Biao Li

List of Publications by Year in descending order

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18 papers	2,326 citations	687363 13 h-index	839539 18 g-index
19 all docs	19 docs citations	19 times ranked	4853 citing authors

#	Article	IF	Citations
1	Quantitative Acetylomics Revealed Acetylation-Mediated Molecular Pathway Network Changes in Human Nonfunctional Pituitary Neuroendocrine Tumors. Frontiers in Endocrinology, 2021, 12, 753606.	3.5	6
2	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. Human Mutation, 2017, 38, 1266-1276.	2.5	14
3	A Probabilistic Model to Predict Clinical Phenotypic Traits from Genome Sequencing. PLoS Computational Biology, 2014, 10, e1003825.	3.2	10
4	MutPred Splice: machine learning-based prediction of exonic variants that disrupt splicing. Genome Biology, 2014, 15, R19.	9.6	135
5	Global human frequencies of predicted nuclear pathogenic variants and the role played by protein hydrophobicity in pathogenicity potential. Scientific Reports, 2014, 4, 7155.	3.3	8
6	SIRT5 Regulates the Mitochondrial Lysine Succinylome and Metabolic Networks. Cell Metabolism, 2013, 18, 920-933.	16.2	549
7	Calibration of Multiple In Silico Tools for Predicting Pathogenicity of Mismatch Repair Gene Missense Substitutions. Human Mutation, 2013, 34, 255-265.	2.5	80
8	Label-free quantitative proteomics of the lysine acetylome in mitochondria identifies substrates of SIRT3 in metabolic pathways. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6601-6606.	7.1	414
9	Evaluating Purifying Selection in the Mitochondrial DNA of Various Mammalian Species. PLoS ONE, 2013, 8, e58993.	2.5	39
10	Comparing Phylogeny and the Predicted Pathogenicity of Protein Variations Reveals Equal Purifying Selection across the Global Human mtDNA Diversity. American Journal of Human Genetics, 2011, 88, 433-439.	6.2	103
11	In silico prediction of deleterious single amino acid polymorphisms from amino acid sequence. Journal of Computational Chemistry, 2011, 32, 1211-1216.	3.3	4
12	In silico functional profiling of human disease-associated and polymorphic amino acid substitutions. Human Mutation, 2010, 31, 335-346.	2.5	57
13	Automated inference of molecular mechanisms of disease from amino acid substitutions. Bioinformatics, 2009, 25, 2744-2750.	4.1	691
14	A functional intronic variant in the tyrosine hydroxylase (TH) gene confers risk of essential hypertension in the Northern Chinese Han population. Clinical Science, 2008, 115, 151-158.	4.3	15
15	Association Study With 33 Single-Nucleotide Polymorphisms in 11 Candidate Genes for Hypertension in Chinese. Hypertension, 2006, 47, 1147-1154.	2.7	90
16	G Protein Î²3 Subunit Gene Variants and Essential Hypertension in the Northern Chinese Han Population. Annals of Human Genetics, 2005, 69, 468-473.	0.8	23
17	Evolution and migration history of the Chinese population inferred from Chinese Y-chromosome evidence. Journal of Human Genetics, 2004, 49, 339-348.	2.3	74
18	Lipoprotein Lipase Gene Polymorphisms and Blood Pressure Levels in the Northern Chinese Han Population. Hypertension Research, 2004, 27, 373-378.	2.7	14