

# Guillaume Lettre

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	From GWAS variant to function: A study of ~148,000 variants for blood cell traits.. <i>Human Genetics and Genomics Advances</i> , <b>2022</b> , 3, 100063	0.8	1
129	Cohort profile: genomic data for 26 622 individuals from the Canadian Longitudinal Study on Aging (CLSA).. <i>BMJ Open</i> , <b>2022</b> , 12, e059021	3	1
128	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. <i>American Journal of Human Genetics</i> , <b>2021</b> , 108, 564-582	11	7
127	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , <b>2021</b> , 108, 874-893	11	5
126	A mechanotoxin-4 (GsMTx4)-sensitive cation channel mediates increased cation permeability in human hereditary spherocytosis of multiple genetic etiologies. <i>Haematologica</i> , <b>2021</b> , 106, 2759-2762	6.6	3
125	Multi-ethnic genome-wide association analyses of white blood cell and platelet traits in the Population Architecture using Genomics and Epidemiology (PAGE) study. <i>BMC Genomics</i> , <b>2021</b> , 22, 432	4.5	0
124	Potential causal role of l-glutamine in sickle cell disease painful crises: A Mendelian randomization analysis. <i>Blood Cells, Molecules, and Diseases</i> , <b>2021</b> , 86, 102504	2.1	3
123	Transcriptomic Profiling of Canine Atrial Fibrillation Models After One Week of Sustained Arrhythmia. <i>Circulation: Arrhythmia and Electrophysiology</i> , <b>2021</b> , 14, e009887	6.4	1
122	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , <b>2021</b> , 108, 1836-1851	11	1
121	Clonal hematopoiesis in sickle cell disease. <i>Blood</i> , <b>2021</b> , 138, 2148-2152	2.2	7
120	Shared genetic pathways contribute to risk of hypertrophic and dilated cardiomyopathies with opposite directions of effect. <i>Nature Genetics</i> , <b>2021</b> , 53, 128-134	36.3	35
119	Blocking HbS Polymerization in SCD. <i>Cell</i> , <b>2020</b> , 180, 819	56.2	
118	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , <b>2020</b> , 182, 1214-1231.e11	56.2	96
117	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. <i>Cell</i> , <b>2020</b> , 182, 1198-1213.e14	56.2	88
116	A genetic association study of heart failure: more evidence for the role of BAG3 in idiopathic dilated cardiomyopathy. <i>ESC Heart Failure</i> , <b>2020</b> , 7, 4384	3.7	4
115	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. <i>Molecular Psychiatry</i> , <b>2020</b> , 25, 2392-2409	15.1	45
114	Validation of Genome-Wide Polygenic Risk Scores for Coronary Artery Disease in French Canadians. <i>Circulation Genomic and Precision Medicine</i> , <b>2019</b> , 12, e002481	5.2	33

