



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 8, 2020 – 11:59 PM BST

PDB ID : 2OJV
Title : Crystal structure of a ternary complex of goat lactoperoxidase with cyanide and iodide ions at 2.4 Å resolution
Authors : Singh, A.K.; Singh, N.; Singh, S.B.; Sharma, S.; Kaur, P.; Singh, T.P.
Deposited on : 2007-01-15
Resolution : 2.40 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

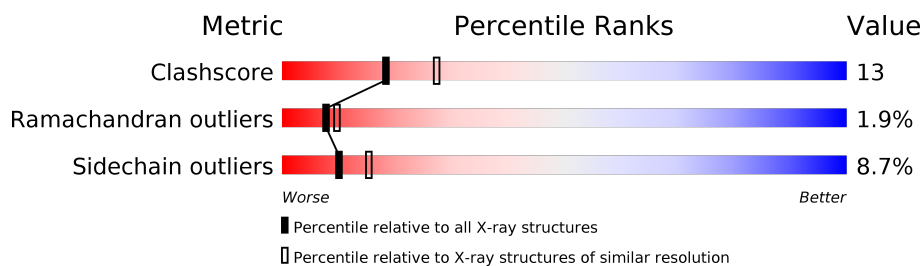
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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))
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	595	
2	B	3	
2	C	3	
2	D	3	
3	E	2	

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
5	CYN	A	2844	-	-	X	-

2 Entry composition [i](#)

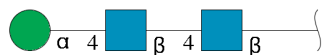
There are 9 unique types of molecules in this entry. The entry contains 5362 atoms, of which 0 are hydrogens and 0 are deuteriums.

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
1	A	595	Total	C	N	O	S	0	0	0
			4753	3021	844	862	26			

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



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

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

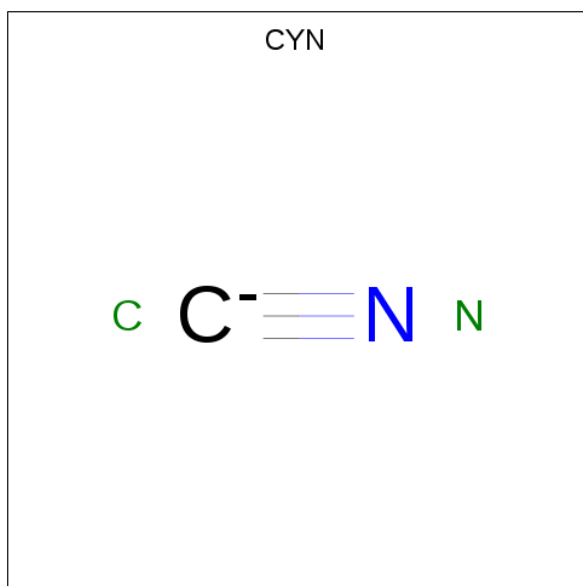


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

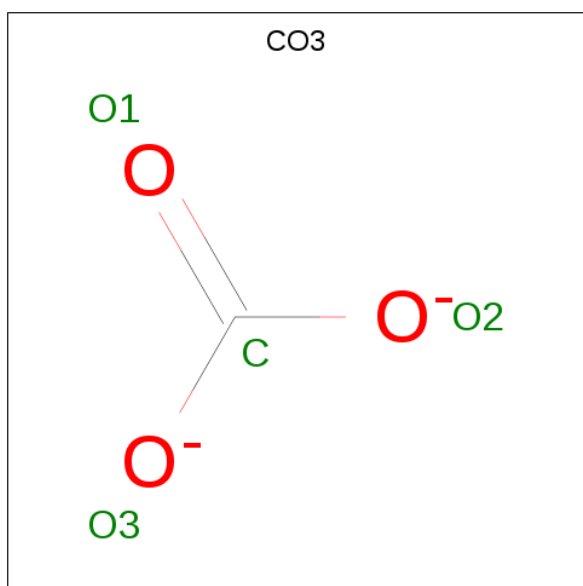
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ca	0	0
			1	1		

- Molecule 5 is CYANIDE ION (three-letter code: CYN) (formula: CN).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	N	0	0
			2	1	1		

- Molecule 6 is CARBONATE ION (three-letter code: CO3) (formula: CO₃).

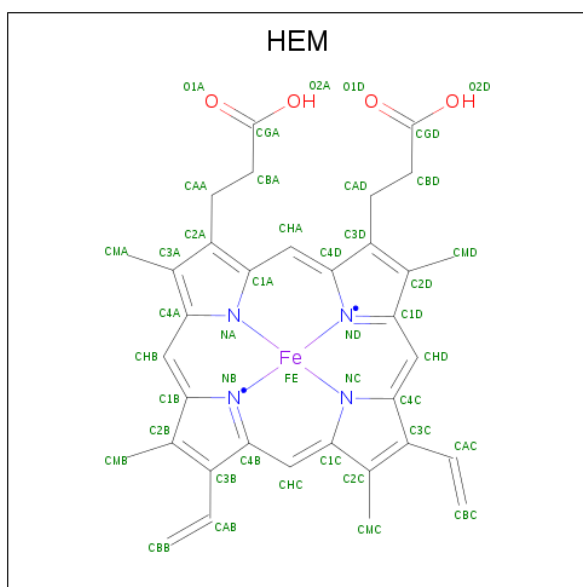


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	1	3		

- Molecule 7 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	8	Total I 8 8	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
8	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 9 is water.

