## Scientific Style

Genus and species names should be in *italics*.


## Abbreviations and Genetic Nomenclature

Avoid using unnecessary abbreviations. The full term for which an abbreviation stands should precede its first use in the text unless it is a standard unit of measurement. Abbreviations should follow the rules and recommendations of the IUPAC-IUB Commission on Biochemical Nomenclature (CBN) at http://www.chem.qmul.ac.uk/iubmb/nomenclature/. Genus or species names, gene symbols, mathematical formulae and any other words to be given special emphasis should be underlined once for italics. Similar signs have to be clearly distinguished, e.g. 1 (one) and I (letter), or 0 (zero) and O (letter). Use S.I. units for linear dimensions, body mass, and clinical chemistry. Use the degree Celsius for temperature.

Gene symbols have to be given in italics; authors should use the approved genetic nomenclature as it can be found for different organisms at corresponding websites; some common examples are given here:

· Human:  http://www.genenames.org/about/guidelines
· Mouse: http://www.informatics.jax.org/mgihome/nomen/
· Rat: http://rgd.mcw.edu/nomen/nomen.shtml
· Chicken: http://www.agnc.msstate.edu/
· Anolis lizard http://lizardbase.org/pages/agnc.html
· *Xenopus*: http://www.xenbase.org/gene/static/geneNomenclature.jsp
· Zebrafish: https://wiki.zfin.org/display/general/ZFIN+Zebrafish+Nomenclature+Guidelines
· *Drosophila*: http://flybase.org/static_pages/docs/nomenclature/nomenclature3.html
· *C. elegans*: http://wiki.wormbase.org/index.php/Nomenclature
· *Arabidopsis*: http://www.arabidopsis.org/portals/nomenclature/guidelines.jsp
· *S. cerevisiae*: http://www.yeastgenome.org/gene_guidelines.shtml
· *S. pombe*: http://www.pombase.org/submit-data/gene-naming-guidelines


If novel alleles of common genes or new genes are discussed, corresponding gene symbols should be approved by the corresponding nomenclature committee prior to submission.


**Standard Abbreviations currently being used are:**

| | | | |
|---|---|---|---|
| chr | Chromosome | FISH | fluorescence in situ hybridization |
| Da | dalton | SSCP | single strand conformational polymorphism |
| kDa | kilodalton | | |
| l | liter | LINE | long interspersed element |
| ml | milliliter | SINE | short interspersed element |
| PCR | polymerase chain reaction | MHC | major histocompatibility complex |
| ORF | open reading frame | HPLC | high performance liquid chromatography |
| cM | centimorgan | | |
| bp | base pair | SSLP | simple sequence length polymorphism |
| SDS | sodium dodecylsulfate | RFLP | restriction fragment length polymorphism |
| PAGE | polyacrylamide gel electrophoresis | | |
| | | PFGE | pulsed field gel electrophoresis |

**Data deposition**

Large-scale datasets, sequences, and mathematical models should be deposited in a relevant public databases prior to submission and accession codes should be provided in the Materials & Methods section. If necessary, please include in the manuscript the relevant information (username and password) for confidential access by peer-reviewers.

Data for which no suitable public database exists should be included, if possible, as dataset files in the Supplementary Material.

Microarray and sequencing-based functional genomics data should be deposited in the ArrayExpress (http://www.ebi.ac.uk/arrayexpress/), GEO (http://www.ncbi.nlm.nih.gov/geo/) or CIBEX (http://cibex.nig.ac.jp/index.jsp) databases in compliance to the MIAME (http://www.mged.org/Workgroups/MIAME/miame.html) standards and the MINSEQE (http://www.mged.org/minseqe/) draft proposal.

Mass spectrometry datasets should be deposited in a machine-readable format (e.g. mzML if possible) in one of the major public database, for example Pride (http://www.ebi.ac.uk/pride/) or PeptideAtlas (http://www.peptideatlas.org) and authors should follow the MIAPE recommendations (http://www.psidev.info/index.php?q=node/91).

Molecular interaction data should be deposited with a member of the International Molecular Exchange Consortium (IMEx, http://www.imexconsortium.org) prior to submission of the manuscript. Authors should follow the MIMIx recommendations (http://www.psidev.info/index.php?q=node/278).

Metabolomics data should be deposited following the recommendations of the Metabolomics Standards Initiative (MSI) (http://metabolomicssociety.org/index.php/resources/metabolomics-standards) in a recognised repository such as MetaboLights (http://www.ebi.ac.uk/metabolights/).

Nucleotide sequence data should be submitted to an International Nucleotide Sequence Database Collaboration member: GenBank (http://www.ncbi.nlm.nih.gov/genbank/), EMBL Nucleotide Sequence Database (http://www.ebi.ac.uk/embl/) or DDBJ (http://www.ddbj.nig.ac.jp/).

Human clinical and genomic datasets: We encourage authors to provide access to genotype and clinical data with as few restrictions as possible while respecting ethical obligations to the patients and relevant medical and legal issues. Such data should be deposited in one of the major public access-controlled repositories such as dbGAP (http://www.ncbi.nlm.nih.gov/gap) or EGA (http://www.ebi.ac.uk/ega). Simple genetic polymorphisms should be submitted to dbSNP (http://www.ncbi.nlm.nih.gov/SNP/).