

Steven P Wilder

List of Publications by Citations

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Version: 2024-04-23

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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	Ensembl 2016. <i>Nucleic Acids Research</i> , 2016 , 44, D710-6	20.1	1094
34	Ensembl 2014. <i>Nucleic Acids Research</i> , 2014 , 42, D749-55	20.1	1087
33	Ensembl 2015. <i>Nucleic Acids Research</i> , 2015 , 43, D662-9	20.1	1013
32	Ensembl 2012. <i>Nucleic Acids Research</i> , 2012 , 40, D84-90	20.1	798
31	Ensembl 2013. <i>Nucleic Acids Research</i> , 2013 , 41, D48-55	20.1	797
30	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
29	Ensembl 2011. <i>Nucleic Acids Research</i> , 2011 , 39, D800-6	20.1	590
28	ENCODE data in the UCSC Genome Browser: year 5 update. <i>Nucleic Acids Research</i> , 2013 , 41, D56-63	20.1	580
27	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
26	Ensembl 2017. <i>Nucleic Acids Research</i> , 2017 , 45, D635-D642	20.1	404
25	Integrative annotation of chromatin elements from ENCODE data. <i>Nucleic Acids Research</i> , 2013 , 41, 827-40.1	20.1	383
24	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. <i>Cell</i> , 2016 , 167, 1398-1414.e34	56.2	334
23	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
22	The ensembl regulatory build. <i>Genome Biology</i> , 2015 , 16, 56	18.3	255
21	Ensembl 10th year. <i>Nucleic Acids Research</i> , 2010 , 38, D557-62	20.1	240
20	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
19	Phylometabonomic patterns of adaptation to high fat diet feeding in inbred mice. <i>PLoS ONE</i> , 2008 , 3, e1668	3.7	83

18	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
17	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
16	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
15	Chromosomal mapping of genetic loci controlling absence epilepsy phenotypes in the WAG/Rij rat. <i>Epilepsia</i> , 2004 , 45, 908-15	6.4	44
14	Ensembl regulation resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	33
13	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
12	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
11	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
10	Chromosomal mapping of quantitative trait loci controlling elastin content in rat aorta. <i>Hypertension</i> , 2005 , 45, 460-6	8.5	18
9	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
8	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
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	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
5	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
4	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
3	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
2	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
1	Comparative analysis of neutrophil and monocyte epigenomes		2

