



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 07:55 PM GMT

PDB ID : 4QD7
Title : Crystal structure of Thioesterase PA1618 from *Pseudomonas aeruginosa*
Authors : Ji, T.; Allen, K.N.; Dunaway-Mariano, D.
Deposited on : 2014-05-13
Resolution : 1.76 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

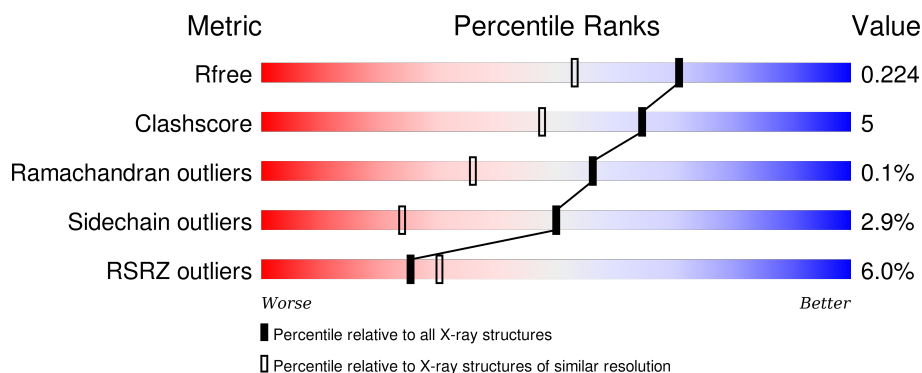
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.76 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}	91344	1609 (1.76-1.76)
Clashscore	102246	1730 (1.76-1.76)
Ramachandran outliers	100387	1711 (1.76-1.76)
Sidechain outliers	100360	1711 (1.76-1.76)
RSRZ outliers	91569	1610 (1.76-1.76)

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. 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	152	<div> <div>87%</div> <div>5% 9%</div> </div>
1	B	152	<div> <div>4%</div> <div>84%</div> <div>7% • 9%</div> </div>
1	C	152	<div> <div>6%</div> <div>82%</div> <div>7% • 9%</div> </div>
1	D	152	<div> <div>7%</div> <div>86%</div> <div>6% 9%</div> </div>
1	E	152	<div> <div>8%</div> <div>82%</div> <div>9% 9%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	152	<p>7% 80% 11% 9%</p>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6941 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 Thioesterase PA1618.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	139	Total	C	N	O	S	Se	0	4	0
			1070	666	194	204	3	3			
1	B	139	Total	C	N	O	S	Se	0	2	0
			1047	658	189	194	3	3			
1	C	139	Total	C	N	O	S	Se	0	0	0
			1053	654	192	201	3	3			
1	D	139	Total	C	N	O	S	Se	0	2	0
			1045	653	187	199	3	3			
1	E	139	Total	C	N	O	S	Se	0	1	0
			1048	654	191	197	3	3			
1	F	139	Total	C	N	O	S	Se	0	2	0
			1051	654	193	198	3	3			

