



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:51 PM UTC

PDB ID : 3R55 / pdb_00003r55
Title : Crystal structure of the complex of goat lactoperoxidase with Pyrazinamide at 2.1 Å resolution
Authors : Singh, R.P.; Pandey, N.; Singh, A.K.; Sinha, M.; Kaur, P.; Sharma, S.; Singh, T.P.
Deposited on : 2011-03-18
Resolution : 2.10 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ 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

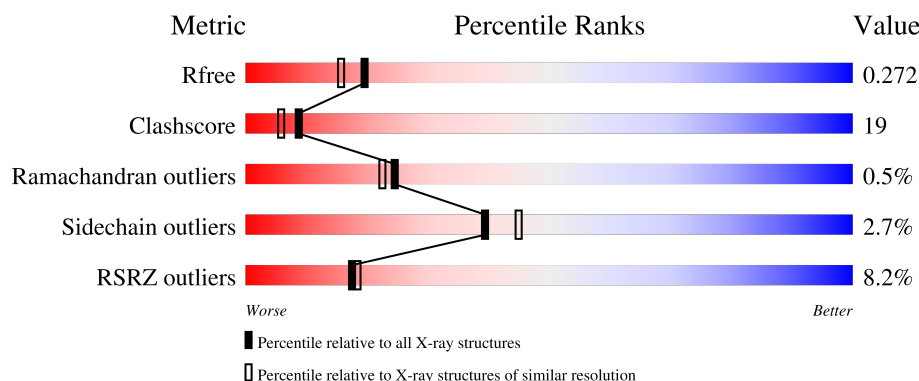
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	8% 79% 17% .
2	B	2	50% 50%
2	C	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
12	MRD	A	628	-	-	X	-
9	PZA	A	619	-	-	X	-
9	PZA	A	620	-	-	X	-

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 5298 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.

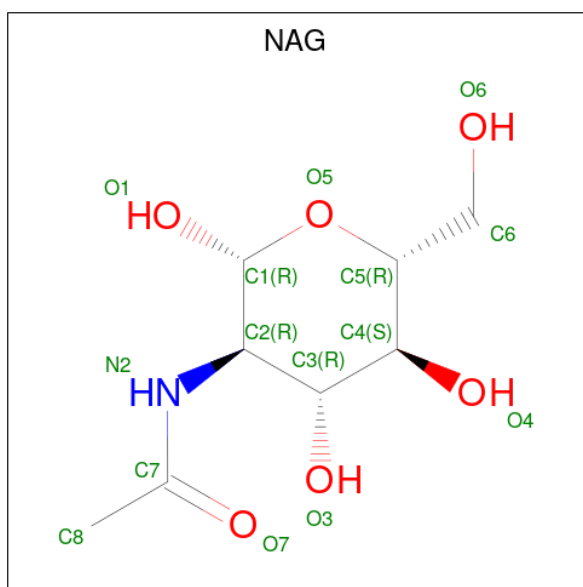
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	595	Total	C	N	O	P	S	0	0	0
			4756	3021	843	865	1	26			

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



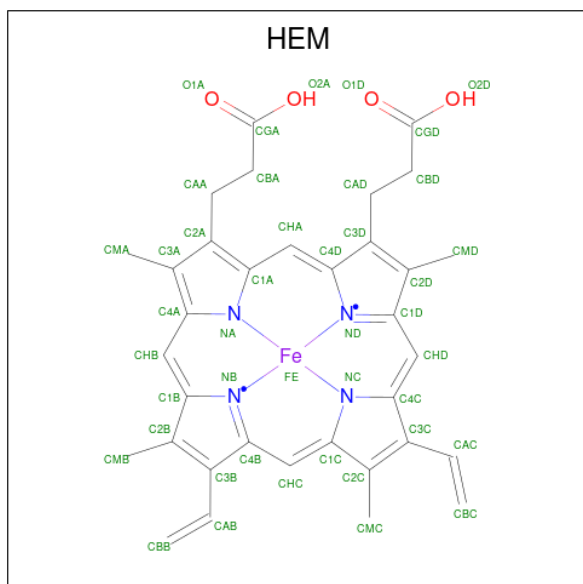
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	C	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 4 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

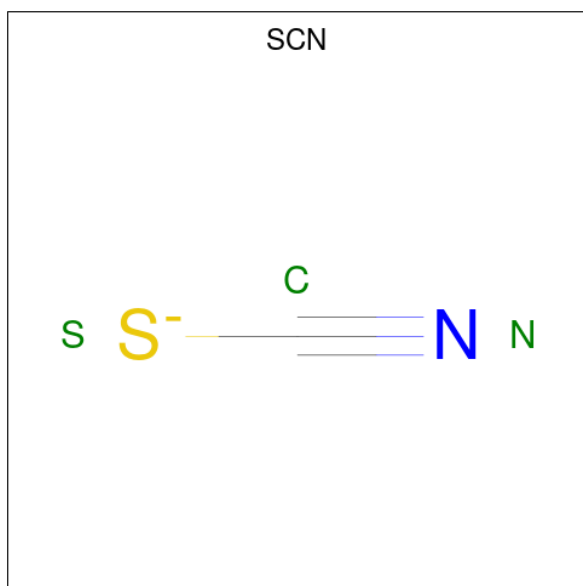
- Molecule 6 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

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

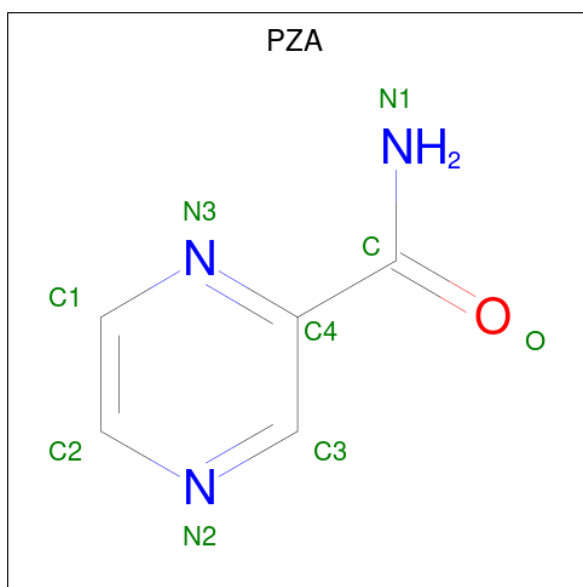
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	12	Total	I	0	0
			12	12		

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



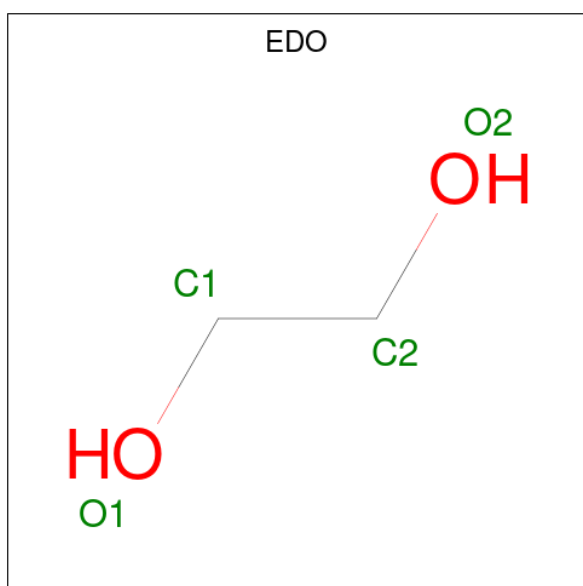
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	S	0	0
			3	1	1	1		

- Molecule 9 is PYRAZINE-2-CARBOXAMIDE (CCD ID: PZA) (formula: C₅H₅N₃O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	N	O	0	0
			9	5	3	1		
9	A	1	Total	C	N	O	0	0
			9	5	3	1		

- Molecule 10 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



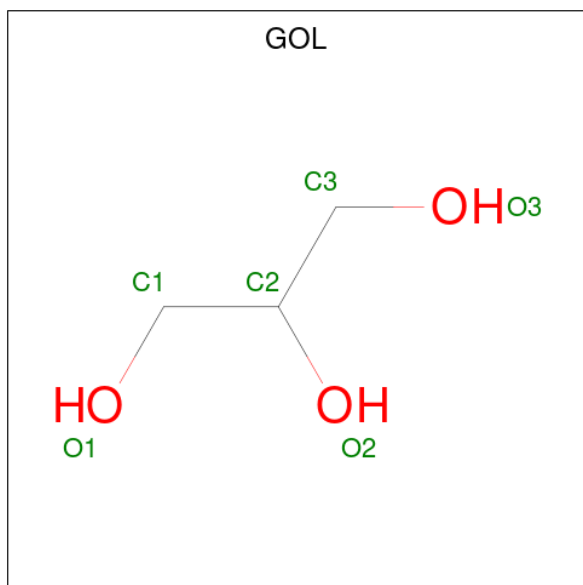
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		

