

Cathy H Wu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/660173/publications.pdf>

Version: 2024-02-01

207
papers

39,349
citations

30551

56
h-index

6024

165
g-index

222
all docs

222
docs citations

222
times ranked

60839
citing authors

#	ARTICLE	IF	CITATIONS
1	Global analysis of switchgrass (<i>Panicum virgatum</i> L.) transcriptomes in response to interactive effects of drought and heat stresses. <i>BMC Plant Biology</i> , 2022, 22, 107.	1.6	4
2	The InterPro protein families and domains database: 20 years on. <i>Nucleic Acids Research</i> , 2021, 49, D344-D354.	6.5	1,385
3	UniProt: the universal protein knowledgebase in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D480-D489.	6.5	4,709
4	Characterization of metabolic responses, genetic variations, and microsatellite instability in ammonia-stressed CHO cells grown in fed-batch cultures. <i>BMC Biotechnology</i> , 2021, 21, 4.	1.7	10
5	Alterations in the Global Proteome and Phosphoproteome in Third Generation EGFR TKI Resistance Reveal Drug Targets to Circumvent Resistance. <i>Cancer Research</i> , 2021, 81, 3051-3066.	0.4	38
6	TnCentral: a Prokaryotic Transposable Element Database and Web Portal for Transposon Analysis. <i>MBio</i> , 2021, 12, e0206021.	1.8	56
7	The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , 2021, 49, D325-D334.	6.5	2,416
8	COVID-19 Knowledge Graph from semantic integration of biomedical literature and databases. <i>Bioinformatics</i> , 2021, 37, 4597-4598.	1.8	17
9	A crowdsourcing open platform for literature curation in UniProt. <i>PLoS Biology</i> , 2021, 19, e3001464.	2.6	74
10	Protein ontology on the semantic web for knowledge discovery. <i>Scientific Data</i> , 2020, 7, 337.	2.4	9
11	piNET: a versatile web platform for downstream analysis and visualization of proteomics data. <i>Nucleic Acids Research</i> , 2020, 48, W85-W93.	6.5	18
12	Understanding ER+ Breast Cancer Dormancy Using Bioinspired Synthetic Matrices for Long-Term 3D Culture and Insights into Late Recurrence. <i>Advanced Biology</i> , 2020, 4, e2000119.	3.0	17
13	OUP accepted manuscript. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	0
14	Using distant supervision to augment manually annotated data for relation extraction. <i>PLoS ONE</i> , 2019, 14, e0216913.	1.1	17
15	UniProt genomic mapping for deciphering functional effects of missense variants. <i>Human Mutation</i> , 2019, 40, 694-705.	1.1	29
16	PIRSitePredict for protein functional site prediction using position-specific rules. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	5
17	Tunable synthetic extracellular matrices to investigate breast cancer response to biophysical and biochemical cues. <i>APL Bioengineering</i> , 2019, 3, 016101.	3.3	26
18	Coordination between TGF- β 2 cellular signaling and epigenetic regulation during epithelial to mesenchymal transition. <i>Epigenetics and Chromatin</i> , 2019, 12, 11.	1.8	21

