

DR THOMAS SHAFEE


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WIKIPEDIA-INTEGRATED ACADEMIC JOURNALS

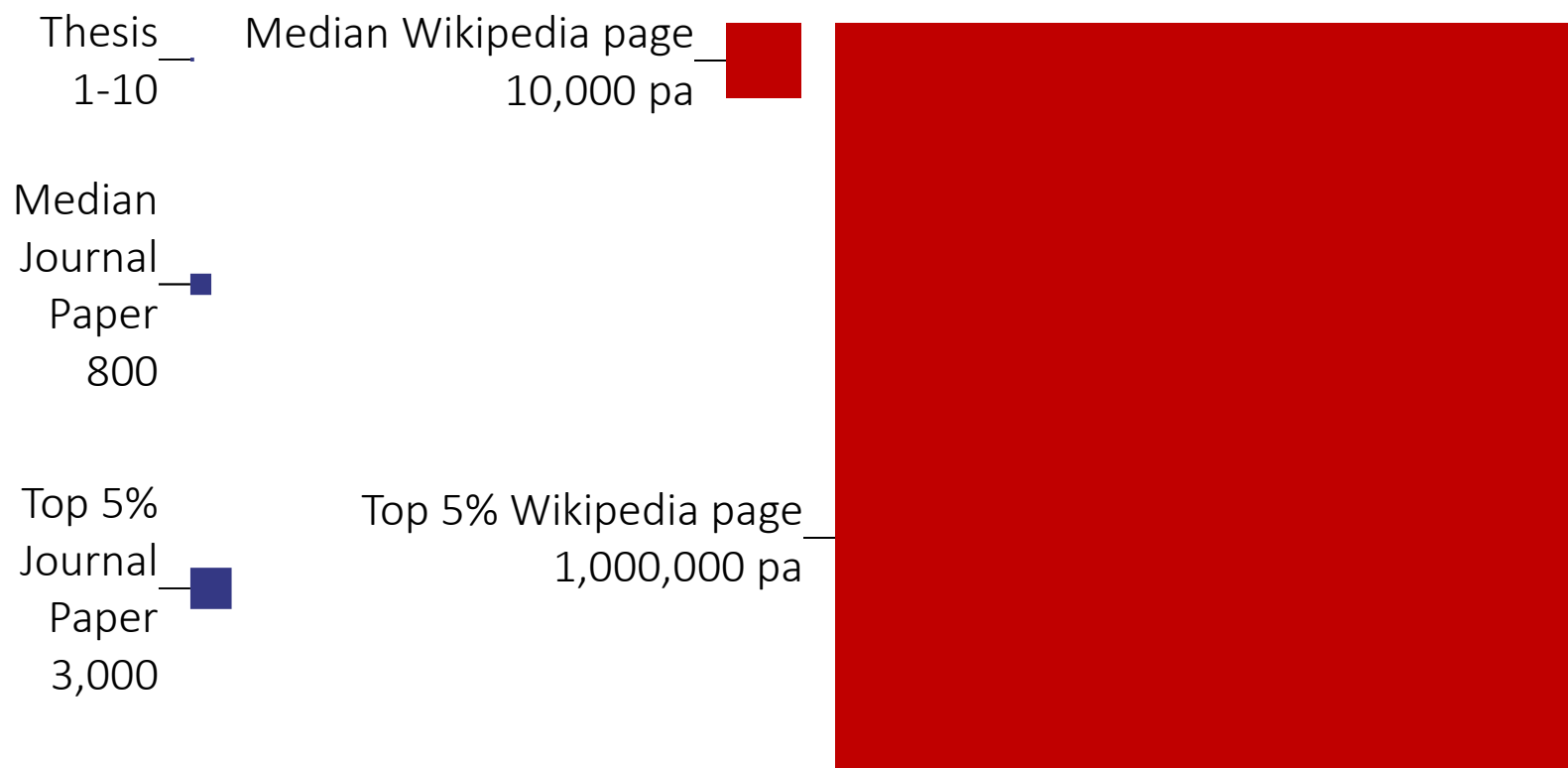
IDEAL PLATFORMS FOR OUTREACH AND PUBLIC COMMUNICATIONS

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A QUESTION OF REACH

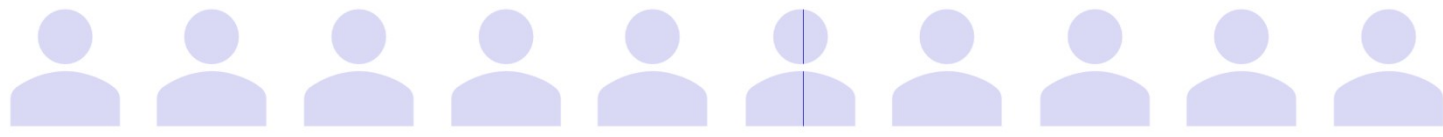
MAXIMISING IMPACT

WHO READS WIKIPEDIA?





WHO READS WIKIPEDIA'S MEDICAL CONTENT?

 General public

 Medical students

 Practicing doctors

 Research scientists

HOW CAN EXPERTS BE ENCOURAGED TO CONTRIBUTE?

MAKING AN IMMEDIATE, REAL-WORLD IMPACT

SIMILARITIES AND DIFFERENCES

	Academic Journal	Wikipedia
Readership size	Small and brief Median article - 800 total Top 5% article - 3000 total	Very large and extended Median article - 10,000 per year Top 5% article - 1,000,000 per year
Readership composition	Other academics, often within narrow field	General public as well as experts and professionals
Peer review	Pre-publication, private review by 2-4 subject specialists	Post-publication public review of a sort by subject generalists 'Good article' - 1 reviewer 'Featured Article' - 5-12 reviewers
Reputation	Varies by journal but generally extremely high	Public generally trust Academics have mixed opinions by improving
Authorship	Small number with relevant, accredited expertise. Organised group with lead and corresponding authors.	Large number with mixed expertise levels. Loose organisation. Many pseudonymous or anonymous.
Timeliness	Static Updated by new publications	Constantly updated Only one consensus version

BRIDGING THE ACADEMIC DIVIDE

- Content published into both Wikipedia and academic corpus



Stable, citable, peer-reviewed version with the credibility of a scholarly journal



