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List of Publications by Year in descending order

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44
papers

4,694
citations

186265

28
h-index

265206

42
g-index

54
all docs

54
docs citations

54
times ranked

6713
citing authors

#	ARTICLE	IF	CITATIONS
1	Ten quick tips for teaching with participatory live coding. PLoS Computational Biology, 2020, 16, e1008090.	3.2	13
2	Assessing graph-based read mappers against a baseline approach highlights strengths and weaknesses of current methods. BMC Genomics, 2020, 21, 282.	2.8	13
3	A high-quality assembly of the nine-spined stickleback (<i>Pungitius pungitius</i>) genome. Genome Biology and Evolution, 2019, 11, 3291-3308.	2.5	54
4	Graph Peak Caller: Calling ChIP-seq peaks on graph-based reference genomes. PLoS Computational Biology, 2019, 15, e1006731.	3.2	23
5	Genomic architecture of haddock (<i>Melanogrammus aeglefinus</i>) shows expansions of innate immune genes and short tandem repeats. BMC Genomics, 2018, 19, 240.	2.8	58
6	The Grayling Genome Reveals Selection on Gene Expression Regulation after Whole-Genome Duplication. Genome Biology and Evolution, 2018, 10, 2785-2800.	2.5	42
7	Loss of stomach, loss of appetite? Sequencing of the ballan wrasse (<i>Labrus bergylta</i>) genome and intestinal transcriptomic profiling illuminate the evolution of loss of stomach function in fish. BMC Genomics, 2018, 19, 186.	2.8	48
8	Mitochondrial genome variation of Atlantic cod. BMC Research Notes, 2018, 11, 397.	1.4	6
9	An improved genome assembly uncovers prolific tandem repeats in Atlantic cod. BMC Genomics, 2017, 18, 95.	2.8	153
10	The genomic mosaicism of hybrid speciation. Science Advances, 2017, 3, e1602996.	10.3	138
11	Coordinates and intervals in graph-based reference genomes. BMC Bioinformatics, 2017, 18, 263.	2.6	22
12	Good enough practices in scientific computing. PLoS Computational Biology, 2017, 13, e1005510.	3.2	254
13	The new era of genome sequencing using high-throughput sequencing technology: generation of the first version of the Atlantic cod genome. , 2016, , 1-20.		1
14	An improved version of the Atlantic cod genome and advancements in functional genomics: implications for the future of cod farming. , 2016, , 45-72.		25
15	Evolutionary redesign of the Atlantic cod (<i>Gadus morhua</i> L.) Toll-like receptor repertoire by gene losses and expansions. Scientific Reports, 2016, 6, 25211.	3.3	89
16	The Atlantic salmon genome provides insights into rediploidization. Nature, 2016, 533, 200-205.	27.8	1,021
17	Evolution of the immune system influences speciation rates in teleost fishes. Nature Genetics, 2016, 48, 1204-1210.	21.4	226
18	Genomic characterization of the Atlantic cod sex-locus. Scientific Reports, 2016, 6, 31235.	3.3	34

