Scopus & SciVal have experience with responsible use of metrics for research assessment
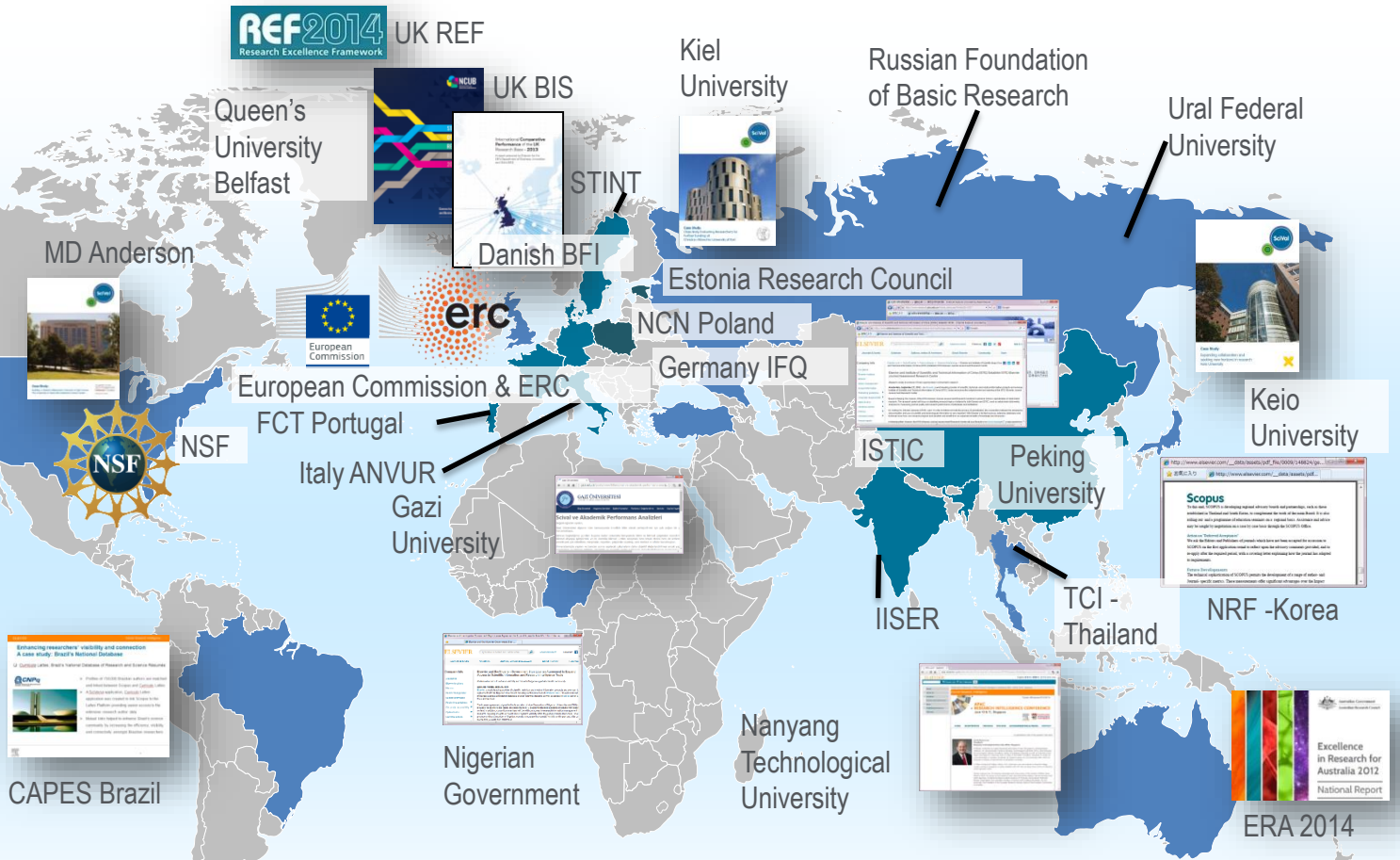
Research metrics: our approach

