

Insuk Lee

List of Publications by Year in descending order

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Version: 2024-02-01

92
papers

7,776
citations

109321

35
h-index

56724

83
g-index

99
all docs

99
docs citations

99
times ranked

11009
citing authors

#	ARTICLE	IF	CITATIONS
1	HumanNet v3: an improved database of human gene networks for disease research. <i>Nucleic Acids Research</i> , 2022, 50, D632-D639.	14.5	53
2	The importance of enhancer methylation for epigenetic regulation of tumorigenesis in squamous lung cancer. <i>Experimental and Molecular Medicine</i> , 2022, 54, 12-22.	7.7	12
3	Viral coinfection promotes tuberculosis immunopathogenesis by type I IFN signaling-dependent impediment of Th1 cell pulmonary influx. <i>Nature Communications</i> , 2022, 13, .	12.8	11
4	Systems biology analysis identifies TNFRSF9 as a functional marker of tumor-infiltrating regulatory T-cell enabling clinical outcome prediction in lung cancer. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 860-868.	4.1	12
5	Chaperone-like protein DAY plays critical roles in photomorphogenesis. <i>Nature Communications</i> , 2021, 12, 4194.	12.8	5
6	Human reference gut microbiome catalog including newly assembled genomes from under-represented Asian metagenomes. <i>Genome Medicine</i> , 2021, 13, 134.	8.2	47
7	Genome-Wide Association Studies in <i>Arabidopsis thaliana</i> : Statistical Analysis and Network-Based Augmentation of Signals. <i>Methods in Molecular Biology</i> , 2021, 2200, 187-210.	0.9	3
8	Dysregulation of TFH-B-TRM lymphocyte cooperation is associated with unfavorable anti-PD-1 responses in EGFR-mutant lung cancer. <i>Nature Communications</i> , 2021, 12, 6068.	12.8	31
9	VirtualCytometry: a webserver for evaluating immune cell differentiation using single-cell RNA sequencing data. <i>Bioinformatics</i> , 2020, 36, 546-551.	4.1	8
10	Single-cell network biology for resolving cellular heterogeneity in human diseases. <i>Experimental and Molecular Medicine</i> , 2020, 52, 1798-1808.	7.7	72
11	Genome-wide identification of differentially methylated promoters and enhancers associated with response to anti-PD-1 therapy in non-small cell lung cancer. <i>Experimental and Molecular Medicine</i> , 2020, 52, 1550-1563.	7.7	99
12	Tumor-Infiltrating Regulatory T-cell Accumulation in the Tumor Microenvironment Is Mediated by IL33/ST2 Signaling. <i>Cancer Immunology Research</i> , 2020, 8, 1393-1406.	3.4	28
13	Single-cell ATAC sequencing analysis: From data preprocessing to hypothesis generation. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1429-1439.	4.1	91
14	Single-cell transcriptome analysis reveals TOX as a promoting factor for T cell exhaustion and a predictor for anti-PD-1 responses in human cancer. <i>Genome Medicine</i> , 2020, 12, 22.	8.2	98
15	BarleyNet: A Network-Based Functional Omics Analysis Server for Cultivated Barley, <i>Hordeum vulgare</i> L.. <i>Frontiers in Plant Science</i> , 2020, 11, 98.	3.6	17
16	Construction of Functional Protein Networks Using Domain Profile Associations. <i>Methods in Molecular Biology</i> , 2020, 2074, 35-44.	0.9	4
17	BiomeNet: a database for construction and analysis of functional interaction networks for any species with a sequenced genome. <i>Bioinformatics</i> , 2019, 36, 1584-1589.	4.1	6
18	Pathway-specific protein domains are predictive for human diseases. <i>PLoS Computational Biology</i> , 2019, 15, e1007052.	3.2	8

