



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 12, 2024 – 08:05 PM EDT

PDB ID : 3CYJ
Title : Crystal structure of a mandelate racemase/muconate lactonizing enzyme-like protein from *Rubrobacter xylanophilus*
Authors : Bonanno, J.B.; Freeman, J.; Bain, K.T.; Zhang, F.; Bravo, J.; Smith, D.; Wasserman, S.; Sauder, J.M.; Burley, S.K.; Almo, S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2008-04-25
Resolution : 2.30 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
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)	:	2.36.2

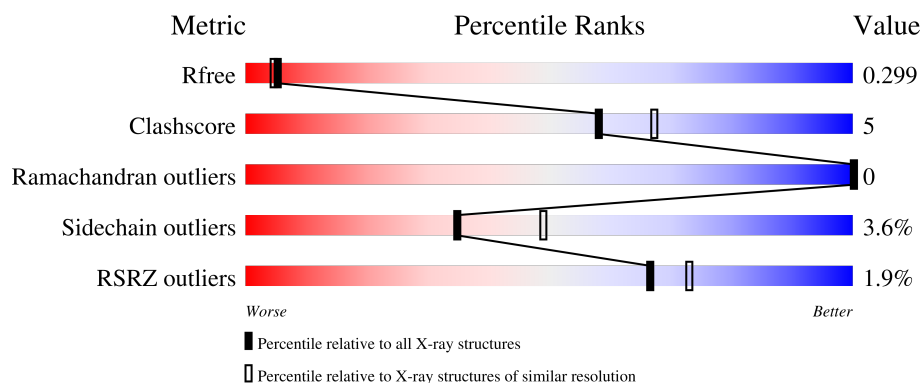
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	372	<div> <div>5%</div> <div>84%</div> <div>11%</div> <div>..</div> </div>
1	B	372	<div> <div>83%</div> <div>11%</div> <div>..</div> </div>
1	C	372	<div> <div>5%</div> <div>87%</div> <div>9%</div> <div>.</div> </div>
1	D	372	<div> <div>84%</div> <div>12%</div> <div>...</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11364 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 Mandelate racemase/muconate lactonizing enzyme-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	359	Total	C	N	O	S	0	2	0
			2704	1703	487	503	11			
1	B	359	Total	C	N	O	S	0	3	0
			2725	1711	498	505	11			
1	C	359	Total	C	N	O	S	0	2	0
			2704	1703	487	503	11			
1	D	359	Total	C	N	O	S	0	1	0
			2705	1698	491	505	11			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	expression tag	UNP Q1ASJ4
A	0	SER	-	expression tag	UNP Q1ASJ4
A	1	LEU	-	expression tag	UNP Q1ASJ4
A	363	GLU	-	expression tag	UNP Q1ASJ4
A	364	GLY	-	expression tag	UNP Q1ASJ4
A	365	HIS	-	expression tag	UNP Q1ASJ4
A	366	HIS	-	expression tag	UNP Q1ASJ4
A	367	HIS	-	expression tag	UNP Q1ASJ4
A	368	HIS	-	expression tag	UNP Q1ASJ4
A	369	HIS	-	expression tag	UNP Q1ASJ4
A	370	HIS	-	expression tag	UNP Q1ASJ4
B	-1	MET	-	expression tag	UNP Q1ASJ4
B	0	SER	-	expression tag	UNP Q1ASJ4
B	1	LEU	-	expression tag	UNP Q1ASJ4
B	363	GLU	-	expression tag	UNP Q1ASJ4
B	364	GLY	-	expression tag	UNP Q1ASJ4
B	365	HIS	-	expression tag	UNP Q1ASJ4
B	366	HIS	-	expression tag	UNP Q1ASJ4
B	367	HIS	-	expression tag	UNP Q1ASJ4
B	368	HIS	-	expression tag	UNP Q1ASJ4
B	369	HIS	-	expression tag	UNP Q1ASJ4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	370	HIS	-	expression tag	UNP Q1ASJ4
C	-1	MET	-	expression tag	UNP Q1ASJ4
C	0	SER	-	expression tag	UNP Q1ASJ4
C	1	LEU	-	expression tag	UNP Q1ASJ4
C	363	GLU	-	expression tag	UNP Q1ASJ4
C	364	GLY	-	expression tag	UNP Q1ASJ4
C	365	HIS	-	expression tag	UNP Q1ASJ4
C	366	HIS	-	expression tag	UNP Q1ASJ4
C	367	HIS	-	expression tag	UNP Q1ASJ4
C	368	HIS	-	expression tag	UNP Q1ASJ4
C	369	HIS	-	expression tag	UNP Q1ASJ4
C	370	HIS	-	expression tag	UNP Q1ASJ4
D	-1	MET	-	expression tag	UNP Q1ASJ4
D	0	SER	-	expression tag	UNP Q1ASJ4
D	1	LEU	-	expression tag	UNP Q1ASJ4
D	363	GLU	-	expression tag	UNP Q1ASJ4
D	364	GLY	-	expression tag	UNP Q1ASJ4
D	365	HIS	-	expression tag	UNP Q1ASJ4
D	366	HIS	-	expression tag	UNP Q1ASJ4
D	367	HIS	-	expression tag	UNP Q1ASJ4
D	368	HIS	-	expression tag	UNP Q1ASJ4
D	369	HIS	-	expression tag	UNP Q1ASJ4
D	370	HIS	-	expression tag	UNP Q1ASJ4

