Bruno A GaÃ«ta

List of Publications by Year
in descending order

41 papers	1,797 citations	361413 20 h-index	345221 36 g-index
41 all docs	41 docs citations	41 times ranked	2734 citing authors

#	Article	IF	Citations
1	Fld1p, a functional homologue of human seipin, regulates the size of lipid droplets in yeast. Journal of Cell Biology, 2008, 180, 473-482.	5.2	411
2	Individual Variation in the Germline Ig Gene Repertoire Inferred from Variable Region Gene Rearrangements. Journal of Immunology, 2010, 184, 6986-6992.	0.8	261
3	Identification of vaccine candidate antigens from a genomic analysis of Porphyromonas gingivalis. Vaccine, 2001, 19, 4135-4142.	3.8	127
4	iHMMune-align: hidden Markov model-based alignment and identification of germline genes in rearranged immunoglobulin gene sequences. Bioinformatics, 2007, 23, 1580-1587.	4.1	117
5	The Inference of Phased Haplotypes for the Immunoglobulin H Chain V Region Gene Loci by Analysis of VDJ Gene Rearrangements. Journal of Immunology, 2012, 188, 1333-1340.	0.8	102
6	Bioinformatics Curriculum Guidelines: Toward a Definition of Core Competencies. PLoS Computational Biology, 2014, 10, e1003496.	3.2	102
7	The development and application of bioinformatics core competencies to improve bioinformatics training and education. PLoS Computational Biology, 2018, 14, e1005772.	3.2	84
8	Genomic screening by 454 pyrosequencing identifies a new human IGHV gene and sixteen other new IGHV allelic variants. Immunogenetics, 2011, 63, 259-265.	2.4	62
9	Chlorogenic acid attenuates virulence factors and pathogenicity of Pseudomonas aeruginosa by regulating quorum sensing. Applied Microbiology and Biotechnology, 2019, 103, 903-915.	3.6	60
10	GOBLET: The Global Organisation for Bioinformatics Learning, Education and Training. PLoS Computational Biology, 2015, 11, e1004143.	3.2	52
11	Divergent human populations show extensive shared IGK rearrangements in peripheral blood B cells. Immunogenetics, 2012, 64, 3-14.	2.4	46
12	IgE Sequences in Individuals Living in an Area of Endemic Parasitism Show Little Mutational Evidence of Antigen Selection. Scandinavian Journal of Immunology, 2011, 73, 496-504.	2.7	38
13	Clustering-based identification of clonally-related immunoglobulin gene sequence sets. Immunome Research, 2010, 6, S4.	0.1	34
14	The GOBLET training portal: a global repository of bioinformatics training materials, courses and trainers. Bioinformatics, 2015, 31, 140-142.	4.1	34
15	Exonuclease activity and P nucleotide addition in the generation of the expressed immunoglobulin repertoire. BMC Immunology, 2004, 5, 19.	2.2	29
16	Partitioning of Rearranged Ig Genes by Mutation Analysis Demonstrates D-D Fusion and V Gene Replacement in the Expressed Human Repertoire. Journal of Immunology, 2004, 172, 340-348.	0.8	25
17	Applying, Evaluating and Refining Bioinformatics Core Competencies (An Update from the Curriculum) Tj ETQq1 1 0.784314 rgBT /Ov	3.2	24
18	Reconsidering the human immunoglobulin heavy-chain locus:. Immunogenetics, 2006, 57, 917-925.	2.4	23

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19	The 5â€²-flanking region of the Î±2MR/LRP gene contains an enhancer-like cluster of Sp1 binding sites. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1994, 1219, 307-313.	2.4	22
20	Benchmarking the performance of human antibody gene alignment utilities using a 454 sequence dataset. Bioinformatics, 2010, 26, 3129-3130.	4.1	22
21	IgE-Associated IGHV Genes from Venom and Peanut Allergic Individuals Lack Mutational Evidence of Antigen Selection. PLoS ONE, 2014, 9, e89730.	2.5	13
22	ISCBâ€™s Initial Reaction to The New England Journal of Medicine Editorial on Data Sharing. PLoS Computational Biology, 2016, 12, e1004816.	3.2	12
23	Saturation mutagenesis of theDrosophilatRNAArggene B-Box intragenic promoter element: requirements for transcription activation and stable complex formation. Nucleic Acids Research, 1990, 18, 1541-1548.	14.5	11
24	Candidate disease gene prediction using Gentrepid: application to a genomeâ€wide association study on coronary artery disease. Molecular Genetics & Genomic Medicine, 2014, 2, 44-57.	1.2	11
25	Improved VCF normalization for accurate VCF comparison. Bioinformatics, 2017, 33, 964-970.	4.1	11
26	Identifying highly mutated IGHD genes in the junctions of rearranged human immunoglobulin heavy chain genes. Journal of Immunological Methods, 2007, 324, 26-37.	1.4	10
27	Analysis of genome-wide association study data using the protein knowledge base. BMC Genetics, 2011, 12, 98.	2.7	10
28	BLAST on the Web. BioTechniques, 2000, 28, 436-439.	1.8	8
29	Combining spatial and chemical information for clustering pharmacophores. BMC Bioinformatics, 2014, 15, S5.	2.6	7
30	Ten simple rules for forming a scientific professional society. PLoS Computational Biology, 2017, 13, e1005226.	3.2	7
31	GentrepidV2.0: a web server for candidate disease gene prediction. BMC Bioinformatics, 2013, 14, 249.	2.6	6
32	MINER: exploratory analysis of gene interaction networks by machine learning from expression data. BMC Genomics, 2009, 10, S17.	2.8	5
33	Parallelizing Optimal Multiple Sequence Alignment by Dynamic Programming. , 2008, , .		4
34	Pairwise alignment of nucleotide sequences using maximal exact matches. BMC Bioinformatics, 2019, 20, 261.	2.6	4
35	ISCBâ€™s initial reaction to New England Journal of Medicine editorial on data sharing. Bioinformatics, 2017, 33, 2968-2968.	4.1	1
36	Cache Friendly Optimisation of de Bruijn Graph based Local Re-assembly in Variant Calling. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 17, 1-1.	3.0	1

#	Article	IF	Citations
37	ISCBâ€™s initial reaction to New England Journal of Medicine editorial on data sharing. F1000Research, 2016, 5, 157.	1.6	1
38	BLAST...What Next?. BioTechniques, 2000, 28, 874-876.	1.8	0
39	Art in Science Competition invites artworks to the annual exhibition on ISMB 2018 in Chicago. PLoS Computational Biology, 2018, 14, e1006139.	3.2	0
40	Undergraduate Education in Bioinformaticsâ€"Progress and Lessons Learnt from an Engineering Degree. , 2021, , 73-77.		0
41	Art in Science Competition invites artworks to the annual exhibition on ISMB 2018 in Chicago. F1000Research, 2018, 7, 337.	1.6	0