Full wwPDB X-ray Structure Validation Report (i)

Oct 30, 2023 – 07:31 PM JST

PDB ID	:	4Y55
Title	:	Crystal structure of Buffalo lactoperoxidase with Rhodanide at 2.09 Angstrom resolution
Authors	:	Gupta, A.; Tyagi, T.K.; Kaur, P.; Sharma, S.; Singh, T.P.
Deposited on	:	2015-02-11
Resolution	:	2.10 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:

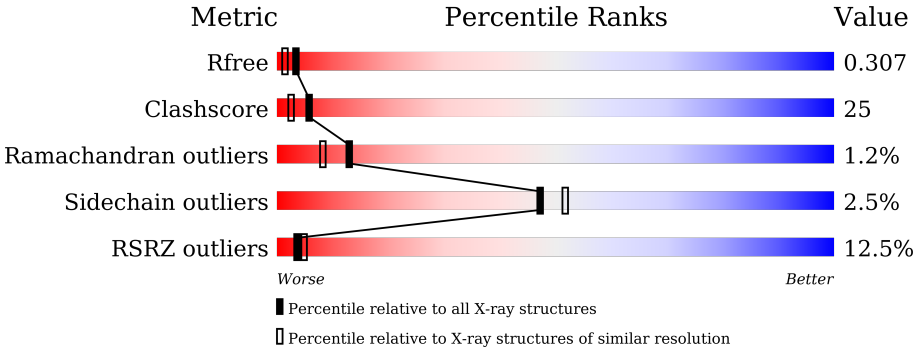
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	12%, 63%, 33%, • •
2	B	3	100%
3	C	2	50%, 50%
3	E	2	100%
4	D	3	100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	B	2	-	-	-	X
2	BMA	B	3	-	-	-	X
4	MAN	D	3	-	-	-	X
7	NO3	A	617	-	-	X	-
7	NO3	A	618	-	-	X	-

2 Entry composition (i)

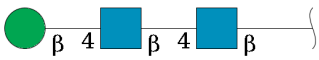
There are 10 unique types of molecules in this entry. The entry contains 5156 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	4770	3032	845	865	1	27	0	0	0

- Molecule 2 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.

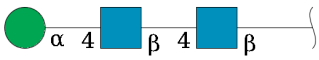


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	3	39	22	2	15	0	0	0

- 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
3	E	2	28	16	2	10	0	0	0

- Molecule 4 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			
4	D	3	39	22	2	15	0	0	0

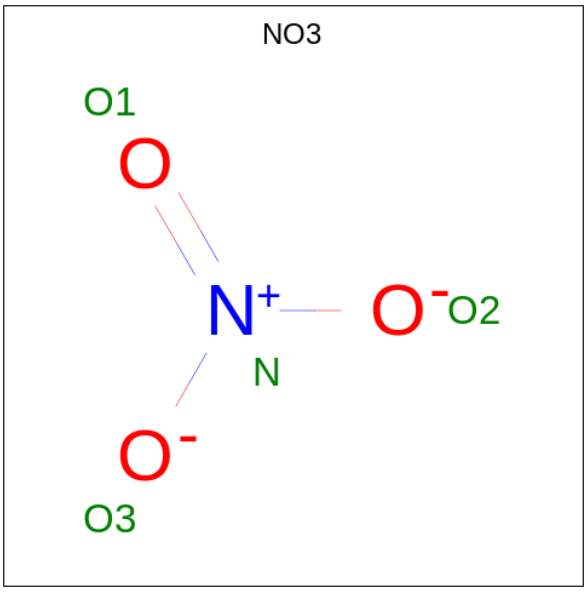
- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 6 is IODIDE ION (three-letter code: IOD) (formula: I).

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

- Molecule 7 is NITRATE ION (three-letter code: NO3) (formula: NO_3).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	N	O		
7	A	1	4	1	3	0	0
			Total	N	O		
7	A	1	4	1	3	0	0

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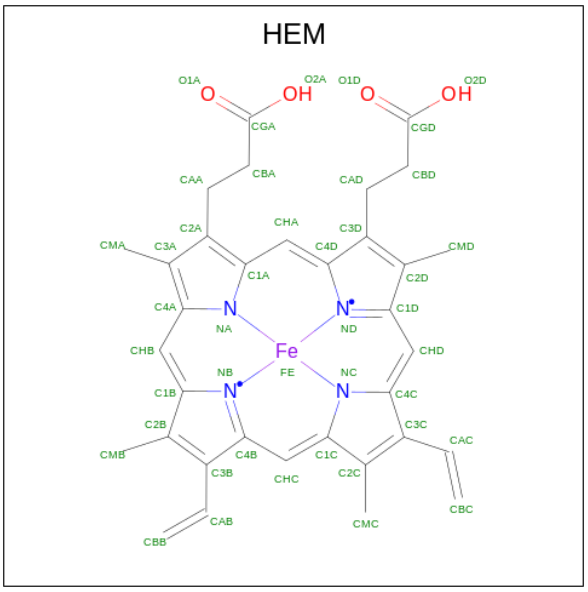
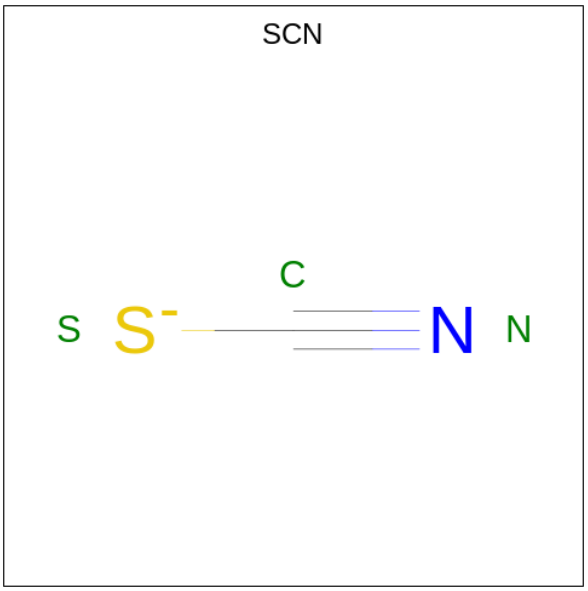
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	N	O		
7	A	1	4	1	3	0	0
			Total	N	O		
7	A	1	4	1	3	0	0

- Molecule 8 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		
8	A	1	43	34	1	4	4	0	0

- Molecule 9 is THIOCYANATE ION (three-letter code: SCN) (formula: CNS).



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

- Molecule 10 is water.

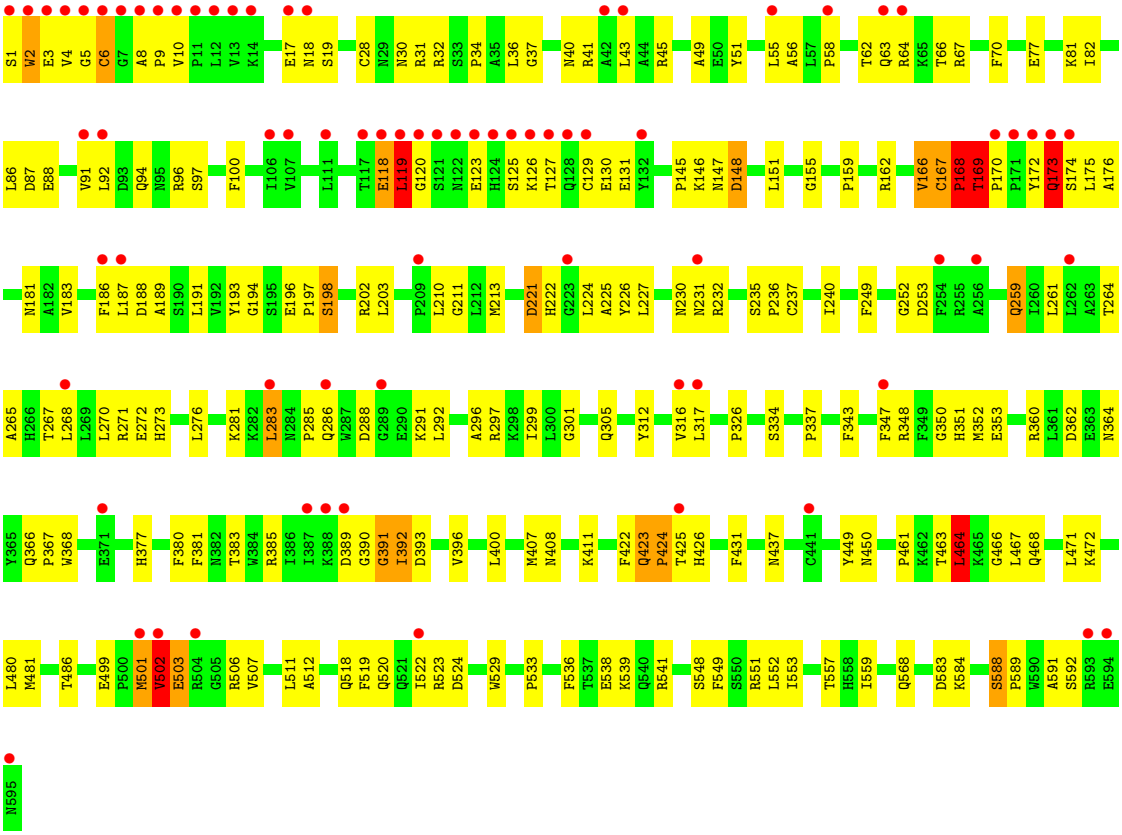
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
10	A	174	174	174	0	0

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: 12% 63% 33%



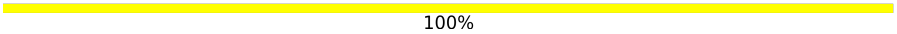
• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B: 100%

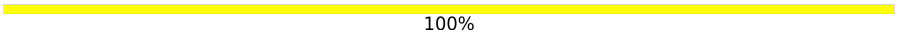
• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:

