List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1756078/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	EWS-FLI-1 Expression Triggers a Ewing's Sarcoma Initiation Program in Primary Human Mesenchymal Stem Cells. Cancer Research, 2008, 68, 2176-2185.	0.9	293
2	Identification of Cancer Stem Cells in Ewing's Sarcoma. Cancer Research, 2009, 69, 1776-1781.	0.9	291
3	EWS-FLI-1 modulates miRNA145 and <i>SOX2</i> expression to initiate mesenchymal stem cell reprogramming toward Ewing sarcoma cancer stem cells. Genes and Development, 2010, 24, 916-932.	5.9	254
4	An Integrated Genome-wide CRISPRa Approach to Functionalize IncRNAs in Drug Resistance. Cell, 2018, 173, 649-664.e20.	28.9	238
5	A STAT3-mediated metabolic switch is involved in tumour transformation and STAT3 addiction. Aging, 2010, 2, 823-842.	3.1	231
6	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
7	Combined CSL and p53 downregulation promotes cancer-associated fibroblast activation. Nature Cell Biology, 2015, 17, 1193-1204.	10.3	170
8	Behavioral and Psychological Effects of Coronavirus Disease-19 Quarantine in Patients With Dementia. Frontiers in Psychiatry, 2020, 11, 578015.	2.6	157
9	Identification of Prognostic Molecular Features in the Reactive Stroma of Human Breast and Prostate Cancer. PLoS ONE, 2011, 6, e18640.	2.5	140
10	Constitutively Active Stat3 Enhances Neu-Mediated Migration and Metastasis in Mammary Tumors via Upregulation of Cten. Cancer Research, 2010, 70, 2558-2567.	0.9	131
11	Extracellular Vesicles Released from Mesenchymal Stromal Cells Modulate miRNA in Renal Tubular Cells and Inhibit ATP Depletion Injury. Stem Cells and Development, 2014, 23, 1809-1819.	2.1	121
12	Prediction of Human Disease Genes by Human-Mouse Conserved Coexpression Analysis. PLoS Computational Biology, 2008, 4, e1000043.	3.2	119
13	PERK induces resistance to cell death elicited by endoplasmic reticulum stress and chemotherapy. Molecular Cancer, 2017, 16, 91.	19.2	115
14	DNA methylation changes measured in preâ€diagnostic peripheral blood samples are associated with smoking and lung cancer risk. International Journal of Cancer, 2017, 140, 50-61.	5.1	115
15	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
16	Shortening of 3′UTRs Correlates with Poor Prognosis in Breast and Lung Cancer. PLoS ONE, 2012, 7, e31129.	2.5	95
17	A TARBP2-Dependent miRNA Expression Profile Underlies Cancer Stem Cell Properties and Provides Candidate Therapeutic Reagents in Ewing Sarcoma. Cancer Cell, 2012, 21, 807-821.	16.8	89
18	Genome-wide discovery of functional transcription factor binding sites by comparative genomics: The case of Stat3. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5117-5122.	7.1	73

#	Article	IF	CITATIONS
19	The IKK/NF-κB signalingÂpathway requires Morgana to drive breast cancer metastasis. Nature Communications, 2017, 8, 1636.	12.8	73
20	Partial inhibition of gp130-Jak-Stat3 signaling prevents Wnt–β-catenin–mediated intestinal tumor growth and regeneration. Science Signaling, 2014, 7, ra92.	3.6	68
21	miR-214 and miR-148b Targeting Inhibits Dissemination of Melanoma and Breast Cancer. Cancer Research, 2016, 76, 5151-5162.	0.9	65
22	Roar: detecting alternative polyadenylation with standard mRNA sequencing libraries. BMC Bioinformatics, 2016, 17, 423.	2.6	64
23	miR-223 Is a Coordinator of Breast Cancer Progression as Revealed by Bioinformatics Predictions. PLoS ONE, 2014, 9, e84859.	2.5	61
24	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
25	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
26	STAT3-mediated activation of microRNA cluster 17Â92 promotes proliferation and survival of ALK-positive anaplastic large cell lymphoma. Haematologica, 2014, 99, 116-124.	3.5	50
27	Reciprocal modulation of mesenchymal stem cells and tumor cells promotes lung cancer metastasis. EBioMedicine, 2018, 29, 128-145.	6.1	50
28	An atlas of tissue-specific conserved coexpression for functional annotation and disease gene prediction. European Journal of Human Genetics, 2011, 19, 1173-1180.	2.8	49
29	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
30	In silico prediction of IncRNA function using tissue specific and evolutionary conserved expression. BMC Bioinformatics, 2017, 18, 144.	2.6	42
