Tero Aittokallio

List of Publications by Year in descending order

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#	Article	lF	CITATIONS
1	A community effort to assess and improve drug sensitivity prediction algorithms. Nature Biotechnology, 2014, 32, 1202-1212.	17.5	653
2	SynergyFinder 2.0: visual analytics of multi-drug combination synergies. Nucleic Acids Research, 2020, 48, W488-W493.	14.5	545
3	Searching for Drug Synergy in Complex Dose–Response Landscapes Using an Interaction Potency Model. Computational and Structural Biotechnology Journal, 2015, 13, 504-513.	4.1	485
4	SynergyFinder: a web application for analyzing drug combination dose–response matrix data. Bioinformatics, 2017, 33, 2413-2415.	4.1	403
5	Graph-based methods for analysing networks in cell biology. Briefings in Bioinformatics, 2006, 7, 243-255.	6.5	368
6	Individualized Systems Medicine Strategy to Tailor Treatments for Patients with Chemorefractory Acute Myeloid Leukemia. Cancer Discovery, 2013, 3, 1416-1429.	9.4	334
7	Toward more realistic drug-target interaction predictions. Briefings in Bioinformatics, 2015, 16, 325-337.	6.5	331
8	Network pharmacology applications to map the unexplored target space and therapeutic potential of natural products. Natural Product Reports, 2015, 32, 1249-1266.	10.3	331
9	Making Sense of Large-Scale Kinase Inhibitor Bioactivity Data Sets: A Comparative and Integrative Analysis. Journal of Chemical Information and Modeling, 2014, 54, 735-743.	5.4	284
10	Quantitative scoring of differential drug sensitivity for individually optimized anticancer therapies. Scientific Reports, 2014, 4, 5193.	3.3	243
11	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	12.8	240
12	Fully-automated and ultra-fast cell-type identification using specific marker combinations from single-cell transcriptomic data. Nature Communications, 2022, 13, 1246.	12.8	163
13	Machine learning and feature selection for drug response prediction in precision oncology applications. Biophysical Reviews, 2019, 11, 31-39.	3.2	148
14	What is synergy? The Saariselkägreement revisited. Frontiers in Pharmacology, 2015, 6, 181.	3.5	147
15	Methods for High-throughput Drug Combination Screening and Synergy Scoring. Methods in Molecular Biology, 2018, 1711, 351-398.	0.9	140
16	Genome-wide Profiling of Interleukin-4 and STAT6 Transcription Factor Regulation of Human Th2 Cell Programming. Immunity, 2010, 32, 852-862.	14.3	139
17	SynergyFinder 3.0: an interactive analysis and consensus interpretation of multi-drug synergies across multiple samples. Nucleic Acids Research, 2022, 50, W739-W743.	14.5	139
18	Dealing with missing values in large-scale studies: microarray data imputation and beyond. Briefings in Bioinformatics, 2010, 11, 253-264.	6.5	137

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19	Integrated drug profiling and CRISPR screening identify essential pathways for CAR T-cell cytotoxicity. Blood, 2020, 135, 597-609.	1.4	134
20	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
21	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. Lancet Oncology, The, 2017, 18, 132-142.	10.7	124
22	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
23	Quantitative Subcellular Proteome and Secretome Profiling of Influenza A Virus-Infected Human Primary Macrophages. PLoS Pathogens, 2011, 7, e1001340.	4.7	122
24	Regularized Machine Learning in the Genetic Prediction of Complex Traits. PLoS Genetics, 2014, 10, e1004754.	3.5	122
25	PP2A inhibition is a druggable MEK inhibitor resistance mechanism in KRAS-mutant lung cancer cells. Science Translational Medicine, 2018, 10, .	12.4	116
26	Network Pharmacology Strategies Toward Multi-Target Anticancer Therapies: From Computational Models to Experimental Design Principles. Current Pharmaceutical Design, 2014, 20, 23-36.	1.9	115
27	Aggressive natural killer-cell leukemiaÂmutational landscape and drug profiling highlight JAK-STAT signaling as therapeutic target. Nature Communications, 2018, 9, 1567.	12.8	107
28	GOlorize: a Cytoscape plug-in for network visualization with Gene Ontology-based layout and coloring. Bioinformatics, 2007, 23, 394-396.	4.1	105
29	A practical comparison of methods for detecting transcription factor binding sites in ChIP-seq experiments. BMC Genomics, 2009, 10, 618.	2.8	105
30	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. Nature Genetics, 2020, 52, 448-457.	21.4	104
31	Improving missing value estimation in microarray data with gene ontology. Bioinformatics, 2006, 22, 566-572.	4.1	101
32	Identification of Novel IL-4/Stat6-Regulated Genes in T Lymphocytes. Journal of Immunology, 2003, 171, 3627-3635.	0.8	99
33	Prediction of drug combination effects with a minimal set of experiments. Nature Machine Intelligence, 2019, 1, 568-577.	16.0	99
34	Early metabolic markers identify potential targets for the prevention of type 2 diabetes. Diabetologia, 2017, 60, 1740-1750.	6.3	96
35	Systematic construction of gene coexpression networks with applications to human T helper cell differentiation process. Bioinformatics, 2007, 23, 2096-2103.	4.1	94
36	Alignment of LCâ€MS images, with applications to biomarker discovery and protein identification. Proteomics, 2008, 8, 650-672.	2.2	92

