

# Nicolas Guex

## List of Publications by Year in descending order

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79  
papers

20,867  
citations

145106

33  
h-index

73587

79  
g-index

99  
all docs

99  
docs citations

99  
times ranked

32596  
citing authors

#	ARTICLE	IF	CITATIONS
1	Soil protist function varies with elevation in the Swiss Alps. <i>Environmental Microbiology</i> , 2022, 24, 1689-1702.	1.8	10
2	SPICA: Swiss portal for immune cell analysis. <i>Nucleic Acids Research</i> , 2022, 50, D1109-D1114.	6.5	5
3	Unexpected post-glacial colonisation route explains the white colour of barn owls ( <i>Tyto alba</i> ) from the British Isles. <i>Molecular Ecology</i> , 2022, 31, 482-497.	2.0	11
4	Genomic consequences of colonisation, migration and genetic drift in barn owl insular populations of the eastern Mediterranean. <i>Molecular Ecology</i> , 2022, 31, 1375-1388.	2.0	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. <i>Soil Biology and Biochemistry</i> , 2022, 169, 108674.	4.2	17
6	Essential role of Cp190 in physical and regulatory boundary formation. <i>Science Advances</i> , 2022, 8, eabl8834.	4.7	27
7	Inhibition of G-protein signalling in cardiac dysfunction of intellectual developmental disorder with cardiac arrhythmia (IDDC) syndrome. <i>Journal of Medical Genetics</i> , 2021, 58, 815-831.	1.5	3
8	Anti-adipogenic signals at the onset of obesity-related inflammation in white adipose tissue. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 227-247.	2.4	22
9	Blood virosphere in febrile Tanzanian children. <i>Emerging Microbes and Infections</i> , 2021, 10, 982-993.	3.0	9
10	Mutation-specific pathophysiological mechanisms define different neurodevelopmental disorders associated with SATB1 dysfunction. <i>American Journal of Human Genetics</i> , 2021, 108, 346-356.	2.6	30
11	CTCF loss has limited effects on global genome architecture in <i>Drosophila</i> despite critical regulatory functions. <i>Nature Communications</i> , 2021, 12, 1011.	5.8	60
12	DBnorm as an R package for the comparison and selection of appropriate statistical methods for batch effect correction in metabolomic studies. <i>Scientific Reports</i> , 2021, 11, 5657.	1.6	14
13	Predicting spatial patterns of soil bacteria under current and future environmental conditions. <i>ISME Journal</i> , 2021, 15, 2547-2560.	4.4	27
14	Unsupervised Analysis of Flow Cytometry Data in a Clinical Setting Captures Cell Diversity and Allows Population Discovery. <i>Frontiers in Immunology</i> , 2021, 12, 633910.	2.2	8
15	Variants in <i>USP48</i> encoding ubiquitin hydrolase are associated with autosomal dominant non-syndromic hereditary hearing loss. <i>Human Molecular Genetics</i> , 2021, 30, 1785-1796.	1.4	6
16	Transcriptomic Signature Differences Between SARS-CoV-2 and Influenza Virus Infected Patients. <i>Frontiers in Immunology</i> , 2021, 12, 666163.	2.2	27
17	Variants in the degron of <i>AFF3</i> are associated with intellectual disability, mesomelic dysplasia, horseshoe kidney, and epileptic encephalopathy. <i>American Journal of Human Genetics</i> , 2021, 108, 857-873.	2.6	19
18	A single-cell morpho-transcriptomic map of brassinosteroid action in the <i>Arabidopsis</i> root. <i>Molecular Plant</i> , 2021, 14, 1985-1999.	3.9	40

