

Tom Goldammer

List of Publications by Year in descending order

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92
papers

2,762
citations

185998

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48
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all docs

92
docs citations

92
times ranked

2961
citing authors

#	ARTICLE	IF	CITATIONS
1	The Early Immune Response of Lymphoid and Myeloid Head-Kidney Cells of Rainbow Trout (<i>Oncorhynchus mykiss</i>) Stimulated with <i>Aeromonas salmonicida</i> . <i>Fishes</i> , 2022, 7, 12.	0.7	3
2	Insights into early ontogenesis: characterization of stress and development key genes of pikeperch (<i>Sander lucioperca</i>) in vivo and in vitro. <i>Fish Physiology and Biochemistry</i> , 2021, 47, 515-532.	0.9	10
3	Effects of Chronic Hypoxia on the Immune Status of Pikeperch (<i>Sander lucioperca</i> Linnaeus, 1758). <i>Biology</i> , 2021, 10, 649.	1.3	8
4	Quality control in scRNA-Seq can discriminate pacemaker cells: the mtRNA bias. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 6585-6592.	2.4	10
5	Comprehensive Characterization of Multitissue Expression Landscape, Co-Expression Networks and Positive Selection in Pikeperch. <i>Cells</i> , 2021, 10, 2289.	1.8	4
6	PIAS Factors from Rainbow Trout Control NF- κ B- and STAT-Dependent Gene Expression. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12815.	1.8	5
7	Analysis of Autozygosity Using Whole-Genome Sequence Data of Full-Sib Families in Pikeperch (<i>Sander</i>) Tj ETQq1 1,0.784314 rgBT /Ove 1.1	1.1	2
8	Early response of salmonid head-kidney cells to stress hormones and toll-like receptor ligands. <i>Fish and Shellfish Immunology</i> , 2020, 98, 950-961.	1.6	23
9	Characterisation of the teleostean κ B-Ras family: The two members NKIRAS1 and NKIRAS2 from rainbow trout influence the activity of NF- κ B in opposite ways. <i>Fish and Shellfish Immunology</i> , 2020, 106, 1004-1013.	1.6	11
10	Comparative Analysis of the Transcriptome and Distribution of Putative SNPs in Two Rainbow Trout (<i>Oncorhynchus mykiss</i>) Breeding Strains by Using Next-Generation Sequencing. <i>Genes</i> , 2020, 11, 841.	1.0	3
11	The synergistic interaction of thermal stress coupled with overstocking strongly modulates the transcriptomic activity and immune capacity of rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Scientific Reports</i> , 2020, 10, 14913.	1.6	18
12	Time-Dependent Effects of Acute Handling on the Brain Monoamine System of the Salmonid <i>Coregonus maraena</i> . <i>Frontiers in Neuroscience</i> , 2020, 14, 591738.	1.4	3
13	Xenogeneic and Stem Cell-Based Therapy for Cardiovascular Diseases: Genetic Engineering of Porcine Cells and Their Applications in Heart Regeneration. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9686.	1.8	5
14	Integrative Cluster Analysis of Whole Hearts Reveals Proliferative Cardiomyocytes in Adult Mice. <i>Cells</i> , 2020, 9, 1144.	1.8	19
15	Dawn to Dusk: Diurnal Rhythm of the Immune Response in Rainbow Trout (<i>Oncorhynchus Mykiss</i>). <i>Biology</i> , 2020, 9, 8.	1.3	17
16	Single-Nucleus Sequencing of an Entire Mammalian Heart: Cell Type Composition and Velocity. <i>Cells</i> , 2020, 9, 318.	1.8	36
17	Gene Profiling in the Adipose Fin of Salmonid Fishes Supports Its Function as a Flow Sensor. <i>Genes</i> , 2020, 11, 21.	1.0	2
18	Single nuclei sequencing of entire mammalian hearts: strain-dependent cell-type composition and velocity. <i>Cardiovascular Research</i> , 2020, 116, 1249-1251.	1.8	13

