

# Manfred G Grabherr

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1817294/publications.pdf>

Version: 2024-02-01

55  
papers

38,928  
citations

159585

30  
h-index

182427

51  
g-index

60  
all docs

60  
docs citations

60  
times ranked

46648  
citing authors

#	ARTICLE	IF	CITATIONS
1	EZTraits: A programmable tool to evaluate multi-site deterministic traits. PLoS ONE, 2022, 17, e0259327.	2.5	0
2	Metatranscriptomics captures dynamic shifts in mycorrhizal coordination in boreal forests. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	12
3	Flexible Machine Learning Algorithms for Clinical Gait Assessment Tools. Sensors, 2022, 22, 4957.	3.8	0
4	Comparative Fungal Community Analyses Using Metatranscriptomics and Internal Transcribed Spacer Amplicon Sequencing from Norway Spruce. MSystems, 2021, 6, .	3.8	16
5	Building de novo reference genome assemblies of complex eukaryotic microorganisms from single nuclei. Scientific Reports, 2020, 10, 1303.	3.3	22
6	Intra- and inter-individual metabolic profiling highlights carnitine and lysophosphatidylcholine pathways as key molecular defects in type 2 diabetes. Scientific Reports, 2019, 9, 9653.	3.3	32
7	Analyzing DNA methylation patterns in subjects diagnosed with schizophrenia using machine learning methods. Journal of Psychiatric Research, 2019, 114, 41-47.	3.1	19
8	Investigation of the host transcriptional response to intracellular bacterial infection using Dictyostelium discoideum as a host model. BMC Genomics, 2019, 20, 961.	2.8	17
9	ACES: a machine learning toolbox for clustering analysis and visualization. BMC Genomics, 2018, 19, 964.	2.8	1
10	Functional and evolutionary genomic inferences in <i>Populus</i> through genome and population sequencing of American and European aspen. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10970-E10978.	7.1	84
11	Special Issue Introduction: The Wonders and Mysteries Next Generation Sequencing Technologies Help Reveal. Genes, 2018, 9, 505.	2.4	0
12	Global characterization of the Dicer-like protein DrnB roles in miRNA biogenesis in the social amoeba <i>Dictyostelium discoideum</i> . RNA Biology, 2018, 15, 937-954.	3.1	9
13	Comparative omics and feeding manipulations in chicken indicate a shift of the endocrine role of visceral fat towards reproduction. BMC Genomics, 2018, 19, 295.	2.8	33
14	Interactions of Freshwater Cyanobacteria with Bacterial Antagonists. Applied and Environmental Microbiology, 2017, 83, .	3.1	39
15	microTaboo: a general and practical solution to the k-disjoint problem. BMC Bioinformatics, 2017, 18, 228.	2.6	0
16	Correspondence on Lovell et al.: identification of chicken genes previously assumed to be evolutionarily lost. Genome Biology, 2017, 18, 112.	8.8	51
17	Reading and editing the <i>Pleurodeles waltl</i> genome reveals novel features of tetrapod regeneration. Nature Communications, 2017, 8, 2286.	12.8	123
18	Evolution of the p53-MDM2 pathway. BMC Evolutionary Biology, 2017, 17, 177.	3.2	23

