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an Open Access Journal by MDPI

CITESCORE 3.1

Structural Genomic Evaluations Using Molecular Modeling

Guest Editor:

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Deadline for manuscript submissions:
closed (10 January 2021)

Message from the Guest Editor

Dear Colleagues,

The field of structural genomics has been expanding rapidly for several years. The need for high quality analyses of protein structures is valuable to drug design efforts and chemotherapeutic applications. Computational analysis provides a general prediction of biochemical function establishing a foundation for further direct experimentation. Specifically, techniques such as domain identification, homology modeling, *in silico* drug screening, and pharmacophore identification allow us to develop a greater understanding of the potential roles of these proteins in signal transduction and gene expression. Putative characterizations of hypothetical proteins open doors to novel insights expanding our knowledge of the pathophysiology of both acute and chronic diseases.