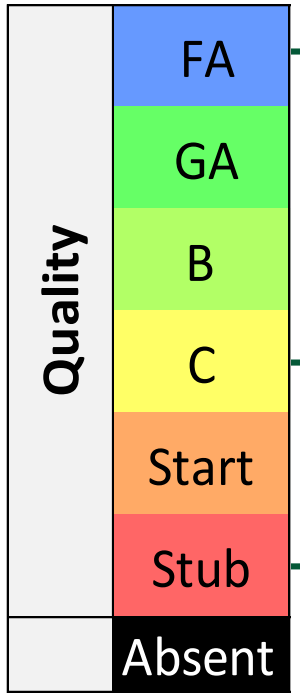
@WikiJMed
@WikiJSci
@WikiJHum

Wikipedia-integrated academic publishing

Maximising reach and impact

WIKIJOURNALS

Example case studies in WikiJournals



Full review articles

Existing high-quality Wikipedia article updated and submitted

- Peripatric speciation
- Rosetta stone

Wikipedia article previously existing but flawed/outdated

- Lysine

Wikipedia article previously completely absent/stub

- Anthracyclines

Article sections

Wikipedia article section that warranted own page

- Gene structure

Wikipedia article previously lacked images

- Cell disassembly during apoptosis

Partner articles

More technical partner

- Dioxins and dioxin-like compounds

Stand-alones

Research articles

- Viewer interaction with YouTube videos about hysterectomy recovery

Case studies

- Acute gastrointestinal bleeding from a chronic cause: a teaching case report

Teaching methods

- A card game for Bell's theorem and its loopholes

Systematic reviews

- Mealtime difficulty in older people with dementia

Image galleries

- Medical gallery of Blausen Medical3

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Journals

WikiJournal of Medicine (WikiJMed.org)

WikiJournal of Science (WikiJSci.org)

PLOS (TopicPagesWiki.plos.org)

Wikipedia

My userpage	Search "User:tshafee"
WikiProject Medicine	Search "WP:MED"

This presentation

bit.ly/WikiJournal2020b

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

Shafee, T; Masukume, G; Kipersztok, L; Das, D; Häggström, M; Heilman, J. (2017). "The evolution of Wikipedia's medical content: past, present and future". *JECH*. 71(10).

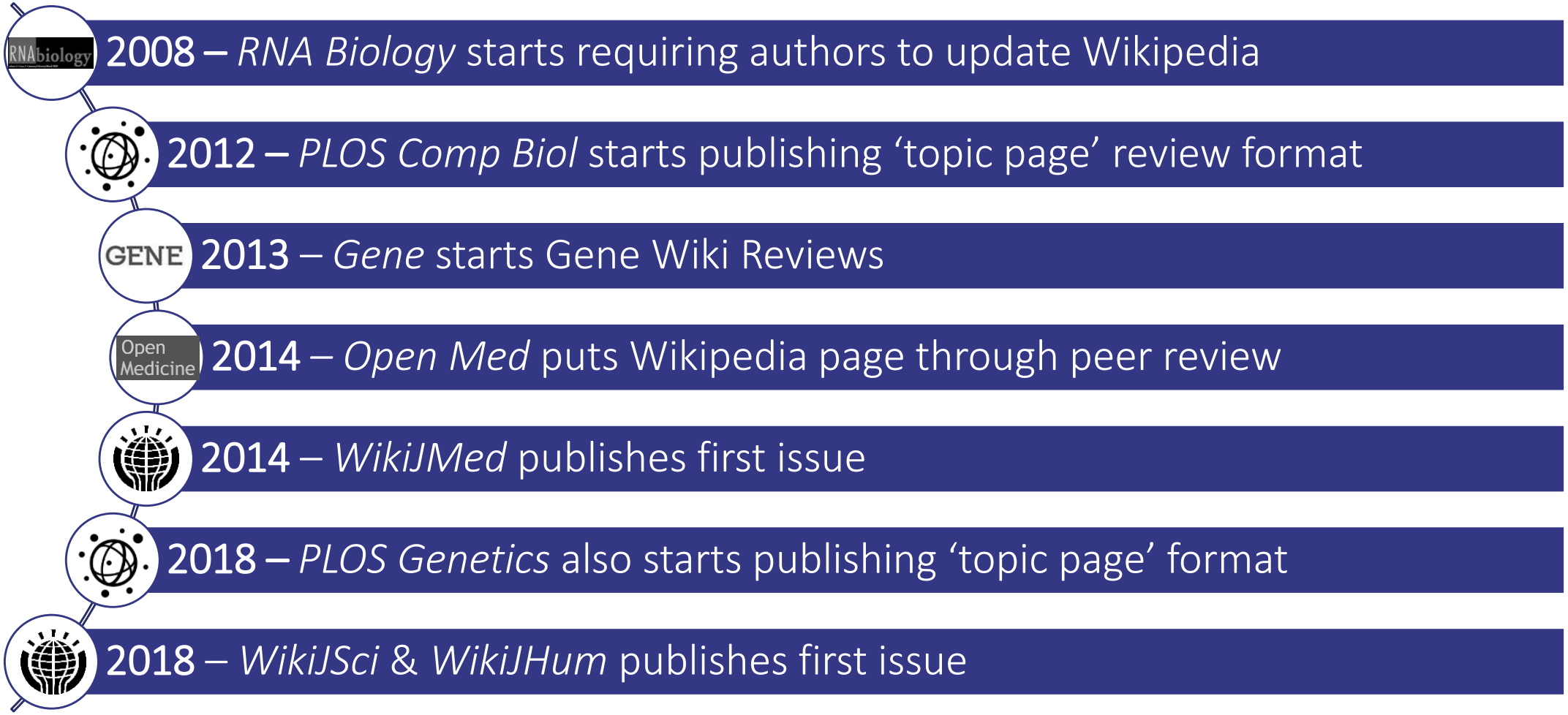
Shafee, T (2017) "Wikipedia-integrated publishing: A comparison of successful models". *Health Inform.* 27(2)

