Barbara E Stranger

List of Publications by Year
in descending order

83	25,594	44069 48	56724 83
papers	citations	h-index	g-index

96	96	96	38903
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The Evolutionary History of Common Genetic Variants Influencing Human Cortical Surface Area. Cerebral Cortex, 2021, 31, 1873-1887.	2.9	21
2	Examining Sex-Differentiated Genetic Effects Across Neuropsychiatric and Behavioral Traits. Biological Psychiatry, 2021, 89, 1127-1137.	1.3	48
3	Systematic evaluation of transcriptomics-based deconvolution methods and references using thousands of clinical samples. Briefings in Bioinformatics, 2021, 22, .	6.5	10
4	5-Hydroxymethylcytosine Profiles in Circulating Cell-Free DNA Associate with Disease Burden in Children with Neuroblastoma. Clinical Cancer Research, 2020, 26, 1309-1317.	7.0	22
5	Pharmacogenomic genotypes define genetic ancestry in patients and enable population-specific genomic implementation. Pharmacogenomics Journal, 2020, 20, 126-135.	2.0	14
6	Association of CNVs with methylation variation. Npj Genomic Medicine, 2020, 5, 41.	3.8	17
7	Determinants of telomere length across human tissues. Science, 2020, 369, .	12.6	257
8	Cell typeâ€“specific genetic regulation of gene expression across human tissues. Science, 2020, 369, .	12.6	210
9	The impact of sex on gene expression across human tissues. Science, 2020, 369, .	12.6	329
10	Integration of genomics and transcriptomics predicts diabetic retinopathy susceptibility genes. ELife, 2020, 9, .	6.0	18
11	The new science of sex differences in neuropsychiatric traits. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 333-334.	1.7	2
12	ImmGen report: sexual dimorphism in the immune system transcriptome. Nature Communications, 2019, 10, 4295.	12.8	155
13	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.	3.0	14
14	Polygenic Adaptation Underlies Evolution of Brain Structures and Behavioral Traits. European Neuropsychopharmacology, 2019, 29, S755-S756.	0.7	1
15	The role of sex in the genomics ofÂhuman complex traits. Nature Reviews Genetics, 2019, 20, 173-190.	16.3	203
16	Sex differences in the genetic architecture of obsessiveâ€“compulsive disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 351-364.	1.7	41
17	Sex differences in gene expression in response to ischemia in the human left ventricular myocardium. Human Molecular Genetics, 2019, 28, 1682-1693.	2.9	26
18	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.	5.5	66

#	Article	IF	Citations
19	Large-Scale trans -eQTLs Affect Hundreds of Transcripts and Mediate Patterns of Transcriptional Co-regulation. American Journal of Human Genetics, 2017, 100, 581-591.	6.2	86
20	Bedside Back to Bench: Building Bridges between Basic and Clinical Genomic Research. Cell, 2017, 169, 6-12.	28.9	103
21	Genetic architecture of age-related cognitive decline in African Americans. Neurology: Genetics, 2017, 3, e125.	1.9	22
22	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.	2.8	59
23	Enhancing GTEx by bridging the gaps between genotype, gene expression, and disease. Nature Genetics, 2017, 49, 1664-1670.	21.4	179
24	Evaluation of Genetic Predisposition for MYCN-Amplified Neuroblastoma. Journal of the National Cancer Institute, 2017, 109, .	6.3	20
25	Assocplots: a Python package for static and interactive visualization of multiple-group GWAS results. Bioinformatics, 2017, 33, 432-434.	4.1	19
26	Imputing Gene Expression in Uncollected Tissues Within and Beyond GTEx. American Journal of Human Genetics, 2016, 98, 697-708.	6.2	51
27	Integrative genomics reveals hypoxia inducible genes that are associated with a poor prognosis in neuroblastoma patients. Oncotarget, 2016, 7, 76816-76826.	1.8	33
28	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.	6.2	122
29	Design and Implementation of the International Genetics and Translational Research in Transplantation Network. Transplantation, 2015, 99, 2401-2412.	1.0	60
30	Expression Quantitative Trait Loci Information Improves Predictive Modeling of Disease Relevance of Non-Coding Genetic Variation. PLoS ONE, 2015, 10, e0140758.	2.5	17
31	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.	7.1	185
32	Accurate and Fast Multiple-Testing Correction in eQTL Studies. American Journal of Human Genetics, 2015, 96, 857-868.	6.2	25
33	The impact of human copy number variation on gene expression: Figure 1. Briefings in Functional Genomics, 2015, 14, 352-357.	2.7	108
34	ImmVar project: Insights and design considerations for future studies of â€œhealthyâ€•immune variation. Seminars in Immunology, 2015, 27, 51-57.	5.6	53
35	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	12.8	533
36	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.	3.5	46

