

第2回 SPARC Japan セミナー2018

(オープンアクセス・サミット2018)

「オープンサイエンス時代のクオリティコントロールを見通す」

生命科学研究における プレプリント活用の現状

大学共同利用機関法人 情報・システム研究機構

データサイエンス共同利用基盤施設

ライフサイエンス統合データベースセンター (DBCLS)

坊農 秀雅

<https://researchmap.jp/bonohu/>

"Utility of preprints in Life Science"

by Hidemasa Bono from Database Center for Life Science (DBCLS)

生命科学研究者の立場から見たOpen Access (OA)



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・ 現状、ゴールド OA一択

- ・ すなわち「オープンアクセス」＝ゴールドOA

+ BioRxiv

・ グリーンOAという言葉自体ほとんど知られてない

- ・ IFの付いてない雑誌は回避される傾向
- ・ ピアレビューを経た論文のみ業績とみなす伝統

‘Preprint’ discussed in *Science*

29 SEPT 2017 VOL 357, ISSUE 6358

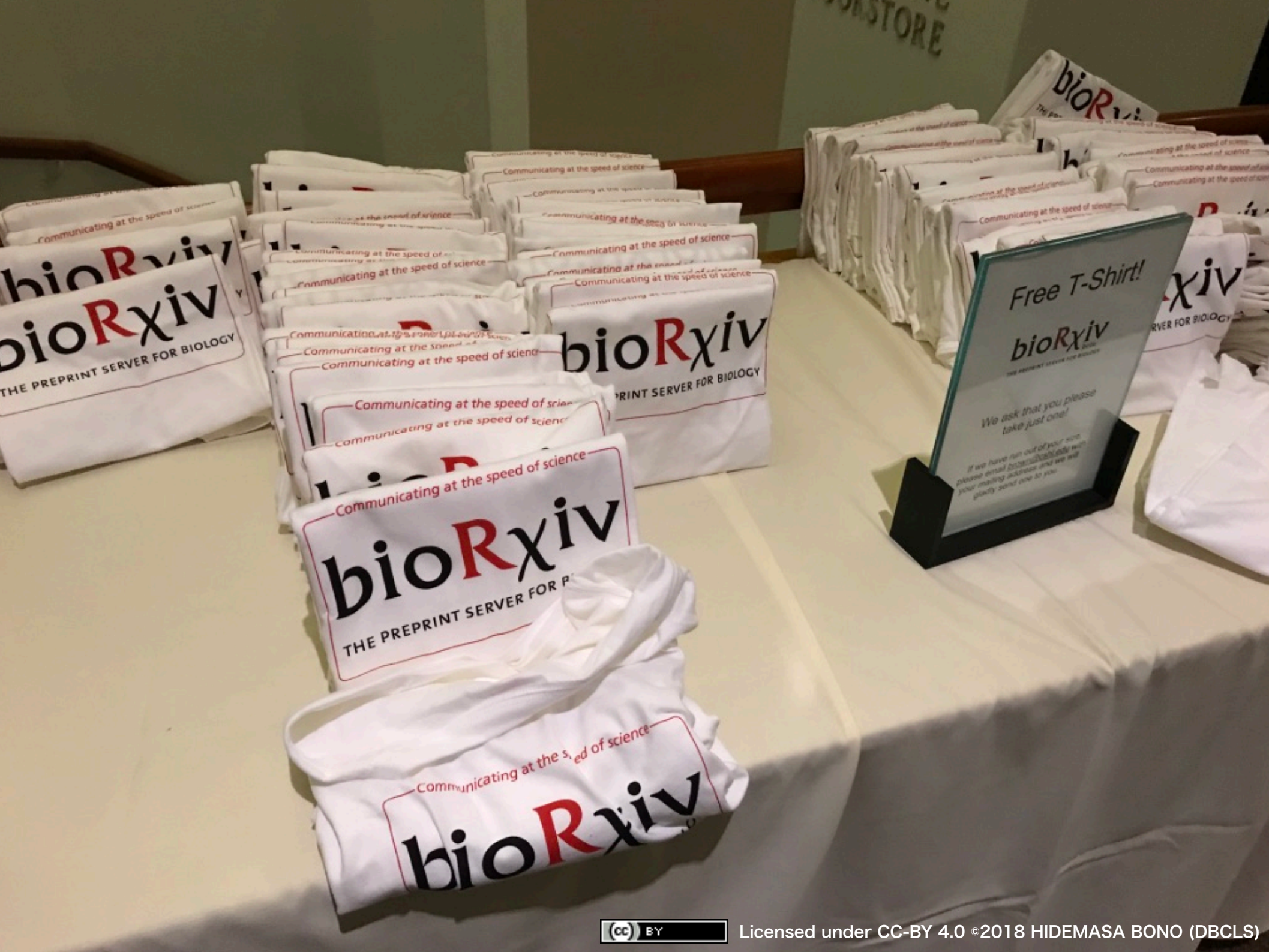


- Preprint ecosystems in Editorial (p1331)
- THE PREPRINT DILEMMA (p1344-1347)
 - Biologists are posting unreviewed papers in record numbers. Here’s a survival guide
- How biologists pioneered preprints — with paper and postage (p1348)
 - Francis Crick and James Watson experimented with preprints as well as DNA.

第2回 SPARC Japan セミナー2017 (オープンアクセス・サミット2017)

「プレプリントとオープンアクセス」坊農秀雅「趣旨説明」より





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口頭発表はもちろん、 ポスター発表もBioRxiv

→これは自分もやらねば…



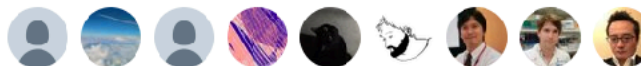
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次の論文はプレプリントサーバー(BioRxiv)に
まず出そう(決意)



20:01 - 2017年11月4日

1件のリツイート 17件のいいね





@bonohu


月曜日のSPARC Japanセミナー「プレプリントとオープンアクセス」に始まって、水曜日から土曜日までBioRxiv をホストしているCSHLでの Genome Informatics Conference。すごくプレプリントな一週間だったなあ

20:09 - 2017年11月4日



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This article is a preprint and has not been peer-reviewed [what does this mean?].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

Hypoxia is an insufficient level of oxygen supply in the cell, and hypoxia-inducible factor is a central regulator of oxygen homeostasis. In order to elucidate functional insights in hypoxic response in data-driven way, we attempted meta-analysis of hypoxic transcriptome for public expression data