



Protein Domain Evolution and Involvement in Diseases

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Deadline for manuscript
submissions:

closed (31 December 2019)

Message from the Guest Editors

Protein domains are structural and functional units harboring specific functions and orchestrating various processes, from enzyme catalysis to signal transduction. The use of protein domains in different contexts, a phenomenon called versatility or promiscuity, permits the molecular tinkering necessary for functional diversification and species evolution. Protein domains are evolutionarily conserved and several domain databases have been developed, providing statistical models allowing automatic protein annotation and experimental 3D structures enabling homology modeling and comparative analyses. These different levels of information (sequence, structure and evolution) available for protein domains can be used to understand the molecular mechanisms of human diseases, providing tools for diagnosis and specific therapeutic approaches. However, challenges remain, particularly for improving the sequence annotation of the dark proteome. This Special Issue will cover a selection of recent research topics in the field of protein domain discovery, annotation and evolution, with a relationship to human diseases. Research papers, up-to-date review articles, and commentaries are welcome.





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Message from the Editor-in-Chief

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