We must offer:
- A basket of metrics
- For all peers
- Generated in an automated and scalable way

When implementing / using metrics:
- Always use judgment with metrics
- There is no perfect or leading metric; always use at least 2
- Selection differs depending on the question
- Take variables into account
- We can't prevent stupidity or irresponsibility

Best practice
- Research community who judge and are judged should ideally define metrics
- No methodological black boxes – no exceptions
- Independent of business and access models
- No aggregate / composite metrics

Response to HEFCE's call for evidence: independent review of the role of metrics in research assessment

30 June 2014

Yes, Elsevier would be interested in participating in a workshop / event to discuss the use of metrics in research assessment and management.

This response covers the following sections:

A. Why is Elsevier responding?
B. For what purposes are research metrics used?
C. Guiding principles for use of metrics in research assessment
D. A model for generating and using metrics in research assessment
E. Implications for using metrics in research assessment
F. Response to the specific questions posed by HEFCE

Empowering Knowledge

Composite metrics should be avoided and all calculation methods must be freely available, not proprietary

Snowball Metrics approach to altmetrics

Vision: Snowball Metrics enable benchmarking by driving quality and efficiency across higher education's research and enterprise activities, regardless of system and supplier

Bottom-up initiative: *Universities define and endorse metrics* to generate a strategic dashboard. The community is their guardian.

There are 4 Snowball Metrics altmetrics buckets:

- **Scholarly Activity** - Number of times that an output has been posted in online tools that are typically used by academic scholars e.g. Mendeley, Zotero

- **Scholarly Commentary** - Number of times that an output has been commented on in online tools that are typically used by academic scholars e.g. research blogs, F1000 Prime

- **Mass Media** - Number of times that an output has been referred to by e.g. newspapers, specialized publications

- **Social Activity** - Number of times that an output has stimulated social media posts e.g. Facebook, Twitter

Snowball Metrics Project Partners

UNIVERSITY OF CAMBRIDGE · UNIVERSITY OF OXFORD · Queen's University Belfast · UCL · Imperial College London · UNIVERSITY OF LEEDS · University of BRISTOL · University of St Andrews · ELSEVIER

Mendeley Readership Statistics ⓘ

135 people have saved this article to Mendeley

Top disciplines
Physics: 29%
Biological Sciences: 17%
Computer and Information Science: 9%

Top demographics
Ph.D. Student: 33%
Post Doc: 11%
Student (Master): 9%

Top countries
United States: 4%
Brazil: 2%
Germany: 2%

View in search results format

March 2014

Ⓜ Save to Mendeley | → View this article in Mendeley

Altmetric for Scopus

Up to now this article has been mentioned **1725** times by **1688** sources.

Sources
■ 40 Facebook users
■ 8 science blogs
■ 33 Google+ users
■ 10 news outlets
■ 1 Pinner
■ 1 Q&A thread
■ 6 Reddit threads
■ 1587 tweeters

Saved to reference managers
■ 4 CiteULike   ■ 134 Mendeley

ies.

ements for formation

June 2012

see details | open report in new tab

This app is provided by **Altmetric**. Learn more here

phage capsids

6

Search   Alerts   My list   My Scopus

1 of 1
View in EMBASE | View at Publisher |

Every article will now display the Article Metrics module in the sidebar

Nature Methods

Volume 10, Issue 6, April 2013, Pages 563-5...

