

Seungchan Kim

List of Publications by Year in descending order

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89
papers

7,376
citations

159585

30
h-index

110387

64
g-index

95
all docs

95
docs citations

95
times ranked

9799
citing authors

#	ARTICLE	IF	CITATIONS
1	Probabilistic Boolean networks: a rule-based uncertainty model for gene regulatory networks. <i>Bioinformatics</i> , 2002, 18, 261-274.	4.1	1,371
2	Identification of Distinct Basal and Luminal Subtypes of Muscle-Invasive Bladder Cancer with Different Sensitivities to Frontline Chemotherapy. <i>Cancer Cell</i> , 2014, 25, 152-165.	16.8	1,358
3	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736.	16.8	482
4	Molecular Dissection of Hyperdiploid Multiple Myeloma by Gene Expression Profiling. <i>Cancer Research</i> , 2007, 67, 2982-2989.	0.9	236
5	Gene expression profile in multiple sclerosis patients and healthy controls: identifying pathways relevant to disease. <i>Human Molecular Genetics</i> , 2003, 12, 2191-2199.	2.9	191
6	Identification of extracellular miRNA in human cerebrospinal fluid by next-generation sequencing. <i>Rna</i> , 2013, 19, 712-722.	3.5	182
7	Coefficient of determination in nonlinear signal processing. <i>Signal Processing</i> , 2000, 80, 2219-2235.	3.7	174
8	MicroRNA-328 is associated with (non-small) cell lung cancer (NSCLC) brain metastasis and mediates NSCLC migration. <i>International Journal of Cancer</i> , 2011, 129, 2621-2631.	5.1	154
9	Inference from Clustering with Application to Gene-Expression Microarrays. <i>Journal of Computational Biology</i> , 2002, 9, 105-126.	1.6	150
10	CAN MARKOV CHAIN MODELS MIMIC BIOLOGICAL REGULATION?. <i>Journal of Biological Systems</i> , 2002, 10, 337-357.	1.4	141
11	Total Extracellular Small RNA Profiles from Plasma, Saliva, and Urine of Healthy Subjects. <i>Scientific Reports</i> , 2017, 7, 44061.	3.3	136
12	Multivariate Measurement of Gene Expression Relationships. <i>Genomics</i> , 2000, 67, 201-209.	2.9	133
13	Growing genetic regulatory networks from seed genes. <i>Bioinformatics</i> , 2004, 20, 1241-1247.	4.1	107
14	General nonlinear framework for the analysis of gene interaction via multivariate expression arrays. <i>Journal of Biomedical Optics</i> , 2000, 5, 411.	2.6	104
15	Identification of combination gene sets for glioma classification. <i>Molecular Cancer Therapeutics</i> , 2002, 1, 1229-36.	4.1	87
16	Fuzzy c-means clustering with prior biological knowledge. <i>Journal of Biomedical Informatics</i> , 2009, 42, 74-81.	4.3	80
17	Strong Feature Sets from Small Samples. <i>Journal of Computational Biology</i> , 2002, 9, 127-146.	1.6	79
18	Systems Analysis of the Human Pulmonary Arterial Hypertension Lung Transcriptome. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2019, 60, 637-649.	2.9	76

