

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	Deep learning for healthcare: review, opportunities and challenges. Briefings in Bioinformatics, 2018, 19, 1236-1246.	3.2	1,459
2	Deep Patient: An Unsupervised Representation to Predict the Future of Patients from the Electronic Health Records. Scientific Reports, 2016, 6, 26094.	1.6	1,036
3	Gene expression elucidates functional impact of polygenic risk for schizophrenia. Nature Neuroscience, 2016, 19, 1442-1453.	7.1	952
4	Artificial Intelligence in Cardiology. Journal of the American College of Cardiology, 2018, 71, 2668-2679.	1.2	690
5	Multiscale Analysis of Independent Alzheimer's Cohorts Finds Disruption of Molecular, Genetic, and Clinical Networks by Human Herpesvirus. Neuron, 2018, 99, 64-82.e7.	3.8	558
6	Identification of type 2 diabetes subgroups through topological analysis of patient similarity. Science Translational Medicine, 2015, 7, 311ra174.	5.8	426
7	Necroptosis activation in Alzheimer's disease. Nature Neuroscience, 2017, 20, 1236-1246.	7.1	305
8	Natural Language Processing of Clinical Notes on Chronic Diseases: Systematic Review. JMIR Medical Informatics, 2019, 7, e12239.	1.3	297
9	Machine-Learning Algorithms to Automate Morphological and Functional Assessments in 2D Echocardiography. Journal of the American College of Cardiology, 2016, 68, 2287-2295.	1.2	291
10	L1000CDS2: LINCS L1000 characteristic direction signatures search engine. Npj Systems Biology and Applications, 2016, 2, .	1.4	250
11	<i>In silico</i> methods for drug repurposing and pharmacology. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2016, 8, 186-210.	6.6	250
12	Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics. Cell Systems, 2015, 1, 72-87.	2.9	241
13	Multiplex qPCR discriminates variants of concern to enhance global surveillance of SARS-CoV-2. PLoS Biology, 2021, 19, e3001236.	2.6	200
14	The Asthma Mobile Health Study, a large-scale clinical observational study using ResearchKit. Nature Biotechnology, 2017, 35, 354-362.	9.4	185
15	Mutations in Tetratricopeptide Repeat Domain 7A Result in a Severe Form of Very Early Onset Inflammatory Bowel Disease. Gastroenterology, 2014, 146, 1028-1039.	0.6	175
16	Androgen Deprivation Therapy and Future Alzheimer's Disease Risk. Journal of Clinical Oncology, 2016, 34, 566-571.	0.8	169
17	Cognitive Machine-Learning Algorithm for Cardiac Imaging. Circulation: Cardiovascular Imaging, 2016, 9, .	1.3	164
18	Deep learning predicts hip fracture using confounding patient and healthcare variables. Npj Digital Medicine, 2019, 2, 31.	5.7	158

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19	Early life stress alters transcriptomic patterning across reward circuitry in male and female mice. <i>Nature Communications</i> , 2019, 10, 5098.	5.8	136
20	Gold Nanoparticle Reprograms Pancreatic Tumor Microenvironment and Inhibits Tumor Growth. <i>ACS Nano</i> , 2016, 10, 10636-10651.	7.3	134
21	Genome-Wide Significant Loci: How Important Are They?. <i>Journal of the American College of Cardiology</i> , 2015, 65, 830-845.	1.2	129
22	A Targetable GATA2-IGF2 Axis Confers Aggressiveness in Lethal Prostate Cancer. <i>Cancer Cell</i> , 2015, 27, 223-239.	7.7	128
23	Proposed Requirements for Cardiovascular Imaging-Related Machine Learning Evaluation (PRIME): A Checklist. <i>JACC: Cardiovascular Imaging</i> , 2020, 13, 2017-2035.	2.3	123
24	Cross-Tissue Regulatory Gene Networks in Coronary Artery Disease. <i>Cell Systems</i> , 2016, 2, 196-208.	2.9	120
25	Early introductions and transmission of SARS-CoV-2 variant B.1.1.7 in the United States. <i>Cell</i> , 2021, 184, 2595-2604.e13.	13.5	113
26	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
27	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
28	Deep representation learning of electronic health records to unlock patient stratification at scale. <i>Npj Digital Medicine</i> , 2020, 3, 96.	5.7	90
29	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
30	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
31	Disease Heritability Inferred from Familial Relationships Reported in Medical Records. <i>Cell</i> , 2018, 173, 1692-1704.e11.	13.5	79
32	Mapping the effects of drugs on the immune system. <i>Nature Biotechnology</i> , 2016, 34, 47-54.	9.4	78
33	Development and clinical application of an integrative genomic approach to personalized cancer therapy. <i>Genome Medicine</i> , 2016, 8, 62.	3.6	71
34	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
35	Integrative approach to sporadic Alzheimer's disease: deficiency of TYROBP in cerebral A β 2 amyloidosis mouse normalizes clinical phenotype and complement subnetwork molecular pathology without reducing A β 2 burden. <i>Molecular Psychiatry</i> , 2019, 24, 431-446.	4.1	67
36	Isolation and Identification of the Follicular Microbiome: Implications for Acne Research. <i>Journal of Investigative Dermatology</i> , 2018, 138, 2033-2040.	0.3	64

