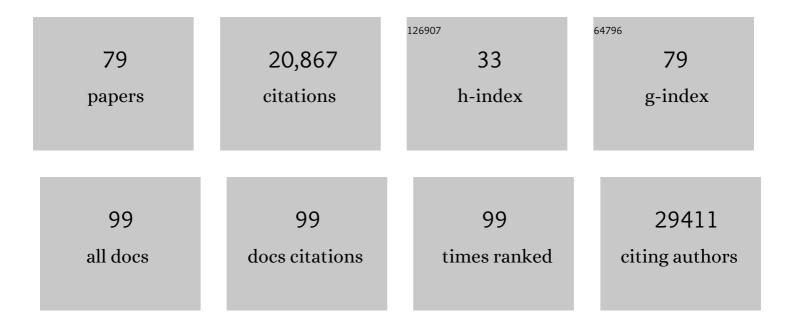
Nicolas Guex

List of Publications by Year in descending order

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NICOLAS CHEY

#	Article	IF	CITATIONS
1	Soil protist function varies with elevation in the Swiss Alps. Environmental Microbiology, 2022, 24, 1689-1702.	3.8	10
2	SPICA: Swiss portal for immune cell analysis. Nucleic Acids Research, 2022, 50, D1109-D1114.	14.5	5
3	Unexpected postâ€glacial colonisation route explains the white colour of barn owls (<i>Tyto alba</i>) from the British Isles. Molecular Ecology, 2022, 31, 482-497.	3.9	11
4	Genomic consequences of colonisation, migration and genetic drift in barn owl insular populations of the eastern Mediterranean. Molecular Ecology, 2022, 31, 1375-1388.	3.9	5
5	Comparative analysis of diversity and environmental niches of soil bacterial, archaeal, fungal and protist communities reveal niche divergences along environmental gradients in the Alps. Soil Biology and Biochemistry, 2022, 169, 108674.	8.8	17
6	Essential role of Cp190 in physical and regulatory boundary formation. Science Advances, 2022, 8, eabl8834.	10.3	27
7	Inhibition of G-protein signalling in cardiac dysfunction of intellectual developmental disorder with cardiac arrhythmia (IDDCA) syndrome. Journal of Medical Genetics, 2021, 58, 815-831.	3.2	3
8	Anti-adipogenic signals at the onset of obesity-related inflammation in white adipose tissue. Cellular and Molecular Life Sciences, 2021, 78, 227-247.	5.4	22
9	Blood virosphere in febrile Tanzanian children. Emerging Microbes and Infections, 2021, 10, 982-993.	6.5	9
10	Mutation-specific pathophysiological mechanisms define different neurodevelopmental disorders associated with SATB1 dysfunction. American Journal of Human Genetics, 2021, 108, 346-356.	6.2	30
11	CTCF loss has limited effects on global genome architecture in Drosophila despite critical regulatory functions. Nature Communications, 2021, 12, 1011.	12.8	60
12	DBnorm as an R package for the comparison and selection of appropriate statistical methods for batch effect correction in metabolomic studies. Scientific Reports, 2021, 11, 5657.	3.3	14
13	Predicting spatial patterns of soil bacteria under current and future environmental conditions. ISME Journal, 2021, 15, 2547-2560.	9.8	27
14	Unsupervised Analysis of Flow Cytometry Data in a Clinical Setting Captures Cell Diversity and Allows Population Discovery. Frontiers in Immunology, 2021, 12, 633910.	4.8	8
15	Variants in <i>USP48</i> encoding ubiquitin hydrolase are associated with autosomal dominant non-syndromic hereditary hearing loss. Human Molecular Genetics, 2021, 30, 1785-1796.	2.9	6
16	Transcriptomic Signature Differences BetweenÂSARS-CoV-2 and Influenza Virus Infected Patients. Frontiers in Immunology, 2021, 12, 666163.	4.8	27
17	Variants in the degron of AFF3 are associated with intellectual disability, mesomelic dysplasia, horseshoe kidney, and epileptic encephalopathy. American Journal of Human Genetics, 2021, 108, 857-873.	6.2	19
18	A single-cell morpho-transcriptomic map of brassinosteroid action in the Arabidopsis root. Molecular Plant, 2021, 14, 1985-1999.	8.3	40

