anticipate that the functional attributes of enzymes are due to the remarkable versatility found in protein structures.

## Enzyme Nomenclature Provides a Systematic Way of Naming Metabolic Reactions

Traditionally, enzymes were named by adding the suffix *-ase* to the name of the substrate upon which they acted, as in *urease* for the urea-hydrolyzing enzyme or *phosphatase* for enzymes hydrolyzing phosphoryl groups from organic phosphate compounds. Other enzymes acquired names bearing little resemblance to their activity, such as the peroxide-decomposing enzyme *catalase* or the proteolytic enzymes *(proteases)* of the digestive tract, *trypsin* and *pepsin*. Because of the confusion that arose from these trivial designations, an International Commission on Enzymes was established to create a systematic basis for enzyme nomenclature. Although common names for many enzymes remain in use, all enzymes now are classified and formally named according to the reaction they catalyze. Six classes of reactions are recognized (Table 13.1). Within each class are subclasses, and under each subclass are sub-subclasses within which individual enzymes are listed. Classes, subclasses, sub-subclasses, and individual entries are each numbered so that a series of four numbers serves to specify a particular enzyme. A systematic name, descriptive of the reaction, is also assigned to each entry. To illustrate, consider the enzyme that catalyzes this reaction:

$$\text{ATP} + \text{D-glucose} \longrightarrow \text{ADP} + \text{D-glucose-6-phosphate}$$

**TABLE 13.1** Systematic Classification of Enzymes According to the Enzyme Commission

| E.C. Number | Systematic Name and Subclasses |
|---|---|
| 1 | *Oxidoreductases* (oxidation–reduction reactions) |
| 1.1 | Acting on CH—OH group of donors |
| 1.1.1 | With NAD or NADP as acceptor |
| 1.1.3 | With $O_2$ as acceptor |
| 1.2 | Acting on the $\diagdown$C=O group of donors |
| 1.2.3 | With $O_2$ as acceptor |
| 1.3 | Acting on the CH—CH group of donors |
| 1.3.1 | With NAD or NADP as acceptor |
| 2 | *Transferases* (transfer of functional groups) |
| 2.1 | Transferring C-1 groups |
| 2.1.1 | Methyltransferases |
| 2.1.2 | Hydroxymethyltransferases and formyltransferases |
| 2.1.3 | Carboxyltransferases and carbamoyltransferases |
| 2.2 | Transferring aldehydic or ketonic residues |
| 2.3 | Acyltransferases |
| 2.4 | Glycosyltransferases |
| 2.6 | Transferring N-containing groups |
| 2.6.1 | Aminotransferases |
| 2.7 | Transferring P-containing groups |
| 2.7.1 | With an alcohol group as acceptor |
| 3 | *Hydrolases* (hydrolysis reactions) |
| 3.1 | Cleaving ester linkage |
| 3.1.1 | Carboxylic ester hydrolases |
| 3.1.3 | Phosphoric monoester hydrolases |
| 3.1.4 | Phosphoric diester hydrolases |
| 4 | *Lyases* (addition to double bonds) |
| 4.1 | C=C lyases |
| 4.1.1 | Carboxy lyases |
| 4.1.2 | Aldehyde lyases |
| 4.2 | C=O lyases |
| 4.2.1 | Hydrolases |
| 4.3 | C=N lyases |
| 4.3.1 | Ammonia-lyases |
| 5 | *Isomerases* (isomerization reactions) |
| 5.1 | Racemases and epimerases |
| 5.1.3 | Acting on carbohydrates |
| 5.2 | *Cis-trans* isomerases |
| 6 | *Ligases* (formation of bonds with ATP cleavage) |
| 6.1 | Forming C—O bonds |
| 6.1.1 | Amino acid–RNA ligases |
| 6.2 | Forming C—S bonds |
| 6.3 | Forming C—N bonds |
| 6.4 | Forming C—C bonds |
| 6.4.1 | Carboxylases |

