2D
7	B	1021	HEM	CAA-CBA-CGA-O2A
7	B	1021	HEM	CAD-CBD-CGD-O1D
7	B	1021	HEM	CAA-CBA-CGA-O1A
7	A	1001	HEM	CAA-CBA-CGA-O2A
7	A	1001	HEM	CAA-CBA-CGA-O1A

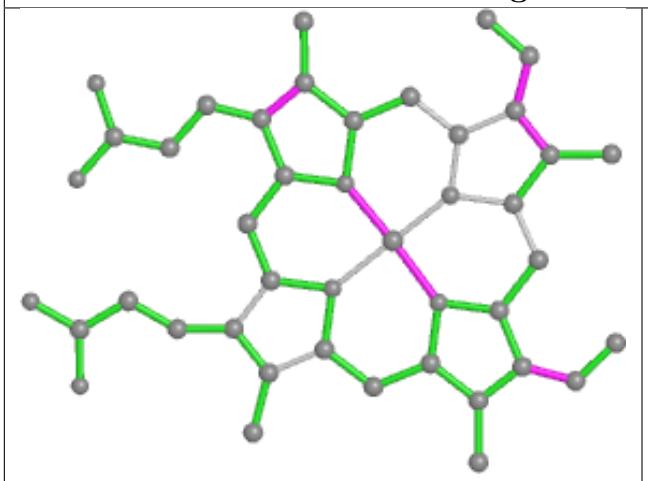
There are no ring outliers.

6 monomers are involved in 48 short contacts:

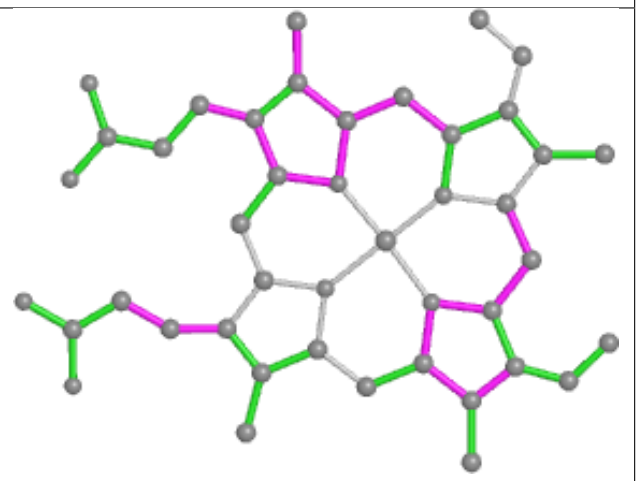
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	2004	PO4	3	0
8	B	5001	PEG	9	0
7	A	1001	HEM	15	0
5	A	2001	PO4	3	0
8	A	5001	PEG	4	0
7	B	1021	HEM	21	0

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.

