

Paul S Meltzer

List of Publications by Year in descending order

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321
papers

42,094
citations

2975

93
h-index

2509

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. <i>Nature Medicine</i> , 2001, 7, 673-679.	30.7	2,352
2	Mutations of a mutS homolog in hereditary nonpolyposis colorectal cancer. <i>Cell</i> , 1993, 75, 1215-1225.	28.9	2,195
3	Vascular Channel Formation by Human Melanoma Cells in Vivo and in Vitro: Vasculogenic Mimicry. <i>American Journal of Pathology</i> , 1999, 155, 739-752.	3.8	1,705
4	Gene-Expression Profiles in Hereditary Breast Cancer. <i>New England Journal of Medicine</i> , 2001, 344, 539-548.	27.0	1,669
5	Rare Structural Variants Disrupt Multiple Genes in Neurodevelopmental Pathways in Schizophrenia. <i>Science</i> , 2008, 320, 539-543.	12.6	1,654
6	High frequency of BRAF mutations in nevi. <i>Nature Genetics</i> , 2003, 33, 19-20.	21.4	1,547
7	Expression profiling using cDNA microarrays. <i>Nature Genetics</i> , 1999, 21, 10-14.	21.4	1,529
8	AIB1, a Steroid Receptor Coactivator Amplified in Breast and Ovarian Cancer. <i>Science</i> , 1997, 277, 965-968.	12.6	1,514
9	High-Resolution Mapping and Characterization of Open Chromatin across the Genome. <i>Cell</i> , 2008, 132, 311-322.	28.9	1,246
10	Mutations in the human Jagged1 gene are responsible for Alagille syndrome. <i>Nature Genetics</i> , 1997, 16, 235-242.	21.4	1,072
11	MicroRNA Expression, Survival, and Response to Interferon in Liver Cancer. <i>New England Journal of Medicine</i> , 2009, 361, 1437-1447.	27.0	778
12	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. <i>Nature</i> , 2018, 555, 371-376.	27.8	649
13	Expression profiling identifies the cytoskeletal organizer ezrin and the developmental homeoprotein Six-1 as key metastatic regulators. <i>Nature Medicine</i> , 2004, 10, 175-181.	30.7	480
14	Functionally defined therapeutic targets in diffuse intrinsic pontine glioma. <i>Nature Medicine</i> , 2015, 21, 555-559.	30.7	473
15	Mechanisms of sarcoma development. <i>Nature Reviews Cancer</i> , 2003, 3, 685-694.	28.4	406
16	MYC-driven accumulation of 2-hydroxyglutarate is associated with breast cancer prognosis. <i>Journal of Clinical Investigation</i> , 2014, 124, 398-412.	8.2	348
17	Comparative genomic hybridization using oligonucleotide microarrays and total genomic DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 17765-17770.	7.1	336
18	Small RNAs with big impacts. <i>Nature</i> , 2005, 435, 745-746.	27.8	324