Nonhybrid, finished micr...
SMRT sequencing data

Chin, C.-S.[a], Alexander, D.H.[a], Marks, P.[a], Klammer, A.A.[a], Drake, J.[a], Heiner, C.[a], Clum, A.[b],
Copeland, A.[b], Huddleston, J.[c], Eichler, E.E.[c], Turner, S.W.[a], Korlach, J.[a] ✉

[a] Pacific Biosciences, Menlo Park, CA, United States
[b] Joint Genome Institute, Walnut Creek, CA, United States
[c] Department of Genome Sciences, University of Washington, Seattle, WA, United States
⊞ View additional affiliations

Abstract   ▼ View references (44)

We present a hierarchical genome-assembly process (HGAP) for high-quality de novo microbial genome assemblies using only a single, long-insert shotgun DNA library in conjunction with Single Molecule, Real-Time (SMRT) DNA sequencing. Our method uses the longest reads as seeds to recruit all other reads for construction of highly accurate preassembled reads through a directed acyclic graph-based consensus procedure, which we follow with assembly using off-the-shelf long-read assemblers. In contrast to hybrid approaches, HGAP does not require highly accurate raw reads for error correction. We demonstrate efficient genome assembly for several microorganisms using as few as three SMRT Cell zero-mode waveguide arrays of sequencing and for BACs using just one SMRT Cell. Long repeat regions can be successfully resolved with this workflow. We also describe a consensus algorithm that incorporates SMRT sequencing primary quality values to produce de novo genome sequence exceeding 99.999% accuracy. © 2013 Nature America, Inc. All rights reserved.

Indexed keywords

EMTREE medical terms: algorithm; article; bacterial cell; bacterial genome; consensus; DNA library; DNA sequence; Escherichia coli; microbial genetics; microorganism; nonhuman; Pedobacter heparinus; priority journal; bacterial artificial chromosome; bacterial genome; DNA sequence; gene library; genetics; human; methodology; nucleotide repeat

MeSH: Chromosomes, Artificial, Bacterial; Escherichia coli; Gene Library; Genome, Bacterial; Humans; Repetitive Sequences, Nucleic Acid; Sequence Analysis, DNA
Medline is the source for the MeSH terms of this document.

References (44)   View in search results format

○ Page ⊟ Export | 🖨 Print | ✉ E-mail | Create bibliography

○ Medini, D., Serruto, D., Parkhill, J., Relman, D.A., Donati, C., Moxon, R., Falkow, S., (...), Rappuoli, R.
1   **Microbiology in the post-genomic era**
    (2008) Nature Reviews Microbiology, 6 (6), pp. 419-430. Cited 170 times.
    doi: 10.1038/nrmicro1901
    View at Publisher

○ Parkhill, J., Wren, B.W.
2   **Bacterial epidemiology and biology - lessons from genome sequencing**

Cited by 111 documents

Complete genome sequence of the petroleum-emulsifying bacterium Pseudomonas stutzeri SLG510A3-8
Hu, B. , Nie, Y. , Geng, S.
(2015) Journal of Biotechnology

Complete genome sequence of Burkholderia pyrrocinia 2327[T], the first industrial bacterium which produced antifungal antibiotic pyrrolnitrin
Kwak, Y. , Shin, J.-H.
(2015) Journal of Biotechnology

Complete genome sequence of Lactobacillus salivarius Ren, a probiotic strain with anti-tumor activity
Sun, E. , Ren, F. , Liu, S.
(2015) Journal of Biotechnology

View all **111** citing documents

Inform me when this document is cited in Scopus:
🏷 Set citation alert | 📶 Set citation feed

Related documents

Reducing assembly complexity of microbial genomes with single-molecule sequencing
Koren, S. , Harhay, G.P. , Smith, T.P.L.
(2013) Genome Biology

One chromosome, one contig: Complete microbial genomes from long-read sequencing and assembly
Koren, S. , Phillippy, A.M.
(2015) Current Opinion in Microbiology

Whole genome complete resequencing of Bacillus subtilis natto by combining long reads with high-quality short reads
Kamada, M. , Hase, S. , Sato, K.
(2014) PLoS ONE

View all related documents based on references

Find more related documents in Scopus based on:
👤 Authors | 🏷 Keywords

Metrics   ❓

💬 111   Citations   99TH PERCENTILE
❄ 20.67 Field-Weighted Citation Impact
Ⓜ 337   Mendeley Readers   99TH PERCENTILE
🎬 12   Blog posts
🐦 84   Tweets on Twitter   99TH PERCENTILE
🗒 4   Mass Media Stories
    21   Mentions in 6 additional sources
                    ❓ Select data provided by Altmetric.com

View all metrics

The Article Metrics module in the sidebar provides at-a-glance information for the researcher. They can quickly see citation impact and scholarly community engagement with the article.

