

Gernot Glöckner

List of Publications by Year in descending order

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121
papers

35,710
citations

46918

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18075

120
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125
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docs citations

125
times ranked

37718
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	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
4	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
5	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
6	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
7	Adaptive divergence across Southern Ocean gradients in the pelagic diatom <i>Fragilariopsis kerguelensis</i> . <i>Molecular Ecology</i> , 2020, 29, 4913-4924.	2.0	15
8	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
9	Loss of a chloroplast encoded function could influence species range in kelp. <i>Ecology and Evolution</i> , 2019, 9, 8759-8770.	0.8	5
10	An aerobic eukaryotic parasite with functional mitochondria that likely lacks a mitochondrial genome. <i>Science Advances</i> , 2019, 5, eaav1110.	4.7	76
11	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
12	Temperature Modulates Sex-Biased Gene Expression in the Gametophytes of the Kelp <i>Saccharina latissima</i> . <i>Frontiers in Marine Science</i> , 2019, 6, .	1.2	16
13	Multiple Roots of Fruiting Body Formation in Amoebozoa. <i>Genome Biology and Evolution</i> , 2018, 10, 591-606.	1.1	39
14	Depletion of Nesprin-2 is associated with an embryonic lethal phenotype in mice. <i>Nucleus</i> , 2018, 9, 503-515.	0.6	10
15	The Chara Genome: Secondary Complexity and Implications for Plant Terrestrialization. <i>Cell</i> , 2018, 174, 448-464.e24.	13.5	420
16	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , 2017, 541, 536-540.	13.7	332
17	A Tripeptidyl peptidase 1 is a binding partner of GPHR (Golgi pH regulator) in <i>Dictyostelium</i> . <i>DMM Disease Models and Mechanisms</i> , 2017, 10, 897-907.	1.2	22
18	Transcriptome reprogramming during developmental switching in <i>Physarum polycephalum</i> involves extensive remodeling of intracellular signaling networks. <i>Scientific Reports</i> , 2017, 7, 12304.	1.6	16

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19	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
20	Improved annotation with de novo transcriptome assembly in four social amoeba species. <i>BMC Genomics</i> , 2017, 18, 120.	1.2	7
21	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
22	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
23	Transcriptomic profiling of <i>Alexandrium fundyense</i> during physical interaction with or exposure to chemical signals from the parasite <i>Amoebophrya</i> . <i>Molecular Ecology</i> , 2016, 25, 1294-1307.	2.0	22
24	The multicellularity genes of dictyostelid social amoebas. <i>Nature Communications</i> , 2016, 7, 12085.	5.8	63
25	Convergent evolution of tRNA gene targeting preferences in compact genomes. <i>Mobile DNA</i> , 2016, 7, 17.	1.3	17
26	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
27	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
28	Genome size shifts: karyotype evolution in <i>C. repis</i> section <i>N. eglectoides</i> (<i>A. steraceae</i>). <i>Plant Biology</i> , 2015, 17, 775-786.	1.8	11
29	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
30	Root of Dictyostelia based on 213 universal proteins. <i>Molecular Phylogenetics and Evolution</i> , 2015, 92, 53-62.	1.2	16
31	Metabarcoding vs. morphological identification to assess diatom diversity in environmental studies. <i>Molecular Ecology Resources</i> , 2015, 15, 526-542.	2.2	212
32	Social Amoebae and Their Genomes: On the Brink to True Multicellularity. <i>Advances in Marine Genomics</i> , 2015, , 363-376.	1.2	2
33	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
34	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
35	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
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	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
38	Pan genome of the phytoplankton <i>Emiliania</i> underpins its global distribution. <i>Nature</i> , 2013, 499, 209-213.	13.7	448
39	High-throughput sequencing of a single chromosome: a moth W chromosome. <i>Chromosome Research</i> , 2013, 21, 491-505.	1.0	45
40	Comparative genomics in the <i>Amoebozoa</i> clade. <i>Biological Reviews</i> , 2013, 88, 215-225.	4.7	14
41	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
42	Conserved Gene Regulatory Function of the Carboxy-Terminal Domain of Dictyostelid C-Module-Binding Factor. <i>Eukaryotic Cell</i> , 2013, 12, 460-468.	3.4	5
43	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
44	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
45	The Mitochondrial Genome of <i>Arctica islandica</i> ; Phylogeny and Variation. <i>PLoS ONE</i> , 2013, 8, e82857.	1.1	16
46	Genome Analysis of Social Amoebae. , 2013, , 35-47.		0
47	GenColors-based comparative genome databases for small eukaryotic genomes. <i>Nucleic Acids Research</i> , 2012, 41, D692-D699.	6.5	7
48	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
49	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
50	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
51	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
52	A comprehensive cDNA library of light- and temperature-stressed <i>Saccharina latissima</i> (Phaeophyceae). <i>European Journal of Phycology</i> , 2012, 47, 83-94.	0.9	22
53	Developmental Gene Regulation by an Ancient Intercellular Communication System in Social Amoebae. <i>Protist</i> , 2012, 163, 25-37.	0.6	25
54	Comparative and functional genomics provide insights into the pathogenicity of dermatophytic fungi. <i>Genome Biology</i> , 2011, 12, R7.	13.9	181

