Barbara E Stranger

List of Publications by Citations

87 papers	20,504 citations	47 h-index	96 g-index
96 ext. papers	23,714 ext. citations	14.2 avg, IF	6.03 L-index

#	Paper	IF	Citations
87	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature*, **2007**, 447, 799-816	50.4	4121
86	A second generation human haplotype map of over 3.1 million SNPs. *Nature*, **2007**, 449, 851-61	50.4	3647
85	Genetics of rheumatoid arthritis contributes to biology and drug discovery. *Nature*, **2014**, 506, 376-81	50.4	1426
84	Genome-wide detection and characterization of positive selection in human populations. *Nature*, **2007**, 449, 913-8	50.4	1367
83	Relative impact of nucleotide and copy number variation on gene expression phenotypes. *Science*, **2007**, 315, 848-53	33.3	1361
82	Population genomics of human gene expression. *Nature Genetics*, **2007**, 39, 1217-24	36.3	936
81	Common regulatory variation impacts gene expression in a cell type-dependent manner. *Science*, **2009**, 325, 1246-50	33.3	607
80	Genome-wide associations of gene expression variation in humans. *PLoS Genetics*, **2005**, 1, e78	6	431
79	Chromatin marks identify critical cell types for fine mapping complex trait variants. *Nature Genetics*, **2013**, 45, 124-30	36.3	422
78	Progress and promise of genome-wide association studies for human complex trait genetics. *Genetics*, **2011**, 187, 367-83	4	406
77	Polarization of the effects of autoimmune and neurodegenerative risk alleles in leukocytes. *Science* , **2014**, 344, 519-23	33.3	372
76	Patterns of cis regulatory variation in diverse human populations. *PLoS Genetics*, **2012**, 8, e1002639	6	361
75	Candidate causal regulatory effects by integration of expression QTLs with complex trait genetic associations. *PLoS Genetics*, **2010**, 6, e1000895	6	339
74	The transcriptional landscape of age in human peripheral blood. *Nature Communications*, **2015**, 6, 8570	17.4	335
73	Common genetic variants modulate pathogen-sensing responses in human dendritic cells. *Science*, **2014**, 343, 1246980	33.3	309
72	Genevar: a database and Java application for the analysis and visualization of SNP-gene associations in eQTL studies. *Bioinformatics*, **2010**, 26, 2474-6	7.2	264
71	Integrative eQTL-based analyses reveal the biology of breast cancer risk loci. *Cell*, **2013**, 152, 633-41	56.2	255

70	Fine-mapping the genetic association of the major histocompatibility complex in multiple sclerosis: HLA and non-HLA effects. *PLoS Genetics*, **2013**, 9, e1003926	6	186
69	Intersection of population variation and autoimmunity genetics in human T cell activation. *Science*, **2014**, 345, 1254665	33.3	175
68	Enhancing GTEx by bridging the gaps between genotype, gene expression, and disease. *Nature Genetics*, **2017**, 49, 1664-1670	36.3	127
67	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	6	127
66	The role of sex in the genomics of human complex traits. *Nature Reviews Genetics*, **2019**, 20, 173-190	30.1	119
65	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, 7219-24	11.5	117
64	Fast-evolving noncoding sequences in the human genome. *Genome Biology*, **2007**, 8, R118	18.3	116
63	Large-scale population study of human cell lines indicates that dosage compensation is virtually complete. *PLoS Genetics*, **2008**, 4, e9	6	113
62	Multilocus analysis of variation and speciation in the closely related species Arabidopsis halleri and A. lyrata. *Genetics*, **2004**, 166, 373-88	4	112
61	Breaking the waves: improved detection of copy number variation from microarray-based comparative genomic hybridization. *Genome Biology*, **2007**, 8, R228	18.3	110
60	The impact of sex on gene expression across human tissues. *Science*, **2020**, 369,	33.3	100
59	Disentangling the Effects of Colocalizing Genomic Annotations to Functionally Prioritize Non-coding Variants within Complex-Trait Loci. *American Journal of Human Genetics*, **2015**, 97, 139-52	11	94
58	CD33: increased inclusion of exon 2 implicates the Ig V-set domain in Alzheimer's disease susceptibility. *Human Molecular Genetics*, **2014**, 23, 2729-36	5.6	93
57	Determinants of telomere length across human tissues. *Science*, **2020**, 369,	33.3	90
56	Common risk alleles for inflammatory diseases are targets of recent positive selection. *American Journal of Human Genetics*, **2013**, 92, 517-29	11	88
55	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, 529-34	11.5	87
54	Bedside Back to Bench: Building Bridges between Basic and Clinical Genomic Research. *Cell*, **2017**, 169, 6-12	56.2	81
53	The GTEx Consortium atlas of genetic regulatory effects across human tissues		81

