

Nuno Barbosa-Morais

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

7,114
citations

94381

37
h-index

138417

58
g-index

67
all docs

67
docs citations

67
times ranked

13735
citing authors

#	ARTICLE	IF	CITATIONS
1	Allosteric Antagonist Modulation of TRPV2 by Piperlongumine Impairs Glioblastoma Progression. <i>ACS Central Science</i> , 2021, 7, 868-881.	5.3	34
2	The splicing factor XAB2 interacts with ERCC1-XPF and XPG for R-loop processing. <i>Nature Communications</i> , 2021, 12, 3153.	5.8	27
3	NineTeen Complex-subunit Salsa is required for efficient splicing of a subset of introns and dorsal-ventral patterning. <i>Rna</i> , 2020, 26, 1935-1956.	1.6	2
4	Unraveling Targetable Systemic and Cell-Type-Specific Molecular Phenotypes of Alzheimer's and Parkinson's Brains With Digital Cytometry. <i>Frontiers in Neuroscience</i> , 2020, 14, 607215.	1.4	6
5	IgE to epitopes of Ara h 2 enhance the diagnostic accuracy of Ara h 2-specific IgE. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2020, 75, 2309-2318.	2.7	36
6	Expression of receptor activator of NF κ B (RANK) drives stemness and resistance to therapy in ER+HER2-breast cancer. <i>Oncotarget</i> , 2020, 11, 1714-1728.	0.8	15
7	Interactive Alternative Splicing Analysis of Human Stem Cells Using psichomics. <i>Methods in Molecular Biology</i> , 2020, 2117, 179-205.	0.4	0
8	Dissecting celastrol with machine learning to unveil dark pharmacology. <i>Chemical Communications</i> , 2019, 55, 6369-6372.	2.2	10
9	Pan-cancer association of a centrosome amplification gene expression signature with genomic alterations and clinical outcome. <i>PLoS Computational Biology</i> , 2019, 15, e1006832.	1.5	35
10	Natural product-drug conjugates for modulation of TRPV1-expressing tumors. <i>Bioorganic and Medicinal Chemistry</i> , 2019, 27, 2531-2536.	1.4	8
11	Light-entrained and brain-tuned circadian circuits regulate ILC3s and gut homeostasis. <i>Nature</i> , 2019, 574, 254-258.	13.7	137
12	psichomics: graphical application for alternative splicing quantification and analysis. <i>Nucleic Acids Research</i> , 2019, 47, e7-e7.	6.5	36
13	Androgen-regulated transcription of ESRP2 drives alternative splicing patterns in prostate cancer. <i>ELife</i> , 2019, 8, .	2.8	56
14	Expansion of DUB functionality by alternative isoforms: USP35, a case study. <i>Journal of Cell Science</i> , 2018, 131, .	1.2	34
15	Over-elongation of centrioles in cancer promotes centriole amplification and chromosome missegregation. <i>Nature Communications</i> , 2018, 9, 1258.	5.8	113
16	PTBP1-Mediated Alternative Splicing Regulates the Inflammatory Secretome and the Pro-tumorigenic Effects of Senescent Cells. <i>Cancer Cell</i> , 2018, 34, 85-102.e9.	7.7	152
17	Decoding a cancer-relevant splicing decision in the RON proto-oncogene using high-throughput mutagenesis. <i>Nature Communications</i> , 2018, 9, 3315.	5.8	46
18	Androgen-dependent alternative mRNA isoform expression in prostate cancer cells. <i>F1000Research</i> , 2018, 7, 1189.	0.8	16

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19	Alternative splicing: the pledge, the turn, and the prestige. <i>Human Genetics</i> , 2017, 136, 1015-1042.	1.8	106
20	<i>Trypanosoma brucei</i> metabolism is under circadian control. <i>Nature Microbiology</i> , 2017, 2, 17032.	5.9	68
21	Neuronal regulation of type 2 innate lymphoid cells via neuromedin U. <i>Nature</i> , 2017, 549, 277-281.	13.7	421
22	PD11-09 MOLECULAR TUMOR GRADING OF NON MUSCLE INVASIVE BLADDER CANCER BASED ON WHOLE TRANSCRIPTOME ANALYSIS. <i>Journal of Urology</i> , 2016, 195, .	0.2	0
23	Molecular tumor grading of non muscle invasive bladder cancer based on whole transcriptome analysis.. <i>Journal of Clinical Oncology</i> , 2016, 34, 467-467.	0.8	1
24	Next-generation RNA Sequencing of Archival Formalin-fixed Paraffin-embedded Urothelial Bladder Cancer. <i>European Urology</i> , 2014, 66, 982-986.	0.9	33
25	Widespread intron retention in mammals functionally tunes transcriptomes. <i>Genome Research</i> , 2014, 24, 1774-1786.	2.4	554
26	<i>T rypanosoma brucei</i> histone H 1 inhibits RNA polymerase I transcription and is important for parasite fitness in vivo. <i>Molecular Microbiology</i> , 2014, 93, 645-663.	1.2	23
27	Latent Regulatory Potential of Human-Specific Repetitive Elements. <i>Molecular Cell</i> , 2013, 49, 262-272.	4.5	62
28	MBNL proteins repress ES-cell-specific alternative splicing and reprogramming. <i>Nature</i> , 2013, 498, 241-245.	13.7	326
29	The Evolutionary Landscape of Alternative Splicing in Vertebrate Species. <i>Science</i> , 2012, 338, 1587-1593.	6.0	905
30	Functional evidence that <i>Drosha</i> overexpression in cervical squamous cell carcinoma affects cell phenotype and microRNA profiles. <i>Journal of Pathology</i> , 2011, 224, 496-507.	2.1	71
31	SIK2 Is a Centrosome Kinase Required for Bipolar Mitotic Spindle Formation that Provides a Potential Target for Therapy in Ovarian Cancer. <i>Cancer Cell</i> , 2010, 18, 109-121.	7.7	126
32	A re-annotation pipeline for Illumina BeadArrays: improving the interpretation of gene expression data. <i>Nucleic Acids Research</i> , 2010, 38, e17-e17.	6.5	200
33	The importance of platform annotation in interpreting microarray data. <i>Lancet Oncology</i> , The, 2010, 11, 717.	5.1	14
34	Association of ESR1 gene tagging SNPs with breast cancer risk. <i>Human Molecular Genetics</i> , 2009, 18, 1131-1139.	1.4	84
35	Isolation of Stool-Derived Mucus Provides a High Yield of Colonocytes Suitable for Early Detection of Colorectal Carcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009, 18, 2006-2013.	1.1	15
36	Considerations for the processing and analysis of GoldenGate-based two-colour Illumina platforms. <i>Statistical Methods in Medical Research</i> , 2009, 18, 437-452.	0.7	18

