HGNC
HUGO Gene Nomenclature Committee

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Nome News Issue 15

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Meetings

Michael travelled to Munich (18-20 September) for the "YAPC: The_Science_of_Perl" conference. This workshop-based conference provided lots of ideas that we hope to use to our advantage in our next upgrade of Genew. Genew4 will be developed for use next year and will enable online editing, and dynamic interaction with our in-house blast database. This will use PHP software as the front end interface for a PostgresQL database.

Sue, Hester, Elspeth and Matt were all at the ASHG meeting in Baltimore (15-19 October) this year, where we shared an exhibitor's booth with HUGO. As an alternative to checking posters directly for use of approved gene symbols, this year we scanned the abstracts in advance. From this information we prepared 46 letters explaining about approved gene symbols and placed them in the pigeon holes at ASHG, asking the authors to visit the booth to discuss their posters with us. This generated nine extra visitors and has since been followed by emails from three other authors.

This new strategy has proven far more successful and less time consuming than some previous ideas. At ASHG last year we visited all 2049 posters over the course of the conference and wrote to 160 authors afterwards explaining about approved gene symbols. Unfortunately, only five authors contacted us as a result.

Genew Database

We are still working towards version 4 of Genew, and in the meantime have added a new gene status, "Approved Non-Human". This currently includes 64 entries that are approved in order to maintain the orthologous symbol in the human series. It is quite likely that most of these genes will ultimately be found in the human genome. Each "Approved Non-Human" gene symbol has links to the appropriate non-human sequence accession ID where possible.

We are also testing a new field designated "Locus Type", where we can store data regarding the type of entry, examples so far include "pseudogene" and "phenotype only".

Gene Family Nomenclature in Nature Genetics

Nature Genetics' new supplement, "A User's Guide to the Human Genome" strongly emphasised the importance of approved gene symbols, under the answer to Question 8: "*How can one find all the members of a human gene family?*". For further details see doi:10.1038/ng973

Funding and Staffing

Our current funding from NIH has been extended until October 2003 to include an extra Post-Doctoral Nomenclature Editor. We have advertised for this position and hope that the new editor will be in post by December 2002. We have successfully continued to obtain travel funds for conference and workshop attendance from: the H-Invitational, HAWK2, The Royal Society and the UCL Graduate School Fund. We would very much like to thank them for their help.

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