



# Many shades of journal publishing: what colour is peer review in a predatory journal?

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# Journal quality criteria

- **Efficiency** - identifying and disseminating significant knowledge in timely manner
- **Focus** - the extent to which a journal publishes the most pertinent and meaningful knowledge
- **Impact** - the extent to which its content reflects and inspires the new, relevant knowledge
- **Scope** – reaching audience, potential contributors to knowledge (regional, national, international)
- **Selectivity** - ability to select better knowledge
- **Composite rating** - determined by the journals' efficiency, focus, impact, scope, and selectivity

Forgionne and Kohli, Information and Management, 2001

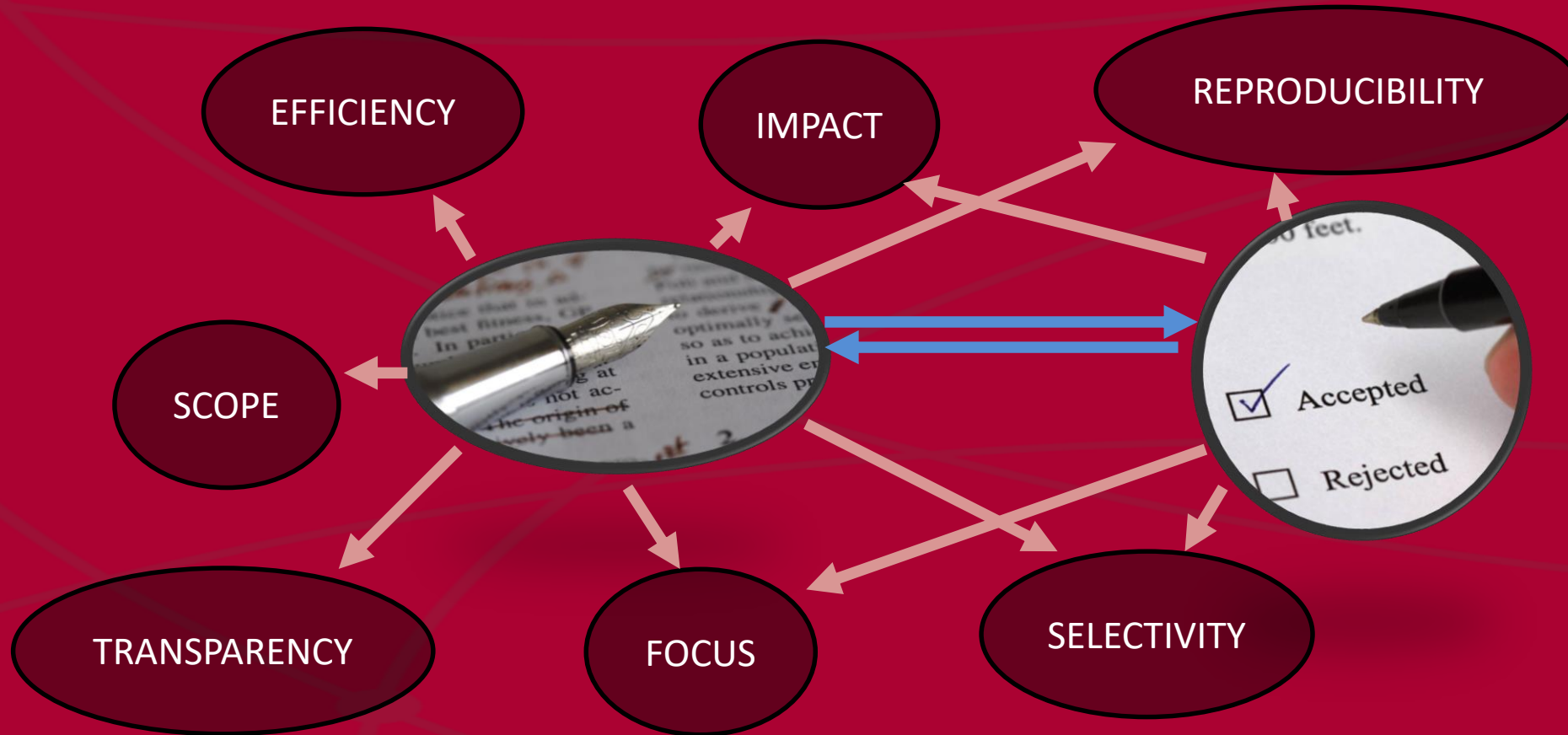


# Journal quality criteria (additional)

- **Transparency and openness** – content, research data, methods, software, editorial policies
- **Reproducibility** – the basic principle of science (repeat, replicate, reproduce and reuse)!
- **Licencing** – article content and research data usage rights



# Editors and peer reviewers





# Peer review

- „The peer-review process is still the gold standard that will continue to drive scholarly publication” (Mayden, 2012)
- **„Peer review involves the unbiased, independent critical assessment of scholarly or research manuscripts submitted to journals by key experts or opinion leaders” (ICMJE)**
- „A good reviewer is competent, knowledgeable, unbiased, objective, punctual, consistent, ethically sound, constructive, and maintains confidentiality” (Garmel, 2010; Kumar, 2009)



# WHY „PREDATORY” JOURNALS?

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## Possible reasons?

- commercialization of the scholarly publishing
- *publish or perish*
- bias in acceptance by well-known „western” journals
- language barriers
- not all research is globally relevant
- different funding levels in different countries/research communities
- simplicity of journal – still paper-centric

## Protein structure and function at low temperatures†

By R. JAENICKE

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D-8400 Regensburg, F.R.G.