WikiJSci Editorial Board (2018). "The aims and scope of WikiJournal of Science". *WikiJournal of Science* 1(1):1

[END]

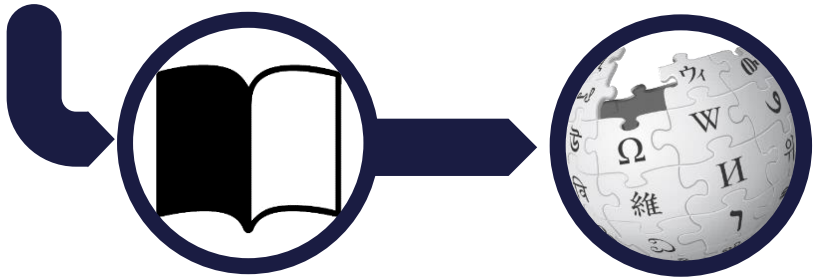
[EXTRA SLIDES]

Development of concepts



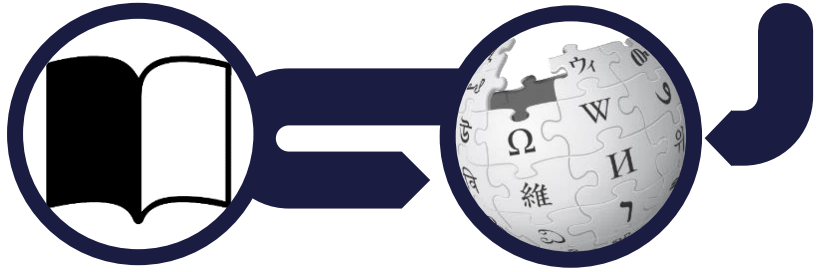
BRIDGING THE ACADEMIC DIVIDE

- Content published into both Wikipedia and academic corpus
  - Stable, citable, peer-reviewed journal version
  - Living version with extreme impact of Wikipedia
- Example journals
  - *PLOS Genetics*
  - *PLOS CompBiol*
  - *PLOS ONE*
  - *Wiki.J.Med*
  - *Wiki.J.Sci*
  - *Wiki.J.Hum*
  - *Open Medicine*
  - *Gene*
  - *RNA Biology*



