

Tópicos de busca bibliográfica

Google-fu et al

Felipe Figueiredo

Instituto Nacional de Traumatologia e Ortopedia

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- Livros

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- Hoje podemos fazer buscas profundas em bases bibliográficas (conteúdo completo das obras)

- **PUBMED** - `www.pubmed.org` (ou `.com`)
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3 Deep Web

- Papers
- Livros

- **Mecanismo de busca**, mantido pelo governo dos EUA (NLM¹ e NIH²)
- Acessa primariamente a base MEDLINE, entre outras
- Referências dos artigos são indexadas e catalogadas para busca
- Links para o conteúdo dos artigos (externos)
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- Exporta referências para gerenciadores bibliográficos (Mendeley, EndNote, etc)

¹National Library of Medicine

²National Institutes of Health

Definition

Base bibliográfica de acesso gratuito de referências de Ciências da Saúde e afins

Disponíveis:

- Índice
- Abstract
- Link para artigo completo (em geral, site da editora)

De acordo com a Wikipédia

Disciplinas: Medicine, nursing, pharmacy, dentistry, veterinary medicine, health care, biology, biochemistry, molecular evolution, biomedicine, history of medicine, health services research, AIDS, toxicology and environmental health, molecular biology, complementary medicine, behavioral sciences, chemical sciences, bioengineering, health policy development, environmental science, marine biology, plant and animal science, biophysics

Definition

Repositório gratuito de artigos Open-Access

Disponíveis:

- Índice
- Abstract
- Conteúdo integral

PUBMED Busca



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The screenshot shows the PubMed website interface in a Chromium browser. The address bar displays the URL: www.ncbi.nlm.nih.gov/pubmed/?Db=pubmed&term=virus%20evolution. The search bar contains the text "virus evolution". The results page shows "Items: 1 to 20 of 38011". The first three results are listed:

- [Viral variants that initiate and drive maturation of V1V2-directed HIV-1 broadly neutralizing antibodies.](#)
Bhiman JN, Anthony C, Doria-Rose NA, Karimanzira O, Schramm CA, Khoza T, Kitchin D, Botha G, Gorman J, Garrett NJ, Abdool Karim SS, Shapiro L, Williamson C, Kwong PD, Mascola JR, Morris L, Moore PL. *Nat Med.* 2015 Oct 12. doi: 10.1038/nm.3963. [Epub ahead of print]
PMID: 26457756
- [The use of the NIS reporter gene for optimizing oncolytic virotherapy.](#)
Miller A, Russell SJ. *Expert Opin Biol Ther.* 2015 Oct 12:1-18. [Epub ahead of print]
PMID: 26457362
- [Transcriptional regulation of gilthead seabream bone morphogenetic protein \(BMP\) 2 gene by bone- and cartilage-related transcription factors.](#)
Marques CL, Leonor Cancela M, Laizé V. *Gene.* 2015 Oct 8. pii: S0378-1119(15)01212-3. doi: 10.1016/j.gene.2015.10.005. [Epub ahead of print]

On the right side, there is a "New feature" section, a "Results by year" bar chart, and a "Related searches" section with links like "influenza virus evolution", "dengue virus evolution", "virus evolution review", "ma virus evolution", and "chikungunya virus evolution". At the bottom, there is a "Show all downloads..." link.

Viral variants that initiate and drive maturation of V1V2-directed HIV-1 broadly neutralizing antibodies. - PubMed - N

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www.ncbi.nlm.nih.gov/pubmed/26457756

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Abstract

Nat Med. 2015 Oct 12. doi: 10.1038/nm.3963. [Epub ahead of print]

Viral variants that initiate and drive maturation of V1V2-directed HIV-1 broadly neutralizing antibodies.

