Barbara E Stranger

List of Publications by Year
in descending order

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83 papers	25,594 citations	44042 48 h-index	56687 83 g-index
96 all docs	96 docs citations	96 times ranked	38903 citing authors

#	Article	IF	Citations
1	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	13.7	4,709
2	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	13.7	4,137
3	Genetics of rheumatoid arthritis contributes to biology and drug discovery. Nature, 2014, 506, 376-381.	13.7	1,974
4	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	13.7	1,788
5	Relative Impact of Nucleotide and Copy Number Variation on Gene Expression Phenotypes. Science, 2007, 315, 848-853.	6.0	1,546
6	Population genomics of human gene expression. Nature Genetics, 2007, 39, 1217-1224.	9.4	1,072
7	Common Regulatory Variation Impacts Gene Expression in a Cell Typeâ€“Dependent Manner. Science, 2009, 325, 1246-1250.	6.0	694
8	Chromatin marks identify critical cell types for fine mapping complex trait variants. Nature Genetics, 2013, 45, 124-130.	9.4	553
9	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	5.8	533
10	Progress and Promise of Genome-Wide Association Studies for Human Complex Trait Genetics. Genetics, 2011, 187, 367-383.	1.2	486
11	Polarization of the Effects of Autoimmune and Neurodegenerative Risk Alleles in Leukocytes. Science, 2014, 344, 519-523.	6.0	480
12	Genome-Wide Associations of Gene Expression Variation in Humans. PLoS Genetics, 2005, 1, e78.	1.5	467
13	Patterns of Cis Regulatory Variation in Diverse Human Populations. PLoS Genetics, 2012, 8, e1002639.	1.5	439
14	Candidate Causal Regulatory Effects by Integration of Expression QTLs with Complex Trait Genetic Associations. PLoS Genetics, 2010, 6, e1000895.	1.5	434
15	Common Genetic Variants Modulate Pathogen-Sensing Responses in Human Dendritic Cells. Science, 2014, 343, 1246980.	6.0	391
16	The impact of sex on gene expression across human tissues. Science, 2020, 369, .	6.0	329
17	Integrative eQTL-Based Analyses Reveal the Biology of Breast Cancer Risk Loci. Cell, 2013, 152, 633-641.	13.5	300
18	Genevar: a database and Java application for the analysis and visualization of SNP-gene associations in eQTL studies. Bioinformatics, 2010, 26, 2474-2476.	1.8	282

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19	Determinants of telomere length across human tissues. Science, 2020, 369, .	6.0	257
20	Fine-Mapping the Genetic Association of the Major Histocompatibility Complex in Multiple Sclerosis: HLA and Non-HLA Effects. PLoS Genetics, 2013, 9, e1003926.	1.5	250
21	Intersection of population variation and autoimmunity genetics in human T cell activation. Science, 2014, 345, 1254665.	6.0	218
22	Cell typeâ€“specific genetic regulation of gene expression across human tissues. Science, 2020, 369, .	6.0	210
23	The role of sex in the genomics ofÂhuman complex traits. Nature Reviews Genetics, 2019, 20, 173-190.	7.7	203
24	Human HLA-G+ extravillous trophoblasts: Immune-activating cells that interact with decidual leukocytes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7219-7224.	3.3	185
25	Enhancing GTEx by bridging the gaps between genotype, gene expression, and disease. Nature Genetics, 2017, 49, 1664-1670.	9.4	179
26	Fast-evolving noncoding sequences in the human genome. Genome Biology, 2007, 8, R118.	13.9	163
27	ImmGen report: sexual dimorphism in the immune system transcriptome. Nature Communications, 2019, 10, 4295.	5.8	155
28	Genome-Wide Association Study and Gene Expression Analysis Identifies CD84 as a Predictor of Response to Etanercept Therapy in Rheumatoid Arthritis. PLoS Genetics, 2013, 9, e1003394.	1.5	146
29	CD33: increased inclusion of exon 2 implicates the Ig V-set domain in Alzheimer's disease susceptibility. Human Molecular Genetics, 2014, 23, 2729-2736.	1.4	128
30	Large-Scale Population Study of Human Cell Lines Indicates that Dosage Compensation Is Virtually Complete. PLoS Genetics, 2008, 4, e9.	1.5	127
31	Multilocus Analysis of Variation and Speciation in the Closely Related Species Arabidopsis halleri and A. lyrata. Genetics, 2004, 166, 373-388.	1.2	124
32	Disentangling the Effects of Colocalizing Genomic Annotations to Functionally Prioritize Non-coding Variants within Complex-Trait Loci. American Journal of Human Genetics, 2015, 97, 139-152.	2.6	122
33	Breaking the waves: improved detection of copy number variation from microarray-based comparative genomic hybridization. Genome Biology, 2007, 8, R228.	13.9	120
34	Interindividual variation in human T regulatory cells. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E1111-20.	3.3	112
35	The impact of human copy number variation on gene expression: Figure 1. Briefings in Functional Genomics, 2015, 14, 352-357.	1.3	108
36	Genomics of alternative splicing: evolution, development and pathophysiology. Human Genetics, 2014, 133, 679-687.	1.8	103

