Andrey Alexeyenko

List of Publications by Year
in descending order

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42
papers

3,203
citations

361296
20
h-index

276775
41
g-index

46
all docs

46
docs citations

46
times ranked

6994
citing authors

#	ARTICLE	IF	CITATIONS
1	EviCor: Interactive Web Platform for Exploration of Molecular Features and Response to Anti-cancer Drugs. Journal of Molecular Biology, 2022, 434, 167528.	2.0	4
2	Individualized discovery of rare cancer drivers in global network context. ELife, 2022, 11, .	2.8	3
3	Robust derivation of transplantable dopamine neurons from human pluripotent stem cells by timed retinoic acid delivery. Nature Communications, 2022, 13, .	5.8	9
4	A Shh/Gli-driven three-node timer motif controls temporal identity and fate of neural stem cells. Science Advances, 2020, 6, .	4.7	9
5	Prediction of response to anti-cancer drugs becomes robust via network integration of molecular data. Scientific Reports, 2019, 9, 2379.	1.6	11
6	Protein profiling and network enrichment analysis in individuals before and after the onset of rheumatoid arthritis. Arthritis Research and Therapy, 2019, 21, 288.	1.6	13
7	Protein profiling of fineâ€needle aspirates reveals subtypeâ€associated immune signatures and involvement of chemokines in breast cancer. Molecular Oncology, 2019, 13, 376-391.	2.1	28
8	Expression of scavenger receptor <scp>MARCO</scp> defines a targetable tumorâ€associated macrophage subset in nonâ€small cell lung cancer. International Journal of Cancer, 2018, 143, 1741-1752.	2.3	65
9	EviNet: a web platform for network enrichment analysis with flexible definition of gene sets. Nucleic Acids Research, 2018, 46, W163-W170.	6.5	22
10	Protein Expression in Tonsillar and Base of Tongue Cancer and in Relation to Human Papillomavirus (HPV) and Clinical Outcome. International Journal of Molecular Sciences, 2018, 19, 978.	1.8	13
11	A fineâ€needle aspirationâ€based protein signature discriminates benign from malignant breast lesions. Molecular Oncology, 2018, 12, 1415-1428.	2.1	15
12	Using Erlang in Research and Education in a Technical University. Computer Science, 2018, 19, 335.	0.4	0
13	RhoA knockout fibroblasts lose tumor-inhibitory capacity in vitro and promote tumor growth in vivo. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1413-E1421.	3.3	30
14	Spatially resolved transcriptome profiling in model plant species. Nature Plants, 2017, 3, 17061.	4.7	135
15	NEArender: an R package for functional interpretation of â€˜omicsâ€™ data via network enrichment analysis. BMC Bioinformatics, 2017, 18, 118.	1.2	16
16	The regulation of hydroxysteroid 17Î²-dehydrogenase type 1 and 2 gene expression in breast cancer cell lines by estradiol, dihydrotestosterone, microRNAs, and genes related to breast cancer. Oncotarget, 2017, 8, 62183-62194.	0.8	14
17	Genome-wide identification of Wig-1 mRNA targets by RIP-Seq analysis. Oncotarget, 2016, 7, 1895-1911.	0.8	14
18	Confrontation of fibroblasts with cancer cells in vitro: gene network analysis of transcriptome changes and differential capacity to inhibit tumor growth. Journal of Experimental and Clinical Cancer Research, 2015, 34, 62.	3.5	11

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19	Identification of Novel Epigenetic Markers of Prostate Cancer by NotI-Microarray Analysis. Disease Markers, 2015, 2015, 1-13.	0.6	41
20	Identifying and Assessing Interesting Subgroups in a Heterogeneous Population. BioMed Research International, 2015, 2015, 1-13.	0.9	3
21	Inhibition of tumor cell proliferation and motility by fibroblasts is both contact and soluble factor dependent. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17188-17193.	3.3	81
22	Distinguishing between driver and passenger mutations in individual cancer genomes by network enrichment analysis. BMC Bioinformatics, 2014, 15, 308.	1.2	68
23	An international effort towards developing standards for best practices in analysis, interpretation and reporting of clinical genome sequencing results in the CLARITY Challenge. Genome Biology, 2014, 15, R53.	13.9	101
24	Efficient de novo assembly of large and complex genomes by massively parallel sequencing of Fosmid pools. BMC Genomics, 2014, 15, 439.	1.2	6
25	MGclus: network clustering employing shared neighbors. Molecular BioSystems, 2013, 9, 1670.	2.9	12
26	The Norway spruce genome sequence and conifer genome evolution. Nature, 2013, 497, 579-584.	13.7	1,303
27	Statistical Assessment of Crosstalk Enrichment between Gene Groups in Biological Networks. PLoS ONE, 2013, 8, e54945.	1.1	34
28	Comparative interactomics with Funcoup 2.0. Nucleic Acids Research, 2012, 40, D821-D828.	6.5	49
29	Network enrichment analysis: extension of gene-set enrichment analysis to gene networks. BMC Bioinformatics, 2012, 13, 226.	1.2	102
30	Comprehensive analysis of the genome transcriptome and proteome landscapes of three tumor cell lines. Genome Medicine, 2012, 4, 86.	3.6	37
31	Network Analysis of Functional Genomics Data: Application to Avian Sex-Biased Gene Expression. Scientific World Journal, The, 2012, 2012, 1-10.	0.8	2
32	Novel Genes and Pathways Modulated by Syndecan-1: Implications for the Proliferation and Cell-Cycle Regulation of Malignant Mesothelioma Cells. PLoS ONE, 2012, 7, e48091.	1.1	41
33	Genetic Association of Sequence Variants Near AGER/NOTCH4 and Dementia. Journal of Alzheimer's Disease, 2011, 24, 475-484.	1.2	9
34	Analysis of lipid pathway genes indicates association of sequence variation near SREBF1/TOM1L2/ATPAF2 with dementia risk. Human Molecular Genetics, 2010, 19, 2068-2078.	1.4	45
35	Genome-wide pathway analysis implicates intracellular transmembrane protein transport in Alzheimer disease. Journal of Human Genetics, 2010, 55, 707-709.	1.1	50
36	Dynamic Zebrafish Interactome Reveals Transcriptional Mechanisms of Dioxin Toxicity. PLoS ONE, 2010, 5, e10465.	1.1	47

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37	Global networks of functional coupling in eukaryotes from comprehensive data integration. Genome Research, 2009, 19, 1107-1116.	2.4	137
38	High-Throughput In Vivo Analysis of Gene Expression in Caenorhabditis elegans. PLoS Biology, 2007, 5, e237.	2.6	346
39	Calcyon mRNA expression in the frontal-striatal circuitry and its relationship to vesicular processes and ADHD. Behavioral and Brain Functions, 2007, 3, 33.	1.4	20
40	Overview and comparison of ortholog databases. Drug Discovery Today: Technologies, 2006, 3, 137-143.	4.0	24
41	Chromosomal clustering of nuclear genes encoding mitochondrial and chloroplast proteins in Arabidopsis. Trends in Genetics, 2006, 22, 589-593.	2.9	6
42	Automatic clustering of orthologs and inparalogs shared by multiple proteomes. Bioinformatics, 2006, 22, e9-e15.	1.8	227