Chun Li

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6615735/publications.pdf

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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	Nonparametric estimation of Spearman's rank correlation with bivariate survival data. Biometrics, 2022, 78, 421-434.	1.4	12
2	Inter-individual variability in structural brain development from late childhood to young adulthood. NeuroImage, 2021, 242, 118450.	4.2	64
3	An empirical comparison of two novel transformation models. Statistics in Medicine, 2020, 39, 562-576.	1.6	6
4	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
5	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
6	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
7	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
8	Covariate-adjusted Spearman's Rank Correlation with Probability-scale Residuals. Biometrics, 2018, 74, 595-605.	1.4	59
9	Modeling continuous response variables using ordinal regression. Statistics in Medicine, 2017, 36, 4316-4335.	1.6	128
10	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
11	Genetic Association Analysis of Drusen Progression. , 2016, 57, 2225.		12
12	Alpha2A adrenergic receptor genetic variation contributes to hyperglycemia after myocardial infarction. International Journal of Cardiology, 2016, 215, 482-486.	1.7	8
13	Probabilityâ€scale residuals for continuous, discrete, and censored data. Canadian Journal of Statistics, 2016, 44, 463-479.	0.9	20
14	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
15	Leveraging Identity-by-Descent for Accurate Genotype Inference in Family Sequencing Data. PLoS Genetics, 2015, 11, e1005271.	3.5	3
16	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
17	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
18	Increased prevalence of EPAS1 variant in cattle with high-altitude pulmonary hypertension. Nature Communications, 2015, 6, 6863.	12.8	69

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19	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
20	A haplotype-based framework for group-wise transmission/disequilibrium tests for rare variant association analysis. Bioinformatics, 2015, 31, 1452-1459.	4.1	14
21	MetaDiff: differential isoform expression analysis using random-effects meta-regression. BMC Bioinformatics, 2015, 16, 208.	2.6	9
22	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
23	Genetic Simulation Tools for Postâ€Genome Wide Association Studies of Complex Diseases. Genetic Epidemiology, 2015, 39, 11-19.	1.3	22
24	Design of DNA Pooling to Allow Incorporation of Covariates in Rare Variants Analysis. PLoS ONE, 2014, 9, e114523.	2.5	1
25	Genotype and risk of major bleeding during warfarin treatment. Pharmacogenomics, 2014, 15, 1973-1983.	1.3	50
26	Improved Variant Calling Accuracy by Merging Replicates in Whole-Exome Sequencing Studies. BioMed Research International, 2014, 2014, 1-7.	1.9	12
27	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
28	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
29	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
30	Human Somatic Variation: Itâ€™s Not Just for Cancer Anymore. Current Genetic Medicine Reports, 2013, 1, 212-218.	1.9	8
31	Tgif1 Regulates Quiescence and Self-Renewal of Hematopoietic Stem Cells. Molecular and Cellular Biology, 2013, 33, 4824-4833.	2.3	26
32	ASAP: an environment for automated preprocessing of sequencing data. BMC Research Notes, 2013, 6, 5.	1.4	4
33	A Common Deletion in the APOBEC3 Genes and Breast Cancer Risk. Journal of the National Cancer Institute, 2013, 105, 573-579.	6.3	141
34	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
35	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
36	Recurrent Tissue-Specific mtDNA Mutations Are Common in Humans. PLoS Genetics, 2013, 9, e1003929.	3.5	130

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37	Genome-Wide Association Study in East Asians Identifies Novel Susceptibility Loci for Breast Cancer. PLoS Genetics, 2012, 8, e1002532.	3.5	137
38	A new residual for ordinal outcomes. Biometrika, 2012, 99, 473-480.	2.4	30
39	Novel Genetic Markers of Breast Cancer Survival Identified by a Genome-Wide Association Study. Cancer Research, 2012, 72, 1182-1189.	0.9	62
40	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
41	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
42	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
43	Periorbital infections after Dermabond closure of traumatic lacerations in three children. Journal of AAPOS, 2012, 16, 168-172.	0.3	5
44	Exome sequencing generates high quality data in non-target regions. BMC Genomics, 2012, 13, 194.	2.8	130
45	Effect of the VKORC1 D36Y variant on warfarin dose requirement and pharmacogenetic dose prediction. Thrombosis and Haemostasis, 2012, 108, 781-788.	3.4	20
46	Meta-analysis identifies common variants associated with body mass index in east Asians. Nature Genetics, 2012, 44, 307-311.	21.4	372
47	Optimized Selection of Unrelated Subjects for Wholeâ€Genome Sequencing Studies of Rare Highâ€Penetrance Alleles. Genetic Epidemiology, 2012, 36, 472-479.	1.3	1
48	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
49	Gene-based interaction analysis by incorporating external linkage disequilibrium information. European Journal of Human Genetics, 2011, 19, 164-172.	2.8	18
50	Link-based quantitative methods to identify differentially coexpressed genes and gene Pairs. BMC Bioinformatics, 2011, 12, 315.	2.6	82
51	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
52	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
53	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
54	Adjustment for local ancestry in genetic association analysis of admixed populations. Bioinformatics, 2011, 27, 670-677.	4.1	59

