



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 19, 2023 – 05:16 AM EDT

PDB ID : 2NQX
Title : Crystal Structure of bovine lactoperoxidase with iodide ions at 2.9A resolution
Authors : Singh, A.K.; Kaur, P.; Singh, N.; Bhushan, A.; Sharma, S.; Singh, T.P.
Deposited on : 2006-11-01
Resolution : 2.95 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 types of validation reports are described at

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

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (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) : 2.36

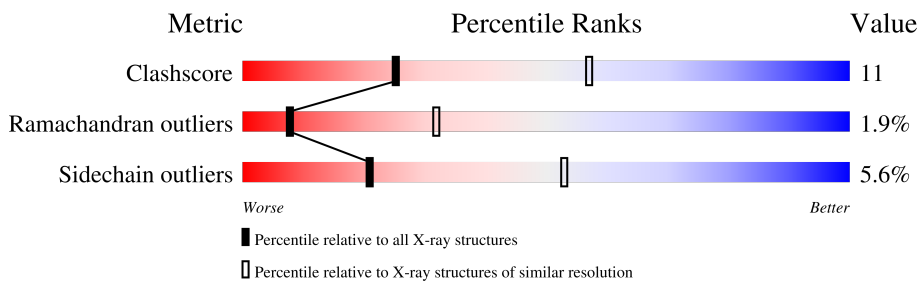
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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	3462 (3.00-2.92)
Ramachandran outliers	138981	3340 (3.00-2.92)
Sidechain outliers	138945	3343 (3.00-2.92)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	595	76% 20% ..
2	B	3	33% 67%
2	D	3	100%
3	C	2	100%
3	E	2	100%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
8	OSM	A	710	-	-	X	-

2 Entry composition i

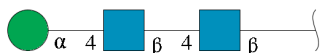
There are 9 unique types of molecules in this entry. The entry contains 5114 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	S			
1	A	595	4770	3037	847	860	26	0	0	0

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



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

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



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

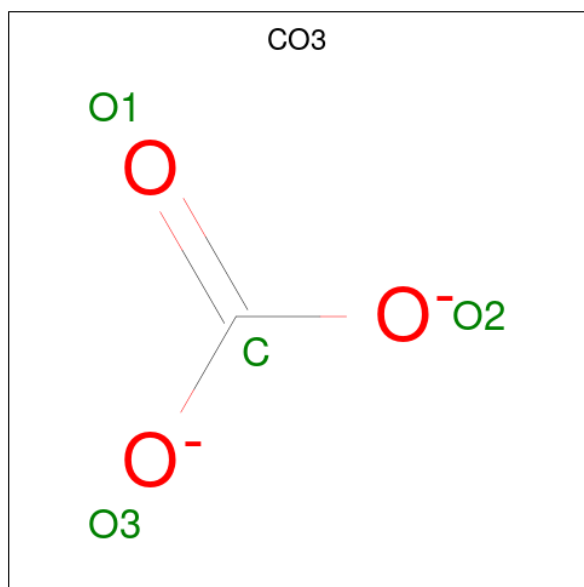
- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 5 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	7	Total I 7 7	0	0

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



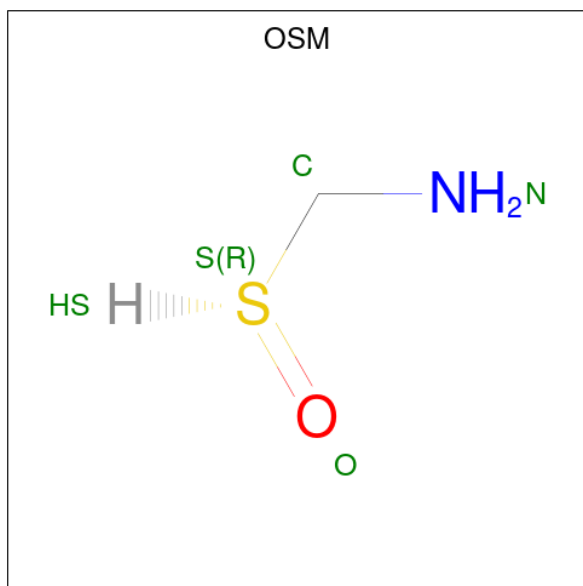
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 4 1 3	0	0

- Molecule 7 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C₃₄H₃₂FeN₄O₄).



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

- Molecule 8 is 1-(OXIDOSULFANYL)METHANAMINE (three-letter code: OSM) (formula: CH_5NOS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			S
8	A	1	4	1	1	1	1	0	0

- Molecule 9 is water.

