Characterizing insertions in coiled coil proteins NATHAN SCHMIDT, WILLIAM DEGRADO, University of California, San Francisco, UCSF TEAM — Coiled coils represent a common motif in proteins and figure largely in the assembly and dynamics required for diverse functions, including membrane fusion, signal transduction, and motors. A hallmark characteristic of coiled coils is a repeating 7-residue geometric and sequence motif. While there has been a great deal of attention given to the regular repeating structures within coiled coil proteins, much less is known about the structure and function of less regular regions in which one or more residues are inserted. Such insertions are often highly conserved and critical to interdomain communication in signaling proteins. Here we develop the "accommodation index" as a parameter that allows automatic detection and classification of insertions based on the three dimensional structure of a protein. Using bacterial histidine kinases as a test system, we show that sequence insertion defects in coiled coils can be accommodated structurally in different ways and used to create bifunctional switches for signal transduction.

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