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Structure-based investigations of the effects of missense mutations associated with human disorders

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Human genome sequence differs among individuals and differences known as non-synonymous single nucleotide polymorphisms (nsSNPs) can be responsible for many human diseases or cause the natural differences among the individuals by affecting the structure, function, interactions and other properties of expressed proteins. From computational standpoint the mono-genetic diseases resulting from missense mutations which affect the wild type characteristics of a specific protein are of specific interest. Using various cases of disorders, it is demonstrated that almost always the mutations do not directly affect the functional properties of the corresponding protein, but rather indirectly alter its wild type characteristics. In addition, it is indicated that disease causing mutations do not necessary destabilize protein stability or protein-protein interactions, but can be stabilizing and still be harmful. Overall, a detailed computational analysis combined with an analysis of the corresponding biological function is needed to make reasonable prediction of the disease association of missense mutations. Once the molecular mechanism of disease is revealed, the disease-causing effect can be targeted with small molecule binding.

Biography

Emil Alexov has completed his PhD in 1991 from Sofia University and Postdoctoral studies from City College of New York and Columbia University. Currently, he is Professor at Department of Physics at Clemson University, SC, USA. He has published more than 110 papers in various journals and serving as an editorial board member of numerous journals.

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