Joaquin Dopazo

List of Publications by Year
in descending order

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347	25,298	11651	9345
papers	citations	70 h-index	143 g-index

375	375	375	39916
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Incidence and Prevalence of Children's Diffuse Lung Disease in Spain. Archivos De Bronconeumologia, 2022, 58, 22-29.	0.8	15
2	Towards a metagenomics machine learning interpretable model for understanding the transition from adenoma to colorectal cancer. Scientific Reports, 2022, 12, 450.	3.3	11
3	Integrating pathway knowledge with deep neural networks to reduce the dimensionality in single-cell RNA-seq data. BioData Mining, 2022, 15, 1.	4.0	12
4	Discovering potential interactions between rare diseases and COVID-19 by combining mechanistic models of viral infection with statistical modeling. Human Molecular Genetics, 2022, , .	2.9	1
5	Detailed stratified GWAS analysis for severe COVID-19 in four European populations. Human Molecular Genetics, 2022, 31, 3945-3966.	2.9	46
6	Protein and functional isoform levels and genetic variants of the BAFF and APRIL pathway components in systemic lupus erythematosus. Scientific Reports, 2022, 12, .	3.3	2
7	CSVS, a crowdsourcing database of the Spanish population genetic variability. Nucleic Acids Research, 2021, 49, D1130-D1137.	14.5	34
8	Genome-scale mechanistic modeling of signaling pathways made easy: A bioconductor/cytoscape/web server framework for the analysis of omic data. Computational and Structural Biotechnology Journal, 2021, 19, 2968-2978.	4.1	9
9	Molecular Genetics in the Next Generation Sequencing Era. , 2021, , 215-230.		0
10	A versatile workflow to integrate RNA-seq genomic and transcriptomic data into mechanistic models of signaling pathways. PLoS Computational Biology, 2021, 17, e1008748.	3.2	6
11	Plastome genomics in South American maize landraces: chloroplast lineages parallel the geographical structuring of nuclear gene pools. Annals of Botany, 2021, 128, 115-125.	2.9	7
12	Implementing Personalized Medicine in COVID-19 in Andalusia: An Opportunity to Transform the Healthcare System. Journal of Personalized Medicine, 2021, 11, 475.	2.5	20
13	Taxonomic variations in the gut microbiome of gout patients with and without tophi might have a functional impact on urate metabolism. Molecular Medicine, 2021, 27, 50.	4.4	31
14	Phylogenetic Analysis of the 2020 West Nile Virus (WNV) Outbreak in Andalusia (Spain). Viruses, 2021, 13, 836.	3.3	13
15	A comprehensive database for integrated analysis of omics data in autoimmune diseases. BMC Bioinformatics, 2021, 22, 343.	2.6	12
16	Predictive Value of MRP-1 in Localized High-Risk Soft Tissue Sarcomas: A Translational Research Associated to ISG-STS 1001 Randomized Phase III Trial. Molecular Cancer Therapeutics, 2021, 20, 2539-2552.	4.1	2
17	Mechanistic modeling of the SARS-CoV-2 disease map. BioData Mining, 2021, 14, 5.	4.0	11
18	Transcriptomic Analysis of a Diabetic Skin-Humanized Mouse Model Dissects Molecular Pathways Underlying the Delayed Wound Healing Response. Genes, 2021, 12, 47.	2.4	6

