

Holger SÃ¼ltmann

List of Publications by Year in descending order

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144
papers

11,397
citations

47006

47
h-index

30922

102
g-index

158
all docs

158
docs citations

158
times ranked

20292
citing authors

#	ARTICLE	IF	CITATIONS
1	Impact of Surgeon's Experience in Rigid Versus Elastic MRI/TRUS-Fusion Biopsy to Detect Significant Prostate Cancer Using Targeted and Systematic Cores. <i>Cancers</i> , 2022, 14, 886.	3.7	3
2	miR-449a Repression Leads to Enhanced NOTCH Signaling in TMPRSS2:ERG Fusion Positive Prostate Cancer Cells. <i>Cancers</i> , 2021, 13, 964.	3.7	5
3	KRAS / GNAS testing by highly sensitive deep targeted next generation sequencing improves the endoscopic ultrasound-guided workup of suspected mucinous neoplasms of the pancreas. <i>Genes Chromosomes and Cancer</i> , 2021, 60, 489-497.	2.8	13
4	DNA Promoter Methylation and ERG Regulate the Expression of CD24 in Prostate Cancer. <i>American Journal of Pathology</i> , 2021, 191, 618-630.	3.8	7
5	Feasibility and Challenges for Sequential Treatments in ALK-Rearranged Non-Small-Cell Lung Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 670483.	2.8	10
6	Earlier extracranial progression and shorter survival in ALK- rearranged lung cancer with positive liquid rebiopsies. <i>Translational Lung Cancer Research</i> , 2021, 10, 2118-2131.	2.8	16
7	Liquid Biopsies beyond Mutation Calling: Genomic and Epigenomic Features of Cell-Free DNA in Cancer. <i>Cancers</i> , 2021, 13, 5615.	3.7	20
8	Early identification of disease progression in ALK-rearranged lung cancer using circulating tumor DNA analysis. <i>Npj Precision Oncology</i> , 2021, 5, 100.	5.4	21
9	Rearranged ERG confers robustness to prostate cancer cells by subverting the function of p53. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2020, 38, 736.e1-736.e10.	1.6	2
10	Longitudinal therapy monitoring of ALK-positive lung cancer by combined copy number and targeted mutation profiling of cell-free DNA. <i>EBioMedicine</i> , 2020, 62, 103103.	6.1	32
11	The ERG-Regulated <i>LINC00920</i> Promotes Prostate Cancer Cell Survival via the 14-3-3 μ FOXO Pathway. <i>Molecular Cancer Research</i> , 2020, 18, 1545-1559.	3.4	10
12	Novel Liquid Biomarker Panels for A Very Early Response Capturing of NSCLC Therapies in Advanced Stages. <i>Cancers</i> , 2020, 12, 954.	3.7	3
13	Circulating MicroRNAs as Potential Biomarkers for Lung Cancer. <i>Recent Results in Cancer Research</i> , 2020, 215, 299-318.	1.8	26
14	Pathways regulating the expression of the immunomodulatory protein glycodelin in non-small cell lung cancer. <i>International Journal of Oncology</i> , 2019, 54, 515-526.	3.3	10
15	Excess hepsin proteolytic activity limits oncogenic signaling and induces ER stress and autophagy in prostate cancer cells. <i>Cell Death and Disease</i> , 2019, 10, 601.	6.3	18
16	Detection of TP53 Mutations in Tissue or Liquid Rebiopsies at Progression Identifies ALK+ Lung Cancer Patients with Poor Survival. <i>Cancers</i> , 2019, 11, 124.	3.7	36
17	Serial liquid biopsies for detection of treatment failure and profiling of resistance mechanisms in <i>KLC1</i> -ALK-rearranged lung cancer. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a004630.	1.2	13
18	Digital PCR After MALDI-Mass Spectrometry Imaging to Combine Proteomic Mapping and Identification of Activating Mutations in Pulmonary Adenocarcinoma. <i>Proteomics - Clinical Applications</i> , 2019, 13, e1800034.	1.6	19

