Raffaele A. Calogero

List of Publications by Year
in descending order

177	8,955	50170 46	49773 87
papers	citations	h-index	g-index

189	189	189	15832
all docs	docs citations	times ranked	citing authors

#	ARTICLE	IF	CITATIONS
1	Mesenchymal Stem Cell-Derived Microvesicles Protect Against Acute Tubular Injury. Journal of the American Society of Nephrology: JASN, 2009, 20, 1053-1067.	3.0	1,144
2	Endothelial progenitor cell–derived microvesicles activate an angiogenic program in endothelial cells by a horizontal transfer of mRNA. Blood, 2007, 110, 2440-2448.	0.6	864
3	Clonal analysis of lineage fate in native haematopoiesis. Nature, 2018, 553, 212-216.	13.7	410
4	ERCC1 and RRM1 gene expressions but not EGFR are predictive of shorter survival in advanced non-small-cell lung cancer treated with cisplatin and gemcitabine. Annals of Oncology, 2006, 17, 1818-1825.	0.6	301
5	Human liver stem cell–derived microvesicles accelerate hepatic regeneration in hepatectomized rats. Journal of Cellular and Molecular Medicine, 2010, 14, 1605-1618.	1.6	277
6	YAP Drives Growth by Controlling Transcriptional Pause Release from Dynamic Enhancers. Molecular Cell, 2015, 60, 328-337.	4.5	228
7	Histone Methyltransferase MMSET/NSD2 Alters EZH2 Binding and Reprograms the Myeloma Epigenome through Global and Focal Changes in H3K36 and H3K27 Methylation. PLoS Genetics, 2014, 10, e1004566.	1.5	178
8	Live-animal imaging of native haematopoietic stem and progenitor cells. Nature, 2020, 578, 278-283.	13.7	171
9	Selection of the mRNA translation initiation region by Escherichia coli ribosomes.. Proceedings of the National Academy of Sciences of the United States of America, 1988, 85, 6427-6431.	3.3	163
10	The Hippo Transducer YAP1 Transforms Activated Satellite Cells and Is a Potent Effector of Embryonal Rhabdomyosarcoma Formation. Cancer Cell, 2014, 26, 273-287.	7.7	152
11	Indole-3-acetic acid improves Escherichia coli's defences to stress. Archives of Microbiology, 2006, 185, 373-382.	1.0	129
12	Dual RNA-seq of Nontypeable Haemophilus influenzae and Host Cell Transcriptomes Reveals Novel Insights into Host-Pathogen Cross Talk. MBio, 2015, 6, e01765-15.	1.8	123
13	Regenerative Reprogramming of the Intestinal Stem Cell State via Hippo Signaling Suppresses Metastatic Colorectal Cancer. Cell Stem Cell, 2020, 27, 590-604.e9.	5.2	112
14	Identification, cloning, nucleotide sequence and chromosomal map location of hns, the structural gene for Escherichia coli DNA-binding protein H-NS. Molecular Genetics and Genomics, 1988, 212, 199-202.	2.4	95
15	Immunotargeting of Antigen xCT Attenuates Stem-like Cell Behavior and Metastatic Progression in Breast Cancer. Cancer Research, 2016, 76, 62-72.	0.4	93
16	oneChannelGUI: a graphical interface to Bioconductor tools, designed for life scientists who are not familiar with R language. Bioinformatics, 2007, 23, 3406-3408.	1.8	91
17	NUAK2 is a critical YAP target in liver cancer. Nature Communications, 2018, 9, 4834.	5.8	88
18	Selection of suitable reference genes for accurate normalization of gene expression profile studies in non-small cell lung cancer. BMC Cancer, 2006, 6, 200.	1.1	85

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19	Ibrutinib inhibits CD20 upregulation on CLL B cells mediated by the CXCR4/SDF-1 axis. Blood, 2016, 128, 1609-1613.	0.6	85
20	A genomic view of estrogen actions in human breast cancer cells by expression profiling of the hormone-responsive transcriptome. Journal of Molecular Endocrinology, 2004, 32, 719-775.	1.1	80
