Silvio Bicciato

List of Publications by Year
in descending order

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		22153	8630
202	23,274	59	146
papers	citations	h-index	g-index

223	223	223	36008
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Role of YAP/TAZ in mechanotransduction. Nature, 2011, 474, 179-183.	27.8	4,288
2	The Hippo Transducer TAZ Confers Cancer Stem Cell-Related Traits on Breast Cancer Cells. Cell, 2011, 147, 759-772.	28.9	1,115
3	YAP/TAZ Incorporation in the Î²-Catenin Destruction Complex Orchestrates the Wnt Response. Cell, 2014, 158, 157-170.	28.9	873
4	Genome-wide association between YAP/TAZ/TEAD andÂAP-1 at enhancers drives oncogenic growth. Nature Cell Biology, 2015, 17, 1218-1227.	10.3	865
5	Tumor-Induced Tolerance and Immune Suppression Depend on the C/EBPÎ² Transcription Factor. Immunity, 2010, 32, 790-802.	14.3	782
6	Tumors induce a subset of inflammatory monocytes with immunosuppressive activity on CD8+ T cells. Journal of Clinical Investigation, 2006, 116, 2777-2790.	8.2	723
7	A Mutant-p53/Smad Complex Opposes p63 to Empower TGFÎ²-Induced Metastasis. Cell, 2009, 137, 87-98.	28.9	717
8	A MicroRNA Targeting Dicer for Metastasis Control. Cell, 2010, 141, 1195-1207.	28.9	619
9	Indoleamine 2,3-dioxygenase is a signaling protein in long-term tolerance by dendritic cells. Nature Immunology, 2011, 12, 870-878.	14.5	577
10	Aryl hydrocarbon receptor control of a disease tolerance defence pathway. Nature, 2014, 511, 184-190.	27.8	574
11	Regeneration of the entire human epidermis using transgenic stem cells. Nature, 2017, 551, 327-332.	27.8	544
12	IL-7 and IL-15 instruct the generation of human memory stem T cells from naive precursors. Blood, 2013, 121, 573-584.	1.4	455
13	Role of TAZ as Mediator of Wnt Signaling. Cell, 2012, 151, 1443-1456.	28.9	419
14	Muscle insulin sensitivity and glucose metabolism are controlled by the intrinsic muscle clock. Molecular Metabolism, 2014, 3, 29-41.	6.5	324
15	Aerobic glycolysis tunes <scp>YAP</scp> / <scp>TAZ</scp> transcriptional activity. EMBO Journal, 2015, 34, 1349-1370.	7.8	306
16	Comparison of computational methods for Hi-C data analysis. Nature Methods, 2017, 14, 679-685.	19.0	301
17	A Relay Pathway between Arginine and Tryptophan Metabolism Confers Immunosuppressive Properties on Dendritic Cells. Immunity, 2017, 46, 233-244.	14.3	241
18	Transcriptional addiction in cancer cells is mediated by YAP/TAZ through BRD4. Nature Medicine, 2018, 24, 1599-1610.	30.7	228

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19	Identification of microRNA expression patterns and definition of a microRNA/mRNA regulatory network in distinct molecular groups of multiple myeloma. Blood, 2009, 114, e20-e26.	1.4	224
20	Human liver-resident CD56bright/CD16neg NK cells are retained within hepatic sinusoids via the engagement of CCR5 and CXCR6 pathways. Journal of Autoimmunity, 2016, 66, 40-50.	6.5	220
21	SHARP1 suppresses breast cancer metastasis by promoting degradation of hypoxia-inducible factors. Nature, 2012, 487, 380-384.	27.8	213
22	Induction of Expandable Tissue-Specific Stem/Progenitor Cells through Transient Expression of YAP/TAZ. Cell Stem Cell, 2016, 19, 725-737.	11.1	204
23	Toward the identification of a tolerogenic signature in IDO-competent dendritic cells. Blood, 2006, 107, 2846-2854.	1.4	183
24	Sterol regulatory element binding protein 1 couples mechanical cues and lipid metabolism. Nature Communications, 2019, 10, 1326.	12.8	158
25	<scp>YAP</scp> enhances the proâ€proliferative transcriptional activity of mutant p53 proteins. EMBO Reports, 2016, 17, 188-201.	4.5	154
26	T Cell Cancer Therapy Requires CD40-CD40L Activation of Tumor Necrosis Factor and Inducible Nitric-Oxide-Synthase-Producing Dendritic Cells. Cancer Cell, 2016, 30, 377-390.	16.8	141
27	Reprogramming normal cells into tumour precursors requires ECM stiffness and oncogene-mediated changes of cell mechanical properties. Nature Materials, 2020, 19, 797-806.	27.5	140
28	Metabotropic glutamate receptor-4 modulates adaptive immunity and restrains neuroinflammation. Nature Medicine, 2010, 16, 897-902.	30.7	138