Bhiman JN^{1,2}, Anthony C³, Dorja-Rose NA⁴, Karimanzira O¹, Schramm CA⁵, Khoza T¹, Kitchin D¹, Bothe G³, Gorman J⁴, Garrett NJ⁶, Abdool Karim SS⁶, Shapiro L^{4,5}, Williamson C^{3,6,7}, Kwong PD⁴, Mascola JR⁴, Morris L^{1,2,6}, Moore PL^{1,2,6}.

Author information

Abstract

The elicitation of broadly neutralizing antibodies (bNAbs) is likely to be essential for a preventative HIV-1 vaccine, but this has not yet been achieved by immunization. In contrast, some HIV-1-infected individuals naturally mount bNAb responses during chronic infection, suggesting that years of maturation may be required for neutralization breadth. Recent studies have shown that viral diversification precedes the emergence of bNAbs, but the significance of this observation is unknown. Here we delineate the key viral events that drove neutralization breadth within the CAP256-VRC26 family of 33 monoclonal antibodies (mAbs) isolated from a superinfected individual. First, we identified minority viral variants, termed bNAb-initiating envelopes, that were distinct from both of the transmitted/founder (T/F) viruses and that efficiently engaged the bNAb precursor. Second, deep sequencing revealed a pool of diverse epitope variants (immunotypes) that were preferentially neutralized by broader members of the antibody lineage. In contrast, a 'dead-end' antibody sublineage unable to neutralize these immunotypes showed limited evolution and failed to develop breadth. Thus, early viral escape at key antibody-virus contact sites selects for antibody sublineages that can tolerate these changes, thereby providing a mechanism for the generation of neutralization breadth within a developing antibody lineage.

PMID: 26457756 [PubMed - as supplied by publisher]

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Bhiman JN^{1,2}, Anthony C³, Dorja-Rose NA⁴, Karimanzira O¹, Schramm CA⁵, Khoza Garrett N⁶, Abdool Karim SS⁶, Shapiro L^{4,5}, Williamson C^{3,6,7}, Kwong PD⁴, Masco

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1. Bhiman JN, Anthony C, Doria-Rose NA, Ka Khoza T, Kitchin D, Botha G, Gorman J, G Shapiro L, Williamson C, Kwong PD, Masoc Nat Med. 2015 Oct 12. doi: 10.1038/nm.3963. [Epub ahead of print]. PMID: 26457756

☐ [The use of the NIS reporter gene for optimizing oncolytic virotherapy.](#)

2. Miller A, Russell SJ. Expert Opin Biol Ther. 2015 Oct 12:1-18. [Epub ahead of print]. PMID: 26457362

☒ [Transcriptional regulation of gilthead seabream bone morphogenetic protein \(BMP\) 2 gene by bone- and cartilage-related transcription factors.](#)

3. Marques CL, Leonor Cancela M, Laizé V. Gene. 2015 Oct 8. pii: S0378-1119(15)01212-3. doi: 10.1016/j.gene.2015.10.005. [Epub ahead of print].

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- Papers
- Livros

Definition

Mecanismo de busca que acessa a base bibliográfica do Google para livros e artigos acadêmicos.

- Escopo: A vida, o universo e tudo o mais³
- Indexa citações
- Facilita acesso ao PDF, caso disponível publicamente
- Exporta referências

³e obrigado pelo peixe

Google Scholar Busca



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The screenshot shows a Google Scholar search results page for the query "virus evolution". The browser window title is "virus evolution - Google Scholar - Chromium". The address bar shows the URL: <https://scholar.google.com.br/scholar?hl=en&q=virus+evolution&btnG=&z=Q>. The search bar contains "virus evolution" and shows "About 2,090,000 results (0.05 sec)".

On the left sidebar, there are filters for "Articles", "Case law", and "My library". Under "Articles", there are sub-filters for "Any time" (Since 2015, Since 2014, Since 2011, Custom range...), "Sort by relevance", and "Sort by date". There are also checkboxes for "include patents" and "include citations", both of which are checked. At the bottom of the sidebar is a "Create alert" button.