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19	PamgeneAnalyzeR: open and reproducible pipeline for kinase profiling. Bioinformatics, 2020, 36, 5117-5119.	4.1	3
20	Key Parameters of Tumor Epitope Immunogenicity Revealed Through a Consortium Approach Improve Neoantigen Prediction. Cell, 2020, 183, 818-834.e13.	28.9	287
21	Greater topoclimatic control of above―versus belowâ€ground communities. Global Change Biology, 2020, 26, 6715-6728.	9.5	11
22	Virosaurus A Reference to Explore and Capture Virus Genetic Diversity. Viruses, 2020, 12, 1248.	3.3	9
23	1-Deoxydihydroceramide causes anoxic death by impairing chaperonin-mediated protein folding. Nature Metabolism, 2019, 1, 996-1008.	11.9	15
24	Differential regulation of RNA polymerase III genes during liver regeneration. Nucleic Acids Research, 2019, 47, 1786-1796.	14.5	12
25	Rapid Recapitulation of Nonalcoholic Steatohepatitis upon Loss of Host Cell Factor 1 Function in Mouse Hepatocytes. Molecular and Cellular Biology, 2019, 39, .	2.3	11
26	Neighbor predation linked to natural competence fosters the transfer of large genomic regions in Vibrio cholerae. ELife, 2019, 8, .	6.0	49
27	Intellectual developmental disorder with cardiac arrhythmia syndrome in a child with compound heterozygous <i>GNB5</i> variants. Clinical Genetics, 2018, 93, 1254-1256.	2.0	11
28	KIAA1109 Variants Are Associated with a Severe Disorder of Brain Development and Arthrogryposis. American Journal of Human Genetics, 2018, 102, 116-132.	6.2	46
29	Towards in the Field Fast Pathogens Detection Using FPGAs. , 2018, , .		0
30	Cycles of gene expression and genome response during mammalian tissue regeneration. Epigenetics and Chromatin, 2018, 11, 52.	3.9	13
31	A systems genetics resource and analysis of sleep regulation in the mouse. PLoS Biology, 2018, 16, e2005750.	5.6	51
32	Cell-free DNA testing of an extended range of chromosomal anomalies: clinical experience with 6,388 consecutive cases. Genetics in Medicine, 2017, 19, 169-175.	2.4	82
33	Genomic Data Clustering on FPGAs for Compression. Lecture Notes in Computer Science, 2017, , 229-240.	1.3	1
34	Diurnal regulation of RNA polymerase III transcription is under the control of both the feeding–fasting response and the circadian clock. Genome Research, 2017, 27, 973-984.	5.5	27
35	Neutrophils and Snail Orchestrate the Establishment of a Pro-tumor Microenvironment in Lung Cancer. Cell Reports, 2017, 21, 3190-3204.	6.4	167
36	Segregated hepatocyte proliferation and metabolic states within the regenerating mouse liver. Hepatology Communications, 2017, 1, 871-885.	4.3	13

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37	GNB5 Mutations Cause an Autosomal-Recessive Multisystem Syndrome with Sinus Bradycardia and Cognitive Disability. American Journal of Human Genetics, 2016, 99, 704-710.	6.2	58
38	Identification of a RAI1-associated disease network through integration of exome sequencing, transcriptomics, and 3D genomics. Genome Medicine, 2016, 8, 105.	8.2	20
39	De novo PIK3R2 variant causes polymicrogyria, corpus callosum hyperplasia and focal cortical dysplasia. European Journal of Human Genetics, 2016, 24, 1359-1362.	2.8	26
40	The SIB Swiss Institute of Bioinformatics' resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	14.5	64
41	TIE-2-expressing monocytes are lymphangiogenic and associate specifically with lymphatics of human breast cancer. Oncolmmunology, 2016, 5, e1073882.	4.6	37
42	West syndrome caused by homozygous variant in the evolutionary conserved gene encoding the mitochondrial elongation factor GUF1. European Journal of Human Genetics, 2016, 24, 1001-1008.	2.8	10
43	Differential Dimerization of Variants Linked to Enhanced S-Cone Sensitivity Syndrome (ESCS) Located in the NR2E3 Ligand-Binding Domain. Human Mutation, 2015, 36, 599-610.	2.5	15
44	Angiogenic Activity of Breast Cancer Patients' Monocytes Reverted by Combined Use of Systems Modeling and Experimental Approaches. PLoS Computational Biology, 2015, 11, e1004050.	3.2	18
45	Wnt directs the endosomal flux of <scp>LDL</scp> â€derived cholesterol and lipid droplet homeostasis. EMBO Reports, 2015, 16, 741-752.	4.5	43
46	Quantifying ChIP-seq data: a spiking method providing an internal reference for sample-to-sample normalization. Genome Research, 2014, 24, 1157-1168.	5.5	143
47	Genome-Wide Analysis of SREBP1 Activity around the Clock Reveals Its Combined Dependency on Nutrient and Circadian Signals. PLoS Genetics, 2014, 10, e1004155.	3.5	45
48	Soil fungal communities of grasslands are environmentally structured at a regional scale in the <scp>A</scp> lps. Molecular Ecology, 2014, 23, 4274-4290.	3.9	125
49	A robust secondâ€generation genomeâ€wide test for fetal aneuploidy based on shotgun sequencing cellâ€free DNA in maternal blood. Prenatal Diagnosis, 2013, 33, 707-710.	2.3	49
50	Plant species distributions along environmental gradients: do belowground interactions with fungi matter?. Frontiers in Plant Science, 2013, 4, 500.	3.6	38
51	Recurrent Structural Motifs in Non-Homologous Protein Structures. International Journal of Molecular Sciences, 2013, 14, 7795-7814.	4.1	5
52	Density-based hierarchical clustering of pyro-sequences on a large scale—the case of fungal ITS1. Bioinformatics, 2013, 29, 1268-1274.	4.1	19
53	TIE-2 and VEGFR Kinase Activities Drive Immunosuppressive Function of TIE-2–Expressing Monocytes in Human Breast Tumors. Clinical Cancer Research, 2013, 19, 3439-3449.	7.0	32
54	PPARβ Interprets a Chromatin Signature of Pluripotency to Promote Embryonic Differentiation at Gastrulation. PLoS ONE, 2013, 8, e83300.	2.5	7

