

Joel T Dudley

List of Publications by Year in descending order

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Version: 2024-02-01

134
papers

11,665
citations

57719

44
h-index

32815

100
g-index

150
all docs

150
docs citations

150
times ranked

22199
citing authors

#	ARTICLE	IF	CITATIONS
1	The Evolution of Mining Electronic Health Records in the Era of Deep Learning. , 2022, , 55-92.		2
2	Early introductions and transmission of SARS-CoV-2 variant B.1.1.7 in the United States. Cell, 2021, 184, 2595-2604.e13.	13.5	113
3	Integrative chemogenomic analysis identifies small molecules that partially rescue Δ F508 Δ CFTR for cystic fibrosis. CPT: Pharmacometrics and Systems Pharmacology, 2021, 10, 500-510.	1.3	3
4	Multiplex qPCR discriminates variants of concern to enhance global surveillance of SARS-CoV-2. PLoS Biology, 2021, 19, e3001236.	2.6	200
5	Phe2vec: Automated disease phenotyping based on unsupervised embeddings from electronic health records. Patterns, 2021, 2, 100337.	3.1	19
6	Repositioning of a novel GABA-B receptor agonist, AZD3355 (Lesogaberan), for the treatment of non-alcoholic steatohepatitis. Scientific Reports, 2021, 11, 20827.	1.6	7
7	Longitudinal Autonomic Nervous System Measures Correlate With Stress and Ulcerative Colitis Disease Activity and Predict Flare. Inflammatory Bowel Diseases, 2021, 27, 1576-1584.	0.9	22
8	Patient similarity network of newly diagnosed multiple myeloma identifies patient subgroups with distinct genetic features and clinical implications. Science Advances, 2021, 7, eabg9551.	4.7	49
9	KRCC1: A potential therapeutic target in ovarian cancer. FASEB Journal, 2020, 34, 2287-2300.	0.2	5
10	Mutation-derived Neoantigen-specific T-cell Responses in Multiple Myeloma. Clinical Cancer Research, 2020, 26, 450-464.	3.2	62
11	Sepsis in the era of data-driven medicine: personalizing risks, diagnoses, treatments and prognoses. Briefings in Bioinformatics, 2020, 21, 1182-1195.	3.2	29
12	miR155 regulation of behavior, neuropathology, and cortical transcriptomics in Alzheimer's disease. Acta Neuropathologica, 2020, 140, 295-315.	3.9	23
13	Deep representation learning of electronic health records to unlock patient stratification at scale. Npj Digital Medicine, 2020, 3, 96.	5.7	90
14	Proposed Requirements for Cardiovascular Imaging-Related Machine Learning Evaluation (PRIME): A Checklist. JACC: Cardiovascular Imaging, 2020, 13, 2017-2035.	2.3	123
15	Integrative genomic meta-analysis reveals novel molecular insights into cystic fibrosis and Δ F508-CFTR rescue. Scientific Reports, 2020, 10, 20553.	1.6	7
16	Systematic Analysis of Environmental Chemicals That Dysregulate Critical Period Plasticity-Related Gene Expression Reveals Common Pathways That Mimic Immune Response to Pathogen. Neural Plasticity, 2020, 2020, 1-10.	1.0	0
17	Identification of therapeutic targets from genetic association studies using hierarchical component analysis. BioData Mining, 2020, 13, 6.	2.2	3
18	A Novel Approach to Safer Glucocorticoid Receptor-Targeted Anti-lymphoma Therapy via REDD1 (Regulated in Development and DNA Damage 1) Inhibition. Molecular Cancer Therapeutics, 2020, 19, 1898-1908.	1.9	7

