

# Tero Aittokallio

## List of Publications by Year in descending order

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Version: 2024-02-01

295  
papers

12,891  
citations

26630

56  
h-index

36028

97  
g-index

326  
all docs

326  
docs citations

326  
times ranked

19351  
citing authors

#	ARTICLE	IF	CITATIONS
1	Implementing a Functional Precision Medicine Tumor Board for Acute Myeloid Leukemia. <i>Cancer Discovery</i> , 2022, 12, 388-401.	9.4	73
2	Fully-automated and ultra-fast cell-type identification using specific marker combinations from single-cell transcriptomic data. <i>Nature Communications</i> , 2022, 13, 1246.	12.8	163
3	What are the current challenges for machine learning in drug discovery and repurposing?. <i>Expert Opinion on Drug Discovery</i> , 2022, 17, 423-425.	5.0	12
4	SynergyFinder 3.0: an interactive analysis and consensus interpretation of multi-drug synergies across multiple samples. <i>Nucleic Acids Research</i> , 2022, 50, W739-W743.	14.5	139
5	Computational Pipeline for Rational Drug Combination Screening in Patient-Derived Cells. <i>Methods in Molecular Biology</i> , 2022, 2449, 327-348.	0.9	4
6	High intratumoral dihydrotestosterone is associated with antiandrogen resistance in VCaP prostate cancer xenografts in castrated mice. <i>IScience</i> , 2022, 25, 104287.	4.1	4
7	Tumor microenvironment as a metapopulation model: The effects of angiogenesis, emigration and treatment modalities. <i>Journal of Theoretical Biology</i> , 2022, 545, 111147.	1.7	1
8	Evaluation of statistical approaches for association testing in noisy drug screening data. <i>BMC Bioinformatics</i> , 2022, 23, 188.	2.6	5
9	Systematic review of computational methods for drug combination prediction. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2807-2814.	4.1	13
10	Tissue-specific identification of multi-omics features for pan-cancer drug response prediction. <i>IScience</i> , 2022, , 104767.	4.1	4
11	Characterizing the Quality of Insight by Interactions: A Case Study. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2021, 27, 3410-3424.	4.4	7
12	RUNX1 mutations in blast-phase chronic myeloid leukemia associate with distinct phenotypes, transcriptional profiles, and drug responses. <i>Leukemia</i> , 2021, 35, 1087-1099.	7.2	32
13	OUP accepted manuscript. <i>Briefings in Bioinformatics</i> , 2021, , .	6.5	6
14	Artificial intelligence, machine learning, and drug repurposing in cancer. <i>Expert Opinion on Drug Discovery</i> , 2021, 16, 977-989.	5.0	68
15	Novel Small Molecule Hsp90/Cdc37 Interface Inhibitors Indirectly Target K-Ras-Signaling. <i>Cancers</i> , 2021, 13, 927.	3.7	11
16	Patient-tailored design for selective co-inhibition of leukemic cell subpopulations. <i>Science Advances</i> , 2021, 7, .	10.3	28
17	Machine Learning of Bone Marrow Histopathology Identifies Genetic and Clinical Determinants in Patients with MDS. <i>Blood Cancer Discovery</i> , 2021, 2, 238-249.	5.0	25
18	Multi-modal meta-analysis of cancer cell line omics profiles identifies ECHDC1 as a novel breast tumor suppressor. <i>Molecular Systems Biology</i> , 2021, 17, e9526.	7.2	8

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19	Re-defining synthetic lethality by phenotypic profiling for precision oncology. Cell Chemical Biology, 2021, 28, 246-256.	5.2	18
20	Inhibition of Arenaviruses by Combinations of Orally Available Approved Drugs. Antimicrobial Agents and Chemotherapy, 2021, 65, .	3.2	27
21	Multi-Omics Marker Analysis Enables Early Prediction of Breast Tumor Progression. Frontiers in Genetics, 2021, 12, 670749.	2.3	9
22	Crowdsourced mapping of unexplored target space of kinase inhibitors. Nature Communications, 2021, 12, 3307.	12.8	41
23	Development of HDAC Inhibitors Exhibiting Therapeutic Potential in T-Cell Prolymphocytic Leukemia. Journal of Medicinal Chemistry, 2021, 64, 8486-8509.	6.4	28
24	Bayesian multi-source regression and monocyte-associated gene expression predict BCL-2 inhibitor resistance in acute myeloid leukemia. Npj Precision Oncology, 2021, 5, 71.	5.4	12
25	Modeling drug combination effects via latent tensor reconstruction. Bioinformatics, 2021, 37, i93-i101.	4.1	9
26	Network-guided identification of cancer-selective combinatorial therapies in ovarian cancer. Briefings in Bioinformatics, 2021, 22, .	6.5	13
27	Drug Combinations as a First Line of Defense against Coronaviruses and Other Emerging Viruses. MBio, 2021, 12, e0334721.	4.1	45
28	Modelling of killer T-cell and cancer cell subpopulation dynamics under immuno- and chemotherapies. Journal of Theoretical Biology, 2020, 488, 110136.	1.7	4
29	Genetic and functional implications of an exonic TRIM55 variant in heart failure. Journal of Molecular and Cellular Cardiology, 2020, 138, 222-233.	1.9	11
30	Cost-effective survival prediction for patients with advanced prostate cancer using clinical trial and real-world hospital registry datasets. International Journal of Medical Informatics, 2020, 133, 104014.	3.3	11
31	Noncanonical effector functions of the T-memory-like T-PLL cell are shaped by cooperative TCL1A and TCR signaling. Blood, 2020, 136, 2786-2802.	1.4	17
32	Improved detection of differentially represented DNA barcodes for high-throughput clonal phenomics. Molecular Systems Biology, 2020, 16, e9195.	7.2	15
33	KIT pathway upregulation predicts dasatinib efficacy in acute myeloid leukemia. Leukemia, 2020, 34, 2780-2784.	7.2	6
34	Leveraging multi-way interactions for systematic prediction of pre-clinical drug combination effects. Nature Communications, 2020, 11, 6136.	12.8	63
35	A relational database to identify differentially expressed genes in the endometrium and endometriosis lesions. Scientific Data, 2020, 7, 284.	5.3	33
36	Systematic mapping of cancer cell target dependencies using high-throughput drug screening in triple-negative breast cancer. Computational and Structural Biotechnology Journal, 2020, 18, 3819-3832.	4.1	6

