Gerhard G Thallinger

List of Publications by Year
in descending order

52	21,254	201674	182427
papers	citations	27	51
		h-index	g-index

53	53	53	30409
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Introducing mothur: Open-Source, Platform-Independent, Community-Supported Software for Describing and Comparing Microbial Communities. Applied and Environmental Microbiology, 2009, 75, 7537-7541.	3.1	18,390
2	Inferring expressed genes by whole-genome sequencing of plasma DNA. Nature Genetics, 2016, 48, 1273-1278.	21.4	295
3	Dimension reduction techniques for the integrative analysis of multi-omics data. Briefings in Bioinformatics, 2016, 17, 628-641.	6.5	280
4	Lipid Data Analyzer: unattended identification and quantitation of lipids in LC-MS data. Bioinformatics, 2011, 27, 572-577.	4.1	173
5	Phylogenomics uncovers early hybridization and adaptive loci shaping the radiation of Lake Tanganyika cichlid fishes. Nature Communications, 2018, 9, 3159.	12.8	162
6	High-quality genome sequence of Pichia pastoris CBS7435. Journal of Biotechnology, 2011, 154, 312-320.	3.8	146
7	The mzTab Data Exchange Format: Communicating Mass-spectrometry-based Proteomics and Metabolomics Experimental Results to a Wider Audience. Molecular and Cellular Proteomics, 2014, 13, 2765-2775.	3.8	130
8	A Toolbox of Diverse Promoters Related to Methanol Utilization: Functionally Verified Parts for Heterologous Pathway Expression in *Pichia pastoris*. ACS Synthetic Biology, 2016, 5, 172-186.	3.8	127
9	Deciphering lipid structures based on platform-independent decision rules. Nature Methods, 2017, 14, 1171-1174.	19.0	116
10	Comprehensive genome and epigenome characterization of CHO cells in response to evolutionary pressures and over time. Biotechnology and Bioengineering, 2016, 113, 2241-2253.	3.3	112
11	Alterations in the Colonic Microbiota in Response to Osmotic Diarrhea. PLoS ONE, 2013, 8, e55817.	2.5	102
12	The *S*phagnum microbiome supports bog ecosystem functioning under extreme conditions. Molecular Ecology, 2014, 23, 4498-4510.	3.9	98
13	Critical Issues in Mycobiota Analysis. Frontiers in Microbiology, 2017, 8, 180.	3.5	83
14	Lipidomic analysis of lipid droplets from murine hepatocytes reveals distinct signatures for nutritional stress. Journal of Lipid Research, 2012, 53, 2141-2152.	4.2	80
15	MetExtract II: A Software Suite for Stable Isotope-Assisted Untargeted Metabolomics. Analytical Chemistry, 2017, 89, 9518-9526.	6.5	80
16	The Human Gastric Microbiome Is Predicated upon Infection with Helicobacter pylori. Frontiers in Microbiology, 2017, 8, 2508.	3.5	75
17	More than Cell Dust: Microparticles Isolated from Cerebrospinal Fluid of Brain Injured Patients Are Messengers Carrying mRNAs, miRNAs, and Proteins. Journal of Neurotrauma, 2013, 30, 1232-1242.	3.4	74
18	Curation of the genome annotation of *Pichia pastoris* (*Komagataella phaffii*) CBS7435 from gene level to protein function. FEMS Yeast Research, 2016, 16, fow051.	2.3	69

