ORCID

CONNECTING RESEARCH AND RESEARCHERS

Getting Credit for Writing Scientific Software

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The Problem: Name Ambiguity

Reliable linking of researchers with their research is impossible using their names

The scholarly record
is broken

The solution: unique author identifiers

http://www.flickr.com/photos/runesteiness/4983827599/

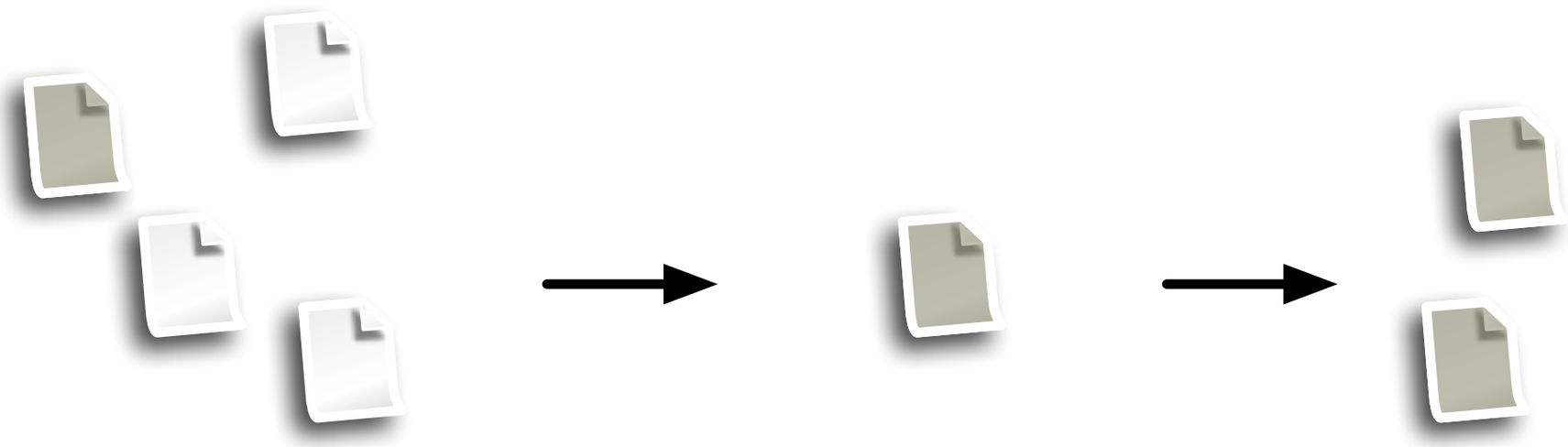
Martin Fenner
http://orcid.org/0000-0003-1419-2405

