

Klopp Christophe

List of Publications by Year in descending order

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Version: 2024-02-01

182
papers

15,257
citations

44069

48
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21540

114
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206
all docs

206
docs citations

206
times ranked

23625
citing authors

#	ARTICLE	IF	CITATIONS
1	An ancient truncated duplication of the anti- $\text{M}\beta$ -allergic hormone receptor type 2 gene is a potential conserved master sex determinant in the Pangasiidae catfish family. <i>Molecular Ecology Resources</i> , 2022, 22, 2411-2428.	4.8	13
2	Generation of a chromosome-level genome assembly for Pacific halibut (<i>Hippoglossus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 707 T Resources, 2022, 22, 2685-2700.	4.8	15
3	Impacts of <i>Mycoplasma agalactiae</i> restriction-modification systems on pan-epigenome dynamics and genome plasticity. <i>Microbial Genomics</i> , 2022, 8, .	2.0	3
4	Development of a polymerase chain reaction (PCR) based genetic sex identification method in the chub mackerel <i>Scomber japonicus</i> and blue mackerel <i>S. australasicus</i>. <i>Nippon Suisan Gakkaishi</i> , 2022, 88, 203-203.	0.1	0
5	Contrasting Gene Decay in Subterranean Vertebrates: Insights from Cavefishes and Fossorial Mammals. <i>Molecular Biology and Evolution</i> , 2021, 38, 589-605.	8.9	43
6	The rise and fall of the ancient northern pike master sex-determining gene. <i>ELife</i> , 2021, 10, .	6.0	24
7	DNAModAnnot: a R toolbox for DNA modification filtering and annotation. <i>Bioinformatics</i> , 2021, 37, 2738-2740.	4.1	7
8	Genetics of nodulation in <i>Aeschynomene evenia</i> uncovers mechanisms of the rhizobium-legume symbiosis. <i>Nature Communications</i> , 2021, 12, 829.	12.8	38
9	The immune system of sturgeons and paddlefish (Acipenseriformes): a review with new data from a chromosome-scale sturgeon genome. <i>Reviews in Aquaculture</i> , 2021, 13, 1709-1729.	9.0	9
10	RADSex: A computational workflow to study sex determination using restriction site-associated DNA sequencing data. <i>Molecular Ecology Resources</i> , 2021, 21, 1715-1731.	4.8	40
11	RNA-Seq Data for Reliable SNP Detection and Genotype Calling: Interest for Coding Variant Characterization and Cis-Regulation Analysis by Allele-Specific Expression in Livestock Species. <i>Frontiers in Genetics</i> , 2021, 12, 655707.	2.3	30
12	A 180 Myr-old female-specific genome region in sturgeon reveals the oldest known vertebrate sex determining system with undifferentiated sex chromosomes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200089.	4.0	41
13	Watch Out for a Second SNP: Focus on Multi-Nucleotide Variants in Coding Regions and Rescued Stop-Gained. <i>Frontiers in Genetics</i> , 2021, 12, 659287.	2.3	2
14	Transcriptome Profiling of the Pacific Oyster <i>Crassostrea gigas</i> Visceral Ganglia over a Reproduction Cycle Identifies Novel Regulatory Peptides. <i>Marine Drugs</i> , 2021, 19, 452.	4.6	4
15	A supernumerary B-sex -chromosome drives male sex determination in the Pach ³ n cavefish, <i>Astyanax mexicanus</i> . <i>Current Biology</i> , 2021, 31, 4800-4809.e9.	3.9	34
16	MINTIA: a metagenomic INserT integrated assembly and annotation tool. <i>PeerJ</i> , 2021, 9, e11885.	2.0	0
17	Neurodevelopment vs. the immune system: Complementary contributions of maternally-inherited gene transcripts and proteins to successful embryonic development in fish. <i>Genomics</i> , 2021, 113, 3811-3826.	2.9	4
18	A duplicated copy of <i>id2b</i> is an unusual sex-determining candidate gene on the Y chromosome of <i>arapaima</i> (<i>Arapaima gigas</i>). <i>Scientific Reports</i> , 2021, 11, 21544.	3.3	8

