Guillaume Lettre

List of Publications by Citations

130 papers	25,027 citations	58 h-index	143 g-index
143 ext. papers	28,887 ext. citations	14.9 avg, IF	5.7 L-index

#	Paper	IF	Citations
130	Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13	50.4	2742
129	Genome-wide association analysis identifies loci for type 2 diabetes and triglyceride levels. *Science*, **2007**, 316, 1331-6	33.3	2364
128	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48	36.3	2267
127	Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*, **2010**, 467, 832-8	50.4	1514
126	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. *Nature Genetics*, **2011**, 43, 333-8	36.3	1394
125	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. *Nature Genetics*, **2009**, 41, 25-34	36.3	1368
124	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
123	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. *Nature Genetics*, **2010**, 42, 949-60	36.3	724
122	Genome partitioning of genetic variation for complex traits using common SNPs. *Nature Genetics*, **2011**, 43, 519-25	36.3	659
121	Human fetal hemoglobin expression is regulated by the developmental stage-specific repressor BCL11A. *Science*, **2008**, 322, 1839-42	33.3	618
120	Deep resequencing of GWAS loci identifies independent rare variants associated with inflammatory bowel disease. *Nature Genetics*, **2011**, 43, 1066-73	36.3	584
119	Identification of ten loci associated with height highlights new biological pathways in human growth. *Nature Genetics*, **2008**, 40, 584-91	36.3	482
118	Genome-wide association study shows BCL11A associated with persistent fetal hemoglobin and amelioration of the phenotype of beta-thalassemia. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 1620-5	11.5	469
117	DNA polymorphisms at the BCL11A, HBS1L-MYB, and beta-globin loci associate with fetal hemoglobin levels and pain crises in sickle cell disease. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 11869-74	11.5	428
116	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
115	An erythroid enhancer of BCL11A subject to genetic variation determines fetal hemoglobin level. *Science*, **2013**, 342, 253-7	33.3	400
114	Genomic inflation factors under polygenic inheritance. *European Journal of Human Genetics*, **2011**, 19, 807-12	5.3	335

113	A common variant of HMGA2 is associated with adult and childhood height in the general population. *Nature Genetics*, **2007**, 39, 1245-50	36.3	330
112	Common variants in the GDF5-UQCC region are associated with variation in human height. *Nature Genetics*, **2008**, 40, 198-203	36.3	315
111	FTO genotype is associated with phenotypic variability of body mass index. *Nature*, **2012**, 490, 267-72	50.4	304
110	Genome-wide association study of coronary heart disease and its risk factors in 8,090 African Americans: the NHLBI CARe Project. *PLoS Genetics*, **2011**, 7, e1001300	6	249
109	Autoimmune diseases: insights from genome-wide association studies. *Human Molecular Genetics*, **2008**, 17, R116-21	5.6	232
108	Developmental apoptosis in C. elegans: a complex CEDnario. *Nature Reviews Molecular Cell Biology*, **2006**, 7, 97-108	48.7	226
107	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. *PLoS Genetics*, **2015**, 11, e1005378	6	220
106	Fine-mapping at three loci known to affect fetal hemoglobin levels explains additional genetic variation. *Nature Genetics*, **2010**, 42, 1049-51	36.3	208
105	Genetic model testing and statistical power in population-based association studies of quantitative traits. *Genetic Epidemiology*, **2007**, 31, 358-62	2.6	203
104	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. *Nature Genetics*, **2013**, 45, 690-6	36.3	192
103	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
102	European ancestry as a risk factor for atrial fibrillation in African Americans. *Circulation*, **2010**, 122, 2009-15	16.7	171
101	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. *American Journal of Human Genetics*, **2014**, 94, 233-45	11	170
100	Deep resequencing of GWAS loci identifies rare variants in CARD9, IL23R and RNF186 that are associated with ulcerative colitis. *PLoS Genetics*, **2013**, 9, e1003723	6	149
99	Genome-wide association analysis of blood-pressure traits in African-ancestry individuals reveals common associated genes in African and non-African populations. *American Journal of Human Genetics*, **2013**, 93, 545-54	11	145
98	Rare variant association studies: considerations, challenges and opportunities. *Genome Medicine*, **2015**, 7, 16	14.4	134
97	Polygenic Versus Monogenic Causes of Hypercholesterolemia Ascertained Clinically. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2016**, 36, 2439-2445	9.4	130
96	Association of sickle cell trait with chronic kidney disease and albuminuria in African Americans. *JAMA - Journal of the American Medical Association*, **2014**, 312, 2115-25	27.4	126

