

Steven P Wilder

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/1460802/steven-p-wilder-publications-by-year.pdf>

Version: 2024-04-23

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

35
papers

9,717
citations

23
h-index

35
g-index

35
ext. papers

11,400
ext. citations

16.4
avg, IF

4.67
L-index

#	Paper	IF	Citations
35	Systems Genetics of Hepatic Metabolome Reveals Octopamine as a Target for Non-Alcoholic Fatty Liver Disease Treatment. <i>Scientific Reports</i> , 2019 , 9, 3656	4.9	9
34	Ensembl 2017. <i>Nucleic Acids Research</i> , 2017 , 45, D635-D642	20.1	404
33	Transcriptome Profiling in Rat Inbred Strains and Experimental Cross Reveals Discrepant Genetic Architecture of Genome-Wide Gene Expression. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 3671-3683	3.2	5
32	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. <i>Cell</i> , 2016 , 167, 1369-1384.e19	56.2	556
31	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. <i>Cell</i> , 2016 , 167, 1415-1429.e19	56.2	637
30	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. <i>Cell</i> , 2016 , 167, 1398-1414.e24	56.2	634
29	Ensembl 2016. <i>Nucleic Acids Research</i> , 2016 , 44, D710-6	20.1	1094
28	Ensembl regulation resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	33
27	Topological analysis of metabolic networks integrating co-segregating transcriptomes and metabolomes in type 2 diabetic rat congenic series. <i>Genome Medicine</i> , 2016 , 8, 101	14.4	14
26	The ensembl regulatory build. <i>Genome Biology</i> , 2015 , 16, 56	18.3	255
25	Ensembl 2015. <i>Nucleic Acids Research</i> , 2015 , 43, D662-9	20.1	1013
24	Ensembl 2014. <i>Nucleic Acids Research</i> , 2014 , 42, D749-55	20.1	1087
23	WiggleTools: parallel processing of large collections of genome-wide datasets for visualization and statistical analysis. <i>Bioinformatics</i> , 2014 , 30, 1008-9	7.2	44
22	Adaptive expression of microRNA-125a in adipose tissue in response to obesity in mice and men. <i>PLoS ONE</i> , 2014 , 9, e91375	3.7	17
21	Integrative annotation of chromatin elements from ENCODE data. <i>Nucleic Acids Research</i> , 2013 , 41, 827-40.1	20.1	383
20	Ensembl 2013. <i>Nucleic Acids Research</i> , 2013 , 41, D48-55	20.1	797
19	ENCODE data in the UCSC Genome Browser: year 5 update. <i>Nucleic Acids Research</i> , 2013 , 41, D56-63	20.1	580

18	Nutrigenomics of high fat diet induced obesity in mice suggests relationships between susceptibility to fatty liver disease and the proteasome. <i>PLoS ONE</i> , 2013 , 8, e82825	3.7	32
17	Ensembl 2012. <i>Nucleic Acids Research</i> , 2012 , 40, D84-90	20.1	798
16	Ensembl 2011. <i>Nucleic Acids Research</i> , 2011 , 39, D800-6	20.1	590
15	Ensembl 10th year. <i>Nucleic Acids Research</i> , 2010 , 38, D557-62	20.1	240
14	ATR-X syndrome protein targets tandem repeats and influences allele-specific expression in a size-dependent manner. <i>Cell</i> , 2010 , 143, 367-78	56.2	297
13	Chromosomal mapping of pancreatic islet morphological features and regulatory hormones in the spontaneously diabetic (Type 2) Goto-Kakizaki rat. <i>Mammalian Genome</i> , 2010 , 21, 499-508	3.2	8
12	Comparative analysis of methods for gene transcription profiling data derived from different microarray technologies in rat and mouse models of diabetes. <i>BMC Genomics</i> , 2009 , 10, 63	4.5	15
11	Functional annotations of diabetes nephropathy susceptibility loci through analysis of genome-wide renal gene expression in rat models of diabetes mellitus. <i>BMC Medical Genomics</i> , 2009 , 2, 41	3.7	10
10	Pathophysiological, genetic and gene expression features of a novel rodent model of the cardio-metabolic syndrome. <i>PLoS ONE</i> , 2008 , 3, e2962	3.7	22
9	Phylometabonomic patterns of adaptation to high fat diet feeding in inbred mice. <i>PLoS ONE</i> , 2008 , 3, e1668	3.7	83
8	Direct quantitative trait locus mapping of mammalian metabolic phenotypes in diabetic and normoglycemic rat models. <i>Nature Genetics</i> , 2007 , 39, 666-72	36.3	132
7	Mapping diabetes QTL in an intercross derived from a congenic strain of the Brown Norway and Goto-Kakizaki rats. <i>Mammalian Genome</i> , 2006 , 17, 538-47	3.2	14
6	Chromosomal mapping of quantitative trait loci controlling elastin content in rat aorta. <i>Hypertension</i> , 2005 , 45, 460-6	8.5	18
5	Polymorphisms in type II SH2 domain-containing inositol 5-phosphatase (INPPL1, SHIP2) are associated with physiological abnormalities of the metabolic syndrome. <i>Diabetes</i> , 2004 , 53, 1900-4	0.9	72
4	Integration of the rat recombination and EST maps in the rat genomic sequence and comparative mapping analysis with the mouse genome. <i>Genome Research</i> , 2004 , 14, 758-65	9.7	22
3	Chromosomal mapping of genetic loci controlling absence epilepsy phenotypes in the WAG/Rij rat. <i>Epilepsia</i> , 2004 , 45, 908-15	6.4	44
2	Polygenic control of idiopathic generalized epilepsy phenotypes in the genetic absence rats from Strasbourg (GAERS). <i>Epilepsia</i> , 2004 , 45, 301-8	6.4	51
1	Comparative analysis of neutrophil and monocyte epigenomes		2