Proteins represent the major components in the living cell that provide the whole repertoire of constituents of cellular organization and metabolism. In the process of evolution, adaptation to extreme conditions mainly referred to temperature, pH and low water activity. With respect to life at low temperatures, effects on protein structure, protein stability and protein folding need consideration.

The sequences and topologies of proteins from psychrophilic, mesophilic and thermophilic organisms are found to be highly homologous. Commonly, adaptive changes refer to multiple alterations of the amino acid sequence, which presently cannot be correlated with specific changes of structure and stability; so far it has not been possible to attribute specific increments in the free energy of stabilization to well-defined amino-acid exchanges in an unambiguous way.

The stability of proteins is limited at high and low temperatures. Their expression and self-organization may be accomplished under conditions strongly deviating from optimum growth conditions. Molecular adaptation to extremes of temperature seems to be accompanied by a flattening of the temperature profile of the free energy of stabilization. In principle, the free energy of stabilization of proteins is small compared to the total molecular energy. As a consequence, molecular adaptation to extremes of physical conditions only requires marginal alterations of the intermolecular interactions and packing density. Careful statistical and structural analyses indicate that altering the number of ion pairs and hydrophobic interactions allows the flexibility of proteins to be adjusted so that full catalytic function is maintained at varying temperatures.

### 1. INTRODUCTION

Proteins as the major components of the living cell provide the basic elements of cellular organization and metabolism. Their structure–function relation is generally assumed to be optimized with respect to the physical conditions characteristic for the natural biotope. Adaptation to extreme conditions during evolution mainly refers to temperature, pH and low water activity (Jaenicke 1981). Low water activity and extremes of pH do not necessarily require molecular adaptation of the cellular inventory as avoidance may take the place of adaptation; for example high salinity or a pH value less than 1 or greater than 11 may be compensated by compatible solutes or proton pumps. In the case of temperature, it is evident that cells are more or less isothermal with respect to their environment. As a consequence, both psychrophiles and thermophiles have to adapt their cell inventory to their respective set of conditions. Strategies promoting thermal stability of proteins have been investigated for many years. The outcome is that in the native state of functional proteins, stabilizing and destabilizing interactions more or less balance each other so that no general mechanism of temperature adaptation can be put forward. Adaptation at the protein level may be

† Dedicated to Professor Hans Neurath on the occasion of his eightieth birthday.

[ 19 ]

## HISTORY OF MEDICINE

### The Triumph over the Most Terrible of the of Death

MD, and Pere Domingo, MD

ago, Edward Jenner performed an the foundation for the eradication of rmed humankind's fight against diste humankind as no other disease ence and diffusion were without parought down at least three empires. d helplessly as their children succie or were disfigured or blinded by it. e to contain smallpox by isolating its y using variolation with varying devever, the definitive solution was not work was done at the end of the 18th ho had developed cowpox from cons rformed Jenner that they were uman form of the disease; he listened and raised it to the status of scientific discover vaccination, but he was the that this technique offered a reliable ilpox. It was also a reliable defense is, such as poliomyelitis, measles, and hough this was not known in Jenner's

lable at <http://www.aconline.org>.

7:635-642.

icia Primària Gràcia, Institut Català de la : la Santa Creu i Sant Pau, Barcelona, or addresses, see end of text.

ays present, filling the churchyard enting with constant fear all whom it en, leaving on those whose lives it as traces of its power, turning the rling at which the mother shuddered, eyes and cheeks of the betrothed horror to the lover (1).

een one of humankind's greatest time immemorial. Even illnesses plague, cholera, and yellow fever a universal and persistent impact. ed to have appeared at the time tural settlements in northeastern 000 BC (2). It probably spread dia by means of Egyptian mer-millennium BC (3). The earliest esions resembling those of small- : faces of mummies from the time h Egyptian Dynasties (1570 to 1085

BC) and in the well-preserved mummy of Ramses V, who died as a young man in 1157 BC (4–6).

The first recorded smallpox epidemic occurred in 1350 BC during the Egyptian–Hittite war. The illness was passed to the Hittite population by Egyptian prisoners and affected soldiers and civilians alike. The Hittite King Suppiluliumas I and his heir, Arnuwandas, were victims; their civilization fell into sharp decline (2).

During the epidemic in Athens in 430 BC, Thucydides noted that those who survived the disease were later immune to it (7). These observations were reiterated by Rhazes (Abu Bakr Muhammad Ibn Zakariya al-Razi), to whom we owe the first medical description of smallpox, *De variolis et morbillis commentarius*, which was written in about AD 910. Rhazes also noted that the illness was transmitted from person to person (8). His explanation of why survivors of smallpox do not develop the disease a second time is the first theory of acquired immunity.

### The Fall of Empires: Variola Rex and the Course of History

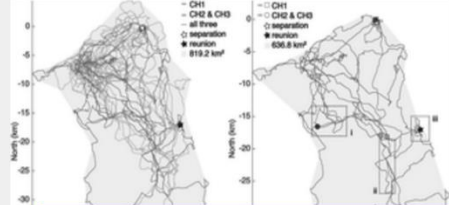
Smallpox greatly affected the development of western civilization. The first stages of the decline of the Roman Empire, around AD 180, coincided with a large-scale epidemic: the plague of Antonine, which killed between 3.5 and 7 million persons (9, 10). The Arab expansion, the Crusades, and the discovery of the West Indies all contributed to the spread of the illness. Unknown in the New World, smallpox was introduced by Spanish and Portuguese conquistadors. It decimated the local population and was instrumental in the fall of the empires of the Aztecs and the Incas. When the Spanish arrived in 1518, Mexico had about 25 million inhabitants; by 1620, this number had diminished to 1.6 million (11). A similar decrease occurred on the eastern coast of what became the United States, where the advent of smallpox had disastrous consequences for the native population (12), and the disease continued to be spread through the relentless process of European colonization (13). The devastating effect of smallpox gave rise to one of the first examples of biological warfare. In a letter written to Colonel Henry Bouquet in 1763, Sir Jeffrey Amherst, com-





