

Joaquin Dopazo

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8769048/publications.pdf>

Version: 2024-02-01

347
papers

25,298
citations

11651

70
h-index

9345

143
g-index

375
all docs

375
docs citations

375
times ranked

39916
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | High-throughput functional annotation and data mining with the Blast2GO suite. <i>Nucleic Acids Research</i> , 2008, 36, 3420-3435. | 14.5 | 3,905 |
| 2 | Differential expression in RNA-seq: A matter of depth. <i>Genome Research</i> , 2011, 21, 2213-2223. | 5.5 | 1,456 |
| 3 | FatiGO: a web tool for finding significant associations of Gene Ontology terms with groups of genes. <i>Bioinformatics</i> , 2004, 20, 578-580. | 4.1 | 1,024 |
| 4 | Qualimap: evaluating next-generation sequencing alignment data. <i>Bioinformatics</i> , 2012, 28, 2678-2679. | 4.1 | 799 |
| 5 | The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. <i>Nature Biotechnology</i> , 2010, 28, 827-838. | 17.5 | 795 |
| 6 | Changes in the pattern of DNA methylation associate with twin discordance in systemic lupus erythematosus. <i>Genome Research</i> , 2010, 20, 170-179. | 5.5 | 569 |
| 7 | A hierarchical unsupervised growing neural network for clustering gene expression patterns. <i>Bioinformatics</i> , 2001, 17, 126-136. | 4.1 | 562 |
| 8 | ETE: a python Environment for Tree Exploration. <i>BMC Bioinformatics</i> , 2010, 11, 24. | 2.6 | 366 |
| 9 | Initial Genomics of the Human Nucleolus. <i>PLoS Genetics</i> , 2010, 6, e1000889. | 3.5 | 324 |
| 10 | Differential Lipid Partitioning Between Adipocytes and Tissue Macrophages Modulates Macrophage Lipotoxicity and M2/M1 Polarization in Obese Mice. <i>Diabetes</i> , 2011, 60, 797-809. | 0.6 | 297 |
| 11 | Babelomics: an integrative platform for the analysis of transcriptomics, proteomics and genomic data with advanced functional profiling. <i>Nucleic Acids Research</i> , 2010, 38, W210-W213. | 14.5 | 283 |
| 12 | A Phylogenetic Analysis of 34 Chloroplast Genomes Elucidates the Relationships between Wild and Domestic Species within the Genus <i>Citrus</i> . <i>Molecular Biology and Evolution</i> , 2015, 32, 2015-2035. | 8.9 | 272 |
| 13 | PupasView: a visual tool for selecting suitable SNPs, with putative pathological effect in genes, for genotyping purposes. <i>Nucleic Acids Research</i> , 2005, 33, W501-W505. | 14.5 | 253 |
| 14 | FatiGO +: a functional profiling tool for genomic data. Integration of functional annotation, regulatory motifs and interaction data with microarray experiments. <i>Nucleic Acids Research</i> , 2007, 35, W91-W96. | 14.5 | 248 |
| 15 | BABELOMICS: a systems biology perspective in the functional annotation of genome-scale experiments. <i>Nucleic Acids Research</i> , 2006, 34, W472-W476. | 14.5 | 240 |
| 16 | SNPeffect 4.0: on-line prediction of molecular and structural effects of protein-coding variants. <i>Nucleic Acids Research</i> , 2012, 40, D935-D939. | 14.5 | 235 |
| 17 | BABELOMICS: a suite of web tools for functional annotation and analysis of groups of genes in high-throughput experiments. <i>Nucleic Acids Research</i> , 2005, 33, W460-W464. | 14.5 | 217 |
| 18 | Paintomics: a web based tool for the joint visualization of transcriptomics and metabolomics data. <i>Bioinformatics</i> , 2011, 27, 137-139. | 4.1 | 211 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | The effects of death and post-mortem cold ischemia on human tissue transcriptomes. <i>Nature Communications</i> , 2018, 9, 490. | 12.8 | 198 |
| 20 | PupaSuite: finding functional single nucleotide polymorphisms for large-scale genotyping purposes. <i>Nucleic Acids Research</i> , 2006, 34, W621-W625. | 14.5 | 194 |
| 21 | Phylemon 2.0: a suite of web-tools for molecular evolution, phylogenetics, phylogenomics and hypotheses testing. <i>Nucleic Acids Research</i> , 2011, 39, W470-W474. | 14.5 | 182 |
| 22 | Controlled Ovarian Stimulation Induces a Functional Genomic Delay of the Endometrium with Potential Clinical Implications. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2008, 93, 4500-4510. | 3.6 | 177 |
| 23 | SNP and haplotype mapping for genetic analysis in the rat. <i>Nature Genetics</i> , 2008, 40, 560-566. | 21.4 | 172 |
| 24 | Mammosphere Formation in Breast Carcinoma Cell Lines Depends upon Expression of E-cadherin. <i>PLoS ONE</i> , 2013, 8, e77281. | 2.5 | 171 |
| 25 | Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892. | 30.7 | 170 |
| 26 | GEPAS: a web-based resource for microarray gene expression data analysis. <i>Nucleic Acids Research</i> , 2003, 31, 3461-3467. | 14.5 | 161 |
| 27 | DNA methylation epigenotypes in breast cancer molecular subtypes. <i>Breast Cancer Research</i> , 2010, 12, R77. | 5.0 | 159 |
| 28 | Genetic evolution and tropism of transmissible gastroenteritis coronaviruses. <i>Virology</i> , 1992, 190, 92-105. | 2.4 | 157 |
| 29 | Phylogenetic Reconstruction Using an Unsupervised Growing Neural Network That Adopts the Topology of a Phylogenetic Tree. <i>Journal of Molecular Evolution</i> , 1997, 44, 226-233. | 1.8 | 155 |
| 30 | IL1 β Induces Mesenchymal Stem Cells Migration and Leucocyte Chemotaxis Through NF- κ B. <i>Stem Cell Reviews and Reports</i> , 2012, 8, 905-916. | 5.6 | 153 |
| 31 | Evolution of the capsid protein genes of foot-and-mouth disease virus: antigenic variation without accumulation of amino acid substitutions over six decades. <i>Journal of Virology</i> , 1992, 66, 3557-3565. | 3.4 | 151 |
| 32 | The human phylome. <i>Genome Biology</i> , 2007, 8, R109. | 8.8 | 150 |
| 33 | Phenotypic characterization of BRCA1 and BRCA2 tumors based in a tissue microarray study with 37 immunohistochemical markers. <i>Breast Cancer Research and Treatment</i> , 2005, 90, 5-14. | 2.5 | 147 |
| 34 | B2G-FAR, a species-centered GO annotation repository. <i>Bioinformatics</i> , 2011, 27, 919-924. | 4.1 | 137 |
| 35 | Human DNA methylomes of neurodegenerative diseases show common epigenomic patterns. <i>Translational Psychiatry</i> , 2016, 6, e718-e718. | 4.8 | 137 |
| 36 | Antigenic structure of the human respiratory syncytial virus G glycoprotein and relevance of hypermutation events for the generation of antigenic variants.. <i>Journal of General Virology</i> , 1997, 78, 2419-2429. | 2.9 | 130 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 37 | Positive Selection, Relaxation, and Acceleration in the Evolution of the Human and Chimp Genome. <i>PLoS Computational Biology</i> , 2006, 2, e38. | 3.2 | 128 |
| 38 | Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. <i>Nature Communications</i> , 2014, 5, 5125. | 12.8 | 122 |
| 39 | A Pan-Cancer Catalogue of Cancer Driver Protein Interaction Interfaces. <i>PLoS Computational Biology</i> , 2015, 11, e1004518. | 3.2 | 122 |
| 40 | Estimating errors and confidence intervals for branch lengths in phylogenetic trees by a bootstrap approach. <i>Journal of Molecular Evolution</i> , 1994, 38, 300-4. | 1.8 | 120 |
| 41 | Phylogeny of viroids, viroidlike satellite RNAs, and the viroidlike domain of hepatitis delta virus RNA.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991, 88, 5631-5634. | 7.1 | 116 |
