Full wwPDB X-ray Structure Validation Report (i)

Feb 4, 2024 – 09:49 PM EST

PDB ID	:	1XIJ
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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

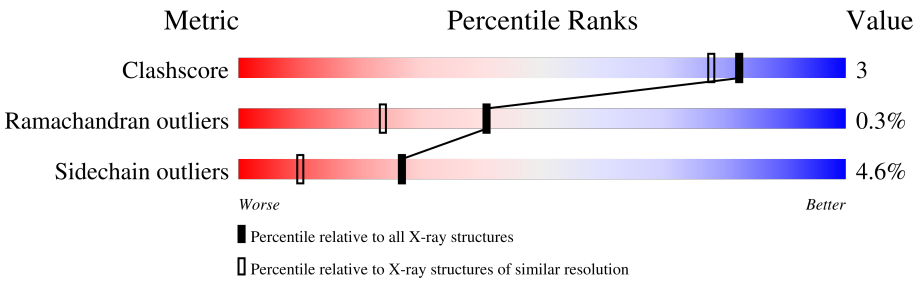
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	388	72% 24% • ••

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
2	THE	A	389	-	X	-	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3418 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.

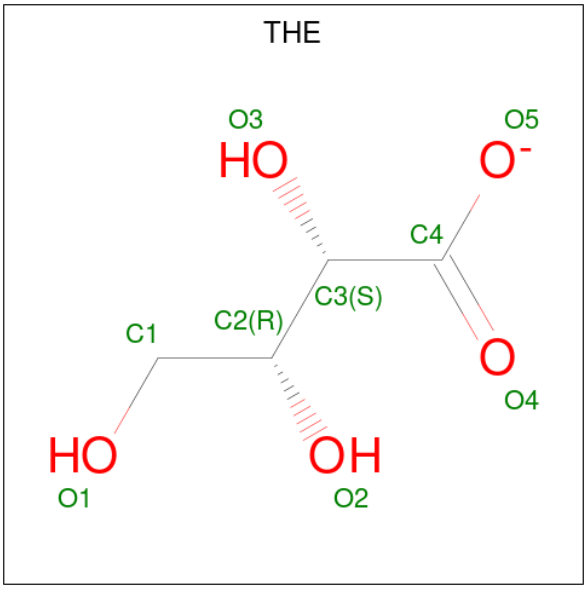
- Molecule 1 is a protein called D-XYLOSE ISOMERASE.

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 THREONATE ION (three-letter code: THE) (formula: $C_4H_7O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	9	4	5	0	0

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

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	377	377	377	0	0

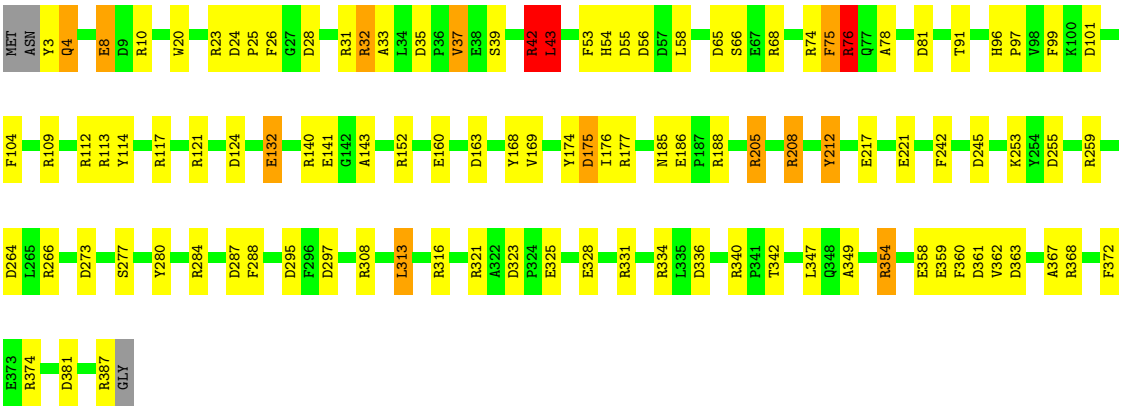
3 Residue-property plots (i)

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. 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. 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

Chain A:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	93.88Å 99.68Å 102.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.70	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-1.70)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.156 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3418	wwPDB-VP
Average B, all atoms ($Å^2$)	10.0	wwPDB-VP

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: THE, MN

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	1.18	3/3103 (0.1%)	2.26	121/4201 (2.9%)