52	Interindividual variation in human T regulatory cells. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, E1111-20	11.5	80
51	Independent and population-specific association of risk variants at the IRGM locus with Crohn's disease. *Human Molecular Genetics*, **2010**, 19, 1828-39	5.6	79
50	ImmGen report: sexual dimorphism in the immune system transcriptome. *Nature Communications*, **2019**, 10, 4295	17.4	73
49	Gene expression levels are a target of recent natural selection in the human genome. *Molecular Biology and Evolution*, **2009**, 26, 649-58	8.3	73
48	Genomics of alternative splicing: evolution, development and pathophysiology. *Human Genetics*, **2014**, 133, 679-87	6.3	71
47	The impact of human copy number variation on gene expression. *Briefings in Functional Genomics*, **2015**, 14, 352-7	4.9	69
46	Sex-biased genetic effects on gene regulation in humans. *Genome Research*, **2012**, 22, 2368-75	9.7	68
45	Cell type-specific genetic regulation of gene expression across human tissues. *Science*, **2020**, 369,	33.3	68
44	IL12A, MPHOSPH9/CDK2AP1 and RGS1 are novel multiple sclerosis susceptibility loci. *Genes and Immunity*, **2010**, 11, 397-405	4.4	62
43	Expression QTL-based analyses reveal candidate causal genes and loci across five tumor types. *Human Molecular Genetics*, **2014**, 23, 5294-302	5.6	61
42	Alzheimer disease susceptibility loci: evidence for a protein network under natural selection. *American Journal of Human Genetics*, **2012**, 90, 720-6	11	57
41	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	7.5	47
40	Large-Scale trans-eQTLs Affect Hundreds of Transcripts and Mediate Patterns of Transcriptional Co-regulation. *American Journal of Human Genetics*, **2017**, 100, 581-591	11	46
39	Primers for 22 candidate genes for ecological adaptations in Brassicaceae. *Molecular Ecology Notes*, **2002**, 2, 258-262		46
38	Design and Implementation of the International Genetics and Translational Research in Transplantation Network. *Transplantation*, **2015**, 99, 2401-12	1.8	44
37	Functional variation and evolution of non-coding DNA. *Current Opinion in Genetics and Development* , **2006**, 16, 559-64	4.9	40
36	ImmVar project: Insights and design considerations for future studies of "healthy" immune variation. *Seminars in Immunology*, **2015**, 27, 51-7	10.7	39
35	Genetic variation in human gene expression. *Mammalian Genome*, **2006**, 17, 503-8	3.2	39