| 42 | Babelomics 5.0: functional interpretation for new generations of genomic data. <i>Nucleic Acids Research</i> , 2015, 43, W117-W121. | 14.5 | 114 |
| 43 | The Prognostic Relevance of the Nonstructural 5A Gene Interferon Sensitivity Determining Region Is Different in Infections with Genotype 1b and 3a Isolates of Hepatitis C Virus. <i>Journal of Infectious Diseases</i> , 1998, 177, 839-847. | 4.0 | 113 |
| 44 | The CD36, CLA-1 (CD36L1), and LIMPII (CD36L2) gene family: cellular distribution, chromosomal location, and genetic evolution. <i>Genomics</i> , 1995, 25, 100-106. | 2.9 | 112 |
| 45 | Systematic Learning of Gene Functional Classes From DNA Array Expression Data by Using Multilayer Perceptrons. <i>Genome Research</i> , 2002, 12, 1703-1715. | 5.5 | 111 |
| 46 | From genes to functional classes in the study of biological systems. <i>BMC Bioinformatics</i> , 2007, 8, 114. | 2.6 | 108 |
| 47 | Next station in microarray data analysis: GEPAS. <i>Nucleic Acids Research</i> , 2006, 34, W486-W491. | 14.5 | 107 |
| 48 | Identification of Genes Involved in Resistance to Interferon- α in Cutaneous T-Cell Lymphoma. <i>American Journal of Pathology</i> , 2002, 161, 1825-1837. | 3.8 | 106 |
| 49 | Sequencing and functional analysis of the genome of a nematode egg-parasitic fungus, <i>Pochonia chlamydsoporia</i> . <i>Fungal Genetics and Biology</i> , 2014, 65, 69-80. | 2.1 | 105 |
| 50 | Discovering molecular functions significantly related to phenotypes by combining gene expression data and biological information. <i>Bioinformatics</i> , 2005, 21, 2988-2993. | 4.1 | 103 |
| 51 | FM19G11, a New Hypoxia-inducible Factor (HIF) Modulator, Affects Stem Cell Differentiation Status. <i>Journal of Biological Chemistry</i> , 2010, 285, 1333-1342. | 3.4 | 99 |
| 52 | COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. <i>Scientific Data</i> , 2020, 7, 136. | 5.3 | 99 |
| 53 | Annotated Draft Genomic Sequence from a <i>Streptococcus pneumoniae</i> Type 19F Clinical Isolate. <i>Microbial Drug Resistance</i> , 2001, 7, 99-125. | 2.0 | 98 |
| 54 | Gene expression correlation and gene ontology-based similarity: an assessment of quantitative relationships. , 2004, 2004, 25-31. | | 98 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 55 | Profiling the venom gland transcriptomes of Costa Rican snakes by 454 pyrosequencing. BMC Genomics, 2011, 12, 259. | 2.8 | 96 |
| 56 | Hypoxia Promotes Efficient Differentiation of Human Embryonic Stem Cells to Functional Endothelium. Stem Cells, 2010, 28, 407-418. | 3.2 | 92 |
| 57 | Phylogenetic relationships of European strains of porcine reproductive and respiratory syndrome virus (PRRSV) inferred from DNA sequences of putative ORF-5 and ORF-7 genes. Virus Research, 1996, 42, 159-165. | 2.2 | 91 |
| 58 | Interoperability with Moby 1.0--It's better than sharing your toothbrush!. Briefings in Bioinformatics, 2008, 9, 220-231. | 6.5 | 91 |
| 59 | PhylomeDB: a database for genome-wide collections of gene phylogenies. Nucleic Acids Research, 2007, 36, D491-D496. | 14.5 | 90 |
| 60 | 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 |
| 61 | PupaSNP Finder: a web tool for finding SNPs with putative effect at transcriptional level. Nucleic Acids Research, 2004, 32, W242-W248. | 14.5 | 86 |
| 62 | GEPAS, an experiment-oriented pipeline for the analysis of microarray gene expression data. Nucleic Acids Research, 2005, 33, W616-W620. | 14.5 | 86 |
| 63 | Molecular profiling related to poor prognosis in thyroid carcinoma. Combining gene expression data and biological information. Oncogene, 2008, 27, 1554-1561. | 5.9 | 86 |
| 64 | Gene expression data preprocessing. Bioinformatics, 2003, 19, 655-656. | 4.1 | 84 |
| 65 | Genome-scale evidence of the nematode-arthropod clade. Genome Biology, 2005, 6, R41. | 9.6 | 83 |
| 66 | Fine-scale evolution: genomic, phenotypic and ecological differentiation in two coexisting <i>Salinibacter ruber</i> strains. ISME Journal, 2010, 4, 882-895. | 9.8 | 81 |
| 67 | Early Transcriptional Defense Responses in Arabidopsis Cell Suspension Culture under High-Light Conditions. Plant Physiology, 2011, 156, 1439-1456. | 4.8 | 81 |
| 68 | Immunogenicity of non-structural proteins of foot-and-mouth disease virus: differences between infected and vaccinated swine. Archives of Virology, 1994, 136, 123-131. | 2.1 | 78 |
| 69 | 267 Spanish Exomes Reveal Population-Specific Differences in Disease-Related Genetic Variation. Molecular Biology and Evolution, 2016, 33, 1205-1218. | 8.9 | 78 |
| 70 | Stress-induced activation of brown adipose tissue prevents obesity in conditions of low adaptive thermogenesis. Molecular Metabolism, 2016, 5, 19-33. | 6.5 | 78 |
| 71 | Methods and approaches in the analysis of gene expression data. Journal of Immunological Methods, 2001, 250, 93-112. | 1.4 | 76 |
| 72 | Multidimensional Gene Set Analysis of Genomic Data. PLoS ONE, 2010, 5, e10348. | 2.5 | 75 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 73 | Mutations in the <i>MORC2</i> gene cause axonal Charcot-Marie-Tooth disease. <i>Brain</i> , 2016, 139, 62-72. | 7.6 | 75 |
| 74 | Functional Interpretation of Microarray Experiments. <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 398-410. | 2.0 | 74 |
| 75 | Genetic Variability and Antigenic Diversity of Foot-and-Mouth Disease Virus. , 1990, , 233-266. | | 74 |
| 76 | Babelomics: advanced functional profiling of transcriptomics, proteomics and genomics experiments. <i>Nucleic Acids Research</i> , 2008, 36, W341-W346. | 14.5 | 73 |
| 77 | Serum metabolomic profiling facilitates the non-invasive identification of metabolic biomarkers associated with the onset and progression of non-small cell lung cancer. <i>Oncotarget</i> , 2016, 7, 12904-12916. | 1.8 | 73 |
| 78 | Whole exome sequencing coupled with unbiased functional analysis reveals new Hirschsprung disease genes. <i>Genome Biology</i> , 2017, 18, 48. | 8.8 | 72 |
| 79 | Phylogenomics and the number of characters required for obtaining an accurate phylogeny of eukaryote model species. <i>Bioinformatics</i> , 2004, 20, i116-i121. | 4.1 | 71 |
| 80 | Exploring the antimicrobial action of a carbon monoxide-releasing compound through whole-genome transcription profiling of <i>Escherichia coli</i> . <i>Microbiology (United Kingdom)</i> , 2009, 155, 813-824. | 1.8 | 71 |
| 81 | Two Novel Mutations in the <i>BCKDK</i> (Branched-Chain Keto-Acid Dehydrogenase Kinase) Gene Are Responsible for a Neurobehavioral Deficit in Two Pediatric Unrelated Patients. <i>Human Mutation</i> , 2014, 35, 470-477. | 2.5 | 70 |
| 82 | Mutation spectrum of <i>EYS</i> in Spanish patients with autosomal recessive retinitis pigmentosa. <i>Human Mutation</i> , 2010, 31, E1772-E1800. | 2.5 | 69 |
| 83 | A Comprehensive DNA Methylation Profile of Epithelial-to-Mesenchymal Transition. <i>Cancer Research</i> , 2014, 74, 5608-5619. | 0.9 | 69 |
| 84 | Whole-genome bisulfite DNA sequencing of a <i>DNMT3B</i> mutant patient. <i>Epigenetics</i> , 2012, 7, 542-550. | 2.7 | 68 |
