

Tero Aittokallio

List of Publications by Year in descending order

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Version: 2024-02-01

295
papers

12,891
citations

30551

56
h-index

40945

97
g-index

326
all docs

326
docs citations

326
times ranked

21184
citing authors

#	ARTICLE	IF	CITATIONS
1	A community effort to assess and improve drug sensitivity prediction algorithms. <i>Nature Biotechnology</i> , 2014, 32, 1202-1212.	9.4	653
2	SynergyFinder 2.0: visual analytics of multi-drug combination synergies. <i>Nucleic Acids Research</i> , 2020, 48, W488-W493.	6.5	545
3	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.	1.9	485
4	SynergyFinder: a web application for analyzing drug combination dose-response matrix data. <i>Bioinformatics</i> , 2017, 33, 2413-2415.	1.8	403
5	Graph-based methods for analysing networks in cell biology. <i>Briefings in Bioinformatics</i> , 2006, 7, 243-255.	3.2	368
6	Individualized Systems Medicine Strategy to Tailor Treatments for Patients with Chemorefractory Acute Myeloid Leukemia. <i>Cancer Discovery</i> , 2013, 3, 1416-1429.	7.7	334
7	Toward more realistic drug-target interaction predictions. <i>Briefings in Bioinformatics</i> , 2015, 16, 325-337.	3.2	331
8	Network pharmacology applications to map the unexplored target space and therapeutic potential of natural products. <i>Natural Product Reports</i> , 2015, 32, 1249-1266.	5.2	331
9	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.	2.5	284
10	Quantitative scoring of differential drug sensitivity for individually optimized anticancer therapies. <i>Scientific Reports</i> , 2014, 4, 5193.	1.6	243
11	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. <i>Nature Communications</i> , 2019, 10, 2674.	5.8	240
12	Fully-automated and ultra-fast cell-type identification using specific marker combinations from single-cell transcriptomic data. <i>Nature Communications</i> , 2022, 13, 1246.	5.8	163
13	Machine learning and feature selection for drug response prediction in precision oncology applications. <i>Biophysical Reviews</i> , 2019, 11, 31-39.	1.5	148
14	What is synergy? The Saariselkä agreement revisited. <i>Frontiers in Pharmacology</i> , 2015, 6, 181.	1.6	147
15	Methods for High-throughput Drug Combination Screening and Synergy Scoring. <i>Methods in Molecular Biology</i> , 2018, 1711, 351-398.	0.4	140
16	Genome-wide Profiling of Interleukin-4 and STAT6 Transcription Factor Regulation of Human Th2 Cell Programming. <i>Immunity</i> , 2010, 32, 852-862.	6.6	139
17	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.	6.5	139
18	Dealing with missing values in large-scale studies: microarray data imputation and beyond. <i>Briefings in Bioinformatics</i> , 2010, 11, 253-264.	3.2	137

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19	Integrated drug profiling and CRISPR screening identify essential pathways for CAR T-cell cytotoxicity. <i>Blood</i> , 2020, 135, 597-609.	0.6	134
20	Susceptibility of low-density lipoprotein particles to aggregate depends on particle lipidome, is modifiable, and associates with future cardiovascular deaths. <i>European Heart Journal</i> , 2018, 39, 2562-2573.	1.0	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. <i>Lancet Oncology</i> , The, 2017, 18, 132-142.	5.1	124
22	Drug Target Commons: A Community Effort to Build a Consensus Knowledge Base for Drug-Target Interactions. <i>Cell Chemical Biology</i> , 2018, 25, 224-229.e2.	2.5	124
23	Quantitative Subcellular Proteome and Secretome Profiling of Influenza A Virus-Infected Human Primary Macrophages. <i>PLoS Pathogens</i> , 2011, 7, e1001340.	2.1	122
24	Regularized Machine Learning in the Genetic Prediction of Complex Traits. <i>PLoS Genetics</i> , 2014, 10, e1004754.	1.5	122
25	PP2A inhibition is a druggable MEK inhibitor resistance mechanism in KRAS-mutant lung cancer cells. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	116
26	Network Pharmacology Strategies Toward Multi-Target Anticancer Therapies: From Computational Models to Experimental Design Principles. <i>Current Pharmaceutical Design</i> , 2014, 20, 23-36.	0.9	115
27	Aggressive natural killer-cell leukemia mutational landscape and drug profiling highlight JAK-STAT signaling as therapeutic target. <i>Nature Communications</i> , 2018, 9, 1567.	5.8	107
28	GOcolorize: a Cytoscape plug-in for network visualization with Gene Ontology-based layout and coloring. <i>Bioinformatics</i> , 2007, 23, 394-396.	1.8	105
29	A practical comparison of methods for detecting transcription factor binding sites in ChIP-seq experiments. <i>BMC Genomics</i> , 2009, 10, 618.	1.2	105
30	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. <i>Nature Genetics</i> , 2020, 52, 448-457.	9.4	104
31	Improving missing value estimation in microarray data with gene ontology. <i>Bioinformatics</i> , 2006, 22, 566-572.	1.8	101
32	Identification of Novel IL-4/Stat6-Regulated Genes in T Lymphocytes. <i>Journal of Immunology</i> , 2003, 171, 3627-3635.	0.4	99
33	Prediction of drug combination effects with a minimal set of experiments. <i>Nature Machine Intelligence</i> , 2019, 1, 568-577.	8.3	99
34	Early metabolic markers identify potential targets for the prevention of type 2 diabetes. <i>Diabetologia</i> , 2017, 60, 1740-1750.	2.9	96
35	Systematic construction of gene coexpression networks with applications to human T helper cell differentiation process. <i>Bioinformatics</i> , 2007, 23, 2096-2103.	1.8	94
36	Alignment of LC-MS images, with applications to biomarker discovery and protein identification. <i>Proteomics</i> , 2008, 8, 650-672.	1.3	92

