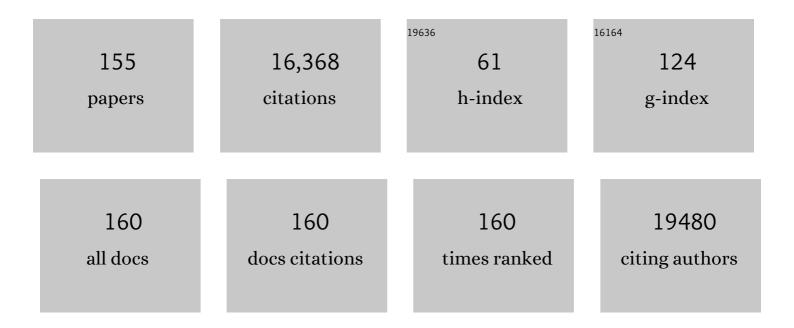
Charlotte Ling

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7462150/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	From The Cover: Epigenetic differences arise during the lifetime of monozygotic twins. Proceedings of the United States of America, 2005, 102, 10604-10609.	3.3	3,169
2	Mechanisms by which common variants in the TCF7L2 gene increase risk of type 2 diabetes. Journal of Clinical Investigation, 2007, 117, 2155-2163.	3.9	683
3	Epigenetics: A Molecular Link Between Environmental Factors and Type 2 Diabetes. Diabetes, 2009, 58, 2718-2725.	0.3	521
4	Epigenetics in Human Obesity and Type 2 Diabetes. Cell Metabolism, 2019, 29, 1028-1044.	7.2	513
5	A Six Months Exercise Intervention Influences the Genome-wide DNA Methylation Pattern in Human Adipose Tissue. PLoS Genetics, 2013, 9, e1003572.	1.5	502
6	Epigenetic regulation of PPARGC1A in human type 2 diabetic islets and effect on insulin secretion. Diabetologia, 2008, 51, 615-622.	2.9	421
7	Genome-Wide DNA Methylation Analysis of Human Pancreatic Islets from Type 2 Diabetic and Non-Diabetic Donors Identifies Candidate Genes That Influence Insulin Secretion. PLoS Genetics, 2014, 10, e1004160.	1.5	408
8	β-Cell Failure in Type 2 Diabetes: Postulated Mechanisms and Prospects for Prevention and Treatment. Diabetes Care, 2014, 37, 1751-1758.	4.3	379
9	Impact of an Exercise Intervention on DNA Methylation in Skeletal Muscle From First-Degree Relatives of Patients With Type 2 Diabetes. Diabetes, 2012, 61, 3322-3332.	0.3	334
10	Altered DNA Methylation and Differential Expression of Genes Influencing Metabolism and Inflammation in Adipose Tissue From Subjects With Type 2 Diabetes. Diabetes, 2014, 63, 2962-2976.	0.3	326
11	Maternal diet and aging alter the epigenetic control of a promoter–enhancer interaction at the <i>Hnf4a</i> gene in rat pancreatic islets. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5449-5454.	3.3	311
12	Increased DNA Methylation and Decreased Expression of PDX-1 in Pancreatic Islets from Patients with Type 2 Diabetes. Molecular Endocrinology, 2012, 26, 1203-1212.	3.7	256
13	Multiple environmental and genetic factors influence skeletal muscle PGC-1α and PGC-1Î ² gene expression in twins. Journal of Clinical Investigation, 2004, 114, 1518-1526.	3.9	251
14	Impact of age, BMI and HbA1c levels on the genome-wide DNA methylation and mRNA expression patterns in human adipose tissue and identification of epigenetic biomarkers in blood. Human Molecular Genetics, 2015, 24, 3792-813.	1.4	223
15	Insulin promoter DNA methylation correlates negatively with insulin gene expression and positively with HbA1c levels in human pancreatic islets. Diabetologia, 2011, 54, 360-367.	2.9	219
16	Blood-based biomarkers of age-associated epigenetic changes in human islets associate with insulin secretion and diabetes. Nature Communications, 2016, 7, 11089.	5.8	201
17	Sex differences in the genome-wide DNA methylation pattern and impact on gene expression, microRNA levels and insulin secretion in human pancreatic islets. Genome Biology, 2014, 15, 522.	3.8	195
18	Effects of short-term high-fat overfeeding on genome-wide DNA methylation in the skeletal muscle of healthy young men. Diabetologia, 2012, 55, 3341-3349.	2.9	179

#	Article	IF	CITATIONS
19	Deoxyribonucleic Acid Methylation and Gene Expression of PPARGC1A in Human Muscle Is Influenced by High-Fat Overfeeding in a Birth-Weight-Dependent Manner. Journal of Clinical Endocrinology and Metabolism, 2010, 95, 3048-3056.	1.8	172
20	β-Cell Failure in Type 2 Diabetes: Postulated Mechanisms and Prospects for Prevention and Treatment. Journal of Clinical Endocrinology and Metabolism, 2014, 99, 1983-1992.	1.8	171
