

Kay Nieselt

List of Publications by Year in descending order

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84
papers

4,842
citations

117625

34
h-index

106344

65
g-index

93
all docs

93
docs citations

93
times ranked

7741
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolutionary Processes in the Emergence and Recent Spread of the Syphilis Agent, <i>Treponema pallidum</i> . <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	16
2	Secondary Metabolite Transcriptomic Pipeline (SeMa-Trap), an expression-based exploration tool for increased secondary metabolite production in bacteria. <i>Nucleic Acids Research</i> , 2022, 50, W682-W689.	14.5	5
3	DamageProfiler: fast damage pattern calculation for ancient DNA. <i>Bioinformatics</i> , 2021, 37, 3652-3653.	4.1	42
4	The Ancient Operational Code is Embedded in the Amino Acid Substitution Matrix and aaRS Phylogenies. <i>Journal of Molecular Evolution</i> , 2020, 88, 136-150.	1.8	9
5	Semantic segmentation of cerebrospinal fluid and brain volume with a convolutional neural network in pediatric hydrocephalus—transfer learning from existing algorithms. <i>Acta Neurochirurgica</i> , 2020, 162, 2463-2474.	1.7	18
6	The Genome of <i>Staphylococcus epidermidis</i> O47. <i>Frontiers in Microbiology</i> , 2020, 11, 2061.	3.5	13
7	2000-year-old pathogen genomes reconstructed from metagenomic analysis of Egyptian mummified individuals. <i>BMC Biology</i> , 2020, 18, 108.	3.8	29
8	The Neuromodulator-Encoding <i>sadA</i> Gene Is Widely Distributed in the Human Skin Microbiome. <i>Frontiers in Microbiology</i> , 2020, 11, 573679.	3.5	9
9	Trace amines produced by skin bacteria accelerate wound healing in mice. <i>Communications Biology</i> , 2020, 3, 277.	4.4	32
10	Draft Genome Sequence of <i>Ochrobactrum</i> sp. Strain MC-1LL, a Bacterial Strain with Antimicrobial Properties, Isolated from Marine Sediments in Nigeria. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
11	Enzyme-Constrained Models and Omics Analysis of <i>Streptomyces coelicolor</i> Reveal Metabolic Changes that Enhance Heterologous Production. <i>IScience</i> , 2020, 23, 101525.	4.1	30
12	MpsAB is important for <i>Staphylococcus aureus</i> virulence and growth at atmospheric CO ₂ levels. <i>Nature Communications</i> , 2019, 10, 3627.	12.8	22
13	Differential transcriptome analysis of enterohemorrhagic <i>Escherichia coli</i> strains reveals differences in response to plant-derived compounds. <i>BMC Microbiology</i> , 2019, 19, 212.	3.3	6
14	The Draft Whole-Genome Sequence of the Antibiotic Producer <i>Empedobacter haloabium</i> ATCC 31962 Provides Indications for Its Taxonomic Reclassification. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
15	Inferring genetic origins and phenotypic traits of George Bähr, the architect of the Dresden Frauenkirche. <i>Scientific Reports</i> , 2018, 8, 2115.	3.3	11
16	Aureo Wiki – The repository of the <i>Staphylococcus aureus</i> research and annotation community. <i>International Journal of Medical Microbiology</i> , 2018, 308, 558-568.	3.6	99
17	Belowground fungal community diversity and composition associated with Norway spruce along an altitudinal gradient. <i>PLoS ONE</i> , 2018, 13, e0208493.	2.5	19
18	Molecular characterization of <i>Treponema pallidum</i> subsp. <i>pallidum</i> in Switzerland and France with a new multilocus sequence typing scheme. <i>PLoS ONE</i> , 2018, 13, e0200773.	2.5	55

