Chuong B Do

List of Publications by Year
in descending order

21 papers	6,019 citations	331670 21 h-index	677142 22 g-index
23 all docs	23 docs citations	23 times ranked	12050 citing authors

#	Article	IF	Citations
1	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. Nature Genetics, 2014, 46, 989-993.	21.4	1,685
2	ProbCons: Probabilistic consistency-based multiple sequence alignment. Genome Research, 2005, 15, 330-340.	5.5	982
3	Comprehensive Research Synopsis and Systematic Meta-Analyses in Parkinson's Disease Genetics: The PDGene Database. PLoS Genetics, 2012, 8, e1002548.	3.5	495
4	Web-Based Genome-Wide Association Study Identifies Two Novel Loci and a Substantial Genetic Component for Parkinson's Disease. PLoS Genetics, 2011, 7, e1002141.	3.5	461
5	CONTRAfold: RNA secondary structure prediction without physics-based models. Bioinformatics, 2006, 22, e90-e98.	4.1	458
6	What is the expectation maximization algorithm?. Nature Biotechnology, 2008, 26, 897-899.	17.5	443
7	Genome-Wide Analysis Points to Roles for Extracellular Matrix Remodeling, the Visual Cycle, and Neuronal Development in Myopia. PLoS Genetics, 2013, 9, e1003299.	3.5	263
8	Germ line variants predispose to both JAK2 V617F clonal hematopoiesis and myeloproliferative neoplasms. Blood, 2016, 128, 1121-1128.	1.4	200
9	Novel Associations for Hypothyroidism Include Known Autoimmune Risk Loci. PLoS ONE, 2012, 7, e34442.	2.5	128
10	Efficient Replication of over 180 Genetic Associations with Self-Reported Medical Data. PLoS ONE, 2011, 6, e23473.	2.5	117
11	Serum Iron Levels and the Risk of Parkinson Disease: A Mendelian Randomization Study. PLoS Medicine, 2013, 10, e1001462.	8.4	116
12	Comparison of Family History and SNPs for Predicting Risk of Complex Disease. PLoS Genetics, 2012, 8, e1002973.	3.5	102
13	A max-margin model for efficient simultaneous alignment and folding of RNA sequences. Bioinformatics, 2008, 24, i68-i76.	4.1	76
14	A genetic variant near olfactory receptor genes influences cilantro preference. Flavour, 2012, 1, .	2.3	72
15	Genetic variants associated with motion sickness point to roles for inner ear development, neurological processes and glucose homeostasis. Human Molecular Genetics, 2015, 24, 2700-2708.	2.9	70
16	Effect of genetic divergence in identifying ancestral origin using HAPAA. Genome Research, 2008, 18, 676-682.	5.5	66
17	Automatic Parameter Learning for Multiple Local Network Alignment. Journal of Computational Biology, 2009, 16, 1001-1022.	1.6	66
18	Genetic variants associated with breast size also influence breast cancer risk. BMC Medical Genetics, 2012, 13, 53.	2.1	65

#	Article	IF	Citations
19	Protein Multiple Sequence Alignment. Methods in Molecular Biology, 2008, 484, 379-413.	0.9	64
20	Multiple alignment of protein sequences with repeats and rearrangements. Nucleic Acids Research, 2006, 34, 5932-5942.	14.5	40
21	A Germline Variant in the TERT Gene Is a Novel Predisposition Allele Associated with Myeloproliferative Neoplasms. Blood, 2012, 120, 707-707.	1.4	2