

Pedro Alexandre Favoretto Galante

List of Publications by Year in descending order

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Version: 2024-02-01

97
papers

2,993
citations

186209

28
h-index

189801

50
g-index

110
all docs

110
docs citations

110
times ranked

5953
citing authors

#	ARTICLE	IF	CITATIONS
1	Monoallelic deleterious <i>MUTYH</i> germline variants as a driver for tumorigenesis. <i>Journal of Pathology</i> , 2022, 256, 214-222.	2.1	12
2	Identification of NID1 as a novel candidate susceptibility gene for familial non-medullary thyroid carcinoma using whole-exome sequencing. <i>Endocrine Connections</i> , 2022, 11, .	0.8	3
3	Whole-genome sequencing of 1,171 elderly admixed individuals from Brazil. <i>Nature Communications</i> , 2022, 13, 1004.	5.8	35
4	The RNA-Binding Protein Musashi1 Regulates a Network of Cell Cycle Genes in Group 4 Medulloblastoma. <i>Cells</i> , 2022, 11, 56.	1.8	3
5	Severe Acute Respiratory Syndrome Coronavirus 2 Variants of Concern: A Perspective for Emerging More Transmissible and Vaccine-Resistant Strains. <i>Viruses</i> , 2022, 14, 827.	1.5	14
6	Association between tumor mutational burden (TMB) and mutational profile and its effect on overall survival: A post hoc analysis of patients with TMB-high and TMB-low metastatic cancer treated with immune checkpoint inhibitors (ICI).. <i>Journal of Clinical Oncology</i> , 2022, 40, 2632-2632.	0.8	0
7	sideRETRO: a pipeline for identifying somatic and polymorphic insertions of processed pseudogenes or retrocopies. <i>Bioinformatics</i> , 2021, 37, 419-421.	1.8	7
8	Synergism of Proneurogenic miRNAs Provides a More Effective Strategy to Target Glioma Stem Cells. <i>Cancers</i> , 2021, 13, 289.	1.7	7
9	Deciphering the Role of Intestinal Crypt Cell Populations in Resistance to Chemotherapy. <i>Cancer Research</i> , 2021, 81, 2730-2744.	0.4	4
10	Reboot: a straightforward approach to identify genes and splicing isoforms associated with cancer patient prognosis. <i>NAR Cancer</i> , 2021, 3, zcab024.	1.6	8
11	Evidence of Cooperation between Hippo Pathway and RAS Mutation in Thyroid Carcinomas. <i>Cancers</i> , 2021, 13, 2306.	1.7	4
12	Molecular Signature Expands the Landscape of Driver Negative Thyroid Cancers. <i>Cancers</i> , 2021, 13, 5184.	1.7	0
13	Chemogenetic modulation of sensory neurons reveals their regulating role in melanoma progression. <i>Acta Neuropathologica Communications</i> , 2021, 9, 183.	2.4	21
14	The RNA-binding protein SERBP1 functions as a novel oncogenic factor in glioblastoma by bridging cancer metabolism and epigenetic regulation. <i>Genome Biology</i> , 2020, 21, 195.	3.8	55
15	Depletion of Ric-8B leads to reduced mTORC2 activity. <i>PLoS Genetics</i> , 2020, 16, e1008255.	1.5	3
16	Gene expression changes associated with trajectories of psychopathology in a longitudinal cohort of children and adolescents. <i>Translational Psychiatry</i> , 2020, 10, 99.	2.4	3
17	Genomic Biomarkers and Underlying Mechanism of Benefit from BCG Immunotherapy in Non-Muscle Invasive Bladder Cancer. <i>Bladder Cancer</i> , 2020, 6, 171-186.	0.2	4
18	Proneural and mesenchymal glioma stem cells display major differences in splicing and lncRNA profiles. <i>Npj Genomic Medicine</i> , 2020, 5, 2.	1.7	29