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55	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
56	Redundant and unique roles of coronin proteins in <i>Dictyostelium</i> . <i>Cellular and Molecular Life Sciences</i> , 2011, 68, 303-313.	2.4	19
57	Origin of land plants: Do conjugating green algae hold the key?. <i>BMC Evolutionary Biology</i> , 2011, 11, 104.	3.2	272
58	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
59	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
60	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
61	Comparative Genomic and Transcriptomic Characterization of the Toxigenic Marine Dinoflagellate <i>Alexandrium ostenfeldii</i> . <i>PLoS ONE</i> , 2011, 6, e28012.	1.1	92
62	Transcriptomic changes arising during light-induced sporulation in <i>Physarum polycephalum</i> . <i>BMC Genomics</i> , 2010, 11, 115.	1.2	23
63	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
64	Genomic characterisation of the ichthyotoxic prymnesiophyte <i>Chrysochromulina polylepis</i> and the expression of polyketide synthase genes in synchronized cultures. <i>European Journal of Phycology</i> , 2010, 45, 215-229.	0.9	21
65	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
66	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
67	A Cytohesin Homolog in <i>Dictyostelium</i> Amoebae. <i>PLoS ONE</i> , 2010, 5, e9378.	1.1	8
68	Centromere sequence and dynamics in <i>Dictyostelium discoideum</i> . <i>Nucleic Acids Research</i> , 2009, 37, 1809-1816.	6.5	27
69	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
70	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
71	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
72	A first glimpse at the transcriptome of <i>Physarum polycephalum</i> . <i>BMC Genomics</i> , 2008, 9, 6.	1.2	38

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73	Chromatophore Genome Sequence of Paulinella Sheds Light on Acquisition of Photosynthesis by Eukaryotes. <i>Current Biology</i> , 2008, 18, 410-418.	1.8	325
74	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
75	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
76	Mitochondrial Genome Evolution in the Social Amoebae. <i>Molecular Biology and Evolution</i> , 2008, 25, 1440-1450.	3.5	32
77	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
78	<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
79	Gain and loss of polyadenylation signals during evolution of green algae. <i>BMC Evolutionary Biology</i> , 2007, 7, 65.	3.2	23
80	The ancestor of the Paulinella chromatophore obtained a carboxysomal operon by horizontal gene transfer from a Nitrococcus-like β -proteobacterium. <i>BMC Evolutionary Biology</i> , 2007, 7, 85.	3.2	90
81	GenColors. <i>Methods in Molecular Biology</i> , 2007, , 75-96.	0.4	8
82	GenColors: annotation and comparative genomics of prokaryotes made easy. <i>Methods in Molecular Biology</i> , 2007, 395, 75-96.	0.4	5
83	Model Host Systems: Tools for Comprehensive Analysis of Host-Pathogen Interactions. , 2006, , 445-456.		0
84	ANALYSIS OF EXPRESSED SEQUENCE TAGS (ESTS) FROM THE POLAR DIATOM FRAGILARIOPSIS CYLINDRUS1. <i>Journal of Phycology</i> , 2006, 42, 78-85.	1.0	46
85	DNA sequence and analysis of human chromosome 8. <i>Nature</i> , 2006, 439, 331-335.	13.7	115
86	Should the draft chimpanzee sequence be finished?. <i>Trends in Genetics</i> , 2006, 22, 122-125.	2.9	19
87	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
88	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
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. <i>Molecular and Cellular Biology</i> , 2006, 26, 8242-8251.	1.1	15
90	The DNA sequence of the human X chromosome. <i>Nature</i> , 2005, 434, 325-337.	13.7	985

