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## **BINDING AND MECHANISM FOR THE MEEVD-TPR2A PEPTIDE—PROTEIN ASSOCIATION AND MODELING THE INTERACTION OF DENGUE PROTEINS WITH NEUTRALIZING ANTIBODIES**

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**T**he interaction between the MEEVD C-terminal peptide from the heat shock protein 90 (Hsp90) and tetratricopeptide repeat A (TPR2A) domain of the heat shock organizing protein (Hop) represents a useful model to study peptide-protein interaction in general. In this work, the mechanism of binding is inferred and the potential of mean force is calculated using the adaptive biasing force (ABF) methodology. Conformational changes of the peptide and the protein receptor induced by binding are observed. The binding free energy is about -8.4 kcal/mol which reproduces the experimental data. The simulations show several transitions from the bound to unbound state along a pathway connecting the binding pocket to the solvent. The MEEVD peptide slowly unbinds breaking the hydrogen bonds first, then moving on the side while interacting with the side chain of residue Asp 5 of the peptide. After this initial movement, the peptide completely moves into the solvent. Analyzing binding transitions intermediate states can be found and they are characterized by the peptide interacting

with a lateral helix; helix A1 of the receptor with mainly Asp 5, Val 4, and Glu 3 of the peptide. The structure of the bound complex obtained after rebinding is structurally very similar to the crystal structure of the complex (0.48 Å RMSD). Structural modeling and energetic analysis of the protein E of dengue has been performed to better understand the interaction of DII E (60aa-250aa), an important epitopic region, and the EDE1 C8 antibody. Molecular dynamic runs of the complex have been performed to evaluate the models. RMSF and intra-molecular interactions were used to evaluate the stability of the structural models.

### **Biography**

Mauro Lapelosa holds a PhD from Rutgers University, USA. He is a Senior Postdoc at the Italian Institute of Technology. He has 15 publications, and his publication H-index is 10. He has been serving as a reviewer of many reputed journals.

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