# Vinh S Le

List of Publications by Year
in descending order



| | | | |
|---|---|---|---|
| 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 | UFBoot2: Improving the Ultrafast Bootstrap Approximation. Molecular Biology and Evolution, 2018, 35, 518-522. | 3.5 | 5,798 |
| 2 | POY version 4: phylogenetic analysis using dynamic homologies. Cladistics, 2010, 26, 72-85. | 1.5 | 186 |
| 3 | IQPNNI: Moving Fast Through Tree Space and Stopping in Time. Molecular Biology and Evolution, 2004, 21, 1565-1571. | 3.5 | 146 |
| 4 | MPBoot: fast phylogenetic maximum parsimony tree inference and bootstrap approximation. BMC Evolutionary Biology, 2018, 18, 11. | 3.2 | 129 |
| 5 | FLU, an amino acid substitution model for influenza proteins. BMC Evolutionary Biology, 2010, 10, 99. | 3.2 | 53 |
| 6 | QMaker: Fast and Accurate Method to Estimate Empirical Models of Protein Evolution. Systematic Biology, 2021, 70, 1046-1060. | 2.7 | 39 |
| 7 | A Vietnamese human genetic variation database. Human Mutation, 2019, 40, 1664-1675. | 1.1 | 36 |
| 8 | FastMG: a simple, fast, and accurate maximum likelihood procedure to estimate amino acid replacement rate matrices from large data sets. BMC Bioinformatics, 2014, 15, 341. | 1.2 | 16 |
| 9 | nQMaker: Estimating Time Nonreversible Amino Acid Substitution Models. Systematic Biology, 2022, 71, 1110-1123. | 2.7 | 9 |
| 10 | FLAVI: An Amino Acid Substitution Model for Flaviviruses. Journal of Molecular Evolution, 2020, 88, 445-452. | 0.8 | 8 |
| 11 | Pairwise alignment with rearrangements. Genome Informatics, 2006, 17, 141-51. | 0.4 | 8 |
| 12 | Random Tree-Puzzle Leads to the Yuleâ€“Harding Distribution. Molecular Biology and Evolution, 2011, 28, 873-877. | 3.5 | 6 |
| 13 | A novel deï¿½novo variant of LAMA2 contributes to merosin deficient congenital muscular dystrophy type 1A: Case report. Biomedical Reports, 2020, 12, 46-50. | 0.9 | 5 |
| 14 | Whole genome analysis of a Vietnamese trio. Journal of Biosciences, 2015, 40, 113-124. | 0.5 | 4 |
| 15 | mPartition: A Model-Based Method for Partitioning Alignments. Journal of Molecular Evolution, 2020, 88, 641-652. | 0.8 | 3 |
| 16 | Response to: A commentary on â€œA Vietnamese human genetic variation databaseâ€• Human Mutation, 2020, 41, 1461-1462. | 1.1 | 2 |
| 17 | De novo homozygous variant of the SCN1A gene in a patient with severe Dravet syndrome complicated by acute encephalopathy. Neurogenetics, 2021, 22, 133-136. | 0.7 | 2 |
| 18 | A Hybrid Approach to Optimize the Number of Recombinations in Ancestral Recombination Graphs. , 2019, , . | | 1 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | pQMaker: empirically estimating amino acid substitution models in a parallel environment. , 2020, , . | | 1 |
| 20 | A Fast and Efficient Method for Estimating Amino Acid Substitution Models. , 2011, , . | | 0 |
| 21 | MVRM: A Hybrid Approach to Predict siRNA Efficacy. , 2015, , . | | 0 |
| 22 | Genomedics: Whole exome analysis system for clinical studies. , 2017, , . | | 0 |
| 23 | Building minimum recombination ancestral recombination graphs for whole genomes. , 2017, , . | | 0 |
| 24 | Exploring the Kinh Vietnamese genomic database for the polymorphisms of the P450 genes towards precision public health. Annals of Human Biology, 2022, 49, 152-155. | 0.4 | 0 |
| 25 | Response to: A commentary on â€œA Vietnamese human genetic variation databaseâ€• , 0, , . | | 0 |