



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 10:21 PM UTC

PDB ID : 5GLA / pdb_00005gla
Title : Crystal structure of the class A beta-lactamase PenL-tTR10 containing 10 residues insertion in omega-loop
Authors : Choi, J.M.; Yi, H.; Kim, H.S.; Lee, S.H.
Deposited on : 2016-07-10
Resolution : 1.50 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 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 : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

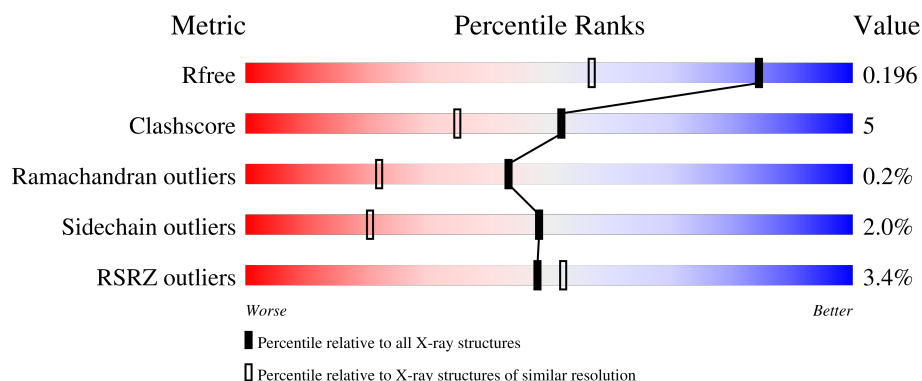
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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}	180053	4037 (1.50-1.50)
Clashscore	190562	4235 (1.50-1.50)
Ramachandran outliers	187476	4153 (1.50-1.50)
Sidechain outliers	187428	4150 (1.50-1.50)
RSRZ outliers	180081	4039 (1.50-1.50)

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	278	4% 88% 8%
1	B	278	3% 85% 9%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 4598 atoms, of which 23 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 Beta-lactamase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	267	Total	C	H	N	O	S	0	0	0
			2007	1238	3	380	378	8			
1	B	266	Total	C	H	N	O	S	0	0	0
			2019	1235	20	379	377	8			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	22	GLY	-	expression tag	UNP A0A2Z4SUB5
A	23	SER	-	expression tag	UNP A0A2Z4SUB5
A	24	HIS	-	expression tag	UNP A0A2Z4SUB5
A	25	MET	-	expression tag	UNP A0A2Z4SUB5
A	173	ILE	-	insertion	UNP A0A2Z4SUB5
A	174	PRO	-	insertion	UNP A0A2Z4SUB5
A	175	GLY	-	insertion	UNP A0A2Z4SUB5
A	176	ASP	-	insertion	UNP A0A2Z4SUB5
A	177	GLU	-	insertion	UNP A0A2Z4SUB5
A	178	ARG	-	insertion	UNP A0A2Z4SUB5
A	179	ASP	-	insertion	UNP A0A2Z4SUB5
A	180	THR	-	insertion	UNP A0A2Z4SUB5
A	181	THR	-	insertion	UNP A0A2Z4SUB5
A	182	THR	-	insertion	UNP A0A2Z4SUB5
B	22	GLY	-	expression tag	UNP A0A2Z4SUB5
B	23	SER	-	expression tag	UNP A0A2Z4SUB5
B	24	HIS	-	expression tag	UNP A0A2Z4SUB5
B	25	MET	-	expression tag	UNP A0A2Z4SUB5
B	173	ILE	-	insertion	UNP A0A2Z4SUB5
B	174	PRO	-	insertion	UNP A0A2Z4SUB5
B	175	GLY	-	insertion	UNP A0A2Z4SUB5
B	176	ASP	-	insertion	UNP A0A2Z4SUB5
B	177	GLU	-	insertion	UNP A0A2Z4SUB5
B	178	ARG	-	insertion	UNP A0A2Z4SUB5
B	179	ASP	-	insertion	UNP A0A2Z4SUB5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	180	THR	-	insertion	UNP A0A2Z4SUB5
B	181	THR	-	insertion	UNP A0A2Z4SUB5
B	182	THR	-	insertion	UNP A0A2Z4SUB5

