# Special Issue

## Protein Domain Evolution and Involvement in Diseases

### 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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### Guest Editors

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### Deadline for manuscript submissions

closed (31 December 2019)

**International Journal of Molecular Sciences**

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**CiteScore 9.0**
**Indexed in PubMed**

mdpi.com/si/20884

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The International Journal of Molecular Sciences (*IJMS*, ISSN 1422-0067) is an open access journal, which was established in 2000. The journal aims to provide a forum for scholarly research on a range of topics, including biochemistry, molecular and cell biology, molecular biophysics, molecular medicine, and all aspects of molecular research in chemistry. *IJMS* publishes both original research and review articles, and regularly publishes special issues to highlight advances at the cutting edge of research. We invite you to read recent articles published in *IJMS* and consider publishing your next paper with us.

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