



# Full wwPDB X-ray Structure Validation Report

Jul 29, 2014 – 10:41 AM EDT

PDB ID : 4M3K  
Title : Structure of a single domain camelid antibody fragment cAb-H7S in complex with the BlaP beta-lactamase from *Bacillus licheniformis*  
Authors : Pain, C.; Kerff, F.; Herman, R.; Sauvage, E.; Preumont, S.; Charlier, P.; Dumoulin, M.  
Deposited on : 2013-08-06  
Resolution : 1.48 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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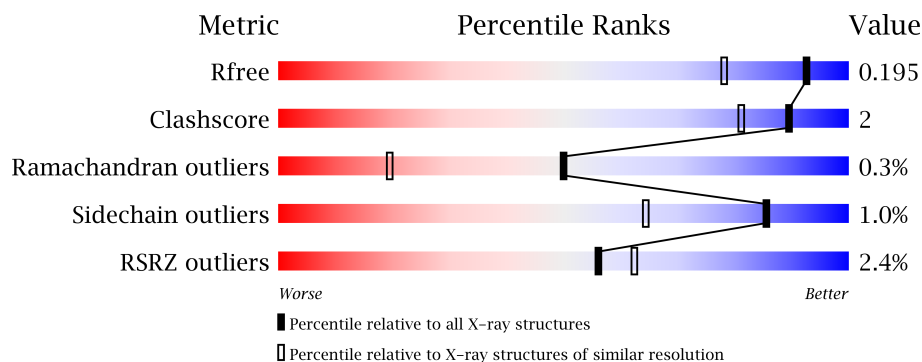
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.16 November 2013  
Xtriage (Phenix) : dev-1439  
EDS : stable23489  
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) : stable23489

# 1 Overall quality at a glance

The reported resolution of this entry is 1.48 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	2222 (1.50-1.46)
Clashscore	79885	2555 (1.50-1.46)
Ramachandran outliers	78287	2496 (1.50-1.46)
Sidechain outliers	78261	2494 (1.50-1.46)
RSRZ outliers	66119	2223 (1.50-1.46)

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	273	
2	B	126	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3224 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 Beta-lactamase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	260	Total	C	N	O	S	0	7	0
			2069	1301	357	407	4			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	197A	PRO	-	INSERTION	UNP P00808
A	197B	GLY	-	INSERTION	UNP P00808
A	296	GLY	-	EXPRESSION TAG	UNP P00808
A	297	PRO	-	EXPRESSION TAG	UNP P00808
A	298	HIS	-	EXPRESSION TAG	UNP P00808
A	299	HIS	-	EXPRESSION TAG	UNP P00808
A	300	HIS	-	EXPRESSION TAG	UNP P00808
A	301	HIS	-	EXPRESSION TAG	UNP P00808
A	302	HIS	-	EXPRESSION TAG	UNP P00808

- Molecule 2 is a protein called Camelid heavy-chain antibody variable fragment cAb-H7S.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	116	Total	C	N	O	S	0	3	0
			884	546	155	177	6			

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Cl	0	0
			1	1		
3	A	1	Total	Cl	0	0
			1	1		

- Molecule 4 is water.

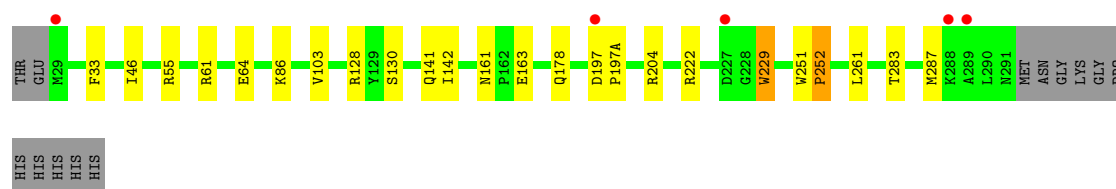
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	197	Total 197	O 197	0	3
4	B	72	Total 72	O 72	0	0

### 3 Residue-property plots

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.