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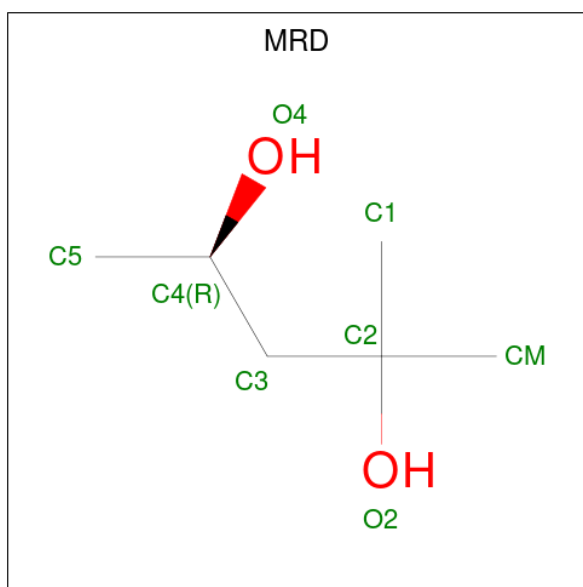
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 11 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



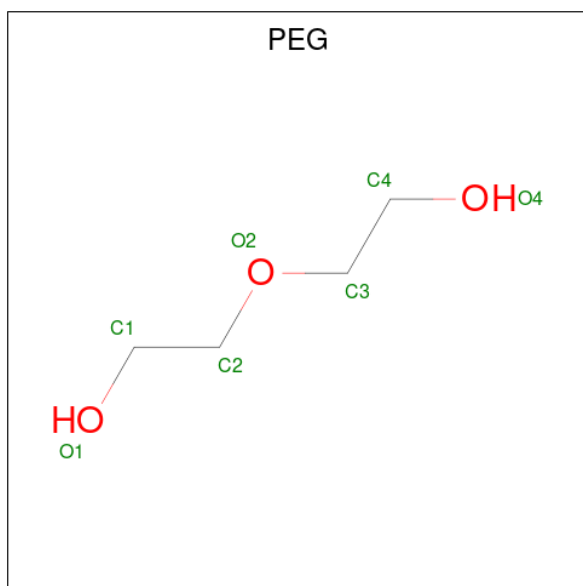
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	C	O	0	0
			6	3	3		
11	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 12 is (4R)-2-METHYLPENTANE-2,4-DIOL (CCD ID: MRD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	A	1	Total	C	O	0	0
			8	6	2		

- Molecule 13 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



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

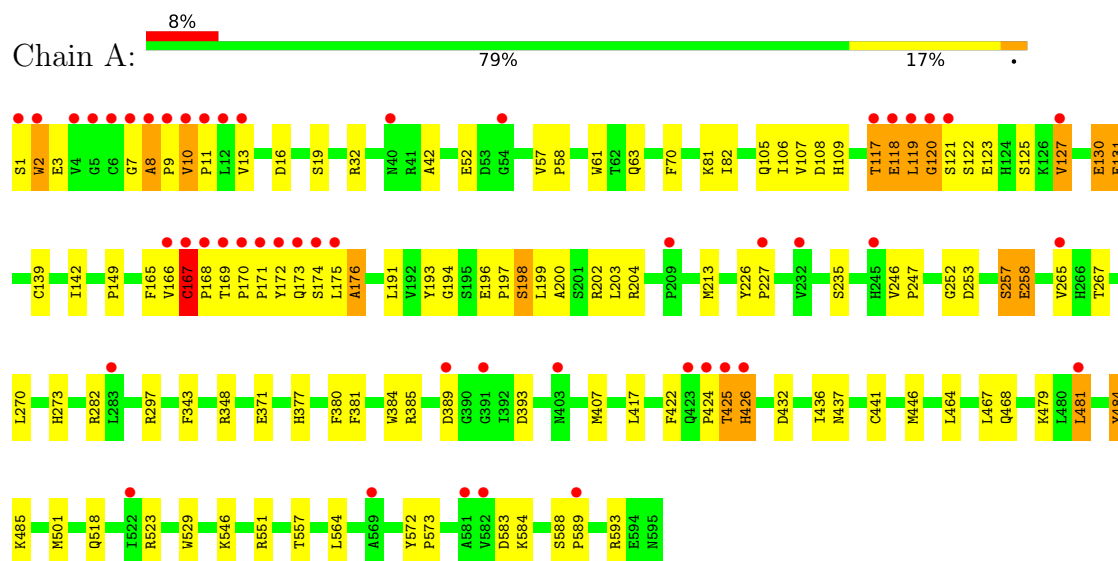
- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	333	Total 333	O 333	0	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

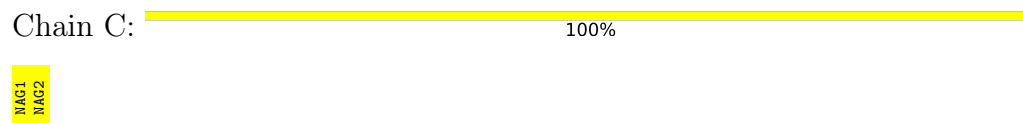
- Molecule 1: Lactoperoxidase



- 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 79.62Å 77.52Å 90.00° 102.24° 90.00°	Depositor
Resolution (Å)	26.40 – 2.10 26.40 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.6 (26.40-2.10) 98.6 (26.40-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.58 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.219 , 0.264 (Not available) , 0.272	Depositor DCC
R_{free} test set	1866 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	42.1	Xtriage
Anisotropy	0.315	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 29.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5298	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.53% 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: HEM, SEP, EDO, ZN, SCN, IOD, PZA, NAG, GOL, MRD, CA, PEG

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	0.54	2/4874 (0.0%)	0.93	24/6619 (0.4%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	481	LEU	C-N	-10.16	1.20	1.33
1	A	176	ALA	C-N	-6.67	1.24	1.33

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	107	VAL	CA-C-N	10.00	134.48	120.29
1	A	107	VAL	C-N-CA	10.00	134.48	120.29
1	A	107	VAL	O-C-N	-9.98	112.19	121.87
1	A	173	GLN	N-CA-C	9.28	124.37	111.56
1	A	257	SER	O-C-N	-8.79	111.54	122.35
1	A	108	ASP	O-C-N	8.55	131.90	122.15
1	A	122	SER	N-CA-C	-8.30	103.06	113.02
1	A	257	SER	CA-C-N	7.81	132.18	120.31
1	A	257	SER	C-N-CA	7.81	132.18	120.31
1	A	119	LEU	CB-CA-C	-7.73	100.51	111.80
1	A	258	GLU	O-C-N	7.45	131.43	122.27
1	A	2	TRP	N-CA-C	-7.41	98.38	108.38
1	A	10	VAL	N-CA-C	-6.45	101.86	108.96
1	A	426	HIS	N-CA-C	-6.30	100.65	110.42
1	A	484	TYR	N-CA-C	-5.78	99.10	108.52
1	A	119	LEU	N-CA-C	5.34	118.80	111.54
1	A	258	GLU	CA-C-N	-5.33	112.41	121.85
1	A	258	GLU	C-N-CA	-5.33	112.41	121.85
1	A	108	ASP	CA-C-N	-5.30	112.25	120.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	108	ASP	C-N-CA	-5.30	112.25	120.31
1	A	226	TYR	CA-C-N	-5.09	115.94	119.66
1	A	226	TYR	C-N-CA	-5.09	115.94	119.66
1	A	167	CYS	CA-C-N	5.09	125.02	119.78
1	A	167	CYS	C-N-CA	5.09	125.02	119.78

There are no chirality outliers.

There are no planarity outliers.

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	4756	0	4640	173	0
2	B	28	0	25	0	0
2	C	28	0	25	1	0
3	A	28	0	26	0	0
4	A	43	0	30	8	0
5	A	1	0	0	0	0
6	A	1	0	0	0	0
7	A	12	0	0	0	0
8	A	3	0	0	0	0
9	A	18	0	10	18	0
10	A	20	0	30	1	0
11	A	12	0	16	2	0
12	A	8	0	14	14	0
13	A	7	0	10	1	0
14	A	333	0	0	5	0
All	All	5298	0	4826	183	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 19.