| 85 | Split decomposition: a technique to analyze viral evolution.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993, 90, 10320-10324. | 7.1 | 67 |
| 86 | GEPAS, a web-based tool for microarray data analysis and interpretation. <i>Nucleic Acids Research</i> , 2008, 36, W308-W314. | 14.5 | 67 |
| 87 | Functional Genomics of 5- to 8-Cell Stage Human Embryos by Blastomere Single-Cell cDNA Analysis. <i>PLoS ONE</i> , 2010, 5, e13615. | 2.5 | 67 |
| 88 | Evidence for short-time divergence and long-time conservation of tissue-specific expression after gene duplication. <i>Briefings in Bioinformatics</i> , 2011, 12, 442-448. | 6.5 | 67 |
| 89 | Potato virus Y group C isolates are a homogeneous pathotype but two different genetic strains.. <i>Journal of General Virology</i> , 1998, 79, 2037-2042. | 2.9 | 66 |
| 90 | High throughput estimation of functional cell activities reveals disease mechanisms and predicts relevant clinical outcomes. <i>Oncotarget</i> , 2017, 8, 5160-5178. | 1.8 | 66 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 91 | Diversification of the expanded teleost-specific toll-like receptor family in Atlantic cod, <i>Gadus morhua</i> . <i>BMC Evolutionary Biology</i> , 2012, 12, 256. | 3.2 | 65 |
| 92 | Gene set-based analysis of polymorphisms: finding pathways or biological processes associated to traits in genome-wide association studies. <i>Nucleic Acids Research</i> , 2009, 37, W340-W344. | 14.5 | 64 |
| 93 | Global Transcriptome Analysis of Primary Cerebrocortical Cells: Identification of Genes Regulated by Triiodothyronine in Specific Cell Types. <i>Cerebral Cortex</i> , 2015, 27, bhv273. | 2.9 | 64 |
| 94 | Primer design for specific diagnosis by PCR of highly variable RNA viruses: Typing of foot-and-mouth disease virus. <i>Virology</i> , 1992, 189, 363-367. | 2.4 | 60 |
| 95 | Joint annotation of coding and non-coding single nucleotide polymorphisms and mutations in the SNPeffect and PupaSuite databases. <i>Nucleic Acids Research</i> , 2008, 36, D825-D829. | 14.5 | 60 |
| 96 | Gene encoding capsid protein VP1 of foot-and-mouth disease virus: a quasispecies model of molecular evolution.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1988, 85, 6811-6815. | 7.1 | 59 |
| 97 | Sequences of isopenicillin N synthetase genes suggest horizontal gene transfer from prokaryotes to eukaryotes. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1990, 241, 164-169. | 2.6 | 58 |
| 98 | ERCC4 Associated with Breast Cancer Risk: A Two-Stage Case-Control Study Using High-throughput Genotyping. <i>Cancer Research</i> , 2006, 66, 9420-9427. | 0.9 | 58 |
| 99 | DNMAD: web-based diagnosis and normalization for microarray data. <i>Bioinformatics</i> , 2004, 20, 3656-3658. | 4.1 | 56 |
| 100 | Genomics and transcriptomics in drug discovery. <i>Drug Discovery Today</i> , 2014, 19, 126-132. | 6.4 | 54 |
| 101 | A RT-PCR assay for the differential diagnosis of vesicular viral diseases of swine. <i>Journal of Virological Methods</i> , 1998, 72, 227-235. | 2.1 | 53 |
| 102 | Selection upon Genome Architecture: Conservation of Functional Neighborhoods with Changing Genes. <i>PLoS Computational Biology</i> , 2010, 6, e1000953. | 3.2 | 53 |
| 103 | Integrating transcriptomic and metabolomic analysis to understand natural leaf senescence in sunflower. <i>Plant Biotechnology Journal</i> , 2016, 14, 719-734. | 8.3 | 53 |
| 104 | COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387. | 7.2 | 53 |
| 105 | Contribution of Mutation and RNA Recombination to the Evolution of a Plant Pathogenic RNA. <i>Journal of Molecular Evolution</i> , 1997, 44, 81-88. | 1.8 | 52 |
| 106 | Improving the management of Inherited Retinal Dystrophies by targeted sequencing of a population-specific gene panel. <i>Scientific Reports</i> , 2016, 6, 23910. | 3.3 | 51 |
| 107 | Integration of transcriptomic and metabolic data reveals hub transcription factors involved in drought stress response in sunflower (<i>Helianthus annuus</i> L.). <i>Plant Molecular Biology</i> , 2017, 94, 549-564. | 3.9 | 51 |
| 108 | Pazopanib for treatment of typical solitary fibrous tumours: a multicentre, single-arm, phase 2 trial. <i>Lancet Oncology</i> , The, 2020, 21, 456-466. | 10.7 | 51 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 109 | An Evolutionary Trade-Off between Protein Turnover Rate and Protein Aggregation Favors a Higher Aggregation Propensity in Fast Degrading Proteins. <i>PLoS Computational Biology</i> , 2011, 7, e1002090. | 3.2 | 50 |
| 110 | Combining Hierarchical Clustering and Self-Organizing Maps for Exploratory Analysis of Gene Expression Patterns. <i>Journal of Proteome Research</i> , 2002, 1, 467-470. | 3.7 | 49 |
| 111 | Highly specific and accurate selection of siRNAs for high-throughput functional assays. <i>Bioinformatics</i> , 2005, 21, 1376-1382. | 4.1 | 49 |
| 112 | Molecular epidemiology of foot-and-mouth disease virus type O. <i>Journal of General Virology</i> , 1993, 74, 2281-2285. | 2.9 | 48 |
| 113 | Bioinformatics methods for the analysis of expression arrays: data clustering and information extraction. <i>Journal of Biotechnology</i> , 2002, 98, 269-283. | 3.8 | 48 |
| 114 | Identification of overexpressed genes in frequently gained/amplified chromosome regions in multiple myeloma. <i>Haematologica</i> , 2006, 91, 184-91. | 3.5 | 48 |
| 115 | New challenges in gene expression data analysis and the extended GEPAS. <i>Nucleic Acids Research</i> , 2004, 32, W485-W491. | 14.5 | 47 |
| 116 | Phylemon: a suite of web tools for molecular evolution, phylogenetics and phylogenomics. <i>Nucleic Acids Research</i> , 2007, 35, W38-W42. | 14.5 | 47 |
| 117 | Exploring the reasons for the large density of triplex-forming oligonucleotide target sequences in the human regulatory regions. <i>BMC Genomics</i> , 2006, 7, 63. | 2.8 | 46 |
| 118 | Fibroblast activation and abnormal extracellular matrix remodelling as common hallmarks in three cancer-prone genodermatoses. <i>British Journal of Dermatology</i> , 2019, 181, 512-522. | 1.5 | 46 |
| 119 | Maslinic Acid-Enriched Diet Decreases Intestinal Tumorigenesis in <i>ApcMin/+</i> Mice through Transcriptomic and Metabolomic Reprogramming. <i>PLoS ONE</i> , 2013, 8, e59392. | 2.5 | 46 |
| 120 | Accelerated phosphatidylcholine turnover in macrophages promotes adipose tissue inflammation in obesity. <i>ELife</i> , 2019, 8, . | 6.0 | 46 |
| 121 | Detailed stratified GWAS analysis for severe COVID-19 in four European populations. <i>Human Molecular Genetics</i> , 2022, 31, 3945-3966. | 2.9 | 46 |
| 122 | Phylogenetic Analysis of Viroid and Viroid-Like Satellite RNAs from Plants: A Reassessment. <i>Journal of Molecular Evolution</i> , 2001, 53, 155-159. | 1.8 | 45 |
| 123 | SNOW, a web-based tool for the statistical analysis of protein-protein interaction networks. <i>Nucleic Acids Research</i> , 2009, 37, W109-W114. | 14.5 | 45 |
| 124 | Papers on normalization, variable selection, classification or clustering of microarray data. <i>Bioinformatics</i> , 2009, 25, 701-702. | 4.1 | 45 |
