Wesley C Warren

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17,338 155 131 59 h-index g-index citations papers 21,656 164 15.7 5.44 L-index avg, IF ext. papers ext. citations

| # | Paper | IF | Citations |
|-----|--|------|-----------|
| 155 | Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014 , 346, 1320-31 | 33.3 | 1182 |
| 154 | Evolutionary and biomedical insights from the rhesus macaque genome. <i>Science</i> , 2007 , 316, 222-34 | 33.3 | 1072 |
| 153 | A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011 , 478, 476-82 | 50.4 | 802 |
| 152 | The genome of a songbird. <i>Nature</i> , 2010 , 464, 757-62 | 50.4 | 655 |
| 151 | Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014 , 346, 1311-20 | 33.3 | 628 |
| 150 | The genome of the Western clawed frog Xenopus tropicalis. <i>Science</i> , 2010 , 328, 633-6 | 33.3 | 579 |
| 149 | Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008 , 453, 175-83 | 50.4 | 545 |
| 148 | Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , 2012 , 483, 169-75 | 50.4 | 517 |
| 147 | A catalog of reference genomes from the human microbiome. <i>Science</i> , 2010 , 328, 994-9 | 33.3 | 508 |
| 146 | Elephant shark genome provides unique insights into gnathostome evolution. <i>Nature</i> , 2014 , 505, 174-9 | 50.4 | 498 |
| 145 | Sequencing of the sea lamprey (Petromyzon marinus) genome provides insights into vertebrate evolution. <i>Nature Genetics</i> , 2013 , 45, 415-21, 421e1-2 | 36.3 | 465 |
| 144 | SNP discovery and allele frequency estimation by deep sequencing of reduced representation libraries. <i>Nature Methods</i> , 2008 , 5, 247-52 | 21.6 | 458 |
| 143 | Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011 , 469, 529-33 | 50.4 | 431 |
| 142 | Mammalian Y chromosomes retain widely expressed dosage-sensitive regulators. <i>Nature</i> , 2014 , 508, 494-9 | 50.4 | 406 |
| 141 | A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. <i>Nature</i> , 2004 , 432, 717-22 | 50.4 | 341 |
| 140 | Comparison of genome degradation in Paratyphi A and Typhi, human-restricted serovars of Salmonella enterica that cause typhoid. <i>Nature Genetics</i> , 2004 , 36, 1268-74 | 36.3 | 308 |
| 139 | Chimpanzee and human Y chromosomes are remarkably divergent in structure and gene content. <i>Nature</i> , 2010 , 463, 536-9 | 50.4 | 286 |

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| 138 | The genomic landscape of rapid repeated evolutionary adaptation to toxic pollution in wild fish. <i>Science</i> , 2016 , 354, 1305-1308 | 33.3 | 250 |
|-----|---|------|-----|
| 137 | Gibbon genome and the fast karyotype evolution of small apes. <i>Nature</i> , 2014 , 513, 195-201 | 50.4 | 241 |
| 136 | The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. <i>Nature Genetics</i> , 2013 , 45, 776-783 | 36.3 | 240 |
| 135 | The draft genome of the parasitic nematode Trichinella spiralis. <i>Nature Genetics</i> , 2011 , 43, 228-35 | 36.3 | 230 |
| 134 | Genome of Rhodnius prolixus, an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 14936-41 | 11.5 | 220 |
| 133 | Characterizing the Major Structural Variant Alleles of the Human Genome. <i>Cell</i> , 2019 , 176, 663-675.e19 | 56.2 | 205 |
| 132 | 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, 20645-50 | 11.5 | 203 |
| 131 | The genome of the platyfish, Xiphophorus maculatus, provides insights into evolutionary adaptation and several complex traits. <i>Nature Genetics</i> , 2013 , 45, 567-72 | 36.3 | 201 |
| 130 | Genome sequence of the tsetse fly (Glossina morsitans): vector of African trypanosomiasis. <i>Science</i> , 2014 , 344, 380-6 | 33.3 | 192 |
| 129 | Sequencing the mouse Y chromosome reveals convergent gene acquisition and amplification on both sex chromosomes. <i>Cell</i> , 2014 , 159, 800-13 | 56.2 | 192 |