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19	Common Molecular Subtypes Among Asian Hepatocellular Carcinoma and Cholangiocarcinoma. <i>Cancer Cell</i> , 2017, 32, 57-70.e3.	16.8	324
20	Fluorescent cDNA microarray hybridization reveals complexity and heterogeneity of cellular genotoxic stress responses. <i>Oncogene</i> , 1999, 18, 3666-3672.	5.9	314
21	Gene Expression Profiling of Human Sarcomas: Insights into Sarcoma Biology. <i>Cancer Research</i> , 2005, 65, 9226-9235.	0.9	312
22	Thyroid Hormone Regulation of Hepatic Genes in Vivo Detected by Complementary DNA Microarray. <i>Molecular Endocrinology</i> , 2000, 14, 947-955.	3.7	303
23	Molecular Subtypes of <i>KIT/PDGFR</i> Wild-Type Gastrointestinal Stromal Tumors. <i>JAMA Oncology</i> , 2016, 2, 922.	7.1	291
24	Data management and analysis for gene expression arrays. <i>Nature Genetics</i> , 1998, 20, 19-23.	21.4	290
25	Succinate Dehydrogenase Mutation Underlies Global Epigenomic Divergence in Gastrointestinal Stromal Tumor. <i>Cancer Discovery</i> , 2013, 3, 648-657.	9.4	288
26	Interaction of the Glucocorticoid Receptor with the Chromatin Landscape. <i>Molecular Cell</i> , 2008, 29, 611-624.	9.7	285
27	Interferon- β links ultraviolet radiation to melanomagenesis in mice. <i>Nature</i> , 2011, 469, 548-553.	27.8	264
28	Rapid generation of region specific probes by chromosome microdissection and their application. <i>Nature Genetics</i> , 1992, 1, 24-28.	21.4	261
29	Melanoma mouse model implicates metabotropic glutamate signaling in melanocytic neoplasia. <i>Nature Genetics</i> , 2003, 34, 108-112.	21.4	260
30	Interaction between the microbiome and TP53 in human lung cancer. <i>Genome Biology</i> , 2018, 19, 123.	8.8	247
31	Sunitinib in patients with chemotherapy-refractory thymoma and thymic carcinoma: an open-label phase 2 trial. <i>Lancet Oncology</i> , 2015, 16, 177-186.	10.7	240
32	The Exomes of the NCI-60 Panel: A Genomic Resource for Cancer Biology and Systems Pharmacology. <i>Cancer Research</i> , 2013, 73, 4372-4382.	0.9	239
33	Cloning a novel member of the human interferon-inducible gene family associated with control of tumorigenicity in a model of human melanoma. <i>Oncogene</i> , 1997, 15, 453-457.	5.9	238
34	High prevalence of MAP2K1 mutations in variant and IGHV4-34 ⁺ expressing hairy-cell leukemias. <i>Nature Genetics</i> , 2014, 46, 8-10.	21.4	236
35	Integrating Global Gene Expression and Radiation Survival Parameters across the 60 Cell Lines of the National Cancer Institute Anticancer Drug Screen. <i>Cancer Research</i> , 2008, 68, 415-424.	0.9	226
36	Soft tissue sarcomas of adults: state of the translational science. <i>Clinical Cancer Research</i> , 2003, 9, 1941-56.	7.0	224

