

Marc Zapatka

List of Publications by Year in descending order

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Version: 2024-02-01

136
papers

21,332
citations

38742

50
h-index

17592

121
g-index

150
all docs

150
docs citations

150
times ranked

29714
citing authors

#	ARTICLE	IF	CITATIONS
1	Clonal evolution in chronic lymphocytic leukemia is scant in relapsed but accelerated in refractory cases after chemo(immune) therapy. <i>Haematologica</i> , 2022, 107, 604-614.	3.5	11
2	Association of mutation signature effectuating processes with mutation hotspots in driver genes and non-coding regions. <i>Nature Communications</i> , 2022, 13, 178.	12.8	12
3	Secondary resistance to idelalisib is characterized by upregulation of IGF1R rather than by MAPK/ERK pathway mutations. <i>Blood</i> , 2022, 139, 3340-3344.	1.4	9
4	A synergistic interaction between HDAC and PARP inhibitors in childhood tumors with chromothripsis. <i>International Journal of Cancer</i> , 2022, 151, 590-606.	5.1	5
5	Comparative parallel multi-omics analysis during the induction of pluripotent and trophectoderm states. <i>Nature Communications</i> , 2022, 13, .	12.8	4
6	A versatile system to introduce clusters of genomic double-strand breaks in large cell populations. <i>Genes Chromosomes and Cancer</i> , 2021, 60, 303-313.	2.8	3
7	Unraveling most abundant mutational signatures in head and neck cancer. <i>International Journal of Cancer</i> , 2021, 148, 115-127.	5.1	19
8	The age of adult pilocytic astrocytoma cells. <i>Oncogene</i> , 2021, 40, 2830-2841.	5.9	6
9	CATCH: A Prospective Precision Oncology Trial in Metastatic Breast Cancer. <i>JCO Precision Oncology</i> , 2021, 5, 676-686.	3.0	20
10	Carbon ion radiotherapy eradicates medulloblastomas with chromothripsis in an orthotopic Li-Fraumeni patient-derived mouse model. <i>Neuro-Oncology</i> , 2021, 23, 2028-2041.	1.2	7
11	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. <i>Leukemia</i> , 2021, 35, 2002-2016.	7.2	34
12	Longitudinal analyses of CLL in mice identify leukemia-related clonal changes including a Myc gain predicting poor outcome in patients. <i>Leukemia</i> , 2021, , .	7.2	3
13	Interleukin-10 receptor signaling promotes the maintenance of a PD-1int TCF-1+ CD8+ T cell population that sustains anti-tumor immunity. <i>Immunity</i> , 2021, 54, 2825-2841.e10.	14.3	57
14	CD8 ⁺ T-cells of CLL-bearing mice acquire a transcriptional program of T-cell activation and exhaustion. <i>Leukemia and Lymphoma</i> , 2020, 61, 351-356.	1.3	17
15	Molecular subgrouping of primary pineal parenchymal tumors reveals distinct subtypes correlated with clinical parameters and genetic alterations. <i>Acta Neuropathologica</i> , 2020, 139, 243-257.	7.7	50
16	IL4I1 Is a Metabolic Immune Checkpoint that Activates the AHR and Promotes Tumor Progression. <i>Cell</i> , 2020, 182, 1252-1270.e34.	28.9	259
17	Chromothripsis in Human Breast Cancer. <i>Cancer Research</i> , 2020, 80, 4918-4931.	0.9	11
18	The landscape of chromothripsis across adult cancer types. <i>Nature Communications</i> , 2020, 11, 2320.	12.8	75

