

Dominique Gauguier

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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	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015 , 47, 1121-1130	36.3	1290
146	Large-scale association analysis identifies new risk loci for coronary artery disease. <i>Nature Genetics</i> , 2013 , 45, 25-33	36.3	1172
145	Metabolic profiling reveals a contribution of gut microbiota to fatty liver phenotype in insulin-resistant mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 12511-6	11.5	854
144	Statistical total correlation spectroscopy: an exploratory approach for latent biomarker identification from metabolic 1H NMR data sets. <i>Analytical Chemistry</i> , 2005 , 77, 1282-9	7.8	729
143	Genome-wide genetic association of complex traits in heterogeneous stock mice. <i>Nature Genetics</i> , 2006 , 38, 879-87	36.3	442
142	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. <i>Nature</i> , 2015 , 526, 112-7	50.4	308
141	Aryl hydrocarbon receptor nuclear translocator-like (BMAL1) is associated with susceptibility to hypertension and type 2 diabetes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 14412-7	11.5	284
140	Chromosomal mapping of genetic loci associated with non-insulin dependent diabetes in the GK rat. <i>Nature Genetics</i> , 1996 , 12, 38-43	36.3	266
139	Progress and prospects in rat genetics: a community view. <i>Nature Genetics</i> , 2008 , 40, 516-22	36.3	234
138	Global microRNA expression profiles in insulin target tissues in a spontaneous rat model of type 2 diabetes. <i>Diabetologia</i> , 2010 , 53, 1099-109	10.3	227
137	Sensitivity to cerebral ischaemic insult in a rat model of stroke is determined by a single genetic locus. <i>Nature Genetics</i> , 1997 , 16, 364-7	36.3	188
136	SNP and haplotype mapping for genetic analysis in the rat. <i>Nature Genetics</i> , 2008 , 40, 560-6	36.3	150
135	A linkage map of the rat genome derived from three F2 crosses. <i>Genome Research</i> , 1997 , 7, 434-40	9.7	146
134	Genetic and environmental effects on complex traits in mice. <i>Genetics</i> , 2006 , 174, 959-84	4	134
133	Pancreatic ectopic fat is characterized by adipocyte infiltration and altered lipid composition. <i>Obesity</i> , 2008 , 16, 522-30	8	132
132	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
131	Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. <i>Nature Genetics</i> , 2013 , 45, 767-75	36.3	131

130	Mapping of quantitative trait loci for blood pressure and cardiac mass in the rat by genome scanning of recombinant inbred strains. <i>Journal of Clinical Investigation</i> , 1995 , 96, 1973-8	15.9	129
129	Genome sequencing reveals loci under artificial selection that underlie disease phenotypes in the laboratory rat. <i>Cell</i> , 2013 , 154, 691-703	56.2	127
128	Genetic influences on the end-stage effector phase of arthritis. <i>Journal of Experimental Medicine</i> , 2001 , 194, 321-30	16.6	127
127	The gene INPPL1, encoding the lipid phosphatase SHIP2, is a candidate for type 2 diabetes in rat and man. <i>Diabetes</i> , 2002 , 51, 2012-7	0.9	113
126	A genetic linkage map of the rat derived from recombinant inbred strains. <i>Mammalian Genome</i> , 1996 , 7, 117-27	3.2	104
125	Initial steps of insulin signaling and glucose transport are defective in the type 2 diabetic rat heart. <i>Cardiovascular Research</i> , 2004 , 61, 288-96	9.9	100
124	MicroRNA-125a is over-expressed in insulin target tissues in a spontaneous rat model of Type 2 Diabetes. <i>BMC Medical Genomics</i> , 2009 , 2, 54	3.7	96
123	Subtle metabolic and liver gene transcriptional changes underlie diet-induced fatty liver susceptibility in insulin-resistant mice. <i>Diabetologia</i> , 2007 , 50, 1867-1879	10.3	94
122	A protocol for high-throughput phenotyping, suitable for quantitative trait analysis in mice. <i>Mammalian Genome</i> , 2006 , 17, 129-46	3.2	88
121	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. <i>Journal of the American College of Cardiology</i> , 2019 , 73, 58-66	15.1	86
120	Implication of gut microbiota metabolites in cardiovascular and metabolic diseases. <i>Cellular and Molecular Life Sciences</i> , 2018 , 75, 3977-3990	10.3	84
119	Phylometabonomic patterns of adaptation to high fat diet feeding in inbred mice. <i>PLoS ONE</i> , 2008 , 3, e1668	3.7	83
118	Metabolic retroconversion of trimethylamine N-oxide and the gut microbiota. <i>Microbiome</i> , 2018 , 6, 73	16.6	82
117	A major quantitative trait locus influences hyperactivity in the WKHA rat. <i>Nature Genetics</i> , 1996 , 14, 471-36.3	36.3	82
116	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
115	Applicability of a "speed" congenic strategy to dissect blood pressure quantitative trait loci on rat chromosome 2. <i>Hypertension</i> , 2000 , 35, 179-87	8.5	71
114	Construction and characterization of a 10-fold genome equivalent rat P1-derived artificial chromosome library. <i>Genomics</i> , 1998 , 50, 306-16	4.3	70
113	Missense mutation in sterile alpha motif of novel protein SamCystin is associated with polycystic kidney disease in (cy/+) rat. <i>Journal of the American Society of Nephrology: JASN</i> , 2005 , 16, 3517-26	12.7	69