21	State-of-the-Art Fusion-Finder Algorithms Sensitivity and Specificity. BioMed Research International, 2013, 2013, 1-6.	0.9	79
22	RAP: RNA-Seq Analysis Pipeline, a new cloud-based NGS web application. BMC Genomics, 2015, 16, S3.	1.2	79
23	The noninflammatory role of high mobility group box 1/tollâ€like receptor 2 axis in the selfâ€renewal of mammary cancer stem cells. FASEB Journal, 2013, 27, 4731-4744.	0.2	78
24	The Human MDM2 Oncoprotein Increases the Transcriptional Activity and the Protein Level of the p53 Homolog p63. Journal of Biological Chemistry, 2002, 277, 2674-2681.	1.6	77
25	Oxysterol-induced up-regulation of MCP-1 expression and synthesis in macrophage cells. Free Radical Biology and Medicine, 2005, 39, 1152-1161.	1.3	76
26	Long non-coding and coding RNAs characterization in Peripheral Blood Mononuclear Cells and Spinal Cord from Amyotrophic Lateral Sclerosis patients. Scientific Reports, 2018, 8, 2378.	1.6	74
27	Global Gene Expression Profiling Of Human Pleural Mesotheliomas: Identification of Matrix Metalloproteinase 14 (MMP-14) as Potential Tumour Target. PLoS ONE, 2009, 4, e7016.	1.1	73
28	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.	3.3	73
29	Extracellular Vesicles Mediate Mesenchymal Stromal Cell-Dependent Regulation of B Cell PI3K-AKT Signaling Pathway and Actin Cytoskeleton. Frontiers in Immunology, 2019, 10, 446.	2.2	73
30	Learning from Nature: Pregnancy Changes the Expression of Inflammation-Related Genes in Patients with Multiple Sclerosis. PLoS ONE, 2010, 5, e8962.	1.1	69
31	Concordant morphologic and gene expression data show that a vaccine halts HER-2/neu preneoplastic lesions. Journal of Clinical Investigation, 2004, 113, 709-717.	3.9	64
32	Indole-3-acetic acid regulates the central metabolic pathways in Escherichia coli. Microbiology (United Kingdom), 2006, 152, 2421-2431.	0.7	63
33	microRNA profiles in urine by next-generation sequencing can stratify bladder cancer subtypes. Oncotarget, 2018, 9, 20658-20669.	0.8	63
34	Transcriptional profiling of endometriosis tissues identifies genes related to organogenesis defects. Journal of Cellular Physiology, 2013, 228, 1927-1934.	2.0	62
35	Nonâ€"Small Cell Lung Cancer Exhibits Transcript Overexpression of Genes Associated with Homologous Recombination and DNA Replication Pathways. Cancer Research, 2009, 69, 3390-3396.	0.4	61
36	Microarray data analysis and mining approaches. Briefings in Functional Genomics & Proteomics, 2008, 6, 265-281.	3.8	59

#	ARTICLE	IF	CITATIONS
37	State of art fusion-finder algorithms are suitable to detect transcription-induced chimeras in normal tissues?. BMC Bioinformatics, 2013, 14, S2.	1.2	56
38	ARX Regulates Cortical Intermediate Progenitor Cell Expansion and Upper Layer Neuron Formation Through Repression of Cdkn1c. Cerebral Cortex, 2015, 25, 322-335.	1.6	56
39	Small non-coding RNA profiling in human biofluids and surrogate tissues from healthy individuals: description of the diverse and most represented species. Oncotarget, 2018, 9, 3097-3111.	0.8	56
40	Are oncoantigens suitable targets for anti-tumour therapy?. Nature Reviews Cancer, 2007, 7, 707-713.	12.8	55
41	Cross platform microarray analysis for robust identification of differentially expressed genes. BMC Bioinformatics, 2007, 8, S5.	1.2	55
42	Characterization of the str operon genes from Spirulina platensis and their evolutionary relationship to those of other prokaryotes. Molecular Genetics and Genomics, 1989, 217, 97-104.	2.4	54
