

Kyungsook Han

List of Publications by Year in descending order

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76
papers

1,437
citations

304743

22
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330143

37
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78
all docs

78
docs citations

78
times ranked

1676
citing authors

#	ARTICLE	IF	CITATIONS
1	A New Approach to Deriving Prognostic Gene Pairs From Cancer Patient-Specific Gene Correlation Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1267-1276.	3.0	4
2	Constructing a Cancer Patient-Specific Network Based on Second-Order Partial Correlations of Gene Expression and DNA Methylation. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, PP, 1-1.	3.0	1
3	Predicting lymph node metastasis and prognosis of individual cancer patients based on miRNA-mediated RNA interactions. BMC Medical Genomics, 2022, 15, 87.	1.5	3
4	Comparative Analysis of Gene Correlation Networks of Breast Cancer Patients Based on Mutations in TP53. Biomolecules, 2022, 12, 979.	4.0	1
5	Multi-Scale Capsule Network for Predicting DNA-Protein Binding Sites. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1793-1800.	3.0	11
6	Predicting TF-DNA Binding Motifs from ChIP-seq Datasets Using the Bag-Based Classifier Combined With a Multi-Fold Learning Scheme. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1743-1751.	3.0	3
7	Predicting Interactions Between Pathogen and Human Proteins Based on the Relation Between Sequence Length and Amino Acid Composition. Current Bioinformatics, 2021, 16, 799-806.	1.5	1
8	GeneCoNet: A web application server for constructing cancer patient-specific gene correlation networks with prognostic gene pairs. Computer Methods and Programs in Biomedicine, 2021, 212, 106465.	4.7	0
9	Constructive Prediction of Potential RNA Aptamers for a Protein Target. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 1476-1482.	3.0	9
10	A Deep Learning Model for RNA-Protein Binding Preference Prediction based on Hierarchical LSTM and Attention Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, PP, 1-1.	3.0	23
11	Constructing cancer patient-specific and group-specific gene networks with multi-omics data. BMC Medical Genomics, 2020, 13, 81.	1.5	10
12	Discovering protein-binding RNA motifs with a generative model of RNA sequences. Computational Biology and Chemistry, 2020, 84, 107171.	2.3	6
13	Predicting protein-binding sites in nucleic acids. , 2020, , 243-255.		0
14	Finding prognostic gene pairs for cancer from patient-specific gene networks. BMC Medical Genomics, 2019, 12, 179.	1.5	8
15	A generative model for constructing nucleic acid sequences binding to a protein. BMC Genomics, 2019, 20, 967.	2.8	10
16	Mutli-Features Prediction of Protein Translational Modification Sites. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1453-1460.	3.0	52
17	Sequence-Based Prediction of Putative Transcription Factor Binding Sites in DNA Sequences of Any Length. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1461-1469.	3.0	3
18	A generalized approach to predicting protein-protein interactions between virus and host. BMC Genomics, 2018, 19, 568.	2.8	41