This can help them decide whether they want to read the article.

Metrics   ❓

💬 111   Citations   99TH PERCENTILE

❄   20.67   Field-Weighted Citation Impact

Ⓜ   337   Mendeley Readers   99TH PERCENTILE

🎬   12   Blog posts

🐦   84   Tweets on Twitter   99TH PERCENTILE

🗒   4   Mass Media Stories

     21   Mentions in 6 additional sources

                    ❓ Select data provided by Altmetric.com

📋 View all metrics

Clicking on "View all metrics" opens up the module for this article.

Metric details

Nonhybrid, finished microbial genome assemblies from long-read SMRT...
Chin C.-S., Alexander D.H., Marks P., Klammer A.A., (...), Korlach J.
(2013) Nature Methods, 10(6), pp. 563-569

Overview	Citations	Scholarly Activity Mendeley, CiteULike, etc.	Scholarly Co... Blogs, Reviews, W...

Overview

Citation Count ""	Field-Weighted Citation Impact ⚖	Citation Benchmarking %
111	**20.67**	**99**th percentile
Cited-by in Scopus ⚙	⚙	Compared to Biotechnology articles of the same age and document type

Mendeley	Mass Media	Blogs	Pubpeer	Twitter	4 Other sources
337 Readers	**4** Items	**12** Posts	**1** Comment	**84** Tweets	**8** Mentions

Engagement highlights

⚙ **Scholarly Activity** - 349 readers from 2 sources

Downloads and posts in common research tools

Mendeley: 337 Readers
Top Discipline: Biological Sciences
Top Demographic: Ph D Student

MENDELEY
Save to Mendeley

citeulike **CiteULike:** 12 Copies

⚙ **Social Activity** - 89 mentions from 3 sources

Mentions characterized by rapid, brief engagement on platforms used by the general population, such as Twitter, Facebook and Google +.

84 tweets from 66 users

4 posts from 4 users

1 post from 1 user

Benchmark highlights ?
Based on 89 mentions from 3 sources

Compared to Biotechnology articles of same age and document type

Overview tab includes:

- Citation and Engagement metric highlights
- Introduces the 4 Snowball Metrics Categories of altmetrics

Metric details

Nonhybrid, finished microbial genome assemblies from long-read SMRT
Chin C.-S., Alexander D.H., Marks P., Klammer A.A., (...), Korlach J.
(2013) Nature Methods, 10(6), pp. 563-569

Overview	**Citations**	Scholarly Activity Mendeley, CiteULike, etc.	Scholarly Co Blogs, Reviews, W