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37	JAK1/2 and BCL2 inhibitors synergize to counteract bone marrow stromal cell-induced protection of AML. <i>Blood</i> , 2017, 130, 789-802.	0.6	90
38	Prediction of human population responses to toxic compounds by a collaborative competition. <i>Nature Biotechnology</i> , 2015, 33, 933-940.	9.4	88
39	Drug response prediction by inferring pathway-response associations with kernelized Bayesian matrix factorization. <i>Bioinformatics</i> , 2016, 32, i455-i463.	1.8	87
40	Comparison of PDQuest and Progenesis software packages in the analysis of two-dimensional electrophoresis gels. <i>Proteomics</i> , 2003, 3, 1936-1946.	1.3	84
41	Target Inhibition Networks: Predicting Selective Combinations of Druggable Targets to Block Cancer Survival Pathways. <i>PLoS Computational Biology</i> , 2013, 9, e1003226.	1.5	84
42	Computational-experimental approach to drug-target interaction mapping: A case study on kinase inhibitors. <i>PLoS Computational Biology</i> , 2017, 13, e1005678.	1.5	84
43	An update on clinical proteomics in Alzheimer's research. <i>Journal of Neurochemistry</i> , 2010, 112, 1386-1414.	2.1	82
44	Obatoclox, Saliphenylhalamide, and Gemcitabine Inhibit Influenza A Virus Infection. <i>Journal of Biological Chemistry</i> , 2012, 287, 35324-35332.	1.6	80
45	Cancer stem cell drugs target K-ras signaling in a stemness context. <i>Oncogene</i> , 2016, 35, 5248-5262.	2.6	78
46	Consistency in drug response profiling. <i>Nature</i> , 2016, 540, E5-E6.	13.7	76
47	Discovery of novel drug sensitivities in T-PLL by high-throughput ex vivo drug testing and mutation profiling. <i>Leukemia</i> , 2018, 32, 774-787.	3.3	75
48	Immune cell contexture in the bone marrow tumor microenvironment impacts therapy response in CML. <i>Leukemia</i> , 2018, 32, 1643-1656.	3.3	75
49	Th1 Response and Cytotoxicity Genes Are Down-Regulated in Cutaneous T-Cell Lymphoma. <i>Clinical Cancer Research</i> , 2006, 12, 4812-4821.	3.2	74
50	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.	0.4	74
51	Comprehensive Drug Testing of Patient-derived Conditionally Reprogrammed Cells from Castration-resistant Prostate Cancer. <i>European Urology</i> , 2017, 71, 319-327.	0.9	74
52	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. <i>Nature Communications</i> , 2016, 7, 12460.	5.8	73
53	Implementing a Functional Precision Medicine Tumor Board for Acute Myeloid Leukemia. <i>Cancer Discovery</i> , 2022, 12, 388-401.	7.7	73
54	Analysis of Inspiratory Flow Shapes in Patients With Partial Upper-Airway Obstruction During Sleep. <i>Chest</i> , 2001, 119, 37-44.	0.4	72

