

Christiaan V Henkel

List of Publications by Year in descending order

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42
papers

3,878
citations

430874

18
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315739

38
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48
all docs

48
docs citations

48
times ranked

8874
citing authors

#	ARTICLE	IF	CITATIONS
1	3D Atlas of the Pituitary Gland of the Model Fish Medaka (<i>Oryzias latipes</i>). <i>Frontiers in Endocrinology</i> , 2021, 12, 719843.	3.5	15
2	Characterization of hormone-producing cell types in the teleost pituitary gland using single-cell RNA-seq. <i>Scientific Data</i> , 2021, 8, 279.	5.3	11
3	Eye-Transcriptome and Genome-Wide Sequencing for Scolecophidia: Implications for Inferring the Visual System of the Ancestral Snake. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	8
4	Unravelling the changes during induced vitellogenesis in female European eel through RNA-Seq: What happens to the liver?. <i>PLoS ONE</i> , 2020, 15, e0236438.	2.5	2
5	Swimming exercise enhances brain plasticity in fish. <i>Royal Society Open Science</i> , 2020, 7, 191640.	2.4	23
6	Title is missing!. , 2020, 15, e0236438.		0
7	Title is missing!. , 2020, 15, e0236438.		0
8	Title is missing!. , 2020, 15, e0236438.		0
9	Title is missing!. , 2020, 15, e0236438.		0
10	Rapid de novo assembly of the European eel genome from nanopore sequencing reads. <i>Scientific Reports</i> , 2017, 7, 7213.	3.3	104
11	De novo whole-genome assembly of a wild type yeast isolate using nanopore sequencing. <i>F1000Research</i> , 2017, 6, 618.	1.6	7
12	De novo whole-genome assembly of a wild type yeast isolate using nanopore sequencing. <i>F1000Research</i> , 2017, 6, 618.	1.6	5
13	Enhancement of <i>Arabidopsis</i> growth characteristics using genome interrogation with artificial transcription factors. <i>PLoS ONE</i> , 2017, 12, e0174236.	2.5	7
14	Snake Genome Sequencing: Results and Future Prospects. <i>Toxins</i> , 2016, 8, 360.	3.4	31
15	Changes in ovarian gene expression profiles and plasma hormone levels in maturing European eel (<i>Anguilla anguilla</i>). <i>Journal of Endocrinology</i> , 2016, 225, 185-196.	1.8	19
16	The <i>Agrobacterium tumefaciens</i> virulence protein VirE3 is a transcriptional activator of the <i>Vf</i> gene. <i>Plant Journal</i> , 2015, 84, 914-924.	5.7	27
17	Using normalization to resolve RNA-Seq biases caused by amplification from minimal input. <i>Physiological Genomics</i> , 2014, 46, 808-820.	2.3	13
18	Genome Sequence of the Octopine-Type <i>Agrobacterium tumefaciens</i> Strain Ach5. <i>Genome Announcements</i> , 2014, 2, .	0.8	19

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19	Targeting oncogene expression to endothelial cells induces proliferation of the myelo-erythroid lineage by repressing the notch pathway. <i>Leukemia</i> , 2013, 27, 2229-2241.	7.2	28
20	The Burmese python genome reveals the molecular basis for extreme adaptation in snakes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20645-20650.	7.1	260
21	Parallel deep transcriptome and proteome analysis of zebrafish larvae. <i>BMC Research Notes</i> , 2013, 6, 428.	1.4	14
22	The king cobra genome reveals dynamic gene evolution and adaptation in the snake venom system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20651-20656.	7.1	412
23	Deep RNA Sequencing of the Skeletal Muscle Transcriptome in Swimming Fish. <i>PLoS ONE</i> , 2013, 8, e53171.	2.5	62
24	The Pituitary Gland of the European Eel Reveals Massive Expression of Genes Involved in the Melanocortin System. <i>PLoS ONE</i> , 2013, 8, e77396.	2.5	15
25	Report from the First Snake Genomics and Integrative Biology Meeting. <i>Standards in Genomic Sciences</i> , 2012, 7, 150-152.	1.5	4
26	Comparison of the Exomes of Common Carp (<i>Cyprinus carpio</i>) and Zebrafish (<i>Danio</i>)	1.1	90
27	Genomics in Eels – Towards Aquaculture and Biology. <i>Marine Biotechnology</i> , 2012, 14, 583-590.	2.4	14
28	First draft genome sequence of the Japanese eel, <i>Anguilla japonica</i> . <i>Gene</i> , 2012, 511, 195-201.	2.2	99
29	Primitive Duplicate Hox Clusters in the European Eel's Genome. <i>PLoS ONE</i> , 2012, 7, e32231.	2.5	128
30	Conserved Expression Signatures between Medaka and Human Pigment Cell Tumors. <i>PLoS ONE</i> , 2012, 7, e37880.	2.5	35
31	Targeting HRASV12G Expression to the Zebrafish Early Hemogenic Progenitors Induces a Myeloproliferative Disorder by Repressing the Notch Pathway. <i>Blood</i> , 2012, 120, 4676-4676.	1.4	1
32	Scaffolding pre-assembled contigs using SSPACE. <i>Bioinformatics</i> , 2011, 27, 578-579.	4.1	2,214
33	Deep sequencing of the innate immune transcriptomic response of zebrafish embryos to <i>Salmonella</i> infection. <i>Fish and Shellfish Immunology</i> , 2011, 31, 716-724.	3.6	79
34	Identification of Common Carp Innate Immune Genes with Whole-Genome Sequencing and RNA-Seq Data. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 165-175.	1.5	23
35	Identification of common carp innate immune genes with whole-genome sequencing and RNA-Seq data. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 169.	1.5	12
36	DNA computing of solutions to knapsack problems. <i>BioSystems</i> , 2007, 88, 156-162.	2.0	31

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37	Application of Mismatch Detection Methods in DNA Computing. Natural Computing, 2006, 5, 151-163.	3.0	1
38	An Algorithm for SAT Without an Extraction Phase. Lecture Notes in Computer Science, 2006, , 67-80.	1.3	1
39	Protein output for DNA computing. Natural Computing, 2005, 4, 1-10.	3.0	16
40	Towards Evolutionary DNA Computing. Lecture Notes in Computer Science, 2005, , 242-257.	1.3	2
41	Application of Mismatch Detection Methods in DNA Computing. Lecture Notes in Computer Science, 2005, , 159-168.	1.3	0
42	DNA computing using single-molecule hybridization detection. Nucleic Acids Research, 2004, 32, 4962-4968.	14.5	26