### Male Circumcision and the Epidemic Emergence of HIV-2 in West Africa

João Dinis Sousa, Marina Padrão Temudo, [ ... ], Anne-Mieke Vandamme



### Cheetah Reunion – The Challenge of Finding Your Friends Again

Tatjana Y. Hubel, Justine Shotton, [ ... ], Alan M. Wilson

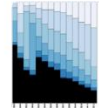


### Tweets

Paul Walk Retweeted

Herbert @hvsdomp

We all know links rot. But did you know linked content changes? A lot? - Scholarly Context Adrift doi.org/10.1371/journa...



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5h

Pablo Iriarte Retweeted

Herbert @hvsdomp

## The Human Genome Project: Under an International Ethical Microscope

Bartha Maria Knoppers and Ruth Chadwick

At first glance, the Human Genome Project (HGP) seems unencumbered by any explicit ethical or legal norms. However, from its beginnings the HGP has spawned a myriad of international (1-9), regional (10-14), and national (15-38) reports and guidelines and, more recently, some legislation (39-47). A review of the last 5 years (December 1989 to July 1994) reveals several areas of international consensus that could serve to harmonize eventual national regulation. Five basic principles underlie this consensus: autonomy, privacy, justice, equity, and quality of respect for human dignity. Ensuring that these international areas of "consensus" are reinforced and adopted by the HGP is an ethical and political challenge—a unique opportunity to direct rather than react.

Autonomy. Genetic testing and the resulting information is highly personal. Because this information could be used to discriminate against individuals on socioeconomic grounds—for example, in selecting employees, immigrants, or insurance applicants—there has been a call for voluntary testing based on autonomous choice, with the participants having full information. The "right" not to know is increasingly raised as a corollary of autonomy. Most genetic information is only predictive and probabilistic—a certain gene may increase the likelihood of developing a disease. Indeed, it is this imprecise nature of genetic information that necessitates further protection against social pressures and a reaffirmation of informed consent procedures. Therefore, counseling has become a prerequisite to the decision to undergo testing. An exception to this principle of individual consent is newborn screening programs for immediately treatable disorders. A recent report from the United States, however, has explicitly recommended that parental consent be obtained (34).

There is consensus limiting genetic testing (including prenatal testing) to tests that are medically therapeutic. Which tests are considered to be therapeutic then re-

mains to be decided by individual countries according to cultural, social, and political norms. Both France (41, 42) and Norway (45) have passed legislation centralizing the elaboration of such "therapeutic" criteria in governmental bodies. Adherence to these criteria effectively curtails the use of genetic tests for sex selection or trait enhancement.

Most genetic testing is further limited to individuals at high risk for serious disorders. Furthermore, there is consensus that predisposition testing should be limited to diseases that are treatable or preventable. Somatic cell therapy is for the most part considered experimental and thus subject to stringent limitations (used only in serious monogenic conditions) as well as to additional safeguards and oversight. Preimplantation embryo testing remains controversial and severely constrained but not totally prohibited, except in Germany (44).

Privacy. Respect for the privacy of the person and for the confidentiality of genetic information is crucial. Although the results of genetic tests could be considered a form of sensitive medical information, genetic testing also reveals information about other family members and is of importance to insurers and employers. Some guidelines would prohibit any communication to all third parties without consent (8, 13, 14, 24, 30). Most guidelines, however, advocate the communication of relevant information to family members at high risk for serious harm without the consent of the patient or of the research participant only when all attempts to elicit voluntary communication have failed. All other disclosures of information—or use of DNA samples (unless anonymous)—would require consent. Furthermore, the collection, storage, and dissemination of genetic information should be subject to special procedures of coding, of removing identifiers, and of obtaining consent for new uses.

In the areas of insurance and employment, the presence or absence of universal health insurance and social security shapes current guidelines. Little is known of the potential discriminatory or stigmatizing effects (or even benefits) of access to genetic information by insurers and employers. Even countries with universal health care recommend rejecting access to or direct testing by employers and insurers for life

and disability insurance. For example, reports from both the Netherlands (28) and the United Kingdom (32) have called for a moratorium on requiring disclosure where life insurance policies are proportionate to income or of moderate size. Only Belgium has specifically included a prohibition on testing or access to genetic information by insurers in its Civil Code (40). The American NIH-DOE report recommends that "Information about past, present or future health status, including genetic information, should not be used to deny health care coverage or services to anyone" (35). Finally, genetic identity testing confirms either filial links (paternity or maternity) or presence at the scene of a crime (forensic testing) and utilizes the same techniques as medical testing (sampling, restriction fragment length polymorphisms (RFLPs), markers, and polymerase chain reaction amplification). Similar privacy concerns arise (38). France has passed legislation requiring court orders for such identity testing (41).

Justice. The international community is united in its concern for vulnerable populations, such as incompetent adults or minors, and for future generations. Although overprotection could make research with these populations impossible, the fact that they cannot decide for themselves and are often in institutions mandates special protection—but not exclusion. Furthermore, in the absence of treatment or prevention, the presymptomatic testing of children for late-onset disease has not been recommended. Where possible, both children and incompetent adults should participate in decision-making.

