

Karin M Verspoor

List of Publications by Year in descending order

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Version: 2024-02-01

181
papers

4,446
citations

172457

29
h-index

149698

56
g-index

204
all docs

204
docs citations

204
times ranked

4843
citing authors

#	ARTICLE	IF	CITATIONS
1	Benchmarks for measurement of duplicate detection methods in nucleotide databases. Database: the Journal of Biological Databases and Curation, 2023, 2023, .	3.0	10
2	Evaluating the dose, indication and agreement with guidelines of antimicrobial use in companion animal practice with natural language processing. JAC-Antimicrobial Resistance, 2022, 4, dlab194.	2.1	6
3	Large-scale protein-protein post-translational modification extraction with distant supervision and confidence calibrated BioBERT. BMC Bioinformatics, 2022, 23, 4.	2.6	4
4	Accuracy of Machine Learning Assisted Detection of Keratoconus: A Systematic Review and Meta-Analysis. Journal of Clinical Medicine, 2022, 11, 478.	2.4	8
5	Overcoming challenges in extracting prescribing habits from veterinary clinics using big data and deep learning. Australian Veterinary Journal, 2022, , .	1.1	0
6	The ChEMU 2022 Evaluation Campaign: Information Extraction in Chemical Patents. Lecture Notes in Computer Science, 2022, , 400-407.	1.3	2
7	Early prediction of incident liver disease using conventional risk factors and gut-microbiome-augmented gradient boosting. Cell Metabolism, 2022, 34, 719-730.e4.	16.2	35
8	COVID-19 Drug Repurposing: A Network-Based Framework for Exploring Biomedical Literature and Clinical Trials for Possible Treatments. Pharmaceutics, 2022, 14, 567.	4.5	6
9	Detection of self-harm and suicidal ideation in emergency department triage notes. Journal of the American Medical Informatics Association: JAMIA, 2022, 29, 472-480.	4.4	17
10	Exploring automatic inconsistency detection for literature-based gene ontology annotation. Bioinformatics, 2022, 38, i273-i281.	4.1	0
11	Uncertainty Estimation and Reduction of Pre-trained Models for Text Regression. Transactions of the Association for Computational Linguistics, 2022, 10, 680-696.	4.8	2
12	Tasks as needs: reframing the paradigm of clinical natural language processing research for real-world decision support. Journal of the American Medical Informatics Association: JAMIA, 2022, 29, 1810-1817.	4.4	20
13	PoLoBag: Polynomial Lasso Bagging for signed gene regulatory network inference from expression data. Bioinformatics, 2021, 36, 5187-5193.	4.1	10
14	ChEMU 2021: Reaction Reference Resolution and Anaphora Resolution in Chemical Patents. Lecture Notes in Computer Science, 2021, , 608-615.	1.3	2
15	Overview of ChEMU 2021: Reaction Reference Resolution and Anaphora Resolution in Chemical Patents. Lecture Notes in Computer Science, 2021, , 292-307.	1.3	3
16	Use and validation of text mining and cluster algorithms to derive insights from Corona Virus Disease-2019 (COVID-19) medical literature. Computer Methods and Programs in Biomedicine Update, 2021, 1, 100010.	3.7	9
17	ChEMU 2020: Natural Language Processing Methods Are Effective for Information Extraction From Chemical Patents. Frontiers in Research Metrics and Analytics, 2021, 6, 654438.	1.9	15
18	Use of a Victorian statewide surveillance program to evaluate the burden of healthcare-associated Staphylococcus aureus bacteraemia and Clostridioides difficile infection in patients with cancer. Internal Medicine Journal, 2021, , .	0.8	0