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19	Pilocytic astrocytoma demethylation and transcriptional landscapes link bZIP transcription factors to immune response. <i>Neuro-Oncology</i> , 2020, 22, 1327-1338.	1.2	10
20	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	27.8	1,966
21	The landscape of viral associations in human cancers. <i>Nature Genetics</i> , 2020, 52, 320-330.	21.4	261
22	Abstract PD2-01: Exploring CDK4/6 inhibitor therapy response and drug resistance development at the single cell level in metastatic breast cancer CTCs. , 2020, , .		0
23	Immune Suppression in CLL Is Mediated By the L-Amino Acid Oxidase IL4I1, a Reason for the Treatment Failure of IDO1 Inhibitors. <i>Blood</i> , 2020, 136, 34-34.	1.4	0
24	Proteogenomic Subtyping of Chronic Lymphocytic Leukemia Identifies a Novel Poor Outcome Subgroup with a Distinct Drug Response Profile. <i>Blood</i> , 2020, 136, 10-11.	1.4	0
25	<i>miRâ€‘16â€‘5p</i> is frequently downâ€‘regulated in astrocytic gliomas and modulates glioma cell proliferation, apoptosis and response to cytotoxic therapy. <i>Neuropathology and Applied Neurobiology</i> , 2019, 45, 441-458.	3.2	50
26	Identification and Analyses of Extra-Cranial and Cranial Rhabdoid Tumor Molecular Subgroups Reveal Tumors with Cytotoxic T Cell Infiltration. <i>Cell Reports</i> , 2019, 29, 2338-2354.e7.	6.4	74
27	Lsd1 as a therapeutic target in Gfi1-activated medulloblastoma. <i>Nature Communications</i> , 2019, 10, 332.	12.8	55
28	Linking aberrant chromatin features in chronic lymphocytic leukemia to transcription factor networks. <i>Molecular Systems Biology</i> , 2019, 15, e8339.	7.2	39
29	MDM4 Is Targeted by 1q Gain and Drives Disease in Burkitt Lymphoma. <i>Cancer Research</i> , 2019, 79, 3125-3138.	0.9	19
30	GENE-06. DISTINCT MOLECULAR SUBGROUPS OF TUMORS OF THE PINEAL REGION CORRELATE WITH CLINICAL PARAMETERS AND GENETIC ALTERATIONS. <i>Neuro-Oncology</i> , 2019, 21, ii81-ii82.	1.2	0
31	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. <i>Nature Communications</i> , 2019, 10, 1459.	12.8	99
32	DECIPHER pooled shRNA library screen identifies PP2A and FGFR signaling as potential therapeutic targets for diffuse intrinsic pontine gliomas. <i>Neuro-Oncology</i> , 2019, 21, 867-877.	1.2	24
33	Comprehensive Analysis of Chromatin States in Atypical Teratoid/Rhabdoid Tumor Identifies Diverging Roles for SWI/SNF and Polycomb in Gene Regulation. <i>Cancer Cell</i> , 2019, 35, 95-110.e8.	16.8	65
34	Mismatch Repair Deficiency Drives Durable Complete Remission by Targeting Programmed Death Receptor 1 in a Metastatic Luminal Breast Cancer Patient. <i>Breast Care</i> , 2019, 14, 53-59.	1.4	13
35	Abstract 1686: Comprehensive genomic and transcriptomic profiling of gastrointestinal stromal tumors. , 2019, , .		0
36	Abstract 3496: Defective DNA damage repair leads to frequent catastrophic genomic events in murine and human tumors. , 2019, , .		0

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37	The landscape of genomic alterations across childhood cancers. <i>Nature</i> , 2018, 555, 321-327.	27.8	1,068
38	Therapeutic targeting of ependymoma as informed by oncogenic enhancer profiling. <i>Nature</i> , 2018, 553, 101-105.	27.8	170
39	Integrative genomic and transcriptomic analysis of leiomyosarcoma. <i>Nature Communications</i> , 2018, 9, 144.	12.8	197
40	DNA methylation-based classification of central nervous system tumours. <i>Nature</i> , 2018, 555, 469-474.	27.8	1,872
41	Analysis of Epstein-Barr Virus Genomes and Expression Profiles in Gastric Adenocarcinoma. <i>Journal of Virology</i> , 2018, 92, .	3.4	47
42	Defective DNA damage repair leads to frequent catastrophic genomic events in murine and human tumors. <i>Nature Communications</i> , 2018, 9, 4760.	12.8	66
43	A novel cloning strategy for one-step assembly of multiplex CRISPR vectors. <i>Scientific Reports</i> , 2018, 8, 17499.	3.3	25
44	Abstract 1352: Inactivation of factors of DNA double-strand break repair by homologous recombination or non-homologous end-joining leads to frequent catastrophic genomic events in murine and human tumors. , 2018, , .		0
45	Abstract 5109: Somatic CRISPR/Cas9-mediated gene editing enables versatile brain tumor modeling. , 2018, , .		0
46	Genomic profiling of Acute lymphoblastic leukemia in ataxia telangiectasia patients reveals tight link between ATM mutations and chromothripsis. <i>Leukemia</i> , 2017, 31, 2048-2056.	7.2	47
47	The branched-chain amino acid transaminase 1 sustains growth of antiestrogen-resistant and ER α -negative breast cancer. <i>Oncogene</i> , 2017, 36, 4124-4134.	5.9	60
48	Tumor-derived exosomes modulate PD-L1 expression in monocytes. <i>Science Immunology</i> , 2017, 2, .	11.9	236
49	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017, 547, 311-317.	27.8	787
50	<i><scp>MED</scp>12</i> mutations and <scp>NOTCH</scp> signalling in chronic lymphocytic leukaemia. <i>British Journal of Haematology</i> , 2017, 179, 421-429.	2.5	29
51	confFuse: High-Confidence Fusion Gene Detection across Tumor Entities. <i>Frontiers in Genetics</i> , 2017, 8, 137.	2.3	9
52	Drug-perturbation-based stratification of blood cancer. <i>Journal of Clinical Investigation</i> , 2017, 128, 427-445.	8.2	124
53	Abstract 509: Genomic profiling of acute lymphoblastic leukemia in ataxia telangiectasia patients reveals tight link between ATM mutations and chromothripsis. , 2017, , .		0
54	Telomere dysfunction and chromothripsis. <i>International Journal of Cancer</i> , 2016, 138, 2905-2914.	5.1	42