| 128 | The genome sequence of the leaf-cutter ant Atta cephalotes reveals insights into its obligate symbiotic lifestyle. <i>PLoS Genetics</i> , 2011 , 7, e1002007 | 6 | 191 |
| 127 | Comparative analysis of the domestic cat genome reveals genetic signatures underlying feline biology and domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 17230-5 | 11.5 | 184 |
| 126 | Divergence and Functional Degradation of a Sex Chromosome-like Supergene. <i>Current Biology</i> , 2016 , 26, 344-50 | 6.3 | 183 |
| 125 | Strict evolutionary conservation followed rapid gene loss on human and rhesus Y chromosomes. <i>Nature</i> , 2012 , 483, 82-6 | 50.4 | 181 |
| 124 | Extensive error in the number of genes inferred from draft genome assemblies. <i>PLoS Computational Biology</i> , 2014 , 10, e1003998 | 5 | 180 |
| 123 | High-resolution comparative analysis of great ape genomes. <i>Science</i> , 2018 , 360, | 33.3 | 178 |
| 122 | Convergent evolution of chicken Z and human X chromosomes by expansion and gene acquisition. <i>Nature</i> , 2010 , 466, 612-6 | 50.4 | 168 |
| 121 | A physical map of the chicken genome. <i>Nature</i> , 2004 , 432, 761-4 | 50.4 | 166 |

| 120 | Genome sequence of Cronobacter sakazakii BAA-894 and comparative genomic hybridization analysis with other Cronobacter species. <i>PLoS ONE</i> , 2010 , 5, e9556 | 3.7 | 166 |
|-----|---|----------------|-----|
| 119 | Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021 , 592, 737- | 7 4 6.4 | 161 |
| 118 | A New Chicken Genome Assembly Provides Insight into Avian Genome Structure. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 109-117 | 3.2 | 143 |
| 117 | Genome of the human hookworm Necator americanus. <i>Nature Genetics</i> , 2014 , 46, 261-269 | 36.3 | 139 |
| 116 | Evolutionary toggling of the MAPT 17q21.31 inversion region. <i>Nature Genetics</i> , 2008 , 40, 1076-83 | 36.3 | 138 |
| 115 | Evolutionary signals of selection on cognition from the great tit genome and methylome. <i>Nature Communications</i> , 2016 , 7, 10474 | 17.4 | 125 |
| 114 | Independent specialization of the human and mouse X chromosomes for the male germ line. <i>Nature Genetics</i> , 2013 , 45, 1083-7 | 36.3 | 111 |
| 113 | Defensins and the convergent evolution of platypus and reptile venom genes. <i>Genome Research</i> , 2008 , 18, 986-94 | 9.7 | 101 |
| 112 | Single haplotype assembly of the human genome from a hydatidiform mole. <i>Genome Research</i> , 2014 , 24, 2066-76 | 9.7 | 98 |
| 111 | Systems biology of the vervet monkey. <i>ILAR Journal</i> , 2013 , 54, 122-43 | 1.7 | 93 |
| 110 | Avian W and mammalian Y chromosomes convergently retained dosage-sensitive regulators. <i>Nature Genetics</i> , 2017 , 49, 387-394 | 36.3 | 92 |
| 109 | The genome of the vervet (Chlorocebus aethiops sabaeus). <i>Genome Research</i> , 2015 , 25, 1921-33 | 9.7 | 84 |
| 108 | Convergence in feeding posture occurs through different genetic loci in independently evolved cave populations of Astyanax mexicanus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 16933-8 | 11.5 | 84 |
| 107 | Specifying and sustaining pigmentation patterns in domestic and wild cats. <i>Science</i> , 2012 , 337, 1536-41 | 33.3 | 84 |
| 106 | INTEGRATE: gene fusion discovery using whole genome and transcriptome data. <i>Genome Research</i> , 2016 , 26, 108-18 | 9.7 | 81 |
| 105 | The role of gene flow in rapid and repeated evolution of cave-related traits in Mexican tetra, Astyanax mexicanus. <i>Molecular Ecology</i> , 2018 , 27, 4397-4416 | 5.7 | 77 |
| 104 | Ancient hybridization and strong adaptation to viruses across African vervet monkey populations. <i>Nature Genetics</i> , 2017 , 49, 1705-1713 | 36.3 | 76 |
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(2008-2014)