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	EXPRESSION TAG	UNP Q9I3A4
A	145	LEU	-	EXPRESSION TAG	UNP Q9I3A4
A	146	GLU	-	EXPRESSION TAG	UNP Q9I3A4
A	147	HIS	-	EXPRESSION TAG	UNP Q9I3A4
A	148	HIS	-	EXPRESSION TAG	UNP Q9I3A4
A	149	HIS	-	EXPRESSION TAG	UNP Q9I3A4
A	150	HIS	-	EXPRESSION TAG	UNP Q9I3A4
A	151	HIS	-	EXPRESSION TAG	UNP Q9I3A4
A	152	HIS	-	EXPRESSION TAG	UNP Q9I3A4
B	1	MSE	-	EXPRESSION TAG	UNP Q9I3A4
B	145	LEU	-	EXPRESSION TAG	UNP Q9I3A4
B	146	GLU	-	EXPRESSION TAG	UNP Q9I3A4
B	147	HIS	-	EXPRESSION TAG	UNP Q9I3A4
B	148	HIS	-	EXPRESSION TAG	UNP Q9I3A4
B	149	HIS	-	EXPRESSION TAG	UNP Q9I3A4
B	150	HIS	-	EXPRESSION TAG	UNP Q9I3A4
B	151	HIS	-	EXPRESSION TAG	UNP Q9I3A4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	152	HIS	-	EXPRESSION TAG	UNP Q9I3A4
C	1	MSE	-	EXPRESSION TAG	UNP Q9I3A4
C	145	LEU	-	EXPRESSION TAG	UNP Q9I3A4
C	146	GLU	-	EXPRESSION TAG	UNP Q9I3A4
C	147	HIS	-	EXPRESSION TAG	UNP Q9I3A4
C	148	HIS	-	EXPRESSION TAG	UNP Q9I3A4
C	149	HIS	-	EXPRESSION TAG	UNP Q9I3A4
C	150	HIS	-	EXPRESSION TAG	UNP Q9I3A4
C	151	HIS	-	EXPRESSION TAG	UNP Q9I3A4
C	152	HIS	-	EXPRESSION TAG	UNP Q9I3A4
D	1	MSE	-	EXPRESSION TAG	UNP Q9I3A4
D	145	LEU	-	EXPRESSION TAG	UNP Q9I3A4
D	146	GLU	-	EXPRESSION TAG	UNP Q9I3A4
D	147	HIS	-	EXPRESSION TAG	UNP Q9I3A4
D	148	HIS	-	EXPRESSION TAG	UNP Q9I3A4
D	149	HIS	-	EXPRESSION TAG	UNP Q9I3A4
D	150	HIS	-	EXPRESSION TAG	UNP Q9I3A4
D	151	HIS	-	EXPRESSION TAG	UNP Q9I3A4
D	152	HIS	-	EXPRESSION TAG	UNP Q9I3A4
E	1	MSE	-	EXPRESSION TAG	UNP Q9I3A4
E	145	LEU	-	EXPRESSION TAG	UNP Q9I3A4
E	146	GLU	-	EXPRESSION TAG	UNP Q9I3A4
E	147	HIS	-	EXPRESSION TAG	UNP Q9I3A4
E	148	HIS	-	EXPRESSION TAG	UNP Q9I3A4
E	149	HIS	-	EXPRESSION TAG	UNP Q9I3A4
E	150	HIS	-	EXPRESSION TAG	UNP Q9I3A4
E	151	HIS	-	EXPRESSION TAG	UNP Q9I3A4
E	152	HIS	-	EXPRESSION TAG	UNP Q9I3A4
F	1	MSE	-	EXPRESSION TAG	UNP Q9I3A4
F	145	LEU	-	EXPRESSION TAG	UNP Q9I3A4
F	146	GLU	-	EXPRESSION TAG	UNP Q9I3A4
F	147	HIS	-	EXPRESSION TAG	UNP Q9I3A4
F	148	HIS	-	EXPRESSION TAG	UNP Q9I3A4
F	149	HIS	-	EXPRESSION TAG	UNP Q9I3A4
F	150	HIS	-	EXPRESSION TAG	UNP Q9I3A4
F	151	HIS	-	EXPRESSION TAG	UNP Q9I3A4
F	152	HIS	-	EXPRESSION TAG	UNP Q9I3A4

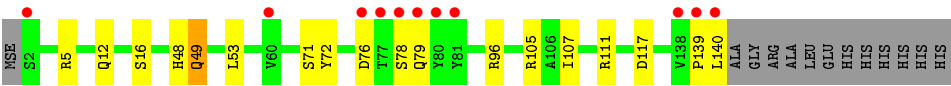
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	118	Total O 118 118	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	105	Total 105	O 105	0	0
2	C	96	Total 96	O 96	0	0
2	D	125	Total 125	O 125	0	0
2	E	91	Total 91	O 91	0	0
2	F	92	Total 92	O 92	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	101.65Å 202.51Å 90.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.87 – 1.76 37.63 – 1.72	Depositor EDS
% Data completeness (in resolution range)	99.5 (35.87-1.76) 97.9 (37.63-1.72)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.60 (at 1.72Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.207 , 0.226 0.205 , 0.224	Depositor DCC
R_{free} test set	1891 reflections (2.06%)	DCC
Wilson B-factor (Å ²)	17.8	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 52.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 97075 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6941	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 45.90 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.2375e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.39	0/1081	0.59	0/1458
1	B	0.37	0/1066	0.58	0/1438
1	C	0.36	0/1067	0.55	0/1444
1	D	0.38	0/1056	0.61	0/1429
1	E	0.33	0/1062	0.52	0/1437
1	F	0.36	0/1061	0.55	0/1436
All	All	0.37	0/6393	0.57	0/8642