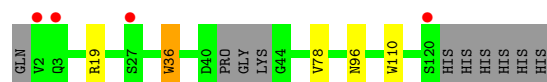
- Molecule 1: Beta-lactamase

Chain A: 



- Molecule 2: Camelid heavy-chain antibody variable fragment cAb-H7S

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	51.82Å 42.94Å 74.82Å 90.00° 105.29° 90.00°	Depositor
Resolution (Å)	36.90 – 1.48 36.90 – 1.48	Depositor EDS
% Data completeness (in resolution range)	98.8 (36.90-1.48) 98.9 (36.90-1.48)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.13 (at 1.48Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, $R_{free}$	0.161 , 0.195 0.160 , 0.195	Depositor DCC
$R_{free}$ test set	2662 reflections (5.36%)	DCC
Wilson B-factor (Å <sup>2</sup> )	15.9	Xtriage
Anisotropy	0.627	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 34.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 52293 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	3224	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.32% 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 ⓘ

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

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	0.82	3/2118 (0.1%)	0.90	5/2867 (0.2%)
2	B	0.74	2/904 (0.2%)	0.81	0/1221
All	All	0.79	5/3022 (0.2%)	0.88	5/4088 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	252	PRO	C-N	12.52	1.58	1.34
1	A	229	TRP	CD2-CE2	6.12	1.48	1.41
1	A	251	TRP	CD2-CE2	5.28	1.47	1.41
2	B	36[A]	TRP	CD2-CE2	5.08	1.47	1.41
2	B	36[B]	TRP	CD2-CE2	5.08	1.47	1.41

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	204	ARG	NE-CZ-NH2	-7.92	116.34	120.30
1	A	128	ARG	NE-CZ-NH1	-6.50	117.05	120.30
1	A	197(A)	PRO	O-C-N	-5.58	113.71	123.20
1	A	55	ARG	NE-CZ-NH1	5.41	123.00	120.30
1	A	204	ARG	NE-CZ-NH1	5.34	122.97	120.30

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	2069	0	2106	9	0
2	B	884	0	855	4	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	197	0	0	1	0
4	B	72	0	0	0	0
All	All	3224	0	2961	13	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 2.

All (13) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:163:GLU:HG3	1:A:178:GLN:HG2	1.87	0.56
1:A:33:PHE:CE1	1:A:46:ILE:HD13	2.42	0.55
1:A:61:ARG:HD2	1:A:64:GLU:OE2	2.07	0.54
2:B:96:ASN:HB2	2:B:110:TRP:CZ3	2.44	0.52
2:B:19[B]:ARG:HH21	2:B:19[B]:ARG:HB3	1.76	0.51
1:A:142[B]:ILE:O	1:A:142[B]:ILE:CG2	2.64	0.46
1:A:86:LYS:NZ	1:A:141[B]:GLN:OE1	2.44	0.44
2:B:19[B]:ARG:NH2	2:B:19[B]:ARG:HB3	2.33	0.43
2:B:36[B]:TRP:CH2	2:B:78:VAL:HG13	2.54	0.42
1:A:229:TRP:CZ2	1:A:252:PRO:HB3	2.55	0.42
1:A:222[B]:ARG:HG3	4:A:507:HOH:O	2.20	0.41
1:A:283:THR:O	1:A:287:MET:HG2	2.21	0.40
1:A:261:LEU:HD23	1:A:261:LEU:N	2.36	0.40

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	265/273 (97%)	259 (98%)	5 (2%)	1 (0%)	43	14
2	B	115/126 (91%)	114 (99%)	1 (1%)	0	100	100
All	All	380/399 (95%)	373 (98%)	6 (2%)	1 (0%)	50	19

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	103	VAL

### 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	226/230 (98%)	222 (98%)	4 (2%)	71	38
2	B	97/103 (94%)	97 (100%)	0	100	100
All	All	323/333 (97%)	319 (99%)	4 (1%)	85	56

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	130	SER
1	A	161[A]	ASN
1	A	161[B]	ASN
1	A	197	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	92	ASN
2	B	96	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 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.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	260/273 (95%)	-0.20	5 (1%) 64 71	11, 15, 30, 47	0
2	B	116/126 (92%)	-0.06	4 (3%) 43 47	13, 20, 35, 60	0
All	All	376/399 (94%)	-0.15	9 (2%) 56 62	11, 18, 34, 60	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	2	VAL	5.2
1	A	29	MET	4.5
1	A	227	ASP	2.6
1	A	288	LYS	2.6
1	A	289	ALA	2.5
2	B	3	GLN	2.4
2	B	27	SER	2.2
2	B	120	SER	2.2
1	A	197	ASP	2.1

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	CL	A	401	1/1	0.02	-	19,19,19,19	0
3	CL	B	201	1/1	0.04	-	17,17,17,17	0

## 6.5 Other polymers

There are no such residues in this entry.