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FOR GENEMARK.HMM (eukaryotic) SOFTWARE

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Please fax the signed agreement to fax: +1 404 603 88 75

EXHIBIT "A"

GeneMark.hmm™ 2.2 and 3.0 (eukaryotic version) description

GeneMark.hmm™ (eukaryotic version) is a data analysis tool designed to predict the presence of protein coding regions from raw DNA sequence text. The program consists of a single executable program (gmhmm) and several files of parameters that represent the statistical characteristics of known protein coding and non-coding regions of individual species.

As an output, GeneMark.hmm™ generates a list of estimated exon boundaries and predicted peptides.

GeneMark.hmm™ program has several other options that are described in the help message displayed if only the command 'gmhmm' is entered.

The GeneMark.hmm™ program does not include the subsystems that performs the statistical analysis and generates the model parameters, matrices of initial and transition probabilities.

The GeneMark.hmm™ 2.2 program includes models for the following organisms:

- H. sapiens
- M. musculus

The GeneMark.hmm™ 3.0 program includes models for the following organisms:

- C. elegans
- A. thaliana
- D. melanogaster
- C. reinhardtii
- Z. maize
- T. aestivum
- H. vulgare
- O. sativa

(Although GeneProbe does not take obligation of the GeneMark.hmm support or maintenance, we will do our best to address your questions, please see <http://www.geneprobe.net/contactus.htm> for faster communication regarding academic distribution use Fax: +1 (404) 603-8875 or e-mail custserv@genepro.com)