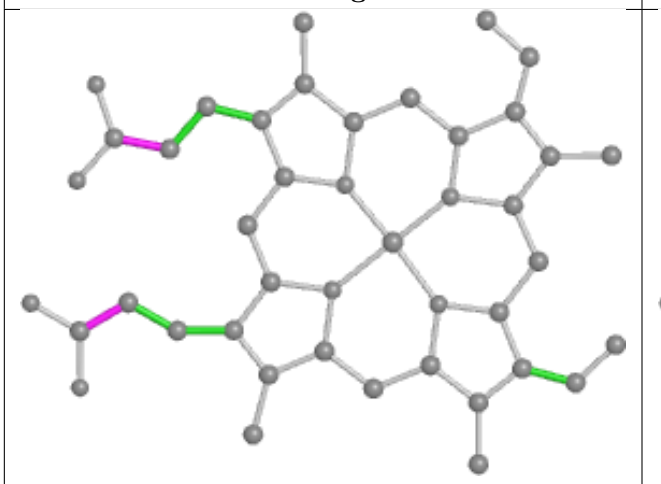
Ligand HEM A 1001



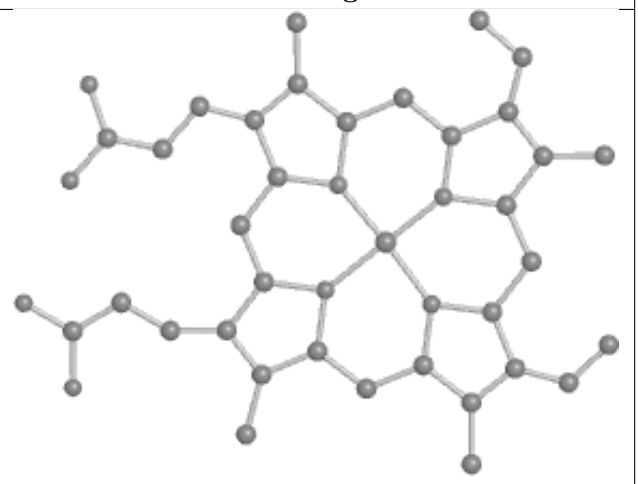
Bond lengths



Bond angles

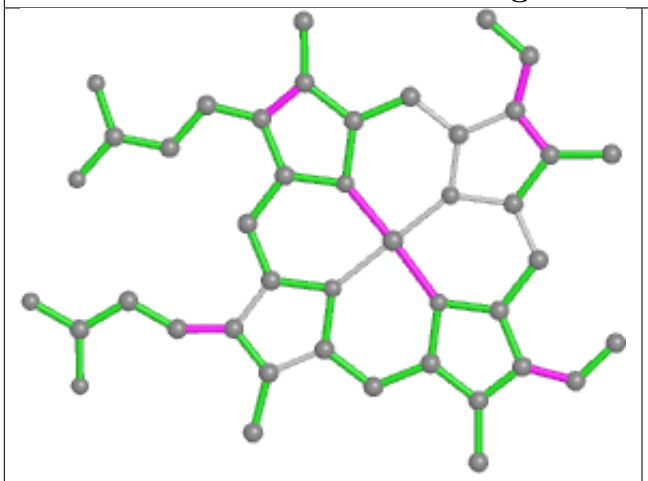


Torsions

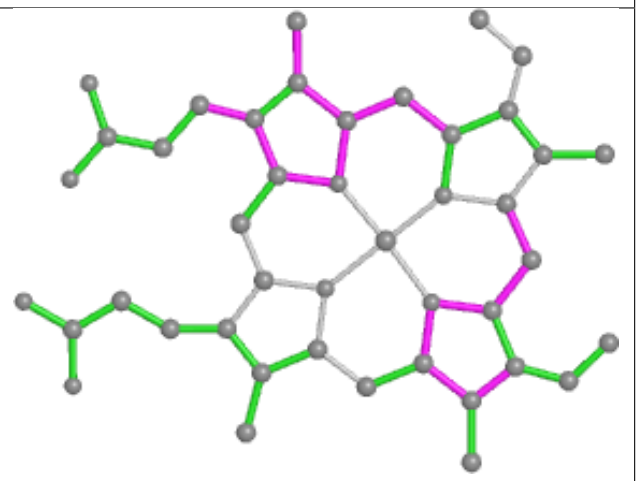


Rings

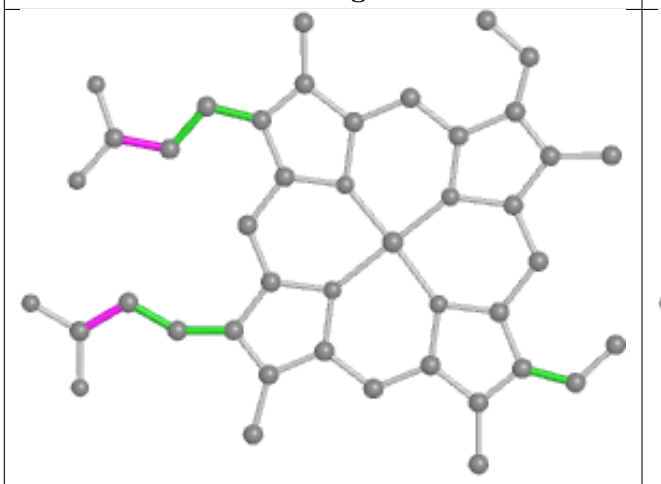
Ligand HEM B 1021



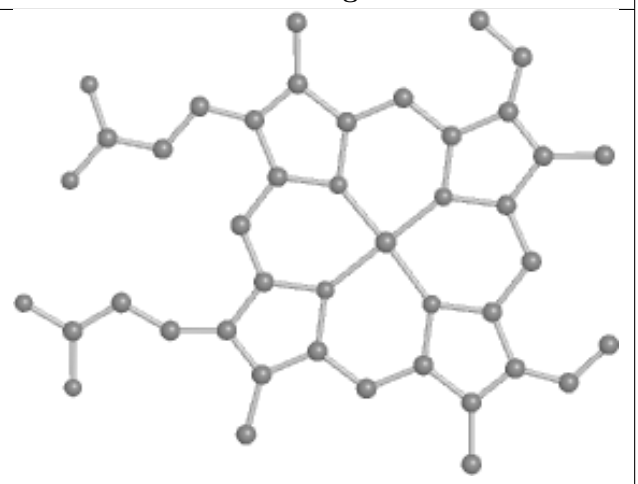
Bond lengths



Bond angles



Torsions



Rings

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%)	0.12	43 (7%)	15	13	4, 17, 43, 67	0
1	B	594/595 (99%)	0.19	45 (7%)	13	12	6, 17, 44, 70	0
All	All	1188/1190 (99%)	0.15	88 (7%)	14	12	4, 17, 43, 70	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	122	SER	11.2
1	B	6	CYS	9.6
1	A	5	GLY	9.1
1	A	2	TRP	8.5
1	A	4	VAL	8.2
1	B	5	GLY	7.9
1	B	121	SER	7.6
1	A	6	CYS	7.4
1	A	122	SER	7.3
1	B	120	GLY	7.1
1	A	595	ASN	6.9
1	A	171	PRO	6.8
1	B	12	LEU	6.7
1	A	121	SER	6.7
1	B	2	TRP	6.7
1	B	1	SER	6.3
1	A	7	GLY	6.1
1	B	7	GLY	5.8
1	B	11	PRO	5.8
1	B	171	PRO	5.6
1	B	4	VAL	5.6
1	A	167	CYS	5.4
1	B	170	PRO	5.4
1	B	174	SER	5.2

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Mol	Chain	Res	Type	RSRZ
1	B	593	ARG	5.2
1	B	172	TYR	5.1
1	A	170	PRO	5.0