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37	Expression-based drug screening of neural progenitor cells from individuals with schizophrenia. <i>Nature Communications</i> , 2018, 9, 4412.	5.8	63
38	Mutation-derived Neoantigen-specific T-cell Responses in Multiple Myeloma. <i>Clinical Cancer Research</i> , 2020, 26, 450-464.	3.2	62
39	Age-Stratified Risk of Unexpected Uterine Sarcoma Following Surgery for Presumed Benign Leiomyoma. <i>Oncologist</i> , 2015, 20, 433-439.	1.9	59
40	Toward clinical genomics in everyday medicine: perspectives and recommendations. <i>Expert Review of Molecular Diagnostics</i> , 2016, 16, 521-532.	1.5	58
41	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
42	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
43	MetaCyto: A Tool for Automated Meta-analysis of Mass and Flow Cytometry Data. <i>Cell Reports</i> , 2018, 24, 1377-1388.	2.9	52
44	REDD1 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
45	Patient similarity network of newly diagnosed multiple myeloma identifies patient subgroups with distinct genetic features and clinical implications. <i>Science Advances</i> , 2021, 7, eabg9551.	4.7	49
46	EHDViz: clinical dashboard development using open-source technologies. <i>BMJ Open</i> , 2016, 6, e010579.	0.8	48
47	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
48	Automated Detection of Off-Label Drug Use. <i>PLoS ONE</i> , 2014, 9, e89324.	1.1	47
49	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
50	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
51	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
52	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
53	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
54	Reflecting health: smart mirrors for personalized medicine. <i>Npj Digital Medicine</i> , 2018, 1, 62.	5.7	36