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19	Genome insights of mercury methylation among <i>Desulfovibrio</i> and <i>Pseudodesulfovibrio</i> strains. <i>Research in Microbiology</i> , 2020, 171, 3-12.	2.1	18
20	Characterization of a Yâ€specific duplication/insertion of the antiâ€Mullerian hormone type II receptor gene based on a chromosomeâ€scale genome assembly of yellow perch, <i>Perca flavescens</i> . <i>Molecular Ecology Resources</i> , 2020, 20, 531-543.	4.8	76
21	Responses to iron oxide and zinc oxide nanoparticles in echinoderm embryos and microalgae: uptake, growth, morphology, and transcriptomic analysis. <i>Nanotoxicology</i> , 2020, 14, 1342-1361.	3.0	15
22	Genome Sequence of the Euryhaline Javafish Medaka, <i>Oryzias javanicus</i> : A Small Aquarium Fish Model for Studies on Adaptation to Salinity. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 907-915.	1.8	22
23	Biological rhythms in the deep-sea hydrothermal mussel <i>Bathymodiolus azoricus</i> . <i>Nature Communications</i> , 2020, 11, 3454.	12.8	30
24	Molecular signatures of muscle growth and composition deciphered by the meta-analysis of age-related public transcriptomics data. <i>Physiological Genomics</i> , 2020, 52, 322-332.	2.3	13
25	Siberian sturgeon multi-tissue reference transcriptome database. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	3
26	Sex chromosome and sex locus characterization in goldfish, <i>Carassius auratus</i> (Linnaeus, 1758). <i>BMC Genomics</i> , 2020, 21, 552.	2.8	28
27	Genome structure and content of the rice rootâ€knot nematode (<i>Meloidogyne graminicola</i>). <i>Ecology and Evolution</i> , 2020, 10, 11006-11021.	1.9	27
28	Domestication modulates the expression of genes involved in neurogenesis in highâ€quality eggs of <i>Sander lucioperca</i> . <i>Molecular Reproduction and Development</i> , 2020, 87, 934-951.	2.0	10
29	Transfer and Transcriptomic Profiling in Liver and Brain of European Eels (<i>Anguilla anguilla</i>) After Dietâ€borne Exposure to Gold Nanoparticles. <i>Environmental Toxicology and Chemistry</i> , 2020, 39, 2450-2461.	4.3	2
30	An integrative atlas of chicken long non-coding genes and their annotations across 25 tissues. <i>Scientific Reports</i> , 2020, 10, 20457.	3.3	20
31	CSA: A high-throughput chromosome-scale assembly pipeline for vertebrate genomes. <i>GigaScience</i> , 2020, 9, .	6.4	4
32	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus</i> . <i>DNA Research</i> , 2020, 27, .	3.4	32
33	Multi-tissue Siberian sturgeon RNA sequencing data. <i>Data in Brief</i> , 2020, 31, 105820.	1.0	2
34	Venom Peptide Repertoire of the European Myrmicine Ant <i>Manica rubida</i> : Identification of Insecticidal Toxins. <i>Journal of Proteome Research</i> , 2020, 19, 1800-1811.	3.7	30
35	Meta-omics Provides Insights into the Impact of Hydrocarbon Contamination on Microbial Mat Functioning. <i>Microbial Ecology</i> , 2020, 80, 286-295.	2.8	15
36	Independent Origin of XY and ZW Sex Determination Mechanisms in Mosquitofish Sister Species. <i>Genetics</i> , 2020, 214, 193-209.	2.9	30

