



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:28 PM GMT

PDB ID : 1XIG
Title : MODES OF BINDING SUBSTRATES AND THEIR ANALOGUES TO THE
ENZYME D-XYLOSE ISOMERASE
Authors : Carrell, H.L.; Glusker, J.P.
Deposited on : 1994-03-07
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
<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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

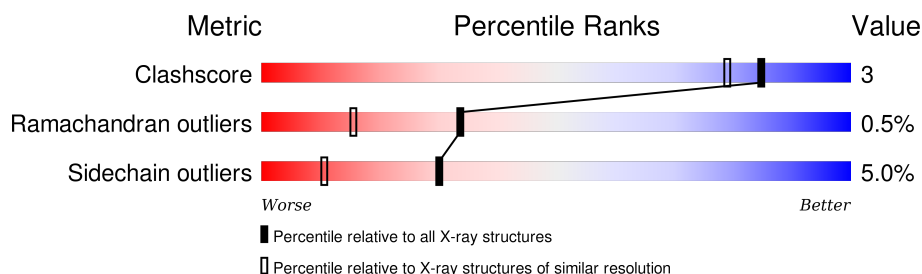
1 Overall quality at a glance

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))
Clashscore	102246	3585 (1.70-1.70)
Ramachandran outliers	100387	3527 (1.70-1.70)
Sidechain outliers	100360	3527 (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 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	388	 68% 27% . .

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3339 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.

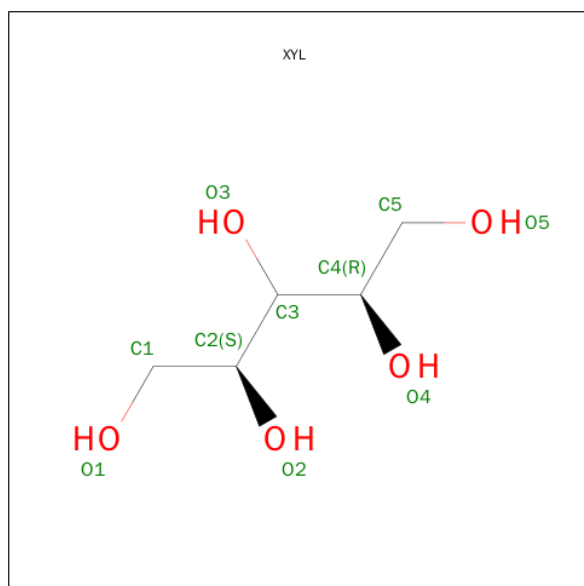
- Molecule 1 is a protein called D-XYLOSE ISOMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	385	3031	1906	545	572	8	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	41	GLN	ARG	CONFLICT	UNP P24300

- Molecule 2 is D-XYLITOL (three-letter code: XYL) (formula: C₅H₁₂O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	10	5	5	0	0

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total 2	Mn 2	0	0

- Molecule 4 is water.

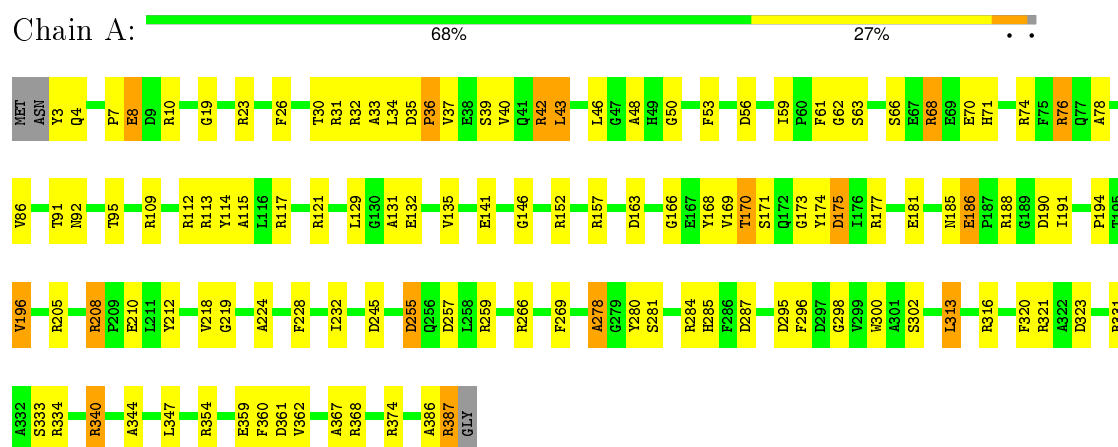
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	296	Total 296	O 296	0	0

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 errors 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.

