

第2回 SPARC Japan セミナー2020

プレプリントは学術情報流通の多様性をどこまで実現できるのか？

生命科学におけるプレプリント やSNS活用の現状と課題

Current status and issues in the use of preprints and
social networking services (SNS) in life science research

広島大学 大学院統合生命科学研究科

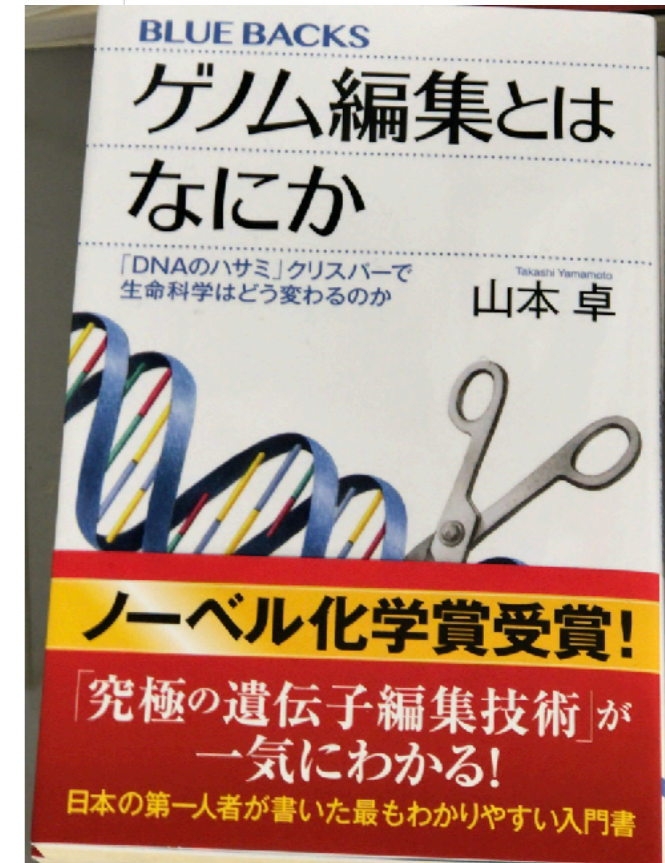
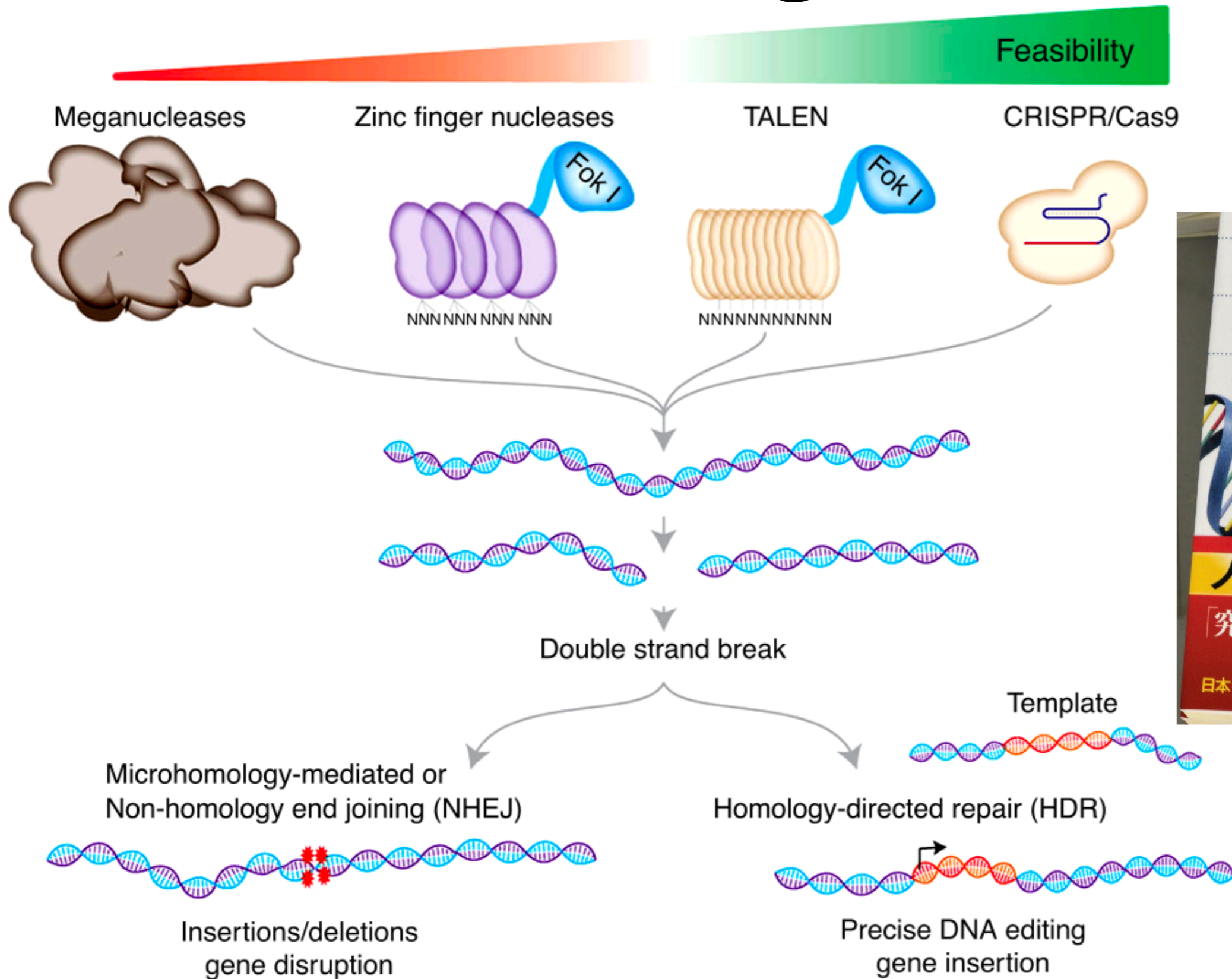
坊農 秀雅

