



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 09:08 PM UTC

PDB ID : 1S5M / pdb_00001s5m
Title : Xylose Isomerase in Substrate and Inhibitor Michaelis States: Atomic Resolution Studies of a Metal-Mediated Hydride Shift
Authors : Fenn, T.D.; Ringe, D.; Petsko, G.A.
Deposited on : 2004-01-21
Resolution : 0.98 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
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

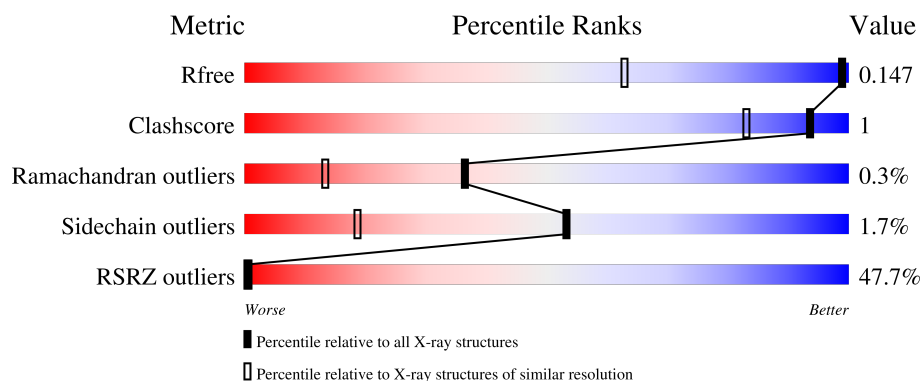
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 0.98 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	1146 (1.02-0.94)
Clashscore	190562	1197 (1.02-0.94)
Ramachandran outliers	187476	1136 (1.02-0.94)
Sidechain outliers	187428	1137 (1.02-0.94)
RSRZ outliers	180081	1144 (1.02-0.94)

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	386	48% 90% 9%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6830 atoms, of which 3140 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.

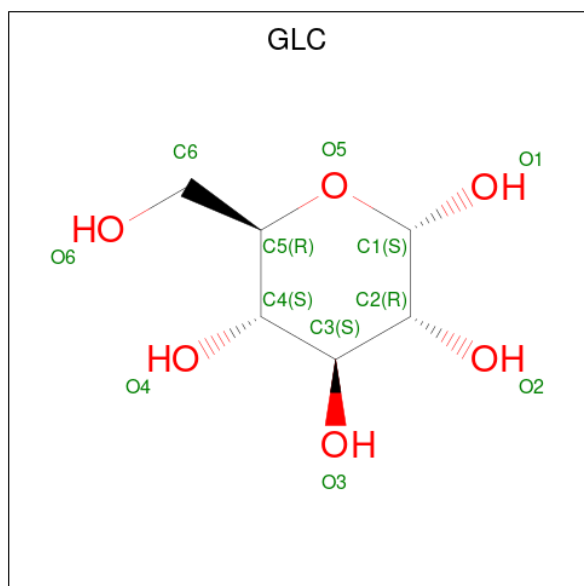
- Molecule 1 is a protein called Xylose isomerase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	386	6378	2036	3128	589	615	10	0	45	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	175	ILE	THR	SEE REMARK 999	UNP P15587

- Molecule 2 is alpha-D-glucopyranose (CCD ID: GLC) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
2	A	1	24	6	12	6	0	0

- Molecule 3 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

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

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total 2	Na 2	0	0

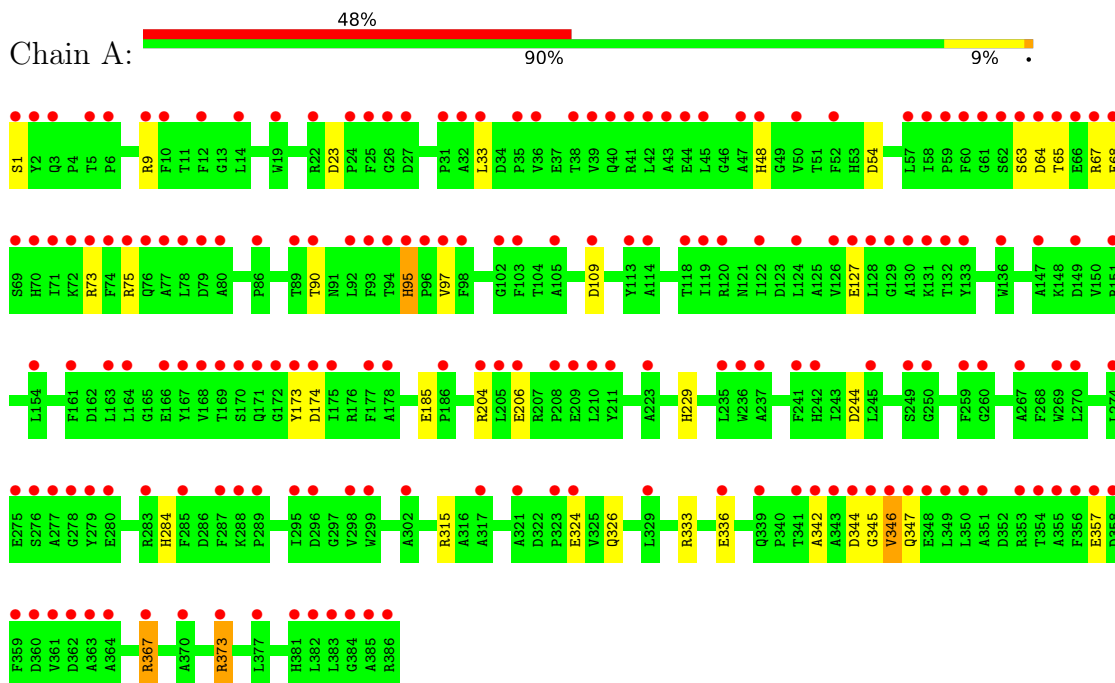
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	411	Total 424	O 424	0	13