which have been archived as microarray and RNA-seq data in public databases, NCBI Gene Expression Omnibus (GEO) and EBI ArrayExpress. While various hypoxic conditions (oxygen concentration and duration of hypoxia) and cell lines are taken in the stored data, we manually curated possible pairs of transcriptome before and after hypoxic stress from microarray and RNA-seq data. As a result, we got 37 pairs in human and 53 pairs

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RESEARCH ARTICLE

Differentiated embryo chondrocyte plays a crucial role in DNA damage response via transcriptional regulation under hypoxic conditions

Hideaki Nakamura, Hidemasa Bono, Keiko Hiyama, Takeshi Kawamoto, Yukio Kato, Takeshi Nakanishi, Masahiko Nishiyama, Eiso Hiyama, Nobuyuki Hirohashi, Eisaburo Sueoka, Lorenz Poellinger, Keiji Tanimoto 

Published: February 21, 2018 <https://doi.org/10.1371/journal.pone.0192136>

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メタ解析手法の論文をプレプリントへ



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Meta-analysis of hypoxic transcriptomes from public databases

 Hidemasa Bono

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

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Abstract

Hypoxia is an insufficient level of oxygen supply in the cell, and hypoxia-inducible factor is a central regulator of oxygen homeostasis. In order to elucidate functional insights in hypoxic response in data-driven way, we attempted meta-analysis of hypoxic transcriptome for public expression data which have been archived as microarray and RNA-seq data in public databases, NCBI Gene Expression Omnibus (GEO) and EBI ArrayExpress. While various hypoxic conditions (oxygen concentration and duration of hypoxia) and cell lines are taken in the stored data, we manually curated possible pairs of transcriptome before and after hypoxic stress from microarray and RNA-seq data. As a result, we got 37 pairs in human and 53 pairs