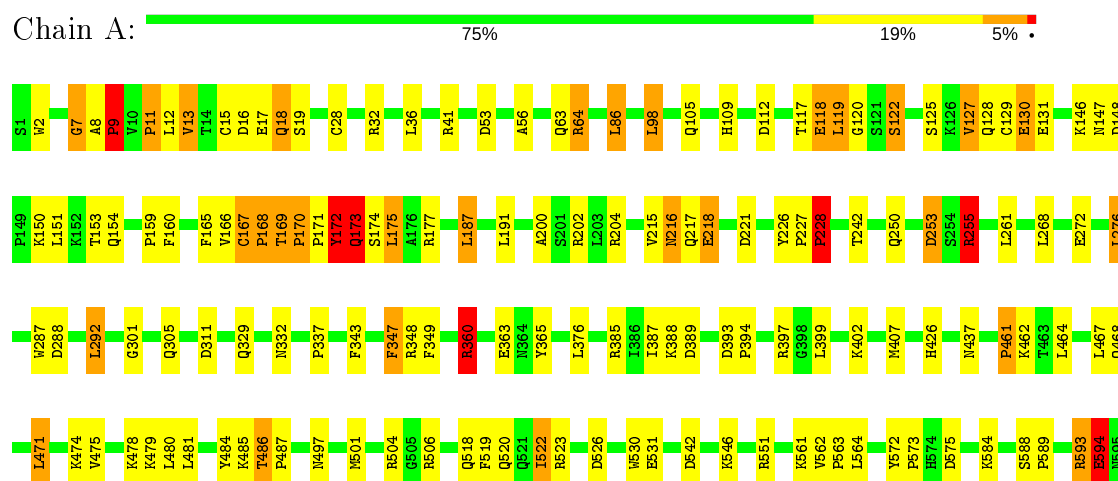
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	406	Total O 406 406	0	0

3 Residue-property plots

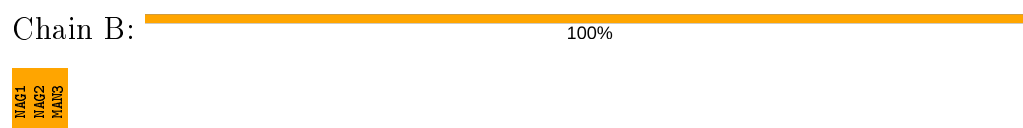
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

- Molecule 1: Lactoperoxidase



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



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



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



MAG1
MAG2
MAIN3

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

Chain E: 

MAG1
MAG2

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	54.20 Å 80.81 Å 77.05 Å 90.00° 102.96° 90.00°	Depositor
Resolution (Å)	74.54 – 2.40	Depositor
% Data completeness (in resolution range)	97.8 (74.54-2.40)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.178 , 0.228	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5362	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

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: CO3, NAG, CA, HEM, IOD, CYN, MAN

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	0.71	1/4882 (0.0%)	1.00	23/6632 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	170	PRO	N-CA	6.27	1.57	1.47

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	172	TYR	CA-CB-CG	-9.83	94.73	113.40
1	A	11	PRO	C-N-CA	-8.82	99.66	121.70
1	A	11	PRO	N-CA-C	7.41	131.36	112.10
1	A	11	PRO	CA-C-N	6.55	131.60	117.20
1	A	255	ARG	NE-CZ-NH2	-6.36	117.12	120.30
1	A	228	PRO	CA-N-CD	-6.18	102.85	111.50
1	A	13	VAL	N-CA-C	6.11	127.49	111.00
1	A	18	GLN	CB-CA-C	5.98	122.37	110.40
1	A	112	ASP	CB-CG-OD2	5.97	123.67	118.30
1	A	461	PRO	CA-N-CD	-5.85	103.31	111.50
1	A	171	PRO	CA-N-CD	-5.80	103.38	111.50
1	A	360	ARG	NE-CZ-NH2	-5.55	117.53	120.30
1	A	311	ASP	CB-CG-OD2	5.42	123.18	118.30
1	A	172	TYR	N-CA-C	5.28	125.26	111.00
1	A	575	ASP	CB-CG-OD2	5.28	123.05	118.30
1	A	53	ASP	CB-CG-OD2	5.28	123.05	118.30
1	A	506	ARG	NE-CZ-NH1	5.25	122.92	120.30
1	A	542	ASP	CB-CG-OD2	5.24	123.01	118.30
1	A	7	GLY	N-CA-C	5.23	126.17	113.10
1	A	253	ASP	CB-CG-OD2	5.20	122.98	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	12	LEU	N-CA-C	5.18	124.99	111.00
1	A	11	PRO	O-C-N	-5.13	114.48	122.70
1	A	11	PRO	CA-N-CD	-5.11	104.35	111.50

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4753	0	4647	122	0
2	B	39	0	34	2	0
2	C	39	0	34	0	0
2	D	39	0	34	2	0
3	E	28	0	25	0	0
4	A	1	0	0	0	0
5	A	2	0	0	2	0
6	A	4	0	0	0	0
7	A	8	0	0	2	0
8	A	43	0	30	3	0
9	A	406	0	0	17	0
All	All	5362	0	4804	129	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 13.

