Luke V. Rasmussen

List of Publications by Year
in descending order

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153	6,520	94269 37	82410 72
papers	citations	h-index	g-index

166	166	166	8945
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Systematic comparison of phenome-wide association study of electronic medical record data and genome-wide association study data. Nature Biotechnology, 2013, 31, 1102-1111.	9.4	846
2	Validation of electronic medical record-based phenotyping algorithms: results and lessons learned from the eMERGE network. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, e147-e154.	2.2	346
3	Electronic Medical Records for Genetic Research: Results of the eMERGE Consortium. Science Translational Medicine, 2011, 3, 79re1.	5.8	302
4	PheKB: a catalog and workflow for creating electronic phenotype algorithms for transportability. Journal of the American Medical Informatics Association: JAMIA, 2016, 23, 1046-1052.	2.2	284
5	Quality Control Procedures for Genomeâ€Wide Association Studies. Current Protocols in Human Genetics, 2011, 68, Unit1.19.	3.5	259
6	Variants Near FOXE1 Are Associated with Hypothyroidism and Other Thyroid Conditions: Using Electronic Medical Records for Genome- and Phenome-wide Studies. American Journal of Human Genetics, 2011, 89, 529-542.	2.6	232
7	Design and Anticipated Outcomes of the eMERGE-PGx Project: A Multicenter Pilot for Preemptive Pharmacogenomics in Electronic Health Record Systems. Clinical Pharmacology and Therapeutics, 2014, 96, 482-489.	2.3	223
8	Big Data and Data Science in Critical Care. Chest, 2018, 154, 1239-1248.	0.4	184
9	Genome- and Phenome-Wide Analyses of Cardiac Conduction Identifies Markers of Arrhythmia Risk. Circulation, 2013, 127, 1377-1385.	1.6	167
10	Natural Language Processing for EHR-Based Pharmacovigilance: A Structured Review. Drug Safety, 2017, 40, 1075-1089.	1.4	133
11	Natural Language Processing for EHR-Based Computational Phenotyping. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 139-153.	1.9	123
12	Recurrent neural networks for classifying relations in clinical notes. Journal of Biomedical Informatics, 2017, 72, 85-95.	2.5	119
13	Desiderata for computable representations of electronic health records-driven phenotype algorithms. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1220-1230.	2.2	110
14	Importance of multi-modal approaches to effectively identify cataract cases from electronic health records. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 225-234.	2.2	106
15	Circulating ACE2-expressing extracellular vesicles block broad strains of SARS-CoV-2. Nature Communications, 2022, 13, 405.	5.8	92
16	Practical challenges in integrating genomic data into the electronic health record. Genetics in Medicine, 2013, 15, 772-778.	1.1	85
17	Clinical text classification with rule-based features and knowledge-guided convolutional neural networks. BMC Medical Informatics and Decision Making, 2019, 19, 71.	1.5	76
18	CSER and eMERGE: current and potential state of the display of genetic information in the electronic health record. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1231-1242.	2.2	73