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55	Uncovering exposures responsible for birth season “ disease effects: a global study. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 275-288.	2.2	33
56	Transcriptional Profiling of Egg Allergy and Relationship to Disease Phenotype. PLoS ONE, 2016, 11, e0163831.	1.1	30
57	Transcriptome-based repurposing of apigenin as a potential anti-fibrotic agent targeting hepatic stellate cells. Scientific Reports, 2017, 7, 42563.	1.6	29
58	Sepsis in the era of data-driven medicine: personalizing risks, diagnoses, treatments and prognoses. Briefings in Bioinformatics, 2020, 21, 1182-1195.	3.2	29
59	Micro <i>scp</i> RNA <i>scp</i> “195 controls <i>scp</i> MICU <i>scp</i> 1 expression and tumor growth in ovarian cancer. EMBO Reports, 2020, 21, e48483.	2.0	29
60	Designing Robust N-of-1 Studies for Precision Medicine: Simulation Study and Design Recommendations. Journal of Medical Internet Research, 2019, 21, e12641.	2.1	29
61	Novel Therapeutics Identification for Fibrosis in Renal Allograft Using Integrative Informatics Approach. Scientific Reports, 2017, 7, 39487.	1.6	28
62	Predicting age by mining electronic medical records with deep learning characterizes differences between chronological and physiological age. Journal of Biomedical Informatics, 2017, 76, 59-68.	2.5	28
63	PatientExploreR: an extensible application for dynamic visualization of patient clinical history from electronic health records in the OMOP common data model. Bioinformatics, 2019, 35, 4515-4518.	1.8	28
64	Deep Learning to Predict Patient Future Diseases from the Electronic Health Records. Lecture Notes in Computer Science, 2016, , 768-774.	1.0	28
65	Regulatory T-cell Genes Drive Altered Immune Microenvironment in Adult Solid Cancers and Allow for Immune Contextual Patient Subtyping. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 103-112.	1.1	27
66	Leveraging Big Data to Transform Drug Discovery. Methods in Molecular Biology, 2019, 1939, 91-118.	0.4	27
67	Translational Bioinformatics Approaches to Drug Development. Advances in Wound Care, 2013, 2, 470-489.	2.6	26
68	Accelerators: Sparking Innovation and Transdisciplinary Team Science in Disparities Research. International Journal of Environmental Research and Public Health, 2017, 14, 225.	1.2	26
69	PI3K inhibitors protect against glucocorticoid-induced skin atrophy. EBioMedicine, 2019, 41, 526-537.	2.7	26
70	Rapamycin Modulates Glucocorticoid Receptor Function, Blocks Atrophogene REDD1, and Protects Skin from Steroid Atrophy. Journal of Investigative Dermatology, 2018, 138, 1935-1944.	0.3	25
71	STORMSeq: An Open-Source, User-Friendly Pipeline for Processing Personal Genomics Data in the Cloud. PLoS ONE, 2014, 9, e84860.	1.1	25
72	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. PLoS Genetics, 2016, 12, e1006137.	1.5	24

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73	miR155 regulation of behavior, neuropathology, and cortical transcriptomics in Alzheimer's disease. <i>Acta Neuropathologica</i> , 2020, 140, 295-315.	3.9	23
74	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
75	Building a Secure Biomedical Data Sharing Decentralized App (DApp): Tutorial. <i>Journal of Medical Internet Research</i> , 2019, 21, e13601.	2.1	22
76	Longitudinal Autonomic Nervous System Measures Correlate With Stress and Ulcerative Colitis Disease Activity and Predict Flare. <i>Inflammatory Bowel Diseases</i> , 2021, 27, 1576-1584.	0.9	22
77	Modern Methods for Delineating Metagenomic Complexity. <i>Cell Systems</i> , 2015, 1, 6-7.	2.9	20
78	Institutional profile: translational pharmacogenomics at the Icahn School of Medicine at Mount Sinai. <i>Pharmacogenomics</i> , 2017, 18, 1381-1386.	0.6	20
79	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
80	Deletion of the glucocorticoid receptor chaperone FKBP51 prevents glucocorticoid-induced skin atrophy. <i>Oncotarget</i> , 2018, 9, 34772-34783.	0.8	20
81	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
82	Phe2vec: Automated disease phenotyping based on unsupervised embeddings from electronic health records. <i>Patterns</i> , 2021, 2, 100337.	3.1	19
83	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
84	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
85	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
86	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
87	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
88	Replicating Cardiovascular Condition-Birth Month Associations. <i>Scientific Reports</i> , 2016, 6, 33166.	1.6	16
89	AN INTEGRATIVE PIPELINE FOR MULTI-MODAL DISCOVERY OF DISEASE RELATIONSHIPS. , 2014, , .		15
90	e-GRASP: an integrated evolutionary and GRASP resource for exploring disease associations. <i>BMC Genomics</i> , 2016, 17, 770.	1.2	15

