James Taylor

List of Publications by Year in descending order

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LAMES TAVIOR

#	Article	IF	CITATIONS
1	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	27.8	15,516
2	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
3	Galaxy: a comprehensive approach for supporting accessible, reproducible, and transparent computational research in the life sciences. Genome Biology, 2010, 11, R86.	9.6	3,082
4	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. Nucleic Acids Research, 2018, 46, W537-W544.	14.5	3,003
5	Initial sequence of the chimpanzee genome and comparison with the human genome. Nature, 2005, 437, 69-87.	27.8	2,222
6	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	27.8	1,943
7	Galaxy: A platform for interactive large-scale genome analysis. Genome Research, 2005, 15, 1451-1455.	5.5	1,795
8	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2016 update. Nucleic Acids Research, 2016, 44, W3-W10.	14.5	1,751
9	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	27.8	1,444
10	Galaxy: A Webâ€Based Genome Analysis Tool for Experimentalists. Current Protocols in Molecular Biology, 2010, 89, Unit 19.10.1-21.	2.9	1,159
11	MetaWRAP—a flexible pipeline for genome-resolved metagenomic data analysis. Microbiome, 2018, 6, 158.	11.1	1,098
12	Architectural Protein Subclasses Shape 3D Organization of Genomes during Lineage Commitment. Cell, 2013, 153, 1281-1295.	28.9	1,050
13	Topologically associating domains are stable units of replication-timing regulation. Nature, 2014, 515, 402-405.	27.8	779
14	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	27.8	657
15	Manipulation of FASTQ data with Galaxy. Bioinformatics, 2010, 26, 1783-1785.	4.1	587
16	Ten Simple Rules for Reproducible Computational Research. PLoS Computational Biology, 2013, 9, e1003285.	3.2	509
17	An encyclopedia of mouse DNA elements (Mouse ENCODE). Genome Biology, 2012, 13, 418.	9.6	410
18	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2020 update. Nucleic Acids Research, 2020, 48, W395-W402.	14.5	322

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19	Next-generation sequencing data interpretation: enhancing reproducibility and accessibility. Nature Reviews Genetics, 2012, 13, 667-672.	16.3	269
20	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. Genome Research, 2007, 17, 1797-1808.	5.5	237
21	The Genome Sequence of the Leaf-Cutter Ant Atta cephalotes Reveals Insights into Its Obligate Symbiotic Lifestyle. PLoS Genetics, 2011, 7, e1002007.	3.5	231
22	Chromatin States in Mouse Sperm Correlate with Embryonic and Adult Regulatory Landscapes. Cell Reports, 2017, 18, 1366-1382.	6.4	231
23	Dissemination of scientific software with Galaxy ToolShed. Genome Biology, 2014, 15, 403.	9.6	205
24	Genomic approaches towards finding cis-regulatory modules in animals. Nature Reviews Genetics, 2012, 13, 469-483.	16.3	200
25	Thyroid hormone signaling specifies cone subtypes in human retinal organoids. Science, 2018, 362, .	12.6	188
26	Evaluation of regulatory potential and conservation scores for detecting cis-regulatory modules in aligned mammalian genome sequences. Genome Research, 2005, 15, 1051-1060.	5.5	185
27	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Research, 2007, 17, 760-774.	5.5	184
28	Lamins Organize the Global Three-Dimensional Genome from the Nuclear Periphery. Molecular Cell, 2018, 71, 802-815.e7.	9.7	153
29	Community-Driven Data Analysis Training for Biology. Cell Systems, 2018, 6, 752-758.e1.	6.2	141
30	Galaxy CloudMan: delivering cloud compute clusters. BMC Bioinformatics, 2010, 11, S4.	2.6	140
31	Measuring the reproducibility and quality of Hi-C data. Genome Biology, 2019, 20, 57.	8.8	125
32	A framework for collaborative analysis of ENCODE data: Making large-scale analyses biologist-friendly. Genome Research, 2007, 17, 960-964.	5.5	122
33	Jetstream. , 2015, , .		121
34	ESPERR: Learning strong and weak signals in genomic sequence alignments to identify functional elements. Genome Research, 2006, 16, 1596-1604.	5.5	111
35	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. Genome Research, 2011, 21, 1659-1671.	5.5	110
36	Using Galaxy to Perform Largeâ€Scale Interactive Data Analyses. Current Protocols in Bioinformatics, 2007, 19, Unit 10.5.	25.8	100

