

Wesley C Warren

List of Publications by Year in descending order

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Version: 2024-02-01

155
papers

24,409
citations

16450

64
h-index

9102

144
g-index

164
all docs

164
docs citations

164
times ranked

29838
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	12.6	1,583
2	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	12.6	1,283
3	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	27.8	1,139
4	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011, 478, 476-482.	27.8	1,016
5	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	12.6	895
6	The genome of a songbird. <i>Nature</i> , 2010, 464, 757-762.	27.8	770
7	The Genome of the Western Clawed Frog <i>Xenopus tropicalis</i> . <i>Science</i> , 2010, 328, 633-636.	12.6	708
8	Elephant shark genome provides unique insights into gnathostome evolution. <i>Nature</i> , 2014, 505, 174-179.	27.8	689
9	Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , 2012, 483, 169-175.	27.8	663
10	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008, 453, 175-183.	27.8	657
11	A Catalog of Reference Genomes from the Human Microbiome. <i>Science</i> , 2010, 328, 994-999.	12.6	621
12	Sequencing of the sea lamprey (<i>Petromyzon marinus</i>) genome provides insights into vertebrate evolution. <i>Nature Genetics</i> , 2013, 45, 415-421.	21.4	588
13	Mammalian Y chromosomes retain widely expressed dosage-sensitive regulators. <i>Nature</i> , 2014, 508, 494-499.	27.8	546
14	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	27.8	541
15	SNP discovery and allele frequency estimation by deep sequencing of reduced representation libraries. <i>Nature Methods</i> , 2008, 5, 247-252.	19.0	534
16	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. <i>Nature</i> , 2004, 432, 717-722.	27.8	391
17	Chimpanzee and human Y chromosomes are remarkably divergent in structure and gene content. <i>Nature</i> , 2010, 463, 536-539.	27.8	381
18	Comparison of genome degradation in Paratyphi A and Typhi, human-restricted serovars of <i>Salmonella enterica</i> that cause typhoid. <i>Nature Genetics</i> , 2004, 36, 1268-1274.	21.4	367

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19	Characterizing the Major Structural Variant Alleles of the Human Genome. <i>Cell</i> , 2019, 176, 663-675.e19.	28.9	364
20	The genomic landscape of rapid repeated evolutionary adaptation to toxic pollution in wild fish. <i>Science</i> , 2016, 354, 1305-1308.	12.6	348
21	Genome of <i>Rhodnius prolixus</i> , 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, 14936-14941.	7.1	329
22	The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. <i>Nature Genetics</i> , 2013, 45, 776-783.	21.4	327
23	Gibbon genome and the fast karyotype evolution of small apes. <i>Nature</i> , 2014, 513, 195-201.	27.8	320
24	High-resolution comparative analysis of great ape genomes. <i>Science</i> , 2018, 360, .	12.6	304
25	Sequencing the Mouse Y Chromosome Reveals Convergent Gene Acquisition and Amplification on Both Sex Chromosomes. <i>Cell</i> , 2014, 159, 800-813.	28.9	291
26	The draft genome of the parasitic nematode <i>Trichinella spiralis</i> . <i>Nature Genetics</i> , 2011, 43, 228-235.	21.4	285
27	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, 17230-17235.	7.1	281
28	Divergence and Functional Degradation of a Sex Chromosome-like Supergene. <i>Current Biology</i> , 2016, 26, 344-350.	3.9	266
29	Extensive Error in the Number of Genes Inferred from Draft Genome Assemblies. <i>PLoS Computational Biology</i> , 2014, 10, e1003998.	3.2	262
30	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
31	Genome Sequence of the Tsetse Fly (<i>Glossina morsitans</i>): Vector of African Trypanosomiasis. <i>Science</i> , 2014, 344, 380-386.	12.6	254
32	The genome of the platyfish, <i>Xiphophorus maculatus</i> , provides insights into evolutionary adaptation and several complex traits. <i>Nature Genetics</i> , 2013, 45, 567-572.	21.4	251
33	Strict evolutionary conservation followed rapid gene loss on human and rhesus Y chromosomes. <i>Nature</i> , 2012, 483, 82-86.	27.8	245
34	The Genome Sequence of the Leaf-Cutter Ant <i>Atta cephalotes</i> Reveals Insights into Its Obligate Symbiotic Lifestyle. <i>PLoS Genetics</i> , 2011, 7, e1002007.	3.5	231
35	A New Chicken Genome Assembly Provides Insight into Avian Genome Structure. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 109-117.	1.8	228
36	Convergent evolution of chicken Z and human X chromosomes by expansion and gene acquisition. <i>Nature</i> , 2010, 466, 612-616.	27.8	210