Benefits: Discovery

Reliable linking of researchers with their research facilitates discovery

Easier to find research outputs by a particular researcher

Easier to find other researchers through co-authors

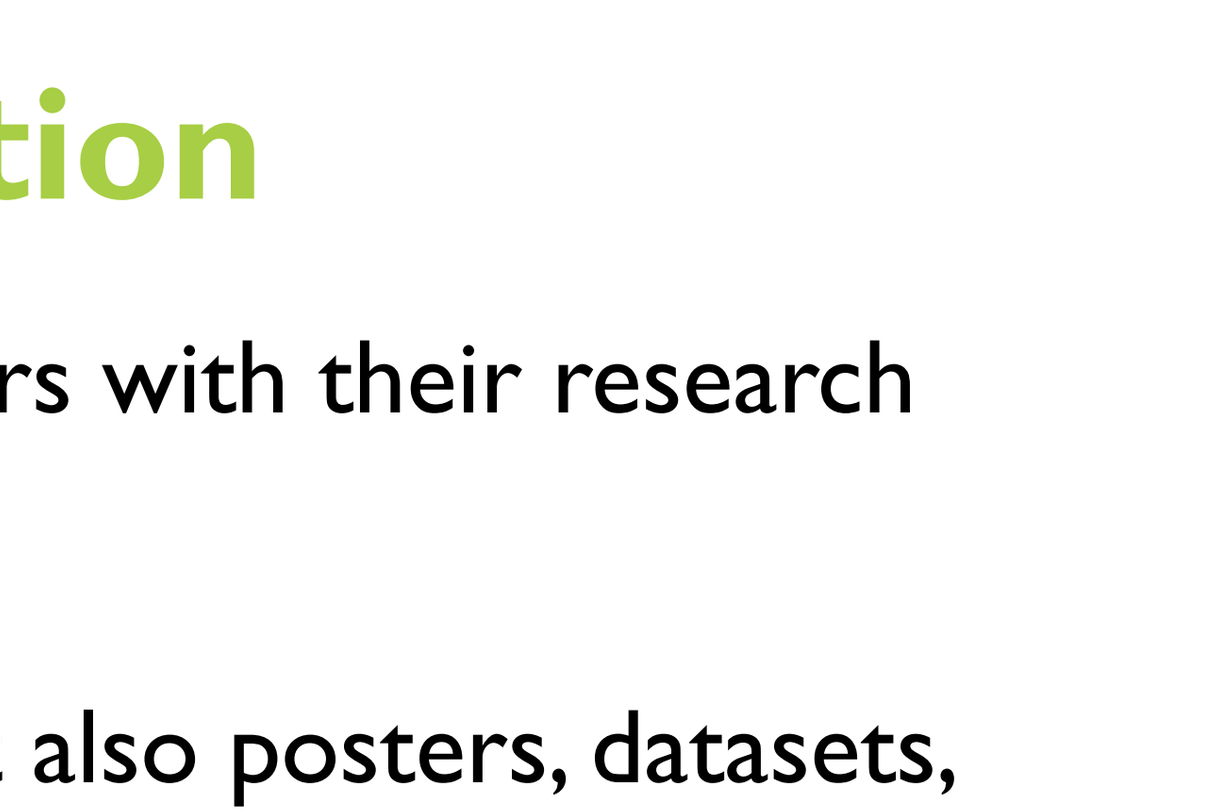


Benefits: Evaluation

Reliable linking of researchers with their research facilitates evaluation

Not just journal articles, but also posters, datasets, book chapters, software, etc.

Not just research outputs, but also funding, people, etc.



Why is ORCID a Solution?

Global	Not limited by discipline, institution or geography
Open	Inclusive and transparently governed not-for-profit Data and source code available under recognized open licenses
Integrated	Third-party seeding of profiles Part of institutional, publisher, and funding agency infrastructure

Who can create an ORCID identifier?

The Researcher

His University/Research Organization

with permission from the researcher

ORCID Members

ORCID launched in October, 2012 and had 27 member organizations as of January 6, 2013:

Universities/Research Organizations: Boston University, CalTech, CERN, Cornell, Harvard University, MSKCC, NYU Langone Medical Center, Universidad de Oviedo, University of Michigan

