

Steven Ge

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

5,365
citations

257101

24
h-index

214527

47
g-index

56
all docs

56
docs citations

56
times ranked

8117
citing authors

#	ARTICLE	IF	CITATIONS
1	ShinyGO: a graphical gene-set enrichment tool for animals and plants. <i>Bioinformatics</i> , 2020, 36, 2628-2629.	1.8	1,793
2	iDEP: an integrated web application for differential expression and pathway analysis of RNA-Seq data. <i>BMC Bioinformatics</i> , 2018, 19, 534.	1.2	803
3	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. <i>Nature Biotechnology</i> , 2010, 28, 827-838.	9.4	795
4	Identification and characterization of lin-28 homolog B (LIN28B) in human hepatocellular carcinoma. <i>Gene</i> , 2006, 384, 51-61.	1.0	272
5	Interpreting expression profiles of cancers by genome-wide survey of breadth of expression in normal tissues. <i>Genomics</i> , 2005, 86, 127-141.	1.3	230
6	Vascular Endothelial Growth Factor- and Thrombin-induced Termination Factor, Down Syndrome Critical Region-1, Attenuates Endothelial Cell Proliferation and Angiogenesis. <i>Journal of Biological Chemistry</i> , 2004, 279, 50537-50554.	1.6	207
7	2.45 GHz radiofrequency fields alter gene expression in cultured human cells. <i>FEBS Letters</i> , 2005, 579, 4829-4836.	1.3	79
8	Atomistic analysis of the field-ion microscopy image of Fe ₃ Al. <i>Physical Review B</i> , 1998, 57, 14203-14208.	1.1	73
9	Implementation of H.264 encoder and decoder on personal computers. <i>Journal of Visual Communication and Image Representation</i> , 2006, 17, 509-532.	1.7	70
10	Gene Expression Profiles of Estrogen Receptor-Positive and Estrogen Receptor-Negative Breast Cancers Are Detectable in Histologically Normal Breast Epithelium. <i>Clinical Cancer Research</i> , 2011, 17, 236-246.	3.2	66
11	Genome-wide survey of interindividual differences of RNA stability in human lymphoblastoid cell lines. <i>Scientific Reports</i> , 2013, 3, 1318.	1.6	66
12	Selective Expression of a Subset of Neuronal Genes in Oligodendroglioma with Chromosome 1p Loss. <i>Brain Pathology</i> , 2004, 14, 34-42.	2.1	57
13	Exploratory bioinformatics investigation reveals importance of <i>cjunc</i> -DNA in early embryo development. <i>BMC Genomics</i> , 2017, 18, 200.	1.2	55
14	Selective field evaporation in field-ion microscopy for ordered alloys. <i>Journal of Applied Physics</i> , 1999, 85, 3488-3493.	1.1	52
15	Interatomic potentials between distinct atoms from first-principles calculation and lattice-inversion method. <i>Journal of Applied Physics</i> , 1997, 82, 578-582.	1.1	49
16	A large quantity of novel human antisense transcripts detected by LongSAGE. <i>Bioinformatics</i> , 2006, 22, 2475-2479.	1.8	49
17	Root isoflavonoids and hairy root transformation influence key bacterial taxa in the soybean rhizosphere. <i>Environmental Microbiology</i> , 2017, 19, 1391-1406.	1.8	42
18	Conserved expression of natural antisense transcripts in mammals. <i>BMC Genomics</i> , 2013, 14, 243.	1.2	40