All (183) 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:2:TRP:CD1	1:A:175:LEU:HD13	1.56	1.41
1:A:167:CYS:CB	1:A:168:PRO:HD2	1.60	1.31
1:A:167:CYS:CB	1:A:168:PRO:CD	2.06	1.27
1:A:120:GLY:HA3	1:A:123:GLU:CD	1.62	1.25
1:A:2:TRP:CB	1:A:175:LEU:HD22	1.72	1.18
1:A:167:CYS:HB2	1:A:168:PRO:CD	1.66	1.17
1:A:7:GLY:C	1:A:9:PRO:HD3	1.73	1.13
1:A:118:GLU:H	1:A:118:GLU:CD	1.55	1.11
1:A:2:TRP:HB2	1:A:175:LEU:HD22	1.23	1.07
1:A:202:ARG:HD3	12:A:628:MRD:H1C1	1.30	1.06
1:A:167:CYS:HB3	1:A:168:PRO:CD	1.82	1.05
1:A:105:GLN:HE21	9:A:619:PZA:H2	1.03	1.02
1:A:167:CYS:HB3	1:A:168:PRO:HD3	1.34	1.02
1:A:120:GLY:C	1:A:123:GLU:HB2	1.87	1.00
1:A:196:GLU:HB3	1:A:198:SEP:O3P	1.63	0.99
1:A:8:ALA:N	1:A:9:PRO:HD3	1.78	0.99
1:A:120:GLY:HA3	1:A:123:GLU:CG	1.93	0.98
1:A:120:GLY:O	1:A:123:GLU:HB2	1.63	0.96
1:A:8:ALA:N	1:A:9:PRO:CD	2.28	0.96
1:A:169:THR:HB	1:A:170:PRO:HD3	1.48	0.95
1:A:8:ALA:HB3	1:A:167:CYS:HA	1.49	0.94
1:A:42:ALA:HB2	1:A:166:VAL:HG11	1.49	0.94
1:A:2:TRP:CD1	1:A:175:LEU:CD1	2.51	0.92
9:A:619:PZA:H5	9:A:620:PZA:C	2.04	0.88
1:A:105:GLN:NE2	9:A:619:PZA:H2	1.73	0.84
1:A:202:ARG:HH11	12:A:628:MRD:H3C1	1.40	0.84
1:A:118:GLU:CD	1:A:118:GLU:N	2.29	0.83
1:A:167:CYS:HB2	1:A:168:PRO:HD2	0.83	0.82
1:A:120:GLY:CA	1:A:123:GLU:HB2	2.09	0.82
1:A:407:MET:HB3	1:A:501:MET:CE	2.12	0.80
1:A:9:PRO:O	1:A:11:PRO:HD3	1.83	0.78
1:A:407:MET:HB3	1:A:501:MET:HE3	1.66	0.77
1:A:2:TRP:NE1	1:A:175:LEU:HD13	2.04	0.73
1:A:165:PHE:CZ	1:A:169:THR:O	2.41	0.73
1:A:81:LYS:HD3	13:A:629:PEG:H42	1.71	0.73
1:A:118:GLU:OE2	1:A:119:LEU:HG	1.89	0.73
1:A:2:TRP:CZ3	1:A:174:SER:HB3	2.24	0.72
1:A:105:GLN:HG3	9:A:619:PZA:N1	2.04	0.72
4:A:603:HEM:HBD2	14:A:752:HOH:O	1.91	0.71
1:A:118:GLU:HG2	1:A:119:LEU:H	1.55	0.71
4:A:603:HEM:HMC1	4:A:603:HEM:HBC2	1.71	0.70
1:A:105:GLN:NE2	9:A:619:PZA:H4	2.07	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:TRP:HB2	1:A:175:LEU:CD2	2.11	0.69
12:A:628:MRD:H5C3	12:A:628:MRD:H1C2	1.75	0.69
1:A:109:HIS:NE2	9:A:619:PZA:C	2.56	0.69
1:A:467:LEU:HD22	1:A:481:LEU:CD1	2.22	0.69
1:A:120:GLY:HA3	1:A:123:GLU:CB	2.22	0.69
1:A:106:ILE:HG13	1:A:265:VAL:HG11	1.75	0.69
1:A:2:TRP:CH2	1:A:174:SER:O	2.46	0.69
1:A:105:GLN:HE21	9:A:619:PZA:H4	1.58	0.68
1:A:118:GLU:N	1:A:118:GLU:OE2	2.26	0.68
1:A:7:GLY:O	1:A:8:ALA:HB3	1.94	0.68
1:A:2:TRP:CG	1:A:175:LEU:HD13	2.22	0.67
1:A:202:ARG:CD	12:A:628:MRD:H1C1	2.17	0.67
1:A:172:TYR:CE2	1:A:174:SER:HB2	2.29	0.67
1:A:8:ALA:CB	1:A:167:CYS:HA	2.23	0.67
1:A:120:GLY:CA	1:A:123:GLU:CD	2.56	0.67
1:A:105:GLN:HG3	9:A:619:PZA:H1	1.60	0.66
1:A:118:GLU:CG	1:A:119:LEU:H	2.08	0.66
1:A:199:LEU:HA	12:A:628:MRD:C1	2.26	0.65
1:A:120:GLY:HA3	1:A:123:GLU:HB2	1.76	0.65
1:A:199:LEU:HA	12:A:628:MRD:H1C3	1.79	0.65
1:A:7:GLY:O	1:A:167:CYS:HA	1.97	0.65
1:A:8:ALA:HB3	1:A:167:CYS:CA	2.26	0.64
1:A:202:ARG:HH11	12:A:628:MRD:C3	2.10	0.64
1:A:481:LEU:HA	1:A:484:TYR:O	1.98	0.64
1:A:381:PHE:CZ	9:A:620:PZA:H4	2.33	0.64
1:A:2:TRP:CG	1:A:175:LEU:HD22	2.31	0.63
1:A:2:TRP:HB3	1:A:175:LEU:HD22	1.77	0.61
1:A:120:GLY:HA3	1:A:123:GLU:OE1	1.99	0.61
1:A:169:THR:N	1:A:170:PRO:CD	2.63	0.61
1:A:117:THR:HG22	1:A:118:GLU:OE2	2.01	0.60
1:A:119:LEU:HD11	1:A:169:THR:HG22	1.82	0.60
1:A:202:ARG:HD3	12:A:628:MRD:C1	2.20	0.60
1:A:197:PRO:HA	10:A:623:EDO:H12	1.83	0.60
1:A:432:ASP:O	1:A:436:ILE:HG12	2.02	0.60
1:A:7:GLY:CA	1:A:9:PRO:HD3	2.32	0.60
1:A:42:ALA:CB	1:A:166:VAL:HG11	2.29	0.59
1:A:119:LEU:HD21	1:A:169:THR:CG2	2.33	0.59
1:A:149:PRO:HG2	11:A:626:GOL:H2	1.85	0.59
1:A:169:THR:H	1:A:170:PRO:HD2	1.67	0.58
1:A:464:LEU:O	1:A:468:GLN:HG3	2.04	0.57
1:A:213:MET:HG2	1:A:273:HIS:CD2	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:TRP:CD2	1:A:175:LEU:HB2	2.39	0.56
1:A:348:ARG:HH11	1:A:437:ASN:HD22	1.53	0.56
1:A:258:GLU:HG3	9:A:619:PZA:N2	2.20	0.56
1:A:120:GLY:CA	1:A:123:GLU:CB	2.79	0.56
1:A:172:TYR:CE2	1:A:174:SER:N	2.69	0.56
1:A:467:LEU:HD22	1:A:481:LEU:HD11	1.88	0.56
1:A:202:ARG:HD2	12:A:628:MRD:H3C1	1.88	0.55
1:A:551:ARG:HD3	1:A:583:ASP:O	2.06	0.55
1:A:2:TRP:CZ2	1:A:174:SER:O	2.59	0.55
