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	Evaluation of low-cost particulate matter sensors OPC N2 and PM Nova for aerosol monitoring. Atmospheric Pollution Research, 2022, 13, 101335.	3.8	14
2	Re-Expression of ERα and AR in Receptor Negative Endocrine Cancers via GSK3 Inhibition. Frontiers in Oncology, 2022, 12, 824594.	2.8	3
3	Expanding the Galaxy's reference data. Bioinformatics Advances, 2022, 2, .	2.4	0
4	PDAUG: a Galaxy based toolset for peptide library analysis, visualization, and machine learning modeling. BMC Bioinformatics, 2022, 23, .	2.6	5
5	GenomicSuperSignature facilitates interpretation of RNA-seq experiments through robust, efficient comparison to public databases. Nature Communications, 2022, 13, .	12.8	6
6	Community-led, integrated, reproducible multi-omics with anvi'o. Nature Microbiology, 2021, 6, 3-6.	13.3	370
7	Using Galaxy to Perform Large-Scale Interactive Data Analyses—An Update. Current Protocols, 2021, 1, e31.	2.9	4
8	SimText: a text mining framework for interactive analysis and visualization of similarities among biomedical entities. Bioinformatics, 2021, 37, 4285-4287.	4.1	2
9	A single-cell RNA-sequencing training and analysis suite using the Galaxy framework. GigaScience, 2020, 9, .	6.4	14
10	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
11	A crowdsourced set of curated structural variants for the human genome. PLoS Computational Biology, 2020, 16, e1007933.	3.2	6
12	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2020 update. Nucleic Acids Research, 2020, 48, W395-W402.	14.5	322
13	Galaxy External Display Applications: closing a dataflow interoperability loop. Nature Methods, 2020, 17, 123-124.	19.0	2
14	Software engineering for scientific big data analysis. GigaScience, 2019, 8, .	6.4	20
15	172. Child Weight Gain Trajectories Associated With Oral Microbiota Composition. Biological Psychiatry, 2019, 85, S71.	1.3	0
16	Sptlc1 is essential for myeloid differentiation and hematopoietic homeostasis. Blood Advances, 2019, 3, 3635-3649.	5.2	4
17	You Wrote It, Now Get It Used. , 2019, , .		0
18	Biology Needs Evolutionary Software Tools: Let's Build Them Right. Molecular Biology and Evolution, 2018, 35, 1372-1375.	8.9	6

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19	Child Weight Gain Trajectories Linked To Oral Microbiota Composition. Scientific Reports, 2018, 8, 14030.	3.3	39
20	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. Nucleic Acids Research, 2018, 46, W537-W544.	14.5	3,003
21	Bioconda: sustainable and comprehensive software distribution for the life sciences. Nature Methods, 2018, 15, 475-476.	19.0	714
22	Recommendations for the packaging and containerizing of bioinformatics software. F1000Research, 2018, 7, 742.	1.6	27
23	Recommendations for the packaging and containerizing of bioinformatics software. F1000Research, 2018, 7, 742.	1.6	29
24	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2016 update. Nucleic Acids Research, 2016, 44, W3-W10.	14.5	1,751
25	Integrative genomic analysis by interoperation of bioinformatics tools in GenomeSpace. Nature Methods, 2016, 13, 245-247.	19.0	44
26	Online Resources for Genomic Analysis Using High-Throughput Sequencing. Cold Spring Harbor Protocols, 2015, 2015, pdb.top083667.	0.3	6
27	Controlling for contamination in re-sequencing studies with a reproducible web-based phylogenetic approach. BioTechniques, 2014, 56, 134-141.	1.8	22
28	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
29	Wrangling Galaxy's reference data. Bioinformatics, 2014, 30, 1917-1919.	4.1	31
30	Dissemination of scientific software with Galaxy ToolShed. Genome Biology, 2014, 15, 403.	9.6	205
31	Analysis of Next-Generation Sequencing Data Using Galaxy. Methods in Molecular Biology, 2014, 1150, 21-43.	0.9	42
32	CloudMap: A Cloud-Based Pipeline for Analysis of Mutant Genome Sequences. Genetics, 2012, 192, 1249-1269.	2.9	281
33	An encyclopedia of mouse DNA elements (Mouse ENCODE). Genome Biology, 2012, 13, 418.	9.6	410
34	Using Galaxy to Perform Large-Scale Interactive Data Analyses. Current Protocols in Bioinformatics, 2012, 38, Unit10.5.	25.8	36
35	Making whole genome multiple alignments usable for biologists. Bioinformatics, 2011, 27, 2426-2428.	4.1	43
36	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

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37	Manipulation of FASTQ data with Galaxy. Bioinformatics, 2010, 26, 1783-1785.	4.1	587
38	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
39	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. Genome Research, 2007, 17, 1797-1808.	5.5	237
40	A framework for collaborative analysis of ENCODE data: Making large-scale analyses biologist-friendly. Genome Research, 2007, 17, 960-964.	5.5	122
41	Quantitative sequence-function relationships in proteins based on gene ontology. BMC Bioinformatics, 2007, 8, 294.	2.6	68
42	Galaxy: A platform for interactive large-scale genome analysis. Genome Research, 2005, 15, 1451-1455.	5.5	1,795