ABSTRACT

Latest achievements have been gained in genome level studies, particularly genome sequencing. As consequence enormous biological information and valuable data are now accessible. This logically advocates computational world to build up additional influential and defined analysis tools. Bioinformatic approach provides time saving and reliable method to study different aspects of proteins.

In this work computational studies have been performed, using different bioinformatics tools/servers, on protein sequences from *B.linens*. The BL-2 strain of specie *B.linens* is short gun genome sequenced microorganism and is important to study due to its variety of applications. Many of its proteins are with unidentifiable functions. The present work describes prediction and assignment of the functions to these unknown hypothetical proteins from *B.linens*, thus assisting the deep perception towards their metabolic tasks in biological systems. Methodology is based on *in silico* studies.

This work provides the account of the physiochemical characterization and functional annotation to query proteins. In addition present scheme of work can be appropriate for researchers to study other hypothetical proteins.