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37	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. Nature Genetics, 2020, 52, 448-457.	21.4	104
38	Phosphoproteome and drug-response effects mediated by the three protein phosphatase 2A inhibitor proteins CIP2A, SET, and PME-1. Journal of Biological Chemistry, 2020, 295, 4194-4211.	3.4	48
39	<i>UBR5</i> Is Coamplified with <i>MYC</i> in Breast Tumors and Encodes an Ubiquitin Ligase That Limits MYC-Dependent Apoptosis. Cancer Research, 2020, 80, 1414-1427.	0.9	35
40	SynToxProfiler: An interactive analysis of drug combination synergy, toxicity and efficacy. PLoS Computational Biology, 2020, 16, e1007604.	3.2	43
41	Reinstated p53 response and high anti-T-cell leukemia activity by the novel alkylating deacetylase inhibitor tinostamustine. Leukemia, 2020, 34, 2513-2518.	7.2	9
42	Breeze: an integrated quality control and data analysis application for high-throughput drug screening. Bioinformatics, 2020, 36, 3602-3604.	4.1	68
43	A normalized drug response metric improves accuracy and consistency of anticancer drug sensitivity quantification in cell-based screening. Communications Biology, 2020, 3, 42.	4.4	23
44	SynergyFinder 2.0: visual analytics of multi-drug combination synergies. Nucleic Acids Research, 2020, 48, W488-W493.	14.5	545
45	Integrated drug profiling and CRISPR screening identify essential pathways for CAR T-cell cytotoxicity. Blood, 2020, 135, 597-609.	1.4	134
46	Multiobjective optimization identifies cancer-selective combination therapies. PLoS Computational Biology, 2020, 16, e1008538.	3.2	9
47	Abstract P6-10-28: Therapeutic stratification of triple negative breast cancer by integrating chemosensitivity & phospho-proteome profiles. , 2020, , .		0
48	SynToxProfiler: An interactive analysis of drug combination synergy, toxicity and efficacy. , 2020, 16, e1007604.		0
49	SynToxProfiler: An interactive analysis of drug combination synergy, toxicity and efficacy. , 2020, 16, e1007604.		0
50	SynToxProfiler: An interactive analysis of drug combination synergy, toxicity and efficacy. , 2020, 16, e1007604.		0
51	SynToxProfiler: An interactive analysis of drug combination synergy, toxicity and efficacy. , 2020, 16, e1007604.		0
52	Multiobjective optimization identifies cancer-selective combination therapies. , 2020, 16, e1008538.		0
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55	Multiobjective optimization identifies cancer-selective combination therapies. , 2020, 16, e1008538.		0
56	Multiobjective optimization identifies cancer-selective combination therapies. , 2020, 16, e1008538.		0
57	Multiobjective optimization identifies cancer-selective combination therapies. , 2020, 16, e1008538.		0
58	Machine learning and feature selection for drug response prediction in precision oncology applications. Biophysical Reviews, 2019, 11, 31-39.	3.2	148
59	Network pharmacology modeling identifies synergistic Aurora B and ZAK interaction in triple-negative breast cancer. Npj Systems Biology and Applications, 2019, 5, 20.	3.0	32
60	Chemogenomic Analysis of the Druggable Kinome and Its Application to Repositioning and Lead Identification Studies. Cell Chemical Biology, 2019, 26, 1608-1622.e6.	5.2	14
61	Novel Screening Method Identifies PI3KÎ±, mTOR, and IGF1R as Key Kinases Regulating Cardiomyocyte Survival. Journal of the American Heart Association, 2019, 8, e013018.	3.7	4
62	Genome-wide off-targets of drugs: risks and opportunities. Cell Biology and Toxicology, 2019, 35, 485-487.	5.3	16
63	Matrix and Tensor Factorization Methods for Toxicogenomic Modeling and Prediction. Challenges and Advances in Computational Chemistry and Physics, 2019, , 57-74.	0.6	1
64	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	12.8	240
65	DNMT Inhibitors Increase Methylation in the Cancer Genome. Frontiers in Pharmacology, 2019, 10, 385.	3.5	67
66	Phenotypic Screening Combined with Machine Learning for Efficient Identification of Breast Cancer-Selective Therapeutic Targets. Cell Chemical Biology, 2019, 26, 970-979.e4.	5.2	34
67	Pharmacological reactivation of MYC-dependent apoptosis induces susceptibility to anti-PD-1 immunotherapy. Nature Communications, 2019, 10, 620.	12.8	60
68	AB0234â€¦AN INTEGRATED PROTEOMICS AND ANTIBODY ANALYSIS OF THE U-ACT-EARLY TRIAL TO IDENTIFY MARKERS OF TREATMENT RESPONSE AND DISEASE PROGRESSION IN EARLY RHEUMATOID ARTHRITIS. , 2019, , .		0
69	1179A novel exonic variant in TRIM55 gene predisposes to heart failure. European Heart Journal, 2019, 40, .	2.2	0
70	JAK/STAT-Activating Genomic Alterations Are a Hallmark of T-PLL. Cancers, 2019, 11, 1833.	3.7	38
71	Prediction of drug combination effects with a minimal set of experiments. Nature Machine Intelligence, 2019, 1, 568-577.	16.0	99
72	Integrated Analysis of Drug Sensitivity and Selectivity to Predict Synergistic Drug Combinations and Target Coaddictions in Cancer. Methods in Molecular Biology, 2019, 1888, 205-217.	0.9	7