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19	3D-MICE: integration of cross-sectional and longitudinal imputation for multi-analyte longitudinal clinical data. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 645-653.	2.2	73
20	Recent Advances in Supervised Dimension Reduction: A Survey. Machine Learning and Knowledge Extraction, 2019, 1, 341-358.	3.2	72
21	Pitfalls of merging GWAS data: lessons learned in the eMERGE network and quality control procedures to maintain high data quality. Genetic Epidemiology, 2011, 35, 887-898.	0.6	71
22	Primary Care Practicesâ€™ Abilities And Challenges In Using Electronic Health Record Data For Quality Improvement. Health Affairs, 2018, 37, 635-643.	2.5	66
23	Statistical and machine learning methods for spatially resolved transcriptomics data analysis. Genome Biology, 2022, 23, 83.	3.8	66
24	Provider perspectives on the integration of patient-reported outcomes in an electronic health record. JAMIA Open, 2019, 2, 73-80.	1.0	65
25	Stakeholder engagement: a key component of integrating genomic information into electronic health records. Genetics in Medicine, 2013, 15, 792-801.	1.1	64
26	Segment convolutional neural networks (Seg-CNNs) for classifying relations in clinical notes. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 93-98.	2.2	62
27	What Every Reader Should Know About Studies Using Electronic Health Record Data but May Be Afraid to Ask. Journal of Medical Internet Research, 2021, 23, e22219.	2.1	61
28	Using natural language processing and machine learning to identify breast cancer local recurrence. BMC Bioinformatics, 2018, 19, 498.	1.2	60
29	Design patterns for the development of electronic health record-driven phenotype extraction algorithms. Journal of Biomedical Informatics, 2014, 51, 280-286.	2.5	55
30	Healthcare provider education to support integration of pharmacogenomics in practice: the eMERGE Network experience. Pharmacogenomics, 2017, 18, 1013-1025.	0.6	55
31	Predicting mortality in critically ill patients with diabetes using machine learning and clinical notes. BMC Medical Informatics and Decision Making, 2020, 20, 295.	1.5	51
32	Prediction of breast cancer distant recurrence using natural language processing and knowledge-guided convolutional neural network. Artificial Intelligence in Medicine, 2020, 110, 101977.	3.8	50
33	Facilitating phenotype transfer using a common data model. Journal of Biomedical Informatics, 2019, 96, 103253.	2.5	49
34	A multidimensional precision medicine approach identifies an autism subtype characterized by dyslipidemia. Nature Medicine, 2020, 26, 1375-1379.	15.2	49
35	Developing a FHIR-based EHR phenotyping framework: A case study for identification of patients with obesity and multiple comorbidities from discharge summaries. Journal of Biomedical Informatics, 2019, 99, 103310.	2.5	48
36	Predicting ICU readmission using grouped physiological and medication trends. Artificial Intelligence in Medicine, 2019, 95, 27-37.	3.8	47

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37	Traditional Chinese medicine clinical records classification with BERT and domain specific corpora. Journal of the American Medical Informatics Association: JAMIA, 2019, 26, 1632-1636.	2.2	46
38	Derivation and Validation of Novel Phenotypes of Multiple Organ Dysfunction Syndrome in Critically Ill Children. JAMA Network Open, 2020, 3, e209271.	2.8	45
39	Anatomic and Advanced Adenoma Detection Rates as Quality Metrics Determined via Natural Language Processing. American Journal of Gastroenterology, 2014, 109, 1844-1849.	0.2	42
40	Evaluating the state of the art in missing data imputation for clinical data. Briefings in Bioinformatics, 2022, 23, .	3.2	42
41	Genomic Information for Clinicians in the Electronic Health Record: Lessons Learned From the Clinical Genome Resource Project and the Electronic Medical Records and Genomics Network. Frontiers in Genetics, 2019, 10, 1059.	1.1	40
42	Cataract research using electronic health records. BMC Ophthalmology, 2011, 11, 32.	0.6	38
43	Classifying relations in clinical narratives using segment graph convolutional and recurrent neural networks (Seg-GCRNs). Journal of the American Medical Informatics Association: JAMIA, 2019, 26, 262-268.	2.2	38
44	Using Tweets to Understand How COVID-19â€“Related Health Beliefs Are Affected in the Age of Social Media: Twitter Data Analysis Study. Journal of Medical Internet Research, 2021, 23, e26302.	2.1	37
45	Validation of an internationally derived patient severity phenotype to support COVID-19 analytics from electronic health record data. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 1411-1420.	2.2	37
46	Development of an optical character recognition pipeline for handwritten form fields from an electronic health record. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, e90-e95.	2.2	36
47	Genome-wide study of resistant hypertension identified from electronic health records. PLoS ONE, 2017, 12, e0171745.	1.1	36
48	A Comparison of Pre-trained Vision-and-Language Models for Multimodal Representation Learning across Medical Images and Reports. , 2020, , .		35
49	Genetic Variants Associated with Serum Thyroid Stimulating Hormone (TSH) Levels in European Americans and African Americans from the eMERGE Network. PLoS ONE, 2014, 9, e111301.	1.1	34
50	Tensor Factorization for Precision Medicine in Heart Failure with Preserved Ejection Fraction. Journal of Cardiovascular Translational Research, 2017, 10, 305-312.	1.1	34
51	Early Prediction of Acute Kidney Injury in Critical Care Setting Using Clinical Notes. , 2018, 2018, 683-686.		34
52	International Analysis of Electronic Health Records of Children and Youth Hospitalized With COVID-19 Infection in 6 Countries. JAMA Network Open, 2021, 4, e2112596.	2.8	33
53	Distinguishing Admissions Specifically for COVID-19 From Incidental SARS-CoV-2 Admissions: National Retrospective Electronic Health Record Study. Journal of Medical Internet Research, 2022, 24, e37931.	2.1	33
54	Developing a portable natural language processing based phenotyping system. BMC Medical Informatics and Decision Making, 2019, 19, 78.	1.5	32

