Professor Claus Wilke-University of Texas at Austin
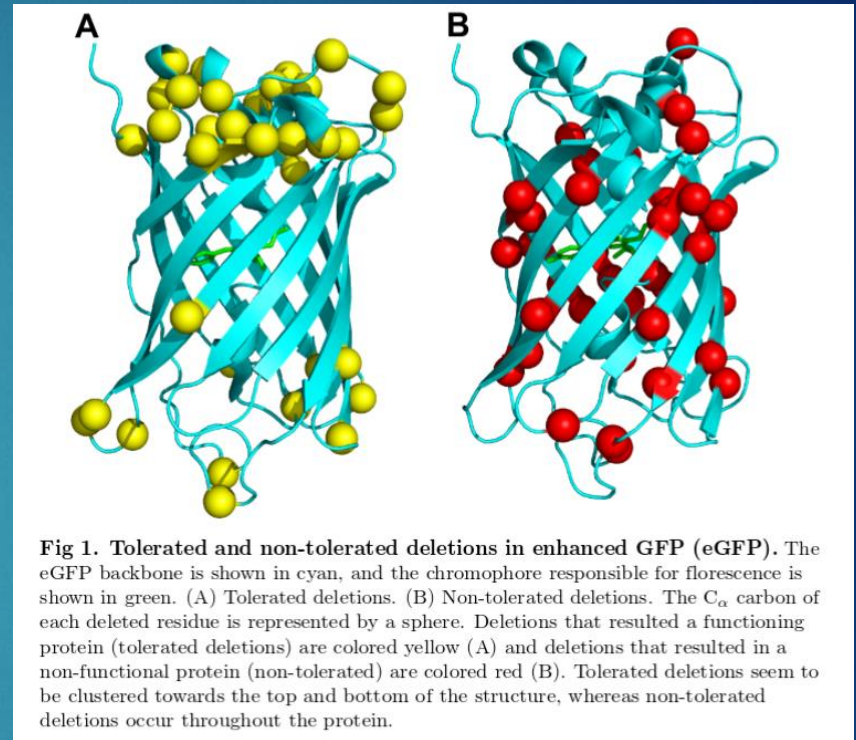## "Structural and Functional Constraints on Protein Evolution"

Fig 1. Tolerated and non-tolerated deletions in enhanced GFP (eGFP). The eGFP backbone is shown in cyan, and the chromophore responsible for florescence is shown in green. (A) Tolerated deletions. (B) Non-tolerated deletions. The C_α carbon of each deleted residue is represented by a sphere. Deletions that resulted a functioning protein (tolerated deletions) are colored yellow (A) and deletions that resulted in a non-functional protein (non-tolerated) are colored red (B). Tolerated deletions seem to be clustered towards the top and bottom of the structure, whereas non-tolerated deletions occur throughout the protein.

Protein-coding genes evolve under constraints imposed by the structural and functional properties of the encoded protein. In particular, buried sites, sites in or near active sites in enzymes, and sites involved in protein-protein interfaces experience increased purifying selection and evolve more slowly than other sites. In this talk, I will discuss the relative strength of this effect. In particular, I will show that even though most active sites of enzymes are located in the protein core, we can disentangle conservation due to solvent accessibility and conservation due to enzymatic activity. We also find that catalytic residues in enzymes exert a long-range effect, causing increased conservation of residues throughout 80% of a typical enzyme structure. Finally, I will show that protein-protein interfaces show surprisingly little sequence divergence, and that interfaces can diverge substantially yet retain the ability to bind to ancestral binding partners.

Friday, October 21; Room 307, SERF; 3:30 - 4:30PM. Pre-talk reception: 3:00 PM in Dabney 568
Anyone interested in meeting with Dr. Wilke, please contact Mike Gilchrist – mikeg@utk.edu