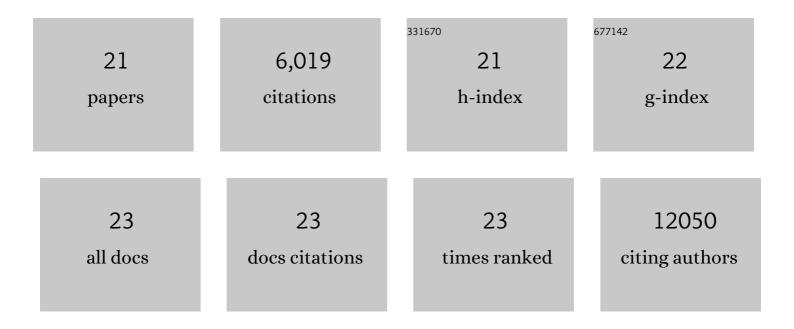
Chuong B Do

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/10588633/publications.pdf Version: 2024-02-01



| # | Article | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Germ line variants predispose to both JAK2 V617F clonal hematopoiesis and myeloproliferative neoplasms. Blood, 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. Human Molecular Genetics, 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. Nature Genetics, 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. PLoS Genetics, 2013, 9, e1003299. | 3.5 | 263 |
| 5 | Serum Iron Levels and the Risk of Parkinson Disease: A Mendelian Randomization Study. PLoS Medicine, 2013, 10, e1001462. | 8.4 | 116 |
| 6 | Comparison of Family History and SNPs for Predicting Risk of Complex Disease. PLoS Genetics, 2012, 8, e1002973. | 3.5 | 102 |
| 7 | Comprehensive Research Synopsis and Systematic Meta-Analyses in Parkinson's Disease Genetics: The PDGene Database. PLoS Genetics, 2012, 8, e1002548. | 3.5 | 495 |
| 8 | Genetic variants associated with breast size also influence breast cancer risk. BMC Medical Genetics, 2012, 13, 53. | 2.1 | 65 |
| 9 | A genetic variant near olfactory receptor genes influences cilantro preference. Flavour, 2012, 1, . | 2.3 | 72 |
| 10 | Novel Associations for Hypothyroidism Include Known Autoimmune Risk Loci. PLoS ONE, 2012, 7, e34442. | 2.5 | 128 |
| 11 | A Germline Variant in the TERT Gene Is a Novel Predisposition Allele Associated with Myeloproliferative Neoplasms. Blood, 2012, 120, 707-707. | 1.4 | 2 |
| 12 | Efficient Replication of over 180 Genetic Associations with Self-Reported Medical Data. PLoS ONE, 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. PLoS Genetics, 2011, 7, e1002141. | 3.5 | 461 |
| 14 | Automatic Parameter Learning for Multiple Local Network Alignment. Journal of Computational Biology, 2009, 16, 1001-1022. | 1.6 | 66 |
| 15 | Protein Multiple Sequence Alignment. Methods in Molecular Biology, 2008, 484, 379-413. | 0.9 | 64 |
| 16 | What is the expectation maximization algorithm?. Nature Biotechnology, 2008, 26, 897-899. | 17.5 | 443 |
| 17 | Effect of genetic divergence in identifying ancestral origin using HAPAA. Genome Research, 2008, 18, 676-682. | 5.5 | 66 |
| 18 | A max-margin model for efficient simultaneous alignment and folding of RNA sequences. Bioinformatics, 2008, 24, i68-i76. | 4.1 | 76 |

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