

# 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  | Full-length transcriptome assembly from RNA-Seq data without a reference genome. <i>Nature Biotechnology</i> , 2011, 29, 644-652.   | 17.5 | 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.   | 12.0 | 7,054     |
| 3  | Genome sequence, comparative analysis and haplotype structure of the domestic dog. <i>Nature</i> , 2005, 438, 803-819.  | 27.8 | 2,215     |
| 4  | The genomic basis of adaptive evolution in threespine sticklebacks. <i>Nature</i> , 2012, 484, 55-61.   | 27.8 | 1,600     |
| 5  | Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.  | 27.8 | 1,442     |
| 6  | 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     |
| 7  | Genome Sequence of <i>Aedes aegypti</i> , a Major Arbovirus Vector. <i>Science</i> , 2007, 316, 1718-1723.  | 12.6 | 1,025     |
| 8  | Evolution of pathogenicity and sexual reproduction in eight <i>Candida</i> genomes. <i>Nature</i> , 2009, 459, 657-662.   | 27.8 | 963       |
| 9  | Computational methods for transcriptome annotation and quantification using RNA-seq. <i>Nature Methods</i> , 2011, 8, 469-477.  | 19.0 | 919       |
| 10 | Evolution of Darwin's finches and their beaks revealed by genome sequencing. <i>Nature</i> , 2015, 518, 371-375.  | 27.8 | 766       |
| 11 | Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007, 447, 167-177.  | 27.8 | 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.                               | 7.1  | 640       |
| 13 | 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       |
| 14 | 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       |
| 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.   | 21.4 | 271       |
| 16 | Genome-wide synteny through highly sensitive sequence alignment: <i>Satsuma</i> . <i>Bioinformatics</i> , 2010, 26, 1145-1151.  | 4.1  | 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. | 7.1  | 217       |
| 18 | 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       |

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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.   | 12.8 | 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.   | 3.0  | 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.   | 7.1  | 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. | 7.1  | 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.  | 0.6  | 76        |
| 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 | Unsupervised genome-wide recognition of local relationship patterns. <i>BMC Genomics</i> , 2013, 14, 347.  | 2.8  | 59        |
| 26 | Correspondence on Lovell et al.: identification of chicken genes previously assumed to be evolutionarily lost. <i>Genome Biology</i> , 2017, 18, 112.  | 8.8  | 51        |
| 27 | Efficient cellular fractionation improves RNA sequencing analysis of mature and nascent transcripts from human tissues. <i>BMC Biotechnology</i> , 2013, 13, 99.   | 3.3  | 47        |
| 28 | Interactions of Freshwater Cyanobacteria with Bacterial Antagonists. <i>Applied and Environmental Microbiology</i> , 2017, 83, .   | 3.1  | 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.   | 3.8  | 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.   | 2.8  | 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.  | 3.3  | 32        |
| 32 | Serendipitous Meta-Transcriptomics: The Fungal Community of Norway Spruce ( <i>Picea abies</i> ). <i>PLoS ONE</i> , 2015, 10, e0139080.  | 2.5  | 27        |
| 33 | High-throughput sequencing of microdissected chromosomal regions. <i>European Journal of Human Genetics</i> , 2010, 18, 457-462.   | 2.8  | 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.  | 3.3  | 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.  | 2.4  | 21        |

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|----|--|-----|-----------|
| 37 | Exploiting Nucleotide Composition to Engineer Promoters. PLoS ONE, 2011, 6, e20136.  | 2.5 | 20        |
| 38 | Analyzing DNA methylation patterns in subjects diagnosed with schizophrenia using machine learning methods. Journal of Psychiatric Research, 2019, 114, 41-47.                           | 3.1 | 19        |
| 39 | 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        |
| 40 | Comparative Fungal Community Analyses Using Metatranscriptomics and Internal Transcribed Spacer Amplicon Sequencing from Norway Spruce. MSystems, 2021, 6, .                             | 3.8 | 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.                                | 2.0 | 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.                       | 4.0 | 15        |
| 43 | Combinatorial identification of DNA methylation patterns over age in the human brain. BMC Bioinformatics, 2016, 17, 393.   | 2.6 | 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, . | 7.1 | 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.                  | 3.1 | 9         |
| 46 | A universal genomic coordinate translator for comparative genomics. BMC Bioinformatics, 2014, 15, 227.   | 2.6 | 7         |
| 47 | PiiL: visualization of DNA methylation and gene expression data in gene pathways. BMC Genomics, 2017, 18, 571.   | 2.8 | 3         |
| 48 | Artificially designed promoters. Bioengineered, 2012, 3, 120-123.  | 3.2 | 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.   | 4.1 | 1         |
| 51 | ACES: a machine learning toolbox for clustering analysis and visualization. BMC Genomics, 2018, 19, 964.   | 2.8 | 1         |
| 52 | microTaboo: a general and practical solution to the k-disjoint problem. BMC Bioinformatics, 2017, 18, 228.   | 2.6 | 0         |
| 53 | Special Issue Introduction: The Wonders and Mysteries Next Generation Sequencing Technologies Help Reveal. Genes, 2018, 9, 505.  | 2.4 | 0         |
| 54 | EZTraits: A programmable tool to evaluate multi-site deterministic traits. PLoS ONE, 2022, 17, e0259327.   | 2.5 | 0         |

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 55 | Flexible Machine Learning Algorithms for Clinical Gait Assessment Tools. Sensors, 2022, 22, 4957. | 3.8 | 0         |