Holger SÃ¼ltmann

List of Publications by Year
in descending order

144 papers	11,397 citations	46984 47 h-index	30894 102 g-index
158 all docs	158 docs citations	158 times ranked	20292 citing authors

#	Article	IF	Citations
1	Variance stabilization applied to microarray data calibration and to the quantification of differential expression. Bioinformatics, 2002, 18, S96-S104.	1.8	2,012
2	Hepatitis B and D Viruses Exploit Sodium Taurocholate Co-transporting Polypeptide for Species-Specific Entry into Hepatocytes. Gastroenterology, 2014, 146, 1070-1083.e6.	0.6	627
3	Circulating miRNAs are correlated with tumor progression in prostate cancer. International Journal of Cancer, 2011, 128, 608-616.	2.3	520
4	The Human let-7a-3 Locus Contains an Epigenetically Regulated MicroRNA Gene with Oncogenic Function. Cancer Research, 2007, 67, 1419-1423.	0.4	437
5	Serum microRNAs as non-invasive biomarkers for cancer. Molecular Cancer, 2010, 9, 306.	7.9	369
6	Extracellular Vesicle-Mediated Transfer of Genetic Information between the Hematopoietic System and the Brain in Response to Inflammation. PLoS Biology, 2014, 12, e1001874.	2.6	312
7	Integrative Genomic Analyses Reveal an Androgen-Driven Somatic Alteration Landscape in Early-Onset Prostate Cancer. Cancer Cell, 2013, 23, 159-170.	7.7	292
8	Yes and PI3K Bind CD95 to Signal Invasion of Glioblastoma. Cancer Cell, 2008, 13, 235-248.	7.7	281
9	Loss of EpCAM expression in breast cancer derived serum exosomes: Role of proteolytic cleavage. Gynecologic Oncology, 2011, 122, 437-446.	0.6	248
10	Extracellular vesicle-mediated transfer of functional RNA in the tumor microenvironment. OncoImmunology, 2015, 4, e1008371.	2.1	227
11	Dependence of Intracellular and Exosomal microRNAs on Viral E6/E7 Oncogene Expression in HPV-positive Tumor Cells. PLoS Pathogens, 2015, 11, e1004712.	2.1	191
12	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. Cancer Cell, 2018, 34, 996-1011.e8.	7.7	190
13	Identification and Classification of Differentially Expressed Genes in Renal Cell Carcinoma by Expression Profiling on a Global Human 31,500-Element cDNA Array. Genome Research, 2001, 11, 1861-1870.	2.4	184
14	Nonlinkage of major histocompatibility complex class I and class II loci in bony fishes. Immunogenetics, 2000, 51, 108-116.	1.2	164
15	Global gene expression analysis reveals specific patterns of cell junctions in non-small cell lung cancer subtypes. Lung Cancer, 2009, 63, 32-38.	0.9	161
16	A field guide for cancer diagnostics using cell€free DNA: From principles to practice and clinical applications. Genes Chromosomes and Cancer, 2018, 57, 123-139.	1.5	155
17	Targeted high throughput sequencing in clinical cancer Settings: formaldehyde fixed-paraffin embedded (FFPE) tumor tissues, input amount and tumor heterogeneity. BMC Medical Genomics, 2011, 4, 68.	0.7	154
18	Identification of a Common Gene Expression Signature in Dilated Cardiomyopathy Across Independent Microarray Studies. Journal of the American College of Cardiology, 2006, 48, 1610-1617.	1.2	153

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19	BAZ2A (TIP5) is involved in epigenetic alterations in prostate cancer and its overexpression predicts disease recurrence. Nature Genetics, 2015, 47, 22-30.	9.4	141
20	TMPRSS2-ERG -specific transcriptional modulation is associated with prostate cancer biomarkers and TGF-β signaling. BMC Cancer, 2011, 11, 507.	1.1	128
