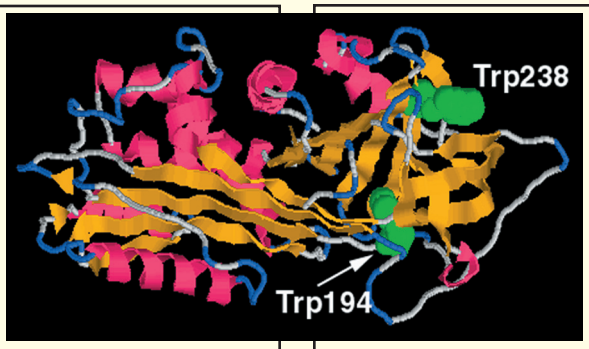
PFAST: Protein Fluorescence and Structure Toolkit

Web-based tool to reveal fluorescence properties of individual tryptophan residues



FAT: Fluorescence Analysis Tool

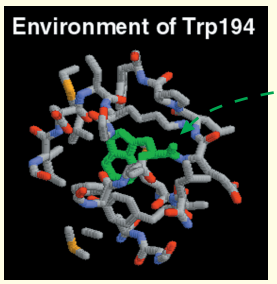
Input: Protein tryptophan fluorescence spectra.
Spectral Analysis Program: Derives individual spectral components from the total protein fluorescence spectrum
Output: Digital and graphical result of decomposition (spectral components, their contribution, Stern-Volmer constants for each component, goodness of fit).

SAT: Structure Analysis Tool

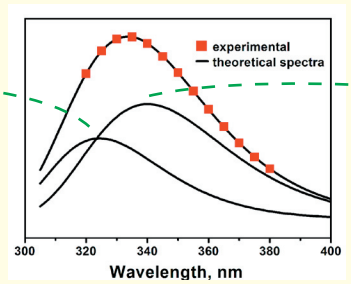
Input: Protein atomic coordinates from Protein Data Bank: www.rcsb.org/pdb/
Structural Analysis Program: Calculates structural parameters of the environment of tryptophan residues (Trps) in protein.
Output: Structural parameters describing the environment of Trps in protein (location of all neighbor atoms around Trps, probability of energy transfer between Trps).

CAT: Correlation Analysis Tool

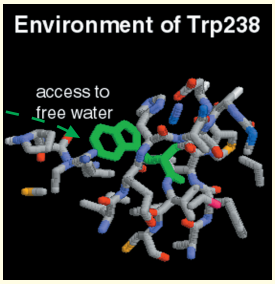
Program of correlation analysis: Assigns spectral components to tryptophan residues based on the methods of multivariate statistical analysis
Output: Probability of assignment and statistical criteria



Component 1
λ = 324 nm



Component 2
λ = 340 nm



Main Applications

- **Proteomics and Interactom:** study the conformational changes of proteins during interactions with ligands, ions, membranes, DNA, RNA and other proteins.
- **Protein Folding:** study of protein structural changes during the folding process

http://www.cs.uri.edu/pfast

Chi Shen[1], Neelima Guduru[1], Nidhi Bansal[1], Rajiv Menon[1], Stephen Jaegle[1], Joan Peckham[1], Yana Reshetnyak[2]
[1]Department of Computer Science, URI; [2]Department of Physics, URI