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- 1979年~1982年 理学部二号館内の回覧誌 Journal of Second Houseを立ち上げ運営
- 1980~1982年 7名を中心とする土曜会を組織・運営
- 1981年 東京大学大学院理学系研究科人類学専攻修士課程 修了
- 1982~1986年 米国テキサス大学ヒューストン校GSBS留学 (Ph.D.)
- 1983~1986年 フルブライトプログラム同期のニュースレターを発行
- 1987~1989年 日本学術振興会PD
- 1989~1991年 東京大学理学部生物学科人類学教室 助手
- 1989年 進化学研究会を発足; SHINKAの発行
- 1991年~2002年 国立遺伝学研究所 進化遺伝研究部門 助教授
- 1991~2009年 日本DNAデータバンクの運営に参加
- 1996年~現在 Molecular Biology and Evolution associate editor
- 1997年~2000年 Anthropological Science 編集長
- 2002年~ 国立遺伝学研究所 集団遺伝研究部門 教授 (現職)
- 2005年~現在 日本学術会議 会員
- 2008年 郷里の福井市で足羽三山文化協議会を発足
- 2009年~現在 Molecular Phylogenetics and Evolution associate editor
- 2009年~現在 Human Biology editorial board member
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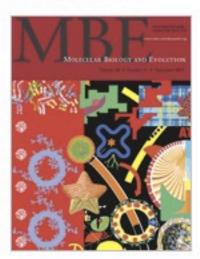
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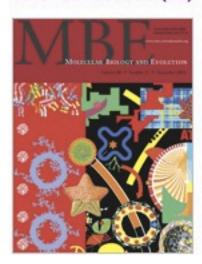
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Evolutionary Patterns of Recently Emerged Animal Duplogs



Kiyoshi Ezawa^{1,2,4}, Kazuho Ikeo^{2,3}, Takashi Gojobori^{2,3} and Naruya Saitou^{1,*}

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Accepted July 19, 2011.

Abstract

Duplogs, or intraspecies paralogs, constitute the important portion of eukaryote genomes and serve as a major source of functional innovation. We conducted detailed analyses of recently emerged animal duplogs. Genome data of three vertebrate species (Homo sapiens, Mus musculus, and Danio rerio),