21	Genetic and epigenetic factors are associated with expression of respiratory chain component NDUFB6 in human skeletal muscle. Journal of Clinical Investigation, 2007, 117, 3427-3435.	3.9	168
22	Identification of CpG-SNPs associated with type 2 diabetes and differential DNA methylation in human pancreatic islets. Diabetologia, 2013, 56, 1036-1046.	2.9	166
23	Age influences DNA methylation and gene expression of COX7A1 in human skeletal muscle. Diabetologia, 2008, 51, 1159-1168.	2.9	164
24	A Central Role for GRB10 in Regulation of Islet Function in Man. PLoS Genetics, 2014, 10, e1004235.	1.5	164
25	Prolactin and growth hormone regulate adiponectin secretion and receptor expression in adipose tissue. Biochemical and Biophysical Research Communications, 2005, 331, 1120-1126.	1.0	162
26	DNA methylation of loci within <i>ABCG1 </i> and <i>PHOSPHO1 </i> in blood DNA is associated with future type 2 diabetes risk. Epigenetics, 2016, 11, 482-488.	1.3	152
27	Genome-Wide Associations between Genetic and Epigenetic Variation Influence mRNA Expression and Insulin Secretion in Human Pancreatic Islets. PLoS Genetics, 2014, 10, e1004735.	1.5	151
28	Epigenetic Alterations in Human Liver From Subjects With Type 2 Diabetes in Parallel With Reduced Folate Levels. Journal of Clinical Endocrinology and Metabolism, 2015, 100, E1491-E1501.	1.8	150
29	DNA methylation in the pathogenesis of type 2 diabetes in humans. Molecular Metabolism, 2018, 14, 12-25.	3.0	148
30	Impact of polyunsaturated and saturated fat overfeeding on the DNA-methylation pattern in human adipose tissue: a randomized controlled trial1–3. American Journal of Clinical Nutrition, 2017, 105, 991-1000.	2.2	127
31	Identification of Functional Prolactin (PRL) Receptor Gene Expression: PRL Inhibits Lipoprotein Lipase Activity in Human White Adipose Tissue. Journal of Clinical Endocrinology and Metabolism, 2003, 88, 1804-1808.	1.8	123
32	Effects of palmitate on genome-wide mRNA expression and DNA methylation patterns in human pancreatic islets. BMC Medicine, 2014, 12, 103.	2.3	123
33	Whole-Genome Bisulfite Sequencing of Human Pancreatic Islets Reveals Novel Differentially Methylated Regions in Type 2 Diabetes Pathogenesis. Diabetes, 2017, 66, 1074-1085.	0.3	122
34	Mitochondrial dysfunction in pancreatic β-cells in Type 2 Diabetes. Molecular and Cellular Endocrinology, 2009, 297, 34-40.	1.6	115
35	Genome-wide analysis of DNA methylation in subjects with type 1 diabetes identifies epigenetic modifications associated with proliferative diabetic retinopathy. BMC Medicine, 2015, 13, 182.	2.3	112
36	Reduced insulin secretion correlates with decreased expression of exocytotic genes in pancreatic islets from patients with type 2 diabetes. Molecular and Cellular Endocrinology, 2012, 364, 36-45.	1.6	111

#	Article	IF	CITATIONS
37	Investigation of Type 2 Diabetes Risk Alleles Support CDKN2A/B, CDKAL1, and TCF7L2 As Susceptibility Genes in a Han Chinese Cohort. PLoS ONE, 2010, 5, e9153.	1.1	109
38	A common variant in MTNR1B, encoding melatonin receptor 1B, is associated with type 2 diabetes and fasting plasma glucose in Han Chinese individuals. Diabetologia, 2009, 52, 830-833.	2.9	103
39	Tight Coupling between Glucose and Mitochondrial Metabolism in Clonal β-Cells Is Required for Robust Insulin Secretion. Journal of Biological Chemistry, 2009, 284, 32395-32404.	1.6	97
40	Dnmt3a is an epigenetic mediator of adipose insulin resistance. ELife, 2017, 6, .	2.8	97
41	NIH working group report—using genomic information to guide weight management: From universal to precision treatment. Obesity, 2016, 24, 14-22.	1.5	96
