Linda Broer

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7186446/publications.pdf

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59	7,121	156536	139680
papers	citations	32 h-index	61 g-index

66	66	66	17029
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	OUP accepted manuscript. Human Reproduction, 2022, , .	0.4	2
2	Genome-wide association meta-analysis identifies 48 risk variants and highlights the role of the stria vascularis in hearing loss. American Journal of Human Genetics, 2022, 109, 1077-1091.	2.6	27
3	A bioinformatics pipeline for estimating mitochondrial DNA copy number and heteroplasmy levels from whole genome sequencing data. NAR Genomics and Bioinformatics, 2022, 4, lqac034.	1.5	12
4	Genome-wide association of phenotypes based on clustering patterns of hand osteoarthritis identifyWNT9Aas novel osteoarthritis gene. Annals of the Rheumatic Diseases, 2021, 80, 367-375.	0.5	26
5	Possible modification of BRSK1 on the risk of alkylating chemotherapy-related reduced ovarian function. Human Reproduction, 2021, 36, 1120-1133.	0.4	8
6	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	3.8	90
7	A comparison of genotyping arrays. European Journal of Human Genetics, 2021, 29, 1611-1624.	1.4	43
8	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183
9	Effect of Genetic Variation in CYP450 on Gonadal Impairment in a European Cohort of Female Childhood Cancer Survivors, Based on a Candidate Gene Approach: Results from the PanCareLIFE Study. Cancers, 2021, 13, 4598.	1.7	8
10	Genetic variation of cisplatin-induced ototoxicity in non-cranial-irradiated pediatric patients using a candidate gene approach: The International PanCareLIFE Study. Pharmacogenomics Journal, 2020, 20, 294-305.	0.9	28
11	Telomere Length and the Risk of Alzheimerâ€™s Disease: The Rotterdam Study. Journal of Alzheimer's Disease, 2020, 73, 707-714.	1.2	45
12	Usefulness of current candidate genetic markers to identify childhood cancer patients at risk for platinum-induced ototoxicity: Results of the European PanCareLIFE cohort study. European Journal of Cancer, 2020, 138, 212-224.	1.3	31
13	Association of candidate pharmacogenetic markers with platinum-induced ototoxicity: PanCareLIFE dataset. Data in Brief, 2020, 32, 106227.	0.5	2
14	Reduced penetrance of pathogenic ACMG variants in a deeply phenotyped cohort study and evaluation of ClinVar classification over time. Genetics in Medicine, 2020, 22, 1812-1820.	1.1	24
15	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.3	26
16	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. American Journal of Human Genetics, 2020, 106, 389-404.	2.6	118
17	Exome Sequencing Analysis Identifies Rare Variants in ATM and RPL8 That Are Associated With Shorter Telomere Length. Frontiers in Genetics, 2020, 11, 337.	1.1	4
18	Rapid Low-Cost Microarray-Based Genotyping for Genetic Screening in Primary Immunodeficiency. Frontiers in Immunology, 2020, 11, 614.	2.2	21

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19	Short-Term, Combined Fasting and Exercise Improves Body Composition in Healthy Males. International Journal of Sport Nutrition and Exercise Metabolism, 2020, 30, 386-395.	1.0	5
20	Metabolomics reveals a link between homocysteine and lipid metabolism and leukocyte telomere length: the ENGAGE consortium. Scientific Reports, 2019, 9, 11623.	1.6	13
21	Disentangling the genetics of lean mass. American Journal of Clinical Nutrition, 2019, 109, 276-287.	2.2	38
22	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
23	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
24	Genetic Determinants of Ototoxicity During and After Childhood Cancer Treatment: Protocol for the PanCareLIFE Study. JMIR Research Protocols, 2019, 8, e11868.	0.5	10
25	MON-208 Association Study of AMH Promoter Polymorphisms and Serum AMH Levels in PCOS Patients. Journal of the Endocrine Society, 2019, 3, .	0.1	0
26	Life-Course Genome-wide Association Study Meta-analysis of Total Body BMD and Assessment of Age-Specific Effects. American Journal of Human Genetics, 2018, 102, 88-102.	2.6	252
27	Genetic variants associated with earlier age at menopause increase the risk of cardiovascular events in women. Menopause, 2018, 25, 451-457.	0.8	22
28	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. PLoS Genetics, 2018, 14, e1007813.	1.5	341
29	Genetic variation in gonadal impairment in female survivors of childhood cancer: a PanCareLIFE study protocol. BMC Cancer, 2018, 18, 930.	1.1	13
30	PanCareLIFE: The scientific basis for a European project to improve long-term care regarding fertility, ototoxicity and health-related quality of life after cancer occurring among children and adolescents. European Journal of Cancer, 2018, 103, 227-237.	1.3	41
31	Body mass index is negatively associated with telomere length: a collaborative cross-sectional meta-analysis of 87 observational studies. American Journal of Clinical Nutrition, 2018, 108, 453-475.	2.2	137
32	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
33	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
34	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	9.4	426
35	Haplotype reference consortium panel: Practical implications of imputations with large reference panels. Human Mutation, 2017, 38, 1025-1032.	1.1	43
36	CYP2C9 Genotypes Modify Benzodiazepine-Related Fall Risk: Original Results From Three Studies With Meta-Analysis. Journal of the American Medical Directors Association, 2017, 18, 88.e1-88.e15.	1.2	19

