

Jacob J Hughey

List of Publications by Year in descending order

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Version: 2024-02-01

159
papers

19,900
citations

36271

51
h-index

14197

128
g-index

186
all docs

186
docs citations

186
times ranked

34770
citing authors

#	ARTICLE	IF	CITATIONS
1	xCell: digitally portraying the tissue cellular heterogeneity landscape. <i>Genome Biology</i> , 2017, 18, 220.	3.8	2,572
2	Reference-based analysis of lung single-cell sequencing reveals a transitional profibrotic macrophage. <i>Nature Immunology</i> , 2019, 20, 163-172.	7.0	2,330
3	Ten Years of Pathway Analysis: Current Approaches and Outstanding Challenges. <i>PLoS Computational Biology</i> , 2012, 8, e1002375.	1.5	1,267
4	Systematic pan-cancer analysis of tumour purity. <i>Nature Communications</i> , 2015, 6, 8971.	5.8	937
5	Variation in the Human Immune System Is Largely Driven by Non-Heritable Influences. <i>Cell</i> , 2015, 160, 37-47.	13.5	828
6	Single-cell NF- κ B dynamics reveal digital activation and analogue information processing. <i>Nature</i> , 2010, 466, 267-271.	13.7	736
7	ImmPort: disseminating data to the public for the future of immunology. <i>Immunologic Research</i> , 2014, 58, 234-239.	1.3	724
8	Discovery and Preclinical Validation of Drug Indications Using Compendia of Public Gene Expression Data. <i>Science Translational Medicine</i> , 2011, 3, 96ra77.	5.8	708
9	Computational Repositioning of the Anticonvulsant Topiramate for Inflammatory Bowel Disease. <i>Science Translational Medicine</i> , 2011, 3, 96ra76.	5.8	534
10	ImmPort, toward repurposing of open access immunological assay data for translational and clinical research. <i>Scientific Data</i> , 2018, 5, 180015.	2.4	529
11	High-Sensitivity Measurements of Multiple Kinase Activities in Live Single Cells. <i>Cell</i> , 2014, 157, 1724-1734.	13.5	483
12	An Environment-Wide Association Study (EWAS) on Type 2 Diabetes Mellitus. <i>PLoS ONE</i> , 2010, 5, e10746.	1.1	470
13	Clinical Interpretation and Implications of Whole-Genome Sequencing. <i>JAMA - Journal of the American Medical Association</i> , 2014, 311, 1035.	3.8	398
14	Comprehensive analysis of normal adjacent to tumor transcriptomes. <i>Nature Communications</i> , 2017, 8, 1077.	5.8	394
15	SMYD3 links lysine methylation of MAP3K2 to Ras-driven cancer. <i>Nature</i> , 2014, 510, 283-287.	13.7	331
16	A longitudinal big data approach for precision health. <i>Nature Medicine</i> , 2019, 25, 792-804.	15.2	329
17	Network-Based Elucidation of Human Disease Similarities Reveals Common Functional Modules Enriched for Pluripotent Drug Targets. <i>PLoS Computational Biology</i> , 2010, 6, e1000662.	1.5	297
18	Minimum information about clinical artificial intelligence modeling: the MI-CLAIM checklist. <i>Nature Medicine</i> , 2020, 26, 1320-1324.	15.2	262

