

# Gernot Glöckner

## List of Publications by Year in descending order

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121  
papers

35,710  
citations

46918

47  
h-index

18075

120  
g-index

125  
all docs

125  
docs citations

125  
times ranked

37718  
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	13.7	21,074
2	Finishing the euchromatic sequence of the human genome. <i>Nature</i> , 2004, 431, 931-945.	13.7	4,232
3	The genome of the social amoeba <i>Dictyostelium discoideum</i> . <i>Nature</i> , 2005, 435, 43-57.	13.7	1,179
4	The DNA sequence of the human X chromosome. <i>Nature</i> , 2005, 434, 325-337.	13.7	985
5	A physical map of the human genome. <i>Nature</i> , 2001, 409, 934-941.	13.7	865
6	The butterfly plant arms-race escalated by gene and genome duplications. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8362-8366.	3.3	458
7	Pan genome of the phytoplankton <i>Emiliania underpins</i> its global distribution. <i>Nature</i> , 2013, 499, 209-213.	13.7	448
8	The Chara Genome: Secondary Complexity and Implications for Plant Terrestrialization. <i>Cell</i> , 2018, 174, 448-464.e24.	13.5	420
9	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , 2017, 541, 536-540.	13.7	332
10	Chromatophore Genome Sequence of <i>Paulinella</i> Sheds Light on Acquisition of Photosynthesis by Eukaryotes. <i>Current Biology</i> , 2008, 18, 410-418.	1.8	325
11	Mutations in a new gene, encoding a zinc-finger protein, cause tricho-rhino-phalangeal syndrome type I. <i>Nature Genetics</i> , 2000, 24, 71-74.	9.4	299
12	Origin of land plants: Do conjugating green algae hold the key?. <i>BMC Evolutionary Biology</i> , 2011, 11, 104.	3.2	272
13	Metabarcoding vs. morphological identification to assess diatom diversity in environmental studies. <i>Molecular Ecology Resources</i> , 2015, 15, 526-542.	2.2	212
14	A comprehensive transcriptome and immune-gene repertoire of the lepidopteran model host <i>Galleria mellonella</i> . <i>BMC Genomics</i> , 2011, 12, 308.	1.2	210
15	Comparative and functional genomics provide insights into the pathogenicity of dermatophytic fungi. <i>Genome Biology</i> , 2011, 12, R7.	13.9	181
16	Sequence and analysis of chromosome 2 of <i>Dictyostelium discoideum</i> . <i>Nature</i> , 2002, 418, 79-85.	13.7	176
17	The Smallest Known Genomes of Multicellular and Toxic Cyanobacteria: Comparison, Minimal Gene Sets for Linked Traits and the Evolutionary Implications. <i>PLoS ONE</i> , 2010, 5, e9235.	1.1	168
18	Phylogeny-wide analysis of social amoeba genomes highlights ancient origins for complex intercellular communication. <i>Genome Research</i> , 2011, 21, 1882-1891.	2.4	145

