Anne-Louise Leutenegger

List of Publications by Year
in descending order

45 papers	3,845 citations	270111 25 h-index	232693 48 g-index
50 all docs	50 docs citations	50 times ranked	8219 citing authors

#	Article	IF	Citations
1	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
2	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
3	Clinical interpretation of variants identified in RNU4ATAC, a non-coding spliceosomal gene. PLoS ONE, 2020, 15, e0235655.	1.1	8
4	Novel Chronic Mouse Model of Cerebral Cavernous Malformations. Stroke, 2020, 51, 1272-1278.	1.0	25
5	New insights into minor splicingâ€"a transcriptomic analysis of cells derived from TALS patients. Rna, 2019, 25, 1130-1149.	1.6	27
6	Whole-Exome Sequencing in the Isolated Populations of Cilento from South Italy. Scientific Reports, 2019, 9, 4059.	1.6	7
7	Strategies for phasing and imputation in a population isolate. Genetic Epidemiology, 2018, 42, 201-213.	0.6	27
8	Detecting the dominance component of heritability in isolated and outbred human populations. Scientific Reports, 2018, 8, 18048.	1.6	3
9	Variation in worldwide incidence of amyotrophic lateral sclerosis: a meta-analysis. International Journal of Epidemiology, 2017, 46, dyw061.	0.9	202
10	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
11	Relationship inference from the genetic data on parents or offspring: A comparative study. Theoretical Population Biology, 2016, 107, 31-38.	0.5	1
12	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
13	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
14	High level of inbreeding in final phase of 1000 Genomes Project. Scientific Reports, 2015, 5, 17453.	1.6	68
15	Genome-wide inbreeding estimation within Lebanese communities using SNP arrays. European Journal of Human Genetics, 2015, 23, 1364-1369.	1.4	11
16	Genetic Variants Modulating CRIPTO Serum Levels Identified by Genome-Wide Association Study in Cilento Isolates. PLoS Genetics, 2015, 11, e1004976.	1.5	13
17	A new Fâ€box protein 7 gene mutation causing typical Parkinson's disease. Movement Disorders, 2015, 30, 1130-1133.	2.2	59
18	FSuite: exploiting inbreeding in dense SNP chip and exome data. Bioinformatics, 2014, 30, 1940-1941.	1.8	30

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19	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
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	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
22	Genetic and Environmental Factors Influencing the Placental Growth Factor (PGF) Variation in Two Populations. PLoS ONE, 2012, 7, e42537.	1.1	11
23	Genetics of VEGF Serum Variation in Human Isolated Populations of Cilento: Importance of VEGF Polymorphisms. PLoS ONE, 2011, 6, e16982.	1.1	68
24	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
25	Does inbreeding affect N-glycosylation of human plasma proteins?. Molecular Genetics and Genomics, 2011, 285, 427-432.	1.0	2
26	Polynesian ecology determines seasonality of biliary atresia. Hepatology, 2011, 54, 1893-1894.	3.6	12
27	Association of TALS Developmental Disorder with Defect in Minor Splicing Component U4atac snRNA. Science, 2011, 332, 240-243.	6.0	195
28	Comparative assessment of methods for estimating individual genome-wide homozygosity-by-descent from human genomic data. BMC Genomics, 2010, 11, 139.	1.2	29
29	Parkinson's disease-related LRRK2 G2019S mutation results from independent mutational events in humans. Human Molecular Genetics, 2010, 19, 1998-2004.	1.4	48
30	Runs of Homozygosity in European Populations. American Journal of Human Genetics, 2008, 83, 359-372.	2.6	958
31	Runs of Homozygosity in European Populations. American Journal of Human Genetics, 2008, 83, 658.	2.6	13
32	LRRK2emph Exon 41 Mutations in Sporadic Parkinson Disease in Europeans. Archives of Neurology, 2007, 64, 425.	4.9	51
33	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
34	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
35	LRRK2G2019S as a Cause of Parkinson's Disease in North African Arabs. New England Journal of Medicine, 2006, 354, 422-423.	13.9	521
36	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

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37	G2019S LRRK2 mutation in French and North African families with Parkinson's disease. Annals of Neurology, 2005, 58, 784-787.	2.8	196
38	Detection of susceptibility loci by genome-wide linkage analysis. BMC Genetics, 2005, 6, S18.	2.7	5
39	Modeling the effect of a genetic factor for a complex trait in a simulated population. BMC Genetics, 2005, 6, S87.	2.7	1
40	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
41	Estimation of the Inbreeding Coefficient through Use of Genomic Data. American Journal of Human Genetics, 2003, 73, 516-523.	2.6	221
42	Presence of Large Deletions in Kindreds with Autism. American Journal of Human Genetics, 2002, 71, 100-115.	2.6	63
43	Impact of parental relationships in maximum lod score affected sib-pair method. Genetic Epidemiology, 2002, 23, 413-425.	0.6	25
44	The Importance of Connections: Joining Components of the Hutterite Pedigree. Genetic Epidemiology, 2001, 21, S230-5.	0.6	11
45	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