42	Helsinki alert of biodiversity and health. Annals of Medicine, 2015, 47, 218-225.	1.5	95
43	Regulation and Function of <i>FTO</i> mRNA Expression in Human Skeletal Muscle and Subcutaneous Adipose Tissue. Diabetes, 2009, 58, 2402-2408.	0.3	94
44	Epigenetic and Transcriptional Alterations in Human Adipose Tissue of Polycystic Ovary Syndrome. Scientific Reports, 2016, 6, 22883.	1.6	93
45	Epigenetic adaptation to regular exercise in humans. Drug Discovery Today, 2014, 19, 1015-1018.	3.2	89
46	A Genome-Wide mQTL Analysis in Human Adipose Tissue Identifies Genetic Variants Associated with DNA Methylation, Gene Expression and Metabolic Traits. PLoS ONE, 2016, 11, e0157776.	1.1	88
47	DNA methylation of the glucagon-like peptide 1 receptor (GLP1R) in human pancreatic islets. BMC Medical Genetics, 2013, 14, 76.	2.1	86
48	The fat cell epigenetic signature in post-obese women is characterized by global hypomethylation and differential DNA methylation of adipogenesis genes. International Journal of Obesity, 2015, 39, 910-919.	1.6	85
49	Regulation of core clock genes in human islets. Metabolism: Clinical and Experimental, 2012, 61, 978-985.	1.5	84
50	Genome-wide DNA promoter methylation and transcriptome analysis in human adipose tissue unravels novel candidate genes for obesity. Molecular Metabolism, 2017, 6, 86-100.	3.0	84
51	Prolactin (PRL) Receptor Gene Expression in Mouse Adipose Tissue: Increases during Lactation and in PRL-Transgenic Mice1. Endocrinology, 2000, 141, 3564-3572.	1.4	83
52	DNA methylation as a diagnostic and therapeutic target in the battle against Type 2 diabetes. Epigenomics, 2015, 7, 451-460.	1.0	83
53	Gestational diabetes and maternal obesity are associated with epigenome-wide methylation changes in children. JCl Insight, 2018, 3, .	2.3	83
54	A Common Variant in TFB1M Is Associated with Reduced Insulin Secretion and Increased Future Risk of Type 2 Diabetes. Cell Metabolism, 2011, 13, 80-91.	7.2	81

#	Article	IF	CITATIONS
55	Epigenome-Wide Association Study of Incident Type 2 Diabetes in a British Population: EPIC-Norfolk Study. Diabetes, 2019, 68, 2315-2326.	0.3	77
56	HDAC7 is overexpressed in human diabetic islets and impairs insulin secretion in rat islets and clonal beta cells. Diabetologia, 2017, 60, 116-125.	2.9	75
57	The effects of high glucose exposure on global gene expression and DNA methylation in human pancreatic islets. Molecular and Cellular Endocrinology, 2018, 472, 57-67.	1.6	72
58	Nesfatin-1 stimulates glucagon and insulin secretion and beta cell NUCB2 is reduced in human type 2 diabetic subjects. Cell and Tissue Research, 2011, 346, 393-405.	1.5	68
59	Young men with low birthweight exhibit decreased plasticity of genome-wide muscle DNA methylation by high-fat overfeeding. Diabetologia, 2014, 57, 1154-1158.	2.9	67
60	Coordinate Changes in Histone Modifications, mRNA Levels, and Metabolite Profiles in Clonal INS-1 832/13 β-Cells Accompany Functional Adaptations to Lipotoxicity. Journal of Biological Chemistry, 2013, 288, 11973-11987.	1.6	66
61	Transcriptional and Epigenetic Changes Influencing Skeletal Muscle Metabolism in Women With Polycystic Ovary Syndrome. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 4465-4477.	1.8	66
62	Decreased expression of genes involved in oxidative phosphorylation in human pancreatic islets from patients with type 2 diabetes. European Journal of Endocrinology, 2011, 165, 589-595.	1.9	64
63	Adipose tissue transcriptomics and epigenomics in low birthweight men and controls: role of high-fat overfeeding. Diabetologia, 2016, 59, 799-812.	2.9	64
64	Short-Term Exercise Training Does Not Stimulate Skeletal Muscle ATP Synthesis in Relatives of Humans With Type 2 Diabetes. Diabetes, 2009, 58, 1333-1341.	0.3	62
