



ScienceDirect Best Practices and Training Webinar

Academic Database Literacy & E-content for Research

Kelwalin Dhanasarnsombut
Customer Consultant Elsevier South East Asia (Thailand)
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- 2. Questions will be answered after presentation.
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- 4. Teaching materials will be sent to you after the training.

Agenda

Introducing Elsevier

Research workflow

Database Literacy

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Q&A, Closing and announcement





Questions from you



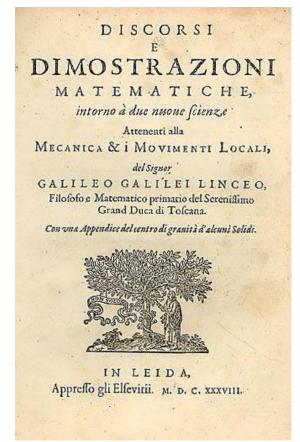
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GENOMICS PROTEOMICS & RIOINFORMATICS

Genomics Proteomics Bioinformatics 10 (2012) 114-121 Original Research

Searching for Non-coding RNAs in Genomic Sequences Using ncRNAscout

Michael Bao 1, Miguel Cervantes Cervantes 2, Ling Zhong 1,3, Jason T.L. Wang 1,3,4

 Bioinformatics Center, New Jerney Institute of Technology, Hevnett, NJ 07102, USA
 Department of Biological Sciences, Rangers University, Revnett, NJ 07102, USA
suppose Science Department, New Jerney Institute of Technology, Newark, NJ 07102, USA Received 21 March 2011; accepted 5 December 2011 Available online 9 June 2012

Receitly non-coding RNA (mRNA) genes have been found to serve many important functions in the cell such as regulation of gene capression at the transcriptional beed. Potentially there are more mRNA undersals syst to be found and hear possible functions see to be resulted. The discovery of artRNAs is a difficult task beause their place sequence indicators study as the start and step codent captived by protons coding KNAs. Current methods willike either sequence motifier or structural parameters to detect zowe larRNAs within genomes. Here, we persent an of number of MRNA index, canned of RNAscout, by stiffaces good by sequence motifier and surrectural parameters. Specifically, our method has three components (i) a measure of the frequency of a sequence, (ii) as measure of the structural parameters within a sequence the into my indicate the presence against constitution in a 4-socie, and (ii) as measure of the frequency of vertiral patterns which as a sequence that my indicate the presence of ncRNA. Experimental results show that, given a genome and a set of known ncRNAs, our method is able to accurately identify and locate a significant number of ncRNA sequences in the genome. The ncRNAscout tool is available for downloading at http://bisinfor-matics.ngt.du/ncRNAscout.

Keywords: Genome-wide ncRNA discovery: Sequence mocific Structural parameter

Non-coding RNA (ncRNA) is a term that describes any RNA that is not translated into a protein or any RNA family aside from mRNA. Non-coding RNAs have many important intracellular functions [1,2]. For example, rRNAs and tRNAs assist in mRNA translation; small nuclear RNAs (snRNAs) splice mRNA; and small nucleo-lar RNAs (snoRNAs) are involved in the medification of rRNAs [3]. Although ncRNA sequences are abundant within genomes [4,5] with numbers comparable to those of protein-coding genes (e), many potential neRNA fami-lies are yet to be discovered and their functions are set to be analyzed. To date, imperfect methods have led to an oversight of ncRNA sequences, even in extensively studied

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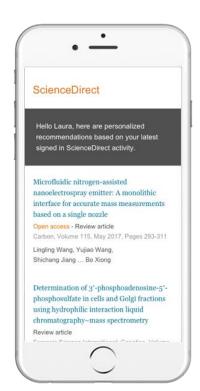
These ncRNA sequences must be identified using new methodologies. The ability to identify potential ncRNA regions within a genome will allow researchers to further the boundaries of knowledge of yet-to-be discovered ncRNA families and their likely intracellular roles.

The difficulty in discovering ncRNA genes within a given genomic sequence chiefly originates from their primary sequences not being evolutionarily conserved. Hence methods used in the discovery of protein-coding regions such as searching for start and stop codons or regions with coding potential, are not effective in search for ncRNA regions [9]. A better method would be to combine sequence and structural features when discovering ncRNA gene

Current tools utilized in ncRNA exploration can be classified into three categories [1,9] (i) ncRNA homology search, (ii) ncRNA prediction, and (iii) ah initio ncRNA

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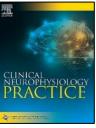














