



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:53 PM GMT

PDB ID : 4U65  
Title : Structure of the periplasmic output domain of the Legionella pneumophila LapD ortholog CdgS9 in complex with Pseudomonas fluorescens LapG  
Authors : Chatterjee, D.; Cooley, R.B.; Boyd, C.D.; Mehl, R.A.; O'Toole, G.A.; Sondermann, H.S.  
Deposited on : 2014-07-27  
Resolution : 2.10 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](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  
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

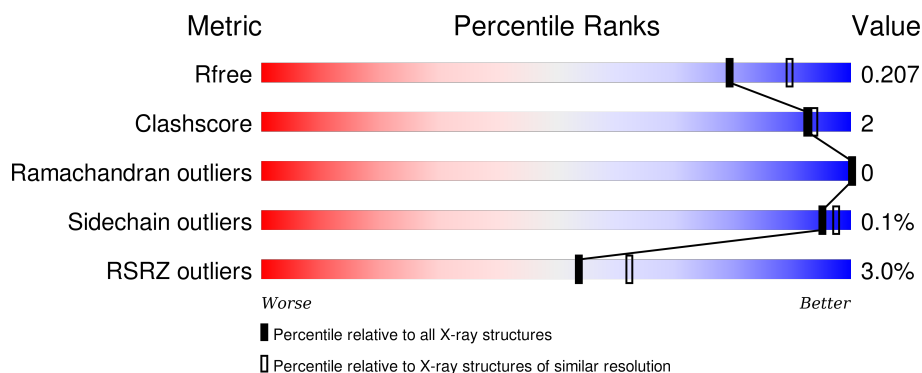
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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	131	<div> <div>3%</div> <div>95%</div> <div>5%</div> </div>
1	B	131	<div> <div>5%</div> <div>89%</div> <div>11%</div> </div>
1	C	131	<div> <div>96%</div> <div>.</div> </div>
1	D	131	<div> <div>9%</div> <div>95%</div> <div>5%</div> <div>.</div> </div>
2	E	197	<div> <div>%</div> <div>89%</div> <div>8%</div> <div>.</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	197	<div><div></div><div>2%</div><div>90%</div><div>8%</div></div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7826 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 Two component histidine kinase, GGDEF domain protein/EAL domain protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	131	Total	C	N	O	S	0	2	0
			1056	678	174	198	6			
1	B	131	Total	C	N	O	S	0	2	0
			1054	676	172	200	6			
1	C	131	Total	C	N	O	S	0	0	0
			1042	670	170	196	6			
1	D	131	Total	C	N	O	S	0	2	0
			1054	676	172	200	6			

- Molecule 2 is a protein called Putative cystine protease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	181	Total	C	N	O	S	0	2	0
			1474	948	248	272	6			
2	F	181	Total	C	N	O	S	0	0	0
			1465	945	246	268	6			

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	F	2	Total	Ca	0	0
			2	2		
3	E	2	Total	Ca	0	0
			2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	113	Total	O	0	0
			113	113		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	70	Total 70	O 70	0	0
4	C	120	Total 120	O 120	0	0
4	D	68	Total 68	O 68	0	0
4	E	163	Total 163	O 163	0	0
4	F	143	Total 143	O 143	0	0

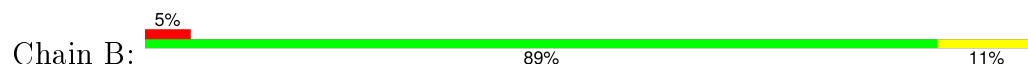
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Two component histidine kinase, GGDEF domain protein/EAL domain protein



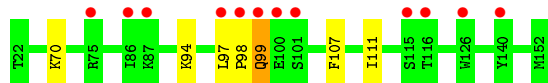
- Molecule 1: Two component histidine kinase, GGDEF domain protein/EAL domain protein



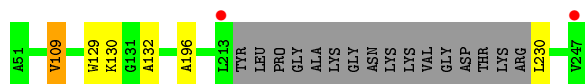
- Molecule 1: Two component histidine kinase, GGDEF domain protein/EAL domain protein