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19	Comprehensive germline mutation analysis and clinical profile in a large cohort of Brazilian xeroderma pigmentosum patients. <i>Journal of the European Academy of Dermatology and Venereology</i> , 2020, 34, 2392-2401.	1.3	17
20	Depletion of Ric-8B leads to reduced mTORC2 activity. , 2020, 16, e1008255.		0
21	Depletion of Ric-8B leads to reduced mTORC2 activity. , 2020, 16, e1008255.		0
22	Depletion of Ric-8B leads to reduced mTORC2 activity. , 2020, 16, e1008255.		0
23	Depletion of Ric-8B leads to reduced mTORC2 activity. , 2020, 16, e1008255.		0
24	Uncovering the mouse olfactory long non-coding transcriptome with a novel machine-learning model. <i>DNA Research</i> , 2019, 26, 365-378.	1.5	8
25	Retroposed copies of RET gene: a somatically acquired event in medullary thyroid carcinoma. <i>BMC Medical Genomics</i> , 2019, 12, 104.	0.7	10
26	The Effects of Neoadjuvant Chemoradiation in Locally Advanced Rectal Cancer—The Impact in Intratumoral Heterogeneity. <i>Frontiers in Oncology</i> , 2019, 9, 974.	1.3	20
27	Antagonism between the RNA-binding protein Musashi1 and miR-137 and its potential impact on neurogenesis and glioblastoma development. <i>Rna</i> , 2019, 25, 768-782.	1.6	25
28	Transposon insertion profiling by sequencing (TIPseq) for mapping LINE-1 insertions in the human genome. <i>Mobile DNA</i> , 2019, 10, 8.	1.3	22
29	Tumor mutational burden (TMB) and BCG responsiveness in high-risk non-muscle invasive bladder cancer (NMIBC).. <i>Journal of Clinical Oncology</i> , 2019, 37, 442-442.	0.8	2
30	Identification and Validation of Potential Differential miRNA Regulation via Alternative Polyadenylation. <i>Methods in Molecular Biology</i> , 2018, 1733, 87-92.	0.4	1
31	Patient-derived conditionally reprogrammed cells maintain intra-tumor genetic heterogeneity. <i>Scientific Reports</i> , 2018, 8, 4097.	1.6	34
32	<i>MRPL53</i>, a New Candidate Gene for Orofacial Clefting, Identified Using an eQTL Approach. <i>Journal of Dental Research</i> , 2018, 97, 33-40.	2.5	8
33	TSC2 rare germline variants in non-tuberous sclerosis patients with neuroendocrine neoplasias. <i>Endocrine-Related Cancer</i> , 2018, 25, L1-L5.	1.6	6
34	miRNA-based signatures in cerebrospinal fluid as potential diagnostic tools for early stage Parkinson’s disease. <i>Oncotarget</i> , 2018, 9, 17455-17465.	0.8	94
35	Histopathological Characterization and Whole Exome Sequencing of Ectopic Thyroid: Fetal Architecture in a Functional Ectopic Gland from Adult Patient. <i>International Journal of Endocrinology</i> , 2018, 2018, 1-10.	0.6	7
36	Tumor mutational burden (TMB), intratumoral genetic heterogeneity (ITGH) and BCG responsiveness in high-risk non-muscle invasive bladder cancer (NMIBC).. <i>Journal of Clinical Oncology</i> , 2018, 36, e16516-e16516.	0.8	1