1:A:348:ARG:HH11	1:A:437:ASN:ND2	2.04	0.54
1:A:467:LEU:CD2	1:A:481:LEU:CD1	2.85	0.54
1:A:169:THR:H	1:A:170:PRO:CD	2.21	0.54
1:A:82:ILE:HD11	1:A:479:LYS:HB3	1.89	0.54
1:A:381:PHE:CZ	9:A:620:PZA:C3	2.91	0.54
1:A:169:THR:HB	1:A:170:PRO:CD	2.31	0.53
1:A:172:TYR:HE2	1:A:174:SER:HB2	1.73	0.53
1:A:16:ASP:CG	1:A:19:SER:HB2	2.35	0.52
1:A:1:SER:O	1:A:2:TRP:CD1	2.63	0.52
1:A:169:THR:N	1:A:170:PRO:HD2	2.24	0.52
1:A:142:ILE:CD1	1:A:436:ILE:HD13	2.39	0.52
1:A:16:ASP:OD1	1:A:19:SER:N	2.42	0.52
1:A:407:MET:CB	1:A:501:MET:CE	2.85	0.51
1:A:142:ILE:HD12	1:A:436:ILE:HD13	1.93	0.51
4:A:603:HEM:HMB2	4:A:603:HEM:HBB2	1.93	0.51
1:A:257:SER:O	1:A:381:PHE:HA	2.11	0.51
4:A:603:HEM:HBB2	4:A:603:HEM:CMB	2.40	0.51
1:A:7:GLY:O	1:A:8:ALA:CB	2.59	0.50
1:A:70:PHE:CG	1:A:485:LYS:HB2	2.47	0.50
1:A:203:LEU:HD11	1:A:252:GLY:HA2	1.94	0.50
1:A:119:LEU:HD21	1:A:169:THR:HG22	1.95	0.49
1:A:32:ARG:HD2	14:A:994:HOH:O	2.13	0.49
1:A:424:PRO:O	1:A:425:THR:HB	2.13	0.49
4:A:603:HEM:HBC2	4:A:603:HEM:CMC	2.40	0.49
1:A:551:ARG:CZ	1:A:584:LYS:HG2	2.43	0.49
1:A:425:THR:O	1:A:425:THR:HG23	2.13	0.49
1:A:377:HIS:HA	1:A:380:PHE:CE2	2.48	0.48
1:A:424:PRO:C	1:A:426:HIS:H	2.19	0.48
1:A:1:SER:O	1:A:2:TRP:CG	2.66	0.48
1:A:172:TYR:OH	1:A:174:SER:HB2	2.13	0.48
1:A:572:TYR:CD1	1:A:573:PRO:HA	2.49	0.48
1:A:118:GLU:CG	1:A:119:LEU:N	2.75	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:417:LEU:HD21	4:A:603:HEM:HMB3	1.96	0.48
1:A:52:GLU:HG2	1:A:57:VAL:HG12	1.96	0.47
1:A:63:GLN:HG2	14:A:927:HOH:O	2.14	0.47
1:A:105:GLN:CG	9:A:619:PZA:N1	2.77	0.47
1:A:118:GLU:OE2	1:A:119:LEU:N	2.48	0.47
1:A:193:TYR:OH	1:A:297:ARG:HA	2.15	0.46
1:A:202:ARG:CD	12:A:628:MRD:H3C1	2.45	0.46
1:A:588:SER:N	1:A:589:PRO:HD2	2.30	0.46
1:A:202:ARG:NH1	12:A:628:MRD:HMC2	2.30	0.46
1:A:120:GLY:CA	1:A:123:GLU:CG	2.80	0.46
1:A:139:CYS:HB2	11:A:627:GOL:O1	2.15	0.46
1:A:123:GLU:HG2	1:A:125:SER:OG	2.16	0.46
1:A:82:ILE:CD1	1:A:479:LYS:HB3	2.46	0.46
1:A:385:ARG:O	1:A:389:ASP:HB3	2.16	0.46
1:A:191:LEU:HA	1:A:253:ASP:HB2	1.97	0.45
1:A:172:TYR:CZ	1:A:174:SER:HB2	2.50	0.45
1:A:199:LEU:CD1	12:A:628:MRD:H1C3	2.46	0.45
9:A:619:PZA:H5	9:A:620:PZA:C4	2.45	0.45
1:A:446:MET:HA	1:A:446:MET:HE2	1.99	0.45
1:A:343:PHE:CD1	1:A:518:GLN:HG2	2.52	0.45
1:A:194:GLY:HA2	1:A:252:GLY:O	2.16	0.45
1:A:551:ARG:HD3	1:A:584:LYS:HA	1.98	0.45
1:A:127:VAL:O	1:A:131:GLU:HB2	2.16	0.45
1:A:523:ARG:HG3	1:A:529:TRP:CE2	2.52	0.44
1:A:467:LEU:CD2	1:A:481:LEU:HD13	2.47	0.44
1:A:2:TRP:CG	1:A:175:LEU:HB2	2.52	0.44
1:A:9:PRO:O	1:A:11:PRO:CD	2.59	0.44
1:A:130:GLU:CD	1:A:426:HIS:HD1	2.25	0.44
1:A:200:ALA:O	1:A:204:ARG:HG3	2.18	0.44
1:A:424:PRO:O	1:A:425:THR:CB	2.64	0.44
1:A:2:TRP:HZ3	1:A:174:SER:HB3	1.77	0.44
1:A:393:ASP:OD1	1:A:557:THR:HB	2.17	0.43
1:A:381:PHE:HZ	9:A:620:PZA:C3	2.29	0.43
1:A:121:SER:C	1:A:123:GLU:H	2.24	0.43
1:A:171:PRO:HG2	14:A:943:HOH:O	2.18	0.43
1:A:199:LEU:HA	12:A:628:MRD:H1C2	1.98	0.43
1:A:422:PHE:CD2	1:A:422:PHE:C	2.96	0.42
1:A:171:PRO:HB2	14:A:943:HOH:O	2.18	0.42
1:A:175:LEU:HD12	1:A:176:ALA:H	1.84	0.42
1:A:572:TYR:CG	1:A:573:PRO:HA	2.55	0.42
1:A:282:ARG:HH11	1:A:282:ARG:HG3	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:16:ASP:OD1	1:A:16:ASP:C	2.62	0.42
1:A:105:GLN:NE2	9:A:619:PZA:N1	2.51	0.41
1:A:381:PHE:CE2	9:A:620:PZA:C3	3.03	0.41
1:A:227:PRO:HD3	1:A:267:THR:HG23	2.02	0.41
1:A:202:ARG:HB3	12:A:628:MRD:H1C1	2.00	0.41
1:A:58:PRO:HG2	1:A:61:TRP:HB2	2.02	0.41
1:A:57:VAL:HG13	1:A:61:TRP:CG	2.55	0.41
1:A:467:LEU:HD23	1:A:481:LEU:HD13	2.02	0.41
1:A:546:LYS:HB2	1:A:546:LYS:NZ	2.36	0.41
1:A:2:TRP:O	1:A:3:GLU:C	2.61	0.41
4:A:603:HEM:C4D	9:A:619:PZA:O	2.73	0.41
1:A:7:GLY:HA2	1:A:9:PRO:HD3	2.02	0.41
4:A:603:HEM:ND	9:A:619:PZA:O	2.54	0.41
1:A:16:ASP:CB	1:A:19:SER:HB2	2.51	0.40
1:A:120:GLY:O	1:A:123:GLU:CB	2.53	0.40
1:A:166:VAL:O	1:A:167:CYS:HB2	2.21	0.40
1:A:246:VAL:HA	1:A:247:PRO:HD3	1.85	0.40
1:A:384:TRP:CH2	2:C:1:NAG:H2	2.56	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	592/595 (100%)	567 (96%)	22 (4%)	3 (0%)	24 22