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37	The sterlet sturgeon genome sequence and the mechanisms of segmental rediploidization. <i>Nature Ecology and Evolution</i> , 2020, 4, 841-852.	7.8	159
38	RNA-Seq transcriptome data of undifferentiated and differentiated gonads of Siberian sturgeon. <i>Data in Brief</i> , 2020, 31, 105741.	1.0	3
39	Transcription Profiling of Monocyte-Derived Macrophages Infected In Vitro With Two Strains of <i>Streptococcus agalactiae</i> Reveals Candidate Pathways Affecting Subclinical Mastitis in Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 689.	2.3	7
40	Identification of the master sex determining gene in Northern pike (<i>Esox lucius</i>) reveals restricted sex chromosome differentiation. <i>PLoS Genetics</i> , 2019, 15, e1008013.	3.5	107
41	Arctic charr brain transcriptome strongly affected by summer seasonal growth but only subtly by feed deprivation. <i>BMC Genomics</i> , 2019, 20, 529.	2.8	6
42	RNA-seq analysis of hepatic gene expression of common Pekin, Muscovy, mule and hinny ducks fed ad libitum or overfed. <i>BMC Genomics</i> , 2019, 20, 13.	2.8	14
43	Transcriptome variation in response to gastrointestinal nematode infection in goats. <i>PLoS ONE</i> , 2019, 14, e0218719.	2.5	7
44	Transcriptomic view of detached lettuce leaves during storage: A crosstalk between wounding, dehydration and senescence. <i>Postharvest Biology and Technology</i> , 2019, 152, 73-88.	6.0	18
45	The genome of the arapaima (<i>Arapaima gigas</i>) provides insights into gigantism, fast growth and chromosomal sex determination system. <i>Scientific Reports</i> , 2019, 9, 5293.	3.3	25
46	Chicken adaptive response to low energy diet: main role of the hypothalamic lipid metabolism revealed by a phenotypic and multi-tissue transcriptomic approach. <i>BMC Genomics</i> , 2019, 20, 1033.	2.8	7
47	Draft Genome Assembly and Annotation of the Gila Topminnow <i>Poeciliopsis occidentalis</i> . <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	2.2	3
48	Structure of the intergenic spacers in chicken ribosomal DNA. <i>Genetics Selection Evolution</i> , 2019, 51, 59.	3.0	9
49	Viruses in the Invasive Hornet <i>Vespa velutina</i> . <i>Viruses</i> , 2019, 11, 1041.	3.3	39
50	Identification of potential chemosignals in the European water vole <i>Arvicola terrestris</i> . <i>Scientific Reports</i> , 2019, 9, 18378.	3.3	10
51	Multi-species annotation of transcriptome and chromatin structure in domesticated animals. <i>BMC Biology</i> , 2019, 17, 108.	3.8	109
52	Domestication may affect the maternal mRNA profile in unfertilized eggs, potentially impacting the embryonic development of Eurasian perch (<i>Perca fluviatilis</i>). <i>PLoS ONE</i> , 2019, 14, e0226878.	2.5	14
53	Environmental transcriptomes of invasive dreissena, a model species in ecotoxicology and invasion biology. <i>Scientific Data</i> , 2019, 6, 234.	5.3	6
54	The Peptide Venom Composition of the Fierce Stinging Ant <i>Tetraponera aethiops</i> (Formicidae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62	3.4	14

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55	Analysis of Transposable Elements Expressed in the Gonads of the Siberian Sturgeon. , 2018, , 115-130.		1
56	Transcriptome profiling of the honeybee parasite Varroa destructor provides new biological insights into the mite adult life cycle. BMC Genomics, 2018, 19, 328.	2.8	33
57	Oyster transcriptome response to Alexandrium exposure is related to saxitoxin load and characterized by disrupted digestion, energy balance, and calcium and sodium signaling. Aquatic Toxicology, 2018, 199, 127-137.	4.0	19
58	Transcriptomic analysis reveals specific metabolic pathways of enterohemorrhagic Escherichia coli O157:H7 in bovine digestive contents. BMC Genomics, 2018, 19, 766.	2.8	14
59	Ten steps to get started in Genome Assembly and Annotation. F1000Research, 2018, 7, 148.	1.6	85
60	One complete and three draft genome sequences of four Brochothrix thermosphacta strains, CD 337, TAP 175, BSAS1 3 and EBP 3070. Standards in Genomic Sciences, 2018, 13, 22.	1.5	10
61	Whole-transcriptome response to wastewater treatment plant and stormwater effluents in the Asian clam, Corbicula fluminea. Ecotoxicology and Environmental Safety, 2018, 165, 96-106.	6.0	20
62	The route to the development of basal stem rot resistance in oil palm (Elaeis guineensis) via the discovery of lignin degradation process in the pathogen Ganoderma boninense. Acta Horticulturae, 2018, , 359-370.	0.2	4
63	Rapid whole-genome based typing and surveillance of avipoxviruses using nanopore sequencing. Journal of Virological Methods, 2018, 261, 34-39.	2.1	31
64	De novo transcriptome analysis to search for sex-differentiation genes in the Siberian sturgeon. General and Comparative Endocrinology, 2018, 268, 96-109.	1.8	18
65	Highly Promiscuous Oxidases Discovered in the Bovine Rumen Microbiome. Frontiers in Microbiology, 2018, 9, 861.	3.5	9
66	Whole-genome sequencing of Aspergillus tubingensis G131 and overview of its secondary metabolism potential. BMC Genomics, 2018, 19, 200.	2.8	25
67	Genomics analysis of Aphanomyces spp. identifies a new class of oomycete effector associated with host adaptation. BMC Biology, 2018, 16, 43.	3.8	62
68	Genetic and transcriptomic analyses provide new insights on the early antiviral response to VHSV in resistant and susceptible rainbow trout. BMC Genomics, 2018, 19, 482.	2.8	17
69	Oak genome reveals facets of long lifespan. Nature Plants, 2018, 4, 440-452.	9.3	303
70	D-GENIES: dot plot large genomes in an interactive, efficient and simple way. PeerJ, 2018, 6, e4958.	2.0	462
71	Fungal diseases affecting oil palm. Burleigh Dodds Series in Agricultural Science, 2018, , 3-22.	0.2	1
72	A fibrolytic potential in the human ileum mucosal microbiota revealed by functional metagenomic. Scientific Reports, 2017, 7, 40248.	3.3	38