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19	Network Integrative Genomic and Transcriptomic Analysis of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Strains Identifies Genes for Antibiotic Resistance and Virulence. <i>MSystems</i> , 2019, 4, .	3.8	15
20	MaizeNet: a co-functional network for network-assisted systems genetics in <i>Zea mays</i> . <i>Plant Journal</i> , 2019, 99, 571-582.	5.7	22
21	HumanNet v2: human gene networks for disease research. <i>Nucleic Acids Research</i> , 2019, 47, D573-D580.	14.5	161
22	Cancer Gene Discovery by Network Analysis of Somatic Mutations Using the MUFFINN Server. <i>Methods in Molecular Biology</i> , 2019, 1907, 37-50.	0.9	1
23	NGSEA: Network-Based Gene Set Enrichment Analysis for Interpreting Gene Expression Phenotypes with Functional Gene Sets. <i>Molecules and Cells</i> , 2019, 42, 579-588.	2.6	13
24	A Genome-Scale Co-Functional Network of Genes Can Accurately Reconstruct Regulatory Circuits Controlled by Two-Component Signaling Systems. <i>Molecules and Cells</i> , 2019, 42, 166-174.	2.6	7
25	araGWAB: Network-based boosting of genome-wide association studies in <i>Arabidopsis thaliana</i> . <i>Scientific Reports</i> , 2018, 8, 2925.	3.3	21
26	Direct Conversion of Mouse Fibroblasts into Cholangiocyte Progenitor Cells. <i>Stem Cell Reports</i> , 2018, 10, 1522-1536.	4.8	11
27	TRRUST v2: an expanded reference database of human and mouse transcriptional regulatory interactions. <i>Nucleic Acids Research</i> , 2018, 46, D380-D386.	14.5	1,288
28	Network-based genetic investigation of virulence-associated phenotypes in methicillin-resistant <i>Staphylococcus aureus</i> . <i>Scientific Reports</i> , 2018, 8, 10796.	3.3	5
29	From sequencing data to gene functions: co-functional network approaches. <i>Animal Cells and Systems</i> , 2017, 21, 77-83.	2.2	27
30	WheatNet: a Genome-Scale Functional Network for Hexaploid Bread Wheat, <i>Triticum aestivum</i> . <i>Molecular Plant</i> , 2017, 10, 1133-1136.	8.3	29
31	Network-Based Gene Function Prediction in Mouse and Other Model Vertebrates Using MouseNet Server. <i>Methods in Molecular Biology</i> , 2017, 1611, 183-198.	0.9	3
32	GWAB: a web server for the network-based boosting of human genome-wide association data. <i>Nucleic Acids Research</i> , 2017, 45, W154-W161.	14.5	29
33	Construction of Functional Gene Networks Using Phylogenetic Profiles. <i>Methods in Molecular Biology</i> , 2017, 1526, 87-98.	0.9	10
34	AraNet: A Network Biology Server for <i>Arabidopsis thaliana</i> and Other Non-Model Plant Species. <i>Methods in Molecular Biology</i> , 2017, 1629, 225-238.	0.9	17
35	TomatoNet: A Genome-wide Co-functional Network for Unveiling Complex Traits of Tomato, a Model Crop for Fleshy Fruits. <i>Molecular Plant</i> , 2017, 10, 652-655.	8.3	18
36	COEXPEDIA: exploring biomedical hypotheses via co-expressions associated with medical subject headings (MeSH). <i>Nucleic Acids Research</i> , 2017, 45, D389-D396.	14.5	84