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55	The Phospholipase C β 2 Mutants R665W and L845F Identified in Ibrutinib-resistant Chronic Lymphocytic Leukemia Patients Are Hypersensitive to the Rho GTPase Rac2 Protein. <i>Journal of Biological Chemistry</i> , 2016, 291, 22136-22148.	3.4	42
56	Recurrent MET fusion genes represent a drug target in pediatric glioblastoma. <i>Nature Medicine</i> , 2016, 22, 1314-1320.	30.7	183
57	In silico SNP analysis of the breast cancer antigen NY-BR-1. <i>BMC Cancer</i> , 2016, 16, 901.	2.6	10
58	Active medulloblastoma enhancers reveal subgroup-specific cellular origins. <i>Nature</i> , 2016, 530, 57-62.	27.8	318
59	DNA methylation dynamics during B cell maturation underlie a continuum of disease phenotypes in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2016, 48, 253-264.	21.4	254
60	Atypical Teratoid/Rhabdoid Tumors Are Comprised of Three Epigenetic Subgroups with Distinct Enhancer Landscapes. <i>Cancer Cell</i> , 2016, 29, 379-393.	16.8	438
61	CITED4 gene silencing in colorectal cancer cells modulates adherens/tight junction gene expression and reduces cell proliferation. <i>Journal of Cancer Research and Clinical Oncology</i> , 2016, 142, 225-237.	2.5	15
62	Whole-Exome Sequencing Revealed No Recurrent Mutations within the PI3K Pathway in Relapsed Chronic Lymphocytic Leukemia Patients Progressing Under Idelalisib Treatment. <i>Blood</i> , 2016, 128, 2770-2770.	1.4	26
63	CLL Exosome-Derived Y RNA hY4 Induces TLR7/8-Mediated Inflammation and PD-L1 Expression in Monocytes. <i>Blood</i> , 2016, 128, 3217-3217.	1.4	1
64	Abstract A30: Chronic lymphocytic leukemia-derived extracellular vesicles mediate NF κ B signaling and pro-inflammatory cytokine release in monocytes. , 2016, , .		0
65	Reprogramming of the ER α and ER β Target Gene Landscape Triggers Tamoxifen Resistance in Breast Cancer. <i>Cancer Research</i> , 2015, 75, 720-731.	0.9	36
66	Somatic CRISPR/Cas9-mediated tumour suppressor disruption enables versatile brain tumour modelling. <i>Nature Communications</i> , 2015, 6, 7391.	12.8	244
67	Progressive Epigenetic Programming during B Cell Maturation Is Reflected in a Continuum of Epigenetic Disease Phenotypes in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2015, 126, 2436-2436.	1.4	1
68	Abstract B25: Progressive epigenetic programming during B cell maturation yields a continuum of clonal disease phenotypes with distinct etiologies in chronic lymphocytic leukemia.. , 2015, , .		0
69	Abstract PR02: Somatic CRISPR/Cas9-mediated tumor suppressor disruption enables versatile brain tumor modeling. , 2015, , .		0
70	STAT3 Single Nucleotide Polymorphism rs4796793 SNP Does Not Correlate with Response to Adjuvant IFN α Therapy in Stage III Melanoma Patients. <i>Frontiers in Medicine</i> , 2014, 1, 47.	2.6	3
71	Capture and Amplification by Tailing and Switching (CATS). <i>RNA Biology</i> , 2014, 11, 817-828.	3.1	68
72	Integrated Pathway-Based Approach Identifies Association between Genomic Regions at CTCF and CACNB2 and Schizophrenia. <i>PLoS Genetics</i> , 2014, 10, e1004345.	3.5	44