Associations: APA, APS, ACM, MLA

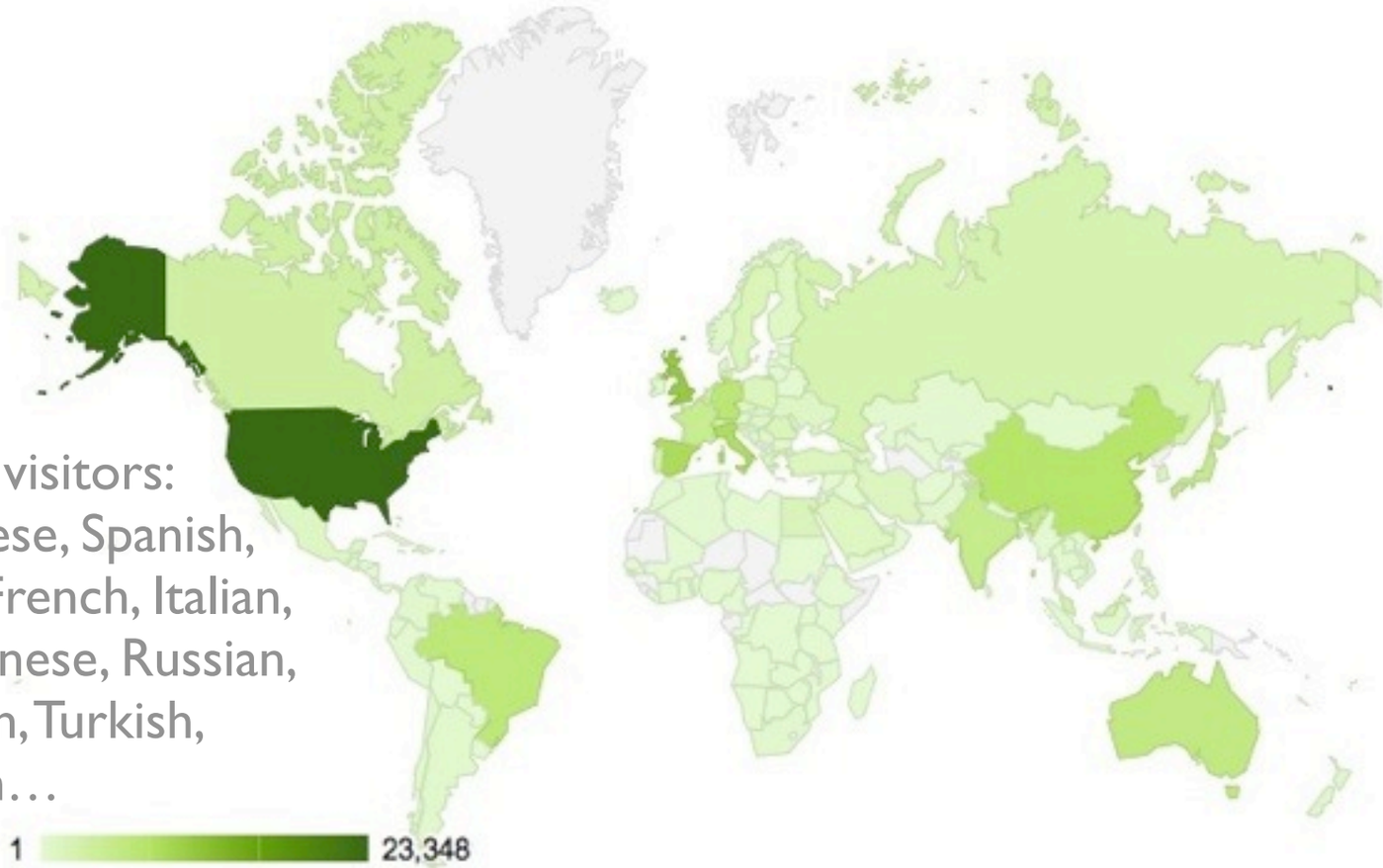
Funders: NIH, Wellcome Trust

Publishers/Publishing Vendors: Aries, Copernicus, Elsevier, Epistemio, Hindawi, Nature, Springer, Wiley Blackwell

Third Party Systems: Faculty of 1000, Thomson Reuters, Figshare, CrossRef

ORCID is international

As of January 14, ORCID had 51,143 registered users.



Languages of visitors:
English, Chinese, Spanish, Portuguese, French, Italian, German, Japanese, Russian, Polish, Korean, Turkish, Dutch, Czech…

27 countries with > 1000 visitors, 68 with >100.

Country / Territory	Visits	% Visits
1. United States	23,347	16.79%
2. United Kingdom	10,621	7.64%
3. Spain	8,538	6.14%
4. Italy	8,284	5.96%
5. China	7,435	5.35%
6. Germany	6,598	4.75%
7. Brazil	6,448	4.64%
8. Australia	5,686	4.09%
9. India	4,955	3.56%
10. Japan	4,853	3.49%

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SEARCH

ORCID
Connecting Research and Researchers

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SIGN IN | REGISTER FOR AN ORCID ID

http://orcid.org/register

Register for an ORCID iD

ORCID provides a persistent digital identifier that distinguishes you from every other researcher and, through integration in key research workflows such as manuscript and grant submission, supports automated linkages between you and your professional activities ensuring that your work is recognized.

First name *

Last name

Email *

Re-enter email *

Password *

Confirm password *

Default privacy for new works

Public

You will be able to add information to your ORCID record about work that you have done. This privacy setting will apply to all works/publications added to your record. You can change this any time.

Notification Email

- [ ] Send me notifications about changes to my ORCID Record.
- [ ] Send me information about events ORCID is sponsoring and ORCID news.

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Martin H. Fenner

0000-0003-1419-2405

View Public ORCID Record

UPDATE

Also known as:

M Fenner
Martin Fenner
Martin Hellmut Fenner
MH Fenner

Country: DE

Websites:

Blog
ScienceCard

Other IDs:

Scopus Author ID 7006600825

Import Research Activities

Add information about you to help distinguish you from other researchers.

0 Affiliations COMING SOON | 42 Works UPDATE | 0 Grants COMING SOON | 0 Patents COMING SOON

Personal Information UPDATE

Biography

Software for Scientists.