Note EDS was not executed.

• Molecule 1: D-XYLOSE ISOMERASE



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	93.90Å 99.70Å 102.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.00 – 1.70	Depositor
% Data completeness (in resolution range)	(Not available) (14.00-1.70)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.162 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3339	wwPDB-VP
Average B, all atoms (Å ²)	11.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MN, XYL

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	1.28	38/3103 (1.2%)	1.90	93/4201 (2.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	5

All (38) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	191	ILE	C-N	10.96	1.59	1.34
1	A	175	ASP	C-N	-10.73	1.09	1.34
1	A	68	ARG	C-N	-8.74	1.14	1.34
1	A	95	THR	C-N	8.61	1.53	1.34
1	A	146	GLY	C-N	8.32	1.48	1.33
1	A	196	VAL	C-N	8.11	1.47	1.33
1	A	3	TYR	C-N	-8.02	1.15	1.34
1	A	255	ASP	C-N	7.97	1.52	1.34
1	A	114	TYR	C-N	7.95	1.52	1.34
1	A	121	ARG	C-N	7.91	1.52	1.34
1	A	280	TYR	C-N	7.66	1.51	1.34
1	A	36	PRO	C-N	7.53	1.51	1.34
1	A	320	PHE	C-N	7.46	1.51	1.34
1	A	302	SER	C-N	7.31	1.50	1.34
1	A	298	GLY	C-N	7.17	1.50	1.34
1	A	115	ALA	C-N	7.00	1.50	1.34
1	A	35	ASP	C-N	6.91	1.47	1.34
1	A	171	SER	C-N	6.77	1.49	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	224	ALA	C-N	6.37	1.44	1.33
1	A	92	ASN	C-N	6.34	1.48	1.34
1	A	30	THR	C-N	6.18	1.48	1.34
1	A	129	LEU	C-N	6.05	1.44	1.33
1	A	112	ARG	C-N	6.03	1.48	1.34
1	A	135	VAL	C-N	5.98	1.47	1.34
1	A	62	GLY	C-N	5.97	1.47	1.34
1	A	278	ALA	C-N	5.91	1.43	1.33
1	A	50	GLY	C-N	-5.85	1.20	1.34
1	A	281	SER	C-N	5.77	1.43	1.33
1	A	63	SER	C-N	5.75	1.47	1.34
1	A	269	PHE	C-N	5.68	1.47	1.34
1	A	219	GLY	C-N	5.64	1.47	1.34
1	A	61	PHE	C-N	-5.50	1.23	1.33
1	A	333	SER	C-N	5.32	1.46	1.34
1	A	386	ALA	C-N	-5.18	1.22	1.34
1	A	19	GLY	C-N	5.18	1.46	1.34
1	A	46	LEU	C-N	5.09	1.42	1.33
1	A	300	TRP	C-N	5.06	1.45	1.34
1	A	71	HIS	C-N	-5.03	1.22	1.34