29	Dynamics of cellular states of fibro-adipogenic progenitors during myogenesis and muscular dystrophy. Nature Communications, 2018, 9, 3670.	12.8	137
30	Mutant p53 Reprograms TNF Signaling in Cancer Cells through Interaction with the Tumor Suppressor DAB2IP. Molecular Cell, 2014, 56, 617-629.	9.7	136
31	Extracellular matrix mechanical cues regulate lipid metabolism through Lipin-1 and SREBP. Nature Cell Biology, 2019, 21, 338-347.	10.3	135
32	Prolylâ€isomerase Pin1 controls normal and cancer stem cells of the breast. EMBO Molecular Medicine, 2014, 6, 99-119.	6.9	130
33	Glucocorticoid receptor signalling activates YAP in breast cancer. Nature Communications, 2017, 8, 14073.	12.8	129
34	Thalidomide Downregulates Angiogenic Genes in Bone Marrow Endothelial Cells of Patients With Active Multiple Myeloma. Journal of Clinical Oncology, 2005, 23, 5334-5346.	1.6	125
35	Unexpected Structural and Functional Consequences of the R33Q Homozygous Mutation in Cardiac Calsequestrin. Circulation Research, 2008, 103, 298-306.	4.5	124
36	Molecular Classification of Multiple Myeloma: A Distinct Transcriptional Profile Characterizes Patients Expressing CCND1 and Negative for 14q32 Translocations. Journal of Clinical Oncology, 2005, 23, 7296-7306.	1.6	123

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37	Generation of human memory stem T cells after haploidentical T-replete hematopoietic stem cell transplantation. Blood, 2015, 125, 2865-2874.	1.4	119
38	Gene expression profiling of plasma cell dyscrasias reveals molecular patterns associated with distinct IGH translocations in multiple myeloma. Oncogene, 2005, 24, 2461-2473.	5.9	118
39	MYC-driven epigenetic reprogramming favors the onset of tumorigenesis by inducing a stem cell-like state. Nature Communications, 2018, 9, 1024.	12.8	114
40	PCA disjoint models for multiclass cancer analysis using gene expression data. Bioinformatics, 2003, 19, 571-578.	4.1	110
41	Human fibrocytic myeloidâ€derived suppressor cells express IDO and promote tolerance via Tregâ€cell expansion. European Journal of Immunology, 2014, 44, 3307-3319.	2.9	104
42	Mechanical cues control mutant p53 stability through a mevalonateâ€“RhoA axis. Nature Cell Biology, 2018, 20, 28-35.	10.3	104
43	A gene expression signature associated with survival in metastatic melanoma. Journal of Translational Medicine, 2006, 4, 50.	4.4	93
44	Novel definition files for human GeneChips based on GeneAnnot. BMC Bioinformatics, 2007, 8, 446.	2.6	93
45	YAP/TAZ activity in stromal cells prevents ageing by controlling cGASâ€“STING. Nature, 2022, 607, 790-798.	27.8	89
46	MRF4 negatively regulates adult skeletal muscle growth by repressing MEF2 activity. Nature Communications, 2016, 7, 12397.	12.8	88
47	Prospective Biomarker Analysis of the Randomized CHER-LOB Study Evaluating the Dual Anti-HER2 Treatment With Trastuzumab and Lapatinib Plus Chemotherapy as Neoadjuvant Therapy for HER2-Positive Breast Cancer. Oncologist, 2015, 20, 1001-1010.	3.7	85
48	P2X7 receptor restrains pathogenic Tfh cell generation in systemic lupus erythematosus. Journal of Experimental Medicine, 2019, 216, 317-336.	8.5	83
49	Single-cell analyses reveal YAP/TAZ as regulators of stemness and cell plasticity in glioblastoma. Nature Cancer, 2021, 2, 174-188.	13.2	83
50	Transcriptomic Profiling of the Development of the Inflammatory Response in Human Monocytes In Vitro. PLoS ONE, 2014, 9, e87680.	2.5	81
51	Integration of Bioinformatic Predictions and Experimental Data to Identify circRNA-miRNA Associations. Genes, 2019, 10, 642.	2.4	81
52	The mutant p53â€D4 complex controls VEGFA isoforms by recruiting lncRNA MALAT1. EMBO Reports, 2017, 18, 1331-1351.	4.5	78
53	Notch is a direct negative regulator of the DNA-damage response. Nature Structural and Molecular Biology, 2015, 22, 417-424.	8.2	68
54	Transcription Factor-Directed Re-wiring of Chromatin Architecture for Somatic Cell Nuclear Reprogramming toward trans-Differentiation. Molecular Cell, 2019, 76, 453-472.e8.	9.7	67