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19	Sleep in the Natural Environment: A Pilot Study. <i>Sensors</i> , 2020, 20, 1378.	2.1	11
20	MEWS++: Enhancing the Prediction of Clinical Deterioration in Admitted Patients through a Machine Learning Model. <i>Journal of Clinical Medicine</i> , 2020, 9, 343.	1.0	37
21	Micro <i>scp</i> >RNA</scp> \approx 195 controls <i>scp</i> >MICU</scp> 1 expression and tumor growth in ovarian cancer. <i>EMBO Reports</i> , 2020, 21, e48483.	2.0	29
22	Sexual dimorphism in atrophic effects of topical glucocorticoids is driven by differential regulation of atrophogene REDD1 in male and female skin. <i>Oncotarget</i> , 2020, 11, 409-418.	0.8	7
23	Identifying Acute Low Back Pain Episodes in Primary Care Practice From Clinical Notes: Observational Study. <i>JMIR Medical Informatics</i> , 2020, 8, e16878.	1.3	19
24	Genome-wide analysis indicates association between heterozygote advantage and healthy aging in humans. <i>BMC Genetics</i> , 2019, 20, 52.	2.7	10
25	Integrative analysis of loss-of-function variants in clinical and genomic data reveals novel genes associated with cardiovascular traits. <i>BMC Medical Genomics</i> , 2019, 12, 108.	0.7	8
26	Transcriptomic Network Interactions in Human Skin Treated with Topical Glucocorticoid Clobetasol Propionate. <i>Journal of Investigative Dermatology</i> , 2019, 139, 2281-2291.	0.3	18
27	Early life stress alters transcriptomic patterning across reward circuitry in male and female mice. <i>Nature Communications</i> , 2019, 10, 5098.	5.8	136
28	Integrative transcriptome imputation reveals tissue-specific and shared biological mechanisms mediating susceptibility to complex traits. <i>Nature Communications</i> , 2019, 10, 3834.	5.8	68
29	A transcriptomic model to predict increase in fibrous cap thickness in response to high-dose statin treatment: Validation by serial intracoronary OCT imaging. <i>EBioMedicine</i> , 2019, 44, 41-49.	2.7	9
30	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
31	Systems Pharmacology Identifies an Arterial Wall Regulatory Gene Network Mediating Coronary Artery Disease Side Effects of Antiretroviral Therapy. <i>Circulation Genomic and Precision Medicine</i> , 2019, 12, e002390.	1.6	9
32	Deep learning predicts hip fracture using confounding patient and healthcare variables. <i>Npj Digital Medicine</i> , 2019, 2, 31.	5.7	158
33	Leveraging Big Data to Transform Drug Discovery. <i>Methods in Molecular Biology</i> , 2019, 1939, 91-118.	0.4	27
34	Lyme Disease Patient Trajectories Learned from Electronic Medical Data for Stratification of Disease Risk and Therapeutic Response. <i>Scientific Reports</i> , 2019, 9, 4460.	1.6	4
35	Predicting Future Cardiovascular Events in Patients With Peripheral Artery Disease Using Electronic Health Record Data. <i>Circulation: Cardiovascular Quality and Outcomes</i> , 2019, 12, e004741.	0.9	40
36	PI3K inhibitors protect against glucocorticoid-induced skin atrophy. <i>EBioMedicine</i> , 2019, 41, 526-537.	2.7	26