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02 Research workflow

Research Workflow



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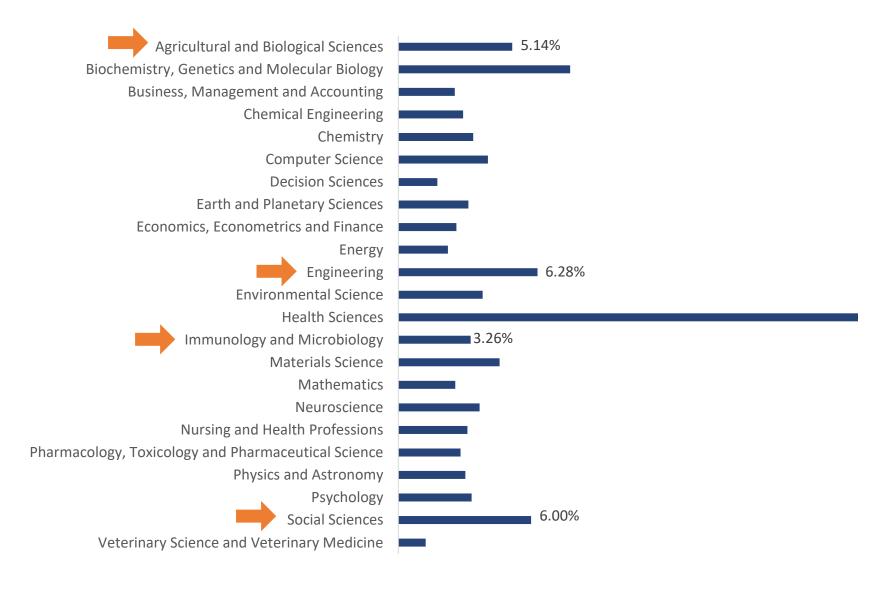
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- How to find research trends?
- How to link research with patents?
- What types of research manuscripts are out there?
- How to find collaborators?
- How to find funding bodies?
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- What should I prepare before writing?
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- How should I approach collaborative writing?
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- What are these metrics in journals?
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03 Database Literacy

