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SÉMINAIRE

Lundi 1 juillet, 14h

*Salle de conférence, 4ème étage, Tour 23-22
IMPMC, Université P. et M. Curie, 4, Place Jussieu, 75005 Paris*

RUBEN ACUMA

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PREDICTION OF THE EFFECTS OF MUTATION ON PROTEIN STABILITY

The effects of amino acid substitution in proteins can be dramatic and predicting its impact may benefit scientists. There are various methods and tools available to address the potential impact of a mutation on the structure of a protein. The identification of these methods, their availability, the time needed to gain enough familiarity with them and their interface, and the difficulty of integrating their results in a global view where all viewpoints can be visualized often limit their use. This is why a web server called SPROUTS has been developed at Tempe. The focus is the thermodynamic contribution to stability. It compiles the predictions from eight distinct algorithms calculating the $\Delta\Delta G$ upon point mutation, together with a prediction of amino acids mainly interacting during the process of folding.