

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	Implementing a Functional Precision Medicine Tumor Board for Acute Myeloid Leukemia. <i>Cancer Discovery</i> , 2022, 12, 388-401.	7.7	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.	5.8	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.	2.5	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.	6.5	139
5	Computational Pipeline for Rational Drug Combination Screening in Patient-Derived Cells. <i>Methods in Molecular Biology</i> , 2022, 2449, 327-348.	0.4	4
6	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
7	Tumor microenvironment as a metapopulation model: The effects of angiogenesis, emigration and treatment modalities. <i>Journal of Theoretical Biology</i> , 2022, 545, 111147.	0.8	1
8	Evaluation of statistical approaches for association testing in noisy drug screening data. <i>BMC Bioinformatics</i> , 2022, 23, 188.	1.2	5
9	Systematic review of computational methods for drug combination prediction. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2807-2814.	1.9	13
10	Tissue-specific identification of multi-omics features for pan-cancer drug response prediction. <i>IScience</i> , 2022, , 104767.	1.9	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.	2.9	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.	3.3	32
13	OUP accepted manuscript. <i>Briefings in Bioinformatics</i> , 2021, , .	3.2	6
14	Artificial intelligence, machine learning, and drug repurposing in cancer. <i>Expert Opinion on Drug Discovery</i> , 2021, 16, 977-989.	2.5	68
15	Novel Small Molecule Hsp90/Cdc37 Interface Inhibitors Indirectly Target K-Ras-Signaling. <i>Cancers</i> , 2021, 13, 927.	1.7	11
16	Patient-tailored design for selective co-inhibition of leukemic cell subpopulations. <i>Science Advances</i> , 2021, 7, .	4.7	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.	2.6	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.	3.2	8

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19	Re-defining synthetic lethality by phenotypic profiling for precision oncology. <i>Cell Chemical Biology</i> , 2021, 28, 246-256.	2.5	18
20	Inhibition of Arenaviruses by Combinations of Orally Available Approved Drugs. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	1.4	27
21	Multi-Omics Marker Analysis Enables Early Prediction of Breast Tumor Progression. <i>Frontiers in Genetics</i> , 2021, 12, 670749.	1.1	9
22	Crowdsourced mapping of unexplored target space of kinase inhibitors. <i>Nature Communications</i> , 2021, 12, 3307.	5.8	41
23	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
24	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
25	Modeling drug combination effects via latent tensor reconstruction. <i>Bioinformatics</i> , 2021, 37, i93-i101.	1.8	9
26	Network-guided identification of cancer-selective combinatorial therapies in ovarian cancer. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	13
27	Drug Combinations as a First Line of Defense against Coronaviruses and Other Emerging Viruses. <i>MBio</i> , 2021, 12, e0334721.	1.8	45
28	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
29	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
30	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
31	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
32	Improved detection of differentially represented DNA barcodes for high-throughput clonal phenomics. <i>Molecular Systems Biology</i> , 2020, 16, e9195.	3.2	15
33	KIT pathway upregulation predicts dasatinib efficacy in acute myeloid leukemia. <i>Leukemia</i> , 2020, 34, 2780-2784.	3.3	6
34	Leveraging multi-way interactions for systematic prediction of pre-clinical drug combination effects. <i>Nature Communications</i> , 2020, 11, 6136.	5.8	63
35	A relational database to identify differentially expressed genes in the endometrium and endometriosis lesions. <i>Scientific Data</i> , 2020, 7, 284.	2.4	33
36	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

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37	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. <i>Nature Genetics</i> , 2020, 52, 448-457.	9.4	104
38	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
39	<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
40	SynToxProfiler: An interactive analysis of drug combination synergy, toxicity and efficacy. <i>PLoS Computational Biology</i> , 2020, 16, e1007604.	1.5	43
41	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
42	Breeze: an integrated quality control and data analysis application for high-throughput drug screening. <i>Bioinformatics</i> , 2020, 36, 3602-3604.	1.8	68
43	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
44	SynergyFinder 2.0: visual analytics of multi-drug combination synergies. <i>Nucleic Acids Research</i> , 2020, 48, W488-W493.	6.5	545
45	Integrated drug profiling and CRISPR screening identify essential pathways for CAR T-cell cytotoxicity. <i>Blood</i> , 2020, 135, 597-609.	0.6	134
46	Multiobjective optimization identifies cancer-selective combination therapies. <i>PLoS Computational Biology</i> , 2020, 16, e1008538.	1.5	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.	1.5	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.	1.4	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.	2.5	14
61	Novel Screening Method Identifies PI3K \pm , mTOR, and IGF1R as Key Kinases Regulating Cardiomyocyte Survival. Journal of the American Heart Association, 2019, 8, e013018.	1.6	4
62	Genome-wide off-targets of drugs: risks and opportunities. Cell Biology and Toxicology, 2019, 35, 485-487.	2.4	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.	5.8	240
65	DNMT Inhibitors Increase Methylation in the Cancer Genome. Frontiers in Pharmacology, 2019, 10, 385.	1.6	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.	2.5	34
67	Pharmacological reactivation of MYC-dependent apoptosis induces susceptibility to anti-PD-1 immunotherapy. Nature Communications, 2019, 10, 620.	5.8	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, .	1.0	0
70	JAK/STAT-Activating Genomic Alterations Are a Hallmark of T-PLL. Cancers, 2019, 11, 1833.	1.7	38
71	Prediction of drug combination effects with a minimal set of experiments. Nature Machine Intelligence, 2019, 1, 568-577.	8.3	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.	0.4	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.	0.4	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.	0.4	60
79	Combined ASRGL1 and p53 immunohistochemistry as an independent predictor of survival in endometrioid endometrial carcinoma. Gynecologic Oncology, 2018, 149, 173-180.	0.6	16
80	Aggressive natural killer-cell leukemia—mutational landscape and drug profiling highlight JAK-STAT signaling as therapeutic target. Nature Communications, 2018, 9, 1567.	5.8	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.	0.4	22
82	Methods for High-throughput Drug Combination Screening and Synergy Scoring. Methods in Molecular Biology, 2018, 1711, 351-398.	0.4	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.	2.5	124
84	Global proteomics profiling improves drug sensitivity prediction: results from a multi-omics, pan-cancer modeling approach. Bioinformatics, 2018, 34, 1353-1362.	1.8	56
85	Novel activities of safe-in-human broad-spectrum antiviral agents. Antiviral Research, 2018, 154, 174-182.	1.9	64
86	Improving the efficacy-safety balance of polypharmacology in multi-target drug discovery. Expert Opinion on Drug Discovery, 2018, 13, 179-192.	2.5	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.	1.9	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.	3.3	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, , .	3.2	25
90	PO-092 Inhibition of the mTORC1-pathway can feedback-activate H-RAS or K-RAS. ESMO Open, 2018, 3, A57.	2.0	0

