Doheon Lee

List of Publications by Year
in descending order

165 papers	6,799 citations	94269 37 h-index	66788 78 g-index
173 all docs	173 docs citations	173 times ranked	10493 citing authors

#	Article	IF	Citations
1	Network‐based classification of breast cancer metastasis. Molecular Systems Biology, 2007, 3, 140.	3.2	1,320
2	Inferring Pathway Activity toward Precise Disease Classification. PLoS Computational Biology, 2008, 4, e1000217.	1.5	475
3	Phytochromes promote seedling light responses by inhibiting four negatively-acting phytochrome-interacting factors. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 7660-7665.	3.3	412
4	Genome-Wide Analysis of Genes Targeted by PHYTOCHROME INTERACTING FACTOR 3-LIKE5 during Seed Germination in <i>Arabidopsis</i> Â. Plant Cell, 2009, 21, 403-419.	3.1	336
5	Normalization of Tumor Vessels by Tie2 Activation and Ang2 Inhibition Enhances Drug Delivery and Produces a Favorable Tumor Microenvironment. Cancer Cell, 2016, 30, 953-967.	7.7	259
6	A Taxonomy of Dirty Data. Data Mining and Knowledge Discovery, 2003, 7, 81-99.	2.4	209
7	On cluster validity index for estimation of the optimal number of fuzzy clusters. Pattern Recognition, 2004, 37, 2009-2025.	5.1	187
8	Gene expression profiling by mRNA sequencing reveals increased expression of immune/inflammation-related genes in the hippocampus of individuals with schizophrenia. Translational Psychiatry, 2013, 3, e321-e321.	2.4	162
9	A feature-based approach to modeling protein‐protein interaction hot spots. Nucleic Acids Research, 2009, 37, 2672-2687.	6.5	161
10	<i>RBSDesigner</i>: software for designing synthetic ribosome binding sites that yields a desired level of protein expression. Bioinformatics, 2010, 26, 2633-2634.	1.8	127
11	Evaluation of the performance of clustering algorithms in kernel-induced feature space. Pattern Recognition, 2005, 38, 607-611.	5.1	122
12	Fuzzy clustering of categorical data using fuzzy centroids. Pattern Recognition Letters, 2004, 25, 1263-1271.	2.6	120
13	Optogenetic Mimicry of the Transient Activation of Dopamine Neurons by Natural Reward Is Sufficient for Operant Reinforcement. PLoS ONE, 2012, 7, e33612.	1.1	118
14	Vascular RhoJ Is an Effective and Selective Target for Tumor Angiogenesis and Vascular Disruption. Cancer Cell, 2014, 25, 102-117.	7.7	109
15	Combining tissue transcriptomics and urine metabolomics for breast cancer biomarker identification. Bioinformatics, 2009, 25, 3151-3157.	1.8	107
16	A kernel-based subtractive clustering method. Pattern Recognition Letters, 2005, 26, 879-891.	2.6	97
17	A protein interaction network associated with asthma. Journal of Theoretical Biology, 2008, 252, 722-731.	0.8	94
18	Density-Induced Support Vector Data Description. IEEE Transactions on Neural Networks, 2007, 18, 284-289.	4.8	92