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73	Variant discovery in the sheep milk transcriptome using RNA sequencing. BMC Genomics, 2017, 18, 170.	2.8	44
74	Long noncoding RNA repertoire in chicken liver and adipose tissue. Genetics Selection Evolution, 2017, 49, 6.	3.0	59
75	About Ganoderma boninense in oil palm plantations of Sumatra and peninsular Malaysia: Ancient population expansion, extensive gene flow and large scale dispersion ability. Fungal Biology, 2017, 121, 529-540.	2.5	30
76	Genetic variability of the activity of bidirectional promoters: a pilot study in bovine muscle. DNA Research, 2017, 24, 221-233.	3.4	2
77	Stable Polycomb-dependent transgenerational inheritance of chromatin states in Drosophila. Nature Genetics, 2017, 49, 876-886.	21.4	81
78	The role of rhizobial (NifV) and plant (FEN1) homocitrate synthases in Aeschynomene/photosynthetic Bradyrhizobium symbiosis. Scientific Reports, 2017, 7, 448.	3.3	21
79	Reconstructing the genome of the most recent common ancestor of flowering plants. Nature Genetics, 2017, 49, 490-496.	21.4	203
80	Draft Genome Sequence of Desulfovibrio BerOc1, a Mercury-Methylating Strain. Genome Announcements, 2017, 5, .	0.8	1
81	De novo transcriptome sequencing and analysis of freshwater snail (Radix balthica) to discover genes and pathways affected by exposure to oxazepam. Ecotoxicology, 2017, 26, 127-140.	2.4	10
82	Draft Genome Sequence of Enterohemorrhagic Escherichia coli O157:H7 Strain MC2 Isolated from Cattle in France. Genome Announcements, 2017, 5, .	0.8	3
83	Evolution of gene expression after whole-genome duplication: New insights from the spotted gar genome. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2017, 328, 709-721.	1.3	52
84	Transcriptomic responses of the endangered freshwater mussel Margaritifera margaritifera to trace metal contamination in the Dronne River, France. Environmental Science and Pollution Research, 2017, 24, 27145-27159.	5.3	26
85	Rapid Discovery of De Novo Deleterious Mutations in Cattle Enhances the Value of Livestock as Model Species. Scientific Reports, 2017, 7, 11466.	3.3	61
86	Analysis of large 16S rRNA Illumina data sets: Impact of singleton read filtering on microbial community description. Molecular Ecology Resources, 2017, 17, e122-e132.	4.8	55
87	Genome Sequence of the Yeast Clavispora lusitaniae Type Strain CBS 6936. Genome Announcements, 2017, 5, .	0.8	16
88	Root transcriptomic responses of grafted grapevines to heterogeneous nitrogen availability depend on rootstock genotype. Journal of Experimental Botany, 2017, 68, 4339-4355.	4.8	42
89	The Rio1p ATPase hinders premature entry into translation of late pre-40S pre-ribosomal particles. Nucleic Acids Research, 2017, 45, 10824-10836.	14.5	20
90	Identification of copy number variation in French dairy and beef breeds using next-generation sequencing. Genetics Selection Evolution, 2017, 49, 77.	3.0	37