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19	Bow-tie architecture of gene regulatory networks in species of varying complexity. <i>Journal of the Royal Society Interface</i> , 2021, 18, 20210069.	3.4	2
20	Early prediction of diagnostic-related groups and estimation of hospital cost by processing clinical notes. <i>Npj Digital Medicine</i> , 2021, 4, 103.	10.9	20
21	The Evolution of Clinical Knowledge During COVID-19: Towards a Global Learning Health System. <i>Yearbook of Medical Informatics</i> , 2021, 30, 176-184.	1.0	7
22	Machine learning with a reduced dimensionality representation of comprehensive Pentacam tomography parameters to identify subclinical keratoconus. <i>Computers in Biology and Medicine</i> , 2021, 138, 104884.	7.0	10
23	Memorization vs. Generalization : Quantifying Data Leakage in NLP Performance Evaluation. , 2021, , .		12
24	ChEMU-Ref: A Corpus for Modeling Anaphora Resolution in the Chemical Domain. , 2021, , .		7
25	Impact of detecting clinical trial elements in exploration of COVID-19 literature. , 2021, , .		0
26	TargetAnalytica: A Text Analytics Framework for Ranking Therapeutic Molecules in the Bibliome. <i>Studies in Big Data</i> , 2021, , 165-184.	1.1	0
27	Automatic consistency assurance for literature-based gene ontology annotation. <i>BMC Bioinformatics</i> , 2021, 22, 565.	2.6	2
28	ChemTables: a dataset for semantic classification on tables in chemical patents. <i>Journal of Cheminformatics</i> , 2021, 13, 97.	6.1	2
29	Quality Matters: Biocuration Experts on the Impact of Duplication and Other Data Quality Issues in Biological Databases. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 91-103.	6.9	14
30	Evaluation of consensus strategies for haplotype phasing. <i>Briefings in Bioinformatics</i> , 2020, 22, .	6.5	4
31	Artificial intelligence for clinical decision support in neurology. <i>Brain Communications</i> , 2020, 2, fcaa096.	3.3	41
32	Classification performance of administrative coding data for detection of invasive fungal infection in paediatric cancer patients. <i>PLoS ONE</i> , 2020, 15, e0238889.	2.5	7
33	Use of cefovecin in dogs and cats attending first-opinion veterinary practices in Australia. <i>Veterinary Record</i> , 2020, 187, e95.	0.3	14
34	Testing Contextualized Word Embeddings to Improve NER in Spanish Clinical Case Narratives. <i>IEEE Access</i> , 2020, 8, 164717-164726.	4.2	10
35	Development of a Self-Harm Monitoring System for Victoria. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 9385.	2.6	8
36	Describing the antimicrobial usage patterns of companion animal veterinary practices; free text analysis of more than 4.4 million consultation records. <i>PLoS ONE</i> , 2020, 15, e0230049.	2.5	38

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37	Evaluating the Performance of Various Machine Learning Algorithms to Detect Subclinical Keratoconus. <i>Translational Vision Science and Technology</i> , 2020, 9, 24.	2.2	37
38	Burden and clinical outcomes of hospital-coded infections in patients with cancer: an 11-year longitudinal cohort study at an Australian cancer centre. <i>Supportive Care in Cancer</i> , 2020, 28, 6023-6034.	2.2	7
39	ChEMU: Named Entity Recognition and Event Extraction of Chemical Reactions from Patents. <i>Lecture Notes in Computer Science</i> , 2020, , 572-579.	1.3	16
40	Overview of ChEMU 2020: Named Entity Recognition and Event Extraction of Chemical Reactions from Patents. <i>Lecture Notes in Computer Science</i> , 2020, , 237-254.	1.3	13
41	Evaluating the Utility of Model Configurations and Data Augmentation on Clinical Semantic Textual Similarity. , 2020, , .		12
42	WikiUMLS: Aligning UMLS to Wikipedia via Cross-lingual Neural Ranking. , 2020, , .		1
43	Improved Topic Representations of Medical Documents to Assist COVID-19 Literature Exploration. , 2020, , .		2
44	Domain Adaptation and Instance Selection for Disease Syndrome Classification over Veterinary Clinical Notes. , 2020, , .		5
45	Learning from Unlabelled Data for Clinical Semantic Textual Similarity. , 2020, , .		9
46	Advanced Methods for Big Data Analytics in Womenâ€™s Health. , 2020, , .		0
47	Title is missing!. , 2020, 15, e0238889.		0
48	Title is missing!. , 2020, 15, e0238889.		0
49	Title is missing!. , 2020, 15, e0238889.		0
50	Title is missing!. , 2020, 15, e0238889.		0
51	Using natural language processing and VetCompass to understand antimicrobial usage patterns in Australia. <i>Australian Veterinary Journal</i> , 2019, 97, 298-300.	1.1	23
52	The current scope of healthcare-associated infection surveillance activities in hospitalized immunocompromised patients: a systematic review. <i>International Journal of Epidemiology</i> , 2019, 48, 1768-1782.	1.9	6
53	Exploring effective approaches for haplotype block phasing. <i>BMC Bioinformatics</i> , 2019, 20, 540.	2.6	24
54	Quantifying semantic similarity of clinical evidence in the biomedical literature to facilitate related evidence synthesis. <i>Journal of Biomedical Informatics</i> , 2019, 100, 103321.	4.3	6