The main results area displays several entries:

- Basic concepts in RNA virus evolution.**
E Domingo, C Escarmis, N Sevilla, A Moya, SF Elena... - The FASEB Journal, 1996 - FASEB
Abstract A hallmark of RNA genomes is the error-prone nature of their replication and retrotranscription. The major biochemical basis of the limited replication fidelity is the absence of proofreading/repair and postreplicative error correction mechanisms that ...
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- Influenza B virus evolution: co-circulating lineages and comparison of evolutionary pattern with those of influenza A and C viruses**
M Yamashita, M Krystal, WM Fitch, P Palese - Virology, 1988 - Elsevier
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- Mechanisms of plant virus evolution**
MJ Roossinck - Annual review of phytopathology, 1997 - annualreviews.org
Abstract Plant viruses utilize several mechanisms to generate the large amount of genetic diversity found both within and between species. Plant RNA viruses and pararetroviruses probably have highly error prone replication mechanisms, that result in numerous ...
Cited by 332 Related articles All 6 versions Cite Save
- Virus evolution and genetic diversity of hantaviruses and their rodent hosts**
A Plyusnin, SP Morzunov - Hantaviruses, 2001 - Springer
Abstract Unlike other members of the Bunyaviridae family, which must be regarded as arboviruses 1, hantaviruses are not transmitted by arthropod vectors, and are exclusively maintained in the populations of their specific rodent hosts. Thus, the prefix "Robo"(from ...
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avirulent strains
T Toyoda, T Sakaguchi, H Hirota, B Gotoh, K Kuma... - Virology, 1989 - Elsevier
Abstract Sequence analysis and comparison of the fusion glycoprotein genes of 11 Newcastle disease **virus** (NDV) isolates indicated a high degree of functional and structural constraint exerted on the change of the glycoprotein. However, synonymous nucleotide ...
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Rearrangements in the 5' nontranslated region and phylogenetic analyses of cucumber mosaic **virus** RNA 3 indicate radial **evolution** of three subgroups asm.org (HTML)
MJ Roossinck, L Zhang, KH Hellwald - Journal of virology, 1999 - Am Soc Microbiol
ABSTRACT Cucumber mosaic **virus** (CMV) has been divided into two subgroups based on serological data, peptide mapping of the coat protein, nucleic acid hybridization, and nucleotide sequence similarity. Analyses of a number of recently isolated strains suggest ...
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What does structure tell us about **virus evolution**? researchgate.net (PDF)
DH Bamford, JM Grimes, DJ Stuart - Current opinion in structural biology, 2005 - Elsevier
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Newcastle disease **virus evolution**: I. Multiple lineages defined by sequence variability of the hemagglutinin-neuraminidase gene
T Sakaguchi, T Toyoda, B Gotoh, NM Inocencio... - Virology, 1989 - Elsevier
Abstract We compared the hemagglutinin-neuraminidase gene sequence among 13 strains of Newcastle disease **virus** (NDV) isolated over the last 50 years. Although overall homology was remarkably high, the sequence variability demonstrated the existence of at least three ...
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⁴Arquivo .RIS (RefMan): importado diretamente no Mendeley

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MLA Bamford, Dennis H., Jonathan M. Grimes, and David I. Stuart. "What does structure tell us about virus evolution?." *Current opinion in structural biology* 15.6 (2005): 655-663.

APA Bamford, D. H., Grimes, J. M., & Stuart, D. I. (2005). What does structure tell us about virus evolution?. *Current opinion in structural biology*, 15(6), 655-663.

Chicago Bamford, Dennis H., Jonathan M. Grimes, and David I. Stuart. "What does structure tell us about virus evolution?." *Current opinion in structural biology* 15, no. 6 (2005): 655-663.