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19	Adrenocortical carcinoma survival rates correlated to genomic copy number variants. <i>Molecular Cancer Therapeutics</i> , 2008, 7, 425-431.	4.1	72
20	Planning interventions in biological networks. <i>ACM Transactions on Intelligent Systems and Technology</i> , 2010, 1, 1-26.	4.5	62
21	miRNA Expression Profiling in Migrating Glioblastoma Cells: Regulation of Cell Migration and Invasion by miR-23b via Targeting of Pyk2. <i>PLoS ONE</i> , 2012, 7, e39818.	2.5	55
22	Uncovering the biology of multiple myeloma among African Americans: a comprehensive genomics approach. <i>Blood</i> , 2013, 121, 3147-3152.	1.4	53
23	Extracellular microRNAs in blood differentiate between ischaemic and haemorrhagic stroke subtypes. <i>Journal of Extracellular Vesicles</i> , 2020, 9, 1713540.	12.2	53
24	A Nonlinear Discrete Dynamical Model for Transcriptional Regulation: Construction and Properties. <i>Biophysical Journal</i> , 2004, 86, 1922-1945.	0.5	46
25	Microarray reveals differences in both tumors and vascular specific gene expression in de novo CD5+ and CD5- diffuse large B-cell lymphomas. <i>Cancer Research</i> , 2003, 63, 60-6.	0.9	46
26	Frataxin deficiency promotes endothelial senescence in pulmonary hypertension. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	38
27	Pathway Implications of Aberrant Global Methylation in Adrenocortical Cancer. <i>PLoS ONE</i> , 2016, 11, e0150629.	2.5	35
28	Editorial [Hot topic: Genomic Signal Processing: Part 1 (Guest Editors: E.R. Dougherty, X. Cai, Y. Huang,)] <i>Tj ETQq0 0 0 rgBT /Overlock 10</i>	1.6	33
29	Prospective Molecular Profiling of Canine Cancers Provides a Clinically Relevant Comparative Model for Evaluating Personalized Medicine (PMed) Trials. <i>PLoS ONE</i> , 2014, 9, e90028.	2.5	33
30	A method to reduce ancestry related germline false positives in tumor only somatic variant calling. <i>BMC Medical Genomics</i> , 2017, 10, 61.	1.5	31
31	Differential Response of Glioma Stem Cells to Arsenic Trioxide Therapy Is Regulated by MNK1 and mRNA Translation. <i>Molecular Cancer Research</i> , 2018, 16, 32-46.	3.4	29
32	EDDY: a novel statistical gene set test method to detect differential genetic dependencies. <i>Nucleic Acids Research</i> , 2014, 42, e60-e60.	14.5	28
33	Multiscale, multimodal analysis of tumor heterogeneity in IDH1 mutant vs wild-type diffuse gliomas. <i>PLoS ONE</i> , 2019, 14, e0219724.	2.5	25
34	Multiresolution Analysis for Optimal Binary Filters. <i>Journal of Mathematical Imaging and Vision</i> , 2001, 14, 53-72.	1.3	22
35	Feature selection algorithms to find strong genes. <i>Pattern Recognition Letters</i> , 2005, 26, 1444-1453.	4.2	22
36	DNA Methylation in Multiple Myeloma Is Weakly Associated with Gene Transcription. <i>PLoS ONE</i> , 2012, 7, e52626.	2.5	20

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37	RNA sequencing of whole blood reveals early alterations in immune cells and gene expression in Parkinson's disease. <i>Nature Aging</i> , 2021, 1, 734-747.	11.6	18
38	Stochastic Transcriptional Regulatory Systems with Time Delays: A Mean-Field Approximation. <i>Journal of Computational Biology</i> , 2006, 13, 1049-1076.	1.6	17
39	Unsupervised morphological granulometric texture segmentation of digital mammograms. <i>Journal of Electronic Imaging</i> , 1999, 8, 65.	0.9	16
40	Genomic profiles of low-grade murine gliomas evolve during progression to glioblastoma. <i>Neuro-Oncology</i> , 2017, 19, 1237-1247.	1.2	16
41	Computational repurposing of therapeutic small molecules from cancer to pulmonary hypertension. <i>Science Advances</i> , 2021, 7, eabh3794.	10.3	16
42	Leveraging Spatial Variation in Tumor Purity for Improved Somatic Variant Calling of Archival Tumor Only Samples. <i>Frontiers in Oncology</i> , 2019, 9, 119.	2.8	15
43	Matrix stiffening induces a pathogenic QKI-miR-7-SRSF1 signaling axis in pulmonary arterial endothelial cells. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2021, 320, L726-L738.	2.9	13
44	Joint learning of logic relationships for studying protein function using phylogenetic profiles and the rosetta stone method. <i>IEEE Transactions on Signal Processing</i> , 2006, 54, 2427-2435.	5.3	12
45	An Algorithm to Learn Causal Relations Between Genes from Steady State Data: Simulation and Its Application to Melanoma Dataset. <i>Lecture Notes in Computer Science</i> , 2005, , 524-534.	1.3	11
46	AKT Pathway Genes Define 5 Prognostic Subgroups in Glioblastoma. <i>PLoS ONE</i> , 2014, 9, e100827.	2.5	11
47	Corrected small-sample estimation of the Bayes error. <i>Bioinformatics</i> , 2003, 19, 944-951.	4.1	9
48	Comparison of Gene Regulatory Networks via Steady-State Trajectories. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2007, 2007, 1-11.	1.4	8
49	Identifying MiRNA and Imaging Features Associated with Metastasis of Lung Cancer to the Brain. , 2009, , .		8
50	IDENTIFYING TARGETS FOR INTERVENTION BY ANALYZING BASINS OF ATTRACTION. , 2010, , 350-361.		8
51	SCUBE1 Controls BMP2-Relevant Pulmonary Endothelial Function. <i>JACC Basic To Translational Science</i> , 2020, 5, 1073-1092.	4.1	8
52	CLUSTERING CONTEXT-SPECIFIC GENE REGULATORY NETWORKS. , 2009, , 444-455.		7
53	KNOWLEDGE-ASSISTED APPROACH TO IDENTIFY PATHWAYS WITH DIFFERENTIAL DEPENDENCIES. , 2016, , .		7
54	DIFFERENTIAL PATHWAY DEPENDENCY DISCOVERY ASSOCIATED WITH DRUG RESPONSE ACROSS CANCER CELL LINES. , 2017, 22, 497-508.		7

