



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 31, 2021 – 03:23 PM EDT

PDB ID : 3M0Y
Title : Crystal structure of Pseudomonas stutzeri L-rhamnose isomerase mutant S329A in complex with L-rhamnose
Authors : Yoshida, H.; Takeda, K.; Izumori, K.; Kamitori, S.
Deposited on : 2010-03-03
Resolution : 1.96 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

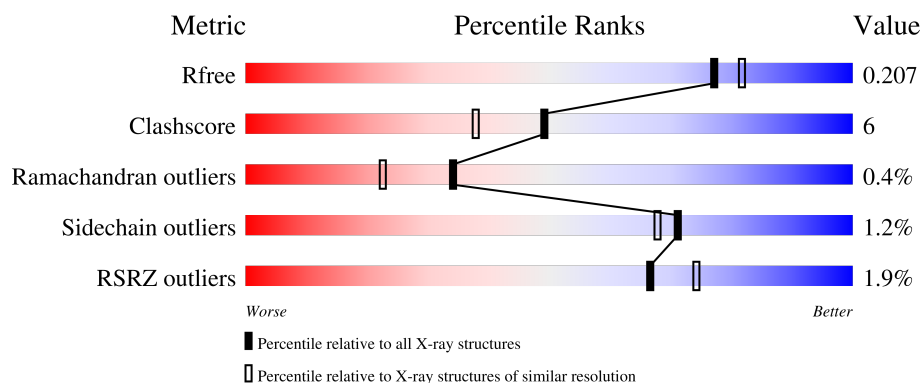
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.96 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}	130704	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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	<div> <div></div> <div>84%</div> <div>12%</div> <div>.</div> </div>
1	B	438	<div> <div>2%</div> <div>83%</div> <div>13%</div> <div>.</div> </div>
1	C	438	<div> <div>3%</div> <div>82%</div> <div>15%</div> <div>.</div> </div>
1	D	438	<div> <div></div> <div>82%</div> <div>13%</div> <div>.</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14508 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
1	A	421	Total	C	N	O	S	0	0	0
			3259	2048	584	618	9			
1	B	421	Total	C	N	O	S	0	0	0
			3259	2048	584	618	9			
1	C	428	Total	C	N	O	S	0	0	0
			3300	2073	591	627	9			
1	D	419	Total	C	N	O	S	0	0	0
			3250	2042	582	617	9			

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	329	ALA	SER	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	329	ALA	SER	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

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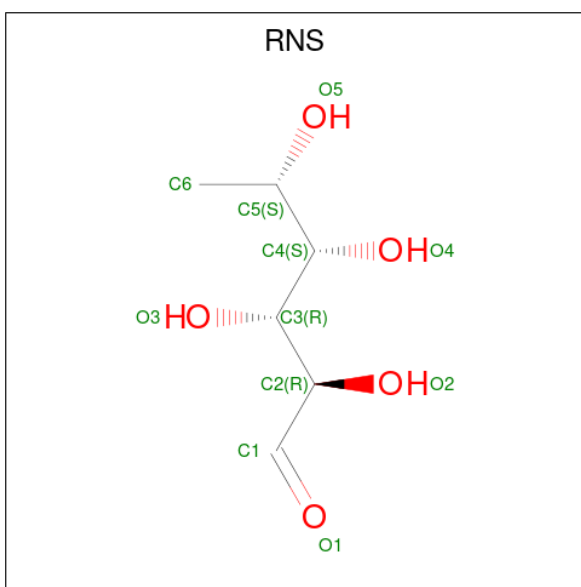
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Chain	Residue	Modelled	Actual	Comment	Reference
C	329	ALA	SER	engineered mutation	UNP Q75WH8
C	431	GLY	-	expression tag	UNP Q75WH8
C	432	SER	-	expression tag	UNP Q75WH8
C	433	HIS	-	expression tag	UNP Q75WH8
C	434	HIS	-	expression tag	UNP Q75WH8
C	435	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	329	ALA	SER	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 (three-letter code: 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 L-RHAMNOSE (three-letter code: RNS) (formula: C₆H₁₂O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			11	6	5		
3	B	1	Total	C	O	0	0
			11	6	5		
3	C	1	Total	C	O	0	0
			11	6	5		
3	D	1	Total	C	O	0	0
			11	6	5		

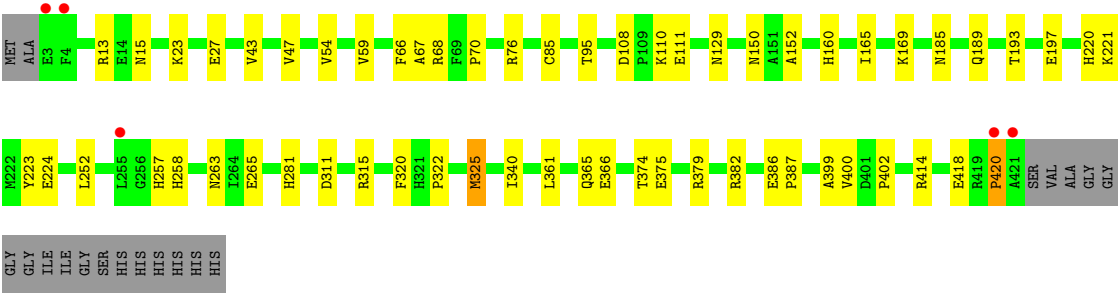
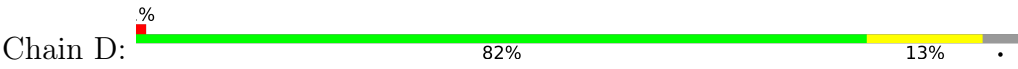
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	382	Total	O	0	0
			382	382		
4	B	348	Total	O	0	0
			348	348		
4	C	310	Total	O	0	0
			310	310		
4	D	348	Total	O	0	0
			348	348		

