

James Taylor

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

115 papers	35,376 citations	47 h-index	135 g-index
135 ext. papers	43,203 ext. citations	15.1 avg, IF	8.29 L-index

#	Paper	IF	Citations
115	Cellular life from the three domains and viruses are transcriptionally active in a hypersaline desert community. <i>Environmental Microbiology</i> , 2021 , 23, 3401-3417	5.2	9
114	Using Galaxy to Perform Large-Scale Interactive Data Analyses-An Update. <i>Current Protocols</i> , 2021 , 1, e31		3
113	An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. <i>Genome Research</i> , 2020 , 30, 472-484	9.7	11
112	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2020 update. <i>Nucleic Acids Research</i> , 2020 , 48, W395-W402	20.1	106
111	The full-length transcriptome of using direct RNA sequencing. <i>Genome Research</i> , 2020 , 30, 299-312	9.7	32
110	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	4.7	3
109	Environmental Factors Driving Spatial Heterogeneity in Desert Halophile Microbial Communities. <i>Frontiers in Microbiology</i> , 2020 , 11, 578669	5.7	2
108	A single-cell RNA-sequencing training and analysis suite using the Galaxy framework. <i>GigaScience</i> , 2020 , 9,	7.6	5
107	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	11.5	4
106	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	7.6	18
105	Cloud bursting galaxy: federated identity and access management. <i>Bioinformatics</i> , 2020 , 36, 1-9	7.2	2
104	Measuring the reproducibility and quality of Hi-C data. <i>Genome Biology</i> , 2019 , 20, 57	18.3	62
103	CloudLaunch: Discover and Deploy Cloud Applications. <i>Future Generation Computer Systems</i> , 2019 , 94, 802-810	7.5	11
102	Halophilic microbial community compositional shift after a rare rainfall in the Atacama Desert. <i>ISME Journal</i> , 2019 , 13, 2737-2749	11.9	33
101	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	10.2	16
100	Biology Needs Evolutionary Software Tools: Let's Build Them Right. <i>Molecular Biology and Evolution</i> , 2018 , 35, 1372-1375	8.3	6
99	Thyroid hormone signaling specifies cone subtypes in human retinal organoids. <i>Science</i> , 2018 , 362,	33.3	101

98	Federated Galaxy: Biomedical Computing at the Frontier 2018 , 2018,		2
97	MetaWRAP-a flexible pipeline for genome-resolved metagenomic data analysis. <i>Microbiome</i> , 2018 , 6, 158	16.6	370
96	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. <i>Nucleic Acids Research</i> , 2018 , 46, W537-W544	20.1	1509
95	Community-Driven Data Analysis Training for Biology. <i>Cell Systems</i> , 2018 , 6, 752-758.e1	10.6	62
94	Practical Computational Reproducibility in the Life Sciences. <i>Cell Systems</i> , 2018 , 6, 631-635	10.6	66
93	Lamins Organize the Global Three-Dimensional Genome from the Nuclear Periphery. <i>Molecular Cell</i> , 2018 , 71, 802-815.e7	17.6	98
92	Chromatin States in Mouse Sperm Correlate with Embryonic and Adult Regulatory Landscapes. <i>Cell Reports</i> , 2017 , 18, 1366-1382	10.6	147
91	A Novel Long Non-Coding RNA in the hTERT Promoter Region Regulates hTERT Expression. <i>Non-coding RNA</i> , 2017 , 4,	7.1	15
90	Jupyter and Galaxy: Easing entry barriers into complex data analyses for biomedical researchers. <i>PLoS Computational Biology</i> , 2017 , 13, e1005425	5	39
89	Natural variation in stochastic photoreceptor specification and color preference in. <i>ELife</i> , 2017 , 6,	8.9	12
88	CloudBridge: a Simple Cross-Cloud Python Library 2016 , 2016,		3
87	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2016 update. <i>Nucleic Acids Research</i> , 2016 , 44, W3-W10	20.1	1220
86	Jetstream 2016 ,		6
85	Genome-wide comparative analysis reveals human-mouse regulatory landscape and evolution. <i>BMC Genomics</i> , 2015 , 16, 87	4.5	46
84	Building and provisioning bioinformatics environments on public and private Clouds 2015 ,		2
83	Open pipelines for integrated tumor genome profiles reveal differences between pancreatic cancer tumors and cell lines. <i>Cancer Medicine</i> , 2015 , 4, 392-403	4.8	8
82	HiFive: a tool suite for easy and efficient HiC and 5C data analysis. <i>Genome Biology</i> , 2015 , 16, 237	18.3	52
81	Enabling cloud bursting for life sciences within Galaxy. <i>Concurrency Computation Practice and Experience</i> , 2015 , 27, 4330-4343	1.4	5

