

Greg Gibson

List of Publications by Year in descending order

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Version: 2024-02-01

186
papers

24,255
citations

31902

53
h-index

8599

146
g-index

215
all docs

215
docs citations

215
times ranked

32912
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Methylation quantitative trait loci are largely consistent across disease states in Crohn's disease. <i>Genes, Genomes, Genetics</i> , 2022, 12, . | 0.8 | 2 |
| 2 | Canalization of the Polygenic Risk for Common Diseases and Traits in the UK Biobank Cohort. <i>Molecular Biology and Evolution</i> , 2022, 39, . | 3.5 | 8 |
| 3 | Generation of human long-lived plasma cells by developmentally regulated epigenetic imprinting. <i>Life Science Alliance</i> , 2022, 5, e202101285. | 1.3 | 19 |
| 4 | Perspectives on rigor and reproducibility in single cell genomics. <i>PLoS Genetics</i> , 2022, 18, e1010210. | 1.5 | 17 |
| 5 | Targeted RNAseq Improves Clinical Diagnosis of Very Early-Onset Pediatric Immune Dysregulation. <i>Journal of Personalized Medicine</i> , 2022, 12, 919. | 1.1 | 1 |
| 6 | TreeMap: a structured approach to fine mapping of eQTL variants. <i>Bioinformatics</i> , 2021, 37, 1125-1134. | 1.8 | 6 |
| 7 | Mucosal Inflammatory and Wound Healing Gene Programmes Reveal Targets for Structuring Behaviour in Paediatric Crohn's Disease. <i>Journal of Crohn's and Colitis</i> , 2021, 15, 273-286. | 0.6 | 20 |
| 8 | Highly elevated polygenic risk scores are better predictors of myocardial infarction risk early in life than later. <i>Genome Medicine</i> , 2021, 13, 13. | 3.6 | 36 |
| 9 | Whole-genome sequencing of African Americans implicates differential genetic architecture in inflammatory bowel disease. <i>American Journal of Human Genetics</i> , 2021, 108, 431-445. | 2.6 | 21 |
| 10 | Transcriptional firing represses bactericidal activity in cystic fibrosis airway neutrophils. <i>Cell Reports Medicine</i> , 2021, 2, 100239. | 3.3 | 25 |
| 11 | Clinical and Host Biological Factors Predict Colectomy Risk in Children Newly Diagnosed With Ulcerative Colitis. <i>Inflammatory Bowel Diseases</i> , 2021, , . | 0.9 | 11 |
| 12 | Extrafollicular IgD+ B cells generate IgE antibody secreting cells in the nasal mucosa. <i>Mucosal Immunology</i> , 2021, 14, 1144-1159. | 2.7 | 21 |
| 13 | Altered splicing associated with the pathology of inflammatory bowel disease. <i>Human Genomics</i> , 2021, 15, 47. | 1.4 | 7 |
| 14 | Machine learning applications for therapeutic tasks with genomics data. <i>Patterns</i> , 2021, 2, 100328. | 3.1 | 14 |
| 15 | Phantom epistasis between unlinked loci. <i>Nature</i> , 2021, 596, E1-E3. | 13.7 | 16 |
| 16 | Stratification of risk of progression to colectomy in ulcerative colitis via measured and predicted gene expression. <i>American Journal of Human Genetics</i> , 2021, 108, 1765-1779. | 2.6 | 6 |
| 17 | Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , 2021, 53, 1300-1310. | 9.4 | 590 |
| 18 | Single-cell RNA-seq of out-of-thaw mesenchymal stromal cells shows tissue-of-origin differences and inter-donor cell-cycle variations. <i>Stem Cell Research and Therapy</i> , 2021, 12, 565. | 2.4 | 16 |