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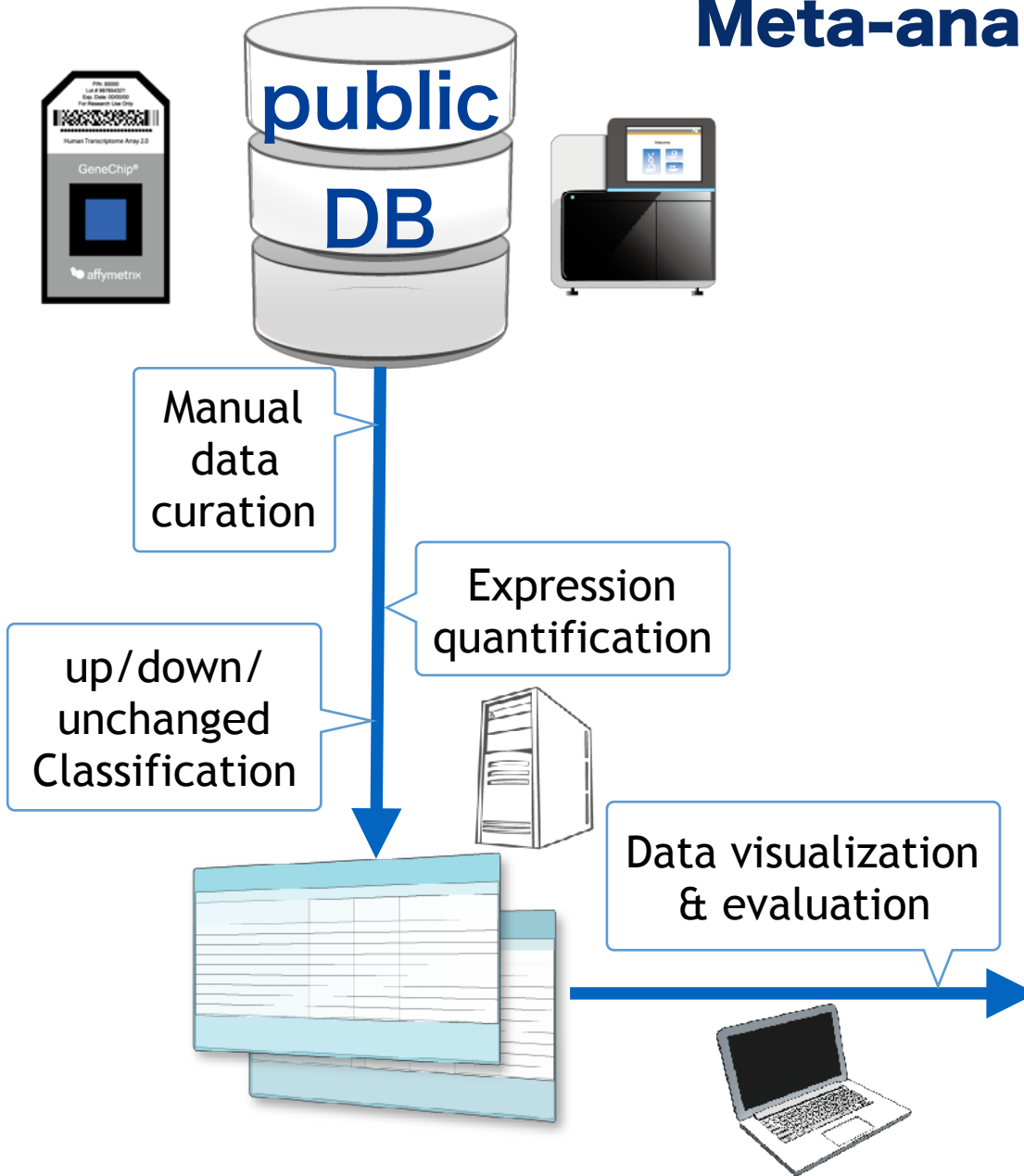
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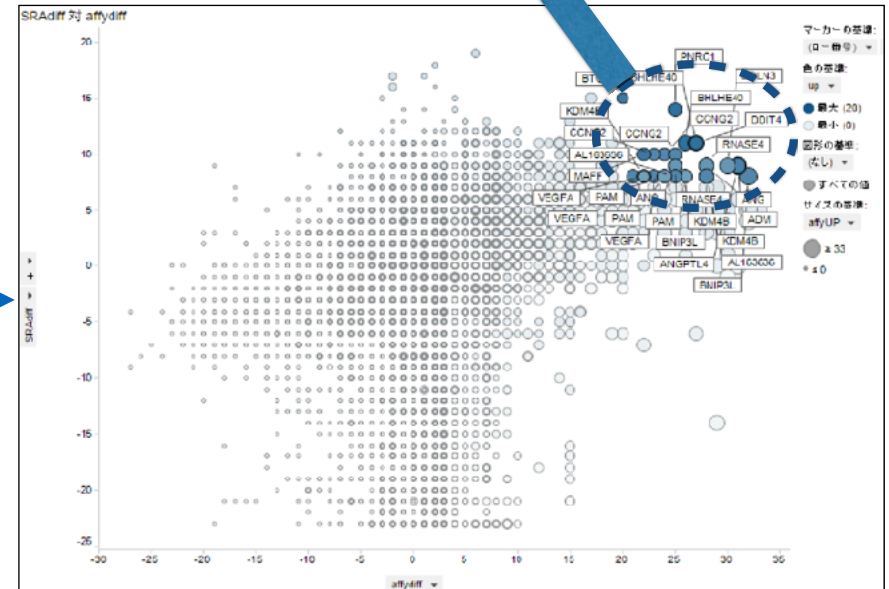
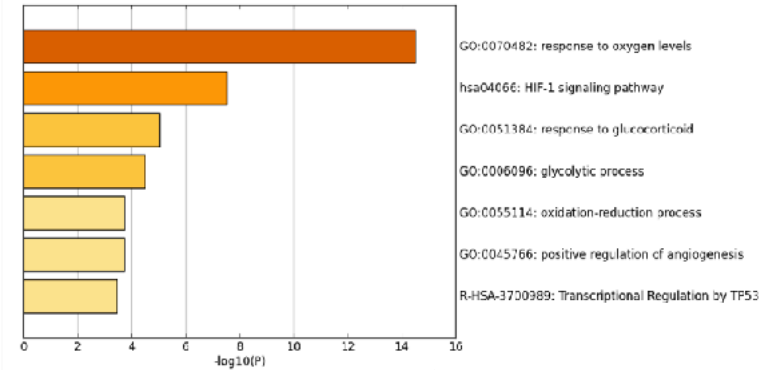


