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The Structure of the FAD-based Redox Sensor Domain of NifL: Insights into Mechanism through X-ray Photoreduction. Jason Key[1], Marco Hefti[2], Erin Purcell[1], Keith Moffat[1], [1]Univ. of Chicago, Chicago, USA, [2]Leiden Univ., Leiden, The Netherlands.

NifL is a modular multi-domain sensor protein responsible for the regulation of nitrogen fixation genes in response to redox state and ADP concentration. Redox is monitored by the N-terminal PAS domain of NifL which contains an FAD cofactor. To explore the mechanism of signal recognition and transduction in NifL, we have determined the crystal structure of the FAD-bound PAS domain of NifL from the organism *Azotobacter Vinelandii* (*Av*NifLF) to 1.04 Å resolution. The structure of *Av*NifLF reveals a novel cavity with two water molecules coordinated to the FAD. We are able to visualize the structural conversion from the oxidized "off" state of the protein toward a reduced "on" state using X-ray photoreduction of the FAD prosthetic group; the X-ray beam itself drives the biologically relevant reaction. A redox-sensitive hydrogen bond is observed in the protein and structural rearrangement within the FAD cavity is evident. We propose that these are the initial structural events in the conversion between signaling states in this bacterial redox sensor. Structural differences propagate more than 7Å from the FAD cavity onto the A and I strands of the β-sheet of the protein, a region implicated in signaling in other PAS domain proteins.