

Paolo Provero

List of Publications by Year in descending order

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Version: 2024-02-01

88
papers

4,758
citations

117625

34
h-index

106344

65
g-index

98
all docs

98
docs citations

98
times ranked

9832
citing authors

#	ARTICLE	IF	CITATIONS
1	Cancer Metabolic Subtypes and Their Association with Molecular and Clinical Features. <i>Cancers</i> , 2022, 14, 2145.	3.7	3
2	The My Active and Healthy Aging ICT platform prevents quality of life decline in older adults: a randomised controlled study. <i>Age and Ageing</i> , 2021, 50, 1261-1267.	1.6	18
3	IL17A critically shapes the transcriptional program of fibroblasts in pancreatic cancer and switches on their protumorigenic functions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	27
4	Deletion of a pseudogene within a fragile site triggers the oncogenic expression of the mitotic CCSE1 gene. <i>Life Science Alliance</i> , 2021, 4, e202101019.	2.8	2
5	The heme synthesis-export system regulates the tricarboxylic acid cycle flux and oxidative phosphorylation. <i>Cell Reports</i> , 2021, 35, 109252.	6.4	29
6	ESDN inhibits melanoma progression by blocking E-selectin expression in endothelial cells via STAT3. <i>Cancer Letters</i> , 2021, 510, 13-23.	7.2	4
7	A live single-cell reporter assay links intratumor heterogeneity to metastatic proclivity in Ewing sarcoma. <i>Science Advances</i> , 2021, 7, .	10.3	5
8	Meta-Analysis of Microdissected Breast Tumors Reveals Genes Regulated in the Stroma but Hidden in Bulk Analysis. <i>Cancers</i> , 2021, 13, 3371.	3.7	9
9	Pseudogenes as Competitive Endogenous RNAs: Target Prediction and Validation. <i>Methods in Molecular Biology</i> , 2021, 2324, 115-129.	0.9	0
10	The chromatin landscape of primary synovial sarcoma organoids is linked to specific epigenetic mechanisms and dependencies. <i>Life Science Alliance</i> , 2021, 4, e202000808.	2.8	18
11	Optic nerve sheath diameter asymmetry in healthy subjects and patients with intracranial hypertension. <i>Neurological Sciences</i> , 2020, 41, 329-333.	1.9	23
12	Interference with the Cannabinoid Receptor CB1R Results in Miswiring of GnRH3 and AgRP1 Axons in Zebrafish Embryos. <i>International Journal of Molecular Sciences</i> , 2020, 21, 168.	4.1	11
13	LIN28B Underlies the Pathogenesis of a Subclass of Ewing Sarcoma. <i>Cell Reports</i> , 2020, 30, 4567-4583.e5.	6.4	20
14	Behavioral and Psychological Effects of Coronavirus Disease-19 Quarantine in Patients With Dementia. <i>Frontiers in Psychiatry</i> , 2020, 11, 578015.	2.6	157
15	Liver-Specific siRNA-Mediated Stat3 or C3 Knockdown Improves the Outcome of Experimental Autoimmune Myocarditis. <i>Molecular Therapy - Methods and Clinical Development</i> , 2020, 18, 62-72.	4.1	5
16	MiR-100 is a predictor of endocrine responsiveness and prognosis in patients with operable luminal breast cancer. <i>ESMO Open</i> , 2020, 5, e000937.	4.5	10
17	Differential Co-Expression Analyses Allow the Identification of Critical Signalling Pathways Altered during Tumour Transformation and Progression. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9461.	4.1	27
18	Proteomics-Based Evidence for a Pro-Oncogenic Role of ESRP1 in Human Colorectal Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2020, 21, 575.	4.1	12

