Dominique Gauguier

List of Publications by Year in Descending Order

147 papers	10,803 citations	50 h-index	103 g-index
152 ext. papers	12,398 ext. citations	9.1 avg, IF	5.07 L-index

#	Paper	IF	Citations
147	Microbiome and metabolome features of the cardiometabolic disease spectrum.. *Nature Medicine*, **2022**,	50.5	4
146	Diet dependent impact of benzoate on diabetes and obesity in mice.. *Biochimie*, **2021**, 194, 35-35	4.6	0
145	Human and preclinical studies of the host-gut microbiome co-metabolite hippurate as a marker and mediator of metabolic health. *Gut*, **2021**, 70, 2105-2114	19.2	13
144	Dominant gut Prevotella copri in gastrectomised non-obese diabetic Goto-Kakizaki rats improves glucose homeostasis through enhanced FXR signalling. *Diabetologia*, **2020**, 63, 1223-1235	10.3	17
143	The Natural Metabolite 4-Cresol Improves Glucose Homeostasis and Enhances Cell Function. *Cell Reports*, **2020**, 30, 2306-2320.e5	10.6	18
142	Plasma and urine metabolomic analyses in aortic valve stenosis reveal shared and biofluid-specific changes in metabolite levels. *PLoS ONE*, **2020**, 15, e0242019	3.7	3
141	Plasma and urine metabolomic analyses in aortic valve stenosis reveal shared and biofluid-specific changes in metabolite levels **2020**, 15, e0242019		
140	Plasma and urine metabolomic analyses in aortic valve stenosis reveal shared and biofluid-specific changes in metabolite levels **2020**, 15, e0242019		
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138	Plasma and urine metabolomic analyses in aortic valve stenosis reveal shared and biofluid-specific changes in metabolite levels **2020**, 15, e0242019		
137	Plasma and urine metabolomic analyses in aortic valve stenosis reveal shared and biofluid-specific changes in metabolite levels **2020**, 15, e0242019		
136	Plasma and urine metabolomic analyses in aortic valve stenosis reveal shared and biofluid-specific changes in metabolite levels **2020**, 15, e0242019		
135	Conserved properties of genetic architecture of renal and fat transcriptomes in rat models of insulin resistance. *DMM Disease Models and Mechanisms*, **2019**, 12,	4.1	2
134	Systems Genetics of Hepatic Metabolome Reveals Octopamine as a Target for Non-Alcoholic Fatty Liver Disease Treatment. *Scientific Reports*, **2019**, 9, 3656	4.9	9
133	Untargeted Mass Spectrometry Lipidomics identifies correlation between serum sphingomyelins and plasma cholesterol. *Lipids in Health and Disease*, **2019**, 18, 38	4.4	12
132	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. *Journal of the American College of Cardiology*, **2019**, 73, 58-66	15.1	86
131	pJRES Binning Algorithm (JBA): a new method to facilitate the recovery of metabolic information from pJRES 1H NMR spectra. *Bioinformatics*, **2019**, 35, 1916-1922	7.2	6

