wwPDB X-ray Structure Validation Summary Report (i)

Jun 23, 2024 – 02:40 AM EDT

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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

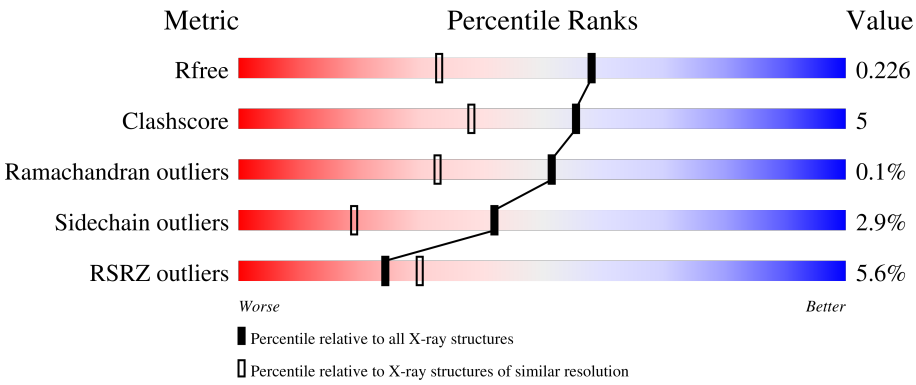
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

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}	130704	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (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 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	152	%, 87%, 5%, 9%
1	B	152	3%, 84%, 7%, •, 9%
1	C	152	6%, 82%, 7%, •, 9%
1	D	152	7%, 86%, 6%, 9%
1	E	152	7%, 82%, 9%, 9%

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Mol	Chain	Length	Quality of chain
1	F	152	7% 80% 11% • 9%

2 Entry composition (i)

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

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
			Total	O		
2	A	118	118	118	0	0

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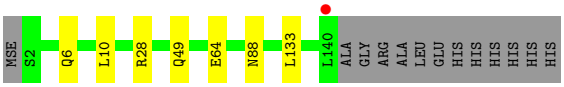
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	B	105	105	105	0	0
			Total	O		
2	C	96	96	96	0	0
			Total	O		
2	D	125	125	125	0	0
			Total	O		
2	E	91	91	91	0	0
			Total	O		
2	F	92	92	92	0	0

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.

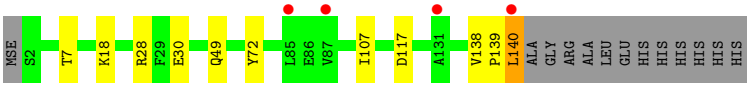
• Molecule 1: Thioesterase PA1618

Chain A:



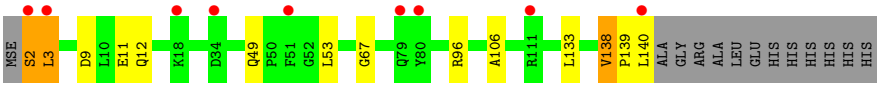
• Molecule 1: Thioesterase PA1618

Chain B:



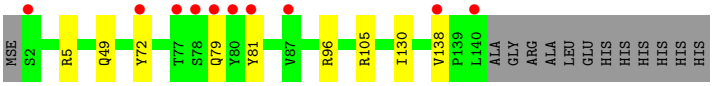
• Molecule 1: Thioesterase PA1618

Chain C:



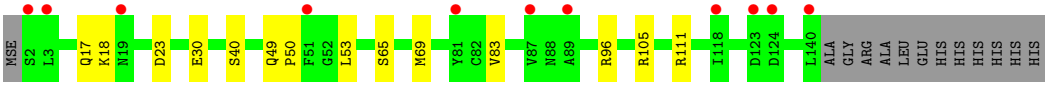
• Molecule 1: Thioesterase PA1618

Chain D:



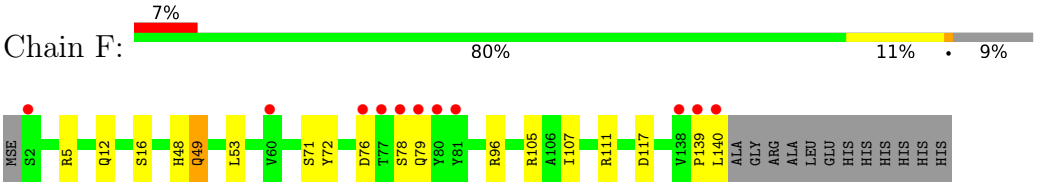
• Molecule 1: Thioesterase PA1618

Chain E:



• Molecule 1: Thioesterase PA1618

Chain F:


7%
80%
11%
9%
MSE
S2
R5
Q12
S16
H48
Q49
L53
V60
S71
Y72
D76
T77
S78
Q79
Y80
Y81
R96
R105
A106
I107
R111
D117
V138
P139
L140
ALA
GLY
ARG
ALA
LEU
GLU
HIS
HIS
HIS
HIS
HIS
HIS

4 Data and refinement statistics (i)

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
$< I/\sigma(I) >$ [1]	1.60 (at 1.72Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.207 , 0.226 0.207 , 0.226	Depositor DCC
R_{free} test set	2000 reflections (2.06%)	wwPDB-VP
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
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	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 $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (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:CE2	1:B:72:TYR:CG	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:CD1	1:F:72:TYR:CB	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:298:HOH:O	2:D:322:HOH:O[3_655]	2.10	0.10
2:A:307:HOH:O	2:D:319: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%)	22	8
All	All	834/912 (91%)	817 (98%)	16 (2%)	1 (0%)	51	33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	139	PRO

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	113/121 (93%)	111 (98%)	2 (2%)	59	40
1	B	111/121 (92%)	108 (97%)	3 (3%)	44	22
1	C	114/121 (94%)	109 (96%)	5 (4%)	28	8
1	D	107/121 (88%)	105 (98%)	2 (2%)	57	37
1	E	111/121 (92%)	107 (96%)	4 (4%)	35	13
1	F	107/121 (88%)	104 (97%)	3 (3%)	43	20
All	All	663/726 (91%)	644 (97%)	19 (3%)	42	19

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

Mol	Chain	Res	Type
1	E	65	SER
1	F	71	SER
1	F	140	LEU
1	F	49	GLN
1	C	138	VAL

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

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 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 (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%)	-0.06	1 (0%)	87	92	11, 18, 28, 35	0
1	B	136/152 (89%)	0.27	4 (2%)	51	57	12, 21, 33, 40	0
1	C	136/152 (89%)	0.46	9 (6%)	18	24	13, 24, 39, 50	0
1	D	136/152 (89%)	0.24	10 (7%)	14	19	10, 17, 40, 48	0
1	E	136/152 (89%)	0.52	11 (8%)	12	16	16, 26, 38, 45	0
1	F	136/152 (89%)	0.40	11 (8%)	12	16	13, 22, 46, 58	0
All	All	816/912 (89%)	0.31	46 (5%)	24	30	10, 21, 37, 58	0

The worst 5 of 46 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	2	SER	8.0
1	F	78	SER	5.4
1	D	140	LEU	5.4
1	F	139	PRO	5.3
1	F	140	LEU	5.1

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 monosaccharides 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.