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37	A physical map of the chicken genome. <i>Nature</i> , 2004, 432, 761-764.	27.8	200
38	Genome Sequence of <i>Cronobacter sakazakii</i> BAA-894 and Comparative Genomic Hybridization Analysis with Other <i>Cronobacter</i> Species. <i>PLoS ONE</i> , 2010, 5, e9556.	2.5	198
39	Evolutionary toggling of the MAPT 17q21.31 inversion region. <i>Nature Genetics</i> , 2008, 40, 1076-1083.	21.4	176
40	Evolutionary signals of selection on cognition from the great tit genome and methylome. <i>Nature Communications</i> , 2016, 7, 10474.	12.8	172
41	Genome of the human hookworm <i>Necator americanus</i> . <i>Nature Genetics</i> , 2014, 46, 261-269.	21.4	166
42	Independent specialization of the human and mouse X chromosomes for the male germ line. <i>Nature Genetics</i> , 2013, 45, 1083-1087.	21.4	164
43	The role of gene flow in rapid and repeated evolution of cave-related traits in Mexican tetra, <i>Astyanax mexicanus</i> . <i>Molecular Ecology</i> , 2018, 27, 4397-4416.	3.9	160
44	The sterlet sturgeon genome sequence and the mechanisms of segmental rediploidization. <i>Nature Ecology and Evolution</i> , 2020, 4, 841-852.	7.8	159
45	Avian W and mammalian Y chromosomes convergently retained dosage-sensitive regulators. <i>Nature Genetics</i> , 2017, 49, 387-394.	21.4	147
46	Defensins and the convergent evolution of platypus and reptile venom genes. <i>Genome Research</i> , 2008, 18, 986-994.	5.5	137
47	Single haplotype assembly of the human genome from a hydatidiform mole. <i>Genome Research</i> , 2014, 24, 2066-2076.	5.5	133
48	3D genomics across the tree of life reveals condensin II as a determinant of architecture type. <i>Science</i> , 2021, 372, 984-989.	12.6	132
49	Convergence in feeding posture occurs through different genetic loci in independently evolved cave populations of <i>Astyanax mexicanus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16933-16938.	7.1	126
50	Systems Biology of the Vervet Monkey. <i>ILAR Journal</i> , 2013, 54, 122-143.	1.8	120
51	INTEGRATE: gene fusion discovery using whole genome and transcriptome data. <i>Genome Research</i> , 2016, 26, 108-118.	5.5	120
52	Clonal polymorphism and high heterozygosity in the celibate genome of the Amazon molly. <i>Nature Ecology and Evolution</i> , 2018, 2, 669-679.	7.8	117
53	Antarctic blackfin icefish genome reveals adaptations to extreme environments. <i>Nature Ecology and Evolution</i> , 2019, 3, 469-478.	7.8	115
54	The genome of the vervet (<i>Chlorocebus aethiops sabaeus</i>). <i>Genome Research</i> , 2015, 25, 1921-1933.	5.5	114

