

# Elin Grundberg

## List of Publications by Year in descending order

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Version: 2024-02-01

77  
papers

16,832  
citations

57631

44  
h-index

66788

78  
g-index

87  
all docs

87  
docs citations

87  
times ranked

27543  
citing authors

#	ARTICLE	IF	CITATIONS
1	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	13.7	1,789
2	Large-scale association analysis identifies new risk loci for coronary artery disease. <i>Nature Genetics</i> , 2013, 45, 25-33.	9.4	1,439
3	Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture. <i>Nature Genetics</i> , 2012, 44, 491-501.	9.4	1,100
4	An atlas of genetic influences on human blood metabolites. <i>Nature Genetics</i> , 2014, 46, 543-550.	9.4	1,084
5	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014, 46, 234-244.	9.4	959
6	Human metabolic individuality in biomedical and pharmaceutical research. <i>Nature</i> , 2011, 477, 54-60.	13.7	916
7	Mapping cis- and trans-regulatory effects across multiple tissues in twins. <i>Nature Genetics</i> , 2012, 44, 1084-1089.	9.4	701
8	Twenty bone-mineral-density loci identified by large-scale meta-analysis of genome-wide association studies. <i>Nature Genetics</i> , 2009, 41, 1199-1206.	9.4	660
9	Epigenome-Wide Scans Identify Differentially Methylated Regions for Age and Age-Related Phenotypes in a Healthy Ageing Population. <i>PLoS Genetics</i> , 2012, 8, e1002629.	1.5	620
10	An atlas of genetic influences on osteoporosis in humans and mice. <i>Nature Genetics</i> , 2019, 51, 258-266.	9.4	557
11	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. <i>Nature</i> , 2015, 526, 112-117.	13.7	483
12	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2011, 43, 984-989.	9.4	481
13	The Architecture of Gene Regulatory Variation across Multiple Human Tissues: The MuTHER Study. <i>PLoS Genetics</i> , 2011, 7, e1002003.	1.5	392
14	Identification of 153 new loci associated with heel bone mineral density and functional involvement of GPC6 in osteoporosis. <i>Nature Genetics</i> , 2017, 49, 1468-1475.	9.4	391
15	Global Analysis of DNA Methylation Variation in Adipose Tissue from Twins Reveals Links to Disease-Associated Variants in Distal Regulatory Elements. <i>American Journal of Human Genetics</i> , 2013, 93, 876-890.	2.6	330
16	Identification of an imprinted master trans regulator at the KLF14 locus related to multiple metabolic phenotypes. <i>Nature Genetics</i> , 2011, 43, 561-564.	9.4	289
17	Cigarette smoking reduces DNA methylation levels at multiple genomic loci but the effect is partially reversible upon cessation. <i>Epigenetics</i> , 2014, 9, 1382-1396.	1.3	285
18	Single-cell analysis of human adipose tissue identifies depot- and disease-specific cell types. <i>Nature Metabolism</i> , 2020, 2, 97-109.	5.1	272

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19	Allele-Specific Chromatin Remodeling in the ZBP2/GSDMB/ORMDL3 Locus Associated with the Risk of Asthma and Autoimmune Disease. <i>American Journal of Human Genetics</i> , 2009, 85, 377-393.	2.6	262
20	Global patterns of cis variation in human cells revealed by high-density allelic expression analysis. <i>Nature Genetics</i> , 2009, 41, 1216-1222.	9.4	206
21	An epigenome-wide association study of total serum immunoglobulin E concentration. <i>Nature</i> , 2015, 520, 670-674.	13.7	193
22	An Integration of Genome-Wide Association Study and Gene Expression Profiling to Prioritize the Discovery of Novel Susceptibility Loci for Osteoporosis-Related Traits. <i>PLoS Genetics</i> , 2010, 6, e1000977.	1.5	191
23	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. <i>PLoS Genetics</i> , 2014, 10, e1004517.	1.5	191
24	Spectrum of mutations in <i>MMACHC</i> , allelic expression, and evidence for genotype-phenotype correlations. <i>Human Mutation</i> , 2009, 30, 1072-1081.	1.1	186
25	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. <i>Human Molecular Genetics</i> , 2008, 17, 2868-2876.	1.4	183
26	A Genome-Wide Association Study Reveals Variants in ARL15 that Influence Adiponectin Levels. <i>PLoS Genetics</i> , 2009, 5, e1000768.	1.5	148
27	Genetic variation in the human vitamin D receptor is associated with muscle strength, fat mass and body weight in Swedish women. <i>European Journal of Endocrinology</i> , 2004, 150, 323-328.	1.9	139
28	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. <i>PLoS Genetics</i> , 2014, 10, e1004423.	1.5	134
29	Antibody Responses after a Single Dose of SARS-CoV-2 mRNA Vaccine. <i>New England Journal of Medicine</i> , 2021, 384, 1959-1961.	13.9	131
30	Type I Collagen $\alpha 1$ Sp1 Polymorphism and the Risk of Cruciate Ligament Ruptures or Shoulder Dislocations. <i>American Journal of Sports Medicine</i> , 2008, 36, 2432-2436.	1.9	114
31	Genetic Determinants of Trabecular and Cortical Volumetric Bone Mineral Densities and Bone Microstructure. <i>PLoS Genetics</i> , 2013, 9, e1003247.	1.5	100
32	Population whole-genome bisulfite sequencing across two tissues highlights the environment as the principal source of human methylome variation. <i>Genome Biology</i> , 2015, 16, 290.	3.8	90
33	Population genomics in a disease targeted primary cell model. <i>Genome Research</i> , 2009, 19, 1942-1952.	2.4	89
34	Eight Common Genetic Variants Associated with Serum DHEAS Levels Suggest a Key Role in Ageing Mechanisms. <i>PLoS Genetics</i> , 2011, 7, e1002025.	1.5	87
35	Characterization of functional methylomes by next-generation capture sequencing identifies novel disease-associated variants. <i>Nature Communications</i> , 2015, 6, 7211.	5.8	84
36	The Presence of Methylation Quantitative Trait Loci Indicates a Direct Genetic Influence on the Level of DNA Methylation in Adipose Tissue. <i>PLoS ONE</i> , 2013, 8, e55923.	1.1	83