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|----|--|-----|-----------|
| 19 | Relationship Between Genomic Risk Scores (GRS) and Coronary Artery Calcium (CAC) Score: A Pilot Study. <i>Clinical Nutrition ESPEN</i> , 2021, 47, 293-298. | 0.5 | 0 |
| 20 | The greater inflammatory pathwayâ€™high clinical potential by innovative predictive, preventive, and personalized medical approach. <i>EPMA Journal</i> , 2020, 11, 1-16. | 3.3 | 24 |
| 21 | Derivation of notochordal cells from human embryonic stem cells reveals unique regulatory networks by single cellâ€™transcriptomics. <i>Journal of Cellular Physiology</i> , 2020, 235, 5241-5255. | 2.0 | 18 |
| 22 | Correlation Patterns Among B7 Family Ligands and Tryptophan Degrading Enzymes in Hepatocellular Carcinoma. <i>Frontiers in Oncology</i> , 2020, 10, 1632. | 1.3 | 5 |
| 23 | Characterization of Donor Variability for Î³Î³ T Cell ex vivo Expansion and Development of an Allogeneic Î³Î³ T Cell Immunotherapy. <i>Frontiers in Medicine</i> , 2020, 7, 588453. | 1.2 | 21 |
| 24 | Canalization and Robustness in Human Genetics and Disease. <i>Annual Review of Genetics</i> , 2020, 54, 189-211. | 3.2 | 22 |
| 25 | Fine-mapping within eQTL credible intervals by expression CROP-seq. <i>Biology Methods and Protocols</i> , 2020, 5, bpa008. | 1.0 | 8 |
| 26 | Pitfalls in Single Clone CRISPR-Cas9 Mutagenesis to Fine-Map Regulatory Intervals. <i>Genes</i> , 2020, 11, 504. | 1.0 | 6 |
| 27 | Tissue specific regulation of transcription in endometrium and association with disease. <i>Human Reproduction</i> , 2020, 35, 377-393. | 0.4 | 43 |
| 28 | Dietary modification, penetrance, and the origins of congenital malformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5097-5099. | 3.3 | 1 |
| 29 | African Ancestry Proportionâ€™Influences Ilealâ€™Gene Expression inâ€™Inflammatory Bowel Disease. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2020, 10, 203-205. | 2.3 | 8 |
| 30 | The Medical Genome Reference Bank contains whole genome and phenotype data of 2570 healthy elderly. <i>Nature Communications</i> , 2020, 11, 435. | 5.8 | 47 |
| 31 | The Effects of Age and Dose on Gene Expression and Segmental Bone Defect Repair After BMPâ€™2 Delivery. <i>JBMR Plus</i> , 2019, 3, e10068. | 1.3 | 13 |
| 32 | The effect of X-linked dosage compensation on complex trait variation. <i>Nature Communications</i> , 2019, 10, 3009. | 5.8 | 44 |
| 33 | TIGAR: An Improved Bayesian Tool for Transcriptomic Data Imputation Enhances Gene Mapping of Complex Traits. <i>American Journal of Human Genetics</i> , 2019, 105, 258-266. | 2.6 | 84 |
| 34 | Biological relevance of computationally predicted pathogenicity of noncoding variants. <i>Nature Communications</i> , 2019, 10, 330. | 5.8 | 44 |
| 35 | Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. <i>Genetics</i> , 2019, 212, 905-918. | 1.2 | 23 |
| 36 | Classification of individuals and the potential to detect sexual contact using the microbiome of the pubic region. <i>Forensic Science International: Genetics</i> , 2019, 41, 177-187. | 1.6 | 21 |

