Christiaan V Henkel

List of Publications by Year
in descending order

42 papers	3,878 citations	430874 18 h-index	315739 38 g-index
48 all docs	48 docs citations	48 times ranked	8874 citing authors

#	Article	IF	Citations
1	Scaffolding pre-assembled contigs using SSPACE. Bioinformatics, 2011, 27, 578-579.	4.1	2,214
2	The king cobra genome reveals dynamic gene evolution and adaptation in the snake venom system. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20651-20656.	7.1	412
3	The Burmese python genome reveals the molecular basis for extreme adaptation in snakes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20645-20650.	7.1	260
4	Primitive Duplicate Hox Clusters in the European Eel's Genome. PLoS ONE, 2012, 7, e32231.	2.5	128
5	Rapid de novo assembly of the European eel genome from nanopore sequencing reads. Scientific Reports, 2017, 7, 7213.	3.3	104
6	First draft genome sequence of the Japanese eel, Anguilla japonica. Gene, 2012, 511, 195-201.	2.2	99
7	Comparison of the Exomes of Common Carp (<i>Cyprinus carpio</i>) and Zebrafish (<i>Danio) Tj ETQq1 1 0.784314 rgBT /Overlock	1.1	90
8	Deep sequencing of the innate immune transcriptomic response of zebrafish embryos to Salmonella infection. Fish and Shellfish Immunology, 2011, 31, 716-724.	3.6	79
9	Deep RNA Sequencing of the Skeletal Muscle Transcriptome in Swimming Fish. PLoS ONE, 2013, 8, e53171.	2.5	62
10	Conserved Expression Signatures between Medaka and Human Pigment Cell Tumors. PLoS ONE, 2012, 7, e37880.	2.5	35
11	DNA computing of solutions to knapsack problems. BioSystems, 2007, 88, 156-162.	2.0	31
12	Snake Genome Sequencing: Results and Future Prospects. Toxins, 2016, 8, 360.	3.4	31
13	Targeting oncogene expression to endothelial cells induces proliferation of the myelo-erythroid lineage by repressing the notch pathway. Leukemia, 2013, 27, 2229-2241.	7.2	28
14	The <i>Agrobacterium tumefaciens</i> virulence protein VirE3 is a transcriptional activator of the F‑box gene <i><scp>VBF</scp></i>. Plant Journal, 2015, 84, 914-924.	5.7	27
15	DNA computing using single-molecule hybridization detection. Nucleic Acids Research, 2004, 32, 4962-4968.	14.5	26
16	Identification of Common Carp Innate Immune Genes with Whole-Genome Sequencing and RNA-Seq Data. Journal of Integrative Bioinformatics, 2011, 8, 165-175.	1.5	23
17	Swimming exercise enhances brain plasticity in fish. Royal Society Open Science, 2020, 7, 191640.	2.4	23
18	Genome Sequence of the Octopine-Type Agrobacterium tumefaciens Strain Ach5. Genome Announcements, 2014, 2, .	0.8	19

#	Article	IF	Citations
19	Changes in ovarian gene expression profiles and plasma hormone levels in maturing European eel () Tj ETQq1 1 0.784314 rgBT /Overl... 2016, 225, 185-196.	1.8	19
20	Protein output for DNA computing. Natural Computing, 2005, 4, 1-10.	3.0	16
21	3D Atlas of the Pituitary Gland of the Model Fish Medaka (Oryzias latipes). Frontiers in Endocrinology, 2021, 12, 719843.	3.5	15
22	The Pituitary Gland of the European Eel Reveals Massive Expression of Genes Involved in the Melanocortin System. PLoS ONE, 2013, 8, e77396.	2.5	15
23	Genomics in Eels â€" Towards Aquaculture and Biology. Marine Biotechnology, 2012, 14, 583-590.	2.4	14
24	Parallel deep transcriptome and proteome analysis of zebrafish larvae. BMC Research Notes, 2013, 6, 428.	1.4	14
25	Using normalization to resolve RNA-Seq biases caused by amplification from minimal input. Physiological Genomics, 2014, 46, 808-820.	2.3	13
26	Identification of common carp innate immune genes with whole-genome sequencing and RNA-Seq data. Journal of Integrative Bioinformatics, 2011, 8, 169.	1.5	12
27	Characterization of hormone-producing cell types in the teleost pituitary gland using single-cell RNA-seq. Scientific Data, 2021, 8, 279.	5.3	11
28	Eye-Transcriptome and Genome-Wide Sequencing for Scolecophidia: Implications for Inferring the Visual System of the Ancestral Snake. Genome Biology and Evolution, 2021, 13, .	2.5	8
29	De novo whole-genome assembly of a wild type yeast isolate using nanopore sequencing. F1000Research, 2017, 6, 618.	1.6	7
30	Enhancement of Arabidopsis growth characteristics using genome interrogation with artificial transcription factors. PLoS ONE, 2017, 12, e0174236.	2.5	7
31	De novo whole-genome assembly of a wild type yeast isolate using nanopore sequencing. F1000Research, 2017, 6, 618.	1.6	5
32	Report from the First Snake Genomics and Integrative Biology Meeting. Standards in Genomic Sciences, 2012, 7, 150-152.	1.5	4
33	Unravelling the changes during induced vitellogenesis in female European eel through RNA-Seq: What happens to the liver?. PLoS ONE, 2020, 15, e0236438.	2.5	2
34	Towards Evolutionary DNA Computing. Lecture Notes in Computer Science, 2005, , 242-257.	1.3	2
35	Application of Mismatch Detection Methods in DNA Computing. Natural Computing, 2006, 5, 151-163.	3.0	1
36	An Algorithm for SAT Without an Extraction Phase. Lecture Notes in Computer Science, 2006, , 67-80.	1.3	1

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37	Targeting HRASV12G Expression to the Zebrafish Early Hemogenic Progenitors Induces a Myeloproliferative Disorder by Repressing the Notch Pathway. Blood, 2012, 120, 4676-4676.	1.4	1
38	Application of Mismatch Detection Methods in DNA Computing. Lecture Notes in Computer Science, 2005, , 159-168.	1.3	0
39	Title is missing!. , 2020, 15, e0236438.		0
40	Title is missing!. , 2020, 15, e0236438.		0
41	Title is missing!. , 2020, 15, e0236438.		0
42	Title is missing!. , 2020, 15, e0236438.		0