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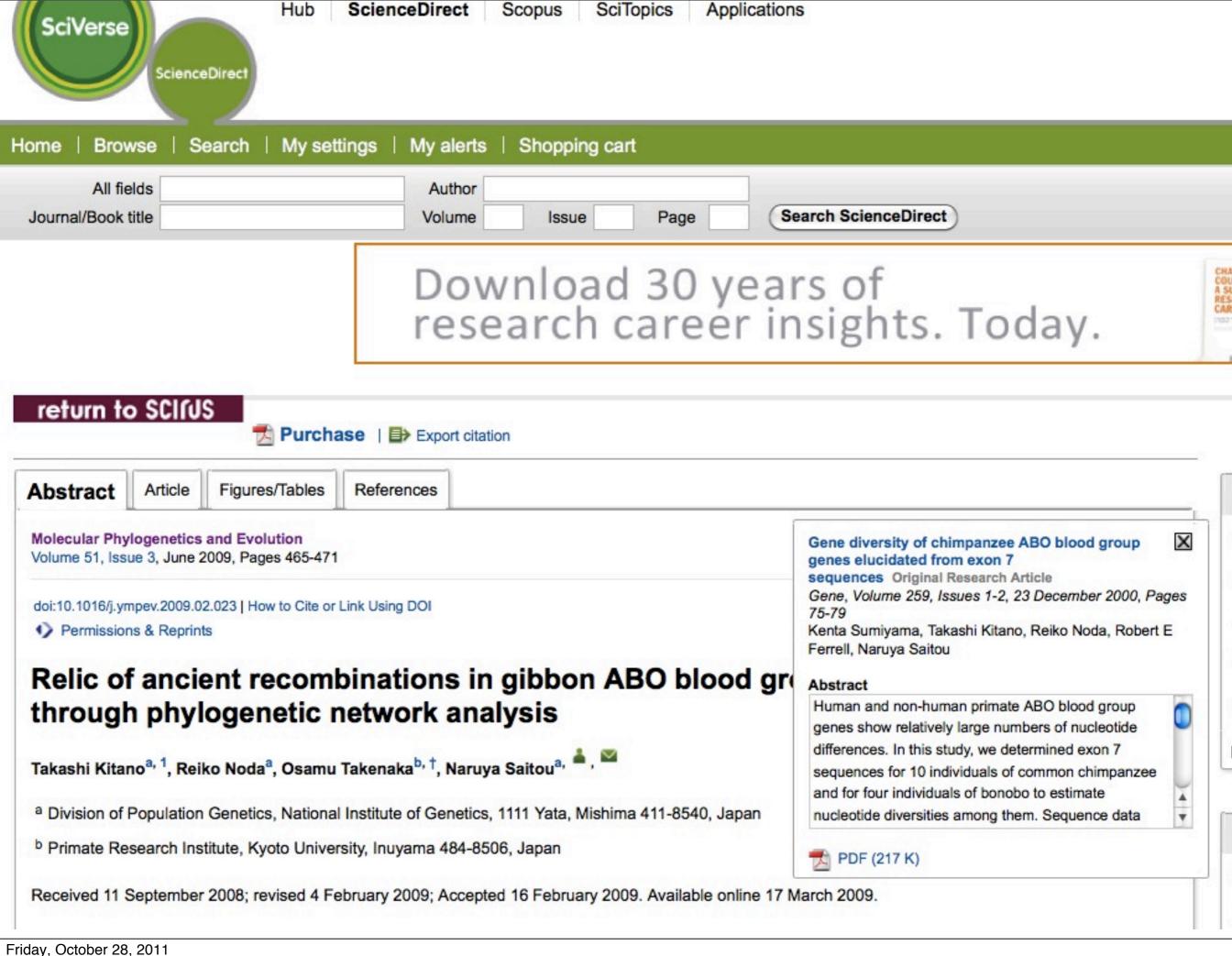
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Anthropological Science

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Advanced CT images reveal nonmetric cranial variations in living humans

NARUYA SAITOU¹⁾, RYOSUKE KIMURA²⁾, HITOSHI FUKASE³⁾, AKIRA YOGI⁴⁾, SADAYUKI MURAYAMA⁴⁾ and HAJIME ISHIDA³⁾

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- 4) Department of Radiology, Faculty of Medicine, University of the Ryukyus, Okinawa

(received September 28, 2010) (accepted October 15, 2010)

Abstract Two mainland Japanese males were examined with a computer tomography (CT) X-ray scanner to reconstruct three-dimensional CT simulation images of their



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Discipline: evolutionary genomics

Research interests: divergence of modern humans specially in Asia; genetic features of human uniqueness; ancient DNA study

Keywords: evolution, genomics, population, aDNA, humanness



Prof. Joseph Salmons, University of Wisconsin-Madison, USA

Discipline: linguistics

Research interests: language change and linguistic reconstruction, especially sound change, in settings from prehistory to the present; how structural aspects of language are intertwined with social aspects, including migration, language, and dialect contact along with geographical and social variation

Keywords: historical linguistics, comparative linguistics, language variation, dialectology, language contact



Prof. Alicia Sanchez-Mazas, University of Geneva, Switzerland

Discipline: population genetics

Research interests: the genetic study of human populations and its application to human peopling history since the emergence of modern humans; the molecular analysis of the HLA polyphormism (human MHC) in worldwide human populations, the statistical analysis of population genetics data; the comparison of genetics with archaeology, palaeontology, and historical linguistics; the

study of HLA molecular evolution

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Exploration for Functional Nucleotide Sequence Candidates within Coding Regions of Mammalian Genes

Rumiko Suzuki^{1,2,†} and Naruya Saitou^{1,2,*}

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Edited by Katsumi Isono

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Received September 12, 2010. Accepted April 14, 2011.