95	Candidate gene association resource (CARe): design, methods, and proof of concept. *Circulation: Cardiovascular Genetics*, **2010**, 3, 267-75		125
94	Genome-wide association study of white blood cell count in 16,388 African Americans: the continental origins and genetic epidemiology network (COGENT). *PLoS Genetics*, **2011**, 7, e1002108	6	111
93	Imputation of exome sequence variants into population- based samples and blood-cell-trait-associated loci in African Americans: NHLBI GO Exome Sequencing Project. *American Journal of Human Genetics*, **2012**, 91, 794-808	11	103
92	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2011**, 88, 6-18	11	103
91	The Polygenic and Monogenic Basis of Blood Traits and Diseases. *Cell*, **2020**, 182, 1214-1231.e11	56.2	96
90	Rare and low-frequency coding variants in CXCR2 and other genes are associated with hematological traits. *Nature Genetics*, **2014**, 46, 629-34	36.3	92
89	Multiple loci are associated with white blood cell phenotypes. *PLoS Genetics*, **2011**, 7, e1002113	6	92
88	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. *Cell*, **2020**, 182, 1198-1213.e14	56.2	88
87	Enhanced statistical tests for GWAS in admixed populations: assessment using African Americans from CARe and a Breast Cancer Consortium. *PLoS Genetics*, **2011**, 7, e1001371	6	86
86	A meta-analysis and genome-wide association study of platelet count and mean platelet volume in african americans. *PLoS Genetics*, **2012**, 8, e1002491	6	84
85	Genome-wide association of anthropometric traits in African- and African-derived populations. *Human Molecular Genetics*, **2010**, 19, 2725-38	5.6	81
84	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2012**, 90, 1116-1117	11	78
83	Identification, replication, and fine-mapping of Loci associated with adult height in individuals of african ancestry. *PLoS Genetics*, **2011**, 7, e1002298	6	77
82	Genetic association analysis highlights new loci that modulate hematological trait variation in Caucasians and African Americans. *Human Genetics*, **2011**, 129, 307-17	6.3	74
81	Variant-aware saturating mutagenesis using multiple Cas9 nucleases identifies regulatory elements at trait-associated loci. *Nature Genetics*, **2017**, 49, 625-634	36.3	73
80	Fine mapping of the association with obesity at the FTO locus in African-derived populations. *Human Molecular Genetics*, **2010**, 19, 2907-16	5.6	72
79	Association of variants at BCL11A and HBS1L-MYB with hemoglobin F and hospitalization rates among sickle cell patients in Cameroon. *PLoS ONE*, **2014**, 9, e92506	3.7	69
78	Human genetic variation alters CRISPR-Cas9 on- and off-targeting specificity at therapeutically implicated loci. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E11257-E11266	11.5	66

