



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 19, 2026 – 05:50 AM UTC

PDB ID : 7DN6 / pdb_00007dn6
Title : Crystal structure of bovine lactoperoxidase with hydrogen peroxide trapped between heme iron and his109 at 1.69 Å resolution
Authors : Singh, P.K.; Singh, A.K.; Kaur, P.; Sharma, S.; Singh, T.P.
Deposited on : 2020-12-08
Resolution : 1.70 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 : 2022.3.0, CSD as543be (2022)
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 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

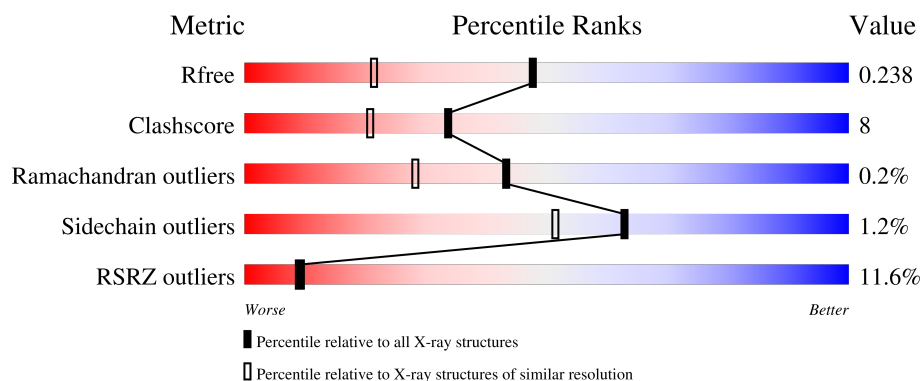
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	12% 85% 13%
2	C	2	50% 50%

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
10	OSM	A	617	-	-	X	-
10	OSM	A	619	-	-	X	-
11	PEO	A	627	-	-	X	-

2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 5568 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.

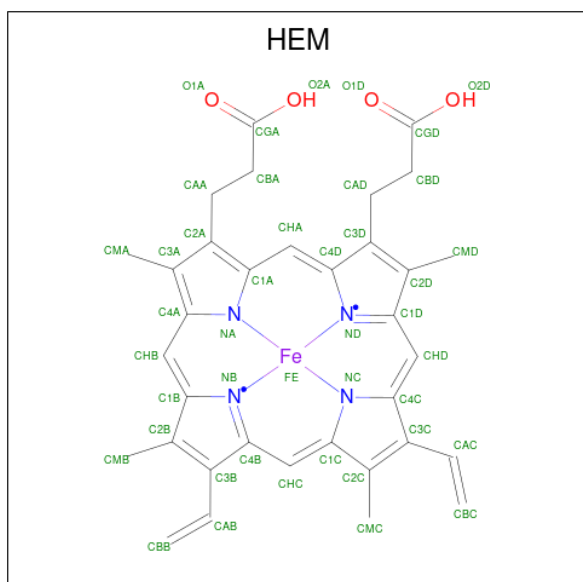
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	595	Total	C	N	O	S	0	0	0
			4770	3037	847	860	26			

- 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	C	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$) (labeled as "Ligand of Interest" by depositor).

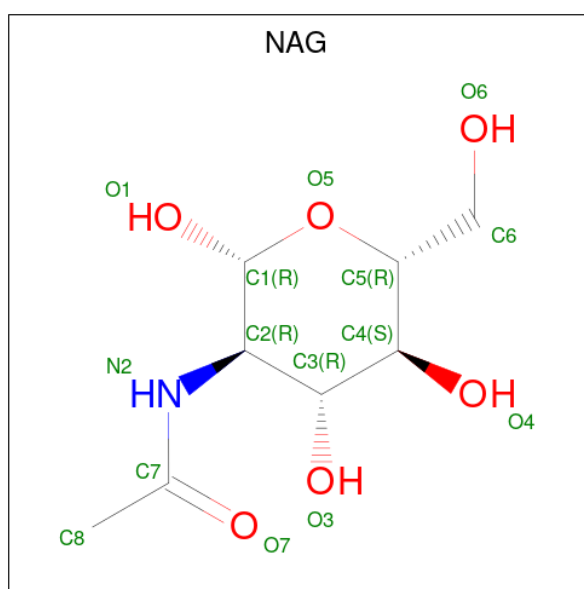


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	Fe	N	O	
			43	34	1	4	4	
							0	0

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

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

- Molecule 6 is IODIDE ION (CCD ID: IOD) (formula: I).

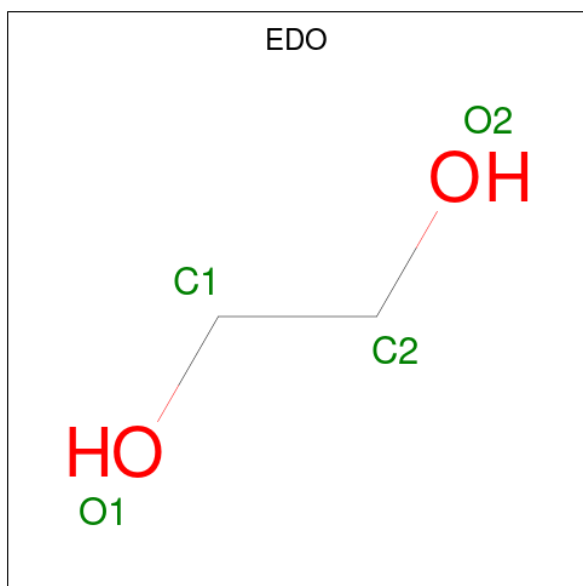
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	19	Total	I		
			19	19	0	0

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

- Molecule 8 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).

