MOONEY LABORATORY WEB SERVICES AND SOFTWARE

C. C. Carlisle and S. D. Mooney

Mooney Lab, Buck Institute for Age Research, 8001 Redwood Blvd
Novato, CA, 94945, USA
[*]*Email: ccarlisle@buckinstitute.org*

The Mooney laboratory provides several webservices for the characterization of proteins and amino acid substitutions in proteins. MutDB is a resource to help determine which single nucleotide polymorphism(s) (SNPs) is/are likely to affect the function of their translated protein product(s). S-BLEST is designed to help a user submit protein structures to identify statistically significant neighbors and the underlying structural environments that make that match using a suite of sequence and structure analysis software tools. Catalytic Residue Predictor (CRP) is a tool to identify the amino acid residues in proteins, which are likely to be involved in catalysis. On the other hand, Protein-Protein Interaction Predictor (PPI) is designed to characterize amino acid residues in proteins likely to be involved in protein binding. Using the web services associated with these utilities, i.e., CRP and PPI Predictor, we have developed extensions for both UCSF Chimera and PyMOL that integrate these tools with both of these structural visualization and modeling programs. The extensions for both of these programs can be downloaded at http://lifescienceweb.org/.