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73	Abstract P2-06-25: A phenotypic screening and machine learning platform efficiently identifies triple negative breast cancer-selective and readily druggable targets. , 2019, , .		0
74	Abstract 2945: Clinical implementation of precision systems oncology in the treatment of ovarian cancer based on ex-vivo drug testing and molecular profiling. Cancer Research, 2019, 79, 2945-2945.	0.9	1
75	Abstract 458: Precision systems medicine in acute myeloid leukemia: real-time translation of tailored therapeutic opportunities arising from ex-vivo drug sensitivity testing and molecular profiling. , 2019, , .		0
76	Abstract A137: Drug screening and molecular profiling identifies INKA1 as a predictive biomarker for sensitivity to MAPK inhibition-antimitotic combination treatment in pancreatic ductal adenocarcinoma. , 2019, , .		0
77	Abstract 2945: Clinical implementation of precision systems oncology in the treatment of ovarian cancer based on ex-vivo drug testing and molecular profiling. , 2019, , .		0
78	Patient-Customized Drug Combination Prediction and Testing for T-cell Prolymphocytic Leukemia Patients. Cancer Research, 2018, 78, 2407-2418.	0.9	60
79	Combined ASRGL1 and p53 immunohistochemistry as an independent predictor of survival in endometrioid endometrial carcinoma. Gynecologic Oncology, 2018, 149, 173-180.	1.4	16
80	Aggressive natural killer-cell leukemia—mutational landscape and drug profiling highlight JAK-STAT signaling as therapeutic target. Nature Communications, 2018, 9, 1567.	12.8	107
81	Secreted frizzled-related protein 2 (SFRP2) expression promotes lesion proliferation via canonical WNT signaling and indicates lesion borders in extraovarian endometriosis. Human Reproduction, 2018, 33, 817-831.	0.9	22
82	Methods for High-throughput Drug Combination Screening and Synergy Scoring. Methods in Molecular Biology, 2018, 1711, 351-398.	0.9	140
83	Drug Target Commons: A Community Effort to Build a Consensus Knowledge Base for Drug-Target Interactions. Cell Chemical Biology, 2018, 25, 224-229.e2.	5.2	124
84	Global proteomics profiling improves drug sensitivity prediction: results from a multi-omics, pan-cancer modeling approach. Bioinformatics, 2018, 34, 1353-1362.	4.1	56
85	Novel activities of safe-in-human broad-spectrum antiviral agents. Antiviral Research, 2018, 154, 174-182.	4.1	64
86	Improving the efficacy-safety balance of polypharmacology in multi-target drug discovery. Expert Opinion on Drug Discovery, 2018, 13, 179-192.	5.0	59
87	Antiandrogens Reduce Intratumoral Androgen Concentrations and Induce Androgen Receptor Expression in Castration-Resistant Prostate Cancer Xenografts. American Journal of Pathology, 2018, 188, 216-228.	3.8	9
88	Discovery of novel drug sensitivities in T-PLL by high-throughput ex vivo drug testing and mutation profiling. Leukemia, 2018, 32, 774-787.	7.2	75
89	Interactive visual analysis of drug–target interaction networks using Drug Target Profiler, with applications to precision medicine and drug repurposing. Briefings in Bioinformatics, 2018, , .	6.5	25
90	PO-092 Inhibition of the mTORC1-pathway can feedback-activate H-RAS or K-RAS. ESMO Open, 2018, 3, A57.	4.5	0

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91	Adrenals Contribute to Growth of Castration-Resistant VCaP Prostate Cancer Xenografts. American Journal of Pathology, 2018, 188, 2890-2901.	3.8	17
92	Drug Target Commons 2.0: a community platform for systematic analysis of drug–target interaction profiles. Database: the Journal of Biological Databases and Curation, 2018, 2018, 1-13.	3.0	36
93	Learning with multiple pairwise kernels for drug bioactivity prediction. Bioinformatics, 2018, 34, i509-i518.	4.1	51
94	ePCR: an R-package for survival and time-to-event prediction in advanced prostate cancer, applied to real-world patient cohorts. Bioinformatics, 2018, 34, 3957-3959.	4.1	5
95	Drug-Sensitivity Screening and Genomic Characterization of 45 HPV-Negative Head and Neck Carcinoma Cell Lines for Novel Biomarkers of Drug Efficacy. Molecular Cancer Therapeutics, 2018, 17, 2060-2071.	4.1	33
96	PP2A inhibition is a druggable MEK inhibitor resistance mechanism in KRAS-mutant lung cancer cells. Science Translational Medicine, 2018, 10, .	12.4	116
97	Susceptibility of low-density lipoprotein particles to aggregate depends on particle lipidome, is modifiable, and associates with future cardiovascular deaths. European Heart Journal, 2018, 39, 2562-2573.	2.2	126
98	Immune cell contexture in the bone marrow tumor microenvironment impacts therapy response in CML. Leukemia, 2018, 32, 1643-1656.	7.2	75
99	Comparative Analysis of Independent Ex Vivo functional Drug Screens Identifies Predictive Biomarkers of BCL-2 Inhibitor Response in AML. Blood, 2018, 132, 2763-2763.	1.4	1
100	Abstract 3277: Identification of internal tandem duplication within the FLT3 gene from AML patient next-generation sequence data. , 2018, , .		0
101	Abstract 3883: Gene expression predicts sex vivo drug sensitivity in acute myeloid leukemia. , 2018, , .		0
102	Abstract 875: Chemical biology approach to phenotypic intra-tumor heterogeneity in high-grade serous ovarian cancer. , 2018, , .		0
103	Abstract 3899: Discovery and clinical implementation of individualized therapies in acute myeloid leukemia based on ex vivo drug sensitivity testing and multi-omics profiling. , 2018, , .		0
104	Expanding the Utility of Midostaurin in Acute Myeloid Leukemia - Predictive Mutational Signatures in Patient Samples without FLT3 mutations and Clinically Applicable Synergistic Drug Combinations. Blood, 2018, 132, 2743-2743.	1.4	0
105	Comprehensive Drug Testing of Patient-derived Conditionally Reprogrammed Cells from Castration-resistant Prostate Cancer. European Urology, 2017, 71, 319-327.	1.9	74
106	Systematic drug sensitivity testing reveals synergistic growth inhibition by dasatinib or mTOR inhibitors with paclitaxel in ovarian granulosa cell tumor cells. Gynecologic Oncology, 2017, 144, 621-630.	1.4	26
107	Whole-genome view of the consequences of a population bottleneck using 2926 genome sequences from Finland and United Kingdom. European Journal of Human Genetics, 2017, 25, 477-484.	2.8	60
108	Matched preclinical designs for improved translatability. Science Translational Medicine, 2017, 9, .	12.4	2