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19	Global DNA methylation reflects spatial heterogeneity and molecular evolution of lung adenocarcinomas. <i>International Journal of Cancer</i> , 2019, 144, 1061-1072.	5.1	22
20	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. <i>Genes Chromosomes and Cancer</i> , 2019, 58, 3-11.	2.8	14
21	Multiple layers of intratumor heterogeneity: clues to clonal evolution of non-small cell lung cancer. <i>Oncotarget</i> , 2019, 10, 1549-1551.	1.8	1
22	Defining molecular risk in ALK+ NSCLC. <i>Oncotarget</i> , 2019, 10, 3093-3103.	1.8	35
23	Hepatitis D virus replication is sensed by MDA5 and induces IFN- γ responses in hepatocytes. <i>Journal of Hepatology</i> , 2018, 69, 25-35.	3.7	101
24	Prospective single center trial of next-generation sequencing analysis in metastatic renal cell cancer: the MORE-TRIAL. <i>Future Science OA</i> , 2018, 4, FSO299.	1.9	3
25	Experimental design and data analysis of Ago-RIP-Seq experiments for the identification of microRNA targets. <i>Briefings in Bioinformatics</i> , 2018, 19, 918-929.	6.5	3
26	Identification of E6/E7-Dependent MicroRNAs in HPV-Positive Cancer Cells. <i>Methods in Molecular Biology</i> , 2018, 1699, 119-134.	0.9	12
27	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. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2018, 36, 161.e19-161.e30.	1.6	26
28	Correlation between genomic index lesions and mpMRI and 68Ga-PSMA-PET/CT imaging features in primary prostate cancer. <i>Scientific Reports</i> , 2018, 8, 16708.	3.3	27
29	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. <i>Cancer Cell</i> , 2018, 34, 996-1011.e8.	16.8	190
30	Molecular signatures in IASLC/ATS/ERS classified growth patterns of lung adenocarcinoma. <i>PLoS ONE</i> , 2018, 13, e0206132.	2.5	12
31	Genome-Based Classification and Therapy of Prostate Cancer. <i>Diagnostics</i> , 2018, 8, 62.	2.6	16
32	Epigenomic profiling of non-small cell lung cancer xenografts uncover LRP12 DNA methylation as predictive biomarker for carboplatin resistance. <i>Genome Medicine</i> , 2018, 10, 55.	8.2	37
33	Genomic features of renal cell carcinoma with venous tumor thrombus. <i>Scientific Reports</i> , 2018, 8, 7477.	3.3	19
34	FGF-2 is a driving force for chromosomal instability and a stromal factor associated with adverse clinico-pathological features in prostate cancer. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2018, 36, 365.e15-365.e26.	1.6	12
35	A field guide for cancer diagnostics using cell-free DNA: From principles to practice and clinical applications. <i>Genes Chromosomes and Cancer</i> , 2018, 57, 123-139.	2.8	155
36	Spatial distribution of <i>EGFR</i> and <i>KRAS</i> mutation frequencies correlates with histological growth patterns of lung adenocarcinomas. <i>International Journal of Cancer</i> , 2017, 141, 1841-1848.	5.1	21