All (129) 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:168:PRO:HG2	1:A:172:TYR:CE1	1.85	1.11
1:A:63:GLN:HG2	9:A:3178:HOH:O	1.50	1.10
1:A:167:CYS:HB3	1:A:168:PRO:HD2	1.34	1.09
1:A:426:HIS:HB3	9:A:3202:HOH:O	1.55	1.05
1:A:2:TRP:HB2	1:A:175:LEU:HD12	1.35	1.03
1:A:169:THR:CG2	1:A:170:PRO:HD3	1.89	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:ARG:HG3	9:A:3237:HOH:O	1.64	0.96
1:A:119:LEU:HD11	1:A:169:THR:HG21	1.48	0.96
1:A:167:CYS:HB3	1:A:168:PRO:CD	1.97	0.95
1:A:169:THR:HG22	1:A:170:PRO:HD3	1.49	0.93
1:A:169:THR:HG22	1:A:170:PRO:CD	2.00	0.91
1:A:118:GLU:HB3	9:A:3243:HOH:O	1.72	0.90
1:A:551:ARG:HD3	1:A:584:LYS:HA	1.55	0.87
1:A:216:ASN:ND2	1:A:218:GLU:H	1.72	0.87
1:A:167:CYS:CB	1:A:168:PRO:HD2	2.07	0.84
1:A:481:LEU:HD21	1:A:487:PRO:HD3	1.56	0.84
5:A:2844:CYN:N	7:A:2852:IOD:I	2.82	0.82
1:A:202:ARG:NH2	7:A:2848:IOD:I	2.83	0.81
1:A:119:LEU:HD11	1:A:169:THR:CG2	2.11	0.81
1:A:169:THR:HG23	1:A:170:PRO:HD3	1.61	0.81
1:A:19:SER:HB3	9:A:3189:HOH:O	1.79	0.81
1:A:130:GLU:HG2	1:A:159:PRO:HG3	1.62	0.80
1:A:172:TYR:O	1:A:173:GLN:HB3	1.81	0.80
1:A:146:LYS:HE2	9:A:3257:HOH:O	1.84	0.77
1:A:216:ASN:HD22	1:A:218:GLU:H	1.31	0.76
1:A:169:THR:CG2	1:A:170:PRO:CD	2.59	0.76
1:A:253:ASP:OD2	1:A:255:ARG:HD3	1.87	0.75
1:A:172:TYR:HD2	1:A:173:GLN:H	1.34	0.74
1:A:481:LEU:CD2	1:A:487:PRO:HD3	2.18	0.73
1:A:167:CYS:CB	1:A:168:PRO:CD	2.63	0.72
1:A:561:LYS:HE2	9:A:2905:HOH:O	1.89	0.72
1:A:365:TYR:CZ	1:A:397:ARG:HG2	2.25	0.72
1:A:146:LYS:O	1:A:147:ASN:HB2	1.88	0.71
1:A:130:GLU:HG3	9:A:3201:HOH:O	1.93	0.69
1:A:174:SER:OG	1:A:175:LEU:N	2.25	0.69
1:A:216:ASN:HD22	1:A:217:GLN:N	1.93	0.67
1:A:467:LEU:HG	1:A:471:LEU:HD22	1.77	0.66
1:A:169:THR:HG22	1:A:170:PRO:HD2	1.77	0.66
1:A:288:ASP:O	1:A:292:LEU:HD22	1.96	0.66
1:A:169:THR:H	1:A:170:PRO:HD2	1.61	0.64
1:A:8:ALA:HB3	9:A:3247:HOH:O	1.97	0.64
1:A:129:CYS:HB2	9:A:3188:HOH:O	1.98	0.63
1:A:119:LEU:CD1	1:A:169:THR:HG21	2.25	0.63
1:A:168:PRO:CG	1:A:172:TYR:CE1	2.75	0.63
8:A:2853:HEM:HBC2	8:A:2853:HEM:HMC2	1.81	0.62
1:A:2:TRP:HB2	1:A:175:LEU:CD1	2.22	0.61
2:B:1:NAG:H61	2:B:2:NAG:C1	2.31	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:PRO:HG2	1:A:172:TYR:HE1	1.58	0.61
1:A:475:VAL:HG12	1:A:479:LYS:HE3	1.81	0.61
1:A:594:GLU:OE2	1:A:594:GLU:HA	2.02	0.59
1:A:8:ALA:N	1:A:9:PRO:CD	2.65	0.59
1:A:64:ARG:HD3	9:A:3249:HOH:O	2.02	0.59
1:A:7:GLY:HA2	1:A:167:CYS:HA	1.84	0.59
1:A:8:ALA:N	1:A:9:PRO:HD2	2.18	0.58
1:A:15:CYS:HG	1:A:28:CYS:HG	0.60	0.58
1:A:216:ASN:HD22	1:A:216:ASN:C	2.07	0.57
1:A:125:SER:HA	1:A:128:GLN:HB3	1.87	0.57
1:A:348:ARG:HH11	1:A:437:ASN:ND2	2.03	0.57
1:A:169:THR:H	1:A:170:PRO:CD	2.18	0.57
1:A:202:ARG:HD2	1:A:250:GLN:HE22	1.69	0.57
1:A:343:PHE:CD1	1:A:518:GLN:HG2	2.40	0.56
1:A:119:LEU:CD1	1:A:169:THR:CG2	2.80	0.56
1:A:125:SER:C	1:A:127:VAL:N	2.60	0.55
1:A:172:TYR:HD2	1:A:173:GLN:N	2.04	0.54
1:A:462:LYS:HD2	9:A:3136:HOH:O	2.09	0.53
1:A:588:SER:N	1:A:589:PRO:CD	2.71	0.53
1:A:530:TRP:CE2	1:A:531:GLU:HG3	2.44	0.53
1:A:16:ASP:O	1:A:17:GLU:HB2	2.09	0.52
1:A:349:PHE:CB	1:A:497:ASN:HD21	2.23	0.52
2:D:1:NAG:H62	2:D:2:NAG:C1	2.40	0.52
1:A:172:TYR:CD2	1:A:173:GLN:N	2.77	0.51
2:B:2:NAG:H3	2:B:3:MAN:O5	2.11	0.51
1:A:187:LEU:HD13	1:A:305:GLN:HA	1.92	0.51
1:A:468:GLN:HG2	1:A:474:LYS:HA	1.92	0.51
1:A:16:ASP:HB3	9:A:3189:HOH:O	2.11	0.50
1:A:216:ASN:HB2	1:A:227:PRO:O	2.11	0.50
1:A:221:ASP:HB2	1:A:226:TYR:CZ	2.45	0.50
1:A:365:TYR:CE1	1:A:397:ARG:HG2	2.48	0.49
1:A:287:TRP:HE3	1:A:292:LEU:HD13	1.78	0.49
1:A:301:GLY:O	1:A:305:GLN:HG3	2.14	0.47
1:A:349:PHE:HA	1:A:497:ASN:HD21	1.80	0.47
1:A:593:ARG:HD3	1:A:593:ARG:HA	1.79	0.47
1:A:216:ASN:ND2	1:A:217:GLN:N	2.63	0.47
1:A:393:ASP:HB2	1:A:394:PRO:HD3	1.96	0.47
1:A:36:LEU:HG	1:A:337:PRO:HD2	1.96	0.47
1:A:485:LYS:O	1:A:486:THR:HB	2.15	0.47
1:A:105:GLN:HE21	5:A:2844:CYN:C	2.28	0.46
1:A:109:HIS:ND1	9:A:2881:HOH:O	2.28	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:ASP:O	1:A:151:LEU:HB2	2.15	0.46
1:A:125:SER:C	1:A:127:VAL:H	2.19	0.46
1:A:172:TYR:O	1:A:173:GLN:CB	2.59	0.46
1:A:348:ARG:HH11	1:A:437:ASN:HD22	1.63	0.45
1:A:407:MET:HB3	1:A:501:MET:CE	2.47	0.45
2:D:2:NAG:H4	2:D:3:MAN:H2	1.65	0.45
1:A:169:THR:N	1:A:170:PRO:HD2	2.31	0.45
1:A:215:VAL:HA	1:A:228:PRO:HD3	1.97	0.45
1:A:131:GLU:HA	1:A:131:GLU:OE2	2.17	0.44
1:A:15:CYS:CB	1:A:28:CYS:HG	2.24	0.44
1:A:150:LYS:O	1:A:154:GLN:N	2.46	0.44
1:A:478:LYS:HB2	1:A:478:LYS:HE3	1.50	0.44
1:A:120:GLY:C	1:A:122:SER:H	2.19	0.43
1:A:332:ASN:ND2	9:A:3196:HOH:O	2.41	0.43
1:A:360:ARG:NH2	1:A:389:ASP:OD2	2.51	0.43
1:A:202:ARG:HD2	1:A:250:GLN:NE2	2.34	0.43
1:A:15:CYS:CB	1:A:28:CYS:SG	3.06	0.43
1:A:572:TYR:HA	1:A:573:PRO:HA	1.62	0.43
1:A:119:LEU:HD21	1:A:169:THR:HG23	2.00	0.43
1:A:272:GLU:HG3	1:A:276:LEU:HD22	2.01	0.43
1:A:562:VAL:HB	1:A:563:PRO:HD2	2.01	0.43
1:A:484:TYR:O	1:A:485:LYS:HB2	2.19	0.42
1:A:160:PHE:HA	9:A:3144:HOH:O	2.19	0.42
1:A:385:ARG:O	1:A:389:ASP:HB3	2.19	0.42
1:A:9:PRO:CG	1:A:41:ARG:CZ	2.96	0.42
1:A:481:LEU:HA	1:A:481:LEU:HD23	1.74	0.42
8:A:2853:HEM:CMC	8:A:2853:HEM:HBC2	2.48	0.42
1:A:594:GLU:OE2	1:A:594:GLU:CA	2.66	0.42
1:A:519:PHE:CD1	1:A:522:ILE:HD11	2.55	0.42
1:A:7:GLY:C	1:A:9:PRO:HD2	2.40	0.42
1:A:387:ILE:HG22	1:A:388:LYS:HG3	2.02	0.42
1:A:588:SER:N	1:A:589:PRO:HD2	2.35	0.41
1:A:98:LEU:HD13	1:A:399:LEU:HD23	2.01	0.41
1:A:200:ALA:O	1:A:204:ARG:HG3	2.21	0.41
1:A:347:PHE:HB3	8:A:2853:HEM:HMD3	2.02	0.41
1:A:86:LEU:HD13	9:A:3037:HOH:O	2.21	0.41
1:A:522:ILE:O	1:A:526:ASP:HB2	2.20	0.41
1:A:9:PRO:O	1:A:11:PRO:HD3	2.20	0.40
1:A:165:PHE:CD1	1:A:165:PHE:N	2.90	0.40
1:A:402:LYS:HA	1:A:402:LYS:HD3	1.95	0.40
1:A:216:ASN:ND2	1:A:216:ASN:C	2.74	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	593/595 (100%)	557 (94%)	25 (4%)	11 (2%)	8	10