65	Extensive changes in the transcriptional profile of human adipose tissue including genes involved in oxidative phosphorylation after a 6â€month exercise intervention. Acta Physiologica, 2014, 211, 188-200.	1.8	62
66	Enhanced mitochondrial metabolism may account for the adaptation to insulin resistance in islets from C57BL/6J mice fed a high-fat diet. Diabetologia, 2006, 50, 74-83.	2.9	61
67	Hepatic <i>DPP4</i> DNA Methylation Associates With Fatty Liver. Diabetes, 2017, 66, 25-35.	0.3	59
68	Genetic variation in the GCKR gene is associated with non-alcoholic fatty liver disease in Chinese people. Molecular Biology Reports, 2011, 38, 1145-1150.	1.0	56
69	Osteocalcin, glucose metabolism, lipid profile and chronic lowâ€grade inflammation in middleâ€aged and elderly Chinese. Diabetic Medicine, 2013, 30, 309-317.	1.2	56
70	PRL Receptor-Mediated Effects in Female Mouse Adipocytes: PRL Induces Suppressors of Cytokine Signaling Expression and Suppresses Insulin-Induced Leptin Production in Adipocytes in Vitro. Endocrinology, 2001, 142, 4880-4890.	1.4	52
71	Sex influences DNA methylation and gene expression in human skeletal muscle myoblasts and myotubes. Stem Cell Research and Therapy, 2019, 10, 26.	2.4	52
72	Abnormal epigenetic changes during differentiation of human skeletal muscle stem cells from obese subjects. BMC Medicine, 2017, 15, 39.	2.3	51

#	Article	IF	CITATIONS
73	ATAC-seq reveals alterations in open chromatin in pancreatic islets from subjects with type 2 diabetes. Scientific Reports, 2019, 9, 7785.	1.6	51
74	Human liver epigenetic alterations in non-alcoholic steatohepatitis are related to insulin action. Epigenetics, 2017, 12, 287-295.	1.3	50
75	Epigenetic regulation of insulin action and secretion – role in the pathogenesis of type 2 diabetes. Journal of Internal Medicine, 2020, 288, 158-167.	2.7	50
76	Epigenetics and obesity: the devil is in the details. BMC Medicine, 2010, 8, 88.	2.3	49
77	36Âh fasting of young men influences adipose tissue DNA methylation of LEP and ADIPOQ in a birth weight-dependent manner. Clinical Epigenetics, 2017, 9, 40.	1.8	48
78	Epigenetic alterations in blood mirror age-associated DNA methylation and gene expression changes in human liver. Epigenomics, 2017, 9, 105-122.	1.0	48
79	Developmental programming: Stateâ€ofâ€theâ€science and future directions–Summary from a Pennington Biomedical symposium. Obesity, 2016, 24, 1018-1026.	1.5	47
80	DNA methylation links genetics, fetal environment, and an unhealthy lifestyle to the development of type 2 diabetes. Clinical Epigenetics, 2017, 9, 105.	1.8	47
81	Diabetes medication associates with DNA methylation of metformin transporter genes in the human liver. Clinical Epigenetics, 2017, 9, 102.	1.8	46
82	Increased resistin expression in the adipose tissue of male prolactin transgenic mice and in male mice with elevated androgen levels. FEBS Letters, 2001, 507, 147-150.	1.3	42
83	Sex Differences in the Methylome and Transcriptome of the Human Liver and Circulating HDL-Cholesterol Levels. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 4395-4408.	1.8	42
84	Interaction between hormone-sensitive lipase and ChREBP in fat cells controls insulin sensitivity. Nature Metabolism, 2019, 1, 133-146.	5.1	42
85	A Single Bout of Electroacupuncture Remodels Epigenetic and Transcriptional Changes in Adipose Tissue in Polycystic Ovary Syndrome. Scientific Reports, 2018, 8, 1878.	1.6	40
86	A Syntenic Cross Species Aneuploidy Genetic Screen Links RCAN1 Expression to β-Cell Mitochondrial Dysfunction in Type 2 Diabetes. PLoS Genetics, 2016, 12, e1006033.	1.5	39
