



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 04:40 PM JST

PDB ID : 6L9T / pdb_00006l9t
Title : Crystal structure of the complex of bovine lactoperoxidase with OSCN at 1.89 Å resolution
Authors : Singh, P.K.; Viswanathan, V.; Pandey, N.; Singh, A.; Sinha, M.; Singh, R.P.; Kaur, P.; Sharma, S.; Singh, T.P.
Deposited on : 2019-11-11
Resolution : 1.89 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	:	4-5-2 with Phenix2.0
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

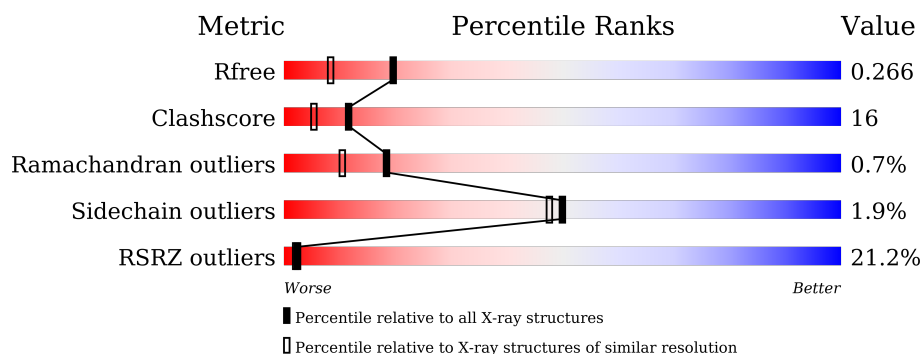
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.89 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	21% 77% 21% .
2	AeA	2	50% 50%
2	AhA	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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	IOD	A	618	-	-	X	-
7	IOD	A	620	-	-	X	-
7	IOD	A	621	-	-	X	-
7	IOD	A	623	-	-	X	-
7	IOD	A	624	-	-	X	-
9	OSM	A	634	-	-	X	-

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 5511 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
			4770	3037	847	860	26			

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



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

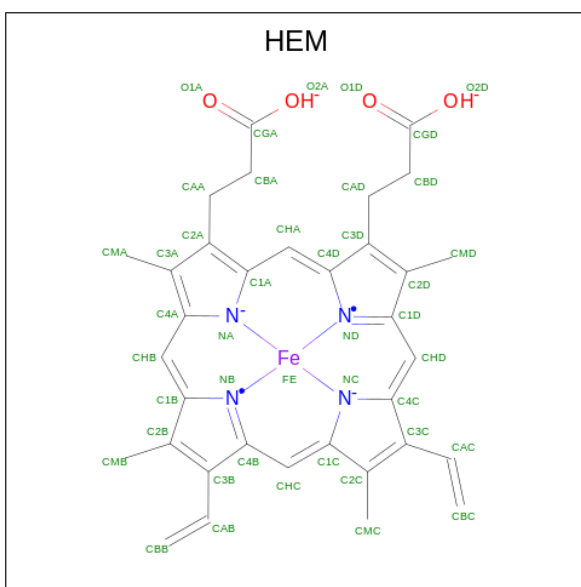
- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

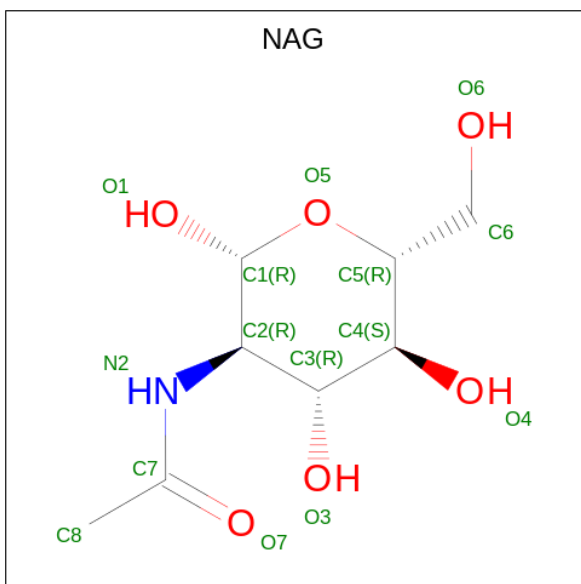
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	0	0
			1	1		

- Molecule 5 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: C₃₄H₃₂FeN₄O₄) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $\text{C}_8\text{H}_{15}\text{NO}_6$) (labeled as "Ligand of Interest" by depositor).

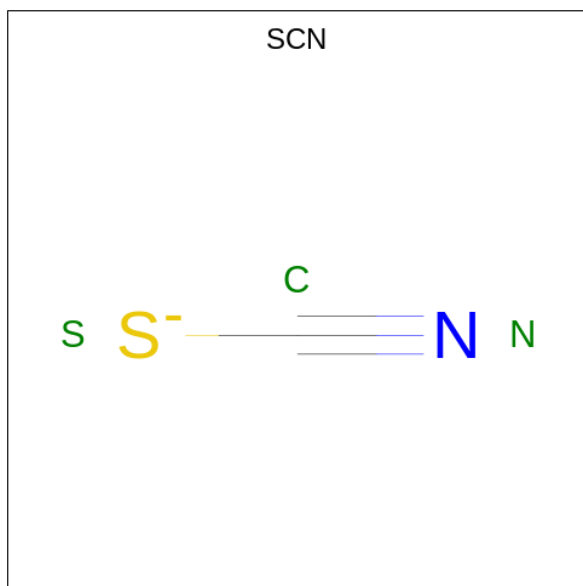


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total 14	C 8	N 1	O 5	0	0
6	A	1	Total 14	C 8	N 1	O 5	0	0

- Molecule 7 is IODIDE ION (CCD ID: IOD) (formula: I).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	19	Total I 19 19	0	0

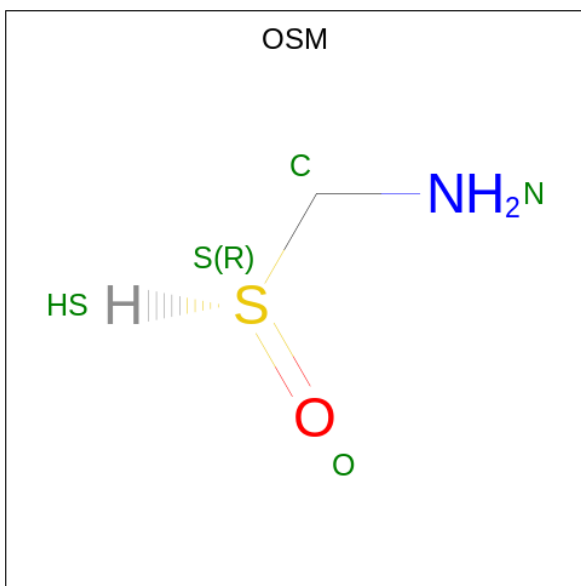
- Molecule 8 is THIOCYANATE ION (CCD ID: SCN) (formula: CNS).



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

- Molecule 9 is 1-(OXIDOSULFANYL)METHANAMINE (CCD ID: OSM) (formula:

CH₅NOS) (labeled as "Ligand of Interest" by depositor).



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

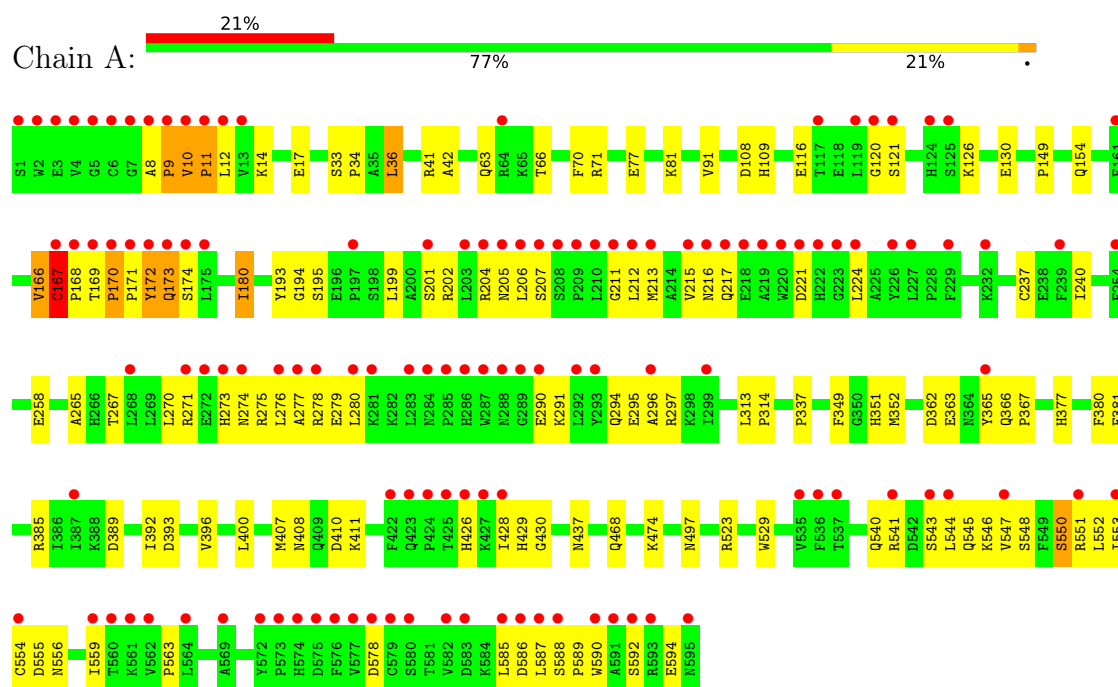
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	562	Total	O	0	0
			562	562		

