Nico Pfeifer

List of Publications by Year
in descending order

57 papers	4,402 citations	201674 27 h-index	149698 56 g-index
65 all docs	65 docs citations	65 times ranked	7584 citing authors

#	Article	IF	Citations
1	Analysis of antibodies from HCV elite neutralizers identifies genetic determinants of broad neutralization. Immunity, 2022, 55, 341-354.e7.	14.3	21
2	Efficient privacy-preserving whole-genome variant queries. Bioinformatics, 2022, 38, 2202-2210.	4.1	5
3	Durability of omicron-neutralising serum activity after mRNA booster immunisation in older adults. Lancet Infectious Diseases, The, 2022, 22, 445-446.	9.1	28
4	Identifying disease-causing mutations with privacy protection. Bioinformatics, 2021, 36, 5205-5213.	4.1	3
5	Adapting the geno2pheno[coreceptor] tool to HIV-1 subtype CRF01_AE by phenotypic validation using clinical isolates from South-East Asia. Journal of Clinical Virology, 2021, 136, 104755.	3.1	1
6	Kinetics and correlates of the neutralizing antibody response to SARS-CoV-2 infection in humans. Cell Host and Microbe, 2021, 29, 917-929.e4.	11.0	132
7	The AIMe registry for artificial intelligence in biomedical research. Nature Methods, 2021, 18, 1128-1131.	19.0	38
8	Evaluation of a Rapid Antigen Test To Detect SARS-CoV-2 Infection and Identify Potentially Infectious Individuals. Journal of Clinical Microbiology, 2021, 59, e0089621.	3.9	55
9	Longitudinal Isolation of Potent Near-Germline SARS-CoV-2-Neutralizing Antibodies from COVID-19 Patients. Cell, 2020, 182, 843-854.e12.	28.9	310
10	openPrimeR for multiplex amplification of highly diverse templates. Journal of Immunological Methods, 2020, 480, 112752.	1.4	36
11	Weighted elastic net for unsupervised domain adaptation with application to age prediction from DNA methylation data. Bioinformatics, 2019, 35, i154-i163.	4.1	11
12	Modeling the Amplification of Immunoglobulins through Machine Learning on Sequence-Specific Features. Scientific Reports, 2019, 9, 10748.	3.3	4
13	Polyclonal and convergent antibody response to Ebola virus vaccine rVSV-ZEBOV. Nature Medicine, 2019, 25, 1589-1600.	30.7	92
14	Unique and assay specific features of NOMe-, ATAC- and DNase I-seq data. Nucleic Acids Research, 2019, 47, 10580-10596.	14.5	31
15	web-rMKL: a web server for dimensionality reduction and sample clustering of multi-view data based on unsupervised multiple kernel learning. Nucleic Acids Research, 2019, 47, W605-W609.	14.5	4
16	A Framework with Randomized Encoding for a Fast Privacy Preserving Calculation of Non-linear Kernels for Machine Learning Applications in Precision Medicine. Lecture Notes in Computer Science, 2019, , 493-511.	1.3	1
17	Whither systems medicine?. Experimental and Molecular Medicine, 2018, 50, e453-e453.	7.7	49
18	geno2pheno[ngs-freq]: a genotypic interpretation system for identifying viral drug resistance using next-generation sequencing data. Nucleic Acids Research, 2018, 46, W271-W277.	14.5	37

#	ARTICLE	IF	CITATIONS
19	Combination therapy with anti-HIV-1 antibodies maintains viral suppression. Nature, 2018, 561, 479-484.	27.8	392
20	Safety and antiviral activity of combination HIV-1 broadly neutralizing antibodies in viremic individuals. Nature Medicine, 2018, 24, 1701-1707.	30.7	195
21	Performance Evaluation of a Genotypic Tropism Test Using HIV-1 CRF01_AE Isolates in Japan. Japanese Journal of Infectious Diseases, 2018, 71, 264-266.	1.2	3
22	XplOit: An Ontology-Based Data Integration Platform Supporting the Development of Predictive Models for Personalized Medicine. Studies in Health Technology and Informatics, 2018, 247, 21-25.	0.3	4
23	Antibody 10-1074 suppresses viremia in HIV-1-infected individuals. Nature Medicine, 2017, 23, 185-191.	30.7	399
24	Genetic sequence-based prediction of long-range chromatin interactions suggests a potential role of short tandem repeat sequences in genome organization. BMC Bioinformatics, 2017, 18, 218.	2.6	15
25	Determination of Phenotypic Resistance Cutoffs From Routine Clinical Data. Journal of Acquired Immune Deficiency Syndromes (1999), 2017, 74, e129-e137.	2.1	3
26	Towards Multiple Kernel Principal Component Analysis for Integrative Analysis of Tumor Samples. Journal of Integrative Bioinformatics, 2017, 14, .	1.5	4
27	Prediction of HIV-1 sensitivity to broadly neutralizing antibodies shows a trend towards resistance over time. PLoS Computational Biology, 2017, 13, e1005789.	3.2	28
28	Using drug exposure for predicting drug resistance â€" A data-driven genotypic interpretation tool. PLoS ONE, 2017, 12, e0174992.	2.5	9
29	Interpretable per case weighted ensemble method for cancer associations. BMC Genomics, 2016, 17, 501.	2.8	5
30	A genotypic method for determining HIV-2 coreceptor usage enables epidemiological studies and clinical decision support. Retrovirology, 2016, 13, 85.	2.0	13
31	Impact of pre-adapted HIV transmission. Nature Medicine, 2016, 22, 606-613.	30.7	87
32	HIV-1 therapy with monoclonal antibody 3BNC117 elicits host immune responses against HIV-1. Science, 2016, 352, 997-1001.	12.6	263
33	Family-Joining: A Fast Distance-Based Method for Constructing Generally Labeled Trees. Molecular Biology and Evolution, 2016, 33, 2720-2734.	8.9	4
34	HIV-1 antibody 3BNC117 suppresses viral rebound in humans during treatment interruption. Nature, 2016, 535, 556-560.	27.8	400
35	Primarily Oseltamivir-Resistant Influenza a (H1N1pdm09) virus Evolving into a Multidrug-Resistant virus Carrying H275Y and I223R Neuraminidase Substitutions. Antiviral Therapy, 2015, 20, 97-100.	1.0	5
36	Identification and analysis of methylation call differences between bisulfite microarray and bisulfite sequencing data with statistical learning techniques. BMC Bioinformatics, 2015, 16, .	2.6	2

