Gerhard G Thallinger

List of Publications by Year
in descending order

52 papers	21,254 citations	201674 27 h-index	182427 51 g-index
53 all docs	53 docs citations	53 times ranked	30409 citing authors

#	Article	IF	Citations
1	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
2	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
3	A map of mass spectrometry-based *in silico* fragmentation prediction and compound identification in metabolomics. Briefings in Bioinformatics, 2021, 22, .	6.5	18
4	Non-linear fitting with joint spatial regularization in arterial spin labeling. Medical Image Analysis, 2021, 71, 102067.	11.6	5
5	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
6	FXR-dependent Rubicon induction impairs autophagy in models of human cholestasis. Journal of Hepatology, 2020, 72, 1122-1131.	3.7	47
7	Identification and Quantification of Oxidized Lipids in LC-MS Lipidomics Data. Studies in Health Technology and Informatics, 2020, 271, 39-48.	0.3	2
8	Gene and miRNA expression in giant cell arteritis—a concise systematic review of significantly modified studies. Clinical Rheumatology, 2019, 38, 307-316.	2.2	3
9	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
10	The CXCR4—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
11	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
12	A Comprehensive FXR Signaling Atlas Derived from Pooled ChIP-seq Data. Studies in Health Technology and Informatics, 2019, 260, 105-112.	0.3	1
13	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
14	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
15	Methanol independent induction in *Pichia pastoris* by simple derepressed overexpression of single transcription factors. Biotechnology and Bioengineering, 2018, 115, 1037-1050.	3.3	64
16	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
17	Cytoplasmic location of NR4A1 in aggressive lymphomas is associated with a favourable cancer specific survival. Scientific Reports, 2018, 8, 14528.	3.3	4
18	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

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19	Phylogenomics uncovers early hybridization and adaptive loci shaping the radiation of Lake Tanganyika cichlid fishes. Nature Communications, 2018, 9, 3159.	12.8	162
20	NR4A3 Suppresses Lymphomagenesis through Induction of Proapoptotic Genes. Cancer Research, 2017, 77, 2375-2386.	0.9	24
21	Enzyme discovery beyond homology: a unique hydroxynitrile lyase in the Bet v1 superfamily. Scientific Reports, 2017, 7, 46738.	3.3	21
22	Deciphering lipid structures based on platform-independent decision rules. Nature Methods, 2017, 14, 1171-1174.	19.0	116
23	MetExtract II: A Software Suite for Stable Isotope-Assisted Untargeted Metabolomics. Analytical Chemistry, 2017, 89, 9518-9526.	6.5	80
24	Critical Issues in Mycobiota Analysis. Frontiers in Microbiology, 2017, 8, 180.	3.5	83
25	The Human Gastric Microbiome Is Predicated upon Infection with Helicobacter pylori. Frontiers in Microbiology, 2017, 8, 2508.	3.5	75
26	Translin and Trax differentially regulate telomere-associated transcript homeostasis. Oncotarget, 2016, 7, 33809-33820.	1.8	9
27	Characterisation of Candida within the Mycobiome/Microbiome of the Lower Respiratory Tract of ICU Patients. PLoS ONE, 2016, 11, e0155033.	2.5	45
28	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
29	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
30	Inferring expressed genes by whole-genome sequencing of plasma DNA. Nature Genetics, 2016, 48, 1273-1278.	21.4	295
31	Dimension reduction techniques for the integrative analysis of multi-omics data. Briefings in Bioinformatics, 2016, 17, 628-641.	6.5	280
32	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
33	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
34	A Physicians' Wish List for the Clinical Application of Intestinal Metagenomics. PLoS Medicine, 2014, 11, e1001627.	8.4	9
35	The *Sphagnum* microbiome supports bog ecosystem functioning under extreme conditions. Molecular Ecology, 2014, 23, 4498-4510.	3.9	98
36	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

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37	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
38	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
39	Peroxidase gene discovery from the horseradish transcriptome. BMC Genomics, 2014, 15, 227.	2.8	22
40	Assessment of lipidomic species in hepatocyte lipid droplets from stressed mouse models. Scientific Data, 2014, 1, 140051.	5.3	10
41	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
42	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
43	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
44	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
45	High-Throughput Characterization and Comparison of Microbial Communities. Biomedizinische Technik, 2013, 58 Suppl 1, .	0.8	2
46	Alterations in the Colonic Microbiota in Response to Osmotic Diarrhea. PLoS ONE, 2013, 8, e55817.	2.5	102
47	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
48	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
49	High-Throughput Characterization and Comparison of Microbial Communities. , 2012, , 37-57.		0
50	High-quality genome sequence of Pichia pastoris CBS7435. Journal of Biotechnology, 2011, 154, 312-320.	3.8	146
51	Lipid Data Analyzer: unattended identification and quantitation of lipids in LC-MS data. Bioinformatics, 2011, 27, 572-577.	4.1	173
52	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