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73	Chromosome 17/17q gain and unaltered profiles in high resolution array-CGH are prognostically informative in neuroblastoma. <i>Genes Chromosomes and Cancer</i> , 2014, 53, 639-649.	2.8	34
74	MiR-328 promotes glioma cell invasion via SFRP1-dependent Wnt-signaling activation. <i>Neuro-Oncology</i> , 2014, 16, 179-190.	1.2	78
75	Genome Sequencing of SHH Medulloblastoma Predicts Genotype-Related Response to Smoothed Inhibition. <i>Cancer Cell</i> , 2014, 25, 393-405.	16.8	627
76	Decoding the regulatory landscape of medulloblastoma using DNA methylation sequencing. <i>Nature</i> , 2014, 510, 537-541.	27.8	378
77	The onset of p53 loss of heterozygosity is differentially induced in various stem cell types and may involve the loss of either allele. <i>Cell Death and Differentiation</i> , 2014, 21, 1419-1431.	11.2	34
78	Resistance Mechanisms for the Bruton's Tyrosine Kinase Inhibitor Ibrutinib. <i>New England Journal of Medicine</i> , 2014, 370, 2286-2294.	27.0	1,042
79	Enhancer hijacking activates GF1 family oncogenes in medulloblastoma. <i>Nature</i> , 2014, 511, 428-434.	27.8	520
80	Abstract 3084: Epigenetic deregulation in H3.3-K27M mutant pediatric high-grade gliomas. , 2014, , .		0
81	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. <i>Nature Genetics</i> , 2013, 45, 927-932.	21.4	674
82	Robust molecular subgrouping and copy-number profiling of medulloblastoma from small amounts of archival tumour material using high-density DNA methylation arrays. <i>Acta Neuropathologica</i> , 2013, 125, 913-916.	7.7	244
83	Reduced H3K27me3 and DNA Hypomethylation Are Major Drivers of Gene Expression in K27M Mutant Pediatric High-Grade Gliomas. <i>Cancer Cell</i> , 2013, 24, 660-672.	16.8	633
84	Tumor microenvironment interactions studied by zonal transcriptional profiling of squamous cell lung carcinoma. <i>Genes Chromosomes and Cancer</i> , 2013, 52, 250-264.	2.8	10
85	Low p14ARF expression in neuroblastoma cells is associated with repressed histone mark status, and enforced expression induces growth arrest and apoptosis. <i>Human Molecular Genetics</i> , 2013, 22, 1735-1745.	2.9	13
86	Genome-wide identification of translationally inhibited and degraded miR-155 targets using RNA-interacting protein-IP. <i>RNA Biology</i> , 2013, 10, 1017-1029.	3.1	33
87	Coverage Bias and Sensitivity of Variant Calling for Four Whole-genome Sequencing Technologies. <i>PLoS ONE</i> , 2013, 8, e66621.	2.5	74
88	Use of tumor genomic profiling to reveal mechanisms of resistance to the BTK inhibitor ibrutinib in chronic lymphocytic leukemia (CLL).. <i>Journal of Clinical Oncology</i> , 2013, 31, 7014-7014.	1.6	19
89	Survivin-specific T-cell reactivity correlates with tumor response and patient survival: a phase-II peptide vaccination trial in metastatic melanoma. <i>Cancer Immunology, Immunotherapy</i> , 2012, 61, 2091-2103.	4.2	69
90	Relevance of PTEN loss in brain metastasis formation in breast cancer patients. <i>Breast Cancer Research</i> , 2012, 14, R49.	5.0	93

