



Definición: Aplicación de los principios de la web 2.0 al quehacer científico.



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Problemas de la situación actual

- Lentitud
- Característica de la información compartida
- Dificultad para reproducir resultados
- Acceso a la información
- Falta de interactividad

Información compartida: Trabajo finalizado,
revisado y de alta calidad

Propuestas “Ciencia 2.0”:

- Blogs
- Wikis
- Preprint server

natureprecedings
Pre-publication research and preliminary findings





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[Graham Martin](#)

Posted 28 September 2007

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Genome activity profiling of monomeric-IgE and Fc-epsilon-RI-aggregation on human mast cells reveals a complex network of genes involved in inflammatory responses

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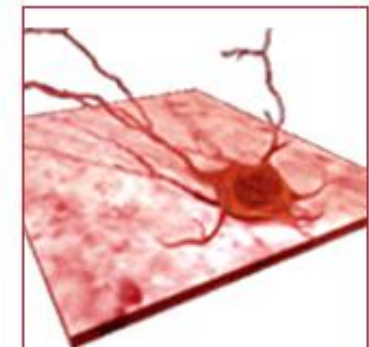
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Document information

doi:10.1038/npre.2007.670.1

DNALinux Virtual Desktop Edition

[Sebastian Bassi](#)¹ & Virginia Gonzalez¹

Correspondence: [\(login to view email address\)](#)

1. Universidad Nacional de Quilmes



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3 votes

-  Document Type: Manuscript
-  Date: Received 09 August 2007 22:11 UTC; Posted 13 August 2007
-  Subjects: [Biotechnology](#), [Bioinformatics](#)
-  Tags: [linux](#) [bioinformatics](#) [emboss](#) [blast](#) [software](#)
-  Abstract: The new version of DNALinux (VDE) is presented. DNALinux VDE is a departure from traditional distributions since it uses a virtual machine to bundle together the operating system and bioinformatics applications. The main advantage of this approach is that a virtualized environment doesn't affect a installed system. With a virtual machine a Linux system can be run under a Windows system, provided that the virtual machine player is installed. The included programs are listed and specifications to add more programs are explained. We believe that DNALinux could be used as a standardized virtual machine for learning, using, developing and testing bioinformatics applications

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hdl:10101/npre.2007.141.1

Characterization of Fut10 and Fut11, Putative Alpha-1-3/4 Fucosyltransferase Genes Important for Vertebrate Development

2 votes

[Santosh Patnaik](#)¹

1. Department of Cell Biology, Albert Einstein College of Medicine, New York, USA



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Document Type: Manuscript



Date: Received 20 June 2007 20:53 UTC; Posted 20 June 2007



Subjects: [Development](#), [Molecular Cell Biology](#)



Tags: [development](#) [fucosyltransferase](#) [GDP-fucose](#) [hydrolysis](#) [morpholino](#)



Abstract: Two new, putative alpha-1-3/4 fucosyltransferases (α 1-3/4 Fuc-Ts), Fuc-TX and Fuc-TXI, were identified in the vertebrate genome and transcriptome sequence databases through sequence homology-based queries. These proteins have a significant sequence similarity to only α 1-3/4 Fuc-Ts, and possess peptide motifs that are evolutionarily conserved among the known vertebrate α 1-3/4 Fuc-Ts. However, Fuc-TX and Fuc-TXI lack the HH[R/W][D/E] sequence that determines the specificity for type 1 or 2 substrates among the known vertebrate enzymes, and Fuc-TXI proteins do not possess a transmembrane domain. The Fut10 and Fut11 genes that encode these proteins are expressed ubiquitously in the adult mouse and in the mouse embryo.

Dificultad para reproducir resultados

Repositorios de datos públicos:

Requisitos: Bases publicas (Genbank, Uniprot, etc) o base de las publicaciones.
Software disponible.

Formatos “machine readable”: Tendencia
XML



Disponibilidad software científico

Tipo de software científico:

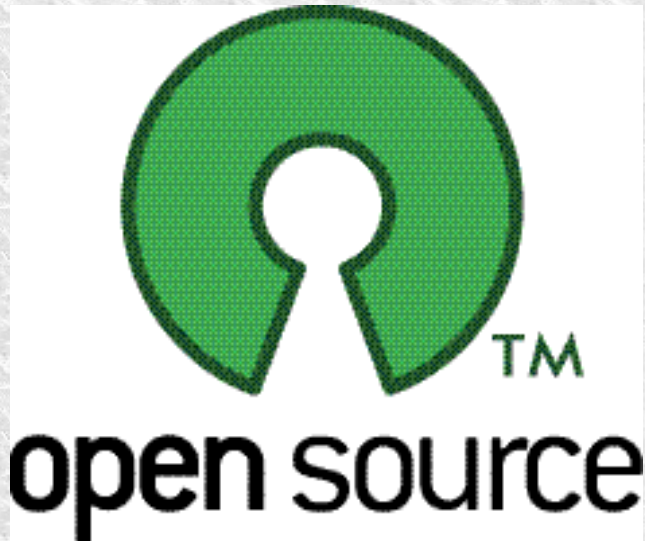
- Uso por los científicos en tareas “generales” (Word, Excel, Sistemas operativos).
- Uso por los científicos en tareas “específicas” (MathLab, SigmaPlot, EndNote), hecho por empresas.
- Hecho por científicos para sus propias investigaciones: EMBOSS, Primer3, gnuplot, etc.

