

Nicholas P Tatonetti

List of Publications by Year in descending order

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Version: 2024-02-01

103
papers

6,650
citations

145106

33
h-index

84171

75
g-index

133
all docs

133
docs citations

133
times ranked

12256
citing authors

#	ARTICLE	IF	CITATIONS
1	No population left behind: Improving paediatric drug safety using informatics and systems biology. <i>British Journal of Clinical Pharmacology</i> , 2022, 88, 1464-1470.	1.1	10
2	System-wide transcriptome damage and tissue identity loss in COVID-19 patients. <i>Cell Reports Medicine</i> , 2022, 3, 100522.	3.3	24
3	Snapshots of nascent RNA reveal cell- and stimulus-specific responses to acute kidney injury. <i>JCI Insight</i> , 2022, 7, .	2.3	3
4	A database of pediatric drug effects to evaluate ontogenic mechanisms from child growth and development. <i>Med</i> , 2022, 3, 579-595.e7.	2.2	1
5	Deep learning on time series laboratory test results from electronic health records for early detection of pancreatic cancer.. <i>Journal of Clinical Oncology</i> , 2022, 40, e16268-e16268.	0.8	0
6	Shotgun transcriptome, spatial omics, and isothermal profiling of SARS-CoV-2 infection reveals unique host responses, viral diversification, and drug interactions. <i>Nature Communications</i> , 2021, 12, 1660.	5.8	132
7	Medical records-based chronic kidney disease phenotype for clinical care and "big data" observational and genetic studies. <i>Npj Digital Medicine</i> , 2021, 4, 70.	5.7	39
8	Identifying Symptom Information in Clinical Notes Using Natural Language Processing. <i>Nursing Research</i> , 2021, 70, 173-183.	0.8	24
9	E-Pedigrees: a large-scale automatic family pedigree prediction application. <i>Bioinformatics</i> , 2021, 37, 3966-3968.	1.8	2
10	Fine-scale genetic ancestry as a potential new tool for precision medicine. <i>Nature Medicine</i> , 2021, 27, 1152-1153.	15.2	3
11	Evaluating risk detection methods to uncover ontogenic-mediated adverse drug effect mechanisms in children. <i>BioData Mining</i> , 2021, 14, 34.	2.2	3
12	Predictions, Pivots, and a Pandemic: a Review of 2020's Top Translational Bioinformatics Publications. <i>Yearbook of Medical Informatics</i> , 2021, 30, 219-225.	0.8	1
13	Plasma kallikrein predicts primary graft dysfunction after heart transplant. <i>Journal of Heart and Lung Transplantation</i> , 2021, 40, 1199-1211.	0.3	11
14	Characterizing shared and distinct symptom clusters in common chronic conditions through natural language processing of nursing notes. <i>Research in Nursing and Health</i> , 2021, 44, 906-919.	0.8	16
15	No Increased Risk of Colorectal Adenomas in Spouses of Patients with Colorectal Neoplasia. <i>Clinical Gastroenterology and Hepatology</i> , 2020, 18, 509-510.	2.4	0
16	Using Machine Learning to Identify Adverse Drug Effects Posing Increased Risk to Women. <i>Patterns</i> , 2020, 1, 100108.	3.1	20
17	Associations between blood type and COVID-19 infection, intubation, and death. <i>Nature Communications</i> , 2020, 11, 5761.	5.8	309
18	Immune complement and coagulation dysfunction in adverse outcomes of SARS-CoV-2 infection. <i>Nature Medicine</i> , 2020, 26, 1609-1615.	15.2	255