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	167	CYS
1	A	168	PRO
1	A	169	THR
1	A	173	GLN
1	A	594	GLU
1	A	242	THR
1	A	486	THR
1	A	56	ALA
1	A	172	TYR
1	A	9	PRO
1	A	166	VAL

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	517/517 (100%)	472 (91%)	45 (9%)	10	15

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	PRO
1	A	13	VAL
1	A	18	GLN
1	A	32	ARG
1	A	64	ARG
1	A	86	LEU
1	A	98	LEU
1	A	117	THR
1	A	118	GLU
1	A	119	LEU
1	A	122	SER
1	A	127	VAL
1	A	130	GLU
1	A	153	THR
1	A	172	TYR
1	A	173	GLN
1	A	175	LEU
1	A	177	ARG
1	A	187	LEU
1	A	191	LEU
1	A	216	ASN
1	A	218	GLU
1	A	228	PRO
1	A	255	ARG
1	A	261	LEU
1	A	268	LEU
1	A	276	LEU
1	A	292	LEU
1	A	329	GLN
1	A	347	PHE
1	A	360	ARG
1	A	363	GLU
1	A	376	LEU
1	A	461	PRO
1	A	464	LEU
1	A	471	LEU
1	A	480	LEU
1	A	504	ARG
1	A	520	GLN
1	A	522	ILE
1	A	523	ARG
1	A	546	LYS
1	A	564	LEU