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37	P4â€495: SINGLE NUCLEI AND SINGLE WHOLE CELL SEQUENCING OF ALZHEIMER'S DISEASE. <i>Alzheimer's and Dementia</i> , 2019, 15, P1503.	0.4	0
38	Clarifying the Potential Role of Microbes in Alzheimerâ€™s Disease. <i>Neuron</i> , 2019, 104, 1036-1037.	3.8	10
39	Critical period plasticity-related transcriptional aberrations in schizophrenia and bipolar disorder. <i>Schizophrenia Research</i> , 2019, 207, 12-21.	1.1	15
40	High-Throughput Identification of the Plasma Proteomic Signature of Inflammatory Bowel Disease. <i>Journal of Crohn's and Colitis</i> , 2019, 13, 462-471.	0.6	18
41	CANDI: an R package and Shiny app for annotating radiographs and evaluating computer-aided diagnosis. <i>Bioinformatics</i> , 2019, 35, 1610-1612.	1.8	4
42	Integrative approach to sporadic Alzheimerâ€™s disease: A deficiency of TYROBP in cerebral A β amyloidosis mouse normalizes clinical phenotype and complement subnetwork molecular pathology without reducing A β burden. <i>Molecular Psychiatry</i> , 2019, 24, 431-446.	4.1	67
43	Natural Language Processing of Clinical Notes on Chronic Diseases: Systematic Review. <i>JMIR Medical Informatics</i> , 2019, 7, e12239.	1.3	297
44	Designing Robust N-of-1 Studies for Precision Medicine: Simulation Study and Design Recommendations. <i>Journal of Medical Internet Research</i> , 2019, 21, e12641.	2.1	29
45	Privacy-Preserving Methods for Feature Engineering Using Blockchain: Review, Evaluation, and Proof of Concept. <i>Journal of Medical Internet Research</i> , 2019, 21, e13600.	2.1	22
46	Building a Secure Biomedical Data Sharing Decentralized App (DApp): Tutorial. <i>Journal of Medical Internet Research</i> , 2019, 21, e13601.	2.1	22
47	SUN-253 Effects of Growth Hormone Stimulation on the Immunologic Cellular Landscape in Pediatric Patients. <i>Journal of the Endocrine Society</i> , 2019, 3, .	0.1	0
48	The next generation of precision medicine: observational studies, electronic health records, biobanks and continuous monitoring. <i>Human Molecular Genetics</i> , 2018, 27, R56-R62.	1.4	48
49	Isolation and Identification of the Follicular Microbiome: Implications for Acne Research. <i>Journal of Investigative Dermatology</i> , 2018, 138, 2033-2040.	0.3	64
50	Rapamycin Modulates Glucocorticoid Receptor Function, Blocks Atrophogene REDD1, and Protects Skin from Steroid Atrophy. <i>Journal of Investigative Dermatology</i> , 2018, 138, 1935-1944.	0.3	25
51	Deep learning for healthcare: review, opportunities and challenges. <i>Briefings in Bioinformatics</i> , 2018, 19, 1236-1246.	3.2	1,459
52	Uncovering exposures responsible for birth season " disease effects: a global study. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2018, 25, 275-288.	2.2	33
53	Regulatory T-cell Genes Drive Altered Immune Microenvironment in Adult Solid Cancers and Allow for Immune Contextual Patient Subtyping. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 103-112.	1.1	27
54	Precision Medicine for Relapsed Multiple Myeloma on the Basis of an Integrative Multiomics Approach. <i>JCO Precision Oncology</i> , 2018, 2018, 1-17.	1.5	20

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55	Deletion of the glucocorticoid receptor chaperone FKBP51 prevents glucocorticoid-induced skin atrophy. <i>Oncotarget</i> , 2018, 9, 34772-34783.	0.8	20
56	Reflecting health: smart mirrors for personalized medicine. <i>Npj Digital Medicine</i> , 2018, 1, 62.	5.7	36
57	Integrative bioinformatics identifies postnatal lead (Pb) exposure disrupts developmental cortical plasticity. <i>Scientific Reports</i> , 2018, 8, 16388.	1.6	13
58	Multiscale Analysis of Independent Alzheimer's Cohorts Finds Disruption of Molecular, Genetic, and Clinical Networks by Human Herpesvirus. <i>Neuron</i> , 2018, 99, 64-82.e7.	3.8	558
59	Expression-based drug screening of neural progenitor cells from individuals with schizophrenia. <i>Nature Communications</i> , 2018, 9, 4412.	5.8	63
60	Disease Heritability Inferred from Familial Relationships Reported in Medical Records. <i>Cell</i> , 2018, 173, 1692-1704.e11.	13.5	79
61	The Rapid Prediction of Carbapenem Resistance in Patients With <i>Klebsiella pneumoniae</i> Bacteremia Using Electronic Medical Record Data. <i>Open Forum Infectious Diseases</i> , 2018, 5, ofy091.	0.4	15
62	The whole is greater than the sum of its parts: combining classical statistical and machine intelligence methods in medicine. <i>Heart</i> , 2018, 104, 1228-1228.	1.2	15
63	MetaCyto: A Tool for Automated Meta-analysis of Mass and Flow Cytometry Data. <i>Cell Reports</i> , 2018, 24, 1377-1388.	2.9	52
64	Adaptive Landscape of Protein Variation in Human Exomes. <i>Molecular Biology and Evolution</i> , 2018, 35, 2015-2025.	3.5	10
65	Association of Hemoglobin A _{1c} Levels With Use of Sulfonylureas, Dipeptidyl Peptidase 4 Inhibitors, and Thiazolidinediones in Patients With Type 2 Diabetes Treated With Metformin. <i>JAMA Network Open</i> , 2018, 1, e181755.	2.8	54
66	Artificial Intelligence in Cardiology. <i>Journal of the American College of Cardiology</i> , 2018, 71, 2668-2679.	1.2	690
67	A 72-Year-Old Patient with Longstanding, Untreated Familial Hypercholesterolemia but no Coronary Artery Calcification: A Case Report. <i>Cureus</i> , 2018, 10, e2452.	0.2	1
68	Automated disease cohort selection using word embeddings from Electronic Health Records. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2018, 23, 145-156.	0.7	17
69	A Network-Biology Informed Computational Drug Repositioning Strategy to Target Disease Risk Trajectories and Comorbidities of Peripheral Artery Disease. <i>AMIA Summits on Translational Science Proceedings</i> , 2018, 2017, 108-117.	0.4	4
70	Novel Therapeutics Identification for Fibrosis in Renal Allograft Using Integrative Informatics Approach. <i>Scientific Reports</i> , 2017, 7, 39487.	1.6	28
71	Transcriptome-based repurposing of apigenin as a potential anti-fibrotic agent targeting hepatic stellate cells. <i>Scientific Reports</i> , 2017, 7, 42563.	1.6	29
72	Deficiency of TYROBP, an adapter protein for TREM2 and CR3 receptors, is neuroprotective in a mouse model of early Alzheimer's pathology. <i>Acta Neuropathologica</i> , 2017, 134, 769-788.	3.9	85