| 102 | High-coverage sequencing and annotated assemblies of the budgerigar genome. <i>GigaScience</i> , 2014 , 3, 11 | 7.6 | 67 | |
|-----|--|------|----|--|
| 101 | The sterlet sturgeon genome sequence and the mechanisms of segmental rediploidization. <i>Nature Ecology and Evolution</i> , 2020 , 4, 841-852 | 12.3 | 65 | |
| 100 | The Physarum polycephalum Genome Reveals Extensive Use of Prokaryotic Two-Component and Metazoan-Type Tyrosine Kinase Signaling. <i>Genome Biology and Evolution</i> , 2015 , 8, 109-25 | 3.9 | 63 | |
| 99 | Antarctic blackfin icefish genome reveals adaptations to extreme environments. <i>Nature Ecology and Evolution</i> , 2019 , 3, 469-478 | 12.3 | 62 | |
| 98 | Generation and annotation of the DNA sequences of human chromosomes 2 and 4. <i>Nature</i> , 2005 , 434, 724-31 | 50.4 | 61 | |
| 97 | Clonal polymorphism and high heterozygosity in the celibate genome of the Amazon molly. <i>Nature Ecology and Evolution</i> , 2018 , 2, 669-679 | 12.3 | 60 | |
| 96 | Third Report on Chicken Genes and Chromosomes 2015. <i>Cytogenetic and Genome Research</i> , 2015 , 145, 78-179 | 1.9 | 57 | |
| 95 | Pangolin genomes and the evolution of mammalian scales and immunity. <i>Genome Research</i> , 2016 , 26, 1312-1322 | 9.7 | 54 | |
| 94 | Developing tools for the study of molluscan immunity: The sequencing of the genome of the eastern oyster, Crassostrea virginica. <i>Fish and Shellfish Immunology</i> , 2015 , 46, 2-4 | 4.3 | 49 | |
| 93 | Genomic analysis reveals hidden biodiversity within colugos, the sister group to primates. <i>Science Advances</i> , 2016 , 2, e1600633 | 14.3 | 49 | |
| 92 | Molecular Adaptations for Sensing and Securing Prey and Insight into Amniote Genome Diversity from the Garter Snake Genome. <i>Genome Biology and Evolution</i> , 2018 , 10, 2110-2129 | 3.9 | 48 | |
| 91 | Origin of INSL3-mediated testicular descent in therian mammals. <i>Genome Research</i> , 2008 , 18, 974-85 | 9.7 | 48 | |
| 90 | Construction and characterization of a new bovine bacterial artificial chromosome library with 10 genome-equivalent coverage. <i>Mammalian Genome</i> , 2000 , 11, 662-3 | 3.2 | 48 | |
| 89 | Glucose and insulin treatment of insulinoma cells results in transcriptional regulation of a common set of genes. <i>Diabetes</i> , 2004 , 53, 1496-508 | 0.9 | 46 | |
| 88 | Digital gene expression for non-model organisms. <i>Genome Research</i> , 2011 , 21, 1905-15 | 9.7 | 44 | |
| 87 | Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. <i>Nature Genetics</i> , 2017 , 49, 1714-1721 | 36.3 | 43 | |
| 86 | A non-human primate system for large-scale genetic studies of complex traits. <i>Human Molecular Genetics</i> , 2012 , 21, 3307-16 | 5.6 | 43 | |
| 85 | Gene discovery and comparative analysis of X-degenerate genes from the domestic cat Y chromosome. <i>Genomics</i> , 2008 , 92, 329-38 | 4.3 | 43 | |

| 84 | Comparative genomic analysis of six Glossina genomes, vectors of African trypanosomes. <i>Genome Biology</i> , 2019 , 20, 187 | 18.3 | 39 |
|----|---|-------------------|----|
| 83 | Profiling of gender-regulated gene transcripts in the filarial nematode Brugia malayi by cDNA oligonucleotide array analysis. <i>Molecular and Biochemical Parasitology</i> , 2005 , 143, 49-57 | 1.9 | 38 |
| 82 | Towards complete and error-free genome assemblies of all vertebrate species | | 38 |
| 81 | Joint MiRNA/mRNA expression profiling reveals changes consistent with development of dysfunctional corpus luteum after weight gain. <i>PLoS ONE</i> , 2015 , 10, e0135163 | 3.7 | 37 |
| 80 | Human-specific tandem repeat expansion and differential gene expression during primate evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 23243-23253 | 11.5 | 37 |