A phosphate group is transferred from ATP to the C-6-OH group of glucose, so the enzyme is a *transferase* (class 2, Table 13.1). Subclass 7 of transferases is *enzymes transferring phosphorus-containing groups,* and sub-subclass 1 covers those *phosphotransferases with an alcohol group as an acceptor.* Entry 2 in this sub-subclass is **ATP:D-glucose-6-phosphotransferase,** and its classification number is **2.7.1.2.** In use, this number is written preceded by the letters **E.C.,** denoting the Enzyme Commission. For example, entry 1 in the same sub-subclass is E.C.2.7.1.1, ATP:D-hexose-6-phosphotransferase, an ATP-dependent enzyme that transfers a phosphate to the 6-OH of hexoses (that is, it is nonspecific regarding its hexose acceptor). These designations can be cumbersome, so in everyday usage, trivial names are commonly used. The glucose-specific enzyme E.C.2.7.1.2 is called *glucokinase,* and the nonspecific E.C.2.7.1.1 is known as *hexokinase. Kinase* is a trivial term for enzymes that are ATP-dependent phosphotransferases.

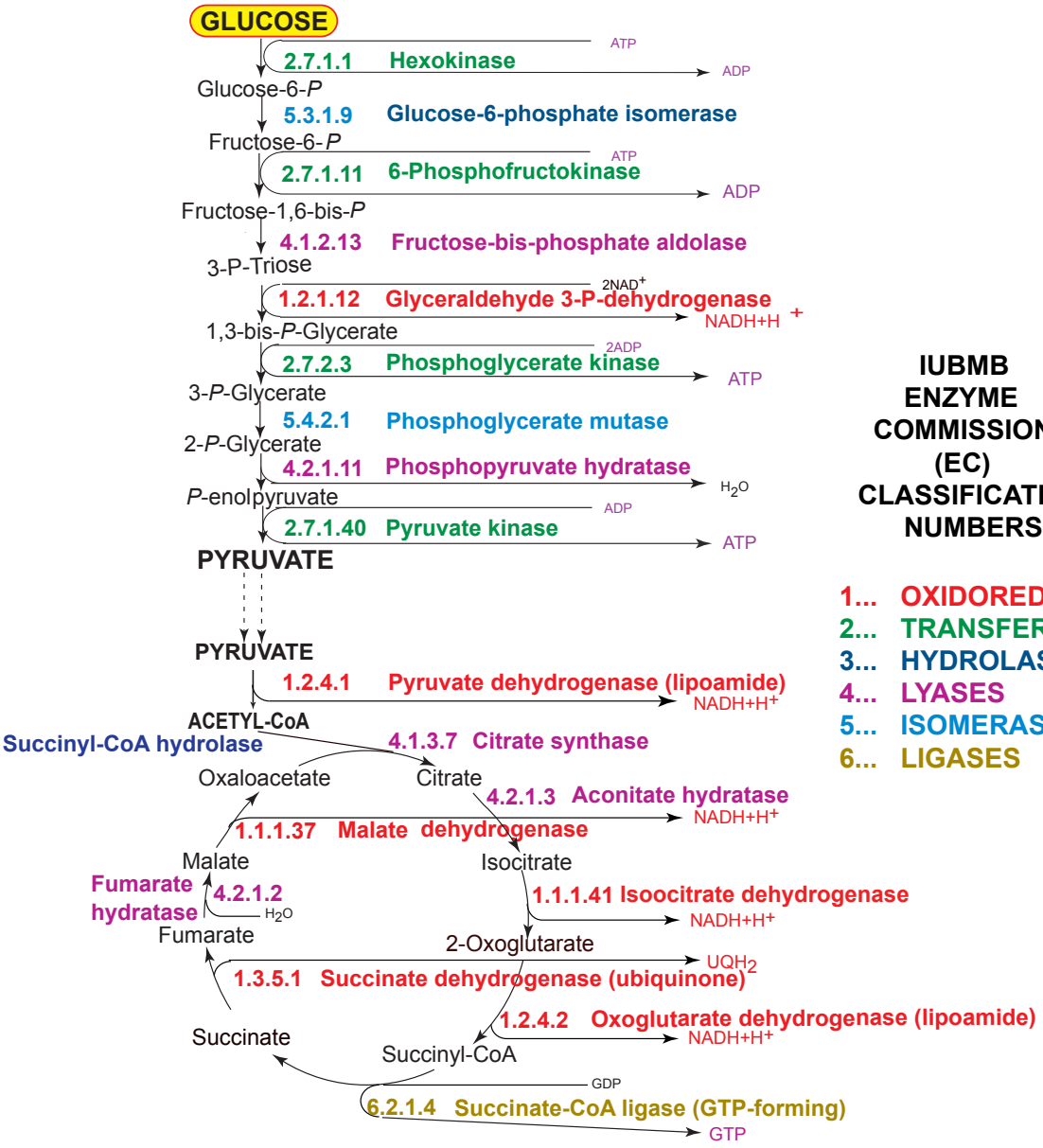
## Coenzymes and Cofactors Are Nonprotein Components Essential to Enzyme Activity

