



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 08:20 am BST

PDB ID : 1FGS
Title : FOLYLPOLYGLUTAMATE SYNTHETASE FROM LACTOBACILLUS CASEI
Authors : Sun, X.; Bogнар, A.; Baker, E.; Smith, C.
Deposited on : 1998-04-29
Resolution : 2.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

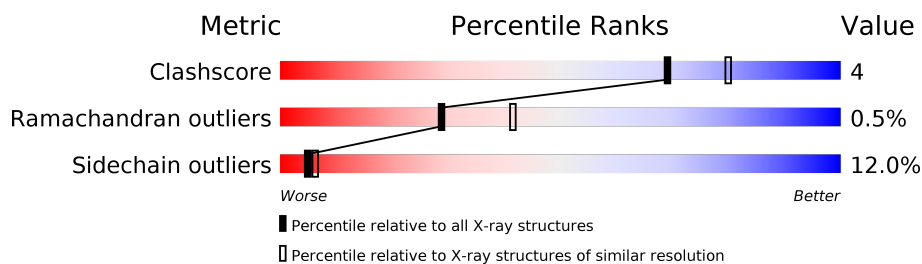
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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))
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)

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 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	428	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3167 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 FOLYLPOLYGLUTAMATE SYNTHETASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	393	Total	C	N	O	S	0	0	0
			2988	1910	524	549	5			

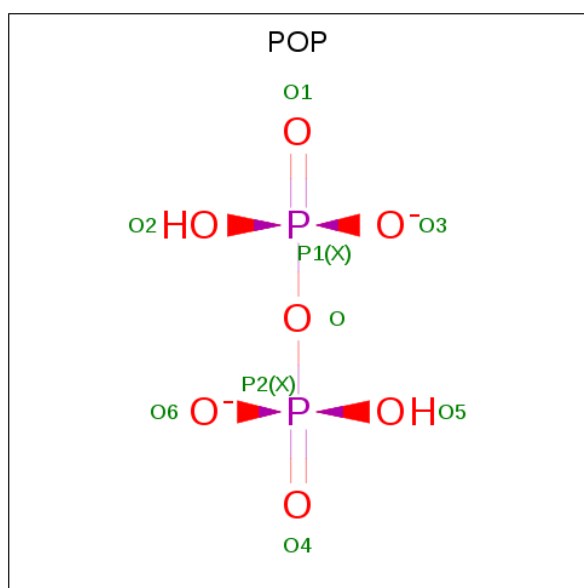
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	128	ALA	GLY	CONFLICT	UNP P15925

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is PYROPHOSPHATE 2- (three-letter code: POP) (formula: H₂O₇P₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			9	7	2		

- Molecule 4 is water.

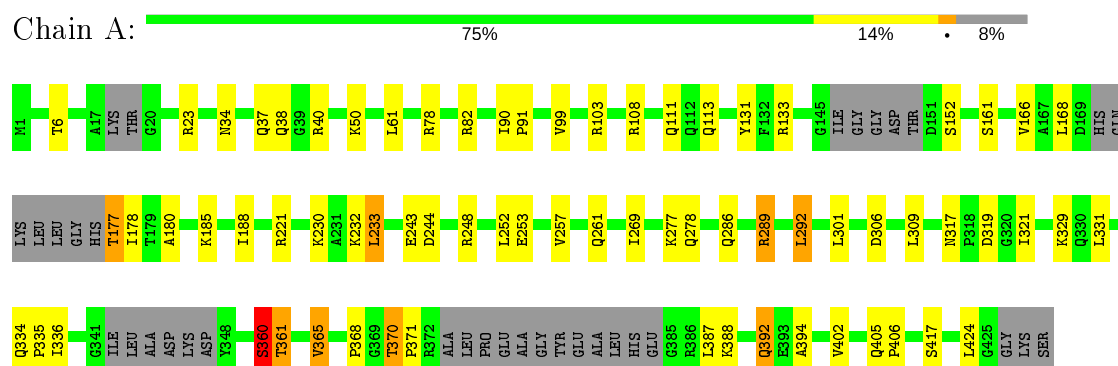
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	169	Total	O	0	0
			169	169		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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. 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. 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.

Note EDS was not executed.

