



**Thursday, November 16, 2017, 12:30 pm**

**Seaver Science Auditorium, Room 150**

SSC Auditorium next to the library

## **Professor Michael Cohen**

*Department of Physiology and Pharmacology  
Oregon Health and Science University*

### **Decoding Protein ADP-ribosylation Networks in Cells Using Chemical Genetic Approaches**

ADP-ribosylation (ADPr) is a reversible posttranslational modification that is essential for cellular function, yet little information exists regarding relevant protein substrates and target specificity. ADPr is catalyzed by a family of 17 enzymes in humans known as poly-ADP-ribose-polymerases (PARP1-16 in humans; also known as ARTDs), which transfer the ADP-ribose moiety from nicotinamide adenine dinucleotide (NAD<sup>+</sup>) to amino acids on target proteins. Progress in understanding the specific role of a given PARP in cells has been severely limited by (i) the inability to identify the direct targets for individual PARPs in a cellular context and (ii) the lack of selective inhibitors for individual PARP family members.

To address the first challenge, my laboratory has designed novel orthogonal NAD<sup>+</sup> analogue-engineered PARP pairs for the identification of direct protein targets of individual PARPs. We have successfully applied this approach toward the identification of the direct targets of the poly-PARP subfamily, and have recently extended this strategy to the mono-PARP subfamily. Most recently, we have used this strategy to identify targets of PARP14. My laboratory is addressing the second challenge by using a structure-based design strategy to generate selective inhibitors of individual mono-PARP family members.

*Hosted by Professor Matt Pratt*

The scientific community is invited

**USC Department of Chemistry**

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