Affiliations

Works UPDATE

Blogs, Wikis und Podcasts im Unterricht Oct-2008 — Public

DOI: 10.1002/biuz.200890080

Fenner, M, 2008, 'Blogs, Wikis und Podcasts im Unterricht', *Biologie in unserer Zeit*, vol. 38, no. 5, pp. 284-286.

Carboplatin plus weekly docetaxel as salvage chemotherapy in docetaxel-resistant and castration-resistant prostate cancer: — Public

World Journal of Urology 2010

DOI: 10.1007/s00345-010-0527-5

Martin Fenner

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Add information about you to help distinguish you from other researchers.

Connecting Research and Researchers

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1		**Fenner, Martin H.** Fenner, M. H.	40	Medicine, Engineering, Chemistry, Social Sciences, Biochemistry, Genetics and Molecular Biology, Neuroscience, Physics and Astronomy, Materials Science, Pharmacology, Toxicology and Pharmaceutics, Multidisciplinary	Medizinische Hochschule Hannover (MHH)	Hannover	Germany

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Thornton Group Software

The following software packages have been made publicly available by members of the Thornton Group.

Software	Description
ArchSchema	ArchSchema is a java program that generates dynamic plots of related Pfam domain architectures. Authors: Asif Tamuri and Roman Laskowski
LIGPLOT	LIGPLOT is a program which plots schematic diagrams of protein-ligand interactions. Authors: Andrew Wallace and Roman Laskowski.
PROCHECK	PROCHECK checks the stereochemical quality of protein structures. Authors: Roman Laskowski. Malcolm MacArthur, David Smith, David Jones, Gail Hutchinson, Louise Morris, David Moss and Janet Thornton.
PROCHECK-COMP	PROCOMP Compares residue-by-residue geometry of a set of closely-related protein structures. PROCOMP is part of PROCHECK (see above). Author: Roman Laskowski.
PROCHECK-NMR	PROCHECK-NMR is a suite of programs that have been derived from the PROCHECK programs to analyse ensembles of protein structures solved by NMR. Authors: Roman Laskowski and Malcolm MacArthur.
QUASIPROX	Quaternary Structure Inference of Proteins from their Crystals. Author: Hannes Posntingl.
SMSD	SMSD (small molecule subgraph detector) is a program to find similar molecules and reactions to a given one. Author: Syed Asad Rahman (asad@ebi.ac.uk).
SURFNET	Program to generate surfaces, and void regions between surfaces, from coordinate data supplied in a PDB file. Author: Roman Laskowski. N.B. This link is still hosted at UCL.

Contact

We would like to encourage laboratories wishing to discuss any collaborations to contact us. For information, comments and/or suggestions please contact us.

PUBLIC

articlemetrics / alm

Article-Level Metrics - Alternative Measures to Gauge the Impact of Research — Read more
http://article-level-metrics.plos.org/

alm /

955 commits

ALM-158 fixed parsing for attributes in scienceseeker XML

mfenner authored 6 hours ago — latest commit 77af3e680e

app	6 hours ago	ALM-158 fixed parsing for attributes in scienceseeker XML [mfenner]
config	10 hours ago	ALM-193 increased timeout for jobs [mfenner]
db	2 days ago	ALM-153 tried to fix scienceseeker namespace errors [mfenner]
features	a day ago	ALM-154 display responses of past 31 days and not 30 days to be in sy... [mfenner]
lib	6 hours ago	ALM-158 fixed parsing for attributes in scienceseeker XML [mfenner]
log	11 months ago	initial checkin of a blank ruby on rails application [jsong-plos]
public	14 days ago	ALM-157 removed precompiled assets [mfenner]
script	8 months ago	Added Cucumber files [mfenner]
spec	6 hours ago	ALM-158 fixed parsing for attributes in scienceseeker XML [mfenner]
vendor	2 days ago	ALM-153 tried to fix scienceseeker namespace errors [mfenner]
.gitignore	7 days ago	ALM-178 don't include data_bags folder in version control [mfenner]

RailsContributors

Rails Contributors - All time

See names mapping →

Showing 2840 people

	Name	Commits
#1	Jeremy Kemper	3977
#2	David Heinemeier Hansson	3595
#3	Aaron Patterson	2962
#4	José Valim	2931
#5	Xavier Noria	1840
#6	Santiago Pastorino	1626
#7	Josh Peek	1230
#8	Rafael Mendonça França	1145
#9	Jon Leighton	1120
#10	Vijay Dev	1090
#11	Pratik Naik	945
#12	Yehuda Katz	895
#13	Carlos Antonio da Silva	888
#14	Michael Koziarski	757
#15	Rick Olson	595
#16	Piotr Sarnacki	537

