

Jacob J Hughey

List of Publications by Year in descending order

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Version: 2024-02-01

159
papers

19,900
citations

36303

51
h-index

14208

128
g-index

186
all docs

186
docs citations

186
times ranked

34770
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of Electronic Health Records Reveals Medication-Related Interference on Point-of-Care Urine Drug Screening Assays. <i>Journal of Analytical Toxicology</i> , 2022, 46, 99-102.	2.8	2
2	Open challenges in developing digital therapeutics in the United States. , 2022, 1, e0000008.		16
3	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.	8.8	7
4	OUP accepted manuscript. <i>Bioinformatics</i> , 2022, , .	4.1	1
5	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.	2.3	15
6	Deep learning from multiple experts improves identification of amyloid neuropathologies. <i>Acta Neuropathologica Communications</i> , 2022, 10, 66.	5.2	12
7	Trans-channel fluorescence learning improves high-content screening for Alzheimer's disease therapeutics. <i>Nature Machine Intelligence</i> , 2022, 4, 583-595.	16.0	9
8	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.	2.8	2
9	Trials and Tribulations—11 Reasons Why We Need to Promote Clinical Trials Data Sharing. <i>JAMA Network Open</i> , 2021, 4, e2035043.	5.9	6
10	Algorithmic Stewardship in Health Care—Reply. <i>JAMA - Journal of the American Medical Association</i> , 2021, 325, 588.	7.4	2
11	Quantifying Variation in Treatment Utilization for Type 2 Diabetes Across Five Major University of California Health Systems. <i>Diabetes Care</i> , 2021, 44, 908-914.	8.6	9
12	Rethinking PICO in the Machine Learning Era: ML-PICO. <i>Applied Clinical Informatics</i> , 2021, 12, 407-416.	1.7	6
13	pmparser and PMDB: resources for large-scale, open studies of the biomedical literature. <i>PeerJ</i> , 2021, 9, e11071.	2.0	2
14	Automated quality control and cell identification of droplet-based single-cell data using dropkick. <i>Genome Research</i> , 2021, 31, 1742-1752.	5.5	25
15	Opportunities and Challenges in Democratizing Immunology Datasets. <i>Frontiers in Immunology</i> , 2021, 12, 647536.	4.8	2
16	Big Data in Nephrology. <i>Nature Reviews Nephrology</i> , 2021, 17, 676-687.	9.6	10
17	Five-year pediatric use of a digital wearable fitness device: lessons from a pilot case study. <i>JAMIA Open</i> , 2021, 4, ooab054.	2.0	2
18	Assessing Clinical Outcomes in a Data-Rich World—A Reality Check on Real-World Data. <i>JAMA Network Open</i> , 2021, 4, e2117826.	5.9	2