Meta-analysis of hypoxic stress



Enrichment Summary

Figure 1. Heatmap of enriched terms across input gene lists, colored by p-values.



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Bono H. *BioRxiv* <https://doi.org/10.1101/267310>

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AUTHORS

[Hidemasa Bono](#)

CATEGORIES

- [Gene Expression \(incl. Microarray and other genome-wide approaches\)](#)

KEYWORD(S)

[human](#)[mouse](#)[genechip](#)[RNA-seq](#)[Hypoxia](#)[meta-analysis](#)

Manually annotated possible pairs of transcriptomes before and after hypoxic stress from public expression data. The data process details are described in BioRxiv (<https://doi.org/10.1101/267310>).

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DATASET

Mouse microarray log ratio data before and after hypoxic stress

Hidemasa Bono 23/01/2018



DATASET

Mouse list of counts after hypoxic stress (up/down/unchanged)

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DATASET

Human RNA-seq ratio data before and after hypoxic stress

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DATASET

Human list of counts after hypoxic stress by RNA-seq (up/down/unch...

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DATASET

Human microarray log ratio data before and after hypoxic stress

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DATASET

Human list of counts after hypoxic stress (up/down/unchanged)

Hidemasa Bono 23/01/2018



DATASET

Mouse list of microarray datasets before and after hypoxic stress

Hidemasa Bono 23/01/2018



DATASET

Human list of microarray datasets before and after hypoxic stress

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DATASET

Human list of RNA-seq datasets before and after hypoxic stress

Hidemasa Bono 23/01/2018

<https://doi.org/10.6084/m9.figshare.c.3983880>



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id	UP	DOWN	UNCHANGED
1007_s_at	7	0	30
1053_at 2	10	25	
117_at 5	0	32	
121_at 2	1	34	
1255_g_at	1	0	36
1294_at 2	0	35	
1316_at 1	0	36	
1320_at 2	0	35	
1405_i_at	10	1	26
1431_at 3	0	34	
1438_at 6	3	28	
1487_at 0	0	37	
1494_f_at	1	0	36
1552256_a_at	9	0	28
1552257_a_at	0	10	27
1552258_at	1	1	35
1552261_at	0	2	35
1552263_at	6	3	28
1552264_a_at	3	4	30
1552266_at	1	1	35
1552269_at	2	4	31
1552271_at	2	0	35

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humanUDN1.5.txt (956.13 kB)

A A

MD5: 66b88cc4cb4dec44d5d5c2c142be3306

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Feb 2018	477	87
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Sep 2018	62	26
Oct 2018	35	18

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- Biophysics
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- Cell Biology
- Clinical Trials
- Developmental Biology
- Ecology

New Results

In renal cell carcinoma, cancerous phenotypes linked to hypoxia-inducible factors are insensitive to the volatile anesthetic isoflurane

