Anne-Louise Leutenegger

List of Publications by Year
in descending order

45 papers	3,845 citations	236833 25 h-index	206029 48 g-index
50 all docs	50 docs citations	50 times ranked	7447 citing authors

#	Article	IF	Citations
1	Runs of Homozygosity in European Populations. American Journal of Human Genetics, 2008, 83, 359-372.	2.6	958
2	LRRK2G2019S as a Cause of Parkinson's Disease in North African Arabs. New England Journal of Medicine, 2006, 354, 422-423.	13.9	521
3	Loss of VPS13C Function in Autosomal-Recessive Parkinsonism Causes Mitochondrial Dysfunction and Increases PINK1/Parkin-Dependent Mitophagy. American Journal of Human Genetics, 2016, 98, 500-513.	2.6	333
4	Estimation of the Inbreeding Coefficient through Use of Genomic Data. American Journal of Human Genetics, 2003, 73, 516-523.	2.6	221
5	Variation in worldwide incidence of amyotrophic lateral sclerosis: a meta-analysis. International Journal of Epidemiology, 2017, 46, dyw061.	0.9	202
6	G2019S LRRK2 mutation in French and North African families with Parkinson's disease. Annals of Neurology, 2005, 58, 784-787.	2.8	196
7	Association of TALS Developmental Disorder with Defect in Minor Splicing Component U4atac snRNA. Science, 2011, 332, 240-243.	6.0	195
8	LRRK2 Haplotype Analyses in European and North African Families with Parkinson Disease: A Common Founder for the G2019S Mutation Dating from the 13th Century. American Journal of Human Genetics, 2005, 77, 330-332.	2.6	130
9	Clinical and demographic factors and outcome of amyotrophic lateral sclerosis in relation to population ancestral origin. European Journal of Epidemiology, 2016, 31, 229-245.	2.5	87
10	Segregation Analysis of Phenotypic Components of Learning Disabilities. I. Nonword Memory and Digit Span. American Journal of Human Genetics, 2000, 67, 631-646.	2.6	73
11	Genetics of VEGF Serum Variation in Human Isolated Populations of Cilento: Importance of VEGF Polymorphisms. PLoS ONE, 2011, 6, e16982.	1.1	68
12	High level of inbreeding in final phase of 1000 Genomes Project. Scientific Reports, 2015, 5, 17453.	1.6	68
13	Presence of Large Deletions in Kindreds with Autism. American Journal of Human Genetics, 2002, 71, 100-115.	2.6	63
14	A new Fâ€box protein 7 gene mutation causing typical Parkinson's disease. Movement Disorders, 2015, 30, 1130-1133.	2.2	59
15	Six Novel Loci Associated with Circulating VEGF Levels Identified by a Meta-analysis of Genome-Wide Association Studies. PLoS Genetics, 2016, 12, e1005874.	1.5	56
16	Consanguinity around the world: what do the genomic data of the HGDP-CEPH diversity panel tell us?. European Journal of Human Genetics, 2011, 19, 583-587.	1.4	52
17	LRRK2emph Exon 41 Mutations in Sporadic Parkinson Disease in Europeans. Archives of Neurology, 2007, 64, 425.	4.9	51
18	Using Genomic Inbreeding Coefficient Estimates for Homozygosity Mapping of Rare Recessive Traits: Application to Taybi-Linder Syndrome. American Journal of Human Genetics, 2006, 79, 62-66.	2.6	48

