# HGNC
HUGO Gene Nomenclature Committee

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# HGNC Newsletter Autumn 2009

**There are currently 28483 approved symbols**

**In this newsletter:** we have made quite a few changes to our website over the last few months, with the addition of a brand new search tool, a permanent statistics feature and a comprehensive ncRNA page.  The HGNC also hosted a two day workshop with colleagues to discuss the important issue of coordinating gene nomenclature across vertebrate species.

## The new List Search

You can now search our database for multiple gene symbols in one step by using our List Search tool, which you can access by clicking on the orange Gene Search button on any page of the HGNC website. Lists of symbols can be typed, pasted or uploaded from a file.  The results include a 'match type' column that shows how each submitted symbol matches the relevant HGNC gene record.  You can also connect to an advanced version of the tool from the results page, which supports case sensitive searching and provides extra options for the results format.  Happy searching!

## ncRNA page update

The HGNC ncRNA webpage presents our work to date on naming ncRNA (non-protein-coding RNA) genes.  The field of RNA research is rapidly expanding with a concomitant increase in the number of ncRNAs identified.  We are actively engaging the RNA research community in order to provide unique names for each sequence that encodes an ncRNA. For instance, our work with both Rfam and miRBase databases for the microRNAs has lead to a unique name for every known human gene encoding a pre-miRNA and each resultant mature miRNA product (e.g. the *MIR100* gene encodes the hsa-mir-100 pre-miRNA).  Another example is our close collaboration with the snoRNA-LBME-db database which has produced a systematic nomenclature for genes encoding the small nucleolar RNAs (snoRNAs): *SNORA#* (small nucleolar RNA, H/ACA box containing #), *SNORD#* (small nucleolar RNA, C/D box containing #) and *SCARNA#* (small Cajal body-specific RNA #). To date we have named about 2000 human genes that encode ncRNAs, transfer RNAs (tRNAs), ribosomal RNAs (rRNAs), spliceosomal RNAs, long ncRNAs and ncRNA host genes.  We hope that this single resource for all classes of ncRNA genes will be a useful tool for researchers.

We continually aim to develop new gene family webpages, or update our existing pages, whenever we feel there is a community need for such a resource. We welcome your suggestions for additional families or gene groupings that could be added to our gene family pages.

## Statistics and Downloads

Our Downloads page has had a makeover and following user requests now includes statistics on the types of entries in our database with quick links to download these data.  For example, you can now see how many protein-coding genes vs. non-coding RNA genes have been given HGNC approved symbols.  For each dataset you can click the blue icon to download the HGNC core fields as a tab delimited text file. Alternatively, click the red icon to download your own selection of data fields from the Custom Downloads page. For a full description of HGNC data fields, visit the Column Name Definitions page.  The custom downloads page also provides a choice of data output formats, including tab delimited text file, html table, and full Gene Report table.

## Meeting News

Susan attended the 11th International Meeting on Human Genome Variation and Complex Genome Analysis HGV2009 in beautiful Tallinn, Estonia from 11th-13th September.  She presented a poster entitled "A Nomenclature for Copy Number Variable Genes?" designed to elicit opinions on potential CNV gene nomenclature schemes from members of the research community. If you have any comments or suggestions on CNV gene naming please email us.

The HGNC hosted a two day meeting in Cambridge this month, GNAS2009, with invited representatives from gene nomenclature groups, vertebrate genomes, genome databases and orthology resources, and gene family experts. The aim of the meeting was to discuss naming genes consistently across vertebrate species, and we are hopeful that, based on very productive discussions, we can produce some common guidelines and proposals for unifying vertebrate gene naming.

Elspeth is currently at the 59th ASHG meeting (20th-24th October) in Honolulu, Hawaii.  If you are at the meeting and have any gene nomenclature questions please go and see Elspeth at booth 333 in the exhibit hall, which HGNC is sharing with HUGO.

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

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