

# Gerhard G Thallinger

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3767056/publications.pdf>

Version: 2024-02-01

52  
papers

21,254  
citations

201385

27  
h-index

182168

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. <i>Metabolites</i> , 2022, 12, 288.	1.3	3
2	Genome sequences of <i>Tropheus moorii</i> and <i>Petrochromis trewavasae</i> , two eco-morphologically divergent cichlid fishes endemic to Lake Tanganyika. <i>Scientific Reports</i> , 2021, 11, 4309.	1.6	4
3	A map of mass spectrometry-based <i>in silico</i> fragmentation prediction and compound identification in metabolomics. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	18
4	Non-linear fitting with joint spatial regularization in arterial spin labeling. <i>Medical Image Analysis</i> , 2021, 71, 102067.	7.0	5
5	BMP7 aberrantly induced in the psoriatic epidermis instructs inflammation-associated Langerhans cells. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 1194-1207.e11.	1.5	12
6	FXR-dependent Rubicon induction impairs autophagy in models of human cholestasis. <i>Journal of Hepatology</i> , 2020, 72, 1122-1131.	1.8	47
7	Identification and Quantification of Oxidized Lipids in LC-MS Lipidomics Data. <i>Studies in Health Technology and Informatics</i> , 2020, 271, 39-48.	0.2	2
8	Gene and miRNA expression in giant cell arteritis—a concise systematic review of significantly modified studies. <i>Clinical Rheumatology</i> , 2019, 38, 307-316.	1.0	3
9	Utility of serological biomarkers for giant cell arteritis in a large cohort of treatment-naïve patients. <i>Clinical Rheumatology</i> , 2019, 38, 317-329.	1.0	32
10	The CXCR4–CXCL12-Axis Is of Prognostic Relevance in DLBCL and Its Antagonists Exert Pro-Apoptotic Effects In Vitro. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4740.	1.8	14
11	Comparison and evaluation of integrative methods for the analysis of multilevel omics data: a study based on simulated and experimental cancer data. <i>Briefings in Bioinformatics</i> , 2019, 20, 671-681.	3.2	23
12	A Comprehensive FXR Signaling Atlas Derived from Pooled ChIP-seq Data. <i>Studies in Health Technology and Informatics</i> , 2019, 260, 105-112.	0.2	1
13	Comparison of tear proteome in allergic rhinoconjunctivitis patients and controls with respect to pollen season. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2018, 73, 1541-1543.	2.7	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. <i>Journal of Proteomics</i> , 2018, 181, 118-130.	1.2	24
15	Methanol independent induction in <i>Pichia pastoris</i> by simple derepressed overexpression of single transcription factors. <i>Biotechnology and Bioengineering</i> , 2018, 115, 1037-1050.	1.7	64
16	A concise review of significantly modified serological biomarkers in giant cell arteritis, as detected by different methods. <i>Autoimmunity Reviews</i> , 2018, 17, 188-194.	2.5	19
17	Cytoplasmic location of NR4A1 in aggressive lymphomas is associated with a favourable cancer specific survival. <i>Scientific Reports</i> , 2018, 8, 14528.	1.6	4
18	The mitochondrial genome of the oribatid mite <i>Paraleius leontonychus</i> : new insights into tRNA evolution and phylogenetic relationships in acariform mites. <i>Scientific Reports</i> , 2018, 8, 7558.	1.6	22