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37	Evaluation of the Myocilin Mutation Gln368Stop Demonstrates Reduced Penetrance for Glaucoma in European Populations. Ophthalmology, 2017, 124, 547-553.	2.5	23
38	Genome-wide association and functional studies identify a role for matrix Gla protein in osteoarthritis of the hand. Annals of the Rheumatic Diseases, 2017, 76, 2046-2053.	0.5	64
39	Low-Frequency Synonymous Coding Variation in CYP2R1 Has Large Effects on Vitamin D Levels and Risk of Multiple Sclerosis. American Journal of Human Genetics, 2017, 101, 227-238.	2.6	112
40	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	5.8	147
41	Burden of genetic risk variants in multiple sclerosis families in the Netherlands. Multiple Sclerosis Journal - Experimental, Translational and Clinical, 2016, 2, 205521731664872.	0.5	6
42	Human age estimation from blood using mRNA, DNA methylation, DNA rearrangement, and telomere length. Forensic Science International: Genetics, 2016, 24, 33-43.	1.6	102
43	Genomewide metaâ€analysis identifies loci associated with <scp>IGF</scp> â€I and <scp>IGFBP</scp> â€3 levels with impact on ageâ€related traits. Aging Cell, 2016, 15, 811-824.	3.0	83
44	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	9.4	284
45	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	1.5	331
46	GWAS and Meta-Analysis in Aging/Longevity. Advances in Experimental Medicine and Biology, 2015, 847, 107-125.	0.8	22
47	GWAS of Longevity in CHARGE Consortium Confirms APOE and FOXO3 Candidacy. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2015, 70, 110-118.	1.7	250
48	Causal mechanisms and balancing selection inferred from genetic associations with polycystic ovary syndrome. Nature Communications, 2015, 6, 8464.	5.8	304
49	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	5.8	533
50	Single nucleotide polymorphisms in CRTC1 and BARX1 are associated with esophageal adenocarcinoma. Journal of Carcinogenesis, 2015, 14, 5.	2.5	14
51	Leukocyte telomere length associates with prospective mortality independent of immune-related parameters and known genetic markers. International Journal of Epidemiology, 2014, 43, 878-886.	0.9	95
52	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	5.8	192
53	Association of adiponectin and leptin with relative telomere length in seven independent cohorts including 11,448 participants. European Journal of Epidemiology, 2014, 29, 629-638.	2.5	23
54	Telomere length in circulating leukocytes is associated with lung function and disease. European Respiratory Journal, 2014, 43, 983-992.	3.1	103

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55	Identification of seven loci affecting mean telomere length and their association with disease. Nature Genetics, 2013, 45, 422-427.	9.4	808
56	Distinguishing true from false positives in genomic studies: p values. European Journal of Epidemiology, 2013, 28, 131-138.	2.5	36
57	Meta-analysis of telomere length in 19â€‰713 subjects reveals high heritability, stronger maternal inheritance and a paternal age effect. European Journal of Human Genetics, 2013, 21, 1163-1168.	1.4	380
58	Association Between Chromosome 9p21 Variants and the Ankle-Brachial Index Identified by a Meta-Analysis of 21 Genome-Wide Association Studies. Circulation: Cardiovascular Genetics, 2012, 5, 100-112.	5.1	98
59	Association of HSP70 and its Co-Chaperones with Alzheimer's Disease. Journal of Alzheimer's Disease, 2011, 25, 93-102.	1.2	21