

# 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	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	19.0	789
2	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	8.8	308
3	Concept annotation in the CRAFT corpus. <i>BMC Bioinformatics</i> , 2012, 13, 161.	2.6	188
4	The CHEMDNER corpus of chemicals and drugs and its annotation principles. <i>Journal of Cheminformatics</i> , 2015, 7, S2.	6.1	166
5	BioC: a minimalist approach to interoperability for biomedical text processing. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat064-bat064.	3.0	123
6	The structural and content aspects of abstracts versus bodies of full text journal articles are different. <i>BMC Bioinformatics</i> , 2010, 11, 492.	2.6	121
7	Big Data in Medicine Is Driving Big Changes. <i>Yearbook of Medical Informatics</i> , 2014, 23, 14-20.	1.0	119
8	The gene normalization task in BioCreative III. <i>BMC Bioinformatics</i> , 2011, 12, S2.	2.6	101
9	BioLemmatizer: a lemmatization tool for morphological processing of biomedical text. <i>Journal of Biomedical Semantics</i> , 2012, 3, 3.	1.6	97
10	Large-scale biomedical concept recognition: an evaluation of current automatic annotators and their parameters. <i>BMC Bioinformatics</i> , 2014, 15, 59.	2.6	94
11	A corpus of full-text journal articles is a robust evaluation tool for revealing differences in performance of biomedical natural language processing tools. <i>BMC Bioinformatics</i> , 2012, 13, 207.	2.6	78
12	A categorization approach to automated ontological function annotation. <i>Protein Science</i> , 2006, 15, 1544-1549.	7.6	59
13	Annotating the biomedical literature for the human variome. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat019-bat019.	3.0	53
14	Automatic English-Chinese name transliteration for development of multilingual resources. , 1998, , .		52
15	Designing Health Websites Based on Usersâ€™ Web-Based Information-Seeking Behaviors: A Mixed-Method Observational Study. <i>Journal of Medical Internet Research</i> , 2016, 18, e145.	4.3	50
16	Combining heterogeneous data sources for accurate functional annotation of proteins. <i>BMC Bioinformatics</i> , 2013, 14, S10.	2.6	41
17	Biomedical Text Mining: State-of-the-Art, Open Problems and Future Challenges. <i>Lecture Notes in Computer Science</i> , 2014, , 271-300.	1.3	41
18	Artificial intelligence for clinical decision support in neurology. <i>Brain Communications</i> , 2020, 2, fcaa096.	3.3	41

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19	Text mining electronic hospital records to automatically classify admissions against disease: Measuring the impact of linking data sources. <i>Journal of Biomedical Informatics</i> , 2016, 64, 158-167.	4.3	39
20	Convolutional neural networks for chemical-disease relation extraction are improved with character-based word embeddings. , 2018, , .		39
21	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
22	High-precision biological event extraction with a concept recognizer. , 2009, , .		38
23	Approximate Subgraph Matching-Based Literature Mining for Biomedical Events and Relations. <i>PLoS ONE</i> , 2013, 8, e60954.	2.5	37
24	Coreference annotation and resolution in the Colorado Richly Annotated Full Text (CRAFT) corpus of biomedical journal articles. <i>BMC Bioinformatics</i> , 2017, 18, 372.	2.6	37
25	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
26	Duplicates, redundancies and inconsistencies in the primary nucleotide databases: a descriptive study. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, baw163.	3.0	36
27	Literature mining of protein-residue associations with graph rules learned through distant supervision. <i>Journal of Biomedical Semantics</i> , 2012, 3, S2.	1.6	35
28	Early prediction of incident liver disease using conventional risk factors and gut-microbiome-augmented gradient boosting. <i>Cell Metabolism</i> , 2022, 34, 719-730.e4.	16.2	35
29	Literature mining of genetic variants for curation: quantifying the importance of supplementary material. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau003-bau003.	3.0	34
30	CQADupStack. , 2015, , .		34
31	The textual characteristics of traditional and Open Access scientific journals are similar. <i>BMC Bioinformatics</i> , 2009, 10, 183.	2.6	33
32	Positive-Unlabeled Learning for inferring drug interactions based on heterogeneous attributes. <i>BMC Bioinformatics</i> , 2017, 18, 140.	2.6	33
33	End-to-End Neural Relation Extraction Using Deep Biaffine Attention. <i>Lecture Notes in Computer Science</i> , 2019, , 729-738.	1.3	33
34	Protein annotation as term categorization in the gene ontology using word proximity networks. <i>BMC Bioinformatics</i> , 2005, 6, S20.	2.6	31
35	TOWARDS EARLY DISCOVERY OF SALIENT HEALTH THREATS: A SOCIAL MEDIA EMOTION CLASSIFICATION TECHNIQUE. , 2016, , .		31
36	PHENOstruct: Prediction of human phenotype ontology terms using heterogeneous data sources. <i>F1000Research</i> , 2015, 4, 259.	1.6	31

