



Nome News Issue 28

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Staff Recruitment

We are currently looking to employ a new Gene Nomenclature Advisor. This post, working in a small team based at University College London, is funded by the National Human Genome Research Institute (NHGRI) for two years in the first instance.

Chromosome Projects

This month we are highlighting our collaboration with the Human Genome Project chromosome-specific annotation groups. Over the past few years, we have been checking the gene data submitted to us from each of these chromosome groups to ensure every gene locus is assigned a unique approved symbol. We have been confirming that symbols are correct for known genes, and where possible we have provided new approved gene symbols for the previously unnamed and newly discovered genes. This has meant that when each human chromosome is published there are a high number of approved symbols available immediately, and indeed Nature now insists that approved symbols are used where they are available in these publications.

A good example of the value of this work is the recently published gene map of the extended human MHC ([PMID:15573121](#)) where 100% of the genes identified had approved symbols.

Furthermore, once chromosomes are published we have continued to work with the data, and have now provided approved symbols for over 98% of all the reported known genes on chromosomes 6, 9,10, 13 and 14.

Downloads

With the new [Genew downloads page](#) working smoothly, it should be noted that the CGI script ([gdlw](#)) is able to produce far more tailored outputs. For instance, the interface allows users to select which columns to output, can limit by chromosome and executes SQL queries and subqueries. Additionally these searches can be saved, either as bookmarks allowing them to be rerun at any time, or as [PHP](#) and [perl](#) code (see the Output format menu on the [custom downloads](#) page.)

The [PHP code](#) option is suitable for embedding into any [PHP](#) web page. This allows an HTML table to be dynamically generated by [gdlw](#) each time the page loads. We already use this feature in our new look [Symbol Report](#) page and plan to use it to automatically update our [gene family pages](#) from Genew.

The perl code option generates a short perl script that uses [LWP::Simple](#) to execute the saved search and prints it to STDOUT. It would be trivial to modify this code to feed the data directly to an application or local database. Another useful output format is 'Show SQL' as it displays the actual SQL query that is being generated by [gdlw](#); this is often helpful when debugging a query.

There is further information on using [gdlw](#) on the [Program Documentation](#) page. If you need help in using any of these features or have suggestions for new [gdlw](#) features please [email](#) us.

Upcoming Meetings

Michael attended the Workshop on Database Issues in Biological Databases (DBiBD) held in Edinburgh, U.K. (8-9 January 2005).

Tam has been selected to participate in the International Workshop on Encoding Information in DNA Sequences to be held in Okinawa, Japan (21-27 February 2005). He will be presenting a poster on the organisation and phylogenetic relationship of chromosome 16 segmental duplications associated with the polycystic kidney disease 1 (*PKD1*) gene.

Publication

Horton R, Wilming L, Rand V, Lovering RC, Bruford EA, Khodiyar VK, Lush MJ, Povey S, Talbot CC, Wright MW, Wain HM, Trowsdale J, Ziegler A & Beck S. Gene Map of the Extended MHC. Nature Reviews Genetics 2004 (5):889-899 (2004) [PMID:15573121](#)

Also, members of HGNC were acknowledged in a recent publication ([PMID:15608191](#)) by [IMGT/GENE-DG](#).

Congratulations

Congratulations to Dr Tina Eyre on passing her PhD viva this month.