Christopher G Chute

List of Publications by Year
in descending order

82 papers	4,949 citations	147801 31 h-index	118850 62 g-index
94 all docs	94 docs citations	94 times ranked	7475 citing authors

#	Article	IF	Citations
1	The Human Phenotype Ontology in 2021. Nucleic Acids Research, 2021, 49, D1207-D1217.	14.5	652
2	The National COVID Cohort Collaborative (N3C): Rationale, design, infrastructure, and deployment. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 427-443.	4.4	342
3	Preemptive Genotyping for Personalized Medicine: Design of the Right Drug, Right Dose, Right Timeâ€"Using Genomic Data to Individualize Treatment Protocol. Mayo Clinic Proceedings, 2014, 89, 25-33.	3.0	250
4	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.	6.2	232
5	Classification, Ontology, and Precision Medicine. New England Journal of Medicine, 2018, 379, 1452-1462.	27.0	220
6	Association Between Immune Dysfunction and COVID-19 Breakthrough Infection After SARS-CoV-2 Vaccination in the US. JAMA Internal Medicine, 2022, 182, 153.	5.1	182
7	Clinical Characterization and Prediction of Clinical Severity of SARS-CoV-2 Infection Among US Adults Using Data From the US National COVID Cohort Collaborative. JAMA Network Open, 2021, 4, e2116901.	5.9	179
8	Genome- and Phenome-Wide Analyses of Cardiac Conduction Identifies Markers of Arrhythmia Risk. Circulation, 2013, 127, 1377-1385.	1.6	167
9	Characterizing Long COVID: Deep Phenotype of a Complex Condition. EBioMedicine, 2021, 74, 103722.	6.1	127
10	ICD-11: an international classification of diseases for the twenty-first century. BMC Medical Informatics and Decision Making, 2021, 21, 206.	3.0	120
11	Desiderata for computable representations of electronic health records-driven phenotype algorithms. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1220-1230.	4.4	110
12	Similar Levels of Urological Symptoms Have Similar Impact on Scottish and American Menâ€"Although Scots Report Less Symptoms. Journal of Urology, 1993, 150, 1701-1705.	0.4	107
13	Associations between HIV infection and clinical spectrum of COVID-19: a population level analysis based on US National COVID Cohort Collaborative (N3C) data. Lancet HIV,the, 2021, 8, e690-e700.	4.7	106
14	Identifying who has long COVID in the USA: a machine learning approach using N3C data. The Lancet Digital Health, 2022, 4, e532-e541.	12.3	104
15	Characteristics, Outcomes, and Severity Risk Factors Associated With SARS-CoV-2 Infection Among Children in the US National COVID Cohort Collaborative. JAMA Network Open, 2022, 5, e2143151.	5.9	102
16	Normalization and standardization of electronic health records for high-throughput phenotyping: the SHARPn consortium. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, e341-e348.	4.4	100
17	Long-term use of immunosuppressive medicines and in-hospital COVID-19 outcomes: a retrospective cohort study using data from the National COVID Cohort Collaborative. Lancet Rheumatology, The, 2022, 4, e33-e41.	3.9	96
18	Predictive Utility of Polygenic Risk Scores for Coronary Heart Disease in Three Major Racial and Ethnic Groups. American Journal of Human Genetics, 2020, 106, 707-716.	6.2	93

