

## Suggested Xenopus Gene Name Guidelines

The following represents a draft proposal for Xenopus gene nomenclature standards. The revised guidelines are in response to some criticisms of the de facto guidelines presently in use. These suggestions are very closely aligned with zebrafish nomenclature standards and are also consistent with mammalian gene naming conventions. The suggestions are the result of an online survey and many e-mails and telephone calls. Respondents (50) were from Britain, Canada, the Czech Republic, France, Germany, Japan, the Netherlands, Switzerland and the USA. In general there was a lot of consensus, although each suggested guideline was objected to by at least one respondent.

### Suggested naming conventions:

\*Xenopus gene names and symbols should be identical to human gene names whenever possible\*.

Note that names are not the same as symbols- please be sure to use the correct form, symbol or name, in the correct place. The JGI field "**name**" should contain the gene symbol, but all in lower case. Please copy the HUGO approved gene symbol directly from NCBI Gene and change the case.

<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?CMD=search&DB=gene>

For example, PAX2 would be entered as pax2

The define field should begin with the full approved gene name. Once again, please get this from Gene. If the gene name is all that you are placing in the define, this is all you need. If you want to include additional contextual information (e.g. transcription factor, zinc finger, whatever), please place a semi-colon at the end of the gene name. For example;

name: pax2  
define: paired box gene 2; paired family transcription factor

In examples where the mammalian gene name is a reference to an original Xenopus name, the Xenopus name will be retained. For example chordin in humans is called chordin-like. In this case the gene would retain the name chordin.

If the human gene name include reference to a third species, for example "disheveled homolog 1 (Drosophila)" do not include the Drosophila in brackets.

If the human name is crazy and the mouse name makes sense, please contact us to discuss the example (we will form a nomenclature committee). When identity is uncertain be cautious. Use a temporary name like “cdx2 like” until more information is available, at which time the name would be changed.

Gene names should not begin with an “X” unless the X is a part of a standard word (e.g. xenobiotic). The species will be listed in another field.

When a gene is duplicated in *Xenopus* relative to mammals, please name the human ortholog with the same name and symbols as the human gene. Metazome will help in assigning this relationship. Name the second gene (in the example of *pax2*), *pax2* gene 2, the symbol would be *pax2.2*

If the two genes are equidistant from the human gene, name one gene *pax2.1* and the other *pax2.2* (name *pax2* gene 1 and *pax2* gene 2)

Orthology to a mammalian gene must be based on more information than a blast result in order to have the mammalian gene name applied. Synteny data from <http://www.metazome.net> will help enormously here. If no additional data is available please use a provisional name.

#### \*GENE SYMBOLS\*

1. Gene symbols should be the same as the HUGO human gene symbol. Look these up at NCBI's Gene .
2. Symbols are short-form representations (or abbreviations) of the descriptive gene name.
3. Symbols should not begin with an X unless part of a gene name abbreviation.
4. Symbols should only contain Latin letters and Arabic numerals and all be in lower case. e.g. SLC4A4 -> *slc4a4*. Please use all lower case, even for terms like ATPase (in a symbol, this would be *atp*).

These guidelines hope to fully integrate *Xenopus* data with that of other model systems, especially mammalian. Other systems, such as zebrafish and chick, have adopted almost identical guidelines and are also using the human gene names. This will make cross-database queries much simpler, as will modifications such as deleting punctuation. Searching for *pax2* will find all of the *pax2* genes, and you will no longer have to do *pax2*, *pax-2*, *pax.2* searches. If you would like to volunteer for the nomenclature committee please contact us. /body>