



# wwPDB X-ray Structure Validation Summary Report

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PDB ID : 2GL2 / pdb\_00002gl2  
Title : Crystal structure of the tetra mutant (T66G,R67G,F68G,Y69G) of bacterial adhesin FadA  
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Deposited on : 2006-04-04  
Resolution : 2.50 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the  symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

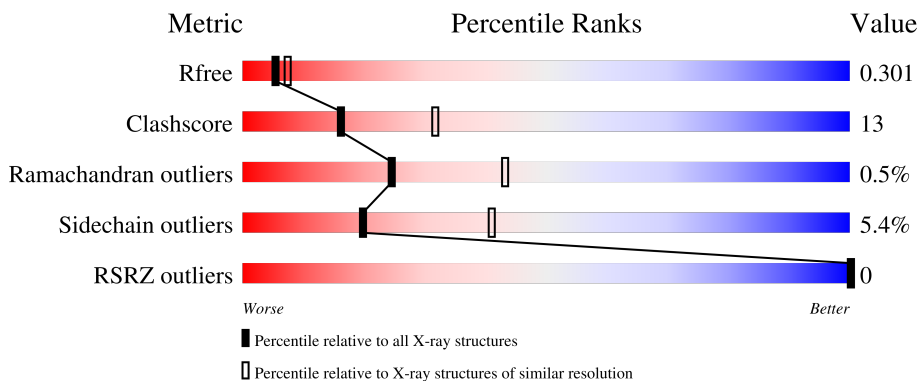
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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))
$R_{free}$	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	119	 62% 21% 13%
1	B	119	 63% 27% 8%

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1912 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 adhesion A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	103	815	496	147	171	1	0	0	0
1	B	109	874	531	163	179	1	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	66	GLY	THR	engineered mutation	GB 57117488
A	67	GLY	ARG	engineered mutation	GB 57117488
A	68	GLY	PHE	engineered mutation	GB 57117488
A	69	GLY	TYR	engineered mutation	GB 57117488
A	112	LEU	-	expression tag	GB 57117488
A	113	GLU	-	expression tag	GB 57117488
A	114	HIS	-	expression tag	GB 57117488
A	115	HIS	-	expression tag	GB 57117488
A	116	HIS	-	expression tag	GB 57117488
A	117	HIS	-	expression tag	GB 57117488
A	118	HIS	-	expression tag	GB 57117488
A	119	HIS	-	expression tag	GB 57117488
B	66	GLY	THR	engineered mutation	GB 57117488
B	67	GLY	ARG	engineered mutation	GB 57117488
B	68	GLY	PHE	engineered mutation	GB 57117488
B	69	GLY	TYR	engineered mutation	GB 57117488
B	112	LEU	-	expression tag	GB 57117488
B	113	GLU	-	expression tag	GB 57117488
B	114	HIS	-	expression tag	GB 57117488
B	115	HIS	-	expression tag	GB 57117488
B	116	HIS	-	expression tag	GB 57117488
B	117	HIS	-	expression tag	GB 57117488
B	118	HIS	-	expression tag	GB 57117488
B	119	HIS	-	expression tag	GB 57117488

- Molecule 2 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
2	A	109	Total 109	O 109	0	0
2	B	114	Total 114	O 114	0	0



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	59.17Å 59.17Å 188.25Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.20 – 2.50 29.20 – 2.50	Depositor EDS
% Data completeness (in resolution range)	89.1 (29.20-2.50) 89.5 (29.20-2.50)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.31 (at 2.51Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.232 , 0.307 0.230 , 0.301	Depositor DCC
$R_{free}$ test set	1182 reflections (10.30%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	40.4	Xtrriage
Anisotropy	0.542	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 26.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	0.165 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	1912	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.15% 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	0.46	0/819	0.75	0/1098
1	B	0.44	0/883	0.77	0/1185
All	All	0.45	0/1702	0.76	0/2283

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	815	0	783	19	0
1	B	874	0	824	27	0
2	A	109	0	0	2	0
2	B	114	0	0	8	0
All	All	1912	0	1607	43	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 13.

The worst 5 of 43 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:B:61:GLN:HE22	1:B:74:GLN:HG2	1.48	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:76:LEU:HA	1:B:79:LYS:HE3	1.73	0.71
1:A:15:ASP:O	1:A:19:GLN:HG2	1.95	0.66
1:B:94:GLN:O	1:B:98:ILE:HG13	1.99	0.63
1:A:93:GLN:HG3	1:B:31:GLU:HG3	1.81	0.63

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	99/119 (83%)	94 (95%)	4 (4%)	1 (1%)	12	24
1	B	105/119 (88%)	104 (99%)	1 (1%)	0	100	100
All	All	204/238 (86%)	198 (97%)	5 (2%)	1 (0%)	24	43

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	62	ALA

### 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	80/91 (88%)	76 (95%)	4 (5%)	22	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	86/91 (94%)	81 (94%)	5 (6%)	18	38
All	All	166/182 (91%)	157 (95%)	9 (5%)	20	41

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	116	HIS
1	B	118	HIS
1	A	53	LEU
1	B	25	GLU
1	B	28	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	41	GLN
1	B	46	ASN
1	B	93	GLN
1	B	61	GLN
1	B	74	GLN

### 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 oligosaccharides 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	103/119 (86%)	-1.37	0 <a href="#">100</a> <a href="#">100</a>	21, 39, 74, 92	0
1	B	109/119 (91%)	-1.37	0 <a href="#">100</a> <a href="#">100</a>	21, 46, 76, 95	0
All	All	212/238 (89%)	-1.37	0 <a href="#">100</a> <a href="#">100</a>	21, 41, 76, 95	0

There are no RSRZ outliers to report.

### 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 oligosaccharides 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.