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37	JAK1/2 and BCL2 inhibitors synergize to counteract bone marrow stromal cell–induced protection of AML. Blood, 2017, 130, 789-802.	1.4	90
38	Prediction of human population responses to toxic compounds by a collaborative competition. Nature Biotechnology, 2015, 33, 933-940.	17.5	88
39	Drug response prediction by inferring pathway-response associations with kernelized Bayesian matrix factorization. Bioinformatics, 2016, 32, i455-i463.	4.1	87
40	Comparison of PDQuest and Progenesis software packages in the analysis of two-dimensional electrophoresis gels. Proteomics, 2003, 3, 1936-1946.	2.2	84
41	Target Inhibition Networks: Predicting Selective Combinations of Druggable Targets to Block Cancer Survival Pathways. PLoS Computational Biology, 2013, 9, e1003226.	3.2	84
42	Computational-experimental approach to drug-target interaction mapping: A case study on kinase inhibitors. PLoS Computational Biology, 2017, 13, e1005678.	3.2	84
43	An update on clinical proteomics in Alzheimer's research. Journal of Neurochemistry, 2010, 112, 1386-1414.	3.9	82
44	Obatoclax, Saliphenylhalamide, and Gemcitabine Inhibit Influenza A Virus Infection. Journal of Biological Chemistry, 2012, 287, 35324-35332.	3.4	80
45	Cancer stem cell drugs target K-ras signaling in a stemness context. Oncogene, 2016, 35, 5248-5262.	5.9	78
46	Consistency in drug response profiling. Nature, 2016, 540, E5-E6.	27.8	76
47	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
48	Immune cell contexture in the bone marrow tumor microenvironment impacts therapy response in CML. Leukemia, 2018, 32, 1643-1656.	7.2	75
49	Th1 Response and Cytotoxicity Genes Are Down-Regulated in Cutaneous T-Cell Lymphoma. Clinical Cancer Research, 2006, 12, 4812-4821.	7.0	74
50	Accumulated Metabolites of Hydroxybutyric Acid Serve as Diagnostic and Prognostic Biomarkers of Ovarian High-Grade Serous Carcinomas. Cancer Research, 2016, 76, 796-804.	0.9	74
51	Comprehensive Drug Testing of Patient-derived Conditionally Reprogrammed Cells from Castration-resistant Prostate Cancer. European Urology, 2017, 71, 319-327.	1.9	74
52	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. Nature Communications, 2016, 7, 12460.	12.8	73
53	Implementing a Functional Precision Medicine Tumor Board for Acute Myeloid Leukemia. Cancer Discovery, 2022, 12, 388-401.	9.4	73
54	Analysis of Inspiratory Flow Shapes in Patients With Partial Upper-Airway Obstruction During Sleep. Chest, 2001, 119, 37-44.	0.8	72

