



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 13, 2017 – 06:42 pm GMT

PDB ID : 3R55
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 wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

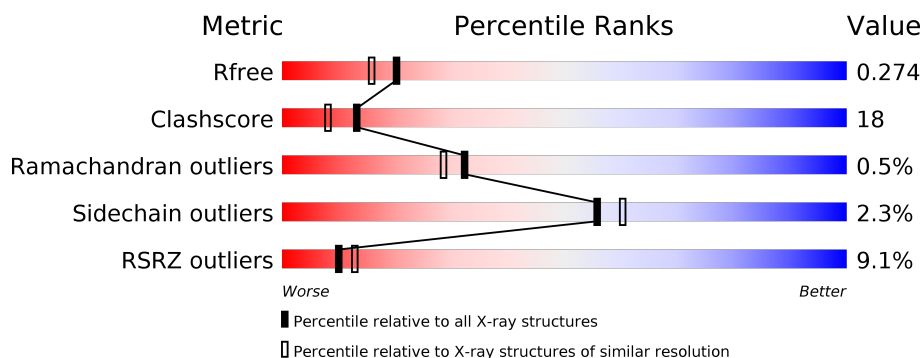
1 Overall quality at a glance

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}	100719	4243 (2.10-2.10)
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)
RSRZ outliers	101464	4275 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	

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	EDO	A	603	-	-	-	X
10	EDO	A	606	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
10	EDO	A	619	-	-	-	X
11	GOL	A	621	-	-	-	X
12	MRD	A	623	-	-	X	X
8	SCN	A	700	-	X	-	-
9	PZA	A	597	-	-	X	X
9	PZA	A	598	-	-	X	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 SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

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

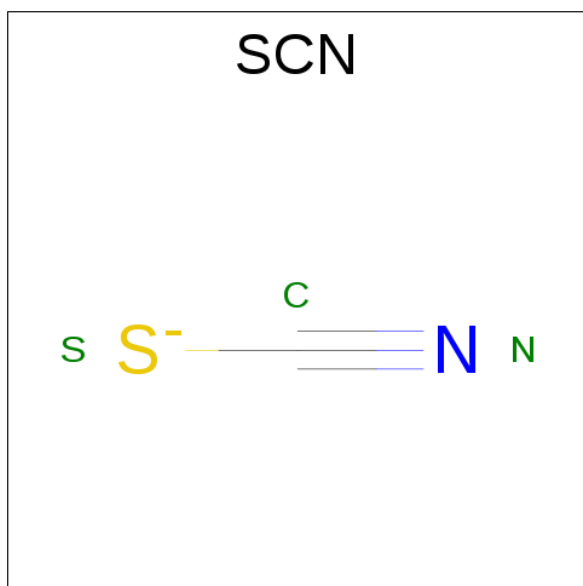
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	2	Total	C	N	O	0	0
			28	16	2	10		

- # HEM

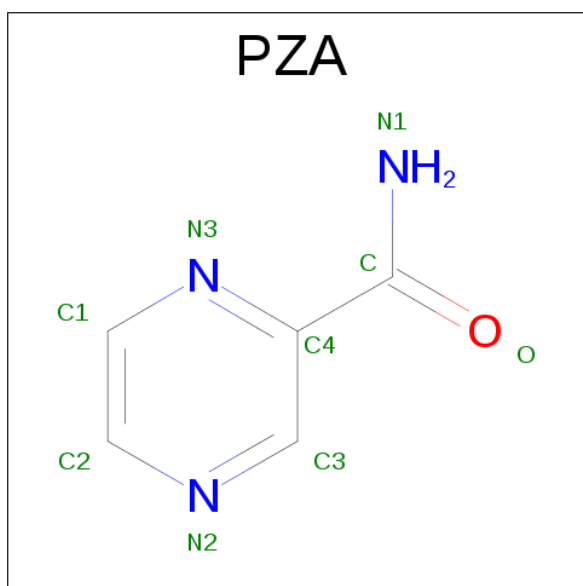
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	12	Total	I	0	0
			12	12		

- Molecule 8 is THIOCYANATE ION (three-letter code: SCN) (formula: CNS).