• Molecule 1: FOLYLPOLYGLUTAMATE SYNTHETASE



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	54.00 Å 46.10 Å 84.90 Å 90.00° 107.30° 90.00°	Depositor
Resolution (Å)	15.00 – 2.40	Depositor
% Data completeness (in resolution range)	(Not available) (15.00-2.40)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT	Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3167	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, POP

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	0.46	0/3048	0.88	7/4159 (0.2%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	370	THR	C-N-CD	-16.79	83.66	120.60
1	A	317	ASN	C-N-CD	-7.20	104.77	120.60
1	A	244	ASP	CB-CG-OD1	6.21	123.89	118.30
1	A	365	VAL	C-N-CD	-5.88	107.67	120.60
1	A	424	LEU	CA-CB-CG	5.77	128.57	115.30
1	A	166	VAL	N-CA-C	-5.18	97.03	111.00
1	A	368	PRO	N-CA-C	5.17	125.53	112.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	2988	0	2995	22	0
2	A	1	0	0	0	0
3	A	9	0	0	0	0
4	A	169	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	3167	0	2995	22	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 4.

All (22) 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:243:GLU:HG3	1:A:248:ARG:HG2	1.60	0.82
1:A:365:VAL:HG12	1:A:388:LYS:HB2	1.73	0.70
1:A:269:ILE:HD11	1:A:292:LEU:HD21	1.80	0.62
1:A:34:ASN:HB3	1:A:37:GLN:HG3	1.82	0.62
1:A:388:LYS:HG3	1:A:394:ALA:HB2	1.82	0.61
1:A:168:LEU:HA	1:A:178:ILE:HD11	1.87	0.56
1:A:252:LEU:HD23	1:A:289:ARG:HG3	1.89	0.54
1:A:336:ILE:HG22	1:A:406:PRO:HG2	1.89	0.53
1:A:233:LEU:HD11	1:A:257:VAL:HG13	1.93	0.51
1:A:6:THR:HG23	1:A:99:VAL:HG11	1.91	0.51
1:A:177:THR:HG23	1:A:180:ALA:HB3	1.93	0.50
1:A:257:VAL:HG11	1:A:331:LEU:HD11	1.97	0.47
1:A:38:GLN:HB2	1:A:133:ARG:HD2	1.96	0.46
1:A:82:ARG:HB3	1:A:82:ARG:HE	1.34	0.45
1:A:292:LEU:HD12	1:A:292:LEU:HA	1.84	0.42
1:A:90:ILE:HA	1:A:91:PRO:HD3	1.72	0.42
1:A:360:SER:HB3	1:A:361:THR:H	1.51	0.42
1:A:392:GLN:HE21	1:A:392:GLN:H	1.68	0.41
1:A:161:SER:HB3	1:A:188:ILE:HD12	2.03	0.41
1:A:61:LEU:HA	1:A:61:LEU:HD23	1.91	0.40
1:A:90:ILE:HD12	1:A:131:TYR:CE2	2.57	0.40
1:A:405:GLN:HA	1:A:406:PRO:HD2	1.93	0.40

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	381/428 (89%)	363 (95%)	16 (4%)	2 (0%)	29	41

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	360	SER
1	A	371	PRO

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	309/344 (90%)	272 (88%)	37 (12%)	5	6

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	ARG
1	A	40	ARG
1	A	50	LYS
1	A	78	ARG
1	A	103	ARG
1	A	108	ARG
1	A	111	GLN
1	A	113	GLN
1	A	152	SER
1	A	177	THR
1	A	185	LYS
1	A	221	ARG
1	A	230	LYS
1	A	232	LYS
1	A	233	LEU
1	A	253	GLU
1	A	261	GLN

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Mol	Chain	Res	Type
1	A	277	LYS
1	A	278	GLN
1	A	286	GLN
1	A	289	ARG
1	A	292	LEU
1	A	301	LEU
1	A	306	ASP
1	A	309	LEU
1	A	319	ASP
1	A	321	ILE
1	A	329	LYS
1	A	334	GLN
1	A	335	PRO
1	A	360	SER
1	A	361	THR
1	A	370	THR
1	A	387	LEU
1	A	392	GLN
1	A	402	VAL
1	A	417	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	110	GLN
1	A	238	GLN
1	A	261	GLN
1	A	262	GLN
1	A	264	ASN
1	A	392	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	POP	A	999	2	6,8,8	1.10	0	13,13,13	0.95	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	POP	A	999	2	-	1/6/6/6	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	999	POP	P1-O-P2-O5

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 ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.