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109	JAK1/2 and BCL2 inhibitors synergize to counteract bone marrow stromal cellâ€‘induced protection of AML. <i>Blood</i> , 2017, 130, 789-802.	1.4	90
110	Early metabolic markers identify potential targets for the prevention of type 2 diabetes. <i>Diabetologia</i> , 2017, 60, 1740-1750.	6.3	96
111	Re: Fatemeh Seyednasrollah, Mehrad Mahmoudian, Liisa Rautakorpi, et al. How Reliable are Trial-based Prognostic Models in Real-world Patients with Metastatic Castration-resistant Prostate Cancer? <i>Eur Urol.</i> 2017;71:838â€‘40. <i>European Urology</i> , 2017, 72, e68-e69.	1.9	0
112	SynergyFinder: a web application for analyzing drug combination doseâ€‘response matrix data. <i>Bioinformatics</i> , 2017, 33, 2413-2415.	4.1	403
113	The inconvenience of data of convenience: computational research beyond post-mortem analyses. <i>Nature Methods</i> , 2017, 14, 937-938.	19.0	9
114	In Search of Systemâ€‘Wide Productivity Gains â€‘The Role of Global Collaborations in Preclinical Translation. <i>Clinical and Translational Science</i> , 2017, 10, 423-425.	3.1	2
115	A Community Challenge for Inferring Genetic Predictors of Gene Essentialities through Analysis of a Functional Screen of Cancer Cell Lines. <i>Cell Systems</i> , 2017, 5, 485-497.e3.	6.2	19
116	Instability of LDL particles predicts future cardiovascular deaths. <i>Atherosclerosis</i> , 2017, 263, e12.	0.8	0
117	Seed-effect modeling improves the consistency of genome-wide loss-of-function screens and identifies synthetic lethal vulnerabilities in cancer cells. <i>Genome Medicine</i> , 2017, 9, 51.	8.2	12
118	C-SPADE: a web-tool for interactive analysis and visualization of drug screening experiments through compound-specific bioactivity dendrograms. <i>Nucleic Acids Research</i> , 2017, 45, W495-W500.	14.5	18
119	Enhanced sensitivity to glucocorticoids in cytarabine-resistant AML. <i>Leukemia</i> , 2017, 31, 1187-1195.	7.2	44
120	Orphan G protein-coupled receptor GPRC5A modulates integrin $\alpha 1$ -mediated epithelial cell adhesion. <i>Cell Adhesion and Migration</i> , 2017, 11, 434-446.	2.7	13
121	Prediction of overall survival for patients with metastatic castration-resistant prostate cancer: development of a prognostic model through a crowdsourced challenge with open clinical trial data. <i>Lancet Oncology</i> , The, 2017, 18, 132-142.	10.7	124
122	Antiviral Properties of Chemical Inhibitors of Cellular Anti-Apoptotic Bcl-2 Proteins. <i>Viruses</i> , 2017, 9, 271.	3.3	39
123	MediSyn: uncertainty-aware visualization of multiple biomedical datasets to support drug treatment selection. <i>BMC Bioinformatics</i> , 2017, 18, 393.	2.6	6
124	Systematic identification of feature combinations for predicting drug response with Bayesian multi-view multi-task linear regression. <i>Bioinformatics</i> , 2017, 33, i359-i368.	4.1	58
125	A DREAM Challenge to Build Prediction Models for Short-Term Discontinuation of Docetaxel in Metastatic Castration-Resistant Prostate Cancer. <i>JCO Clinical Cancer Informatics</i> , 2017, 1, 1-15.	2.1	12
126	Identification and Clinical Exploration of Individualized Targeted Therapeutic Approaches in Acute Myeloid Leukemia Patients By Integrating Drug Response and Deep Molecular Profiles. <i>Blood</i> , 2017, 130, 854-854.	1.4	1



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127	Computational-experimental approach to drug-target interaction mapping: A case study on kinase inhibitors. PLoS Computational Biology, 2017, 13, e1005678.	3.2	84
128	Rapalogs can promote cancer cell stemness <i>in vitro</i> in a Galectin-1 and H-ras-dependent manner. Oncotarget, 2017, 8, 44550-44566.	1.8	20
129	Abstract 5560: Systemic map of protein phosphatase 2A (PP2A)-regulated phosphotargets and drug responses in cancer cells. , 2017, , .		1
130	Abstract 410: Identifying ovarian cancer specific targeted drugs using high-throughput drug sensitivity profiles of primary cancer cells. , 2017, , .		0
131	Abstract A26: Prediction of synergistic anticancer drug combinations by integrating chemical and genetic screens. , 2017, , .		0
132	Multi-Omics Studies towards Novel Modulators of Influenza A Virus-Host Interaction. Viruses, 2016, 8, 269.	3.3	23
133	Consistency in drug response profiling. Nature, 2016, 540, E5-E6.	27.8	76
134	Identification of selective cytotoxic and synthetic lethal drug responses in triple negative breast cancer cells. Molecular Cancer, 2016, 15, 34.	19.2	57
135	Systematic drug screening reveals specific vulnerabilities and co-resistance patterns in endocrine-resistant breast cancer. BMC Cancer, 2016, 16, 378.	2.6	11
136	Drug response prediction by inferring pathway-response associations with kernelized Bayesian matrix factorization. Bioinformatics, 2016, 32, i455-i463.	4.1	87
137	Unstable LDL – Novel mechanism of atherogenesis and link to cardiovascular deaths. Atherosclerosis, 2016, 252, e208.	0.8	0
138	The Hydroxysteroid (17 $\beta$ ) Dehydrogenase Family Gene HSD17B12 Is Involved in the Prostaglandin Synthesis Pathway, the Ovarian Function, and Regulation of Fertility. Endocrinology, 2016, 157, 3719-3730.	2.8	43
139	Phosphoproteomics to Characterize Host Response During Influenza A Virus Infection of Human Macrophages. Molecular and Cellular Proteomics, 2016, 15, 3203-3219.	3.8	66
140	Optimized design and analysis of preclinical intervention studies in vivo. Scientific Reports, 2016, 6, 30723.	3.3	36
141	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. Nature Communications, 2016, 7, 12460.	12.8	73
142	Transcriptional response networks for elucidating mechanisms of action of multitargeted agents. Drug Discovery Today, 2016, 21, 1063-1075.	6.4	28
143	Cancer stem cell drugs target K-ras signaling in a stemness context. Oncogene, 2016, 35, 5248-5262.	5.9	78
144	Liver lipid metabolism is altered by increased circulating estrogen to androgen ratio in male mouse. Journal of Proteomics, 2016, 133, 66-75.	2.4	7