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37	A Comparison of the Whole Genome Approach of MeDIP-Seq to the Targeted Approach of the Infinium HumanMethylation450 BeadChip® for Methylome Profiling. <i>PLoS ONE</i> , 2012, 7, e50233.	1.1	83
38	Global Analysis of the Impact of Environmental Perturbation on cis-Regulation of Gene Expression. <i>PLoS Genetics</i> , 2011, 7, e1001279.	1.5	81
39	Targeted screening of cis-regulatory variation in human haplotypes. <i>Genome Research</i> , 2009, 19, 118-127.	2.4	78
40	Functional variation in allelic methylomes underscores a strong genetic contribution and reveals novel epigenetic alterations in the human epigenome. <i>Genome Biology</i> , 2017, 18, 50.	3.8	71
41	A genome-wide approach to identifying novel-imprinted genes. <i>Human Genetics</i> , 2008, 122, 625-634.	1.8	70
42	Fibroblast growth factor-23 is associated with parathyroid hormone and renal function in a population-based cohort of elderly men. <i>European Journal of Endocrinology</i> , 2008, 158, 125-129.	1.9	60
43	ASCL2 reciprocally controls key trophoblast lineage decisions during hemochorial placenta development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	53
44	Humoral immune responses during SARS-CoV-2 mRNA vaccine administration in seropositive and seronegative individuals. <i>BMC Medicine</i> , 2021, 19, 169.	2.3	52
45	Tissue Effect on Genetic Control of Transcript Isoform Variation. <i>PLoS Genetics</i> , 2009, 5, e1000608.	1.5	50
46	Assessment of gene-by-sex interaction effect on bone mineral density. <i>Journal of Bone and Mineral Research</i> , 2012, 27, 2051-2064.	3.1	47
47	Identification of Novel Loci Associated With Hip Shape: A Meta-Analysis of Genomewide Association Studies. <i>Journal of Bone and Mineral Research</i> , 2019, 34, 241-251.	3.1	47
48	Global miRNA expression and correlation with mRNA levels in primary human bone cells. <i>Rna</i> , 2015, 21, 1433-1443.	1.6	43
49	Expression of Phosphofructokinase in Skeletal Muscle Is Influenced by Genetic Variation and Associated With Insulin Sensitivity. <i>Diabetes</i> , 2014, 63, 1154-1165.	0.3	41
50	Vitamin D Receptor 3' Haplotypes Are Unequally Expressed in Primary Human Bone Cells and Associated With Increased Fracture Risk: The MrOS Study in Sweden and Hong Kong. <i>Journal of Bone and Mineral Research</i> , 2007, 22, 832-840.	3.1	37
51	Dominant gut <i>Prevotella copri</i> in gastrectomised non-obese diabetic Goto-Kakizaki rats improves glucose homeostasis through enhanced FXR signalling. <i>Diabetologia</i> , 2020, 63, 1223-1235.	2.9	37
52	Genomic answers for children: Dynamic analyses of >1000 pediatric rare disease genomes. <i>Genetics in Medicine</i> , 2022, 24, 1336-1348.	1.1	37
53	Systematic assessment of the human osteoblast transcriptome in resting and induced primary cells. <i>Physiological Genomics</i> , 2008, 33, 301-311.	1.0	32
54	Impact of Common Variation in Bone-Related Genes on Type 2 Diabetes and Related Traits. <i>Diabetes</i> , 2012, 61, 2176-2186.	0.3	31

