

Suzanne B R Jacobs

List of Publications by Year in descending order

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12
papers

1,789
citations

933264

10
h-index

1199470

12
g-index

13
all docs

13
docs citations

13
times ranked

5334
citing authors

#	ARTICLE	IF	CITATIONS
1	Interaction Between Type 2 Diabetes Prevention Strategies and Genetic Determinants of Coronary Artery Disease on Cardiometabolic Risk Factors. <i>Diabetes</i> , 2020, 69, 112-120.	0.3	13
2	Analysis of Glucocorticoid-Related Genes Reveal <i>CCHCR1</i> as a New Candidate Gene for Type 2 Diabetes. <i>Journal of the Endocrine Society</i> , 2020, 4, bvaa121.	0.1	8
3	Gain-of-Function Claims for Type-2-Diabetes-Associated Coding Variants in <i>SLC16A11</i> Are Not Supported by the Experimental Data. <i>Cell Reports</i> , 2019, 29, 778-780.	2.9	6
4	Polyunsaturated Fatty Acid Desaturation Is a Mechanism for Glycolytic NAD ⁺ Recycling. <i>Cell Metabolism</i> , 2019, 29, 856-870.e7.	7.2	87
5	The <i>SLC16A11</i> risk haplotype is associated with decreased insulin action, higher transaminases and large-size adipocytes. <i>European Journal of Endocrinology</i> , 2019, 180, 99-107.	1.9	19
6	A Low-Frequency Inactivating <i>AKT2</i> Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017, 66, 2019-2032.	0.3	47
7	A Loss-of-Function Splice Acceptor Variant in <i>IGF2</i> Is Protective for Type 2 Diabetes. <i>Diabetes</i> , 2017, 66, 2903-2914.	0.3	52
8	Type 2 Diabetes Variants Disrupt Function of <i>SLC16A11</i> through Two Distinct Mechanisms. <i>Cell</i> , 2017, 170, 199-212.e20.	13.5	121
9	Association of a Low-Frequency Variant in <i>HNF1A</i> With Type 2 Diabetes in a Latino Population. <i>JAMA - Journal of the American Medical Association</i> , 2014, 311, 2305.	3.8	230
10	Sequence variants in <i>SLC16A11</i> are a common risk factor for type 2 diabetes in Mexico. <i>Nature</i> , 2014, 506, 97-101.	13.7	439
11	Loss-of-function mutations in <i>SLC30A8</i> protect against type 2 diabetes. <i>Nature Genetics</i> , 2014, 46, 357-363.	9.4	428
12	Genome-wide meta-analysis identifies new susceptibility loci for migraine. <i>Nature Genetics</i> , 2013, 45, 912-917.	9.4	338