

Seungchan Kim

List of Publications by Year in descending order

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Version: 2024-02-01

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	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
2	Frataxin deficiency promotes endothelial senescence in pulmonary hypertension. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	38
3	Computational repurposing of therapeutic small molecules from cancer to pulmonary hypertension. <i>Science Advances</i> , 2021, 7, eabh3794.	10.3	16
4	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
5	SCUBE1 Controls BMPR2-Relevant Pulmonary Endothelial Function. <i>JACC Basic To Translational Science</i> , 2020, 5, 1073-1092.	4.1	8
6	Extracellular microRNAs in blood differentiate between ischaemic and haemorrhagic stroke subtypes. <i>Journal of Extracellular Vesicles</i> , 2020, 9, 1713540.	12.2	53
7	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
8	Probing glioblastoma and its microenvironment using single-nucleus and single-cell sequencing. , 2019, , .		1
9	Multiscale, multimodal analysis of tumor heterogeneity in IDH1 mutant vs wild-type diffuse gliomas. <i>PLoS ONE</i> , 2019, 14, e0219724.	2.5	25
10	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
11	MicroRNA 7 Regulates YAP/TAZ Signaling in Pulmonary Vascular Stiffness and Pulmonary Hypertension. <i>FASEB Journal</i> , 2019, 33, 681.8.	0.5	0
12	Multiscale, multimodal analysis of tumor heterogeneity in IDH1 mutant vs wild-type diffuse gliomas. , 2019, 14, e0219724.		0
13	Multiscale, multimodal analysis of tumor heterogeneity in IDH1 mutant vs wild-type diffuse gliomas. , 2019, 14, e0219724.		0
14	Multiscale, multimodal analysis of tumor heterogeneity in IDH1 mutant vs wild-type diffuse gliomas. , 2019, 14, e0219724.		0
15	Multiscale, multimodal analysis of tumor heterogeneity in IDH1 mutant vs wild-type diffuse gliomas. , 2019, 14, e0219724.		0
16	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
17	GPU-Accelerated Differential Dependency Network Analysis. , 2018, , .		0
18	Phenotype Classification Using Moment Features of Single-Cell Data. <i>Cancer Informatics</i> , 2018, 17, 117693511877170.	1.9	1

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19	Genomic profiles of low-grade murine gliomas evolve during progression to glioblastoma. <i>Neuro-Oncology</i> , 2017, 19, 1237-1247.	1.2	16
20	Total Extracellular Small RNA Profiles from Plasma, Saliva, and Urine of Healthy Subjects. <i>Scientific Reports</i> , 2017, 7, 44061.	3.3	136
21	DIFFERENTIAL PATHWAY DEPENDENCY DISCOVERY ASSOCIATED WITH DRUG RESPONSE ACROSS CANCER CELL LINES. , 2017, 22, 497-508.		7
22	Contextualization of drug-mediator relations using evidence networks. <i>BMC Bioinformatics</i> , 2017, 18, 252.	2.6	2
23	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
24	KNOWLEDGE-ASSISTED APPROACH TO IDENTIFY PATHWAYS WITH DIFFERENTIAL DEPENDENCIES. , 2016, , .		7
25	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736.	16.8	482
26	Pathway Implications of Aberrant Global Methylation in Adrenocortical Cancer. <i>PLoS ONE</i> , 2016, 11, e0150629.	2.5	35
27	KNOWLEDGE-ASSISTED APPROACH TO IDENTIFY PATHWAYS WITH DIFFERENTIAL DEPENDENCIES. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2016, 21, 33-44.	0.7	7
28	AKT Pathway Genes Define 5 Prognostic Subgroups in Glioblastoma. <i>PLoS ONE</i> , 2014, 9, e100827.	2.5	11
29	Initial Experience with Genomic Profiling of Heavily Pretreated Breast Cancers. <i>Annals of Surgical Oncology</i> , 2014, 21, 3216-3222.	1.5	4
30	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
31	Template-based intervention in Boolean network models of biological systems. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2014, 2014, 11.	1.4	2
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	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
34	Learning contextual gene set interaction networks of cancer with condition specificity. <i>BMC Genomics</i> , 2013, 14, 110.	2.8	2
35	Identification of extracellular miRNA in human cerebrospinal fluid by next-generation sequencing. <i>Rna</i> , 2013, 19, 712-722.	3.5	182
36	Uncovering the biology of multiple myeloma among African Americans: a comprehensive genomics approach. <i>Blood</i> , 2013, 121, 3147-3152.	1.4	53