113	Integrative analysis of vascular endothelial cell genomic features identifies AIDA as a coronary artery disease candidate gene. <i>Genome Biology</i> , <b>2019</b> , 20, 133	18.3	11
112	Pleiotropic effects for Parkin and LRRK2 in leprosy type-1 reactions and Parkinson's disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 15616-15624	11.5	35
111	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , <b>2019</b> , 51, 452-469	36.3	44
110	Whole genome sequence association with E-selectin levels reveals loss-of-function variant in African Americans. <i>Human Molecular Genetics</i> , <b>2019</b> , 28, 515-523	5.6	10
109	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol Use. <i>Biological Psychiatry</i> , <b>2019</b> , 85, 946-955	7.9	35
108	14q32 and let-7 microRNAs regulate transcriptional networks in fetal and adult human erythroblasts. <i>Human Molecular Genetics</i> , <b>2018</b> , 27, 1411-1420	5.6	14
107	Neuropilin-1 expression in adipose tissue macrophages protects against obesity and metabolic syndrome. <i>Science Immunology</i> , <b>2018</b> , 3,	28	27
106	The genetics of platelet count and volume in humans. <i>Platelets</i> , <b>2018</b> , 29, 125-130	3.6	26
105	PHACTR1 splicing isoforms and eQTLs in atherosclerosis-relevant human cells. <i>BMC Medical Genetics</i> , <b>2018</b> , 19, 97	2.1	12
104	A common functional PIEZO1 deletion allele associates with red blood cell density in sickle cell disease patients. <i>American Journal of Hematology</i> , <b>2018</b> , 93, E362-E365	7.1	9
103	Variants at the APOE /C1/C2/C4 Locus Modulate Cholesterol Efflux Capacity Independently of High-Density Lipoprotein Cholesterol. <i>Journal of the American Heart Association</i> , <b>2018</b> , 7, e009545	6	14
102	Common Hb globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. <i>PLoS Genetics</i> , <b>2018</b> , 14, e1007293	6	25
101	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , <b>2018</b> , 50, 26-41	36.3	186
100	Lp-PLA2, scavenger receptor class B type I gene (SCARB1) rs10846744 variant, and cardiovascular disease. <i>PLoS ONE</i> , <b>2018</b> , 13, e0204352	3.7	2
99	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , <b>2017</b> , 542, 186-190	50.4	412
98	Variant-aware saturating mutagenesis using multiple Cas9 nucleases identifies regulatory elements at trait-associated loci. <i>Nature Genetics</i> , <b>2017</b> , 49, 625-634	36.3	73
97	Genome-wide association study of erythrocyte density in sickle cell disease patients. <i>Blood Cells, Molecules, and Diseases</i> , <b>2017</b> , 65, 60-65	2.1	8
96	Frameshift indels introduced by genome editing can lead to in-frame exon skipping. <i>PLoS ONE</i> , <b>2017</b> , 12, e0178700	3.7	53

95	Rare coding variants pinpoint genes that control human hematological traits. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006925	6	28
94	Polygenic determinants in extremes of high-density lipoprotein cholesterol. <i>Journal of Lipid Research</i> , <b>2017</b> , 58, 2162-2170	6.3	33
93	The osteoarthritis and height GDF5 locus yields its secrets. <i>Nature Genetics</i> , <b>2017</b> , 49, 1165-1166	36.3	2
92	Human genetic variation alters CRISPR-Cas9 on- and off-targeting specificity at therapeutically implicated loci. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E11257-E11266	11.5	66
91	An erythroid-specific ATP2B4 enhancer mediates red blood cell hydration and malaria susceptibility. <i>Journal of Clinical Investigation</i> , <b>2017</b> , 127, 3065-3074	15.9	24
90	Polygenic Versus Monogenic Causes of Hypercholesterolemia Ascertained Clinically. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , <b>2016</b> , 36, 2439-2445	9.4	130
89	Fetal haemoglobin in sickle-cell disease: from genetic epidemiology to new therapeutic strategies. <i>Lancet, The</i> , <b>2016</b> , 387, 2554-64	40	55
88	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. <i>American Journal of Human Genetics</i> , <b>2016</b> , 99, 40-55	11	61
87	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. <i>American Journal of Human Genetics</i> , <b>2016</b> , 99, 22-39	11	42
86	Testing the role of predicted gene knockouts in human anthropometric trait variation. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 2082-2092	5.6	7
85	An Essential Erythroid-Specific Enhancer of ATP2B4 Associated with Red Blood Cell Traits and Malaria Susceptibility. <i>Blood</i> , <b>2016</b> , 128, 1250-1250	2.2	1
84	Lower Methylation of the ANGPTL2 Gene in Leukocytes from Post-Acute Coronary Syndrome Patients. <i>PLoS ONE</i> , <b>2016</b> , 11, e0153920	3.7	17
83	Whole-genome sequencing in French Canadians from Quebec. <i>Human Genetics</i> , <b>2016</b> , 135, 1213-1221	6.3	13
82	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. <i>American Journal of Human Genetics</i> , <b>2016</b> , 99, 8-21	11	47
81	Whole-Exome Sequencing Identifies Loci Associated with Blood Cell Traits and Reveals a Role for Alternative GFI1B Splice Variants in Human Hematopoiesis. <i>American Journal of Human Genetics</i> , <b>2016</b> , 99, 481-8	11	31
80	Comparison of DNA methylation profiles in human fetal and adult red blood cell progenitors. <i>Genome Medicine</i> , <b>2015</b> , 7, 1	14.4	65
79	Rare variant association studies: considerations, challenges and opportunities. <i>Genome Medicine</i> , <b>2015</b> , 7, 16	14.4	134
78	Myocardial Infarction-Associated SNP at 6p24 Interferes With MEF2 Binding and Associates With PHACTR1 Expression Levels in Human Coronary Arteries. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , <b>2015</b> , 35, 1472-1479	9.4	62

