Lennart Đ¡ Karssen

List of Publications by Year
in descending order

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37	4,588	236925	330143
papers	citations	25 h-index	37 g-index

38	38	38	12334
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Identification of seven loci affecting mean telomere length and their association with disease. Nature Genetics, 2013, 45, 422-427.	21.4	808
2	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615
3	Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. Nature Genetics, 2013, 45, 314-318.	21.4	398
4	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	21.4	365
5	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	21.4	310
6	The Genome of the Netherlands: design, and project goals. European Journal of Human Genetics, 2014, 22, 221-227.	2.8	246
7	Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma. Nature Genetics, 2014, 46, 1126-1130.	21.4	212
8	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. PLoS Genetics, 2012, 8, e1002490.	3.5	181
9	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	8.4	178
10	Characteristics of de novo structural changes in the human genome. Genome Research, 2015, 25, 792-801.	5.5	115
11	Genome-wide meta-analysis of 158,000 individuals of European ancestry identifies three loci associated with chronic back pain. PLoS Genetics, 2018, 14, e1007601.	3.5	112
12	Improved imputation quality of low-frequency and rare variants in European samples using the â€˜Genome of The Netherlandsâ€™. European Journal of Human Genetics, 2014, 22, 1321-1326.	2.8	92
13	Meta-analysis of genome-wide association studies identifies novel loci that influence cupping and the glaucomatous process. Nature Communications, 2014, 5, 4883.	12.8	89
14	Population-specific genotype imputations using minimac or IMPUTE2. Nature Protocols, 2015, 10, 1285-1296.	12.0	84
15	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. PLoS Genetics, 2015, 11, e1005230.	3.5	77
16	Insight into the genetic architecture of back pain and its risk factors from a study of 509,000 individuals. Pain, 2019, 160, 1361-1373.	4.2	74
17	Insight in Genome-Wide Association of Metabolite Quantitative Traits by Exome Sequence Analyses. PLoS Genetics, 2015, 11, e1004835.	3.5	70
18	Large scale international replication and meta-analysis study confirms association of the 15q14 locus with myopia. The CREAM consortium. Human Genetics, 2012, 131, 1467-1480.	3.8	67

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19	Meta-analysis of genome-wide association studies in five cohorts reveals common variants in RBFOX1, a regulator of tissue-specific splicing, associated with refractive error. Human Molecular Genetics, 2013, 22, 2754-2764.	2.9	60
20	The GenABEL Project for statistical genomics. F1000Research, 2016, 5, 914.	1.6	55
21	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. Nature Communications, 2015, 6, 6065.	12.8	45
22	Analysis of genetically independent phenotypes identifies shared genetic factors associated with chronic musculoskeletal pain conditions. Communications Biology, 2020, 3, 329.	4.4	42
23	Association Analysis of Bitter Receptor Genes in Five Isolated Populations Identifies a Significant Correlation between TAS2R43 Variants and Coffee Liking. PLoS ONE, 2014, 9, e92065.	2.5	41
24	Genome-Wide Meta-Analysis of Myopia and Hyperopia Provides Evidence for Replication of 11 Loci. PLoS ONE, 2014, 9, e107110.	2.5	40
25	A Genome-Wide Screen for Interactions Reveals a New Locus on 4p15 Modifying the Effect of Waist-to-Hip Ratio on Total Cholesterol. PLoS Genetics, 2011, 7, e1002333.	3.5	29
26	Non-additive genome-wide association scan reveals a new gene associated with habitual coffee consumption. Scientific Reports, 2016, 6, 31590.	3.3	25
27	Genome-wide association study for refractive astigmatism reveals genetic co-determination with spherical equivalent refractive error: the CREAM consortium. Human Genetics, 2015, 134, 131-146.	3.8	24
28	A Genome-Wide Association Study in isolated populations reveals new genes associated to common food likings. Reviews in Endocrine and Metabolic Disorders, 2016, 17, 209-219.	5.7	22
29	â€˜Omicsâ€™ biomarkers associated with chronic low back pain: protocol of a retrospective longitudinal study. BMJ Open, 2016, 6, e012070.	1.9	19
30	Plasma N-glycome composition associates with chronic low back pain. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 2124-2133.	2.4	18
31	Replication of 15 loci involved in human plasma protein N-glycosylation in 4802 samples from four cohorts. Glycobiology, 2021, 31, 82-88.	2.5	15
32	PheLiGe: an interactive database of billions of human genotypeâ€“phenotype associations. Nucleic Acids Research, 2021, 49, D1347-D1350.	14.5	13
33	The Challenges of Genome-Wide Interaction Studies: Lessons to Learn from the Analysis of HDL Blood Levels. PLoS ONE, 2014, 9, e109290.	2.5	13
34	Genome-wide association analysis on five isolated populations identifies variants of the HLA-DOA gene associated with white wine liking. European Journal of Human Genetics, 2015, 23, 1717-1722.	2.8	12
35	CollapsABEL: an R library for detecting compound heterozygote alleles in genome-wide association studies. BMC Bioinformatics, 2016, 17, 156.	2.6	10
36	Variants in TTC25 affect autistic trait in patients with autism spectrum disorder and general population. European Journal of Human Genetics, 2017, 25, 982-987.	2.8	5

#	Article	IF	Citations
37	Analytical and simulation methods for estimating the potential predictive ability of genetic profiling: a comparison of methods and results. European Journal of Human Genetics, 2012, 20, 1270-1274.	2.8	4