All (93) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	76	ARG	NE-CZ-NH2	-18.78	110.91	120.30
1	A	266	ARG	NE-CZ-NH1	15.95	128.28	120.30
1	A	284	ARG	NE-CZ-NH2	-14.51	113.05	120.30
1	A	331	ARG	NE-CZ-NH2	-13.53	113.53	120.30
1	A	266	ARG	NE-CZ-NH2	-13.29	113.66	120.30
1	A	259	ARG	NE-CZ-NH1	13.16	126.88	120.30
1	A	10	ARG	NE-CZ-NH1	12.19	126.40	120.30
1	A	368	ARG	NE-CZ-NH2	-12.05	114.28	120.30
1	A	117	ARG	NE-CZ-NH2	-11.73	114.44	120.30
1	A	74	ARG	NE-CZ-NH1	11.65	126.13	120.30
1	A	109	ARG	NE-CZ-NH1	-10.87	114.86	120.30
1	A	173	GLY	O-C-N	-10.32	106.18	122.70
1	A	42	ARG	CD-NE-CZ	9.71	137.19	123.60
1	A	74	ARG	NE-CZ-NH2	-9.68	115.46	120.30
1	A	10	ARG	CD-NE-CZ	9.65	137.11	123.60
1	A	68	ARG	NE-CZ-NH2	9.51	125.06	120.30
1	A	3	TYR	C-N-CA	9.47	145.39	121.70
1	A	334	ARG	NE-CZ-NH2	-9.16	115.72	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	56	ASP	CB-CG-OD1	8.54	125.98	118.30
1	A	188	ARG	NE-CZ-NH2	-8.51	116.05	120.30
1	A	23	ARG	CD-NE-CZ	8.33	135.26	123.60
1	A	295	ASP	CB-CG-OD1	8.21	125.69	118.30
1	A	3	TYR	O-C-N	-8.20	109.57	122.70
1	A	321	ARG	NE-CZ-NH2	-8.02	116.29	120.30
1	A	168	TYR	CB-CG-CD1	-7.86	116.29	121.00
1	A	163	ASP	CB-CG-OD1	7.79	125.31	118.30
1	A	259	ARG	NE-CZ-NH2	-7.78	116.41	120.30
1	A	177	ARG	NE-CZ-NH2	7.65	124.13	120.30
1	A	23	ARG	NE-CZ-NH1	7.63	124.12	120.30
1	A	173	GLY	CA-C-N	7.57	133.85	117.20
1	A	76	ARG	NH1-CZ-NH2	7.41	127.56	119.40
1	A	257	ASP	CB-CG-OD2	-7.38	111.66	118.30
1	A	168	TYR	O-C-N	-7.30	111.01	122.70
1	A	113	ARG	NE-CZ-NH2	-7.08	116.76	120.30
1	A	316	ARG	NE-CZ-NH2	-6.99	116.80	120.30
1	A	113	ARG	NE-CZ-NH1	6.88	123.74	120.30
1	A	287	ASP	CB-CG-OD1	6.65	124.29	118.30
1	A	266	ARG	CD-NE-CZ	6.62	132.87	123.60
1	A	157	ARG	NE-CZ-NH1	6.60	123.60	120.30
1	A	10	ARG	NH1-CZ-NH2	-6.55	112.19	119.40
1	A	331	ARG	NH1-CZ-NH2	6.55	126.61	119.40
1	A	361	ASP	CB-CG-OD2	-6.54	112.42	118.30
1	A	152	ARG	NE-CZ-NH1	6.50	123.55	120.30
1	A	368	ARG	CD-NE-CZ	6.39	132.55	123.60
1	A	257	ASP	CB-CG-OD1	6.33	124.00	118.30
1	A	74	ARG	CD-NE-CZ	6.33	132.46	123.60
1	A	152	ARG	CD-NE-CZ	6.27	132.38	123.60
1	A	296	PHE	O-C-N	-6.25	112.70	122.70
1	A	374	ARG	NE-CZ-NH2	-6.21	117.20	120.30
1	A	42	ARG	NE-CZ-NH2	6.15	123.38	120.30
1	A	313	LEU	CA-CB-CG	6.15	129.44	115.30
1	A	8	GLU	CA-CB-CG	6.14	126.91	113.40
1	A	255	ASP	CB-CG-OD2	-6.02	112.88	118.30
1	A	177	ARG	NE-CZ-NH1	-6.00	117.30	120.30
1	A	35	ASP	CB-CG-OD1	5.95	123.66	118.30
1	A	374	ARG	NE-CZ-NH1	5.90	123.25	120.30
1	A	387	ARG	NE-CZ-NH2	-5.89	117.36	120.30
1	A	212	TYR	CB-CG-CD1	-5.84	117.50	121.00
1	A	26	PHE	O-C-N	-5.83	113.30	123.20
1	A	367	ALA	O-C-N	5.81	131.99	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	321	ARG	NE-CZ-NH1	5.79	123.20	120.30
1	A	135	VAL	CA-CB-CG2	-5.72	102.31	110.90
1	A	191	ILE	O-C-N	-5.68	113.62	122.70
1	A	121	ARG	NE-CZ-NH2	-5.66	117.47	120.30
1	A	194	PRO	O-C-N	-5.66	113.64	122.70
1	A	188	ARG	NE-CZ-NH1	5.66	123.13	120.30
1	A	295	ASP	CB-CG-OD2	-5.64	113.23	118.30
1	A	48	ALA	CB-CA-C	-5.62	101.68	110.10
1	A	191	ILE	CA-C-O	5.54	131.72	120.10
1	A	367	ALA	C-N-CA	-5.48	107.99	121.70
1	A	68	ARG	CG-CD-NE	5.47	123.28	111.80
1	A	31	ARG	O-C-N	5.46	131.44	122.70
1	A	168	TYR	CB-CG-CD2	5.45	124.27	121.00
1	A	43	LEU	CA-CB-CG	5.45	127.83	115.30
1	A	340	ARG	CD-NE-CZ	5.43	131.20	123.60
1	A	368	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	A	190	ASP	O-C-N	5.42	131.37	122.70
1	A	23	ARG	O-C-N	-5.41	114.05	122.70
1	A	78	ALA	O-C-N	-5.40	114.06	122.70
1	A	35	ASP	CB-CG-OD2	-5.38	113.45	118.30
1	A	168	TYR	CA-C-O	5.37	131.38	120.10
1	A	61	PHE	C-N-CA	5.35	133.54	122.30
1	A	280	TYR	C-N-CA	-5.34	108.36	121.70
1	A	208	ARG	NE-CZ-NH2	-5.23	117.68	120.30
1	A	387	ARG	NE-CZ-NH1	5.21	122.91	120.30
1	A	7	PRO	O-C-N	-5.20	114.38	122.70
1	A	152	ARG	NE-CZ-NH2	-5.19	117.70	120.30
1	A	42	ARG	O-C-N	-5.12	114.50	122.70
1	A	205	ARG	CD-NE-CZ	5.12	130.77	123.60
1	A	174	TYR	CB-CG-CD1	5.11	124.07	121.00
1	A	284	ARG	NE-CZ-NH1	5.07	122.84	120.30
1	A	181	GLU	OE1-CD-OE2	5.05	129.36	123.30
1	A	344	ALA	O-C-N	5.03	130.74	122.70

