BjÃ¶rn A GrÃ¼ning

List of Publications by Year
in descending order

52 papers	10,502 citations	394421 19 h-index	182427 51 g-index
72 all docs	72 docs citations	72 times ranked	21459 citing authors

#	Article	IF	Citations
1	Packaging research artefacts with RO-Crate. Data Science, 2022, 5, 97-138.	0.9	52
2	Pluripotency factors determine gene expression repertoire at zygotic genome activation. Nature Communications, 2022, 13, 788.	12.8	9
3	Democratizing data-independent acquisition proteomics analysis on public cloud infrastructures via the Galaxy framework. GigaScience, 2022, 11, .	6.4	13
4	Ten simple rules for making a software tool workflow-ready. PLoS Computational Biology, 2022, 18, e1009823.	3.2	7
5	Galaxy workflows for fragment-based virtual screening: a case study on the SARS-CoV-2 main protease. Journal of Cheminformatics, 2022, 14, 22.	6.1	2
6	Expanding the Galaxy's reference data. Bioinformatics Advances, 2022, 2, .	2.4	0
7	MaxQuant and MSstats in Galaxy Enable Reproducible Cloud-Based Analysis of Quantitative Proteomics Experiments for Everyone. Journal of Proteome Research, 2022, 21, 1558-1565.	3.7	8
8	Loop detection using Hi-C data with HiCExplorer. GigaScience, 2022, 11, .	6.4	17
9	ChiRA: an integrated framework for chimeric read analysis from RNA-RNA interactome and RNA structurome data. GigaScience, 2021, 10, .	6.4	6
10	Tool recommender system in Galaxy using deep learning. GigaScience, 2021, 10, .	6.4	9
11	BioContainers Registry: Searching Bioinformatics and Proteomics Tools, Packages, and Containers. Journal of Proteome Research, 2021, 20, 2056-2061.	3.7	19
12	User-friendly, scalable tools and workflows for single-cell RNA-seq analysis. Nature Methods, 2021, 18, 327-328.	19.0	26
13	Robust and efficient single-cell Hi-C clustering with approximate k-nearest neighbor graphs. Bioinformatics, 2021, 37, 4006-4013.	4.1	9
14	A constructivist-based proposal for bioinformatics teaching practices during lockdown. PLoS Computational Biology, 2021, 17, e1008922.	3.2	6
15	Fostering accessible online education using Galaxy as an e-learning platform. PLoS Computational Biology, 2021, 17, e1008923.	3.2	15
16	A SARS-CoV-2 sequence submission tool for the European Nucleotide Archive. Bioinformatics, 2021, 37, 3983-3985.	4.1	3
17	Galaxy-ML: An accessible, reproducible, and scalable machine learning toolkit for biomedicine. PLoS Computational Biology, 2021, 17, e1009014.	3.2	14
18	Ready-to-use public infrastructure for global SARS-CoV-2 monitoring. Nature Biotechnology, 2021, 39, 1178-1179.	17.5	21