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37	miRNA Expression Profiling in Migrating Glioblastoma Cells: Regulation of Cell Migration and Invasion by miR-23b via Targeting of Pyk2. PLoS ONE, 2012, 7, e39818.	2.5	55
38	DNA Methylation in Multiple Myeloma Is Weakly Associated with Gene Transcription. PLoS ONE, 2012, 7, e52626.	2.5	20
39	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
40	Context-specific gene regulatory networks subdivide intrinsic subtypes of breast cancer. BMC Bioinformatics, 2011, 12, S3.	2.6	4
41	MicroRNA-328 is associated with (non-small) cell lung cancer (NSCLC) brain metastasis and mediates NSCLC migration. International Journal of Cancer, 2011, 129, 2621-2631.	5.1	154
42	IDENTIFYING TARGETS FOR INTERVENTION BY ANALYZING BASINS OF ATTRACTION. , 2010, , 350-361.		8
43	Planning interventions in biological networks. ACM Transactions on Intelligent Systems and Technology, 2010, 1, 1-26.	4.5	62
44	CLUSTERING CONTEXT-SPECIFIC GENE REGULATORY NETWORKS. , 2009, , 444-455.		7
45	Fuzzy c-means clustering with prior biological knowledge. Journal of Biomedical Informatics, 2009, 42, 74-81.	4.3	80
46	Modeling of Gene Regulatory Network Dynamics Using Threshold Logic. Annals of the New York Academy of Sciences, 2009, 1158, 71-81.	3.8	5
47	Prediction of Pairwise Gene Interaction Using Threshold Logic. Annals of the New York Academy of Sciences, 2009, 1158, 276-286.	3.8	4
48	Identifying MiRNA and Imaging Features Associated with Metastasis of Lung Cancer to the Brain. , 2009, , .		8
49	Editorial [Hot topic: Genomic Signal Processing: Part 1 (Guest Editors: E.R. Dougherty, X. Cai, Y. Huang,)] Tj ETQq1 1.0.784314.rgBT /C 1.6 33		
50	Context-specific gene regulations in cancer gene expression data. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2009, , 75-86.	0.7	2
51	Parallel programming to identify cellular contexts. , 2008, , .		0
52	Adrenocortical carcinoma survival rates correlated to genomic copy number variants. Molecular Cancer Therapeutics, 2008, 7, 425-431.	4.1	72
53	Molecular Dissection of Hyperdiploid Multiple Myeloma by Gene Expression Profiling. Cancer Research, 2007, 67, 2982-2989.	0.9	236
54	Comparison of Gene Regulatory Networks via Steady-State Trajectories. Eurasip Journal on Bioinformatics and Systems Biology, 2007, 2007, 1-11.	1.4	8