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	8	ALA
1	A	167	CYS
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	515/516 (100%)	501 (97%)	14 (3%)	39 45

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	VAL
1	A	13	VAL
1	A	117	THR
1	A	118	GLU
1	A	127	VAL
1	A	130	GLU
1	A	131	GLU
1	A	235	SER
1	A	270	LEU
1	A	371	GLU
1	A	425	THR
1	A	441	CYS
1	A	564	LEU
1	A	593	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	ASN
1	A	102	GLN
1	A	105	GLN
1	A	124	HIS
1	A	128	GLN
1	A	147	ASN
1	A	259	GLN
1	A	329	GLN
1	A	437	ASN
1	A	468	GLN
1	A	497	ASN

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Mol	Chain	Res	Type
1	A	568	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	SEP	A	198	1	8,9,10	1.67	1 (12%)	7,12,14	1.34	1 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	SEP	A	198	1	-	4/6/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	198	SEP	P-O1P	3.56	1.61	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	198	SEP	OG-CB-CA	2.36	110.44	108.14

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	198	SEP	CB-OG-P-O1P
1	A	198	SEP	CB-OG-P-O2P
1	A	198	SEP	CB-OG-P-O3P
1	A	198	SEP	CA-CB-OG-P

There are no ring outliers.

1 monomer is involved in 1 short contact:

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

5.5 Carbohydrates [i](#)

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	B	1	2,1	14,14,15	0.49	0	17,19,21	0.83	0
2	NAG	B	2	2	14,14,15	1.09	2 (14%)	17,19,21	1.45	3 (17%)
2	NAG	C	1	2,1	14,14,15	0.66	0	17,19,21	0.73	0
2	NAG	C	2	2	14,14,15	0.42	0	17,19,21	2.20	4 (23%)

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

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2	NAG	C8-C7	2.60	1.55	1.50
2	B	2	NAG	C1-C2	2.03	1.55	1.52

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	NAG	C1-O5-C5	6.92	121.46	112.19
2	B	2	NAG	C4-C3-C2	3.29	115.84	111.02
2	C	2	NAG	C4-C3-C2	-2.91	106.76	111.02
2	B	2	NAG	C1-O5-C5	-2.68	108.59	112.19
2	C	2	NAG	C1-C2-N2	2.56	114.47	110.43
2	C	2	NAG	O5-C5-C4	2.53	116.98	110.83
2	B	2	NAG	C2-N2-C7	2.17	125.81	122.90

There are no chirality outliers.

All (2) torsion outliers are listed below:

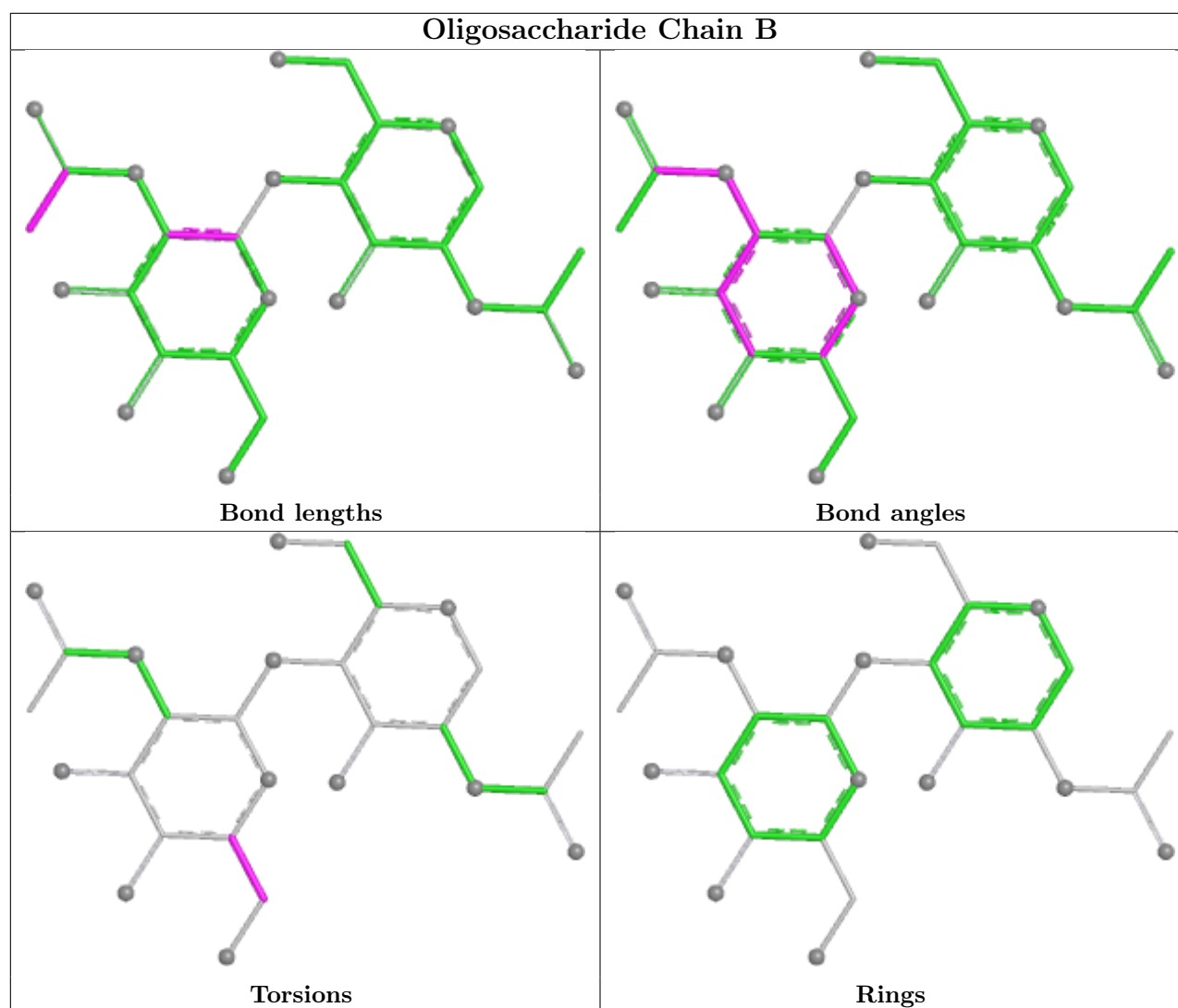
Mol	Chain	Res	Type	Atoms
2	B	2	NAG	C4-C5-C6-O6
2	B	2	NAG	O5-C5-C6-O6

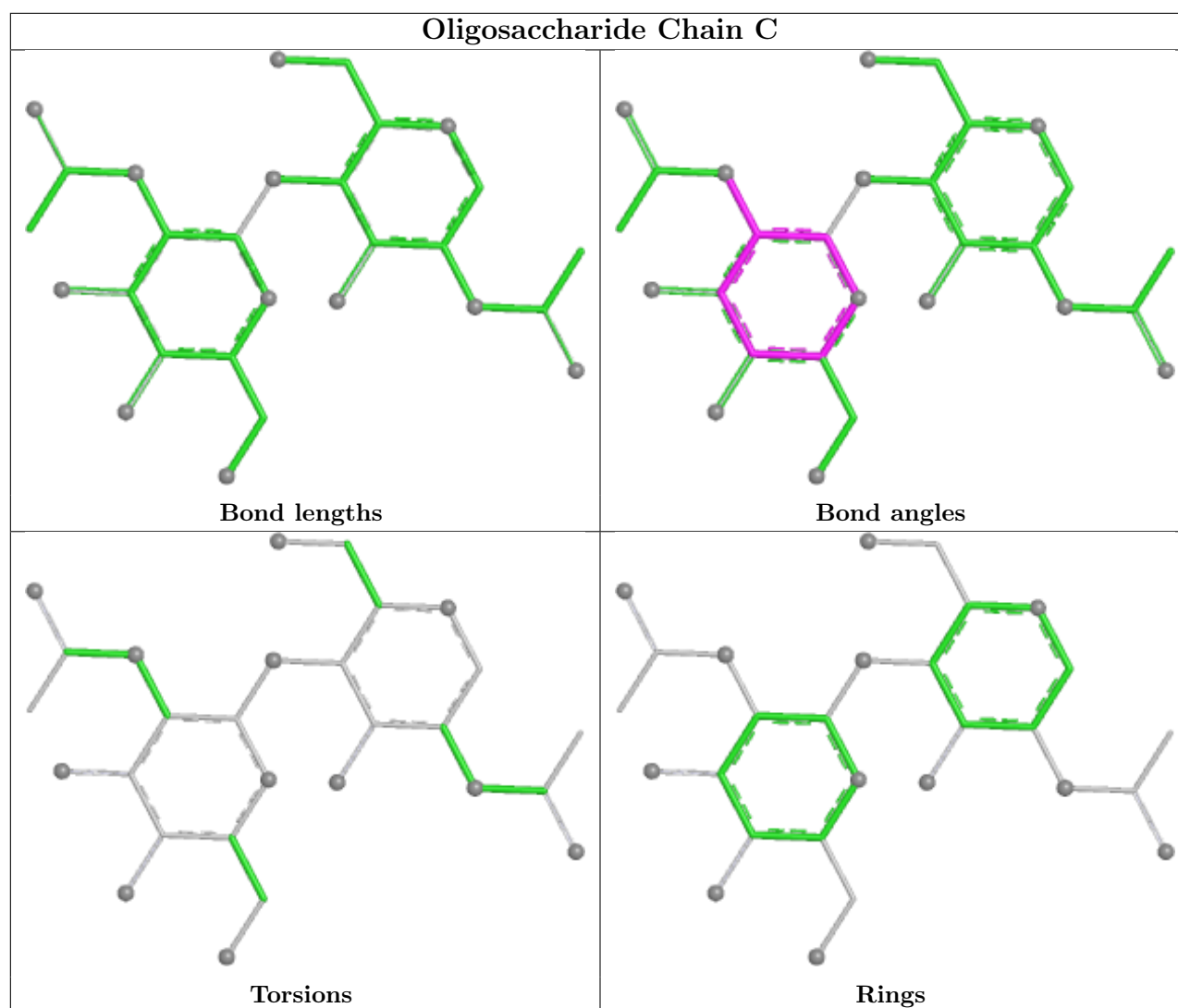
There are no ring outliers.

