



## Combating Infectious Diseases by Bioinformatics Approach

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**ABSTRACT:** Beta-lactamases are a superfamily of enzymes, which degrade the  $\beta$ -lactam class of antibiotics. They are produced endogenously by the bacterial cells, which when exposed to the  $\beta$ -lactam class of antibiotics inactivate them by cleaving the  $\beta$ -lactam ring. Based on the presence or absence of metallic ligand,  $\beta$ -lactamases have been divided into two broad functional classes.  $\beta$ -Lactamases are a constitutively evolving and expanding superfamily of enzymes, which could be further subdivided on the basis of presence/absence of conserved motifs. Our work shows that they also contain family specific patterns/motifs which useful in recognizing and assigning newly discovered  $\beta$ -lactamases to one or the other family or subfamily. We have also developed a database Comprehensive Beta-lactamase Molecular Annotation Resource (CBMAR) that contains comprehensive information about different types of  $\beta$ -lactamases. Analysis of  $\beta$ -lactamase from *Yersinia enterocolitica* shows that not only the three-dimensional structure, other factors are also responsible for their production and efficacy. © 2014 iGlobal Research and Publishing Foundation. All rights reserved.

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