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37	Statistical issues in the analysis of Illumina data. <i>BMC Bioinformatics</i> , 2008, 9, 85.	1.2	90
38	Spike-in validation of an Illumina-specific variance-stabilizing transformation. <i>BMC Research Notes</i> , 2008, 1, 18.	0.6	13
39	Species-Specific Transcription in Mice Carrying Human Chromosome 21. <i>Science</i> , 2008, 322, 434-438.	6.0	260
40	Tissue-specific splicing factor gene expression signatures. <i>Nucleic Acids Research</i> , 2008, 36, 4823-4832.	6.5	172
41	Association of single-nucleotide polymorphisms in the cell cycle genes with breast cancer in the British population. <i>Carcinogenesis</i> , 2008, 29, 333-341.	1.3	68
42	Pediatric Malignant Germ Cell Tumors Show Characteristic Transcriptome Profiles. <i>Cancer Research</i> , 2008, 68, 4239-4247.	0.4	83
43	High-resolution aCGH and expression profiling identifies a novel genomic subtype of ER negative breast cancer. <i>Genome Biology</i> , 2007, 8, R215.	13.9	275
44	MicroRNA expression profiling of human breast cancer identifies new markers of tumor subtype. <i>Genome Biology</i> , 2007, 8, R214.	13.9	828
45	Global microRNA profiles in cervical squamous cell carcinoma depend on Drosha expression levels. <i>Journal of Pathology</i> , 2007, 212, 368-377.	2.1	162
46	A gene-expression signature to predict survival in breast cancer across independent data sets. <i>Oncogene</i> , 2007, 26, 1507-1516.	2.6	225
47	Using array-comparative genomic hybridization to define molecular portraits of primary breast cancers. <i>Oncogene</i> , 2007, 26, 1959-1970.	2.6	97
48	New androgen receptor genomic targets show an interaction with the ETS1 transcription factor. <i>EMBO Reports</i> , 2007, 8, 871-878.	2.0	240
49	Cell Cycle Genes Are the Evolutionarily Conserved Targets of the E2F4 Transcription Factor. <i>PLoS ONE</i> , 2007, 2, e1061.	1.1	51
50	Genome-wide identification of functionally distinct subsets of cellular mRNAs associated with two nucleocytoplasmic-shuttling mammalian splicing factors. <i>Genome Biology</i> , 2006, 7, R113.	13.9	68
51	A consensus prognostic gene expression classifier for ER positive breast cancer. <i>Genome Biology</i> , 2006, 7, R101.	13.9	82
52	MMASS: an optimized array-based method for assessing CpG island methylation. <i>Nucleic Acids Research</i> , 2006, 34, e136-e136.	6.5	44
53	Diversity of human U2AF splicing factors.. <i>FEBS Journal</i> , 2006, 273, 4807-4816.	2.2	38
54	ASD: a bioinformatics resource on alternative splicing. <i>Nucleic Acids Research</i> , 2006, 34, D46-D55.	6.5	205

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55	PACK: Profile Analysis using Clustering and Kurtosis to find molecular classifiers in cancer. <i>Bioinformatics</i> , 2006, 22, 2269-2275.	1.8	61
56	A variational Bayesian mixture modelling framework for cluster analysis of gene-expression data. <i>Bioinformatics</i> , 2005, 21, 3025-3033.	1.8	73
57	Systematic genome-wide annotation of spliceosomal proteins reveals differential gene family expansion. <i>Genome Research</i> , 2005, 16, 66-77.	2.4	92
58	Diversity of Vertebrate Splicing Factor U2AF35. <i>Journal of Biological Chemistry</i> , 2004, 279, 27039-27049.	1.6	47
59	Expression microarray reproducibility is improved by optimising purification steps in RNA amplification and labelling. <i>BMC Genomics</i> , 2004, 5, 9.	1.2	45
60	Allosteric Antagonist Modulation of TRPV2 by Piperlongumine Impairs Glioblastoma Progression. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1