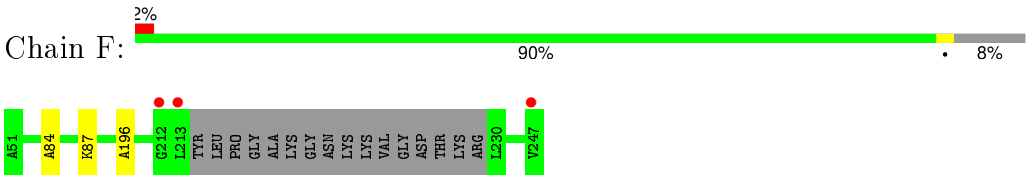
- Molecule 1: Two component histidine kinase, GGDEF domain protein/EAL domain protein



- Molecule 2: Putative cystine protease



- Molecule 2: Putative cystine protease



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.85Å 73.67Å 88.22Å 90.00° 92.88° 90.00°	Depositor
Resolution (Å)	44.06 – 2.10 46.02 – 2.10	Depositor EDS
% Data completeness (in resolution range)	97.6 (44.06-2.10) 92.8 (46.02-2.10)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.95 (at 2.10Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, $R_{free}$	0.170 , 0.211 0.170 , 0.207	Depositor DCC
$R_{free}$ test set	1889 reflections (3.57%)	DCC
Wilson B-factor (Å <sup>2</sup> )	23.7	Xtriage
Anisotropy	0.582	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 58.5	EDS
Estimated twinning fraction	0.015 for k,h,-l 0.014 for -k,-h,-l 0.106 for h,-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 55781 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7826	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.60% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA

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	0.27	0/1082	0.47	0/1467
1	B	0.26	0/1077	0.52	0/1461
1	C	0.25	0/1065	0.46	0/1445
1	D	0.27	0/1077	0.47	0/1461
2	E	0.24	0/1510	0.41	0/2048
2	F	0.24	0/1501	0.43	0/2036
All	All	0.25	0/7312	0.46	0/9918

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	98	PRO	Peptide
1	D	99	GLN	Peptide

## 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	1056	0	1057	6	0
1	B	1054	0	1048	12	0
1	C	1042	0	1040	4	0
1	D	1054	0	1048	6	0
2	E	1474	0	1448	5	0
2	F	1465	0	1449	2	0
3	E	2	0	0	0	0
3	F	2	0	0	0	0
4	A	113	0	0	0	0
4	B	70	0	0	0	0
4	C	120	0	0	0	0
4	D	68	0	0	0	0
4	E	163	0	0	0	0
4	F	143	0	0	0	0
All	All	7826	0	7090	29	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 2.