Living version with extreme impact of Wikipedia

- Example journals



PLOS Genetics

PLOS CompBiol



Wiki.J.Med

Wiki.J.Sci

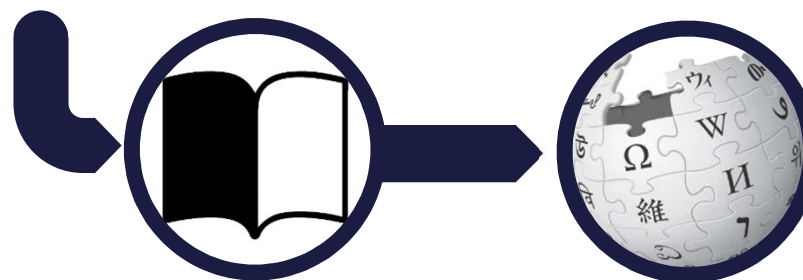
Wiki.J.Hum

GENE

Gene

RNAbiology

RNA Biology



JOURNAL FIRST

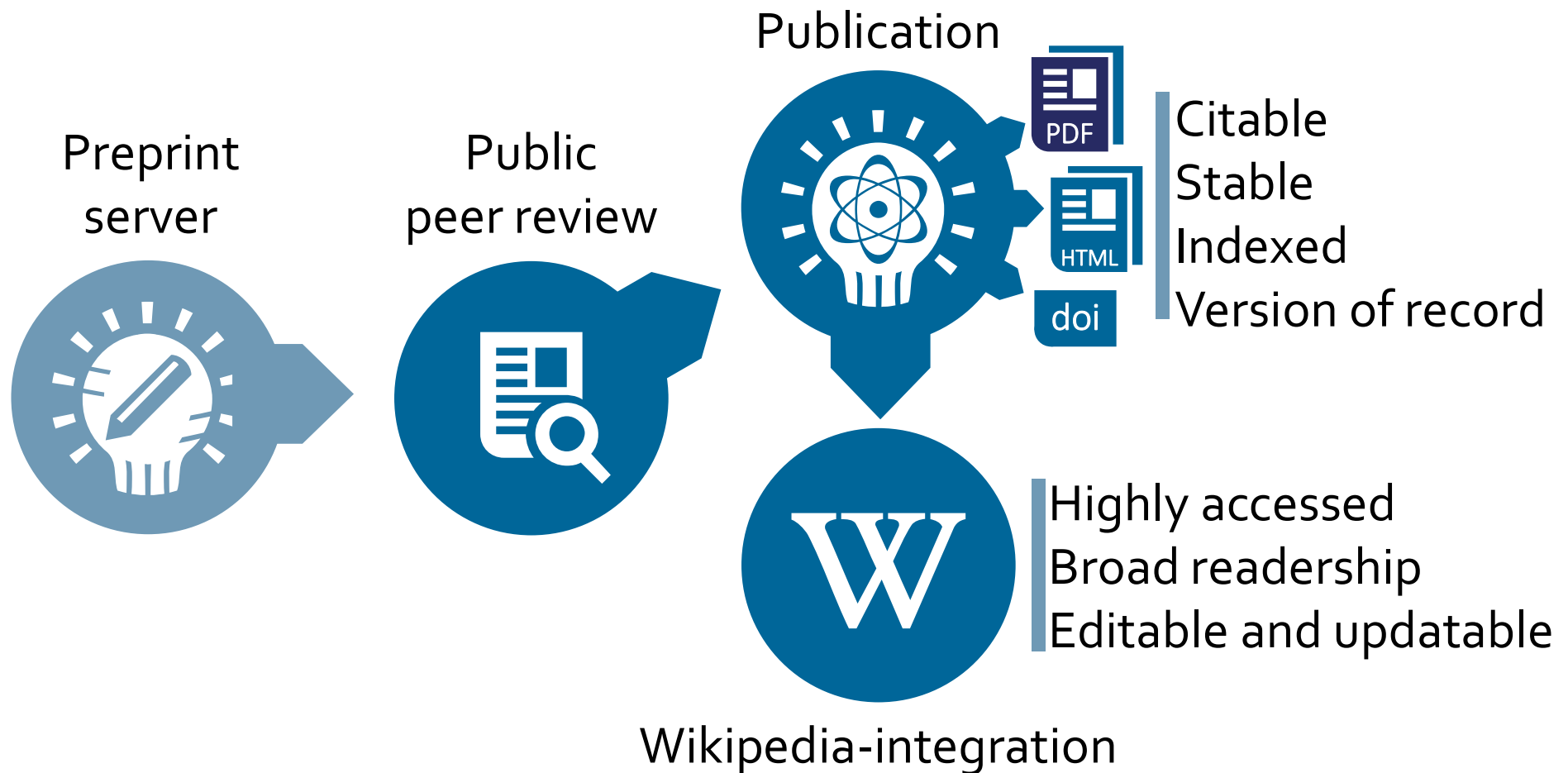


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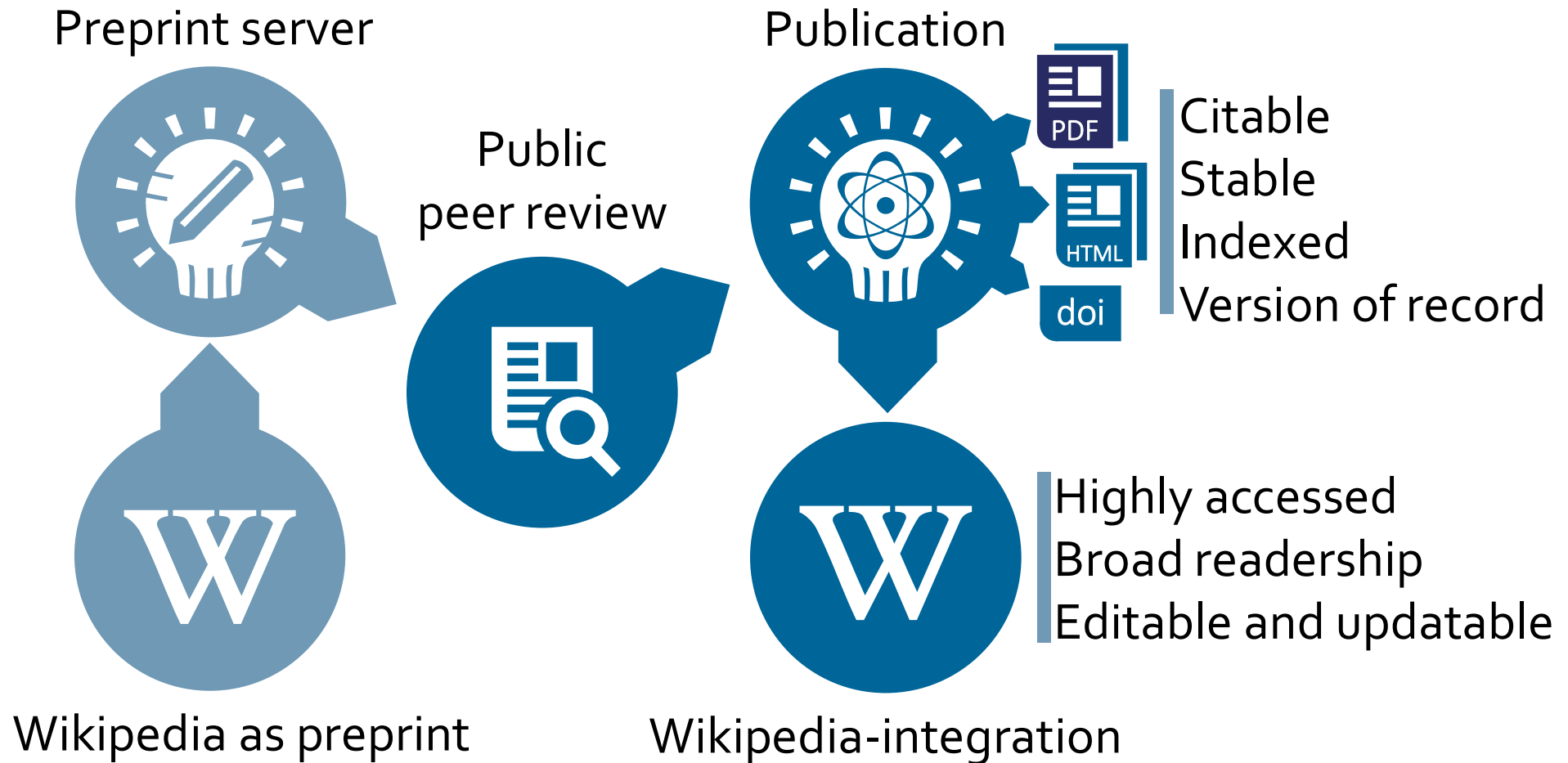


PARALLEL

A WIKIJOURNAL'S PUBLISHING FLOW



A WIKIJOURNAL'S PUBLISHING FLOW



ACADEMIC AND WIKIPEDIC VERSIONS

PLOS COMPUTATIONAL BIOLOGY

TOPIC PAGE
Transcriptomics technologies

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Abstract

Transcriptomics technologies are the techniques used to study an organism's **transcriptome**, the sum of all of its **RNA transcripts**. The information content of an organism is recorded in the DNA of its **genome** and **expressed** through **transcription**. Here, **mRNA** serves as a transient intermediary molecule in the information network, whilst **noncoding RNAs** perform additional diverse functions. A transcriptome captures a snapshot in time of the total transcripts present in a **cell**.

The first attempts to study the whole transcriptome began in the early 1990s, and technological advances since the late 1990s have made transcriptomics a widespread discipline. Transcriptomics has been defined by repeated technological innovations that transform the

References [edit source]

 The 2017 version of this article has passed academic peer review and been published in the journal **PLOS Computational Biology** [1]. The published version can be read and cited **here** [2] and the peer review **here**.

Published version

1. ^ Lowe R, Shirley N, Bleackley M, Dolan S, Shafee T (2017). "Transcription technologies" [2]. *PLOS Computational Biology*. 13 (5): e1005457. PMC 5436640 [3]. PMID 28545146 [4]. doi:10.1371/journal.pcbi.1005457 [5].