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55	An evaluation of the NQF Quality Data Model for representing Electronic Health Record driven phenotyping algorithms. AMIA ... Annual Symposium proceedings, 2012, 2012, 911-20.	0.2	32
56	Review and evaluation of electronic health records-driven phenotype algorithm authoring tools for clinical and translational research. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1251-1260.	2.2	30
57	A case study evaluating the portability of an executable computable phenotype algorithm across multiple institutions and electronic health record environments. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 1540-1546.	2.2	29
58	Pharmacogenomic clinical decision support design and multi-site process outcomes analysis in the eMERGE Network. Journal of the American Medical Informatics Association: JAMIA, 2019, 26, 143-148.	2.2	28
59	Implementation of workflow engine technology to deliver basic clinical decision support functionality. BMC Medical Research Methodology, 2011, 11, 43.	1.4	27
60	Making work visible for electronic phenotype implementation: Lessons learned from the eMERGE network. Journal of Biomedical Informatics, 2019, 99, 103293.	2.5	27
61	Electronic medical records and genomics (eMERGE) network exploration in cataract: several new potential susceptibility loci. Molecular Vision, 2014, 20, 1281-95.	1.1	27
62	Participant choices for return of genomic results in the eMERGE Network. Genetics in Medicine, 2020, 22, 1821-1829.	1.1	25
63	Early Prediction of Acute Kidney Injury in Critical Care Setting Using Clinical Notes and Structured Multivariate Physiological Measurements. Studies in Health Technology and Informatics, 2019, 264, 368-372.	0.2	25
64	Association of Pathogenic Variants in Hereditary Cancer Genes With Multiple Diseases. JAMA Oncology, 2022, 8, 835.	3.4	25
65	The Electronic Health Record for Translational Research. Journal of Cardiovascular Translational Research, 2014, 7, 607-614.	1.1	24
66	Cancer classification and pathway discovery using non-negative matrix factorization. Journal of Biomedical Informatics, 2019, 96, 103247.	2.5	24
67	MedGCN: Medication recommendation and lab test imputation via graph convolutional networks. Journal of Biomedical Informatics, 2022, 127, 104000.	2.5	23
68	Practical considerations for implementing genomic information resources. Applied Clinical Informatics, 2016, 07, 870-882.	0.8	21
69	Empowering genomic medicine by establishing critical sequencing result data flows: the eMERGE example. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 1375-1381.	2.2	21
70	Assessing the spatial implications of interactions among strategic forest management options using a Windows-based harvest simulator. Computers and Electronics in Agriculture, 2002, 33, 179-196.	3.7	20
71	A deep-learning-based unsupervised model on esophageal manometry using variational autoencoder. Artificial Intelligence in Medicine, 2021, 112, 102006.	3.8	19
72	International Changes in COVID-19 Clinical Trajectories Across 315 Hospitals and 6 Countries: Retrospective Cohort Study. Journal of Medical Internet Research, 2021, 23, e31400.	2.1	19