77	Small island, big genetic discoveries. <i>Nature Genetics</i> , <b>2015</b> , 47, 1224-5	36.3	11
76	Validation of fatty acid intakes estimated by a food frequency questionnaire using erythrocyte fatty acid profiling in the Montreal Heart Institute Biobank. <i>Journal of Human Nutrition and Dietetics</i> , <b>2015</b> , 28, 646-58	3.1	12
75	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005378	6	220
74	Crispr-Cas9 Saturating Mutagenesis Reveals an Achilles Heel in the BCL11A Erythroid Enhancer for Fetal Hemoglobin Induction (by Genome Editing). <i>Blood</i> , <b>2015</b> , 126, 638-638	2.2	3
73	Prospective Evaluation of Fetal Haemoglobin Induction in Maternal Erythrocytes: A Preliminary Analysis of a Cohort of 345 Parturients. <i>Blood</i> , <b>2015</b> , 126, 3370-3370	2.2	
72	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. <i>American Journal of Human Genetics</i> , <b>2014</b> , 94, 233-45	11	170
71	A variational Bayes discrete mixture test for rare variant association. <i>Genetic Epidemiology</i> , <b>2014</b> , 38, 21-30	2.6	12
70	Rare and low-frequency variants in human common diseases and other complex traits. <i>Journal of Medical Genetics</i> , <b>2014</b> , 51, 705-14	5.8	21
69	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , <b>2014</b> , 46, 1173-86	36.3	1339
68	Large multiethnic Candidate Gene Study for C-reactive protein levels: identification of a novel association at CD36 in African Americans. <i>Human Genetics</i> , <b>2014</b> , 133, 985-95	6.3	25
67	Rare and low-frequency coding variants in CXCR2 and other genes are associated with hematological traits. <i>Nature Genetics</i> , <b>2014</b> , 46, 629-34	36.3	92
66	Strategies to fine-map genetic associations with lipid levels by combining epigenomic annotations and liver-specific transcription profiles. <i>Genomics</i> , <b>2014</b> , 104, 105-12	4.3	10
65	Trans-ethnic meta-analysis of white blood cell phenotypes. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 6944-605.6	5.6	45
64	Lessons and Implications from Genome-Wide Association Studies (GWAS) Findings of Blood Cell Phenotypes. <i>Genes</i> , <b>2014</b> , 5, 51-64	4.2	12
63	Whole-exome imputation of sequence variants identified two novel alleles associated with adult body height in African Americans. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 6607-15	5.6	11
62	Nonsense mutations in BAG3 are associated with early-onset dilated cardiomyopathy in French Canadians. <i>Canadian Journal of Cardiology</i> , <b>2014</b> , 30, 1655-61	3.8	43
61	Association of sickle cell trait with chronic kidney disease and albuminuria in African Americans. <i>JAMA - Journal of the American Medical Association</i> , <b>2014</b> , 312, 2115-25	27.4	126
60	Association of variants at BCL11A and HBS1L-MYB with hemoglobin F and hospitalization rates among sickle cell patients in Cameroon. <i>PLoS ONE</i> , <b>2014</b> , 9, e92506	3.7	69

