Network analysis of the conformational change of c-Src, a tyrosine kinase, by molecular dynamics simulation

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Non-receptor tyrosine kinase c-Src plays a critical role in numerous cellular signaling pathways. Activation of c-Src involves a change from its inactive to the active state accompanied by large-scale conformational change depending on the phosphorylation state of two major phosphorylation sites, Tyr416 and Tyr527. A detailed mechanism for the entire conformational transition of c-Src via phosphorylation control of Tyr416 and Tyr527 is still elusive. In this study, we investigated the inactive to active conformational change of c-Src by targeted molecular dynamics simulation. Based on the simulation, we proposed a dynamical scenario for the activation process of c-Src. A detailed study of the conformational transition pathway based on network analysis suggests that Lys321 plays a key role in the c-Src activation process.

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Biography

Sangwook Wu received his BA degree in Biochemistry from Yonsei University, Korea in 1990. After working as a Scientist at Samsung Display Devices during 1995-1999, he obtained his PhD in Theoretical Condensed Matter Physics from Iowa State University during 1999-2005. He joined the Computational Biophysics Lab at UNC-Chapel Hill (Dr. Lee Pedersen) as postdoctoral research associate during 2005-2014. From 2014 to the present, he has been a faculty member at Pukyong National University in Korea. His research interests are in the areas of computational dynamics of biological macromolecules.

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