Yvonne BÃ¶ttcher

List of Publications by Year
in descending order

35 papers	6,730 citations	393982 19 h-index	377514 34 g-index
37 all docs	37 docs citations	37 times ranked	14102 citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
2	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
3	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. PLoS Medicine, 2017, 14, e1002383.	3.9	341
4	Genetics and epigenetics in obesity. Metabolism: Clinical and Experimental, 2019, 92, 37-50.	1.5	230
5	Many obesity-associated SNPs strongly associate with DNA methylation changes at proximal promoters and enhancers. Genome Medicine, 2015, 7, 103.	3.6	124
6	The genetics of fat distribution. Diabetologia, 2014, 57, 1276-1286.	2.9	116
7	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
8	Adipose Tissue Expression and Genetic Variants of the Bone Morphogenetic Protein Receptor 1A Gene (BMPR1A) Are Associated With Human Obesity. Diabetes, 2009, 58, 2119-2128.	0.3	73
9	FGF6 and FGF9 regulate UCP1 expression independent of brown adipogenesis. Nature Communications, 2020, 11, 1421.	5.8	67
10	Genetic Variation in the Visfatin Gene (PBEF1) and Its Relation to Glucose Metabolism and Fat-Depot-Specific Messenger Ribonucleic Acid Expression in Humans. Journal of Clinical Endocrinology and Metabolism, 2006, 91, 2725-2731.	1.8	64
11	ENPP1 Variants and Haplotypes Predispose to Early Onset Obesity and Impaired Glucose and Insulin Metabolism in German Obese Children. Journal of Clinical Endocrinology and Metabolism, 2006, 91, 4948-4952.	1.8	55
12	Hypoxia-inducible factor 3A gene expression and methylation in adipose tissue is related to adipose tissue dysfunction. Scientific Reports, 2016, 6, 27969.	1.6	49
13	Global DNA methylation levels in human adipose tissue are related to fat distribution and glucose homeostasis. Diabetologia, 2014, 57, 2374-2383.	2.9	42
14	Cardiometabolic risk markers, adipocyte fatty acid binding protein (aFABP) and the impact of high-intensity interval training (HIIT) in obese adolescents. Metabolism: Clinical and Experimental, 2017, 68, 77-87.	1.5	37
15	The genetics of euthyroid familial goiter. Trends in Endocrinology and Metabolism, 2005, 16, 314-319.	3.1	36
16	Age- and gender-specific norms for the German version of the Three-Factor Eating-Questionnaire (TFEQ). Appetite, 2015, 91, 241-247.	1.8	31
17	Brown adipose tissue (BAT) specific vaspin expression is increased after obesogenic diets and cold exposure and linked to acute changes in DNA-methylation. Molecular Metabolism, 2017, 6, 482-493.	3.0	29
18	DNA methylation signature in blood mirrors successful weight-loss during lifestyle interventions: the CENTRAL trial. Genome Medicine, 2020, 12, 97.	3.6	28

#	Article	IF	Citations
19	Adipose tissue depot specific promoter methylation of TMEM18. Journal of Molecular Medicine, 2014, 92, 881-888.	1.7	21
20	Epigenetic signatures associated with maternal body mass index or gestational weight gain: a systematic review. Journal of Developmental Origins of Health and Disease, 2021, 12, 373-383.	0.7	19
21	R1467H variant in the rho guanine nucleotide exchange factor 11 (ARHGEF11) is associated with impaired glucose tolerance and type 2 diabetes in German Caucasians. Journal of Human Genetics, 2008, 53, 365-367.	1.1	16
22	IRS1 DNA promoter methylation and expression in human adipose tissue are related to fat distribution and metabolic traits. Scientific Reports, 2017, 7, 12369.	1.6	16
23	The role of rs2237781 within GRM8 in eating behavior. Brain and Behavior, 2013, 3, 495-502.	1.0	14
24	DNA methylation patterns reflect individual's lifestyle independent of obesity. Clinical and Translational Medicine, 2022, 12, .	1.7	13
25	(Epi)genetic regulation of CRTC1 in human eating behaviour and fat distribution. EBioMedicine, 2019, 44, 476-488.	2.7	12
26	Developmentally Driven Changes in Adipogenesis in Different Fat Depots Are Related to Obesity. Frontiers in Endocrinology, 2020, 11, 138.	1.5	12
27	Cohort profile: Epigenetics in Pregnancy (EPIPREG) â€“ population-based sample of European and South Asian pregnant women with epigenome-wide DNA methylation (850k) in peripheral blood leukocytes. PLoS ONE, 2021, 16, e0256158.	1.1	11
28	Serglycin Is Involved in Adipose Tissue Inflammation in Obesity. Journal of Immunology, 2022, 208, 121-132.	0.4	8
29	m6A Regulators in Human Adipose Tissue - Depot-Specificity and Correlation With Obesity. Frontiers in Endocrinology, 2021, 12, 778875.	1.5	7
30	Maternal Glucose and LDL-Cholesterol Levels Are Related to Placental Leptin Gene Methylation, and, Together With Nutritional Factors, Largely Explain a Higher Methylation Level Among Ethnic South Asians. Frontiers in Endocrinology, 2021, 12, 809916.	1.5	7
31	DNA methylation of SSPN is linked to adipose tissue distribution and glucose metabolism. FASEB Journal, 2018, 32, 6898-6910.	0.2	6
32	Genetically programmed changes in transcription of the novel progranulin regulator. Journal of Molecular Medicine, 2020, 98, 1139-1148.	1.7	4
33	Role of the DNA repair genes H2AX and HMGB1 in human fat distribution and lipid profiles. BMJ Open Diabetes Research and Care, 2020, 8, e000831.	1.2	4
34	Upâ€“toâ€“date on the evidence linking miRNA-related epitranscriptomic modifications and disease settings. Can these modifications affect cross-kingdom regulation?. RNA Biology, 2021, , 1-14.	1.5	3
35	37â€ƒDNA methylation pattern in blood may reflect individualsâ€™ daily lifestyle. Adipositas - Ursachen Folgeerkrankungen Therapie, 2021, 15, .	0.2	0