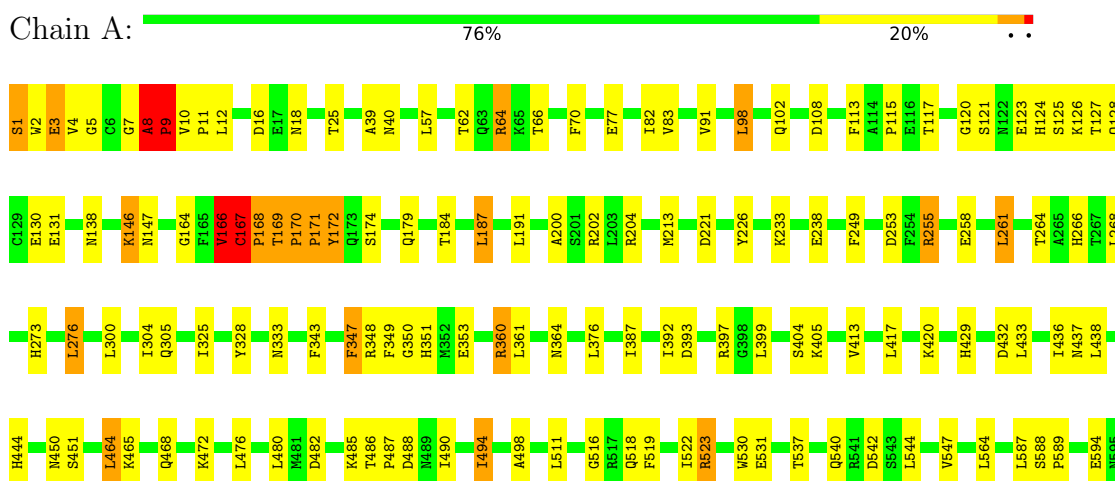
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	151	Total 151	O 151	0	0

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.

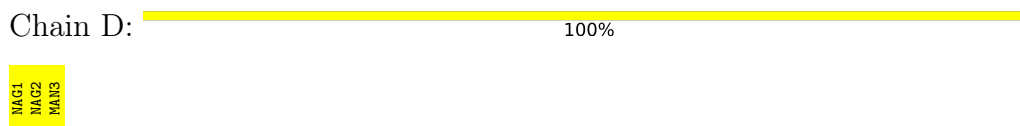
- Molecule 1: Lactoperoxidase



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



MAG1
MAG2

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

Chain E:

100%

MAG1
MAG2

4 Data and refinement statistics

Xtrriage (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	54.53Å 80.55Å 78.03Å 90.00° 103.74° 90.00°	Depositor
Resolution (Å)	25.00 – 2.95	Depositor
% Data completeness (in resolution range)	98.5 (25.00-2.95)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.17	Depositor
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.196 , 0.236	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	5114	wwPDB-VP
Average B, all atoms (Å ²)	25.0	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: HEM, MAN, CO3, OSM, NAG, CA, IOD

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	0/4898	0.67	12/6645 (0.2%)

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	1	2

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	166	VAL	CA-CB-CG2	-12.08	92.78	110.90
1	A	167	CYS	CA-CB-SG	-9.96	96.07	114.00
1	A	166	VAL	N-CA-CB	9.76	132.98	111.50
1	A	1	SER	O-C-N	-8.71	108.77	122.70
1	A	8	ALA	CB-CA-C	7.77	121.76	110.10
1	A	18	ASN	N-CA-CB	7.20	123.56	110.60
1	A	166	VAL	C-N-CA	6.79	138.69	121.70
1	A	486	THR	N-CA-CB	6.77	123.17	110.30
1	A	2	TRP	N-CA-C	6.26	127.91	111.00
1	A	138	ASN	N-CA-C	5.55	125.99	111.00
1	A	172	TYR	N-CA-C	5.40	125.58	111.00
1	A	167	CYS	CB-CA-C	-5.07	100.26	110.40