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19	Predicting Interactions between Virus and Host Proteins Using Repeat Patterns and Composition of Amino Acids. <i>Journal of Healthcare Engineering</i> , 2018, 2018, 1-9.	1.9	35
20	Finding Protein-Binding Nucleic Acid Sequences Using a Long Short-Term Memory Neural Network. <i>Lecture Notes in Computer Science</i> , 2018, , 827-830.	1.3	0
21	Finding Potential RNA Aptamers for a Protein Target Using Sequence and Structure Features. <i>Lecture Notes in Computer Science</i> , 2018, , 888-892.	1.3	0
22	An improved method for predicting interactions between virus and human proteins. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1650024.	0.8	23
23	WIG1 is crucial for AGO2-mediated ACOT7 mRNA silencing via miRNA-dependent and -independent mechanisms. <i>Nucleic Acids Research</i> , 2017, 45, 6894-6910.	14.5	9
24	Data of protein-RNA binding sites. <i>Data in Brief</i> , 2017, 10, 561-563.	1.0	0
25	Predicting protein-binding regions in RNA using nucleotide profiles and compositions. <i>BMC Systems Biology</i> , 2017, 11, 16.	3.0	16
26	miRNA-Disease Association Prediction with Collaborative Matrix Factorization. <i>Complexity</i> , 2017, 2017, 1-9.	1.6	73
27	Predicting Transcription Factor Binding Sites in DNA Sequences Without Prior Knowledge. <i>Lecture Notes in Computer Science</i> , 2016, , 386-391.	1.3	1
28	PRIdictor: Protein-RNA Interaction predictor. <i>BioSystems</i> , 2016, 139, 17-22.	2.0	48
29	An efficient algorithm for planar drawing of RNA structures with pseudoknots of any type. <i>Journal of Bioinformatics and Computational Biology</i> , 2016, 14, 1650009.	0.8	1
30	PNImodeler: web server for inferring protein-binding nucleotides from sequence data. <i>BMC Genomics</i> , 2015, 16, S6.	2.8	16
31	Predicting protein-binding RNA nucleotides with consideration of binding partners. <i>Computer Methods and Programs in Biomedicine</i> , 2015, 120, 3-15.	4.7	6
32	Sequence-based prediction of protein-binding sites in DNA: Comparative study of two SVM models. <i>Computer Methods and Programs in Biomedicine</i> , 2014, 117, 158-167.	4.7	15
33	Prediction of Protein-Protein Interactions Based on Protein-Protein Correlation Using Least Squares Regression. <i>Current Protein and Peptide Science</i> , 2014, 15, 553-560.	1.4	103
34	PPISearchEngine: gene ontology-based search for protein-protein interactions. <i>Computer Methods in Biomechanics and Biomedical Engineering</i> , 2013, 16, 691-698.	1.6	2
35	Classification of diffusion tensor images for the early detection of Alzheimer's disease. <i>Computers in Biology and Medicine</i> , 2013, 43, 1313-1320.	7.0	40
36	Predicting protein-binding RNA nucleotides using the feature-based removal of data redundancy and the interaction propensity of nucleotide triplets. <i>Computers in Biology and Medicine</i> , 2013, 43, 1687-1697.	7.0	23

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37	ModuleSearch: finding functional modules in a protein-protein interaction network. Computer Methods in Biomechanics and Biomedical Engineering, 2012, 15, 691-699.	1.6	6
38	Prediction of protein-protein interactions between viruses and human by an SVM model. BMC Bioinformatics, 2012, 13, S5.	2.6	83
39	Prediction of RNA-binding amino acids from protein and RNA sequences. BMC Bioinformatics, 2011, 12, S7.	2.6	20
40	InfarctSizer: computing infarct volume from brain images of a stroke animal model. Computer Methods in Biomechanics and Biomedical Engineering, 2011, 14, 497-504.	1.6	6
41	An ontology-based search engine for protein-protein interactions. BMC Bioinformatics, 2010, 11, S23.	2.6	5
42	Predicting RNA-Binding Sites in Proteins Using the Interaction Propensity of Amino Acid Triplets. Protein and Peptide Letters, 2010, 17, 1102-1110.	0.9	3
43	A reliability measure of protein-protein interactions and a reliability measure-based search engine. Computer Methods in Biomechanics and Biomedical Engineering, 2010, 13, 97-104.	1.6	0
44	PseudoViewer3: generating planar drawings of large-scale RNA structures with pseudoknots. Bioinformatics, 2009, 25, 1435-1437.	4.1	145
45	Prediction of Binding Motifs in Hepatitis C Virus NS5A and Human Proteins. Protein and Peptide Letters, 2008, 15, 494-504.	0.9	0
46	Prediction of RNA-Binding Residues in Proteins Using the Interaction Propensities of Amino Acids and Nucleotides. Lecture Notes in Computer Science, 2008, , 114-121.	1.3	0
47	Estimating the Reliability of Protein-Protein Interactions. , 2007, , .		0
48	Analysis of HCV Envelope Proteins Interacting with Human Proteins. , 2007, , .		0
49	Discovering Inter-Domain Paths between Hepatitis C Virus NS5A and Human Liver Proteins. , 2007, , .		0
50	Identifying Functional Groups by Finding Cliques and Near-Cliques in Protein Interaction Networks. , 2007, , .		2
51	Prediction of Interacting Motif Pairs Using Stochastic Boosting. , 2007, , .		1
52	PRI-Modeler: Extracting RNA structural elements from PDB files of protein-RNA complexes. FEBS Letters, 2007, 581, 1881-1890.	2.8	18
53	Multi-Layered Networks for Visualizing the Interactions between Heterogeneous Proteins. , 2007, , .		0
54	Hepatitis C virus contact map prediction based on binary encoding strategy. Computational Biology and Chemistry, 2007, 31, 233-238.	2.3	12