JOURNAL FIRST

- Compatible with any OA journal
- Simplest workflow
- Well-suited to topics that are missing/start/stub on Wikipedia



WIKIPEDIA FIRST

- Restricted by Wikipedia's CC-BY-SA license
- May be only option for highly-developed pages (full replacement typically more difficult Class B and above)

PARALLEL

- Compatible with closed journal
- Two versions can be tailored to different audiences
- Increased work for authors and reviewers

ACADEMIC AND WIKIPEDIC VERSIONS

OPEN ACCESS Freely available online

PLOS COMPUTATIONAL BIOLOGY

Topic Page

Circular Permutation in Proteins

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This is a "Topic Page" article for *PLoS Computational Biology*.

Circular permutation describes a type of relationship between proteins, whereby the proteins have a changed order of amino acids in their protein sequence, such that the sequence of the first portion of one protein (adjacent to the N-terminus) is related to that of the second portion of the other protein (near its C-terminus), and vice versa (see Figure 1). This is directly analogous to the mathematical notion of a cyclic permutation over the set of residues in a protein.

Circular permutation can be the result of evolutionary events, post-translational modifications, or artificially engineered mutations. The result is a protein structure with different connectivity, but overall similar three-dimensional (3D) shape. The homology

permuted variants of cyclic wild-type proteins [10]. SISYPHUS is a database that contains a collection of hand-curated manual alignments of proteins with non-trivial relationships, several of which have circular permutations [11].

Evolution

There are two main models that are currently being used to explain the evolution of circularly permuted proteins: *permutation by duplication* and *fission and fusion*. The two models have compelling examples supporting them, but the relative contribution of each model in evolution is still under debate [12]. Other, less common, mechanisms have been proposed, such as "cut and paste" [13] or "exon shuffling."

References [edit source]

 (2012) (reviewer reports): "Circular permutation in proteins", *PLOS Computational Biology*, **8** (3): e1002445, 2012, doi:10.1371/JOURNAL.PCBI.1002445, ISSN 1553-734X, PMC 3320104, PMID 22496628, Wikidata Q5121672

1. ^ [a] [b] [c] Cunningham BA, Hemperly JJ, Hopp TP, Edelman GM (July 1979). "Favin versus concanavalin A: Circularly permuted amino acid sequences". *Proceedings of the National Academy of Sciences of the United States of America*. **76** (7): 3218–22. Bibcode:1979PNAS...76.3218C. doi:10.1073/pnas.76.7.3218. PMC 383795. PMID 16592676.
2. ^ Einspahr H, Parks EH, Suguna K, Subramanian E, Suddath FL (December 1986). "The crystal structure of pea lectin at 3.0-A resolution". *The Journal of Biological Chemistry*. **261** (35): 16518–27. PMID 3782132.
3. ^ Carrington DM, Auffret A, Hanke DE (1985). "Polypeptide ligation occurs during post-translational modification of concanavalin A". *Nature*. **313** (5997): 64–7.

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The Free Encyclopedia

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Circular permutation in proteins

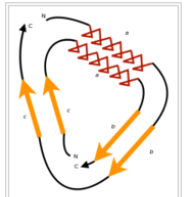
From Wikipedia, the free encyclopedia
(Redirected from Circular permutant)

A **circular permutation** is a relationship between proteins whereby the proteins have a changed order of amino acids in their peptide sequence. The result is a protein structure with different connectivity, but overall similar three-dimensional (3D) shape. In 1979, the first pair of circularly permuted proteins – concanavalin A and lectin – were discovered; over 2000 such proteins are now known.

Circular permutation can occur as the result of evolutionary events, posttranslational modifications, or artificially engineered mutations. The two main models proposed to explain the evolution of circularly permuted proteins are *permutation by duplication* and *fission and fusion*. Permutation by duplication occurs when a gene undergoes duplication to form a tandem repeat, before redundant sections of the protein are removed; this relationship is found between saposin and swaposin. Fission and fusion occurs when partial proteins fuse to form a single polypeptide, such as in nicotinamide nucleotide transhydrogenases.

Circular permutations are routinely engineered in the laboratory to improve their catalytic activity or thermostability, or to investigate properties of the original protein.

