



The Pied Piper

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Conference Watch

January 3-7 , 2007

PSB 2007

Wailea, Maui, USA

March 6-9, 2007

[Computational Cell Biology](#)

Cold Spring Harbor, NY, USA

May 8-12 , 2007

[Biology of Genomes](#)

Cold Spring Harbor, NY, USA

July 19-25 , 2007

ISMB

Vienna, Austria

November 1-5, 2007

[Genome Informatics](#)

Cold Spring Harbor, NY, USA

Announcing the New Cardiovascular Disease Portal

The new [Cardiovascular Portal](#) at [RGD](#) provides a comprehensive resource that integrates diverse data types and analysis tools. This dynamic portal offers researchers a unique opportunity to locate related cardiovascular disease information in one centralized location. The [Cardiovascular Disease Portal homepage](#) offers users a summary of data within the portal and several options to view and access data. The portal homepage invites users to customize a results page by allowing users to narrow results by specific disease or disease category. Once a specific disease is chosen, the disease portal will provide a list of related genes, QTL, and strains along with a genomic view of these objects as well as access to related Genome Browser results. The portal also offers sections for [Phenotypes](#), [Biological Processes](#) and [Pathways](#) related to cardiovascular disease. We invite you to visit the new [Cardiovascular Disease Portal](#) at [RGD](#) and take advantage of this excellent resource for cardiovascular disease information.

Genome Repair Kit Now Available at RGD

A [Genome Repair Kit](#) is now available at the Rat Genome Database. The Genome Repair Kit will allow users to report any conflicts they find in the genome sequence or annotations and view currently submitted conflicts. The Genome Repair kit is accessible from the navigation bar on the RGD web site, under "[Genome Conflicts](#)".

RGD's [Genome Browser](#) (GBrowser) now includes conflict tracks. In order to alert users to potential problem areas, RGD has mapped the positions of [6 regions](#), covering 250 Kb to 6Mb each, that differ in chromosomal assignment between the Baylor 3.4 and Celera assemblies. Additional conflicts will continue to be added as they are found.

Have you identified regions of conflict or other sequence errors? Let us know! [RGD](#) has a simple [form you can use to report conflicts](#). We will contact you for details, add the data to GBrowse, and forward these conflicts to the appropriate place, such as Baylor or RGD curation staff, for resolution. Please [Contact RGD](#) with any questions.

[Genome Repair Kit](#)

NCBI Releases Update for the Rat Genome

NCBI released an update for the rat genome that includes re-annotation of the reference genome assembly and addition of an alternate genome assembly. The reference assembly, representing the BN/SsNHsdMCW

New @ RGD

New Data in RGD:

RGD Data Scoreboard:

Data totals available below and at [RGD homepage](#)

Strains

inbred	573
congenic	354
consomic	44
mutant	75
coisogenic	8
outbred	21
recombinant inbred	57
transgenic	30
segregating inbred	13
Total	1175

genome, is based on RGSC v3.4 'November 2004 update' generated by the Human Genome Sequencing Center at the Baylor College of Medicine as a component of the Rat Genome Sequencing Consortium. The alternate assembly, representing a mixture of the Brown Norway and Sprague-Dawley genomes, is based on Celera Genomics' January 2003 whole genome shotgun (WGS) assembly.

The NCBI Map Viewer provides graphical displays of several types of maps, including sequence maps, two genetic maps, and a radiation hybrid map. Map features that can be seen on the sequence map include NCBI contigs (the 'Contig' map), the WGS sequences (the 'Component' map), and the location of genes, STSs, ESTs, and gene models predicted by Gnomon. By default, data and annotations from the reference assembly is shown. Please see the instructions on how to view data from the alternate assembly. Documentation is provided below to describe the resource features and methods used, tutorials, and statistics.

You can find genes or markers of interest by submitting a query against the whole genome or one chromosome at a time. Results are indicated both graphically, as tick marks on the chromosomes, or in a tabular format. The results table includes links to a chromosome graphical view where the gene or marker can be seen in the context of additional data. For genes, a particularly useful display includes the Gene, Ab initio (i.e. the Gnomon predicted gene models), and Rn RNA (i.e. rat ESTs and mRNAs) sequence maps. Use the "Maps & Options" window to configure each display.

