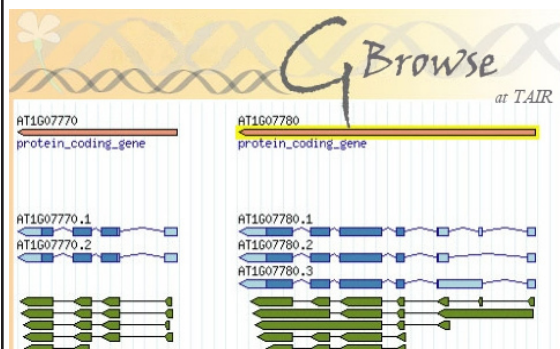




TAIR Newsletter Fall 2007

GBrowse now available at TAIR

The Generic Genome browser, developed by the Generic Model Organism Database (GMOD) project, is now available at TAIR. Search or browse a map of the *Arabidopsis* ge-



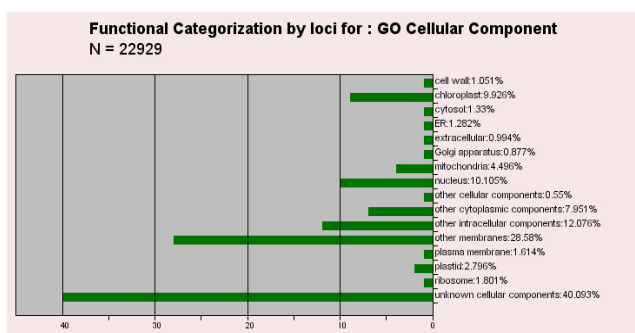
nome (including genes, cDNAs and ESTs, insertion mutants, SNPs, markers and BACs) or upload your own annotation track. Tracks can be easily customized by turning on and off specific data types, collapsing and expanding tracks, or changing track order. We also added a track with a VISTA plot displaying nucleotide similarity of the *Arabidopsis* genome to the poplar genome. See Mayor *et al* 2000 Bioinformatics article for more information on the VISTA tool.

Perlegen SNPs now available

249,052 high-quality SNPs discovered with Perlegen resequencing arrays now available from TAIR polymorphism search and SeqViewer. More than 1 million SNPs discovered at various false discovery rates are available at the TAIR FTP site, as are 13,470 predictions of highly polymorphic or deleted regions. See the Clark *et al*. 2007 Science article for more details.

New Bar Charts for GO Classification

You can view the current GO annotation of the whole genome or your set of genes in either



pie chart (based on annotation numbers) or the new bar chart (based on gene numbers) format. To see the bar charts, select 'Gene Bar Chart' when drawing results from Functional Categorization. Formulas that define the percentages in each slice/bar are provided. When using charts generated using TAIR in publications, please provide the date of analysis for reference purposes.

AraCyc Metabolic Pathway Updates

(<http://www.arabidopsis.org/biocyc/index.jsp>)

50 new pathways have been added, and 65 updated in the recent two releases, AraCyc 4.0 and 4.1. To date, 85% of the 283 total pathways have been experimentally confirmed. The remaining pathways lack sufficient experimental data to be confirmed. However, they have

been validated by a curator who has assessed that their computational prediction was justified based on a number of clues from the literature. In addition, in the July release of 4.0, the AraCyc genes have been updated to reflect the latest function annotations of the TAIR 7 Arabidopsis genome release. As a result, a significant proportion of gene assignments to reactions (which are based on the functional annotations of genes) have been updated: 1327 old assignments (19% of total) have been removed and 952 new assignments have been added.

Note: if you prefer not to receive future email updates from us, please log in to your TAIR account and update your profile by unchecking the 'Email me monthly TAIR release notes' check box.

To view previous news releases, go to <http://arabidopsis.org/news/news.jsp>

TAIR is committed to providing the best possible service to the Arabidopsis community. Should you have any questions or suggestions please contact us at curator@arabidopsis.org