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19	Mutational Characterization of Cutaneous Melanoma Supports Divergent Pathways Model for Melanoma Development. Cancers, 2021, 13, 5219.	3.7	5
20	COVID19 Disease Map, a computational knowledge repository of virusâ€“host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	7.2	53
21	Deciphering Genomic Heterogeneity and the Internal Composition of Tumour Activities through a Hierarchical Factorisation Model. Mathematics, 2021, 9, 2833.	2.2	0
22	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
23	Real world evidence of calcifediol or vitamin D prescription and mortality rate of COVID-19 in a retrospective cohort of hospitalized Andalusian patients. Scientific Reports, 2021, 11, 23380.	3.3	39
24	Highly accurate whole-genome imputation of SARS-CoV-2 from partial or low-quality sequences. GigaScience, 2021, 10, .	6.4	2
25	Association of a single nucleotide polymorphism in the ubxn6 gene with long-term non-progression phenotype in HIV-positive individuals. Clinical Microbiology and Infection, 2020, 26, 107-114.	6.0	3
26	Mechanistic models of signaling pathways deconvolute the glioblastoma single-cell functional landscape. NAR Cancer, 2020, 2, zcaa011.	3.1	11
27	SMN1 copyâ€number and sequence variant analysis from nextâ€generation sequencing data. Human Mutation, 2020, 41, 2073-2077.	2.5	17
28	Mechanistic Models of Signaling Pathways Reveal the Drug Action Mechanisms behind Gender-Specific Gene Expression for Cancer Treatments. Cells, 2020, 9, 1579.	4.1	7
29	Immune Cell Associations with Cancer Risk. IScience, 2020, 23, 101296.	4.1	6
30	Drug repurposing for COVID-19 using machine learning and mechanistic models of signal transduction circuits related to SARS-CoV-2 infection. Signal Transduction and Targeted Therapy, 2020, 5, 290.	17.1	39
31	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. Scientific Data, 2020, 7, 136.	5.3	99
32	Platform to study intracellular polystyrene nanoplastic pollution and clinical outcomes. Stem Cells, 2020, 38, 1321-1325.	3.2	23
33	Pazopanib for treatment of typical solitary fibrous tumours: a multicentre, single-arm, phase 2 trial. Lancet Oncology, The, 2020, 21, 456-466.	10.7	51
34	The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. F1000Research, 2020, 9, 1229.	1.6	5
35	A comparison of mechanistic signaling pathway activity analysis methods. Briefings in Bioinformatics, 2019, 20, 1655-1668.	6.5	33
36	Exploring the druggable space around the Fanconi anemia pathway using machine learning and mechanistic models. BMC Bioinformatics, 2019, 20, 370.	2.6	26

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37	Antibiotic resistance and metabolic profiles as functional biomarkers that accurately predict the geographic origin of city metagenomics samples. Biology Direct, 2019, 14, 15.	4.6	17
38	Fibroblast activation and abnormal extracellular matrix remodelling as common hallmarks in three cancerâ€prone genodermatoses. British Journal of Dermatology, 2019, 181, 512-522.	1.5	46
39	Differential metabolic activity and discovery of therapeutic targets using summarized metabolic pathway models. Npj Systems Biology and Applications, 2019, 5, 7.	3.0	30
40	PyCellBase, an efficient python package for easy retrieval of biological data from heterogeneous sources. BMC Bioinformatics, 2019, 20, 159.	2.6	0
41	Using mechanistic models for the clinical interpretation of complex genomic variation. Scientific Reports, 2019, 9, 18937.	3.3	20
42	Precision medicine needs pioneering clinical bioinformaticians. Briefings in Bioinformatics, 2019, 20, 752-766.	6.5	40
43	Accelerated phosphatidylcholine turnover in macrophages promotes adipose tissue inflammation in obesity. ELife, 2019, 8, .	6.0	46
44	The effects of death and post-mortem cold ischemia on human tissue transcriptomes. Nature Communications, 2018, 9, 490.	12.8	198
45	A framework for genomic sequencing on clusters of multicore and manycore processors. International Journal of High Performance Computing Applications, 2018, 32, 393-406.	3.7	2
46	The first complete genomic structure of Butyrivibrio fibrisolvens and its chromid. Microbial Genomics, 2018, 4, .	2.0	9
47	The modular network structure of the mutational landscape of Acute Myeloid Leukemia. PLoS ONE, 2018, 13, e0202926.	2.5	5
48	Models of cell signaling uncover molecular mechanisms of high-risk neuroblastoma and predict disease outcome. Biology Direct, 2018, 13, 16.	4.6	26
49	Gene Expression Integration into Pathway Modules Reveals a Pan-Cancer Metabolic Landscape. Cancer Research, 2018, 78, 6059-6072.	0.9	40
50	Whole exome sequencing coupled with unbiased functional analysis reveals new Hirschsprung disease genes. Genome Biology, 2017, 18, 48.	8.8	72
51	ATGC transcriptomics: a web-based application to integrate, explore and analyze de novo transcriptomic data. BMC Bioinformatics, 2017, 18, 121.	2.6	6
52	Integration of transcriptomic and metabolic data reveals hub transcription factors involved in drought stress response in sunflower (Helianthus annuus L.). Plant Molecular Biology, 2017, 94, 549-564.	3.9	51
53	HGVA: the Human Genome Variation Archive. Nucleic Acids Research, 2017, 45, W189-W194.	14.5	6
54	Reference genome assessment from a population scale perspective: an accurate profile of variability and noise. Bioinformatics, 2017, 33, 3511-3517.	4.1	0