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19	Metaproteomics Analysis of SARS-CoV-2-Infected Patient Samples Reveals Presence of Potential Coinfecting Microorganisms. Journal of Proteome Research, 2021, 20, 1451-1454.	3.7	15
20	A proteomics sample metadata representation for multiomics integration and big data analysis. Nature Communications, 2021, 12, 5854.	12.8	45
21	NanoGalaxy: Nanopore long-read sequencing data analysis in Galaxy. GigaScience, 2020, 9, .	6.4	23
22	Intuitive, reproducible high-throughput molecular dynamics in Galaxy: a tutorial. Journal of Cheminformatics, 2020, 12, 54.	6.1	13
23	The ChemicalToolbox: reproducible, user-friendly cheminformatics analysis on the Galaxy platform. Journal of Cheminformatics, 2020, 12, 40.	6.1	21
24	No more business as usual: Agile and effective responses to emerging pathogen threats require open data and open analytics. PLoS Pathogens, 2020, 16, e1008643.	4.7	22
25	Galaxy HiCExplorer 3: a web server for reproducible Hi-C, capture Hi-C and single-cell Hi-C data analysis, quality control and visualization. Nucleic Acids Research, 2020, 48, W177-W184.	14.5	188
26	Ewastools: Infinium Human Methylation BeadChip pipeline for population epigenetics integrated into Galaxy. GigaScience, 2020, 9, .	6.4	12
27	Survey of metaproteomics software tools for functional microbiome analysis. PLoS ONE, 2020, 15, e0241503.	2.5	28
28	Pou5f3, SoxB1, and Nanog remodel chromatin on high nucleosome affinity regions at zygotic genome activation. Genome Research, 2019, 29, 383-395.	5.5	49
29	Software engineering for scientific big data analysis. GigaScience, 2019, 8, .	6.4	20
30	The RNA workbench 2.0: next generation RNA data analysis. Nucleic Acids Research, 2019, 47, W511-W515.	14.5	13
31	GraphClust2: Annotation and discovery of structured RNAs with scalable and accessible integrative clustering. GigaScience, 2019, 8, .	6.4	12
32	Accessible and reproducible mass spectrometry imaging data analysis in Galaxy. GigaScience, 2019, 8, .	6.4	22
33	Impact of angiogenic activation and inhibition on miRNA profiles of human retinal endothelial cells. Experimental Eye Research, 2019, 181, 98-104.	2.6	18
34	Update on the moFF Algorithm for Label-Free Quantitative Proteomics. Journal of Proteome Research, 2019, 18, 728-731.	3.7	13
35	The de.NBI / ELIXIR-DE training platform - Bioinformatics training in Germany and across Europe within ELIXIR. F1000Research, 2019, 8, 1877.	1.6	1
36	The de.NBI / ELIXIR-DE training platform - Bioinformatics training in Germany and across Europe within ELIXIR. F1000Research, 2019, 8, 1877.	1.6	3

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37	High-resolution TADs reveal DNA sequences underlying genome organization in flies. Nature Communications, 2018, 9, 189.	12.8	652
38	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. Nucleic Acids Research, 2018, 46, W537-W544.	14.5	3,003
39	Recommendations for the packaging and containerizing of bioinformatics software. F1000Research, 2018, 7, 742.	1.6	27
40	Recommendations for the packaging and containerizing of bioinformatics software. F1000Research, 2018, 7, 742.	1.6	29
41	The RNA workbench: best practices for RNA and high-throughput sequencing bioinformatics in Galaxy. Nucleic Acids Research, 2017, 45, W560-W566.	14.5	38
42	EBF1 binds to EBNA2 and promotes the assembly of EBNA2 chromatin complexes in B cells. PLoS Pathogens, 2017, 13, e1006664.	4.7	25
43	Four simple recommendations to encourage best practices in research software. F1000Research, 2017, 6, 876.	1.6	88
44	Jupyter and Galaxy: Easing entry barriers into complex data analyses for biomedical researchers. PLoS Computational Biology, 2017, 13, e1005425.	3.2	53
45	ENASearch: A Python library for interacting with ENA's API. Journal of Open Source Software, 2017, 2, 418.	4.6	1
46	deepTools2: a next generation web server for deep-sequencing data analysis. Nucleic Acids Research, 2016, 44, W160-W165.	14.5	5,157
47	Anatomy of BioJS, an open source community for the life sciences. ELife, 2015, 4, .	6.0	29
48	Characterization and Phylogenetic Analysis of the Mitochondrial Genome of Glarea lozoyensis Indicates High Diversity within the Order Helotiales. PLoS ONE, 2013, 8, e74792.	2.5	9
49	Galaxy tools and workflows for sequence analysis with applications in molecular plant pathology. PeerJ, 2013, 1, e167.	2.0	159
50	Genome Sequence of the Fungus Glarea lozoyensis: the First Genome Sequence of a Species from the Helotiaceae Family. Eukaryotic Cell, 2012, 11, 250-250.	3.4	20
51	Small-molecule conversion of toxic oligomers to nontoxic Î²-sheetâ€"rich amyloid fibrils. Nature Chemical Biology, 2012, 8, 93-101.	8.0	400
52	Genome Sequence of Streptomyces sp. Strain TÃ¼6071. Journal of Bacteriology, 2011, 193, 4278-4279.	2.2	8