43	The Human Tumor Suppressor ARF Interacts with Spinophilin/Neurabin II, a Type 1 Protein-phosphatase-binding Protein. Journal of Biological Chemistry, 2001, 276, 14161-14169.	1.6	53
44	Sparsely-connected autoencoder (SCA) for single cell RNAseq data mining. Npj Systems Biology and Applications, 2021, 7, 1.	1.4	53
45	miR-135b Coordinates Progression of ErbB2-Driven Mammary Carcinomas through Suppression of MID1 and MTCH2. American Journal of Pathology, 2013, 182, 2058-2070.	1.9	52
46	Bisphenol A effects on gene expression in adipocytes from children: association with metabolic disorders. Journal of Molecular Endocrinology, 2015, 54, 289-303.	1.1	52
47	Involvement of Inflammatory Chemokines in Survival of Human Monocytes Fed with Malarial Pigment. Infection and Immunity, 2010, 78, 4912-4921.	1.0	51
48	YAPâ€TEAD signaling promotes basal cell carcinoma development via a câ€JUN/AP1 axis. EMBO Journal, 2018, 37, .	3.5	51
49	Novel insights into Notum and glypicans regulation in colorectal cancer. Oncotarget, 2015, 6, 41237-41257.	0.8	50
50	Deregulation of MicroRNAs mediated control of carnitine cycle in prostate cancer: molecular basis and pathophysiological consequences. Oncogene, 2017, 36, 6030-6040.	2.6	49
51	Reproducible bioinformatics project: a community for reproducible bioinformatics analysis pipelines. BMC Bioinformatics, 2018, 19, 349.	1.2	49
52	Arx acts as a regional key selector gene in the ventral telencephalon mainly through its transcriptional repression activity. Developmental Biology, 2009, 334, 59-71.	0.9	48
53	Prdm5 Regulates Collagen Gene Transcription by Association with RNA Polymerase II in Developing Bone. PLoS Genetics, 2012, 8, e1002711.	1.5	48
54	MicroRNA miR-34a downregulates FOXP1 during DNA damage response to limit BCR signalling in chronic lymphocytic leukaemia B cells. Leukemia, 2019, 33, 403-414.	3.3	46

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55	Different miRNA Profiles in Plasma Derived Small and Large Extracellular Vesicles from Patients with Neurodegenerative Diseases. International Journal of Molecular Sciences, 2021, 22, 2737.	1.8	44
56	Comparative gene expression profiling reveals partially overlapping but distinct genomic actions of different antiestrogens in human breast cancer cells. Journal of Cellular Biochemistry, 2006, 98, 1163-1184.	1.2	43
57	Excision Repair Cross Complementing-1 and Topoisomerase IIÎ± Gene Expression in Small-Cell Lung Cancer Patients Treated with Platinum and Etoposide: A Retrospective Study. Journal of Thoracic Oncology, 2008, 3, 583-589.	0.5	41
58	Interleukin 12-activated lymphocytes influence tumor genetic programs. Cancer Research, 2001, 61, 3518-23.	0.4	40
59	Piroxicam and Cisplatin in a Mouse Model of Peritoneal Mesothelioma. Clinical Cancer Research, 2006, 12, 6133-6143.	3.2	39
60	Mechanism of translational initiation in prokaryotes. FEBS Letters, 1986, 207, 198-204.	1.3	38
61	Characterization of RNA-binding domains of hepatitis delta antigen. Journal of General Virology, 1993, 74, 2473-2478.	1.3	38
62	Inflammation and breast cancer. Inflammatory component of mammary carcinogenesis in ErbB2 transgenic mice. Breast Cancer Research, 2007, 9, 211.	2.2	38
63	LSD1 mediates MYCN control of epithelial-mesenchymal transition through silencing of metastatic suppressor NDRG1 gene. Oncotarget, 2017, 8, 3854-3869.	0.8	37