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37	Mutations in BRCA2 and taxane resistance in prostate cancer. <i>Scientific Reports</i> , 2017, 7, 4574.	3.3	32
38	PARP inhibition in BRCA2-mutated prostate cancer. <i>Annals of Oncology</i> , 2017, 28, 189-191.	1.2	12
39	QSEA modelling of genome-wide DNA methylation from sequencing enrichment experiments. <i>Nucleic Acids Research</i> , 2017, 45, e44-e44.	14.5	39
40	Patient-specific molecular alterations are associated with metastatic clear cell renal cell cancer progressing under tyrosine kinase inhibitor therapy. <i>Oncotarget</i> , 2017, 8, 74049-74057.	1.8	14
41	<i>ERG</i> gene fusion variants induce TGF- β signaling and epithelial to mesenchymal transition in human prostate cancer cells. <i>Oncotarget</i> , 2017, 8, 25115-25130.	1.8	23
42	Mutation analysis of circulating plasma DNA to determine response to EGFR tyrosine kinase inhibitor therapy of lung adenocarcinoma patients. <i>Scientific Reports</i> , 2016, 6, 33505.	3.3	44
43	Cross-talk between AMPK and EGFR dependent Signaling in Non-Small Cell Lung Cancer. <i>Scientific Reports</i> , 2016, 6, 27514.	3.3	8
44	Spatial niche formation but not malignant progression is a driving force for intratumoural heterogeneity. <i>Nature Communications</i> , 2016, 7, ncomms11845.	12.8	44
45	Low Input Whole-Exome Sequencing to Determine the Representation of the Tumor Exome in Circulating DNA of Non-Small Cell Lung Cancer Patients. <i>PLoS ONE</i> , 2016, 11, e0161012.	2.5	39
46	A cancer specific hypermethylation signature of the TERT promoter predicts biochemical relapse in prostate cancer: a retrospective cohort study. <i>Oncotarget</i> , 2016, 7, 57726-57736.	1.8	55
47	Ago-RIP-Seq identifies Polycomb repressive complex I member CBX7 as a major target of <i>miR-375</i> in prostate cancer progression. <i>Oncotarget</i> , 2016, 7, 59589-59603.	1.8	38
48	Extracellular vesicle-mediated transfer of functional RNA in the tumor microenvironment. <i>Oncotarget</i> , 2015, 4, e1008371.	4.6	227
49	Dependence of Intracellular and Exosomal microRNAs on Viral E6/E7 Oncogene Expression in HPV-positive Tumor Cells. <i>PLoS Pathogens</i> , 2015, 11, e1004712.	4.7	191
50	BAZ2A (TIP5) is involved in epigenetic alterations in prostate cancer and its overexpression predicts disease recurrence. <i>Nature Genetics</i> , 2015, 47, 22-30.	21.4	141
51	Comparative Analysis and Modeling of the Severity of Steatohepatitis in DDC-Treated Mouse Strains. <i>PLoS ONE</i> , 2014, 9, e111006.	2.5	11
52	Extracellular Vesicle-Mediated Transfer of Genetic Information between the Hematopoietic System and the Brain in Response to Inflammation. <i>PLoS Biology</i> , 2014, 12, e1001874.	5.6	312
53	Novel RNA Markers in Prostate Cancer: Functional Considerations and Clinical Translation. <i>BioMed Research International</i> , 2014, 2014, 1-12.	1.9	12
54	Hepatitis B and D Viruses Exploit Sodium Taurocholate Co-transporting Polypeptide for Species-Specific Entry into Hepatocytes. <i>Gastroenterology</i> , 2014, 146, 1070-1083.e6.	1.3	627

