Nora C Toussaint

List of Publications by Year
in descending order

36 papers	4,968 citations	236925 25 h-index	361022 35 g-index
39 all docs	39 docs citations	39 times ranked	8535 citing authors

#	Article	IF	Citations
1	Precision microbiome reconstitution restores bile acid mediated resistance to Clostridium difficile. Nature, 2015, 517, 205-208.	27.8	1,506
2	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	16.8	623
3	Ecological Modeling from Time-Series Inference: Insight into Dynamics and Stability of Intestinal Microbiota. PLoS Computational Biology, 2013, 9, e1003388.	3.2	487
4	Intestinal Microbiota Containing Barnesiella Species Cures Vancomycin-Resistant Enterococcus faecium Colonization. Infection and Immunity, 2013, 81, 965-973.	2.2	391
5	Proton Pump Inhibitors Alter Specific Taxa in the Human Gastrointestinal Microbiome: A Crossover Trial. Gastroenterology, 2015, 149, 883-885.e9.	1.3	268
6	Characterization of a Novel Orthomyxo-like Virus Causing Mass Die-Offs of Tilapia. MBio, 2016, 7, e00431-16.	4.1	181
7	Loss of Microbiota-Mediated Colonization Resistance to *Clostridium difficile* Infection With Oral Vancomycin Compared With Metronidazole. Journal of Infectious Diseases, 2015, 212, 1656-1665.	4.0	157
8	HLA-DR15 Molecules Jointly Shape an Autoreactive T Cell Repertoire in Multiple Sclerosis. Cell, 2020, 183, 1264-1281.e20.	28.9	133
9	Gut Microbiota and Tacrolimus Dosing in Kidney Transplantation. PLoS ONE, 2015, 10, e0122399.	2.5	133
10	Gut Microbial Community Structure and Complications After Kidney Transplantation. Transplantation, 2014, 98, 697-705.	1.0	131
11	Combined mutation in Vhl, Trp53 and Rb1 causes clear cell renal cell carcinoma in mice. Nature Medicine, 2017, 23, 869-877.	30.7	101
12	The Tumor Profiler Study: integrated, multi-omic, functional tumor profiling for clinical decision support. Cancer Cell, 2021, 39, 288-293.	16.8	71
13	Genomic and Geographic Context for the Evolution of High-Risk Carbapenem-Resistant *Enterobacter cloacae* Complex Clones ST171 and ST78. MBio, 2018, 9, .	4.1	67
14	BALL - biochemical algorithms library 1.3. BMC Bioinformatics, 2010, 11, 531.	2.6	62
15	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
16	Barrett's esophagus is associated with a distinct oral microbiome. Clinical and Translational Gastroenterology, 2018, 9, e135.	2.5	49
17	Bioinformatics for precision oncology. Briefings in Bioinformatics, 2019, 20, 778-788.	6.5	49
18	Increasing Dietary Fiber Intake Is Associated with a Distinct Esophageal Microbiome. Clinical and Translational Gastroenterology, 2018, 9, e199.	2.5	42

#	Article	IF	Citations
19	Binding Pocket Optimization by Computational Protein Design. PLoS ONE, 2012, 7, e52505.	2.5	39
20	SCIM: universal single-cell matching with unpaired feature sets. Bioinformatics, 2020, 36, i919-i927.	4.1	37
21	Universal peptide vaccines â€" Optimal peptide vaccine design based on viral sequence conservation. Vaccine, 2011, 29, 8745-8753.	3.8	35
22	Comparative analysis of mRNA and protein degradation in prostate tissues indicates high stability of proteins. Nature Communications, 2019, 10, 2524.	12.8	35
23	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
24	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
25	OptiTope--a 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
26	Novel Machine Learning Methods for MHC Class I Binding Prediction. Lecture Notes in Computer Science, 2010, , 98-109.	1.3	30
27	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
28	NGS-pipe: a flexible, easily extendable and highly configurable framework for NGS analysis. Bioinformatics, 2018, 34, 107-108.	4.1	25
29	Inferring latent task structure for Multitask Learning by Multiple Kernel Learning. BMC Bioinformatics, 2010, 11, S5.	2.6	24
30	Towards <i>in silico</i> design of epitope-based vaccines. Expert Opinion on Drug Discovery, 2009, 4, 1047-1060.	5.0	18
31	Features of Circulating Parainfluenza Virus Required for Growth in Human Airway. MBio, 2016, 7, e00235.	4.1	18
32	SwissMTB: establishing comprehensive molecular cancer diagnostics in Swiss clinics. BMC Medical Informatics and Decision Making, 2018, 18, 89.	3.0	18
33	Exploiting physico-chemical properties in string kernels. BMC Bioinformatics, 2010, 11, S7.	2.6	17
34	Convergent network effects along the axis of gene expression during prostate cancer progression. Genome Biology, 2020, 21, 302.	8.8	17
35	T-cell epitope prediction based on self-tolerance. , 2011, , .		5
36	An exact algorithm for side-chain placement in protein design. Optimization Letters, 2011, 5, 393-406.	1.6	4