

# 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  
h-index

21540

114  
g-index

206  
all docs

206  
docs citations

206  
times ranked

23625  
citing authors

#	ARTICLE	IF	CITATIONS
1	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	27.8	2,860
2	ijvenn: an interactive Venn diagram viewer. <i>BMC Bioinformatics</i> , 2014, 15, 293.	2.6	1,528
3	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
4	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
5	The BioMart community portal: an innovative alternative to large, centralized data repositories. <i>Nucleic Acids Research</i> , 2015, 43, W589-W598.	14.5	682
6	Metabolic adaptation to a high-fat diet is associated with a change in the gut microbiota. <i>Gut</i> , 2012, 61, 543-553.	12.1	511
7	An Immune-Related Gene Evolved into the Master Sex-Determining Gene in Rainbow Trout, <i>Oncorhynchus mykiss</i> . <i>Current Biology</i> , 2012, 22, 1423-1428.	3.9	466
8	D-GENIES: dot plot large genomes in an interactive, efficient and simple way. <i>PeerJ</i> , 2018, 6, e4958.	2.0	462
9	Oak genome reveals facets of long lifespan. <i>Nature Plants</i> , 2018, 4, 440-452.	9.3	303
10	Gene evolution and gene expression after whole genome duplication in fish: the PhyloFish database. <i>BMC Genomics</i> , 2016, 17, 368.	2.8	288
11	Involvement of tissue bacteria in the onset of diabetes in humans: evidence for a concept. <i>Diabetologia</i> , 2011, 54, 3055-3061.	6.3	283
12	Functional metagenomics to mine the human gut microbiome for dietary fiber catabolic enzymes. <i>Genome Research</i> , 2010, 20, 1605-1612.	5.5	228
13	Microbial ecology of the rumen evaluated by 454 GS FLX pyrosequencing is affected by starch and oil supplementation of diets. <i>FEMS Microbiology Ecology</i> , 2013, 83, 504-514.	2.7	224
14	Design and Characterization of a 52K SNP Chip for Goats. <i>PLoS ONE</i> , 2014, 9, e86227.	2.5	220
15	Reconstructing the genome of the most recent common ancestor of flowering plants. <i>Nature Genetics</i> , 2017, 49, 490-496.	21.4	203
16	The sterlet sturgeon genome sequence and the mechanisms of segmental rediploidization. <i>Nature Ecology and Evolution</i> , 2020, 4, 841-852.	7.8	159
17	Detection of Haplotypes Associated with Prenatal Death in Dairy Cattle and Identification of Deleterious Mutations in GART, SHBG and SLC37A2. <i>PLoS ONE</i> , 2013, 8, e65550.	2.5	137
18	Generation and analysis of a 29,745 unique Expressed Sequence Tags from the Pacific oyster ( <i>Crassostrea gigas</i> ) assembled into a publicly accessible database: the GigasDatabase. <i>BMC Genomics</i> , 2009, 10, 341.	2.8	127

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19	Identification of large intergenic non-coding RNAs in bovine muscle using next-generation transcriptomic sequencing. BMC Genomics, 2014, 15, 499.	2.8	120
20	<i>De novo</i> assembly of maritime pine transcriptome: implications for forest breeding and biotechnology. Plant Biotechnology Journal, 2014, 12, 286-299.	8.3	115
21	Multi-species annotation of transcriptome and chromatin structure in domesticated animals. BMC Biology, 2019, 17, 108.	3.8	109
22	Decoding the oak genome: public release of sequence data, assembly, annotation and publication strategies. Molecular Ecology Resources, 2016, 16, 254-265.	4.8	108
23	Identification of the master sex determining gene in Northern pike ( <i>Esox lucius</i> ) reveals restricted sex chromosome differentiation. PLoS Genetics, 2019, 15, e1008013.	3.5	107
24	Attenuated sensing of SHH by Ptch1 underlies evolution of bovine limbs. Nature, 2014, 511, 46-51.	27.8	106
25	Compacting and correcting Trinity and Oases RNA-Seq <i>de novo</i> assemblies. PeerJ, 2017, 5, e2988.	2.0	105
26	Gonad transcriptome analysis of pearl oyster <i>Pinctada margaritifera</i> : identification of potential sex differentiation and sex determining genes. BMC Genomics, 2014, 15, 491.	2.8	100
27	Third Report on Chicken Genes and Chromosomes 2015. Cytogenetic and Genome Research, 2015, 145, 78-179.	1.1	97
28	The genome of the white-rot fungus <i>Pycnoporus cinnabarinus</i> : a basidiomycete model with a versatile arsenal for lignocellulosic biomass breakdown. BMC Genomics, 2014, 15, 486.	2.8	91
29	High-resolution genetic maps of <i>Eucalyptus</i> improve <i>Eucalyptus grandis</i> genome assembly. New Phytologist, 2015, 206, 1283-1296.	7.3	90
30	Characterization and Comparative Analysis of the Milk Transcriptome in Two Dairy Sheep Breeds using RNA Sequencing. Scientific Reports, 2016, 5, 18399.	3.3	88
31	Ten steps to get started in Genome Assembly and Annotation. F1000Research, 2018, 7, 148.	1.6	85
32	Transcriptome profiling of the feeding-to-fasting transition in chicken liver. BMC Genomics, 2008, 9, 611.	2.8	83
33	Bioinformatic analysis of ESTs collected by Sanger and pyrosequencing methods for a keystone forest tree species: oak. BMC Genomics, 2010, 11, 650.	2.8	82
34	Transcriptional profiling of bud dormancy induction and release in oak by next-generation sequencing. BMC Genomics, 2013, 14, 236.	2.8	82
35	Stable Polycomb-dependent transgenerational inheritance of chromatin states in <i>Drosophila</i> . Nature Genetics, 2017, 49, 876-886.	21.4	81
36	Novel Insights into the Bovine Polled Phenotype and Horn Ontogenesis in Bovidae. PLoS ONE, 2013, 8, e63512.	2.5	78