112	Dissection of a quantitative trait locus for genetic hypertension on rat chromosome 10. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995 , 92, 8778-82	11.5	69
111	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. <i>Diabetes</i> , 2006 , 55, 3166-74	0.9	67
110	Gender differences in hypertrophy, insulin resistance and ischemic injury in the aging type 2 diabetic rat heart. <i>Journal of Molecular and Cellular Cardiology</i> , 2004 , 37, 547-55	5.8	64
109	Large scale association analysis identifies three susceptibility loci for coronary artery disease. <i>PLoS ONE</i> , 2011 , 6, e29427	3.7	63
108	A resource for the simultaneous high-resolution mapping of multiple quantitative trait loci in rats: the NIH heterogeneous stock. <i>Genome Research</i> , 2009 , 19, 150-8	9.7	63
107	Genome-wide diversity in the levant reveals recent structuring by culture. <i>PLoS Genetics</i> , 2013 , 9, e1003316	3.6	59
106	Microbial-Host Co-metabolites Are Prodromal Markers Predicting Phenotypic Heterogeneity in Behavior, Obesity, and Impaired Glucose Tolerance. <i>Cell Reports</i> , 2017 , 20, 136-148	10.6	57
105	Progression of diet-induced diabetes in C57BL6J mice involves functional dissociation of Ca ²⁺ (+) channels from secretory vesicles. <i>Diabetes</i> , 2010 , 59, 1192-201	0.9	57
104	Association between angiotensin-converting enzyme gene polymorphisms and diabetic nephropathy: case-control, haplotype, and family-based study in three European populations. <i>Journal of the American Society of Nephrology: JASN</i> , 2007 , 18, 1284-91	12.7	57
103	Homology-directed repair in rodent zygotes using Cas9 and TALEN engineered proteins. <i>Scientific Reports</i> , 2015 , 5, 14410	4.9	56
102	Complete genome searches for quantitative trait loci controlling blood pressure and related traits in four segregating populations derived from Dahl hypertensive rats. <i>Mammalian Genome</i> , 1999 , 10, 259-65	3.2	55
101	Genetic dissection of region around the Sa gene on rat chromosome 1: evidence for multiple loci affecting blood pressure. <i>Hypertension</i> , 2001 , 38, 216-21	8.5	54
100	Plaque burden in HIV-infected patients is associated with serum intestinal microbiota-generated trimethylamine. <i>Aids</i> , 2015 , 29, 443-52	3.5	52
99	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
98	Analysis of quantitative trait loci for blood pressure on rat chromosomes 2 and 13. Age-related differences in effect. <i>Hypertension</i> , 1996 , 28, 1118-22	8.5	51
97	Successful isolation of a rat chromosome 1 blood pressure quantitative trait locus in reciprocal congenic strains. <i>Hypertension</i> , 1998 , 32, 639-46	8.5	50
96	The genes and gene organization of the Ly49 region of the rat natural killer cell gene complex. <i>European Journal of Immunology</i> , 2005 , 35, 261-72	6.1	48
95	A gene-based genetic linkage and comparative map of the rat X chromosome. <i>Genomics</i> , 1997 , 40, 253-61.3	4.3	45