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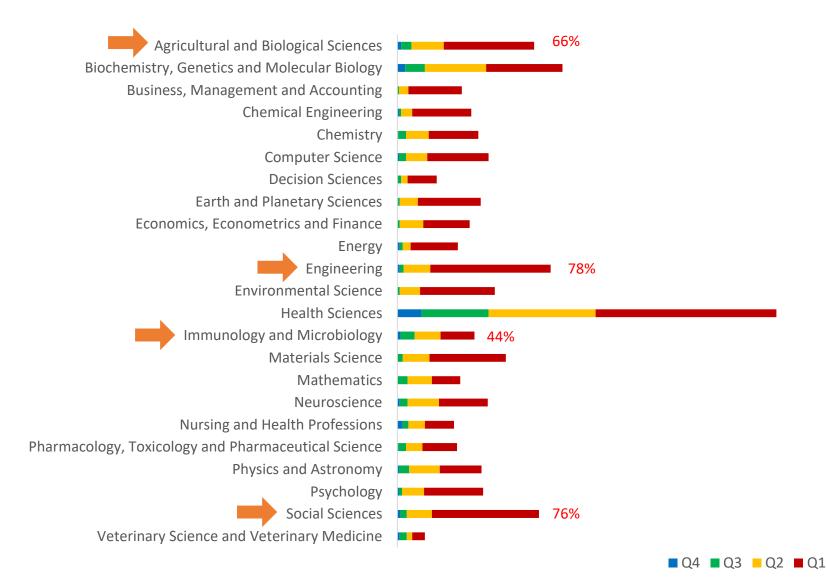
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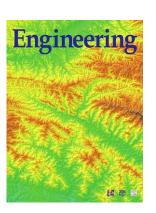
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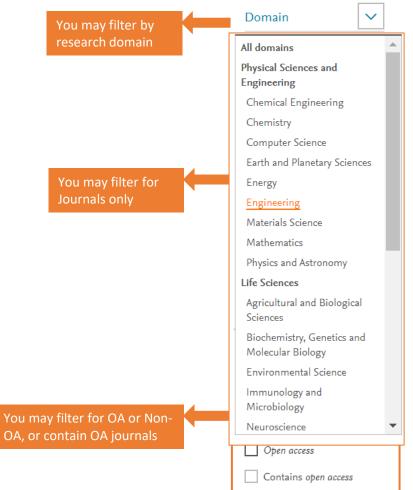
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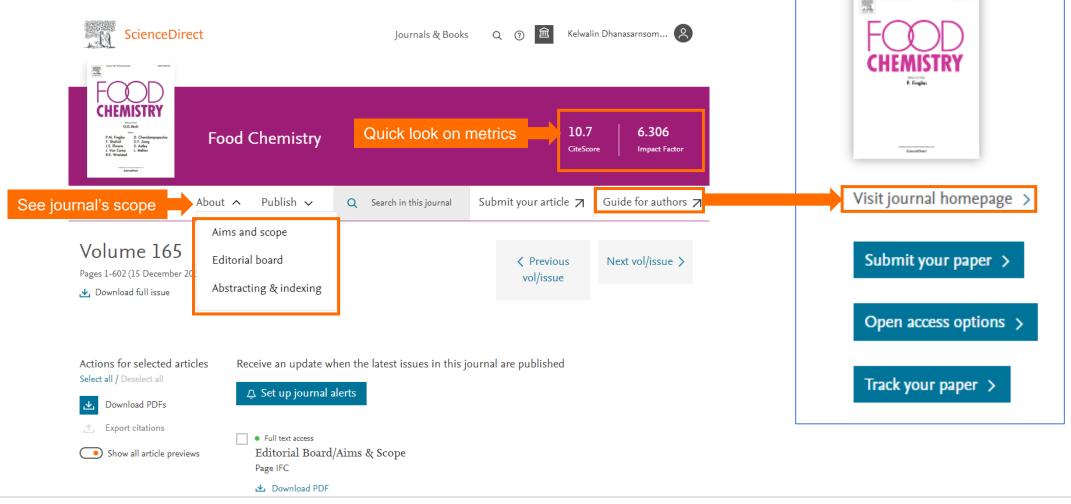
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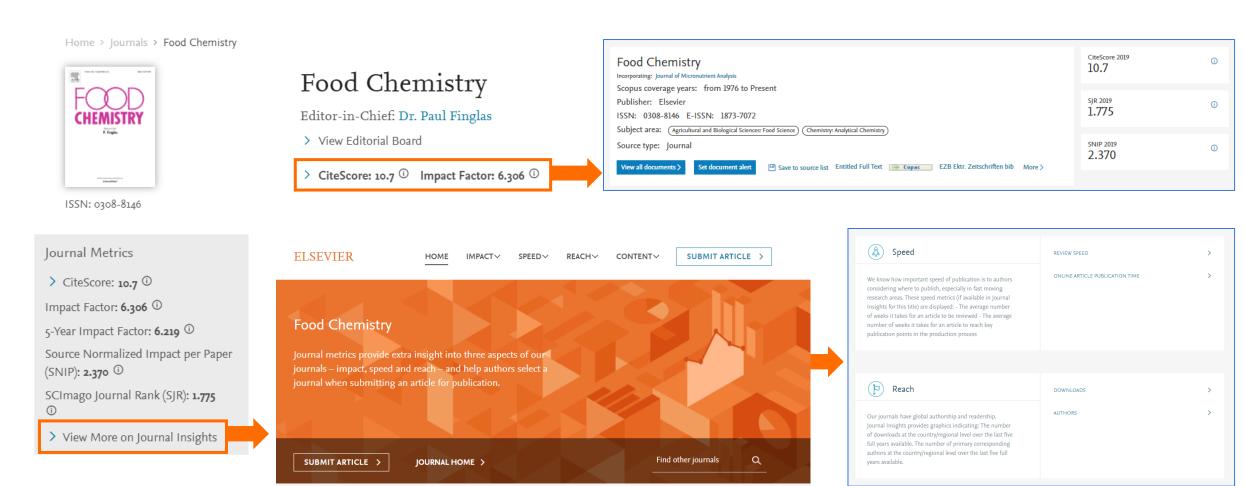
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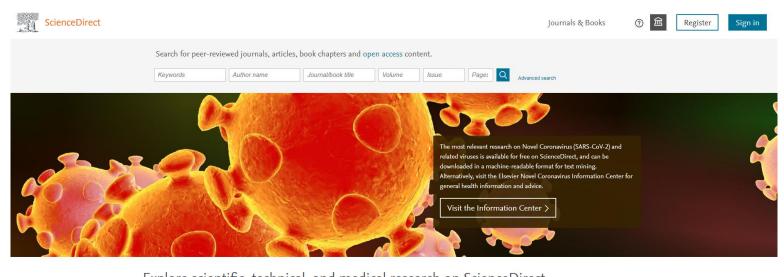