Many enzymes carry out their catalytic function relying solely on their protein structure. Many others require nonprotein components, called **cofactors** (Table 13.2). Cofactors may be metal ions or organic molecules referred to as **coenzymes.** Coenzymes and cofactors provide proteins with chemically versatile functions not found in amino acid side chains. Many coenzymes are vitamins or contain vitamins as part of their structure. Usually coenzymes are actively involved in the catalytic reaction of the enzyme, often serving as intermediate carriers of functional groups in the conversion of substrates to products. In most cases, a coenzyme is firmly associated with its enzyme, perhaps even by covalent bonds, and it is difficult to separate the two. Such tightly bound coenzymes are referred to as **prosthetic groups** of the enzyme. The catalytically active complex of protein and prosthetic group is called the **holoenzyme.** The protein without the prosthetic group is called the **apoenzyme;** it is catalytically inactive.

**TABLE 13.2 Enzyme Cofactors: Some Metal Ions and Coenzymes and the Enzymes with Which They Are Associated**

| Metal Ions and Some Enzymes That Require Them | | Coenzymes Serving as Transient Carriers of Specific Atoms or Functional Groups | | |
|---|---|---|---|---|
| Metal Ion | Enzyme | Coenzyme | Entity Transferred | Representative Enzymes Using Coenzymes |
| $Fe^{2+}$ or $Fe^{3+}$ | Cytochrome oxidase<br>Catalase<br>Peroxidase | Thiamine pyrophosphate (TPP)<br>Flavin adenine dinucleotide (FAD)<br>Nicotinamide adenine dinucleotide (NAD) | Aldehydes<br>Hydrogen atoms<br>Hydride ion ($:H^-$) | Pyruvate dehydrogenase<br>Succinate dehydrogenase<br>Alcohol dehydrogenase |
| $Cu^{2+}$ | Cytochrome oxidase | | | |
| $Zn^{2+}$ | DNA polymerase<br>Carbonic anhydrase<br>Alcohol dehydrogenase | Coenzyme A (CoA)<br>Pyridoxal phosphate (PLP) | Acyl groups<br>Amino groups | Acetyl-CoA carboxylase<br>Aspartate aminotransferase |
| $Mg^{2+}$ | Hexokinase<br>Glucose-6-phosphatase | 5′-Deoxyadenosylcobalamin (vitamin $B_{12}$) | H atoms and alkyl groups | Methylmalonyl-CoA mutase |
| $Mn^{2+}$ | Arginase | Biotin (biocytin) | $CO_2$ | Propionyl-CoA carboxylase |
| $K^+$ | Pyruvate kinase (also requires $Mg^{2+}$) | Tetrahydrofolate (THF) | Other one-carbon groups, such as formyl and methyl groups | Thymidylate synthase |
| $Ni^{2+}$ | Urease | | | |
| Mo | Nitrate reductase | | | |
| Se | Glutathione peroxidase | | | |