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



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	53.99Å 79.93Å 76.31Å 90.00° 102.18° 90.00°	Depositor
Resolution (Å)	35.33 – 1.89 35.33 – 1.89	Depositor EDS
% Data completeness (in resolution range)	99.9 (35.33-1.89) 99.9 (35.33-1.89)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.49 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.205 , 0.264 0.211 , 0.266	Depositor DCC
R_{free} test set	2580 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	21.5	Xtriage
Anisotropy	0.788	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 56.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5511	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.18% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: IOD, OSM, SCN, HEM, NAG, CA, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.06	1/4898 (0.0%)	1.38	11/6645 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	205	ASN	C-O	5.07	1.30	1.23

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	167	CYS	CA-C-N	9.36	131.54	119.84
1	A	167	CYS	C-N-CA	9.36	131.54	119.84
1	A	10	VAL	CA-C-N	8.65	130.66	119.84
1	A	10	VAL	C-N-CA	8.65	130.66	119.84
1	A	194	GLY	CA-C-O	-8.04	115.78	122.29
1	A	9	PRO	CA-C-N	6.56	134.27	122.13
1	A	9	PRO	C-N-CA	6.56	134.27	122.13
1	A	408	ASN	CB-CA-C	5.80	119.66	109.80
1	A	265	ALA	CA-C-N	5.43	127.55	120.28
1	A	265	ALA	C-N-CA	5.43	127.55	120.28
1	A	166	VAL	O-C-N	5.14	128.91	122.59

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	4770	0	4688	136	0
2	AeA	28	0	25	1	0
2	AhA	28	0	25	0	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
5	A	43	0	30	18	0
6	A	28	0	26	1	0
7	A	19	0	0	16	0
8	A	27	0	0	3	0
9	A	4	0	5	16	0
10	A	562	0	0	33	0
All	All	5511	0	4799	155	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 16.

All (155) 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:108:ASP:OD2	5:A:603:HEM:CMD	1.68	1.37
1:A:258:GLU:OE2	5:A:603:HEM:CMB	1.73	1.34
5:A:603:HEM:HBD2	9:A:634:OSM:HN2	1.12	1.10
1:A:170:PRO:HB2	1:A:171:PRO:HD3	1.32	1.09
1:A:170:PRO:HG2	1:A:171:PRO:HD2	1.31	1.09
1:A:216:ASN:HA	8:A:625:SCN:S	1.93	1.08
1:A:167:CYS:HB2	1:A:168:PRO:HD3	1.23	1.07
9:A:634:OSM:H1	10:A:884:HOH:O	1.55	1.06
1:A:170:PRO:HB2	1:A:171:PRO:CD	1.87	1.04
1:A:167:CYS:CB	1:A:168:PRO:HD3	1.85	1.02
1:A:429:HIS:O	7:A:621:IOD:I	2.48	1.02
7:A:619:IOD:I	10:A:748:HOH:O	2.46	1.02
1:A:258:GLU:OE2	5:A:603:HEM:HMB1	0.84	1.01
1:A:130:GLU:OE1	1:A:426:HIS:ND1	1.94	1.01
1:A:108:ASP:CG	5:A:603:HEM:HMD1	1.87	0.99
1:A:410:ASP:OD1	10:A:701:HOH:O	1.81	0.98
1:A:109:HIS:NE2	9:A:634:OSM:S	2.03	0.96
1:A:108:ASP:OD2	5:A:603:HEM:HMD1	0.77	0.94
1:A:173:GLN:NE2	10:A:703:HOH:O	1.99	0.94
1:A:109:HIS:CE1	9:A:634:OSM:HS	1.85	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:LEU:HD12	1:A:337:PRO:HD2	1.49	0.93
1:A:258:GLU:CD	5:A:603:HEM:HMB1	1.94	0.92
1:A:170:PRO:CG	1:A:171:PRO:HD2	2.01	0.89
1:A:170:PRO:CB	1:A:171:PRO:CD	2.50	0.87
1:A:195:SER:O	10:A:702:HOH:O	1.92	0.86
9:A:634:OSM:C	10:A:884:HOH:O	2.16	0.86
5:A:603:HEM:CBD	9:A:634:OSM:HN2	1.86	0.86
5:A:603:HEM:HBD2	9:A:634:OSM:N	1.91	0.85
1:A:63:GLN:O	1:A:71:ARG:NH1	2.09	0.83
1:A:207:SER:HA	10:A:992:HOH:O	1.78	0.83
5:A:603:HEM:CHA	9:A:634:OSM:H2	2.08	0.83
1:A:224:LEU:HD13	1:A:271:ARG:NH1	1.94	0.82
1:A:351:HIS:HD1	1:A:437:ASN:HD21	1.25	0.82
1:A:559:ILE:HA	8:A:627:SCN:S	2.20	0.80
7:A:620:IOD:I	10:A:1117:HOH:O	2.69	0.79
1:A:550:SER:OG	1:A:563:PRO:O	2.00	0.79
1:A:8:ALA:H	1:A:9:PRO:HD3	1.46	0.79
1:A:10:VAL:HG23	1:A:41:ARG:NH2	1.99	0.78
1:A:168:PRO:HG2	1:A:172:TYR:HB2	1.64	0.78
8:A:633:SCN:S	9:A:634:OSM:S	2.83	0.77
1:A:167:CYS:HB2	1:A:168:PRO:CD	2.12	0.76
1:A:12:LEU:HB2	1:A:14:LYS:HE2	1.69	0.74
6:A:605:NAG:O4	10:A:704:HOH:O	2.06	0.73
1:A:221:ASP:HB3	1:A:224:LEU:HB2	1.70	0.73
1:A:167:CYS:CB	1:A:168:PRO:CD	2.68	0.71
1:A:377:HIS:NE2	7:A:618:IOD:I	2.93	0.71
5:A:603:HEM:C1A	9:A:634:OSM:H2	2.27	0.70
1:A:204:ARG:O	10:A:706:HOH:O	2.10	0.70
1:A:108:ASP:CG	5:A:603:HEM:CMD	2.57	0.70
1:A:199:LEU:HA	7:A:624:IOD:I	2.63	0.69
1:A:290:GLU:OE2	10:A:705:HOH:O	2.10	0.69
1:A:578:ASP:OD1	10:A:708:HOH:O	2.12	0.68
1:A:294:GLN:OE1	10:A:707:HOH:O	2.12	0.66
1:A:116:GLU:O	10:A:709:HOH:O	2.13	0.66
1:A:8:ALA:N	1:A:9:PRO:CD	2.58	0.66
7:A:615:IOD:I	10:A:1167:HOH:O	2.84	0.66
1:A:291:LYS:CD	10:A:886:HOH:O	2.43	0.65
1:A:586:ASP:N	10:A:716:HOH:O	2.26	0.65
1:A:362:ASP:O	1:A:365:TYR:N	2.28	0.64
1:A:237:CYS:O	10:A:710:HOH:O	2.14	0.64
1:A:541:ARG:O	1:A:545:GLN:HB2	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:258:GLU:CD	5:A:603:HEM:CMB	2.60	0.64
7:A:617:IOD:I	10:A:862:HOH:O	2.85	0.64
1:A:540:GLN:O	1:A:544:LEU:N	2.28	0.64
1:A:8:ALA:H	1:A:9:PRO:CD	2.10	0.63
5:A:603:HEM:HMC1	5:A:603:HEM:HBC2	1.81	0.63
1:A:224:LEU:HD13	1:A:271:ARG:HH11	1.64	0.63
7:A:623:IOD:I	9:A:634:OSM:C	3.18	0.62
1:A:170:PRO:CB	1:A:171:PRO:HD2	2.26	0.62
1:A:206:LEU:O	10:A:711:HOH:O	2.16	0.61
1:A:548:SER:OG	1:A:551:ARG:CB	2.49	0.61
1:A:548:SER:OG	1:A:551:ARG:N	2.30	0.61
1:A:36:LEU:CD1	1:A:337:PRO:HD2	2.26	0.61
1:A:17:GLU:OE2	10:A:712:HOH:O	2.17	0.60
1:A:224:LEU:CD1	1:A:271:ARG:NH1	2.65	0.60
1:A:36:LEU:HD12	1:A:337:PRO:CD	2.28	0.60
1:A:291:LYS:HD2	10:A:886:HOH:O	2.01	0.59
1:A:548:SER:HG	1:A:551:ARG:H	1.50	0.58
1:A:363:GLU:HA	7:A:611:IOD:I	2.73	0.58
1:A:169:THR:OG1	1:A:170:PRO:HD3	2.04	0.58
1:A:237:CYS:HA	1:A:381:PHE:O	2.03	0.58
1:A:213:MET:HG2	1:A:273:HIS:CD2	2.40	0.56
1:A:551:ARG:NH2	1:A:555:ASP:OD1	2.41	0.54
1:A:377:HIS:CD2	7:A:618:IOD:I	3.32	0.53
1:A:170:PRO:CG	1:A:171:PRO:CD	2.77	0.53
1:A:212:LEU:HD13	10:A:1210:HOH:O	2.07	0.53
1:A:468:GLN:HG2	1:A:474:LYS:HA	1.90	0.53
5:A:603:HEM:C4D	9:A:634:OSM:H2	2.44	0.53
1:A:149:PRO:HB2	7:A:620:IOD:I	2.80	0.51
1:A:173:GLN:CD	10:A:703:HOH:O	2.47	0.51
1:A:166:VAL:HG13	1:A:180:ILE:HG12	1.92	0.51
1:A:215:VAL:HG23	1:A:217:GLN:HE21	1.75	0.50
1:A:540:GLN:NE2	10:A:715:HOH:O	2.43	0.50
1:A:548:SER:OG	1:A:551:ARG:HB2	2.12	0.50
1:A:377:HIS:HA	1:A:380:PHE:CE2	2.48	0.49
1:A:400:LEU:HD11	1:A:553:ILE:HD13	1.93	0.49
1:A:77:GLU:OE2	1:A:81:LYS:NZ	2.41	0.49
1:A:267:THR:CG2	1:A:392:ILE:HD13	2.43	0.49
1:A:172:TYR:CE2	1:A:174:SER:HB2	2.48	0.48
1:A:202:ARG:HD3	7:A:624:IOD:I	2.84	0.48
1:A:207:SER:N	10:A:739:HOH:O	2.45	0.48
1:A:523:ARG:HG3	1:A:529:TRP:CE2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:66:THR:HB	1:A:70:PHE:N	2.29	0.47
1:A:392:ILE:O	1:A:396:VAL:HG23	2.14	0.47
1:A:215:VAL:HG23	1:A:217:GLN:NE2	2.28	0.47
7:A:623:IOD:I	9:A:634:OSM:H1	2.84	0.47
1:A:393:ASP:HB2	10:A:844:HOH:O	2.15	0.47
1:A:91:VAL:HG12	1:A:411:LYS:HD3	1.96	0.47
1:A:277:ALA:O	1:A:280:LEU:HB2	2.15	0.46
1:A:273:HIS:HE1	1:A:296:ALA:HB3	1.80	0.46
1:A:588:SER:N	1:A:589:PRO:CD	2.79	0.46
1:A:217:GLN:OE1	2:AeA:2:NAG:O6	2.32	0.46
1:A:8:ALA:N	1:A:9:PRO:HD3	2.13	0.45
1:A:291:LYS:HD3	10:A:886:HOH:O	2.13	0.45
1:A:592:SER:OG	1:A:594:GLU:OE1	2.35	0.45
1:A:385:ARG:O	1:A:389:ASP:HB3	2.16	0.45
1:A:273:HIS:CE1	1:A:296:ALA:HB3	2.52	0.45
1:A:274:ASN:HB3	1:A:278:ARG:NH1	2.31	0.45
1:A:548:SER:HG	1:A:551:ARG:HB2	1.82	0.44
1:A:109:HIS:CD2	9:A:634:OSM:S	3.03	0.44
1:A:544:LEU:O	1:A:547:VAL:HG22	2.17	0.44
5:A:603:HEM:CBD	9:A:634:OSM:N	2.65	0.44
1:A:430:GLY:HA2	7:A:621:IOD:I	2.88	0.44
1:A:42:ALA:HB2	1:A:166:VAL:HG21	1.98	0.44
1:A:291:LYS:O	1:A:295:GLU:HB2	2.18	0.44
1:A:154:GLN:OE1	10:A:713:HOH:O	2.21	0.44
1:A:276:LEU:HD21	1:A:585:LEU:HD23	2.00	0.44
1:A:556:ASN:HA	10:A:724:HOH:O	2.17	0.44
1:A:544:LEU:HG	1:A:590:TRP:HH2	1.82	0.43
1:A:121:SER:C	1:A:126:LYS:HD3	2.43	0.43
1:A:211:GLY:HA2	10:A:780:HOH:O	2.17	0.43
1:A:34:PRO:HD2	7:A:610:IOD:I	2.89	0.43
1:A:221:ASP:HB2	1:A:271:ARG:NH2	2.33	0.43
1:A:270:LEU:HD13	10:A:1010:HOH:O	2.18	0.43
1:A:10:VAL:HG23	1:A:41:ARG:HH22	1.76	0.42
1:A:275:ARG:O	1:A:279:GLU:HG2	2.18	0.42
1:A:172:TYR:CD1	1:A:172:TYR:O	2.73	0.42
1:A:349:PHE:HA	1:A:497:ASN:HD21	1.84	0.42
1:A:221:ASP:CB	1:A:271:ARG:NH2	2.83	0.42
1:A:193:TYR:CZ	1:A:297:ARG:HA	2.55	0.42
1:A:313:LEU:N	1:A:314:PRO:CD	2.83	0.42
1:A:407:MET:HE3	1:A:407:MET:C	2.45	0.42
1:A:10:VAL:HA	1:A:11:PRO:HD3	1.91	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:543:SER:HA	1:A:546:LYS:HG3	2.02	0.41
1:A:366:GLN:O	1:A:367:PRO:C	2.63	0.41
1:A:169:THR:N	1:A:170:PRO:CD	2.83	0.41
1:A:544:LEU:HG	1:A:590:TRP:CH2	2.56	0.41
1:A:258:GLU:OE2	5:A:603:HEM:C2B	2.64	0.40
1:A:540:GLN:CD	10:A:715:HOH:O	2.64	0.40
1:A:553:ILE:O	1:A:554:CYS:C	2.64	0.40
5:A:603:HEM:C4D	9:A:634:OSM:C	3.04	0.40
1:A:33:SER:O	1:A:36:LEU:HB2	2.21	0.40
1:A:199:LEU:HD13	7:A:624:IOD:I	2.91	0.40
1:A:294:GLN:OE1	1:A:294:GLN:HA	2.21	0.40
1:A:352:MET:CB	1:A:407:MET:HG2	2.52	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%)	553 (93%)	36 (6%)	4 (1%)	18 10

