Chun Li

List of Publications by Year in descending order

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104	6,924	50276	62596
papers	citations	46 h-index	80 g-index

105	105	105	11528
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic Determinants of Response to Warfarin during Initial Anticoagulation. New England Journal of Medicine, 2008, 358, 999-1008.	27.0	516
2	Genome-wide association study identifies a new breast cancer susceptibility locus at 6q25.1. Nature Genetics, 2009, 41, 324-328.	21.4	481
3	Allelic Heterogeneity at the Serotonin Transporter Locus (SLC6A4) Confers Susceptibility to Autism and Rigid-Compulsive Behaviors. American Journal of Human Genetics, 2005, 77, 265-279.	6.2	378
4	Meta-analysis identifies common variants associated with body mass index in east Asians. Nature Genetics, 2012, 44, 307-311.	21.4	372
5	Genetic Variation Near the Hepatocyte Nuclear Factor-4Î± Gene Predicts Susceptibility to Type 2 Diabetes. Diabetes, 2004, 53, 1141-1149.	0.6	255
6	Large-scale genetic study in East Asians identifies six new loci associated with colorectal cancer risk. Nature Genetics, 2014, 46, 533-542.	21.4	212
7	Identification of New Genetic Risk Variants for Type 2 Diabetes. PLoS Genetics, 2010, 6, e1001127.	3.5	193
8	The Finlandâ€“United States Investigation of Nonâ€“Insulinâ€Dependent Diabetes Mellitus Genetics (FUSION) Study. I. An Autosomal Genome Scan for Genes That Predispose to Type 2 Diabetes. American Journal of Human Genetics, 2000, 67, 1174-1185.	6.2	186
9	Genetic evidence implicating multiple genes in the MET receptor tyrosine kinase pathway in autism spectrum disorder. Autism Research, 2008, 1, 159-168.	3.8	143
10	A Common Deletion in the APOBEC3 Genes and Breast Cancer Risk. Journal of the National Cancer Institute, 2013, 105, 573-579.	6.3	141
11	Genome-Wide Association Study in East Asians Identifies Novel Susceptibility Loci for Breast Cancer. PLoS Genetics, 2012, 8, e1002532.	3.5	137
12	Genome-wide association analysis in East Asians identifies breast cancer susceptibility loci at 1q32.1, 5q14.3 and 15q26.1. Nature Genetics, 2014, 46, 886-890.	21.4	135
13	Genome-wide and Ordered-Subset linkage analyses provide support for autism loci on 17q and 19p with evidence of phenotypic and interlocus genetic correlates. BMC Medical Genetics, 2005, 6, 1.	2.1	130
14	Exome sequencing generates high quality data in non-target regions. BMC Genomics, 2012, 13, 194.	2.8	130
15	Recurrent Tissue-Specific mtDNA Mutations Are Common in Humans. PLoS Genetics, 2013, 9, e1003929.	3.5	130
16	Modeling continuous response variables using ordinal regression. Statistics in Medicine, 2017, 36, 4316-4335.	1.6	128
17	The Finlandâ€“United States Investigation of Nonâ€“Insulin-Dependent Diabetes Mellitus Genetics (FUSION) Study. II. An Autosomal Genome Scan for Diabetes-Related Quantitative-Trait Loci. American Journal of Human Genetics, 2000, 67, 1186-1200.	6.2	121
18	Identification of a Functional Genetic Variant at 16q12.1 for Breast Cancer Risk: Results from the Asia Breast Cancer Consortium. PLoS Genetics, 2010, 6, e1001002.	3.5	107

