

Hierarquia KEGG

▼ Metabolism

► Overview

▼ Carbohydrate metabolism

▼ 00010 Glycolysis / Gluconeogenesis [PATH:[ko00010](#)]

[K00844](#) HK; hexokinase [EC:[2.7.1.1](#)]

[K12407](#) GCK; glucokinase [EC:[2.7.1.2](#)]

[K00845](#) glk; glucokinase [EC:[2.7.1.2](#)]

[K01810](#) GPI, pgi; glucose-6-phosphate isomerase [EC:[5.3.1.9](#)]

[K06859](#) pgi1; glucose-6-phosphate isomerase, archaeal [EC:[5.3.1.9](#)]

[K13810](#) tal-pgi; transaldolase / glucose-6-phosphate isomerase [EC:[2.2.1.2](#) [5.3.1.9](#)]

[K15916](#) pgi-pmi; glucose/mannose-6-phosphate isomerase [EC:[5.3.1.9](#) [5.3.1.8](#)]

[K00850](#) pfkA, PFK; 6-phosphofructokinase 1 [EC:[2.7.1.11](#)]

[K16370](#) pfkB; 6-phosphofructokinase 2 [EC:[2.7.1.11](#)]

[K03841](#) FBP, fbp; fructose-1,6-bisphosphatase I [EC:[3.1.3.11](#)]

[K02446](#) glpX; fructose-1,6-bisphosphatase II [EC:[3.1.3.11](#)]

[K11532](#) glpX-SEBP; fructose-1,6-bisphosphatase II / sedoheptulose-1,7-bisphosphatase [EC:[3.1.3.11](#) [3.1.3.37](#)]

[K01086](#) fbp-SEBP; fructose-1,6-bisphosphatase I / sedoheptulose-1,7-bisphosphatase [EC:[3.1.3.11](#) [3.1.3.37](#)]

[K04041](#) fbp3; fructose-1,6-bisphosphatase III [EC:[3.1.3.11](#)]

[K01623](#) ALDO; fructose-bisphosphate aldolase, class I [EC:[4.1.2.13](#)]

[K11645](#) fbaB; fructose-bisphosphate aldolase, class I [EC:[4.1.2.13](#)]

[K01624](#) FBA, fbaA; fructose-bisphosphate aldolase, class II [EC:[4.1.2.13](#)]

[K01622](#) K01622; fructose 1,6-bisphosphate aldolase/phosphatase [EC:[4.1.2.13](#) [3.1.3.11](#)]

KEGG Orthology (KO)

- Integrar a informação genômica às redes protéicas através dos números EC.
- Utiliza identificadores comuns nos genomas e nas vias metabólicas.
- Grupos eram formados por análise manual de um banco de similaridades combinada com características evolutivas.
- Informação propagada utilizando ferramentas computacionais (KOALA)
- Peça chave para o sistema hierárquico do KEGG.
- 18949 KOs com 5320103 proteínas.