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

Chain E: 

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

Chain D: 

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	54.01Å 80.05Å 76.80Å 90.00° 102.64° 90.00°	Depositor
Resolution (Å)	35.33 – 2.10 35.30 – 2.10	Depositor EDS
% Data completeness (in resolution range)	97.4 (35.33-2.10) 97.4 (35.30-2.10)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.87 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.236 , 0.298 0.252 , 0.307	Depositor DCC
R_{free} test set	1821 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	34.0	Xtriage
Anisotropy	0.391	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 39.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	5156	wwPDB-VP
Average B, all atoms (Å^2)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.05% 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: SCN, SEP, MAN, HEM, NO3, NAG, IOD, CA, BMA

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	0.72	2/4886 (0.0%)	0.95	24/6627 (0.4%)

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 (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	424	PRO	N-CD	5.83	1.56	1.47
1	A	353	GLU	CD-OE1	5.23	1.31	1.25

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	118	GLU	CB-CA-C	-14.60	81.21	110.40
1	A	169	THR	N-CA-CB	-11.69	88.08	110.30
1	A	423	GLN	CB-CA-C	10.92	132.24	110.40
1	A	119	LEU	CB-CA-C	10.43	130.01	110.20
1	A	502	VAL	CB-CA-C	10.00	130.39	111.40
1	A	168	PRO	N-CA-CB	-9.25	92.20	103.30
1	A	119	LEU	N-CA-CB	-8.55	93.29	110.40
1	A	56	ALA	N-CA-CB	-7.99	98.91	110.10
1	A	67	ARG	NE-CZ-NH1	7.21	123.90	120.30
1	A	56	ALA	O-C-N	-6.97	111.55	122.70
1	A	118	GLU	N-CA-C	6.84	129.47	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	503	GLU	N-CA-CB	-6.74	98.47	110.60
1	A	502	VAL	N-CA-C	-6.24	94.16	111.00
1	A	501	MET	C-N-CA	6.00	136.71	121.70
1	A	464	LEU	CB-CA-C	-5.93	98.92	110.20
1	A	67	ARG	NE-CZ-NH2	-5.92	117.34	120.30
1	A	168	PRO	N-CA-C	5.82	127.22	112.10
1	A	96	ARG	NE-CZ-NH1	5.72	123.16	120.30
1	A	486	THR	N-CA-CB	5.59	120.93	110.30
1	A	148	ASP	C-N-CD	5.54	140.03	128.40
1	A	56	ALA	CA-C-N	5.48	129.26	117.20
1	A	96	ARG	NE-CZ-NH2	-5.35	117.63	120.30
1	A	348	ARG	NE-CZ-NH1	5.21	122.91	120.30
1	A	221	ASP	CB-CG-OD1	5.02	122.82	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	169	THR	Peptide
1	A	391	GLY	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4770	0	4676	244	2
2	B	39	0	34	0	0
3	C	28	0	25	1	0
3	E	28	0	25	0	0
4	D	39	0	34	0	0
5	A	1	0	0	0	0
6	A	6	0	0	1	0
7	A	16	0	0	4	0
8	A	43	0	30	4	0
9	A	12	0	0	0	0
10	A	174	0	0	15	0
All	All	5156	0	4824	248	2

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 25.

