



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 04:42 am GMT

PDB ID : 4XIS
Title : A METAL-MEDIATED HYDRIDE SHIFT MECHANISM FOR XYLOSE ISOMERASE BASED ON THE 1.6 ANGSTROMS STREPTOMYCES RUBIGINOSUS STRUCTURES WITH XYLITOL AND D-XYLOSE
Authors : Whitlow, M.; Howard, A.J.
Deposited on : 1991-03-25
Resolution : 1.60 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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

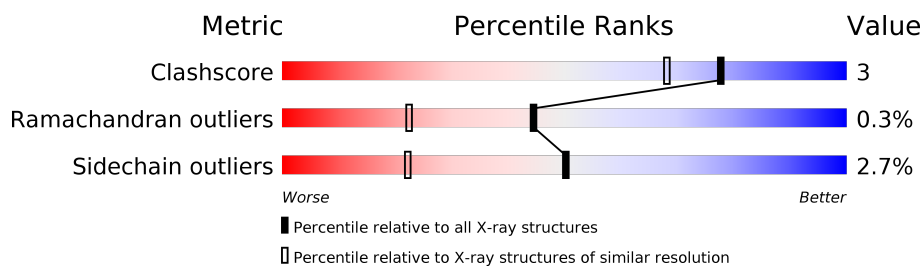
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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	112137	2967 (1.60-1.60)
Ramachandran outliers	110173	2887 (1.60-1.60)
Sidechain outliers	110143	2886 (1.60-1.60)

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	387	

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	XLS	A	393	X	-	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3527 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 XYLOSE ISOMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	387	Total	C	N	O	S	0	17	1
			3100	1940	575	576	9			

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

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	2	Total	C	O	0	0
			20	10	10		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Mn	0	1
			3	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	400	Total	O	0	4
			404	404		

Note EDS was not executed.

Chain A:

85% 11%

R2 R10 R23 D24 P25 A29 T30 R31 R32 R41 R42 D65 R74 F75 R76 T91 N92 L93 F94 T95 H96 P97 V98 R109 D110 R113 R117 K118 T119 I120 R121 D124 E132 R152 R157 R177 N185 E196 P197

Y212 V218 G219 H230 F242 D245 L246 N247 G248 R266 F269 R284 D287 R292 D296 R316 R331 R334 E337 R340 L347 R368 D381 R387 G398

4 Data and refinement statistics

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	94.64Å 99.97Å 103.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.60	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-1.60)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.135 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3527	wwPDB-VP
Average B, all atoms (Å ²)	16.0	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: XYZ, XLS, 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	1.20	5/3265 (0.2%)	1.72	88/4413 (2.0%)

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	4
2	A	1	0
All	All	1	4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	132[A]	GLU	CG-CD	-7.63	1.40	1.51
1	A	132[B]	GLU	CG-CD	-7.63	1.40	1.51
1	A	113	ARG	CZ-NH2	5.92	1.40	1.33
1	A	132[A]	GLU	CD-OE2	5.71	1.31	1.25
1	A	132[B]	GLU	CD-OE2	5.71	1.31	1.25

All (88) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	132[A]	GLU	CB-CG-CD	15.23	155.32	114.20
1	A	132[B]	GLU	CB-CG-CD	15.23	155.32	114.20
1	A	113	ARG	NE-CZ-NH1	14.21	127.41	120.30
1	A	331	ARG	NE-CZ-NH1	13.59	127.10	120.30
1	A	331	ARG	NE-CZ-NH2	-12.31	114.15	120.30
1	A	74	ARG	CD-NE-CZ	11.87	140.22	123.60

