

L1000CDS2: LINCS L1000 characteristic direction signa

Npj Systems Biology and Applications

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DOI: [10.1038/npjbsa.2016.15](https://doi.org/10.1038/npjbsa.2016.15)

Citation Report

#	ARTICLE	IF	CITATIONS
1	An open RNA-Seq data analysis pipeline tutorial with an example of reprocessing data from a recent Zika virus study. <i>F1000Research</i> , 2016, 5, 1574.	1.6	30
2	GEN3VA: aggregation and analysis of gene expression signatures from related studies. <i>BMC Bioinformatics</i> , 2016, 17, 461.	2.6	17
3	Concerted changes in transcriptional regulation of genes involved in DNA methylation, demethylation, and folate-mediated one-carbon metabolism pathways in the NCI-60 cancer cell line panel in response to cancer drug treatment. <i>Clinical Epigenetics</i> , 2016, 8, 73.	4.1	21
4	A review of connectivity map and computational approaches in pharmacogenomics. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw112.	6.5	182
5	Drug repositioning beyond the low-hanging fruits. <i>Current Opinion in Systems Biology</i> , 2017, 3, 95-102.	2.6	11
6	seqFISH Accurately Detects Transcripts in Single Cells and Reveals Robust Spatial Organization in the Hippocampus. <i>Neuron</i> , 2017, 94, 752-758.e1.	8.1	100
7	Common and cell-type specific responses to anti-cancer drugs revealed by high throughput transcript profiling. <i>Nature Communications</i> , 2017, 8, 1186.	12.8	78
8	Clustergrammer, a web-based heatmap visualization and analysis tool for high-dimensional biological data. <i>Scientific Data</i> , 2017, 4, 170151.	5.3	176
9	Reversal of cancer gene expression correlates with drug efficacy and reveals therapeutic targets. <i>Nature Communications</i> , 2017, 8, 16022.	12.8	151
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16	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.	6.2	327
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21	A meta-analysis portal for human breast cancer transcriptomics data: BreastCancerVis. , 2018, , .		0
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