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37	Conceptualising health information seeking behaviours and exploratory search: result of a qualitative study. <i>Health and Technology</i> , 2015, 5, 45-55.	3.6	30
38	Overview of the BioCreative VI Precision Medicine Track: mining protein interactions and mutations for precision medicine. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	30
39	Exploiting graph kernels for high performance biomedical relation extraction. <i>Journal of Biomedical Semantics</i> , 2018, 9, 7.	1.6	29
40	Web Forum Retrieval and Text Analytics: A Survey. <i>Foundations and Trends in Information Retrieval</i> , 2018, 12, 1-163.	6.8	27
41	Text Mining Improves Prediction of Protein Functional Sites. <i>PLoS ONE</i> , 2012, 7, e32171.	2.5	27
42	Uncovering protein interaction in abstracts and text using a novel linear model and word proximity networks. <i>Genome Biology</i> , 2008, 9, S11.	9.6	26
43	Mutation extraction tools can be combined for robust recognition of genetic variants in the literature. <i>F1000Research</i> , 2014, 3, 18.	1.6	26
44	Ontology quality assurance through analysis of term transformations. <i>Bioinformatics</i> , 2009, 25, i77-i84.	4.1	25
45	Exploring effective approaches for haplotype block phasing. <i>BMC Bioinformatics</i> , 2019, 20, 540.	2.6	24
46	Better Health Explorer. , 2015, , .		23
47	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
48	Mutation extraction tools can be combined for robust recognition of genetic variants in the literature. <i>F1000Research</i> , 2014, 3, 18.	1.6	22
49	HIGH-PRECISION BIOLOGICAL EVENT EXTRACTION: EFFECTS OF SYSTEM AND OF DATA. <i>Computational Intelligence</i> , 2011, 27, 681-701.	3.2	21
50	Comparing CNN and LSTM character-level embeddings in BiLSTM-CRF models for chemical and disease named entity recognition. , 2018, , .		21
51	Improving Chemical Named Entity Recognition in Patents with Contextualized Word Embeddings. , 2019, , .		21
52	Evaluating a variety of text-mined features for automatic protein function prediction with GOstruct. <i>Journal of Biomedical Semantics</i> , 2015, 6, 9.	1.6	20
53	From POS tagging to dependency parsing for biomedical event extraction. <i>BMC Bioinformatics</i> , 2019, 20, 72.	2.6	20
54	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

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55	Associating disease-related genetic variants in intergenic regions to the genes they impact. PeerJ, 2014, 2, e639.	2.0	20
56	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
57	A close look at protein function prediction evaluation protocols. GigaScience, 2015, 4, 41.	6.4	18
58	The Colorado Richly Annotated Full Text (CRAFT) Corpus: Multi-Model Annotation in the Biomedical Domain. , 2017, , 1379-1394.		18
59	What Can We Get From 1000 Tokens? A Case Study of Multilingual POS Tagging For Resource-Poor Languages. , 2014, , .		18
60	Evaluation of a Machine Learning Duplicate Detection Method for Bioinformatics Databases. , 2015, , .		17
61	Appraising the Quality of Systematic Reviews for Age-Related Macular Degeneration Interventions. JAMA Ophthalmology, 2018, 136, 1051.	2.5	17
62	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
63	Exploring Species-Based Strategies for Gene Normalization. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 462-471.	3.0	16
64	A two-tiered unsupervised clustering approach for drug repositioning through heterogeneous data integration. BMC Bioinformatics, 2018, 19, 129.	2.6	16
65	ChEMU: Named Entity Recognition and Event Extraction of Chemical Reactions from Patents. Lecture Notes in Computer Science, 2020, , 572-579.	1.3	16
66	BioC interoperability track overview. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau053-bau053.	3.0	15
67	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
68	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
69	Roles for Text Mining in Protein Function Prediction. Methods in Molecular Biology, 2014, 1159, 95-108.	0.9	15
70	Quality Matters: Biocuration Experts on the Impact of Duplication and Other Data Quality Issues in Biological Databases. Genomics, Proteomics and Bioinformatics, 2020, 18, 91-103.	6.9	14
71	Use of cefovecin in dogs and cats attending first-opinion veterinary practices in Australia. Veterinary Record, 2020, 187, e95.	0.3	14
72	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