All (248) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:519:PHE:HA	1:A:522:ILE:CD1	1.62	1.27
1:A:391:GLY:HA3	10:A:846:HOH:O	1.43	1.14
1:A:519:PHE:CD1	1:A:522:ILE:CD1	2.31	1.13
1:A:2:TRP:HZ3	1:A:4:VAL:N	1.52	1.07
1:A:519:PHE:HA	1:A:522:ILE:CG1	1.83	1.07
1:A:167:CYS:HB3	1:A:168:PRO:HD3	1.37	1.06
1:A:519:PHE:O	1:A:522:ILE:HG13	1.57	1.03
1:A:407:MET:HB3	1:A:501:MET:CE	1.88	1.02
1:A:519:PHE:CD1	1:A:522:ILE:HD11	1.96	1.00
1:A:221:ASP:OD2	10:A:790:HOH:O	1.80	0.99
1:A:167:CYS:CB	1:A:168:PRO:CD	2.40	0.98
1:A:519:PHE:HA	1:A:522:ILE:HG12	1.46	0.97
1:A:2:TRP:CZ3	1:A:4:VAL:N	2.27	0.97
1:A:519:PHE:CA	1:A:522:ILE:HD11	1.94	0.97
1:A:43:LEU:CD2	1:A:181:ASN:HB2	1.94	0.96
1:A:519:PHE:HD1	1:A:522:ILE:CD1	1.74	0.96
1:A:519:PHE:O	1:A:522:ILE:CG1	2.13	0.96
1:A:91:VAL:HG11	1:A:411:LYS:HD3	1.48	0.95
1:A:519:PHE:CA	1:A:522:ILE:CD1	2.44	0.94
1:A:519:PHE:HA	1:A:522:ILE:HD11	1.47	0.94
1:A:213:MET:HG2	1:A:273:HIS:CD2	2.03	0.93
1:A:519:PHE:CB	1:A:522:ILE:HD11	1.99	0.92
1:A:167:CYS:HB3	1:A:168:PRO:CD	1.99	0.91
1:A:2:TRP:CZ3	1:A:4:VAL:HG23	2.05	0.91
1:A:64:ARG:HG3	1:A:64:ARG:HH11	1.36	0.89
1:A:501:MET:SD	1:A:506:ARG:HA	2.12	0.88
1:A:519:PHE:CA	1:A:522:ILE:HG12	2.04	0.86
1:A:91:VAL:CG1	1:A:411:LYS:HD3	2.08	0.84
1:A:118:GLU:O	1:A:118:GLU:CG	2.22	0.81
1:A:43:LEU:HD23	1:A:181:ASN:HB2	1.60	0.81
1:A:167:CYS:HB2	1:A:168:PRO:HD2	1.63	0.81
1:A:424:PRO:O	6:A:613:IOD:I	2.69	0.81
1:A:172:TYR:OH	1:A:174:SER:HB2	1.81	0.80
1:A:519:PHE:C	1:A:522:ILE:HG12	2.03	0.79
1:A:100:PHE:CE1	1:A:316:VAL:HG22	2.17	0.79
1:A:288:ASP:O	1:A:292:LEU:HG	1.83	0.79
1:A:463:THR:O	1:A:466:GLY:N	2.15	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:ARG:HG3	1:A:64:ARG:NH1	1.97	0.78
1:A:519:PHE:CA	1:A:522:ILE:CG1	2.58	0.77
1:A:519:PHE:CG	1:A:522:ILE:HD11	2.19	0.77
1:A:196:GLU:HB2	1:A:198:SEP:O1P	1.83	0.77
1:A:43:LEU:HD21	1:A:181:ASN:HB2	1.67	0.77
1:A:519:PHE:CD1	1:A:522:ILE:HD13	2.20	0.76
1:A:197:PRO:HD2	1:A:198:SEP:O1P	1.86	0.75
1:A:186:PHE:CE2	1:A:337:PRO:HB2	2.21	0.75
1:A:130:GLU:OE2	1:A:426:HIS:ND1	2.17	0.74
1:A:202:ARG:HH22	1:A:231:ASN:HB2	1.52	0.74
1:A:51:TYR:CD1	1:A:55:LEU:O	2.40	0.73
1:A:172:TYR:CZ	1:A:174:SER:HB2	2.23	0.73
1:A:2:TRP:HE3	1:A:3:GLU:N	1.87	0.73
1:A:407:MET:HB3	1:A:501:MET:HE2	1.70	0.73
1:A:120:GLY:HA3	1:A:123:GLU:HB3	1.70	0.72
1:A:10:VAL:HG11	1:A:41:ARG:NH1	2.05	0.72
1:A:407:MET:HB3	1:A:501:MET:HE1	1.70	0.71
1:A:519:PHE:C	1:A:522:ILE:CG1	2.58	0.71
1:A:501:MET:SD	1:A:506:ARG:CA	2.79	0.70
1:A:167:CYS:CB	1:A:168:PRO:HD2	2.20	0.70
1:A:2:TRP:CE3	1:A:3:GLU:CA	2.74	0.70
1:A:167:CYS:HB2	1:A:168:PRO:CD	2.18	0.70
1:A:268:LEU:O	1:A:552:LEU:HD21	1.92	0.70
1:A:63:GLN:OE1	1:A:63:GLN:N	2.20	0.69
1:A:6:CYS:HG	1:A:167:CYS:HG	0.73	0.69
1:A:385:ARG:HD3	1:A:389:ASP:OD2	1.93	0.69
1:A:2:TRP:CE3	1:A:3:GLU:N	2.62	0.68
1:A:2:TRP:CE3	1:A:4:VAL:HG23	2.28	0.68
1:A:259:GLN:HE22	1:A:261:LEU:HB2	1.56	0.68
1:A:2:TRP:HZ3	1:A:4:VAL:H	0.78	0.68
1:A:502:VAL:CG1	1:A:503:GLU:H	2.06	0.68
1:A:186:PHE:CE2	1:A:337:PRO:CB	2.77	0.68
1:A:519:PHE:HA	1:A:522:ILE:HD13	1.70	0.67
1:A:77:GLU:OE2	1:A:81:LYS:NZ	2.23	0.67
1:A:186:PHE:O	1:A:188:ASP:N	2.27	0.66
1:A:118:GLU:O	1:A:118:GLU:HG2	1.95	0.66
1:A:63:GLN:CD	1:A:63:GLN:H	1.97	0.66
1:A:100:PHE:HE1	1:A:316:VAL:CG2	2.08	0.65
1:A:286:GLN:OE1	1:A:286:GLN:N	2.27	0.65
1:A:2:TRP:HE3	1:A:3:GLU:CA	2.10	0.64
1:A:312:TYR:CZ	1:A:316:VAL:HG21	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:213:MET:HG2	1:A:273:HIS:HD2	1.62	0.64
1:A:551:ARG:HD3	1:A:583:ASP:O	1.97	0.64
1:A:186:PHE:HE2	1:A:337:PRO:CB	2.11	0.64
1:A:9:PRO:HG2	10:A:765:HOH:O	1.97	0.63
1:A:227:LEU:HG	1:A:270:LEU:HD22	1.79	0.63
1:A:100:PHE:CE1	1:A:316:VAL:CG2	2.81	0.63
1:A:91:VAL:CG1	1:A:411:LYS:CD	2.76	0.63
1:A:464:LEU:O	1:A:468:GLN:HG3	1.98	0.63
1:A:227:LEU:HD23	10:A:740:HOH:O	1.97	0.63
1:A:146:LYS:O	1:A:147:ASN:HB2	1.98	0.62
1:A:523:ARG:HG3	1:A:529:TRP:CZ2	2.33	0.62
1:A:17:GLU:O	1:A:18:ASN:HB3	1.99	0.62
1:A:58:PRO:HD3	1:A:162:ARG:CZ	2.29	0.62
1:A:502:VAL:HB	1:A:507:VAL:O	1.99	0.61
1:A:88:GLU:O	1:A:91:VAL:HG22	2.00	0.61
1:A:8:ALA:HB3	1:A:9:PRO:HD3	1.82	0.61
1:A:100:PHE:CZ	1:A:316:VAL:HG22	2.34	0.61
1:A:172:TYR:HE2	1:A:175:LEU:H	1.49	0.61
1:A:450:ASN:OD1	1:A:461:PRO:HD2	2.01	0.61
1:A:237:CYS:HA	1:A:381:PHE:O	2.02	0.60
1:A:91:VAL:HG23	1:A:91:VAL:O	2.02	0.60
1:A:1:SER:O	1:A:2:TRP:HB3	1.99	0.60
1:A:551:ARG:HD3	1:A:584:LYS:HA	1.84	0.60
1:A:172:TYR:CG	1:A:173:GLN:N	2.70	0.60
1:A:286:GLN:NE2	1:A:592:SER:OG	2.35	0.60
1:A:2:TRP:CE3	1:A:4:VAL:N	2.69	0.59
1:A:501:MET:HG2	1:A:506:ARG:C	2.22	0.59
1:A:18:ASN:O	1:A:19:SER:C	2.41	0.59
1:A:351:HIS:HD1	1:A:437:ASN:HD21	1.48	0.59
1:A:221:ASP:HB2	1:A:226:TYR:CZ	2.38	0.58
1:A:5:GLY:HA3	10:A:717:HOH:O	2.02	0.58
1:A:148:ASP:O	1:A:151:LEU:HB2	2.04	0.58
1:A:368:TRP:CH2	1:A:390:GLY:N	2.72	0.58
1:A:425:THR:HG22	1:A:425:THR:O	2.04	0.57
1:A:172:TYR:O	1:A:173:GLN:HB3	2.03	0.57
1:A:166:VAL:O	1:A:167:CYS:HB2	2.04	0.57
1:A:422:PHE:CE2	1:A:423:GLN:O	2.57	0.57
1:A:559:ILE:N	1:A:559:ILE:HD13	2.20	0.57
1:A:230:ASN:OD1	1:A:231:ASN:N	2.38	0.56
1:A:286:GLN:H	1:A:286:GLN:CD	2.07	0.56
1:A:501:MET:SD	1:A:506:ARG:C	2.84	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:TRP:CE3	1:A:2:TRP:C	2.78	0.56
1:A:125:SER:O	1:A:129:CYS:HB2	2.06	0.56
1:A:377:HIS:HA	1:A:380:PHE:CE2	2.40	0.55
8:A:621:HEM:HMB2	8:A:621:HEM:HBB2	1.87	0.55
1:A:146:LYS:O	1:A:147:ASN:CB	2.54	0.55
1:A:519:PHE:HD1	1:A:522:ILE:HD12	1.64	0.55
10:A:833:HOH:O	3:C:1:NAG:H81	2.06	0.54
1:A:366:GLN:O	1:A:367:PRO:C	2.43	0.54
1:A:264:THR:HG23	1:A:392:ILE:HG13	1.89	0.54
1:A:268:LEU:HD23	1:A:549:PHE:CE2	2.42	0.54
1:A:31:ARG:HD2	7:A:618:NO3:O1	2.07	0.54
1:A:281:LYS:NZ	1:A:285:PRO:O	2.40	0.53
1:A:87:ASP:N	7:A:617:NO3:O1	2.41	0.53
1:A:393:ASP:OD1	1:A:557:THR:HB	2.08	0.53
1:A:2:TRP:CE3	1:A:3:GLU:HA	2.44	0.52
1:A:188:ASP:O	1:A:189:ALA:C	2.47	0.52
1:A:288:ASP:HB2	1:A:291:LYS:H	1.74	0.52
1:A:519:PHE:HD1	1:A:522:ILE:HD11	1.45	0.52
1:A:519:PHE:CG	1:A:522:ILE:CD1	2.84	0.52
1:A:283:LEU:HD21	1:A:591:ALA:HB2	1.90	0.52
1:A:66:THR:HB	1:A:70:PHE:N	2.25	0.52
1:A:407:MET:CB	1:A:501:MET:HE1	2.40	0.51
1:A:32:ARG:NH2	1:A:334:SER:OG	2.43	0.51
1:A:169:THR:N	1:A:170:PRO:CD	2.73	0.51
1:A:283:LEU:CD2	1:A:591:ALA:HA	2.40	0.51
1:A:193:TYR:OH	1:A:297:ARG:HA	2.10	0.51
1:A:385:ARG:O	1:A:389:ASP:HB2	2.10	0.51
1:A:364:ASN:N	1:A:364:ASN:HD22	2.08	0.51
1:A:471:LEU:O	1:A:472:LYS:C	2.50	0.51
1:A:77:GLU:HB2	1:A:145:PRO:HG3	1.94	0.50
1:A:45:ARG:CZ	1:A:49:ALA:HB2	2.42	0.50
1:A:92:LEU:O	1:A:94:GLN:OE1	2.29	0.50
1:A:272:GLU:O	1:A:276:LEU:HB2	2.12	0.50
1:A:551:ARG:CD	1:A:583:ASP:O	2.59	0.50
1:A:92:LEU:HB2	10:A:843:HOH:O	2.11	0.49
1:A:210:LEU:HD22	10:A:853:HOH:O	2.10	0.49
1:A:281:LYS:HD2	1:A:285:PRO:HA	1.94	0.49
1:A:467:LEU:HD11	1:A:471:LEU:HD11	1.93	0.49
1:A:592:SER:OG	1:A:592:SER:O	2.29	0.49
1:A:62:THR:HG22	1:A:64:ARG:H	1.77	0.49
1:A:392:ILE:HG23	1:A:396:VAL:HG23	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:191:LEU:HA	1:A:253:ASP:HB2	1.95	0.49
1:A:467:LEU:HG	1:A:471:LEU:HD12	1.94	0.49
1:A:82:ILE:CD1	1:A:480:LEU:HD23	2.43	0.48
1:A:235:SER:OG	10:A:842:HOH:O	2.20	0.48
1:A:350:GLY:HA3	8:A:621:HEM:CBC	2.44	0.48
1:A:203:LEU:HD21	1:A:252:GLY:HA2	1.94	0.48
1:A:326:PRO:O	1:A:523:ARG:NH2	2.43	0.48
1:A:10:VAL:HG11	1:A:41:ARG:CZ	2.42	0.48
1:A:264:THR:O	1:A:267:THR:HB	2.14	0.48
1:A:481:MET:HA	1:A:481:MET:CE	2.44	0.48
1:A:317:LEU:O	1:A:502:VAL:HG11	2.14	0.47
1:A:524:ASP:OD2	10:A:874:HOH:O	2.20	0.47
1:A:183:VAL:HG11	10:A:732:HOH:O	2.14	0.47
8:A:621:HEM:HMC2	8:A:621:HEM:HBC2	1.97	0.47
1:A:588:SER:N	1:A:589:PRO:CD	2.77	0.47
1:A:464:LEU:HD13	1:A:481:MET:HG3	1.95	0.47
1:A:2:TRP:CZ3	1:A:4:VAL:CG2	2.88	0.47
1:A:97:SER:HB3	1:A:568:GLN:O	2.14	0.47
1:A:183:VAL:CG1	10:A:732:HOH:O	2.63	0.47
1:A:202:ARG:HH22	1:A:231:ASN:CB	2.22	0.47
1:A:316:VAL:HG12	1:A:316:VAL:O	2.15	0.47
1:A:501:MET:CG	1:A:506:ARG:C	2.83	0.47
1:A:502:VAL:HG13	1:A:503:GLU:H	1.79	0.47
1:A:100:PHE:HE1	1:A:316:VAL:HG23	1.80	0.46
1:A:2:TRP:CE3	1:A:3:GLU:C	2.88	0.46
1:A:211:GLY:HA3	1:A:292:LEU:HB2	1.98	0.46
1:A:2:TRP:C	1:A:2:TRP:CD2	2.88	0.46
1:A:343:PHE:CD1	1:A:518:GLN:HG2	2.51	0.46
1:A:501:MET:SD	1:A:506:ARG:O	2.74	0.46
1:A:119:LEU:HD13	10:A:779:HOH:O	2.15	0.46
1:A:28:CYS:HA	1:A:34:PRO:HB3	1.98	0.46
1:A:362:ASP:C	1:A:362:ASP:OD1	2.53	0.46
1:A:37:GLY:HA3	1:A:186:PHE:CZ	2.50	0.46
1:A:588:SER:CB	1:A:589:PRO:HD3	2.46	0.45
1:A:172:TYR:CE2	1:A:174:SER:HB2	2.51	0.45
1:A:213:MET:CB	1:A:270:LEU:HD11	2.47	0.45
1:A:224:LEU:HD23	1:A:224:LEU:N	2.32	0.44
1:A:131:GLU:CG	10:A:770:HOH:O	2.65	0.44
1:A:265:ALA:HA	1:A:268:LEU:HB2	1.99	0.44
1:A:392:ILE:HG23	1:A:396:VAL:CG2	2.48	0.44
1:A:400:LEU:HD11	1:A:553:ILE:HD13	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:296:ALA:O	1:A:299:ILE:N	2.49	0.44
1:A:368:TRP:CH2	1:A:390:GLY:CA	3.01	0.44
1:A:352:MET:HB3	1:A:407:MET:HG2	1.98	0.44
1:A:502:VAL:HG12	1:A:503:GLU:H	1.80	0.44
1:A:536:PHE:O	1:A:541:ARG:NH1	2.51	0.43
1:A:236:PRO:O	1:A:240:ILE:HG12	2.19	0.43
1:A:87:ASP:O	1:A:411:LYS:HE3	2.19	0.43
1:A:511:LEU:O	1:A:512:ALA:C	2.51	0.43
1:A:213:MET:HB3	1:A:270:LEU:HD11	2.01	0.43
1:A:221:ASP:HB2	1:A:226:TYR:CE2	2.54	0.43
1:A:548:SER:OG	1:A:551:ARG:HB2	2.19	0.43
1:A:2:TRP:HE3	1:A:3:GLU:C	2.23	0.42
1:A:175:LEU:HD23	1:A:176:ALA:N	2.34	0.42
1:A:301:GLY:O	1:A:305:GLN:HG3	2.19	0.42
1:A:368:TRP:HZ3	1:A:389:ASP:OD1	2.02	0.42
1:A:194:GLY:HA2	1:A:252:GLY:O	2.19	0.42
1:A:273:HIS:CE1	1:A:296:ALA:HB3	2.54	0.42
1:A:360:ARG:HH12	1:A:389:ASP:CG	2.22	0.42
1:A:407:MET:CB	1:A:501:MET:CE	2.79	0.42
1:A:523:ARG:HG3	1:A:529:TRP:CE2	2.55	0.42
1:A:202:ARG:NH2	1:A:231:ASN:ND2	2.68	0.42
1:A:501:MET:HG2	1:A:507:VAL:N	2.35	0.42
1:A:86:LEU:HB2	7:A:617:NO3:O1	2.19	0.42
1:A:30:ASN:O	1:A:34:PRO:HA	2.20	0.41
1:A:36:LEU:O	1:A:186:PHE:HZ	2.02	0.41
1:A:159:PRO:HD2	1:A:431:PHE:CE2	2.55	0.41
1:A:385:ARG:O	1:A:389:ASP:CB	2.68	0.41
1:A:126:LYS:CG	1:A:127:THR:N	2.83	0.41
1:A:502:VAL:CG1	1:A:503:GLU:N	2.80	0.41
1:A:519:PHE:CD1	1:A:522:ILE:HD12	2.42	0.41
1:A:58:PRO:HD3	1:A:162:ARG:NH1	2.36	0.41
1:A:265:ALA:O	1:A:268:LEU:N	2.53	0.41
1:A:449:TYR:OH	1:A:499:GLU:OE2	2.33	0.41
1:A:18:ASN:C	1:A:19:SER:O	2.58	0.41
1:A:31:ARG:NH1	7:A:618:NO3:O1	2.38	0.41
1:A:225:ALA:O	1:A:271:ARG:NH2	2.49	0.41
1:A:240:ILE:HD13	1:A:240:ILE:HA	1.91	0.41
1:A:407:MET:SD	1:A:408:ASN:N	2.93	0.41
1:A:43:LEU:HD21	1:A:181:ASN:CB	2.43	0.41
1:A:230:ASN:ND2	1:A:232:ARG:HG2	2.36	0.40
1:A:522:ILE:HG13	1:A:523:ARG:N	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:621:HEM:HBC2	8:A:621:HEM:CMC	2.51	0.40
1:A:426:HIS:HB3	10:A:818:HOH:O	2.21	0.40
1:A:249:PHE:CE2	1:A:383:THR:HG22	2.56	0.40
1:A:392:ILE:O	1:A:396:VAL:HG23	2.22	0.40
1:A:151:LEU:HD23	1:A:155:GLY:O	2.21	0.40
1:A:422:PHE:CD2	1:A:423:GLN:O	2.75	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:222:HIS:CE1	1:A:538:GLU:OE2[2_555]	1.68	0.52
1:A:222:HIS:ND1	1:A:538:GLU:OE2[2_555]	1.88	0.32

