



Nome News Issue 31

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Meetings attended

Last month, Elspeth, Matt and Michael travelled to the Jackson Laboratory in Maine to meet with our counterparts from the Mouse Genomic Nomenclature Committee ([MGNC](#)). This was a productive and enjoyable meeting, in which we discussed specific gene families, policy issues, phenotype-based nomenclature, and especially the standardisation of nomenclature across species as part of our collaboration on the HUMOT (Human & Mouse Orthologous Gene Nomenclature) Project. Staff from the Rat Genome Database ([RGD](#)) were also in attendance to discuss co-ordinating gene nomenclature for all three species.

Hot Topic

Our current hot topic: 'Does it matter if a disease phenotype and its causative cloned gene have the SAME symbol?', we are asking you to vote on the following two options:

- 1) Introduce a new symbol or add some extra letter to the phenotype symbol, in each case as a temporary solution.
- 2) Keep the original phenotype-derived name and symbol until more is known about the normal function of the gene.

Your response so far shows how divisive this issue is, with 58% voting for option 1 and 42% voting for option 2. Therefore we would encourage all who have not voted yet to email us at hgnc@genenames.org to ensure your view is taken into account.

FTP download page to be retired

We are planning to take down our static FTP download page very soon, as this has been superseded by our new [enhanced download](#) page. Please update your bookmarks and scripts to ensure they point to the new download page. If you have any questions about this please contact us at hgnc@genenames.org.

If you would like to be added to our Nome News mailing list or if you have questions or comments on any human gene nomenclature issue, please email us at: hgnc@genenames.org

HUGOA

Having attended the [Gene Ontology \(GO\) Annotation Camp](#) at Stanford University, Varsha is now adding GO terms to the [UniProt](#) database at the European Bioinformatics Institute ([EBI](#)), under the tutelage of Ruth. To date the HUGOA project has resulted in the annotation of 553 terms to 124 proteins .

New Orthology Search Tool

The [HGNC](#), [MGI](#), [Homologene](#), [Ensembl](#), [PhIGs](#) and [Inparanoid](#) each provide their own orthology information, and previously researchers had to check each of these resources to confirm an orthology prediction. However, we have now collated all of the information from these resources into the HUMOT Comparison of Orthology Predictions (HCOP) database. The [HCOP](#) search engine returns the known orthology assertions for human and mouse genes and also the official nomenclatures (where assigned), sequence accessions, aliases, database identifiers, and chromosomal locations.

The HCOP will make orthology searching quicker and help to expedite the HUMOT project itself when making orthology assertions between human and mouse genes. Indeed, prior to making HCOP public we used it to generate comparative files, which are especially useful in identifying human/mouse ortholog pairs with different approved gene symbols. In each case we will attempt to change either the human or mouse approved nomenclature (whenever possible), so that ortholog pairs have the equivalent nomenclature.

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