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19	Where Have All the Emergencies Gone? The Impact of the COVID-19 Pandemic on Obstetric and Gynecologic Procedures and Consults at a New York City Hospital. <i>Journal of Minimally Invasive Gynecology</i> , 2020, 28, 1411-1419.e1.	0.3	24
20	Comparative analysis, applications, and interpretation of electronic health record-based stroke phenotyping methods. <i>BioData Mining</i> , 2020, 13, 21.	2.2	12
21	Prevalence of progressive multifocal leukoencephalopathy (PML) in adults and children with systemic lupus erythematosus. <i>Lupus Science and Medicine</i> , 2020, 7, e000388.	1.1	9
22	Association of Neighborhood Deprivation Index With Success in Cancer Care Crowdfunding. <i>JAMA Network Open</i> , 2020, 3, e2026946.	2.8	25
23	Low Rates of Screening for Celiac Disease Among Family Members. <i>Clinical Gastroenterology and Hepatology</i> , 2019, 17, 463-468.	2.4	5
24	Artificial Intelligence for Drug Toxicity and Safety. <i>Trends in Pharmacological Sciences</i> , 2019, 40, 624-635.	4.0	149
25	Challenges with quality of race and ethnicity data in observational databases. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2019, 26, 730-736.	2.2	116
26	ROMOP: a light-weight R package for interfacing with OMOP-formatted electronic health record data. <i>JAMIA Open</i> , 2019, 2, 10-14.	1.0	11
27	Informatics and Computational Methods in Natural Product Drug Discovery: A Review and Perspectives. <i>Frontiers in Genetics</i> , 2019, 10, 368.	1.1	95
28	Translational medicine in the Age of Big Data. <i>Briefings in Bioinformatics</i> , 2019, 20, 457-462.	3.2	12
29	The Next Generation of Drug Safety Science: Coupling Detection, Corroboration, and Validation to Discover Novel Drug Effects and Drug-Drug Interactions. <i>Clinical Pharmacology and Therapeutics</i> , 2018, 103, 177-179.	2.3	9
30	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
31	Pharmacological risk factors associated with hospital readmission rates in a psychiatric cohort identified using prescriptome data mining. <i>BMC Medical Informatics and Decision Making</i> , 2018, 18, 79.	1.5	10
32	Disease Heritability Inferred from Familial Relationships Reported in Medical Records. <i>Cell</i> , 2018, 173, 1692-1704.e11.	13.5	79
33	Pathogen population structure can explain hospital outbreaks. <i>ISME Journal</i> , 2018, 12, 2835-2843.	4.4	4
34	Structural and functional cardiac profile after prolonged duration of mechanical unloading: potential implications for myocardial recovery. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2018, 315, H1463-H1476.	1.5	16
35	Tissue-Specific Analysis of Pharmacological Pathways. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2018, 7, 453-463.	1.3	6
36	Low Screening Rates for Diabetes Mellitus Among Family Members of Affected Relatives. <i>AMIA ... Annual Symposium proceedings</i> , 2018, 2018, 1471-1477.	0.2	1

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37	Reply. Journal of the American College of Cardiology, 2017, 69, 1877-1878.	1.2	0
38	Development of A Machine Learning Algorithm to Classify Drugs Of Unknown Fetal Effect. Scientific Reports, 2017, 7, 12839.	1.6	27
39	Procedure prediction from symbolic Electronic Health Records via time intervals analytics. Journal of Biomedical Informatics, 2017, 75, 70-82.	2.5	26
40	Climate Classification is an Important Factor in Assessing Quality-of-Care Across Hospitals. Scientific Reports, 2017, 7, 4948.	1.6	11
41	Prognosis of Clinical Outcomes with Temporal Patterns and Experiences with One Class Feature Selection. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 555-563.	1.9	22
42	Ten Simple Rules to Enable Multi-site Collaborations through Data Sharing. PLoS Computational Biology, 2017, 13, e1005278.	1.5	29
43	Systems biology approaches for identifying adverse drug reactions and elucidating their underlying biological mechanisms. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2016, 8, 104-122.	6.6	42
44	A novel, rapid method to compare the therapeutic windows of oral anticoagulants using the Hill coefficient. Scientific Reports, 2016, 6, 29387.	1.6	10
45	Coupling Data Mining and Laboratory Experiments to Discover Drug Interactions Causing QT Prolongation. Journal of the American College of Cardiology, 2016, 68, 1756-1764.	1.2	63
46	Predicting G protein-coupled receptor downstream signaling by tissue expression. Bioinformatics, 2016, 32, 3435-3443.	1.8	13
47	Replicating Cardiovascular Condition-Birth Month Associations. Scientific Reports, 2016, 6, 33166.	1.6	16
48	Investigation of 7-dehydrocholesterol reductase pathway to elucidate off-target prenatal effects of pharmaceuticals: a systematic review. Pharmacogenomics Journal, 2016, 16, 411-429.	0.9	35
49	A curated and standardized adverse drug event resource to accelerate drug safety research. Scientific Data, 2016, 3, 160026.	2.4	145
50	A Computational Drug Repositioning Approach for Targeting Oncogenic Transcription Factors. Cell Reports, 2016, 15, 2348-2356.	2.9	29
51	Improving condition severity classification with an efficient active learning based framework. Journal of Biomedical Informatics, 2016, 61, 44-54.	2.5	18
52	An Integrative Data Science Pipeline to Identify Novel Drug Interactions that Prolong the QT Interval. Drug Safety, 2016, 39, 433-441.	1.4	30
53	A Pharmacovigilance Signaling System Based on FDA Regulatory Action and Post-Marketing Adverse Event Reports. Drug Safety, 2016, 39, 561-575.	1.4	34
54	Mapping the effects of drugs on the immune system. Nature Biotechnology, 2016, 34, 47-54.	9.4	78

