

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 : 7/16/18 at 12:28:44
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
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Order : 2

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