77	Comparison of DNA methylation profiles in human fetal and adult red blood cell progenitors. *Genome Medicine*, **2015**, 7, 1	14.4	65
76	Recent progress in the study of the genetics of height. *Human Genetics*, **2011**, 129, 465-72	6.3	64
75	Genome-wide comparison of African-ancestry populations from CARe and other cohorts reveals signals of natural selection. *American Journal of Human Genetics*, **2011**, 89, 368-81	11	63
74	Myocardial Infarction-Associated SNP at 6p24 Interferes With MEF2 Binding and Associates With PHACTR1 Expression Levels in Human Coronary Arteries. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2015**, 35, 1472-1479	9.4	62
73	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. *American Journal of Human Genetics*, **2016**, 99, 40-55	11	61
72	Fetal haemoglobin in sickle-cell disease: from genetic epidemiology to new therapeutic strategies. *Lancet, The*, **2016**, 387, 2554-64	40	55
71	Frameshift indels introduced by genome editing can lead to in-frame exon skipping. *PLoS ONE*, **2017**, 12, e0178700	3.7	53
70	Common genetic variation in eight genes of the GH/IGF1 axis does not contribute to adult height variation. *Human Genetics*, **2007**, 122, 129-39	6.3	51
69	Genetic regulation of adult stature. *Current Opinion in Pediatrics*, **2009**, 21, 515-22	3.2	50
68	Genome-wide association analysis of red blood cell traits in African Americans: the COGENT Network. *Human Molecular Genetics*, **2013**, 22, 2529-38	5.6	48
67	C. elegans GLA-3 is a novel component of the MAP kinase MPK-1 signaling pathway required for germ cell survival. *Genes and Development*, **2006**, 20, 2279-92	12.6	47
66	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. *American Journal of Human Genetics*, **2016**, 99, 8-21	11	47
65	Trans-ethnic meta-analysis of white blood cell phenotypes. *Human Molecular Genetics*, **2014**, 23, 6944-60	5.6	45
64	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. *Molecular Psychiatry*, **2020**, 25, 2392-2409	15.1	45
63	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
62	Nonsense mutations in BAG3 are associated with early-onset dilated cardiomyopathy in French Canadians. *Canadian Journal of Cardiology*, **2014**, 30, 1655-61	3.8	43
61	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. *American Journal of Human Genetics*, **2016**, 99, 22-39	11	42
60	The search for genetic modifiers of disease severity in the hemoglobinopathies. *Cold Spring Harbor Perspectives in Medicine*, **2012**, 2,	5.4	40

59	Multi-ethnic analysis of lipid-associated loci: the NHLBI CARe project. *PLoS ONE*, **2012**, 7, e36473	3.7	39
58	Pleiotropic effects for Parkin and LRRK2 in leprosy type-1 reactions and Parkinson's disease. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 15616-15624	11.5	35
57	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol Use. *Biological Psychiatry*, **2019**, 85, 946-955	7.9	35
56	Shared genetic pathways contribute to risk of hypertrophic and dilated cardiomyopathies with opposite directions of effect. *Nature Genetics*, **2021**, 53, 128-134	36.3	35
55	Validation of Genome-Wide Polygenic Risk Scores for Coronary Artery Disease in French Canadians. *Circulation Genomic and Precision Medicine*, **2019**, 12, e002481	5.2	33
54	Polygenic determinants in extremes of high-density lipoprotein cholesterol. *Journal of Lipid Research*, **2017**, 58, 2162-2170	6.3	33
53	Whole-Exome Sequencing Identifies Loci Associated with Blood Cell Traits and Reveals a Role for Alternative GFI1B Splice Variants in Human Hematopoiesis. *American Journal of Human Genetics*, **2016**, 99, 481-8	11	31
52	Rare coding variants pinpoint genes that control human hematological traits. *PLoS Genetics*, **2017**, 13, e1006925	6	28
51	Neuropilin-1 expression in adipose tissue macrophages protects against obesity and metabolic syndrome. *Science Immunology*, **2018**, 3,	28	27
50	The genetics of platelet count and volume in humans. *Platelets*, **2018**, 29, 125-130	3.6	26
49	Common β-globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. *PLoS Genetics*, **2018**, 14, e1007293	6	25
48	Large multiethnic Candidate Gene Study for C-reactive protein levels: identification of a novel association at CD36 in African Americans. *Human Genetics*, **2014**, 133, 985-95	6.3	25
47	An erythroid-specific ATP2B4 enhancer mediates red blood cell hydration and malaria susceptibility. *Journal of Clinical Investigation*, **2017**, 127, 3065-3074	15.9	24
46	Modifier genes in Mendelian disorders: the example of hemoglobin disorders. *Annals of the New York Academy of Sciences*, **2010**, 1214, 47-56	6.5	23
45	Rare and low-frequency variants in human common diseases and other complex traits. *Journal of Medical Genetics*, **2014**, 51, 705-14	5.8	21
44	Association of linear growth impairment in pediatric Crohn's disease and a known height locus: a pilot study. *Annals of Human Genetics*, **2010**, 74, 489-97	2.2	19
43	Lower Methylation of the ANGPTL2 Gene in Leukocytes from Post-Acute Coronary Syndrome Patients. *PLoS ONE*, **2016**, 11, e0153920	3.7	17
42	14q32 and let-7 microRNAs regulate transcriptional networks in fetal and adult human erythroblasts. *Human Molecular Genetics*, **2018**, 27, 1411-1420	5.6	14

