

# Zhiyong

## List of Publications by Year in descending order

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Version: 2024-02-01

191  
papers

18,606  
citations

25034

57  
h-index

20358

116  
g-index

196  
all docs

196  
docs citations

196  
times ranked

18455  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Database resources of the national center for biotechnology information. <i>Nucleic Acids Research</i> , 2022, 50, D20-D26.  | 14.5 | 887       |
| 2  | Global-Local attention network with multi-task uncertainty loss for abnormal lymph node detection in MR images. <i>Medical Image Analysis</i> , 2022, 77, 102345.  | 11.6 | 13        |
| 3  | DeepLensNet: Deep Learning Automated Diagnosis and Quantitative Classification of Cataract Type and Severity. <i>Ophthalmology</i> , 2022, 129, 571-584.   | 5.2  | 23        |
| 4  | Predicting myocardial infarction through retinal scans and minimal personal information. <i>Nature Machine Intelligence</i> , 2022, 4, 55-61.  | 16.0 | 30        |
| 5  | Detecting visually significant cataract using retinal photograph-based deep learning. <i>Nature Aging</i> , 2022, 2, 264-271.  | 11.6 | 14        |
| 6  | PhenoRerank: A re-ranking model for phenotypic concept recognition pre-trained on human phenotype ontology. <i>Journal of Biomedical Informatics</i> , 2022, 129, 104059.  | 4.3  | 2         |
| 7  | Machine Learning Approach to Facilitate Knowledge Synthesis at the Intersection of Liver Cancer, Epidemiology, and Health Disparities Research. <i>JCO Clinical Cancer Informatics</i> , 2022, , .   | 2.1  | 0         |
| 8  | Recent advances in biomedical literature mining. <i>Briefings in Bioinformatics</i> , 2021, 22, .  | 6.5  | 59        |
| 9  | LitCovid: an open database of COVID-19 literature. <i>Nucleic Acids Research</i> , 2021, 49, D1534-D1540.  | 14.5 | 189       |
| 10 | COVID-19-CT-CXR: A Freely Accessible and Weakly Labeled Chest X-Ray and CT Image Collection on COVID-19 From Biomedical Literature. <i>IEEE Transactions on Big Data</i> , 2021, 7, 3-12.  | 6.1  | 55        |
| 11 | Database resources of the National Center for Biotechnology Information. <i>Nucleic Acids Research</i> , 2021, 49, D10-D17.  | 14.5 | 545       |
| 12 | Recent advances of automated methods for searching and extracting genomic variant information from biomedical literature. <i>Briefings in Bioinformatics</i> , 2021, 22, .   | 6.5  | 13        |
| 13 | PhenoTagger: a hybrid method for phenotype concept recognition using human phenotype ontology. <i>Bioinformatics</i> , 2021, 37, 1884-1890.  | 4.1  | 18        |
| 14 | NLM-Chem, a new resource for chemical entity recognition in PubMed full text literature. <i>Scientific Data</i> , 2021, 8, 91.   | 5.3  | 26        |
| 15 | Learning Few-Shot Chest X-Ray Diagnosis Using Images From The Published Scientific Literature. , 2021, , .   |      | 3         |
| 16 | Multimodal, multitask, multiattention (M3) deep learning detection of reticular pseudodrusen: Toward automated and accessible classification of age-related macular degeneration. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2021, 28, 1135-1148. | 4.4  | 11        |
| 17 | LitSuggest: a web-based system for literature recommendation and curation using machine learning. <i>Nucleic Acids Research</i> , 2021, 49, W352-W358.   | 14.5 | 28        |
| 18 | NLM-Gene, a richly annotated gold standard dataset for gene entities that addresses ambiguity and multi-species gene recognition. <i>Journal of Biomedical Informatics</i> , 2021, 118, 103779.  | 4.3  | 9         |