A current list of other genomes viewable in the NCBI Map Viewer is provided on the [Map Viewer home page](#). Also consider reviewing the resources listed on the [Genomic Biology site](#).

Available Documentation:

- [NCBI Handbook: Map Viewer chapter](#) - resource description
- [NCBI Handbook: Map Viewer Exercises](#) - tutorials and examples
- [Map Viewer Help](#) - details about navigation and customizing your display
- [Genome Assembly](#) - description of genome assembly and annotation process
- [Gnomon](#) - description of NCBI's Hidden Markov Model (HMM) ab initio prediction program

[Access to full article courtesy of NCBI](#)



CiteXplore – integrating biomedical literature and data

Today the European Molecular Biology Laboratory's [European Bioinformatics Institute \[EMBL-EBI\]](#) launches CiteXplore, a new freely accessible literature resource service.

Biological researchers require two crucial sources of information: scientific literature published in peer reviewed journals and databases storing key biological data such as DNA and protein sequences, functions and structures of molecules and microarray data. Tools that integrate these two sources of information are desperately sought.

EMBL-EBI scientists have developed CiteXplore, a tool that links electronic literature resources to bioinformatics databases, to fulfil this need. It integrates abstracts from various resources including the US National Library of Medicine's MEDLINE database of abstracts from peer-reviewed biomedical journals, biological abstracts from patent applications from the European Patent Office, and Chinese Biological Abstracts from the Shanghai Information Center for Life Sciences, Chinese Academy of Sciences. From these abstracts CiteXplore links to full-text articles at various locations such as PubMedCentral and publisher websites.

CiteXplore also provides a direct link between the scientific literature and the EMBL-EBI's biological databases. "When you are reading an abstract describing a specific gene or protein, typically you want more information on it, for example its sequence or its function, as well as easy access to the full paper," says Peter Stoehr, who coordinates CiteXplore. CiteXplore uses powerful text-mining tools developed by EMBL-EBI researchers to link literature and databases automatically, so that at the touch of a button the biological terms are identified in the text and you can call up the record of the molecule that you are looking for.

In future, the range of literature resources hosted in CiteXplore will be extended for better coverage of other

Genes

known	9886
variants	100
pseudo	600
predicted	12711
alleles	39
Total	23336
Annotated	11777

QTLs

Rat	1172
Mouse	2466
Human	556

Ontologies

Strains	
Phenotypes	976
Diseases	522
Genes	
GO	81434
Phenotypes	2104
Diseases	2390
Pathway	1977
QTLs	
Phenotypes	4099
Diseases	1670

News from RGD:

[RGD](#) adds link to [PhysGen](#)



The PhysGen Logo appears on the upper portion of RGD pages and links directly to the PhysGen homepage.

Read other [news from RGD](#)

[Submit to Pied Piper](#)

domains such as plant science, agricultural and food sciences, and to integrate it with UK PubMedCentral, a recently launched project led by a consortium comprising the British Library, University of Manchester and EMBL-EBI.

CiteXplore is freely available at www.ebi.ac.uk/citexplore.

Source: [EMBL-EBI Press Release, November 27, 2006](#)

Submit information about your rat research, an upcoming conference or new, exciting tools that aid in rat research to The Pied Piper.
*[*Click here to see requirements](#)*

Neurons Grown from Embryonic Stem Cells Restore Function in Paralyzed Rats

For the first time, researchers have enticed transplants of embryonic stem cell-derived motor neurons in the spinal cord to connect with muscles and partially restore function in paralyzed animals. The study suggests that similar techniques may be useful for treating such disorders as spinal cord injury, transverse myelitis, amyotrophic lateral sclerosis (ALS), and spinal muscular atrophy. The study was funded in part by the NIH's National Institute of Neurological Disorders and Stroke (NINDS).

The researchers, led by Douglas Kerr, M.D., Ph.D., of The Johns Hopkins University School of Medicine, used a combination of transplanted motor neurons, chemicals capable of overcoming signals that inhibit axon growth, and a nerve growth factor to attract axons to muscles. The report is published in the July 2006 issue of *Annals of Neurology*. *

"This work is a remarkable advance that can help us understand how stem cells might be used to treat injuries and disease and begin to fulfill their great promise. The successful demonstration of functional restoration is proof of the principle and an important step forward. We must remember, however, that we still have a great distance to go," says Elias A. Zerhouni, Director of the National Institutes of Health.