1 monomer is involved in 1 short contact:

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

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





5.6 Ligand geometry [i](#)

Of 29 ligands modelled in this entry, 14 are monoatomic - leaving 15 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	$\# Z > 2$
10	EDO	A	622	-	3,3,3	0.44	0	2,2,2	0.40	0
10	EDO	A	625	-	3,3,3	0.48	0	2,2,2	0.42	0
12	MRD	A	628	-	7,7,7	0.31	0	9,10,10	0.62	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	A	601	1	14,14,15	0.77	1 (7%)	17,19,21	1.71	3 (17%)
8	SCN	A	618	-	1,2,2	3.20	1 (100%)	0,1,1	-	-
9	PZA	A	619	4	9,9,9	0.47	0	11,11,11	2.14	5 (45%)
3	NAG	A	602	1	14,14,15	0.42	0	17,19,21	0.80	1 (5%)
10	EDO	A	623	-	3,3,3	0.43	0	2,2,2	0.32	0
4	HEM	A	603	9,1	50,50,50	1.94	10 (20%)	67,82,82	1.46	9 (13%)
10	EDO	A	621	-	3,3,3	0.46	0	2,2,2	0.47	0
9	PZA	A	620	-	9,9,9	0.47	0	11,11,11	1.75	3 (27%)
11	GOL	A	626	-	5,5,5	0.23	0	5,5,5	0.28	0
13	PEG	A	629	-	6,6,6	0.44	0	5,5,5	0.30	0
11	GOL	A	627	-	5,5,5	0.33	0	5,5,5	0.50	0
10	EDO	A	624	-	3,3,3	0.42	0	2,2,2	0.39	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	EDO	A	622	-	-	1/1/1/1	-
10	EDO	A	625	-	-	1/1/1/1	-
12	MRD	A	628	-	-	2/5/5/5	-
3	NAG	A	601	1	-	0/6/23/26	0/1/1/1
9	PZA	A	619	4	-	4/4/4/4	0/1/1/1
3	NAG	A	602	1	-	0/6/23/26	0/1/1/1
10	EDO	A	623	-	-	0/1/1/1	-
4	HEM	A	603	9,1	-	4/14/54/54	-
10	EDO	A	621	-	-	1/1/1/1	-
9	PZA	A	620	-	-	0/4/4/4	0/1/1/1
11	GOL	A	626	-	-	4/4/4/4	-
13	PEG	A	629	-	-	4/4/4/4	-
11	GOL	A	627	-	-	2/4/4/4	-
10	EDO	A	624	-	-	0/1/1/1	-

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	603	HEM	C3D-C2D	7.31	1.52	1.36
4	A	603	HEM	FE-ND	5.69	2.12	1.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	603	HEM	FE-NB	3.87	2.06	1.94
4	A	603	HEM	FE-NA	3.32	2.06	1.95
4	A	603	HEM	FE-NC	3.29	2.06	1.95
8	A	618	SCN	C-N	3.20	1.26	1.15
4	A	603	HEM	CAB-C3B	3.16	1.55	1.47
4	A	603	HEM	CAC-C3C	3.03	1.55	1.47
3	A	601	NAG	C8-C7	2.32	1.55	1.50
4	A	603	HEM	CMA-C3A	2.26	1.55	1.50
4	A	603	HEM	CMC-C2C	2.10	1.55	1.50
4	A	603	HEM	CMB-C2B	2.02	1.54	1.50

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	603	HEM	C4D-ND-C1D	5.45	111.66	105.21
3	A	601	NAG	C1-O5-C5	4.26	117.89	112.19
4	A	603	HEM	CMD-C2D-C1D	3.69	130.81	125.03
3	A	601	NAG	O5-C1-C2	-3.60	105.72	111.29
9	A	619	PZA	C4-C-N1	3.59	119.76	116.22
4	A	603	HEM	C3B-C2B-C1B	3.40	108.96	106.41
3	A	601	NAG	C1-C2-N2	3.14	115.38	110.43
9	A	619	PZA	C1-N3-C4	3.13	120.96	116.93
9	A	619	PZA	C2-N2-C3	2.65	121.50	116.85
4	A	603	HEM	CBD-CAD-C3D	-2.65	105.20	112.53
9	A	619	PZA	C2-C1-N3	-2.61	118.51	122.19
9	A	619	PZA	C4-C3-N2	-2.59	118.58	121.97
4	A	603	HEM	C1B-NB-C4B	2.54	108.22	105.21
4	A	603	HEM	C2B-C1B-NB	-2.53	106.94	109.84
9	A	620	PZA	C1-N3-C4	2.51	120.16	116.93
9	A	620	PZA	C4-C-N1	2.50	118.68	116.22
9	A	620	PZA	C3-C4-N3	-2.43	118.74	121.60
4	A	603	HEM	CAD-C3D-C4D	2.28	128.67	124.70
4	A	603	HEM	CHC-C1C-NC	2.17	126.81	124.45
4	A	603	HEM	CHA-C4D-ND	2.10	126.97	124.37
3	A	602	NAG	C1-O5-C5	2.01	114.87	112.19

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	A	626	GOL	O1-C1-C2-C3
12	A	628	MRD	C2-C3-C4-C5

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Mol	Chain	Res	Type	Atoms
11	A	626	GOL	C1-C2-C3-O3
11	A	627	GOL	O1-C1-C2-C3
10	A	622	EDO	O1-C1-C2-O2
13	A	629	PEG	O1-C1-C2-O2
11	A	626	GOL	O1-C1-C2-O2
9	A	619	PZA	N1-C-C4-N3
9	A	619	PZA	O-C-C4-N3
13	A	629	PEG	C4-C3-O2-C2
13	A	629	PEG	C1-C2-O2-C3
10	A	621	EDO	O1-C1-C2-O2
11	A	626	GOL	O2-C2-C3-O3
11	A	627	GOL	O1-C1-C2-O2
9	A	619	PZA	N1-C-C4-C3
9	A	619	PZA	O-C-C4-C3
10	A	625	EDO	O1-C1-C2-O2
4	A	603	HEM	CAA-CBA-CGA-O2A
4	A	603	HEM	CAA-CBA-CGA-O1A
4	A	603	HEM	CAD-CBD-CGD-O1D
4	A	603	HEM	CAD-CBD-CGD-O2D
12	A	628	MRD	C2-C3-C4-O4
13	A	629	PEG	O2-C3-C4-O4