Traditional algorithms for sequence alignment and structure alignment are not able to detect circular permutations between proteins. New non-linear approaches have been developed that overcome this and are able to detect topology-independent similarities.



Schematic representation of a circular permutation in two proteins. The first protein (outer circle) has the sequence a-b-c. After the permutation the second protein (inner circle) has the sequence c-a-b. The letters N and C indicate the location of the amino- and carboxy-termini of the protein sequences and how their positions change relative to each other.

Contents [hide]

1 History
2 Evolution
2.1 Permutation by duplication
2.1.1 Saposin and swaposin
2.2 Fission and fusion
2.2.1 Transhydrogenases
2.3 Other processes that can lead to circular permutations
2.3.1 Post-translational modification
3 The role of circular permutations in protein engineering
4 Algorithmic detection of circular permutations
5 References
6 Further reading

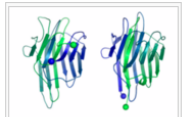
History [edit source | edit]

In 1979, Bruce Cunningham and his colleagues discovered the first instance of a circularly permuted protein in nature.[1] After determining the peptide sequence of the lectin protein favin, they noticed its similarity to a known protein – concanavalin A – except that the ends were circularly permuted. Later work confirmed the circular permutation between the pair[2] and showed that concanavalin A is permuted post-translationally[3] through cleavage and an unusual protein ligation.[4]

