Anton Nekrutenko

List of Publications by Year
in descending order

96 papers	22,425 citations	66343 42 h-index	42399 92 g-index
120 all docs	120 docs citations	120 times ranked	32668 citing authors

#	Article	IF	Citations
1	Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space. Cell Genomics, 2022, 2, 100085.	6.5	59
2	Selection Analysis Identifies Clusters of Unusual Mutational Changes in Omicron Lineage BA.1 That Likely Impact Spike Function. Molecular Biology and Evolution, 2022, 39, .	8.9	84
3	Detection of SARS-CoV-2 intra-host recombination during superinfection with Alpha and Epsilon variants in New York City. Nature Communications, 2022, 13, .	12.8	22
4	Sequencing error profiles of Illumina sequencing instruments. NAR Genomics and Bioinformatics, 2021, 3, lqab019.	3.2	188
5	Increased yields of duplex sequencing data by a series of quality control tools. NAR Genomics and Bioinformatics, 2021, 3, lqab002.	3.2	6
6	Using Galaxy to Perform Large‐Scale Interactive Data Analyses—An Update. Current Protocols, 2021, 1, e31.	2.9	4
7	Fostering accessible online education using Galaxy as an e-learning platform. PLoS Computational Biology, 2021, 17, e1008923.	3.2	15
8	Reproducible and accessible analysis of transposon insertion sequencing in Galaxy for qualitative essentiality analyses. BMC Microbiology, 2021, 21, 168.	3.3	1
9	GYAN: Accelerating Bioinformatics Tools in Galaxy with GPU-Aware Computation Mapping. , 2021, , .		1
10	Stepwise Evolution and Exceptional Conservation of ORF1a/b Overlap in Coronaviruses. Molecular Biology and Evolution, 2021, 38, 5678-5684.	8.9	6
11	Ready-to-use public infrastructure for global SARS-CoV-2 monitoring. Nature Biotechnology, 2021, 39, 1178-1179.	17.5	21
12	HyPhy 2.5—A Customizable Platform for Evolutionary Hypothesis Testing Using Phylogenies. Molecular Biology and Evolution, 2020, 37, 295-299.	8.9	342
13	A single-cell RNA-sequencing training and analysis suite using the Galaxy framework. GigaScience, 2020, 9, .	6.4	14
14	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
15	In memory of James Taylor: the birth of Galaxy. Genome Biology, 2020, 21, 105.	8.8	1
16	Family reunion via error correction: an efficient analysis of duplex sequencing data. BMC Bioinformatics, 2020, 21, 96.	2.6	10
17	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2020 update. Nucleic Acids Research, 2020, 48, W395-W402.	14.5	322
18	A High-Resolution View of Adaptive Event Dynamics in a Plasmid. Genome Biology and Evolution, 2019, 11, 3022-3034.	2.5	11

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19	Predicting runtimes of bioinformatics tools based on historical data: five years of Galaxy usage. Bioinformatics, 2019, 35, 3453-3460.	4.1	11
20	Bottleneck and selection in the germline and maternal age influence transmission of mitochondrial DNA in human pedigrees. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25172-25178.	7.1	71
21	Biology Needs Evolutionary Software Tools: Let's Build Them Right. Molecular Biology and Evolution, 2018, 35, 1372-1375.	8.9	6
22	Child Weight Gain Trajectories Linked To Oral Microbiota Composition. Scientific Reports, 2018, 8, 14030.	3.3	39
23	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. Nucleic Acids Research, 2018, 46, W537-W544.	14.5	3,003
24	Community-Driven Data Analysis Training for Biology. Cell Systems, 2018, 6, 752-758.e1.	6.2	141
25	Practical Computational Reproducibility in the Life Sciences. Cell Systems, 2018, 6, 631-635.	6.2	100
26	Jupyter and Galaxy: Easing entry barriers into complex data analyses for biomedical researchers. PLoS Computational Biology, 2017, 13, e1005425.	3.2	53
27	Streamlined analysis of duplex sequencing data with Du Novo. Genome Biology, 2016, 17, 180.	8.8	24
28	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2016 update. Nucleic Acids Research, 2016, 44, W3-W10.	14.5	1,751
29	Integrative genomic analysis by interoperation of bioinformatics tools in GenomeSpace. Nature Methods, 2016, 13, 245-247.	19.0	44
30	Online Resources for Genomic Analysis Using High-Throughput Sequencing. Cold Spring Harbor Protocols, 2015, 2015, pdb.top083667.	0.3	6
31	StructureFold: genome-wide RNA secondary structure mapping and reconstruction *in vivo*. Bioinformatics, 2015, 31, 2668-2675.	4.1	43
32	Controlling for contamination in re-sequencing studies with a reproducible web-based phylogenetic approach. BioTechniques, 2014, 56, 134-141.	1.8	22
33	Maternal age effect and severe germ-line bottleneck in the inheritance of human mitochondrial DNA. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15474-15479.	7.1	201
34	Wrangling Galaxy's reference data. Bioinformatics, 2014, 30, 1917-1919.	4.1	31
35	Dissemination of scientific software with Galaxy ToolShed. Genome Biology, 2014, 15, 403.	9.6	205
36	Web-based visual analysis for high-throughput genomics. BMC Genomics, 2013, 14, 397.	2.8	45

