

Rafael C Jimenez

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

4,610
citations

331670

21
h-index

197818

49
g-index

55
all docs

55
docs citations

55
times ranked

8813
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Ten simple rules to run a successful BioHackathon. PLoS Computational Biology, 2020, 16, e1007808. | 3.2 | 7 |
| 2 | The bio.tools registry of software tools and data resources for the life sciences. Genome Biology, 2019, 20, 164. | 8.8 | 39 |
| 3 | Implementation and relevance of FAIR data principles in biopharmaceutical R&D. Drug Discovery Today, 2019, 24, 933-938. | 6.4 | 95 |
| 4 | Community Organizations: Changing the Culture in Which Research Software Is Developed and Sustained. Computing in Science and Engineering, 2019, 21, 8-24. | 1.2 | 22 |
| 5 | Uniform resolution of compact identifiers for biomedical data. Scientific Data, 2018, 5, 180029. | 5.3 | 50 |
| 6 | Recommendations for the packaging and containerizing of bioinformatics software. F1000Research, 2018, 7, 742. | 1.6 | 27 |
| 7 | Recommendations for the packaging and containerizing of bioinformatics software. F1000Research, 2018, 7, 742. | 1.6 | 29 |
| 8 | BioCIDER: a Contextualisation InDEx for biological Resources discovery. Bioinformatics, 2017, 33, 2607-2608. | 4.1 | 1 |
| 9 | Discovering and linking public omics data sets using the Omics Discovery Index. Nature Biotechnology, 2017, 35, 406-409. | 17.5 | 159 |
| 10 | BioContainers: an open-source and community-driven framework for software standardization. Bioinformatics, 2017, 33, 2580-2582. | 4.1 | 205 |
| 11 | Four simple recommendations to encourage best practices in research software. F1000Research, 2017, 6, 876. | 1.6 | 88 |
| 12 | General guidelines for biomedical software development. F1000Research, 2017, 6, 273. | 1.6 | 7 |
| 13 | General guidelines for biomedical software development. F1000Research, 2017, 6, 273. | 1.6 | 15 |
| 14 | A community proposal to integrate proteomics activities in ELIXIR. F1000Research, 2017, 6, 875. | 1.6 | 13 |
| 15 | The future of metabolomics in ELIXIR. F1000Research, 2017, 6, 1649. | 1.6 | 19 |
| 16 | The future of metabolomics in ELIXIR. F1000Research, 2017, 6, 1649. | 1.6 | 11 |
| 17 | Identifiers for the 21st century: How to design, provision, and reuse persistent identifiers to maximize utility and impact of life science data. PLoS Biology, 2017, 15, e2001414. | 5.6 | 97 |
| 18 | Tools and data services registry: a community effort to document bioinformatics resources. Nucleic Acids Research, 2016, 44, D38-D47. | 14.5 | 113 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Top 10 metrics for life science software good practices. F1000Research, 2016, 5, 2000. | 1.6 | 14 |
| 20 | Data integration in biological research: an overview. Journal of Biological Research, 2015, 22, 9. | 2.1 | 59 |
| 21 | Future opportunities and trends for e-infrastructures and life sciences: going beyond the grid to enable life science data analysis. Frontiers in Genetics, 2015, 6, 197. | 2.3 | 8 |
| 22 | The GOBLET training portal: a global repository of bioinformatics training materials, courses and trainers. Bioinformatics, 2015, 31, 140-142. | 4.1 | 34 |
| 23 | The MIntAct project—IntAct as a common curation platform for 11 molecular interaction databases. Nucleic Acids Research, 2014, 42, D358-D363. | 14.5 | 1,634 |
| 24 | KEGGViewer, a BioJS component to visualize KEGG Pathways. F1000Research, 2014, 3, 43. | 1.6 | 11 |
| 25 | PsicquicGraph, a BioJS component to visualize molecular interactions from PSICQUIC servers. F1000Research, 2014, 3, 44. | 1.6 | 5 |
| 26 | Sequence, a BioJS component for visualising sequences. F1000Research, 2014, 3, 52. | 1.6 | 9 |
| 27 | BioJS: an open source standard for biological visualisation – its status in 2014. F1000Research, 2014, 3, 55. | 1.6 | 22 |
| 28 | wigExplorer, a BioJS component to visualise wig data. F1000Research, 2014, 3, 53. | 1.6 | 4 |
| 29 | wigExplorer, a BioJS component to visualise wig data. F1000Research, 2014, 3, 53. | 1.6 | 3 |
| 30 | BioJS: an open source JavaScript framework for biological data visualization. Bioinformatics, 2013, 29, 1103-1104. | 4.1 | 110 |
| 31 | Best practices in bioinformatics training for life scientists. Briefings in Bioinformatics, 2013, 14, 528-537. | 6.5 | 51 |
| 32 | Bioinformatics Workflows and Web Services in Systems Biology Made Easy for Experimentalists. Methods in Molecular Biology, 2013, 1021, 299-310. | 0.9 | 4 |
| 33 | iAnn: an event sharing platform for the life sciences. Bioinformatics, 2013, 29, 1919-1921. | 4.1 | 6 |
| 34 | Integration of Cardiac Proteome Biology and Medicine by a Specialized Knowledgebase. Circulation Research, 2013, 113, 1043-1053. | 4.5 | 65 |
| 35 | A new reference implementation of the PSICQUIC web service. Nucleic Acids Research, 2013, 41, W601-W606. | 14.5 | 91 |
| 36 | Proteomics Data Exchange and Storage: The Need for Common Standards and Public Repositories. Methods in Molecular Biology, 2013, 1007, 317-333. | 0.9 | 11 |

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|----|--|------|-----------|
| 37 | Teaching the Fundamentals of Biological Data Integration Using Classroom Games. PLoS Computational Biology, 2012, 8, e1002789. | 3.2 | 21 |
| 38 | Bioinformatics Training Network (BTN): a community resource for bioinformatics trainers. Briefings in Bioinformatics, 2012, 13, 383-389. | 6.5 | 23 |
| 39 | The IntAct molecular interaction database in 2012. Nucleic Acids Research, 2012, 40, D841-D846. | 14.5 | 962 |
| 40 | MyDas, an Extensible Java DAS Server. PLoS ONE, 2012, 7, e44180. | 2.5 | 2 |
| 41 | PSICQUIC and PSISCORE: accessing and scoring molecular interactions. Nature Methods, 2011, 8, 528-529. | 19.0 | 274 |
| 42 | myKaryoView: A Light-Weight Client for Visualization of Genomic Data. PLoS ONE, 2011, 6, e26345. | 2.5 | 5 |
| 43 | easyDAS: Automatic creation of DAS servers. BMC Bioinformatics, 2011, 12, 23. | 2.6 | 6 |
| 44 | DAS Writeback: A Collaborative Annotation System. BMC Bioinformatics, 2011, 12, 143. | 2.6 | 4 |
| 45 | Dasty3, a WEB framework for DAS. Bioinformatics, 2011, 27, 2616-2617. | 4.1 | 14 |
| 46 | OntoDas " a tool for facilitating the construction of complex queries to the Gene Ontology. BMC Bioinformatics, 2008, 9, 437. | 2.6 | 4 |
| 47 | Integrating biological data " the Distributed Annotation System. BMC Bioinformatics, 2008, 9, S3. | 2.6 | 87 |
| 48 | The Protein Feature Ontology: a tool for the unification of protein feature annotations. Bioinformatics, 2008, 24, 2767-2772. | 4.1 | 19 |
| 49 | Dasty2, an Ajax protein DAS client. Bioinformatics, 2008, 24, 2119-2121. | 4.1 | 25 |