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|----|---|-----|-----------|
| 37 | Blood-Derived DNA Methylation Signatures of Crohn's Disease and Severity of Intestinal Inflammation. <i>Gastroenterology</i> , 2019, 156, 2254-2265.e3. | 0.6 | 91 |
| 38 | Molecular Genetic and Immune Functional Responses Distinguish Bone Marrow Mesenchymal Stromal Cells from Hepatic Stellate Cells. <i>Stem Cells</i> , 2019, 37, 1075-1082. | 1.4 | 14 |
| 39 | Clinical utility of RNA sequencing to resolve unusual GNE myopathy with a novel promoter deletion. <i>Muscle and Nerve</i> , 2019, 60, 98-103. | 1.0 | 15 |
| 40 | On the utilization of polygenic risk scores for therapeutic targeting. <i>PLoS Genetics</i> , 2019, 15, e1008060. | 1.5 | 74 |
| 41 | Clinical and biological predictors of response to standardised paediatric colitis therapy (PROTECT): a multicentre inception cohort study. <i>Lancet, The</i> , 2019, 393, 1708-1720. | 6.3 | 121 |
| 42 | Cardiac Toxicity From Ethanol Exposure in Human-Induced Pluripotent Stem Cell-Derived Cardiomyocytes. <i>Toxicological Sciences</i> , 2019, 169, 280-292. | 1.4 | 16 |
| 43 | PolyQTL: Bayesian multiple eQTL detection with control for population structure and sample relatedness. <i>Bioinformatics</i> , 2019, 35, 1061-1063. | 1.8 | 6 |
| 44 | Ulcerative colitis mucosal transcriptomes reveal mitochondriopathy and personalized mechanisms underlying disease severity and treatment response. <i>Nature Communications</i> , 2019, 10, 38. | 5.8 | 215 |
| 45 | Regional gene expression analysis of multiple tissues in an experimental animal model of post-traumatic osteoarthritis. <i>Osteoarthritis and Cartilage</i> , 2019, 27, 294-303. | 0.6 | 15 |
| 46 | Going to the negative: genomics for optimized medical prescription. <i>Nature Reviews Genetics</i> , 2019, 20, 1-2. | 7.7 | 34 |
| 47 | Differential transcriptome and development of human peripheral plasma cell subsets. <i>JCI Insight</i> , 2019, 4, . | 2.3 | 41 |
| 48 | Potency Analysis of Mesenchymal Stromal Cells Using a Combinatorial Assay Matrix Approach. <i>Cell Reports</i> , 2018, 22, 2504-2517. | 2.9 | 150 |
| 49 | Signatures of negative selection in the genetic architecture of human complex traits. <i>Nature Genetics</i> , 2018, 50, 746-753. | 9.4 | 304 |
| 50 | Replicability and Prediction: Lessons and Challenges from GWAS. <i>Trends in Genetics</i> , 2018, 34, 504-517. | 2.9 | 138 |
| 51 | Enhanced Contribution of HLA in Pediatric Onset Ulcerative Colitis. <i>Inflammatory Bowel Diseases</i> , 2018, 24, 829-838. | 0.9 | 23 |
| 52 | Pervasive Modulation of Obesity Risk by the Environment and Genomic Background. <i>Genes</i> , 2018, 9, 411. | 1.0 | 16 |
| 53 | Individualized Transcriptional Resolution of Complicated Malaria in a Colombian Study. <i>Journal of Personalized Medicine</i> , 2018, 8, 29. | 1.1 | 2 |
| 54 | Bowel Location Rather Than Disease Subtype Dominates Transcriptomic Heterogeneity in Pediatric IBD. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2018, 6, 474-476.e3. | 2.3 | 10 |

