

Julien Gagneur

List of Publications by Year in descending order

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Version: 2024-02-01

68
papers

8,632
citations

81743

39
h-index

91712

69
g-index

97
all docs

97
docs citations

97
times ranked

14050
citing authors

#	ARTICLE	IF	CITATIONS
1	Partitioning RNAs by length improves transcriptome reconstruction from short-read RNA-seq data. <i>Nature Biotechnology</i> , 2022, 40, 741-750.	9.4	7
2	Clinical implementation of RNA sequencing for Mendelian disease diagnostics. <i>Genome Medicine</i> , 2022, 14, 38.	3.6	85
3	Detection of aberrant splicing events in RNA-seq data using FRASER. <i>Nature Communications</i> , 2021, 12, 529.	5.8	78
4	Detection of aberrant gene expression events in RNA sequencing data. <i>Nature Protocols</i> , 2021, 16, 1276-1296.	5.5	58
5	Transcriptome-directed analysis for Mendelian disease diagnosis overcomes limitations of conventional genomic testing. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	87
6	Base-resolution models of transcription-factor binding reveal soft motif syntax. <i>Nature Genetics</i> , 2021, 53, 354-366.	9.4	325
7	MTSplice predicts effects of genetic variants on tissue-specific splicing. <i>Genome Biology</i> , 2021, 22, 94.	3.8	23
8	Predicting mean ribosome load for 5â€™UTR of any length using deep learning. <i>PLoS Computational Biology</i> , 2021, 17, e1008982.	1.5	17
9	Assessing predictions of the impact of variants on splicing in CAGI5. <i>Human Mutation</i> , 2019, 40, 1215-1224.	1.1	18
10	Global donor and acceptor splicing site kinetics in human cells. <i>ELife</i> , 2019, 8, .	2.8	51
11	Quantification of Proteins and Histone Marks in Drosophila Embryos Reveals Stoichiometric Relationships Impacting Chromatin Regulation. <i>Developmental Cell</i> , 2019, 51, 632-644.e6.	3.1	50
12	The Kipoi repository accelerates community exchange and reuse of predictive models for genomics. <i>Nature Biotechnology</i> , 2019, 37, 592-600.	9.4	118
13	CAGI 5 splicing challenge: Improved exon skipping and intron retention predictions with MMSplice. <i>Human Mutation</i> , 2019, 40, 1243-1251.	1.1	10
14	Quantification and discovery of sequence determinants of proteinâ€™mRNA amount in human tissues. <i>Molecular Systems Biology</i> , 2019, 15, e8513.	3.2	63
15	MMSplice: modular modeling improves the predictions of genetic variant effects on splicing. <i>Genome Biology</i> , 2019, 20, 48.	3.8	140
16	Deep learning: new computational modelling techniques for genomics. <i>Nature Reviews Genetics</i> , 2019, 20, 389-403.	7.7	717
17	A deep proteome and transcriptome abundance atlas of 29 healthy human tissues. <i>Molecular Systems Biology</i> , 2019, 15, e8503.	3.2	576
18	Modeling positional effects of regulatory sequences with spline transformations increases prediction accuracy of deep neural networks. <i>Bioinformatics</i> , 2018, 34, 1261-1269.	1.8	29

