

A Next Generation Connectivity Map: L1000 Platform a

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Repositioning Drugs for Systemic Lupus Erythematosus. , 2016, , 567-575.		2
2	Efficient Generation of Transcriptomic Profiles by Random Composite Measurements. <i>Cell</i> , 2017, 171, 1424-1436.e18.	13.5	95
3	l1kdeconv: an R package for peak calling analysis with LINCS L1000 data. <i>BMC Bioinformatics</i> , 2017, 18, 356.	1.2	14
4	Omics Advances in Ecotoxicology. <i>Environmental Science & Technology</i> , 2018, 52, 3842-3851.	4.6	123
5	From gene networks to drugs: systems pharmacology approaches for AUD. <i>Psychopharmacology</i> , 2018, 235, 1635-1662.	1.5	15
6	RASâ€™MAPK Reactivation Facilitates Acquired Resistance in <i>FGFR1</i>-Amplified Lung Cancer and Underlies a Rationale for Upfront FGFRâ€™MEK Blockade. <i>Molecular Cancer Therapeutics</i> , 2018, 17, 1526-1539.	1.9	39
7	Deep learning improves prediction of drugâ€™drug and drugâ€™food interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4304-E4311.	3.3	325
8	High-Throughput Gene Expression Profiles to Define Drug Similarity and Predict Compound Activity. <i>Assay and Drug Development Technologies</i> , 2018, 16, 162-176.	0.6	33
9	Pharmacogenomics and big genomic data: from lab to clinic and back again. <i>Human Molecular Genetics</i> , 2018, 27, R72-R78.	1.4	28
10	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	13.5	1,417
11	A Library of Phosphoproteomic and Chromatin Signatures for Characterizing Cellular Responses to Drug Perturbations. <i>Cell Systems</i> , 2018, 6, 424-443.e7.	2.9	68
12	Chemical probes and drug leads from advances in synthetic planning and methodology. <i>Nature Reviews Drug Discovery</i> , 2018, 17, 333-352.	21.5	182
13	L1000FWD: fireworks visualization of drug-induced transcriptomic signatures. <i>Bioinformatics</i> , 2018, 34, 2150-2152.	1.8	109
14	The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. <i>Cell Systems</i> , 2018, 6, 13-24.	2.9	327
15	Genome-Wide Expression Profiles Drive Discovery of Novel Compounds that Reduce Binge Drinking in Mice. <i>Neuropsychopharmacology</i> , 2018, 43, 1257-1266.	2.8	39
16	Drug repositioning: current approaches and their implications in the precision medicine era. <i>Expert Review of Precision Medicine and Drug Development</i> , 2018, 3, 49-61.	0.4	48
18	In silico cancer research towards 3R. <i>BMC Cancer</i> , 2018, 18, 408.	1.1	83
19	Multi-target drug repositioning by bipartite block-wise sparse multi-task learning. <i>BMC Systems Biology</i> , 2018, 12, 55.	3.0	8

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20	Emerging Approaches for the Identification of Protein Targets of Small Molecules - A Practitionersâ€™ Perspective. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 8504-8535.	2.9	55
21	InDePTH: detection of hub genes for developing gene expression networks under anticancer drug treatment. <i>Oncotarget</i> , 2018, 9, 29097-29111.	0.8	8
22	Systematic polypharmacology and drug repurposing via an integrated L1000-based Connectivity Map database mining. <i>Royal Society Open Science</i> , 2018, 5, 181321.	1.1	36
23	Predicting Small Molecule Potency to Inhibit Estrogen Receptors using Machine Learning and Deep Learning Approaches. , 2018, , .		1
24	Sustainable data and metadata management at the BD2K-LINCS Data Coordination and Integration Center. <i>Scientific Data</i> , 2018, 5, 180117.	2.4	22
25	Polypharmacology or Promiscuity? Structural Interactions of Resveratrol With Its Bandwagon of Targets. <i>Frontiers in Pharmacology</i> , 2018, 9, 1201.	1.6	35
26	Report: NIA workshop on translating genetic variants associated with longevity into drug targets. <i>GeroScience</i> , 2018, 40, 523-538.	2.1	5
27	BET Inhibition Improves NASH and Liver Fibrosis. <i>Scientific Reports</i> , 2018, 8, 17257.	1.6	27
28	Integrative bioinformatics identifies postnatal lead (Pb) exposure disrupts developmental cortical plasticity. <i>Scientific Reports</i> , 2018, 8, 16388.	1.6	13
29	Gene Expression Analyses in Breast Cancer: Sample Matters. <i>JNCI Cancer Spectrum</i> , 2018, 2, pky019.	1.4	0
30	Drug and disease signature integration identifies synergistic combinations in glioblastoma. <i>Nature Communications</i> , 2018, 9, 5315.	5.8	78
31	Genome-wide mega-analysis identifies 16 loci and highlights diverse biological mechanisms in the common epilepsies. <i>Nature Communications</i> , 2018, 9, 5269.	5.8	331
32	The Inner Ear Heat Shock Transcriptional Signature Identifies Compounds That Protect Against Aminoglycoside Ototoxicity. <i>Frontiers in Cellular Neuroscience</i> , 2018, 12, 445.	1.8	14
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39	Expression-based drug screening of neural progenitor cells from individuals with schizophrenia. <i>Nature Communications</i> , 2018, 9, 4412.	5.8	63
40	A Qualitative Modeling Approach for Whole Genome Prediction Using High-Throughput Toxicogenomics Data and Pathway-Based Validation. <i>Frontiers in Pharmacology</i> , 2018, 9, 1072.	1.6	6
41	Using Machine Learning to Predict Synergistic Antimalarial Compound Combinations With Novel Structures. <i>Frontiers in Pharmacology</i> , 2018, 9, 1096.	1.6	27
42	A Comparison of the TempO-Seq S1500+ Platform to RNA-Seq and Microarray Using Rat Liver Mode of Action Samples. <i>Frontiers in Genetics</i> , 2018, 9, 485.	1.1	51
43	Harnessing the biological complexity of Big Data from LINCS gene expression signatures. <i>PLoS ONE</i> , 2018, 13, e0201937.	1.1	9
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