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|----|---|-----|-----------|
| 55 | Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018, 103, 691-706. | 2.6 | 326 |
| 56 | Factors of the bone marrow microniche that support human plasma cell survival and immunoglobulin secretion. <i>Nature Communications</i> , 2018, 9, 3698. | 5.8 | 95 |
| 57 | Disease-specific regulation of gene expression in a comparative analysis of juvenile idiopathic arthritis and inflammatory bowel disease. <i>Genome Medicine</i> , 2018, 10, 48. | 3.6 | 46 |
| 58 | Population genetics and GWAS: A primer. <i>PLoS Biology</i> , 2018, 16, e2005485. | 2.6 | 36 |
| 59 | Bone Marrow–Derived Mesenchymal Stromal Cells from Patients with Sickle Cell Disease Display Intact Functionality. <i>Biology of Blood and Marrow Transplantation</i> , 2017, 23, 736-745. | 2.0 | 15 |
| 60 | Prediction of complicated disease course for children newly diagnosed with Crohn's disease: a multicentre inception cohort study. <i>Lancet, The</i> , 2017, 389, 1710-1718. | 6.3 | 482 |
| 61 | The Genetic Architecture of Gene Expression in Peripheral Blood. <i>American Journal of Human Genetics</i> , 2017, 100, 228-237. | 2.6 | 178 |
| 62 | Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. <i>Nature Communications</i> , 2017, 8, 483. | 5.8 | 22 |
| 63 | Constraints on eQTL Fine Mapping in the Presence of Multisite Local Regulation of Gene Expression. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2533-2544. | 0.8 | 23 |
| 64 | Transcriptional risk scores link GWAS to eQTLs and predict complications in Crohn's disease. <i>Nature Genetics</i> , 2017, 49, 1517-1521. | 9.4 | 146 |
| 65 | Individualization of pubic hair bacterial communities and the effects of storage time and temperature. <i>Forensic Science International: Genetics</i> , 2017, 26, 12-20. | 1.6 | 26 |
| 66 | Immune dysfunctionality of replicative senescent mesenchymal stromal cells is corrected by IFN γ priming. <i>Blood Advances</i> , 2017, 1, 628-643. | 2.5 | 43 |
| 67 | Cryptic Genetic Variation in Evolutionary Developmental Genetics. <i>Biology</i> , 2016, 5, 28. | 1.3 | 21 |
| 68 | Genomic insights into ayurvedic and western approaches to personalized medicine. <i>Journal of Genetics</i> , 2016, 95, 209-228. | 0.4 | 59 |
| 69 | On the Evaluation of Module Preservation. <i>Cell Systems</i> , 2016, 3, 17-19. | 2.9 | 5 |
| 70 | Autosomal genetic control of human gene expression does not differ across the sexes. <i>Genome Biology</i> , 2016, 17, 248. | 3.8 | 15 |
| 71 | A Burden of Rare Variants Associated with Extremes of Gene Expression in Human Peripheral Blood. <i>American Journal of Human Genetics</i> , 2016, 98, 299-309. | 2.6 | 84 |
| 72 | Exome sequencing of patients with histiocytoid cardiomyopathy reveals a de novo <i>NDUFB11</i> mutation that plays a role in the pathogenesis of histiocytoid cardiomyopathy. <i>American Journal of Medical Genetics, Part A</i> , 2015, 167, 2114-2121. | 0.7 | 38 |

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|----|---|------|-----------|
| 73 | Mature Cystic Fibrosis Airway Neutrophils Suppress T Cell Function: Evidence for a Role of Arginase 1 but Not Programmed Death-Ligand 1. <i>Journal of Immunology</i> , 2015, 194, 5520-5528. | 0.4 | 60 |
| 74 | DICER1 and microRNA regulation in post-traumatic stress disorder with comorbid depression. <i>Nature Communications</i> , 2015, 6, 10106. | 5.8 | 81 |
| 75 | Mesenchymal Stromal Cells Derived From Crohn's Patients Deploy Indoleamine 2,3-dioxygenase-mediated Immune Suppression, Independent of Autophagy. <i>Molecular Therapy</i> , 2015, 23, 1248-1261. | 3.7 | 47 |
| 76 | GTE _x detects genetic effects. <i>Science</i> , 2015, 348, 640-641. | 6.0 | 44 |
| 77 | Omic personality: implications of stable transcript and methylation profiles for personalized medicine. <i>Genome Medicine</i> , 2015, 7, 88. | 3.6 | 13 |
| 78 | Expression quantitative trait locus analysis for translational medicine. <i>Genome Medicine</i> , 2015, 7, 60. | 3.6 | 69 |
| 79 | Blood gene expression profiles suggest altered immune function associated with symptoms of generalized anxiety disorder. <i>Brain, Behavior, and Immunity</i> , 2015, 43, 184-191. | 2.0 | 45 |
| 80 | PLOS Genetics Data Sharing Policy: In Pursuit of Functional Utility. <i>PLoS Genetics</i> , 2015, 11, e1005716. | 1.5 | 10 |
| 81 | Transcription Profiling of Malaria-Naïve and Semi-immune Colombian Volunteers in a <i>Plasmodium vivax</i> Sporozoite Challenge. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003978. | 1.3 | 32 |
| 82 | PART of the WHOLE: A Case Study in Wellness-Oriented Personalized Medicine. <i>Yale Journal of Biology and Medicine</i> , 2015, 88, 397-406. | 0.2 | 1 |
| 83 | Comparative transcriptomics and metabolomics in a rhesus macaque drug administration study. <i>Frontiers in Cell and Developmental Biology</i> , 2014, 2, 54. | 1.8 | 15 |
| 84 | SDS, a structural disruption score for assessment of missense variant deleteriousness. <i>Frontiers in Genetics</i> , 2014, 5, 82. | 1.1 | 13 |
| 85 | A Longitudinal Study of Health Improvement in the Atlanta CHDWB Wellness Cohort. <i>Journal of Personalized Medicine</i> , 2014, 4, 489-507. | 1.1 | 13 |
| 86 | Single cell transcriptional analysis reveals novel innate immune cell types. <i>PeerJ</i> , 2014, 2, e452. | 0.9 | 11 |
| 87 | Characterization of Distinct Classes of Differential Gene Expression in Osteoblast Cultures from Non-Syndromic Craniosynostosis Bone. <i>Journal of Genomics</i> , 2014, 2, 121-130. | 0.6 | 9 |
| 88 | A simulation study of gene-by-environment interactions in GWAS implies ample hidden effects. <i>Frontiers in Genetics</i> , 2014, 5, 225. | 1.1 | 45 |
| 89 | Systems Genomics of Metabolic Phenotypes in Wild-Type <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2014, 197, 781-793. | 1.2 | 69 |
| 90 | Hemani et al. reply. <i>Nature</i> , 2014, 514, E5-E6. | 13.7 | 12 |