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55	Overview of the BioCreative VI Precision Medicine Track: mining protein interactions and mutations for precision medicine. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	30
56	Automated assessment of biological database assertions using the scientific literature. BMC Bioinformatics, 2019, 20, 216.	2.6	3
57	End-to-End Neural Relation Extraction Using Deep Biaffine Attention. Lecture Notes in Computer Science, 2019, , 729-738.	1.3	33
58	From POS tagging to dependency parsing for biomedical event extraction. BMC Bioinformatics, 2019, 20, 72.	2.6	20
59	Hospital-coded infections in patients with cancer: Evaluating disease burden and outcomes in Australian cancer patients. Infection, Disease and Health, 2019, 24, S2.	1.1	1
60	Search Effectiveness in Nonredundant Sequence Databases: Assessments and Solutions. Journal of Computational Biology, 2019, 26, 605-617.	1.6	1
61	Improving Chemical Named Entity Recognition in Patents with Contextualized Word Embeddings. , 2019, , .		21
62	Findings of the WMT 2019 Biomedical Translation Shared Task: Evaluation for MEDLINE Abstracts and Biomedical Terminologies. , 2019, , .		9
63	Characterizing the Scope of Exposome Research Through Topic Modeling and Ontology Analysis. Studies in Health Technology and Informatics, 2019, 264, 1530-1531.	0.3	2
64	A Bag-of-concepts Model Improves Relation Extraction in a Narrow Knowledge Domain with Limited Data. , 2019, , .		1
65	Comparative Analysis of Sequence Clustering Methods for Deduplication of Biological Databases. Journal of Data and Information Quality, 2018, 9, 1-27.	2.1	6
66	A two-tiered unsupervised clustering approach for drug repositioning through heterogeneous data integration. BMC Bioinformatics, 2018, 19, 129.	2.6	16
67	Web Forum Retrieval and Text Analytics: A Survey. Foundations and Trends in Information Retrieval, 2018, 12, 1-163.	6.8	27
68	CommViz: Visualization of semantic patterns in large social communication networks. Information Visualization, 2018, 17, 66-88.	1.9	3
69	The randomized information coefficient: assessing dependencies in noisy data. Machine Learning, 2018, 107, 509-549.	5.4	8
70	BioCreative VI Precision Medicine Track system performance is constrained by entity recognition and variations in corpus characteristics. Database: the Journal of Biological Databases and Curation, 2018, .	3.0	4
71	Semantic-Based Policy Composition for Privacy-Demanding Data Linkage. , 2018, , .		1
72	Appraising the Quality of Systematic Reviews for Age-Related Macular Degeneration Interventions. JAMA Ophthalmology, 2018, 136, 1051.	2.5	17