#	ARTICLE	IF	CITATIONS
19	Phylogenomics uncovers early hybridization and adaptive loci shaping the radiation of Lake Tanganyika cichlid fishes. <i>Nature Communications</i> , 2018, 9, 3159.	5.8	162
20	NR4A3 Suppresses Lymphomagenesis through Induction of Proapoptotic Genes. <i>Cancer Research</i> , 2017, 77, 2375-2386.	0.4	24
21	Enzyme discovery beyond homology: a unique hydroxynitrile lyase in the Bet v1 superfamily. <i>Scientific Reports</i> , 2017, 7, 46738.	1.6	21
22	Deciphering lipid structures based on platform-independent decision rules. <i>Nature Methods</i> , 2017, 14, 1171-1174.	9.0	116
23	MetExtract II: A Software Suite for Stable Isotope-Assisted Untargeted Metabolomics. <i>Analytical Chemistry</i> , 2017, 89, 9518-9526.	3.2	80
24	Critical Issues in Mycobiota Analysis. <i>Frontiers in Microbiology</i> , 2017, 8, 180.	1.5	83
25	The Human Gastric Microbiome Is Predicated upon Infection with <i>Helicobacter pylori</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2508.	1.5	75
26	Translin and Trax differentially regulate telomere-associated transcript homeostasis. <i>Oncotarget</i> , 2016, 7, 33809-33820.	0.8	9
27	Characterisation of <i>Candida</i> within the Mycobiome/Microbiome of the Lower Respiratory Tract of ICU Patients. <i>PLoS ONE</i> , 2016, 11, e0155033.	1.1	45
28	Curation of the genome annotation of <i>Pichia pastoris</i> ( <i>Komagataella phaffii</i> ) CBS7435 from gene level to protein function. <i>FEMS Yeast Research</i> , 2016, 16, fow051.	1.1	69
29	Comprehensive genome and epigenome characterization of CHO cells in response to evolutionary pressures and over time. <i>Biotechnology and Bioengineering</i> , 2016, 113, 2241-2253.	1.7	112
30	Inferring expressed genes by whole-genome sequencing of plasma DNA. <i>Nature Genetics</i> , 2016, 48, 1273-1278.	9.4	295
31	Dimension reduction techniques for the integrative analysis of multi-omics data. <i>Briefings in Bioinformatics</i> , 2016, 17, 628-641.	3.2	280
32	A Toolbox of Diverse Promoters Related to Methanol Utilization: Functionally Verified Parts for Heterologous Pathway Expression in <i>Pichia pastoris</i> . <i>ACS Synthetic Biology</i> , 2016, 5, 172-186.	1.9	127
33	ATGL and CGI-58 are lipid droplet proteins of the hepatic stellate cell line HSC-T6. <i>Journal of Lipid Research</i> , 2015, 56, 1972-1984.	2.0	32
34	A Physicians' Wish List for the Clinical Application of Intestinal Metagenomics. <i>PLoS Medicine</i> , 2014, 11, e1001627.	3.9	9
35	The <i>Sphagnum</i> microbiome supports bog ecosystem functioning under extreme conditions. <i>Molecular Ecology</i> , 2014, 23, 4498-4510.	2.0	98
36	The mzTab Data Exchange Format: Communicating Mass-spectrometry-based Proteomics and Metabolomics Experimental Results to a Wider Audience. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2765-2775.	2.5	130

#	ARTICLE	IF	CITATIONS
37	Towards improved membrane protein production in <i>Pichia pastoris</i> : General and specific transcriptional response to membrane protein overexpression. <i>New Biotechnology</i> , 2014, 31, 538-552.	2.4	37
38	NR4A1-mediated apoptosis suppresses lymphomagenesis and is associated with a favorable cancer-specific survival in patients with aggressive B-cell lymphomas. <i>Blood</i> , 2014, 123, 2367-2377.	0.6	37
39	Peroxidase gene discovery from the horseradish transcriptome. <i>BMC Genomics</i> , 2014, 15, 227.	1.2	22
40	Assessment of lipidomic species in hepatocyte lipid droplets from stressed mouse models. <i>Scientific Data</i> , 2014, 1, 140051.	2.4	10
41	Comparative Genome Analysis of <i>Campylobacter fetus</i> Subspecies Revealed Horizontally Acquired Genetic Elements Important for Virulence and Niche Specificity. <i>PLoS ONE</i> , 2014, 9, e85491.	1.1	33
42	Resolving Tumor Heterogeneity: Genes Involved in Chordoma Cell Development Identified by Low-Template Analysis of Morphologically Distinct Cells. <i>PLoS ONE</i> , 2014, 9, e87663.	1.1	17
43	More than Cell Dust: Microparticles Isolated from Cerebrospinal Fluid of Brain Injured Patients Are Messengers Carrying mRNAs, miRNAs, and Proteins. <i>Journal of Neurotrauma</i> , 2013, 30, 1232-1242.	1.7	74
44	The impact of genetic stress by ATGL deficiency on the lipidome of lipid droplets from murine hepatocytes. <i>Journal of Lipid Research</i> , 2013, 54, 2185-2194.	2.0	18
45	High-Throughput Characterization and Comparison of Microbial Communities. <i>Biomedizinische Technik</i> , 2013, 58 Suppl 1, .	0.9	2
46	Alterations in the Colonic Microbiota in Response to Osmotic Diarrhea. <i>PLoS ONE</i> , 2013, 8, e55817.	1.1	102
47	Complete Mitochondrial DNA Sequences of the Threadfin Cichlid ( <i>Petrochromis trewavasae</i> ) and the Blunthead Cichlid ( <i>Tropheus moorii</i> ) and Patterns of Mitochondrial Genome Evolution in Cichlid Fishes. <i>PLoS ONE</i> , 2013, 8, e67048.	1.1	41
48	Lipidomic analysis of lipid droplets from murine hepatocytes reveals distinct signatures for nutritional stress. <i>Journal of Lipid Research</i> , 2012, 53, 2141-2152.	2.0	80
49	High-Throughput Characterization and Comparison of Microbial Communities. , 2012, , 37-57.		0
50	High-quality genome sequence of <i>Pichia pastoris</i> CBS7435. <i>Journal of Biotechnology</i> , 2011, 154, 312-320.	1.9	146
51	Lipid Data Analyzer: unattended identification and quantitation of lipids in LC-MS data. <i>Bioinformatics</i> , 2011, 27, 572-577.	1.8	173
52	Introducing mothur: Open-Source, Platform-Independent, Community-Supported Software for Describing and Comparing Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7537-7541.	1.4	18,390