Email: bonohu@hiroshima-u.ac.jp

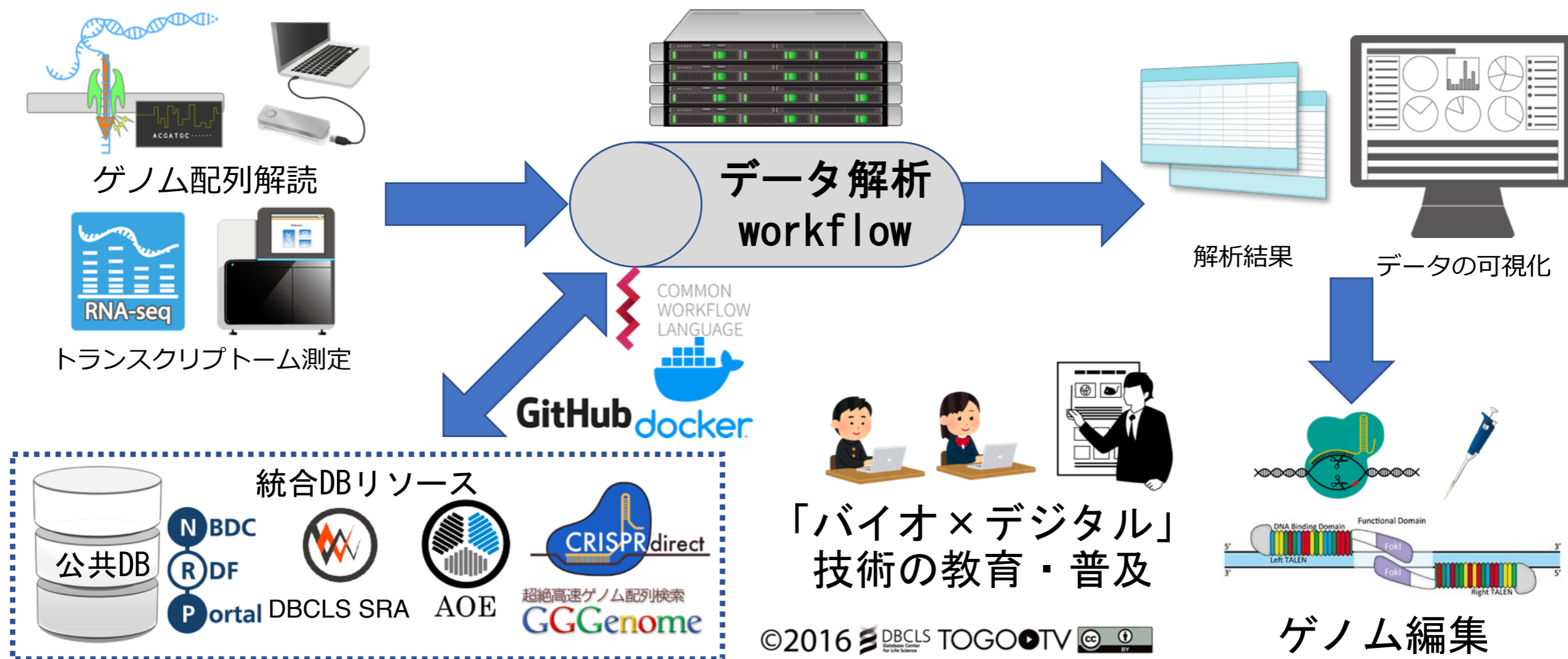
<https://bonohu.hiroshima-u.ac.jp>



Genome editing



ゲノム編集データ解析基盤技術の開発



+ バイオインフォマティクスによる遺伝子機能解析研究

<https://bonohu.hiroshima-u.ac.jp/> 3

本日の話

プレプリント+研究者版SNS

- ・ プレプリント利用実例とその課題
 - ・ bioRxiv
 - ・ F1000research
 - ・ biohackRxiv
- ・ 研究者版SNS
 - ・ ResearchGate
 - ・ Twitter

私の場合の実例は

<https://bonohu.hiroshima-u.ac.jp/>
の左カラムから



The screenshot shows the 'bonohulab' website, which is a personal academic profile page for Prof. Bono. The page is organized into several sections:

- About Me:** Identifies the user as a researcher at Hiroshima University, Graduate School of Integrated Life Sciences, Genomics Information Science Research Room. It also mentions the alias 'a.k.a. bonohulab'.
- Social:** A column of buttons linking to various social and academic platforms: Twitter, Instagram, Google Scholar, and ResearchGate.
- Link:** A column of buttons linking to specific resources: 広島大学 研究者総覧 (Hiroshima University Researcher Roster), ぼうのブログ (Bono's Blog), bonohu blog, bioRxiv, Europe PMC, f1000research, Figshare, ImpactStory, ORCID, PubMed, and ResearchMap.
- Japanese top:** A section with a date (Nov 21, 2020) and a link to 'Prof. Bono'.
- bonohulab と:** A section describing the lab's focus on genome data analysis and base technology.
- ニュース (News):** A list of recent research news items, including mentions of FANTOM, functional annotation, Database Issue, and various publications in 2020.
- もっとニュースを見る (See more news):** A link to view additional news.
- 研究内容 (Research Content):** A section titled '1. ゲノム編集データ解析基' (Genome editing data analysis base).

メタ解析手法の論文をプレプリントへ



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New Results

Meta-analysis of hypoxic transcriptomes from public databases

 Hidemasa Bono

doi: <https://doi.org/10.1101/267310>

This article is a preprint and has not been peer-reviewed [what does this mean?].

Abstract

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前回2018年10月末



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Meta-analysis of hypoxic transcriptomes from public databases

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ARTICLE USAGE

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Article usage: February 2018 to October 2018

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Total	907	327
Feb 2018	477	87
Mar 2018	112	54
Apr 2018	51	27
May 2018	37	23
Jun 2018	21	19

2020年11月末現在



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Meta-analysis of hypoxic transcriptomes from public databases

Hidemasa Bono, Kiichi Hirota

doi: <https://doi.org/10.1101/267310>

Now published in *Biomedicine* doi: [10.3390/biomedicines8010010](https://doi.org/10.3390/biomedicines8010010)

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Last 6 months

This month

Article usage: February 2018 to November 2020

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COVID-19 SARS-CoV-2 preprints from medRxiv and bioRxiv

Subject Area

Bioinformatics

Subject Areas

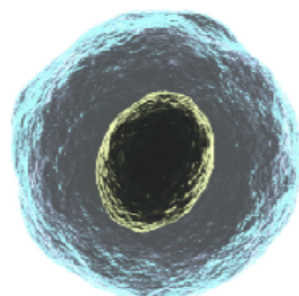
All Articles

Animal Behavior and Cognition

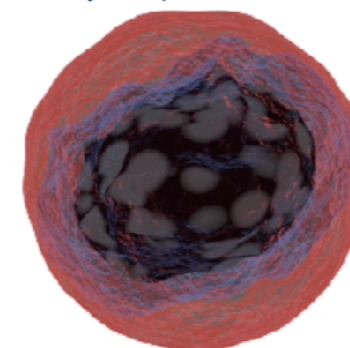
Biochemistry

その一方で、全く変化なし！

出してみte感じたプレプリントのメリット&デメリット



- すぐに公開できる
 - 先取制の担保(査読で止めて出し抜くのを阻止)
- DOIで引用可能
 - 研究費申請のリファレンス
- 現状APC無料
- 査読誌への投稿可
 - 生命科学系はほぼ可に
- EuroPMCから検索可能



- 一度公開すると論文が出せないかもという恐怖
 - 実はそうではなくなっている現実の認識不足
- 査読論文に出すスタイルを変えたくない
- 査読論文しか評価されない現実

変化したのは

- medRxivがCOVID-19の影響で広く知られるように
 - 査読論文との違い無視
 - プレプリントに関する無理解も露呈
- 一部の共同研究者が査読誌投稿前にbioRxivに出すように
 - 早く研究成果を世に知らせたい
- プレプリントの受け皿が増殖
 - 各種査読論文誌が投稿と同時に（例: MDPIの[preprints.org](https://www.mdpi.com/preprints)）
 - bioRxivが受け付けてくれない（例: Hackathonのレポート）

今月(2020/12)に入ってからの変化



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Peer Review: Implementing a "publish, then review" model of publishing



Michael B Eisen , Anna Akhmanova, Timothy E Behrens, Diane M Harper, Detlef Weigel, Mone Zaidi
eLife, United Kingdom

Editorial · Dec 1, 2020

Cited 0 Views 22,556 Annotations **8**

Cite as: eLife 2020;9:e64910 DOI: 10.7554/eLife.64910

Article

Abstract

Abstract

From July 2021 eLife will only review manuscripts already published as preprints, and will focus its editorial process on producing public reviews to be posted alongside the preprints.