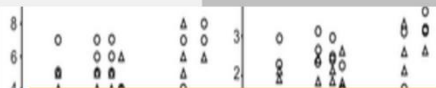
The continuing debate on the desirability of germline modification is sparked by a desire for justice toward future generations and prevention of eugenic uses of the technology. Although most guidelines advocate a total prohibition of germline modification, others have taken a more cautious approach, suggesting continuing discussion of its technical and ethical aspects and the development of adequate safeguards. The 1991 CIOMS Declaration of Inuyama (5) considered continued discussion of its technical and ethical aspects to be essential. Nevertheless, Austria (39), France (41), Germany (44), Norway (45), and Switzerland (47) prohibit germline alteration by statute.

Equity. Although not explicitly mentioned as a governing principle, equity is a recurring part of the ongoing discussion. How do we ensure equity of access to genetic research, testing, and information: equal costs; equal resources; and equal sharing of information? There is a potential danger and the accompanying fear of genetic testing increasing social inequality, of access to testing being linked to willingness

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### Deforestation Impacts on Bat Functional Diversity in Tropical Landscapes

Rodrigo García-Morales, Claudia E. Moreno, [ ... ], Eva S. Ávila-Gómez



### Ear Structures of the Naked Mole-Rat, *Heterocephalus glaber*, and Its Relatives (Rodentia: Bathyergidae)

Matthew J. Mason, Hannah L. Cornwall, Ewan St. J. Smith



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# The defects of peer review

- slow
- expensive
- highly subjective
- „something of a lottery”
- biased against innovative papers, women, non-prestigious institutions, low income countries, language, negative studies...
- easily abused
- inconsistent
- unable to detect errors or fraud

**FRAUDULENT RESULTS**

Andrew Wakefield, Lancet, 1998 – MMR vaccines and autism

Haruko Obokata. Nature, 2014 – stem cell research

Hwang Woo-suk, Science, 2004 i 2005 – have „succeeded” in creating human embryonic stem cells by cloning

Jan Hendrik Schön, Science et al. – semiconductors

Jon Sudbø, Lancet, 2009 – oncology

Yoshitaka Fujii, anesthesiology – fabricated more than 183 papers!

Diederik Stapel, psychology – 54 papers retracted!

paper generators – SCIdgen, Mathgen

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J Linnell MD, A P Dillon MD, S E Davies MD  
University Departments of Paediatric Gastroenterology  
(S H Murch MB, D M Casson MRCP, M Malik MRCP,  
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Radiology (A Valentine MRCP), Royal Free Hospital and School of  
Medicine, London NW3 2QG, UK  
Correspondence to: Dr A J Wakefield

computer, to study  
and controls. Urinary methylmalonic acid  
patients and controls were compared by a two-sample t test.  
Urinary creatinine was estimated by routine spectrophotometric  
assay.  
Children were screened for antiendomyxal antibodies and  
boys were screened for fragile-X if this had not been done



# Irreproducible research

IS THERE A CRISIS?

More than 70% of researchers have tried and failed to reproduce another scientist's experiments, and more than half have failed to reproduce their own experiments.



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# „Predatory” journals (J. Beall)

- **Editorial bodies** – editors are not named; without affiliations
- **Contact** – missing or fraudulent contact information
- **Fees** – costs associated with publishing are hidden or unclear
- **Journal name** – doesn't reflect the scope; imitates name of a prestigious journal; contain the national or international affiliation that does not match information on publisher's location
- **Indexing and metrics** – false information on indexing, false metrics
- **Journal scope** – is too broad
- **Peer review** – missing information on the peer review process, sometimes without peer review
- **Spam e-mails** – journal sends e-mails requesting submissions or inviting researchers to be members of the editorial board



## Small study

- 50 „predatory” publishers/journals were analyzed
- publisher name, URL address, note on fees, fees (USD), note on peer review
- author guidelines, reviewer guidelines, ethical policies were collected as a separate files
- screenshot of the publisher web site was captured
- simple content analysis – with **peer review** in focus



List of Journals

IPASJ International Journal of Computer Science (IJCS) ISSN 2321-5992

IPASJ International Journal of Information Technology (IJIT) ISSN 2321-5976

IPASJ International Journal of Electronics & Communication (IJEC) ISSN 2321-5984

IPASJ International Journal of Electrical Engineering (IJEE) ISSN 2321-600X

IPASJ International Journal of Mechanical Engineering (IJME) ISSN 2321-6441

IPASJ International Journal of Management (IJM) ISSN 2321-645X

Our Other Journals

International Journal of Emerging Trends & Technology in Computer Science, ISSN 2278-6856, www.ijettes.org, Email id: editor@ijettes.org

International Journal of Application or Innovation in Engineering & Management, ISSN 2319 - 4847, www.ijaem.org, Email id: editor@ijaem.org

Indexing Details

IJCS	IJEC	IS
ISSN 2321-5992	ISSN 2321-5984	

HIGHLIGHTS

6- Year Old Publication House  
All Journals Have Impact Factor More than 2.5  
1000+ Reviewer Board  
10000+ Authors Share their Research work  
200+ Successful Issue Published  
50+ Conference Associate  
Publication Fee is Low as compared to other journals

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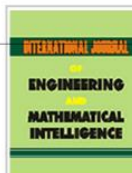
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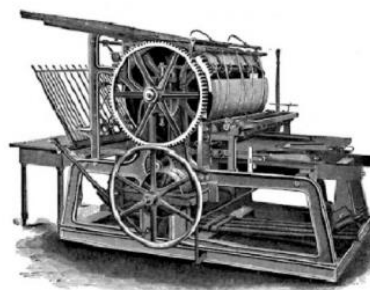
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Knowledge is the root of all good- Imam Ali (AS), Publish your work & enhance your good.