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55	Silencing c-Myc Translation As a Therapeutic Strategy through Targeting PI3K Delta and CK1 Epsilon in Hematological Malignancies. <i>Blood</i> , 2016, 128, 291-291.	0.6	1
56	Using a Novel Ontology to Inform the Discovery of Therapeutic Peptides from Animal Venoms. <i>AMIA Summits on Translational Science Proceedings</i> , 2016, 2016, 209-18.	0.4	3
57	In Search of 'Birth Month Genes': Using Existing Data Repositories to Locate Genes Underlying Birth Month-Disease Relationships. <i>AMIA Summits on Translational Science Proceedings</i> , 2016, 2016, 189-98.	0.4	1
58	VenomKB, a new knowledge base for facilitating the validation of putative venom therapies. <i>Scientific Data</i> , 2015, 2, 150065.	2.4	9
59	Systems Pharmacology Augments Drug Safety Surveillance. <i>Clinical Pharmacology and Therapeutics</i> , 2015, 97, 151-158.	2.3	43
60	Improving Detection of Arrhythmia Drug-Drug Interactions in Pharmacovigilance Data through the Implementation of Similarity-Based Modeling. <i>PLoS ONE</i> , 2015, 10, e0129974.	1.1	17
61	Birth month affects lifetime disease risk: a phenome-wide method. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 1042-1053.	2.2	106
62	Toward a complete dataset of drug-drug interaction information from publicly available sources. <i>Journal of Biomedical Informatics</i> , 2015, 55, 206-217.	2.5	97
63	Outcomes Prediction via Time Intervals Related Patterns. , 2015, , .		19
64	3D Pharmacophoric Similarity improves Multi Adverse Drug Event Identification in Pharmacovigilance. <i>Scientific Reports</i> , 2015, 5, 8809.	1.6	18
65	An Active Learning Framework for Efficient Condition Severity Classification. <i>Lecture Notes in Computer Science</i> , 2015, , 13-24.	1.0	5
66	Development and validation of a classification approach for extracting severity automatically from electronic health records. <i>Journal of Biomedical Semantics</i> , 2015, 6, 14.	0.9	16
67	Connectivity Homology Enables Inter-Species Network Models of Synthetic Lethality. <i>PLoS Computational Biology</i> , 2015, 11, e1004506.	1.5	30
68	Disruption of the mTOR-eIF4F Axis By Selectively Targeting PI3Kdelta and Proteasome Potently Inhibits Cap Dependent Translation of c-Myc in Aggressive Lymphomas. <i>Blood</i> , 2015, 126, 593-593.	0.6	0
69	Are All Vaccines Created Equal? Using Electronic Health Records to Discover Vaccines Associated With Clinician-Coded Adverse Events. <i>AMIA Summits on Translational Science Proceedings</i> , 2015, 2015, 196-200.	0.4	6
70	A knowledge-based, automated method for phenotyping in the EHR using only clinical pathology reports. <i>AMIA Summits on Translational Science Proceedings</i> , 2015, 2015, 64-8.	0.4	2
71	An Assessment of Family History Information Captured in an Electronic Health Record. <i>AMIA ... Annual Symposium proceedings</i> , 2015, 2015, 2035-42.	0.2	22
72	Pharmacological inhibition of cystine-glutamate exchange induces endoplasmic reticulum stress and ferroptosis. <i>ELife</i> , 2014, 3, e02523.	2.8	1,296

