# Guillaume Lettre

List of Publications by Year
in descending order



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|---|---|---|---|
| 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 | From GWAS variant to function: A study of â¼148,000 variants for blood cell traits. Human Genetics and Genomics Advances, 2022, 3, 100063. | 1.0 | 9 |
| 2 | Transcriptome-wide association study in UK Biobank Europeans identifies associations with blood cell traits. Human Molecular Genetics, 2022, 31, 2333-2347. | 1.4 | 6 |
| 3 | Importance of genetic testing in unexplained cardiac arrest. European Heart Journal, 2022, 43, 3071-3081. | 1.0 | 36 |
| 4 | Cohort profile: genomic data for 26 622 individuals from the Canadian Longitudinal Study on Aging (CLSA). BMJ Open, 2022, 12, e059021. | 0.8 | 17 |
| 5 | One step closer to linking GWAS SNPs with the right genes. Nature Genetics, 2022, 54, 748-749. | 9.4 | 4 |
| 6 | 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 |
| 7 | 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 |
| 8 | 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 |
| 9 | 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 |
| 10 | 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 |
| 11 | 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 |
| 12 | Transcriptomic Profiling of Canine Atrial Fibrillation Models After One Week of Sustained Arrhythmia. Circulation: Arrhythmia and Electrophysiology, 2021, 14, e009887. | 2.1 | 6 |
| 13 | 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 |
| 14 | Clonal hematopoiesis in sickle cell disease. Blood, 2021, 138, 2148-2152. | 0.6 | 29 |
| 15 | Understanding the molecular events preceding and leading to atrial fibrillation. Heart Rhythm, 2021, 18, 2126-2127. | 0.3 | 1 |
| 16 | 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 |
| 17 | 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 |
| 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 | 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 |
| 20 | A genetic association study of heart failure: more evidence for the role of BAG3 in idiopathic dilated cardiomyopathy. ESC Heart Failure, 2020, 7, 4384-4389. | 1.4 | 11 |
| 21 | Blocking HbS Polymerization in SCD. Cell, 2020, 180, 819. | 13.5 | 2 |
| 22 | 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 |
| 23 | 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 |
| 24 | 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 |
| 25 | Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469. | 9.4 | 89 |
| 26 | 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 |
| 27 | 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 |
| 28 | 14q32 and let-7 microRNAs regulate transcriptional networks in fetal and adult human erythroblasts. Human Molecular Genetics, 2018, 27, 1411-1420. | 1.4 | 25 |
| 29 | Neuropilin-1 expression in adipose tissue macrophages protects against obesity and metabolic syndrome. Science Immunology, 2018, 3, . | 5.6 | 41 |
| 30 | The genetics of platelet count and volume in humans. Platelets, 2018, 29, 125-130. | 1.1 | 44 |
| 31 | Lp-PLA2, scavenger receptor class B type I gene (SCARB1) rs10846744 variant, and cardiovascular disease. PLoS ONE, 2018, 13, e0204352. | 1.1 | 2 |
| 32 | PHACTR1 splicing isoforms and eQTLs in atherosclerosis-relevant human cells. BMC Medical Genetics, 2018, 19, 97. | 2.1 | 20 |
| 33 | 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 |
| 34 | 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 |
| 35 | Common Î±-globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. PLoS Genetics, 2018, 14, e1007293. | 1.5 | 45 |
| 36 | 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 |