Citations

111 Cited-by documents

🔆 About Snowball Metric

Citation Count

111

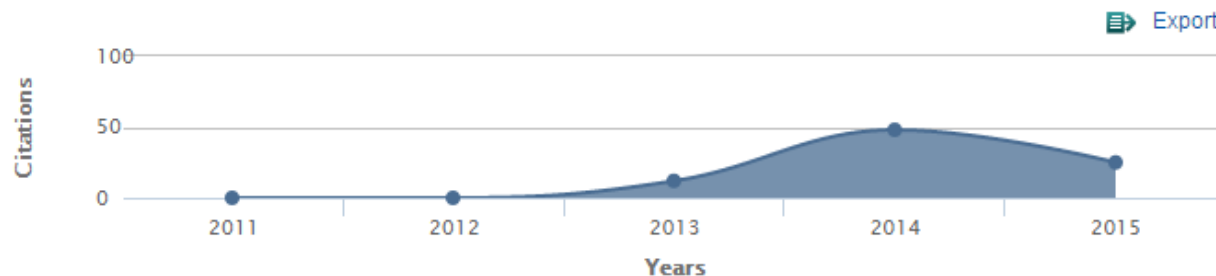Cited-by in Scopus 🔆

99

Citation Benchmarking   %

99th percentile ▬▬▬▬▬

Compared to Biotechnology articles of the same
age and document type

Cited by

📤 Export

111 Citations

Date range: 2011 ▾ to 2015 ▾

○ Exclude self citations
○ Exclude citations from books
Edit the data for this graph.   Update

(Graph: Citations vs Years 2011–2015, peaking near 50 in 2014)

Benchmarking ❓

Measures of activity relative to specific research domains, based on Cited-by in Scopus

Compared to Biotechnology ▾ articles of same age and document type

All Citations   ▬▬▬▬ 99TH PERCENTILE

Citation tab includes:

- Citation Count
- Field-Weighted Citation Impact
- Citation Percentile Benchmarking

Benchmarking is a ranking comparison for the article as compared to other similar articles of the same document type and publishing timeline. Percentile benchmarks show how citations or activity received by this article compare with the averages for similar articles

Metric details

Nonhybrid, finished microbial genome assemblies from long-read SMRT

Chin C.-S., Alexander D.H., Marks P., Klammer A.A., (...), Korlach J.
(2013) Nature Methods, 10(6), pp. 563-569

Overview	Citations	**Scholarly Activity** Mendeley, CiteULike, etc.	Scholarly C Blogs, Reviews

⚙ Scholarly Activity

349 readers from 2 sources

Indirect measurement of activity by people using scholarly platforms such as Mendeley, and CiteULike.

⚙ About Snowball Metric

Mendeley Readers ♏	CiteULike 🔖
337 Readers Save to Mendeley	**12**

Mendeley Reader demographics

View publication in Mendeley

By discipline

- 55% Biological Sciences
- 6% Computer And Information Science
- 1% Arts And Literature

View all

By academic status

- 21% Ph D Student
- 9% Student Master
- 7% Post Doc

View all

By country

- 5% United States
- 2% Germany
- 1% Belgium
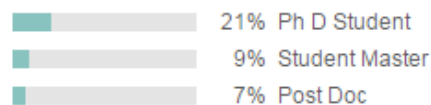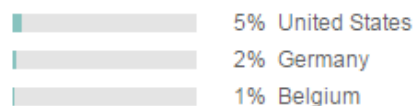
View all

* Data provided by altmetric.com

Indirect measurement of activity by people using scholarly platforms such as Mendeley, and CiteULike.

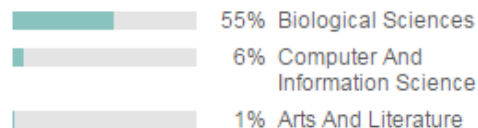**Mendeley Readers** 🅜

337 Readers

Save to Mendeley

CiteULike

12

Scholarly Activity tab includes:

- Percentile Benchmarks for Scholarly Activity, Mendeley, and CiteULike

Mendeley Reader demographics
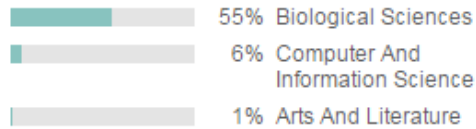
View publication in Mendeley

By discipline

55% Biological Sciences

6% Computer And Information Science

1% Arts And Literature

View all

By academic status

21% Ph D Student

9% Student Master

7% Post Doc

View all

By country

5% United States

2% Germany

1% Belgium
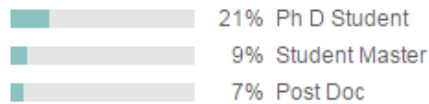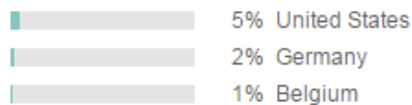
View all

Benchmarking ❓

Measures of activity relative to specific research domains, based on all sources of Scholarly Activity

Compared to [Biotechnology ▼] articles of same age and document type

All Scholarly Activity - 349   99TH PERCENTILE

Mendeley - 337   99TH PERCENTILE

CiteULike - 12   99TH PERCENTILE

❓ *Select data provided by Altmetric.co*

Met...