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37	Bedside Back to Bench: Building Bridges between Basic and Clinical Genomic Research. Cell, 2017, 169, 6-12.	13.5	103
38	Extensive genetic diversity and substructuring among zebrafish strains revealed through copy number variant analysis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 529-534.	3.3	102
39	Common Risk Alleles for Inflammatory Diseases Are Targets of Recent Positive Selection. American Journal of Human Genetics, 2013, 92, 517-529.	2.6	100
40	Gene Expression Levels Are a Target of Recent Natural Selection in the Human Genome. Molecular Biology and Evolution, 2008, 26, 649-658.	3.5	96
41	Independent and population-specific association of risk variants at the IRGM locus with Crohn's disease. Human Molecular Genetics, 2010, 19, 1828-1839.	1.4	93
42	Sex-biased genetic effects on gene regulation in humans. Genome Research, 2012, 22, 2368-2375.	2.4	92
43	Large-Scale trans -eQTLs Affect Hundreds of Transcripts and Mediate Patterns of Transcriptional Co-regulation. American Journal of Human Genetics, 2017, 100, 581-591.	2.6	86
44	Alzheimer Disease Susceptibility Loci: Evidence for a Protein Network under Natural Selection. American Journal of Human Genetics, 2012, 90, 720-726.	2.6	71
45	Expression QTL-based analyses reveal candidate causal genes and loci across five tumor types. Human Molecular Genetics, 2014, 23, 5294-5302.	1.4	71
46	IL12A, MPHOSPH9/CDK2AP1 and RGS1 are novel multiple sclerosis susceptibility loci. Genes and Immunity, 2010, 11, 397-405.	2.2	70
47	Genetic analysis of isoform usage in the human anti-viral response reveals influenza-specific regulation of ERAP2 transcripts under balancing selection. Genome Research, 2018, 28, 1812-1825.	2.4	66
48	Design and Implementation of the International Genetics and Translational Research in Transplantation Network. Transplantation, 2015, 99, 2401-2412.	0.5	60
49	Neuroblastoma survivors are at increased risk for second malignancies: A report from the International Neuroblastoma Risk Group Project. European Journal of Cancer, 2017, 72, 177-185.	1.3	59
50	ImmVar project: Insights and design considerations for future studies of â€œhealthyâ€•immune variation. Seminars in Immunology, 2015, 27, 51-57.	2.7	53
51	Imputing Gene Expression in Uncollected Tissues Within and Beyond GTEx. American Journal of Human Genetics, 2016, 98, 697-708.	2.6	51
52	Primers for 22 candidate genes for ecological adaptations in Brassicaceae. Molecular Ecology Notes, 2002, 2, 258-262.	1.7	48
53	Functional variation and evolution of non-coding DNA. Current Opinion in Genetics and Development, 2006, 16, 559-564.	1.5	48
54	Examining Sex-Differentiated Genetic Effects Across Neuropsychiatric and Behavioral Traits. Biological Psychiatry, 2021, 89, 1127-1137.	0.7	48