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55	A new parallel pipeline for DNA methylation analysis of long reads datasets. BMC Bioinformatics, 2017, 18, 161.	2.6	12
56	Graph-theoretical comparison of normal and tumor networks in identifying BRCA genes. BMC Systems Biology, 2017, 11, 110.	3.0	14
57	VISMapper: ultra-fast exhaustive cartography of viral insertion sites for gene therapy. BMC Bioinformatics, 2017, 18, 421.	2.6	1
58	High throughput estimation of functional cell activities reveals disease mechanisms and predicts relevant clinical outcomes. Oncotarget, 2017, 8, 5160-5178.	1.8	66
59	Genomic expression differences between cutaneous cells from red hair color individuals and black hair color individuals based on bioinformatic analysis. Oncotarget, 2017, 8, 11589-11599.	1.8	5
60	Serum metabolomic profiling facilitates the non-invasive identification of metabolic biomarkers associated with the onset and progression of non-small cell lung cancer. Oncotarget, 2016, 7, 12904-12916.	1.8	73
61	Objective review of de novo standâ€alone error correction methods for <scp>NGS</scp> data. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2016, 6, 111-146.	14.6	21
62	Improving the management of Inherited Retinal Dystrophies by targeted sequencing of a population-specific gene panel. Scientific Reports, 2016, 6, 23910.	3.3	51
63	The pan-cancer pathological regulatory landscape. Scientific Reports, 2016, 6, 39709.	3.3	29
64	The transcriptomics of an experimentally evolved plant-virus interaction. Scientific Reports, 2016, 6, 24901.	3.3	19
65	Integrating transcriptomic and metabolomic analysis to understand natural leaf senescence in sunflower. Plant Biotechnology Journal, 2016, 14, 719-734.	8.3	53
66	Web-based network analysis and visualization using CellMaps. Bioinformatics, 2016, 32, 3041-3043.	4.1	15
67	Screening of CD96 and ASXL1 in 11 patients with Opitz C or Bohringâ€“Opitz syndromes. American Journal of Medical Genetics, Part A, 2016, 170, 24-31.	1.2	13
68	Integrated gene set analysis for microRNA studies. Bioinformatics, 2016, 32, 2809-2816.	4.1	23
69	Identification of the Photoreceptor Transcriptional Co-Repressor SAMD11 as Novel Cause of Autosomal Recessive Retinitis Pigmentosa. Scientific Reports, 2016, 6, 35370.	3.3	13
70	Dysfunctional mitochondrial fission impairs cell reprogramming. Cell Cycle, 2016, 15, 3240-3250.	2.6	36
71	Actionable pathways: interactive discovery of therapeutic targets using signaling pathway models. Nucleic Acids Research, 2016, 44, W212-W216.	14.5	27
72	HPG pore: an efficient and scalable framework for nanopore sequencing data. BMC Bioinformatics, 2016, 17, 107.	2.6	9