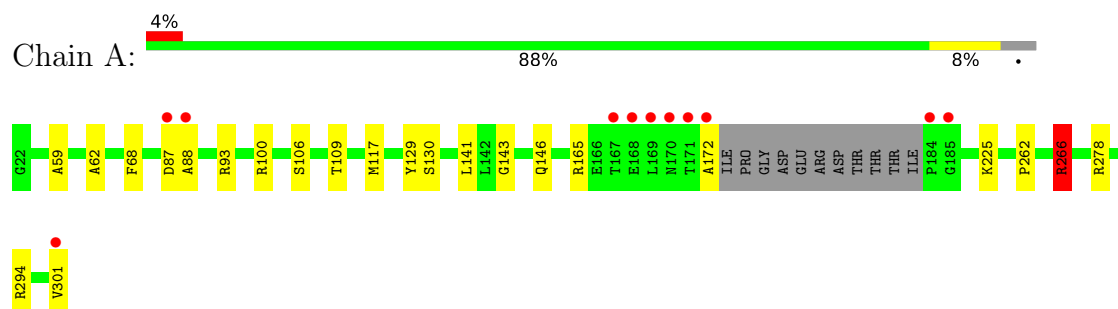
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	297	Total 297	O 297	0	0
2	B	275	Total 275	O 275	0	0

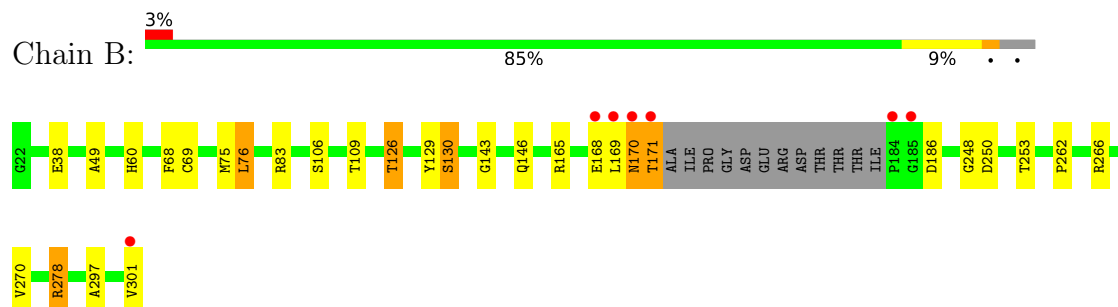
3 Residue-property plots [i](#)

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: Beta-lactamase



• Molecule 1: Beta-lactamase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	35.03Å 92.55Å 68.87Å 90.00° 92.61° 90.00°	Depositor
Resolution (Å)	32.24 – 1.50 32.24 – 1.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (32.24-1.50) 99.8 (32.24-1.50)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.11 (at 1.50Å)	Xtriage
Refinement program	PHENIX 1.8_1069	Depositor
R, R_{free}	0.169 , 0.196 0.170 , 0.196	Depositor DCC
R_{free} test set	3533 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	13.5	Xtriage
Anisotropy	0.031	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 38.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.045 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4598	wwPDB-VP
Average B, all atoms (Å ²)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.35% 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](#)

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	0.57	4/2034 (0.2%)	0.73	1/2757 (0.0%)
1	B	0.54	2/2029 (0.1%)	0.80	6/2750 (0.2%)
All	All	0.56	6/4063 (0.1%)	0.77	7/5507 (0.1%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	186	ASP	C-O	-7.42	1.14	1.23
1	A	278	ARG	C-O	-6.87	1.15	1.24
1	B	129	TYR	C-O	-6.82	1.15	1.24
1	A	129	TYR	C-O	-6.22	1.15	1.24
1	A	100	ARG	C-O	-5.49	1.17	1.24
1	A	266	ARG	C-O	-5.28	1.17	1.23

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	278	ARG	NE-CZ-NH2	7.16	125.64	119.20
1	B	171	THR	N-CA-CB	6.08	121.83	111.50
1	B	76	LEU	O-C-N	5.91	128.41	122.08
1	B	278	ARG	NE-CZ-NH1	-5.75	115.75	121.50
1	A	266	ARG	N-CA-C	5.19	115.90	108.74
1	B	75	MET	CA-C-N	5.16	127.96	120.79
1	B	75	MET	C-N-CA	5.16	127.96	120.79

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	2004	3	2003	17	0
1	B	1999	20	1998	24	0
2	A	297	0	0	8	0
2	B	275	0	0	6	0
All	All	4575	23	4001	41	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 5.