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19	Reanalysis of Chinese <i>Treponema pallidum</i> samples: all Chinese samples cluster with SS14-like group of syphilis-causing treponemes. <i>BMC Research Notes</i> , 2018, 11, 16.	1.4	6
20	Ancient genomes reveal a high diversity of <i>Mycobacterium leprae</i> in medieval Europe. <i>PLoS Pathogens</i> , 2018, 14, e1006997.	4.7	98
21	DACCOR—Detection, characterization, and reconstruction of repetitive regions in bacterial genomes. <i>PeerJ</i> , 2018, 6, e4742.	2.0	3
22	Fast and simple protein-alignment-guided assembly of orthologous gene families from microbiome sequencing reads. <i>Microbiome</i> , 2017, 5, 11.	11.1	31
23	Expression of Desmoglein 2, Desmocollin 3 and Plakophilin 2 in Placenta and Bone Marrow-Derived Mesenchymal Stromal Cells. <i>Stem Cell Reviews and Reports</i> , 2017, 13, 258-266.	5.6	5
24	Origin of modern syphilis and emergence of a pandemic <i>Treponema pallidum</i> cluster. <i>Nature Microbiology</i> , 2017, 2, 16245.	13.3	138
25	Ancient Egyptian mummy genomes suggest an increase of Sub-Saharan African ancestry in post-Roman periods. <i>Nature Communications</i> , 2017, 8, 15694.	12.8	131
26	dRNA-seq transcriptional profiling of the FK506 biosynthetic gene cluster in <i>Streptomyces tsukubaensis</i> NRRL18488 and general analysis of the transcriptome. <i>RNA Biology</i> , 2017, 14, 1617-1626.	3.1	14
27	Improving ancient DNA genome assembly. <i>PeerJ</i> , 2017, 5, e3126.	2.0	15
28	EAGER: efficient ancient genome reconstruction. <i>Genome Biology</i> , 2016, 17, 60.	8.8	305
29	Bone marrow-derived mesenchymal stromal cells differ in their attachment to fibronectin-derived peptides from term placenta-derived mesenchymal stromal cells. <i>Stem Cell Research and Therapy</i> , 2016, 7, 29.	5.5	13
30	Pan-Tetris: an interactive visualisation for Pan-genomes. <i>BMC Bioinformatics</i> , 2015, 16, S3.	2.6	22
31	A Whole-Genome Microarray Study of <i>Arabidopsis thaliana</i> Semisolid Callus Cultures Exposed to Microgravity and Nonmicrogravity Related Spaceflight Conditions for 5 Days on Board of Shenzhou 8. <i>BioMed Research International</i> , 2015, 2015, 1-15.	1.9	42
32	A Novel Point Mutation Promotes Growth Phase-Dependent Daptomycin Tolerance in <i>Staphylococcus aureus</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 5366-5376.	3.2	90
33	Differential RNA-seq (dRNA-seq) for annotation of transcriptional start sites and small RNAs in <i>Helicobacter pylori</i> . <i>Methods</i> , 2015, 86, 89-101.	3.8	47
34	Emergence of Coding and its Specificity as a Physico-Informatic Problem. <i>Origins of Life and Evolution of Biospheres</i> , 2015, 45, 249-255.	1.9	18
35	Insight into the evolution and origin of leprosy bacilli from the genome sequence of <i>Mycobacterium lepromatosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4459-4464.	7.1	134
36	Parallel detection of ancient pathogens via array-based DNA capture. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130375.	4.0	38

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37	Global Transcriptional Start Site Mapping Using Differential RNA Sequencing Reveals Novel Antisense RNAs in Escherichia coli. Journal of Bacteriology, 2015, 197, 18-28.	2.2	287
38	Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. Nature, 2014, 514, 494-497.	27.8	506
39	inPHAP: Interactive visualization of genotype and phased haplotype data. BMC Bioinformatics, 2014, 15, 200.	2.6	9
40	Mycobacterium leprae genomes from a British medieval leprosy hospital: towards understanding an ancient epidemic. BMC Genomics, 2014, 15, 270.	2.8	60
41	Altering gene expression by aminocoumarins: the role of DNA supercoiling in Staphylococcus aureus. BMC Genomics, 2014, 15, 291.	2.8	22
42	Metabolic and transcriptional activities of Staphylococcus aureus challenged with high-doses of daptomycin. International Journal of Medical Microbiology, 2014, 304, 931-940.	3.6	22
43	Low Osteogenic Differentiation Potential of Placenta-Derived Mesenchymal Stromal Cells Correlates with Low Expression of the Transcription Factors Runx2 and Twist2. Stem Cells and Development, 2013, 22, 2859-2872.	2.1	42
44	Visualizing dimensionality reduction of systems biology data. Data Mining and Knowledge Discovery, 2013, 27, 146-165.	3.7	5
45	High-Resolution Transcriptome Maps Reveal Strain-Specific Regulatory Features of Multiple Campylobacter jejuni Isolates. PLoS Genetics, 2013, 9, e1003495.	3.5	260
46	Genome-Wide Comparison of Medieval and Modern <i>Mycobacterium leprae</i> . Science, 2013, 341, 179-183.	12.6	313
47	Characterization of a <i>mazEF</i> Toxin-Antitoxin Homologue from Staphylococcus equorum. Journal of Bacteriology, 2013, 195, 115-125.	2.2	33
48	Non-coding RNA, Prediction. , 2013, , 1534-1538.		0
49	REVEAL--visual eQTL analytics. Bioinformatics, 2012, 28, i542-i548.	4.1	0
50	Phylogeny of the Staphylococcal Major Autolysin and Its Use in Genus and Species Typing. Journal of Bacteriology, 2012, 194, 2630-2636.	2.2	29
51	Metabolic Switches and Adaptations Deduced from the Proteomes of Streptomyces coelicolor Wild Type and <i>phoP</i> Mutant Grown in Batch Culture. Molecular and Cellular Proteomics, 2012, 11, M111.013797.	3.8	54
52	Yersinia pestis: New Evidence for an Old Infection. PLoS ONE, 2012, 7, e49803.	2.5	33
53	Transcriptomic studies of phosphate control of primary and secondary metabolism in Streptomyces coelicolor. Applied Microbiology and Biotechnology, 2012, 95, 61-75.	3.6	45
54	iHAT: interactive Hierarchical Aggregation Table for Genetic Association Data. BMC Bioinformatics, 2012, 13, S2.	2.6	16