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73	Human DNA methylomes of neurodegenerative diseases show common epigenomic patterns. Translational Psychiatry, 2016, 6, e718-e718.	4.8	137
74	267 Spanish Exomes Reveal Population-Specific Differences in Disease-Related Genetic Variation. Molecular Biology and Evolution, 2016, 33, 1205-1218.	8.9	78
75	Stress-induced activation of brown adipose tissue prevents obesity in conditions of low adaptive thermogenesis. Molecular Metabolism, 2016, 5, 19-33.	6.5	78
76	Progress in pharmacogenetics: consortiums and new strategies. Drug Metabolism and Personalized Therapy, 2016, 31, 17-23.	0.6	12
77	Chronic subordination stress selectively downregulates the insulin signaling pathway in liver and skeletal muscle but not in adipose tissue of male mice. Stress, 2016, 19, 214-224.	1.8	10
78	Highly sensitive and ultrafast read mapping for RNA-seq analysis. DNA Research, 2016, 23, 93-100.	3.4	19
79	Assessment of Targeted Next-Generation Sequencing as a Tool for the Diagnosis of Charcot-Marie-Tooth Disease and Hereditary Motor Neuropathy. Journal of Molecular Diagnostics, 2016, 18, 225-234.	2.8	36
80	Differential Features between Chronic Skin Inflammatory Diseases Revealed in Skin-Humanized Psoriasis and Atopic Dermatitis Mouse Models. Journal of Investigative Dermatology, 2016, 136, 136-145.	0.7	37
81	Mutations in theMORC2gene cause axonal Charcotâ€“Marieâ€“Tooth disease. Brain, 2016, 139, 62-72.	7.6	75
82	The Mutational Landscape of Acute Promyelocytic Leukemia Reveals an Interacting Network of Co-Occurrences and Recurrent Mutations. PLoS ONE, 2016, 11, e0148346.	2.5	23
83	Comparative gene expression study of the vestibular organ of the Igf1 deficient mouse using whole-transcript arrays. Hearing Research, 2015, 330, 62-77.	2.0	12
84	Exome sequencing reveals a high genetic heterogeneity on familial Hirschsprung disease. Scientific Reports, 2015, 5, 16473.	3.3	29
85	SEQUENCING OF 150 CITRUS VARIETIES: LINKING GENOTYPES TO PHENOTYPES. Acta Horticulturae, 2015, , 585-589.	0.2	1
86	Using activation status of signaling pathways as mechanism-based biomarkers to predict drug sensitivity. Scientific Reports, 2015, 5, 18494.	3.3	40
87	Familyâ€based genomeâ€wide association study in Patagonia confirms the association of the DMD locus and cleft lip and palate. European Journal of Oral Sciences, 2015, 123, 381-384.	1.5	13
88	Identification of epistatic interactions through genome-wide association studies in sporadic medullary and juvenile papillary thyroid carcinomas. BMC Medical Genomics, 2015, 8, 83.	1.5	15
89	The EGR2 gene is involved in axonal Charcotâ€'Marieâ€'Tooth disease. European Journal of Neurology, 2015, 22, 1548-1555.	3.3	24
90	A Pan-Cancer Catalogue of Cancer Driver Protein Interaction Interfaces. PLoS Computational Biology, 2015, 11, e1004518.	3.2	122

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91	Assessing the impact of mutations found in next generation sequencing data over human signaling pathways. Nucleic Acids Research, 2015, 43, W270-W275.	14.5	16
92	Babelomics 5.0: functional interpretation for new generations of genomic data. Nucleic Acids Research, 2015, 43, W117-W121.	14.5	114
93	Therapeutic targets for olive pollen allergy defined by gene markers modulated by Ole e 1-derived peptides. Molecular Immunology, 2015, 64, 252-261.	2.2	5
94	Concurrent and Accurate Short Read Mapping on Multicore Processors. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 995-1007.	3.0	2
95	PTMcode v2: a resource for functional associations of post-translational modifications within and between proteins. Nucleic Acids Research, 2015, 43, D494-D502.	14.5	90
96	Involvement of a citrus meiotic recombination TTC-repeat motif in the formation of gross deletions generated by ionizing radiation and MULE activation. BMC Genomics, 2015, 16, 69.	2.8	15
97	Deregulation of key signaling pathways involved in oocyte maturation in FMR1 premutation carriers with Fragile X-associated primary ovarian insufficiency. Gene, 2015, 571, 52-57.	2.2	17
98	A parallel and sensitive software tool for methylation analysis on multicore platforms. Bioinformatics, 2015, 31, 3130-3138.	4.1	9
99	A Phylogenetic Analysis of 34 Chloroplast Genomes Elucidates the Relationships between Wild and Domestic Species within the GenusCitrus. Molecular Biology and Evolution, 2015, 32, 2015-2035.	8.9	272
100	Whole-exome sequencing reveals ZNF408 as a new gene associated with autosomal recessive retinitis pigmentosa with vitreal alterations. Human Molecular Genetics, 2015, 24, 4037-4048.	2.9	41
101	Fast inexact mapping using advanced tree exploration on backward search methods. BMC Bioinformatics, 2015, 16, 18.	2.6	2
102	BRCA1 Alternative splicing landscape in breast tissue samples. BMC Cancer, 2015, 15, 219.	2.6	17
103	Reâ€evaluation casts doubt on the pathogenicity of homozygous USH2A p.C759F. American Journal of Medical Genetics, Part A, 2015, 167, 1597-1600.	1.2	21
104	Global Transcriptome Analysis of Primary Cerebrocortical Cells: Identification of Genes Regulated by Triiodothyronine in Specific Cell Types. Cerebral Cortex, 2015, 27, bhv273.	2.9	64
105	Combined Genetic and High-Throughput Strategies for Molecular Diagnosis of Inherited Retinal Dystrophies. PLoS ONE, 2014, 9, e88410.	2.5	32
106	Exome Sequencing Reveals Novel and Recurrent Mutations with Clinical Significance in Inherited Retinal Dystrophies. PLoS ONE, 2014, 9, e116176.	2.5	16
107	Capturing the biological impact of CDKN2A and MC1R genes as an early predisposing event in melanoma and non melanoma skin cancer. Oncotarget, 2014, 5, 1439-1451.	1.8	35
108	A Comprehensive DNA Methylation Profile of Epithelial-to-Mesenchymal Transition. Cancer Research, 2014, 74, 5608-5619.	0.9	69