94	Chromosomal mapping of genetic loci controlling absence epilepsy phenotypes in the WAG/Rij rat. <i>Epilepsia</i> , 2004 , 45, 908-15	6.4	44
93	Serum IgE concentration and other immune manifestations of treatment with gold salts are linked to the MHC and IL4 regions in the rat. <i>Genomics</i> , 1996 , 31, 111-4	4.3	42
92	Analysis of distribution in the human, pig, and rat genomes points toward a general subtelomeric origin of minisatellite structures. <i>Genomics</i> , 1998 , 52, 62-71	4.3	39
91	Genome-wide association study in a Lebanese cohort confirms PHACTR1 as a major determinant of coronary artery stenosis. <i>PLoS ONE</i> , 2012 , 7, e38663	3.7	38
90	Loss of Cardioprotective Effects at the Locus as a Result of Gene-Smoking Interactions. <i>Circulation</i> , 2017 , 135, 2336-2353	16.7	36
89	G/T substitution in intron 1 of the UNC13B gene is associated with increased risk of nephropathy in patients with type 1 diabetes. <i>Diabetes</i> , 2008 , 57, 2843-50	0.9	33
88	A high-resolution consensus linkage map of the rat, integrating radiation hybrid and genetic maps. <i>Genomics</i> , 2001 , 75, 57-69	4.3	33
87	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
86	Characteristics of the aortic elastic network and related phenotypes in seven inbred rat strains. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2005 , 288, H769-77	5.2	29
85	European rational approach for the genetics of diabetic complications--EURAGEDIC: patient populations and strategy. <i>Nephrology Dialysis Transplantation</i> , 2008 , 23, 161-8	4.3	27
84	A pharmacogenetic approach to blood pressure in Lyon hypertensive rats. A chromosome 2 locus influences the response to a calcium antagonist. <i>Journal of Clinical Investigation</i> , 1997 , 100, 2000-6	15.9	27
83	Inheritance of diabetes mellitus as consequence of gestational hyperglycemia in rats. <i>Diabetes</i> , 1990 , 39, 734-739	0.9	27
82	Integration of the human exposome with the human genome to advance medicine. <i>Biochimie</i> , 2018 , 152, 155-158	4.6	25
81	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. <i>Diabetologia</i> , 2004 , 47, 1096-106	10.3	25
80	mQTL.NMR: an integrated suite for genetic mapping of quantitative variations of (1)H NMR-based metabolic profiles. <i>Analytical Chemistry</i> , 2015 , 87, 4377-84	7.8	24
79	Untargeted metabolome quantitative trait locus mapping associates variation in urine glycerate to mutant glycerate kinase. <i>Journal of Proteome Research</i> , 2012 , 11, 631-42	5.6	23
78	Marker-assisted congenic screening (MACS): a database tool for the efficient production and characterization of congenic lines. <i>Mammalian Genome</i> , 2003 , 14, 350-6	3.2	23
77	A gene map of the rat derived from linkage analysis and related regions in the mouse and human genomes. <i>Mammalian Genome</i> , 1999 , 10, 675-86	3.2	23

76	T2DM GWAS in the Lebanese population confirms the role of TCF7L2 and CDKAL1 in disease susceptibility. <i>Scientific Reports</i> , 2014 , 4, 7351	4.9	22
75	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
74	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
73	Biological roles of microRNAs in the control of insulin secretion and action. <i>Physiological Genomics</i> , 2017 , 49, 1-10	3.6	21
72	Genetic and environmental influences on total plasma homocysteine and its role in coronary artery disease risk. <i>Atherosclerosis</i> , 2012 , 222, 180-6	3.1	21
71	Quantitative trait locus dissection in congenic strains of the Goto-Kakizaki rat identifies a region conserved with diabetes loci in human chromosome 1q. <i>Physiological Genomics</i> , 2004 , 19, 1-10	3.6	20
70	Thymectomy and radiation-induced type 1 diabetes in nonlymphopenic BB rats. <i>Diabetes</i> , 2002 , 51, 2975-81	5.8	20
69	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. <i>Human Molecular Genetics</i> , 2002 , 11, 2165-73	5.6	20
68	Rat chromosome 9 bears a major susceptibility locus for IgE response. <i>European Journal of Immunology</i> , 2000 , 30, 1698-705	6.1	20
67	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. <i>Mammalian Genome</i> , 1998 , 9, 910-2	3.2	19
66	The Natural Metabolite 4-Cresol Improves Glucose Homeostasis and Enhances ECell Function. <i>Cell Reports</i> , 2020 , 30, 2306-2320.e5	10.6	18
65	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. <i>Scientific Reports</i> , 2016 , 6, 35278	4.9	18
64	Chromosomal mapping of quantitative trait loci controlling elastin content in rat aorta. <i>Hypertension</i> , 2005 , 45, 460-6	8.5	18
63	Dominant gut <i>Prevotella copri</i> in gastrectomised non-obese diabetic Goto-Kakizaki rats improves glucose homeostasis through enhanced FXR signalling. <i>Diabetologia</i> , 2020 , 63, 1223-1235	10.3	17
62	Broad-ranging natural metabotype variation drives physiological plasticity in healthy control inbred rat strains. <i>Journal of Proteome Research</i> , 2011 , 10, 1675-89	5.6	17
61	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
60	Detailed comparative gene map of rat chromosome 1 with mouse and human genomes and physical mapping of an evolutionary chromosomal breakpoint. <i>Genomics</i> , 2000 , 64, 32-43	4.3	16
59	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

