

Molecular Phylogenetics

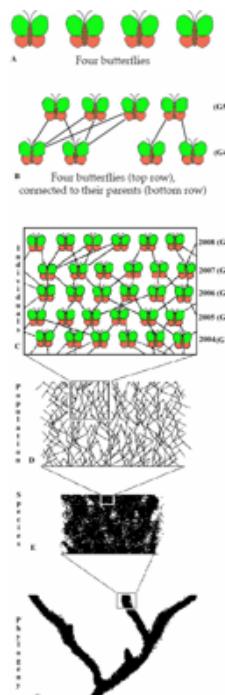
EEOB 563

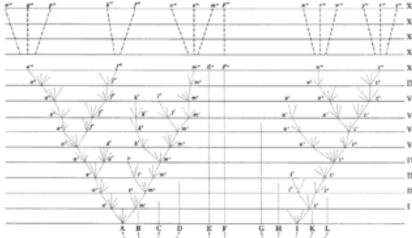
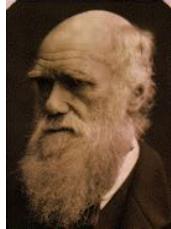
Phylogeny (*from phylum – tribe, and genesis – origin*)

- the term introduced by E. Haeckel in the second half of the XIX century and now has two somewhat different meanings.
- (1) Phylogeny in wide sense is a historical development of organisms
- (2) Phylogeny in narrow sense includes not all aspects of historic development, but only succession of branching of a genealogical (i.e. a phylogenetic) tree.
- Usually represented by a phylogenetic tree.

What is a phylogenetic tree?

- A tree is a mathematical structure which is used to model the actual evolutionary history of a group of sequences or organisms.
- The actual pattern of historical relationships is an evolutionary tree which we try to estimate





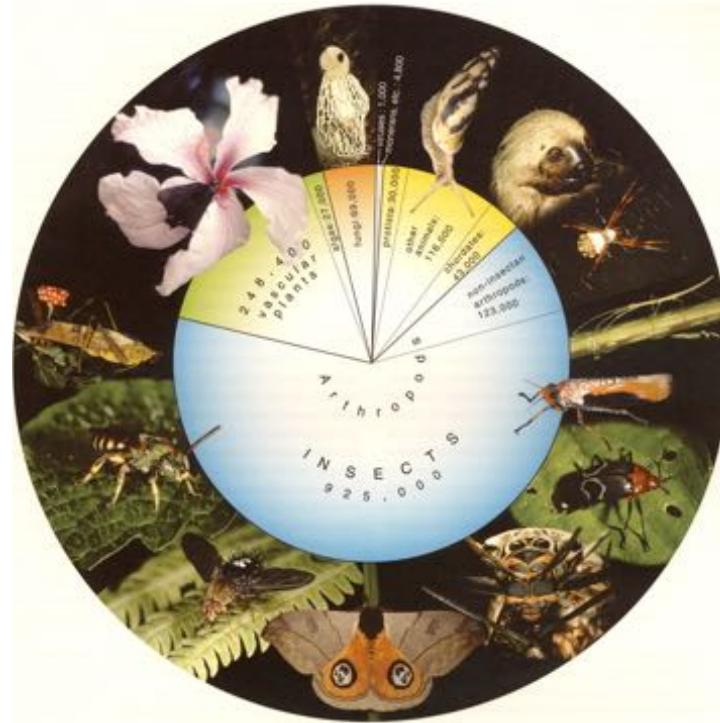
"The time will come I believe, though I shall not live to see it, when we shall have fairly true genealogical (phylogenetic) trees of each great kingdom of nature"

Darwin's letter to Thomas Huxley (1857)



"... there is, after all, one true tree of life [...]. It exists. It is in principle knowable. We don't know it all yet. By 2050 we should –or if we do not, we shall have been defeated only at the terminal twigs, by the sheer number of species."