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|----|--|------|-----------|
| 19 | Artificial Intelligence in Action: Addressing the COVID-19 Pandemic with Natural Language Processing. Annual Review of Biomedical Data Science, 2021, 4, 313-339.  | 6.5  | 38        |
| 20 | Improving Interpretability in Machine Diagnosis. Ophthalmology Science, 2021, 1, 100038.   | 2.5  | 8         |
| 21 | Editor's introduction to the special section on the 7th Biomedical Linked Annotation Hackathon (BLAH7). Genomics and Informatics, 2021, 19, e20.   | 0.8  | 0         |
| 22 | BERT-GT: cross-sentence <i>n</i> -ary relation extraction with BERT and Graph Transformer. Bioinformatics, 2021, 36, 5678-5685.  | 4.1  | 19        |
| 23 | Artificial Intelligence in Age-Related Macular Degeneration (AMD). , 2021, , 101-112.  |      | 3         |
| 24 | Evolving use of ancestry, ethnicity, and race in genetics research—A survey spanning seven decades. American Journal of Human Genetics, 2021, 108, 2215-2223.  | 6.2  | 27        |
| 25 | Benchmarking Effectiveness and Efficiency of Deep Learning Models for Semantic Textual Similarity in the Clinical Domain: Validation Study. JMIR Medical Informatics, 2021, 9, e27386.                                   | 2.6  | 5         |
| 26 | Multi-task deep learning-based survival analysis on the prognosis of late AMD using the longitudinal data in AREDS.. AMIA ... Annual Symposium proceedings, 2021, 2021, 506-515.   | 0.2  | 0         |
| 27 | FullMeSH: improving large-scale MeSH indexing with full text. Bioinformatics, 2020, 36, 1533-1541.   | 4.1  | 26        |
| 28 | Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2020, 48, D9-D16.   | 14.5 | 381       |
| 29 | Better synonyms for enriching biomedical search. Journal of the American Medical Informatics Association: JAMIA, 2020, 27, 1894-1902.  | 4.4  | 6         |
| 30 | Predicting risk of late age-related macular degeneration using deep learning. Npj Digital Medicine, 2020, 3, 111.  | 10.9 | 33        |
| 31 | Ten tips for a text-mining-ready article: How to improve automated discoverability and interpretability. PLoS Biology, 2020, 18, e3000716.   | 5.6  | 10        |
| 32 | TeamTat: a collaborative text annotation tool. Nucleic Acids Research, 2020, 48, W5-W11.   | 14.5 | 34        |
| 33 | Deep learning with sentence embeddings pre-trained on biomedical corpora improves the performance of finding similar sentences in electronic medical records. BMC Medical Informatics and Decision Making, 2020, 20, 73. | 3.0  | 15        |
| 34 | BioConceptVec: Creating and evaluating literature-based biomedical concept embeddings on a large scale. PLoS Computational Biology, 2020, 16, e1007617.  | 3.2  | 43        |
| 35 | Deep Learning Automated Detection of Reticular Pseudodrusen from Fundus Autofluorescence Images or Color Fundus Photographs in AREDS2. Ophthalmology, 2020, 127, 1674-1687.  | 5.2  | 19        |
| 36 | Keep up with the latest coronavirus research. Nature, 2020, 579, 193-193.  | 27.8 | 230       |

