Elin Grundberg

List of Publications by Year
in descending order

77 papers	16,832 citations	57719 44 h-index	66879 78 g-index
87 all docs	87 docs citations	87 times ranked	27543 citing authors

#	Article	IF	Citations
1	Blood DNA methylation at TXNIP and glycemic changes in response to weight-loss diet interventions: the POUNDS lost trial. International Journal of Obesity, 2022, 46, 1122-1127.	1.6	13
2	Genomic answers for children: Dynamic analyses of >1000 pediatric rare disease genomes. Genetics in Medicine, 2022, 24, 1336-1348.	1.1	37
3	eP422: Diagnostic rate of genetic testing in a pediatric research cohort with clinical insurance denials. Genetics in Medicine, 2022, 24, S264.	1.1	0
4	Cross-reactive antibodies elicited to conserved epitopes on SARS-CoV-2 spike protein after infection and vaccination. Scientific Reports, 2022, 12, 6496.	1.6	20
5	Adipose methylome integrative-omic analyses reveal genetic and dietary metabolic health drivers and insulin resistance classifiers. Genome Medicine, 2022, 14, .	3.6	6
6	ASCL2 reciprocally controls key trophoblast lineage decisions during hemochorial placenta development. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	53
7	AKR1C2 and AKR1C3 expression in adipose tissue: Association with body fat distribution and regulatory variants. Molecular and Cellular Endocrinology, 2021, 527, 111220.	1.6	11
8	Antibody Responses after a Single Dose of SARS-CoV-2 mRNA Vaccine. New England Journal of Medicine, 2021, 384, 1959-1961.	13.9	131
9	Humoral immune responses during SARS-CoV-2 mRNA vaccine administration in seropositive and seronegative individuals. BMC Medicine, 2021, 19, 169.	2.3	52
10	Immune cell residency in the nasal mucosa may partially explain respiratory disease severity across the age range. Scientific Reports, 2021, 11, 15927.	1.6	16
11	Intersection of regulatory pathways controlling hemostasis and hemochorial placentation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	19
12	Single-cell analysis of human adipose tissue identifies depot- and disease-specific cell types. Nature Metabolism, 2020, 2, 97-109.	5.1	272
13	Dominant gut Prevotella copri in gastrectomised non-obese diabetic Gotoâ€“Kakizaki rats improves glucose homeostasis through enhanced FXR signalling. Diabetologia, 2020, 63, 1223-1235.	2.9	37
14	Capturing functional epigenomes for insight into metabolic diseases. Molecular Metabolism, 2020, 38, 100936.	3.0	9
15	Customized MethylC-Capture Sequencing to Evaluate Variation in the Human Sperm DNA Methylome Representative of Altered Folate Metabolism. Environmental Health Perspectives, 2019, 127, 87002.	2.8	20
16	Mendelian Randomization Analysis Reveals a Causal Influence of Circulating Sclerostin Levels on Bone Mineral Density and Fractures. Journal of Bone and Mineral Research, 2019, 34, 1824-1836.	3.1	24
17	Dissecting features of epigenetic variants underlying cardiometabolic risk using full-resolution epigenome profiling in regulatory elements. Nature Communications, 2019, 10, 1209.	5.8	16
18	An atlas of genetic influences on osteoporosis in humans and mice. Nature Genetics, 2019, 51, 258-266.	9.4	557