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19	Guidelines for Genome-Scale Analysis of Biological Rhythms. <i>Journal of Biological Rhythms</i> , 2017, 32, 380-393.	1.4	237
20	A common rejection module (CRM) for acute rejection across multiple organs identifies novel therapeutics for organ transplantation. <i>Journal of Experimental Medicine</i> , 2013, 210, 2205-2221.	4.2	201
21	Creation and implications of a phenome-genome network. <i>Nature Biotechnology</i> , 2006, 24, 55-62.	9.4	190
22	Phenotype risk scores identify patients with unrecognized Mendelian disease patterns. <i>Science</i> , 2018, 359, 1233-1239.	6.0	164
23	Cross-tissue Analysis of Gene and Protein Expression in Normal and Cancer Tissues. <i>Scientific Reports</i> , 2016, 6, 24799.	1.6	155
24	Autoimmune Disease Classification by Inverse Association with SNP Alleles. <i>PLoS Genetics</i> , 2009, 5, e1000792.	1.5	151
25	Reversal of cancer gene expression correlates with drug efficacy and reveals therapeutic targets. <i>Nature Communications</i> , 2017, 8, 16022.	5.8	151
26	Ageing disrupts cell subpopulation dynamics and diminishes the function of mesenchymal stem cells. <i>Scientific Reports</i> , 2014, 4, 7144.	1.6	140
27	Assessment of a Deep Learning Model Based on Electronic Health Record Data to Forecast Clinical Outcomes in Patients With Rheumatoid Arthritis. <i>JAMA Network Open</i> , 2019, 2, e190606.	2.8	135
28	A Meta-analysis of Lung Cancer Gene Expression Identifies <i>PTK7</i> as a Survival Gene in Lung Adenocarcinoma. <i>Cancer Research</i> , 2014, 74, 2892-2902.	0.4	131
29	Translational Bioinformatics: Coming of Age. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2008, 15, 709-714.	2.2	129
30	Microfluidic platform for real-time signaling analysis of multiple single T cells in parallel. <i>Lab on A Chip</i> , 2008, 8, 1700.	3.1	127
31	A Noisy Paracrine Signal Determines the Cellular NF- κ B Response to Lipopolysaccharide. <i>Science Signaling</i> , 2009, 2, ra65.	1.6	124
32	Robust meta-analysis of gene expression using the elastic net. <i>Nucleic Acids Research</i> , 2015, 43, e79-e79.	6.5	124
33	Prototype of running clinical trials in an untrustworthy environment using blockchain. <i>Nature Communications</i> , 2019, 10, 917.	5.8	114
34	Defective Signaling in the JAK-STAT Pathway Tracks with Chronic Inflammation and Cardiovascular Risk in Aging Humans. <i>Cell Systems</i> , 2016, 3, 374-384.e4.	2.9	107
35	Type 2 Diabetes Risk Alleles Demonstrate Extreme Directional Differentiation among Human Populations, Compared to Other Diseases. <i>PLoS Genetics</i> , 2012, 8, e1002621.	1.5	106
36	Releasing a preprint is associated with more attention and citations for the peer-reviewed article. <i>ELife</i> , 2019, 8, .	2.8	101

