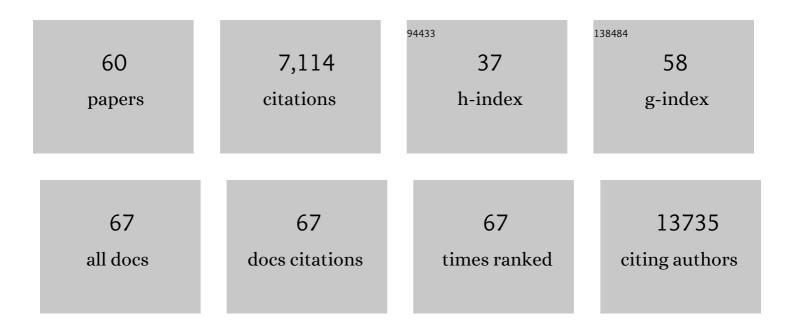
Nuno Barbosa-Morais

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2976761/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Allosteric Antagonist Modulation of TRPV2 by Piperlongumine Impairs Glioblastoma Progression. ACS Central Science, 2021, 7, 868-881.	11.3	34
2	The splicing factor XAB2 interacts with ERCC1-XPF and XPG for R-loop processing. Nature Communications, 2021, 12, 3153.	12.8	27
3	NineTeen Complex-subunit Salsa is required for efficient splicing of a subset of introns and dorsal–ventral patterning. Rna, 2020, 26, 1935-1956.	3.5	2
4	Unraveling Targetable Systemic and Cell-Type-Specific Molecular Phenotypes of Alzheimer's and Parkinson's Brains With Digital Cytometry. Frontiers in Neuroscience, 2020, 14, 607215.	2.8	6
5	lgE to epitopes of Ara h 2 enhance the diagnostic accuracy of Ara h 2â€specific IgE. Allergy: European Journal of Allergy and Clinical Immunology, 2020, 75, 2309-2318.	5.7	36
6	Expression of receptor activator of NFkB (RANK) drives stemness and resistance to therapy in ER+HER2- breast cancer. Oncotarget, 2020, 11, 1714-1728.	1.8	15
7	Interactive Alternative Splicing Analysis of Human Stem Cells Using psichomics. Methods in Molecular Biology, 2020, 2117, 179-205.	0.9	0
8	Dissecting celastrol with machine learning to unveil dark pharmacology. Chemical Communications, 2019, 55, 6369-6372.	4.1	10
9	Pan-cancer association of a centrosome amplification gene expression signature with genomic alterations and clinical outcome. PLoS Computational Biology, 2019, 15, e1006832.	3.2	35
10	Natural product–drug conjugates for modulation of TRPV1-expressing tumors. Bioorganic and Medicinal Chemistry, 2019, 27, 2531-2536.	3.0	8
11	Light-entrained and brain-tuned circadian circuits regulate ILC3s and gut homeostasis. Nature, 2019, 574, 254-258.	27.8	137
12	psichomics: graphical application for alternative splicing quantification and analysis. Nucleic Acids Research, 2019, 47, e7-e7.	14.5	36
13	Androgen-regulated transcription of ESRP2 drives alternative splicing patterns in prostate cancer. ELife, 2019, 8, .	6.0	56
14	Expansion of DUB functionality by alternative isoforms: USP35, a case study. Journal of Cell Science, 2018, 131, .	2.0	34
15	Over-elongation of centrioles in cancer promotes centriole amplification and chromosome missegregation. Nature Communications, 2018, 9, 1258.	12.8	113
16	PTBP1-Mediated Alternative Splicing Regulates the Inflammatory Secretome and the Pro-tumorigenic Effects of Senescent Cells. Cancer Cell, 2018, 34, 85-102.e9.	16.8	152
17	Decoding a cancer-relevant splicing decision in the RON proto-oncogene using high-throughput mutagenesis. Nature Communications, 2018, 9, 3315.	12.8	46
18	Androgen-dependent alternative mRNA isoform expression in prostate cancer cells. F1000Research, 2018, 7, 1189.	1.6	16