| 79 | Sequencing strategies and characterization of 721 vervet monkey genomes for future genetic analyses of medically relevant traits. <i>BMC Biology</i> , 2015 , 13, 41 | 7.3 | 36 |
| 78 | Proteomics and deep sequencing comparison of seasonally active venom glands in the platypus reveals novel venom peptides and distinct expression profiles. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1354-64 | 7.6 | 35 |
| 77 | The landscape of extreme genomic variation in the highly adaptable Atlantic killifish. <i>Genome Biology and Evolution</i> , 2017 , 9, 659-676 | 3.9 | 34 |
| 76 | 3D genomics across the tree of life reveals condensin II as a determinant of architecture type. <i>Science</i> , 2021 , 372, 984-989 | 33.3 | 33 |
| 75 | Opsin Repertoire and Expression Patterns in Horseshoe Crabs: Evidence from the Genome of Limulus polyphemus (Arthropoda: Chelicerata). <i>Genome Biology and Evolution</i> , 2016 , 8, 1571-89 | 3.9 | 33 |
| 74 | Physical Mapping and Refinement of the Painted Turtle Genome (Chrysemys picta) Inform Amniote Genome Evolution and Challenge Turtle-Bird Chromosomal Conservation. <i>Genome Biology and Evolution</i> , 2015 , 7, 2038-50 | 3.9 | 32 |
| 73 | A High-Resolution SNP Array-Based Linkage Map Anchors a New Domestic Cat Draft Genome Assembly and Provides Detailed Patterns of Recombination. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 160 | 7 ³ 16 | 32 |
| 72 | Transcriptome analysis of female and male Xiphophorus maculatus Jp 163 A. <i>PLoS ONE</i> , 2011 , 6, e1837 | 93.7 | 31 |
| 71 | A limited role for gene duplications in the evolution of platypus venom. <i>Molecular Biology and Evolution</i> , 2012 , 29, 167-77 | 8.3 | 30 |
| 70 | A new domestic cat genome assembly based on long sequence reads empowers feline genomic medicine and identifies a novel gene for dwarfism. <i>PLoS Genetics</i> , 2020 , 16, e1008926 | 6 | 29 |
| 69 | Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. <i>Science</i> , 2020 , 370, | 33.3 | 28 |
| 68 | The Novel Evolution of the Sperm Whale Genome. <i>Genome Biology and Evolution</i> , 2017 , 9, 3260-3264 | 3.9 | 27 |
| 67 | Applications and efficiencies of the first cat 63K DNA array. <i>Scientific Reports</i> , 2018 , 8, 7024 | 4.9 | 26 |

(2018-2013)

| To the Root of the Curl: A Signature of a Recent Selective Sweep Identifies a Mutation That Defines the Cornish Rex Cat Breed. <i>PLoS ONE</i> , 2013 , 8, e67105 | 3.7 | 26 | |
|---|--|---|---|
| A proposal to sequence the genome of a garter snake (Thamnophis sirtalis). <i>Standards in Genomic Sciences</i> , 2011 , 4, 257-70 | | 24 | |
| Physical map-assisted whole-genome shotgun sequence assemblies. <i>Genome Research</i> , 2006 , 16, 768-7 | 5 9.7 | 24 | |
| Genome sequence of the basal haplorrhine primate Tarsius syrichta reveals unusual insertions. <i>Nature Communications</i> , 2016 , 7, 12997 | 17.4 | 22 | |
| Fosmid-based physical mapping of the Histoplasma capsulatum genome. <i>Genome Research</i> , 2004 , 14, 1603-9 | 9.7 | 20 | |
| The quail genome: insights into social behaviour, seasonal biology and infectious disease response. <i>BMC Biology</i> , 2020 , 18, 14 | 7.3 | 19 | |
| The roles of plasticity and evolutionary change in shaping gene expression variation in natural populations of extremophile fish. <i>Molecular Ecology</i> , 2017 , 26, 6384-6399 | 5.7 | 18 | |
| The Cyprinodon variegatus genome reveals gene expression changes underlying differences in skull morphology among closely related species. <i>BMC Genomics</i> , 2017 , 18, 424 | 4.5 | 18 | |
| Higher-order genome organization in platypus and chicken sperm and repositioning of sex chromosomes during mammalian evolution. <i>Chromosoma</i> , 2009 , 118, 53-69 | 2.8 | 18 | |
| X. couchianus and X. hellerii genome models provide genomic variation insight among Xiphophorus species. <i>BMC Genomics</i> , 2016 , 17, 37 | 4.5 | 18 | |