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37	Systematic identification of interaction effects between genome- and environment-wide associations in type 2 diabetes mellitus. <i>Human Genetics</i> , 2013, 132, 495-508.	1.8	98
38	Population-level rhythms in human skin with implications for circadian medicine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12313-12318.	3.3	97
39	PDX-MI: Minimal Information for Patient-Derived Tumor Xenograft Models. <i>Cancer Research</i> , 2017, 77, e62-e66.	0.4	92
40	Live-cell measurements of kinase activity in single cells using translocation reporters. <i>Nature Protocols</i> , 2018, 13, 155-169.	5.5	90
41	Widespread parainflammation in human cancer. <i>Genome Biology</i> , 2016, 17, 145.	3.8	87
42	Computational Discovery of Niclosamide Ethanolamine, a Repurposed Drug Candidate That Reduces Growth of Hepatocellular Carcinoma Cells In Vitro and in Mice by Inhibiting Cell Division Cycle 37 Signaling. <i>Gastroenterology</i> , 2017, 152, 2022-2036.	0.6	81
43	ZeitZeiger: supervised learning for high-dimensional data from an oscillatory system. <i>Nucleic Acids Research</i> , 2016, 44, e80-e80.	6.5	76
44	Evidence for widespread dysregulation of circadian clock progression in human cancer. <i>PeerJ</i> , 2018, 6, e4327.	0.9	75
45	The Case for Algorithmic Stewardship for Artificial Intelligence and Machine Learning Technologies. <i>JAMA - Journal of the American Medical Association</i> , 2020, 324, 1397.	3.8	69
46	Analysis of the Genetic Basis of Disease in the Context of Worldwide Human Relationships and Migration. <i>PLoS Genetics</i> , 2013, 9, e1003447.	1.5	67
47	Sex differences in disease risk from reported genome-wide association study findings. <i>Human Genetics</i> , 2012, 131, 353-364.	1.8	64
48	Anti-CD44 Antibody Treatment Lowers Hyperglycemia and Improves Insulin Resistance, Adipose Inflammation, and Hepatic Steatosis in Diet-Induced Obese Mice. <i>Diabetes</i> , 2015, 64, 867-875.	0.3	62
49	Computational modeling of mammalian signaling networks. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 194-209.	6.6	61
50	LimoRhyde: A Flexible Approach for Differential Analysis of Rhythmic Transcriptome Data. <i>Journal of Biological Rhythms</i> , 2019, 34, 5-18.	1.4	61
51	Disease Risk Factors Identified Through Shared Genetic Architecture and Electronic Medical Records. <i>Science Translational Medicine</i> , 2014, 6, 234ra57.	5.8	58
52	Diabetes Irreversibly Depletes Bone Marrow-Derived Mesenchymal Progenitor Cell Subpopulations. <i>Diabetes</i> , 2014, 63, 3047-3056.	0.3	58
53	Extreme Evolutionary Disparities Seen in Positive Selection across Seven Complex Diseases. <i>PLoS ONE</i> , 2010, 5, e12236.	1.1	55
54	Peptidomic Identification of Serum Peptides Diagnosing Preeclampsia. <i>PLoS ONE</i> , 2013, 8, e65571.	1.1	52

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55	MetaCyto: A Tool for Automated Meta-analysis of Mass and Flow Cytometry Data. <i>Cell Reports</i> , 2018, 24, 1377-1388.	2.9	52
56	NF- κ B signaling dynamics is controlled by a dose-sensing autoregulatory loop. <i>Science Signaling</i> , 2019, 12, .	1.6	52
57	Machine learning identifies a compact gene set for monitoring the circadian clock in human blood. <i>Genome Medicine</i> , 2017, 9, 19.	3.6	51
58	The Ultimate Model Organism. <i>Science</i> , 2008, 320, 325-327.	6.0	48
59	Are minor alleles more likely to be risk alleles?. <i>BMC Medical Genomics</i> , 2018, 11, 3.	0.7	48
60	Meta-Analysis of Vaginal Microbiome Data Provides New Insights Into Preterm Birth. <i>Frontiers in Microbiology</i> , 2020, 11, 476.	1.5	47
61	Whole genome sequencing in support of wellness and health maintenance. <i>Genome Medicine</i> , 2013, 5, 58.	3.6	46
62	Achieving high-sensitivity for clinical applications using augmented exome sequencing. <i>Genome Medicine</i> , 2015, 7, 71.	3.6	46
63	Microfluidic single-cell transcriptional analysis rationally identifies novel surface marker profiles to enhance cell-based therapies. <i>Nature Communications</i> , 2016, 7, 11945.	5.8	46
64	Solving Immunology?. <i>Trends in Immunology</i> , 2017, 38, 116-127.	2.9	45
65	Single-cell variation leads to population invariance in NF- κ B signaling dynamics. <i>Molecular Biology of the Cell</i> , 2015, 26, 583-590.	0.9	44
66	Precision annotation of digital samples in NCBI's gene expression omnibus. <i>Scientific Data</i> , 2017, 4, 170125.	2.4	44
67	Repurpose terbutaline sulfate for amyotrophic lateral sclerosis using electronic medical records. <i>Scientific Reports</i> , 2015, 5, 8580.	1.6	43
68	Investigation of maternal environmental exposures in association with self-reported preterm birth. <i>Reproductive Toxicology</i> , 2014, 45, 1-7.	1.3	42
69	Differential Phasing between Circadian Clocks in the Brain and Peripheral Organs in Humans. <i>Journal of Biological Rhythms</i> , 2016, 31, 588-597.	1.4	42
70	The 10,000 Immunomes Project: Building a Resource for Human Immunology. <i>Cell Reports</i> , 2018, 25, 513-522.e3.	2.9	40
71	A robust and interpretable end-to-end deep learning model for cytometry data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21373-21380.	3.3	40
72	Protected Health Information filter (Philter): accurately and securely de-identifying free-text clinical notes. <i>Npj Digital Medicine</i> , 2020, 3, 57.	5.7	38

