# Christiaan V Henkel

List of Publications by Year
in descending order

| 42 papers | 3,878 citations | 430442<br>18 h-index | 315357<br>38 g-index |
|---|---|---|---|
| 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 (Oryzias latipes). Frontiers in Endocrinology, 2021, 12, 719843. | 1.5 | 15 |
| 2 | Characterization of hormone-producing cell types in the teleost pituitary gland using single-cell RNA-seq. Scientific Data, 2021, 8, 279. | 2.4 | 11 |
| 3 | Eye-Transcriptome and Genome-Wide Sequencing for Scolecophidia: Implications for Inferring the Visual System of the Ancestral Snake. Genome Biology and Evolution, 2021, 13, . | 1.1 | 8 |
| 4 | Unravelling the changes during induced vitellogenesis in female European eel through RNA-Seq: What happens to the liver?. PLoS ONE, 2020, 15, e0236438. | 1.1 | 2 |
| 5 | Swimming exercise enhances brain plasticity in fish. Royal Society Open Science, 2020, 7, 191640. | 1.1 | 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. Scientific Reports, 2017, 7, 7213. | 1.6 | 104 |
| 11 | De novo whole-genome assembly of a wild type yeast isolate using nanopore sequencing. F1000Research, 2017, 6, 618. | 0.8 | 7 |
| 12 | De novo whole-genome assembly of a wild type yeast isolate using nanopore sequencing. F1000Research, 2017, 6, 618. | 0.8 | 5 |
| 13 | Enhancement of Arabidopsis growth characteristics using genome interrogation with artificial transcription factors. PLoS ONE, 2017, 12, e0174236. | 1.1 | 7 |
| 14 | Snake Genome Sequencing: Results and Future Prospects. Toxins, 2016, 8, 360. | 1.5 | 31 |
| 15 | Changes in ovarian gene expression profiles and plasma hormone levels in maturing European eel () Tj ETQq1 1 0.784314 rgBT /Overlock 2016, 225, 185-196. | 0.8 | 19 |
| 16 | The <i>Agrobacterium tumefaciens</i> virulence protein VirE3 is a transcriptional activator of the Fâ€box gene <i><scp>VBF</scp></i>. Plant Journal, 2015, 84, 914-924. | 2.8 | 27 |
| 17 | Using normalization to resolve RNA-Seq biases caused by amplification from minimal input. Physiological Genomics, 2014, 46, 808-820. | 1.0 | 13 |
| 18 | Genome Sequence of the Octopine-Type Agrobacterium tumefaciens Strain Ach5. Genome Announcements, 2014, 2, . | 0.8 | 19 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 19 | Targeting oncogene expression to endothelial cells induces proliferation of the myelo-erythroid lineage by repressing the notch pathway. Leukemia, 2013, 27, 2229-2241. | 3.3 | 28 |
| 20 | 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. | 3.3 | 260 |
| 21 | Parallel deep transcriptome and proteome analysis of zebrafish larvae. BMC Research Notes, 2013, 6, 428. | 0.6 | 14 |
| 22 | 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. | 3.3 | 412 |
| 23 | Deep RNA Sequencing of the Skeletal Muscle Transcriptome in Swimming Fish. PLoS ONE, 2013, 8, e53171. | 1.1 | 62 |
| 24 | The Pituitary Gland of the European Eel Reveals Massive Expression of Genes Involved in the Melanocortin System. PLoS ONE, 2013, 8, e77396. | 1.1 | 15 |
| 25 | Report from the First Snake Genomics and Integrative Biology Meeting. Standards in Genomic Sciences, 2012, 7, 150-152. | 1.5 | 4 |
| 26 | Comparison of the Exomes of Common Carp (<i>Cyprinus carpio</i>) and Zebrafish (<i>Danio) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 46 | 0.5 | 90 |
| 27 | Genomics in Eels â€" Towards Aquaculture and Biology. Marine Biotechnology, 2012, 14, 583-590. | 1.1 | 14 |
| 28 | First draft genome sequence of the Japanese eel, Anguilla japonica. Gene, 2012, 511, 195-201. | 1.0 | 99 |
| 29 | Primitive Duplicate Hox Clusters in the European Eel's Genome. PLoS ONE, 2012, 7, e32231. | 1.1 | 128 |
| 30 | Conserved Expression Signatures between Medaka and Human Pigment Cell Tumors. PLoS ONE, 2012, 7, e37880. | 1.1 | 35 |
| 31 | Targeting HRASV12G Expression to the Zebrafish Early Hemogenic Progenitors Induces a Myeloproliferative Disorder by Repressing the Notch Pathway. Blood, 2012, 120, 4676-4676. | 0.6 | 1 |
| 32 | Scaffolding pre-assembled contigs using SSPACE. Bioinformatics, 2011, 27, 578-579. | 1.8 | 2,214 |
| 33 | Deep sequencing of the innate immune transcriptomic response of zebrafish embryos to Salmonella infection. Fish and Shellfish Immunology, 2011, 31, 716-724. | 1.6 | 79 |
| 34 | Identification of Common Carp Innate Immune Genes with Whole-Genome Sequencing and RNA-Seq Data. Journal of Integrative Bioinformatics, 2011, 8, 165-175. | 1.0 | 23 |
| 35 | Identification of common carp innate immune genes with whole-genome sequencing and RNA-Seq data. Journal of Integrative Bioinformatics, 2011, 8, 169. | 1.0 | 12 |
| 36 | DNA computing of solutions to knapsack problems. BioSystems, 2007, 88, 156-162. | 0.9 | 31 |

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|---|---------|----|-----------| 
| 37 | Application of Mismatch Detection Methods in DNA Computing. Natural Computing, 2006, 5, 151-163. | 1.8 | 1 |
| 38 | An Algorithm for SAT Without an Extraction Phase. Lecture Notes in Computer Science, 2006, , 67-80. | 1.0 | 1 |
| 39 | Protein output for DNA computing. Natural Computing, 2005, 4, 1-10. | 1.8 | 16 |
| 40 | Towards Evolutionary DNA Computing. Lecture Notes in Computer Science, 2005, , 242-257. | 1.0 | 2 |
| 41 | Application of Mismatch Detection Methods in DNA Computing. Lecture Notes in Computer Science, 2005, , 159-168. | 1.0 | 0 |
| 42 | DNA computing using single-molecule hybridization detection. Nucleic Acids Research, 2004, 32, 4962-4968. | 6.5 | 26 |