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	11	PRO
1	A	167	CYS
1	A	170	PRO
1	A	120	GLY

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	518/518 (100%)	508 (98%)	10 (2%)	50 47

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	LEU
1	A	172	TYR
1	A	173	GLN
1	A	180	ILE
1	A	201	SER
1	A	240	ILE
1	A	428	ILE
1	A	550	SER
1	A	552	LEU
1	A	587	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	ASN
1	A	128	GLN
1	A	217	GLN
1	A	231	ASN
1	A	273	HIS
1	A	329	GLN
1	A	366	GLN
1	A	468	GLN
1	A	497	ASN
1	A	558	HIS

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 ⓘ

4 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	AeA	1	1,2	14,14,15	0.78	0	17,19,21	1.62	6 (35%)
2	NAG	AeA	2	2	14,14,15	0.56	0	17,19,21	2.27	3 (17%)
2	NAG	AhA	1	1,2	14,14,15	0.42	0	17,19,21	1.04	1 (5%)
2	NAG	AhA	2	2	14,14,15	0.74	0	17,19,21	2.08	5 (29%)

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	AeA	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	AeA	2	2	-	0/6/23/26	0/1/1/1
2	NAG	AhA	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	AhA	2	2	-	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	AeA	2	NAG	C1-O5-C5	6.99	121.66	112.19
2	AhA	2	NAG	C4-C3-C2	4.56	117.71	111.02
2	AeA	2	NAG	C4-C3-C2	-4.30	104.71	111.02
2	AhA	2	NAG	O5-C5-C4	-3.59	102.08	110.83
2	AhA	2	NAG	O5-C5-C6	3.15	112.14	107.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AhA	2	NAG	C2-N2-C7	3.06	127.26	122.90
2	AhA	1	NAG	O5-C5-C6	2.91	111.76	107.20
2	AhA	2	NAG	O5-C1-C2	2.55	115.32	111.29
2	AeA	2	NAG	O3-C3-C2	2.48	114.60	109.47
2	AeA	1	NAG	C6-C5-C4	2.37	118.55	113.00
2	AeA	1	NAG	O5-C1-C2	2.34	114.98	111.29
2	AeA	1	NAG	C1-O5-C5	2.34	115.36	112.19
2	AeA	1	NAG	O7-C7-N2	2.18	125.95	121.95
2	AeA	1	NAG	O7-C7-C8	-2.08	118.20	122.06
2	AeA	1	NAG	O4-C4-C5	2.04	114.37	109.30

There are no chirality outliers.

