

# 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	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
2	Using Galaxy to Perform Large-scale Interactive Data Analyses—An Update. <i>Current Protocols</i> , 2021, 1, e31.	1.3	4
3	Cloud bursting galaxy: federated identity and access management. <i>Bioinformatics</i> , 2020, 36, 1-9.	1.8	11
4	Systematic integration of GATA transcription factors and epigenomes via IDEAS paints the regulatory landscape of hematopoietic cells. <i>IUBMB Life</i> , 2020, 72, 27-38.	1.5	8
5	Environmental Factors Driving Spatial Heterogeneity in Desert Halophile Microbial Communities. <i>Frontiers in Microbiology</i> , 2020, 11, 578669.	1.5	12
6	A single-cell RNA-sequencing training and analysis suite using the Galaxy framework. <i>GigaScience</i> , 2020, 9, .	3.3	14
7	Hidden dynamic signatures drive substrate selectivity in the disordered phosphoproteome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23606-23616.	3.3	9
8	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
9	An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. <i>Genome Research</i> , 2020, 30, 472-484.	2.4	38
10	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2020 update. <i>Nucleic Acids Research</i> , 2020, 48, W395-W402.	6.5	322
11	The full-length transcriptome of <i>C. elegans</i> using direct RNA sequencing. <i>Genome Research</i> , 2020, 30, 299-312.	2.4	77
12	CloudLaunch: Discover and deploy cloud applications. <i>Future Generation Computer Systems</i> , 2019, 94, 802-810.	4.9	23
13	Halophilic microbial community compositional shift after a rare rainfall in the Atacama Desert. <i>ISME Journal</i> , 2019, 13, 2737-2749.	4.4	62
14	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
15	Phosphorylation Sites with S/T-P Motif: Possible Basal Anti-Aggregation Mechanism. <i>Biophysical Journal</i> , 2019, 116, 65a.	0.2	0
16	Measuring the reproducibility and quality of Hi-C data. <i>Genome Biology</i> , 2019, 20, 57.	3.8	125
17	Biology Needs Evolutionary Software Tools: Let's Build Them Right. <i>Molecular Biology and Evolution</i> , 2018, 35, 1372-1375.	3.5	6
18	Thyroid hormone signaling specifies cone subtypes in human retinal organoids. <i>Science</i> , 2018, 362, .	6.0	188

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19	Federated Galaxy: Biomedical Computing at the Frontier. , 2018, 2018, .		9
20	MetaWRAPâ€”a flexible pipeline for genome-resolved metagenomic data analysis. Microbiome, 2018, 6, 158.	4.9	1,098
21	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. Nucleic Acids Research, 2018, 46, W537-W544.	6.5	3,003
22	Community-Driven Data Analysis Training for Biology. Cell Systems, 2018, 6, 752-758.e1.	2.9	141
23	Practical Computational Reproducibility in the Life Sciences. Cell Systems, 2018, 6, 631-635.	2.9	100
24	Lamins Organize the Global Three-Dimensional Genome from the Nuclear Periphery. Molecular Cell, 2018, 71, 802-815.e7.	4.5	153
25	A Novel Long Non-Coding RNA in the hTERT Promoter Region Regulates hTERT Expression. Non-coding RNA, 2018, 4, 1.	1.3	28
26	Chromatin States in Mouse Sperm Correlate with Embryonic and Adult Regulatory Landscapes. Cell Reports, 2017, 18, 1366-1382.	2.9	231
27	Jupyter and Galaxy: Easing entry barriers into complex data analyses for biomedical researchers. PLoS Computational Biology, 2017, 13, e1005425.	1.5	53
28	Natural variation in stochastic photoreceptor specification and color preference in Drosophila. ELife, 2017, 6, .	2.8	27
29	Jetstream. , 2016, , .		11
30	CloudBridge. , 2016, 2016, .		6
31	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2016 update. Nucleic Acids Research, 2016, 44, W3-W10.	6.5	1,751
32	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
33	HiFive: a tool suite for easy and efficient HiC and 5C data analysis. Genome Biology, 2015, 16, 237.	3.8	72
34	Enabling cloud bursting for life sciences within Galaxy. Concurrency Computation Practice and Experience, 2015, 27, 4330-4343.	1.4	7
35	Ribosome A and P sites revealed by length analysis of ribosome profiling data. Nucleic Acids Research, 2015, 43, 3680-3687.	6.5	43
36	Jetstream. , 2015, , .		121

