

Andrey A Yurchenko

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

1,432
citations

471061

17
h-index

377514

34
g-index

54
all docs

54
docs citations

54
times ranked

2703
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic legacy of the African cheetah, <i>Acinonyx jubatus</i> . <i>Genome Biology</i> , 2015, 16, 277.	3.8	167
2	Genome-wide Evidence Reveals that African and Eurasian Golden Jackals Are Distinct Species. <i>Current Biology</i> , 2015, 25, 2158-2165.	1.8	156
3	Chromosomal-Level Assembly of the Asian Seabass Genome Using Long Sequence Reads and Multi-layered Scaffolding. <i>PLoS Genetics</i> , 2016, 12, e1005954.	1.5	105
4	Comparison of carnivore, omnivore, and herbivore mammalian genomes with a new leopard assembly. <i>Genome Biology</i> , 2016, 17, 211.	3.8	101
5	Pangolin genomes and the evolution of mammalian scales and immunity. <i>Genome Research</i> , 2016, 26, 1312-1322.	2.4	95
6	Scans for signatures of selection in Russian cattle breed genomes reveal new candidate genes for environmental adaptation and acclimation. <i>Scientific Reports</i> , 2018, 8, 12984.	1.6	85
7	Parallelism in eco-morphology and gene expression despite variable evolutionary and genomic backgrounds in a Holarctic fish. <i>PLoS Genetics</i> , 2020, 16, e1008658.	1.5	73
8	De novo transcriptome assembly, annotation and comparison of four ecological and evolutionary model salmonid fish species. <i>BMC Genomics</i> , 2018, 19, 32.	1.2	63
9	Genome-wide genotyping uncovers genetic profiles and history of the Russian cattle breeds. <i>Heredity</i> , 2018, 120, 125-137.	1.2	61
10	High-density genotyping reveals signatures of selection related to acclimation and economically important traits in 15 local sheep breeds from Russia. <i>BMC Genomics</i> , 2019, 20, 294.	1.2	57
11	RAS mutations drive proliferative chronic myelomonocytic leukemia via a KMT2A-PLK1 axis. <i>Nature Communications</i> , 2021, 12, 2901.	5.8	44
12	Robust forensic matching of confiscated horns to individual poached African rhinoceros. <i>Current Biology</i> , 2018, 28, R13-R14.	1.8	27
13	Demographic History, Adaptation, and NRAP Convergent Evolution at Amino Acid Residue 100 in the World Northernmost Cattle from Siberia. <i>Molecular Biology and Evolution</i> , 2021, 38, 3093-3110.	3.5	27
14	Genome-wide association study and scan for signatures of selection point to candidate genes for body temperature maintenance under the cold stress in Siberian cattle populations. <i>BMC Genetics</i> , 2019, 20, 26.	2.7	25
15	A matrix metalloproteinase 9 (MMP9) gene single nucleotide polymorphism is associated with predisposition to tick-borne encephalitis virus-induced severe central nervous system disease. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 763-767.	1.1	24
16	Genomic differentiation and intercontinental population structure of mosquito vectors <i>Culex pipiens pipiens</i> and <i>Culex pipiens molestus</i> . <i>Scientific Reports</i> , 2020, 10, 7504.	1.6	24
17	The Population Origins and Expansion of Feral Cats in Australia. <i>Journal of Heredity</i> , 2016, 107, 104-114.	1.0	21
18	The functional genetic architecture of egg-laying and live-bearing reproduction in common lizards. <i>Nature Ecology and Evolution</i> , 2021, 5, 1546-1556.	3.4	19

