Paul S Meltzer

List of Publications by Year
in descending order

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321 papers	42,094 citations	2963 93 h-index	2500 196 g-index
339 all docs	339 docs citations	339 times ranked	46670 citing authors

#	Article	IF	Citations
1	Classification and diagnostic prediction of cancers using gene expression profiling and artificial neural networks. Nature Medicine, 2001, 7, 673-679.	15.2	2,352
2	Mutations of a mutS homolog in hereditary nonpolyposis colorectal cancer. Cell, 1993, 75, 1215-1225.	13.5	2,195
3	Vascular Channel Formation by Human Melanoma Cells in Vivo and in Vitro: Vasculogenic Mimicry. American Journal of Pathology, 1999, 155, 739-752.	1.9	1,705
4	Gene-Expression Profiles in Hereditary Breast Cancer. New England Journal of Medicine, 2001, 344, 539-548.	13.9	1,669
5	Rare Structural Variants Disrupt Multiple Genes in Neurodevelopmental Pathways in Schizophrenia. Science, 2008, 320, 539-543.	6.0	1,654
6	High frequency of BRAF mutations in nevi. Nature Genetics, 2003, 33, 19-20.	9.4	1,547
7	Expression profiling using cDNA microarrays. Nature Genetics, 1999, 21, 10-14.	9.4	1,529
8	AIB1, a Steroid Receptor Coactivator Amplified in Breast and Ovarian Cancer. Science, 1997, 277, 965-968.	6.0	1,514
9	High-Resolution Mapping andÂCharacterization of Open Chromatin across the Genome. Cell, 2008, 132, 311-322.	13.5	1,246
10	Mutations in the human Jagged1 gene are responsible for Alagille syndrome. Nature Genetics, 1997, 16, 235-242.	9.4	1,072
11	MicroRNA Expression, Survival, and Response to Interferon in Liver Cancer. New England Journal of Medicine, 2009, 361, 1437-1447.	13.9	778
12	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. Nature, 2018, 555, 371-376.	13.7	649
13	Expression profiling identifies the cytoskeletal organizer ezrin and the developmental homeoprotein Six-1 as key metastatic regulators. Nature Medicine, 2004, 10, 175-181.	15.2	480
14	Functionally defined therapeutic targets in diffuse intrinsic pontine glioma. Nature Medicine, 2015, 21, 555-559.	15.2	473
15	Mechanisms of sarcoma development. Nature Reviews Cancer, 2003, 3, 685-694.	12.8	406
16	MYC-driven accumulation of 2-hydroxyglutarate is associated with breast cancer prognosis. Journal of Clinical Investigation, 2014, 124, 398-412.	3.9	348
17	Comparative genomic hybridization using oligonucleotide microarrays and total genomic DNA. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 17765-17770.	3.3	336
18	Small RNAs with big impacts. Nature, 2005, 435, 745-746.	13.7	324

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19	Common Molecular Subtypes Among Asian Hepatocellular Carcinoma and Cholangiocarcinoma. Cancer Cell, 2017, 32, 57-70.e3.	7.7	324
20	Fluorescent cDNA microarray hybridization reveals complexity and heterogeneity of cellular genotoxic stress responses. Oncogene, 1999, 18, 3666-3672.	2.6	314
21	Gene Expression Profiling of Human Sarcomas: Insights into Sarcoma Biology. Cancer Research, 2005, 65, 9226-9235.	0.4	312
22	Thyroid Hormone Regulation of Hepatic Genes in Vivo Detected by Complementary DNA Microarray. Molecular Endocrinology, 2000, 14, 947-955.	3.7	303
23	Molecular Subtypes of<i>KIT/PDGFRA</i>Wild-Type Gastrointestinal Stromal Tumors. JAMA Oncology, 2016, 2, 922.	3.4	291
24	Data management and analysis for gene expression arrays. Nature Genetics, 1998, 20, 19-23.	9.4	290