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37	Intratumoral Genetic Heterogeneity in Rectal Cancer. <i>Annals of Surgery</i> , 2017, 265, e4-e6.	2.1	56
38	A straightforward assay to evaluate DNA integrity and optimize next-generation sequencing for clinical diagnosis in oncology. <i>Experimental and Molecular Pathology</i> , 2017, 103, 294-299.	0.9	18
39	A genetic cluster of patients with variant xeroderma pigmentosum with two different founder mutations. <i>British Journal of Dermatology</i> , 2017, 176, 1270-1278.	1.4	23
40	High IL-1R8 expression in breast tumors promotes tumor growth and contributes to impaired antitumor immunity. <i>Oncotarget</i> , 2017, 8, 49470-49483.	0.8	24
41	Unveiling the Impact of the Genomic Architecture on the Evolution of Vertebrate microRNAs. <i>Frontiers in Genetics</i> , 2017, 8, 34.	1.1	14
42	MiRIAD update: using alternative polyadenylation, protein interaction network analysis and additional species to enhance exploration of the role of intragenic miRNAs and their host genes. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	10
43	Measuring plasma levels of three microRNAs can improve the accuracy for identification of malignant breast lesions in women with BI-RADS 4 mammography. <i>Oncotarget</i> , 2017, 8, 83940-83948.	0.8	7
44	Functional genomics analyses of RNA-binding proteins reveal the splicing regulator SNRPB as an oncogenic candidate in glioblastoma. <i>Genome Biology</i> , 2016, 17, 125.	3.8	83
45	Host gene constraints and genomic context impact the expression and evolution of human microRNAs. <i>Nature Communications</i> , 2016, 7, 11438.	5.8	47
46	MicroRNA Expression Signature Is Altered in the Cardiac Remodeling Induced by High Fat Diets. <i>Journal of Cellular Physiology</i> , 2016, 231, 1771-1783.	2.0	27
47	Signaling transcript profile of the asexual intraerythrocytic development cycle of <i>Plasmodium falciparum</i> induced by melatonin and cAMP. <i>Genes and Cancer</i> , 2016, 7, 323-339.	0.6	16
48	A Mouse Model of Targeted Musashi1 Expression in Whole Intestinal Epithelium Suggests Regulatory Roles in Cell Cycle and Stemness. <i>Stem Cells</i> , 2015, 33, 3621-3634.	1.4	25
49	Comprehensive cancer-gene panels can be used to estimate mutational load and predict clinical benefit to PD-1 blockade in clinical practice. <i>Oncotarget</i> , 2015, 6, 34221-34227.	0.8	198
50	Alternative Polyadenylation Allows Differential Negative Feedback of Human miRNA miR-579 on Its Host Gene ZFR. <i>PLoS ONE</i> , 2015, 10, e0121507.	1.1	24
51	The use of personalized biomarkers and liquid biopsies to monitor treatment response and disease recurrence in locally advanced rectal cancer after neoadjuvant chemoradiation. <i>Oncotarget</i> , 2015, 6, 38360-38371.	0.8	52
52	Identification of agonists for a group of human odorant receptors. <i>Frontiers in Pharmacology</i> , 2015, 6, 35.	1.6	37
53	Comprehensive evaluation of the effectiveness of gene expression signatures to predict complete response to neoadjuvant chemoradiotherapy and guide surgical intervention in rectal cancer. <i>Cancer Genetics</i> , 2015, 208, 319-326.	0.2	45
54	A Genome-Wide Landscape of Retrocopies in Primate Genomes. <i>Genome Biology and Evolution</i> , 2015, 7, 2265-2275.	1.1	46

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55	ICRmax: An optimized approach to detect tumor-specific interchromosomal rearrangements for clinical application. <i>Genomics</i> , 2015, 105, 265-272.	1.3	4
56	Recurrent somatic mutation in DROSHA induces microRNA profile changes in Wilms tumour. <i>Nature Communications</i> , 2014, 5, 4039.	5.8	159
57	Overexpression of miR-21-5p as a predictive marker for complete tumor regression to neoadjuvant chemoradiotherapy in rectal cancer patients. <i>BMC Medical Genomics</i> , 2014, 7, 68.	0.7	58
58	miRIADâ€™integrating microRNA inter- and intragenic data. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, .	1.4	85
59	Mutational analysis of genes coding for cell surface proteins in colorectal cancer cell lines reveal novel altered pathways, druggable mutations and mutated epitopes for targeted therapy. <i>Oncotarget</i> , 2014, 5, 9199-9213.	0.8	31
60	Setting Up an Intronic miRNA Database. <i>Methods in Molecular Biology</i> , 2013, 936, 69-76.	0.4	6
61	The Human Cell Surfaceome of Breast Tumors. <i>BioMed Research International</i> , 2013, 2013, 1-11.	0.9	6
62	Gene Copy-Number Polymorphism Caused by Retrotransposition in Humans. <i>PLoS Genetics</i> , 2013, 9, e1003242.	1.5	88
63	RCpedia: a database of retrocopied genes. <i>Bioinformatics</i> , 2013, 29, 1235-1237.	1.8	32
64	SPLOOCE. <i>RNA Biology</i> , 2012, 9, 1339-1343.	1.5	7
65	SurfaceomeDB: a cancer-orientated database for genes encoding cell surface proteins. <i>Cancer Immunity</i> , 2012, 12, 15.	3.2	7
66	HPV-58 Molecular Variants Exhibit Different Transcriptional Activity. <i>Intervirology</i> , 2011, 54, 146-150.	1.2	8
67	Temporal blastemal cell gene expression analysis in the kidney reveals new Wnt and related signaling pathway genes to be essential for Wilms' tumor onset. <i>Cell Death and Disease</i> , 2011, 2, e224-e224.	2.7	23
68	PVALB, a New $\frac{1}{4}$ thle Adenoma Diagnostic Marker Identified through Gene Expression. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2011, 96, E151-E160.	1.8	22
69	Analysis of allelic differential expression in the human genome using allele-specific serial analysis of gene expression tags. <i>Genome</i> , 2011, 54, 120-127.	0.9	5
70	Alternative splicing and genetic diversity: silencers are more frequently modified by SNVs associated with alternative exon/intron borders. <i>Nucleic Acids Research</i> , 2011, 39, 4942-4948.	6.5	11
71	Distinct patterns of somatic alterations in a lymphoblastoid and a tumor genome derived from the same individual. <i>Nucleic Acids Research</i> , 2011, 39, 6056-6068.	6.5	19
72	Common Promoter Elements in Odorant and Vomeronasal Receptor Genes. <i>PLoS ONE</i> , 2011, 6, e29065.	1.1	32