#	ARTICLE	IF	CITATIONS
19	Pattern Discovery for Wide-Window Open Information Extraction in Biomedical Literature. , 2018, , .		7
20	Automatic gene annotation using GO terms from cellular component domain. BMC Medical Informatics and Decision Making, 2018, 18, 119.	1.5	16
21	PENNER: Pattern-enhanced Nested Named Entity Recognition in Biomedical Literature. , 2018, , .		4
22	iTextMine: integrated text-mining system for large-scale knowledge extraction from the literature. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	22
23	Cloud-based Semantic Integration and Knowledge Discovery Systems in Precision Medicine. , 2018, , .		0
24	Transcriptional profiling of liver during the critical embryo-to-hatchling transition period in the chicken (Gallus gallus). BMC Genomics, 2018, 19, 695.	1.2	25
25	RESTful API for iPTMnet. , 2018, , .		0
26	iPTMnet: an integrated resource for protein post-translational modification network discovery. Nucleic Acids Research, 2018, 46, D542-D550.	6.5	120
27	Completing sparse and disconnected protein-protein network by deep learning. BMC Bioinformatics, 2018, 19, 103.	1.2	16
28	Integrative annotation and knowledge discovery of kinase post-translational modifications and cancer-associated mutations through federated protein ontologies and resources. Scientific Reports, 2018, 8, 6518.	1.6	31
29	DEXTER: Disease-Expression Relation Extraction from Text. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	11
30	Protein Complex Mention Recognition with Web-Based Knowledge Learning. Lecture Notes in Computer Science, 2018, , 190-197.	1.0	0
31	Predicting nsSNPs that Disrupt Protein-Protein Interactions Using Docking. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1082-1093.	1.9	1
32	InterPro in 2017â€”beyond protein family and domain annotations. Nucleic Acids Research, 2017, 45, D190-D199.	6.5	1,358
33	eGARD: Extracting associations between genomic anomalies and drug responses from text. PLoS ONE, 2017, 12, e0189663.	1.1	14
34	Protein Ontology (PRO): enhancing and scaling up the representation of protein entities. Nucleic Acids Research, 2017, 45, D339-D346.	6.5	73
35	eGenPub, a text mining system for extending computationally mapped bibliography for UniProt Knowledgebase by capturing centrality. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	6
36	Protein Bioinformatics Databases and Resources. Methods in Molecular Biology, 2017, 1558, 3-39.	0.4	154

#	ARTICLE	IF	CITATIONS
37	Analysis of Protein Phosphorylation and Its Functional Impact on Protein-Protein Interactions via Text Mining of the Scientific Literature. <i>Methods in Molecular Biology</i> , 2017, 1558, 213-232.	0.4	7
38	iPTMnet: Integrative Bioinformatics for Studying PTM Networks. <i>Methods in Molecular Biology</i> , 2017, 1558, 333-353.	0.4	26
39	Evolutionary analysis and interaction prediction for protein-protein interaction network in geometric space. <i>PLoS ONE</i> , 2017, 12, e0183495.	1.1	12
40	Noise Reduction Methods for Distantly Supervised Biomedical Relation Extraction. , 2017, , .		12
41	BioC-compatible full-text passage detection for protein-protein interactions using extended dependency graph. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw072.	1.4	6
42	Enhancing interacting residue prediction with integrated contact matrix prediction in protein-protein interaction. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2016, 2016, 17.	1.4	1
43	Protein-protein interaction prediction based on multiple kernels and partial network with linear programming. <i>BMC Systems Biology</i> , 2016, 10, .	3.0	3
44	Overview of the interactive task in BioCreative V. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw119.	1.4	36
45	BioCreative V BioC track overview: collaborative biocurator assistant task for BioGRID. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw121.	1.4	28
46	Prediction of residue-residue contact matrix for protein-protein interaction with Fisher score features and deep learning. <i>Methods</i> , 2016, 110, 97-105.	1.9	41
47	miRiaD: A Text Mining Tool for Detecting Associations of microRNAs with Diseases. <i>Journal of Biomedical Semantics</i> , 2016, 7, 9.	0.9	16
48	Inference of protein-protein interaction networks from multiple heterogeneous data. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2016, 2016, 8.	1.4	13
49	Computational clustering for viral reference proteomes: Table 1.. <i>Bioinformatics</i> , 2016, 32, 2041-2043.	1.8	3
50	Scalable Text Mining Assisted Curation of Post-Translationally Modified Proteoforms in the Protein Ontology. <i>CEUR Workshop Proceedings</i> , 2016, 1747, .	2.3	0
51	Construction of phosphorylation interaction networks by text mining of full-length articles using the eFIP system. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	1.4	23
52	UniRef clusters: a comprehensive and scalable alternative for improving sequence similarity searches. <i>Bioinformatics</i> , 2015, 31, 926-932.	1.8	1,223
53	An Integrated Approach for Analyzing Clinical Genomic Variant Data from Next-Generation Sequencing. <i>Journal of Biomolecular Techniques</i> , 2015, 26, 19-28.	0.8	9
54	Toll-Like Receptor Signaling in Vertebrates: Testing the Integration of Protein, Complex, and Pathway Data in the Protein Ontology Framework. <i>PLoS ONE</i> , 2015, 10, e0122978.	1.1	2

