

James Taylor

List of Publications by Citations

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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	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012 , 489, 57-74	50.4	11449
114	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
113	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
112	Initial sequence of the chimpanzee genome and comparison with the human genome. <i>Nature</i> , 2005 , 437, 69-87	50.4	1828
111	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004 , 428, 493-521	50.4	1689
110	Galaxy: a platform for interactive large-scale genome analysis. <i>Genome Research</i> , 2005 , 15, 1451-5	9.7	1509
109	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. <i>Nucleic Acids Research</i> , 2018 , 46, W537-W544	20.1	1509
108	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2016 update. <i>Nucleic Acids Research</i> , 2016 , 44, W3-W10	20.1	1220
107	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014 , 515, 355-64	50.4	1026
106	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
105	Architectural protein subclasses shape 3D organization of genomes during lineage commitment. <i>Cell</i> , 2013 , 153, 1281-95	56.2	848
104	Topologically associating domains are stable units of replication-timing regulation. <i>Nature</i> , 2014 , 515, 402-5	50.4	563
103	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008 , 453, 175-83	50.4	545
102	Manipulation of FASTQ data with Galaxy. <i>Bioinformatics</i> , 2010 , 26, 1783-5	7.2	450
101	MetaWRAP-a flexible pipeline for genome-resolved metagenomic data analysis. <i>Microbiome</i> , 2018 , 6, 158	16.6	370
100	Ten simple rules for reproducible computational research. <i>PLoS Computational Biology</i> , 2013 , 9, e1003285		343
99	An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , 2012 , 13, 418	18.3	340

98	Next-generation sequencing data interpretation: enhancing reproducibility and accessibility. <i>Nature Reviews Genetics</i> , 2012 , 13, 667-72	30.1	215
97	28-way vertebrate alignment and conservation track in the UCSC Genome Browser. <i>Genome Research</i> , 2007 , 17, 1797-808	9.7	204
96	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
95	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
94	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
93	Genomic approaches towards finding cis-regulatory modules in animals. <i>Nature Reviews Genetics</i> , 2012 , 13, 469-83	30.1	156
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	Dissemination of scientific software with Galaxy ToolShed. <i>Genome Biology</i> , 2014 , 15, 403	18.3	136
90	Galaxy CloudMan: delivering cloud compute clusters. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 12, S4	3.6	111
89	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2020 update. <i>Nucleic Acids Research</i> , 2020 , 48, W395-W402	20.1	106
88	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
87	Thyroid hormone signaling specifies cone subtypes in human retinal organoids. <i>Science</i> , 2018 , 362,	33.3	101
86	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. <i>Genome Research</i> , 2011 , 21, 1659-71	9.7	100
85	Lamins Organize the Global Three-Dimensional Genome from the Nuclear Periphery. <i>Molecular Cell</i> , 2018 , 71, 802-815.e7	17.6	98
84	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
83	Harnessing cloud computing with Galaxy Cloud. <i>Nature Biotechnology</i> , 2011 , 29, 972-4	44.5	85
82	Using galaxy to perform large-scale interactive data analyses. <i>Current Protocols in Bioinformatics</i> , 2007 , Chapter 10, Unit 10.5	24.2	84
81	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

