



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 13, 2023 – 11:40 AM JST

PDB ID : 5X2Y
Title : Crystal structure of Pseudomonas putida methionine gamma-lyase C116H mutant without sulfate ion
Authors : Shiba, T.; Sato, D.; Harada, S.
Deposited on : 2017-02-02
Resolution : 1.79 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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

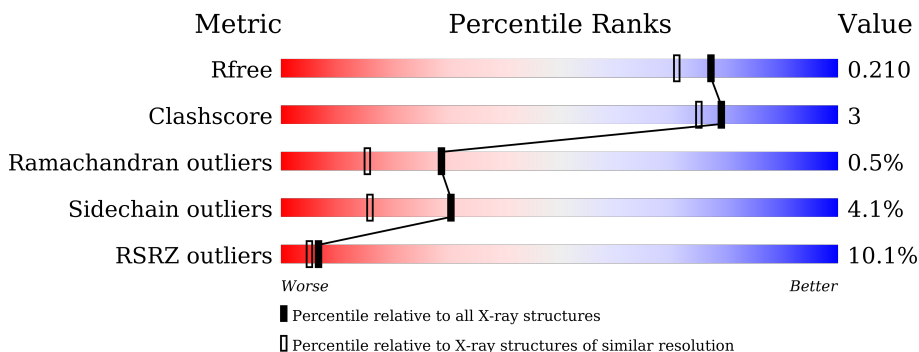
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.79 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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	398	 10% 87% 10% ...
1	B	398	 11% 88% 10% .
1	C	398	 8% 87% 8% .
1	D	398	 11% 88% 8% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12462 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-methionine gamma-lyase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	392	2970	1874	525	554	1	16	0	0	0
1	B	392	2966	1872	525	552	1	16	0	0	0
1	C	382	2884	1820	510	537	1	16	0	0	0
1	D	390	2946	1858	520	551	1	16	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	116	HIS	CYS	engineered mutation	UNP P13254
B	116	HIS	CYS	engineered mutation	UNP P13254
C	116	HIS	CYS	engineered mutation	UNP P13254
D	116	HIS	CYS	engineered mutation	UNP P13254

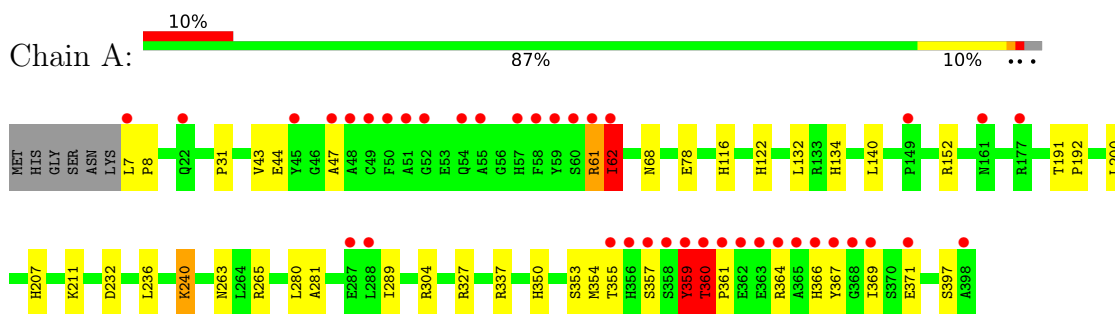
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	129	Total 129	O 129	0	0
2	B	196	Total 196	O 196	0	0
2	C	176	Total 176	O 176	0	0
2	D	195	Total 195	O 195	0	0

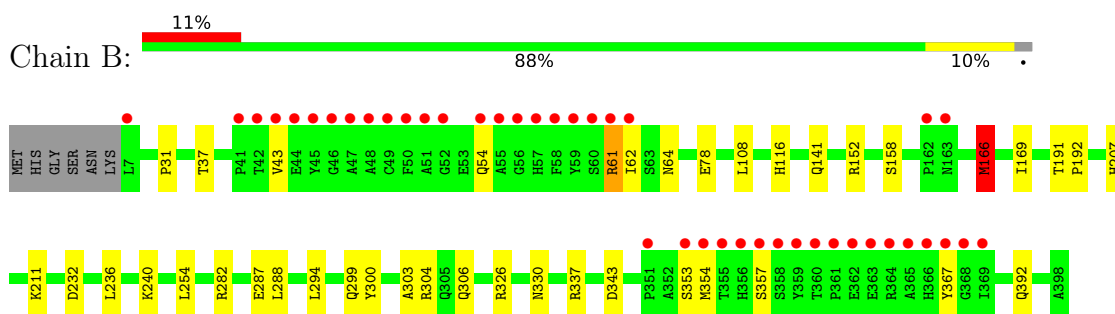
3 Residue-property plots [i](#)

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.