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73	Disease Risk Factors Identified Through Shared Genetic Architecture and Electronic Medical Records. <i>Science Translational Medicine</i> , 2014, 6, 234ra57.	5.8	58
74	Coherent Functional Modules Improve Transcription Factor Target Identification, Cooperativity Prediction, and Disease Association. <i>PLoS Genetics</i> , 2014, 10, e1004122.	1.5	29
75	Insight into the Interactions between Novel Coumarin Derivatives and Human A ₃ Adenosine Receptors. <i>ChemMedChem</i> , 2014, 9, 2245-2253.	1.6	13
76	Stimulated Reporting: The Impact of US Food and Drug Administration-Issued Alerts on the Adverse Event Reporting System (FAERS). <i>Drug Safety</i> , 2014, 37, 971-980.	1.4	54
77	Insight into the Functional and Structural Properties of 3-Arylcoumarin as an Interesting Scaffold in Monoamine Oxidase...B Inhibition. <i>ChemMedChem</i> , 2014, 9, 1488-1500.	1.6	35
78	Monoamine Oxidase (MAO) Inhibitory Activity: 3-Phenylcoumarins versus 4-Hydroxy-3-phenylcoumarins. <i>ChemMedChem</i> , 2014, 9, 1672-1676.	1.6	16
79	Similarity-based modeling in large-scale prediction of drug-drug interactions. <i>Nature Protocols</i> , 2014, 9, 2147-2163.	5.5	178
80	Synthesis, pharmacological study and docking calculations of new benzo[<i>f</i>]coumarin derivatives as dual inhibitors of enzymatic systems involved in neurodegenerative diseases. <i>Future Medicinal Chemistry</i> , 2014, 6, 371-383.	1.1	28
81	Bridging Islands of Information to Establish an Integrated Knowledge Base of Drugs and Health Outcomes of Interest. <i>Drug Safety</i> , 2014, 37, 557-567.	1.4	49
82	Impact of Major Bleeding on Long-Term Mortality in Anemic Versus Nonanemic Patients Undergoing Percutaneous Coronary Intervention Using Bivalirudin. <i>American Journal of Cardiology</i> , 2014, 113, 1481-1486.	0.7	12
83	The Weber Effect and the United States Food and Drug Administration's Adverse Event Reporting System (FAERS): Analysis of Sixty-Two Drugs Approved from 2006 to 2010. <i>Drug Safety</i> , 2014, 37, 283-294.	1.4	106
84	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
85	State of the Art and Development of a Drug-Drug Interaction Large Scale Predictor Based on 3D Pharmacophoric Similarity. <i>Current Drug Metabolism</i> , 2014, 15, 490-501.	0.7	16
86	Pathway analysis of genome-wide data improves warfarin dose prediction. <i>BMC Genomics</i> , 2013, 14, S11.	1.2	14
87	Connecting the Dots: Applications of Network Medicine in Pharmacology and Disease. <i>Clinical Pharmacology and Therapeutics</i> , 2013, 94, 659-669.	2.3	35
88	Web-scale pharmacovigilance: listening to signals from the crowd. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2013, 20, 404-408.	2.2	180
89	Comparative study of the 3-phenylcoumarin scaffold: Synthesis, X-ray structural analysis and semiempirical calculations of a selected series of compounds. <i>Journal of Molecular Structure</i> , 2013, 1050, 185-191.	1.8	2
90	MAO Inhibitory Activity of 2-Arylbenzofurans versus 3-Arylcoumarins: Synthesis, in-vitro Study, and Docking Calculations. <i>ChemMedChem</i> , 2013, 8, 956-966.	1.6	32

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91	Novel (coumarin-3-yl)carbamates as selective MAO-B inhibitors: Synthesis, inÂvitro and inÂvivo assays, theoretical evaluation of ADMEÂproperties and docking study. European Journal of Medicinal Chemistry, 2013, 63, 151-161.	2.6	50
92	Genetic variants associated with warfarin dose in African-American individuals: a genome-wide association study. Lancet, The, 2013, 382, 790-796.	6.3	237
93	High-Throughput Methods for Combinatorial Drug Discovery. Science Translational Medicine, 2013, 5, 205rv1.	5.8	139
94	Response to 'Use of an algorithm for identifying hidden drug--drug interactions in adverse event reports' by Gooden et al. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 591-591.	2.2	0
95	Detection of Drug-Drug Interactions by Modeling Interaction Profile Fingerprints. PLoS ONE, 2013, 8, e58321.	1.1	96
96	Genome Wide Analysis of Drug-Induced Torsades de Pointes: Lack of Common Variants with Large Effect Sizes. PLoS ONE, 2013, 8, e78511.	1.1	57
97	Data-Driven Prediction of Drug Effects and Interactions. Science Translational Medicine, 2012, 4, 125ra31.	5.8	610
98	A novel signal detection algorithm for identifying hidden drug-drug interactions in adverse event reports. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 79-85.	2.2	165
99	Interpretome: a freely available, modular, and secure personal genome interpretation engine. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2012, , 339-350.	0.7	12
100	Detecting Drug Interactions From Adverse-Event Reports: Interaction Between Paroxetine and Pravastatin Increases Blood Glucose Levels. Clinical Pharmacology and Therapeutics, 2011, 90, 133-142.	2.3	183
101	Cooperative transcription factor associations discovered using regulatory variation. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 13353-13358.	3.3	53
102	An integrative method for scoring candidate genes from association studies: application to warfarin dosing. BMC Bioinformatics, 2010, 11, S9.	1.2	14
103	Predicting drug side-effects by chemical systems biology. Genome Biology, 2009, 10, 238.	13.9	59