80	Dynamics of mitochondrial heteroplasmy in three families investigated via a repeatable re-sequencing study. <i>Genome Biology</i> , 2011 , 12, R59	18.3	83
79	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
78	Jetstream 2015 ,		68
77	Practical Computational Reproducibility in the Life Sciences. <i>Cell Systems</i> , 2018 , 6, 631-635	10.6	66
76	Integrative approach reveals composition of endoparasitoid wasp venoms. <i>PLoS ONE</i> , 2013 , 8, e64125	3.7	64
75	Measuring the reproducibility and quality of Hi-C data. <i>Genome Biology</i> , 2019 , 20, 57	18.3	62
74	Community-Driven Data Analysis Training for Biology. <i>Cell Systems</i> , 2018 , 6, 752-758.e1	10.6	62
73	Windshield splatter analysis with the Galaxy metagenomic pipeline. <i>Genome Research</i> , 2009 , 19, 2144-53	9.7	61
72	Finding cis-regulatory elements using comparative genomics: some lessons from ENCODE data. <i>Genome Research</i> , 2007 , 17, 775-86	9.7	61
71	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. <i>Nature</i> , 2005 , 434, 724-31	50.4	61
70	HiFive: a tool suite for easy and efficient HiC and 5C data analysis. <i>Genome Biology</i> , 2015 , 16, 237	18.3	52
69	Experimental validation of predicted mammalian erythroid cis-regulatory modules. <i>Genome Research</i> , 2006 , 16, 1480-92	9.7	49
68	Genome-wide comparative analysis reveals human-mouse regulatory landscape and evolution. <i>BMC Genomics</i> , 2015 , 16, 87	4.5	46
67	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
66	Jupyter and Galaxy: Easing entry barriers into complex data analyses for biomedical researchers. <i>PLoS Computational Biology</i> , 2017 , 13, e1005425	5	39
65	CloudMan as a platform for tool, data, and analysis distribution. <i>BMC Bioinformatics</i> , 2012 , 13, 315	3.6	36
64	Web-based visual analysis for high-throughput genomics. <i>BMC Genomics</i> , 2013 , 14, 397	4.5	35
63	Making whole genome multiple alignments usable for biologists. <i>Bioinformatics</i> , 2011 , 27, 2426-8	7.2	35

62	Integrating diverse databases into an unified analysis framework: a Galaxy approach. <i>Database: the Journal of Biological Databases and Curation</i> , 2011 , 2011, bar011	5	34
61	Halophilic microbial community compositional shift after a rare rainfall in the Atacama Desert. <i>ISME Journal</i> , 2019 , 13, 2737-2749	11.9	33
60	The full-length transcriptome of using direct RNA sequencing. <i>Genome Research</i> , 2020 , 30, 299-312	9.7	32
59	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
58	Using Galaxy to perform large-scale interactive data analyses. <i>Current Protocols in Bioinformatics</i> , 2012 , Chapter 10, Unit10.5	24.2	31
57	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
56	Comparative analyses of bidirectional promoters in vertebrates. <i>BMC Bioinformatics</i> , 2008 , 9 Suppl 6, S9	3.6	27
55	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
54	Wrangling Galaxy's reference data. <i>Bioinformatics</i> , 2014 , 30, 1917-9	7.2	22
53	NGS analyses by visualization with Trackster. <i>Nature Biotechnology</i> , 2012 , 30, 1036-9	44.5	22
52	Using cloud computing infrastructure with CloudBioLinux, CloudMan, and Galaxy. <i>Current Protocols in Bioinformatics</i> , 2012 , Chapter 11, Unit11.9	24.2	21
51	The anatomy of successful computational biology software. <i>Nature Biotechnology</i> , 2013 , 31, 894-7	44.5	18
50	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
49	Galaxy: A Gateway to Tools in e-Science. <i>Computer Communications and Networks</i> , 2011 , 145-177	0.5	17
48	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
47	Chromosome Conformation Paints Reveal the Role of Lamina Association in Genome Organization and Regulation		16
46	A Novel Long Non-Coding RNA in the hTERT Promoter Region Regulates hTERT Expression. <i>Non-coding RNA</i> , 2017 , 4,	7.1	15
45	The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications. <i>Journal of Biomedical Semantics</i> , 2011 , 2, 4	2.2	15