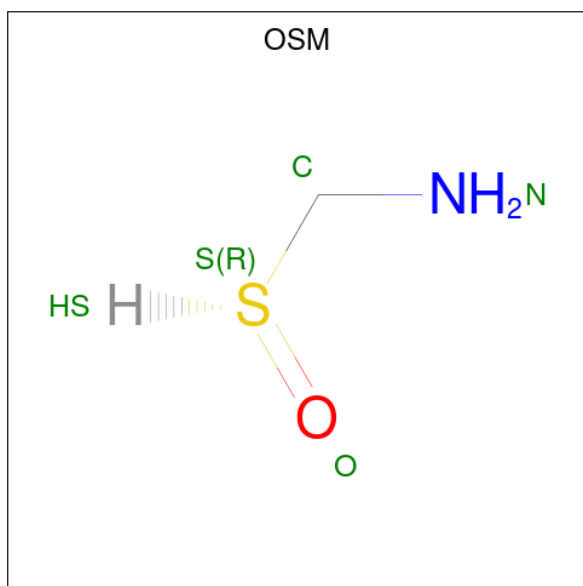


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 9 is ZINC ION (CCD ID: ZN) (formula: Zn).

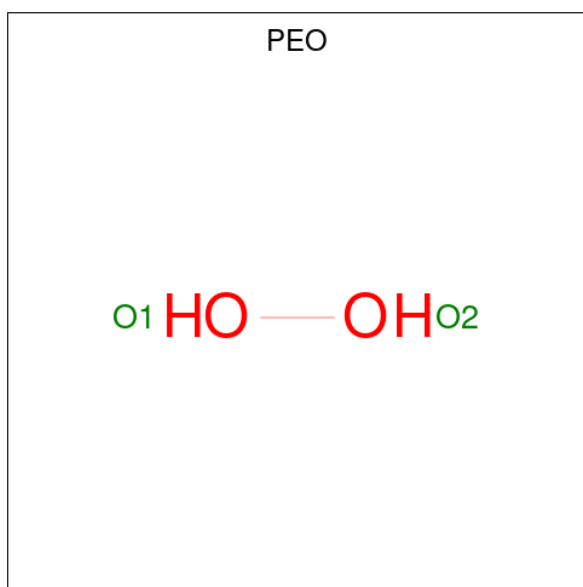
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	1	Total	Zn	0	0
			1	1		

- Molecule 10 is 1-(OXIDOSULFANYL)METHANAMINE (CCD ID: OSM) (formula: CH₅NOS).



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

- Molecule 11 is HYDROGEN PEROXIDE (CCD ID: PEO) (formula: H₂O₂).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	1	Total	O	0	0
			2	2		

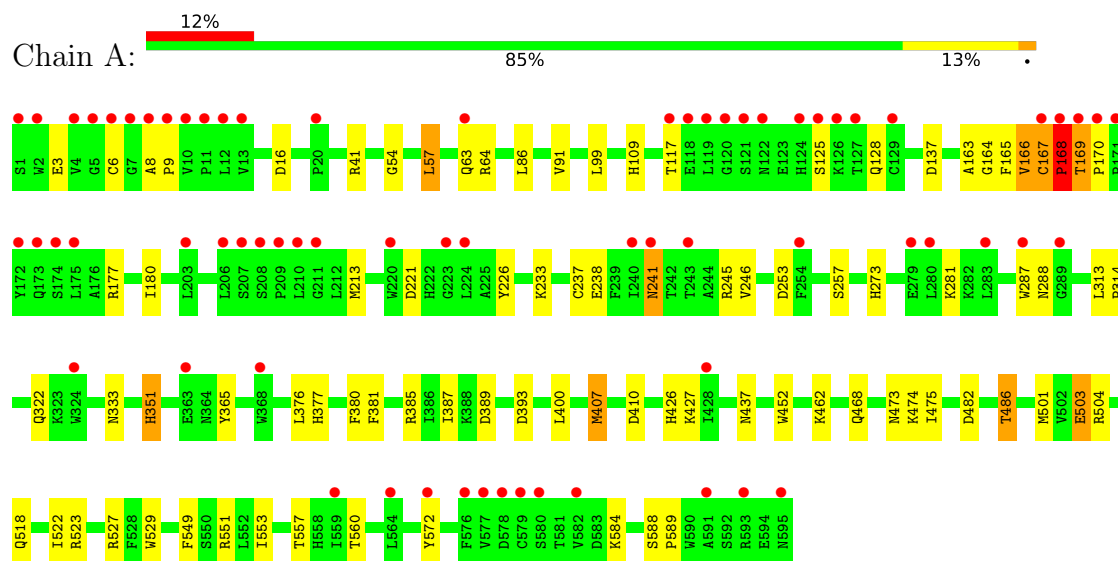
- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	654	Total	O	0	0
			654	654		

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



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	53.91Å 79.69Å 76.97Å 90.00° 102.23° 90.00°	Depositor
Resolution (Å)	39.41 – 1.70 39.41 – 1.70	Depositor EDS
% Data completeness (in resolution range)	97.6 (39.41-1.70) 97.6 (39.41-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.52 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.197 , 0.235 0.204 , 0.238	Depositor DCC
R_{free} test set	3464 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	24.5	Xtriage
Anisotropy	0.116	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 37.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5568	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.64% 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, GOL, CA, OSM, HEM, EDO, NAG, PEO, 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	1.07	4/4898 (0.1%)	1.39	22/6645 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	486	THR	C-N	11.75	1.47	1.33
1	A	57	LEU	C-N	10.88	1.47	1.33
1	A	167	CYS	C-N	7.46	1.51	1.33
1	A	452	TRP	C-O	5.10	1.30	1.24