21	Genome-wide DNA Methylation Events in *TMPRSS2–ERG* Fusion-Negative Prostate Cancers Implicate an EZH2-Dependent Mechanism with *miR-26a* Hypermethylation. Cancer Discovery, 2012, 2, 1024-1035.	7.7	127
22	Equivalence test in quantitative reverse transcription polymerase chain reaction: confirmation of reference genes suitable for normalization. Analytical Biochemistry, 2004, 335, 1-9.	1.1	121
23	The maternal embryonic leucine zipper kinase (MELK) is upregulated in high-grade prostate cancer. Journal of Molecular Medicine, 2013, 91, 237-248.	1.7	117
24	ERBB2 and TOP2A in Breast Cancer: A Comprehensive Analysis of Gene Amplification, RNA Levels, and Protein Expression and Their Influence on Prognosis and Prediction. Clinical Cancer Research, 2010, 16, 2391-2401.	3.2	113
25	Effects of infiltrating lymphocytes and estrogen receptor on gene expression and prognosis in breast cancer. Breast Cancer Research and Treatment, 2009, 116, 69-77.	1.1	106
26	Organization of Mhc Class II B Genes in the Zebrafish (Brachydanio rerio). Genomics, 1994, 23, 1-14.	1.3	103
27	Hepatitis D virus replication is sensed by MDA5 and induces IFN-β/λ responses in hepatocytes. Journal of Hepatology, 2018, 69, 25-35.	1.8	101
28	Gene Expression Profiling Unravels Cancer-Related Hepatic Molecular Signatures in Steatohepatitis but Not in Steatosis. PLoS ONE, 2012, 7, e46584.	1.1	97
29	Integration of pathway knowledge into a reweighted recursive feature elimination approach for risk stratification of cancer patients. Bioinformatics, 2010, 26, 2136-2144.	1.8	94
30	Ubiquitin carboxyl-terminal hydrolase 1 (UCHL1) is a potential tumour suppressor in prostate cancer and is frequently silenced by promoter methylation. Molecular Cancer, 2011, 10, 129.	7.9	88
31	A Contig Map of the *Mhc* Class I Genomic Region in the Zebrafish Reveals Ancient Synteny. Journal of Immunology, 2000, 164, 5296-5305.	0.4	85
32	Linkage Relationships and Haplotype Polymorphism Among Cichlid Mhc Class II B Loci. Genetics, 1998, 149, 1527-1537.	1.2	85
33	EZH2 Depletion Blocks the Proliferation of Colon Cancer Cells. PLoS ONE, 2011, 6, e21651.	1.1	84
34	Systematic analysis of T7 RNA polymerase based in vitro linear RNA amplification for use in microarray experiments. BMC Genomics, 2004, 5, 29.	1.2	79
35	Prognostic Role of E2F1 and Members of the CDKN2A Network in Gastrointestinal Stromal Tumors. Clinical Cancer Research, 2005, 11, 6589-6597.	3.2	79
36	The anterior gradient 2 (AGR2) gene is overexpressed in prostate cancer and may be useful as a urine sediment marker for prostate cancer detection. Prostate, 2011, 71, 575-587.	1.2	79

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37	Differential expression of apoptotic genes PDIA3 and MAP3K5 distinguishes between low- and high-risk prostate cancer. Molecular Cancer, 2009, 8, 130.	7.9	70
38	Identification of Clinically Relevant Protein Targets in Prostate Cancer with 2D-DIGE Coupled Mass Spectrometry and Systems Biology Network Platform. PLoS ONE, 2011, 6, e16833.	1.1	67
39	Serum miR-142-3p is associated with early relapse in operable lung adenocarcinoma patients. Lung Cancer, 2013, 80, 223-227.	0.9	65
40	Gene expression in kidney cancer is associated with cytogenetic abnormalities, metastasis formation, and patient survival. Clinical Cancer Research, 2005, 11, 646-55.	3.2	64
41	Role of miR-34a as a suppressor of L1CAM in endometrial carcinoma. Oncotarget, 2014, 5, 462-472.	0.8	63
