

# GeneMark

Version 2.5p (09.08.06)

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## PROGRAM INFORMATION

Sequence : Corynebacterium phage TouchMeNot complete sequence, 40526 bp, circularly permuted, Cluster  
Analysis Date : 3/18/18 at 3:49:27  
Pages : 21  
Sequence Length : 40526 bp  
GC Content : 60.03%

Window Length : 96 bp  
Window Step : 12 bp  
Threshold Value : 0.500

PS-Version : 1.2

GeneMark Options : PostScript graph,  
Mark ORFs / splice sites,  
List ORFs,  
List regions and/or splice sites,

## Matrix notes & comments

For details on the model building procedure see:  
Besemer J. and Borodovsky M.  
"Heuristic approach to deriving models for gene finding"  
NAR, 1999, Vol. 27, No. 19, pp. 3911-3920

## MATRIX INFORMATION

Matrix : Heuristic, GC = 60  
Author : Borodovsky Laboratory - Georgia Tech  
Order : 2

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