59	Using height association studies to gain insights into human idiopathic short and syndromic stature phenotypes. <i>Pediatric Nephrology</i> , <b>2013</b> , 28, 557-62	3.2	5
58	Genome-wide association analysis of blood-pressure traits in African-ancestry individuals reveals common associated genes in African and non-African populations. <i>American Journal of Human Genetics</i> , <b>2013</b> , 93, 545-54	11	145
57	An erythroid enhancer of BCL11A subject to genetic variation determines fetal hemoglobin level. <i>Science</i> , <b>2013</b> , 342, 253-7	33.3	400
56	The non-synonymous polymorphism at position 114 of the WRN protein affects cholesterol efflux in vitro and correlates with cholesterol levels in vivo. <i>Experimental Gerontology</i> , <b>2013</b> , 48, 533-8	4.5	5
55	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. <i>Nature Genetics</i> , <b>2013</b> , 45, 690-6	36.3	192
54	Deep resequencing of GWAS loci identifies rare variants in CARD9, IL23R and RNF186 that are associated with ulcerative colitis. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003723	6	149
53	Genome-wide association analysis of red blood cell traits in African Americans: the COGENT Network. <i>Human Molecular Genetics</i> , <b>2013</b> , 22, 2529-38	5.6	48
52	Fine-Mapping and Genome Editing Reveal An Essential Erythroid Enhancer At The HbF-Associated BCL11A Locus. <i>Blood</i> , <b>2013</b> , 122, 437-437	2.2	1
51	Ultraconserved elements in the human genome: association and transmission analyses of highly constrained single-nucleotide polymorphisms. <i>Genetics</i> , <b>2012</b> , 192, 253-66	4	13
50	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , <b>2012</b> , 490, 267-72	50.4	304
49	Imputation of exome sequence variants into population-based samples and blood-cell-trait-associated loci in African Americans: NHLBI GO Exome Sequencing Project. <i>American Journal of Human Genetics</i> , <b>2012</b> , 91, 794-808	11	103
48	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. <i>American Journal of Human Genetics</i> , <b>2012</b> , 90, 1116-1117	11	78
47	A meta-analysis and genome-wide association study of platelet count and mean platelet volume in african americans. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002491	6	84
46	The search for genetic modifiers of disease severity in the Ehemoglobinopathies. <i>Cold Spring Harbor Perspectives in Medicine</i> , <b>2012</b> , 2,	5.4	40
45	Pooled DNA resequencing of 68 myocardial infarction candidate genes in French canadians. <i>Circulation: Cardiovascular Genetics</i> , <b>2012</b> , 5, 547-54		9
44	Multi-ethnic analysis of lipid-associated loci: the NHLBI CARE project. <i>PLoS ONE</i> , <b>2012</b> , 7, e36473	3.7	39
43	Deep resequencing of GWAS loci identifies independent rare variants associated with inflammatory bowel disease. <i>Nature Genetics</i> , <b>2011</b> , 43, 1066-73	36.3	584
42	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. <i>Nature Genetics</i> , <b>2011</b> , 43, 333-8	36.3	1394

41	Genome partitioning of genetic variation for complex traits using common SNPs. <i>Nature Genetics</i> , <b>2011</b> , 43, 519-25	36.3	659
40	Genomic inflation factors under polygenic inheritance. <i>European Journal of Human Genetics</i> , <b>2011</b> , 19, 807-12	5.3	335
39	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. <i>American Journal of Human Genetics</i> , <b>2011</b> , 88, 6-18	11	103
38	Genome-wide comparison of African-ancestry populations from CARE and other cohorts reveals signals of natural selection. <i>American Journal of Human Genetics</i> , <b>2011</b> , 89, 368-81	11	63
37	Genetic association analysis highlights new loci that modulate hematological trait variation in Caucasians and African Americans. <i>Human Genetics</i> , <b>2011</b> , 129, 307-17	6.3	74
36	Recent progress in the study of the genetics of height. <i>Human Genetics</i> , <b>2011</b> , 129, 465-72	6.3	64
35	Multiple loci are associated with white blood cell phenotypes. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002113	6	92
34	Enhanced statistical tests for GWAS in admixed populations: assessment using African Americans from CARE and a Breast Cancer Consortium. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1001371	6	86
33	Genome-wide association study of white blood cell count in 16,388 African Americans: the continental origins and genetic epidemiology network (COGENT). <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002108	6	111
32	Identification, replication, and fine-mapping of Loci associated with adult height in individuals of african ancestry. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002298	6	77
31	Genome-wide association study of coronary heart disease and its risk factors in 8,090 African Americans: the NHLBI CARE Project. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1001300	6	249
30	Association of linear growth impairment in pediatric Crohn's disease and a known height locus: a pilot study. <i>Annals of Human Genetics</i> , <b>2010</b> , 74, 489-97	2.2	19
29	Biological, clinical and population relevance of 95 loci for blood lipids. <i>Nature</i> , <b>2010</b> , 466, 707-13	50.4	2742
28	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , <b>2010</b> , 467, 832-8	50.4	1514
27	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , <b>2010</b> , 42, 949-60	36.3	724
26	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , <b>2010</b> , 42, 937-48	36.3	2267
25	Fine-mapping at three loci known to affect fetal hemoglobin levels explains additional genetic variation. <i>Nature Genetics</i> , <b>2010</b> , 42, 1049-51	36.3	208
24	Modifier genes in Mendelian disorders: the example of hemoglobin disorders. <i>Annals of the New York Academy of Sciences</i> , <b>2010</b> , 1214, 47-56	6.5	23

