Shay Tzur

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11683113/publications.pdf

Version: 2024-02-01

42 papers	2,831 citations	279798 23 h-index	276875 41 g-index
43 all docs	43 docs citations	43 times ranked	4321 citing authors

#	Article	IF	Citations
1	Missense mutations in the APOL1 gene are highly associated with end stage kidney disease risk previously attributed to the MYH9 gene. Human Genetics, 2010, 128, 345-350.	3.8	539
2	The Dawn of Human Matrilineal Diversity. American Journal of Human Genetics, 2008, 82, 1130-1140.	6.2	392
3	Maternal traces of deep common ancestry and asymmetric gene flow between Pygmy hunterâ€“gatherers and Bantu-speaking farmers. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 1596-1601.	7.1	157
4	The Matrilineal Ancestry of Ashkenazi Jewry: Portrait of a Recent Founder Event. American Journal of Human Genetics, 2006, 78, 487-497.	6.2	140
5	Exome Sequencing Reveals SYCE1 Mutation Associated With Autosomal Recessive Primary Ovarian Insufficiency. Journal of Clinical Endocrinology and Metabolism, 2014, 99, E2129-E2132.	3.6	128
6	APOL1 Risk Variants Predict Histopathology and Progression to ESRD in HIV-Related Kidney Disease. Journal of the American Society of Nephrology: JASN, 2012, 23, 343-350.	6.1	107
7	Counting the Founders: The Matrilineal Genetic Ancestry of the Jewish Diaspora. PLoS ONE, 2008, 3, e2062.	2.5	101
8	The Genographic Project Public Participation Mitochondrial DNA Database. PLoS Genetics, 2007, 3, e104.	3.5	99
9	Gain-of-function mutation of microRNA-140 in human skeletal dysplasia. Nature Medicine, 2019, 25, 583-590.	30.7	86
10	APOL1 allelic variants are associated with lower age of dialysis initiation and thereby increased dialysis vintage in African and Hispanic Americans with non-diabetic end-stage kidney disease. Nephrology Dialysis Transplantation, 2012, 27, 1498-1505.	0.7	85
11	High Population Frequencies of APOL1 Risk Variants Are Associated with Increased Prevalence of Non-Diabetic Chronic Kidney Disease in the Igbo People from South-Eastern Nigeria. Nephron Clinical Practice, 2013, 123, 123-128.	2.3	82
12	African ancestry allelic variation at the MYH9 gene contributes to increased susceptibility to non-diabetic end-stage kidney disease in Hispanic Americans. Human Molecular Genetics, 2010, 19, 1816-1827.	2.9	75
13	Deficiency of the sphingosine-1-phosphate lyase SGPL1 is associated with congenital nephrotic syndrome and congenital adrenal calcifications. Human Mutation, 2017, 38, 365-372.	2.5	71
14	No Evidence from Genome-Wide Data of a Khazar Origin for the Ashkenazi Jews. Human Biology, 2013, 85, 859-900.	0.2	68
15	Absence of APOL1 Risk Variants Protects against HIV-Associated Nephropathy in the Ethiopian Population. American Journal of Nephrology, 2011, 34, 452-459.	3.1	66
16	The population genetics of chronic kidney disease: insights from the MYH9â€“APOL1 locus. Nature Reviews Nephrology, 2011, 7, 313-326.	9.6	58
17	Possible incipient sympatric ecological speciation in blind mole rats (Spalax). Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2587-2592.	7.1	58
18	The Genomic History of the Bronze Age Southern Levant. Cell, 2020, 181, 1146-1157.e11.	28.9	51