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55	Specifying and Sustaining Pigmentation Patterns in Domestic and Wild Cats. <i>Science</i> , 2012, 337, 1536-1541.	12.6	110
56	Ancient hybridization and strong adaptation to viruses across African vervet monkey populations. <i>Nature Genetics</i> , 2017, 49, 1705-1713.	21.4	107
57	Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. <i>Science</i> , 2020, 370, .	12.6	105
58	Developing tools for the study of molluscan immunity: The sequencing of the genome of the eastern oyster, <i>Crassostrea virginica</i> . <i>Fish and Shellfish Immunology</i> , 2015, 46, 2-4.	3.6	100
59	Third Report on Chicken Genes and Chromosomes 2015. <i>Cytogenetic and Genome Research</i> , 2015, 145, 78-179.	1.1	97
60	Pangolin genomes and the evolution of mammalian scales and immunity. <i>Genome Research</i> , 2016, 26, 1312-1322.	5.5	95
61	The <i>Physarum polycephalum</i> Genome Reveals Extensive Use of Prokaryotic Two-Component and Metazoan-Type Tyrosine Kinase Signaling. <i>Genome Biology and Evolution</i> , 2016, 8, 109-125.	2.5	87
62	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. <i>Nature</i> , 2005, 434, 724-731.	27.8	85
63	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.	7.1	82
64	A RAD-Tag Genetic Map for the Platyfish (<i>Xiphophorus maculatus</i>) Reveals Mechanisms of Karyotype Evolution Among Teleost Fish. <i>Genetics</i> , 2014, 197, 625-641.	2.9	80
65	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.	3.5	79
66	High-coverage sequencing and annotated assemblies of the budgerigar genome. <i>GigaScience</i> , 2014, 3, 11.	6.4	75
67	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.	2.5	72
68	Comparative genomic analysis of six <i>Glossina</i> genomes, vectors of African trypanosomes. <i>Genome Biology</i> , 2019, 20, 187.	8.8	71
69	Genomic analysis reveals hidden biodiversity within colugos, the sister group to primates. <i>Science Advances</i> , 2016, 2, e1600633.	10.3	64
70	A chromosome-level genome of <i>Astyanax mexicanus</i> surface fish for comparing population-specific genetic differences contributing to trait evolution. <i>Nature Communications</i> , 2021, 12, 1447.	12.8	60
71	Construction and characterization of a new bovine bacterial artificial chromosome library with 10 genome-equivalent coverage. <i>Mammalian Genome</i> , 2000, 11, 662-663.	2.2	57
72	Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. <i>Nature Genetics</i> , 2017, 49, 1714-1721.	21.4	57

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73	Origin of INSL3-mediated testicular descent in therian mammals. <i>Genome Research</i> , 2008, 18, 974-985.	5.5	55
74	A non-human primate system for large-scale genetic studies of complex traits. <i>Human Molecular Genetics</i> , 2012, 21, 3307-3316.	2.9	51
75	Digital gene expression for non-model organisms. <i>Genome Research</i> , 2011, 21, 1905-1915.	5.5	50
76	Opsin Repertoire and Expression Patterns in Horseshoe Crabs: Evidence from the Genome of <i>Limulus polyphemus</i> (Arthropoda: Chelicerata). <i>Genome Biology and Evolution</i> , 2016, 8, 1571-1589.	2.5	50
77	Glucose and Insulin Treatment of Insulinoma Cells Results in Transcriptional Regulation of a Common Set of Genes. <i>Diabetes</i> , 2004, 53, 1496-1508.	0.6	48
78	Gene discovery and comparative analysis of X-degenerate genes from the domestic cat Y chromosome. Sequence data from this article have been deposited with the EMBL/GenBank Data Libraries under Accession No. EU879967-EU879988. <i>Genomics</i> , 2008, 92, 329-338.	2.9	47
79	Physical Mapping and Refinement of the Painted Turtle Genome (<i>Chrysemys picta</i>) Inform Amniote Genome Evolution and Challenge Turtle-Bird Chromosomal Conservation. <i>Genome Biology and Evolution</i> , 2015, 7, 2038-2050.	2.5	46
80	Transcriptome Analysis of Female and Male <i>Xiphophorus maculatus</i> Jp 163 A. <i>PLoS ONE</i> , 2011, 6, e18379.	2.5	45
81	Sequencing strategies and characterization of 721 vervet monkey genomes for future genetic analyses of medically relevant traits. <i>BMC Biology</i> , 2015, 13, 41.	3.8	45
82	The Landscape of Extreme Genomic Variation in the Highly Adaptable Atlantic Killifish. <i>Genome Biology and Evolution</i> , 2017, 9, 659-676.	2.5	43
83	Joint MiRNA/mRNA Expression Profiling Reveals Changes Consistent with Development of Dysfunctional Corpus Luteum after Weight Gain. <i>PLoS ONE</i> , 2015, 10, e0135163.	2.5	42
84	Profiling of gender-regulated gene transcripts in the filarial nematode <i>Brugia malayi</i> by cDNA oligonucleotide array analysis. <i>Molecular and Biochemical Parasitology</i> , 2005, 143, 49-57.	1.1	41
85	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, 1607-1616.	1.8	41
86	The quail genome: insights into social behaviour, seasonal biology and infectious disease response. <i>BMC Biology</i> , 2020, 18, 14.	3.8	40
87	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, 1354-1364.	3.8	39
88	Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. <i>Genome Research</i> , 2019, 29, 576-589.	5.5	39
89	Applications and efficiencies of the first cat 63K DNA array. <i>Scientific Reports</i> , 2018, 8, 7024.	3.3	38
90	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, .	7.1	34

