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HSAP: Human endogenous retroviruses Structure Analysis Program

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Human endogenous retroviruses (HERVs) comprise up to 8% of the human genome and are believed to have a significant impact on the human genome structure and function related to human evolution and disease. They have structural genes, gag, pol, env, and LTR elements in their flanking region. Bioinformatic analysis of HERV shows performed using the RepeatMasker program to identify repeat sequences. Following the analysis of the Repeat Masker, we used a mergence algorithm that makes to define more precisely HERV families and to ascribe individual members for their families. Using this information, we developed a program, named HSAP (HERVs Structure Analysis Program). The HSAP shows structural features of HERVs in the genome database by searching LTR-gag-pol-env-LTR sequences. In addition, it also shows graphical representation of HERV structures. Therefore, the HSAP could be of great use the exploring of HERV features and biological roles in human genome.