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DH Bamford, JM Grimes, DI Stuart - Current opinion in structural ..., 2005 - europepmc.org

Viruses are the most abundant life form and infect practically all organisms. Consequently, these obligate parasites are a major cause of human suffering and economic loss. The organization and origins of this enormous virosphere are profound open questions in ...

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- Iniciado em 2004, digitalizou milhões de livros + OCR para extrair a íntegra do texto
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⁵<https://books.google.com/>

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Cleber Cristiano Prodanov e Ernani Cesar de Freitas

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1 Review

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5 TRABALHOS ACADÊMICOS E CIENTÍFICOS NOS CURSOS DE GRADUAÇÃO E PÓS-GRADUAÇÃO

Trabalhos científicos ou acadêmicos consistem em escritos que resultam do desenvolvimento de pesquisas realizadas tanto em Curso de Graduação quanto de Pós-graduação.

São vários os tipos de trabalhos acadêmicos e suas denominações e não há consenso sobre os significados dos diversos termos empregados. Por isso, adotamos, neste trabalho, o entendimento que é dado pela ABNT ou, quando inexistente, o mais aceito, tendo por base a literatura sobre o assunto.

Esta obra não contempla todos os tipos de trabalhos acadêmicos ou científicos. O interesse está voltado para aqueles típicos de disciplinas, conclusão de cursos de graduação e pós-graduação, projeto de pesquisa, além de redação e formatação de artigo.

Nos cursos de graduação, os universitários devem ser orientados a progredir gradativamente da simples informação para a autodescoberta do conhecimento e para a criatividade.

Dessa forma, os cursos de graduação caracterizam-se pela integração social dos universitários, não somente pela sua instrumentalização, mas, principalmente, pela formação de uma comunidade acadêmica.

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[By John Barrow]

WITH A BIOGRAPHICAL INTRODUCTION

BY

HENRY KINGSLEY

AUTHOR OF GEOFFREY HAMLYN

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Example (Buscando a frase...)

“Life depends on the ability of cells to store, retrieve, and translate the genetic instructions required to make and maintain a living organism.”

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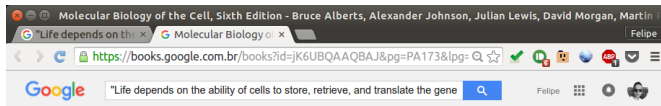
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Result 1 of 1 in this book for "Life depends on the ability of cells to store, retrieve, and translate the genetic instructions required to make and maintain a living organism."

Clear search

BASIC GENETIC MECHANISMS

DNA, Chromosomes, and Genomes

CHAPTER 4

IN THIS CHAPTER
THE STRUCTURE AND FUNCTION OF DNA
CHROMOSOMAL DNA AND ITS PACKAGING IN THE CHROMATIN FIBER
CHROMATIN STRUCTURE AND FUNCTION
THE GLOBAL STRUCTURE OF CHROMOSOMES

Life depends on the ability of cells to store, retrieve, and translate the genetic instructions required to make and maintain a living organism. This *hereditary information* is passed on from a cell to its daughter cells at cell division, and from one generation of an organism to the next through the organism's reproductive cells. The instructions are stored within every living cell as its *genes*, the information-containing elements that determine the characteristics of a species as a whole and of the individuals within it.
As soon as genetics emerged as a science at the beginning of the twentieth century, scientists became intrigued by the chemical structure of genes. The information in genes is copied and transmitted from cell to daughter cell millions of times during the life of a multicellular organism, and it survives the process essentially unchanged. What form of molecule could be capable of such accurate and almost unlimited replication and also be able to exert precise control, directing multicellular development as well as the daily life of every cell? What kind of instructions does the genetic information contain? And how can the enormous amount

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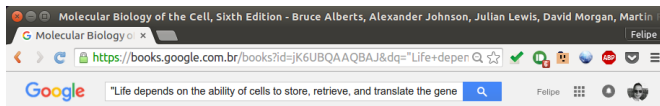
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DT Felson, JJ Anderson, A Naimark... - *Annals of internal medicine* ..., 1988 - Am Coll Physicians
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A highly pleiotropic amino acid polymorphism in the *Drosophila* insulin receptor contributes to life-history adaptation

