

Cardiovascular Physiology and Muscle Content Meetings

Two large-scale additions were made to the Gene Ontology in October 2007 as the result of specialized content meetings with experts in the domains of blood pressure regulation and muscle development. The blood pressure meeting, held at the Medical College of Wisconsin, brought about the addition of 119 new terms and the refinement of many definitions and relationships. The more detailed global view of blood pressure regulation and the revised ontology structure take into account many of the intertwined processes that contribute to this important biological area. The muscle meeting, which took place at the University of Padua, Italy, resulted in a greatly expanded representation of muscle development with the addition of 159 new terms.

To see the blood pressure regulation and muscle terms, respectively, go to the AmiGO Advanced Search, type `mtg_cardio` or `mtg_muscle` in the query box, and select Search type 'All fields': http://amigo.geneontology.org/advanced_query

If you would like to participate in the community annotation of gene products to these new terms, please visit the community annotation wikis.

Cardiovascular physiology: <http://wiki.geneontology.org/index.php/Cardiovascular>
Muscle development: http://wiki.geneontology.org/index.php/Muscle_Biology

How to Get Started with GO: Annotation SOPs

To foster best practices in groups starting to make their own GO annotations, the Gene Ontology Consortium has produced a new guide to annotation which provides a general introduction to ways in which groups can make literature-based, electronic, and sequence-based annotations. We have also provided guidance on which method is best for different user needs. If your workflow or needs are not addressed in this guide, please contact GO.

View the SOP guide: <http://www.geneontology.org/GO.annotation.SOP.shtml>

Evidence Code Update

GOC has released a major revision of the Evidence Code Guide, incorporating recent changes to code usage, and including examples of when specific evidence codes should and should not be used. The new guidelines will help curators select the correct codes and standardize usage across groups. Other improvements include 'last updated' date stamps showing when changes were made regarding each code, and grouping of codes based on how they are assigned, e.g., IMP, IDA, IGI, IPI and IEP are classed together as 'experimental evidence codes'. Documentation for ISS is unchanged but flagged as 'under review', as the usage of this code is under discussion; details will be included in a future newsletter.

View the evidence code guide: <http://www.geneontology.org/GO.evidence.shtml>

With (or) From field

The 'With (or) From' field is used to hold an additional identifier for annotations that use certain evidence codes. Currently the field is mandatory for annotations using the evidence codes IC, ISS and IEA, and recommended for annotations using the evidence codes IPI, IGI or IGC. The identifier must be a valid database accession ID. For IC, the GO term on the basis of which the annotation was made must be placed in the field. For the other evidence codes, it will be the structurally similar gene/protein or the interacting partner molecule.

See the GO annotation file format guide for more information:
<http://www.geneontology.org/GO.format.annotation.shtml>

Cardiovascular Gene Ontology Annotation Initiative

A new University College London-based Cardiovascular Gene Ontology Annotation initiative started on 1 November 2007. The project is supported by the British Heart Foundation, and aims to prioritize the annotation of human genes associated with the cardiovascular system, in order to provide full GO annotation to genes associated with cardiovascular processes. For more information, please visit this URL:

<http://www.ucl.ac.uk/medicine/cardiovascular-genetics/geneontology.html>

New Subcellular Location2GO mapping (spsl2go)

The UniProt GOA group at EBI are pleased to announce a new mapping of UniProtKB subcellular locations to GO terms. The mapping was produced in collaboration with Serenella Ferro Rojas of the Swiss Institute of Bioinformatics. To date, 269 subcellular location terms from the comment (CC) lines of UniProtKB entries have been manually mapped to the equivalent GO terms. The new mapping has been applied electronically to enhance the electronic GO annotations (assigned the IEA evidence code) in our latest GOA release, providing 418,185 new associations with 396,734 proteins.

The `spsl2go` mapping file is available from the GOA FTP site:

<ftp://ftp.ebi.ac.uk/pub/databases/GO/goa/external2go/spsl2go>

and from the Gene Ontology Consortium website:
<http://www.geneontology.org/external2go/spsl2go>

The GO reference for this mapping is `GO_REF:0000023`.

Upcoming Meetings

1-5 Dec 2007: ASCB 47th Annual Meeting
Washington, D.C.
<http://www.ascb.org/meetings/>

6-9 Dec 2007: Rat Genomics & Models
Cold Spring Harbor, New York
<http://meetings.cshl.edu/meetings/rodent07.shtml>

5-9 Jan 2008: Genetic Analysis: Model Organisms to Human Biology
San Diego, California
<http://www.gsa-modelorganisms.org/>

12-16 Jan 2008: Plant and Animal Genome XVI
San Diego, California
<http://www.intl-pag.org/>

View Expanded Newsletter Online: <http://www.geneontology.org/newsletter/archive/200711.shtml>

To Receive Future Newsletters: Subscribe to the GO Friends mailing list (gofriends@geneontology.org)

Contact the Gene Ontology Consortium: Please send comments or questions to gohelp@geneontology.org