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|----|--|------|-----------|
| 37 | Automated abnormality classification of chest radiographs using deep convolutional neural networks. <i>Npj Digital Medicine</i> , 2020, 3, 70.   | 10.9 | 133       |
| 38 | An Empirical Study of Multi-Task Learning on BERT for Biomedical Text Mining. , 2020, , .  |      | 49        |
| 39 | PDC - a probabilistic distributional clustering algorithm: a case study on suicide articles in PubMed. <i>AMIA Summits on Translational Science Proceedings</i> , 2020, 2020, 259-268.   | 0.4  | 0         |
| 40 | LitSense: making sense of biomedical literature at sentence level. <i>Nucleic Acids Research</i> , 2019, 47, W594-W599.  | 14.5 | 37        |
| 41 | ML-Net: multi-label classification of biomedical texts with deep neural networks. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2019, 26, 1279-1285.   | 4.4  | 83        |
| 42 | PubMed Text Similarity Model and its application to curation efforts in the Conserved Domain Database. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .   | 3.0  | 10        |
| 43 | Coinheritance of generalized pustular psoriasis and familial Behçet-like autoinflammatory syndrome with variants in <i>IL36RN</i> and <i>TNFAIP3</i> in the heterozygous state. <i>Journal of Dermatology</i> , 2019, 46, 907-910. | 1.2  | 7         |
| 44 | A Deep Learning Approach for Automated Detection of Geographic Atrophy from Color Fundus Photographs. <i>Ophthalmology</i> , 2019, 126, 1533-1540.   | 5.2  | 55        |
| 45 | BioWordVec, Improving biomedical word embeddings with subword information and MeSH. <i>Scientific Data</i> , 2019, 6, 52.  | 5.3  | 268       |
| 46 | Tracking human genes along the translational continuum. <i>Npj Genomic Medicine</i> , 2019, 4, 25.   | 3.8  | 2         |
| 47 | Fine-Grained Lesion Annotation in CT Images With Knowledge Mined From Radiology Reports. , 2019, , .   |      | 0         |
| 48 | A Text-Mining System for Concept Annotation in Biomedical Full Text Articles. , 2019, , .  |      | 1         |
| 49 | Biomedical Mention Disambiguation using a Deep Learning Approach. , 2019, , .  |      | 9         |
| 50 | 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        |
| 51 | PMC text mining subset in BioC: about three million full-text articles and growing. <i>Bioinformatics</i> , 2019, 35, 3533-3535.   | 4.1  | 51        |
| 52 | PubTator central: automated concept annotation for biomedical full text articles. <i>Nucleic Acids Research</i> , 2019, 47, W587-W593.   | 14.5 | 248       |
| 53 | Exploring semi-supervised variational autoencoders for biomedical relation extraction. <i>Methods</i> , 2019, 166, 112-119.  | 3.8  | 45        |
| 54 | Text Mining for Drug Discovery. <i>Methods in Molecular Biology</i> , 2019, 1939, 231-252.   | 0.9  | 30        |

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|----|--|------|-----------|
| 55 | Using deep learning to identify translational research in genomic medicine beyond bench to bedside. Database: the Journal of Biological Databases and Curation, 2019, 2019, .  | 3.0  | 4         |
| 56 | BioSentVec: creating sentence embeddings for biomedical texts. , 2019, , .   |      | 91        |
| 57 | A self-attention based deep learning method for lesion attribute detection from CT reports. , 2019, , .  |      | 14        |
| 58 | Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2019, 47, D23-D28.  | 14.5 | 502       |
| 59 | DeepSeeNet: A Deep Learning Model for Automated Classification of Patient-based Age-related Macular Degeneration Severity from Color Fundus Photographs. Ophthalmology, 2019, 126, 565-575.                          | 5.2  | 220       |
| 60 | ChestX-ray: Hospital-Scale Chest X-ray Database and Benchmarks on Weakly Supervised Classification and Localization of Common Thorax Diseases. Advances in Computer Vision and Pattern Recognition, 2019, , 369-392. | 1.3  | 45        |
| 61 | Transfer Learning in Biomedical Natural Language Processing: An Evaluation of BERT and ELMo on Ten Benchmarking Datasets. , 2019, , .  |      | 360       |
| 62 | Introduction to BLAH5 special issue: recent progress on interoperability of biomedical text mining. Genomics and Informatics, 2019, 17, e12.   | 0.8  | 0         |
| 63 | A multi-task deep learning model for the classification of Age-related Macular Degeneration. AMIA Summits on Translational Science Proceedings, 2019, 2019, 505-514.   | 0.4  | 8         |
| 64 | Opportunities and obstacles for deep learning in biology and medicine. Journal of the Royal Society Interface, 2018, 15, 20170387.   | 3.4  | 1,282     |
| 65 | Generalizing biomedical relation classification with neural adversarial domain adaptation. Bioinformatics, 2018, 34, 2973-2981.  | 4.1  | 30        |
| 66 | tmVar 2.0: integrating genomic variant information from literature with dbSNP and ClinVar for precision medicine. Bioinformatics, 2018, 34, 80-87.   | 4.1  | 79        |
| 67 | A Deep Phenotype Association Study Reveals Specific Phenotype Associations with Genetic Variants in Age-related Macular Degeneration. Ophthalmology, 2018, 125, 559-568.   | 5.2  | 30        |
| 68 | TieNet: Text-Image Embedding Network for Common Thorax Disease Classification and Reporting in Chest X-Rays. , 2018, , .   |      | 261       |
| 69 | How user intelligence is improving PubMed. Nature Biotechnology, 2018, 36, 937-945.  | 17.5 | 46        |
| 70 | Sentence Similarity Measures Revisited. , 2018, , .  |      | 5         |
| 71 | PubMed Labs: an experimental system for improving biomedical literature search. Database: the Journal of Biological Databases and Curation, 2018, 2018, .  | 3.0  | 15        |
| 72 | Assisting document triage for human kinome curation via machine learning. Database: the Journal of Biological Databases and Curation, 2018, 2018, .  | 3.0  | 2         |