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	166	VAL	CA

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1	SER	Mainchain
1	A	166	VAL	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	4690	99	0
2	B	39	0	34	0	0
2	D	39	0	34	0	0
3	C	28	0	25	0	0
3	E	28	0	25	0	0
4	A	1	0	0	0	0
5	A	7	0	0	2	0
6	A	4	0	0	0	0
7	A	43	0	30	10	0
8	A	4	0	5	2	0
9	A	151	0	0	1	0
All	All	5114	0	4843	103	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 (103) 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:258:GLU:OE2	7:A:709:HEM:HMB3	1.68	0.94
1:A:351:HIS:HD1	1:A:437:ASN:HD21	1.20	0.88
1:A:258:GLU:HG3	8:A:710:OSM:HS	1.37	0.87
1:A:170:PRO:HB2	1:A:171:PRO:CD	2.06	0.86
1:A:487:PRO:HA	1:A:490:ILE:HD13	1.57	0.86
1:A:487:PRO:HA	1:A:490:ILE:CD1	2.04	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8:ALA:CB	1:A:9:PRO:HD2	2.08	0.84
1:A:123:GLU:OE2	1:A:125:SER:HB3	1.80	0.82
1:A:9:PRO:HG2	1:A:167:CYS:O	1.81	0.81
1:A:8:ALA:HB1	1:A:9:PRO:CD	2.14	0.78
1:A:8:ALA:O	1:A:10:VAL:HG22	1.84	0.77
1:A:167:CYS:HB2	1:A:168:PRO:HD3	1.67	0.77
1:A:8:ALA:CB	1:A:9:PRO:CD	2.65	0.75
1:A:170:PRO:CB	1:A:171:PRO:CD	2.65	0.74
7:A:709:HEM:HMB1	7:A:709:HEM:HBB2	1.68	0.74
1:A:170:PRO:CB	1:A:171:PRO:HD3	2.25	0.67
1:A:169:THR:H	1:A:170:PRO:CD	2.08	0.67
1:A:170:PRO:HB2	1:A:171:PRO:HD2	1.75	0.66
1:A:213:MET:HG2	1:A:273:HIS:CD2	2.29	0.66
1:A:258:GLU:HG3	8:A:710:OSM:S	2.35	0.66
7:A:709:HEM:HBC2	7:A:709:HEM:HMC2	1.77	0.66
1:A:253:ASP:OD2	1:A:255:ARG:HD3	1.97	0.65
1:A:544:LEU:O	1:A:547:VAL:HG22	1.98	0.64
1:A:351:HIS:HD1	1:A:437:ASN:ND2	1.95	0.63
1:A:8:ALA:HB3	1:A:9:PRO:HD2	1.79	0.63
1:A:82:ILE:HG21	1:A:494:ILE:HD11	1.83	0.60
1:A:125:SER:HA	1:A:128:GLN:HB3	1.85	0.59
1:A:108:ASP:OD2	7:A:709:HEM:HMD1	2.04	0.58
1:A:328:TYR:HD1	1:A:523:ARG:HD3	1.68	0.57
1:A:328:TYR:CD1	1:A:523:ARG:HD3	2.40	0.57
1:A:519:PHE:CD1	1:A:522:ILE:HD11	2.40	0.56
1:A:8:ALA:HB1	1:A:9:PRO:HD2	1.81	0.56
1:A:221:ASP:HB2	1:A:226:TYR:CZ	2.42	0.55
1:A:167:CYS:HB2	1:A:168:PRO:CD	2.36	0.55
1:A:249:PHE:CZ	1:A:387:ILE:HD11	2.43	0.53
1:A:8:ALA:O	1:A:9:PRO:C	2.46	0.53
1:A:258:GLU:CD	7:A:709:HEM:HMB3	2.30	0.52
1:A:5:GLY:O	1:A:7:GLY:N	2.42	0.52
1:A:464:LEU:O	1:A:468:GLN:HG3	2.09	0.52
1:A:117:THR:HG22	1:A:164:GLY:HA2	1.90	0.52
1:A:102:GLN:OE1	1:A:261:LEU:HB3	2.11	0.50
1:A:123:GLU:HG2	1:A:125:SER:H	1.76	0.50
1:A:537:THR:OG1	1:A:540:GLN:HG3	2.10	0.50
1:A:200:ALA:O	1:A:204:ARG:HG3	2.12	0.49
1:A:450:ASN:HD21	1:A:487:PRO:HB2	1.76	0.49
1:A:300:LEU:O	1:A:304:ILE:HG12	2.12	0.49
1:A:8:ALA:HB1	1:A:9:PRO:HD3	1.92	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:530:TRP:CE2	1:A:531:GLU:HG3	2.47	0.49
1:A:113:PHE:O	1:A:115:PRO:HD3	2.13	0.48
1:A:108:ASP:CG	7:A:709:HEM:HMD1	2.34	0.48
1:A:120:GLY:HA3	1:A:123:GLU:OE1	2.13	0.48
1:A:108:ASP:OD2	7:A:709:HEM:HMD2	2.14	0.47
1:A:325:ILE:HD11	1:A:516:GLY:HA2	1.96	0.47
1:A:420:LYS:HA	1:A:429:HIS:O	2.13	0.47
1:A:169:THR:N	1:A:170:PRO:CD	2.74	0.47
1:A:348:ARG:HD3	1:A:437:ASN:OD1	2.14	0.47
1:A:170:PRO:HB3	1:A:171:PRO:HD3	1.96	0.47
1:A:25:THR:O	1:A:184:THR:HG22	2.15	0.47
1:A:350:GLY:HA3	7:A:709:HEM:CBC	2.45	0.47
1:A:77:GLU:HG3	5:A:704:IOD:I	2.85	0.46
1:A:276:LEU:HD12	1:A:587:LEU:HD11	1.96	0.46
1:A:417:LEU:HD22	1:A:433:LEU:HD22	1.98	0.45
1:A:261:LEU:HD12	1:A:261:LEU:HA	1.83	0.45
1:A:9:PRO:O	1:A:10:VAL:HG13	2.16	0.45
1:A:146:LYS:O	1:A:147:ASN:HB2	2.17	0.45
1:A:124:HIS:O	1:A:128:GLN:N	2.47	0.45
1:A:123:GLU:HB3	1:A:126:LYS:HE2	1.97	0.45
1:A:127:THR:HG22	1:A:131:GLU:CG	2.47	0.44
1:A:233:LYS:HE2	1:A:238:GLU:OE1	2.17	0.44
7:A:709:HEM:HBC2	7:A:709:HEM:CMC	2.47	0.44
1:A:450:ASN:ND2	1:A:488:ASP:OD1	2.47	0.44
1:A:98:LEU:HD13	1:A:399:LEU:HD23	2.00	0.44
1:A:62:THR:HG22	1:A:64:ARG:HG3	2.01	0.43
1:A:530:TRP:HZ2	5:A:707:IOD:I	2.70	0.43
1:A:39:ALA:O	1:A:40:ASN:HB2	2.18	0.43
1:A:364:ASN:HD22	1:A:364:ASN:N	2.15	0.43
7:A:709:HEM:HMB1	7:A:709:HEM:CBB	2.43	0.43
1:A:66:THR:HB	1:A:70:PHE:O	2.19	0.43
1:A:83:VAL:HG12	1:A:413:VAL:HB	2.00	0.43
1:A:393:ASP:O	1:A:397:ARG:HG3	2.19	0.43
1:A:476:LEU:HD21	1:A:498:ALA:HB1	2.00	0.43
1:A:120:GLY:CA	1:A:123:GLU:OE1	2.67	0.43
1:A:187:LEU:HB3	1:A:305:GLN:HG2	2.01	0.42
1:A:465:LYS:HE3	9:A:736:HOH:O	2.18	0.42
1:A:179:GLN:HG2	1:A:444:HIS:NE2	2.34	0.42
1:A:169:THR:H	1:A:170:PRO:HD2	1.83	0.42
1:A:3:GLU:C	1:A:4:VAL:CG2	2.88	0.42
1:A:360:ARG:O	1:A:361:LEU:HD23	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:464:LEU:HD22	1:A:468:GLN:OE1	2.20	0.42
1:A:168:PRO:HG2	1:A:172:TYR:CG	2.55	0.41
1:A:10:VAL:HA	1:A:11:PRO:HD3	1.90	0.41
1:A:468:GLN:O	1:A:472:LYS:N	2.54	0.41
1:A:438:LEU:HD21	1:A:494:ILE:HB	2.02	0.41
1:A:482:ASP:O	1:A:485:LYS:NZ	2.53	0.41
1:A:264:THR:HG23	1:A:392:ILE:HB	2.03	0.41
1:A:187:LEU:HD13	1:A:305:GLN:HA	2.02	0.41
1:A:432:ASP:O	1:A:436:ILE:HG12	2.20	0.41
1:A:347:PHE:C	1:A:349:PHE:H	2.24	0.40
1:A:353:GLU:HA	1:A:405:LYS:O	2.21	0.40
1:A:191:LEU:O	1:A:266:HIS:HE1	2.04	0.40
1:A:249:PHE:HZ	1:A:387:ILE:HD11	1.86	0.40
1:A:343:PHE:CD1	1:A:518:GLN:HG2	2.57	0.40
1:A:588:SER:OG	1:A:589:PRO:HD3	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	593/595 (100%)	543 (92%)	39 (7%)	11 (2%)	8 32

