

Greg Gibson

List of Publications by Year in descending order

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Version: 2024-02-01

186
papers

24,255
citations

36691

53
h-index

9865

146
g-index

215
all docs

215
docs citations

215
times ranked

36716
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 Marrowâ€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	GTEx 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
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.	1.8	94
156	Population Genomics: Finding the Variants of Mass Disruption. <i>Current Biology</i> , 2003, 13, R901-R903.	1.8	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.	2.0	54
158	Merging Ecology, Molecular Evolution, and Functional Genetics. <i>Molecular Ecology</i> , 2003, 12, 1109-1112.	2.0	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.	0.8	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.	1.2	133
161	Microarray Analysis. <i>PLoS Biology</i> , 2003, 1, e15.	2.6	30
162	Unusual genetic architecture of natural variation affecting drug resistance in <i>Drosophila melanogaster</i> . <i>Genetical Research</i> , 2002, 80, 205-213.	0.3	10

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163	Enabling Population and Quantitative Genomics. <i>Genetical Research</i> , 2002, 80, 1-6.	0.3	20
164	The evolution of developmental regulatory pathways. <i>Current Opinion in Genetics and Development</i> , 2002, 12, 695-700.	1.5	14
165	Developmental Evolution: Getting Robust About Robustness. <i>Current Biology</i> , 2002, 12, R347-R349.	1.8	18
166	A genetic attack on the defense complex. <i>BioEssays</i> , 2002, 24, 487-489.	1.2	4
167	Microarrays in ecology and evolution: a preview. <i>Molecular Ecology</i> , 2002, 11, 17-24.	2.0	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.	9.4	595
169	Evolution: A complement for evolutionary genetics. <i>Current Biology</i> , 2001, 11, R74-R76.	1.8	0
170	Developmental evolution: The unbearable likeness of beings. <i>Current Biology</i> , 2001, 11, R345-R348.	1.8	2
171	Assessing Gene Significance from cDNA Microarray Expression Data via Mixed Models. <i>Journal of Computational Biology</i> , 2001, 8, 625-637.	0.8	987
172	Quantitative Trait Loci for the Monoamine-Related Traits Heart Rate and Headless Behavior in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2001, 157, 283-294.	1.2	21
173	Canalization in evolutionary genetics: a stabilizing theory?. <i>BioEssays</i> , 2000, 22, 372-380.	1.2	311
174	Haplotype dimorphism in a SNP collection from <i>Drosophila melanogaster</i> . , 2000, 288, 63-75.		33
175	Genetic variation for the positioning of wing veins in <i>Drosophila melanogaster</i> . <i>Evolution & Development</i> , 2000, 2, 16-24.	1.1	90
176	Evolution: Hox genes and the cellared wine principle. <i>Current Biology</i> , 2000, 10, R452-R455.	1.8	21
177	Canalization in evolutionary genetics: a stabilizing theory?. , 2000, 22, 372.		18
178	Quantitative Trait Loci Affecting Components of Wing Shape in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2000, 155, 671-683.	1.2	123
179	Axial variation in the threespine stickleback: genetic and environmental factors. <i>Evolution & Development</i> , 1999, 1, 100-112.	1.1	28
180	Absence of Protein Polymorphism in the Ras Genes of <i>Drosophila melanogaster</i> . <i>Journal of Molecular Evolution</i> , 1999, 49, 583-590.	0.8	22

#	ARTICLE	IF	CITATIONS
181	Developmental evolution: Going beyond the "just so"™. <i>Current Biology</i> , 1999, 9, R942-R945.	1.8	6
182	Insect evolution: Redesigning the fruitfly. <i>Current Biology</i> , 1999, 9, R86-R89.	1.8	15
183	Potential Variance Affecting Homeotic Ultrabithorax and Antennapedia Phenotypes in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 1999, 151, 1081-1091.	1.2	56
184	Is Function of the <i>Drosophila</i> Homeotic Gene <i>Ultrabithorax</i> Canalized?. <i>Genetics</i> , 1997, 147, 1155-1168.	1.2	55
185	Epistasis and Pleiotropy as Natural Properties of Transcriptional Regulation. <i>Theoretical Population Biology</i> , 1996, 49, 58-89.	0.5	111
186	The specificities of sex combs reduced and Antennapedia are defined by a distinct portion of each protein that includes the homeodomain. <i>Cell</i> , 1990, 62, 1087-1103.	13.5	206