Site stripping based on likelihood ratio reduction is a useful tool to evaluate the impact of non-clock-like behavior on viral phylogenetic reconstructions

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#	Paper	IF	Citations
9	Exploring full-genome sequences for phylogenetic support of HIV-1 transmission events. *Aids*, **2005** , 19, 1551-2	3.5	11
8	[HIV-1 diversity: a tool for studying the pandemic]. *Cadernos De Saude Publica*, **2006**, 22, 473-84	3.2	5
7	Phylogenetic analysis reveals a correlation between the expansion of very virulent infectious bursal disease virus and reassortment of its genome segment B. *Journal of Virology*, **2006**, 80, 8503-9	6.6	91
6	Analysis of the overdispersed clock in the short-term evolution of hepatitis C virus: Using the E1/E2 gene sequences to infer infection dates in a single source outbreak. *Molecular Biology and Evolution* , **2006**, 23, 1242-53	8.3	10
5	Evolutionary analyses of European H1N2 swine influenza A virus by placing timestamps on the multiple reassortment events. *Virus Research*, **2008**, 131, 271-8	6.4	21
4	Population dynamics of HIV-1 subtype B in a cohort of men-having-sex-with-men in Rome, Italy. *Journal of Acquired Immune Deficiency Syndromes (1999)*, **2010**, 55, 156-60	3.1	42
3	Viral phylodynamics and the search for an heffective number of infectionsh. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2010**, 365, 1879-90	5.8	95
2	Use of phylogenetics in the molecular epidemiology and evolutionary studies of viral infections. *Critical Reviews in Clinical Laboratory Sciences*, **2010**, 47, 5-49	9.4	48
1	The mode and tempo of hepatitis C virus evolution within and among hosts. *BMC Evolutionary Biology*, **2011**, 11, 131	3	107