OxFOS

Oxford Forum of Open Scholarship

Welcome to our in-person conference day

Wednesday 4 March 2026, 10:00-18:00

go.glam.ox.ac.uk/OxFOS26

#OxFOS26

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OxFOS

Oxford Forum of Open Scholarship

Reimagining ‘open’
Sharing research outside of traditional formats

Wednesday 4 March 2026

go.glam.ox.ac.uk/OxFOS26

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#OxFOS26

Beyond the Journal Article: Building a New National Publication Culture in the Netherlands

Dr Ana Ranitovic
Chief of Open Science & Open Science Programme Manager

Oxford Forum for Open Scholarship · March 4, 2026

Image source: Pjotr Wiese
National Open Science Festival 2025

What counts as a research output?

Journal articles?

Books?

Datasets?

Software?

Policy reports?

Teaching materials?

New Vision for Publication Culture

- Coordinated by Chiefs of Open Science, developed by the community
- Approved by all Dutch universities (Dec 2025)
- National framework, disciplinary flexibility

By 2030, research outputs in all their forms will be recognized as essential scholarly contributions, valued for their quality, integrity, openness, and societal relevance.

All contributions recognized

Quality > Quantity

Integrity > Prestige

Why a new publication culture?

- **Publish-or-perish pressures** prioritize volume and journal prestige over quality.
- **Prestige-driven evaluation** over real scientific contribution.
- **Diverse outputs undervalued** - data, software, peer review, and societal work rarely count in careers.
- **Reproducibility at risk** as replication studies and negative results go unrewarded.
- **Rising publication costs** (APCs) strain budgets and create inequities.
- **Peer review overload** slows dissemination and weakens quality control.

Universiteiten
van Nederland

SOO 50.04A

Position Paper
17 november 2025

Vision on Publication Culture
Chiefs Open Science

Content

Framework for a new publication culture

Guiding principles

- **Fit-for-purpose**
- **Open**
- **Sustainable**

Practical framework

- **Audience & Quality:** Research is published in a way that enables us to reach the relevant audiences and to show that our research meets the quality standards expected by these audiences.
- **Openness & Timeliness**: Research is published in an open and timely way.
- **Cost effectiveness:** Research is published in a way that safeguards financial sustainability of our scholarly communication infrastructures.

What needs to change?

- **Open and sovereign infrastructures**
  Invest in federated repositories and national platforms to ensure long-term accessibility and digital autonomy.
- **Support and skills**
  Train researchers and professional staff in responsible publishing, FAIR data, and AI literacy.
- **Norm-setting with the academic community**
  Change must be co-created by researchers across disciplines.
- **Recognition & Rewards reform**
  Replace quantity-driven metrics with quality-focused assessment aligned with mission and societal value.
- **Anchoring in policy**
  Align funding policies, evaluation protocols, and career frameworks with the new publication culture.

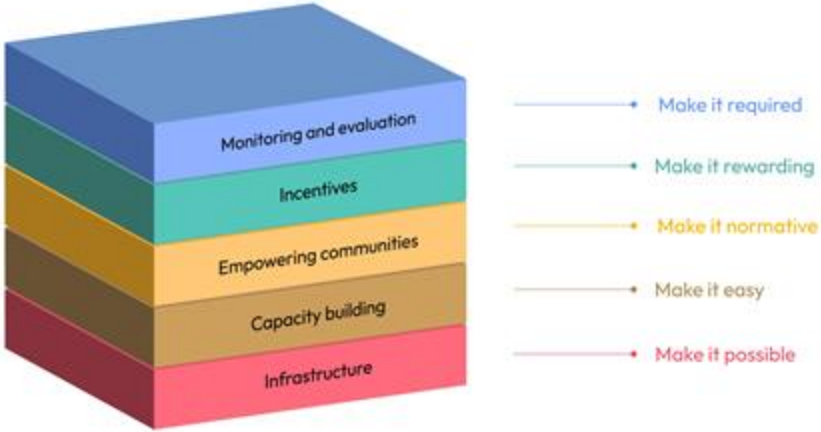
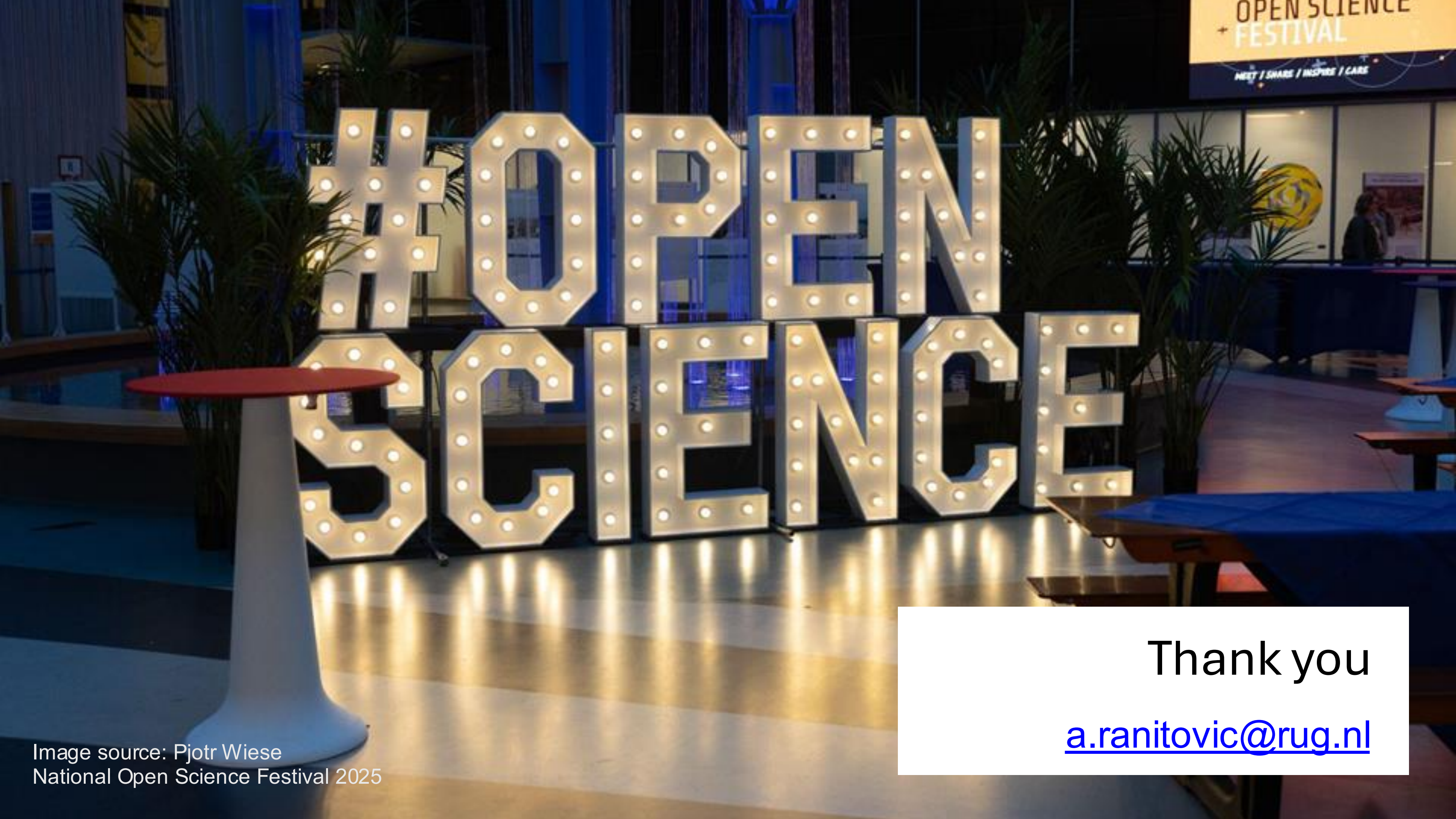


Image source: Openscience.nl

In closing

If publication culture concerns why, where, when, and how researchers publish their work, and the implications this has for their careers, the quality of research, and the accessibility of knowledge…

…then what kind of publication culture do we want?



Thank you

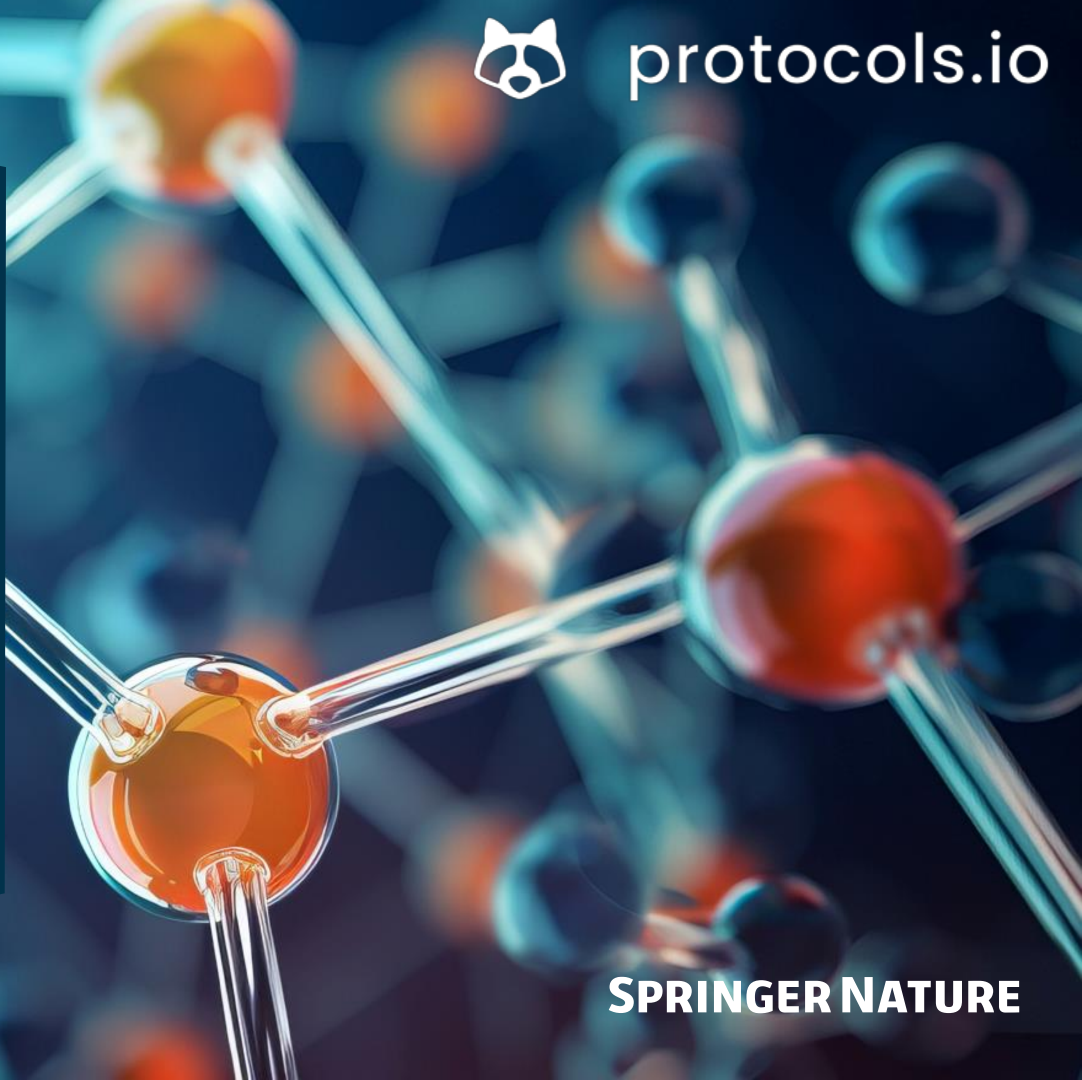
a.ranitovic@rug.nl

Image source: Pjotr Wiese
National Open Science Festival 2025

protocols.io

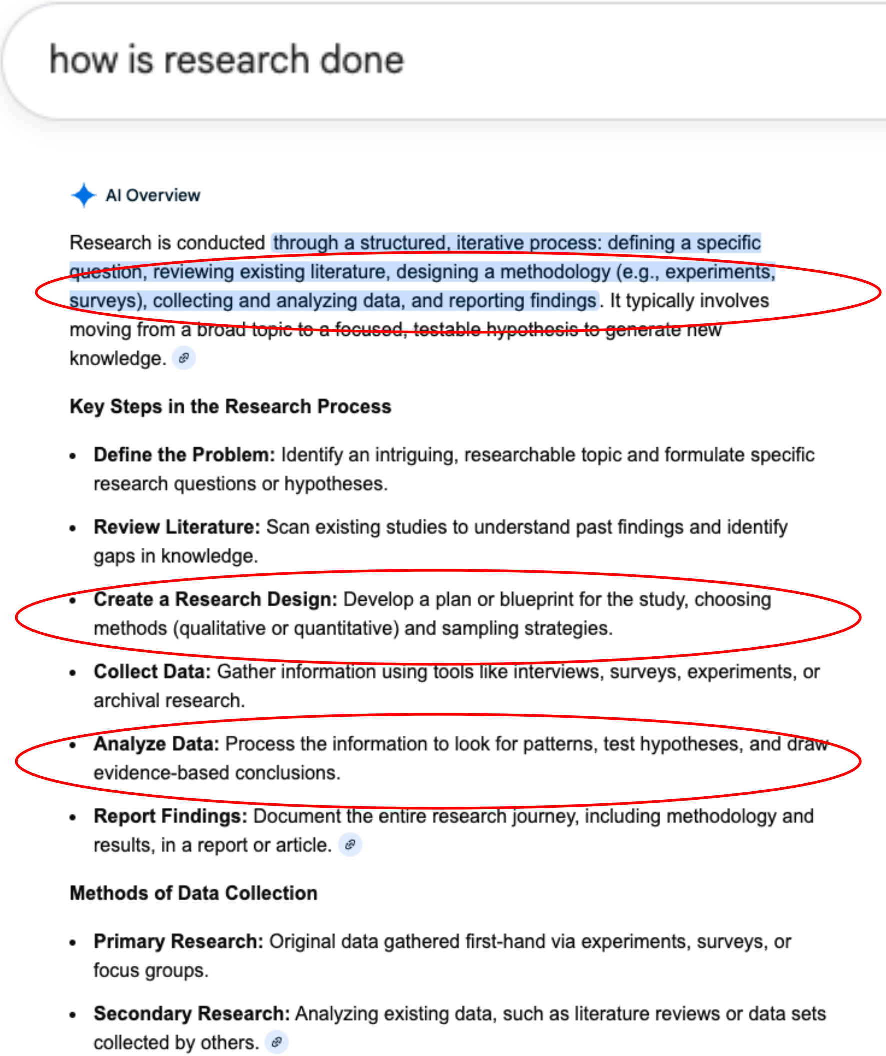
Show Your Working!

The Case for Publishing and Recognizing Research Methods



Emma Ganley, PhD
emma@protocols.io
4th March 2026
OxFOS, University of Oxford

SPRINGER NATURE



how is research done

AI Overview

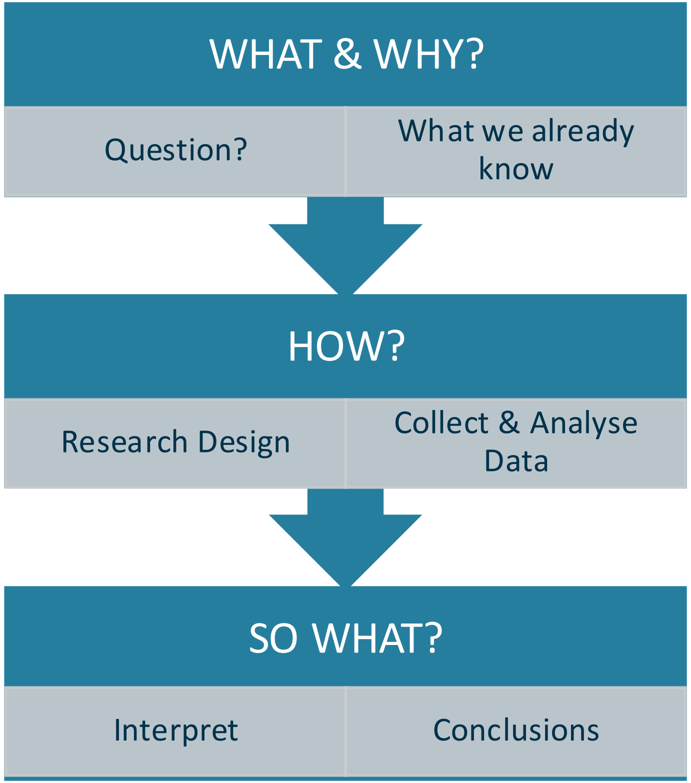
Research is conducted through a structured, iterative process: defining a specific question, reviewing existing literature, designing a methodology (e.g., experiments, surveys), collecting and analyzing data, and reporting findings. It typically involves moving from a broad topic to a focused, testable hypothesis to generate new knowledge.

Key Steps in the Research Process

- **Define the Problem:** Identify an intriguing, researchable topic and formulate specific research questions or hypotheses.
- **Review Literature:** Scan existing studies to understand past findings and identify gaps in knowledge.
- **Create a Research Design:** Develop a plan or blueprint for the study, choosing methods (qualitative or quantitative) and sampling strategies.
- **Collect Data:** Gather information using tools like interviews, surveys, experiments, or archival research.
- **Analyze Data:** Process the information to look for patterns, test hypotheses, and draw evidence-based conclusions.
- **Report Findings:** Document the entire research journey, including methodology and results, in a report or article.

Methods of Data Collection

- **Primary Research:** Original data gathered first-hand via experiments, surveys, or focus groups.
- **Secondary Research:** Analyzing existing data, such as literature reviews or data sets collected by others.



WHAT & WHY?

Question?

What we already know

HOW?

Research Design

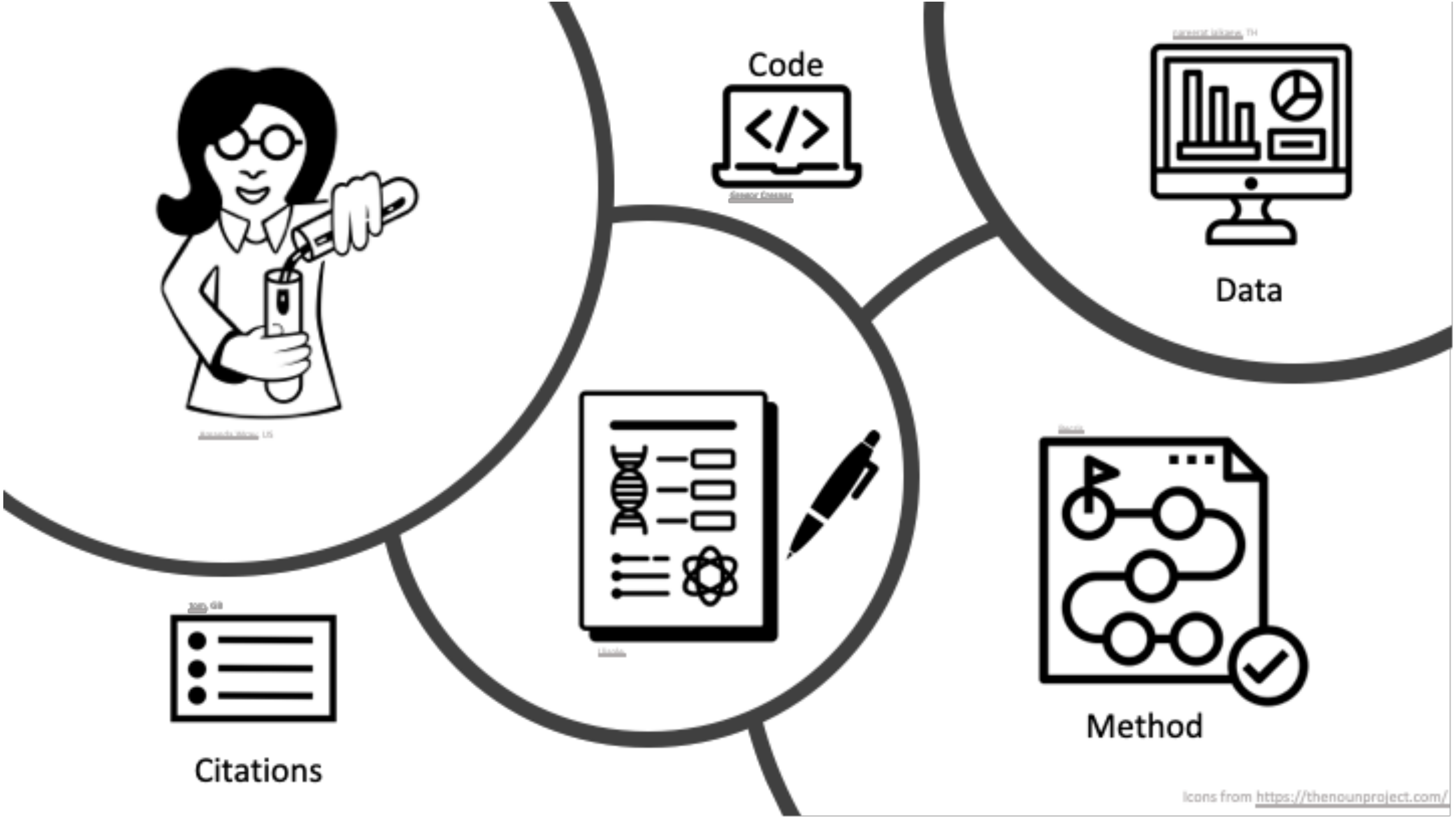
Collect & Analyse Data

SO WHAT?

Interpret

Conclusions

SPRINGER NATURE



Code

Data

Method

Citations

Icons from https://thenounproject.com/

Open Methods – the next frontier in open science

Building on open access publications and FAIR data principles

The open science movement has focused on:

- Open access publications
- Open & FAIR data and code

Data sharing needs methods sharing

- Complete methods are needed to accurately interpret data and results

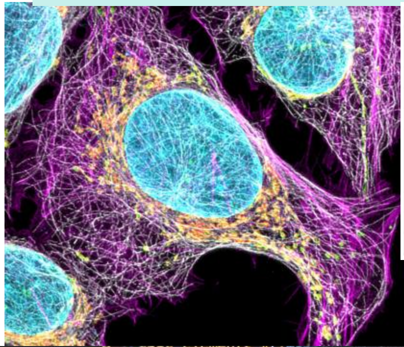
Policy recommendations for methods availability and sharing

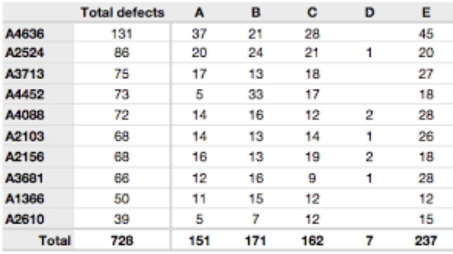
- Promoting Reusable and Open Methods and Protocols (PRO-MaP) from the European Commission
- UNESCO recommendation on Open Science

Results and Data Need Methods

"I THINK YOU SHOULD BE MORE EXPLICIT HERE IN STEP TWO."

"Then a miracle occurs..."





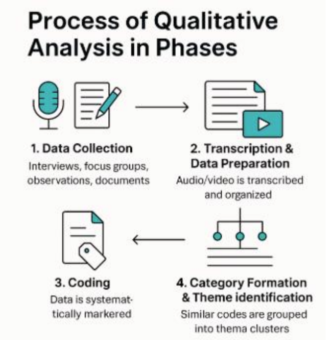
	Total defects	A	B	C	D	E
A4636	131	37	21	28		45
A2524	86	20	24	21	1	20
A3713	75	17	13	18		27
A4452	73	5	33	17		18
A4088	72	14	16	12	2	28
A2103	68	14	13	14	1	26
A2156	68	16	13	19	2	18
A3681	66	12	16	9	1	28
A1366	50	11	15	12		12
A2610	39	5	7	12		15
Total	728	151	171	162	7	237

```
(def config-files ["standalone/configuration/standalone.
                   "standalone/configuration/standalone-
                   "standalone/configuration/standalone-
                   "domain/configuration/domain.xml"])

(defn println-err [& args]
  (binding [*out* *err*]
    (apply println args)))

(defn metadata-url
  "Return the metadata url, but only for full binary dis
  [url]
  (if (.endsWith url "dist-bin.zip")
    (.replaceFirst url "/[^/]*$" "/build-metadata.json")

(defprotocol BinArtifact
```



Process of Qualitative Analysis in Phases

1. Data Collection
Interviews, focus groups, observations, documents

2. Transcription & Data Preparation
Audio/video is transcribed and organized

3. Coding
Data is systematically markered

4. Category Formation & Theme identification
Similar codes are grouped into thema clusters

Daniel Gonzales
@dgonzales1990

2017: “Devices were fabricated as previously described [ref 8]”

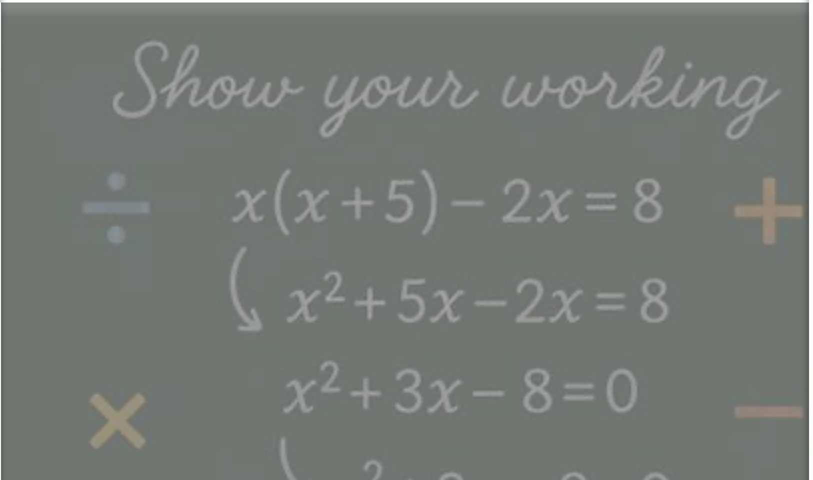
[ref 8] 2015: “Devices were fabricated as previously described [ref 4]”

[ref 4] 2013: “Devices were fabricated as previously described [ref 2]”

[ref 2] 2009: “Devices were fabricated with conventional methods”

13:16 - 17. Jan. 2018

230 Retweets 798 „Gefällt mir“-Angaben



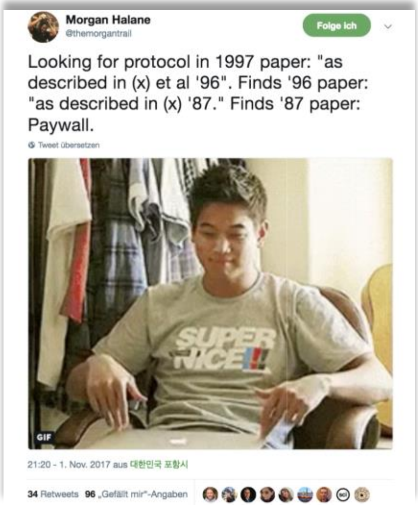
Hagen M. Gegner
@hi_hagen

I am currently reading through so many papers to better understand methods.

"Blabla as described elsewhere" tell me your secrets without Schnitzeljagd! :D

I am really appreciating the methods detailed protocols.io et al. platforms.

9:54 AM · May 4, 2020 from Essen, Germany

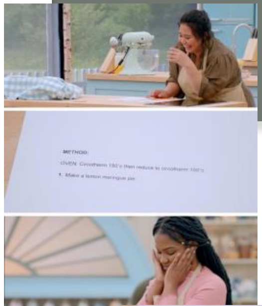


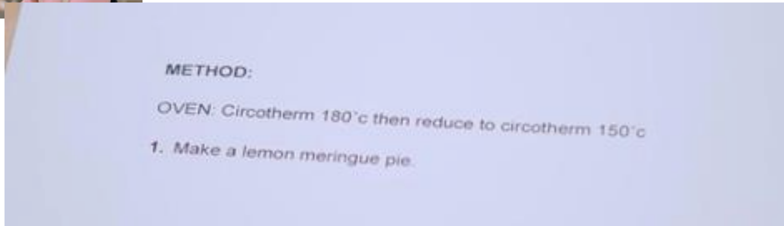
Morgan Halane
@themorgantrail

Looking for protocol in 1997 paper: "as described in (x) et al '96". Finds '96 paper: "as described in (x) '87." Finds '87 paper: Paywall.

21:20 - 1. Nov. 2017 aus 대한민국 포항시

34 Retweets 96 „Gefällt mir“-Angaben





METHOD:

OVEN: Circotherm 180°c then reduce to circotherm 150°c

1. Make a lemon meringue pie.

Dr. Julia Gauberg
@JuliaTheEvoDiva

All I want is to find the original protocol 😢

1:10 AM · May 24, 2022

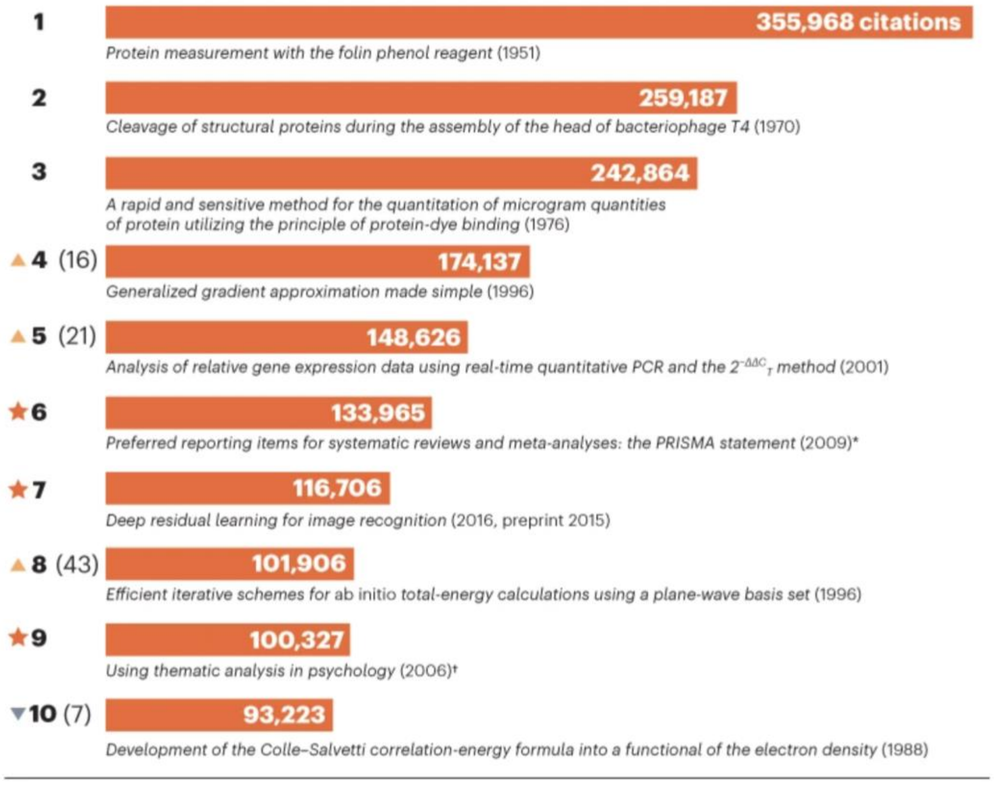
NEWS FEATURE | 15 April 2025 | Clarification 22 April 2025

These are the most-cited research papers of all time

Some studies have received hundreds of thousands of citations, *Nature*'s updated analysis shows.

TOP TEN CITED PAPERS

Just 3 papers have more than 200,000 citations each, according to the Web of Science database. All three cover biological laboratory techniques. This update to a 2014 list of most-cited articles shows that the top three papers remain unchanged. But there have been shifts in the positions of others (triangles), and some additions that were not on the previous list (orange stars). For alternative rankings from two other databases, and a median ranking across all three, see Supplementary information (go.nature.com/425g9dn).



Nature **640**, 591 (2025)
doi: https://doi.org/10.1038/d41586-025-01124-w

protocols.io: Share method details before, during, and after publication

Open Access Repository

Discover and publish detailed scientific protocols

Free to Read

Free to Publish

25 000+ public protocols

Private Collaboration Tool

Private space to securely create, share, and optimise protocols within your team or organisation

88 000+ private protocols

Step-by-step Protocols

Dynamic & Interactive
Update and improve in real-time.

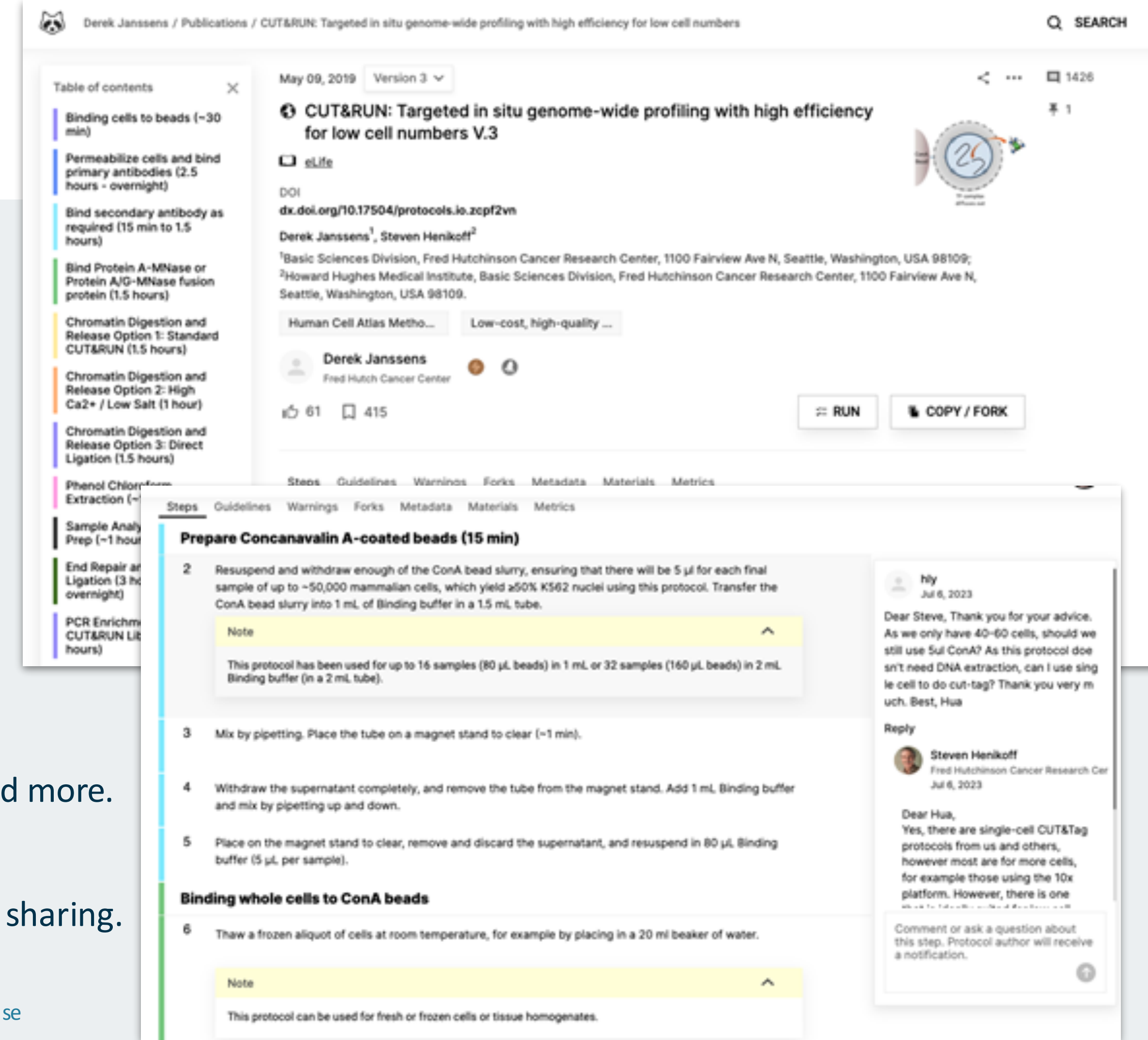
Versioning, Forking & History
Track changes over time.

Collaborative
Concurrent editing & commenting.

Standardized & Searchable
Easy to find and follow.

Multimedia-Enabled
Add videos, images, plate maps, and more.

Private and Secure
Granular permissions and selective sharing.



May 09, 2019

CUT&RUN: Targeted in situ genome-wide profiling with high efficiency for low cell numbers V.3

eLife

DOI
dx.doi.org/10.17504/protocols.io.zcpf2vn

Derek Janssens[1], Steven Henikoff[2]

[1]Basic Sciences Division, Fred Hutchinson Cancer Research Center, 1100 Fairview Ave N, Seattle, Washington, USA 98109; [2]Howard Hughes Medical Institute, Basic Sciences Division, Fred Hutchinson Cancer Research Center, 1100 Fairview Ave N, Seattle, Washington, USA 98109.

Derek Janssens
Fred Hutch Cancer Center

Prepare Concanavalin A-coated beads (15 min)

2 Resuspend and withdraw enough of the ConA bead slurry, ensuring that there will be 5 µl for each final sample of up to ~50,000 mammalian cells, which yield ≥50% K562 nuclei using this protocol. Transfer the ConA bead slurry into 1 mL of Binding buffer in a 1.5 mL tube.

Note
This protocol has been used for up to 16 samples (80 µL beads) in 1 mL or 32 samples (160 µL beads) in 2 mL Binding buffer (in a 2 mL tube).

3 Mix by pipetting. Place the tube on a magnet stand to clear (~1 min).

4 Withdraw the supernatant completely, and remove the tube from the magnet stand. Add 1 mL Binding buffer and mix by pipetting up and down.

5 Place on the magnet stand to clear, remove and discard the supernatant, and resuspend in 80 µL Binding buffer (5 µL per sample).

Binding whole cells to ConA beads

6 Thaw a frozen aliquot of cells at room temperature, for example by placing in a 20 ml beaker of water.

Note
This protocol can be used for fresh or frozen cells or tissue homogenates.

hly
Jul 6, 2023
Dear Steve, Thank you for your advice. As we only have 40-60 cells, should we still use 5ul ConA? As this protocol doesn't need DNA extraction, can I use single cell to do cut-tag? Thank you very much. Best, Hua

Reply

Steven Henikoff
Fred Hutchinson Cancer Research Cer
Jul 6, 2023

Dear Hua,
Yes, there are single-cell CUT&Tag protocols from us and others, however most are for more cells, for example those using the 10x platform. However, there is one

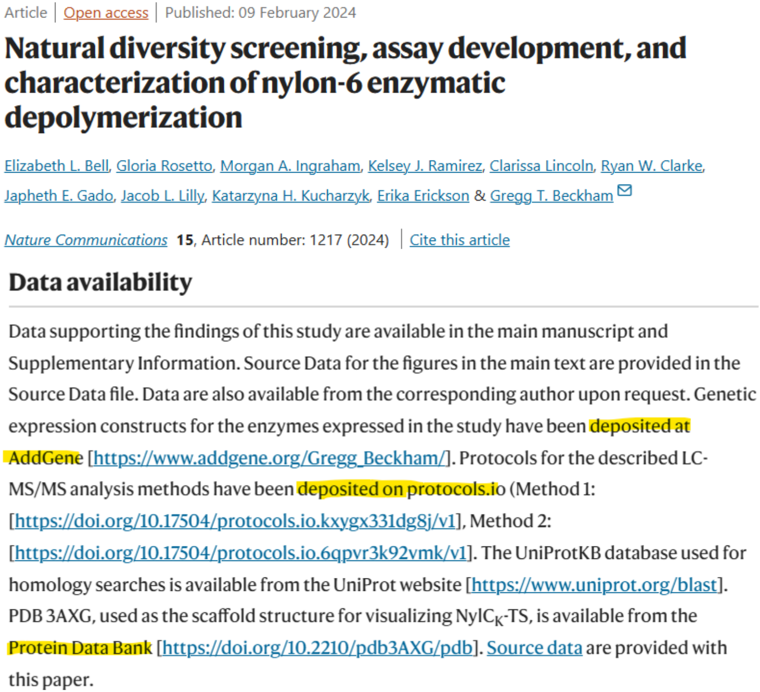
Comment or ask a question about this step. Protocol author will receive a notification.

Version: Updated for same purpose | **Fork**: Adapted for a different purpose

Modular publishing

Publish discrete research outputs

- Expression constructs → AddGene
- Protocols → protocols.io
- Molecular structure → Protein Data Bank



Article | Open access | Published: 09 February 2024

Natural diversity screening, assay development, and characterization of nylon-6 enzymatic depolymerization

Elizabeth L. Bell, Gloria Rosetto, Morgan A. Ingraham, Kelsey J. Ramirez, Clarissa Lincoln, Ryan W. Clarke, Japheth E. Gado, Jacob L. Lilly, Katarzyna H. Kucharzyk, Erika Erickson & Gregg T. Beckham

Nature Communications **15**, Article number: 1217 (2024) | Cite this article

Data availability

Data supporting the findings of this study are available in the main manuscript and Supplementary Information. Source Data for the figures in the main text are provided in the Source Data file. Data are also available from the corresponding author upon request. Genetic expression constructs for the enzymes expressed in the study have been deposited at AddGene [https://www.addgene.org/Gregg_Beckham/]. Protocols for the described LC-MS/MS analysis methods have been deposited on protocols.io (Method 1: [https://doi.org/10.17504/protocols.io.kxygx331dg8j/v1], Method 2: [https://doi.org/10.17504/protocols.io.6qpvr3k92vmk/v1]. The UniProtKB database used for homology searches is available from the UniProt website [https://www.uniprot.org/blast]. PDB 3AXG, used as the scaffold structure for visualizing NylC$_K$-TS, is available from the Protein Data Bank [https://doi.org/10.2210/pdb3AXG/pdb]. Source data are provided with this paper.

Citations to protocols appear in:

- Data Availability Statements
- Materials & Methods section of paper
- Reference list

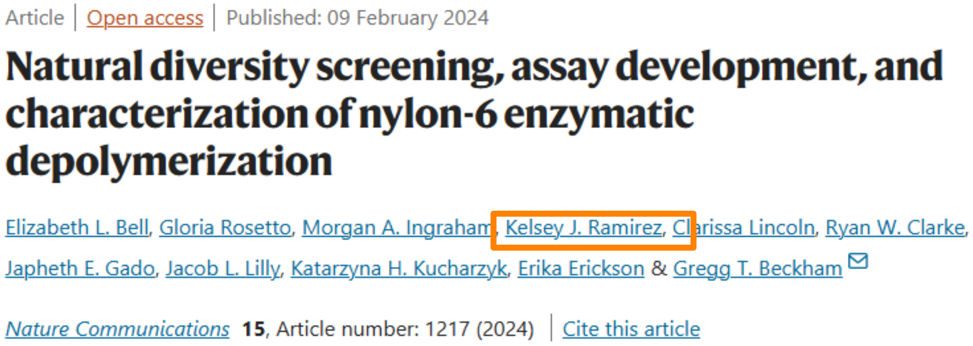
SPRINGER NATURE

https://doi.org/10.1038/s41467-024-45523-5

Author Credit for Method Development

Paper vs protocol - Separate research outputs with distinct author lists

Paper



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Protocol

Jan 07, 2024 Version 1

Analysis of products from deconstructed nylon-6 by UHPLC-MS/MS (dMRM) V.1

Nature Communications

DOI

dx.doi.org/10.17504/protocols.io.kxygx331dg8j/v1

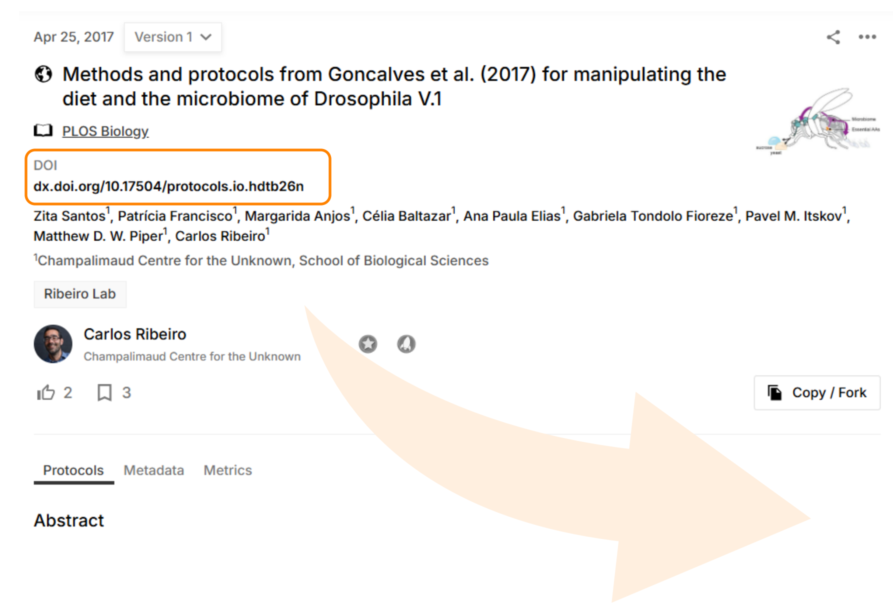
Kelsey J. Ramirez[1,2], Morgan A. Ingraham[1,2], Elizabeth L. Bell[1,2], Gregg T. Beckham[1,2]

[1]Renewable Resources and Enabling Sciences Center, National Renewable Energy Laboratory, Golden, CO, USA;

[2]BOTTLE Consortium, Golden, CO, USA

Publish detailed methods on protocols.io

Link protocols (or a collection of protocols) in your materials and methods section



Apr 25, 2017

Methods and protocols from Goncalves et al. (2017) for manipulating the diet and the microbiome of Drosophila V.1

PLOS Biology

DOI
dx.doi.org/10.17504/protocols.io.hdtb26n

Zita Santos[1], Patrícia Francisco[1], Margarida Anjos[1], Célia Baltazar[1], Ana Paula Elias[1], Gabriela Tondolo Fioreze[1], Pavel M. Itskov[1], Matthew D. W. Piper[1], Carlos Ribeiro[1]

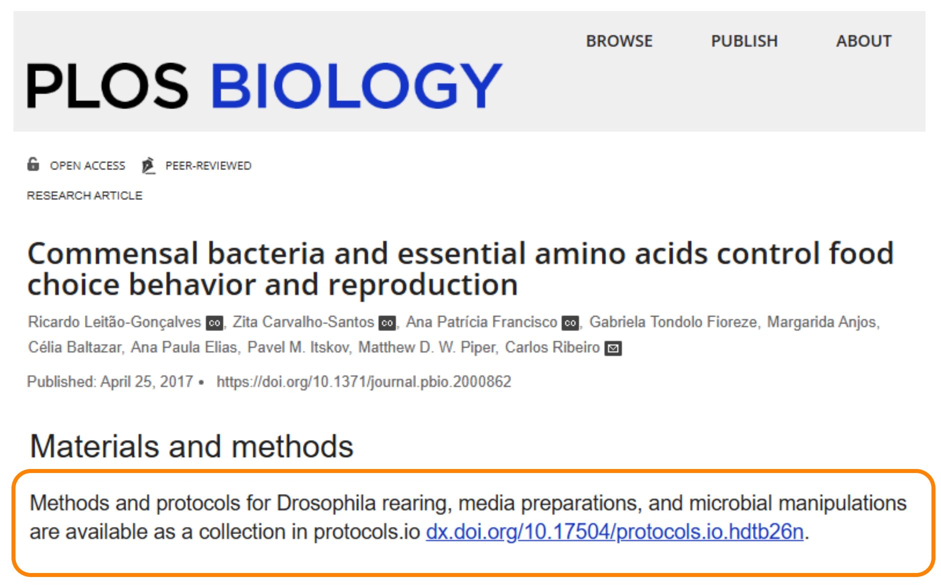
[1]Champalimaud Centre for the Unknown, School of Biological Sciences

Ribeiro Lab

Carlos Ribeiro
Champalimaud Centre for the Unknown

2 3

Abstract



PLOS BIOLOGY

OPEN ACCESS PEER-REVIEWED

RESEARCH ARTICLE

Commensal bacteria and essential amino acids control food choice behavior and reproduction

Ricardo Leitão-Gonçalves, Zita Carvalho-Santos, Ana Patrícia Francisco, Gabriela Tondolo Fioreze, Margarida Anjos, Célia Baltazar, Ana Paula Elias, Pavel M. Itskov, Matthew D. W. Piper, Carlos Ribeiro

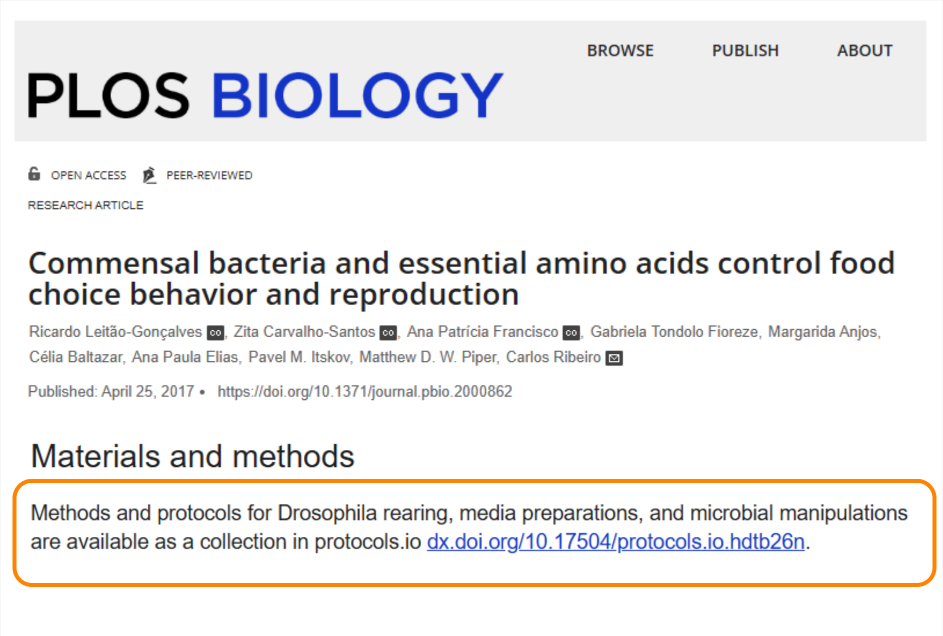
Published: April 25, 2017 • https://doi.org/10.1371/journal.pbio.2000862

Materials and methods

Methods and protocols for Drosophila rearing, media preparations, and microbial manipulations are available as a collection in protocols.io dx.doi.org/10.17504/protocols.io.hdtb26n.

Publishing – dynamic permanence

Viewers notified new version avaliable when following link from publication



RESEARCH ARTICLE

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Published: April 25, 2017 • https://doi.org/10.1371/journal.pbio.2000862

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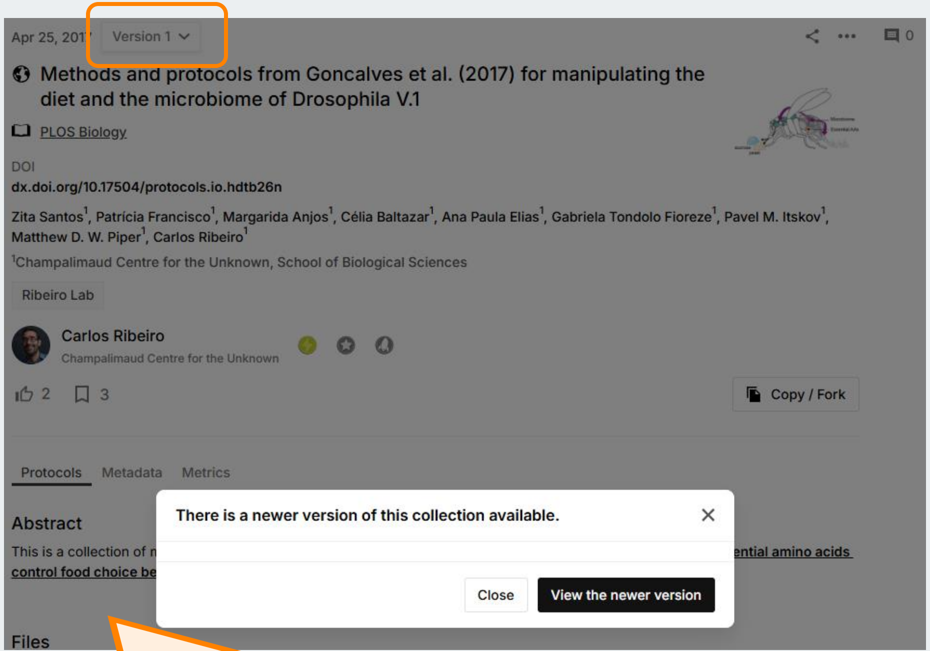

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[1]Champalimaud Centre for the Unknown, School of Biological Sciences

Ribeiro Lab

Carlos Ribeiro
Champalimaud Centre for the Unknown

Abstract

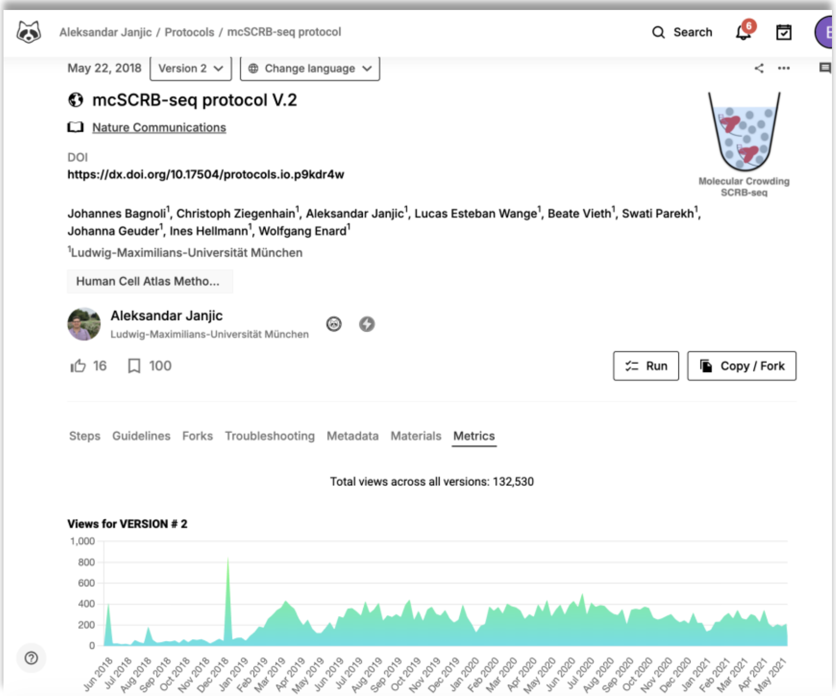
This is a collection of r
ential amino acids
control food choice be

Files

There is a newer version of this collection available.

Metrics on protocols.io

Easily trackable reuse of protocols



mcSCRB-seq protocol V.2

Nature Communications

DOI
https://dx.doi.org/10.17504/protocols.io.p9kdr4w

Johannes Bagnoli[1], Christoph Ziegenhain[1], Aleksandar Janjic[1], Lucas Esteban Wange[1], Beate Vieth[1], Swati Parekh[1], Johanna Geuder[1], Ines Hellmann[1], Wolfgang Enard[1]

[1]Ludwig-Maximilians-Universität München

Human Cell Atlas Metho...

Aleksandar Janjic
Ludwig-Maximilians-Universität München

16 100

Total views across all versions: 132,530

Views for VERSION # 2

nature > nature communications > articles > article

Article | Open access | Published: 26 July 2018

Sensitive and powerful single-cell RNA sequencing using mcSCRB-seq

Johannes W. Bagnoli, Christoph Ziegenhain, Aleksandar Janjic, Lucas E. Wange, Beate Vieth, Swati Parekh, Johanna Geuder, Ines Hellmann & Wolfgang Enard

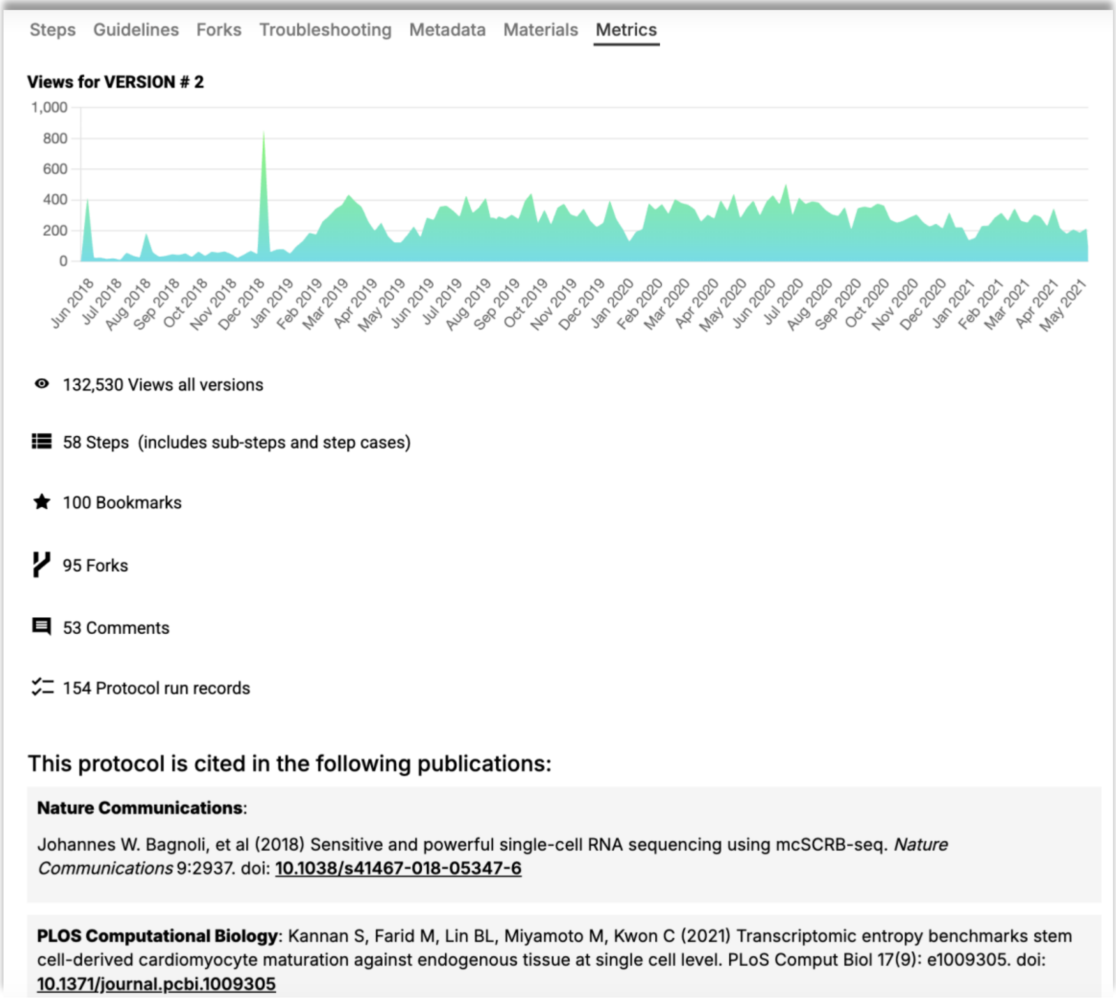
Nature Communications **9**, Article number: 2937 (2018)

44k Accesses | **256** Citations | **87** Altmetric

>132,000 views across all versions

>44,000 Accesses

https://www.protocols.io/view/mcscrb-seq-protocol-5qpvo4d7g4o1/v2
https://www.nature.com/articles/s41467-018-05347-6



132,530 Views all versions

58 Steps (includes sub-steps and step cases)

100 Bookmarks

95 Forks

53 Comments

154 Protocol run records

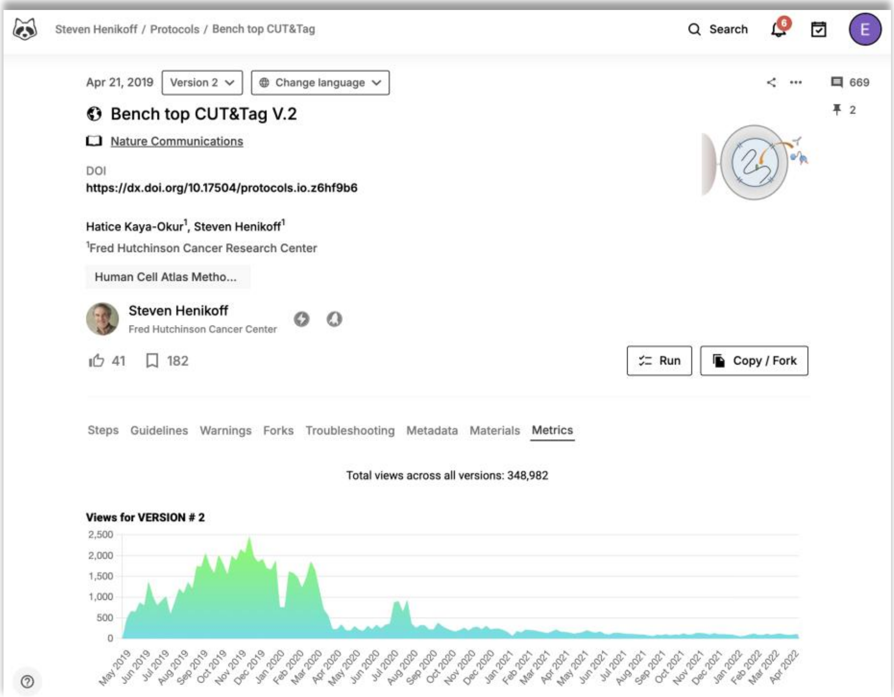
This protocol is cited in the following publications:

Nature Communications:

Johannes W. Bagnoli, et al (2018) Sensitive and powerful single-cell RNA sequencing using mcSCRB-seq. *Nature Communications* 9:2937. doi: 10.1038/s41467-018-05347-6

PLOS Computational Biology: Kannan S, Farid M, Lin BL, Miyamoto M, Kwon C (2021) Transcriptomic entropy benchmarks stem cell-derived cardiomyocyte maturation against endogenous tissue at single cell level. PLoS Comput Biol 17(9): e1009305. doi: 10.1371/journal.pcbi.1009305

Value of step-by-step method



Apr 21, 2019

Bench top CUT&Tag V.2

Nature Communications

DOI
https://dx.doi.org/10.17504/protocols.io.z6hf9b6

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Human Cell Atlas Metho...

Steven Henikoff
Fred Hutchinson Cancer Center

41 182

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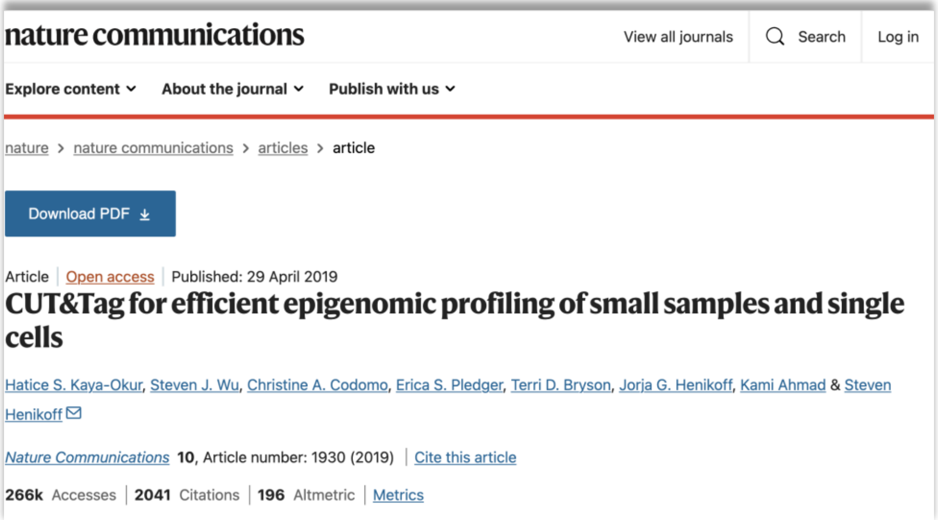

nature > nature communications > articles > article

Article | Open access | Published: 29 April 2019

CUT&Tag for efficient epigenomic profiling of small samples and single cells

Hatice S. Kaya-Okur, Steven J. Wu, Christine A. Codomo, Erica S. Pledger, Terri D. Bryson, Jorja G. Henikoff, Kami Ahmad & Steven Henikoff

Nature Communications **10**, Article number: 1930 (2019) | Cite this article

266k Accesses | **2041** Citations | **196** Altmetric | Metrics

>348,000 views across all versions

>266,000 Accesses

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	Indexed with a persistent identifier	Defined conditions for access	Linked to other data, use common vocabulary	Clear usage licenses and provenance
protocols.io Part of SPRINGER NATURE	Indexed on google scholar	CC-BY License	Open API Integrations (ELNs & Data Locations)	Versioning Forking Running

Enhancing your profile with protocol publications

Visibility and opportunities for early career researchers

Dr Jacopo Cerasoni
Post Doc, Loyola University Chicago

"Although my PhD was specific to a time period in a region, I managed to add this methodological aspect that sort of went past those boundaries."

"Another really good thing that I think this protocol has done for my career is the recognition it gave me.

I was lucky enough to have been invited to lectures and practical sessions at various universities."

Q&A

protocols.io

Unlocking CRyPTIC: How can a big, open dataset help fight the world's most deadly infectious disease?

Jeremy Westhead

UNIVERSITY OF OXFORD

MODERNISING
MEDICAL
MICROBIOLOGY

Gates Foundation

CRyPTIC

wellcome

Tuberculosis kills more than any other infectious disease

https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(24)00158-0

Mycobacterium Tuberculosis

https://www.who.int/teams/global-programme-on-tuberculosis-and-lung-health/tb-reports/global-tuberculosis-report-2024/tb-disease-burden/1-1-tb-incidence

Treatment

- First randomised clinical trial
  - Evaluating Streptomycin for treatment of pulmonary TB
  - 1946
- Many more antibiotics now available
  - WHO lists 15 antibiotics for current/past treatment
- Resistance is growing

Drug resistance

- Drug susceptible TB (DS-TB)
- Multi-drug resistant TB (MDR-TB)
  - Rifampicin and Isoniazid resistant
- Pre-extensively drug resistant TB (Pre-XDR-TB)
  - MDR-TB
  - Resistant to at least one of Moxifloxacin and Levofloxacin
- Extensively-drug resistant TB (XDR-TB)
  - Pre-XDR-TB
  - Resistant to at least one of Bedaquiline and Linezolid

Detecting drug resistance (laboratory)

- Grow a culture from a patient
  - Weeks from sample
- Visually see Mycobacteria through a microscope
- Drug susceptibility testing (DST)
  - Attempt to grow the culture in various dilutions of various drugs
  - Requires a second growth time-frame

Detecting drug resistance (genetics)

- Grow a culture from a patient
- Whole genome sequence (WGS) the sample
- Ensure that the sample is Mycobacterium Tuberculosis
- Assemble a genome
- Look for mutations associated with resistance to drugs
    - Requires a large dataset of both genotypes and phenotypes

Comprehensive Resistance Prediction for Tuberculosis: an International Consortium (CRyPTIC)

- Project ran from 2016-2021
- Collecting both genotypes and phenotypes from clinical patients worldwide
- The aim was to achieve sufficiently accurate genetic prediction of resistance to most anti-TB drugs to allow WGS to replace culture-based DST

CRyPTIC datasets

- Initial dataset was the largest ever global study of TB at the time
  - 15,211 sample from 27 countries on 5 continents
- Since the project end, additional samples have been received
- Latest release contains 53,897 samples with genotypes and at least one DST
- Licensed under the CC-BY 4.0 license
  - Freedom to use the dataset (including commercial) provided the author is credited

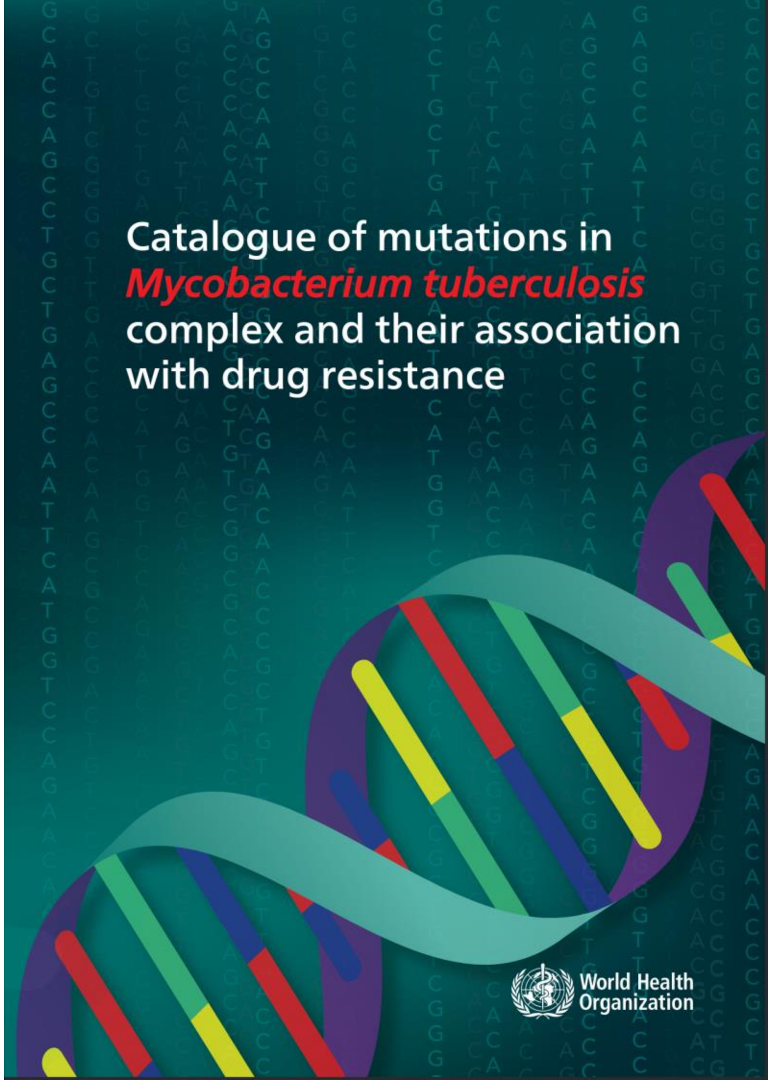
https://crypticproject.info/datasets/

CRyPTIC dataset publication

- Results tables published to Zenodo
    - High-level mutations
    - DST phenotypes
- Raw genetic data published to the European Nucleotide Archive (ENA)
    - De-facto standard for publication of genetic data
    - ENA identifiers are included in results table to enable linking

Dataset uses

- Initial dataset contributed towards the WHO *Catalogue of mutations in Mycobacterium tuberculosis complex and their association with drug resistance*
- Utilised genotypic and phenotypic results, as well as expert clinical knowledge to link mutations to drug resistance



Catalogue of mutations in *Mycobacterium tuberculosis* complex and their association with drug resistance

World Health Organization

Dataset uses

- Recent dataset was used to automate this process, producing a comparable catalogue without the addition of clinical input

Rapidly and reproducibly building a comprehensive catalogue of resistance-associated variants for *M. tuberculosis*

Dylan Adlard[1], Kerri M Malone[2], Jeremy Westhead[1], Martin Hunt[1,2], Hieu Thai[1], Matthew Colpus[1], Robert D Turner[1], Shaheed V Omar[3], David W Eyre[1,4,5], Nazir Ismail[6], Timothy M Walker[1], Timothy EA Peto[1,4,5], Derrick W Crook[1,4,5], Zamin Iqbal[2,7], and Philip W Fowler*[1,4,5]

[1]Nuffield Department of Medicine, John Radcliffe Hospital, University of Oxford, Headley Way, Oxford, U.K.

[2]European Bioinformatics Institute, Cambridge, UK

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[4]Health Protection Research Unit in Healthcare Associated Infections and Antimicrobial Resistance, University of Oxford, Oxford, U.K.

[5]National Institute of Health Research Oxford Biomedical Research Centre, John Radcliffe Hospital, Headley Way, Oxford, UK

[6]Department of Clinical Microbiology and Infectious Diseases, University of the Witwatersrand, Johannesburg, South Africa

[7]Milner Centre for Evolution, University of Bath, UK

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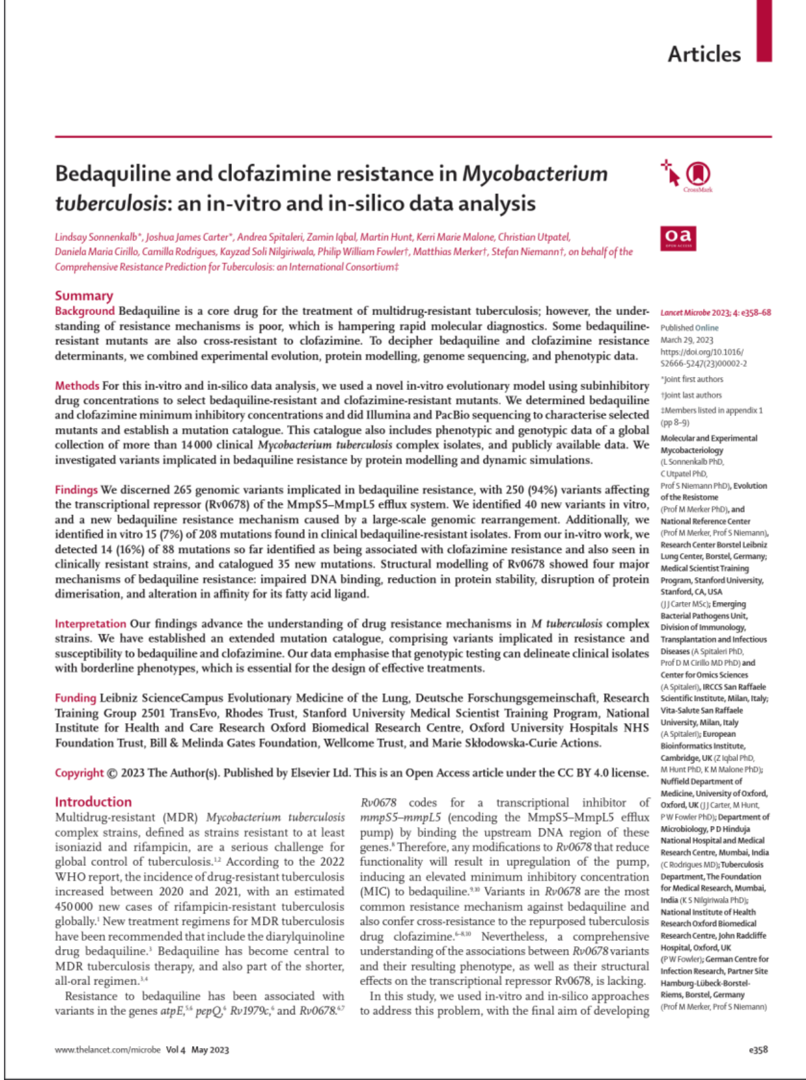
*To whom correspondence should be addressed: philip.fowler@ndm.ox.ac.uk, @philipwfowler.bsky.social

Dataset uses

- Enhancing the understanding of mechanisms behind resistance to new drugs



Bedaquiline and clofazimine resistance in *Mycobacterium tuberculosis*: an in-vitro and in-silico data analysis

Lindsay Sonnenkalb, Joshua James Carter*, Andrea Spitaleri, Zamin Iqbal, Martin Hunt, Kerri Marie Malone, Christian Utpatel, Daniela Maria Cirillo, Camilla Rodrigues, Kayzad Soli Nilgiriwala, Philip William Fowler†, Matthias Merker†, Stefan Niemann†, on behalf of the Comprehensive Resistance Prediction for Tuberculosis: an International Consortium‡*

Summary

Background Bedaquiline is a core drug for the treatment of multidrug-resistant tuberculosis; however, the understanding of resistance mechanisms is poor, which is hampering rapid molecular diagnostics. Some bedaquiline-resistant mutants are also cross-resistant to clofazimine. To decipher bedaquiline and clofazimine resistance determinants, we combined experimental evolution, protein modelling, genome sequencing, and phenotypic data.

Methods For this in-vitro and in-silico data analysis, we used a novel in-vitro evolutionary model using subinhibitory drug concentrations to select bedaquiline-resistant and clofazimine-resistant mutants. We determined bedaquiline and clofazimine minimum inhibitory concentrations and did Illumina and PacBio sequencing to characterise selected mutants and establish a mutation catalogue. This catalogue also includes phenotypic and genotypic data of a global collection of more than 14 000 clinical *Mycobacterium tuberculosis* complex isolates, and publicly available data. We investigated variants implicated in bedaquiline resistance by protein modelling and dynamic simulations.

Findings We discerned 265 genomic variants implicated in bedaquiline resistance, with 250 (94%) variants affecting the transcriptional repressor (Rv0678) of the MmpS5–MmpL5 efflux system. We identified 40 new variants in vitro, and a new bedaquiline resistance mechanism caused by a large-scale genomic rearrangement. Additionally, we identified in vitro 15 (7%) of 208 mutations found in clinical bedaquiline-resistant isolates. From our in-vitro work, we detected 14 (16%) of 88 mutations so far identified as being associated with clofazimine resistance and also seen in clinically resistant strains, and catalogued 35 new mutations. Structural modelling of Rv0678 showed four major mechanisms of bedaquiline resistance: impaired DNA binding, reduction in protein stability, disruption of protein dimerisation, and alteration in affinity for its fatty acid ligand.

Interpretation Our findings advance the understanding of drug resistance mechanisms in *M tuberculosis* complex strains. We have established an extended mutation catalogue, comprising variants implicated in resistance and susceptibility to bedaquiline and clofazimine. Our data emphasise that genotypic testing can delineate clinical isolates with borderline phenotypes, which is essential for the design of effective treatments.

Funding Leibniz ScienceCampus Evolutionary Medicine of the Lung, Deutsche Forschungsgemeinschaft, Research Training Group 2501 TransEvo, Rhodes Trust, Stanford University Medical Scientist Training Program, National Institute for Health and Care Research Oxford Biomedical Research Centre, Oxford University Hospitals NHS Foundation Trust, Bill & Melinda Gates Foundation, Wellcome Trust, and Marie Skłodowska-Curie Actions.

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†Joint last authors

‡Members listed in appendix 1 (pp 8–9)

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Introduction

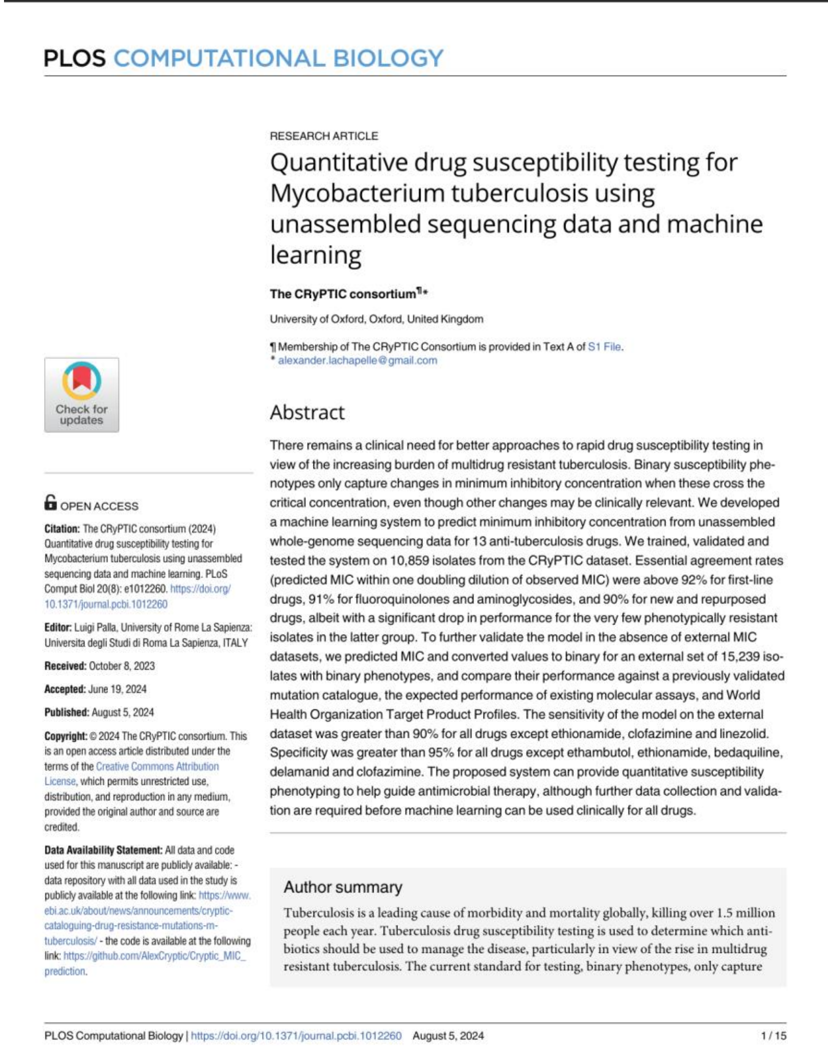
Multidrug-resistant (MDR) *Mycobacterium tuberculosis* complex strains, defined as strains resistant to at least isoniazid and rifampicin, are a serious challenge for global control of tuberculosis.[1,2] According to the 2022 WHO report, the incidence of drug-resistant tuberculosis increased between 2020 and 2021, with an estimated 450 000 new cases of rifampicin-resistant tuberculosis globally.[1] New treatment regimens for MDR tuberculosis have been recommended that include the diarylquinoline drug bedaquiline.[3] Bedaquiline has become central to MDR tuberculosis therapy, and also part of the shorter, all-oral regimen.[3,4]

Resistance to bedaquiline has been associated with variants in the genes *atpE*,[5,6] *pepQ*,[6] *Rv1979c*,[6] and *Rv0678*.[6,7] *Rv0678* codes for a transcriptional inhibitor of *mmpS5–mmpL5* (encoding the MmpS5–MmpL5 efflux pump) by binding the upstream DNA region of these genes.[8] Therefore, any modifications to *Rv0678* that reduce functionality will result in upregulation of the pump, inducing an elevated minimum inhibitory concentration (MIC) to bedaquiline.[9,10] Variants in *Rv0678* are the most common resistance mechanism against bedaquiline and also confer cross-resistance to the repurposed tuberculosis drug clofazimine.[6–8,10] Nevertheless, a comprehensive understanding of the associations between *Rv0678* variants and their resulting phenotype, as well as their structural effects on the transcriptional repressor Rv0678, is lacking.

In this study, we used in-vitro and in-silico approaches to address this problem, with the final aim of developing

Dataset uses

- Applying machine learning to enable DST prediction without full genome assembly



PLOS COMPUTATIONAL BIOLOGY

RESEARCH ARTICLE

Quantitative drug susceptibility testing for Mycobacterium tuberculosis using unassembled sequencing data and machine learning

The CRyPTIC consortium¶*

University of Oxford, Oxford, United Kingdom

¶ Membership of The CRyPTIC Consortium is provided in Text A of S1 File.
* alexander.lachapelle@gmail.com

Check for updates

OPEN ACCESS

Citation: The CRyPTIC consortium (2024) Quantitative drug susceptibility testing for Mycobacterium tuberculosis using unassembled sequencing data and machine learning. PLoS Comput Biol 20(8): e1012260. https://doi.org/10.1371/journal.pcbi.1012260

Editor: Luigi Palla, University of Rome La Sapienza: Universita degli Studi di Roma La Sapienza, ITALY

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Data Availability Statement: All data and code used for this manuscript are publicly available: - data repository with all data used in the study is publicly available at the following link: https://www.ebi.ac.uk/about/news/announcements/cryptic-cataloguing-drug-resistance-mutations-m-tuberculosis/ - the code is available at the following link: https://github.com/AlexCryptic/Cryptic_MIC_prediction.

Abstract

There remains a clinical need for better approaches to rapid drug susceptibility testing in view of the increasing burden of multidrug resistant tuberculosis. Binary susceptibility phenotypes only capture changes in minimum inhibitory concentration when these cross the critical concentration, even though other changes may be clinically relevant. We developed a machine learning system to predict minimum inhibitory concentration from unassembled whole-genome sequencing data for 13 anti-tuberculosis drugs. We trained, validated and tested the system on 10,859 isolates from the CRyPTIC dataset. Essential agreement rates (predicted MIC within one doubling dilution of observed MIC) were above 92% for first-line drugs, 91% for fluoroquinolones and aminoglycosides, and 90% for new and repurposed drugs, albeit with a significant drop in performance for the very few phenotypically resistant isolates in the latter group. To further validate the model in the absence of external MIC datasets, we predicted MIC and converted values to binary for an external set of 15,239 isolates with binary phenotypes, and compare their performance against a previously validated mutation catalogue, the expected performance of existing molecular assays, and World Health Organization Target Product Profiles. The sensitivity of the model on the external dataset was greater than 90% for all drugs except ethionamide, clofazimine and linezolid. Specificity was greater than 95% for all drugs except ethambutol, ethionamide, bedaquiline, delamanid and clofazimine. The proposed system can provide quantitative susceptibility phenotyping to help guide antimicrobial therapy, although further data collection and validation are required before machine learning can be used clinically for all drugs.

Author summary

Tuberculosis is a leading cause of morbidity and mortality globally, killing over 1.5 million people each year. Tuberculosis drug susceptibility testing is used to determine which antibiotics should be used to manage the disease, particularly in view of the rise in multidrug resistant tuberculosis. The current standard for testing, binary phenotypes, only capture

Thanks

- The CRyPTIC consortium
- Wellcome Trust
- MRC Newton Fund
- Bill & Melinda Gates Foundation

Base4NFDI

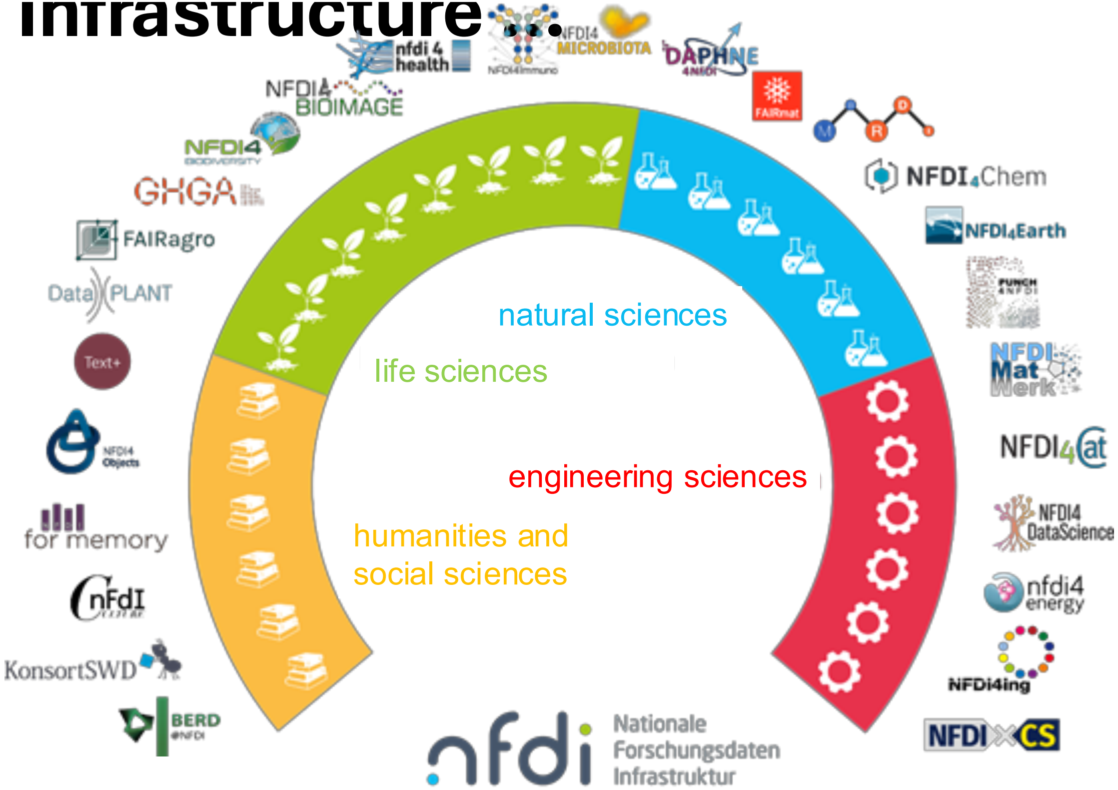
Growing Interoperable RDM Basic Services Across Domains

Najla Rettberg

March 4 2026 Oxford Forum for Open Scholarship

Funded by **DFG** as part of **NFDI**. Grant Numbers: 521453681, 521460392, 521462155, 521463400, 521466146, 521471126, 521473512, 521474032, 521475185, 521476232

NFDI: The German National Research Data Infrastructure …



→ 2018: 10-yr funding: 90 mi/pa

→26 discipline-specific consortia providing RDM services

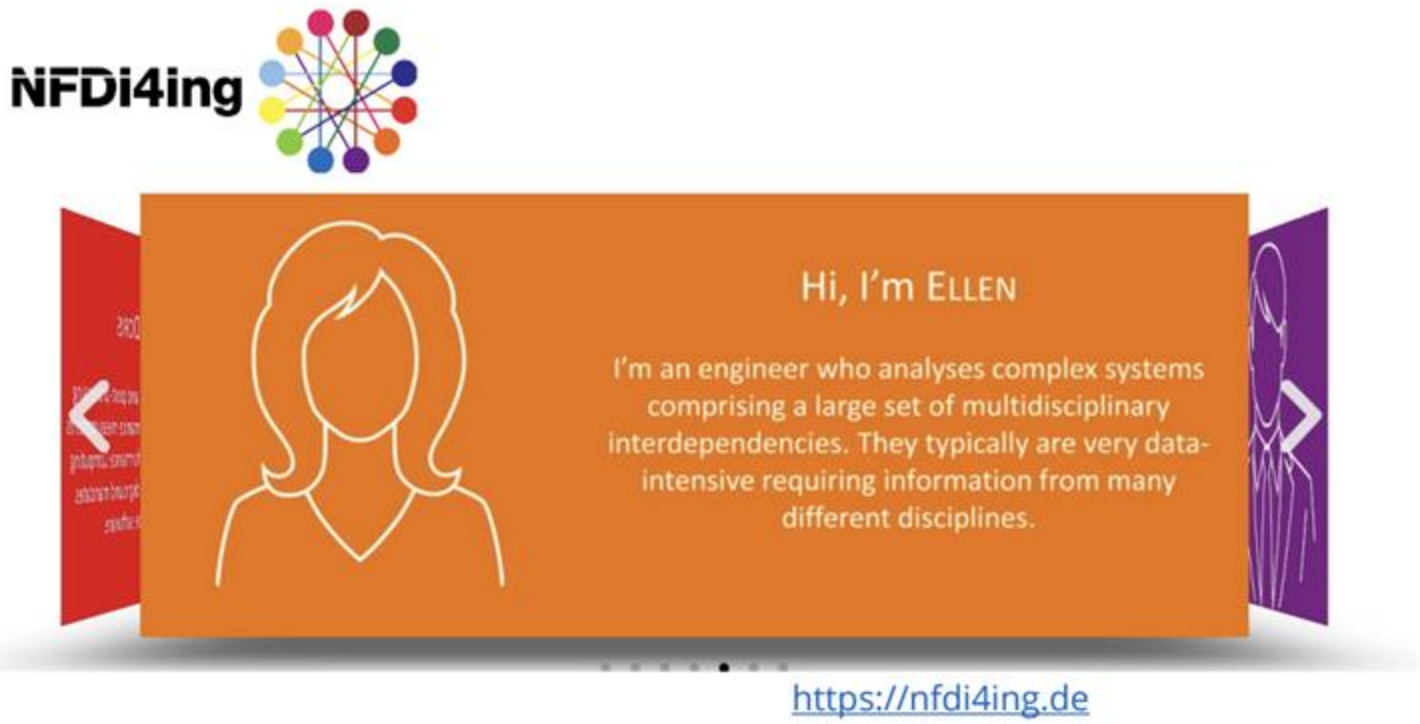
Data as a common good for excellent research, organised by the scientific community in Germany.

Snapshot from today‘s NFDI landscape

NFDI4Chem

https://www.nfdi4chem.de

Snapshot from today‘s NFDI landscape



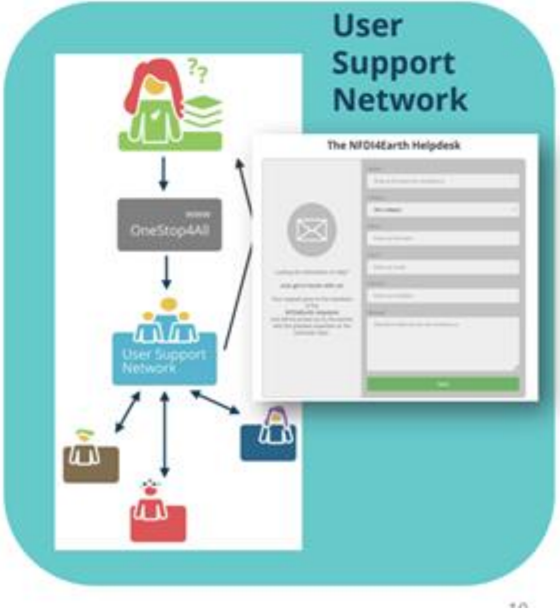
NFDi4ing

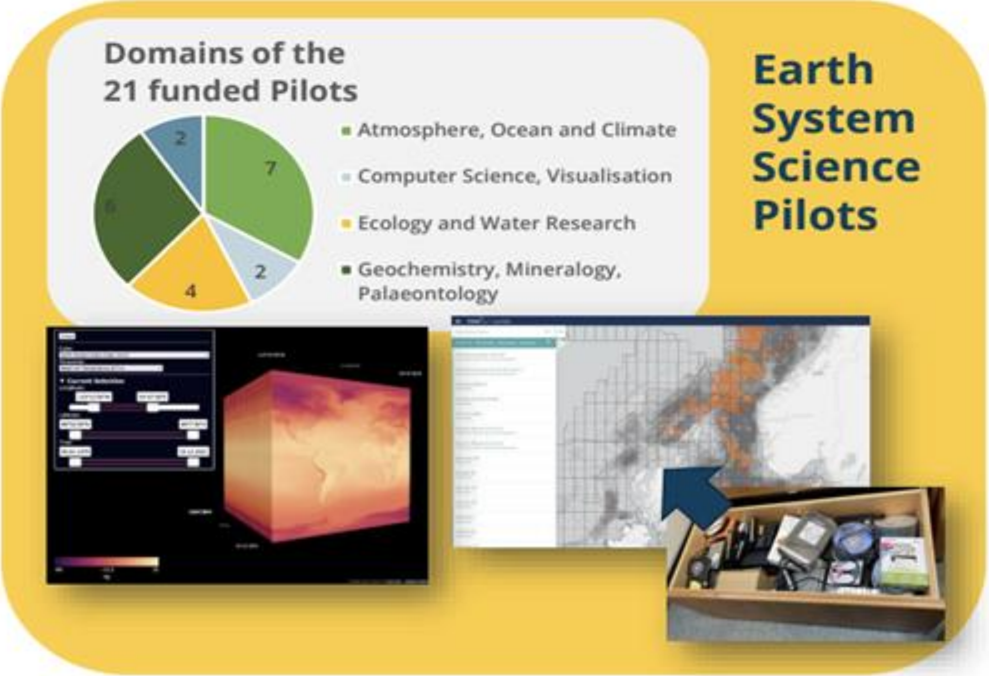
Hi, I’m Ellen

I’m an engineer who analyses complex systems comprising a large set of multidisciplinary interdependencies. They typically are very data-intensive requiring information from many different disciplines.

https://nfdi4ing.de

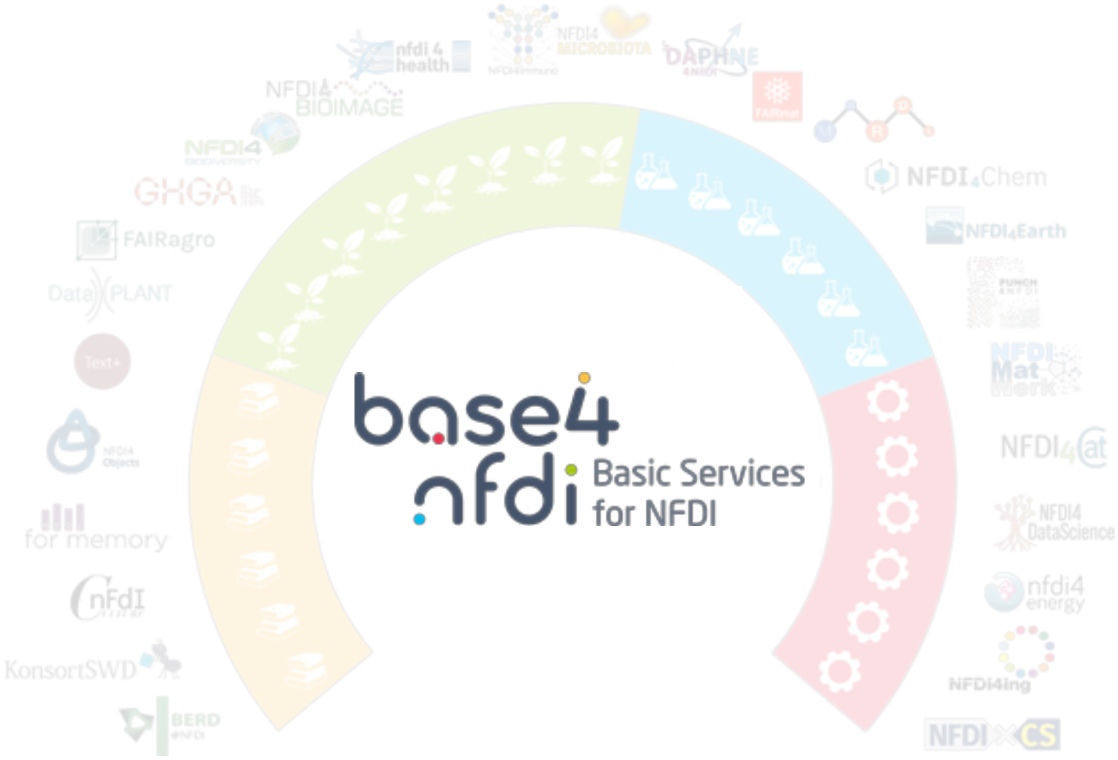
Snapshot from today‘s NFDI landscape





https://www.nfdi4earth.de

Building ‘horizontal’ services



Base4NFDI integrates infrastructure and establishes **cross-disciplinary services as common, interoperable solutions.**

NFDI Basic Services under development

IAM4nfdi
Identity and Access Management
for the German National Research
Data Infrastructure

TS4nfdi
Terminology Services
for the German National Research
Data Infrastructure

PID4nfdi
Persistent Identifier Services
for the German National Research
Data Infrastructure

Jupyter®4nfdi
A central JupyterHub
for the German National Research
Data Infrastructure

DMP4nfdi
Data Management Plans
for the German National Research
Data Infrastructure

RDMT4nfdi
Research Data Management Training
for the German National Research
Data Infrastructure

KGI4nfdi
Knowledge Graph Infrastructure
for the German National Research
Data Infrastructure

nfdi.software
A Research Software Marketplace
for the German National Research
Data Infrastructure

ACCT4nfdi
Accounting Infrastructures
for the German National Research
Data Infrastructure

… further Basic Services to follow!

https://base4nfdi.de/

Developing Services Researchers actually want

The Community ‘vote’ on the services

“Synergy effects can be expected through interdisciplinary cooperation.” (Biodiversity)

“A central service connected to IAM4NFDI will be very important to us.” (Cultural heritage)

“We are unsure if this tool will succeed in having broad community acceptance in the future.” (Material sciences)

Step by Step integration across disciplines

DMP4NFDI incubator dashboard

Dashboards provide:

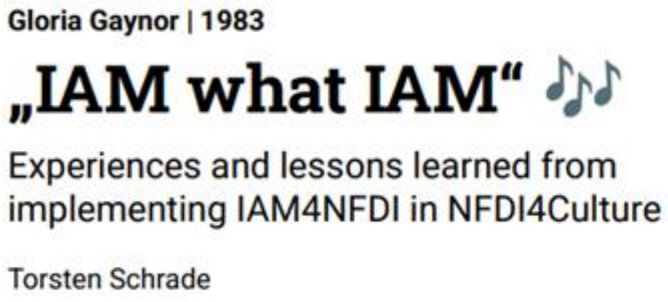
- Transparency of progress
- Visibility of use cases
- Ev ption

https://dmp.services.base4nfdi.de/incubator/

The IAM4NFDI Incubator aims to develop, foster and mature new ideas in the field of identity and access management. The incubator will investigate new technologies that currently have no place (yet) in the services ecosystem of the IAM4NFDI project. This may include to test and experiment with potential new features for existing CAAI solutions. You can find more information about IAM4NFDI in our documentation.

Coscine is an open-source platform for research data management (RDM) and can be used by all researchers of every

Incubators: Sharing success stories



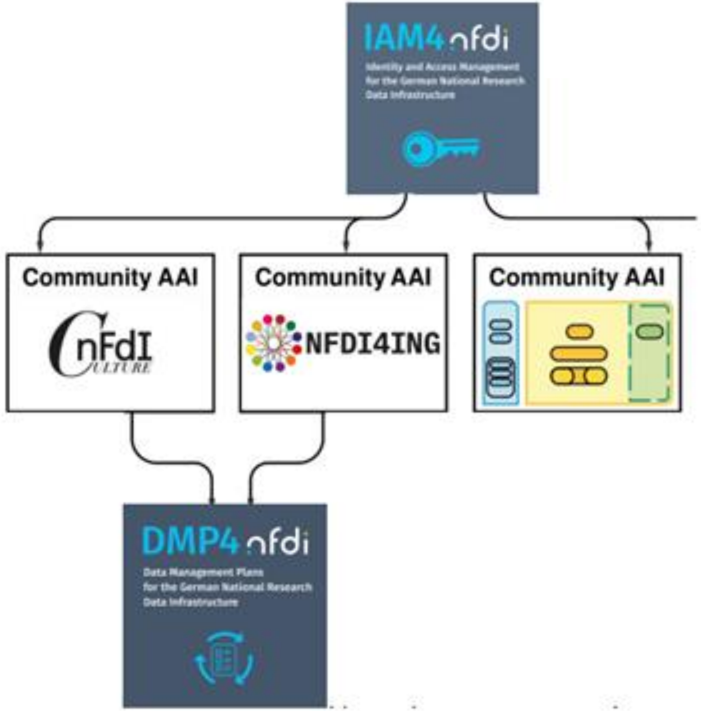
Gloria Gaynor | 1983

„IAM what IAM“ 🎶

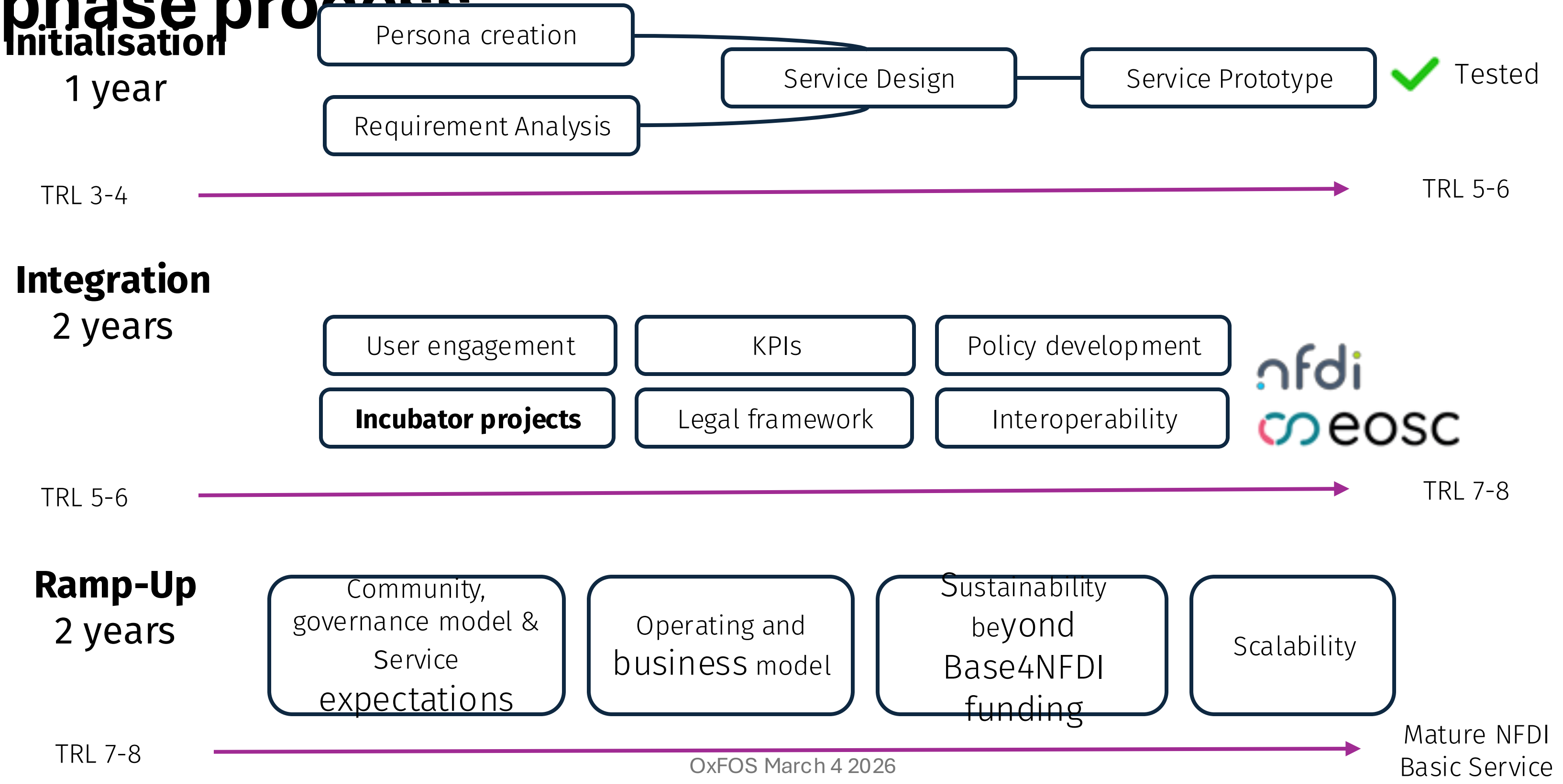
Experiences and lessons learned from implementing IAM4NFDI in NFDI4Culture

Torsten Schrade

Through IAM4NFDI we have been able to integrate and reuse basic services from other consortia such as DMP4NFDI (roll out in 09/2025)



Technical development of the services: **three-phase process**



Initialisation
1 year

Persona creation

Requirement Analysis

Service Design

Service Prototype

✓ Tested

TRL 3-4 → TRL 5-6

Integration
2 years

User engagement

KPIs

Policy development

Incubator projects

Legal framework

Interoperability

nfdi
eosc

TRL 5-6 → TRL 7-8

Ramp-Up
2 years

Community, governance model & Service expectations

Operating and business model

Sustainability beyond Base4NFDI funding

Scalability

TRL 7-8 → Mature NFDI Basic Service

Open Governance and Sustainability

Business and operational models

- **Transition to operations**- Project basis to permanent operations
- **Ownership** of scientific information infrastructures
- **Holistic governance approach for scientific information infrastructures** at the political level
- **Agreements -** closing the gap with service providers and HPC

A joint NFDI operation model as the way forward

Underpinning an Open Scholarship Environment

1. Openly governed services, selected and built by the research community.

2. Reuse of Infrastructure in a **heterogenous technical and organisational environment**.

3. **Ensuring sustainable services** through viable governance and business models.

→ **… building infrastructure takes time, at least 10 years!**

This is a participatory effort:

The ‘Human Factor”

Support, training, skills

are at the heart of a service

(it’s not just TRL)

A good service takes a combination of communities and competencies

base4 nfdi Basic Services for NFDI

Questions? Send an email: base4nfdi-office@lists.nfdi.de

Check our website: www.base4nfdi.de

Unfortunately, Clair couldn’t make her session today but we’re leaving this placeholder to acknowledge her work on open software

FAIRwDDI : a French research project on research data reuse

Oxford Forum of Open Scholarship (OxFOS): Reimagining ‘open’: Sharing research outside of traditional formats

Paul Colin, Alina Danciu – Sciences Po, Center for Socio-Political Data (CDSP), CNRS

4 March 2026

20 years of open sciences

One of the French Socio-Political Data Center's (CDSP) main missions is to serve the French and International social sciences and humanities (SSH) communities **by facilitating the reuse of surveys and data, both quantitative and qualitative, in the field of sociology and political science,** since 2005.

A **support and research unit** (UAR 828) set up in 2005 by Sciences Po and the French National Research Center (CNRS)

A team of 25 developers, data managers, panel managers and survey specialists

Research protocol

Qualitative study

- 8 interviews with SSH secondary users

Mostly questionnaire data reusers.

Quantitative study

- Distribution of questionnaires to the French community of secondary data users via several mailing lists

170 completed questionnaires ; 124 reusers ; 64 reported data reuse dropouts

Research questions

Data reuse : “**Data reuse is use of data one which did not collect oneself**” (Fear, 2013)

- What difficulties do data reusers encounter ?
- What are the causes of dropout ?

First findings : three dimensions for data reuse

Following Latour's science anthropology (1987 ; 1999) we propose three complementary dimensions for understanding data-reuse practices.

- **Align research questions with data :** defining questions from data or ensuring that available data can meaningfully address the research question
- **Align data with the field :** assessing the data's validity and relevance
- **Align data with the production** : generating new knowledge through visualization (graphs, tables) and analysis.

We have also identified exogenous factors : **time, reusers data literacy, legal and ethical issues, lack of recognition**.

Supporting researcher’s needs for data reuse

To respond to recurring needs and questions, we developed **two key resources**:

🗂️ [**ReQuest Data Bank**]()

- 65000 **quantitative research questions from more than 250 questionnaires**

📘 **DDI (Data Documentation Initiative) Metadata Made Simple Guide**

- A simple introduction to **data documentation** and **metadata structuring**

DDI Metadata Made Simple:

Your Top Questions Answered

Credits

Texts:
The texts are published under the Creative Commons CC BY SA license. You are free to share and adapt them, provided that you credit the authors. The first two slides come from Metadata management in the real world: Open Science in France – Data Policy can make a difference

Illustrations slide "Supporting researcher's needs for data reuse"
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Who Owns Our Epistemologies? Positivism Creep and Open Research

Thomas A. Graves
Annayah M.B. Prosser
Madeleine Pownall

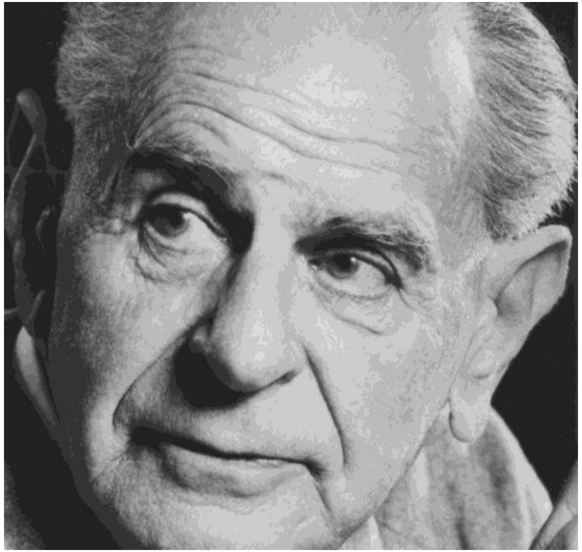
At LSE: "Should Reproducibility be the aim for Open Qualitative Research?"

- 4 June 2025
- London Open Science & Scholarship Festival
- LSE Open Research Working Group panel events
- Annayah: open science has promoted positivism creep into qualitative research where it is not epistemologically appropriate.
- Conclusion - most qualitative research is not reproducible because it does not aim for generalisability or objectivity.

Chair and panellists at event "Should Reproducibility be the aim for Open Qualitative Research?". Left to right: Dr Matteo M. Galizzi (chair), Kirsty Wallis, Dr Annayah M.B. Prosser, Dr Matthew Hanchard, Dr Madeleine Pownall. Photo by Lucy Lambe.

What do we mean by positivism?

- Emphasises observable, empirical evidence and scientific methods.
- Believes in objective truths about the world that can be refuted (Braun & Clarke, 2022: 292).
- Associated with the scientific method and reproducible experimentation.
- Popper rejected positivism, defined as seeking verification of facts, suggesting instead that research should seek to prove untruths false (2002).
- We also include Popper's falsificationism in our broad understanding of "positivist" research due to its belief in the existence of objective facts and the aim of science being to find generalisable theories that describe the world.

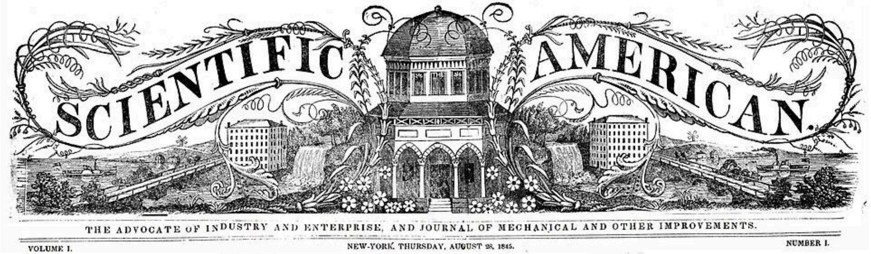


Karl Popper formal LSE staff portrait, courtesy LSE Library.

Where do many qualitative approaches differ?

- Many qualitative methods seek to document *particular* events/experiences/phenomena which cannot be reproduced or generalised.
- Many qualitative researchers give researcher subjectivity/positionality and interpretation of phenomena from different perspectives an important role in their research – so the aim is not to be objective and dispassionate.
- Some qualitative researchers reject the possibility of objective knowledge about the world in favour of subjective analysis of discourses, so verification is impossible.

1845 logo of *Scientific American* (public domain).



What is Positivism Creep?

- The subtle infiltration of positivist assumptions into methodologies where they do not belong (Braun & Clarke 2022)
- Infiltration of positivist assumptions is also a broader societal trend e.g. through "scientistic" perspectives – the view that only scientific knowledge is legitimate (Stenmark, 1997).

Open Research and Positivism

- Open science movement spread due to the replication crisis in behavioural and natural sciences.
- Replication crisis identified questionable research practices such as p-hacking, HARKing, cherry-picking, and data-fishing (Andrade, 2021), all of which are specific to quantitative, positivist approaches.
- Open science practices such as preregistration, data and code sharing therefore seen as ways of redressing QRPs and therefore as linked with positivist values such as reproducibility, replication, and generalisability (Prosser et al., 2023).
- BUT open research practices can also have different benefits to non-positivist research!

No! Not that kind of cherry picking! (Photo by Matt Ryall, 2012, CC BY 2.0)

Some Open Research Mandates Presume all Research is Positivist

E.g. European Commission policy since 2017 and UKRI draft research data policy (2025) requiring FAIR data deposits.

Interoperability and re-usability imply a need for data to be reproducible.

E.g. requirements to share data within short time frames e.g. UKRI draft policy suggesting requiring data sharing of all data not shared elsewhere within 2 years of end of funding

Incompatible with some research methods/styles where fruits of research are not be seen for significant periods after data collection.

E.g. anthropologists & ethnographers spend years/decades organising and publishing findings from extended fieldwork trips.

- "research period" is also often not separable from ordinary life, e.g. for

Open research requirements of funders determine which epistemologies are acceptable – thus funding bodies "own" our epistemologies!

What can be done?

- Methodological & epistemological pluralism.
- Reflexivity (positionality statements, preregistration, and self-reflective research methods, practice, and writing).
- Qual researchers resist positivism creep using "qualitative sensibility" (Braun & Clarke, 2022).
- Research can be open without being positivist.
- Be guided by your field's (and your own research field's) ethical context in deciding which open research practices to use.
- Open research mandates (especially for open data) should be domain-specific and flexible rather than blanket policies applying to all research areas.
- Where new requirements for open practices are introduced, funders should increase the duration of funding to allow for greater labour hours demanded by such requirements.

Summary

- Many mainstream conceptualisations and requirements of open research/open science proceed from positivist assumptions.
- This leads to the introduction of positivist methods and approaches in qualitative research methods where they may not be epistemologically appropriate.
- Therefore, we argue for open research policies and research methodologies which facilitate epistemological pluralism and reflexivity.