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91	The genome of the social amoeba <i>Dictyostelium discoideum</i> . <i>Nature</i> , 2005, 435, 43-57.	13.7	1,179
92	Gene Organization Features in A/T-Rich Organisms. <i>Journal of Molecular Evolution</i> , 2005, 60, 90-98.	0.8	22
93	DictyMOLD-a <i>Dictyostelium discoideum</i> genome browser database. <i>Bioinformatics</i> , 2005, 21, 696-697.	1.8	1
94	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
95	GenColors: accelerated comparative analysis and annotation of prokaryotic genomes at various stages of completeness. <i>Bioinformatics</i> , 2005, 21, 3669-3671.	1.8	16
96	The <i>Dictyostelium</i> genome encodes numerous RasGEFs with multiple biological roles. <i>Genome Biology</i> , 2005, 6, R68.	13.9	36
97	Comparative analysis of the <i>Borrelia garinii</i> genome. <i>Nucleic Acids Research</i> , 2004, 32, 6038-6046.	6.5	109
98	Finishing the euchromatic sequence of the human genome. <i>Nature</i> , 2004, 431, 931-945.	13.7	4,232
99	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
100	Identification and phylogenetic analysis of <i>Dictyostelium discoideum</i> kinesin proteins. <i>BMC Genomics</i> , 2003, 4, 47.	1.2	31
101	Evolutionary Analyses of ABC Transporters of <i>Dictyostelium discoideum</i> . <i>Eukaryotic Cell</i> , 2002, 1, 643-652.	3.4	75
102	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
103	Sequence and analysis of chromosome 2 of <i>Dictyostelium discoideum</i> . <i>Nature</i> , 2002, 418, 79-85.	13.7	176
104	A physical map of the human genome. <i>Nature</i> , 2001, 409, 934-941.	13.7	865
105	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	13.7	21,074
106	Multifunctional Centromere Binding Factor 1 Is Essential for Chromosome Segregation in the Human Pathogenic Yeast <i>Candida glabrata</i> . <i>Molecular and Cellular Biology</i> , 2001, 21, 4875-4888.	1.1	17
107	The <i>Dictyostelium discoideum</i> family of Rho-related proteins. <i>Nucleic Acids Research</i> , 2001, 29, 1068-1079.	6.5	96
108	The Complex Repeats of <i>Dictyostelium discoideum</i> . <i>Genome Research</i> , 2001, 11, 585-594.	2.4	47

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109	The Complex Repeats of <i>Dictyostelium discoideum</i> . <i>Genome Research</i> , 2001, 11, 585-594.	2.4	56
110	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
111	RUMMAGE – a high-throughput sequence annotation system. <i>Trends in Genetics</i> , 2000, 16, 519-521.	2.9	25
112	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
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	Comparative Genome Sequence Analysis of the Bpa/Str Region in Mouse and Man. <i>Genome Research</i> , 2000, 10, 758-775.	2.4	48
115	Large Scale Sequencing and Analysis of AT Rich Eukaryote Genomes. <i>Current Genomics</i> , 2000, 1, 289-299.	0.7	14
116	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
117	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
118	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
119	Cloning and characterization of <i>LRG5</i> , a gene involved in blue light signaling in <i>Chlamydomonas</i> gametogenesis. <i>Plant Journal</i> , 1997, 12, 677-683.	2.8	6
120	Cloning and characterization of <i>LRG5</i> , a gene involved in blue light signaling in <i>Chlamydomonas</i> gametogenesis. <i>Plant Journal</i> , 1997, 12, 677-683.	2.8	14
121	<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