Dawkins (2003), A Devil's Chaplain



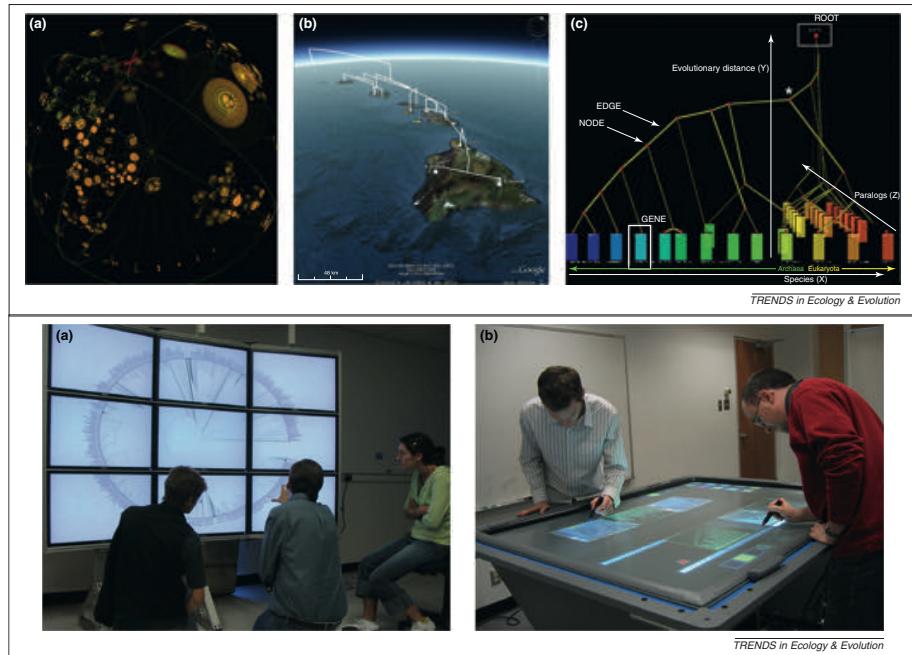
The AToL initiative (Assembling the Tree of Life) is a large research effort sponsored by the National Science Foundation. Its goal is to reconstruct the evolutionary origins of all living things.



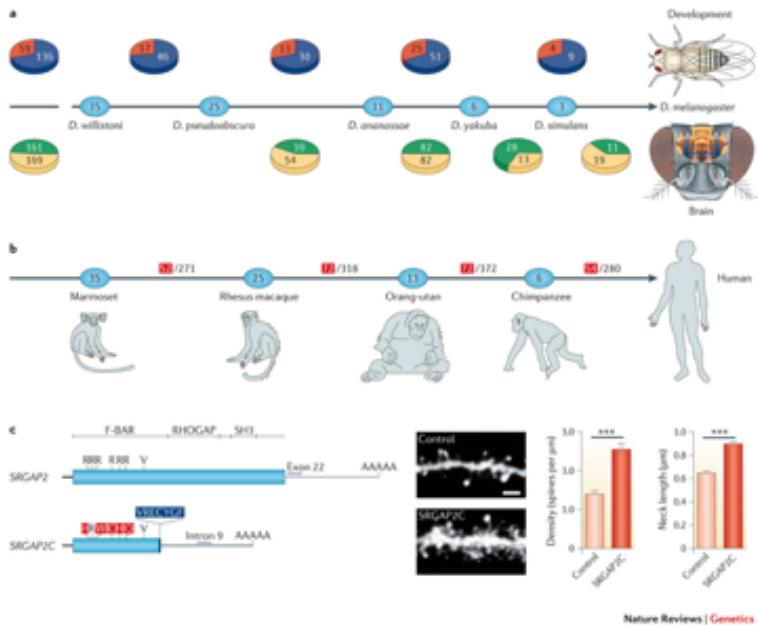
The Protist Ribosomal Reference database (PRiRe) is a catalog of unicellular eukaryotic Small Subunit rRNA sequences with curated metadata. Gruen L, Becher D, Ander S, Baas D, Benney C, Blinov I, Bothe C, Borodagel G, de Vargas C, Deselle J, Del Campo J, Dierssen JH, Duhaime M, Edwards R, Helmuth M, Hoehn MA, Laro E, Le Moal N, Lepage R, Ward P, Manktelow K, McMurtry J, Mora S, O'Kelly S, Pichot J, Probert L, Reuterle M, Sturm K, Sturm T, Vilela D, Zommermann P, Chisholm R., 40(21), Nov 27 2012, Rochester Institute of Technology.