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: Xylose isomerase



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	85.86Å 92.97Å 98.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 0.98 50.00 – 0.98	Depositor EDS
% Data completeness (in resolution range)	94.9 (50.00-0.98) 90.5 (50.00-0.98)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.11 (at 0.95Å)	Xtriage
Refinement program	SHELXL-97, CNS	Depositor
R, R_{free}	0.111 , 0.129 0.145 , 0.147	Depositor DCC
R_{free} test set	11433 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	8.9	Xtriage
Anisotropy	0.147	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.49 , 53.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	6830	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.03% 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: GLC, MN, NA

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	1.02	8/3323 (0.2%)	1.38	33/4494 (0.7%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	73	ARG	CZ-NH2	7.27	1.43	1.33
1	A	73	ARG	CZ-NH1	7.08	1.42	1.32
1	A	95	HIS	CD2-NE2	-7.07	1.30	1.37
1	A	67	ARG	CD-NE	6.10	1.54	1.46
1	A	315	ARG	CZ-NH2	5.90	1.41	1.33
1	A	336	GLU	CB-CG	-5.84	1.34	1.52
1	A	33	LEU	CB-CG	-5.64	1.42	1.53
1	A	315	ARG	NE-CZ	-5.19	1.27	1.33

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	73	ARG	CD-NE-CZ	32.89	170.44	124.40
1	A	204[A]	ARG	CD-NE-CZ	13.47	143.27	124.40
1	A	204[B]	ARG	CD-NE-CZ	13.47	143.27	124.40
1	A	95	HIS	CG-CD2-NE2	8.77	115.97	107.20
1	A	373	ARG	NE-CZ-NH2	8.58	126.92	119.20
1	A	174[A]	ASP	CA-C-O	8.37	130.76	121.39
1	A	174[B]	ASP	CA-C-O	8.37	130.76	121.39
1	A	336	GLU	CB-CG-CD	7.04	124.57	112.60
1	A	284[A]	HIS	CG-CD2-NE2	6.84	114.04	107.20
1	A	344	ASP	CA-CB-CG	6.50	119.10	112.60
1	A	346	VAL	CA-CB-CG1	6.33	121.17	110.40
1	A	75	ARG	CD-NE-CZ	6.27	133.17	124.40
1	A	67	ARG	CD-NE-CZ	-6.22	115.69	124.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	315	ARG	CD-NE-CZ	-6.17	115.76	124.40
1	A	9[A]	ARG	NE-CZ-NH2	-6.11	113.70	119.20
1	A	229	HIS	ND1-CE1-NE2	5.98	114.38	108.40
1	A	244	ASP	CA-CB-CG	5.95	118.55	112.60
1	A	127	GLU	OE1-CD-OE2	5.82	136.87	122.90
1	A	95	HIS	CB-CG-ND1	5.74	131.30	122.70
1	A	54	ASP	CA-CB-CG	5.72	118.32	112.60
1	A	23	ASP	CB-CA-C	5.64	121.29	110.17
1	A	367	ARG	CD-NE-CZ	-5.57	116.60	124.40
1	A	109	ASP	CA-CB-CG	5.53	118.13	112.60
1	A	357	GLU	CB-CG-CD	5.44	121.85	112.60
1	A	64	ASP	CA-C-N	5.33	127.37	120.44
1	A	64	ASP	C-N-CA	5.33	127.37	120.44
1	A	284[A]	HIS	CE1-NE2-CD2	-5.18	103.82	109.00
1	A	347	GLN	OE1-CD-NE2	-5.13	117.47	122.60
1	A	63	SER	CA-CB-OG	-5.06	100.98	111.10
1	A	173[A]	TYR	CA-C-N	-5.02	115.34	122.77
1	A	173[A]	TYR	C-N-CA	-5.02	115.34	122.77
1	A	173[B]	TYR	CA-C-N	-5.02	115.34	122.77
1	A	173[B]	TYR	C-N-CA	-5.02	115.34	122.77

There are no chirality outliers.