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73	Exploiting graph kernels for high performance biomedical relation extraction. Journal of Biomedical Semantics, 2018, 9, 7.	1.6	29
74	Crowdsourcing critical appraisal of research evidence (CrowdCARE) was found to be a valid approach to assessing clinical research quality. Journal of Clinical Epidemiology, 2018, 104, 8-14.	5.0	15
75	The Dagstuhl Perspectives Workshop on Performance Modeling and Prediction. ACM SIGIR Forum, 2018, 52, 91-101.	0.5	8
76	Convolutional neural networks for chemical-disease relation extraction are improved with character-based word embeddings. , 2018, , .		39
77	Comparing CNN and LSTM character-level embeddings in BiLSTM-CRF models for chemical and disease named entity recognition. , 2018, , .		21
78	The Use of Web-Based Technologies in Health Research Participation: Qualitative Study of Consumer and Researcher Experiences. Journal of Medical Internet Research, 2018, 20, e12094.	4.3	14
79	Findings of the WMT 2018 Biomedical Translation Shared Task: Evaluation on Medline test sets. , 2018, , .		1
80	An Improved Neural Network Model for Joint. , 2018, , .		4
81	DrKnow: A Diagnostic Learning Tool with Feedback from Automated Clinical Decision Support. AMIA ... Annual Symposium proceedings, 2018, 2018, 1348-1357.	0.2	0
82	Duplicates, redundancies and inconsistencies in the primary nucleotide databases: a descriptive study. Database: the Journal of Biological Databases and Curation, 2017, 2017, baw163.	3.0	36
83	Literature consistency of bioinformatics sequence databases is effective for assessing record quality. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	8
84	Automated detection of records in biological sequence databases that are inconsistent with the literature. Journal of Biomedical Informatics, 2017, 71, 229-240.	4.3	12
85	Positive-Unlabeled Learning for inferring drug interactions based on heterogeneous attributes. BMC Bioinformatics, 2017, 18, 140.	2.6	33
86	Learning Biological Sequence Types Using the Literature. , 2017, , .		2
87	Multi-field query expansion is effective for biomedical dataset retrieval. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	8
88	Coreference annotation and resolution in the Colorado Richly Annotated Full Text (CRAFT) corpus of biomedical journal articles. BMC Bioinformatics, 2017, 18, 372.	2.6	37
89	The Colorado Richly Annotated Full Text (CRAFT) Corpus: Multi-Model Annotation in the Biomedical Domain. , 2017, , 1379-1394.		18
90	Diagnostic Machine Learning Models for Acute Abdominal Pain: Towards an e-Learning Tool for Medical Students. Studies in Health Technology and Informatics, 2017, 245, 447-451.	0.3	10

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91	A Framework to Adjust Dependency Measure Estimates for Chance. , 2016, , .		12
92	The Pre-Eclampsia Ontology: A Disease Ontology Representing the Domain Knowledge Specific to Pre-Eclampsia. PLoS ONE, 2016, 11, e0162828.	2.5	7
93	TOWARDS EARLY DISCOVERY OF SALIENT HEALTH THREATS: A SOCIAL MEDIA EMOTION CLASSIFICATION TECHNIQUE. , 2016, , .		31
94	Towards a Methodology for Nursing-Specific Clinical Decision Support Systems (CDSS). Journal of Decision Systems, 2016, 25, 23-34.	3.2	3
95	What are health website visitors doing. , 2016, , .		2
96	Evaluation of CD-HIT for constructing non-redundant databases. , 2016, , .		10
97	A categorical analysis of coreference resolution errors in biomedical texts. Journal of Biomedical Informatics, 2016, 60, 309-318.	4.3	7
98	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
99	Text mining electronic hospital records to automatically classify admissions against disease: Measuring the impact of linking data sources. Journal of Biomedical Informatics, 2016, 64, 158-167.	4.3	39
100	A physarum-inspired prize-collecting steiner tree approach to identify subnetworks for drug repositioning. BMC Systems Biology, 2016, 10, 128.	3.0	10
101	Thematic issue of the Second combined Bio-ontologies and Phenotypes Workshop. Journal of Biomedical Semantics, 2016, 7, 66.	1.6	0
102	Establishing a baseline for literature mining human genetic variants and their relationships to disease cohorts. BMC Medical Informatics and Decision Making, 2016, 16, 68.	3.0	13
103	Gene Ontology synonym generation rules lead to increased performance in biomedical concept recognition. Journal of Biomedical Semantics, 2016, 7, 52.	1.6	9
104	Coreference resolution improves extraction of Biological Expression Language statements from texts. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw076.	3.0	9
105	Supervised Learning for Detection of Duplicates in Genomic Sequence Databases. PLoS ONE, 2016, 11, e0159644.	2.5	10
106	Designing Health Websites Based on Usersâ€™ Web-Based Information-Seeking Behaviors: A Mixed-Method Observational Study. Journal of Medical Internet Research, 2016, 18, e145.	4.3	50
107	Finding and Exploring Health Information with a Slider-Based User Interface. Studies in Health Technology and Informatics, 2016, 227, 106-12.	0.3	1
108	Special issue on bio-ontologies and phenotypes. Journal of Biomedical Semantics, 2015, 6, 40.	1.6	1