After the discovery of a natural circularly permuted protein, researchers looked for a way to emulate this process. In 1983, David Goldenberg and Thomas Creighton were able to create a circularly permuted version of a protein by chemically ligating the termini to create a cyclic protein, then introducing new termini elsewhere using trypsin.[5] In 1989, Kaarlin Luger and her colleagues introduced a genetic method for making circular permutations by carefully fragmenting and ligating DNA.[6] This method allowed for permutations to be introduced at arbitrary sites.[6]

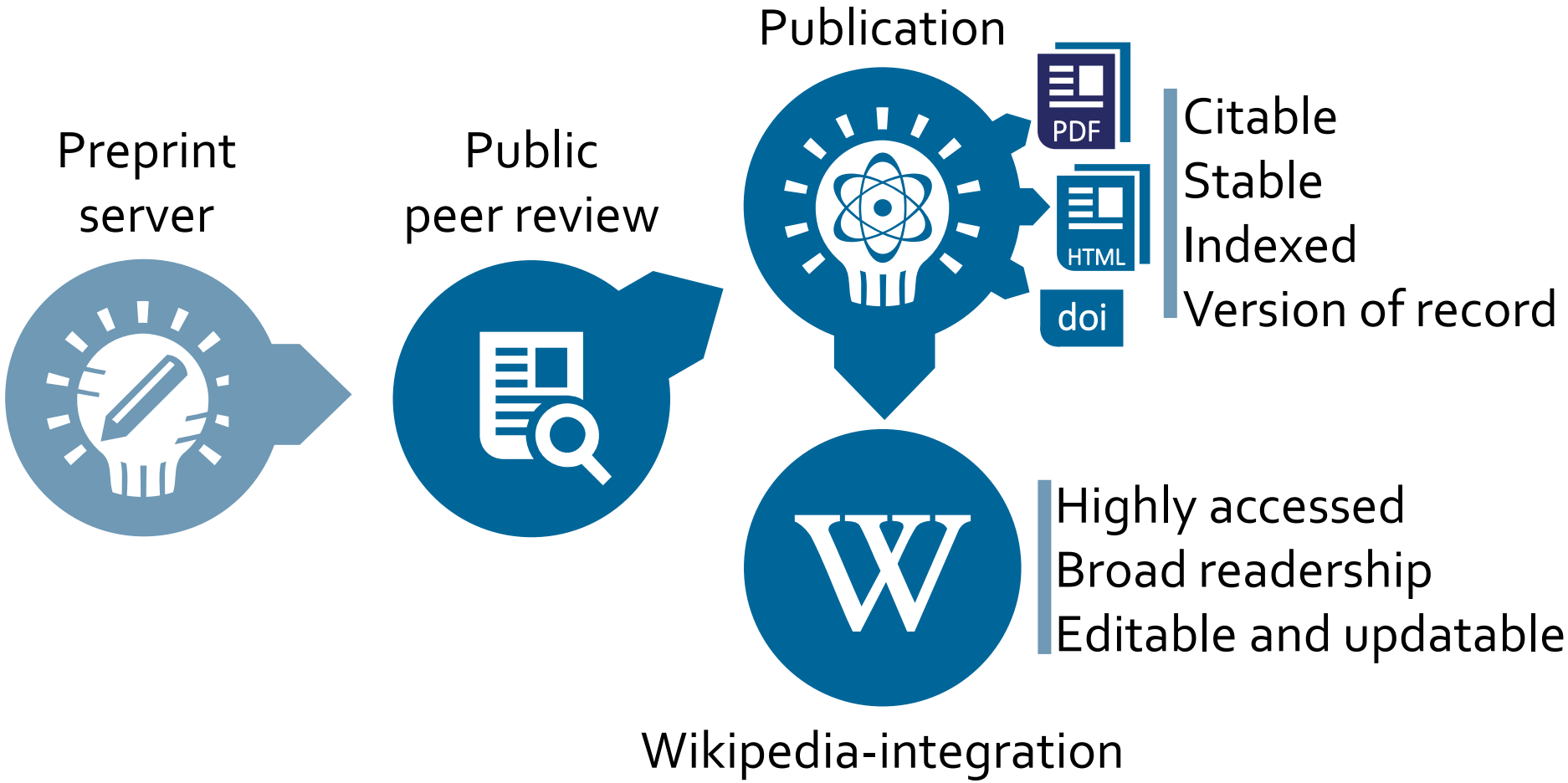
Despite the early discovery of post-translational circular permutations and the suggestion of a possible genetic mechanism for evolving circular permutants, it was not until 1995 that the first circularly permuted pair of genes were discovered. Saposins are a class of proteins involved in sphingolipid catabolism and antigen presentation of lipids in humans. Chris Ponting and Robert Russell identified a circularly permuted version of a saposin inserted into plant aspartic proteinase, which they nicknamed swaposin.[7] Saposin and swaposin were the first known case of two natural genes related by a circular permutation.[7]