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Mol	Chain	Res	Type
1	A	593	ARG
1	A	594	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	GLN
1	A	147	ASN
1	A	216	ASN
1	A	222	HIS
1	A	245	HIS
1	A	250	GLN
1	A	329	GLN
1	A	423	GLN
1	A	437	ASN
1	A	468	GLN
1	A	497	ASN
1	A	520	GLN
1	A	570	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

11 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	B	1	1,2	14,14,15	0.58	0	17,19,21	1.47	3 (17%)
2	NAG	B	2	2	14,14,15	0.55	0	17,19,21	1.63	2 (11%)
2	MAN	B	3	2	11,11,12	0.66	0	15,15,17	1.52	3 (20%)
2	NAG	C	1	1,2	14,14,15	0.61	0	17,19,21	0.80	0
2	NAG	C	2	2	14,14,15	0.75	1 (7%)	17,19,21	1.35	1 (5%)
2	MAN	C	3	2	11,11,12	0.58	0	15,15,17	1.03	1 (6%)
2	NAG	D	1	1,2	14,14,15	0.81	1 (7%)	17,19,21	1.43	2 (11%)
2	NAG	D	2	2	14,14,15	0.58	0	17,19,21	1.79	4 (23%)
2	MAN	D	3	2	11,11,12	0.52	0	15,15,17	1.68	2 (13%)
3	NAG	E	1	1,3	14,14,15	0.65	0	17,19,21	2.23	5 (29%)
3	NAG	E	2	3	14,14,15	0.53	0	17,19,21	0.88	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	B	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	B	2	2	-	3/6/23/26	0/1/1/1
2	MAN	B	3	2	-	2/2/19/22	0/1/1/1
2	NAG	C	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1
2	MAN	C	3	2	-	2/2/19/22	0/1/1/1
2	NAG	D	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	1/6/23/26	0/1/1/1
2	MAN	D	3	2	-	2/2/19/22	1/1/1/1
3	NAG	E	1	1,3	-	0/6/23/26	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)
2	D	1	NAG	O5-C1	-2.19	1.40	1.43
2	C	2	NAG	O5-C1	-2.08	1.40	1.43

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2	NAG	C1-O5-C5	5.28	119.34	112.19
2	D	3	MAN	C1-O5-C5	5.10	119.10	112.19
3	E	1	NAG	O5-C5-C6	5.00	115.04	107.20
3	E	1	NAG	C4-C3-C2	4.42	117.49	111.02
2	B	2	NAG	C4-C3-C2	4.12	117.06	111.02
2	C	2	NAG	C1-O5-C5	3.85	117.41	112.19
3	E	1	NAG	O5-C1-C2	-3.83	105.23	111.29
3	E	1	NAG	C1-O5-C5	-3.68	107.20	112.19
2	B	2	NAG	O5-C5-C6	3.60	112.85	107.20
2	B	3	MAN	C1-O5-C5	3.53	116.97	112.19
2	D	1	NAG	O5-C1-C2	-3.51	105.75	111.29
2	B	3	MAN	C1-C2-C3	3.33	113.76	109.67
2	B	1	NAG	C2-N2-C7	-3.27	118.25	122.90
2	B	1	NAG	O5-C1-C2	-3.11	106.38	111.29
2	D	1	NAG	C6-C5-C4	-3.03	105.91	113.00
3	E	1	NAG	C2-N2-C7	-2.57	119.25	122.90
2	D	2	NAG	C2-N2-C7	-2.41	119.47	122.90
2	D	3	MAN	C1-C2-C3	2.41	112.62	109.67
2	C	3	MAN	C1-O5-C5	2.34	115.37	112.19
2	D	2	NAG	C4-C3-C2	-2.29	107.66	111.02
2	D	2	NAG	O5-C5-C6	2.25	110.73	107.20
2	B	1	NAG	O4-C4-C5	2.20	114.76	109.30
2	B	3	MAN	O5-C1-C2	2.04	113.92	110.77

There are no chirality outliers.

All (16) torsion outliers are listed below:

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

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Mol	Chain	Res	Type	Atoms
2	B	2	NAG	O5-C5-C6-O6

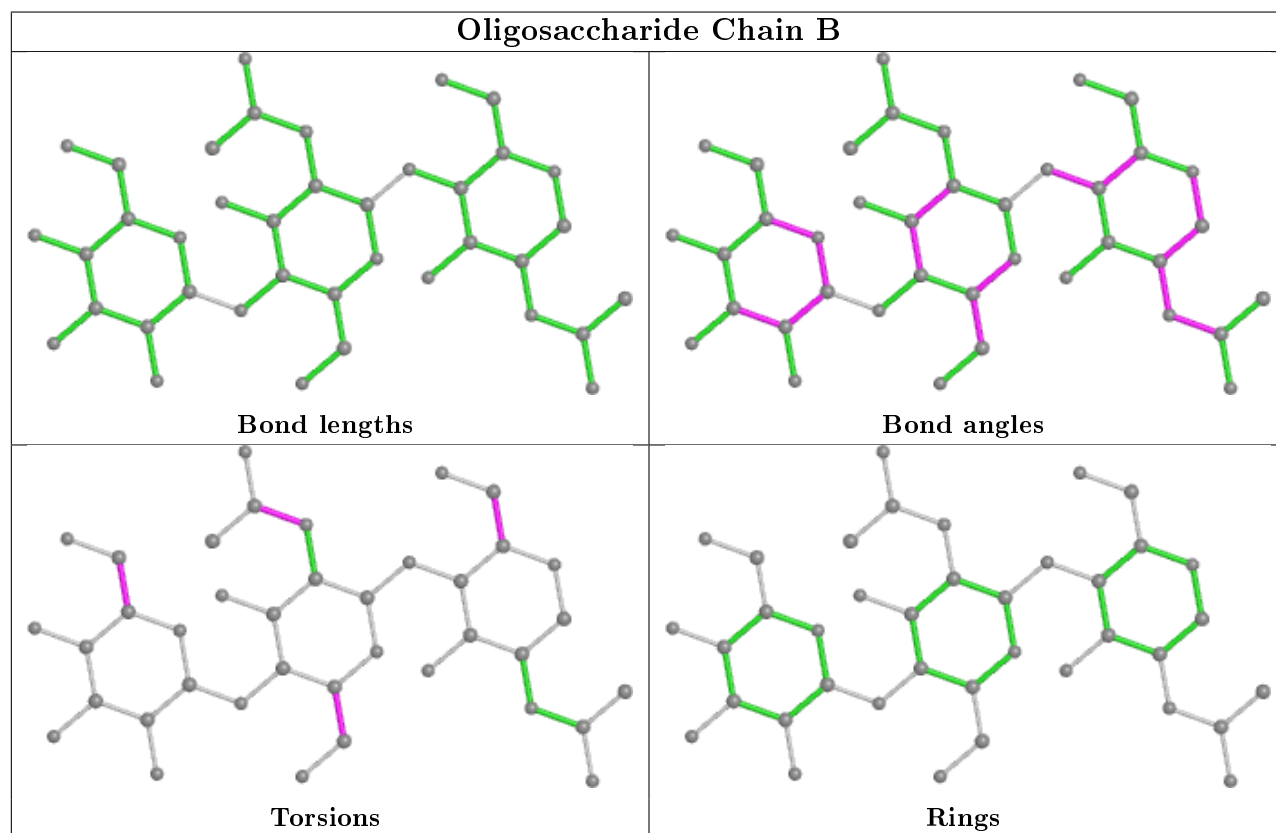
All (1) ring outliers are listed below:

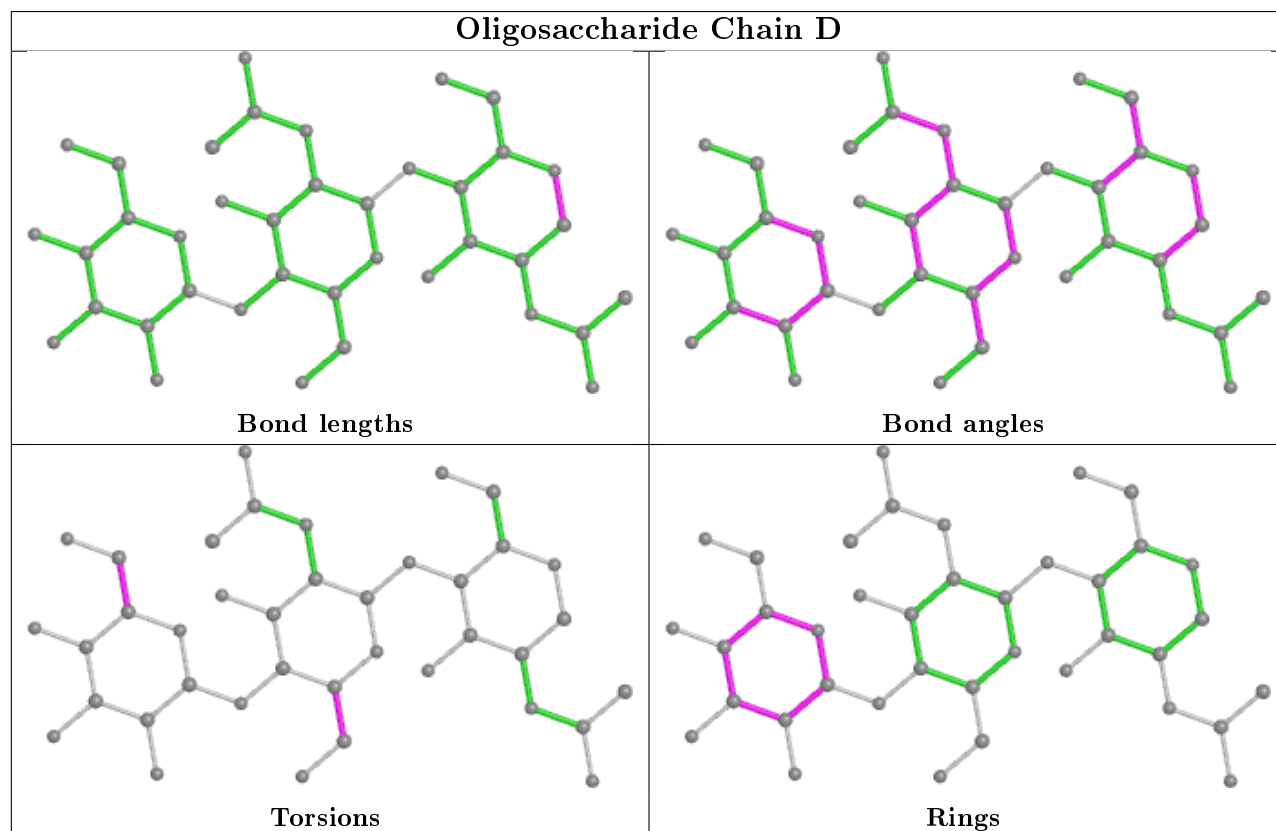
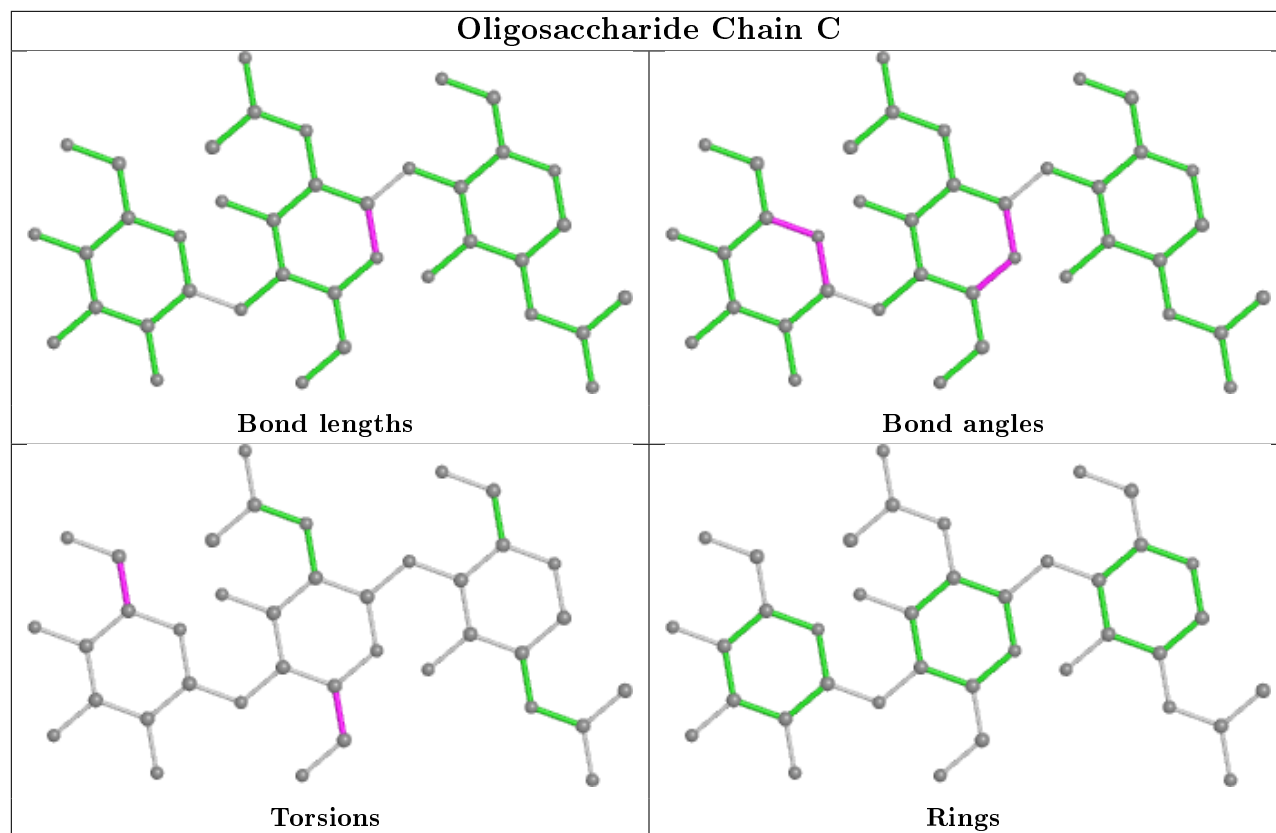
Mol	Chain	Res	Type	Atoms
2	D	3	MAN	C1-C2-C3-C4-C5-O5