Nuno Barbosa-Morais

#	Article	IF	CITATIONS
19	Alternative splicing: the pledge, the turn, and the prestige. Human Genetics, 2017, 136, 1015-1042.	3.8	106
20	Trypanosoma brucei metabolism is under circadian control. Nature Microbiology, 2017, 2, 17032.	13.3	68
21	Neuronal regulation of type 2 innate lymphoid cells via neuromedin U. Nature, 2017, 549, 277-281.	27.8	421
22	PD11-09 MOLECULAR TUMOR GRADING OF NON MUSCLE INVASIVE BLADDER CANCER BASED ON WHOLE TRANSCRIPTOME ANALYSIS. Journal of Urology, 2016, 195, .	0.4	0
23	Molecular tumor grading of non muscle invasive bladder cancer based on whole transcriptome analysis Journal of Clinical Oncology, 2016, 34, 467-467.	1.6	1
24	Next-generation RNA Sequencing of Archival Formalin-fixed Paraffin-embedded Urothelial Bladder Cancer. European Urology, 2014, 66, 982-986.	1.9	33
25	Widespread intron retention in mammals functionally tunes transcriptomes. Genome Research, 2014, 24, 1774-1786.	5.5	554
26	T rypanosoma brucei histone H 1 inhibits RNA polymerase I transcription and is important for parasite fitness in vivo. Molecular Microbiology, 2014, 93, 645-663.	2.5	23
27	Latent Regulatory Potential of Human-Specific Repetitive Elements. Molecular Cell, 2013, 49, 262-272.	9.7	62
28	MBNL proteins repress ES-cell-specific alternative splicing and reprogramming. Nature, 2013, 498, 241-245.	27.8	326
29	The Evolutionary Landscape of Alternative Splicing in Vertebrate Species. Science, 2012, 338, 1587-1593.	12.6	905
30	Functional evidence that <i>Drosha</i> overexpression in cervical squamous cell carcinoma affects cell phenotype and microRNA profiles. Journal of Pathology, 2011, 224, 496-507.	4.5	71
31	SIK2 Is a Centrosome Kinase Required for Bipolar Mitotic Spindle Formation that Provides a Potential Target for Therapy in Ovarian Cancer. Cancer Cell, 2010, 18, 109-121.	16.8	126
32	A re-annotation pipeline for Illumina BeadArrays: improving the interpretation of gene expression data. Nucleic Acids Research, 2010, 38, e17-e17.	14.5	200
33	The importance of platform annotation in interpreting microarray data. Lancet Oncology, The, 2010, 11, 717.	10.7	14
34	Association of ESR1 gene tagging SNPs with breast cancer risk. Human Molecular Genetics, 2009, 18, 1131-1139.	2.9	84
35	Isolation of Stool-Derived Mucus Provides a High Yield of Colonocytes Suitable for Early Detection of Colorectal Carcinoma. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 2006-2013.	2.5	15
36	Considerations for the processing and analysis of GoldenGate-based two-colour Illumina platforms. Statistical Methods in Medical Research, 2009, 18, 437-452.	1.5	18

#	Article	IF	CITATIONS
37	Statistical issues in the analysis of Illumina data. BMC Bioinformatics, 2008, 9, 85.	2.6	90
38	Spike-in validation of an Illumina-specific variance-stabilizing transformation. BMC Research Notes, 2008, 1, 18.	1.4	13
39	Species-Specific Transcription in Mice Carrying Human Chromosome 21. Science, 2008, 322, 434-438.	12.6	260
40	Tissue-specific splicing factor gene expression signatures. Nucleic Acids Research, 2008, 36, 4823-4832.	14.5	172
41	Association of single-nucleotide polymorphisms in the cell cycle genes with breast cancer in the British population. Carcinogenesis, 2008, 29, 333-341.	2.8	68
42	Pediatric Malignant Germ Cell Tumors Show Characteristic Transcriptome Profiles. Cancer Research, 2008, 68, 4239-4247.	0.9	83
43	High-resolution aCCH and expression profiling identifies a novel genomic subtype of ER negative breast cancer. Genome Biology, 2007, 8, R215.	9.6	275
44	MicroRNA expression profiling of human breast cancer identifies new markers of tumor subtype. Genome Biology, 2007, 8, R214.	9.6	828
45	Global microRNA profiles in cervical squamous cell carcinoma depend on Drosha expression levels. Journal of Pathology, 2007, 212, 368-377.	4.5	162
46	A gene-expression signature to predict survival in breast cancer across independent data sets. Oncogene, 2007, 26, 1507-1516.	5.9	225
47	Using array-comparative genomic hybridization to define molecular portraits of primary breast cancers. Oncogene, 2007, 26, 1959-1970.	5.9	97
48	New androgen receptor genomic targets show an interaction with the ETS1 transcription factor. EMBO Reports, 2007, 8, 871-878.	4.5	240
49	Cell Cycle Genes Are the Evolutionarily Conserved Targets of the E2F4 Transcription Factor. PLoS ONE, 2007, 2, e1061.	2.5	51
50	Genome-wide identification of functionally distinct subsets of cellular mRNAs associated with two nucleocytoplasmic-shuttling mammalian splicing factors. Genome Biology, 2006, 7, R113.	9.6	68
51	A consensus prognostic gene expression classifier for ER positive breast cancer. Genome Biology, 2006, 7, R101.	9.6	82
52	MMASS: an optimized array-based method for assessing CpG island methylation. Nucleic Acids Research, 2006, 34, e136-e136.	14.5	44
53	Diversity of human U2AF splicing factors. FEBS Journal, 2006, 273, 4807-4816.	4.7	38
54	ASD: a bioinformatics resource on alternative splicing. Nucleic Acids Research, 2006, 34, D46-D55.	14.5	205

#	Article	IF	CITATIONS
55	PACK: Profile Analysis using Clustering and Kurtosis to find molecular classifiers in cancer. Bioinformatics, 2006, 22, 2269-2275.	4.1	61
56	A variational Bayesian mixture modelling framework for cluster analysis of gene-expression data. Bioinformatics, 2005, 21, 3025-3033.	4.1	73
57	Systematic genome-wide annotation of spliceosomal proteins reveals differential gene family expansion. Genome Research, 2005, 16, 66-77.	5.5	92
58	Diversity of Vertebrate Splicing Factor U2AF35. Journal of Biological Chemistry, 2004, 279, 27039-27049.	3.4	47
59	Expression microarray reproducibility is improved by optimising purification steps in RNA amplification and labelling. BMC Genomics, 2004, 5, 9.	2.8	45
60	Allosteric Antagonist Modulation of TRPV2 by Piperlongumine Impairs Glioblastoma Progression. SSRN Electronic Journal, 0, , .	0.4	1