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73	An ancillary genomics system to support the return of pharmacogenomic results. Journal of the American Medical Informatics Association: JAMIA, 2019, 26, 306-310.	2.2	18
74	Toward <scp>crossâ€platform</scp> electronic health record<scp>â€driven</scp> phenotyping using Clinical Quality Language. Learning Health Systems, 2020, 4, e10233.	1.1	17
75	Desiderata for the development of next-generation electronic health record phenotype libraries. GigaScience, 2021, 10, .	3.3	17
76	A Mendelian Randomization Approach Using 3-HMG-Coenzyme-A Reductase Gene Variation to Evaluate the Association of Statin-Induced Low-Density Lipoprotein Cholesterol Lowering With Noncardiovascular Disease Phenotypes. JAMA Network Open, 2021, 4, e2112820.	2.8	16
77	Multi-View Graph Convolutional Network and Its Applications on Neuroimage Analysis for Parkinson's Disease. AMIA ... Annual Symposium proceedings, 2018, 2018, 1147-1156.	0.2	16
78	Proactive vs Reactive Machine Learning in Health Care. JAMA - Journal of the American Medical Association, 2022, 327, 623.	3.8	16
79	Spatiotemporal localization of proteins in mycobacteria. Cell Reports, 2021, 37, 110154.	2.9	16
80	Developing a data element repository to support EHR-driven phenotype algorithm authoring and execution. Journal of Biomedical Informatics, 2016, 62, 232-242.	2.5	15
81	Identifying Breast Cancer Distant Recurrences from Electronic Health Records Using Machine Learning. Journal of Healthcare Informatics Research, 2019, 3, 283-299.	5.3	15
82	Genomic considerations for FHIRÂ®; eMERGE implementation lessons. Journal of Biomedical Informatics, 2021, 118, 103795.	2.5	15
83	A rural community's involvement in the design and usability testing of a computerâ€based informed consent process for the personalized medicine research project. American Journal of Medical Genetics, Part A, 2014, 164, 129-140.	0.7	14
84	Effects of 2 Forms of Practice Facilitation on Cardiovascular Prevention in Primary Care. Medical Care, 2020, 58, 344-351.	1.1	14
85	Performanceâ€weightedâ€voting model: An ensemble machine learning method for cancer type classification using wholeâ€exome sequencing mutation. Quantitative Biology, 2020, 8, 347-358.	0.3	14
86	Deep learning for cancer type classification and driver gene identification. BMC Bioinformatics, 2021, 22, 491.	1.2	14
87	Supervised Nonnegative Matrix Factorization to Predict ICU Mortality Risk. , 2018, 2018, 1189-1194.		13
88	A Modular Architecture for Electronic Health Record-Driven Phenotyping. AMIA Summits on Translational Science Proceedings, 2015, 2015, 147-51.	0.4	13
89	A multi-institution evaluation of clinical profile anonymization. Journal of the American Medical Informatics Association: JAMIA, 2016, 23, e131-e137.	2.2	12
90	Deep Generative Classifiers for Thoracic Disease Diagnosis with Chest X-ray Images. , 2018, 2018, 1209-1214.		12

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91	Integrating hypertension phenotype and genotype with hybrid non-negative matrix factorization. Bioinformatics, 2019, 35, 1395-1403.	1.8	12
92	Predictive modeling of bacterial infections and antibiotic therapy needs in critically ill adults. Journal of Biomedical Informatics, 2020, 109, 103540.	2.5	12
93	<scp>Dataâ€driven</scp> discovery of probable Alzheimer's disease and related dementia subphenotypes using electronic health records. Learning Health Systems, 2020, 4, e10246.	1.1	12
94	Subphenotyping depression using machine learning and electronic health records. Learning Health Systems, 2020, 4, e10241.	1.1	12
95	A novel normalization and differential abundance test framework for microbiome data. Bioinformatics, 2020, 36, 3959-3965.	1.8	12
96	Agingâ€related cell typeâ€specific pathophysiologic immune responses that exacerbate disease severity in aged COVIDâ€19 patients. Aging Cell, 2022, 21, e13544.	3.0	11
97	Preoperative magnetic resonance imaging use and oncologic outcomes in premenopausal breast cancer patients. Npj Breast Cancer, 2020, 6, 49.	2.3	10
98	Somatic genetic aberrations in benign breast disease and the risk of subsequent breast cancer. Npj Breast Cancer, 2020, 6, 24.	2.3	10
99	Multinational characterization of neurological phenotypes in patients hospitalized with COVID-19. Scientific Reports, 2021, 11, 20238.	1.6	10
100	A Prototype for Executable and Portable Electronic Clinical Quality Measures Using the KNIME Analytics Platform. AMIA Summits on Translational Science Proceedings, 2015, 2015, 127-31.	0.4	10
101	Optimizing the evaluation of gene-targeted panels for tumor mutational burden estimation. Scientific Reports, 2021, 11, 21072.	1.6	9
102	A Template for Authoring and Adapting Genomic Medicine Content in the eMERGE Infobutton Project. AMIA ... Annual Symposium proceedings, 2014, 2014, 944-53.	0.2	9
103	Advances in Machine Learning Approaches to Heart Failure with Preserved Ejection Fraction. Heart Failure Clinics, 2022, 18, 287-300.	1.0	9
104	Challenges to electronic clinical quality measurement using third-party platforms in primary care practices: the healthy hearts in the heartland experience. JAMIA Open, 2019, 2, 423-428.	1.0	8
105	Hyperchloremia in critically ill patients: association with outcomes and prediction using electronic health record data. BMC Medical Informatics and Decision Making, 2020, 20, 302.	1.5	8
106	Unsupervised phenotyping of sepsis using nonnegative matrix factorization of temporal trends from a multivariate panel of physiological measurements. BMC Medical Informatics and Decision Making, 2021, 21, 95.	1.5	8
107	Contralateral Breast Cancer Event Detection Using Nature Language Processing. AMIA ... Annual Symposium proceedings, 2017, 2017, 1885-1892.	0.2	8
108	Improving the Accuracy of Scores to Predict Gastrostomy after Intracerebral Hemorrhage with Machine Learning. Journal of Stroke and Cerebrovascular Diseases, 2018, 27, 3570-3574.	0.7	7

