Lennart Đ¡ Karssen

List of Publications by Year
in descending order

37 papers	4,588 citations	236925 25 h-index	330143 37 g-index
38 all docs	38 docs citations	38 times ranked	12334 citing authors

#	Article	IF	Citations
1	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
2	PheLiGe: an interactive database of billions of human genotype–phenotype associations. Nucleic Acids Research, 2021, 49, D1347-D1350.	14.5	13
3	Analysis of genetically independent phenotypes identifies shared genetic factors associated with chronic musculoskeletal pain conditions. Communications Biology, 2020, 3, 329.	4.4	42
4	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
5	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
6	Plasma N-glycome composition associates with chronic low back pain. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 2124-2133.	2.4	18
7	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
8	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615
9	'Omics' biomarkers associated with chronic low back pain: protocol of a retrospective longitudinal study. BMJ Open, 2016, 6, e012070.	1.9	19
10	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
11	Non-additive genome-wide association scan reveals a new gene associated with habitual coffee consumption. Scientific Reports, 2016, 6, 31590.	3.3	25
12	CollapsABEL: an R library for detecting compound heterozygote alleles in genome-wide association studies. BMC Bioinformatics, 2016, 17, 156.	2.6	10
13	The GenABEL Project for statistical genomics. F1000Research, 2016, 5, 914.	1.6	55
14	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. PLoS Genetics, 2015, 11, e1005230.	3.5	77
15	Population-specific genotype imputations using minimac or IMPUTE2. Nature Protocols, 2015, 10, 1285-1296.	12.0	84
16	Insight in Genome-Wide Association of Metabolite Quantitative Traits by Exome Sequence Analyses. PLoS Genetics, 2015, 11, e1004835.	3.5	70
17	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
18	Characteristics of de novo structural changes in the human genome. Genome Research, 2015, 25, 792-801.	5.5	115

#	Article	IF	Citations
19	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
20	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	21.4	310
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	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	21.4	365
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	Improved imputation quality of low-frequency and rare variants in European samples using the 'Genome of The Netherlands'. European Journal of Human Genetics, 2014, 22, 1321-1326.	2.8	92
26	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
27	The Genome of the Netherlands: design, and project goals. European Journal of Human Genetics, 2014, 22, 221-227.	2.8	246
28	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
29	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
30	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
31	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
32	Identification of seven loci affecting mean telomere length and their association with disease. Nature Genetics, 2013, 45, 422-427.	21.4	808
33	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	8.4	178
34	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. PLoS Genetics, 2012, 8, e1002490.	3.5	181
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	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