MASS PROTEOMETRY

Mammalian-PERFECT

An Amino Acid Sequence Database for Proteomics Research

A comprehensive amino acid sequence database with reduced redundancy

Mammalian-PERFECT Benefits point

◆ Dramatic reduction of protein identification time

Mammalian-PERFECT is a database containing human, mouse, and rat sequences that manages to reduce redundancy. Search time is dramatically reduced compared to EST databases using mass spectrometry or other data.

◆ Longer sequences than ESTs for improved accuracy

Mammalian-PERFECT's consensus sequences are much longer than ESTs, leading to improved accuracy.

◆ Good sequence quality

Our unique Genome Refined Consensus method maximally improves sequence reliability

◆ Comprehensiveness

VTS(virtual transcribed sequences) contained in Mammalian-PERFECT are much more effective than ESTs for identifying low-expression genes and unknown genes

◆ Simultaneous evaluation/searching of known and unknown proteins

Optimal candidate amino acid sequence identified from among a large pool:

NCBInr (known proteins) + Consensus sequences (expressed mRNA fragments) + VTS (low expression/time-specific)

◆ Easy set-up for use with other major protein search engines

The database is easily adapted for use with other major search engines.
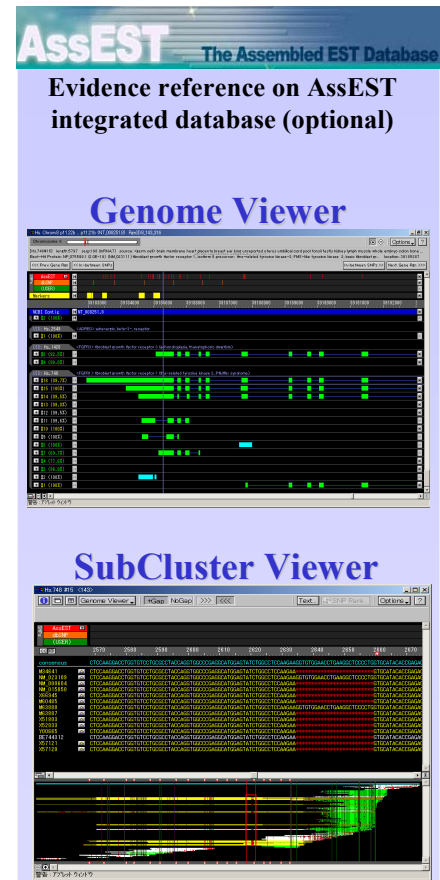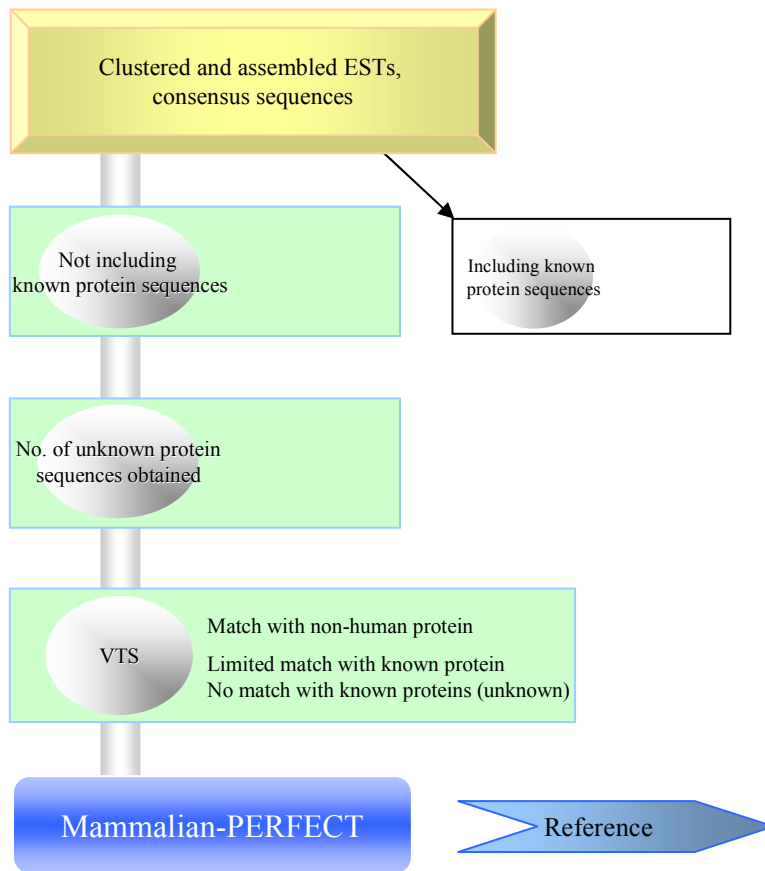
Mammalian-PERFECT contains:

- **Consensus sequences(assembled EST)**
- **Genome Refined Consensus sequences**
- **VTS (virtual transcribed sequences)**
- **Added services: NCBInr (non-redundant protein database)**
  Already divided into human, mouse, rat, and cow genomes
- **NCBI Nr + consensus sequences + VTS (known/unknown candidate pool)**

Format: Multi-FASTA file on CD/DVD. Data revised quarterly.

Mammalian-PERFECT Summary

Clustered and assembled ESTs, consensus sequences

Not including known protein sequences

Including known protein sequences

No. of unknown protein sequences obtained

VTS

Match with non-human protein
Limited match with known protein
No match with known proteins (unknown)

Mammalian-PERFECT

Reference

AssEST The Assembled EST Database

Evidence reference on AssEST integrated database (optional)

Genome Viewer

SubCluster Viewer

Comparison with EST data

Comparison between EST sequence (dbEST) and Mammalian-PERFECT

	dbEST	Mammalian-PERFECT
① No. of sequences (redundancy)	42,600,000 amino acid sequences	1,800,00 amino acid sequences
② Sequence length	Short	Long
③Sequence quality	Some poor quality sequences	High quality sequences with Genome Refined Consensus (pat. pend.)
④ Comprehensiveness	No low-expression sequences	Includes low-expression sequences
⑤ Search speed	Very slow because of ①	Fast because of ①
⑥Identification accuracy	Low because of ②-④	High because of because of ②-④
⑦Sequence data processing	Manually by user	Automatic
⑧ Related searches	Manually by user	Linkable to AssEST or VTS-Express

For estimates and other information, contact:

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