44	Clues to function in gene deserts. <i>Trends in Biotechnology</i> , 2005 , 23, 269-71	15.1	15
43	The repressive genome compartment is established early in the cell cycle before forming the lamina associated domains		14
42	Natural variation in stochastic photoreceptor specification and color preference in. <i>ELife</i> , 2017 , 6,	8.9	12
41	Bioconda: A sustainable and comprehensive software distribution for the life sciences		12
40	An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. <i>Genome Research</i> , 2020 , 30, 472-484	9.7	11
39	CloudLaunch: Discover and Deploy Cloud Applications. <i>Future Generation Computer Systems</i> , 2019 , 94, 802-810	7.5	11
38	QuASAR: Quality Assessment of Spatial Arrangement Reproducibility in Hi-C Data		11
37	Leveraging the national cyberinfrastructure for biomedical research. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2014 , 21, 195-9	8.6	10
36	Web-based analysis of (Epi-) genome data using EpiGRAPH and Galaxy. <i>Methods in Molecular Biology</i> , 2010 , 628, 275-96	1.4	10
35	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
34	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
33	Phylogenomic resources at the UCSC Genome Browser. <i>Methods in Molecular Biology</i> , 2008 , 422, 133-44	1.4	7
32	Biology Needs Evolutionary Software Tools: Let's Build Them Right. <i>Molecular Biology and Evolution</i> , 2018 , 35, 1372-1375	8.3	6
31	Measuring the reproducibility and quality of Hi-C data		6
30	TADs pair homologous chromosomes to promote interchromosomal gene regulation		6
29	Jetstream 2016 ,		6
28	Enabling cloud bursting for life sciences within Galaxy. <i>Concurrency Computation Practice and Experience</i> , 2015 , 27, 4330-4343	1.4	5
27	Online resources for genomic analysis using high-throughput sequencing. <i>Cold Spring Harbor Protocols</i> , 2015 , 2015, 324-35	1.2	5

26	MetaWRAP - a flexible pipeline for genome-resolved metagenomic data analysis		5
25	A single-cell RNA-sequencing training and analysis suite using the Galaxy framework. <i>GigaScience</i> , 2020 , 9,	7.6	5
24	A reference model for deploying applications in virtualized environments. <i>Concurrency Computation Practice and Experience</i> , 2012 , 24, 1349-1361	1.4	4
23	Community-driven data analysis training for biology		4
22	The full-length transcriptome of <i>C. elegans</i> using direct RNA sequencing		4
21	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
20	CloudBridge: a Simple Cross-Cloud Python Library 2016 , 2016,		3
19	2014 ,		3
18	Genome-wide comparative analysis reveals human- mouse regulatory landscape and evolution		3
17	Practical computational reproducibility in the life sciences		3
16	Lamins organize the global three-dimensional genome from the nuclear periphery		3
15	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
14	Using Galaxy to Perform Large-Scale Interactive Data Analyses-An Update. <i>Current Protocols</i> , 2021 , 1, e31		3
13	Building and provisioning bioinformatics environments on public and private Clouds 2015 ,		2
12	Lessons learned from Galaxy, a Web-based platform for high-throughput genomic analyses 2012 ,		2
11	Cellular life from the three domains and viruses are transcriptionally active in a hypersaline desert community		2
10	A guide and best practices for R/Bioconductor tool integration in Galaxy. <i>F1000Research</i> , 5, 2757	3.6	2
9	Environmental Factors Driving Spatial Heterogeneity in Desert Halophile Microbial Communities. <i>Frontiers in Microbiology</i> , 2020 , 11, 578669	5.7	2

8	Cloud bursting galaxy: federated identity and access management. <i>Bioinformatics</i> , 2020 , 36, 1-9	7.2	2
7	Federated Galaxy: Biomedical Computing at the Frontier 2018 , 2018,		2
6	2011 ,		1
5	Understanding trivial challenges of microbial genomics: An assembly example		1
4	Enhancing pre-defined workflows with ad hoc analytics using Galaxy, Docker and Jupyter		1
3	Temporal regulation of green and red cone specification in human retinas and retinal organoids		1
2	The DNA60IFX contest. <i>Genome Biology</i> , 2013 , 14, 124		18.3
1	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		