The Chaperonin-60 Universal Target is a Barcode for Bacteria That Enables the Non-Assembly of Metagenomic Sequence Data LiWu M, Chumerinck TJ, Hennigsean SM, Hilt JE, Kuykendall P, Nov 28 2012, PLoS One

The Effect of Geographical Scale of Sampling on DNA Barcoding Performance. Bhattacharya DT, Fujisawa T, Eble M, Monaghan MT, Stoeck M, Friedrich L, Geiger J, Harrison J, Fraser CR, Miller L, Nilsson MH, Berendsohn TG, Vrabel AP., 2010 Oct 1;8(10):881-899. DOI: 10.1016/j.ydbio.2010.07.016, Systematic Biology



Space, time, form: viewing the Tree of Life
Roderic D.M. Page



Why molecular phylogenetics?

- The stream of heredity makes phylogeny: in a sense, it is phylogeny. Complete genetic analysis would provide the most priceless data for the mapping of this stream. **George G. Simpson, 1945**



- "I do not fully understand why we are not proclaiming the message from the housetops ... We finally have a method that can sort homology from analogy." **Stephen J. Gould , 1985**



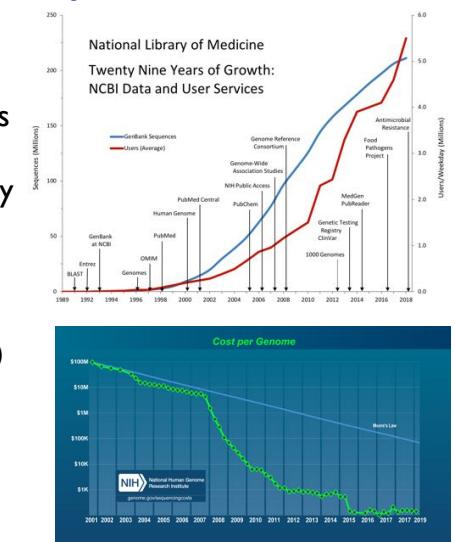
J. Theoret. Biol. (1965) 8, 357–366

Molecules as Documents of Evolutionary History

EMILE ZUCKERKANDL AND LINUS PAULING

Molecules as documents of evolutionary history

- "We may ask the question where in the now living systems the greatest amount of information of their past history has survived and how it can be extracted"
- "Best fit are the different types of macromolecules (sequences) which carry the genetic information"

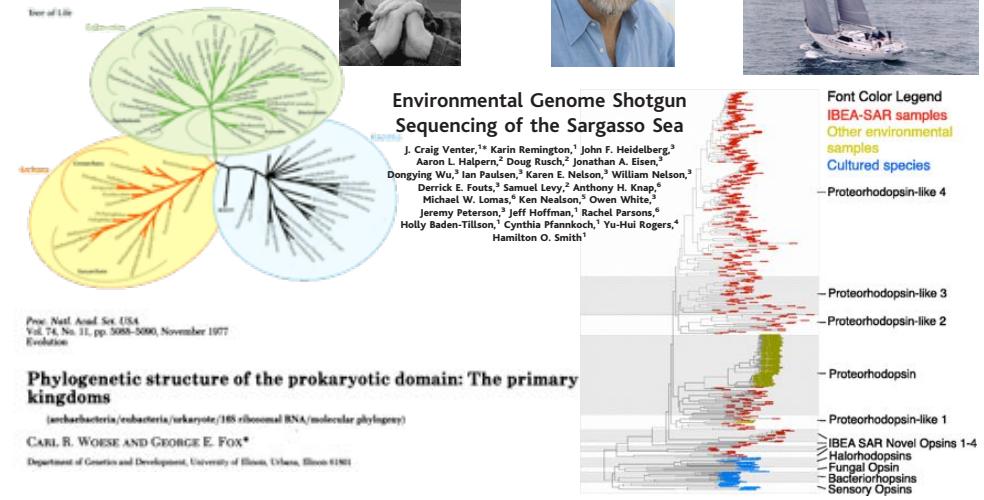


Applications of Phylogenetic Analysis

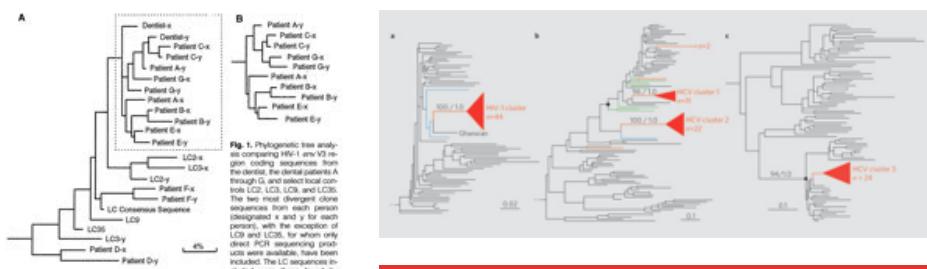
- Systematics and classification
- Discovering new life forms
- Phylogeography and speciation
- Molecular evolution
- Genomics
- Epidemiology and forensics
- Biotechnology
- Agriculture
- Conservation