| 125 | Fixation of mutations at the VP1 gene of foot-and-mouth disease virus. Can quasispecies define a transient molecular clock?. <i>Gene</i> , 1991, 103, 147-153. | 2.2 | 44 |
| 126 | Large deletions in the 5'-untranslated region of foot-and-mouth disease virus of serotype C. <i>Virus Research</i> , 1995, 35, 155-167. | 2.2 | 43 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 127 | Comparison of vaccine strains and the virus causing the 1986 foot-and-mouth disease outbreak in Spain: epizootiological analysis. <i>Virus Research</i> , 1990, 15, 45-55. | 2.2 | 42 |
| 128 | Selective Pressures at a Codon-level Predict Deleterious Mutations in Human Disease Genes. <i>Journal of Molecular Biology</i> , 2006, 358, 1390-1404. | 4.2 | 42 |
| 129 | Understanding disease mechanisms with models of signaling pathway activities. <i>BMC Systems Biology</i> , 2014, 8, 121. | 3.0 | 42 |
| 130 | Functional analysis of multiple genomic signatures demonstrates that classification algorithms choose phenotype-related genes. <i>Pharmacogenomics Journal</i> , 2010, 10, 310-323. | 2.0 | 41 |
| 131 | Whole-exome sequencing reveals ZNF408 as a new gene associated with autosomal recessive retinitis pigmentosa with vitreal alterations. <i>Human Molecular Genetics</i> , 2015, 24, 4037-4048. | 2.9 | 41 |
| 132 | Evolutionary analysis of the picornavirus family. <i>Journal of Molecular Evolution</i> , 1995, 40, 362-371. | 1.8 | 40 |
| 133 | Novel genes detected by transcriptional profiling from whole-blood cells in patients with early onset of acute coronary syndrome. <i>Clinica Chimica Acta</i> , 2013, 421, 184-190. | 1.1 | 40 |
| 134 | Using activation status of signaling pathways as mechanism-based biomarkers to predict drug sensitivity. <i>Scientific Reports</i> , 2015, 5, 18494. | 3.3 | 40 |
| 135 | Gene Expression Integration into Pathway Modules Reveals a Pan-Cancer Metabolic Landscape. <i>Cancer Research</i> , 2018, 78, 6059-6072. | 0.9 | 40 |
| 136 | Precision medicine needs pioneering clinical bioinformaticians. <i>Briefings in Bioinformatics</i> , 2019, 20, 752-766. | 6.5 | 40 |
| 137 | A web-based interactive framework to assist in the prioritization of disease candidate genes in whole-exome sequencing studies. <i>Nucleic Acids Research</i> , 2014, 42, W88-W93. | 14.5 | 39 |
| 138 | Drug repurposing for COVID-19 using machine learning and mechanistic models of signal transduction circuits related to SARS-CoV-2 infection. <i>Signal Transduction and Targeted Therapy</i> , 2020, 5, 290. | 17.1 | 39 |
| 139 | Real world evidence of calcifediol or vitamin D prescription and mortality rate of COVID-19 in a retrospective cohort of hospitalized Andalusian patients. <i>Scientific Reports</i> , 2021, 11, 23380. | 3.3 | 39 |
| 140 | Grape antioxidant dietary fiber inhibits intestinal polyposis in <i>Apc Min/+</i> mice: relation to cell cycle and immune response. <i>Carcinogenesis</i> , 2013, 34, 1881-1888. | 2.8 | 38 |
| 141 | Use of estimated evolutionary strength at the codon level improves the prediction of disease-related protein mutations in humans. <i>Human Mutation</i> , 2008, 29, 198-204. | 2.5 | 37 |
| 142 | VARIANT: Command Line, Web service and Web interface for fast and accurate functional characterization of variants found by Next-Generation Sequencing. <i>Nucleic Acids Research</i> , 2012, 40, W54-W58. | 14.5 | 37 |
| 143 | Differential Features between Chronic Skin Inflammatory Diseases Revealed in Skin-Humanized Psoriasis and Atopic Dermatitis Mouse Models. <i>Journal of Investigative Dermatology</i> , 2016, 136, 136-145. | 0.7 | 37 |
| 144 | Prophet, a web-based tool for class prediction using microarray data. <i>Bioinformatics</i> , 2007, 23, 390-391. | 4.1 | 36 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 145 | Association Study of 69 Genes in the Ret Pathway Identifies Low-penetrance Loci in Sporadic Medullary Thyroid Carcinoma. <i>Cancer Research</i> , 2007, 67, 9561-9567. | 0.9 | 36 |
| 146 | The AnnoLite and AnnoLyze programs for comparative annotation of protein structures. <i>BMC Bioinformatics</i> , 2007, 8, S4. | 2.6 | 36 |
| 147 | Mutation Screening of Multiple Genes in Spanish Patients with Autosomal Recessive Retinitis Pigmentosa by Targeted Resequencing. <i>PLoS ONE</i> , 2011, 6, e27894. | 2.5 | 36 |
| 148 | Dysfunctional mitochondrial fission impairs cell reprogramming. <i>Cell Cycle</i> , 2016, 15, 3240-3250. | 2.6 | 36 |
| 149 | Assessment of Targeted Next-Generation Sequencing as a Tool for the Diagnosis of Charcot-Marie-Tooth Disease and Hereditary Motor Neuropathy. <i>Journal of Molecular Diagnostics</i> , 2016, 18, 225-234. | 2.8 | 36 |
| 150 | Point Mutant Frequencies in the <i>pol</i> Gene of Human Immunodeficiency Virus Type 1 Are Two- to Threefold Lower Than Those of <i>env</i> . <i>AIDS Research and Human Retroviruses</i> , 1996, 12, 1117-1128. | 1.1 | 35 |
| 151 | Capturing the biological impact of CDKN2A and MC1R genes as an early predisposing event in melanoma and non melanoma skin cancer. <i>Oncotarget</i> , 2014, 5, 1439-1451. | 1.8 | 35 |
| 152 | A strain-type clustering of potato virus Y based on the genetic distance between isolates calculated by RFLP analysis of the amplified coat protein gene. <i>Archives of Virology</i> , 1996, 141, 2425-2442. | 2.1 | 34 |
| 153 | The protease MT1-MMP drives a combinatorial proteolytic program in activated endothelial cells. <i>FASEB Journal</i> , 2012, 26, 4481-4494. | 0.5 | 34 |
| 154 | CSVS, a crowdsourcing database of the Spanish population genetic variability. <i>Nucleic Acids Research</i> , 2021, 49, D1130-D1137. | 14.5 | 34 |
| 155 | Estimation of the intrinsic rate of natural increase and its error by both algebraic and resampling approaches. <i>Bioinformatics</i> , 1993, 9, 535-540. | 4.1 | 33 |
| 156 | A novel candidate region linked to development of both pheochromocytoma and head/neck paraganglioma. <i>Genes Chromosomes and Cancer</i> , 2005, 42, 260-268. | 2.8 | 33 |
| 157 | Exploring the Link between Germline and Somatic Genetic Alterations in Breast Carcinogenesis. <i>PLoS ONE</i> , 2010, 5, e14078. | 2.5 | 33 |
| 158 | Exome sequencing identifies a new mutation in SERAC1 in a patient with 3-methylglutaconic aciduria. <i>Molecular Genetics and Metabolism</i> , 2013, 110, 73-77. | 1.1 | 33 |
| 159 | A New Overgrowth Syndrome is due to Mutations in <i>RNF125</i> . <i>Human Mutation</i> , 2014, 35, 1436-1441. | 2.5 | 33 |
| 160 | A comparison of mechanistic signaling pathway activity analysis methods. <i>Briefings in Bioinformatics</i> , 2019, 20, 1655-1668. | 6.5 | 33 |
| 161 | Title is missing!. <i>Artificial Intelligence Review</i> , 2003, 20, 39-51. | 15.7 | 32 |
| 162 | Extensive Translatome Remodeling during ER Stress Response in Mammalian Cells. <i>PLoS ONE</i> , 2012, 7, e35915. | 2.5 | 32 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 163 | Combined Genetic and High-Throughput Strategies for Molecular Diagnosis of Inherited Retinal Dystrophies. PLoS ONE, 2014, 9, e88410. | 2.5 | 32 |
