Enzyme Commission Classification

The Enzyme Commission (EC) number is a numerical classification scheme for enzymes, established by the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology (IUBMB). It categorizes enzymes based on the chemical reaction they catalyze.

Hierarchical Structure: The system is hierarchical, consisting of four numbers separated by periods (e.g., EC X.Y.Z.W).

EC X (Class): The first digit indicates one of the seven main classes of enzymatic reactions:

Class	Reaction catalyzed
EC 1	Oxidation/reduction reactions; transfer of H and O atoms or electrons from one substance to another
EC 2	Transfer of a functional group from one substance to another. The group may be methyl-, acyl-, amino- or phosphate group
EC 3	Formation of two products from a substrate by hydrolysis
EC 4	Non-hydrolytic addition or removal of groups from substrates. C-C, C-N, C-O or C-S bonds may be cleaved
EC 5	Intramolecule rearrangement, i.e. isomerization changes within a single molecule
EC 6	Join together two molecules by synthesis of new C-O, C-S, C-N or C-C bonds with simultaneous breakdown of ATP
EC 7	Catalyse the movement of ions or molecules across membranes or their separation within membranes

EC X.Y (Subclass): The second digit generally indicates the type of group or bond acted upon (e.g., the type of donor in oxidoreductases, the type of group transferred in transferases).

EC X.Y.Z (Sub-subclass): The third digit provides more specific information about the reaction, such as the type of acceptor group (for oxidoreductases and transferases) or the specific bond hydrolyzed (for hydrolases).

EC X.Y.Z.W (Serial Number): The fourth digit is a serial number specific to the enzyme within its sub-subclass, essentially identifying the specific substrate.

The EC classification system serves **several critical purposes** in biochemistry and related fields:

- **Standardization and Unambiguity:** Provides a unique, universally recognized identifier for each distinct enzyme function, eliminating confusion arising from multiple common names or names based on discovery rather than function.
- **Database Organization:** Essential for organizing and querying biochemical databases (e.g., BRENDA, KEGG, UniProt, PDB). Users can search for enzymes based on the reactions they catalyze.
- **Functional Annotation:** Aids in predicting and annotating the function of newly discovered genes and proteins identified through sequencing or structural genomics projects. If a protein shares significant sequence or structural similarity with an enzyme of known EC number, it suggests a similar function.
- **Metabolic Pathway Analysis:** Helps in understanding and reconstructing metabolic pathways by clearly defining the catalytic steps involved.
- **Drug Discovery:** Identifying enzymes by their function (EC number) is crucial for selecting targets for drug development.