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73	The Asthma Mobile Health Study, a large-scale clinical observational study using ResearchKit. <i>Nature Biotechnology</i> , 2017, 35, 354-362.	9.4	185
74	Institutional profile: translational pharmacogenomics at the Icahn School of Medicine at Mount Sinai. <i>Pharmacogenomics</i> , 2017, 18, 1381-1386.	0.6	20
75	Necroptosis activation in Alzheimer's disease. <i>Nature Neuroscience</i> , 2017, 20, 1236-1246.	7.1	305
76	Intracoronary Imaging, Cholesterol Efflux, and Transcriptomics after Intensive Statin Treatment in Diabetes. <i>Scientific Reports</i> , 2017, 7, 7001.	1.6	12
77	Predicting age by mining electronic medical records with deep learning characterizes differences between chronological and physiological age. <i>Journal of Biomedical Informatics</i> , 2017, 76, 59-68.	2.5	28
78	Intracoronary Imaging, Cholesterol Efflux, and Transcriptomes After Intensive Statin Treatment. <i>Journal of the American College of Cardiology</i> , 2017, 69, 628-640.	1.2	56
79	Accelerators: Sparking Innovation and Transdisciplinary Team Science in Disparities Research. <i>International Journal of Environmental Research and Public Health</i> , 2017, 14, 225.	1.2	26
80	High-Throughput Characterization of Blood Serum Proteomics of IBD Patients with Respect to Aging and Genetic Factors. <i>PLoS Genetics</i> , 2017, 13, e1006565.	1.5	41
81	Transcriptional Profiling of Egg Allergy and Relationship to Disease Phenotype. <i>PLoS ONE</i> , 2016, 11, e0163831.	1.1	30
82	Deep Patient: An Unsupervised Representation to Predict the Future of Patients from the Electronic Health Records. <i>Scientific Reports</i> , 2016, 6, 26094.	1.6	1,036
83	EHDViz: clinical dashboard development using open-source technologies. <i>BMJ Open</i> , 2016, 6, e010579.	0.8	48
84	L1000CDS2: LINCS L1000 characteristic direction signatures search engine. <i>Npj Systems Biology and Applications</i> , 2016, 2, .	1.4	250
85	Influence of age on androgen deprivation therapy-associated Alzheimer's disease. <i>Scientific Reports</i> , 2016, 6, 35695.	1.6	12
86	Reply to R.L. Bowen et al, M. Froehner et al, J.L. Leow et al, and C. Brady et al. <i>Journal of Clinical Oncology</i> , 2016, 34, 2804-2805.	0.8	1
87	Gene expression elucidates functional impact of polygenic risk for schizophrenia. <i>Nature Neuroscience</i> , 2016, 19, 1442-1453.	7.1	952
88	Healthcare Data Mining with Matrix Models. , 2016, , .		2
89	Deep phenotyping predicts Huntington's genotype. <i>Nature Biotechnology</i> , 2016, 34, 823-824.	9.4	3
90	Machine-Learning Algorithms to Automate Morphological and Functional Assessments in 2D Echocardiography. <i>Journal of the American College of Cardiology</i> , 2016, 68, 2287-2295.	1.2	291