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55	Upregulation of translational machinery and distinct genetic subgroups characterise hyperdiploidy in multiple myeloma. British Journal of Haematology, 2007, 136, 565-573.	2.5	66
56	The Reconstruction of Transcriptional Networks Reveals Critical Genes with Implications for Clinical Outcome of Multiple Myeloma. Clinical Cancer Research, 2011, 17, 7402-7412.	7.0	65
57	Molecular characterization of human multiple myeloma cell lines by integrative genomics: Insights into the biology of the disease. Genes Chromosomes and Cancer, 2007, 46, 226-238.	2.8	62
58	Integration of genomic and gene expression data of childhood ALL without known aberrations identifies subgroups with specific genetic hallmarks. Genes Chromosomes and Cancer, 2009, 48, 22-38.	2.8	62
59	Bimodal CD40/Fas-Dependent Crosstalk between iNKT Cells and Tumor-Associated Macrophages Impairs Prostate Cancer Progression. Cell Reports, 2018, 22, 3006-3020.	6.4	62
60	The early expansion of anergic NKG2A^{pos}/CD56^{dim}/CD16^{neg} natural killer represents a therapeutic target in haploidentical hematopoietic stem cell transplantation. Haematologica, 2018, 103, 1390-1402.	3.5	61
61	d <scp>NTP</scp> metabolism links mechanical cues and <scp>YAP</scp> / <scp>TAZ</scp> to cell growth and oncogeneâ€induced senescence. EMBO Journal, 2018, 37, .	7.8	60
62	The calcineurin-NFAT pathway controls activity-dependent circadian gene expression in slow skeletal muscle. Molecular Metabolism, 2015, 4, 823-833.	6.5	58
63	Mutant p53 improves cancer cellsâ€™ resistance to endoplasmic reticulum stress by sustaining activation of the UPR regulator ATF6. Oncogene, 2019, 38, 6184-6195.	5.9	56
64	F-actin dynamics regulates mammalian organ growth and cell fate maintenance. Journal of Hepatology, 2019, 71, 130-142.	3.7	56
65	APTANI: a computational tool to select aptamers through sequence-structure motif analysis of HT-SELEX data. Bioinformatics, 2016, 32, 161-164.	4.1	55
66	Dynamic Transcriptional and Epigenetic Regulation of Human Epidermal Keratinocyte Differentiation. Stem Cell Reports, 2016, 6, 618-632.	4.8	55
67	Pattern identification and classification in gene expression data using an autoassociative neural network model. Biotechnology and Bioengineering, 2003, 81, 594-606.	3.3	54
68	MDP, a database linking drug response data to genomic information, identifies dasatinib and statins as a combinatorial strategy to inhibit YAP/TAZ in cancer cells. Oncotarget, 2015, 6, 38854-38865.	1.8	54
69	Integrative Genomics Analyses Reveal Molecularly Distinct Subgroups of B-Cell Chronic Lymphocytic Leukemia Patients with 13q14 Deletion. Clinical Cancer Research, 2010, 16, 5641-5653.	7.0	52
70	MCM7and its hosted miR-25, 93 and 106b cluster elicit YAP/TAZ oncogenic activity in lung cancer. Carcinogenesis, 2017, 38, 64-75.	2.8	52
71	Mutant p53 induces Golgi tubulo-vesiculation driving a prometastatic secretome. Nature Communications, 2020, 11, 3945.	12.8	52
72	Deficiency of immunoregulatory indoleamine 2,3-dioxygenase 1in juvenile diabetes. JCI Insight, 2018, 3, .	5.0	51

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73	Computational analysis of flow-cytometry antigen expression profiles in childhood acute lymphoblastic leukemia: an MLL/AF4 identification. Leukemia, 2003, 17, 1557-1565.	7.2	49
74	Circulating mucosal-associated invariant T cells identify patients responding to anti-PD-1 therapy. Nature Communications, 2021, 12, 1669.	12.8	48
75	lncRNA profiling in early-stage chronic lymphocytic leukemia identifies transcriptional fingerprints with relevance in clinical outcome. Blood Cancer Journal, 2016, 6, e468-e468.	6.2	47
76	Engagement of Nuclear Coactivator 7 by 3-Hydroxyanthranilic Acid Enhances Activation of Aryl Hydrocarbon Receptor in Immunoregulatory Dendritic Cells. Frontiers in Immunology, 2019, 10, 1973.	4.8	47
77	Transcriptional features of multiple myeloma patients with chromosome 1q gain. Leukemia, 2007, 21, 1113-1116.	7.2	45
78	Phenotypes and gene expression profiles of Saccharopolyspora erythraea rifampicin-resistant (rif) mutants affected in erythromycin production. Microbial Cell Factories, 2009, 8, 18.	4.0	45
