

Taras K Oleksyk

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

25,319
citations

331259

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264894

42
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all docs

45
docs citations

45
times ranked

49274
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic diversity and selection in Puerto Rican horses. <i>Scientific Reports</i> , 2022, 12, 515.	1.6	4
2	ESTIMATION OF THE FREQUENCY OF GENETIC VARIANTS ASSOCIATED WITH VITAMIN D LEVELS AND OSTEOPOROSIS IN THE POPULATION OF UKRAINE. <i>Problemi Endokrinnoi Patologii</i> , 2022, 79, 53-59.	0.0	0
3	Genomics of Adaptation and Speciation. <i>Genes</i> , 2022, 13, 1187.	1.0	2
4	Genome diversity in Ukraine. <i>GigaScience</i> , 2021, 10, .	3.3	9
5	Molecular Phylogeny and Evolution of Amazon Parrots in the Greater Antilles. <i>Genes</i> , 2021, 12, 608.	1.0	2
6	Chromosome-Level Genome Assemblies Expand Capabilities of Genomics for Conservation Biology. <i>Genes</i> , 2021, 12, 1336.	1.0	12
7	Genome-wide sequence analyses of ethnic populations across Russia. <i>Genomics</i> , 2020, 112, 442-458.	1.3	19
8	Genomes of Three Closely Related Caribbean Amazons Provide Insight for Species History and Conservation. <i>Genes</i> , 2019, 10, 54.	1.0	8
9	Innovative assembly strategy contributes to understanding the evolution and conservation genetics of the endangered <i>Solenodon paradoxus</i> from the island of Hispaniola. <i>GigaScience</i> , 2018, 7, .	3.3	12
10	A Recurrent BRCA2 Mutation Explains the Majority of Hereditary Breast and Ovarian Cancer Syndrome Cases in Puerto Rico. <i>Cancers</i> , 2018, 10, 419.	1.7	22
11	Mitogenomic sequences support a north-south subspecies subdivision within <i>Solenodon paradoxus</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 662-670.	0.7	9
12	Genomic legacy of the African cheetah, <i>Acinonyx jubatus</i> . <i>Genome Biology</i> , 2015, 16, 277.	3.8	167
13	Putting Russia on the genome map. <i>Science</i> , 2015, 350, 747-747.	6.0	8
14	SmileFinder: a resampling-based approach to evaluate signatures of selection from genome-wide sets of matching allele frequency data in two or more diploid populations. <i>GigaScience</i> , 2015, 4, 1.	3.3	241
15	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
16	Sequencing rare and common APOL1 coding variants to determine kidney disease risk. <i>Kidney International</i> , 2015, 88, 754-763.	2.6	30
17	The Genome Russia project: closing the largest remaining omission on the world Genome map. <i>GigaScience</i> , 2015, 4, 53.	3.3	16
18	GWATCH: a web platform for automated gene association discovery analysis. <i>GigaScience</i> , 2014, 3, 18.	3.3	5

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19	Isolation and characterization of microsatellite loci in the critically endangered Puerto Rican parrot (<i>Amazona vittata</i>). <i>Conservation Genetics Resources</i> , 2014, 6, 885-889.	0.4	2
20	Colonization of islands in the Mona Passage by endemic dwarf geckoes (genus <i>Tropidura</i>). <i>Systematic Zoology</i> , 2014, 63, 4488-4500.	0.8	10
21	Reconstructing Native American Migrations from Whole-Genome and Whole-Exome Data. <i>PLoS Genetics</i> , 2013, 9, e1004023.	1.5	185
22	The <i>Sp185/333</i> immune response genes and proteins are expressed in cells dispersed within all major organs of the adult purple sea urchin. <i>Innate Immunity</i> , 2013, 19, 569-587.	1.1	33
23	Evidence for selection at HIV host susceptibility genes in a West Central African human population. <i>BMC Evolutionary Biology</i> , 2012, 12, 237.	3.2	20
24	A locally funded Puerto Rican parrot (<i>Amazona vittata</i>) genome sequencing project increases avian data and advances young researcher education. <i>GigaScience</i> , 2012, 1, 14.	3.3	40
25	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012, 491, 56-65.	13.7	7,199
26	Reconciling Apparent Conflicts between Mitochondrial and Nuclear Phylogenies in African Elephants. <i>PLoS ONE</i> , 2011, 6, e20642.	1.1	43
27	History Shaped the Geographic Distribution of Genomic Admixture on the Island of Puerto Rico. <i>PLoS ONE</i> , 2011, 6, e16513.	1.1	87
28	Worldwide Distribution of the MYH9 Kidney Disease Susceptibility Alleles and Haplotypes: Evidence of Historical Selection in Africa. <i>PLoS ONE</i> , 2010, 5, e11474.	1.1	33
29	Genome-wide scans for footprints of natural selection. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 185-205.	1.8	343
30	Genetics of Focal Segmental Glomerulosclerosis and Human Immunodeficiency Virus-Associated Collapsing Glomerulopathy: The Role of MYH9 Genetic Variation. <i>Seminars in Nephrology</i> , 2010, 30, 111-125.	0.6	30
31	Association of Trypanolytic ApoL1 Variants with Kidney Disease in African Americans. <i>Science</i> , 2010, 329, 841-845.	6.0	1,725
32	Genome and gene alterations by insertions and deletions in the evolution of human and chimpanzee chromosome 22. <i>BMC Genomics</i> , 2009, 10, 51.	1.2	17
33	Extended IL10 haplotypes and their association with HIV progression to AIDS. <i>Genes and Immunity</i> , 2009, 10, 309-322.	2.2	37
34	MYH9 is a major-effect risk gene for focal segmental glomerulosclerosis. <i>Nature Genetics</i> , 2008, 40, 1175-1184.	9.4	636
35	Evaluation of <i>IL10</i> , <i>IL19</i> and <i>IL20</i> gene polymorphisms and chronic hepatitis B infection outcome. <i>International Journal of Immunogenetics</i> , 2008, 35, 255-264.	0.8	41
36	Identifying Selected Regions from Heterozygosity and Divergence Using a Light-Coverage Genomic Dataset from Two Human Populations. <i>PLoS ONE</i> , 2008, 3, e1712.	1.1	50

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37	Genetics of cattails in radioactively contaminated areas around Chernobyl. <i>Molecular Ecology</i> , 2006, 15, 2611-2625.	2.0	12
38	Behavioral Risk Exposure and Host Genetics of Susceptibility to HIV-1 Infection. <i>Journal of Infectious Diseases</i> , 2006, 193, 16-26.	1.9	49
39	Independent Occurrences of Multiple Repeats in the Control Region of Mitochondrial DNA of White-Tailed Deer. <i>Journal of Heredity</i> , 2006, 97, 235-243.	1.0	18
40	Single nucleotide polymorphisms and haplotypes in the IL10 region associated with HCV clearance. <i>Genes and Immunity</i> , 2005, 6, 347-357.	2.2	79
41	Evaluating association and transmission of eight inflammatory genes with Viliuisk encephalomyelitis susceptibility. <i>International Journal of Immunogenetics</i> , 2004, 31, 121-128.	1.2	7
42	High levels of fluctuating asymmetry in populations of <i>Apodemus flavicollis</i> from the most contaminated areas in Chernobyl. <i>Journal of Environmental Radioactivity</i> , 2004, 73, 1-20.	0.9	42
43	Frequency distributions of ¹³⁷ Cs in fish and mammal populations. <i>Journal of Environmental Radioactivity</i> , 2002, 61, 55-74.	0.9	16