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37	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
38	RNA-Seq reveals genotype-specific molecular responses to water deficit in eucalyptus. <i>BMC Genomics</i> , 2011, 12, 538.	2.8	67
39	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. <i>BMC Biology</i> , 2013, 11, 50.	3.8	63
40	A Comparison between Transcriptome Sequencing and 16S Metagenomics for Detection of Bacterial Pathogens in Wildlife. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003929.	3.0	62
41	Genomics analysis of <i>Aphanomyces</i> spp. identifies a new class of oomycete effector associated with host adaptation. <i>BMC Biology</i> , 2018, 16, 43.	3.8	62
42	Rapid Discovery of De Novo Deleterious Mutations in Cattle Enhances the Value of Livestock as Model Species. <i>Scientific Reports</i> , 2017, 7, 11466.	3.3	61
43	Long noncoding RNA repertoire in chicken liver and adipose tissue. <i>Genetics Selection Evolution</i> , 2017, 49, 6.	3.0	59
44	Strengthening insights into host responses to mastitis infection in ruminants by combining heterogeneous microarray data sources. <i>BMC Genomics</i> , 2011, 12, 225.	2.8	58
45	Analysis of large 16S rRNA Illumina data sets: Impact of singleton read filtering on microbial community description. <i>Molecular Ecology Resources</i> , 2017, 17, e122-e132.	4.8	55
46	NG6: Integrated next generation sequencing storage and processing environment. <i>BMC Genomics</i> , 2012, 13, 462.	2.8	53
47	Genome-Wide Study of Structural Variants in Bovine Holstein, MontbÃ©liarde and Normande Dairy Breeds. <i>PLoS ONE</i> , 2015, 10, e0135931.	2.5	52
48	Evolution of gene expression after wholeâ€genome duplication: New insights from the spotted gar genome. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2017, 328, 709-721.	1.3	52
49	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
50	Comprehensive RNA-Seq profiling to evaluate lactating sheep mammary gland transcriptome. <i>Scientific Data</i> , 2016, 3, 160051.	5.3	50
51	The oak gene expression atlas: insights into Fagaceae genome evolution and the discovery of genes regulated during bud dormancy release. <i>BMC Genomics</i> , 2015, 16, 112.	2.8	49
52	The red coral ( <i>Corallium rubrum</i> ) transcriptome: a new resource for population genetics and local adaptation studies. <i>Molecular Ecology Resources</i> , 2015, 15, 1205-1215.	4.8	47
53	Evolutionary Origins of Rhizarian Parasites. <i>Molecular Biology and Evolution</i> , 2016, 33, 980-983.	8.9	47
54	Development of SNP genotyping arrays in two shellfish species. <i>Molecular Ecology Resources</i> , 2014, 14, 820-830.	4.8	44