"This study provides a 'recipe' for using stem cells to reconnect the nervous system," says Dr. Kerr. "It raises the notion that we can eventually achieve this in humans, although we have a long way to go."

[Read Full Article](#)

Source: [NIH News](#)

Researchers Identify Role of Protein Important for Stem Cell Growth; Study Leads to Recovery in Animal Model of Stroke

For the first time, researchers have found that a protein signal important in embryonic development promotes survival and proliferation of stem cells. Stimulating receptors for this protein, called Notch, led to functional recovery in rats with brain damage from stroke. The results suggest potential new ways of treating stroke and neurodegenerative diseases.

The study was conducted by Ronald D.G. McKay, Ph.D., Andreas Androutsellis-Theotokis, Ph.D., and colleagues at the National Institute of Neurological Disorders and Stroke (NINDS) in Bethesda, Maryland, and published in the August 17, 2006, issue of *Nature*. *

"This is a new role for the Notch receptor," Dr. McKay says. Previous studies have shown that Notch is important for proper development of embryos, and that it regulates chemical chain reactions, or pathways, that are central to cancer and diabetes. However, this is the first study to show that Notch controls stem cell division and survival and that it can prompt functional recovery after brain injury in an animal model.

Dr. McKay and his colleagues tested chemicals that increase Notch activity in cultured neural stem cells (NSCs). NSCs can form all of the cells that make up the nervous system, but they do not normally develop into other kinds of tissue. The researchers found that one of these chemicals, Dll4, rapidly reduced cell death. They also found that Notch is part of the pathway by which insulin controls cell survival, and they identified several other genes that control cells' responses to Notch. Pumping Dll4 into the brains of normal rats for 7 days increased the number of dividing cells. Many of the newly generated cells showed a marker that is common on immature neurons. These cells survived for at least 45 days in an immature state. These findings suggest that Notch may be important for maintaining populations of stem cells in the brain and other parts of the body.

The researchers also tested Dll4 in cultures of human embryonic stem cells and pancreatic stem cells and found that it improved survival and proliferation of those cells. The results suggested that Notch may be an

important control signal for many different kinds of stem cells.

[Read Full Article](#)

Source: [NINDS](#)

Drug Prevents Brain Swelling After Stroke

A drug long used to treat diabetes significantly reduces brain swelling, neuron loss, and death after stroke in rats, researchers have found. The finding may lead to improved ways of treating stroke and other disorders in humans.

The drug, called glibenclamide or glyburide, appears to work by blocking channels, or pore-like structures, that open in cell membranes when the brain is deprived of oxygen. The opening of these channels allows sodium ions and water to flow into the cells, causing them to swell (a condition called edema). The flow of sodium into cells also triggers a flood of sodium and water into surrounding tissues, which increases intracranial pressure and damages cells. Current treatments for brain edema are only moderately effective, and the swelling is believed to be responsible for much of the brain damage and death that occurs in people who have severe strokes.

The study was led by J. Marc Simard, M.D., Ph.D., of the University of Maryland at Baltimore School of Medicine. It was funded in part by the National Institute of Neurological Disorders and Stroke (NINDS) and appeared in the April 2006 issue of Nature Medicine.

[Read Full Article](#)

Source: [NINDS](#)



RGD in the Community

Upcoming RGD Activities:

Victoria Petri, PhD, RGD Research Scientist, will attend the upcoming GO Consortium Meeting January 8-10, 2007.

Recent RGD Activities:

Howard Jacob, PhD, RGD PI and Human Molecular Genetics Center Director, participated The Rat Genome Meeting in Melbourne Australia, December 1-2, 2006. Dr. Jacob's presentation was entitled: "The Rat Genome; from Genes to Engineered Tissues".

Victoria Petri, PhD, RGD Research Scientist, attended the Phenotype and Trait Ontology (PATO) Meeting, December 1-2, 2006 at Stanford University.

Mary Shimoyama, MS, RGD Program Manager, attended The 20th International Mammalian Genome Conference in Charleston, South Carolina November 12-15, 2006.

Anne Kwitek, PhD, RGD Co-PI and Andrew Patzer, Bioinformatics Managing Director, participated in the [ISMB Meeting](#), August 6-10, 2006 in Fortaleza, Brazil.