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|----|--|------|-----------|
| 73 | Overview of the BioCreative VI text-mining services for Kinome Curation Track. Database: the Journal of Biological Databases and Curation, 2018, 2018, .                 | 3.0  | 3         |
| 74 | Best Match: New relevance search for PubMed. PLoS Biology, 2018, 16, e2005343.   | 5.6  | 90        |
| 75 | LitVar: a semantic search engine for linking genomic variant data in PubMed and PMC. Nucleic Acids Research, 2018, 46, W530-W536.  | 14.5 | 96        |
| 76 | PubMed Phrases, an open set of coherent phrases for searching biomedical literature. Scientific Data, 2018, 5, 180104.   | 5.3  | 13        |
| 77 | A Fast Deep Learning Model for Textual Relevance in Biomedical Information Retrieval. , 2018, , .  |      | 25        |
| 78 | ezTag: tagging biomedical concepts via interactive learning. Nucleic Acids Research, 2018, 46, W523-W529.  | 14.5 | 27        |
| 79 | Extracting chemicalâ€“protein relations with ensembles of SVM and deep learning models. Database: the Journal of Biological Databases and Curation, 2018, 2018, .        | 3.0  | 85        |
| 80 | A Field Sensor: computing the composition and intent of PubMed queries. Database: the Journal of Biological Databases and Curation, 2018, 2018, .                        | 3.0  | 4         |
| 81 | Scaling up data curation using deep learning: An application to literature triage in genomic variation resources. PLoS Computational Biology, 2018, 14, e1006390.        | 3.2  | 33        |
| 82 | PSB 2019 Workshop on Text Mining and Visualization for Precision Medicine. , 2018, , .   |      | 0         |
| 83 | NegBio: a high-performance tool for negation and uncertainty detection in radiology reports. AMIA Summits on Translational Science Proceedings, 2018, 2017, 188-196.     | 0.4  | 18        |
| 84 | Bridging the gap: Incorporating a semantic similarity measure for effectively mapping PubMed queries to documents. Journal of Biomedical Informatics, 2017, 75, 122-127. | 4.3  | 33        |
| 85 | DIGNiFI: Discovering causative genes for orphan diseases using protein-protein interaction networks. BMC Systems Biology, 2017, 11, 23.                                  | 3.0  | 12        |
| 86 | MeSH Now: automatic MeSH indexing at PubMed scale via learning to rank. Journal of Biomedical Semantics, 2017, 8, 15.  | 1.6  | 57        |
| 87 | ChestX-Ray8: Hospital-Scale Chest X-Ray Database and Benchmarks on Weakly-Supervised Classification and Localization of Common Thorax Diseases. , 2017, , .              |      | 2,038     |
| 88 | Towards PubMed 2.0. ELife, 2017, 6, .  | 6.0  | 86        |
| 89 | On expert curation and scalability: UniProtKB/Swiss-Prot as a case study. Bioinformatics, 2017, 33, 3454-3460.   | 4.1  | 91        |
| 90 | Deep learning for extracting protein-protein interactions from biomedical literature. , 2017, , .  |      | 61        |