80	Ribosome A and P sites revealed by length analysis of ribosome profiling data. <i>Nucleic Acids Research</i> , 2015 , 43, 3680-7	20.1	32
79	Jetstream 2015 ,		68
78	Online resources for genomic analysis using high-throughput sequencing. <i>Cold Spring Harbor Protocols</i> , 2015 , 2015, 324-35	1.2	5
77	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014 , 515, 355-64	50.4	1026
76	Topologically associating domains are stable units of replication-timing regulation. <i>Nature</i> , 2014 , 515, 402-5	50.4	563
75	Dissemination of scientific software with Galaxy ToolShed. <i>Genome Biology</i> , 2014 , 15, 403	18.3	136
74	Leveraging the national cyberinfrastructure for biomedical research. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2014 , 21, 195-9	8.6	10
73	2014 ,		3
72	Wrangling Galaxy's reference data. <i>Bioinformatics</i> , 2014 , 30, 1917-9	7.2	22
71	The 3rd DBCLS BioHackathon: improving life science data integration with Semantic Web technologies. <i>Journal of Biomedical Semantics</i> , 2013 , 4, 6	2.2	22
70	Web-based visual analysis for high-throughput genomics. <i>BMC Genomics</i> , 2013 , 14, 397	4.5	35
69	The anatomy of successful computational biology software. <i>Nature Biotechnology</i> , 2013 , 31, 894-7	44.5	18
68	The DNA60IFX contest. <i>Genome Biology</i> , 2013 , 14, 124	18.3	
67	Architectural protein subclasses shape 3D organization of genomes during lineage commitment. <i>Cell</i> , 2013 , 153, 1281-95	56.2	848
66	Ten simple rules for reproducible computational research. <i>PLoS Computational Biology</i> , 2013 , 9, e1003285		343
65	Parasitoid wasp venom SERCA regulates Drosophila calcium levels and inhibits cellular immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 9427-32	11.5	43
64	Integrative approach reveals composition of endoparasitoid wasp venoms. <i>PLoS ONE</i> , 2013 , 8, e64125	3.7	64
63	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012 , 489, 57-74	50.4	11449

62	Next-generation sequencing data interpretation: enhancing reproducibility and accessibility. <i>Nature Reviews Genetics</i> , 2012 , 13, 667-72	30.1	215
61	Using cloud computing infrastructure with CloudBioLinux, CloudMan, and Galaxy. <i>Current Protocols in Bioinformatics</i> , 2012 , Chapter 11, Unit11.9	24.2	21
60	Using Galaxy to perform large-scale interactive data analyses. <i>Current Protocols in Bioinformatics</i> , 2012 , Chapter 10, Unit10.5	24.2	31
59	NGS analyses by visualization with Trackster. <i>Nature Biotechnology</i> , 2012 , 30, 1036-9	44.5	22
58	CloudMan as a platform for tool, data, and analysis distribution. <i>BMC Bioinformatics</i> , 2012 , 13, 315	3.6	36
57	A reference model for deploying applications in virtualized environments. <i>Concurrency Computation Practice and Experience</i> , 2012 , 24, 1349-1361	1.4	4
56	Genomic approaches towards finding cis-regulatory modules in animals. <i>Nature Reviews Genetics</i> , 2012 , 13, 469-83	30.1	156
55	Lessons learned from Galaxy, a Web-based platform for high-throughput genomic analyses 2012 ,		2
54	An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , 2012 , 13, 418	18.3	340
53	Dynamics of mitochondrial heteroplasmy in three families investigated via a repeatable re-sequencing study. <i>Genome Biology</i> , 2011 , 12, R59	18.3	83
52	The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications. <i>Journal of Biomedical Semantics</i> , 2011 , 2, 4	2.2	15
51	Harnessing cloud computing with Galaxy Cloud. <i>Nature Biotechnology</i> , 2011 , 29, 972-4	44.5	85
50	2011 ,		1
49	Making whole genome multiple alignments usable for biologists. <i>Bioinformatics</i> , 2011 , 27, 2426-8	7.2	35
48	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. <i>Genome Research</i> , 2011 , 21, 1659-71	9.7	100
47	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	6	191
46	Integrating diverse databases into a unified analysis framework: a Galaxy approach. <i>Database: the Journal of Biological Databases and Curation</i> , 2011 , 2011, bar011	5	34
45	Galaxy: A Gateway to Tools in e-Science. <i>Computer Communications and Networks</i> , 2011 , 145-177	0.5	17