42	A simple strand-specific RNA-Seq library preparation protocol combining the Illumina TruSeq RNA and the dUTP methods. Biochemical and Biophysical Research Communications, 2012, 422, 643-646.	1.0	62
43	Combinatorial RNAi for quantitative protein network analysis. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6579-6584.	3.3	55
44	A cancer specific hypermethylation signature of the TERT promoter predicts biochemical relapse in prostate cancer: a retrospective cohort study. Oncotarget, 2016, 7, 57726-57736.	0.8	55
45	Class I Mhc genes of cichlid fishes: identification, expression, and polymorphism. Immunogenetics, 1997, 46, 63-72.	1.2	53
46	microRNA biomarkers in body fluids of prostate cancer patients. Methods, 2013, 59, 132-137.	1.9	51
47	Subtractive gene expression profiling of articular cartilage and mesenchymal stem cells: serpins as cartilage-relevant differentiation markers. Osteoarthritis and Cartilage, 2008, 16, 48-60.	0.6	50
48	arrayMagic: two-colour cDNA microarray quality control and preprocessing. Bioinformatics, 2005, 21, 554-556.	1.8	48
49	Reduced expression of vacuole membrane protein 1 affects the invasion capacity of tumor cells. Oncogene, 2008, 27, 1320-1326.	2.6	48
50	Mhc class II B gene evolution in East African cichlid fishes. Immunogenetics, 2000, 51, 556-575.	1.2	46
51	Peroxiredoxins 3 and 4 Are Overexpressed in Prostate Cancer Tissue and Affect the Proliferation of Prostate Cancer Cells in Vitro. Journal of Proteome Research, 2012, 11, 2452-2466.	1.8	46
52	Polymorphism and estimation of the number of MhcCyca class I and class I genes in laboratory strains of the common carp (Cyprinus carpio L.). Developmental and Comparative Immunology, 1993, 17, 141-156.	1.0	45
53	From ORFeome to Biology: A Functional Genomics Pipeline. Genome Research, 2004, 14, 2136-2144.	2.4	44
54	Identification and meta-analysis of a small gene expression signature for the diagnosis of estrogen receptor status in invasive ductal breast cancer. International Journal of Cancer, 2006, 119, 2974-2979.	2.3	44

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55	Estimating large-scale signaling networks through nested effect models with intervention effects from microarray data. Bioinformatics, 2008, 24, 2650-2656.	1.8	44
56	Mutation analysis of circulating plasma DNA to determine response to EGFR tyrosine kinase inhibitor therapy of lung adenocarcinoma patients. Scientific Reports, 2016, 6, 33505.	1.6	44
57	Spatial niche formation but not malignant progression is a driving force for intratumoural heterogeneity. Nature Communications, 2016, 7, ncomms11845.	5.8	44
58	Transcription alterations of members of the ubiquitin–proteasome network in prostate carcinoma. Prostate Cancer and Prostatic Diseases, 2011, 14, 38-45.	2.0	42
59	Identification of cellular targets for the human papillomavirus E6 and E7 oncogenes by RNA interference and transcriptome analyses. Journal of Molecular Medicine, 2007, 85, 1253-1262.	1.7	41
60	Marked Gene Transcript Level Alterations Occur Early During Radical Prostatectomy. European Urology, 2008, 53, 333-346.	0.9	40
61	QSEA–modelling of genome-wide DNA methylation from sequencing enrichment experiments. Nucleic Acids Research, 2017, 45, e44-e44.	6.5	39
62	Low Input Whole-Exome Sequencing to Determine the Representation of the Tumor Exome in Circulating DNA of Non-Small Cell Lung Cancer Patients. PLoS ONE, 2016, 11, e0161012.	1.1	39