例: BioHackrXiv



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TogoEx: the integration of gene expression data


AUTHORS

Hidemasa Bono, Takeya Kasukawa

AUTHOR ASSERTIONS

Conflict of Interest: No ▼

Public Data: Not applicable ▼



TogoEx: the integration of gene expression data

Hidemasa Bono¹ and Takeya Kasukawa²

1 DBCLS, Japan 2 RIKEN, Japan

Abstract

Gene expression data have potential to obtain many new biomedical findings by reusing and integrating publicly available datasets since most of the datasets were usually analyzed only focusing on what their data producers have interests to (like genes of interests). However, we have several issues to overcome for the efficient reuse of the public expression data: current available metadata for gene expression data is not sufficient enough to re-use; and human resources are too lacking to tackle the integration of gene expression data. In the ELIXIR Biohackathon-Europe 2019, we discussed what was necessary to achieve a new analysis interface to utilize the FANTOM6 data (quantified transcriptomic responses in human dermal fibroblasts using Capped Analysis of Gene Expression (CAGE) by knock-down of long non-coding RNAs (lncRNAs)). We then considered possible solutions against the issues, and decided implementation plans and scheduled to implement it.

Introduction

Gene expression data have been archived in public repositories, the NCBI Gene Expression Omnibus (GEO; <https://www.ncbi.nlm.nih.gov/geo/>) and the EBI ArrayExpress (AE; <https://www.ebi.ac.uk/arrayexpress/>). Unlike the International Nucleotide Sequence Database (<https://www.insdc.org/>), these two databases have not been exchanging data with each

ページ: 1 / 4

自動ズーム

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Abstract

Report on the group 'TogoEx' in the BioHackathon Europe 2019.

Preprint DOI

10.37044/osf.io/esrc9

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1-2 of 2 ARTICLES

OPINION ARTICLE  metrics

BioHackathon 2015: Semantics of data for life sciences and reproducible research [version 1; peer review: 2 approved]

Rutger A. Vos, Toshiaki Katayama, Hiroyuki Mishima, Shin Kawano, Shuichi Kawashima, Jin-Dong Kim, Yuki Moriya, Toshiaki Tokimatsu, Atsuko Yamaguchi, Yasunori Yamamoto, Hongyan Wu, Peter Amstutz, Erick Antezana, Nobuyuki P. Aoki, Kazuharu Arakawa, Jerven T. Bolleman, Evan Bolton, Raoul J. P. Bonnal, Hidemasa Bono, Kees Burger, Hirokazu Chiba, Kevin B. Cohen, Eric W. Deutsch, Jesualdo T. Fernández-Breis, Gang Fu, Takatomo Fujisawa, Atsushi Fukushima, Alexander García, Naohisa Goto, Tudor Groza, Colin Hercus, Robert Hoehndorf, Kotone Itaya, Nick Juty, Takeshi Kawashima, Jee-Hyub Kim, Akira R. Kinjo, Masaaki Kotera, Kouji Kozaki, Sadahiro Kumagai, Tatsuya Kushida, Thomas Lütteke, Masaaki Matsubara, Joe Miyamoto, Attayeb Mohsen, Hiroshi Mori, Yuki Naito, Takeru Nakazato, Jeremy Nguyen-Xuan, Kozo Nishida, Naoki Nishida, Hiroyo Nishide, Soichi Ogishima, Tazro Ohta, Shujiro Okuda, Benedict Paten, Jean-Luc Perret, Philip Prathipati, Pjotr Prins, Núria Queralt-Rosinach, Daisuke Shinmachi, Shinya Suzuki, Tsuyosi Tabata, Terue Takatsuki, Kieron Taylor, Mark Thompson, Ikuo Uchiyama, Bruno Vieira, Chih-Hsuan Wei, Mark Wilkinson, Issaku Yamada, Ryota Yamanaka, Kazutoshi Yoshitake, Akiyasu C. Yoshizawa, Michel Dumontier, Kenjiro Kosaki, Toshihisa Takagi

 **PEER REVIEWERS** *Jeremy G. Frey; James P. Balhoff and Gaurav Vaidya*
FUNDER National Bioscience Database Center

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OPINION ARTICLE  metrics

BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services [version 1; peer review: 2 approved with reservations]

ResearchGate (RG)

研究者向けのSNS

- 2008年にBostonで設立→2013年からBerlinに本部
- 2016年の公称利用者数 900万人
 - 自分は2015年ごろから登録して使っている模様
- researchmap / ORCID的な業績リスト集的な側面も
 - 基本誰かが登録しないといけないようだが、自動で入る印象
- Following/Followersもあるが、特にそこに制約はない
 - それは関係なく、登録者同士でやりとり可能
- 業績に対する統計値の可視化がリアルタイムに

RGトップページ



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39.7 · PhD · [Edit](#)

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Overview

Research

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Introduction

Development of database technologies for genome editing and functional genomics by bioinformatic approach

Languages

English · Japanese

Disciplines

Bioinformatics Molecular Biology Genetics Databases Data Mining

Skills and expertise (12)

Gene Expression Genomics Bioinformatics ... Biology Next ... Sequencing
Gene Regulation Bioinformatics Transcriptomics Differential ... Expression
Expression Profiling Microarray Analysis [View all](#)