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37	DNase-chip: a high-resolution method to identify DNase I hypersensitive sites using tiled microarrays. <i>Nature Methods</i> , 2006, 3, 503-509.	19.0	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. <i>New England Journal of Medicine</i> , 2021, 385, 2066-2076.	27.0	210
40	Pim-1 is up-regulated by constitutively activated FLT3 and plays a role in FLT3-mediated cell survival. <i>Blood</i> , 2005, 105, 1759-1767.	1.4	209
41	A specific missense mutation in GTF2I occurs at high frequency in thymic epithelial tumors. <i>Nature Genetics</i> , 2014, 46, 844-849.	21.4	208
42	DNA Breaks and End Resection Measured Genome-wide by End Sequencing. <i>Molecular Cell</i> , 2016, 63, 898-911.	9.7	206
43	Activating Signal Cointegrator 2 Belongs to a Novel Steady-State Complex That Contains a Subset of Trithorax Group Proteins. <i>Molecular and Cellular Biology</i> , 2003, 23, 140-149.	2.3	202
44	Point Mutations in Exon 1B of APC Reveal Gastric Adenocarcinoma and Proximal Polyposis of the Stomach as a Familial Adenomatous Polyposis Variant. <i>American Journal of Human Genetics</i> , 2016, 98, 830-842.	6.2	201
45	Transcription Program of Human Herpesvirus 8 (Kaposi's Sarcoma-Associated Herpesvirus). <i>Journal of Virology</i> , 2001, 75, 4843-4853.	3.4	198
46	Genome-Wide Identification of PAX3-FKHR Binding Sites in Rhabdomyosarcoma Reveals Candidate Target Genes Important for Development and Cancer. <i>Cancer Research</i> , 2010, 70, 6497-6508.	0.9	195
47	Genome-Wide Analysis of Menin Binding Provides Insights into MEN1 Tumorigenesis. <i>PLoS Genetics</i> , 2006, 2, e51.	3.5	193
48	Gene expression profile in multiple sclerosis patients and healthy controls: identifying pathways relevant to disease. <i>Human Molecular Genetics</i> , 2003, 12, 2191-2199.	2.9	191
49	A Nuclear Factor, ASC-2, as a Cancer-amplified Transcriptional Coactivator Essential for Ligand-dependent Transactivation by Nuclear Receptors in Vivo. <i>Journal of Biological Chemistry</i> , 1999, 274, 34283-34293.	3.4	190
50	Analyses of Resected Human Brain Metastases of Breast Cancer Reveal the Association between Up-Regulation of Hexokinase 2 and Poor Prognosis. <i>Molecular Cancer Research</i> , 2009, 7, 1438-1445.	3.4	185
51	A Polymorphism in IRF4 Affects Human Pigmentation through a Tyrosinase-Dependent MITF/TFAP2A Pathway. <i>Cell</i> , 2013, 155, 1022-1033.	28.9	184
52	Molecular classification of familial non- <i>BRCA1/BRCA2</i> breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 2532-2537.	7.1	182
53	Specific Chromosomal Aberrations and Amplification of the AIB1 Nuclear Receptor Coactivator Gene in Pancreatic Carcinomas. <i>American Journal of Pathology</i> , 1999, 154, 525-536.	3.8	181
54	Genome-wide association study identifies two susceptibility loci for osteosarcoma. <i>Nature Genetics</i> , 2013, 45, 799-803.	21.4	181

