Yoo-Ah Kim

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11556537/publications.pdf

Version: 2024-02-01

471371 395590 44 1,488 17 33 citations h-index g-index papers 49 49 49 2200 all docs docs citations times ranked citing authors

#	Article	IF	CITATIONS
1	Mutational Signatures: From Methods to Mechanisms. Annual Review of Biomedical Data Science, 2021, 4, 189-206.	2.8	19
2	RepairSig: Deconvolution of DNA damage and repair contributions to the mutational landscape of cancer. Cell Systems, 2021, 12, 994-1003.e4.	2.9	6
3	The language of a virus. Science, 2021, 371, 233-234.	6.0	4
4	Network Module Detection to Decipher Heterogeneity of Cancer Mutations. , 2021, , 151-166.		0
5	Identifying Drug Sensitivity Subnetworks with NETPHIX. IScience, 2020, 23, 101619.	1.9	5
6	Network-based approaches elucidate differences within APOBEC and clock-like signatures in breast cancer. Genome Medicine, 2020, 12, 52.	3.6	20
7	Hidden Markov models lead to higher resolution maps of mutation signature activity in cancer. Genome Medicine, 2019, 11, 49.	3.6	22
8	WeSME: uncovering mutual exclusivity of cancer drivers and beyond. Bioinformatics, 2017, 33, 814-821.	1.8	79
9	BeWith: A Between-Within method to discover relationships between cancer modules via integrated analysis of mutual exclusivity, co-occurrence and functional interactions. PLoS Computational	1.5	38
	Biology, 2017, 13, e1005695.		
10	Biology, 2017, 13, e1005695. Data Migration., 2016, , 487-491.		0
10		1.5	O 51
	Data Migration., 2016, , 487-491. Understanding Genotype-Phenotype Effects in Cancer via Network Approaches. PLoS Computational	1.5 1.8	
11	Data Migration., 2016, , 487-491. Understanding Genotype-Phenotype Effects in Cancer via Network Approaches. PLoS Computational Biology, 2016, 12, e1004747. MEMCover: integrated analysis of mutual exclusivity and functional network reveals dysregulated		51
11 12	Data Migration., 2016, , 487-491. Understanding Genotype-Phenotype Effects in Cancer via Network Approaches. PLoS Computational Biology, 2016, 12, e1004747. MEMCover: integrated analysis of mutual exclusivity and functional network reveals dysregulated pathways across multiple cancer types. Bioinformatics, 2015, 31, i284-i292. Sex- and Tissue-Specific Functions of Drosophila Doublesex Transcription Factor Target Genes.	1.8	51 87
11 12 13	Data Migration., 2016, , 487-491. Understanding Genotype-Phenotype Effects in Cancer via Network Approaches. PLoS Computational Biology, 2016, 12, e1004747. MEMCover: integrated analysis of mutual exclusivity and functional network reveals dysregulated pathways across multiple cancer types. Bioinformatics, 2015, 31, i284-i292. Sex- and Tissue-Specific Functions of Drosophila Doublesex Transcription Factor Target Genes. Developmental Cell, 2014, 31, 761-773. Delay monitoring for wireless sensor networks: An architecture using air sniffers. Ad Hoc Networks,	1.8 3.1	51 87 122
11 12 13	Data Migration., 2016, , 487-491. Understanding Genotype-Phenotype Effects in Cancer via Network Approaches. PLoS Computational Biology, 2016, 12, e1004747. MEMCover: integrated analysis of mutual exclusivity and functional network reveals dysregulated pathways across multiple cancer types. Bioinformatics, 2015, 31, i284-i292. Sex- and Tissue-Specific Functions of Drosophila Doublesex Transcription Factor Target Genes. Developmental Cell, 2014, 31, 761-773. Delay monitoring for wireless sensor networks: An architecture using air sniffers. Ad Hoc Networks, 2014, 13, 549-559. Comparative validation of the <i>D. melanogaster < i > modENCODE transcriptome annotation. Genome</i>	1.8 3.1 3.4	51 87 122 8
11 12 13 14	Data Migration., 2016, , 487-491. Understanding Genotype-Phenotype Effects in Cancer via Network Approaches. PLoS Computational Biology, 2016, 12, e1004747. MEMCover: integrated analysis of mutual exclusivity and functional network reveals dysregulated pathways across multiple cancer types. Bioinformatics, 2015, 31, i284-i292. Sex- and Tissue-Specific Functions of Drosophila Doublesex Transcription Factor Target Genes. Developmental Cell, 2014, 31, 761-773. Delay monitoring for wireless sensor networks: An architecture using air sniffers. Ad Hoc Networks, 2014, 13, 549-559. Comparative validation of the <i>D. melanogaster</i> i> modENCODE transcriptome annotation. Genome Research, 2014, 24, 1209-1223. Module cover - a new approach to genotype-phenotype studies. Pacific Symposium on Biocomputing	1.8 3.1 3.4 2.4	51 87 122 8