Condiciones para publicación de trabajos sobre software

Disponibilidad de manera gratuita para comunidad académica.

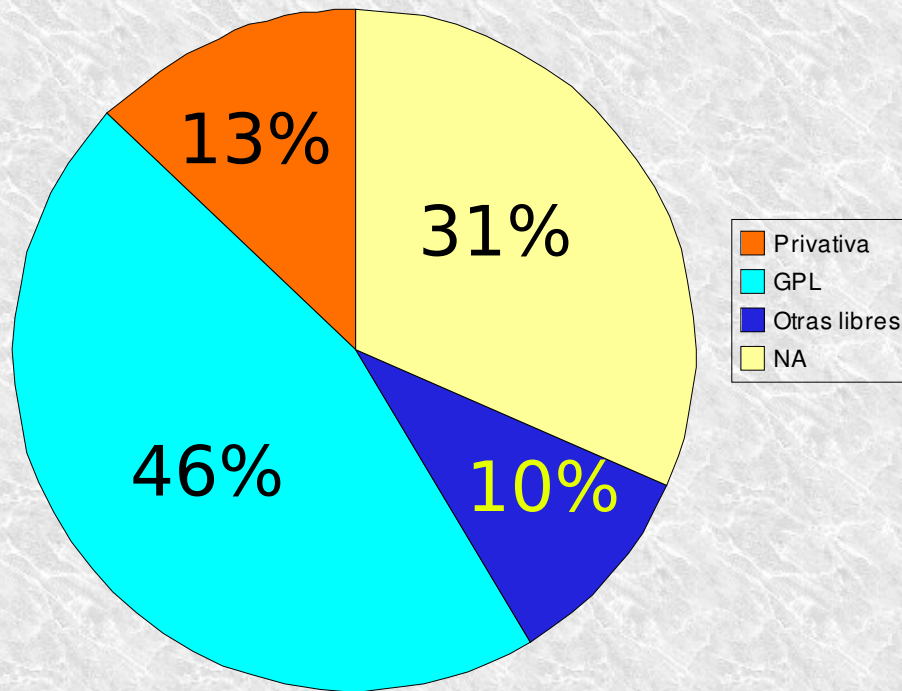
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Código fuente: Solo en casos que sea relevante como la presentación de un algoritmo nuevo o mejor que uno conocido.

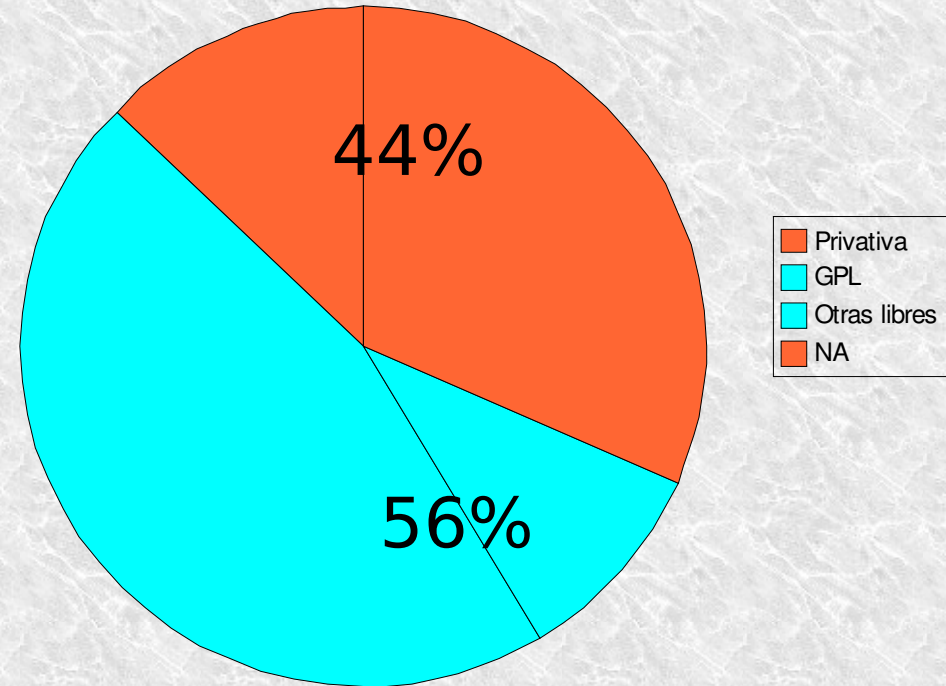


Licencias de software en ciencia

Software científico



Software científico



En base a todas las publicaciones aparecidas en “Bioinformatics” desde Enero a junio de 2007.

Ejemplo: Caso BIP (Biology in Python)

Acceso a la información: Open Access (OA).

