MatÃºÅ¡ KalaÅ¡

List of Publications by Year
in descending order

22 papers	832 citations	759233 12 h-index	677142 22 g-index
26 all docs	26 docs citations	26 times ranked	1704 citing authors

#	Article	IF	Citations
1	BioSimulators: a central registry of simulation engines and services for recommending specific tools. Nucleic Acids Research, 2022, 50, W108-W114.	14.5	11
2	Galaxy: A Decade of Realising CWFR Concepts. Data Intelligence, 2022, 4, 358-371.	1.5	3
3	biotoolsSchema: a formalized schema for bioinformatics software description. GigaScience, 2021, 10, .	6.4	7
4	Bioimage analysis workflows: community resources to navigate through a complex ecosystem. F1000Research, 2021, 10, 320.	1.6	12
5	Perspectives on automated composition of workflows in the life sciences. F1000Research, 2021, 10, 897.	1.6	7
6	Community curation of bioinformatics software and data resources. Briefings in Bioinformatics, 2020, 21, 1697-1705.	6.5	12
7	The bio.tools registry of software tools and data resources for the life sciences. Genome Biology, 2019, 20, 164.	8.8	39
8	Norwegian e-Infrastructure for Life Sciences (NeLS). F1000Research, 2018, 7, 968.	1.6	10
9	Robust Cross-Platform Workflows: How Technical and Scientific Communities Collaborate to Develop, Test and Share Best Practices for Data Analysis. Data Science and Engineering, 2017, 2, 232-244.	6.4	19
10	ReGaTE: Registration of Galaxy Tools in Elixir. GigaScience, 2017, 6, 1-4.	6.4	14
11	Using registries to integrate bioinformatics tools and services into workbench environments. International Journal on Software Tools for Technology Transfer, 2016, 18, 581-586.	1.9	5
12	Tools and data services registry: a community effort to document bioinformatics resources. Nucleic Acids Research, 2016, 44, D38-D47.	14.5	113
13	BioHackathon series in 2011 and 2012: penetration of ontology and linked data in life science domains. Journal of Biomedical Semantics, 2014, 5, 5.	1.6	47
14	FreeContact: fast and free software for protein contact prediction from residue co-evolution. BMC Bioinformatics, 2014, 15, 85.	2.6	146
15	Community-driven development for computational biology at Sprints, Hackathons and Codefests. BMC Bioinformatics, 2014, 15, S7.	2.6	42
16	The Genomic HyperBrowser: an analysis web server for genome-scale data. Nucleic Acids Research, 2013, 41, W133-W141.	14.5	32
17	EDAM: an ontology of bioinformatics operations, types of data and identifiers, topics and formats. Bioinformatics, 2013, 29, 1325-1332.	4.1	215
18	Sprints, Hackathons and Codefests as community gluons in computational biology. EMBnet Journal, 2013, 19, 40.	0.6	5

#	Article	IF	Citations
19	Interoperable Semantic Web services (Tutorials). Nature Precedings, 2011, , .	0.1	0
20	Identifying elemental genomic track types and representing them uniformly. BMC Bioinformatics, 2011, 12, 494.	2.6	20
21	The EMBRACE web service collection. Nucleic Acids Research, 2010, 38, W683-W688.	14.5	40
22	BioXSD: the common data-exchange format for everyday bioinformatics web services. Bioinformatics, 2010, 26, i540-i546.	4.1	20