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Na 1 1	0	0
2	C	1	Total Na 1 1	0	0

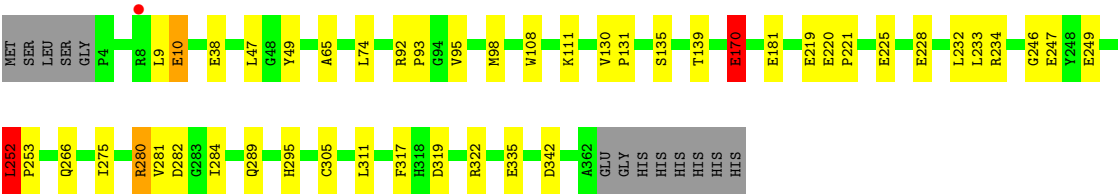
- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	113	Total	O	0	0
			113	113		
4	B	137	Total	O	0	0
			137	137		
4	C	112	Total	O	0	0
			112	112		
4	D	150	Total	O	0	0
			150	150		



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	193.10Å 193.10Å 113.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.30 48.28 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.2 (20.00-2.30) 98.2 (48.28-2.30)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	0.16	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.55 (at 2.29Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.243 , 0.292 0.252 , 0.299	Depositor DCC
R_{free} test set	4688 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	28.2	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 45.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.57$, $\langle L^2 \rangle = 0.42$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11364	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 69.77 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.4988e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: GOL, 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	0.90	2/2773 (0.1%)	0.83	2/3769 (0.1%)
1	B	0.97	3/2795 (0.1%)	0.88	5/3793 (0.1%)
1	C	0.90	2/2773 (0.1%)	0.82	0/3769
1	D	0.99	3/2769 (0.1%)	0.89	4/3761 (0.1%)
All	All	0.94	10/11110 (0.1%)	0.85	11/15092 (0.1%)

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	B	0	1

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	250[A]	TRP	CB-CG	8.02	1.64	1.50
1	C	250[B]	TRP	CB-CG	8.02	1.64	1.50
1	A	250[A]	TRP	CB-CG	6.94	1.62	1.50
1	A	250[B]	TRP	CB-CG	6.94	1.62	1.50
1	B	220	GLU	CG-CD	6.33	1.61	1.51