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19	Mathematical modeling of translation initiation for the estimation of its efficiency to computationally design mRNA sequences with desired expression levels in prokaryotes. BMC Systems Biology, 2010, 4, 71.	3.0	82
20	Dynamic changes in DNA methylation and hydroxymethylation when hES cells undergo differentiation toward a neuronal lineage. Human Molecular Genetics, 2014, 23, 657-667.	1.4	82
21	Compositional and functional differences of the mucosal microbiota along the intestine of healthy individuals. Scientific Reports, 2020, 10, 14977.	1.6	78
22	A novel initialization scheme for the fuzzy c-means algorithm for color clustering. Pattern Recognition Letters, 2004, 25, 227-237.	2.6	76
23	Fuzzy cluster validation index based on inter-cluster proximity. Pattern Recognition Letters, 2003, 24, 2561-2574.	2.6	73
24	A cluster validation index for GK cluster analysis based on relative degree of sharing. Information Sciences, 2004, 168, 225-242.	4.0	72
25	Predicting Pharmacodynamic Drug-Drug Interactions through Signaling Propagation Interference on Protein-Protein Interaction Networks. PLoS ONE, 2015, 10, e0140816.	1.1	65
26	Discovering Health Benefits of Phytochemicals with Integrated Analysis of the Molecular Network, Chemical Properties and Ethnopharmacological Evidence. Nutrients, 2018, 10, 1042.	1.7	62
27	Differential activation of immune/inflammatory response-related co-expression modules in the hippocampus across the major psychiatric disorders. Molecular Psychiatry, 2016, 21, 376-385.	4.1	60
28	Building the process-drug–side effect network to discover the relationship between biological Processes and side effects. BMC Bioinformatics, 2011, 12, S2.	1.2	54
29	Modularized learning of genetic interaction networks from biological annotations and mRNA expression data. Bioinformatics, 2005, 21, 2739-2747.	1.8	52
30	PLPD: reliable protein localization prediction from imbalanced and overlapped datasets. Nucleic Acids Research, 2006, 34, 4655-4666.	6.5	50
31	Transcriptome sequencing of the choroid plexus in schizophrenia. Translational Psychiatry, 2016, 6, e964-e964.	2.4	50
32	Improving support vector data description using local density degree. Pattern Recognition, 2005, 38, 1768-1771.	5.1	48
33	Detecting clusters of different geometrical shapes in microarray gene expression data. Bioinformatics, 2005, 21, 1927-1934.	1.8	48
34	Multivariate classification of urine metabolome profiles for breast cancer diagnosis. BMC Bioinformatics, 2010, 11, S4.	1.2	45
35	Fuzzy Branching Temporal Logic. IEEE Transactions on Systems, Man, and Cybernetics, 2004, 34, 1045-1055.	5.5	42
36	Association between SNPs and gene expression in multiple regions of the human brain. Translational Psychiatry, 2012, 2, e113-e113.	2.4	40

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37	A k-populations algorithm for clustering categorical data. Pattern Recognition, 2005, 38, 1131-1134.	5.1	39
38	AsiDesigner: exon-based siRNA design server considering alternative splicing. Nucleic Acids Research, 2008, 36, W97-W103.	6.5	39
39	Specificity of molecular interactions in transient protein-protein interaction interfaces. Proteins: Structure, Function and Bioinformatics, 2006, 65, 593-606.	1.5	37
40	Dysregulated signaling hubs of liver lipid metabolism reveal hepatocellular carcinoma pathogenesis. Nucleic Acids Research, 2016, 44, 5529-5539.	6.5	35
41	Regression trees for regulatory element identification. Bioinformatics, 2004, 20, 750-757.	1.8	34
42	The association of Alu repeats with the generation of potential AU-rich elements (ARE) at 3' untranslated regions.. BMC Genomics, 2004, 5, 97.	1.2	34
43	Architecture of basic building blocks in protein and domain structural interaction networks. Bioinformatics, 2005, 21, 1479-1486.	1.8	26
44	SNP@Ethnos: a database of ethnically variant single-nucleotide polymorphisms. Nucleic Acids Research, 2007, 35, D711-D715.	6.5	26
45	Protein comparison at the domain architecture level. BMC Bioinformatics, 2009, 10, S5.	1.2	26
46	ETM-DB: integrated Ethiopian traditional herbal medicine and phytochemicals database. BMC Complementary and Alternative Medicine, 2019, 19, 212.	3.7	26
47	Somatic deletions implicated in functional diversity of brain cells of individuals with schizophrenia and unaffected controls. Scientific Reports, 2015, 4, 3807.	1.6	25
48	Prediction of compound-target interactions of natural products using large-scale drug and protein information. BMC Bioinformatics, 2016, 17, 219.	1.2	24
49	Transcription of human endogenous retroviruses in human brain by RNA-seq analysis. PLoS ONE, 2019, 14, e0207353.	1.1	24
50	Identification of temporal association rules from time-series microarray data sets. BMC Bioinformatics, 2009, 10, S6.	1.2	22
51	Analysis of AML genes in dysregulated molecular networks. BMC Bioinformatics, 2009, 10, S2.	1.2	22
52	Generation and application of drug indication inference models using typed network motif comparison analysis. BMC Medical Informatics and Decision Making, 2013, 13, S2.	1.5	21
53	Prediction of drugs having opposite effects on disease genes in a directed network. BMC Systems Biology, 2016, 10, 2.	3.0	21
54	A method to improve protein subcellular localization prediction by integrating various biological data sources. BMC Bioinformatics, 2009, 10, S43.	1.2	20