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|---|---|---|---|
| 37 | Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190. | 13.7 | 544 |
| 38 | Variant-aware saturating mutagenesis using multiple Cas9 nucleases identifies regulatory elements at trait-associated loci. Nature Genetics, 2017, 49, 625-634. | 9.4 | 96 |
| 39 | Genome-wide association study of erythrocyte density in sickle cell disease patients. Blood Cells, Molecules, and Diseases, 2017, 65, 60-65. | 0.6 | 13 |
| 40 | Polygenic determinants in extremes of high-density lipoprotein cholesterol. Journal of Lipid Research, 2017, 58, 2162-2170. | 2.0 | 49 |
| 41 | The osteoarthritis and height GDF5 locus yields its secrets. Nature Genetics, 2017, 49, 1165-1166. | 9.4 | 7 |
| 42 | 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 |
| 43 | Frameshift indels introduced by genome editing can lead to in-frame exon skipping. PLoS ONE, 2017, 12, e0178700. | 1.1 | 77 |
| 44 | Rare coding variants pinpoint genes that control human hematological traits. PLoS Genetics, 2017, 13, e1006925. | 1.5 | 39 |
| 45 | An erythroid-specific ATP2B4 enhancer mediates red blood cell hydration and malaria susceptibility. Journal of Clinical Investigation, 2017, 127, 3065-3074. | 3.9 | 48 |
| 46 | Whole-genome sequencing in French Canadians from Quebec. Human Genetics, 2016, 135, 1213-1221. | 1.8 | 16 |
| 47 | Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21. | 2.6 | 60 |
| 48 | 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 |
| 49 | Polygenic Versus Monogenic Causes of Hypercholesterolemia Ascertained Clinically. Arteriosclerosis, Thrombosis, and Vascular Biology, 2016, 36, 2439-2445. | 1.1 | 174 |
| 50 | Fetal haemoglobin in sickle-cell disease: from genetic epidemiology to new therapeutic strategies. Lancet, The, 2016, 387, 2554-2564. | 6.3 | 73 |
| 51 | Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55. | 2.6 | 82 |
| 52 | 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 |
| 53 | Testing the role of predicted gene knockouts in human anthropometric trait variation. Human Molecular Genetics, 2016, 25, 2082-2092. | 1.4 | 10 |
| 54 | 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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|---|---|---|---|
| 55 | Lower Methylation of the ANGPTL2 Gene in Leukocytes from Post-Acute Coronary Syndrome Patients. PLoS ONE, 2016, 11, e0153920. | 1.1 | 18 |
| 56 | 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 |
| 57 | 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 |
| 58 | Comparison of DNA methylation profiles in human fetal and adult red blood cell progenitors. Genome Medicine, 2015, 7, 1. | 3.6 | 104 |
| 59 | Rare variant association studies: considerations, challenges and opportunities. Genome Medicine, 2015, 7, 16. | 3.6 | 176 |
| 60 | 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 |
| 61 | Small island, big genetic discoveries. Nature Genetics, 2015, 47, 1224-1225. | 9.4 | 17 |
| 62 | 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 |
| 63 | 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 |
| 64 | Lessons and Implications from Genome-Wide Association Studies (GWAS) Findings of Blood Cell Phenotypes. Genes, 2014, 5, 51-64. | 1.0 | 12 |
| 65 | 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 |
| 66 | 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 |
| 67 | 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 |
| 68 | 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 |
| 69 | A Variational Bayes Discrete Mixture Test for Rare Variant Association. Genetic Epidemiology, 2014, 38, 21-30. | 0.6 | 12 |
| 70 | Rare and low-frequency variants in human common diseases and other complex traits. Journal of Medical Genetics, 2014, 51, 705-714. | 1.5 | 29 |
| 71 | 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 |
| 72 | 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 |

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|---|---|---|---|
| 73 | 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 |
| 74 | 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 |
| 75 | Trans-ethnic meta-analysis of white blood cell phenotypes. Human Molecular Genetics, 2014, 23, 6944-6960. | 1.4 | 60 |
| 76 | 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 |
| 77 | 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 |
| 78 | Using height association studies to gain insights into human idiopathic short and syndromic stature phenotypes. Pediatric Nephrology, 2013, 28, 557-562. | 0.9 | 6 |
| 79 | 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 |
| 80 | An Erythroid Enhancer of BCL11A Subject to Genetic Variation Determines Fetal Hemoglobin Level. Science, 2013, 342, 253-257. | 6.0 | 518 |
| 81 | 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 |
| 82 | 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 |
| 83 | 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 |
| 84 | 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 |
| 85 | Fine-Mapping and Genome Editing Reveal An Essential Erythroid Enhancer At The HbF-Associated BCL11A Locus. Blood, 2013, 122, 437-437. | 0.6 | 1 |
| 86 | 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 |
| 87 | 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 |
| 88 | Pooled DNA Resequencing of 68 Myocardial Infarction Candidate Genes in French Canadians. Circulation: Cardiovascular Genetics, 2012, 5, 547-554. | 5.1 | 10 |
| 89 | Ultraconserved Elements in the Human Genome: Association and Transmission Analyses of Highly Constrained Single-Nucleotide Polymorphisms. Genetics, 2012, 192, 253-266. | 1.2 | 17 |
| 90 | FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272. | 13.7 | 383 |

