# Nome News Issue 40

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*< Previous Issue*

*Next Issue >*

## New Gene Family Resources

We continually develop new gene family webpages, or update our existing pages, wherever we feel there is a community need for such a resource. For example, we have recently established a Voltage-Gated Ion Channel resource that includes all of the human genes that encode these channels. These data were derived from the latest compendium of voltage-gated ion channels as published by the Nomenclature Committee of the International Union of Pharmacology (NC-IUPHAR) in 2005. Other recent additions are the protein tyrosine phosphatase (PTP) family, and the proteoglycans. A resource page for the non-protein-coding RNAs in the HGNC database has also been generated. We welcome suggestions for other families that could be added to our gene family pages.

## HCOP Update

The HGNC Comparison of Orthology Predictions search tool, HCOP, enables users to compare orthologs predicted for human genes in 5 other genomes (mouse, rat, dog, chicken and fruitfly).

We have now added human-mouse and human-rat orthology annotations from the Evola (Evolutionary Annotation) dataset, part of the H-Invitational Database(H-InvDB), to the HCOP search tool. This means there are now 9 independent orthology datasets available for comparison in HCOP.

Users can assess the reliability of the prediction from the number of these different sources that identify a particular orthologous pair. We intend to further expand HCOP to include orthology information from other orthology prediction databases and other species, and would welcome your comments and suggestions.

## Upcoming Meetings

### HGM2007

The 12th HUGO Human Genome Meeting, HGM2007, will be held from 21-24th May 2007 in Montreal, Canada. Members of the HGNC, MGNC and RGNC will be attending this meeting, so please come and see us in booth 509 to discuss gene nomenclature or other issues.

### HGVS 2007

Tam and Sue will be attending the Human Genome Variation Society (HGVS) meeting "Pharmacogenetics and Human Genome Variation" which is being held on the 21st of May as a satellite event to HGM2007 in Montreal, Canada. Tam will present a poster as a follow-up on the issue of copy number variants which was discussed at last years HGVS/HGNC side meeting.

## Transfer RNA Gene Nomenclature

The HGNC recently reviewed the nomenclature for the genes encoding the cytoplasmic transfer RNAs. To reflect the current usage in the literature the stem symbol for the transfer RNAs has been updated to "TRNAx", where "x" is the single letter code for the amino acid transferred by the specific tRNA molecule. Due to the highly repetitive nature of the tRNA gene family, and the high incidence of pseudogenes, the HGNC will only name genes for cytoplasmic tRNAs for which there is transcriptional evidence, genomic location and sequence available. The current HGNC cytoplasmic tRNA gene records can be viewed from the non-protein-coding RNA resource page.

## IGSF4 Family Nomenclature

Following extensive discussions with the scientific community a new nomenclature system for the IGSF4 family has been agreed. The new stem symbol and name is CADM, "cell adhesion molecule". It was agreed that the numbering of the family should be based on Biederer's analysis of this family (Biederer, 2006) with IGSF4 (alias TSLC1, NECL2, SynCAM1) renamed as CADM1, IGSF4D (alias NECL3, SynCAM2) as CADM2, IGSF4B (alias TSLL1, NECL1, SynCAM3) as CADM3, IGSF4C (alias TSLL2, NECL4, SynCAM4) as CADM4.

## Nature Publishing Group

Elspeth and Sue enjoyed a recent meeting with Chris Gunter from Nature and Magdalena Skipper from Nature Reviews Genetics, discussing the use of approved gene nomenclature in these journals and others within the Nature Publishing Group. Both have agreed to ensure that their author guidelines will include a note on using approved gene nomenclature, and they aim for this to be included in a standardised set of guidelines for all Nature-titled journals. We hope that if both Nature and Nature Reviews Genetics take a more "hardline" stance on nomenclature (as Nature Genetics already do) that this will encourage other high impact journals to use standardised gene nomenclature more systematically.

## Meetings Attended

Ruth attended the Gene Ontology (GO) Consortium meeting in Cambridge, 8-10th January, and presented a poster entitled "Summary of the collaboration between HGNC and GOA". During the meeting evidence codes, user advocacy, ontology development and other aspects of GO were discussed.

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:
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