Joel T Dudley

List of Publications by Year
in descending order

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134

papers

11,665

citations

57758

44

h-index

32842

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.	28.9	113
3	Integrative chemogenomic analysis identifies small molecules that partially rescue Î”F508â€CFTR for cystic fibrosis. CPT: Pharmacometrics and Systems Pharmacology, 2021, 10, 500-510.	2.5	3
4	Multiplex qPCR discriminates variants of concern to enhance global surveillance of SARS-CoV-2. PLoS Biology, 2021, 19, e3001236.	5.6	200
5	Phe2vec: Automated disease phenotyping based on unsupervised embeddings from electronic health records. Patterns, 2021, 2, 100337.	5.9	19
6	Repositioning of a novel GABA-B receptor agonist, AZD3355 (Lesogaberan), for the treatment of non-alcoholic steatohepatitis. Scientific Reports, 2021, 11, 20827.	3.3	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.	1.9	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.	10.3	49
9	KRCC1: A potential therapeutic target in ovarian cancer. FASEB Journal, 2020, 34, 2287-2300.	0.5	5
10	Mutation-derived Neoantigen-specific T-cell Responses in Multiple Myeloma. Clinical Cancer Research, 2020, 26, 450-464.	7.0	62
11	Sepsis in the era of data-driven medicine: personalizing risks, diagnoses, treatments and prognoses. Briefings in Bioinformatics, 2020, 21, 1182-1195.	6.5	29
12	miR155 regulation of behavior, neuropathology, and cortical transcriptomics in Alzheimer's disease. Acta Neuropathologica, 2020, 140, 295-315.	7.7	23
13	Deep representation learning of electronic health records to unlock patient stratification at scale. Npj Digital Medicine, 2020, 3, 96.	10.9	90
14	Proposed Requirements for Cardiovascular Imaging-Related Machine Learning Evaluation (PRIME): A Checklist. JACC: Cardiovascular Imaging, 2020, 13, 2017-2035.	5.3	123
15	Integrative genomic meta-analysis reveals novel molecular insights into cystic fibrosis and Î”F508-CFTR rescue. Scientific Reports, 2020, 10, 20553.	3.3	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.	2.2	0
17	Identification of therapeutic targets from genetic association studies using hierarchical component analysis. BioData Mining, 2020, 13, 6.	4.0	3
18	A Novel Approach to Safer Glucocorticoid Receptorâ€“Targeted Anti-lymphoma Therapy via REDD1 (Regulated in Development and DNA Damage 1) Inhibition. Molecular Cancer Therapeutics, 2020, 19, 1898-1908.	4.1	7

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19	Sleep in the Natural Environment: A Pilot Study. Sensors, 2020, 20, 1378.	3.8	11
20	MEWS++: Enhancing the Prediction of Clinical Deterioration in Admitted Patients through a Machine Learning Model. Journal of Clinical Medicine, 2020, 9, 343.	2.4	37
21	Micro <scp>RNA</scp> â€•195 controls <scp>MICU</scp> 1 expression and tumor growth in ovarian cancer. EMBO Reports, 2020, 21, e48483.	4.5	29
22	Sexual dimorphism in atrophic effects of topical glucocorticoids is driven by differential regulation of atrophogene REDD1 in male and female skin. Oncotarget, 2020, 11, 409-418.	1.8	7
23	Identifying Acute Low Back Pain Episodes in Primary Care Practice From Clinical Notes: Observational Study. JMIR Medical Informatics, 2020, 8, e16878.	2.6	19
24	Genome-wide analysis indicates association between heterozygote advantage and healthy aging in humans. BMC Genetics, 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. BMC Medical Genomics, 2019, 12, 108.	1.5	8
26	Transcriptomic Network Interactions in Human Skin Treated with Topical Glucocorticoid Clobetasol Propionate. Journal of Investigative Dermatology, 2019, 139, 2281-2291.	0.7	18
27	Early life stress alters transcriptomic patterning across reward circuitry in male and female mice. Nature Communications, 2019, 10, 5098.	12.8	136
28	Integrative transcriptome imputation reveals tissue-specific and shared biological mechanisms mediating susceptibility to complex traits. Nature Communications, 2019, 10, 3834.	12.8	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. EBioMedicine, 2019, 44, 41-49.	6.1	9
30	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.	4.1	28
31	Systems Pharmacology Identifies an Arterial Wall Regulatory Gene Network Mediating Coronary Artery Disease Side Effects of Antiretroviral Therapy. Circulation Genomic and Precision Medicine, 2019, 12, e002390.	3.6	9
32	Deep learning predicts hip fracture using confounding patient and healthcare variables. Npj Digital Medicine, 2019, 2, 31.	10.9	158
33	Leveraging Big Data to Transform Drug Discovery. Methods in Molecular Biology, 2019, 1939, 91-118.	0.9	27
34	Lyme Disease Patient Trajectories Learned from Electronic Medical Data for Stratification of Disease Risk and Therapeutic Response. Scientific Reports, 2019, 9, 4460.	3.3	4
35	Predicting Future Cardiovascular Events in Patients With Peripheral Artery Disease Using Electronic Health Record Data. Circulation: Cardiovascular Quality and Outcomes, 2019, 12, e004741.	2.2	40
36	PI3K inhibitors protect against glucocorticoid-induced skin atrophy. EBioMedicine, 2019, 41, 526-537.	6.1	26

