

A

PROBE DESIGN

ClustalW parameter

Divergent size filter (%) : Show alignment

Probe design parameters

Probe size Min :

Probe size Max :

Maximum degeneracy :

Minimum degeneracy :

Inosine threshold (%) :

Specificity step parameter

E-Value threshold tBLASTn :

Launch Step 3 Repeat Step Reinitialize Help

Initialization

Research...

Step 1 : Reference sequence extraction [OK]
: Homologous protein accession numbers listing [OK]
: ClustalW [OK]
Step 2 : Potential probes research [OK]

Length : Position : Sequence : Degeneracy : Inosine (%)

24 : 172 : GAYAA YTT YTT YTT CAIGAYGAR : 128 : 8.33
--> 4 oligopeptide(s)

24 : 643 : TAYTGYAARCCIRTITGGTAYTGG : 32 : 8.33
--> 3 oligopeptide(s)

24 : 958 : GCIAGYCARAGYCGRCRRGTITTY : 128 : 8.33
--> 2 oligopeptide(s)

Save Results

B