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55	Immunohistochemical Loss of Succinate Dehydrogenase Subunit A (SDHA) in Gastrointestinal Stromal Tumors (GISTs) Signals SDHA Germline Mutation. <i>American Journal of Surgical Pathology</i> , 2013, 37, 234-240.	3.7	178
56	Differential responses of stress genes to low dose-rate gamma irradiation. <i>Molecular Cancer Research</i> , 2003, 1, 445-52.	3.4	177
57	Expression Profiling of Synovial Sarcoma by cDNA Microarrays. <i>American Journal of Pathology</i> , 2002, 161, 1587-1595.	3.8	173
58	Microarray expression profiling in melanoma reveals a BRAF mutation signature. <i>Oncogene</i> , 2004, 23, 4060-4067.	5.9	169
59	Evidence for an Unanticipated Relationship between Undifferentiated Pleomorphic Sarcoma and Embryonal Rhabdomyosarcoma. <i>Cancer Cell</i> , 2011, 19, 177-191.	16.8	167
60	Telomere capture stabilizes chromosome breakage. <i>Nature Genetics</i> , 1993, 4, 252-255.	21.4	160
61	Recurrent epimutation of <i>SDHC</i> in gastrointestinal stromal tumors. <i>Science Translational Medicine</i> , 2014, 6, 268ra177.	12.4	158
62	A Molecular Function Map of Ewing's Sarcoma. <i>PLoS ONE</i> , 2009, 4, e5415.	2.5	158
63	Expression profiling in cancer using cDNA microarrays. <i>Electrophoresis</i> , 1999, 20, 223-229.	2.4	157
64	TRAIL induces apoptosis in triple-negative breast cancer cells with a mesenchymal phenotype. <i>Breast Cancer Research and Treatment</i> , 2009, 113, 217-230.	2.5	157
65	Molecular determinants of human uveal melanoma invasion and metastasis. <i>Clinical and Experimental Metastasis</i> , 2002, 19, 233-246.	3.3	149
66	Molecular cytogenetic analysis of <i>i(12p)</i> -negative human male germ cell tumors. <i>Genes Chromosomes and Cancer</i> , 1993, 8, 230-236.	2.8	141
67	A genome-based strategy uncovers frequent BRAF mutations in melanoma. <i>Cancer Cell</i> , 2002, 2, 5-7.	16.8	139
68	Identification of cryptic sites of DNA sequence amplification in human breast cancer by chromosome microdissection. <i>Nature Genetics</i> , 1994, 8, 155-161.	21.4	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. <i>Haematologica</i> , 2011, 96, 558-566.	3.5	135
70	Biology of childhood osteogenic sarcoma and potential targets for therapeutic development: meeting summary. <i>Clinical Cancer Research</i> , 2003, 9, 5442-53.	7.0	135
71	Multivariate Measurement of Gene Expression Relationships. <i>Genomics</i> , 2000, 67, 201-209.	2.9	133
72	Expression of multiple molecular phenotypes by aggressive melanoma tumor cells: role in vasculogenic mimicry. <i>Critical Reviews in Oncology/Hematology</i> , 2002, 44, 17-27.	4.4	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. <i>Clinical Cancer Research</i> , 2009, 15, 6148-6157.	7.0	132
74	Stress-specific signatures: expression profiling of p53 wild-type and -null human cells. <i>Oncogene</i> , 2005, 24, 4572-4579.	5.9	131
75	Toward a Drug Development Path That Targets Metastatic Progression in Osteosarcoma. <i>Clinical Cancer Research</i> , 2014, 20, 4200-4209.	7.0	127
76	Positively selected enhancer elements endow osteosarcoma cells with metastatic competence. <i>Nature Medicine</i> , 2018, 24, 176-185.	30.7	126
77	Gene-target recognition among members of the Myc superfamily and implications for oncogenesis. <i>Nature Genetics</i> , 2000, 24, 113-119.	21.4	125
78	Array comparative genomic hybridization-based characterization of genetic alterations in pulmonary neuroendocrine tumors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 13040-13045.	7.1	123
79	Characterization of the 12q13-15 amplicon in soft tissue tumors. <i>Cancer Genetics and Cytogenetics</i> , 1995, 83, 32-36.	1.0	119
80	Expression of the cytoskeleton linker protein ezrin in human cancers. <i>Clinical and Experimental Metastasis</i> , 2007, 24, 69-78.	3.3	118
81	Generation of band-specific painting probes from a single microdissected chromosome. <i>Human Molecular Genetics</i> , 1993, 2, 1117-1121.	2.9	116
82	Rapid Generation of Whole Chromosome Painting Probes (WCPs) by Chromosome Microdissection. <i>Genomics</i> , 1994, 22, 101-107.	2.9	115
83	Loss-of-Function Fibroblast Growth Factor Receptor-2 Mutations in Melanoma. <i>Molecular Cancer Research</i> , 2009, 7, 41-54.	3.4	112
84	Genome-wide depletion of replication initiation events in highly transcribed regions. <i>Genome Research</i> , 2011, 21, 1822-1832.	5.5	112
85	Effects of ligand and thyroid hormone receptor isoforms on hepatic gene expression profiles of thyroid hormone receptor knockout mice. <i>EMBO Reports</i> , 2003, 4, 581-587.	4.5	110
86	Nm23-H1 Suppresses Tumor Cell Motility by Down-regulating the Lysophosphatidic Acid Receptor <i><i>EDG2</i></i> . <i>Cancer Research</i> , 2007, 67, 7238-7246.	0.9	110
87	Genome-wide expression changes induced by HTLV-1 Tax: evidence for MLK-3 mixed lineage kinase involvement in Tax-mediated NF- κ B activation. <i>Oncogene</i> , 2001, 20, 4484-4496.	5.9	109
88	Transcriptional activation by the thyroid hormone receptor through ligand-dependent receptor recruitment and chromatin remodelling. <i>Nature Communications</i> , 2015, 6, 7048.	12.8	106
89	General nonlinear framework for the analysis of gene interaction via multivariate expression arrays. <i>Journal of Biomedical Optics</i> , 2000, 5, 411.	2.6	104
90	An Integrated Prognostic Classifier for Stage I Lung Adenocarcinoma Based on mRNA, microRNA, and DNA Methylation Biomarkers. <i>Journal of Thoracic Oncology</i> , 2015, 10, 1037-1048.	1.1	103