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73	Establishing a baseline for literature mining human genetic variants and their relationships to disease cohorts. <i>BMC Medical Informatics and Decision Making</i> , 2016, 16, 68.	3.0	13
74	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
75	A UIMA wrapper for the NCBO annotator. <i>Bioinformatics</i> , 2010, 26, 1800-1801.	4.1	12
76	A Framework to Adjust Dependency Measure Estimates for Chance. , 2016, , .		12
77	Automated detection of records in biological sequence databases that are inconsistent with the literature. <i>Journal of Biomedical Informatics</i> , 2017, 71, 229-240.	4.3	12
78	Visualization and Language Processing for Supporting Analysis across the Biomedical Literature. <i>Lecture Notes in Computer Science</i> , 2010, , 420-429.	1.3	12
79	Evaluating the Utility of Model Configurations and Data Augmentation on Clinical Semantic Textual Similarity. , 2020, , .		12
80	Memorization vs. Generalization : Quantifying Data Leakage in NLP Performance Evaluation. , 2021, , .		12
81	Dynamic document delivery: generating natural language texts on demand. , 0, , .		11
82	Automatic English-Chinese name transliteration for development of multilingual resources. , 1998, , .		11
83	Towards a Semantic Lexicon for Biological Language Processing. <i>Comparative and Functional Genomics</i> , 2005, 6, 61-66.	2.0	11
84	Assessing the Impact of Case Sensitivity and Term Information Gain on Biomedical Concept Recognition. <i>PLoS ONE</i> , 2015, 10, e0119091.	2.5	11
85	U-Compare bio-event meta-service: compatible BioNLP event extraction services. <i>BMC Bioinformatics</i> , 2011, 12, 481.	2.6	10
86	Representing annotation compositionality and provenance for the Semantic Web. <i>Journal of Biomedical Semantics</i> , 2013, 4, 38.	1.6	10
87	Evaluation of CD-HIT for constructing non-redundant databases. , 2016, , .		10
88	A physarum-inspired prize-collecting steiner tree approach to identify subnetworks for drug repositioning. <i>BMC Systems Biology</i> , 2016, 10, 128.	3.0	10
89	Benchmarks for measurement of duplicate detection methods in nucleotide databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2023, 2023, .	3.0	10
90	Testing Contextualized Word Embeddings to Improve NER in Spanish Clinical Case Narratives. <i>IEEE Access</i> , 2020, 8, 164717-164726.	4.2	10

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91	PoLoBag: Polynomial Lasso Bagging for signed gene regulatory network inference from expression data. <i>Bioinformatics</i> , 2021, 36, 5187-5193.	4.1	10
92	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
93	Supervised Learning for Detection of Duplicates in Genomic Sequence Databases. <i>PLoS ONE</i> , 2016, 11, e0159644.	2.5	10
94	Diagnostic Machine Learning Models for Acute Abdominal Pain: Towards an e-Learning Tool for Medical Students. <i>Studies in Health Technology and Informatics</i> , 2017, 245, 447-451.	0.3	10
95	Gene Ontology synonym generation rules lead to increased performance in biomedical concept recognition. <i>Journal of Biomedical Semantics</i> , 2016, 7, 52.	1.6	9
96	Coreference resolution improves extraction of Biological Expression Language statements from texts. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw076.	3.0	9
97	Use and validation of text mining and cluster algorithms to derive insights from Corona Virus Disease-2019 (COVID-19) medical literature. <i>Computer Methods and Programs in Biomedicine Update</i> , 2021, 1, 100010.	3.7	9
98	Findings of the WMT 2019 Biomedical Translation Shared Task: Evaluation for MEDLINE Abstracts and Biomedical Terminologies. , 2019, , .		9
99	Learning from Unlabelled Data for Clinical Semantic Textual Similarity. , 2020, , .		9
100	Acquisition and evaluation of verb subcategorization resources for biomedicine. <i>Journal of Biomedical Informatics</i> , 2013, 46, 228-237.	4.3	8
101	Approaches to verb subcategorization for biomedicine. <i>Journal of Biomedical Informatics</i> , 2013, 46, 212-227.	4.3	8
102	Optimizing graph-based patterns to extract biomedical events from the literature. <i>BMC Bioinformatics</i> , 2015, 16, S2.	2.6	8
103	Literature consistency of bioinformatics sequence databases is effective for assessing record quality. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	8
104	Multi-field query expansion is effective for biomedical dataset retrieval. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	8
105	The randomized information coefficient: assessing dependencies in noisy data. <i>Machine Learning</i> , 2018, 107, 509-549.	5.4	8
106	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
107	The Dagstuhl Perspectives Workshop on Performance Modeling and Prediction. <i>ACM SIGIR Forum</i> , 2018, 52, 91-101.	0.5	8
108	Accuracy of Machine Learning Assisted Detection of Keratoconus: A Systematic Review and Meta-Analysis. <i>Journal of Clinical Medicine</i> , 2022, 11, 478.	2.4	8