Non... long-read SMRT sequencing data Back to article

Chin...
(201...

	Scholarly Commentary Blogs, Reviews, Wikipedia, etc.	Mass Media	Social Activity Twitter, Facebook, etc.

Scholarly Commentary tab includes:

- Blog posts, reviews, Wikipedia articles, etc. by experts and scholars*

Scholarly Commentary

16 mentions
Reviews, articles and blogs by experts and scholars, such as F1000Prime, research blogs, and Wikipedia.

☀ About Snowball Metrics

📖 Blogs

Microbial sequencing at Nature Methods
Methagora
29 September 2014

Over the years, Nature Methods has publishe...
sequence data for microbial studies. We cove...
the stage for a molecular taxonomy of microb...

**Our review of "Nonhybrid, finished microbial...
sequencing data", aka the HGAP paper**
In between lines of code
19 June 2014

As it is out in the open that I was one of the...
though I could as well make my review public...
February 2013) online at Publons. The review...

**Our review of "Nonhybrid, finished microbial...
sequencing data", aka the HGAP paper**
In between lines of code
19 June 2014

As it is out in the open that I was one of the...
though I could as well make my review public...
February 2013) online at Publons. The review...

An outsiders guide to bacterial genome sequencing on the Pacific Biosciences RS
Pathogens: Genes and Genomes
27 February 2014

It had to happen eventually. My Twitter feed in recent times had become unbearable with the insufferably smug PacBio mafia (that’s you Keith, Lex, Adam and David) crowing about

📖 Post-publication peer reviews

📖 Pubpeer
| 1 comment from PubPeer

P Publons

2 comments from Publons
Massive parallel sequencing
George Church
01 January 2014

Massive parallel sequencing or massively parallel sequencing is any of several high-throughput approaches to DNA sequencing using the concept of massively parallel processing; it is also called next-generation sequencing (NGS) or second-generation sequenci

* Data provided by altmetric.com

Met... | Email

Nor... long-read SMRT sequencing data Back to article
Chin...
(201...

| | Scholarly Commentary
Blogs, Reviews, Wikipedia, etc. | **Mass Media** | Social Activity
Twitter, Facebook, etc. |

Mass Media tab includes:

- Coverage of this article in the mass media, e.g. newspapers and trade magazines*

⚙ **Mass Media**

4 stories from 4 sources
Coverage of research output in the mass media

⚙ About Snowball Metric

定序間的釘孤枝！−淺談次世代基因定序技術
Pansci
26 May 2015

次世代基因定序技術已然發展10年，而為什麼叫做次世代（Next-Generation）呢？那第一代去哪裡了？我為何要關心次世代定序技術？乾我何事？要回答到你懂這些問題以前，你必須必備大一生物學；不難拉，大概有點概念就可以。再來要有基礎的統計學概念以及數理概念，一樣不難拉，高中程度就可以。可是你問我，我高中都在談戀愛怎辦？沒關係，就讓我娓娓道來。

New Cost-Effective Genome Assembly Process
Medical News Today
08 May 2013

The U.S. Department of Energy Joint Genome Institute (DOE JGI) is among the world leaders in sequencing the genomes of microbes, focusing on their potential applications in the fields of bioenergy and environment. As a national user facility, the DOE JGI i