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109	Understanding disease mechanisms with models of signaling pathway activities. BMC Systems Biology, 2014, 8, 121.	3.0	42
110	Acceleration of short and long DNA read mapping without loss of accuracy using suffix array. Bioinformatics, 2014, 30, 3396-3398.	4.1	16
111	Molecular interactions between sugar beet andPolymyxa betaeduring its life cycle. Annals of Applied Biology, 2014, 164, 244-256.	2.5	10
112	The role of the interactome in the maintenance of deleterious variability in human populations. Molecular Systems Biology, 2014, 10, 752.	7.2	28
113	Deciphering intrafamilial phenotypic variability by exome sequencing in a Bardetâ€“Biedl family. Molecular Genetics & Genomic Medicine, 2014, 2, 124-133.	1.2	13
114	Two Novel Mutations in theBCKDK(Branched-Chain Keto-Acid Dehydrogenase Kinase) Gene Are Responsible for a Neurobehavioral Deficit in Two Pediatric Unrelated Patients. Human Mutation, 2014, 35, 470-477.	2.5	70
115	A web-based interactive framework to assist in the prioritization of disease candidate genes in whole-exome sequencing studies. Nucleic Acids Research, 2014, 42, W88-W93.	14.5	39
116	Novel RP1 mutations and a recurrent BBS1variant explain the co-existence of two distinct retinal phenotypes in the same pedigree. BMC Genetics, 2014, 15, 143.	2.7	18
117	The Activation of the Sox2 RR2 Pluripotency Transcriptional Reporter in Human Breast Cancer Cell Lines is Dynamic and Labels Cells with Higher Tumorigenic Potential. Frontiers in Oncology, 2014, 4, 308.	2.8	17
118	A web tool for the design and management of panels of genes for targeted enrichment and massive sequencing for clinical applications. Nucleic Acids Research, 2014, 42, W83-W87.	14.5	6
119	Sequencing and functional analysis of the genome of a nematode egg-parasitic fungus, Pochonia chlamydosporia. Fungal Genetics and Biology, 2014, 65, 69-80.	2.1	105
120	A New Overgrowth Syndrome is due to Mutations inRNF125. Human Mutation, 2014, 35, 1436-1441.	2.5	33
121	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. Nature Communications, 2014, 5, 5125.	12.8	122
122	Pathway network inference from gene expression data. BMC Systems Biology, 2014, 8, S7.	3.0	30
123	ngsCAT: a tool to assess the efficiency of targeted enrichment sequencing. Bioinformatics, 2014, 30, 1767-1768.	4.1	9
124	A novel locus for a hereditary recurrent neuropathy on chromosome 21q21. Neuromuscular Disorders, 2014, 24, 660-665.	0.6	4
125	Genomics and transcriptomics in drug discovery. Drug Discovery Today, 2014, 19, 126-132.	6.4	54
126	Permanent Cardiac Sarcomere Changes in a Rabbit Model of Intrauterine Growth Restriction. PLoS ONE, 2014, 9, e113067.	2.5	21

