



S N BOSE NATIONAL CENTRE FOR BASIC SCIENCES

Block JD, Sector III, Salt Lake, Kolkata 700 106

DEPARTMENTAL SEMINAR

Chemical, Biological & Macro-Molecular Sciences

11th January,2022

4.00 PM

ONLINE

SPEAKER



Prof. Ruchi Anand,
Department of Chemistry, Indian Institute of Technology Bombay

Allostery in Biological Systems Abstract

Allostery in biological systems influence various important functions. Here, we discuss two enzyme systems that exhibit two different type of allostery. In the first system conformational allostery results in formation of a molecular tunnel where passage of reactive intermediate occurs to enable function of a bifunctional enzyme involved in the important purine biosynthetic pathway, essential for synthesis of DNA/RNA. The second system exhibits primarily dynamic allostery, where we explore how entry of phenol in one domain influence ATPase activity in the tandemly located AAA+ ATP hydrolysis domain.

Briefly, in the first system ammonia is produced in the glutaminase domain and it travels to the FGAM synthetase domain, via a ~ 25 Å long transient hydrophobic tunnel converting formylglycinamideribonucleotide (FGAR) to formylglycinamidineribonucleotide (FGAM). The allosteric pathway and the identity of the tunnel remained elusive for more than two decades. In this work using a combination of molecular dynamics, crystallography, mutagenesis and biochemistry we delineated the allosteric trigger that passes the signal 25 Å away to open a dual gated transient tunnel[1]. The work provided insights as to how long distance communication plays a crucial role in controlling reactivity at multiple active centres and in enabling formation of molecular tunnel that traverses within the enzyme. The second enzyme is involved in triggering stress related genes by activating sigma 54 dependent RNA polymerase. The enzyme MopR senses pollutant phenol [2] and in response to it, the tandemly located ATPase domain assembles into a molecular motor that brings about activation of the polymerase. Here, we explore questions as to how the enzyme exclusively finds phenol and how long distance hinge regions are paramount in maintaining the allosteric communication via a conserved network of hydrogen bonds that pass the allosteric cues via dynamic allostery.

- [1] Sharma, N. et. al.,(2020) Science Advances, 2020, 6: eaay7919
- [2] Ray et. al (216) ACS Chemical Biology, 2016, 11, 8, 2357-2365

HOST FACULTY

Prof. Rajib K Mitra and Dr. Suman Chakrabarty CHEMICAL, BIOLOGICAL & MACRO-MOLECULAR SCIENCES