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	167	CYS	CA-C-N	14.71	138.23	119.84
1	A	167	CYS	C-N-CA	14.71	138.23	119.84
1	A	486	THR	CA-C-N	10.29	130.06	119.56
1	A	486	THR	C-N-CA	10.29	130.06	119.56
1	A	473	ASN	CB-CA-C	7.61	120.99	110.34
1	A	57	LEU	CA-C-N	7.46	127.38	119.85
1	A	57	LEU	C-N-CA	7.46	127.38	119.85
1	A	168	PRO	N-CA-CB	-7.42	95.46	103.25
1	A	57	LEU	O-C-N	-6.80	114.21	121.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	170	PRO	N-CA-C	5.79	117.76	110.70
1	A	486	THR	O-C-N	-5.64	116.02	121.94
1	A	241	ASN	N-CA-C	-5.24	98.49	107.61
1	A	137	ASP	CB-CA-C	5.24	120.84	110.42
1	A	426	HIS	CB-CA-C	5.19	118.69	109.65
1	A	288	ASN	CA-C-N	5.16	125.67	119.94
1	A	288	ASN	C-N-CA	5.16	125.67	119.94
1	A	253	ASP	CA-C-N	5.15	127.69	120.28
1	A	253	ASP	C-N-CA	5.15	127.69	120.28
1	A	166	VAL	CA-C-N	5.13	134.32	121.80
1	A	166	VAL	C-N-CA	5.13	134.32	121.80
1	A	351	HIS	CA-CB-CG	-5.09	108.71	113.80
1	A	177	ARG	CB-CG-CD	-5.07	99.65	111.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	167	CYS	Peptide

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	4689	68	0
2	C	28	0	25	1	0
3	A	43	0	30	0	0
4	A	1	0	0	0	0
5	A	28	0	26	0	0
6	A	19	0	0	4	0
7	A	6	0	8	0	0
8	A	4	0	6	0	0
9	A	1	0	0	0	0
10	A	12	0	14	5	0
11	A	2	0	0	2	0
12	A	654	0	0	28	0
All	All	5568	0	4798	75	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 8.

All (75) 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:407:MET:CG	1:A:501:MET:HE3	1.81	1.09
1:A:407:MET:HG3	1:A:501:MET:CE	1.83	1.08
1:A:407:MET:HG3	1:A:501:MET:HE3	1.09	1.05
1:A:407:MET:CG	1:A:501:MET:CE	2.37	1.01
1:A:117:THR:HG22	1:A:164:GLY:HA2	1.40	1.00
1:A:3:GLU:OE1	12:A:701:HOH:O	1.88	0.92
6:A:623:IOD:I	12:A:1166:HOH:O	2.58	0.91
1:A:109:HIS:NE2	11:A:627:PEO:O1	2.09	0.84
1:A:351:HIS:HD1	1:A:437:ASN:HD21	1.22	0.83
6:A:620:IOD:I	11:A:627:PEO:O1	2.67	0.83
1:A:462:LYS:HD2	12:A:816:HOH:O	1.79	0.81
1:A:410:ASP:OD1	12:A:702:HOH:O	2.05	0.74
1:A:365:TYR:O	12:A:703:HOH:O	2.07	0.71
6:A:622:IOD:I	12:A:1343:HOH:O	2.79	0.70
1:A:165:PHE:CZ	1:A:169:THR:O	2.45	0.70
1:A:86:LEU:O	12:A:704:HOH:O	2.12	0.68
1:A:407:MET:HG2	1:A:501:MET:CE	2.23	0.65
10:A:617:OSM:N	12:A:716:HOH:O	2.30	0.63
10:A:617:OSM:H2	12:A:883:HOH:O	1.98	0.63
1:A:385:ARG:O	1:A:389:ASP:HB3	2.01	0.61
1:A:407:MET:CG	1:A:501:MET:HE2	2.26	0.60