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 (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	221	GLU	CD-OE2	-9.41	1.15	1.25
1	A	217	GLU	CD-OE1	-8.49	1.16	1.25
1	A	141	GLU	CD-OE1	-5.90	1.19	1.25

All (121) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	340	ARG	NE-CZ-NH1	35.51	138.06	120.30
1	A	340	ARG	CD-NE-CZ	26.06	160.08	123.60
1	A	340	ARG	NE-CZ-NH2	-25.81	107.40	120.30
1	A	76	ARG	NE-CZ-NH2	-24.13	108.24	120.30
1	A	331	ARG	NE-CZ-NH2	-16.20	112.20	120.30
1	A	10	ARG	CD-NE-CZ	16.14	146.19	123.60
1	A	68	ARG	NE-CZ-NH2	15.93	128.27	120.30
1	A	387	ARG	CA-C-O	14.84	151.27	120.10
1	A	266	ARG	NE-CZ-NH2	-14.79	112.90	120.30
1	A	74	ARG	NE-CZ-NH2	-13.85	113.38	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	152	ARG	NE-CZ-NH2	-13.83	113.39	120.30
1	A	188	ARG	NE-CZ-NH1	13.18	126.89	120.30
1	A	124	ASP	CB-CG-OD1	12.72	129.75	118.30
1	A	334	ARG	NE-CZ-NH2	-12.42	114.09	120.30
1	A	74	ARG	NE-CZ-NH1	12.28	126.44	120.30
1	A	76	ARG	NH1-CZ-NH2	12.27	132.90	119.40
1	A	387	ARG	CD-NE-CZ	12.25	140.75	123.60
1	A	387	ARG	NE-CZ-NH1	11.96	126.28	120.30
1	A	266	ARG	NE-CZ-NH1	11.15	125.87	120.30
1	A	163	ASP	CB-CG-OD1	10.32	127.58	118.30
1	A	56	ASP	CB-CG-OD1	10.23	127.51	118.30
1	A	188	ARG	NE-CZ-NH2	-9.95	115.33	120.30
1	A	42	ARG	NE-CZ-NH1	9.88	125.24	120.30
1	A	32	ARG	NE-CZ-NH1	9.80	125.20	120.30
1	A	42	ARG	CD-NE-CZ	9.79	137.31	123.60
1	A	259	ARG	NE-CZ-NH1	9.66	125.13	120.30
1	A	331	ARG	NH1-CZ-NH2	9.56	129.92	119.40
1	A	28	ASP	CB-CG-OD1	9.51	126.86	118.30
1	A	112	ARG	NE-CZ-NH1	-9.49	115.56	120.30
1	A	81	ASP	CB-CG-OD1	9.46	126.82	118.30
1	A	316	ARG	NE-CZ-NH2	-9.19	115.70	120.30
1	A	75	PHE	CB-CG-CD2	-9.04	114.47	120.80
1	A	387	ARG	NE-CZ-NH2	-9.03	115.78	120.30
1	A	23	ARG	CD-NE-CZ	8.95	136.13	123.60
1	A	104	PHE	CB-CG-CD2	-8.52	114.84	120.80
1	A	280	TYR	CB-CG-CD1	8.45	126.07	121.00
1	A	358	GLU	OE1-CD-OE2	-8.41	113.20	123.30
1	A	208	ARG	NE-CZ-NH1	8.22	124.41	120.30
1	A	284	ARG	NE-CZ-NH2	-8.19	116.20	120.30
1	A	10	ARG	NE-CZ-NH2	7.91	124.26	120.30
1	A	175	ASP	CB-CG-OD2	-7.81	111.27	118.30
1	A	117	ARG	NE-CZ-NH1	7.78	124.19	120.30
1	A	368	ARG	NE-CZ-NH1	7.73	124.17	120.30
1	A	152	ARG	NE-CZ-NH1	7.72	124.16	120.30
1	A	242	PHE	CB-CG-CD2	-7.71	115.40	120.80
1	A	143	ALA	O-C-N	7.47	134.65	122.70
1	A	295	ASP	CB-CG-OD2	7.46	125.01	118.30
1	A	280	TYR	CB-CG-CD2	-7.41	116.56	121.00
1	A	140	ARG	NE-CZ-NH2	-7.40	116.60	120.30
1	A	76	ARG	CG-CD-NE	-7.35	96.36	111.80
1	A	368	ARG	NE-CZ-NH2	-7.26	116.67	120.30
1	A	245	ASP	CB-CG-OD1	7.19	124.77	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	68	ARG	NH1-CZ-NH2	-7.11	111.58	119.40
1	A	31	ARG	NE-CZ-NH2	7.10	123.85	120.30
1	A	295	ASP	CB-CG-OD1	7.07	124.67	118.30
1	A	295	ASP	OD1-CG-OD2	-6.84	110.31	123.30
1	A	277	SER	CB-CA-C	6.72	122.88	110.10
