## Yoo-Ah Kim

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11556537/publications.pdf Version: 2024-02-01



<u> Үоо-Ан Кім</u>

#	Article	IF	CITATIONS
1	Chapter 5: Network Biology Approach to Complex Diseases. PLoS Computational Biology, 2012, 8, e1002820.	1.5	239
2	Identifying Causal Genes and Dysregulated Pathways in Complex Diseases. PLoS Computational Biology, 2011, 7, e1001095.	1.5	163
3	Comparative validation of the <i>D. melanogaster</i> modENCODE transcriptome annotation. Genome Research, 2014, 24, 1209-1223.	2.4	147
4	Sex- and Tissue-Specific Functions of Drosophila Doublesex Transcription Factor Target Genes. Developmental Cell, 2014, 31, 761-773.	3.1	122
5	MEMCover: integrated analysis of mutual exclusivity and functional network reveals dysregulated pathways across multiple cancer types. Bioinformatics, 2015, 31, i284-i292.	1.8	87
6	Distributed Channel Assignment for Multi-radio Wireless Networks. , 2006, , .		80
7	WeSME: uncovering mutual exclusivity of cancer drivers and beyond. Bioinformatics, 2017, 33, 814-821.	1.8	79
8	Understanding Genotype-Phenotype Effects in Cancer via Network Approaches. PLoS Computational Biology, 2016, 12, e1004747.	1.5	51
9	Algorithms for data migration with cloning. , 2003, , .		42
10	Bridging the Gap between Genotype and Phenotype via Network Approaches. Frontiers in Genetics, 2012, 3, 227.	1.1	38
11	BeWith: A Between-Within method to discover relationships between cancer modules via integrated analysis of mutual exclusivity, co-occurrence and functional interactions. PLoS Computational Biology, 2017, 13, e1005695.	1.5	38
12	Approximation Algorithms for Data Broadcast in Wireless Networks. IEEE Transactions on Mobile Computing, 2012, 11, 1237-1248.	3.9	35
13	Network integration meets network dynamics. BMC Biology, 2010, 8, 48.	1.7	29
14	Algorithms for Minimizing Response Time in Broadcast Scheduling. Algorithmica, 2004, 38, 597-608.	1.0	28
15	Algorithms for Data Migration with Cloning. SIAM Journal on Computing, 2004, 33, 448-461.	0.8	27
16	Modeling information flow in biological networks. Physical Biology, 2011, 8, 035012.	0.8	26
17	Data migration to minimize the total completion time. Journal of Algorithms, 2005, 55, 42-57.	0.9	25
18	Hidden Markov models lead to higher resolution maps of mutation signature activity in cancer. Genome Medicine, 2019, 11, 49.	3.6	22

Үоо-Ан Кім

#	Article	IF	CITATIONS
19	Network-based approaches elucidate differences within APOBEC and clock-like signatures in breast cancer. Genome Medicine, 2020, 12, 52.	3.6	20
20	Fault-tolerant monitor placement for out-of-band wireless sensor network monitoring. Ad Hoc Networks, 2012, 10, 62-74.	3.4	19
21	Mutational Signatures: From Methods to Mechanisms. Annual Review of Biomedical Data Science, 2021, 4, 189-206.	2.8	19
22	On generalized gossiping and broadcasting. Journal of Algorithms, 2006, 59, 81-106.	0.9	18
23	Broadcasting in Heterogeneous Networks. Algorithmica, 2007, 48, 1-21.	1.0	14
24	Module cover - a new approach to genotype-phenotype studies. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2013, , 135-46.	0.7	14
25	Algorithms for Minimizing Response Time in Broadcast Scheduling. Lecture Notes in Computer Science, 2002, , 425-438.	1.0	13
26	MODULE COVER $\hat{a} \in \hat{A}$ NEW APPROACH TO GENOTYPE-PHENOTYPE STUDIES. , 2012, , .		12
27	Data Migration in Heterogeneous Storage Systems. , 2011, , .		10
28	Delay monitoring for wireless sensor networks: An architecture using air sniffers. , 2009, , .		8
29	Delay monitoring for wireless sensor networks: An architecture using air sniffers. Ad Hoc Networks, 2014, 13, 549-559.	3.4	8
30	Equivalence of two linear programming relaxations for broadcast scheduling. Operations Research Letters, 2004, 32, 473-478.	0.5	7
31	Data migration on parallel disks: Algorithms and evaluation. Algorithmica, 2006, 45, 137-158.	1.0	6
32	Sniffer channel selection for monitoring wireless LANs. Computer Communications, 2012, 35, 1994-2003.	3.1	6
33	RepairSig: Deconvolution of DNA damage and repair contributions to the mutational landscape of cancer. Cell Systems, 2021, 12, 994-1003.e4.	2.9	6
34	Designing Infrastructure-Based Overlay Networks for Delay-Sensitive Group Communications. , 2007, ,		5
35	Identifying Drug Sensitivity Subnetworks with NETPHIX. IScience, 2020, 23, 101619.	1.9	5
36	Meta Analysis of Microarray Data Using Gene Regulation Pathways. , 2008, , .		4

Үоо-Ан Кім

#	Article	IF	CITATIONS
37	The language of a virus. Science, 2021, 371, 233-234.	6.0	4
38	Sniffer Channel Selection for Monitoring Wireless LANs. Lecture Notes in Computer Science, 2009, , 489-498.	1.0	4
39	Broadcasting on Networks of Workstations. Algorithmica, 2010, 57, 848-868.	1.0	2
40	Improved Approximation Algorithms for Data Migration. Algorithmica, 2012, 63, 347-362.	1.0	1
41	A Computational Inference Framework for analyzing Gene Regulation Pathway using Microarray Data. , 2006, , .		0
42	Data Migration. , 2016, , 487-491.		0
43	Data Migration. , 2008, , 217-220.		0
44	Network Module Detection to Decipher Heterogeneity of Cancer Mutations. , 2021, , 151-166.		0