Abstract

The primary role of a protein coding gene is to encode amino acids. Therefore, synonymous sites of codons, which do not change the encoded amino acid, are regarded as evolving neutrally. However, if a certain region of a protein coding gene contains a functional nucleotide element (e.g. splicing signals), synonymous sites in the region may have selective pressure. The existence of such elements would be detected by searching regions of low nucleotide substitution. We explored invariant nucleotide sequences in 10 790 orthologous genes of six mammalian species (Homo sapiens, Macaca mulatta, Mus musculus, Rattus

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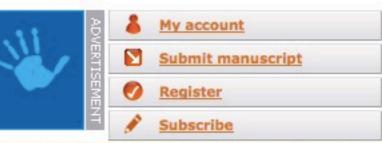




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Journal of Human Genetics 56, 257 (April 2011) | doi:10.1038/jhg.2011.8

A Commentary on The Soliga, an isolated tribe from Southern India: genetic diversity and phylogenetic affinities

Naruya Saitou

The Subcontinent India is located at the South-Central part of Eurasia, and has been the cross-roads of human dispersal. Now in this issue of Journal of Human Genetics, Rene J Herrera and collaborators showed a new genetic connection between one isolated tribe in India, Soliga and Aborigines in Australia.2 The Soliga tribe is distributed in the state of Karnataka, Southern India, and phenotypically resemble the Australian Aborigines. This study may be the first one to show that a particular human population in this Subcontinent may be phylogenetically close to Aborigines.

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MISHIMA - a new method for high speed multiple alignment of nucleotide sequences of bacterial genome scale data

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Abstract

Background

Large nucleotide sequence datasets are becoming increasingly common objects of comparison. Complete bacterial genomes are reported almost everyday. This creates challenges for developing new multiple sequence alignment methods. Conventional multiple alignment methods are based on pairwise alignment and/or progressive alignment techniques. These approaches have performance problems when the number of sequences is large and when dealing with genome scale sequences.

Results

We present a new method of multiple sequence alignment, called MISHIMA (Method for Inferring Sequence History In terms of Multiple Alignment), that does not depend on pairwise sequence comparison. A new algorithm