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	37	VAL	CA

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	170	THR	Mainchain
1	A	196	VAL	Mainchain
1	A	210	GLU	Mainchain
1	A	278	ALA	Mainchain
1	A	53	PHE	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	3031	0	2894	17	0
2	A	10	0	9	0	0
3	A	2	0	0	0	0
4	A	296	0	0	4	0
All	All	3339	0	2903	17	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 3.

All (17) 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:59:ILE:HG21	1:A:68:ARG:HG2	1.73	0.71
1:A:354:ARG:HB3	1:A:359:GLU:HG3	1.79	0.64
1:A:340:ARG:HD2	4:A:637:HOH:O	1.98	0.63
1:A:141:GLU:OE2	4:A:587:HOH:O	2.17	0.58
1:A:186:GLU:OE1	1:A:255:ASP:HB3	2.08	0.54
1:A:166:GLY:O	1:A:170:THR:HG23	2.08	0.52
1:A:32:ARG:NH1	1:A:33:ALA:O	2.42	0.51
1:A:340:ARG:CD	4:A:637:HOH:O	2.58	0.48
1:A:36:PRO:O	1:A:40:VAL:HG23	2.14	0.47
1:A:245:ASP:OD1	1:A:285:HIS:HD2	1.98	0.47
1:A:86:VAL:O	1:A:131:ALA:HA	2.17	0.45
1:A:228:PHE:CZ	1:A:232:ILE:HD11	2.52	0.44
1:A:360:PHE:CD2	1:A:362:VAL:HG12	2.53	0.44
1:A:208:ARG:NH1	4:A:582:HOH:O	2.34	0.43
1:A:323:ASP:OD2	1:A:387:ARG:NH2	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:354:ARG:NE	1:A:359:GLU:OE2	2.52	0.41
1:A:34:LEU:HD13	1:A:39:SER:OG	2.21	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	383/388 (99%)	369 (96%)	12 (3%)	2 (0%)	34 15

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	186	GLU
1	A	218	VAL

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	302/304 (99%)	287 (95%)	15 (5%)	30 11

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	GLN
1	A	8	GLU
1	A	37	VAL
1	A	42	ARG
1	A	43	LEU
1	A	66	SER
1	A	70	GLU
1	A	76	ARG
1	A	91	THR
1	A	132	GLU
1	A	169	VAL
1	A	175	ASP
1	A	185	ASN
1	A	313	LEU
1	A	347	LEU

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

Mol	Chain	Res	Type
1	A	4	GLN
1	A	285	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	XYL	A	389	3	9,9,9	1.38	2 (22%)	10,11,11	1.48	2 (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
2	XYL	A	389	3	-	0/12/12/12	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	389	XYL	O1-C1	-3.16	1.28	1.42
2	A	389	XYL	O2-C2	-2.53	1.37	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	389	XYL	O1-C1-C2	-2.17	106.38	111.10
2	A	389	XYL	O5-C5-C4	2.71	116.99	111.10

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.