

# 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	The Evolutionary History of Common Genetic Variants Influencing Human Cortical Surface Area. <i>Cerebral Cortex</i> , 2021, 31, 1873-1887.	1.6	21
2	Examining Sex-Differentiated Genetic Effects Across Neuropsychiatric and Behavioral Traits. <i>Biological Psychiatry</i> , 2021, 89, 1127-1137.	0.7	48
3	Systematic evaluation of transcriptomics-based deconvolution methods and references using thousands of clinical samples. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	10
4	5-Hydroxymethylcytosine Profiles in Circulating Cell-Free DNA Associate with Disease Burden in Children with Neuroblastoma. <i>Clinical Cancer Research</i> , 2020, 26, 1309-1317.	3.2	22
5	Pharmacogenomic genotypes define genetic ancestry in patients and enable population-specific genomic implementation. <i>Pharmacogenomics Journal</i> , 2020, 20, 126-135.	0.9	14
6	Association of CNVs with methylation variation. <i>Npj Genomic Medicine</i> , 2020, 5, 41.	1.7	17
7	Determinants of telomere length across human tissues. <i>Science</i> , 2020, 369, .	6.0	257
8	Cell type-specific genetic regulation of gene expression across human tissues. <i>Science</i> , 2020, 369, .	6.0	210
9	The impact of sex on gene expression across human tissues. <i>Science</i> , 2020, 369, .	6.0	329
10	Integration of genomics and transcriptomics predicts diabetic retinopathy susceptibility genes. <i>ELife</i> , 2020, 9, .	2.8	18
11	The new science of sex differences in neuropsychiatric traits. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019, 180, 333-334.	1.1	2
12	ImmGen report: sexual dimorphism in the immune system transcriptome. <i>Nature Communications</i> , 2019, 10, 4295.	5.8	155
13	5-Hydroxymethylcytosine Profiles Are Prognostic of Outcome in Neuroblastoma and Reveal Transcriptional Networks That Correlate With Tumor Phenotype. <i>JCO Precision Oncology</i> , 2019, 3, 1-12.	1.5	14
14	Polygenic Adaptation Underlies Evolution of Brain Structures and Behavioral Traits. <i>European Neuropsychopharmacology</i> , 2019, 29, S755-S756.	0.3	1
15	The role of sex in the genomics of human complex traits. <i>Nature Reviews Genetics</i> , 2019, 20, 173-190.	7.7	203
16	Sex differences in the genetic architecture of obsessive-compulsive disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019, 180, 351-364.	1.1	41
17	Sex differences in gene expression in response to ischemia in the human left ventricular myocardium. <i>Human Molecular Genetics</i> , 2019, 28, 1682-1693.	1.4	26
18	Genetic analysis of isoform usage in the human anti-viral response reveals influenza-specific regulation of <i>ERAP2</i> transcripts under balancing selection. <i>Genome Research</i> , 2018, 28, 1812-1825.	2.4	66