Current affiliation

Edit 

Hiroshima University

Location

Hiroshima, Japan



Department

Graduate school of Integrated Sciences for Life

Position

Professor

Time period

Apr 2020 - Present

Role

Development of database technologies for genome editing and functional genomics by bioinformatic approach

RGのお知らせ機能(updates)



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Overview

Research

Experience **New**

Stats

About me

Introduction

Development of database technologies for genome editing and functional genomics by bioinformatic approach

Languages

English · Japanese

Disciplines

Bioinformatics Molecular Biology Genetics Databases Data Mining

Skills and expertise (12)

Gene Expression Genomics Bioinformatics ... Biology Next ... Sequencing
Gene Regulation Bioinformatics Transcriptomics Differential ... Expression
Expression Profiling Microarray Analysis View all

Updates



You have a new citation on: [Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs](#)

4h ago

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You have 2 new citations on: [KEGG: kyoto Encyclopedia of Genes and Genomes](#)

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Hiroshima University

Location

Hiroshima, Japan

Department

Graduate school of Integrated Sciences for Life

Position

Professor

Time period

Apr 2020 - Present

Role

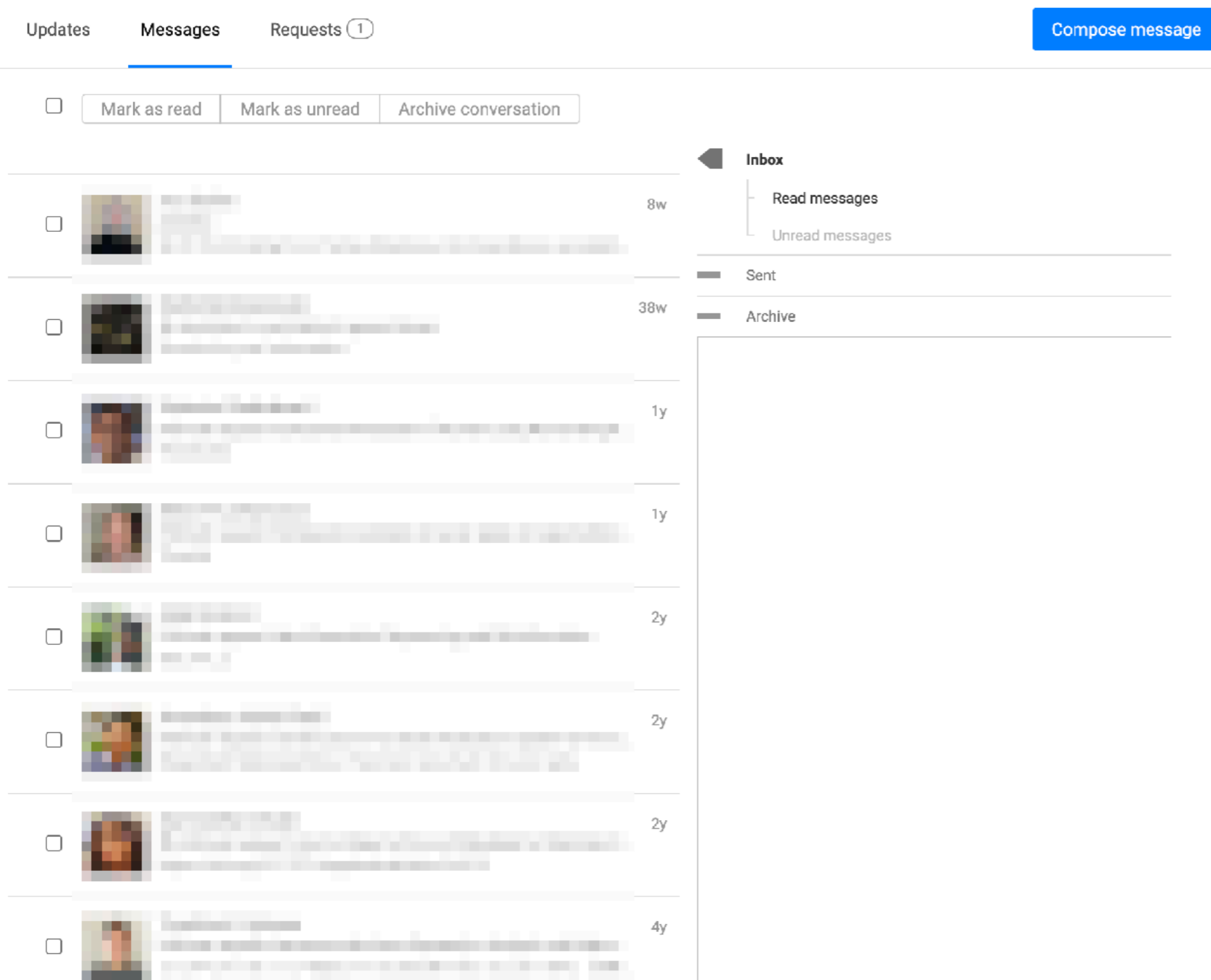
Development of database technologies for genome editing and functional genomics by bioinformatic approach



RGのSNS (Messages)