There are no planarity outliers.

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	3250	3128	2961	9	0
2	A	12	12	10	0	0
3	A	2	0	0	0	0
4	A	2	0	0	0	0
5	A	424	0	0	4	0
All	All	3690	3140	2971	9	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 1.

All (9) 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:95:HIS:HD2	1:A:97:VAL:H	1.40	0.68
1:A:48[A]:HIS:HD2	5:A:2324:HOH:O	1.90	0.54
1:A:333:ARG:NH2	1:A:367:ARG:HD3	2.27	0.50
1:A:324[A]:GLU:OE2	1:A:373:ARG:NH2	2.47	0.48
1:A:345:GLY:N	5:A:2410:HOH:O	2.48	0.45
1:A:326[A]:GLN:NE2	5:A:2112:HOH:O	2.52	0.41
1:A:95:HIS:CD2	1:A:97:VAL:H	2.28	0.41
1:A:342:ALA:HB1	5:A:2410:HOH:O	2.20	0.41

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	408/386 (106%)	394 (97%)	13 (3%)	1 (0%)	43	16

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	185	GLU

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	326/302 (108%)	321 (98%)	5 (2%)	57 20

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	SER
1	A	65	THR
1	A	68	GLU
1	A	90	THR
1	A	346	VAL

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	95	HIS
1	A	308	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](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 4 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	GLC	A	1001	3	12,12,12	1.11	1 (8%)	17,17,17	2.00	5 (29%)

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	GLC	A	1001	3	-	0/2/22/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	GLC	O5-C1	3.44	1.51	1.42

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	GLC	O5-C5-C6	4.42	117.39	106.44
2	A	1001	GLC	C1-O5-C5	-4.11	105.70	113.65
2	A	1001	GLC	C6-C5-C4	-3.44	104.57	113.02
2	A	1001	GLC	O6-C6-C5	-2.69	102.17	111.33
2	A	1001	GLC	C3-C4-C5	-2.35	105.97	110.23

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 ⓘ

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	386/386 (100%)	2.23	184 (47%) 0 1	4, 12, 28, 60	24 (6%)

All (184) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	385[A]	ALA	9.5
1	A	65	THR	9.0
1	A	25	PHE	8.5
1	A	1	SER	8.4
1	A	24	PRO	8.2
1	A	346	VAL	7.4
1	A	75	ARG	7.3
1	A	356	PHE	6.9
1	A	173[A]	TYR	6.9
1	A	343	ALA	6.8
1	A	33	LEU	6.5
1	A	126	VAL	6.2
1	A	59	PRO	5.7
1	A	350	LEU	5.4
1	A	9[A]	ARG	5.4
1	A	168	VAL	5.4
1	A	132	THR	5.3
1	A	347	GLN	5.2
1	A	174[A]	ASP	5.2
1	A	386[A]	ARG	5.2
1	A	204[A]	ARG	5.1
1	A	68	GLU	5.1
1	A	206[A]	GLU	5.0
1	A	36	VAL	4.9
1	A	351	ALA	4.9
1	A	169	THR	4.9
1	A	383	LEU	4.9