1:A:221:ASP:HB2	1:A:226:TYR:CZ	2.38	0.58
1:A:287:TRP:O	12:A:706:HOH:O	2.18	0.57
1:A:246:VAL:HG11	1:A:387:ILE:HG13	1.87	0.57
1:A:377:HIS:HA	1:A:380:PHE:CE2	2.41	0.56
1:A:117:THR:CG2	1:A:164:GLY:HA2	2.26	0.56
1:A:125:SER:HA	1:A:128:GLN:HB3	1.88	0.56
1:A:54:GLY:HA2	12:A:973:HOH:O	2.06	0.56
1:A:407:MET:HG2	1:A:501:MET:HE2	1.84	0.56
1:A:6:CYS:N	12:A:727:HOH:O	2.39	0.55
1:A:3:GLU:OE2	1:A:3:GLU:HA	2.08	0.54
1:A:64:ARG:NH2	12:A:725:HOH:O	2.38	0.54
1:A:238:GLU:O	1:A:241:ASN:O	2.25	0.54
1:A:16:ASP:OD1	1:A:16:ASP:C	2.51	0.54
1:A:333:ASN:HD22	10:A:619:OSM:HS	1.56	0.54
1:A:523:ARG:HG3	1:A:529:TRP:CE2	2.43	0.54
1:A:560:THR:OG1	12:A:708:HOH:O	2.19	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:237:CYS:HA	1:A:381:PHE:O	2.09	0.52
1:A:527:ARG:HD2	10:A:619:OSM:HN2	1.74	0.52
1:A:41:ARG:NH1	12:A:733:HOH:O	2.43	0.51
1:A:588:SER:OG	1:A:589:PRO:HD3	2.11	0.51
1:A:117:THR:HG22	1:A:164:GLY:CA	2.29	0.50
1:A:213:MET:HG2	1:A:273:HIS:CD2	2.46	0.50
1:A:551:ARG:HD3	1:A:584:LYS:HA	1.93	0.50
1:A:233:LYS:CE	12:A:1010:HOH:O	2.60	0.49
1:A:365:TYR:HB2	1:A:572:TYR:CD2	2.48	0.49
1:A:333:ASN:ND2	10:A:619:OSM:HS	2.12	0.48
1:A:117:THR:HG23	1:A:163:ALA:C	2.39	0.47
1:A:588:SER:N	1:A:589:PRO:CD	2.78	0.47
1:A:518:GLN:O	1:A:522:ILE:HG23	2.15	0.47
1:A:313:LEU:N	1:A:314:PRO:CD	2.78	0.46
1:A:8:ALA:HB3	1:A:9:PRO:HD3	1.96	0.46
1:A:475:ILE:HG23	12:A:1042:HOH:O	2.16	0.46
1:A:468:GLN:HG2	1:A:474:LYS:HA	1.97	0.45
1:A:400:LEU:HD11	1:A:553:ILE:HD13	1.98	0.45
1:A:99:LEU:HD21	1:A:549:PHE:CD1	2.52	0.45
1:A:322:GLN:OE1	12:A:709:HOH:O	2.20	0.45
1:A:503:GLU:HG2	1:A:504:ARG:HG3	1.99	0.45
12:A:1146:HOH:O	2:C:2:NAG:H82	2.17	0.44
1:A:221:ASP:HB2	1:A:226:TYR:CE1	2.52	0.43
1:A:63:GLN:H	1:A:63:GLN:CD	2.26	0.43
1:A:376:LEU:HD13	12:A:1060:HOH:O	2.19	0.43
1:A:169:THR:HG21	12:A:1230:HOH:O	2.18	0.43
1:A:245:ARG:NH2	12:A:754:HOH:O	2.50	0.43
1:A:64:ARG:O	12:A:711:HOH:O	2.22	0.43
1:A:407:MET:C	1:A:407:MET:SD	3.02	0.43
1:A:233:LYS:HE3	12:A:1010:HOH:O	2.20	0.42
1:A:393:ASP:OD1	1:A:557:THR:HB	2.19	0.42
1:A:427:LYS:HG2	12:A:1176:HOH:O	2.19	0.41
1:A:257:SER:O	1:A:381:PHE:HA	2.20	0.41
1:A:482:ASP:OD2	12:A:710:HOH:O	2.21	0.41
6:A:611:IOD:I	12:A:959:HOH:O	2.93	0.41
1:A:166:VAL:HG12	1:A:180:ILE:HG12	2.03	0.41
1:A:281:LYS:NZ	12:A:706:HOH:O	2.47	0.41
1:A:57:LEU:HD23	1:A:57:LEU:HA	1.87	0.41

