



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 01:59 am GMT

PDB ID : 3PV2  
Title : Structure of Legionella fallonii DegQ (wt)  
Authors : Wrase, R.; Scott, H.; Hilgenfeld, R.; Hansen, G.  
Deposited on : 2010-12-06  
Resolution : 2.15 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

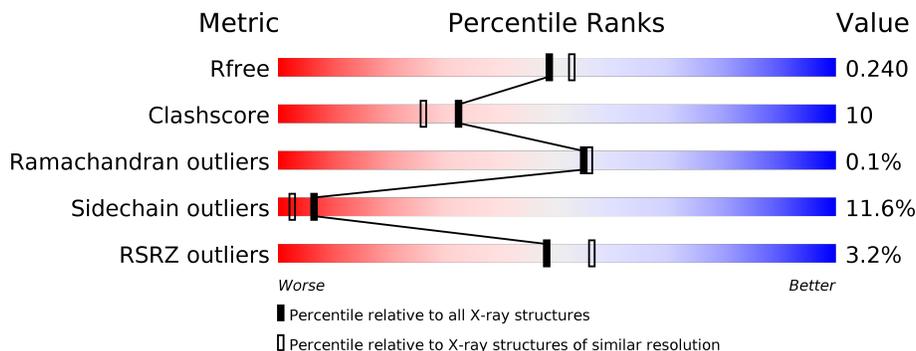
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.15 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))
$R_{free}$	100719	1170 (2.16-2.16)
Clashscore	112137	1278 (2.16-2.16)
Ramachandran outliers	110173	1256 (2.16-2.16)
Sidechain outliers	110143	1255 (2.16-2.16)
RSRZ outliers	101464	1175 (2.16-2.16)

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  $\geq 3$ , 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	451	
1	B	451	
1	C	451	
1	D	451	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12098 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 DegQ.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	384	Total 2895	C 1838	N 504	O 546	S 7	0	4	0
1	B	388	Total 2925	C 1856	N 509	O 554	S 6	0	4	0
1	C	388	Total 2922	C 1852	N 512	O 551	S 7	0	4	0
1	D	383	Total 2888	C 1833	N 502	O 546	S 7	0	4	0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	123	Total 123	O 123	0	0
2	B	128	Total 128	O 128	0	0
2	C	105	Total 105	O 105	0	0
2	D	112	Total 112	O 112	0	0





## 4 Data and refinement statistics i

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	136.70Å 136.70Å 327.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	36.93 – 2.15 36.93 – 2.15	Depositor EDS
% Data completeness (in resolution range)	98.1 (36.93-2.15) 98.1 (36.93-2.15)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.04	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.87 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, $R_{free}$	0.211 , 0.251 0.202 , 0.240	Depositor DCC
$R_{free}$ test set	6107 reflections (5.29%)	DCC
Wilson B-factor (Å <sup>2</sup> )	36.7	Xtriage
Anisotropy	0.575	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 42.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.004 for -h,1/3*h-1/3*k-1/3*l,-4/3*h-8/3*k +1/3*l 0.005 for -1/3*h+1/3*k+1/3*l,-k,8/3*h+4/ 3*k+1/3*l 0.007 for -2/3*h-1/3*k-1/3*l,-1/3*h-2/3*k+ 1/3*l,-4/3*h+4/3*k+1/3*l 0.003 for 1/3*h+2/3*k-1/3*l,-k,-8/3*h-4/3* k-1/3*l 0.004 for -1/3*h-2/3*k+1/3*l,-2/3*h-1/3*k- 1/3*l,4/3*h-4/3*k-1/3*l 0.002 for -h,2/3*h+1/3*k+1/3*l,4/3*h+8/3 *k-1/3*l 0.018 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	12098	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.00% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  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	1.04	0/2932	1.00	4/3971 (0.1%)
1	B	1.01	0/2964	0.95	1/4015 (0.0%)
1	C	0.93	0/2959	0.91	2/4006 (0.0%)
1	D	0.95	0/2925	0.94	1/3961 (0.0%)
All	All	0.98	0/11780	0.95	8/15953 (0.1%)

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	145	ILE	CB-CA-C	-5.73	100.13	111.60
1	C	327	ARG	NE-CZ-NH2	-5.69	117.46	120.30
1	C	102	LEU	CA-CB-CG	5.51	127.98	115.30
1	D	436	LEU	CA-CB-CG	5.29	127.47	115.30
1	A	436	LEU	CA-CB-CG	5.22	127.31	115.30

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	2895	0	3022	77	0
1	B	2925	0	3044	40	0
1	C	2922	0	3047	62	0
1	D	2888	0	3011	65	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	123	0	0	0	0
2	B	128	0	0	2	0
2	C	105	0	0	4	0
2	D	112	0	0	4	0
All	All	12098	0	12124	237	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 10.

The worst 5 of 237 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:D:72:ILE:HD13	1:D:80:ILE:CD1	1.74	1.17
1:A:72:ILE:CD1	1:A:80:ILE:HD11	1.74	1.16
1:A:72:ILE:HD13	1:A:80:ILE:HD11	1.19	1.11
1:D:72:ILE:HD13	1:D:80:ILE:HD11	1.32	1.08
1:A:72:ILE:HD13	1:A:80:ILE:CD1	1.86	1.04

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	378/451 (84%)	373 (99%)	5 (1%)	0	100 100
1	B	384/451 (85%)	376 (98%)	6 (2%)	2 (0%)	32 25
1	C	382/451 (85%)	369 (97%)	13 (3%)	0	100 100
1	D	377/451 (84%)	370 (98%)	5 (1%)	2 (0%)	32 25
All	All	1521/1804 (84%)	1488 (98%)	29 (2%)	4 (0%)	55 41

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	190[A]	PRO
1	D	190[B]	PRO
1	B	190[A]	PRO
1	B	190[B]	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	319/372 (86%)	283 (89%)	36 (11%)	7 2
1	B	322/372 (87%)	292 (91%)	30 (9%)	10 5
1	C	321/372 (86%)	282 (88%)	39 (12%)	6 2
1	D	318/372 (86%)	274 (86%)	44 (14%)	4 1
All	All	1280/1488 (86%)	1131 (88%)	149 (12%)	6 2

5 of 149 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	26	GLN
1	C	219	VAL
1	D	313	SER
1	C	91	LEU
1	C	145	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	349	GLN
1	C	97	GLN
1	D	307	GLN
1	C	15	ASN
1	C	22	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](#)

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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	384/451 (85%)	-0.27	9 (2%) 61 68	31, 46, 76, 117	0
1	B	388/451 (86%)	-0.17	9 (2%) 61 68	31, 48, 78, 133	0
1	C	388/451 (86%)	0.01	23 (5%) 23 30	32, 53, 96, 112	0
1	D	383/451 (84%)	-0.14	9 (2%) 61 68	34, 51, 79, 117	0
All	All	1543/1804 (85%)	-0.14	50 (3%) 48 56	31, 49, 87, 133	0

The worst 5 of 50 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	29	LEU	6.6
1	B	61	ARG	5.6
1	A	61	ARG	5.4
1	C	31	ASN	5.3
1	D	211	ILE	5.0

### 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.