| The Genome and Adult Somatic Transcriptome of the Mormyrid Electric Fish Paramormyrops kingsleyae. <i>Genome Biology and Evolution</i> , 2017 , 9, 3525-3530 | 3.9 | 16 | |
| A 3-way hybrid approach to generate a new high-quality chimpanzee reference genome (Pan_tro_3.0). <i>GigaScience</i> , 2017 , 6, 1-6 | 7.6 | 16 | |
| Complexities of gene expression patterns in natural populations of an extremophile fish (Poecilia mexicana, Poeciliidae). <i>Molecular Ecology</i> , 2017 , 26, 4211-4225 | 5.7 | 15 | |
| Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. <i>Genome Research</i> , 2019 , 29, 576-589 | 9.7 | 15 | |
| Mutations in the Kinesin-2 Motor KIF3B Cause an Autosomal-Dominant Ciliopathy. <i>American Journal of Human Genetics</i> , 2020 , 106, 893-904 | 11 | 14 | |
| Echidna venom gland transcriptome provides insights into the evolution of monotreme venom. <i>PLoS ONE</i> , 2013 , 8, e79092 | 3.7 | 14 | |
| The genomics of ecological flexibility, large brains, and long lives in capuchin monkeys revealed with fecalFACS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118, | 11.5 | 14 | |
| Long-term experimental hybridisation results in the evolution of a new sex chromosome in swordtail fish. <i>Nature Communications</i> , 2018 , 9, 5136 | 17.4 | 14 | |
| | the Cornish Rex Cat Breed. PLoS ONE, 2013, 8, e67105 A proposal to sequence the genome of a garter snake (Thamnophis sirtalis). Standards in Genomic Sciences, 2011, 4, 257-70 Physical map-assisted whole-genome shotgun sequence assemblies. Genome Research, 2006, 16, 768-7 Genome sequence of the basal haplorrhine primate Tarsius syrichta reveals unusual insertions. Nature Communications, 2016, 7, 12997 Fosmid-based physical mapping of the Histoplasma capsulatum genome. Genome Research, 2004, 14, 1603-9 The quail genome: insights into social behaviour, seasonal biology and infectious disease response. BMC Biology, 2020, 18, 14 The roles of plasticity and evolutionary change in shaping gene expression variation in natural populations of extremophile fish. Molecular Ecology, 2017, 26, 6384-6399 The Cyprinodon variegatus genome reveals gene expression changes underlying differences in skull morphology among closely related species. BMC Genomics, 2017, 18, 424 Higher-order genome organization in platypus and chicken sperm and repositioning of sex chromosomes during mammalian evolution. Chromosoma, 2009, 118, 53-69 X. couchianus and X. hellerii genome models provide genomic variation insight among Xiphophorus species. BMC Genomics, 2016, 17, 37 The Genome and Adult Somatic Transcriptome of the Mormyrid Electric Fish Paramormyrops kingsleyae. Genomics, 2016, 17, 37 The Genome and Adult Somatic Transcriptome of the Mormyrid Electric Fish Paramormyrops kingsleyae. Genomics, 2017, 6, 1-6 Complexities of gene expression patterns in natural populations of an extremophile fish (Poecilia mexicana, Poeciliidae). Molecular Ecology, 2017, 26, 4211-4225 Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. Genome Research, 2019, 29, 576-589 Wutations in the Kinesin-2 Motor KIF3B Cause an Autosomal-Dominant Ciliopathy. American Journal of Human Genetics, 2020, 106, 893-904 Echidna venom gland transcriptome provides insights into the evolution of monot | A proposal to sequence the genome of a garter snake (Thamnophis sirtalis). Standards in Genomic Sciences, 2011, 4, 257-70 Physical map-assisted whole-genome shotgun sequence assemblies. Genome Research, 2006, 16, 768-75-97 Genome sequence of the basal haplorrhine primate Tarsius syrichta reveals unusual insertions. Nature Communications, 2016, 7, 12997 Fosmid-based physical mapping of the Histoplasma capsulatum genome. Genome Research, 2004, 14, 1603-9 