87	The SNARE Protein SNAP23 and the SNARE-Interacting Protein Munc18c in Human Skeletal Muscle Are Implicated in Insulin Resistance/Type 2 Diabetes. Diabetes, 2010, 59, 1870-1878.	0.3	38
88	Epigenetic programming of adipose-derived stem cells in low birthweight individuals. Diabetologia, 2016, 59, 2664-2673.	2.9	36
89	PPARG gene Pro12Ala variant contributes to the development of non-alcoholic fatty liver in middle-aged and older Chinese population. Molecular and Cellular Endocrinology, 2012, 348, 255-259.	1.6	35
90	Epigenetic markers associated with metformin response and intolerance in drug-naÃ ⁻ ve patients with type 2 diabetes. Science Translational Medicine, 2020, 12, .	5.8	34

#	Article	IF	CITATIONS
91	Differences in Prolactin Receptor (PRLR) in Mouse and Human Fallopian Tubes: Evidence for Multiple Regulatory Mechanisms Controlling PRLR Isoform Expression in Mice1. Biology of Reproduction, 2008, 79, 748-757.	1.2	33
92	Epigenetics of type 2 diabetes mellitus and weight change — a tool for precision medicine?. Nature Reviews Endocrinology, 2022, 18, 433-448.	4.3	33
93	Progressive prostate hyperplasia in adult prolactin transgenic mice is not dependent on elevated serum androgen levels. Prostate, 2002, 53, 24-33.	1.2	32
94	Scavenger Receptor Class B Type I in the Rat Ovary: Possible Role in High Density Lipoprotein Cholesterol Uptake and in the Recognition of Apoptotic Granulosa Cells*. Endocrinology, 1999, 140, 2494-2500.	1.4	31
95	The Potential Use of DNA Methylation Biomarkers to Identify Risk and Progression of Type 2 Diabetes. Frontiers in Endocrinology, 2015, 6, 43.	1.5	31
96	Does epigenetic dysregulation of pancreatic islets contribute to impaired insulin secretion and type 2 diabetes?. Biochemistry and Cell Biology, 2015, 93, 511-521.	0.9	31
97	Genetic and Nongenetic Regulation of CAPN10 mRNA Expression in Skeletal Muscle. Diabetes, 2005, 54, 3015-3020.	0.3	30
98	Effect of exercise on DNA methylation and metabolism in human adipose tissue and skeletal muscle. Epigenomics, 2013, 5, 603-605.	1.0	30
99	Glucolipotoxicity Alters Insulin Secretion via Epigenetic Changes in Human Islets. Diabetes, 2019, 68, 1965-1974.	0.3	30
100	Prolactin Suppresses Malonyl-CoA Concentration in Human Adipose Tissue. Hormone and Metabolic Research, 2009, 41, 747-751.	0.7	29
101	Does DNA Methylation of PPARGC1A Influence Insulin Action in First Degree Relatives of Patients with Type 2 Diabetes?. PLoS ONE, 2013, 8, e58384.	1.1	29
102	Molecular correlates for maximal oxygen uptake and type 1 fibers. American Journal of Physiology - Endocrinology and Metabolism, 2008, 294, E1152-E1159.	1.8	28
103	MC1568 improves insulin secretion in islets from type 2 diabetes patients and rescues β-cell dysfunction caused by Hdac7 upregulation. Acta Diabetologica, 2018, 55, 1231-1235.	1.2	28
104	Lifestyle Intervention in Pregnant Women With Obesity Impacts Cord Blood DNA Methylation, Which Associates With Body Composition in the Offspring. Diabetes, 2021, 70, 854-866.	0.3	28
105	Epigenetic Changes in Islets of Langerhans Preceding the Onset of Diabetes. Diabetes, 2020, 69, 2503-2517.	0.3	27
106	Genetic Variation in ATP5O Is Associated with Skeletal Muscle ATP50 mRNA Expression and Glucose Uptake in Young Twins. PLoS ONE, 2009, 4, e4793.	1.1	26
107	A Single Nucleotide Polymorphism Associates With the Response of Muscle ATP Synthesis to Long-Term Exercise Training in Relatives of Type 2 Diabetic Humans. Diabetes Care, 2012, 35, 350-357.	4.3	25
108	Human adipogenesis is associated with genome-wide DNA methylation and gene-expression changes. Epigenomics, 2016, 8, 1601-1617.	1.0	25

#	Article	IF	CITATIONS
109	Calpain-10 Expression Is Elevated in Pancreatic Islets from Patients with Type 2 Diabetes. PLoS ONE, 2009, 4, e6558.	1.1	24