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109	CQADupStack. , 2015, , .		34
110	Better Health Explorer. , 2015, , .		23
111	Better health information exploration. , 2015, , .		0
112	Interoperability of text corpus annotations with the semantic web. BMC Proceedings, 2015, 9, .	1.6	1
113	The CHEMDNER corpus of chemicals and drugs and its annotation principles. Journal of Cheminformatics, 2015, 7, S2.	6.1	166
114	A close look at protein function prediction evaluation protocols. GigaScience, 2015, 4, 41.	6.4	18
115	Conceptualising health information seeking behaviours and exploratory search: result of a qualitative study. Health and Technology, 2015, 5, 45-55.	3.6	30
116	Optimizing graph-based patterns to extract biomedical events from the literature. BMC Bioinformatics, 2015, 16, S2.	2.6	8
117	Evaluation of a Machine Learning Duplicate Detection Method for Bioinformatics Databases. , 2015, , .		17
118	Summary of the BioLINK SIG 2013 meeting at ISMB/ECCB 2013. Bioinformatics, 2015, 31, 297-298.	4.1	1
119	Evaluating a variety of text-mined features for automatic protein function prediction with GOstruct. Journal of Biomedical Semantics, 2015, 6, 9.	1.6	20
120	Drawing on millions of biomedical journal publications to do predictive biology. , 2015, , .		0
121	PHENOstruct: Prediction of human phenotype ontology terms using heterogeneous data sources. F1000Research, 2015, 4, 259.	1.6	31
122	Assessing the Impact of Case Sensitivity and Term Information Gain on Biomedical Concept Recognition. PLoS ONE, 2015, 10, e0119091.	2.5	11
123	DTMBIO 2015. , 2015, , .		0
124	Big Data in Medicine Is Driving Big Changes. Yearbook of Medical Informatics, 2014, 23, 14-20.	1.0	119
125	Two platforms for research in Human Communication Science: The AusTalk corpus and the Alveo Virtual Laboratory. , 2014, , .		1
126	BioC interoperability track overview. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau053-bau053.	3.0	15

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127	Biomedical Text Mining: State-of-the-Art, Open Problems and Future Challenges. Lecture Notes in Computer Science, 2014, , 271-300.	1.3	41
128	Literature mining of genetic variants for curation: quantifying the importance of supplementary material. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau003-bau003.	3.0	34
129	Annokey: an annotation tool based on key term search of the NCBI Entrez Gene database. Source Code for Biology and Medicine, 2014, 9, 15.	1.7	6
130	Large-scale biomedical concept recognition: an evaluation of current automatic annotators and their parameters. BMC Bioinformatics, 2014, 15, 59.	2.6	94
131	Roles for Text Mining in Protein Function Prediction. Methods in Molecular Biology, 2014, 1159, 95-108.	0.9	15
132	Mutation extraction tools can be combined for robust recognition of genetic variants in the literature. F1000Research, 2014, 3, 18.	1.6	26
133	What Can We Get From 1000 Tokens? A Case Study of Multilingual POS Tagging For Resource-Poor Languages. , 2014, , .		18
134	Associating disease-related genetic variants in intergenic regions to the genes they impact. PeerJ, 2014, 2, e639.	2.0	20
135	Integrating UIMA with Alveo, a human communication science virtual laboratory. , 2014, , .		1
136	Mapping biomedical vocabularies: a semi-automated term matching approach. Studies in Health Technology and Informatics, 2014, 202, 16-9.	0.3	0
137	Mutation extraction tools can be combined for robust recognition of genetic variants in the literature. F1000Research, 2014, 3, 18.	1.6	22
138	Combining heterogeneous data sources for accurate functional annotation of proteins. BMC Bioinformatics, 2013, 14, S10.	2.6	41
139	Acquisition and evaluation of verb subcategorization resources for biomedicine. Journal of Biomedical Informatics, 2013, 46, 228-237.	4.3	8
140	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	19.0	789
141	Approaches to verb subcategorization for biomedicine. Journal of Biomedical Informatics, 2013, 46, 212-227.	4.3	8
142	Annotating the biomedical literature for the human variome. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat019-bat019.	3.0	53
143	BioC: a minimalist approach to interoperability for biomedical text processing. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat064-bat064.	3.0	123
144	Representing annotation compositionality and provenance for the Semantic Web. Journal of Biomedical Semantics, 2013, 4, 38.	1.6	10