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19	Identification of Novel Loci Associated With Hip Shape: A Meta-Analysis of Genomewide Association Studies. Journal of Bone and Mineral Research, 2019, 34, 241-251.	3.1	47
20	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. Genome Biology, 2017, 18, 50.	3.8	71
21	Identification of 153 new loci associated with heel bone mineral density and functional involvement of GPC6 in osteoporosis. Nature Genetics, 2017, 49, 1468-1475.	9.4	391
22	Higher chylomicron remnants and LDL particle numbers associate with CD36 SNPs and DNA methylation sites that reduce CD36. Journal of Lipid Research, 2016, 57, 2176-2184.	2.0	26
23	Genetic risk factors for decreased bone mineral accretion in children with asthma receiving multiple oral corticosteroid bursts. Journal of Allergy and Clinical Immunology, 2015, 136, 1240-1246.e8.	1.5	13
24	Population whole-genome bisulfite sequencing across two tissues highlights the environment as the principal source of human methylome variation. Genome Biology, 2015, 16, 290.	3.8	90
25	Characterization of functional methylomes by next-generation capture sequencing identifies novel disease-associated variants. Nature Communications, 2015, 6, 7211.	5.8	84
26	An epigenome-wide association study of total serum immunoglobulin E concentration. Nature, 2015, 520, 670-674.	13.7	193
27	Global miRNA expression and correlation with mRNA levels in primary human bone cells. Rna, 2015, 21, 1433-1443.	1.6	43
28	Wholeâ€genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	13.7	483
29	Cigarette smoking reduces DNA methylation levels at multiple genomic loci but the effect is partially reversible upon cessation. Epigenetics, 2014, 9, 1382-1396.	1.3	285
30	Phenotypic Dissection of Bone Mineral Density Reveals Skeletal Site Specificity and Facilitates the Identification of Novel Loci in the Genetic Regulation of Bone Mass Attainment. PLoS Genetics, 2014, 10, e1004423.	1.5	134
31	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. PLoS Genetics, 2014, 10, e1004517.	1.5	191
32	Interrogating causal pathways linking genetic variants, small molecule metabolites, and circulating lipids. Genome Medicine, 2014, 6, 25.	3.6	17
33	An atlas of genetic influences on human blood metabolites. Nature Genetics, 2014, 46, 543-550.	9.4	1,084
34	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
35	Expression of Phosphofructokinase in Skeletal Muscle Is Influenced by Genetic Variation and Associated With Insulin Sensitivity. Diabetes, 2014, 63, 1154-1165.	0.3	41
36	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	9.4	1,439

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37	Global Analysis of DNA Methylation Variation in Adipose Tissue from Twins Reveals Links to Disease-Associated Variants in Distal Regulatory Elements. American Journal of Human Genetics, 2013, 93, 876-890.	2.6	330
38	Genetic Determinants of Trabecular and Cortical Volumetric Bone Mineral Densities and Bone Microstructure. PLoS Genetics, 2013, 9, e1003247.	1.5	100
39	The Presence of Methylation Quantitative Trait Loci Indicates a Direct Genetic Influence on the Level of DNA Methylation in Adipose Tissue. PLoS ONE, 2013, 8, e55923.	1.1	83
40	Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture. Nature Genetics, 2012, 44, 491-501.	9.4	1,100
41	Assessment of gene-by-sex interaction effect on bone mineral density. Journal of Bone and Mineral Research, 2012, 27, 2051-2064.	3.1	47
42	Impact of Common Variation in Bone-Related Genes on Type 2 Diabetes and Related Traits. Diabetes, 2012, 61, 2176-2186.	0.3	31
43	Epigenome-Wide Scans Identify Differentially Methylated Regions for Age and Age-Related Phenotypes in a Healthy Ageing Population. PLoS Genetics, 2012, 8, e1002629.	1.5	620
44	Mapping cis- and trans-regulatory effects across multiple tissues in twins. Nature Genetics, 2012, 44, 1084-1089.	9.4	701
45	A Comparison of the Whole Genome Approach of MeDIP-Seq to the Targeted Approach of the Infinium HumanMethylation450 BeadChipÂ® for Methylome Profiling. PLoS ONE, 2012, 7, e50233.	1.1	83
46	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. Nature Genetics, 2011, 43, 984-989.	9.4	481
47	Human metabolic individuality in biomedical and pharmaceutical research. Nature, 2011, 477, 54-60.	13.7	916
48	Identification of an imprinted master trans regulator at the KLF14 locus related to multiple metabolic phenotypes. Nature Genetics, 2011, 43, 561-564.	9.4	289
49	The Architecture of Gene Regulatory Variation across Multiple Human Tissues: The MuTHER Study. PLoS Genetics, 2011, 7, e1002003.	1.5	392
50	Global Analysis of the Impact of Environmental Perturbation on cis-Regulation of Gene Expression. PLoS Genetics, 2011, 7, e1001279.	1.5	81
51	Eight Common Genetic Variants Associated with Serum DHEAS Levels Suggest a Key Role in Ageing Mechanisms. PLoS Genetics, 2011, 7, e1002025.	1.5	87
52	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
53	An Integration of Genome-Wide Association Study and Gene Expression Profiling to Prioritize the Discovery of Novel Susceptibility Loci for Osteoporosis-Related Traits. PLoS Genetics, 2010, 6, e1000977.	1.5	191
54	Cell culture-induced aberrant methylation of the imprinted IG DMR in human lymphoblastoid cell lines. Epigenetics, 2010, 5, 50-60.	1.3	30