110	Two common genetic variants near nuclear-encoded OXPHOS genes are associated with insulin secretion in vivo. European Journal of Endocrinology, 2011, 164, 765-771.	1.9	24
111	Impact of the peroxisome proliferator activated receptor-Î ³ coactivator-1Î ² (PGC-1Î ²) Ala2O3Pro polymorphism on in vivo metabolism, PGC-1Î ² expression and fibre type composition in human skeletal muscle. Diabetologia, 2007, 50, 1615-1620.	2.9	23
112	Liver DNA methylation of FADS2 associates with FADS2 genotypex. Clinical Epigenetics, 2019, 11, 10.	1.8	23
113	Serum aromatic and branched hain amino acids associated with NASH demonstrate divergent associations with serum lipids. Liver International, 2021, 41, 754-763.	1.9	23
114	Telomere length in blood and skeletal muscle in relation to measures of glycaemia and insulinaemia. Diabetic Medicine, 2012, 29, e377-81.	1.2	22
115	Lysine demethylase inhibition protects pancreatic β cells from apoptosis and improves β-cell function. Molecular and Cellular Endocrinology, 2018, 460, 47-56.	1.6	22
116	Prolactin (PRL) Receptor Gene Expression in Mouse Adipose Tissue: Increases during Lactation and in PRL-Transgenic Mice. Endocrinology, 2000, 141, 3564-3572.	1.4	22
117	The Association of Mitochondrial Content with Prevalent and Incident Type 2 Diabetes. Journal of Clinical Endocrinology and Metabolism, 2010, 95, 1909-1915.	1.8	21
118	Elevated Serum Chemokine CXC Ligand 5 Levels Are Associated with Hypercholesterolemia But Not a Worsening of Insulin Resistance in Chinese People. Journal of Clinical Endocrinology and Metabolism, 2010, 95, 3926-3932.	1.8	21
119	A common variant near the PRL gene is associated with increased adiposity in males. Molecular Genetics and Metabolism, 2011, 102, 78-81.	0.5	21
120	First-Degree Relatives of Type 2 Diabetic Patients Have Reduced Expression of Genes Involved in Fatty Acid Metabolism in Skeletal Muscle. Journal of Clinical Endocrinology and Metabolism, 2012, 97, E1332-E1337.	1.8	21
121	Transcriptome and proteome analysis of soleus muscle of hormone-sensitive lipase-null mice. Journal of Lipid Research, 2005, 46, 2614-2623.	2.0	20
122	Fetal Hyperglycemia Changes Human Preadipocyte Function in Adult Life. Journal of Clinical Endocrinology and Metabolism, 2017, 102, 1141-1150.	1.8	20
123	VPS39-deficiency observed in type 2 diabetes impairs muscle stem cell differentiation via altered autophagy and epigenetics. Nature Communications, 2021, 12, 2431.	5.8	20
124	Developmental and hormonal regulation of progesterone receptor A-form expression in female mouse lung in vivo: interaction with glucocorticoid receptors. Journal of Endocrinology, 2006, 190, 857-870.	1.2	19
125	Relationships of Plasma Adiponectin Level and Adiponectin Receptors 1 and 2 Gene Expression to Insulin Sensitivity and Glucose and Fat Metabolism in Monozygotic and Dizygotic Twins. Journal of Clinical Endocrinology and Metabolism, 2007, 92, 2835-2839.	1.8	18
126	Scavenger Receptor Class B Type I in the Rat Ovary: Possible Role in High Density Lipoprotein Cholesterol Uptake and in the Recognition of Apoptotic Granulosa Cells. Endocrinology, 1999, 140, 2494-2500.	1.4	17

#	Article	IF	CITATIONS
127	Type 2 diabetes classification: a data-driven cluster study of the Danish Centre for Strategic Research in Type 2 Diabetes (DD2) cohort. BMJ Open Diabetes Research and Care, 2022, 10, e002731.	1.2	17
128	Genetic and Nongenetic Determinants of Skeletal Muscle Glucose Transporter 4 Messenger Ribonucleic Acid Levels and Insulin Action in Twins. Journal of Clinical Endocrinology and Metabolism, 2006, 91, 702-708.	1.8	16
