Dr Thomas Shafee

@WikiJMed
@WikiJSci
@WikiJHum

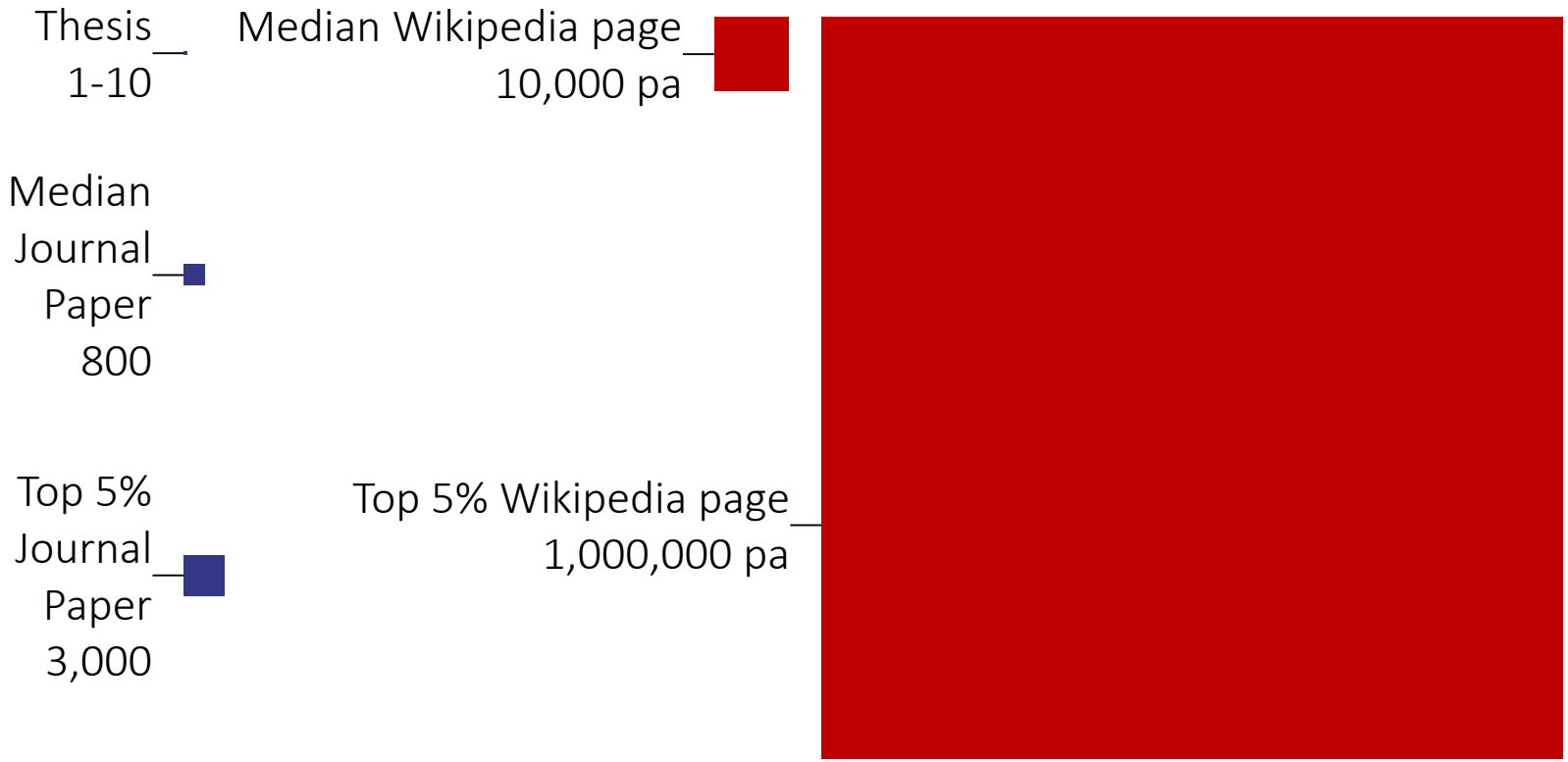
Wikipedia-integrated academic journals

Ideal platforms for outreach and public communications

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

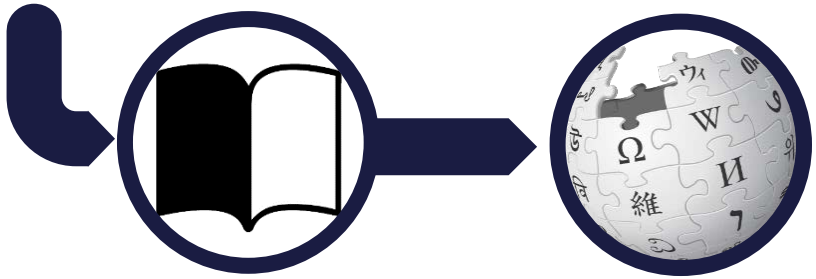
Wiki.J.Med

Wiki.J.Sci

Wiki.J.Hum

Gene

RNA Biology

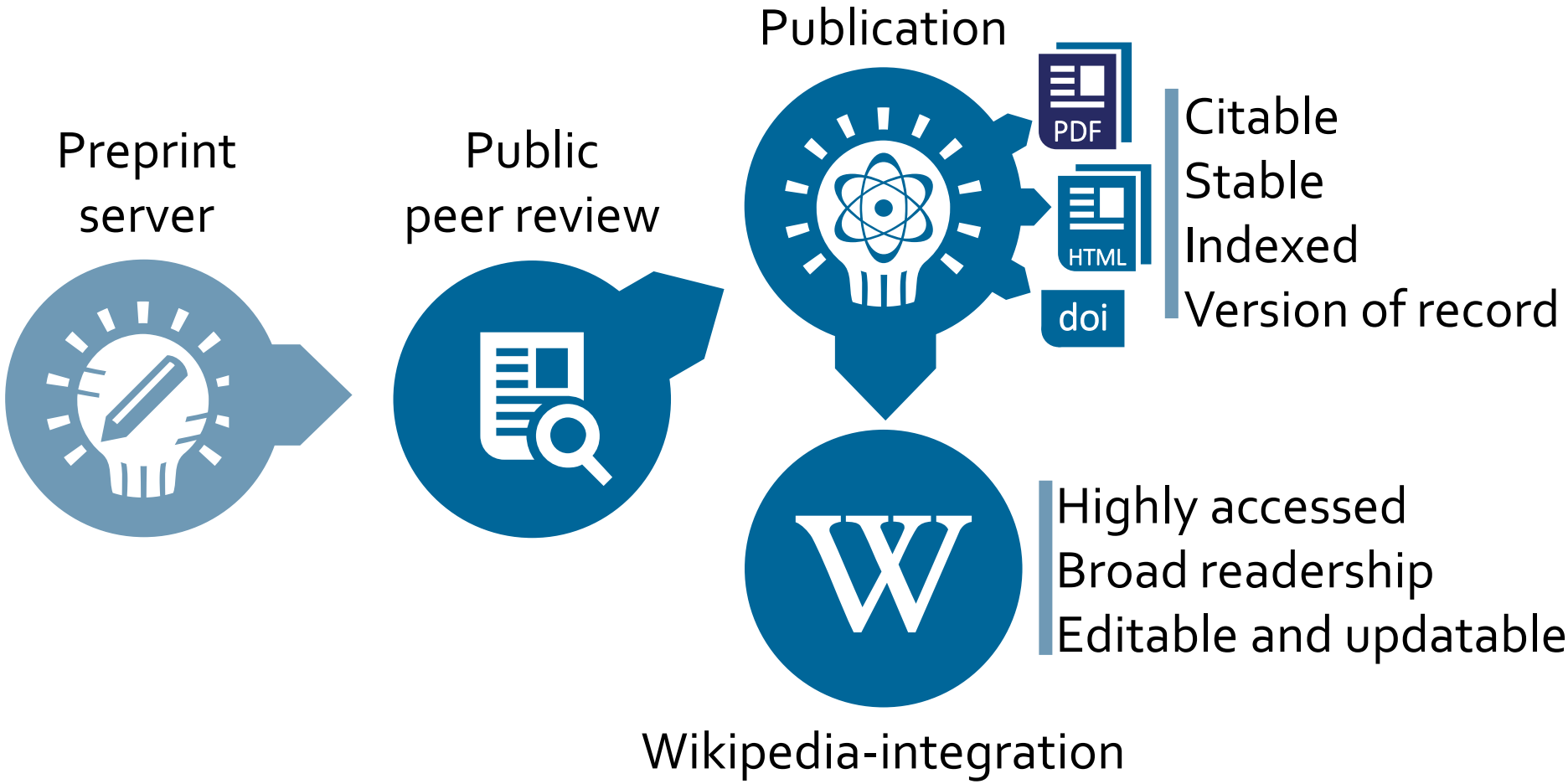


JOURNAL FIRST

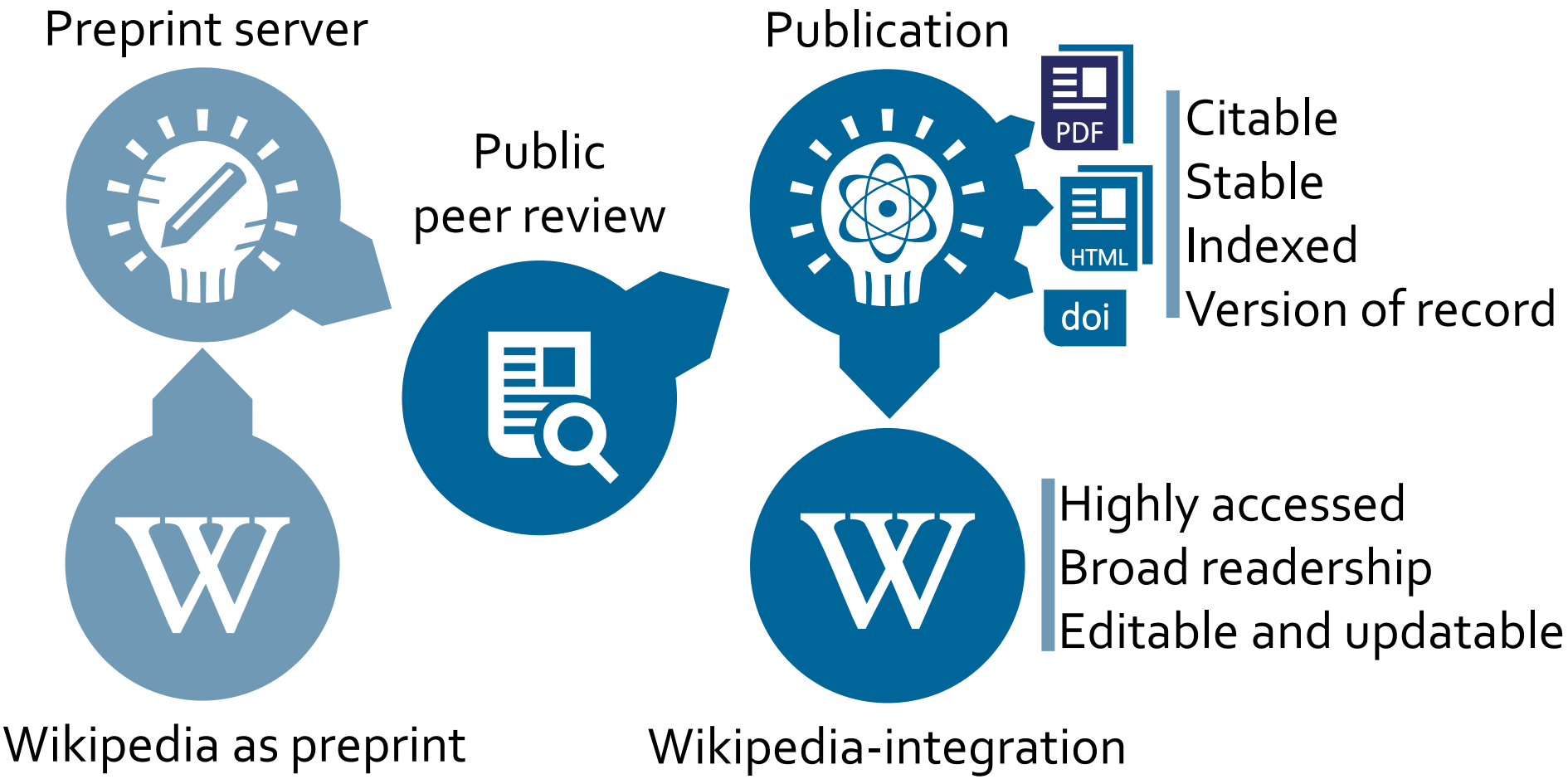
WIKIPEDIA FIRST

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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* T.Shafee@LaTrobe.edu.au

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*** [i] The published version can be read and cited here and the peer review here.

Published version

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

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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.

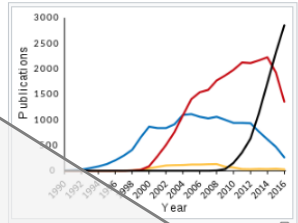