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19	Cbf genes of the Fr-A2 allele are differentially regulated between long-term cold acclimated crown tissue of freeze-resistant and "susceptible, winter wheat mutant lines. <i>BMC Plant Biology</i> , 2009, 9, 34.	1.6	36
20	Elevated expression and potential roles of human Sp5, a member of Sp transcription factor family, in human cancers. <i>Biochemical and Biophysical Research Communications</i> , 2006, 340, 758-766.	1.0	35
21	Gene expression profiles in acute myeloid leukemia with common translocations using SAGE. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 1030-1035.	3.3	32
22	Genome-wide analysis of antisense transcription with Affymetrix exon array. <i>BMC Genomics</i> , 2008, 9, 27.	1.2	32
23	ATOH1 Promotes Leptomeningeal Dissemination and Metastasis of Sonic Hedgehog Subgroup Medulloblastomas. <i>Cancer Research</i> , 2017, 77, 3766-3777.	0.4	29
24	A cross disciplinary study of link decay and the effectiveness of mitigation techniques. <i>BMC Bioinformatics</i> , 2013, 14, S5.	1.2	28
25	Gene expression profile analysis of human hepatocellular carcinoma using SAGE and LongSAGE. <i>BMC Medical Genomics</i> , 2009, 2, 5.	0.7	27
26	AraPath: a knowledgebase for pathway analysis in Arabidopsis. <i>Bioinformatics</i> , 2012, 28, 2291-2292.	1.8	27
27	iDEP Web Application for RNA-Seq Data Analysis. <i>Methods in Molecular Biology</i> , 2021, 2284, 417-443.	0.4	27
28	Comparative analysis of methicillin-sensitive and resistant <i>Staphylococcus aureus</i> exposed to emodin based on proteomic profiling. <i>Biochemical and Biophysical Research Communications</i> , 2017, 494, 318-324.	1.0	19
29	Evaluating the impact of health awareness events on Google search frequency. <i>Preventive Medicine Reports</i> , 2019, 15, 100887.	0.8	19
30	Investigation of the Transcriptome of Prairie Cord Grass, a New Cellulosic Biomass Crop. <i>Plant Genome</i> , 2010, 3, .	1.6	17
31	Identification of metagenes and their Interactions through Large-scale Analysis of Arabidopsis Gene Expression Data. <i>BMC Genomics</i> , 2012, 13, 237.	1.2	13
32	SAGE detects microRNA precursors. <i>BMC Genomics</i> , 2006, 7, 285.	1.2	12
33	Hydrotropism in the primary roots of maize. <i>New Phytologist</i> , 2020, 226, 1796-1808.	3.5	11
34	Regulation of Gene Expression with Thyroid Hormone in Rats with Myocardial Infarction. <i>PLoS ONE</i> , 2012, 7, e40161.	1.1	11
35	Learning the parts of objects by auto-association. <i>Neural Networks</i> , 2002, 15, 285-295.	3.3	10
36	nCov2019: an R package for studying the COVID-19 coronavirus pandemic. <i>PeerJ</i> , 2021, 9, e11421.	0.9	10

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37	Annotating nonspecific SAGE tags with microarray data. <i>Genomics</i> , 2006, 87, 173-180.	1.3	7
38	Large-scale analysis of expression signatures reveals hidden links among diverse cellular processes. <i>BMC Systems Biology</i> , 2011, 5, 87.	3.0	7
39	Influence of estradiol on bovine trophectoderm and uterine gene transcripts around maternal recognition of pregnancy. <i>Biology of Reproduction</i> , 2021, 105, 381-392.	1.2	6
40	Early gene response of human brain microvascular endothelial cells to <i>Listeria monocytogenes</i> infection. <i>Canadian Journal of Microbiology</i> , 2011, 57, 441-446.	0.8	5
41	Influence of conceptus presence and preovulatory estradiol exposure on uterine gene transcripts and proteins around maternal recognition of pregnancy in beef cattle. <i>Molecular and Cellular Endocrinology</i> , 2022, 540, 111508.	1.6	5
42	Subfamily-specific differential contribution of individual monomers and the tether sequence to mouse L1 promoter activity. <i>Mobile DNA</i> , 2022, 13, 13.	1.3	5
43	Efficient algorithm for 2-D arithmetic Fourier transform. <i>IEEE Transactions on Signal Processing</i> , 1997, 45, 2136-2140.	3.2	4
44	PPIinfer: a Bioconductor package for inferring functionally related proteins using protein interaction networks. <i>F1000Research</i> , 0, 6, 1969.	0.8	4
45	Extending MapMan Ontology to Tobacco for Visualization of Gene Expression. <i>Dataset Papers in Biology</i> , 2013, 2013, 1-7.	0.5	4
46	Meta-Analysis of Gene Expression Signatures Reveals Hidden Links among Diverse Biological Processes in Arabidopsis. <i>PLoS ONE</i> , 2014, 9, e108567.	1.1	2
47	Identifying Nonspecific SAGE Tags by Context of Gene Expression. <i>Methods in Molecular Biology</i> , 2008, 387, 199-204.	0.4	2
48	PPIinfer: a Bioconductor package for inferring functionally related proteins using protein interaction networks. <i>F1000Research</i> , 0, 6, 1969.	0.8	2
49	ArraySearch: A Web-Based Genomic Search Engine. <i>Comparative and Functional Genomics</i> , 2012, 2012, 1-10.	2.0	1
50	Application of bioinformatics to analyze the expression of tissue-specific and housekeeping genes in cancer. , 0, , 20-34.		0