41	Variants at the APOE /C1/C2/C4 Locus Modulate Cholesterol Efflux Capacity Independently of High-Density Lipoprotein Cholesterol. *Journal of the American Heart Association*, **2018**, 7, e009545	6	14
40	Ultraconserved elements in the human genome: association and transmission analyses of highly constrained single-nucleotide polymorphisms. *Genetics*, **2012**, 192, 253-66	4	13
39	Whole-genome sequencing in French Canadians from Quebec. *Human Genetics*, **2016**, 135, 1213-1221	6.3	13
38	PHACTR1 splicing isoforms and eQTLs in atherosclerosis-relevant human cells. *BMC Medical Genetics*, **2018**, 19, 97	2.1	12
37	A variational Bayes discrete mixture test for rare variant association. *Genetic Epidemiology*, **2014**, 38, 21-30	2.6	12
36	Validation of fatty acid intakes estimated by a food frequency questionnaire using erythrocyte fatty acid profiling in the Montreal Heart Institute Biobank. *Journal of Human Nutrition and Dietetics*, **2015**, 28, 646-58	3.1	12
35	Lessons and Implications from Genome-Wide Association Studies (GWAS) Findings of Blood Cell Phenotypes. *Genes*, **2014**, 5, 51-64	4.2	12
34	Small island, big genetic discoveries. *Nature Genetics*, **2015**, 47, 1224-5	36.3	11
33	Integrative analysis of vascular endothelial cell genomic features identifies AIDA as a coronary artery disease candidate gene. *Genome Biology*, **2019**, 20, 133	18.3	11
32	Whole-exome imputation of sequence variants identified two novel alleles associated with adult body height in African Americans. *Human Molecular Genetics*, **2014**, 23, 6607-15	5.6	11
31	Strategies to fine-map genetic associations with lipid levels by combining epigenomic annotations and liver-specific transcription profiles. *Genomics*, **2014**, 104, 105-12	4.3	10
30	Whole genome sequence association with E-selectin levels reveals loss-of-function variant in African Americans. *Human Molecular Genetics*, **2019**, 28, 515-523	5.6	10
29	A common functional PIEZO1 deletion allele associates with red blood cell density in sickle cell disease patients. *American Journal of Hematology*, **2018**, 93, E362-E365	7.1	9
28	Pooled DNA resequencing of 68 myocardial infarction candidate genes in French canadians. *Circulation: Cardiovascular Genetics*, **2012**, 5, 547-54		9
27	Genome-wide association study of erythrocyte density in sickle cell disease patients. *Blood Cells, Molecules, and Diseases*, **2017**, 65, 60-65	2.1	8
26	Testing the role of predicted gene knockouts in human anthropometric trait variation. *Human Molecular Genetics*, **2016**, 25, 2082-2092	5.6	7
25	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. *American Journal of Human Genetics*, **2021**, 108, 564-582	11	7
24	Clonal hematopoiesis in sickle cell disease. *Blood*, **2021**, 138, 2148-2152	2.2	7