Chisato Sumi, Yoshiyuki Matsuo, Teppei Iwai,  Hidemasa Bono,  Kiichi Hirota

doi: <https://doi.org/10.1101/375311>

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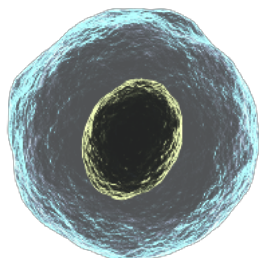
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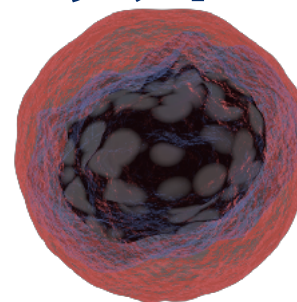
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Sumi C, Matsuo Y, Iwai T, **Bono H**, Hirota K
bioRxiv [25 Jul 2018]
Cited: 0 times (PPR:PPR45785)
- [Suppression of mitochondrial oxygen metabolism mediated by the transcription factor HIF-1 alleviates propofol-induced cell toxicity](#)
Sumi C, Okamoto A, Tanaka H, Kusunoki M, Shoji T, Uba T, Adachi T, Iwai T, Nishi K, Harada H, **Bono H**, Matsuo Y, Hirota K
Sci Rep [12 Jun 2018, 8(1):8987]
Cited: 0 times (PMID:29895831 PMCID:PMC5997661) [Free full text article](#)
- [Promotion of malignant phenotype after disruption of the three-dimensional structure of cultured spheroids from colorectal cancer](#)
Piulats JM, Kondo J, Endo H, Ono H, Hagihara T, Okuyama H, Nishizawa Y, Tomita Y, Ohue M, Okita K, Oyama H, **Bono H**, Masuko T, Inoue M
Oncotarget [23 Mar 2018, 9(22):15968-15983]
Cited: 0 times (PMID:29662620 PMCID:PMC5882311) [Free full text article](#)
- [Meta-analysis of hypoxic transcriptomes from public databases](#) Preprint
Bono H
bioRxiv [23 Feb 2018]
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 EuroPMCから検索可能

出してみて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



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Direct PCR amplification of 16S rRNA genes offers accelerated bacterial identification using the MinION™ nanopore sequencer

Shinichi Kai,  Yoshiyuki Matsuo, So Nakagawa, Kirill Kryukov, Shino Matsukawa, Hiromasa Tanaka, Teppei Iwai, Tadashi Imanishi,  Kiichi Hirota

doi: <https://doi.org/10.1101/435859>

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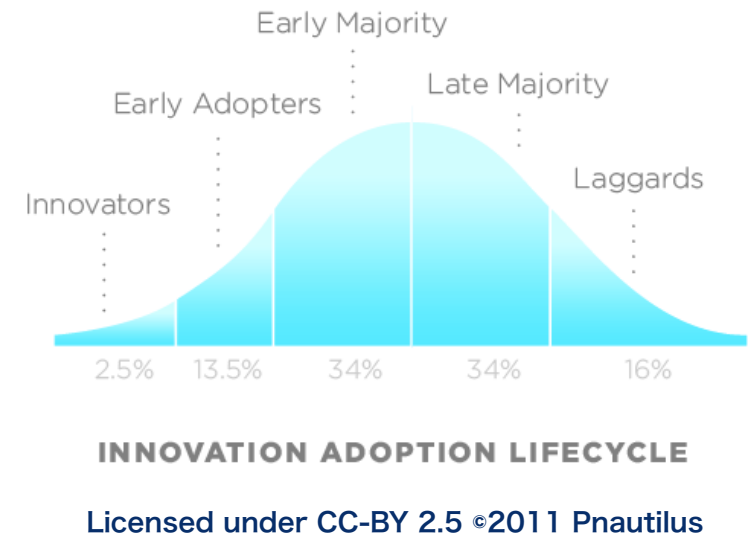
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- Biochemistry
- Bioengineering
- Bioinformatics
- Biophysics
- Cancer Biology

クオリティコントロール

生命科学研究において

- **査読論文だけ、** を続けられるか？
 - 金銭的な問題
 - 査読のコスト
- プレプリントと査読論文の**併用**に移行できるか？
 - 現状、ビッグラボなど、Early adopter
- TwitterなどのSMSでもっと議論が盛り上がれば、**プレプリント**だけでもコミュニケーションはできるのでは？
 - 匿名性の問題



謝辞

- ・ 共同研究者
 - ・ 関西医科大学 広田喜一
 - ・ 広島大学原爆放射線医科学研究所 谷本圭司
- ・ ライフサイエンス統合データベースセンター(DBCLS)