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|-----|---|-----|-----------|
| 91  | BioCreative VI Precision Medicine Track: creating a training corpus for mining protein-protein interactions affected by mutations. , 2017, , .  |     | 6         |
| 92  | Deep Learning for Biomedical Information Retrieval: Learning Textual Relevance from Click Logs. , 2017, , .   |     | 16        |
| 93  | Mining Related Articles for Automatic Journal Cataloging. Journal of Data and Information Science, 2017, 1, 45-59.  | 1.1 | 0         |
| 94  | DIGNiFI. , 2016, , .  |     | 0         |
| 95  | Text Mining Genotype-Phenotype Relationships from Biomedical Literature for Database Curation and Precision Medicine. PLoS Computational Biology, 2016, 12, e1005017.   | 3.2 | 81        |
| 96  | Discovering biomedical semantic relations in PubMed queries for information retrieval and database curation. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw025.                    | 3.0 | 5         |
| 97  | BioCreative V CDR task corpus: a resource for chemical disease relation extraction. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw068.   | 3.0 | 350       |
| 98  | Improving chemical disease relation extraction with rich features and weakly labeled data. Journal of Cheminformatics, 2016, 8, 53.   | 6.1 | 62        |
| 99  | Text mining for precision medicine: automating disease-mutation relationship extraction from biomedical literature. Journal of the American Medical Informatics Association: JAMIA, 2016, 23, 766-772.          | 4.4 | 52        |
| 100 | Text Mining for Precision Medicine: Bringing Structure to EHRs and Biomedical Literature to Understand Genes and Health. Advances in Experimental Medicine and Biology, 2016, 939, 139-166.                     | 1.6 | 46        |
| 101 | Assessing the state of the art in biomedical relation extraction: overview of the BioCreative V chemical-disease relation (CDR) task. Database: the Journal of Biological Databases and Curation, 2016, 2016, . | 3.0 | 123       |
| 102 | Overview of the interactive task in BioCreative V. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw119.  | 3.0 | 36        |
| 103 | TaggerOne: joint named entity recognition and normalization with semi-Markov Models. Bioinformatics, 2016, 32, 2839-2846.   | 4.1 | 221       |
| 104 | Mining chemical patents with an ensemble of open systems. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw065.   | 3.0 | 12        |
| 105 | Crowdsourcing in biomedicine: challenges and opportunities. Briefings in Bioinformatics, 2016, 17, 23-32.   | 6.5 | 82        |
| 106 | Beyond accuracy: creating interoperable and scalable text-mining web services. Bioinformatics, 2016, 32, 1907-1910.   | 4.1 | 37        |
| 107 | A survey of current trends in computational drug repositioning. Briefings in Bioinformatics, 2016, 17, 2-12.  | 6.5 | 459       |
| 108 | Community challenges in biomedical text mining over 10 years: success, failure and the future. Briefings in Bioinformatics, 2016, 17, 132-144.  | 6.5 | 161       |