ほぼすべて日本国外から（私の場合）

Notifications



その内容

- 別刷り(PDF)請求
- オープンアクセスなのに！
- 雑誌特集号への寄稿依頼
- ポスドク申し込み

RGのResearch researchmap的な機能



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Overview Research Experience **New** Stats Scores Following

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Research items

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Conference Paper (1)

Thesis (1)

Data (155)

Research

Presentation

Poster (2)

Preprint (14)

Full-texts (84)

Questions (1)

Answers

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Search by publication title or keyword

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FANTOM enters 20th year: expansion of transcriptomic atlases and functional annotation of non-coding RNAs

Article Full-text available November 2020 · Nucleic Acids Research

Imad Abugessaisa · Jordan A Ramilowski · Marina Lizio · [...] · Takeya Kasukawa

Add to project Add supplementary resources

Characterization of brown adipose tissue thermogenesis in the naked mole-rat (Heterocephalus glaber), a heterothermic mammal

Article November 2020 · Scientific Reports

Yuki Oiwa · Kaori Oka · Hironobu Yasui · [...] · Kyoko Miura

Add full-text Add to project Add supplementary resources

Construction of TUATinsecta database that integrated plant and insect database for screening phytophagous insect metabolic products with medicinal potential

Article Full-text available October 2020 · Scientific Reports

Wakana Nakane · Hisashi Nakamura · Takeru Nakazato · [...] · Hiroko Tabunoki

- 誰かが登録しないとダメらしい（自動じゃない？）
- PDFを登録するのが前提のインターフェース
- プレプリントはmust
- 査読論文はスキップ可
- 勝手に収集してくる？

RGのScores



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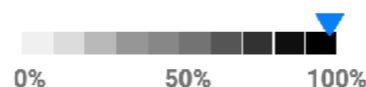


Breakdown:

- 99.64% Publications
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36

h-index
35

excluding self-citations

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KEGG: kyoto Encyclopedia of Genes and Genomes

[Article](#) February 1999 · Nucleic Acids Research




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Publication由来


h-index

Google Scholarとほぼ一致

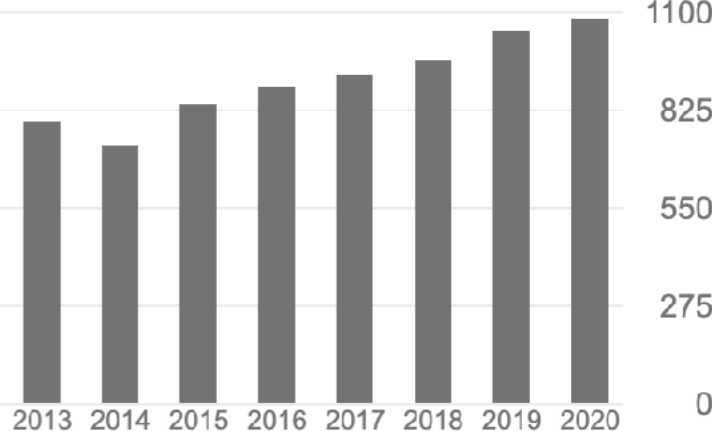
 共著者を追加
共著者の候補があります。
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Hidemasa Bono 
[フォロー](#)

Graduate School of Integrated Sciences for Life, [Hiroshima University](#).
 確認したメール アドレス: hiroshima-u.ac.jp - [ホームページ](#)
[Transcriptomics](#) [Genomics](#) [Bioinformatics](#) [Database Biology](#) [Genome editing](#)

引用先	すべて	2015 年以來
引用	13941	5759
h 指標	36	20
i10 指標	56	34



☐ タイトル
 


	引用先	年
<input type="checkbox"/> KEGG: Kyoto encyclopedia of genes and genomes H Ogata, S Goto, K Sato, W Fujibuchi, H Bono, M Kanehisa Nucleic acids research 27 (1), 29-34	3555	1999
<input type="checkbox"/> The transcriptional landscape of the mammalian genome P Carninci, T Kasukawa, S Katayama, J Gough, MC Frith, N Maeda, ... science 309 (5740), 1559-1563	3449	2005
<input type="checkbox"/> Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Y Okazaki, M Furuno, T Kasukawa, J Adachi, H Bono, S Kondo, I Nikaido, ... Nature 420 (6915), 563-573	1760	2002

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RGのStats

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Overview Research Experience **New** Stats Scores Following