# GLYCOLYSIS & TCA CYCLE - ENZYMES & EC REFERENCE NUMBERS




**IUBMB ENZYME COMMISSION (EC) CLASSIFICATION NUMBERS**

1... OXIDOREDUCTASES
2... TRANSFERASES
3... HYDROLASES
4... LYASES
5... ISOMERASES
6... LIGASES

## ENZYMES

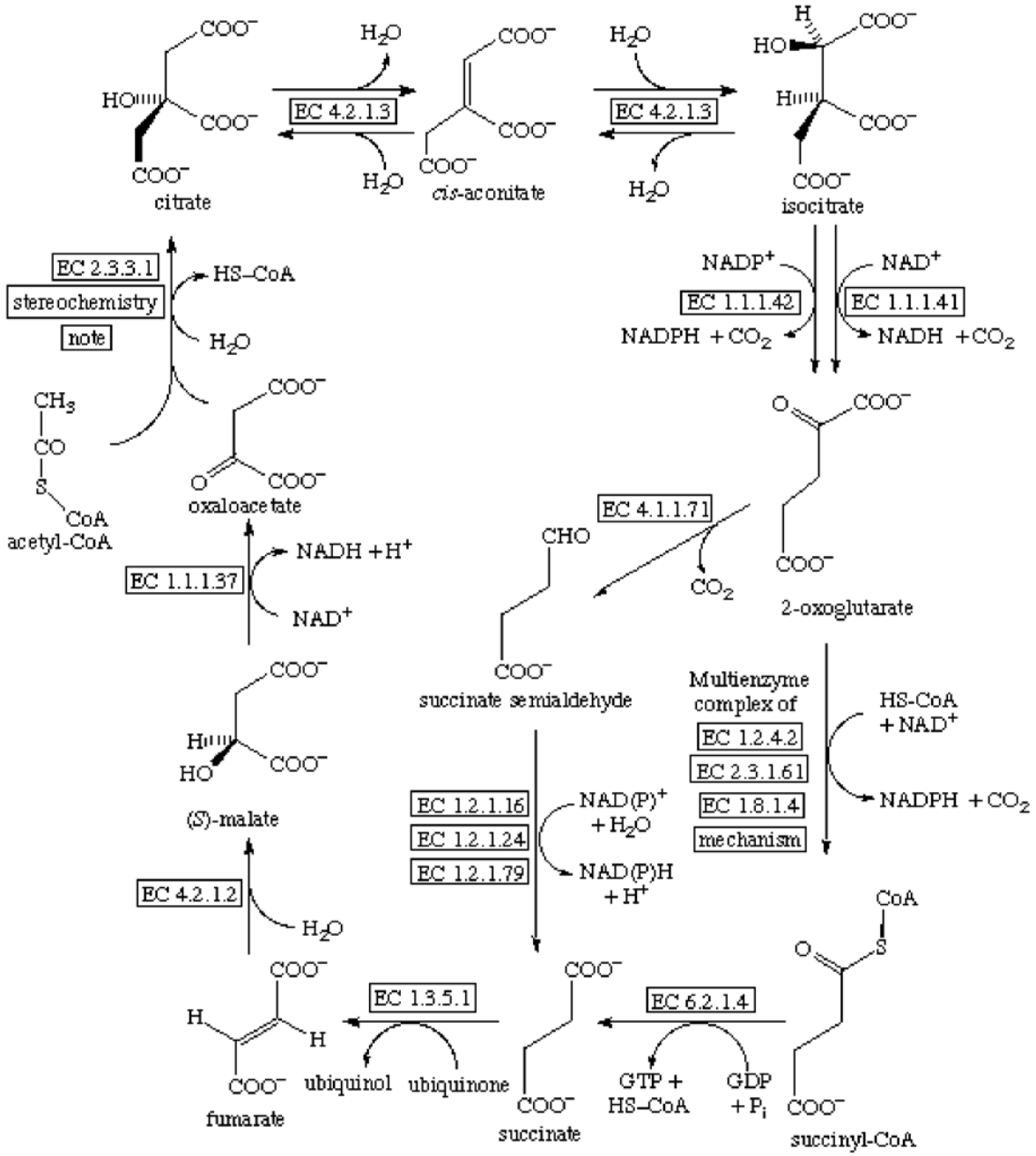
1.1.1.37 Malate dehydrogenase
1.1.1.41 Isocitrate dehydrogenase
1.2.1.12 Glyceraldehyde-3-P dehydrogenase
1.2.4.1 Pyruvate dehydrogenase (lipoamide)
1.2.4.2 Oxoglutarate dehydrogenase (lipoamide)
1.3.5.1 Succinate dehydrogenase (ubiquinone)
2.7.1.1 Hexokinase
2.7.1.11 6-Phosphofructokinase
2.7.1.40 Pyruvate kinase
2.7.2.3 Phosphoglycerate kinase
3.1.2.3 Succinyl-CoA hydrolase
4.1.2.13 Fructose-bis-phosphate aldolase
4.1.3.7 Citrate synthase
4.2.1.2 Fumarate hydratase
4.2.1.3 Aconitate hydratase
4.2.1.11 Phosphopyruvate hydratase
5.3.1.9 Glucose-6-phosphate isomerase
5.4.2.1 Phosphoglycerate mutase
6.2.1.4 Succinate-CoA ligase