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109	The Pre-Eclampsia Ontology: A Disease Ontology Representing the Domain Knowledge Specific to Pre-Eclampsia. PLoS ONE, 2016, 11, e0162828.	2.5	7
110	A categorical analysis of coreference resolution errors in biomedical texts. Journal of Biomedical Informatics, 2016, 60, 309-318.	4.3	7
111	Classification performance of administrative coding data for detection of invasive fungal infection in paediatric cancer patients. PLoS ONE, 2020, 15, e0238889.	2.5	7
112	Burden and clinical outcomes of hospital-coded infections in patients with cancer: an 11-year longitudinal cohort study at an Australian cancer centre. Supportive Care in Cancer, 2020, 28, 6023-6034.	2.2	7
113	The Evolution of Clinical Knowledge During COVID-19: Towards a Global Learning Health System. Yearbook of Medical Informatics, 2021, 30, 176-184.	1.0	7
114	ChEMU-Ref: A Corpus for Modeling Anaphora Resolution in the Chemical Domain. , 2021, , .		7
115	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
116	Comparative Analysis of Sequence Clustering Methods for Deduplication of Biological Databases. Journal of Data and Information Quality, 2018, 9, 1-27.	2.1	6
117	The current scope of healthcare-associated infection surveillance activities in hospitalized immunocompromised patients: a systematic review. International Journal of Epidemiology, 2019, 48, 1768-1782.	1.9	6
118	Quantifying semantic similarity of clinical evidence in the biomedical literature to facilitate related evidence synthesis. Journal of Biomedical Informatics, 2019, 100, 103321.	4.3	6
119	Detection of protein catalytic sites in the biomedical literature. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2013, , 433-44.	0.7	6
120	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
121	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
122	Extracting structured information from free-text medication prescriptions using dependencies. , 2012, , .		5
123	Natural Language Processing. , 2013, , 1495-1498.		5
124	Domain Adaptation and Instance Selection for Disease Syndrome Classification over Veterinary Clinical Notes. , 2020, , .		5
125	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
126	Evaluation of consensus strategies for haplotype phasing. Briefings in Bioinformatics, 2020, 22, .	6.5	4



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127	An Improved Neural Network Model for Joint. , 2018, , .		4
128	Large-scale protein-protein post-translational modification extraction with distant supervision and confidence calibrated BioBERT. BMC Bioinformatics, 2022, 23, 4.	2.6	4
129	LARGE-SCALE TESTING OF BIBLIOME INFORMATICS USING PFAM PROTEIN FAMILIES. , 2005, , .		3
130	Pattern Learning through Distant Supervision for Extraction of Protein-Residue Associations in the Biomedical Literature. , 2011, , .		3
131	Towards a Methodology for Nursing-Specific Clinical Decision Support Systems (CDSS). Journal of Decision Systems, 2016, 25, 23-34.	3.2	3
132	CommViz: Visualization of semantic patterns in large social communication networks. Information Visualization, 2018, 17, 66-88.	1.9	3
133	Automated assessment of biological database assertions using the scientific literature. BMC Bioinformatics, 2019, 20, 216.	2.6	3
134	Overview of ChEMU 2021: Reaction Reference Resolution and Anaphora Resolution in Chemical Patents. Lecture Notes in Computer Science, 2021, , 292-307.	1.3	3
135	Large-scale testing of bibliome informatics using Pfam protein families. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2006, , 76-87.	0.7	3
136	Leveraging Gene Ontology Annotations to Improve a Memory-Based Language Understanding System. , 2010, , .		2
137	What are health website visitors doing. , 2016, , .		2
138	Learning Biological Sequence Types Using the Literature. , 2017, , .		2
139	ChEMU 2021: Reaction Reference Resolution and Anaphora Resolution in Chemical Patents. Lecture Notes in Computer Science, 2021, , 608-615.	1.3	2
140	Bow-tie architecture of gene regulatory networks in species of varying complexity. Journal of the Royal Society Interface, 2021, 18, 20210069.	3.4	2
141	A Semantics-Enhanced Language Model for Unsupervised Word Sense Disambiguation. , 2008, , 287-298.		2
142	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
143	DETECTION OF PROTEIN CATALYTIC SITES IN THE BIOMEDICAL LITERATURE. , 2012, , .		2
144	Improved Topic Representations of Medical Documents to Assist COVID-19 Literature Exploration. , 2020, , .		2

