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Atlanta, Georgia**

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FOR GENEMARK.HMM-ES SOFTWARE PACKAGE

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"The protein coding regions have been predicted by the GeneMark.hmm program."

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Signature Date

Typed or Printed Name Institution

Address

Address

Telephone E-mail

Type & version of operating system: Solaris____, IRIX____, DEC____, LINUX_2-6-5, AIX____ .
Type of machine 32 bit ____, 64 bit ____ .

Please fax the signed agreement to fax #: +1 404 255-20-67

EXHIBIT "A"

The GeneMark.hmm-ES software developed in 2005-2008 includes program GeneMark.hmm -E (the GeneMark.hmm-ES name refers to the software system that includes the latest version of GeneMark.hmm-E along with the modules that allow for unsupervised estimation of HMM parameters)

Description:

The self-training program GeneMark.hmm-ES is a software tool for genomic data analysis designed to predict protein coding regions in novel eukaryotic genomic sequences. The matrices of species specific parameters of the probabilistic models are estimated by an iterative unsupervised procedure that uses raw genomic data as an input to the program.

Although Gene Probe does not take obligation of the GeneMark.hmm-ES support or maintenance, we will do our best to address your questions, please see <http://www.geneprobe.net/contactus.htm>

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