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	8	ALA
1	A	9	PRO
1	A	12	LEU
1	A	169	THR
1	A	174	SER
1	A	3	GLU

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Mol	Chain	Res	Type
1	A	166	VAL
1	A	170	PRO
1	A	171	PRO
1	A	168	PRO
1	A	167	CYS

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	518/518 (100%)	489 (94%)	29 (6%)	21 53

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	PRO
1	A	16	ASP
1	A	57	LEU
1	A	64	ARG
1	A	91	VAL
1	A	98	LEU
1	A	121	SER
1	A	130	GLU
1	A	146	LYS
1	A	187	LEU
1	A	202	ARG
1	A	255	ARG
1	A	261	LEU
1	A	268	LEU
1	A	276	LEU
1	A	333	ASN
1	A	347	PHE
1	A	360	ARG
1	A	376	LEU
1	A	404	SER
1	A	451	SER

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Mol	Chain	Res	Type
1	A	464	LEU
1	A	480	LEU
1	A	494	ILE
1	A	511	LEU
1	A	523	ARG
1	A	542	ASP
1	A	564	LEU
1	A	594	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	109	HIS
1	A	122	ASN
1	A	147	ASN
1	A	266	HIS
1	A	333	ASN
1	A	364	ASN
1	A	423	GLN
1	A	497	ASN
1	A	520	GLN
1	A	545	GLN
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](#)

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

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	0.52	0	17,19,21	0.85	0
2	NAG	B	2	2	14,14,15	0.61	0	17,19,21	1.41	2 (11%)
2	MAN	B	3	2	11,11,12	0.58	0	15,15,17	1.16	2 (13%)
3	NAG	C	1	3,1	14,14,15	0.52	0	17,19,21	0.81	1 (5%)
3	NAG	C	2	3	14,14,15	0.63	0	17,19,21	1.09	2 (11%)
2	NAG	D	1	2,1	14,14,15	0.48	0	17,19,21	0.90	1 (5%)
2	NAG	D	2	2	14,14,15	0.43	0	17,19,21	2.07	2 (11%)
2	MAN	D	3	2	11,11,12	0.58	0	15,15,17	1.18	2 (13%)
3	NAG	E	1	3,1	14,14,15	0.54	0	17,19,21	1.04	2 (11%)
3	NAG	E	2	3	14,14,15	0.52	0	17,19,21	0.89	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	B	2	2	-	0/6/23/26	0/1/1/1
2	MAN	B	3	2	-	2/2/19/22	0/1/1/1
3	NAG	C	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	0/6/23/26	0/1/1/1
2	NAG	D	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
2	MAN	D	3	2	-	0/2/19/22	0/1/1/1
3	NAG	E	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2	NAG	C1-O5-C5	7.30	122.09	112.19
2	B	2	NAG	C4-C3-C2	4.26	117.26	111.02
2	B	3	MAN	C1-O5-C5	3.04	116.32	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	1	NAG	C4-C3-C2	2.79	115.11	111.02
2	D	3	MAN	O5-C5-C6	2.64	111.35	107.20
2	D	3	MAN	C1-O5-C5	2.61	115.73	112.19
3	C	2	NAG	C4-C3-C2	2.55	114.75	111.02
2	D	2	NAG	O5-C5-C4	2.27	116.35	110.83
3	C	2	NAG	C3-C4-C5	2.25	114.25	110.24
2	B	3	MAN	O5-C5-C6	2.25	110.73	107.20
3	E	2	NAG	C4-C3-C2	2.24	114.30	111.02
3	C	1	NAG	C4-C3-C2	2.21	114.26	111.02
3	E	1	NAG	O5-C5-C6	2.14	110.56	107.20
2	D	1	NAG	C4-C3-C2	2.11	114.11	111.02
2	B	2	NAG	O5-C5-C6	2.02	110.37	107.20

There are no chirality outliers.

