

Manfred G Grabherr

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

38,928
citations

159358

30
h-index

182168

51
g-index

60
all docs

60
docs citations

60
times ranked

46648
citing authors

#	ARTICLE	IF	CITATIONS
1	Full-length transcriptome assembly from RNA-Seq data without a reference genome. <i>Nature Biotechnology</i> , 2011, 29, 644-652.	9.4	17,264
2	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.	5.5	7,054
3	Genome sequence, comparative analysis and haplotype structure of the domestic dog. <i>Nature</i> , 2005, 438, 803-819.	13.7	2,215
4	The genomic basis of adaptive evolution in threespine sticklebacks. <i>Nature</i> , 2012, 484, 55-61.	13.7	1,600
5	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.	13.7	1,442
6	Genome sequence and analysis of the Irish potato famine pathogen <i>Phytophthora infestans</i> . <i>Nature</i> , 2009, 461, 393-398.	13.7	1,405
7	Genome Sequence of <i>Aedes aegypti</i> , a Major Arbovirus Vector. <i>Science</i> , 2007, 316, 1718-1723.	6.0	1,025
8	Evolution of pathogenicity and sexual reproduction in eight <i>Candida</i> genomes. <i>Nature</i> , 2009, 459, 657-662.	13.7	963
9	Computational methods for transcriptome annotation and quantification using RNA-seq. <i>Nature Methods</i> , 2011, 8, 469-477.	9.0	919
10	Evolution of Darwin's finches and their beaks revealed by genome sequencing. <i>Nature</i> , 2015, 518, 371-375.	13.7	766
11	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007, 447, 167-177.	13.7	661
12	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.	3.3	640
13	The genome of the green anole lizard and a comparative analysis with birds and mammals. <i>Nature</i> , 2011, 477, 587-591.	13.7	575
14	Genomic Analysis of the Basal Lineage Fungus <i>Rhizopus oryzae</i> Reveals a Whole-Genome Duplication. <i>PLoS Genetics</i> , 2009, 5, e1000549.	1.5	332
15	A cis-acting regulatory mutation causes premature hair graying and susceptibility to melanoma in the horse. <i>Nature Genetics</i> , 2008, 40, 1004-1009.	9.4	271
16	Genome-wide synteny through highly sensitive sequence alignment: <i>Satsuma</i> . <i>Bioinformatics</i> , 2010, 26, 1145-1151.	1.8	258
17	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.	3.3	217
18	An Improved Canine Genome and a Comprehensive Catalogue of Coding Genes and Non-Coding Transcripts. <i>PLoS ONE</i> , 2014, 9, e91172.	1.1	206

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19	Reading and editing the <i>Pleurodeles waltl</i> genome reveals novel features of tetrapod regeneration. <i>Nature Communications</i> , 2017, 8, 2286.	5.8	123
20	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.	1.3	103
21	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.	3.3	91
22	Functional and evolutionary genomic inferences in <i>Populus</i> through genome and population sequencing of American and European aspen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10970-E10978.	3.3	84
23	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.	0.3	76
24	Coordinated Changes in Gene Expression Throughout Encystation of <i>Giardia intestinalis</i> . <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004571.	1.3	69
25	Unsupervised genome-wide recognition of local relationship patterns. <i>BMC Genomics</i> , 2013, 14, 347.	1.2	59
26	Correspondence on Lovell et al.: identification of chicken genes previously assumed to be evolutionarily lost. <i>Genome Biology</i> , 2017, 18, 112.	3.8	51
27	Efficient cellular fractionation improves RNA sequencing analysis of mature and nascent transcripts from human tissues. <i>BMC Biotechnology</i> , 2013, 13, 99.	1.7	47
28	Interactions of Freshwater Cyanobacteria with Bacterial Antagonists. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	39
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.	1.8	34
30	Comparative omics and feeding manipulations in chicken indicate a shift of the endocrine role of visceral fat towards reproduction. <i>BMC Genomics</i> , 2018, 19, 295.	1.2	33
31	Intra- and inter-individual metabolic profiling highlights carnitine and lysophosphatidylcholine pathways as key molecular defects in type 2 diabetes. <i>Scientific Reports</i> , 2019, 9, 9653.	1.6	32
32	Serendipitous Meta-Transcriptomics: The Fungal Community of Norway Spruce (<i>Picea abies</i>). <i>PLoS ONE</i> , 2015, 10, e0139080.	1.1	27
33	High-throughput sequencing of microdissected chromosomal regions. <i>European Journal of Human Genetics</i> , 2010, 18, 457-462.	1.4	23
34	Evolution of the p53-MDM2 pathway. <i>BMC Evolutionary Biology</i> , 2017, 17, 177.	3.2	23
35	Building de novo reference genome assemblies of complex eukaryotic microorganisms from single nuclei. <i>Scientific Reports</i> , 2020, 10, 1303.	1.6	22
36	Identification of Repetitive Elements in the Genome of <i>Oreochromis niloticus</i> : Tilapia Repeat Masker. <i>Marine Biotechnology</i> , 2010, 12, 121-125.	1.1	21

