

James Taylor

List of Publications by Year in descending order

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103
papers

47,407
citations

41258

49
h-index

43802

91
g-index

135
all docs

135
docs citations

135
times ranked

69200
citing authors

#	ARTICLE	IF	CITATIONS
1	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	13.7	15,516
2	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	13.7	4,709
3	Galaxy: a comprehensive approach for supporting accessible, reproducible, and transparent computational research in the life sciences. <i>Genome Biology</i> , 2010, 11, R86.	13.9	3,082
4	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, W537-W544.	6.5	3,003
5	Initial sequence of the chimpanzee genome and comparison with the human genome. <i>Nature</i> , 2005, 437, 69-87.	13.7	2,222
6	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943
7	Galaxy: A platform for interactive large-scale genome analysis. <i>Genome Research</i> , 2005, 15, 1451-1455.	2.4	1,795
8	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2016 update. <i>Nucleic Acids Research</i> , 2016, 44, W3-W10.	6.5	1,751
9	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	13.7	1,444
10	Galaxy: A Web-Based Genome Analysis Tool for Experimentalists. <i>Current Protocols in Molecular Biology</i> , 2010, 89, Unit 19.10.1-21.	2.9	1,159
11	MetaWRAP—a flexible pipeline for genome-resolved metagenomic data analysis. <i>Microbiome</i> , 2018, 6, 158.	4.9	1,098
12	Architectural Protein Subclasses Shape 3D Organization of Genomes during Lineage Commitment. <i>Cell</i> , 2013, 153, 1281-1295.	13.5	1,050
13	Topologically associating domains are stable units of replication-timing regulation. <i>Nature</i> , 2014, 515, 402-405.	13.7	779
14	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008, 453, 175-183.	13.7	657
15	Manipulation of FASTQ data with Galaxy. <i>Bioinformatics</i> , 2010, 26, 1783-1785.	1.8	587
16	Ten Simple Rules for Reproducible Computational Research. <i>PLoS Computational Biology</i> , 2013, 9, e1003285.	1.5	509
17	An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , 2012, 13, 418.	13.9	410
18	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2020 update. <i>Nucleic Acids Research</i> , 2020, 48, W395-W402.	6.5	322

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19	Next-generation sequencing data interpretation: enhancing reproducibility and accessibility. <i>Nature Reviews Genetics</i> , 2012, 13, 667-672.	7.7	269
20	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. <i>Genome Research</i> , 2007, 17, 1797-1808.	2.4	237
21	The Genome Sequence of the Leaf-Cutter Ant <i>Atta cephalotes</i> Reveals Insights into Its Obligate Symbiotic Lifestyle. <i>PLoS Genetics</i> , 2011, 7, e1002007.	1.5	231
22	Chromatin States in Mouse Sperm Correlate with Embryonic and Adult Regulatory Landscapes. <i>Cell Reports</i> , 2017, 18, 1366-1382.	2.9	231
23	Dissemination of scientific software with Galaxy ToolShed. <i>Genome Biology</i> , 2014, 15, 403.	13.9	205
24	Genomic approaches towards finding cis-regulatory modules in animals. <i>Nature Reviews Genetics</i> , 2012, 13, 469-483.	7.7	200
25	Thyroid hormone signaling specifies cone subtypes in human retinal organoids. <i>Science</i> , 2018, 362, .	6.0	188
26	Evaluation of regulatory potential and conservation scores for detecting cis-regulatory modules in aligned mammalian genome sequences. <i>Genome Research</i> , 2005, 15, 1051-1060.	2.4	185
27	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. <i>Genome Research</i> , 2007, 17, 760-774.	2.4	184
28	Lamins Organize the Global Three-Dimensional Genome from the Nuclear Periphery. <i>Molecular Cell</i> , 2018, 71, 802-815.e7.	4.5	153
29	Community-Driven Data Analysis Training for Biology. <i>Cell Systems</i> , 2018, 6, 752-758.e1.	2.9	141
30	Galaxy CloudMan: delivering cloud compute clusters. <i>BMC Bioinformatics</i> , 2010, 11, S4.	1.2	140
31	Measuring the reproducibility and quality of Hi-C data. <i>Genome Biology</i> , 2019, 20, 57.	3.8	125
32	A framework for collaborative analysis of ENCODE data: Making large-scale analyses biologist-friendly. <i>Genome Research</i> , 2007, 17, 960-964.	2.4	122
33	Jetstream. , 2015, , .		121
34	ESPERR: Learning strong and weak signals in genomic sequence alignments to identify functional elements. <i>Genome Research</i> , 2006, 16, 1596-1604.	2.4	111
35	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. <i>Genome Research</i> , 2011, 21, 1659-1671.	2.4	110
36	Using Galaxy to Perform Large-Scale Interactive Data Analyses. <i>Current Protocols in Bioinformatics</i> , 2007, 19, Unit 10.5.	25.8	100

