Guillaume Lettre

List of Publications by Year
in descending order

131 papers	31,119 citations	18465 62 h-index	14197 128 g-index
143 all docs	143 docs citations	143 times ranked	38144 citing authors

#	Article	IF	Citations
1	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
2	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
3	Genome-Wide Association Analysis Identifies Loci for Type 2 Diabetes and Triglyceride Levels. Science, 2007, 316, 1331-1336.	6.0	2,623
4	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
5	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
6	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. Nature Genetics, 2011, 43, 333-338.	9.4	1,685
7	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	9.4	1,572
8	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, 949-960.	9.4	836
9	Genome partitioning of genetic variation for complex traits using common SNPs. Nature Genetics, 2011, 43, 519-525.	9.4	834
10	Human Fetal Hemoglobin Expression Is Regulated by the Developmental Stage-Specific Repressor BCL11A. Science, 2008, 322, 1839-1842.	6.0	759
11	Deep resequencing of GWAS loci identifies independent rare variants associated with inflammatory bowel disease. Nature Genetics, 2011, 43, 1066-1073.	9.4	698
12	Genome-wide association study shows BCL11A associated with persistent fetal hemoglobin and amelioration of the phenotype of Î²-thalassemia. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 1620-1625.	3.3	561
13	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
14	Identification of ten loci associated with height highlights new biological pathways in human growth. Nature Genetics, 2008, 40, 584-591.	9.4	537
15	An Erythroid Enhancer of BCL11A Subject to Genetic Variation Determines Fetal Hemoglobin Level. Science, 2013, 342, 253-257.	6.0	518
16	DNA polymorphisms at the BCL11A , HBS1L-MYB , and Î²- 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, 11869-11874.	3.3	510
17	Genomic inflation factors under polygenic inheritance. European Journal of Human Genetics, 2011, 19, 807-812.	1.4	460
18	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	13.5	388

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19	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	13.7	383
20	A common variant of HMGA2 is associated with adult and childhood height in the general population. Nature Genetics, 2007, 39, 1245-1250.	9.4	373
21	Common variants in the GDF5-UQCC region are associated with variation in human height. Nature Genetics, 2008, 40, 198-203.	9.4	369
22	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	13.5	353
23	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.	1.5	331
24	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.	1.5	290
25	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
26	Autoimmune diseases: insights from genome-wide association studies. Human Molecular Genetics, 2008, 17, R116-R121.	1.4	275
27	Developmental apoptosis in C. elegans: a complex CEDnario. Nature Reviews Molecular Cell Biology, 2006, 7, 97-108.	16.1	269
28	Fine-mapping at three loci known to affect fetal hemoglobin levels explains additional genetic variation. Nature Genetics, 2010, 42, 1049-1051.	9.4	243
29	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. Nature Genetics, 2013, 45, 690-696.	9.4	232
30	Genetic model testing and statistical power in population-based association studies of quantitative traits. Genetic Epidemiology, 2007, 31, 358-362.	0.6	224
31	European Ancestry as a Risk Factor for Atrial Fibrillation in African Americans. Circulation, 2010, 122, 2009-2015.	1.6	219
32	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	2.6	193
33	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, 545-554.	2.6	189
34	Deep Resequencing of GWAS Loci Identifies Rare Variants in CARD9, IL23R and RNF186 That Are Associated with Ulcerative Colitis. PLoS Genetics, 2013, 9, e1003723.	1.5	185
35	Rare variant association studies: considerations, challenges and opportunities. Genome Medicine, 2015, 7, 16.	3.6	176
36	Polygenic Versus Monogenic Causes of Hypercholesterolemia Ascertained Clinically. Arteriosclerosis, Thrombosis, and Vascular Biology, 2016, 36, 2439-2445.	1.1	174

