

# Greg Gibson

## List of Publications by Year in descending order

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Version: 2024-02-01

186  
papers

24,255  
citations

31976

53  
h-index

8630

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>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	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, .	8.9	8
3	Generation of human long-lived plasma cells by developmentally regulated epigenetic imprinting. <i>Life Science Alliance</i> , 2022, 5, e202101285.	2.8	19
4	Perspectives on rigor and reproducibility in single cell genomics. <i>PLoS Genetics</i> , 2022, 18, e1010210.	3.5	17
5	Targeted RNAseq Improves Clinical Diagnosis of Very Early-Onset Pediatric Immune Dysregulation. <i>Journal of Personalized Medicine</i> , 2022, 12, 919.	2.5	1
6	TreeMap: a structured approach to fine mapping of eQTL variants. <i>Bioinformatics</i> , 2021, 37, 1125-1134.	4.1	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.	1.3	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.	8.2	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.	6.2	21
10	Transcriptional firing represses bactericidal activity in cystic fibrosis airway neutrophils. <i>Cell Reports Medicine</i> , 2021, 2, 100239.	6.5	25
11	Clinical and Host Biological Factors Predict Colectomy Risk in Children Newly Diagnosed With Ulcerative Colitis. <i>Inflammatory Bowel Diseases</i> , 2021, , .	1.9	11
12	Extrafollicular IgD+ B cells generate IgE antibody secreting cells in the nasal mucosa. <i>Mucosal Immunology</i> , 2021, 14, 1144-1159.	6.0	21
13	Altered splicing associated with the pathology of inflammatory bowel disease. <i>Human Genomics</i> , 2021, 15, 47.	2.9	7
14	Machine learning applications for therapeutic tasks with genomics data. <i>Patterns</i> , 2021, 2, 100328.	5.9	14
15	Phantom epistasis between unlinked loci. <i>Nature</i> , 2021, 596, E1-E3.	27.8	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.	6.2	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.	21.4	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.	5.5	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.	1.2	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.	6.1	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.	4.1	18
22	Correlation Patterns Among B7 Family Ligands and Tryptophan Degrading Enzymes in Hepatocellular Carcinoma. <i>Frontiers in Oncology</i> , 2020, 10, 1632.	2.8	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.	2.6	21
24	Canalization and Robustness in Human Genetics and Disease. <i>Annual Review of Genetics</i> , 2020, 54, 189-211.	7.6	22
25	Fine-mapping within eQTL credible intervals by expression CROP-seq. <i>Biology Methods and Protocols</i> , 2020, 5, bpaa008.	2.2	8
26	Pitfalls in Single Clone CRISPR-Cas9 Mutagenesis to Fine-Map Regulatory Intervals. <i>Genes</i> , 2020, 11, 504.	2.4	6
27	Tissue specific regulation of transcription in endometrium and association with disease. <i>Human Reproduction</i> , 2020, 35, 377-393.	0.9	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.	7.1	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.	4.5	8
30	The Medical Genome Reference Bank contains whole genome and phenotype data of 2570 healthy elderly. <i>Nature Communications</i> , 2020, 11, 435.	12.8	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.	2.7	13