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145	Accumulated Metabolites of Hydroxybutyric Acid Serve as Diagnostic and Prognostic Biomarkers of Ovarian High-Grade Serous Carcinomas. <i>Cancer Research</i> , 2016, 76, 796-804.	0.9	74
146	Systematic Identification of MicroRNAs That Impact on Proliferation of Prostate Cancer Cells and Display Changed Expression in Tumor Tissue. <i>European Urology</i> , 2016, 69, 1120-1128.	1.9	53
147	CIP2A Promotes T-Cell Activation and Immune Response to <i>Listeria monocytogenes</i> Infection. <i>PLoS ONE</i> , 2016, 11, e0152996.	2.5	17
148	Abstract PR17: Characterization of ascites and tumor-derived ovarian cancer stem-like cells.. , 2016, , .		0
149	Abstract 608: Comprehensive drug testing of patient-derived conditionally reprogrammed cells from castration-resistant prostate cancer. , 2016, , .		1
150	Abstract 4679: Acquisition of cytarabine resistance leads to increased glucocorticoid sensitivity in AML. , 2016, , .		0
151	Mutational Landscape of Aggressive Natural Killer Cell Leukemia and Drug Sensitivity Profiling Reveal Therapeutic Options in Natural Killer Cell Malignancies. <i>Blood</i> , 2016, 128, 2921-2921.	1.4	0
152	From drug response profiling to target addiction scoring in cancer cell models. <i>DMM Disease Models and Mechanisms</i> , 2015, 8, 1255-1264.	2.4	13
153	Label-free quantitative phosphoproteomics with novel pairwise abundance normalization reveals synergistic RAS and CIP2A signaling. <i>Scientific Reports</i> , 2015, 5, 13099.	3.3	49
154	What is synergy? The Saarisek agreement revisited. <i>Frontiers in Pharmacology</i> , 2015, 6, 181.	3.5	147
155	Toward more realistic drug-target interaction predictions. <i>Briefings in Bioinformatics</i> , 2015, 16, 325-337.	6.5	331
156	Network pharmacology applications to map the unexplored target space and therapeutic potential of natural products. <i>Natural Product Reports</i> , 2015, 32, 1249-1266.	10.3	331
157	TIMMA-R: an R package for predicting synergistic multi-targeted drug combinations in cancer cell lines or patient-derived samples. <i>Bioinformatics</i> , 2015, 31, 1866-1868.	4.1	15
158	Impact of normalization methods on high-throughput screening data with high hit rates and drug testing with dose-response data. <i>Bioinformatics</i> , 2015, 31, 3815-3821.	4.1	31
159	Relevance Rank Platform (RRP) for Functional Filtering of High Content Protein-Protein Interaction Data*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 3274-3283.	3.8	19
160	Systematic Mapping of Kinase Addiction Combinations in Breast Cancer Cells by Integrating Drug Sensitivity and Selectivity Profiles. <i>Chemistry and Biology</i> , 2015, 22, 1144-1155.	6.0	22
161	Prediction of human population responses to toxic compounds by a collaborative competition. <i>Nature Biotechnology</i> , 2015, 33, 933-940.	17.5	88
162	MicroRNA-135b regulates ER $\alpha$ , AR and HIF1AN and affects breast and prostate cancer cell growth. <i>Molecular Oncology</i> , 2015, 9, 1287-1300.	4.6	45

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163	Identification of drug candidates and repurposing opportunities through compound–target interaction networks. <i>Expert Opinion on Drug Discovery</i> , 2015, 10, 1333-1345.	5.0	54
164	Searching for Drug Synergy in Complex Dose–Response Landscapes Using an Interaction Potency Model. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 504-513.	4.1	485
165	Specific cancer-associated mutations in the switch III region of Ras increase tumorigenicity by nanocluster augmentation. <i>ELife</i> , 2015, 4, e08905.	6.0	45
166	Abstract P6-02-01: Identification of subgroups of triple negative breast cancer cells with selective responses to mTOR, CDK, mitotic and proteasome inhibitors. , 2015, , .		0
167	Abstract 3746: Novel therapeutic possibilities for chemorefractory ovarian cancer patients identified by functional ex vivo drug sensitivity testing of primary cells from ascites. , 2015, , .		1
168	Abstract 5328: Protein phosphatase 2A activity is a major determinant of therapy response in cancer cells. , 2015, , .		0
169	Abstract 1700: Dasatinib and everolimus show synergistic growth inhibition with paclitaxel in an ovarian granulosa cell tumor model. , 2015, , .		1
170	Abstract POSTER-TECH-1111: High-throughput drug sensitivity and resistance testing of ovarian cancer cell lines provides useful strategy for assessing drug repositioning and therapeutic possibilities of emerging drugs. , 2015, , .		0
171	Abstract B32: Pro-apoptotic functions of AMPK revealed by Myc. , 2015, , .		0
172	JAK1/2 and BCL2 Inhibitors Synergize to Counter-Act Bone Marrow Stromal Cell-Induced Protection of AML. <i>Blood</i> , 2015, 126, 867-867.	1.4	0
173	Novel Lignan and Stilbenoid Mixture Shows Anticarcinogenic Efficacy in Preclinical PC-3M-luc2 Prostate Cancer Model. <i>PLoS ONE</i> , 2014, 9, e93764.	2.5	27
174	Network Pharmacology Strategies Toward Multi-Target Anticancer Therapies: From Computational Models to Experimental Design Principles. <i>Current Pharmaceutical Design</i> , 2014, 20, 23-36.	1.9	115
175	Regularized Machine Learning in the Genetic Prediction of Complex Traits. <i>PLoS Genetics</i> , 2014, 10, e1004754.	3.5	122
176	Phosphoproteomics Combined with Quantitative 14-3-3-affinity Capture Identifies SIRT1 and RAI as Novel Regulators of Cytosolic Double-stranded RNA Recognition Pathway. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2604-2617.	3.8	14
177	Intra-Tissue Steroid Profiling Indicates Differential Progesterone and Testosterone Metabolism in the Endometrium and Endometriosis Lesions. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2014, 99, E2188-E2197.	3.6	55
178	Ovarian Endometriosis Signatures Established through Discovery and Directed Mass Spectrometry Analysis. <i>Journal of Proteome Research</i> , 2014, 13, 4983-4994.	3.7	17
179	Statistical detection of quantitative protein biomarkers provides insights into signaling networks deregulated in acute myeloid leukemia. <i>Proteomics</i> , 2014, 14, 2443-2453.	2.2	10
180	Making Sense of Large-Scale Kinase Inhibitor Bioactivity Data Sets: A Comparative and Integrative Analysis. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 735-743.	5.4	284