Hundreds of examples of protein pairs related by a circular permutation were subsequently discovered in nature or produced in the laboratory. As of February 2012, the Circular Permutation Database[8] contains 2,238 circularly permuted protein pairs with known structures, and many more are known without structures.[9] The CyBase database collects proteins that are cyclic, some of which are permuted variants of cyclic wild-type proteins.[10] SISYPHUS is a database that contains a collection of hand-curated manual alignments



Two proteins that are related by a circular permutation. Concanavalin A (left), from the Protein Data Bank (PDB: 3ona), and peanut lectin (right), from PDB: 2pel, which is homologous to favin. The termini of the proteins are highlighted by blue and green spheres, and the sequence of residues is indicated by the gradient from blue (N-terminus) to green (C-terminus). The fold of the two proteins is highly similar, however, the N- and C-termini are located on different positions of the protein.[11]

A WikiJournal's publishing flow



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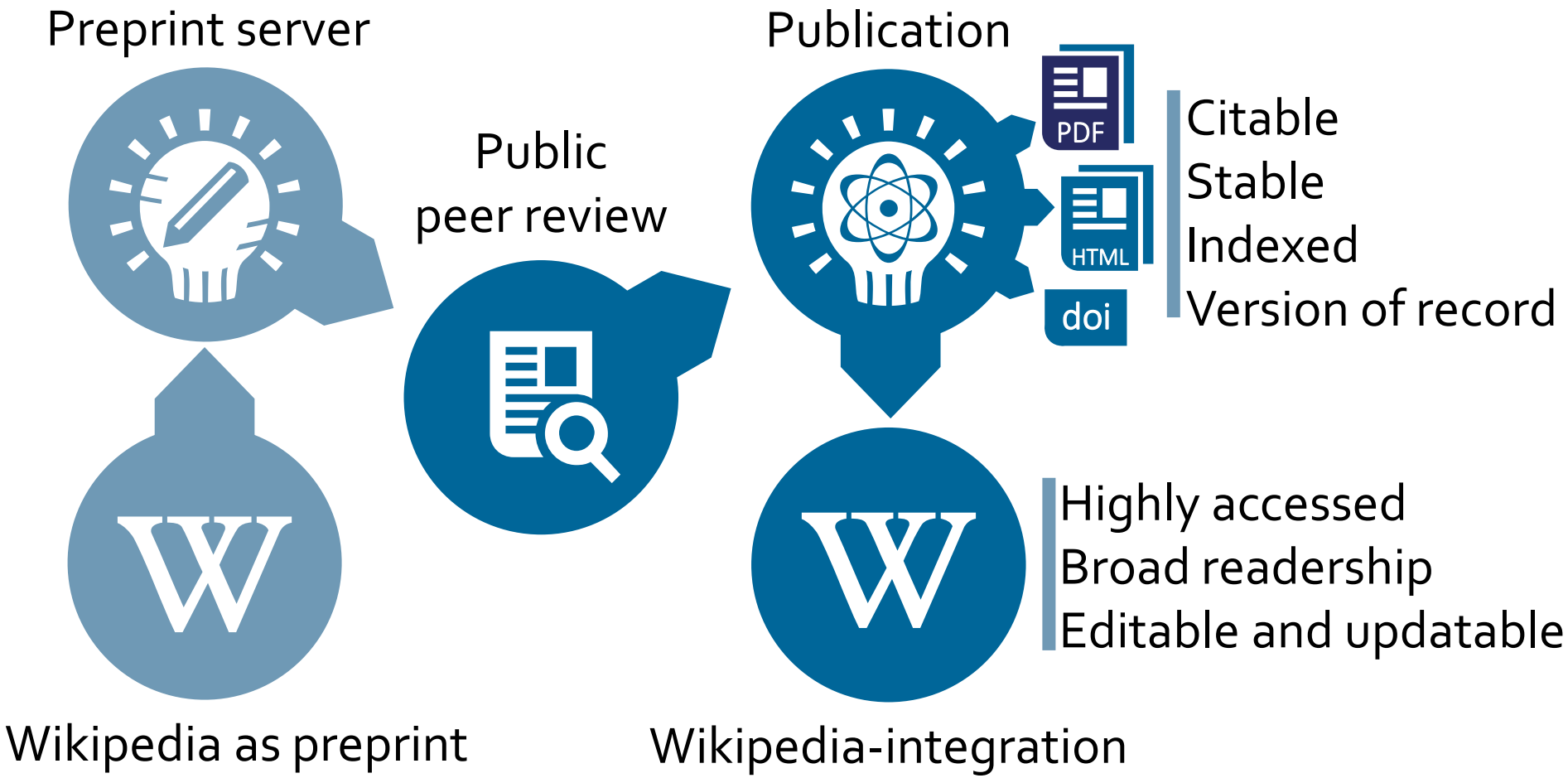