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91	Separate amplified regions encompassing CDK4 and MDM2 in human sarcomas. , 1996, 17, 254-259.		102
92	An Unliganded Thyroid Hormone β 2 Receptor Activates the Cyclin D1/Cyclin-Dependent Kinase/Retinoblastoma/E2F Pathway and Induces Pituitary Tumorigenesis. Molecular and Cellular Biology, 2005, 25, 124-135.	2.3	100
93	Oncogenic ETS fusions deregulate E2F3 target genes in Ewing sarcoma and prostate cancer. Genome Research, 2013, 23, 1797-1809.	5.5	99
94	DNA Methylation Profiling Identifies Global Methylation Differences and Markers of Adrenocortical Tumors. Journal of Clinical Endocrinology and Metabolism, 2012, 97, E1004-E1013.	3.6	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.	2.8	97
97	Harnessing synthetic lethality to predict the response to cancer treatment. Nature Communications, 2018, 9, 2546.	12.8	97
98	Repeat expansions confer WRN dependence in microsatellite-unstable cancers. Nature, 2020, 586, 292-298.	27.8	95
99	Data analysis and integration: of steps and arrows. Nature Genetics, 1999, 22, 213-215.	21.4	93
100	Disease fingerprinting with cDNA microarrays reveals distinct gene expression profiles in lethal type 1 and type 2 cytokine-mediated inflammatory reactions. FASEB Journal, 2001, 15, 2545-2547.	0.5	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.	2.3	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.	2.9	90
103	Focus on sarcomas. Cancer Cell, 2002, 2, 175-178.	16.8	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.	7.0	89
105	Characterization of the metastatic phenotype of a panel of established osteosarcoma cells. Oncotarget, 2015, 6, 29469-29481.	1.8	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.	9.4	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.	2.2	87
108	Lineage of origin in rhabdomyosarcoma informs pharmacological response. Genes and Development, 2014, 28, 1578-1591.	5.9	87