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19	An ultra-high density SNP-based linkage map for enhancing the pikeperch (<i>Sander lucioperca</i>) genome assembly to chromosome-scale. <i>Scientific Reports</i> , 2020, 10, 22335.	1.6	7
20	At Least Two Genes Encode Many Variants of <i>Irak3</i> in Rainbow Trout, but Neither the Full-Length Factor Nor Its Variants Interfere Directly With the TLR-Mediated Stimulation of Inflammation. <i>Frontiers in Immunology</i> , 2019, 10, 2246.	2.2	12
21	The First Highly Contiguous Genome Assembly of Pikeperch (<i>Sander lucioperca</i>), an Emerging Aquaculture Species in Europe. <i>Genes</i> , 2019, 10, 708.	1.0	33
22	A molecular survey of programmed cell death in rainbow trout: Structural and functional specifications of apoptotic key molecules. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2019, 230, 57-69.	0.7	7
23	Evolutionary expression differences of creatine synthesis-related genes: Implications for skeletal muscle metabolism in fish. <i>Scientific Reports</i> , 2019, 9, 5429.	1.6	22
24	Identification of molecular stress indicators in pikeperch <i>Sander lucioperca</i> correlating with rising water temperatures. <i>Aquaculture</i> , 2019, 501, 260-271.	1.7	35
25	Under control: The innate immunity of fish from the inhibitors' perspective. <i>Fish and Shellfish Immunology</i> , 2018, 77, 328-349.	1.6	100
26	Characterization of <i>igf1</i> and <i>igf2</i> genes during maraena whitefish (<i>Coregonus maraena</i>) ontogeny and the effect of temperature on embryogenesis and <i>igf</i> expression. <i>Growth Hormone and IGF Research</i> , 2018, 40, 32-43.	0.5	15
27	Gradual and Acute Temperature Rise Induces Crossing Endocrine, Metabolic, and Immunological Pathways in Maraena Whitefish (<i>Coregonus maraena</i>). <i>Frontiers in Genetics</i> , 2018, 9, 241.	1.1	28
28	Siglecs: A journey through the evolution of sialic acid-binding immunoglobulin-type lectins. <i>Developmental and Comparative Immunology</i> , 2018, 86, 219-231.	1.0	128
29	Multiple gene and transcript variants encoding trout C-polysaccharide binding proteins are differentially but strongly induced after infection with <i>Aeromonas salmonicida</i> . <i>Fish and Shellfish Immunology</i> , 2017, 60, 509-519.	1.6	9
30	Microarray-predicted marker genes and molecular pathways indicating crowding stress in rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Aquaculture</i> , 2017, 473, 355-365.	1.7	35
31	Identification of genes involved in cold-shock response in rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Journal of Genetics</i> , 2017, 96, 701-706.	0.4	9
32	Functional Annotation of All Salmonid Genomes (FAASG): an international initiative supporting future salmonid research, conservation and aquaculture. <i>BMC Genomics</i> , 2017, 18, 484.	1.2	99
33	ST2 from rainbow trout quenches TLR signalling, localises at the nuclear membrane and allows the nuclear translocation of MYD88. <i>Developmental and Comparative Immunology</i> , 2017, 67, 139-152.	1.0	10
34	Adverse Husbandry of Maraena Whitefish Directs the Immune System to Increase Mobilization of Myeloid Cells and Proinflammatory Responses. <i>Frontiers in Immunology</i> , 2016, 7, 631.	2.2	28
35	Toll-like receptors in maraena whitefish: Evolutionary relationship among salmonid fishes and patterns of response to <i>Aeromonas salmonicida</i> . <i>Fish and Shellfish Immunology</i> , 2016, 54, 391-401.	1.6	47
36	Transcriptome sequencing of maraena whitefish (<i>Coregonus maraena</i>). <i>Marine Genomics</i> , 2016, 29, 27-29.	0.4	9