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19	PamgeneAnalyzer: open and reproducible pipeline for kinase profiling. <i>Bioinformatics</i> , 2020, 36, 5117-5119.	1.8	3
20	Key Parameters of Tumor Epitope Immunogenicity Revealed Through a Consortium Approach Improve Neoantigen Prediction. <i>Cell</i> , 2020, 183, 818-834.e13.	13.5	287
21	Greater topoclimatic control of above- versus below-ground communities. <i>Global Change Biology</i> , 2020, 26, 6715-6728.	4.2	11
22	Virosaurus A Reference to Explore and Capture Virus Genetic Diversity. <i>Viruses</i> , 2020, 12, 1248.	1.5	9
23	1-Deoxydihydroceramide causes anoxic death by impairing chaperonin-mediated protein folding. <i>Nature Metabolism</i> , 2019, 1, 996-1008.	5.1	15
24	Differential regulation of RNA polymerase III genes during liver regeneration. <i>Nucleic Acids Research</i> , 2019, 47, 1786-1796.	6.5	12
25	Rapid Recapitulation of Nonalcoholic Steatohepatitis upon Loss of Host Cell Factor 1 Function in Mouse Hepatocytes. <i>Molecular and Cellular Biology</i> , 2019, 39, .	1.1	11
26	Neighbor predation linked to natural competence fosters the transfer of large genomic regions in <i>Vibrio cholerae</i> . <i>ELife</i> , 2019, 8, .	2.8	49
27	Intellectual developmental disorder with cardiac arrhythmia syndrome in a child with compound heterozygous <i>GNB5</i> variants. <i>Clinical Genetics</i> , 2018, 93, 1254-1256.	1.0	11
28	KIAA1109 Variants Are Associated with a Severe Disorder of Brain Development and Arthrogryposis. <i>American Journal of Human Genetics</i> , 2018, 102, 116-132.	2.6	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. <i>Epigenetics and Chromatin</i> , 2018, 11, 52.	1.8	13
31	A systems genetics resource and analysis of sleep regulation in the mouse. <i>PLoS Biology</i> , 2018, 16, e2005750.	2.6	51
32	Cell-free DNA testing of an extended range of chromosomal anomalies: clinical experience with 6,388 consecutive cases. <i>Genetics in Medicine</i> , 2017, 19, 169-175.	1.1	82
33	Genomic Data Clustering on FPGAs for Compression. <i>Lecture Notes in Computer Science</i> , 2017, , 229-240.	1.0	1
34	Diurnal regulation of RNA polymerase III transcription is under the control of both the feeding- fasting response and the circadian clock. <i>Genome Research</i> , 2017, 27, 973-984.	2.4	27
35	Neutrophils and Snail Orchestrate the Establishment of a Pro-tumor Microenvironment in Lung Cancer. <i>Cell Reports</i> , 2017, 21, 3190-3204.	2.9	167
36	Segregated hepatocyte proliferation and metabolic states within the regenerating mouse liver. <i>Hepatology Communications</i> , 2017, 1, 871-885.	2.0	13

