



wwPDB X-ray Structure Validation Summary Report i

Feb 27, 2014 – 04:49 PM GMT

PDB ID : 1GC2
Title : CRYSTAL STRUCTURE OF THE PYRIDOXAL-5'-PHOSPHATEDEPENDENT L-METHIONINE GAMMA-LYASE FROM PSEUDOMONAS PUTIDA
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Deposited on : 2000-07-06
Resolution : 2.00 Å(reported)

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We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

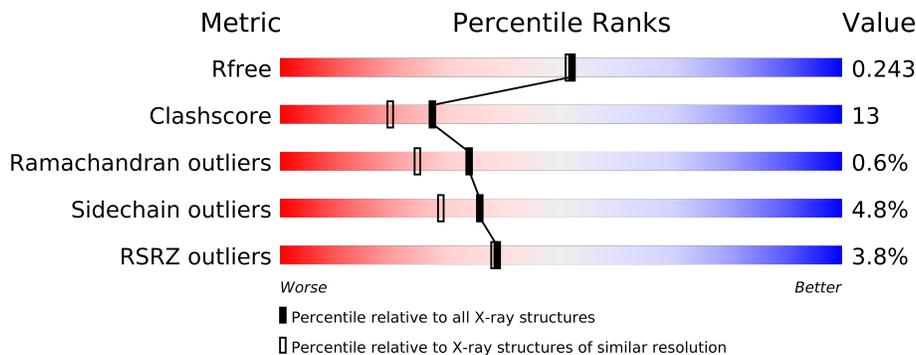
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.00 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}	66092	4888 (2.00-2.00)
Clashscore	79885	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)
RSRZ outliers	66119	4890 (2.00-2.00)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	398	
1	B	398	
1	C	398	
1	D	398	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12444 atoms, of which 0 are hydrogen and 0 are deuterium.

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 METHIONINE GAMMA-LYASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	373	2820	1778	498	527	1	16	0	0	0
1	B	370	2799	1764	495	523	1	16	0	0	0
1	C	375	2837	1789	500	531	1	16	0	0	0
1	D	370	2799	1764	495	523	1	16	0	0	0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	274	Total	O	0	0
			274	274		
2	B	346	Total	O	0	0
			346	346		
2	C	307	Total	O	0	0
			307	307		
2	D	262	Total	O	0	0
			262	262		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

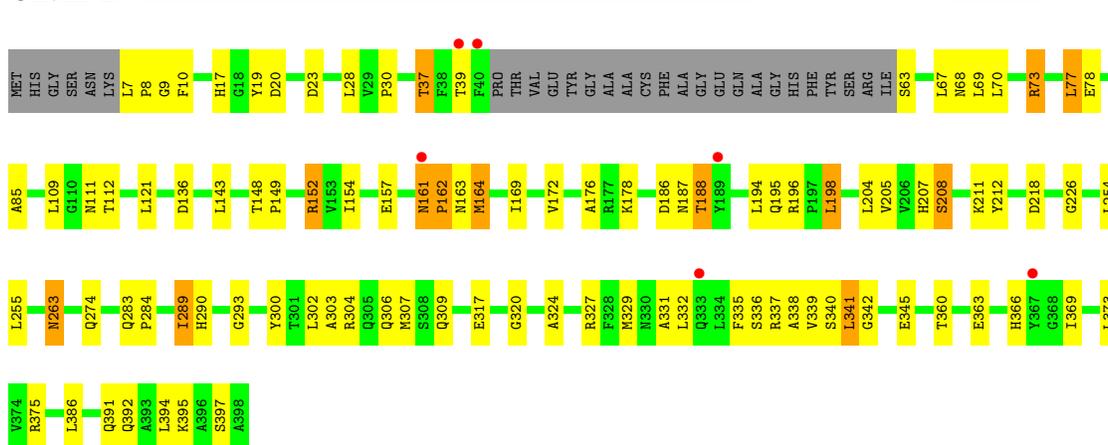
- Molecule 1: METHIONINE GAMMA-LYASE

Chain A:



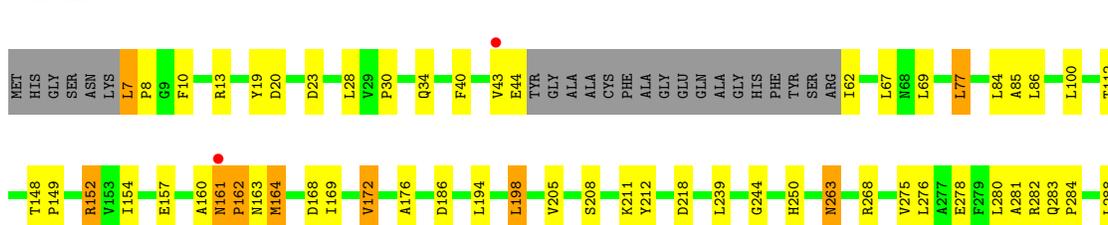
- Molecule 1: METHIONINE GAMMA-LYASE

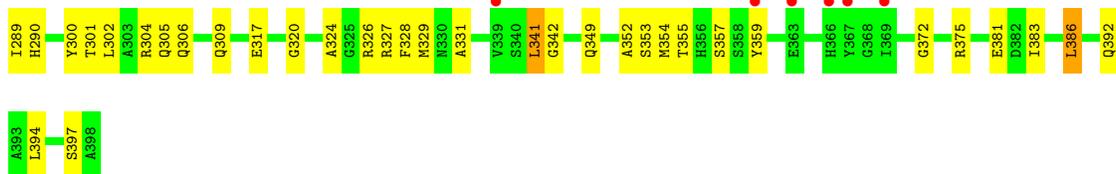
Chain B:



- Molecule 1: METHIONINE GAMMA-LYASE

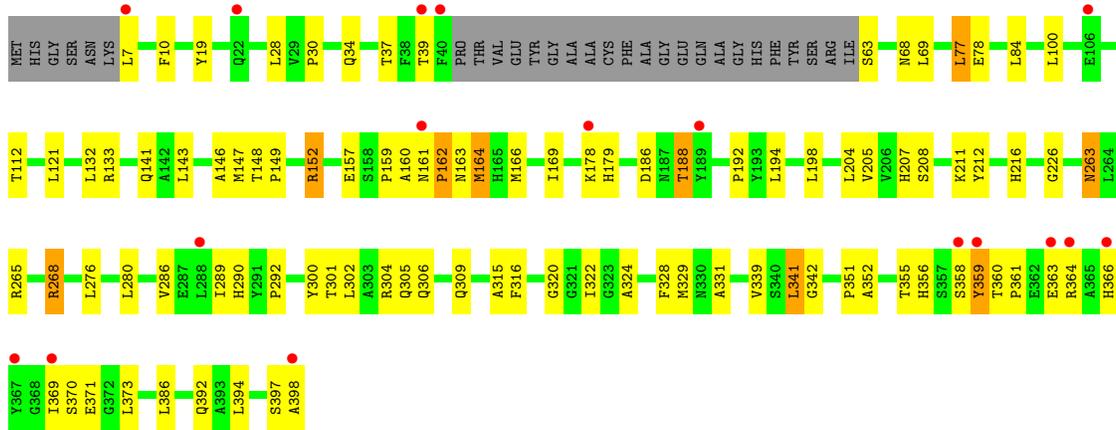
Chain C:





● Molecule 1: METHIONINE GAMMA-LYASE

Chain D:



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	133.58Å 133.58Å 213.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	83.43 – 2.00 94.45 – 2.00	Depositor EDS
% Data completeness (in resolution range)	94.9 (83.43-2.00) 95.0 (94.45-2.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.96 (at 2.00Å)	Xtrriage
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.211 , 0.243 0.212 , 0.243	Depositor DCC
R_{free} test set	12353 reflections (9.97%)	DCC
Wilson B-factor (Å ²)	29.9	Xtrriage
Anisotropy	0.388	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 50.4	EDS
Estimated twinning fraction	No twinning to report.	Xtrriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Outliers	0 of 130029 reflections	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12444	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.36% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	0.31	0/2853	0.60	1/3873 (0.0%)
1	B	0.32	0/2831	0.61	1/3841 (0.0%)
1	C	0.31	0/2870	0.61	1/3896 (0.0%)
1	D	0.31	0/2831	0.60	1/3841 (0.0%)
All	All	0.31	0/11385	0.60	4/15451 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	208	SER	N-CA-C	-5.46	96.26	111.00
1	C	208	SER	N-CA-C	-5.43	96.33	111.00
1	B	208	SER	N-CA-C	-5.35	96.56	111.00
1	A	208	SER	N-CA-C	-5.14	97.12	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2820	0	2800	66	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2799	0	2776	78	0
1	C	2837	0	2817	81	0
1	D	2799	0	2777	90	0
2	A	274	0	0	1	0
2	B	346	0	0	5	0
2	C	307	0	0	7	0
2	D	262	0	0	10	0
All	All	12444	0	11170	291	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 13.

