Function Alignment

Introduction

Function Alignment is a tool that lists alignments of functional prediction for genes. It can be accessed via the second-level menu of Find Functions, as shown in Figure 1.

![Figure 1: Access Function Search.](image)

Keyword Search

The page of Function Alignment, as shown in Figure 2, searches alignments of functional prediction for genes in selected genomes by keyword. User first enters keyword, next selects COG or Pfam or both as filter to look for specific functions and genes.
The result page is split into two parts through tab view: COG and Pfam. If the Function Alignment search involves only one type of function, then either COG or Pfam tab view is displayed, not both (Figure 1).
User can also access Function Alignment from pages of **Gene Cart and Function Cart**.

**Genome Filter**

The Genome Filter is provided to limit the scope of search. The search is conducted on the genomes that user has saved through the **Genome Browser**. If user saves nothing, by default, it’s all genomes in IMG database. However, user can override the selection via the **Genome Filter** provided in the page.

For more information about **Genome Filter**, go to “Home > User Guide > Site Map”.

**Search Specifications**

All searches are case-insensitive. The “list” search has to be separated by “,”.
User can use a percent sign (%) as a wildcard in the middle of a keyword. The results will include any genes with zero or more additional characters at that position. For example, "hydro%ase" in “Gene Product Name” will get results with "hydrolase" and "hydrogenase", etc. If user wants only a single character of the keyword to be variable, type an underscore (_) in that position. Searching for "hydro_ase" will get results with "hydrolase," not "hydrogenase."