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	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
2	PlantÂphenotype relationship corpus for biomedical relationships between plants and phenotypes. Scientific Data, 2022, 9, .	2.4	4
3	Paeonia lactiflora extract suppresses cisplatin-induced muscle wasting via downregulation of muscle-specific ubiquitin E3 ligases, NF-ÎºB signaling, and cytokine levels. Journal of Ethnopharmacology, 2021, 266, 113403.	2.0	1
4	Integrated Network-Based Computational Analysis for Drug Development. , 2021, , 169-183.		1
5	EGR1/GADD45Î± Activation by ROS of Non-Thermal Plasma Mediates Cell Death in Thyroid Carcinoma. Cancers, 2021, 13, 351.	1.7	14
6	Network Analysis to Identify the Risk of Epidemic Spreading. Applied Sciences (Switzerland), 2021, 11, 2997.	1.3	4
7	Context-aware multi-token concept recognition of biological entities. BMC Bioinformatics, 2021, 22, 337.	1.2	2
8	An interactive retrieval system for clinical trial studies with context-dependent protocol elements. PLoS ONE, 2020, 15, e0238290.	1.1	1
9	Reliable Data Collection in Participatory Trials to Assess Digital Healthcare Applications. IEEE Access, 2020, 8, 79472-79490.	2.6	6
10	Compositional and functional differences of the mucosal microbiota along the intestine of healthy individuals. Scientific Reports, 2020, 10, 14977.	1.6	78
11	A Deep Learning-Based Approach for Identifying the Medicinal Uses of Plant-Derived Natural Compounds. Frontiers in Pharmacology, 2020, 11, 584875.	1.6	13
12	Literature mining for context-specific molecular relations using multimodal representations (COMMODAR). BMC Bioinformatics, 2020, 21, 250.	1.2	2
13	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
14	ETM-DB: integrated Ethiopian traditional herbal medicine and phytochemicals database. BMC Complementary and Alternative Medicine, 2019, 19, 212.	3.7	26
15	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
16	CODA-ML: context-specific biological knowledge representation for systemic physiology analysis. BMC Bioinformatics, 2019, 20, 248.	1.2	2
17	Concept embedding to measure semantic relatedness for biomedical information ontologies. Journal of Biomedical Informatics, 2019, 94, 103182.	2.5	19
18	Meta-path Based Prioritization of Functional Drug Actions with Multi-Level Biological Networks. Scientific Reports, 2019, 9, 5469.	1.6	1

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19	Visualizing multifunctional PPI network with Gene Ontology annotation. , 2019, , .		0
20	Shared co-expression networks in frontal cortex of the normal aged brain and schizophrenia. Schizophrenia Research, 2019, 204, 253-261.	1.1	6
21	Transcription of human endogenous retroviruses in human brain by RNA-seq analysis. PLoS ONE, 2019, 14, e0207353.	1.1	24
22	Synergistic Effects of Sanghuang–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
23	Deconvoluting essential gene signatures for cancer growth from genomic expression in compound-treated cells. Bioinformatics, 2019, 35, 1167-1173.	1.8	2
24	In silico profiling of systemic effects of drugs to predict unexpected interactions. Scientific Reports, 2018, 8, 1612.	1.6	13
25	Annotating activation/inhibition relationships to protein-protein interactions using gene ontology relations. BMC Systems Biology, 2018, 12, 9.	3.0	8
26	CONET: a virtual human system-centered platform for drug discovery. Frontiers of Computer Science, 2018, 12, 1-3.	1.6	15
27	Identification of common coexpression modules based on quantitative network comparison. BMC Bioinformatics, 2018, 19, 213.	1.2	5
28	CORUS: Blockchain-Based Trustworthy Evaluation System for Efficacy of Healthcare Remedies. , 2018, , .		12
29	Topological motifs populate complex networks through grouped attachment. Scientific Reports, 2018, 8, 12670.	1.6	5
30	A Data-Driven Approach for Identifying Medicinal Combinations of Natural Products. IEEE Access, 2018, 6, 58106-58118.	2.6	11