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55	Cell culture-induced aberrant methylation of the imprinted IG DMR in human lymphoblastoid cell lines. <i>Epigenetics</i> , 2010, 5, 50-60.	1.3	30
56	Higher chylomicron remnants and LDL particle numbers associate with CD36 SNPs and DNA methylation sites that reduce CD36. <i>Journal of Lipid Research</i> , 2016, 57, 2176-2184.	2.0	26
57	Mendelian Randomization Analysis Reveals a Causal Influence of Circulating Sclerostin Levels on Bone Mineral Density and Fractures. <i>Journal of Bone and Mineral Research</i> , 2019, 34, 1824-1836.	3.1	24
58	Estimation of physical performance and measurements of habitual physical activity may capture men with high risk to fall Data from the Mr Os Sweden cohort. <i>Archives of Gerontology and Geriatrics</i> , 2009, 49, e72-e76.	1.4	22
59	Common Sequence Variation in <i>FLNB</i> Regulates Bone Structure in Women in the General Population and <i>FLNB</i> mRNA Expression in Osteoblasts In Vitro. <i>Journal of Bone and Mineral Research</i> , 2009, 24, 1989-1997.	3.1	21
60	Customized MethylC-Capture Sequencing to Evaluate Variation in the Human Sperm DNA Methylome Representative of Altered Folate Metabolism. <i>Environmental Health Perspectives</i> , 2019, 127, 87002.	2.8	20
61	Cross-reactive antibodies elicited to conserved epitopes on SARS-CoV-2 spike protein after infection and vaccination. <i>Scientific Reports</i> , 2022, 12, 6496.	1.6	20
62	Intersection of regulatory pathways controlling hemostasis and hemochorial placentation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	19
63	Interrogating causal pathways linking genetic variants, small molecule metabolites, and circulating lipids. <i>Genome Medicine</i> , 2014, 6, 25.	3.6	17
64	Dissecting features of epigenetic variants underlying cardiometabolic risk using full-resolution epigenome profiling in regulatory elements. <i>Nature Communications</i> , 2019, 10, 1209.	5.8	16
65	Immune cell residency in the nasal mucosa may partially explain respiratory disease severity across the age range. <i>Scientific Reports</i> , 2021, 11, 15927.	1.6	16
66	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. <i>Bone</i> , 2006, 39, 1343-1351.	1.4	13
67	Genetic risk factors for decreased bone mineral accretion in children with asthma receiving multiple oral corticosteroid bursts. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 136, 1240-1246.e8.	1.5	13
68	Blood DNA methylation at TXNIP and glycemic changes in response to weight-loss diet interventions: the POUNDS lost trial. <i>International Journal of Obesity</i> , 2022, 46, 1122-1127.	1.6	13
69	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. <i>Maturitas</i> , 2005, 50, 153-160.	1.0	12
70	The COMT val158met polymorphism is associated with prevalent fractures in Swedish men. <i>Bone</i> , 2008, 42, 107-112.	1.4	12
71	AKR1C2 and AKR1C3 expression in adipose tissue: Association with body fat distribution and regulatory variants. <i>Molecular and Cellular Endocrinology</i> , 2021, 527, 111220.	1.6	11
72	Capturing functional epigenomes for insight into metabolic diseases. <i>Molecular Metabolism</i> , 2020, 38, 100936.	3.0	9

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73	Adipose methylome integrative-omic analyses reveal genetic and dietary metabolic health drivers and insulin resistance classifiers. <i>Genome Medicine</i> , 2022, 14, .	3.6	6
74	The Impact of Estradiol on Bone Mineral Density Is Modulated by the Specific Estrogen Receptor- $\alpha$ Cofactor Retinoblastoma-Interacting Zinc Finger Protein-1 Insertion/Deletion Polymorphism. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2007, 92, 2300-2306.	1.8	5
75	Analysis of the Impact of Genetic Variation on Human Gene Expression. <i>Methods in Molecular Biology</i> , 2010, 628, 321-339.	0.4	5
76	Large-scale analysis of circulating glutamate and adipose gene expression in relation to abdominal obesity. <i>Amino Acids</i> , 0, , .	1.2	3
77	eP422: Diagnostic rate of genetic testing in a pediatric research cohort with clinical insurance denials. <i>Genetics in Medicine</i> , 2022, 24, S264.	1.1	0