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91	Replicating Cardiovascular Condition-Birth Month Associations. <i>Scientific Reports</i> , 2016, 6, 33166.	1.6	16
92	Gold Nanoparticle Reprograms Pancreatic Tumor Microenvironment and Inhibits Tumor Growth. <i>ACS Nano</i> , 2016, 10, 10636-10651.	7.3	134
93	e-GRASP: an integrated evolutionary and GRASP resource for exploring disease associations. <i>BMC Genomics</i> , 2016, 17, 770.	1.2	15
94	<i>In silico</i> methods for drug repurposing and pharmacology. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2016, 8, 186-210.	6.6	250
95	Blood and Intestine eQTLs from an Anti-TNF-Resistant Crohn's Disease Cohort Inform IBD Genetic Association Loci. <i>Clinical and Translational Gastroenterology</i> , 2016, 7, e177.	1.3	40
96	Development and clinical application of an integrative genomic approach to personalized cancer therapy. <i>Genome Medicine</i> , 2016, 8, 62.	3.6	71
97	Cross-Tissue Regulatory Gene Networks in Coronary Artery Disease. <i>Cell Systems</i> , 2016, 2, 196-208.	2.9	120
98	Dysregulation of miRNA-9 in a Subset of Schizophrenia Patient-Derived Neural Progenitor Cells. <i>Cell Reports</i> , 2016, 15, 1024-1036.	2.9	107
99	Cognitive Machine-Learning Algorithm for Cardiac Imaging. <i>Circulation: Cardiovascular Imaging</i> , 2016, 9, .	1.3	164
100	Comparative analyses of population-scale phenomic data in electronic medical records reveal race-specific disease networks. <i>Bioinformatics</i> , 2016, 32, i101-i110.	1.8	39
101	Toward clinical genomics in everyday medicine: perspectives and recommendations. <i>Expert Review of Molecular Diagnostics</i> , 2016, 16, 521-532.	1.5	58
102	Androgen Deprivation Therapy and Future Alzheimer's Disease Risk. <i>Journal of Clinical Oncology</i> , 2016, 34, 566-571.	0.8	169
103	Mapping the effects of drugs on the immune system. <i>Nature Biotechnology</i> , 2016, 34, 47-54.	9.4	78
104	Deep Learning to Predict Patient Future Diseases from the Electronic Health Records. <i>Lecture Notes in Computer Science</i> , 2016, , 768-774.	1.0	28
105	Network Modeling Reveals CDC42BPA and CLEC11A As Novel Driver Genes of t(4; 14) Multiple Myeloma. <i>Blood</i> , 2016, 128, 802-802.	0.6	1
106	Systems Genetic Analyses Highlight a TGF β 2-FOXO3 Dependent Striatal Astrocyte Network Conserved across Species and Associated with Stress, Sleep, and Huntington's Disease. <i>PLoS Genetics</i> , 2016, 12, e1006137.	1.5	24
107	Data-Driven Identification of Risk Factors of Patient Satisfaction at a Large Urban Academic Medical Center. <i>PLoS ONE</i> , 2016, 11, e0156076.	1.1	20
108	Integrative Analysis of Disease Signatures Shows Inflammation Disrupts Juvenile Experience-Dependent Cortical Plasticity. <i>ENeuro</i> , 2016, 3, ENEURO.0240-16.2016.	0.9	19