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73	A potential role for intragenic miRNAs on their hosts' interactome. BMC Genomics, 2010, 11, 533.	1.2	142
74	Alternative splicing enriched cDNA libraries identify breast cancer-associated transcripts. BMC Genomics, 2010, 11, S4.	1.2	10
75	DSEGeo: Software tools for cross-platform analysis of gene expression data in GEO. Journal of Biomedical Informatics, 2010, 43, 709-715.	2.5	13
76	Systematic detection of putative tumor suppressor genes through the combined use of exome and transcriptome sequencing. Genome Biology, 2010, 11, R114.	13.9	35
77	Application of Bioinformatics in Cancer Research. , 2010, , 211-233.		7
78	Transcriptome-guided characterization of genomic rearrangements in a breast cancer cell line. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1886-1891.	3.3	104
79	A comprehensive in silico expression analysis of RNA binding proteins in normal and tumor tissue; identification of potential players in tumor formation. RNA Biology, 2009, 6, 426-433.	1.5	51
80	Bioinformatics construction of the human cell surfaceome. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16752-16757.	3.3	119
81	A score system for quality evaluation of RNA sequence tags: an improvement for gene expression profiling. BMC Bioinformatics, 2009, 10, 170.	1.2	2
82	Evaluation of a large-scale biomedical data annotation initiative. BMC Bioinformatics, 2009, 10, S10.	1.2	16
83	Towards large-scale sample annotation in gene expression repositories. BMC Bioinformatics, 2009, 10, S9.	1.2	7
84	Identification of FAM46D as a novel cancer/testis antigen using EST data and serological analysis. Genomics, 2009, 94, 153-160.	1.3	23
85	Different Evolutionary Strategies for the Origin of Caspase-1 Inhibitors. Journal of Molecular Evolution, 2008, 66, 591-597.	0.8	14
86	Differential gene expression analysis of iodide-treated rat thyroid follicular cell line PCCI3. Genomics, 2008, 91, 356-366.	1.3	29
87	Genome-Wide Detection of Serpentine Receptor-Like Proteins in Malaria Parasites. PLoS ONE, 2008, 3, e1889.	1.1	43
88	Automatic correspondence of tags and genes (ACTG): a tool for the analysis of SAGE, MPSS and SBS data. Bioinformatics, 2007, 23, 903-905.	1.8	10
89	Sense-antisense pairs in mammals: functional and evolutionary considerations. Genome Biology, 2007, 8, R40.	13.9	55
90	Alternative splicing: a bioinformatics perspective. Molecular BioSystems, 2007, 3, 473.	2.9	13

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91	Identification of potential regulatory motifs in odorant receptor genes by analysis of promoter sequences. <i>Genome Research</i> , 2006, 16, 1091-1098.	2.4	59
92	The impact of SNPs on the interpretation of SAGE and MPSS experimental data. <i>Nucleic Acids Research</i> , 2004, 32, 6104-6110.	6.5	34
93	Detection and evaluation of intron retention events in the human transcriptome. <i>Rna</i> , 2004, 10, 757-765.	1.6	193
94	Splicing factors are differentially expressed in tumors. <i>Genetics and Molecular Research</i> , 2004, 3, 512-20.	0.3	21
95	A novel human G protein-coupled receptor is over-expressed in prostate cancer. <i>Genetics and Molecular Research</i> , 2004, 3, 521-31.	0.3	6
96	ORESTES are enriched in rare exon usage variants affecting the encoded proteins. <i>Comptes Rendus - Biologies</i> , 2003, 326, 979-985.	0.1	13
97	The generation and utilization of a cancer-oriented representation of the human transcriptome by using expressed sequence tags. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 13418-13423.	3.3	105