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55	Variant discovery in the sheep milk transcriptome using RNA sequencing. BMC Genomics, 2017, 18, 170.	2.8	44
56	Assessment of replicate bias in 454 pyrosequencing and a multi-purpose read-filtering tool. BMC Research Notes, 2011, 4, 149.	1.4	43
57	Contrasting Gene Decay in Subterranean Vertebrates: Insights from Cavefishes and Fossorial Mammals. Molecular Biology and Evolution, 2021, 38, 589-605.	8.9	43
58	De Novo sequencing and transcriptome analysis for <i>Tetramorium bicarinatum</i> : a comprehensive venom gland transcriptome analysis from an ant species. BMC Genomics, 2014, 15, 987.	2.8	42
59	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
60	A 180 Myr-old female-specific genome region in sturgeon reveals the oldest known vertebrate sex determining system with undifferentiated sex chromosomes. Philosophical Transactions of the Royal Society B: Biological Sciences, 2021, 376, 20200089.	4.0	41
61	RADSex: A computational workflow to study sex determination using restriction site-associated DNA sequencing data. Molecular Ecology Resources, 2021, 21, 1715-1731.	4.8	40
62	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
63	High-Throughput Sequencing Analyses of XX Genital Ridges Lacking FOXL2 Reveal DMRT1 Up-Regulation Before SOX9 Expression During the Sex-Reversal Process in Goats1. Biology of Reproduction, 2014, 91, 153.	2.7	39
64	Viruses in the Invasive Hornet <i>Vespa velutina</i> . Viruses, 2019, 11, 1041.	3.3	39
65	A fibrolytic potential in the human ileum mucosal microbiota revealed by functional metagenomic. Scientific Reports, 2017, 7, 40248.	3.3	38
66	Genetics of nodulation in <i>Aeschynomene evenia</i> uncovers mechanisms of the rhizobium-legume symbiosis. Nature Communications, 2021, 12, 829.	12.8	38
67	Identification of copy number variation in French dairy and beef breeds using next-generation sequencing. Genetics Selection Evolution, 2017, 49, 77.	3.0	37
68	Pyrosequencing-based transcriptomic resources in the pond snail <i>Lymnaea stagnalis</i> , with a focus on genes involved in molecular response to diquat-induced stress. Ecotoxicology, 2012, 21, 2222-2234.	2.4	35
69	Profiling the venom gland transcriptome of <i>Tetramorium bicarinatum</i> (Hymenoptera: Formicidae): The first transcriptome analysis of an ant species. Toxicon, 2013, 70, 70-81.	1.6	35
70	A unigene set for European beech ( <i>Fagus sylvatica</i> L.) and its use to decipher the molecular mechanisms involved in dormancy regulation. Molecular Ecology Resources, 2015, 15, 1192-1204.	4.8	35
71	Novel Avian Coronavirus and Fulminating Disease in Guinea Fowl, France. Emerging Infectious Diseases, 2014, 20, 105-8.	4.3	34
72	GigaTON: an extensive publicly searchable database providing a new reference transcriptome in the pacific oyster <i>Crassostrea gigas</i> . BMC Bioinformatics, 2015, 16, 401.	2.6	34

