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CMPD: Cancer Mutant Proteome Database

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Abstract : Whole-exome sequencing focuses on the protein coding regions of disease/cancer associated genes based on a priori knowledge is the most cost-effective method to study the association between genetic alterations and disease. Recent advances in high throughput sequencing technologies and proteomic techniques has provided an opportunity to integrate genomics and proteomics, allowing readily detectable mutated peptides corresponding to mutated genes. Since sequence database search is the most widely used method for protein identification using Mass spectrometry (MS)-based proteomics technology, a mutant proteome database is required to better approximate the real protein pool to improve disease-associated mutated protein identification. Large-scale whole exome/genome sequencing studies were launched by National Cancer Institute (NCI), Broad Institute, and The Cancer Genome Atlas (TCGA), which provide not only a comprehensive report on the analysis of coding variants in diverse samples cell lines but a invaluable resource for extensive research community. No existing database is available for the collection of mutant protein sequences related to the identified variants in these studies. CMPD is designed to address this issue, serving as a bridge between genomic data and proteomic studies and focusing on protein sequence-altering variations originated from both germline and cancer-associated somatic variations.

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