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	74	ARG	NE-CZ-NH1	11.49	126.05	120.30
1	A	157	ARG	NE-CZ-NH2	11.34	125.97	120.30
1	A	266[A]	ARG	CD-NE-CZ	10.27	137.98	123.60
1	A	266[B]	ARG	CD-NE-CZ	10.27	137.98	123.60
1	A	188	ARG	NE-CZ-NH2	-10.21	115.20	120.30
1	A	188	ARG	NE-CZ-NH1	9.46	125.03	120.30
1	A	381	ASP	CB-CG-OD1	9.17	126.55	118.30
1	A	74	ARG	NE-CZ-NH2	-9.09	115.75	120.30
1	A	124	ASP	CB-CG-OD1	8.82	126.24	118.30
1	A	10	ARG	NE-CZ-NH1	8.81	124.71	120.30
1	A	368	ARG	NE-CZ-NH1	8.68	124.64	120.30
1	A	31	ARG	NE-CZ-NH2	-8.63	115.99	120.30
1	A	23[A]	ARG	CD-NE-CZ	8.61	135.66	123.60
1	A	23[B]	ARG	CD-NE-CZ	8.61	135.66	123.60
1	A	10	ARG	NE-CZ-NH2	-8.51	116.04	120.30
1	A	292	ARG	NE-CZ-NH2	8.44	124.52	120.30
1	A	177	ARG	NE-CZ-NH2	-8.07	116.26	120.30
1	A	266[A]	ARG	NE-CZ-NH2	-8.05	116.28	120.30
1	A	266[B]	ARG	NE-CZ-NH2	-8.05	116.28	120.30
1	A	113	ARG	NE-CZ-NH2	-8.00	116.30	120.30
1	A	340[A]	ARG	CD-NE-CZ	7.98	134.78	123.60
1	A	340[B]	ARG	CD-NE-CZ	7.98	134.78	123.60
1	A	121	ARG	NE-CZ-NH2	-7.94	116.33	120.30
1	A	284	ARG	NE-CZ-NH1	7.89	124.25	120.30
1	A	31	ARG	NE-CZ-NH1	7.78	124.19	120.30
1	A	23[A]	ARG	CG-CD-NE	7.64	127.85	111.80
1	A	23[B]	ARG	CG-CD-NE	7.64	127.85	111.80
1	A	316	ARG	NE-CZ-NH1	7.64	124.12	120.30
1	A	205[A]	ARG	NE-CZ-NH1	7.50	124.05	120.30
1	A	205[B]	ARG	NE-CZ-NH1	7.50	124.05	120.30
1	A	295	ASP	CB-CG-OD1	7.41	124.97	118.30
1	A	340[A]	ARG	NE-CZ-NH2	-7.31	116.64	120.30
1	A	340[B]	ARG	NE-CZ-NH2	-7.31	116.64	120.30
1	A	177	ARG	NE-CZ-NH1	7.31	123.95	120.30
1	A	208	ARG	NE-CZ-NH2	-7.23	116.69	120.30
1	A	387[A]	ARG	NE-CZ-NH1	7.15	123.88	120.30
1	A	387[B]	ARG	NE-CZ-NH1	7.15	123.88	120.30
1	A	284	ARG	NE-CZ-NH2	-7.01	116.79	120.30
1	A	76[A]	ARG	NE-CZ-NH1	7.01	123.80	120.30
1	A	76[B]	ARG	NE-CZ-NH1	7.01	123.80	120.30
1	A	266[A]	ARG	NE-CZ-NH1	6.98	123.79	120.30
1	A	266[B]	ARG	NE-CZ-NH1	6.98	123.79	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	340[A]	ARG	NE-CZ-NH1	6.61	123.60	120.30
1	A	340[B]	ARG	NE-CZ-NH1	6.61	123.60	120.30
1	A	132[A]	GLU	OE1-CD-OE2	-6.56	115.42	123.30
1	A	132[B]	GLU	OE1-CD-OE2	-6.56	115.42	123.30
1	A	42	ARG	NE-CZ-NH1	6.48	123.54	120.30
1	A	121	ARG	NE-CZ-NH1	6.40	123.50	120.30
1	A	109	ARG	NE-CZ-NH2	-6.32	117.14	120.30
1	A	334	ARG	NE-CZ-NH1	6.26	123.43	120.30
1	A	24	ASP	CB-CA-C	6.24	122.88	110.40
1	A	109	ARG	NE-CZ-NH1	6.18	123.39	120.30
1	A	32	ARG	NE-CZ-NH1	6.17	123.39	120.30
1	A	76[A]	ARG	NE-CZ-NH2	-6.16	117.22	120.30
1	A	76[B]	ARG	NE-CZ-NH2	-6.16	117.22	120.30
1	A	124	ASP	CB-CG-OD2	-6.16	112.76	118.30
1	A	245	ASP	CB-CG-OD1	5.96	123.66	118.30
1	A	152	ARG	NE-CZ-NH2	-5.95	117.33	120.30
1	A	41	ARG	NE-CZ-NH1	5.94	123.27	120.30
1	A	205[A]	ARG	NE-CZ-NH2	-5.91	117.34	120.30
1	A	205[B]	ARG	NE-CZ-NH2	-5.91	117.34	120.30
1	A	152	ARG	NE-CZ-NH1	5.87	123.23	120.30
1	A	347	LEU	CB-CG-CD2	5.80	120.86	111.00
1	A	132[A]	GLU	CG-CD-OE1	5.78	129.86	118.30
1	A	132[B]	GLU	CG-CD-OE1	5.78	129.86	118.30
1	A	117	ARG	NE-CZ-NH1	5.76	123.18	120.30
1	A	287	ASP	CB-CG-OD1	5.73	123.45	118.30
1	A	212	TYR	CB-CG-CD1	-5.70	117.58	121.00
1	A	42	ARG	NE-CZ-NH2	-5.67	117.46	120.30
1	A	242	PHE	CB-CG-CD2	-5.54	116.92	120.80
1	A	269	PHE	CB-CG-CD1	-5.50	116.95	120.80
1	A	76[A]	ARG	CA-CB-CG	5.48	125.46	113.40
1	A	76[B]	ARG	CA-CB-CG	5.48	125.46	113.40
1	A	208	ARG	NE-CZ-NH1	5.48	123.04	120.30
1	A	242	PHE	CB-CG-CD1	5.45	124.61	120.80
1	A	205[A]	ARG	CD-NE-CZ	5.42	131.19	123.60
1	A	205[B]	ARG	CD-NE-CZ	5.42	131.19	123.60
1	A	65	ASP	CB-CG-OD1	5.34	123.10	118.30
1	A	337	GLU	CG-CD-OE1	5.30	128.91	118.30
1	A	110	ASP	CB-CG-OD1	5.22	123.00	118.30
1	A	287	ASP	CB-CG-OD2	-5.17	113.65	118.30
1	A	157	ARG	NH1-CZ-NH2	-5.03	113.87	119.40