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37	Association of Sickle Cell Trait With Chronic Kidney Disease and Albuminuria in African Americans. JAMA - Journal of the American Medical Association, 2014, 312, 2115.	3.8	167
38	Shared genetic pathways contribute to risk of hypertrophic and dilated cardiomyopathies with opposite directions of effect. Nature Genetics, 2021, 53, 128-134.	9.4	155
39	Candidate Gene Association Resource (CARe). Circulation: Cardiovascular Genetics, 2010, 3, 267-275.	5.1	139
40	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.	1.5	133
41	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.	2.6	123
42	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	2.6	122
43	Rare and low-frequency coding variants in CXCR2 and other genes are associated with hematological traits. Nature Genetics, 2014, 46, 629-634.	9.4	113
44	Enhanced Statistical Tests for GWAS in Admixed Populations: Assessment using African Americans from CARe and a Breast Cancer Consortium. PLoS Genetics, 2011, 7, e1001371.	1.5	110
45	Multiple Loci Are Associated with White Blood Cell Phenotypes. PLoS Genetics, 2011, 7, e1002113.	1.5	106
46	Comparison of DNA methylation profiles in human fetal and adult red blood cell progenitors. Genome Medicine, 2015, 7, 1.	3.6	104
47	A Meta-Analysis and Genome-Wide Association Study of Platelet Count and Mean Platelet Volume in African Americans. PLoS Genetics, 2012, 8, e1002491.	1.5	97
48	Variant-aware saturating mutagenesis using multiple Cas9 nucleases identifies regulatory elements at trait-associated loci. Nature Genetics, 2017, 49, 625-634.	9.4	96
49	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.	3.3	96
50	Identification, Replication, and Fine-Mapping of Loci Associated with Adult Height in Individuals of African Ancestry. PLoS Genetics, 2011, 7, e1002298.	1.5	93
51	Genome-wide association of anthropometric traits in African- and African-derived populations. Human Molecular Genetics, 2010, 19, 2725-2738.	1.4	90
52	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
53	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	4.1	83
54	Fine mapping of the association with obesity at the FTO locus in African-derived populations. Human Molecular Genetics, 2010, 19, 2907-2916.	1.4	82

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55	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	2.6	82
56	Genetic association analysis highlights new loci that modulate hematological trait variation in Caucasians and African Americans. Human Genetics, 2011, 129, 307-317.	1.8	81
57	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.	1.1	80
58	Genome-wide Comparison of African-Ancestry Populations from CARe and Other Cohorts Reveals Signals of Natural Selection. American Journal of Human Genetics, 2011, 89, 368-381.	2.6	79
59	Myocardial Infarctionâ€“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.	1.1	78
60	Frameshift indels introduced by genome editing can lead to in-frame exon skipping. PLoS ONE, 2017, 12, e0178700.	1.1	77
61	Recent progress in the study of the genetics of height. Human Genetics, 2011, 129, 465-472.	1.8	73
62	Fetal haemoglobin in sickle-cell disease: from genetic epidemiology to new therapeutic strategies. Lancet, The, 2016, 387, 2554-2564.	6.3	73
63	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and AlcoholÂUse. Biological Psychiatry, 2019, 85, 946-955.	0.7	69
64	Trans-ethnic meta-analysis of white blood cell phenotypes. Human Molecular Genetics, 2014, 23, 6944-6960.	1.4	60
65	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	2.6	60
66	Genetic regulation of adult stature. Current Opinion in Pediatrics, 2009, 21, 515-522.	1.0	59
67	Validation of Genome-Wide Polygenic Risk Scores for Coronary Artery Disease in French Canadians. Circulation Genomic and Precision Medicine, 2019, 12, e002481.	1.6	59
68	Genome-wide association analysis of red blood cell traits in African Americans: the COGENT Network. Human Molecular Genetics, 2013, 22, 2529-2538.	1.4	57
69	Nonsense Mutations in BAG3 are Associated With Early-Onset Dilated Cardiomyopathy in French Canadians. Canadian Journal of Cardiology, 2014, 30, 1655-1661.	0.8	57
70	Common genetic variation in eight genes of the GH/IGF1 axis does not contribute to adult height variation. Human Genetics, 2007, 122, 129-139.	1.8	54
71	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, 2279-2292.	2.7	53
72	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.	2.6	50

