

Henrik Björn Nielsen

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

30,459
citations

147566

31
h-index

182168

51
g-index

51
all docs

51
docs citations

51
times ranked

35277
citing authors

#	ARTICLE	IF	CITATIONS
1	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010, 464, 59-65.	13.7	9,342
2	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	13.7	5,800
3	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013, 500, 541-546.	13.7	3,641
4	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014, 32, 834-841.	9.4	1,664
5	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015, 528, 262-266.	13.7	1,627
6	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , 2016, 535, 376-381.	13.7	1,506
7	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014, 32, 822-828.	9.4	909
8	Recovery of gut microbiota of healthy adults following antibiotic exposure. <i>Nature Microbiology</i> , 2018, 3, 1255-1265.	5.9	483
9	The MAP kinase substrate MKS1 is a regulator of plant defense responses. <i>EMBO Journal</i> , 2005, 24, 2579-2589.	3.5	480
10	Transcriptome Responses to Combinations of Stresses in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2013, 161, 1783-1794.	2.3	478
11	<i>Arabidopsis</i> MAP kinase 4 regulates gene expression through transcription factor release in the nucleus. <i>EMBO Journal</i> , 2008, 27, 2214-2221.	3.5	445
12	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013, 10, 1196-1199.	9.0	442
13	Early Divergent Strains of <i>Yersinia pestis</i> in Eurasia 5,000 Years Ago. <i>Cell</i> , 2015, 163, 571-582.	13.5	425
14	A catalog of the mouse gut metagenome. <i>Nature Biotechnology</i> , 2015, 33, 1103-1108.	9.4	422
15	<i>Arabidopsis</i> MAP kinase 4 regulates salicylic acid- and jasmonic acid/ethylene-dependent responses via EDS1 and PAD4. <i>Plant Journal</i> , 2006, 47, 532-546.	2.8	352
16	<i>Oscillospira</i> and related bacteria: From metagenomic species to metabolic features. <i>Environmental Microbiology</i> , 2017, 19, 835-841.	1.8	320
17	<i>Arabidopsis</i> Mitogen-Activated Protein Kinase Kinases MKK1 and MKK2 Have Overlapping Functions in Defense Signaling Mediated by MEK1, MPK4, and MKS1. <i>Plant Physiology</i> , 2008, 148, 212-222.	2.3	266
18	Improved metagenome binning and assembly using deep variational autoencoders. <i>Nature Biotechnology</i> , 2021, 39, 555-560.	9.4	251

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19	Host genetics and the rumen microbiome jointly associate with methane emissions in dairy cows. <i>PLoS Genetics</i> , 2018, 14, e1007580.	1.5	198
20	Autoimmunity in <i>Arabidopsis thaliana</i> Is Mediated by Epigenetic Regulation of an Immune Receptor. <i>PLoS Pathogens</i> , 2010, 6, e1001137.	2.1	170
21	Transcriptomes of the desiccation-tolerant resurrection plant <i>Craterostigma plantagineum</i> . <i>Plant Journal</i> , 2010, 63, 212-228.	2.8	149
22	The transcriptionally active regions in the genome of <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2009, 73, 1043-1057.	1.2	146
23	Design of oligonucleotides for microarrays and perspectives for design of multi-transcriptome arrays. <i>Nucleic Acids Research</i> , 2003, 31, 3491-3496.	6.5	100
24	Towards the biogeography of prokaryotic genes. <i>Nature</i> , 2022, 601, 252-256.	13.7	85
25	Microarray analysis reveals transcriptional plasticity in the reef building coral <i>Acropora millepora</i> . <i>Molecular Ecology</i> , 2009, 18, 3062-3075.	2.0	80
26	<i>Arabidopsis</i> VARIEGATED 3 encodes a chloroplast-targeted, zinc-finger protein required for chloroplast and palisade cell development. <i>Journal of Cell Science</i> , 2004, 117, 4807-4818.	1.2	65
27	Metabolic and gut microbiome changes following GLP-1 or dual GLP-1/GLP-2 receptor agonist treatment in diet-induced obese mice. <i>Scientific Reports</i> , 2019, 9, 15582.	1.6	64
28	Probe selection for DNA microarrays using OligoWiz. <i>Nature Protocols</i> , 2007, 2, 2677-2691.	5.5	60
29	Transcription analysis using high-density micro-arrays of <i>Aspergillus nidulans</i> wild-type and <i>creA</i> mutant during growth on glucose or ethanol. <i>Fungal Genetics and Biology</i> , 2006, 43, 593-603.	0.9	59
30	New weakly expressed cell cycle-regulated genes in yeast. <i>Yeast</i> , 2005, 22, 1191-1201.	0.8	48
31	Promiscuous and specific phospholipid binding by domains in ZAC, a membrane-associated <i>Arabidopsis</i> protein with an ARF GAP zinc finger and a C2 domain. <i>Plant Molecular Biology</i> , 2000, 44, 799-814.	2.0	35
32	Transcriptome differentiation along the dorso-ventral axis in laser-captured microdissected rat hippocampal granular cell layer. <i>Neuroscience</i> , 2010, 170, 731-741.	1.1	31
33	Fecal Microbiota Transplantation from Overweight or Obese Donors in Cachectic Patients with Advanced Gastroesophageal Cancer: A Randomized, Double-blind, Placebo-Controlled, Phase II Study. <i>Clinical Cancer Research</i> , 2021, 27, 3784-3792.	3.2	30
34	Lazarus1, a DUF300 Protein, Contributes to Programmed Cell Death Associated with <i>Arabidopsis thaliana</i> and the Hypersensitive Response. <i>PLoS ONE</i> , 2010, 5, e12586.	1.1	25
35	Capturing One of the Human Gut Microbiome's Most Wanted: Reconstructing the Genome of a Novel Butyrate-Producing, Clostridial Scavenger from Metagenomic Sequence Data. <i>Frontiers in Microbiology</i> , 2016, 7, 783.	1.5	24
36	GlycA, a novel marker for low grade inflammation, reflects gut microbiome diversity and is more accurate than high sensitive CRP in reflecting metabolomic profile. <i>Metabolomics</i> , 2020, 16, 76.	1.4	23

