



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 18, 2024 – 03:18 PM EDT

PDB ID : 3WHS
Title : Crystal structure of Bacillus subtilis gamma-glutamyltranspeptidase in complex with acivicin
Authors : Wada, K.; Fukuyama, K.
Deposited on : 2013-08-30
Resolution : 1.80 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
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)	:	2.37.1

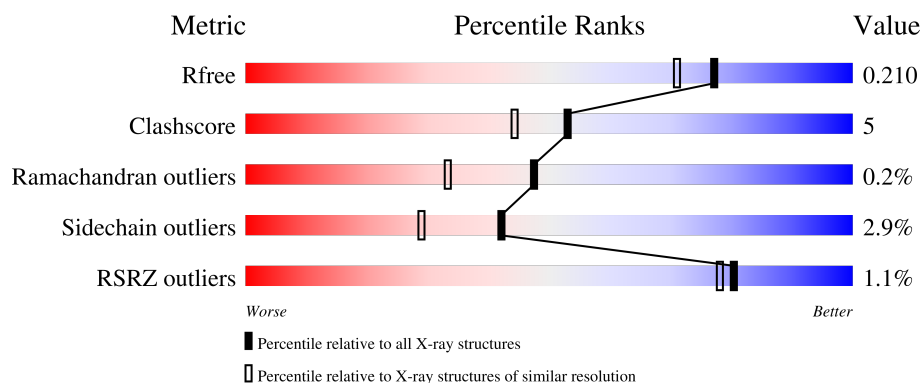
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	418	
2	B	185	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4466 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 Gamma-glutamyltranspeptidase large chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	359	Total	C	N	O	S	0	0	0
			2778	1767	458	543	10			

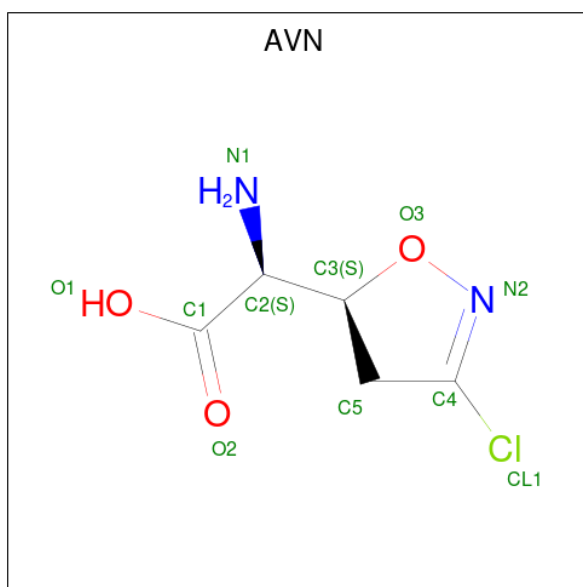
There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	MET	-	expression tag	UNP P54422
A	-14	ASN	-	expression tag	UNP P54422
A	-13	HIS	-	expression tag	UNP P54422
A	-12	LYS	-	expression tag	UNP P54422
A	-11	VAL	-	expression tag	UNP P54422
A	-10	HIS	-	expression tag	UNP P54422
A	-9	HIS	-	expression tag	UNP P54422
A	-8	HIS	-	expression tag	UNP P54422
A	-7	HIS	-	expression tag	UNP P54422
A	-6	HIS	-	expression tag	UNP P54422
A	-5	HIS	-	expression tag	UNP P54422
A	-4	ILE	-	expression tag	UNP P54422
A	-3	GLU	-	expression tag	UNP P54422
A	-2	GLY	-	expression tag	UNP P54422
A	-1	ARG	-	expression tag	UNP P54422
A	0	HIS	-	expression tag	UNP P54422

- Molecule 2 is a protein called Gamma-glutamyltranspeptidase small chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	183	Total	C	N	O	S	0	0	0
			1387	875	231	276	5			

- Molecule 3 is (2S)-AMINO[(5S)-3-CHLORO-4,5-DIHYDROISOXAZOL-5-YL]ACETIC ACID (three-letter code: AVN) (formula: C₅H₇ClN₂O₃).

