Special Issue

Structure, Function and Evolution of Protein Domains

Message from the Guest Editor

This Special Issue welcomes both original research articles and reviews on any aspect of protein domains, with special emphasis on their structure, function, potential evolutionary origins, and relationship with one another. We also encourage articles on sequence repeats of diverse lengths, of which there are many well-known examples, including (but not limited to) TPR/PPR, HEAT, Armadillo, WD40, Ankyrin, Kelch, and LRR (Leu-Rich Repeat). Several repeat families exhibit conservation of structure, such as an array of alpha-helices, or similarity of three-dimensional structures and folds, even though they may differ in amino acid sequence. How the structural and functional units have evolved to produce the larger repeats and complex domains with a distinct specificity for substrates and ligands remains an important unsolved mystery in molecular evolution. Finally, hitherto unrecognized domains and motifs that may be unraveled by novel strategies of sequence or structure alignment are also highly welcome, as well as genetic engineering studies to generate novel chimeric domains.

Guest Editor

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Deadline for manuscript submissions

closed (28 February 2022)

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Message from the Editor-in-Chief

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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