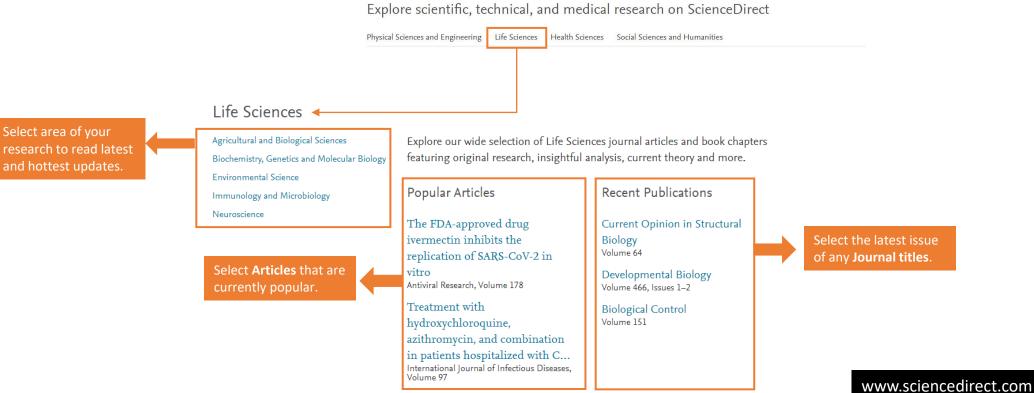


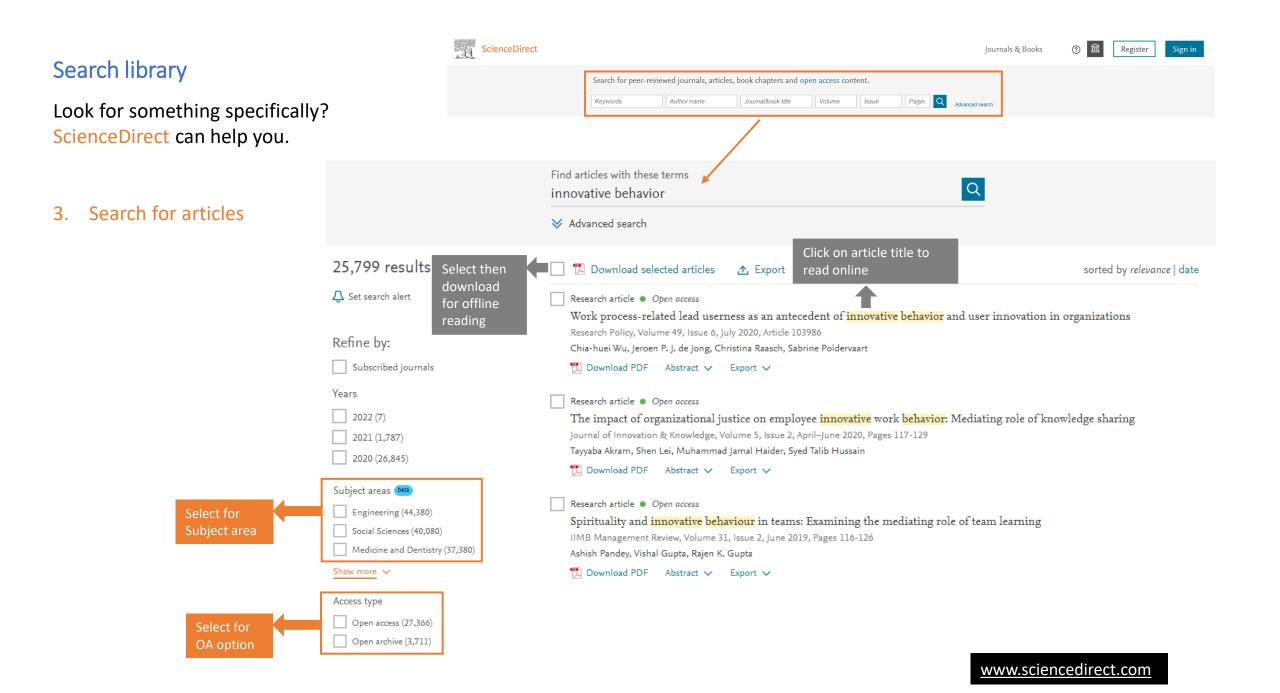
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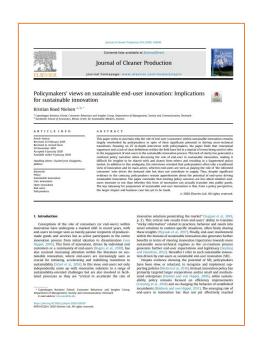
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Is music a mediator impacting car following when driver's personalities are considered

Jianwei Niu ^a 🌣 ⊠, Chuang Ma ^a, Jing Liu ^a, Lei Li ^a, Tingjiang Hu ^b, Linghua Ran ^c

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Highlights

- · Introverts are susceptible to music, and prefer slow tempo and classical music.
- · Pop music aroused more than classical one and induce closer headway time.
- · Medium music tempo was most appropriate for keeping stable car following.