1	A	363	ASP	CB-CG-OD1	6.69	124.32	118.30
1	A	297	ASP	CB-CG-OD1	6.67	124.31	118.30
1	A	101	ASP	CB-CG-OD2	-6.64	112.33	118.30
1	A	168	TYR	CG-CD1-CE1	-6.62	116.00	121.30
1	A	273	ASP	CB-CG-OD2	6.59	124.23	118.30
1	A	10	ARG	NH1-CZ-NH2	-6.58	112.17	119.40
1	A	10	ARG	NE-CZ-NH1	6.55	123.58	120.30
1	A	121	ARG	NE-CZ-NH2	-6.49	117.06	120.30
1	A	321	ARG	NE-CZ-NH1	6.48	123.54	120.30
1	A	334	ARG	NE-CZ-NH1	6.46	123.53	120.30
1	A	74	ARG	CD-NE-CZ	6.46	132.64	123.60
1	A	65	ASP	CB-CG-OD2	6.43	124.08	118.30
1	A	24	ASP	CB-CA-C	6.42	123.24	110.40
1	A	43	LEU	CA-CB-CG	6.41	130.05	115.30
1	A	174	TYR	CB-CG-CD1	6.35	124.81	121.00
1	A	255	ASP	CB-CG-OD2	6.30	123.97	118.30
1	A	8	GLU	CA-CB-CG	6.27	127.20	113.40
1	A	160	GLU	OE1-CD-OE2	6.19	130.72	123.30
1	A	266	ARG	CD-NE-CZ	6.00	132.00	123.60
1	A	3	TYR	CB-CG-CD2	-5.98	117.41	121.00
1	A	35	ASP	CB-CG-OD1	5.96	123.66	118.30
1	A	331	ARG	CG-CD-NE	-5.96	99.30	111.80
1	A	361	ASP	CB-CG-OD2	-5.86	113.03	118.30
1	A	175	ASP	OD1-CG-OD2	5.85	134.42	123.30
1	A	328	GLU	OE1-CD-OE2	-5.85	116.28	123.30
1	A	99	PHE	CB-CG-CD2	-5.85	116.70	120.80
1	A	132	GLU	N-CA-CB	-5.82	100.12	110.60
1	A	113	ARG	CD-NE-CZ	5.81	131.73	123.60
1	A	20	TRP	CH2-CZ2-CE2	-5.80	111.59	117.40
1	A	372	PHE	CB-CG-CD1	5.79	124.85	120.80
1	A	336	ASP	CB-CG-OD1	5.78	123.50	118.30
1	A	325	GLU	OE1-CD-OE2	5.77	130.22	123.30
1	A	308	ARG	NE-CZ-NH1	5.77	123.18	120.30
1	A	212	TYR	CB-CG-CD2	5.76	124.45	121.00
1	A	354	ARG	NE-CZ-NH1	5.67	123.14	120.30
1	A	287	ASP	CB-CG-OD1	5.62	123.36	118.30
1	A	177	ARG	NE-CZ-NH1	-5.59	117.50	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	313	LEU	CA-CB-CG	5.55	128.06	115.30
1	A	42	ARG	NH1-CZ-NH2	-5.53	113.32	119.40
1	A	65	ASP	CB-CA-C	5.52	121.44	110.40
1	A	168	TYR	CB-CG-CD1	-5.41	117.76	121.00
1	A	124	ASP	CB-CG-OD2	-5.40	113.44	118.30
1	A	31	ARG	NH1-CZ-NH2	-5.38	113.48	119.40
1	A	323	ASP	CB-CG-OD1	5.37	123.13	118.30
1	A	308	ARG	NE-CZ-NH2	-5.36	117.62	120.30
1	A	163	ASP	OD1-CG-OD2	-5.34	113.16	123.30
1	A	20	TRP	CZ3-CH2-CZ2	5.33	128.00	121.60
1	A	4	GLN	CB-CG-CD	5.33	125.45	111.60
1	A	381	ASP	CB-CG-OD1	5.31	123.08	118.30
1	A	349	ALA	CB-CA-C	-5.30	102.14	110.10
1	A	264	ASP	CB-CG-OD1	5.30	123.07	118.30
1	A	23	ARG	NE-CZ-NH2	-5.29	117.65	120.30
1	A	205	ARG	NE-CZ-NH1	5.27	122.94	120.30
1	A	342	THR	O-C-N	5.27	131.13	122.70
1	A	23	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	A	367	ALA	N-CA-CB	5.22	117.40	110.10
1	A	374	ARG	NE-CZ-NH2	-5.21	117.69	120.30
1	A	354	ARG	NE-CZ-NH2	-5.20	117.70	120.30
1	A	132	GLU	CA-CB-CG	5.17	124.78	113.40
1	A	109	ARG	NE-CZ-NH1	-5.16	117.72	120.30
1	A	114	TYR	CB-CG-CD2	-5.14	117.91	121.00
1	A	176	ILE	O-C-N	5.14	130.92	122.70
1	A	288	PHE	CB-CG-CD1	-5.13	117.21	120.80
1	A	208	ARG	CB-CG-CD	-5.01	98.58	111.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	53	PHE	Peptide