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55	Social deficits in the AY-9944 mouse model of atypical absence epilepsy. Behavioural Brain Research, 2013, 236, 23-29.	1.2	19
56	Concept embedding to measure semantic relatedness for biomedical information ontologies. Journal of Biomedical Informatics, 2019, 94, 103182.	2.5	19
57	BioCAD: an information fusion platform for bio-network inference and analysis. BMC Bioinformatics, 2007, 8, S2.	1.2	18
58	Predicting unintended effects of drugs based on off-target tissue effects. Biochemical and Biophysical Research Communications, 2016, 469, 399-404.	1.0	18
59	Ranking the sequences of fuzzy values. Information Sciences, 2004, 160, 41-52.	4.0	17
60	Mathematical modeling of humoral immune response suppression by passively administered antibodies in mice. Journal of Theoretical Biology, 2006, 241, 830-851.	0.8	17
61	DAhunter: a web-based server that identifies homologous proteins by comparing domain architecture. Nucleic Acids Research, 2008, 36, W60-W64.	6.5	17
62	Discovering context-specific relationships from biological literature by using multi-level context terms. BMC Medical Informatics and Decision Making, 2012, 12, S1.	1.5	17
63	Accommodating subjective vagueness through a fuzzy extension to the relational data model. Information Systems, 1993, 18, 363-374.	2.4	16
64	Prediction of Extracellular Matrix Proteins Based on Distinctive Sequence and Domain Characteristics. Journal of Computational Biology, 2010, 17, 97-105.	0.8	16
65	Inferring disease association using clinical factors in a combinatorial manner and their use in drug repositioning. Bioinformatics, 2013, 29, 2017-2023.	1.8	16
66	CODA: Integrating multi-level context-oriented directed associations for analysis of drug effects. Scientific Reports, 2017, 7, 7519.	1.6	16
67	Towards clustering of incomplete microarray data without the use of imputation. Bioinformatics, 2007, 23, 107-113.	1.8	15
68	Rule-based multi-scale simulation for drug effect pathway analysis. BMC Medical Informatics and Decision Making, 2013, 13, S4.	1.5	15
69	CONET: a virtual human system-centered platform for drug discovery. Frontiers of Computer Science, 2018, 12, 1-3.	1.6	15
70	Inferring new drug indications using the complementarity between clinical disease signatures and drug effects. Journal of Biomedical Informatics, 2016, 59, 248-257.	2.5	14
71	EGR1/GADD45α Activation by ROS of Non-Thermal Plasma Mediates Cell Death in Thyroid Carcinoma. Cancers, 2021, 13, 351.	1.7	14
72	bZIPDB : A database of regulatory information for human bZIP transcription factors. BMC Genomics, 2007, 8, 136.	1.2	13