The quail genome: insights into social behaviour, seasonal biology and infectious disease response. BMC Biology, 2020, 18, 14 The roles of plasticity and evolutionary change in shaping gene expression variation in natural populations of extremophile fish. Molecular Ecology, 2017, 26, 6384-6399 The Cyprinodon variegatus genome reveals gene expression changes underlying differences in skull morphology among closely related species. BMC Genomics, 2017, 18, 424 Higher-order genome organization in platypus and chicken sperm and repositioning of sex chromosomes during mammalian evolution. Chromosoma, 2009, 118, 53-69 2.8 X. couchianus and X. hellerii genome models provide genomic variation insight among Xiphophorus species. BMC Genomics, 2016, 17, 37 The Genome and Adult Somatic Transcriptome of the Mormyrid Electric Fish Paramormyrops kingsleyae. Genome Biology and Evolution, 2017, 9, 3525-3530 A.3-way hybrid approach to generate a new high-quality chimpanzee reference genome (Pan_tro_3.0). GigaScience, 2017, 6, 1-6 Complexities of gene expression patterns in natural populations of an extremophile fish (Poecilia mexicana, Poeciliidae). Molecular Ecology, 2017, 26, 4211-4225 Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. Genome Research, 2019, 29, 576-589 Mutations in the Kinesin-2 Motor KIF3B Cause an Autosomal-Dominant Ciliopathy. American Journal of Human Genetics, 2020, 106, 893-904 Echidna venom gland transcriptome provides insights into the evolution of monotreme venom. PLos | the Cornish Rex Cat Breed. PLoS ONE, 2013, 8, e67105 A proposal to sequence the genome of a garter snake (Thamnophis sirtalis). Standards in Genomic Sciences, 2011, 4, 257-70 Physical map-assisted whole-genome shotgun sequence assemblies. Genome Research, 2006, 16, 768-75-9,7 Physical map-assisted whole-genome shotgun sequence assemblies. Genome Research, 2006, 16, 768-75-9,7 Genome sequence of the basal haplorrhine primate Tarsius syrichta reveals unusual insertions. Nature Communications, 2016, 7, 12997 Fosmid-based physical mapping of the Histoplasma capsulatum genome. Genome Research, 2004, 14, 1603-9 The quail genome: insights into social behaviour, seasonal biology and infectious disease response. BMC Biology, 2020, 18, 14 The roles of plasticity and evolutionary change in shaping gene expression variation in natural populations of extremophile fish. Molecular Ecology, 2017, 26, 6384-6399 The Cyprinodon variegatus genome reveals gene expression changes underlying differences in skull morphology among closely related species. BMC Genomics, 2017, 18, 424 Higher-order genome organization in platypus and chicken sperm and repositioning of sex chromosomes during mammalian evolution. Chromosoma, 2009, 118, 53-69 X. couchianus and X. hellerii genome models provide genomic variation insight among Xiphophorus species. BMC Genome, 2016, 17, 37 The Genome and Adult Somalic Transcriptome of the Mormyrid Electric Fish Paramormyrops kingsleyae. Genome Biology and Evolution, 2017, 9, 3525-3530 A3-way hybrid approach to generate a new high-quality chimpanzee reference genome (Pana, 10, 3, 3). GigaScience, 2017, 6, 1-6 Complexities of gene expression patterns in natural populations of an extremophile fish (Poecilia mexicana, Poecilidae). Molecular Ecology, 2017, 26, 4211-4225 Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. Genome Research, 2019, 29, 576-589 Mutations in the Kinesin-2 Motor KIF3B Cause an Autosomal-Dominant Ciliopathy. |

| 48 | Whole Body Melanoma Transcriptome Response in Medaka. <i>PLoS ONE</i> , 2015 , 10, e0143057 | 3.7 | 13 |
|----|---|------|----|
| 47 | Characterizing the chromosomes of the platypus (Ornithorhynchus anatinus). <i>Chromosome Research</i> , 2007 , 15, 961-74 | 4.4 | 13 |