58	Genetic control of plasma lipid levels in a cross derived from normoglycaemic Brown Norway and spontaneously diabetic Goto-Kakizaki rats. <i>Diabetologia</i> , 2006 , 49, 2679-88	10.3	15
57	Regenerating 1 and 3b gene expression in the pancreas of type 2 diabetic Goto-Kakizaki (GK) rats. <i>PLoS ONE</i> , 2014 , 9, e90045	3.7	15
56	Protease inhibitor 15, a candidate gene for abdominal aortic internal elastic lamina ruptures in the rat. <i>Physiological Genomics</i> , 2014 , 46, 418-28	3.6	14
55	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
54	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. <i>Diabetes</i> , 2004 , 53, 1111-8	0.9	14
53	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
52	Caffeine Impact on Metabolic Syndrome Components Is Modulated by a CYP1A2 Variant. <i>Annals of Nutrition and Metabolism</i> , 2016 , 68, 1-11	4.5	14
51	MWASTools: an R/bioconductor package for metabolome-wide association studies. <i>Bioinformatics</i> , 2018 , 34, 890-892	7.2	13
50	J-Resolved H NMR 1D-Projections for Large-Scale Metabolic Phenotyping Studies: Application to Blood Plasma Analysis. <i>Analytical Chemistry</i> , 2017 , 89, 11405-11412	7.8	13
49	Genetic association analysis of inositol polyphosphate phosphatase-like 1 (INPPL1, SHIP2) variants with essential hypertension. <i>Journal of Medical Genetics</i> , 2007 , 44, 603-5	5.8	13
48	Human and preclinical studies of the host-gut microbiome co-metabolite hippurate as a marker and mediator of metabolic health. <i>Gut</i> , 2021 , 70, 2105-2114	19.2	13
47	Molecular genetics of the transcription factor GLIS3 identifies its dual function in beta cells and neurons. <i>Genomics</i> , 2018 , 110, 98-111	4.3	12
46	Glycomics investigation into insulin action. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2006 , 1760, 652-68	4	12
45	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. <i>Journal of Immunology</i> , 2004 , 172, 6354-61	5.3	12
44	Untargeted Mass Spectrometry Lipidomics identifies correlation between serum sphingomyelins and plasma cholesterol. <i>Lipids in Health and Disease</i> , 2019 , 18, 38	4.4	12
43	Higher maternal than paternal inheritance of diabetes in GK rats. <i>Diabetes</i> , 1994 , 43, 220-224	0.9	12
42	The SAM domain of ANKS6 has different interacting partners and mutations can induce different cystic phenotypes. <i>Kidney International</i> , 2015 , 88, 299-310	9.9	11
41	A multiplexed targeted assay for high-throughput quantitative analysis of serum methylamines by ultra performance liquid chromatography coupled to high resolution mass spectrometry. <i>Archives of Biochemistry and Biophysics</i> , 2016 , 597, 12-20	4.1	11