1	B	594	GLU	4.9
1	B	173	GLN	4.6
1	B	595	ASN	4.5
1	A	124	HIS	4.5
1	A	120	GLY	4.5
1	B	167	CYS	4.3
1	B	8	ALA	4.3
1	A	174	SER	4.3
1	A	574	HIS	4.3
1	A	8	ALA	4.2
1	A	1	SER	4.2
1	A	594	GLU	4.1
1	A	593	ARG	3.8
1	A	12	LEU	3.8
1	A	123	GLU	3.7
1	B	169	THR	3.7
1	A	173	GLN	3.6
1	A	3	GLU	3.6
1	B	124	HIS	3.5
1	B	14	THR	3.5
1	A	172	TYR	3.4
1	A	11	PRO	3.3
1	A	286	HIS	3.2
1	B	119	LEU	3.2
1	B	147	ASN	3.1
1	A	15	CYS	3.1
1	B	3	GLU	3.1
1	A	232	VAL	3.0
1	A	63	GLN	3.0
1	A	14	THR	3.0
1	A	117	THR	2.9
1	B	286	HIS	2.9
1	B	17	GLU	2.9
1	A	127	VAL	2.8
1	A	168	PRO	2.7
1	A	129	CYS	2.7
1	B	574	HIS	2.6
1	A	18	GLN	2.5
1	B	242	THR	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	10	VAL	2.5
1	A	16	ASP	2.5
1	B	123	GLU	2.5
1	B	175	LEU	2.5
1	A	119	LEU	2.5
1	B	322	GLN	2.5
1	B	16	ASP	2.4
1	A	466	GLY	2.3
1	B	146	LYS	2.3
1	B	235	SER	2.3
1	B	117	THR	2.2
1	B	9	PRO	2.2
1	A	9	PRO	2.2
1	B	10	VAL	2.2
1	B	63	GLN	2.1
1	B	18	GLN	2.1
1	A	131	GLU	2.1
1	B	425	THR	2.1
1	A	469	ALA	2.0
1	A	322	GLN	2.0
1	B	284	ASN	2.0
1	B	588	SER	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	B	198	10/11	0.68	0.48	24,26,32,32	0
1	SEP	A	198	10/11	0.77	0.36	22,23,29,29	0

