Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 12:27 pm BST

PDB ID	:	5XGB
Title	:	Crystal structure of the PAS-GGDEF-EAL domain of PA0861 from Pseudomonas aeruginosa
Authors	:	Liu, C.; Liew, C.W.; Sreekanth, R.; Lescar, J.
Deposited on	:	2017-04-13
Resolution	:	2.28 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 ①) were used in the production of this report:

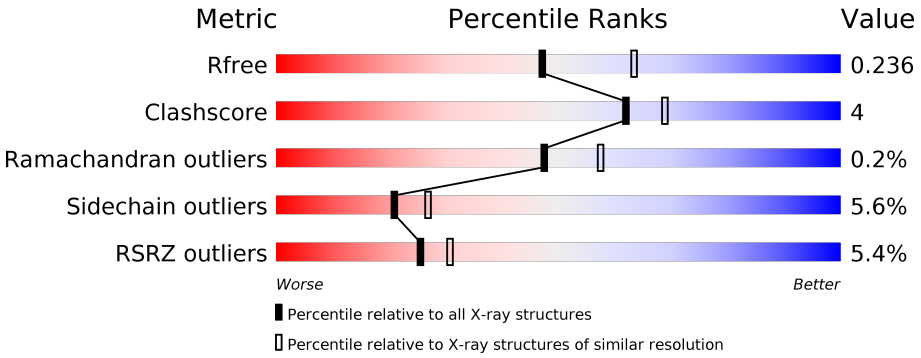
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.28 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	6980 (2.30-2.26)
Clashscore	141614	7711 (2.30-2.26)
Ramachandran outliers	138981	7597 (2.30-2.26)
Sidechain outliers	138945	7598 (2.30-2.26)
RSRZ outliers	127900	6849 (2.30-2.26)

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% 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	568	5% 84% 12%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4621 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 Uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	551	Total	C	N	O	S	0	0	0
			4318	2723	761	811	23			

- Molecule 2 is water.

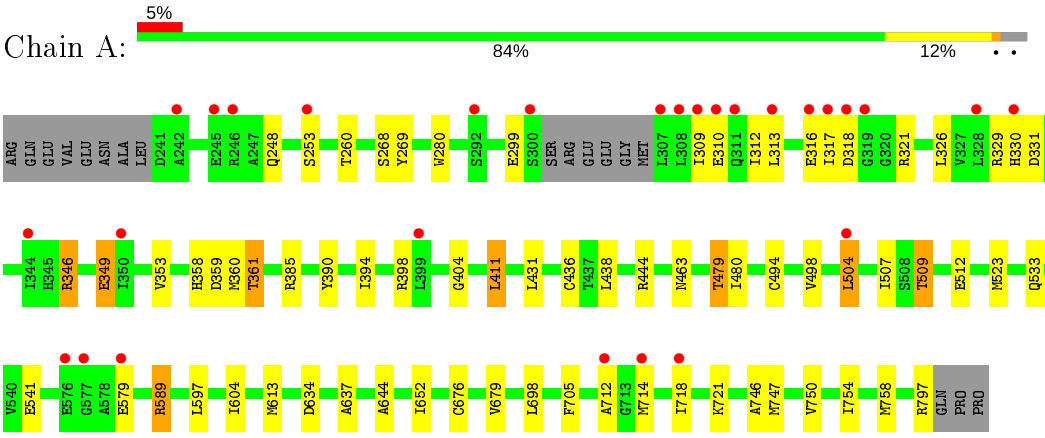
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	303	Total	O	0	0
			303	303		

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 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: Uncharacterized protein

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α, β, γ	134.72Å 134.72Å 210.45Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	70.15 – 2.28 70.15 – 2.28	Depositor EDS
% Data completeness (in resolution range)	100.0 (70.15-2.28) 100.0 (70.15-2.28)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.92 (at 2.27Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.193 , 0.229 0.193 , 0.236	Depositor DCC
R_{free} test set	818 reflections (2.43%)	wwPDB-VP
Wilson B-factor (Å^2)	37.4	Xtriage
Anisotropy	0.179	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 65.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4621	wwPDB-VP
Average B, all atoms (Å^2)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.52% 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

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	0.51	0/4395	0.68	0/5950

There are no bond length outliers.

There are no bond angle outliers.