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91	A Limited Role for Gene Duplications in the Evolution of Platypus Venom. <i>Molecular Biology and Evolution</i> , 2012, 29, 167-177.	8.9	33
92	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.	3.9	33
93	The Novel Evolution of the Sperm Whale Genome. <i>Genome Biology and Evolution</i> , 2017, 9, 3260-3264.	2.5	33
94	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.	2.5	32
95	<i>X. couchianus</i> and <i>X. hellerii</i> genome models provide genomic variation insight among <i>Xiphophorus</i> species. <i>BMC Genomics</i> , 2016, 17, 37.	2.8	32
96	Genome sequence of the basal haplorrhine primate <i>Tarsius syrichta</i> reveals unusual insertions. <i>Nature Communications</i> , 2016, 7, 12997.	12.8	32
97	A proposal to sequence the genome of a garter snake (<i>Thamnophis sirtalis</i>). <i>Standards in Genomic Sciences</i> , 2011, 4, 257-270.	1.5	31
98	The <i>Cyprinodon variegatus</i> genome reveals gene expression changes underlying differences in skull morphology among closely related species. <i>BMC Genomics</i> , 2017, 18, 424.	2.8	29
99	Sequence analysis in <i>Bos taurus</i> reveals pervasiveness of Xâ€“Y arms races in mammalian lineages. <i>Genome Research</i> , 2020, 30, 1716-1726.	5.5	29
100	Mutations in the Kinesin-2 Motor KIF3B Cause an Autosomal-Dominant Ciliopathy. <i>American Journal of Human Genetics</i> , 2020, 106, 893-904.	6.2	29
101	The Genome and Adult Somatic Transcriptome of the Mormyrid Electric Fish <i>Paramormyrops kingsleyae</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 3525-3530.	2.5	28
102	Ultracontinuous Single Haplotype Genome Assemblies for the Domestic Cat (<i>Felis catus</i>) and Asian Leopard Cat (<i>Prionailurus bengalensis</i>). <i>Journal of Heredity</i> , 2021, 112, 165-173.	2.4	28
103	Physical map-assisted whole-genome shotgun sequence assemblies. <i>Genome Research</i> , 2006, 16, 768-775.	5.5	27
104	Long-term experimental hybridisation results in the evolution of a new sex chromosome in swordtail fish. <i>Nature Communications</i> , 2018, 9, 5136.	12.8	27
105	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.	4.8	24
106	The Developmental and Genetic Architecture of the Sexually Selected Male Ornament of Swordtails. <i>Current Biology</i> , 2021, 31, 911-922.e4.	3.9	24
107	Fosmid-Based Physical Mapping of the <i>Histoplasma capsulatum</i> Genome. <i>Genome Research</i> , 2004, 14, 1603-1609.	5.5	23
108	Higher-order genome organization in platypus and chicken sperm and repositioning of sex chromosomes during mammalian evolution. <i>Chromosoma</i> , 2009, 118, 53-69.	2.2	22