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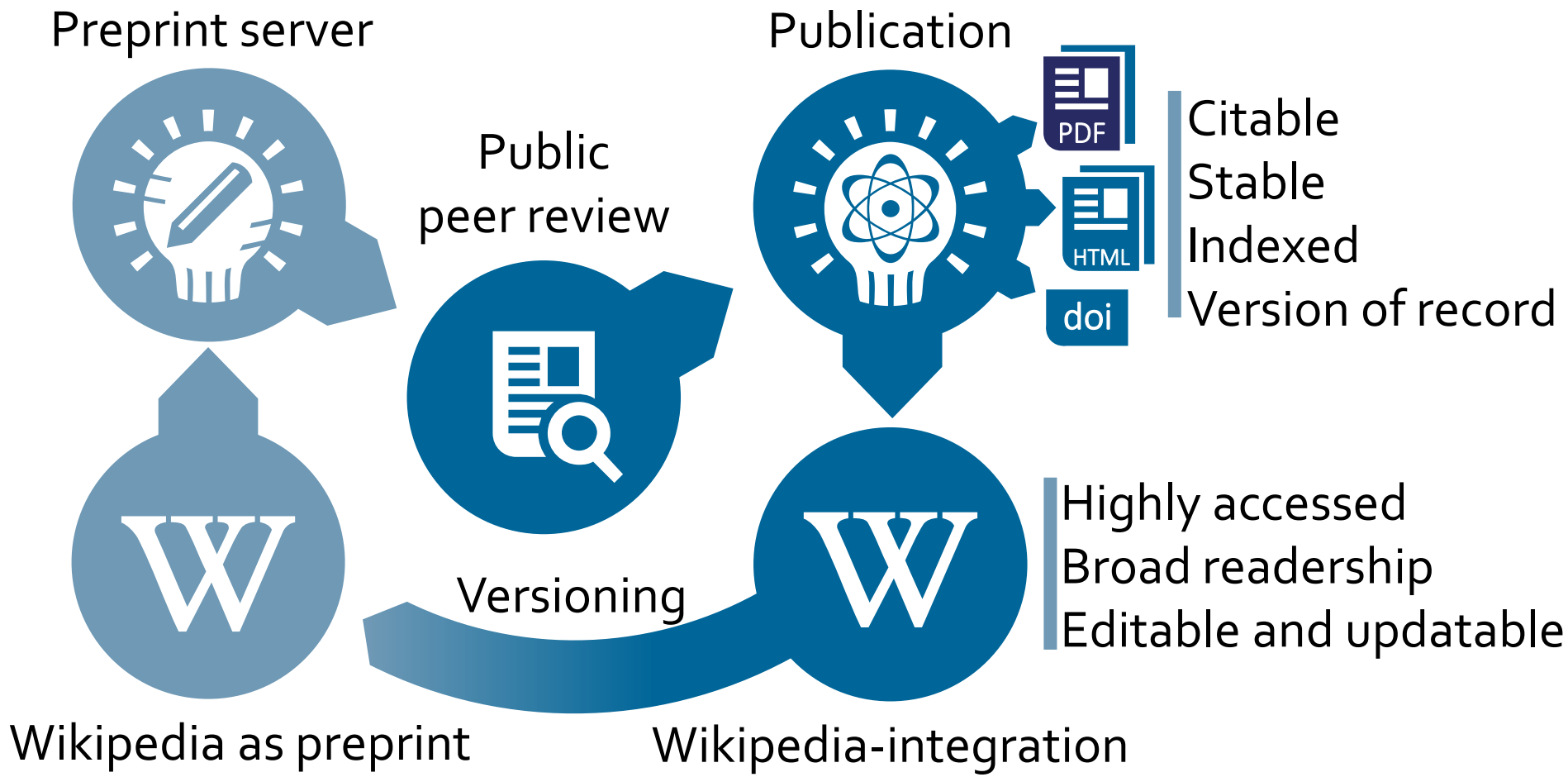

Possible journal partnership system

- One-off partnering with subject-specialist journals
  - Specialist journal: Invite authors, identify peer reviewers
  - WikiJournal: Advises on wikipedia policy compliance, readability and formatting
- Resulting article co-published in specialist journal & WikiJournal
- Then copied into Wikipedia per 'journal-first' model

- Co-publishing example:
  - Staniszewska, S., et al. (2017). GRIPP2 reporting checklists: tools to improve reporting of patient and public involvement in research. ***Research involvement and engagement***, ***3***(1), 13.
  - Staniszewska, S., et al. (2017). GRIPP2 reporting checklists: tools to improve reporting of patient and public involvement in research. ***British Medical Journal 358***(1), j3453

Committee on Publication Ethics

- WikiJMed ethics statement audited and approved by COPE
- WikiJMed.org/Ethics_statement
- Attribution of CC material
  - **Images / videos / other media:** Attribution and license type at end of the figure legend
  - **Text <1 paragraph / <10% of final work:** Hyperlink to contributor list 'Acknowledgements' section
  - **Text >1 paragraph / >10% of final work:** Hyperlink to the full contributor list included in the author list (typically as a hyperlinked "*et al*"). Treated as “Large group authorship”.
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- **Peer reviewing** of article submissions. Does require expertise in the subject at hand.
- Help **preparing** & **formatting** submitted articles
- Join an **editorial board** and share your ideas about journal management
- Will hire a **technical editor**.

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 but 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

Shafee, T. et al. (2017). Evolution of Wikipedia's medical content: past, present and future. JECH. 71(10)