

Open Access Journal Platforms: A Novel Model For Open Science In Microbiology

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Background: project drivers

External drivers

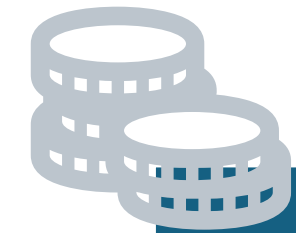
- Funder mandates
- Competition from commercial publishers

Internal drivers

- Early Career Forum
- Charitable objectives

Background: funders and authors

<https://beta.sherpa.ac.uk/>



Funder mandates

- UKRI
- Plan S
- US (OSTP)



Author geography

- ~15% UK
- ~15% EU
- ~15% USA
- ~10% China

Our questions

- What do funders mean by ‘immediate’?
 - Version of record, on the day of publication, CC BY
- What do our Society members want?
 - Easy funder compliance, rapid publication, low or no APC
- Can we make this technically viable?
 - Cost, time, and maintenance
- Can we make this financially sustainable?
 - Publishing costs money!

Our idea

<https://bit.ly/4bJ5Bn1>

- Convert a journal into an Open Research Platform
- Offer transparent peer review and rapid publication.
- Driven by the publisher's existing technology stack.
- Financially sustainable without grants or high APCs.

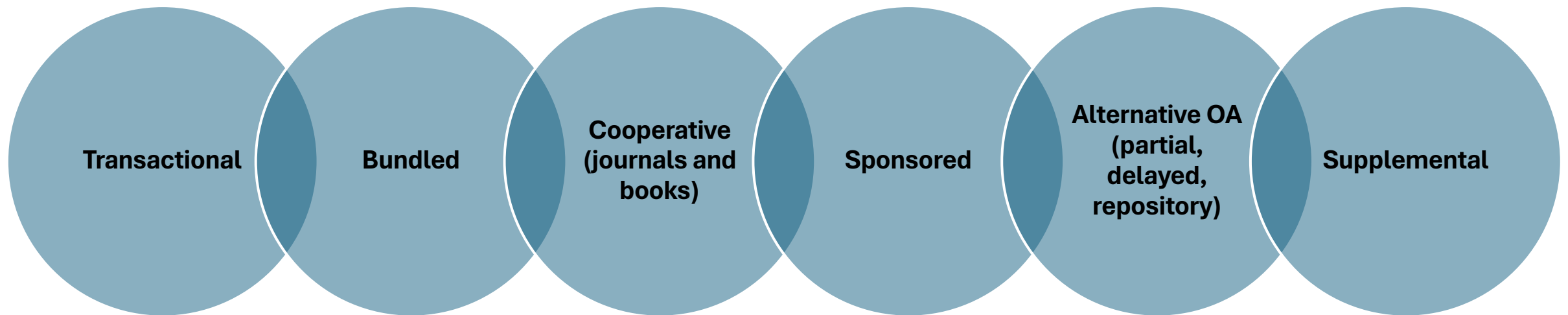
Our goals

<https://bit.ly/4bJ5Bn1>

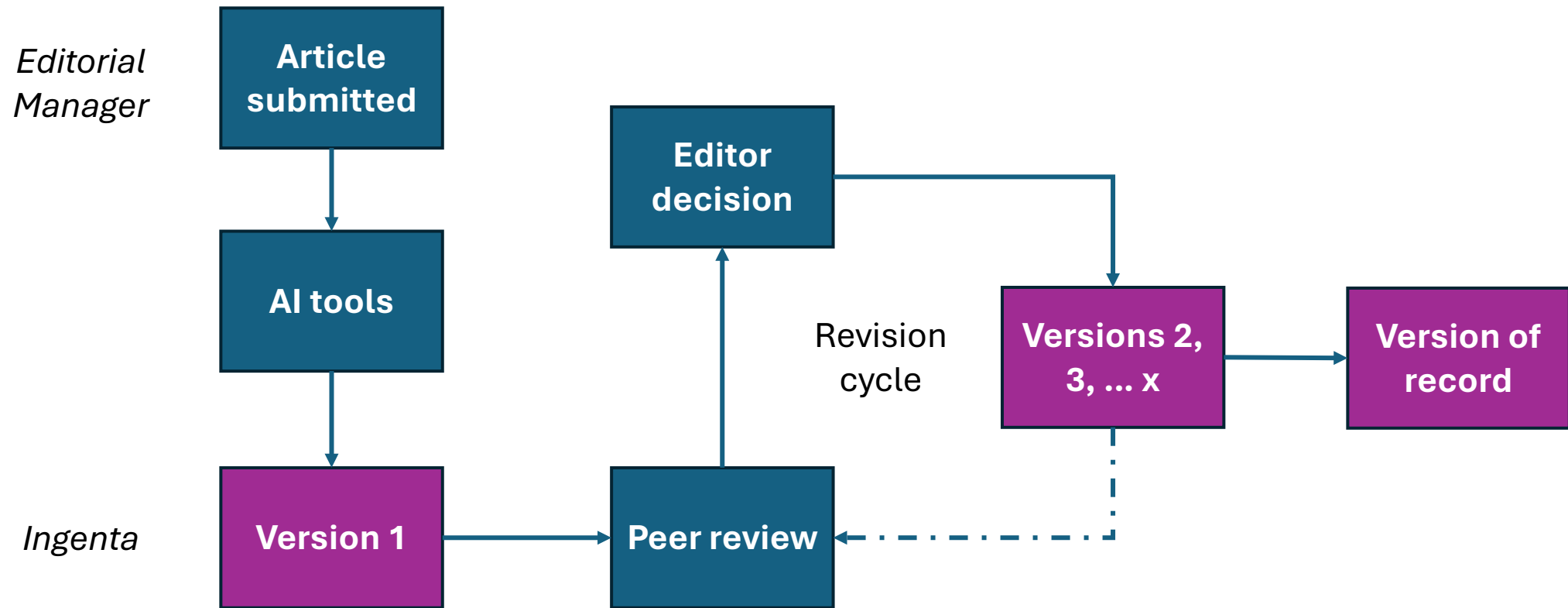
- Make publishing faster
- Reduce the risk of research misconduct
- Provide more transparency
- Be financially sustainable

Finances

<https://zenodo.org/records/11242106>



The open research platform workflow



ACCESS MICROBIOLOGY

an open research platform

Research Article | Open Access

Version 1: Genetic diversity and genomic epidemiology of SARS-CoV-2 during the first three years of pandemic in Morocco: Comprehensive sequence analysis, including the unique B.1.528 lineage in Morocco

Soulandi Djourwe¹, Abderrahim Malki², Néhémie Nzoyikorera³, Joseph Nyandwi⁴, Samuel Privat Zebsoubo⁵, Kawthar Bellamine⁶ and Amale Bousfiha⁷

 View Affiliations

Version Posted: 22 May 2024 | <https://doi.org/10.1099/acmi.0.000853.v1>

This is a **preprint**, which is a preliminary version of an article and has not completed peer review.

 Info  Sections



PDF



Tools



Share



Version status

Status: Under review

Review status breakdown

KEY:     