25	Succinate Dehydrogenase Mutation Underlies Global Epigenomic Divergence in Gastrointestinal Stromal Tumor. Cancer Discovery, 2013, 3, 648-657.	7.7	288
26	Interaction of the Glucocorticoid Receptor with the Chromatin Landscape. Molecular Cell, 2008, 29, 611-624.	4.5	285
27	Interferon-Î³ links ultraviolet radiation to melanomagenesis in mice. Nature, 2011, 469, 548-553.	13.7	264
28	Rapid generation of region specific probes by chromosome microdissection and their application. Nature Genetics, 1992, 1, 24-28.	9.4	261
29	Melanoma mouse model implicates metabotropic glutamate signaling in melanocytic neoplasia. Nature Genetics, 2003, 34, 108-112.	9.4	260
30	Interaction between the microbiome and TP53 in human lung cancer. Genome Biology, 2018, 19, 123.	3.8	247
31	Sunitinib in patients with chemotherapy-refractory thymoma and thymic carcinoma: an open-label phase 2 trial. Lancet Oncology, The, 2015, 16, 177-186.	5.1	240
32	The Exomes of the NCI-60 Panel: A Genomic Resource for Cancer Biology and Systems Pharmacology. Cancer Research, 2013, 73, 4372-4382.	0.4	239
33	Cloning a novel member of the human interferon-inducible gene family associated with control of tumorigenicity in a model of human melanoma. Oncogene, 1997, 15, 453-457.	2.6	238
34	High prevalence of MAP2K1 mutations in variant and IGHV4-34â€"expressing hairy-cell leukemias. Nature Genetics, 2014, 46, 8-10.	9.4	236
35	Integrating Global Gene Expression and Radiation Survival Parameters across the 60 Cell Lines of the National Cancer Institute Anticancer Drug Screen. Cancer Research, 2008, 68, 415-424.	0.4	226
36	Soft tissue sarcomas of adults: state of the translational science. Clinical Cancer Research, 2003, 9, 1941-56.	3.2	224

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37	DNase-chip: a high-resolution method to identify DNase I hypersensitive sites using tiled microarrays. Nature Methods, 2006, 3, 503-509.	9.0	222
38	Activity of durvalumab plus olaparib in metastatic castration-resistant prostate cancer in men with and without DNA damage repair mutations. , 2018, 6, 141.		214
39	New Horizons in the Treatment of Osteosarcoma. New England Journal of Medicine, 2021, 385, 2066-2076.	13.9	210
40	Pim-1 is up-regulated by constitutively activated FLT3 and plays a role in FLT3-mediated cell survival. Blood, 2005, 105, 1759-1767.	0.6	209
41	A specific missense mutation in GTF2I occurs at high frequency in thymic epithelial tumors. Nature Genetics, 2014, 46, 844-849.	9.4	208
42	DNA Breaks and End Resection Measured Genome-wide by End Sequencing. Molecular Cell, 2016, 63, 898-911.	4.5	206
43	Activating Signal Cointegrator 2 Belongs to a Novel Steady-State Complex That Contains a Subset of Trithorax Group Proteins. Molecular and Cellular Biology, 2003, 23, 140-149.	1.1	202
44	Point Mutations in Exon 1B of APC Reveal Gastric Adenocarcinoma and Proximal Polyposis of the Stomach as a Familial Adenomatous Polyposis Variant. American Journal of Human Genetics, 2016, 98, 830-842.	2.6	201
45	Transcription Program of Human Herpesvirus 8 (Kaposi's Sarcoma-Associated Herpesvirus). Journal of Virology, 2001, 75, 4843-4853.	1.5	198
46	Genome-Wide Identification of PAX3-FKHR Binding Sites in Rhabdomyosarcoma Reveals Candidate Target Genes Important for Development and Cancer. Cancer Research, 2010, 70, 6497-6508.	0.4	195