31	Discovering Health Benefits of Phytochemicals with Integrated Analysis of the Molecular Network, Chemical Properties and Ethnopharmacological Evidence. Nutrients, 2018, 10, 1042.	1.7	62
32	A systematic approach to identify therapeutic effects of natural products based on human metabolite information. BMC Bioinformatics, 2018, 19, 205.	1.2	7
33	Phenotype-oriented network analysis for discovering pharmacological effects of natural compounds. Scientific Reports, 2018, 8, 11667.	1.6	11
34	Petri net-based prediction of therapeutic targets that recover abnormally phosphorylated proteins in muscle atrophy. BMC Systems Biology, 2018, 12, 26.	3.0	3
35	Deep learning-based classification with improved time resolution for physical activities of children. PeerJ, 2018, 6, e5764.	0.9	11
36	CODA: Integrating multi-level context-oriented directed associations for analysis of drug effects. Scientific Reports, 2017, 7, 7519.	1.6	16

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37	HIDEEP: a systems approach to predict hormone impacts on drug efficacy based on effect paths. Scientific Reports, 2017, 7, 16600.	1.6	6
38	Coupling effects on turning points of infectious diseases epidemics in scale-free networks. BMC Bioinformatics, 2017, 18, 250.	1.2	2
39	Transcriptome sequencing of the choroid plexus in schizophrenia. Translational Psychiatry, 2016, 6, e964-e964.	2.4	50
40	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
41	Dysregulated signaling hubs of liver lipid metabolism reveal hepatocellular carcinoma pathogenesis. Nucleic Acids Research, 2016, 44, 5529-5539.	6.5	35
42	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
43	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
44	Prediction of compound-target interactions of natural products using large-scale drug and protein information. BMC Bioinformatics, 2016, 17, 219.	1.2	24
45	A corpus for plant-chemical relationships in the biomedical domain. BMC Bioinformatics, 2016, 17, 386.	1.2	10
46	Context-specific functional module based drug efficacy prediction. BMC Bioinformatics, 2016, 17, 275.	1.2	3
47	Predicting unintended effects of drugs based on off-target tissue effects. Biochemical and Biophysical Research Communications, 2016, 469, 399-404.	1.0	18
48	Prediction of drugs having opposite effects on disease genes in a directed network. BMC Systems Biology, 2016, 10, 2.	3.0	21
49	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
50	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
51	Somatic deletions implicated in functional diversity of brain cells of individuals with schizophrenia and unaffected controls. Scientific Reports, 2015, 4, 3807.	1.6	25
52	Inference of brain pathway activities for Alzheimer's disease classification. BMC Medical Informatics and Decision Making, 2015, 15, S1.	1.5	6
53	Context-based resolution of semantic conflicts in biological pathways. BMC Medical Informatics and Decision Making, 2015, 15, S3.	1.5	5
54	SoloDel: a probabilistic model for detecting low-frequent somatic deletions from unmatched sequencing data. Bioinformatics, 2015, 31, 3105-3113.	1.8	3

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55	Predicting Pharmacodynamic Drug-Drug Interactions through Signaling Propagation Interference on Protein-Protein Interaction Networks. PLoS ONE, 2015, 10, e0140816.	1.1	65
56	Context-specific biological network construction. , 2014, , .		0
57	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
58	Vascular RhoJ Is an Effective and Selective Target for Tumor Angiogenesis and Vascular Disruption. Cancer Cell, 2014, 25, 102-117.	7.7	109
59	Anomalies in Network Bridges Involved in Bile Acid Metabolism Predict Outcomes of Colorectal Cancer Patients. PLoS ONE, 2014, 9, e107925.	1.1	4
60	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
61	Rule-based multi-scale simulation for drug effect pathway analysis. BMC Medical Informatics and Decision Making, 2013, 13, S4.	1.5	15
62	BSML. , 2013, , .		2