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37	P4â€495: SINGLE NUCLEI AND SINGLE WHOLE CELL SEQUENCING OF ALZHEIMER'S DISEASE. Alzheimer's and Dementia, 2019, 15, P1503.	0.8	0
38	Clarifying the Potential Role of Microbes in Alzheimerâ€™s Disease. Neuron, 2019, 104, 1036-1037.	8.1	10
39	Critical period plasticity-related transcriptional aberrations in schizophrenia and bipolar disorder. Schizophrenia Research, 2019, 207, 12-21.	2.0	15
40	High-Throughput Identification of the Plasma Proteomic Signature of Inflammatory Bowel Disease. Journal of Crohn's and Colitis, 2019, 13, 462-471.	1.3	18
41	CANDI: an R package and Shiny app for annotating radiographs and evaluating computer-aided diagnosis. Bioinformatics, 2019, 35, 1610-1612.	4.1	4
42	Integrative approach to sporadic Alzheimerâ€™s disease:Âdeficiency of TYROBPÂin cerebral AÎ² amyloidosis mouse normalizes clinical phenotype and complement subnetwork molecular pathology without reducing AÎ² burden. Molecular Psychiatry, 2019, 24, 431-446.	7.9	67
43	Natural Language Processing of Clinical Notes on Chronic Diseases: Systematic Review. JMIR Medical Informatics, 2019, 7, e12239.	2.6	297
44	Designing Robust N-of-1 Studies for Precision Medicine: Simulation Study and Design Recommendations. Journal of Medical Internet Research, 2019, 21, e12641.	4.3	29
45	Privacy-Preserving Methods for Feature Engineering Using Blockchain: Review, Evaluation, and Proof of Concept. Journal of Medical Internet Research, 2019, 21, e13600.	4.3	22
46	Building a Secure Biomedical Data Sharing Decentralized App (DApp): Tutorial. Journal of Medical Internet Research, 2019, 21, e13601.	4.3	22
47	SUN-253 Effects of Growth Hormone Stimulation on the Immunologic Cellular Landscape in Pediatric Patients. Journal of the Endocrine Society, 2019, 3, .	0.2	0
48	The next generation of precision medicine: observational studies, electronic health records, biobanks and continuous monitoring. Human Molecular Genetics, 2018, 27, R56-R62.	2.9	48
49	Isolation and Identification of the FollicularÂMicrobiome: Implications forÂAcne Research. Journal of Investigative Dermatology, 2018, 138, 2033-2040.	0.7	64
50	Rapamycin Modulates Glucocorticoid Receptor Function, Blocks Atrophogene REDD1, and Protects Skin from SteroidÂAtrophy. Journal of Investigative Dermatology, 2018, 138, 1935-1944.	0.7	25
51	Deep learning for healthcare: review, opportunities and challenges. Briefings in Bioinformatics, 2018, 19, 1236-1246.	6.5	1,459
52	Uncovering exposures responsible for birth season â€“ disease effects: a global study. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 275-288.	4.4	33
53	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.	2.5	27
54	Precision Medicine for Relapsed Multiple Myeloma on the Basis of an Integrative Multiomics Approach. JCO Precision Oncology, 2018, 2018, 1-17.	3.0	20