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%)	563 (95%)	29 (5%)	1 (0%)	43	28

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	168	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	518/518 (100%)	512 (99%)	6 (1%)	63	51

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	91	VAL
1	A	168	PRO
1	A	169	THR
1	A	407	MET
1	A	486	THR
1	A	503	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	333	ASN
1	A	556	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 ⓘ

2 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	C	1	1,2	14,14,15	0.82	0	17,19,21	1.19	3 (17%)
2	NAG	C	2	2	14,14,15	0.66	0	17,19,21	2.34	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	C	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	NAG	C1-O5-C5	6.71	121.17	112.19
2	C	2	NAG	C4-C3-C2	-3.80	105.44	111.02
2	C	2	NAG	O3-C3-C2	2.78	115.18	109.40
2	C	2	NAG	O5-C1-C2	-2.53	107.38	111.29
2	C	1	NAG	O4-C4-C5	2.37	115.17	109.32
2	C	1	NAG	O5-C1-C2	-2.31	107.72	111.29
2	C	2	NAG	C1-C2-N2	2.27	114.02	110.43
2	C	1	NAG	C1-O5-C5	-2.00	109.50	112.19

There are no chirality outliers.

All (4) torsion outliers are listed below:

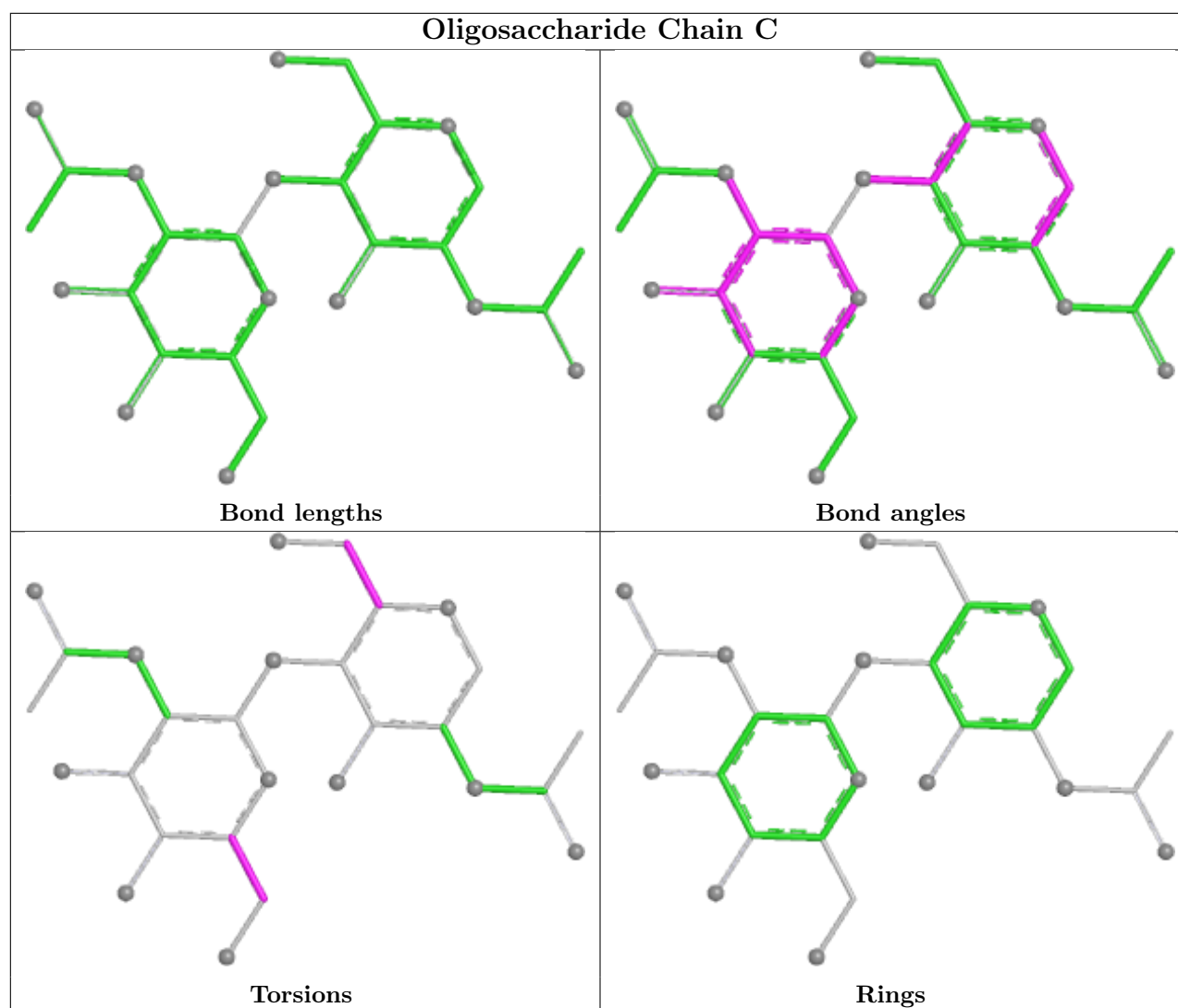
Mol	Chain	Res	Type	Atoms
2	C	2	NAG	C4-C5-C6-O6
2	C	2	NAG	O5-C5-C6-O6
2	C	1	NAG	C4-C5-C6-O6
2	C	1	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	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 30 ligands modelled in this entry, 21 are monoatomic - leaving 9 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
11	PEO	A	627	3	1,1,1	0.39	0	-		
10	OSM	A	617	-	1,3,3	0.31	0	0,2,2	-	-
10	OSM	A	618	-	1,3,3	0.29	0	0,2,2	-	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	EDO	A	615	-	3,3,3	0.72	0	2,2,2	0.05	0
7	GOL	A	614	-	5,5,5	0.25	0	5,5,5	0.35	0
3	HEM	A	601	1,11	50,50,50	1.79	13 (26%)	67,82,82	1.64	10 (14%)
10	OSM	A	619	-	1,3,3	0.12	0	0,2,2	-	-
5	NAG	A	630	1	14,14,15	0.61	0	17,19,21	1.35	2 (11%)
5	NAG	A	603	1	14,14,15	0.52	0	17,19,21	1.65	2 (11%)

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
10	OSM	A	617	-	-	0/0/1/1	-
10	OSM	A	618	-	-	0/0/1/1	-
8	EDO	A	615	-	-	1/1/1/1	-
7	GOL	A	614	-	-	4/4/4/4	-
3	HEM	A	601	1,11	-	4/14/54/54	-
10	OSM	A	619	-	-	0/0/1/1	-
5	NAG	A	630	1	-	2/6/23/26	0/1/1/1
5	NAG	A	603	1	-	0/6/23/26	0/1/1/1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	601	HEM	C1B-NB	-4.69	1.32	1.40
3	A	601	HEM	C4D-ND	-4.68	1.32	1.40
3	A	601	HEM	FE-NB	4.05	2.07	1.94
3	A	601	HEM	FE-NC	3.20	2.05	1.95
3	A	601	HEM	C1C-NC	-3.01	1.33	1.39
3	A	601	HEM	O1D-CGD	2.79	1.31	1.22
3	A	601	HEM	C4B-NB	-2.51	1.33	1.38
3	A	601	HEM	C4A-NA	-2.44	1.35	1.39
3	A	601	HEM	C1A-NA	-2.42	1.35	1.39
3	A	601	HEM	FE-NA	2.27	2.02	1.95
3	A	601	HEM	CBD-CAD	2.20	1.59	1.51
3	A	601	HEM	C4C-NC	-2.14	1.35	1.39
3	A	601	HEM	C1C-C2C	-2.08	1.41	1.45