130	MWASTools: an R/bioconductor package for metabolome-wide association studies. *Bioinformatics*, **2018**, 34, 890-892	7.2	13
129	Metabolic retroconversion of trimethylamine N-oxide and the gut microbiota. *Microbiome*, **2018**, 6, 73	16.6	82
128	Molecular genetics of the transcription factor GLIS3 identifies its dual function in beta cells and neurons. *Genomics*, **2018**, 110, 98-111	4.3	12
127	Integration of the human exposome with the human genome to advance medicine. *Biochimie*, **2018**, 152, 155-158	4.6	25
126	Implication of gut microbiota metabolites in cardiovascular and metabolic diseases. *Cellular and Molecular Life Sciences*, **2018**, 75, 3977-3990	10.3	84
125	Biological roles of microRNAs in the control of insulin secretion and action. *Physiological Genomics*, **2017**, 49, 1-10	3.6	21
124	Loss of Cardioprotective Effects at the Locus as a Result of Gene-Smoking Interactions. *Circulation*, **2017**, 135, 2336-2353	16.7	36
123	Genomic regulation of type 2 diabetes endophenotypes: Contribution from genetic studies in the Goto-Kakizaki rat. *Biochimie*, **2017**, 143, 56-65	4.6	7
122	J-Resolved H NMR 1D-Projections for Large-Scale Metabolic Phenotyping Studies: Application to Blood Plasma Analysis. *Analytical Chemistry*, **2017**, 89, 11405-11412	7.8	13
121	Microbial-Host Co-metabolites Are Prodromal Markers Predicting Phenotypic Heterogeneity in Behavior, Obesity, and Impaired Glucose Tolerance. *Cell Reports*, **2017**, 20, 136-148	10.6	57
120	MetaboSignal: a network-based approach for topological analysis of metabotype regulation via metabolic and signaling pathways. *Bioinformatics*, **2017**, 33, 773-775	7.2	9
119	Transcriptome Profiling in Rat Inbred Strains and Experimental Cross Reveals Discrepant Genetic Architecture of Genome-Wide Gene Expression. *G3: Genes, Genomes, Genetics*, **2016**, 6, 3671-3683	3.2	5
118	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. *Scientific Reports*, **2016**, 6, 35278	4.9	18
117	Application of quantitative metabolomics in systems genetics in rodent models of complex phenotypes. *Archives of Biochemistry and Biophysics*, **2016**, 589, 158-67	4.1	10
116	A multiplexed targeted assay for high-throughput quantitative analysis of serum methylamines by ultra performance liquid chromatography coupled to high resolution mass spectrometry. *Archives of Biochemistry and Biophysics*, **2016**, 597, 12-20	4.1	11
115	Topological analysis of metabolic networks integrating co-segregating transcriptomes and metabolomes in type 2 diabetic rat congenic series. *Genome Medicine*, **2016**, 8, 101	14.4	14
114	Caffeine Impact on Metabolic Syndrome Components Is Modulated by a CYP1A2 Variant. *Annals of Nutrition and Metabolism*, **2016**, 68, 1-11	4.5	14
113	The SAM domain of ANKS6 has different interacting partners and mutations can induce different cystic phenotypes. *Kidney International*, **2015**, 88, 299-310	9.9	11

112	mQTL.NMR: an integrated suite for genetic mapping of quantitative variations of (1)H NMR-based metabolic profiles. *Analytical Chemistry*, **2015**, 87, 4377-84	7.8	24
111	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. *Nature*, **2015**, 526, 112-7	50.4	308
110	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. *Nature Genetics*, **2015**, 47, 1121-1130	36.3	1290
109	Circulating lipid levels and risk of coronary artery disease in a large group of patients undergoing coronary angiography. *Journal of Thrombosis and Thrombolysis*, **2015**, 39, 15-22	5.1	10
108	Homology-directed repair in rodent zygotes using Cas9 and TALEN engineered proteins. *Scientific Reports*, **2015**, 5, 14410	4.9	56
107	ANKS3 Co-Localises with ANKS6 in Mouse Renal Cilia and Is Associated with Vasopressin Signaling and Apoptosis In Vivo in Mice. *PLoS ONE*, **2015**, 10, e0136781	3.7	9
106	Plaque burden in HIV-infected patients is associated with serum intestinal microbiota-generated trimethylamine. *Aids*, **2015**, 29, 443-52	3.5	52
105	Association of coronary artery disease and chronic kidney disease in Lebanese population. *International Journal of Clinical and Experimental Medicine*, **2015**, 8, 15866-77		1
104	T2DM GWAS in the Lebanese population confirms the role of TCF7L2 and CDKAL1 in disease susceptibility. *Scientific Reports*, **2014**, 4, 7351	4.9	22
103	Association of hypertension with coronary artery disease onset in the Lebanese population. *SpringerPlus*, **2014**, 3, 533		5
102	Protease inhibitor 15, a candidate gene for abdominal aortic internal elastic lamina ruptures in the rat. *Physiological Genomics*, **2014**, 46, 418-28	3.6	14
101	Regenerating 1 and 3b gene expression in the pancreas of type 2 diabetic Goto-Kakizaki (GK) rats. *PLoS ONE*, **2014**, 9, e90045	3.7	15
100	Adaptive expression of microRNA-125a in adipose tissue in response to obesity in mice and men. *PLoS ONE*, **2014**, 9, e91375	3.7	17
99	Genetic control of differential acetylation in diabetic rats. *PLoS ONE*, **2014**, 9, e94555	3.7	4
98	Large-scale association analysis identifies new risk loci for coronary artery disease. *Nature Genetics*, **2013**, 45, 25-33	36.3	1172
97	Genome sequencing reveals loci under artificial selection that underlie disease phenotypes in the laboratory rat. *Cell*, **2013**, 154, 691-703	56.2	127
96	Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. *Nature Genetics*, **2013**, 45, 767-75	36.3	131
95	Genome-wide diversity in the levant reveals recent structuring by culture. *PLoS Genetics*, **2013**, 9, e1003316	6	59