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109	Conjugated equine estrogen and medroxyprogesterone acetate are associated with decreased risk of breast cancer relative to bioidentical hormone therapy and controls. PLoS ONE, 2018, 13, e0197064.	1.1	7
110	Machine Learning in Causal Inference: Application in Pharmacovigilance. Drug Safety, 2022, 45, 459-476.	1.4	7
111	Evaluation of structured data from electronic health records to identify clinical classification criteria attributes for systemic lupus erythematosus. Lupus Science and Medicine, 2021, 8, e000488.	1.1	6
112	Genetic-Based Hypertension Subtype Identification Using Informative SNPs. Genes, 2020, 11, 1265.	1.0	5
113	What Is Asked in Clinical Data Request Forms? A Multi-site Thematic Analysis of Forms Towards Better Data Access Support. AMIA ... Annual Symposium proceedings, 2014, 2014, 616-25.	0.2	5
114	Development of a repository of computable phenotype definitions using the clinical quality language. JAMIA Open, 2021, 4, ooab094.	1.0	5
115	Ductal Carcinoma In Situ of Breast: From Molecular Etiology to Therapeutic Management. Endocrinology, 2022, 163, .	1.4	5
116	Efficient Queries of Stand-off Annotations for Natural Language Processing on Electronic Medical Records. Biomedical Informatics Insights, 2016, 8, BII.S38916.	4.6	4
117	The genomic CDS sandbox: An assessment among domain experts. Journal of Biomedical Informatics, 2016, 60, 84-94.	2.5	4
118	Efficient Genomic Interval Queries Using Augmented Range Trees. Scientific Reports, 2019, 9, 5059.	1.6	4
119	Phenotyping Multiple Organ Dysfunction Syndrome Using Temporal Trends in Critically Ill Children. , 2019, 2019, 968-972.		4
120	A Decompositional Approach to Executing Quality Data Model Algorithms on the i2b2 Platform. AMIA Summits on Translational Science Proceedings, 2016, 2016, 167-75.	0.4	4
121	Classifying Clinical Trial Eligibility Criteria to Facilitate Phased Cohort Identification Using Clinical Data Repositories. AMIA ... Annual Symposium proceedings, 2017, 2017, 1754-1763.	0.2	4
122	Design and validation of a FHIR-based EHR-driven phenotyping toolbox. Journal of the American Medical Informatics Association: JAMIA, 0, , .	2.2	4
123	Portable Phenotyping System: A Portable Machine-Learning Approach to i2b2 Obesity Challenge. , 2018, , .		3
124	Supervised subgraph augmented non-negative matrix factorization for interpretable manufacturing time series data analytics. IISE Transactions, 2020, 52, 120-131.	1.6	3
125	Infobuttons for Genomic Medicine: Requirements and Barriers. Applied Clinical Informatics, 2021, 12, 383-390.	0.8	3
126	National Trends in Disease Activity for COVID-19 Among Children in the US. Frontiers in Pediatrics, 2021, 9, 700656.	0.9	3

