StAT

Rapid query and pharma focused analysis of abstracts from MEDLINE

InPharmix Incorporated

Statistical Analysis of Text (StAT)

Description:

StAT searches the MEDLINE literature database of more than 7 million records using a user-supplied query. The resulting abstracts are analyzed statistically to extract and highlight the most important findings in the abstracts. ***StAT*** has an integrated MEDLINE interface, a pharma-specific knowledge domain and user-friendly web based interface. ***StAT*** allows the researcher to quickly explore the literature and is particularly helpful when there is limited time but many concepts to explore, as when conducting genomic research. An integrated MEDLINE interface, larger data set size and a pharma-specific knowledge domain differentiate StAT from other similar tools.

Use:

The user may enter a MEDLINE query (which is searched automatically), upload a local text file or paste a set of abstracts into the ***StAT*** input page.

Results:

StAT returns a list of key words, key sentences and highlighted abstracts ranked by uniqueness based on a background set of pharmaceutical literature.

Advantages:

StAT returns a brief summary of the literature relating to a gene, disease, drug etc. that highlights the key features of the literature with particular emphasis on pharma related concepts.

Ordering Information:

StAT is available free of charge at the InPharmix web site. User registration is required. Stand-alone versions (PC, Mac and UNIX) are also available. Contact InPharmix for pricing information.

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Example:

When a researcher has a long list of genes to analyze, as is frequently the case with the results from a library or gene chip experiment, the time and effort involved in examining the literature can be significant. ***StAT*** allows the researcher to quickly search and analyze the literature concerning a gene in an effective manner. For example, consider the protein Zinc-alpha-2-glycoprotein (ZAG) for which MEDLINE has 59 abstracts. The researcher could examine these abstracts individually, a time consuming and tedious task. ***StAT*** speeds up the review process by quickly identifying a ranked list of the key sentences and most important abstracts for the user. In our ZAG example, the researcher learns that ZAG is a ubiquitous serum protein, that it has a non-peptidic MHC like binding groove and that an X-ray crystal structure is available, all without reviewing the entire body of publications.

Ranked Sentences:

Score	Link to Marked Abstract	Key Sentence
4355 272	0010376801	Zinc-alpha2-glycoprotein (Znalpha2gp) is a soluble major histocompatibility complex homolog widespread in body fluids and in glandular epithelia; the authors recently demonstrated its presence in stratified epithelia
4252 354	0009328826	Zinc-alpha 2-glycoprotein (Zn alpha 2gp) is almost ubiquitous in body fluids, and its antibody labels the corresponding secretory epithelia
4250 250	0010206894	The 2.8 angstrom crystal structure of ZAG resembles a class I major histocompatibility complex (MHC) heavy chain, but ZAG does not bind the class I light chain beta2-microglobulin

Marked Abstract:

>0010206894

Crystal structure of human ZAG, a fat-depleting factor related to MHC molecules. Zn-alpha2-glycoprotein (ZAG) is a soluble protein that is present in serum and other body fluids. ZAG stimulates lipid degradation in adipocytes and causes the extensive fat losses associated with some advanced cancers. The 2.8 angstrom crystal structure of ZAG resembles a class I major histocompatibility complex (MHC) heavy chain, but ZAG does not bind the class I light chain beta2-microglobulin. The ZAG structure includes a large groove analogous to class I MHC peptide binding grooves. Instead of a peptide, the ZAG groove contains a non-peptidic compound that may be implicated in lipid catabolism under normal or pathological conditions.

The ***StAT*** results include links back to the original MEDLINE records. In just a few minutes, the researcher can make an informed decision on the merits of a given gene for further research.

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