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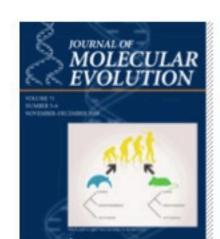
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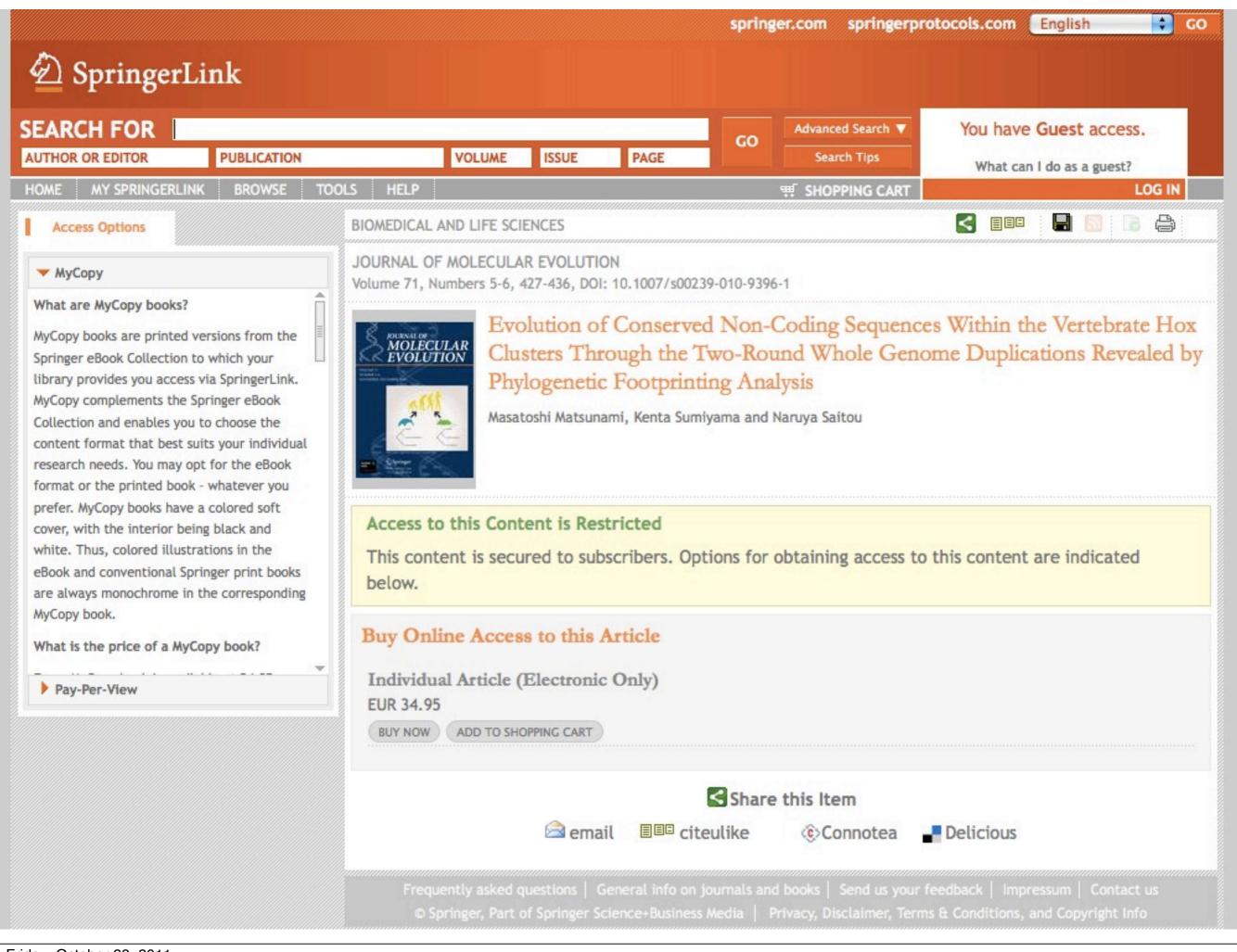
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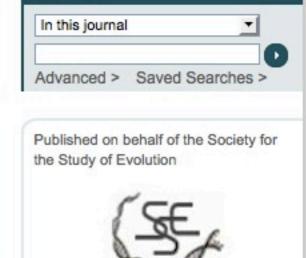
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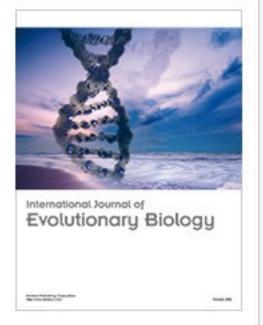


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BMC Evolutionary Biology 2011, 11:303

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Hitchhiking parasites co-evolve

BMC Evolutionary Biology 2011, 11:284

Combining sequence data from rare mockingbirds and their host-specific parasites on the Galapogos Islands increases confidence in the inferred mockingbird phylogeny than using host data alone, leading to more accurate predictions about population structure and effective conservation.



Language linked to scavenging

BMC Evolutionary Biology 2011, 11:261

Derek Bickerton and Eors Szathmary discuss current thinking in the role of human confrontational scavenging in the emergence of language and the high degree of cooperation seen, and directions for future research in this area.

