Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 02:49 pm BST

PDB ID	:	2JGP
Title	:	Structure of the TycC5-6 PCP-C bidomain of the tyrocidine synthetase TycC
Authors	:	Samel, S.A.; Schoenafinger, G.; Knappe, T.A.; Marahiel, M.A.; Essen, L.-O.
Deposited on	:	2007-02-13
Resolution	:	1.85 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:

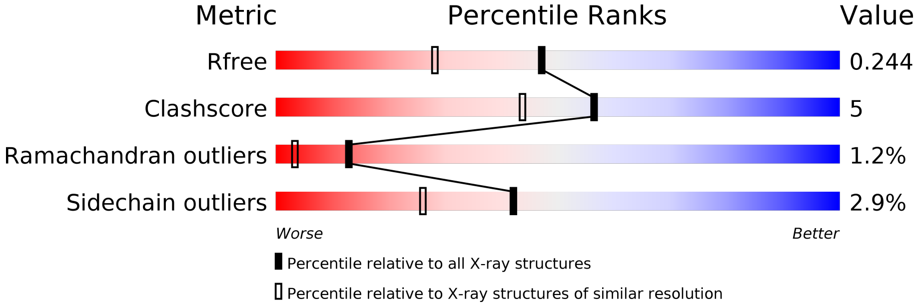
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 1.85 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	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	520	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4477 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.

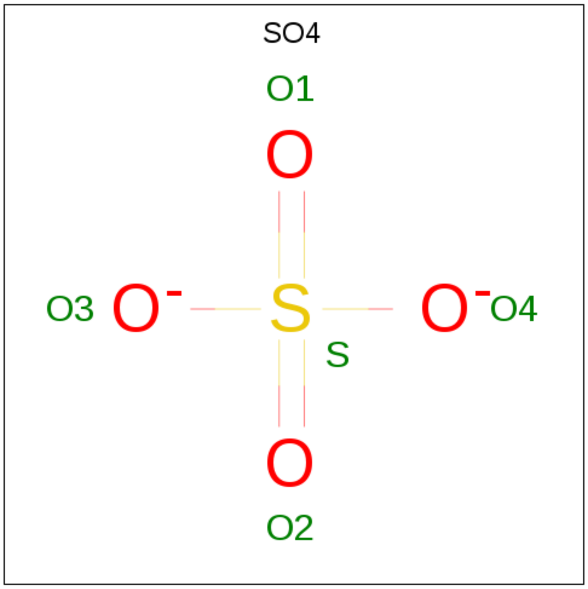
- Molecule 1 is a protein called TYROCIDINE SYNTHETASE 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	520	4161	2655	695	795	16	35	2	0

There is a discrepancy between the modelled and reference sequences:

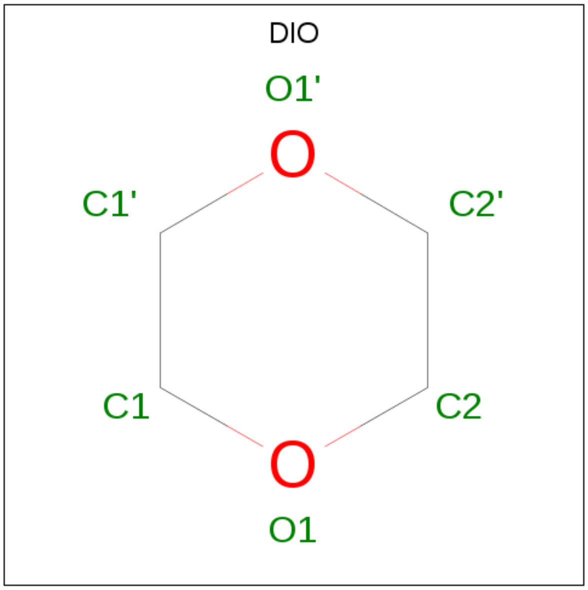
Chain	Residue	Modelled	Actual	Comment	Reference
A	183	GLU	GLN	conflict	UNP O30409