#	ARTICLE	IF	CITATIONS
55	miRTex: A Text Mining System for miRNA-Gene Relation Extraction. <i>PLoS Computational Biology</i> , 2015, 11, e1004391.	1.5	50
56	RNA-Seq Analysis of Abdominal Fat in Genetically Fat and Lean Chickens Highlights a Divergence in Expression of Genes Controlling Adiposity, Hemostasis, and Lipid Metabolism. <i>PLoS ONE</i> , 2015, 10, e0139549.	1.1	49
57	Protein-protein interaction network inference from multiple kernels with optimization based on random walk by linear programming. , 2015, , .		3
58	The InterPro protein families database: the classification resource after 15 years. <i>Nucleic Acids Research</i> , 2015, 43, D213-D221.	6.5	1,205
59	Oncogenic fusion protein EWS-FLI1 is a network hub that regulates alternative splicing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1307-16.	3.3	109
60	Evolutionary Model Selection and Parameter Estimation for Protein-Protein Interaction Network Based on Differential Evolution Algorithm. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 622-631.	1.9	16
61	UniProt: a hub for protein information. <i>Nucleic Acids Research</i> , 2015, 43, D204-D212.	6.5	4,370
62	RLIMS-P 2.0: A Generalizable Rule-Based Information Extraction System for Literature Mining of Protein Phosphorylation Information. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 17-29.	1.9	42
63	Gene Ontology Consortium: going forward. <i>Nucleic Acids Research</i> , 2015, 43, D1049-D1056.	6.5	2,743
64	pGenN, a Gene Normalization Tool for Plant Genes and Proteins in Scientific Literature. <i>PLoS ONE</i> , 2015, 10, e0135305.	1.1	12
65	Bioinformatics Knowledge Map for Analysis of Beta-Catenin Function in Cancer. <i>PLoS ONE</i> , 2015, 10, e0141773.	1.1	12
66	An extended dependency graph for relation extraction in biomedical texts. , 2015, , .		16
67	Development of Bioinformatics Pipeline for Analyzing Clinical Pediatric NGS Data. <i>AMIA Summits on Translational Science Proceedings</i> , 2015, 2015, 207-11.	0.4	2
68	DDI2PPI. , 2014, , .		0
69	RLIMS-P: an online text-mining tool for literature-based extraction of protein phosphorylation information. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau081-bau081.	1.4	23
70	Docking features for predicting binding loss due to protein mutation. , 2014, , .		1
71	Integrative Computational and Experimental Approaches to Establish a Post-Myocardial Infarction Knowledge Map. <i>PLoS Computational Biology</i> , 2014, 10, e1003472.	1.5	10
72	Protein Ontology: a controlled structured network of protein entities. <i>Nucleic Acids Research</i> , 2014, 42, D415-D421.	6.5	63

#	ARTICLE	IF	CITATIONS
73	BioC interoperability track overview. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau053-bau053.	1.4	15
74	A generalizable NLP framework for fast development of pattern-based biomedical relation extraction systems. BMC Bioinformatics, 2014, 15, 285.	1.2	20
75	Activities at the Universal Protein Resource (UniProt). Nucleic Acids Research, 2014, 42, D191-D198.	6.5	1,162
76	Elevated FGF21 secretion, PGC-1 α and ketogenic enzyme expression are hallmarks of iron-sulfur cluster depletion in human skeletal muscle. Human Molecular Genetics, 2014, 23, 24-39.	1.4	59
77	Software for pre-processing Illumina next-generation sequencing short read sequences. Source Code for Biology and Medicine, 2014, 9, 8.	1.7	196
78	iSimp in BioC standard format: enhancing the interoperability of a sentence simplification system. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau038-bau038.	1.4	9
79	BioCreative-IV virtual issue. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau039-bau039.	1.4	43
80	SkateBase, an elasmobranch genome project and collection of molecular resources for chondrichthyan fishes. F1000Research, 2014, 3, 191.	0.8	61
81	Structural and functional studies of S-adenosyl-L-methionine binding proteins: a ligand-centric approach. BMC Structural Biology, 2013, 13, 6.	2.3	50
82	ngsShoRT. , 2013, , .		4
83	A framework for biomedical figure segmentation towards image-based document retrieval. BMC Systems Biology, 2013, 7, S8.	3.0	16
84	Transcription factors and genetic circuits orchestrating the complex, multilayered response of Clostridium acetobutylicum to butanol and butyrate stress. BMC Systems Biology, 2013, 7, 120.	3.0	65
85	A fast Peptide Match service for UniProt Knowledgebase. Bioinformatics, 2013, 29, 2808-2809.	1.8	101
86	An Image-Text Approach for Extracting Experimental Evidence of Protein-Protein Interactions in the Biomedical Literature. , 2013, , .		1
87	Text Mining of Protein Phosphorylation Information Using a Generalizable Rule-Based Approach. , 2013, , .		1
88	Construction of protein phosphorylation networks by data mining, text mining and ontology integration: analysis of the spindle checkpoint. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat038.	1.4	15
89	An overview of the BioCreative 2012 Workshop Track III: interactive text mining task. Database: the Journal of Biological Databases and Curation, 2013, 2013, bas056-bas056.	1.4	68
90	BioC: a minimalist approach to interoperability for biomedical text processing. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat064-bat064.	1.4	123