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Transcriptomics technologies

From Wikipedia, the free encyclopedia

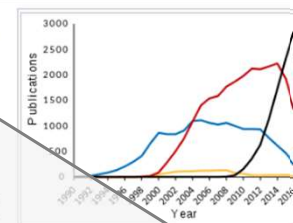
Transcriptomics technologies are the techniques used to study an organism's **transcriptome**, the sum of all of its RNA transcripts. The information content of an organism is recorded in the DNA of its **genome** and expressed through **transcription**. Here, **mRNA** serves as a transient intermediary molecule in the information network, whilst **non-coding RNAs** perform additional diverse functions. A transcriptome captures a snapshot in time of the total transcripts present in a **cell**.

The first attempts to study the whole transcriptome began in the early 1990s, and technological advances since the late 1990s have made transcriptomics a widespread discipline. Transcriptomics has been defined by repeated technological innovations that transform the field: **microarrays**, which quantify a set of predetermined sequences, and **RNA-Seq**, which uses high-throughput sequencing to capture all sequences.

Measuring the expression of an organism's genes in different tissues, conditions, or time points gives information on how genes are **regulated** and reveal details of an organism's biology. It can also help to infer the functions of previously **unannotated** genes. Transcriptomic analysis has enabled the study of how gene expression changes in different organisms and has been instrumental in the understanding of human **disease**. An analysis of gene expression in its entirety allows detection of broad coordinated trends which cannot be discerned by more **targeted assays**.

History [edit]

Transcriptomics has been characterised by the development of new techniques which have redefined what is possible every decade or so and render previous technologies obsolete. The first attempt at capturing a partial human transcriptome was published in 1991 and reported 609 mRNA sequences from the human brain.^[2] In 2008, two human transcriptomes, composed of millions of transcript-derived sequences covering 16,000 genes, were published^{[3][4]} and, by 2015, transcriptomes had been published for hundreds of individuals.^{[5][6]} Transcriptomes of different disease states, tissues or even single cells are now routinely generated.^{[6][7][8]} This explosion in transcriptomics has been driven by the rapid development of new technologies with improved sensitivity and



Transcriptomics method use over time. Published papers referring to RNA-Seq (black), RNA microarray (red), expressed sequence tag (blue) and serial/cap analysis of gene expression (yellow) since 1990 [1].

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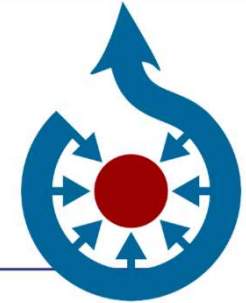
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- Reader subscription / author fee (e.g. *Gene*, *RNA Biol*)
 - Typically charge subscription fees
 - Article processing fee of \$3300 and \$2000 respectively
- OA journal fee waiver (e.g. *PLOS*)
 - For Topic Page review articles, *PLOS* waives its usual \$2250 processing fee
- Charitable foundation and volunteerism (e.g. *WikiJournals*)
 - Web hosting cost is covered by the Wikimedia Foundation
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AN INTERCONNECTED SET OF PLATFORMS

A MASSIVE MEDIA REPOSITORY



- Multimedia file repository
 - Images
 - Video
 - Sound
- Public domain / Freely-licensed
 - Creative commons licenses
- Content scope
 - Educational
 - Informative
 - Instructional
- Like all Wikimedia projects, free and volunteer-run

THE FUTURE OF DATA



- Free, open, structured knowledge base
- Humans and machine readable and editable
Multilingual, queryable
- Standardised, centralised, highly interlinked
Statements, sources, and connections to other databases

Item	Property	Value
Q42	P69	Q691283
Douglas Adams	educated at	St John's College

PROJECT AND COLLABORATION FORMATS

Institutional
/ Long-term

Wikipedian in Residence
Formal, ongoing partnerships

Repeating meetups
Edit-a-thons / Wikibombs

Individual
/ Short-term

Treasurehunts (content, images, citations)
Edit training (Wikipedia, Wikidata, Commons)

INTERNATIONAL PROJECTS

- Wikimedia chapters (e.g. Wikimedia.org.au)
- Wikipedia in Education
 - Wikipedia editing as part of assessed student coursework
- GLAMWiki
 - Documentation, Digitisation, Reference hunting, Digital integration
- WikiJournals
 - Academic journals that dual-publish 1) stable version of record, 2) into Wikipedia
- ORCID integration
- WikiCite
- 1Lib1Ref



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[WikiJournal of Science \(WikiJSci.org\)](#)
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