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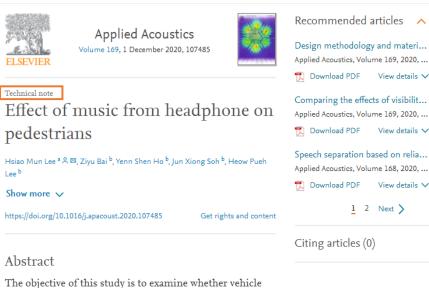
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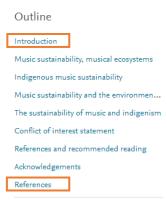
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Indigenous music sustainability during climate change

Klisala Harrison 🖾

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Indigenous music sustainability forms a cohesive concept due to shared sustainability threats globally among different Indigenous peoples historically and contemporaneously, shared aspects of music culture, and current ways of Indigenous pursuing music sustainability. During colonization, forced geographical relocations and cultural assimilations of Indigenous peoples threatened or Part of special issue:

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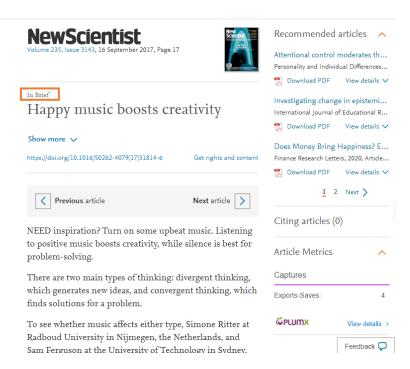
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Video Article

A publication item whose primary content is a video accompanied by a description of that video.

Journal Pre-proof

Robotic Assisted Lower Ureteric Reimplantation with Psoas Hitch repair following an latrogenic Injury

Sarah Marie Norton , Sophie Sharpe , Usman M. Haroon , Barry B. $\operatorname{McGuire}$

PII: S2590-0897(20)30037-2

DOI: https://doi.org/10.1016/j.urolvj.2020.100062

Reference: UROLVJ 100062

To appear in: Urology Video Journal

Received date: 18 September 2019 Revised date: 20 September 2020 Accepted date: 11 October 2020

Please cite this article as: Sarah Marie Norton, Sophie Sharpe, Usman M. Haroon, Barry B. McGuire, Robotic Assisted Lower Ureteric Reimplantation with Psoas Hitch repair following an latrogenic Injury, *Urology Video Journal* (2020), doi: https://doi.org/10.1016/j.urolvj.2020.100062



Background Objective

Outline

Method

Operative Method

Results

Conclusion Keywords

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Declaration of Competing Interest

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Sarah Marie Norton ™, Sophie Sharpe, Usman M. Haroon, Barry B. McGuire

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Background

The risk of injury to the ureter during an abdominal hysterectomy is estimated at 1.3% [1]. This injury often occurs following ligation of the uterine vessels as the ureter crosses under the artery.

Patient Consent

Written informed patient consent for the publication of this video case report was obtained from the patient.

The following is the video related to this article Video 1.



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Navigate with ease with Outline ScienceDirect Highlights Abstract Graphical abstract 1. Introduction Go to the specific section 2. PTMs can cause a switch between the different functio... 3. Homologs of moonlighting Proteins might not have b... 4. Even a single amino acid change can alter protein funct.. 5. Conclusions Transparency document References Show full outline 🗸 Figures (3) Download picture Tables (1) Table 1 Understand content quickly

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Journal of Proteomics
Volume 134, 16 February 2016, Pages 19-24



Protein species and moonlighting proteins: Very small changes in a protein's covalent structure can change its biochemical function ★

Constance J. Jeffery ⊠

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Highlights

- Moonlighting proteins have two or more physiologically relevant biochemical or biophysical functions.
- Post-translational modifications can toggle a moonlighting protein between two functions.
- Small differences between protein species can result in a homolog of a moonlighting protein with only one of the functions.
- A single amino acid difference can cause the gain of a "neomorphic moonlighting function".

Abstract

In the past few decades, hundreds of moonlighting proteins have been identified that perform two or more distinct and physiologically relevant biochemical or biophysical functions that are not due to gene fusions, multiple RNA splice variants, or pleiotropic effects. For this special issue on protein species, this article discusses three topics related to moonlighting proteins that illustrate how small changes or differences in protein covalent structures can result in different functions.

Part of special issue:

Towards deciphering proteomes via the proteoform, protein speciation, moonlighting and protein code concepts