94	Nutrigenomics of high fat diet induced obesity in mice suggests relationships between susceptibility to fatty liver disease and the proteasome. *PLoS ONE*, **2013**, 8, e82825	3.7	32
93	Genetic and environmental influences on total plasma homocysteine and its role in coronary artery disease risk. *Atherosclerosis*, **2012**, 222, 180-6	3.1	21
92	Untargeted metabolome quantitative trait locus mapping associates variation in urine glycerate to mutant glycerate kinase. *Journal of Proteome Research*, **2012**, 11, 631-42	5.6	23
91	Genome-wide association study in a Lebanese cohort confirms PHACTR1 as a major determinant of coronary artery stenosis. *PLoS ONE*, **2012**, 7, e38663	3.7	38
90	Mapping Metabolomic Quantitative Trait Loci (mQTL): A Link Between Metabolome-Wide Association Studies and Systems Biology **2012**, 233-254		1
89	Broad-ranging natural metabotype variation drives physiological plasticity in healthy control inbred rat strains. *Journal of Proteome Research*, **2011**, 10, 1675-89	5.6	17
88	Large scale association analysis identifies three susceptibility loci for coronary artery disease. *PLoS ONE*, **2011**, 6, e29427	3.7	63
87	Progression of diet-induced diabetes in C57BL6J mice involves functional dissociation of Ca2(+) channels from secretory vesicles. *Diabetes*, **2010**, 59, 1192-201	0.9	57
86	Global microRNA expression profiles in insulin target tissues in a spontaneous rat model of type 2 diabetes. *Diabetologia*, **2010**, 53, 1099-109	10.3	227
85	Chromosomal mapping of pancreatic islet morphological features and regulatory hormones in the spontaneously diabetic (Type 2) Goto-Kakizaki rat. *Mammalian Genome*, **2010**, 21, 499-508	3.2	8
84	Comparative analysis of methods for gene transcription profiling data derived from different microarray technologies in rat and mouse models of diabetes. *BMC Genomics*, **2009**, 10, 63	4.5	15
83	Functional annotations of diabetes nephropathy susceptibility loci through analysis of genome-wide renal gene expression in rat models of diabetes mellitus. *BMC Medical Genomics*, **2009**, 2, 41	3.7	10
82	MicroRNA-125a is over-expressed in insulin target tissues in a spontaneous rat model of Type 2 Diabetes. *BMC Medical Genomics*, **2009**, 2, 54	3.7	96
81	A resource for the simultaneous high-resolution mapping of multiple quantitative trait loci in rats: the NIH heterogeneous stock. *Genome Research*, **2009**, 19, 150-8	9.7	63
80	Pancreatic ectopic fat is characterized by adipocyte infiltration and altered lipid composition. *Obesity*, **2008**, 16, 522-30	8	132
79	SNP and haplotype mapping for genetic analysis in the rat. *Nature Genetics*, **2008**, 40, 560-6	36.3	150
78	Progress and prospects in rat genetics: a community view. *Nature Genetics*, **2008**, 40, 516-22	36.3	234
77	G/T substitution in intron 1 of the UNC13B gene is associated with increased risk of nephropathy in patients with type 1 diabetes. *Diabetes*, **2008**, 57, 2843-50	0.9	33

