

# Chuong B Do

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10588633/publications.pdf>

Version: 2024-02-01

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	Germ line variants predispose to both JAK2 V617F clonal hematopoiesis and myeloproliferative neoplasms. <i>Blood</i> , 2016, 128, 1121-1128.	1.4	200
2	Genetic variants associated with motion sickness point to roles for inner ear development, neurological processes and glucose homeostasis. <i>Human Molecular Genetics</i> , 2015, 24, 2700-2708.	2.9	70
3	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. <i>Nature Genetics</i> , 2014, 46, 989-993.	21.4	1,685
4	Genome-Wide Analysis Points to Roles for Extracellular Matrix Remodeling, the Visual Cycle, and Neuronal Development in Myopia. <i>PLoS Genetics</i> , 2013, 9, e1003299.	3.5	263
5	Serum Iron Levels and the Risk of Parkinson Disease: A Mendelian Randomization Study. <i>PLoS Medicine</i> , 2013, 10, e1001462.	8.4	116
6	Comparison of Family History and SNPs for Predicting Risk of Complex Disease. <i>PLoS Genetics</i> , 2012, 8, e1002973.	3.5	102
7	Comprehensive Research Synopsis and Systematic Meta-Analyses in Parkinson's Disease Genetics: The PDGene Database. <i>PLoS Genetics</i> , 2012, 8, e1002548.	3.5	495
8	Genetic variants associated with breast size also influence breast cancer risk. <i>BMC Medical Genetics</i> , 2012, 13, 53.	2.1	65
9	A genetic variant near olfactory receptor genes influences cilantro preference. <i>Flavour</i> , 2012, 1, .	2.3	72
10	Novel Associations for Hypothyroidism Include Known Autoimmune Risk Loci. <i>PLoS ONE</i> , 2012, 7, e34442.	2.5	128
11	A Germline Variant in the TERT Gene Is a Novel Predisposition Allele Associated with Myeloproliferative Neoplasms. <i>Blood</i> , 2012, 120, 707-707.	1.4	2
12	Efficient Replication of over 180 Genetic Associations with Self-Reported Medical Data. <i>PLoS ONE</i> , 2011, 6, e23473.	2.5	117
13	Web-Based Genome-Wide Association Study Identifies Two Novel Loci and a Substantial Genetic Component for Parkinson's Disease. <i>PLoS Genetics</i> , 2011, 7, e1002141.	3.5	461
14	Automatic Parameter Learning for Multiple Local Network Alignment. <i>Journal of Computational Biology</i> , 2009, 16, 1001-1022.	1.6	66
15	Protein Multiple Sequence Alignment. <i>Methods in Molecular Biology</i> , 2008, 484, 379-413.	0.9	64
16	What is the expectation maximization algorithm?. <i>Nature Biotechnology</i> , 2008, 26, 897-899.	17.5	443
17	Effect of genetic divergence in identifying ancestral origin using HAPAA. <i>Genome Research</i> , 2008, 18, 676-682.	5.5	66
18	A max-margin model for efficient simultaneous alignment and folding of RNA sequences. <i>Bioinformatics</i> , 2008, 24, i68-i76.	4.1	76

#	ARTICLE	IF	CITATIONS
19	Multiple alignment of protein sequences with repeats and rearrangements. <i>Nucleic Acids Research</i> , 2006, 34, 5932-5942.	14.5	40
20	CONTRAFold: RNA secondary structure prediction without physics-based models. <i>Bioinformatics</i> , 2006, 22, e90-e98.	4.1	458
21	ProbCons: Probabilistic consistency-based multiple sequence alignment. <i>Genome Research</i> , 2005, 15, 330-340.	5.5	982