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91	Draft genome sequence and characterization of commensal <i>Escherichia coli</i> strain BG1 isolated from bovine gastro-intestinal tract. <i>Standards in Genomic Sciences</i> , 2017, 12, 61.	1.5	9
92	Tench (<i>Tinca tinca</i>) high-throughput transcriptomics reveal feed dependent gut profiles. <i>Aquaculture</i> , 2017, 479, 200-207.	3.5	1
93	Discovery of carbamate degrading enzymes by functional metagenomics. <i>PLoS ONE</i> , 2017, 12, e0189201.	2.5	32
94	Compacting and correcting Trinity and Oases RNA-Seq <i>de novo</i> assemblies. <i>PeerJ</i> , 2017, 5, e2988.	2.0	105
95	Construction of a large collection of small genome variations in French dairy and beef breeds using whole-genome sequences. <i>Genetics Selection Evolution</i> , 2016, 48, 87.	3.0	15
96	Gene evolution and gene expression after whole genome duplication in fish: the PhyloFish database. <i>BMC Genomics</i> , 2016, 17, 368.	2.8	288
97	The impact of long-term hydrocarbon exposure on the structure, activity, and biogeochemical functioning of microbial mats. <i>Marine Pollution Bulletin</i> , 2016, 111, 115-125.	5.0	14
98	Complete Genome Sequence of <i>Lactococcus lactis</i> subsp. <i>lactis</i> A12, a Strain Isolated from Wheat Sourdough. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
99	Characterization and Comparative Analysis of the Milk Transcriptome in Two Dairy Sheep Breeds using RNA Sequencing. <i>Scientific Reports</i> , 2016, 5, 18399.	3.3	88
100	Comprehensive RNA-Seq profiling to evaluate lactating sheep mammary gland transcriptome. <i>Scientific Data</i> , 2016, 3, 160051.	5.3	50
101	A gene-based map of the Nod factor-independent <i>Aeschynomene evenia</i> sheds new light on the evolution of nodulation and legume genomes. <i>DNA Research</i> , 2016, 23, 365-376.	3.4	22
102	The Extent of mRNA Editing Is Limited in Chicken Liver and Adipose, but Impacted by Tissular Context, Genotype, Age, and Feeding as Exemplified with a Conserved Edited Site in COG3. <i>Genes, Genomes, Genetics</i> , 2016, 6, 321-335.	1.8	13
103	Evolutionary Origins of Rhizarian Parasites. <i>Molecular Biology and Evolution</i> , 2016, 33, 980-983.	8.9	47
104	Jflow: a workflow management system for web applications. <i>Bioinformatics</i> , 2016, 32, 456-458.	4.1	3
105	Decoding the oak genome: public release of sequence data, assembly, annotation and publication strategies. <i>Molecular Ecology Resources</i> , 2016, 16, 254-265.	4.8	108
106	Targeted genomic enrichment and sequencing of CyHV-3 from carp tissues confirms low nucleotide diversity and mixed genotype infections. <i>PeerJ</i> , 2016, 4, e2516.	2.0	27
107	GigaTON: an extensive publicly searchable database providing a new reference transcriptome in the pacific oyster <i>Crassostrea gigas</i> . <i>BMC Bioinformatics</i> , 2015, 16, 401.	2.6	34
108	RNA-seq de novo Assembly Reveals Differential Gene Expression in <i>Glossina palpalis gambiense</i> Infected with <i>Trypanosoma brucei gambiense</i> vs. Non-Infected and Self-Cured Flies. <i>Frontiers in Microbiology</i> , 2015, 6, 1259.	3.5	26