#	ARTICLE	IF	CITATIONS
91	Prediction of contact matrix for protein-protein interaction. <i>Bioinformatics</i> , 2013, 29, 1018-1025.	1.8	15
92	Use of the Protein Ontology for Multi-Faceted Analysis of Biological Processes: A Case Study of the Spindle Checkpoint. <i>Frontiers in Genetics</i> , 2013, 4, 62.	1.1	7
93	Reorganizing the protein space at the Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2012, 40, D71-D75.	6.5	1,196
94	The eFIP system for text mining of protein interaction networks of phosphorylated proteins. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas044-bas044.	1.4	20
95	Text mining for the biocuration workflow. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas020-bas020.	1.4	132
96	Pathway curation: Application of text-mining tools eGIFT and RLIMS-P. , 2012, , .		2
97	Building a classifier for identifying sentences pertaining to disease-drug relationships in tardive dyskinesia. , 2012, , .		3
98	BioCreative-2012 Virtual Issue. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas049-bas049.	1.4	19
99	InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , 2012, 40, D306-D312.	6.5	921
100	Predicting Ligand Binding Residues and Functional Sites Using Multipositional Correlations with Graph Theoretic Clustering and Kernel CCA. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 992-1001.	1.9	11
101	Robust segmentation of biomedical figures for image-based document retrieval. , 2012, , .		6
102	iSimp: A sentence simplification system for biomedical text. , 2012, , .		21
103	An Automatic System for Extracting Figures and Captions in Biomedical PDF Documents. , 2011, , .		9
104	Omics-Based Molecular Target and Biomarker Identification. <i>Methods in Molecular Biology</i> , 2011, 719, 547-571.	0.4	42
105	Protein Bioinformatics Databases and Resources. <i>Methods in Molecular Biology</i> , 2011, 694, 3-24.	0.4	27
106	The Human Proteome Project: Current State and Future Direction. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.009993.	2.5	294
107	The representation of protein complexes in the Protein Ontology (PRO). <i>BMC Bioinformatics</i> , 2011, 12, 371.	1.2	14
108	Overview of the BioCreative III Workshop. <i>BMC Bioinformatics</i> , 2011, 12, S1.	1.2	88

