

# Rafael C Jimenez

## List of Publications by Year in descending order

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Version: 2024-02-01

49  
papers

4,610  
citations

331259

21  
h-index

197535

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.	1.5	7
2	The bio.tools registry of software tools and data resources for the life sciences. Genome Biology, 2019, 20, 164.	3.8	39
3	Implementation and relevance of FAIR data principles in biopharmaceutical R&D. Drug Discovery Today, 2019, 24, 933-938.	3.2	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.	2.4	50
6	Recommendations for the packaging and containerizing of bioinformatics software. F1000Research, 2018, 7, 742.	0.8	27
7	Recommendations for the packaging and containerizing of bioinformatics software. F1000Research, 2018, 7, 742.	0.8	29
8	BioCIDER: a Contextualisation InDEx for biological Resources discovery. Bioinformatics, 2017, 33, 2607-2608.	1.8	1
9	Discovering and linking public omics data sets using the Omics Discovery Index. Nature Biotechnology, 2017, 35, 406-409.	9.4	159
10	BioContainers: an open-source and community-driven framework for software standardization. Bioinformatics, 2017, 33, 2580-2582.	1.8	205
11	Four simple recommendations to encourage best practices in research software. F1000Research, 2017, 6, 876.	0.8	88
12	General guidelines for biomedical software development. F1000Research, 2017, 6, 273.	0.8	7
13	General guidelines for biomedical software development. F1000Research, 2017, 6, 273.	0.8	15
14	A community proposal to integrate proteomics activities in ELIXIR. F1000Research, 2017, 6, 875.	0.8	13
15	The future of metabolomics in ELIXIR. F1000Research, 2017, 6, 1649.	0.8	19
16	The future of metabolomics in ELIXIR. F1000Research, 2017, 6, 1649.	0.8	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.	2.6	97
18	Tools and data services registry: a community effort to document bioinformatics resources. Nucleic Acids Research, 2016, 44, D38-D47.	6.5	113

#	ARTICLE	IF	CITATIONS
19	Top 10 metrics for life science software good practices. F1000Research, 2016, 5, 2000.	0.8	14
20	Data integration in biological research: an overview. Journal of Biological Research, 2015, 22, 9.	2.2	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.	1.1	8
22	The GOBLET training portal: a global repository of bioinformatics training materials, courses and trainers. Bioinformatics, 2015, 31, 140-142.	1.8	34
23	The MIntAct project—IntAct as a common curation platform for 11 molecular interaction databases. Nucleic Acids Research, 2014, 42, D358-D363.	6.5	1,634
24	KEGGViewer, a BioJS component to visualize KEGG Pathways. F1000Research, 2014, 3, 43.	0.8	11
25	PsicquicGraph, a BioJS component to visualize molecular interactions from PSICQUIC servers. F1000Research, 2014, 3, 44.	0.8	5
26	Sequence, a BioJS component for visualising sequences. F1000Research, 2014, 3, 52.	0.8	9
27	BioJS: an open source standard for biological visualisation – its status in 2014. F1000Research, 2014, 3, 55.	0.8	22
28	wigExplorer, a BioJS component to visualise wig data. F1000Research, 2014, 3, 53.	0.8	4
29	wigExplorer, a BioJS component to visualise wig data. F1000Research, 2014, 3, 53.	0.8	3
30	BioJS: an open source JavaScript framework for biological data visualization. Bioinformatics, 2013, 29, 1103-1104.	1.8	110
31	Best practices in bioinformatics training for life scientists. Briefings in Bioinformatics, 2013, 14, 528-537.	3.2	51
32	Bioinformatics Workflows and Web Services in Systems Biology Made Easy for Experimentalists. Methods in Molecular Biology, 2013, 1021, 299-310.	0.4	4
33	iAnn: an event sharing platform for the life sciences. Bioinformatics, 2013, 29, 1919-1921.	1.8	6
34	Integration of Cardiac Proteome Biology and Medicine by a Specialized Knowledgebase. Circulation Research, 2013, 113, 1043-1053.	2.0	65
35	A new reference implementation of the PSICQUIC web service. Nucleic Acids Research, 2013, 41, W601-W606.	6.5	91
36	Proteomics Data Exchange and Storage: The Need for Common Standards and Public Repositories. Methods in Molecular Biology, 2013, 1007, 317-333.	0.4	11

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37	Teaching the Fundamentals of Biological Data Integration Using Classroom Games. PLoS Computational Biology, 2012, 8, e1002789.	1.5	21
38	Bioinformatics Training Network (BTN): a community resource for bioinformatics trainers. Briefings in Bioinformatics, 2012, 13, 383-389.	3.2	23
39	The IntAct molecular interaction database in 2012. Nucleic Acids Research, 2012, 40, D841-D846.	6.5	962
40	MyDas, an Extensible Java DAS Server. PLoS ONE, 2012, 7, e44180.	1.1	2
41	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. Nature Methods, 2011, 8, 528-529.	9.0	274
42	myKaryoView: A Light-Weight Client for Visualization of Genomic Data. PLoS ONE, 2011, 6, e26345.	1.1	5
43	easyDAS: Automatic creation of DAS servers. BMC Bioinformatics, 2011, 12, 23.	1.2	6
44	DAS Writeback: A Collaborative Annotation System. BMC Bioinformatics, 2011, 12, 143.	1.2	4
45	Dasty3, a WEB framework for DAS. Bioinformatics, 2011, 27, 2616-2617.	1.8	14
46	OntoDas " a tool for facilitating the construction of complex queries to the Gene Ontology. BMC Bioinformatics, 2008, 9, 437.	1.2	4
47	Integrating biological data " the Distributed Annotation System. BMC Bioinformatics, 2008, 9, S3.	1.2	87
48	The Protein Feature Ontology: a tool for the unification of protein feature annotations. Bioinformatics, 2008, 24, 2767-2772.	1.8	19
49	Dasty2, an Ajax protein DAS client. Bioinformatics, 2008, 24, 2119-2121.	1.8	25