47	Genome-Wide Analysis of Menin Binding Provides Insights into MEN1 Tumorigenesis. PLoS Genetics, 2006, 2, e51.	1.5	193
48	Gene expression profile in multiple sclerosis patients and healthy controls: identifying pathways relevant to disease. Human Molecular Genetics, 2003, 12, 2191-2199.	1.4	191
49	A Nuclear Factor, ASC-2, as a Cancer-amplified Transcriptional Coactivator Essential for Ligand-dependent Transactivation by Nuclear Receptors in Vivo. Journal of Biological Chemistry, 1999, 274, 34283-34293.	1.6	190
50	Analyses of Resected Human Brain Metastases of Breast Cancer Reveal the Association between Up-Regulation of Hexokinase 2 and Poor Prognosis. Molecular Cancer Research, 2009, 7, 1438-1445.	1.5	185
51	A Polymorphism in IRF4 Affects Human Pigmentation through a Tyrosinase-Dependent MITF/TFAP2A Pathway. Cell, 2013, 155, 1022-1033.	13.5	184
52	Molecular classification of familial non-BRCA1/BRCA2 breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 2532-2537.	3.3	182
53	Specific Chromosomal Aberrations and Amplification of the AIB1 Nuclear Receptor Coactivator Gene in Pancreatic Carcinomas. American Journal of Pathology, 1999, 154, 525-536.	1.9	181
54	Genome-wide association study identifies two susceptibility loci for osteosarcoma. Nature Genetics, 2013, 45, 799-803.	9.4	181

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55	Immunohistochemical Loss of Succinate Dehydrogenase Subunit A (SDHA) in Gastrointestinal Stromal Tumors (GISTs) Signals SDHA Germline Mutation. American Journal of Surgical Pathology, 2013, 37, 234-240.	2.1	178
56	Differential responses of stress genes to low dose-rate gamma irradiation. Molecular Cancer Research, 2003, 1, 445-52.	1.5	177
57	Expression Profiling of Synovial Sarcoma by cDNA Microarrays. American Journal of Pathology, 2002, 161, 1587-1595.	1.9	173
58	Microarray expression profiling in melanoma reveals a BRAF mutation signature. Oncogene, 2004, 23, 4060-4067.	2.6	169
59	Evidence for an Unanticipated Relationship between Undifferentiated Pleomorphic Sarcoma and Embryonal Rhabdomyosarcoma. Cancer Cell, 2011, 19, 177-191.	7.7	167
60	Telomere capture stabilizes chromosome breakage. Nature Genetics, 1993, 4, 252-255.	9.4	160
61	Recurrent epimutation of <i>SDHC</i> in gastrointestinal stromal tumors. Science Translational Medicine, 2014, 6, 268ra177.	5.8	158
62	A Molecular Function Map of Ewing's Sarcoma. PLoS ONE, 2009, 4, e5415.	1.1	158
63	Expression profiling in cancer using cDNA microarrays. Electrophoresis, 1999, 20, 223-229.	1.3	157
64	TRAIL induces apoptosis in triple-negative breast cancer cells with a mesenchymal phenotype. Breast Cancer Research and Treatment, 2009, 113, 217-230.	1.1	157
65	Molecular determinants of human uveal melanoma invasion and metastasis. Clinical and Experimental Metastasis, 2002, 19, 233-246.	1.7	149
66	Molecular cytogenetic analysis of i(12p)-negative human male germ cell tumors. Genes Chromosomes and Cancer, 1993, 8, 230-236.	1.5	141
67	A genome-based strategy uncovers frequent BRAF mutations in melanoma. Cancer Cell, 2002, 2, 5-7.	7.7	139
68	Identification of cryptic sites of DNA sequence amplification in human breast cancer by chromosome microdissection. Nature Genetics, 1994, 8, 155-161.	9.4	137
69	Methylation profiling of mediastinal gray zone lymphoma reveals a distinctive signature with elements shared by classical Hodgkin's lymphoma and primary mediastinal large B-cell lymphoma. Haematologica, 2011, 96, 558-566.	1.7	135