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37	Exploiting Nucleotide Composition to Engineer Promoters. PLoS ONE, 2011, 6, e20136.	1.1	20
38	Analyzing DNA methylation patterns in subjects diagnosed with schizophrenia using machine learning methods. Journal of Psychiatric Research, 2019, 114, 41-47.	1.5	19
39	Investigation of the host transcriptional response to intracellular bacterial infection using Dictyostelium discoideum as a host model. BMC Genomics, 2019, 20, 961.	1.2	17
40	Comparative Fungal Community Analyses Using Metatranscriptomics and Internal Transcribed Spacer Amplicon Sequencing from Norway Spruce. MSystems, 2021, 6, .	1.7	16
41	A practical guide to build <i>de-novo</i> assemblies for single tissues of non-model organisms: the example of a Neotropical frog. PeerJ, 2017, 5, e3702.	0.9	16
42	RNA-sequence data normalization through in silico prediction of reference genes: the bacterial response to DNA damage as case study. BioData Mining, 2017, 10, 30.	2.2	15
43	Combinatorial identification of DNA methylation patterns over age in the human brain. BMC Bioinformatics, 2016, 17, 393.	1.2	13
44	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, .	3.3	12
45	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.	1.5	9
46	A universal genomic coordinate translator for comparative genomics. BMC Bioinformatics, 2014, 15, 227.	1.2	7
47	PiiL: visualization of DNA methylation and gene expression data in gene pathways. BMC Genomics, 2017, 18, 571.	1.2	3
48	Artificially designed promoters. Bioengineered, 2012, 3, 120-123.	1.4	2
49	Modular and configurable optimal sequence alignment software: Cola. Source Code for Biology and Medicine, 2014, 9, 12.	1.7	2
50	Whiteboard: a framework for the programmatic visualization of complex biological analyses: Fig. 1.. Bioinformatics, 2015, 31, 2054-2055.	1.8	1
51	ACES: a machine learning toolbox for clustering analysis and visualization. BMC Genomics, 2018, 19, 964.	1.2	1
52	microTaboo: a general and practical solution to the k-disjoint problem. BMC Bioinformatics, 2017, 18, 228.	1.2	0
53	Special Issue Introduction: The Wonders and Mysteries Next Generation Sequencing Technologies Help Reveal. Genes, 2018, 9, 505.	1.0	0
54	EZTraits: A programmable tool to evaluate multi-site deterministic traits. PLoS ONE, 2022, 17, e0259327.	1.1	0

#	ARTICLE	IF	CITATIONS
55	Flexible Machine Learning Algorithms for Clinical Gait Assessment Tools. Sensors, 2022, 22, 4957.	2.1	0