Discovering new life forms



Disease Transmission and Medical Forensics



Molecular Epidemiology of HIV Transmission in a Dental Practice

Chin-Yih Ou, Carol A. Ciesielinski, Gerald Myers, Claudio I. Bandea, Chi-Cheng Luo, Bette T. M. Korber, James I. Mullins, Gerald Schochetman, Ruth L. Berkman, James I. Economou, John J. Witte, Lawrence C. Furman, Glen A. Satten, Kersti A. MacInnes, James W. Curran, Harold W. Jaffe, Laboratory Investigation Group,* Epidemiologic Investigation Group†

Nature 444, 896-897 (6 December 2006) doi:10.1038/nature05364; Received 4 November 2006; Accepted 24 November 2006; Published online 6 December 2006

Molecular Epidemiology: HIV-1 and HCV sequences from Libyan outbreak

Tulio de Oliveira¹, Oliver G. Pobur¹, Andrew Rambaut², Marco Salemi³, Sharon Caselli⁴, Massimo Ciuccozzi⁵, Giovanni Rezza⁵, Guido Castelli-Gattinara⁶, Roberto D'Arrigo⁶, Massimo Antonucci⁶, Luc Perrin⁶, Vittorio Colizzi⁶, Carlo Federico Perino⁶ and Bengt Hazuda Study Group^{1,2}

In 1998, outbreaks of human immunodeficiency virus type 1 (HIV-1) and hepatitis C virus (HCV) infection were reported in children attending Al-Fateh Hospital in Bengazi, Libya. Here we used molecular phylogenetic techniques to analyse new virus sequences from these outbreaks. We find that the HIV-1 and HCV strains were already circulating and prevalent in this hospital and its environs before the arrival in March 1998 of the foreign medical staff (five Bulgarian nurses and a Palestinian doctor) who stand accused of transmitting the HIV strain to the children.

Ou et al. 1992

Applications of Phylogenetic Analysis

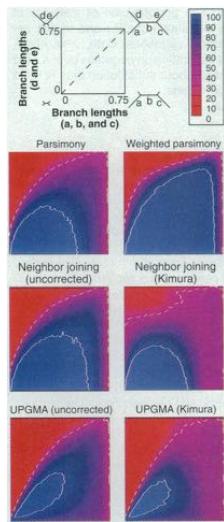
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- Conservation

“Simple identification via phylogenetic classification of organisms has, to date, yielded more patent filings than any other use of phylogeny in industry.”

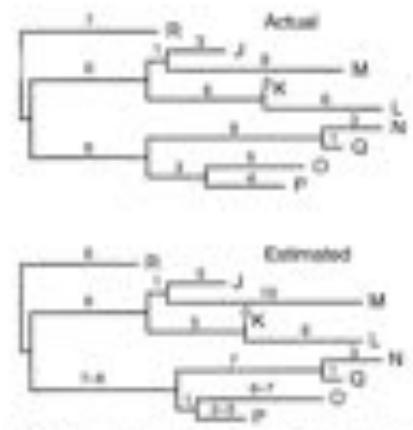
Bader et al. (2001)



How do we know that phylogenetics work?



a) simulations



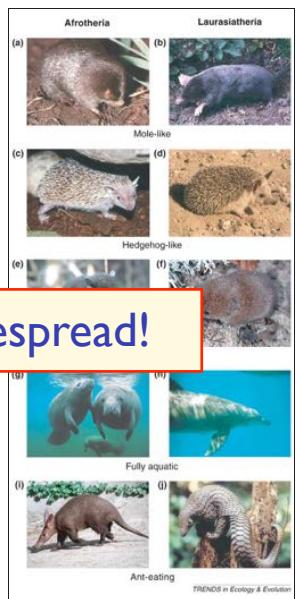
b) experimental phylogenies

ARTICLE [https://doi.org/10.1038/sj.tee.1901583](#) Application and Accuracy of Molecular Phylogenies