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109	Complexities of gene expression patterns in natural populations of an extremophile fish (<i>Poecilia</i>). <i>Journal of Herpetology</i> , 2017, 51, 1-10.	3.9	21
110	Molecular genetic analysis of the melanoma regulatory locus in <i>Xiphophorus</i> interspecies hybrids. <i>Molecular Carcinogenesis</i> , 2017, 56, 1935-1944.	2.7	21
111	Comparison of <i>Xiphophorus</i> and human melanoma transcriptomes reveals conserved pathway interactions. <i>Pigment Cell and Melanoma Research</i> , 2018, 31, 496-508.	3.3	21
112	The genome of the stable fly, <i>Stomoxys calcitrans</i> , reveals potential mechanisms underlying reproduction, host interactions, and novel targets for pest control. <i>BMC Biology</i> , 2021, 19, 41.	3.8	19
113	Characterizing the chromosomes of the platypus (<i>Ornithorhynchus anatinus</i>). <i>Chromosome Research</i> , 2007, 15, 961-974.	2.2	18
114	Echidna Venom Gland Transcriptome Provides Insights into the Evolution of Monotreme Venom. <i>PLoS ONE</i> , 2013, 8, e79092.	2.5	18
115	Dramatic changes in gene expression in different forms of <i>Crithidia fasciculata</i> reveal potential mechanisms for insect-specific adhesion in kinetoplastid parasites. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007570.	3.0	18
116	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.	6.4	17
117	The Piranha Genome Provides Molecular Insight Associated to Its Unique Feeding Behavior. <i>Genome Biology and Evolution</i> , 2019, 11, 2099-2106.	2.5	17
118	Chromosome-scale genome assembly of the sea louse <i>Caligus rogercresseyi</i> by SMRT sequencing and Hi-C analysis. <i>Scientific Data</i> , 2021, 8, 60.	5.3	17
119	Tumorigenic circulating tumor cells from xenograft mouse models of non-metastatic NSCLC patients reveal distinct single cell heterogeneity and drug responses. <i>Molecular Cancer</i> , 2022, 21, 73.	19.2	16
120	Increased production of peptide deformylase eliminates retention of formylmethionine in bovine somatotropin overproduced in <i>Escherichia coli</i> . <i>Gene</i> , 1996, 174, 235-238.	2.2	15
121	Identification and analysis of divergent immune gene families within the Tasmanian devil genome. <i>BMC Genomics</i> , 2015, 16, 1017.	2.8	14
122	Whole Body Melanoma Transcriptome Response in Medaka. <i>PLoS ONE</i> , 2015, 10, e0143057.	2.5	14
123	Germ cell and tumor associated piRNAs in the medaka and <i>Xiphophorus</i> melanoma models. <i>BMC Genomics</i> , 2016, 17, 357.	2.8	13
124	A domestic cat whole exome sequencing resource for trait discovery. <i>Scientific Reports</i> , 2021, 11, 7159.	3.3	13
125	Patterns of Genome-Wide Variation in <i>Glossina fuscipes fuscipes</i> Tsetse Flies from Uganda. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1573-1584.	1.8	12
126	A proteinaceous organic matrix regulates carbonate mineral production in the marine teleost intestine. <i>Scientific Reports</i> , 2016, 6, 34494.	3.3	11