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109	Chromothripsis and Focal Copy Number Alterations Determine Poor Outcome in Malignant Melanoma. <i>Cancer Research</i> , 2013, 73, 1454-1460.	0.9	86
110	Provocative questions in osteosarcoma basic and translational biology: A report from the Children's Oncology Group. <i>Cancer</i> , 2019, 125, 3514-3525.	4.1	86
111	SCLC-CellMiner: A Resource for Small Cell Lung Cancer Cell Line Genomics and Pharmacology Based on Genomic Signatures. <i>Cell Reports</i> , 2020, 33, 108296.	6.4	86
112	The Synovial Sarcoma-associated SS18-SSX2 Fusion Protein Induces Epigenetic Gene (De)Regulation. <i>Cancer Research</i> , 2006, 66, 9474-9482.	0.9	85
113	Antagonistic Cross-Regulation between Sox9 and Sox10 Controls an Anti-tumorigenic Program in Melanoma. <i>PLoS Genetics</i> , 2015, 11, e1004877.	3.5	85
114	Lipid defect underlies selective skin barrier impairment of an epidermal-specific deletion of Gata-3. <i>Journal of Cell Biology</i> , 2006, 175, 661-670.	5.2	80
115	Unfavorable prognosis of <i>CRTC1</i> - <i>MAML2</i> positive mucoepidermoid tumors with <i>CDKN2A</i> deletions. <i>Genes Chromosomes and Cancer</i> , 2010, 49, 59-69.	2.8	80
116	Nonrandom chromosome alterations in rhabdomyosarcoma. <i>Cancer Genetics and Cytogenetics</i> , 1985, 16, 189-197.	1.0	79
117	<i>CDC91L1</i> (PIG-U) is a newly discovered oncogene in human bladder cancer. <i>Nature Medicine</i> , 2004, 10, 374-381.	30.7	79
118	Suppressor role of activating transcription factor 2 (ATF2) in skin cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 1674-1679.	7.1	78
119	Twelve amplified and expressed genes localized in a single domain in glioma. <i>Human Genetics</i> , 1996, 98, 625-628.	3.8	77
120	A chromatin structure-based model accurately predicts <i>DNA</i> replication timing in human cells. <i>Molecular Systems Biology</i> , 2014, 10, 722.	7.2	77
121	The gene expression response of breast cancer to growth regulators: patterns and correlation with tumor expression profiles. <i>Cancer Research</i> , 2003, 63, 7158-66.	0.9	75
122	Thyroid Hormone Responsive Genes in Cultured Human Fibroblasts. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2005, 90, 936-943.	3.6	74
123	Translocation 1;7 in hematologic disorders: A brief review of 22 cases. <i>Cancer Genetics and Cytogenetics</i> , 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. <i>Genomics</i> , 1992, 14, 680-684.	2.9	71
125	Generation and analysis of melanoma SAGE libraries: SAGE advice on the melanoma transcriptome. <i>Oncogene</i> , 2004, 23, 2264-2274.	5.9	71
126	Alterations in genomic profiles during tumor progression in a mouse model of follicular thyroid carcinoma. <i>Carcinogenesis</i> , 2003, 24, 1467-1479.	2.8	68

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127	Identification and Cloning of the Human Homolog (JAG1) of the Rat Jagged1 Gene from the Alagille Syndrome Critical Region at 20p12. <i>Genomics</i> , 1997, 43, 376-379.	2.9	67
128	Biological indicators for the identification of ionizing radiation exposure in humans. <i>Expert Review of Molecular Diagnostics</i> , 2001, 1, 211-219.	3.1	66
129	NUP98â€“PHF23 Is a Chromatin-Modifying Oncoprotein That Causes a Wide Array of Leukemias Sensitive to Inhibition of PHD Histone Reader Function. <i>Cancer Discovery</i> , 2014, 4, 564-577.	9.4	66
130	Hypoxia Modulates EWS-FLI1 Transcriptional Signature and Enhances the Malignant Properties of Ewing's Sarcoma Cells <i>In vitro</i> . <i>Cancer Research</i> , 2010, 70, 4015-4023.	0.9	65
131	Melanoblast transcriptome analysis reveals pathways promoting melanoma metastasis. <i>Nature Communications</i> , 2020, 11, 333.	12.8	65
132	Phenol oxidase activation in <i>Drosophila</i> : A cascade of reactions. <i>Biochemical Genetics</i> , 1975, 13, 85-108.	1.7	64
133	Genomic aberrations in pediatric diffuse intrinsic pontine gliomas. <i>Neuro-Oncology</i> , 2012, 14, 326-332.	1.2	62
134	Discovery and validation of methylation markers for endometrial cancer. <i>International Journal of Cancer</i> , 2014, 135, 1860-1868.	5.1	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. <i>Developmental Biology</i> , 2003, 254, 188-199.	2.0	61
136	Expression and Mutational Status of c-kit in Thymic Epithelial Tumors. <i>Journal of Thoracic Oncology</i> , 2010, 5, 1447-1453.	1.1	61
137	Mutant thyroid hormone receptor beta represses the expression and transcriptional activity of peroxisome proliferator-activated receptor gamma during thyroid carcinogenesis. <i>Cancer Research</i> , 2003, 63, 5274-80.	0.9	61
138	Molecular Grading of Ductal Carcinoma <i>In situ</i> of the Breast. <i>Clinical Cancer Research</i> , 2008, 14, 8244-8252.	7.0	60
139	RNA Sequencing of the NCI-60: Integration into CellMiner and CellMiner CDB. <i>Cancer Research</i> , 2019, 79, 3514-3524.	0.9	58
140	Differentially Painting Human Chromosome Arms with Combined Binary Ratio-labeling Fluorescence In Situ Hybridization. <i>Genome Research</i> , 2000, 10, 861-865.	5.5	56
141	ATP11B mediates platinum resistance in ovarian cancer. <i>Journal of Clinical Investigation</i> , 2013, 123, 2119-2130.	8.2	56
142	Genome-Wide Methylation Patterns in Papillary Thyroid Cancer Are Distinct Based on Histological Subtype and Tumor Genotype. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2014, 99, E329-E337.	3.6	55
143	The second European interdisciplinary Ewing sarcoma research summit - A joint effort to deconstructing the multiple layers of a complex disease. <i>Oncotarget</i> , 2016, 7, 8613-8624.	1.8	55
144	Assessment of Automated Image Analysis of Breast Cancer Tissue Microarrays for Epidemiologic Studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 992-999.	2.5	54