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73	A genome-wide association study identifies only two ancestry specific variants associated with spontaneous preterm birth. <i>Scientific Reports</i> , 2018, 8, 226.	1.6	37
74	Improving the phenotype risk score as a scalable approach to identifying patients with Mendelian disease. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2019, 26, 1437-1447.	2.2	35
75	Heterogeneity in HIV and cellular transcription profiles in cell line models of latent and productive infection: implications for HIV latency. <i>Retrovirology</i> , 2019, 16, 32.	0.9	35
76	<i>In silico</i> and <i>in vitro</i> drug screening identifies new therapeutic approaches for Ewing sarcoma. <i>Oncotarget</i> , 2017, 8, 4079-4095.	0.8	34
77	Expression-Based Genome-Wide Association Study Links Vitamin D Binding Protein With Autoantigenicity in Type 1 Diabetes. <i>Diabetes</i> , 2016, 65, 1341-1349.	0.3	33
78	Finding disease-related genomic experiments within an international repository: first steps in translational bioinformatics. <i>AMIA ... Annual Symposium proceedings</i> , 2006, , 106-10.	0.2	32
79	Self-reported dietary adherence, disease-specific symptoms, and quality of life are associated with healthcare provider follow-up in celiac disease. <i>BMC Gastroenterology</i> , 2017, 17, 156.	0.8	31
80	Eating breakfast and avoiding late-evening snacking sustains lipid oxidation. <i>PLoS Biology</i> , 2020, 18, e3000622.	2.6	31
81	Organ Size Control Is Dominant over Rb Family Inactivation to Restrict Proliferation <i>In Vivo</i> . <i>Cell Reports</i> , 2014, 8, 371-381.	2.9	30
82	Application of Machine Learning for Cytometry Data. <i>Frontiers in Immunology</i> , 2021, 12, 787574.	2.2	30
83	PatientExploreR: an extensible application for dynamic visualization of patient clinical history from electronic health records in the OMOP common data model. <i>Bioinformatics</i> , 2019, 35, 4515-4518.	1.8	28
84	CHARACTERISTICS OF DRUG COMBINATION THERAPY IN ONCOLOGY BY ANALYZING CLINICAL TRIAL DATA ON CLINICALTRIALS.GOV., 2014, , .		27
85	Protein Microarrays Discover Angiotensinogen and PRKRIP1 as Novel Targets for Autoantibodies in Chronic Renal Disease. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.000497.	2.5	26
86	Robust prediction of clinical outcomes using cytometry data. <i>Bioinformatics</i> , 2019, 35, 1197-1203.	1.8	25
87	Automated quality control and cell identification of droplet-based single-cell data using droppick. <i>Genome Research</i> , 2021, 31, 1742-1752.	2.4	25
88	Comparing Ethnicity-Specific Reference Intervals for Clinical Laboratory Tests from EHR Data. <i>journal of applied laboratory medicine</i> , The, 2018, 3, 366-377.	0.6	24
89	Cox regression increases power to detect genotype-phenotype associations in genomic studies using the electronic health record. <i>BMC Genomics</i> , 2019, 20, 805.	1.2	24
90	Reanalysis of the Rituximab in ANCA-Associated Vasculitis trial identifies granulocyte subsets as a novel early marker of successful treatment. <i>Arthritis Research and Therapy</i> , 2015, 17, 262.	1.6	23