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109	Important role of kallikrein 6 for the development of keratinocyte proliferative resistance to topical glucocorticoids. <i>Oncotarget</i> , 2016, 7, 69479-69488.	0.8	12
110	Integrative Network Analysis of Newly Diagnosed Multiple Myeloma Identifies a Novel RNA-Seq Based High Riskgene Signature. <i>Blood</i> , 2016, 128, 3285-3285.	0.6	1
111	Aberrant a-to-I RNA Editing and Prognostic Impact of Adar in Multiple Myeloma Patients with 1q Amplification. <i>Blood</i> , 2016, 128, 357-357.	0.6	0
112	Modern Methods for Delineating Metagenomic Complexity. <i>Cell Systems</i> , 2015, 1, 6-7.	2.9	20
113	<scp>REDD</scp>1 functions at the crossroads between the therapeutic and adverse effects of topical glucocorticoids. <i>EMBO Molecular Medicine</i> , 2015, 7, 42-58.	3.3	51
114	Computational and Experimental Advances in Drug Repositioning for Accelerated Therapeutic Stratification. <i>Current Topics in Medicinal Chemistry</i> , 2015, 15, 5-20.	1.0	81
115	Age-Stratified Risk of Unexpected Uterine Sarcoma Following Surgery for Presumed Benign Leiomyoma. <i>Oncologist</i> , 2015, 20, 433-439.	1.9	59
116	Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics. <i>Cell Systems</i> , 2015, 1, 72-87.	2.9	241
117	A Targetable GATA2-IGF2 Axis Confers Aggressiveness in Lethal Prostate Cancer. <i>Cancer Cell</i> , 2015, 27, 223-239.	7.7	128
118	Genome-Wide Significant Loci: How Important Are They?. <i>Journal of the American College of Cardiology</i> , 2015, 65, 830-845.	1.2	129
119	Genomic and Network Patterns of Schizophrenia Genetic Variation in Human Evolutionary Accelerated Regions. <i>Molecular Biology and Evolution</i> , 2015, 32, 1148-1160.	3.5	98
120	Identification of type 2 diabetes subgroups through topological analysis of patient similarity. <i>Science Translational Medicine</i> , 2015, 7, 311ra174.	5.8	426
121	Integrative network modeling approaches to personalized cancer medicine. <i>Personalized Medicine</i> , 2015, 12, 245-257.	0.8	12
122	Patient-Specific Mutation-Derived Tumor Antigens As Targets for Cancer Immunotherapy in Multiple Myeloma. <i>Blood</i> , 2015, 126, 1851-1851.	0.6	0
123	Towards a Network-Based Molecular Taxonomy of Newly Diagnosed Multiple Myeloma. <i>Blood</i> , 2015, 126, 840-840.	0.6	0
124	Personalized medicine: from genotypes, molecular phenotypes and the quantified self, towards improved medicine. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2015, , 342-6.	0.7	12
125	AN INTEGRATIVE PIPELINE FOR MULTI-MODAL DISCOVERY OF DISEASE RELATIONSHIPS. , 2014, , .		15
126	PERSONALIZED MEDICINE: FROM GENOTYPES, MOLECULAR PHENOTYPES AND THE QUANTIFIED SELF, TOWARDS IMPROVED MEDICINE. , 2014, , .		13

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127	Mutations in Tetratricopeptide Repeat Domain 7A Result in a Severe Form of Very Early Onset Inflammatory Bowel Disease. <i>Gastroenterology</i> , 2014, 146, 1028-1039.	0.6	175
128	Weighted Gene Co-Expression Network Analysis (WGCNA) Identifies Highly Proliferative Myeloma Subgroup Responsive to CDK4/ARK5 Inhibition. <i>Blood</i> , 2014, 124, 3445-3445.	0.6	9
129	STORMSeq: An Open-Source, User-Friendly Pipeline for Processing Personal Genomics Data in the Cloud. <i>PLoS ONE</i> , 2014, 9, e84860.	1.1	25
130	Automated Detection of Off-Label Drug Use. <i>PLoS ONE</i> , 2014, 9, e89324.	1.1	47
131	An Integrative Network Approach for Genomic Discovery and Personalized Therapy in Relapsed Multiple Myeloma. <i>Blood</i> , 2014, 124, 3426-3426.	0.6	0
132	The promise of genomics-based drug repurposing. <i>Clinical Advances in Hematology and Oncology</i> , 2014, 12, 601-3.	0.3	0
133	Translational Bioinformatics Approaches to Drug Development. <i>Advances in Wound Care</i> , 2013, 2, 470-489.	2.6	26
134	Using integrative informatics to bridge toxicogenomics and disease biology. <i>ISEE Conference Abstracts</i> , 2013, 2013, 5939.	0.0	0