



Structure, Function and Evolution of Protein Domains

Guest Editor:

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Deadline for manuscript
submissions:
closed (28 February 2022)

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.





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Message from the Editor-in-Chief

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