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73	A supernumerary X-chromosome drives male sex determination in the Pachón cavefish, <i>Astyanax mexicanus</i> . <i>Current Biology</i> , 2021, 31, 4800-4809.e9.	3.9	34
74	sigReannot: an oligo-set re-annotation pipeline based on similarities with the Ensembl transcripts and Unigene clusters. <i>BMC Proceedings</i> , 2009, 3, S3.	1.6	33
75	Identification and development of new polymorphic microsatellite markers using genome assembly for <i>Ganoderma boninense</i> , causal agent of oil palm basal stem rot disease. <i>Mycological Progress</i> , 2015, 14, 1.	1.4	33
76	Transcriptome profiling of the honeybee parasite <i>Varroa destructor</i> provides new biological insights into the mite adult life cycle. <i>BMC Genomics</i> , 2018, 19, 328.	2.8	33
77	Gene-based single nucleotide polymorphism discovery in bovine muscle using next-generation transcriptomic sequencing. <i>BMC Genomics</i> , 2013, 14, 307.	2.8	32
78	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
79	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus</i> . <i>DNA Research</i> , 2020, 27, .	3.4	32
80	Discovery of carbamate degrading enzymes by functional metagenomics. <i>PLoS ONE</i> , 2017, 12, e0189201.	2.5	32
81	Rapid whole-genome based typing and surveillance of avipoxviruses using nanopore sequencing. <i>Journal of Virological Methods</i> , 2018, 261, 34-39.	2.1	31
82	About <i>Ganoderma boninense</i> in oil palm plantations of Sumatra and peninsular Malaysia: Ancient population expansion, extensive gene flow and large scale dispersion ability. <i>Fungal Biology</i> , 2017, 121, 529-540.	2.5	30
83	Biological rhythms in the deep-sea hydrothermal mussel <i>Bathymodiolus azoricus</i> . <i>Nature Communications</i> , 2020, 11, 3454.	12.8	30
84	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
85	Independent Origin of XY and ZW Sex Determination Mechanisms in Mosquitofish Sister Species. <i>Genetics</i> , 2020, 214, 193-209.	2.9	30
86	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
87	Sex chromosome and sex locus characterization in goldfish, <i>Carassius auratus</i> (Linnaeus, 1758). <i>BMC Genomics</i> , 2020, 21, 552.	2.8	28
88	Genome structure and content of the rice root-knot nematode ( <i>Meloidogyne graminicola</i> ). <i>Ecology and Evolution</i> , 2020, 10, 11006-11021.	1.9	27
89	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
90	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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91	Transcriptomic responses of the endangered freshwater mussel <i>Margaritifera margaritifera</i> to trace metal contamination in the Dronne River, France. <i>Environmental Science and Pollution Research</i> , 2017, 24, 27145-27159.	5.3	26
92	Genome Sequence of <i>Weissella confusa</i> LBAE C39-2, Isolated from a Wheat Sourdough. <i>Journal of Bacteriology</i> , 2012, 194, 1608-1609.	2.2	25
93	Field Monitoring of Avian Influenza Viruses: Whole-Genome Sequencing and Tracking of Neuraminidase Evolution Using 454 Pyrosequencing. <i>Journal of Clinical Microbiology</i> , 2012, 50, 2881-2887.	3.9	25
94	Whole-genome sequencing of <i>Aspergillus tubingensis</i> G131 and overview of its secondary metabolism potential. <i>BMC Genomics</i> , 2018, 19, 200.	2.8	25
95	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
96	Expanding Duplication of Free Fatty Acid Receptor-2 (GPR43) Genes in the Chicken Genome. <i>Genome Biology and Evolution</i> , 2015, 7, 1332-1348.	2.5	24
97	The rise and fall of the ancient northern pike master sex-determining gene. <i>ELife</i> , 2021, 10, .	6.0	24
98	The chicken RH map: current state of progress and microchromosome mapping. <i>Cytogenetic and Genome Research</i> , 2007, 117, 14-21.	1.1	22
99	Genome Sequences of Three <i>Leuconostoc citreum</i> Strains, LBAE C10, LBAE C11, and LBAE E16, Isolated from Wheat Sourdoughs. <i>Journal of Bacteriology</i> , 2012, 194, 1610-1611.	2.2	22
100	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
101	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
102	The role of rhizobial (NifV) and plant (FEN1) homocitrate synthases in <i>Aeschynomene</i> /photosynthetic <i>Bradyrhizobium</i> symbiosis. <i>Scientific Reports</i> , 2017, 7, 448.	3.3	21
103	Fine mapping of complex traits in non-model species: using next generation sequencing and advanced intercross lines in Japanese quail. <i>BMC Genomics</i> , 2012, 13, 551.	2.8	20
104	The Rio1p ATPase hinders premature entry into translation of late pre-40S pre-ribosomal particles. <i>Nucleic Acids Research</i> , 2017, 45, 10824-10836.	14.5	20
105	Whole-transcriptome response to wastewater treatment plant and stormwater effluents in the Asian clam, <i>Corbicula fluminea</i> . <i>Ecotoxicology and Environmental Safety</i> , 2018, 165, 96-106.	6.0	20
106	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
107	A 3.7 Mb Deletion Encompassing ZEB2 Causes a Novel Polled and Multisystemic Syndrome in the Progeny of a Somatic Mosaic Bull. <i>PLoS ONE</i> , 2012, 7, e49084.	2.5	19
108	Whole-genome, deep pyrosequencing analysis of a duck influenza A virus evolution in swine cells. <i>Infection, Genetics and Evolution</i> , 2013, 18, 31-41.	2.3	19