All (41) 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:143:GLY:O	1:A:146:GLN:NE2	1.73	1.20
1:B:69:CYS:SG	1:B:171:THR:OG1	2.10	1.07
1:A:87:ASP:OD2	1:A:88:ALA:N	2.01	0.93
1:B:171:THR:HA	1:B:250:ASP:OD1	1.77	0.84
1:B:171:THR:OG1	1:B:248:GLY:HA3	1.77	0.83
1:B:171:THR:HG21	1:B:253:THR:OG1	1.83	0.77
1:B:171:THR:HB	1:B:250:ASP:N	1.99	0.77
1:B:170:ASN:HB2	2:B:463:HOH:O	1.90	0.70
1:B:262:PRO:HB2	1:B:266:ARG:HB2	1.82	0.61
1:B:83:ARG:HD2	2:B:502:HOH:O	2.01	0.59
1:B:169:LEU:O	1:B:170:ASN:O	2.20	0.59
1:A:225:LYS:HE3	2:A:422:HOH:O	2.05	0.57
1:B:266:ARG:NH2	2:B:409:HOH:O	2.38	0.56
1:B:170:ASN:O	1:B:171:THR:C	2.51	0.52
1:A:172:ALA:HB1	2:A:406:HOH:O	2.10	0.51
1:A:106:SER:HB3	1:A:109:THR:OG1	2.11	0.51
1:A:165:ARG:NH1	2:A:412:HOH:O	2.44	0.50
1:A:87:ASP:OD2	1:A:87:ASP:C	2.54	0.49
1:B:143:GLY:O	1:B:146:GLN:NE2	2.33	0.49
1:A:59:ALA:HB1	1:A:62:ALA:HB2	1.95	0.48
1:B:38:GLU:OE2	1:B:60:HIS:HE1	1.97	0.48
1:A:262:PRO:HB2	1:A:266:ARG:HG3	1.97	0.47
1:A:225:LYS:CE	2:A:422:HOH:O	2.62	0.47
1:B:165:ARG:NH2	2:B:414:HOH:O	2.47	0.47
1:A:294:ARG:NH1	2:A:413:HOH:O	2.44	0.47
1:B:266:ARG:CZ	2:B:409:HOH:O	2.63	0.47
1:B:266:ARG:NE	2:B:409:HOH:O	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:301:VAL:O	1:A:301:VAL:HG13	2.16	0.45
1:B:126:THR:O	1:B:130:SER:HA	2.18	0.44
1:A:141:LEU:C	1:A:141:LEU:HD23	2.43	0.44
1:A:93:ARG:NH2	2:A:410:HOH:O	2.43	0.43
1:A:117:MET:HE3	2:A:573:HOH:O	2.17	0.43
1:B:49:ALA:HA	1:B:270:VAL:O	2.17	0.43
1:A:93:ARG:NE	2:A:410:HOH:O	2.49	0.42
1:B:169:LEU:O	1:B:170:ASN:C	2.63	0.42
1:B:171:THR:HB	1:B:248:GLY:C	2.46	0.41
1:B:168:GLU:OE1	1:B:168:GLU:N	2.50	0.41
1:A:146:GLN:H	1:A:146:GLN:CD	2.28	0.40
1:B:171:THR:CB	1:B:248:GLY:HA3	2.49	0.40
1:B:297:ALA:O	1:B:301:VAL:HG13	2.22	0.40
1:B:106:SER:HB3	1:B:109:THR:OG1	2.22	0.40

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	263/278 (95%)	254 (97%)	9 (3%)	0	100	100
1	B	262/278 (94%)	255 (97%)	6 (2%)	1 (0%)	30	12
All	All	525/556 (94%)	509 (97%)	15 (3%)	1 (0%)	43	22

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	170	ASN

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	197/207 (95%)	194 (98%)	3 (2%)	57	31
1	B	197/207 (95%)	192 (98%)	5 (2%)	42	14
All	All	394/414 (95%)	386 (98%)	8 (2%)	48	20

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	68	PHE
1	A	130	SER
1	A	266	ARG
1	B	68	PHE
1	B	76	LEU
1	B	126	THR
1	B	130	SER
1	B	278	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	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 oligosaccharides 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	267/278 (96%)	-0.11	11 (4%) 41 45	6, 11, 26, 42	0
1	B	266/278 (95%)	-0.01	7 (2%) 57 61	6, 12, 24, 40	1 (0%)
All	All	533/556 (95%)	-0.06	18 (3%) 48 52	6, 11, 26, 42	1 (0%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	88	ALA	7.1
1	A	171	THR	5.9
1	B	185	GLY	5.2
1	B	170	ASN	4.5
1	B	184	PRO	4.4
1	A	172	ALA	4.3
1	B	301	VAL	4.0
1	B	171	THR	3.8
1	A	185	GLY	3.7
1	A	170	ASN	3.2
1	B	169	LEU	3.1
1	A	167	THR	3.1
1	A	169	LEU	3.1
1	A	168	GLU	2.4
1	B	168	GLU	2.3
1	A	301	VAL	2.3
1	A	184	PRO	2.1
1	A	87	ASP	2.0

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 oligosaccharides 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.