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37	SoyNet: a database of co-functional networks for soybean <i>Glycine max.</i> <i>Nucleic Acids Research</i> , 2017, 45, D1082-D1089.	14.5	56
38	Functional gene networks based on the gene neighborhood in metagenomes. <i>Animal Cells and Systems</i> , 2017, 21, 301-306.	2.2	10
39	Network perturbation by recurrent regulatory variants in cancer. <i>PLoS Computational Biology</i> , 2017, 13, e1005449.	3.2	5
40	Microvesicles from brain-extract-treated mesenchymal stem cells improve neurological functions in a rat model of ischemic stroke. <i>Scientific Reports</i> , 2016, 6, 33038.	3.3	84
41	Generation of Integration-free Induced Neural Stem Cells from Mouse Fibroblasts. <i>Journal of Biological Chemistry</i> , 2016, 291, 14199-14212.	3.4	24
42	MouseNet v2: a database of gene networks for studying the laboratory mouse and eight other model vertebrates. <i>Nucleic Acids Research</i> , 2016, 44, D848-D854.	14.5	40
43	Function-driven discovery of disease genes in zebrafish using an integrated genomics big data resource. <i>Nucleic Acids Research</i> , 2016, 44, gkw897.	14.5	24
44	Network-assisted investigation of virulence and antibiotic-resistance systems in <i>Pseudomonas aeruginosa</i> . <i>Scientific Reports</i> , 2016, 6, 26223.	3.3	28
45	A single gene of a commensal microbe affects host susceptibility to enteric infection. <i>Nature Communications</i> , 2016, 7, 11606.	12.8	31
46	Weighted mutual information analysis substantially improves domain-based functional network models. <i>Bioinformatics</i> , 2016, 32, 2824-2830.	4.1	20
47	MUFFINN: cancer gene discovery via network analysis of somatic mutation data. <i>Genome Biology</i> , 2016, 17, 129.	8.8	126
48	An integrated systems biology approach identifies positive cofactor 4 as a factor that increases reprogramming efficiency. <i>Nucleic Acids Research</i> , 2016, 44, 1203-1215.	14.5	20
49	Systematic comparison of variant calling pipelines using gold standard personal exome variants. <i>Scientific Reports</i> , 2015, 5, 17875.	3.3	284
50	TRRUST: a reference database of human transcriptional regulatory interactions. <i>Scientific Reports</i> , 2015, 5, 11432.	3.3	339
51	FlyNet: a versatile network prioritization server for the <i>Drosophila</i> community. <i>Nucleic Acids Research</i> , 2015, 43, W91-W97.	14.5	18
52	Modes of Interaction between Individuals Dominate the Topologies of Real World Networks. <i>PLoS ONE</i> , 2015, 10, e0121248.	2.5	4
53	Network-assisted genetic dissection of pathogenicity and drug resistance in the opportunistic human pathogenic fungus <i>Cryptococcus neoformans</i> . <i>Scientific Reports</i> , 2015, 5, 8767.	3.3	31
54	Network-assisted crop systems genetics: network inference and integrative analysis. <i>Current Opinion in Plant Biology</i> , 2015, 24, 61-70.	7.1	40

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55	Patterns of Metabolite Changes Identified from Large-Scale Gene Perturbations in Arabidopsis Using a Genome-Scale Metabolic Network. <i>Plant Physiology</i> , 2015, 167, 1685-1698.	4.8	55
56	Editorial overview: Genome studies and molecular genetics: data-driven approaches to genotype-to-phenotype studies in crops. <i>Current Opinion in Plant Biology</i> , 2015, 24, iv-vi.	7.1	1
57	AraNet v2: an improved database of co-functional gene networks for the study of Arabidopsis thaliana and 27 other nonmodel plant species. <i>Nucleic Acids Research</i> , 2015, 43, D996-D1002.	14.5	150
58	EcoliNet: a database of cofunctional gene network for Escherichia coli. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	3.0	31
59	RiceNet v2: an improved network prioritization server for rice genes. <i>Nucleic Acids Research</i> , 2015, 43, W122-W127.	14.5	95
60	Network-assisted approaches for human disease research. <i>Animal Cells and Systems</i> , 2015, 19, 231-235.	2.2	13
61	Pathway-Dependent Effectiveness of Network Algorithms for Gene Prioritization. <i>PLoS ONE</i> , 2015, 10, e0130589.	2.5	15
62	Co-Inheritance Analysis within the Domains of Life Substantially Improves Network Inference by Phylogenetic Profiling. <i>PLoS ONE</i> , 2015, 10, e0139006.	2.5	22
63	WormNet v3: a network-assisted hypothesis-generating server for Caenorhabditis elegans. <i>Nucleic Acids Research</i> , 2014, 42, W76-W82.	14.5	59
64	YeastNet v3: a public database of data-specific and integrated functional gene networks for <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2014, 42, D731-D736.	14.5	75
65	MORPHIN: a web tool for human disease research by projecting model organism biology onto a human integrated gene network. <i>Nucleic Acids Research</i> , 2014, 42, W147-W153.	14.5	16
66	Complementarity between distance- and probability-based methods of gene neighbourhood identification for pathway reconstruction. <i>Molecular BioSystems</i> , 2014, 10, 24-29.	2.9	25
67	JiffyNet: a web-based instant protein network modeler for newly sequenced species. <i>Nucleic Acids Research</i> , 2013, 41, W192-W197.	14.5	31
68	Network approaches to the genetic dissection of phenotypes in animals and humans. <i>Animal Cells and Systems</i> , 2013, 17, 75-79.	2.2	15
69	RIDDLE: Reflective diffusion and local extension reveal functional associations for unannotated gene sets via proximity in a gene network. <i>Genome Biology</i> , 2012, 13, R125.	9.6	16
70	Metabolomics as a Hypothesis-Generating Functional Genomics Tool for the Annotation of Arabidopsis thaliana Genes of Unknown Function. <i>Frontiers in Plant Science</i> , 2012, 3, 15.	3.6	82
71	Towards understanding how molecular networks evolve in plants. <i>Current Opinion in Plant Biology</i> , 2012, 15, 177-184.	7.1	61
72	Probabilistic functional gene societies. <i>Progress in Biophysics and Molecular Biology</i> , 2011, 106, 435-442.	2.9	10

