



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 18, 2026 – 12:58 AM UTC

PDB ID : 3ITO / pdb_00003ito
Title : Crystal structure of Pseudomonas stutzeri L-rhamnose isomerase mutant D327N in complex with D-psicose
Authors : Yoshida, H.; Yamaji, M.; Ishii, T.; Izumori, K.; Kamitori, S.
Deposited on : 2009-08-28
Resolution : 1.90 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

<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

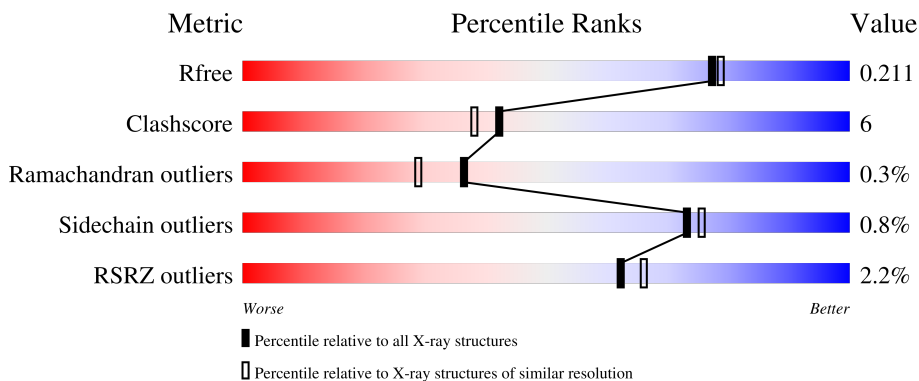
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	438	 83% 13% .
1	B	438	 82% 14% .
1	C	438	 82% 15% .
1	D	438	 81% 14% .

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 14564 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 L-rhamnose isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	421	3260	2048	585	618	9	0	0	0
1	B	421	3260	2048	585	618	9	0	0	0
1	C	428	3301	2073	592	627	9	0	0	0
1	D	419	3251	2042	583	617	9	0	0	0

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	150	ASN	ASP	engineered mutation	UNP Q75WH8
A	327	ASN	ASP	engineered mutation	UNP Q75WH8
A	431	GLY	-	expression tag	UNP Q75WH8
A	432	SER	-	expression tag	UNP Q75WH8
A	433	HIS	-	expression tag	UNP Q75WH8
A	434	HIS	-	expression tag	UNP Q75WH8
A	435	HIS	-	expression tag	UNP Q75WH8
A	436	HIS	-	expression tag	UNP Q75WH8
A	437	HIS	-	expression tag	UNP Q75WH8
A	438	HIS	-	expression tag	UNP Q75WH8
B	150	ASN	ASP	engineered mutation	UNP Q75WH8
B	327	ASN	ASP	engineered mutation	UNP Q75WH8
B	431	GLY	-	expression tag	UNP Q75WH8
B	432	SER	-	expression tag	UNP Q75WH8
B	433	HIS	-	expression tag	UNP Q75WH8
B	434	HIS	-	expression tag	UNP Q75WH8
B	435	HIS	-	expression tag	UNP Q75WH8
B	436	HIS	-	expression tag	UNP Q75WH8
B	437	HIS	-	expression tag	UNP Q75WH8
B	438	HIS	-	expression tag	UNP Q75WH8
C	150	ASN	ASP	engineered mutation	UNP Q75WH8

Continued on next page...