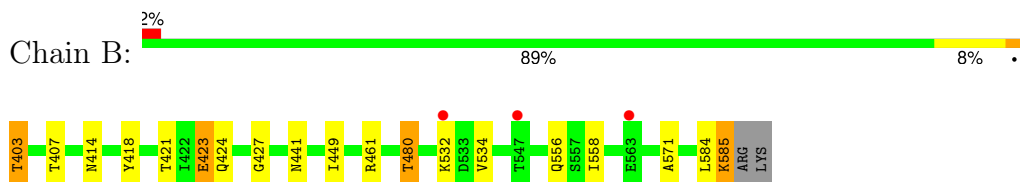


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			10	5	2	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	197	Total	O	0	0
			197	197		
4	B	94	Total	O	0	0
			94	94		

- Molecule 1: Gamma-glutamyltranspeptidase large chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	60.08Å 71.67Å 144.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.04 – 1.80 30.04 – 1.80	Depositor EDS
% Data completeness (in resolution range)	96.8 (30.04-1.80) 96.8 (30.04-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.08 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.183 , 0.209 0.182 , 0.210	Depositor DCC
R_{free} test set	2883 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	22.2	Xtriage
Anisotropy	0.070	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 49.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4466	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.22% 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: AVN

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	0.60	0/2836	0.66	0/3834
2	B	0.61	0/1415	0.69	1/1924 (0.1%)
All	All	0.60	0/4251	0.67	1/5758 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	403	THR	CA-CB-OG1	-5.19	98.11	109.00

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	2778	0	2762	36	0
2	B	1387	0	1367	15	0
3	B	10	0	6	1	0
4	A	197	0	0	6	0
4	B	94	0	0	1	0
All	All	4466	0	4135	45	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 (45) 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:351:GLY:H	1:A:383:GLN:HE21	1.16	0.94
1:A:185:SER:O	1:A:189:GLU:HG2	1.74	0.87
2:B:480:THR:HG23	4:B:702:HOH:O	1.75	0.87
1:A:271:THR:HG21	2:B:461:ARG:HH12	1.41	0.85
1:A:111:ASP:HB3	1:A:271:THR:HG22	1.57	0.85
1:A:271:THR:HG23	1:A:273:ASP:OD1	1.79	0.81
2:B:407:THR:OG1	2:B:480:THR:HG21	1.87	0.75
1:A:394:GLN:HE22	2:B:449:ILE:H	1.33	0.75
1:A:378:ASP:HB3	1:A:381:LYS:HE2	1.73	0.71
2:B:424:GLN:H	2:B:441:ASN:HD21	1.39	0.71
1:A:53:HIS:HD2	1:A:55:LEU:H	1.40	0.69
2:B:584:LEU:O	2:B:585:LYS:HB2	1.94	0.67
1:A:133:ILE:HG21	1:A:141:LYS:HZ3	1.60	0.65
2:B:480:THR:HG22	2:B:558:ILE:H	1.60	0.64
1:A:359:LYS:HA	4:A:696:HOH:O	1.99	0.62
1:A:351:GLY:H	1:A:383:GLN:NE2	1.96	0.57
1:A:103:LYS:NZ	1:A:103:LYS:HB3	2.22	0.55
1:A:102:GLY:H	2:B:414:ASN:ND2	2.06	0.53
1:A:82:ASN:ND2	1:A:91:ILE:H	2.08	0.52
1:A:271:THR:CG2	1:A:273:ASP:OD1	2.53	0.51
2:B:427:GLY:HA2	2:B:441:ASN:HD22	1.78	0.49
1:A:378:ASP:O	1:A:381:LYS:HG2	2.13	0.48
1:A:82:ASN:HD21	1:A:91:ILE:H	1.60	0.48
1:A:196:GLU:OE2	1:A:200:ARG:NH1	2.47	0.48
2:B:556:GLN:HE21	2:B:571:ALA:HA	1.79	0.48
1:A:360:GLU:OE1	1:A:382:TYR:OH	2.25	0.47
1:A:133:ILE:HG21	1:A:141:LYS:NZ	2.28	0.47
1:A:102:GLY:H	2:B:414:ASN:HD22	1.62	0.46
1:A:53:HIS:CD2	1:A:55:LEU:H	2.27	0.46
1:A:166:MET:HG2	4:A:685:HOH:O	2.16	0.45
1:A:84:THR:HA	1:A:181:PHE:CZ	2.52	0.45
1:A:108:THR:HG22	4:A:574:HOH:O	2.17	0.45
1:A:307:HIS:CE1	4:A:696:HOH:O	2.70	0.44
1:A:141:LYS:HB3	4:A:692:HOH:O	2.17	0.44
1:A:103:LYS:NZ	1:A:103:LYS:CB	2.80	0.43
1:A:351:GLY:N	1:A:383:GLN:HE21	1.97	0.43
2:B:424:GLN:H	2:B:441:ASN:ND2	2.12	0.43
1:A:276:ILE:HG23	1:A:289:PRO:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:321:TYR:CD2	2:B:534:VAL:HG11	2.55	0.42
1:A:53:HIS:HE1	4:A:550:HOH:O	2.02	0.42
2:B:403:THR:HG21	3:B:600:AVN:N2	2.35	0.42
1:A:308:PHE:CZ	1:A:362:GLN:HG2	2.55	0.41
1:A:88:MET:O	2:B:421:THR:HA	2.21	0.40
1:A:337:SER:CB	1:A:391:GLN:HE22	2.35	0.40
1:A:103:LYS:HB3	1:A:103:LYS:HZ2	1.87	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	357/418 (85%)	353 (99%)	4 (1%)	0	100	100
2	B	181/185 (98%)	177 (98%)	3 (2%)	1 (1%)	25	12
All	All	538/603 (89%)	530 (98%)	7 (1%)	1 (0%)	47	33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	423	GLU

