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# DESCRIPTION

**Gene: X** is the open access mirror journal of **Gene**

*Gene: X* offers authors with high-quality research who want to publish in a gold open access journal the opportunity to make their work immediately, permanently, and freely accessible.

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*Gene* and *Gene: X* have the same aims and scope. A unified editorial team manages rigorous peer-review for both titles using the same submission system. The author's choice of journal is blinded to referees, ensuring the editorial process is identical.

For more information please refer to our FAQs for authors

*Gene* publishes papers that focus on the **regulation**, **expression**, **function** and **evolution** of **genes** in all biological contexts, including all prokaryotic and eukaryotic organisms, as well as viruses.

*Gene* strives to be a very diverse journal and topics in all fields will be considered for publication. Although not limited to the following, some general topics include:

- DNA Organization, Replication & Evolution -Focus on genomic DNA (chromosomal organization, comparative genomics, DNA replication, DNA repair, mobile DNA, mitochondrial DNA, chloroplast DNA).
- Expression & Function - Focus on functional RNAs (microRNAs, tRNAs, rRNAs, mRNA splicing, alternative polyadenylation)
- Regulation - Focus on processes that mediate gene-read out (epigenetics, chromatin, histone code, transcription, translation, protein degradation).
- Cell Signaling - Focus on mechanisms that control information flow into the nucleus to control gene expression (kinase and phosphatase pathways controlled by extra-cellular ligands, Wnt, Notch, TGFbeta/BMPs, FGFs, IGFs etc.)
• Profiling of gene expression and genetic variation - Focus on high throughput approaches (e.g., DeepSeq, ChIP-Seq, Affymetrix microarrays, proteomics) that define gene regulatory circuitry, molecular pathways and protein/protein networks.

• Genetics - Focus on development in model organisms (e.g., mouse, frog, fruit fly, worm), human genetic variation, population genetics, as well as agricultural and veterinary genetics.

• Molecular Pathology & Regenerative Medicine - Focus on the deregulation of molecular processes in human diseases and mechanisms supporting regeneration of tissues through pluripotent or multipotent stem cells.

Gene encourages submission of novel manuscripts that present a reasonable level of analysis, functional relevance and/or mechanistic insight. Gene also welcomes papers that have predominantly a descriptive component but improve the essential basis of knowledge for subsequent functional studies, or provide important confirmation of recently published discoveries.

The primary criteria for acceptance are that the work is original and scientifically sound. The journal appreciates that standards of novelty are arbitrary, differ among disciplines and geographic locations, as well as change with time. In partnership with Editors, Referees and Authors, the journal will promote the revision of papers to ensure that accepted papers are reasonably complete and competitive with concurrent submissions in a given field.

ABSTRACTING AND INDEXING

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**General points**
- Make sure you use uniform lettering and sizing of your original artwork.
- Preferred fonts: Arial (or Helvetica), Times New Roman (or Times), Symbol, Courier.
- Number the illustrations according to their sequence in the text.
- Use a logical naming convention for your artwork files.
- Indicate per figure if it is a single, 1.5 or 2-column fitting image.
- For Word submissions only, you may still provide figures and their captions, and tables within a single file at the revision stage.
• Please note that individual figure files larger than 10 MB must be provided in separate source files. A detailed guide on electronic artwork is available.

You are urged to visit this site; some excerpts from the detailed information are given here.

Formats
Regardless of the application used, when your electronic artwork is finalized, please 'save as' or convert the images to one of the following formats (note the resolution requirements for line drawings, halftones, and line/halftone combinations given below):

EPS (or PDF): Vector drawings. Embed the font or save the text as 'graphics'.
TIFF (or JPG): Color or grayscale photographs (halftones): always use a minimum of 300 dpi.
TIFF (or JPG): Bitmapped line drawings: use a minimum of 1000 dpi.
TIFF (or JPG): Combinations bitmapped line/half-tone (color or grayscale): a minimum of 500 dpi is required.

Please do not:
• Supply files that are optimized for screen use (e.g., GIF, BMP, PICT, WPG); the resolution is too low.
• Supply files that are too low in resolution.
• Submit graphics that are disproportionately large for the content.

Only if a laser-quality printer is not available (dot matrix printers are unsatisfactory) should you present professionally drawn figures in black ink on white paper. Always use large and bold lettering and heavy smoothlines to permit photographic reduction. Ensure that all symbols in the figure are large and match the explanations in the legend. Sequence figures should be either 60 nucleotides (or amino acids) in width (to fit into a single printed column), or 120-150 nt. As a rule no more than a single page is allowed for sequence figures. Add bp, nt, kb or kDa symbols above the numerals in marker lanes. Legends should be typed/printed double-spaced, on pages separate from the figures themselves. The maximum size of figures is A4: present larger figures on two or more sheets.

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Please make sure that artwork files are in an acceptable format (TIFF (or JPEG), EPS (or PDF) or MS Office files) and with the correct resolution. If, together with your accepted article, you submit usable color figures then Elsevier will ensure, at no additional charge, that these figures will appear in color online (e.g., ScienceDirect and other sites) in addition to color reproduction in print. Further information on the preparation of electronic artwork.

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Ensure that each illustration has a caption. A caption should comprise a brief title (not on the figure itself) and a description of the illustration. Keep text in the illustrations themselves to a minimum but explain all symbols and abbreviations used.

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