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55	Activation of AMP-activated protein kinase sensitizes lung cancer cells and H1299 xenografts to erlotinib. <i>Lung Cancer</i> , 2014, 86, 151-157.	2.0	12
56	Long Noncoding RNA: <i>lncRNAs</i> to Cancer. <i>European Urology</i> , 2014, 65, 1152-1153.	1.9	22
57	Evolving therapeutic concepts in prostate cancer based on genome-wide analyses (Review). <i>International Journal of Oncology</i> , 2014, 45, 1337-1344.	3.3	14
58	Role of miR-34a as a suppressor of L1CAM in endometrial carcinoma. <i>Oncotarget</i> , 2014, 5, 462-472.	1.8	63
59	Serum miR-142-3p is associated with early relapse in operable lung adenocarcinoma patients. <i>Lung Cancer</i> , 2013, 80, 223-227.	2.0	65
60	The maternal embryonic leucine zipper kinase (MELK) is upregulated in high-grade prostate cancer. <i>Journal of Molecular Medicine</i> , 2013, 91, 237-248.	3.9	117
61	Integrative Genomic Analyses Reveal an Androgen-Driven Somatic Alteration Landscape in Early-Onset Prostate Cancer. <i>Cancer Cell</i> , 2013, 23, 159-170.	16.8	292
62	microRNA biomarkers in body fluids of prostate cancer patients. <i>Methods</i> , 2013, 59, 132-137.	3.8	51
63	A Cancer-Indicative microRNA Pattern in Normal Prostate Tissue. <i>International Journal of Molecular Sciences</i> , 2013, 14, 5239-5249.	4.1	18
64	Characterization of Transcriptional Changes in ERG Rearrangement-Positive Prostate Cancer Identifies the Regulation of Metabolic Sensors Such as Neuropeptide Y. <i>PLoS ONE</i> , 2013, 8, e55207.	2.5	32
65	ERG Induces Epigenetic Activation of Tudor Domain-Containing Protein 1 (TDRD1) in ERG Rearrangement-Positive Prostate Cancer. <i>PLoS ONE</i> , 2013, 8, e59976.	2.5	26
66	Early Detection of Lung Cancer by Molecular Markers in Endobronchial Epithelial-Lining Fluid. <i>Journal of Thoracic Oncology</i> , 2012, 7, 1001-1008.	1.1	16
67	Peroxiredoxins 3 and 4 Are Overexpressed in Prostate Cancer Tissue and Affect the Proliferation of Prostate Cancer Cells in Vitro. <i>Journal of Proteome Research</i> , 2012, 11, 2452-2466.	3.7	46
68	A simple strand-specific RNA-Seq library preparation protocol combining the Illumina TruSeq RNA and the dUTP methods. <i>Biochemical and Biophysical Research Communications</i> , 2012, 422, 643-646.	2.1	62
69	Genome-wide DNA Methylation Events in <i>TMPRSS2-ERG</i> Fusion-Negative Prostate Cancers Implicate an EZH2-Dependent Mechanism with <i>miR-26a</i> Hypermethylation. <i>Cancer Discovery</i> , 2012, 2, 1024-1035.	9.4	127
70	Establishment and comparative characterization of novel squamous cell non-small cell lung cancer cell lines and their corresponding tumor tissue. <i>Lung Cancer</i> , 2012, 75, 45-57.	2.0	28
71	Gene Expression Profiling Unravels Cancer-Related Hepatic Molecular Signatures in Steatohepatitis but Not in Steatosis. <i>PLoS ONE</i> , 2012, 7, e46584.	2.5	97
72	Graph based fusion of miRNA and mRNA expression data improves clinical outcome prediction in prostate cancer. <i>BMC Bioinformatics</i> , 2011, 12, 488.	2.6	35

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73	Matrix-Dependent Regulation of AKT in Hepsin-Overexpressing PC3 Prostate Cancer Cells. <i>Neoplasia</i> , 2011, 13, 579-IN2.	5.3	27
74	EZH2 Depletion Blocks the Proliferation of Colon Cancer Cells. <i>PLoS ONE</i> , 2011, 6, e21651.	2.5	84
75	Transcription alterations of members of the ubiquitin-proteasome network in prostate carcinoma. <i>Prostate Cancer and Prostatic Diseases</i> , 2011, 14, 38-45.	3.9	42
76	Loss of EpCAM expression in breast cancer derived serum exosomes: Role of proteolytic cleavage. <i>Gynecologic Oncology</i> , 2011, 122, 437-446.	1.4	248
77	TMPRSS2-ERG -specific transcriptional modulation is associated with prostate cancer biomarkers and TGF- β^2 signaling. <i>BMC Cancer</i> , 2011, 11, 507.	2.6	128
78	Ubiquitin carboxyl-terminal hydrolase 1 (UCHL1) is a potential tumour suppressor in prostate cancer and is frequently silenced by promoter methylation. <i>Molecular Cancer</i> , 2011, 10, 129.	19.2	88
79	Targeted high throughput sequencing in clinical cancer Settings: formaldehyde fixed-paraffin embedded (FFPE) tumor tissues, input amount and tumor heterogeneity. <i>BMC Medical Genomics</i> , 2011, 4, 68.	1.5	154
80	The anterior gradient 2 (AGR2) gene is overexpressed in prostate cancer and may be useful as a urine sediment marker for prostate cancer detection. <i>Prostate</i> , 2011, 71, 575-587.	2.3	79
81	Circulating miRNAs are correlated with tumor progression in prostate cancer. <i>International Journal of Cancer</i> , 2011, 128, 608-616.	5.1	520
82	pathClass: an R-package for integration of pathway knowledge into support vector machines for biomarker discovery. <i>Bioinformatics</i> , 2011, 27, 1442-1443.	4.1	30
83	Antibody-Mediated Signal Amplification for Reverse Phase Protein Array-Based Protein Quantification. <i>Methods in Molecular Biology</i> , 2011, 785, 55-64.	0.9	5
84	Identification of Clinically Relevant Protein Targets in Prostate Cancer with 2D-DIGE Coupled Mass Spectrometry and Systems Biology Network Platform. <i>PLoS ONE</i> , 2011, 6, e16833.	2.5	67
85	Sensitivity and resistance towards isoliquiritigenin, doxorubicin and methotrexate in T cell acute lymphoblastic leukaemia cell lines by pharmacogenomics. <i>Naunyn-Schmiedeberg's Archives of Pharmacology</i> , 2010, 382, 221-234.	3.0	20
86	Increasing the sensitivity of reverse phase protein arrays by antibody-mediated signal amplification. <i>Proteome Science</i> , 2010, 8, 36.	1.7	17
87	ERBB2 and TOP2A in Breast Cancer: A Comprehensive Analysis of Gene Amplification, RNA Levels, and Protein Expression and Their Influence on Prognosis and Prediction. <i>Clinical Cancer Research</i> , 2010, 16, 2391-2401.	7.0	113
88	Integration of pathway knowledge into a reweighted recursive feature elimination approach for risk stratification of cancer patients. <i>Bioinformatics</i> , 2010, 26, 2136-2144.	4.1	94
89	Serum microRNAs as non-invasive biomarkers for cancer. <i>Molecular Cancer</i> , 2010, 9, 306.	19.2	369
90	Gene expression analysis of endobronchial epithelial lining fluid in the evaluation of indeterminate pulmonary nodules. <i>Journal of Thoracic and Cardiovascular Surgery</i> , 2009, 138, 474-479.	0.8	14

