The Enzyme Function Initiative is developing such tools to predict in vitro enzymatic and in vivo physiological functions of unknown enzymes.

Uniprot, a web base resources that hold protein sequence and functional information, has over 44 million protein sequences (derived from nucleotide sequences) and most have no well defined protein function.

Metabolic Docker: uses molecular docking as a basis for predicting the function of enzymes. It supports docking both ground state and high energy intermediate forms of metabolites and commercially available compounds to protein structures

Other Types of Enzymes

The three enzymes studied above are all hydrolases - enzymes that catalyze the hydrolysis of bonds (either amide or acetal). This is only one class of six different reaction types that have been categorized by the Enzyme Commission of the International Union of Biochemistry and Molecular Biology. The six types (all external links) include:

**EC1: Oxidoreductases** - oxidation/reduction reactions (we will discuss these in Chapter 8B)

**EC2: Transferases** - acyl, glycosyl, 1C, N, O, aldehydes, ketones, etc

**EC3: Hydrolases**

**EC4: Lyases** - cleavage of C-C, C-O, C-N, C-S, etc. bonds

**EC5: Isomerases** - racemases, epimerases, cis-trans isomerases

**EC6: Ligases** - form C-C, C-O, C-N, etc bonds

Other Links

Enzyme Nomenclature Database: Interactive site to search information on enzymes using EC system of nomenclature.

BRENDA: (Braunschweig Enzyme Database) Comprehensive Enzyme Information System

KEGG PATHWAY: collection of manually drawn pathway maps representing our knowledge on the molecular interaction and reaction networks using KEGG, Kyoto Encyclopedia of Genes and Genomes

FMM (From Metabolite to Metabolite) - reconstructs metabolic pathways from one metabolite to another

References
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