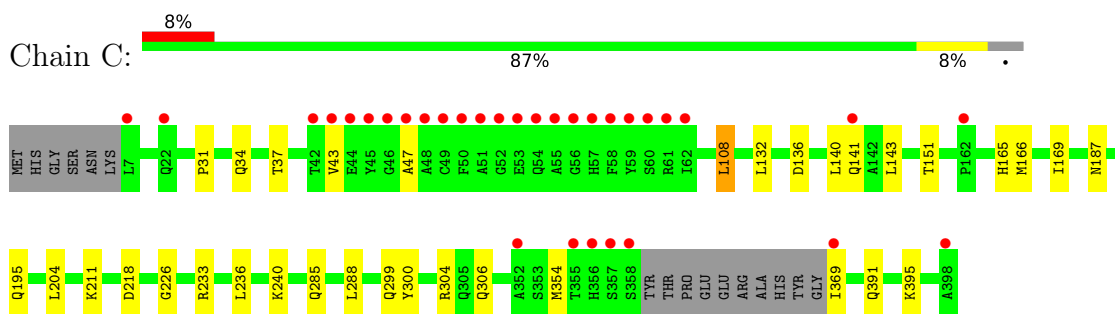
- Molecule 1: L-methionine gamma-lyase



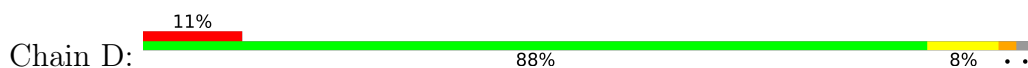
- Molecule 1: L-methionine gamma-lyase

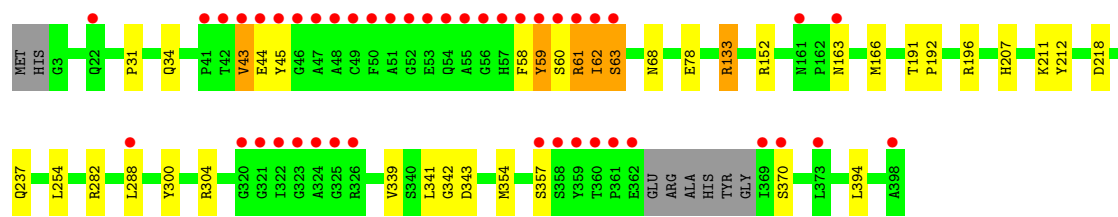


- Molecule 1: L-methionine gamma-lyase



- Molecule 1: L-methionine gamma-lyase





4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	154.79Å 153.38Å 80.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.79 20.00 – 1.79	Depositor EDS
% Data completeness (in resolution range)	97.0 (20.00-1.79) 97.1 (20.00-1.79)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.40 (at 1.79Å)	Xtrriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.173 , 0.204 0.183 , 0.210	Depositor DCC
R_{free} test set	8763 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	18.4	Xtrriage
Anisotropy	0.051	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 45.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.011 for k,h,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12462	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.78% 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: LLP

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	0.59	0/3010	0.78	3/4086 (0.1%)
1	B	0.65	0/3006	0.81	6/4081 (0.1%)
1	C	0.61	0/2919	0.79	1/3960 (0.0%)
1	D	0.64	0/2983	0.81	5/4047 (0.1%)
All	All	0.62	0/11918	0.80	15/16174 (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	A	0	3
1	B	0	2
1	D	0	1
All	All	0	6

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	282	ARG	NE-CZ-NH2	7.61	124.10	120.30
1	B	232	ASP	CB-CG-OD1	6.26	123.93	118.30
1	B	282	ARG	NE-CZ-NH2	6.21	123.40	120.30
1	B	343	ASP	CB-CG-OD1	6.02	123.72	118.30
1	D	152	ARG	NE-CZ-NH1	5.62	123.11	120.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	359	TYR	Peptide
1	A	360	THR	Peptide
1	A	62	ILE	Peptide
1	B	367	TYR	Peptide
1	B	61	ARG	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	2970	0	2926	29	0
1	B	2966	0	2922	20	0
1	C	2884	0	2853	17	0
1	D	2946	0	2909	18	0
2	A	129	0	0	0	0
2	B	196	0	0	0	0
2	C	176	0	0	0	0
2	D	195	0	0	2	0
All	All	12462	0	11610	66	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.