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19	Somatic alterations compromised molecular diagnosis of DOCK8 hyper-IgE syndrome caused by a novel intronic splice site mutation. <i>Scientific Reports</i> , 2018, 8, 16719.	1.6	5
20	OUTRIDER: A Statistical Method for Detecting Aberrantly Expressed Genes in RNA Sequencing Data. <i>American Journal of Human Genetics</i> , 2018, 103, 907-917.	2.6	112
21	OCR-Stats: Robust estimation and statistical testing of mitochondrial respiration activities using Seahorse XF Analyzer. <i>PLoS ONE</i> , 2018, 13, e0199938.	1.1	55
22	Inhibition of oxidative stress in cholinergic projection neurons fully rescues aging-associated olfactory circuit degeneration in <i>Drosophila</i> . <i>ELife</i> , 2018, 7, .	2.8	21
23	GenoGAM 2.0: scalable and efficient implementation of genome-wide generalized additive models for gigabase-scale genomes. <i>BMC Bioinformatics</i> , 2018, 19, 247.	1.2	1
24	Bioinformatics advances biology and medicine by turning big data troves into knowledge. <i>Informatik-Spektrum</i> , 2017, 40, 153-160.	1.0	2
25	Genetic diagnosis of Mendelian disorders via RNA sequencing. <i>Nature Communications</i> , 2017, 8, 15824.	5.8	432
26	Chromatin-remodeling factor SMARCD2 regulates transcriptional networks controlling differentiation of neutrophil granulocytes. <i>Nature Genetics</i> , 2017, 49, 742-752.	9.4	87
27	GenoGAM: genome-wide generalized additive models for ChIP-Seq analysis. <i>Bioinformatics</i> , 2017, 33, 2258-2265.	1.8	9
28	TT-seq captures enhancer landscapes immediately after T-cell stimulation. <i>Molecular Systems Biology</i> , 2017, 13, 920.	3.2	44
29	Mutations in MDH2, Encoding a Krebs Cycle Enzyme, Cause Early-Onset Severe Encephalopathy. <i>American Journal of Human Genetics</i> , 2017, 100, 151-159.	2.6	63
30	Cis-regulatory elements explain most of the mRNA stability variation across genes in yeast. <i>Rna</i> , 2017, 23, 1648-1659.	1.6	63
31	Caenorhabditis elegans CES-1 Snail Represses pig-1 MELK Expression To Control Asymmetric Cell Division. <i>Genetics</i> , 2017, 206, 2069-2084.	1.2	13
32	Measures of RNA metabolism rates: Toward a definition at the level of single bonds. <i>Transcription</i> , 2017, 8, 75-80.	1.7	8
33	Accurate Promoter and Enhancer Identification in 127 ENCODE and Roadmap Epigenomics Cell Types and Tissues by GenoSTAN. <i>PLoS ONE</i> , 2017, 12, e0169249.	1.1	73
34	Meiotic Interactors of a Mitotic Gene TAO3 Revealed by Functional Analysis of its Rare Variant. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2255-2263.	0.8	5
35	Determinants of scpRNA metabolism in the Schizosaccharomyces pombe genome. <i>Molecular Systems Biology</i> , 2016, 12, 857.	3.2	81
36	TT-seq maps the human transient transcriptome. <i>Science</i> , 2016, 352, 1225-1228.	6.0	384