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55	Genome-Wide RNA Polymerase II Profiles and RNA Accumulation Reveal Kinetics of Transcription and Associated Epigenetic Changes During Diurnal Cycles. PLoS Biology, 2012, 10, e1001442.	5.6	178
56	A multiplicity of factors contributes to selective RNA polymerase III occupancy of a subset of RNA polymerase III genes in mouse liver. Genome Research, 2012, 22, 666-680.	5.5	56
57	Defining and searching for structural motifs using DeepView/Swiss-PdbViewer. BMC Bioinformatics, 2012, 13, 173.	2.6	260
58	A Missense Mutation in Myelin Oligodendrocyte Glycoprotein as a Cause of Familial Narcolepsy with Cataplexy. American Journal of Human Genetics, 2012, 91, 396.	6.2	0
59	A Missense Mutation in Myelin Oligodendrocyte Glycoprotein as a Cause of Familial Narcolepsy with Cataplexy. American Journal of Human Genetics, 2011, 89, 474-479.	6.2	55
60	Hyaline Fibromatosis Syndrome inducing mutations in the ectodomain of anthrax toxin receptor 2 can be rescued by proteasome inhibitors. EMBO Molecular Medicine, 2011, 3, 208-221.	6.9	45
61	Multiple Imputations Applied to the DREAM3 Phosphoproteomics Challenge: A Winning Strategy. PLoS ONE, 2010, 5, e8012.	2.5	6
62	Evolutionary Trajectories of Primate Genes Involved in HIV Pathogenesis. Molecular Biology and Evolution, 2009, 26, 2865-2875.	8.9	50
63	Automated comparative protein structure modeling with SWISSâ€MODEL and Swissâ€PdbViewer: A historical perspective. Electrophoresis, 2009, 30, S162-73.	2.4	1,574
64	Natural variation of potato allene oxide synthase 2 causes differential levels of jasmonates and pathogen resistance in Arabidopsis. Planta, 2008, 228, 293-306.	3.2	48
65	Expression, purification, and characterization of multiple, multifunctional human glucocorticoid receptor proteins. Protein Expression and Purification, 2008, 62, 29-35.	1.3	7
66	High-Throughput SHAPE Analysis Reveals Structures in HIV-1 Genomic RNA Strongly Conserved across Distinct Biological States. PLoS Biology, 2008, 6, e96.	5.6	351
67	ShapeFinder: A software system for high-throughput quantitative analysis of nucleic acid reactivity information resolved by capillary electrophoresis. Rna, 2008, 14, 1979-1990.	3.5	209
68	A Geographic Variant of the <i>Staphylococcus aureus</i> Pantonâ€Valentine Leukocidin Toxin and the Origin of Communityâ€Associated Methicillinâ€Resistant <i>S. aureus</i> USA300. Journal of Infectious Diseases, 2008, 197, 187-194.	4.0	66
69	Modeling the pore structure of voltage-gated sodium channels in closed, open, and fast-inactivated conformation reveals details of site 1 toxin and local anesthetic binding. Journal of Molecular Modeling, 2006, 12, 813-822.	1.8	36
70	SWISS-MODEL: an automated protein homology-modeling server. Nucleic Acids Research, 2003, 31, 3381-3385.	14.5	4,722
71	Protein Tertiary Structure Modeling. Current Protocols in Protein Science, 2001, 23, Unit2.8.	2.8	3
72	Automated protein modelling - the proteome in 3D. Pharmacogenomics, 2000, 1, 257-266.	1.3	49

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73	Protein structure computing in the genomic era. Research in Microbiology, 2000, 151, 107-112.	2.1	111
74	Protein modelling for all. Trends in Biochemical Sciences, 1999, 24, 364-367.	7.5	452
75	Loss of LKB1 Kinase Activity in Peutz-Jeghers Syndrome, and Evidence for Allelic and Locus Heterogeneity. American Journal of Human Genetics, 1998, 63, 1641-1650.	6.2	194
76	New Insulin-Like Proteins with Atypical Disulfide Bond Pattern Characterized in <i>Caenorhabditis elegans</i> by Comparative Sequence Analysis and Homology Modeling. Genome Research, 1998, 8, 348-353.	5.5	138
77	SWISSâ€MODEL and the Swissâ€₽db Viewer: An environment for comparative protein modeling. Electrophoresis, 1997, 18, 2714-2723.	2.4	10,267
78	Large-Scale Comparative Protein Modelling. Principles and Practice, 1997, , 177-186.	0.3	6
79	Glyoxysomal malate dehydrogenase and malate synthase from soybean cotyledons (Clycine max L.): enzyme association, antibody production and cDNA cloning. Planta, 1995, 197, 369-75.	3.2	39