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55	Deletion of the glucocorticoid receptor chaperone FKBP51 prevents glucocorticoid-induced skin atrophy. Oncotarget, 2018, 9, 34772-34783.	1.8	20
56	Reflecting health: smart mirrors for personalized medicine. Npj Digital Medicine, 2018, 1, 62.	10.9	36
57	Integrative bioinformatics identifies postnatal lead (Pb) exposure disrupts developmental cortical plasticity. Scientific Reports, 2018, 8, 16388.	3.3	13
58	Multiscale Analysis of Independent Alzheimerâ€™s Cohorts Finds Disruption of Molecular, Genetic, and Clinical Networks by Human Herpesvirus. Neuron, 2018, 99, 64-82.e7.	8.1	558
59	Expression-based drug screening of neural progenitor cells from individuals with schizophrenia. Nature Communications, 2018, 9, 4412.	12.8	63
60	Disease Heritability Inferred from Familial Relationships Reported in Medical Records. Cell, 2018, 173, 1692-1704.e11.	28.9	79
61	The Rapid Prediction of Carbapenem Resistance in Patients With Klebsiella pneumoniae Bacteremia Using Electronic Medical Record Data. Open Forum Infectious Diseases, 2018, 5, ofy091.	0.9	15
62	The whole is greater than the sum of its parts: combining classical statistical and machine intelligence methods in medicine. Heart, 2018, 104, 1228-1228.	2.9	15
63	MetaCyto: A Tool for Automated Meta-analysis of Mass and Flow Cytometry Data. Cell Reports, 2018, 24, 1377-1388.	6.4	52
64	Adaptive Landscape of Protein Variation in Human Exomes. Molecular Biology and Evolution, 2018, 35, 2015-2025.	8.9	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. JAMA Network Open, 2018, 1, e181755.	5.9	54
66	Artificial Intelligence in Cardiology. Journal of the American College of Cardiology, 2018, 71, 2668-2679.	2.8	690
67	A 72-Year-Old Patient with Longstanding, Untreated Familial Hypercholesterolemia but no Coronary Artery Calcification: A Case Report. Cureus, 2018, 10, e2452.	0.5	1
68	Automated disease cohort selection using word embeddings from Electronic Health Records. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 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. AMIA Summits on Translational Science Proceedings, 2018, 2017, 108-117.	0.4	4
70	Novel Therapeutics Identification for Fibrosis in Renal Allograft Using Integrative Informatics Approach. Scientific Reports, 2017, 7, 39487.	3.3	28
71	Transcriptome-based repurposing of apigenin as a potential anti-fibrotic agent targeting hepatic stellate cells. Scientific Reports, 2017, 7, 42563.	3.3	29
72	Deficiency of TYROBP, an adapter protein for TREM2 and CR3 receptors, is neuroprotective in a mouse model of early Alzheimerâ€™s pathology. Acta Neuropathologica, 2017, 134, 769-788.	7.7	85