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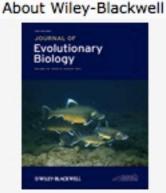
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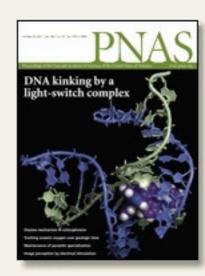
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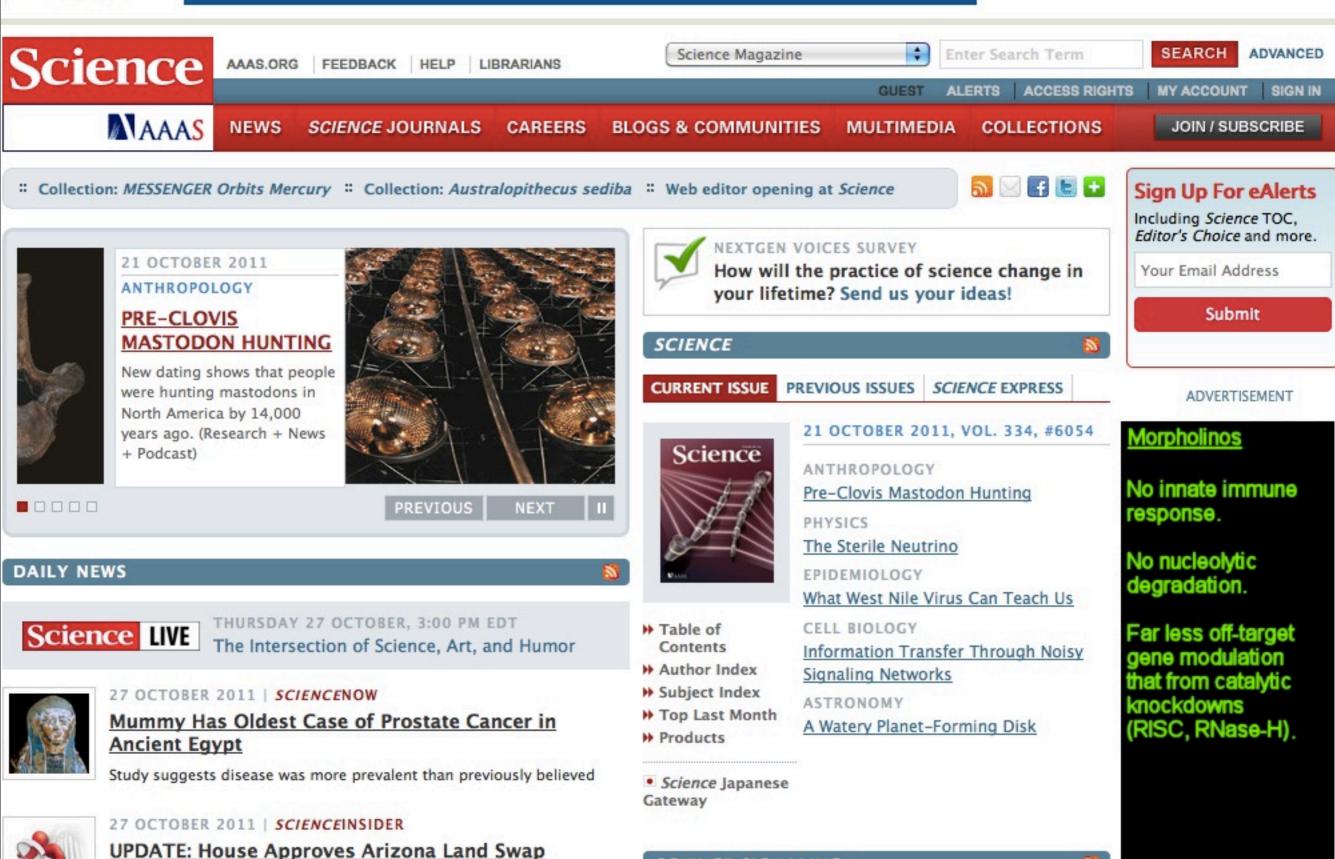