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19	The Structure and Gene Repertoire of an Ancient Red Algal Plastid Genome. <i>Journal of Molecular Evolution</i> , 2000, 51, 382-390.	0.8	126
20	Identification and characterization of a new conjugation/type IVA secretion system (trb/tra) of <i>Legionella pneumophila</i> Corby localized on two mobile genomic islands. <i>International Journal of Medical Microbiology</i> , 2008, 298, 411-428.	1.5	122
21	DNA sequence and analysis of human chromosome 8. <i>Nature</i> , 2006, 439, 331-335.	13.7	115
22	Endosymbiotic Gene Transfer and Transcriptional Regulation of Transferred Genes in <i>Paulinella chromatophora</i> . <i>Molecular Biology and Evolution</i> , 2011, 28, 407-422.	3.5	110
23	Comparative analysis of the <i>Borrelia garinii</i> genome. <i>Nucleic Acids Research</i> , 2004, 32, 6038-6046.	6.5	109
24	The <i>Dictyostelium discoideum</i> family of Rho-related proteins. <i>Nucleic Acids Research</i> , 2001, 29, 1068-1079.	6.5	96
25	Comparative Genomic and Transcriptomic Characterization of the Toxigenic Marine Dinoflagellate <i>Alexandrium ostenfeldii</i> . <i>PLoS ONE</i> , 2011, 6, e28012.	1.1	92
26	The ancestor of the <i>Paulinella chromatophore</i> obtained a carboxysomal operon by horizontal gene transfer from a Nitrococcus-like $\beta$ -proteobacterium. <i>BMC Evolutionary Biology</i> , 2007, 7, 85.	3.2	90
27	<i>Legionella</i> pathogenicity: Genome structure, regulatory networks and the host cell response. <i>International Journal of Medical Microbiology</i> , 2007, 297, 577-587.	1.5	88
28	High tandem repeat content in the genome of the short-lived annual fish <i>Nothobranchius furzeri</i> : a new vertebrate model for aging research. <i>Genome Biology</i> , 2009, 10, R16.	13.9	87
29	The <i>Physarum polycephalum</i> Genome Reveals Extensive Use of Prokaryotic Two-Component and Metazoan-Type Tyrosine Kinase Signaling. <i>Genome Biology and Evolution</i> , 2016, 8, 109-125.	1.1	87
30	The origins of eukaryotic-like proteins in <i>Legionella pneumophila</i> . <i>International Journal of Medical Microbiology</i> , 2010, 300, 470-481.	1.5	86
31	Proteomic analysis of <i>Legionella</i> -containing phagosomes isolated from <i>Dictyostelium</i> . <i>International Journal of Medical Microbiology</i> , 2009, 299, 489-508.	1.5	82
32	Comparative analyses of <i>Legionella</i> species identifies genetic features of strains causing Legionnairesâ€™ disease. <i>Genome Biology</i> , 2014, 15, 505.	3.8	82
33	An aerobic eukaryotic parasite with functional mitochondria that likely lacks a mitochondrial genome. <i>Science Advances</i> , 2019, 5, eaav1110.	4.7	76
34	Evolutionary Analyses of ABC Transporters of <i>Dictyostelium discoideum</i> . <i>Eukaryotic Cell</i> , 2002, 1, 643-652.	3.4	75
35	Comparative gene expression in toxic versus non-toxic strains of the marine dinoflagellate <i>Alexandrium minutum</i> . <i>BMC Genomics</i> , 2010, 11, 248.	1.2	73
36	The Genome of the Foraminiferan <i>Reticulomyxa filosa</i> . <i>Current Biology</i> , 2014, 24, 11-18.	1.8	73

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37	Cyanobacterial diversity in the hot spring, pelagic and benthic habitats of a tropical soda lake. <i>FEMS Microbiology Ecology</i> , 2013, 85, 389-401.	1.3	71
38	The transcriptome of <i>Spodoptera exigua</i> larvae exposed to different types of microbes. <i>Insect Biochemistry and Molecular Biology</i> , 2012, 42, 557-570.	1.2	70
39	The multicellularity genes of dictyostelid social amoebas. <i>Nature Communications</i> , 2016, 7, 12085.	5.8	63
40	Comparative analyses of <i>Legionella</i> species identifies genetic features of strains causing Legionnaires' disease. <i>Genome Biology</i> , 2014, 15, 505.	13.9	62
41	Large-Scale Sequencing of Two Regions in Human Chromosome 7q22: Analysis of 650 kb of Genomic Sequence around the <i>EPO</i> and <i>CUTL1</i> Loci Reveals 17 Genes. <i>Genome Research</i> , 1998, 8, 1060-1073.	2.4	57
42	Analysis of phenotypic evolution in <i>Dictyostelia</i> highlights developmental plasticity as a likely consequence of colonial multicellularity. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20130976.	1.2	57
43	UNDERSTANDING NITROGEN LIMITATION IN <i>AUREOCOCCUS ANOPHAGEFFERENS</i> (PELAGOPHYCEAE) THROUGH cDNA AND qRT-PCR ANALYSIS. <i>Journal of Phycology</i> , 2008, 44, 1235-1249.	1.0	56
44	A new class of ice-binding proteins discovered in a salt-stress-induced cDNA library of the psychrophilic diatom <i>Fragilariopsis cylindrus</i> (Bacillariophyceae). <i>European Journal of Phycology</i> , 2008, 43, 423-433.	0.9	56
45	The Complex Repeats of <i>Dictyostelium discoideum</i> . <i>Genome Research</i> , 2001, 11, 585-594.	2.4	56
46	The nuclear envelope protein Nesprin-2 has roles in cell proliferation and differentiation during wound healing. <i>Nucleus</i> , 2012, 3, 172-186.	0.6	52
47	Comparative genome analysis: selection pressure on the <i>Borrelia</i> vls cassettes is essential for infectivity. <i>BMC Genomics</i> , 2006, 7, 211.	1.2	50
48	Comparative Genome Sequence Analysis of the Bpa/Str Region in Mouse and Man. <i>Genome Research</i> , 2000, 10, 758-775.	2.4	48
49	The Complex Repeats of <i>Dictyostelium discoideum</i> . <i>Genome Research</i> , 2001, 11, 585-594.	2.4	47
50	ANALYSIS OF EXPRESSED SEQUENCE TAGS (ESTS) FROM THE POLAR DIATOM FRAGILARIOPSIS CYLINDRUS1. <i>Journal of Phycology</i> , 2006, 42, 78-85.	1.0	46
51	High-throughput sequencing of a single chromosome: a moth W chromosome. <i>Chromosome Research</i> , 2013, 21, 491-505.	1.0	45
52	EST analysis of the scaly green flagellate <i>Mesostigma viride</i> (Streptophyta): implications for the evolution of green plants (Viridiplantae). <i>BMC Plant Biology</i> , 2006, 6, 2.	1.6	42
53	Genomic Insights into Processes Driving the Infection of <i>Alexandrium tamarense</i> by the Parasitoid <i>Amoebophrya</i> sp. <i>Eukaryotic Cell</i> , 2014, 13, 1439-1449.	3.4	42
54	From Green to Red: Horizontal Gene Transfer of the Phycoerythrin Gene Cluster between <i>Planktothrix</i> Strains. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6803-6812.	1.4	39