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73	MKEM: a Multi-level Knowledge Emergence Model for mining undiscovered public knowledge. BMC Bioinformatics, 2010, 11, S3.	1.2	13
74	In silico profiling of systemic effects of drugs to predict unexpected interactions. Scientific Reports, 2018, 8, 1612.	1.6	13
75	Synergistic Effects of Sanghuangâ€"Danshen Bioactives on Arterial Stiffness in a Randomized Clinical Trial of Healthy Smokers: An Integrative Approach to in silico Network Analysis. Nutrients, 2019, 11, 108.	1.7	13
76	A Deep Learning-Based Approach for Identifying the Medicinal Uses of Plant-Derived Natural Compounds. Frontiers in Pharmacology, 2020, 11, 584875.	1.6	13
77	Comparative analysis of the JAK/STAT signaling through erythropoietin receptor and thrombopoietin receptor using a systems approach. BMC Bioinformatics, 2009, 10, S53.	1.2	12
78	Inference of combinatorial Boolean rules of synergistic gene sets from cancer microarray datasets. Bioinformatics, 2010, 26, 1506-1512.	1.8	12
79	CORUS: Blockchain-Based Trustworthy Evaluation System for Efficacy of Healthcare Remedies. , 2018, , .		12
80	Possibilistic support vector machines. Pattern Recognition, 2005, 38, 1325-1327.	5.1	11
81	Computational identification of altered metabolism using gene expression and metabolic pathways. Biotechnology and Bioengineering, 2009, 103, 835-843.	1.7	11
82	A Data-Driven Approach for Identifying Medicinal Combinations of Natural Products. IEEE Access, 2018, 6, 58106-58118.	2.6	11
83	Phenotype-oriented network analysis for discovering pharmacological effects of natural compounds. Scientific Reports, 2018, 8, 11667.	1.6	11
84	Deep learning-based classification with improved time resolution for physical activities of children. PeerJ, 2018, 6, e5764.	0.9	11
85	A corpus for plant-chemical relationships in the biomedical domain. BMC Bioinformatics, 2016, 17, 386.	1.2	10
86	Meta-analysis method for discovering reliable biomarkers by integrating statistical and biological approaches: An application to liver toxicity. Biochemical and Biophysical Research Communications, 2016, 471, 274-281.	1.0	10
87	Exploring molecular links between lymph node invasion and cancer prognosis in human breast cancer. BMC Systems Biology, 2011, 5, S4.	3.0	8
88	Context-dependent transcriptional regulations between signal transduction pathways. BMC Bioinformatics, 2011, 12, 19.	1.2	8
89	Annotating activation/inhibition relationships to protein-protein interactions using gene ontology relations. BMC Systems Biology, 2018, 12, 9.	3.0	8
90	Integration of Immune Models Using Petri Nets. Lecture Notes in Computer Science, 2004, , 205-216.	1.0	7

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91	H-CORE: Enabling genome-scale Bayesian analysis of biological systems without prior knowledge. BioSystems, 2007, 90, 197-210.	0.9	7
92	Prediction of cancer prognosis with the genetic basis of transcriptional variations. Genomics, 2011, 97, 350-357.	1.3	7
93	Predicting disease phenotypes based on the molecular networks with Condition-Responsive Correlation. International Journal of Data Mining and Bioinformatics, 2011, 5, 131.	0.1	7
94	SigCS base: an integrated genetic information resource for human cerebral stroke. BMC Systems Biology, 2011, 5, S10.	3.0	7
95	A systematic approach to identify therapeutic effects of natural products based on human metabolite information. BMC Bioinformatics, 2018, 19, 205.	1.2	7
96	COMPARISON OF TYPE-2 FUZZY VALUES WITH SATISFACTION FUNCTION. International Journal of Uncertainty, Fuzziness and Knowlege-Based Systems, 2004, 12, 601-611.	0.9	6
97	In silico analysis of lactate producing metabolic network in Lactococcus lactis. Enzyme and Microbial Technology, 2004, 35, 654-662.	1.6	6
98	Fuzzy Continuous Petri Net-Based Approach for Modeling Immune Systems. Lecture Notes in Computer Science, 2006, , 278-285.	1.0	6
99	Computational identification of combinatorial regulation and transcription factor binding sites. Biotechnology and Bioengineering, 2007, 97, 1594-1602.	1.7	6
100	Inference of combinatorial neuronal synchrony with Bayesian networks. Journal of Neuroscience Methods, 2010, 186, 130-139.	1.3	6
101	Genome-wide DNA-binding specificity of PIL5, an Arabidopsis basic Helix-Loop-Helix (bHLH) transcription factor. International Journal of Data Mining and Bioinformatics, 2010, 4, 588.	0.1	6
102	Inference of brain pathway activities for Alzheimer's disease classification. BMC Medical Informatics and Decision Making, 2015, 15, S1.	1.5	6
103	HIDEEP: a systems approach to predict hormone impacts on drug efficacy based on effect paths. Scientific Reports, 2017, 7, 16600.	1.6	6
104	Shared co-expression networks in frontal cortex of the normal aged brain and schizophrenia. Schizophrenia Research, 2019, 204, 253-261.	1.1	6
105	Reliable Data Collection in Participatory Trials to Assess Digital Healthcare Applications. IEEE Access, 2020, 8, 79472-79490.	2.6	6
106	Enabling Large-Scale Bayesian Network Learning by Preserving Intercluster Directionality. IEICE Transactions on Information and Systems, 2007, E90-D, 1018-1027.	0.4	6
107	Design of Autonomous Underwater Vehicles for Cage Aquafarms. Intelligent Vehicles Symposium, 2009 IEEE, 2007, , .	0.0	5
108	Patome: a database server for biological sequence annotation and analysis in issued patents and published patent applications. Nucleic Acids Research, 2007, 35, D47-D50.	6.5	5