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91	Molecular Cancer Phenotype in Normal Prostate Tissue. <i>European Urology</i> , 2009, 55, 885-891.	1.9	23
92	In vitro-targeted gene identification in patients with hepatitis C using a genome-wide microarray technology. <i>Hepatology</i> , 2009, 49, 378-386.	7.3	19
93	Effects of infiltrating lymphocytes and estrogen receptor on gene expression and prognosis in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2009, 116, 69-77.	2.5	106
94	Reverse-phase protein arrays for application-oriented cancer research. <i>Proteomics - Clinical Applications</i> , 2009, 3, 1140-1150.	1.6	6
95	Global gene expression analysis reveals specific patterns of cell junctions in non-small cell lung cancer subtypes. <i>Lung Cancer</i> , 2009, 63, 32-38.	2.0	161
96	Differential expression of apoptotic genes PDIA3 and MAP3K5 distinguishes between low- and high-risk prostate cancer. <i>Molecular Cancer</i> , 2009, 8, 130.	19.2	70
97	Contact spotting of protein microarrays coupled with spike-in of normalizer protein permits time-resolved analysis of ERBB receptor signaling. <i>Proteomics</i> , 2008, 8, 1586-1594.	2.2	13
98	Metastases and multiple myeloma generate distinct transcriptional footprints in osteocytes <i>in vivo</i> . <i>Journal of Pathology</i> , 2008, 214, 617-626.	4.5	24
99	Loss of p16 ^{INK4A} downregulation and enables RB/E2F1-dependent cell cycle promotion in gastrointestinal stromal tumours (GISTs). <i>Journal of Pathology</i> , 2008, 215, 253-262.	4.5	36
100	Increased KIT signalling with upregulation of cyclin D correlates to accelerated proliferation and shorter disease-free survival in gastrointestinal stromal tumours (GISTs) with KIT exon 11 deletions. <i>Journal of Pathology</i> , 2008, 216, 225-235.	4.5	20
101	Reduced expression of vacuole membrane protein 1 affects the invasion capacity of tumor cells. <i>Oncogene</i> , 2008, 27, 1320-1326.	5.9	48
102	Yes and PI3K Bind CD95 to Signal Invasion of Glioblastoma. <i>Cancer Cell</i> , 2008, 13, 235-248.	16.8	281
103	Marked Gene Transcript Level Alterations Occur Early During Radical Prostatectomy. <i>European Urology</i> , 2008, 53, 333-346.	1.9	40
104	Subtractive gene expression profiling of articular cartilage and mesenchymal stem cells: serpins as cartilage-relevant differentiation markers. <i>Osteoarthritis and Cartilage</i> , 2008, 16, 48-60.	1.3	50
105	Genomic analysis reveals poor separation of human cardiomyopathies of ischemic and nonischemic etiologies. <i>Physiological Genomics</i> , 2008, 34, 88-94.	2.3	22
106	Predicting pathway membership via domain signatures. <i>Bioinformatics</i> , 2008, 24, 2137-2142.	4.1	17
107	Estimating large-scale signaling networks through nested effect models with intervention effects from microarray data. <i>Bioinformatics</i> , 2008, 24, 2650-2656.	4.1	44
108	Infrared-based protein detection arrays for quantitative proteomics. <i>Expert Opinion on Drug Discovery</i> , 2008, 3, 273-283.	5.0	2