63	Ago-RIP-Seq identifies Polycomb repressive complex I member CBX7 as a major target of *miR-375* in prostate cancer progression. Oncotarget, 2016, 7, 59589-59603.	0.8	38
64	Analysis of pigmented villonodular synovitis with genome-wide complementary DNA microarray and tissue array technology reveals insight into potential novel therapeutic approaches. Arthritis and Rheumatism, 2006, 54, 1009-1019.	6.7	37
65	Epigenomic profiling of non-small cell lung cancer xenografts uncover LRP12 DNA methylation as predictive biomarker for carboplatin resistance. Genome Medicine, 2018, 10, 55.	3.6	37
66	Loss of 9p leads to p16INK4A down-regulation and enables RB/E2F1-dependent cell cycle promotion in gastrointestinal stromal tumours (GISTs). Journal of Pathology, 2008, 215, 253-262.	2.1	36
67	Detection of TP53 Mutations in Tissue or Liquid Rebiopsies at Progression Identifies ALK+ Lung Cancer Patients with Poor Survival. Cancers, 2019, 11, 124.	1.7	36
68	Graph based fusion of miRNA and mRNA expression data improves clinical outcome prediction in prostate cancer. BMC Bioinformatics, 2011, 12, 488.	1.2	35
69	Defining molecular risk in ALK+ NSCLC. Oncotarget, 2019, 10, 3093-3103.	0.8	35
70	Mutations in BRCA2 and taxane resistance in prostate cancer. Scientific Reports, 2017, 7, 4574.	1.6	32
71	Longitudinal therapy monitoring of ALK-positive lung cancer by combined copy number and targeted mutation profiling of cell-free DNA. EBioMedicine, 2020, 62, 103103.	2.7	32
72	Characterization of Transcriptional Changes in ERG Rearrangement-Positive Prostate Cancer Identifies the Regulation of Metabolic Sensors Such as Neuropeptide Y. PLoS ONE, 2013, 8, e55207.	1.1	32

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73	Conservation of *Mhc* Class III Region Synteny Between Zebrafish and Human as Determined by Radiation Hybrid Mapping. Journal of Immunology, 2000, 165, 6984-6993.	0.4	31
74	The differentiation antigen NY-BR-1 is a potential target for antibody-based therapies in breast cancer. International Journal of Cancer, 2007, 120, 2635-2642.	2.3	31
75	Major histocompatibility complex class II A genes in cichlid fishes: identification, expression, linkage relationships, and haplotype variation. Immunogenetics, 2000, 51, 576-586.	1.2	30
76	`pathClass`: an R-package for integration of pathway knowledge into support vector machines for biomarker discovery. Bioinformatics, 2011, 27, 1442-1443.	1.8	30
77	Identification of aberrant chromosomal regions from gene expression microarray studies applied to human breast cancer. Bioinformatics, 2007, 23, 2273-2280.	1.8	28
78	Establishment and comparative characterization of novel squamous cell non-small cell lung cancer cell lines and their corresponding tumor tissue. Lung Cancer, 2012, 75, 45-57.	0.9	28
79	Matrix-Dependent Regulation of AKT in Hepsin-Overexpressing PC3 Prostate Cancer Cells. Neoplasia, 2011, 13, 579-IN2.	2.3	27
80	Correlation between genomic index lesions and mpMRI and 68Ga-PSMA-PET/CT imaging features in primary prostate cancer. Scientific Reports, 2018, 8, 16708.	1.6	27
81	Overexpression of nuclear AR-V7 protein in primary prostate cancer is an independent negative prognostic marker in men with high-risk disease receiving adjuvant therapy. Urologic Oncology: Seminars and Original Investigations, 2018, 36, 161.e19-161.e30.	0.8	26
82	Circulating MicroRNAs as Potential Biomarkers for Lung Cancer. Recent Results in Cancer Research, 2020, 215, 299-318.	1.8	26