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109	Synthetic inter-species cooperation of host and virus for targeted genetic evolution. Journal of Biotechnology, 2011, 153, 35-41.	1.9	5
110	Electronic Medical Records privacy preservation through k-anonymity clustering method. , 2012, , .		5
111	Context-based resolution of semantic conflicts in biological pathways. BMC Medical Informatics and Decision Making, 2015, 15, S3.	1.5	5
112	Identification of common coexpression modules based on quantitative network comparison. BMC Bioinformatics, 2018, 19, 213.	1.2	5
113	Topological motifs populate complex networks through grouped attachment. Scientific Reports, 2018, 8, 12670.	1.6	5
114	Synergistic mechanisms of Sanghuangâ€"Danshen phytochemicals on postprandial vascular dysfunction in healthy subjects: A network biology approach based on a clinical trial. Scientific Reports, 2019, 9, 9746.	1.6	5
115	A Bayesian ensemble approach with a disease gene network predicts damaging effects of missense variants of human cancers. Human Genetics, 2013, 132, 15-27.	1.8	4
116	A Systems Biological Approach to Understanding the Mechanisms Underlying the Therapeutic Potential of Red Ginseng Supplements against Metabolic Diseases. Molecules, 2020, 25, 1967.	1.7	4
117	Network Analysis to Identify the Risk of Epidemic Spreading. Applied Sciences (Switzerland), 2021, 11, 2997.	1.3	4
118	Anomalies in Network Bridges Involved in Bile Acid Metabolism Predict Outcomes of Colorectal Cancer Patients. PLoS ONE, 2014, 9, e107925.	1.1	4
119	Machineâ€Learned Lightâ€Field Camera that Reads Facial Expression from Highâ€Contrast and Illumination Invariant 3D Facial Images. Advanced Intelligent Systems, 0, , 2100182.	3.3	4
120	PlantÂphenotype relationship corpus for biomedical relationships between plants and phenotypes. Scientific Data, 2022, 9, .	2.4	4
121	Mining metastasis related genes by primary-secondary tumor comparisons from large-scale databases. BMC Bioinformatics, 2009, 10, S2.	1.2	3
122	SoloDel: a probabilistic model for detecting low-frequent somatic deletions from unmatched sequencing data. Bioinformatics, 2015, 31, 3105-3113.	1.8	3
123	Context-specific functional module based drug efficacy prediction. BMC Bioinformatics, 2016, 17, 275.	1.2	3
124	Petri net-based prediction of therapeutic targets that recover abnormally phosphorylated proteins in muscle atrophy. BMC Systems Biology, 2018, 12, 26.	3.0	3
125	Component-based software architecture for biosystem reverse engineering. Biotechnology and Bioprocess Engineering, 2005, 10, 400-407.	1.4	2
126	Voting Fuzzy k-NN to Predict Protein Subcellular Localization from Normalized Amino Acid Pair Compositions. Lecture Notes in Computer Science, 2005, , 180-185.	1.0	2

