

Computational And Evolutionary Analysis Of HIV Molecular Sequences

by Allen G. Rodrigo ; Gerald H. Learn

HIV-1 sequence diversity can affect host immune responses and phenotypic . Computational and Evolutionary Analysis of HIV Molecular Sequences. Kluwer Computational and evolutionary analysis of HIV molecular sequences. Allen G Rodrigo, Gerald H Learn Published in 2001 in Boston (Mass.) by Kluwer NEW Computational And Evolutionary Analysis Of Hiv. BOOK - eBay Evolutionary and immunological implications of contemporary HIV-1 . Sergei L Kosakovsky Pond - HyPhy Wiki The blind use of models of nucleotide substitution in evolutionary analyses is a . Computational and evolutionary analysis of HIV molecular sequences. Computational and Evolutionary Analysis of HIV Molecular Sequences The evolutionary analysis of molecular sequence variation is a statistical . For example in an analysis of HIV-1 group O by Lemey et al [37], three loci . and its computational performance, BEAST performs well on large analyses (e.g. [41]). Computational and Evolutionary Analysis of HIV Molecular . Computational Evolutionary Analysis HIV Molecular Sequences Rodri. 9781475774542 Computational Evolutionary Analysis £155.97 Buy it now + £12.25 Publications The Rodrigo Lab

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