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	393	XLS	C2

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	177	ARG	Sidechain
1	A	208	ARG	Sidechain
1	A	331	ARG	Sidechain
1	A	41	ARG	Sidechain

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	3100	0	2952	20	0
2	A	20	0	5	1	0
3	A	3	0	0	0	0
4	A	404	0	0	8	0
All	All	3527	0	2957	21	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 (21) 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:96:HIS:HD2	1:A:98:VAL:H	1.32	0.76
1:A:92:ASN:HD21	1:A:95:THR:H	1.36	0.73
1:A:340[B]:ARG:NH2	4:A:528:HOH:O	1.68	0.67
1:A:93:LEU:HD21	4:A:618:HOH:O	1.97	0.63
1:A:248:GLY:HA2	4:A:608:HOH:O	2.00	0.61
1:A:218:VAL:HG11	4:A:608:HOH:O	2.00	0.61
1:A:219:GLY:H	1:A:247:ASN:HD21	1.54	0.56
1:A:24:ASP:HB2	1:A:25:PRO:HD2	1.87	0.56
1:A:96:HIS:CD2	1:A:98:VAL:H	2.19	0.54
1:A:92:ASN:C	1:A:92:ASN:HD22	2.14	0.50
1:A:92:ASN:ND2	1:A:94:PHE:H	2.10	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:340[B]:ARG:NE	4:A:528:HOH:O	2.40	0.49
1:A:337:GLU:HG2	1:A:340[A]:ARG:NH2	2.27	0.49
1:A:91:THR:HG21	4:A:618:HOH:O	2.13	0.48
1:A:92:ASN:HD22	1:A:94:PHE:H	1.64	0.46
2:A:393:XLS:H3	2:A:394:XYO:O5	1.45	0.46
1:A:381:ASP:HB3	1:A:387[B]:ARG:HD2	1.98	0.45
1:A:119:THR:N	4:A:618:HOH:O	2.49	0.45
1:A:92:ASN:ND2	1:A:95:THR:H	2.07	0.45
1:A:118:LYS:HB3	4:A:618:HOH:O	2.19	0.42
1:A:23[B]:ARG:HG2	1:A:29:ALA:N	2.36	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	402/387 (104%)	387 (96%)	14 (4%)	1 (0%)	51 27

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	317/303 (105%)	308 (97%)	9 (3%)	49 21

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	ARG
1	A	23[A]	ARG
1	A	23[B]	ARG
1	A	91	THR
1	A	92	ASN
1	A	185	ASN
1	A	230	HIS
1	A	247	ASN
1	A	347	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	77	GLN
1	A	92	ASN
1	A	96	HIS
1	A	215	ASN
1	A	222	GLN
1	A	230	HIS
1	A	247	ASN

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](#)

2 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
2	XLS	A	393	3,2	9,9,9	2.62	2 (22%)	11,11,11	2.57	3 (27%)
2	XYS	A	394	3,2	10,10,10	2.03	2 (20%)	14,14,14	3.67	7 (50%)

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	XLS	A	393	3,2	1/1/3/4	0/10/12/12	0/0/0/0
2	XYS	A	394	3,2	-	0/0/17/17	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	394	XYS	O5-C1	-5.15	1.35	1.43
2	A	393	XLS	O2-C2	-4.39	1.34	1.43
2	A	394	XYS	C1-C2	2.61	1.58	1.52
2	A	393	XLS	O1-C1	5.84	1.44	1.19

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	393	XLS	O1-C1-C2	-3.42	115.82	125.13
2	A	394	XYS	C1-C2-C3	-2.74	105.70	110.65
2	A	394	XYS	O2-C2-C3	3.19	117.30	110.36
2	A	394	XYS	C5-O5-C1	3.35	118.60	112.80
2	A	394	XYS	O4-C4-C5	3.79	116.89	109.18
2	A	393	XLS	C3-C2-C1	3.89	123.35	111.10
2	A	394	XYS	O1-C1-C2	4.17	121.19	109.42
2	A	394	XYS	O1-C1-O5	5.10	123.52	109.72
2	A	393	XLS	O2-C2-C1	5.73	123.89	110.30
2	A	394	XYS	O5-C5-C4	9.68	125.96	110.79

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	393	XLS	C2

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	393	XLS	1	0
2	A	394	XYS	1	0

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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 [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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.