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55	Breeze: an integrated quality control and data analysis application for high-throughput drug screening. <i>Bioinformatics</i> , 2020, 36, 3602-3604.	1.8	68
56	Artificial intelligence, machine learning, and drug repurposing in cancer. <i>Expert Opinion on Drug Discovery</i> , 2021, 16, 977-989.	2.5	68
57	DNMT Inhibitors Increase Methylation in the Cancer Genome. <i>Frontiers in Pharmacology</i> , 2019, 10, 385.	1.6	67
58	Reproducibility-Optimized Test Statistic for Ranking Genes in Microarray Studies. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 423-431.	1.9	66
59	Phosphoproteomics to Characterize Host Response During Influenza A Virus Infection of Human Macrophages. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3203-3219.	2.5	66
60	Novel activities of safe-in-human broad-spectrum antiviral agents. <i>Antiviral Research</i> , 2018, 154, 174-182.	1.9	64
61	Leveraging multi-way interactions for systematic prediction of pre-clinical drug combination effects. <i>Nature Communications</i> , 2020, 11, 6136.	5.8	63
62	Identification of Novel Genes Regulated by IL-12, IL-4, or TGF- β 2 during the Early Polarization of CD4+ Lymphocytes. <i>Journal of Immunology</i> , 2003, 171, 5328-5336.	0.4	61
63	Whole-genome view of the consequences of a population bottleneck using 2926 genome sequences from Finland and United Kingdom. <i>European Journal of Human Genetics</i> , 2017, 25, 477-484.	1.4	60
64	Patient-Customized Drug Combination Prediction and Testing for T-cell Prolymphocytic Leukemia Patients. <i>Cancer Research</i> , 2018, 78, 2407-2418.	0.4	60
65	Pharmacological reactivation of MYC-dependent apoptosis induces susceptibility to anti-PD-1 immunotherapy. <i>Nature Communications</i> , 2019, 10, 620.	5.8	60
66	Improving the efficacy-safety balance of polypharmacology in multi-target drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2018, 13, 179-192.	2.5	59
67	Systematic identification of feature combinations for predicting drug response with Bayesian multi-view multi-task linear regression. <i>Bioinformatics</i> , 2017, 33, i359-i368.	1.8	58
68	Identification of selective cytotoxic and synthetic lethal drug responses in triple negative breast cancer cells. <i>Molecular Cancer</i> , 2016, 15, 34.	7.9	57
69	Global proteomics profiling improves drug sensitivity prediction: results from a multi-omics, pan-cancer modeling approach. <i>Bioinformatics</i> , 2018, 34, 1353-1362.	1.8	56
70	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.	2.5	55
71	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.	1.8	55
72	Identification of drug candidates and repurposing opportunities through compound-target interaction networks. <i>Expert Opinion on Drug Discovery</i> , 2015, 10, 1333-1345.	2.5	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. <i>American Journal of Pathology</i> , 2014, 184, 2163-2173.	1.9	53
74	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.	0.9	53
75	Missing value imputation improves clustering and interpretation of gene expression microarray data. <i>BMC Bioinformatics</i> , 2008, 9, 202.	1.2	52
76	Integrating probe-level expression changes across generations of Affymetrix arrays. <i>Nucleic Acids Research</i> , 2005, 33, e193-e193.	6.5	51
77	Learning with multiple pairwise kernels for drug bioactivity prediction. <i>Bioinformatics</i> , 2018, 34, i509-i518.	1.8	51
78	Label-free quantitative phosphoproteomics with novel pairwise abundance normalization reveals synergistic RAS and CIP2A signaling. <i>Scientific Reports</i> , 2015, 5, 13099.	1.6	49
79	Phosphoproteome and drug-response effects mediated by the three protein phosphatase 2A inhibitor proteins CIP2A, SET, and PME-1. <i>Journal of Biological Chemistry</i> , 2020, 295, 4194-4211.	1.6	48
80	A model of a snorer's upper airway. <i>Mathematical Biosciences</i> , 2001, 170, 79-90.	0.9	46
81	MicroRNA-135b regulates ER α , AR and HIF1AN and affects breast and prostate cancer cell growth. <i>Molecular Oncology</i> , 2015, 9, 1287-1300.	2.1	45
82	Specific cancer-associated mutations in the switch III region of Ras increase tumorigenicity by nanocluster augmentation. <i>ELife</i> , 2015, 4, e08905.	2.8	45
83	Drug Combinations as a First Line of Defense against Coronaviruses and Other Emerging Viruses. <i>MBio</i> , 2021, 12, e0334721.	1.8	45
84	Enhanced sensitivity to glucocorticoids in cytarabine-resistant AML. <i>Leukemia</i> , 2017, 31, 1187-1195.	3.3	44
85	The Hydroxysteroid (17 β) Dehydrogenase Family Gene HSD17B12 Is Involved in the Prostaglandin Synthesis Pathway, the Ovarian Function, and Regulation of Fertility. <i>Endocrinology</i> , 2016, 157, 3719-3730.	1.4	43
86	SynToxProfiler: An interactive analysis of drug combination synergy, toxicity and efficacy. <i>PLoS Computational Biology</i> , 2020, 16, e1007604.	1.5	43
87	Computational Strategies for Analyzing Data in Gene Expression Microarray Experiments. <i>Journal of Bioinformatics and Computational Biology</i> , 2003, 01, 541-586.	0.3	41
88	A statistical score for assessing the quality of multiple sequence alignments. <i>BMC Bioinformatics</i> , 2006, 7, 484.	1.2	41
89	Quality classification of tandem mass spectrometry data. <i>Bioinformatics</i> , 2006, 22, 400-406.	1.8	41
90	Chk1 Targeting Reactivates PP2A Tumor Suppressor Activity in Cancer Cells. <i>Cancer Research</i> , 2013, 73, 6757-6769.	0.4	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. <i>Cell Death and Disease</i> , 2013, 4, e742-e742.	2.7	41
92	Crowdsourced mapping of unexplored target space of kinase inhibitors. <i>Nature Communications</i> , 2021, 12, 3307.	5.8	41
93	Genetic variants and their interactions in disease risk prediction – machine learning and network perspectives. <i>BioData Mining</i> , 2013, 6, 5.	2.2	40
94	Antiviral Properties of Chemical Inhibitors of Cellular Anti-Apoptotic Bcl-2 Proteins. <i>Viruses</i> , 2017, 9, 271.	1.5	39
95	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.	1.5	38
96	JAK/STAT-Activating Genomic Alterations Are a Hallmark of T-PLL. <i>Cancers</i> , 2019, 11, 1833.	1.7	38
97	Geometrical distortions in two-dimensional gels: applicable correction methods. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2005, 815, 25-37.	1.2	37
98	Optimized design and analysis of preclinical intervention studies in vivo. <i>Scientific Reports</i> , 2016, 6, 30723.	1.6	36
99	Drug Target Commons 2.0: a community platform for systematic analysis of drug–target interaction profiles. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, 1-13.	1.4	36
100	Sleep quality, daytime sleepiness and fasting insulin levels in women with chronic obstructive pulmonary disease. <i>Respiratory Medicine</i> , 2005, 99, 856-863.	1.3	35
101	Improved Statistical Modeling of Tumor Growth and Treatment Effect in Preclinical Animal Studies with Highly Heterogeneous Responses <i>In Vivo</i> . <i>Clinical Cancer Research</i> , 2012, 18, 4385-4396.	3.2	35
102	<i>UBR5</i> Is Coamplified with <i>MYC</i> in Breast Tumors and Encodes an Ubiquitin Ligase That Limits MYC-Dependent Apoptosis. <i>Cancer Research</i> , 2020, 80, 1414-1427.	0.4	35
103	Phenotypic Screening Combined with Machine Learning for Efficient Identification of Breast Cancer-Selective Therapeutic Targets. <i>Cell Chemical Biology</i> , 2019, 26, 970-979.e4.	2.5	34
104	Drug-Sensitivity Screening and Genomic Characterization of 45 HPV-Negative Head and Neck Carcinoma Cell Lines for Novel Biomarkers of Drug Efficacy. <i>Molecular Cancer Therapeutics</i> , 2018, 17, 2060-2071.	1.9	33
105	A relational database to identify differentially expressed genes in the endometrium and endometriosis lesions. <i>Scientific Data</i> , 2020, 7, 284.	2.4	33
106	Network pharmacology modeling identifies synergistic Aurora B and ZAK interaction in triple-negative breast cancer. <i>Npj Systems Biology and Applications</i> , 2019, 5, 20.	1.4	32
107	RUNX1 mutations in blast-phase chronic myeloid leukemia associate with distinct phenotypes, transcriptional profiles, and drug responses. <i>Leukemia</i> , 2021, 35, 1087-1099.	3.3	32
108	Hierarchical grid transformation for image warping in the analysis of two-dimensional electrophoresis gels. <i>Proteomics</i> , 2002, 2, 1504-1515.	1.3	31