44	Manipulation of FASTQ data with Galaxy. <i>Bioinformatics</i> , 2010 , 26, 1783-5	7.2	450
43	Galaxy: a web-based genome analysis tool for experimentalists. <i>Current Protocols in Molecular Biology</i> , 2010 , Chapter 19, Unit 19.10.1-21	2.9	961
42	Galaxy: a comprehensive approach for supporting accessible, reproducible, and transparent computational research in the life sciences. <i>Genome Biology</i> , 2010 , 11, R86	18.3	2579
41	Galaxy CloudMan: delivering cloud compute clusters. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 12, S4	3.6	111
40	Web-based analysis of (Epi-) genome data using EpiGRAPH and Galaxy. <i>Methods in Molecular Biology</i> , 2010 , 628, 275-96	1.4	10
39	Windshield splatter analysis with the Galaxy metagenomic pipeline. <i>Genome Research</i> , 2009 , 19, 2144-53	9.7	61
38	Primary sequence and epigenetic determinants of in vivo occupancy of genomic DNA by GATA1. <i>Nucleic Acids Research</i> , 2009 , 37, 7024-38	20.1	27
37	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008 , 453, 175-83	50.4	545
36	Comparative analyses of bidirectional promoters in vertebrates. <i>BMC Bioinformatics</i> , 2008 , 9 Suppl 6, S9	3.6	27
35	Toward the commoditization of translational genomic research: Design and implementation features of the Galaxy genomic workbench. <i>Summit on Translational Bioinformatics</i> , 2008 , 2008, 56-60		
34	Phylogenomic resources at the UCSC Genome Browser. <i>Methods in Molecular Biology</i> , 2008 , 422, 133-44	1.4	7
33	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. <i>Genome Research</i> , 2007 , 17, 760-74	9.7	163
32	Finding cis-regulatory elements using comparative genomics: some lessons from ENCODE data. <i>Genome Research</i> , 2007 , 17, 775-86	9.7	61
31	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007 , 447, 799-816	50.4	4121
30	28-way vertebrate alignment and conservation track in the UCSC Genome Browser. <i>Genome Research</i> , 2007 , 17, 1797-808	9.7	204
29	Using galaxy to perform large-scale interactive data analyses. <i>Current Protocols in Bioinformatics</i> , 2007 , Chapter 10, Unit 10.5	24.2	84
28	A framework for collaborative analysis of ENCODE data: making large-scale analyses biologist-friendly. <i>Genome Research</i> , 2007 , 17, 960-4	9.7	105
27	Experimental validation of predicted mammalian erythroid cis-regulatory modules. <i>Genome Research</i> , 2006 , 16, 1480-92	9.7	49

26	ESPERR: learning strong and weak signals in genomic sequence alignments to identify functional elements. <i>Genome Research</i> , 2006 , 16, 1596-604	9.7	97
25	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, 565-73	8.3	73
24	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. <i>Nature</i> , 2005 , 434, 724-31	50.4	61
23	Initial sequence of the chimpanzee genome and comparison with the human genome. <i>Nature</i> , 2005 , 437, 69-87	50.4	1828
22	Clues to function in gene deserts. <i>Trends in Biotechnology</i> , 2005 , 23, 269-71	15.1	15
21	Evaluation of regulatory potential and conservation scores for detecting cis-regulatory modules in aligned mammalian genome sequences. <i>Genome Research</i> , 2005 , 15, 1051-60	9.7	164
20	Galaxy: a platform for interactive large-scale genome analysis. <i>Genome Research</i> , 2005 , 15, 1451-5	9.7	1509
19	Regulatory potential scores from genome-wide three-way alignments of human, mouse, and rat. <i>Genome Research</i> , 2004 , 14, 700-7	9.7	84
18	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004 , 428, 493-521	50.4	1689
17	Understanding trivial challenges of microbial genomics: An assembly example		1
16	Genome-wide comparative analysis reveals human- mouse regulatory landscape and evolution		3
15	Chromosome Conformation Paints Reveal the Role of Lamina Association in Genome Organization and Regulation		16
14	Measuring the reproducibility and quality of Hi-C data		6
13	Practical computational reproducibility in the life sciences		3
12	QuASAR: Quality Assessment of Spatial Arrangement Reproducibility in Hi-C Data		11
11	Bioconda: A sustainable and comprehensive software distribution for the life sciences		12
10	Community-driven data analysis training for biology		4
9	MetaWRAP - a flexible pipeline for genome-resolved metagenomic data analysis		5

8	TADs pair homologous chromosomes to promote interchromosomal gene regulation	6
7	The repressive genome compartment is established early in the cell cycle before forming the lamina associated domains	14
6	The full-length transcriptome of <i>C. elegans</i> using direct RNA sequencing	4
5	Cellular life from the three domains and viruses are transcriptionally active in a hypersaline desert community	2
4	Enhancing pre-defined workflows with ad hoc analytics using Galaxy, Docker and Jupyter	1
3	A guide and best practices for R/Bioconductor tool integration in Galaxy. <i>F1000Research</i> , 5, 2757	3.6 2
2	Lamins organize the global three-dimensional genome from the nuclear periphery	3
1	Temporal regulation of green and red cone specification in human retinas and retinal organoids	1