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73	The Asthma Mobile Health Study, a large-scale clinical observational study using ResearchKit. Nature Biotechnology, 2017, 35, 354-362.	17.5	185
74	Institutional profile: translational pharmacogenomics at the Icahn School of Medicine at Mount Sinai. Pharmacogenomics, 2017, 18, 1381-1386.	1.3	20
75	Necroptosis activation in Alzheimer's disease. Nature Neuroscience, 2017, 20, 1236-1246.	14.8	305
76	Intracoronary Imaging, Cholesterol Efflux, and Transcriptomics after Intensive Statin Treatment in Diabetes. Scientific Reports, 2017, 7, 7001.	3.3	12
77	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.	4.3	28
78	Intracoronary Imaging, Cholesterol Efflux, and Transcriptomes After IntensiveÂStatinÂTreatment. Journal of the American College of Cardiology, 2017, 69, 628-640.	2.8	56
79	Accelerators: Sparking Innovation and Transdisciplinary Team Science in Disparities Research. International Journal of Environmental Research and Public Health, 2017, 14, 225.	2.6	26
80	High-Throughput Characterization of Blood Serum Proteomics of IBD Patients with Respect to Aging and Genetic Factors. PLoS Genetics, 2017, 13, e1006565.	3.5	41
81	Transcriptional Profiling of Egg Allergy and Relationship to Disease Phenotype. PLoS ONE, 2016, 11, e0163831.	2.5	30
82	Deep Patient: An Unsupervised Representation to Predict the Future of Patients from the Electronic Health Records. Scientific Reports, 2016, 6, 26094.	3.3	1,036
83	EHDViz: clinical dashboard development using open-source technologies. BMJ Open, 2016, 6, e010579.	1.9	48
84	L1000CDS2: LINCS L1000 characteristic direction signatures search engine. Npj Systems Biology and Applications, 2016, 2, .	3.0	250
85	Influence of age on androgen deprivation therapy-associated Alzheimerâ€™s disease. Scientific Reports, 2016, 6, 35695.	3.3	12
86	Reply to R.L. Bowen et al, M. Froehner et al, J.L. Leow et al, and C. Brady et al. Journal of Clinical Oncology, 2016, 34, 2804-2805.	1.6	1
87	Gene expression elucidates functional impact of polygenic risk for schizophrenia. Nature Neuroscience, 2016, 19, 1442-1453.	14.8	952
88	Healthcare Data Mining with Matrix Models. , 2016, , .		2
89	Deep phenotyping predicts Huntington's genotype. Nature Biotechnology, 2016, 34, 823-824.	17.5	3
90	Machine-Learning Algorithms to Automate Morphological and Functional Assessments in 2D Echocardiography. Journal of the American College of Cardiology, 2016, 68, 2287-2295.	2.8	291

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91	Replicating Cardiovascular Condition-Birth Month Associations. Scientific Reports, 2016, 6, 33166.	3.3	16
92	Gold Nanoparticle Reprograms Pancreatic Tumor Microenvironment and Inhibits Tumor Growth. ACS Nano, 2016, 10, 10636-10651.	14.6	134
93	e-GRASP: an integrated evolutionary and GRASP resource for exploring disease associations. BMC Genomics, 2016, 17, 770.	2.8	15
94	<i>In silico</i> methods for drug repurposing and pharmacology. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 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. Clinical and Translational Gastroenterology, 2016, 7, e177.	2.5	40
96	Development and clinical application of an integrative genomic approach to personalized cancer therapy. Genome Medicine, 2016, 8, 62.	8.2	71
97	Cross-Tissue Regulatory Gene Networks in Coronary Artery Disease. Cell Systems, 2016, 2, 196-208.	6.2	120
98	Dysregulation of miRNA-9 in a Subset of Schizophrenia Patient-Derived Neural Progenitor Cells. Cell Reports, 2016, 15, 1024-1036.	6.4	107
99	Cognitive Machine-Learning Algorithm for Cardiac Imaging. Circulation: Cardiovascular Imaging, 2016, 9, .	2.6	164
100	Comparative analyses of population-scale phenomic data in electronic medical records reveal race-specific disease networks. Bioinformatics, 2016, 32, i101-i110.	4.1	39
101	Toward clinical genomics in everyday medicine: perspectives and recommendations. Expert Review of Molecular Diagnostics, 2016, 16, 521-532.	3.1	58
102	Androgen Deprivation Therapy and Future Alzheimerâ€™s Disease Risk. Journal of Clinical Oncology, 2016, 34, 566-571.	1.6	169
103	Mapping the effects of drugs on the immune system. Nature Biotechnology, 2016, 34, 47-54.	17.5	78
104	Deep Learning to Predict Patient Future Diseases from the Electronic Health Records. Lecture Notes in Computer Science, 2016, , 768-774.	1.3	28
105	Network Modeling Reveals CDC42BPA and CLEC11A As Novel Driver Genes of t(4; 14) Multiple Myeloma. Blood, 2016, 128, 802-802.	1.4	1
106	Systems Genetic Analyses Highlight a TGFÎ²-FOXO3 Dependent Striatal Astrocyte Network Conserved across Species and Associated with Stress, Sleep, and Huntingtonâ€™s Disease. PLoS Genetics, 2016, 12, e1006137.	3.5	24
107	Data-Driven Identification of Risk Factors of Patient Satisfaction at a Large Urban Academic Medical Center. PLoS ONE, 2016, 11, e0156076.	2.5	20
108	Integrative Analysis of Disease Signatures Shows Inflammation Disrupts Juvenile Experience-Dependent Cortical Plasticity. ENeuro, 2016, 3, ENEURO.0240-16.2016.	1.9	19