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19	Large-Scale trans-eQTLs Affect Hundreds of Transcripts and Mediate Patterns of Transcriptional Co-regulation. <i>American Journal of Human Genetics</i> , 2017, 100, 581-591.	2.6	86
20	Bedside Back to Bench: Building Bridges between Basic and Clinical Genomic Research. <i>Cell</i> , 2017, 169, 6-12.	13.5	103
21	Genetic architecture of age-related cognitive decline in African Americans. <i>Neurology: Genetics</i> , 2017, 3, e125.	0.9	22
22	Neuroblastoma survivors are at increased risk for second malignancies: A report from the International Neuroblastoma Risk Group Project. <i>European Journal of Cancer</i> , 2017, 72, 177-185.	1.3	59
23	Enhancing GTEx by bridging the gaps between genotype, gene expression, and disease. <i>Nature Genetics</i> , 2017, 49, 1664-1670.	9.4	179
24	Evaluation of Genetic Predisposition for MYCN-Amplified Neuroblastoma. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	3.0	20
25	Assocplots: a Python package for static and interactive visualization of multiple-group GWAS results. <i>Bioinformatics</i> , 2017, 33, 432-434.	1.8	19
26	Imputing Gene Expression in Uncollected Tissues Within and Beyond GTEx. <i>American Journal of Human Genetics</i> , 2016, 98, 697-708.	2.6	51
27	Integrative genomics reveals hypoxia inducible genes that are associated with a poor prognosis in neuroblastoma patients. <i>Oncotarget</i> , 2016, 7, 76816-76826.	0.8	33
28	Disentangling the Effects of Colocalizing Genomic Annotations to Functionally Prioritize Non-coding Variants within Complex-Trait Loci. <i>American Journal of Human Genetics</i> , 2015, 97, 139-152.	2.6	122
29	Design and Implementation of the International Genetics and Translational Research in Transplantation Network. <i>Transplantation</i> , 2015, 99, 2401-2412.	0.5	60
30	Expression Quantitative Trait Loci Information Improves Predictive Modeling of Disease Relevance of Non-Coding Genetic Variation. <i>PLoS ONE</i> , 2015, 10, e0140758.	1.1	17
31	Human HLA-G+ extravillous trophoblasts: Immune-activating cells that interact with decidual leukocytes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 7219-7224.	3.3	185
32	Accurate and Fast Multiple-Testing Correction in eQTL Studies. <i>American Journal of Human Genetics</i> , 2015, 96, 857-868.	2.6	25
33	The impact of human copy number variation on gene expression: Figure 1. <i>Briefings in Functional Genomics</i> , 2015, 14, 352-357.	1.3	108
34	ImmVar project: Insights and design considerations for future studies of "healthy" immune variation. <i>Seminars in Immunology</i> , 2015, 27, 51-57.	2.7	53
35	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015, 6, 8570.	5.8	533
36	Regulation of Gene Expression in Autoimmune Disease Loci and the Genetic Basis of Proliferation in CD4+ Effector Memory T Cells. <i>PLoS Genetics</i> , 2014, 10, e1004404.	1.5	46

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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.	3.3	112
38	Common Genetic Variants Modulate Pathogen-Sensing Responses in Human Dendritic Cells. Science, 2014, 343, 1246980.	6.0	391
39	Genetics of rheumatoid arthritis contributes to biology and drug discovery. Nature, 2014, 506, 376-381.	13.7	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.	1.4	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.	6.0	218
43	Genomics of alternative splicing: evolution, development and pathophysiology. Human Genetics, 2014, 133, 679-687.	1.8	103
44	Polarization of the Effects of Autoimmune and Neurodegenerative Risk Alleles in Leukocytes. Science, 2014, 344, 519-523.	6.0	480
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	Chromatin marks identify critical cell types for fine mapping complex trait variants. Nature Genetics, 2013, 45, 124-130.	9.4	553
47	Integrative eQTL-Based Analyses Reveal the Biology of Breast Cancer Risk Loci. Cell, 2013, 152, 633-641.	13.5	300
48	Genetics of human gene expression. Current Opinion in Genetics and Development, 2013, 23, 627-634.	1.5	25
49	Common Risk Alleles for Inflammatory Diseases Are Targets of Recent Positive Selection. American Journal of Human Genetics, 2013, 92, 517-529.	2.6	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.	1.5	250
51	Balancing Selection on a Regulatory Region Exhibiting Ancient Variation That Predates Humanâ€œNeandertal Divergence. PLoS Genetics, 2013, 9, e1003404.	1.5	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.	1.5	146
53	Analysis of caseâ€œcontrol association studies with known risk variants. Bioinformatics, 2012, 28, 1729-1737.	1.8	36
54	Patterns of Cis Regulatory Variation in Diverse Human Populations. PLoS Genetics, 2012, 8, e1002639.	1.5	439