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145	Automatic consistency assurance for literature-based gene ontology annotation. BMC Bioinformatics, 2021, 22, 565.	2.6	2
146	ChemTables: a dataset for semantic classification on tables in chemical patents. Journal of Cheminformatics, 2021, 13, 97.	6.1	2
147	The ChEMU 2022 Evaluation Campaign: Information Extraction in Chemical Patents. Lecture Notes in Computer Science, 2022, , 400-407.	1.3	2
148	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
149	Two platforms for research in Human Communication Science: The AusTalk corpus and the Alveo Virtual Laboratory. , 2014, , .		1
150	Special issue on bio-ontologies and phenotypes. Journal of Biomedical Semantics, 2015, 6, 40.	1.6	1
151	Interoperability of text corpus annotations with the semantic web. BMC Proceedings, 2015, 9, .	1.6	1
152	Summary of the BioLINK SIG 2013 meeting at ISMB/ECCB 2013. Bioinformatics, 2015, 31, 297-298.	4.1	1
153	Semantic-Based Policy Composition for Privacy-Demanding Data Linkage. , 2018, , .		1
154	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
155	Search Effectiveness in Nonredundant Sequence Databases: Assessments and Solutions. Journal of Computational Biology, 2019, 26, 605-617.	1.6	1
156	Integrating UIMA with Alveo, a human communication science virtual laboratory. , 2014, , .		1
157	Findings of the WMT 2018 Biomedical Translation Shared Task: Evaluation on Medline test sets. , 2018, , .		1
158	A Bag-of-concepts Model Improves Relation Extraction in a Narrow Knowledge Domain with Limited Data. , 2019, , .		1
159	WikiUMLS: Aligning UMLS to Wikipedia via Cross-lingual Neural Ranking. , 2020, , .		1
160	Finding and Exploring Health Information with a Slider-Based User Interface. Studies in Health Technology and Informatics, 2016, 227, 106-12.	0.3	1
161	Knowledge Integration in OpenWorlds: Utilizing the Mathematics of Hierarchical Structure. , 2007, , .		0
162	Exploiting Term Relations for Semantic Hierarchy Construction. , 2008, , .		0

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163	Better health information exploration. , 2015, , .		0
164	Drawing on millions of biomedical journal publications to do predictive biology. , 2015, , .		0
165	Thematic issue of the Second combined Bio-ontologies and Phenotypes Workshop. Journal of Biomedical Semantics, 2016, 7, 66.	1.6	0
166	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
167	Impact of detecting clinical trial elements in exploration of COVID-19 literature. , 2021, , .		0
168	Applied Text Mining. , 2013, , 33-37.		0
169	Unstructured Information Management Architecture (UIMA). , 2013, , 2320-2324.		0
170	DTMBIO 2015. , 2015, , .		0
171	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. F1000Research, 0, 8, 1677.	1.6	0
172	TargetAnalytica: A Text Analytics Framework for Ranking Therapeutic Molecules in the Bibliome. Studies in Big Data, 2021, , 165-184.	1.1	0
173	DrKnow: A Diagnostic Learning Tool with Feedback from Automated Clinical Decision Support. AMIA ... Annual Symposium proceedings, 2018, 2018, 1348-1357.	0.2	0
174	Advanced Methods for Big Data Analytics in Women's Health. , 2020, , .		0
175	Overcoming challenges in extracting prescribing habits from veterinary clinics using big data and deep learning. Australian Veterinary Journal, 2022, , .	1.1	0
176	Mapping biomedical vocabularies: a semi-automated term matching approach. Studies in Health Technology and Informatics, 2014, 202, 16-9.	0.3	0
177	Exploring automatic inconsistency detection for literature-based gene ontology annotation. Bioinformatics, 2022, 38, i273-i281.	4.1	0
178	Title is missing!. , 2020, 15, e0238889.		0
179	Title is missing!. , 2020, 15, e0238889.		0
180	Title is missing!. , 2020, 15, e0238889.		0

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181	Title is missing!. , 2020, 15, e0238889.		0