31	A comparison of machine learning techniques for survival prediction in breast cancer. BioData Mining, 2011, 4, 12.	4.0	41
32	Epigenetic Features of Human Mesenchymal Stem Cells Determine Their Permissiveness for Induction of Relevant Transcriptional Changes by SYT-SSX1. PLoS ONE, 2009, 4, e7904.	2.5	40
33	Renal Regenerative Potential of Extracellular Vesicles Derived from miRNA-Engineered Mesenchymal Stromal Cells. International Journal of Molecular Sciences, 2019, 20, 2381.	4.1	40
34	miR-146a Exerts Differential Effects on Melanoma Growth and Metastatization. Molecular Cancer Research, 2016, 14, 548-562.	3.4	39
35	miR-221/222 control luminal breast cancer tumor progression by regulating different targets. Cell Cycle, 2014, 13, 1811-1826.	2.6	38
36	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

#	Article	IF	CITATIONS
37	Choice of Alternative Polyadenylation Sites, Mediated by the RNA-Binding Protein Elavl3, Plays a Role in Differentiation of Inhibitory Neuronal Progenitors. Frontiers in Cellular Neuroscience, 2018, 12, 518.	3.7	33
38	An exclusive cellular and molecular network governs intestinal smooth muscle cell differentiation in vertebrates. Development (Cambridge), 2017, 144, 464-478.	2.5	31
39	Evolutionary Rewiring of Human Regulatory Networks by Waves of Genome Expansion. American Journal of Human Genetics, 2018, 102, 207-218.	6.2	31
40	Identification of functional TFAP2A and SP1 binding sites in new TFAP2A-modulated genes. BMC Genomics, 2010, 11, 355.	2.8	30
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	p130Cas promotes invasiveness of three-dimensional ErbB2-transformed mammary acinar structures by enhanced activation of mTOR/p70S6K and Rac1. European Journal of Cell Biology, 2011, 90, 237-248.	3.6	29
43	The heme synthesis-export system regulates the tricarboxylic acid cycle flux and oxidative phosphorylation. Cell Reports, 2021, 35, 109252.	6.4	29
44	Evolution of Promoter Affinity for Transcription Factors in the Human Lineage. Molecular Biology and Evolution, 2011, 28, 2173-2183.	8.9	28
45	Targeting Cancer Stem–like Cells as an Approach to Defeating Cellular Heterogeneity in Ewing Sarcoma. Cancer Research, 2014, 74, 6610-6622.	0.9	28
46	IRF4 Mediates the Oncogenic Effects of STAT3 in Anaplastic Large Cell Lymphomas. Cancers, 2018, 10, 21.	3.7	28
47	Differential Co-Expression Analyses Allow the Identification of Critical Signalling Pathways Altered during Tumour Transformation and Progression. International Journal of Molecular Sciences, 2020, 21, 9461.	4.1	27
48	IL17A critically shapes the transcriptional program of fibroblasts in pancreatic cancer and switches on their protumorigenic functions. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	27
49	Modeling the Spread of Vector-Borne Diseases on Bipartite Networks. PLoS ONE, 2010, 5, e13796.	2.5	27
50	The scaffold protein p140Cap limits ERBB2-mediated breast cancer progression interfering with Rac GTPase-controlled circuitries. Nature Communications, 2017, 8, 14797.	12.8	26
51	MicroRNAs-143 and -145 induce epithelial to mesenchymal transition and modulate the expression of junction proteins. Cell Death and Differentiation, 2017, 24, 1750-1760.	11.2	26
52	Postâ€ŧranscriptional gene expression control by <scp>NANOS</scp> is upâ€regulated and functionally important in <scp>pR</scp> bâ€deficient cells. EMBO Journal, 2014, 33, 2201-2215.	7.8	25
53	Rictor/mTORC2 deficiency enhances keratinocyte stress tolerance via mitohormesis. Cell Death and Differentiation, 2017, 24, 731-746.	11.2	24
54	Genome-wide Identification and Characterization of Fixed Human-Specific Regulatory Regions. American Journal of Human Genetics, 2014, 95, 39-48.	6.2	23

#	Article	IF	CITATIONS
55	The Length of the Expressed 3′ UTR Is an Intermediate Molecular Phenotype Linking Genetic Variants to Complex Diseases. Frontiers in Genetics, 2019, 10, 714.	2.3	23
56	Optic nerve sheath diameter asymmetry in healthy subjects and patients with intracranial hypertension. Neurological Sciences, 2020, 41, 329-333.	1.9	23
57	CLOE: identification of putative functional relationships among genes by comparison of expression profiles between two species. BMC Bioinformatics, 2004, 5, 179.	2.6	21
58	Morgana acts as a protoâ€oncogene through inhibition of a <scp>ROCK–PTEN</scp> pathway. Journal of Pathology, 2014, 234, 152-163.	4.5	21