#	ARTICLE	IF	CITATIONS
109	BioCreative III interactive task: an overview. BMC Bioinformatics, 2011, 12, S4.	1.2	65
110	A comprehensive protein-centric ID mapping service for molecular data integration. Bioinformatics, 2011, 27, 1190-1191.	1.8	70
111	The Protein Ontology: a structured representation of protein forms and complexes. Nucleic Acids Research, 2011, 39, D539-D545.	6.5	102
112	Protein-Centric Data Integration for Functional Analysis of Comparative Proteomics Data. Methods in Molecular Biology, 2011, 694, 323-339.	0.4	3
113	eFIP: A Tool for Mining Functional Impact of Phosphorylation from Literature. Methods in Molecular Biology, 2011, 694, 63-75.	0.4	10
114	Structure-Guided Rule-Based Annotation of Protein Functional Sites in UniProt Knowledgebase. Methods in Molecular Biology, 2011, 694, 91-105.	0.4	7
115	Representative Proteomes: A Stable, Scalable and Unbiased Proteome Set for Sequence Analysis and Functional Annotation. PLoS ONE, 2011, 6, e18910.	1.1	94
116	Proteomic Analysis of Pathways Involved in Estrogen-Induced Growth and Apoptosis of Breast Cancer Cells. PLoS ONE, 2011, 6, e20410.	1.1	28
117	Document classification for mining host pathogen protein-protein interactions. Artificial Intelligence in Medicine, 2010, 49, 155-160.	3.8	16
118	Community annotation in biology. Biology Direct, 2010, 5, 12.	1.9	21
119	Protein Bioinformatics Infrastructure for the Integration and Analysis of Multiple High-Throughput Omics Data. Advances in Bioinformatics, 2010, 2010, 1-19.	5.7	19
120	Prediction of Catalytic Residues in Proteins Using a Consensus of Prediction (CoP) Approach. , 2010, , .		0
121	Molecular Mechanisms Mediating the Effect of Mono-(2-Ethylhexyl) Phthalate on Hormone-Stimulated Steroidogenesis in MA-10 Mouse Tumor Leydig Cells. Endocrinology, 2010, 151, 3348-3362.	1.4	78
122	Predicting ligand binding residues using multi-positional correlations and kernel canonical correlation analysis. , 2010, , .		2
123	Phylogenomic Analysis of Marine Roseobacters. PLoS ONE, 2010, 5, e11604.	1.1	29
124	Systems Integration of Biodefense Omics Data for Analysis of Pathogen-Host Interactions and Identification of Potential Targets. PLoS ONE, 2009, 4, e7162.	1.1	18
125	Studying Biocuration Workflows. Nature Precedings, 2009, , .	0.1	1
126	Biocuration Workflow Catalogue. Nature Precedings, 2009, , .	0.1	0

#	ARTICLE	IF	CITATIONS
127	Predicting functional sites in biological sequences using canonical correlation analysis. , 2009, , .		0
128	InterPro: the integrative protein signature database. Nucleic Acids Research, 2009, 37, D211-D215.	6.5	1,712
129	TGF-beta signaling proteins and the Protein Ontology. BMC Bioinformatics, 2009, 10, S3.	1.2	9
130	Sequence signatures in envelope protein may determine whether flaviviruses produce hemorrhagic or encephalitic syndromes. Virus Genes, 2009, 39, 1-9.	0.7	16
131	BioTagger-GM: A Gene/Protein Name Recognition System. Journal of the American Medical Informatics Association: JAMIA, 2009, 16, 247-255.	2.2	54
132	Mining impact of protein modifications on protein-protein interactions from literature. , 2009, , .		0
133	iProLINK: A Framework for Linking Text Mining with Ontology and Systems Biology. , 2008, , .		2
134	Protein bioinformatics. , 2008, , 203-222.		1
135	Document Classification for Mining Host Pathogen Protein-Protein Interactions. , 2008, , .		6
136	Integrated Bioinformatics for Radiation-Induced Pathway Analysis from Proteomics and Microarray Data. Journal of Proteomics and Bioinformatics, 2008, 01, 047-060.	0.4	20
137	Dependence network modeling for biomarker identification. Bioinformatics, 2007, 23, 198-206.	1.8	64
138	Challenges and Solutions in Proteomics. Current Genomics, 2007, 8, 21-28.	0.7	12
139	UniRef: comprehensive and non-redundant UniProt reference clusters. Bioinformatics, 2007, 23, 1282-1288.	1.8	1,144
140	New developments in the InterPro database. Nucleic Acids Research, 2007, 35, D224-D228.	6.5	444
141	Mapping Gene/Protein Names in Free Text to Biomedical Databases. , 2007, , .		4
142	Comparative bioinformatics analyses and profiling of lysosome-related organelle proteomes. International Journal of Mass Spectrometry, 2007, 259, 147-160.	0.7	49
143	Framework for a Protein Ontology. BMC Bioinformatics, 2007, 8, S1.	1.2	78
144	A comparison study on algorithms of detecting long forms for short forms in biomedical text. BMC Bioinformatics, 2007, 8, S5.	1.2	25