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19	Evaluation of coverage variation of SNP chips for genome-wide association studies. European Journal of Human Genetics, 2008, 16, 635-643.	2.8	106
20	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
21	DCGL: an R package for identifying differentially coexpressed genes and links from gene expression microarray data. Bioinformatics, 2010, 26, 2637-2638.	4.1	98
22	Evaluation of Breast Cancer Susceptibility Loci in Chinese Women. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2357-2365.	2.5	92
23	Genome-wide association study identifies breast cancer risk variant at 10q21.2: results from the Asia Breast Cancer Consortium. Human Molecular Genetics, 2011, 20, 4991-4999.	2.9	92
24	Genetic and Clinical Predictors for Breast Cancer Risk Assessment and Stratification Among Chinese Women. Journal of the National Cancer Institute, 2010, 102, 972-981.	6.3	90
25	Common genetic determinants of breast-cancer risk in East Asian women: a collaborative study of 23 637 breast cancer cases and 25 579 controls. Human Molecular Genetics, 2013, 22, 2539-2550.	2.9	86
26	Link-based quantitative methods to identify differentially coexpressed genes and gene Pairs. BMC Bioinformatics, 2011, 12, 315.	2.6	82
27	Underestimation of Soft Tissue Entrapment by Computed Tomography in Orbital Floor Fractures in the Pediatric Population. Ophthalmology, 2008, 115, 1620-1625.	5.2	81
28	Relative contribution of CYP2C9 and VKORC1 genotypes and early INR response to the prediction of warfarin sensitivity during initiation of therapy. Blood, 2009, 113, 3925-3930.	1.4	79
29	GWAsimulator: a rapid whole-genome simulation program. Bioinformatics, 2008, 24, 140-142.	4.1	77
30	A Large Set of Finnish Affected Sibling Pair Families With Type 2 Diabetes Suggests Susceptibility Loci on Chromosomes 6, 11, and 14. Diabetes, 2004, 53, 821-829.	0.6	73
31	Evaluation of 11 Breast Cancer Susceptibility Loci in African-American Women. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 2761-2764.	2.5	73
32	The Finlandâ€“United States Investigation of Nonâ€“Insulin-Dependent Diabetes Mellitus Genetics (FUSION) Study. I. An Autosomal Genome Scan for Genes That Predispose to Type 2 Diabetes. American Journal of Human Genetics, 2000, 67, 1174-1185.	6.2	71
33	Replication and Functional Genomic Analyses of the Breast Cancer Susceptibility Locus at 6q25.1 Generalize Its Importance in Women of Chinese, Japanese, and European Ancestry. Cancer Research, 2011, 71, 1344-1355.	0.9	71
34	Genetic Association Analysis Using Data from Triads and Unrelated Subjects. American Journal of Human Genetics, 2005, 76, 592-608.	6.2	69
35	Increased prevalence of EPAS1 variant in cattle with high-altitude pulmonary hypertension. Nature Communications, 2015, 6, 6863.	12.8	69
36	Inter-individual variability in structural brain development from late childhood to young adulthood. NeuroImage, 2021, 242, 118450.	4.2	64

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37	Novel Genetic Markers of Breast Cancer Survival Identified by a Genome-Wide Association Study. Cancer Research, 2012, 72, 1182-1189.	0.9	62
38	Adjustment for local ancestry in genetic association analysis of admixed populations. Bioinformatics, 2011, 27, 670-677.	4.1	59
39	Covariate-adjusted Spearman's Rank Correlation with Probability-scale Residuals. Biometrics, 2018, 74, 595-605.	1.4	59
40	Assessing Whether an Allele Can Account in Part for a Linkage Signal: The Genotype-IBD Sharing Test (GIST). American Journal of Human Genetics, 2004, 74, 418-431.	6.2	58
41	Longitudinal follow-up of hypermetropic children identified during preschool vision screening. Journal of AAPOS, 2010, 14, 211-215.	0.3	57
42	Genetics of serum concentration of IL-6 and TNFÎ± in systemic lupus erythematosus and rheumatoid arthritis: a candidate gene analysis. Clinical Rheumatology, 2015, 34, 1375-1382.	2.2	56
43	Assessing departure from Hardyâ€Weinberg equilibrium in the presence of disease association. Genetic Epidemiology, 2008, 32, 589-599.	1.3	53
44	Racial disparity in amniotic fluid concentrations of tumor necrosis factor (TNF)-Î± and soluble TNF receptors in spontaneous preterm birth. American Journal of Obstetrics and Gynecology, 2008, 198, 533.e1-533.e10.	1.3	50
45	Genotype and risk of major bleeding during warfarin treatment. Pharmacogenomics, 2014, 15, 1973-1983.	1.3	50
46	The age-dependent effect of anisometropia magnitude on anisometropic amblyopia severity. Journal of AAPOS, 2008, 12, 150-156.	0.3	48
47	Beta-1-adrenoceptor genetic variants and ethnicity independently affect response to beta-blockade. Pharmacogenetics and Genomics, 2008, 18, 895-902.	1.5	48
48	Morphometric Changes in the Rat Optic Nerve Following Short-term Intermittent Elevations in Intraocular Pressure. , 2010, 51, 6431.		47
49	ATOM: a powerful gene-based association test by combining optimally weighted markers. Bioinformatics, 2009, 25, 497-503.	4.1	45
50	Plasma Biomarkers of Oxidative Stress and Genetic Variants in Age-Related Macular Degeneration. American Journal of Ophthalmology, 2012, 153, 460-467.e1.	3.3	41
51	Common MMP-7 Polymorphisms and Breast Cancer Susceptibility: A Multistage Study of Association and Functionality. Cancer Research, 2008, 68, 6453-6459.	0.9	39
52	Prioritized Subset Analysis: Improving Power in Genome-wide Association Studies. Human Heredity, 2008, 65, 129-141.	0.8	39
53	Genetic polymorphisms in the MMPâ€7 gene and breast cancer survival. International Journal of Cancer, 2009, 124, 208-214.	5.1	39
54	Genetic polymorphisms in the IGFBP3 gene: association with breast cancer risk and blood IGFBP-3 protein levels among Chinese women. Cancer Epidemiology Biomarkers and Prevention, 2004, 13, 1290-5.	2.5	31

