

Gennady Churakov

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9697689/publications.pdf>

Version: 2024-02-01

21
papers

1,374
citations

623734

14
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713466

21
g-index

22
all docs

22
docs citations

22
times ranked

1894
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Retroposed Elements as Archives for the Evolutionary History of Placental Mammals. <i>PLoS Biology</i> , 2006, 4, e91. | 5.6 | 238 |
| 2 | Evolutionary history of 7SL RNA-derived SINEs in Supraprimates. <i>Trends in Genetics</i> , 2007, 23, 158-161. | 6.7 | 204 |
| 3 | Mesozoic retroposons reveal parrots as the closest living relatives of passerine birds. <i>Nature Communications</i> , 2011, 2, 443. | 12.8 | 175 |
| 4 | Rodent Evolution: Back to the Root. <i>Molecular Biology and Evolution</i> , 2010, 27, 1315-1326. | 8.9 | 131 |
| 5 | The genome of the vervet (<i>Chlorocebus aethiops sabaues</i>). <i>Genome Research</i> , 2015, 25, 1921-1933. | 5.5 | 114 |
| 6 | Mosaic retroposon insertion patterns in placental mammals. <i>Genome Research</i> , 2009, 19, 868-875. | 5.5 | 79 |
| 7 | Genomic analysis reveals hidden biodiversity within colugos, the sister group to primates. <i>Science Advances</i> , 2016, 2, e1600633. | 10.3 | 64 |
| 8 | Multiple Lineages of Ancient CR1 Retroposons Shaped the Early Genome Evolution of Amniotes. <i>Genome Biology and Evolution</i> , 2015, 7, 205-217. | 2.5 | 62 |
| 9 | Exploring Massive Incomplete Lineage Sorting in Arctoids (Laurasiatheria, Carnivora). <i>Molecular Biology and Evolution</i> , 2015, 32, msv188. | 8.9 | 48 |
| 10 | Incomplete Lineage Sorting and Hybridization Statistics for Large-Scale Retroposon Insertion Data. <i>PLoS Computational Biology</i> , 2016, 12, e1004812. | 3.2 | 47 |
| 11 | A novel web-based TinT application and the chronology of the Primate Alu retroposon activity. <i>BMC Evolutionary Biology</i> , 2010, 10, 376. | 3.2 | 45 |
| 12 | A Novel Abundant Family of Retroposed Elements (DAS-SINEs) in the Nine-Banded Armadillo (<i>Dasyurus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T | 8.9 | 39 |
| 13 | Speciation network in Laurasiatheria: retrophylogenomic signals. <i>Genome Research</i> , 2017, 27, 997-1003. | 5.5 | 38 |
| 14 | Genome sequence of the basal haplorrhine primate <i>Tarsius syrichta</i> reveals unusual insertions. <i>Nature Communications</i> , 2016, 7, 12997. | 12.8 | 32 |
| 15 | The Beaver's Phylogenetic Lineage Illuminated by Retroposon Reads. <i>Scientific Reports</i> , 2017, 7, 43562. | 3.3 | 13 |
| 16 | The multic comparative 2-n-way genome suite. <i>Genome Research</i> , 2020, 30, 1508-1516. | 5.5 | 13 |
| 17 | Ancient Traces of Tailless Retropseudogenes in Therian Genomes. <i>Genome Biology and Evolution</i> , 2015, 7, 889-900. | 2.5 | 9 |
| 18 | GPAC's Genome Presence/Absence Compiler: A Web Application to Comparatively Visualize Multiple Genome-Level Changes. <i>Molecular Biology and Evolution</i> , 2015, 32, 275-286. | 8.9 | 9 |

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|----|--|-----|-----------|
| 19 | The Volcano Rabbit in the Phylogenetic Network of Lagomorphs. <i>Genome Biology and Evolution</i> , 2019, 11, 11-16. | 2.5 | 6 |
| 20 | First evidence of miniature transposable elements in sponges (Porifera). <i>Hydrobiologia</i> , 2012, 687, 43-47. | 2.0 | 2 |
| 21 | Euarchontoglires Challenged by Incomplete Lineage Sorting. <i>Genes</i> , 2022, 13, 774. | 2.4 | 2 |