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	601	HEM	C1B-NB-C4B	5.37	111.57	105.21
3	A	601	HEM	CHC-C4B-NB	5.04	129.85	124.42
3	A	601	HEM	C3B-C4B-NB	-4.61	106.16	109.47
5	A	603	NAG	O5-C1-C2	-4.29	104.66	111.29
3	A	601	HEM	CHB-C1B-NB	3.01	128.09	124.37
3	A	601	HEM	C1D-C2D-C3D	-2.81	104.03	106.98
3	A	601	HEM	CHD-C1D-C2D	-2.79	120.62	125.03
5	A	630	NAG	C2-N2-C7	-2.76	119.20	122.90
3	A	601	HEM	C3D-C4D-ND	2.73	113.17	110.17
3	A	601	HEM	C2D-C1D-ND	2.69	113.01	109.90
5	A	630	NAG	O5-C5-C4	-2.60	104.51	110.83
5	A	603	NAG	C1-C2-N2	-2.22	106.94	110.43
3	A	601	HEM	O2D-CGD-CBD	2.17	120.84	114.00
3	A	601	HEM	CMC-C2C-C1C	-2.04	121.14	124.73

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	614	GOL	O1-C1-C2-C3
7	A	614	GOL	C1-C2-C3-O3
7	A	614	GOL	O2-C2-C3-O3
5	A	630	NAG	C4-C5-C6-O6
7	A	614	GOL	O1-C1-C2-O2
5	A	630	NAG	O5-C5-C6-O6
3	A	601	HEM	CAD-CBD-CGD-O2D
3	A	601	HEM	CAA-CBA-CGA-O1A
3	A	601	HEM	CAA-CBA-CGA-O2A
8	A	615	EDO	O1-C1-C2-O2
3	A	601	HEM	CAD-CBD-CGD-O1D

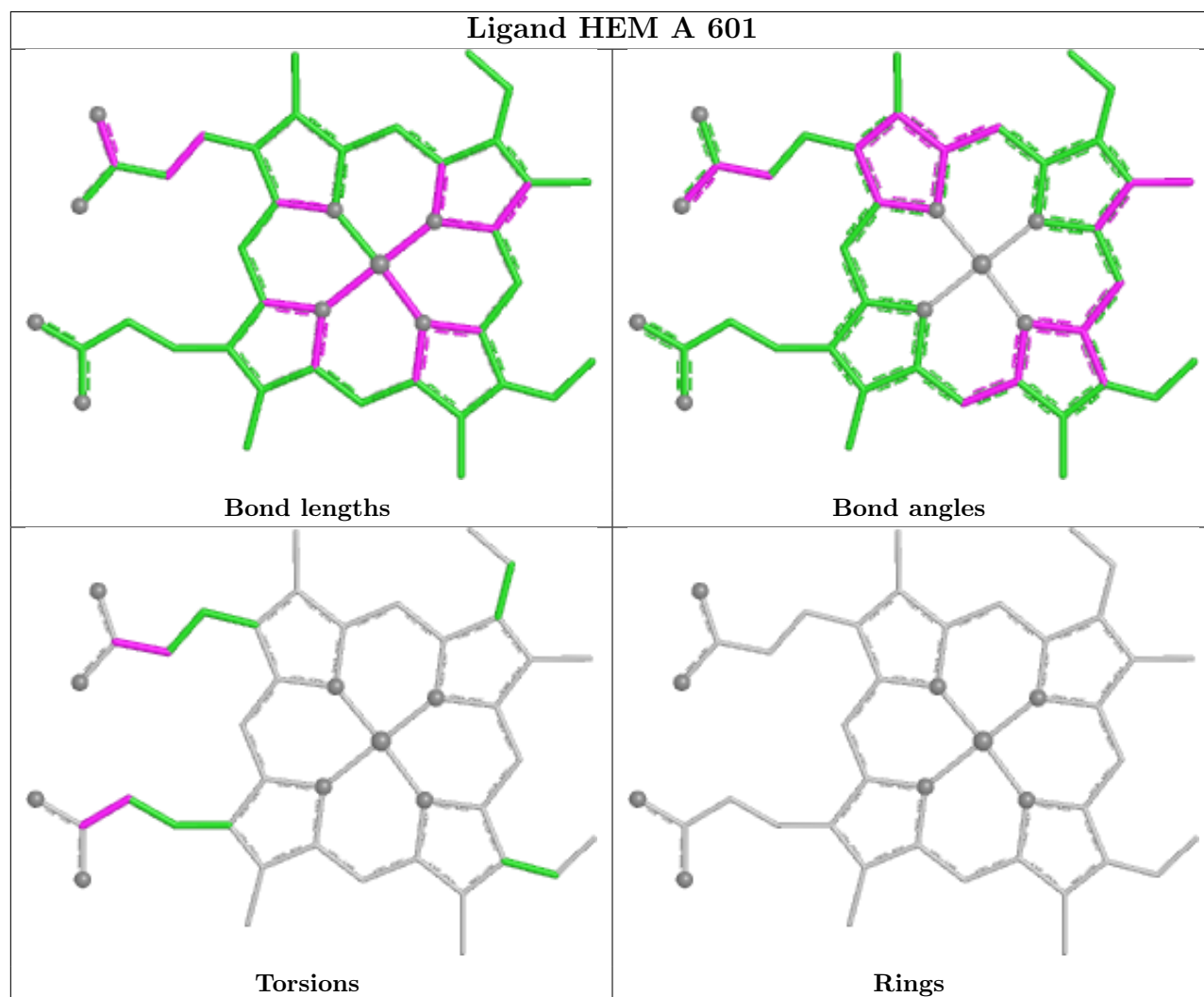
There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	A	627	PEO	2	0
10	A	617	OSM	2	0
10	A	619	OSM	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 ⓘ