- Molecule 1: L-rhamnose isomerase



● 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	74.72Å 104.94Å 114.99Å 90.00° 108.06° 90.00°	Depositor
Resolution (Å)	42.21 – 1.96 42.21 – 1.96	Depositor EDS
% Data completeness (in resolution range)	91.1 (42.21-1.96) 91.2 (42.21-1.96)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.76 (at 1.97Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.183 , 0.216 0.175 , 0.207	Depositor DCC
R_{free} test set	11025 reflections (9.41%)	wwPDB-VP
Wilson B-factor (Å ²)	19.0	Xtriage
Anisotropy	0.286	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 50.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.019 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14508	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.81% 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: RNS, 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	0.32	0/3331	0.54	0/4517
1	B	0.31	0/3331	0.54	0/4517
1	C	0.30	0/3372	0.52	0/4571
1	D	0.31	0/3322	0.53	0/4504
All	All	0.31	0/13356	0.53	0/18109

There are no bond length outliers.

There are no bond angle outliers.

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	3259	0	3165	35	0
1	B	3259	0	3165	35	0
1	C	3300	0	3205	43	0
1	D	3250	0	3152	39	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	11	0	11	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	11	0	11	0	0
3	C	11	0	11	0	0
3	D	11	0	11	0	0
4	A	382	0	0	3	0
4	B	348	0	0	2	0
4	C	310	0	0	1	0
4	D	348	0	0	2	0
All	All	14508	0	12731	152	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 152 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:129:ASN:H	1:A:160:HIS:HE1	1.12	0.91
1:B:129:ASN:H	1:B:160:HIS:HE1	1.21	0.85
1:A:129:ASN:H	1:A:160:HIS:CE1	1.98	0.82
1:B:129:ASN:H	1:B:160:HIS:CE1	2.04	0.76
1:D:129:ASN:H	1:D:160:HIS:HE1	1.33	0.75

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%)	407 (97%)	11 (3%)	1 (0%)	47 38
1	B	419/438 (96%)	408 (97%)	10 (2%)	1 (0%)	47 38
1	C	426/438 (97%)	413 (97%)	10 (2%)	3 (1%)	22 11
1	D	417/438 (95%)	404 (97%)	11 (3%)	2 (0%)	29 17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1681/1752 (96%)	1632 (97%)	42 (2%)	7 (0%)	34 22

5 of 7 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 ⓘ

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	329/340 (97%)	325 (99%)	4 (1%)	71 68
1	B	329/340 (97%)	322 (98%)	7 (2%)	53 46
1	C	332/340 (98%)	329 (99%)	3 (1%)	78 77
1	D	328/340 (96%)	326 (99%)	2 (1%)	86 85
All	All	1318/1360 (97%)	1302 (99%)	16 (1%)	71 68

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	325	MET
1	C	374	THR
1	B	354	LEU
1	C	371	LEU
1	B	325	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	160	HIS
1	C	344	ASN
1	C	258	HIS
1	C	368	ASN
1	B	8	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 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	RNS	D	2004	2	8,10,10	0.50	0	9,13,13	0.80	0
3	RNS	B	2002	2	8,10,10	0.51	0	9,13,13	0.93	1 (11%)
3	RNS	C	2003	2	8,10,10	0.44	0	9,13,13	0.95	1 (11%)
3	RNS	A	2001	2	8,10,10	0.48	0	9,13,13	0.83	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	RNS	D	2004	2	-	0/12/14/14	-
3	RNS	B	2002	2	-	0/12/14/14	-
3	RNS	C	2003	2	-	0/12/14/14	-
3	RNS	A	2001	2	-	0/12/14/14	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	C	2003	RNS	C3-C4-C5	-2.56	109.65	113.19
3	B	2002	RNS	C3-C4-C5	-2.31	109.99	113.19

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 [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%)	-0.33	3 (0%) 87 92	11, 18, 30, 47	0
1	B	421/438 (96%)	-0.10	9 (2%) 63 72	12, 20, 36, 52	0
1	C	428/438 (97%)	0.12	15 (3%) 44 53	13, 24, 43, 66	0
1	D	419/438 (95%)	-0.12	5 (1%) 79 84	12, 19, 32, 53	0
All	All	1689/1752 (96%)	-0.11	32 (1%) 66 74	11, 20, 36, 66	0

The worst 5 of 32 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	319	GLY	10.4
1	C	427	GLY	6.1
1	B	314	ALA	5.5
1	B	423	VAL	5.0
1	B	4	PHE	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 monosaccharides 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	RNS	B	2002	11/11	0.91	0.12	19,23,27,28	0
3	RNS	A	2001	11/11	0.93	0.12	18,20,25,25	0
3	RNS	D	2004	11/11	0.93	0.13	19,23,29,30	0
3	RNS	C	2003	11/11	0.94	0.10	26,28,32,32	0
2	MN	B	503	1/1	0.98	0.05	23,23,23,23	0
2	MN	C	506	1/1	0.99	0.05	23,23,23,23	0
2	MN	D	507	1/1	0.99	0.07	19,19,19,19	0
2	MN	D	508	1/1	0.99	0.04	20,20,20,20	0
2	MN	A	502	1/1	0.99	0.05	20,20,20,20	0
2	MN	A	501	1/1	0.99	0.05	18,18,18,18	0
2	MN	B	504	1/1	0.99	0.04	23,23,23,23	0
2	MN	C	505	1/1	0.99	0.06	22,22,22,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.