BIOLOGY COLLOQUIUM

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Crystal Structures of the Y29F and Y29A mutants of Vitreoscilla hemoglobin

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Many bacteria use hemoglobin as an oxygen-storage and oxygen-delivery vehicle. Many bacterial hemoglobins are directly associated with flavoprotein partners; others, including the dimeric hemoglobins from Vitreoscilla spp., interact with flavoproteins but in a less intimate way. Profs. Dale Webster and Ben Stark in our department have been studying Vitreoscilla hemoglobin for several decades, and in recent years their investigations have led to potential interest in this protein both as a tool in bioremediation and as a component of chimeric expression systems. Dr. Stark and his collaborator, Dr. Kanak Dikshit, have characterized the oxygen-binding and biophysical characteristics of several mutants of Vitreoscilla hemoglobin, including three mutants at residue 28, which is a tyrosine in the wild-type protein. Our lab has recently obtained high-resolution (1.75 and 1.85A) crystal structures of the tyr->phe and tyr-ala mutants. We will describe these structural studies and the implications they might have on our understanding of this protein's properties. The alanine mutant is ordered through most of the "D" region, which is completely disordered in the wild-type and phenylalanine proteins.