79	Induction of immunosuppressive functions and NF-ÎºB by FLIP in monocytes. Nature Communications, 2018, 9, 5193.	12.8	45
80	Altered peritumoral microRNA expression predicts head and neck cancer patients with a high risk of recurrence. Modern Pathology, 2017, 30, 1387-1401.	5.5	44
81	Disabled Homolog 2 Controls Prometastatic Activity of Tumor-Associated Macrophages. Cancer Discovery, 2020, 10, 1758-1773.	9.4	44
82	Transcriptional profiling of human bronchial epithelial cell BEAS-2B exposed to diesel and biomass ultrafine particles. BMC Genomics, 2018, 19, 302.	2.8	43
83	Computational methods for the integrative analysis of single-cell data. Briefings in Bioinformatics, 2021, 22, 20-29.	6.5	43
84	Epigenomic landscape of human colorectal cancer unveils an aberrant core of pan-cancer enhancers orchestrated by YAP/TAZ. Nature Communications, 2021, 12, 2340.	12.8	43
85	Strategies for comparing gene expression profiles from different microarray platforms: Application to a caseâ€“control experiment. Analytical Biochemistry, 2006, 353, 43-56.	2.4	40
86	Identification of a molecular signature predictive of sensitivity to differentiation induction in acute myeloid leukemia. Leukemia, 2006, 20, 1751-1758.	7.2	38
87	A-MADMAN: Annotation-based microarray data meta-analysis tool. BMC Bioinformatics, 2009, 10, 201.	2.6	38
88	Alterations of redox and iron metabolism accompany the development of <scp>HIV</scp> latency. EMBO Journal, 2020, 39, e102209.	7.8	37
89	Comparative genomics and transcriptional profiles of Saccharopolyspora erythraea NRRL 2338 and a classically improved erythromycin over-producing strain. Microbial Cell Factories, 2012, 11, 32.	4.0	36
90	P2X7 Receptor Activity Limits Accumulation of T Cells within Tumors. Cancer Research, 2020, 80, 3906-3919.	0.9	36

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91	Hmgb3 Is Regulated by MicroRNA-206 during Muscle Regeneration. PLoS ONE, 2012, 7, e43464.	2.5	35
92	TIM4 expression by dendritic cells mediates uptake of tumor-associated antigens and anti-tumor responses. Nature Communications, 2021, 12, 2237.	12.8	35
93	Integrative genomic analysis reveals distinct transcriptional and genetic features associated with chromosome 13 deletion in multiple myeloma. Haematologica, 2007, 92, 56-65.	3.5	34
94	Mining of Biological Data II : Assessing Data Structure and Class Homogeneity by Cluster Analysis. Metabolic Engineering, 2000, 2, 228-238.	7.0	33
95	A locally adaptive statistical procedure (LAP) to identify differentially expressed chromosomal regions. Bioinformatics, 2006, 22, 2658-2666.	4.1	33
96	Integrated analysis of microRNA and mRNA expression profiles in physiological myelopoiesis: role of hsa-mir-299-5p in CD34+ progenitor cells commitment. Cell Death and Disease, 2010, 1, e28-e28.	6.3	33
97	PI3K Inhibitors Curtail MYC-Dependent Mutant p53 Gain-of-Function in Head and Neck Squamous Cell Carcinoma. Clinical Cancer Research, 2020, 26, 2956-2971.	7.0	33
98	A comparative transcriptomic analysis of astrocytes differentiation from human neural progenitor cells. European Journal of Neuroscience, 2016, 44, 2858-2870.	2.6	32
99	Genomic expression during human myelopoiesis. BMC Genomics, 2007, 8, 264.	2.8	31
100	Cancer gene prioritization by integrative analysis of mRNA expression and DNA copy number data: a comparative review. Briefings in Bioinformatics, 2013, 14, 27-35.	6.5	31
101	Single-keratinocyte transcriptomic analyses identify different clonal types and proliferative potential mediated by FOXM1 in human epidermal stem cells. Nature Communications, 2021, 12, 2505.	12.8	31
102	Glycolysis downregulation is a hallmark of HIVâ€1 latency and sensitizes infected cells to oxidative stress. EMBO Molecular Medicine, 2021, 13, e13901.	6.9	30
103	Comparative genomics revealed key molecular targets to rapidly convert a reference rifamycin-producing bacterial strain into an overproducer by genetic engineering. Metabolic Engineering, 2014, 26, 1-16.	7.0	29