63	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
64	Social deficits in the AY-9944 mouse model of atypical absence epilepsy. Behavioural Brain Research, 2013, 236, 23-29.	1.2	19
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	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
67	Rule-based whole body modeling for analyzing multi-compound effects. , 2012, , .		2
68	TNMCA. , 2012, , .		2
69	Association between SNPs and gene expression in multiple regions of the human brain. Translational Psychiatry, 2012, 2, e113-e113.	2.4	40
70	Electronic Medical Records privacy preservation through k-anonymity clustering method. , 2012, , .		5
71	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
72	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

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73	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
74	Prediction of cancer prognosis with the genetic basis of transcriptional variations. Genomics, 2011, 97, 350-357.	1.3	7
75	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
76	SigCS base: an integrated genetic information resource for human cerebral stroke. BMC Systems Biology, 2011, 5, S10.	3.0	7
77	Exploring molecular links between lymph node invasion and cancer prognosis in human breast cancer. BMC Systems Biology, 2011, 5, S4.	3.0	8
78	Context-dependent transcriptional regulations between signal transduction pathways. BMC Bioinformatics, 2011, 12, 19.	1.2	8
79	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
80	Synthetic inter-species cooperation of host and virus for targeted genetic evolution. Journal of Biotechnology, 2011, 153, 35-41.	1.9	5
81	Predicting tissue-specific expressions based on sequence characteristics. BMB Reports, 2011, 44, 250-255.	1.1	0
82	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
83	MKEM: a Multi-level Knowledge Emergence Model for mining undiscovered public knowledge. BMC Bioinformatics, 2010, 11, S3.	1.2	13
84	Multivariate classification of urine metabolome profiles for breast cancer diagnosis. BMC Bioinformatics, 2010, 11, S4.	1.2	45
85	Inference of combinatorial neuronal synchrony with Bayesian networks. Journal of Neuroscience Methods, 2010, 186, 130-139.	1.3	6
86	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
87	Prediction of Extracellular Matrix Proteins Based on Distinctive Sequence and Domain Characteristics. Journal of Computational Biology, 2010, 17, 97-105.	0.8	16
88	Inference of combinatorial Boolean rules of synergistic gene sets from cancer microarray datasets. Bioinformatics, 2010, 26, 1506-1512.	1.8	12
89	A new perspective of integrative genome-wide association analysis considering trans eSNP effect. , 2010, , .		1
90	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

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91	PSExplorer: whole parameter space exploration for molecular signaling pathway dynamics. Bioinformatics, 2010, 26, 2477-2479.	1.8	0
92	<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
93	Relationships between genetic polymorphisms and transcriptional profiles for outcome prediction in anticancer agent treatment. BMB Reports, 2010, 43, 836-841.	1.1	2
94	Disease Classification Based on the Activities of Interacting Molecular Modules with Condition-Responsive Correlation. , 2009, , .		0
95	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
96	Combining tissue transcriptomics and urine metabolomics for breast cancer biomarker identification. Bioinformatics, 2009, 25, 3151-3157.	1.8	107
97	A feature-based approach to modeling protein–protein interaction hot spots. Nucleic Acids Research, 2009, 37, 2672-2687.	6.5	161
98	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
99	A method to improve protein subcellular localization prediction by integrating various biological data sources. BMC Bioinformatics, 2009, 10, S43.	1.2	20
100	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
