j. s. karling Distinguished Lectureship

DEPARTMENT OF BIOLOGICAL SCIENCES SEMINAR

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La Jolla, California

Friday, September 14, 2012
11:00 am
PFEN 241, Dean's Auditorium

Reception AT 10:30 AM , Hallway by 241

"Molecular recognition and signaling in the human GPCR Superfamily"

GPCRs constitute the largest protein families in the human genome and play essential roles in normal cell processes, most notably in cell signaling. The human GPCR family contains more than 800 members and recognizes thousands of different ligands and activates a number of signaling pathways through interactions with a small number of binding partners. GPCRs have also been implicated in numerous human diseases, and represent more than 30-40% of drug targets. Delivering GPCR structures in close collaboration with the community on specific receptor systems is of immense value to the basic science community interested in cell signaling and molecular recognition, as well as the applied science community interested in drug discovery. This work is being followed up with additional biophysical characterization including NMR spectroscopy and community wide assessments with computational biology groups throughout the world. Crystal structures are now available for rhodopsin, adrenergic, and adenosine receptors in both inactive and activated forms, as well as for chemokine, dopamine, histamine, lipid, and all four opioid receptors in inactive conformations. A review of the common structural features seen in these receptors and the scope of structural diversity of GPCRs at different levels of homology provides insight into our growing understanding of the biology of GPCR action and their impact on drug discovery. Given the current set of GPCR structural data, a distinct modularity is now being observed between the extracellular (ligand-binding) and intracellular (signaling) regions. The rapidly expanding repertoire of GPCR structures provides a solid framework for experimental and molecular modeling studies, and helps to chart a roadmap for comprehensive structural coverage of the whole superfamily and an understanding of GPCR biological and therapeutic mechanisms. With the rapid accumulation of this data, one can now start to investigate GPCR evolution, and expanding this understanding to human evolution and cognition.

For more information on Dr. Stevens and his research, go to: http://stevens.scripps.edu/members.shtml