For further detail, see the preprint at: Graves, T.A., Pownall, M., & Prosser, A.M.B. (2025). 'Getting Creeped Out? Open Science, Qualitative Methods, and the Dangers of Positivism Creep.' SocArXiv. https://doi.org/10.31235/osf.io/nphjc_v1

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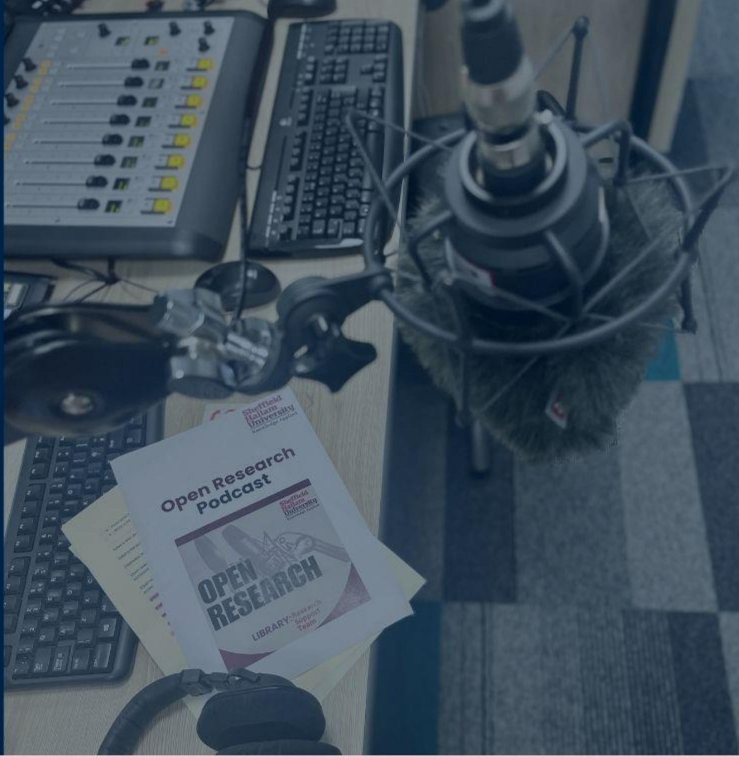

REIMAGINING ‘OPEN’:

CASE STUDY - SHU OPEN RESEARCH PODCAST

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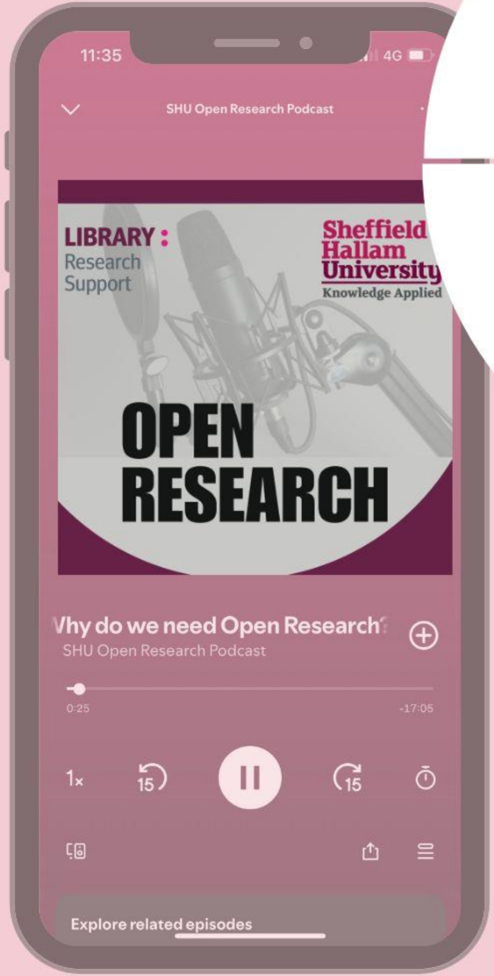

Vhy do we need Open Research

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share experience

showcase expertise

enable open practice

foster transdisciplinary dialogue

discovery

preservation

metadata

licensing

infrastructure of openness

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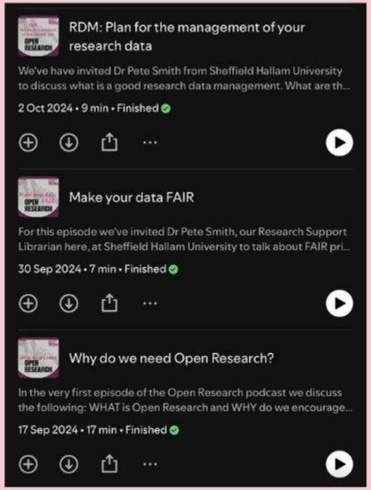
concept

theory + practice



RDM: Plan for the management of your research data

We've have invited Dr Pete Smith from Sheffield Hallam University to discuss what is a good research data management. What are th...

2 Oct 2024 • 9 min • Finished ✓

Make your data FAIR

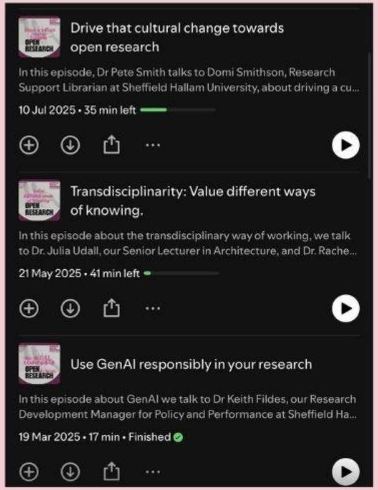
For this episode we've invited Dr Pete Smith, our Research Support Librarian here, at Sheffield Hallam University to talk about FAIR pri...

30 Sep 2024 • 7 min • Finished ✓

Why do we need Open Research?

In the very first episode of the Open Research podcast we discuss the following: WHAT is Open Research and WHY do we encourage...

17 Sep 2024 • 17 min • Finished ✓



Drive that cultural change towards open research

In this episode, Dr Pete Smith talks to Domi Smithson, Research Support Librarian at Sheffield Hallam University, about driving a cu...

10 Jul 2025 • 35 min left

Transdisciplinarity: Value different ways of knowing.

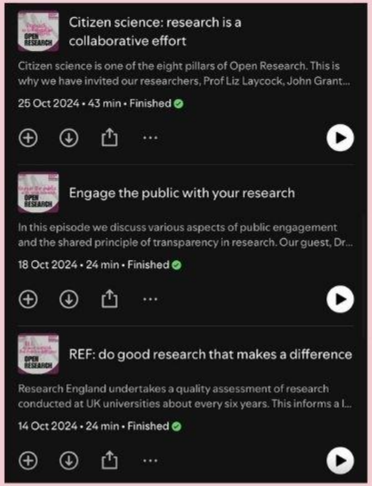
In this episode about the transdisciplinary way of working, we talk to Dr. Julia Udall, our Senior Lecturer in Architecture, and Dr. Rache...

21 May 2025 • 41 min left

Use GenAI responsibly in your research

In this episode about GenAI we talk to Dr Keith Fildes, our Research Development Manager for Policy and Performance at Sheffield Ha...

19 Mar 2025 • 17 min • Finished ✓



Citizen science: research is a collaborative effort

Citizen science is one of the eight pillars of Open Research. This is why we have invited our researchers, Prof Liz Laycock, John Grant...

25 Oct 2024 • 43 min • Finished ✓

Engage the public with your research

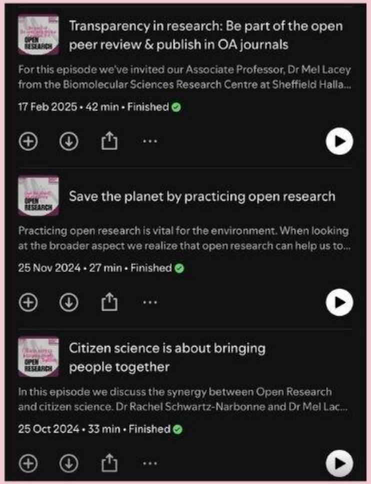
In this episode we discuss various aspects of public engagement and the shared principle of transparency in research. Our guest, Dr...

18 Oct 2024 • 24 min • Finished ✓

REF: do good research that makes a difference

Research England undertakes a quality assessment of research conducted at UK universities about every six years. This informs a l...

14 Oct 2024 • 24 min • Finished ✓



Transparency in research: Be part of the open peer review & publish in OA journals

For this episode we've invited our Associate Professor, Dr Mel Lacey from the Biomolecular Sciences Research Centre at Sheffield Halla...

17 Feb 2025 • 42 min • Finished ✓

Save the planet by practicing open research

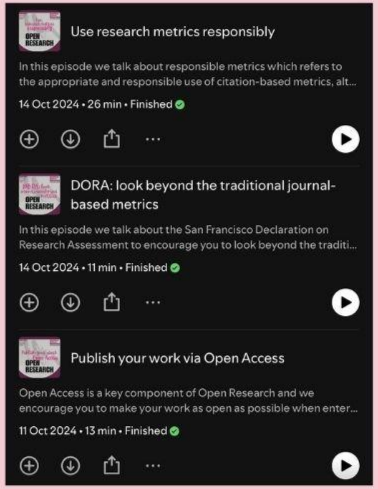
Practicing open research is vital for the environment. When looking at the broader aspect we realize that open research can help us to...

25 Nov 2024 • 27 min • Finished ✓

Citizen science is about bringing people together

In this episode we discuss the synergy between Open Research and citizen science. Dr Rachel Schwartz-Narbonne and Dr Mel Lac...

25 Oct 2024 • 33 min • Finished ✓



Use research metrics responsibly

In this episode we talk about responsible metrics which refers to the appropriate and responsible use of citation-based metrics, alt...

14 Oct 2024 • 26 min • Finished ✓

DORA: look beyond the traditional journal-based metrics

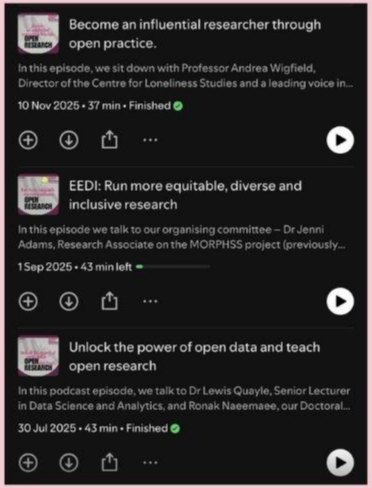
In this episode we talk about the San Francisco Declaration on Research Assessment to encourage you to look beyond the traditi...

14 Oct 2024 • 11 min • Finished ✓

Publish your work via Open Access

Open Access is a key component of Open Research and we encourage you to make your work as open as possible when enter...

11 Oct 2024 • 13 min • Finished ✓



Become an influential researcher through open practice.

In this episode, we sit down with Professor Andrea Wigfield, Director of the Centre for Loneliness Studies and a leading voice in...

10 Nov 2025 • 37 min • Finished ✓

EEDI: Run more equitable, diverse and inclusive research

In this episode we talk to our organising committee – Dr Jenni Adams, Research Associate on the MORPHSS project (previously...

1 Sep 2025 • 43 min left

Unlock the power of open data and teach open research

In this podcast episode, we talk to Dr Lewis Quayle, Senior Lecturer in Data Science and Analytics, and Ronak Naeemaee, our Doctoral...

30 Jul 2025 • 43 min • Finished ✓

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A podcast journey:

- learning
- exploring
- evolving

“In the very first episode of the Open Research podcast we discuss the following: WHAT is Open Research and WHY do we encourage researchers to practice Open Research here, at our university and beyond.”

“In this episode, we dive into the growing role of visual data in research—from images and videos to graphs, maps, and other visual materials—and explore how visuals can reveal insights that text or numbers alone may miss. We discuss the types of visual data commonly used across different fields, and how researchers can mobilise data in meaningful ways, drawing on Bruno Latour’s concept of the “mobilisation of data.” We also tackle the challenges of reproducibility with visual data, examining how interpretation, documentation, and metadata impact the ability to replicate and reuse findings. The episode offers practical approaches and best practices for managing, sharing, and documenting visual data effectively, as well as highlighting tools and platforms that support open and reproducible research. Finally, we consider the institutional role in fostering a culture that values open, shareable, and reproducible visual outputs, with insights from Dr Ester Ehiyazaryan-White, Senior Lecturer in Childhood and Early Childhood at Sheffield Hallam University and our UKRN Local Network Lead on how these practices are evolving and what opportunities and challenges lie ahead for researchers.

Further read: Hansson, Karin & Dahlgren, Anna (2022). Open research data repositories: Practices, norms, and metadata for sharing images. Journal of the Association for Information Science and Technology, 73(2), 303–316. DOI: 10.1002/asi.24571“

episode description

OA
Citizen Science
blogs
FAIR
RDM
preprints
PLS

Ethics
open peer review
DORA
CARE
culture
REF

AI
OERs
maps
protocols
participants
tools
EEDI
code
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reproducibility
impact

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EEDI

guests

UKRN Local Network Lead
Dean of Research
Open Research Manager
Lecturer in Architectural Science
Director of the Centre for Loneliness Studies
Research Support Librarians
Senior Lecturer in Architecture
Senior Lecturer in Childhood and Early Childhood
Senior Lecturer in Sustainable Construction and Climate Change
Senior Lecturer in Environmental Chemistry
Senior Lecturer in Data Science and Analytics
Associate Professor
Doctoral Researcher
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audience

everyone
at the University and beyond!

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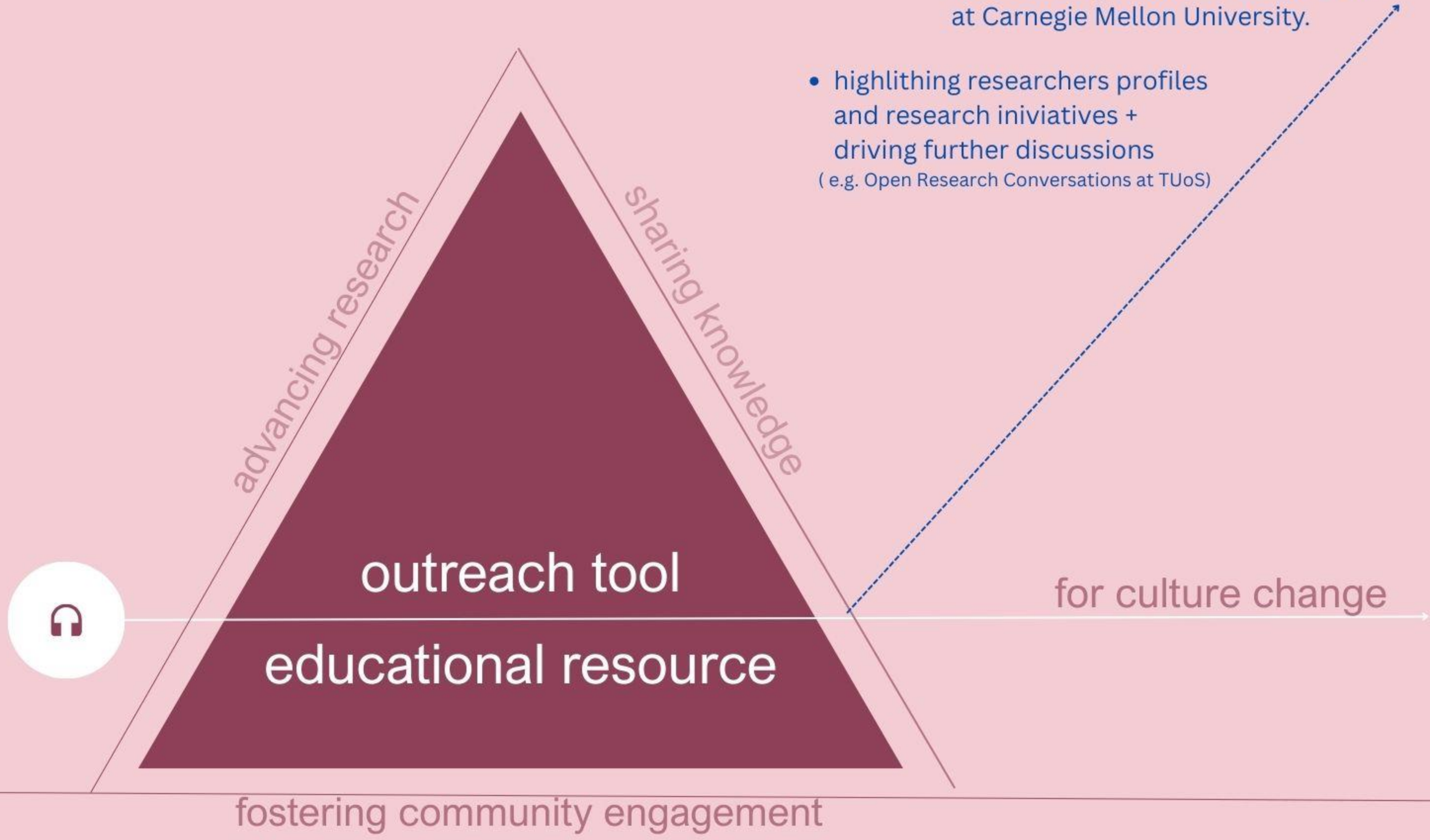
academic library as a facilitator



- a resource to the Project on Open and Evolving Metaliteracies (POEM) at Carnegie Mellon University.
- highlithing researchers profiles and research iniviatives + driving further discussions (e.g. Open Research Conversations at TUoS)

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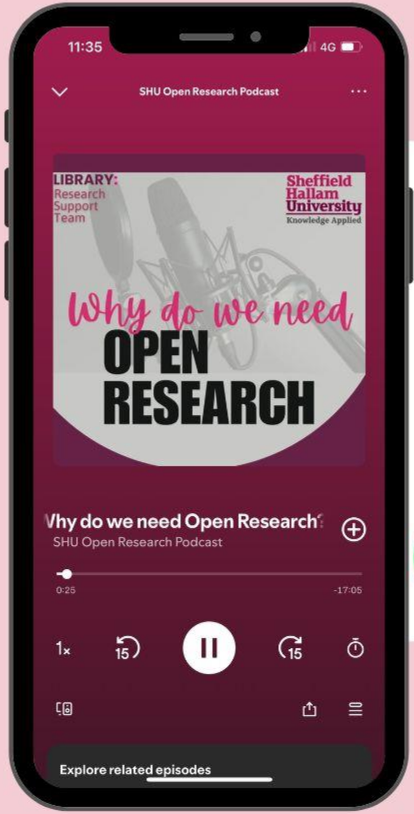

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Thurs, 5th March, ONLINE 13:00-15:00,
Cultivating FAIR data across disciplines

Fri, 6th March, ONLINE 11:00-12:00,
How to do open research safely

We'd love to hear what you thought of todays event

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