70	Biology of childhood osteogenic sarcoma and potential targets for therapeutic development: meeting summary. Clinical Cancer Research, 2003, 9, 5442-53.	3.2	135
71	Multivariate Measurement of Gene Expression Relationships. Genomics, 2000, 67, 201-209.	1.3	133
72	Expression of multiple molecular phenotypes by aggressive melanoma tumor cells: role in vasculogenic mimicry. Critical Reviews in Oncology/Hematology, 2002, 44, 17-27.	2.0	132

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73	Vorinostat Inhibits Brain Metastatic Colonization in a Model of Triple-Negative Breast Cancer and Induces DNA Double-Strand Breaks. Clinical Cancer Research, 2009, 15, 6148-6157.	3.2	132
74	Stress-specific signatures: expression profiling of p53 wild-type and -null human cells. Oncogene, 2005, 24, 4572-4579.	2.6	131
75	Toward a Drug Development Path That Targets Metastatic Progression in Osteosarcoma. Clinical Cancer Research, 2014, 20, 4200-4209.	3.2	127
76	Positively selected enhancer elements endow osteosarcoma cells with metastatic competence. Nature Medicine, 2018, 24, 176-185.	15.2	126
77	Gene-target recognition among members of the Myc superfamily and implications for oncogenesis. Nature Genetics, 2000, 24, 113-119.	9.4	125
78	Array comparative genomic hybridization-based characterization of genetic alterations in pulmonary neuroendocrine tumors. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 13040-13045.	3.3	123
79	Characterization of the 12q13-15 amplicon in soft tissue tumors. Cancer Genetics and Cytogenetics, 1995, 83, 32-36.	1.0	119
80	Expression of the cytoskeleton linker protein ezrin in human cancers. Clinical and Experimental Metastasis, 2007, 24, 69-78.	1.7	118
81	Generation of band-specific painting probes from a single microdissected chromosome. Human Molecular Genetics, 1993, 2, 1117-1121.	1.4	116
82	Rapid Generation of Whole Chromosome Painting Probes (WCPs) by Chromosome Microdissection. Genomics, 1994, 22, 101-107.	1.3	115
83	Loss-of-Function Fibroblast Growth Factor Receptor-2 Mutations in Melanoma. Molecular Cancer Research, 2009, 7, 41-54.	1.5	112
84	Genome-wide depletion of replication initiation events in highly transcribed regions. Genome Research, 2011, 21, 1822-1832.	2.4	112
85	Effects of ligand and thyroid hormone receptor isoforms on hepatic gene expression profiles of thyroid hormone receptor knockout mice. EMBO Reports, 2003, 4, 581-587.	2.0	110
86	Nm23-H1 Suppresses Tumor Cell Motility by Down-regulating the Lysophosphatidic Acid Receptor <i>EDG2</i>. Cancer Research, 2007, 67, 7238-7246.	0.4	110
87	Genome-wide expression changes induced by HTLV-1 Tax: evidence for MLK-3 mixed lineage kinase involvement in Tax-mediated NF-Î°B activation. Oncogene, 2001, 20, 4484-4496.	2.6	109
88	Transcriptional activation by the thyroid hormone receptor through ligand-dependent receptor recruitment and chromatin remodelling. Nature Communications, 2015, 6, 7048.	5.8	106
89	General nonlinear framework for the analysis of gene interaction via multivariate expression arrays. Journal of Biomedical Optics, 2000, 5, 411.	1.4	104
90	An Integrated Prognostic Classifier for Stage I Lung Adenocarcinoma Based on mRNA, microRNA, and DNA Methylation Biomarkers. Journal of Thoracic Oncology, 2015, 10, 1037-1048.	0.5	103