A new cost-effective genome assembly process
Nanowerk
05 May 2013

A new cost-effective genome assembly process
EurekAlert!
05 May 2013

(DOE/Joint Genome Institute) Genome assembly, the molecular equivalent of trying to put together a multi-million piece jigsaw puzzle without knowing what the picture on the cover of the box is, remains challenging due to the very large number of very sma

❓ *Select data provided by Altmetric.co...*

* Data provided by altmetric.com

Metr

Social Activity tab includes:

- Mentions of this article in social media*

Nor...   ...ong-read SMRT sequencing data Back to article
Chin...
(201...

| Scholarly Commentary | Mass Media | **Social Activity** |
| Blogs, Reviews, Wikipedia, etc. | | Twitter, Facebook, etc. |

Social activity

89 mentions from 3 sources
Mentions characterized by rapid, brief engagement on platforms used by the general population, such as Twitter, Facebook and Google +.

About Snowball Metrics

Twitter	Facebook	Google +
84 Tweets	**4** Posts	**1** Post

Twitter – 84 tweets from 66 accounts

Jason Chin @infoecho | 07 January

Moon♥ @LovelyMoonB | 31 October 2014

Nicole Cloonan @ncloonan | 14 October 2014

Joon @joonomics | 14 October 2014

View 10 more

Facebook – 4 posts from 4 accounts

Vaccini - Clínica de Vacinação | 01 April
Vacinas da rede pública e privada são de boa qualidade. Mesmo que você já tenha tido HPV, deve tomar a vacina.

Sociedade Brasileira de Imunizações (SBIm) | 26 March
"Existe diferença entre as vacinas da rede pública e da rede particular?" "Quem esquece de tomar a 2ª dose de uma vacina na data prevista deve recomeçar o esquema vacinal?" "Já tive hepatite B, preciso me vacinar?" Confira as respostas para essas perguntas

Integromics- IT for Life Sciences | 06 May 2013
Hierarchical Genome Assembly: New de novo assembly method , uses @PacBio 's technology http://t.co/zbS5rFqla7

Molecular Creativity | 06 May 2013
Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data
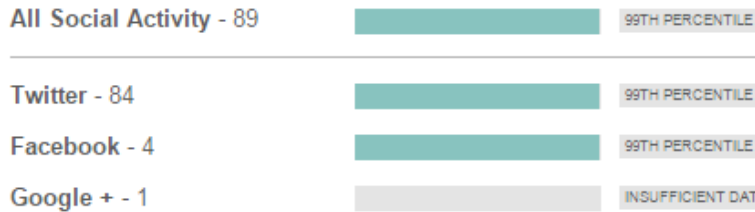http://www.nature.com/nmeth/journal/vaop/ncurrent/full/nmeth.2474.html
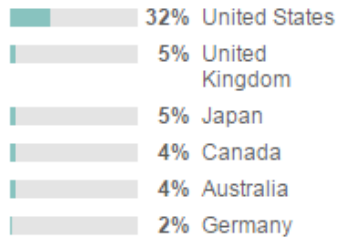
Google + – 1 post from 1 account

* Data provided by altmetric.com

Benchmarking ❓

Measures of activity relative to specific research domains, based on all sources of Social Activity

Compared to [Biotechnology ▾] *articles of same age and document type*

All Social Activity - 89	▇▇▇▇▇▇	99TH PERCENTILE
Twitter - 84	▇▇▇▇▇▇	99TH PERCENTILE
Facebook - 4	▇▇▇▇▇▇	99TH PERCENTILE
Google + - 1	▇▇▇▇▇▇	INSUFFICIENT DATA

Twitter demographics

▇▇	**32%**	United States
▌	**5%**	United Kingdom
▌	**5%**	Japan
▌	**4%**	Canada
▌	**4%**	Australia
▌	**2%**	Germany

View all

Social Activity tab includes:

- Percentile Benchmarks for Social Activity and underlying data sources
- Twitter demographic map