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19	eQTL Mapping Using Transcription Factor Affinity. <i>Methods in Molecular Biology</i> , 2020, 2082, 39-49.	0.9	1
20	The Length of the Expressed 3' UTR Is an Intermediate Molecular Phenotype Linking Genetic Variants to Complex Diseases. <i>Frontiers in Genetics</i> , 2019, 10, 714.	2.3	23
21	SP1 and STAT3 Functionally Synergize to Induce the RhoU Small GTPase and a Subclass of Non-canonical WNT Responsive Genes Correlating with Poor Prognosis in Breast Cancer. <i>Cancers</i> , 2019, 11, 101.	3.7	21
22	Renal Regenerative Potential of Extracellular Vesicles Derived from miRNA-Engineered Mesenchymal Stromal Cells. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2381.	4.1	40
23	Reciprocal modulation of mesenchymal stem cells and tumor cells promotes lung cancer metastasis. <i>EBioMedicine</i> , 2018, 29, 128-145.	6.1	50
24	An Integrated Genome-wide CRISPRa Approach to Functionalize lncRNAs in Drug Resistance. <i>Cell</i> , 2018, 173, 649-664.e20.	28.9	238
25	Evolutionary Rewiring of Human Regulatory Networks by Waves of Genome Expansion. <i>American Journal of Human Genetics</i> , 2018, 102, 207-218.	6.2	31
26	IRF4 Mediates the Oncogenic Effects of STAT3 in Anaplastic Large Cell Lymphomas. <i>Cancers</i> , 2018, 10, 21.	3.7	28
27	Soluble Neuregulin1 Down-Regulates Myelination Genes in Schwann Cells. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 157.	2.9	11
28	Choice of Alternative Polyadenylation Sites, Mediated by the RNA-Binding Protein Elavl3, Plays a Role in Differentiation of Inhibitory Neuronal Progenitors. <i>Frontiers in Cellular Neuroscience</i> , 2018, 12, 518.	3.7	33
29	An exclusive cellular and molecular network governs intestinal smooth muscle cell differentiation in vertebrates. <i>Development (Cambridge)</i> , 2017, 144, 464-478.	2.5	31
30	Rictor/mTORC2 deficiency enhances keratinocyte stress tolerance via mitohormesis. <i>Cell Death and Differentiation</i> , 2017, 24, 731-746.	11.2	24
31	PERK induces resistance to cell death elicited by endoplasmic reticulum stress and chemotherapy. <i>Molecular Cancer</i> , 2017, 16, 91.	19.2	115
32	The scaffold protein p140Cap limits ERBB2-mediated breast cancer progression interfering with Rac GTPase-controlled circuitries. <i>Nature Communications</i> , 2017, 8, 14797.	12.8	26
33	Dysregulation of Blimp1 transcriptional repressor unleashes p130Cas/ErbB2 breast cancer invasion. <i>Scientific Reports</i> , 2017, 7, 1145.	3.3	17
34	The IKK/NF- κ B signaling pathway requires Morgana to drive breast cancer metastasis. <i>Nature Communications</i> , 2017, 8, 1636.	12.8	73
35	A functional strategy to characterize expression Quantitative Trait Loci. <i>Human Genetics</i> , 2017, 136, 1477-1487.	3.8	4
36	MicroRNAs-143 and -145 induce epithelial to mesenchymal transition and modulate the expression of junction proteins. <i>Cell Death and Differentiation</i> , 2017, 24, 1750-1760.	11.2	26

