



Nome News Issue 11

Issue 11. March 2002

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Email Increase

We had the highest ever number of emails in one month in January this year, a grand total of 818. During this time we succeeded in approving 154 new symbols.

Meetings

Hester and Elspeth attended The Human Annotation Workshop (Wellcome Trust Genome Campus, Hinxton, UK) 1 - 3 March, at which Hester spoke on "The Nomenclature Revolution".

Ruth will be attending The Ontologies Workshop. From Genotype to Phenotype: Linking Bioinformatics and Medical Informatics Ontologies (Manchester, UK) 23 - 24 March and will be speaking on "Nomenclature: The Language of Genomics".

Once again at the [HGM meeting](#) (Shanghai, China) 14 - 17 April 2002 we are able to offer poster prizes for the two posters which contain the HIGHEST NUMBER of correct gene symbols. This will be judged by members of the HGNC team with a score of +1 for use of a correct symbol and -3 for an incorrect one. The prizes are a year's subscription to Nature Genetics, and a year's subscription to Nature Reviews Genetics, whom we would like to thank for their support. Please come and see us at booth 7B to discuss nomenclature.

Gene Families

STARD START domain containing
DCLRE DNA cross-link repair (PSO2 homolog, S. cerevisiae)
TRP transient receptor potential cation channel

Symbol Updates

[SNAI](#) snail homologs

Publications

Wain, H.M, Lush M, Ducluzeau, F, Povey, S. Genew: The Human Nomenclature Database. [Nucleic Acids Research](#) 2002 Vol. 30, No. 1 169-171. PMID: 11752283

BLAST

Our lblast database system described at the O'Reilly Bioinformatics Technology Conference by Michael, comprises a set of Perl scripts that provide active maintenance of sequence annotation and automatic sequence importation into the lblast database. Thus reflecting changes made to the Genew database on an ongoing basis. The lblast database is assembled from five scattered sources of sequence data into a co-ordinated body:

1. Legacy sequences (229 unsorted sequences from our previous filing system).
2. Sequences held within Genew (2700+).
3. Bulk submissions (1300+ provided by chromosome sequencing consortia).
4. SRS downloads (18000+ accession IDs and Ref_Seq IDs from Genew).
5. User_contrib (~200 sequences that have been searched against the lblast database in the previous 4 weeks).

Perl Scripts

We have two new Perl scripts online:

[srs_get.pl](#)

This program takes a list of accession numbers or refseq ID's from a file or STDIN, attempts to download them from any one of a number specified SRS servers and prints the data to STDOUT.

[mini_srs_get.pl](#)

This is a simplified version of srs_get.pl.

New Downloadable Files

<http://www.gene.ucl.ac.uk/public-files/nomen/chr20.txt>

Chromosome 20 Specific

HGNC	Symbol	Previous symbol	Alias	Acc ID	Location
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