#	ARTICLE	IF	CITATIONS
181	PhosFox: a bioinformatics tool for peptide-level processing of LC-MS/MS-based phosphoproteomic data. Proteome Science, 2014, 12, 36.	1.7	12
182	Castration Induces Up-Regulation of Intratumoral Androgen Biosynthesis and Androgen Receptor Expression in an Orthotopic VCaP Human Prostate Cancer Xenograft Model. American Journal of Pathology, 2014, 184, 2163-2173.	3.8	53
183	A community effort to assess and improve drug sensitivity prediction algorithms. Nature Biotechnology, 2014, 32, 1202-1212.	17.5	653
184	Quantitative scoring of differential drug sensitivity for individually optimized anticancer therapies. Scientific Reports, 2014, 4, 5193.	3.3	243
185	A Two-Step Learning Approach for Solving Full and Almost Full Cold Start Problems in Dyadic Prediction. Lecture Notes in Computer Science, 2014, , 517-532.	1.3	12
186	Abstract 982: Analysis of clonal evolution of leukemia in vivo following novel targeted treatments. , 2014, , .		0
187	Abstract 5384: Systematic high-throughput drug sensitivity and resistance testing (DSRT) of ovarian cancer cell lines indicates novel therapeutic possibilities with existing and emerging drugs. , 2014, , .		0
188	Abstract 4184: Drug set enrichment analysis : A computational approach to identify functional drug sets. , 2014, , .		0
189	Abstract LB-31: Castration induces upregulation of intratumoral androgen biosynthesis and androgen receptor expression in orthotopic VCaP human prostate cancer xenograft model. , 2014, , .		0
190	Stroma-Derived Factors Significantly Impact the Drug Response Profiles of Patient-Derived Primary AML Cells: Implications for Drug Sensitivity Testing. Blood, 2014, 124, 3505-3505.	1.4	0
191	AML Specific Targeted Drugs Identified By Drug Sensitivity and Resistance Testing: Comparison of Ex Vivo Patient Cells with in Vitro Cell Lines. Blood, 2014, 124, 2163-2163.	1.4	1
192	Genetic variants and their interactions in disease risk prediction – machine learning and network perspectives. BioData Mining, 2013, 6, 5.	4.0	40
193	Predicting drug–target interactions through integrative analysis of chemogenetic assays in yeast. Molecular BioSystems, 2013, 9, 768.	2.9	6
194	Chk1 Targeting Reactivates PP2A Tumor Suppressor Activity in Cancer Cells. Cancer Research, 2013, 73, 6757-6769.	0.9	41
195	Individualized Systems Medicine Strategy to Tailor Treatments for Patients with Chemorefractory Acute Myeloid Leukemia. Cancer Discovery, 2013, 3, 1416-1429.	9.4	334
196	Target Inhibition Networks: Predicting Selective Combinations of Druggable Targets to Block Cancer Survival Pathways. PLoS Computational Biology, 2013, 9, e1003226.	3.2	84
197	Anticancer compound ABT-263 accelerates apoptosis in virus-infected cells and imbalances cytokine production and lowers survival rates of infected mice. Cell Death and Disease, 2013, 4, e742-e742.	6.3	41
198	Parallel Feature Selection for Regularized Least-Squares. Lecture Notes in Computer Science, 2013, , 280-294.	1.3	0

#	ARTICLE	IF	CITATIONS
199	Abstract 5588: Functional drug sensitivity and resistance profiling of AML patient cells defines a disease-specific combination of druggable signal addictions.. , 2013, , .		0
200	Abstract A34: Development of a drug sensitivity testing pipeline towards the establishment of precision medicine for ovarian cancer. , 2013, , .		0
201	Abstract B21: Characterization of primary high-grade serous ovarian cancer cell lines: Cell line and growth condition specific differences in stem cell marker expression and high-throughput drug screening. , 2013, , .		0
202	Stromal Cell Supported High-Throughput Drug Testing Of Primary Leukemia Cells For Comprehensive Assessment Of Sensitivity To Novel Therapies. Blood, 2013, 122, 1668-1668.	1.4	0
203	Identification Of AML Subtype-Selective Drugs By Functional Ex Vivo Drug Sensitivity and Resistance Testing and Genomic Profiling. Blood, 2013, 122, 482-482.	1.4	0
204	Pravastatin-induced improvement in coronary reactivity and circulating ATP and ADP levels in young adults with type 1 diabetes. Frontiers in Physiology, 2012, 3, 338.	2.8	8
205	Obatoclox, Saliphenylhalamide, and Gemcitabine Inhibit Influenza A Virus Infection. Journal of Biological Chemistry, 2012, 287, 35324-35332.	3.4	80
206	Improved Statistical Modeling of Tumor Growth and Treatment Effect in Preclinical Animal Studies with Highly Heterogeneous Responses <i>In Vivo</i>. Clinical Cancer Research, 2012, 18, 4385-4396.	7.0	35
207	Optimized detection of transcription factor-binding sites in ChIP-seq experiments. Nucleic Acids Research, 2012, 40, e1-e1.	14.5	6
208	The rocky road to personalized medicine: computational and statistical challenges. Personalized Medicine, 2012, 9, 109-114.	1.5	4
209	A multilevel layout algorithm for visualizing physical and genetic interaction networks, with emphasis on their modular organization. BioData Mining, 2012, 5, 2.	4.0	11
210	461 Identification of Personalized Therapeutic Strategies and Associated Biomarkers in Adult Acute Myeloid Leukemia Using a Functional Drug Sensitivity and Resistance Testing Platform. European Journal of Cancer, 2012, 48, 142-143.	2.8	0
211	Wrapper-based selection of genetic features in genome-wide association studies through fast matrix operations. Algorithms for Molecular Biology, 2012, 7, 11.	1.2	28
212	Mining high-throughput screens for cancer drug targetsâ€”lessons from yeast chemicalâ€”genomic profiling and synthetic lethality. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2012, 2, 263-272.	6.8	6
213	Abstract 895: Quantitative drug sensitivity and resistance testing (DSRT) of primary ex vivo AML blasts highlights mTOR and MEK as potential key molecular driver signals of therapeutic significance. , 2012, , .		0
214	Abstract 3188: Development of a cancer pharmacopeia-wideex-vivodrug sensitivity and resistance testing (DSRT) platform for AML: Towards individually optimized therapy and improved understanding of drug resistance patterns. , 2012, , .		0
215	High-Throughput Ex Vivo Drug Sensitivity and Resistance Testing (DSRT) Integrated with Deep Genomic and Molecular Profiling Reveal New Therapy Options with Targeted Drugs in Subgroups of Relapsed Chemorefractory AML. Blood, 2012, 120, 288-288.	1.4	1
216	Fast and parallelized greedy forward selection of genetic variants in Genome-wide association studies. , 2011, , .		1