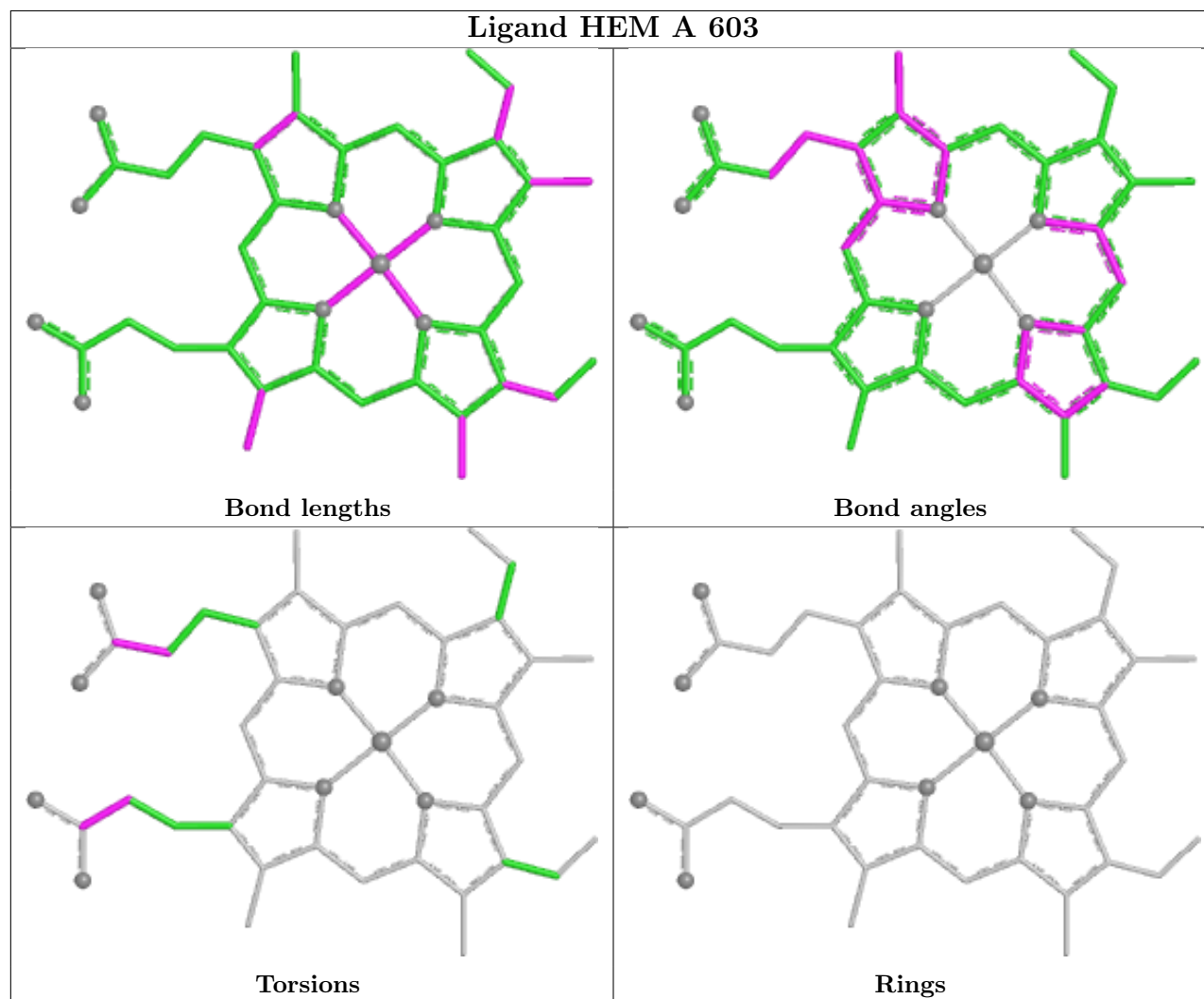
There are no ring outliers.

8 monomers are involved in 42 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	A	628	MRD	14	0
9	A	619	PZA	14	0
10	A	623	EDO	1	0
4	A	603	HEM	8	0
9	A	620	PZA	6	0
11	A	626	GOL	1	0
13	A	629	PEG	1	0
11	A	627	GOL	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 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	594/595 (99%)	0.71	49 (8%) 17 18	29, 41, 70, 101	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	172	TYR	10.6
1	A	2	TRP	8.9
1	A	173	GLN	7.9
1	A	171	PRO	6.4
1	A	1	SER	6.0
1	A	170	PRO	5.7
1	A	167	CYS	5.6
1	A	119	LEU	5.0
1	A	265	VAL	5.0
1	A	169	THR	4.6
1	A	12	LEU	4.5
1	A	174	SER	4.4
1	A	10	VAL	4.2
1	A	117	THR	4.2
1	A	8	ALA	3.7
1	A	4	VAL	3.6
1	A	227	PRO	3.6
1	A	9	PRO	3.5
1	A	5	GLY	3.2
1	A	11	PRO	3.2
1	A	175	LEU	3.1
1	A	13	VAL	3.0
1	A	7	GLY	3.0
1	A	283	LEU	2.8
1	A	168	PRO	2.8
1	A	426	HIS	2.7
1	A	6	CYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	391	GLY	2.7
1	A	481	LEU	2.6
1	A	232	VAL	2.6
1	A	403	ASN	2.6
1	A	118	GLU	2.5
1	A	121	SER	2.5
1	A	389	ASP	2.4
1	A	245	HIS	2.4
1	A	209	PRO	2.4
1	A	54	GLY	2.3
1	A	522	ILE	2.3
1	A	127	VAL	2.2
1	A	424	PRO	2.2
1	A	166	VAL	2.2
1	A	581	ALA	2.2
1	A	582	VAL	2.1
1	A	425	THR	2.1
1	A	40	ASN	2.1
1	A	120	GLY	2.1
1	A	569	ALA	2.1
1	A	423	GLN	2.0
1	A	589	PRO	2.0

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

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

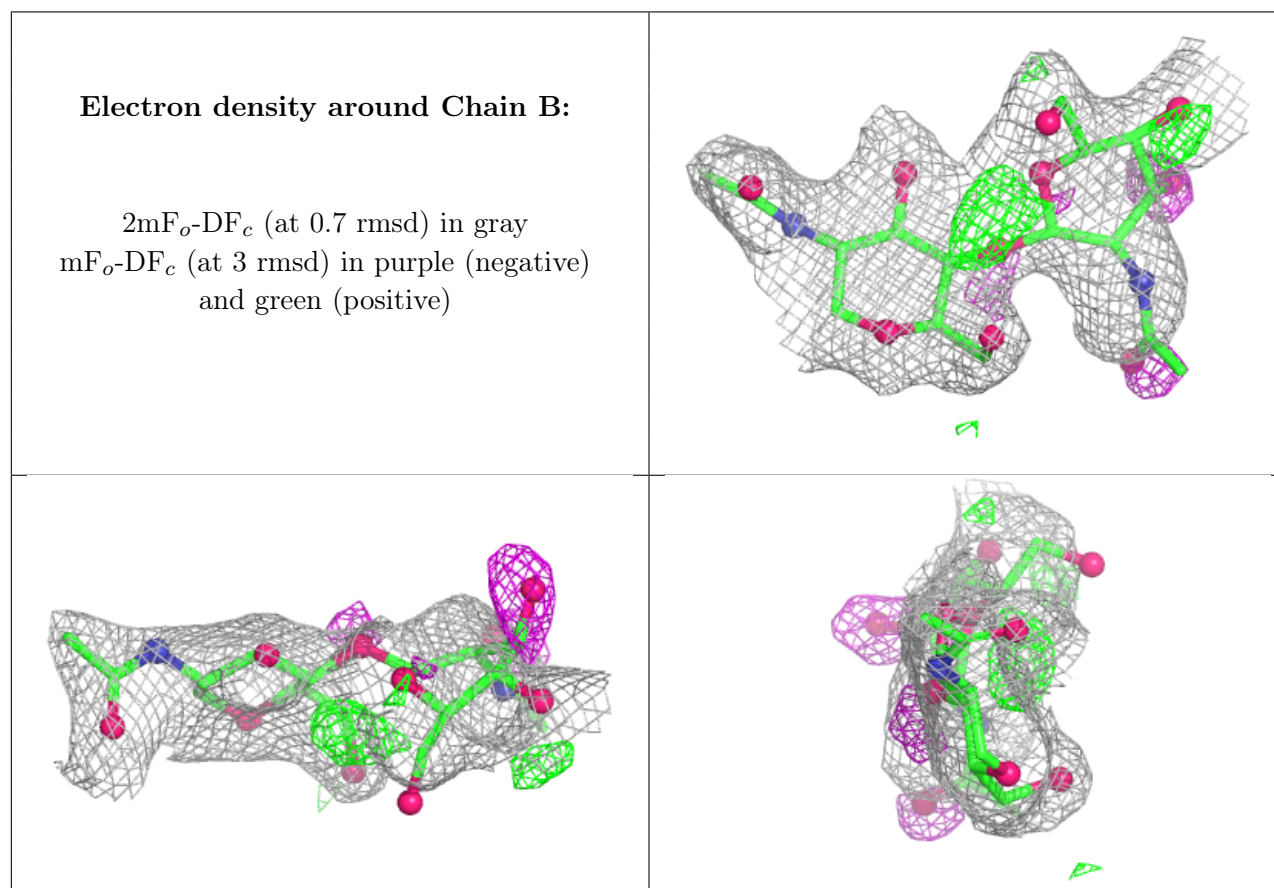
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	SEP	A	198	10/11	0.85	0.13	39,40,41,41	0