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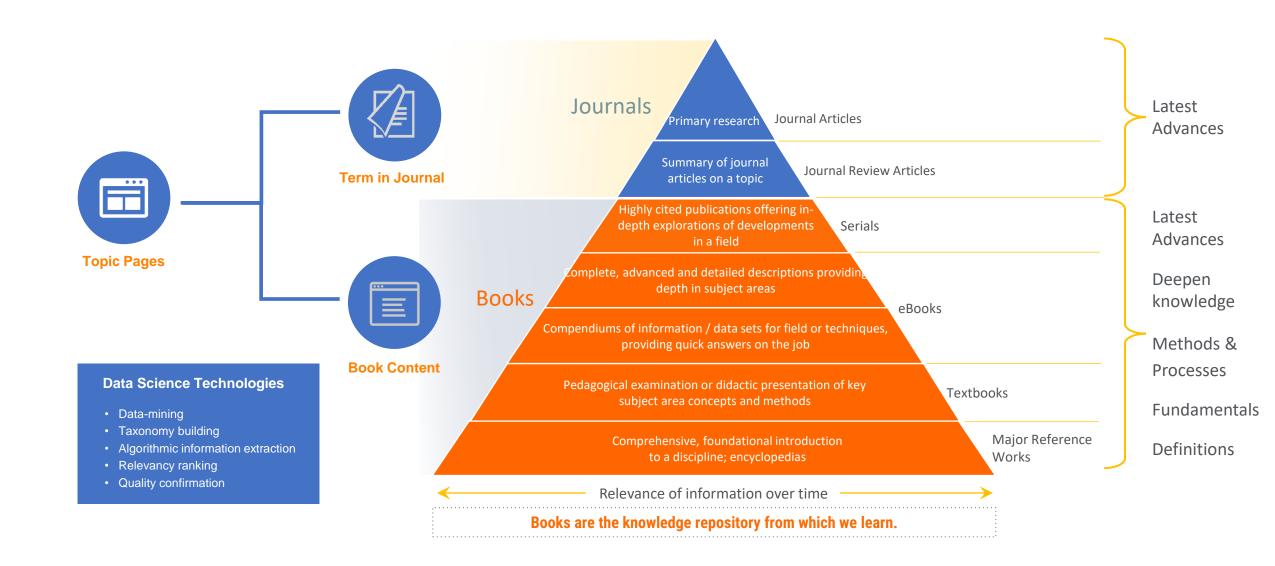
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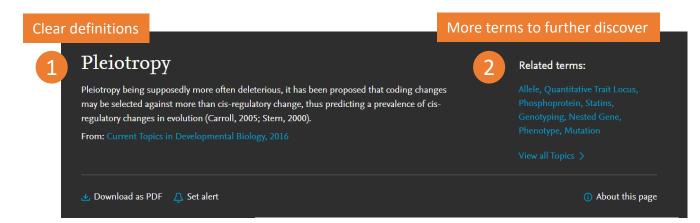
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4 Pleiotropy

Pleiotropy means that a single gene affects two or more characters. In the context of life history evolution, pleiotropy means that a single gene affects the fitness of the organism at two or more ages. It is convenient to categorize the combinations of age-specific pleiotropic effects as shown in Table 1. If a new mutation improves fitness in both young and old animals, then it is likely to be favored by natural selection, and will increase in the population. Conversely, a gene that decreases fitness in both young and old organisms will be eliminated by natural selection. The more interesting cases in Table 1 are those in which the fitness effects on young and old organisms are

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Abstract

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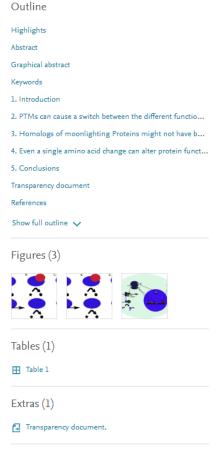
Biological significance

For this special issue on protein species, this article discusses three topics related to moonlighting proteins: Post-translational modifications (PTMs) that can cause a switch between functions, homologs that share only one of multiple functions, and proteins in which a single amino acid mutation results in the creation of a new function. The examples included illustrate that even in an average protein of hundreds of amino acids, a relatively small difference in sequence or PTMs can result in a large difference in function, which can be important in predicting protein functions, regulation of protein functions, and in the evolution of new functions.

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Journal of Proteomics Volume 134, 16 February 2016, Pages 19-24



Protein species and moonlighting proteins: Very small changes in a protein's covalent structure can change its biochemical function ★