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%)	533 (90%)	52 (9%)	7 (1%)	13 8

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	167	CYS
1	A	173	GLN
1	A	187	LEU
1	A	502	VAL
1	A	2	TRP
1	A	464	LEU
1	A	166	VAL

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%)	503 (98%)	13 (2%)	47 52

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

Mol	Chain	Res	Type
1	A	6	CYS
1	A	40	ASN
1	A	119	LEU
1	A	168	PRO
1	A	173	GLN
1	A	259	GLN
1	A	283	LEU
1	A	347	PHE
1	A	392	ILE
1	A	520	GLN
1	A	533	PRO
1	A	539	LYS
1	A	588	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	GLN
1	A	217	GLN
1	A	259	GLN
1	A	364	ASN
1	A	468	GLN
1	A	497	ASN
1	A	570	ASN

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	1.26	0	8,12,14	2.32	4 (50%)

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	-	1/5/8/10	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	198	SEP	OG-P-O1P	-3.99	95.28	106.47
1	A	198	SEP	P-OG-CB	3.80	128.76	118.30
1	A	198	SEP	O3P-P-O2P	2.79	118.30	107.64
1	A	198	SEP	O3P-P-OG	2.09	112.28	106.73

There are no chirality outliers.

All (1) torsion outliers are listed below:

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

There are no ring outliers.

1 monomer is involved in 2 short contacts:

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

5.5 Carbohydrates (i)

10 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NAG	B	1	2,1	14,14,15	0.95	1 (7%)	17,19,21	2.38	8 (47%)
2	NAG	B	2	2	14,14,15	0.48	0	17,19,21	1.34	2 (11%)
2	BMA	B	3	2	11,11,12	0.69	0	15,15,17	1.61	3 (20%)
3	NAG	C	1	1,3	14,14,15	0.69	0	17,19,21	0.93	0
3	NAG	C	2	3	14,14,15	0.60	0	17,19,21	0.66	0
4	NAG	D	1	4,1	14,14,15	1.03	1 (7%)	17,19,21	1.49	6 (35%)
4	NAG	D	2	4	14,14,15	0.62	0	17,19,21	2.29	6 (35%)
4	MAN	D	3	4	11,11,12	0.36	0	15,15,17	1.17	2 (13%)
3	NAG	E	1	1,3	14,14,15	0.53	0	17,19,21	1.63	3 (17%)
3	NAG	E	2	3	14,14,15	0.52	0	17,19,21	1.49	4 (23%)

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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	E	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1	NAG	O5-C1	-2.71	1.39	1.43
2	B	1	NAG	O5-C1	-2.46	1.39	1.43

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	D	2	NAG	C4-C3-C2	-5.71	102.64	111.02
4	D	2	NAG	C1-O5-C5	4.83	118.73	112.19
3	E	1	NAG	C1-O5-C5	4.67	118.52	112.19
2	B	1	NAG	C6-C5-C4	4.16	122.75	113.00
2	B	3	BMA	C1-C2-C3	4.03	114.62	109.67
2	B	1	NAG	C1-C2-N2	-3.92	103.79	110.49
2	B	1	NAG	C1-O5-C5	-3.76	107.10	112.19
2	B	1	NAG	C4-C3-C2	3.68	116.42	111.02
4	D	3	MAN	C1-C2-C3	3.40	113.84	109.67
2	B	2	NAG	C1-O5-C5	3.39	116.79	112.19
3	E	2	NAG	C4-C3-C2	-3.39	106.06	111.02
2	B	1	NAG	O4-C4-C5	3.21	117.27	109.30
2	B	1	NAG	O5-C5-C4	-3.09	103.30	110.83
2	B	3	BMA	C1-O5-C5	2.98	116.23	112.19
2	B	1	NAG	O4-C4-C3	-2.97	103.47	110.35
4	D	2	NAG	O5-C5-C6	2.83	111.65	107.20
4	D	1	NAG	C2-N2-C7	2.66	126.69	122.90
2	B	2	NAG	C1-C2-N2	2.46	114.69	110.49
4	D	2	NAG	C1-C2-N2	2.42	114.62	110.49
3	E	1	NAG	C3-C4-C5	2.39	114.50	110.24
2	B	3	BMA	O5-C5-C6	2.28	110.78	107.20
3	E	2	NAG	O5-C1-C2	-2.28	107.69	111.29
4	D	1	NAG	O5-C5-C6	-2.25	103.67	107.20
4	D	1	NAG	O5-C1-C2	-2.19	107.84	111.29
4	D	1	NAG	O3-C3-C2	2.18	113.98	109.47
4	D	1	NAG	O7-C7-N2	2.15	125.91	121.95
3	E	2	NAG	O3-C3-C2	2.15	113.92	109.47
4	D	2	NAG	C2-N2-C7	-2.15	119.85	122.90
3	E	1	NAG	O5-C5-C6	2.12	110.52	107.20
3	E	2	NAG	O7-C7-C8	-2.11	118.14	122.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	D	2	NAG	C8-C7-N2	2.02	119.52	116.10
4	D	1	NAG	O7-C7-C8	-2.01	118.32	122.06
4	D	3	MAN	C3-C4-C5	2.01	113.82	110.24
2	B	1	NAG	C3-C4-C5	-2.00	106.67	110.24