| 164 | Self-organizing tree-growing network for the classification of protein sequences. Protein Science, 1998, 7, 2613-2622. | 7.6 | 31 |
| 165 | Evidence for systems-level molecular mechanisms of tumorigenesis. BMC Genomics, 2007, 8, 185. | 2.8 | 31 |
| 166 | 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 |
| 167 | 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 |
| 168 | Ontology-Driven Approaches to Analyzing Data in Functional Genomics. , 2006, 316, 67-86. | | 30 |
| 169 | Pathway network inference from gene expression data. BMC Systems Biology, 2014, 8, S7. | 3.0 | 30 |
| 170 | Differential metabolic activity and discovery of therapeutic targets using summarized metabolic pathway models. Npj Systems Biology and Applications, 2019, 5, 7. | 3.0 | 30 |
| 171 | ISACGH: a web-based environment for the analysis of Array CGH and gene expression which includes functional profiling. Nucleic Acids Research, 2007, 35, W81-W85. | 14.5 | 29 |
| 172 | Exome sequencing reveals a high genetic heterogeneity on familial Hirschsprung disease. Scientific Reports, 2015, 5, 16473. | 3.3 | 29 |
| 173 | The pan-cancer pathological regulatory landscape. Scientific Reports, 2016, 6, 39709. | 3.3 | 29 |
| 174 | Gene set internal coherence in the context of functional profiling. BMC Genomics, 2009, 10, 197. | 2.8 | 28 |
| 175 | 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 |
| 176 | A map of human microRNA variation uncovers unexpectedly high levels of variability. Genome Medicine, 2012, 4, 62. | 8.2 | 28 |
| 177 | The role of the interactome in the maintenance of deleterious variability in human populations. Molecular Systems Biology, 2014, 10, 752. | 7.2 | 28 |
| 178 | Development, Characterization and Experimental Validation of a Cultivated Sunflower (Helianthus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 | 2.5 | 28 |
| 179 | Genome Maps, a new generation genome browser. Nucleic Acids Research, 2013, 41, W41-W46. | 14.5 | 27 |
| 180 | Actionable pathways: interactive discovery of therapeutic targets using signaling pathway models. Nucleic Acids Research, 2016, 44, W212-W216. | 14.5 | 27 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 181 | Defining the Genomic Signature of Totipotency and Pluripotency during Early Human Development. PLoS ONE, 2013, 8, e62135. | 2.5 | 27 |
| 182 | Comparing Bacterial Genomes Through Conservation Profiles. Genome Research, 2003, 13, 991-998. | 5.5 | 26 |
| 183 | Models of cell signaling uncover molecular mechanisms of high-risk neuroblastoma and predict disease outcome. Biology Direct, 2018, 13, 16. | 4.6 | 26 |
| 184 | Exploring the druggable space around the Fanconi anemia pathway using machine learning and mechanistic models. BMC Bioinformatics, 2019, 20, 370. | 2.6 | 26 |
| 185 | Self-organizing tree growing network for classifying amino acids. Bioinformatics, 1998, 14, 376-377. | 4.1 | 25 |
| 186 | DBAli tools: mining the protein structure space. Nucleic Acids Research, 2007, 35, W393-W397. | 14.5 | 25 |
| 187 | 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 |
| 188 | The <i>EGR2</i> gene is involved in axonal Charcot-Marie-Tooth disease. European Journal of Neurology, 2015, 22, 1548-1555. | 3.3 | 24 |
| 189 | Assessing the Biological Significance of Gene Expression Signatures and Co-Expression Modules by Studying Their Network Properties. PLoS ONE, 2011, 6, e17474. | 2.5 | 24 |
| 190 | Molecular Characterization of Human Immunodeficiency Virus Type 1 Isolates from Venezuela. AIDS Research and Human Retroviruses, 1995, 11, 605-616. | 1.1 | 23 |
| 191 | Inferring the functional effect of gene expression changes in signaling pathways. Nucleic Acids Research, 2013, 41, W213-W217. | 14.5 | 23 |
| 192 | Integrated gene set analysis for microRNA studies. Bioinformatics, 2016, 32, 2809-2816. | 4.1 | 23 |
| 193 | Platform to study intracellular polystyrene nanoplastic pollution and clinical outcomes. Stem Cells, 2020, 38, 1321-1325. | 3.2 | 23 |
| 194 | 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 |
| 195 | A procedure for detecting selection in highly variable viral genomes: evidence of positive selection in antigenic regions of capsid protein VP1 of foot-and-mouth disease virus. Journal of Virological Methods, 1998, 74, 215-221. | 2.1 | 22 |
| 196 | Parallel implementation of DNAmI program on message-passing architectures. Parallel Computing, 1998, 24, 701-716. | 2.1 | 22 |
| 197 | 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 |
| 198 | Formulating and testing hypotheses in functional genomics. Artificial Intelligence in Medicine, 2009, 45, 97-107. | 6.5 | 21 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 199 | Analysis of chronic lymphocytic leukemia transcriptomic profile: differences between molecular subgroups. <i>Leukemia and Lymphoma</i> , 2009, 50, 68-79. | 1.3 | 21 |
| 200 | <i>Fortunella margarita</i> Transcriptional Reprogramming Triggered by <i>Xanthomonas citri</i> subsp. <i>citri</i> . <i>BMC Plant Biology</i> , 2011, 11, 159. | 3.6 | 21 |
| 201 | Re-evaluation casts doubt on the pathogenicity of homozygous <i>USH2A</i> p.C759F. <i>American Journal of Medical Genetics, Part A</i> , 2015, 167, 1597-1600. | 1.2 | 21 |
| 202 | Objective review of <i>de novo</i> stand-alone error correction methods for NGS data. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2016, 6, 111-146. | 14.6 | 21 |
| 203 | Permanent Cardiac Sarcomere Changes in a Rabbit Model of Intrauterine Growth Restriction. <i>PLoS ONE</i> , 2014, 9, e113067. | 2.5 | 21 |
| 204 | Monte Carlo simulation in phylogenies: An application to test the constancy of evolutionary rates. <i>Journal of Molecular Evolution</i> , 1994, 38, 305-9. | 1.8 | 20 |
| 205 | A method for determining the position and size of optimal sequence regions for phylogenetic analysis. <i>Journal of Molecular Evolution</i> , 1995, 41, 1128-38. | 1.8 | 20 |
| 206 | Microarray Data Processing and Analysis. , 2002, , 43-63. | | 20 |
| 207 | Supervised Neural Networks for Clustering Conditions in DNA Array Data After Reducing Noise by Clustering Gene Expression Profiles. , 2002, , 91-103. | | 20 |
| 208 | Functional profiling of microarray experiments using text-mining derived bioentities. <i>Bioinformatics</i> , 2007, 23, 3098-3099. | 4.1 | 20 |
| 209 | Select Your SNPs (SYSNPs): a web tool for automatic and massive selection of SNPs. <i>International Journal of Data Mining and Bioinformatics</i> , 2012, 6, 324. | 0.1 | 20 |
| 210 | Using mechanistic models for the clinical interpretation of complex genomic variation. <i>Scientific Reports</i> , 2019, 9, 18937. | 3.3 | 20 |
| 211 | Implementing Personalized Medicine in COVID-19 in Andalusia: An Opportunity to Transform the Healthcare System. <i>Journal of Personalized Medicine</i> , 2021, 11, 475. | 2.5 | 20 |
| 212 | Functional assessment of time course microarray data. <i>BMC Bioinformatics</i> , 2009, 10, S9. | 2.6 | 19 |
| 213 | Role of <i>CPI</i> in restoring skin homeostasis in cutaneous field of cancerization: effects of topical application of a film-forming medical device containing photolyase and UV filters. <i>Experimental Dermatology</i> , 2013, 22, 494-496. | 2.9 | 19 |