6.3 Carbohydrates (i)

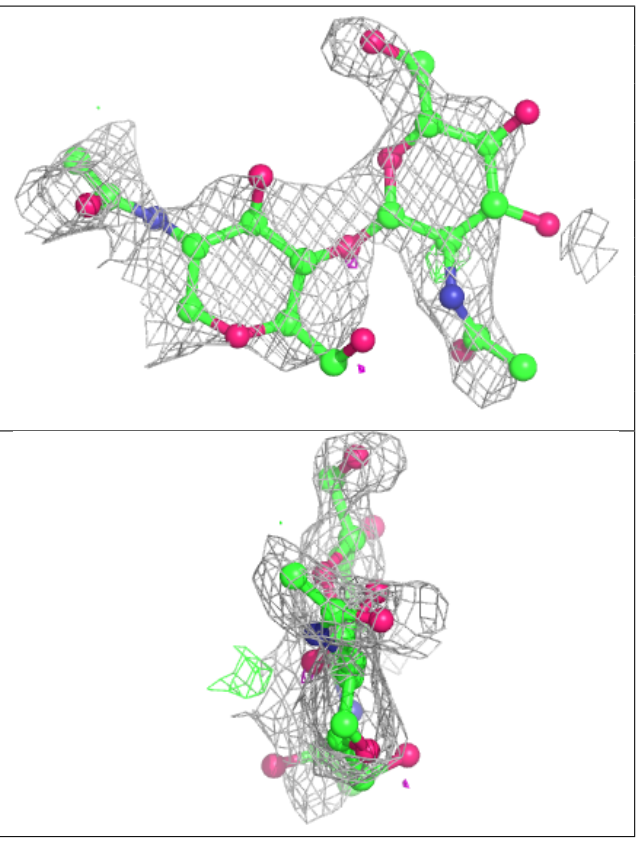
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	F	2	14/15	0.45	0.57	51,53,54,55	0
3	BMA	D	3	11/12	0.69	0.74	55,57,57,57	0
3	BMA	H	3	11/12	0.70	0.64	46,47,47,48	0
2	NAG	G	2	14/15	0.72	0.56	43,45,45,45	0
2	NAG	E	2	14/15	0.73	0.42	39,41,42,42	0
2	NAG	C	2	14/15	0.75	0.57	49,52,52,53	0
2	NAG	C	1	14/15	0.81	0.49	35,40,42,46	0
3	NAG	H	2	14/15	0.83	0.31	39,40,42,44	0
3	NAG	D	2	14/15	0.84	0.49	46,49,50,53	0
2	NAG	F	1	14/15	0.87	0.35	37,42,44,48	0
2	NAG	E	1	14/15	0.89	0.18	29,31,33,36	0
3	NAG	D	1	14/15	0.90	0.18	31,34,37,42	0
3	NAG	H	1	14/15	0.90	0.19	29,31,33,36	0
2	NAG	G	1	14/15	0.92	0.20	33,35,37,40	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.

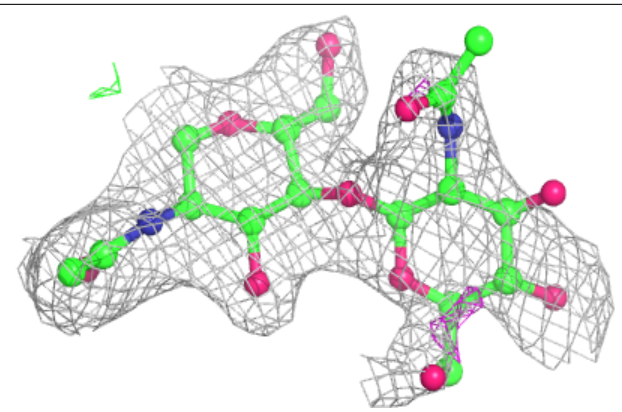
Electron density around Chain C:

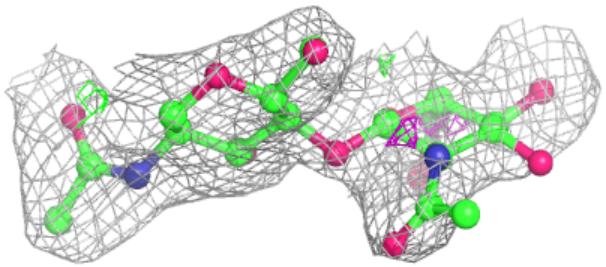
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)