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19	The Role of Electronic Health Records in Advancing Genomic Medicine. Annual Review of Genomics and Human Genetics, 2021, 22, 219-238.	6.2	11
20	Optogenetic stimulation of VIPergic SCN neurons induces photoperiodic-like changes in the mammalian circadian clock. European Journal of Neuroscience, 2021, 54, 7063-7071.	2.6	9
21	The risks of using the chi-square periodogram to estimate the period of biological rhythms. PLoS Computational Biology, 2021, 17, e1008567.	3.2	14
22	Age- and Sex-Associated Variations in the Sensitivity of Serological Tests Among Individuals Infected With SARS-CoV-2. JAMA Network Open, 2021, 4, e210337.	5.9	12
23	Case-control study of the association of chronic acid suppression and social determinants of health with COVID-19 infection. Scientific Reports, 2021, 11, 20987.	3.3	1
24	Application of Machine Learning for Cytometry Data. Frontiers in Immunology, 2021, 12, 787574.	4.8	30
25	The risks of using the chi-square periodogram to estimate the period of biological rhythms. , 2021, 17, e1008567.		0
26	The risks of using the chi-square periodogram to estimate the period of biological rhythms. , 2021, 17, e1008567.		0
27	The risks of using the chi-square periodogram to estimate the period of biological rhythms. , 2021, 17, e1008567.		0
28	Protected Health Information filter (Philter): accurately and securely de-identifying free-text clinical notes. Npj Digital Medicine, 2020, 3, 57.	10.9	38
29	CovidCounties is an interactive real time tracker of the COVID19 pandemic at the level of US counties. Scientific Data, 2020, 7, 405.	5.3	11
30	A robust and interpretable end-to-end deep learning model for cytometry data. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 21373-21380.	7.1	40
31	Accuracy of medical billing data against the electronic health record in the measurement of colorectal cancer screening rates. BMJ Open Quality, 2020, 9, e000856.	1.1	9
32	The Case for Algorithmic Stewardship for Artificial Intelligence and Machine Learning Technologies. JAMA - Journal of the American Medical Association, 2020, 324, 1397.	7.4	69
33	Minimum information about clinical artificial intelligence modeling: the MI-CLAIM checklist. Nature Medicine, 2020, 26, 1320-1324.	30.7	262
34	Distinct Components of Photoperiodic Light Are Differentially Encoded by the Mammalian Circadian Clock. Journal of Biological Rhythms, 2020, 35, 353-367.	2.6	9
35	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.	1.1	7
36	Eating breakfast and avoiding late-evening snacking sustains lipid oxidation. PLoS Biology, 2020, 18, e3000622.	5.6	31

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37	Meta-Analysis of Vaginal Microbiome Data Provides New Insights Into Preterm Birth. <i>Frontiers in Microbiology</i> , 2020, 11, 476.	3.5	47
38	Tracing diagnosis trajectories over millions of patients reveal an unexpected risk in schizophrenia. <i>Scientific Data</i> , 2019, 6, 201.	5.3	10
39	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.	4.4	35
40	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.	2.0	35
41	Discovering Cross-Reactivity in Urine Drug Screening Immunoassays through Large-Scale Analysis of Electronic Health Records. <i>Clinical Chemistry</i> , 2019, 65, 1522-1531.	3.2	17
42	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.	4.1	28
43	A longitudinal big data approach for precision health. <i>Nature Medicine</i> , 2019, 25, 792-804.	30.7	329
44	NF- κ B signaling dynamics is controlled by a dose-sensing autoregulatory loop. <i>Science Signaling</i> , 2019, 12, .	3.6	52
45	Assessment of Postdonation Outcomes in US Living Kidney Donors Using Publicly Available Data Sets. <i>JAMA Network Open</i> , 2019, 2, e191851.	5.9	10
46	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.	5.9	135
47	Prototype of running clinical trials in an untrustworthy environment using blockchain. <i>Nature Communications</i> , 2019, 10, 917.	12.8	114
48	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.	2.1	11
49	Cox regression increases power to detect genotype-phenotype associations in genomic studies using the electronic health record. <i>BMC Genomics</i> , 2019, 20, 805.	2.8	24
50	Robust prediction of clinical outcomes using cytometry data. <i>Bioinformatics</i> , 2019, 35, 1197-1203.	4.1	25
51	LimoRhyde: A Flexible Approach for Differential Analysis of Rhythmic Transcriptome Data. <i>Journal of Biological Rhythms</i> , 2019, 34, 5-18.	2.6	61
52	Reference-based analysis of lung single-cell sequencing reveals a transitional profibrotic macrophage. <i>Nature Immunology</i> , 2019, 20, 163-172.	14.5	2,330
53	Releasing a preprint is associated with more attention and citations for the peer-reviewed article. <i>ELife</i> , 2019, 8, .	6.0	101
54	Symphony: simulating large-scale, rhythmic data. <i>PeerJ</i> , 2019, 7, e6985.	2.0	8