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Highlights

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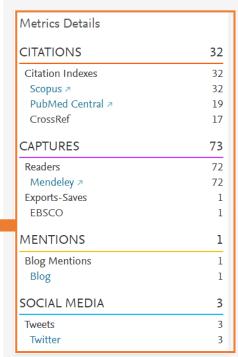
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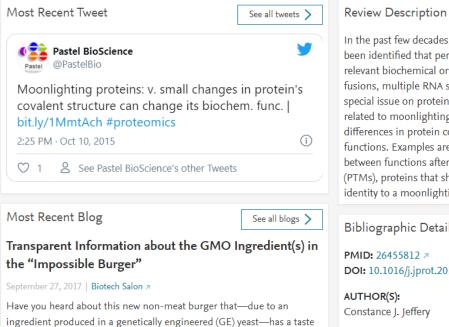
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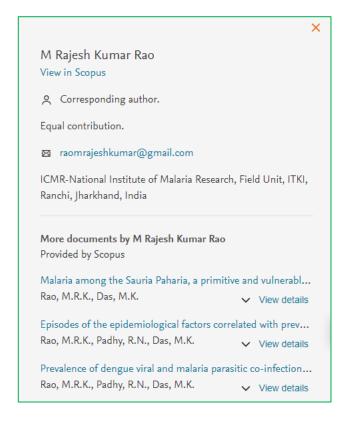
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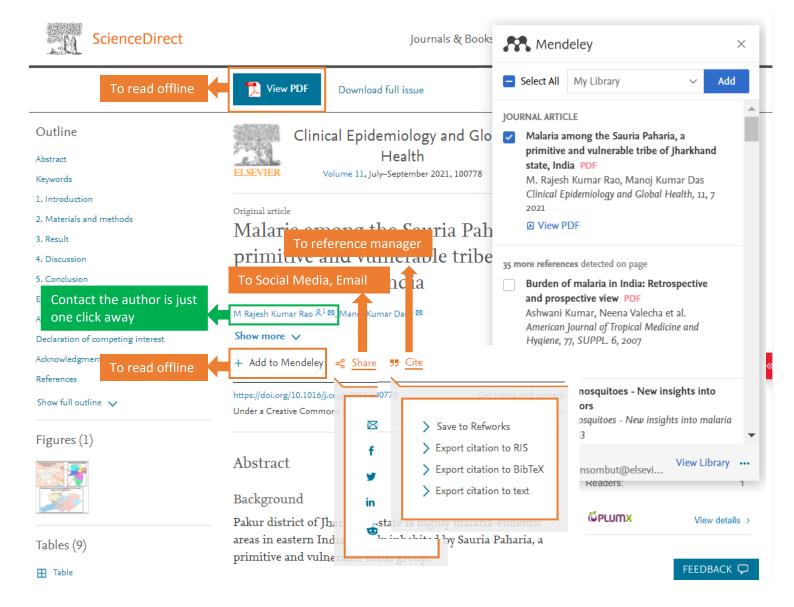
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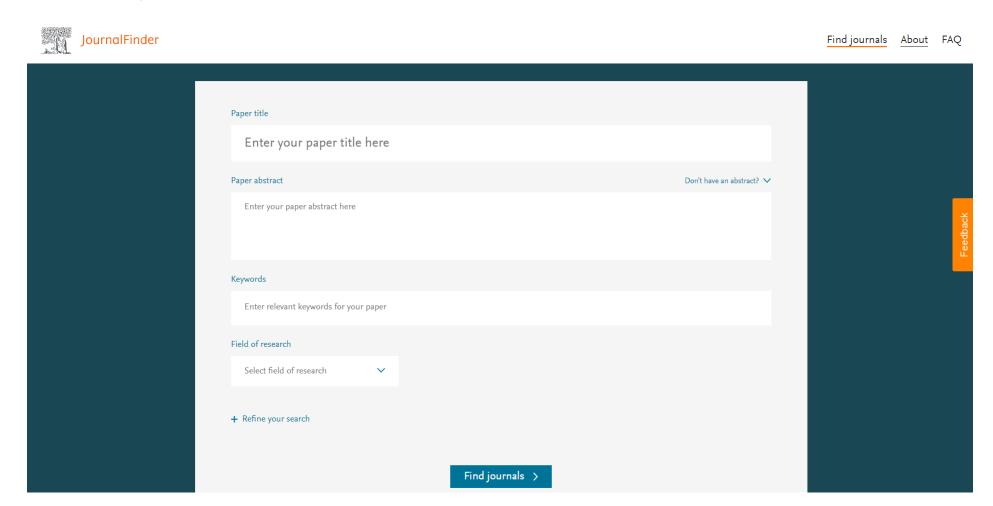
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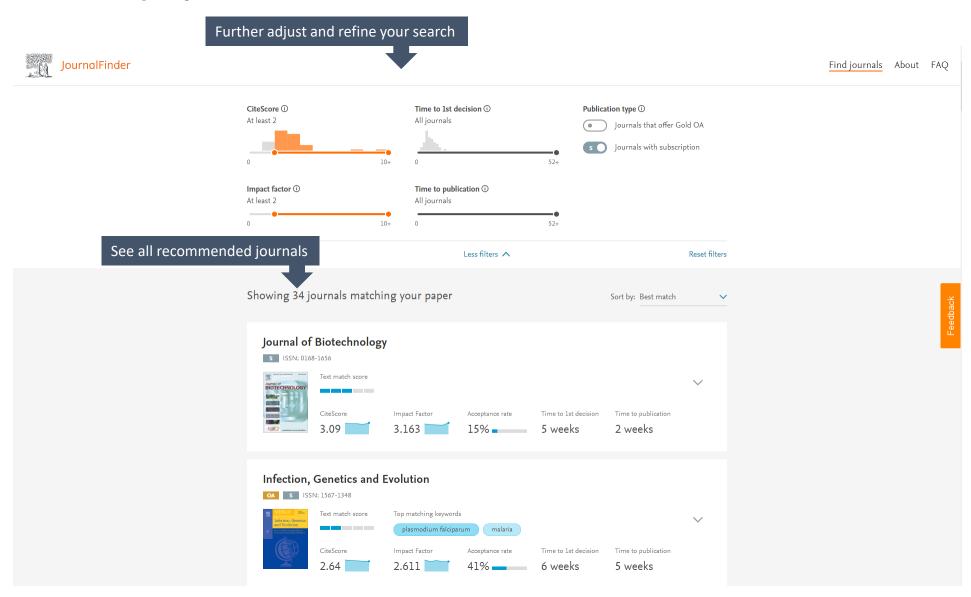
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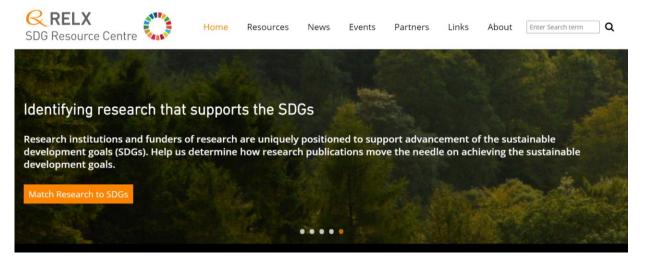
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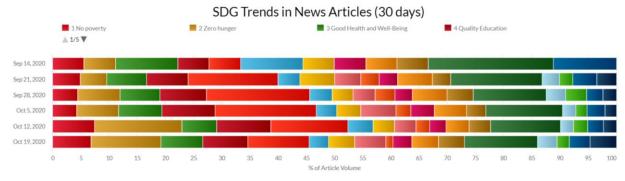
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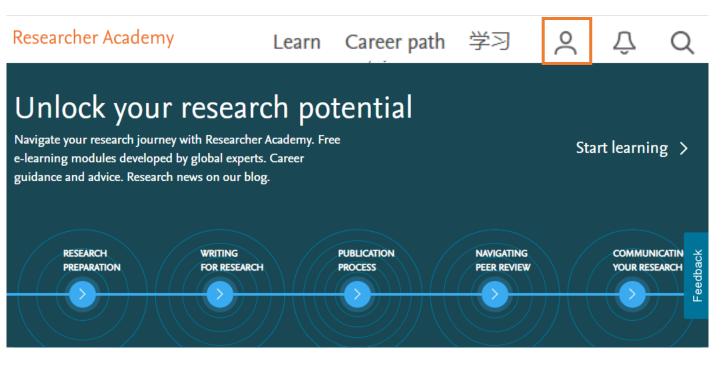