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109	A Comparison between Transcriptome Sequencing and 16S Metagenomics for Detection of Bacterial Pathogens in Wildlife. PLoS Neglected Tropical Diseases, 2015, 9, e0003929.	3.0	62
110	Genome-Wide Study of Structural Variants in Bovine Holstein, Montb�liarde and Normande Dairy Breeds. PLoS ONE, 2015, 10, e0135931.	2.5	52
111	The BioMart community portal: an innovative alternative to large, centralized data repositories. Nucleic Acids Research, 2015, 43, W589-W598.	14.5	682
112	Combined QTL and Selective Sweep Mappings with Coding SNP Annotation and cis-eQTL Analysis Revealed PARK2 and JAG2 as New Candidate Genes for Adiposity Regulation. G3: Genes, Genomes, Genetics, 2015, 5, 517-529.	1.8	17
113	Comparison of whole-genome (13X) and capture (87X) resequencing methods for SNP and genotype callings. Animal Genetics, 2015, 46, 82-86.	1.7	2
114	A unigene set for European beech (Fagus sylvatica L.) and its use to decipher the molecular mechanisms involved in dormancy regulation. Molecular Ecology Resources, 2015, 15, 1192-1204.	4.8	35
115	Contrasted effects of natural complex mixtures of PAHs and metals on oxygen cycle in a microbial mat. Chemosphere, 2015, 135, 189-201.	8.2	9
116	Third Report on Chicken Genes and Chromosomes 2015. Cytogenetic and Genome Research, 2015, 145, 78-179.	1.1	97
117	Intra-host viral variability in children clinically infected with H1N1 (2009) pandemic influenza. Infection, Genetics and Evolution, 2015, 33, 47-54.	2.3	8
118	The oak gene expression atlas: insights into Fagaceae genome evolution and the discovery of genes regulated during bud dormancy release. BMC Genomics, 2015, 16, 112.	2.8	49
119	The red coral (Corallium rubrum) transcriptome: a new resource for population genetics and local adaptation studies. Molecular Ecology Resources, 2015, 15, 1205-1215.	4.8	47
120	Expanding Duplication of Free Fatty Acid Receptor-2 (GPR43) Genes in the Chicken Genome. Genome Biology and Evolution, 2015, 7, 1332-1348.	2.5	24
121	Identification and development of new polymorphic microsatellite markers using genome assembly for Ganoderma boninense, causal agent of oil palm basal stem rot disease. Mycological Progress, 2015, 14, 1.	1.4	33
122	High-resolution genetic maps of Eucalyptus improve Eucalyptus grandis genome assembly. New Phytologist, 2015, 206, 1283-1296.	7.3	90
123	Combining GWAS and RNA-Seq Approaches for Detection of the Causal Mutation for Hereditary Junctional Epidermolysis Bullosa in Sheep. PLoS ONE, 2015, 10, e0126416.	2.5	15
124	Genome-Wide Characterization of RNA Editing in Chicken Embryos Reveals Common Features among Vertebrates. PLoS ONE, 2015, 10, e0126776.	2.5	15
125	Design and Characterization of a 52K SNP Chip for Goats. PLoS ONE, 2014, 9, e86227.	2.5	220
126	DNA Methylation and Transcription in a Distal Region Upstream from the Bovine AlphaS1 Casein Gene after Once or Twice Daily Milking. PLoS ONE, 2014, 9, e111556.	2.5	39