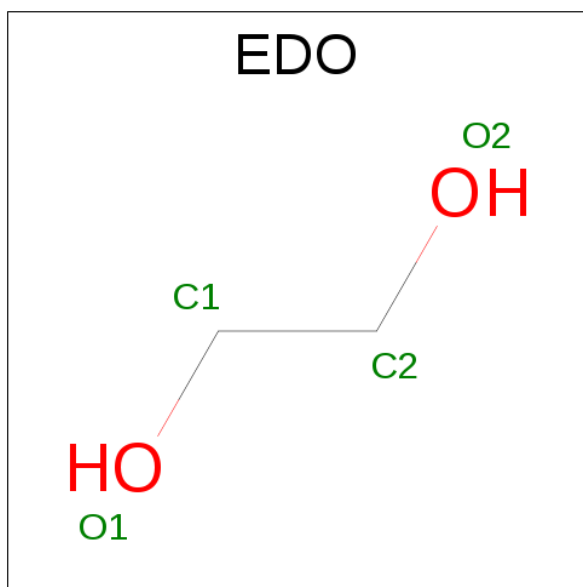
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	S	0	0
			3	1	1	1		

- Molecule 9 is PYRAZINE-2-CARBOXAMIDE (three-letter code: 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 (three-letter code: EDO) (formula: $C_2H_6O_2$).



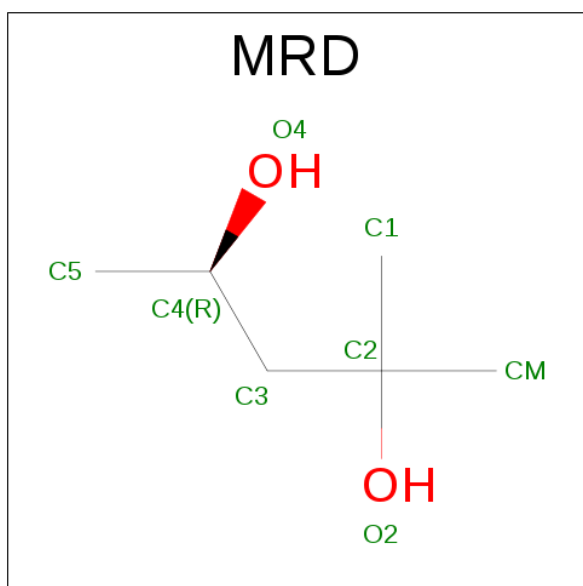
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 11 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



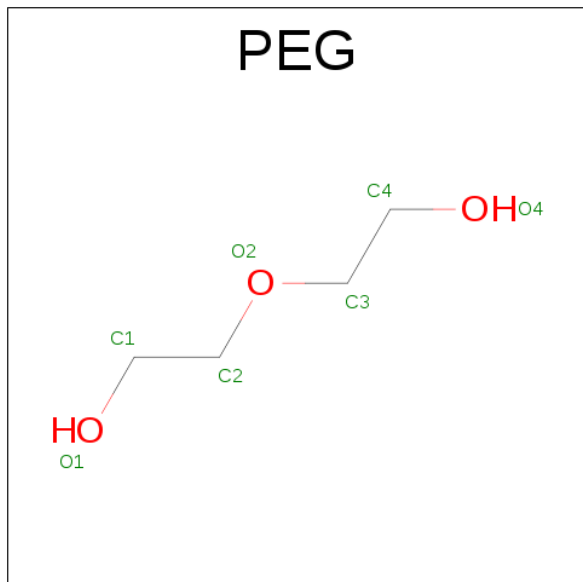
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	C	O	0	0
			6	3	3		
11	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 12 is (4R)-2-METHYLPENTANE-2,4-DIOL (three-letter code: 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 (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