23	Using height association studies to gain insights into human idiopathic short and syndromic stature phenotypes. *Pediatric Nephrology*, **2013**, 28, 557-62	3.2	5
22	The non-synonymous polymorphism at position 114 of the WRN protein affects cholesterol efflux in vitro and correlates with cholesterol levels in vivo. *Experimental Gerontology*, **2013**, 48, 533-8	4.5	5
21	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. *American Journal of Human Genetics*, **2021**, 108, 874-893	11	5
20	A genetic association study of heart failure: more evidence for the role of BAG3 in idiopathic dilated cardiomyopathy. *ESC Heart Failure*, **2020**, 7, 4384	3.7	4
19	Crispr-Cas9 Saturating Mutagenesis Reveals an Achilles Heel in the BCL11A Erythroid Enhancer for Fetal Hemoglobin Induction (by Genome Editing). *Blood*, **2015**, 126, 638-638	2.2	3
18	The Polygenic and Monogenic Basis of Blood Traits and Diseases		3
17	A mechanotoxin-4 (GsMTx4)-sensitive cation channel mediates increased cation permeability in human hereditary spherocytosis of multiple genetic etiologies. *Haematologica*, **2021**, 106, 2759-2762	6.6	3
16	Potential causal role of l-glutamine in sickle cell disease painful crises: A Mendelian randomization analysis. *Blood Cells, Molecules, and Diseases*, **2021**, 86, 102504	2.1	3
15	The osteoarthritis and height GDF5 locus yields its secrets. *Nature Genetics*, **2017**, 49, 1165-1166	36.3	2
14	Lp-PLA2, scavenger receptor class B type I gene (SCARB1) rs10846744 variant, and cardiovascular disease. *PLoS ONE*, **2018**, 13, e0204352	3.7	2
13	Fine-Mapping and Genome Editing Reveal An Essential Erythroid Enhancer At The HbF-Associated BCL11A Locus. *Blood*, **2013**, 122, 437-437	2.2	1
12	An Essential Erythroid-Specific Enhancer of ATP2B4 Associated with Red Blood Cell Traits and Malaria Susceptibility. *Blood*, **2016**, 128, 1250-1250	2.2	1
11	From GWAS variant to function: A study of ~148,000 variants for blood cell traits.. *Human Genetics and Genomics Advances*, **2022**, 3, 100063	0.8	1
10	Whole genome sequencing association analysis of quantitative red blood cell phenotypes: the NHLBI TOPMed program		1
9	Validation of genome-wide polygenic risk scores for coronary artery disease in French Canadians		1
8	From GWAS Variant to Function: a Study of ~148,000 Variants for Blood Cell Traits		1
7	CRISPR perturbations at many coronary artery disease loci impair vascular endothelial cell functions		1
6	Transcriptomic Profiling of Canine Atrial Fibrillation Models After One Week of Sustained Arrhythmia. *Circulation: Arrhythmia and Electrophysiology*, **2021**, 14, e009887	6.4	1

5	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. *American Journal of Human Genetics*, **2021**, 108, 1836-1851	11	1
4	Cohort profile: genomic data for 26 622 individuals from the Canadian Longitudinal Study on Aging (CLSA).. *BMJ Open*, **2022**, 12, e059021	3	1
3	Multi-ethnic genome-wide association analyses of white blood cell and platelet traits in the Population Architecture using Genomics and Epidemiology (PAGE) study. *BMC Genomics*, **2021**, 22, 432	4.5	0
2	Blocking HbS Polymerization in SCD. *Cell*, **2020**, 180, 819	56.2	
1	Prospective Evaluation of Fetal Haemoglobin Induction in Maternal Erythrocytes: A Preliminary Analysis of a Cohort of 345 Parturients. *Blood*, **2015**, 126, 3370-3370	2.2	