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55	Threshold Logic Gene Regulatory Networks. , 2007, , .		6
56	Learning Context-Specific Gene Regulatory Networks via In-Silico Conditioning. , 2007, , .		1
57	Prioritizing Molecular Signatures by Combining ACGH and Global Gene Expression Profiling. , 2007, , .		0
58	Germline copy number polymorphisms involving larger than 100 kb are uncommon in normal subjects. Prostate, 2007, 67, 227-233.	2.3	3
59	MINING MOLECULAR CONTEXTS OF CANCER VIA IN-SILICO CONDITIONING. , 2007, , .		7
60	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
61	Planning for Gene Regulatory Network Intervention. , 2006, , .		3
62	Parallel Computation and Visualization Tools for Codetermination Analysis of Multivariate Gene Expression Relations. , 2006, , 297-310.		1
63	Joint learning of logic relationships for studying protein function using phylogenetic profiles and the rosetta stone method. IEEE Transactions on Signal Processing, 2006, 54, 2427-2435.	5.3	12
64	Stochastic Transcriptional Regulatory Systems with Time Delays: A Mean-Field Approximation. Journal of Computational Biology, 2006, 13, 1049-1076.	1.6	17
65	Quantization of Global Gene Expression Data. , 2006, , .		6
66	Feature selection algorithms to find strong genes. Pattern Recognition Letters, 2005, 26, 1444-1453.	4.2	22
67	An Algorithm to Learn Causal Relations Between Genes from Steady State Data: Simulation and Its Application to Melanoma Dataset. Lecture Notes in Computer Science, 2005, , 524-534.	1.3	11
68	Growing genetic regulatory networks from seed genes. Bioinformatics, 2004, 20, 1241-1247.	4.1	107
69	A Nonlinear Discrete Dynamical Model for Transcriptional Regulation: Construction and Properties. Biophysical Journal, 2004, 86, 1922-1945.	0.5	46
70	Gene expression profile in multiple sclerosis patients and healthy controls: identifying pathways relevant to disease. Human Molecular Genetics, 2003, 12, 2191-2199.	2.9	191
71	Corrected small-sample estimation of the Bayes error. Bioinformatics, 2003, 19, 944-951.	4.1	9
72	Parallel Computation and Visualization Tools for Codetermination Analysis of Multivariate Gene Expression Relations. , 2003, , 227-240.		1

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73	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
74	<title>Granulometric classifiers from small samples</title>. , 2002, 4667, 100.		0
75	Probabilistic Boolean networks: a rule-based uncertainty model for gene regulatory networks. <i>Bioinformatics</i> , 2002, 18, 261-274.	4.1	1,371
76	CAN MARKOV CHAIN MODELS MIMIC BIOLOGICAL REGULATION?. <i>Journal of Biological Systems</i> , 2002, 10, 337-357.	1.4	141
77	Strong Feature Sets from Small Samples. <i>Journal of Computational Biology</i> , 2002, 9, 127-146.	1.6	79
78	Inference from Clustering with Application to Gene-Expression Microarrays. <i>Journal of Computational Biology</i> , 2002, 9, 105-126.	1.6	150
79	Identification of combination gene sets for glioma classification. <i>Molecular Cancer Therapeutics</i> , 2002, 1, 1229-36.	4.1	87
80	<title>Parallel computing methods for analyzing gene expression relationships</title>. , 2001, 4266, 213.		6
81	<title>Time series inference from clustering</title>. , 2001, , .		0
82	<title>Finding robust linear expression-based classifiers</title>. , 2001, 4266, 207.		0
83	Multiresolution Analysis for Optimal Binary Filters. <i>Journal of Mathematical Imaging and Vision</i> , 2001, 14, 53-72.	1.3	22
84	Coefficient of determination in nonlinear signal processing. <i>Signal Processing</i> , 2000, 80, 2219-2235.	3.7	174
85	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
86	Multivariate Measurement of Gene Expression Relationships. <i>Genomics</i> , 2000, 67, 201-209.	2.9	133
87	Unsupervised morphological granulometric texture segmentation of digital mammograms. <i>Journal of Electronic Imaging</i> , 1999, 8, 65.	0.9	16
88	<title>Fast run-length-based algorithm for one-dimensional flat opening</title>. , 1998, 3452, 158.		1
89	Extracellular Micrnas in Blood Differentiate Between Ischemic and Hemorrhagic Stroke Subtypes. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0