#	Article	IF	Citations
37	Interindividual variation in human T regulatory cells. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E1111-20.	7.1	112
38	Common Genetic Variants Modulate Pathogen-Sensing Responses in Human Dendritic Cells. Science, 2014, 343, 1246980.	12.6	391
39	Genetics of rheumatoid arthritis contributes to biology and drug discovery. Nature, 2014, 506, 376-381.	27.8	1,974
40	CD33: increased inclusion of exon 2 implicates the Ig V-set domain in Alzheimer's disease susceptibility. Human Molecular Genetics, 2014, 23, 2729-2736.	2.9	128
41	O3-04-05: EXPRESSION QTL ANALYSIS FROM PRIMARY IMMUNE CELLS IDENTIFIES NOVEL REGULATORY EFFECTS UNDERLYING ALZHEIMER'S DISEASE SUSCEPTIBILITY. , 2014, 10, P216-P216.		0
42	Intersection of population variation and autoimmunity genetics in human T cell activation. Science, 2014, 345, 1254665.	12.6	218
43	Genomics of alternative splicing: evolution, development and pathophysiology. Human Genetics, 2014, 133, 679-687.	3.8	103
44	Polarization of the Effects of Autoimmune and Neurodegenerative Risk Alleles in Leukocytes. Science, 2014, 344, 519-523.	12.6	480
45	Expression QTL-based analyses reveal candidate causal genes and loci across five tumor types. Human Molecular Genetics, 2014, 23, 5294-5302.	2.9	71
46	Chromatin marks identify critical cell types for fine mapping complex trait variants. Nature Genetics, 2013, 45, 124-130.	21.4	553
47	Integrative eQTL-Based Analyses Reveal the Biology of Breast Cancer Risk Loci. Cell, 2013, 152, 633-641.	28.9	300
48	Genetics of human gene expression. Current Opinion in Genetics and Development, 2013, 23, 627-634.	3.3	25
49	Common Risk Alleles for Inflammatory Diseases Are Targets of Recent Positive Selection. American Journal of Human Genetics, 2013, 92, 517-529.	6.2	100
50	Fine-Mapping the Genetic Association of the Major Histocompatibility Complex in Multiple Sclerosis: HLA and Non-HLA Effects. PLoS Genetics, 2013, 9, e1003926.	3.5	250
51	Balancing Selection on a Regulatory Region Exhibiting Ancient Variation That Predates Humanâ€“Neandertal Divergence. PLoS Genetics, 2013, 9, e1003404.	3.5	26
52	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.	3.5	146
53	Analysis of caseâ€“control association studies with known risk variants. Bioinformatics, 2012, 28, 1729-1737.	4.1	36
54	Patterns of Cis Regulatory Variation in Diverse Human Populations. PLoS Genetics, 2012, 8, e1002639.	3.5	439

#	Article	IF	Citations
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, 529-534.	7.1	102
56	Sex-biased genetic effects on gene regulation in humans. Genome Research, 2012, 22, 2368-2375.	5.5	92
57	Systems and genome-wide approaches unite to provide a route to personalized medicine. Genome Medicine, 2012, 4, 29.	8.2	1
58	Coordinating GWAS results with gene expression in a systems immunologic paradigm in autoimmunity. Current Opinion in Immunology, 2012, 24, 544-551.	5.5	14
59	Alzheimer Disease Susceptibility Loci: Evidence for a Protein Network under Natural Selection. American Journal of Human Genetics, 2012, 90, 720-726.	6.2	71
60	Progress and Promise of Genome-Wide Association Studies for Human Complex Trait Genetics. Genetics, 2011, 187, 367-383.	2.9	486
61	IL12A, MPHOSPH9/CDK2AP1 and RGS1 are novel multiple sclerosis susceptibility loci. Genes and Immunity, 2010, 11, 397-405.	4.1	70
62	Independent and population-specific association of risk variants at the IRGM locus with Crohn's disease. Human Molecular Genetics, 2010, 19, 1828-1839.	2.9	93
63	Candidate Causal Regulatory Effects by Integration of Expression QTLs with Complex Trait Genetic Associations. PLoS Genetics, 2010, 6, e1000895.	3.5	434
64	Genevar: a database and Java application for the analysis and visualization of SNP-gene associations in eQTL studies. Bioinformatics, 2010, 26, 2474-2476.	4.1	282
65	Common Regulatory Variation Impacts Gene Expression in a Cell Typeâ€“Dependent Manner. Science, 2009, 325, 1246-1250.	12.6	694
66	Gene Expression Levels Are a Target of Recent Natural Selection in the Human Genome. Molecular Biology and Evolution, 2008, 26, 649-658.	8.9	96
67	Large-Scale Population Study of Human Cell Lines Indicates that Dosage Compensation Is Virtually Complete. PLoS Genetics, 2008, 4, e9.	3.5	127
68	Modifier Effects between Regulatory and Protein-Coding Variation. PLoS Genetics, 2008, 4, e1000244.	3.5	33
69	Breaking the waves: improved detection of copy number variation from microarray-based comparative genomic hybridization. Genome Biology, 2007, 8, R228.	9.6	120
70	Fast-evolving noncoding sequences in the human genome. Genome Biology, 2007, 8, R118.	9.6	163
71	Relative Impact of Nucleotide and Copy Number Variation on Gene Expression Phenotypes. Science, 2007, 315, 848-853.	12.6	1,546
72	Population genomics of human gene expression. Nature Genetics, 2007, 39, 1217-1224.	21.4	1,072

#	Article	IF	Citations
73	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
74	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	27.8	1,788
75	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	27.8	4,137
76	Functional variation and evolution of non-coding DNA. Current Opinion in Genetics and Development, 2006, 16, 559-564.	3.3	48
77	From DNA to RNA to disease and back: The 'central dogma' of regulatory disease variation. Human Genomics, 2006, 2, 383.	2.9	21
78	Genetic variation in human gene expression. Mammalian Genome, 2006, 17, 503-508.	2.2	40
79	The genetics of regulatory variation in the human genome. Human Genomics, 2005, 2, 126.	2.9	21
80	Genome-Wide Associations of Gene Expression Variation in Humans. PLoS Genetics, 2005, 1, e78.	3.5	467
81	Multilocus Analysis of Variation and Speciation in the Closely Related Species Arabidopsis halleri and A. lyrata. Genetics, 2004, 166, 373-388.	2.9	124
82	Nucleotide variation at the myrosinase-encoding locus, TGG1, and quantitative myrosinase enzyme activity variation in Arabidopsis thaliana. Molecular Ecology, 2004, 14, 295-309.	3.9	10
83	Primers for 22 candidate genes for ecological adaptations in Brassicaceae. Molecular Ecology Notes, 2002, 2, 258-262.	1.7	48