All (6) torsion outliers are listed below:

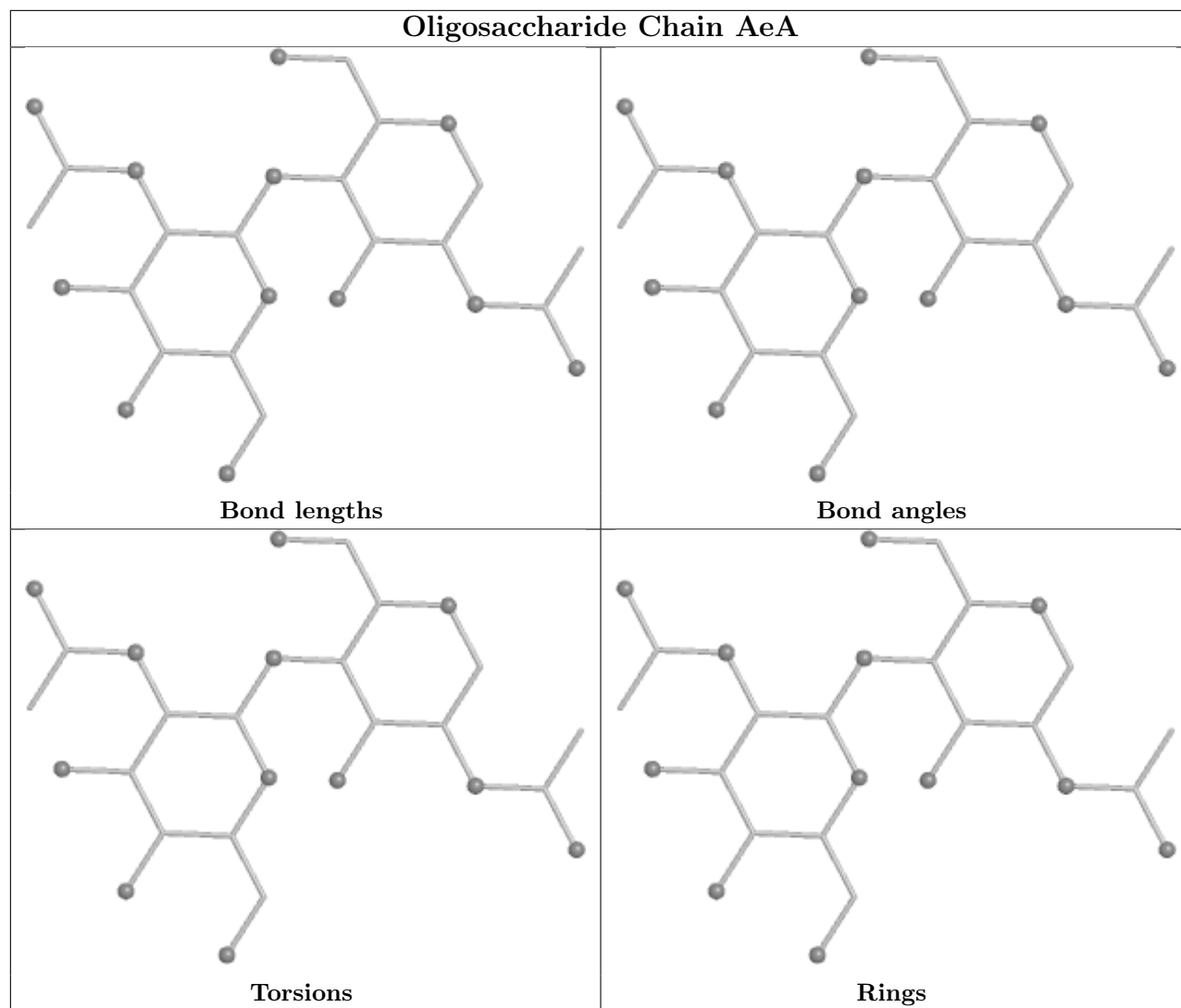
Mol	Chain	Res	Type	Atoms
2	AhA	2	NAG	C1-C2-N2-C7
2	AhA	2	NAG	O5-C5-C6-O6
2	AhA	2	NAG	C4-C5-C6-O6
2	AhA	1	NAG	O5-C5-C6-O6
2	AhA	1	NAG	C4-C5-C6-O6
2	AhA	2	NAG	C3-C2-N2-C7

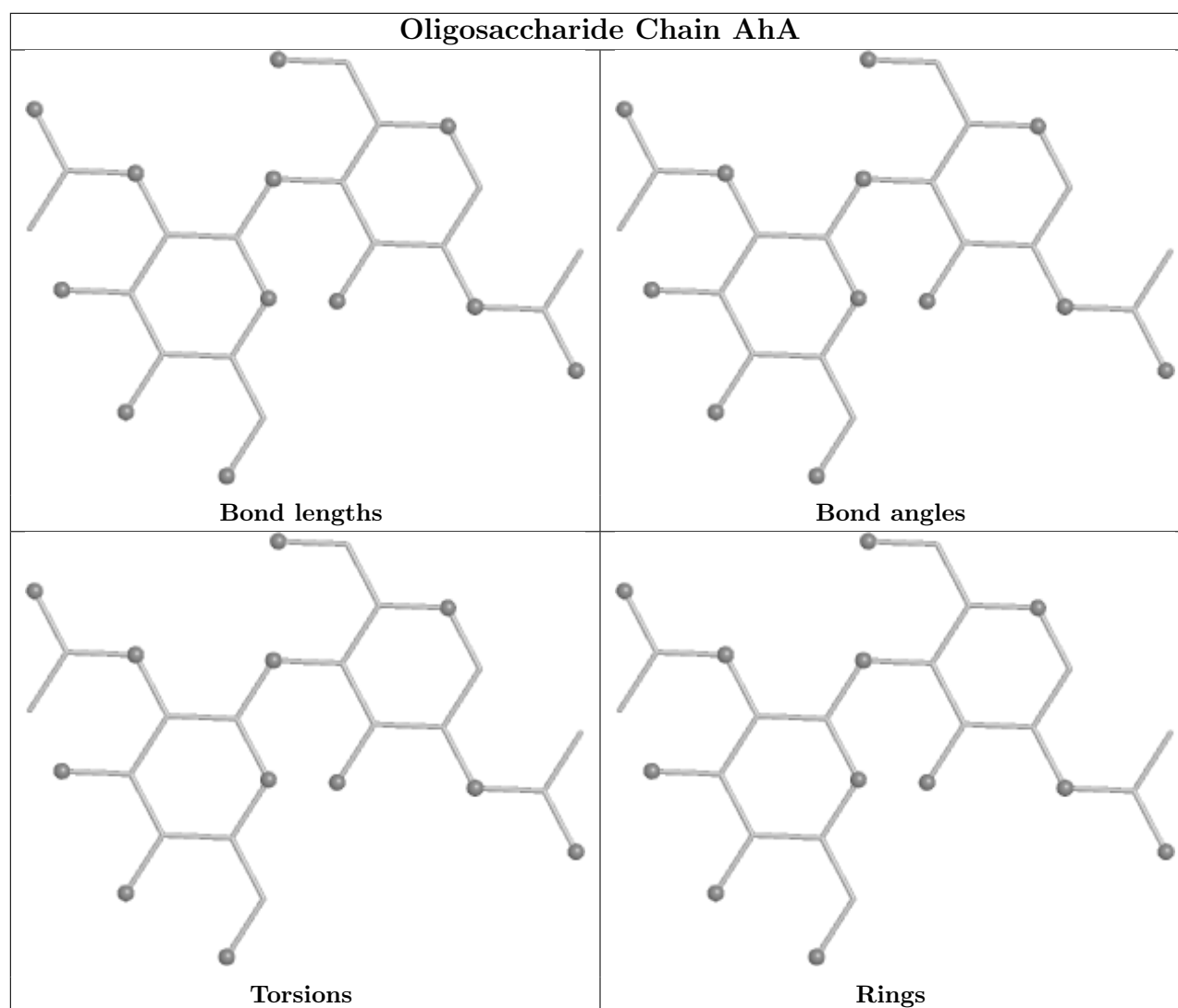
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	AeA	2	NAG	1	0

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





5.6 Ligand geometry [i](#)

Of 34 ligands modelled in this entry, 21 are monoatomic - leaving 13 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	$\# Z > 2$
8	SCN	A	628	-	1,2,2	1.35	0	0,1,1	-	-
8	SCN	A	626	-	1,2,2	1.06	0	0,1,1	-	-
8	SCN	A	632	-	1,2,2	0.26	0	0,1,1	-	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	A	605	1	14,14,15	0.57	0	17,19,21	1.03	1 (5%)
6	NAG	A	604	1	14,14,15	0.61	0	17,19,21	0.99	0
9	OSM	A	634	7,5	1,3,3	0.02	0	0,2,2	-	-
8	SCN	A	627	-	1,2,2	1.19	0	0,1,1	-	-
8	SCN	A	625	-	1,2,2	1.61	0	0,1,1	-	-
8	SCN	A	633	-	1,2,2	0.10	0	0,1,1	-	-
8	SCN	A	631	7	1,2,2	0.08	0	0,1,1	-	-
5	HEM	A	603	9,1	50,50,50	1.54	8 (16%)	66,82,82	1.72	15 (22%)
8	SCN	A	630	-	1,2,2	0.36	0	0,1,1	-	-
8	SCN	A	629	-	1,2,2	0.76	0	0,1,1	-	-

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
6	NAG	A	605	1	-	0/6/23/26	0/1/1/1
6	NAG	A	604	1	-	1/6/23/26	0/1/1/1
9	OSM	A	634	7,5	-	0/0/1/1	-
5	HEM	A	603	9,1	-	4/14/54/54	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	603	HEM	FE-NB	4.25	2.08	1.94
5	A	603	HEM	FE-NC	4.14	2.09	1.95
5	A	603	HEM	C1B-NB	-3.33	1.34	1.40
5	A	603	HEM	CBD-CGD	2.51	1.56	1.50
5	A	603	HEM	C1C-C2C	-2.39	1.40	1.45
5	A	603	HEM	C3B-C4B	2.22	1.49	1.44
5	A	603	HEM	C1C-NC	-2.20	1.35	1.39
5	A	603	HEM	FE-NA	2.00	2.01	1.95