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Mol	Chain	Res	Type	RSRZ
1	A	69	SER	4.8
1	A	60	PHE	4.7
1	A	74	PHE	4.7
1	A	357	GLU	4.7
1	A	76	GLN	4.6
1	A	355	ALA	4.6
1	A	22	ARG	4.6
1	A	61	GLY	4.6
1	A	70	HIS	4.5
1	A	147	ALA	4.5
1	A	86	PRO	4.4
1	A	178	ALA	4.4
1	A	78	LEU	4.4
1	A	359	PHE	4.3
1	A	66	GLU	4.3
1	A	163[A]	LEU	4.3
1	A	367	ARG	4.2
1	A	64	ASP	4.2
1	A	277[A]	ALA	4.2
1	A	89	THR	4.2
1	A	128	LEU	4.2
1	A	6	PRO	4.1
1	A	43	ALA	4.1
1	A	354	THR	4.1
1	A	72	LYS	4.1
1	A	349[A]	LEU	4.1
1	A	172	GLY	4.0
1	A	44	GLU	4.0
1	A	342	ALA	4.0
1	A	98	PHE	4.0
1	A	79	ASP	3.9
1	A	323	PRO	3.9
1	A	161	PHE	3.9
1	A	120	ARG	3.9
1	A	278	GLY	3.8
1	A	32	ALA	3.8
1	A	151[A]	ARG	3.7
1	A	119	ILE	3.7
1	A	280	GLU	3.7
1	A	71	ILE	3.7
1	A	361	VAL	3.7
1	A	276[A]	SER	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	80	ALA	3.6
1	A	131	LYS	3.6
1	A	39	VAL	3.5
1	A	73	ARG	3.5
1	A	210	LEU	3.5
1	A	58	ILE	3.5
1	A	298	VAL	3.4
1	A	250[A]	GLY	3.4
1	A	130	ALA	3.4
1	A	175[A]	ILE	3.4
1	A	358	ASP	3.3
1	A	40[A]	GLN	3.3
1	A	279	TYR	3.3
1	A	324[A]	GLU	3.3
1	A	136	TRP	3.3
1	A	299	TRP	3.3
1	A	63	SER	3.3
1	A	345	GLY	3.3
1	A	283[A]	ARG	3.3
1	A	114	ALA	3.3
1	A	348[A]	GLU	3.2
1	A	57	LEU	3.2
1	A	2	TYR	3.2
1	A	285	PHE	3.2
1	A	287[A]	PHE	3.2
1	A	363	ALA	3.1
1	A	384	GLY	3.1
1	A	96	PRO	3.1
1	A	50[A]	VAL	3.1
1	A	122	ILE	3.1
1	A	38	THR	3.1
1	A	167	TYR	3.1
1	A	177[A]	PHE	3.1
1	A	208	PRO	3.0
1	A	362	ASP	3.0
1	A	67	ARG	3.0
1	A	45	LEU	3.0
1	A	370	ALA	3.0
1	A	288	LYS	3.0
1	A	149	ASP	2.9
1	A	205[A]	LEU	2.9
1	A	360	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	237	ALA	2.9
1	A	127	GLU	2.9
1	A	223	ALA	2.9
1	A	42	LEU	2.8
1	A	52	PHE	2.8
1	A	129	GLY	2.8
1	A	353	ARG	2.8
1	A	62	SER	2.8
1	A	344	ASP	2.7
1	A	12	PHE	2.7
1	A	260	GLY	2.7
1	A	267	ALA	2.7
1	A	164[A]	LEU	2.7
1	A	382	LEU	2.7
1	A	113	TYR	2.6
1	A	373	ARG	2.6
1	A	186	PRO	2.6
1	A	211	TYR	2.6
1	A	90	THR	2.6
1	A	241	PHE	2.6
1	A	19	TRP	2.5
1	A	249[A]	SER	2.5
1	A	31	PRO	2.5
1	A	296	ASP	2.5
1	A	235	LEU	2.5
1	A	329	LEU	2.5
1	A	381	HIS	2.5
1	A	93	PHE	2.5
1	A	103	PHE	2.4
1	A	5	THR	2.4
1	A	209	GLU	2.4
1	A	170	SER	2.4
1	A	274	LEU	2.3
1	A	3[A]	GLN	2.3
1	A	35	PRO	2.3
1	A	171	GLN	2.3
1	A	317	ALA	2.3
1	A	48[A]	HIS	2.3
1	A	95	HIS	2.3
1	A	295	ILE	2.3
1	A	336	GLU	2.3
1	A	133	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	341	THR	2.3
1	A	339	GLN	2.3
1	A	275	GLU	2.3
1	A	27	ASP	2.3
1	A	92	LEU	2.3
1	A	124	LEU	2.2
1	A	166	GLU	2.2
1	A	10[A]	PHE	2.2
1	A	321	ALA	2.2
1	A	236	TRP	2.2
1	A	269	TRP	2.2
1	A	14	LEU	2.2
1	A	97	VAL	2.2
1	A	41[A]	ARG	2.2
1	A	289	PRO	2.1
1	A	109	ASP	2.1
1	A	270	LEU	2.1
1	A	377	LEU	2.1
1	A	77	ALA	2.1
1	A	105	ALA	2.1
1	A	364	ALA	2.1
1	A	245	LEU	2.1
1	A	26	GLY	2.1
1	A	242	HIS	2.1
1	A	94	THR	2.0
1	A	118	THR	2.0
1	A	47	ALA	2.0
1	A	302	ALA	2.0
1	A	259	PHE	2.0
1	A	102	GLY	2.0
1	A	154	LEU	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

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. 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	GLC	A	1001	12/12	0.92	0.15	10,16,28,32	0
4	NA	A	2005	1/1	0.94	0.12	26,26,26,26	0
4	NA	A	2004	1/1	0.98	0.10	19,19,19,19	0
3	MN	A	2001	1/1	1.00	0.03	8,8,8,8	1
3	MN	A	2002	1/1	1.00	0.01	7,7,7,7	1

6.5 Other polymers

There are no such residues in this entry.