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109	Filtering strategies for improving protein identification in high-throughput MS/MS studies. <i>Proteomics</i> , 2009, 9, 848-860.	1.3	31
110	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.	1.8	31
111	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.	3.2	29
112	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.	3.0	29
113	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.	1.9	29
114	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.	1.6	28
115	Wrapper-based selection of genetic features in genome-wide association studies through fast matrix operations. <i>Algorithms for Molecular Biology</i> , 2012, 7, 11.	0.3	28
116	Transcriptional response networks for elucidating mechanisms of action of multitargeted agents. <i>Drug Discovery Today</i> , 2016, 21, 1063-1075.	3.2	28
117	Patient-tailored design for selective co-inhibition of leukemic cell subpopulations. <i>Science Advances</i> , 2021, 7, .	4.7	28
118	Development of HDAC Inhibitors Exhibiting Therapeutic Potential in T-Cell Prolymphocytic Leukemia. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 8486-8509.	2.9	28
119	Effect of medroxyprogesterone on inspiratory flow shapes during sleep in postmenopausal women. <i>Respiratory Physiology and Neurobiology</i> , 2003, 134, 131-143.	0.7	27
120	A comparative evaluation of software for the analysis of liquid chromatography-tandem mass spectrometry data from isotope coded affinity tag experiments. <i>Proteomics</i> , 2005, 5, 2748-2760.	1.3	27
121	Novel Lignan and Stilbenoid Mixture Shows Anticarcinogenic Efficacy in Preclinical PC-3M-luc2 Prostate Cancer Model. <i>PLoS ONE</i> , 2014, 9, e93764.	1.1	27
122	Inhibition of Arenaviruses by Combinations of Orally Available Approved Drugs. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	1.4	27
123	Systematic drug sensitivity testing reveals synergistic growth inhibition by dasatinib or mTOR inhibitors with paclitaxel in ovarian granulosa cell tumor cells. <i>Gynecologic Oncology</i> , 2017, 144, 621-630.	0.6	26
124	Interactive visual analysis of drug-target interaction networks using Drug Target Profiler, with applications to precision medicine and drug repurposing. <i>Briefings in Bioinformatics</i> , 2018, .	3.2	25
125	Machine Learning of Bone Marrow Histopathology Identifies Genetic and Clinical Determinants in Patients with MDS. <i>Blood Cancer Discovery</i> , 2021, 2, 238-249.	2.6	25
126	Probe-level estimation improves the detection of differential splicing in Affymetrix exon array studies. <i>Genome Biology</i> , 2009, 10, R77.	13.9	23