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2	NAG	C4-C5-C6-O6
4	D	3	MAN	C4-C5-C6-O6
3	E	1	NAG	O5-C5-C6-O6
4	D	3	MAN	O5-C5-C6-O6
2	B	2	NAG	O5-C5-C6-O6
3	E	1	NAG	C4-C5-C6-O6
4	D	2	NAG	O5-C5-C6-O6
3	E	2	NAG	C4-C5-C6-O6
3	E	2	NAG	O5-C5-C6-O6
4	D	2	NAG	C4-C5-C6-O6

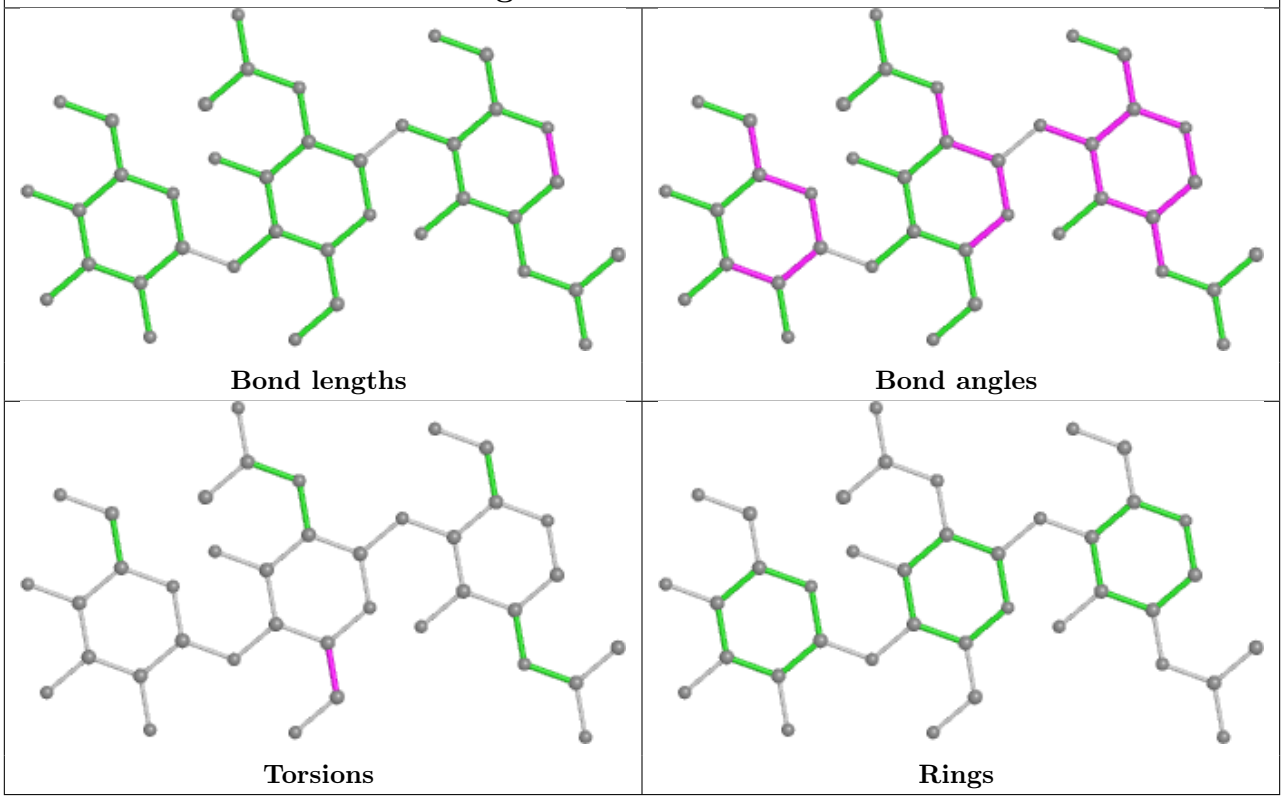
There are no ring outliers.

1 monomer is involved in 1 short contact:

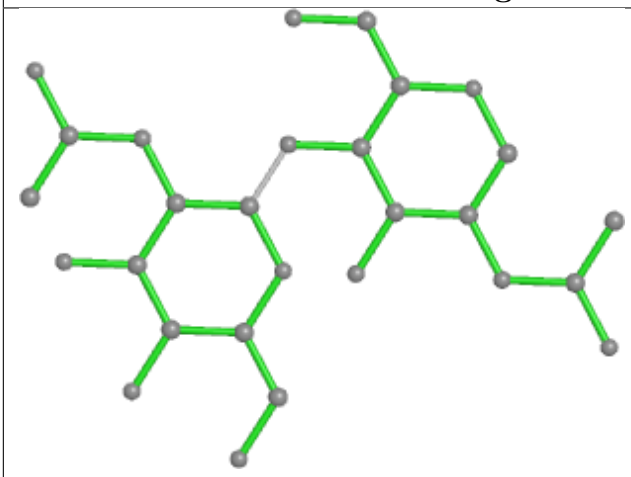
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1	NAG	1	0