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	177	ARG	NE-CZ-NH1	-6.49	117.06	120.30
1	B	280	ARG	NE-CZ-NH1	6.27	123.44	120.30
1	D	252	LEU	CB-CG-CD2	-5.93	100.92	111.00
1	D	342	ASP	CB-CG-OD1	5.87	123.58	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	280	ARG	NE-CZ-NH2	-5.54	117.53	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	224	SER	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	2704	0	2648	32	0
1	B	2725	0	2690	27	0
1	C	2704	0	2648	27	0
1	D	2705	0	2653	24	1
2	A	1	0	0	0	0
2	C	1	0	0	0	0
3	A	6	0	8	0	0
3	C	6	0	8	0	0
4	A	113	0	0	1	1
4	B	137	0	0	2	0
4	C	112	0	0	0	0
4	D	150	0	0	1	0
All	All	11364	0	10655	104	1

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 5.

The worst 5 of 104 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:47:LEU:C	1:A:47:LEU:HD23	1.81	1.01
1:C:93:PRO:HB3	1:C:250[B]:TRP:CD2	2.02	0.94
1:D:282:ASP:HB2	4:D:497:HOH:O	1.78	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:40:HIS:CE1	1:C:45:LYS:HD3	2.14	0.82
1:D:252:LEU:HD23	1:D:284:ILE:HD11	1.60	0.82

All (1) 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:D:289:GLN:OE1	4:A:442:HOH:O[7_556]	2.16	0.04

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	359/372 (96%)	350 (98%)	9 (2%)	0	100	100
1	B	360/372 (97%)	353 (98%)	7 (2%)	0	100	100
1	C	359/372 (96%)	352 (98%)	7 (2%)	0	100	100
1	D	358/372 (96%)	351 (98%)	7 (2%)	0	100	100
All	All	1436/1488 (96%)	1406 (98%)	30 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	267/282 (95%)	254 (95%)	13 (5%)	25	35
1	B	271/282 (96%)	262 (97%)	9 (3%)	38	53
1	C	267/282 (95%)	259 (97%)	8 (3%)	41	57
1	D	268/282 (95%)	257 (96%)	11 (4%)	30	43
All	All	1073/1128 (95%)	1032 (96%)	41 (4%)	35	47

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	314	LEU
1	D	232	LEU
1	C	355	SER
1	D	170	GLU
1	D	252	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	303	HIS
1	C	266	GLN
1	D	303	HIS
1	D	40	HIS
1	B	295	HIS

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

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	GOL	A	372	-	5,5,5	0.44	0	5,5,5	1.19	1 (20%)
3	GOL	C	372	-	5,5,5	0.28	0	5,5,5	0.71	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	GOL	A	372	-	-	3/4/4/4	-
3	GOL	C	372	-	-	0/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	372	GOL	O2-C2-C1	2.18	118.21	109.18

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	372	GOL	O1-C1-C2-C3
3	A	372	GOL	O1-C1-C2-O2
3	A	372	GOL	O2-C2-C3-O3

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	359/372 (96%)	0.14	4 (1%) 80 85	35, 45, 57, 70	0
1	B	359/372 (96%)	-0.19	2 (0%) 89 92	31, 39, 53, 65	0
1	C	359/372 (96%)	0.28	20 (5%) 24 30	36, 45, 60, 71	0
1	D	359/372 (96%)	-0.21	1 (0%) 94 96	29, 39, 52, 61	0
All	All	1436/1488 (96%)	0.01	27 (1%) 66 73	29, 42, 56, 71	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	250[A]	TRP	8.0
1	A	250[A]	TRP	8.0
1	C	355	SER	5.7
1	A	355	SER	5.0
1	C	356	GLU	3.7

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	GOL	A	372	6/6	0.87	0.17	50,54,58,60	0
2	NA	C	371	1/1	0.89	0.16	58,58,58,58	0
3	GOL	C	372	6/6	0.90	0.18	53,57,60,66	0
2	NA	A	371	1/1	0.91	0.16	55,55,55,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.