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37	Harnessing cloud computing with Galaxy Cloud. Nature Biotechnology, 2011, 29, 972-974.	17.5	100
38	Practical Computational Reproducibility in the Life Sciences. Cell Systems, 2018, 6, 631-635.	6.2	100
39	Regulatory Potential Scores From Genome-Wide Three-Way Alignments of Human, Mouse, and Rat. Genome Research, 2004, 14, 700-707.	5.5	93
40	Dynamics of mitochondrial heteroplasmy in three families investigated via a repeatable re-sequencing study. Genome Biology, 2011, 12, R59.	8.8	93
41	Integrative Approach Reveals Composition of Endoparasitoid Wasp Venoms. PLoS ONE, 2013, 8, e64125.	2.5	92
42	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. Nature, 2005, 434, 724-731.	27.8	85
43	Strong and Weak Male Mutation Bias at Different Sites in the Primate Genomes: Insights from the Human-Chimpanzee Comparison. Molecular Biology and Evolution, 2006, 23, 565-573.	8.9	84
44	The full-length transcriptome of <i>C. elegans</i> using direct RNA sequencing. Genome Research, 2020, 30, 299-312.	5.5	77
45	HiFive: a tool suite for easy and efficient HiC and 5C data analysis. Genome Biology, 2015, 16, 237.	8.8	72
46	Parasitoid wasp venom SERCA regulates <i>Drosophila</i> calcium levels and inhibits cellular immunity. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 9427-9432.	7.1	70
47	Finding cis-regulatory elements using comparative genomics: Some lessons from ENCODE data. Genome Research, 2007, 17, 775-786.	5.5	69
48	Windshield splatter analysis with the Galaxy metagenomic pipeline. Genome Research, 2009, 19, 2144-2153.	5.5	68
49	Genome-wide comparative analysis reveals human-mouse regulatory landscape and evolution. BMC Genomics, 2015, 16, 87.	2.8	62
50	Halophilic microbial community compositional shift after a rare rainfall in the Atacama Desert. ISME Journal, 2019, 13, 2737-2749.	9.8	62
51	Experimental validation of predicted mammalian erythroid cis-regulatory modules. Genome Research, 2006, 16, 1480-1492.	5.5	56
52	Jupyter and Galaxy: Easing entry barriers into complex data analyses for biomedical researchers. PLoS Computational Biology, 2017, 13, e1005425.	3.2	53
53	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
54	Web-based visual analysis for high-throughput genomics. BMC Genomics, 2013, 14, 397.	2.8	45

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55	Making whole genome multiple alignments usable for biologists. Bioinformatics, 2011, 27, 2426-2428.	4.1	43
56	CloudMan as a platform for tool, data, and analysis distribution. BMC Bioinformatics, 2012, 13, 315.	2.6	43
57	Ribosome A and P sites revealed by length analysis of ribosome profiling data. Nucleic Acids Research, 2015, 43, 3680-3687.	14.5	43
58	Characterization of Button Loci that Promote Homologous Chromosome Pairing and Cell-Type-Specific Interchromosomal Gene Regulation. Developmental Cell, 2019, 51, 341-356.e7.	7.0	41
59	An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. Genome Research, 2020, 30, 472-484.	5.5	38
60	Using Galaxy to Perform Largeâ€6cale Interactive Data Analyses. Current Protocols in Bioinformatics, 2012, 38, Unit10.5.	25.8	36
61	Wrangling Galaxy's reference data. Bioinformatics, 2014, 30, 1917-1919.	4.1	31
62	Comparative analyses of bidirectional promoters in vertebrates. BMC Bioinformatics, 2008, 9, S9.	2.6	30
63	Primary sequence and epigenetic determinants of in vivo occupancy of genomic DNA by GATA1. Nucleic Acids Research, 2009, 37, 7024-7038.	14.5	29
64	A Novel Long Non-Coding RNA in the hTERT Promoter Region Regulates hTERT Expression. Non-coding RNA, 2018, 4, 1.	2.6	28
65	Natural variation in stochastic photoreceptor specification and color preference in Drosophila. ELife, 2017, 6, .	6.0	27
66	NGS analyses by visualization with Trackster. Nature Biotechnology, 2012, 30, 1036-1039.	17.5	26
67	The 3rd DBCLS BioHackathon: improving life science data integration with Semantic Web technologies. Journal of Biomedical Semantics, 2013, 4, 6.	1.6	26
68	The anatomy of successful computational biology software. Nature Biotechnology, 2013, 31, 894-897.	17.5	25
69	Using Cloud Computing Infrastructure with CloudBioLinux, CloudMan, and Galaxy. Current Protocols in Bioinformatics, 2012, 38, Unit11.9.	25.8	23
70	CloudLaunch: Discover and deploy cloud applications. Future Generation Computer Systems, 2019, 94, 802-810.	7.5	23
71	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
72	Cellular life from the three domains and viruses are transcriptionally active in a hypersaline desert community. Environmental Microbiology, 2021, 23, 3401-3417.	3.8	20