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%)	0.77	69 (11%) 9 9	16, 31, 100, 173	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	168	PRO	8.7
1	A	174	SER	7.5
1	A	169	THR	7.4
1	A	4	VAL	7.3
1	A	171	PRO	6.3
1	A	119	LEU	6.1
1	A	2	TRP	6.0
1	A	173	GLN	5.8
1	A	12	LEU	5.3
1	A	10	VAL	5.3
1	A	5	GLY	4.9
1	A	175	LEU	4.5
1	A	220	TRP	4.5
1	A	8	ALA	4.3
1	A	172	TYR	4.2
1	A	13	VAL	4.2
1	A	125	SER	4.0
1	A	117	THR	4.0
1	A	9	PRO	4.0
1	A	167	CYS	3.7
1	A	283	LEU	3.7
1	A	6	CYS	3.7
1	A	170	PRO	3.7
1	A	127	THR	3.5
1	A	120	GLY	3.5
1	A	287	TRP	3.4
1	A	63	GLN	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	129	CYS	3.3
1	A	582	VAL	3.3
1	A	1	SER	3.3
1	A	126	LYS	3.3
1	A	280	LEU	3.2
1	A	124	HIS	3.2
1	A	207	SER	3.1
1	A	209	PRO	3.0
1	A	240	ILE	3.0
1	A	11	PRO	3.0
1	A	7	GLY	3.0
1	A	223	GLY	3.0
1	A	572	TYR	2.9
1	A	254	PHE	2.8
1	A	580	SER	2.8
1	A	368	TRP	2.7
1	A	577	VAL	2.7
1	A	118	GLU	2.7
1	A	121	SER	2.7
1	A	591	ALA	2.7
1	A	224	LEU	2.6
1	A	324	TRP	2.5
1	A	20	PRO	2.5
1	A	243	THR	2.4
1	A	211	GLY	2.4
1	A	564	LEU	2.3
1	A	279	GLU	2.3
1	A	206	LEU	2.3
1	A	210	LEU	2.3
1	A	576	PHE	2.3
1	A	208	SER	2.3
1	A	579	CYS	2.2
1	A	289	GLY	2.2
1	A	559	ILE	2.2
1	A	241	ASN	2.2
1	A	363	GLU	2.2
1	A	595	ASN	2.2
1	A	578	ASP	2.1
1	A	203	LEU	2.1
1	A	428	ILE	2.1
1	A	122	ASN	2.0
1	A	593	ARG	2.0

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

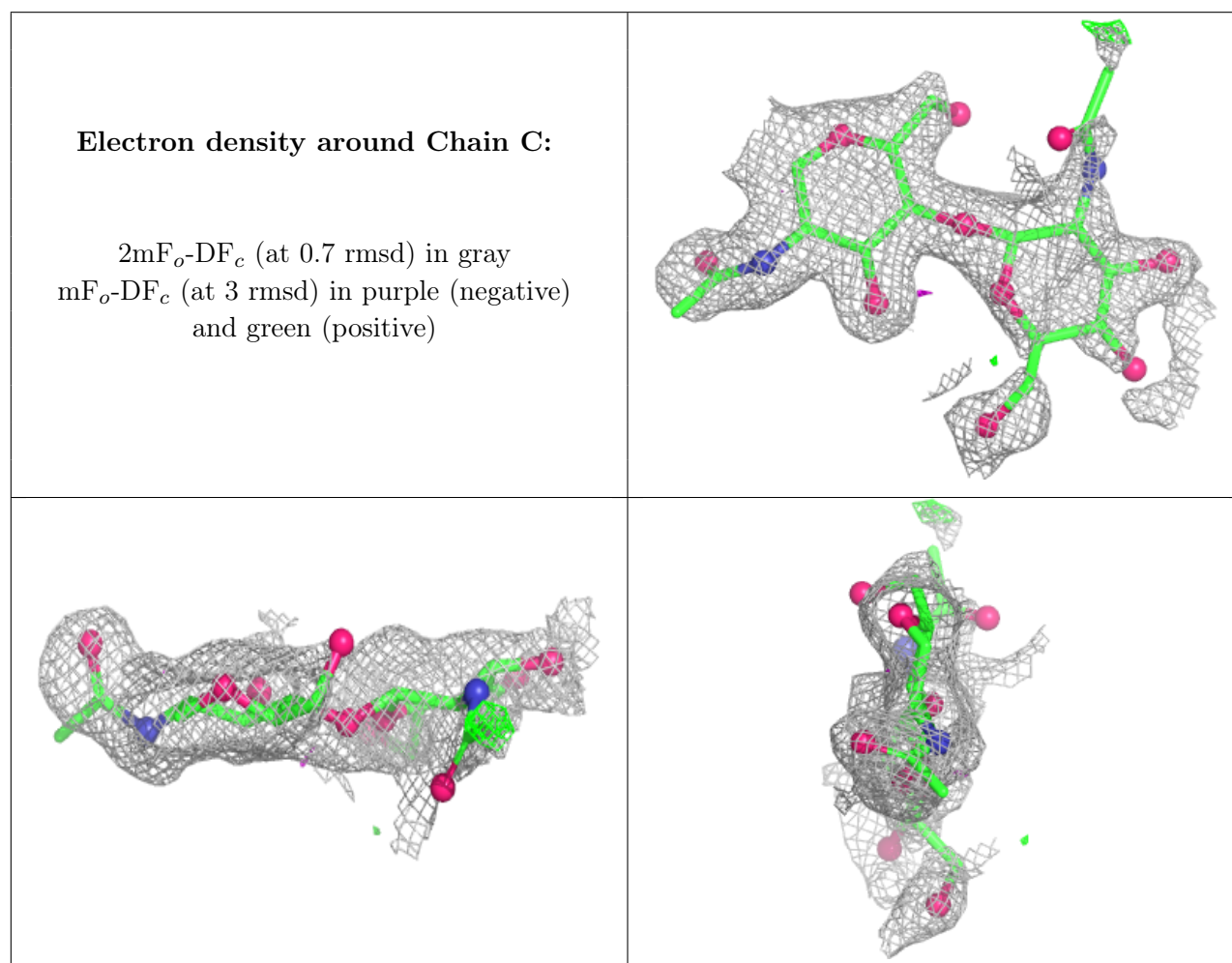
There are no non-standard protein/DNA/RNA residues in this entry.

