Special Issue

Molecular Recognition in Protein and Peptide Nanotechnology

Message from the Guest Editors

During the last four decades, a growing body of evidence has been accumulating on the specific interaction and molecular recognition of the complementary peptides, i.e., sense and antisense peptides specified by the complementary DNA and RNA sequences. The interaction of sense and antisense peptides can be described with the set of rules combining physico-chemical properties of amino acids with bidirectional coding and stereochemical interaction. This natural genetic coding algorithm for complementary peptide interactions is neither expensive nor time-consuming, and enables simple and efficient design of interacting protein and peptide motifs. It represents a powerful new tool for the investigation and modeling of natural or de novo designed protein and peptide ligand-acceptor (receptor) systems.

Different applications include:

- Investigation of ligand and receptor structure, function and evolution
- Screening of protein and peptide ligands and acceptors (receptors)
- Development of vaccines, diagnostic tests and biomaterials
- Label-free technology to track drug candidates
- Peptidomimetics
- Investigation of peptide nucleic acids interaction

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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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