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91	Heterogeneity in recent-onset type 1 diabetes – a clinical trial perspective. <i>Diabetes/Metabolism Research and Reviews</i> , 2015, 31, 588-594.	1.7	22
92	The microfluidic multitrapping nanophysiometer for hematologic cancer cell characterization reveals temporal sensitivity of the calcein-AM efflux assay. <i>Scientific Reports</i> , 2014, 4, 5117.	1.6	20
93	Digitally deconvolving the tumor microenvironment. <i>Genome Biology</i> , 2016, 17, 175.	3.8	20
94	Translational bioinformatics applications in genome medicine. <i>Genome Medicine</i> , 2009, 1, 64.	3.6	19
95	Single-Cell and Population NF- κ B Dynamic Responses Depend on Lipopolysaccharide Preparation. <i>PLoS ONE</i> , 2013, 8, e53222.	1.1	18
96	Discovering Cross-Reactivity in Urine Drug Screening Immunoassays through Large-Scale Analysis of Electronic Health Records. <i>Clinical Chemistry</i> , 2019, 65, 1522-1531.	1.5	17
97	Big data opens a window onto wellness. <i>Nature Biotechnology</i> , 2017, 35, 720-721.	9.4	16
98	Open challenges in developing digital therapeutics in the United States. , 2022, 1, e0000008.		16
99	IDENTIFICATION OF DISCRIMINATING BIOMARKERS FOR HUMAN DISEASE USING INTEGRATIVE NETWORK BIOLOGY. , 2008, , .		15
100	Individualized Constellation of Killer Cell Immunoglobulin-Like Receptors and Cognate HLA Class I Ligands that Controls Natural Killer Cell Antiviral Immunity Predisposes COVID-19. <i>Frontiers in Genetics</i> , 2022, 13, 845474.	1.1	15
101	The risks of using the chi-square periodogram to estimate the period of biological rhythms. <i>PLoS Computational Biology</i> , 2021, 17, e1008567.	1.5	14
102	Comparison of automated and human assignment of MeSH terms on publicly-available molecular datasets. <i>Journal of Biomedical Informatics</i> , 2011, 44, S39-S43.	2.5	13
103	Cancer Cell’s Autonomous Parainflammation Mimics Immune Cell Infiltration. <i>Cancer Research</i> , 2017, 77, 3740-3744.	0.4	12
104	Age- and Sex-Associated Variations in the Sensitivity of Serological Tests Among Individuals Infected With SARS-CoV-2. <i>JAMA Network Open</i> , 2021, 4, e210337.	2.8	12
105	Deep learning from multiple experts improves identification of amyloid neuropathologies. <i>Acta Neuropathologica Communications</i> , 2022, 10, 66.	2.4	12
106	Risky Business: Meeting the Structural Needs of Transdisciplinary Science. <i>Journal of Pediatrics</i> , 2017, 191, 255-258.	0.9	11
107	Combinatorial processing of bacterial and host-derived innate immune stimuli at the single-cell level. <i>Molecular Biology of the Cell</i> , 2019, 30, 282-292.	0.9	11
108	CovidCounties is an interactive real time tracker of the COVID19 pandemic at the level of US counties. <i>Scientific Data</i> , 2020, 7, 405.	2.4	11