59	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. Cancers, 2019, 11, 101.	3.7	21
60	LIN28B Underlies the Pathogenesis of a Subclass of Ewing Sarcoma. Cell Reports, 2020, 30, 4567-4583.e5.	6.4	20
61	Functional Annotation and Identification of Candidate Disease Genes by Computational Analysis of Normal Tissue Gene Expression Data. PLoS ONE, 2008, 3, e2439.	2.5	20
62	Identification of p130Cas/ErbB2-dependent invasive signatures in transformed mammary epithelial cells. Cell Cycle, 2013, 12, 2409-2422.	2.6	18
63	The My Active and Healthy Aging ICT platform prevents quality of life decline in older adults: a randomised controlled study. Age and Ageing, 2021, 50, 1261-1267.	1.6	18
64	The chromatin landscape of primary synovial sarcoma organoids is linked to specific epigenetic mechanisms and dependencies. Life Science Alliance, 2021, 4, e202000808.	2.8	18
65	Dysregulation of Blimp1 transcriptional repressor unleashes p130Cas/ErbB2 breast cancer invasion. Scientific Reports, 2017, 7, 1145.	3.3	17
66	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
67	Proteomics-Based Evidence for a Pro-Oncogenic Role of ESRP1 in Human Colorectal Cancer Cells. International Journal of Molecular Sciences, 2020, 21, 575.	4.1	12
68	Drug repositioning for orphan genetic diseases through Conserved Anticoexpressed Gene Clusters (CAGCs). BMC Bioinformatics, 2013, 14, 288.	2.6	11
69	Soluble Neuregulin1 Down-Regulates Myelination Genes in Schwann Cells. Frontiers in Molecular Neuroscience, 2018, 11, 157.	2.9	11
70	Interference with the Cannabinoid Receptor CB1R Results in Miswiring of GnRH3 and AgRP1 Axons in Zebrafish Embryos. International Journal of Molecular Sciences, 2020, 21, 168.	4.1	11
71	Toward robust network based complex systems: from evolutionary cellular automata to biological models. Intelligenza Artificiale, 2011, 5, 37-47.	1.6	10
72	MiR-100 is a predictor of endocrine responsiveness and prognosis in patients with operable luminal breast cancer. ESMO Open, 2020, 5, e000937.	4.5	10

#	Article	IF	CITATIONS
73	Accurate Data Processing Improves the Reliability of Affymetrix Gene Expression Profiles from FFPE Samples. PLoS ONE, 2014, 9, e86511.	2.5	10
74	A Signature Inferred from Drosophila Mitotic Genes Predicts Survival of Breast Cancer Patients. PLoS ONE, 2011, 6, e14737.	2.5	9
75	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. Frontiers in Endocrinology, 2013, 4, 203.	3.5	9
76	Meta-Analysis of Microdissected Breast Tumors Reveals Genes Regulated in the Stroma but Hidden in Bulk Analysis. Cancers, 2021, 13, 3371.	3.7	9
77	Identification of Functionalcis-regulatory Polymorphisms in the Human Genome. Human Mutation, 2013, 34, 735-742.	2.5	8
78	OTX2 regulates the expression of TAp63 leading to macular and cochlear neuroepithelium development. Aging, 2015, 7, 928-936.	3.1	7
79	Liver-Specific siRNA-Mediated Stat3 or C3 Knockdown Improves the Outcome of Experimental Autoimmune Myocarditis. Molecular Therapy - Methods and Clinical Development, 2020, 18, 62-72.	4.1	5
80	A live single-cell reporter assay links intratumor heterogeneity to metastatic proclivity in Ewing sarcoma. Science Advances, 2021, 7, .	10.3	5
81	Hepatocyte Growth Factor-mediated satellite cells niche perturbation promotes development of distinct sarcoma subtypes. ELife, 2016, 5, .	6.0	5
82	A functional strategy to characterize expression Quantitative Trait Loci. Human Genetics, 2017, 136, 1477-1487.	3.8	4
83	ESDN inhibits melanoma progression by blocking E-selectin expression in endothelial cells via STAT3. Cancer Letters, 2021, 510, 13-23.	7.2	4
84	Chromas from chromatin: sonification of the epigenome. F1000Research, 2016, 5, 274.	1.6	3
85	Cancer Metabolic Subtypes and Their Association with Molecular and Clinical Features. Cancers, 2022, 14, 2145.	3.7	3
86	Deletion of a pseudogene within a fragile site triggers the oncogenic expression of the mitotic CCSER1 gene. Life Science Alliance, 2021, 4, e202101019.	2.8	2
87	eQTL Mapping Using Transcription Factor Affinity. Methods in Molecular Biology, 2020, 2082, 39-49.	0.9	1
88	Pseudogenes as Competitive Endogenous RNAs: Target Prediction and Validation. Methods in Molecular Biology, 2021, 2324, 115-129.	0.9	0