76	Genomic organization and mutation screening of the human ortholog of Pkdr1 associated with polycystic kidney disease in the rat. *European Journal of Medical Genetics*, **2008**, 51, 325-31	2.6	1
75	Pathophysiological, genetic and gene expression features of a novel rodent model of the cardio-metabolic syndrome. *PLoS ONE*, **2008**, 3, e2962	3.7	22
74	European rational approach for the genetics of diabetic complications--EURAGEDIC: patient populations and strategy. *Nephrology Dialysis Transplantation*, **2008**, 23, 161-8	4.3	27
73	Phylometabonomic patterns of adaptation to high fat diet feeding in inbred mice. *PLoS ONE*, **2008**, 3, e1668	3.7	83
72	Direct quantitative trait locus mapping of mammalian metabolic phenotypes in diabetic and normoglycemic rat models. *Nature Genetics*, **2007**, 39, 666-72	36.3	132
71	Subtle metabolic and liver gene transcriptional changes underlie diet-induced fatty liver susceptibility in insulin-resistant mice. *Diabetologia*, **2007**, 50, 1867-1879	10.3	94
70	Aryl hydrocarbon receptor nuclear translocator-like (BMAL1) is associated with susceptibility to hypertension and type 2 diabetes. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 14412-7	11.5	284
69	Association between angiotensin-converting enzyme gene polymorphisms and diabetic nephropathy: case-control, haplotype, and family-based study in three European populations. *Journal of the American Society of Nephrology: JASN*, **2007**, 18, 1284-91	12.7	57
68	Genetic association analysis of inositol polyphosphate phosphatase-like 1 (INPPL1, SHIP2) variants with essential hypertension. *Journal of Medical Genetics*, **2007**, 44, 603-5	5.8	13
67	Diabetes quantitative trait locus research: from physiology to genetics and back. *Diabetologia*, **2006** , 49, 431-3	10.3	3
66	Genetic control of plasma lipid levels in a cross derived from normoglycaemic Brown Norway and spontaneously diabetic Goto-Kakizaki rats. *Diabetologia*, **2006**, 49, 2679-88	10.3	15
65	Analysis of 14 candidate genes for diabetic nephropathy on chromosome 3q in European populations: strongest evidence for association with a variant in the promoter region of the adiponectin gene. *Diabetes*, **2006**, 55, 3166-74	0.9	67
64	Genetic and environmental effects on complex traits in mice. *Genetics*, **2006**, 174, 959-84	4	134
63	Metabolic profiling reveals a contribution of gut microbiota to fatty liver phenotype in insulin-resistant mice. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 12511-6	11.5	854
62	Glycomics investigation into insulin action. *Biochimica Et Biophysica Acta - General Subjects*, **2006**, 1760, 652-68	4	12
61	Genomic organization of the rat Clock gene and sequence analysis in inbred rat strains. *Genomics*, **2006**, 87, 208-17	4.3	3
60	Genome-wide genetic association of complex traits in heterogeneous stock mice. *Nature Genetics*, **2006**, 38, 879-87	36.3	442
59	A protocol for high-throughput phenotyping, suitable for quantitative trait analysis in mice. *Mammalian Genome*, **2006**, 17, 129-46	3.2	88

58	Mapping diabetes QTL in an intercross derived from a congenic strain of the Brown Norway and Goto-Kakizaki rats. *Mammalian Genome*, **2006**, 17, 538-47	3.2	14
57	Statistical total correlation spectroscopy: an exploratory approach for latent biomarker identification from metabolic 1H NMR data sets. *Analytical Chemistry*, **2005**, 77, 1282-9	7.8	729
56	The genes and gene organization of the Ly49 region of the rat natural killer cell gene complex. *European Journal of Immunology*, **2005**, 35, 261-72	6.1	48
55	The rat as a model physiological system **2005**,		3
54	Characteristics of the aortic elastic network and related phenotypes in seven inbred rat strains. *American Journal of Physiology - Heart and Circulatory Physiology*, **2005**, 288, H769-77	5.2	29
53	Chromosomal mapping of quantitative trait loci controlling elastin content in rat aorta. *Hypertension*, **2005**, 45, 460-6	8.5	18
52	Missense mutation in sterile alpha motif of novel protein SamCystin is associated with polycystic kidney disease in (cy/+) rat. *Journal of the American Society of Nephrology: JASN*, **2005**, 16, 3517-26	12.7	69
51	Quantitative trait locus dissection in congenic strains of the Goto-Kakizaki rat identifies a region conserved with diabetes loci in human chromosome 1q. *Physiological Genomics*, **2004**, 19, 1-10	3.6	20
50	Studies of congenic lines in the Brown Norway rat model of Th2-mediated immunopathological disorders show that the aurothiopropanol sulfonate-induced immunological disorder (Aiid3) locus on chromosome 9 plays a major role compared to Aiid2 on chromosome 10. *Journal of Immunology*, **2004**, 172, 6354-61	5.3	12
49	Transforming growth factor-beta 1 production is correlated with genetically determined ACE expression in congenic rats: a possible link between ACE genotype and diabetic nephropathy. *Diabetes*, **2004**, 53, 1111-8	0.9	14
48	Polymorphisms in type II SH2 domain-containing inositol 5-phosphatase (INPPL1, SHIP2) are associated with physiological abnormalities of the metabolic syndrome. *Diabetes*, **2004**, 53, 1900-4	0.9	72
47	Integration of the rat recombination and EST maps in the rat genomic sequence and comparative mapping analysis with the mouse genome. *Genome Research*, **2004**, 14, 758-65	9.7	22
46	Initial steps of insulin signaling and glucose transport are defective in the type 2 diabetic rat heart. *Cardiovascular Research*, **2004**, 61, 288-96	9.9	100
45	Chromosomal mapping of genetic loci controlling absence epilepsy phenotypes in the WAG/Rij rat. *Epilepsia*, **2004**, 45, 908-15	6.4	44
44	Polygenic control of idiopathic generalized epilepsy phenotypes in the genetic absence rats from Strasbourg (GAERS). *Epilepsia*, **2004**, 45, 301-8	6.4	51
43	Enhanced insulin secretion and cholesterol metabolism in congenic strains of the spontaneously diabetic (Type 2) Goto Kakizaki rat are controlled by independent genetic loci in rat chromosome 8. *Diabetologia*, **2004**, 47, 1096-106	10.3	25
42	Gender differences in hypertrophy, insulin resistance and ischemic injury in the aging type 2 diabetic rat heart. *Journal of Molecular and Cellular Cardiology*, **2004**, 37, 547-55	5.8	64
41	Marker-assisted congenic screening (MACS): a database tool for the efficient production and characterization of congenic lines. *Mammalian Genome*, **2003**, 14, 350-6	3.2	23

