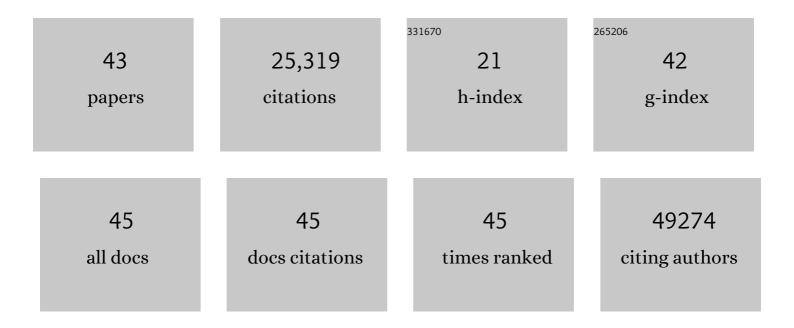
## Taras K Oleksyk

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6294731/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
2	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199
3	Association of Trypanolytic ApoL1 Variants with Kidney Disease in African Americans. Science, 2010, 329, 841-845.	12.6	1,725
4	MYH9 is a major-effect risk gene for focal segmental glomerulosclerosis. Nature Genetics, 2008, 40, 1175-1184.	21.4	636
5	Genome-wide scans for footprints of natural selection. Philosophical Transactions of the Royal Society B: Biological Sciences, 2010, 365, 185-205.	4.0	343
6	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. GigaScience, 2015, 4, 1.	6.4	241
7	Reconstructing Native American Migrations from Whole-Genome and Whole-Exome Data. PLoS Genetics, 2013, 9, e1004023.	3.5	185
8	Genomic legacy of the African cheetah, Acinonyx jubatus. Genome Biology, 2015, 16, 277.	8.8	167
9	History Shaped the Geographic Distribution of Genomic Admixture on the Island of Puerto Rico. PLoS ONE, 2011, 6, e16513.	2.5	87
10	Single nucleotide polymorphisms and haplotypes in the IL10 region associated with HCV clearance. Genes and Immunity, 2005, 6, 347-357.	4.1	79
11	Identifying Selected Regions from Heterozygosity and Divergence Using a Light-Coverage Genomic Dataset from Two Human Populations. PLoS ONE, 2008, 3, e1712.	2.5	50
12	Behavioral Risk Exposure and Host Genetics of Susceptibility to HIVâ€i Infection. Journal of Infectious Diseases, 2006, 193, 16-26.	4.0	49
13	Reconciling Apparent Conflicts between Mitochondrial and Nuclear Phylogenies in African Elephants. PLoS ONE, 2011, 6, e20642.	2.5	43
14	High levels of fluctuating asymmetry in populations of Apodemus flavicollis from the most contaminated areas in Chornobyl. Journal of Environmental Radioactivity, 2004, 73, 1-20.	1.7	42
15	Evaluation of <i>IL10</i> , <i>IL19</i> and <i>IL20</i> gene polymorphisms and chronic hepatitis B infection outcome. International Journal of Immunogenetics, 2008, 35, 255-264.	1.8	41
16	A locally funded Puerto Rican parrot (Amazona vittata) genome sequencing project increases avian data and advances young researcher education. GigaScience, 2012, 1, 14.	6.4	40
17	Extended IL10 haplotypes and their association with HIV progression to AIDS. Genes and Immunity, 2009, 10, 309-322.	4.1	37
18	Worldwide Distribution of the MYH9 Kidney Disease Susceptibility Alleles and Haplotypes: Evidence of Historical Selection in Africa. PLoS ONE, 2010, 5, e11474.	2.5	33

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19	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. Innate Immunity, 2013, 19, 569-587.	2.4	33
20	Genetics of Focal Segmental Glomerulosclerosis and Human Immunodeficiency Virus–Associated Collapsing Glomerulopathy: The Role of MYH9 Genetic Variation. Seminars in Nephrology, 2010, 30, 111-125.	1.6	30
21	Sequencing rare and common APOL1 coding variants to determine kidney disease risk. Kidney International, 2015, 88, 754-763.	5.2	30
22	A Recurrent BRCA2 Mutation Explains the Majority of Hereditary Breast and Ovarian Cancer Syndrome Cases in Puerto Rico. Cancers, 2018, 10, 419.	3.7	22
23	Evidence for selection at HIV host susceptibility genes in a West Central African human population. BMC Evolutionary Biology, 2012, 12, 237.	3.2	20
24	Genome-wide sequence analyses of ethnic populations across Russia. Genomics, 2020, 112, 442-458.	2.9	19
25	Independent Occurrences of Multiple Repeats in the Control Region of Mitochondrial DNA of White-Tailed Deer. Journal of Heredity, 2006, 97, 235-243.	2.4	18
26	Genome and gene alterations by insertions and deletions in the evolution of human and chimpanzee chromosome 22. BMC Genomics, 2009, 10, 51.	2.8	17
27	Frequency distributions of 137Cs in fish and mammal populations. Journal of Environmental Radioactivity, 2002, 61, 55-74.	1.7	16
28	The Genome Russia project: closing the largest remaining omission on the world Genome map. GigaScience, 2015, 4, 53.	6.4	16
29	Genetics of cattails in radioactively contaminated areas around Chornobyl. Molecular Ecology, 2006, 15, 2611-2625.	3.9	12
30	Innovative assembly strategy contributes to understanding the evolution and conservation genetics of the endangered Solenodon paradoxus from the island of Hispaniola. GigaScience, 2018, 7, .	6.4	12
31	Chromosome-Level Genome Assemblies Expand Capabilities of Genomics for Conservation Biology. Genes, 2021, 12, 1336.	2.4	12
32	Colonization of islands in the Mona Passage by endemic dwarf geckoes (genus) Tj ETQq0 0 0 rgBT /Overlock 10 Tr 4488-4500.	f 50 227 <sup>-</sup> 1.9	Td ( <i>Sphae 10</i>
33	Mitogenomic sequences support a north–south subspecies subdivision within Solenodon paradoxus. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2017, 28, 662-670.	0.7	9
34	Genome diversity in Ukraine. GigaScience, 2021, 10, .	6.4	9
35	Putting Russia on the genome map. Science, 2015, 350, 747-747.	12.6	8
36	Genomes of Three Closely Related Caribbean Amazons Provide Insight for Species History and Conservation. Genes, 2019, 10, 54.	2.4	8

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#	Article	IF	CITATIONS
37	Evaluating association and transmission of eight inflammatory genes with Viliuisk encephalomyelitis susceptibility. International Journal of Immunogenetics, 2004, 31, 121-128.	1.2	7
38	GWATCH: a web platform for automated gene association discovery analysis. GigaScience, 2014, 3, 18.	6.4	5
39	Genetic diversity and selection in Puerto Rican horses. Scientific Reports, 2022, 12, 515.	3.3	4
40	Isolation and characterization of microsatellite loci in the critically endangered Puerto Rican parrot (Amazona vittata). Conservation Genetics Resources, 2014, 6, 885-889.	0.8	2
41	Molecular Phylogeny and Evolution of Amazon Parrots in the Greater Antilles. Genes, 2021, 12, 608.	2.4	2
42	Genomics of Adaptation and Speciation. Genes, 2022, 13, 1187.	2.4	2
43	ESTIMATION OF THE FREQUENCY OF GENETIC VARIANTS ASSOCIATED WITH VITAMIN D LEVELS AND OSTEOPOROSIS IN THE POPULATION OF UKRAINE. Problemi Endokrinnoi Patologii, 2022, 79, 53-59.	0.2	Ο