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73	Pleiotropic effects for Parkin and LRRK2 in leprosy type-1 reactions and Parkinsonâ€™s disease. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15616-15624.	3.3	50
74	Polygenic determinants in extremes of high-density lipoprotein cholesterol. Journal of Lipid Research, 2017, 58, 2162-2170.	2.0	49
75	The Search for Genetic Modifiers of Disease Severity in the Â-Hemoglobinopathies. Cold Spring Harbor Perspectives in Medicine, 2012, 2, a015032-a015032.	2.9	48
76	An erythroid-specific ATP2B4 enhancer mediates red blood cell hydration and malaria susceptibility. Journal of Clinical Investigation, 2017, 127, 3065-3074.	3.9	48
77	Multi-Ethnic Analysis of Lipid-Associated Loci: The NHLBI CARe Project. PLoS ONE, 2012, 7, e36473.	1.1	46
78	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, 481-488.	2.6	45
79	Common Î±-globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. PLoS Genetics, 2018, 14, e1007293.	1.5	45
80	The genetics of platelet count and volume in humans. Platelets, 2018, 29, 125-130.	1.1	44
81	Neuropilin-1 expression in adipose tissue macrophages protects against obesity and metabolic syndrome. Science Immunology, 2018, 3, .	5.6	41
82	Rare coding variants pinpoint genes that control human hematological traits. PLoS Genetics, 2017, 13, e1006925.	1.5	39
83	Importance of genetic testing in unexplained cardiac arrest. European Heart Journal, 2022, 43, 3071-3081.	1.0	36
84	Large multiethnic Candidate Gene Study for C-reactive protein levels: identification of a novel association at CD36 in African Americans. Human Genetics, 2014, 133, 985-995.	1.8	31
85	Rare and low-frequency variants in human common diseases and other complex traits. Journal of Medical Genetics, 2014, 51, 705-714.	1.5	29
86	Clonal hematopoiesis in sickle cell disease. Blood, 2021, 138, 2148-2152.	0.6	29
87	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	2.6	28
88	Modifier genes in Mendelian disorders: the example of hemoglobin disorders. Annals of the New York Academy of Sciences, 2010, 1214, 47-56.	1.8	27
89	Integrative analysis of vascular endothelial cell genomic features identifies AIDA as a coronary artery disease candidate gene. Genome Biology, 2019, 20, 133.	3.8	26
90	14q32 and let-7 microRNAs regulate transcriptional networks in fetal and adult human erythroblasts. Human Molecular Genetics, 2018, 27, 1411-1420.	1.4	25

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91	Variants at the APOE/C1/C2/C4 Locus Modulate Cholesterol Efflux Capacity Independently of Highâ€Density Lipoprotein Cholesterol. Journal of the American Heart Association, 2018, 7, e009545.	1.6	25
92	Association of Linear Growth Impairment in Pediatric Crohn's Disease and a Known Height Locus: A Pilot Study. Annals of Human Genetics, 2010, 74, 489-497.	0.3	24
93	PHACTR1 splicing isoforms and eQTLs in atherosclerosis-relevant human cells. BMC Medical Genetics, 2018, 19, 97.	2.1	20
94	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, 646-658.	1.3	18
95	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.	2.6	18
96	Lower Methylation of the ANGPTL2 Gene in Leukocytes from Post-Acute Coronary Syndrome Patients. PLoS ONE, 2016, 11, e0153920.	1.1	18
97	Ultraconserved Elements in the Human Genome: Association and Transmission Analyses of Highly Constrained Single-Nucleotide Polymorphisms. Genetics, 2012, 192, 253-266.	1.2	17
98	Small island, big genetic discoveries. Nature Genetics, 2015, 47, 1224-1225.	9.4	17
99	Cohort profile: genomic data for 26 622 individuals from the Canadian Longitudinal Study on Aging (CLSA). BMJ Open, 2022, 12, e059021.	0.8	17
100	Whole-genome sequencing in French Canadians from Quebec. Human Genetics, 2016, 135, 1213-1221.	1.8	16
101	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.	2.0	15
102	Whole genome sequence association with E-selectin levels reveals loss-of-function variant in African Americans. Human Molecular Genetics, 2019, 28, 515-523.	1.4	15
103	Whole-exome imputation of sequence variants identified two novel alleles associated with adult body height in African Americans. Human Molecular Genetics, 2014, 23, 6607-6615.	1.4	14
104	Strategies to fine-map genetic associations with lipid levels by combining epigenomic annotations and liver-specific transcription profiles. Genomics, 2014, 104, 105-112.	1.3	14
105	Potential causal role of l-glutamine in sickle cell disease painful crises: A Mendelian randomization analysis. Blood Cells, Molecules, and Diseases, 2021, 86, 102504.	0.6	14
106	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.	2.6	14
107	Genome-wide association study of erythrocyte density in sickle cell disease patients. Blood Cells, Molecules, and Diseases, 2017, 65, 60-65.	0.6	13
108	Lessons and Implications from Genome-Wide Association Studies (GWAS) Findings of Blood Cell Phenotypes. Genes, 2014, 5, 51-64.	1.0	12