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109	The Role of Electronic Health Records in Advancing Genomic Medicine. Annual Review of Genomics and Human Genetics, 2021, 22, 219-238.	2.5	11
110	TOWARDS A CYTOKINE-CELL INTERACTION KNOWLEDGEBASE OF THE ADAPTIVE IMMUNE SYSTEM. , 2008, , .		10
111	Is the crowd better as an assistant or a replacement in ontology engineering? An exploration through the lens of the Gene Ontology. Journal of Biomedical Informatics, 2016, 60, 199-209.	2.5	10
112	Tracing diagnosis trajectories over millions of patients reveal an unexpected risk in schizophrenia. Scientific Data, 2019, 6, 201.	2.4	10
113	Assessment of Postdonation Outcomes in US Living Kidney Donors Using Publicly Available Data Sets. JAMA Network Open, 2019, 2, e191851.	2.8	10
114	Big Data in Nephrology. Nature Reviews Nephrology, 2021, 17, 676-687.	4.1	10
115	Accuracy of medical billing data against the electronic health record in the measurement of colorectal cancer screening rates. BMJ Open Quality, 2020, 9, e000856.	0.4	9
116	Distinct Components of Photoperiodic Light Are Differentially Encoded by the Mammalian Circadian Clock. Journal of Biological Rhythms, 2020, 35, 353-367.	1.4	9
117	Quantifying Variation in Treatment Utilization for Type 2 Diabetes Across Five Major University of California Health Systems. Diabetes Care, 2021, 44, 908-914.	4.3	9
118	Optogenetic stimulation of VIPergic SCN neurons induces photoperiodic-like changes in the mammalian circadian clock. European Journal of Neuroscience, 2021, 54, 7063-7071.	1.2	9
119	Enabling precision medicine in neonatology, an integrated repository for preterm birth research. Scientific Data, 2018, 5, 180219.	2.4	9
120	Trans-channel fluorescence learning improves high-content screening for Alzheimer's disease therapeutics. Nature Machine Intelligence, 2022, 4, 583-595.	8.3	9
121	Validating pathophysiological models of aging using clinical electronic medical records. Journal of Biomedical Informatics, 2010, 43, 358-364.	2.5	8
122	Gene expression deconvolution in linear space. Nature Methods, 2012, 9, 9-9.	9.0	8
123	Symphony: simulating large-scale, rhythmic data. PeerJ, 2019, 7, e6985.	0.9	8
124	SYSTEMATIC IDENTIFICATION OF RISK FACTORS FOR ALZHEIMER'S DISEASE THROUGH SHARED GENETIC ARCHITECTURE AND ELECTRONIC MEDICAL RECORDS. , 2012, , .		7
125	Open data informatics and data repurposing for IBD. Nature Reviews Gastroenterology and Hepatology, 2018, 15, 715-716.	8.2	7
126	Recent Advances in Systems and Network Medicine: Meeting Report from the First International Conference in Systems and Network Medicine. Systems Medicine (New Rochelle, N Y), 2020, 3, 22-35.	1.4	7