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127	High-Throughput Sequencing Analyses of XX Genital Ridges Lacking FOXL2 Reveal DMRT1 Up-Regulation Before SOX9 Expression During the Sex-Reversal Process in Goats1. <i>Biology of Reproduction</i> , 2014, 91, 153.	2.7	39
128	Complete Genome Sequence of a Field Strain of Peste des Petits Ruminants Virus Isolated during 2010-2014 Epidemics in Senegal. <i>Genome Announcements</i> , 2014, 2, .	0.8	14
129	Novel Avian Coronavirus and Fulminating Disease in Guinea Fowl, France. <i>Emerging Infectious Diseases</i> , 2014, 20, 105-8.	4.3	34
130	Development of <sc>SNP</sc>-genotyping arrays in two shellfish species. <i>Molecular Ecology Resources</i> , 2014, 14, 820-830.	4.8	44
131	De Novo sequencing and transcriptome analysis for <i>Tetramorium bicarinatum</i> : a comprehensive venom gland transcriptome analysis from an ant species. <i>BMC Genomics</i> , 2014, 15, 987.	2.8	42
132	Re-Sequencing Data for Refining Candidate Genes and Polymorphisms in QTL Regions Affecting Adiposity in Chicken. <i>PLoS ONE</i> , 2014, 9, e111299.	2.5	11
133	jvenn: an interactive Venn diagram viewer. <i>BMC Bioinformatics</i> , 2014, 15, 293.	2.6	1,528
134	The rainbow trout genome provides novel insights into evolution after whole-genome duplication in vertebrates. <i>Nature Communications</i> , 2014, 5, 3657.	12.8	814
135	Generation and characterization of the sea bass <i>Dicentrarchus labrax</i> brain and liver transcriptomes. <i>Gene</i> , 2014, 544, 56-66.	2.2	32
136	An integrative method to normalize RNA-Seq data. <i>BMC Bioinformatics</i> , 2014, 15, 188.	2.6	17
137	The genome of the white-rot fungus <i>Pycnoporus cinnabarinus</i> : a basidiomycete model with a versatile arsenal for lignocellulosic biomass breakdown. <i>BMC Genomics</i> , 2014, 15, 486.	2.8	91
138	Gonad transcriptome analysis of pearl oyster <i>Pinctada margaritifera</i> : identification of potential sex differentiation and sex determining genes. <i>BMC Genomics</i> , 2014, 15, 491.	2.8	100
139	Identification of large intergenic non-coding RNAs in bovine muscle using next-generation transcriptomic sequencing. <i>BMC Genomics</i> , 2014, 15, 499.	2.8	120
140	<i>De novo</i> assembly of maritime pine transcriptome: implications for forest breeding and biotechnology. <i>Plant Biotechnology Journal</i> , 2014, 12, 286-299.	8.3	115
141	The Loss of Adipokine Genes in the Chicken Genome and Implications for Insulin Metabolism. <i>Molecular Biology and Evolution</i> , 2014, 31, 2637-2646.	8.9	51
142	Whole-genome sequencing of 234 bulls facilitates mapping of monogenic and complex traits in cattle. <i>Nature Genetics</i> , 2014, 46, 858-865.	21.4	697
143	Attenuated sensing of SHH by Ptch1 underlies evolution of bovine limbs. <i>Nature</i> , 2014, 511, 46-51.	27.8	106
144	RNAbrowse: RNA-Seq De Novo Assembly Results Browser. <i>PLoS ONE</i> , 2014, 9, e96821.	2.5	19

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145	Transcriptional profiling of bud dormancy induction and release in oak by next-generation sequencing. BMC Genomics, 2013, 14, 236.	2.8	82
146	High-density linkage mapping in a pine tree reveals a genomic region associated with inbreeding depression and provides clues to the extent and distribution of meiotic recombination. BMC Biology, 2013, 11, 50.	3.8	63
147	Gene-based single nucleotide polymorphism discovery in bovine muscle using next-generation transcriptomic sequencing. BMC Genomics, 2013, 14, 307.	2.8	32
148	Microbial ecology of the rumen evaluated by 454 GS FLX pyrosequencing is affected by starch and oil supplementation of diets. FEMS Microbiology Ecology, 2013, 83, 504-514.	2.7	224
149	Profiling the venom gland transcriptome of Tetramorium bicarinatum (Hymenoptera: Formicidae): The first transcriptome analysis of an ant species. Toxicon, 2013, 70, 70-81.	1.6	35
150	Whole-genome, deep pyrosequencing analysis of a duck influenza A virus evolution in swine cells. Infection, Genetics and Evolution, 2013, 18, 31-41.	2.3	19
151	Novel Insights into the Bovine Polled Phenotype and Horn Ontogenesis in Bovidae. PLoS ONE, 2013, 8, e63512.	2.5	78
152	Detection of Haplotypes Associated with Prenatal Death in Dairy Cattle and Identification of Deleterious Mutations in GART, SHBG and SLC37A2. PLoS ONE, 2013, 8, e65550.	2.5	137
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