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	4318	0	4303	38	0
2	A	303	0	0	0	0
All	All	4621	0	4303	38	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 (38) 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:358:HIS:HD2	1:A:360:MET:CE	1.95	0.78
1:A:358:HIS:CD2	1:A:360:MET:HE2	2.28	0.69
1:A:712:ALA:HB3	1:A:747:MET:SD	2.33	0.68
1:A:536:HIS:HB2	1:A:539:ASP:HB3	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:358:HIS:CD2	1:A:360:MET:CE	2.80	0.62
1:A:358:HIS:HD2	1:A:360:MET:HE2	1.60	0.61
1:A:312:ILE:HG22	1:A:317:ILE:HB	1.85	0.59
1:A:411:LEU:HB3	1:A:498:VAL:HG22	1.86	0.57
1:A:404:GLY:H	1:A:463:ASN:HD22	1.53	0.57
1:A:404:GLY:H	1:A:463:ASN:ND2	2.02	0.57
1:A:509:THR:HG22	1:A:512:GLU:H	1.70	0.56
1:A:721:LYS:HG2	1:A:758:MET:HE1	1.88	0.55
1:A:358:HIS:HD2	1:A:360:MET:HE1	1.71	0.55
1:A:313:LEU:HD22	1:A:341:GLY:HA3	1.91	0.53
1:A:346:ARG:HG2	1:A:349:GLU:HB2	1.91	0.52
1:A:313:LEU:HD13	1:A:353:VAL:HG21	1.93	0.51
1:A:746:ALA:O	1:A:750:VAL:HG23	2.11	0.51
1:A:260:THR:HB	1:A:269:TYR:HB3	1.94	0.50
1:A:652:ILE:HD11	1:A:679:VAL:HG11	1.93	0.49
1:A:589:ARG:HG2	1:A:597:LEU:HD22	1.93	0.49
1:A:310:GLU:HA	1:A:313:LEU:HD12	1.95	0.49
1:A:390:TYR:CZ	1:A:394:ILE:HD11	2.49	0.48
1:A:438:LEU:HD23	1:A:480:ILE:HD13	1.96	0.47
1:A:411:LEU:N	1:A:411:LEU:HD23	2.30	0.46
1:A:714:MET:O	1:A:718:ILE:HG12	2.16	0.45
1:A:431:LEU:HD11	1:A:494:CYS:SG	2.57	0.44
1:A:359:ASP:OD1	1:A:361:THR:HB	2.18	0.43
1:A:604:ILE:HG23	1:A:613:MET:HE3	2.00	0.43
1:A:644:ALA:HA	1:A:676:CYS:O	2.18	0.43
1:A:504:LEU:HD23	1:A:507:ILE:HB	2.00	0.43
1:A:358:HIS:CD2	1:A:360:MET:HE1	2.52	0.42
1:A:438:LEU:HG	1:A:479:THR:HG23	2.01	0.42
1:A:394:ILE:O	1:A:398:ARG:HB2	2.20	0.41
1:A:523:MET:HB3	1:A:533:GLN:HG2	2.03	0.41
1:A:754:ILE:O	1:A:758:MET:HG3	2.20	0.41
1:A:652:ILE:HD11	1:A:679:VAL:CG1	2.51	0.41
1:A:299:GLU:HA	1:A:326:LEU:HD11	2.03	0.41
1:A:634:ASP:HB3	1:A:637:ALA:HB2	2.03	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	547/568 (96%)	526 (96%)	20 (4%)	1 (0%)	47 57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	316	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	461/476 (97%)	435 (94%)	26 (6%)	21 27

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	248	GLN
1	A	253	SER
1	A	268	SER
1	A	280	TRP
1	A	309	ILE
1	A	318	ASP
1	A	321	ARG
1	A	329	ARG
1	A	330	HIS
1	A	331	ASP

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Mol	Chain	Res	Type
1	A	346	ARG
1	A	349	GLU
1	A	361	THR
1	A	385	ARG
1	A	411	LEU
1	A	436	CYS
1	A	444	ARG
1	A	479	THR
1	A	504	LEU
1	A	509	THR
1	A	541	GLU
1	A	579	GLU
1	A	589	ARG
1	A	698	LEU
1	A	705	PHE
1	A	797	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	358	HIS
1	A	373	GLN
1	A	425	HIS
1	A	463	ASN
1	A	481	GLN
1	A	493	ASN
1	A	583	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

There are no ligands in this entry.

5.7 Other polymers

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

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	551/568 (97%)	0.25	30 (5%) 25 31	23, 46, 94, 122	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	307	LEU	6.2
1	A	317	ILE	5.9
1	A	330	HIS	5.4
1	A	242	ALA	4.9
1	A	399	LEU	4.3
1	A	319	GLY	4.2
1	A	318	ASP	4.1
1	A	712	ALA	4.1
1	A	308	LEU	3.8
1	A	246	ARG	3.8
1	A	577	GLY	3.7
1	A	309	ILE	3.4
1	A	245	GLU	3.1
1	A	579	GLU	3.1
1	A	253	SER	3.1
1	A	333	SER	3.0
1	A	300	SER	3.0
1	A	313	LEU	3.0
1	A	350	ILE	2.8
1	A	344	ILE	2.7
1	A	718	ILE	2.7
1	A	292	SER	2.5
1	A	504	LEU	2.5
1	A	328	LEU	2.5
1	A	714	MET	2.4
1	A	576	GLU	2.3
1	A	310	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	539	ASP	2.2
1	A	316	GLU	2.2
1	A	311	GLN	2.1

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 carbohydrates 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.