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Journals



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## Fees (#50)

- 9 journals not charging (new - probably will charge in the future)
- 5 journals – information on charges not available
- 4 journals – price on demand (contact address)
- 32 journals have fees (\$40-\$500) – differences between local and foreign authors
- article processing charges, article processing fees, article publishing fee, handling fee, manuscript processing fee, page fee
- upon acceptance



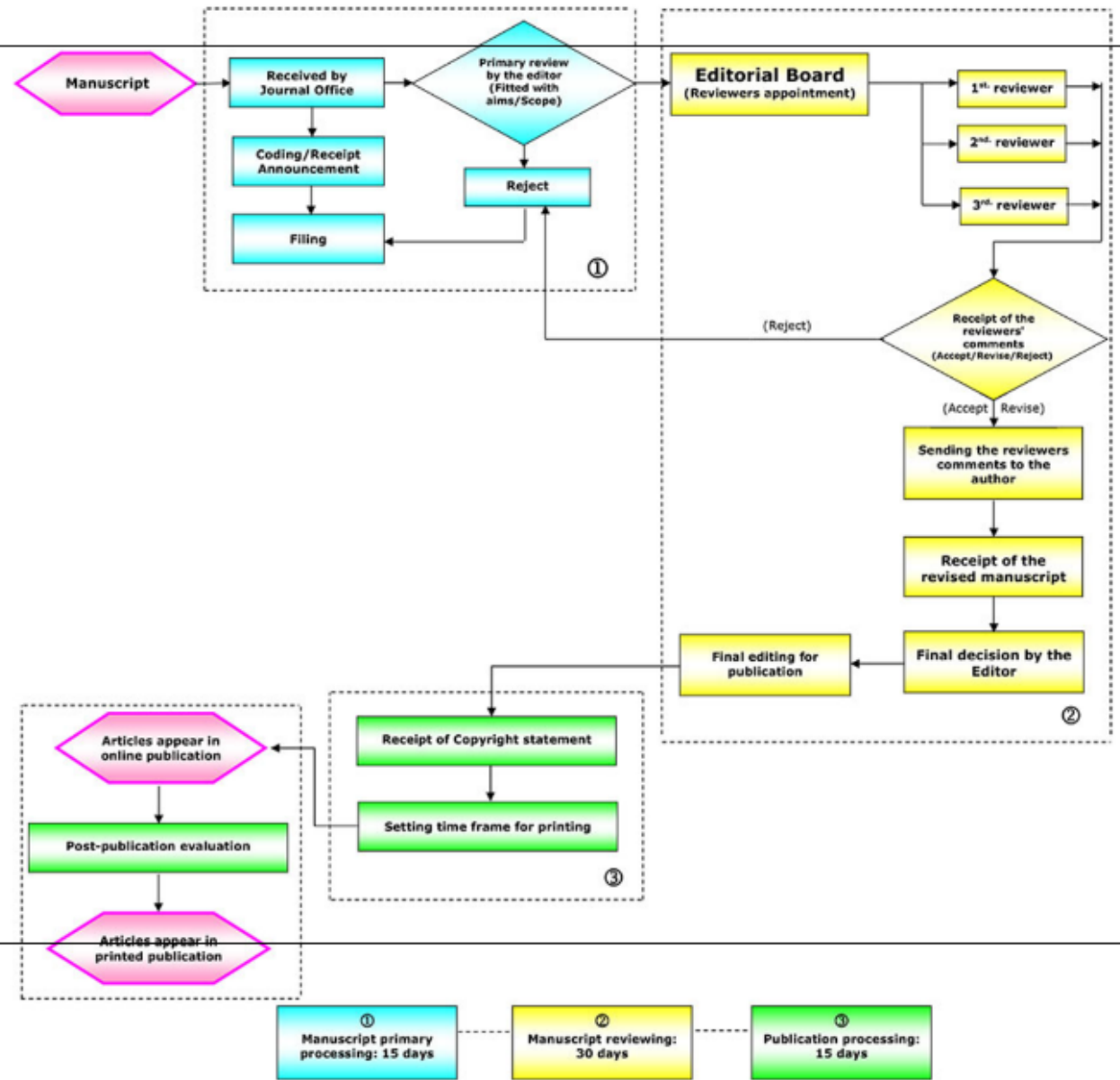


## Ethical policy (#50)

- 31 journals have a kind of ethical policy as a separate document
- all ethical policies have a note on **peer review**, manuscript originality and plagiarism
- 27 have a note on disclosure and conflict of interest

# PEERE

- only 14 journals have guidelines document
- 21 journal have a note on peer review
- 37 have information on peer review (double blind)
- 9 journals have double blind peer review
- ethical issues (plagiarism, fraud, confidentiality, conflict of interest)



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# „Predatory” journals

- **Editorial bodies** – editors are named; with affiliations
- **Contact** – contact information present
- **Fees** – 80% transparent information on fees
- **Journal name** – „international” character
- **Indexing and metrics** – not present
- **Journal scope** – not too broad
- **Peer review** – information on peer review process present

Limitations of the study:

- small sample
- accuracy of the presented information was not checked



# THE FUTURE OF PREDATORY PUBLISHERS?

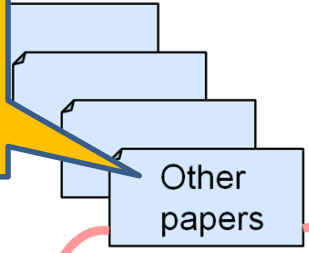
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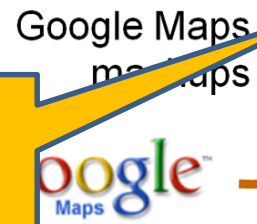
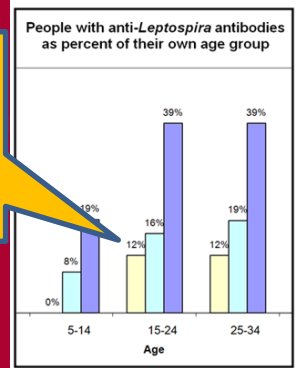
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INCLUSION OF EXISTING RESEARCH DATA