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0
2	A	1	5	4	1	0	0

- Molecule 3 is 1,4-DIETHYLENE DIOXIDE (three-letter code: DIO) (formula: $C_4H_8O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 4 2	0	0
3	A	1	Total C O 6 4 2	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Na 1 1	0	0

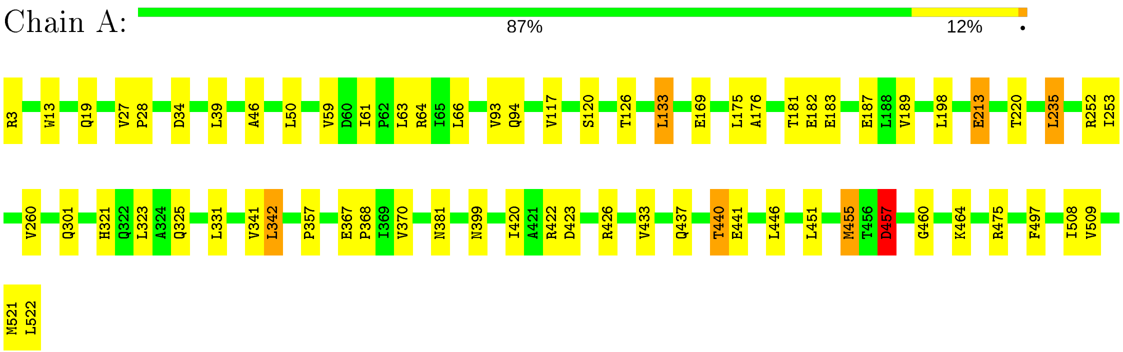
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	293	Total O 293 293	0	0

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 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.

- Molecule 1: TYROCIDINE SYNTHETASE 3



4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	84.97Å 84.97Å 164.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.81 – 1.85 19.82 – 1.85	Depositor EDS
% Data completeness (in resolution range)	98.6 (19.81-1.85) 98.6 (19.82-1.85)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.12 (at 1.85Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.208 , 0.238 0.214 , 0.244	Depositor DCC
R_{free} test set	1766 reflections (3.41%)	wwPDB-VP
Wilson B-factor (Å^2)	33.6	Xtriage
Anisotropy	0.131	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 53.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4477	wwPDB-VP
Average B, all atoms (Å^2)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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: NA, DIO, SO4

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	0.37	1/4259 (0.0%)	0.74	6/5783 (0.1%)

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	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	460	GLY	C-N	-7.94	1.15	1.34

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	457	ASP	CB-CG-OD2	-28.52	92.63	118.30
1	A	455	MET	O-C-N	-22.29	87.04	122.70
1	A	457	ASP	CB-CG-OD1	15.23	132.00	118.30
1	A	460	GLY	C-N-CA	6.67	138.37	121.70
1	A	455	MET	CA-C-N	5.61	129.54	117.20
1	A	460	GLY	O-C-N	-5.40	114.06	122.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	455	MET	Mainchain
1	A	457	ASP	Sidechain

