Abstract

The prediction for the unknown proteins from Mycobacterium tuberculosis KZN 1435 were carried out for characterization of the proteins in their respective families. In Mycobacterium tuberculosis KZN 1435 out of 1560 genes for hypothetical proteins, functions were predicted for 1221 hypothetical protein whereas, structures for 803 unknown proteins were revealed. The Bioinformatics web tools like CDD-BLAST, INTERPROSCAN, PFAM and COGs were used for the prediction of functions in the proteins by searching protein databases for the presence of conserved domains; whereas, tertiary structures were constructed using PS2 Server-Protein Structure Prediction server. This study was helpful in understanding functional characteristics of hypothetical proteins in Mycobacterium tuberculosis KZN 1435 as well as their role in the life cycle of the bacterium.
Comparative Functional Genomics Studies for Understanding the Hypothetical Proteins in Mycobacterium tuberculosis KZN 1435

References

- Chih-Chieh C, Jenn-Kang H, Jinn-Moon Y (PS)2: protein structure prediction server Nucl.
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