104	Allosteric modulation of metabotropic glutamate receptor 4 activates IDO1-dependent, immunoregulatory signaling in dendritic cells. Neuropharmacology, 2016, 102, 59-71.	4.1	29
105	A novel RNA aptamer identifies plasma membrane ATP synthase beta subunit as an early marker and therapeutic target in aggressive cancer. Breast Cancer Research and Treatment, 2019, 176, 271-289.	2.5	29
106	The Proteasome Inhibitor Bortezomib Controls Indoleamine 2,3-Dioxygenase 1 Breakdown and Restores Immune Regulation in Autoimmune Diabetes. Frontiers in Immunology, 2017, 8, 428.	4.8	28
107	A computational procedure to identify significant overlap of differentially expressed and genomic imbalanced regions in cancer datasets â€. Nucleic Acids Research, 2009, 37, 5057-5070.	14.5	27
108	SPPS of difficult sequences. Chemical Biology and Drug Design, 1997, 49, 103-111.	1.1	27

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109	MafB is a downstream target of the IL-10/STAT3 signaling pathway, involved in the regulation of macrophage de-activation. Biochimica Et Biophysica Acta - Molecular Cell Research, 2014, 1843, 955-964.	4.1	27
110	Complete gene expression profiling of Saccharopolyspora erythraea using GeneChip DNA microarrays. Microbial Cell Factories, 2007, 6, 37.	4.0	25
111	Mining of Biological Data I: Identifying Discriminating Features Via Mean Hypothesis Testing. Metabolic Engineering, 2000, 2, 218-227.	7.0	24
112	The tissue inhibitor of metalloproteinases 1 increases the clonogenic efficiency of human hematopoietic progenitor cells through CD63/PI3K/Akt signaling. Experimental Hematology, 2015, 43, 974-985.e1.	0.4	24
113	Class IA PI3Ks regulate subcellular and functional dynamics of IDO1. EMBO Reports, 2020, 21, e49756.	4.5	24
114	Quantitative phenotypic analysis of multistress response inZygosaccharomyces rouxiicomplex. FEMS Yeast Research, 2014, 14, 586-600.	2.3	23
115	High NRF2 Levels Correlate with Poor Prognosis in Colorectal Cancer Patients and with Sensitivity to the Kinase Inhibitor AT9283 In Vitro. Biomolecules, 2020, 10, 1365.	4.0	22
116	PREDA: an R-package to identify regional variations in genomic data. Bioinformatics, 2011, 27, 2446-2447.	4.1	21
117	Aptamers against mouse and human tumor-infiltrating myeloid cells as reagents for targeted chemotherapy. Science Translational Medicine, 2020, 12, .	12.4	21
118	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.	2.8	20
119	Cell-Type-Specific Analysis of Molecular Pathology in Autism Identifies Common Genes and Pathways Affected Across Neocortical Regions. Molecular Neurobiology, 2020, 57, 2279-2289.	4.0	20
120	UCbase 2.0: ultraconserved sequences database (2014 update). Database: the Journal of Biological Databases and Curation, 2014, 2014, bau062-bau062.	3.0	19
121	Enzymatic Inactivation of Oxysterols in Breast Tumor Cells Constraints Metastasis Formation by Reprogramming the Metastatic Lung Microenvironment. Frontiers in Immunology, 2018, 9, 2251.	4.8	19
122	APTANI2: update of aptamer selection through sequence-structure analysis. Bioinformatics, 2020, 36, 2266-2268.	4.1	19
123	Aberrant transcriptional and post-transcriptional regulation of SPAG5, a YAP-TAZ-TEAD downstream effector, fuels breast cancer cell proliferation. Cell Death and Differentiation, 2021, 28, 1493-1511.	11.2	19
124	Transcriptional, epigenetic and retroviral signatures identify regulatory regions involved in hematopoietic lineage commitment. Scientific Reports, 2016, 6, 24724.	3.3	18
125	Artificial Intelligence for Hospital Health Care: Application Cases and Answers to Challenges in European Hospitals. Healthcare (Switzerland), 2021, 9, 961.	2.0	18
126	CXCL5-mediated accumulation of mature neutrophils in lung cancer tissues impairs the differentiation program of anticancer CD8 T cells and limits the efficacy of checkpoint inhibitors. OncoImmunology, 2022, 11, 2059876.	4.6	18

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127	PTPN11 mutations in childhood acute lymphoblastic leukemia occur as a secondary event associated with high hyperdiploidy. Leukemia, 2010, 24, 232-235.	7.2	17