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73	Galaxy: A Gateway to Tools in e-Science. Computer Communications and Networks, 2011, , 145-177.	0.8	20
74	The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications. Journal of Biomedical Semantics, 2011, 2, 4.	1.6	19
75	Clues to function in gene deserts. Trends in Biotechnology, 2005, 23, 269-271.	9.3	15
76	A single-cell RNA-sequencing training and analysis suite using the Galaxy framework. GigaScience, 2020, 9, .	6.4	14
77	Leveraging the national cyberinfrastructure for biomedical research. Journal of the American Medical Informatics Association: JAMIA, 2014, 21, 195-199.	4.4	12
78	Environmental Factors Driving Spatial Heterogeneity in Desert Halophile Microbial Communities. Frontiers in Microbiology, 2020, 11, 578669.	3.5	12
79	Jetstream. , 2016, , .		11
80	Cloud bursting galaxy: federated identity and access management. Bioinformatics, 2020, 36, 1-9.	4.1	11
81	Web-Based Analysis of (Epi-) Genome Data Using EpiGRAPH and Galaxy. Methods in Molecular Biology, 2010, 628, 275-296.	0.9	10
82	Federated Galaxy: Biomedical Computing at the Frontier. , 2018, 2018, .		9
83	Hidden dynamic signatures drive substrate selectivity in the disordered phosphoproteome. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 23606-23616.	7.1	9
84	Open pipelines for integrated tumor genome profiles reveal differences between pancreatic cancer tumors and cell lines. Cancer Medicine, 2015, 4, 392-403.	2.8	8
85	Systematic integration of GATA transcription factors and epigenomes via IDEAS paints the regulatory landscape of hematopoietic cells. IUBMB Life, 2020, 72, 27-38.	3.4	8
86	Enabling cloud bursting for life sciences within Galaxy. Concurrency Computation Practice and Experience, 2015, 27, 4330-4343.	2.2	7
87	Phylogenomic Resources at the UCSC Genome Browser. Methods in Molecular Biology, 2008, 422, 133-144.	0.9	7
88	Online Resources for Genomic Analysis Using High-Throughput Sequencing. Cold Spring Harbor Protocols, 2015, 2015, pdb.top083667.	0.3	6
89	CloudBridge. , 2016, 2016, .		6
90	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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91	Lessons learned from Galaxy, a Web-based platform for high-throughput genomic analyses. , 2012, , .		5
92	A reference model for deploying applications in virtualized environments. Concurrency Computation Practice and Experience, 2012, 24, 1349-1361.	2.2	4
93	Galaxy Cluster to Cloud - Genomics at Scale. , 2014, , .		4
94	Using Galaxy to Perform Largeâ€Scale Interactive Data Analyses—An Update. Current Protocols, 2021, 1, e31.	2.9	4
95	The DNA60IFX contest. Genome Biology, 2013, 14, 124.	8.8	3
96	A guide and best practices for R/Bioconductor tool integration in Galaxy. F1000Research, 0, 5, 2757.	1.6	3
97	Building and provisioning bioinformatics environments on public and private Clouds. , 2015, , .		2
98	The Galaxy Track Browser: Transforming the genome browser from visualization tool to analysis tool. , 2011, , .		1
99	Rigorous Mapping of Orthologous Bidirectional Promoters inVertebrates Defines their Evolutionary History. , 2007, , .		0
100	A sustainable national gateway for biological computation. , 2013, , .		0
101	Phosphorylation Sites with S/T-P Motif: Possible Basal Anti-Aggregation Mechanism. Biophysical Journal, 2019, 116, 65a.	0.5	0
102	Toward the commoditization of translational genomic research: Design and implementation features of the Galaxy genomic workbench. Summit on Translational Bioinformatics, 2008, 2008, 56-60.	0.7	0
103	Rigorous Mapping of Orthologous Bidirectional Promoters inVertebrates Defines their Evolutionary History. , 2007, , .		0