83	ERG Induces Epigenetic Activation of Tudor Domain-Containing Protein 1 (TDRD1) in ERG Rearrangement-Positive Prostate Cancer. PLoS ONE, 2013, 8, e59976.	1.1	26
84	Identification of Seven Genes in the Major Histocompatibility Complex Class I Region of the Zebrafish. Scandinavian Journal of Immunology, 2000, 51, 577-585.	1.3	24
85	Metastases and multiple myeloma generate distinct transcriptional footprints in osteocytes *in vivo*. Journal of Pathology, 2008, 214, 617-626.	2.1	24
86	Molecular Cancer Phenotype in Normal Prostate Tissue. European Urology, 2009, 55, 885-891.	0.9	23
87	*TMPRSS2:ERG* gene fusion variants induce TGF-Î² signaling and epithelial to mesenchymal transition in human prostate cancer cells. Oncotarget, 2017, 8, 25115-25130.	0.8	23
88	Genomic analysis reveals poor separation of human cardiomyopathies of ischemic and nonischemic etiologies. Physiological Genomics, 2008, 34, 88-94.	1.0	22
89	Long Noncoding RNA: â€œLNCsâ€•to Cancer. European Urology, 2014, 65, 1152-1153.	0.9	22
90	Global DNA methylation reflects spatial heterogeneity and molecular evolution of lung adenocarcinomas. International Journal of Cancer, 2019, 144, 1061-1072.	2.3	22

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91	Spatial distribution of *EGFR* and *KRAS* mutation frequencies correlates with histological growth patterns of lung adenocarcinomas. International Journal of Cancer, 2017, 141, 1841-1848.	2.3	21
92	Early identification of disease progression in ALK-rearranged lung cancer using circulating tumor DNA analysis. Npj Precision Oncology, 2021, 5, 100.	2.3	21
93	Identification and Linkage of the Proteasome Activator Complex PA28 Subunit Genes in Zebrafish. Scandinavian Journal of Immunology, 2000, 51, 571-576.	1.3	20
94	Increased KIT signalling with up‑regulation of cyclin D correlates to accelerated proliferation and shorter disease‑free survival in gastrointestinal stromal tumours (GISTs) with *KIT* exon 11 deletions. Journal of Pathology, 2008, 216, 225-235.	2.1	20
95	Sensitivity and resistance towards isoliquiritigenin, doxorubicin and methotrexate in T cell acute lymphoblastic leukaemia cell lines by pharmacogenomics. Naunyn-Schmiedeberg's Archives of Pharmacology, 2010, 382, 221-234.	1.4	20
96	Liquid Biopsies beyond Mutation Calling: Genomic and Epigenomic Features of Cell-Free DNA in Cancer. Cancers, 2021, 13, 5615.	1.7	20
97	Isolation of Mhc Class II DMA and DMB cDNA Sequences in a Marsupial: The Gray Short-Tailed Opossum (Monodelphis domestica). Journal of Molecular Evolution, 1998, 47, 578-585.	0.8	19
98	Functional Profiling: From Microarrays via Cell-Based Assays to Novel Tumor Relevant Modulators of the Cell Cycle. Cancer Research, 2005, 65, 7733-7742.	0.4	19
99	In vitro-targeted gene identification in patients with hepatitis C using a genome-wide microarray technology. Hepatology, 2009, 49, 378-386.	3.6	19
100	Genomic features of renal cell carcinoma with venous tumor thrombus. Scientific Reports, 2018, 8, 7477.	1.6	19
101	Digital PCR After MALDI‑Mass Spectrometry Imaging to Combine Proteomic Mapping and Identification of Activating Mutations in Pulmonary Adenocarcinoma. Proteomics - Clinical Applications, 2019, 13, e1800034.	0.8	19
102	A Cancer-Indicative microRNA Pattern in Normal Prostate Tissue. International Journal of Molecular Sciences, 2013, 14, 5239-5249.	1.8	18
103	Excess hepsin proteolytic activity limits oncogenic signaling and induces ER stress and autophagy in prostate cancer cells. Cell Death and Disease, 2019, 10, 601.	2.7	18