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55	NKAP is a novel RS-related protein that interacts with RNA and RNA binding proteins. <i>Nucleic Acids Research</i> , 2014, 42, 3177-3193.	6.5	39
56	Multiple Roots of Fruiting Body Formation in Amoebozoa. <i>Genome Biology and Evolution</i> , 2018, 10, 591-606.	1.1	39
57	A first glimpse at the transcriptome of <i>Physarum polycephalum</i> . <i>BMC Genomics</i> , 2008, 9, 6.	1.2	38
58	The <i>Dictyostelium</i> genome encodes numerous RasGEFs with multiple biological roles. <i>Genome Biology</i> , 2005, 6, R68.	13.9	36
59	Responses of the kelp <i>Saccharina latissima</i> (Phaeophyceae) to the warming Arctic: from physiology to transcriptomics. <i>Physiologia Plantarum</i> , 2020, 168, 5-26.	2.6	33
60	Mitochondrial Genome Evolution in the Social Amoebae. <i>Molecular Biology and Evolution</i> , 2008, 25, 1440-1450.	3.5	32
61	Transcriptomic response of the toxic prymnesiophyte <i>Prymnesium parvum</i> (N. Carter) to phosphorus and nitrogen starvation. <i>Harmful Algae</i> , 2012, 18, 1-15.	2.2	32
62	Identification and phylogenetic analysis of <i>Dictyostelium discoideum</i> kinesin proteins. <i>BMC Genomics</i> , 2003, 4, 47.	1.2	31
63	The Actinome of <i>Dictyostelium discoideum</i> in Comparison to Actins and Actin-Related Proteins from Other Organisms. <i>PLoS ONE</i> , 2008, 3, e2654.	1.1	30
64	Genomic Structure of a Novel LIM Domain Gene (ZNF185) in Xq28 and Comparisons with the Orthologous Murine Transcript. <i>Genomics</i> , 1997, 43, 329-338.	1.3	29
65	Unusual combinatorial involvement of poly-A/T tracts in organizing genes and chromatin in <i>Dictyostelium</i> . <i>Genome Research</i> , 2012, 22, 1098-1106.	2.4	29
66	Non-LTR retrotransposons with unique integration preferences downstream of <i>Dictyostelium discoideum</i> tRNA genes. <i>Molecular Genetics and Genomics</i> , 1999, 262, 772-780.	2.4	28
67	Transfer RNA gene-targeted integration: an adaptation of retrotransposable elements to survive in the compact <i>Dictyostelium discoideum</i> genome. <i>Cytogenetic and Genome Research</i> , 2005, 110, 288-298.	0.6	28
68	Centromere sequence and dynamics in <i>Dictyostelium discoideum</i> . <i>Nucleic Acids Research</i> , 2009, 37, 1809-1816.	6.5	27
69	RpkA, a Highly Conserved GPCR with a Lipid Kinase Domain, Has a Role in Phagocytosis and Anti-Bacterial Defense. <i>PLoS ONE</i> , 2011, 6, e27311.	1.1	26
70	RUMMAGE – a high-throughput sequence annotation system. <i>Trends in Genetics</i> , 2000, 16, 519-521.	2.9	25
71	Developmental Gene Regulation by an Ancient Intercellular Communication System in Social Amoebae. <i>Protist</i> , 2012, 163, 25-37.	0.6	25
72	<i>Chlamydomonas</i> mutants affected in the light-dependent step of sexual differentiation.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993, 90, 6981-6985.	3.3	23