The worst 5 of 291 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:186:ASP:OD1	1:B:188:THR:HG23	1.74	0.88
1:C:169:ILE:H	1:C:306:GLN:HE22	1.19	0.86
1:A:7:LEU:HD12	1:A:8:PRO:HD2	1.56	0.85
1:C:161:ASN:H	1:C:161:ASN:HD22	1.22	0.84
1:D:286:VAL:HG11	1:D:289:ILE:HD11	1.60	0.83

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	368/398 (92%)	353 (96%)	13 (4%)	2 (0%)	38 29
1	B	365/398 (92%)	351 (96%)	13 (4%)	1 (0%)	50 44
1	C	370/398 (93%)	357 (96%)	11 (3%)	2 (0%)	38 29
1	D	365/398 (92%)	347 (95%)	14 (4%)	4 (1%)	21 10
All	All	1468/1592 (92%)	1408 (96%)	51 (4%)	9 (1%)	33 24

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	162	PRO
1	A	361	PRO
1	B	162	PRO
1	C	359	TYR
1	D	162	PRO

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	289/306 (94%)	280 (97%)	9 (3%)	52 49
1	B	286/306 (94%)	268 (94%)	18 (6%)	25 18
1	C	291/306 (95%)	277 (95%)	14 (5%)	35 28
1	D	286/306 (94%)	272 (95%)	14 (5%)	35 28
All	All	1152/1224 (94%)	1097 (95%)	55 (5%)	35 28

5 of 55 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	345	GLU
1	C	100	LEU
1	D	268	ARG
1	B	386	LEU
1	C	7	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	306	GLN
1	C	161	ASN
1	D	274	GLN
1	B	349	GLN
1	B	391	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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	A	211	1	24,24,25	3.90	6 (25%)	30,32,34	2.33	11 (36%)
1	LLP	B	211	1	24,24,25	4.06	6 (25%)	30,32,34	2.34	12 (40%)
1	LLP	C	211	1	24,24,25	3.91	6 (25%)	30,32,34	2.32	11 (36%)
1	LLP	D	211	1	24,24,25	3.97	6 (25%)	30,32,34	2.37	12 (40%)

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	A	211	1	-	0/15/17/19	0/1/1/1
1	LLP	B	211	1	-	0/15/17/19	0/1/1/1
1	LLP	C	211	1	-	0/15/17/19	0/1/1/1
1	LLP	D	211	1	-	0/15/17/19	0/1/1/1

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	211	LLP	O-C	18.49	1.24	1.11
1	D	211	LLP	O-C	17.94	1.23	1.11
1	A	211	LLP	O-C	17.59	1.23	1.11
1	C	211	LLP	O-C	17.57	1.23	1.11
1	D	211	LLP	C3-C2	4.08	1.43	1.40

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	211	LLP	C4-C4'-NZ	5.53	121.83	111.52
1	D	211	LLP	C4-C4'-NZ	5.41	121.59	111.52
1	A	211	LLP	C4-C4'-NZ	5.08	120.97	111.52
1	C	211	LLP	C4-C4'-NZ	4.87	120.58	111.52
1	D	211	LLP	C4'-C4-C5	4.70	124.01	119.70

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	373/398 (93%)	0.27	25 (6%) 17 17	21, 33, 59, 88	0
1	B	370/398 (92%)	0.09	6 (1%) 68 69	20, 32, 46, 58	0
1	C	375/398 (94%)	0.14	8 (2%) 60 61	21, 33, 51, 79	0
1	D	370/398 (92%)	0.27	17 (4%) 31 30	23, 37, 56, 89	0
All	All	1488/1592 (93%)	0.19	56 (3%) 38 38	20, 33, 53, 89	0

The worst 5 of 56 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	161	ASN	7.5
1	A	43	VAL	7.4
1	C	43	VAL	5.7
1	A	360	THR	5.7
1	A	161	ASN	5.6

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
1	LLP	C	211	24/25	0.13	0.20	23,29,29,30	0
1	LLP	A	211	24/25	0.15	0.13	24,31,33,34	0
1	LLP	B	211	24/25	0.12	-0.00	24,30,30,32	0
1	LLP	D	211	24/25	0.12	-0.17	26,33,34,35	0

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.