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127	Early Prediction of Mortality in Critical Care Setting in Sepsis Patients Using Structured Features and Unstructured Clinical Notes. , 2021, , .		3
128	Using Machine Learning to Integrate Socio-Behavioral Factors in Predicting Cardiovascular-Related Mortality Risk. Studies in Health Technology and Informatics, 2019, 264, 433-437.	0.2	3
129	Characterizing Design Patterns of EHR-Driven Phenotype Extraction Algorithms. , 2018, , .		2
130	Implementing a Portable Clinical NLP System with a Common Data Model -- a Lisp Perspective. , 2018, 2018, 461-466.		2
131	Using Machine Learning to Predict Hyperchloremia in Critically Ill Patients. , 2019, 2019, 1703-1707.		2
132	Characterizing phenotypic abnormalities associated with high-risk individuals developing lung cancer using electronic health records from the All of Us researcher workbench. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 2313-2324.	2.2	2
133	Facilitating reproducible research through direct connection of data analysis with manuscript preparation: StatTag for connecting statistical software to Microsoft Word. JAMIA Open, 2020, 3, 342-358.	1.0	2
134	Prototype Development: Context-Driven Dynamic XML Ophthalmologic Data Capture Application. JMIR Medical Informatics, 2017, 5, e27.	1.3	2
135	Solutions for Unexpected Challenges Encountered when Integrating Research Genomics Results into the EHR. ACI Open, 2020, 04, e132-e135.	0.2	2
136	Predictive Modeling of the Risk of Acute Kidney Injury in Critical Care: A Systematic Investigation of The Class Imbalance Problem. AMIA Summits on Translational Science Proceedings, 2019, 2019, 809-818.	0.4	2
137	Phenoflow: A Microservice Architecture for Portable Workflow-based Phenotype Definitions. AMIA Summits on Translational Science Proceedings, 2021, 2021, 142-151.	0.4	2
138	Applicability of Pharmacogenomically Guided Medication Treatment during Hospitalization of At-Risk Minority Patients. Journal of Personalized Medicine, 2021, 11, 1343.	1.1	2
139	A multi-site cognitive task analysis for biomedical query mediation. International Journal of Medical Informatics, 2016, 93, 74-84.	1.6	1
140	The Genomic Medical Record and Omic Ancillary Systems. Computers in Health Care, 2020, , 253-275.	0.2	1
141	Rich Text Formatted EHR Narratives: A Hidden and Ignored Trove. Studies in Health Technology and Informatics, 2019, 264, 472-476.	0.2	1
142	CQL4NLP: Development and Integration of FHIR NLP Extensions in Clinical Quality Language for EHR-driven Phenotyping. AMIA Summits on Translational Science Proceedings, 2021, 2021, 624-633.	0.4	1
143	Under-specification as the source of ambiguity and vagueness in narrative phenotype algorithm definitions. BMC Medical Informatics and Decision Making, 2022, 22, 23.	1.5	1
144	Using an Unsupervised Clustering Model to Detect the Early Spread of SARS-CoV-2 Worldwide. Genes, 2022, 13, 648.	1.0	1

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145	Generating and Reporting Electronic Clinical Quality Measures from Electronic Health Records: Strategies from EvidenceNOW Cooperatives. Applied Clinical Informatics, 2022, 13, 485-494.	0.8	1
146	Development and validation of MicrobEx: an open-source package for microbiology culture concept extraction. JAMIA Open, 2022, 5, .	1.0	1
147	Psychiatric manifestations of rare variation in medically actionable genes: a PheWAS approach. BMC Genomics, 2022, 23, 385.	1.2	1
148	Facilitating Genetics Aware Clinical Decision Support: Putting the eMERGE Infrastructure into Practice. ACI Open, 2021, 05, e54-e58.	0.2	0
149	Antiplatelet Medications and Biomarkers of Hemostasis May Explain the Association of Hematoma Appearance and Subsequent Hematoma Expansion After Intracerebral Hemorrhage. Neurocritical Care, 2021, , 1.	1.2	0
150	Integration of NLP2FHIR Representation with Deep Learning Models for EHR Phenotyping: A Pilot Study on Obesity Datasets. AMIA Summits on Translational Science Proceedings, 2021, 2021, 410-419.	0.4	0
151	802â€...An electronic health record-based approach to identify and characterize patients with immune checkpoint inhibitor-associated arthritis. , 2021, 9, A838-A839.		0
152	Abstract P2-09-15: Frequency of germline mutations in breast cancer susceptibility genes among women under age 50 presenting with parity associated breast cancer. Cancer Research, 2022, 82, P2-09-15-P2-09-15.	0.4	0
153	Unsupervised clustering analysis of SARS-Cov-2 population structure reveals six major subtypes at early stage across the world. , 2021, , .		0