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109	Important role of kallikrein 6 for the development of keratinocyte proliferative resistance to topical glucocorticoids. Oncotarget, 2016, 7, 69479-69488.	1.8	12
110	Integrative Network Analysis of Newly Diagnosed Multiple Myeloma Identifies a Novel RNA-Seq Based High Riskgene Signature. Blood, 2016, 128, 3285-3285.	1.4	1
111	Aberrant a-to-I RNA Editing and Prognostic Impact of Adar in Multiple Myeloma Patients with 1q Amplification. Blood, 2016, 128, 357-357.	1.4	0
112	Modern Methods for Delineating Metagenomic Complexity. Cell Systems, 2015, 1, 6-7.	6.2	20
113	<scp>REDD</scp>1 functions at the crossroads between the therapeutic and adverse effects of topical glucocorticoids. EMBO Molecular Medicine, 2015, 7, 42-58.	6.9	51
114	Computational and Experimental Advances in Drug Repositioning for Accelerated Therapeutic Stratification. Current Topics in Medicinal Chemistry, 2015, 15, 5-20.	2.1	81
115	Age-Stratified Risk of Unexpected Uterine Sarcoma Following Surgery for Presumed Benign Leiomyoma. Oncologist, 2015, 20, 433-439.	3.7	59
116	Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics. Cell Systems, 2015, 1, 72-87.	6.2	241
117	A Targetable GATA2-IGF2 Axis Confers Aggressiveness in Lethal Prostate Cancer. Cancer Cell, 2015, 27, 223-239.	16.8	128
118	Genome-Wide Significant Loci: HowÂImportant Are They?. Journal of the American College of Cardiology, 2015, 65, 830-845.	2.8	129
119	Genomic and Network Patterns of Schizophrenia Genetic Variation in Human Evolutionary Accelerated Regions. Molecular Biology and Evolution, 2015, 32, 1148-1160.	8.9	98
120	Identification of type 2 diabetes subgroups through topological analysis of patient similarity. Science Translational Medicine, 2015, 7, 311ra174.	12.4	426
121	Integrative network modeling approaches to personalized cancer medicine. Personalized Medicine, 2015, 12, 245-257.	1.5	12
122	Patient-Specific Mutation-Derived Tumor Antigens As Targets for Cancer Immunotherapy in Multiple Myeloma. Blood, 2015, 126, 1851-1851.	1.4	0
123	Towards a Network-Based Molecular Taxonomy of Newly Diagnosed Multiple Myeloma. Blood, 2015, 126, 840-840.	1.4	0
124	Personalized medicine: from genotypes, molecular phenotypes and the quantified self, towards improved medicine. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 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. Gastroenterology, 2014, 146, 1028-1039.	1.3	175
128	Weighted Gene Co-Expression Network Analysis (WGCNA) Identifies Highly Proliferative Myeloma Subgroup Responsive to CDK4/ARK5 Inhibition. Blood, 2014, 124, 3445-3445.	1.4	9
129	STORMSeq: An Open-Source, User-Friendly Pipeline for Processing Personal Genomics Data in the Cloud. PLoS ONE, 2014, 9, e84860.	2.5	25
130	Automated Detection of Off-Label Drug Use. PLoS ONE, 2014, 9, e89324.	2.5	47
131	An Integrative Network Approach for Genomic Discovery and Personalized Therapy in Relapsed Multiple Myeloma. Blood, 2014, 124, 3426-3426.	1.4	0
132	The promise of genomics-based drug repurposing. Clinical Advances in Hematology and Oncology, 2014, 12, 601-3.	0.3	0
133	Translational Bioinformatics Approaches to Drug Development. Advances in Wound Care, 2013, 2, 470-489.	5.1	26
134	Using integrative informatics to bridge toxicogenomics and disease biology. ISEE Conference Abstracts, 2013, 2013, 5939.	0.0	0