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55	ImmPort, toward repurposing of open access immunological assay data for translational and clinical research. <i>Scientific Data</i> , 2018, 5, 180015.	5.3	529
56	Tau-independent Phase Analysis: A Novel Method for Accurately Determining Phase Shifts. <i>Journal of Biological Rhythms</i> , 2018, 33, 223-232.	2.6	2
57	A genome-wide association study identifies only two ancestry specific variants associated with spontaneous preterm birth. <i>Scientific Reports</i> , 2018, 8, 226.	3.3	37
58	Live-cell measurements of kinase activity in single cells using translocation reporters. <i>Nature Protocols</i> , 2018, 13, 155-169.	12.0	90
59	Phenotype risk scores identify patients with unrecognized Mendelian disease patterns. <i>Science</i> , 2018, 359, 1233-1239.	12.6	164
60	The 10,000 Immunomes Project: Building a Resource for Human Immunology. <i>Cell Reports</i> , 2018, 25, 513-522.e3.	6.4	40
61	Comparing Ethnicity-Specific Reference Intervals for Clinical Laboratory Tests from EHR Data. <i>Journal of Applied Laboratory Medicine</i> , 2018, 3, 366-377.	1.3	24
62	Pulling the covers in electronic health records for an association study with self-reported sleep behaviors. <i>Chronobiology International</i> , 2018, 35, 1702-1712.	2.0	2
63	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.	7.1	97
64	Open data informatics and data repurposing for IBD. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2018, 15, 715-716.	17.8	7
65	MetaCyto: A Tool for Automated Meta-analysis of Mass and Flow Cytometry Data. <i>Cell Reports</i> , 2018, 24, 1377-1388.	6.4	52
66	Are minor alleles more likely to be risk alleles?. <i>BMC Medical Genomics</i> , 2018, 11, 3.	1.5	48
67	Enabling precision medicine in neonatology, an integrated repository for preterm birth research. <i>Scientific Data</i> , 2018, 5, 180219.	5.3	9
68	Evidence for widespread dysregulation of circadian clock progression in human cancer. <i>PeerJ</i> , 2018, 6, e4327.	2.0	75
69	Translational informatics of population health: How large biomolecular and clinical datasets unite. , 2018, , .		0
70	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.	1.3	81
71	Machine learning identifies a compact gene set for monitoring the circadian clock in human blood. <i>Genome Medicine</i> , 2017, 9, 19.	8.2	51
72	Solving Immunology?. <i>Trends in Immunology</i> , 2017, 38, 116-127.	6.8	45

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73	PDX-MI: Minimal Information for Patient-Derived Tumor Xenograft Models. <i>Cancer Research</i> , 2017, 77, e62-e66.	0.9	92
74	Comprehensive analysis of normal adjacent to tumor transcriptomes. <i>Nature Communications</i> , 2017, 8, 1077.	12.8	394
75	Precision annotation of digital samples in NCBI's gene expression omnibus. <i>Scientific Data</i> , 2017, 4, 170125.	5.3	44
76	Big data opens a window onto wellness. <i>Nature Biotechnology</i> , 2017, 35, 720-721.	17.5	16
77	Guidelines for Genome-Scale Analysis of Biological Rhythms. <i>Journal of Biological Rhythms</i> , 2017, 32, 380-393.	2.6	237
78	Reversal of cancer gene expression correlates with drug efficacy and reveals therapeutic targets. <i>Nature Communications</i> , 2017, 8, 16022.	12.8	151
79	Cancer Cell's "Autonomous Parainflammation Mimics Immune Cell Infiltration. <i>Cancer Research</i> , 2017, 77, 3740-3744.	0.9	12
80	Risky Business: Meeting the Structural Needs of Transdisciplinary Science. <i>Journal of Pediatrics</i> , 2017, 191, 255-258.	1.8	11
81	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.	2.0	31
82	xCell: digitally portraying the tissue cellular heterogeneity landscape. <i>Genome Biology</i> , 2017, 18, 220.	8.8	2,572
83	<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.	1.8	34
84	Widespread parainflammation in human cancer. <i>Genome Biology</i> , 2016, 17, 145.	8.8	87
85	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.	6.2	107
86	Digitally deconvolving the tumor microenvironment. <i>Genome Biology</i> , 2016, 17, 175.	8.8	20
87	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.	2.6	3
88	Cross-tissue Analysis of Gene and Protein Expression in Normal and Cancer Tissues. <i>Scientific Reports</i> , 2016, 6, 24799.	3.3	155
89	ZeitZeiger: supervised learning for high-dimensional data from an oscillatory system. <i>Nucleic Acids Research</i> , 2016, 44, e80-e80.	14.5	76
90	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.	4.4	3

