

Vinh S Le

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

6,452
citations

1162889

8
h-index

887953

17
g-index

26
all docs

26
docs citations

26
times ranked

9623
citing authors

#	ARTICLE	IF	CITATIONS
1	nQMaker: Estimating Time Nonreversible Amino Acid Substitution Models. <i>Systematic Biology</i> , 2022, 71, 1110-1123.	2.7	9
2	Exploring the Kinh Vietnamese genomic database for the polymorphisms of the P450 genes towards precision public health. <i>Annals of Human Biology</i> , 2022, 49, 152-155.	0.4	0
3	QMaker: Fast and Accurate Method to Estimate Empirical Models of Protein Evolution. <i>Systematic Biology</i> , 2021, 70, 1046-1060.	2.7	39
4	De novo homozygous variant of the SCN1A gene in a patient with severe Dravet syndrome complicated by acute encephalopathy. <i>Neurogenetics</i> , 2021, 22, 133-136.	0.7	2
5	Response to: A commentary on "A Vietnamese human genetic variation database". <i>Human Mutation</i> , 2020, 41, 1461-1462.	1.1	2
6	mPartition: A Model-Based Method for Partitioning Alignments. <i>Journal of Molecular Evolution</i> , 2020, 88, 641-652.	0.8	3
7	FLAVI: An Amino Acid Substitution Model for Flaviviruses. <i>Journal of Molecular Evolution</i> , 2020, 88, 445-452.	0.8	8
8	A novel de novo variant of LAMA2 contributes to merosin deficient congenital muscular dystrophy type 1A: Case report. <i>Biomedical Reports</i> , 2020, 12, 46-50.	0.9	5
9	pQMaker: empirically estimating amino acid substitution models in a parallel environment. , 2020, , .		1
10	A Vietnamese human genetic variation database. <i>Human Mutation</i> , 2019, 40, 1664-1675.	1.1	36
11	A Hybrid Approach to Optimize the Number of Recombinations in Ancestral Recombination Graphs. , 2019, , .		1
12	UFBoot2: Improving the Ultrafast Bootstrap Approximation. <i>Molecular Biology and Evolution</i> , 2018, 35, 518-522.	3.5	5,798
13	MPBoot: fast phylogenetic maximum parsimony tree inference and bootstrap approximation. <i>BMC Evolutionary Biology</i> , 2018, 18, 11.	3.2	129
14	Genomedics: Whole exome analysis system for clinical studies. , 2017, , .		0
15	Building minimum recombination ancestral recombination graphs for whole genomes. , 2017, , .		0
16	MVRM: A Hybrid Approach to Predict siRNA Efficacy. , 2015, , .		0
17	Whole genome analysis of a Vietnamese trio. <i>Journal of Biosciences</i> , 2015, 40, 113-124.	0.5	4
18	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.	1.2	16

#	ARTICLE	IF	CITATIONS
19	Random Tree-Puzzle Leads to the Yule-Harding Distribution. <i>Molecular Biology and Evolution</i> , 2011, 28, 873-877.	3.5	6
20	A Fast and Efficient Method for Estimating Amino Acid Substitution Models. , 2011, , .		0
21	FLU, an amino acid substitution model for influenza proteins. <i>BMC Evolutionary Biology</i> , 2010, 10, 99.	3.2	53
22	POY version 4: phylogenetic analysis using dynamic homologies. <i>Cladistics</i> , 2010, 26, 72-85.	1.5	186
23	Pairwise alignment with rearrangements. <i>Genome Informatics</i> , 2006, 17, 141-51.	0.4	8
24	IQPNNI: Moving Fast Through Tree Space and Stopping in Time. <i>Molecular Biology and Evolution</i> , 2004, 21, 1565-1571.	3.5	146
25	Response to: A commentary on "A Vietnamese human genetic variation database", 0, , .		0