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91	Hotspot Mutations in H3F3A and IDH1 Define Distinct Epigenetic and Biological Subgroups of Glioblastoma. <i>Cancer Cell</i> , 2012, 22, 425-437.	16.8	1,551
92	Genome Sequencing of Pediatric Medulloblastoma Links Catastrophic DNA Rearrangements with TP53 Mutations. <i>Cell</i> , 2012, 148, 59-71.	28.9	743
93	Driver mutations in histone H3.3 and chromatin remodelling genes in paediatric glioblastoma. <i>Nature</i> , 2012, 482, 226-231.	27.8	2,129
94	Dissecting the genomic complexity underlying medulloblastoma. <i>Nature</i> , 2012, 488, 100-105.	27.8	765
95	RNAi screening in glioma stem-like cells identifies PFKFB4 as a key molecule important for cancer cell survival. <i>Oncogene</i> , 2012, 31, 3235-3243.	5.9	123
96	Abstract 4872: ICGC PedBrain Tumor - Next-generation sequencing identifies novel subgroup-specific mutations and copy number aberrations in medulloblastoma. <i>Cancer Research</i> , 2012, 72, 4872-4872.	0.9	1
97	Monitoring CSF Proteome Alterations in Amyotrophic Lateral Sclerosis: Obstacles and Perspectives in Translating a Novel Marker Panel to the Clinic. <i>PLoS ONE</i> , 2012, 7, e44401.	2.5	44
98	Bronchoalveolar lavage fluid of lung cancer patients: Mapping the uncharted waters using proteomics technology. <i>Lung Cancer</i> , 2011, 72, 136-138.	2.0	12
99	Proteomic Bronchiolitis Obliterans Syndrome Risk Monitoring in Lung Transplant Recipients. <i>Transplantation</i> , 2011, 92, 477-485.	1.0	13
100	MicroRNA miR-885-5p targets CDK2 and MCM5, activates p53 and inhibits proliferation and survival. <i>Cell Death and Differentiation</i> , 2011, 18, 974-984.	11.2	133
101	Postoperative serum proteomic profiles may predict recurrence-free survival in high-risk primary breast cancer. <i>Journal of Cancer Research and Clinical Oncology</i> , 2011, 137, 1773-1783.	2.5	9
102	The FRA2C common fragile site maps to the borders of MYCN amplicons in neuroblastoma and is associated with gross chromosomal rearrangements in different cancers. <i>Human Molecular Genetics</i> , 2011, 20, 1488-1501.	2.9	42
103	ERCC5 p.Asp1104His and ERCC2 p.Lys751Gln Polymorphisms Are Independent Prognostic Factors for the Clinical Course of Melanoma. <i>Journal of Investigative Dermatology</i> , 2011, 131, 1280-1290.	0.7	28
104	Merkel Cell Polyomavirus Status Is Not Associated with Clinical Course of Merkel Cell Carcinoma. <i>Journal of Investigative Dermatology</i> , 2011, 131, 1631-1638.	0.7	153
105	Abstract 4724: Identification of a CpG-island methylator phenotype (CIMP) in a subgroup of pilocytic astrocytoma with favorable prognosis. , 2011, , .		0
106	Serum proteomics and disease-specific biomarkers of patients with advanced gastric cancer. <i>Oncology Letters</i> , 2010, 1, 327-333.	1.8	5
107	BRCA1-associated breast and ovarian cancer risks in Poland: no association with commonly studied polymorphisms. <i>Breast Cancer Research and Treatment</i> , 2010, 119, 201-211.	2.5	70
108	Polymorphisms in the BRCA1 and ABCB1 genes modulate menopausal hormone therapy associated breast cancer risk in postmenopausal women. <i>Breast Cancer Research and Treatment</i> , 2010, 120, 727-736.	2.5	58