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55	Extensive genetic diversity and substructuring among zebrafish strains revealed through copy number variant analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 529-534.	3.3	102
56	Sex-biased genetic effects on gene regulation in humans. <i>Genome Research</i> , 2012, 22, 2368-2375.	2.4	92
57	Systems and genome-wide approaches unite to provide a route to personalized medicine. <i>Genome Medicine</i> , 2012, 4, 29.	3.6	1
58	Coordinating GWAS results with gene expression in a systems immunologic paradigm in autoimmunity. <i>Current Opinion in Immunology</i> , 2012, 24, 544-551.	2.4	14
59	Alzheimer Disease Susceptibility Loci: Evidence for a Protein Network under Natural Selection. <i>American Journal of Human Genetics</i> , 2012, 90, 720-726.	2.6	71
60	Progress and Promise of Genome-Wide Association Studies for Human Complex Trait Genetics. <i>Genetics</i> , 2011, 187, 367-383.	1.2	486
61	IL12A, MPHOSP9/CDK2AP1 and RGS1 are novel multiple sclerosis susceptibility loci. <i>Genes and Immunity</i> , 2010, 11, 397-405.	2.2	70
62	Independent and population-specific association of risk variants at the IRGM locus with Crohn's disease. <i>Human Molecular Genetics</i> , 2010, 19, 1828-1839.	1.4	93
63	Candidate Causal Regulatory Effects by Integration of Expression QTLs with Complex Trait Genetic Associations. <i>PLoS Genetics</i> , 2010, 6, e1000895.	1.5	434
64	Genevar: a database and Java application for the analysis and visualization of SNP-gene associations in eQTL studies. <i>Bioinformatics</i> , 2010, 26, 2474-2476.	1.8	282
65	Common Regulatory Variation Impacts Gene Expression in a Cell Type-Dependent Manner. <i>Science</i> , 2009, 325, 1246-1250.	6.0	694
66	Gene Expression Levels Are a Target of Recent Natural Selection in the Human Genome. <i>Molecular Biology and Evolution</i> , 2008, 26, 649-658.	3.5	96
67	Large-Scale Population Study of Human Cell Lines Indicates that Dosage Compensation Is Virtually Complete. <i>PLoS Genetics</i> , 2008, 4, e9.	1.5	127
68	Modifier Effects between Regulatory and Protein-Coding Variation. <i>PLoS Genetics</i> , 2008, 4, e1000244.	1.5	33
69	Breaking the waves: improved detection of copy number variation from microarray-based comparative genomic hybridization. <i>Genome Biology</i> , 2007, 8, R228.	13.9	120
70	Fast-evolving noncoding sequences in the human genome. <i>Genome Biology</i> , 2007, 8, R118.	13.9	163
71	Relative Impact of Nucleotide and Copy Number Variation on Gene Expression Phenotypes. <i>Science</i> , 2007, 315, 848-853.	6.0	1,546
72	Population genomics of human gene expression. <i>Nature Genetics</i> , 2007, 39, 1217-1224.	9.4	1,072

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73	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	13.7	4,709
74	Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , 2007, 449, 913-918.	13.7	1,788
75	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , 2007, 449, 851-861.	13.7	4,137
76	Functional variation and evolution of non-coding DNA. <i>Current Opinion in Genetics and Development</i> , 2006, 16, 559-564.	1.5	48
77	From DNA to RNA to disease and back: The 'central dogma' of regulatory disease variation. <i>Human Genomics</i> , 2006, 2, 383.	1.4	21
78	Genetic variation in human gene expression. <i>Mammalian Genome</i> , 2006, 17, 503-508.	1.0	40
79	The genetics of regulatory variation in the human genome. <i>Human Genomics</i> , 2005, 2, 126.	1.4	21
80	Genome-Wide Associations of Gene Expression Variation in Humans. <i>PLoS Genetics</i> , 2005, 1, e78.	1.5	467
81	Multilocus Analysis of Variation and Speciation in the Closely Related Species <i>Arabidopsis halleri</i> and <i>A. lyrata</i> . <i>Genetics</i> , 2004, 166, 373-388.	1.2	124
82	Nucleotide variation at the myrosinase-encoding locus, TGG1, and quantitative myrosinase enzyme activity variation in <i>Arabidopsis thaliana</i> . <i>Molecular Ecology</i> , 2004, 14, 295-309.	2.0	10
83	Primers for 22 candidate genes for ecological adaptations in Brassicaceae. <i>Molecular Ecology Notes</i> , 2002, 2, 258-262.	1.7	48