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creator
publicationYear
publisher
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has_metadata

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13 documents found in 264ms
Page 1 of 2

1. NCAR Command Language (NCL) [version 6.0.0]
doi:10.5065/D6WD3XH5 Software : Data analysis and visualization software
Brown, Dave • Brownrigg, Richard • Haley, Mary • Huang, Wei

2. A case study for efficient management of high throughput primary lab datasource code [version 1.1]
doi:10.5447/IPK/2011/0 Software : source code
Colmsee, Christian • Flemming, Steffen • Klapperstück, Matthias • Lange, Matthias • Scholz, Uwe

3. Workspace
doi:10.4231/D3FF3KZ9Q Software
Clark, S

4. Crystal Viewer Tool
doi:10.4231/D3VH5CH5N Software
Mehrotra, Saumitra

5. Crystal Viewer Tool
doi:10.4231/D3NC5SB92 Software
Paul, Abhijeet

6. Demuxipy - software for demultiplexing hierarchically tagged 454 reads
doi:10.6079/J9DMUX Software
Brant C. Faircloth

7. Illumiprocessor - software for Illumina read quality filtering
doi:10.6079/J9ILL Software
Brant C. Faircloth

8. Medici [version 1.4]
doi:10.4231/D3KP7TQ85 Software : Simulation Tool
Clark, Steven

9. Meep [version 2.0]
doi:10.4231/D3JQ0ST8G Software : Simulation Tool
Ouyang, Jing • Wang, Xufeng • Qi, Minghao

10. Polymer Modeler [version 3.2]
doi:10.4231/D3PG1HN27 Software : Simulation Tool
Haley, Benjamin • Wilson, Nate • Li, Chunyu • Arguelles, Andrea • Jaramillo, Eugenio • (et. al.)

Brief reports

Open Access

RMol: A Toolset for Transforming SD/Molfile structure information into R Objects

Martin Grabner, **Kurt Varmuza** and **Matthias Dehmer**

Source Code for Biology and Medicine 2012, **7**:12 doi:10.1186/1751-0473-7-12
Published: 14 November 2012

Abstract (provisional)

Background

The graph-theoretical analysis of molecular networks has a long tradition in chemoinformatics. As demonstrated frequently, a well designed format to encode chemical structures and structure-related information of organic compounds is the Molfile format. But when it comes to use modern programming languages for statistical data analysis in Bio- and Chemoinformatics, R as one of the most powerful free languages lacks tools to process R Molfile data collections and import molecular network data into R.

Results

We design an R object which allows a lossless information mapping of structural information from Molfiles into R objects. This provides the basis to use the RMol object as an anchor for connecting Molfile data collections with R libraries for analyzing graphs. Associated with the RMol objects, a set of R functions completes the toolset to organize, describe and manipulate the converted data sets. Further, we bypass R-typical limits for manipulating large data sets by storing R objects in bz-compressed serialized files instead of employing RData files.

Conclusions

By design, RMol is a R tool set without dependencies to other libraries or programming languages. It is useful to integrate into pipelines for serialized batch analysis by using network data and, therefore, helps to process sdf-data sets in R effeciently. It is freely available under the BSD licence. The script source can be downloaded from http://sourceforge.net/p/rmol-toolset.

Source Code for Biology and Medicine
Volume 7

Viewing options
Abstract
Provisional PDF (327KB)

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RESEARCH ARTICLE

PIPS: Pathogenicity Island Prediction Software

Siomar C. Soares, Vinícius A. C. Abreu, Rommel T. J. Ramos, Louise Cerdeira, Artur Silva, Jan Baumbach, Eva Trost, Andreas Tauch, Raphael Hirata Jr., Ana L. Mattos-Guaraldi, Anderson Miyoshi, Vasco Azevedo

Article Usage

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Feb 15, 2012 (publication date) through Jan 30, 2013*

