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Genetics Research

Genetics Research is a key forum for original research on all aspects of human and animal genetics, reporting key findings on genes, mutations and molecular interactions leading to a better understanding of human disease. The journal focuses on the use of new technologies, such as massive parallel sequencing together with bioinformatics analysis, to produce increasingly detailed views of how genes function in tissues and how these genes perform, individually or collectively, in disease aetiology. The journal publishes original work, review articles, short papers, computational studies, and novel methods and techniques in research covering humans and well-established genetic organisms (such as the mouse and rat). Key subject areas include medical genetics, genomics, human evolutionary and population genetics, bioinformatics, genetics of complex traits, molecular and developmental genetics, Evo-Devo, quantitative and statistical genetics, behavioural genetics and environmental genetics. The breadth and quality of research make the journal an invaluable resource for medical geneticists, molecular biologists, animal breeders, and researchers involved in genetic basis of diseases, evolutionary and developmental studies.

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Equations should be typed within the manuscript in an editable format, aligned left, and each equation should be numbered.

$$x + y = z - a,$$
 (1)
$$x^2 + ty = abz - a\beta$$
 (2)

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Journal

Beaudoin, N., Serizet, C., Gosti, F. & Giraudat, J. Jr (2000 *a*). Interactions between abscisic acid. *Plant Cell* **12**, 1103–1116.

Oliver, T. R., Feingold, E., Yu, K., Cheung, V., Tinker, S., Yadav-Shah, M., Masse, N. & Sherman, S. L. (2008). New insight into human nondisjunction of chromosome 21 in oocyte. *PloS Genetics* **4**, e1000033.

Book

Jeffreys, H. (1961). Theory of Probability, 3rd edn. Oxford, UK: Oxford University Press.

Goffinet, B. & Mangin, B. (1998). Testing of goodness of fit. In *Biostatistical Analysis*, p. 50. Rahway, NJ: Prentice-Hall.

Hoffman, A. A. (2000). Laboratory and field heritabilities. In *Genetic Variation in the Wild* (ed. T. A. Mousseau, B. Sinervo & J. A. Endler), pp. 200–218. New York: Oxford University Press.

Online publications

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Koga, A., Sasaki, S., Naruse, K., Shimada, A. & Sakaizumi, M. (2010). Occurrence of a short variant of the *Tol2* transposable element in natural populations of the medaka fish. *Genetics Research*, published online 7 December 2010. doi: 10.1017/S0016672310000479.

References to websites should state the date that the website was accessed, as well as the URL.

Weisstein, E. W. (2005). Euler–Lagrange differential equation. Available at http://mathworld.wolfram.com/eulerlagrangedifferentialequation.html (accessed 10 April 2006).

PhD thesis

Yekutieli, D. (2001). Theoretical results needed for applying the false discovery rate in statistical problems. PhD thesis, Department of Statistics and Operations Research, Tel Aviv University, Tel Aviv, Israel.

Nomenclature

Whenever possible, employ standardized nomenclature. Refer to the following publications for guidance: Novick, R. P. *et al.* (*Bacteriological Reviews* **40**, pp. 168–189, 1976) for plasmids, and O'Brien (Ed.), *Genetic Maps* **6**, Cold Spring Harbor 1993, for recent information on most species and recent gene lists. Gene abbreviations should generally be typed in italic. Note that '+' as the symbol for a wild-type allele should not be italicized.

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(Revised 15 January 2016)