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|-----|---|-----|-----------|
| 109 | Pressing needs of biomedical text mining in biocuration and beyond: opportunities and challenges. Database: the Journal of Biological Databases and Curation, 2016, 2016, bau161. | 3.0 | 30        |
| 110 | The CHEMDNER corpus of chemicals and drugs and its annotation principles. Journal of Cheminformatics, 2015, 7, S2.  | 6.1 | 166       |
| 111 | tmChem: a high performance approach for chemical named entity recognition and normalization. Journal of Cheminformatics, 2015, 7, S3.   | 6.1 | 203       |
| 112 | Scaling drug indication curation through crowdsourcing. Database: the Journal of Biological Databases and Curation, 2015, 2015, .   | 3.0 | 34        |
| 113 | GNormPlus: An Integrative Approach for Tagging Genes, Gene Families, and Protein Domains. BioMed Research International, 2015, 2015, 1-7.   | 1.9 | 155       |
| 114 | Text Mining for Translational Bioinformatics. BioMed Research International, 2015, 2015, 1-2.   | 1.9 | 4         |
| 115 | Identifying named entities from PubMed® for enriching semantic categories. BMC Bioinformatics, 2015, 16, 57.  | 2.6 | 10        |
| 116 | Challenges in clinical natural language processing for automated disorder normalization. Journal of Biomedical Informatics, 2015, 57, 28-37.                                      | 4.3 | 125       |
| 117 | SimConcept: A Hybrid Approach for Simplifying Composite Named Entities in Biomedical Text. IEEE Journal of Biomedical and Health Informatics, 2015, 19, 1385-1391.                | 6.3 | 18        |
| 118 | Crowdsourcing and mining crowd data. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 267-9.  | 0.7 | 2         |
| 119 | LabeledIn: Cataloging labeled indications for human drugs. Journal of Biomedical Informatics, 2014, 52, 448-456.  | 4.3 | 35        |
| 120 | Text mining tools for assisting literature curation. , 2014, , .  |     | 2         |
| 121 | Overview of the gene ontology task at BioCreative IV. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau086-bau086.                                      | 3.0 | 45        |
| 122 | SimConcept. , 2014, 2014, 138-146.  |     | 13        |
| 123 | tmBioC: improving interoperability of text-mining tools with BioC. Database: the Journal of Biological Databases and Curation, 2014, 2014, .                                      | 3.0 | 8         |
| 124 | Hybrid curation of gene-mutation relations combining automated extraction and crowdsourcing. Database: the Journal of Biological Databases and Curation, 2014, 2014, .            | 3.0 | 35        |
| 125 | BioC interoperability track overview. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau053-bau053.  | 3.0 | 15        |
| 126 | BC4GO: a full-text corpus for the BioCreative IV GO task. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau074-bau074.                                  | 3.0 | 36        |



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|-----|--|------|-----------|
| 127 | NCBI disease corpus: A resource for disease name recognition and concept normalization. Journal of Biomedical Informatics, 2014, 47, 1-10.                                   | 4.3  | 525       |
| 128 | Author name disambiguation for <scp>P</scp>ub<scp>M</scp>ed. Journal of the Association for Information Science and Technology, 2014, 65, 765-781.                           | 2.9  | 68        |
| 129 | CROWDSOURCING AND MINING CROWD DATA. , 2014, , .   |      | 3         |
| 130 | BioCreative-IV virtual issue. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau039-bau039.   | 3.0  | 43        |
| 131 | Accessing Biomedical Literature in the Current Information Landscape. Methods in Molecular Biology, 2014, 1159, 11-31.   | 0.9  | 32        |
| 132 | Automated Disease Normalization with Low Rank Approximations. , 2014, , .  |      | 8         |
| 133 | Automatic extraction of drug indications from FDA drug labels. AMIA ... Annual Symposium proceedings, 2014, 2014, 787-94.  | 0.2  | 4         |
| 134 | Pathway-based drug repositioning using causal inference. BMC Bioinformatics, 2013, 14, S3.   | 2.6  | 71        |
| 135 | PubTator: a web-based text mining tool for assisting biocuration. Nucleic Acids Research, 2013, 41, W518-W522.   | 14.5 | 523       |
| 136 | tmVar: a text mining approach for extracting sequence variants in biomedical literature. Bioinformatics, 2013, 29, 1433-1439.  | 4.1  | 197       |
| 137 | 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. | 3.0  | 68        |
| 138 | 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       |
| 139 | Toward Creating a Gold Standard of Drug Indications from FDA Drug Labels. , 2013, , .  |      | 5         |
| 140 | DNorm: disease name normalization with pairwise learning to rank. Bioinformatics, 2013, 29, 2909-2917.   | 4.1  | 436       |
| 141 | Developing Topic-specific Search Filters for PubMed with Click-through Data. Methods of Information in Medicine, 2013, 52, 395-402.  | 1.2  | 9         |
| 142 | Large-Scale Event Extraction from Literature with Multi-Level Gene Normalization. PLoS ONE, 2013, 8, e55814.   | 2.5  | 83        |
| 143 | Predicting clicks of PubMed articles. AMIA ... Annual Symposium proceedings, 2013, 2013, 947-56.   | 0.2  | 0         |
| 144 | Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2012, 40, D13-D25.  | 14.5 | 510       |