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127	Multi-Omics Studies towards Novel Modulators of Influenza A Virusâ€™Host Interaction. <i>Viruses</i> , 2016, 8, 269.	1.5	23
128	A normalized drug response metric improves accuracy and consistency of anticancer drug sensitivity quantification in cell-based screening. <i>Communications Biology</i> , 2020, 3, 42.	2.0	23
129	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.	6.2	22
130	Secreted frizzled-related protein 2 (SFRP2) expression promotes lesion proliferation via canonical WNT signaling and indicates lesion borders in extraovarian endometriosis. <i>Human Reproduction</i> , 2018, 33, 817-831.	0.4	22
131	Analysis of similarity of electrophoretic patterns in mRNA differential display. <i>Electrophoresis</i> , 2000, 21, 2947-2956.	1.3	21
132	Automated detection of differentially expressed fragments in mRNA differential display. <i>Electrophoresis</i> , 2001, 22, 1935-1945.	1.3	21
133	Rapalogs can promote cancer cell stemness <i>in vitro</i> in a Galectin-1 and H-ras-dependent manner. <i>Oncotarget</i> , 2017, 8, 44550-44566.	0.8	20
134	Classification of Nasal Inspiratory Flow Shapes by Attributed Finite Automata. <i>Journal of Biomedical Informatics</i> , 1999, 32, 34-55.	0.7	19
135	Model-based prediction of sequence alignment quality. <i>Bioinformatics</i> , 2008, 24, 2165-2171.	1.8	19
136	Relevance Rank Platform (RRP) for Functional Filtering of High Content Proteinâ€™Protein Interaction Data*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 3274-3283.	2.5	19
137	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.	2.9	19
138	Medroxyprogesterone improves nocturnal breathing in postmenopausal women with chronic obstructive pulmonary disease. <i>Respiratory Research</i> , 2005, 6, 28.	1.4	18
139	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.	6.5	18
140	Re-defining synthetic lethality by phenotypic profiling for precision oncology. <i>Cell Chemical Biology</i> , 2021, 28, 246-256.	2.5	18
141	Climacteric vasomotor symptoms do not predict nocturnal breathing abnormalities in postmenopausal women. <i>Maturitas</i> , 2001, 39, 29-37.	1.0	17
142	Inspiratory flow shape clustering: An automated method to monitor upper airway performance during sleep. <i>Computer Methods and Programs in Biomedicine</i> , 2007, 85, 8-18.	2.6	17
143	Ovarian Endometriosis Signatures Established through Discovery and Directed Mass Spectrometry Analysis. <i>Journal of Proteome Research</i> , 2014, 13, 4983-4994.	1.8	17
144	Adrenals Contribute to Growth of Castration-Resistant VCaP Prostate Cancer Xenografts. <i>American Journal of Pathology</i> , 2018, 188, 2890-2901.	1.9	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. <i>Blood</i> , 2020, 136, 2786-2802.	0.6	17
146	CIP2A Promotes T-Cell Activation and Immune Response to <i>Listeria monocytogenes</i> Infection. <i>PLoS ONE</i> , 2016, 11, e0152996.	1.1	17
147	Quantitative maps of genetic interactions in yeast - Comparative evaluation and integrative analysis. <i>BMC Systems Biology</i> , 2011, 5, 45.	3.0	16
148	Combined ASRGL1 and p53 immunohistochemistry as an independent predictor of survival in endometrioid endometrial carcinoma. <i>Gynecologic Oncology</i> , 2018, 149, 173-180.	0.6	16
149	Genome-wide off-targets of drugs: risks and opportunities. <i>Cell Biology and Toxicology</i> , 2019, 35, 485-487.	2.4	16
150	Improving the false nearest neighbors method with graphical analysis. <i>Physical Review E</i> , 1999, 60, 416-421.	0.8	15
151	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.	1.8	15
152	Improved detection of differentially represented DNA barcodes for high-throughput clonal phenomics. <i>Molecular Systems Biology</i> , 2020, 16, e9195.	3.2	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. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2604-2617.	2.5	14
154	Chemogenomic Analysis of the Druggable Kinome and Its Application to Repositioning and Lead Identification Studies. <i>Cell Chemical Biology</i> , 2019, 26, 1608-1622.e6.	2.5	14
155	A human ImmunoChip cDNA microarray provides a comprehensive tool to study immune responses. <i>Journal of Immunological Methods</i> , 2005, 303, 122-134.	0.6	13
156	From drug response profiling to target addiction scoring in cancer cell models. <i>DMM Disease Models and Mechanisms</i> , 2015, 8, 1255-1264.	1.2	13
157	Orphan G protein-coupled receptor GPRC5A modulates integrin $\alpha 1$ -mediated epithelial cell adhesion. <i>Cell Adhesion and Migration</i> , 2017, 11, 434-446.	1.1	13
158	Network-guided identification of cancer-selective combinatorial therapies in ovarian cancer. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	13
159	Systematic review of computational methods for drug combination prediction. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2807-2814.	1.9	13
160	Feature learning with a genetic algorithm for fluorescence fingerprinting of plant species. <i>Pattern Recognition Letters</i> , 2003, 24, 2663-2673.	2.6	12
161	Overnight variability in transcutaneous carbon dioxide predicts vascular impairment in women. <i>Experimental Physiology</i> , 2008, 93, 880-891.	0.9	12
162	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.	1.8	12

#	ARTICLE	IF	CITATIONS
163	PhosFox: a bioinformatics tool for peptide-level processing of LC-MS/MS-based phosphoproteomic data. <i>Proteome Science</i> , 2014, 12, 36.	0.7	12
164	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.	3.6	12
165	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.	1.0	12
166	Bayesian multi-source regression and monocyte-associated gene expression predict BCL-2 inhibitor resistance in acute myeloid leukemia. <i>Npj Precision Oncology</i> , 2021, 5, 71.	2.3	12
167	A Two-Step Learning Approach for Solving Full and Almost Full Cold Start Problems in Dyadic Prediction. <i>Lecture Notes in Computer Science</i> , 2014, , 517-532.	1.0	12
168	What are the current challenges for machine learning in drug discovery and repurposing?. <i>Expert Opinion on Drug Discovery</i> , 2022, 17, 423-425.	2.5	12
169	A multilevel layout algorithm for visualizing physical and genetic interaction networks, with emphasis on their modular organization. <i>BioData Mining</i> , 2012, 5, 2.	2.2	11
170	Systematic drug screening reveals specific vulnerabilities and co-resistance patterns in endocrine-resistant breast cancer. <i>BMC Cancer</i> , 2016, 16, 378.	1.1	11
171	Genetic and functional implications of an exonic TRIM55 variant in heart failure. <i>Journal of Molecular and Cellular Cardiology</i> , 2020, 138, 222-233.	0.9	11
172	Cost-effective survival prediction for patients with advanced prostate cancer using clinical trial and real-world hospital registry datasets. <i>International Journal of Medical Informatics</i> , 2020, 133, 104014.	1.6	11
173	Novel Small Molecule Hsp90/Cdc37 Interface Inhibitors Indirectly Target K-Ras-Signaling. <i>Cancers</i> , 2021, 13, 927.	1.7	11
174	Electrophoretic Signal Comparison Applied to mRNA Differential Display Analysis. <i>BioTechniques</i> , 2003, 34, 116-122.	0.8	10
175	Can carotid body perfusion act as a respiratory controller?. <i>Journal of Theoretical Biology</i> , 2007, 249, 737-748.	0.8	10
176	Predicting Quantitative Genetic Interactions by Means of Sequential Matrix Approximation. <i>PLoS ONE</i> , 2008, 3, e3284.	1.1	10
177	Resampling Reveals Sample-Level Differential Expression in Clinical Genome-Wide Studies. <i>OMICS A Journal of Integrative Biology</i> , 2009, 13, 381-396.	1.0	10
178	Statistical detection of quantitative protein biomarkers provides insights into signaling networks deregulated in acute myeloid leukemia. <i>Proteomics</i> , 2014, 14, 2443-2453.	1.3	10
179	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
180	The inconvenience of data of convenience: computational research beyond post-mortem analyses. <i>Nature Methods</i> , 2017, 14, 937-938.	9.0	9