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55	Breeze: an integrated quality control and data analysis application for high-throughput drug screening. Bioinformatics, 2020, 36, 3602-3604.	4.1	68
56	Artificial intelligence, machine learning, and drug repurposing in cancer. Expert Opinion on Drug Discovery, 2021, 16, 977-989.	5.0	68
57	DNMT Inhibitors Increase Methylation in the Cancer Genome. Frontiers in Pharmacology, 2019, 10, 385.	3.5	67
58	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
59	Phosphoproteomics to Characterize Host Response During Influenza A Virus Infection of Human Macrophages. Molecular and Cellular Proteomics, 2016, 15, 3203-3219.	3.8	66
60	Novel activities of safe-in-human broad-spectrum antiviral agents. Antiviral Research, 2018, 154, 174-182.	4.1	64
61	Leveraging multi-way interactions for systematic prediction of pre-clinical drug combination effects. Nature Communications, 2020, 11, 6136.	12.8	63
62	Identification of Novel Genes Regulated by IL-12, IL-4, or TGF-Î ² during the Early Polarization of CD4+ Lymphocytes. Journal of Immunology, 2003, 171, 5328-5336.	0.8	61
63	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
64	Patient-Customized Drug Combination Prediction and Testing for T-cell Prolymphocytic Leukemia Patients. Cancer Research, 2018, 78, 2407-2418.	0.9	60
65	Pharmacological reactivation of MYC-dependent apoptosis induces susceptibility to anti-PD-1 immunotherapy. Nature Communications, 2019, 10, 620.	12.8	60
66	Improving the efficacy-safety balance of polypharmacology in multi-target drug discovery. Expert Opinion on Drug Discovery, 2018, 13, 179-192.	5.0	59
67	Systematic identification of feature combinations for predicting drug response with Bayesian multi-view multi-task linear regression. Bioinformatics, 2017, 33, i359-i368.	4.1	58
68	Identification of selective cytotoxic and synthetic lethal drug responses in triple negative breast cancer cells. Molecular Cancer, 2016, 15, 34.	19.2	57
69	Global proteomics profiling improves drug sensitivity prediction: results from a multi-omics, pan-cancer modeling approach. Bioinformatics, 2018, 34, 1353-1362.	4.1	56
70	Quantitative Proteomics Analysis of the Nuclear Fraction of Human CD4+ Cells in the Early Phases of IL-4-induced Th2 Differentiation. Molecular and Cellular Proteomics, 2010, 9, 1937-1953.	3.8	55
71	Intra-Tissue Steroid Profiling Indicates Differential Progesterone and Testosterone Metabolism in the Endometrium and Endometriosis Lesions. Journal of Clinical Endocrinology and Metabolism, 2014, 99, E2188-E2197.	3.6	55
72	Identification of drug candidates and repurposing opportunities through compound–target interaction networks. Expert Opinion on Drug Discovery, 2015, 10, 1333-1345.	5.0	54

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73	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
74	Systematic Identification of MicroRNAs That Impact on Proliferation of Prostate Cancer Cells and Display Changed Expression in Tumor Tissue. European Urology, 2016, 69, 1120-1128.	1.9	53
75	Missing value imputation improves clustering and interpretation of gene expression microarray data. BMC Bioinformatics, 2008, 9, 202.	2.6	52
76	Integrating probe-level expression changes across generations of Affymetrix arrays. Nucleic Acids Research, 2005, 33, e193-e193.	14.5	51
77	Learning with multiple pairwise kernels for drug bioactivity prediction. Bioinformatics, 2018, 34, i509-i518.	4.1	51
78	Label-free quantitative phosphoproteomics with novel pairwise abundance normalization reveals synergistic RAS and CIP2A signaling. Scientific Reports, 2015, 5, 13099.	3.3	49
79	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
80	A model of a snorer's upper airway. Mathematical Biosciences, 2001, 170, 79-90.	1.9	46
81	MicroRNAâ€135b regulates ERα, AR and HIF1AN and affects breast and prostate cancer cell growth. Molecular Oncology, 2015, 9, 1287-1300.	4.6	45
82	Specific cancer-associated mutations in the switch III region of Ras increase tumorigenicity by nanocluster augmentation. ELife, 2015, 4, e08905.	6.0	45
83	Drug Combinations as a First Line of Defense against Coronaviruses and Other Emerging Viruses. MBio, 2021, 12, e0334721.	4.1	45
84	Enhanced sensitivity to glucocorticoids in cytarabine-resistant AML. Leukemia, 2017, 31, 1187-1195.	7.2	44
85	The Hydroxysteroid (17β) 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
86	SynToxProfiler: An interactive analysis of drug combination synergy, toxicity and efficacy. PLoS Computational Biology, 2020, 16, e1007604.	3.2	43
87	Computational Strategies for Analyzing Data in Gene Expression Microarray Experiments. Journal of Bioinformatics and Computational Biology, 2003, 01, 541-586.	0.8	41
88	A statistical score for assessing the quality of multiple sequence alignments. BMC Bioinformatics, 2006, 7, 484.	2.6	41
89	Quality classification of tandem mass spectrometry data. Bioinformatics, 2006, 22, 400-406.	4.1	41
90	Chk1 Targeting Reactivates PP2A Tumor Suppressor Activity in Cancer Cells. Cancer Research, 2013, 73, 6757-6769.	0.9	41