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37	GNB5 Mutations Cause an Autosomal-Recessive Multisystem Syndrome with Sinus Bradycardia and Cognitive Disability. <i>American Journal of Human Genetics</i> , 2016, 99, 704-710.	2.6	58
38	Identification of a RAI1-associated disease network through integration of exome sequencing, transcriptomics, and 3D genomics. <i>Genome Medicine</i> , 2016, 8, 105.	3.6	20
39	De novo PIK3R2 variant causes polymicrogyria, corpus callosum hyperplasia and focal cortical dysplasia. <i>European Journal of Human Genetics</i> , 2016, 24, 1359-1362.	1.4	26
40	The SIB Swiss Institute of Bioinformaticsâ€™ resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016, 44, D27-D37.	6.5	64
41	TIE-2-expressing monocytes are lymphangiogenic and associate specifically with lymphatics of human breast cancer. <i>OncImmunology</i> , 2016, 5, e1073882.	2.1	37
42	West syndrome caused by homozygous variant in the evolutionary conserved gene encoding the mitochondrial elongation factor GUF1. <i>European Journal of Human Genetics</i> , 2016, 24, 1001-1008.	1.4	10
43	Differential Dimerization of Variants Linked to Enhanced S-Cone Sensitivity Syndrome (ESCS) Located in the NR2E3 Ligand-Binding Domain. <i>Human Mutation</i> , 2015, 36, 599-610.	1.1	15
44	Angiogenic Activity of Breast Cancer Patientsâ€™ Monocytes Reverted by Combined Use of Systems Modeling and Experimental Approaches. <i>PLoS Computational Biology</i> , 2015, 11, e1004050.	1.5	18
45	Wnt directs the endosomal flux of <sc>LDL</sc> â€derived cholesterol and lipid droplet homeostasis. <i>EMBO Reports</i> , 2015, 16, 741-752.	2.0	43
46	Quantifying ChIP-seq data: a spiking method providing an internal reference for sample-to-sample normalization. <i>Genome Research</i> , 2014, 24, 1157-1168.	2.4	143
47	Genome-Wide Analysis of SREBP1 Activity around the Clock Reveals Its Combined Dependency on Nutrient and Circadian Signals. <i>PLoS Genetics</i> , 2014, 10, e1004155.	1.5	45
48	Soil fungal communities of grasslands are environmentally structured at a regional scale in the <sc>A</sc>ps. <i>Molecular Ecology</i> , 2014, 23, 4274-4290.	2.0	125
49	A robust secondâ€generation genomeâ€wide test for fetal aneuploidy based on shotgun sequencing cellâ€free DNA in maternal blood. <i>Prenatal Diagnosis</i> , 2013, 33, 707-710.	1.1	49
50	Plant species distributions along environmental gradients: do belowground interactions with fungi matter?. <i>Frontiers in Plant Science</i> , 2013, 4, 500.	1.7	38
51	Recurrent Structural Motifs in Non-Homologous Protein Structures. <i>International Journal of Molecular Sciences</i> , 2013, 14, 7795-7814.	1.8	5
52	Density-based hierarchical clustering of pyro-sequences on a large scaleâ€the case of fungal ITS1. <i>Bioinformatics</i> , 2013, 29, 1268-1274.	1.8	19
53	TIE-2 and VEGFR Kinase Activities Drive Immunosuppressive Function of TIE-2â€Expressing Monocytes in Human Breast Tumors. <i>Clinical Cancer Research</i> , 2013, 19, 3439-3449.	3.2	32
54	PPARÎ² Interprets a Chromatin Signature of Pluripotency to Promote Embryonic Differentiation at Gastrulation. <i>PLoS ONE</i> , 2013, 8, e83300.	1.1	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. <i>PLoS Biology</i> , 2012, 10, e1001442.	2.6	178
56	A multiplicity of factors contributes to selective RNA polymerase III occupancy of a subset of RNA polymerase III genes in mouse liver. <i>Genome Research</i> , 2012, 22, 666-680.	2.4	56
57	Defining and searching for structural motifs using DeepView/Swiss-PdbViewer. <i>BMC Bioinformatics</i> , 2012, 13, 173.	1.2	260
58	A Missense Mutation in Myelin Oligodendrocyte Glycoprotein as a Cause of Familial Narcolepsy with Cataplexy. <i>American Journal of Human Genetics</i> , 2012, 91, 396.	2.6	0
59	A Missense Mutation in Myelin Oligodendrocyte Glycoprotein as a Cause of Familial Narcolepsy with Cataplexy. <i>American Journal of Human Genetics</i> , 2011, 89, 474-479.	2.6	55
60	Hyaline Fibromatosis Syndrome inducing mutations in the ectodomain of anthrax toxin receptor 2 can be rescued by proteasome inhibitors. <i>EMBO Molecular Medicine</i> , 2011, 3, 208-221.	3.3	45
61	Multiple Imputations Applied to the DREAM3 Phosphoproteomics Challenge: A Winning Strategy. <i>PLoS ONE</i> , 2010, 5, e8012.	1.1	6
62	Evolutionary Trajectories of Primate Genes Involved in HIV Pathogenesis. <i>Molecular Biology and Evolution</i> , 2009, 26, 2865-2875.	3.5	50
63	Automated comparative protein structure modeling with SWISS-MODEL and Swiss-PdbViewer: A historical perspective. <i>Electrophoresis</i> , 2009, 30, S162-73.	1.3	1,574
64	Natural variation of potato allene oxide synthase 2 causes differential levels of jasmonates and pathogen resistance in <i>Arabidopsis</i> . <i>Planta</i> , 2008, 228, 293-306.	1.6	48
65	Expression, purification, and characterization of multiple, multifunctional human glucocorticoid receptor proteins. <i>Protein Expression and Purification</i> , 2008, 62, 29-35.	0.6	7
66	High-Throughput SHAPE Analysis Reveals Structures in HIV-1 Genomic RNA Strongly Conserved across Distinct Biological States. <i>PLoS Biology</i> , 2008, 6, e96.	2.6	351
67	ShapeFinder: A software system for high-throughput quantitative analysis of nucleic acid reactivity information resolved by capillary electrophoresis. <i>Rna</i> , 2008, 14, 1979-1990.	1.6	209
68	A Geographic Variant of the <i>Staphylococcus aureus</i> Pantón-Valentine Leukocidin Toxin and the Origin of Community-Associated Methicillin-Resistant <i>S. aureus</i> USA300. <i>Journal of Infectious Diseases</i> , 2008, 197, 187-194.	1.9	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. <i>Journal of Molecular Modeling</i> , 2006, 12, 813-822.	0.8	36
70	SWISS-MODEL: an automated protein homology-modeling server. <i>Nucleic Acids Research</i> , 2003, 31, 3381-3385.	6.5	4,722
71	Protein Tertiary Structure Modeling. <i>Current Protocols in Protein Science</i> , 2001, 23, Unit2.8.	2.8	3
72	Automated protein modelling - the proteome in 3D. <i>Pharmacogenomics</i> , 2000, 1, 257-266.	0.6	49

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73	Protein structure computing in the genomic era. <i>Research in Microbiology</i> , 2000, 151, 107-112.	1.0	111
74	Protein modelling for all. <i>Trends in Biochemical Sciences</i> , 1999, 24, 364-367.	3.7	452
75	Loss of LKB1 Kinase Activity in Peutz-Jeghers Syndrome, and Evidence for Allelic and Locus Heterogeneity. <i>American Journal of Human Genetics</i> , 1998, 63, 1641-1650.	2.6	194
76	New Insulin-Like Proteins with Atypical Disulfide Bond Pattern Characterized in <i>Caenorhabditis elegans</i> by Comparative Sequence Analysis and Homology Modeling. <i>Genome Research</i> , 1998, 8, 348-353.	2.4	138
77	SWISS-MODEL and the Swiss-Pdb Viewer: An environment for comparative protein modeling. <i>Electrophoresis</i> , 1997, 18, 2714-2723.	1.3	10,267
78	Large-Scale Comparative Protein Modelling. <i>Principles and Practice</i> , 1997, , 177-186.	0.3	6
79	Glyoxysomal malate dehydrogenase and malate synthase from soybean cotyledons ( <i>Glycine max</i> L.): enzyme association, antibody production and cDNA cloning. <i>Planta</i> , 1995, 197, 369-75.	1.6	39