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

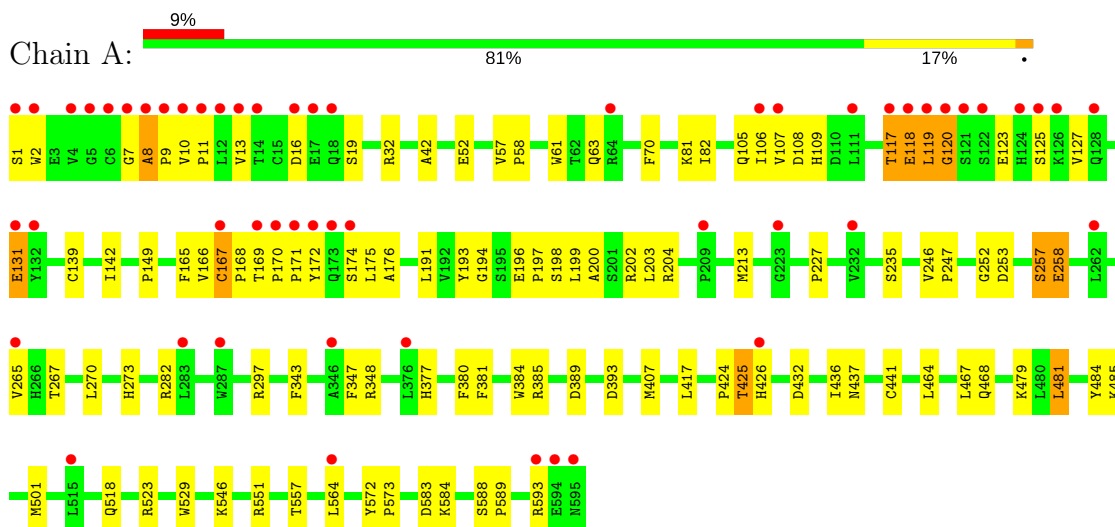
- Molecule 14 is water.

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

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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



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 43.98 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.6 (26.40-2.10) 98.6 (43.98-2.10)	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 0.234 , 0.274	Depositor DCC
R_{free} test set	1864 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	42.1	Xtriage
Anisotropy	0.315	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 39.5	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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, ZN, SCN, NAG, SEP, CA, EDO, MRD, HEM, PEG, PZA, IOD

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.44	2/4874 (0.0%)	0.60	6/6619 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	481	LEU	C-N	-5.84	1.20	1.34
1	A	258	GLU	CD-OE2	-5.18	1.20	1.25

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	257	SER	O-C-N	-6.98	111.54	122.70
1	A	107	VAL	O-C-N	-6.57	112.19	122.70
1	A	108	ASP	O-C-N	5.75	131.90	122.70
1	A	258	GLU	O-C-N	5.46	131.43	122.70
1	A	107	VAL	C-N-CA	5.11	134.48	121.70

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	168	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	28	0	26	0	0
3	A	56	0	50	1	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	178	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 18.

The worst 5 of 178 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	1.20
1:A:2:TRP:CB	1:A:175:LEU:HD22	1.72	1.18

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	592/595 (100%)	567 (96%)	22 (4%)	3 (0%)	32 28

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 [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	515/516 (100%)	503 (98%)	12 (2%)	56 60

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	235	SER
1	A	270	LEU
1	A	441	CYS
1	A	131	GLU
1	A	425	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	147	ASN
1	A	259	GLN
1	A	468	GLN
1	A	128	GLN
1	A	437	ASN

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	9,9,10	1.79	2 (22%)	9,12,14	1.30	1 (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
1	SEP	A	198	1	-	0/5/8/10	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	198	SEP	P-O1P	3.17	1.61	1.50
1	A	198	SEP	CA-C	3.32	1.54	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	2.31	110.44	108.17

There are no chirality outliers.

There are no torsion outliers.