34	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	6	37
33	Modifier effects between regulatory and protein-coding variation. *PLoS Genetics*, **2008**, 4, e1000244	6	30
32	Genetic analysis of isoform usage in the human anti-viral response reveals influenza-specific regulation of transcripts under balancing selection. *Genome Research*, **2018**, 28, 1812-1825	9.7	29
31	Integrative genomics reveals hypoxia inducible genes that are associated with a poor prognosis in neuroblastoma patients. *Oncotarget*, **2016**, 7, 76816-76826	3.3	26
30	Analysis of case-control association studies with known risk variants. *Bioinformatics*, **2012**, 28, 1729-37	7.2	25
29	Imputing Gene Expression in Uncollected Tissues Within and Beyond GTEx. *American Journal of Human Genetics*, **2016**, 98, 697-708	11	25
28	Sex differences in the genetic architecture of obsessive-compulsive disorder. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2019**, 180, 351-364	3.5	25
27	Balancing selection on a regulatory region exhibiting ancient variation that predates human-neandertal divergence. *PLoS Genetics*, **2013**, 9, e1003404	6	21
26	The genetics of regulatory variation in the human genome. *Human Genomics*, **2005**, 2, 126-31	6.8	20
25	Accurate and fast multiple-testing correction in eQTL studies. *American Journal of Human Genetics*, **2015**, 96, 857-68	11	18
24	From DNA to RNA to disease and back: the Scentral dogmaSof regulatory disease variation. *Human Genomics*, **2006**, 2, 383-90	6.8	18
23	Sex differences in gene expression in response to ischemia in the human left ventricular myocardium. *Human Molecular Genetics*, **2019**, 28, 1682-1693	5.6	18
22	Genetics of human gene expression. *Current Opinion in Genetics and Development*, **2013**, 23, 627-34	4.9	17
21	Evaluation of Genetic Predisposition for MYCN-Amplified Neuroblastoma. *Journal of the National Cancer Institute*, **2017**, 109,	9.7	17
20	Genetic architecture of age-related cognitive decline in African Americans. *Neurology: Genetics*, **2017**, 3, e125	3.8	16
19	Expression Quantitative Trait Loci Information Improves Predictive Modeling of Disease Relevance of Non-Coding Genetic Variation. *PLoS ONE*, **2015**, 10, e0140758	3.7	16
18	Assocplots: a Python package for static and interactive visualization of multiple-group GWAS results. *Bioinformatics*, **2017**, 33, 432-434	7.2	14
17	Coordinating GWAS results with gene expression in a systems immunologic paradigm in autoimmunity. *Current Opinion in Immunology*, **2012**, 24, 544-51	7.8	13

16	Examining Sex-Differentiated Genetic Effects Across Neuropsychiatric and Behavioral Traits. *Biological Psychiatry*, **2021**, 89, 1127-1137	7.9	12
15	5-Hydroxymethylcytosine Profiles in Circulating Cell-Free DNA Associate with Disease Burden in Children with Neuroblastoma. *Clinical Cancer Research*, **2020**, 26, 1309-1317	12.9	11
14	5-Hydroxymethylcytosine Profiles Are Prognostic of Outcome in Neuroblastoma and Reveal Transcriptional Networks That Correlate With Tumor Phenotype. *JCO Precision Oncology*, **2019**, 3,	3.6	8
13	Nucleotide variation at the myrosinase-encoding locus, TGG1, and quantitative myrosinase enzyme activity variation in Arabidopsis thaliana. *Molecular Ecology*, **2005**, 14, 295-309	5.7	8
12	Pharmacogenomic genotypes define genetic ancestry in patients and enable population-specific genomic implementation. *Pharmacogenomics Journal*, **2020**, 20, 126-135	3.5	8
11	Polygenic selection underlies evolution of human brain structure and behavioral traits		6
10	The Evolutionary History of Common Genetic Variants Influencing Human Cortical Surface Area. *Cerebral Cortex*, **2021**, 31, 1873-1887	5.1	6
9	Integration of genomics and transcriptomics predicts diabetic retinopathy susceptibility genes. *ELife*, **2020**, 9,	8.9	5
8	Association of CNVs with methylation variation. *Npj Genomic Medicine*, **2020**, 5, 41	6.2	4
7	Examining sex-differentiated genetic effects across neuropsychiatric and behavioral traits		3
6	Systems and genome-wide approaches unite to provide a route to personalized medicine. *Genome Medicine*, **2012**, 4, 29	14.4	1
5	Genetic analysis of isoform usage in the human anti-viral response reveals influenza-specific regulation of ERAP2 transcripts under balancing selection		1
4	Sex differences in the genetic architecture of obsessive-compulsive disorder		1
3	The Evolutionary History of Common Genetic Variants Influencing Human Cortical Surface Area		1
2	Systematic evaluation of transcriptomics-based deconvolution methods and references using thousands of clinical samples. *Briefings in Bioinformatics*, **2021**, 22,	13.4	1
1	O3-04-05: EXPRESSION QTL ANALYSIS FROM PRIMARY IMMUNE CELLS IDENTIFIES NOVEL REGULATORY EFFECTS UNDERLYING ALZHEIMERS DISEASE SUSCEPTIBILITY **2014**, 10, P216-P216		