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109	Postmenopausal estrogen monotherapy-associated breast cancer risk is modified by CYP17A1_-34_T>C polymorphism. <i>Breast Cancer Research and Treatment</i> , 2010, 120, 737-744.	2.5	19
110	Polymorphisms in genes of the steroid receptor superfamily modify postmenopausal breast cancer risk associated with menopausal hormone therapy. <i>International Journal of Cancer</i> , 2010, 126, 2935-2946.	5.1	29
111	qPCR in gastrointestinal stromal tumors: Evaluation of reference genes and expression analysis of KIT and the alternative receptor tyrosine kinases FLT3, CSF1-R, PDGFRB, MET and AXL. <i>BMC Molecular Biology</i> , 2010, 11, 100.	3.0	14
112	Proteomic analysis of field cancerization in pharynx and oesophagus: a prospective pilot study. <i>Journal of Pathology</i> , 2010, 221, 462-470.	4.5	24
113	Data-Mining in klinischen Datensätzen - Bericht der Arbeitsgruppe Bioinformatik der DGKL. <i>Laboratoriums Medizin</i> , 2010, 34, 227-233.	0.6	3
114	Identification of serum proteins as prognostic and predictive markers of colorectal cancer using surface enhanced laser desorption ionization-time of flight mass spectrometry. <i>Oncology Reports</i> , 2010, 24, 57-64.	2.6	20
115	Implementation of Smith-Waterman Algorithm in OpenCL for GPUs. , 2010, , .		8
116	Serum Amyloid A As a Prognostic Marker in Melanoma Identified by Proteomic Profiling. <i>Journal of Clinical Oncology</i> , 2009, 27, 2199-2208.	1.6	107
117	Differential Clinical Significance of Individual NKG2D Ligands in Melanoma: Soluble ULBP2 as an Indicator of Poor Prognosis Superior to S100B. <i>Clinical Cancer Research</i> , 2009, 15, 5208-5215.	7.0	168
118	CCM2 Mediates Death Signaling by the TrkA Receptor Tyrosine Kinase. <i>Neuron</i> , 2009, 63, 585-591.	8.1	58
119	Breast cancer: a candidate gene approach across the estrogen metabolic pathway. <i>Breast Cancer Research and Treatment</i> , 2008, 108, 137-149.	2.5	74
120	Impact of the CCR5 gene polymorphism on the survival of metastatic melanoma patients receiving immunotherapy. <i>Cancer Immunology, Immunotherapy</i> , 2008, 57, 685-691.	4.2	83
121	Divergent mechanisms underlie Smad4-mediated positive regulation of the three genes encoding the basement membrane component laminin-332 (laminin-5). <i>BMC Cancer</i> , 2008, 8, 215.	2.6	14
122	Ontological Analysis and Pathway Modelling in Drug Discovery. <i>Pharmaceutical Medicine</i> , 2008, 22, 99-105.	1.9	2
123	Microphthalmia-Associated Transcription Factor Gene Amplification in Metastatic Melanoma Is a Prognostic Marker for Patient Survival, But Not a Predictive Marker for Chemosensitivity and Chemotherapy Response. <i>Clinical Cancer Research</i> , 2007, 13, 6344-6350.	7.0	67
124	Basement membrane component laminin-5 is a target of the tumor suppressor Smad4. <i>Oncogene</i> , 2007, 26, 1417-1427.	5.9	32
125	High-level inducible Smad4-reexpression in the cervical cancer cell line C4-II is associated with a gene expression profile that predicts a preferential role of Smad4 in extracellular matrix composition. <i>BMC Cancer</i> , 2007, 7, 209.	2.6	8
126	Using gene expression data and network topology to detect substantial pathways, clusters and switches during oxygen deprivation of <i>Escherichia coli</i> . <i>BMC Bioinformatics</i> , 2007, 8, 149.	2.6	11

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127	CCR5 gene polymorphism in patients with cutaneous melanoma: Impact on survival following immunotherapy. <i>Journal of Clinical Oncology</i> , 2007, 25, 21071-21071.	1.6	0
128	Discovering functional gene expression patterns in the metabolic network of <i>Escherichia coli</i> with wavelets transforms. <i>BMC Bioinformatics</i> , 2006, 7, 119.	2.6	17
129	Oligonucleotide array-based comparative genomic hybridization (aCGH) of 90 neuroblastomas reveals aberration patterns closely associated with relapse pattern and outcome. <i>Genes Chromosomes and Cancer</i> , 2006, 45, 1130-1142.	2.8	72
130	Smad4 deficiency in cervical carcinoma cells. <i>Oncogene</i> , 2005, 24, 810-819.	5.9	35
131	Differential proteome analysis of conditioned media to detect Smad4 regulated secreted biomarkers in colon cancer. <i>Proteomics</i> , 2005, 5, 2587-2601.	2.2	86
132	Loss of Smad4 correlates with loss of the invasion suppressor E-cadherin in advanced colorectal carcinomas. <i>Journal of Pathology</i> , 2004, 202, 412-420.	4.5	48
133	Tumor suppressor Smad4 mediates downregulation of the anti-adhesive invasion-promoting matricellular protein SPARC: Landscaping activity of Smad4 as revealed by "secretome" analysis. <i>Proteomics</i> , 2004, 4, 1324-1334.	2.2	41
134	NoBP, a Nuclear Fibroblast Growth Factor 3 Binding Protein, Is Cell Cycle Regulated and Promotes Cell Growth. <i>Molecular and Cellular Biology</i> , 2001, 21, 4996-5007.	2.3	29
135	Tumor suppressor Smad4 mediates down-regulation of the anti-adhesive invasion-promoting matricellular protein SPARC. , 0, 2004, .		0
136	Viren und Krebs: Umfassende Suche nach viralen Sequenzen. , 0, , .		0