

Yvonne BÄjtcher

List of Publications by Year in descending order

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Version: 2024-02-01

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	Serglycin Is Involved in Adipose Tissue Inflammation in Obesity. <i>Journal of Immunology</i> , 2022, 208, 121-132.	0.4	8
2	DNA methylation patterns reflect individual's lifestyle independent of obesity. <i>Clinical and Translational Medicine</i> , 2022, 12, .	1.7	13
3	Epigenetic signatures associated with maternal body mass index or gestational weight gain: a systematic review. <i>Journal of Developmental Origins of Health and Disease</i> , 2021, 12, 373-383.	0.7	19
4	Cohort profile: Epigenetics in Pregnancy (EPIPREG) – population-based sample of European and South Asian pregnant women with epigenome-wide DNA methylation (850k) in peripheral blood leukocytes. <i>PLoS ONE</i> , 2021, 16, e0256158.	1.1	11
5	37-Å-DNA methylation pattern in blood may reflect individuals'™ daily lifestyle. <i>Adipositas - Ursachen Folgeerkrankungen Therapie</i> , 2021, 15, .	0.2	0
6	Up-to-date on the evidence linking miRNA-related epitranscriptomic modifications and disease settings. Can these modifications affect cross-kingdom regulation?. <i>RNA Biology</i> , 2021, , 1-14.	1.5	3
7	m6A Regulators in Human Adipose Tissue - Depot-Specificity and Correlation With Obesity. <i>Frontiers in Endocrinology</i> , 2021, 12, 778875.	1.5	7
8	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. <i>Frontiers in Endocrinology</i> , 2021, 12, 809916.	1.5	7
9	DNA methylation signature in blood mirrors successful weight-loss during lifestyle interventions: the CENTRAL trial. <i>Genome Medicine</i> , 2020, 12, 97.	3.6	28
10	FGF6 and FGF9 regulate UCP1 expression independent of brown adipogenesis. <i>Nature Communications</i> , 2020, 11, 1421.	5.8	67
11	Genetically programmed changes in transcription of the novel progranulin regulator. <i>Journal of Molecular Medicine</i> , 2020, 98, 1139-1148.	1.7	4
12	Role of the DNA repair genes <i>H2AX</i> and <i>HMGB1</i> in human fat distribution and lipid profiles. <i>BMJ Open Diabetes Research and Care</i> , 2020, 8, e000831.	1.2	4
13	Developmentally Driven Changes in Adipogenesis in Different Fat Depots Are Related to Obesity. <i>Frontiers in Endocrinology</i> , 2020, 11, 138.	1.5	12
14	(Epi)genetic regulation of CRTCL in human eating behaviour and fat distribution. <i>EBioMedicine</i> , 2019, 44, 476-488.	2.7	12
15	Genetics and epigenetics in obesity. <i>Metabolism: Clinical and Experimental</i> , 2019, 92, 37-50.	1.5	230
16	DNA methylation of <i>SSPN</i> is linked to adipose tissue distribution and glucose metabolism. <i>FASEB Journal</i> , 2018, 32, 6898-6910.	0.2	6
17	Brown adipose tissue (BAT) specific vaspin expression is increased after obesogenic diets and cold exposure and linked to acute changes in DNA-methylation. <i>Molecular Metabolism</i> , 2017, 6, 482-493.	3.0	29
18	Cardiometabolic risk markers, adipocyte fatty acid binding protein (aFABP) and the impact of high-intensity interval training (HIIT) in obese adolescents. <i>Metabolism: Clinical and Experimental</i> , 2017, 68, 77-87.	1.5	37

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19	IRS1 DNA promoter methylation and expression in human adipose tissue are related to fat distribution and metabolic traits. <i>Scientific Reports</i> , 2017, 7, 12369.	1.6	16
20	Genome-wide DNA promoter methylation and transcriptome analysis in human adipose tissue unravels novel candidate genes for obesity. <i>Molecular Metabolism</i> , 2017, 6, 86-100.	3.0	84
21	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. <i>PLoS Medicine</i> , 2017, 14, e1002383.	3.9	341
22	Hypoxia-inducible factor 3A gene expression and methylation in adipose tissue is related to adipose tissue dysfunction. <i>Scientific Reports</i> , 2016, 6, 27969.	1.6	49
23	Many obesity-associated SNPs strongly associate with DNA methylation changes at proximal promoters and enhancers. <i>Genome Medicine</i> , 2015, 7, 103.	3.6	124
24	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	13.7	1,328
25	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
26	Age- and gender-specific norms for the German version of the Three-Factor Eating-Questionnaire (TFEQ). <i>Appetite</i> , 2015, 91, 241-247.	1.8	31
27	Global DNA methylation levels in human adipose tissue are related to fat distribution and glucose homeostasis. <i>Diabetologia</i> , 2014, 57, 2374-2383.	2.9	42
28	Adipose tissue depot specific promoter methylation of TMEM18. <i>Journal of Molecular Medicine</i> , 2014, 92, 881-888.	1.7	21
29	The genetics of fat distribution. <i>Diabetologia</i> , 2014, 57, 1276-1286.	2.9	116
30	The role of rs2237781 within <i>GRM8</i> in eating behavior. <i>Brain and Behavior</i> , 2013, 3, 495-502.	1.0	14
31	Adipose Tissue Expression and Genetic Variants of the Bone Morphogenetic Protein Receptor 1A Gene (<i>BMPRI1A</i>) Are Associated With Human Obesity. <i>Diabetes</i> , 2009, 58, 2119-2128.	0.3	73
32	R1467H variant in the rho guanine nucleotide exchange factor 11 (<i>ARHGEF11</i>) is associated with impaired glucose tolerance and type 2 diabetes in German Caucasians. <i>Journal of Human Genetics</i> , 2008, 53, 365-367.	1.1	16
33	Genetic Variation in the Visfatin Gene (<i>PBEF1</i>) and Its Relation to Glucose Metabolism and Fat-Depot-Specific Messenger Ribonucleic Acid Expression in Humans. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2006, 91, 2725-2731.	1.8	64
34	ENPP1 Variants and Haplotypes Predispose to Early Onset Obesity and Impaired Glucose and Insulin Metabolism in German Obese Children. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2006, 91, 4948-4952.	1.8	55
35	The genetics of euthyroid familial goiter. <i>Trends in Endocrinology and Metabolism</i> , 2005, 16, 314-319.	3.1	36