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|-----|--|------|-----------|
| 91 | Wellness and Health Omics Linked to the Environment: The WHOLE Approach to Personalized Medicine. <i>Advances in Experimental Medicine and Biology</i> , 2014, 799, 1-14. | 0.8 | 8 |
| 92 | Directions for the drivers. <i>Nature</i> , 2014, 512, 31-32. | 13.7 | 3 |
| 93 | Gene expression profiles associated with acute myocardial infarction and risk of cardiovascular death. <i>Genome Medicine</i> , 2014, 6, 40. | 3.6 | 50 |
| 94 | AACDS: A database for personal genome interpretation. <i>EMBnet Journal</i> , 2014, 20, 780. | 0.2 | 0 |
| 95 | Of flies, mice and men: a systematic approach to understanding the early life origins of chronic lung disease. <i>Thorax</i> , 2013, 68, 380-384. | 2.7 | 34 |
| 96 | Geographical, Environmental and Pathophysiological Influences on the Human Blood Transcriptome. <i>Current Genetic Medicine Reports</i> , 2013, 1, 203-211. | 1.9 | 8 |
| 97 | From personalized to public health genomics. <i>Genome Medicine</i> , 2013, 5, 60. | 3.6 | 4 |
| 98 | What if we had whole-genome sequence data for millions of individuals?. <i>Genome Medicine</i> , 2013, 5, 80. | 3.6 | 3 |
| 99 | Rare allelic forms of <i>PRDM9</i> associated with childhood leukemogenesis. <i>Genome Research</i> , 2013, 23, 419-430. | 2.4 | 45 |
| 100 | Congruence of Additive and Non-Additive Effects on Gene Expression Estimated from Pedigree and SNP Data. <i>PLoS Genetics</i> , 2013, 9, e1003502. | 1.5 | 79 |
| 101 | Blood-Informative Transcripts Define Nine Common Axes of Peripheral Blood Gene Expression. <i>PLoS Genetics</i> , 2013, 9, e1003362. | 1.5 | 53 |
| 102 | Genetic and Nongenetic Variation Revealed for the Principal Components of Human Gene Expression. <i>Genetics</i> , 2013, 195, 1117-1128. | 1.2 | 23 |
| 103 | Genetic risk prediction in a small cohort of healthy adults in Atlanta. <i>Genetical Research</i> , 2013, 95, 30-37. | 0.3 | 3 |
| 104 | Whole genome sequencing in support of wellness and health maintenance. <i>Genome Medicine</i> , 2013, 5, 58. | 3.6 | 46 |
| 105 | Complex Genetic Architecture of Cardiac Disease in a Wild Type Inbred Strain of <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2013, 8, e62909. | 1.1 | 5 |
| 106 | Guidelines for Genome-Wide Association Studies. <i>PLoS Genetics</i> , 2012, 8, e1002812. | 1.5 | 88 |
| 107 | Sexual dimorphism in multiple aspects of 3D facial symmetry and asymmetry defined by spatially dense geometric morphometrics. <i>Journal of Anatomy</i> , 2012, 221, 97-114. | 0.9 | 84 |
| 108 | Effect of Normalization on Statistical and Biological Interpretation of Gene Expression Profiles. <i>Frontiers in Genetics</i> , 2012, 3, 160. | 1.1 | 27 |