#	Article	IF	Citations
19	A Biallelic Mutation in the Homologous Recombination Repair Gene SPIDR Is Associated With Human Gonadal Dysgenesis. Journal of Clinical Endocrinology and Metabolism, 2017, 102, 681-688.	3.6	47
20	Lysine acetyltransferase 8 is involved in cerebral development and syndromic intellectual disability. Journal of Clinical Investigation, 2020, 130, 1431-1445.	8.2	40
21	Congenital dilated cardiomyopathy caused by biallelic mutations in Filamin C. European Journal of Human Genetics, 2016, 24, 1792-1796.	2.8	36
22	Phylogenetic applications of whole Y-chromosome sequences and the Near Eastern origin of Ashkenazi Levites. Nature Communications, 2013, 4, 2928.	12.8	31
23	No Evidence from Genome-wide Data of a Khazar Origin fo the Ashkenazi Jews. Human Biology, 2013, 85, 859.	0.2	30
24	Lethal neonatal rigidity and multifocal seizure syndrome â€“ Report of another family with a BRAT1 mutation. European Journal of Paediatric Neurology, 2015, 19, 240-242.	1.6	28
25	Whole-exome sequencing reveals POC5 as a novel gene associated with autosomal recessive retinitis pigmentosa. Human Molecular Genetics, 2018, 27, 614-624.	2.9	26
26	A null variant in the apolipoprotein L3 gene is associated with non-diabetic nephropathy. Nephrology Dialysis Transplantation, 2018, 33, 323-330.	0.7	25
27	A de novo GABRA2 missense mutation in severe early-onset epileptic encephalopathy with a choreiform movement disorder. European Journal of Paediatric Neurology, 2018, 22, 516-524.	1.6	23
28	Intellectual disability and non-compaction cardiomyopathy with a de novo NONO mutation identified by exome sequencing. European Journal of Human Genetics, 2016, 24, 1635-1638.	2.8	22
29	Clinical Heterogeneity and Phenotypic Expansion of NaPi-IIaâ€“Associated Disease. Journal of Clinical Endocrinology and Metabolism, 2017, 102, 4604-4614.	3.6	22
30	Variant in SCYL1 gene causes aberrant splicing in a family with cerebellar ataxia, recurrent episodes of liver failure, and growth retardation. European Journal of Human Genetics, 2019, 27, 263-268.	2.8	22
31	Mutations inTAX1BP3Cause Dilated Cardiomyopathy with Septo-Optic Dysplasia. Human Mutation, 2015, 36, 439-442.	2.5	21
32	Primary Coenzyme Q deficiency Due to Novel ADCK3 Variants, Studies in Fibroblasts and Review of Literature. Neurochemical Research, 2019, 44, 2372-2384.	3.3	15
33	The genetic variation in the R1a clade among the Ashkenazi Levitesâ€™ Y chromosome. Scientific Reports, 2017, 7, 14969.	3.3	13
34	Odour-genes covariance within a natural population of subterranean Spalax galili blind mole rats. Biological Journal of the Linnean Society, 0, 96, 483-490.	1.6	12
35	A founder effect for p47phox Trp193Ter chronic granulomatous disease in Kavkazi Jews. Blood Cells, Molecules, and Diseases, 2015, 55, 320-327.	1.4	12
36	A novel 154-bp deletion in the human mitochondrial DNA control region in healthy individuals. Human Mutation, 2008, 29, 1387-1391.	2.5	11

#	Article	IF	Citations
37	Biallelic mutations in EXOC3L2 cause a novel syndrome that affects the brain, kidney and blood. Journal of Medical Genetics, 2019, 56, 340-346.	3.2	9
38	Linkage disequilibrium analysis reveals an albuminuria risk haplotype containing three missense mutations in the cubilin gene with striking differences among European and African ancestry populations. BMC Nephrology, 2012, 13, 142.	1.8	7
39	Exome sequencing identified a novelde novo OPA1mutation in a consanguineous family presenting with optic atrophy. Genetical Research, 2016, 98, e10.	0.9	5
40	Big data analysis of human mitochondrial DNA substitution models: a regression approach. BMC Genomics, 2018, 19, 759.	2.8	5
41	Exome sequencing identified mutations in CASK and MYBPC3 as the cause of a complex dilated cardiomyopathy phenotype. Genetical Research, 2016, 98, e8.	0.9	3
42	Strictly conserved tri-nucleotide motif â€œCATâ€•is associated with TAS DNA protein-binding sites in human mitochondrial DNA control region. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2017, 28, 250-253.	0.7	3