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127	Expression signatures of early-stage and advanced medaka melanomas. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2018, 208, 20-28.	2.6	11
128	Fixation of allelic gene expression landscapes and expression bias pattern shape the transcriptome of the clonal Amazon molly. <i>Genome Research</i> , 2021, 31, 372-379.	5.5	11
129	Venkatesh et al. reply. <i>Nature</i> , 2014, 511, E9-E10.	27.8	10
130	Response to Hron et al.. <i>Genome Biology</i> , 2015, 16, 165.	8.8	10
131	Explainable artificial intelligence in high-throughput drug repositioning for subgroup stratifications with interventionable potential. <i>Journal of Biomedical Informatics</i> , 2021, 118, 103792.	4.3	10
132	Neuronal Ceroid Lipofuscinosis in a Domestic Cat Associated with a DNA Sequence Variant That Creates a Premature Stop Codon in <i>CLN6</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2741-2751.	1.8	9
133	Mining the 99 Lives Cat Genome Sequencing Consortium database implicates genes and variants for the <i>Ticked</i> locus in domestic cats (<i>Felis catus</i>). <i>Animal Genetics</i> , 2021, 52, 321-332.	1.7	9
134	Epigenetic Regulation of Cancer Immune Cells. <i>Seminars in Cancer Biology</i> , 2021, , .	9.6	9
135	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.	0.6	8
136	Tsetse fly (<i>Glossina pallidipes</i>) midgut responses to <i>Trypanosoma brucei</i> challenge. <i>Parasites and Vectors</i> , 2017, 10, 614.	2.5	8
137	Gene expression variation and parental allele inheritance in a <i>Xiphophorus</i> interspecies hybridization model. <i>PLoS Genetics</i> , 2018, 14, e1007875.	3.5	8
138	A 50K SNP array reveals genetic structure for bald eagles (<i>Haliaeetus leucocephalus</i>). <i>Conservation Genetics</i> , 2020, 21, 65-76.	1.5	8
139	Genome Assemblies across the Diverse Evolutionary Spectrum of <i>Leishmania</i> Protozoan Parasites. <i>Microbiology Resource Announcements</i> , 2021, 10, e0054521.	0.6	8
140	Single Circulating-Tumor-Cell-Targeted Sequencing to Identify Somatic Variants in Liquid Biopsies in Non-Small-Cell Lung Cancer Patients. <i>Current Issues in Molecular Biology</i> , 2022, 44, 750-763.	2.4	7
141	Building and Improving Reference Genome Assemblies. <i>Proceedings of the IEEE</i> , 2017, , 1-14.	21.3	6
142	Expression Signatures of Cisplatin- and Trametinib-Treated Early-Stage Medaka Melanomas. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2267-2276.	1.8	6
143	Cloning of the cDNAs coding for cat growth hormone and prolactin. <i>Gene</i> , 1996, 168, 247-249.	2.2	5
144	Basal Vertebrates Clarify the Evolutionary History of Ciliopathy-Associated Genes <i>Tmem138</i> and <i>Tmem216</i> . <i>Molecular Biology and Evolution</i> , 2013, 30, 62-65.	8.9	5

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145	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.	4.8	5
146	On the origin of SCPP genes. <i>Evolution & Development</i> , 2014, 16, 125-126.	2.0	4
147	The enigma of the platypus genome. <i>Australian Journal of Zoology</i> , 2009, 57, 157.	1.0	2
148	Discordant Genome Assemblies Drastically Alter the Interpretation of Single-Cell RNA Sequencing Data Which Can Be Mitigated by a Novel Integration Method. <i>Cells</i> , 2022, 11, 608.	4.1	2
149	No bull: Upholding community standards in public sharing of biological datasets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4277-E4277.	7.1	1
150	The practical use of genome sequencing data in the management of a feline colony pedigree. <i>BMC Veterinary Research</i> , 2017, 13, 225.	1.9	1
151	The Evolution of Viviparity in Vertebrates. <i>Advances in Anatomy, Embryology and Cell Biology</i> , 2021, 234, 7-19.	1.6	1
152	Genome mapping overview. , 2005, , .		0
153	Global assessment of organ specific basal gene expression over a diurnal cycle with analyses of gene copies exhibiting cyclic expression patterns. <i>BMC Genomics</i> , 2020, 21, 787.	2.8	0
154	Comparative analysis of cancer driver genes between human and six non-human primates (LB182). <i>FASEB Journal</i> , 2014, 28, LB182.	0.5	0
155	Avian genomics. , 2022, , 7-16.		0