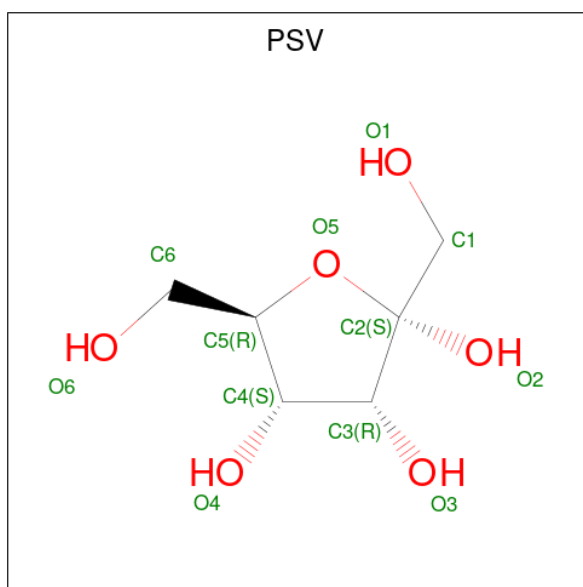
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	327	ASN	ASP	engineered mutation	UNP Q75WH8
C	431	GLY	-	expression tag	UNP Q75WH8
C	432	SER	-	expression tag	UNP Q75WH8
C	433	HIS	-	expression tag	UNP Q75WH8
C	434	HIS	-	expression tag	UNP Q75WH8
C	435	HIS	-	expression tag	UNP Q75WH8
C	436	HIS	-	expression tag	UNP Q75WH8
C	437	HIS	-	expression tag	UNP Q75WH8
C	438	HIS	-	expression tag	UNP Q75WH8
D	150	ASN	ASP	engineered mutation	UNP Q75WH8
D	327	ASN	ASP	engineered mutation	UNP Q75WH8
D	431	GLY	-	expression tag	UNP Q75WH8
D	432	SER	-	expression tag	UNP Q75WH8
D	433	HIS	-	expression tag	UNP Q75WH8
D	434	HIS	-	expression tag	UNP Q75WH8
D	435	HIS	-	expression tag	UNP Q75WH8
D	436	HIS	-	expression tag	UNP Q75WH8
D	437	HIS	-	expression tag	UNP Q75WH8
D	438	HIS	-	expression tag	UNP Q75WH8

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Mn 2 2	0	0
2	B	2	Total Mn 2 2	0	0
2	C	2	Total Mn 2 2	0	0
2	D	2	Total Mn 2 2	0	0

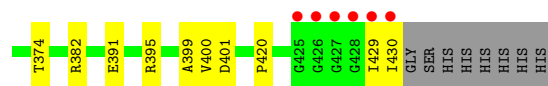
- Molecule 3 is alpha-D-psicofuranose (CCD ID: PSV) (formula: C₆H₁₂O₆).



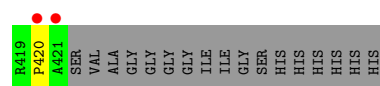
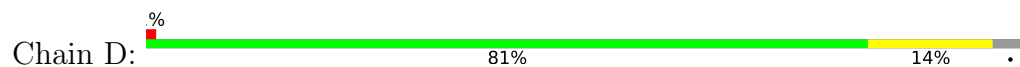
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 12 6 6	0	0
3	B	1	Total C O 12 6 6	0	0
3	C	1	Total C O 12 6 6	0	0
3	D	1	Total C O 12 6 6	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	385	Total O 385 385	0	0
4	B	345	Total O 345 345	0	0
4	C	339	Total O 339 339	0	0
4	D	367	Total O 367 367	0	0



- Molecule 1: L-rhamnose isomerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	74.76Å 104.73Å 115.03Å 90.00° 108.24° 90.00°	Depositor
Resolution (Å)	42.15 – 1.90 42.15 – 1.90	Depositor EDS
% Data completeness (in resolution range)	92.3 (42.15-1.90) 92.3 (42.15-1.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.88 (at 1.89Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.176 , 0.211 0.175 , 0.211	Depositor DCC
R_{free} test set	12186 reflections (9.97%)	wwPDB-VP
Wilson B-factor (Å ²)	12.3	Xtrriage
Anisotropy	0.029	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 44.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.025 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14564	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.85% 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: MN, PSV

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	0.35	0/3332	0.82	5/4518 (0.1%)
1	B	0.34	0/3332	0.83	5/4518 (0.1%)
1	C	0.34	0/3373	0.81	4/4572 (0.1%)
1	D	0.34	0/3323	0.83	6/4505 (0.1%)
All	All	0.34	0/13360	0.82	20/18113 (0.1%)

There are no bond length outliers.

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	401	ASP	CA-C-N	6.40	125.90	119.24
1	A	401	ASP	C-N-CA	6.40	125.90	119.24
1	B	246	GLY	CA-C-N	5.81	126.21	119.47
1	B	246	GLY	C-N-CA	5.81	126.21	119.47
1	D	255	LEU	N-CA-C	5.78	118.32	111.33

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	3260	0	3167	41	0
1	B	3260	0	3167	39	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3301	0	3207	42	0
1	D	3251	0	3154	42	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	12	0	10	0	0
3	B	12	0	10	1	0
3	C	12	0	10	0	0
3	D	12	0	9	0	0
4	A	385	0	0	5	0
4	B	345	0	0	1	0
4	C	339	0	0	1	0
4	D	367	0	0	1	0
All	All	14564	0	12734	164	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 6.