Stats history

Time: Weekly ▾

Research Interest



Citations



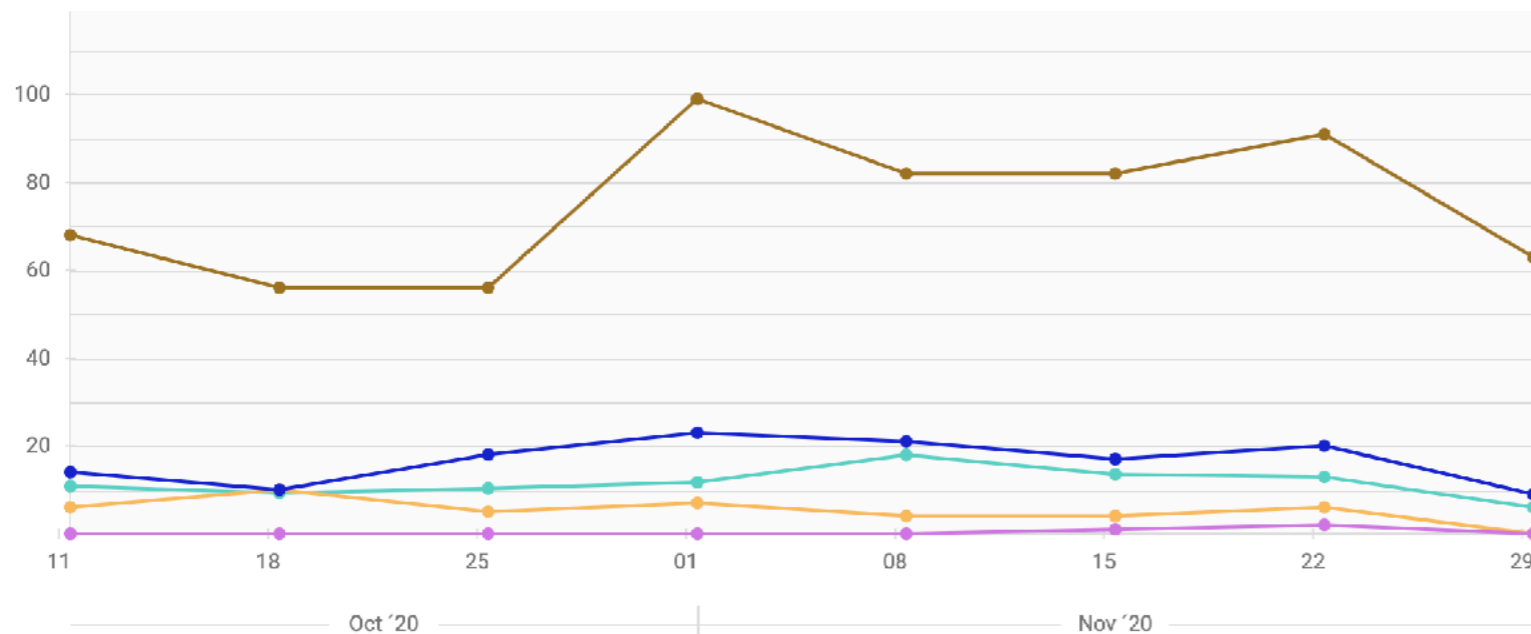
Recommendations



Reads



Full-text reads





- アクセス数(Reads)だけでなく、Full-text readsは別に
- 被引用(Citations)も
- Recommendations
- Research Interest

RG

他の機能

Project

Functional annotation of public transcriptome data

 Hidemasa Bono ·  Hiromasa Ono

Goal: Annotating public gene expression data & database biology

Updates 0 new 0

Recommendations 0 new 0

Followers 0 new 8

Reads ⓘ 0 new 54

Overview

Project log

References (7)

Add research

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Projects (4)

Functional annotation of public transcriptome data

Project

Add update

Indexing data in Sequence Read Archive

Project

Add update

Development of database technologies for genome editing

Project

Add update

Functional genomics by bioinformatic approach

Project

Add update

Research referenced in this project

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TogoEx: the integration of gene expression data

Preprint Full-text · Jul 2020

 Hidemasa Bono ·  Takeya Kasukawa

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An integrated index of public gene expression databases and its application for meta-analysis of hypoxic transcriptomes

Poster Full-text · May 2019

 Hidemasa Bono

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Meta-Analysis of Hypoxic Transcriptomes from Public Databases