The first attempts to study the whole transcriptome began in the early 1990s, and technological advances since the late 1990s have made transcriptomics a widespread discipline. Transcriptomics has been defined by repeated technological innovations that transform the field. There are two key contemporary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

Contents [show]

History [edit]

Transcriptomics has been characterised by the development of new techniques which have redefined what is possible every decade or so and rendered 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 economy.[9][10][11][12]



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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  www.WikiJMed.org/Ethics_statement

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SOOOOO... WHO PAYS?

- 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
  - Editors donate volunteer labour so no fees of any kind

The wider Wikimedia ecosystem

An interconnected set of platforms

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The Free Encyclopedia

Wiktionary
The free dictionary

Wikiquote

WIKIBOOKS

WIKISOURCE

WIKINEWS

WIKIVERSITY

WIKISPECIES
free species directory

MediaWiki

WIKIDATA

WIKIMEDIA
COMMONS

wiki
voyage

WIKIMEDIA
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FOUNDATION

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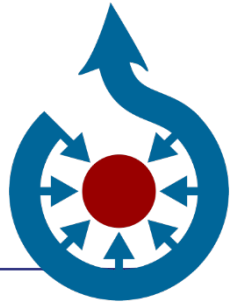

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  - Sound
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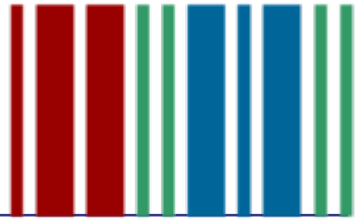
- Content scope
  - Educational
  - Informative
  - Instructional
- Like all Wikimedia projects, free and volunteer-run

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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Journals

WikiJournal of Medicine (WikiJMed.org)

WikiJournal of Science (WikiJSci.org)

PLOS (TopicPagesWiki.plos.org)

Wikipedia

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Shafee, T; Mietchen, D; Su, A. (2017). "Academics can help shape Wikipedia". *Science*. 357 (6351): 557–558.

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