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An Abstract of Sundry Papers and Proposals for Improving the Inland Navigation of Pennsylvania and Maryland, by Opening a Communication between the Tide-Waters of Delaware and Chesapeake Bay

Transactions of the American Philosophical Society, Vol. 1, Jan. 1, 1769 - Jan. 1, 1771 (Jan. 1, 1769 - Jan. 1, 1771), pp. 293-300

doi:10.2307/1005040

This article consists of 12 page(s).

Modelo de negocios asociado al OA:

El que publica, paga. Publicidad.
Impresiones.

Actualidad: 2800 publicaciones listadas en
www.doaj.org

Clasificación: OA nativas y “migrantes”.
Acceso semirestringido.

Desventajas:

¿Independencia editorial?

¿Uso de fondos públicos para competir con negocio privado ya establecido? (ej. de BMC)

¿Presupuesto de investigación?



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RESEARCH ARTICLE



The Diploid Genome Sequence of an Individual Human

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Presented here is a genome sequence of an individual human. It was produced from ~32 million random DNA fragments, sequenced by Sanger dideoxy technology and assembled into 4,528 scaffolds, comprising 2,810 million bases (Mb) of contiguous sequence with approximately 7.5-fold coverage for any given region. We developed a modified version of the Celera assembler to facilitate the identification and comparison of alternate

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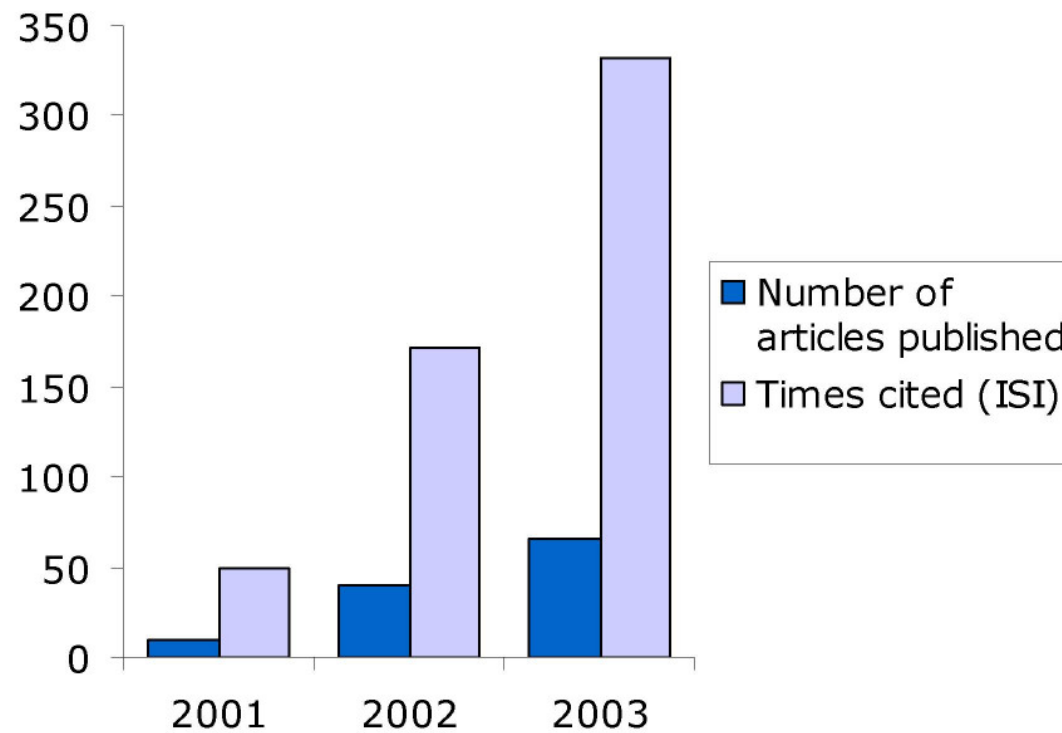
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BMC Bioinformatics



Oposición al OA: Partnership for Research Integrity in Science & Medicine (PRISM)



Objetivo: "educate policy makers and the American people about the risks posed by government intervention in scholarly publishing."
(resumen: Hacer lobby).

Comentario de Wired: It takes several logical steps, and maybe some leaps, to link that mission to research integrity.



PRISM

Partnership for Research Integrity in Science & Medicine

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The Partnership for Research Integrity in Science and Medicine (PRISM) was formed to advocate for policies that ensure the quality, integrity, and economic viability of peer-reviewed journals.

PRISM supports new approaches to access and new economic models that offer choices to suit diverse budgets and needs. Publishers have been at the forefront in testing new models to expand access for subscribers and non-subscribers alike.

PRISM expresses concerns about the unintended consequences of unfunded government mandates and mandatory one-size-fits-all policies that underestimate the complexities and differing needs of the scientific community and scientific journals.

PRISM seeks to educate all stakeholders about the importance of maintaining the integrity of published information, and sustaining the incentives for all publishers to invest in the system of independent publishing that continues to sustain the public's trust in scientific and medical research.



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