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37	Online Resources for Genomic Analysis Using High-Throughput Sequencing. Cold Spring Harbor Protocols, 2015, 2015, pdb.top083667.	0.2	6
38	Genome-wide comparative analysis reveals human-mouse regulatory landscape and evolution. BMC Genomics, 2015, 16, 87.	1.2	62
39	Building and provisioning bioinformatics environments on public and private Clouds. , 2015, , .		2
40	Galaxy Cluster to Cloud - Genomics at Scale. , 2014, , .		4
41	Wrangling Galaxy's reference data. Bioinformatics, 2014, 30, 1917-1919.	1.8	31
42	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	13.7	1,444
43	Topologically associating domains are stable units of replication-timing regulation. Nature, 2014, 515, 402-405.	13.7	779
44	Dissemination of scientific software with Galaxy ToolShed. Genome Biology, 2014, 15, 403.	13.9	205
45	Leveraging the national cyberinfrastructure for biomedical research. Journal of the American Medical Informatics Association: JAMIA, 2014, 21, 195-199.	2.2	12
46	The 3rd DBCLS BioHackathon: improving life science data integration with Semantic Web technologies. Journal of Biomedical Semantics, 2013, 4, 6.	0.9	26
47	Web-based visual analysis for high-throughput genomics. BMC Genomics, 2013, 14, 397.	1.2	45
48	The anatomy of successful computational biology software. Nature Biotechnology, 2013, 31, 894-897.	9.4	25
49	The DNA60iFX contest. Genome Biology, 2013, 14, 124.	3.8	3
50	Architectural Protein Subclasses Shape 3D Organization of Genomes during Lineage Commitment. Cell, 2013, 153, 1281-1295.	13.5	1,050
51	Ten Simple Rules for Reproducible Computational Research. PLoS Computational Biology, 2013, 9, e1003285.	1.5	509
52	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.	3.3	70
53	A sustainable national gateway for biological computation. , 2013, , .		0
54	Integrative Approach Reveals Composition of Endoparasitoid Wasp Venoms. PLoS ONE, 2013, 8, e64125.	1.1	92

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55	Lessons learned from Galaxy, a Web-based platform for high-throughput genomic analyses. , 2012, , .		5
56	An encyclopedia of mouse DNA elements (Mouse ENCODE). Genome Biology, 2012, 13, 418.	13.9	410
57	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	13.7	15,516
58	Next-generation sequencing data interpretation: enhancing reproducibility and accessibility. Nature Reviews Genetics, 2012, 13, 667-672.	7.7	269
59	Using Cloud Computing Infrastructure with CloudBioLinux, CloudMan, and Galaxy. Current Protocols in Bioinformatics, 2012, 38, Unit11.9.	25.8	23
60	Using Galaxy to Perform Large-scale Interactive Data Analyses. Current Protocols in Bioinformatics, 2012, 38, Unit10.5.	25.8	36
61	NGS analyses by visualization with Trackster. Nature Biotechnology, 2012, 30, 1036-1039.	9.4	26
62	CloudMan as a platform for tool, data, and analysis distribution. BMC Bioinformatics, 2012, 13, 315.	1.2	43
63	A reference model for deploying applications in virtualized environments. Concurrency Computation Practice and Experience, 2012, 24, 1349-1361.	1.4	4
64	Genomic approaches towards finding cis-regulatory modules in animals. Nature Reviews Genetics, 2012, 13, 469-483.	7.7	200
65	Harnessing cloud computing with Galaxy Cloud. Nature Biotechnology, 2011, 29, 972-974.	9.4	100
66	The Galaxy Track Browser: Transforming the genome browser from visualization tool to analysis tool. , 2011, , .		1
67	Dynamics of mitochondrial heteroplasmy in three families investigated via a repeatable re-sequencing study. Genome Biology, 2011, 12, R59.	3.8	93
68	The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications. Journal of Biomedical Semantics, 2011, 2, 4.	0.9	19
69	Making whole genome multiple alignments usable for biologists. Bioinformatics, 2011, 27, 2426-2428.	1.8	43
70	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. Genome Research, 2011, 21, 1659-1671.	2.4	110
71	The Genome Sequence of the Leaf-Cutter Ant <i>Atta cephalotes</i> Reveals Insights into Its Obligate Symbiotic Lifestyle. PLoS Genetics, 2011, 7, e1002007.	1.5	231
72	Integrating diverse databases into an unified analysis framework: a Galaxy approach. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar011-bar011.	1.4	46