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 carbohydrates 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$
3	NAG	A	599	1,3	14,14,15	0.49	0	15,19,21	0.90	0
3	NAG	A	600	3	14,14,15	1.05	1 (7%)	15,19,21	1.38	2 (13%)
3	NAG	A	601	1,3	14,14,15	0.65	0	15,19,21	0.72	0
3	NAG	A	602	3	14,14,15	0.42	0	15,19,21	2.17	3 (20%)

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
3	NAG	A	599	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	600	3	-	0/6/23/26	0/1/1/1
3	NAG	A	601	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	602	3	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	600	NAG	C8-C7	2.49	1.55	1.50

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	NAG	C4-C3-C2	-2.91	106.76	111.02
3	A	600	NAG	C1-O5-C5	-2.60	108.59	112.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	NAG	C1-C2-N2	2.33	114.47	110.49
3	A	600	NAG	C4-C3-C2	3.29	115.84	111.02
3	A	602	NAG	C1-O5-C5	6.74	121.46	112.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	601	NAG	1	0

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	$\# Z > 2$
2	NAG	A	596	1	14,14,15	0.75	1 (7%)	15,19,21	1.83	3 (20%)
9	PZA	A	597	4	9,9,9	0.45	0	11,11,11	2.20	5 (45%)
9	PZA	A	598	-	9,9,9	0.45	0	11,11,11	1.77	3 (27%)
10	EDO	A	603	-	3,3,3	0.48	0	2,2,2	0.46	0
2	NAG	A	604	1	14,14,15	0.42	0	15,19,21	0.73	0
10	EDO	A	605	-	3,3,3	0.46	0	2,2,2	0.38	0
10	EDO	A	606	-	3,3,3	0.46	0	2,2,2	0.30	0
10	EDO	A	614	-	3,3,3	0.44	0	2,2,2	0.37	0
4	HEM	A	618	1,9	28,50,50	2.21	6 (21%)	17,82,82	1.55	1 (5%)
10	EDO	A	619	-	3,3,3	0.50	0	2,2,2	0.41	0
11	GOL	A	621	-	5,5,5	0.17	0	5,5,5	0.22	0
11	GOL	A	622	-	5,5,5	0.32	0	5,5,5	0.42	0
12	MRD	A	623	-	7,7,7	0.28	0	9,10,10	0.55	0
13	PEG	A	625	-	6,6,6	0.44	0	5,5,5	0.31	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	SCN	A	700	-	1,2,2	3.21	1 (100%)	0,1,1	0.00	-

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	596	1	-	0/6/23/26	0/1/1/1
9	PZA	A	597	4	-	0/4/4/4	0/1/1/1
9	PZA	A	598	-	-	0/4/4/4	0/1/1/1
10	EDO	A	603	-	-	0/1/1/1	0/0/0/0
2	NAG	A	604	1	-	0/6/23/26	0/1/1/1
10	EDO	A	605	-	-	0/1/1/1	0/0/0/0
10	EDO	A	606	-	-	0/1/1/1	0/0/0/0
10	EDO	A	614	-	-	0/1/1/1	0/0/0/0
4	HEM	A	618	1,9	-	0/6/54/54	0/0/8/8
10	EDO	A	619	-	-	0/1/1/1	0/0/0/0
11	GOL	A	621	-	-	0/4/4/4	0/0/0/0
11	GOL	A	622	-	-	0/4/4/4	0/0/0/0
12	MRD	A	623	-	-	0/5/5/5	0/0/0/0
13	PEG	A	625	-	-	0/4/4/4	0/0/0/0
8	SCN	A	700	-	-	0/0/0/0	0/0/0/0

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	618	HEM	C3B-C2B	-4.71	1.34	1.40
4	A	618	HEM	C3C-C2C	-4.21	1.34	1.40
2	A	596	NAG	C8-C7	2.23	1.55	1.50
4	A	618	HEM	C4D-ND	2.41	1.39	1.36
8	A	700	SCN	C-N	3.21	1.26	1.15