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55	Analysis of the Impact of Genetic Variation on Human Gene Expression. Methods in Molecular Biology, 2010, 628, 321-339.	0.4	5
56	Targeted screening of cis-regulatory variation in human haplotypes. Genome Research, 2009, 19, 118-127.	2.4	78
57	Tissue Effect on Genetic Control of Transcript Isoform Variation. PLoS Genetics, 2009, 5, e1000608.	1.5	50
58	A Genome-Wide Association Study Reveals Variants in ARL15 that Influence Adiponectin Levels. PLoS Genetics, 2009, 5, e1000768.	1.5	148
59	Population genomics in a disease targeted primary cell model. Genome Research, 2009, 19, 1942-1952.	2.4	89
60	Spectrum of mutations inMMACHC, allelic expression, and evidence for genotypeÃ¢Â€Â“phenotype correlations. Human Mutation, 2009, 30, 1072-1081.	1.1	186
61	Twenty bone-mineral-density loci identified by large-scale meta-analysis of genome-wide association studies. Nature Genetics, 2009, 41, 1199-1206.	9.4	660
62	Global patterns of cis variation in human cells revealed by high-density allelic expression analysis. Nature Genetics, 2009, 41, 1216-1222.	9.4	206
63	Estimation of physical performance and measurements of habitual physical activity may capture men with high risk to fallâ€”Data from the Mr Os Sweden cohort. Archives of Gerontology and Geriatrics, 2009, 49, e72-e76.	1.4	22
64	Allele-Specific Chromatin Remodeling in the ZPBP2/GSDMB/ORMDL3 Locus Associated with the Risk of Asthma and Autoimmune Disease. American Journal of Human Genetics, 2009, 85, 377-393.	2.6	262
65	Common Sequence Variation in FLNB Regulates Bone Structure in Women in the General Population and FLNB mRNA Expression in Osteoblasts In Vitro. Journal of Bone and Mineral Research, 2009, 24, 1989-1997.	3.1	21
66	A genome-wide approach to identifying novel-imprinted genes. Human Genetics, 2008, 122, 625-634.	1.8	70
67	The COMT val158met polymorphism is associated with prevalent fractures in Swedish men. Bone, 2008, 42, 107-112.	1.4	12
68	Type I Collagen Î±1 Sp1 Polymorphism and the Risk of Cruciate Ligament Ruptures or Shoulder Dislocations. American Journal of Sports Medicine, 2008, 36, 2432-2436.	1.9	114
69	Fibroblast growth factor-23 is associated with parathyroid hormone and renal function in a population-based cohort of elderly men. European Journal of Endocrinology, 2008, 158, 125-129.	1.9	60
70	Systematic assessment of the human osteoblast transcriptome in resting and induced primary cells. Physiological Genomics, 2008, 33, 301-311.	1.0	32
71	A risk haplotype of STAT4 for systemic lupus erythematosus is over-expressed, correlates with anti-dsDNA and shows additive effects with two risk alleles of IRF5. Human Molecular Genetics, 2008, 17, 2868-2876.	1.4	183
72	The Impact of Estradiol on Bone Mineral Density Is Modulated by the Specific Estrogen Receptor-Î± Cofactor Retinoblastoma-Interacting Zinc Finger Protein-1 Insertion/Deletion Polymorphism. Journal of Clinical Endocrinology and Metabolism, 2007, 92, 2300-2306.	1.8	5

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73	Vitamin D Receptor 3â€² Haplotypes Are Unequally Expressed in Primary Human Bone Cells and Associated With Increased Fracture Risk: The MrOS Study in Sweden and Hong Kong. Journal of Bone and Mineral Research, 2007, 22, 832-840.	3.1	37
74	The positive effect of dietary vitamin D intake on bone mineral density in men is modulated by the polyadenosine repeat polymorphism of the vitamin D receptor. Bone, 2006, 39, 1343-1351.	1.4	13
75	A TA-repeat polymorphism in the gene for the estrogen receptor alpha does not correlate with muscle strength or body composition in young adult Swedish women. Maturitas, 2005, 50, 153-160.	1.0	12
76	Genetic variation in the human vitamin D receptor is associated with muscle strength, fat mass and body weight in Swedish women. European Journal of Endocrinology, 2004, 150, 323-328.	1.9	139
77	Large-scale analysis of circulating glutamate and adipose gene expression in relation to abdominal obesity. Amino Acids, 0, , .	1.2	3