#	ARTICLE	IF	CITATIONS
55	MINING MOLECULAR CONTEXTS OF CANCER VIA IN-SILICO CONDITIONING. , 2007, , .		7
56	KNOWLEDGE-ASSISTED APPROACH TO IDENTIFY PATHWAYS WITH DIFFERENTIAL DEPENDENCIES. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 33-44.	0.7	7
57	<title>Parallel computing methods for analyzing gene expression relationships</title>. , 2001, 4266, 213.		6
58	Quantization of Global Gene Expression Data. , 2006, , .		6
59	Threshold Logic Gene Regulatory Networks. , 2007, , .		6
60	Modeling of Gene Regulatory Network Dynamics Using Threshold Logic. Annals of the New York Academy of Sciences, 2009, 1158, 71-81.	3.8	5
61	Prediction of Pairwise Gene Interaction Using Threshold Logic. Annals of the New York Academy of Sciences, 2009, 1158, 276-286.	3.8	4
62	Biomarkers associated with metastasis of lung cancer to brain predict patient survival. International Journal of Data Mining and Bioinformatics, 2011, 5, 287.	0.1	4
63	Context-specific gene regulatory networks subdivide intrinsic subtypes of breast cancer. BMC Bioinformatics, 2011, 12, S3.	2.6	4
64	Initial Experience with Genomic Profiling of Heavily Pretreated Breast Cancers. Annals of Surgical Oncology, 2014, 21, 3216-3222.	1.5	4
65	Planning for Gene Regulatory Network Intervention. , 2006, , .		3
66	Germline copy number polymorphisms involving larger than 100 kb are uncommon in normal subjects. Prostate, 2007, 67, 227-233.	2.3	3
67	Mining molecular contexts of cancer via in-silico conditioning. Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2007, 6, 169-79.	0.4	3
68	Learning contextual gene set interaction networks of cancer with condition specificity. BMC Genomics, 2013, 14, 110.	2.8	2
69	Template-based intervention in Boolean network models of biological systems. Eurasip Journal on Bioinformatics and Systems Biology, 2014, 2014, 11.	1.4	2
70	Contextualization of drug-mediator relations using evidence networks. BMC Bioinformatics, 2017, 18, 252.	2.6	2
71	Context-specific gene regulations in cancer gene expression data. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2009, , 75-86.	0.7	2
72	<title>Fast run-length-based algorithm for one-dimensional flat opening</title>. , 1998, 3452, 158.		1

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73	Parallel Computation and Visualization Tools for Codetermination Analysis of Multivariate Gene Expression Relations. , 2003, , 227-240.		1
74	Parallel Computation and Visualization Tools for Codetermination Analysis of Multivariate Gene Expression Relations. , 2006, , 297-310.		1
75	Learning Context-Specific Gene Regulatory Networks via In-Silico Conditioning. , 2007, , .		1
76	Phenotype Classification Using Moment Features of Single-Cell Data. Cancer Informatics, 2018, 17, 117693511877170.	1.9	1
77	Probing glioblastoma and its microenvironment using single-nucleus and single-cell sequencing. , 2019, , .		1
78	<title>Time series inference from clustering</title>. , 2001, , .		0
79	<title>Finding robust linear expression-based classifiers</title>. , 2001, 4266, 207.		0
80	<title>Granulometric classifiers from small samples</title>. , 2002, 4667, 100.		0
81	Prioritizing Molecular Signatures by Combining ACGH and Global Gene Expression Profiling. , 2007, , .		0
82	Parallel programming to identify cellular contexts. , 2008, , .		0
83	GPU-Accelerated Differential Dependency Network Analysis. , 2018, , .		0
84	Extracellular Micrnas in Blood Differentiate Between Ischemic and Hemorrhagic Stroke Subtypes. SSRN Electronic Journal, 0, , .	0.4	0
85	MicroRNA 7 Regulates YAP/TAZ Signaling in Pulmonary Vascular Stiffness and Pulmonary Hypertension. FASEB Journal, 2019, 33, 681.8.	0.5	0
86	Multiscale, multimodal analysis of tumor heterogeneity in IDH1 mutant vs wild-type diffuse gliomas. , 2019, 14, e0219724.		0
87	Multiscale, multimodal analysis of tumor heterogeneity in IDH1 mutant vs wild-type diffuse gliomas. , 2019, 14, e0219724.		0
88	Multiscale, multimodal analysis of tumor heterogeneity in IDH1 mutant vs wild-type diffuse gliomas. , 2019, 14, e0219724.		0
89	Multiscale, multimodal analysis of tumor heterogeneity in IDH1 mutant vs wild-type diffuse gliomas. , 2019, 14, e0219724.		0