23	Genome-wide association of anthropometric traits in African- and African-derived populations. <i>Human Molecular Genetics</i> , <b>2010</b> , 19, 2725-38	5.6	81
22	Candidate gene association resource (CARE): design, methods, and proof of concept. <i>Circulation: Cardiovascular Genetics</i> , <b>2010</b> , 3, 267-75		125
21	European ancestry as a risk factor for atrial fibrillation in African Americans. <i>Circulation</i> , <b>2010</b> , 122, 2009-167	16.7	171
20	Fine mapping of the association with obesity at the FTO locus in African-derived populations. <i>Human Molecular Genetics</i> , <b>2010</b> , 19, 2907-16	5.6	72
19	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. <i>Nature Genetics</i> , <b>2009</b> , 41, 25-34	36.3	1368
18	Genetic regulation of adult stature. <i>Current Opinion in Pediatrics</i> , <b>2009</b> , 21, 515-22	3.2	50
17	Identification of ten loci associated with height highlights new biological pathways in human growth. <i>Nature Genetics</i> , <b>2008</b> , 40, 584-91	36.3	482
16	Common variants in the GDF5-UQCC region are associated with variation in human height. <i>Nature Genetics</i> , <b>2008</b> , 40, 198-203	36.3	315
15	Genome-wide association study shows BCL11A associated with persistent fetal hemoglobin and amelioration of the phenotype of beta-thalassemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 1620-5	11.5	469
14	DNA polymorphisms at the BCL11A, HBS1L-MYB, and beta-globin loci associate with fetal hemoglobin levels and pain crises in sickle cell disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 11869-74	11.5	428
13	Autoimmune diseases: insights from genome-wide association studies. <i>Human Molecular Genetics</i> , <b>2008</b> , 17, R116-21	5.6	232
12	Human fetal hemoglobin expression is regulated by the developmental stage-specific repressor BCL11A. <i>Science</i> , <b>2008</b> , 322, 1839-42	33.3	618
11	Genetic model testing and statistical power in population-based association studies of quantitative traits. <i>Genetic Epidemiology</i> , <b>2007</b> , 31, 358-62	2.6	203
10	A common variant of HMGA2 is associated with adult and childhood height in the general population. <i>Nature Genetics</i> , <b>2007</b> , 39, 1245-50	36.3	330
9	Common genetic variation in eight genes of the GH/IGF1 axis does not contribute to adult height variation. <i>Human Genetics</i> , <b>2007</b> , 122, 129-39	6.3	51
8	Genome-wide association analysis identifies loci for type 2 diabetes and triglyceride levels. <i>Science</i> , <b>2007</b> , 316, 1331-6	33.3	2364
7	C. elegans GLA-3 is a novel component of the MAP kinase MPK-1 signaling pathway required for germ cell survival. <i>Genes and Development</i> , <b>2006</b> , 20, 2279-92	12.6	47
6	Developmental apoptosis in C. elegans: a complex CEDnario. <i>Nature Reviews Molecular Cell Biology</i> , <b>2006</b> , 7, 97-108	48.7	226

5	The Polygenic and Monogenic Basis of Blood Traits and Diseases	3
4	Whole genome sequencing association analysis of quantitative red blood cell phenotypes: the NHLBI TOPMed program	1
3	Validation of genome-wide polygenic risk scores for coronary artery disease in French Canadians	1
2	From GWAS Variant to Function: a Study of ~148,000 Variants for Blood Cell Traits	1
1	CRISPR perturbations at many coronary artery disease loci impair vascular endothelial cell functions	1