The Gene Ontology Newsletter

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RSC Publishing is GO!

Beginning in February 2007, all Royal Society of Chemistry (RSC) Publishing electronic journal articles will be enhanced to highlight compounds and scientific concepts. These highlighted words are hyperlinks to allow readers to download structures of chemical compounds, link to topic-specific online databases, and find related articles. Terms from the Gene Ontology and the Sequence Ontology, as well as several other classification systems, will be used to highlight the scientific concepts in the articles. Compounds and ontology terms will be published as RSS feeds, enabling automated discovery of relevant research. More information is available from the Project Prospect website:

http://www.rsc.org/Publishing/Journals/ProjectProspect/index.asp

Gene of the Quarter: MSH2

MSH2 is a member of a highly conserved family of proteins involved in DNA mismatch repair that includes *E. coli* MutS and *S. cerevisiae* Msh2p. Mutations in human *MSH2* result in hereditary nonpolyposis colorectal cancer (HNPCC) and several sporadic cancers. Linking the human *MSH2* gene to HNPCC was facilitated by prior characterization of *E. coli MutS* and *S. cerevisiae MSH2* (Fishel R, et al. (1993) Cell 75:1027).

specific damaged DNA bridge DNA b

In order to summarize the knowledge in the published literature for MSH2, 125 GO annotations based on

(http://www.geneontology.org/GO.current.annotations.shtml).

experimental evidence, were made for human MSH2 and its predicted orthologs. The annotations are consistent with the known role of MSH2 in DNA repair but the variety of terms used in the annotations illustrates the level of experimental knowledge in each species and may point to subtle functional differences. MSH2 annotations (including a full version of the graphic shown above) can be viewed at http://www.geneontology.org/images/RefGenomeGraphs/609309.html or downloaded with other annotations for an organism from the GO website

About "Gene of the Quarter": In 2006, the GO consortium initiated the reference genome project to provide complete GO annotations for orthologs of human disease genes in a set of 12 model organisms. Please contact go-help@geneontology.org with comments, additional annotations, or suggestions for disease-related genes to annotate.

GO Now is_a Complete

In January, Biological Process became the final ontology to be made "is_a complete", meaning each term in the hierarchy has at least one is_a relationship path to the top node (see Newsletter Issue 1). This change also resulted in various improvements to the ontology such as the introduction of new top-level terms to distinguish single cell, multi-cellular and multi-organism processes.

New Genomes GO Annotated

TIGR has released GO annotations for three genomes from tick-borne bacteria: Neorickettsia sennetsu, Ehrlichia chaffeensis and Anaplasma phagocytophilum. These and other annotations may be downloaded from http://www.geneontology.org/ GO.current.annotations.shtml.

TIGR GO Annotation Courses

Prokaryotic Annotation Training and Analysis Courses in 2007: March 27-29, June 12-14, August 21-23, October 16-18

New Eukaryotic Annotation Training and Analysis Courses in 2007: March 6-8, June 26-28, September 18-20

http://www.tigr.org/edutraining/training/

There will not be a GOC annotation camp this year.

Upcoming Meetings

PAMGO workshop August 8-10, 2007 Virginia Bioinformatics Institute http://pamgo.vbi.vt.edu/activities.php

2nd International Biocurator Meeting October 25-28, 2007 Dolce Hayes Mansion, San Jose, CA http://biocurator.org/Mtg2007

New Evidence Code: Inferred from Genomic Context (IGC)

A new evidence code, "Inferred from Genomic Context" (IGC), has been added to the GO set for use when an annotation attached to a gene product is derived using information about other gene products in a genome. These additional genes can be neighbors, as in operons and syntenic regions, or spread throughout the genome. An example of an IGC-based annotation is metabolic pathway reconstruction, where the presence of an entire set of required genes is evidence that each gene in the set can be annotated to the biological process in question. See http://www.geneontology.org/GO.evidence.shtmI for additional documentation on IGC.

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