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55	Enriching targeted sequencing experiments for rare disease alleles. Bioinformatics, 2011, 27, 2112-2118.	4.1	8
56	Morphometric Changes in the Rat Optic Nerve Following Short-term Intermittent Elevations in Intraocular Pressure. , 2010, 51, 6431.		47
57	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
58	DCGL: an R package for identifying differentially coexpressed genes and links from gene expression microarray data. Bioinformatics, 2010, 26, 2637-2638.	4.1	98
59	Identification of New Genetic Risk Variants for Type 2 Diabetes. PLoS Genetics, 2010, 6, e1001127.	3.5	193
60	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
61	Evaluation of Breast Cancer Susceptibility Loci in Chinese Women. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2357-2365.	2.5	92
62	Longitudinal follow-up of hypermetropic children identified during preschool vision screening. Journal of AAPOS, 2010, 14, 211-215.	0.3	57
63	Test of Association Between Two Ordinal Variables While Adjusting for Covariates. Journal of the American Statistical Association, 2010, 105, 612-620.	3.1	13
64	ATOM: a powerful gene-based association test by combining optimally weighted markers. Bioinformatics, 2009, 25, 497-503.	4.1	45
65	GRK5 Gln41Leu polymorphism is not associated with sensitivity to Î²₁-adrenergic blockade in humans. Pharmacogenomics, 2009, 10, 1581-1587.	1.3	21
66	Genetic polymorphisms in the MMPâ€7 gene and breast cancer survival. International Journal of Cancer, 2009, 124, 208-214.	5.1	39
67	Genome-wide association study identifies a new breast cancer susceptibility locus at 6q25.1. Nature Genetics, 2009, 41, 324-328.	21.4	481
68	Evaluation of 11 Breast Cancer Susceptibility Loci in African-American Women. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 2761-2764.	2.5	73
69	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
70	Estrogen Exposure, Metabolism, and Enzyme Variants in a Model for Breast Cancer Risk Prediction. Cancer Informatics, 2009, 7, CIN.S2262.	1.9	19
71	Evaluating cost efficiency of SNP chips in genomeâ€wide association studies. Genetic Epidemiology, 2008, 32, 387-395.	1.3	23
72	Assessing departure from Hardyâ€Weinberg equilibrium in the presence of disease association. Genetic Epidemiology, 2008, 32, 589-599.	1.3	53

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73	A prevalenceâ€based association test for caseâ€control studies. Genetic Epidemiology, 2008, 32, 600-605.	1.3	16
74	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
75	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
76	Evaluation of coverage variation of SNP chips for genome-wide association studies. European Journal of Human Genetics, 2008, 16, 635-643.	2.8	106
77	The age-dependent effect of anisometropia magnitude on anisometropic amblyopia severity. Journal of AAPOS, 2008, 12, 150-156.	0.3	48
78	Underestimation of Soft Tissue Entrapment by Computed Tomography in Orbital Floor Fractures in the Pediatric Population. Ophthalmology, 2008, 115, 1620-1625.	5.2	81
79	Genetic Determinants of Response to Warfarin during Initial Anticoagulation. New England Journal of Medicine, 2008, 358, 999-1008.	27.0	516
80	Common MMP-7 Polymorphisms and Breast Cancer Susceptibility: A Multistage Study of Association and Functionality. Cancer Research, 2008, 68, 6453-6459.	0.9	39
81	GWAsimulator: a rapid whole-genome simulation program. Bioinformatics, 2008, 24, 140-142.	4.1	77
82	Prioritized Subset Analysis: Improving Power in Genome-wide Association Studies. Human Heredity, 2008, 65, 129-141.	0.8	39
83	A Statistical Reappraisal of the Findings of an Esophageal Cancer Genome-Wide Association Study. Cancer Research, 2008, 68, 3074-3075.	0.9	1
84	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
85	Associations of Plasma-Soluble Fas Ligand with Aging and Age-Related Macular Degeneration. , 2008, 49, 1345.		20
86	USE OF COX-2 INHIBITORS IN PATIENTS WITH RETINAL VENOUS OCCLUSIVE DISEASE. Retina, 2008, 28, 134-137.	1.7	3
87	Beta-1-adrenoceptor genetic variants and ethnicity independently affect response to beta-blockade. Pharmacogenetics and Genomics, 2008, 18, 895-902.	1.5	48
88	First-Time Failure Rates of Candidates for Board Certification. JAMA Ophthalmology, 2008, 126, 548.	2.4	7
89	Strategy for encoding and comparison of gene expression signatures. Genome Biology, 2007, 8, R133.	8.8	24
90	Effects of Environment, Genetics and Data Analysis Pitfalls in an Esophageal Cancer Genome-Wide Association Study. PLoS ONE, 2007, 2, e958.	2.5	6

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91	Variations in the Î±2A-adrenergic receptor gene and their functional effects. Clinical Pharmacology and Therapeutics, 2006, 79, 173-185.	4.7	28
92	Haplotype association analysis for late onset diseases using nuclear family data. Genetic Epidemiology, 2006, 30, 220-230.	1.3	4
93	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
94	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
95	Genetic Association Analysis Using Data from Triads and Unrelated Subjects. American Journal of Human Genetics, 2005, 76, 592-608.	6.2	69
96	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
97	Detecting Geneâ€Gene Interaction in Linkage Analysis. Current Protocols in Human Genetics, 2005, 46, Unit 1.15.	3.5	2
98	Genetic Variation Near the Hepatocyte Nuclear Factor-4Î± Gene Predicts Susceptibility to Type 2 Diabetes. Diabetes, 2004, 53, 1141-1149.	0.6	255
99	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
100	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
101	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
102	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
103	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
104	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