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37	Harnessing cloud computing with Galaxy Cloud. <i>Nature Biotechnology</i> , 2011, 29, 972-974.	9.4	100
38	Practical Computational Reproducibility in the Life Sciences. <i>Cell Systems</i> , 2018, 6, 631-635.	2.9	100
39	Regulatory Potential Scores From Genome-Wide Three-Way Alignments of Human, Mouse, and Rat. <i>Genome Research</i> , 2004, 14, 700-707.	2.4	93
40	Dynamics of mitochondrial heteroplasmy in three families investigated via a repeatable re-sequencing study. <i>Genome Biology</i> , 2011, 12, R59.	3.8	93
41	Integrative Approach Reveals Composition of Endoparasitoid Wasp Venoms. <i>PLoS ONE</i> , 2013, 8, e64125.	1.1	92
42	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. <i>Nature</i> , 2005, 434, 724-731.	13.7	85
43	Strong and Weak Male Mutation Bias at Different Sites in the Primate Genomes: Insights from the Human-Chimpanzee Comparison. <i>Molecular Biology and Evolution</i> , 2006, 23, 565-573.	3.5	84
44	The full-length transcriptome of <i>C. elegans</i> using direct RNA sequencing. <i>Genome Research</i> , 2020, 30, 299-312.	2.4	77
45	HiFive: a tool suite for easy and efficient HiC and 5C data analysis. <i>Genome Biology</i> , 2015, 16, 237.	3.8	72
46	Parasitoid wasp venom SERCA regulates <i>Drosophila</i> calcium levels and inhibits cellular immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 9427-9432.	3.3	70
47	Finding cis-regulatory elements using comparative genomics: Some lessons from ENCODE data. <i>Genome Research</i> , 2007, 17, 775-786.	2.4	69
48	Windshield splatter analysis with the Galaxy metagenomic pipeline. <i>Genome Research</i> , 2009, 19, 2144-2153.	2.4	68
49	Genome-wide comparative analysis reveals human-mouse regulatory landscape and evolution. <i>BMC Genomics</i> , 2015, 16, 87.	1.2	62
50	Halophilic microbial community compositional shift after a rare rainfall in the Atacama Desert. <i>ISME Journal</i> , 2019, 13, 2737-2749.	4.4	62
51	Experimental validation of predicted mammalian erythroid cis-regulatory modules. <i>Genome Research</i> , 2006, 16, 1480-1492.	2.4	56
52	Jupyter and Galaxy: Easing entry barriers into complex data analyses for biomedical researchers. <i>PLoS Computational Biology</i> , 2017, 13, e1005425.	1.5	53
53	Integrating diverse databases into an unified analysis framework: a Galaxy approach. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar011-bar011.	1.4	46
54	Web-based visual analysis for high-throughput genomics. <i>BMC Genomics</i> , 2013, 14, 397.	1.2	45

