

New database activities for functional genomics in KRIBB

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Functional genomics is widely discussed term that has different meanings for different scientists. The several hundred functional genomics websites that have sprung up over the 12 months clearly demonstrates that interpretations of functional genomics are diverse. One example is EST database from NCBI. The dbEST is a division of GenBank that contains sequence data and other information on "single-pass" cDNA sequences and The entry of dbEST is more than 2,000,000. The most important species in dbEST entries is human and the number of entry is about 55% among total species. EST sequences may be used to find the function of unknown sequences or find complete full length cDNA sequences. But dbEST is simple collection of EST sequences. Scientists searching dbEST only can use keyword and retrieve some sequence entries related keywords. Human EST in dbEST is composed of more than 70 human organs or libraries. To turn to EST sequences to account, we analyzed dbEST, than human EST sequences in dbEST were grouped in human organs or tissue libraries. This new database of EST sequences can be downloaded by users in each group of each library, and can be used to search sequence similarity by BLAST and FASTA programs. In the future, new EST database will be extended to *in-silico cloning* system.