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37	Simultaneous characterization of sense and antisense genomic processes by the double-stranded hidden Markov model. <i>Nucleic Acids Research</i> , 2016, 44, e44-e44.	6.5	4
38	Temporal Expression Profiling Identifies Pathways Mediating Effect of Causal Variant on Phenotype. <i>PLoS Genetics</i> , 2015, 11, e1005195.	1.5	17
39	Negative feedback buffers effects of regulatory variants. <i>Molecular Systems Biology</i> , 2015, 11, 785.	3.2	33
40	Biallelic Mutations in NBAS Cause Recurrent Acute Liver Failure with Onset in Infancy. <i>American Journal of Human Genetics</i> , 2015, 97, 163-169.	2.6	110
41	Annotation of genomics data using bidirectional hidden Markov models unveils variations in Pol II transcription cycle. <i>Molecular Systems Biology</i> , 2014, 10, 768.	3.2	21
42	An Evaluation of High-Throughput Approaches to QTL Mapping in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2014, 196, 853-865.	1.2	86
43	Mitochondrial protein sorting as a therapeutic target for ATP synthase disorders. <i>Nature Communications</i> , 2014, 5, 5585.	5.8	29
44	Yeast Growth Plasticity Is Regulated by Environment-Specific Multi-QTL Interactions. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 769-777.	0.8	34
45	Genotyping 1000 yeast strains by next-generation sequencing. <i>BMC Genomics</i> , 2013, 14, 90.	1.2	47
46	Transcriptome Surveillance by Selective Termination of Noncoding RNA Synthesis. <i>Cell</i> , 2013, 155, 1075-1087.	13.5	201
47	Genotype-Environment Interactions Reveal Causal Pathways That Mediate Genetic Effects on Phenotype. <i>PLoS Genetics</i> , 2013, 9, e1003803.	1.5	72
48	The Genomic and Transcriptomic Landscape of a HeLa Cell Line. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1213-1224.	0.8	355
49	Experimental Relocation of the Mitochondrial ATP9 Gene to the Nucleus Reveals Forces Underlying Mitochondrial Genome Evolution. <i>PLoS Genetics</i> , 2012, 8, e1002876.	1.5	48
50	Selective Phenotyping, Entropy Reduction, and the Mastermind game. <i>BMC Bioinformatics</i> , 2011, 12, 406.	1.2	15
51	Model-based gene set analysis for Bioconductor. <i>Bioinformatics</i> , 2011, 27, 1882-1883.	1.8	56
52	Antisense expression increases gene expression variability and locus interdependency. <i>Molecular Systems Biology</i> , 2011, 7, 468.	3.2	173
53	A yeast-based assay identifies drugs active against human mitochondrial disorders. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11989-11994.	3.3	73
54	GOing Bayesian: model-based gene set analysis of genome-scale data. <i>Nucleic Acids Research</i> , 2010, 38, 3523-3532.	6.5	190

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55	Genome-wide allele- and strand-specific expression profiling. <i>Molecular Systems Biology</i> , 2009, 5, 274.	3.2	31
56	Bidirectional promoters generate pervasive transcription in yeast. <i>Nature</i> , 2009, 457, 1033-1037.	13.7	872
57	Combinatorial binding predicts spatio-temporal cis-regulatory activity. <i>Nature</i> , 2009, 462, 65-70.	13.7	361
58	Dissecting the Genetic Basis of Resistance to Malaria Parasites in <i>Anopheles gambiae</i> . <i>Science</i> , 2009, 326, 147-150.	6.0	106
59	Identification of mitochondrial disease genes through integrative analysis of multiple datasets. <i>Methods</i> , 2008, 46, 248-255.	1.9	10
60	Dynamic Regulation by Polycomb Group Protein Complexes Controls Pattern Formation and the Cell Cycle in <i>Drosophila</i> . <i>Developmental Cell</i> , 2008, 15, 877-889.	3.1	178
61	4DXpress: a database for cross-species expression pattern comparisons. <i>Nucleic Acids Research</i> , 2007, 36, D847-D853.	6.5	33
62	Capturing cellular machines by systematic screens of protein complexes. <i>Trends in Microbiology</i> , 2006, 14, 336-339.	3.5	10
63	Assessing Systems Properties of Yeast Mitochondria through an Interaction Map of the Organelle. <i>PLoS Genetics</i> , 2006, 2, e170.	1.5	67
64	From molecular networks to qualitative cell behavior. <i>FEBS Letters</i> , 2005, 579, 1867-1871.	1.3	31
65	A physical and functional map of the human TNF- α /NF- κ B signal transduction pathway. <i>Nature Cell Biology</i> , 2004, 6, 97-105.	4.6	970
66	Computation of elementary modes: a unifying framework and the new binary approach. <i>BMC Bioinformatics</i> , 2004, 5, 175.	1.2	207
67	Modular decomposition of protein-protein interaction networks. <i>Genome Biology</i> , 2004, 5, R57.	13.9	100
68	Hierarchical analysis of dependency in metabolic networks. <i>Bioinformatics</i> , 2003, 19, 1027-1034.	1.8	56