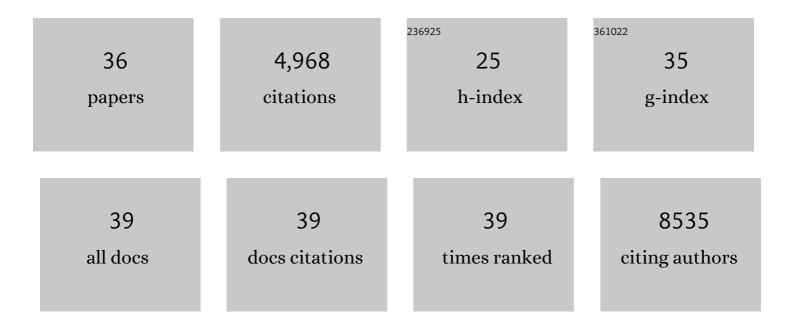
Nora C Toussaint

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1394845/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Tracing Clonal Dynamics Reveals that Two- and Three-dimensional Patient-derived Cell Models Capture Tumor Heterogeneity of Clear Cell Renal Cell Carcinoma. European Urology Focus, 2021, 7, 152-162.	3.1	34
2	The Tumor Profiler Study: integrated, multi-omic, functional tumor profiling for clinical decision support. Cancer Cell, 2021, 39, 288-293.	16.8	71
3	HLA-DR15 Molecules Jointly Shape an Autoreactive T Cell Repertoire in Multiple Sclerosis. Cell, 2020, 183, 1264-1281.e20.	28.9	133
4	Convergent network effects along the axis of gene expression during prostate cancer progression. Genome Biology, 2020, 21, 302.	8.8	17
5	SCIM: universal single-cell matching with unpaired feature sets. Bioinformatics, 2020, 36, i919-i927.	4.1	37
6	Comparative analysis of mRNA and protein degradation in prostate tissues indicates high stability of proteins. Nature Communications, 2019, 10, 2524.	12.8	35
7	Bioinformatics for precision oncology. Briefings in Bioinformatics, 2019, 20, 778-788.	6.5	49
8	Barrett's esophagus is associated with a distinct oral microbiome. Clinical and Translational Gastroenterology, 2018, 9, e135.	2.5	49
9	NGS-pipe: a flexible, easily extendable and highly configurable framework for NGS analysis. Bioinformatics, 2018, 34, 107-108.	4.1	25
10	Genomic Surveillance Reveals Diversity of Multidrug-Resistant Organism Colonization and Infection: A Prospective Cohort Study in Liver Transplant Recipients. Clinical Infectious Diseases, 2018, 67, 905-912.	5.8	60
11	Increasing Dietary Fiber Intake Is Associated with a Distinct Esophageal Microbiome. Clinical and Translational Gastroenterology, 2018, 9, e199.	2.5	42
12	SwissMTB: establishing comprehensive molecular cancer diagnostics in Swiss clinics. BMC Medical Informatics and Decision Making, 2018, 18, 89.	3.0	18
13	Genomic and Geographic Context for the Evolution of High-Risk Carbapenem-Resistant <i>Enterobacter cloacae</i> Complex Clones ST171 and ST78. MBio, 2018, 9, .	4.1	67
14	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	16.8	623
15	Combined mutation in Vhl, Trp53 and Rb1 causes clear cell renal cell carcinoma in mice. Nature Medicine, 2017, 23, 869-877.	30.7	101
16	Characterization of a Novel Orthomyxo-like Virus Causing Mass Die-Offs of Tilapia. MBio, 2016, 7, e00431-16.	4.1	181
17	Features of Circulating Parainfluenza Virus Required for Growth in Human Airway. MBio, 2016, 7, e00235.	4.1	18
18	Proton Pump Inhibitors Alter Specific Taxa in the Human Gastrointestinal Microbiome: A Crossover Trial. Gastroenterology, 2015, 149, 883-885.e9.	1.3	268

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#	Article	lF	CITATIONS
19	Loss of Microbiota-Mediated Colonization Resistance to <i>Clostridium difficile</i> Infection With Oral Vancomycin Compared With Metronidazole. Journal of Infectious Diseases, 2015, 212, 1656-1665.	4.0	157
20	Precision microbiome reconstitution restores bile acid mediated resistance to Clostridium difficile. Nature, 2015, 517, 205-208.	27.8	1,506
21	Gut Microbiota and Tacrolimus Dosing in Kidney Transplantation. PLoS ONE, 2015, 10, e0122399.	2.5	133
22	Gut Microbial Community Structure and Complications After Kidney Transplantation. Transplantation, 2014, 98, 697-705.	1.0	131
23	In melanoma, <scp>H</scp> ippo signaling is affected by copy number alterations and <scp>YAP</scp> 1 overexpression impairs patient survival. Pigment Cell and Melanoma Research, 2014, 27, 671-673.	3.3	28
24	Intestinal Microbiota Containing Barnesiella Species Cures Vancomycin-Resistant Enterococcus faecium Colonization. Infection and Immunity, 2013, 81, 965-973.	2.2	391
25	Ecological Modeling from Time-Series Inference: Insight into Dynamics and Stability of Intestinal Microbiota. PLoS Computational Biology, 2013, 9, e1003388.	3.2	487
26	Binding Pocket Optimization by Computational Protein Design. PLoS ONE, 2012, 7, e52505.	2.5	39
27	Universal peptide vaccines – Optimal peptide vaccine design based on viral sequence conservation. Vaccine, 2011, 29, 8745-8753.	3.8	35
28	An exact algorithm for side-chain placement in protein design. Optimization Letters, 2011, 5, 393-406.	1.6	4
29	T-cell epitope prediction based on self-tolerance. , 2011, , .		5
30	BALL - biochemical algorithms library 1.3. BMC Bioinformatics, 2010, 11, 531.	2.6	62
31	Inferring latent task structure for Multitask Learning by Multiple Kernel Learning. BMC Bioinformatics, 2010, 11, S5.	2.6	24
32	Exploiting physico-chemical properties in string kernels. BMC Bioinformatics, 2010, 11, S7.	2.6	17
33	Novel Machine Learning Methods for MHC Class I Binding Prediction. Lecture Notes in Computer Science, 2010, , 98-109.	1.3	30
34	OptiTopea web server for the selection of an optimal set of peptides for epitope-based vaccines. Nucleic Acids Research, 2009, 37, W617-W622.	14.5	32
35	Towards <i>in silico</i> design of epitope-based vaccines. Expert Opinion on Drug Discovery, 2009, 4, 1047-1060.	5.0	18
36	A Mathematical Framework for the Selection of an Optimal Set of Peptides for Epitope-Based Vaccines. PLoS Computational Biology, 2008, 4, e1000246.	3.2	32