64	Functional and Physical Interaction of the Human ARF Tumor Suppressor with Tat-binding Protein-1. Journal of Biological Chemistry, 2004, 279, 6345-6353.	1.6	36
65	Optimizing a Massive Parallel Sequencing Workflow for Quantitative miRNA Expression Analysis. PLoS ONE, 2012, 7, e31630.	1.1	36
66	A regulatory microRNA network controls endothelial cell phenotypic switch during sprouting angiogenesis. ELife, 2020, 9, .	2.8	35
67	The cellular apoptosis susceptibility *CAS/CSE1L* gene protects ovarian cancer cells from death by suppressing RASSF1C. FASEB Journal, 2012, 26, 2446-2456.	0.2	34
68	Mutant SOD1 and mitochondrial damage alter expression and splicing of genes controlling neuritogenesis in models of neurodegeneration. Human Mutation, 2011, 32, 168-182.	1.1	33
69	A novel infection- and inflammation-associated molecular signature in peripheral blood of myasthenia gravis patients. Immunobiology, 2016, 221, 1227-1236.	0.8	33
70	Cell-to-Cell Signaling Influences the Fate of Prostate Cancer Stem Cells and Their Potential to Generate More Aggressive Tumors. PLoS ONE, 2012, 7, e31467.	1.1	32
71	Transcriptional Profiling of Polycythemia Vera Identifies Gene Expression Patterns Both Dependent and Independent from the Action of JAK2V617F. Clinical Cancer Research, 2010, 16, 4339-4352.	3.2	31
72	Recombinant human lactoferrin induces human and mouse dendritic cell maturation *via* Tollâ€like receptors 2 and 4. FASEB Journal, 2014, 28, 416-429.	0.2	31

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73	miR-129-5p: A key factor and therapeutic target in amyotrophic lateral sclerosis. Progress in Neurobiology, 2020, 190, 101803.	2.8	31
74	Deletion in a (T)8 microsatellite abrogates expression regulation by 3'-UTR. Nucleic Acids Research, 2003, 31, 6561-6569.	6.5	30
75	A computational search for box C/D snoRNA genes in the Drosophila melanogaster genome. Bioinformatics, 2004, 20, 3293-3301.	1.8	29
76	Genomic and Proteomic Analyses of Prdm5 Reveal Interactions with Insulator Binding Proteins in Embryonic Stem Cells. Molecular and Cellular Biology, 2013, 33, 4504-4516.	1.1	29
77	Luminal breast cancer-specific circular RNAs uncovered by a novel tool for data analysis. Oncotarget, 2018, 9, 14580-14596.	0.8	29
78	SETD2 and histone H3 lysine 36 methylation deficiency in advanced systemic mastocytosis. Leukemia, 2018, 32, 139-148.	3.3	28
79	An integrated approach of immunogenomics and bioinformatics to identify new Tumor Associated Antigens (TAA) for mammary cancer immunological prevention. BMC Bioinformatics, 2005, 6, S7.	1.2	27
80	Genes regulated by hepatocyte growth factor as targets to sensitize ovarian cancer cells to cisplatin. Molecular Cancer Therapeutics, 2006, 5, 1126-1135.	1.9	27
81	The <i>MET</i> oncogene transforms human primary bone-derived cells into osteosarcomas by targeting committed osteo-progenitors. Journal of Bone and Mineral Research, 2012, 27, 1322-1334.	3.1	27
82	Safety and efficacy of the Russian COVID-19 vaccine: more information needed. Lancet, The, 2020, 396, e53.	6.3	27
83	Conjugated Linoleic Acid Alters Global Gene Expression in Human Intestinal-Like Caco-2 Cells in an Isomer-Specific Manner3. Journal of Nutrition, 2007, 137, 2359-2365.	1.3	26
84	Apoptosis Induced by Piroxicam plus Cisplatin Combined Treatment Is Triggered by p21 in Mesothelioma. PLoS ONE, 2011, 6, e23569.	1.1	26
85	Oxidative stress controls the choice of alternative last exons via a Brahma–BRCA1–CstF pathway. Nucleic Acids Research, 2017, 45, 902-914.	6.5	26