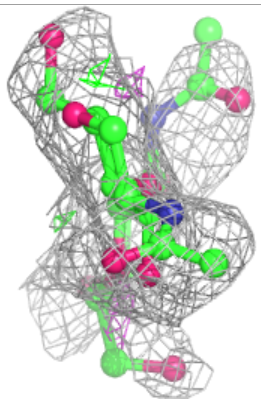


Electron density around Chain E:

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

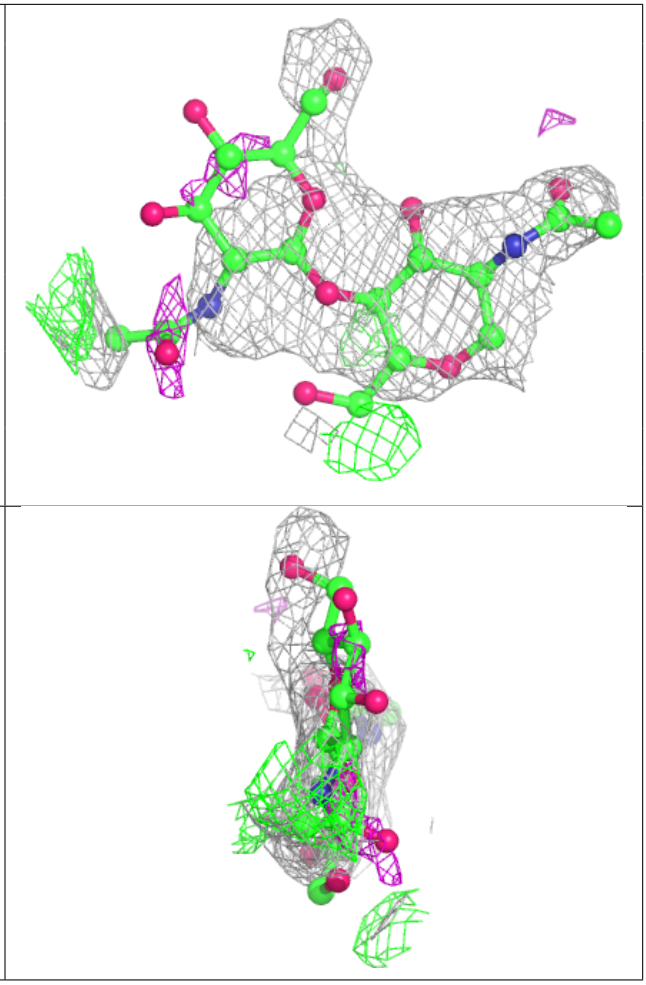