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19	New filovirus disease classification and nomenclature. Nature Reviews Microbiology, 2019, 17, 261-263.	28.6	84
20	Outcomes of SARS-CoV-2 Infection in Patients With Chronic Liver Disease and Cirrhosis: A National COVID Cohort Collaborative Study. Gastroenterology, 2021, 161, 1487-1501.e5.	1.3	79
21	Some experiences and opportunities for big data in translational research. Genetics in Medicine, 2013, 15, 802-809.	2.4	76
22	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.	4.4	73
23	Analyzing the heterogeneity and complexity of Electronic Health Record oriented phenotyping algorithms. AMIA ... Annual Symposium proceedings, 2011, 2011, 274-83.	0.2	68
24	The eMERGE genotype set of 83,717 subjects imputed to ~40â€‰million variants genome wide and association with the herpes zoster medical record phenotype. Genetic Epidemiology, 2019, 43, 63-81.	1.3	63
25	Fast Healthcare Interoperability Resources (FHIR) as a Meta Model to Integrate Common Data Models: Development of a Tool and Quantitative Validation Study. JMIR Medical Informatics, 2019, 7, e15199.	2.6	50
26	Association Between Glucagon-Like Peptide 1 Receptor Agonist and Sodiumâ€“Glucose Cotransporter 2 Inhibitor Use and COVID-19 Outcomes. Diabetes Care, 2021, 44, 1564-1572.	8.6	43
27	Probing the Virtual Proteome to Identify Novel Disease Biomarkers. Circulation, 2018, 138, 2469-2481.	1.6	42
28	Practical considerations in genomic decision support: The eMERGE experience. Journal of Pathology Informatics, 2015, 6, 50.	1.7	42
29	SMART-on-FHIR implemented over i2b2. Journal of the American Medical Informatics Association: JAMIA, 2017, 24, 398-402.	4.4	39
30	Semantic integration of clinical laboratory tests from electronic health records for deep phenotyping and biomarker discovery. Npj Digital Medicine, 2019, 2, .	10.9	39
31	Synergies between centralized and federated approaches to data quality: a report from the national COVID cohort collaborative. Journal of the American Medical Informatics Association: JAMIA, 2022, 29, 609-618.	4.4	39
32	The GA4GH Phenopacket schema defines a computable representation of clinical data. Nature Biotechnology, 2022, 40, 817-820.	17.5	38
33	Genome-wide study of resistant hypertension identified from electronic health records. PLoS ONE, 2017, 12, e0171745.	2.5	36
34	On beyond Gruber: â€œOntologiesâ€•in todayâ€™s biomedical information systems and the limits of OWL. Journal of Biomedical Informatics: X, 2019, 100, 100002.	4.2	35
35	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.	2.5	34
36	The SHARPn project on secondary use of Electronic Medical Record data: progress, plans, and possibilities. AMIA ... Annual Symposium proceedings, 2011, 2011, 248-56.	0.2	30

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37	The Return of Actionable Variants Empirical (RAVE) Study, a Mayo Clinic Genomic Medicine Implementation Study: Design and Initial Results. Mayo Clinic Proceedings, 2018, 93, 1600-1610.	3.0	29
38	A Census of Disease Ontologies. Annual Review of Biomedical Data Science, 2018, 1, 305-331.	6.5	29
39	Network-based analysis reveals distinct association patterns in a semantic MEDLINE-based drug-disease-gene network. Journal of Biomedical Semantics, 2014, 5, 33.	1.6	24
40	Use of Hydroxychloroquine, Remdesivir, and Dexamethasone Among Adults Hospitalized With COVID-19 in the United States. Annals of Internal Medicine, 2021, 174, 1395-1403.	3.9	24
41	Genomic Medicine, Health Information Technology, and Patient Care. JAMA - Journal of the American Medical Association, 2013, 309, 1467.	7.4	23
42	Clinical element models in the SHARPn consortium. Journal of the American Medical Informatics Association: JAMIA, 2016, 23, 248-256.	4.4	23
43	A Simple Standard for Sharing Ontological Mappings (SSSOM). Database: the Journal of Biological Databases and Curation, 2022, 2022, .	3.0	23
44	Feature engineering with clinical expert knowledge: A case study assessment of machine learning model complexity and performance. PLoS ONE, 2020, 15, e0231300.	2.5	22
45	EXPLORING THE PHARMACOGENOMICS KNOWLEDGE BASE (PHARMGKB) FOR REPOSITIONING BREAST CANCER DRUGS BY LEVERAGING WEB ONTOLOGY LANGUAGE (OWL) AND CHEMINFORMATICS APPROACHES. , 2013, , .		21
46	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.	4.4	21
47	NSAID use and clinical outcomes in COVID-19 patients: a 38-center retrospective cohort study. Virology Journal, 2022, 19, 84.	3.4	19
48	Mining severe drug-drug interaction adverse events using Semantic Web technologies: a case study. BioData Mining, 2015, 8, 12.	4.0	18
49	Transformation of standardized clinical models based on OWL technologies: from CEM to OpenEHR archetypes. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 536-544.	4.4	18
50	A conceptual model for translating omic data into clinical action. Journal of Pathology Informatics, 2015, 6, 46.	1.7	17
51	Post-recovery COVID-19 and incident heart failure in the National COVID Cohort Collaborative (N3C) study. Nature Communications, 2022, 13, .	12.8	17
52	ICD-11 extension codes support detailed clinical abstraction and comprehensive classification. BMC Medical Informatics and Decision Making, 2021, 21, 278.	3.0	16
53	Developing a data element repository to support EHR-driven phenotype algorithm authoring and execution. Journal of Biomedical Informatics, 2016, 62, 232-242.	4.3	15
54	Interface Terminologies, Reference Terminologies and Aggregation Terminologies: A Strategy for Better Integration. Studies in Health Technology and Informatics, 2017, 245, 940-944.	0.3	15

