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RANDOM SUBCLONING, PAIRWISE END SEQUENCING, AND THE MOLECULAR EVOLUTION OF THE VERTEBRATE TRYPSINOGENS

by

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ABSTRACT

Mathematical theory for random subcloning is presented and discussed in detail. The pairwise end sequencing strategy for mapping and sequencing is presented in a general form; specific examples are analyzed with the aid of computer simulations. The evolution of the vertebrate trypsinogen multigene family is discussed in the context of newly sequenced trypsinogen genes from the lamprey *Petromyzon marinus* and the tunicate *Boltenia villosa*.