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	596	NAG	O5-C1-C2	-4.14	105.72	111.47
4	A	618	HEM	CBD-CAD-C3D	-3.81	105.20	112.47
9	A	597	PZA	C4-C3-N2	-2.97	118.58	122.04
9	A	597	PZA	C2-C1-N3	-2.76	118.51	122.17
9	A	598	PZA	C3-C4-N3	-2.52	118.74	121.64

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 42 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	597	PZA	14	0
9	A	598	PZA	6	0
10	A	606	EDO	1	0
4	A	618	HEM	8	0
11	A	621	GOL	1	0
11	A	622	GOL	1	0
12	A	623	MRD	14	0
13	A	625	PEG	1	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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%)	0.67	54 (9%) 10 13	29, 41, 70, 101	0

The worst 5 of 54 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	172	TYR	12.9
1	A	2	TRP	11.0
1	A	173	GLN	9.8
1	A	12	LEU	9.0
1	A	1	SER	8.6

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
1	SEP	A	198	10/11	0.89	0.17	-	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
3	NAG	A	601	14/15	0.79	0.19	0.63	38,40,43,47	0
3	NAG	A	599	14/15	0.85	0.17	0.50	39,44,46,50	0
3	NAG	A	602	14/15	0.71	0.31	-	51,55,56,56	0
3	NAG	A	600	14/15	0.60	0.36	-	54,57,58,58	0

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
9	PZA	A	598	9/9	0.75	0.40	11.15	38,38,39,39	9
10	EDO	A	603	4/4	0.78	0.31	8.63	38,38,39,40	0
10	EDO	A	606	4/4	0.77	0.22	8.03	35,36,37,37	0
12	MRD	A	623	8/8	0.74	0.42	7.79	28,33,36,36	0
11	GOL	A	621	6/6	0.83	0.24	5.86	40,40,40,40	0
9	PZA	A	597	9/9	0.66	0.41	5.66	39,39,40,41	0
10	EDO	A	619	4/4	0.76	0.20	3.41	42,42,43,43	0
8	SCN	A	700	3/3	0.80	0.21	1.15	56,56,56,56	0
4	HEM	A	618	43/43	0.97	0.20	0.45	28,29,32,33	0
13	PEG	A	625	7/7	0.69	0.25	0.31	51,51,53,53	7
10	EDO	A	614	4/4	0.86	0.18	0.05	49,49,49,49	0
10	EDO	A	605	4/4	0.92	0.12	0.01	41,42,42,43	0
5	CA	A	607	1/1	0.96	0.16	-0.08	36,36,36,36	0
11	GOL	A	622	6/6	0.74	0.22	-0.08	62,63,63,63	0
7	IOD	A	616	1/1	0.98	0.04	-1.07	55,55,55,55	1
7	IOD	A	624	1/1	0.97	0.07	-1.43	54,54,54,54	1
7	IOD	A	615	1/1	1.00	0.09	-1.45	46,46,46,46	0
7	IOD	A	609	1/1	1.00	0.09	-1.78	33,33,33,33	0
7	IOD	A	612	1/1	0.98	0.04	-1.97	49,49,49,49	0
7	IOD	A	611	1/1	0.98	0.04	-2.07	61,61,61,61	0
7	IOD	A	626	1/1	0.98	0.04	-2.40	57,57,57,57	1
7	IOD	A	610	1/1	0.98	0.07	-2.44	56,56,56,56	1
2	NAG	A	604	14/15	0.75	0.30	-	39,39,40,40	0
2	NAG	A	596	14/15	0.85	0.35	-	47,50,52,52	0
6	ZN	A	608	1/1	0.95	0.04	-	61,61,61,61	0
7	IOD	A	620	1/1	0.98	0.07	-	57,57,57,57	1
7	IOD	A	613	1/1	0.96	0.07	-	66,66,66,66	1
7	IOD	A	627	1/1	0.91	0.08	-	57,57,57,57	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
7	IOD	A	617	1/1	0.98	0.05	-	57,57,57,57	1

6.5 Other polymers [i](#)

There are no such residues in this entry.