| 214 | The transcriptomics of an experimentally evolved plant-virus interaction. <i>Scientific Reports</i> , 2016, 6, 24901. | 3.3 | 19 |
| 215 | Highly sensitive and ultrafast read mapping for RNA-seq analysis. <i>DNA Research</i> , 2016, 23, 93-100. | 3.4 | 19 |
| 216 | Evolutionary relationships among bean common mosaic virus strains and closely related potyviruses. <i>Virus Research</i> , 1994, 31, 39-48. | 2.2 | 18 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 217 | Molecular epidemiology of HIV-1 in Madrid. <i>Virus Research</i> , 1994, 31, 331-342. | 2.2 | 18 |
| 218 | Confidence limits for resolution estimation in image averaging by random subsampling. <i>Ultramicroscopy</i> , 1995, 60, 385-391. | 1.9 | 18 |
| 219 | Novel RP1 mutations and a recurrent BBS1 variant explain the co-existence of two distinct retinal phenotypes in the same pedigree. <i>BMC Genetics</i> , 2014, 15, 143. | 2.7 | 18 |
| 220 | Genetic characterization of populations of a de novo arisen sugar beet pest, <i>aubeonymus mariaefranciscaae</i> (coleoptera, curculionidae), by RAPD analysis. <i>Journal of Molecular Evolution</i> , 1997, 45, 24-31. | 1.8 | 17 |
| 221 | Gene expression analysis of chromosomal regions with gain or loss of genetic material detected by comparative genomic hybridization. <i>Genes Chromosomes and Cancer</i> , 2004, 41, 353-365. | 2.8 | 17 |
| 222 | Analysis of Normal-Tumour Tissue Interaction in Tumours: Prediction of Prostate Cancer Features from the Molecular Profile of Adjacent Normal Cells. <i>PLoS ONE</i> , 2011, 6, e16492. | 2.5 | 17 |
| 223 | Pathways systematically associated to Hirschsprung's disease. <i>Orphanet Journal of Rare Diseases</i> , 2013, 8, 187. | 2.7 | 17 |
| 224 | The Activation of the Sox2 RR2 Pluripotency Transcriptional Reporter in Human Breast Cancer Cell Lines is Dynamic and Labels Cells with Higher Tumorigenic Potential. <i>Frontiers in Oncology</i> , 2014, 4, 308. | 2.8 | 17 |
| 225 | Deregulation of key signaling pathways involved in oocyte maturation in FMR1 premutation carriers with Fragile X-associated primary ovarian insufficiency. <i>Gene</i> , 2015, 571, 52-57. | 2.2 | 17 |
| 226 | BRCA1 Alternative splicing landscape in breast tissue samples. <i>BMC Cancer</i> , 2015, 15, 219. | 2.6 | 17 |
| 227 | Antibiotic resistance and metabolic profiles as functional biomarkers that accurately predict the geographic origin of city metagenomics samples. <i>Biology Direct</i> , 2019, 14, 15. | 4.6 | 17 |
| 228 | SMN1 copy number and sequence variant analysis from next generation sequencing data. <i>Human Mutation</i> , 2020, 41, 2073-2077. | 2.5 | 17 |
| 229 | Whole-exome sequencing identifies novel compound heterozygous mutations in USH2A in Spanish patients with autosomal recessive retinitis pigmentosa. <i>Molecular Vision</i> , 2013, 19, 2187-95. | 1.1 | 17 |
| 230 | Large-scale transcriptional profiling and functional assays reveal important roles for Rho-GTPase signalling and SCL during haematopoietic differentiation of human embryonic stem cells. <i>Human Molecular Genetics</i> , 2011, 20, 4932-4946. | 2.9 | 16 |
| 231 | Exome Sequencing Reveals Novel and Recurrent Mutations with Clinical Significance in Inherited Retinal Dystrophies. <i>PLoS ONE</i> , 2014, 9, e116176. | 2.5 | 16 |
| 232 | Acceleration of short and long DNA read mapping without loss of accuracy using suffix array. <i>Bioinformatics</i> , 2014, 30, 3396-3398. | 4.1 | 16 |
| 233 | Assessing the impact of mutations found in next generation sequencing data over human signaling pathways. <i>Nucleic Acids Research</i> , 2015, 43, W270-W275. | 14.5 | 16 |
| 234 | Design of primers for PCR amplification of highly variable genomes. <i>Bioinformatics</i> , 1993, 9, 123-125. | 4.1 | 15 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 235 | Primary genetic characterization of HIV-1 isolates from WHO-sponsored vaccine evaluation sites by the RNase-A mismatch method. <i>Virus Research</i> , 1995, 39, 251-259. | 2.2 | 15 |
| 236 | Early peroxisome proliferator-activated receptor gamma regulated genes involved in expansion of pancreatic beta cell mass. <i>BMC Medical Genomics</i> , 2011, 4, 86. | 1.5 | 15 |
| 237 | Identification of epistatic interactions through genome-wide association studies in sporadic medullary and juvenile papillary thyroid carcinomas. <i>BMC Medical Genomics</i> , 2015, 8, 83. | 1.5 | 15 |
| 238 | Involvement of a citrus meiotic recombination TTC-repeat motif in the formation of gross deletions generated by ionizing radiation and MULE activation. <i>BMC Genomics</i> , 2015, 16, 69. | 2.8 | 15 |
| 239 | Web-based network analysis and visualization using CellMaps. <i>Bioinformatics</i> , 2016, 32, 3041-3043. | 4.1 | 15 |
| 240 | Incidence and Prevalence of Children's Diffuse Lung Disease in Spain. <i>Archivos De Bronconeumologia</i> , 2022, 58, 22-29. | 0.8 | 15 |
| 241 | A computer program for the design of PCR primers for diagnosis of highly variable genomes. <i>Journal of Virological Methods</i> , 1993, 41, 157-165. | 2.1 | 14 |
| 242 | Graph-theoretical comparison of normal and tumor networks in identifying BRCA genes. <i>BMC Systems Biology</i> , 2017, 11, 110. | 3.0 | 14 |
| 243 | Bioinformatics and cancer: an essential alliance. <i>Clinical and Translational Oncology</i> , 2006, 8, 409-415. | 2.4 | 13 |
| 244 | Biological processes, properties and molecular wiring diagrams of candidate low-penetrance breast cancer susceptibility genes. <i>BMC Medical Genomics</i> , 2008, 1, 62. | 1.5 | 13 |
| 245 | Deciphering intrafamilial phenotypic variability by exome sequencing in a Bardet-Biedl family. <i>Molecular Genetics & Genomic Medicine</i> , 2014, 2, 124-133. | 1.2 | 13 |
| 246 | Family-based genome-wide association study in Patagonia confirms the association of the <i>DMD</i> locus and cleft lip and palate. <i>European Journal of Oral Sciences</i> , 2015, 123, 381-384. | 1.5 | 13 |
| 247 | Screening of CD96 and ASXL1 in 11 patients with Opitz C or Bohring-Opitz syndromes. <i>American Journal of Medical Genetics, Part A</i> , 2016, 170, 24-31. | 1.2 | 13 |
| 248 | Identification of the Photoreceptor Transcriptional Co-Repressor SAMD11 as Novel Cause of Autosomal Recessive Retinitis Pigmentosa. <i>Scientific Reports</i> , 2016, 6, 35370. | 3.3 | 13 |
| 249 | Phylogenetic Analysis of the 2020 West Nile Virus (WNV) Outbreak in Andalusia (Spain). <i>Viruses</i> , 2021, 13, 836. | 3.3 | 13 |
| 250 | Estimates by computer simulation of genetic distances from comparisons of RNase A mismatch cleavage patterns. <i>Journal of Virological Methods</i> , 1993, 45, 73-82. | 2.1 | 12 |
| 251 | Serial Expression Analysis: a web tool for the analysis of serial gene expression data. <i>Nucleic Acids Research</i> , 2010, 38, W239-W245. | 14.5 | 12 |
| 252 | Natural Selection on Functional Modules, a Genome-Wide Analysis. <i>PLoS Computational Biology</i> , 2011, 7, e1001093. | 3.2 | 12 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 253 | Comparative gene expression study of the vestibular organ of the Igf1 deficient mouse using whole-transcript arrays. <i>Hearing Research</i> , 2015, 330, 62-77. | 2.0 | 12 |
