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Expressed sequence tag (EST) clustering database

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Abstract

The sequence tag alignment and consensus knowledgebase (STACK) is an international collaborative project on EST clustering.

Content

The sequence tag alignment and consensus knowledgebase (STACK) is an international collaborative project on EST clustering. STACK uses a different algorithm to cluster ESTs than other EST databases such as UniGene and TIGR, and claims to produce longer EST consensus sequences than the other databases without sacrificing multiple alignment accuracy. It is possible to search sequences against STACK using the full range of BLAST programs at this site. The [South African National Bioinformatics Institute](#) (SANBI) homepage through which STACK is accessed has links to people, positions and courses at SANBI, to the tuberculosis *Mycobacterium tuberculosis* information site, including MycDB, and to a new HIV Africa website.

Navigation

Moving around is easy, with none of the links progressing too far. The site is well documented and explained, enabling easy use.

Reporter's comments

Timeliness

The site was last modified on 1 December 1999 with the addition of HIV Africa.

Best feature

Searching STACK with BLAST is excellent with the results easy to understand and links to the EST clusters easy to follow. In addition, a good feature is the ability to search for ESTs from defined organs. The STACK database and programs are also downloadable to local machines.

Worst feature

The links to the EST multiple alignment data are not easy to follow and could be made more robust.

Wish list

A useful feature to add in the light of large sequencing projects would be the ability to submit batch processes, containing multiple search sequences, direct to the STACK server.

Related websites

Other EST clustering systems are found at [UniGene](#) and [TIGR gene indices](#).

Table of links

[South African National Bioinformatics Institute \(SANBI\). STACK: sequence tag alignment and consensus knowledgebase](#)

[South African National Bioinformatics Institute](#)

[UniGene](#)

[TIGR gene indices](#)

References

1. South African National Bioinformatics Institute (SANBI). STACK: sequence tag alignment and consensus knowledgebase.