Miriam S Udler

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/9012168/publications.pdf

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28	2,033	471061	500791
papers	citations	17	28
		h-index	g-index

36	36	36	4391
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic analysis of dietary intake identifies new loci and functional links with metabolic traits. Nature Human Behaviour, 2022, 6, 155-163.	6.2	22
2	Heterogeneity of Diabetes: Î²-Cells, Phenotypes, and Precision Medicine: Proceedings of an International Symposium of the Canadian Institutes of Health Researchâ€™s Institute of Nutrition, Metabolism and Diabetes and the U.S. National Institutes of Healthâ€™s National Institute of Diabetes and Digestive and Kidney Diseases. Diabetes Care, 2022, 45, 3-22.	4.3	14
3	Rare coding variants in 35 genes associate with circulating lipid levelsâ€”A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	2.6	24
4	Type 2 Diabetes Partitioned Polygenic Scores Associate With Disease Outcomes in 454,193 Individuals Across 13 Cohorts. Diabetes Care, 2022, 45, 674-683.	4.3	29
5	Separating the direct effects of traits on atherosclerotic cardiovascular disease from those mediated by type 2 diabetes. Diabetologia, 2022, 65, 790-799.	2.9	9
6	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250
7	Inherited basis of visceral, abdominal subcutaneous and gluteofemoral fat depots. Nature Communications, 2022, 13, .	5.8	43
8	Variance-quantitative trait loci enable systematic discovery of gene-environment interactions for cardiometabolic serum biomarkers. Nature Communications, 2022, 13, .	5.8	14
9	Genetic Loci and Physiologic Pathways Involved in Gestational Diabetes Mellitus Implicated Through Clustering. Diabetes, 2021, 70, 268-281.	0.3	10
10	Identifying subgroups of people at risk for type 2 diabetes. Nature Medicine, 2021, 27, 23-25.	15.2	3
11	Genetic determinants of daytime napping and effects on cardiometabolic health. Nature Communications, 2021, 12, 900.	5.8	136
12	Randomized prospective evaluation of genome sequencing versus standard-of-care as a first molecular diagnostic test. Genetics in Medicine, 2021, 23, 1689-1696.	1.1	17
13	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. Nature Communications, 2021, 12, 3505.	5.8	49
14	Genome-wide association analyses highlight etiological differences underlying newly defined subtypes of diabetes. Nature Genetics, 2021, 53, 1534-1542.	9.4	81
15	Defining Heterogeneity Among Women With Gestational Diabetes Mellitus. Diabetes, 2020, 69, 2064-2074.	0.3	29
16	A Long Non-coding RNA, LOC157273, Is an Effector Transcript at the Chromosome 8p23.1-PPP1R3B Metabolic Traits and Type 2 Diabetes Risk Locus. Frontiers in Genetics, 2020, 11, 615.	1.1	14
17	Case 6-2020: A 34-Year-Old Woman with Hyperglycemia. New England Journal of Medicine, 2020, 382, 745-753.	13.9	12
18	Pleiotropy-Based Decomposition of Genetic Risk Scores: Association and Interaction Analysis for Type 2 Diabetes and CAD. American Journal of Human Genetics, 2020, 106, 646-658.	2.6	17

#	Article	IF	Citations
19	Type 2 Diabetes: Multiple Genes, Multiple Diseases. Current Diabetes Reports, 2019, 19, 55.	1.7	48
20	Genetic Risk Scores for Diabetes Diagnosis and Precision Medicine. Endocrine Reviews, 2019, 40, 1500-1520.	8.9	192
21	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	13.7	248
22	Type 2 diabetes genetic loci informed by multi-trait associations point to disease mechanisms and subtypes: A soft clustering analysis. PLoS Medicine, 2018, 15, e1002654.	3.9	373
23	A Decade of Genetic and Metabolomic Contributions to Type 2 Diabetes Risk Prediction. Current Diabetes Reports, 2017, 17, 135.	1.7	19
24	Effect of Genetic African Ancestry on eGFR and Kidney Disease. Journal of the American Society of Nephrology: JASN, 2015, 26, 1682-1692.	3.0	75
25	Evaluating the power to discriminate between highly correlated SNPs in genetic association studies. Genetic Epidemiology, 2010, 34, 463-468.	0.6	48
26	Fine scale mapping of the breast cancer 16q12 locus. Human Molecular Genetics, 2010, 19, 2507-2515.	1.4	68
27	FGFR2 variants and breast cancer risk: fine-scale mapping using African American studies and analysis of chromatin conformation. Human Molecular Genetics, 2009, 18, 1692-1703.	1.4	110
28	Common germline polymorphisms in COMT, CYP19A1, ESR1, PGR, SULT1E1 and STS and survival after a diagnosis of breast cancer. International Journal of Cancer, 2009, 125, 2687-2696.	2.3	34