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91	Separate amplified regions encompassingCDK4 andMDM2 in human sarcomas. , 1996, 17, 254-259.		102
92	An Unliganded Thyroid Hormone Î² Receptor Activates the Cyclin D1/Cyclin-Dependent Kinase/Retinoblastoma/E2F Pathway and Induces Pituitary Tumorigenesis. Molecular and Cellular Biology, 2005, 25, 124-135.	1.1	100
93	Oncogenic ETS fusions deregulate E2F3 target genes in Ewing sarcoma and prostate cancer. Genome Research, 2013, 23, 1797-1809.	2.4	99
94	DNA Methylation Profiling Identifies Global Methylation Differences and Markers of Adrenocortical Tumors. Journal of Clinical Endocrinology and Metabolism, 2012, 97, E1004-E1013.	1.8	98
95	Clinical differentiation between proteus syndrome and hemihyperplasia: Description of a distinct form of hemihyperplasia. , 1998, 79, 311-318.		97
96	Archival Fine-Needle Aspiration Cytopathology (FNAC) Samples. Journal of Molecular Diagnostics, 2010, 12, 739-745.	1.2	97
97	Harnessing synthetic lethality to predict the response to cancer treatment. Nature Communications, 2018, 9, 2546.	5.8	97
98	Repeat expansions confer WRN dependence in microsatellite-unstable cancers. Nature, 2020, 586, 292-298.	13.7	95
99	Data analysis and integration: of steps and arrows. Nature Genetics, 1999, 22, 213-215.	9.4	93
100	Disease fingerprinting with cDNA microarrays reveals distinct gene expression profiles in lethal typeâ€1 and typeâ€2 cytokineâ€mediated inflammatory reactions. FASEB Journal, 2001, 15, 2545-2547.	0.2	92
101	A p21-ZEB1 Complex Inhibits Epithelial-Mesenchymal Transition through the MicroRNA 183-96-182 Cluster. Molecular and Cellular Biology, 2014, 34, 533-550.	1.1	92
102	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. Human Molecular Genetics, 2014, 23, 6616-6633.	1.4	90
103	Focus on sarcomas. Cancer Cell, 2002, 2, 175-178.	7.7	89
104	<i>SLFN11</i> Is a Transcriptional Target of EWS-FLI1 and a Determinant of Drug Response in Ewing Sarcoma. Clinical Cancer Research, 2015, 21, 4184-4193.	3.2	89
105	Characterization of the metastatic phenotype of a panel of established osteosarcoma cells. Oncotarget, 2015, 6, 29469-29481.	0.8	89
106	A Genome-Wide Scan Identifies Variants in <i>NFIB</i> Associated with Metastasis in Patients with Osteosarcoma. Cancer Discovery, 2015, 5, 920-931.	7.7	88
107	Separate and variably shaped chromosome arm domains are disclosed by chromosome arm painting in human cell nuclei. Chromosome Research, 1998, 6, 25-33.	1.0	87
108	Lineage of origin in rhabdomyosarcoma informs pharmacological response. Genes and Development, 2014, 28, 1578-1591.	2.7	87

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109	Chromothripsis and Focal Copy Number Alterations Determine Poor Outcome in Malignant Melanoma. Cancer Research, 2013, 73, 1454-1460.	0.4	86
110	Provocative questions in osteosarcoma basic and translational biology: A report from the Children's Oncology Group. Cancer, 2019, 125, 3514-3525.	2.0	86
111	SCLC-CellMiner: A Resource for Small Cell Lung Cancer Cell Line Genomics and Pharmacology Based on Genomic Signatures. Cell Reports, 2020, 33, 108296.	2.9	86
112	The Synovial Sarcomaâ€"Associated SS18-SSX2 Fusion Protein Induces Epigenetic Gene (De)Regulation. Cancer Research, 2006, 66, 9474-9482.	0.4	85
113	Antagonistic Cross-Regulation between Sox9 and Sox10 Controls an Anti-tumorigenic Program in Melanoma. PLoS Genetics, 2015, 11, e1004877.	1.5	85