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73	Gain and loss of polyadenylation signals during evolution of green algae. BMC Evolutionary Biology, 2007, 7, 65.	3.2	23
74	Transcriptomic changes arising during light-induced sporulation in <i>Physarum polycephalum</i> . BMC Genomics, 2010, 11, 115.	1.2	23
75	Gene Organization Features in A/T-Rich Organisms. Journal of Molecular Evolution, 2005, 60, 90-98.	0.8	22
76	A comprehensive cDNA library of light- and temperature-stressed <i>Saccharina latissima</i> (Phaeophyceae). European Journal of Phycology, 2012, 47, 83-94.	0.9	22
77	Transcriptomic profiling of <i>Alexandrium fundyense</i> during physical interaction with or exposure to chemical signals from the parasite <i>Amoebophrya</i> . Molecular Ecology, 2016, 25, 1294-1307.	2.0	22
78	A Tripeptidyl peptidase 1 is a binding partner of GPHR (Golgi pH regulator) in <i>Dictyostelium</i> . DMM Disease Models and Mechanisms, 2017, 10, 897-907.	1.2	22
79	Genomic characterisation of the ichthyotoxic prymnesiophyte <i>Chrysochromulina polylepis</i> and the expression of polyketide synthase genes in synchronized cultures. European Journal of Phycology, 2010, 45, 215-229.	0.9	21
80	Should the draft chimpanzee sequence be finished?. Trends in Genetics, 2006, 22, 122-125.	2.9	19
81	Redundant and unique roles of coronin proteins in <i>Dictyostelium</i> . Cellular and Molecular Life Sciences, 2011, 68, 303-313.	2.4	19
82	Multifunctional Centromere Binding Factor 1 Is Essential for Chromosome Segregation in the Human Pathogenic Yeast <i>Candida glabrata</i> . Molecular and Cellular Biology, 2001, 21, 4875-4888.	1.1	17
83	Convergent evolution of tRNA gene targeting preferences in compact genomes. Mobile DNA, 2016, 7, 17.	1.3	17
84	GenColors: accelerated comparative analysis and annotation of prokaryotic genomes at various stages of completeness. Bioinformatics, 2005, 21, 3669-3671.	1.8	16
85	The Mitochondrial Genome of <i>Arctica islandica</i> ; Phylogeny and Variation. PLoS ONE, 2013, 8, e82857.	1.1	16
86	Root of Dictyostelia based on 213 universal proteins. Molecular Phylogenetics and Evolution, 2015, 92, 53-62.	1.2	16
87	Transcriptome reprogramming during developmental switching in <i>Physarum polycephalum</i> involves extensive remodeling of intracellular signaling networks. Scientific Reports, 2017, 7, 12304.	1.6	16
88	Temperature Modulates Sex-Biased Gene Expression in the Gametophytes of the Kelp <i>Saccharina latissima</i> . Frontiers in Marine Science, 2019, 6, .	1.2	16
89	Role of RNA Polymerase III Transcription Factors in the Selection of Integration Sites by the <i>Dictyostelium</i> Non-Long Terminal Repeat Retrotransposon TRE5-A. Molecular and Cellular Biology, 2006, 26, 8242-8251.	1.1	15
90	Adaptive divergence across Southern Ocean gradients in the pelagic diatom <i>Fragilariopsis kerguelensis</i> . Molecular Ecology, 2020, 29, 4913-4924.	2.0	15