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127	Assessing Differential Expression Measurements by Highly Parallel Pyrosequencing and DNA Microarrays: A Comparative Study. OMICS A Journal of Integrative Biology, 2013, 17, 53-59.	2.0	2
128	Intrauterine growth restriction is associated with cardiac ultrastructural and gene expression changes related to the energetic metabolism in a rabbit model. American Journal of Physiology - Heart and Circulatory Physiology, 2013, 305, H1752-H1760.	3.2	24
129	Pathways systematically associated to Hirschsprungâ€™s disease. Orphanet Journal of Rare Diseases, 2013, 8, 187.	2.7	17
130	Molecular Pattern in Olive Pollen Response. Journal of Allergy and Clinical Immunology, 2013, 131, AB44.	2.9	0
131	Exome sequencing identifies a new mutation in SERAC1 in a patient with 3-methylglutaconic aciduria. Molecular Genetics and Metabolism, 2013, 110, 73-77.	1.1	33
132	Novel genes detected by transcriptional profiling from whole-blood cells in patients with early onset of acute coronary syndrome. Clinica Chimica Acta, 2013, 421, 184-190.	1.1	40
133	Grape antioxidant dietary fiber inhibits intestinal polyposis in Apc Min/+ mice: relation to cell cycle and immune response. Carcinogenesis, 2013, 34, 1881-1888.	2.8	38
134	Inferring the functional effect of gene expression changes in signaling pathways. Nucleic Acids Research, 2013, 41, W213-W217.	14.5	23
135	Genome Maps, a new generation genome browser. Nucleic Acids Research, 2013, 41, W41-W46.	14.5	27
136	Mammosphere Formation in Breast Carcinoma Cell Lines Depends upon Expression of E-cadherin. PLoS ONE, 2013, 8, e77281.	2.5	171
137	Role of <scp>CPI</scp>â€17 in restoring skin homoeostasis in cutaneous field of cancerization: effects of topical application of a filmâ€forming medical device containing photolyase and <scp>UV</scp> filters. Experimental Dermatology, 2013, 22, 494-496.	2.9	19
138	A dynamic pipeline for RNA sequencing on multicore processors. , 2013, , .		6
139	Multicore and Cloud-Based Solutions for Genomic Variant Analysis. Lecture Notes in Computer Science, 2013, , 273-284.	1.3	2
140	Maslinic Acid-Enriched Diet Decreases Intestinal Tumorigenesis in ApcMin/+ Mice through Transcriptomic and Metabolomic Reprogramming. PLoS ONE, 2013, 8, e59392.	2.5	46
141	Defining the Genomic Signature of Totipotency and Pluripotency during Early Human Development. PLoS ONE, 2013, 8, e62135.	2.5	27
142	Whole-exome sequencing identifies novel compound heterozygous mutations in USH2A in Spanish patients with autosomal recessive retinitis pigmentosa. Molecular Vision, 2013, 19, 2187-95.	1.1	17
143	The protease MT1â€MMP drives a combinatorial proteolytic program in activated endothelial cells. FASEB Journal, 2012, 26, 4481-4494.	0.5	34
144	Qualimap: evaluating next-generation sequencing alignment data. Bioinformatics, 2012, 28, 2678-2679.	4.1	799

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145	Discovering the hidden sub-network component in a ranked list of genes or proteins derived from genomic experiments. Nucleic Acids Research, 2012, 40, e158-e158.	14.5	22
146	VARIANT: Command Line, Web service and Web interface for fast and accurate functional characterization of variants found by Next-Generation Sequencing. Nucleic Acids Research, 2012, 40, W54-W58.	14.5	37
147	Inferring the regulatory network behind a gene expression experiment. Nucleic Acids Research, 2012, 40, W168-W172.	14.5	10
148	Whole-genome bisulfite DNA sequencing of a DNMT3B mutant patient. Epigenetics, 2012, 7, 542-550.	2.7	68
149	CellBase, a comprehensive collection of RESTful web services for retrieving relevant biological information from heterogeneous sources. Nucleic Acids Research, 2012, 40, W609-W614.	14.5	31
150	Select Your SNPs (SYSNPs): a web tool for automatic and massive selection of SNPs. International Journal of Data Mining and Bioinformatics, 2012, 6, 324.	0.1	20
151	Extensive Translatome Remodeling during ER Stress Response in Mammalian Cells. PLoS ONE, 2012, 7, e35915.	2.5	32
152	Using GPUs for the Exact Alignment of Short-Read Genetic Sequences by Means of the Burrows-Wheeler Transform. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1245-1256.	3.0	28
153	SNPeffect 4.0: on-line prediction of molecular and structural effects of protein-coding variants. Nucleic Acids Research, 2012, 40, D935-D939.	14.5	235
154	Diversification of the expanded teleost-specific toll-like receptor family in Atlantic cod, Gadus morhua. BMC Evolutionary Biology, 2012, 12, 256.	3.2	65
155	IL1Î² Induces Mesenchymal Stem Cells Migration and Leucocyte Chemotaxis Through NF-ÎºB. Stem Cell Reviews and Reports, 2012, 8, 905-916.	5.6	153
156	Transdifferentiation of MALME-3M and MCF-7 Cells toward Adipocyte-like Cells is Dependent on Clathrin-mediated Endocytosis. SpringerPlus, 2012, 1, 44.	1.2	5
157	Four new loci associations discovered by pathway-based and network analyses of the genome-wide variability profile of Hirschsprungâ€™s disease. Orphanet Journal of Rare Diseases, 2012, 7, 103.	2.7	7
158	A map of human microRNA variation uncovers unexpectedly high levels of variability. Genome Medicine, 2012, 4, 62.	8.2	28
159	Variable selection for multifactorial genomic data. Chemometrics and Intelligent Laboratory Systems, 2012, 110, 113-122.	3.5	7
160	Development, Characterization and Experimental Validation of a Cultivated Sunflower (Helianthus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.5	28
161	Protein Interactions for Functional Genomics. International Journal of Knowledge Discovery in Bioinformatics, 2012, 3, 15-30.	0.8	0
162	Using Papers Citations for Selecting the Best Genomic Databases. , 2011, , .		1