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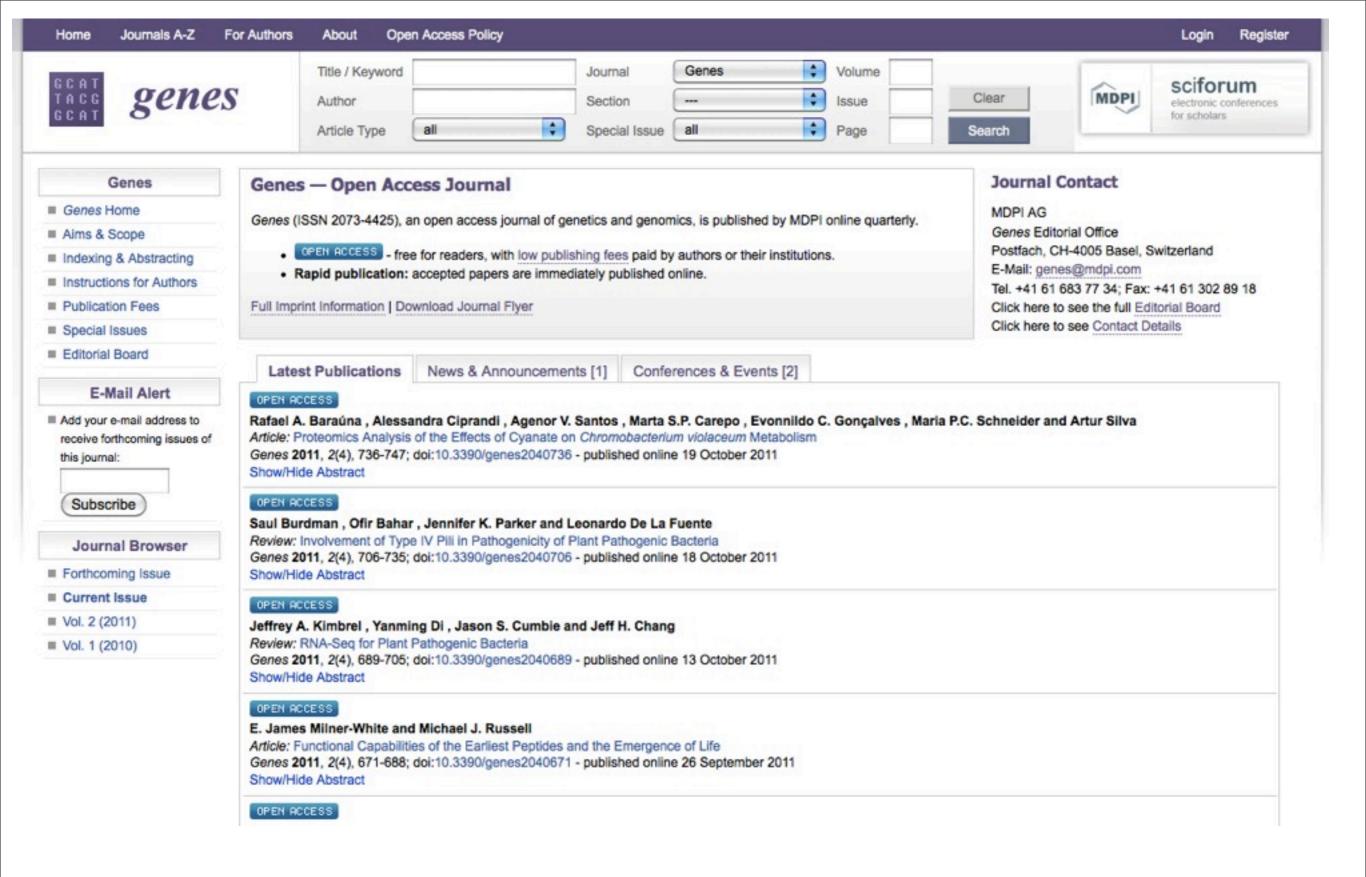
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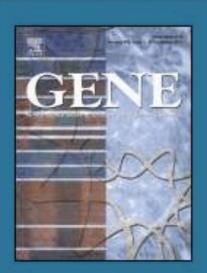
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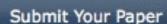
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