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19	Methanol independent induction in *Pichia pastoris* by simple derepressed overexpression of single transcription factors. Biotechnology and Bioengineering, 2018, 115, 1037-1050.	3.3	64
20	FXR-dependent Rubicon induction impairs autophagy in models of human cholestasis. Journal of Hepatology, 2020, 72, 1122-1131.	3.7	47
21	Characterisation of Candida within the Mycobiome/Microbiome of the Lower Respiratory Tract of ICU Patients. PLoS ONE, 2016, 11, e0155033.	2.5	45
22	Complete Mitochondrial DNA Sequences of the Threadfin Cichlid (Petrochromis trewavasae) and the Blunthead Cichlid (Tropheus moorii) and Patterns of Mitochondrial Genome Evolution in Cichlid Fishes. PLoS ONE, 2013, 8, e67048.	2.5	41
23	Towards improved membrane protein production in Pichia pastoris: General and specific transcriptional response to membrane protein overexpression. New Biotechnology, 2014, 31, 538-552.	4.4	37
24	NR4A1-mediated apoptosis suppresses lymphomagenesis and is associated with a favorable cancer-specific survival in patients with aggressive B-cell lymphomas. Blood, 2014, 123, 2367-2377.	1.4	37
25	Comparative Genome Analysis of Campylobacter fetus Subspecies Revealed Horizontally Acquired Genetic Elements Important for Virulence and Niche Specificity. PLoS ONE, 2014, 9, e85491.	2.5	33
26	ATGL and CGI-58 are lipid droplet proteins of the hepatic stellate cell line HSC-T6. Journal of Lipid Research, 2015, 56, 1972-1984.	4.2	32
27	Utility of serological biomarkers for giant cell arteritis in a large cohort of treatment-naïve patients. Clinical Rheumatology, 2019, 38, 317-329.	2.2	32
28	NR4A3 Suppresses Lymphomagenesis through Induction of Proapoptotic Genes. Cancer Research, 2017, 77, 2375-2386.	0.9	24
29	Myristic acid induces proteomic and secretomic changes associated with steatosis, cytoskeleton remodeling, endoplasmic reticulum stress, protein turnover and exosome release in HepG2 cells. Journal of Proteomics, 2018, 181, 118-130.	2.4	24
30	Comparison and evaluation of integrative methods for the analysis of multilevel omics data: a study based on simulated and experimental cancer data. Briefings in Bioinformatics, 2019, 20, 671-681.	6.5	23
31	Peroxidase gene discovery from the horseradish transcriptome. BMC Genomics, 2014, 15, 227.	2.8	22
32	The mitochondrial genome of the oribatid mite Paraleius leontonychus: new insights into tRNA evolution and phylogenetic relationships in acariform mites. Scientific Reports, 2018, 8, 7558.	3.3	22
33	Enzyme discovery beyond homology: a unique hydroxynitrile lyase in the Bet v1 superfamily. Scientific Reports, 2017, 7, 46738.	3.3	21
34	A concise review of significantly modified serological biomarkers in giant cell arteritis, as detected by different methods. Autoimmunity Reviews, 2018, 17, 188-194.	5.8	19
35	The impact of genetic stress by ATGL deficiency on the lipidome of lipid droplets from murine hepatocytes. Journal of Lipid Research, 2013, 54, 2185-2194.	4.2	18
36	A map of mass spectrometry-based *in silico* fragmentation prediction and compound identification in metabolomics. Briefings in Bioinformatics, 2021, 22, .	6.5	18

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37	Resolving Tumor Heterogeneity: Genes Involved in Chordoma Cell Development Identified by Low-Template Analysis of Morphologically Distinct Cells. PLoS ONE, 2014, 9, e87663.	2.5	17
38	The CXCR4â€"CXCL12-Axis Is of Prognostic Relevance in DLBCL and Its Antagonists Exert Pro-Apoptotic Effects In Vitro. International Journal of Molecular Sciences, 2019, 20, 4740.	4.1	14
39	BMP7 aberrantly induced in the psoriatic epidermis instructs inflammation-associated Langerhans cells. Journal of Allergy and Clinical Immunology, 2020, 145, 1194-1207.e11.	2.9	12
40	Assessment of lipidomic species in hepatocyte lipid droplets from stressed mouse models. Scientific Data, 2014, 1, 140051.	5.3	10
41	A Physicians' Wish List for the Clinical Application of Intestinal Metagenomics. PLoS Medicine, 2014, 11, e1001627.	8.4	9
42	Translin and Trax differentially regulate telomere-associated transcript homeostasis. Oncotarget, 2016, 7, 33809-33820.	1.8	9
43	Non-linear fitting with joint spatial regularization in arterial spin labeling. Medical Image Analysis, 2021, 71, 102067.	11.6	5
44	Comparison of tear proteome in allergic rhinoconjunctivitis patients and controls with respect to pollen season. Allergy: European Journal of Allergy and Clinical Immunology, 2018, 73, 1541-1543.	5.7	4
45	Cytoplasmic location of NR4A1 in aggressive lymphomas is associated with a favourable cancer specific survival. Scientific Reports, 2018, 8, 14528.	3.3	4
46	Genome sequences of Tropheus moorii and Petrochromis trewavasae, two eco-morphologically divergent cichlid fishes endemic to Lake Tanganyika. Scientific Reports, 2021, 11, 4309.	3.3	4
47	Gene and miRNA expression in giant cell arteritisâ€"a concise systematic review of significantly modified studies. Clinical Rheumatology, 2019, 38, 307-316.	2.2	3
48	Characterization of Constituents with Potential Anti-Inflammatory Activity in Chinese Lonicera Species by UHPLC-HRMS Based Metabolite Profiling. Metabolites, 2022, 12, 288.	2.9	3
49	High-Throughput Characterization and Comparison of Microbial Communities. Biomedizinische Technik, 2013, 58 Suppl 1, .	0.8	2
50	Identification and Quantification of Oxidized Lipids in LC-MS Lipidomics Data. Studies in Health Technology and Informatics, 2020, 271, 39-48.	0.3	2
51	A Comprehensive FXR Signaling Atlas Derived from Pooled ChIP-seq Data. Studies in Health Technology and Informatics, 2019, 260, 105-112.	0.3	1
52	High-Throughput Characterization and Comparison of Microbial Communities. , 2012, , 37-57.		0