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37	Structurally diverse genes encode Tlr2 in rainbow trout: The conserved receptor cannot be stimulated by classical ligands to activate NF- κ B in vitro. <i>Developmental and Comparative Immunology</i> , 2016, 54, 75-88.	1.0	21
38	<i>Aeromonas salmonicida</i> Infection Only Moderately Regulates Expression of Factors Contributing to Toll-Like Receptor Signaling but Massively Activates the Cellular and Humoral Branches of Innate Immunity in Rainbow Trout (<i>Oncorhynchus mykiss</i>). <i>Journal of Immunology Research</i> , 2015, 2015, 1-16.	0.9	42
39	Impact of Thermal Stress on Kidney-Specific Gene Expression in Farmed Regional and Imported Rainbow Trout. <i>Marine Biotechnology</i> , 2015, 17, 576-592.	1.1	48
40	Cloning and characterization of the proximal promoter region of rainbow trout (<i>Oncorhynchus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62	1.6	16
41	The Mammalian Cervical Vertebrae Blueprint Depends on the <i>Tbr1</i> (<i>brachyury</i>) Gene. <i>Genetics</i> , 2015, 199, 873-883.	1.2	14
42	Comprehensive and comparative transcription analyses of the complement pathway in rainbow trout. <i>Fish and Shellfish Immunology</i> , 2015, 42, 98-107.	1.6	30
43	Identification and de novo sequencing of housekeeping genes appropriate for gene expression analyses in farmed maraena whitefish (<i>Coregonus maraena</i>) during crowding stress. <i>Fish Physiology and Biochemistry</i> , 2015, 41, 397-412.	0.9	22
44	GRP94 is encoded by two differentially expressed genes during development of rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Fish Physiology and Biochemistry</i> , 2014, 40, 1917-1926.	0.9	9
45	Creatine metabolism differs between mammals and rainbow trout (<i>Oncorhynchus mykiss</i>). SpringerPlus, 2014, 3, 510.	1.2	33
46	Transcriptome Profiling Reveals Insight into Distinct Immune Responses to <i>Aeromonas salmonicida</i> in Gill of Two Rainbow Trout Strains. <i>Marine Biotechnology</i> , 2014, 16, 333-348.	1.1	54
47	The proximal promoter of a novel interleukin-8-encoding gene in rainbow trout (<i>Oncorhynchus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 62 2014, 46, 155-164.	1.0	23
48	Characterization of the interleukin 1 receptor-associated kinase 4 (IRAK4)-encoding gene in salmonid fish: The functional copy is rearranged in <i>Oncorhynchus mykiss</i> and that factor can impair TLR signaling in mammalian cells. <i>Fish and Shellfish Immunology</i> , 2014, 36, 206-214.	1.6	37
49	Comparison of splenic transcriptome activity of two rainbow trout strains differing in robustness under regional aquaculture conditions. <i>Molecular Biology Reports</i> , 2013, 40, 1955-1966.	1.0	18
50	Novel insights into the peritoneal inflammation of rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Fish and Shellfish Immunology</i> , 2013, 35, 1192-1199.	1.6	46
51	Transcriptome Profiling of Gill Tissue in Regionally Bred and Globally Farmed Rainbow Trout Strains Reveals Different Strategies for Coping with Thermal Stress. <i>Marine Biotechnology</i> , 2013, 15, 445-460.	1.1	75
52	Iron-sulfur cluster scaffold (ISCU) gene is duplicated in salmonid fish and tissue and temperature dependent expressed in rainbow trout. <i>Gene</i> , 2013, 512, 251-258.	1.0	3
53	Identification of differentially expressed protective genes in liver of two rainbow trout strains. <i>Veterinary Immunology and Immunopathology</i> , 2012, 145, 305-315.	0.5	19
54	Duplicated NELL2 genes show different expression patterns in two rainbow trout strains after temperature and pathogen challenge. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2012, 163, 65-73.	0.7	4