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91	Cloning and characterization of <i>LRC5</i> , a gene involved in blue light signaling in <i>Chlamydomonas</i> gametogenesis. <i>Plant Journal</i> , 1997, 12, 677-683.	2.8	14
92	Comparative genomics in the <i>A</i> moebozoa clade. <i>Biological Reviews</i> , 2013, 88, 215-225.	4.7	14
93	Is geographical variation driving the transcriptomic responses to multiple stressors in the kelp <i>Saccharina latissima</i> ?. <i>BMC Plant Biology</i> , 2019, 19, 513.	1.6	14
94	Large Scale Sequencing and Analysis of AT Rich Eukaryote Genomes. <i>Current Genomics</i> , 2000, 1, 289-299.	0.7	14
95	A set of genes conserved in sequence and expression traces back the establishment of multicellularity in social amoebae. <i>BMC Genomics</i> , 2016, 17, 871.	1.2	13
96	Genome size shifts: karyotype evolution in <i>C</i> repis section <i>N</i> eglectoides ( <i>A</i> steraceae). <i>Plant Biology</i> , 2015, 17, 775-786.	1.8	11
97	Template jumping by a LINE reverse transcriptase has created a SINE-like 5S rRNA retropseudogene in <i>Dictyostelium</i> . <i>Molecular Genetics and Genomics</i> , 2004, 271, 98-102.	1.0	10
98	The function of the inner nuclear envelope protein SUN1 in mRNA export is regulated by phosphorylation. <i>Scientific Reports</i> , 2017, 7, 9157.	1.6	10
99	Depletion of Nesprin-2 is associated with an embryonic lethal phenotype in mice. <i>Nucleus</i> , 2018, 9, 503-515.	0.6	10
100	Knock-out of a putative transporter results in altered blue-light signalling in <i>Chlamydomonas</i> . <i>Plant Journal</i> , 2002, 31, 577-587.	2.8	8
101	GenColors. <i>Methods in Molecular Biology</i> , 2007, , 75-96.	0.4	8
102	A Cytohesin Homolog in <i>Dictyostelium</i> Amoebae. <i>PLoS ONE</i> , 2010, 5, e9378.	1.1	8
103	GenColors-based comparative genome databases for small eukaryotic genomes. <i>Nucleic Acids Research</i> , 2012, 41, D692-D699.	6.5	7
104	Improved annotation with de novo transcriptome assembly in four social amoeba species. <i>BMC Genomics</i> , 2017, 18, 120.	1.2	7
105	RNAseq and quantitative proteomic analysis of <i>Dictyostelium</i> knock-out cells lacking the core autophagy proteins ATG9 and/or ATG16. <i>BMC Genomics</i> , 2021, 22, 444.	1.2	7
106	Increased Heat Resilience of Intraspecific Outbred Compared to Inbred Lineages in the Kelp <i>Laminaria digitata</i> : Physiology and Transcriptomics. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	7
107	Cloning and characterization of <i>LRC5</i> , a gene involved in blue light signaling in <i>Chlamydomonas</i> gametogenesis. <i>Plant Journal</i> , 1997, 12, 677-683.	2.8	6
108	Conserved Gene Regulatory Function of the Carboxy-Terminal Domain of <i>Dictyostelid</i> C-Module-Binding Factor. <i>Eukaryotic Cell</i> , 2013, 12, 460-468.	3.4	5

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109	Loss of a chloroplast encoded function could influence species range in kelp. <i>Ecology and Evolution</i> , 2019, 9, 8759-8770.	0.8	5
110	Transcriptomic Responses to Darkness and the Survival Strategy of the Kelp <i>Saccharina latissima</i> in the Early Polar Night. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	5
111	Abundantly expressed class of noncoding RNAs conserved through the multicellular evolution of dictyostelid social amoebas. <i>Genome Research</i> , 2021, 31, 436-447.	2.4	5
112	GenColors: annotation and comparative genomics of prokaryotes made easy. <i>Methods in Molecular Biology</i> , 2007, 395, 75-96.	0.4	5
113	Comparative analysis of the PCOLCE region in <i>Fugu rubripes</i> using a new automated annotation tool. <i>Mammalian Genome</i> , 2000, 11, 213-219.	1.0	3
114	Presence of male mitochondria in somatic tissues and their functional importance at the whole animal level in the marine bivalve <i>Arctica islandica</i> . <i>Communications Biology</i> , 2021, 4, 1104.	2.0	3
115	The C-Terminal SynMuv/DdDUF926 Domain Regulates the Function of the N-Terminal Domain of DdNKAP. <i>PLoS ONE</i> , 2016, 11, e0168617.	1.1	3
116	Analysis of organellar genomes in brown algae reveals an independent introduction of similar foreign sequences into the mitochondrial genome. <i>Genomics</i> , 2021, 113, 646-654.	1.3	2
117	TRE5-A retrotransposition profiling reveals putative RNA polymerase III transcription complex binding sites on the <i>Dictyostelium</i> extrachromosomal rDNA element. <i>PLoS ONE</i> , 2017, 12, e0175729.	1.1	2
118	Social Amoebae and Their Genomes: On the Brink to True Multicellularity. <i>Advances in Marine Genomics</i> , 2015, , 363-376.	1.2	2
119	DictyMOLD-a <i>Dictyostelium discoideum</i> genome browser database. <i>Bioinformatics</i> , 2005, 21, 696-697.	1.8	1
120	Model Host Systems: Tools for Comprehensive Analysis of Host-Pathogen Interactions. , 2006, , 445-456.		0
121	Genome Analysis of Social Amoebae. , 2013, , 35-47.		0