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PLOS	1,651	402	41	**2,094**
PMC	203	97	n.a.	**300**
Totals	**1,854**	**499**	**41**	**2,394**
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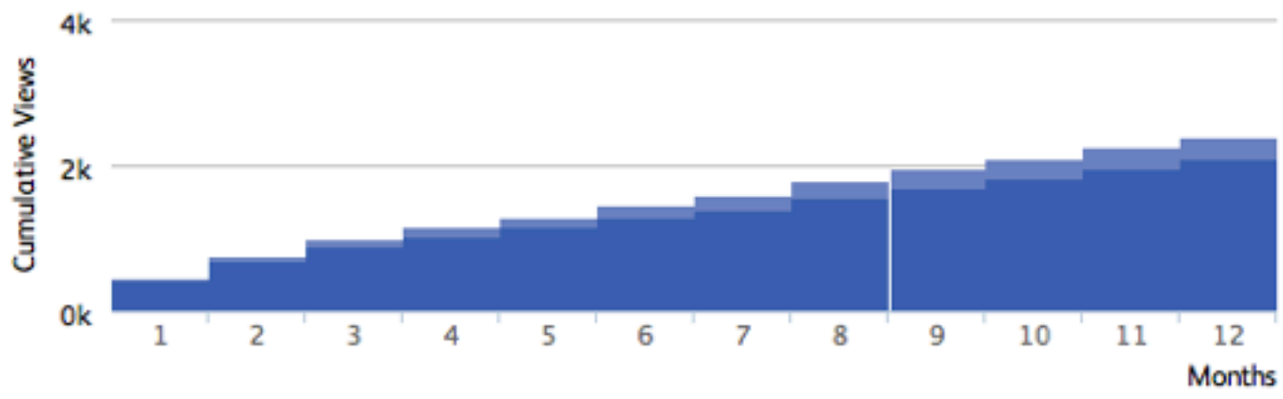

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alm

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software

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(2012) Article-Level Metrics - Alternative Measures to Gauge the Impact of Research *GitHub*

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DOI: 10.1002/biuz.200890080
Fenner, M, 2008, 'Blogs, Wikis und Podcasts im Unterricht', *Biologie in unserer Zeit*, vol. 38, no. 5, pp. 284-286.

Carboplatin plus weekly docetaxel as salvage chemotherapy in docetaxel-resistant and castration-resistant prostate cancer: World Journal of Urology 2010 — Public

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martin fenner

Status Martin Fenner

TYPE

- journal_article (414,851)
- conference_paper (7,734)

YEAR

- 2012 (29,988)
- 2011 (28,623)
- 2010 (27,776)
- 2009 (27,567)
- 2008 (23,125)
- 2007 (20,026)
- 2006 (17,717)
- 2005 (15,207)
- 2004 (14,018)
- 2003 (12,395)

OA STATUS

- Other (412,570)
- Open Access (10,015)

PUBLICATION

- ChemInform (3,714)
- Journal of the American Chemical Society (2,684)
- Nature (2,375)
- PLoS ONE (2,335)

SORT BY: **RELEVANCE** PUBLICATION YEAR

PAGE 1 OF 422,585 RESULTS

Duplication: stop favouring applicant with longest list

Published **6 Mar 2008** in **Nature** , volume **452** , issue **7183** , on pages **29** to **29**

Martin Fenner

dx.doi.org/10.1038/452029a More IN YOUR PROFILE

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Published **22 Mar 2012** in **Nature Materials** , volume **11** , issue **4**

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dx.doi.org/10.1038/nmat3283 More IN YOUR PROFILE

ORCID: Unique Identifiers for Authors and Contributors

Published **2011** in **Information Standards Quarterly** , volume **23** , issue **3** , on page **10**

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CrossRef search interface

cr-search /

65 commits

Do not use MongoData in app.rb where Sinatra settings (with mongo col… ···

kjw authored a day ago latest commit 334f0e0797

.bundle	6 months ago	Add bundler support. [Karl Ward]
conf	a day ago	Remove some history. [kjw]
lib	a day ago	Do not use MongoData in app.rb where Sinatra settings (with mongo col… [kjw]
public	6 days ago	New "beta" logo and shorter search box. [kjw]
views	6 days ago	Mention need to set content type to json on /links requests. [kjw]
Gemfile	18 days ago	Fix up ORCID updates and deposits. [kjw]
Gemfile.lock	2 months ago	Few fixes to result.rb. [Karl Ward]
Rakefile	18 days ago	Fix up ORCID updates and deposits. [kjw]
app.rb	a day ago	Do not use MongoData in app.rb where Sinatra settings (with mongo col… [kjw]
config.ru	6 months ago	Merge branch 'master' of github.com:CrossRef/cr-search [kjw]
urls.txt	4 months ago	Siege urls.txt file. Slight correct to API docs. [kjw]