

# Open Research Europe



Open Science Days IV, University of Belgrade

3<sup>rd</sup> November 2022

Alicia Estacio Gomez | Content Acquisition Editor | F1000

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# Background

Who | What | When | Where | Why | How

# Open Research Europe (ORE)

- ✓ **Public Procurement** – 5.8 Million EUR contract signed in March 2020 with F1000Research for 4 years.
- ✓ **Open access publishing venue** for Horizon 2020, Horizon Europe and Euratom beneficiaries within 6 subject areas.

**Open Research Europe platform was launched in March 2021**

278 publications on the platform (October 2022)

[open-research-europe.ec.europa.eu](https://open-research-europe.ec.europa.eu)

# Ambitions of the European Commission

**To lead by example** in operationalising open science principles within scientific publishing & exploring **sustainable** open access publishing **business models**

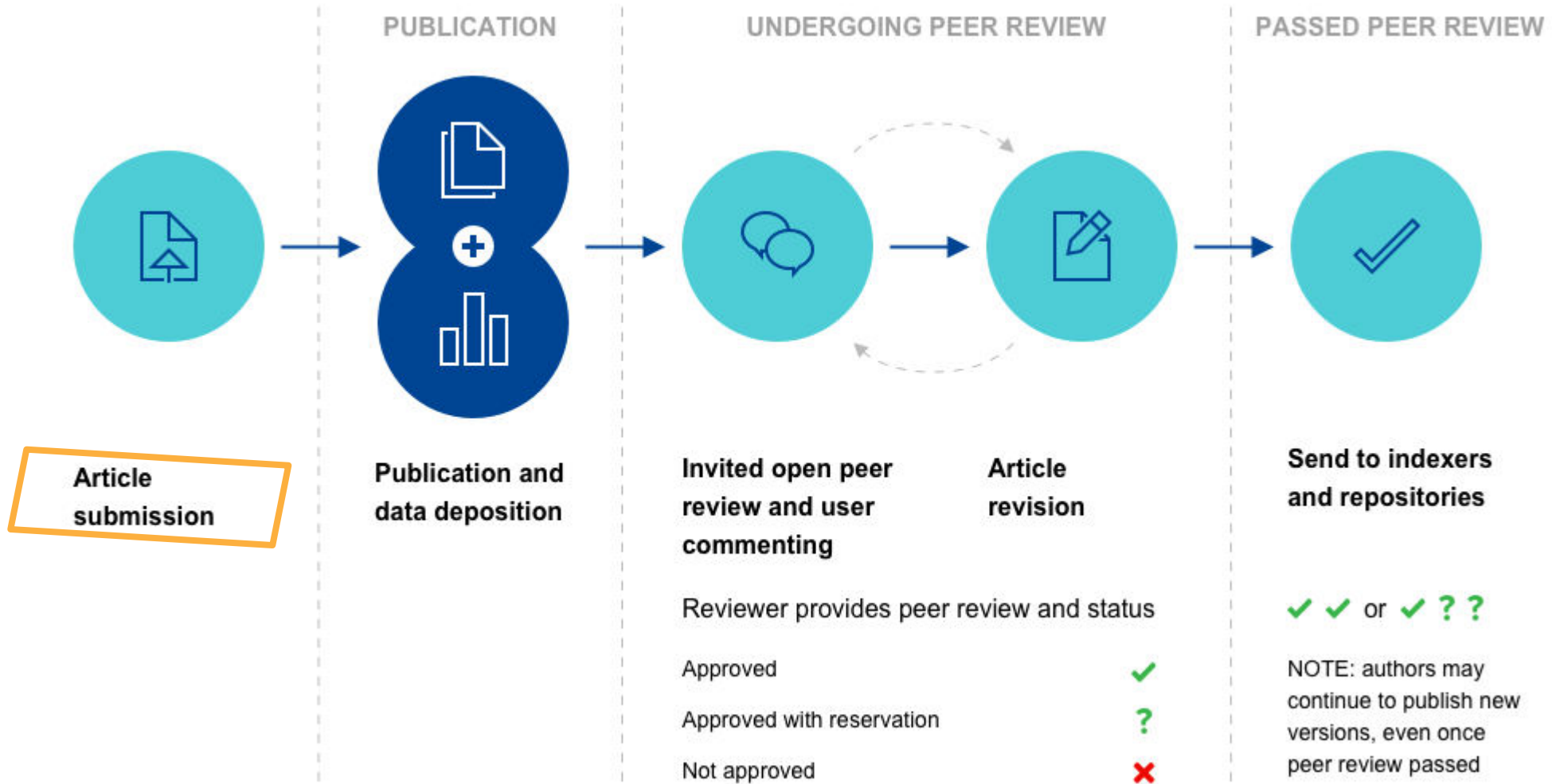
- ✓ **Open peer-review, and early sharing of research**
- ✓ **Immediate publication**
- ✓ **New generation article metrics**
- ✓ **Transparency & cost-effectiveness (APCs paid for by the Commission – 780 EUR)**
- ✓ **Aligned with the EC policy and principles**
- ✓

[open-research-europe.ec.europa.eu/article-processing-charges](https://open-research-europe.ec.europa.eu/article-processing-charges)

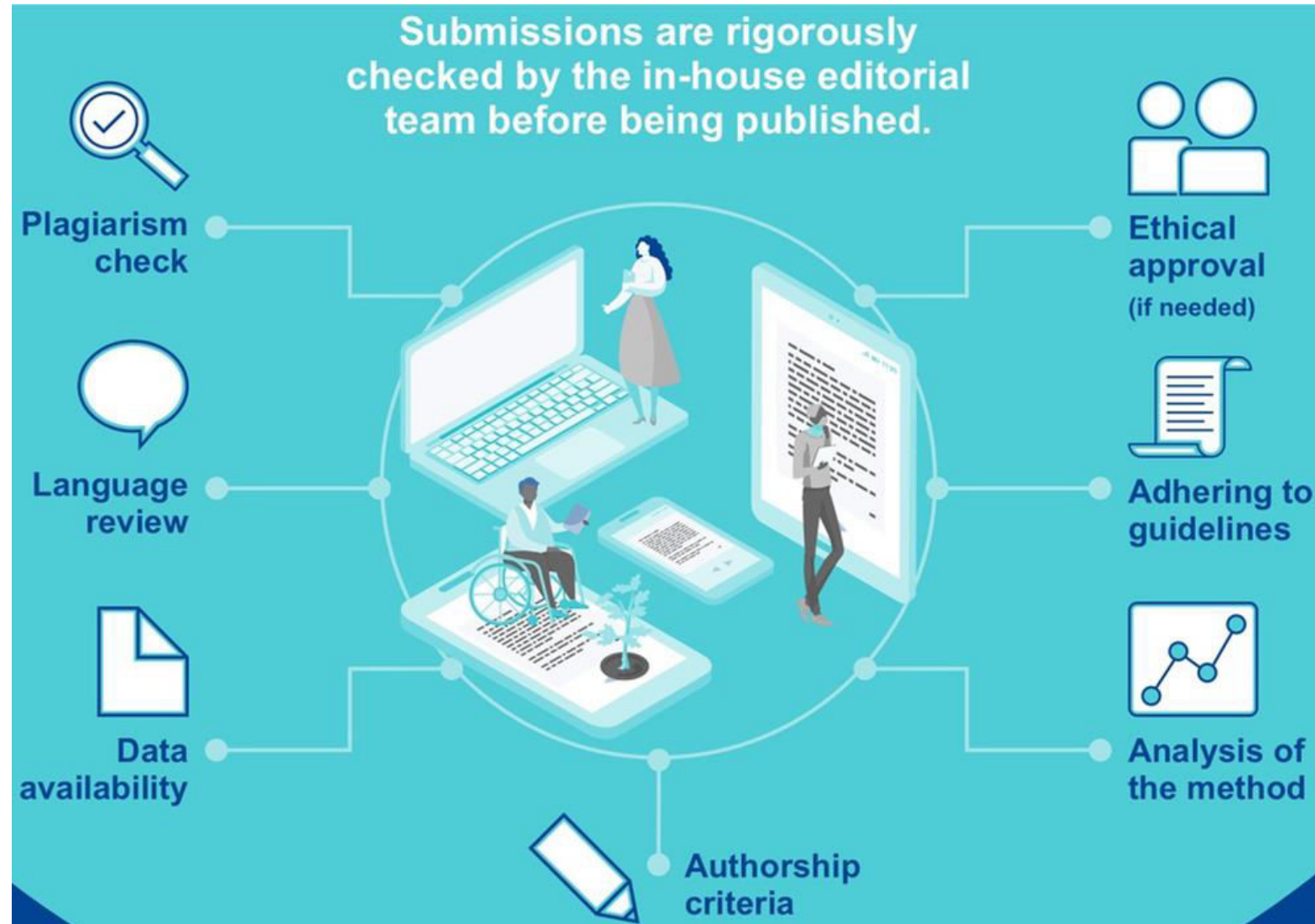
# ORE: How it works

The publishing model

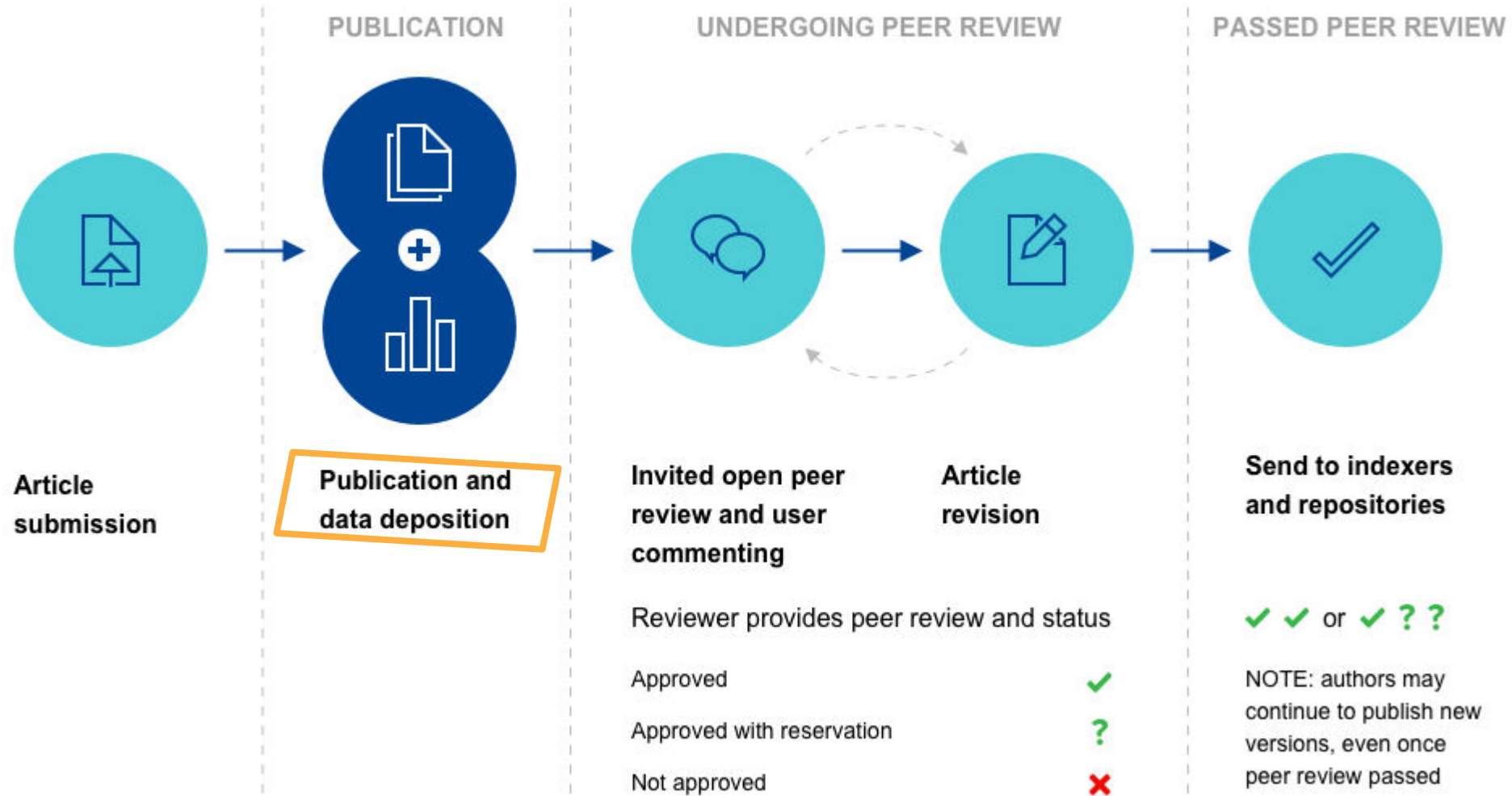
# Open Research Europe Publishing Model



# Pre-Publication Checks

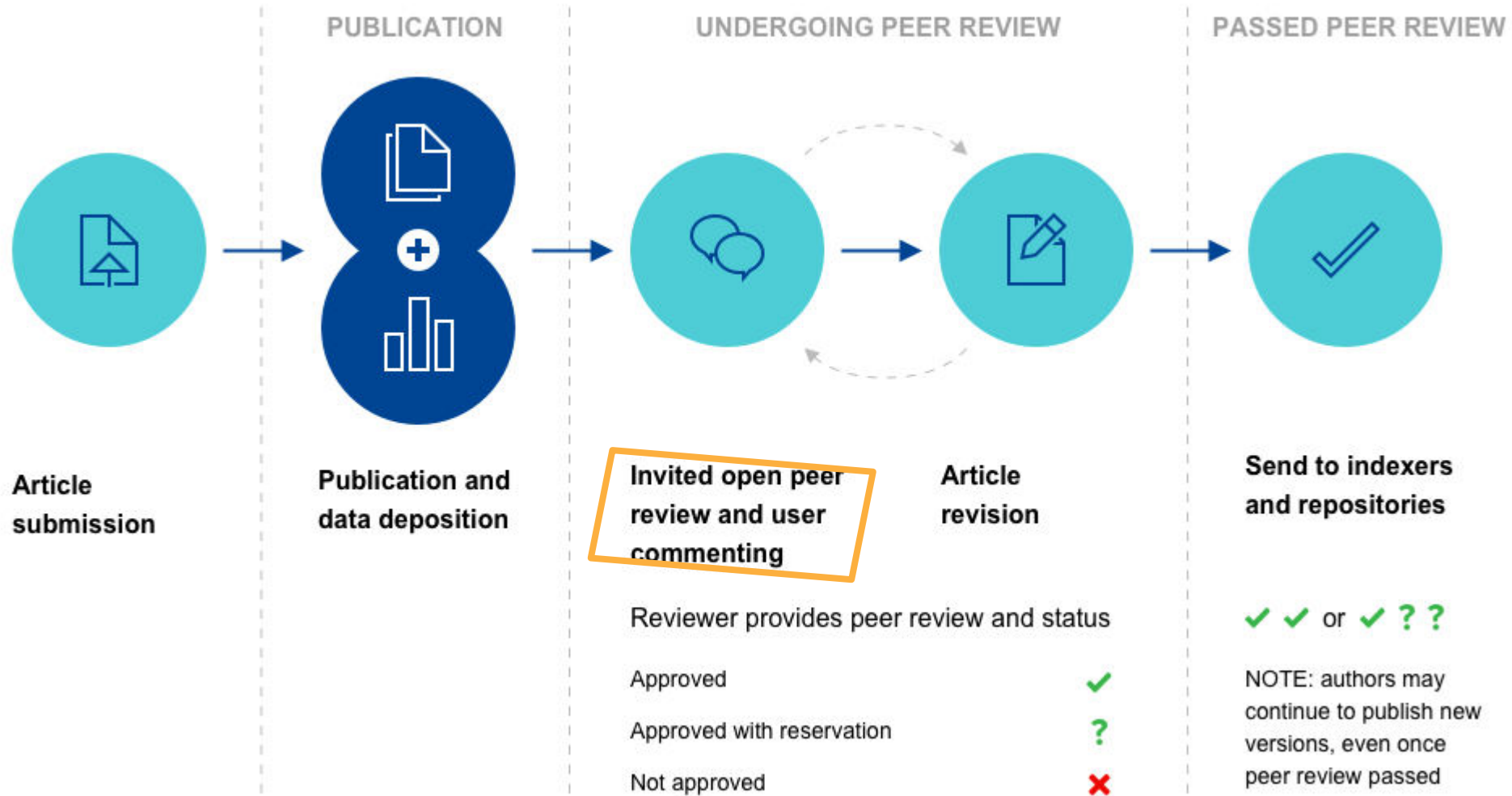


# Open Research Europe Publishing Model





# Open Research Europe Publishing Model



# Selecting reviewers – author selection

Once an article has been conditionally accepted, authors are directed to the peer reviewing section of their ORE account to select reviewers.

1.

ORE requires authors to suggest 5 reviewers (which must be verified) – articles will not be published without them.

1.

The ORE editorial management system and the editorial team support authors in making the author suggestions.

Selection is made two ways:

**1. Through knowledge of their field of research**

•

**2. Using the ORE peer review selector tool**

•

# Reviewer verification

Once the names have been selected, they await verification by the ORE editorial team.

- **Qualified** – reviewers are checked they have the correct expertise
- 
- **Expert** - at least 3 articles as lead author in a relevant topic, with at least 1 article having been published in the last 5 years
- **Impartial** - no co-authoring with lead authors in the 3 years preceding; don't work at the same institution; are not a close collaborator with an author, no competing interests
- **Global:** For any given article, we require authors to suggest geographically-diverse reviewers
- 
- **Diverse:** reviewers should be diverse with regards to their gender, location and career stage
- **Additional expertise:** e.g., statistics experts required if necessary
-

# Open Research Europe Publishing Model

## ✓ APPROVED

The paper is scientifically sound in its current form and only minor, if any, improvements are suggested

## ? APPROVED WITH RESERVATIONS

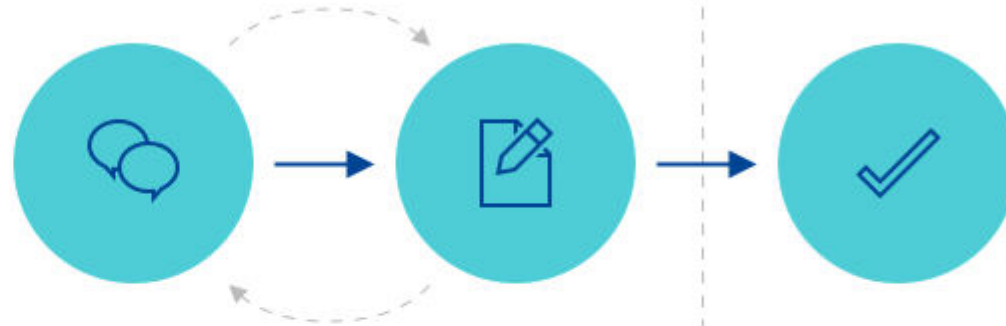
A number of small changes, sometimes more significant revisions are required to address specific details and improve the papers academic merit.

## ✗ NOT APPROVED

Fundamental flaws in the paper seriously undermine the findings and conclusions

UNDERGOING PEER REVIEW

PASSED PEER REVIEW



**Invited open peer review and user commenting**

**Article revision**

**Send to indexers and repositories**

Reviewer provides peer review and status

Approved



Approved with reservation



Not approved



✓ ✓ or ✓ ? ?

NOTE: authors may continue to publish new versions, even once peer review passed

# Passing Peer Review

- Revisions are made through new versions of the article that are linked together (versions are limitless)
- 
- Authors need to achieve a certain 'threshold' of reviewer status to pass peer review and be indexed:

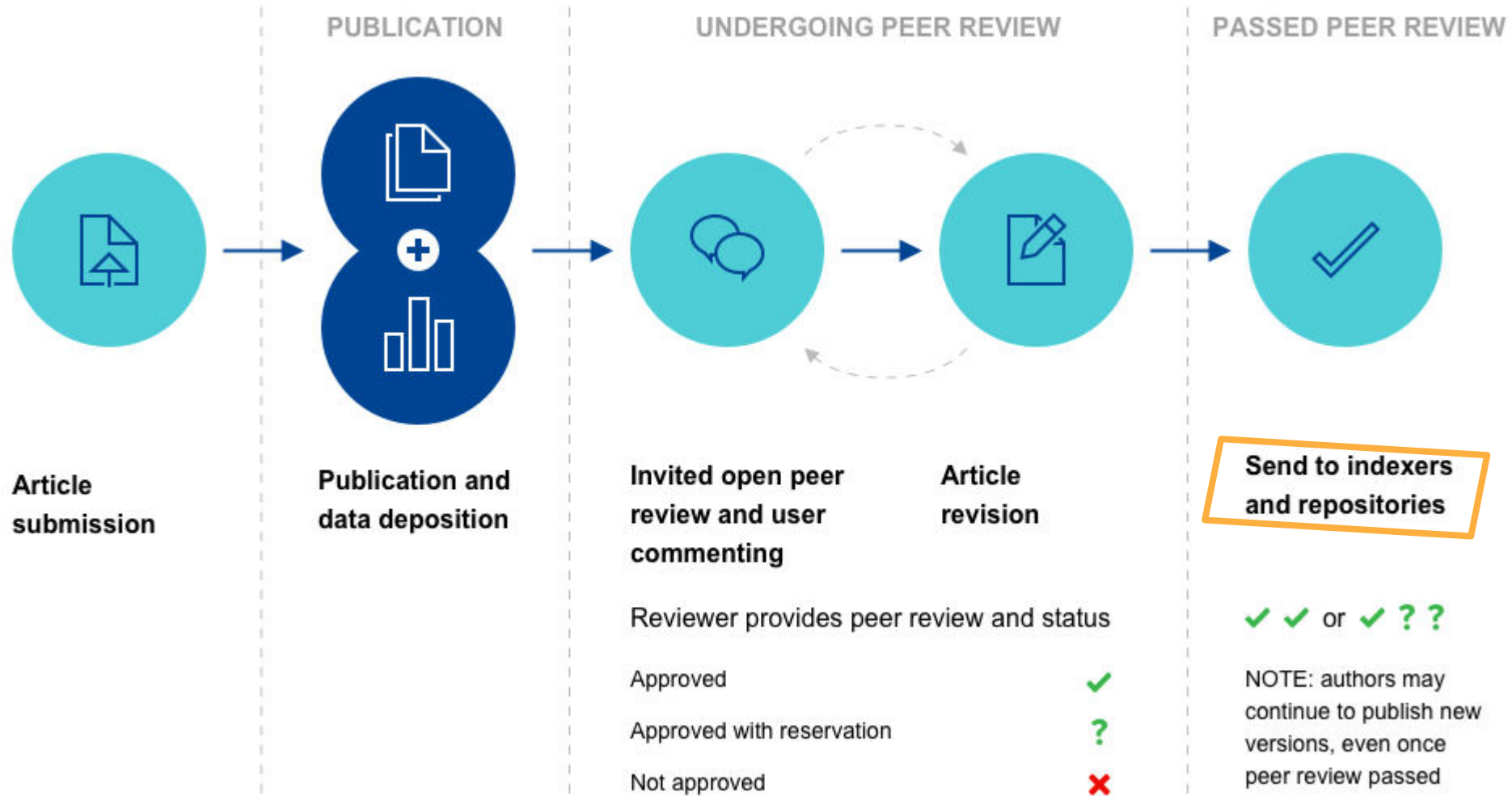


**2 'Approved' Status**



**2 'Approved with reservations' + 1 'Approved' Status**

# Open Research Europe Publishing Model



# Publication

154 Views

50 Downloads

4 Citations

Cite

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Home > Articles > A new nomenclature for the livestock-associated Mycobacterium ...

RESEARCH ARTICLE

## REVISED A new nomenclature for the livestock-associated *Mycobacterium tuberculosis* complex based on phylogenomics [version 2; peer review: 2 approved]

Michaela Zwyer, Cengiz Çavusoglu , Giovanni Ghielmetti , Maria Lodovica Pacciarini, Erika Scaltriti, Dick Van Soolingen, Anna Dötsch, Miriam Reinhard, Sebastien Gagneux , Daniela Brites  

This article is included in [Evolution and Ecology gateway](#)



This article is included in [Evolutionary Biology collection](#)



This article is included in [Excellent Science gateway](#)



Article

Authors

Metrics

### Open Peer Review

Approval Status   

Version 2

(Revision)

01 Dec 21

1

2



[view](#)



[view](#)

Version 1

25 Aug 21

↑




[view](#)

↑



[view](#)

1. **Lorraine Michelet**, Paris-Est University, Marne-la-Vallée, France
2. **Liliana C. M. Salvador** , University of Georgia, Athens, GA, USA

### Comments on this article

All Comments (0)

# Responses and New Versions

**Reviewer Report** 7 Views Ⓢ

? **Approved with reservations** ⓘ

13 Oct 2021 VERSION 1

Liliana C. M. Salvador , Department of Infectious Diseases, College of Veterinary Medicine, University of Georgia, Athens, GA, USA

[Cite this Report](#)

[Responses \(1\)](#)

**Summary**

Zwyer *et al.* proposed a new nomenclature for three species of the Mycobacterium tuberculosis complex *M. bovis*, *M. orygis* and *M. caprae* by combining phylogenetics with genomics. The goals of their study was to define lineages and sub-lineages based on genetic diversity patterns by analysing a subset of 830 whole genomes extracted from (and representative of) different parts of the world). The authors have found three main lineages La1, La2, and La3, representing respectively, *M. bovis*, *M. caprae* and *M. orygis*. Within La1, the authors have identified eight sublineages (La1.1-La1.8), which presented distinct geographical patterns (some restricted to an area, while others globally widespread). The authors have also found specific markers (SNPs) to molecularly characterize the different MTBC groups.

**General comments**

This manuscript is highly relevant for the molecular characterization of MTBC and for future molecular epidemiological and evolutionary studies. There is a large need to extend the current classification system (L1-L7 involving *M. tuberculosis* and *M. africanum*) to other species of the complex and the authors did it using a dataset of 853 genomes from across the world. Overall, I find the manuscript well thought out, very relevant, and timely. I only have a few comments below regarding the analysis performed, which could impact the presented results.

**General comments/questions**

- Selection of isolates: authors mentioned that they chose 50 genomes per continent. What if the same amount of genomes was taken from an endemic place versus a non-endemic place. How does the local prevalence of the disease affect the genetic diversity that we see in the 50 isolates? Are the 50 genomes enough to characterize well the genetic diversity of a specific place?
- What is MTBC-Livestock associated? How is it defined? Are there any other MTBC species that infect livestock that are not included? Are there any "MTBC-Livestock associated" lineages that infect the same or even more other types of animals like, for example, badgers or white-tailed deer (both reservoirs for *M. bovis*)?

Is the work clearly and accurately presented and does it cite the current literature?

Yes

Is the study design appropriate and does the work have academic merit?

Yes

Are sufficient details of methods and analysis provided to allow replication by others?

Yes

If applicable, is the statistical analysis and its interpretation appropriate?

Not applicable

Are all the source data underlying the results available to ensure full reproducibility?

Yes

Are the conclusions drawn adequately supported by the results?

Partly

**Competing Interests**

No competing interests were disclosed.

**Reviewer Expertise**

phylogenetics, phylogenetics, bioinformatics, M. bovis

*I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.*



AUTHOR RESPONSE 1 DECEMBER 2021

**Daniela Brites**  
Swiss Tropical and Public Health Institute, Basel, Switzerland

We thank the reviewer for her positive feedback.

As for the selection of isolates; the aim of this analysis was to have balanced phylogenetic inference of the total diversity of the MTBC. However, we were not so interested in maximizing genetic diversity within each lineage but rather to have an even representation of endemic and non-endemic places (which we believe to have achieved by sampling randomly each lineage in each continent) at a global scale and show that there is no reason to treat *M. bovis* differently than the human adapted lineages; at least not in what concerns the tree topology. Certainly, as very well pointed out by the reviewer, 50 genomes might not be enough to represent all diversity of *M. bovis* in Africa for instance, but that should be true also for other groups of the MTBC. As to the definition of livestock associated, a similar question was also raised by the other reviewer, revealing that we failed to pass on more clearly why we consider *M. bovis*, *M. orygis* and *M. caprae* as livestock-associated MTBC members. We have added to the Introduction a few considerations defending this point of view, which we hope addresses the reviewer's concerns.

At the core of considering these species as livestock-associated is the strong evidence that the evolutionary success of *M. bovis*, *M. orygis* and *M. caprae* is associated with the fact that these pathogens are able to cause sustainable infections in livestock species. The fact that these are multi-host pathogens allows them to linger in other animal reservoirs, and in more recent times (post bTB surveillance), this might play a crucial role for these lineages by avoiding local extinctions. However at a global and evolutionary scale, migration and population expansion of *M. bovis* (possibly also *M. caprae* and *M. orygis*, to be confirmed as more data becomes available) are most likely a consequence of cattle husbandry and movements. We think that distinguishes *M. bovis*, *M. orygis* and *M. caprae* from other animal MTBC members, which are also multi-host pathogens (e.g. *M. microti*).

**Competing Interests:** No competing interests were disclosed.

[View less](#)

**RESPOND** Report a concern



**REVISED** **Amendments from Version 1**

Definition of livestock associated MTBC members was added to the introduction.  
Rational for considering *M. orygis* as livestock associated MTBC member was added to the introduction.  
10 duplicated WGS were removed from the analysis.  
Suite of markers to identify lineages and sublineages was added to TBProfiler.

**See the detailed response from the author(s) to the review by Lorraine Michelet**  
**See the detailed response from the author(s) to the review by Liliana C. M. Salvador**



# Open data example

## Data availability

### Underlying data

European Nucleotide Archive (EBI-EMBL): A new nomenclature for the livestock-associated *Mycobacterium tuberculosis* complex based on phylogenomics. Accession number: PRJEB46653, <https://identifiers.org/ena.embl:PRJEB46653>

European Nucleotide Archive (EBI-EMBL): Whole Genome sequencing (WGS) of *Mycobacterium bovis* spoligotype SB0120 and SB0841 isolates circulating in Italy. Accession number PRJEB46575, <https://identifiers.org/ena.embl:PRJEB46575>

Zenodo: A new nomenclature for the livestock-associated *Mycobacterium tuberculosis* complex based on phylogenomics, <https://doi.org/10.5281/zenodo.5153095><sup>90</sup>

This project contains the following underlying data:

- Table 1: Accession numbers and metadata associated with the 829 WGS used of La1, La2 and La3.
- Table 2 - Accession numbers and metadata associated with the 1,221 WGS used as representatives of the whole MTBC.

### Extended data

Zenodo: A new nomenclature for the livestock-associated *Mycobacterium tuberculosis* complex based on phylogenomics, <https://doi.org/10.5281/zenodo.5730685>

This project contains the following extended data:

- Figure 1: Distribution of the raw pairwise SNP distances between and within main La1 groups.
- Table 3: Spoligotypes patterns inferred from the WGS and used to complement the geographic distribution of La1 sublineages.
- Table 4: Single nucleotide polymorphisms (SNPs) specific to livestock-associated MTBC lineages and sublineages. Coordinates based on the *M. tuberculosis* H37Rv annotation (NC\_000962.3) are given (Position\_ref), and the lineage and or sublineage classification (PhylogeneticSNP). Additionally, the gene-based position is indicated (Position\_gene) as well as the kind of mutation based on SnpEff annotation<sup>50</sup>. SNPs used to create the new KvarQ testsuite are indicated.
- Table 5: KvarQ results of lineage and sublineage typing done with the new testsuite implemented.

# New generation metrics

154 Views | 50 Downloads | 4 Citations

“ Cite | ↓

Home > Articles > A new nomenclature for the livestock-associated *Mycobacterium* ...

RESEARCH ARTICLE

## REVISED A new nomenclature for the livestock-associated *Mycobacterium tuberculosis* complex based on phylogenomics [version 2; peer review: 2 approved]

Michaela Zwyer, Cengiz Çavusoglu, Giovanni Ghielmetti, Maria Lodovica Pacciarini, Erika Scaltriti, Dick Van Soolingen, Anna Dötsch, Miriam Reinhard, Sebastien Gagneux, Daniela Brites

This article is included in Evolution and Ecology gateway

This article is included in Evolutionary Biology collection

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Article


Authors

Metrics


Cited


 DIMENSIONS  
4  
VERSION 1 (1)  
VERSION 2 (3)

 CROSSREF  
4

 GOOGLE SCHOLAR  
4


Discussed

 0 COMMENTS view >

 TWITTER  
2

Data provided by Altmetric

Saved

 MENDELEY  
6  
VERSION 2 (6)

Data provided by Altmetric

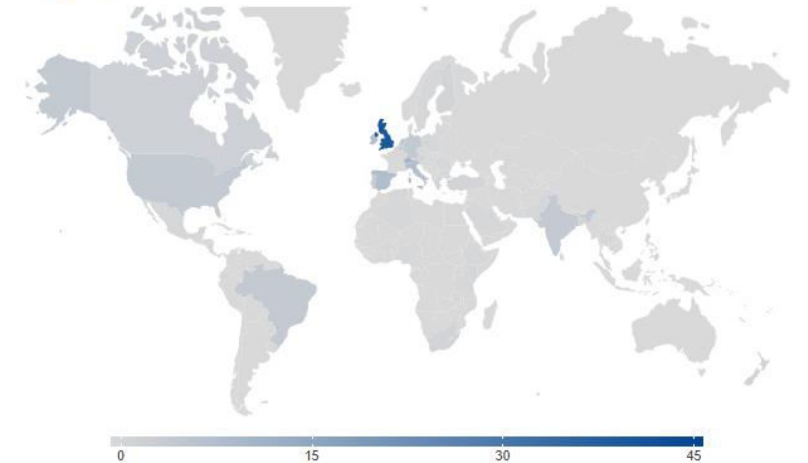
Unless indicated otherwise, values are totals across all versions of this article

Reach

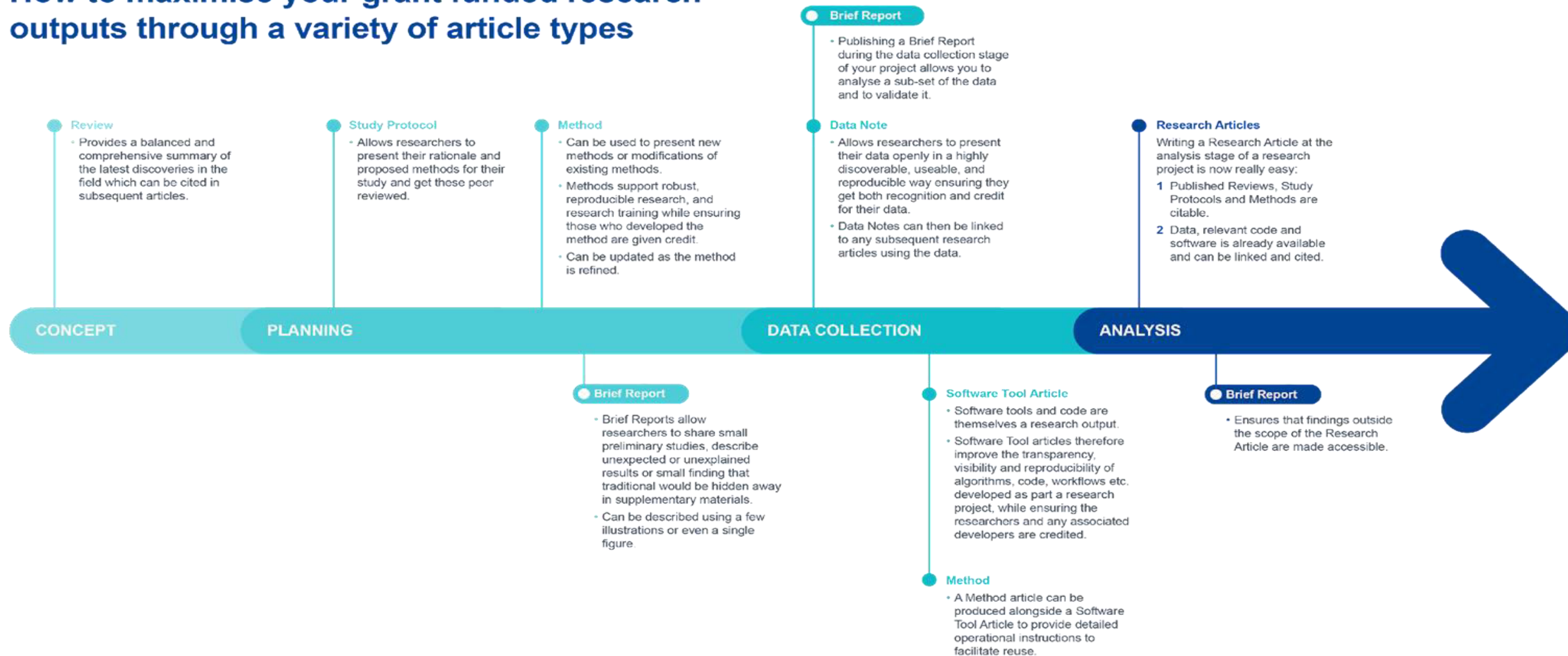
Article Views & Downloads

	HTML Page Views	PDF Downloads	XML Downloads	TOTAL
Open Research Europe	154	50	0	204
Zenodo	47	51	n/a	98
TOTALS	201	101	0	302

Sessions per country



# How to maximise your grant funded research outputs through a variety of article types



## Open Research Europe

# Supporting research across all disciplines

	Natural sciences	Engineering and technology	Medical and health sciences	Agricultural and veterinary sciences	Social sciences	Humanities and the arts
Case Study	•	•	•	•	•	•
Research Article	•	•	•	•	•	•
Brief Report	•	•	•	•	•	•
Data Note	•	•	•	•	•	•
Method Article	•	•	•	•	•	•
Open Letter	•	•	•	•	•	•
Software Tool Article	•	•	•	•	•	•
Review	•	•	•	•	•	•
Case Report	•	•	•	•		
Registered Report	•	•	•	•	•	
Clinical Practice Article	•	•	•	•		
Study Protocol	•	•	•	•	•	
Systematic Review	•	•	•	•	•	
Essay					•	•

# ORE: the platform so far

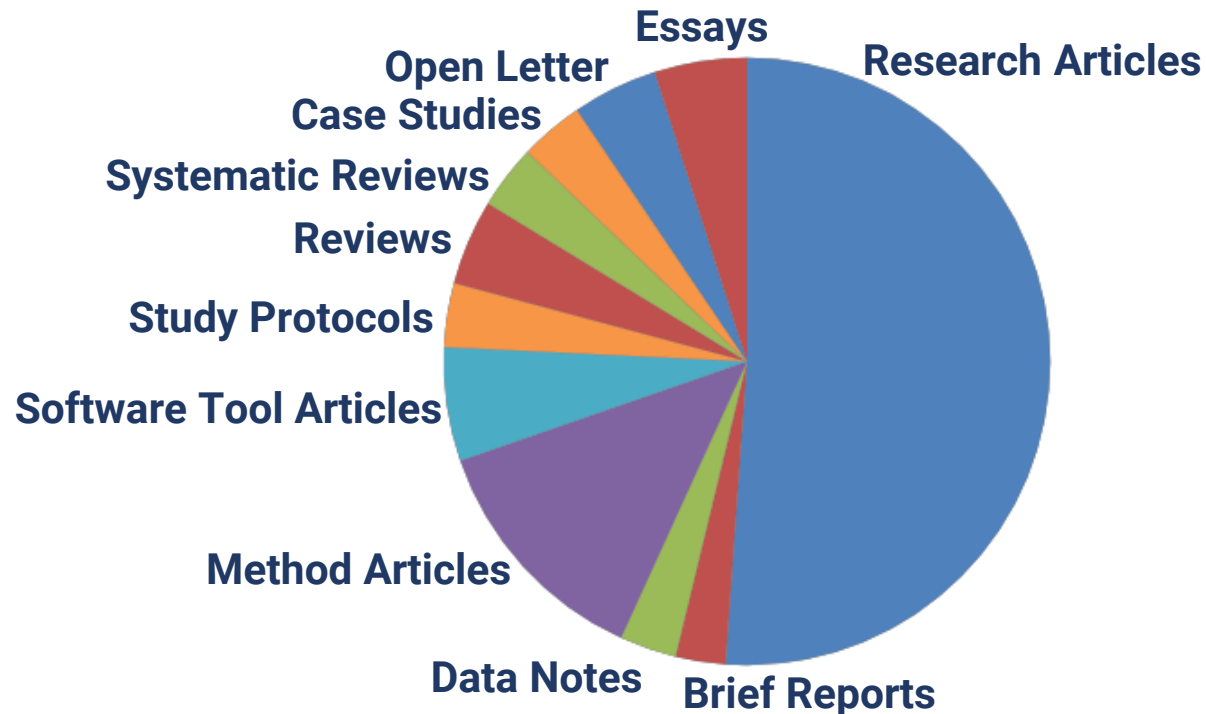
Stats | Major milestones | Content curation |

# Progress of the platform so far

**278** published articles

**216** articles completed peer review

**164** articles passed peer review



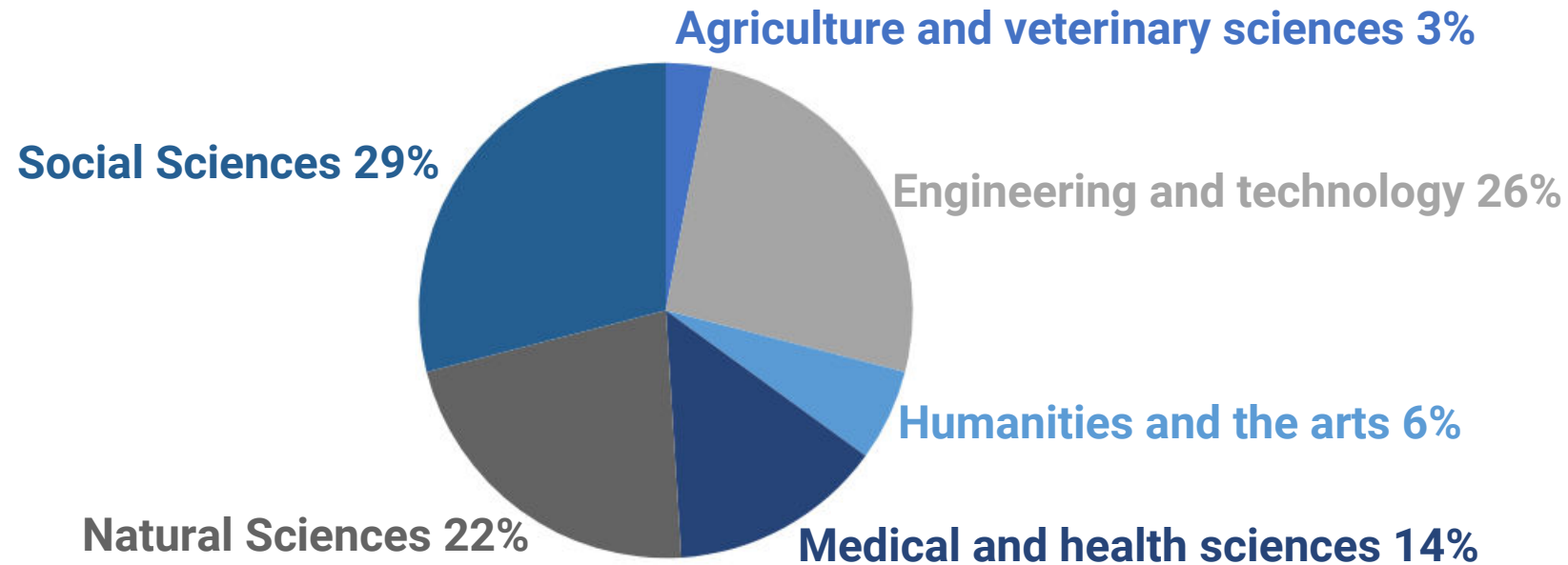
## Currently indexed in:

- ✓ Google Scholar
- ✓ DOAJ Seal
- ✓ INSPEC
- ✓ Scopus (accepted)
- ✓ ERIH Plus (accepted)

# Progress of the platform so far

## Subjects areas

- ✓ Agricultural and veterinary sciences
- ✓ Humanities and the arts
- ✓ Natural sciences
- ✓ Engineering and technology
- ✓ Medical and health sciences
- ✓ Social sciences



# Progress of the platform so far

## Community Gateways

- ✓ Dedicated hubs housing all content related to a specific subject area
- ✓ Led by Community Gateway Advisors



### Cell, Molecular and Structural Biology

**Cell Biology** studies the structure, function and behaviour of cells, considering them the fundamental units of life. Potential topics include but are not limited to: Cell Signalling, Cell Metabolism, Cell Polarity, Cell Cycle, Membrane-trafficking, non-membrane-bound organelles, cytoskeleton, molecular machines.

**Molecular and Structural Biology** investigates cellular interactions at the molecular level, with special focus on genes and proteins. Potential topics include Molecular Genetics, Molecular Evolution, and Molecular Neuroscience, among others.

This Community Gateway is led by [Dr Gautam Dey](#) and [Dr Katalin Solymosi](#).



### Chemical Engineering

Chemical Engineering is a multi-disciplinary branch of engineering research that combines natural and experimental sciences with life sciences, mathematics, and economics to design, develop, produce, transform, transport, operate and manage the industrial processes that turn raw materials into valuable products. This Community Gateway is led by [Prof. Manuel A. Rodrigo](#).



### Civil Engineering

Civil Engineering brings together advanced knowledge of the physical and natural sciences, mathematics, computational methods, and economics to facilitate the development of vital projects for the benefit of society. This Community Gateway is led by [Dr. Sakdirat Kaewunruen](#).



### Clinical Medicine

The Clinical Medicine Community Gateway focuses on improving patient outcomes, from diagnosis to end-of-life care, and is led by [Dr. Clementina Cocuzza](#).



# Progress of the platform so far

## Collections

- ✓ Compilations of content for Horizon funded communities, projects or conferences.
- ✓ Overseen by Horizon- funded Guest Advisors



### Energy Storage

Energy storage refers to the capture of energy and the effective delivery of it for future use. As the energy crisis has intensified, energy storage has become a major focus of research in both industry and academia.



### Energy Systems Modelling

The transition to a clean and renewable energy system is recognised as one of the biggest challenges the world faces this century. Energy models are key to the transformation of the energy system, facilitating the transition towards sustainable energy sources. This collection will be publishing papers from the 2021 [EMP-E conference](#).



### Epigenetics

The word epigenetic literally means “on top of” changes in genetic sequence. It mostly involves modifications of gene activity and expression, either coming from external or environmental factors, or even part of normal development, without changing the nucleotide sequence. This collection is being led by [Dr. Germano Cecere](#) and [Dr. Jop Kind](#).



### Evolutionary Biology

Evolutionary Biology studies the processes that generate diversity on earth. In this collection [Dr. Mehmet Somel](#) and [Dr. Claudio Ottoni](#) aim to attract research on understanding how species have managed to evolve and adapt to changing environments.

# ORE: Open Research Publishing

The benefits

# What are the benefits?

- **Fast** – articles are published rapidly
- **Inclusive** – can publish all research outputs
- **Open** – fulfils Commission's OA & data sharing requirements
- **Reproducible** – data is published alongside article
- **Transparent** – open, author-driven, peer review
- **Easy** – costs are met directly by the Commission



# Want to know more? Online resources

## Publishing with Open Research Europe

### What is Open Research Europe?

Open Research Europe is the European Commission's publishing service, providing all Horizon 2020 and Horizon Europe beneficiaries and their researchers with the option of an easy, high quality peer-reviewed venue to publish their papers open access, at no cost to them, and in full compliance with the European Commission's **open access policies**.

Through building Open Research Europe, the Commission aims to:

- Provide a high-quality service that meets general and discipline-specific standards of scientific publishing.
- Reinforce its position as a funder that leads by example in operationalizing open science.
- Encourage technology-enabled innovation in scholarly communication.
- Support the integrity and transparency of the research process and reproducibility of research.
- Contribute towards transparency and cost effectiveness in scientific publishing, as well as towards the exploration of sustainable open access business models.

- Links to Blog
- 
- Videos
- 
- FAQs
- 
- Twitter account

<https://think.f1000research.com/open-research-europe-submission/>



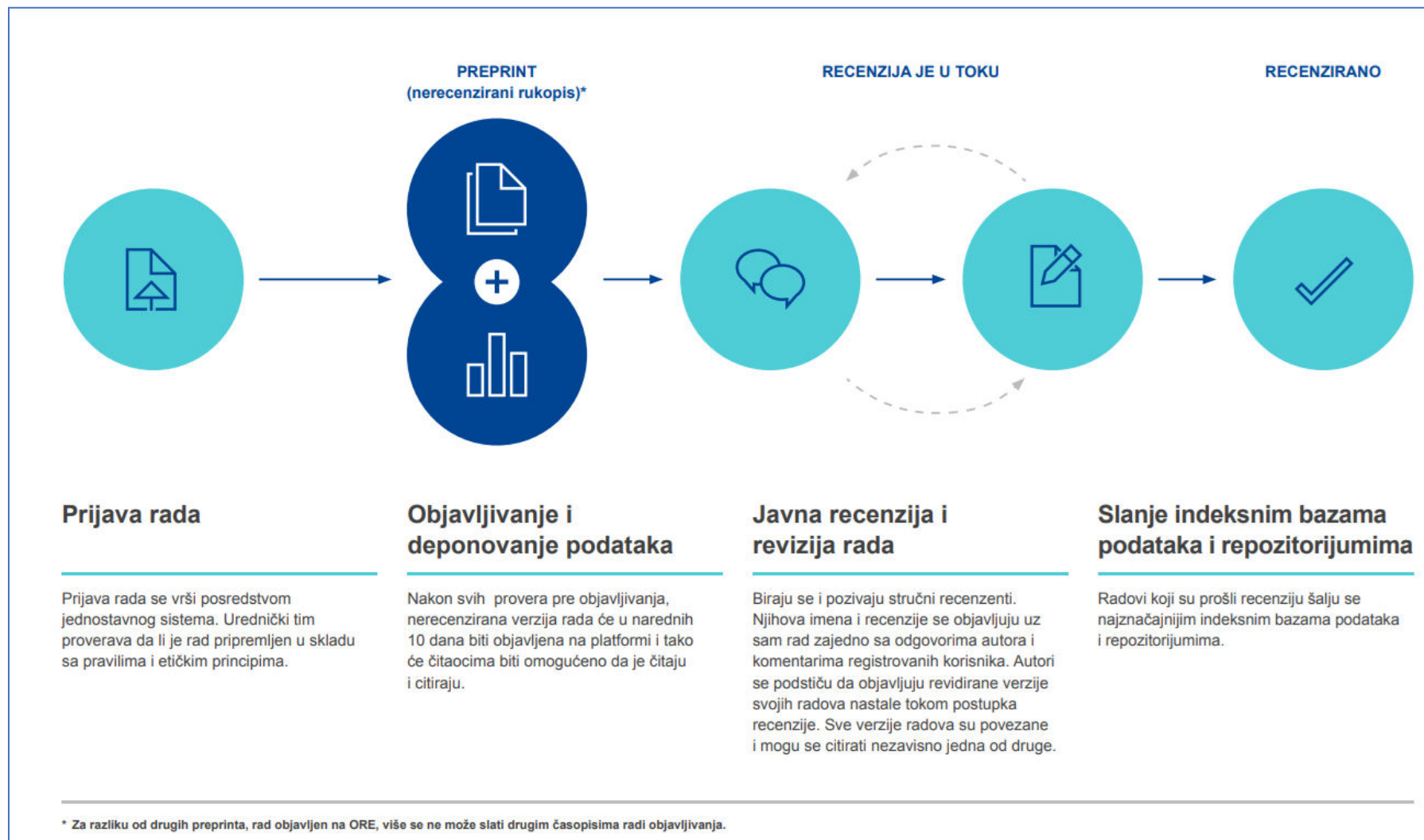
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# CoARA: Coalition for Advancing Research Assessment

- 
- European University Association, European Commission, Science Europe + 20 research organizations drafted an agreement.
  
- It is based on 10 commitments, “establishes a common direction for research assessment reform, while respecting organizations' autonomy”.
  
- 
- Opened for signatories in September 2022- 119 organisations have already signed.
  
- 
- Timeframe: Signatories to share their action plan by the end of 2023 or within one year of signing.

Commitments	• <b>What we do in ORE</b>
<ul style="list-style-type: none"> <li>Recognise the <b>diversity</b> of contributions to, and careers in, research in accordance with the needs and nature of the research</li> </ul>	<ul style="list-style-type: none"> <li>✓ Wide range of article types.</li> <li>✓ We publish confirmatory, negative and null results.</li> </ul>
<p>Base research assessment primarily on qualitative evaluation for which <b>peer review</b> is central, supported by responsible use of quantitative indicators.</p> <ul style="list-style-type: none"> <li></li> </ul>	<ul style="list-style-type: none"> <li>✓ Open &amp; transparent peer review</li> </ul>
<p><b>Abandon inappropriate uses</b> in research assessment of journal- and publication-based metrics, i.e. Journal Impact Factor (JIF) and h-index.</p>	<ul style="list-style-type: none"> <li>✓ No impact factor, article-level metrics are the focus</li> <li></li> </ul>
<ul style="list-style-type: none"> <li><b>Review &amp; develop</b> research assessment criteria, tools</li> </ul>	<ul style="list-style-type: none"> <li>✓ Advisor recruitment</li> </ul>



# Price Transparency

Transparent about the costs & the breakdown for the price that the Commission pays per article.





**Open Research Europe requires that, where possible, the source data underlying the results are made available at publication**

- ✓ However, the sharing of research data **must**:
- ✓
- ✓ Protect the confidentiality, security and privacy of individuals
- ✓
- ✓ Respect the terms of consent by individuals who are involved in research
- ✓
- ✓ Be consistent with Horizon Europe legal, ethical & regulatory frameworks

[open-research-europe.ec.europa.eu/data-guidelines](https://open-research-europe.ec.europa.eu/data-guidelines)