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37	In silico prediction of lncRNA function using tissue specific and evolutionary conserved expression. BMC Bioinformatics, 2017, 18, 144.	2.6	42
38	DNA methylation changes measured in pre-diagnostic peripheral blood samples are associated with smoking and lung cancer risk. International Journal of Cancer, 2017, 140, 50-61.	5.1	115
39	Roar: detecting alternative polyadenylation with standard mRNA sequencing libraries. BMC Bioinformatics, 2016, 17, 423.	2.6	64
40	The fusion protein SS18-SSX1 employs core Wnt pathway transcription factors to induce a partial Wnt signature in synovial sarcoma. Scientific Reports, 2016, 6, 22113.	3.3	33
41	Deep Sequencing Reveals a Novel miR-22 Regulatory Network with Therapeutic Potential in Rhabdomyosarcoma. Cancer Research, 2016, 76, 6095-6106.	0.9	30
42	Alternative Polyadenylation in Triple-Negative Breast Tumors Allows NRAS and c-JUN to Bypass PUMILIO Posttranscriptional Regulation. Cancer Research, 2016, 76, 7231-7241.	0.9	47
43	miR-146a Exerts Differential Effects on Melanoma Growth and Metastatization. Molecular Cancer Research, 2016, 14, 548-562.	3.4	39
44	miR-214 and miR-148b Targeting Inhibits Dissemination of Melanoma and Breast Cancer. Cancer Research, 2016, 76, 5151-5162.	0.9	65
45	The RNA Binding Protein IMP2 Preserves Glioblastoma Stem Cells by Preventing let-7 Target Gene Silencing. Cell Reports, 2016, 15, 1634-1647.	6.4	103
46	Subtype-Specific Metagene-Based Prediction of Outcome after Neoadjuvant and Adjuvant Treatment in Breast Cancer. Clinical Cancer Research, 2016, 22, 337-345.	7.0	58
47	Chromas from chromatin: sonification of the epigenome. F1000Research, 2016, 5, 274.	1.6	3
48	Hepatocyte Growth Factor-mediated satellite cells niche perturbation promotes development of distinct sarcoma subtypes. ELife, 2016, 5, .	6.0	5
49	AKI Recovery Induced by Mesenchymal Stromal Cell-Derived Extracellular Vesicles Carrying MicroRNAs. Journal of the American Society of Nephrology: JASN, 2015, 26, 2349-2360.	6.1	212
50	The Dlx5 and Foxg1 transcription factors, linked via miRNA-9 and -200, are required for the development of the olfactory and GnRH system. Molecular and Cellular Neurosciences, 2015, 68, 103-119.	2.2	51
51	Combined CSL and p53 downregulation promotes cancer-associated fibroblast activation. Nature Cell Biology, 2015, 17, 1193-1204.	10.3	170
52	Total Binding Affinity Profiles of Regulatory Regions Predict Transcription Factor Binding and Gene Expression in Human Cells. PLoS ONE, 2015, 10, e0143627.	2.5	17
53	OTX2 regulates the expression of TAp63 leading to macular and cochlear neuroepithelium development. Aging, 2015, 7, 928-936.	3.1	7
54	miR-223 Is a Coordinator of Breast Cancer Progression as Revealed by Bioinformatics Predictions. PLoS ONE, 2014, 9, e84859.	2.5	61

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55	STAT3-mediated activation of microRNA cluster 17Å92 promotes proliferation and survival of ALK-positive anaplastic large cell lymphoma. <i>Haematologica</i> , 2014, 99, 116-124.	3.5	50
56	Partial inhibition of gp130-Jak-Stat3 signaling prevents Wntâ€“Î²-cateninâ€“mediated intestinal tumor growth and regeneration. <i>Science Signaling</i> , 2014, 7, ra92.	3.6	68
57	Postâ€“transcriptional gene expression control by <sc>NANOS</sc> is upâ€“regulated and functionally important in <sc>pR</sc> bâ€“deficient cells. <i>EMBO Journal</i> , 2014, 33, 2201-2215.	7.8	25
58	Morgana acts as a protoâ€“oncogene through inhibition of a <sc>ROCKâ€“PTEN</sc> pathway. <i>Journal of Pathology</i> , 2014, 234, 152-163.	4.5	21
59	miR-221/222 control luminal breast cancer tumor progression by regulating different targets. <i>Cell Cycle</i> , 2014, 13, 1811-1826.	2.6	38
60	Extracellular Vesicles Released from Mesenchymal Stromal Cells Modulate miRNA in Renal Tubular Cells and Inhibit ATP Depletion Injury. <i>Stem Cells and Development</i> , 2014, 23, 1809-1819.	2.1	121
61	Genome-wide Identification and Characterization of Fixed Human-Specific Regulatory Regions. <i>American Journal of Human Genetics</i> , 2014, 95, 39-48.	6.2	23
62	Targeting Cancer Stemâ€“like Cells as an Approach to Defeating Cellular Heterogeneity in Ewing Sarcoma. <i>Cancer Research</i> , 2014, 74, 6610-6622.	0.9	28
63	Accurate Data Processing Improves the Reliability of Affymetrix Gene Expression Profiles from FFPE Samples. <i>PLoS ONE</i> , 2014, 9, e86511.	2.5	10
64	Identification of Functional cis-regulatory Polymorphisms in the Human Genome. <i>Human Mutation</i> , 2013, 34, 735-742.	2.5	8
65	Drug repositioning for orphan genetic diseases through Conserved Anticoexpressed Gene Clusters (CAGCs). <i>BMC Bioinformatics</i> , 2013, 14, 288.	2.6	11
66	Profiling, Bioinformatic, and Functional Data on the Developing Olfactory/GnRH System Reveal Cellular and Molecular Pathways Essential for This Process and Potentially Relevant for the Kallmann Syndrome. <i>Frontiers in Endocrinology</i> , 2013, 4, 203.	3.5	9
67	Identification of p130Cas/ErbB2-dependent invasive signatures in transformed mammary epithelial cells. <i>Cell Cycle</i> , 2013, 12, 2409-2422.	2.6	18
68	A TARBP2-Dependent miRNA Expression Profile Underlies Cancer Stem Cell Properties and Provides Candidate Therapeutic Reagents in Ewing Sarcoma. <i>Cancer Cell</i> , 2012, 21, 807-821.	16.8	89
69	Shortening of 3â€“UTRs Correlates with Poor Prognosis in Breast and Lung Cancer. <i>PLoS ONE</i> , 2012, 7, e31129.	2.5	95
70	A Signature Inferred from Drosophila Mitotic Genes Predicts Survival of Breast Cancer Patients. <i>PLoS ONE</i> , 2011, 6, e14737.	2.5	9
71	Identification of Prognostic Molecular Features in the Reactive Stroma of Human Breast and Prostate Cancer. <i>PLoS ONE</i> , 2011, 6, e18640.	2.5	140
72	Toward robust network based complex systems: from evolutionary cellular automata to biological models. <i>Intelligenza Artificiale</i> , 2011, 5, 37-47.	1.6	10