104	Predicting pathway membership via domain signatures. Bioinformatics, 2008, 24, 2137-2142.	1.8	17
105	Increasing the sensitivity of reverse phase protein arrays by antibody-mediated signal amplification. Proteome Science, 2010, 8, 36.	0.7	17
106	Extraction and processing of high quality RNA from impalpable and macroscopically invisible prostate cancer for microarray gene expression analysis. International Journal of Oncology, 2005, 27, 713-20.	1.4	17
107	Early Detection of Lung Cancer by Molecular Markers in Endobronchial Epithelial-Lining Fluid. Journal of Thoracic Oncology, 2012, 7, 1001-1008.	0.5	16
108	Genome-Based Classification and Therapy of Prostate Cancer. Diagnostics, 2018, 8, 62.	1.3	16

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109	Earlier extracranial progression and shorter survival in ALK- rearranged lung cancer with positive liquid rebiopsies. Translational Lung Cancer Research, 2021, 10, 2118-2131.	1.3	16
110	Discrimination of Direct and Indirect Interactions in a Network of Regulatory Effects. Journal of Computational Biology, 2007, 14, 1217-1228.	0.8	15
111	Mhc class I gene of African lungfish. Immunogenetics, 2000, 51, 491-495.	1.2	14
112	Gene expression analysis of endobronchial epithelial lining fluid in the evaluation of indeterminate pulmonary nodules. Journal of Thoracic and Cardiovascular Surgery, 2009, 138, 474-479.	0.4	14
113	Evolving therapeutic concepts in prostate cancer based on genome-wide analyses (Review). International Journal of Oncology, 2014, 45, 1337-1344.	1.4	14
114	Patient-specific molecular alterations are associated with metastatic clear cell renal cell cancer progressing under tyrosine kinase inhibitor therapy. Oncotarget, 2017, 8, 74049-74057.	0.8	14
115	Next generation sequencing of the cellular and liquid fraction of pancreatic cyst fluid supports discrimination of IPMN from pseudocysts and reveals cases with multiple mutated driver clones: First findings from the prospective ZYSTEUS biomarker study. Genes Chromosomes and Cancer, 2019, 58, 3-11.	1.5	14
116	Contact spotting of protein microarrays coupled with spike-in of normalizer protein permits time-resolved analysis of ERBB receptor signaling. Proteomics, 2008, 8, 1586-1594.	1.3	13
117	Serial liquid biopsies for detection of treatment failure and profiling of resistance mechanisms in <i>KLC1â€"ALK</i>-rearranged lung cancer. Journal of Physical Education and Sports Management, 2019, 5, a004630.	0.5	13
118	KRAS / GNAS â€testing by highly sensitive deep targeted next generation sequencing improves the endoscopic ultrasoundâ€guided workup of suspected mucinous neoplasms of the pancreas. Genes Chromosomes and Cancer, 2021, 60, 489-497.	1.5	13
119	Novel RNA Markers in Prostate Cancer: Functional Considerations and Clinical Translation. BioMed Research International, 2014, 2014, 1-12.	0.9	12
120	Activation of AMP-activated protein kinase sensitizes lung cancer cells and H1299 xenografts to erlotinib. Lung Cancer, 2014, 86, 151-157.	0.9	12
121	PARP inhibition in BRCA2-mutated prostate cancer. Annals of Oncology, 2017, 28, 189-191.	0.6	12
122	Identification of E6/E7-Dependent MicroRNAs in HPV-Positive Cancer Cells. Methods in Molecular Biology, 2018, 1699, 119-134.	0.4	12
123	Molecular signatures in IASLC/ATS/ERS classified growth patterns of lung adenocarcinoma. PLoS ONE, 2018, 13, e0206132.	1.1	12
