

Angel Rubio

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

2,304
citations

257450

24
h-index

214800

47
g-index

65
all docs

65
docs citations

65
times ranked

3623
citing authors

#	ARTICLE	IF	CITATIONS
1	Rediscover: an R package to identify mutually exclusive mutations. <i>Bioinformatics</i> , 2022, 38, 844-845.	4.1	8
2	On the identifiability of the isoform deconvolution problem: application to select the proper fragment length in an RNA-seq library. <i>Bioinformatics</i> , 2022, , .	4.1	0
3	SOX9 Triggers Different Epithelial to Mesenchymal Transition States to Promote Pancreatic Cancer Progression. <i>Cancers</i> , 2022, 14, 916.	3.7	6
4	BOSO: A novel feature selection algorithm for linear regression with high-dimensional data. <i>PLoS Computational Biology</i> , 2022, 18, e1010180.	3.2	3
5	Comparison of Typical Controllers for Direct Yaw Moment Control Applied on an Electric Race Car. <i>Vehicles</i> , 2021, 3, 127-144.	3.1	8
6	An extended reconstruction of human gut microbiota metabolism of dietary compounds. <i>Nature Communications</i> , 2021, 12, 4728.	12.8	19
7	Integration of CRISPR-Cas9, shRNA with other genomic data provides reliable predictions of gene essentiality. <i>EBioMedicine</i> , 2020, 51, 102577.	6.1	0
8	DrugSniper, a Tool to Exploit Loss-Of-Function Screens, Identifies CREBBP as a Predictive Biomarker of VOLASERTIB in Small Cell Lung Carcinoma (SCLC). <i>Cancers</i> , 2020, 12, 1824.	3.7	6
9	ISOGO: Functional annotation of protein-coding splice variants. <i>Scientific Reports</i> , 2020, 10, 1069.	3.3	6
10	Integration of CLIP experiments of RNA-binding proteins: a novel approach to predict context-dependent splicing factors from transcriptomic data. <i>BMC Genomics</i> , 2019, 20, 521.	2.8	4
11	TranscriptAchilles: a genome-wide platform to predict isoform biomarkers of gene essentiality in cancer. <i>GigaScience</i> , 2019, 8, .	6.4	3
12	Upstream analysis of alternative splicing: a review of computational approaches to predict context-dependent splicing factors. <i>Briefings in Bioinformatics</i> , 2019, 20, 1358-1375.	6.5	53
13	A Computational Based Approach for Identification and Validation of Gene Mutations As Surrogate Markers of Gene Essentiality in Acute Myeloid Leukemia. <i>Blood</i> , 2019, 134, 1414-1414.	1.4	0
14	The aberrant splicing of BAF45d links splicing regulation and transcription in glioblastoma. <i>Neuro-Oncology</i> , 2018, 20, 930-941.	1.2	29
15	Comparison of RNA-seq and microarray platforms for splice event detection using a cross-platform algorithm. <i>BMC Genomics</i> , 2018, 19, 703.	2.8	20
16	Oncogenic activity of SOX1 in glioblastoma. <i>Scientific Reports</i> , 2017, 7, 46575.	3.3	27
17	In-silico gene essentiality analysis of polyamine biosynthesis reveals APRT as a potential target in cancer. <i>Scientific Reports</i> , 2017, 7, 14358.	3.3	10
18	EventPointer: an effective identification of alternative splicing events using junction arrays. <i>BMC Genomics</i> , 2016, 17, 467.	2.8	31

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19	A large-scale analysis of alternative splicing reveals a key role of QKI in lung cancer. <i>Molecular Oncology</i> , 2016, 10, 1437-1449.	4.6	60
20	Data stream visualization framework for smart cities. <i>Soft Computing</i> , 2016, 20, 1671-1681.	3.6	7
21	Combined clinical and genomic signatures for the prognosis of early stage non-small cell lung cancer based on gene copy number alterations. <i>BMC Genomics</i> , 2015, 16, 752.	2.8	12
22	Advances in network-based metabolic pathway analysis and gene expression data integration. <i>Briefings in Bioinformatics</i> , 2015, 16, 265-279.	6.5	25
23	Code Profiling in R: A Review of Existing Methods and an Introduction to Package GUIProfiler. <i>R Journal</i> , 2015, 7, 275.	1.8	5
24	Abstract 2124: Analysis of the functional relevance of novel alternative splicing events in non-small cell lung cancer. , 2015, , .		0
25	In-Silico Prediction of Key Metabolic Differences between Two Non-Small Cell Lung Cancer Subtypes. <i>PLoS ONE</i> , 2014, 9, e103998.	2.5	25
26	Identification of Alternative Splicing Events Regulated by the Oncogenic Factor SRSF1 in Lung Cancer. <i>Cancer Research</i> , 2014, 74, 1105-1115.	0.9	77
27	Channel and feature selection for a surface electromyographic pattern recognition task. <i>Expert Systems With Applications</i> , 2014, 41, 5190-5200.	7.6	44
28	Improving miRNA-mRNA interaction predictions. <i>BMC Genomics</i> , 2014, 15, S2.	2.8	26
29	Integrating gene and protein expression data with genome-scale metabolic networks to infer functional pathways. <i>BMC Systems Biology</i> , 2013, 7, 134.	3.0	5
30	Joint analysis of miRNA and mRNA expression data. <i>Briefings in Bioinformatics</i> , 2013, 14, 263-278.	6.5	104
31	Selection of human tissue-specific elementary flux modes using gene expression data. <i>Bioinformatics</i> , 2013, 29, 2009-2016.	4.1	38
32	CalMaTe: a method and software to improve allele-specific copy number of SNP arrays for downstream segmentation. <i>Bioinformatics</i> , 2012, 28, 1793-1794.	4.1	16
33	Integrating tracer-based metabolomics data and metabolic fluxes in a linear fashion via Elementary Carbon Modes. <i>Metabolic Engineering</i> , 2012, 14, 344-353.	7.0	10
34	Getting DNA copy numbers without control samples. <i>Algorithms for Molecular Biology</i> , 2012, 7, 19.	1.2	1
35	Quantification of miRNA-mRNA Interactions. <i>PLoS ONE</i> , 2012, 7, e30766.	2.5	67
36	Exploring the connectivity structure in metabolic networks: Going beyond graphs via discrete optimization. , 2011, , .		0