#	ARTICLE	IF	CITATIONS
145	Computational analysis and identification of amino acid sites in dengue E proteins relevant to development of diagnostics and vaccines. <i>Virus Genes</i> , 2007, 35, 175-186.	0.7	34
146	Integration of bioinformatics resources for functional analysis of gene expression and proteomic data. <i>Frontiers in Bioscience - Landmark</i> , 2007, 12, 5071.	3.0	30
147	PIRSF family classification system for protein functional and evolutionary analysis. <i>Evolutionary Bioinformatics</i> , 2007, 2, 197-209.	0.6	35
148	Proteomic and Bioinformatic Characterization of the Biogenesis and Function of Melanosomes. <i>Journal of Proteome Research</i> , 2006, 5, 3135-3144.	1.8	183
149	PIRSF Family Classification System for Protein Functional and Evolutionary Analysis. <i>Evolutionary Bioinformatics</i> , 2006, 2, 117693430600200.	0.6	35
150	Quantitative Assessment of Dictionary-based Protein Named Entity Tagging. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2006, 13, 497-507.	2.2	35
151	Prediction of catalytic residues using Support Vector Machine with selected protein sequence and structural properties. <i>BMC Bioinformatics</i> , 2006, 7, 312.	1.2	105
152	Substring selection for biomedical document classification. <i>Bioinformatics</i> , 2006, 22, 2136-2142.	1.8	20
153	The Universal Protein Resource (UniProt): an expanding universe of protein information. <i>Nucleic Acids Research</i> , 2006, 34, D187-D191.	6.5	961
154	Framework for a protein ontology. , 2006, , .		1
155	A comparison study of biomedical short form definition detection algorithms. , 2006, , .		2
156	BioThesaurus: a web-based thesaurus of protein and gene names. <i>Bioinformatics</i> , 2006, 22, 103-105.	1.8	106
157	Computational identification of strain-, species- and genus-specific proteins. <i>BMC Bioinformatics</i> , 2005, 6, 279.	1.2	16
158	Protein Name Tagging Guidelines: Lessons Learned. <i>Comparative and Functional Genomics</i> , 2005, 6, 72-76.	2.0	15
159	The PIR SuperFamily (PIRSF) classification system. , 2005, , .		0
160	DynGO: a tool for visualizing and mining of Gene Ontology and its associations. <i>BMC Bioinformatics</i> , 2005, 6, 201.	1.2	35
161	Plant Protein Annotation in the UniProt Knowledgebase. <i>Plant Physiology</i> , 2005, 138, 59-66.	2.3	42
162	Dynamically generating a protein entity dictionary using online resources. , 2005, , .		0

#	ARTICLE	IF	CITATIONS
163	PIRSF: family classification system at the Protein Information Resource. Nucleic Acids Research, 2004, 32, 112D-114.	6.5	193
164	InterPro, progress and status in 2005. Nucleic Acids Research, 2004, 33, D201-D205.	6.5	478
165	The Universal Protein Resource (UniProt). Nucleic Acids Research, 2004, 33, D154-D159.	6.5	1,681
166	Protein sequence databases. Current Opinion in Chemical Biology, 2004, 8, 76-80.	2.8	201
167	The iProClass integrated database for protein functional analysis. Computational Biology and Chemistry, 2004, 28, 87-96.	1.1	86
168	iProLINK: an integrated protein resource for literature mining. Computational Biology and Chemistry, 2004, 28, 409-416.	1.1	40
169	UniProt: the Universal Protein knowledgebase. Nucleic Acids Research, 2004, 32, 115D-119.	6.5	2,994
170	Gene and Protein Profiling of the Response of MAË10 Leydig Tumor Cells to Human Chorionic Gonadotropin. Journal of Andrology, 2004, 25, 900-913.	2.0	26
171	BIO-AJAX. SIGMOD Record, 2004, 33, 51-57.	0.7	17
172	Update on genome completion and annotations: Protein Information Resource. Human Genomics, 2004, 1, 229.	1.4	25
173	A FAMILY CLASSIFICATION APPROACH TO FUNCTIONAL ANNOTATION OF PROTEINS. , 2004, , 417-434.		1
174	Protein family classification and functional annotation. Computational Biology and Chemistry, 2003, 27, 37-47.	1.1	103
175	iProClass: an integrated database of protein family, function and structure information. Nucleic Acids Research, 2003, 31, 390-392.	6.5	41
176	The Protein Information Resource. Nucleic Acids Research, 2003, 31, 345-347.	6.5	385
177	The PIR for Functional Genomics and Proteomics. , 2003, , 431-442.		0
178	The Protein Information Resource for Functional Genomics and Proteomics. , 2003, , 117-137.		0
179	The Protein Information Resource: an integrated public resource of functional annotation of proteins. Nucleic Acids Research, 2002, 30, 35-37.	6.5	186
180	Accomplishments and challenges in literature data mining for biology. Bioinformatics, 2002, 18, 1553-1561.	1.8	229

