



FIGURE 27.22. Consistency index (CI). A CI score has been plotted for the whole genome of hepatitis C viruses. First, an alignment of whole genomes of different hepatitis C viruses was made. Then a phylogenetic tree was inferred for the complete alignment. Third, small regions of the whole alignment were analyzed to determine how consistent the data in that region was relative to the tree of the whole genome. A sliding window of different base pair lengths was used and the CI for each position in an alignment of complete genomes was averaged over this window. Window sizes are 100 (red), 300 (blue), or 500 (black) nucleotides. (Redrawn from Hraber P.T. et al. 2006. *Virol. J.* **3**: 103, Fig. 3a.)