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|-----|--|------|-----------|
| 109 | Using Blood Informative Transcripts in Geographical Genomics: Impact of Lifestyle on Gene Expression in Fijians. <i>Frontiers in Genetics</i> , 2012, 3, 243. | 1.1 | 26 |
| 110 | Rare and common variants: twenty arguments. <i>Nature Reviews Genetics</i> , 2012, 13, 135-145. | 7.7 | 1,077 |
| 111 | The Effects of Weak Genetic Perturbations on the Transcriptome of the Wing Imaginal Disc and Its Association With Wing Shape in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2011, 187, 1171-1184. | 1.2 | 7 |
| 112 | Common genetic variation and performance on standardized cognitive tests. <i>European Journal of Human Genetics</i> , 2010, 18, 815-820. | 1.4 | 90 |
| 113 | Geographical genomics of human leukocyte gene expression variation in southern Morocco. <i>Nature Genetics</i> , 2010, 42, 62-67. | 9.4 | 142 |
| 114 | Hints of hidden heritability in GWAS. <i>Nature Genetics</i> , 2010, 42, 558-560. | 9.4 | 258 |
| 115 | Missing heritability and strategies for finding the underlying causes of complex disease. <i>Nature Reviews Genetics</i> , 2010, 11, 446-450. | 7.7 | 1,511 |
| 116 | Genotype-by-Diet Interactions Drive Metabolic Phenotype Variation in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2010, 185, 1009-1019. | 1.2 | 86 |
| 117 | Insights from GWAS into the quantitative genetics of transcription in humans. <i>Genetical Research</i> , 2010, 92, 361-369. | 0.3 | 10 |
| 118 | Consent and Internet-Enabled Human Genomics. <i>PLoS Genetics</i> , 2010, 6, e1000965. | 1.5 | 29 |
| 119 | Maternal Influences on the Transmission of Leukocyte Gene Expression Profiles in Population Samples from Brisbane, Australia. <i>PLoS ONE</i> , 2010, 5, e14479. | 1.1 | 13 |
| 120 | Genomic Consequences of Background Effects on <i>scalloped</i> Mutant Expressivity in the Wing of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2009, 181, 1065-1076. | 1.2 | 55 |
| 121 | Strain-Dependent Differences in Several Reproductive Traits Are Not Accompanied by Early Postmating Transcriptome Changes in Female <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2009, 181, 1273-1280. | 1.2 | 12 |
| 122 | Finding the missing heritability of complex diseases. <i>Nature</i> , 2009, 461, 747-753. | 13.7 | 7,490 |
| 123 | Decanalization and the origin of complex disease. <i>Nature Reviews Genetics</i> , 2009, 10, 134-140. | 7.7 | 269 |
| 124 | Statistical Genetics: Gene Mapping Through Linkage and Association. <i>Genes, Brain and Behavior</i> , 2009, 8, 127-128. | 1.1 | 0 |
| 125 | A genome-wide study of common SNPs and CNVs in cognitive performance in the CANTAB. <i>Human Molecular Genetics</i> , 2009, 18, 4650-4661. | 1.4 | 131 |
| 126 | Metabolomics of Genotype by Diet Interactions underlying Metabolic Syndrome in <i>Drosophila</i> . <i>FASEB Journal</i> , 2009, 23, 505.4. | 0.2 | 0 |