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73	p130Cas promotes invasiveness of three-dimensional ErbB2-transformed mammary acinar structures by enhanced activation of mTOR/p70S6K and Rac1. <i>European Journal of Cell Biology</i> , 2011, 90, 237-248.	3.6	29
74	A comparison of machine learning techniques for survival prediction in breast cancer. <i>BioData Mining</i> , 2011, 4, 12.	4.0	41
75	An atlas of tissue-specific conserved coexpression for functional annotation and disease gene prediction. <i>European Journal of Human Genetics</i> , 2011, 19, 1173-1180.	2.8	49
76	Evolution of Promoter Affinity for Transcription Factors in the Human Lineage. <i>Molecular Biology and Evolution</i> , 2011, 28, 2173-2183.	8.9	28
77	Identification of functional TFAP2A and SP1 binding sites in new TFAP2A-modulated genes. <i>BMC Genomics</i> , 2010, 11, 355.	2.8	30
78	A STAT3-mediated metabolic switch is involved in tumour transformation and STAT3 addiction. <i>Aging</i> , 2010, 2, 823-842.	3.1	231
79	Constitutively Active Stat3 Enhances Neu-Mediated Migration and Metastasis in Mammary Tumors via Upregulation of Cten. <i>Cancer Research</i> , 2010, 70, 2558-2567.	0.9	131
80	EWS-FLI-1 modulates miRNA145 and <i>SOX2</i> expression to initiate mesenchymal stem cell reprogramming toward Ewing sarcoma cancer stem cells. <i>Genes and Development</i> , 2010, 24, 916-932.	5.9	254
81	Modeling the Spread of Vector-Borne Diseases on Bipartite Networks. <i>PLoS ONE</i> , 2010, 5, e13796.	2.5	27
82	Epigenetic Features of Human Mesenchymal Stem Cells Determine Their Permissiveness for Induction of Relevant Transcriptional Changes by SYT-SSX1. <i>PLoS ONE</i> , 2009, 4, e7904.	2.5	40
83	Identification of Cancer Stem Cells in Ewing's Sarcoma. <i>Cancer Research</i> , 2009, 69, 1776-1781.	0.9	291
84	Genome-wide discovery of functional transcription factor binding sites by comparative genomics: The case of Stat3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5117-5122.	7.1	73
85	EWS-FLI-1 Expression Triggers a Ewing's Sarcoma Initiation Program in Primary Human Mesenchymal Stem Cells. <i>Cancer Research</i> , 2008, 68, 2176-2185.	0.9	293
86	Prediction of Human Disease Genes by Human-Mouse Conserved Coexpression Analysis. <i>PLoS Computational Biology</i> , 2008, 4, e1000043.	3.2	119
87	Functional Annotation and Identification of Candidate Disease Genes by Computational Analysis of Normal Tissue Gene Expression Data. <i>PLoS ONE</i> , 2008, 3, e2439.	2.5	20
88	CLOE: identification of putative functional relationships among genes by comparison of expression profiles between two species. <i>BMC Bioinformatics</i> , 2004, 5, 179.	2.6	21