| 254 | Progress in pharmacogenetics: consortiums and new strategies. <i>Drug Metabolism and Personalized Therapy</i> , 2016, 31, 17-23. | 0.6 | 12 |
| 255 | A new parallel pipeline for DNA methylation analysis of long reads datasets. <i>BMC Bioinformatics</i> , 2017, 18, 161. | 2.6 | 12 |
| 256 | A comprehensive database for integrated analysis of omics data in autoimmune diseases. <i>BMC Bioinformatics</i> , 2021, 22, 343. | 2.6 | 12 |
| 257 | Integrating pathway knowledge with deep neural networks to reduce the dimensionality in single-cell RNA-seq data. <i>BioData Mining</i> , 2022, 15, 1. | 4.0 | 12 |
| 258 | Mechanistic models of signaling pathways deconvolute the glioblastoma single-cell functional landscape. <i>NAR Cancer</i> , 2020, 2, zcaa011. | 3.1 | 11 |
| 259 | Mechanistic modeling of the SARS-CoV-2 disease map. <i>BioData Mining</i> , 2021, 14, 5. | 4.0 | 11 |
| 260 | Evolution and Tropism of Transmissible Gastroenteritis Coronavirus. <i>Advances in Experimental Medicine and Biology</i> , 1994, 342, 35-42. | 1.6 | 11 |
| 261 | Towards a metagenomics machine learning interpretable model for understanding the transition from adenoma to colorectal cancer. <i>Scientific Reports</i> , 2022, 12, 450. | 3.3 | 11 |
| 262 | Analysis of genetic variability of populations of herpes simplex viruses. <i>Virus Research</i> , 1993, 28, 249-261. | 2.2 | 10 |
| 263 | Comparative study of the genetic variability in thymidine kinase and glycoprotein B genes of herpes simplex viruses by the RNase A mismatch cleavage method. <i>Virus Research</i> , 1995, 35, 205-214. | 2.2 | 10 |
| 264 | An Approach to Inferring Transcriptional Regulation Among Genes From Large-Scale Expression Data. <i>Comparative and Functional Genomics</i> , 2003, 4, 148-154. | 2.0 | 10 |
| 265 | Functional signatures identified in B-cell non-Hodgkin lymphoma profiles. <i>Leukemia and Lymphoma</i> , 2009, 50, 1699-1708. | 1.3 | 10 |
| 266 | Functional genomics and networks: new approaches in the extraction of complex gene modules. <i>Expert Review of Proteomics</i> , 2010, 7, 55-63. | 3.0 | 10 |
| 267 | Inferring the regulatory network behind a gene expression experiment. <i>Nucleic Acids Research</i> , 2012, 40, W168-W172. | 14.5 | 10 |
| 268 | Molecular interactions between sugar beet and <i>Polymyxa betae</i> during its life cycle. <i>Annals of Applied Biology</i> , 2014, 164, 244-256. | 2.5 | 10 |
| 269 | Chronic subordination stress selectively downregulates the insulin signaling pathway in liver and skeletal muscle but not in adipose tissue of male mice. <i>Stress</i> , 2016, 19, 214-224. | 1.8 | 10 |
| 270 | Improved Class Prediction in DNA Microarray Gene Expression Data by Unsupervised Reduction of the Dimensionality followed by Supervised Learning with a Perceptron. <i>Journal of Signal Processing Systems</i> , 2003, 35, 245-253. | 1.0 | 9 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 271 | HCAD, closing the gap between breakpoints and genes. <i>Nucleic Acids Research</i> , 2004, 33, D511-D513. | 14.5 | 9 |
| 272 | Direct functional assessment of the composite phenotype through multivariate projection strategies. <i>Genomics</i> , 2008, 92, 373-383. | 2.9 | 9 |
| 273 | ngsCAT: a tool to assess the efficiency of targeted enrichment sequencing. <i>Bioinformatics</i> , 2014, 30, 1767-1768. | 4.1 | 9 |
| 274 | A parallel and sensitive software tool for methylation analysis on multicore platforms. <i>Bioinformatics</i> , 2015, 31, 3130-3138. | 4.1 | 9 |
| 275 | HPG pore: an efficient and scalable framework for nanopore sequencing data. <i>BMC Bioinformatics</i> , 2016, 17, 107. | 2.6 | 9 |
| 276 | The first complete genomic structure of <i>Butyrivibrio fibrisolvens</i> and its chromid. <i>Microbial Genomics</i> , 2018, 4, . | 2.0 | 9 |
| 277 | Genome-scale mechanistic modeling of signaling pathways made easy: A bioconductor/cytoscape/web server framework for the analysis of omic data. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2968-2978. | 4.1 | 9 |
| 278 | Identification of optimal regions for phylogenetic studies on VP1 gene of foot-and-mouth disease virus: analysis of types A and O Argentinean viruses. <i>Veterinary Research</i> , 2001, 32, 31-45. | 3.0 | 9 |
| 279 | CLEAR-test: Combining inference for differential expression and variability in microarray data analysis. <i>Journal of Biomedical Informatics</i> , 2008, 41, 33-45. | 4.3 | 8 |
| 280 | New phylogenetic venues opened by a novel implementation of the DNAmI algorithm. <i>Bioinformatics</i> , 1998, 14, 544-545. | 4.1 | 7 |
| 281 | Advances in Cluster Analysis of Microarray Data. , 2005, , 153-173. | | 7 |
| 282 | Four new loci associations discovered by pathway-based and network analyses of the genome-wide variability profile of Hirschsprung's disease. <i>Orphanet Journal of Rare Diseases</i> , 2012, 7, 103. | 2.7 | 7 |
| 283 | Variable selection for multifactorial genomic data. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2012, 110, 113-122. | 3.5 | 7 |
| 284 | Mechanistic Models of Signaling Pathways Reveal the Drug Action Mechanisms behind Gender-Specific Gene Expression for Cancer Treatments. <i>Cells</i> , 2020, 9, 1579. | 4.1 | 7 |
| 285 | Plastome genomics in South American maize landraces: chloroplast lineages parallel the geographical structuring of nuclear gene pools. <i>Annals of Botany</i> , 2021, 128, 115-125. | 2.9 | 7 |
| 286 | Expression profiles and biological function. , 2000, 11, 106-17. | | 7 |
| 287 | Sequence analysis of HIV-1vif gene in Spanish isolates. <i>Virus Genes</i> , 1995, 9, 283-288. | 1.6 | 6 |
| 288 | RT-PCR in foot-and-mouth. <i>Veterinary Quarterly</i> , 1998, 20, 34-36. | 6.7 | 6 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 289 | Ontologies and Functional Genomics. , 2005, , 99-112. | | 6 |
| 290 | A dynamic pipeline for RNA sequencing on multicore processors. , 2013, , . | | 6 |
| 291 | 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 |
| 292 | ATGC transcriptomics: a web-based application to integrate, explore and analyze de novo transcriptomic data. BMC Bioinformatics, 2017, 18, 121. | 2.6 | 6 |
| 293 | HGVA: the Human Genome Variation Archive. Nucleic Acids Research, 2017, 45, W189-W194. | 14.5 | 6 |
| 294 | Immune Cell Associations with Cancer Risk. IScience, 2020, 23, 101296. | 4.1 | 6 |
| 295 | 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 |
| 296 | 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 |
| 297 | A new type of unsupervised growing neural network for biological sequence classification that adopts the topology of a phylogenetic tree. Lecture Notes in Computer Science, 1997, , 932-941. | 1.3 | 5 |
| 298 | Gene expression analysis of the endometrium reveals that controlled ovarian stimulation induces a genomic delay with potential clinical implications. Fertility and Sterility, 2007, 88, S43-S44. | 1.0 | 5 |
