Immunoinformatics of Human Bcl-2-Associated Athanogene 6 (BAG6)

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AFFILIATIONS

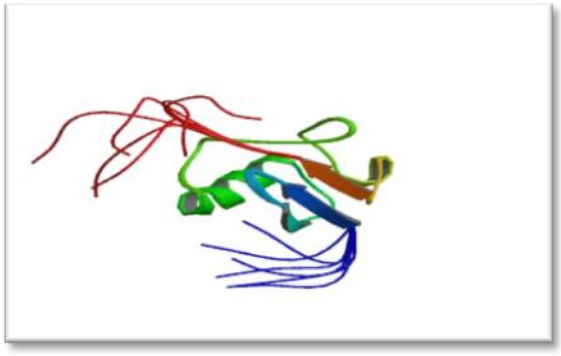
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I. Abstract

Human BAG-6 is a biologically important protein and contains a chain of 1132 residues with conserved SDL sequence motif. It is a large proline-rich and ATP independent molecular chaperone protein[1]. Human Bag-6 protein takes part in apoptosis and is linked with acute diarrhea and discrete sub-aortic stenosis[2]. It plays a vital role in preventing the aggregation of misfolded and hydrophobic patches containing proteins. It Triggers the NK cells cytotoxic against the closely related tumor cells as well as myeloid dendritic cells. It maintains the property of foreign proteins in a soluble state[3]. It is linked with two such biological functions; one is protein degradation of defective polypeptides and another one is tail-anchored / type II Transmembrane protein biogenesis performances in mammals[4]. The discovery of BAG6 is considered to be the hallmark of adaptive immunity. There have been several studies of BAG6 illustrating its biochemical, physiological and immunological properties. Still, there are limited studies on BAG6 that focused on molecular phylogenetic analyses and genetic variants in human populations. Hence, there is a need for a comprehensive characterization of the BAG6 protein for establishing its role in antigen presentation in an immune response. Therefore, the aim of this study is to comprehensively characterize the BAG6 protein using various perspectives such as molecular evolution, mapping of mutational hotspots, and signaling pathways. Herein, we identified that orthologs of Human BAG-6 protein were identified in various vertebrate species and fishes have a second copy of BAG6 due to whole genome duplication. Mutational hotspot of BAG6 was established with a library of 126 pathogenic mutations. These mutational hotpots serve as the platform for future studies for mutational characterization of BAG6. Pathway analyses reveal that BAG6 is a central hub connecting several biological pathways. In this comprehensive computational study, we endeavor to get more knowledge on this protein complex regarding evolutionary analysis.

II. Image



Solution Structure of the N-terminal Ubiquitin-like Domain in the Human BAG-6 Protein(1WX9.PDB)[5].

III. Reference

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IV. Biography

Dr. Abhishek Kumar is a Research Scientist at the University of Kiel, Kiel, Germany. He has published more than 25 research papers on sequence analysis. Dr. Ravi Tandon is an Assistant Professor at Jawaharlal Nehru University. He is serving more than 5 years in Biotechnology Department of Jawaharlal Nehru University, Delhi, India. Dr. Alisha Parveen is currently pursuing Ph.D. from Medical Research Center, Medical Faculty of Mannheim, University of Heidelberg, Mannheim, Germany. She has successfully submitted her Ph.D. Research thesis and waiting for her Defence. Kayenat Parveen is a student, recently she has completed her M.Sc. with specialization in Bioinformatics. She is currently working on research papers in collaboration with Dr. Abhishek Kumar and Dr. Ravi Tandon.

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