THE MUTDB WEB TOOL FOR SNP ANALYSIS

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Single Nucleotide Polymorphisms (SNPs), the commonest types of genetic variation, have proven to be very important in the study of human health. One challenge in SNPs research is the enormous amount of data and data distribution among different resources. To assist researchers in this emerging field we have developed a new version of MutDB which is a comprehensive, up-to-date, and user friendly web application providing annotations for non-synonymous SNPs on coding areas in human genome. Currently, MutDB integrates data from dbSNP and SwissProt to provide researchers with a centralized tool to examine those mutations. For each mutation the application provides wide range of annotations on chromosome, transcription and gene product levels. and phenotype implications. We present the location of the SNP on the genome, mrna and protein as well as mapping to the different nomenclature systems. Using *Mutpred* we present predictions for the effect of a SNP on multiple post translational modification processes, the impact on the protein structure and functions associated with the variant. Future directions: include mutations and annotations from ParmGKB database, alleles frequencies, and data from cancer research.