#	ARTICLE	IF	CITATIONS
217	Probabilistic Analysis of Probe Reliability in Differential Gene Expression Studies with Short Oligonucleotide Arrays. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 217-225.	3.0	29
218	PolyAlign: A Versatile LC-MS Data Alignment Tool for Landmark-Selected and -Automated Use. <i>International Journal of Proteomics</i> , 2011, 2011, 1-9.	2.0	9
219	Quantitative maps of genetic interactions in yeast - Comparative evaluation and integrative analysis. <i>BMC Systems Biology</i> , 2011, 5, 45.	3.0	16
220	Quantitative Subcellular Proteome and Secretome Profiling of Influenza A Virus-Infected Human Primary Macrophages. <i>PLoS Pathogens</i> , 2011, 7, e1001340.	4.7	122
221	Quantitative Proteomics Analysis of the Nuclear Fraction of Human CD4+ Cells in the Early Phases of IL-4-induced Th2 Differentiation. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1937-1953.	3.8	55
222	Genome-wide Profiling of Interleukin-4 and STAT6 Transcription Factor Regulation of Human Th2 Cell Programming. <i>Immunity</i> , 2010, 32, 852-862.	14.3	139
223	Mahalanobis distance screening of Arabidopsis mutants with chlorophyll fluorescence. <i>Photosynthesis Research</i> , 2010, 105, 273-283.	2.9	8
224	An update on clinical proteomics in Alzheimer's research. <i>Journal of Neurochemistry</i> , 2010, 112, 1386-1414.	3.9	82
225	Genetic Variants and Their Interactions in the Prediction of Increased Pre-Clinical Carotid Atherosclerosis: The Cardiovascular Risk in Young Finns Study. <i>PLoS Genetics</i> , 2010, 6, e1001146.	3.5	38
226	Genome-Wide Scoring of Positive and Negative Epistasis through Decomposition of Quantitative Genetic Interaction Fitness Matrices. <i>PLoS ONE</i> , 2010, 5, e11611.	2.5	3
227	Early suppression of immune response pathways characterizes children with prediabetes in genome-wide gene expression profiling. <i>Journal of Autoimmunity</i> , 2010, 35, 70-76.	6.5	29
228	Dealing with missing values in large-scale studies: microarray data imputation and beyond. <i>Briefings in Bioinformatics</i> , 2010, 11, 253-264.	6.5	137
229	Nocturnal transcutaneous carbon dioxide tension in postmenopausal estrogen users and non-users. <i>Menopause International</i> , 2009, 15, 107-112.	1.6	2
230	Transcutaneous carbon dioxide profile during sleep reveals metabolic risk factors in post-menopausal females. <i>European Respiratory Journal</i> , 2009, 34, 1132-1139.	6.7	4
231	Genoscape: a Cytoscape plug-in to automate the retrieval and integration of gene expression data and molecular networks. <i>Bioinformatics</i> , 2009, 25, 2617-2618.	4.1	12
232	Resampling Reveals Sample-Level Differential Expression in Clinical Genome-Wide Studies. <i>OMICS A Journal of Integrative Biology</i> , 2009, 13, 381-396.	2.0	10
233	Optimized detection of differential expression in global profiling experiments: case studies in clinical transcriptomic and quantitative proteomic datasets. <i>Briefings in Bioinformatics</i> , 2009, 10, 547-555.	6.5	29
234	A practical comparison of methods for detecting transcription factor binding sites in ChIP-seq experiments. <i>BMC Genomics</i> , 2009, 10, 618.	2.8	105

#	ARTICLE	IF	CITATIONS
235	Filtering strategies for improving protein identification in high-throughput MS/MS studies. Proteomics, 2009, 9, 848-860.	2.2	31
236	Understanding sleep-disordered breathing through mathematical modelling. Sleep Medicine Reviews, 2009, 13, 333-343.	8.5	6
237	Probe-level estimation improves the detection of differential splicing in Affymetrix exon array studies. Genome Biology, 2009, 10, R77.	9.6	23
238	Module Finding Approaches for Protein Interaction Networks. , 2009, , 335-353.		3
239	Alignment of LC-MS images, with applications to biomarker discovery and protein identification. Proteomics, 2008, 8, 650-672.	2.2	92
240	Overnight variability in transcutaneous carbon dioxide predicts vascular impairment in women. Experimental Physiology, 2008, 93, 880-891.	2.0	12
241	Missing value imputation improves clustering and interpretation of gene expression microarray data. BMC Bioinformatics, 2008, 9, 202.	2.6	52
242	Overnight features of transcutaneous carbon dioxide measurement as predictors of metabolic status. Artificial Intelligence in Medicine, 2008, 42, 55-65.	6.5	6
243	Model-based prediction of sequence alignment quality. Bioinformatics, 2008, 24, 2165-2171.	4.1	19
244	Reproducibility-Optimized Test Statistic for Ranking Genes in Microarray Studies. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 423-431.	3.0	66
245	Predicting Quantitative Genetic Interactions by Means of Sequential Matrix Approximation. PLoS ONE, 2008, 3, e3284.	2.5	10
246	Parameter estimation of a respiratory control model from noninvasive carbon dioxide measurements during sleep. Mathematical Medicine and Biology, 2007, 24, 225-249.	1.2	6
247	Systematic construction of gene coexpression networks with applications to human T helper cell differentiation process. Bioinformatics, 2007, 23, 2096-2103.	4.1	94
248	GOLORize: a Cytoscape plug-in for network visualization with Gene Ontology-based layout and coloring. Bioinformatics, 2007, 23, 394-396.	4.1	105
249	Predicting Gene Expression from Combined Expression and Promoter Profile Similarity with Application to Missing Value Imputation. , 2007, , 97-104.		1
250	Computer-assisted identification of multitrace electrophoretic patterns in differential display experiments. Electrophoresis, 2007, 28, 879-893.	2.4	4
251	Can carotid body perfusion act as a respiratory controller?. Journal of Theoretical Biology, 2007, 249, 737-748.	1.7	10
252	Inspiratory flow shape clustering: An automated method to monitor upper airway performance during sleep. Computer Methods and Programs in Biomedicine, 2007, 85, 8-18.	4.7	17