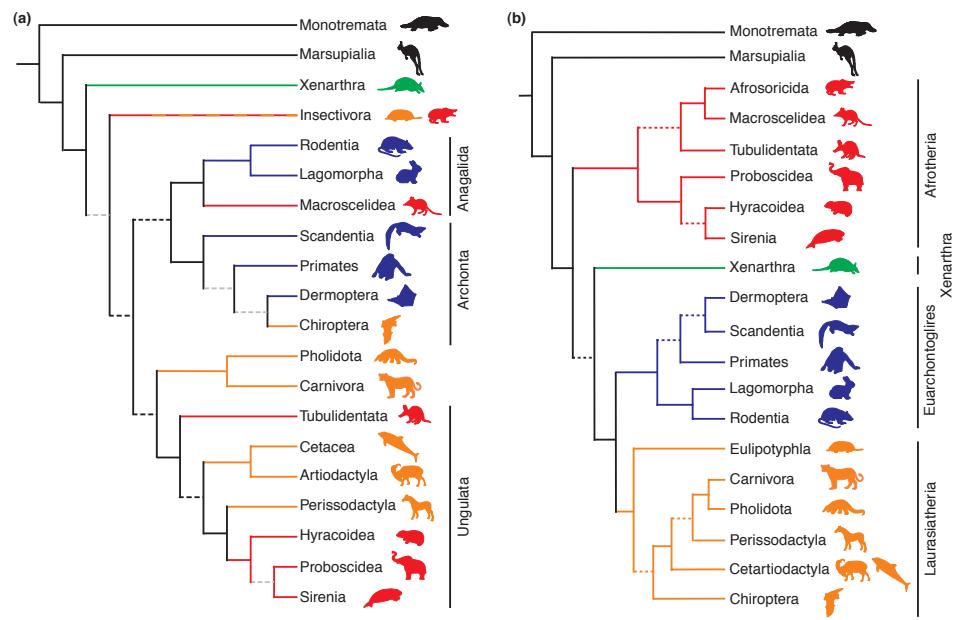
David M. Hillis, John P. Huelsenbeck, Clifford W. Cunningham

Niche	Placental Mammals	Australian Marsupials
Burrower	Mole	Marsupial mole
Anteater	Anteater	Numbat (marsupial)
Mouse	Mouse	Marsupial mouse
Climber	Spotted quoll	
Glider	Flying squirrel	Flying phalanger
Cat	Bobcat	Tasmanian "tiger cat"
Wolf	Wolf	Tasmanian wolf

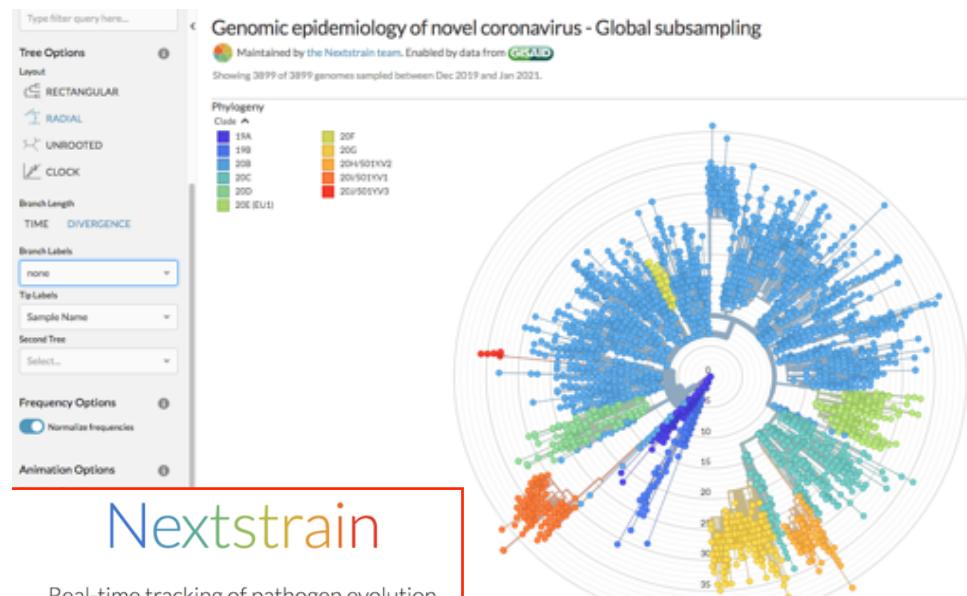
Convergence is widespread!