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	C	1	14/15	-	-	29,40,48,55	0
2	NAG	C	2	14/15	-	-	64,77,89,91	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.



6.4 Ligands ⓘ

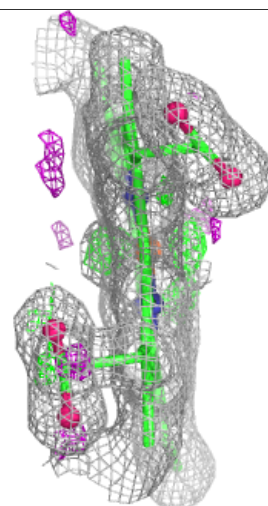
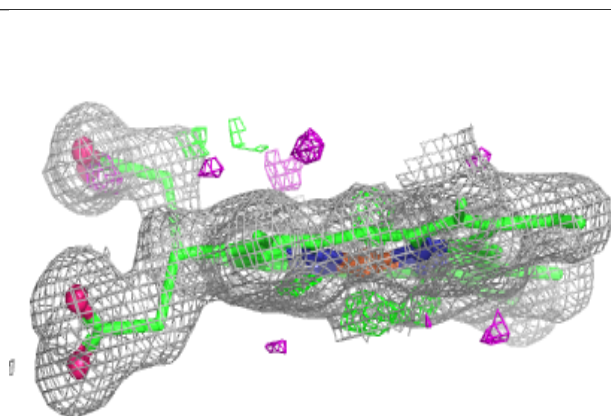
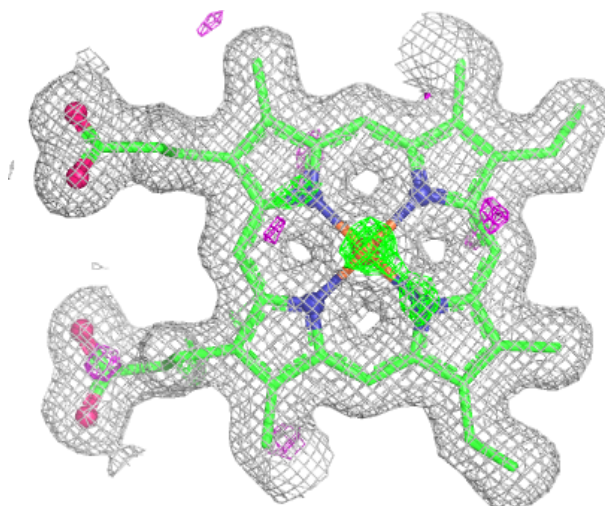
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NAG	A	603	14/15	0.82	0.11	43,51,56,56	0
5	NAG	A	630	14/15	0.84	0.11	37,44,50,59	0
10	OSM	A	619	4/4	0.84	0.23	30,32,36,37	4
6	IOD	A	610	1/1	0.87	0.12	60,60,60,60	1
8	EDO	A	615	4/4	0.88	0.13	29,31,31,31	0
7	GOL	A	614	6/6	0.88	0.14	35,42,52,53	0
10	OSM	A	617	4/4	0.91	0.14	40,42,43,53	0
10	OSM	A	618	4/4	0.92	0.13	35,35,36,38	0
6	IOD	A	626	1/1	0.93	0.11	45,45,45,45	0
6	IOD	A	606	1/1	0.93	0.09	47,47,47,47	1
11	PEO	A	627	2/2	0.93	0.10	16,16,16,29	0
6	IOD	A	611	1/1	0.94	0.08	48,48,48,48	1
6	IOD	A	623	1/1	0.95	0.10	51,51,51,51	1
6	IOD	A	609	1/1	0.95	0.08	40,40,40,40	1
6	IOD	A	612	1/1	0.95	0.08	46,46,46,46	1
6	IOD	A	613	1/1	0.95	0.17	42,42,42,42	1
6	IOD	A	625	1/1	0.96	0.07	40,40,40,40	1
6	IOD	A	622	1/1	0.96	0.07	41,41,41,41	1
6	IOD	A	628	1/1	0.96	0.08	54,54,54,54	1
6	IOD	A	629	1/1	0.96	0.19	58,58,58,58	1
6	IOD	A	621	1/1	0.96	0.06	45,45,45,45	1
6	IOD	A	608	1/1	0.97	0.06	32,32,32,32	0
6	IOD	A	605	1/1	0.97	0.05	32,32,32,32	1
6	IOD	A	607	1/1	0.97	0.06	44,44,44,44	1
9	ZN	A	616	1/1	0.97	0.07	39,39,39,39	0
6	IOD	A	624	1/1	0.98	0.04	39,39,39,39	1
3	HEM	A	601	43/43	0.98	0.06	16,18,23,25	0
6	IOD	A	620	1/1	0.99	0.02	28,28,28,28	1
4	CA	A	602	1/1	0.99	0.03	20,20,20,20	0
6	IOD	A	604	1/1	1.00	0.01	19,19,19,19	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 HEM A 601:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.