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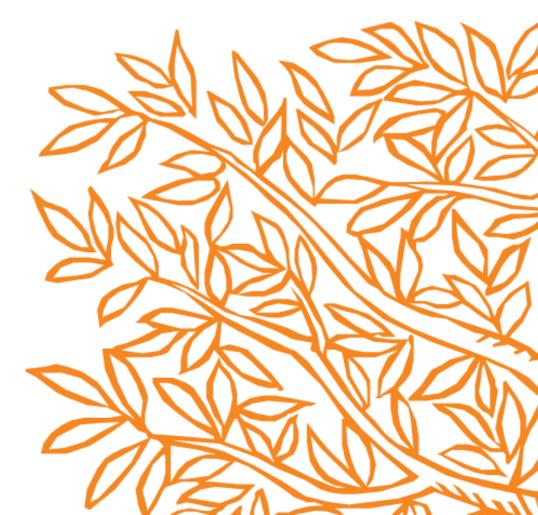
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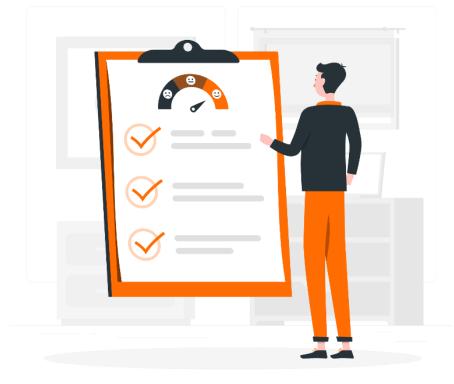




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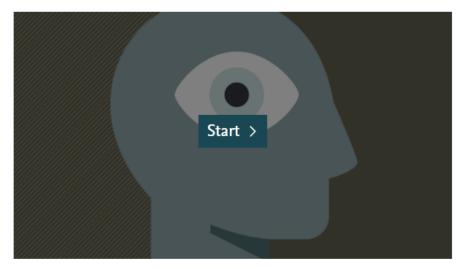


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<Thailand> ScienceDirect Best Practices and Training Webinar



Description

Agenda

- Research Workflow
- Database Literacy: ScienceDirect
- Elsevier's Author Companion: Journal Finder
- Elsevier's e-Learning Source: Research Academy
- Q&A

Presenters

· Kelwalin Dhanasarnsombut | Customer Consultant



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