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55	FSDB: A frameshift signal database. <i>Computational Biology and Chemistry</i> , 2007, 31, 298-302.	2.3	23
56	Comparative Analysis of the Interaction Networks of HIV-1 and Human Proteins. <i>Lecture Notes in Computer Science</i> , 2007, , 339-346.	1.3	0
57	Mining Molecular Structure Data for the Patterns of Interactions Between Protein and RNA. <i>Lecture Notes in Computer Science</i> , 2007, , 94-101.	1.3	0
58	PseudoViewer: web application and web service for visualizing RNA pseudoknots and secondary structures. <i>Nucleic Acids Research</i> , 2006, 34, W416-W422.	14.5	83
59	Web Service for Predicting Interacting Proteins and Application to Human and HIV-1 Proteins. <i>Lecture Notes in Computer Science</i> , 2006, , 631-640.	1.3	2
60	Dynamic Visualization of Signal Transduction Pathways from Database Information. <i>Lecture Notes in Computer Science</i> , 2005, , 663-672.	1.3	0
61	A Database Server for Predicting Protein-Protein Interactions. <i>Lecture Notes in Computer Science</i> , 2004, , 271-278.	1.3	1
62	Predicting genes expressed via -1 and +1 frameshifts. <i>Nucleic Acids Research</i> , 2004, 32, 4884-4892.	14.5	58
63	WebInterViewer: visualizing and analyzing molecular interaction networks. <i>Nucleic Acids Research</i> , 2004, 32, W89-W95.	14.5	25
64	HPID: The Human Protein Interaction Database. <i>Bioinformatics</i> , 2004, 20, 2466-2470.	4.1	88
65	Three-dimensional visualization of protein interaction networks. <i>Computers in Biology and Medicine</i> , 2004, 34, 127-139.	7.0	4
66	Prediction of Protein Functions Using Protein Interaction Data. <i>Lecture Notes in Computer Science</i> , 2004, , 317-324.	1.3	0
67	Prediction of Binding Sites in Protein-Nucleic Acid Complexes. <i>Lecture Notes in Computer Science</i> , 2004, , 309-316.	1.3	0
68	Prevention of passively transferred experimental autoimmune myasthenia gravis by an in vitro selected RNA aptamer. <i>FEBS Letters</i> , 2003, 548, 85-89.	2.8	32
69	Computational analysis of hydrogen bonds in protein-RNA complexes for interaction patterns. <i>FEBS Letters</i> , 2003, 552, 231-239.	2.8	54
70	PSEUDOVIEWER2: visualization of RNA pseudoknots of any type. <i>Nucleic Acids Research</i> , 2003, 31, 3432-3440.	14.5	63
71	Visualization and analysis of protein interactions. <i>Bioinformatics</i> , 2003, 19, 317-318.	4.1	25
72	Complexity management in visualizing protein interaction networks. <i>Bioinformatics</i> , 2003, 19, i177-i179.	4.1	19

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73	A fast layout algorithm for protein interaction networks. <i>Bioinformatics</i> , 2003, 19, 1882-1888.	4.1	35
74	Mining RNA Structure Elements from the Structure Data of Protein-RNA Complexes. <i>Lecture Notes in Computer Science</i> , 2003, , 352-359.	1.3	0
75	PseudoViewer: automatic visualization of RNA pseudoknots. <i>Bioinformatics</i> , 2002, 18, S321-S328.	4.1	26
76	Simulation studies of the effects of user mobility on the handoff performance of mobile communications. <i>Simulation Modelling Practice and Theory</i> , 2002, 10, 497-512.	3.8	1