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91	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
92	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
93	Critical period plasticity-related transcriptional aberrations in schizophrenia and bipolar disorder. <i>Schizophrenia Research</i> , 2019, 207, 12-21.	1.1	15
94	PERSONALIZED MEDICINE: FROM GENOTYPES, MOLECULAR PHENOTYPES AND THE QUANTIFIED SELF, TOWARDS IMPROVED MEDICINE. , 2014, , .		13
95	Integrative bioinformatics identifies postnatal lead (Pb) exposure disrupts developmental cortical plasticity. <i>Scientific Reports</i> , 2018, 8, 16388.	1.6	13
96	Integrative network modeling approaches to personalized cancer medicine. <i>Personalized Medicine</i> , 2015, 12, 245-257.	0.8	12
97	Influence of age on androgen deprivation therapy-associated Alzheimer's disease. <i>Scientific Reports</i> , 2016, 6, 35695.	1.6	12
98	Intracoronary Imaging, Cholesterol Efflux, and Transcriptomics after Intensive Statin Treatment in Diabetes. <i>Scientific Reports</i> , 2017, 7, 7001.	1.6	12
99	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
100	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
101	Sleep in the Natural Environment: A Pilot Study. <i>Sensors</i> , 2020, 20, 1378.	2.1	11
102	Adaptive Landscape of Protein Variation in Human Exomes. <i>Molecular Biology and Evolution</i> , 2018, 35, 2015-2025.	3.5	10
103	Genome-wide analysis indicates association between heterozygote advantage and healthy aging in humans. <i>BMC Genetics</i> , 2019, 20, 52.	2.7	10
104	Clarifying the Potential Role of Microbes in Alzheimer's Disease. <i>Neuron</i> , 2019, 104, 1036-1037.	3.8	10
105	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
106	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
107	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
108	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

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109	Integrative genomic meta-analysis reveals novel molecular insights into cystic fibrosis and $\Delta F508$ -CFTR rescue. <i>Scientific Reports</i> , 2020, 10, 20553.	1.6	7
110	A Novel Approach to Safer Glucocorticoid Receptor-Targeted Anti-lymphoma Therapy via REDD1 (Regulated in Development and DNA Damage 1) Inhibition. <i>Molecular Cancer Therapeutics</i> , 2020, 19, 1898-1908.	1.9	7
111	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
112	Repositioning of a novel GABA-B receptor agonist, AZD3355 (Lesogaberan), for the treatment of non-alcoholic steatohepatitis. <i>Scientific Reports</i> , 2021, 11, 20827.	1.6	7
113	KRCC1: A potential therapeutic target in ovarian cancer. <i>FASEB Journal</i> , 2020, 34, 2287-2300.	0.2	5
114	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
115	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
116	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
117	Deep phenotyping predicts Huntington's genotype. <i>Nature Biotechnology</i> , 2016, 34, 823-824.	9.4	3
118	Identification of therapeutic targets from genetic association studies using hierarchical component analysis. <i>BioData Mining</i> , 2020, 13, 6.	2.2	3
119	Integrative chemogenomic analysis identifies small molecules that partially rescue $\Delta F508$ -CFTR for cystic fibrosis. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2021, 10, 500-510.	1.3	3
120	Healthcare Data Mining with Matrix Models. , 2016, , .		2
121	The Evolution of Mining Electronic Health Records in the Era of Deep Learning. , 2022, , 55-92.		2
122	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
123	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
124	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
125	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
126	P4-495: SINGLE NUCLEI AND SINGLE WHOLE CELL SEQUENCING OF ALZHEIMER'S DISEASE. <i>Alzheimer's and Dementia</i> , 2019, 15, P1503.	0.4	0

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127	Systematic Analysis of Environmental Chemicals That Dysregulate Critical Period Plasticity-Related Gene Expression Reveals Common Pathways That Mimic Immune Response to Pathogen. <i>Neural Plasticity</i> , 2020, 2020, 1-10.	1.0	0
128	Using integrative informatics to bridge toxicogenomics and disease biology. ISEE Conference Abstracts, 2013, 2013, 5939.	0.0	0
129	An Integrative Network Approach for Genomic Discovery and Personalized Therapy in Relapsed Multiple Myeloma. <i>Blood</i> , 2014, 124, 3426-3426.	0.6	0
130	Patient-Specific Mutation-Derived Tumor Antigens As Targets for Cancer Immunotherapy in Multiple Myeloma. <i>Blood</i> , 2015, 126, 1851-1851.	0.6	0
131	Towards a Network-Based Molecular Taxonomy of Newly Diagnosed Multiple Myeloma. <i>Blood</i> , 2015, 126, 840-840.	0.6	0
132	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
133	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
134	The promise of genomics-based drug repurposing. <i>Clinical Advances in Hematology and Oncology</i> , 2014, 12, 601-3.	0.3	0