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55	Advanced comparative cytogenetic analysis of X chromosomes in river buffalo, cattle, sheep, and human. <i>Chromosome Research</i> , 2012, 20, 413-425.	1.0	13
56	Comparative molecular characterization of the regucalcin (RGN) gene in rainbow trout (<i>Oncorhynchus mykiss</i>) and maraena whitefish (<i>Coregonus maraena</i>). <i>Molecular Biology Reports</i> , 2012, 39, 4291-4300.	1.0	9
57	Salmonid Tollip and MyD88 factors can functionally replace their mammalian orthologues in TLR-mediated trout SAA promoter activation. <i>Developmental and Comparative Immunology</i> , 2011, 35, 81-87.	1.0	42
58	MARCH5 gene is duplicated in rainbow trout, but only fish-specific gene copy is up-regulated after VHSV infection. <i>Fish and Shellfish Immunology</i> , 2011, 31, 1041-1050.	1.6	18
59	Annotation of novel transcripts putatively relevant for bovine fat metabolism. <i>Molecular Biology Reports</i> , 2011, 38, 2975-2986.	1.0	5
60	Peptidylarginine deiminase gene is differentially expressed in freshwater and brackish water rainbow trout. <i>Molecular Biology Reports</i> , 2010, 37, 2333-2339.	1.0	31
61	Molecular characterization of PRR13 and its tissue-specific expression in rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Fish Physiology and Biochemistry</i> , 2010, 36, 1271-1276.	0.9	6
62	Acetylcysteine impairs survival of luteal cells through mitochondrial dysfunction. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2010, 77A, 310-320.	1.1	23
63	Analysis of structure and gene expression of bovine CCDC3 gene indicates a function in fat metabolism. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2010, 156, 19-25.	0.7	10
64	Cloning and expression of activation induced cytidine deaminase from <i>Bos taurus</i> . <i>Veterinary Immunology and Immunopathology</i> , 2010, 134, 151-159.	0.5	5
65	Toll-like receptor signaling in bony fish. <i>Veterinary Immunology and Immunopathology</i> , 2010, 134, 139-150.	0.5	379
66	A High-Resolution Radiation Hybrid Map of Sheep Chromosome X and Comparison with Human and Cattle. <i>Cytogenetic and Genome Research</i> , 2009, 125, 40-45.	0.6	9
67	Evolutionary Break Point Analysis between the Proximal Half of Bovine Chromosome 27 and Conserved Segments of the Human Genome. <i>Cytogenetic and Genome Research</i> , 2009, 125, 33-39.	0.6	2
68	Novel transcripts discovered by mining genomic DNA from defined regions of bovine chromosome 6. <i>BMC Genomics</i> , 2009, 10, 186.	1.2	37
69	Cytogenetic anchoring of radiation hybrid and virtual maps of sheep chromosome X and comparison of X chromosomes in sheep, cattle, and human. <i>Chromosome Research</i> , 2009, 17, 497-506.	1.0	14
70	Characterization of Dehydrololichyl diphosphate synthase gene in rainbow trout (<i>Oncorhynchus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 260-265.	0.7	18
71	Characterization of two key molecules of teleost innate immunity from rainbow trout (<i>Oncorhynchus mykiss</i>): MyD88 and SAA. <i>Veterinary Immunology and Immunopathology</i> , 2009, 131, 122-126.	0.5	57
72	Cloning and tissue-specific expression of a .DELTA.-COP homologue in a freshwater and a brackish water-adapted strain of rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Genes and Genetic Systems</i> , 2009, 84, 239-243.	0.2	4