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19	Whole Genome Sequencing and Re-sequencing of the Sable Antelope (<i>Hippotragus niger</i>): A Resource for Monitoring Diversity in <i>ex Situ</i> and <i>in Situ</i> Populations. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1785-1793.	0.8	18
20	XPC deficiency increases risk of hematologic malignancies through mutator phenotype and characteristic mutational signature. <i>Nature Communications</i> , 2020, 11, 5834.	5.8	17
21	Chromosome and Genome Divergence between the Cryptic Eurasian Malaria Vector-Species <i>Anopheles messeae</i> and <i>Anopheles daciae</i> . <i>Genes</i> , 2020, 11, 165.	1.0	17
22	Increased risk of internal tumors in DNA repair-deficient xeroderma pigmentosum patients: analysis of four international cohorts. <i>Orphanet Journal of Rare Diseases</i> , 2022, 17, 104.	1.2	17
23	Eco-geographic units, population hierarchy, and a two-level conservation strategy with reference to a critically endangered salmonid, Sakhalin taimen <i>Parahucho perryi</i> . <i>Conservation Genetics</i> , 2015, 16, 431-441.	0.8	14
24	Chromosome-Level Assembly of the Common Lizard (<i>Zootoca vivipara</i>) Genome. <i>Genome Biology and Evolution</i> , 2020, 12, 1953-1960.	1.1	13
25	DNA polymerase zeta contributes to heterochromatin replication to prevent genome instability. <i>EMBO Journal</i> , 2021, 40, e104543.	3.5	12
26	B Chromosomes of the Asian Seabass (<i>Lates calcarifer</i>) Contribute to Genome Variations at the Level of Individuals and Populations. <i>Genes</i> , 2018, 9, 464.	1.0	11
27	Whole-Genome Analysis of <i>Mycobacterium tuberculosis</i> from Patients with Tuberculous Spondylitis, Russia. <i>Emerging Infectious Diseases</i> , 2018, 24, 579-583.	2.0	9
28	Exome-wide search and functional annotation of genes associated in patients with severe tick-borne encephalitis in a Russian population. <i>BMC Medical Genomics</i> , 2019, 12, 61.	0.7	9
29	Cloning and Functional Analysis of SaCLC1, a Gene Belonging to the Chloride Channel Family (CLC), from the Halophyte <i>Suaeda altissima</i> (L.) Pall.. <i>Doklady Biochemistry and Biophysics</i> , 2018, 481, 186-189.	0.3	8
30	In silico Analyses of Transcriptomes of the Marine Green Microalga <i>Dunaliella tertiolecta</i> : Identification of Sequences Encoding P-type ATPases. <i>Molecular Biology</i> , 2018, 52, 520-531.	0.4	8
31	Genotyping and Whole-Genome Resequencing of Welsh Sheep Breeds Reveal Candidate Genes and Variants for Adaptation to Local Environment and Socioeconomic Traits. <i>Frontiers in Genetics</i> , 2021, 12, 612492.	1.1	8
32	Whole-Genome Resequencing Points to Candidate DNA Loci Affecting Body Temperature under Cold Stress in Siberian Cattle Populations. <i>Life</i> , 2021, 11, 959.	1.1	8
33	Analytical ϵ -back-off of whole genome sequencing quality for the Genome Russia project using a small cohort for autoimmune hepatitis. <i>PLoS ONE</i> , 2018, 13, e0200423.	1.1	7
34	Resequencing and signatures of selection scan in two Siberian native sheep breeds point to candidate genetic variants for adaptation and economically important traits. <i>Animal Genetics</i> , 2021, 52, 126-131.	0.6	6
35	Frequency and Genomic Aspects of Intrinsic Resistance to Vismodegib in Locally Advanced Basal Cell Carcinoma. <i>Clinical Cancer Research</i> , 2022, 28, 1422-1432.	3.2	6
36	Population genetic structure and phylogeography of sterlet (<i>Acipenser ruthenus</i>), Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 67 Td (A and Analysis, 2019, 30, 156-164.	0.7	5

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37	Transcriptome of the bivalve <i>Limecola balthica</i> L. from Western Pacific: A new resource for studies of European populations. <i>Marine Genomics</i> , 2018, 40, 58-63.	0.4	4
38	Association of ABCB9 and COL22A1 Gene Polymorphism with Human Predisposition to Severe Forms of Tick-Borne Encephalitis. <i>Russian Journal of Genetics</i> , 2019, 55, 368-377.	0.2	4
39	Resequencing the Yaroslavl cattle genomes reveals signatures of selection and a rare haplotype on <sc>BTA28</sc> likely to be related to breed phenotypes. <i>Animal Genetics</i> , 2022, 53, 680-684.	0.6	4
40	A panel of microsatellite loci for population studies of Sakhalin taimen <i>Parahucho perryi</i> (Brevoort). <i>Russian Journal of Genetics</i> , 2012, 48, 831-837.	0.2	2
41	Exome-wide survey of the Siberian Caucasian population. <i>BMC Medical Genetics</i> , 2019, 20, 51.	2.1	2
42	The Iberian legacy into a young genetic xeroderma pigmentosum cluster in central Brazil. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2020, 852, 503164.	0.9	2
43	Genomic profiling of late-onset basal cell carcinomas from two brothers with nevoid basal cell carcinoma syndrome. <i>Journal of the European Academy of Dermatology and Venereology</i> , 2021, 35, 396-402.	1.3	2
44	A Novel Case of Gorlin Syndrome Mosaicism Involving an SMO Gene Mutation: Clinical, Histological and Molecular Analysis of Basaloid Tumours. <i>Acta Dermato-Venereologica</i> , 2021, 101, adv00434.	0.6	2
45	The new Internal Transcribed Spacer 2 diagnostic tool clarifies the taxonomic position and geographic distribution of the North American malaria vector <i>Anopheles punctipennis</i> . <i>Malaria Journal</i> , 2021, 20, 141.	0.8	2
46	First description of ultramutated endometrial cancer caused by germline loss-of-function and somatic exonuclease domain mutations in POLE gene. <i>Genetics and Molecular Biology</i> , 2020, 43, e20200100.	0.6	2
47	A rare splice site mutation in the gene encoding glucokinase/hexokinase 4 in a patient with MODY type 2. <i>Vavilovskii Zhurnal Genetiki i Seleksii</i> , 2020, 24, 299-305.	0.4	1