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127	Systematic identification of ACE2 expression modulators reveals cardiomyopathy as a risk factor for mortality in COVID-19 patients. <i>Genome Biology</i> , 2022, 23, 15.	3.8	7
128	Trials and Tribulations—11 Reasons Why We Need to Promote Clinical Trials Data Sharing. <i>JAMA Network Open</i> , 2021, 4, e2035043.	2.8	6
129	Rethinking PICO in the Machine Learning Era: ML-PICO. <i>Applied Clinical Informatics</i> , 2021, 12, 407-416.	0.8	6
130	ENABLING INTEGRATIVE GENOMIC ANALYSIS OF HIGH-IMPACT HUMAN DISEASES THROUGH TEXT MINING. , 2007, , .		6
131	NOVEL INTEGRATION OF HOSPITAL ELECTRONIC MEDICAL RECORDS AND GENE EXPRESSION MEASUREMENTS TO IDENTIFY GENETIC MARKERS OF MATURATION. , 2007, , .		5
132	DO CANCER CLINICAL TRIAL POPULATIONS TRULY REPRESENT CANCER PATIENTS? A COMPARISON OF OPEN CLINICAL TRIALS TO THE CANCER GENOME ATLAS. , 2016, , .		5
133	It takes a genome to understand a village: Population scale precision medicine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12344-12346.	3.3	4
134	Genetic analysis in a patient with nine primary malignant neoplasms: A rare case of Li-Fraumeni syndrome. <i>Oncology Reports</i> , 2016, 35, 1519-1528.	1.2	3
135	Immune modulators in disease: integrating knowledge from the biomedical literature and gene expression. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2016, 23, 617-626.	2.2	3
136	Allogeneic Antibodies Identify GVL Targets CHAF1b and NuSAP1 in AML Patients.. <i>Blood</i> , 2007, 110, 168-168.	0.6	3
137	Intra-microfluidic pinocytic loading of human T cells. , 2007, , .		2
138	Serological Targeted Analysis of an ITIH4 Peptide Isoform: A Preterm Birth Biomarker and Its Associated SNP Implications. <i>Journal of Genetics and Genomics</i> , 2015, 42, 507-510.	1.7	2
139	Tau-independent Phase Analysis: A Novel Method for Accurately Determining Phase Shifts. <i>Journal of Biological Rhythms</i> , 2018, 33, 223-232.	1.4	2
140	Pulling the covers in electronic health records for an association study with self-reported sleep behaviors. <i>Chronobiology International</i> , 2018, 35, 1702-1712.	0.9	2
141	A Computational Approach to Identify Interfering Medications on Urine Drug Screening Assays without Data from Confirmatory Testing. <i>Journal of Analytical Toxicology</i> , 2021, 45, 325-330.	1.7	2
142	Algorithmic Stewardship in Health Care—Reply. <i>JAMA - Journal of the American Medical Association</i> , 2021, 325, 588.	3.8	2
143	pmparser and PMDB: resources for large-scale, open studies of the biomedical literature. <i>PeerJ</i> , 2021, 9, e11071.	0.9	2
144	Opportunities and Challenges in Democratizing Immunology Datasets. <i>Frontiers in Immunology</i> , 2021, 12, 647536.	2.2	2

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145	Five-year pediatric use of a digital wearable fitness device: lessons from a pilot case study. JAMIA Open, 2021, 4, ooab054.	1.0	2
146	Assessing Clinical Outcomes in a Data-Rich World—A Reality Check on Real-World Data. JAMA Network Open, 2021, 4, e2117826.	2.8	2
147	A SYSTEMATIC ASSESSMENT OF LINKING GENE EXPRESSION WITH GENETIC VARIANTS FOR PRIORITIZING CANDIDATE TARGETS. , 2014, , .		2
148	Analysis of Electronic Health Records Reveals Medication-Related Interference on Point-of-Care Urine Drug Screening Assays. Journal of Analytical Toxicology, 2022, 46, 99-102.	1.7	2
149	RImmPort. , 2014, , .		1
150	Towards the characterization of normal peripheral immune cells with data from ImmPort. , 2014, , .		1
151	Case—control study of the association of chronic acid suppression and social determinants of health with COVID-19 infection. Scientific Reports, 2021, 11, 20987.	1.6	1
152	COMPUTATIONAL DRUG REPOSITIONING. , 2012, , .		1
153	COMPUTATIONAL APPROACHES TO DRUG REPURPOSING AND PHARMACOLOG- SESSION INTRODUCTION. , 2013, , .		1
154	OUP accepted manuscript. Bioinformatics, 2022, , .	1.8	1
155	Selected proceedings of the First Summit on Translational Bioinformatics 2008. BMC Bioinformatics, 2009, 10, 11.	1.2	0
156	Translational informatics of population health: How large biomolecular and clinical datasets unite. , 2018, , .		0
157	The risks of using the chi-square periodogram to estimate the period of biological rhythms. , 2021, 17, e1008567.		0
158	The risks of using the chi-square periodogram to estimate the period of biological rhythms. , 2021, 17, e1008567.		0
159	The risks of using the chi-square periodogram to estimate the period of biological rhythms. , 2021, 17, e1008567.		0