

# Peter Tonellato

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7495808/publications.pdf>

Version: 2024-02-01

58  
papers

3,625  
citations

361413

20  
h-index

197818

49  
g-index

61  
all docs

61  
docs citations

61  
times ranked

5246  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	27.8	1,943
2	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	5.6	290
3	A Genomic-Systems Biology Map for Cardiovascular Function. <i>Science</i> , 2001, 294, 1723-1726.	12.6	166
4	Biomedical Cloud Computing With Amazon Web Services. <i>PLoS Computational Biology</i> , 2011, 7, e1002147.	3.2	110
5	Rat Genome Database (RGD): mapping disease onto the genome. <i>Nucleic Acids Research</i> , 2002, 30, 125-128.	14.5	96
6	Genomic map of cardiovascular phenotypes of hypertension in female Dahl S rats. <i>Physiological Genomics</i> , 2003, 15, 243-257.	2.3	91
7	Genetically defined risk of salt sensitivity in an intercross of Brown Norway and Dahl S rats. <i>Physiological Genomics</i> , 2000, 2, 107-115.	2.3	78
8	A Call to Action. <i>American Journal of Clinical Pathology</i> , 2010, 133, 832-834.	0.7	66
9	A Unique Morphological Phenotype in Chemoresistant Triple-Negative Breast Cancer Reveals Metabolic Reprogramming and PLIN4 Expression as a Molecular Vulnerability. <i>Molecular Cancer Research</i> , 2019, 17, 2492-2507.	3.4	63
10	Evolutionary Dynamics of Oncogenes and Tumor Suppressor Genes: Higher Intensities of Purifying Selection than Other Genes. <i>Molecular Biology and Evolution</i> , 2003, 20, 964-968.	8.9	57
11	RNA-Seq of the Caribbean reef-building coral <i>Orbicella faveolata</i> (Scleractinia-Merulinidae) under bleaching and disease stress expands models of coral innate immunity. <i>PeerJ</i> , 2016, 4, e1616.	2.0	56
12	Individualized patient-centered lifestyle recommendations: An expert system for communicating patient specific cardiovascular risk information and prioritizing lifestyle options. <i>Journal of Biomedical Informatics</i> , 2012, 45, 1164-1174.	4.3	46
13	Automated Construction of High-Density Comparative Maps Between Rat, Human, and Mouse. <i>Genome Research</i> , 2001, 11, 1935-1943.	5.5	40
14	Phylogenetics of rat inbred strains. <i>Mammalian Genome</i> , 2003, 14, 61-64.	2.2	40
15	BN phenome: detailed characterization of the cardiovascular, renal, and pulmonary systems of the sequenced rat. <i>Physiological Genomics</i> , 2006, 25, 303-313.	2.3	40
16	High-Density Rat Radiation Hybrid Maps Containing Over 24,000 SSLPs, Genes, and ESTs Provide a Direct Link to the Rat Genome Sequence. <i>Genome Research</i> , 2004, 14, 750-757.	5.5	36
17	A decision support system for cost-effective diagnosis. <i>Artificial Intelligence in Medicine</i> , 2010, 50, 149-161.	6.5	28
18	Tools and strategies for physiological genomics: the Rat Genome Database. <i>Physiological Genomics</i> , 2005, 23, 246-256.	2.3	25

#	ARTICLE	IF	CITATIONS
19	COSMOS: Python library for massively parallel workflows. <i>Bioinformatics</i> , 2014, 30, 2956-2958.	4.1	23
20	Identification of Hypertension-Related QTLs in African American Sib Pairs. <i>Hypertension</i> , 2002, 40, 634-639.	2.7	22
21	Differential gene expression associated with dietary methylmercury (MeHg) exposure in rainbow trout ( <i>Oncorhynchus mykiss</i> ) and zebrafish ( <i>Danio rerio</i> ). <i>Ecotoxicology</i> , 2013, 22, 740-751.	2.4	22
22	Integrative Genomics: In Silico Coupling of Rat Physiology and Complex Traits With Mouse and Human Data. <i>Genome Research</i> , 2004, 14, 651-660.	5.5	19
23	A Systems Approach to Designing Effective Clinical Trials Using Simulations. <i>Circulation</i> , 2013, 127, 517-526.	1.6	19
24	Genomic characteristics of trastuzumab-resistant Her2-positive metastatic breast cancer. <i>Journal of Cancer Research and Clinical Oncology</i> , 2017, 143, 1255-1262.	2.5	19
25	A novel approach for high-quality microarray processing using third-dye array visualization technology. <i>IEEE Transactions on Nanobioscience</i> , 2003, 2, 193-201.	3.3	17
26	High-Throughput Scanning of the Rat Genome Using Interspersed Repetitive Sequence-PCR Markers. <i>Genomics</i> , 2000, 69, 287-294.	2.9	16
27	Multiple approaches to data-mining of proteomic data based on statistical and pattern classification methods. <i>Proteomics</i> , 2003, 3, 1704-1709.	2.2	14
28	Automated Analysis of Conserved Synteny for the Zebrafish Genome. <i>Methods in Cell Biology</i> , 2004, 77, 255-271.	1.1	14
29	Histopathologic Alterations Associated with Global Gene Expression Due to Chronic Dietary TCDD Exposure in Juvenile Zebrafish. <i>PLoS ONE</i> , 2014, 9, e100910.	2.5	12
30	MC-GenomeKey: a multicloud system for the detection and annotation of genomic variants. <i>BMC Bioinformatics</i> , 2017, 18, 49.	2.6	10
31	Personalized Anticoagulation. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	8
32	Female reproductive impacts of dietary methylmercury in yellow perch ( <i>Perca flavescens</i> ) and zebrafish ( <i>Danio rerio</i> ). <i>Chemosphere</i> , 2018, 195, 301-311.	8.2	8
33	Quantification of the Contribution of Type 1 and Type 2 Angiotensin II Receptors to the Net Tissue Specific Effect of Angiotensin II. <i>Annals of Biomedical Engineering</i> , 2000, 28, 653-664.	2.5	7
34	Peptide Identification Using Peptide Amino Acid Attribute Vectors. <i>Journal of Proteome Research</i> , 2004, 3, 813-820.	3.7	7
35	Big Data Cohort Extraction to Facilitate Machine Learning to Improve Statin Treatment. <i>Western Journal of Nursing Research</i> , 2017, 39, 42-62.	1.4	7
36	A strengths-based data capture model: mining data-driven and person-centered health assets. <i>JAMIA Open</i> , 2018, 1, 11-14.	2.0	7