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|---|---|---|---|
| 91 | 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 |
| 92 | 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 |
| 93 | Multi-Ethnic Analysis of Lipid-Associated Loci: The NHLBI CARe Project. PLoS ONE, 2012, 7, e36473. | 1.1 | 46 |
| 94 | Deep resequencing of GWAS loci identifies independent rare variants associated with inflammatory bowel disease. Nature Genetics, 2011, 43, 1066-1073. | 9.4 | 698 |
| 95 | Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. Nature Genetics, 2011, 43, 333-338. | 9.4 | 1,685 |
| 96 | Genome partitioning of genetic variation for complex traits using common SNPs. Nature Genetics, 2011, 43, 519-525. | 9.4 | 834 |
| 97 | Genomic inflation factors under polygenic inheritance. European Journal of Human Genetics, 2011, 19, 807-812. | 1.4 | 460 |
| 98 | 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 |
| 99 | 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 |
| 100 | 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 |
| 101 | Recent progress in the study of the genetics of height. Human Genetics, 2011, 129, 465-472. | 1.8 | 73 |
| 102 | Multiple Loci Are Associated with White Blood Cell Phenotypes. PLoS Genetics, 2011, 7, e1002113. | 1.5 | 106 |
| 103 | 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 |
| 104 | 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 |
| 105 | Identification, Replication, and Fine-Mapping of Loci Associated with Adult Height in Individuals of African Ancestry. PLoS Genetics, 2011, 7, e1002298. | 1.5 | 93 |
| 106 | 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 |
| 107 | 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 |
| 108 | Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713. | 13.7 | 3,249 |

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|---|---|---|---|
| 109 | Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838. | 13.7 | 1,789 |
| 110 | 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 |
| 111 | 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 |
| 112 | Fine-mapping at three loci known to affect fetal hemoglobin levels explains additional genetic variation. Nature Genetics, 2010, 42, 1049-1051. | 9.4 | 243 |
| 113 | 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 |
| 114 | Genome-wide association of anthropometric traits in African- and African-derived populations. Human Molecular Genetics, 2010, 19, 2725-2738. | 1.4 | 90 |
| 115 | Candidate Gene Association Resource (CARe). Circulation: Cardiovascular Genetics, 2010, 3, 267-275. | 5.1 | 139 |
| 116 | European Ancestry as a Risk Factor for Atrial Fibrillation in African Americans. Circulation, 2010, 122, 2009-2015. | 1.6 | 219 |
| 117 | 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 |
| 118 | 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 |
| 119 | Genetic regulation of adult stature. Current Opinion in Pediatrics, 2009, 21, 515-522. | 1.0 | 59 |
| 120 | Identification of ten loci associated with height highlights new biological pathways in human growth. Nature Genetics, 2008, 40, 584-591. | 9.4 | 537 |
| 121 | Common variants in the GDF5-UQCC region are associated with variation in human height. Nature Genetics, 2008, 40, 198-203. | 9.4 | 369 |
| 122 | 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 |
| 123 | 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 |
| 124 | Autoimmune diseases: insights from genome-wide association studies. Human Molecular Genetics, 2008, 17, R116-R121. | 1.4 | 275 |
| 125 | Human Fetal Hemoglobin Expression Is Regulated by the Developmental Stage-Specific Repressor BCL11A. Science, 2008, 322, 1839-1842. | 6.0 | 759 |
| 126 | Genome-Wide Association Analysis Identifies Loci for Type 2 Diabetes and Triglyceride Levels. Science, 2007, 316, 1331-1336. | 6.0 | 2,623 |

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|---|---|---|---|
| 127 | Genetic model testing and statistical power in population-based association studies of quantitative traits. Genetic Epidemiology, 2007, 31, 358-362. | 0.6 | 224 |
| 128 | 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 |
| 129 | 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 |
| 130 | Developmental apoptosis in C. elegans: a complex CEDnario. Nature Reviews Molecular Cell Biology, 2006, 7, 97-108. | 16.1 | 269 |
| 131 | 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 |