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

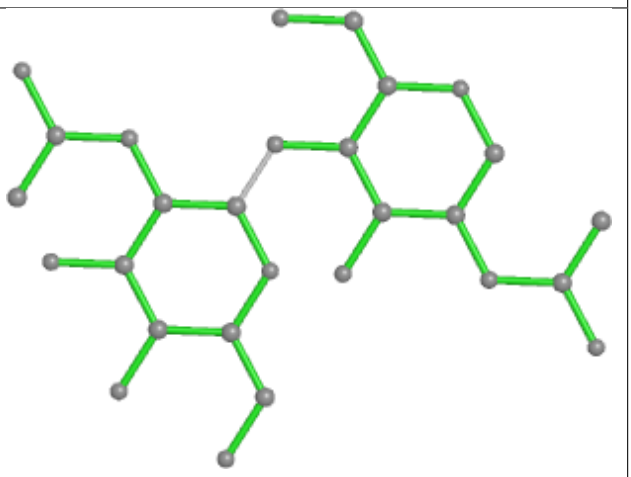
Oligosaccharide Chain B



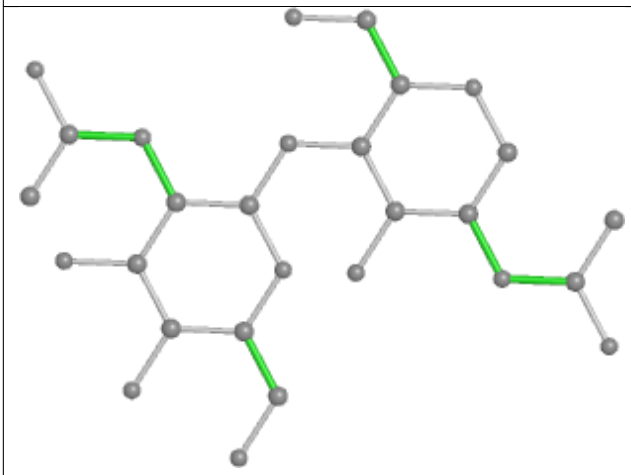
Oligosaccharide Chain C



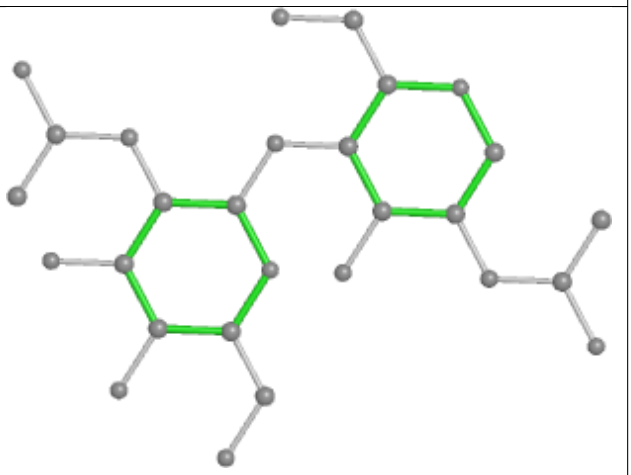
Bond lengths



Bond angles

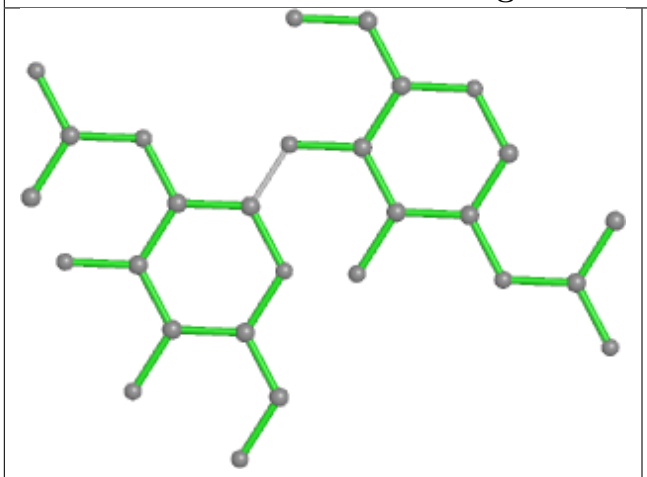


Torsions

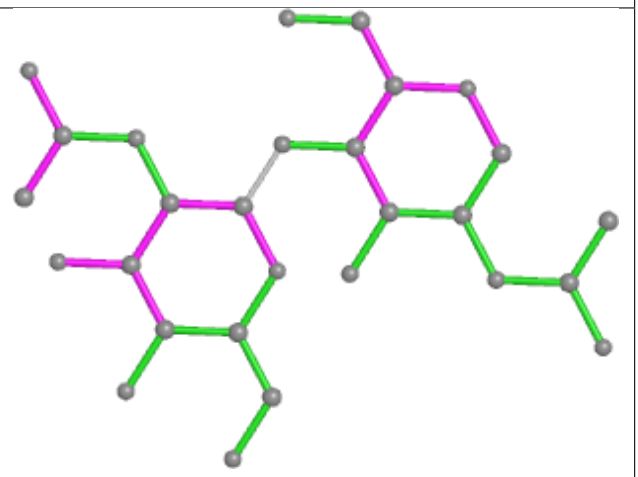


Rings

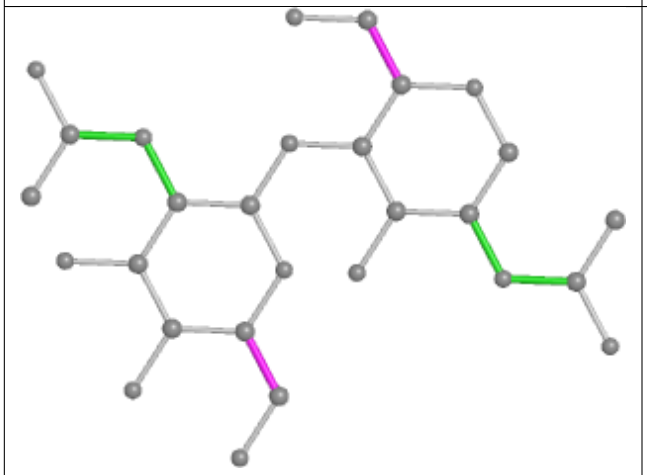
Oligosaccharide Chain E



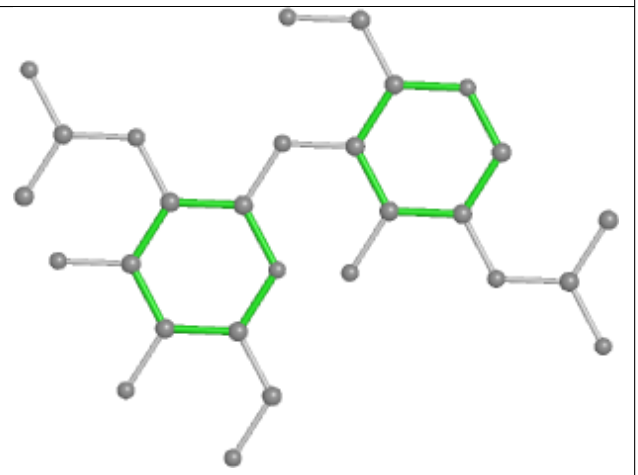
Bond lengths



Bond angles

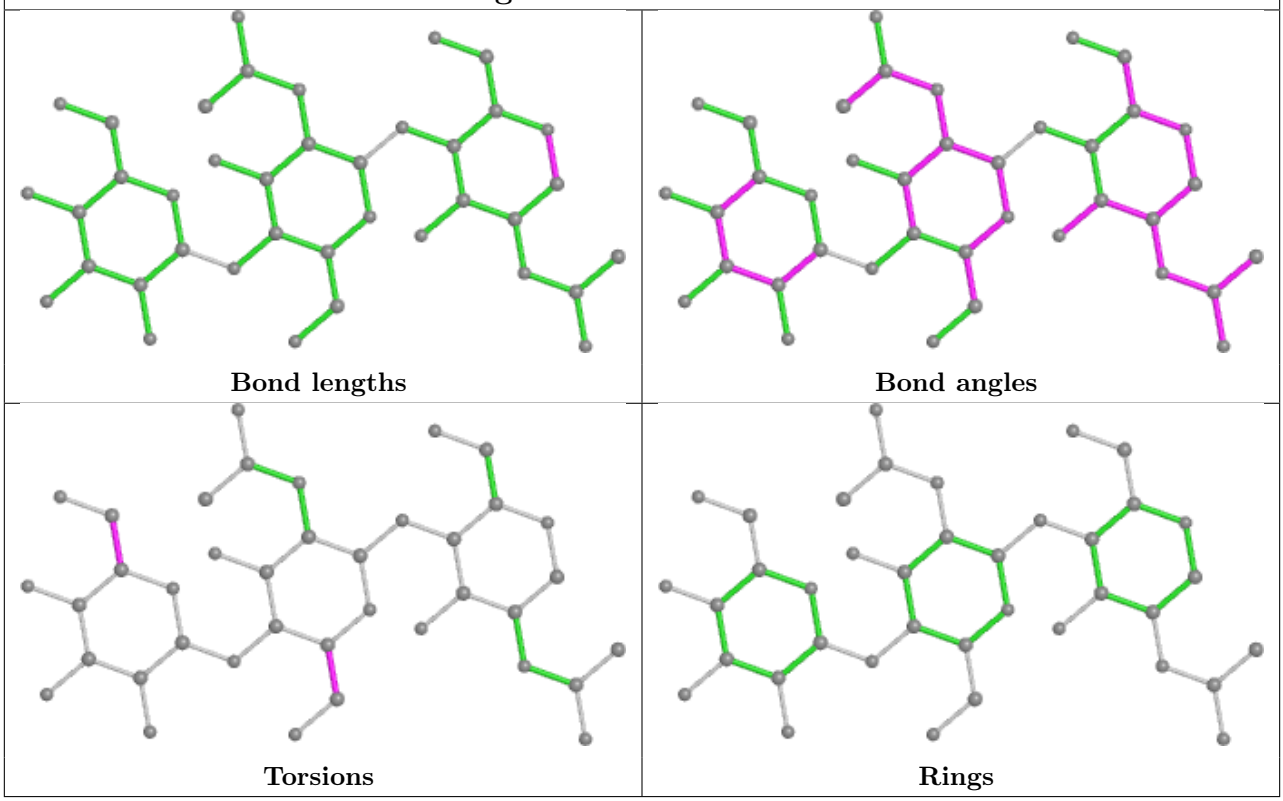


Torsions



Rings

Oligosaccharide Chain D



5.6 Ligand geometry (i)

Of 16 ligands modelled in this entry, 7 are monoatomic - leaving 9 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
9	SCN	A	622	-	1,2,2	1.04	0	0,1,1	-	-
9	SCN	A	625	-	1,2,2	0.36	0	0,1,1	-	-
9	SCN	A	623	-	1,2,2	0.01	0	0,1,1	-	-
7	NO3	A	618	-	1,3,3	0.42	0	0,3,3	-	-
7	NO3	A	617	-	1,3,3	0.71	0	0,3,3	-	-
7	NO3	A	619	-	1,3,3	3.62	1 (100%)	0,3,3	-	-
7	NO3	A	620	-	1,3,3	0.87	0	0,3,3	-	-
9	SCN	A	624	-	1,2,2	0.63	0	0,1,1	-	-
8	HEM	A	621	10,1	41,50,50	1.62	8 (19%)	45,82,82	1.89	17 (37%)

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	HEM	A	621	10,1	-	4/12/54/54	-

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	621	HEM	C4D-ND	-5.09	1.31	1.40
7	A	619	NO3	O1-N	-3.62	1.07	1.24
8	A	621	HEM	C1B-NB	-3.57	1.34	1.40
8	A	621	HEM	FE-NB	3.04	2.11	1.96
8	A	621	HEM	C4B-NB	-2.95	1.32	1.38
8	A	621	HEM	CHB-C1B	2.50	1.41	1.35
8	A	621	HEM	C4D-C3D	2.29	1.49	1.45
8	A	621	HEM	O1D-CGD	2.26	1.29	1.22
8	A	621	HEM	C1A-CHA	-2.14	1.35	1.41

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	A	621	HEM	C1B-NB-C4B	4.16	109.37	105.07
8	A	621	HEM	CHA-C4D-ND	3.89	129.19	124.38
8	A	621	HEM	CHA-C4D-C3D	-3.78	118.22	125.33
8	A	621	HEM	CBA-CAA-C2A	-3.27	107.04	112.62
8	A	621	HEM	CBD-CAD-C3D	-2.97	104.36	112.63
8	A	621	HEM	O2A-CGA-O1A	-2.84	116.21	123.30
8	A	621	HEM	O2A-CGA-CBA	2.62	122.46	114.03
8	A	621	HEM	C4A-C3A-C2A	2.62	108.82	107.00
8	A	621	HEM	C4B-C3B-C2B	-2.58	105.07	107.11
8	A	621	HEM	CAA-CBA-CGA	2.58	120.99	113.76
8	A	621	HEM	CHD-C1D-C2D	-2.57	120.96	124.98
8	A	621	HEM	CMC-C2C-C3C	2.44	129.25	124.68
8	A	621	HEM	CMD-C2D-C1D	2.40	128.69	125.04
8	A	621	HEM	C3C-C4C-NC	-2.16	106.87	110.94
8	A	621	HEM	CHC-C4B-NB	2.13	126.75	124.43
8	A	621	HEM	C2D-C1D-ND	2.13	112.43	109.88
8	A	621	HEM	C3D-C4D-ND	2.11	112.51	110.17

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	621	HEM	CAA-CBA-CGA-O1A
8	A	621	HEM	CAD-CBD-CGD-O1D
8	A	621	HEM	CAD-CBD-CGD-O2D
8	A	621	HEM	CAA-CBA-CGA-O2A

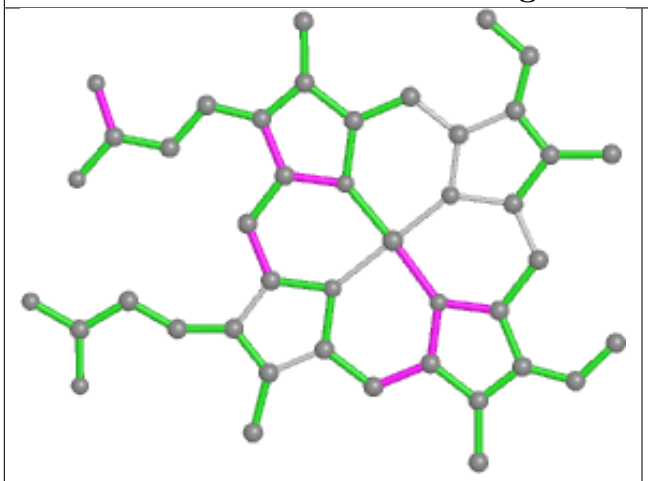
There are no ring outliers.