#	ARTICLE	IF	CITATIONS
37	Single Circulating-Tumor-Cell-Targeted Sequencing to Identify Somatic Variants in Liquid Biopsies in Non-Small-Cell Lung Cancer Patients. <i>Current Issues in Molecular Biology</i> , 2022, 44, 750-763.	2.4	7
38	Producing personalized statin treatment plans to optimize clinical outcomes using big data and machine learning. <i>Journal of Biomedical Informatics</i> , 2022, 128, 104029.	4.3	7
39	Assessment of Chemokinetic Behavior of Inflammatory Lung Macrophages in a Linear Under-Agarose Assay. <i>Journal of Leukocyte Biology</i> , 1990, 48, 297-305.	3.3	5
40	Western influenced lifestyle and Kv2.1 association as predicted biomarkers for Tunisian colorectal cancer. <i>BMC Cancer</i> , 2020, 20, 1086.	2.6	5
41	Discovering Associations Among Older Adults' Characteristics and Planned Nursing Interventions Using Electronic Health Record Data. <i>Research and Theory for Nursing Practice</i> , 2019, 33, 58-80.	0.4	5
42	Personalized long-term prediction of cognitive function: Using sequential assessments to improve model performance. <i>Journal of Biomedical Informatics</i> , 2017, 76, 78-86.	4.3	4
43	Evaluation of cfDNA as an early detection assay for dense tissue breast cancer. <i>Scientific Reports</i> , 2022, 12, 8458.	3.3	3
44	Deriving clinical action from whole-genome analysis. <i>Personalized Medicine</i> , 2012, 9, 247-252.	1.5	2
45	Exploring Older Adults' Strengths, Problems, and Wellbeing Using De-identified Electronic Health Record Data. <i>AMIA ... Annual Symposium proceedings</i> , 2018, 2018, 1263-1272.	0.2	2
46	Mathematical analysis of type-I and type-IIb muscle fiber force generation in renal hypertension. <i>Annals of Biomedical Engineering</i> , 1996, 24, 489-499.	2.5	1
47	Application of statistical machine learning in identifying candidate biomarkers of resistant to anti-cancer drugs in ovarian cancer. , 2014, , .		1
48	Mutational Forks: Inferring Deregulated Flow of Signal Transduction Based on Patient-Specific Mutations. , 2019, , .		1
49	Development, implementation and participant evaluation of combining text messaging and peer group support in a weight management programme for African-American women. <i>Journal of Research in Nursing</i> , 2020, 25, 475-491.	0.9	1
50	Using Comparative Genomics to Leverage Animal Models in the Identification of Cancer Genes. Examples in Prostate Cancer. <i>Cancer Genomics and Proteomics</i> , 2005, 2, 137-144.	2.0	1
51	Optimization of a Gene Analysis Application. <i>Computing Letters</i> , 2006, 2, 81-88.	0.5	0
52	Erratum to "Optimization of a Gene Analysis Application" <i>Computing Letters</i> , 2006, 2, 163.	0.5	0
53	P3-077: A Translational Research Strategy to Individualize Prediction of Long-Term Cognitive Trajectory. , 2016, 12, P847-P847.		0
54	O1-06-01: Using Big Data To Individualize Prediction Of Long-Term Cognitive Trajectory. , 2016, 12, P185-P186.		0

#	ARTICLE	IF	CITATIONS
55	Preliminary analysis and assessment of breast cancer risk in Japanese women.. Journal of Clinical Oncology, 2017, 35, e13092-e13092.	1.6	0
56	A simulation platform to examine heterogeneity influence on treatment. AMIA Summits on Translational Science Proceedings, 2012, 2012, 19-24.	0.4	0
57	Using simulation and optimization approach to improve outcome through warfarin precision treatment. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 412-423.	0.7	0
58	A community call to action: mitigating COVID pandemicâ€™s impact on mental health. Future Virology, 2022, , .	1.8	0