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55	Making whole genome multiple alignments usable for biologists. <i>Bioinformatics</i> , 2011, 27, 2426-2428.	1.8	43
56	CloudMan as a platform for tool, data, and analysis distribution. <i>BMC Bioinformatics</i> , 2012, 13, 315.	1.2	43
57	Ribosome A and P sites revealed by length analysis of ribosome profiling data. <i>Nucleic Acids Research</i> , 2015, 43, 3680-3687.	6.5	43
58	Characterization of Button Loci that Promote Homologous Chromosome Pairing and Cell-Type-Specific Interchromosomal Gene Regulation. <i>Developmental Cell</i> , 2019, 51, 341-356.e7.	3.1	41
59	An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. <i>Genome Research</i> , 2020, 30, 472-484.	2.4	38
60	Using Galaxy to Perform Large-Scale Interactive Data Analyses. <i>Current Protocols in Bioinformatics</i> , 2012, 38, Unit10.5.	25.8	36
61	Wrangling Galaxy's reference data. <i>Bioinformatics</i> , 2014, 30, 1917-1919.	1.8	31
62	Comparative analyses of bidirectional promoters in vertebrates. <i>BMC Bioinformatics</i> , 2008, 9, S9.	1.2	30
63	Primary sequence and epigenetic determinants of in vivo occupancy of genomic DNA by GATA1. <i>Nucleic Acids Research</i> , 2009, 37, 7024-7038.	6.5	29
64	A Novel Long Non-Coding RNA in the hTERT Promoter Region Regulates hTERT Expression. <i>Non-coding RNA</i> , 2018, 4, 1.	1.3	28
65	Natural variation in stochastic photoreceptor specification and color preference in <i>Drosophila</i> . <i>ELife</i> , 2017, 6, .	2.8	27
66	NGS analyses by visualization with Trackster. <i>Nature Biotechnology</i> , 2012, 30, 1036-1039.	9.4	26
67	The 3rd DBCLS BioHackathon: improving life science data integration with Semantic Web technologies. <i>Journal of Biomedical Semantics</i> , 2013, 4, 6.	0.9	26
68	The anatomy of successful computational biology software. <i>Nature Biotechnology</i> , 2013, 31, 894-897.	9.4	25
69	Using Cloud Computing Infrastructure with CloudBioLinux, CloudMan, and Galaxy. <i>Current Protocols in Bioinformatics</i> , 2012, 38, Unit11.9.	25.8	23
70	CloudLaunch: Discover and deploy cloud applications. <i>Future Generation Computer Systems</i> , 2019, 94, 802-810.	4.9	23
71	No more business as usual: Agile and effective responses to emerging pathogen threats require open data and open analytics. <i>PLoS Pathogens</i> , 2020, 16, e1008643.	2.1	22
72	Cellular life from the three domains and viruses are transcriptionally active in a hypersaline desert community. <i>Environmental Microbiology</i> , 2021, 23, 3401-3417.	1.8	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.	0.9	19
75	Clues to function in gene deserts. Trends in Biotechnology, 2005, 23, 269-271.	4.9	15
76	A single-cell RNA-sequencing training and analysis suite using the Galaxy framework. GigaScience, 2020, 9, .	3.3	14
77	Leveraging the national cyberinfrastructure for biomedical research. Journal of the American Medical Informatics Association: JAMIA, 2014, 21, 195-199.	2.2	12
78	Environmental Factors Driving Spatial Heterogeneity in Desert Halophile Microbial Communities. Frontiers in Microbiology, 2020, 11, 578669.	1.5	12
79	Jetstream. , 2016, , .		11
80	Cloud bursting galaxy: federated identity and access management. Bioinformatics, 2020, 36, 1-9.	1.8	11
81	Web-Based Analysis of (Epi-) Genome Data Using EpiGRAPH and Galaxy. Methods in Molecular Biology, 2010, 628, 275-296.	0.4	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.	3.3	9
84	Open pipelines for integrated tumor genome profiles reveal differences between pancreatic cancer tumors and cell lines. Cancer Medicine, 2015, 4, 392-403.	1.3	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.	1.5	8
86	Enabling cloud bursting for life sciences within Galaxy. Concurrency Computation Practice and Experience, 2015, 27, 4330-4343.	1.4	7
87	Phylogenomic Resources at the UCSC Genome Browser. Methods in Molecular Biology, 2008, 422, 133-144.	0.4	7
88	Online Resources for Genomic Analysis Using High-Throughput Sequencing. Cold Spring Harbor Protocols, 2015, 2015, pdb.top083667.	0.2	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.	3.5	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.	1.4	4
93	Galaxy Cluster to Cloud - Genomics at Scale. , 2014, , .		4
94	Using Galaxy to Perform Largeâ€Scale Interactive Data Analysesâ€An Update. Current Protocols, 2021, 1, e31.	1.3	4
95	The DNA60IFX contest. Genome Biology, 2013, 14, 124.	3.8	3
96	A guide and best practices for R/Bioconductor tool integration in Galaxy. F1000Research, 0, 5, 2757.	0.8	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.	0.2	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