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109	Identification of aberrant chromosomal regions from gene expression microarray studies applied to human breast cancer. <i>Bioinformatics</i> , 2007, 23, 2273-2280.	4.1	28
110	Discrimination of Direct and Indirect Interactions in a Network of Regulatory Effects. <i>Journal of Computational Biology</i> , 2007, 14, 1217-1228.	1.6	15
111	Combinatorial RNAi for quantitative protein network analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 6579-6584.	7.1	55
112	[454] TARGETED IDENTIFICATION OF IRON REGULATED GENES IN PATIENTS WITH HEMOCHROMATOSIS AND HEPATITIS C USING A CUSTOM-MADE WHOLE GENOME cDNA MICROARRAY. <i>Journal of Hepatology</i> , 2007, 46, S173.	3.7	0
113	The Human <i>let-7a-3</i> Locus Contains an Epigenetically Regulated MicroRNA Gene with Oncogenic Function. <i>Cancer Research</i> , 2007, 67, 1419-1423.	0.9	437
114	The differentiation antigen NY-BR-1 is a potential target for antibody-based therapies in breast cancer. <i>International Journal of Cancer</i> , 2007, 120, 2635-2642.	5.1	31
115	Identification of cellular targets for the human papillomavirus E6 and E7 oncogenes by RNA interference and transcriptome analyses. <i>Journal of Molecular Medicine</i> , 2007, 85, 1253-1262.	3.9	41
116	Identification of a Common Gene Expression Signature in Dilated Cardiomyopathy Across Independent Microarray Studies. <i>Journal of the American College of Cardiology</i> , 2006, 48, 1610-1617.	2.8	153
117	Analysis of pigmented villonodular synovitis with genome-wide complementary DNA microarray and tissue array technology reveals insight into potential novel therapeutic approaches. <i>Arthritis and Rheumatism</i> , 2006, 54, 1009-1019.	6.7	37
118	Identification and meta-analysis of a small gene expression signature for the diagnosis of estrogen receptor status in invasive ductal breast cancer. <i>International Journal of Cancer</i> , 2006, 119, 2974-2979.	5.1	44
119	Functional Profiling: From Microarrays via Cell-Based Assays to Novel Tumor Relevant Modulators of the Cell Cycle. <i>Cancer Research</i> , 2005, 65, 7733-7742.	0.9	19
120	arrayMagic: two-colour cDNA microarray quality control and preprocessing. <i>Bioinformatics</i> , 2005, 21, 554-556.	4.1	48
121	Prognostic Role of <i>E2F1</i> and Members of the <i>CDKN2A</i> Network in Gastrointestinal Stromal Tumors. <i>Clinical Cancer Research</i> , 2005, 11, 6589-6597.	7.0	79
122	Gene expression in kidney cancer is associated with cytogenetic abnormalities, metastasis formation, and patient survival. <i>Clinical Cancer Research</i> , 2005, 11, 646-55.	7.0	64
123	Extraction and processing of high quality RNA from impalpable and macroscopically invisible prostate cancer for microarray gene expression analysis. <i>International Journal of Oncology</i> , 2005, 27, 713-20.	3.3	17
124	From ORFeome to Biology: A Functional Genomics Pipeline. <i>Genome Research</i> , 2004, 14, 2136-2144.	5.5	44
125	Systematic analysis of T7 RNA polymerase based in vitro linear RNA amplification for use in microarray experiments. <i>BMC Genomics</i> , 2004, 5, 29.	2.8	79
126	Equivalence test in quantitative reverse transcription polymerase chain reaction: confirmation of reference genes suitable for normalization. <i>Analytical Biochemistry</i> , 2004, 335, 1-9.	2.4	121