Data fusion



MASHUPS

**PLOS COMPUTATIONAL BIOLOGY**

Shotton *et al.* 2009, Adventures in semantic publishing

**PLOS NEGLECTED TROPICAL DISEASES**  
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**RESEARCH ARTICLE**

Impact of Environment and Social Gradient on *Leptospira* Infection in Urban Slums

Reis *et al.* 2008, original

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Asserted Class Hierarchy

- + owl:Thing
- + cito:Manifestation
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Citation typing ontology

turn all highlighting on | date | disease | habitat | institution | organism | person | place | protein | taxon

Top | Abstract | Author Summary | Introduction | Methods | Results | Discussion | Supporting Information | Acknowledgements | References | Data Fusion Supplements

**SEMANTICALLY ENHANCED VERSION OF A RESEARCH ARTICLE FROM PLOS NEGLECTED TROPICAL DISEASES**

Impact of Environment and Social Gradient on *Leptospira* Infection in Urban Slums

document summary

Reis *et al.* 2008, enhanced

*Leptospira interrogans* serova Copenhageni *Leptospira kirschneri* serovar Grippityphosa *leptospira spirochete*

**leptospirosis** mammals

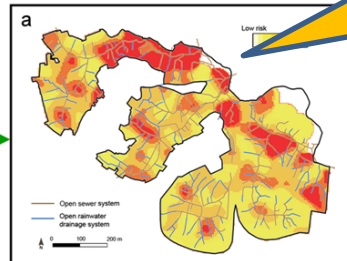
meningococcal disease Mumbai New York America occupational disease open drainage system

open rainwater drainage system open sewer drainage system

Pau de Lima pulmonary hemorrhage syndrome rats

*Rattus norvegicus* refuse deposit Rio de Janeiro Salvador Sao Paulo

Document summary



Interactive Fig. 3

- Table 1 data
- Fig. 2 data
- Fig. S2 data

Downloadable datasets

S1: Technical details

S2: Annotation guidelines

Reis *et al.* Portuguese abstract

RDF1: Details of article

RDF2: Details of citations

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## Introduction

At present, one billion of the world's population resides in **slum settlements** [1]. This number is expected to double in the next 25 years [1]. The growth of large urban populations which are marginalized from basic services has created a new set of global health challenges [2],[3]. As part of the Millennium Development Goals [4], a major priority has been to address the underlying poor sanitation and environmental degradation in slum communities which, in turn, are the cause of a spectrum of neglected diseases which affect these populations [2],[3],[5].

**Leptospirosis** is a paradigm for an urban health problem that has emerged due to recent growth of **slums** [6],[7]. The disease, caused by the **Leptospira spirochete**, produces life-threatening manifestations, such as **Weil's disease** and severe **pulmonary hemorrhage syndrome** for which fatality is more than 10% and 50%, respectively [7]–[9]. **Leptospirosis** is transmitted during direct contact with animal reservoirs or water and soil contaminated with their urine [8],[9]. Changes in the urban environment due to expanding slum communities has produced conditions for rodent-borne transmission [6],[10]. Urban epidemics of **leptospirosis** now occur in **cities** throughout the developing world during seasonal heavy rainfall and flooding [6],[11]–[18]. There is scarce data on the burden of specific diseases that affect slum populations [2], however **leptospirosis** appears to have become a major infectious disease problem in this population. In **Brazil** alone, more than 10,000 cases of severe **leptospirosis** are reported each year due to outbreaks in **urban centers** [19], whereas roughly 3,000, 8,000 and 1,500 cases are reported annually for **meningococcal disease**, **visceral leishmaniasis** and **dengue hemorrhagic fever**, respectively, which are other infectious diseases associated with urban poverty [20]–[22]. Case fatality (10%) from **leptospirosis** [19] is comparable to that observed for **meningococcal disease**, **visceral leishmaniasis** and **dengue hemorrhagic fever** (20%, 8% and 10%, respectively) in this setting [20],[23],[24]. Furthermore, **leptospirosis** is associated with extreme weather events, as exemplified by the El Niño-associated outbreak in **Guayaquil** in 1998 [25]. **Leptospirosis** is therefore expected to become an increasingly important slum health problem as predicted global climate change [26],[27] and growth of the world's slum population [1] evolves.

Urban **leptospirosis** is a disease of poor environments since it disproportionately affects communities that lack adequate sewage systems and refuse collection services [6],[10],[11]. In this setting, outbreaks are often due to transmission of a single serovar, **L. interrogans serovar Copenhageni**, which is associated with the **Rattus norvegicus** reservoir [6], [28]–[30]. Elucidation of the specific determinants of poverty which have led to the emergence of urban **leptospirosis** is essential in guiding community-based interventions which, to date, have been uniformly unsuccessful. Herein, we report the findings of a large seroprevalence survey performed in a Brazilian slum community (*favela*). Geographical Information System (GIS) methods were used to identify sources for **Leptospira** transmission in the **slum environment**. Furthermore, we evaluated whether relative differences in socioeconomic status among slum residents contributed to the risk of **Leptospira infection**, in addition to the attributes of the environment in which they reside.