The worst 5 of 164 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:B:129:ASN:H	1:B:160:HIS:HE1	1.16	0.93
1:A:129:ASN:H	1:A:160:HIS:HE1	1.14	0.90
1:C:217:PHE:HB3	1:C:252:LEU:HG	1.61	0.82
1:A:129:ASN:H	1:A:160:HIS:CE1	1.98	0.82
1:C:129:ASN:H	1:C:160:HIS:HE1	1.25	0.81

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	419/438 (96%)	408 (97%)	10 (2%)	1 (0%)	43	36
1	B	419/438 (96%)	406 (97%)	12 (3%)	1 (0%)	43	36
1	C	426/438 (97%)	415 (97%)	9 (2%)	2 (0%)	24	16
1	D	417/438 (95%)	405 (97%)	11 (3%)	1 (0%)	43	36
All	All	1681/1752 (96%)	1634 (97%)	42 (2%)	5 (0%)	36	29

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	317	VAL
1	A	224	GLU
1	B	224	GLU
1	C	224	GLU
1	D	224	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	330/341 (97%)	327 (99%)	3 (1%)	70	73
1	B	330/341 (97%)	326 (99%)	4 (1%)	63	63
1	C	333/341 (98%)	331 (99%)	2 (1%)	78	81
1	D	329/341 (96%)	327 (99%)	2 (1%)	78	81
All	All	1322/1364 (97%)	1311 (99%)	11 (1%)	73	75

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	371	LEU
1	C	374	THR
1	D	374	THR
1	D	371	LEU
1	B	110	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	258	HIS
1	D	328	GLN
1	B	281	HIS
1	B	258	HIS
1	D	344	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 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 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	$\# Z > 2$
3	PSV	B	602	2	11,12,12	0.41	0	10,18,18	0.63	0
3	PSV	D	604	2	11,12,12	0.38	0	10,18,18	0.56	0
3	PSV	A	601	2	11,12,12	0.31	0	10,18,18	0.51	0
3	PSV	C	603	2	11,12,12	0.38	0	10,18,18	0.61	0

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	PSV	B	602	2	-	3/5/24/24	0/1/1/1
3	PSV	D	604	2	-	3/5/24/24	0/1/1/1
3	PSV	A	601	2	-	3/5/24/24	0/1/1/1
3	PSV	C	603	2	-	3/5/24/24	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	603	PSV	O5-C5-C6-O6
3	B	602	PSV	C4-C5-C6-O6
3	C	603	PSV	C4-C5-C6-O6
3	B	602	PSV	O5-C5-C6-O6
3	D	604	PSV	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	602	PSV	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	421/438 (96%)	-0.35	4 (0%) 79 82	5, 11, 23, 35	0
1	B	421/438 (96%)	-0.13	11 (2%) 57 61	6, 13, 27, 46	0
1	C	428/438 (97%)	0.05	18 (4%) 40 43	6, 15, 33, 57	0
1	D	419/438 (95%)	-0.25	5 (1%) 76 79	6, 12, 25, 48	0
All	All	1689/1752 (96%)	-0.17	38 (2%) 62 66	5, 13, 28, 57	0

The worst 5 of 38 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	427	GLY	6.8
1	C	319	GLY	5.5
1	B	316	GLY	4.9
1	C	317	VAL	4.6
1	C	316	GLY	4.6

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [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. 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(\AA^2)	Q<0.9
3	PSV	B	602	12/12	0.80	0.16	26,30,33,37	0
3	PSV	C	603	12/12	0.83	0.15	26,31,34,38	0
3	PSV	D	604	12/12	0.90	0.10	15,21,27,30	0
3	PSV	A	601	12/12	0.91	0.10	12,19,25,29	0
2	MN	B	504	1/1	0.98	0.06	22,22,22,22	0
2	MN	B	503	1/1	0.99	0.06	25,25,25,25	0
2	MN	A	501	1/1	0.99	0.05	13,13,13,13	0
2	MN	C	505	1/1	0.99	0.06	21,21,21,21	0
2	MN	D	508	1/1	0.99	0.04	14,14,14,14	0
2	MN	D	507	1/1	1.00	0.02	13,13,13,13	0
2	MN	A	502	1/1	1.00	0.02	13,13,13,13	0
2	MN	C	506	1/1	1.00	0.03	18,18,18,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.