#	Article	IF	CITATIONS
19	Sniffer channel selection for monitoring wireless LANs. Computer Communications, 2012, 35, 1994-2003.	3.1	6
20	Fault-tolerant monitor placement for out-of-band wireless sensor network monitoring. Ad Hoc Networks, 2012, 10, 62-74.	3.4	19
21	Improved Approximation Algorithms for Data Migration. Algorithmica, 2012, 63, 347-362.	1.0	1
22	Bridging the Gap between Genotype and Phenotype via Network Approaches. Frontiers in Genetics, 2012, 3, 227.	1.1	38
23	MODULE COVER – A NEW APPROACH TO GENOTYPE-PHENOTYPE STUDIES. , 2012, , .		12
24	Data Migration in Heterogeneous Storage Systems. , 2011, , .		10
25	Modeling information flow in biological networks. Physical Biology, 2011, 8, 035012.	0.8	26
26	Identifying Causal Genes and Dysregulated Pathways in Complex Diseases. PLoS Computational Biology, 2011, 7, e1001095.	1.5	163
27	Broadcasting on Networks of Workstations. Algorithmica, 2010, 57, 848-868.	1.0	2
28	Network integration meets network dynamics. BMC Biology, 2010, 8, 48.	1.7	29
29	Delay monitoring for wireless sensor networks: An architecture using air sniffers. , 2009, , .		8
30	Sniffer Channel Selection for Monitoring Wireless LANs. Lecture Notes in Computer Science, 2009, , 489-498.	1.0	4
31	Meta Analysis of Microarray Data Using Gene Regulation Pathways. , 2008, , .		4
32	Data Migration. , 2008, , 217-220.		0
33	Designing Infrastructure-Based Overlay Networks for Delay-Sensitive Group Communications. , 2007, ,		5
34	Broadcasting in Heterogeneous Networks. Algorithmica, 2007, 48, 1-21.	1.0	14
35	Distributed Channel Assignment for Multi-radio Wireless Networks. , 2006, , .		80
36	A Computational Inference Framework for analyzing Gene Regulation Pathway using Microarray Data. , 2006, , .		0

#	Article	IF	CITATIONS
37	On generalized gossiping and broadcasting. Journal of Algorithms, 2006, 59, 81-106.	0.9	18
38	Data migration on parallel disks: Algorithms and evaluation. Algorithmica, 2006, 45, 137-158.	1.0	6
39	Data migration to minimize the total completion time. Journal of Algorithms, 2005, 55, 42-57.	0.9	25
40	Algorithms for Minimizing Response Time in Broadcast Scheduling. Algorithmica, 2004, 38, 597-608.	1.0	28
41	Equivalence of two linear programming relaxations for broadcast scheduling. Operations Research Letters, 2004, 32, 473-478.	0.5	7
42	Algorithms for Data Migration with Cloning. SIAM Journal on Computing, 2004, 33, 448-461.	0.8	27
43	Algorithms for data migration with cloning. , 2003, , .		42
44	Algorithms for Minimizing Response Time in Broadcast Scheduling. Lecture Notes in Computer Science, 2002, , 425-438.	1.0	13