The IUBMB Enzyme Commission (EC) Numbers are all 4-figure numbers, the first of which denotes one of ONLY 6 CLASSES of enzyme as shown above. These identify the biochemical nature of every reaction and are worth memorising

Designed by Donald Nicholson © 2002 IUBMB

# Citric acid cycle

When cursor points to a box further details will be displayed in a tooltip window. If you click on the box you will change to appropriate reaction scheme or enzyme specification.




© IUBMB 2003

---

**Note:** The bold bond shows the carboxymethyl group originating from the acetyl-CoA.

---

The overall reaction is:

$$CH_3\text{-}CO\text{-}S\text{-}CoA + H_2O + GDP + P_i = \mathbf{2}\ CO_2 + \mathbf{4}\ \mathbf{x}\ 2H + HS\text{-}CoA + GTP$$

---

Cyanobacteria lack EC 1.2.4.2 oxoglutarate dehydrogenase (succinyl-transferring). Instead they convert 2-oxoglutarate to succinate semialdehye, see Zhang S, Bryant DA. The tricarboxylic acid cycle in

cyanobacteria. *Science* 334 (2011) 1551-1553. [PMID: 22174252]

---

Return to:

enzymes homepage.
stereochemistry of EC 2.3.3.1 citrate (*Si*)-synthase
oxo-acid dehydrogenase complex reactions
EC 1.1.1.37 malate dehydrogenase
EC 1.1.1.41 isocitrate dehydrogenase ($NAD^+$)
EC 1.1.1.42 isocitrate dehydrogenase ($NADP^+$)
EC 1.2.1.16 succinate-semialdehyde dehydrogenase [$NAD(P)^+$]
EC 1.2.1.24 succinate-semialdehyde dehydrogenase ($NAD^+$)
EC 1.2.1.79 succinate-semialdehyde dehydrogenase ($NADP^+$)
EC 1.2.4.2 oxoglutarate dehydrogenase (succinyl-transferring)
EC 1.3.5.1 succinate dehydrogenase (ubiquinone)
EC 1.8.1.4 dihydrolipoamide dehydrogenase
EC 2.3.1.61 dihydrolipoyllysine-residue succinyltransferase
EC 2.3.3.1 citrate (*Si*)-synthase
EC 4.1.1.71 2-oxoglutarate decarboxylase
EC 4.2.1.2 fumarate hydratase
EC 4.2.1.3 aconitate hydratase
EC 6.2.1.4 succinate-CoA ligase (GDP-forming)