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	OpenMS â€" An open-source software framework for mass spectrometry. BMC Bioinformatics, 2008, 9, 163.	2.6	556
2	HIV-1 antibody 3BNC117 suppresses viral rebound in humans during treatment interruption. Nature, 2016, 535, 556-560.	27.8	400
3	Antibody 10-1074 suppresses viremia in HIV-1-infected individuals. Nature Medicine, 2017, 23, 185-191.	30.7	399
4	Combination therapy with anti-HIV-1 antibodies maintains viral suppression. Nature, 2018, 561, 479-484.	27.8	392
5	Longitudinal Isolation of Potent Near-Germline SARS-CoV-2-Neutralizing Antibodies from COVID-19 Patients. Cell, 2020, 182, 843-854.e12.	28.9	310
6	HIV-1 therapy with monoclonal antibody 3BNC117 elicits host immune responses against HIV-1. Science, 2016, 352, 997-1001.	12.6	263
7	TOPP--the OpenMS proteomics pipeline. Bioinformatics, 2007, 23, e191-e197.	4.1	249
8	Safety and antiviral activity of combination HIV-1 broadly neutralizing antibodies in viremic individuals. Nature Medicine, 2018, 24, 1701-1707.	30.7	195
9	Integrating different data types by regularized unsupervised multiple kernel learning with application to cancer subtype discovery. Bioinformatics, 2015, 31, i268-i275.	4.1	145
10	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
11	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
12	Widespread Impact of HLA Restriction on Immune Control and Escape Pathways of HIV-1. Journal of Virology, 2012, 86, 5230-5243.	3.4	114
13	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
14	Polyclonal and convergent antibody response to Ebola virus vaccine rVSV-ZEBOV. Nature Medicine, 2019, 25, 1589-1600.	30.7	92
15	Impact of pre-adapted HIV transmission. Nature Medicine, 2016, 22, 606-613.	30.7	87
16	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
17	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
18	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

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19	Whither systems medicine?. Experimental and Molecular Medicine, 2018, 50, e453-e453.	7.7	49
20	LC-MSsim â€" a simulation software for liquid chromatography mass spectrometry data. BMC Bioinformatics, 2008, 9, 423.	2.6	42
21	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
22	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
23	The AIMe registry for artificial intelligence in biomedical research. Nature Methods, 2021, 18, 1128-1131.	19.0	38
24	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
25	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
26	openPrimeR for multiplex amplification of highly diverse templates. Journal of Immunological Methods, 2020, 480, 112752.	1.4	36
27	Unique and assay specific features of NOMe-, ATAC- and DNase I-seq data. Nucleic Acids Research, 2019, 47, 10580-10596.	14.5	31
28	Distinct HIV-1 Escape Patterns Selected by Cytotoxic T Cells with Identical Epitope Specificity. Journal of Virology, 2013, 87, 2253-2263.	3.4	30
29	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
30	Durability of omicron-neutralising serum activity after mRNA booster immunisation in older adults. Lancet Infectious Diseases, The, 2022, 22, 445-446.	9.1	28
31	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
32	TICO: a tool for improving predictions of prokaryotic translation initiation sites. Bioinformatics, 2005, 21, 3568-3569.	4.1	23
33	Personalized HIV therapy to control drug resistance. Drug Discovery Today: Technologies, 2014, 11, 57-64.	4.0	23
34	Analysis of antibodies from HCV elite neutralizers identifies genetic determinants of broad neutralization. Immunity, 2022, 55, 341-354.e7.	14.3	21
35	Improving HIV coreceptor usage prediction in the clinic using hints from next-generation sequencing data. Bioinformatics, 2012, 28, i589-i595.	4.1	18
36	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

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37	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
38	A genotypic method for determining HIV-2 coreceptor usage enables epidemiological studies and clinical decision support. Retrovirology, 2016, 13, 85.	2.0	13
39	Weighted elastic net for unsupervised domain adaptation with application to age prediction from DNA methylation data. Bioinformatics, 2019, 35, i154-i163.	4.1	11
40	Using drug exposure for predicting drug resistance â€" A data-driven genotypic interpretation tool. PLoS ONE, 2017, 12, e0174992.	2.5	9
41	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
42	Interpretable per case weighted ensemble method for cancer associations. BMC Genomics, 2016, 17, 501.	2.8	5
43	Efficient privacy-preserving whole-genome variant queries. Bioinformatics, 2022, 38, 2202-2210.	4.1	5
44	Improved therapy-success prediction with GSS estimated from clinical HIV-1 sequences. Journal of the International AIDS Society, 2014, 17, 19743.	3.0	4
45	Family-Joining: A Fast Distance-Based Method for Constructing Generally Labeled Trees. Molecular Biology and Evolution, 2016, 33, 2720-2734.	8.9	4
46	Towards Multiple Kernel Principal Component Analysis for Integrative Analysis of Tumor Samples. Journal of Integrative Bioinformatics, 2017, 14, .	1.5	4
47	Modeling the Amplification of Immunoglobulins through Machine Learning on Sequence-Specific Features. Scientific Reports, 2019, 9, 10748.	3.3	4
48	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
49	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
50	Determination of Phenotypic Resistance Cutoffs From Routine Clinical Data. Journal of Acquired Immune Deficiency Syndromes (1999), 2017, 74, e129-e137.	2.1	3
51	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
52	Identifying disease-causing mutations with privacy protection. Bioinformatics, 2021, 36, 5205-5213.	4.1	3
53	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
54	Effects of sequence alterations on results from genotypic tropism testing. Journal of Clinical Virology, 2015, 65, 68-73.	3.1	1

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55	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
56	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
57	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