The worst 5 of 66 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:D:63:SER:HB3	1:D:68:ASN:HD21	1.43	0.82
1:B:166:MET:H	1:B:299:GLN:HE22	1.33	0.75
1:C:169:ILE:H	1:C:306:GLN:HE22	1.41	0.69
1:C:166:MET:H	1:C:299:GLN:HE22	1.41	0.68
1:D:60:SER:O	1:D:63:SER:HB2	1.99	0.62

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	389/398 (98%)	379 (97%)	6 (2%)	4 (1%)	15 5
1	B	389/398 (98%)	378 (97%)	9 (2%)	2 (0%)	29 15
1	C	377/398 (95%)	368 (98%)	9 (2%)	0	100 100
1	D	385/398 (97%)	374 (97%)	10 (3%)	1 (0%)	41 27
All	All	1540/1592 (97%)	1499 (97%)	34 (2%)	7 (0%)	29 15

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	62	ILE
1	B	62	ILE
1	A	367	TYR
1	A	61	ARG
1	D	45	TYR

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	301/306 (98%)	288 (96%)	13 (4%)	29 14
1	B	300/306 (98%)	287 (96%)	13 (4%)	29 14
1	C	293/306 (96%)	284 (97%)	9 (3%)	40 25
1	D	300/306 (98%)	286 (95%)	14 (5%)	26 12
All	All	1194/1224 (98%)	1145 (96%)	49 (4%)	30 16

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	140	LEU
1	D	43	VAL
1	C	141	GLN
1	C	288	LEU
1	D	59	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	299	GLN
1	D	187	ASN
1	C	305	GLN
1	D	22	GLN
1	D	207	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](#)

4 non-standard protein/DNA/RNA residues 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
1	LLP	B	211	1	23,24,25	2.83	5 (21%)	25,32,34	1.61	6 (24%)
1	LLP	C	211	1	23,24,25	2.37	5 (21%)	25,32,34	1.45	6 (24%)
1	LLP	D	211	1	23,24,25	2.64	5 (21%)	25,32,34	1.49	6 (24%)
1	LLP	A	211	1	23,24,25	2.46	5 (21%)	25,32,34	1.45	4 (16%)

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
1	LLP	B	211	1	-	6/16/17/19	0/1/1/1
1	LLP	C	211	1	-	5/16/17/19	0/1/1/1
1	LLP	D	211	1	-	6/16/17/19	0/1/1/1
1	LLP	A	211	1	-	4/16/17/19	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	211	LLP	C3-C2	7.85	1.48	1.40
1	D	211	LLP	C3-C2	7.01	1.47	1.40
1	B	211	LLP	C4'-NZ	6.26	1.48	1.27
1	A	211	LLP	C3-C2	6.15	1.47	1.40
1	B	211	LLP	C4-C5	6.11	1.49	1.42

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	211	LLP	C4-C3-C2	-3.41	118.08	120.19
1	A	211	LLP	OP3-P-OP4	-3.12	98.42	106.73
1	D	211	LLP	C3-C4-C5	-2.84	116.08	118.26
1	B	211	LLP	O3-C3-C2	2.79	123.58	117.49
1	A	211	LLP	C6-N1-C2	2.67	124.12	119.17

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	211	LLP	O-C-CA-CB
1	B	211	LLP	O-C-CA-CB
1	C	211	LLP	O-C-CA-CB
1	D	211	LLP	O-C-CA-CB
1	B	211	LLP	C4-C4'-NZ-CE

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	391/398 (98%)	0.62	39 (9%) 7 5	12, 25, 73, 128	0
1	B	391/398 (98%)	0.33	42 (10%) 6 4	10, 18, 79, 98	0
1	C	381/398 (95%)	0.32	32 (8%) 11 8	10, 20, 70, 114	0
1	D	389/398 (97%)	0.47	44 (11%) 5 3	10, 18, 79, 119	0
All	All	1552/1592 (97%)	0.44	157 (10%) 7 5	10, 20, 77, 128	0

The worst 5 of 157 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	367	TYR	21.0
1	C	59	TYR	12.6
1	A	365	ALA	12.4
1	D	59	TYR	12.2
1	C	55	ALA	10.6

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
1	LLP	D	211	24/25	0.96	0.09	10,19,23,24	0
1	LLP	B	211	24/25	0.97	0.09	11,19,24,27	0
1	LLP	C	211	24/25	0.97	0.07	12,16,21,22	0
1	LLP	A	211	24/25	0.97	0.07	13,20,22,24	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.