

Ionas Erb

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

2,088
citations

394421

19
h-index

361022

35
g-index

45
all docs

45
docs citations

45
times ranked

4151
citing authors

#	ARTICLE	IF	CITATIONS
1	Understanding sequencing data as compositions: an outlook and review. <i>Bioinformatics</i> , 2018, 34, 2870-2878.	4.1	224
2	A field guide for the compositional analysis of any-omics data. <i>GigaScience</i> , 2019, 8, .	6.4	187
3	Genome and transcriptome analysis of the Mesoamerican common bean and the role of gene duplications in establishing tissue and temporal specialization of genes. <i>Genome Biology</i> , 2016, 17, 32.	8.8	166
4	Multiple sequence alignment modeling: methods and applications. <i>Briefings in Bioinformatics</i> , 2016, 17, 1009-1023.	6.5	153
5	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. <i>Genome Biology</i> , 2016, 17, 251.	8.8	131
6	SwissRegulon: a database of genome-wide annotations of regulatory sites. <i>Nucleic Acids Research</i> , 2007, 35, D127-D131.	14.5	123
7	MotEvo: integrated Bayesian probabilistic methods for inferring regulatory sites and motifs on multiple alignments of DNA sequences. <i>Bioinformatics</i> , 2012, 28, 487-494.	4.1	114
8	The functional importance of telomere clustering: Global changes in gene expression result from SIR factor dispersion. <i>Genome Research</i> , 2009, 19, 611-625.	5.5	110
9	Alignathon: a competitive assessment of whole-genome alignment methods. <i>Genome Research</i> , 2014, 24, 2077-2089.	5.5	102
10	Third Report on Chicken Genes and Chromosomes 2015. <i>Cytogenetic and Genome Research</i> , 2015, 145, 78-179.	1.1	97
11	Using the T-Coffee package to build multiple sequence alignments of protein, RNA, DNA sequences and 3D structures. <i>Nature Protocols</i> , 2011, 6, 1669-1682.	12.0	87
12	How should we measure proportionality on relative gene expression data?. <i>Theory in Biosciences</i> , 2016, 135, 21-36.	1.4	77
13	T-Coffee: Tree-Based Consistency Objective Function for Alignment Evaluation. <i>Methods in Molecular Biology</i> , 2014, 1079, 117-129.	0.9	56
14	Principal Component Analysis of the Effects of Environmental Enrichment and (-)-epigallocatechin-3-gallate on Age-Associated Learning Deficits in a Mouse Model of Down Syndrome. <i>Frontiers in Behavioral Neuroscience</i> , 2015, 9, 330.	2.0	44
15	Combined Treatment With Environmental Enrichment and (-)-Epigallocatechin-3-Gallate Ameliorates Learning Deficits and Hippocampal Alterations in a Mouse Model of Down Syndrome. <i>ENEURO</i> .0103-16.2016.	1.9	42
16	Impaired development of neocortical circuits contributes to the neurological alterations in DYRK1A haploinsufficiency syndrome. <i>Neurobiology of Disease</i> , 2019, 127, 210-222.	4.4	35
17	Transcription Factor Binding Site Positioning in Yeast: Proximal Promoter Motifs Characterize TATA-Less Promoters. <i>PLoS ONE</i> , 2011, 6, e24279.	2.5	30
18	Genome-wide Expression Profiling, In Vivo DNA Binding Analysis, and Probabilistic Motif Prediction Reveal Novel Abf1 Target Genes during Fermentation, Respiration, and Sporulation in Yeast. <i>Molecular Biology of the Cell</i> , 2008, 19, 2193-2207.	2.1	29

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19	BlastRâ€”fast and accurate database searches for non-coding RNAs. <i>Nucleic Acids Research</i> , 2011, 39, 6886-6895.	14.5	28
20	Large multiple sequence alignments with a root-to-leaf regressive method. <i>Nature Biotechnology</i> , 2019, 37, 1466-1470.	17.5	25
21	Use of ChIP-Seq data for the design of a multiple promoter-alignment method. <i>Nucleic Acids Research</i> , 2012, 40, e52-e52.	14.5	23
22	Amalgams: data-driven amalgamation for the dimensionality reduction of compositional data. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa076.	3.2	19
23	Interpretable Log Contrasts for the Classification of Health Biomarkers: a New Approach to Balance Selection. <i>MSystems</i> , 2020, 5, .	3.8	16
24	Partial correlations in compositional data analysis. <i>Applied Computing and Geosciences</i> , 2020, 6, 100026.	2.2	15
25	Examining microbeâ€”metabolite correlations by linear methods. <i>Nature Methods</i> , 2021, 18, 37-39.	19.0	15
26	Multi-Information in the Thermodynamic Limit. <i>Journal of Statistical Physics</i> , 2004, 115, 949-976.	1.2	13
27	Timeâ€”course and dynamics of obesityâ€”related behavioral changes induced by energyâ€”dense foods in mice. <i>Addiction Biology</i> , 2018, 23, 531-543.	2.6	13
28	On a Notion of Linear Replicator Equations. <i>Journal of Dynamics and Differential Equations</i> , 2005, 17, 427-451.	1.9	12
29	Extinction and reinstatement of an operant responding maintained by food in different models of obesity. <i>Addiction Biology</i> , 2018, 23, 544-555.	2.6	11
30	Editorial:â€”Compositional data analysis and related methods applied to genomicsâ€”a first special issue from <i>NAR Genomics and Bioinformatics</i> . <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa103.	3.2	10
31	Efficient and Interpretable Prediction of Protein Functional Classes by Correspondence Analysis and Compact Set Relations. <i>PLoS ONE</i> , 2013, 8, e75542.	2.5	7
32	Multiple Sequence Alignment Computation Using the T-Coffee Regressive Algorithm Implementation. <i>Methods in Molecular Biology</i> , 2021, 2231, 89-97.	0.9	6
33	Pergola: Boosting Visualization and Analysis of Longitudinal Data by Unlocking Genomic Analysis Tools. <i>IScience</i> , 2018, 9, 244-257.	4.1	5
34	The Information-Geometric Perspective of Compositional Data Analysis. , 2021, , 21-43.		5
35	Pergola-web: a web server for the visualization and analysis of longitudinal behavioral data using repurposed genomics tools and standards. <i>Nucleic Acids Research</i> , 2019, 47, W600-W604.	14.5	2
36	Protocol for Measuring Compulsive-like Feeding Behavior in Mice. <i>Bio-protocol</i> , 2019, 9, e3308.	0.4	1