86	SeqBox: RNAseq/ChIPseq reproducible analysis on a consumer game computer. Bioinformatics, 2018, 34, 871-872.	1.8	26
87	rCASC: reproducible classification analysis of single-cell sequencing data. GigaScience, 2019, 8, .	3.3	26
88	Data discrepancies and substandard reporting of interim data of Sputnik V phase 3 trial. Lancet, The, 2021, 397, 1881-1883.	6.3	26
89	Prdm5 suppresses ApcMin-driven intestinal adenomas and regulates monoacylglycerol lipase expression. Oncogene, 2014, 33, 3342-3350.	2.6	25
90	MicroRNAs from saliva of anopheline mosquitoes mimic human endogenous miRNAs and may contribute to vector-host-pathogen interactions. Scientific Reports, 2019, 9, 2955.	1.6	25

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91	Chemical synthesis and in vivo hyperexpression of a modular gene coding for Escherichia coli translational initiation factor IF1. Molecular Genetics and Genomics, 1987, 208, 63-69.	2.4	22
92	RNA-Seq profiling in peripheral blood mononuclear cells of amyotrophic lateral sclerosis patients and controls. Scientific Data, 2019, 6, 190006.	2.4	22
93	Site-directed mutagenesis of Escherichia coli translation initiation factor IF1. Identification of the amino acids involved in its ribosomal binding and recycling. Protein Engineering, Design and Selection, 1989, 3, 133-138.	1.0	21
94	Dissecting an alternative splicing analysis workflow for GeneChipÂ®Exon 1.0 ST Affymetrix arrays. BMC Genomics, 2008, 9, 571.	1.2	21
95	The long intergenic non-coding RNA CCR492 functions as a let-7 competitive endogenous RNA to regulate c-Myc expression. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 1322-1332.	0.9	21
96	p190 RhoGAP promotes contact inhibition in epithelial cells by repressing YAP activity. Journal of Cell Biology, 2018, 217, 3183-3201.	2.3	21
97	Characterization of a genetic mouse model of lung cancer: a promise to identify Non-Small Cell Lung Cancer therapeutic targets and biomarkers. BMC Genomics, 2014, 15, S1.	1.2	20
98	Cardioprotective mIGF-1/SIRT1 signaling induces hypertension, leukocytosis and fear response in mice. Aging, 2012, 4, 402-416.	1.4	20
99	The Hay Wells Syndrome-Derived TAp63&alpha;Q540L Mutant has Impaired Transcriptional and Cell Growth Regulatory Activity. Cell Cycle, 2006, 5, 78-87.	1.3	19
100	Epidermal growth factor ligand/receptor loop and downstream signaling activation pattern in completely resected nonsmall cell lung cancer. Cancer, 2007, 110, 1321-1328.	2.0	19
101	Critical Roles for Rictor/Sin1 Complexes in Interferon-dependent Gene Transcription and Generation of Antiproliferative Responses. Journal of Biological Chemistry, 2014, 289, 6581-6591.	1.6	19
102	Chimera: a Bioconductor package for secondary analysis of fusion products. Bioinformatics, 2014, 30, 3556-3557.	1.8	18
103	Impact of Mycobacterium tuberculosis RD1-locus on human primary dendritic cell immune functions. Scientific Reports, 2015, 5, 17078.	1.6	18
104	Mimicking p14ARF Phosphorylation Influences Its Ability to Restrain Cell Proliferation. PLoS ONE, 2013, 8, e53631.	1.1	18
105	Reinitiation of protein synthesis in Escherichia coli can be induced by mRNA cis -elements unrelated to canonical translation initiation signals. FEBS Letters, 2000, 468, 73-78.	1.3	16
106	Alternative splicing detection workflow needs a careful combination of sample prep and bioinformatics analysis. BMC Bioinformatics, 2015, 16, S2.	1.2	16