129	The expression of myosin heavy chain (MHC) genes in human skeletal muscle is related to metabolic characteristics involved in the pathogenesis of type 2 diabetes. Molecular Genetics and Metabolism, 2011, 103, 275-281.	0.5	16
130	Epigenetic markers to further understand insulin resistance. Diabetologia, 2016, 59, 2295-2297.	2.9	16
131	Prevalence of non-alcoholic fatty liver disease and its relation to hypoadiponectinaemia in the middle-aged and elderly Chinese population. Archives of Medical Science, 2011, 4, 665-672.	0.4	15
132	The Lysine Demethylase KDM5B Regulates Islet Function and Glucose Homeostasis. Journal of Diabetes Research, 2019, 2019, 1-15.	1.0	15
133	Novel Subgroups of Type 2 Diabetes Display Different Epigenetic Patterns That Associate With Future Diabetic Complications. Diabetes Care, 2022, 45, 1621-1630.	4.3	15
134	Less pronounced response to exercise in healthy relatives to type 2 diabetic subjects compared with controls. Journal of Applied Physiology, 2015, 119, 953-960.	1.2	13
135	Electroacupuncture Mimics Exercise-Induced Changes in Skeletal Muscle Gene Expression in Women With Polycystic Ovary Syndrome. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 2027-2041.	1.8	13
136	Regulation of skeletal muscle <i>PPAR</i> δmRNA expression in twins. Journal of Physiology, 2007, 584, 1011-1017.	1.3	12
137	Fasting unmasks differential fat and muscle transcriptional regulation of metabolic gene sets in low versus normal birth weight men. EBioMedicine, 2019, 47, 341-351.	2.7	11
138	PRL Receptor-Mediated Effects in Female Mouse Adipocytes: PRL Induces Suppressors of Cytokine Signaling Expression and Suppresses Insulin-Induced Leptin Production in Adipocytes in Vitro. Endocrinology, 2001, 142, 4880-4890.	1.4	11
139	Isolation of differentially expressed aldose reductase in ovaries after estrogen withdrawal from hypophysectomized diethylstilbestrol treated rats: increased expression during apoptosis. Molecular and Cellular Endocrinology, 2000, 164, 183-190.	1.6	9
140	Statin therapy is associated with epigenetic modifications in individuals with Type 2 diabetes. Epigenomics, 2021, 13, 919-925.	1.0	9
141	Epigenome- and Transcriptome-wide Changes in Muscle Stem Cells from Low Birth Weight Men. Endocrine Research, 2020, 45, 58-71.	0.6	7
142	Adipose methylome integrative-omic analyses reveal genetic and dietary metabolic health drivers and insulin resistance classifiers. Genome Medicine, 2022, 14, .	3.6	6
143	Differential DNA Methylation and Expression of miRNAs in Adipose Tissue From Twin Pairs Discordant for Type 2 Diabetes. Diabetes, 2021, 70, 2402-2418.	0.3	5
144	Excess of glucocorticoids during late gestation impairs the recovery of offspring's βâ€cell function after a postnatal injury. FASEB Journal, 2021, 35, e21828.	0.2	2

#	Article	IF	CITATIONS
145	Pharmacoepigenetics in type 2 diabetes: is it clinically relevant?. Diabetologia, 2022, , 1.	2.9	2
146	Epigenetics and Type 2 Diabetes. , 2011, , 135-145.		1
147	Epigenetics in the Pathophysiology of Type 2 Diabetes. , 2012, , 225-232.		1
148	Epigenetic Modifications and Type 2 Diabetes in Humans. Frontiers in Diabetes, 2014, , 102-110.	0.4	1
149	Genetic Epidemiology of Type 2 Diabetes. , 0, , 95-110.		1
150	Epigenetic Epidemiology of Obesity and Type 2 Diabetes. , 2022, , 445-474.		1
151	Epigenetics of Diabetes in Humans. , 2012, , 321-329.		0
152	Epigenetics in Type 2 Diabetes. , 2016, , 241-258.		0
153	Genome-Wide DNA and Histone Modification Studies in Metabolic Disease. , 2016, , 255-270.		0
154	Genome editing (CRISPR-Cas9) to identify and characterise functional variants determining metformin response. , 2018, 13, .		0
155	Basics of Molecular Genetics: Lessons from Type 2 Diabetes. , 0, , 367-376.		0