| 46 | Increased production of peptide deformylase eliminates retention of formylmethionine in bovine somatotropin overproduced in Escherichia coli. <i>Gene</i> , 1996 , 174, 235-8 | 3.8 | 13 |
| 45 | A chromosome-level genome of Astyanax mexicanus surface fish for comparing population-specific genetic differences contributing to trait evolution. <i>Nature Communications</i> , 2021 , 12, 1447 | 17.4 | 13 |
| 44 | A guinea fowl genome assembly provides new evidence on evolution following domestication and selection in galliformes. <i>Molecular Ecology Resources</i> , 2019 , 19, 997-1014 | 8.4 | 11 |
| 43 | Identification and analysis of divergent immune gene families within the Tasmanian devil genome. <i>BMC Genomics</i> , 2015 , 16, 1017 | 4.5 | 10 |
| 42 | Response to Hron et al. <i>Genome Biology</i> , 2015 , 16, 165 | 18.3 | 10 |
| 41 | The Developmental and Genetic Architecture of the Sexually Selected Male Ornament of Swordtails. <i>Current Biology</i> , 2021 , 31, 911-922.e4 | 6.3 | 10 |
| 40 | Molecular genetic analysis of the melanoma regulatory locus in Xiphophorus interspecies hybrids. <i>Molecular Carcinogenesis</i> , 2017 , 56, 1935-1944 | 5 | 9 |
| 39 | The genome of the stable fly, Stomoxys calcitrans, reveals potential mechanisms underlying reproduction, host interactions, and novel targets for pest control. <i>BMC Biology</i> , 2021 , 19, 41 | 7.3 | 9 |
| 38 | Patterns of Genome-Wide Variation in Glossina fuscipes fuscipes Tsetse Flies from Uganda. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 1573-84 | 3.2 | 9 |
| 37 | Germ cell and tumor associated piRNAs in the medaka and Xiphophorus melanoma models. <i>BMC Genomics</i> , 2016 , 17, 357 | 4.5 | 9 |
| 36 | A proteinaceous organic matrix regulates carbonate mineral production in the marine teleost intestine. <i>Scientific Reports</i> , 2016 , 6, 34494 | 4.9 | 8 |
| 35 | Venkatesh et al. reply. <i>Nature</i> , 2014 , 511, E9-10 | 50.4 | 8 |
| 34 | Expression signatures of early-stage and advanced medaka melanomas. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2018 , 208, 20-28 | 3.2 | 8 |
| 33 | Tsetse fly (Glossina pallidipes) midgut responses to Trypanosoma brucei challenge. <i>Parasites and Vectors</i> , 2017 , 10, 614 | 4 | 7 |
| 32 | Comparison of Xiphophorus and human melanoma transcriptomes reveals conserved pathway interactions. <i>Pigment Cell and Melanoma Research</i> , 2018 , 31, 496-508 | 4.5 | 7 |
| 31 | The Piranha Genome Provides Molecular Insight Associated to Its Unique Feeding Behavior. <i>Genome Biology and Evolution</i> , 2019 , 11, 2099-2106 | 3.9 | 7 |

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| 30 | Dramatic changes in gene expression in different forms of Crithidia fasciculata reveal potential mechanisms for insect-specific adhesion in kinetoplastid parasites. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007570 | 4.8 | 7 |
|----|---|------|---|
| 29 | A Resource of Genome-Wide Single Nucleotide Polymorphisms (Snps) for the Conservation and Management of Golden Eagles. <i>Journal of Raptor Research</i> , 2017 , 51, 368-377 | 0.9 | 6 |
| 28 | Sequence analysis in reveals pervasiveness of X-Y arms races in mammalian lineages. <i>Genome Research</i> , 2020 , 30, 1716-1726 | 9.7 | 6 |
| 27 | Expression Signatures of Cisplatin- and Trametinib-Treated Early-Stage Medaka Melanomas. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 2267-2276 | 3.2 | 5 |
| 26 | Diversity of Immunoglobulin Light Chain Genes in Non-Teleost Ray-Finned Fish Uncovers IgL Subdivision into Five Ancient Isotypes. <i>Frontiers in Immunology</i> , 2018 , 9, 1079 | 8.4 | 5 |
| 25 | Cloning of the cDNAs coding for cat growth hormone and prolactin. <i>Gene</i> , 1996 , 168, 247-9 | 3.8 | 5 |
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