32	The effect of X-linked dosage compensation on complex trait variation. <i>Nature Communications</i> , 2019, 10, 3009.	12.8	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.	6.2	84
34	Biological relevance of computationally predicted pathogenicity of noncoding variants. <i>Nature Communications</i> , 2019, 10, 330.	12.8	44
35	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. <i>Genetics</i> , 2019, 212, 905-918.	2.9	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.	3.1	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.	1.3	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.	3.2	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.	2.2	15
40	On the utilization of polygenic risk scores for therapeutic targeting. <i>PLoS Genetics</i> , 2019, 15, e1008060.	3.5	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.	13.7	121
42	Cardiac Toxicity From Ethanol Exposure in Human-Induced Pluripotent Stem Cell-Derived Cardiomyocytes. <i>Toxicological Sciences</i> , 2019, 169, 280-292.	3.1	16
43	PolyQTL: Bayesian multiple eQTL detection with control for population structure and sample relatedness. <i>Bioinformatics</i> , 2019, 35, 1061-1063.	4.1	6
44	Ulcerative colitis mucosal transcriptomes reveal mitochondriopathy and personalized mechanisms underlying disease severity and treatment response. <i>Nature Communications</i> , 2019, 10, 38.	12.8	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.	1.3	15
46	Going to the negative: genomics for optimized medical prescription. <i>Nature Reviews Genetics</i> , 2019, 20, 1-2.	16.3	34
47	Differential transcriptome and development of human peripheral plasma cell subsets. <i>JCI Insight</i> , 2019, 4, .	5.0	41
48	Potency Analysis of Mesenchymal Stromal Cells Using a Combinatorial Assay Matrix Approach. <i>Cell Reports</i> , 2018, 22, 2504-2517.	6.4	150
49	Signatures of negative selection in the genetic architecture of human complex traits. <i>Nature Genetics</i> , 2018, 50, 746-753.	21.4	304
50	Replicability and Prediction: Lessons and Challenges from GWAS. <i>Trends in Genetics</i> , 2018, 34, 504-517.	6.7	138
51	Enhanced Contribution of HLA in Pediatric Onset Ulcerative Colitis. <i>Inflammatory Bowel Diseases</i> , 2018, 24, 829-838.	1.9	23
52	Pervasive Modulation of Obesity Risk by the Environment and Genomic Background. <i>Genes</i> , 2018, 9, 411.	2.4	16
53	Individualized Transcriptional Resolution of Complicated Malaria in a Colombian Study. <i>Journal of Personalized Medicine</i> , 2018, 8, 29.	2.5	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.	4.5	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. American Journal of Human Genetics, 2018, 103, 691-706.	6.2	326
56	Factors of the bone marrow microniche that support human plasma cell survival and immunoglobulin secretion. Nature Communications, 2018, 9, 3698.	12.8	95
57	Disease-specific regulation of gene expression in a comparative analysis of juvenile idiopathic arthritis and inflammatory bowel disease. Genome Medicine, 2018, 10, 48.	8.2	46
58	Population genetics and GWAS: A primer. PLoS Biology, 2018, 16, e2005485.	5.6	36
59	Bone Marrowâ€Derived Mesenchymal Stromal Cells from Patients with Sickle Cell Disease Display Intact Functionality. Biology of Blood and Marrow Transplantation, 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. Lancet, The, 2017, 389, 1710-1718.	13.7	482
61	The Genetic Architecture of Gene Expression in Peripheral Blood. American Journal of Human Genetics, 2017, 100, 228-237.	6.2	178