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73	Systematic prediction of gene function in <i>Arabidopsis thaliana</i> using a probabilistic functional gene network. <i>Nature Protocols</i> , 2011, 6, 1429-1442.	12.0	41
74	Genetic dissection of the biotic stress response using a genome-scale gene network for rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 18548-18553.	7.1	170
75	Prioritizing candidate disease genes by network-based boosting of genome-wide association data. <i>Genome Research</i> , 2011, 21, 1109-1121.	5.5	646
76	Towards Establishment of a Rice Stress Response Interactome. <i>PLoS Genetics</i> , 2011, 7, e1002020.	3.5	199
77	Rational association of genes with traits using a genome-scale gene network for <i>Arabidopsis thaliana</i> . <i>Nature Biotechnology</i> , 2010, 28, 149-156.	17.5	332
78	Predicting genetic modifier loci using functional gene networks. <i>Genome Research</i> , 2010, 20, 1143-1153.	5.5	83
79	Assessment of effectiveness of the network-guided genetic screen. <i>Molecular BioSystems</i> , 2010, 6, 1803.	2.9	3
80	Rational Extension of the Ribosome Biogenesis Pathway Using Network-Guided Genetics. <i>PLoS Biology</i> , 2009, 7, e1000213.	5.6	156
81	Effects of Functional Bias on Supervised Learning of a Gene Network Model. <i>Methods in Molecular Biology</i> , 2009, 541, 463-475.	0.9	12
82	A single gene network accurately predicts phenotypic effects of gene perturbation in <i>Caenorhabditis elegans</i> . <i>Nature Genetics</i> , 2008, 40, 181-188.	21.4	284
83	Integrating Functional Genomics Data. <i>Methods in Molecular Biology</i> , 2008, 453, 267-278.	0.9	8
84	Network-guided genetic screening: building, testing and using gene networks to predict gene function. <i>Briefings in Functional Genomics & Proteomics</i> , 2008, 7, 217-227.	3.8	24
85	24 Bioinformatic Prediction of Yeast Gene Function. <i>Methods in Microbiology</i> , 2007, , 597-628.	0.8	4
86	Broad network-based predictability of <i>Saccharomyces cerevisiae</i> gene loss-of-function phenotypes. <i>Genome Biology</i> , 2007, 8, R258.	9.6	87
87	An Improved, Bias-Reduced Probabilistic Functional Gene Network of Baker's Yeast, <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2007, 2, e988.	2.5	174
88	A high-accuracy consensus map of yeast protein complexes reveals modular nature of gene essentiality. <i>BMC Bioinformatics</i> , 2007, 8, 236.	2.6	239
89	Protein interaction networks from yeast to human. <i>Current Opinion in Structural Biology</i> , 2004, 14, 292-299.	5.7	323
90	A Probabilistic Functional Network of Yeast Genes. <i>Science</i> , 2004, 306, 1555-1558.	12.6	640

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91	The Conserved CA/TG motif at Mu termini: T Specifies Stable Transpososome Assembly. <i>Journal of Molecular Biology</i> , 2003, 330, 261-275.	4.2	16
92	Patterns of sequence conservation at termini of long terminal repeat (LTR) retrotransposons and DNA transposons in the human genome: lessons from phage Mu. <i>Nucleic Acids Research</i> , 2003, 31, 4531-4540.	14.5	10