114	Lipid defect underlies selective skin barrier impairment of an epidermal-specific deletion of Gata-3. Journal of Cell Biology, 2006, 175, 661-670.	2.3	80
115	Unfavorable prognosis of <i>CRTC1â€MAML2</i> positive mucoepidermoid tumors with <i>CDKN2A</i> deletions. Genes Chromosomes and Cancer, 2010, 49, 59-69.	1.5	80
116	Nonrandom chromosome alterations in rhabdomyosarcoma. Cancer Genetics and Cytogenetics, 1985, 16, 189-197.	1.0	79
117	CDC91L1 (PIG-U) is a newly discovered oncogene in human bladder cancer. Nature Medicine, 2004, 10, 374-381.	15.2	79
118	Suppressor role of activating transcription factor 2 (ATF2) in skin cancer. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 1674-1679.	3.3	78
119	Twelve amplified and expressed genes localized in a single domain in glioma. Human Genetics, 1996, 98, 625-628.	1.8	77
120	A chromatin structureâ€based model accurately predicts <scp>DNA</scp> replication timing in human cells. Molecular Systems Biology, 2014, 10, 722.	3.2	77
121	The gene expression response of breast cancer to growth regulators: patterns and correlation with tumor expression profiles. Cancer Research, 2003, 63, 7158-66.	0.4	75
122	Thyroid Hormone Responsive Genes in Cultured Human Fibroblasts. Journal of Clinical Endocrinology and Metabolism, 2005, 90, 936-943.	1.8	74
123	Translocation 1;7 in hematologic disorders: A brief review of 22 cases. Cancer Genetics and Cytogenetics, 1985, 18, 207-213.	1.0	72
124	Rapid generation of region-specific genomic clones by chromosome microdissection: Isolation of DNA from a region frequently deleted in malignant melanoma. Genomics, 1992, 14, 680-684.	1.3	71
125	Generation and analysis of melanoma SAGE libraries: SAGE advice on the melanoma transcriptome. Oncogene, 2004, 23, 2264-2274.	2.6	71
126	Alterations in genomic profiles during tumor progression in a mouse model of follicular thyroid carcinoma. Carcinogenesis, 2003, 24, 1467-1479.	1.3	68

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127	Identification and Cloning of the Human Homolog (JAG1) of the RatJagged1Gene from the Alagille Syndrome Critical Region at 20p12. Genomics, 1997, 43, 376-379.	1.3	67
128	Biological indicators for the identification of ionizing radiation exposure in humans. Expert Review of Molecular Diagnostics, 2001, 1, 211-219.	1.5	66
129	NUP98â€“PHF23 Is a Chromatin-Modifying Oncoprotein That Causes a Wide Array of Leukemias Sensitive to Inhibition of PHD Histone Reader Function. Cancer Discovery, 2014, 4, 564-577.	7.7	66
130	Hypoxia Modulates EWS-FLI1 Transcriptional Signature and Enhances the Malignant Properties of Ewing's Sarcoma Cells <i>In vitro</i>. Cancer Research, 2010, 70, 4015-4023.	0.4	65
131	Melanoblast transcriptome analysis reveals pathways promoting melanoma metastasis. Nature Communications, 2020, 11, 333.	5.8	65
132	Phenol oxidase activation in Drosophila: A cascade of reactions. Biochemical Genetics, 1975, 13, 85-108.	0.8	64
133	Genomic aberrations in pediatric diffuse intrinsic pontine gliomas. Neuro-Oncology, 2012, 14, 326-332.	0.6	62
134	Discovery and validation of methylation markers for endometrial cancer. International Journal of Cancer, 2014, 135, 1860-1868.	2.3	62