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## Common variants at ten loci influence QT interval duration in the QTGEN Study

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The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line

The FANTOM Consortium & Riken Omics Science Center<sup>1</sup>

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ScienceDirect - Gene : Architecture of the large membrane-bound mucins - Mozilla Firefox

2.1. The nine gene candidates

2.2. *MUC3/MUC3A* and *MUC3B*

2.3. *MUC11* and *MUC12*

2.4. *MUC17*

2.5. The cluster of large membrane-bound mucins

2.6. *MUC16*

2.7. *MUC4*

3. General structure of the apomucins (mucin polypeptides)

3.1. SEA domain

3.2. EGF domain

3.3. NIDO-AMOP- $\rightarrow$ WF-D domains

4. Alternative splicing of mucins

References

**1. Introduction**

Epithelial mucins are heavily O-glycosylated proteins found in the mucus layer or at the cell surface of many epitheliums. They are responsible for the physical properties of mucus gels and are involved in epithelial cell protection. There is still no clear definition of a "mucin" and the increasing number of genes with the symbol *MUC* is unfortunately not helping the scientific community ([Dekker et al., 2002] and [Rose and Voynow, 2006]). In a first approach, we can propose the term mucin refers at least to the highly O-glycosylated epithelial molecules mainly found in the mucus layer. There are two structurally distinct families of mucins. The first one is made of the five *MUC19* that form oligomeric structures (Thornton et al., in press). The other family is made of membrane-bound mucins are made of at least a mucin-like domain, i.e. a large portion of amino acids that carry the O-glycans. The Ser/Thr/Pro repeat sequences are typically subject to a VNTR (variable number of TR) polymorphism. This region is expected to be highly polymorphic. Our goal in this review is to give a clear definition of mucins, which are located primarily, but not exclusively, at the cell surface, as their respective genes encode mucins. The O-glycosylated extracellular portion may be released into the mucus gel by proteolysis of mucus gels in contrast to small mucin molecules. We will only dwell here on the large membrane-bound mucins. Concerning the small mucin *MUC1* which was the first mucin characterized, several reviews have been published [Patton et al., 1995] and [Taylor-Papadimitriou et al., 1999]. Even though the large membrane-bound mucins due to sometimes the complexity and repetitive sequence databases can be useful tools to find new genes and to help in the characterization of new genes, it is important to bring new data from database analysis in order to bring some clarification.

**2. Domains of the membrane-bound mucins**

**2.1. The nine gene candidates**

To date, several cDNA genomic sequences claiming to come from seven putative membrane-bound mucins: *MUC12*, *MUC16* and *MUC17*. *MUC4* was mapped to 3q29, *MUC16* has been localized to 11p15, *MUC11*, *MUC12* and *MUC17* are organized in a cluster of genes on 7q22.1 (Table 1).

Table 1.

General features of the human and mouse large membrane-bound mucins

Human				Mouse	
Gene	Location	aa/TR <sup>1</sup>	Exons	Gene	Location
<i>MUC3/3A/3B</i>	7q22.1	17	> 11 (13?)		
<i>MUC4</i>	3q29	16	25	<i>Muc4</i>	16B3
<i>MUC11/12</i>	7q22.1		> 11 (13?)		

Done

Dekker et al., 2002 J. Dekker, J.W. Rossen, H.A. Buller and A.W. Einerhand, The MUC family: an obituary, *Trends Biochem. Sci.* **27** (2002), pp. 126–131. [Article](#) | [PDF \(72 K\)](#) | [View Record in Scopus](#) | [Cited By in Scopus \(119\)](#)

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**Defining mucins: family values:**

- There are two approaches to the definition of mucins but both are unsatisfactory when it comes to defining the relationships of the mucin-encoding genes.

- Using this criterion to define mucins would be similar to conflating all lipoproteins based on their modification with lipid moieties and calling the encoding genes ?LIP-number?.

**All in the family?:**

- MUC3* was one of the first *MUC* proteins found, in 1990 [4], but it has recently been discovered that there are, in fact, two closely related and adjacent genes (*MUC3A* and *MUC3B*) with 98% homology [26].

**Conclusions: families and orphans:**

- Based on sequence homology, two families of mucins can be distinguished: (1) the mucin genes at locus 11p15, which probably encode mucus-forming mucins; and (2) the mucin genes at loci 7q22, 3q and 1q21, presumably encoding membrane-bound mucins.

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# Influence of synoptic patterns on surface ozone variability over the eastern United States from 1980 to 2012

L. Shen et al.

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Research article

## Influence of synoptic patterns on surface ozone variability over the eastern United States from 1980 to 2012

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Received

**Abstract.** We investigate the effect of synoptic patterns on surface ozone variability over the eastern United States during the summer months. Daily MDA8 JJA ozone shows a bimodal distribution with a peak in the afternoon and a minimum in the morning. The variability in daily weather. We find that the leading EOF patterns explain 53 % of the variance in daily MDA8 ozone over the eastern United States associated with the North American monsoon system when its west boundary is located over the Bermuda High and an enhanced Gr activity, while the southern peak ap

the total number of days the jet traverses the Midwest and northeast each summer. In the Midwest and northeast, we find that the correlation coefficient  $r$  between detrended mean JJA MDA8 ozone and the polar jet frequency ranges between  $-0.76$  and  $-0.93$  over 1980–2012 depending on the time period selected, suggesting that polar jet frequency could provide a simple metric to predict ozone variability in future climate regimes. In the southeast, the influence of the Bermuda High on mean JJA MDA8 ozone depends on the location of its west edge. For