Versions

1

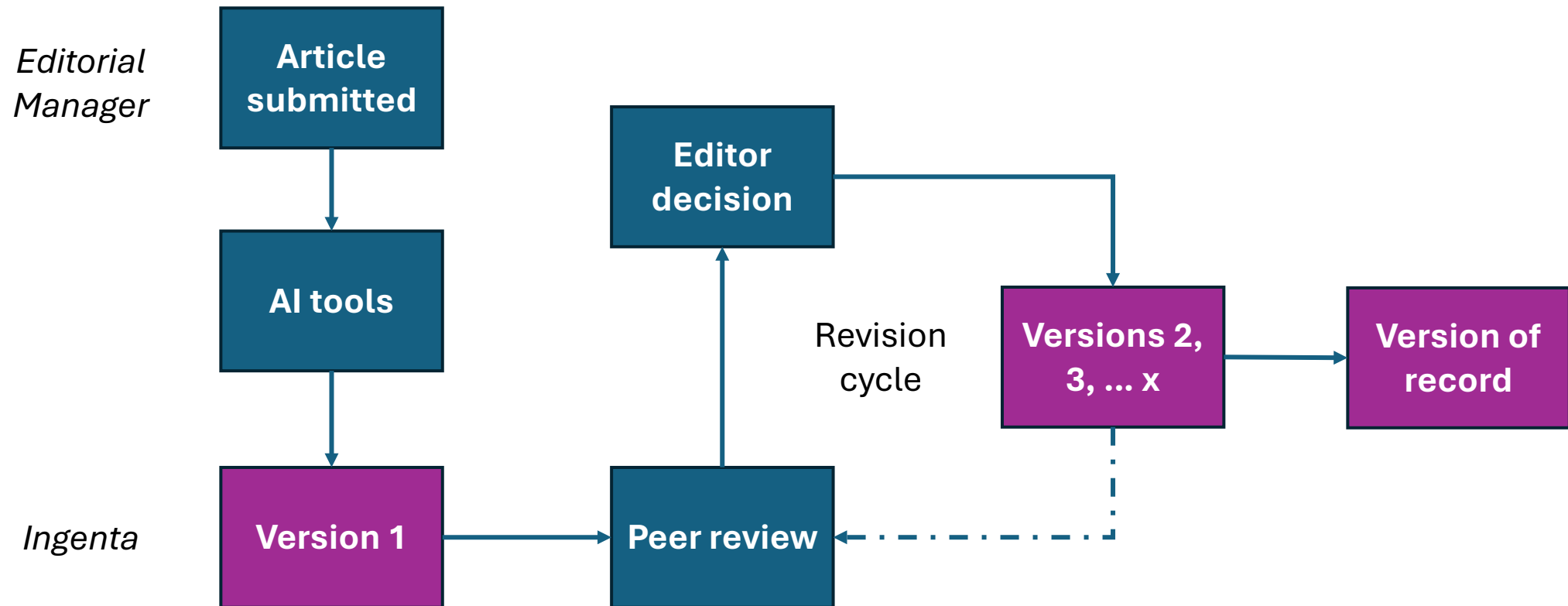
Review Tools




read

During the three years following the emergence of the COVID-19 pandemic, the African continent, like other regions of the world, was significantly impacted by COVID-19. In Morocco, the COVID-19 pandemic has been marked by the emergence and spread of several SARS-CoV-2 variants, leading to a substantial increase in the incidence of infections and deaths. Nevertheless, there has been a persistent lack of

The open research platform workflow



Version 2: Comparative virulome analysis of four *Staphylococcus epidermidis* strains from human skin and platelet concentrates using whole genome sequencing

Basit Yousuf¹, Annika Flint², Kelly Weedmark³, Franco Pagotto⁴ and Sandra Ramirez-Arcos⁵ 

 View Affiliations

Version Posted: 29 February 2024 | <https://doi.org/10.1099/acmi.0.000780.v2>

This is an [author-accepted-manuscript](#). Click [here](#) to see the published [Version of Record](#).

 Info  Sections

 PDF  Tools  Share

Staphylococcus epidermidis is one of the predominant bacterial contaminants in platelet concentrates (PCs), a blood component used to treat bleeding disorders. PCs are a unique niche that triggers biofilm formation, the main contributor to *S. epidermidis* infections. We performed whole genome sequencing of four *S. epidermidis* strains isolated from the skin of healthy human volunteers (AZ22 and AZ39) and contaminated PCs (ST10002 and ST11003) to unravel phylogenetic relationships and decipher virulence mechanisms compared to 25 complete *S. epidermidis* genomes in GenBank. AZ39 and ST11003 formed a separate unique lineage with 14.1.R1 and SE95 strains, while AZ22 formed a cluster with 1457 and ST10002 closely grouped with FDAAGOS_161. The four isolates were assigned to sequence types ST1175, ST1174, ST73, and ST16, respectively. All four genomes exhibited biofilm-associated genes *ebh*, *ebp*, *sdrG*, *sdrH*, and *atl*. Additionally, AZ22 had *sdrF* and *aap*, whereas ST10002 had *aap* and *icaABCDR*. Notably, AZ39 possesses truncated *ebh* and *sdrG* and harbors a toxin encoding gene. All isolates carry multiple antibiotic resistance genes conferring resistance to fosfomycin (*fosB*), β -lactams (*blaZ*) and fluoroquinolones (*norA*). This study revealed a unique lineage for *S. epidermidis* and provided insight into the genetic basis of virulence and antibiotic resistance in transfusion-associated *S. epidermidis* strains.