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19	Pathogens in Urine from a Female Patient with Overactive Bladder Syndrome Detected by Culture-independent High Throughput Sequencing: A Case Report. <i>Open Microbiology Journal</i> , 2014, 8, 148-153.	0.7	18
20	The chloroplast genome of the diatom <i>Seminavis robusta</i> : New features introduced through multiple mechanisms of horizontal gene transfer. <i>Marine Genomics</i> , 2014, 16, 17-27.	1.1	43
21	Hybrid speciation through sorting of parental incompatibilities in Italian sparrows. <i>Molecular Ecology</i> , 2014, 23, 5831-5842.	3.9	60
22	On the middle ground between open source and commercial software - the case of the Newbler program. <i>Genome Biology</i> , 2014, 15, 113.	9.6	94
23	Palindromic Sequence Artifacts Generated during Next Generation Sequencing Library Preparation from Historic and Ancient DNA. <i>PLoS ONE</i> , 2014, 9, e89676.	2.5	27
24	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.	3.1	39
25	Alterations of microbiota in urine from women with interstitial cystitis. <i>BMC Microbiology</i> , 2012, 12, 205.	3.3	195
26	Environmental microbiology through the lens of high-throughput DNA sequencing: Synopsis of current platforms and bioinformatics approaches. <i>Journal of Microbiological Methods</i> , 2012, 91, 106-113.	1.6	115
27	Genome Fragmentation Is Not Confined to the Peridinin Plastid in Dinoflagellates. <i>PLoS ONE</i> , 2012, 7, e38809.	2.5	13
28	Assessing diversity of the female urine microbiota by high throughput sequencing of 16S rDNA amplicons. <i>BMC Microbiology</i> , 2011, 11, 244.	3.3	241
29	Complete Genome Sequence of the Commensal <i>Enterococcus faecalis</i> 62, Isolated from a Healthy Norwegian Infant. <i>Journal of Bacteriology</i> , 2011, 193, 2377-2378.	2.2	46
30	The genome sequence of Atlantic cod reveals a unique immune system. <i>Nature</i> , 2011, 477, 207-210.	27.8	730
31	Genome Evolution of a Tertiary Dinoflagellate Plastid. <i>PLoS ONE</i> , 2011, 6, e19132.	2.5	56
32	Genomic organization and gene expression of the multiple globins in Atlantic cod: conservation of globin-flanking genes in chordates infers the origin of the vertebrate globin clusters. <i>BMC Evolutionary Biology</i> , 2010, 10, 315.	3.2	22
33	Identification and Quantification of Genomic Repeats and Sample Contamination in Assemblies of 454 Pyrosequencing Reads. <i>Sequencing</i> , 2010, 2010, 1-12.	0.5	13
34	A novel totivirus and piscine reovirus (PRV) in Atlantic salmon (<i>Salmo salar</i>) with cardiomyopathy syndrome (CMS). <i>Virology Journal</i> , 2010, 7, 309.	3.4	113
35	A genome-wide analysis of nonribosomal peptide synthetase gene clusters and their peptides in a <i>Planktothrix rubescens</i> strain. <i>BMC Genomics</i> , 2009, 10, 396.	2.8	89
36	Large-scale sequence analyses of Atlantic cod. <i>New Biotechnology</i> , 2009, 25, 263-271.	4.4	73

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37	A solid-phase method for preparing human DNA from urine for diagnostic purposes. <i>Clinical Biochemistry</i> , 2009, 42, 1128-1135.	1.9	15
38	Multiple-locus variable-number tandem repeat analysis of <i>Legionella pneumophila</i> using multi-colored capillary electrophoresis. <i>Journal of Microbiological Methods</i> , 2008, 73, 111-117.	1.6	18
39	Expression of <i>Patella vulgata</i> Orthologs of engrailed and dpp-BMP2/4 in Adjacent Domains during Molluscan Shell Development Suggests a Conserved Compartment Boundary Mechanism. <i>Developmental Biology</i> , 2002, 246, 341-355.	2.0	115
40	Characterisation of two snail genes in the gastropod mollusc <i>Patella vulgata</i> . Implications for understanding the ancestral function of the snail-related genes in Bilateria. <i>Development Genes and Evolution</i> , 2002, 212, 186-195.	0.9	25
41	Novel and conserved roles for orthodenticle / otx and orthopedia / otp orthologs in the gastropod mollusc <i>Patella vulgata</i> . <i>Development Genes and Evolution</i> , 2002, 212, 330-337.	0.9	46
42	A lophotrochozoan twist gene is expressed in the ectomesoderm of the gastropod mollusk <i>Patella vulgata</i> . <i>Evolution & Development</i> , 2002, 4, 334-343.	2.0	32
43	Hedgehog crosses the snail's midline. <i>Nature</i> , 2002, 417, 811-812.	27.8	211
44	The stringlike genes of the limpet <i>Patella vulgata</i> . <i>Gene</i> , 1996, 172, 261-265.	2.2	4