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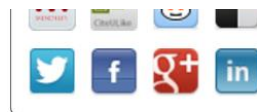
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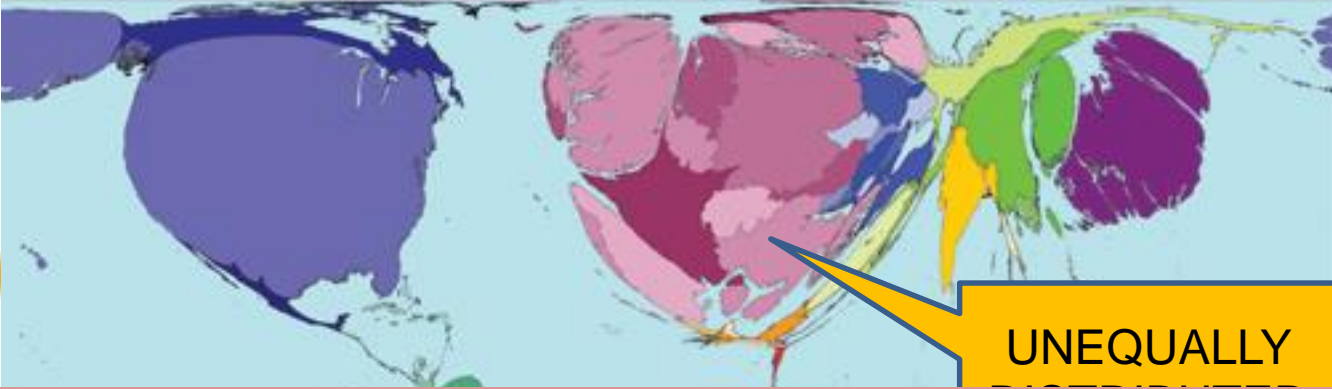
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**Mutational dynamics and phylogenetic utility of noncoding chloroplast DNA**

Thomas Borsch · Dietmar Quandt

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**Abstract** Introns and spacers are a rich and well-appreciated information source for evolutionary studies in plants. Compared to coding sequences, the mutational dynamics of introns and spacers is very different, involving frequent microstructural changes in addition to substitutions of individual nucleotides. An understanding of the biology of sequence change is required for correct application of molecular characters in phylogenetic analyses, including homology assessment, alignment coding, and tree inference. The widely used term “indel” is very general, and different kinds of microstructural mutations, such as simple sequence repeats, short tandem repeats, homonucleotide repeats, inversions, inverted repeats, and deletions, need to be distinguished. Noncoding DNA has been indispensable for analyses at the species level because coding sequences usually do not offer sufficient variability. A variety of introns and spacers has been successfully applied for phylogeny inference at deeper levels (major lineages of angiosperms and land plants) in past years, and phylogenetic structure *R* in intron and spacer data sets usually outperforms that of coding-sequence data sets. In order to fully utilize their potential, the molecular evolution and applicability of the most important noncoding markers (the *trnT-trnF* region comprising two spacers and a group I

intron; the *trnS-G* region comprising one spacer and a group II intron in *trnG*; the group II introns in *petD*, *trnI6*, *trnI8*, and *trnK*; and the *atpB-rbcL* and *psbA-trnG* spacers) are reviewed. The study argues for the use of noncoding DNA in a spectrum of applications from deep-level phylogenetics to speciation studies and barcoding, and aims at outlining molecular evolutionary principles needed for effective analysis.

**Keywords** Spacers · Introns · Phylogenetic structure *R* · Molecular evolution · SSRs · Inversions · Mutational hotspots · DNA barcoding

**Introduction**

The application of noncoding chloroplast DNA sequence data in plant molecular systematics has been steadily increasing over the last decade. Sequencing of rapidly evolving spacers and introns was initially proposed for unravelling evolutionary patterns among closely related species (Taberlet et al. 1991; Manen and Natali 1995). The idea was to use universal amplification primers that anneal to conserved genes and thereby span more variable spacers and introns. At about the same time, pronounced differences in mutational dynamics and consequently in levels of variability between coding and noncoding plastid regions were pointed out by Morton and Clegg (1993), Clegg et al. (1994), and others. As compared to coding genes, the sequences of introns and spacers are functionally less constrained. This, however, describes average sequence conservation. Introns in particular possess a well-conserved secondary structure that leads to a mosaic of highly conserved and extremely variable parts (Cech 1988; Michel et al. 1989; Cech et al. 1994; Kelchner 2002; Borsch et al.

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**Severe fever with thrombocytopenia syndrome, an emerging zoonosis**

Quan Liu PhD #, Bao He PhD #, Si-Yang Huang PhD #, Feng Wei PhD #, Prof Xing-Quan Zhu PhD #

**Summary**

Severe fever with thrombocytopenia syndrome (SFTS) is an emerging haemorrhagic fever that was first described in rural areas of China. The causative agent, SFTS virus (SFTSV), is a novel phlebovirus in the Bunyaviridae family. Since the first report in 2010, SFTS has been found in 11 provinces of China, with about 2500 reported cases, and an average case-fatality rate of 7-3%. The disease was also reported in Japan and Korea in 2012; Heartland virus, another phlebovirus genetically closely related to SFTSV, was isolated from two patients in the USA. The disease has become a substantial risk to public health, not only in China, but also in other parts of the world. The virus could undergo rapid evolution by gene mutation, reassortment, and homologous recombination in tick vectors and vertebrate reservoir hosts. No specific treatment of SFTS is available, and avoiding tick bites is an important measure to prevent the infection and transmission of SFTSV. This Review provides information on the molecular characteristics and ecology of this emerging tick-borne virus and describes the epidemiology, clinical signs, pathogenesis, diagnosis, treatment, and prevention of human infection with SFTSV.

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