40	Genetics and functional genomics of type 2 diabetes mellitus. *Genome Biology*, **2003**, 4, 241	18.3	6
39	Thymectomy and radiation-induced type 1 diabetes in nonlymphopenic BB rats. *Diabetes*, **2002**, 51, 2975-81	6.9	20
38	Characterization of a major modifier locus for polycystic kidney disease (Modpkdr1) in the Han:SPRD(cy/+) rat in a region conserved with a mouse modifier locus for Alport syndrome. *Human Molecular Genetics*, **2002**, 11, 2165-73	5.6	20
37	The gene INPPL1, encoding the lipid phosphatase SHIP2, is a candidate for type 2 diabetes in rat and man. *Diabetes*, **2002**, 51, 2012-7	0.9	113
36	Localization, cDNA sequence and genomic organization of the rat seipin gene (Bscl2) and sequence analysis in inbred rat models of Type 2 diabetes mellitus. *Cytogenetic and Genome Research*, **2002**, 98, 71-4	1.9	2
35	Approaches to the analysis of complex quantitative phenotypes and marker map construction based on the analysis of rat models of hypertension. *Methods in Molecular Biology*, **2002**, 195, 225-51	1.4	2
34	A dominant modifier of transgene methylation is mapped by QTL analysis to mouse chromosome 13. *Genome Research*, **2001**, 11, 382-8	9.7	9
33	Genetic dissection of region around the Sa gene on rat chromosome 1: evidence for multiple loci affecting blood pressure. *Hypertension*, **2001**, 38, 216-21	8.5	54
32	Genetic influences on the end-stage effector phase of arthritis. *Journal of Experimental Medicine*, **2001**, 194, 321-30	16.6	127
31	A high-resolution consensus linkage map of the rat, integrating radiation hybrid and genetic maps. *Genomics*, **2001**, 75, 57-69	4.3	33
30	Applicability of a "speed" congenic strategy to dissect blood pressure quantitative trait loci on rat chromosome 2. *Hypertension*, **2000**, 35, 179-87	8.5	71
29	Rat chromosome 9 bears a major susceptibility locus for IgE response. *European Journal of Immunology*, **2000**, 30, 1698-705	6.1	20
28	Detailed comparative gene map of rat chromosome 1 with mouse and human genomes and physical mapping of an evolutionary chromosomal breakpoint. *Genomics*, **2000**, 64, 32-43	4.3	16
27	Complete genome searches for quantitative trait loci controlling blood pressure and related traits in four segregating populations derived from Dahl hypertensive rats. *Mammalian Genome*, **1999**, 10, 259-65	3.2	55
26	Linkage and physical mapping of rat microsatellites derived from minisatellite loci. *Mammalian Genome*, **1999**, 10, 405-9	3.2	9
25	A gene map of the rat derived from linkage analysis and related regions in the mouse and human genomes. *Mammalian Genome*, **1999**, 10, 675-86	3.2	23
24	Report on rat chromosome 4. *Journal of Experimental Animal Science*, **1999**, 40, 37-46		
23	Localization of tub and uncoupling proteins (Ucp) 2 and 3 to a region of rat chromosome 1 linked to glucose intolerance and adiposity in the Goto-Kakizaki (GK) type 2 diabetic rat. *Mammalian Genome*, **1998**, 9, 910-2	3.2	19

