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*VABILO NA PREDAVANJE
V OKVIRU DOKTORSKEGA ŠTUDIJA
KEMIJSKE ZNANOSTI*

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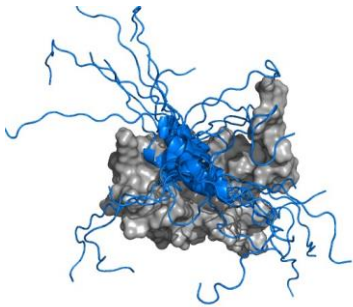
z naslovom:

**New lights on the protein interaction
horizon**

v sredo, 20. marca 2019 ob 15:00 uri
v predavalnici 1 v 1. nadstropju Fakultete
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Vljudno vabljeni!

Abstract:



Protein interactions are usually mediated by structured interfaces leading to well-defined contact patterns. The classical models are undergoing a dramatic revision, when both conformational and interaction dynamics are taken into account. Recent data indicate plasticity of the templated folding pathways, resulting in alternative structures upon binding to different partners. Furthermore, considerable variations:

polymorphism or extensive conformational exchange are frequently observed in protein complexes, with important biological consequences. This phenomenon, where conformational heterogeneity is linked to function is termed as fuzziness, which is represented from enzymes to membraneless organelles.

Conformational fluctuations are usually modulated by non-native, transient contacts, which complement suboptimal binding motifs to improve affinity. As a further layer of complexity, redundant sequence motifs establish multivalent, weak interactions in supramolecular assemblies, such as signalosomes or non-membrane bound cellular compartments. Further problems arise from simultaneous involvement of proteins in multiple activities to facilitate dynamic adaptation to stochastic cellular conditions. Here I propose a uniform model to describe the complex relationships between sequences, structures and functions of proteins. In this model, both native and non-native interactions should be characterized along the binding trajectory together with their functional impacts. The interaction mechanism is defined by the relative contributions of these two contact types in different stages along the pathway, which determines the spatial and temporal plasticity of the recognition process. I will also show how novel prediction methods exploit these principles providing exciting future perspectives for biotechnology and drug design.

References

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