

CPSC 335 Project 4 Report

Output:

----- Dynamic Programming -----

String to Match = PIEPCMGA

Best Score: 30

sp|Q12517|DCP1_YEAST mRNA-decapping enzyme subunit 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=DCP1 PE=1 SV=1

PIEPCMGA

PLE*CMGV

3.06277 s

String to Match = TQGASNIGE

Best Score: 36

sp|Q08213|NGL1_YEAST RNA exonuclease NGL1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NGL1 PE=1 SV=1

TQGASN*IGE

TDGASNVIGE

4.37292 s

String to Match = ALAKLIRYGG

Best Score: 35

sp|P15108|HSC82_YEAST ATP-dependent molecular chaperone HSC82 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=HSC82 PE=1 SV=4

ALAKLIRYGG

ALAKLLRYNS

4.7688 s

String to Match = CSNPNLSDFGR

Best Score: 37

sp|Q03088|SVL3_YEAST Styryl dye vacuolar localization protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SVL3 PE=1 SV=1

CSNPNLSDFGR

PSSINMSDFGR

5.648 s

String to Match = MYPEPTIDE

Best Score: 35

sp|P25558|BUD3_YEAST Bud site selection protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BUD3 PE=1 SV=2

MYPEPTIDE

LFP*PTIDE

3.75069 s