62	Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. Nature Communications, 2017, 8, 483.	12.8	22
63	Constraints on eQTL Fine Mapping in the Presence of Multisite Local Regulation of Gene Expression. G3: Genes, Genomes, Genetics, 2017, 7, 2533-2544.	1.8	23
64	Transcriptional risk scores link GWAS to eQTLs and predict complications in Crohn's disease. Nature Genetics, 2017, 49, 1517-1521.	21.4	146
65	Individualization of pubic hair bacterial communities and the effects of storage time and temperature. Forensic Science International: Genetics, 2017, 26, 12-20.	3.1	26
66	Immune dysfunctionality of replicative senescent mesenchymal stromal cells is corrected by IFN $\gamma$ priming. Blood Advances, 2017, 1, 628-643.	5.2	43
67	Cryptic Genetic Variation in Evolutionary Developmental Genetics. Biology, 2016, 5, 28.	2.8	21
68	Genomic insights into ayurvedic and western approaches to personalized medicine. Journal of Genetics, 2016, 95, 209-228.	0.7	59
69	On the Evaluation of Module Preservation. Cell Systems, 2016, 3, 17-19.	6.2	5
70	Autosomal genetic control of human gene expression does not differ across the sexes. Genome Biology, 2016, 17, 248.	8.8	15
71	A Burden of Rare Variants Associated with Extremes of Gene Expression in Human Peripheral Blood. American Journal of Human Genetics, 2016, 98, 299-309.	6.2	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. American Journal of Medical Genetics, Part A, 2015, 167, 2114-2121.	1.2	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.	0.8	60
74	DICER1 and microRNA regulation in post-traumatic stress disorder with comorbid depression. <i>Nature Communications</i> , 2015, 6, 10106.	12.8	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.	8.2	47
76	GTE <sub>x</sub> detects genetic effects. <i>Science</i> , 2015, 348, 640-641.	12.6	44
77	Omic personality: implications of stable transcript and methylation profiles for personalized medicine. <i>Genome Medicine</i> , 2015, 7, 88.	8.2	13
78	Expression quantitative trait locus analysis for translational medicine. <i>Genome Medicine</i> , 2015, 7, 60.	8.2	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.	4.1	45
80	PLOS Genetics Data Sharing Policy: In Pursuit of Functional Utility. <i>PLoS Genetics</i> , 2015, 11, e1005716.	3.5	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.	3.0	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.	3.7	15
84	SDS, a structural disruption score for assessment of missense variant deleteriousness. <i>Frontiers in Genetics</i> , 2014, 5, 82.	2.3	13
85	A Longitudinal Study of Health Improvement in the Atlanta CHDWB Wellness Cohort. <i>Journal of Personalized Medicine</i> , 2014, 4, 489-507.	2.5	13
86	Single cell transcriptional analysis reveals novel innate immune cell types. <i>PeerJ</i> , 2014, 2, e452.	2.0	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.	0.9	9
88	A simulation study of gene-by-environment interactions in GWAS implies ample hidden effects. <i>Frontiers in Genetics</i> , 2014, 5, 225.	2.3	45
89	Systems Genomics of Metabolic Phenotypes in Wild-Type <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2014, 197, 781-793.	2.9	69
90	Hemani et al. reply. <i>Nature</i> , 2014, 514, E5-E6.	27.8	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.	1.6	8
92	Directions for the drivers. <i>Nature</i> , 2014, 512, 31-32.	27.8	3