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|-----|--|------|-----------|
| 127 | The environmental contribution to gene expression profiles. <i>Nature Reviews Genetics</i> , 2008, 9, 575-581. | 7.7 | 221 |
| 128 | A gene expression signature of confinement in peripheral blood of red wolves (<i>Canis rufus</i>). <i>Molecular Ecology</i> , 2008, 17, 2782-2791. | 2.0 | 18 |
| 129 | Cryptic genetic variation. <i>Current Biology</i> , 2008, 18, R989-R990. | 1.8 | 38 |
| 130 | A Genome-Wide Gene Expression Signature of Environmental Geography in Leukocytes of Moroccan Amazighs. <i>PLoS Genetics</i> , 2008, 4, e1000052. | 1.5 | 97 |
| 131 | Genetic Variation for Cardiac Dysfunction in <i>Drosophila</i> . <i>PLoS ONE</i> , 2007, 2, e601. | 1.1 | 33 |
| 132 | Quantitative trait transcripts for nicotine resistance in <i>Drosophila melanogaster</i> . <i>Nature Genetics</i> , 2007, 39, 264-268. | 9.4 | 68 |
| 133 | Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218. | 13.7 | 1,886 |
| 134 | Human Evolution: Thrifty Genes and the Dairy Queen. <i>Current Biology</i> , 2007, 17, R295-R296. | 1.8 | 17 |
| 135 | Human Genetics: The Hidden Text of Genome-wide Associations. <i>Current Biology</i> , 2007, 17, R929-R932. | 1.8 | 15 |
| 136 | Biology's next top model. <i>Current Biology</i> , 2006, 16, R37-R38. | 1.8 | 0 |
| 137 | Evolution: The Plastic Transcriptome. <i>Current Biology</i> , 2006, 16, R285-R287. | 1.8 | 6 |
| 138 | Epidermal Growth Factor Receptor and Transforming Growth Factor- β Signaling Contributes to Variation for Wing Shape in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2006, 173, 1417-1431. | 1.2 | 100 |
| 139 | [11] Analysis of Variance of Microarray Data. <i>Methods in Enzymology</i> , 2006, 411, 214-233. | 0.4 | 29 |
| 140 | Genetic variation for dorsal-ventral patterning of the <i>Drosophila melanogaster</i> eggshell. <i>Evolution & Development</i> , 2005, 7, 81-88. | 1.1 | 2 |
| 141 | Mutation accumulation of the transcriptome. <i>Nature Genetics</i> , 2005, 37, 458-460. | 9.4 | 9 |
| 142 | The quantitative genetics of transcription. <i>Trends in Genetics</i> , 2005, 21, 616-623. | 2.9 | 266 |
| 143 | Gene expression profiles associated with the transition to parasitism in <i>Ancylostoma caninum</i> larvae. <i>Molecular and Biochemical Parasitology</i> , 2005, 143, 39-48. | 0.5 | 50 |
| 144 | SYSTEMS BIOLOGY: The Origins of Stability. <i>Science</i> , 2005, 310, 237-237. | 6.0 | 2 |

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|-----|--|-----|-----------|
| 145 | Replication of an Egfr-Wing Shape Association in a Wild-Caught Cohort of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2005, 169, 2115-2125. | 1.2 | 41 |
| 146 | EVOLUTION: The Synthesis and Evolution of a Supermodel. <i>Science</i> , 2005, 307, 1890-1891. | 6.0 | 77 |
| 147 | Nucleotide Variation in the Egfr Locus of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2004, 167, 1199-1212. | 1.2 | 21 |
| 148 | Use of regression methods to identify motifs that modulate germline transcription in <i>Drosophila melanogaster</i> . <i>Genetical Research</i> , 2004, 83, 177-188. | 0.3 | 5 |
| 149 | Effects of Population Structure and Sex on Association Between Serotonin Receptors and <i>Drosophila</i> Heart Rate. <i>Genetics</i> , 2004, 168, 1963-1974. | 1.2 | 12 |
| 150 | Association Between Nucleotide Variation in Egfr and Wing Shape in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2004, 167, 1187-1198. | 1.2 | 58 |
| 151 | Anomalies in the Expression Profile of Interspecific Hybrids of <i>Drosophila melanogaster</i> and <i>Drosophila simulans</i> . <i>Genome Research</i> , 2004, 14, 373-379. | 2.4 | 140 |
| 152 | Uncovering cryptic genetic variation. <i>Nature Reviews Genetics</i> , 2004, 5, 681-690. | 7.7 | 477 |
| 153 | Genes Regulated by Mating, Sperm, or Seminal Proteins in Mated Female <i>Drosophila melanogaster</i> . <i>Current Biology</i> , 2004, 14, 1509-1514. | 1.8 | 287 |
| 154 | Extensive Sex-Specific Nonadditivity of Gene Expression in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2004, 167, 1791-1799. | 1.2 | 201 |
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| 156 | Population Genomics: Finding the Variants of Mass Disruption. <i>Current Biology</i> , 2003, 13, R901-R903. | 1.8 | 4 |
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