#	ARTICLE	IF	CITATIONS
253	Automated Pattern Ranking in Differential Display Data Analysis. , 2006, 317, 111-122.		2
254	A statistical score for assessing the quality of multiple sequence alignments. BMC Bioinformatics, 2006, 7, 484.	2.6	41
255	Graph-based methods for analysing networks in cell biology. Briefings in Bioinformatics, 2006, 7, 243-255.	6.5	368
256	Non-invasive respiratory monitoring during wakefulness and sleep in pre- and postmenopausal women. Respiratory Physiology and Neurobiology, 2006, 150, 66-74.	1.6	7
257	Model-Based Analysis of Mechanisms Responsible for Sleep-Induced Carbon Dioxide Differences. Bulletin of Mathematical Biology, 2006, 68, 315-341.	1.9	7
258	Improving missing value estimation in microarray data with gene ontology. Bioinformatics, 2006, 22, 566-572.	4.1	101
259	Th1 Response and Cytotoxicity Genes Are Down-Regulated in Cutaneous T-Cell Lymphoma. Clinical Cancer Research, 2006, 12, 4812-4821.	7.0	74
260	Quality classification of tandem mass spectrometry data. Bioinformatics, 2006, 22, 400-406.	4.1	41
261	Improving Identification of Differentially Expressed Genes by Integrative Analysis of Affymetrix and Illumina Arrays. OMICS A Journal of Integrative Biology, 2006, 10, 369-380.	2.0	7
262	Inference of Gene Coexpression Networks by Integrative Analysis across Microarray Experiments. Journal of Integrative Bioinformatics, 2006, 3, 137-147.	1.5	0
263	Geometrical distortions in two-dimensional gels: applicable correction methods. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2005, 815, 25-37.	2.3	37
264	A human ImmunoChip cDNA microarray provides a comprehensive tool to study immune responses. Journal of Immunological Methods, 2005, 303, 122-134.	1.4	13
265	A comparative evaluation of software for the analysis of liquid chromatography-tandem mass spectrometry data from isotope coded affinity tag experiments. Proteomics, 2005, 5, 2748-2760.	2.2	27
266	Integrating probe-level expression changes across generations of Affymetrix arrays. Nucleic Acids Research, 2005, 33, e193-e193.	14.5	51
267	Sleep quality, daytime sleepiness and fasting insulin levels in women with chronic obstructive pulmonary disease. Respiratory Medicine, 2005, 99, 856-863.	2.9	35
268	Medroxyprogesterone improves nocturnal breathing in postmenopausal women with chronic obstructive pulmonary disease. Respiratory Research, 2005, 6, 28.	3.6	18
269	Statistical Methods for Identifying Conserved Residues in Multiple Sequence Alignment. Statistical Applications in Genetics and Molecular Biology, 2004, 3, 1-28.	0.6	7
270	Genetic Feature Learning Algorithm for Fluorescence Fingerprinting of Plants. Lecture Notes in Computer Science, 2004, , 371-383.	1.3	4



#	ARTICLE	IF	CITATIONS
271	Kinetics and STAT4- or STAT6-mediated regulation of genes involved in lymphocyte polarization to Th1 and Th2 cells. <i>European Journal of Immunology</i> , 2003, 33, 1105-1116.	2.9	28
272	Feature learning with a genetic algorithm for fluorescence fingerprinting of plant species. <i>Pattern Recognition Letters</i> , 2003, 24, 2663-2673.	4.2	12
273	State of vigilance, oestrogen replacement therapy, and lipid profile as modifiers of nocturnal movement-induced heart rate responses. <i>Clinical Physiology and Functional Imaging</i> , 2003, 23, 293-299.	1.2	0
274	Comparison of PDQuest and Progenesis software packages in the analysis of two-dimensional electrophoresis gels. <i>Proteomics</i> , 2003, 3, 1936-1946.	2.2	84
275	Effect of medroxyprogesterone on inspiratory flow shapes during sleep in postmenopausal women. <i>Respiratory Physiology and Neurobiology</i> , 2003, 134, 131-143.	1.6	27
276	Efficient estimation of emission probabilities in profile hidden Markov models. <i>Bioinformatics</i> , 2003, 19, 2359-2368.	4.1	8
277	Identification of Novel Genes Regulated by IL-12, IL-4, or TGF- $\beta$ 2 during the Early Polarization of CD4+ Lymphocytes. <i>Journal of Immunology</i> , 2003, 171, 5328-5336.	0.8	61
278	Computational Strategies for Analyzing Data in Gene Expression Microarray Experiments. <i>Journal of Bioinformatics and Computational Biology</i> , 2003, 01, 541-586.	0.8	41
279	Identification of Novel IL-4/Stat6-Regulated Genes in T Lymphocytes. <i>Journal of Immunology</i> , 2003, 171, 3627-3635.	0.8	99
280	Prediction of Inspiratory Flow Shapes During Sleep with a Mathematic Model of Upper Airway Forces. <i>Sleep</i> , 2003, 26, 857-863.	1.1	7
281	Electrophoretic Signal Comparison Applied to mRNA Differential Display Analysis. <i>BioTechniques</i> , 2003, 34, 116-122.	1.8	10
282	Hierarchical grid transformation for image warping in the analysis of two-dimensional electrophoresis gels. <i>Proteomics</i> , 2002, 2, 1504-1515.	2.2	31
283	Adjustment of the Human Respiratory System to Increased Upper Airway Resistance During Sleep. <i>Bulletin of Mathematical Biology</i> , 2002, 64, 3-28.	1.9	8
284	Climacteric vasomotor symptoms do not predict nocturnal breathing abnormalities in postmenopausal women. <i>Maturitas</i> , 2001, 39, 29-37.	2.4	17
285	A model of a snorer's upper airway. <i>Mathematical Biosciences</i> , 2001, 170, 79-90.	1.9	46
286	Testing for Periodicity in Signals: An Application to Detect Partial Upper Airway Obstruction during Sleep. <i>Journal of Theoretical Medicine</i> , 2001, 3, 231-245.	0.5	8
287	Automated detection of differentially expressed fragments in mRNA differential display. <i>Electrophoresis</i> , 2001, 22, 1935-1945.	2.4	21
288	Analysis of Inspiratory Flow Shapes in Patients With Partial Upper-Airway Obstruction During Sleep. <i>Chest</i> , 2001, 119, 37-44.	0.8	72

#	ARTICLE	IF	CITATIONS
289	Analysis of similarity of electrophoretic patterns in mRNA differential display. Electrophoresis, 2000, 21, 2947-2956.	2.4	21
290	Detection of high-frequency respiratory movements during sleep. Computer Methods and Programs in Biomedicine, 2000, 61, 171-185.	4.7	8
291	Improving the false nearest neighbors method with graphical analysis. Physical Review E, 1999, 60, 416-421.	2.1	15
292	Classification of Nasal Inspiratory Flow Shapes by Attributed Finite Automata. Journal of Biomedical Informatics, 1999, 32, 34-55.	0.7	19
293	Phenotypic Screening Combined with Machine Learning for Efficient Identification of Breast Cancer-Selective Therapeutic Targets. SSRN Electronic Journal, 0, , .	0.4	0
294	Chemogenomic Analysis of the Druggable Kinome and Its Application to Repositioning and Lead Identification Studies. SSRN Electronic Journal, 0, , .	0.4	0
295	Module Finding Approaches for Protein Interaction Networks. , 0, , 422-443.		0