Full wwPDB X-ray Structure Validation Report ⓘ

Nov 7, 2023 – 03:49 PM JST

PDB ID	:	7D95
Title	:	Crystal structure of acivicin-bound GATase subunit of Methanocaldococcus jannaschii GMP synthetase
Authors	:	Bellur, A.; Dongre, A.; Kumar, S.; Balaram, H.
Deposited on	:	2020-10-12
Resolution	:	1.67 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:

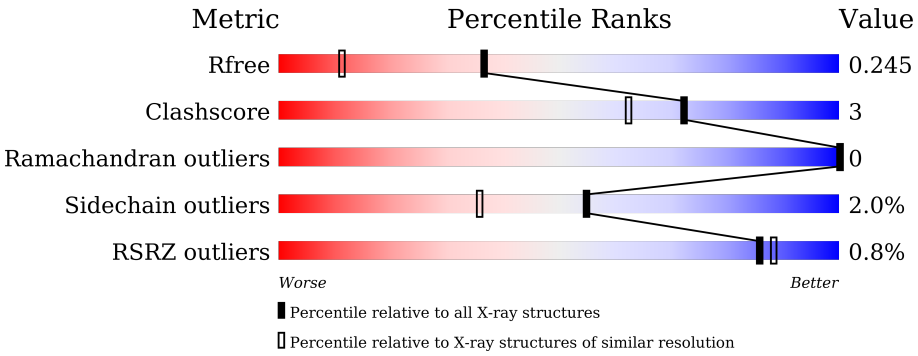
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

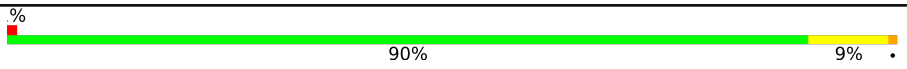
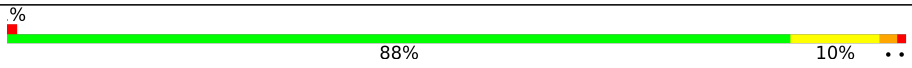
The reported resolution of this entry is 1.67 Å.

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	6780 (1.70-1.66)
Clashscore	141614	7310 (1.70-1.66)
Ramachandran outliers	138981	7173 (1.70-1.66)
Sidechain outliers	138945	7172 (1.70-1.66)
RSRZ outliers	127900	6661 (1.70-1.66)

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 <=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	188	
1	B	188	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3206 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 GMP synthase [glutamine-hydrolyzing] subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	188	Total	C	N	O	S	0	0	0
			1468	939	247	275	7			
1	B	188	Total	C	N	O	S	0	0	0
			1472	941	247	277	7			

- Molecule 2 is water.

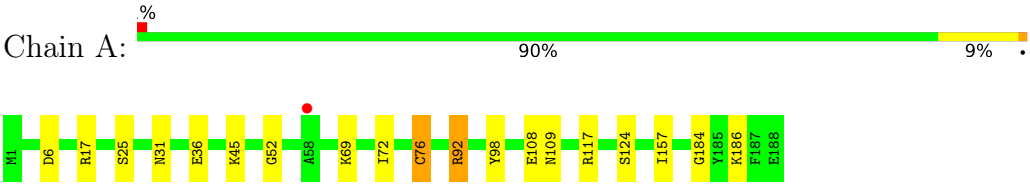
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	131	Total	O	0	0
			131	131		
2	B	135	Total	O	0	0
			135	135		

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.

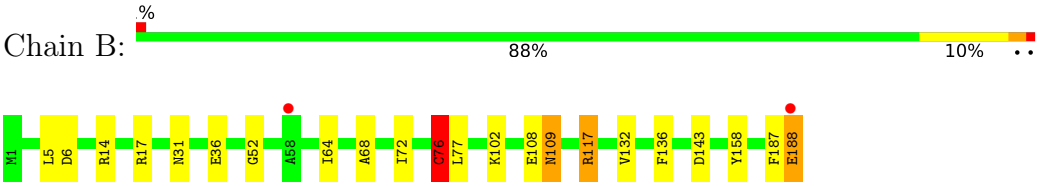
• Molecule 1: GMP synthase [glutamine-hydrolyzing] subunit A

Chain A:



• Molecule 1: GMP synthase [glutamine-hydrolyzing] subunit A

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α, β, γ	65.35Å 65.35Å 97.37Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	56.59 – 1.67 36.91 – 1.67	Depositor EDS
% Data completeness (in resolution range)	99.5 (56.59-1.67) 99.6 (36.91-1.67)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.84 (at 1.67Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.197 , 0.234 0.210 , 0.245	Depositor DCC
R_{free} test set	2703 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	21.4	Xtriage
Anisotropy	0.197	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 32.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.029 for -h,-k,l 0.469 for h,-h-k,-l 0.034 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	3206	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.62% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 5CS, SNN

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	1.13	2/1473 (0.1%)	1.05	4/1990 (0.2%)
1	B	1.14	3/1477 (0.2%)	1.02	5/1995 (0.3%)
All	All	1.13	5/2950 (0.2%)	1.04	9/3985 (0.2%)

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	1
1	B	0	1
All	All	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	36	GLU	CD-OE1	8.92	1.35	1.25
1	A	36	GLU	CD-OE2	-7.48	1.17	1.25
1	B	36	GLU	CD-OE2	6.49	1.32	1.25
1	A	25	SER	CB-OG	-5.70	1.34	1.42
1	B	158	TYR	CE1-CZ	5.38	1.45	1.38

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	17	ARG	NE-CZ-NH2	-8.21	116.19	120.30
1	A	17	ARG	NE-CZ-NH1	7.33	123.96	120.30
1	B	17	ARG	NE-CZ-NH2	-6.19	117.21	120.30
1	A	92	ARG	NE-CZ-NH1	5.87	123.23	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	14	ARG	NE-CZ-NH2	-5.84	117.38	120.30
1	A	6	ASP	CB-CG-OD2	-5.61	113.25	118.30
1	B	6	ASP	CB-CG-OD2	-5.56	113.30	118.30
1	B	17	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	B	143	ASP	CB-CG-OD1	5.00	122.80	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	108	GLU	Mainchain
1	B	76	5CS	Mainchain

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	1468	0	1443	10	1
1	B	1472	0	1447	10	1
2	A	131	0	0	4	0
2	B	135	0	0	0	0
All	All	3206	0	2890	20	1

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.

All (20) 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:69:LYS:HD3	2:A:323:HOH:O	1.61	1.00
1:B:187:PHE:O	1:B:188:GLU:HB2	1.57	0.98
1:A:69:LYS:HD2	2:A:217:HOH:O	1.82	0.78
1:B:187:PHE:O	1:B:188:GLU:CB	2.33	0.72
1:A:92:ARG:NH2	2:A:201:HOH:O	2.08	0.71
1:B:188:GLU:OE2	1:B:188:GLU:HA	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:68:ALA:HB3	1:B:72:ILE:HD11	1.88	0.54
1:B:108:GLU:O	1:B:109:SNN:C	2.56	0.54
1:A:98:TYR:CE1	1:A:124:SER:HB3	2.43	0.53
1:A:92:ARG:HG2	2:A:263:HOH:O	2.12	0.49
1:A:52:GLY:O	1:A:76:5CS:HF	2.13	0.49
1:A:72:ILE:HG12	1:A:157:ILE:HG12	1.97	0.46
1:B:52:GLY:H	1:B:76:5CS:HF	1.81	0.46
1:A:72:ILE:HD11	1:A:157:ILE:HG23	1.98	0.46
1:A:184:GLY:O	1:A:186:LYS:HE2	2.19	0.42
1:A:98:TYR:CZ	1:A:124:SER:HB3	2.56	0.41
1:B:5:LEU:HD21	1:B:64:ILE:CD1	2.49	0.41
1:B:76:5CS:HD	1:B:77:LEU:H	1.85	0.41
1:B:76:5CS:HD	1:B:77:LEU:N	2.36	0.40
1:B:132:VAL:CG1	1:B:136:PHE:HB2	2.51	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:117:ARG:CG	1:B:117:ARG:NH1[1_665]	2.18	0.02

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	183/188 (97%)	181 (99%)	2 (1%)	0	100	100
1	B	183/188 (97%)	181 (99%)	2 (1%)	0	100	100
All	All	366/376 (97%)	362 (99%)	4 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	152/158 (96%)	150 (99%)	2 (1%)	69 54
1	B	153/158 (97%)	149 (97%)	4 (3%)	46 25
All	All	305/316 (96%)	299 (98%)	6 (2%)	55 36

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	ASN
1	A	45	LYS
1	B	31	ASN
1	B	102	LYS
1	B	117	ARG
1	B	188	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	ASN
1	B	31	ASN