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91	Adrenals Contribute to Growth of Castration-Resistant VCaP Prostate Cancer Xenografts. <i>American Journal of Pathology</i> , 2018, 188, 2890-2901.	1.9	17
92	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
93	Learning with multiple pairwise kernels for drug bioactivity prediction. <i>Bioinformatics</i> , 2018, 34, i509-i518.	1.8	51
94	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
95	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
96	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
97	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
98	Immune cell contexture in the bone marrow tumor microenvironment impacts therapy response in CML. <i>Leukemia</i> , 2018, 32, 1643-1656.	3.3	75
99	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
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. <i>Blood</i> , 2018, 132, 2743-2743.	0.6	0
105	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
106	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
107	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
108	Matched preclinical designs for improved translatability. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	2

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109	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
110	Early metabolic markers identify potential targets for the prevention of type 2 diabetes. <i>Diabetologia</i> , 2017, 60, 1740-1750.	2.9	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;71:838-40. <i>European Urology</i> , 2017, 72, e68-e69.	0.9	0
112	SynergyFinder: a web application for analyzing drug combination dose-response matrix data. <i>Bioinformatics</i> , 2017, 33, 2413-2415.	1.8	403
113	The inconvenience of data of convenience: computational research beyond post-mortem analyses. <i>Nature Methods</i> , 2017, 14, 937-938.	9.0	9
114	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
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.	2.9	19
116	Instability of LDL particles predicts future cardiovascular deaths. <i>Atherosclerosis</i> , 2017, 263, e12.	0.4	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.	3.6	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.	6.5	18
119	Enhanced sensitivity to glucocorticoids in cytarabine-resistant AML. <i>Leukemia</i> , 2017, 31, 1187-1195.	3.3	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.	1.1	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.	5.1	124
122	Antiviral Properties of Chemical Inhibitors of Cellular Anti-Apoptotic Bcl-2 Proteins. <i>Viruses</i> , 2017, 9, 271.	1.5	39
123	MediSyn: uncertainty-aware visualization of multiple biomedical datasets to support drug treatment selection. <i>BMC Bioinformatics</i> , 2017, 18, 393.	1.2	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.	1.8	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.	1.0	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.	0.6	1

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127	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
128	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
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. <i>Viruses</i> , 2016, 8, 269.	1.5	23
133	Consistency in drug response profiling. <i>Nature</i> , 2016, 540, E5-E6.	13.7	76
134	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
135	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
136	Drug response prediction by inferring pathway-response associations with kernelized Bayesian matrix factorization. <i>Bioinformatics</i> , 2016, 32, i455-i463.	1.8	87
137	Unstable LDL - Novel mechanism of atherogenesis and link to cardiovascular deaths. <i>Atherosclerosis</i> , 2016, 252, e208.	0.4	0
138	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
139	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
140	Optimized design and analysis of preclinical intervention studies <i>in vivo</i> . <i>Scientific Reports</i> , 2016, 6, 30723.	1.6	36
141	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
142	Transcriptional response networks for elucidating mechanisms of action of multitargeted agents. <i>Drug Discovery Today</i> , 2016, 21, 1063-1075.	3.2	28
143	Cancer stem cell drugs target K-ras signaling in a stemness context. <i>Oncogene</i> , 2016, 35, 5248-5262.	2.6	78
144	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

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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.	0.4	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.	0.9	53
147	CIP2A Promotes T-Cell Activation and Immune Response to <i>Listeria monocytogenes</i> Infection. <i>PLoS ONE</i> , 2016, 11, e0152996.	1.1	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.	0.6	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.	1.2	13
153	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
154	What is synergy? The SaarisekÅ agreement revisited. <i>Frontiers in Pharmacology</i> , 2015, 6, 181.	1.6	147
155	Toward more realistic drug-target interaction predictions. <i>Briefings in Bioinformatics</i> , 2015, 16, 325-337.	3.2	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.	5.2	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.	1.8	15
158	Impact of normalization methods on high-throughput screening data with high hit rates and drug testing with doseâ€™response data. <i>Bioinformatics</i> , 2015, 31, 3815-3821.	1.8	31
159	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
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.	6.2	22
161	Prediction of human population responses to toxic compounds by a collaborative competition. <i>Nature Biotechnology</i> , 2015, 33, 933-940.	9.4	88
162	MicroRNAâ€™135b regulates ERÎ±, AR and HIF1AN and affects breast and prostate cancer cell growth. <i>Molecular Oncology</i> , 2015, 9, 1287-1300.	2.1	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.	2.5	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.	1.9	485
165	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
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
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