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	3031	0	2900	15	2
2	A	9	0	6	0	0
3	A	1	0	0	0	0
4	A	377	0	0	4	4
All	All	3418	0	2906	15	4

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 (15) 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:25:PRO:HG2	1:A:26:PHE:CD1	2.39	0.57
1:A:25:PRO:HG2	1:A:26:PHE:CE1	2.48	0.47
1:A:32:ARG:NH1	1:A:33:ALA:O	2.47	0.47
1:A:42:ARG:HE	1:A:42:ARG:HA	1.82	0.45
1:A:37:VAL:HB	1:A:78:ALA:HB2	1.98	0.45
1:A:205:ARG:HD2	4:A:772:HOH:O	2.16	0.45
1:A:58:LEU:HD11	1:A:75:PHE:CG	2.52	0.45
1:A:212:TYR:HB3	4:A:739:HOH:O	2.18	0.44
1:A:76:ARG:HD3	4:A:770:HOH:O	2.17	0.44
1:A:208:ARG:NH1	4:A:582:HOH:O	2.35	0.42
1:A:360:PHE:CD2	1:A:362:VAL:HG12	2.55	0.42
1:A:54:HIS:O	1:A:55:ASP:C	2.58	0.42
1:A:39:SER:O	1:A:43:LEU:HB2	2.21	0.41
1:A:96:HIS:ND1	1:A:97:PRO:HD2	2.36	0.41
1:A:354:ARG:HB3	1:A:359:GLU:HG3	2.03	0.40

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:253:LYS:NZ	4:A:737:HOH:O[4_566]	1.97	0.23
4:A:509:HOH:O	4:A:733:HOH:O[6_555]	2.05	0.15
4:A:629:HOH:O	4:A:715:HOH:O[3_656]	2.11	0.09
1:A:253:LYS:CE	4:A:737:HOH:O[4_566]	2.12	0.08

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%)	372 (97%)	10 (3%)	1 (0%)	41 24

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	186	GLU

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%)	288 (95%)	14 (5%)	27 10

All (14) 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	76	ARG
1	A	91	THR
1	A	132	GLU
1	A	169	VAL

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Mol	Chain	Res	Type
1	A	175	ASP
1	A	185	ASN
1	A	313	LEU
1	A	347	LEU

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	4	GLN
1	A	41	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 1 is 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	THE	A	389	3	7,8,8	1.99	4 (57%)	7,10,10	4.86	4 (57%)

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	THE	A	389	3	-	5/10/10/10	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	389	THE	O2-C2	3.05	1.49	1.43
2	A	389	THE	O5-C4	-2.42	1.22	1.30
2	A	389	THE	C3-C4	-2.26	1.49	1.52
2	A	389	THE	O3-C3	2.20	1.46	1.42

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	389	THE	O5-C4-O4	-9.28	103.02	124.09
2	A	389	THE	O5-C4-C3	7.34	133.10	113.27
2	A	389	THE	O2-C2-C1	-3.67	100.54	109.14
2	A	389	THE	O3-C3-C4	2.54	115.98	110.66

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	389	THE	O2-C2-C3-C4
2	A	389	THE	O3-C3-C4-O5
2	A	389	THE	O3-C3-C4-O4
2	A	389	THE	C2-C3-C4-O5
2	A	389	THE	C2-C3-C4-O4

There are no ring outliers.

No monomer is involved in short contacts.

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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.