128	A gene expression signature of Retinoblastoma loss-of-function predicts resistance to neoadjuvant chemotherapy in ER-positive/HER2-positive breast cancer patients. Breast Cancer Research and Treatment, 2018, 170, 329-341.	2.5	17
129	WoPPER: Web server for Position Related data analysis of gene Expression in Prokaryotes. Nucleic Acids Research, 2017, 45, W109-W115.	14.5	16
130	ETV7 regulates breast cancer stem-like cell features by repressing IFN-response genes. Cell Death and Disease, 2021, 12, 742.	6.3	16
131	Motif discovery in promoters of genes co-localized and co-expressed during myeloid cells differentiation. Nucleic Acids Research, 2009, 37, 533-549.	14.5	15
132	Isoprenylcysteine carboxy methyltransferase (ICMT) is associated with tumor aggressiveness and its expression is controlled by the p53 tumor suppressor. Journal of Biological Chemistry, 2019, 294, 5060-5073.	3.4	15
133	Exome sequencing and bioinformatic approaches reveals rare sequence variants involved in cell signalling and elastic fibre homeostasis: new evidence in the development of ectopic calcification. Cellular Signalling, 2019, 59, 131-140.	3.6	15
134	Aging: a portrait from gene expression profile in blood cells. Aging, 2016, 8, 1802-1821.	3.1	15
135	CCR1 and CCR5 mediate cancer-induced myelopoiesis and differentiation of myeloid cells in the tumor. , 2022, 10, e003131.		15
136	Transcriptional profiles in melanocytes from clinically unaffected skin distinguish the neoplastic growth pattern in patients with melanoma. British Journal of Dermatology, 2007, 156, 62-71.	1.5	14
137	MICAL2 is expressed in cancer associated neo-angiogenic capillary endothelia and it is required for endothelial cell viability, motility and VEGF response. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2019, 1865, 2111-2124.	3.8	14
138	EphB6 Regulates TFEB-Lysosomal Pathway and Survival of Disseminated Indolent Breast Cancer Cells. Cancers, 2021, 13, 1079.	3.7	14
139	Fatal cytokine release syndrome by an aberrant FLIP/STAT3 axis. Cell Death and Differentiation, 2022, 29, 420-438.	11.2	14
140	Gene expression profiling of human fibrocytic myeloid-derived suppressor cells (f-MDSCs). Genomics Data, 2014, 2, 389-392.	1.3	12
141	Computational methods for analyzing genome-wide chromosome conformation capture data. Current Opinion in Biotechnology, 2018, 54, 98-105.	6.6	12
142	GATA Factor-Mediated Gene Regulation in Human Erythropoiesis. IScience, 2020, 23, 101018.	4.1	11
143	COVID-19 health policy evaluation: integrating health and economic perspectives with a data envelopment analysis approach. European Journal of Health Economics, 2022, 23, 1263-1285.	2.8	11
144	Algorithm for automatic genotype calling of single nucleotide polymorphisms using the full course of TaqMan real-time data. Nucleic Acids Research, 2006, 34, e56-e56.	14.5	10

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145	Mutated clones driving leukemic transformation are already detectable at the single-cell level in CD34-positive cells in the chronic phase of primary myelofibrosis. Npj Precision Oncology, 2021, 5, 4.	5.4	10
146	Identifying and discriminating seismic patterns leading flank eruptions at Mt. Etna Volcano during 1981â€“1996. Journal of Volcanology and Geothermal Research, 2001, 106, 211-228.	2.1	9
147	Microarray data mining using Bioconductor packages. BMC Proceedings, 2009, 3, S9.	1.6	9
148	GDA, a web-based tool for Genomics and Drugs integrated analysis. Nucleic Acids Research, 2018, 46, W148-W156.	14.5	9
149	Identifying seismicity patterns leading flank eruptions at Mt. Etna Volcano during 1981-1996. Geophysical Research Letters, 1999, 26, 2105-2108.	4.0	8
150	Computational Methods for the Integrative Analysis of Genomics and Pharmacological Data. Frontiers in Oncology, 2020, 10, 185.	2.8	8
151	Gene expression profile correlates with molecular and clinical features in patients with myelofibrosis. Blood Advances, 2021, 5, 1452-1462.	5.2	8
152	An improved system for automated peptide synthesis. Chemical Engineering and Technology, 1995, 18, 210-215.	1.5	7
153	Fermentation Diagnosis by Multivariate Statistical Analysis. Applied Biochemistry and Biotechnology, 2002, 102-103, 049-062.	2.9	7