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 [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	1070	0	1038	6	0
1	B	1047	0	1031	8	0
1	C	1053	0	1041	8	0
1	D	1045	0	1001	9	0
1	E	1048	0	1029	11	0
1	F	1051	0	1017	24	0
2	A	118	0	0	0	4
2	B	105	0	0	0	0
2	C	96	0	0	0	0
2	D	125	0	0	1	3

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	91	0	0	1	0
2	F	92	0	0	4	0
All	All	6941	0	6157	63	4

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.

The worst 5 of 63 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:F:72:TYR:CZ	1:F:72:TYR:CD1	2.39	1.09
1:B:72:TYR:CG	1:B:72:TYR:CE2	2.41	1.02
1:D:72:TYR:CE2	1:D:72:TYR:CG	2.43	0.97
1:A:28:ARG:CD	1:A:28:ARG:CZ	2.47	0.92
1:F:72:TYR:CB	1:F:72:TYR:CD1	2.53	0.92

All (4) 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)
2:A:307:HOH:O	2:D:322:HOH:O[3_655]	1.99	0.21
2:A:264:HOH:O	2:A:265:HOH:O[4_566]	2.04	0.16
2:A:307:HOH:O	2:D:319:HOH:O[3_655]	2.10	0.10
2:A:298:HOH:O	2:D:322:HOH:O[3_655]	2.10	0.10

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	141/152 (93%)	138 (98%)	3 (2%)	0	100	100
1	B	139/152 (91%)	137 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	137/152 (90%)	135 (98%)	2 (2%)	0	100	100
1	D	139/152 (91%)	136 (98%)	3 (2%)	0	100	100
1	E	138/152 (91%)	135 (98%)	3 (2%)	0	100	100
1	F	140/152 (92%)	136 (97%)	3 (2%)	1 (1%)	26	10
All	All	834/912 (91%)	817 (98%)	16 (2%)	1 (0%)	56	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	139	PRO

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	113/121 (93%)	111 (98%)	2 (2%)	66	46
1	B	111/121 (92%)	108 (97%)	3 (3%)	52	27
1	C	114/121 (94%)	109 (96%)	5 (4%)	35	11
1	D	107/121 (88%)	105 (98%)	2 (2%)	65	43
1	E	111/121 (92%)	107 (96%)	4 (4%)	42	16
1	F	107/121 (88%)	104 (97%)	3 (3%)	51	25
All	All	663/726 (91%)	644 (97%)	19 (3%)	50	24

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	138	VAL
1	D	49	GLN
1	E	83	VAL
1	C	49	GLN
1	F	49	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

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 [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	136/152 (89%)	-0.03	1 (0%) 89 92	11, 18, 28, 35	0
1	B	136/152 (89%)	0.30	6 (4%) 38 44	12, 21, 33, 40	0
1	C	136/152 (89%)	0.49	9 (6%) 22 27	13, 24, 39, 50	0
1	D	136/152 (89%)	0.27	10 (7%) 17 23	10, 17, 40, 48	0
1	E	136/152 (89%)	0.55	12 (8%) 12 15	16, 26, 38, 45	0
1	F	136/152 (89%)	0.42	11 (8%) 15 18	13, 22, 46, 58	0
All	All	816/912 (89%)	0.33	49 (6%) 25 30	10, 21, 37, 58	0

The worst 5 of 49 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	2	SER	8.1
1	D	140	LEU	5.4
1	F	78	SER	5.4
1	F	139	PRO	5.3
1	F	140	LEU	5.2

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 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.