135	Microarray analysis of knockout mice identifies cyclin D2 as a possible mediator for the action of thyroid hormone during the postnatal development of the cerebellum. Developmental Biology, 2003, 254, 188-199.	0.9	61
136	Expression and Mutational Status of c-kit in Thymic Epithelial Tumors. Journal of Thoracic Oncology, 2010, 5, 1447-1453.	0.5	61
137	Mutant thyroid hormone receptor beta represses the expression and transcriptional activity of peroxisome proliferator-activated receptor gamma during thyroid carcinogenesis. Cancer Research, 2003, 63, 5274-80.	0.4	61
138	Molecular Grading of Ductal Carcinoma <i>In situ</i> of the Breast. Clinical Cancer Research, 2008, 14, 8244-8252.	3.2	60
139	RNA Sequencing of the NCI-60: Integration into CellMiner and CellMiner CDB. Cancer Research, 2019, 79, 3514-3524.	0.4	58
140	Differentially Painting Human Chromosome Arms with Combined Binary Ratio-labeling Fluorescence In Situ Hybridization. Genome Research, 2000, 10, 861-865.	2.4	56
141	ATP11B mediates platinum resistance in ovarian cancer. Journal of Clinical Investigation, 2013, 123, 2119-2130.	3.9	56
142	Genome-Wide Methylation Patterns in Papillary Thyroid Cancer Are Distinct Based on Histological Subtype and Tumor Genotype. Journal of Clinical Endocrinology and Metabolism, 2014, 99, E329-E337.	1.8	55
143	The second European interdisciplinary Ewing sarcoma research summit - A joint effort to deconstructing the multiple layers of a complex disease. Oncotarget, 2016, 7, 8613-8624.	0.8	55
144	Assessment of Automated Image Analysis of Breast Cancer Tissue Microarrays for Epidemiologic Studies. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 992-999.	1.1	54

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145	Molecular cytogenetic characterization and physical mapping of 12q13â€“15 amplification in human cancers. Genes Chromosomes and Cancer, 1996, 17, 205-214.	1.5	53
146	Spotting the target: microarrays for disease gene discovery. Current Opinion in Genetics and Development, 2001, 11, 258-263.	1.5	51
147	Related subunits of NF-Î°B map to two distinct loci associated with translocations in leukemia, NFKB1 and NFKB2. Genomics, 1992, 13, 287-292.	1.3	50
148	Complete sequence analysis of a gene (OS-9) ubiquitously expressed in human tissues and amplified in sarcomas. Molecular Carcinogenesis, 1996, 15, 270-275.	1.3	50
149	Transgenic Targeting of a Dominant Negative Corepressor to Liver Blocks Basal Repression by Thyroid Hormone Receptor and Increases Cell Proliferation. Journal of Biological Chemistry, 2001, 276, 15066-15072.	1.6	49
150	The NCI-60 Methylome and Its Integration into CellMiner. Cancer Research, 2017, 77, 601-612.	0.4	48
151	Preferential Localization of Human Origins of DNA Replication at the 5â€²-Ends of Expressed Genes and at Evolutionarily Conserved DNA Sequences. PLoS ONE, 2011, 6, e17308.	1.1	47
152	Alpha-globulins suppress human leukocyte tumor necrosis factor secretion. European Journal of Immunology, 1989, 19, 939-942.	1.6	46
153	Verapamil suppresses the emergence of P-glycoprotein-mediated multi-drug resistance. , 1996, 66, 520-525.		46
154	Large-Scale Profiling of Archival Lymph Nodes Reveals Pervasive Remodeling of the Follicular Lymphoma Methylome. Cancer Research, 2009, 69, 758-764.	0.4	46
155	Imprints and <i>DPPA3</i> are bypassed during pluripotency- and differentiation-coupled methylation reprogramming in testicular germ cell tumors. Genome Research, 2016, 26, 1490-1504.	2.4	44