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37	RNAâ€"DNA differences in human mitochondria restore ancestral form of 16S ribosomal RNA. Genome Research, 2013, 23, 1789-1796.	5.5	49
38	The anatomy of successful computational biology software. Nature Biotechnology, 2013, 31, 894-897.	17.5	25
39	Ten Simple Rules for Reproducible Computational Research. PLoS Computational Biology, 2013, 9, e1003285.	3.2	509
40	A sustainable national gateway for biological computation. , 2013, , .		0
41	Lessons learned from Galaxy, a Web-based platform for high-throughput genomic analyses. , 2012, , .		5
42	Next-generation sequencing data interpretation: enhancing reproducibility and accessibility. Nature Reviews Genetics, 2012, 13, 667-672.	16.3	269
43	Using Galaxy to Perform Largeâ€Scale Interactive Data Analyses. Current Protocols in Bioinformatics, 2012, 38, Unit10.5.	25.8	36
44	NGS analyses by visualization with Trackster. Nature Biotechnology, 2012, 30, 1036-1039.	17.5	26
45	A reference model for deploying applications in virtualized environments. Concurrency Computation Practice and Experience, 2012, 24, 1349-1361.	2.2	4
46	Harnessing cloud computing with Galaxy Cloud. Nature Biotechnology, 2011, 29, 972-974.	17.5	100
47	Dynamics of mitochondrial heteroplasmy in three families investigated via a repeatable re-sequencing study. Genome Biology, 2011, 12, R59.	8.8	93
48	A Massively Parallel Sequencing Approach Uncovers Ancient Origins and High Genetic Variability of Endangered Przewalski's Horses. Genome Biology and Evolution, 2011, 3, 1096-1106.	2.5	51
49	Making whole genome multiple alignments usable for biologists. Bioinformatics, 2011, 27, 2426-2428.	4.1	43
50	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
51	Galaxy: A Gateway to Tools in e-Science. Computer Communications and Networks, 2011, , 145-177.	0.8	20
52	Galaxy CloudMan: delivering cloud compute clusters. BMC Bioinformatics, 2010, 11, S4.	2.6	140
53	Complete Khoisan and Bantu genomes from southern Africa. Nature, 2010, 463, 943-947.	27.8	400
54	Manipulation of FASTQ data with Galaxy. Bioinformatics, 2010, 26, 1783-1785.	4.1	587

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55	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
56	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
57	Web-Based Analysis of (Epi-) Genome Data Using EpiGRAPH and Galaxy. Methods in Molecular Biology, 2010, 628, 275-296.	0.9	10
58	Windshield splatter analysis with the Galaxy metagenomic pipeline. Genome Research, 2009, 19, 2144-2153.	5.5	68
59	High-Resolution Mapping of Evolutionary Trajectories in a Phage. Genome Biology and Evolution, 2009, 1, 294-307.	2.5	10
60	Transcriptome of embryonic and neonatal mouse cortex by high-throughput RNA sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12741-12746.	7.1	72
61	Wheels within Wheels: Clues to the Evolution of the Gnas and Gnal Loci. Molecular Biology and Evolution, 2008, 25, 2745-2757.	8.9	9
62	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
63	Rapid asymmetric evolution of a dual-coding tumor suppressor INK4a/ARF locus contradicts its function. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 12807-12812.	7.1	22
64	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. Genome Research, 2007, 17, 1797-1808.	5.5	237
65	A First Look at ARFome: Dual-Coding Genes in Mammalian Genomes. PLoS Computational Biology, 2007, 3, e91.	3.2	68
66	Using Galaxy to Perform Large‐Scale Interactive Data Analyses. Current Protocols in Bioinformatics, 2007, 19, Unit 10.5.	25.8	100
67	A framework for collaborative analysis of ENCODE data: Making large-scale analyses biologist-friendly. Genome Research, 2007, 17, 960-964.	5.5	122
68	mNSC1 shows no evidence of protein-coding capacity. Gene, 2006, 370, 83-85.	2.2	2
69	Functionality of unspliced XBP1 is required to explain evolution of overlapping reading frames. Trends in Genetics, 2006, 22, 645-648.	6.7	31
70	Rapid and asymmetric divergence of duplicate genes in the human gene coexpression network. BMC Bioinformatics, 2006, 7, 46.	2.6	45
71	Oscillating Evolution of a Mammalian Locus with Overlapping Reading Frames: An XLÎ±s/ALEX Relay. PLoS Genetics, 2005, 1, e18.	3.5	39
72	Galaxy: A platform for interactive large-scale genome analysis. Genome Research, 2005, 15, 1451-1455.	5.5	1,795