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	4161	0	4084	41	0
2	A	10	0	0	0	0
3	A	12	0	16	1	0
4	A	1	0	0	0	0
5	A	293	0	0	1	0
All	All	4477	0	4100	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:508:ILE:HD12	1:A:509:VAL:N	2.01	0.76
1:A:117:VAL:HG12	1:A:120:SER:HB3	1.72	0.71
1:A:117:VAL:CG1	1:A:120:SER:HB3	2.21	0.70
1:A:323:LEU:CD2	1:A:508:ILE:HD13	2.23	0.69
1:A:117:VAL:HG12	1:A:117:VAL:O	1.95	0.66
1:A:220:THR:HG21	3:A:1525:DIO:H22	1.82	0.61
1:A:252:ARG:NH1	1:A:253:ILE:HD11	2.15	0.61
1:A:420:ILE:HG23	1:A:422:ARG:HB2	1.83	0.60
1:A:175:LEU:HD23	1:A:175:LEU:C	2.24	0.57
1:A:521:MET:O	1:A:522:LEU:HB2	2.05	0.57
1:A:446:LEU:HD13	1:A:451:LEU:HD11	1.85	0.57
1:A:508:ILE:HD12	1:A:508:ILE:C	2.26	0.56
1:A:3:ARG:NH2	1:A:28:PRO:O	2.38	0.55
1:A:3:ARG:NH2	1:A:27:VAL:HG12	2.22	0.53
1:A:126:THR:HG21	1:A:189:VAL:HG11	1.90	0.53
1:A:175:LEU:HD23	1:A:176:ALA:N	2.25	0.52
1:A:19:GLN:NE2	5:A:2020:HOH:O	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:LEU:HD13	1:A:497:PHE:CZ	2.47	0.49
1:A:3:ARG:NH2	1:A:27:VAL:CG1	2.77	0.48
1:A:175:LEU:HD23	1:A:176:ALA:C	2.34	0.48
1:A:126:THR:HG21	1:A:189:VAL:CG1	2.44	0.47
1:A:321:HIS:CE1	1:A:331:LEU:HD22	2.49	0.47
1:A:13:TRP:CH2	1:A:59:VAL:HG21	2.50	0.47
1:A:50:LEU:HD22	1:A:61:ILE:O	2.14	0.47
1:A:381:ASN:ND2	1:A:399:ASN:HD22	2.14	0.45
1:A:117:VAL:O	1:A:117:VAL:CG1	2.63	0.45
1:A:446:LEU:CD1	1:A:451:LEU:HD11	2.46	0.45
1:A:301:GLN:NE2	1:A:464:LYS:O	2.50	0.44
1:A:50:LEU:HD11	1:A:63:LEU:HA	2.00	0.44
1:A:34:ASP:HB3	1:A:39:LEU:HD11	2.00	0.44
1:A:367:GLU:N	1:A:368:PRO:CD	2.82	0.43
1:A:323:LEU:HD22	1:A:508:ILE:HD13	2.00	0.42
1:A:181:THR:HG22	1:A:182:GLU:N	2.35	0.41
1:A:213:GLU:N	1:A:213:GLU:CD	2.73	0.41
1:A:175:LEU:CD2	1:A:175:LEU:C	2.88	0.41
1:A:46:ALA:HB1	1:A:66:LEU:HD23	2.02	0.41
1:A:440:THR:HG22	1:A:440:THR:O	2.20	0.41
1:A:181:THR:HG22	1:A:183:GLU:H	1.85	0.40
1:A:357:PRO:HD3	1:A:433:VAL:HG13	2.02	0.40
1:A:93:VAL:HG11	1:A:260:VAL:HB	2.04	0.40
1:A:235:LEU:CD1	1:A:370:VAL:HG21	2.50	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	520/520 (100%)	489 (94%)	25 (5%)	6 (1%)	13	3

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	213	GLU
1	A	440	THR
1	A	441	GLU
1	A	133	LEU
1	A	475	ARG
1	A	423	ASP

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	452/450 (100%)	439 (97%)	13 (3%)	42	26

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

Mol	Chain	Res	Type
1	A	64	ARG
1	A	94	GLN
1	A	133	LEU
1	A	169	GLU
1	A	187	GLU
1	A	198	LEU
1	A	235	LEU
1	A	325	GLN
1	A	341	VAL
1	A	342	LEU
1	A	426	ARG
1	A	437	GLN
1	A	457	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	143	GLN

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Mol	Chain	Res	Type
1	A	267	GLN
1	A	280	GLN
1	A	325	GLN
1	A	381	ASN
1	A	427	ASN
1	A	500	HIS
1	A	510	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 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	$\#\|Z\| > 2$
2	SO4	A	1524	-	4,4,4	0.17	0	6,6,6	0.16	0
2	SO4	A	1523	-	4,4,4	0.13	0	6,6,6	0.11	0
3	DIO	A	1526	-	6,6,6	0.49	0	6,6,6	0.53	0
3	DIO	A	1525	-	6,6,6	0.49	0	6,6,6	0.47	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	DIO	A	1526	-	-	-	0/1/1/1
3	DIO	A	1525	-	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1525	DIO	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	460:GLY	C	461:GLN	N	1.15

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.