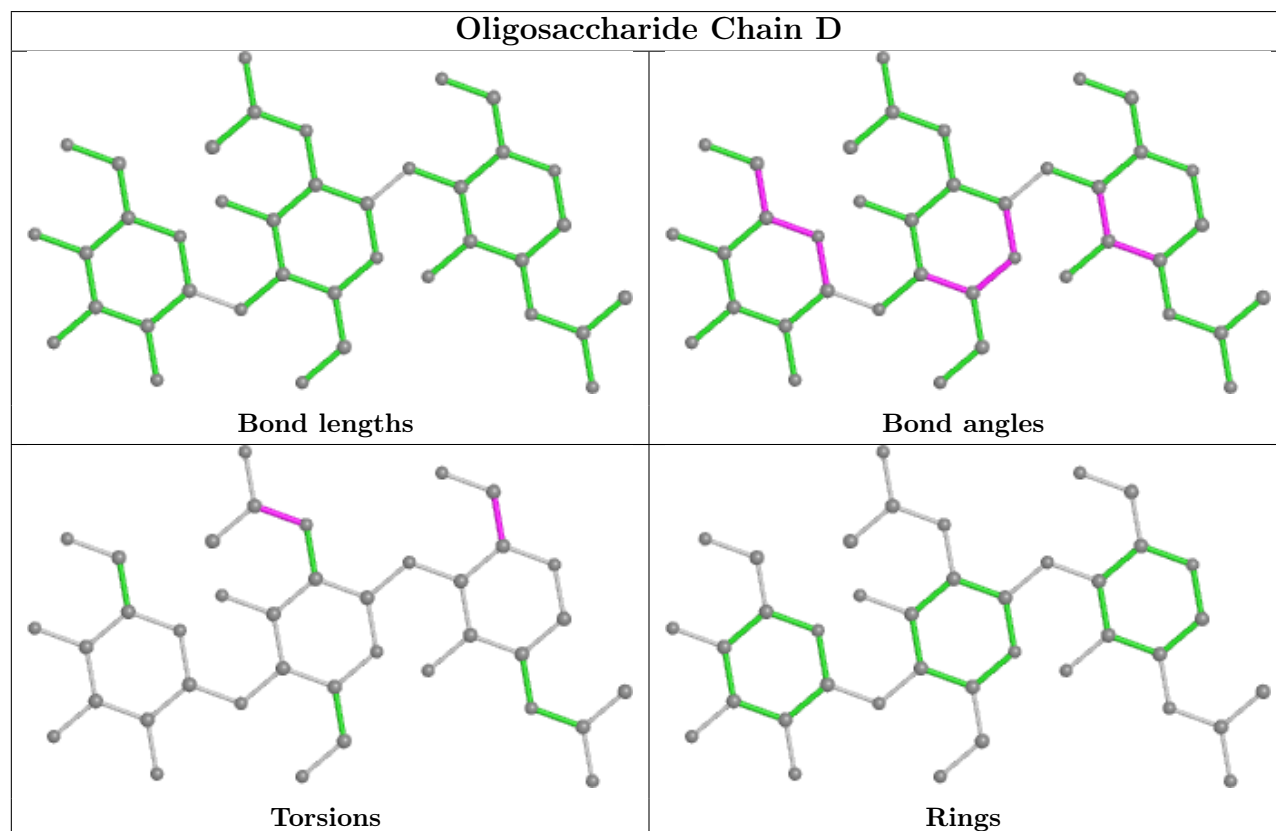
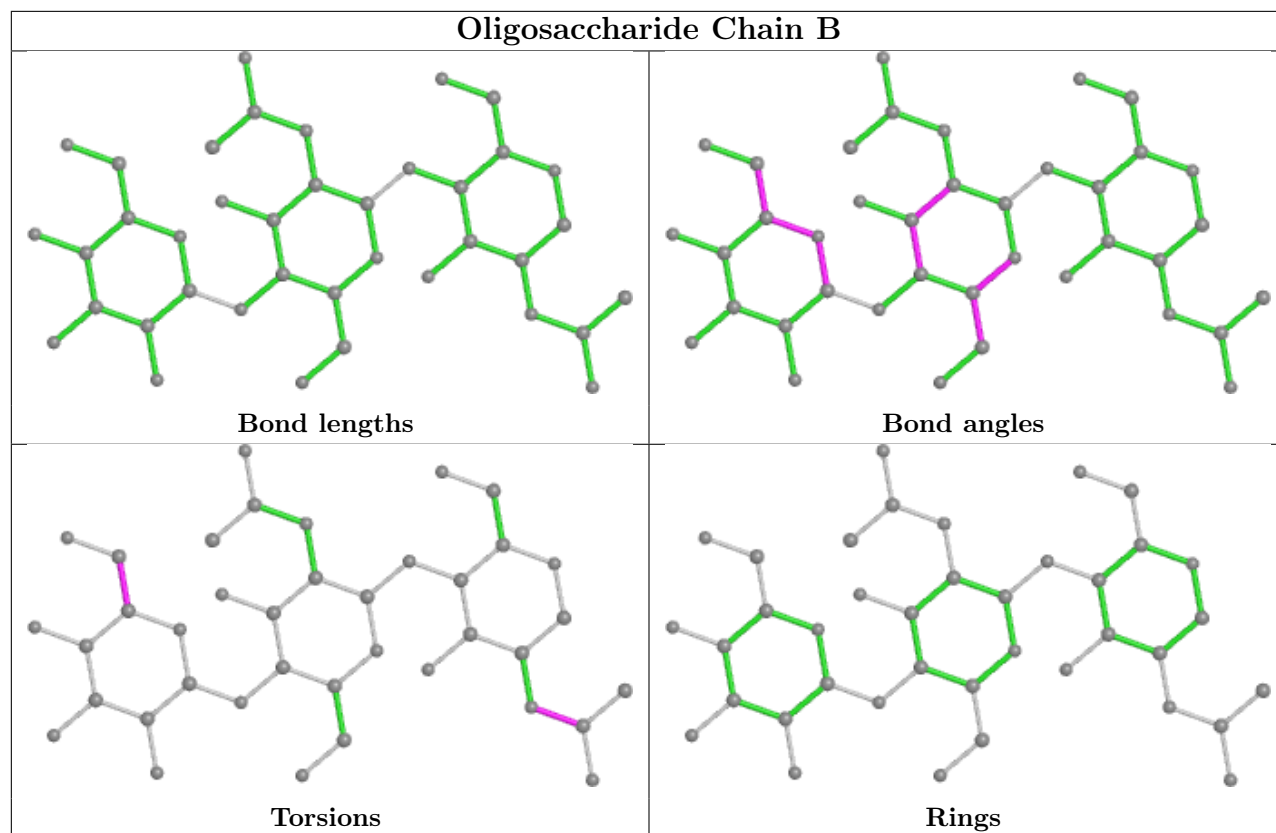
All (14) torsion outliers are listed below:

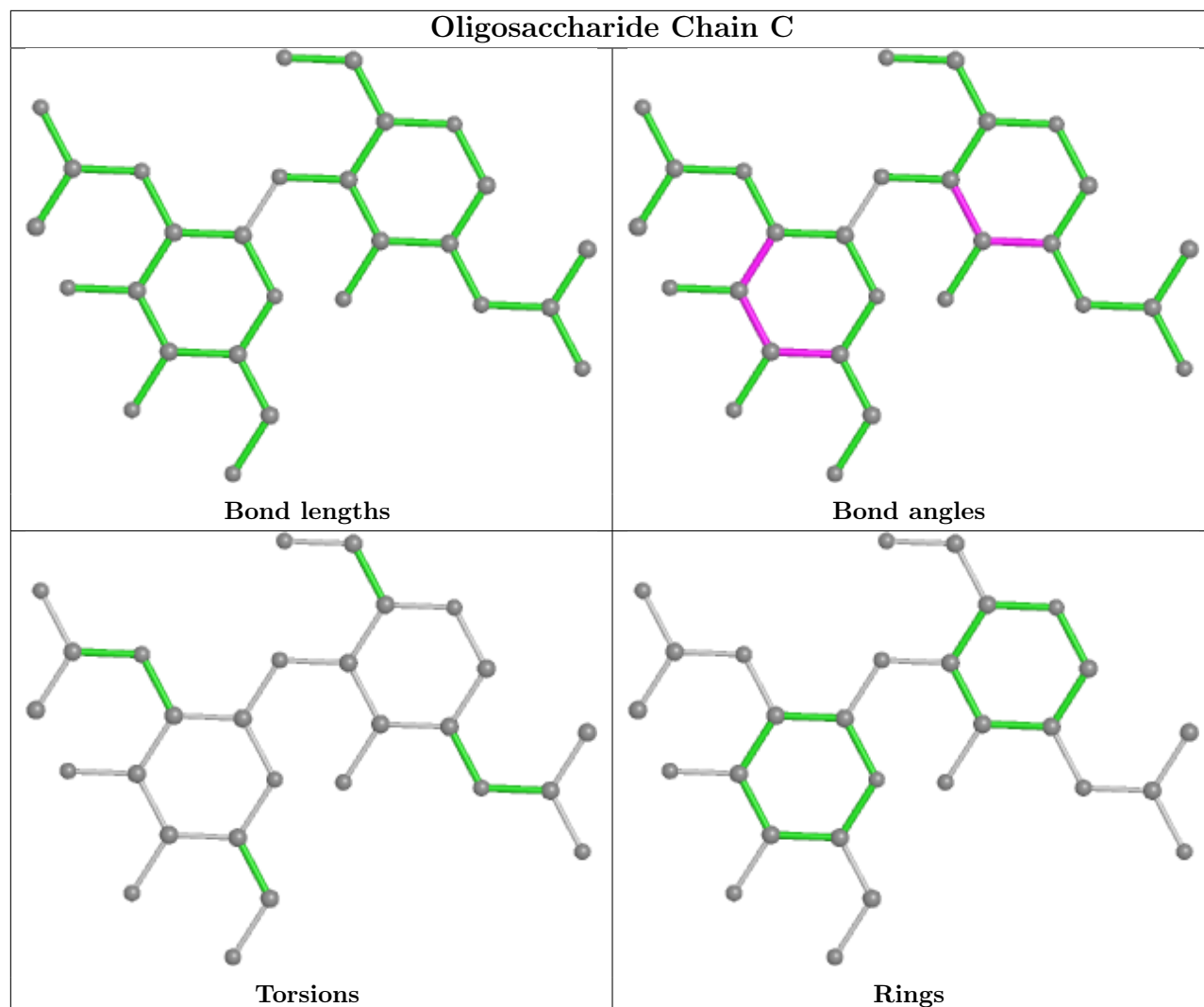
Mol	Chain	Res	Type	Atoms
3	E	1	NAG	C8-C7-N2-C2
3	E	1	NAG	O7-C7-N2-C2
3	E	2	NAG	C8-C7-N2-C2
3	E	2	NAG	O7-C7-N2-C2
2	D	1	NAG	O5-C5-C6-O6
2	B	1	NAG	C8-C7-N2-C2
2	D	2	NAG	C8-C7-N2-C2
2	D	2	NAG	O7-C7-N2-C2
2	B	3	MAN	O5-C5-C6-O6
2	D	1	NAG	C4-C5-C6-O6
2	B	1	NAG	O7-C7-N2-C2
2	B	3	MAN	C4-C5-C6-O6
3	E	2	NAG	C4-C5-C6-O6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