#	ARTICLE	IF	CITATIONS
181	New techniques for extracting features from protein sequences. IBM Systems Journal, 2001, 40, 426-441.	3.1	80
182	iProClass: an integrated, comprehensive and annotated protein classification database. Nucleic Acids Research, 2001, 29, 52-54.	6.5	32
183	Protein Information Resource: a community resource for expert annotation of protein data. Nucleic Acids Research, 2001, 29, 29-32.	6.5	72
184	ProClass protein family database. Nucleic Acids Research, 2000, 28, 273-276.	6.5	18
185	The Protein Information Resource (PIR). Nucleic Acids Research, 2000, 28, 41-44.	6.5	165
186	The PIR-International Protein Sequence Database. Nucleic Acids Research, 1999, 27, 39-43.	6.5	149
187	ProClass Protein Family Database. Nucleic Acids Research, 1999, 27, 272-274.	6.5	28
188	GENE FAMILY IDENTIFICATION NETWORK DESIGN FOR PROTEIN SEQUENCE ANALYSIS. International Journal on Artificial Intelligence Tools, 1999, 08, 419-432.	0.7	3
189	Title is missing!. Applied Intelligence, 1997, 7, 27-38.	3.3	12
190	Artificial neural networks for molecular sequence analysis. Computers & Chemistry, 1997, 21, 237-256.	1.2	95
191	[5] Gene classification artificial neural system. Methods in Enzymology, 1996, 266, 71-88.	0.4	22
192	A Protein Class Database Organized with ProSite Protein Groups and PIR Superfamilies. Journal of Computational Biology, 1996, 3, 547-561.	0.8	14
193	Motif identification neural design for rapid and sensitive protein family search. Bioinformatics, 1996, 12, 109-118.	1.8	16
194	Neural networks for molecular sequence classification. Mathematics and Computers in Simulation, 1995, 40, 23-33.	2.4	13
195	Title is missing!. Machine Learning, 1995, 21, 177-193.	3.4	2
196	Neural networks for full-scale protein sequence classification: Sequence encoding with singular value decomposition. Machine Learning, 1995, 21, 177-193.	3.4	77
197	Back-propagation and counter-propagation neural networks for phylogenetic classification of ribosomal RNA sequences. Nucleic Acids Research, 1994, 22, 4291-4299.	6.5	46
198	Neural Networks for Molecular Sequence Classification. , 1994, , 279-305.		3

#	ARTICLE	IF	CITATIONS
199	Classification neural networks for rapid sequence annotation and automated database organization. Computers & Chemistry, 1993, 17, 219-227.	1.2	18
200	PROTEIN CLASSIFICATION ARTIFICIAL NEURAL SYSTEM: A FILTER PROGRAM FOR DATABASE SEARCH. , 1993, , .		0
201	CANS: an interactive neural network system for CRAY supercomputers. , 1992, , .		3
202	Protein classification artificial neural system. Protein Science, 1992, 1, 667-677.	3.1	112
203	Protein classification using a neural network database system. , 1991, , .		8
204	Neural networks for molecular sequence database management. , 1991, , .		4
205	Using an artificial neural system to determine the knowledge based of an expert system. , 1990, , .		4
206	Artificial neural system for gene classification using a domain database. , 1990, , .		10
207	Annotation of Protein Sequences. , 0, , 131-147.		0