22	Construction and characterization of a 10-fold genome equivalent rat P1-derived artificial chromosome library. *Genomics*, **1998**, 50, 306-16	4.3	70
21	Analysis of distribution in the human, pig, and rat genomes points toward a general subtelomeric origin of minisatellite structures. *Genomics*, **1998**, 52, 62-71	4.3	39
20	Successful isolation of a rat chromosome 1 blood pressure quantitative trait locus in reciprocal congenic strains. *Hypertension*, **1998**, 32, 639-46	8.5	50
19	A gene-based genetic linkage and comparative map of the rat X chromosome. *Genomics*, **1997**, 40, 253-61	4.3	45
18	A linkage map of the rat genome derived from three F2 crosses. *Genome Research*, **1997**, 7, 434-40	9.7	146
17	Sensitivity to cerebral ischaemic insult in a rat model of stroke is determined by a single genetic locus. *Nature Genetics*, **1997**, 16, 364-7	36.3	188
16	Integrated genetic mapping of 64 rat microsatellite markers from different sources. *Mammalian Genome*, **1997**, 8, 282-3	3.2	9
15	A pharmacogenetic approach to blood pressure in Lyon hypertensive rats. A chromosome 2 locus influences the response to a calcium antagonist. *Journal of Clinical Investigation*, **1997**, 100, 2000-6	15.9	27
14	Serum IgE concentration and other immune manifestations of treatment with gold salts are linked to the MHC and IL4 regions in the rat. *Genomics*, **1996**, 31, 111-4	4.3	42
13	A genetic linkage map of the rat derived from recombinant inbred strains. *Mammalian Genome*, **1996**, 7, 117-27	3.2	104
12	Chromosomal mapping of genetic loci associated with non-insulin dependent diabetes in the GK rat. *Nature Genetics*, **1996**, 12, 38-43	36.3	266
11	A major quantitative trait locus influences hyperactivity in the WKHA rat. *Nature Genetics*, **1996**, 14, 471-3	36.3	82
10	Analysis of quantitative trait loci for blood pressure on rat chromosomes 2 and 13. Age-related differences in effect. *Hypertension*, **1996**, 28, 1118-22	8.5	51
9	Two polymorphic dinucleotide repeats in the rat dystrophin gene, including the conserved 3RUTR repeat. *Mammalian Genome*, **1995**, 6, 668-9	3.2	3
8	Dissection of a quantitative trait locus for genetic hypertension on rat chromosome 10. *Proceedings of the National Academy of Sciences of the United States of America*, **1995**, 92, 8778-82	11.5	69
7	Mapping of quantitative trait loci for blood pressure and cardiac mass in the rat by genome scanning of recombinant inbred strains. *Journal of Clinical Investigation*, **1995**, 96, 1973-8	15.9	129
6	Higher maternal than paternal inheritance of diabetes in GK rats. *Diabetes*, **1994**, 43, 220-224	0.9	12
5	Inheritance of diabetes mellitus as consequence of gestational hyperglycemia in rats. *Diabetes*, **1990**, 39, 734-739	0.9	27

4	The Microbial Metabolite 4-Cresol Improves Glucose Homeostasis and Enhances β Cell Function	1
3	Microbiome Determinants and Physiological Effects of the Benzoate-Hippurate Microbial-Host Co-Metabolic Pathway	1
2	Metabolic retroconversion of trimethylamine N-oxide and the gut microbiota	4
1	Microbiome Inhibition of IRAK-4 by Trimethylamine Mediates Metabolic and Immune Benefits in High-Fat-Diet-induced Insulin Resistance	2