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37	Effects of sequence alterations on results from genotypic tropism testing. Journal of Clinical Virology, 2015, 65, 68-73.	3.1	1
38	Integrating different data types by regularized unsupervised multiple kernel learning with application to cancer subtype discovery. Bioinformatics, 2015, 31, i268-i275.	4.1	145
39	CRF19_cpx is an Evolutionary fit HIV-1 Variant Strongly Associated With Rapid Progression to AIDS in Cuba. EBioMedicine, 2015, 2, 244-254.	6.1	56
40	Improved therapy-success prediction with GSS estimated from clinical HIV-1 sequences. Journal of the International AIDS Society, 2014, 17, 19743.	3.0	4
41	Association Between HIV-1 Coreceptor Usage and Resistance to Broadly Neutralizing Antibodies. Journal of Acquired Immune Deficiency Syndromes (1999), 2014, 67, 107-112.	2.1	13
42	Transmitted Escape Mutations Lead to Accelerated HIV-1 Disease Progression and Largely Define the Relative Contribution of HLA Alleles to Control. AIDS Research and Human Retroviruses, 2014, 30, A40-A40.	1.1	0
43	Personalized HIV therapy to control drug resistance. Drug Discovery Today: Technologies, 2014, 11, 57-64.	4.0	23
44	Modelling binding between CCR5 and CXCR4 receptors and their ligands suggests the surface electrostatic potential of the co-receptor to be a key player in the HIV-1 tropism. Retrovirology, 2013, 10, 130.	2.0	24
45	Distinct HIV-1 Escape Patterns Selected by Cytotoxic T Cells with Identical Epitope Specificity. Journal of Virology, 2013, 87, 2253-2263.	3.4	30
46	A genome-to-genome analysis of associations between human genetic variation, HIV-1 sequence diversity, and viral control. ELife, 2013, 2, e01123.	6.0	126
47	Improving HIV coreceptor usage prediction in the clinic using hints from next-generation sequencing data. Bioinformatics, 2012, 28, i589-i595.	4.1	18
48	Correlates of Protective Cellular Immunity Revealed by Analysis of Population-Level Immune Escape Pathways in HIV-1. Journal of Virology, 2012, 86, 13202-13216.	3.4	99
49	Widespread Impact of HLA Restriction on Immune Control and Escape Pathways of HIV-1. Journal of Virology, 2012, 86, 5230-5243.	3.4	114
50	Optimal de novo Design of MRM Experiments for Rapid Assay Development in Targeted Proteomics. Journal of Proteome Research, 2010, 9, 2696-2704.	3.7	40
51	Improving Peptide Identification in Proteome Analysis by a Two-Dimensional Retention Time Filtering Approach. Journal of Proteome Research, 2009, 8, 4109-4115.	3.7	36
52	OpenMS â€" An open-source software framework for mass spectrometry. BMC Bioinformatics, 2008, 9, 163.	2.6	556
53	LC-MSsim â€" a simulation software for liquid chromatography mass spectrometry data. BMC Bioinformatics, 2008, 9, 423.	2.6	42
54	Gradient-Based Optimization of Kernel-Target Alignment for Sequence Kernels Applied to Bacterial Gene Start Detection. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 216-226.	3.0	39

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55	Statistical learning of peptide retention behavior in chromatographic separations: a new kernel-based approach for computational proteomics. BMC Bioinformatics, 2007, 8, 468.	2.6	70
56	TOPP--the OpenMS proteomics pipeline. Bioinformatics, 2007, 23, e191-e197.	4.1	249
57	TICO: a tool for improving predictions of prokaryotic translation initiation sites. Bioinformatics, 2005, 21, 3568-3569.	4.1	23