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55	A new residual for ordinal outcomes. Biometrika, 2012, 99, 473-480.	2.4	30
56	Variations in the Î±2A-adrenergic receptor gene and their functional effects. Clinical Pharmacology and Therapeutics, 2006, 79, 173-185.	4.7	28
57	Genetic Variations in the Î± _{2A} -Adrenoreceptor Are Associated With Blood Pressure Response to the Agonist Dexmedetomidine. Circulation: Cardiovascular Genetics, 2011, 4, 179-187.	5.1	27
58	Tgif1 Regulates Quiescence and Self-Renewal of Hematopoietic Stem Cells. Molecular and Cellular Biology, 2013, 33, 4824-4833.	2.3	26
59	Genetic variation in the presynaptic norepinephrine transporter is associated with blood pressure responses to exercise in healthy humans. Pharmacogenetics and Genomics, 2011, 21, 171-178.	1.5	25
60	Strategy for encoding and comparison of gene expression signatures. Genome Biology, 2007, 8, R133.	8.8	24
61	Rare Coding Variants and Breast Cancer Risk: Evaluation of Susceptibility Loci Identified in Genome-Wide Association Studies. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 622-628.	2.5	24
62	Evaluating cost efficiency of SNP chips in genomeâ€wide association studies. Genetic Epidemiology, 2008, 32, 387-395.	1.3	23
63	Whole-Exome Sequencing Identifies Novel Somatic Mutations in Chinese Breast Cancer Patients. Journal of Molecular and Genetic Medicine: an International Journal of Biomedical Research, 2015, 09, .	0.1	22
64	Genetic Simulation Tools for Postâ€Genome Wide Association Studies of Complex Diseases. Genetic Epidemiology, 2015, 39, 11-19.	1.3	22
65	Haplotype Analyses of CYP19A1 Gene Variants and Breast Cancer Risk: Results from the Shanghai Breast Cancer Study. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 27-32.	2.5	21
66	GRK5 Gln41Leu polymorphism is not associated with sensitivity to Î²₁-adrenergic blockade in humans. Pharmacogenomics, 2009, 10, 1581-1587.	1.3	21
67	Associations of Plasma-Soluble Fas Ligand with Aging and Age-Related Macular Degeneration. , 2008, 49, 1345.		20
68	Effect of the VKORC1 D36Y variant on warfarin dose requirement and pharmacogenetic dose prediction. Thrombosis and Haemostasis, 2012, 108, 781-788.	3.4	20
69	Probabilityâ€scale residuals for continuous, discrete, and censored data. Canadian Journal of Statistics, 2016, 44, 463-479.	0.9	20
70	Joint analyses of multi-tissue Hi-C and eQTL data demonstrate close spatial proximity between eQTLs and their target genes. BMC Genetics, 2019, 20, 43.	2.7	20
71	Estrogen Exposure, Metabolism, and Enzyme Variants in a Model for Breast Cancer Risk Prediction. Cancer Informatics, 2009, 7, CIN.S2262.	1.9	19
72	Gene-based interaction analysis by incorporating external linkage disequilibrium information. European Journal of Human Genetics, 2011, 19, 164-172.	2.8	18