Article Full-text · Jan 2020 · Biomedicines

 Hidemasa Bono ·  Kiichi Hirota

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2 Citations

Projectで論文がまとめられる

RG job情報がメールで

- ・ 海外のばかりですが
- ・ JREC-IN的な
- ・ 広告メールもたまに ↓

ResearchGate <no-reply@researchgatemail.net>

11月26日 木曜日 13:07

宛先: 坊農 秀雅 <bonohu@hiroshima-u.ac.jp>

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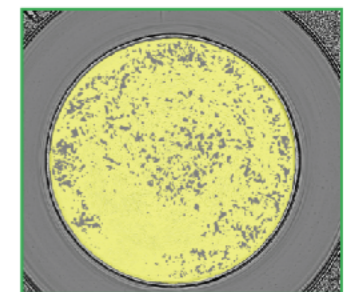
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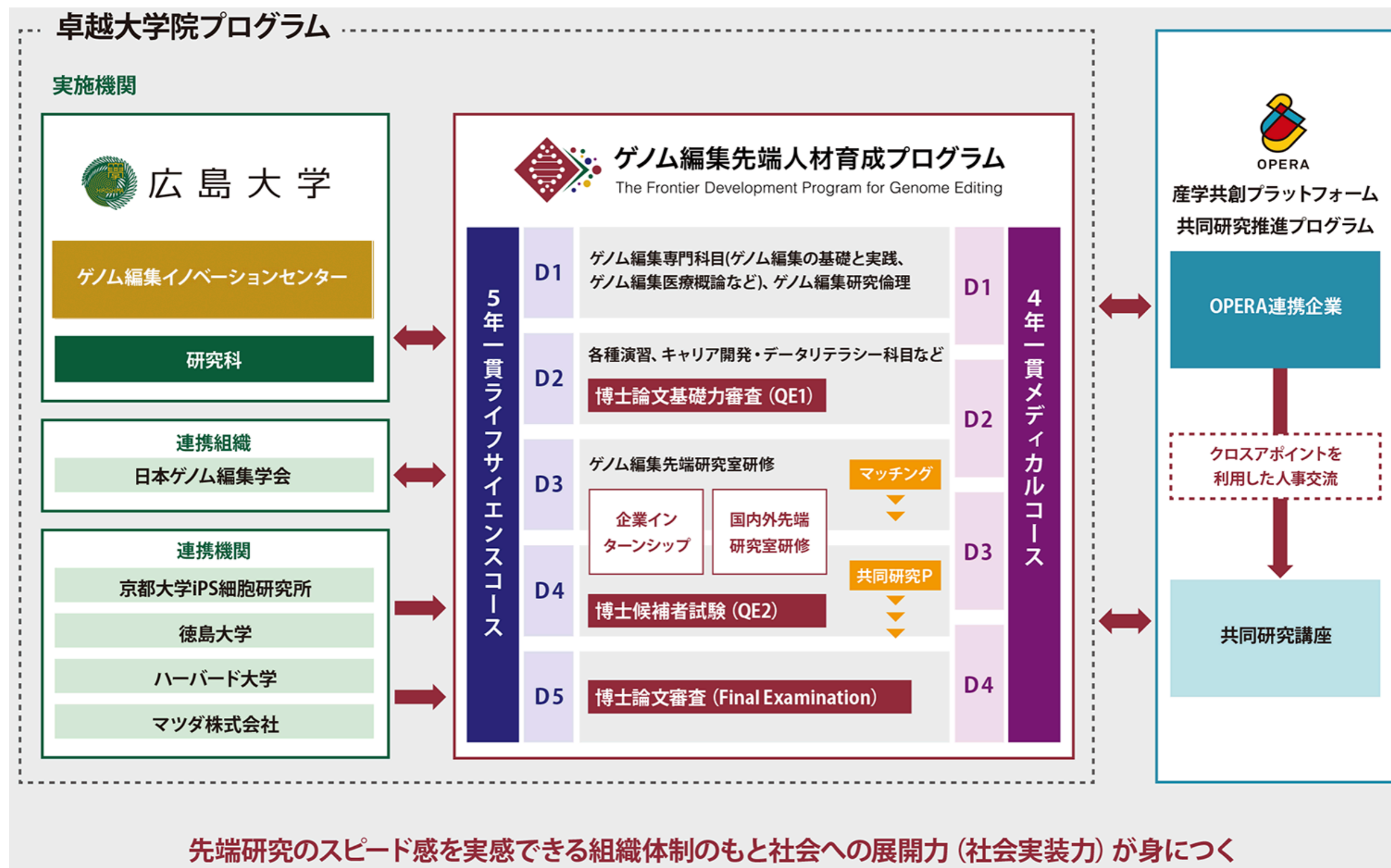
まとめ

プレプリントと研究者向けのSNS

- ・プレプリント、RGともに日本では**利用が進んでない**
 - ・ Full-text取得目的での利用はされている？（ググって）
- ・ しかし、匿名（のつもり）でのtwitter利用は進んでいる
 - ・ 実名にしないのは自信がない、今後に影響するから？
- ・ それゆえ、欧米のように**プレプリントを義務付けるべき**
 - ・ **査読論文しか評価しない評価基準を改訂していくべき**
 - ・ 何より**研究者の意識を変える教育、啓蒙活動**を

広島大学 卓越大学院プログラム

ゲノム編集先端人材育成プログラム



バイオインフォマティクスの講義を担当

2020年度はオンデマンドで

7. 配列類似性検索

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Graduate School of Integrated Sciences for Life,
Hiroshima University

坊農秀雅 (Hidemasa Bono)

Email: bonohu@hiroshima-u.ac.jp
<http://bonohu.hiroshima-u.ac.jp/>



BI20_08.mp4



BI20_07.pdf



BI20_07.mp4



BI20_06.pdf



BI20_06.mp4

公共DBからのデータ取得

広島大学大学院統合生命科学研究科
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ビッグデータを取り扱う のリラシー

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生命科学 データ解析

Dr. Bono
生命科学
データ解析
坊農秀雅



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生命科学分野の公共データ

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バイオインフォマティクス 歴史 (History)

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ChIP-chip への応用

博士課程前期 専門的教育科目
Master course Specialized Education
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ガイダンス (Guidance)

広島大学大学院統合生命科学研究科
Graduate School of Integrated Sciences for Life,
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博士課程前期 専門的教育科目

Master course Specialized Education

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生命科学 データ解析

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