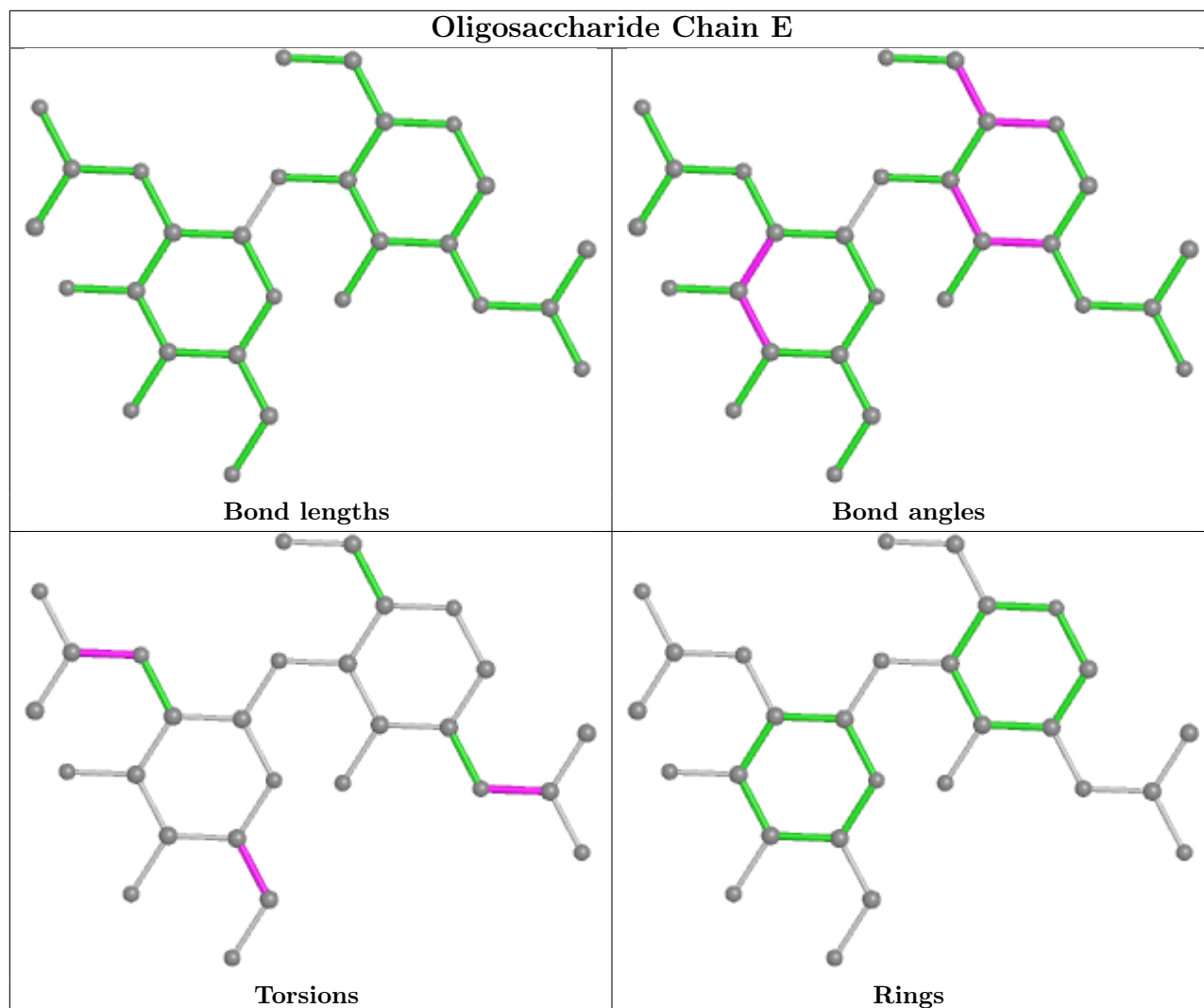
There are no ring outliers.

No monomer is involved in short contacts.