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91	Differential Phasing between Circadian Clocks in the Brain and Peripheral Organs in Humans. <i>Journal of Biological Rhythms</i> , 2016, 31, 588-597.	2.6	42
92	Microfluidic single-cell transcriptional analysis rationally identifies novel surface marker profiles to enhance cell-based therapies. <i>Nature Communications</i> , 2016, 7, 11945.	12.8	46
93	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.	7.1	4
94	Expression-Based Genome-Wide Association Study Links Vitamin D α 25(OH) ₂ Binding Protein With Autoantigenicity in Type 1 Diabetes. <i>Diabetes</i> , 2016, 65, 1341-1349.	0.6	33
95	Is the crowd better as an assistant or a replacement in ontology engineering? An exploration through the lens of the Gene Ontology. <i>Journal of Biomedical Informatics</i> , 2016, 60, 199-209.	4.3	10
96	DO CANCER CLINICAL TRIAL POPULATIONS TRULY REPRESENT CANCER PATIENTS? A COMPARISON OF OPEN CLINICAL TRIALS TO THE CANCER GENOME ATLAS. , 2016, , .		5
97	Repurpose terbutaline sulfate for amyotrophic lateral sclerosis using electronic medical records. <i>Scientific Reports</i> , 2015, 5, 8580.	3.3	43
98	Single-cell variation leads to population invariance in NF- κ B signaling dynamics. <i>Molecular Biology of the Cell</i> , 2015, 26, 583-590.	2.1	44
99	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.	3.5	23
100	Systematic pan-cancer analysis of tumour purity. <i>Nature Communications</i> , 2015, 6, 8971.	12.8	937
101	Variation in the Human Immune System Is Largely Driven by Non-Heritable Influences. <i>Cell</i> , 2015, 160, 37-47.	28.9	828
102	Heterogeneity in recent-onset type 1 diabetes – a clinical trial perspective. <i>Diabetes/Metabolism Research and Reviews</i> , 2015, 31, 588-594.	4.0	22
103	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.	3.9	2
104	Robust meta-analysis of gene expression using the elastic net. <i>Nucleic Acids Research</i> , 2015, 43, e79-e79.	14.5	124
105	Achieving high-sensitivity for clinical applications using augmented exome sequencing. <i>Genome Medicine</i> , 2015, 7, 71.	8.2	46
106	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.	0.6	62
107	Disease Risk Factors Identified Through Shared Genetic Architecture and Electronic Medical Records. <i>Science Translational Medicine</i> , 2014, 6, 234ra57.	12.4	58
108	RlmmPort. , 2014, , .		1