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145	Approximate Subgraph Matching-Based Literature Mining for Biomedical Events and Relations. PLoS ONE, 2013, 8, e60954.	2.5	37
146	Natural Language Processing. , 2013, , 1495-1498.		5
147	Applied Text Mining. , 2013, , 33-37.		0
148	Unstructured Information Management Architecture (UIMA). , 2013, , 2320-2324.		0
149	Detection of protein catalytic sites in the biomedical literature. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2013, , 433-44.	0.7	6
150	Extracting structured information from free-text medication prescriptions using dependencies. , 2012, , .		5
151	Concept annotation in the CRAFT corpus. BMC Bioinformatics, 2012, 13, 161.	2.6	188
152	A corpus of full-text journal articles is a robust evaluation tool for revealing differences in performance of biomedical natural language processing tools. BMC Bioinformatics, 2012, 13, 207.	2.6	78
153	Literature mining of protein-residue associations with graph rules learned through distant supervision. Journal of Biomedical Semantics, 2012, 3, S2.	1.6	35
154	BioLemmatizer: a lemmatization tool for morphological processing of biomedical text. Journal of Biomedical Semantics, 2012, 3, 3.	1.6	97
155	Text Mining Improves Prediction of Protein Functional Sites. PLoS ONE, 2012, 7, e32171.	2.5	27
156	DETECTION OF PROTEIN CATALYTIC SITES IN THE BIOMEDICAL LITERATURE. , 2012, , .		2
157	Pattern Learning through Distant Supervision for Extraction of Protein-Residue Associations in the Biomedical Literature. , 2011, , .		3
158	HIGH-PRECISION BIOLOGICAL EVENT EXTRACTION: EFFECTS OF SYSTEM AND OF DATA. Computational Intelligence, 2011, 27, 681-701.	3.2	21
159	U-Compare bio-event meta-service: compatible BioNLP event extraction services. BMC Bioinformatics, 2011, 12, 481.	2.6	10
160	The gene normalization task in BioCreative III. BMC Bioinformatics, 2011, 12, S2.	2.6	101
161	The structural and content aspects of abstracts versus bodies of full text journal articles are different. BMC Bioinformatics, 2010, 11, 492.	2.6	121
162	A UIMA wrapper for the NCBO annotator. Bioinformatics, 2010, 26, 1800-1801.	4.1	12

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163	Leveraging Gene Ontology Annotations to Improve a Memory-Based Language Understanding System. , 2010, , .		2
164	Exploring Species-Based Strategies for Gene Normalization. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 462-471.	3.0	16
165	Visualization and Language Processing for Supporting Analysis across the Biomedical Literature. Lecture Notes in Computer Science, 2010, , 420-429.	1.3	12
166	Ontology quality assurance through analysis of term transformations. Bioinformatics, 2009, 25, i77-i84.	4.1	25
167	The textual characteristics of traditional and Open Access scientific journals are similar. BMC Bioinformatics, 2009, 10, 183.	2.6	33
168	High-precision biological event extraction with a concept recognizer. , 2009, , .		38
169	Uncovering protein interaction in abstracts and text using a novel linear model and word proximity networks. Genome Biology, 2008, 9, S11.	9.6	26
170	Exploiting Term Relations for Semantic Hierarchy Construction. , 2008, , .		0
171	A Semantics-Enhanced Language Model for Unsupervised Word Sense Disambiguation. , 2008, , 287-298.		2
172	Knowledge Integration in OpenWorlds: Utilizing the Mathematics of Hierarchical Structure. , 2007, , .		0
173	A categorization approach to automated ontological function annotation. Protein Science, 2006, 15, 1544-1549.	7.6	59
174	Large-scale testing of bibliome informatics using Pfam protein families. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2006, , 76-87.	0.7	3
175	LARGE-SCALE TESTING OF BIBLIOME INFORMATICS USING PFAM PROTEIN FAMILIES. , 2005, , .		3
176	Protein annotation as term categorization in the gene ontology using word proximity networks. BMC Bioinformatics, 2005, 6, S20.	2.6	31
177	Towards a Semantic Lexicon for Biological Language Processing. Comparative and Functional Genomics, 2005, 6, 61-66.	2.0	11
178	Automatic English-Chinese name transliteration for development of multilingual resources. , 1998, , .		11
179	Automatic English-Chinese name transliteration for development of multilingual resources. , 1998, , .		52
180	Dynamic document delivery: generating natural language texts on demand. , 0, , .		11

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181	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. F1000Research, 0, 8, 1677.	1.6	0