

GENOME RESEARCH

... the new genetics

Here's why:

1. Genome Research publishes the best and most creative research on physical and genetic mapping, DNA sequencing, gene discovery, informatics, statistical and mathematical methods, technology development, and gene function.

A Novel In Vivo Method to Detect DNA Sequence Variation
Malek Faham and David R. Cox

The Genexpress Index: A Resource for Gene Discovery and the Genic Map of the Human Genome
Rémi Houlgatte, Régine Mariage-Samson, Simone Duprat, Anne Tessier, Simone Bentolila, Bernard Lamy, and Charles Auffray

A Biometrical Genome Search in Rats Reveals the Multigenic Basis of Blood Pressure Variation
Nichola J. Schork, Josä E. Krieger, Maria R. Trolliet, Klebber G. Franchini, George Koike, Eduardo M. Krieger, Eric S. Lander, Victor J. Dzau, and Howard J. Jacob

Karyotype Distributions in a Stochastic Model of Reciprocal Translocation
David Sankoff and Vincent Ferretti

A Physical Map of Chromosome 2 of *Arabidopsis thaliana*
Eve Ann Zachgo, Ming Li Wang, Julia Dewdney, David Bouchez, Christine Camilleri, Stephen Belmonte, Lu Huang, Maureen Dolan, and Howard M. Goodman

2. Genome Research supplements and enhances editorial content with electronic presentations on the World Wide Web.

Check out the example at <http://www.cshl.org/journals/gr/supplement/> and on-line abstracts for 1996 issues.

3. Genome Research publishes review articles that put current research accomplishments into perspective.

Hyper-recombination and Bloom's Syndrome: Microbes Again Provide Clues About Cancer
Rodney Rothstein and Serge Gangloff

Around the Genomes: The *Drosophila* Genome Project
Gerald M. Rubin

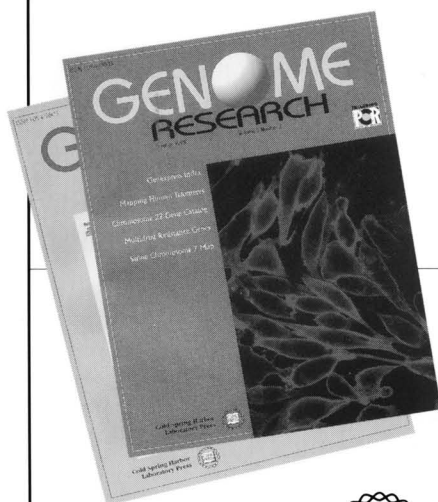
4. Genome Research is expanding the "PCR Methods and Applications" section to incorporate more methods germane to genome research — henceforth, the "Genome Methods" section.

Cross-screening: A New Method to Assemble Clones Rapidly and Unambiguously into Contigs
John Locke, Greg Rairdan, Heather McDermid, David Nash, David Pilgrim, John Bell, Kenneth Roy, and Ross Hodgetts

5. Genome Research has also begun publishing letters — concise reports describing the structure, sequence, expression, and/or other biologically relevant features of a gene, with supplementary data made available electronically.

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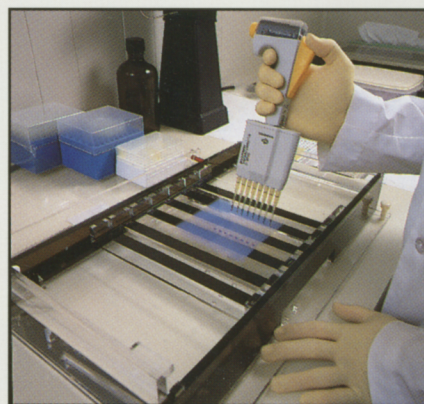
Using the Human Transcript Map



Now you can place almost any human sequence in one of the 1,000 genetically anchored bins on the recently published radiation hybrid-based human transcript map¹. Armed with this knowledge, you can look up all of the transcripts that have been mapped to that bin and simply purchase transcript-specific STS primer pairs, cDNA clones, and YAC clones for most of the transcripts. BAC clones containing the transcripts can be determined by PCR-based or hybridization-based screening.

Over the course of the next year, tens of thousands of additional transcripts will be added to this resource which is being updated and released over the world wide web by Mark Boguski, Greg Schuler, and the staff at NCBI². Most of these new transcripts will be based on the invaluable cDNA resource made possible by the I.M.A.G.E. Consortium³, the end-sequencing of which is being performed by Washington University and has been made possible by the generous support of Merck & Company⁴. The expansion of the transcript map is being accelerated by a significant donation from Sandoz to map 10,000 brain related transcripts⁵.

The resources needed to make the maximum use of this new tool are available from Research Genetics. Visit our web site at <http://www.resgen.com> or e-mail Kay Swanson (kswanson@resgen.com) or Jim Hudson (hudson@resgen.com) for more information. If you would like a free copy of the transcript map, please send a name and address via e-mail to kpollack@resgen.com.



References

1. Schuler, G., Boguski, M., et al, *Science* Oct, 25, 1996.
2. <http://www.ncbi.nlm.nih.gov/SCIENCE96>
3. <http://www-bio.llnl.gov/bbrp/image/image.html>
4. <http://genome.wustl.edu/est/esthmpg.html>
5. Research Genetics Resources, Vol. 3, No. 2, pg.1

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