Received: 20/02/2024 | Version Posted: 29/02/2024

Version status

Status: Accepted

Review status breakdown

KEY:     

	Versions	
	1	2
Review Tools	 read	
Reviewer 1	 read	
Reviewer 2	 read	
Editor	 read	 read

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Volume 6, Issue 4

Research Article | Open Access


Comparative virulome analysis of four *Staphylococcus epidermidis* strains from human skin and platelet concentrates using whole genome sequencing


Basit Yousuf^{1,2}, Annika Flint³, Kelly Weedmark³, Franco Pagotto^{2,3} and Sandra Ramirez-Arcos^{1,2} 

 View Affiliations

Published: 03 April 2024 | <https://doi.org/10.1099/acmi.0.000780.v3>

 Info  Sections

 Side by side view

 PDF

 Tools

 Share

Graphical Abstract

Graphical Abstract

Virulome profile of four *Staphylococcus epidermidis* strains isolated from platelet concentrates and human skin.





Version status

Status: Published Version of Record

 Version history

Review status breakdown

KEY:     

	Versions	
	1	2
Review Tools		
	read	
Reviewer 1		
	read	

Technology choices

Off-the-shelf

- Set-up costs
- Additional annual fees
- Vendor tie-in
- Training

Existing
technology

- Set-up costs
- Annual fees already locked in
- Familiar systems (no training)

What we had to change

Back-end

- Authentication & authorization
- Content ingestion (single)
- Data feeds
- Analytics (including COUNTER)
- SEO
- WebCMS

User interface

- Homepage
- Publisher-controlled pages
- Journal home pages
- Article display
- Article tools
- Search functionality

What we had to change

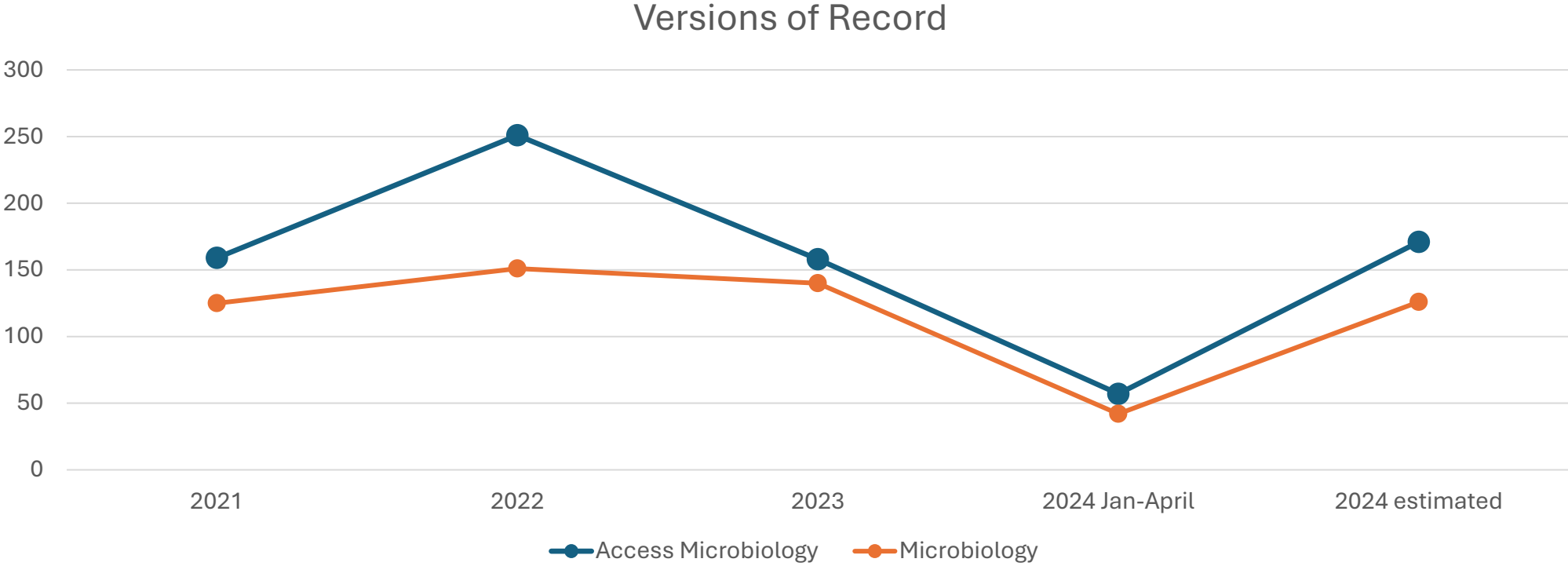
Back-end

- ~~Authentication & authorization~~
- **Content ingestion (versioned)**
- **Review ingestion (versioned)**
- Data feeds
- Analytics (including COUNTER)
- SEO
- WebCMS