#	ARTICLE	IF	CITATIONS
181	Antiandrogens Reduce Intratumoral Androgen Concentrations and Induce Androgen Receptor Expression in Castration-Resistant Prostate Cancer Xenografts. <i>American Journal of Pathology</i> , 2018, 188, 216-228.	1.9	9
182	Reinstated p53 response and high anti-T-cell leukemia activity by the novel alkylating deacetylase inhibitor tinostamustine. <i>Leukemia</i> , 2020, 34, 2513-2518.	3.3	9
183	Multi-Omics Marker Analysis Enables Early Prediction of Breast Tumor Progression. <i>Frontiers in Genetics</i> , 2021, 12, 670749.	1.1	9
184	Modeling drug combination effects via latent tensor reconstruction. <i>Bioinformatics</i> , 2021, 37, i93-i101.	1.8	9
185	Multiobjective optimization identifies cancer-selective combination therapies. <i>PLoS Computational Biology</i> , 2020, 16, e1008538.	1.5	9
186	Detection of high-frequency respiratory movements during sleep. <i>Computer Methods and Programs in Biomedicine</i> , 2000, 61, 171-185.	2.6	8
187	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
188	Adjustment of the Human Respiratory System to Increased Upper Airway Resistance During Sleep. <i>Bulletin of Mathematical Biology</i> , 2002, 64, 3-28.	0.9	8
189	Efficient estimation of emission probabilities in profile hidden Markov models. <i>Bioinformatics</i> , 2003, 19, 2359-2368.	1.8	8
190	Mahalanobis distance screening of Arabidopsis mutants with chlorophyll fluorescence. <i>Photosynthesis Research</i> , 2010, 105, 273-283.	1.6	8
191	Pravastatin-induced improvement in coronary reactivity and circulating ATP and ADP levels in young adults with type 1 diabetes. <i>Frontiers in Physiology</i> , 2012, 3, 338.	1.3	8
192	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.	3.2	8
193	Prediction of Inspiratory Flow Shapes During Sleep with a Mathematic Model of Upper Airway Forces. <i>Sleep</i> , 2003, 26, 857-863.	0.6	7
194	Statistical Methods for Identifying Conserved Residues in Multiple Sequence Alignment. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2004, 3, 1-28.	0.2	7
195	Non-invasive respiratory monitoring during wakefulness and sleep in pre- and postmenopausal women. <i>Respiratory Physiology and Neurobiology</i> , 2006, 150, 66-74.	0.7	7
196	Model-Based Analysis of Mechanisms Responsible for Sleep-Induced Carbon Dioxide Differences. <i>Bulletin of Mathematical Biology</i> , 2006, 68, 315-341.	0.9	7
197	Improving Identification of Differentially Expressed Genes by Integrative Analysis of Affymetrix and Illumina Arrays. <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 369-380.	1.0	7
198	Liver lipid metabolism is altered by increased circulating estrogen to androgen ratio in male mouse. <i>Journal of Proteomics</i> , 2016, 133, 66-75.	1.2	7

#	ARTICLE	IF	CITATIONS
199	Integrated Analysis of Drug Sensitivity and Selectivity to Predict Synergistic Drug Combinations and Target Coaddictions in Cancer. <i>Methods in Molecular Biology</i> , 2019, 1888, 205-217.	0.4	7
200	Characterizing the Quality of Insight by Interactions: A Case Study. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2021, 27, 3410-3424.	2.9	7
201	Parameter estimation of a respiratory control model from noninvasive carbon dioxide measurements during sleep. <i>Mathematical Medicine and Biology</i> , 2007, 24, 225-249.	0.8	6
202	Overnight features of transcutaneous carbon dioxide measurement as predictors of metabolic status. <i>Artificial Intelligence in Medicine</i> , 2008, 42, 55-65.	3.8	6
203	Understanding sleep-disordered breathing through mathematical modelling. <i>Sleep Medicine Reviews</i> , 2009, 13, 333-343.	3.8	6
204	Optimized detection of transcription factor-binding sites in ChIP-seq experiments. <i>Nucleic Acids Research</i> , 2012, 40, e1-e1.	6.5	6
205	Mining high-throughput screens for cancer drug targets—lessons from yeast chemical-genomic profiling and synthetic lethality. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2012, 2, 263-272.	4.6	6
206	Predicting drug-target interactions through integrative analysis of chemogenetic assays in yeast. <i>Molecular BioSystems</i> , 2013, 9, 768.	2.9	6
207	MediSyn: uncertainty-aware visualization of multiple biomedical datasets to support drug treatment selection. <i>BMC Bioinformatics</i> , 2017, 18, 393.	1.2	6
208	KIT pathway upregulation predicts dasatinib efficacy in acute myeloid leukemia. <i>Leukemia</i> , 2020, 34, 2780-2784.	3.3	6
209	Systematic mapping of cancer cell target dependencies using high-throughput drug screening in triple-negative breast cancer. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3819-3832.	1.9	6
210	OUP accepted manuscript. <i>Briefings in Bioinformatics</i> , 2021, , .	3.2	6
211	ePCR: an R-package for survival and time-to-event prediction in advanced prostate cancer, applied to real-world patient cohorts. <i>Bioinformatics</i> , 2018, 34, 3957-3959.	1.8	5
212	Evaluation of statistical approaches for association testing in noisy drug screening data. <i>BMC Bioinformatics</i> , 2022, 23, 188.	1.2	5
213	Genetic Feature Learning Algorithm for Fluorescence Fingerprinting of Plants. <i>Lecture Notes in Computer Science</i> , 2004, , 371-383.	1.0	4
214	Computer-assisted identification of multitrace electrophoretic patterns in differential display experiments. <i>Electrophoresis</i> , 2007, 28, 879-893.	1.3	4
215	Transcutaneous carbon dioxide profile during sleep reveals metabolic risk factors in post-menopausal females. <i>European Respiratory Journal</i> , 2009, 34, 1132-1139.	3.1	4
216	The rocky road to personalized medicine: computational and statistical challenges. <i>Personalized Medicine</i> , 2012, 9, 109-114.	0.8	4