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	603	HEM	CMD-C2D-C1D	4.37	131.70	125.04
5	A	603	HEM	CHC-C4B-NB	4.34	129.13	124.42
5	A	603	HEM	C1B-NB-C4B	4.02	109.22	105.07
5	A	603	HEM	C3B-C2B-C1B	3.57	109.13	106.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	603	HEM	CHD-C1D-ND	3.34	128.05	124.42
5	A	603	HEM	C4B-C3B-C2B	-3.28	104.51	107.11
5	A	603	HEM	CHA-C4D-C3D	-3.24	119.25	125.33
5	A	603	HEM	CAD-C3D-C4D	2.93	129.77	124.66
5	A	603	HEM	CHA-C4D-ND	2.79	127.82	124.37
5	A	603	HEM	C4C-NC-C1C	2.69	107.99	105.35
6	A	605	NAG	O5-C1-C2	-2.65	107.10	111.29
5	A	603	HEM	O2D-CGD-CBD	2.39	121.70	114.03
5	A	603	HEM	C3D-C4D-ND	2.34	112.77	110.17
5	A	603	HEM	C1A-CHA-C4D	-2.34	120.79	126.34
5	A	603	HEM	CHD-C1D-C2D	-2.26	121.44	124.98
5	A	603	HEM	O2D-CGD-O1D	-2.19	117.84	123.30

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	604	NAG	C4-C5-C6-O6
5	A	603	HEM	CAA-CBA-CGA-O1A
5	A	603	HEM	CAA-CBA-CGA-O2A
5	A	603	HEM	CAD-CBD-CGD-O1D
5	A	603	HEM	CAD-CBD-CGD-O2D

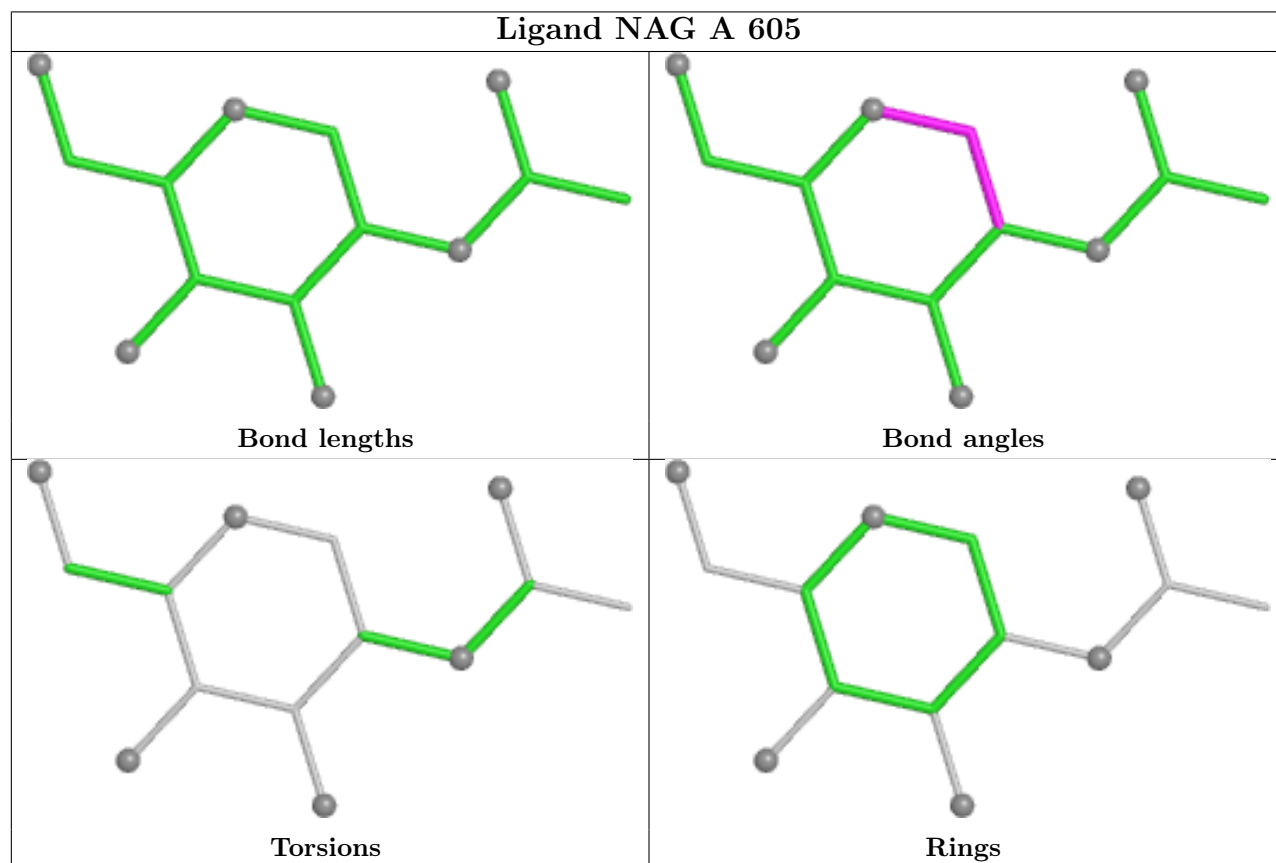
There are no ring outliers.

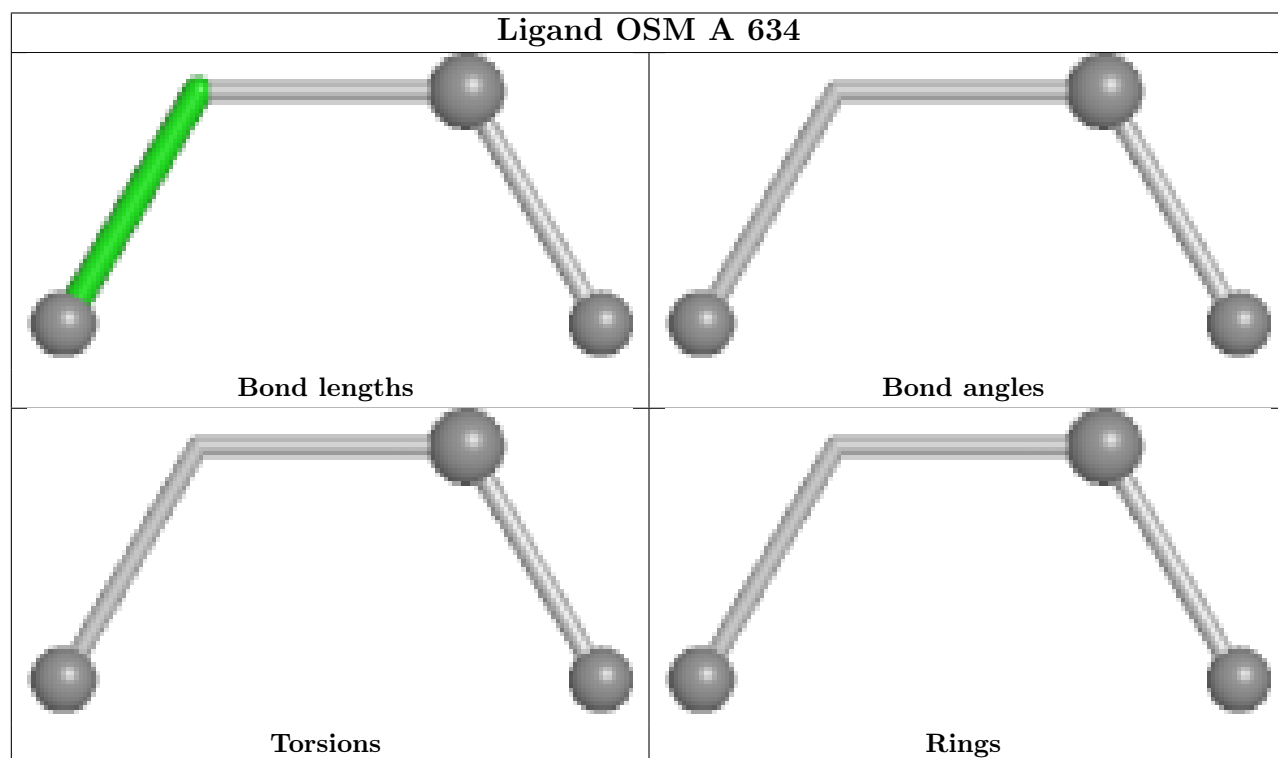
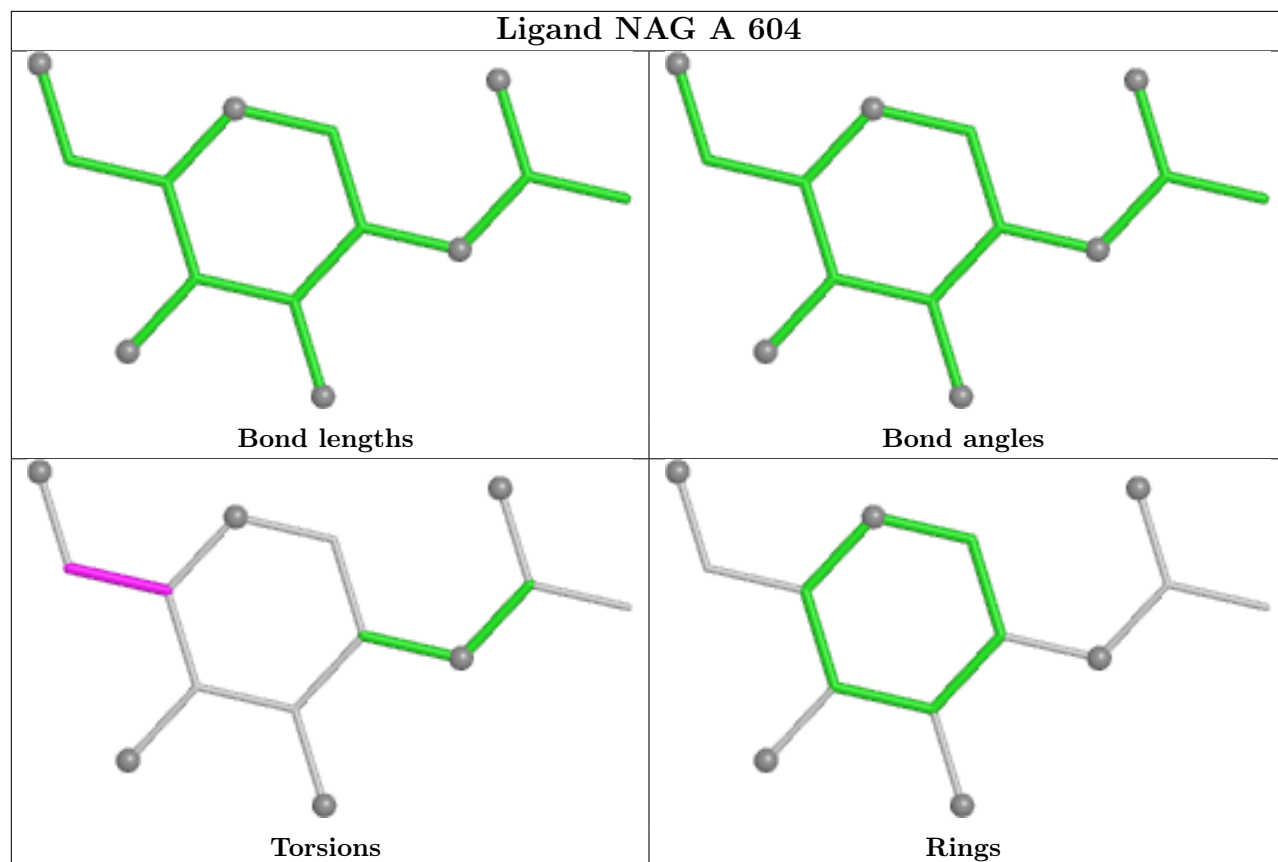
6 monomers are involved in 29 short contacts:

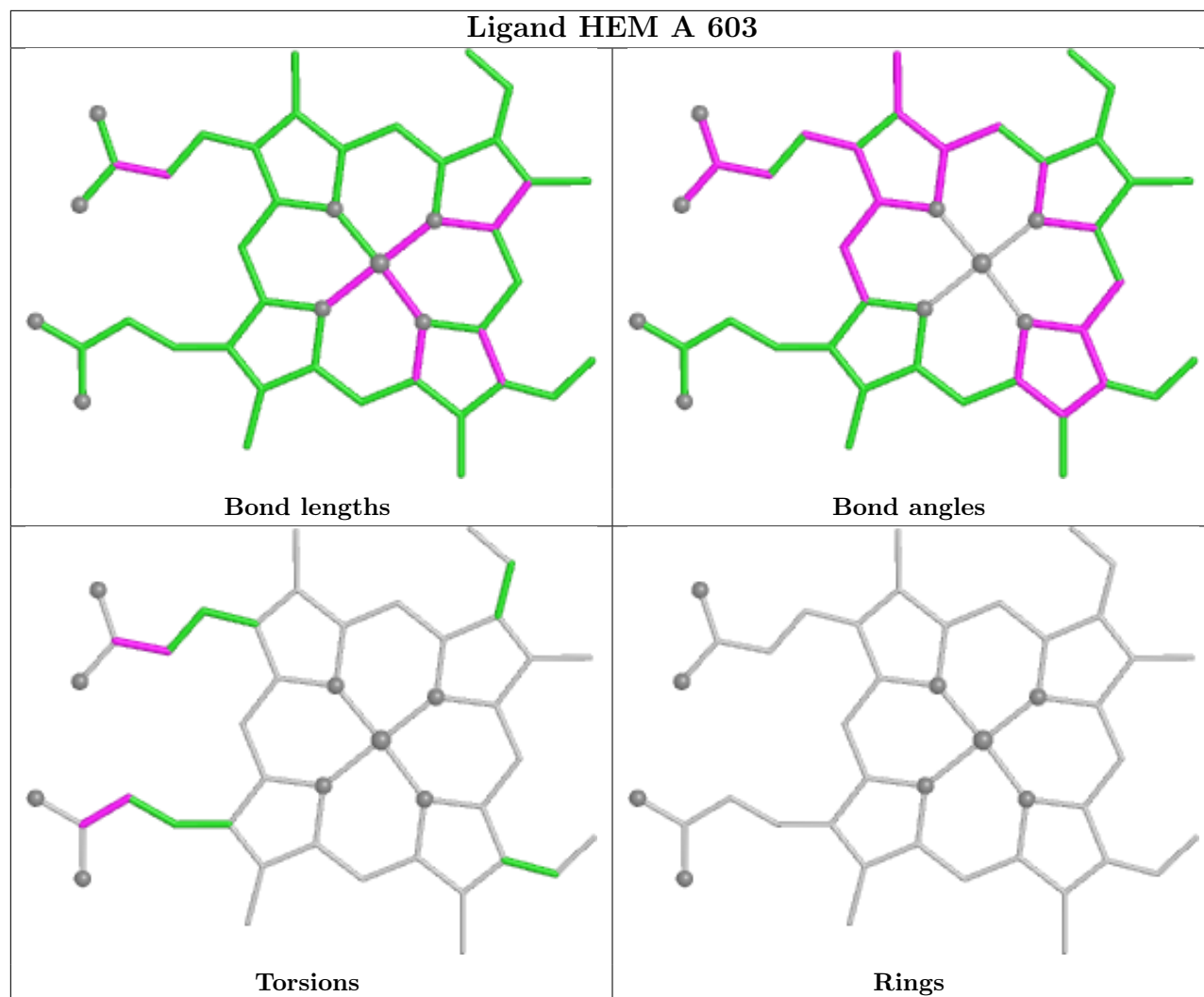
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	605	NAG	1	0
9	A	634	OSM	16	0
8	A	627	SCN	1	0
8	A	625	SCN	1	0
8	A	633	SCN	1	0
5	A	603	HEM	18	0

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 ⓘ

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	595/595 (100%)	1.01	126 (21%) 2 2	12, 30, 80, 158	0

All (126) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	168	PRO	8.3
1	A	224	LEU	7.7
1	A	169	THR	7.4
1	A	2	TRP	7.2
1	A	8	ALA	7.1
1	A	172	TYR	7.0
1	A	11	PRO	7.0
1	A	9	PRO	7.0
1	A	174	SER	6.5
1	A	280	LEU	6.5
1	A	13	VAL	6.2
1	A	12	LEU	6.1
1	A	175	LEU	6.0
1	A	287	TRP	5.6
1	A	119	LEU	5.4
1	A	170	PRO	5.4
1	A	283	LEU	5.4
1	A	220	TRP	5.2
1	A	10	VAL	5.2
1	A	4	VAL	5.1
1	A	222	HIS	4.9
1	A	428	ILE	4.7
1	A	227	LEU	4.6
1	A	223	GLY	4.6
1	A	209	PRO	4.5
1	A	208	SER	4.4
1	A	7	GLY	4.2