All (29) 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:70:LYS:HG3	1:B:94:LYS:HE3	1.73	0.71
1:A:33:PHE:HZ	1:B:148:ASN:HD22	1.41	0.67
1:D:97:LEU:HB3	1:D:99:GLN:OE1	1.99	0.63
1:B:116:THR:HG21	1:B:136:SER:HB2	1.85	0.59
1:D:70:LYS:HG3	1:D:94:LYS:HE2	1.85	0.58
1:B:85:ASP:HB3	1:B:91:ILE:HD11	1.85	0.57
1:A:33:PHE:HZ	1:B:148:ASN:ND2	2.03	0.56
1:A:126:TRP:CD2	2:E:196:ALA:HB1	2.42	0.54
1:C:126:TRP:CD2	2:F:196:ALA:HB1	2.42	0.54
1:B:101:SER:HA	1:B:102:ASP:CB	2.39	0.53
1:C:53:LEU:HD22	1:C:65:MET:HG3	1.91	0.52
1:B:101:SER:HA	1:B:102:ASP:HB3	1.92	0.51
1:B:104:PRO:HB2	1:B:106:TRP:CD1	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:109:VAL:HG13	2:E:132:ALA:HB1	1.93	0.50
1:C:65:MET:HG2	1:C:92:ILE:HD12	1.94	0.49
1:B:77:TYR:HE2	2:E:230:LEU:HB3	1.78	0.49
1:D:99:GLN:O	1:D:99:GLN:HG2	2.14	0.47
1:B:99:GLN:N	1:B:99:GLN:OE1	2.49	0.45
1:C:66:ASP:HA	1:C:92:ILE:HD13	1.99	0.44
1:B:34:PHE:CD1	1:B:141:VAL:HG22	2.53	0.44
1:D:99:GLN:OE1	1:D:99:GLN:N	2.43	0.43
1:A:53:LEU:HD22	1:A:65:MET:HG3	1.99	0.43
1:D:107:PHE:CE2	1:D:111:ILE:HD13	2.54	0.43
1:A:78:PHE:O	1:A:96:GLN:NE2	2.44	0.41
1:A:33:PHE:CZ	1:B:148:ASN:ND2	2.83	0.41
1:D:99:GLN:H	1:D:99:GLN:CD	2.23	0.41
2:F:84:ALA:HA	2:F:87:LYS:HE3	2.02	0.41
2:E:129:TRP:CZ3	2:E:130:LYS:HE2	2.56	0.40
2:E:230:LEU:HA	2:E:230:LEU:HD12	1.92	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	131/131 (100%)	129 (98%)	2 (2%)	0	100	100
1	B	131/131 (100%)	128 (98%)	3 (2%)	0	100	100
1	C	129/131 (98%)	128 (99%)	1 (1%)	0	100	100
1	D	131/131 (100%)	129 (98%)	2 (2%)	0	100	100
2	E	179/197 (91%)	176 (98%)	3 (2%)	0	100	100
2	F	177/197 (90%)	172 (97%)	5 (3%)	0	100	100
All	All	878/918 (96%)	862 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	120/118 (102%)	120 (100%)	0	100	100
1	B	120/118 (102%)	120 (100%)	0	100	100
1	C	118/118 (100%)	118 (100%)	0	100	100
1	D	120/118 (102%)	120 (100%)	0	100	100
2	E	155/166 (93%)	154 (99%)	1 (1%)	90	94
2	F	154/166 (93%)	154 (100%)	0	100	100
All	All	787/804 (98%)	786 (100%)	1 (0%)	95	97

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	109	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	84	GLN

### 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 [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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 ⓘ

### 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<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	131/131 (100%)	-0.02	4 (3%) 52 61	18, 28, 57, 87	0
1	B	131/131 (100%)	0.31	6 (4%) 36 45	22, 40, 70, 86	0
1	C	131/131 (100%)	-0.22	0 100 100	18, 28, 49, 70	0
1	D	131/131 (100%)	0.29	12 (9%) 11 15	22, 40, 75, 98	0
2	E	181/197 (91%)	-0.32	2 (1%) 82 86	17, 26, 51, 74	0
2	F	181/197 (91%)	-0.29	3 (1%) 73 78	16, 26, 49, 78	0
All	All	886/918 (96%)	-0.07	27 (3%) 54 62	16, 29, 62, 98	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	77	TYR	7.2
1	B	116	THR	6.8
1	D	99	GLN	5.3
1	D	116	THR	5.3
2	F	212	GLY	4.7
2	F	247	VAL	4.4
2	F	213	LEU	4.2
1	A	98	PRO	4.1
1	D	140	TYR	4.1
1	A	97	LEU	4.0
1	A	99	GLN	3.7
1	B	115	SER	3.6
1	B	126	TRP	3.3
1	B	113	TRP	3.3
1	D	86	ILE	3.3
1	D	98	PRO	3.1
1	D	87	LYS	3.1
1	D	115	SER	3.0
1	D	126	TRP	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	33	PHE	2.8
1	D	100	GLU	2.5
2	E	247	VAL	2.5
1	B	114	PRO	2.4
1	D	97	LEU	2.3
2	E	213	LEU	2.2
1	D	101	SER	2.0
1	D	75	ARG	2.0

## 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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	CA	E	302	1/1	0.97	0.07	-2.65	36,36,36,36	0
3	CA	F	302	1/1	0.99	0.05	-3.77	35,35,35,35	0
3	CA	F	301	1/1	0.99	0.04	-4.25	36,36,36,36	0
3	CA	E	301	1/1	0.99	0.06	-5.71	32,32,32,32	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.