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	296/348 (85%)	288 (97%)	8 (3%)	44	31
2	B	155/157 (99%)	150 (97%)	5 (3%)	39	25
All	All	451/505 (89%)	438 (97%)	13 (3%)	42	29

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	LYS
1	A	87	MET
1	A	103	LYS
1	A	184	ASP
1	A	196	GLU
1	A	263	LYS
1	A	271	THR
1	A	359	LYS
2	B	418	TYR
2	B	423	GLU
2	B	480	THR
2	B	532	LYS
2	B	585	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	53	HIS
1	A	82	ASN
1	A	281	GLN
1	A	307	HIS
1	A	309	ASN
1	A	346	ASN
1	A	363	GLN
1	A	383	GLN
1	A	391	GLN
1	A	394	GLN
2	B	414	ASN
2	B	424	GLN
2	B	441	ASN
2	B	554	ASN
2	B	556	GLN
2	B	576	ASN

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 ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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	$\# Z > 2$
3	AVN	B	600	2	9,10,11	2.37	3 (33%)	8,13,15	3.42	2 (25%)

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	AVN	B	600	2	-	3/7/15/17	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	600	AVN	C4-N2	5.59	1.32	1.26
3	B	600	AVN	C5-C3	-2.68	1.49	1.53
3	B	600	AVN	C3-C2	-2.47	1.50	1.53

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	600	AVN	C3-O3-N2	-8.73	99.96	109.03
3	B	600	AVN	O3-C3-C5	-3.60	102.01	104.45

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	600	AVN	O2-C1-C2-N1
3	B	600	AVN	O1-C1-C2-N1
3	B	600	AVN	C1-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	600	AVN	1	0

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	359/418 (85%)	-0.15	3 (0%) 86 84	14, 23, 35, 52	0
2	B	183/185 (98%)	-0.14	3 (1%) 72 68	14, 22, 33, 44	0
All	All	542/603 (89%)	-0.15	6 (1%) 80 78	14, 22, 35, 52	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	37	GLU	5.7
1	A	210	ASN	3.9
1	A	38	TYR	3.2
2	B	563	GLU	2.8
2	B	547	THR	2.7
2	B	532	LYS	2.2

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	AVN	B	600	10/11	0.96	0.12	14,18,22,24	0

6.5 Other polymers [i](#)

There are no such residues in this entry.