

# Si Quang Le

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4174485/publications.pdf>

Version: 2024-02-01

19  
papers

11,376  
citations

759233

12  
h-index

940533

16  
g-index

19  
all docs

19  
docs citations

19  
times ranked

25724  
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole genome analysis of a Vietnamese trio. <i>Journal of Biosciences</i> , 2015, 40, 113-124.	1.1	4
2	FastMG: a simple, fast, and accurate maximum likelihood procedure to estimate amino acid replacement rate matrices from large data sets. <i>BMC Bioinformatics</i> , 2014, 15, 341.	2.6	16
3	Reappraisal of known malaria resistance loci in a large multicenter study. <i>Nature Genetics</i> , 2014, 46, 1197-1204.	21.4	206
4	Imputation-Based Meta-Analysis of Severe Malaria in Three African Populations. <i>PLoS Genetics</i> , 2013, 9, e1003509.	3.5	95
5	Modeling Protein Evolution with Several Amino Acid Replacement Matrices Depending on Site Rates. <i>Molecular Biology and Evolution</i> , 2012, 29, 2921-2936.	8.9	201
6	Detecting Bad SNPs from Illumina BeadChips Using Jeffreys Distance. , 2012, , .		0
7	A Maximum Likelihood Method for Detecting Bad Samples from Illumina BeadChips Data. , 2012, , .		0
8	ReplacementMatrix: a web server for maximum-likelihood estimation of amino acid replacement rate matrices. <i>Bioinformatics</i> , 2011, 27, 2758-2760.	4.1	15
9	SNP detection and genotyping from low-coverage sequencing data on multiple diploid samples. <i>Genome Research</i> , 2011, 21, 952-960.	5.5	142
10	FLU, an amino acid substitution model for influenza proteins. <i>BMC Evolutionary Biology</i> , 2010, 10, 99.	3.2	53
11	A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010, 467, 1061-1073.	27.8	7,209
12	Accounting for Solvent Accessibility and Secondary Structure in Protein Phylogenetics Is Clearly Beneficial. <i>Systematic Biology</i> , 2010, 59, 277-287.	5.6	107
13	An Improved General Amino Acid Replacement Matrix. <i>Molecular Biology and Evolution</i> , 2008, 25, 1307-1320.	8.9	2,748
14	Phylogenetic mixture models for proteins. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 3965-3976.	4.0	202
15	Empirical profile mixture models for phylogenetic reconstruction. <i>Bioinformatics</i> , 2008, 24, 2317-2323.	4.1	292
16	Exploiting Temporal Relations in Mining Hepatitis Data. <i>New Generation Computing</i> , 2007, 25, 247-262.	3.3	11
17	Association-Based Dissimilarity Measures for Categorical Data: Limitation and Improvement. <i>Lecture Notes in Computer Science</i> , 2006, , 493-498.	1.3	1
18	An association-based dissimilarity measure for categorical data. <i>Pattern Recognition Letters</i> , 2005, 26, 2549-2557.	4.2	54

#	ARTICLE	IF	CITATIONS
19	Mining hepatitis data with temporal abstraction. , 2003, , .		20