156	Characterization of a highly conserved gene (OS4) amplified with CDK4 in human sarcomas. Oncogene, 1997, 15, 1289-1294.	2.6	43
157	A small protein encoded by a putative lncRNA regulates apoptosis and tumorigenicity in human colorectal cancer cells. ELife, 2020, 9, .	2.8	43
158	Bromodomain and Extraterminal Protein Inhibitor JQ1 Suppresses Thyroid Tumor Growth in a Mouse Model. Clinical Cancer Research, 2017, 23, 430-440.	3.2	42
159	Biomarker significance of plasma and tumor miR-21, miR-221, and miR-106a in osteosarcoma. Oncotarget, 2017, 8, 96738-96752.	0.8	41
160	Role of glutathione and its associated enzymes in multidrug-resistant human myeloma cells. Biochemical Pharmacology, 1989, 38, 787-793.	2.0	40
161	Detection of Antisense and Ribozyme Accessible Sites on Native mRNAs: Application to NCOA3 mRNA. Molecular Therapy, 2001, 4, 454-460.	3.7	39
162	Inhibition of Polo-like kinase 1 prevents the growth of metastatic breast cancer cells in the brain. Clinical and Experimental Metastasis, 2011, 28, 899-908.	1.7	39

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163	EWS-FLI1 employs an E2F switch to drive target gene expression. Nucleic Acids Research, 2015, 43, 2780-2789.	6.5	39
164	Copy Number Aberrations of Genes Regulating Normal Thymus Development in Thymic Epithelial Tumors. Clinical Cancer Research, 2013, 19, 1960-1971.	3.2	38
165	Distinct methylation profiles characterize fusion-positive and fusion-negative rhabdomyosarcoma. Modern Pathology, 2015, 28, 1214-1224.	2.9	38
166	Current state of pediatric sarcoma biology and opportunities for future discovery: A report from the sarcoma translational research workshop. Cancer Genetics, 2016, 209, 182-194.	0.2	38
167	Epigenome-wide DNA methylation analysis of small cell lung cancer cell lines suggests potential chemotherapy targets. Clinical Epigenetics, 2020, 12, 93.	1.8	38
168	NCI-60 Whole Exome Sequencing and Pharmacological CellMiner Analyses. PLoS ONE, 2014, 9, e101670.	1.1	38
169	Chromosome arm-specific multicolor FISH. Genes Chromosomes and Cancer, 2001, 30, 105-109.	1.5	37
170	Advanced Bone Formation in Mice with a Dominant-negative Mutation in the Thyroid Hormone Receptor Î² Gene due to Activation of Wnt/Î²-Catenin Protein Signaling. Journal of Biological Chemistry, 2012, 287, 17812-17822.	1.6	37
171	G-Cimp Status Prediction Of Glioblastoma Samples Using mRNA Expression Data. PLoS ONE, 2012, 7, e47839.	1.1	37
172	Transcript Mapping in a 46-kb Sequenced Region at the Core of 12q13.3 Amplification in Human Cancers. Genomics, 1997, 42, 295-301.	1.3	35
173	A combined approach identifies a limited number of new thyroid hormone target genes in post-natal mouse cerebellum. Journal of Molecular Endocrinology, 2007, 39, 17-28.	1.1	35
174	Identification of RECQ1-regulated transcriptome uncovers a role of RECQ1 in regulation of cancer cell migration and invasion. Cell Cycle, 2014, 13, 2431-2445.	1.3	35
175	Targeting loss of the Hippo signaling pathway in <i>NF2</i>-deficient papillary kidney cancers. Oncotarget, 2018, 9, 10723-10733.	0.8	35
176	Lucky draw in the gene raffle. Nature, 2002, 417, 906-907.	13.7	34
177	Constitutive Fmsâ€like tyrosine kinase 3 activation results in specific changes in gene expression in myeloid leukaemic cells. British Journal of Haematology, 2007, 138, 603-615.	1.2	34
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