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73	A first generation whole genome RH map of the river buffalo with comparison to domestic cattle. BMC Genomics, 2008, 9, 631.	1.2	78
74	A radiation hybrid map of river buffalo <i>(Bubalus bubalis)</i> chromosome 7 and comparative mapping to the cattle and human genomes. Cytogenetic and Genome Research, 2007, 119, 235-241.	0.6	13
75	Generation of an improved cytogenetic and comparative map of Bos taurus chromosome BTA27. Chromosome Research, 2007, 15, 203-213.	1.0	7
76	A gene-based high-resolution comparative radiation hybrid map as a framework for genome sequence assembly of a bovine chromosome 6 region associated with QTL for growth, body composition, and milk performance traits. BMC Genomics, 2006, 7, 53.	1.2	25
77	Bovine NALP5, NALP8, and NALP9 Genes: Assignment to a QTL Region and the Expression in Adult Tissues, Oocytes, and Preimplantation Embryos. Biology of Reproduction, 2006, 74, 577-584.	1.2	33
78	Assignment of chromosome rearrangements between X chromosomes of human and cattle by laser microdissection and Zoo-FISH. Chromosome Research, 2005, 13, 569-574.	1.0	14
79	The bovine PPARGC1A gene: molecular characterization and association of an SNP with variation of milk fat synthesis. Physiological Genomics, 2005, 21, 1-13.	1.0	127
80	A 1463 Gene Cattle-Human Comparative Map With Anchor Points Defined by Human Genome Sequence Coordinates. Genome Research, 2004, 14, 1424-1437.	2.4	133
81	Targeted Generation of 16 Sequence-Tagged Sites for Bovine Chromosome Region 5q21-q25 by Microdissection. Chromosome Research, 2004, 12, 309-315.	1.0	2
82	High-resolution comparative mapping between human chromosomes 4 and 8 and bovine chromosome 27 provides genes and segments serving as positional candidates for udder health in cattle. Genomics, 2004, 84, 696-706.	1.3	16
83	Application of disease-associated differentially expressed genes â€œ Mining for functional candidate genes for mastitis resistance in cattle. Genetics Selection Evolution, 2003, 35, S19-34.	1.2	24
84	The telomeric region of BTA18 containing a potential QTL region for health in cattle exhibits high similarity to the HSA19q region in humansâ€™††Sequence data from this article have been deposited with the GenBank Data Libraries under accession numbers AJ459269-AJ459294.. Genomics, 2003, 81, 270-278.	1.3	15
85	A comparative radiation hybrid map of bovine chromosome 18 and homologous chromosomes in human and mice. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 2106-2111.	3.3	31
86	Targeted Construction of a High-Resolution, Integrated, Comprehensive, and Comparative Map for a Region Specific to Bovine Chromosome 6 Based on Radiation Hybrid Mapping. Genomics, 2002, 79, 768-776.	1.3	21
87	Identification and chromosome assignment of 23 genes expressed in meat and dairy cattle. Chromosome Research, 2002, 10, 411-418.	1.0	7
88	Isolation and characterization of hepatic and intestinal expressed sequence tags potentially involved in trait differentiation between cows of different metabolic type. Mammalian Genome, 2001, 12, 528-537.	1.0	23
89	Detection of QTL for milk production traits in cattle by application of a specifically developed marker map of BTA6. Animal Genetics, 1999, 30, 333-339.	0.6	61
90	High-Resolution Human/Goat Comparative Map of the Goat Polled/Intersex Syndrome (PIS): The Human Homologue Is Contained in a Human YAC from HSA3q23. Genomics, 1999, 56, 31-39.	1.3	37

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91	Detection and functional characterisation of the transcription factor peroxisome proliferator-activated receptor gamma in lutein cells. <i>Journal of Endocrinology</i> , 1998, 159, 429-439.	1.2	59
92	STAT5A encoding gene maps to Chromosome 19 in cattle and goat and to Chromosome 11 in sheep. <i>Mammalian Genome</i> , 1997, 8, 705-706.	1.0	15