



# wwPDB X-ray Structure Validation Summary Report i

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PDB ID : 4MLD  
Title : X-ray structure of ComE D58E REC domain from Streptococcus pneumoniae  
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Deposited on : 2013-09-06  
Resolution : 2.88 Å (reported)

This is a wwPDB 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/ValidationPDFNotes.html>

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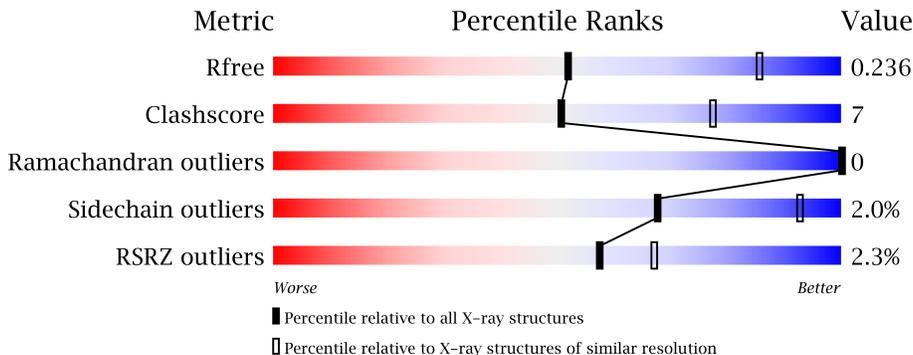
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : **FAILED**  
Xtriage (Phenix) : dev-1439  
EDS : stable23161  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable23161

# 1 Overall quality at a glance

The reported resolution of this entry is 2.88 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))
$R_{free}$	66092	1360 (2.90-2.86)
Clashscore	79885	1696 (2.90-2.86)
Ramachandran outliers	78287	1647 (2.90-2.86)
Sidechain outliers	78261	1650 (2.90-2.86)
RSRZ outliers	66119	1362 (2.90-2.86)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	143	
1	B	143	
1	C	143	
1	D	143	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4468 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Response regulator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	133	1121	726	179	213	3	0	0	0
1	B	132	1113	720	178	212	3	0	0	0
1	C	132	1113	720	178	212	3	0	0	0
1	D	133	1121	726	179	213	3	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	58	GLU	ASP	ENGINEERED MUTATION	UNP Q8DMW5
B	58	GLU	ASP	ENGINEERED MUTATION	UNP Q8DMW5
C	58	GLU	ASP	ENGINEERED MUTATION	UNP Q8DMW5
D	58	GLU	ASP	ENGINEERED MUTATION	UNP Q8DMW5



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.85Å 90.85Å 140.25Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.40 – 2.88 45.43 – 2.88	Depositor EDS
% Data completeness (in resolution range)	99.7 (45.40-2.88) 99.9 (45.43-2.88)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	0.17	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.28 (at 2.91Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3.928)	Depositor
R, $R_{free}$	0.195 , 0.239 0.190 , 0.236	Depositor DCC
$R_{free}$ test set	739 reflections (5.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	58.4	Xtriage
Anisotropy	0.980	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 48.9	EDS
Estimated twinning fraction	0.064 for h,-h-k,-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 14816 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4468	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.46% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality

### 5.1 Standard geometry

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	0.24	0/1141	0.43	0/1536
1	B	0.24	0/1133	0.43	0/1525
1	C	0.25	0/1133	0.43	0/1525
1	D	0.23	0/1141	0.42	0/1536
All	All	0.24	0/4548	0.43	0/6122

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1121	0	1128	18	0
1	B	1113	0	1117	19	0
1	C	1113	0	1117	14	0
1	D	1121	0	1128	18	0
All	All	4468	0	4490	66	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 7.

The worst 5 of 66 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:112:ILE:HA	1:B:112:ILE:HA	1.75	0.68
1:B:50:GLU:HB2	1:B:79:ASN:OD1	1.95	0.67
1:C:112:ILE:HA	1:D:112:ILE:HA	1.79	0.65
1:D:60:ASP:HA	1:D:65:GLU:HA	1.78	0.65
1:B:76:ARG:HH21	1:B:103:SER:H	1.45	0.62

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	131/143 (92%)	127 (97%)	4 (3%)	0	100	100
1	B	130/143 (91%)	126 (97%)	4 (3%)	0	100	100
1	C	130/143 (91%)	125 (96%)	5 (4%)	0	100	100
1	D	131/143 (92%)	126 (96%)	5 (4%)	0	100	100
All	All	522/572 (91%)	504 (97%)	18 (3%)	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	126/136 (93%)	124 (98%)	2 (2%)	75	95
1	B	125/136 (92%)	122 (98%)	3 (2%)	61	91
1	C	125/136 (92%)	123 (98%)	2 (2%)	75	95
1	D	126/136 (93%)	123 (98%)	3 (2%)	61	91
All	All	502/544 (92%)	492 (98%)	10 (2%)	68	93

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	132	LEU
1	C	14	VAL
1	D	85	VAL
1	B	61	ILE
1	C	51	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	D	52	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

Mogul failed to run properly - this section will therefore be empty.

## 5.5 Carbohydrates ⓘ

Mogul failed to run properly - this section will therefore be empty.

## 5.6 Ligand geometry ⓘ

Mogul failed to run properly - this section will therefore be empty.

## 5.7 Other polymers ⓘ

Mogul failed to run properly - this section will therefore be empty.

## 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, 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	133/143 (93%)	0.21	3 (2%) 57 67	47, 63, 94, 121	0
1	B	132/143 (92%)	0.14	2 (1%) 70 80	48, 69, 97, 122	0
1	C	132/143 (92%)	0.36	5 (3%) 38 46	48, 64, 95, 122	0
1	D	133/143 (93%)	0.08	2 (1%) 70 80	52, 68, 105, 122	0
All	All	530/572 (92%)	0.20	12 (2%) 57 67	47, 66, 99, 122	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	50	GLU	5.3
1	D	51	VAL	2.8
1	C	49	ASP	2.7
1	B	50	GLU	2.6
1	A	50	GLU	2.5

### 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

There are no such residues in this entry.