101	Protein comparison at the domain architecture level. BMC Bioinformatics, 2009, 10, S5.	1.2	26
102	Mining metastasis related genes by primary-secondary tumor comparisons from large-scale databases. BMC Bioinformatics, 2009, 10, S2.	1.2	3
103	Identification of temporal association rules from time-series microarray data sets. BMC Bioinformatics, 2009, 10, S6.	1.2	22
104	Analysis of AML genes in dysregulated molecular networks. BMC Bioinformatics, 2009, 10, S2.	1.2	22
105	Pathway level analysis by augmenting activities of transcription factor target genes. IET Systems Biology, 2009, 3, 534-542.	0.8	0
106	Computational identification of altered metabolism using gene expression and metabolic pathways. Biotechnology and Bioengineering, 2009, 103, 835-843.	1.7	11
107	Special Issue on Artificial Immune Systems. Mathematical Modelling and Algorithms, 2009, 8, 101-102.	0.5	2
108	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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109	Analysis of AML Genes in Dysregulated Molecular Networks. Summit on Translational Bioinformatics, 2009, 2009, 1-18.	0.7	0
110	A protein interaction network associated with asthma. Journal of Theoretical Biology, 2008, 252, 722-731.	0.8	94
111	Genome-Wide DNA-Binding Specificity of PIL5, a Arabidopsis Basic Helix-Loop-Helix (bHLH) Transcription Factor. , 2008, , .		1
112	AsiDesigner: exon-based siRNA design server considering alternative splicing. Nucleic Acids Research, 2008, 36, W97-W103.	6.5	39
113	Inferring Pathway Activity toward Precise Disease Classification. PLoS Computational Biology, 2008, 4, e1000217.	1.5	475
114	DAhunter: a web-based server that identifies homologous proteins by comparing domain architecture. Nucleic Acids Research, 2008, 36, W60-W64.	6.5	17
115	Identification of temporal association rules from time-series microarray data set. , 2008, , .		0
116	Systems Bioinformatics Research Trends. Journal of Korean Society of Medical Informatics, 2008, 14, 313.	0.3	0
117	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
118	Design of Autonomous Underwater Vehicles for Cage Aquafarms. Intelligent Vehicles Symposium, 2009 IEEE, 2007, , .	0.0	5
119	Intelligent Navigation of Autonomous Underwater Vehicles for Cage Aquafarm Surveillance. , 2007, , .		0
120	Towards clustering of incomplete microarray data without the use of imputation. Bioinformatics, 2007, 23, 107-113.	1.8	15
121	SNP@Ethnos: a database of ethnically variant single-nucleotide polymorphisms. Nucleic Acids Research, 2007, 35, D711-D715.	6.5	26
122	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
123	Networkâ€based classification of breast cancer metastasis. Molecular Systems Biology, 2007, 3, 140.	3.2	1,320
124	Density-Induced Support Vector Data Description. IEEE Transactions on Neural Networks, 2007, 18, 284-289.	4.8	92
125	Stochastic Simulation Model for Patterned Neural Multi-Electrode Arrays. , 2007, , .		1
126	Computational identification of combinatorial regulation and transcription factor binding sites. Biotechnology and Bioengineering, 2007, 97, 1594-1602.	1.7	6

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127	H-CORE: Enabling genome-scale Bayesian analysis of biological systems without prior knowledge. BioSystems, 2007, 90, 197-210.	0.9	7
128	BioCAD: an information fusion platform for bio-network inference and analysis. BMC Bioinformatics, 2007, 8, S2.	1.2	18
129	bZIPDB : A database of regulatory information for human bZIP transcription factors. BMC Genomics, 2007, 8, 136.	1.2	13
130	Enabling Large-Scale Bayesian Network Learning by Preserving Intercluster Directionality. IEICE Transactions on Information and Systems, 2007, E90-D, 1018-1027.	0.4	6
131	Specificity of molecular interactions in transient protein-protein interaction interfaces. Proteins: Structure, Function and Bioinformatics, 2006, 65, 593-606.	1.5	37
132	Mathematical modeling of humoral immune response suppression by passively administered antibodies in mice. Journal of Theoretical Biology, 2006, 241, 830-851.	0.8	17