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91	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
92	Crowdsourced mapping of unexplored target space of kinase inhibitors. Nature Communications, 2021, 12, 3307.	12.8	41
93	Genetic variants and their interactions in disease risk prediction – machine learning and network perspectives. BioData Mining, 2013, 6, 5.	4.0	40
94	Antiviral Properties of Chemical Inhibitors of Cellular Anti-Apoptotic Bcl-2 Proteins. Viruses, 2017, 9, 271.	3.3	39
95	Genetic Variants and Their Interactions in the Prediction of Increased Pre-Clinical Carotid Atherosclerosis: The Cardiovascular Risk in Young Finns Study. PLoS Genetics, 2010, 6, e1001146.	3.5	38
96	JAK/STAT-Activating Genomic Alterations Are a Hallmark of T-PLL. Cancers, 2019, 11, 1833.	3.7	38
97	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
98	Optimized design and analysis of preclinical intervention studies in vivo. Scientific Reports, 2016, 6, 30723.	3.3	36
99	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
100	Sleep quality, daytime sleepiness and fasting insulin levels in women with chronic obstructive pulmonary disease. Respiratory Medicine, 2005, 99, 856-863.	2.9	35
101	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
102	<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
103	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
104	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
105	A relational database to identify differentially expressed genes in the endometrium and endometriosis lesions. Scientific Data, 2020, 7, 284.	5.3	33
106	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
107	RUNX1 mutations in blast-phase chronic myeloid leukemia associate with distinct phenotypes, transcriptional profiles, and drug responses. Leukemia, 2021, 35, 1087-1099.	7.2	32
108	Hierarchical grid transformation for image warping in the analysis of two-dimensional electrophoresis gels. Proteomics, 2002, 2, 1504-1515.	2.2	31

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109	Filtering strategies for improving protein identification in high-throughput MS/MS studies. Proteomics, 2009, 9, 848-860.	2.2	31
110	Impact of normalization methods on high-throughput screening data with high hit rates and drug testing with dose–response data. Bioinformatics, 2015, 31, 3815-3821.	4.1	31
111	Optimized detection of differential expression in global profiling experiments: case studies in clinical transcriptomic and quantitative proteomic datasets. Briefings in Bioinformatics, 2009, 10, 547-555.	6.5	29
112	Early suppression of immune response pathways characterizes children with prediabetes in genome-wide gene expression profiling. Journal of Autoimmunity, 2010, 35, 70-76.	6.5	29
113	Probabilistic Analysis of Probe Reliability in Differential Gene Expression Studies with Short Oligonucleotide Arrays. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 217-225.	3.0	29
114	Kinetics and STAT4- or STAT6-mediated regulation of genes involved in lymphocyte polarization to Th1 and Th2 cells. European Journal of Immunology, 2003, 33, 1105-1116.	2.9	28
115	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
116	Transcriptional response networks for elucidating mechanisms of action of multitargeted agents. Drug Discovery Today, 2016, 21, 1063-1075.	6.4	28
117	Patient-tailored design for selective co-inhibition of leukemic cell subpopulations. Science Advances, 2021, 7, .	10.3	28
118	Development of HDAC Inhibitors Exhibiting Therapeutic Potential in T-Cell Prolymphocytic Leukemia. Journal of Medicinal Chemistry, 2021, 64, 8486-8509.	6.4	28
119	Effect of medroxyprogesterone on inspiratory flow shapes during sleep in postmenopausal women. Respiratory Physiology and Neurobiology, 2003, 134, 131-143.	1.6	27
120	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
121	Novel Lignan and Stilbenoid Mixture Shows Anticarcinogenic Efficacy in Preclinical PC-3M-luc2 Prostate Cancer Model. PLoS ONE, 2014, 9, e93764.	2.5	27
122	Inhibition of Arenaviruses by Combinations of Orally Available Approved Drugs. Antimicrobial Agents and Chemotherapy, 2021, 65, .	3.2	27
123	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
124	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
125	Machine Learning of Bone Marrow Histopathology Identifies Genetic and Clinical Determinants in Patients with MDS. Blood Cancer Discovery, 2021, 2, 238-249.	5.0	25
126	Probe-level estimation improves the detection of differential splicing in Affymetrix exon array studies. Genome Biology, 2009, 10, R77.	9.6	23