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163	Differential expression in RNA-seq: A matter of depth. Genome Research, 2011, 21, 2213-2223.	5.5	1,456
164	Differential Lipid Partitioning Between Adipocytes and Tissue Macrophages Modulates Macrophage Lipotoxicity and M2/M1 Polarization in Obese Mice. Diabetes, 2011, 60, 797-809.	0.6	297
165	Gene-expression Profiling And Differential Pathways In The Sensitization And Tolerance To Allergens. Journal of Allergy and Clinical Immunology, 2011, 127, AB263-AB263.	2.9	0
166	Fortunella margarita Transcriptional Reprogramming Triggered by Xanthomonas citri subsp. citri. BMC Plant Biology, 2011, 11, 159.	3.6	21
167	Analysis of Normal-Tumour Tissue Interaction in Tumours: Prediction of Prostate Cancer Features from the Molecular Profile of Adjacent Normal Cells. PLoS ONE, 2011, 6, e16492.	2.5	17
168	myKaryoView: A Light-Weight Client for Visualization of Genomic Data. PLoS ONE, 2011, 6, e26345.	2.5	5
169	Mutation Screening of Multiple Genes in Spanish Patients with Autosomal Recessive Retinitis Pigmentosa by Targeted Resequencing. PLoS ONE, 2011, 6, e27894.	2.5	36
170	Early peroxisome proliferator-activated receptor gamma regulated genes involved in expansion of pancreatic beta cell mass. BMC Medical Genomics, 2011, 4, 86.	1.5	15
171	A large scale survey reveals that chromosomal copy-number alterations significantly affect gene modules involved in cancer initiation and progression. BMC Medical Genomics, 2011, 4, 37.	1.5	5
172	Profiling the venom gland transcriptomes of Costa Rican snakes by 454 pyrosequencing. BMC Genomics, 2011, 12, 259.	2.8	96
173	Early Transcriptional Defense Responses in Arabidopsis Cell Suspension Culture under High-Light Conditions Â Â Â. Plant Physiology, 2011, 156, 1439-1456.	4.8	81
174	Paintomics: a web based tool for the joint visualization of transcriptomics and metabolomics data. Bioinformatics, 2011, 27, 137-139.	4.1	211
175	B2G-FAR, a species-centered GO annotation repository. Bioinformatics, 2011, 27, 919-924.	4.1	137
176	Large-scale transcriptional profiling and functional assays reveal important roles for Rho-GTPase signalling and SCL during haematopoietic differentiation of human embryonic stem cells. Human Molecular Genetics, 2011, 20, 4932-4946.	2.9	16
177	Evidence for short-time divergence and long-time conservation of tissue-specific expression after gene duplication. Briefings in Bioinformatics, 2011, 12, 442-448.	6.5	67
178	Phylemon 2.0: a suite of web-tools for molecular evolution, phylogenetics, phylogenomics and hypotheses testing. Nucleic Acids Research, 2011, 39, W470-W474.	14.5	182
179	An Evolutionary Trade-Off between Protein Turnover Rate and Protein Aggregation Favors a Higher Aggregation Propensity in Fast Degrading Proteins. PLoS Computational Biology, 2011, 7, e1002090.	3.2	50
180	Natural Selection on Functional Modules, a Genome-Wide Analysis. PLoS Computational Biology, 2011, 7, e1001093.	3.2	12

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