93	Gene expression profiles associated with acute myocardial infarction and risk of cardiovascular death. <i>Genome Medicine</i> , 2014, 6, 40.	8.2	50
94	AACDS: A database for personal genome interpretation. <i>EMBnet Journal</i> , 2014, 20, 780.	0.6	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.	5.6	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.	8.2	4
98	What if we had whole-genome sequence data for millions of individuals?. <i>Genome Medicine</i> , 2013, 5, 80.	8.2	3
99	Rare allelic forms of <i>PRDM9</i> associated with childhood leukemogenesis. <i>Genome Research</i> , 2013, 23, 419-430.	5.5	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.	3.5	79
101	Blood-Informative Transcripts Define Nine Common Axes of Peripheral Blood Gene Expression. <i>PLoS Genetics</i> , 2013, 9, e1003362.	3.5	53
102	Genetic and Nongenetic Variation Revealed for the Principal Components of Human Gene Expression. <i>Genetics</i> , 2013, 195, 1117-1128.	2.9	23
103	Genetic risk prediction in a small cohort of healthy adults in Atlanta. <i>Genetical Research</i> , 2013, 95, 30-37.	0.9	3
104	Whole genome sequencing in support of wellness and health maintenance. <i>Genome Medicine</i> , 2013, 5, 58.	8.2	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.	2.5	5
106	Guidelines for Genome-Wide Association Studies. <i>PLoS Genetics</i> , 2012, 8, e1002812.	3.5	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.	1.5	84
108	Effect of Normalization on Statistical and Biological Interpretation of Gene Expression Profiles. <i>Frontiers in Genetics</i> , 2012, 3, 160.	2.3	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.	2.3	26
110	Rare and common variants: twenty arguments. <i>Nature Reviews Genetics</i> , 2012, 13, 135-145.	16.3	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.	2.9	7
112	Common genetic variation and performance on standardized cognitive tests. <i>European Journal of Human Genetics</i> , 2010, 18, 815-820.	2.8	90
113	Geographical genomics of human leukocyte gene expression variation in southern Morocco. <i>Nature Genetics</i> , 2010, 42, 62-67.	21.4	142
114	Hints of hidden heritability in GWAS. <i>Nature Genetics</i> , 2010, 42, 558-560.	21.4	258
115	Missing heritability and strategies for finding the underlying causes of complex disease. <i>Nature Reviews Genetics</i> , 2010, 11, 446-450.	16.3	1,511
116	Genotype-by-Diet Interactions Drive Metabolic Phenotype Variation in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2010, 185, 1009-1019.	2.9	86
117	Insights from GWAS into the quantitative genetics of transcription in humans. <i>Genetical Research</i> , 2010, 92, 361-369.	0.9	10
118	Consent and Internet-Enabled Human Genomics. <i>PLoS Genetics</i> , 2010, 6, e1000965.	3.5	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.	2.5	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.	2.9	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.	2.9	12
122	Finding the missing heritability of complex diseases. <i>Nature</i> , 2009, 461, 747-753.	27.8	7,490
123	Decanalization and the origin of complex disease. <i>Nature Reviews Genetics</i> , 2009, 10, 134-140.	16.3	269
124	Statistical Genetics: Gene Mapping Through Linkage and Association. <i>Genes, Brain and Behavior</i> , 2009, 8, 127-128.	2.2	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.	2.9	131
126	Metabolomics of Genotype by Diet Interactions underlying Metabolic Syndrome in <i>Drosophila</i> . <i>FASEB Journal</i> , 2009, 23, 505.4.	0.5	0