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|-----|---|------|-----------|
| 145 | Prioritizing PubMed articles for the Comparative Toxicogenomic Database utilizing semantic information. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas042-bas042.                      | 3.0  | 12        |
| 146 | Biocuration workflows and text mining: overview of the BioCreative 2012 Workshop Track II. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas043-bas043.                                   | 3.0  | 67        |
| 147 | Linking multiple disease-related resources through UMLS. , 2012, , .  |      | 9         |
| 148 | Improving Online Access to Drug-Related Information. , 2012, , .  |      | 1         |
| 149 | BioCreative-2012 Virtual Issue. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas049-bas049.  | 3.0  | 19        |
| 150 | Accelerating literature curation with text-mining tools: a case study of using PubTator to curate genes in PubMed abstracts. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas041-bas041. | 3.0  | 83        |
| 151 | Systematic identification of pharmacogenomics information from clinical trials. Journal of Biomedical Informatics, 2012, 45, 870-878.   | 4.3  | 26        |
| 152 | A Network Approach for Computational Drug Repositioning. , 2012, , .  |      | 0         |
| 153 | A new method for computational drug repositioning using drug pairwise similarity. , 2012, 2012, 1-4.  |      | 63        |
| 154 | Improving links between literature and biological data with text mining: a case study with GEO, PDB and MEDLINE. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas026.                    | 3.0  | 21        |
| 155 | Automatic identification and normalization of dosage forms in drug monographs. BMC Medical Informatics and Decision Making, 2012, 12, 9.  | 3.0  | 2         |
| 156 | SR4GN: A Species Recognition Software Tool for Gene Normalization. PLoS ONE, 2012, 7, e38460.   | 2.5  | 71        |
| 157 | Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2011, 39, D38-D51.   | 14.5 | 582       |
| 158 | Semi-automatic semantic annotation of PubMed queries: A study on quality, efficiency, satisfaction. Journal of Biomedical Informatics, 2011, 44, 310-318.   | 4.3  | 68        |
| 159 | A context-blocks model for identifying clinical relationships in patient records. BMC Bioinformatics, 2011, 12, S3.   | 2.6  | 14        |
| 160 | Overview of the BioCreative III Workshop. BMC Bioinformatics, 2011, 12, S1.   | 2.6  | 88        |
| 161 | The gene normalization task in BioCreative III. BMC Bioinformatics, 2011, 12, S2.   | 2.6  | 101       |
| 162 | The Protein-Protein Interaction tasks of BioCreative III: classification/ranking of articles and linking bio-ontology concepts to full text. BMC Bioinformatics, 2011, 12, S3.                                      | 2.6  | 121       |

| #   | ARTICLE  | IF   | CITATIONS |
|-----|--|------|-----------|
| 163 | BioCreative III interactive task: an overview. BMC Bioinformatics, 2011, 12, S4.   | 2.6  | 65        |
| 164 | Recommending MeSH terms for annotating biomedical articles. Journal of the American Medical Informatics Association: JAMIA, 2011, 18, 660-667.                       | 4.4  | 107       |
| 165 | Extraction of data deposition statements from the literature: a method for automatically tracking research results. Bioinformatics, 2011, 27, 3306-3312.             | 4.1  | 27        |
| 166 | PubMed and beyond: a survey of web tools for searching biomedical literature. Database: the Journal of Biological Databases and Curation, 2011, 2011, baq036-baq036. | 3.0  | 375       |
| 167 | Click-words: learning to predict document keywords from a user perspective. Bioinformatics, 2010, 26, 2767-2775.   | 4.1  | 11        |
| 168 | Extracting Rx information from clinical narrative. Journal of the American Medical Informatics Association: JAMIA, 2010, 17, 536-539.                                | 4.4  | 26        |
| 169 | Automatic integration of drug indications from multiple health resources. , 2010, , .  |      | 24        |
| 170 | Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2010, 38, D5-D16.   | 14.5 | 417       |
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