107	Development, Function, and Clinical Significance of Plasmacytoid Dendritic Cells in Chronic Myeloid Leukemia. Cancer Research, 2018, 78, 6223-6234.	0.4	16
108	Kohonen neural networks and genetic classification. Mathematical and Computer Modelling, 2007, 45, 34-60.	2.0	15

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109	Transcriptional Analysis of an E2F Gene Signature as a Biomarker of Activity of the Cyclin-Dependent Kinase Inhibitor PHA-793887 in Tumor and Skin Biopsies from a Phase I Clinical Study. Molecular Cancer Therapeutics, 2010, 9, 1265-1273.	1.9	15
110	Functional and pharmacodynamic evaluation of metronomic cyclophosphamide and docetaxel regimen in castration-resistant prostate cancer. Future Oncology, 2013, 9, 1375-1388.	1.1	15
111	BRAF mutations in non-small cell lung cancer: has finally Janus opened the door?. Critical Reviews in Oncology/Hematology, 2016, 101, 32-39.	2.0	15
112	Xenopatients show the need for precision medicine approach to chemotherapy in ovarian cancer. Oncotarget, 2016, 7, 26181-26191.	0.8	15
113	A hypoxic signature marks tumors formed by disseminated tumor cells in the BALB-neuT mammary cancer model. Oncotarget, 2016, 7, 33081-33095.	0.8	15
114	Extracellular Vesicles Derived From Plasma of Patients With Neurodegenerative Disease Have Common Transcriptomic Profiling. Frontiers in Aging Neuroscience, 2022, 14, 785741.	1.7	15
115	Amplification of repeat-containing transcribed sequences (ARTS): a transcriptome fingerprinting strategy to detect functionally relevant microsatellite mutations in cancer. Nucleic Acids Research, 2003, 31, 33e-33.	6.5	14
116	Immune prevention of mammary carcinogenesis in HER-2/neu transgenic mice: a microarray scenario. Cancer Immunology, Immunotherapy, 2005, 54, 599-610.	2.0	14
117	Regulation of leukemic cell differentiation and retinoid-induced gene expression by statins. Molecular Cancer Therapeutics, 2009, 8, 615-625.	1.9	14
118	The TRPA1 channel is a cardiac target of mIGF-1/SIRT1 signaling. American Journal of Physiology - Heart and Circulatory Physiology, 2014, 307, H939-H944.	1.5	14
119	Differential Expression Analysis in Single-Cell Transcriptomics. Methods in Molecular Biology, 2019, 1979, 425-432.	0.4	14
120	Evolution of HER2-positive mammary carcinoma: HER2 loss reveals claudin-low traits in cancer progression. Oncogenesis, 2021, 10, 77.	2.1	14
121	RRE: a tool for the extraction of non-coding regions surrounding annotated genes from genomic datasets. Bioinformatics, 2004, 20, 2848-2850.	1.8	13
122	Oncoantigens as anti-tumor vaccination targets: the chance of a lucky strike?. Cancer Immunology, Immunotherapy, 2008, 57, 1685-1694.	2.0	13
123	Molecular and functional characterization of urine€derived podocytes from patients with Alport syndrome. Journal of Pathology, 2020, 252, 88-100.	2.1	13
124	Sparsely Connected Autoencoders: A Multi-Purpose Tool for Single Cell omics Analysis. International Journal of Molecular Sciences, 2021, 22, 12755.	1.8	13
125	Cloning and characterization of a developmentally regulated sea urchin cDNA encoding glutamine synthetase. Gene, 1995, 152, 205-208.	1.0	12
126	Atorvastatin modulates anti-proliferative and pro-proliferative signals in Her2/neu-positive mammary cancer. Biochemical Pharmacology, 2011, 82, 1079-1089.	2.0	12

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127	A Mathematical-Biological Joint Effort to Investigate the Tumor-Initiating Ability of Cancer Stem Cells. PLoS ONE, 2014, 9, e106193.	1.1	12