#	ARTICLE	IF	CITATIONS
217	Novel Screening Method Identifies PI3K $\hat{+}$, mTOR, and IGF1R as Key Kinases Regulating Cardiomyocyte Survival. <i>Journal of the American Heart Association</i> , 2019, 8, e013018.	1.6	4
218	Modelling of killer T-cell and cancer cell subpopulation dynamics under immuno- and chemotherapies. <i>Journal of Theoretical Biology</i> , 2020, 488, 110136.	0.8	4
219	Computational Pipeline for Rational Drug Combination Screening in Patient-Derived Cells. <i>Methods in Molecular Biology</i> , 2022, 2449, 327-348.	0.4	4
220	High intratumoral dihydrotestosterone is associated with antiandrogen resistance in VCaP prostate cancer xenografts in castrated mice. <i>IScience</i> , 2022, 25, 104287.	1.9	4
221	Tissue-specific identification of multi-omics features for pan-cancer drug response prediction. <i>IScience</i> , 2022, , 104767.	1.9	4
222	Genome-Wide Scoring of Positive and Negative Epistasis through Decomposition of Quantitative Genetic Interaction Fitness Matrices. <i>PLoS ONE</i> , 2010, 5, e11611.	1.1	3
223	Module Finding Approaches for Protein Interaction Networks. , 2009, , 335-353.		3
224	Automated Pattern Ranking in Differential Display Data Analysis. , 2006, 317, 111-122.		2
225	Nocturnal transcutaneous carbon dioxide tension in postmenopausal estrogen users and non-users. <i>Menopause International</i> , 2009, 15, 107-112.	1.6	2
226	Matched preclinical designs for improved translatability. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	2
227	In Search of System-Wide Productivity Gains -The Role of Global Collaborations in Preclinical Translation. <i>Clinical and Translational Science</i> , 2017, 10, 423-425.	1.5	2
228	Predicting Gene Expression from Combined Expression and Promoter Profile Similarity with Application to Missing Value Imputation. , 2007, , 97-104.		1
229	Fast and parallelized greedy forward selection of genetic variants in Genome-wide association studies. , 2011, , .		1
230	Matrix and Tensor Factorization Methods for Toxicogenomic Modeling and Prediction. <i>Challenges and Advances in Computational Chemistry and Physics</i> , 2019, , 57-74.	0.6	1
231	Comparative Analysis of Independent Ex Vivo functional Drug Screens Identifies Predictive Biomarkers of BCL-2 Inhibitor Response in AML. <i>Blood</i> , 2018, 132, 2763-2763.	0.6	1
232	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.	0.6	1
233	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. <i>Blood</i> , 2012, 120, 288-288.	0.6	1
234	AML Specific Targeted Drugs Identified By Drug Sensitivity and Resistance Testing: Comparison of Ex Vivo Patient Cells with in Vitro Cell Lines. <i>Blood</i> , 2014, 124, 2163-2163.	0.6	1

#	ARTICLE	IF	CITATIONS
235	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
236	Abstract 1700: Dasatinib and everolimus show synergistic growth inhibition with paclitaxel in an ovarian granulosa cell tumor model. , 2015, , .		1
237	Abstract 608: Comprehensive drug testing of patient-derived conditionally reprogrammed cells from castration-resistant prostate cancer. , 2016, , .		1
238	Abstract 5560: Systemic map of protein phosphatase 2A (PP2A)-regulated phosphotargets and drug responses in cancer cells. , 2017, , .		1
239	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.	0.4	1
240	Tumor microenvironment as a metapopulation model: The effects of angiogenesis, emigration and treatment modalities. Journal of Theoretical Biology, 2022, 545, 111147.	0.8	1
241	State of vigilance, oestrogen replacement therapy, and lipid profile as modifiers of nocturnal movement-induced heart rate responses. Clinical Physiology and Functional Imaging, 2003, 23, 293-299.	0.5	0
242	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.	1.3	0
243	Unstable LDL â€™ Novel mechanism of atherogenesis and link to cardiovascular deaths. Atherosclerosis, 2016, 252, e208.	0.4	0
244	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? Eur Urol. 2017;71:838â€™40. European Urology, 2017, 72, e68-e69.	0.9	0
245	Instability of LDL particles predicts future cardiovascular deaths. Atherosclerosis, 2017, 263, e12.	0.4	0
246	PO-092 Inhibition of the mTORC1-pathway can feedback-activate H-RAS or K-RAS. ESMO Open, 2018, 3, A57.	2.0	0
247	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
248	1179A novel exonic variant in TRIM55 gene predisposes to heart failure. European Heart Journal, 2019, 40, .	1.0	0
249	Inference of Gene Coexpression Networks by Integrative Analysis across Microarray Experiments. Journal of Integrative Bioinformatics, 2006, 3, 137-147.	1.0	0
250	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
251	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
252	Parallel Feature Selection for Regularized Least-Squares. Lecture Notes in Computer Science, 2013, , 280-294.	1.0	0