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127	The environmental contribution to gene expression profiles. Nature Reviews Genetics, 2008, 9, 575-581.	16.3	221
128	A gene expression signature of confinement in peripheral blood of red wolves ( <i>Canis rufus</i> ). Molecular Ecology, 2008, 17, 2782-2791.	3.9	18
129	Cryptic genetic variation. Current Biology, 2008, 18, R989-R990.	3.9	38
130	A Genome-Wide Gene Expression Signature of Environmental Geography in Leukocytes of Moroccan Amazighs. PLoS Genetics, 2008, 4, e1000052.	3.5	97
131	Genetic Variation for Cardiac Dysfunction in Drosophila. PLoS ONE, 2007, 2, e601.	2.5	33
132	Quantitative trait transcripts for nicotine resistance in Drosophila melanogaster. Nature Genetics, 2007, 39, 264-268.	21.4	68
133	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	27.8	1,886
134	Human Evolution: Thrifty Genes and the Dairy Queen. Current Biology, 2007, 17, R295-R296.	3.9	17
135	Human Genetics: The Hidden Text of Genome-wide Associations. Current Biology, 2007, 17, R929-R932.	3.9	15
136	Biology's next top model. Current Biology, 2006, 16, R37-R38.	3.9	0
137	Evolution: The Plastic Transcriptome. Current Biology, 2006, 16, R285-R287.	3.9	6
138	Epidermal Growth Factor Receptor and Transforming Growth Factor- $\beta$ Signaling Contributes to Variation for Wing Shape in Drosophila melanogaster. Genetics, 2006, 173, 1417-1431.	2.9	100
139	[11] Analysis of Variance of Microarray Data. Methods in Enzymology, 2006, 411, 214-233.	1.0	29
140	Genetic variation for dorsal-ventral patterning of the Drosophila melanogaster eggshell. Evolution & Development, 2005, 7, 81-88.	2.0	2
141	Mutation accumulation of the transcriptome. Nature Genetics, 2005, 37, 458-460.	21.4	9
142	The quantitative genetics of transcription. Trends in Genetics, 2005, 21, 616-623.	6.7	266
143	Gene expression profiles associated with the transition to parasitism in Ancylostoma caninum larvae. Molecular and Biochemical Parasitology, 2005, 143, 39-48.	1.1	50
144	SYSTEMS BIOLOGY: The Origins of Stability. Science, 2005, 310, 237-237.	12.6	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.	2.9	41
146	EVOLUTION: The Synthesis and Evolution of a Supermodel. <i>Science</i> , 2005, 307, 1890-1891.	12.6	77
147	Nucleotide Variation in the Egfr Locus of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2004, 167, 1199-1212.	2.9	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.	0.9	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.	2.9	12
150	Association Between Nucleotide Variation in Egfr and Wing Shape in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2004, 167, 1187-1198.	2.9	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.	5.5	140
152	Uncovering cryptic genetic variation. <i>Nature Reviews Genetics</i> , 2004, 5, 681-690.	16.3	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.	3.9	287
154	Extensive Sex-Specific Nonadditivity of Gene Expression in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2004, 167, 1791-1799.	2.9	201
155	Evidence that Egfr Contributes to Cryptic Genetic Variation for Photoreceptor Determination in Natural Populations of <i>Drosophila melanogaster</i> . <i>Current Biology</i> , 2003, 13, 1888-1893.	3.9	94
156	Population Genomics: Finding the Variants of Mass Disruption. <i>Current Biology</i> , 2003, 13, R901-R903.	3.9	4
157	Contrasting selection pressures on components of the Ras-mediated signal transduction pathway in <i>Drosophila</i> . <i>Molecular Ecology</i> , 2003, 12, 1315-1323.	3.9	54
158	Merging Ecology, Molecular Evolution, and Functional Genetics. <i>Molecular Ecology</i> , 2003, 12, 1109-1112.	3.9	30
159	Introduction: Special Issue on Selected Papers from the 2002 SID International Symposium. <i>Journal of the Society for Information Display</i> , 2003, 11, 79.	2.1	0
160	Mixed-Model Reanalysis of Primate Data Suggests Tissue and Species Biases in Oligonucleotide-Based Gene Expression Profiles. <i>Genetics</i> , 2003, 165, 747-757.	2.9	133
161	Microarray Analysis. <i>PLoS Biology</i> , 2003, 1, e15.	5.6	30
162	Unusual genetic architecture of natural variation affecting drug resistance in <i>Drosophila melanogaster</i> . <i>Genetical Research</i> , 2002, 80, 205-213.	0.9	10

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163	Enabling Population and Quantitative Genomics. <i>Genetical Research</i> , 2002, 80, 1-6.	0.9	20
164	The evolution of developmental regulatory pathways. <i>Current Opinion in Genetics and Development</i> , 2002, 12, 695-700.	3.3	14
165	Developmental Evolution: Getting Robust About Robustness. <i>Current Biology</i> , 2002, 12, R347-R349.	3.9	18
166	A genetic attack on the defense complex. <i>BioEssays</i> , 2002, 24, 487-489.	2.5	4
167	Microarrays in ecology and evolution: a preview. <i>Molecular Ecology</i> , 2002, 11, 17-24.	3.9	167
168	The contributions of sex, genotype and age to transcriptional variance in <i>Drosophila melanogaster</i> . <i>Nature Genetics</i> , 2001, 29, 389-395.	21.4	595
169	Evolution: A complement for evolutionary genetics. <i>Current Biology</i> , 2001, 11, R74-R76.	3.9	0
170	Developmental evolution: The unbearable likeness of beings. <i>Current Biology</i> , 2001, 11, R345-R348.	3.9	2
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