

# Andrey Alexeyenko

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1826827/publications.pdf>

Version: 2024-02-01

42  
papers

3,203  
citations

361045

20  
h-index

276539

41  
g-index

46  
all docs

46  
docs citations

46  
times ranked

6994  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Norway spruce genome sequence and conifer genome evolution. <i>Nature</i> , 2013, 497, 579-584.	13.7	1,303
2	High-Throughput In Vivo Analysis of Gene Expression in <i>Caenorhabditis elegans</i> . <i>PLoS Biology</i> , 2007, 5, e237.	2.6	346
3	Automatic clustering of orthologs and inparalogs shared by multiple proteomes. <i>Bioinformatics</i> , 2006, 22, e9-e15.	1.8	227
4	Global networks of functional coupling in eukaryotes from comprehensive data integration. <i>Genome Research</i> , 2009, 19, 1107-1116.	2.4	137
5	Spatially resolved transcriptome profiling in model plant species. <i>Nature Plants</i> , 2017, 3, 17061.	4.7	135
6	Network enrichment analysis: extension of gene-set enrichment analysis to gene networks. <i>BMC Bioinformatics</i> , 2012, 13, 226.	1.2	102
7	An international effort towards developing standards for best practices in analysis, interpretation and reporting of clinical genome sequencing results in the CLARITY Challenge. <i>Genome Biology</i> , 2014, 15, R53.	13.9	101
8	Inhibition of tumor cell proliferation and motility by fibroblasts is both contact and soluble factor dependent. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17188-17193.	3.3	81
9	Distinguishing between driver and passenger mutations in individual cancer genomes by network enrichment analysis. <i>BMC Bioinformatics</i> , 2014, 15, 308.	1.2	68
10	Expression of scavenger receptor <i>MARCO</i> defines a targetable tumor-associated macrophage subset in non-small cell lung cancer. <i>International Journal of Cancer</i> , 2018, 143, 1741-1752.	2.3	65
11	Genome-wide pathway analysis implicates intracellular transmembrane protein transport in Alzheimer disease. <i>Journal of Human Genetics</i> , 2010, 55, 707-709.	1.1	50
12	Comparative interactomics with Funcoup 2.0. <i>Nucleic Acids Research</i> , 2012, 40, D821-D828.	6.5	49
13	Dynamic Zebrafish Interactome Reveals Transcriptional Mechanisms of Dioxin Toxicity. <i>PLoS ONE</i> , 2010, 5, e10465.	1.1	47
14	Analysis of lipid pathway genes indicates association of sequence variation near <i>SREBF1/TOM1L2/ATPAF2</i> with dementia risk. <i>Human Molecular Genetics</i> , 2010, 19, 2068-2078.	1.4	45
15	Identification of Novel Epigenetic Markers of Prostate Cancer by NotI-Microarray Analysis. <i>Disease Markers</i> , 2015, 2015, 1-13.	0.6	41
16	Novel Genes and Pathways Modulated by Syndecan-1: Implications for the Proliferation and Cell-Cycle Regulation of Malignant Mesothelioma Cells. <i>PLoS ONE</i> , 2012, 7, e48091.	1.1	41
17	Comprehensive analysis of the genome transcriptome and proteome landscapes of three tumor cell lines. <i>Genome Medicine</i> , 2012, 4, 86.	3.6	37
18	Statistical Assessment of Crosstalk Enrichment between Gene Groups in Biological Networks. <i>PLoS ONE</i> , 2013, 8, e54945.	1.1	34

#	ARTICLE	IF	CITATIONS
19	RhoA knockout fibroblasts lose tumor-inhibitory capacity in vitro and promote tumor growth in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1413-E1421.	3.3	30
20	Protein profiling of fineâ€needle aspirates reveals subtypeâ€associated immune signatures and involvement of chemokines in breast cancer. <i>Molecular Oncology</i> , 2019, 13, 376-391.	2.1	28
21	Overview and comparison of ortholog databases. <i>Drug Discovery Today: Technologies</i> , 2006, 3, 137-143.	4.0	24
22	EviNet: a web platform for network enrichment analysis with flexible definition of gene sets. <i>Nucleic Acids Research</i> , 2018, 46, W163-W170.	6.5	22
23	Calcyon mRNA expression in the frontal-striatal circuitry and its relationship to vesicular processes and ADHD. <i>Behavioral and Brain Functions</i> , 2007, 3, 33.	1.4	20
24	NEArender: an R package for functional interpretation of â€omicsâ€™ data via network enrichment analysis. <i>BMC Bioinformatics</i> , 2017, 18, 118.	1.2	16
25	A fineâ€needle aspirationâ€based protein signature discriminates benign from malignant breast lesions. <i>Molecular Oncology</i> , 2018, 12, 1415-1428.	2.1	15
26	Genome-wide identification of Wig-1 mRNA targets by RIP-Seq analysis. <i>Oncotarget</i> , 2016, 7, 1895-1911.	0.8	14
27	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. <i>Oncotarget</i> , 2017, 8, 62183-62194.	0.8	14
28	Protein Expression in Tonsillar and Base of Tongue Cancer and in Relation to Human Papillomavirus (HPV) and Clinical Outcome. <i>International Journal of Molecular Sciences</i> , 2018, 19, 978.	1.8	13
29	Protein profiling and network enrichment analysis in individuals before and after the onset of rheumatoid arthritis. <i>Arthritis Research and Therapy</i> , 2019, 21, 288.	1.6	13
30	MGclus: network clustering employing shared neighbors. <i>Molecular BioSystems</i> , 2013, 9, 1670.	2.9	12
31	Confrontation of fibroblasts with cancer cells in vitro: gene network analysis of transcriptome changes and differential capacity to inhibit tumor growth. <i>Journal of Experimental and Clinical Cancer Research</i> , 2015, 34, 62.	3.5	11
32	Prediction of response to anti-cancer drugs becomes robust via network integration of molecular data. <i>Scientific Reports</i> , 2019, 9, 2379.	1.6	11
33	Genetic Association of Sequence Variants Near AGER/NOTCH4 and Dementia. <i>Journal of Alzheimer's Disease</i> , 2011, 24, 475-484.	1.2	9
34	A Shh/Gli-driven three-node timer motif controls temporal identity and fate of neural stem cells. <i>Science Advances</i> , 2020, 6, .	4.7	9
35	Robust derivation of transplantable dopamine neurons from human pluripotent stem cells by timed retinoic acid delivery. <i>Nature Communications</i> , 2022, 13, .	5.8	9
36	Chromosomal clustering of nuclear genes encoding mitochondrial and chloroplast proteins in Arabidopsis. <i>Trends in Genetics</i> , 2006, 22, 589-593.	2.9	6

#	ARTICLE	IF	CITATIONS
37	Efficient de novo assembly of large and complex genomes by massively parallel sequencing of Fosmid pools. BMC Genomics, 2014, 15, 439.	1.2	6
38	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
39	Identifying and Assessing Interesting Subgroups in a Heterogeneous Population. BioMed Research International, 2015, 2015, 1-13.	0.9	3
40	Individualized discovery of rare cancer drivers in global network context. ELife, 2022, 11, .	2.8	3
41	Network Analysis of Functional Genomics Data: Application to Avian Sex-Biased Gene Expression. Scientific World Journal, The, 2012, 2012, 1-10.	0.8	2
42	Using Erlang in Research and Education in a Technical University. Computer Science, 2018, 19, 335.	0.4	0