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37	Crosstalk. Trends in Plant Science, 2006, 11, 63-64.	4.3	21
38	The chemical interactome space between the human host and the genetically defined gut metabotypes. ISME Journal, 2013, 7, 730-742.	4.4	21
39	Improving comparability between microarray probe signals by thermodynamic intensity correction. Nucleic Acids Research, 2007, 35, e48.	6.5	19
40	Impaired Uptake and/or Utilization of Leucine by <i>Saccharomyces cerevisiae</i> Is Suppressed by the <i>SPT15-300</i> Allele of the TATA-Binding Protein Gene. Applied and Environmental Microbiology, 2009, 75, 6055-6061.	1.4	19
41	Transcriptomic variation in a coral reveals pathways of clonal organisation. Marine Genomics, 2009, 2, 119-125.	0.4	18
42	TIMP1 overexpression mediates resistance of MCF-7 human breast cancer cells to fulvestrant and down-regulates progesterone receptor expression. Tumor Biology, 2013, 34, 3839-3851.	0.8	18
43	Functional Associations by Response Overlap (FARO), a Functional Genomics Approach Matching Gene Expression Phenotypes. PLoS ONE, 2007, 2, e676.	1.1	17
44	Distinct developmental defense activations in barley embryos identified by transcriptome profiling. Plant Molecular Biology, 2006, 61, 589-601.	2.0	15
45	Controlled indole-3-acetaldoxime production through ethanol-induced expression of CYP79B2. Planta, 2009, 229, 1209-1217.	1.6	13
46	Advanced Dental Cleaning is Associated with Reduced Risk of COPD Exacerbations – A Randomized Controlled Trial. International Journal of COPD, 2021, Volume 16, 3203-3215.	0.9	13
47	Predicting facial characteristics from complex polygenic variations. Forensic Science International: Genetics, 2015, 19, 263-268.	1.6	11
48	Analysis of cell death inducing compounds. Archives of Toxicology, 2007, 81, 803-811.	1.9	8
49	Conjugated C-6 hydroxylated bile acids in serum relate to human metabolic health and gut Clostridia species. Scientific Reports, 2021, 11, 13252.	1.6	8
50	Analysis of a gene panel for targeted sequencing of colorectal cancer samples. Oncotarget, 2018, 9, 9043-9060.	0.8	8
51	Novel genes involved in pathophysiology of gonadotropin-dependent adrenal tumors in mice. Molecular and Cellular Endocrinology, 2017, 444, 9-18.	1.6	5