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55	Regulation of Gene Expression in Autoimmune Disease Loci and the Genetic Basis of Proliferation in CD4+ Effector Memory T Cells. PLoS Genetics, 2014, 10, e1004404.	1.5	46
56	Sex differences in the genetic architecture of obsessiveâ€“compulsive disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 351-364.	1.1	41
57	Genetic variation in human gene expression. Mammalian Genome, 2006, 17, 503-508.	1.0	40
58	Analysis of caseâ€“control association studies with known risk variants. Bioinformatics, 2012, 28, 1729-1737.	1.8	36
59	Modifier Effects between Regulatory and Protein-Coding Variation. PLoS Genetics, 2008, 4, e1000244.	1.5	33
60	Integrative genomics reveals hypoxia inducible genes that are associated with a poor prognosis in neuroblastoma patients. Oncotarget, 2016, 7, 76816-76826.	0.8	33
61	Balancing Selection on a Regulatory Region Exhibiting Ancient Variation That Predates Humanâ€“Neandertal Divergence. PLoS Genetics, 2013, 9, e1003404.	1.5	26
62	Sex differences in gene expression in response to ischemia in the human left ventricular myocardium. Human Molecular Genetics, 2019, 28, 1682-1693.	1.4	26
63	Genetics of human gene expression. Current Opinion in Genetics and Development, 2013, 23, 627-634.	1.5	25
64	Accurate and Fast Multiple-Testing Correction in eQTL Studies. American Journal of Human Genetics, 2015, 96, 857-868.	2.6	25
65	Genetic architecture of age-related cognitive decline in African Americans. Neurology: Genetics, 2017, 3, e125.	0.9	22
66	5-Hydroxymethylcytosine Profiles in Circulating Cell-Free DNA Associate with Disease Burden in Children with Neuroblastoma. Clinical Cancer Research, 2020, 26, 1309-1317.	3.2	22
67	The genetics of regulatory variation in the human genome. Human Genomics, 2005, 2, 126.	1.4	21
68	From DNA to RNA to disease and back: The 'central dogma' of regulatory disease variation. Human Genomics, 2006, 2, 383.	1.4	21
69	The Evolutionary History of Common Genetic Variants Influencing Human Cortical Surface Area. Cerebral Cortex, 2021, 31, 1873-1887.	1.6	21
70	Evaluation of Genetic Predisposition for MYCN-Amplified Neuroblastoma. Journal of the National Cancer Institute, 2017, 109, .	3.0	20
71	Assocplots: a Python package for static and interactive visualization of multiple-group GWAS results. Bioinformatics, 2017, 33, 432-434.	1.8	19
72	Integration of genomics and transcriptomics predicts diabetic retinopathy susceptibility genes. ELife, 2020, 9, .	2.8	18

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73	Expression Quantitative Trait Loci Information Improves Predictive Modeling of Disease Relevance of Non-Coding Genetic Variation. PLoS ONE, 2015, 10, e0140758.	1.1	17
74	Association of CNVs with methylation variation. Npj Genomic Medicine, 2020, 5, 41.	1.7	17
75	Coordinating GWAS results with gene expression in a systems immunologic paradigm in autoimmunity. Current Opinion in Immunology, 2012, 24, 544-551.	2.4	14
76	5-Hydroxymethylcytosine Profiles Are Prognostic of Outcome in Neuroblastoma and Reveal Transcriptional Networks That Correlate With Tumor Phenotype. JCO Precision Oncology, 2019, 3, 1-12.	1.5	14
77	Pharmacogenomic genotypes define genetic ancestry in patients and enable population-specific genomic implementation. Pharmacogenomics Journal, 2020, 20, 126-135.	0.9	14
78	Nucleotide variation at the myrosinase-encoding locus, TGG1, and quantitative myrosinase enzyme activity variation in Arabidopsis thaliana. Molecular Ecology, 2004, 14, 295-309.	2.0	10
79	Systematic evaluation of transcriptomics-based deconvolution methods and references using thousands of clinical samples. Briefings in Bioinformatics, 2021, 22, .	3.2	10
80	The new science of sex differences in neuropsychiatric traits. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 333-334.	1.1	2
81	Systems and genome-wide approaches unite to provide a route to personalized medicine. Genome Medicine, 2012, 4, 29.	3.6	1
82	Polygenic Adaptation Underlies Evolution of Brain Structures and Behavioral Traits. European Neuropsychopharmacology, 2019, 29, S755-S756.	0.3	1
83	O3-04-05: EXPRESSION QTL ANALYSIS FROM PRIMARY IMMUNE CELLS IDENTIFIES NOVEL REGULATORY EFFECTS UNDERLYING ALZHEIMER'S DISEASE SUSCEPTIBILITY. , 2014, 10, P216-P216.		0