128	A computational approach based on the colored Petri net formalism for studying multiple sclerosis. BMC Bioinformatics, 2019, 20, 623.	1.2	12
129	Multi-level model for the investigation of oncoantigen-driven vaccination effect. BMC Bioinformatics, 2013, 14, S11.	1.2	11
130	DNA damage and transcriptional regulation in iPSC-derived neurons from Ataxia Telangiectasia patients. Scientific Reports, 2019, 9, 651.	1.6	11
131	Microarray Probe Expression Measures, Data Normalization and Statistical Validation. Comparative and Functional Genomics, 2003, 4, 442-446.	2.0	10
132	AP-2Î± regulates migration of GN-11 neurons via a specific genetic programme involving the Axl receptor tyrosine kinase. BMC Biology, 2009, 7, 25.	1.7	10
133	HashClone: a new tool to quantify the minimal residual disease in B-cell lymphoma from deep sequencing data. BMC Bioinformatics, 2017, 18, 516.	1.2	10
134	Selection of mRNA by Ribosomes During Prokaryotic Translational Initiation. , 1988, , 317-330.		10
135	Translational modulation in hepatitis B virus preS-S open reading frame expression. Journal of General Virology, 1992, 73, 139-148.	1.3	9
136	Use of a constrain phage displayed-peptide library for the isolation of peptides binding to HIV-1 nucleocapsid protein (NCp7). FEBS Letters, 1995, 361, 85-88.	1.3	9
137	Microarray Data Analysis and Mining. , 2004, 94, 67-90.		9
138	Circulating Extracellular Vesicles Contain Liver-Derived RNA Species as Indicators of Severe Cholestasis-Induced Early Liver Fibrosis in Mice. Antioxidants and Redox Signaling, 2022, 36, 480-504.	2.5	9
139	The effect of trans-10, cis-12 conjugated linoleic acid on gene expression profiles related to lipid metabolism in human intestinal-like Caco-2 cells. Genes and Nutrition, 2009, 4, 103-112.	1.2	8
140	Docker4Circ: A Framework for the Reproducible Characterization of circRNAs from RNA-Seq Data. International Journal of Molecular Sciences, 2020, 21, 293.	1.8	8
141	Relationship between size of mRNA ribosomal binding site and initiation factor function. Biochimie, 1987, 69, 957-963.	1.3	7
142	Toward a Long-Lasting Immune Prevention of HER2 Mammary Carcinomas: Directions from Transgenic Mice. Cell Cycle, 2004, 3, 702-704.	1.3	7
143	Laser capture microdissection for transcriptomic profiles in human skin biopsies. BMC Molecular Biology, 2018, 19, 7.	3.0	7
144	PIK3R1W624R Is an Actionable Mutation in High Grade Serous Ovarian Carcinoma. Cells, 2020, 9, 442.	1.8	7

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145	Frequent mutations of FBXO11 highlight BCL6 as a therapeutic target in Burkitt lymphoma. Blood Advances, 2021, 5, 5239-5257.	2.5	7
146	METâ†14 promotes a ligand-dependent, AKT-driven invasive growth. Life Science Alliance, 2022, 5, e202201409.	1.3	7
147	Expression inE. coliand purification of a chimeric p22-NS3 recombinant antigen of Hepatitis C Virus (HCV). FEBS Letters, 1993, 324, 253-257.	1.3	6
148	VIRTLAB: a virtual molecular biology laboratory. Bioinformatics, 1998, 14, 815-816.	1.8	6
149	miRNA profiles of canine cutaneous mast cell tumours with early nodal metastasis and evaluation as potential biomarkers. Scientific Reports, 2020, 10, 18918.	1.6	6
150	Identification of Altered miRNAs in Cerumen of Dogs Affected by Otitis Externa. Frontiers in Immunology, 2020, 11, 914.	2.2	6
151	Early stability and late random tumor progression of a HER2-positive primary breast cancer patient-derived xenograft. Scientific Reports, 2021, 11, 1563.	1.6	6
152	Computational Analysis of circRNA Expression Data. Methods in Molecular Biology, 2021, 2284, 181-192.	0.4	6