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73	Galaxy: A Gateway to Tools in e-Science. Computer Communications and Networks, 2011, , 145-177.	0.8	20
74	Galaxy CloudMan: delivering cloud compute clusters. BMC Bioinformatics, 2010, 11, S4.	1.2	140
75	Manipulation of FASTQ data with Galaxy. Bioinformatics, 2010, 26, 1783-1785.	1.8	587
76	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
77	Galaxy: a comprehensive approach for supporting accessible, reproducible, and transparent computational research in the life sciences. Genome Biology, 2010, 11, R86.	13.9	3,082
78	Web-Based Analysis of (Epi-) Genome Data Using EpiGRAPH and Galaxy. Methods in Molecular Biology, 2010, 628, 275-296.	0.4	10
79	Windshield splatter analysis with the Galaxy metagenomic pipeline. Genome Research, 2009, 19, 2144-2153.	2.4	68
80	Primary sequence and epigenetic determinants of in vivo occupancy of genomic DNA by GATA1. Nucleic Acids Research, 2009, 37, 7024-7038.	6.5	29
81	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	13.7	657
82	Comparative analyses of bidirectional promoters in vertebrates. BMC Bioinformatics, 2008, 9, S9.	1.2	30
83	Phylogenomic Resources at the UCSC Genome Browser. Methods in Molecular Biology, 2008, 422, 133-144.	0.4	7
84	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
85	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. Genome Research, 2007, 17, 1797-1808.	2.4	237
86	Using Galaxy to Perform Large-Scale Interactive Data Analyses. Current Protocols in Bioinformatics, 2007, 19, Unit 10.5.	25.8	100
87	A framework for collaborative analysis of ENCODE data: Making large-scale analyses biologist-friendly. Genome Research, 2007, 17, 960-964.	2.4	122
88	Rigorous Mapping of Orthologous Bidirectional Promoters in Vertebrates Defines their Evolutionary History. , 2007, , .		0
89	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Research, 2007, 17, 760-774.	2.4	184
90	Finding cis-regulatory elements using comparative genomics: Some lessons from ENCODE data. Genome Research, 2007, 17, 775-786.	2.4	69

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91	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
92	Rigorous Mapping of Orthologous Bidirectional Promoters in Vertebrates Defines their Evolutionary History. , 2007, , .		0
93	Experimental validation of predicted mammalian erythroid cis-regulatory modules. <i>Genome Research</i> , 2006, 16, 1480-1492.	2.4	56
94	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
95	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
96	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. <i>Nature</i> , 2005, 434, 724-731.	13.7	85
97	Initial sequence of the chimpanzee genome and comparison with the human genome. <i>Nature</i> , 2005, 437, 69-87.	13.7	2,222
98	Clues to function in gene deserts. <i>Trends in Biotechnology</i> , 2005, 23, 269-271.	4.9	15
99	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
100	Galaxy: A platform for interactive large-scale genome analysis. <i>Genome Research</i> , 2005, 15, 1451-1455.	2.4	1,795
101	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
102	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943
103	A guide and best practices for R/Bioconductor tool integration in Galaxy. <i>F1000Research</i> , 0, 5, 2757.	0.8	3