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145	Molecular cytogenetic characterization and physical mapping of 12q13-15 amplification in human cancers. <i>Genes Chromosomes and Cancer</i> , 1996, 17, 205-214.	2.8	53
146	Spotting the target: microarrays for disease gene discovery. <i>Current Opinion in Genetics and Development</i> , 2001, 11, 258-263.	3.3	51
147	Related subunits of NF- κ B map to two distinct loci associated with translocations in leukemia, NFKB1 and NFKB2. <i>Genomics</i> , 1992, 13, 287-292.	2.9	50
148	Complete sequence analysis of a gene (OS-9) ubiquitously expressed in human tissues and amplified in sarcomas. <i>Molecular Carcinogenesis</i> , 1996, 15, 270-275.	2.7	50
149	Transgenic Targeting of a Dominant Negative Corepressor to Liver Blocks Basal Repression by Thyroid Hormone Receptor and Increases Cell Proliferation. <i>Journal of Biological Chemistry</i> , 2001, 276, 15066-15072.	3.4	49
150	The NCI-60 Methylome and Its Integration into CellMiner. <i>Cancer Research</i> , 2017, 77, 601-612.	0.9	48
151	Preferential Localization of Human Origins of DNA Replication at the 5'-Ends of Expressed Genes and at Evolutionarily Conserved DNA Sequences. <i>PLoS ONE</i> , 2011, 6, e17308.	2.5	47
152	Alpha-globulins suppress human leukocyte tumor necrosis factor secretion. <i>European Journal of Immunology</i> , 1989, 19, 939-942.	2.9	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. <i>Cancer Research</i> , 2009, 69, 758-764.	0.9	46
155	Imprints and <i>DPPA3</i> are bypassed during pluripotency- and differentiation-coupled methylation reprogramming in testicular germ cell tumors. <i>Genome Research</i> , 2016, 26, 1490-1504.	5.5	44
156	Characterization of a highly conserved gene (OS4) amplified with CDK4 in human sarcomas. <i>Oncogene</i> , 1997, 15, 1289-1294.	5.9	43
157	A small protein encoded by a putative lncRNA regulates apoptosis and tumorigenicity in human colorectal cancer cells. <i>ELife</i> , 2020, 9, .	6.0	43
158	Bromodomain and Extraterminal Protein Inhibitor JQ1 Suppresses Thyroid Tumor Growth in a Mouse Model. <i>Clinical Cancer Research</i> , 2017, 23, 430-440.	7.0	42
159	Biomarker significance of plasma and tumor miR-21, miR-221, and miR-106a in osteosarcoma. <i>Oncotarget</i> , 2017, 8, 96738-96752.	1.8	41
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