

John Boyle

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

838
citations

687363

13
h-index

580821

25
g-index

34
all docs

34
docs citations

34
times ranked

1457
citing authors

#	ARTICLE	IF	CITATIONS
1	Is there a gender gap in chemical sciences scholarly communication?. Chemical Science, 2020, 11, 2277-2301.	7.4	40
2	Managing Chaos: Bridging the cultural divide between engineers and scientists working within the life sciences. Computing in Science and Engineering, 2019, , 1-1.	1.2	2
3	Chemlistem: chemical named entity recognition using recurrent neural networks. Journal of Cheminformatics, 2018, 10, 59.	6.1	26
4	Improving the learning of chemical-protein interactions from literature using transfer learning and specialized word embeddings. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	34
5	There and back again. Nature Biotechnology, 2013, 31, 13-15.	17.5	0
6	Biology must develop its own big-data systems. Nature, 2013, 499, 7-7.	27.8	21
7	There and back again. Bioentrepreneur, 2012, , .	0.2	0
8	Mining PeptideAtlas for Biomarkers and Therapeutics in Human Disease. Current Pharmaceutical Design, 2012, 18, 748-754.	1.9	2
9	Interfaces to PeptideAtlas: a case study of standard data access systems. Briefings in Bioinformatics, 2012, 13, 615-626.	6.5	1
10	Methods for visual mining of genomic and proteomic data atlases. BMC Bioinformatics, 2012, 13, 58.	2.6	8
11	EPEPT: A web service for enhanced P-value estimation in permutation tests. BMC Bioinformatics, 2011, 12, 411.	2.6	6
12	SEQADAPT: an adaptable system for the tracking, storage and analysis of high throughput sequencing experiments. BMC Bioinformatics, 2010, 11, 377.	2.6	0
13	QTIPS: A novel method of unsupervised determination of isotopic amino acid distribution in SILAC experiments. Journal of the American Society for Mass Spectrometry, 2010, 21, 1417-1422.	2.8	12
14	mspecLINE: bridging knowledge of human disease with the proteome. BMC Medical Genomics, 2010, 3, 7.	1.5	9
15	Genome-Wide Analysis of Effectors of Peroxisome Biogenesis. PLoS ONE, 2010, 5, e11953.	2.5	24
16	Howdah - A Flexible Pipeline Framework for Analyzing Genomic Data. , 2010, , .		0
17	An Integration Architecture Designed to Deal with the Issues of Biological Scope, Scale and Complexity. Lecture Notes in Computer Science, 2010, , 179-191.	1.3	1
18	Adaptable data management for systems biology investigations. BMC Bioinformatics, 2009, 10, 79.	2.6	18

#	ARTICLE	IF	CITATIONS
19	Cytoscape: A Community-Based Framework for Network Modeling. <i>Methods in Molecular Biology</i> , 2009, 563, 219-239.	0.9	191
20	Managing Chaos: Lessons Learned Developing Software in the Life Sciences. <i>Computing in Science and Engineering</i> , 2009, 11, 20-29.	1.2	17
21	Programming Languages. , 2009, , 403-440.		1
22	Systems biology driven software design for the research enterprise. <i>BMC Bioinformatics</i> , 2008, 9, 295.	2.6	19
23	Genome-wide analysis of signaling networks regulating fatty acid-induced gene expression and organelle biogenesis. <i>Journal of Cell Biology</i> , 2008, 181, 281-292.	5.2	55
24	A Case Study on 3-D Reconstruction and Shape Description of Peroxisomes in Yeast. , 2007, , .		1
25	Yng1 PHD Finger Binding to H3 Trimethylated at K4 Promotes NuA3 HAT Activity at K14 of H3 and Transcription at a Subset of Targeted ORFs. <i>Molecular Cell</i> , 2006, 24, 785-796.	9.7	283
26	Gene-Expression Omnibus integration and clustering Tools in SeqExpress. <i>Bioinformatics</i> , 2005, 21, 2550-2551.	4.1	22
27	SeqExpress: desktop analysis and visualization tool for gene expression experiments. <i>Bioinformatics</i> , 2004, 20, 1649-1650.	4.1	9
28	From WIMPS to 3D: The Development of AMAZE. <i>Journal of Visual Languages and Computing</i> , 1996, 7, 291-319.	1.8	19
29	Design of a 3D User Interface to a Database. <i>Workshops in Computing</i> , 1995, , 127-142.	0.4	3
30	The Design of 3D Metaphors for Database Visualisation. , 1995, , 185-202.		4
31	Design of a 3D user interface to a database. <i>Lecture Notes in Computer Science</i> , 1994, , 171-185.	1.3	6