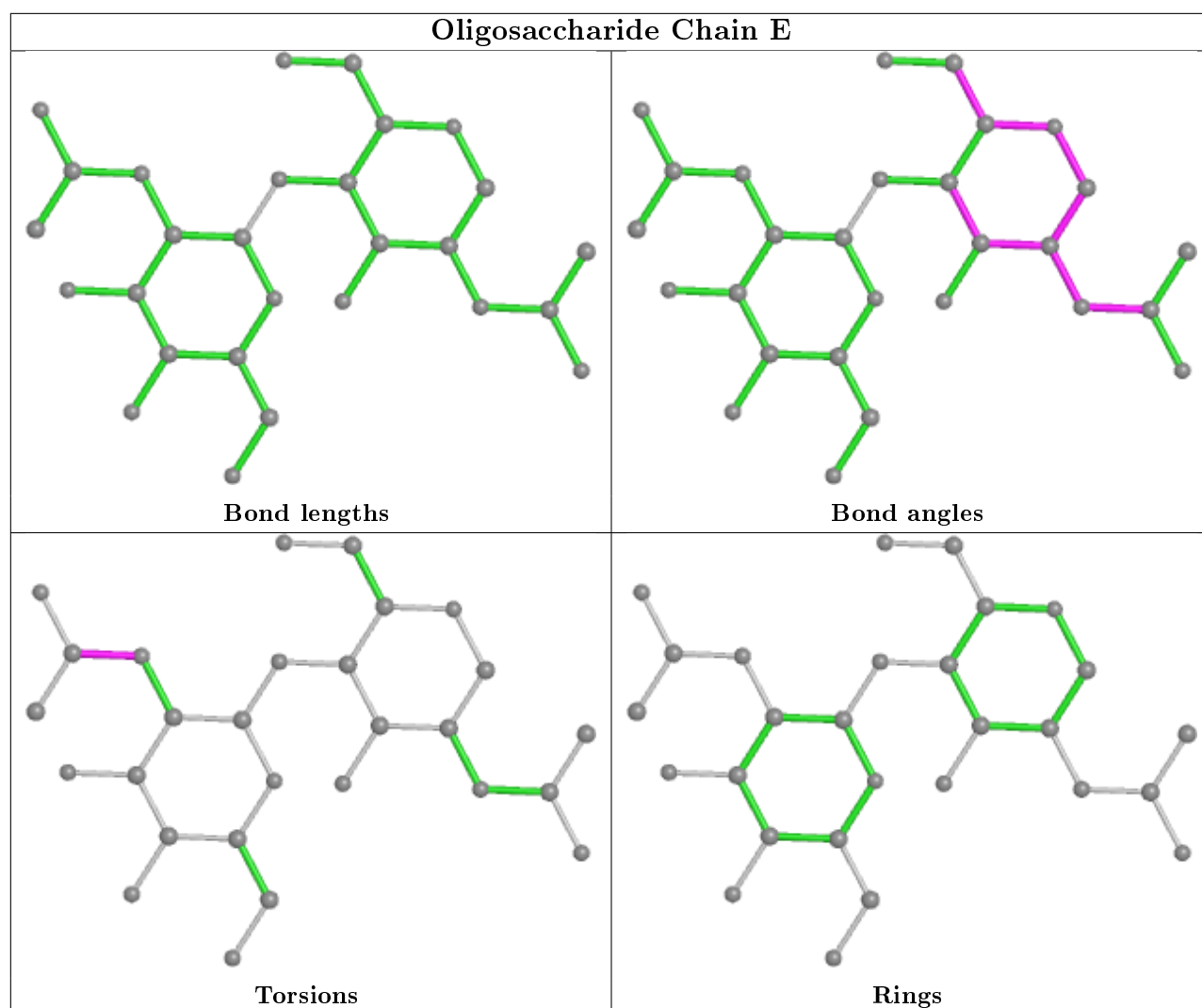
6 monomers are involved in 4 short contacts:

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







5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 9 are monoatomic - leaving 3 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	CYN	A	2844	8	0,1,1	0.00	-	-		
8	HEM	A	2853	1,5	27,50,50	2.25	7 (25%)	17,82,82	1.10	1 (5%)
6	CO3	A	688	-	0,3,3	0.00	-	0,3,3	0.00	-

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	2853	1,5	-	0/6/54/54	-

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	2853	HEM	C3C-C2C	-4.94	1.33	1.40
8	A	2853	HEM	C3D-C2D	4.78	1.51	1.37
8	A	2853	HEM	C3B-C2B	-4.12	1.34	1.40
8	A	2853	HEM	C3C-CAC	3.98	1.56	1.47
8	A	2853	HEM	C3B-CAB	3.59	1.55	1.47
8	A	2853	HEM	CAA-C2A	2.98	1.56	1.52
8	A	2853	HEM	CAD-C3D	2.06	1.55	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	2853	HEM	CBD-CAD-C3D	-2.01	108.78	112.48

There are no chirality outliers.

There are no torsion outliers.

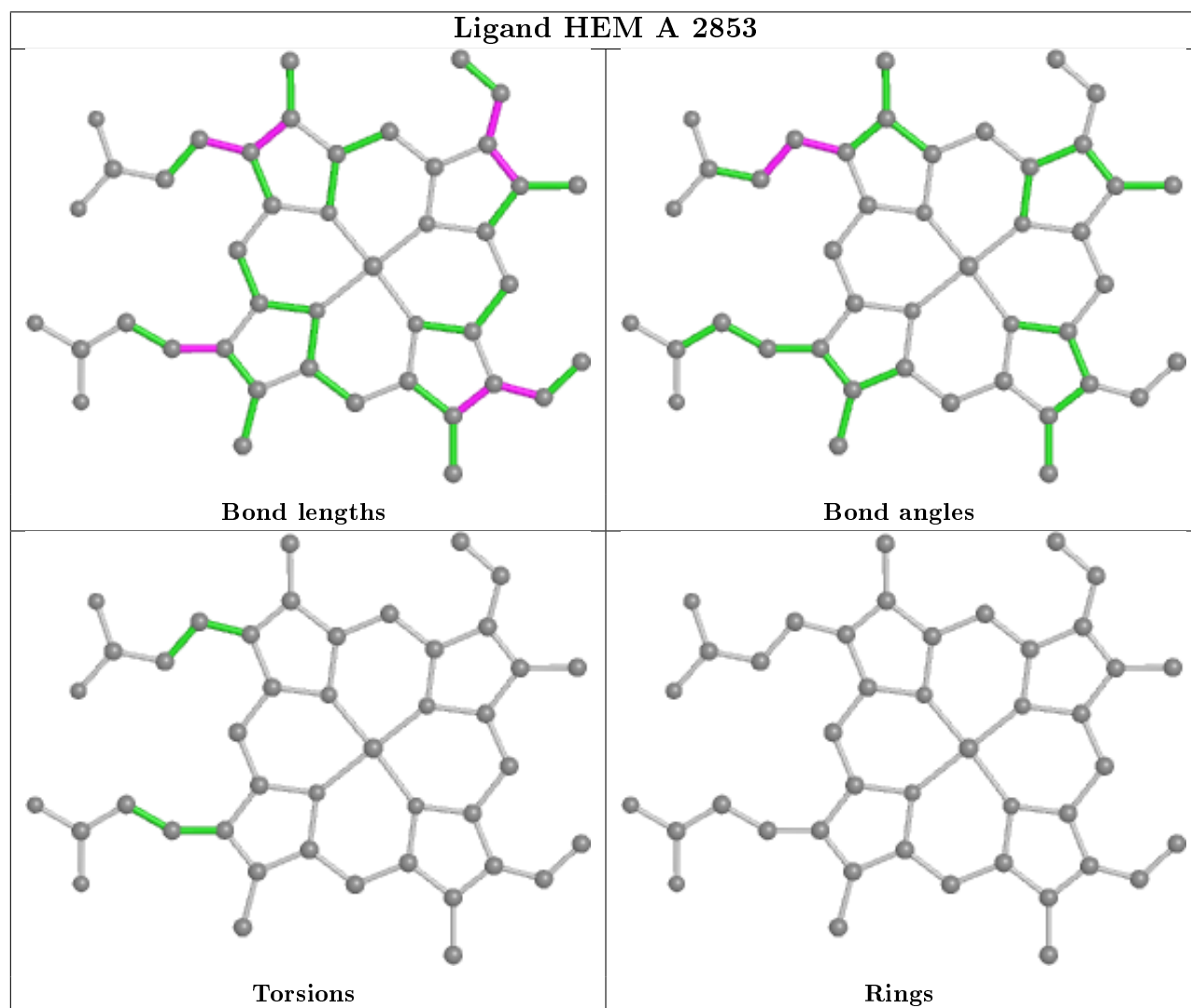
There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	2844	CYN	2	0
8	A	2853	HEM	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.