#	ARTICLE	IF	CITATIONS
253	Abstract 5588: Functional drug sensitivity and resistance profiling of AML patient cells defines a disease-specific combination of druggable signal addictions.. , 2013, , .		0
254	Abstract A34: Development of a drug sensitivity testing pipeline towards the establishment of precision medicine for ovarian cancer. , 2013, , .		0
255	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
256	Stromal Cell Supported High-Throughput Drug Testing Of Primary Leukemia Cells For Comprehensive Assessment Of Sensitivity To Novel Therapies. Blood, 2013, 122, 1668-1668.	0.6	0
257	Identification Of AML Subtype-Selective Drugs By Functional Ex Vivo Drug Sensitivity and Resistance Testing and Genomic Profiling. Blood, 2013, 122, 482-482.	0.6	0
258	Abstract 982: Analysis of clonal evolution of leukemia in vivo following novel targeted treatments. , 2014, , .		0
259	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
260	Abstract 4184: Drug set enrichment analysis : A computational approach to identify functional drug sets. , 2014, , .		0
261	Abstract LB-31: Castration induces upregulation of intratumoral androgen biosynthesis and androgen receptor expression in orthotopic VCaP human prostate cancer xenograft model. , 2014, , .		0
262	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.	0.6	0
263	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
264	Abstract 5328: Protein phosphatase 2A activity is a major determinant of therapy response in cancer cells. , 2015, , .		0
265	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
266	Abstract B32: Pro-apoptotic functions of AMPK revealed by Myc. , 2015, , .		0
267	JAK1/2 and BCL2 Inhibitors Synergize to Counter-Act Bone Marrow Stromal Cell-Induced Protection of AML. Blood, 2015, 126, 867-867.	0.6	0
268	Abstract PR17: Characterization of ascites and tumor-derived ovarian cancer stem-like cells.. , 2016, , .		0
269	Abstract 4679: Acquisition of cytarabine resistance leads to increased glucocorticoid sensitivity in AML. , 2016, , .		0
270	Mutational Landscape of Aggressive Natural Killer Cell Leukemia and Drug Sensitivity Profiling Reveal Therapeutic Options in Natural Killer Cell Malignancies. Blood, 2016, 128, 2921-2921.	0.6	0

#	ARTICLE	IF	CITATIONS
271	Abstract 410: Identifying ovarian cancer specific targeted drugs using high-throughput drug sensitivity profiles of primary cancer cells. , 2017, , .		0
272	Abstract A26: Prediction of synergistic anticancer drug combinations by integrating chemical and genetic screens. , 2017, , .		0
273	Phenotypic Screening Combined with Machine Learning for Efficient Identification of Breast Cancer-Selective Therapeutic Targets. SSRN Electronic Journal, 0, , .	0.4	0
274	Abstract 3277: Identification of internal tandem duplication within theFLT3gene from AML patient next-generation sequence data. , 2018, , .		0
275	Abstract 3883: Gene expression predictsex vivodrug sensitivity in acute myeloid leukemia. , 2018, , .		0
276	Abstract 875: Chemical biology approach to phenotypic intra-tumor heterogeneity in high-grade serous ovarian cancer. , 2018, , .		0
277	Abstract 3899: Discovery and clinical implementation of individualized therapies in acute myeloid leukemia based onex vivodrug sensitivity testing and multi-omics profiling. , 2018, , .		0
278	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.	0.6	0
279	Chemogenomic Analysis of the Druggable Kinome and Its Application to Repositioning and Lead Identification Studies. SSRN Electronic Journal, 0, , .	0.4	0
280	Abstract P2-06-25: A phenotypic screening and machine learning platform efficiently identifies triple negative breast cancer-selective and readily druggable targets. , 2019, , .		0
281	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
282	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
283	Abstract P6-10-28: Therapeutic stratification of triple negative breast cancer by integrating chemosensitivity & phospho-proteome profiles. , 2020, , .		0
284	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
285	SynToxProfiler: An interactive analysis of drug combination synergy, toxicity and efficacy. , 2020, 16, e1007604.		0
286	SynToxProfiler: An interactive analysis of drug combination synergy, toxicity and efficacy. , 2020, 16, e1007604.		0
287	SynToxProfiler: An interactive analysis of drug combination synergy, toxicity and efficacy. , 2020, 16, e1007604.		0
288	SynToxProfiler: An interactive analysis of drug combination synergy, toxicity and efficacy. , 2020, 16, e1007604.		0

#	ARTICLE	IF	CITATIONS
289	Multiobjective optimization identifies cancer-selective combination therapies. , 2020, 16, e1008538.		0
290	Multiobjective optimization identifies cancer-selective combination therapies. , 2020, 16, e1008538.		0
291	Multiobjective optimization identifies cancer-selective combination therapies. , 2020, 16, e1008538.		0
292	Multiobjective optimization identifies cancer-selective combination therapies. , 2020, 16, e1008538.		0
293	Multiobjective optimization identifies cancer-selective combination therapies. , 2020, 16, e1008538.		0
294	Multiobjective optimization identifies cancer-selective combination therapies. , 2020, 16, e1008538.		0
295	Module Finding Approaches for Protein Interaction Networks. , 0, , 422-443.		0