Springer et al. 2004



Springer et al. 2004



Nextstrain

Real-time tracking of pathogen evolution

Nextstrain is an open-source project to harness the scientific and public health potential of pathogen genome data. We provide a continually-updated view of publicly available data alongside powerful analytic and visualization tools for use by the community. Our goal is to aid epidemiological understanding and improve outbreak response. If you have any questions, or simply want to say hi, please give us a shout at hello@nextstrain.org.

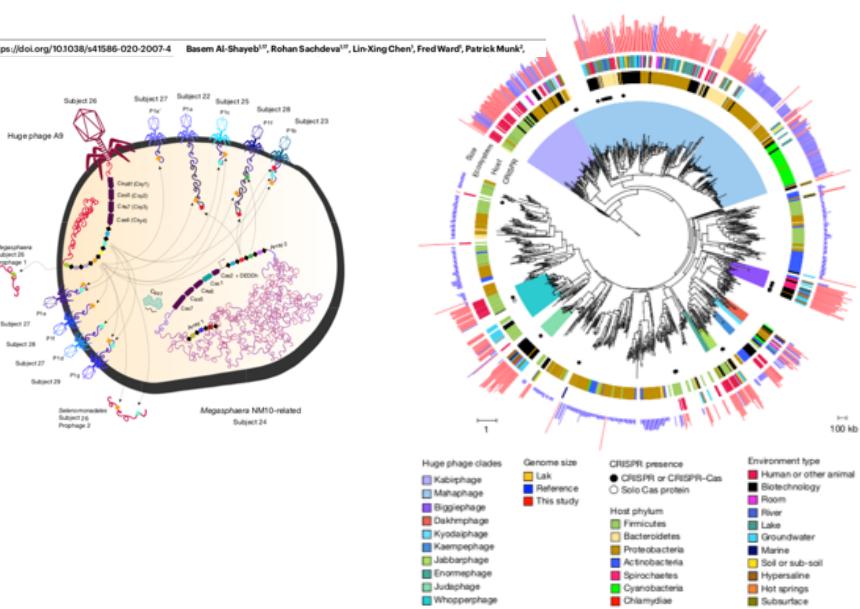
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Article

Clades of huge phages from across Earth's ecosystems

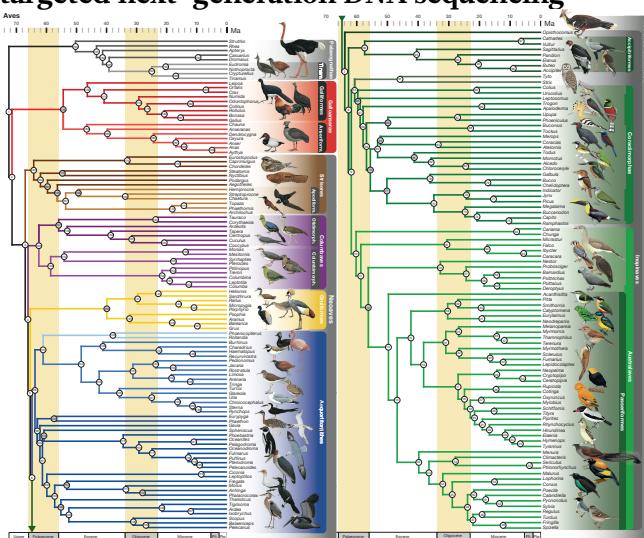
<https://doi.org/10.1038/s41586-020-2007-4> Basem Al-Shayeb^{1,2*}, Rohan Sachdeva^{1,2}, Lin-Xing Chen¹, Fred Ward¹, Patrick Munk¹,



LETTER

doi:10.1038/nature15697

A comprehensive phylogeny of birds (Aves) using targeted next-generation DNA sequencing



Article

One thousand plant transcriptomes and the phylogenomics of green plants

<https://doi.org/10.1038/s41586-019-1693-2> One Thousand Plant Transcriptomes Initiative