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Mol	Chain	Res	Type	RSRZ
1	A	579	CYS	4.1
1	A	582	VAL	4.1
1	A	5	GLY	4.1
1	A	206	LEU	4.1
1	A	288	ASN	4.0
1	A	221	ASP	4.0
1	A	587	LEU	4.0
1	A	1	SER	4.0
1	A	277	ALA	3.9
1	A	572	TYR	3.8
1	A	425	THR	3.8
1	A	580	SER	3.8
1	A	562	VAL	3.7
1	A	219	ALA	3.5
1	A	561	LYS	3.5
1	A	212	LEU	3.5
1	A	591	ALA	3.5
1	A	423	GLN	3.4
1	A	560	THR	3.4
1	A	211	GLY	3.3
1	A	274	ASN	3.3
1	A	426	HIS	3.3
1	A	210	LEU	3.3
1	A	173	GLN	3.3
1	A	6	CYS	3.3
1	A	121	SER	3.3
1	A	592	SER	3.3
1	A	272	GLU	3.2
1	A	273	HIS	3.2
1	A	289	GLY	3.1
1	A	292	LEU	3.1
1	A	276	LEU	3.1
1	A	167	CYS	3.1
1	A	577	VAL	3.0
1	A	271	ARG	3.0
1	A	171	PRO	3.0
1	A	554	CYS	2.9
1	A	239	PHE	2.9
1	A	286	HIS	2.9
1	A	215	VAL	2.9
1	A	536	PHE	2.8
1	A	590	TRP	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	595	ASN	2.8
1	A	120	GLY	2.8
1	A	537	THR	2.8
1	A	3	GLU	2.8
1	A	543	SER	2.7
1	A	205	ASN	2.7
1	A	424	PRO	2.7
1	A	544	LEU	2.7
1	A	564	LEU	2.7
1	A	559	ILE	2.7
1	A	285	PRO	2.6
1	A	585	LEU	2.6
1	A	124	HIS	2.5
1	A	541	ARG	2.5
1	A	588	SER	2.5
1	A	254	PHE	2.5
1	A	574	HIS	2.5
1	A	293	TYR	2.4
1	A	268	LEU	2.4
1	A	117	THR	2.4
1	A	547	VAL	2.4
1	A	290	GLU	2.4
1	A	125	SER	2.4
1	A	229	PHE	2.3
1	A	296	ALA	2.3
1	A	216	ASN	2.3
1	A	201	SER	2.3
1	A	593	ARG	2.3
1	A	218	GLU	2.3
1	A	161	PHE	2.3
1	A	213	MET	2.3
1	A	427	LYS	2.3
1	A	284	ASN	2.3
1	A	281	LYS	2.3
1	A	551	ARG	2.3
1	A	232	LYS	2.3
1	A	573	PRO	2.2
1	A	203	LEU	2.2
1	A	226	TYR	2.2
1	A	422	PHE	2.2
1	A	576	PHE	2.2
1	A	583	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	569	ALA	2.2
1	A	575	ASP	2.2
1	A	578	ASP	2.2
1	A	64	ARG	2.2
1	A	586	ASP	2.1
1	A	217	GLN	2.1
1	A	387	ILE	2.1
1	A	197	PRO	2.1
1	A	278	ARG	2.1
1	A	553	ILE	2.0
1	A	207	SER	2.0
1	A	299	ILE	2.0
1	A	365	TYR	2.0
1	A	204	ARG	2.0
1	A	535	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

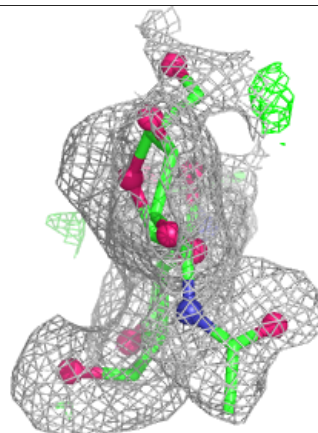
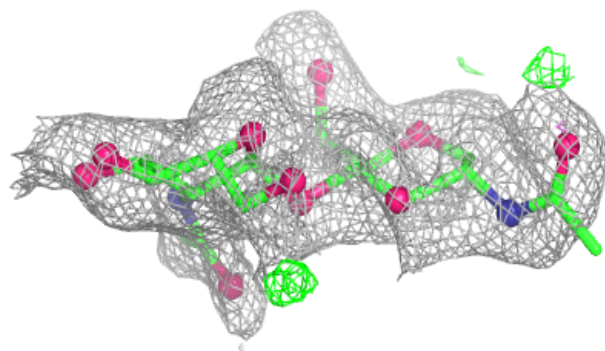
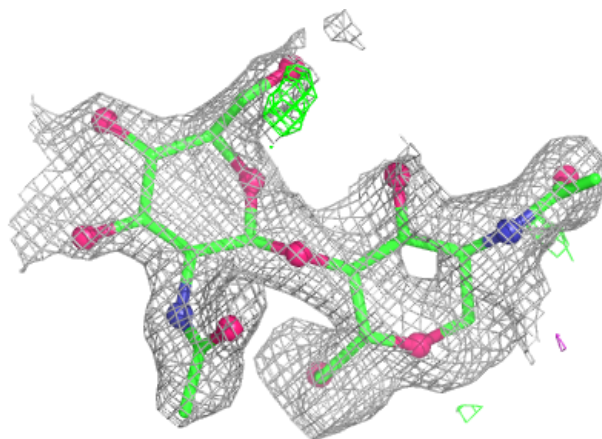
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

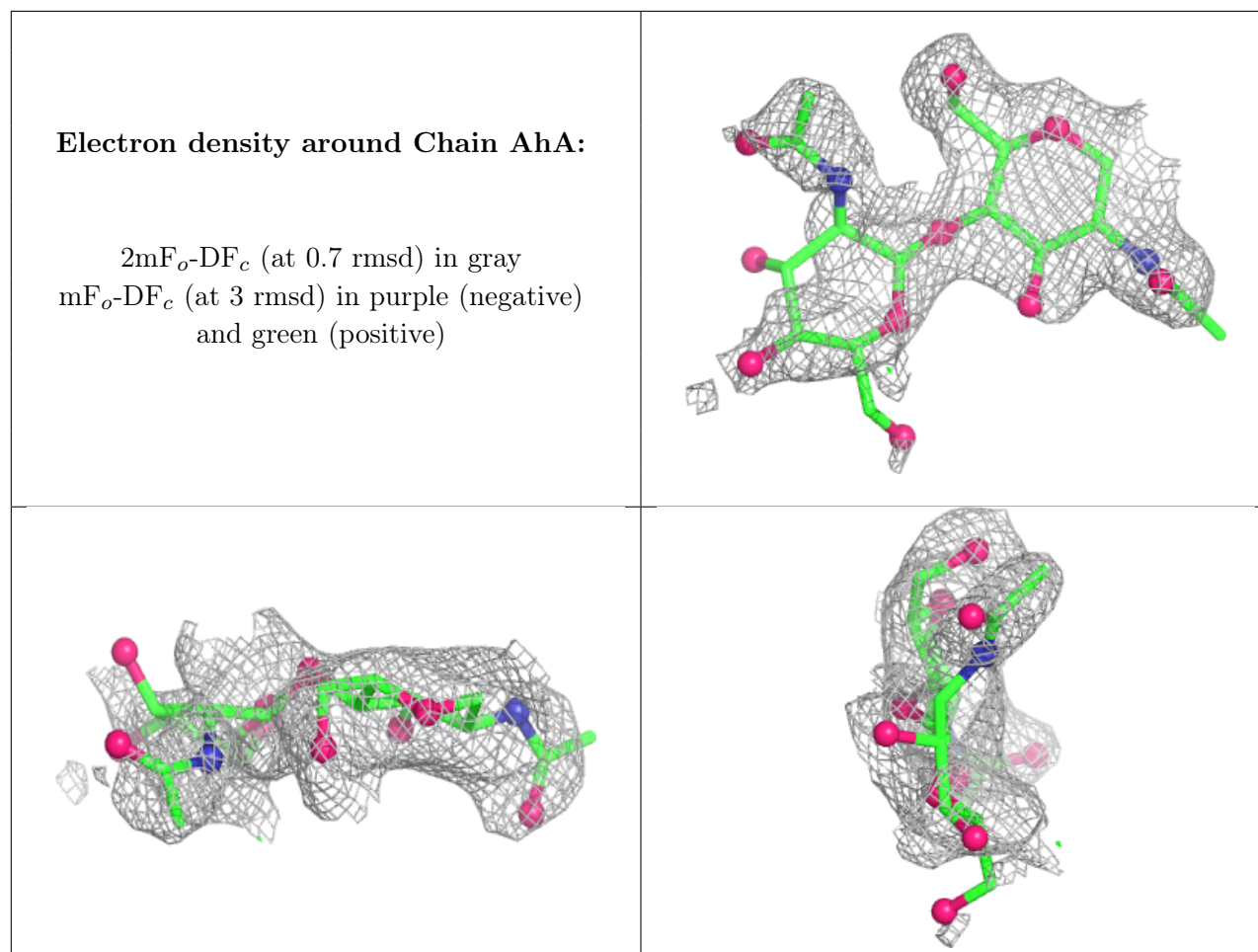
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAG	AeA	1	14/15	-	-	36,57,61,65	0
2	NAG	AeA	2	14/15	-	-	56,69,71,71	0
2	NAG	AhA	1	14/15	-	-	45,54,59,69	0
2	NAG	AhA	2	14/15	-	-	66,74,84,86	0

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 AeA:

$2mF_o-DF_c$ (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	NAG	A	604	14/15	0.69	0.16	50,58,67,71	0
6	NAG	A	605	14/15	0.88	0.10	33,38,41,42	0
7	IOD	A	617	1/1	0.89	0.13	64,64,64,64	1
4	ZN	A	602	1/1	0.92	0.11	54,54,54,54	0
7	IOD	A	614	1/1	0.94	0.17	75,75,75,75	1
7	IOD	A	609	1/1	0.94	0.08	37,37,37,37	0
7	IOD	A	618	1/1	0.94	0.13	61,61,61,61	1
8	SCN	A	626	3/3	0.94	0.10	17,17,18,19	3
7	IOD	A	622	1/1	0.95	0.14	91,91,91,91	0
8	SCN	A	629	3/3	0.95	0.07	9,9,9,11	3
8	SCN	A	632	3/3	0.95	0.10	14,14,16,16	3