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127	Multi-Omics Studies towards Novel Modulators of Influenza A Virus–Host Interaction. Viruses, 2016, 8, 269.	3.3	23
128	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
129	Systematic Mapping of Kinase Addiction Combinations in Breast Cancer Cells by Integrating Drug Sensitivity and Selectivity Profiles. Chemistry and Biology, 2015, 22, 1144-1155.	6.0	22
130	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
131	Analysis of similarity of electrophoretic patterns in mRNA differential display. Electrophoresis, 2000, 21, 2947-2956.	2.4	21
132	Automated detection of differentially expressed fragments in mRNA differential display. Electrophoresis, 2001, 22, 1935-1945.	2.4	21
133	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
134	Classification of Nasal Inspiratory Flow Shapes by Attributed Finite Automata. Journal of Biomedical Informatics, 1999, 32, 34-55.	0.7	19
135	Model-based prediction of sequence alignment quality. Bioinformatics, 2008, 24, 2165-2171.	4.1	19
136	Relevance Rank Platform (RRP) for Functional Filtering of High Content Protein–Protein Interaction Data*. Molecular and Cellular Proteomics, 2015, 14, 3274-3283.	3.8	19
137	A Community Challenge for Inferring Genetic Predictors of Gene Essentialities through Analysis of a Functional Screen of Cancer Cell Lines. Cell Systems, 2017, 5, 485-497.e3.	6.2	19
138	Medroxyprogesterone improves nocturnal breathing in postmenopausal women with chronic obstructive pulmonary disease. Respiratory Research, 2005, 6, 28.	3.6	18
139	C-SPADE: a web-tool for interactive analysis and visualization of drug screening experiments through compound-specific bioactivity dendrograms. Nucleic Acids Research, 2017, 45, W495-W500.	14.5	18
140	Re-defining synthetic lethality by phenotypic profiling for precision oncology. Cell Chemical Biology, 2021, 28, 246-256.	5.2	18
141	Climacteric vasomotor symptoms do not predict nocturnal breathing abnormalities in postmenopausal women. Maturitas, 2001, 39, 29-37.	2.4	17
142	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
143	Ovarian Endometriosis Signatures Established through Discovery and Directed Mass Spectrometry Analysis. Journal of Proteome Research, 2014, 13, 4983-4994.	3.7	17
144	Adrenals Contribute to Growth of Castration-Resistant VCaP Prostate Cancer Xenografts. American Journal of Pathology, 2018, 188, 2890-2901.	3.8	17