#	Article	IF	Citations
19	Parkinson's disease-related LRRK2 G2019S mutation results from independent mutational events in humans. Human Molecular Genetics, 2010, 19, 1998-2004.	1.4	48
20	Inbreeding Coefficient Estimation with Dense SNP Data: Comparison of Strategies and Application to HapMap III. Human Heredity, 2014, 77, 49-62.	0.4	46
21	Juvenile-Onset Parkinsonism as a Result of the First Mutation in the Adenosine Triphosphate Orientation Domain of PINK1. Archives of Neurology, 2006, 63, 1257.	4.9	43
22	FSuite: exploiting inbreeding in dense SNP chip and exome data. Bioinformatics, 2014, 30, 1940-1941.	1.8	30
23	Comparative assessment of methods for estimating individual genome-wide homozygosity-by-descent from human genomic data. BMC Genomics, 2010, 11, 139.	1.2	29
24	A novel locus for autosomal dominant â€œuncomplicatedâ€•hereditary spastic paraplegia maps to chromosome 8p21.1-q13.3. Human Genetics, 2007, 122, 261-273.	1.8	27
25	Strategies for phasing and imputation in a population isolate. Genetic Epidemiology, 2018, 42, 201-213.	0.6	27
26	New insights into minor splicingâ€”a transcriptomic analysis of cells derived from TALS patients. Rna, 2019, 25, 1130-1149.	1.6	27
27	Impact of parental relationships in maximum lod score affected sib-pair method. Genetic Epidemiology, 2002, 23, 413-425.	0.6	25
28	Novel Chronic Mouse Model of Cerebral Cavernous Malformations. Stroke, 2020, 51, 1272-1278.	1.0	25
29	Runs of Homozygosity in European Populations. American Journal of Human Genetics, 2008, 83, 658.	2.6	13
30	Genetic Variants Modulating CRIPTO Serum Levels Identified by Genome-Wide Association Study in Cilento Isolates. PLoS Genetics, 2015, 11, e1004976.	1.5	13
31	Polynesian ecology determines seasonality of biliary atresia. Hepatology, 2011, 54, 1893-1894.	3.6	12
32	The Importance of Connections: Joining Components of the Hutterite Pedigree. Genetic Epidemiology, 2001, 21, S230-5.	0.6	11
33	Genetic and Environmental Factors Influencing the Placental Growth Factor (PGF) Variation in Two Populations. PLoS ONE, 2012, 7, e42537.	1.1	11
34	Genome-wide inbreeding estimation within Lebanese communities using SNP arrays. European Journal of Human Genetics, 2015, 23, 1364-1369.	1.4	11
35	Multiethnic genomeâ€wide association study of differentiated thyroid cancer in the <scp>EPITHYR</scp> consortium. International Journal of Cancer, 2021, 148, 2935-2946.	2.3	11
36	Could Inbred Cases Identified in GWAS Data Succeed in Detecting Rare Recessive Variants Where Affected Sib-Pairs Have Failed?. Human Heredity, 2012, 74, 142-152.	0.4	8

#	Article	IF	Citations
37	Clinical interpretation of variants identified in RNU4ATAC, a non-coding spliceosomal gene. PLoS ONE, 2020, 15, e0235655.	1.1	8
38	Does anonymous sperm donation increase the risk for unions between relatives and the incidence of autosomal recessive diseases due to consanguinity?. Human Reproduction, 2014, 29, 394-399.	0.4	7
39	Whole-Exome Sequencing in the Isolated Populations of Cilento from South Italy. Scientific Reports, 2019, 9, 4059.	1.6	7
40	Genetics of PlGF plasma levels highlights a role of its receptors and supports the link between angiogenesis and immunity. Scientific Reports, 2021, 11, 16821.	1.6	6
41	Detection of susceptibility loci by genome-wide linkage analysis. BMC Genetics, 2005, 6, S18.	2.7	5
42	Detecting the dominance component of heritability in isolated and outbred human populations. Scientific Reports, 2018, 8, 18048.	1.6	3
43	Does inbreeding affect N-glycosylation of human plasma proteins?. Molecular Genetics and Genomics, 2011, 285, 427-432.	1.0	2
44	Modeling the effect of a genetic factor for a complex trait in a simulated population. BMC Genetics, 2005, 6, S87.	2.7	1
45	Relationship inference from the genetic data on parents or offspring: A comparative study. Theoretical Population Biology, 2016, 107, 31-38.	0.5	1