Victoria Petri, PhD, RGD Research Scientist and Jennifer Smith, MS, RGD Scientific Curator, both attended the [GO Annotation Camp](#), July 10-14, 2006 at Stanford University.



Facts and Functions of RGD

Registering Data with RGD

The scientific community is encouraged to register [Gene](#), [QTL](#) and [Strain](#) data with [RGD](#). Registering data with RGD ensures accurate public data records and maintains proper nomenclature compliance for objects.

RGD also accepts registration of non-public data. Non-public registrations will be held from public database release until the author instructs RGD to release the data.

To register your data with RGD please choose one of the registration forms below or visit the [Submit Data](#) section at RGD. Please refer to [RGD's Nomenclature](#) page as a guide in obtaining proper nomenclature for you submission.

RGD Data Submission Forms

[Strain Registration](#)
[Gene Registration](#)
[QTL Registration](#)

If you would like to see a particular tool or data type featured in a future installment of "Facts and Functions of RGD", please send your idea to rgdnewsletter@mcw.edu

RGD Resources:

ANEX University of Tokushima Rat Database	http://www.anex.med.tokushima-u.ac.jp/rat/index-e.html
ARB Rat Genetic Database	http://www.niams.nih.gov/rtbc/ratgbase/
Baylor College of Medicine	http://www.hgsc.bcm.tmc.edu/
Ensembl	http://www.ensembl.org/Rattus_norvegicus/
Entrez Genome Database for Rattus norvegicus	http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=genomeprj&cmd=Retrieve&dopt=Overview&list_uids=10621
IDP-MHC Rat Sequence Database:	http://www.ebi.ac.uk/ipd/mhc/rt1/index.html
ILAR -Institute for Laboratory Animal Research	http://dels.nas.edu/ilar_n/ilarhome/
Japan RGD Mirror Site	http://rat.lab.nig.ac.jp/
Mammalian Gene Collection	http://mgc.nci.nih.gov/
National Bio Resource Project Rat Japan	http://www.anim.med.kyoto-u.ac.jp/nbr
NCBI	http://www.ncbi.nlm.nih.gov/
NHGRI Rat Genome Sequencing Homepage	http://www.genome.gov/10001855
NIH Animal Genetic Resource	http://dvrnet.ors.od.nih.gov/gen_repository.asp/

**NIH Animal Genetic Resource:
list of rat strains and stocks** http://dvrnet.ors.od.nih.gov/rat_strains.htm/

**NIH Autoimmune Rat Model
Repository** <http://dvrnet.ors.od.nih.gov/ratcenter/index.html>

NIH Rat Genomics and Genetics <http://www.nih.gov/science/models/rat/>

PGA <http://pga.mcw.edu/>

RatMap <http://ratmap.gen.gu.se/>

Rat Community Forum @ RGD <http://rgd.mcw.edu/RCF/>

RGD <http://rgd.mcw.edu/>

RGNC <http://rgnc.gen.gu.se/>

RGSC <http://www.hgsc.bcm.tmc.edu/projects/rat>

RRRC <http://www.nrrrc.missouri.edu/>

TIGR Rat Gene Index <http://compbio.dfci.harvard.edu/tgi/>

UCSC <http://www.genome.ucsc.edu/>

**University of Iowa Rat EST
Project** <http://ratest.uiowa.edu/>

VISTA at LBL <http://pipeline.lbl.gov/rat/>

**Wellcome Trust Centre Rat
Mapping Resources** http://www.well.ox.ac.uk/rat_mapping_resources/

**Whitehead/MIT Genetic Maps
of Rat Genome** <http://www.genome.wi.mit.edu/rat/public/>

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If you are having difficulties viewing this newsletter please go to <http://rgd.mcw.edu/newsletter> to view it as a page in your web browser.

The Bioinformatics Research Center is a part of the Medical College of Wisconsin. RGD is funded by grant HL64541 from the National Heart, Lung, and Blood Institute on behalf of the NIH. Please read [our disclaimer](#).

We also encourage you to register for The Rat Community Forum (RCF) at <http://rgd.mcw.edu/RCF/>. Simply click **Login** to register. (If you are a member of the RCF, you are automatically subscribed to *The Pied*

Piper.)

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This Newsletter was constructed by Angela Zuniga-Meyer.