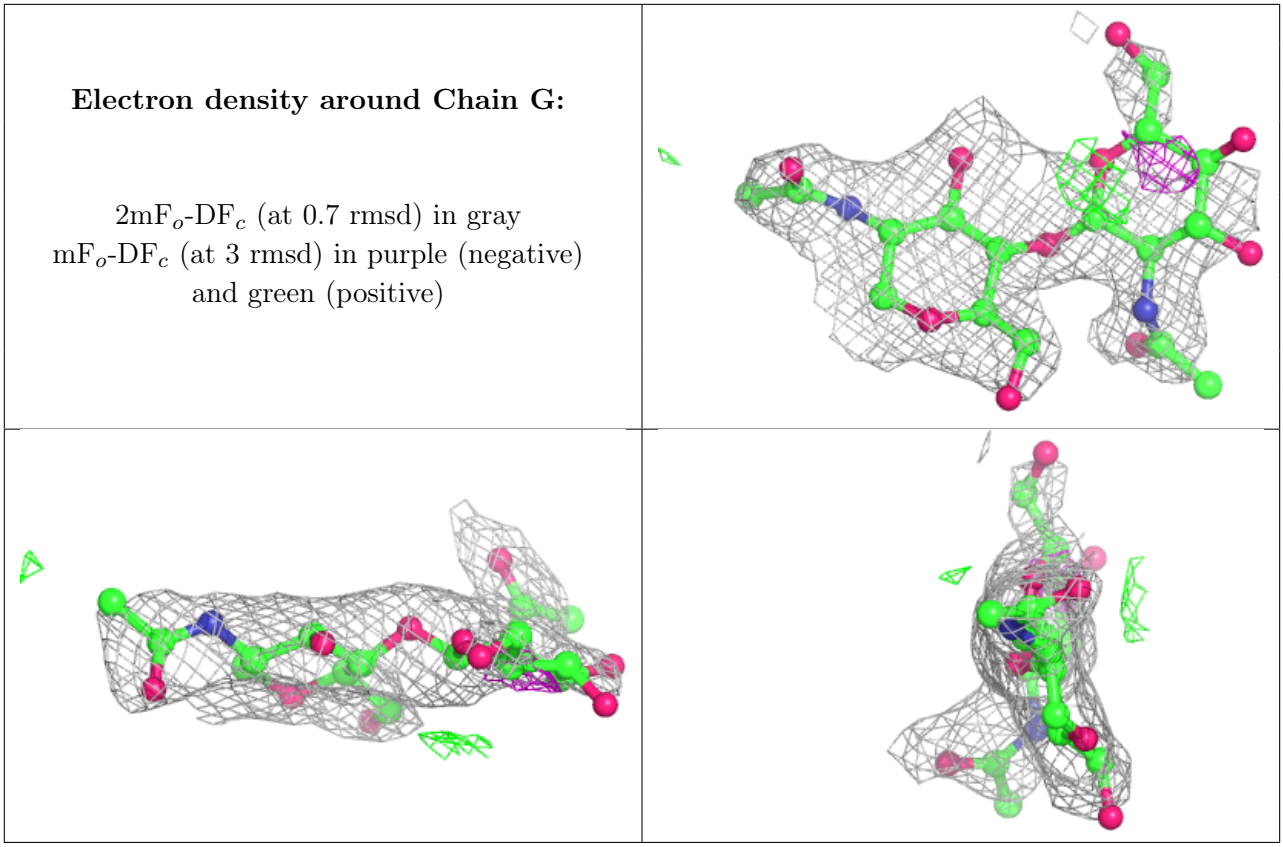
Electron density around Chain F:

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



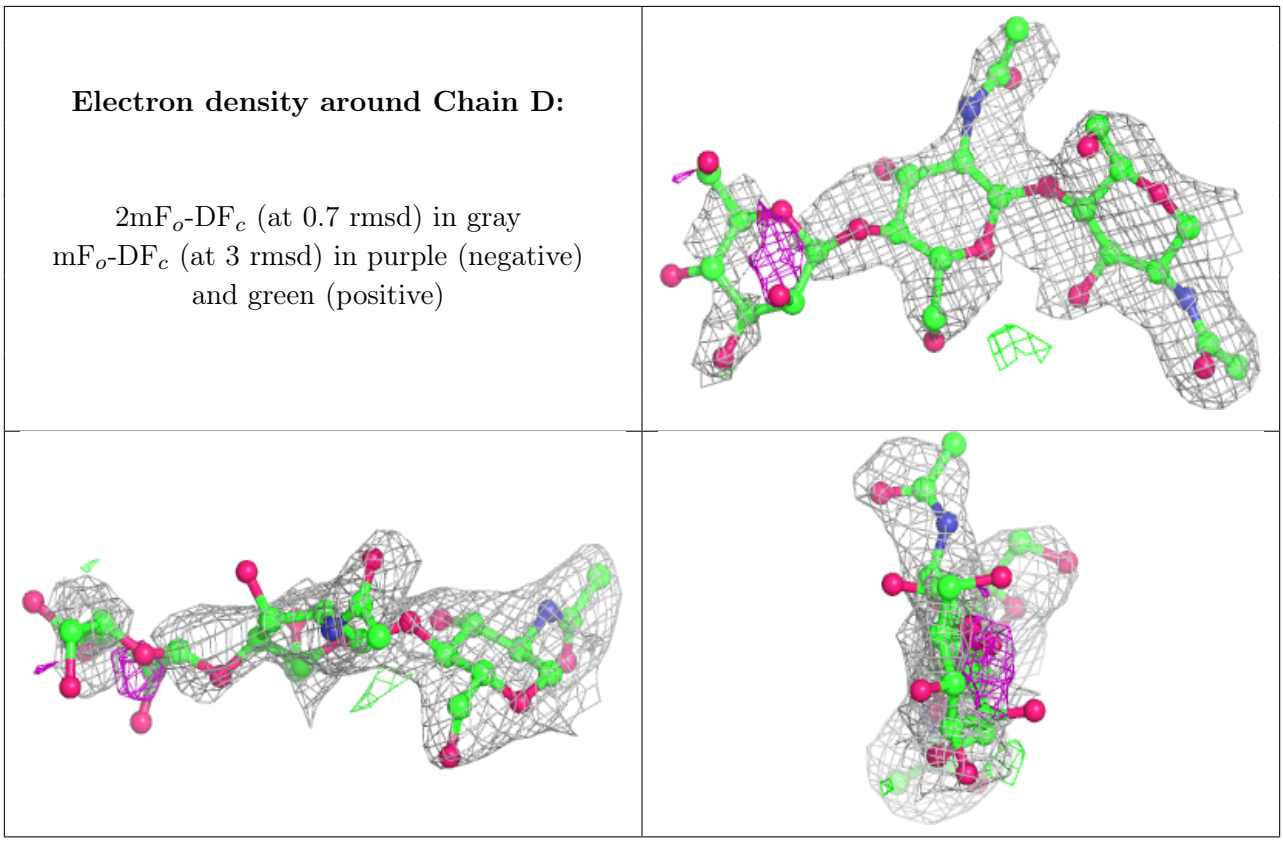
Electron density around Chain G:

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



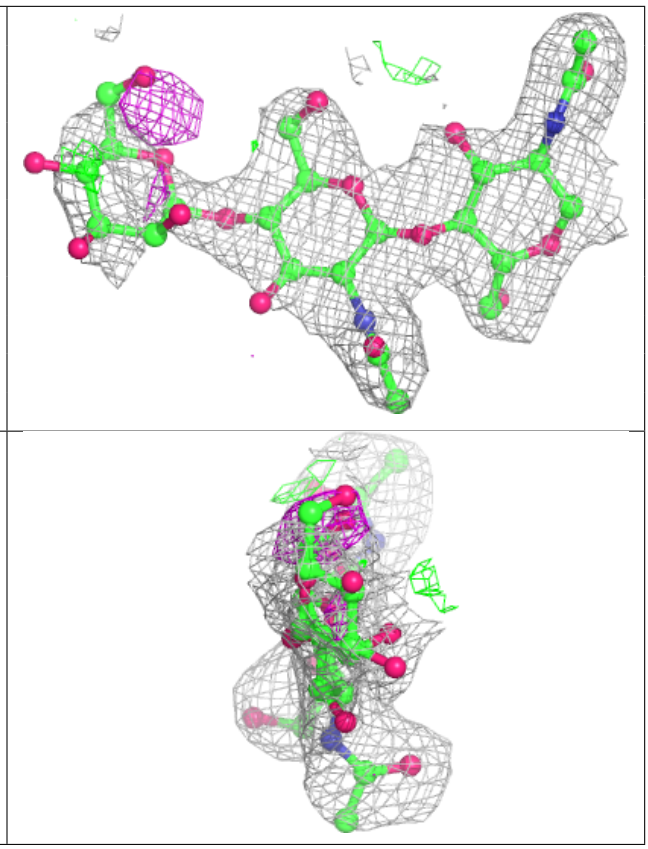
Electron density around Chain D:

$2mF_o$-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 H:

$2mF_o$-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.