40	Circulating lipid levels and risk of coronary artery disease in a large group of patients undergoing coronary angiography. <i>Journal of Thrombosis and Thrombolysis</i> , 2015 , 39, 15-22	5.1	10
39	Application of quantitative metabolomics in systems genetics in rodent models of complex phenotypes. <i>Archives of Biochemistry and Biophysics</i> , 2016 , 589, 158-67	4.1	10
38	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
37	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
36	ANKS3 Co-Localises with ANKS6 in Mouse Renal Cilia and Is Associated with Vasopressin Signaling and Apoptosis In Vivo in Mice. <i>PLoS ONE</i> , 2015 , 10, e0136781	3.7	9
35	Integrated genetic mapping of 64 rat microsatellite markers from different sources. <i>Mammalian Genome</i> , 1997 , 8, 282-3	3.2	9
34	A dominant modifier of transgene methylation is mapped by QTL analysis to mouse chromosome 13. <i>Genome Research</i> , 2001 , 11, 382-8	9.7	9
33	Linkage and physical mapping of rat microsatellites derived from minisatellite loci. <i>Mammalian Genome</i> , 1999 , 10, 405-9	3.2	9
32	MetaboSignal: a network-based approach for topological analysis of metabotype regulation via metabolic and signaling pathways. <i>Bioinformatics</i> , 2017 , 33, 773-775	7.2	9
31	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
30	Genomic regulation of type 2 diabetes endophenotypes: Contribution from genetic studies in the Goto-Kakizaki rat. <i>Biochimie</i> , 2017 , 143, 56-65	4.6	7
29	Genetics and functional genomics of type 2 diabetes mellitus. <i>Genome Biology</i> , 2003 , 4, 241	18.3	6
28	pJRES Binning Algorithm (JBA): a new method to facilitate the recovery of metabolic information from pJRES 1H NMR spectra. <i>Bioinformatics</i> , 2019 , 35, 1916-1922	7.2	6
27	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
26	Association of hypertension with coronary artery disease onset in the Lebanese population. <i>SpringerPlus</i> , 2014 , 3, 533		5
25	Genetic control of differential acetylation in diabetic rats. <i>PLoS ONE</i> , 2014 , 9, e94555	3.7	4
24	Metabolic retroconversion of trimethylamine N-oxide and the gut microbiota		4
23	Microbiome and metabolome features of the cardiometabolic disease spectrum.. <i>Nature Medicine</i> , 2022 ,	50.5	4

22	Diabetes quantitative trait locus research: from physiology to genetics and back. <i>Diabetologia</i> , 2006 , 49, 431-3	10.3	3
21	Genomic organization of the rat Clock gene and sequence analysis in inbred rat strains. <i>Genomics</i> , 2006 , 87, 208-17	4.3	3
20	The rat as a model physiological system 2005 ,		3
19	Two polymorphic dinucleotide repeats in the rat dystrophin gene, including the conserved 3RUTR repeat. <i>Mammalian Genome</i> , 1995 , 6, 668-9	3.2	3
18	Plasma and urine metabolomic analyses in aortic valve stenosis reveal shared and biofluid-specific changes in metabolite levels. <i>PLoS ONE</i> , 2020 , 15, e0242019	3.7	3
17	Conserved properties of genetic architecture of renal and fat transcriptomes in rat models of insulin resistance. <i>DMM Disease Models and Mechanisms</i> , 2019 , 12,	4.1	2
16	Localization, cDNA sequence and genomic organization of the rat seipin gene (Bscl2) and sequence analysis in inbred rat models of Type 2 diabetes mellitus. <i>Cytogenetic and Genome Research</i> , 2002 , 98, 71-4	1.9	2
15	Approaches to the analysis of complex quantitative phenotypes and marker map construction based on the analysis of rat models of hypertension. <i>Methods in Molecular Biology</i> , 2002 , 195, 225-51	1.4	2
14	Microbiome Inhibition of IRAK-4 by Trimethylamine Mediates Metabolic and Immune Benefits in High-Fat-Diet-induced Insulin Resistance		2
13	Genomic organization and mutation screening of the human ortholog of Pkdr1 associated with polycystic kidney disease in the rat. <i>European Journal of Medical Genetics</i> , 2008 , 51, 325-31	2.6	1
12	Association of coronary artery disease and chronic kidney disease in Lebanese population. <i>International Journal of Clinical and Experimental Medicine</i> , 2015 , 8, 15866-77		1
11	The Microbial Metabolite 4-Cresol Improves Glucose Homeostasis and Enhances ECell Function		1
10	Microbiome Determinants and Physiological Effects of the Benzoate-Hippurate Microbial-Host Co-Metabolic Pathway		1
9	Mapping Metabolomic Quantitative Trait Loci (mQTL): A Link Between Metabolome-Wide Association Studies and Systems Biology 2012 , 233-254		1
8	Diet dependent impact of benzoate on diabetes and obesity in mice.. <i>Biochimie</i> , 2021 , 194, 35-35	4.6	0
7	Report on rat chromosome 4. <i>Journal of Experimental Animal Science</i> , 1999 , 40, 37-46		
6	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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