User interface

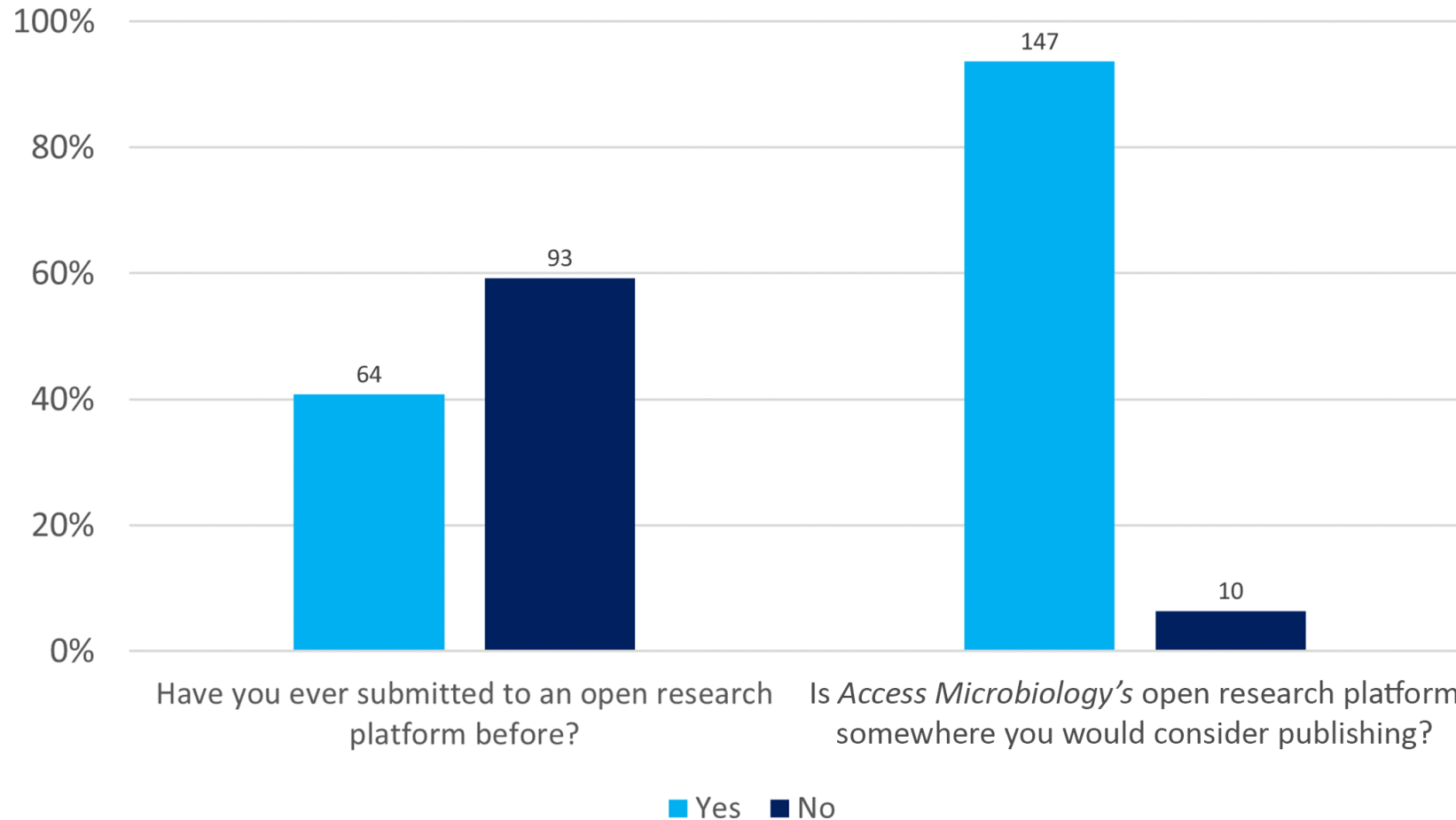
- Homepage
- Publisher-controlled pages
- Journal home pages
- **Article versioning**
- **Article display with reviews**
- Article tools
- **Search functionality**

Success metrics: publish more content



Success metrics: community acceptance

<https://bit.ly/452ygAU>



Success metrics: community acceptance

<https://bit.ly/452ygAU>

“Very glad to see this society trying to embrace modern scientific publishing, unlike some which seem to see it as a revenue stream and [are] actively fighting open access.”

Thank you for your attention

Tasha Mellins-Cohen

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