#	ARTICLE	IF	CITATIONS
19	RNA-sequence data normalization through in silico prediction of reference genes: the bacterial response to DNA damage as case study. <i>BioData Mining</i> , 2017, 10, 30.	4.0	15
20	PiiL: visualization of DNA methylation and gene expression data in gene pathways. <i>BMC Genomics</i> , 2017, 18, 571.	2.8	3
21	Characterization of the <i>Giardia intestinalis</i> secretome during interaction with human intestinal epithelial cells: The impact on host cells. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0006120.	3.0	103
22	A practical guide to build <i>de-novo</i> assemblies for single tissues of non-model organisms: the example of a Neotropical frog. <i>PeerJ</i> , 2017, 5, e3702.	2.0	16
23	Combinatorial identification of DNA methylation patterns over age in the human brain. <i>BMC Bioinformatics</i> , 2016, 17, 393.	2.6	13
24	Coordinated Changes in Gene Expression Throughout Encystation of <i>Giardia intestinalis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004571.	3.0	69
25	Serendipitous Meta-Transcriptomics: The Fungal Community of Norway Spruce ( <i>Picea abies</i> ). <i>PLoS ONE</i> , 2015, 10, e0139080.	2.5	27
26	Function of Isolated Pancreatic Islets From Patients at Onset of Type 1 Diabetes: Insulin Secretion Can Be Restored After Some Days in a Nondiabetogenic Environment In Vitro. <i>Diabetes</i> , 2015, 64, 2506-2512.	0.6	76
27	Evolution of Darwin's finches and their beaks revealed by genome sequencing. <i>Nature</i> , 2015, 518, 371-375.	27.8	766
28	Whiteboard: a framework for the programmatic visualization of complex biological analyses: Fig. 1.. <i>Bioinformatics</i> , 2015, 31, 2054-2055.	4.1	1
29	Genome and physiology of the ascomycete filamentous fungus <i>Xeromyces bisporus</i> , the most xerophilic organism isolated to date. <i>Environmental Microbiology</i> , 2015, 17, 496-513.	3.8	34
30	A universal genomic coordinate translator for comparative genomics. <i>BMC Bioinformatics</i> , 2014, 15, 227.	2.6	7
31	Modular and configurable optimal sequence alignment software: Cola. <i>Source Code for Biology and Medicine</i> , 2014, 9, 12.	1.7	2
32	An Improved Canine Genome and a Comprehensive Catalogue of Coding Genes and Non-Coding Transcripts. <i>PLoS ONE</i> , 2014, 9, e91172.	2.5	206
33	De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis. <i>Nature Protocols</i> , 2013, 8, 1494-1512.	12.0	7,054
34	Unsupervised genome-wide recognition of local relationship patterns. <i>BMC Genomics</i> , 2013, 14, 347.	2.8	59
35	Broad-scale phylogenomics provides insights into retrovirus host evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20146-20151.	7.1	91
36	Efficient cellular fractionation improves RNA sequencing analysis of mature and nascent transcripts from human tissues. <i>BMC Biotechnology</i> , 2013, 13, 99.	3.3	47

#	ARTICLE	IF	CITATIONS
37	Artificially designed promoters. <i>Bioengineered</i> , 2012, 3, 120-123.	3.2	2
38	Population-scale sequencing reveals genetic differentiation due to local adaptation in Atlantic herring. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19345-19350.	7.1	217
39	The genomic basis of adaptive evolution in threespine sticklebacks. <i>Nature</i> , 2012, 484, 55-61.	27.8	1,600
40	The genome of the green anole lizard and a comparative analysis with birds and mammals. <i>Nature</i> , 2011, 477, 587-591.	27.8	575
41	Obligate biotrophy features unraveled by the genomic analysis of rust fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9166-9171.	7.1	640
42	Computational methods for transcriptome annotation and quantification using RNA-seq. <i>Nature Methods</i> , 2011, 8, 469-477.	19.0	919
43	Full-length transcriptome assembly from RNA-Seq data without a reference genome. <i>Nature Biotechnology</i> , 2011, 29, 644-652.	17.5	17,264
44	Exploiting Nucleotide Composition to Engineer Promoters. <i>PLoS ONE</i> , 2011, 6, e20136.	2.5	20
45	Identification of Repetitive Elements in the Genome of <i>Oreochromis niloticus</i> : Tilapia Repeat Masker. <i>Marine Biotechnology</i> , 2010, 12, 121-125.	2.4	21
46	High-throughput sequencing of microdissected chromosomal regions. <i>European Journal of Human Genetics</i> , 2010, 18, 457-462.	2.8	23
47	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.	27.8	1,442
48	Genome-wide synteny through highly sensitive sequence alignment: <i>Satsuma</i> . <i>Bioinformatics</i> , 2010, 26, 1145-1151.	4.1	258
49	Genomic Analysis of the Basal Lineage Fungus <i>Rhizopus oryzae</i> Reveals a Whole-Genome Duplication. <i>PLoS Genetics</i> , 2009, 5, e1000549.	3.5	332
50	Evolution of pathogenicity and sexual reproduction in eight <i>Candida</i> genomes. <i>Nature</i> , 2009, 459, 657-662.	27.8	963
51	Genome sequence and analysis of the Irish potato famine pathogen <i>Phytophthora infestans</i> . <i>Nature</i> , 2009, 461, 393-398.	27.8	1,405
52	A cis-acting regulatory mutation causes premature hair graying and susceptibility to melanoma in the horse. <i>Nature Genetics</i> , 2008, 40, 1004-1009.	21.4	271
53	Genome Sequence of <i>Aedes aegypti</i> , a Major Arbovirus Vector. <i>Science</i> , 2007, 316, 1718-1723.	12.6	1,025
54	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007, 447, 167-177.	27.8	661

#	ARTICLE	IF	CITATIONS
55	Genome sequence, comparative analysis and haplotype structure of the domestic dog. Nature, 2005, 438, 803-819.	27.8	2,215