153	Identification of TENM4 as a Novel Cancer Stem Cell-Associated Molecule and Potential Target in Triple Negative Breast Cancer. Cancers, 2021, 13, 894.	1.7	6
154	MET Exon 14 Skipping: A Case Study for the Detection of Genetic Variants in Cancer Driver Genes by Deep Learning. International Journal of Molecular Sciences, 2021, 22, 4217.	1.8	6
155	Purification of recombinant hepatitis delta antigen expressed inE. colicells. FEBS Letters, 1993, 318, 322-324.	1.3	5
156	Application of the Euro Clonality nextâ€generation sequencingâ€based marker screening approach to detect immunoglobulin heavy chain rearrangements in mantle cell lymphoma patients: first data from the Fondazione Italiana Linfomi MCL0208 trial. British Journal of Haematology, 2021, 194, 378-381.	1.2	5
157	Mathematical Approach to Predict the Drug Effects on Cancer Stem Cell Models. Electronic Notes in Theoretical Computer Science, 2011, 277, 29-39.	0.9	4
158	Transcriptional analysis of the Aurora inhibitor Danusertib leading to biomarker identification in TP53 wild type cells. Gene, 2012, 494, 202-208.	1.0	4
159	Laniakea@ReCaS: exploring the potential of customisable Galaxy on-demand instances as a cloud-based service. BMC Bioinformatics, 2021, 22, 544.	1.2	4
160	Oncoantigens for an immune prevention of cancer. American Journal of Cancer Research, 2011, 1, 255-264.	1.4	4
161	Towards a long-lasting immune prevention of HER2 mammary carcinomas: directions from transgenic mice. Cell Cycle, 2004, 3, 704-6.	1.3	4
162	A versatile mathematical work-flow to explore how Cancer Stem Cell fate influences tumor progression. BMC Systems Biology, 2015, 9, S1.	3.0	3

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163	Neutron diffraction evidence for substrate-triggered intermolecular interactions in the ribosomal protein IF-2. Chemical Physics Letters, 1987, 139, 116-118.	1.2	2
164	RME/AGEE a computer tool for restriction enzyme mapping training. Biochemical Education, 1996, 24, 160-163.	0.1	1
165	Gene Ontology Rewritten for Computing Gene Functional Similarity. , 2010, , .		1
166	Digging in the RNA-seq Garbage: Evaluating the Characteristics of Unmapped RNA-seq Reads in Normal Tissues. , 2012, , .		1
167	Look for methods, not conclusions. Cell Death and Disease, 2019, 10, 931.	2.7	1
168	Circulating miRNome of Trachemys scripta after elective gonadectomy under general anesthesia. Scientific Reports, 2021, 11, 14712.	1.6	1
169	Quantifying Entire Transcriptomes by Aligned RNA-Seq Data. Methods in Molecular Biology, 2015, 1269, 163-172.	0.4	1
170	A chimeric recombinant antigen of the Hepatitis C virus expressed in E.coli. Protein Engineering, Design and Selection, 0, , .	1.0	0
171	Purification of Recombinant Proteins with High Isoelectric Points. , 2004, 94, 225-238.		0
172	Genome-Wide Search for Splicing Defects Associated with Amyotrophic Lateral Sclerosis (ALS). , 2009, , .		0
173	Cancer stem cell based adjuvant for oncoantingen-driven vaccination. , 2011, , .		0
174	Message from the IIBM 2012 Workshop Co-Chairs. , 2012, , .		0
175	ParallelHashClone: A Parallel Implementation of HashClone Suite for Clonality Assessment from NGS Data. , 2018, , .		0
176	Computational Analysis of Single-Cell RNA-Seq Data. Methods in Molecular Biology, 2021, 2284, 289-301.	0.4	0
177	A pipeline to detect antibody-targetable cancer stem cell proteins.. Journal of Clinical Oncology, 2012, 30, e13527-e13527.	0.8	0