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73	Reconciling the Numbers: ESTs Versus Protein-Coding Genes. Molecular Biology and Evolution, 2004, 21, 1278-1282.	8.9	17
74	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	27.8	1,943
75	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. Nature, 2004, 432, 695-716.	27.8	2,421
76	Identification of Novel Exons from Rat–Mouse Comparisons. Journal of Molecular Evolution, 2004, 59, 703-708.	1.8	12
77	COMPARATIVE GENOMICS. Annual Review of Genomics and Human Genetics, 2004, 5, 15-56.	6.2	156
78	Detection of gene duplications and block duplications in eukaryotic genomes. Journal of Structural and Functional Genomics, 2003, 3, 27-34.	1.2	21
79	An evolutionary approach reveals a high protein-coding capacity of the human genome. Trends in Genetics, 2003, 19, 306-310.	6.7	33
80	Subgenome-specific markers in allopolyploid cotton Gossypium hirsutum: implications for evolutionary analysis of polyploids. Gene, 2003, 306, 99-103.	2.2	10
81	Evolutionary Dynamics of Oncogenes and Tumor Suppressor Genes: Higher Intensities of Purifying Selection than Other Genes. Molecular Biology and Evolution, 2003, 20, 964-968.	8.9	57
82	ETOPE: evolutionary test of predicted exons. Nucleic Acids Research, 2003, 31, 3564-3567.	14.5	17
83	Detection of gene duplications and block duplications in eukaryotic genomes. , 2003, , 27-34.		1
84	Detection of gene duplications and block duplications in eukaryotic genomes. Journal of Structural and Functional Genomics, 2003, 3, 27-34.	1.2	12
85	Signatures of Domain Shuffling in the Human Genome. Genome Research, 2002, 12, 1642-1650.	5.5	91
86	The KA/KS Ratio Test for Assessing the Protein-Coding Potential of Genomic Regions: An Empirical and Simulation Study. Genome Research, 2002, 12, 198-202.	5.5	233
87	Bushbaby Growth Hormone Is Much More Similar to Nonprimate Growth Hormones than to Rhesus Monkey and Human Growth Hormones. Molecular Biology and Evolution, 2001, 18, 55-60.	8.9	29
88	Evolutionary analyses of the human genome. Nature, 2001, 409, 847-849.	27.8	442
89	Transposable elements are found in a large number of human protein-coding genes. Trends in Genetics, 2001, 17, 619-621.	6.7	383
90	Evolution of Microsatellite Alleles in Four Species of Mice (Genus Apodemus). Journal of Molecular Evolution, 2000, 51, 166-172.	1.8	51

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91	Isolation of binary species-specific PCR-based markers and their value for diagnostic applications. Gene, 2000, 249, 47-51.	2.2	11
92	Densities, length proportions, and other distributional features of repetitive sequences in the human genome estimated from 430 megabases of genomic sequence. Gene, 2000, 259, 81-88.	2.2	91
93	Assessment of Compositional Heterogeneity Within and Between Eukaryotic Genomes. Genome Research, 2000, 10, 1986-1995.	5.5	15
94	Representational difference analysis to distinguish cryptic species. Molecular Ecology, 1999, 8, 1235-1237.	3.9	16
95	Representational difference analysis to distinguish cryptic species. Molecular Ecology, 1999, 8, 1235.	3.9	3
96	A guide and best practices for R/Bioconductor tool integration in Galaxy. F1000Research, 0, 5, 2757.	1.6	3