133	PLPD: reliable protein localization prediction from imbalanced and overlapped datasets. Nucleic Acids Research, 2006, 34, 4655-4666.	6.5	50
134	BioCAD. , 2006, , .		0
135	Fuzzy Continuous Petri Net-Based Approach for Modeling Immune Systems. Lecture Notes in Computer Science, 2006, , 278-285.	1.0	6
136	Evaluation of the performance of clustering algorithms in kernel-induced feature space. Pattern Recognition, 2005, 38, 607-611.	5.1	122
137	A k-populations algorithm for clustering categorical data. Pattern Recognition, 2005, 38, 1131-1134.	5.1	39
138	Improving support vector data description using local density degree. Pattern Recognition, 2005, 38, 1768-1771.	5.1	48
139	A kernel-based subtractive clustering method. Pattern Recognition Letters, 2005, 26, 879-891.	2.6	97
140	Possibilistic support vector machines. Pattern Recognition, 2005, 38, 1325-1327.	5.1	11
141	Component-based software architecture for biosystem reverse engineering. Biotechnology and Bioprocess Engineering, 2005, 10, 400-407.	1.4	2
142	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
143	Modularized learning of genetic interaction networks from biological annotations and mRNA expression data. Bioinformatics, 2005, 21, 2739-2747.	1.8	52
144	Detecting clusters of different geometrical shapes in microarray gene expression data. Bioinformatics, 2005, 21, 1927-1934.	1.8	48

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145	Architecture of basic building blocks in protein and domain structural interaction networks. Bioinformatics, 2005, 21, 1479-1486.	1.8	26
146	Assessing the Quality of Fuzzy Partitions Using Relative Intersection. IEICE Transactions on Information and Systems, 2005, E88-D, 594-602.	0.4	1
147	Mathematical Modeling of Immune Suppression. Lecture Notes in Computer Science, 2005, , 182-192.	1.0	2
148	Regression trees for regulatory element identification. Bioinformatics, 2004, 20, 750-757.	1.8	34
149	Integration of Immune Models Using Petri Nets. Lecture Notes in Computer Science, 2004, , 205-216.	1.0	7
150	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
151	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
152	On cluster validity index for estimation of the optimal number of fuzzy clusters. Pattern Recognition, 2004, 37, 2009-2025.	5.1	187
153	Fuzzy clustering of categorical data using fuzzy centroids. Pattern Recognition Letters, 2004, 25, 1263-1271.	2.6	120
154	In silico analysis of lactate producing metabolic network in Lactococcus lactis. Enzyme and Microbial Technology, 2004, 35, 654-662.	1.6	6
155	A novel initialization scheme for the fuzzy c-means algorithm for color clustering. Pattern Recognition Letters, 2004, 25, 227-237.	2.6	76
156	Ranking the sequences of fuzzy values. Information Sciences, 2004, 160, 41-52.	4.0	17
157	A cluster validation index for GK cluster analysis based on relative degree of sharing. Information Sciences, 2004, 168, 225-242.	4.0	72
158	Fuzzy Branching Temporal Logic. IEEE Transactions on Systems, Man, and Cybernetics, 2004, 34, 1045-1055.	5.5	42
159	A Taxonomy of Dirty Data. Data Mining and Knowledge Discovery, 2003, 7, 81-99.	2.4	209
160	Fuzzy cluster validation index based on inter-cluster proximity. Pattern Recognition Letters, 2003, 24, 2561-2574.	2.6	73
161	Learning Rules to Extract Protein Interactions from Biomedical Text. Lecture Notes in Computer Science, 2003, , 148-158.	1.0	2
162	Decision Trees for Multiple Abstraction Levels of Data. Lecture Notes in Computer Science, 2001, , 76-87.	1.0	0

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163	Extending semantics of relational operators for vague queries. Microprocessing and Microprogramming, 1993, 39, 165-168.	0.3	1
164	Accommodating subjective vagueness through a fuzzy extension to the relational data model. Information Systems, 1993, 18, 363-374.	2.4	16
165	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