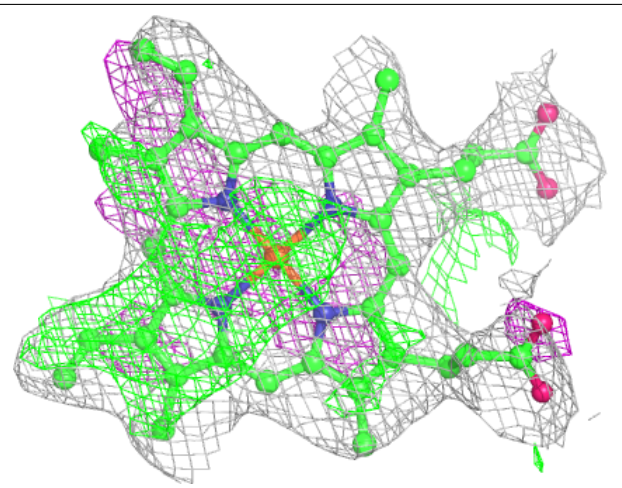
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	NAG	B	607	14/15	0.74	0.45	34,37,37,37	0
8	PEG	B	5001	7/7	0.78	0.48	30,31,31,31	0
7	HEM	A	1001	43/43	0.79	0.30	15,16,17,18	0
7	HEM	B	1021	43/43	0.80	0.29	12,14,15,16	0
8	PEG	A	5001	7/7	0.81	0.37	30,30,31,31	0
4	NAG	A	604	14/15	0.84	0.38	27,29,32,32	0
6	CA	B	1000	1/1	0.86	0.08	22,22,22,22	0
5	PO4	B	2003	5/5	0.91	0.30	52,52,52,52	0
5	PO4	B	2004	5/5	0.92	0.33	56,56,56,56	0
5	PO4	A	2001	5/5	0.92	0.37	63,63,63,63	0
5	PO4	A	2002	5/5	0.95	0.21	53,53,53,53	0
6	CA	A	1000	1/1	0.98	0.08	13,13,13,13	0

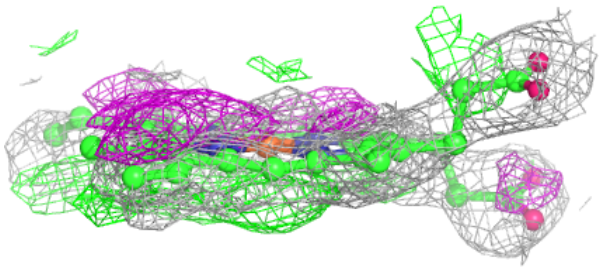
The following is a graphical depiction of the model fit to experimental electron density of all

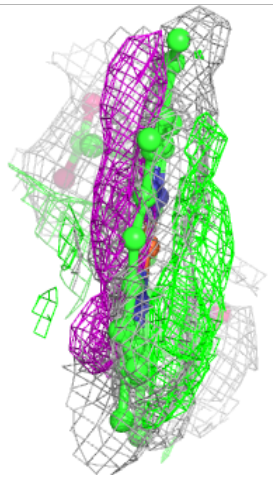
instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around HEM A 1001:

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

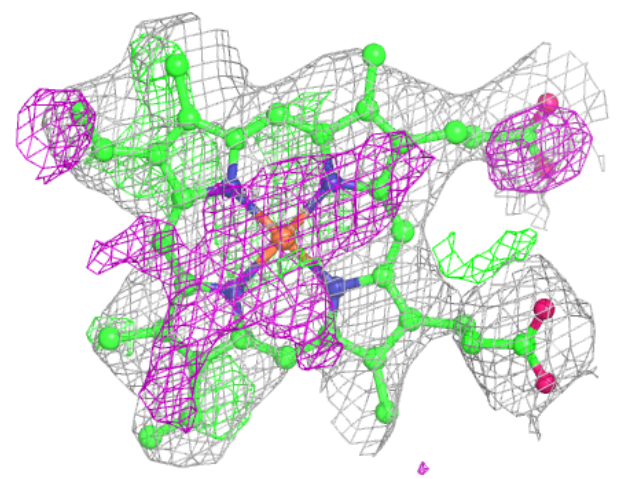


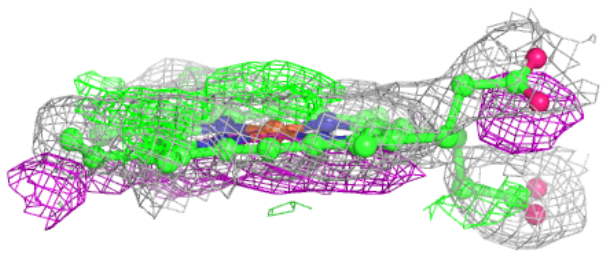


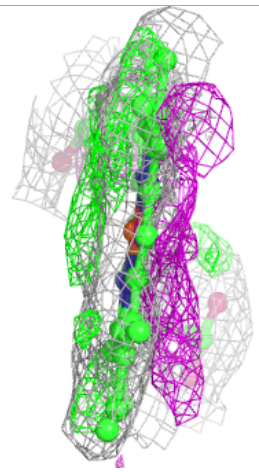


Electron density around HEM B 1021:

$2mF_o$-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.