Daniel Blankenberg

List of Publications by Year
in descending order

42 papers	11,773 citations	279798 23 h-index	289244 40 g-index
55 all docs	55 docs citations	55 times ranked	21569 citing authors

#	Article	IF	Citations
1	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. Nucleic Acids Research, 2018, 46, W537-W544.	14.5	3,003
2	Galaxy: A platform for interactive large-scale genome analysis. Genome Research, 2005, 15, 1451-1455.	5.5	1,795
3	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2016 update. Nucleic Acids Research, 2016, 44, W3-W10.	14.5	1,751
4	Galaxy: A Web‐Based Genome Analysis Tool for Experimentalists. Current Protocols in Molecular Biology, 2010, 89, Unit 19.10.1-21.	2.9	1,159
5	Bioconda: sustainable and comprehensive software distribution for the life sciences. Nature Methods, 2018, 15, 475-476.	19.0	714
6	Manipulation of FASTQ data with Galaxy. Bioinformatics, 2010, 26, 1783-1785.	4.1	587
7	An encyclopedia of mouse DNA elements (Mouse ENCODE). Genome Biology, 2012, 13, 418.	9.6	410
8	Community-led, integrated, reproducible multi-omics with anvi'o. Nature Microbiology, 2021, 6, 3-6.	13.3	370
9	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2020 update. Nucleic Acids Research, 2020, 48, W395-W402.	14.5	322
10	CloudMap: A Cloud-Based Pipeline for Analysis of Mutant Genome Sequences. Genetics, 2012, 192, 1249-1269.	2.9	281
11	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. Genome Research, 2007, 17, 1797-1808.	5.5	237
12	Dissemination of scientific software with Galaxy ToolShed. Genome Biology, 2014, 15, 403.	9.6	205
13	Maternal age effect and severe germ-line bottleneck in the inheritance of human mitochondrial DNA. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15474-15479.	7.1	201
14	A framework for collaborative analysis of ENCODE data: Making large-scale analyses biologist-friendly. Genome Research, 2007, 17, 960-964.	5.5	122
15	Quantitative sequence-function relationships in proteins based on gene ontology. BMC Bioinformatics, 2007, 8, 294.	2.6	68
16	Integrating diverse databases into an unified analysis framework: a Galaxy approach. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar011-bar011.	3.0	46
17	Integrative genomic analysis by interoperation of bioinformatics tools in GenomeSpace. Nature Methods, 2016, 13, 245-247.	19.0	44
18	Making whole genome multiple alignments usable for biologists. Bioinformatics, 2011, 27, 2426-2428.	4.1	43

#	Article	IF	Citations
19	Analysis of Next-Generation Sequencing Data Using Galaxy. Methods in Molecular Biology, 2014, 1150, 21-43.	0.9	42
20	Child Weight Gain Trajectories Linked To Oral Microbiota Composition. Scientific Reports, 2018, 8, 14030.	3.3	39
21	Using Galaxy to Perform Large‐Scale Interactive Data Analyses. Current Protocols in Bioinformatics, 2012, 38, Unit10.5.	25.8	36
22	Wrangling Galaxy's reference data. Bioinformatics, 2014, 30, 1917-1919.	4.1	31
23	Recommendations for the packaging and containerizing of bioinformatics software. F1000Research, 2018, 7, 742.	1.6	29
24	Recommendations for the packaging and containerizing of bioinformatics software. F1000Research, 2018, 7, 742.	1.6	27
25	Controlling for contamination in re-sequencing studies with a reproducible web-based phylogenetic approach. BioTechniques, 2014, 56, 134-141.	1.8	22
26	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
27	Software engineering for scientific big data analysis. GigaScience, 2019, 8, .	6.4	20
28	A single-cell RNA-sequencing training and analysis suite using the Galaxy framework. GigaScience, 2020, 9, .	6.4	14
29	Evaluation of low-cost particulate matter sensors OPC N2 and PM Nova for aerosol monitoring. Atmospheric Pollution Research, 2022, 13, 101335.	3.8	14
30	Online Resources for Genomic Analysis Using High-Throughput Sequencing. Cold Spring Harbor Protocols, 2015, 2015, pdb.top083667.	0.3	6
31	Biology Needs Evolutionary Software Tools: Let's Build Them Right. Molecular Biology and Evolution, 2018, 35, 1372-1375.	8.9	6
32	A crowdsourced set of curated structural variants for the human genome. PLoS Computational Biology, 2020, 16, e1007933.	3.2	6
33	GenomicSuperSignature facilitates interpretation of RNA-seq experiments through robust, efficient comparison to public databases. Nature Communications, 2022, 13, .	12.8	6
34	PDAUG: a Galaxy based toolset for peptide library analysis, visualization, and machine learning modeling. BMC Bioinformatics, 2022, 23, .	2.6	5
35	Sptlc1 is essential for myeloid differentiation and hematopoietic homeostasis. Blood Advances, 2019, 3, 3635-3649.	5.2	4
36	Using Galaxy to Perform Large‐Scale Interactive Data Analyses—An Update. Current Protocols, 2021, 1, e31.	2.9	4

#	ARTICLE	IF	CITATIONS
37	Re-Expression of ERα and AR in Receptor Negative Endocrine Cancers via GSK3 Inhibition. Frontiers in Oncology, 2022, 12, 824594.	2.8	3
38	Galaxy External Display Applications: closing a dataflow interoperability loop. Nature Methods, 2020, 17, 123-124.	19.0	2
39	SimText: a text mining framework for interactive analysis and visualization of similarities among biomedical entities. Bioinformatics, 2021, 37, 4285-4287.	4.1	2
40	172. Child Weight Gain Trajectories Associated With Oral Microbiota Composition. Biological Psychiatry, 2019, 85, S71.	1.3	0
41	You Wrote It, Now Get It Used. , 2019, , .		0
42	Expanding the Galaxy's reference data. Bioinformatics Advances, 2022, 2, .	2.4	0