Annalise B. Paaby^{1,2}, Alan O. Bergland³, Emily L. Behrman¹ and Paul S. Schmidt¹

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- 102. Kelley, J.L., Peyton, J.T., **Fiston-Lavier, A.-S.**, Teets N.M., Yee, M.-C., Johnston, J.C., Bustamante, C.D., Lee, R.E., Denlinger, D.L. (2014). Compact genome of the Antarctic midge is likely an adaptation to an extreme environment. *Nature Communications*, **5**, #4611, doi:10.1038/ncomms5611.
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Trends in Ecology & Evolution Cell Press

Volume 22, Issue 3, March 2007, Pages 156–165

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Parasites: proxies for host genealogy and ecology?

Caroline M. Nieberding^{1,2}, Isabelle Olivieri³

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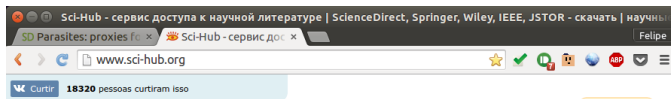
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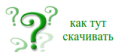


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Parasites: proxies for host genealogy and ecology?

Caroline M. Nieberding^{1,2} and Isabelle Olivier³

¹ Zoogeographical Research Unit, University of Liège, B 4000 Sart Tilman, Belgium
² Institute of Biology, Leiden University, 2300 RA Leiden, the Netherlands
³ Institut des Sciences de l'Evolution, Université Montpellier 2, 34095 Montpellier cedex 05, France

Genetic information is used extensively to reconstruct the evolutionary and demographic history of organisms. Recently, it has been suggested that genetic information from some parasites can complement genetic data from their hosts. This approach relies upon the hypothesis that such parasites share a common history with their host. In some cases, parasites provide an additional source of information because parasite data can better reconstruct the common history. Here, we discuss which parasite traits are important in determining their usefulness for analysing host history. The key is the matching of the traits of the parasite (e.g. effective population size, generation time, mutation rate and level of host specificity) with the timescales (phylogenetic, phylogeographic and demographic) that are relevant to the issues of concern in host history.

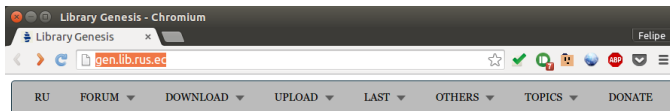
Whiteman and Parker [6] partly summarized the theoretical framework for using parasites as proxies for their host evolutionary history. Here, we further explain why parasites have become used as host 'proxies'. We emphasize that such 'proxy' parasites should share the host genealogical history and provide a better resolution of this common history than would the host itself. We argue that the choice of the most relevant parasite varies with the timescale of the analysis (phylogenetic, phylogeographic or demographic; see Glossary) and that parasites could be most useful at the phylogeographic and demographic scales. A better understanding of the relationship between parasites and their hosts is needed to address the questions that can be addressed.

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2	M. W. Service (auth.)	Mosquito Ecology: Field Sampling Methods 978-1-85166-798-7, 978-94-011-1868-2	Springer Netherlands	1993		English	30 Mb	pdf	[1] [2] [3] [4] [edit]	
3	John B. Silver	Mosquito Ecology: Field Sampling Methods (Third Edition) [3rd ed.] 1402066651, 9781402066658	Springer	2008	1500	English	27 Mb	pdf	[1] [2] [3] [4] [edit]	
4	J. R. McNeill	Mosquito Empires: Ecology and War in the Greater Caribbean, 1620-1914 (New Approaches to the Americas) [1 ed.]		2010	390	English	3 Mb	pdf	[1] [2] [3] [4] [edit]	

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