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109	CHARACTERISTICS OF DRUG COMBINATION THERAPY IN ONCOLOGY BY ANALYZING CLINICAL TRIAL DATA ON CLINICALTRIALS.GOV. , 2014, , .		27
110	Towards the characterization of normal peripheral immune cells with data from ImmPort. , 2014, , .		1
111	Clinical Interpretation and Implications of Whole-Genome Sequencing. JAMA - Journal of the American Medical Association, 2014, 311, 1035.	7.4	398
112	Organ Size Control Is Dominant over Rb Family Inactivation to Restrict Proliferation In Vivo. Cell Reports, 2014, 8, 371-381.	6.4	30
113	High-Sensitivity Measurements of Multiple Kinase Activities in Live Single Cells. Cell, 2014, 157, 1724-1734.	28.9	483
114	Diabetes Irreversibly Depletes Bone Marrow-Derived Mesenchymal Progenitor Cell Subpopulations. Diabetes, 2014, 63, 3047-3056.	0.6	58
115	ImmPort: disseminating data to the public for the future of immunology. Immunologic Research, 2014, 58, 234-239.	2.9	724
116	A Meta-analysis of Lung Cancer Gene Expression Identifies <i>PTK7</i> as a Survival Gene in Lung Adenocarcinoma. Cancer Research, 2014, 74, 2892-2902.	0.9	131
117	Investigation of maternal environmental exposures in association with self-reported preterm birth. Reproductive Toxicology, 2014, 45, 1-7.	2.9	42
118	SMYD3 links lysine methylation of MAP3K2 to Ras-driven cancer. Nature, 2014, 510, 283-287.	27.8	331
119	The microfluidic multitrap nanophysiometer for hematologic cancer cell characterization reveals temporal sensitivity of the calcein-AM efflux assay. Scientific Reports, 2014, 4, 5117.	3.3	20
120	Aging disrupts cell subpopulation dynamics and diminishes the function of mesenchymal stem cells. Scientific Reports, 2014, 4, 7144.	3.3	140
121	A SYSTEMATIC ASSESSMENT OF LINKING GENE EXPRESSION WITH GENETIC VARIANTS FOR PRIORITIZING CANDIDATE TARGETS. , 2014, , .		2
122	Systematic identification of interaction effects between genome- and environment-wide associations in type 2 diabetes mellitus. Human Genetics, 2013, 132, 495-508.	3.8	98
123	A common rejection module (CRM) for acute rejection across multiple organs identifies novel therapeutics for organ transplantation. Journal of Experimental Medicine, 2013, 210, 2205-2221.	8.5	201
124	Analysis of the Genetic Basis of Disease in the Context of Worldwide Human Relationships and Migration. PLoS Genetics, 2013, 9, e1003447.	3.5	67
125	Whole genome sequencing in support of wellness and health maintenance. Genome Medicine, 2013, 5, 58.	8.2	46
126	Single-Cell and Population NF- κ B Dynamic Responses Depend on Lipopolysaccharide Preparation. PLoS ONE, 2013, 8, e53222.	2.5	18