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127	Special Issue on Artificial Immune Systems. Mathematical Modelling and Algorithms, 2009, 8, 101-102.	0.5	2
128	Intelligent PSR estimator for feature extraction of a passive sonar target. International Journal of Control, Automation and Systems, 2010, 8, 677-682.	1.6	2
129	Rule-based whole body modeling for analyzing multi-compound effects. , 2012, , .		2
130	TNMCA. , 2012, , .		2
131	Prioritization of SNPs for Genome-Wide Association Studies Using an Interaction Model of Genetic Variation, Gene Expression, and Trait Variation. Molecules and Cells, 2012, 33, 351-362.	1.0	2
132	BSML. , 2013, , .		2
133	Coupling effects on turning points of infectious diseases epidemics in scale-free networks. BMC Bioinformatics, 2017, 18, 250.	1.2	2
134	CODA-ML: context-specific biological knowledge representation for systemic physiology analysis. BMC Bioinformatics, 2019, 20, 248.	1.2	2
135	Deconvoluting essential gene signatures for cancer growth from genomic expression in compound-treated cells. Bioinformatics, 2019, 35, 1167-1173.	1.8	2
136	Literature mining for context-specific molecular relations using multimodal representations (COMMODAR). BMC Bioinformatics, 2020, 21, 250.	1.2	2
137	Learning Rules to Extract Protein Interactions from Biomedical Text. Lecture Notes in Computer Science, 2003, , 148-158.	1.0	2
138	Relationships between genetic polymorphisms and transcriptional profiles for outcome prediction in anticancer agent treatment. BMB Reports, 2010, 43, 836-841.	1.1	2
139	Context-aware multi-token concept recognition of biological entities. BMC Bioinformatics, 2021, 22, 337.	1.2	2
140	Mathematical Modeling of Immune Suppression. Lecture Notes in Computer Science, 2005, , 182-192.	1.0	2
141	Extending semantics of relational operators for vague queries. Microprocessing and Microprogramming, 1993, 39, 165-168.	0.3	1
142	Stochastic Simulation Model for Patterned Neural Multi-Electrode Arrays. , 2007, , .		1
143	Genome-Wide DNA-Binding Specificity of PIL5, a Arabidopsis Basic Helix-Loop-Helix (bHLH) Transcription Factor. , 2008, , .		1
144	A new perspective of integrative genome-wide association analysis considering trans eSNP effect. , 2010, , .		1

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145	Meta-path Based Prioritization of Functional Drug Actions with Multi-Level Biological Networks. Scientific Reports, 2019, 9, 5469.	1.6	1
146	An interactive retrieval system for clinical trial studies with context-dependent protocol elements. PLoS ONE, 2020, 15, e0238290.	1.1	1
147	Paeonia lactiflora extract suppresses cisplatin-induced muscle wasting via downregulation of muscle-specific ubiquitin E3 ligases, NF-I°B signaling, and cytokine levels. Journal of Ethnopharmacology, 2021, 266, 113403.	2.0	1
148	Integrated Network-Based Computational Analysis for Drug Development. , 2021, , 169-183.		1
149	Assessing the Quality of Fuzzy Partitions Using Relative Intersection. IEICE Transactions on Information and Systems, 2005, E88-D, 594-602.	0.4	1
150	BioCAD. , 2006, , .		0
151	Intelligent Navigation of Autonomous Underwater Vehicles for Cage Aquafarm Surveillance. , 2007, , .		0
152	Identification of temporal association rules from time-series microarray data set. , 2008, , .		0
153	Disease Classification Based on the Activities of Interacting Molecular Modules with Condition-Responsive Correlation. , 2009, , .		0
154	Pathway level analysis by augmenting activities of transcription factor target genes. IET Systems Biology, 2009, 3, 534-542.	0.8	0
155	PSExplorer: whole parameter space exploration for molecular signaling pathway dynamics. Bioinformatics, 2010, 26, 2477-2479.	1.8	0
156	Context-specific biological network construction. , 2014, , .		0
157	Association analysis of the perturbation of interactions in biological pathways and anticancer drug activity. Biochemical and Biophysical Research Communications, 2016, 470, 137-143.	1.0	0
158	Visualizing multifunctional PPI network with Gene Ontology annotation. , 2019, , .		0
159	Decision Trees for Multiple Abstraction Levels of Data. Lecture Notes in Computer Science, 2001, , 76-87.	1.0	0
160	Systems Bioinformatics Research Trends. Journal of Korean Society of Medical Informatics, 2008, 14, 313.	0.3	0
161	Computational identification of significantly regulated metabolic reactions by integration of data on enzyme activity and gene expression. BMB Reports, 2008, 41, 609-614.	1.1	0
162	CONVIRT: A web-based tool for transcriptional regulatory site identification using a conserved virtual chromosome. BMB Reports, 2009, 42, 823-828.	1.1	0

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163	Predicting tissue-specific expressions based on sequence characteristics. BMB Reports, 2011, 44, 250-255.	1.1	0
164	Analysis of AML Genes in Dysregulated Molecular Networks. Summit on Translational Bioinformatics, 2009, 2009, 1-18.	0.7	0
165	Paeonia lactiflora extract improves the muscle function of mdx mice, an animal model of Duchenne muscular dystrophy, via downregulating the high mobility group box 1 protein. Journal of Ethnopharmacology, 2022, 289, 115079.	2.0	0