154	Impact of probe annotation on the integration of miRNAâ€“mRNA expression profiles for miRNA target detection. Nucleic Acids Research, 2010, 38, e97-e97.	14.5	7
155	ASB2 is a direct target of FLI1 that sustains NF-Î°B pathway activation in germinal center-derived diffuse large B-cell lymphoma. Journal of Experimental and Clinical Cancer Research, 2021, 40, 357.	8.6	7
156	Marker Identification and Classification of Cancer Types Using Gene Expression Data and SIMCA. Methods of Information in Medicine, 2004, 43, 4-8.	1.2	6
157	Acute Leukemia Subclassification: A Marker Protein Expression Perspective. Hematology, 2004, 9, 165-170.	1.5	6
158	Integrative analysis of copy number and gene expression data suggests novel pathogenetic mechanisms in primary myelofibrosis. International Journal of Cancer, 2016, 138, 1657-1669.	5.1	6
159	Chromosome positioning in interphase nuclei of hematopoietic stem cell and myeloid precursor. Hematology Reports, 2018, 10, 7515.	0.8	6
160	RNA-seq in DMD urinary stem cells recognized muscle-related transcription signatures and addressed the identification of atypical mutations by whole-genome sequencing. Human Genetics and Genomics Advances, 2022, 3, 100054.	1.7	6
161	RNA aptamers specific for transmembrane p24 trafficking protein 6 and Clusterin for the targeted delivery of imaging reagents and RNA therapeutics to human Î² cells. Nature Communications, 2022, 13, 1815.	12.8	6
162	Immunophenotype signature as a tool to define prognostic subgroups in childhood acute myeloid leukemia. Leukemia, 2006, 20, 888-891.	7.2	5

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163	CRITICAL ANALYSIS OF TRANSCRIPTIONAL AND POST-TRANSCRIPTIONAL REGULATORY NETWORKS IN MULTIPLE MYELOMA. , 2009, , 397-408.		5
164	Artificial neural network technologies to identify biomarkers for therapeutic intervention. Current Opinion in Molecular Therapeutics, 2004, 6, 616-23.	2.8	5
165	Automation of the liquid-phase synthesis of biopolymers. Journal of Chemical Technology and Biotechnology, 1998, 71, 77-83.	3.2	4
166	Synthetic Peptides Derived from the Angiostatin K4 Domain Inhibit Endothelial Cell Migration. ChemBioChem, 2003, 4, 1238-1242.	2.6	4
167	Anticancer innovative therapy congress: Highlights from the 10th anniversary edition. Cytokine and Growth Factor Reviews, 2021, 59, 1-8.	7.2	4
168	Genome-Wide Definition of Promoter and Enhancer Usage during Neural Induction of Human Embryonic Stem Cells. PLoS ONE, 2015, 10, e0126590.	2.5	4
169	Urine-Derived Stem Cells Express 571 Neuromuscular Disorders Causing Genes, Making Them a Potential in vitro Model for Rare Genetic Diseases. Frontiers in Physiology, 2021, 12, 716471.	2.8	4
170	Disjoint PCA models for marker identification and classification of cancer types using gene expression data. , 0, , .		3
171	A multifactorial â€˜Consensus Signatureâ€™ by in silico analysis to predict response to neoadjuvant anthracycline-based chemotherapy in triple-negative breast cancer. Npj Breast Cancer, 2015, 1, 15003.	5.2	3
172	Characterization of GECPAR, a noncoding RNA that regulates the transcriptional program of diffuse large B cell lymphoma. Haematologica, 2021, , .	3.5	3
173	Human T cells engineered with a leukemia lipid-specific TCR enables donor-unrestricted recognition of CD1c-expressing leukemia. Nature Communications, 2021, 12, 4844.	12.8	3
174	Computational Analysis of Hi-C Data. Methods in Molecular Biology, 2021, 2157, 103-125.	0.9	3
175	Differential proteomic profile of leukemic CD34+ progenitor cells from chronic myeloid leukemia patients. Oncotarget, 2018, 9, 21758-21769.	1.8	3
176	A comprehensive molecular and morphological study of the effects of space flight on human capillary endothelial cells: sample quality assessment and preliminary results.. Frontiers in Physiology, 0, 9, .	2.8	3
177	The Genome-Wide Impact of Nipblb Loss-of-Function on Zebrafish Gene Expression. International Journal of Molecular Sciences, 2020, 21, 9719.	4.1	2
178	Marker identification and classification of cancer types using gene expression data and SIMCA. Methods of Information in Medicine, 2004, 43, 4-8.	1.2	2