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 11 ligands modelled in this entry, 8 are monoatomic - leaving 3 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
7	HEM	A	709	1	41,50,50	1.99	7 (17%)	45,82,82	1.75	9 (20%)
6	CO3	A	688	-	2,3,3	0.41	0	2,3,3	0.23	0
8	OSM	A	710	-	1,3,3	0.02	0	0,2,2	-	-

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	HEM	A	709	1	-	2/12/54/54	-
8	OSM	A	710	-	-	0/0/1/1	-

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	709	HEM	C3D-C2D	7.68	1.53	1.36
7	A	709	HEM	C3C-CAC	4.15	1.56	1.47
7	A	709	HEM	C3C-C2C	-3.26	1.35	1.40
7	A	709	HEM	CAB-C3B	3.14	1.56	1.47
7	A	709	HEM	FE-NB	2.81	2.10	1.96
7	A	709	HEM	CAA-C2A	2.45	1.55	1.52
7	A	709	HEM	FE-ND	2.20	2.07	1.96

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	709	HEM	C4D-ND-C1D	6.31	111.59	105.07
7	A	709	HEM	C4C-CHD-C1D	3.86	127.65	122.56
7	A	709	HEM	C4B-CHC-C1C	3.67	127.40	122.56
7	A	709	HEM	C1B-NB-C4B	2.83	107.99	105.07
7	A	709	HEM	CAD-C3D-C4D	2.61	129.21	124.66
7	A	709	HEM	C3B-C2B-C1B	2.34	108.22	106.49
7	A	709	HEM	C2B-C1B-NB	-2.08	107.38	109.84
7	A	709	HEM	CMC-C2C-C3C	2.06	128.53	124.68
7	A	709	HEM	CMD-C2D-C1D	2.01	128.09	125.04

There are no chirality outliers.

All (2) torsion outliers are listed below:

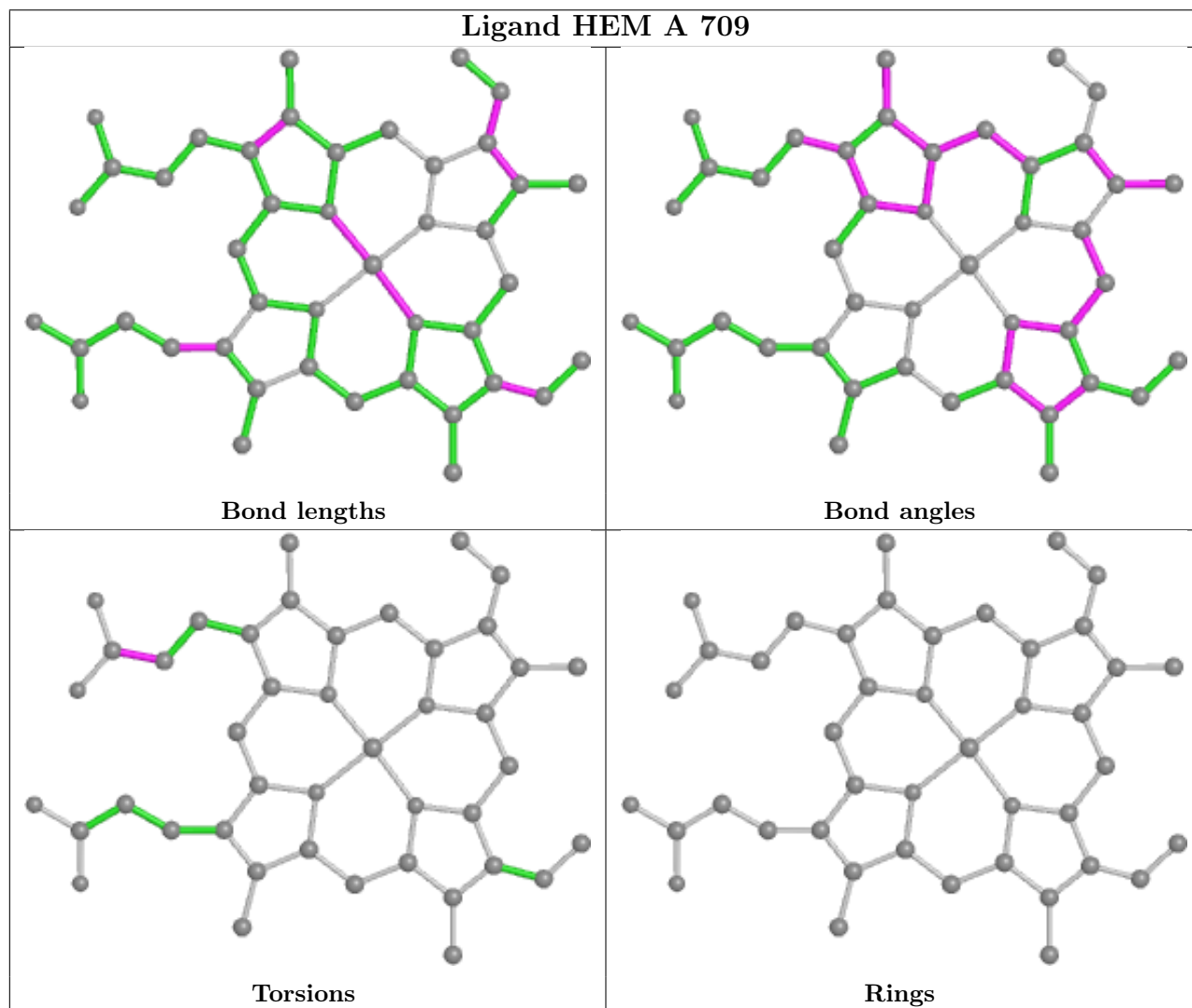
Mol	Chain	Res	Type	Atoms
7	A	709	HEM	CAD-CBD-CGD-O2D
7	A	709	HEM	CAD-CBD-CGD-O1D

There are no ring outliers.

2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	709	HEM	10	0
8	A	710	OSM	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 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.