124	FGF-2 is a driving force for chromosomal instability and a stromal factor associated with adverse clinico-pathological features in prostate cancer. Urologic Oncology: Seminars and Original Investigations, 2018, 36, 365.e15-365.e26.	0.8	12
125	New family of Mhc class II A genes identified from cDNA sequences in the cichlid fish Aulonocara hansbaenschi. Immunogenetics, 1999, 49, 544-548.	1.2	11
126	Comparative Analysis and Modeling of the Severity of Steatohepatitis in DDC-Treated Mouse Strains. PLoS ONE, 2014, 9, e111006.	1.1	11

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127	Pathways regulating the expression of the immunomodulatory protein glycodelin in non‐small cell lung cancer. International Journal of Oncology, 2019, 54, 515-526.	1.4	10
128	The ERG-Regulated <i>LINC00920</i> Promotes Prostate Cancer Cell Survival via the 14-3-3ïµâ€œFOXO Pathway. Molecular Cancer Research, 2020, 18, 1545-1559.	1.5	10
129	Feasibility and Challenges for Sequential Treatments in ALK-Rearranged Non-Small-Cell Lung Cancer. Frontiers in Oncology, 2021, 11, 670483.	1.3	10
130	Cross-talk between AMPK and EGFR dependent Signaling in Non-Small Cell Lung Cancer. Scientific Reports, 2016, 6, 27514.	1.6	8
131	DNA Promoter Methylation and ERG Regulate the Expression of CD24 in Prostate Cancer. American Journal of Pathology, 2021, 191, 618-630.	1.9	7
132	cDNA Sequence Coding for the ??-Chain of the Third Complement Component in the African Lungfish. Scandinavian Journal of Immunology, 1999, 49, 367-375.	1.3	6
133	Reverse‐phase protein arrays for application‐orientated cancer research. Proteomics - Clinical Applications, 2009, 3, 1140-1150.	0.8	6
134	miR-449a Repression Leads to Enhanced NOTCH Signaling in TMPRSS2:ERG Fusion Positive Prostate Cancer Cells. Cancers, 2021, 13, 964.	1.7	5
135	Antibody-Mediated Signal Amplification for Reverse Phase Protein Array-Based Protein Quantification. Methods in Molecular Biology, 2011, 785, 55-64.	0.4	5
136	Prospective single center trial of next-generation sequencing analysis in metastatic renal cell cancer: the MORE-TRIAL. Future Science OA, 2018, 4, FSO299.	0.9	3
137	Experimental design and data analysis of Ago-RIP-Seq experiments for the identification of microRNA targets. Briefings in Bioinformatics, 2018, 19, 918-929.	3.2	3
138	Novel Liquid Biomarker Panels for A Very Early Response Capturing of NSCLC Therapies in Advanced Stages. Cancers, 2020, 12, 954.	1.7	3
139	Impact of Surgeon's Experience in Rigid Versus Elastic MRI/TRUS-Fusion Biopsy to Detect Significant Prostate Cancer Using Targeted and Systematic Cores. Cancers, 2022, 14, 886.	1.7	3
140	Infrared-based protein detection arrays for quantitative proteomics. Expert Opinion on Drug Discovery, 2008, 3, 273-283.	2.5	2
141	Rearranged ERG confers robustness to prostate cancer cells by subverting the function of p53. Urologic Oncology: Seminars and Original Investigations, 2020, 38, 736.e1-736.e10.	0.8	2
142	Multiple layers of intratumor heterogeneity: clues to clonal evolution of non-small cell lung cancer. Oncotarget, 2019, 10, 1549-1551.	0.8	1
143	[454] TARGETED IDENTIFICATION OF IRON REGULATED GENES IN PATIENTS WITH HEMOCHROMATOSIS AND HEPATITIS C USING A CUSTOM-MADE WHOLE GENOME cDNA MICROARRAY. Journal of Hepatology, 2007, 46, S173.	1.8	0
144	Recent advances in transcription profiling of human cancer. Current Opinion in Molecular Therapeutics, 2004, 6, 593-9.	2.8	0