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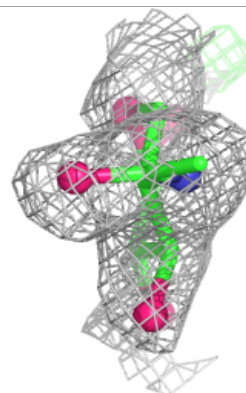
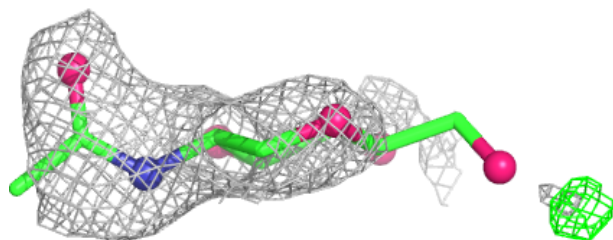
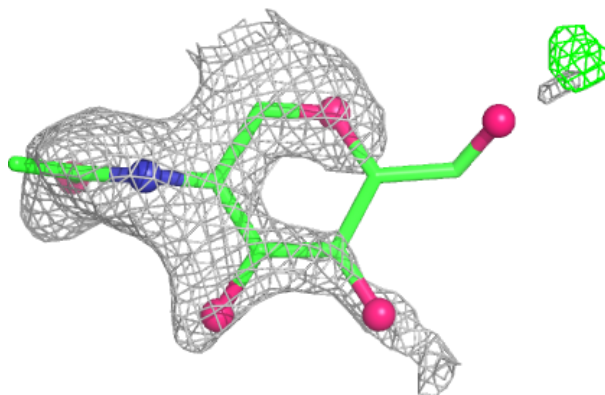
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
9	OSM	A	634	4/4	0.95	0.13	24,30,33,35	0
8	SCN	A	631	3/3	0.96	0.10	21,21,21,23	3
7	IOD	A	616	1/1	0.96	0.09	42,42,42,42	1
7	IOD	A	615	1/1	0.96	0.09	55,55,55,55	1
7	IOD	A	611	1/1	0.97	0.05	32,32,32,32	1
8	SCN	A	625	3/3	0.97	0.09	6,6,6,6	3
7	IOD	A	620	1/1	0.97	0.07	39,39,39,39	1
8	SCN	A	627	3/3	0.97	0.13	3,3,4,4	3
8	SCN	A	630	3/3	0.98	0.07	12,12,12,14	3
7	IOD	A	613	1/1	0.98	0.04	36,36,36,36	1
7	IOD	A	610	1/1	0.98	0.13	68,68,68,68	1
5	HEM	A	603	43/43	0.98	0.06	12,14,19,24	0
8	SCN	A	628	3/3	0.99	0.07	0,0,0,0	3
7	IOD	A	612	1/1	0.99	0.03	33,33,33,33	0
7	IOD	A	624	1/1	0.99	0.04	29,29,29,29	1
3	CA	A	601	1/1	0.99	0.02	17,17,17,17	0
7	IOD	A	607	1/1	0.99	0.04	29,29,29,29	1
8	SCN	A	633	3/3	0.99	0.07	13,13,13,13	3
7	IOD	A	608	1/1	0.99	0.02	25,25,25,25	1
7	IOD	A	623	1/1	1.00	0.01	18,18,18,18	1
7	IOD	A	606	1/1	1.00	0.02	18,18,18,18	0
7	IOD	A	621	1/1	1.00	0.07	31,31,31,31	1
7	IOD	A	619	1/1	1.00	0.03	30,30,30,30	1

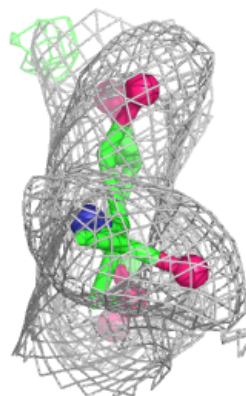
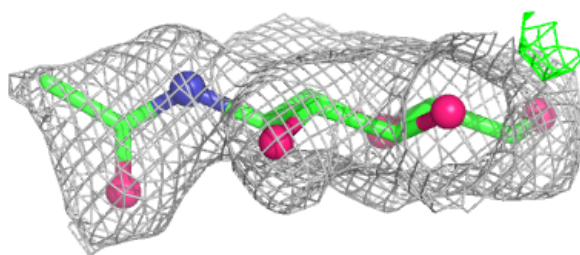
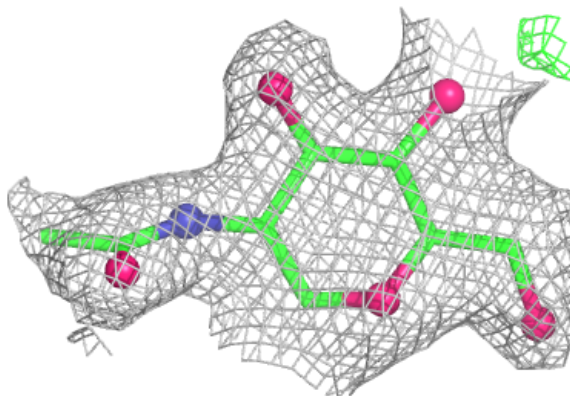
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NAG A 604:

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

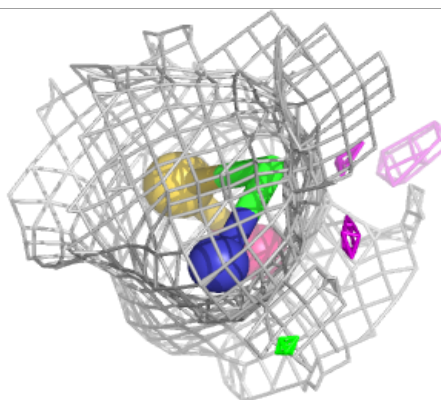
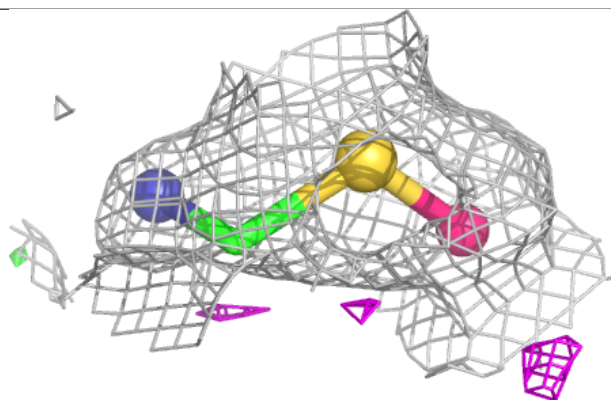
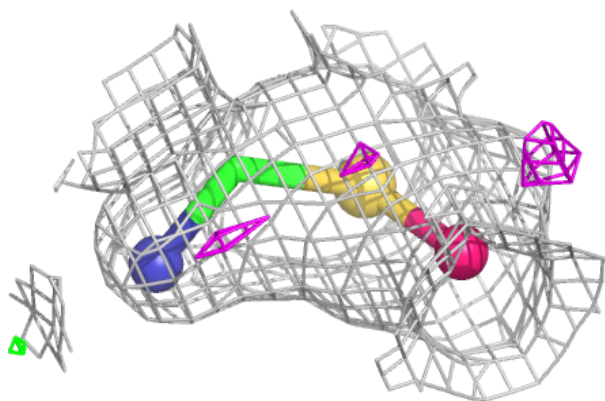
**Electron density around NAG A 605:**

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



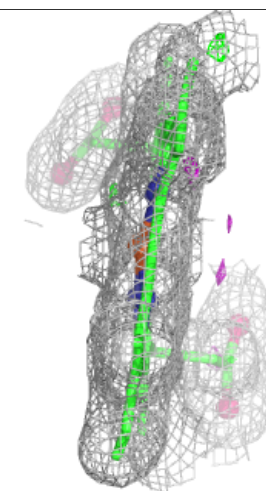
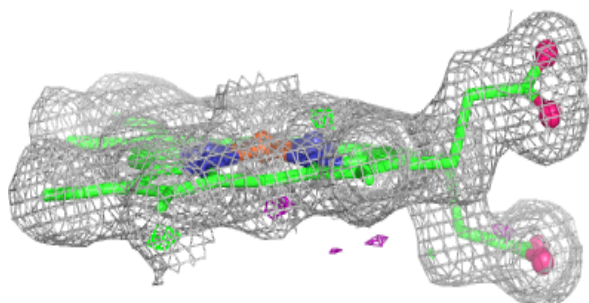
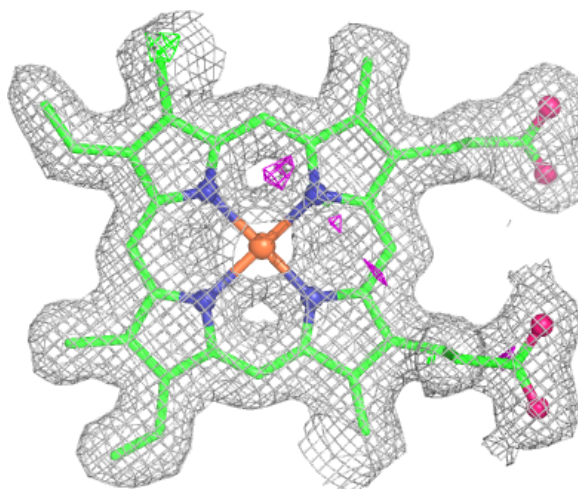
Electron density around OSM A 634:

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



Electron density around HEM A 603:

$2mF_o-DF_c$ (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.