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Terminal - captainnemo@Zelda: ~/Desktop/project-4-team-dio
File Edit View Terminal Tabs Help
captainnemo@Zelda:~/Desktop/project-4-team-dio$ make
g++ -std=c++11 project4_main.cc -o experiment
./project4_test
load_protein still works: passed, score 1/1
local_alignment trivial equal cases: passed, score 2/2
local_alignment trivial deletion/insertion cases: passed, score 2/2
local_alignment trivial substitution cases: passed, score 2/2
local_alignment simple local cases: passed, score 2/2
TOTAL SCORE = 9 / 9

captainnemo@Zelda:~/Desktop/project-4-team-dio$ ./experiment
----- Dynamic Programming -----
String to Match = PIEPCMGGA
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
PIEPCMGGA
PLE*CMGV
40.5078
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
45.3196
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
51.888
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
55.2778
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
46.2354
captainnemo@Zelda:~/Desktop/project-4-team-dio$
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