3 monomers are involved in 8 short contacts:

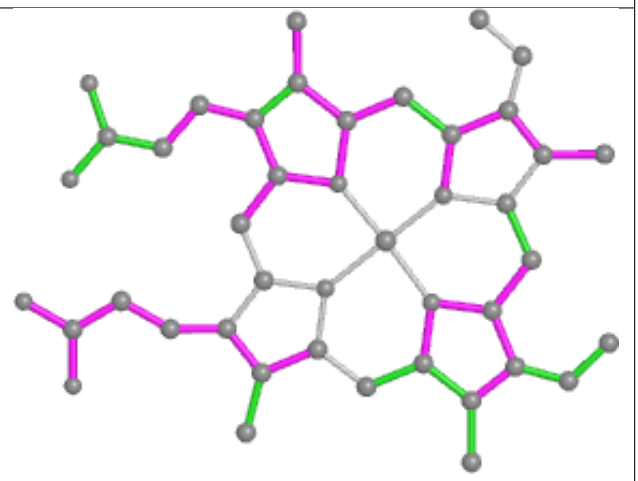
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	618	NO3	2	0
7	A	617	NO3	2	0
8	A	621	HEM	4	0

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.

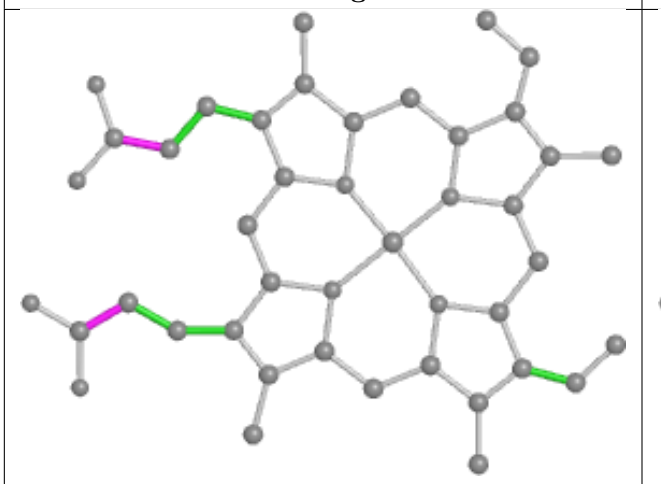
Ligand HEM A 621



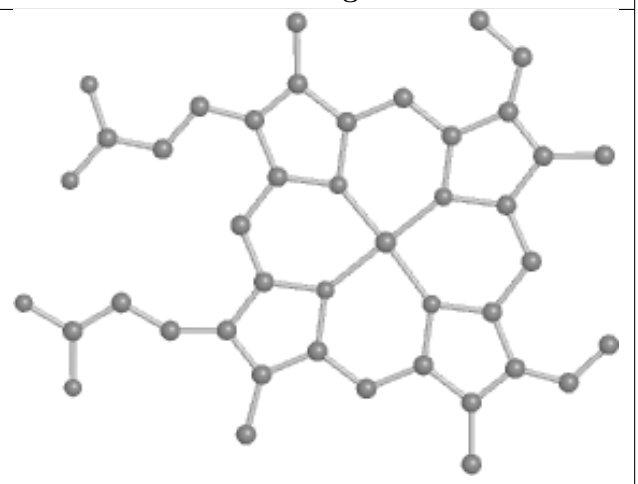
Bond lengths



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%)	0.81	74 (12%) 3 5	26, 46, 100, 159	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	TRP	19.7
1	A	1	SER	17.0
1	A	172	TYR	13.3
1	A	122	ASN	11.8
1	A	173	GLN	9.7
1	A	7	GLY	9.4
1	A	268	LEU	8.6
1	A	4	VAL	8.1
1	A	174	SER	8.0
1	A	8	ALA	8.0
1	A	120	GLY	7.9
1	A	121	SER	7.5
1	A	13	VAL	7.2
1	A	595	ASN	7.1
1	A	170	PRO	7.1
1	A	18	ASN	6.5
1	A	171	PRO	5.0
1	A	119	LEU	5.0
1	A	125	SER	4.5
1	A	3	GLU	4.5
1	A	254	PHE	4.5
1	A	5	GLY	4.3
1	A	123	GLU	4.1
1	A	126	LYS	4.1
1	A	10	VAL	4.1
1	A	64	ARG	3.9
1	A	92	LEU	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	593	ARG	3.8
1	A	12	LEU	3.7
1	A	42	ALA	3.7
1	A	129	CYS	3.7
1	A	91	VAL	3.7
1	A	124	HIS	3.6
1	A	522	ILE	3.6
1	A	14	LYS	3.4
1	A	186	PHE	3.4
1	A	316	VAL	3.3
1	A	6	CYS	3.3
1	A	118	GLU	3.2
1	A	502	VAL	3.2
1	A	58	PRO	3.1
1	A	387	ILE	3.1
1	A	317	LEU	3.0
1	A	231	ASN	2.9
1	A	117	THR	2.9
1	A	504	ARG	2.8
1	A	389	ASP	2.8
1	A	9	PRO	2.8
1	A	501	MET	2.8
1	A	289	GLY	2.8
1	A	107	VAL	2.7
1	A	262	LEU	2.7
1	A	209	PRO	2.7
1	A	128	GLN	2.6
1	A	132	TYR	2.6
1	A	223	GLY	2.6
1	A	127	THR	2.5
1	A	286	GLN	2.5
1	A	63	GLN	2.4
1	A	43	LEU	2.3
1	A	187	LEU	2.3
1	A	347	PHE	2.3
1	A	17	GLU	2.3
1	A	11	PRO	2.2
1	A	388	LYS	2.2
1	A	111	LEU	2.2
1	A	283	LEU	2.1
1	A	256	ALA	2.1
1	A	425	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	594	GLU	2.1
1	A	441	CYS	2.1
1	A	106	ILE	2.1
1	A	55	LEU	2.0
1	A	371	GLU	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	0.94	0.12	38,55,65,66	0

6.3 Carbohydrates (i)

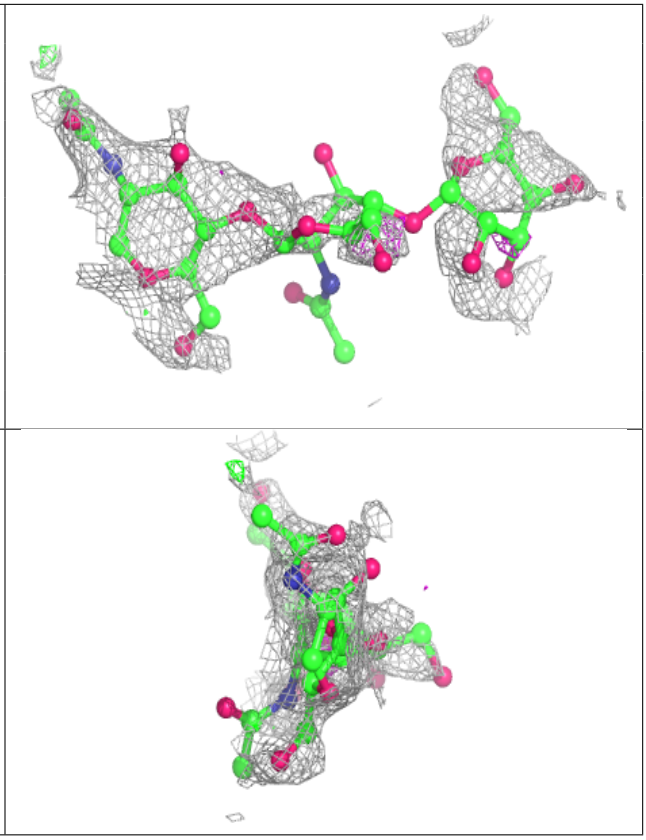
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

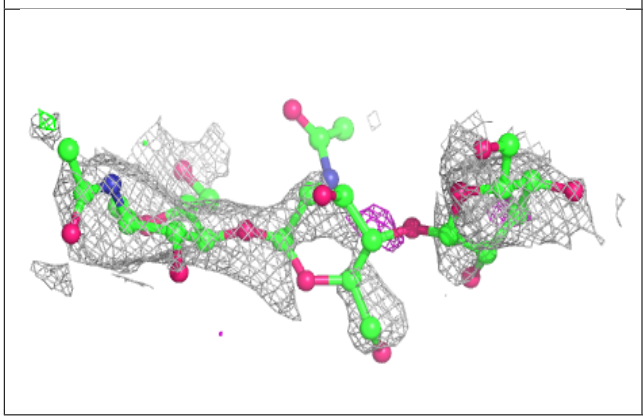
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	BMA	B	3	11/12	0.40	0.46	110,122,129,132	0
4	MAN	D	3	11/12	0.56	0.43	78,81,84,84	0
2	NAG	B	2	14/15	0.69	0.59	114,128,137,137	0
3	NAG	C	2	14/15	0.71	0.33	81,97,111,113	0
3	NAG	E	2	14/15	0.72	0.36	78,99,104,109	0
2	NAG	B	1	14/15	0.72	0.29	76,82,102,106	0
3	NAG	E	1	14/15	0.74	0.24	60,75,86,100	0
4	NAG	D	2	14/15	0.81	0.31	69,79,89,103	0
3	NAG	C	1	14/15	0.88	0.13	58,68,73,83	0
4	NAG	D	1	14/15	0.91	0.14	44,57,62,71	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:

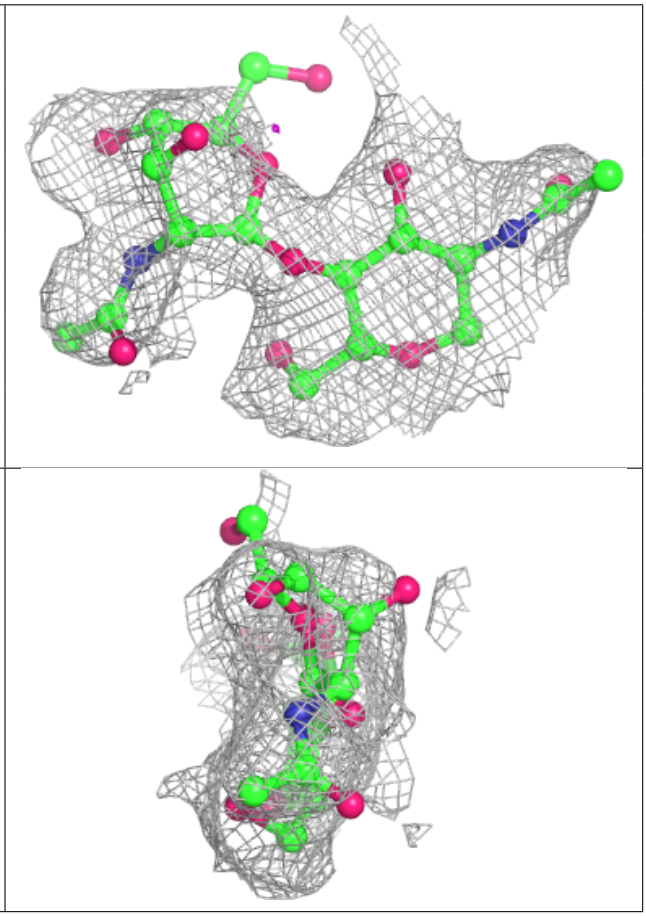
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

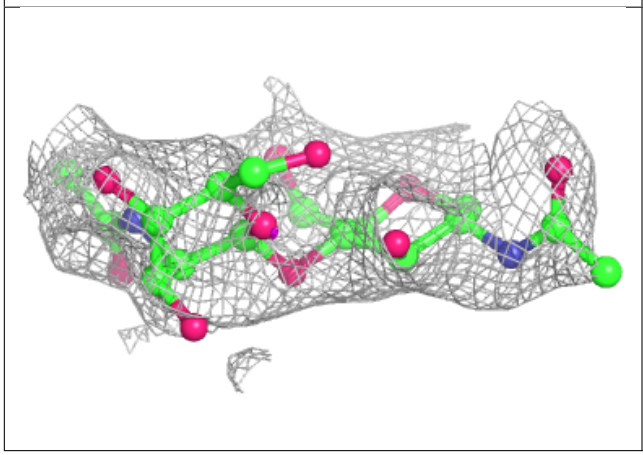




Electron density around Chain C:

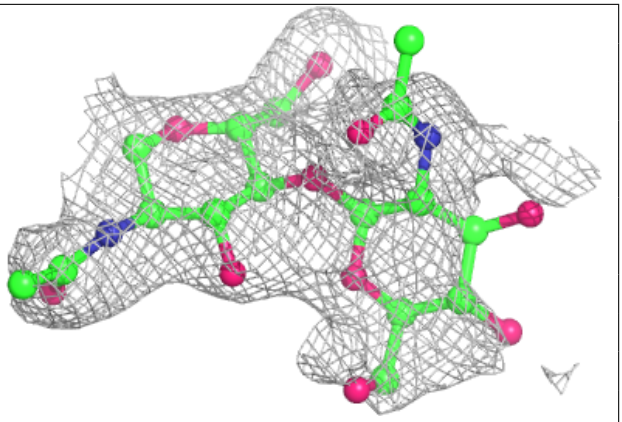
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

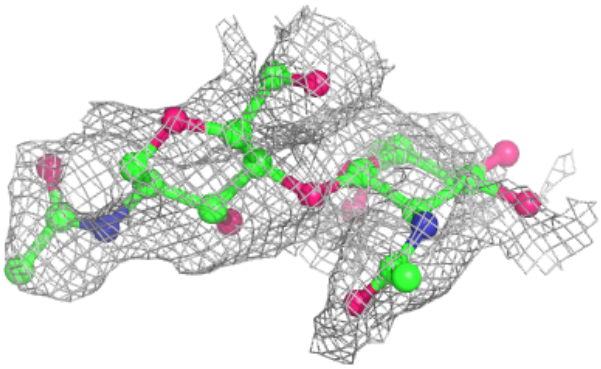


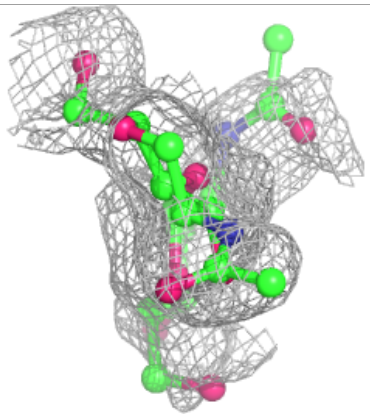


Electron density around Chain E:

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

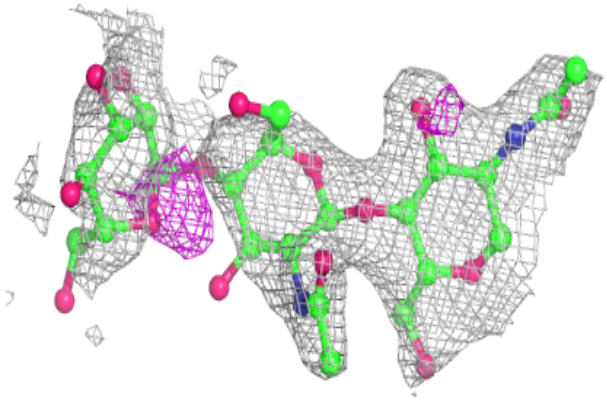


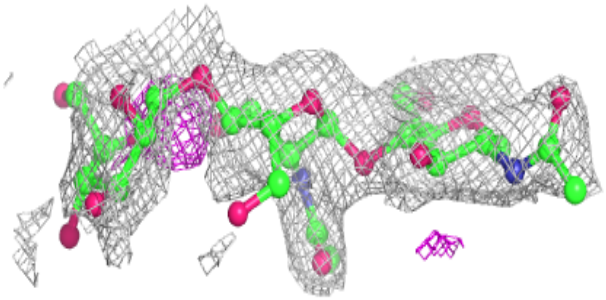


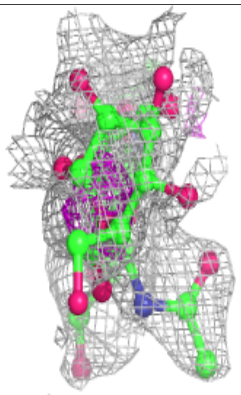


Electron density around Chain D:

$2mF_o$-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)

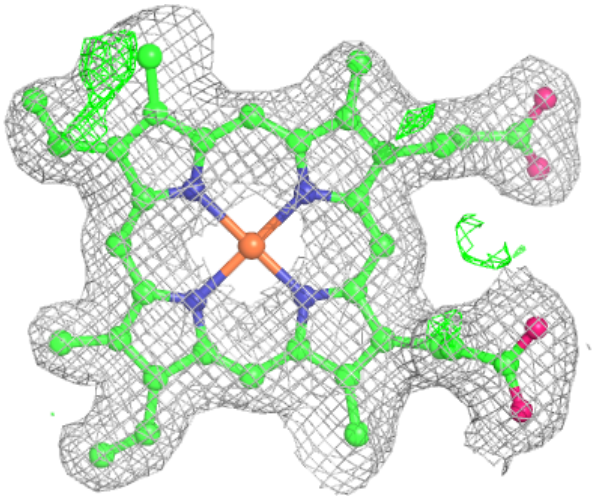
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

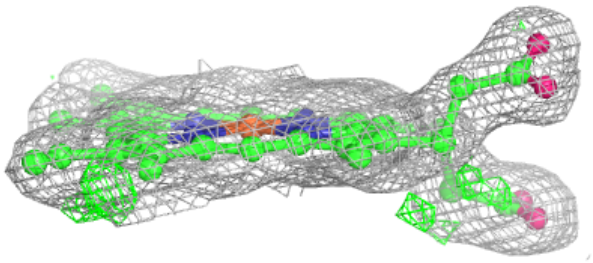
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	IOD	A	612	1/1	0.76	0.21	147,147,147,147	0
7	NO3	A	617	4/4	0.84	0.53	58,62,63,75	0
9	SCN	A	623	3/3	0.86	0.17	44,44,46,57	0
9	SCN	A	622	3/3	0.88	0.16	41,41,53,53	0
5	CA	A	611	1/1	0.92	0.11	37,37,37,37	0
7	NO3	A	620	4/4	0.93	0.10	41,44,50,53	0
6	IOD	A	616	1/1	0.93	0.12	88,88,88,88	0
7	NO3	A	618	4/4	0.93	0.13	44,47,52,53	0
9	SCN	A	624	3/3	0.94	0.22	34,34,37,38	0
8	HEM	A	621	43/43	0.96	0.22	25,32,37,40	0
6	IOD	A	614	1/1	0.96	0.05	74,74,74,74	0
9	SCN	A	625	3/3	0.96	0.18	31,31,44,51	0
6	IOD	A	613	1/1	0.97	0.03	79,79,79,79	0
6	IOD	A	626	1/1	0.98	0.03	56,56,56,56	0
7	NO3	A	619	4/4	0.98	0.17	17,17,21,46	0
6	IOD	A	615	1/1	0.99	0.10	33,33,33,33	0

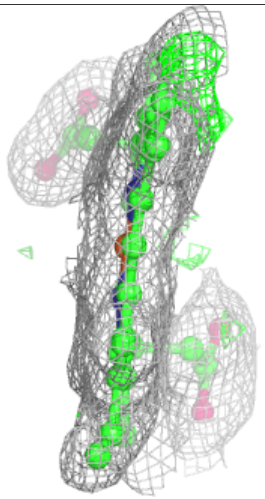
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around HEM A 621:

$2mF_o$-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.