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127	Peptidomic Identification of Serum Peptides Diagnosing Preeclampsia. PLoS ONE, 2013, 8, e65571.	2.5	52
128	COMPUTATIONAL APPROACHES TO DRUG REPURPOSING AND PHARMACOLOGY- SESSION INTRODUCTION. , 2013, , .		1
129	Ten Years of Pathway Analysis: Current Approaches and Outstanding Challenges. PLoS Computational Biology, 2012, 8, e1002375.	3.2	1,267
130	Type 2 Diabetes Risk Alleles Demonstrate Extreme Directional Differentiation among Human Populations, Compared to Other Diseases. PLoS Genetics, 2012, 8, e1002621.	3.5	106
131	SYSTEMATIC IDENTIFICATION OF RISK FACTORS FOR ALZHEIMER'S DISEASE THROUGH SHARED GENETIC ARCHITECTURE AND ELECTRONIC MEDICAL RECORDS. , 2012, , .		7
132	Gene expression deconvolution in linear space. Nature Methods, 2012, 9, 9-9.	19.0	8
133	Sex differences in disease risk from reported genome-wide association study findings. Human Genetics, 2012, 131, 353-364.	3.8	64
134	COMPUTATIONAL DRUG REPOSITIONING. , 2012, , .		1
135	Discovery and Preclinical Validation of Drug Indications Using Compendia of Public Gene Expression Data. Science Translational Medicine, 2011, 3, 96ra77.	12.4	708
136	Comparison of automated and human assignment of MeSH terms on publicly-available molecular datasets. Journal of Biomedical Informatics, 2011, 44, S39-S43.	4.3	13
137	Protein Microarrays Discover Angiotensinogen and PRKRIP1 as Novel Targets for Autoantibodies in Chronic Renal Disease. Molecular and Cellular Proteomics, 2011, 10, M110.000497.	3.8	26
138	Computational Repositioning of the Anticonvulsant Topiramate for Inflammatory Bowel Disease. Science Translational Medicine, 2011, 3, 96ra76.	12.4	534
139	Validating pathophysiological models of aging using clinical electronic medical records. Journal of Biomedical Informatics, 2010, 43, 358-364.	4.3	8
140	Computational modeling of mammalian signaling networks. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2010, 2, 194-209.	6.6	61
141	Single-cell NF- κ B dynamics reveal digital activation and analogue information processing. Nature, 2010, 466, 267-271.	27.8	736
142	Extreme Evolutionary Disparities Seen in Positive Selection across Seven Complex Diseases. PLoS ONE, 2010, 5, e12236.	2.5	55
143	Network-Based Elucidation of Human Disease Similarities Reveals Common Functional Modules Enriched for Pluripotent Drug Targets. PLoS Computational Biology, 2010, 6, e1000662.	3.2	297
144	An Environment-Wide Association Study (EWAS) on Type 2 Diabetes Mellitus. PLoS ONE, 2010, 5, e10746.	2.5	470

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145	Autoimmune Disease Classification by Inverse Association with SNP Alleles. PLoS Genetics, 2009, 5, e1000792.	3.5	151
146	Selected proceedings of the First Summit on Translational Bioinformatics 2008. BMC Bioinformatics, 2009, 10, 11.	2.6	0
147	Translational bioinformatics applications in genome medicine. Genome Medicine, 2009, 1, 64.	8.2	19
148	A Noisy Paracrine Signal Determines the Cellular NF- κ B Response to Lipopolysaccharide. Science Signaling, 2009, 2, ra65.	3.6	124
149	Translational Bioinformatics: Coming of Age. Journal of the American Medical Informatics Association: JAMIA, 2008, 15, 709-714.	4.4	129
150	Microfluidic platform for real-time signaling analysis of multiple single T cells in parallel. Lab on A Chip, 2008, 8, 1700.	6.0	127
151	The Ultimate Model Organism. Science, 2008, 320, 325-327.	12.6	48
152	IDENTIFICATION OF DISCRIMINATING BIOMARKERS FOR HUMAN DISEASE USING INTEGRATIVE NETWORK BIOLOGY. , 2008, , .		15
153	TOWARDS A CYTOKINE-CELL INTERACTION KNOWLEDGEBASE OF THE ADAPTIVE IMMUNE SYSTEM. , 2008, , .		10
154	Intra-microfluidic pinocytic loading of human T cells. , 2007, , .		2
155	NOVEL INTEGRATION OF HOSPITAL ELECTRONIC MEDICAL RECORDS AND GENE EXPRESSION MEASUREMENTS TO IDENTIFY GENETIC MARKERS OF MATURATION. , 2007, , .		5
156	ENABLING INTEGRATIVE GENOMIC ANALYSIS OF HIGH-IMPACT HUMAN DISEASES THROUGH TEXT MINING. , 2007, , .		6
157	Allogeneic Antibodies Identify GVL Targets CHAF1b and NuSAP1 in AML Patients.. Blood, 2007, 110, 168-168.	1.4	3
158	Creation and implications of a phenome-genome network. Nature Biotechnology, 2006, 24, 55-62.	17.5	190
159	Finding disease-related genomic experiments within an international repository: first steps in translational bioinformatics. AMIA ... Annual Symposium proceedings, 2006, , 106-10.	0.2	32