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	5CS	A	76	1	10,16,17	1.91	4 (40%)	10,21,23	5.79	4 (40%)
1	SNN	B	109	1	7,8,8	3.95	3 (42%)	7,11,11	2.88	4 (57%)
1	5CS	B	76	1	10,16,17	1.98	4 (40%)	10,21,23	5.38	5 (50%)
1	SNN	A	109	1	7,8,8	1.35	1 (14%)	7,11,11	1.69	1 (14%)

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	5CS	A	76	1	-	6/11/24/26	0/1/1/1
1	SNN	B	109	1	-	-	0/1/1/1
1	5CS	B	76	1	-	7/11/24/26	0/1/1/1
1	SNN	A	109	1	-	-	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	109	SNN	C4-CA	-7.63	1.45	1.53
1	B	109	SNN	C5-N1	-6.14	1.28	1.37
1	B	76	5CS	OF-CF	-4.01	1.38	1.44
1	A	76	5CS	OF-CF	-3.47	1.39	1.44
1	A	109	SNN	C5-N1	-3.16	1.32	1.37
1	A	76	5CS	CE-CF	2.86	1.59	1.52
1	B	76	5CS	CE-CF	2.80	1.59	1.52
1	B	109	SNN	O5-C5	2.77	1.28	1.23
1	B	76	5CS	CE-CD	-2.67	1.50	1.53
1	A	76	5CS	OJ2-CJ	2.44	1.29	1.22
1	A	76	5CS	O-C	2.08	1.28	1.19
1	B	76	5CS	OJ2-CJ	2.04	1.28	1.22

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	76	5CS	CE-CF-CI	12.09	136.19	115.08
1	A	76	5CS	OF-CF-CI	-11.35	87.42	109.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	76	5CS	OF-CF-CI	-10.97	88.17	109.23
1	B	76	5CS	CE-CF-CI	10.93	134.16	115.08
1	A	76	5CS	CD-CE-CF	-5.82	98.97	107.78
1	B	76	5CS	CD-CE-CF	-4.84	100.45	107.78
1	B	109	SNN	O5-C5-C4	4.49	132.32	126.39
1	A	76	5CS	OJ1-CJ-OJ2	-3.92	115.18	124.09
1	B	109	SNN	O-C-CA	-3.81	123.43	126.18
1	B	76	5CS	OJ1-CJ-OJ2	-3.74	115.59	124.09
1	B	109	SNN	CA-C-N1	3.23	109.79	107.30
1	B	109	SNN	O5-C5-N1	-3.19	120.71	125.00
1	A	109	SNN	CA-C-N1	3.13	109.72	107.30
1	B	76	5CS	OJ1-CJ-CI	2.95	124.53	114.22

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	76	5CS	CE-CD-SG-CB
1	A	76	5CS	CF-CI-CJ-OJ1
1	A	76	5CS	CF-CI-CJ-OJ2
1	A	76	5CS	CE-CF-CI-NI
1	A	76	5CS	OF-CF-CI-CJ
1	A	76	5CS	CE-CF-CI-CJ
1	B	76	5CS	CE-CD-SG-CB
1	B	76	5CS	CF-CI-CJ-OJ1
1	B	76	5CS	CF-CI-CJ-OJ2
1	B	76	5CS	CE-CF-CI-NI
1	B	76	5CS	OF-CF-CI-CJ
1	B	76	5CS	CE-CF-CI-CJ
1	B	76	5CS	CA-CB-SG-CD

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	76	5CS	1	0
1	B	109	SNN	1	0
1	B	76	5CS	3	0

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

6.1 Protein, DNA and RNA chains

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, 95^{th} 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	186/188 (98%)	-0.53	1 (0%)	91	92	15, 23, 36, 57	0
1	B	186/188 (98%)	-0.52	2 (1%)	80	83	14, 23, 36, 55	0
All	All	372/376 (98%)	-0.52	3 (0%)	86	88	14, 23, 36, 57	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	58	ALA	3.0
1	B	188	GLU	2.3
1	B	58	ALA	2.2

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

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, 95^{th} 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	5CS	A	76	16/17	0.89	0.14	15,27,36,38	0
1	SNN	B	109	8/8	0.90	0.07	23,24,30,31	0
1	5CS	B	76	16/17	0.91	0.14	14,26,37,42	0
1	SNN	A	109	8/8	0.92	0.09	21,22,23,24	0

6.3 Carbohydrates

There are no monosaccharides 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.