Tentative Outline
Special Issue for Current Medicinal Chemistry

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Conformational allostery- and folding-controlled Medication

Aims & Scope:

Protein functional motions are encoded by their 3-dimensional structures where constituent residues are physicochemically connected to have controlled fluctuations near their equilibrium state. Such network formed over a designed fold is woven by hydrophobic collapses of a polypeptide chain entropically driven by water. Hence, 'correct' functional motions of proteins are secured by (1) correct folding of the proteins and (2) their correct contact topology in the folded state. A strategic perturbation in either the folding process or the contact topology, at loci even far away from the functional sites, could modulate the molecular functions. The employment of a single small-molecule compound (or functional peptide) or leveraging the combinatorial effect of multiple of them were evidenced to conformationally select a given (healthy) protein fold, or selectively inhibit a specific enzyme via allosteric drugs. The latter is particularly useful when the structure and sequence of a catalytic pocket are highly conserved among those in paralogs.

Topics to be covered (main bioactive component):

- Protein dynamics
- Theoretical biophysics

Keywords: Allostery, Folding, Molecular mechanics, Allosteric inhibition, Conformational selection

Schedule: The final articles will be delivered by February 2018.