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55	An eQTL biological data visualization challenge and approaches from the visualization community. BMC Bioinformatics, 2012, 13, S8.	2.6	9
56	iHAT: Interactive hierarchical aggregation table. , 2011, , .		2
57	TIALA — Time series alignment analysis. , 2011, , .		4
58	Mayday SeaSight: Combined Analysis of Deep Sequencing and Microarray Data. PLoS ONE, 2011, 6, e16345.	2.5	17
59	The PII protein GlnK is a pleiotropic regulator for morphological differentiation and secondary metabolism in Streptomyces coelicolor. Applied Microbiology and Biotechnology, 2011, 92, 1219-1236.	3.6	34
60	nocoRNac: Characterization of non-coding RNAs in prokaryotes. BMC Bioinformatics, 2011, 12, 40.	2.6	39
61	MGV: a generic graph viewer for comparative omics data. Bioinformatics, 2011, 27, 2248-2255.	4.1	13
62	Mayday - integrative analytics for expression data. BMC Bioinformatics, 2010, 11, 121.	2.6	102
63	The dynamic architecture of the metabolic switch in Streptomyces coelicolor. BMC Genomics, 2010, 11, 10.	2.8	171
64	Phosphoglycerate kinase 1 a promoting enzyme for peritoneal dissemination in gastric cancer. International Journal of Cancer, 2010, 126, 1513-1520.	5.1	121
65	Phosphoglycerate Kinase 1 Promoting Tumor Progression and Metastasis in Gastric Cancer - Detected in a Tumor Mouse Model Using Positron Emission Tomography/Magnetic Resonance Imaging. Cellular Physiology and Biochemistry, 2010, 26, 147-154.	1.6	40
66	Noncoding RNA of Glutamine Synthetase I Modulates Antibiotic Production in Streptomyces coelicolor. Journal of Bacteriology, 2010, 192, 1160-1164.	2.2	49
67	Circadian Expression of Clock- and Tumor Suppressor Genes in Human Oral Mucosa. Cellular Physiology and Biochemistry, 2010, 26, 155-166.	1.6	36
68	Integrative systems biology visualization with MAYDAY. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	9
69	¹⁸ F-FDG-PET/CT to Select Patients with Peritoneal Carcinomatosis for Cytoreductive Surgery and Hyperthermic Intraperitoneal Chemotherapy. Annals of Surgical Oncology, 2009, 16, 1295-1303.	1.5	141
70	SpRay: A visual analytics approach for gene expression data. , 2009, , .		13
71	Lactate modulates gene expression in human mesenchymal stem cells. Langenbeck's Archives of Surgery, 2008, 393, 297-301.	1.9	37
72	PGK1 a Potential Marker for Peritoneal Dissemination in Gastric Cancer. Cellular Physiology and Biochemistry, 2008, 21, 429-436.	1.6	63

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73	Chromatin modifications induced by PML-RAR $\hat{\pm}$ repress critical targets in leukemogenesis as analyzed by ChIP-Chip. <i>Blood</i> , 2008, 111, 2887-2895.	1.4	73
74	Basement Membrane Remodeling in Skeletal Muscles of Patients with Limb Ischemia Involves Regulation of Matrix Metalloproteinases and Tissue Inhibitor of Matrix Metalloproteinases. <i>Journal of Vascular Research</i> , 2007, 44, 202-213.	1.4	32
75	Comparative analysis of structured RNAs in <i>S. cerevisiae</i> indicates a multitude of different functions. <i>BMC Biology</i> , 2007, 5, 25.	3.8	32
76	On the maximal cliques in c-max-tolerance graphs and their application in clustering molecular sequences. <i>Algorithms for Molecular Biology</i> , 2006, 1, 9.	1.2	7
77	Progression-Specific Genes Identified by Expression Profiling of Matched Ductal Carcinomas <i>in situ</i> and Invasive Breast Tumors, Combining Laser Capture Microdissection and Oligonucleotide Microarray Analysis. <i>Cancer Research</i> , 2006, 66, 5278-5286.	0.9	224
78	Mayday-a microarray data analysis workbench. <i>Bioinformatics</i> , 2006, 22, 1010-1012.	4.1	47
79	A Framework for Visualization of Microarray Data and Integrated Meta Information. <i>Information Visualization</i> , 2005, 4, 164-175.	1.9	19
80	Open reading frames provide a rich pool of potential natural antisense transcripts in fungal genomes. <i>Nucleic Acids Research</i> , 2005, 33, 5034-5044.	14.5	22
81	cDNA microarray analysis reveals novel candidate genes expressed in human peripheral blood following exhaustive exercise. <i>Physiological Genomics</i> , 2005, 23, 287-294.	2.3	61
82	DIALIGN P: fast pair-wise and multiple sequence alignment using parallel processors. <i>BMC Bioinformatics</i> , 2004, 5, 128.	2.6	35
83	Identification of a novel mouse Iroquois homeobox gene, <i>lrx5</i> , and chromosomal localisation of all members of the mouse Iroquois gene family. , 2000, 218, 160-174.		57
84	Graphs in sequence spaces: a review of statistical geometry. <i>Biophysical Chemistry</i> , 1997, 66, 111-131.	2.8	14