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127	Recent advances in transcription profiling of human cancer. <i>Current Opinion in Molecular Therapeutics</i> , 2004, 6, 593-9.	2.8	0
128	Variance stabilization applied to microarray data calibration and to the quantification of differential expression. <i>Bioinformatics</i> , 2002, 18, S96-S104.	4.1	2,012
129	Identification and Classification of Differentially Expressed Genes in Renal Cell Carcinoma by Expression Profiling on a Global Human 31,500-Element cDNA Array. <i>Genome Research</i> , 2001, 11, 1861-1870.	5.5	184
130	Identification and Linkage of the Proteasome Activator Complex PA28 Subunit Genes in Zebrafish. <i>Scandinavian Journal of Immunology</i> , 2000, 51, 571-576.	2.7	20
131	Identification of Seven Genes in the Major Histocompatibility Complex Class I Region of the Zebrafish. <i>Scandinavian Journal of Immunology</i> , 2000, 51, 577-585.	2.7	24
132	Major histocompatibility complex class II A genes in cichlid fishes: identification, expression, linkage relationships, and haplotype variation. <i>Immunogenetics</i> , 2000, 51, 576-586.	2.4	30
133	Mhc class II B gene evolution in East African cichlid fishes. <i>Immunogenetics</i> , 2000, 51, 556-575.	2.4	46
134	Nonlinkage of major histocompatibility complex class I and class II loci in bony fishes. <i>Immunogenetics</i> , 2000, 51, 108-116.	2.4	164
135	Mhc class I gene of African lungfish. <i>Immunogenetics</i> , 2000, 51, 491-495.	2.4	14
136	Conservation of Mhc Class III Region Synteny Between Zebrafish and Human as Determined by Radiation Hybrid Mapping. <i>Journal of Immunology</i> , 2000, 165, 6984-6993.	0.8	31
137	A Contig Map of the Mhc Class I Genomic Region in the Zebrafish Reveals Ancient Synteny. <i>Journal of Immunology</i> , 2000, 164, 5296-5305.	0.8	85
138	cDNA Sequence Coding for the C-chain of the Third Complement Component in the African Lungfish. <i>Scandinavian Journal of Immunology</i> , 1999, 49, 367-375.	2.7	6
139	New family of Mhc class II A genes identified from cDNA sequences in the cichlid fish <i>Aulonocara hansbaenschi</i> . <i>Immunogenetics</i> , 1999, 49, 544-548.	2.4	11
140	Isolation of Mhc Class II DMA and DMB cDNA Sequences in a Marsupial: The Gray Short-Tailed Opossum (<i>Monodelphis domestica</i>). <i>Journal of Molecular Evolution</i> , 1998, 47, 578-585.	1.8	19
141	Linkage Relationships and Haplotype Polymorphism Among Cichlid Mhc Class II B Loci. <i>Genetics</i> , 1998, 149, 1527-1537.	2.9	85
142	Class I Mhc genes of cichlid fishes: identification, expression, and polymorphism. <i>Immunogenetics</i> , 1997, 46, 63-72.	2.4	53
143	Organization of Mhc Class II B Genes in the Zebrafish (<i>Brachydanio rerio</i>). <i>Genomics</i> , 1994, 23, 1-14.	2.9	103
144	Polymorphism and estimation of the number of MhcCyca class I and class I genes in laboratory strains of the common carp (<i>Cyprinus carpio</i> L.). <i>Developmental and Comparative Immunology</i> , 1993, 17, 141-156.	2.3	45