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109	A Variational Bayes Discrete Mixture Test for Rare Variant Association. Genetic Epidemiology, 2014, 38, 21-30.	0.6	12
110	A genetic association study of heart failure: more evidence for the role of BAG3 in idiopathic dilated cardiomyopathy. ESC Heart Failure, 2020, 7, 4384-4389.	1.4	11
111	Pooled DNA Resequencing of 68 Myocardial Infarction Candidate Genes in French Canadians. Circulation: Cardiovascular Genetics, 2012, 5, 547-554.	5.1	10
112	Testing the role of predicted gene knockouts in human anthropometric trait variation. Human Molecular Genetics, 2016, 25, 2082-2092.	1.4	10
113	From GWAS variant to function: A study of â^¼148,000 variants for blood cell traits. Human Genetics and Genomics Advances, 2022, 3, 100063.	1.0	9
114	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, 533-538.	1.2	7
115	The osteoarthritis and height GDF5 locus yields its secrets. Nature Genetics, 2017, 49, 1165-1166.	9.4	7
116	Using height association studies to gain insights into human idiopathic short and syndromic stature phenotypes. Pediatric Nephrology, 2013, 28, 557-562.	0.9	6
117	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.	1.2	6
118	Transcriptomic Profiling of Canine Atrial Fibrillation Models After One Week of Sustained Arrhythmia. Circulation: Arrhythmia and Electrophysiology, 2021, 14, e009887.	2.1	6
119	Transcriptome-wide association study in UK Biobank Europeans identifies associations with blood cell traits. Human Molecular Genetics, 2022, 31, 2333-2347.	1.4	6
120	Motif-Raptor: a cell type-specific and transcription factor centric approach for post-GWAS prioritization of causal regulators. Bioinformatics, 2021, 37, 2103-2111.	1.8	5
121	A <i>Grammastola spatulata</i> mechanotoxin-4 (GsMTx4)-sensitive cation channel mediates increased cation permeability in human hereditary spherocytosis of multiple genetic etiologies. Haematologica, 2021, 106, 2759-2762.	1.7	5
122	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.	0.6	5
123	One step closer to linking GWAS SNPs with the right genes. Nature Genetics, 2022, 54, 748-749.	9.4	4
124	Lp-PLA2, scavenger receptor class B type I gene (SCARB1) rs10846744 variant, and cardiovascular disease. PLoS ONE, 2018, 13, e0204352.	1.1	2
125	Blocking HbS Polymerization in SCD. Cell, 2020, 180, 819.	13.5	2
126	An Essential Erythroid-Specific Enhancer of ATP2B4 Associated with Red Blood Cell Traits and Malaria Susceptibility. Blood, 2016, 128, 1250-1250.	0.6	2

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127	Understanding the molecular events preceding and leading to atrial fibrillation. Heart Rhythm, 2021, 18, 2126-2127.	0.3	1
128	Fine-Mapping and Genome Editing Reveal An Essential Erythroid Enhancer At The HbF-Associated BCL11A Locus. Blood, 2013, 122, 437-437.	0.6	1
129	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2012, 90, 1116-1117.	2.6	0
130	Abstract 17913: Inhibition of CETP by Dalcetrapib Results in a Modest Increase in Cholesterol Efflux Capacity Associated With an Increase in Large HDL Particles, but Does Not Impact Carotid Intima-Media Thickness in a dal-PLAQUE-2 Substudy. Circulation, 2014, 130, .	1.6	0
131	Prospective Evaluation of Fetal Haemoglobin Induction in Maternal Erythrocytes: A Preliminary Analysis of a Cohort of 345 Parturients. Blood, 2015, 126, 3370-3370.	0.6	0