| 299 | myKaryoView: A Light-Weight Client for Visualization of Genomic Data. PLoS ONE, 2011, 6, e26345. | 2.5 | 5 |
| 300 | 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 |
| 301 | 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 |
| 302 | 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 |
| 303 | The modular network structure of the mutational landscape of Acute Myeloid Leukemia. PLoS ONE, 2018, 13, e0202926. | 2.5 | 5 |
| 304 | The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. F1000Research, 2020, 9, 1229. | 1.6 | 5 |
| 305 | 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 |
| 306 | Functional profiling and gene expression analysis of chromosomal copy number alterations. Bioinformation, 2007, 1, 432-435. | 0.5 | 5 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 307 | Mutational Characterization of Cutaneous Melanoma Supports Divergent Pathways Model for Melanoma Development. <i>Cancers</i> , 2021, 13, 5219. | 3.7 | 5 |
| 308 | Unsupervised reduction of the dimensionality followed by supervised learning with a perceptron improves the classification of conditions in DNA microarray gene expression data. , 0, , . | | 4 |
| 309 | The Use of Go Terms to Understand the Biological Significance of Microarray Differential Gene Expression Data. , 2004, , 233-247. | | 4 |
| 310 | A novel locus for a hereditary recurrent neuropathy on chromosome 21q21. <i>Neuromuscular Disorders</i> , 2014, 24, 660-665. | 0.6 | 4 |
| 311 | Association of a single nucleotide polymorphism in the ubxn6 gene with long-term non-progression phenotype in HIV-positive individuals. <i>Clinical Microbiology and Infection</i> , 2020, 26, 107-114. | 6.0 | 3 |
| 312 | <i>Salinibacter Ruber: Genomics and Biogeography.</i> , 2005, , 255-266. | | 3 |
| 313 | Assessing Dissimilarity of Genes by Comparing Their RNase A Mismatch Cleavage Patterns. <i>Genetics</i> , 1996, 144, 1975-1983. | 2.9 | 3 |
| 314 | A function-centric approach to the biological interpretation of microarray time-series. <i>Genome Informatics</i> , 2006, 17, 57-66. | 0.4 | 3 |
| 315 | Functional Profiling Methods in Cancer. <i>Methods in Molecular Biology</i> , 2009, 576, 363-374. | 0.9 | 2 |
| 316 | Assessing Differential Expression Measurements by Highly Parallel Pyrosequencing and DNA Microarrays: A Comparative Study. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 53-59. | 2.0 | 2 |
| 317 | Concurrent and Accurate Short Read Mapping on Multicore Processors. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 995-1007. | 3.0 | 2 |
| 318 | Fast inexact mapping using advanced tree exploration on backward search methods. <i>BMC Bioinformatics</i> , 2015, 16, 18. | 2.6 | 2 |
| 319 | A framework for genomic sequencing on clusters of multicore and manycore processors. <i>International Journal of High Performance Computing Applications</i> , 2018, 32, 393-406. | 3.7 | 2 |
| 320 | Predictive Value of MRP-1 in Localized High-Risk Soft Tissue Sarcomas: A Translational Research Associated to ISG-ST5 1001 Randomized Phase III Trial. <i>Molecular Cancer Therapeutics</i> , 2021, 20, 2539-2552. | 4.1 | 2 |
| 321 | Multicore and Cloud-Based Solutions for Genomic Variant Analysis. <i>Lecture Notes in Computer Science</i> , 2013, , 273-284. | 1.3 | 2 |
| 322 | Protein Interactions for Functional Genomics. , 2009, , 223-238. | | 2 |
| 323 | Highly accurate whole-genome imputation of SARS-CoV-2 from partial or low-quality sequences. <i>GigaScience</i> , 2021, 10, . | 6.4 | 2 |
| 324 | Protein and functional isoform levels and genetic variants of the BAFF and APRIL pathway components in systemic lupus erythematosus. <i>Scientific Reports</i> , 2022, 12, . | 3.3 | 2 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 325 | Reducing the effect of the data order in algorithms for constructing phylogenetic trees. <i>Bioinformatics</i> , 1988, 4, 307-307. | 4.1 | 1 |
| 326 | Using gene ontology on genome-scale studies to find significant associations of biologically relevant terms to groups of genes. , 0, , . | | 1 |
| 327 | Integrative Data Analysis and Visualization: Introduction to Critical Problems, Goals and Challenges. , 2005, , 1-9. | | 1 |
| 328 | Clustering " Class Discovery in the Post-Genomic Era. , 2007, , 123-148. | | 1 |
| 329 | Expression and Microarrays. <i>Methods in Molecular Biology</i> , 2008, 453, 245-255. | 0.9 | 1 |
| 330 | Using Papers Citations for Selecting the Best Genomic Databases. , 2011, , . | | 1 |
| 331 | SEQUENCING OF 150 CITRUS VARIETIES: LINKING GENOTYPES TO PHENOTYPES. <i>Acta Horticulturae</i> , 2015, , 585-589. | 0.2 | 1 |
| 332 | VISMapper: ultra-fast exhaustive cartography of viral insertion sites for gene therapy. <i>BMC Bioinformatics</i> , 2017, 18, 421. | 2.6 | 1 |
| 333 | Using Perceptrons for Supervised Classification of DNA Microarray Samples: Obtaining the Optimal Level of Information and Finding Differentially Expressed Genes. <i>Lecture Notes in Computer Science</i> , 2002, , 577-582. | 1.3 | 1 |
| 334 | New Trends in the Analysis of Functional Genomic Data. <i>Mathematics in Industry</i> , 2008, , 576-580. | 0.3 | 1 |
| 335 | Discovering potential interactions between rare diseases and COVID-19 by combining mechanistic models of viral infection with statistical modeling. <i>Human Molecular Genetics</i> , 2022, , . | 2.9 | 1 |
| 336 | Multiple sequence editing by spreadsheet. <i>Bioinformatics</i> , 1990, 6, 401-402. | 4.1 | 0 |
| 337 | Quantitative characterization of antigens using monoclonal antibody reactivities. <i>Bioinformatics</i> , 1993, 9, 101-107. | 4.1 | 0 |
| 338 | O-93. <i>Fertility and Sterility</i> , 2006, 86, S40. | 1.0 | 0 |
| 339 | Gene-expression Profiling And Differential Pathways In The Sensitization And Tolerance To Allergens. <i>Journal of Allergy and Clinical Immunology</i> , 2011, 127, AB263-AB263. | 2.9 | 0 |
| 340 | Molecular Pattern in Olive Pollen Response. <i>Journal of Allergy and Clinical Immunology</i> , 2013, 131, AB44. | 2.9 | 0 |
| 341 | Reference genome assessment from a population scale perspective: an accurate profile of variability and noise. <i>Bioinformatics</i> , 2017, 33, 3511-3517. | 4.1 | 0 |
| 342 | PyCellBase, an efficient python package for easy retrieval of biological data from heterogeneous sources. <i>BMC Bioinformatics</i> , 2019, 20, 159. | 2.6 | 0 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 343 | Molecular Genetics in the Next Generation Sequencing Era. , 2021, , 215-230. | | 0 |
| 344 | Differentiating Positive Selection from Acceleration and Relaxation in Human and Chimp. PLoS Computational Biology, 2005, preprint, e38. | 3.2 | 0 |
| 345 | Protein Interactions for Functional Genomics. International Journal of Knowledge Discovery in Bioinformatics, 2012, 3, 15-30. | 0.8 | 0 |
| 346 | Increased De Novo Phosphatidylcholine Synthesis in Macrophages Promotes Adipose Tissue Inflammation in Obesity. SSRN Electronic Journal, 0, , . | 0.4 | 0 |
| 347 | Deciphering Genomic Heterogeneity and the Internal Composition of Tumour Activities through a Hierarchical Factorisation Model. Mathematics, 2021, 9, 2833. | 2.2 | 0 |