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73	Catecholamine pathway gene variation is associated with norepinephrine and epinephrine concentrations at rest and after exercise. Pharmacogenetics and Genomics, 2012, 22, 254-260.	1.5	18
74	A prevalenceâ€based association test for caseâ€control studies. Genetic Epidemiology, 2008, 32, 600-605.	1.3	16
75	The Short-term Effects of Antioxidant and Zinc Supplements on Oxidative Stress Biomarker Levels in Plasma: A Pilot Investigation. American Journal of Ophthalmology, 2012, 153, 1104-1109.e2.	3.3	16
76	Soft Tissue Metrics in Thyroid Eye Disease: An International Thyroid Eye Disease Society Reliability Study. Ophthalmic Plastic and Reconstructive Surgery, 2018, 34, 544-546.	0.8	16
77	Genomewide association study of tenofovir pharmacokinetics and creatinine clearance in AIDS Clinical Trials Group protocol A5202. Pharmacogenetics and Genomics, 2015, 25, 450-461.	1.5	15
78	Efficacy of Abiraterone and Enzalutamide in Pre- and Postdocetaxel Castration-Resistant Prostate Cancer: A Trial-Level Meta-Analysis. Prostate Cancer, 2017, 2017, 1-8.	0.6	15
79	A haplotype-based framework for group-wise transmission/disequilibrium tests for rare variant association analysis. Bioinformatics, 2015, 31, 1452-1459.	4.1	14
80	Test of Association Between Two Ordinal Variables While Adjusting for Covariates. Journal of the American Statistical Association, 2010, 105, 612-620.	3.1	13
81	Improved Variant Calling Accuracy by Merging Replicates in Whole-Exome Sequencing Studies. BioMed Research International, 2014, 2014, 1-7.	1.9	12
82	A Variant in the Osteoprotegerin Gene Is Associated with Coronary Atherosclerosis in Patients with Rheumatoid Arthritis: Results from a Candidate Gene Study. International Journal of Molecular Sciences, 2015, 16, 3885-3894.	4.1	12
83	Genetic Association Analysis of Drusen Progression. , 2016, 57, 2225.		12
84	Nonparametric estimation of Spearman's rank correlation with bivariate survival data. Biometrics, 2022, 78, 421-434.	1.4	12
85	MetaDiff: differential isoform expression analysis using random-effects meta-regression. BMC Bioinformatics, 2015, 16, 208.	2.6	9
86	Enriching targeted sequencing experiments for rare disease alleles. Bioinformatics, 2011, 27, 2112-2118.	4.1	8
87	Human Somatic Variation: Itâ€™s Not Just for Cancer Anymore. Current Genetic Medicine Reports, 2013, 1, 212-218.	1.9	8
88	Alpha2A adrenergic receptor genetic variation contributes to hyperglycemia after myocardial infarction. International Journal of Cardiology, 2016, 215, 482-486.	1.7	8
89	First-Time Failure Rates of Candidates for Board Certification. JAMA Ophthalmology, 2008, 126, 548.	2.4	7
90	An evaluation of allele frequency estimation accuracy using pooled sequencing data. International Journal of Computational Biology and Drug Design, 2013, 6, 279.	0.3	6

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91	An empirical comparison of two novel transformation models. Statistics in Medicine, 2020, 39, 562-576.	1.6	6
92	Effects of Environment, Genetics and Data Analysis Pitfalls in an Esophageal Cancer Genome-Wide Association Study. PLoS ONE, 2007, 2, e958.	2.5	6
93	Periorbital infections after Dermabond closure of traumatic lacerations in three children. Journal of AAPOS, 2012, 16, 168-172.	0.3	5
94	A novel, noninvasive assay shows that distal airway oxygen tension is low in cystic fibrosis, but not in primary ciliary dyskinesia. Pediatric Pulmonology, 2019, 54, 27-32.	2.0	5
95	The failure rate of candidates for board certification: an educational outcome measure. Transactions of the American Ophthalmological Society, 2006, 104, 129-42.	1.4	5
96	Haplotype association analysis for late onset diseases using nuclear family data. Genetic Epidemiology, 2006, 30, 220-230.	1.3	4
97	ASAP: an environment for automated preprocessing of sequencing data. BMC Research Notes, 2013, 6, 5.	1.4	4
98	USE OF COX-2 INHIBITORS IN PATIENTS WITH RETINAL VENOUS OCCLUSIVE DISEASE. Retina, 2008, 28, 134-137.	1.7	3
99	Leveraging Identity-by-Descent for Accurate Genotype Inference in Family Sequencing Data. PLoS Genetics, 2015, 11, e1005271.	3.5	3
100	Detecting Geneâ€Gene Interaction in Linkage Analysis. Current Protocols in Human Genetics, 2005, 46, Unit 1.15.	3.5	2
101	Frequency of Cystic Fibrosis Transmembrane Conductance Regulator Variants in Individuals Evaluated for Primary Ciliary Dyskinesia. Journal of Pediatrics, 2019, 215, 172-177.e2.	1.8	2
102	A Statistical Reappraisal of the Findings of an Esophageal Cancer Genome-Wide Association Study. Cancer Research, 2008, 68, 3074-3075.	0.9	1
103	Optimized Selection of Unrelated Subjects for Wholeâ€Genome Sequencing Studies of Rare Highâ€Penetrance Alleles. Genetic Epidemiology, 2012, 36, 472-479.	1.3	1
104	Design of DNA Pooling to Allow Incorporation of Covariates in Rare Variants Analysis. PLoS ONE, 2014, 9, e114523.	2.5	1