179	Database Mining Tools for Bioprocess Analysis. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 1998, 31, 405-410.	0.4	1
180	Quantification of Data Clusters for Bioprocess Performance Classification via Artificial Neural Networks. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 1998, 31, 439-444.	0.4	1

#	Article	IF	Citations
181	A novel algorithm for the coupling control in solidâ€phase peptide synthesis. Chemical Biology and Drug Design, 1997, 50, 231-237.	1.1	1
182	In silico analysis of a multifactorial consensus signature (ConSig) for predicting response to anthracycline (A)-based neoadjuvant chemotherapy (NAC) in triple-negative breast cancer (TNBC) patients (pts).. Journal of Clinical Oncology, 2014, 32, 1025-1025.	1.6	1
183	A COMPUTATIONAL PROCEDURE FOR THE INTEGRATIVE ANALYSIS OF GENOMIC DATA AT THE SINGLE SAMPLE LEVEL. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2007, 40, 243-248.	0.4	0
184	Mutations and Drugs Portal (MDP): A Database Linking Drug Response Data and Genomic Information. , 2016, , .		0
185	Gene signatures as potential predictive markers of response to neoadjuvant chemotherapy in ER+/HER2+ breast cancer patients. Annals of Oncology, 2017, 28, v25-v26.	1.2	0
186	NEXT GENERATION SEQUENCING AND EXPERIMENTAL MYOLOGY. Neuromuscular Disorders, 2018, 28, S145.	0.6	0
187	PO-298 MYC favours the onset of tumour initiating cells by inducing epigenetic reprogramming of mammary epithelial cells towards a stem cell-like state. ESMO Open, 2018, 3, A137-A138.	4.5	0
188	P.134Physical and transcriptional characterization of human urinary stem cell populations. Neuromuscular Disorders, 2019, 29, S87.	0.6	0
189	P.386Genome and transcriptome analysis of COLVI genes and characterization of a new promising cellular model. Neuromuscular Disorders, 2019, 29, S194.	0.6	0
190	THE NONCODING RNA GECPAR IS INVOLVED IN WNT SIGNALING AND HAS TUMOR-SUPPRESSOR ACTIVITY IN DIFFUSE LARGE B CELL LYMPHOMA. Hematological Oncology, 2019, 37, 77-77.	1.7	0
191	Gene Expression Profiling of Plasma Cell Dyscrasias: The Role of IGH Translocations in the Heterogeneity of Multiple Myeloma.. Blood, 2004, 104, 4845-4845.	1.4	0
192	Identification of New Genomic Lesions in Childhood ALL without Known Genetic Aberrations: A Microarray Study of Gene Expression and Genotype Data.. Blood, 2006, 108, 2066-2066.	1.4	0
193	Proteomic Profile Of CD34+ Cells From Chronic Myeloid Leukemia Patients and From Normal Donors. Blood, 2013, 122, 2712-2712.	1.4	0
194	Revealing the Generation of Human Memory Stem T Cells in Haploidentical T-Replete Hematopoietic Stem Cell Transplantation. Blood, 2014, 124, 192-192.	1.4	0
195	Integrative Analysis of Copy Number and Gene Expression Data Suggests Novel Pathogenetic Mechanisms in Primary Myelofibrosis. Blood, 2015, 126, 2830-2830.	1.4	0
196	Abstract 1449:In vivotargeted silencing of CCR1 and CCR5 repolarizes pro-tumoral myeloid cells in retinoblastoma positive neutrophils with a strong anti-tumor activity. , 2016, , .		0
197	Abstract P6-01-05: Novel cytotoxic RNA aptamers that distinguish between metastasis-prone and indolent breast and prostate cancers. , 2017, , .		0
198	Abstract P1-09-13: A RB-1 loss-of-function gene-signature (RBsig) predicts resistance to neoadjuvant chemotherapy in HER2+/ER+ breast cancer patients. , 2017, , .		0

#	Article	IF	Citations
199	A RB-1 loss of function gene-signature (RBsig) as a tool to predict response to neoadjuvant chemotherapy (CT) plus anti-HER2 agents (H): A substudy of the NeoALTTO trial (BIG 1-06).. Journal of Clinical Oncology, 2018, 36, 570-570.	1.6	0
200	Abstract PR16: RNA aptamers specific for tumor-infiltrating myeloid cells. , 2020, , .		0
201	Abstract CT261: METAMECH -A Master Observational Trial empowering mechanobiology translational research and mechanobased proof of concept trials in breast cancer. , 2020, , .		0
202	Abstract PO-07: The FLI1 direct target ASB2 promotes NF-KB pathway activation in diffuse large B-cell lymphoma of the germinal center B-cell type. , 2020, , .		0