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37	Segmentation of genomic and transcriptomic microarrays data reveals major correlation between DNA copy number aberrations and gene loci expression. <i>Genomics</i> , 2011, 97, 86-93.	2.9	23
38	Do elementary flux modes combine linearly at the atomic level? Integrating tracer-based metabolomics data and elementary flux modes. <i>BioSystems</i> , 2011, 105, 140-146.	2.0	6
39	Genetic and Epigenetic Modifications of Sox2 Contribute to the Invasive Phenotype of Malignant Gliomas. <i>PLoS ONE</i> , 2011, 6, e26740.	2.5	187
40	Abstract 3307: The multitasking of Sox2: Maintaining the stemness and inducing the malignant phenotype of gliomas. , 2011, , .		0
41	Improvements to previous algorithms to predict gene structure and isoform concentrations using Affymetrix Exon arrays. <i>BMC Bioinformatics</i> , 2010, 11, 578.	2.6	4
42	Development of a novel splice array platform and its application in the identification of alternative splice variants in lung cancer. <i>BMC Genomics</i> , 2010, 11, 352.	2.8	25
43	ACNE: a summarization method to estimate allele-specific copy numbers for Affymetrix SNP arrays. <i>Bioinformatics</i> , 2010, 26, 1827-1833.	4.1	20
44	Genome-Wide Proximal Promoter Analysis and Interpretation. <i>Methods in Molecular Biology</i> , 2010, 593, 157-174.	0.9	0
45	Computing the shortest elementary flux modes in genome-scale metabolic networks. <i>Bioinformatics</i> , 2009, 25, 3158-3165.	4.1	184
46	FactorY, a bioinformatic resource for genome-wide promoter analysis. <i>Computers in Biology and Medicine</i> , 2009, 39, 385-387.	7.0	10
47	Decreasing the Apparent Inertia of an Impedance Haptic Device by Using Force Feedforward. <i>IEEE Transactions on Control Systems Technology</i> , 2009, 17, 833-838.	5.2	35
48	Integrative Oncogenomic Analysis of Microarray Data in Hematologic Malignancies. <i>Methods in Molecular Biology</i> , 2009, 576, 231-277.	0.9	5
49	<i>BCR-ABL1</i> -induced expression of <i>HSPA8</i> promotes cell survival in chronic myeloid leukaemia. <i>British Journal of Haematology</i> , 2008, 142, 571-582.	2.5	33
50	SPACE: an algorithm to predict and quantify alternatively spliced isoforms using microarrays. <i>Genome Biology</i> , 2008, 9, R46.	9.6	26
51	Cytosolic and Plastoglobule-targeted Carotenoid Dioxygenases from <i>Crocus sativus</i> Are Both Involved in Î ² -Ionone Release. <i>Journal of Biological Chemistry</i> , 2008, 283, 24816-24825.	3.4	235
52	Identification of a gene-pathway associated with non-alcoholic steatohepatitis. <i>Journal of Hepatology</i> , 2007, 46, 708-718.	3.7	52
53	GARBAN II: An integrative framework for extracting biological information from proteomic and genomic data. <i>Proteomics</i> , 2006, 6, S12-S15.	2.2	6
54	Correlation between Gene Expression and GO Semantic Similarity. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2005, 2, 330-338.	3.0	194

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55	Loop Shaping for Transparency and Stability Robustness in Time-Delayed Bilateral Telemanipulation. Journal of Dynamic Systems, Measurement and Control, Transactions of the ASME, 2004, 126, 650-656.	1.6	10
56	Experimental Quantitative Comparison of Different Control Architectures for Master-Slave Teleoperation. IEEE Transactions on Control Systems Technology, 2004, 12, 2-11.	5.2	93
57	Stability Analysis of a 1 DOF Haptic Interface Using the Routh-Hurwitz Criterion. IEEE Transactions on Control Systems Technology, 2004, 12, 583-588.	5.2	149
58	Functional proteomics of nonalcoholic steatohepatitis: Mitochondrial proteins as targets of S-adenosylmethionine. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 3065-3070.	7.1	154
59	GARBAN: genomic analysis and rapid biological annotation of cDNA microarray and proteomic data. Bioinformatics, 2003, 19, 2158-2160.	4.1	27
60	Swing-up control problem for a self-erecting double inverted pendulum. IET Control Theory and Applications, 2002, 149, 169-175.	1.7	53
61	Transparent telemanipulation in the presence of time delay. , 0, , .		14
62	A Direct Yaw-Moment Control Logic for an Electric 2WD Formula SAE Using an Error-Cube Proportional Derivative Controller. SAE International Journal of Connected and Automated Vehicles, 0, 3, 139-148.	0.4	3