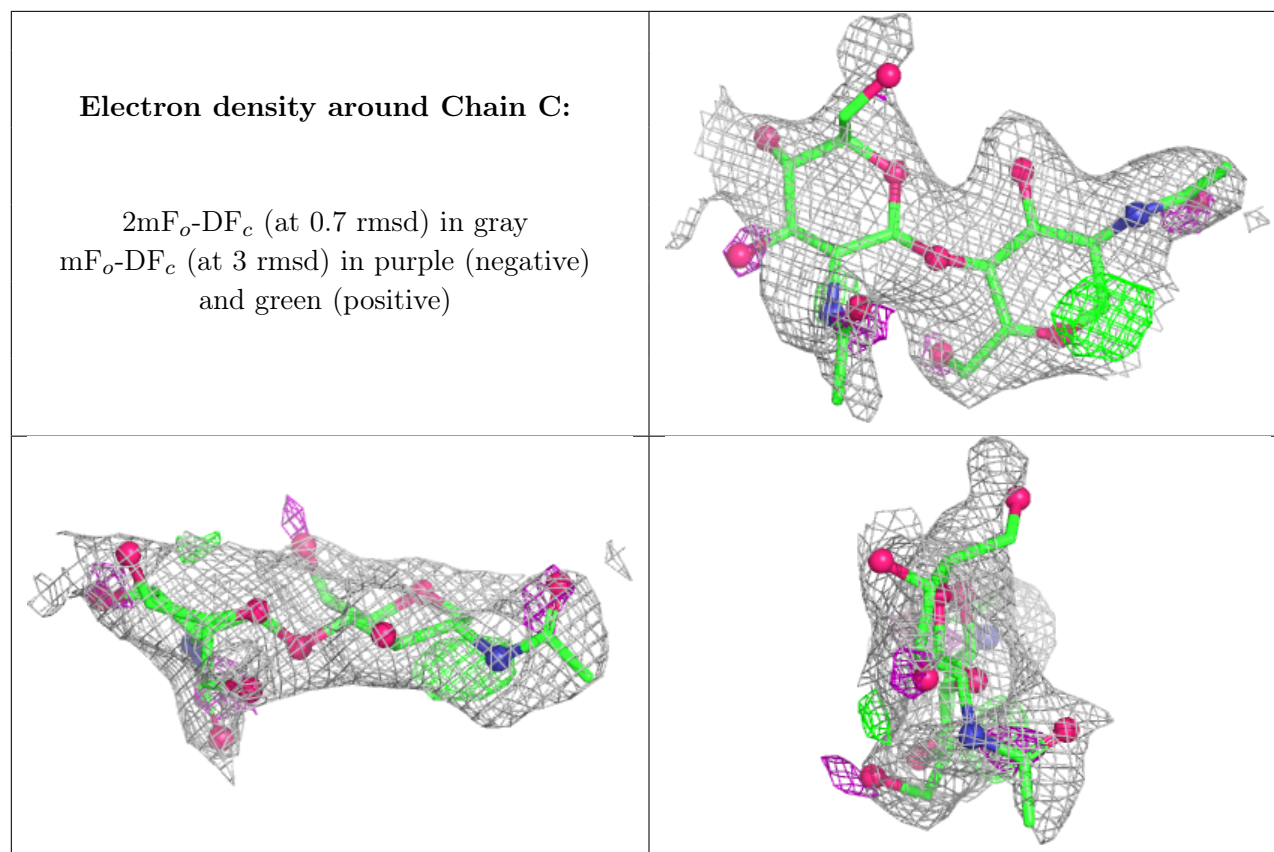
6.3 Carbohydrates [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAG	B	2	14/15	0.44	0.17	54,57,58,58	0
2	NAG	C	2	14/15	0.61	0.13	51,55,56,56	0
2	NAG	C	1	14/15	0.73	0.12	38,40,43,47	0
2	NAG	B	1	14/15	0.76	0.11	39,44,46,50	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 [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
13	PEG	A	629	7/7	0.62	0.16	51,51,53,53	7
9	PZA	A	619	9/9	0.64	0.28	39,39,40,41	0
9	PZA	A	620	9/9	0.67	0.24	38,38,39,39	9
3	NAG	A	602	14/15	0.67	0.12	39,39,40,40	0
3	NAG	A	601	14/15	0.69	0.13	47,50,52,52	0
11	GOL	A	627	6/6	0.71	0.15	62,63,63,63	0
10	EDO	A	621	4/4	0.72	0.21	38,38,39,40	0
12	MRD	A	628	8/8	0.74	0.25	28,33,36,36	0
8	SCN	A	618	3/3	0.78	0.18	56,56,56,56	0
11	GOL	A	626	6/6	0.82	0.15	40,40,40,40	0
10	EDO	A	623	4/4	0.82	0.15	35,36,37,37	0
10	EDO	A	624	4/4	0.84	0.15	49,49,49,49	0
10	EDO	A	625	4/4	0.85	0.17	42,42,43,43	0
10	EDO	A	622	4/4	0.89	0.10	41,42,42,43	0

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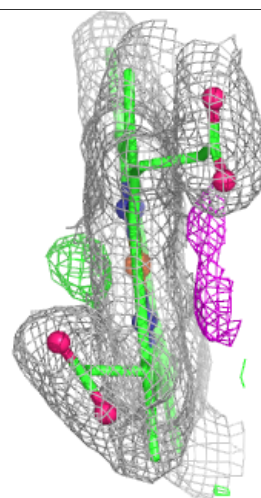
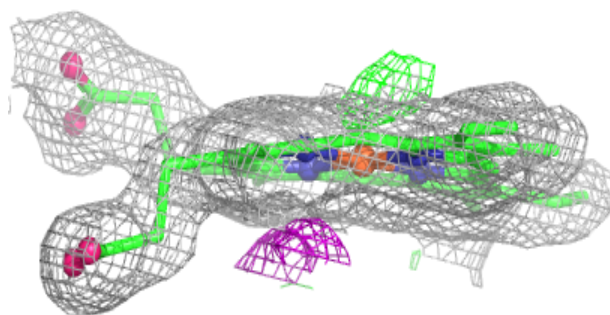
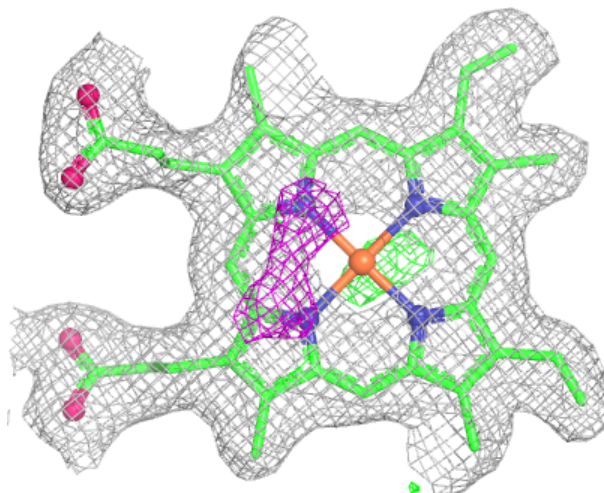
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	IOD	A	617	1/1	0.94	0.08	57,57,57,57	1
7	IOD	A	614	1/1	0.95	0.06	57,57,57,57	1
7	IOD	A	610	1/1	0.96	0.06	66,66,66,66	1
6	ZN	A	605	1/1	0.96	0.05	61,61,61,61	0
7	IOD	A	615	1/1	0.96	0.05	54,54,54,54	1
7	IOD	A	607	1/1	0.96	0.05	56,56,56,56	1
4	HEM	A	603	43/43	0.97	0.07	28,29,32,33	0
7	IOD	A	616	1/1	0.97	0.06	57,57,57,57	1
7	IOD	A	612	1/1	0.97	0.06	55,55,55,55	1
7	IOD	A	613	1/1	0.97	0.05	57,57,57,57	1
7	IOD	A	608	1/1	0.97	0.06	61,61,61,61	0
5	CA	A	604	1/1	0.99	0.05	36,36,36,36	0
7	IOD	A	611	1/1	0.99	0.03	46,46,46,46	0
7	IOD	A	606	1/1	0.99	0.02	33,33,33,33	0
7	IOD	A	609	1/1	0.99	0.04	49,49,49,49	0

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

Electron density around HEM A 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 ⓘ

There are no such residues in this entry.