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55	Clinical Data Retrieval and Analysis. I've Seen a Case Like That Before. Annals of the New York Academy of Sciences, 1992, 670, 133-140.	3.8	13
56	A study paradigm integrating prospective epidemiologic cohorts and electronic health records to identify disease biomarkers. Nature Communications, 2018, 9, 3522.	12.8	13
57	Cancer based pharmacogenomics network supported with scientific evidences: from the view of drug repurposing. BioData Mining, 2015, 8, 9.	4.0	12
58	Sharing ontology between ICD 11 and SNOMED CT will enable seamless re-use and semantic interoperability. Studies in Health Technology and Informatics, 2013, 192, 343-6.	0.3	11
59	Harmonizing units and values of quantitative data elements in a very large nationally pooled electronic health record (EHR) dataset. Journal of the American Medical Informatics Association: JAMIA, 2022, 29, 1172-1182.	4.4	11
60	Overview of ICD-11 architecture and structure. BMC Medical Informatics and Decision Making, 2021, 21, 378.	3.0	11
61	The rendering of human phenotype and rare diseases in ICDâ€11. Journal of Inherited Metabolic Disease, 2018, 41, 563-569.	3.6	10
62	Semantic Alignment between ICD-11 and SNOMED CT. Studies in Health Technology and Informatics, 2015, 216, 790-4.	0.3	10
63	INCORPORATING EXPERT TERMINOLOGY AND DISEASE RISK FACTORS INTO CONSUMER HEALTH VOCABULARIES. , 2012, , .		9
64	Association Between COVID-19 and Mortality in Hip Fracture Surgery in the National COVID Cohort Collaborative (N3C): A Retrospective Cohort Study. Journal of the American Academy of Orthopaedic Surgeons Global Research and Reviews, 2022, 6, .	0.7	9
65	Developing an ETL tool for converting the PCORnet CDM into the OMOP CDM to facilitate the COVID-19 data integration. Journal of Biomedical Informatics, 2022, 127, 104002.	4.3	9
66	ICD-11 and SNOMED CT Common Ontology: circulatory system. Studies in Health Technology and Informatics, 2014, 205, 1043-7.	0.3	9
67	Postcoordination of codes in ICD-11. BMC Medical Informatics and Decision Making, 2021, 21, 379.	3.0	9
68	Mining drug-drug interaction patterns from linked data: A case study for Warfarin, Clopidogrel, and Simvastatin. , 2013, , .		6
69	The Pluripotent Rendering of Clinical Data for Precision Medicine. Studies in Health Technology and Informatics, 2017, 245, 337-340.	0.3	5
70	The horizontal and vertical nature of patient phenotype retrieval: new directions for clinical text processing. Proceedings, 2002, , 165-9.	0.6	4
71	Ankle Fracture and Length of Stay in US Adult Population Using Data From the National COVID Cohort Collaborative. Foot & Ankle Orthopaedics, 2022, 7, 24730114221077282.	0.2	4
72	Preferences for Updates on General Research Results: A Survey of Participants in Genomic Research from Two Institutions. Journal of Personalized Medicine, 2021, 11, 399.	2.5	3

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73	Adverse Drug Event-based Stratification of Tumor Mutations: A Case Study of Breast Cancer Patients Receiving Aromatase Inhibitors. AMIA ... Annual Symposium proceedings, 2014, 2014, 1160-9.	0.2	3
74	Characterizing Design Patterns of EHR-Driven Phenotype Extraction Algorithms. , 2018, , .		2
75	INTEGRATING VA'S NDF-RT DRUG TERMINOLOGY WITH PHARMGKB: PRELIMINARY RESULTS. , 2011, , .		2
76	Comorbidity Characterization Among eMERGE Institutions: A Pilot Evaluation with the Johns Hopkins Adjusted Clinical GroupsÂ® System. AMIA Summits on Translational Science Proceedings, 2019, 2019, 145-152.	0.4	2
77	Ensuring a safe(r) harbor: Excising personally identifiable information from structured electronic health record data. Journal of Clinical and Translational Science, 2022, 6, e10.	0.6	2
78	Developing a modular architecture for creation of rule-based clinical diagnostic criteria. BioData Mining, 2016, 9, 33.	4.0	1
79	Simplifying complex clinical element models to encourage adoption. AMIA Summits on Translational Science Proceedings, 2014, 2014, 26-31.	0.4	1
80	Drug Normalization for Cancer Therapeutic and Druggable Genome Target Discovery. AMIA Summits on Translational Science Proceedings, 2015, 2015, 72-6.	0.4	1
81	Adverse Drug Events-based Tumor Stratification for Ovarian Cancer Patients Receiving Platinum Therapy. AMIA Summits on Translational Science Proceedings, 2015, 2015, 51-5.	0.4	0
82	A Pilot Study on Modeling of Diagnostic Criteria Using OWL and SWRL. Studies in Health Technology and Informatics, 2015, 216, 1093.	0.3	0