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145	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
146	CIP2A Promotes T-Cell Activation and Immune Response to Listeria monocytogenes Infection. PLoS ONE, 2016, 11, e0152996.	2.5	17
147	Quantitative maps of genetic interactions in yeast - Comparative evaluation and integrative analysis. BMC Systems Biology, 2011, 5, 45.	3.0	16
148	Combined ASRGL1 and p53 immunohistochemistry as an independent predictor of survival in endometrioid endometrial carcinoma. Gynecologic Oncology, 2018, 149, 173-180.	1.4	16
149	Genome-wide off-targets of drugs: risks and opportunities. Cell Biology and Toxicology, 2019, 35, 485-487.	5.3	16
150	Improving the false nearest neighbors method with graphical analysis. Physical Review E, 1999, 60, 416-421.	2.1	15
151	TIMMA-R: an R package for predicting synergistic multi-targeted drug combinations in cancer cell lines or patient-derived samples. Bioinformatics, 2015, 31, 1866-1868.	4.1	15
152	Improved detection of differentially represented DNA barcodes for highâ€ŧhroughput clonal phenomics. Molecular Systems Biology, 2020, 16, e9195.	7.2	15
153	Phosphoproteomics Combined with Quantitative 14-3-3-affinity Capture Identifies SIRT1 and RAI as Novel Regulators of Cytosolic Double-stranded RNA Recognition Pathway. Molecular and Cellular Proteomics, 2014, 13, 2604-2617.	3.8	14
154	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
155	A human ImmunoChip cDNA microarray provides a comprehensive tool to study immune responses. Journal of Immunological Methods, 2005, 303, 122-134.	1.4	13
156	From drug response profiling to target addiction scoring in cancer cell models. DMM Disease Models and Mechanisms, 2015, 8, 1255-1264.	2.4	13
157	Orphan G protein-coupled receptor GPRC5A modulates integrin $\langle b \rangle \hat{l}^2 \langle b \rangle 1$ -mediated epithelial cell adhesion. Cell Adhesion and Migration, 2017, 11, 434-446.	2.7	13
158	Network-guided identification of cancer-selective combinatorial therapies in ovarian cancer. Briefings in Bioinformatics, 2021, 22, .	6.5	13
159	Systematic review of computational methods for drug combination prediction. Computational and Structural Biotechnology Journal, 2022, 20, 2807-2814.	4.1	13
160	Feature learning with a genetic algorithm for fluorescence fingerprinting of plant species. Pattern Recognition Letters, 2003, 24, 2663-2673.	4.2	12
161	Overnight variability in transcutaneous carbon dioxide predicts vascular impairment in women. Experimental Physiology, 2008, 93, 880-891.	2.0	12
162	Genoscape: a Cytoscape plug-in to automate the retrieval and integration of gene expression data and molecular networks. Bioinformatics, 2009, 25, 2617-2618.	4.1	12

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163	PhosFox: a bioinformatics tool for peptide-level processing of LC-MS/MS-based phosphoproteomic data. Proteome Science, 2014, 12, 36.	1.7	12
164	Seed-effect modeling improves the consistency of genome-wide loss-of-function screens and identifies synthetic lethal vulnerabilities in cancer cells. Genome Medicine, 2017, 9, 51.	8.2	12
165	A DREAM Challenge to Build Prediction Models for Short-Term Discontinuation of Docetaxel in Metastatic Castration-Resistant Prostate Cancer. JCO Clinical Cancer Informatics, 2017, 1, 1-15.	2.1	12
166	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
167	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
168	What are the current challenges for machine learning in drug discovery and repurposing?. Expert Opinion on Drug Discovery, 2022, 17, 423-425.	5.0	12
169	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
170	Systematic drug screening reveals specific vulnerabilities and co-resistance patterns in endocrine-resistant breast cancer. BMC Cancer, 2016, 16, 378.	2.6	11
171	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
172	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
173	Novel Small Molecule Hsp90/Cdc37 Interface Inhibitors Indirectly Target K-Ras-Signaling. Cancers, 2021, 13, 927.	3.7	11
174	Electrophoretic Signal Comparison Applied to mRNA Differential Display Analysis. BioTechniques, 2003, 34, 116-122.	1.8	10
175	Can carotid body perfusion act as a respiratory controller?. Journal of Theoretical Biology, 2007, 249, 737-748.	1.7	10
176	Predicting Quantitative Genetic Interactions by Means of Sequential Matrix Approximation. PLoS ONE, 2008, 3, e3284.	2.5	10
177	Resampling Reveals Sample-Level Differential Expression in Clinical Genome-Wide Studies. OMICS A Journal of Integrative Biology, 2009, 13, 381-396.	2.0	10
178	Statistical detection of quantitative protein biomarkers provides insights into signaling networks deregulated in acute myeloid leukemia. Proteomics, 2014, 14, 2443-2453.	2.2	10
179	PolyAlign: A Versatile LC-MS Data Alignment Tool for Landmark-Selected and -Automated Use. International Journal of Proteomics, 2011, 2011, 1-9.	2.0	9
180	The inconvenience of data of convenience: computational research beyond post-mortem analyses. Nature Methods, 2017, 14, 937-938.	19.0	9

#	Article	IF	CITATIONS
181	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
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