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109	Oyster transcriptome response to Alexandrium exposure is related to saxitoxin load and characterized by disrupted digestion, energy balance, and calcium and sodium signaling. <i>Aquatic Toxicology</i> , 2018, 199, 127-137.	4.0	19
110	RNAbrowse: RNA-Seq De Novo Assembly Results Browser. <i>PLoS ONE</i> , 2014, 9, e96821.	2.5	19
111	De novo transcriptome analysis to search for sex-differentiation genes in the Siberian sturgeon. <i>General and Comparative Endocrinology</i> , 2018, 268, 96-109.	1.8	18
112	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
113	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
114	An integrative method to normalize RNA-Seq data. <i>BMC Bioinformatics</i> , 2014, 15, 188.	2.6	17
115	Combined QTL and Selective Sweep Mappings with Coding SNP Annotation and cis-eQTL Analysis Revealed <i>PARK2</i> and <i>JAG2</i> as New Candidate Genes for Adiposity Regulation. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 517-529.	1.8	17
116	Genetic and transcriptomic analyses provide new insights on the early antiviral response to VHSV in resistant and susceptible rainbow trout. <i>BMC Genomics</i> , 2018, 19, 482.	2.8	17
117	Genome Sequence of the Yeast <i>Clavispora lusitaniae</i> Type Strain CBS 6936. <i>Genome Announcements</i> , 2017, 5, .	0.8	16
118	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
119	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
120	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
121	Combining GWAS and RNA-Seq Approaches for Detection of the Causal Mutation for Hereditary Junctional Epidermolysis Bullosa in Sheep. <i>PLoS ONE</i> , 2015, 10, e0126416.	2.5	15
122	Genome-Wide Characterization of RNA Editing in Chicken Embryos Reveals Common Features among Vertebrates. <i>PLoS ONE</i> , 2015, 10, e0126776.	2.5	15
123	Generation of a chromosome-level genome assembly for Pacific halibut ( <i>Hippoglossus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TFS Resources, 2022, 22, 2685-2700.	4.8	15
124	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
125	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
126	Transcriptomic analysis reveals specific metabolic pathways of enterohemorrhagic <i>Escherichia coli</i> O157:H7 in bovine digestive contents. <i>BMC Genomics</i> , 2018, 19, 766.	2.8	14



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127	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
128	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
129	The Peptide Venom Composition of the Fierce Stinging Ant <i>Tetraponera aethiops</i> (Formicidae: Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.4	14
130	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>G3: Genes, Genomes, Genetics</i> , 2016, 6, 321-335.	1.8	13
131	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
132	An ancient truncated duplication of the anti- $\text{M}\beta$ 1/4llergic 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
133	Characterization of rainbow trout gonad, brain and gill deep cDNA repertoires using a Roche 454-Titanium sequencing approach. <i>Gene</i> , 2012, 500, 32-39.	2.2	11
134	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
135	De novo transcriptome sequencing and analysis of freshwater snail ( <i>Radix balthica</i> ) to discover genes and pathways affected by exposure to oxazepam. <i>Ecotoxicology</i> , 2017, 26, 127-140.	2.4	10
136	One complete and three draft genome sequences of four <i>Brochothrix thermosphacta</i> strains, CD 337, TAP 175, BSAS1 3 and EBP 3070. <i>Standards in Genomic Sciences</i> , 2018, 13, 22.	1.5	10
137	Identification of potential chemosignals in the European water vole <i>Arvicola terrestris</i> . <i>Scientific Reports</i> , 2019, 9, 18378.	3.3	10
138	Domestication modulates the expression of genes involved in neurogenesis in high-quality eggs of <i>Sander lucioperca</i> . <i>Molecular Reproduction and Development</i> , 2020, 87, 934-951.	2.0	10
139	Contrasted effects of natural complex mixtures of PAHs and metals on oxygen cycle in a microbial mat. <i>Chemosphere</i> , 2015, 135, 189-201.	8.2	9
140	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
141	Highly Promiscuous Oxidases Discovered in the Bovine Rumen Microbiome. <i>Frontiers in Microbiology</i> , 2018, 9, 861.	3.5	9
142	Structure of the intergenic spacers in chicken ribosomal DNA. <i>Genetics Selection Evolution</i> , 2019, 51, 59.	3.0	9
143	The immune system of sturgeons and paddlefish ( <i>Acipenseriformes</i> ): a review with new data from a chromosome-scale sturgeon genome. <i>Reviews in Aquaculture</i> , 2021, 13, 1709-1729.	9.0	9
144	Non PCR-amplified Transcripts and AFLP fragments as reduced representations of the quail genome for 454 Titanium sequencing. <i>BMC Research Notes</i> , 2010, 3, 214.	1.4	8

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145	Intra-host viral variability in children clinically infected with H1N1 (2009) pandemic influenza. <i>Infection, Genetics and Evolution</i> , 2015, 33, 47-54.	2.3	8
146	A duplicated copy of id2b is an unusual sex-determining candidate gene on the Y chromosome of arapaima ( <i>Arapaima gigas</i> ). <i>Scientific Reports</i> , 2021, 11, 21544.	3.3	8
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