Ernesto J Fuentes, J Proteomics Bioinform 2017, 10:10 (Suppl)
DOI: 10.4172/0974-276X-C1-103

Design of PDZ domain specificity

Ernesto J Fuentes
University of Iowa, USA

Molecular recognition is critical for the function and regulation of signal transduction in all cell types. PSD-95/Dlg1/ZO-1 (PDZ) domains are among the most abundant protein-protein interaction modules in the human proteome, commonly found in multi-domain signal scaffolding proteins. PDZ domains typically recognize a variety of short amino acid motifs, including the C-termini and internal peptide sequences of partner proteins. How PDZ domains accommodate these diverse interaction partners while providing specificity remains poorly understood. The overall goal of our studies is to define the molecular basis underlying PDZ domain specificity towards its known ligands. In this presentation, I will discuss recent studies that reveal, how specificity is obtained and rationally altered in model PDZ domains that bind C-terminal and internal peptide sequences? In addition, I will provide examples for how conformational dynamics and structure both contribute to molecular recognition of altered PDZ proteins? These studies have important implications for the evolution, design and regulation of protein-ligand interactions.

Biography

Ernesto J Fuentes began his Post-graduate education at the University of Dayton (Dayton, Ohio) with a Master's degree in Developmental Biology. He has obtained a PhD degree in Biochemistry from University of Illinois under the mentorship of Dr. A Joshua Wand. He has pursed Post-doctoral training at the University of North Carolina in the areas of protein NMR dynamics with Dr. Andrew Lee and Rho-family GTPase function with Dr. Channing Der. His current research broadly focuses on elucidating the molecular mechanisms that regulate signal transduction. Our recent work has focused on two systems: the regulation of Rho-family GTPase signal transduction and bacterial two component systems.

ernesto-fuentes@uiowa.edu

Notes: