BİYOİNFORMATİK PROJE KODU ÇIKTILARI / **OGÜN ATALAY**

NCBI veritabanından 10 adet DNA sırası indiriniz. (DNA.fasta)

1.SORU A) Nucleotides sayılarını hesaplayınız.

Nucleotide Counts (excluding N):

A: 2321

T: 2429

G: 3248

C: 2906

1.SORU B) Sıraları RNA’ya çeviriniz.

(Kod içerisinde RNA\_Dosyası.fasta olarak otomatik kaydediyor. Dosya içeriği aşagıda verilmiştir.)

* >X98449.1 Feline herpesvirus type 1 gE gene
* AUGGGACUGCUUGUUACCAUCCUCGUGAUAUUAUUGAUUGUUACUUCAUCAAGUUCUACU
* AUUCAUCAAGUAACGAUGACAGAAGGUGCCGCACUUUUAGUCGAUGGGGAUGGGAUCGAC
* CCACCUUUAAACAAAACUUCACAUUUUUUGCGAGGUUGGACAUUUCUAGAGACUCCGAAA
* GGAUGUACAGGAGAGGUGAGUGUUCUAAAAGUAUGUAUAGAUCGUGGGGUAUGUCCGGAU
* GAUAUCGUUAUAAAUAAGAGAUGUGGUCACAAAAUGCUUGAAACCCCACUAGCGUUGGCG
* GAAUUUGGAAUUUCUAAUAGUUCUCUCAUCAGAACCAAAGACGUAUAUUUCGUGAAUAAG
* ACCGUGUUUCCAAUUCUCACACCCGAAAAAAGUGGCCUUGGUAUUCAGGGGGCCACUACG
* AAUAUAUCCGGGAUAUAUACCCUGCAUGAGCACGGUGAUAAUGGAUGGAGUCAUCAAUCU
* ACAUUUUUUGUGACCGUAAAGGCAAAACAUCCCGGACCAUCGUUAACCCCAGCACCGGUU
* CACUUAAUAACACCACAUCGCCAUGGGGCACAUUUCCACGUAAGAAACUAUCAUUCGCAU
* GUCUACAUUCCGGGAGAUAAGUUCUUAUUAGAAAUGCACCUCAAAUCAGAUAUCUAUGAU
* CCAGAAUUUUCAGCAACAAUAGACUGGUAUUUUAUGGAGACUGAUAUAAAAUGCCCAGUU
* UUUAGAAUUUAUGAAACUUGUAUAUUUCACCCCCAUGCCGCAUCCUGUCUACAUCCGGAA
* GAUCCCUCAUGCAGUUUUACAUCACCACUUCGAGCGGUAUCUUUAAUUAAUAGAUUUUAU
* CCAAAAUGCGAUCACAGAUAUGCCGAUUGGACAUCCAGAUGUAUCAACACUCCAAGUAUA
* AAUCAUAUGCCAUAUAUCGAACAGCCGGCCAAUAACGUGGAUCUAAAGUUUAUCAAUGUA
* CCCACCAACGCUUCUGGGUUGUACGUAUUCAUACUUCGUUAUAAUGGACAUCCGGAAGAA
* UGGACCUAUACACUCAUAUCAACAGGAGCUAAAUUUUUGAAUGUGAUUAGGGAUCUGACA
* CGCCCACGUCUUGGUAGUCAUCAAAUAGAGACCGAUAUUAGCACAUCUUCGCAGUCGCCU
* ACCACGGAGACACCACGAAACAUACAUAUAACGUGGGCGAGACGUUAUCUAAAGGUUAUC
* AUAGGAAUAAUUUGCGUAGCUGGUAUCCUUUUGAUUGUAAUCUCUAUCACAUGUUAUAUU
* CGAUUUCGUCAUAUGCGAUAUAAACCAUAUGAAGUGAUCAACCCAUUCCCUGCGGUAUAU
* ACCAGCAUUCCUAGUAACGAUCCCGACGAACUCUACUUUGAACGUAUCGCAUCGAACGAC
* GAAGAAUCGGCAGAUGAUUCUUUUGAUGAAUCAGAUGAGGAGGAGCCAUUGAAUAAUCAU
* CAUAUUUCAACAACCCAACAUACUGAUAUUAAUCCAGAAAAAUCCGGAUCUGGGUACAGU
* GUAUGGUUUCGUGAUACAGAAGAUACAUCACCUCAGCCCCUACACGCUCCUCCAGAUUAC
* AGUCGCGUAGUUAAAAGAUUAAAGUCUAUUUUAAAAUGA
* >PQ082960.1 Suid alphaherpesvirus 1 isolate HN5 gE (US8) gene, complete cds
* AUGCGGCCCUUUCUGCUGCGCGCCGCGCAGCUCCUGGCGCUGCUGGCCCUGGCGCUCUCC
* ACCGAGGCCCCGAGCCUCUCCGCCGAGACGACCCCGGGCCCCGUCACCGAGGUCCCGAGU
* CCCUCGGCCGAGGUCUGGGACGACCUCUCCACCGAGGCCGACGACGAUGACCUCAACGGC
* GACCUCGACGGCGACGACCGCCGCGCGGGCUUCGGCUCGGCCCUCGCAUCCCUGAGGGAG
* GCGCCCCCGGCCCAUCUGGUGAACGUGUCCGAGGGCGCCAACUUCACCCUCGACGCGCGC
* GGCGACGGCGCCGUGCUGGCCGGGAUCUGGACGUUCCUGCCCGUCCGCGGCUGCGACGCC
* GUGUCGGUGACCACGGUGUGCUUCGAGACCGCGUGCCACCCGGACCUGGUGCUGGGCCGC
* GCCUGCGUCCCCGAGGCCCCGGAGAUGGGCAUCGGCGACUACCUGCCGCCCGAGGUGCCG
* CGGCUCCGGCGCGAGCCGCCCAUCGUCACCCCGGAGCGGUGGUCGCCGCACCUGAGCGUC
* CUGCGGGCCACGCCCAACGACACGGGCCUCUACACGCUGCACGACGCCUCGGGGCCGCGG
* GCCGUGUUCUUUGUGGCGGUGGGCGACCGGCCGCCCGCGCCGGCGGACCCGGUGGGCCCC
* GCGCGCCACGAGCCCCGCUUCCACGCGCUCGGCUUCCACUCGCAGCUCUUCUCGCCCGGG
* GACACGUUCGACCUGAUGCCGCGCGUGGUCUCGGACAUGGGCGACUCGCGCGAGAACUUU
* ACCGCCACGCUGGACUGGUACUACGCGCGCGCGCCCCCGCGGUGCCUGCUGUACUACGUG
* UACGAGCCCUGCAUCUACCACCCGCGCGCGCCCGAGUGCCUGCGCCCGGUGGACCCGGCG
* UGCAGCUUCACCUCGCCGGCGCGCGCGCGGCUGGUGGCGCGCCGCGCGUACGCCUCGUGC
* AGCCCGCUGCUCGGGGACCGGUGGCUGACCGCCUGCCCCUUCGACGCCUUCGGCGAGGAG
* GUGCACACGAACGCCACCGCGGACGAGUCGGGGCUGUACGUGCUCGUGAUGACCCACAAC
* GGCCACGUCGCCACCUGGGACUACACGCUCGUCGCCACCGCGGCCGAGUACGUCACGGUC
* AUCAAGGAGCUGACGGCCCCGGCCCGGGCCCCGGGCACCCCGUGGGGCCCCGGCGGCGGC
* GACGACGCGAUCUACGUGGACGGCGUCACGACGCCGGCGCCGCCCGCGCGCCCGUGGAAC
* CCGUACGGCCGGACGACGCCCGGGCGGCUGUUUGUGCUGGCGCUGGGCUCCUUCGUGAUG
* ACGUGCGUCGUCGGGGGGGCCAUCUGGCUCUGCGUGCUGUGCUCCCGGCGCCGGGCGGCC
* UCGCGGCCGUUCCGGGUGCCGACGCGGGCGCGGACGCACAUGCUCUCUCCGGUGUACACC
* AGCCUGCCCACGCACGAGGACUACUACGACGGCGACGACGACGACGACGAGGAGGCGGGC
* GUCAUCCGCCGGCGGCCCGCCUCCCCCAGCGGAGACAGCGGCUACGAGGGGCCGUACGCG
* AGCCUGGACCCCGAGGACGAGUUCAGCAGCGACGAGGACGACGGGCUGUACGUGCGCCCC
* GAGGAGGCGCCCCGCUCCGGCUUCGACGUCUGGUUCCGCGAUCCGGAGAAACCGGAAGUG
* ACGAAUGGACCCAACUAUGGCGUGACCGCCAACCGCCUGUUGAUGUCCCGCCCCGCUUAA
* >AY864513.1 Drosophila simulans strain ZIM-12 hemomucin (Hum) gene, partial cds
* CUUCAAGGACUAUAUGUAAGUGCCUGCCGUUCCAAUUGACGUAAUUCCCGUGCUAAUCCU
* UGGAGAAAUCCCCACUUCGUACAGUGUGACCCCGCCCAAAGACCUGAAAGGGGCGCUGGA
* AUCGAACUUUCACCUGGAGGGAGCGGAGCGACUGCUGGAGGGGCGGGUCUACGGCCCGGA
* GUGCCUGAUAGCCCGCAACAACGAGAUCUACACCGGCAUCCACGGCGGUGAGGUCAUCAA
* GCUAACGUCCAACCAUGUCACGCAUGUCACCAAGAUCGGCCAGCCCUGCGGUGCGUAUUU
* UCGAGUCCUAUAAAGGGAGUUUCAUUUUAUAAUAGUAAUCCCCUUGCAGAGGAUAUCUAC
* GAGGAGUCCAGGUGCGGCCGUCCUCUGGGUCUGGCCUUUGAUACGCAGGCUAACAACCUC
* AUCGUCGCUGACGCCUACUACGGCCUGUGGCAGGUGGACCUGGGCACCAAUAAGAAGACC
* CUGCUGGUCUCGCCCGCCCAGGAGCUUGCCGGCAAGUCCAUCAACCGCCCUGCCAAGAUU
* UUCAACGGUGUGACCGUGAGCAAACAGGGCGACAUCUACUGGACGGACUCCUCGUCGGAC
* UUCACCAUCGAAGACCUCGUCUUUGCCAGCUUUGCUAACCCCUCCGGCCGGUGAGUUCAU
* CGCAAAUUAUAGCGCAACUGUCUAAUAUUGCUAGUUUUCAAAGUGAUAGCUAUUCGGAAU
* AGGGCUACAGUGGUACCCCAUUACAUUGAAUGUCUUUACAAAACGAGUUUUGUGACCCAU
* UUAAGAUUAUUUAAAACGCUUGUAGCGGACUCGAGUGAUUCGCCUAAUUAAUCUCAAUUA
* AGAUUACUUCAAUUAGCUUACUUCAGUUAGCUUAAUUCUUAUAAUUAAGGGACAAGUUAC
* AGAAGUAUGACUGUAAGACGAACGCAAACCGGUUUCUCGAUCGGGUCUAAUGGUUACUCU
* AACGGCCUUUGCUUUCUUCUACCUUUCAGUCUUUUCAAAUACAACCGCUCGAAGAAUGUU
* AGCGAGGUGCUGCUGGACGAACUGGCCUUCGCCAACGGAUUGGCCCUCAGUCCCAACGAG
* GACUUCAUCGUGGUAGCCGAGACCGGAGCGAUGCGUCUGACUAAGUAUCACCUGAAGGGU
* GCGAAGGCCGGUCAGAGCGAGGUGUUCGUCGACGGAUUGCCCGGUUUGCCCGAUAACCUG
* ACGCCCGACGCCGAGGGCAUCUGGGUGCCAUUGGUCCAGAGCGCGGAUAGCGAGCAUCCC
* AACGGCUUCACCCUGUUCACUCGCUUCCCCAGCGUGCGCCUCUUCCUGGCCCGCAUGCUG
* GCUUUGUUCGAGCUGCCCUUCCGCUACCUGAACAGCGUAUAUCCGAACAAGUUCUCGCAG
* CGAUUCGUUCACUUCGUUGGACACAUGGAGAGCAUCACUGUGUUGGCGCCCAAGCGAACG
* ACUGUCGUGCGUGUGGACUGGAACGGCAACAUUGUGGGCUCGCUGCAUGGCUUCGACAAG
* UCGGCCGCCACGGUAUCACACGUCCUGGAGUUCCAAGACUUCUUGUUCCUGGGCUCUCCC
* ACCAAUCAGUACCUGGCGCGUGUCAAGUCGCCAAAGGCCAAACAGCCCACGCUGAAGGUG
* CGCAAUGUUCGCGUCGAGGGCGAGGGCUUGGAGGCGUCCAUUGGUGUGCCACCCAGCACA
* GCCACUCCUAAACCCAAGGCGGCUCCCAGCACCACCACUCCAAAACCCACAACGACAACU
* ACUACGCCGAAACCCACUACCACAACGACAACUACUACAACCACGCCAAAACCCACUACC
* ACAACGACAACCAAGAAGCCAACGACCACUACCACCACCACGACAACCACGCCGAAGCCA
* ACCACUACUAAGCCGCCGGCAACUAAGCCAUCUACGACUACAACCACCACCACUACUCNU
* AAGCCAACUACUACUACUACUACUACUCCAGCGC
* >MK867787.1 Microliabum humile isolate HUM internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence
* UCGAACCCUGCAGAGCAGAAUGACACGUGAACAUGUACUUGGAAUCGGACGCCAAACGUG
* ACUAACCAUUGUUAUGAUCGUAGGUGUCCCCCAAUGUGCGAUCAUGAUUCCUUUUACAGG
* GCACCAUGAAUGUAUGUUGGUUAUAAACAAACCCCCGGCACAACACGUGCCAAGGAUAAC
* AAAACUAAAAAGUGCGCGUCAUGUGUACCUCCGUUUGCGGUGUGUGCACUGUUCGUGUCA
* ACUUUAUAAUCAUAAACGACUCUCGGCAACGGAUAUCUCGGCUCACGCAUCGAUGAAGAA
* CGCAGCAAAAUGCGAUACUUGGUGUGAAUUGCAGAAUCCCGUGAACCAUCGAGUUUUUGA
* ACGCAAGUUGCGCCCAAAGCCAUCUGGUUGAGGGCACGUCUGCCUGGGCGUCACGCAUCG
* UAUCGCCCCCCACCAUGACAUGGUGUCGGGGGCGGAGUUUGGCCUCCCGUACGUAUGUUG
* CGGUUGGCUUAAACAGAAGUCUCUUUUGGUCGACGCACGGCUAGUGGUGGUUGAUAAGAC
* CUUCGUCUGGCGACCGUUUGUCUAGAACCAUAAGUGAGCGCUUCUUAAAGACCCCAAUGU
* GUCAUCUUGUGAUGAUGCUUCGA
* >LT717484.1 Lasianthus cyaneus chloroplast partial rbcL gene for DNA, specimen voucher USTH: 012472
* UUUUAUGUCACCCACAAACAGAGACUAAAGCAAGUGUUGGAUUCAAGGCUGGUGUUAAAG
* AGUACAAAUUGACUUAUUAUACUCCUGAAUACGAAACCAAAGAUACUGAUAUCUUGGCAG
* CAUUCCGAGUAACUCCUCAACCCGGAGUUCCGCCCGAAGAAGCAGGUGCCGCGGUAGCUG
* CCGAAUCUUCUACUGGUACAUGGACAACCGUGUGGACCGAUGGACUUACCAGUCUUGAUC
* GUUACAAGGGGCGAUGCUACCACAUCGAGCCAGUUCCUGGAGAAGAAGAUCAAUAUAUUG
* CUUAUGUAGCUUACCCCUUAGACCUUUUUGAAGAAGGUUCUGUUACUAACAUGUUUACUU
* CCAUUGUAGGUAAUGUAUUUGGGUUCAAAGCCCUGCGUGCUCUACGUCUGGAAGAUUUGC
* GAAUCCCUAUUUCUUAUGUUAAAACCUUCCAAGGCCCGCCUCACGGCAUCCAAGUUGAGA
* GAGAUAAAUUGAACAAAUACGGUCGUCCCCUGUUGGGAUGUACUAUUAAACCUAAAUUGG
* GUUUAUCUGCUAAAAACUACGGUAGAGCGGUUUAUGAAUGUCUUCGCGGUGGACUUGAUU
* UUACCAAAGAUGAUGAAAACGUGAACUCCCAACCAUUUAUGCGUUGGAGAGAUCGAUUCU
* UAUUUGUAGCAAAAA
* >LT717473.1 Lasianthus verticillatus chloroplast partial rbcL gene for DNA, specimen voucher USTH: 012464
* AUUUCCCCCCCCAACAGAGACUAAAGCAAGUGCCUUGAUCGUUACAAAGGCGAUGCUACC
* ACAUCGAGCCCGUUGCUGGAGAAGAAAAUCAAUAUAUUGCUUAUGUAGCUUACCCCUUAG
* ACCUUUUUGAAGAAGGCUCUGUUACUAACAUGUUUACUUCCAUUGUGGGUAAUGUAUUUG
* GGUUCAAAGCUCUGCGCGCUCUACGUCUGGAAGAUCUGCGAAUCCCCCCUGCUUAUUUUA
* AAACUUUCCAAGGCCCGCCUCAUGGCAUCCAGGUUGAGAGAGAUAAAUUGAACAAAUACG
* GUCGUCCCCUAUUGGGAUGUACAAUUAAACCUAAAUUGGGGUUAUCCGCUAAAAACUAUG
* GUAGAGCGGAUAAUGAAUGUCUCCGCGGUGUACUUGAUUUUACAAAAGAUGAUGACAACG
* UGAACUCCCAACCCUUUAUGCGUUGGAG
* >HQ247764.1 Equid herpesvirus 2 strain BB9 glycoprotein H (gH) gene, partial cds
* UUUUUGGCAUGGUGGGCUAUUGGGGGGCGAGGGCUUGCAACGCCCUCUCCCUCUACACCG
* GGGUUUUCAGGGUCUUCGGGAUCUCCUGGAACACGGGCGAGUGUGUCUGCGACCACCAGG
* AAAAUUUUGCCAACAACAAAGAGUGUCAACUAUACUGAAAUGAUUGAAAAAAAUCCAUCU
* CUGACGAUUGAUCUGGGAAACCAAACCAAGUAUCAGCUCAACUGGACGGACGUGGUUAAG
* GUGAUCCCGGGGGAACUGAUUGAGAAGAUGUGGGAGGAGUCUAAUGUUACGGAGUCUUUG
* UGGUUUACUCUUAACAAGUUUACAGAUGUUUAUAAAAAGGAUACAAUCUUUAAAAAUUUU
* ACGGGGCAUUUUACUACAAAAUAUGUGUGUAAUGUUUCCCAAGGGGAACCUAAUUAUAAU
* GUUUCUCAGAGGGAGGUAAAAGAAAUUAAGGAAUAUGAUGGGAAAUUUGGGAUUCCAGCU
* CCAGUUGUCCUGUCUG
* >NR\_152932.1 Entoloma mirum TUR K. Kokkonen 99/14 TUR ITS region; from TYPE material
* UUGAAUAAACUUGGUUGGGUUGCUGCUGGCUCUCAGGAGCAUGUGCACACCUAAUGCCAU
* UUUUAACCACCUGUGCACCCUCUGUAGAUUCUGAAGUACCUUUCGAGGAAACUCGGUUUG
* AGAACUGCUGUGCUGAAAAGCCAGCUUUUCUUGCAUUUCAGGUCUAUGUUUUUAUAUACC
* CCACAAGAAUGUAUUAGAAUGUUGUCAAUAGGCCUCUGUGCCUUUAAAACAAAUACAACU
* UUCAACAACGGAUCUCUUGGCUCUCGCAUCGAUGAAGAACGCAGCGAAAUGCGAUAAGUA
* AUGUGAAUUGCAGAAUUCAGUGAAUCAUCGAAUCUUUGAACGCACCUUGCGCUCCUUGGU
* AUUCCGAGGAGCAUGCCUGUUUGAGUGUCAUGAAAUUCUCAACCUUUCUGGCUUUGGCUG
* GUCAGGCUUGGAUUGUGGGAGCUGCUGGCUUUGCAGAAAAGUCAGCUCUCCUUAAAUGCA
* UUAGCAAAAUCUUUGCUAGGCCAUCUUUGGUGUGAUAAUUAUCUAUGCCACUGAUGCUUA
* GCUUCCUUGCAAGAGGGUGGUUUAGCUUCUAACUGUCCAUCUUGGACAAUUUUUUGACAA
* U
* >M81739.1 S.aureofaciens hydroxyurea resistance (hur) gene, complete cds
* GAUCGCCGAGCGGGUGCCGGGGCUGCGCGGGGAGGCCUUCGACCGGGCCGUGGCCGAGGG
* GACCCACACGGGAUGGGCCGAGGGGGCGGAGAAGGCCUUCGAGGCGACGGGGAUGCGGGG
* GACGCCGGCGGUGCUGGUGGACGGGAAGCCGGUGGGGGCGAAGGACGGGUCGAUGUUCGA
* CGCGGCCGGGUUCGCGCGGACCCUCAAGGGGCGGGCGUGGCUGCGUAGGGUCGGGGCCGU
* GGUGGAGAUUCCGGCGGAGUUGGUCGAGGUGCAGCUGCGGUACGGCGGCGCGGCGGGGCG
* GGAGUUCGUCGAGGGGCUGCCGGGGCGGGUGGCGGAGUUCCUGGAGCGGUGGGGGCUGCG
* GGUGGCGGGGCCCGCGAUGCACGGGAUGACGGCCCUGGUGCUGCCGGUGGUGCGGGCGGA
* CGGUACGGAGGCGGCGUUGAAGCUGCUGGUCCCGGAUGAGGAGAGCGCGGGGGAGCCGGU
* CGCGCUGCGCGCGUGGGACGGGCGGGGCUGCGUACGGCUGCUGGAGUGGGACGGGCCUAC
* GGGGACGCUGUUGCUGGAGCGGCUGGACGCGGGGCGGCACCUGUCGGGGCUGGUGGAGCG
* GGACGCGCGGGCGGCGGUGACGGUGGUGGCGGGGCUGCUGGCGCGGCUGACGUCGGUGCG
* GGCGCCGGAGGGGCUGCGGGGGCUGGGGGAGGUCGCGGCGGGGUUGCUGGCGGGGGUGCC
* GGAGGCGGCCGGGCGGCUGGCGGACGCGGGGGAGCGGAGGCUGUUGCGGGACUGCGCGGC
* GGCGUUGGCGGAGGUGGCGGCGGAGCCGGGGGACCGGUUGCUGCACUGGGACCUGCACUU
* CGGGAACGUGCUGGCGGGUGAGCGGGAGCCGUGGCUGGCGAUCGACCCGAAGCCGCUGGC
* GGGGGACCCGGGGUUCGAGUUGCUGCCGGCGUUGGUGAACGGGUUCCGGGCGGGUGAGGU
* CGGGUGGCGGUUCGACCUGCUGACGGGGGUGGUGGGGCUGGACCGGGAGCGGGCGCGGGC
* GUGGACGCUCGGGCGGGUGGUGCAGAACUGUCUGUGGGAGGUGGAGGACGGGGAGGUGGC
* GCUGCCGGAGCGGGAAGUGGCGGUGGCGGAGGUGUUGUUGGGGCGGGCGGGGUGAGUGGG
* GCCUCGGAGGGCCGACGGGUGCGGGUGCGGGUGCGGGUGCUUCCGUAGGGCCGUCGGCGG
* UACCGGGCGGUGGCGGCGUUCGCCCGGGGCGGGGCGGGGCGGGUGCGGGGGGCGUCGUGA
* CGGCGGGUCCGGGGCGUUCCUCGGGGAUCCUGCCGGUUGACCCGUGCCGGGUUGGGCGCC
* GGGCGUGGUGCCGGAGCGUCGUGGCGGCGGGCUCGGGUUGCCCCUUGGGGUUCUCGCCGG
* UCGGGGCCGGGUGGGCCGGCACCGCGCCUUGGCUGGUGGGGUGGGGUGCGGUGCCGGUCA
* GGGUUCCAGGACGACCUUGCCGGUGGUGCCGCGGGUUUCGAGGGCGUGGUGGGCGGCCGC
* CGCUUCGGCCAGGGGGUAGCGCUGAACGGCGGGGCGCAGCGGCCGGUGGCGGCUUCGGCG
* AGGGCGCGGGUUUCAGGACGCGCAGGGGGUCGGGGGCUCCGACGGCUUCGAGCAUGGCGG
* GGCCGAGGACGUGGUGGGUGGUGAUGCCGCGGGCGGUGAGGUCGUCCUGUUCGGCUUCGG
* UGAGGGUGAGGGGCCGGAGGACCAACCGUGAACGAGGUGGCGGGCGCCGGGGGCGAGGAG
* GCCGAGGGCGGUCCGUGCGGUGGUGCCGCCGACGGAGUCGAAGAGGACGGUGGCGCCGUC
* GGGGUGGUGGGCGCGGACGGUGUCGGCCCAGUGGCCGGUGGUG
* >D00360.1 Bacteriophage phi-80 cor gene, complete cds
* CUGCAGCACCAAUAUUCUCGUCAUACUCCUUGAUAAGCUGCGACAUGGCCUGCGCCAGCC
* CAUCAACCGAGAUAUUAUCUGAUACCAGAAUGCCGUACUUCUGGCCGCUCAGCGCCGGGG
* AAGCGGCAGGCGUAACCGUCAUUGACGUGGCGCUGUUCACGGAUGAAAUCUGGAACAGUU
* GCACCGGGUUAGACAUCACGAUAAUUGUCUGGCCAGCGCGAACCUGGCUGGCCGGUGCCG
* UCCAGUUUGUACCCGUCCCGGUGGCGGUAUUUCUAUUAAUGGCGAUGGUGCCGGUGUUAU
* AAAGCAUAUUUUCUCCAGGCAAUAAAAAAACCCCGCCGGAGCGAGGUUUAUGUUUAAGCG
* UAGUGGGUUAUUUGCAGGUUGUUUCGGUAAAUGUAUUCGCACUUACCCAGCGCCAGCUGA
* AAGGAUAUCCAGCCCGGUACUGCGUCUGGUUGUUUUGUUUACGCACACCGUAAAUCUGAA
* CCGUAGUUUCCUGACCGCCAACGAUUGCAGUGCGCGUGCAAACUGGUUCCUGUUUCUCAA
* UUACGCCAGCGCAUCCUGUGAGCAUGACAGCGCCUGCCGUGCAGAUAAUCAGUUUUCUCA
* UUUUGAUAGUAUCCAGAGGUAUUCAUGAACUUAGACAAUACCAACAUGAAAGAGGUGGGU
* AUAAUUGGUUUGAUAGAUCAAUUAUCAGUUAUUGAUCGCCAAACGAUCAAUCAGUCAUAG
* GCCGCUGUAUUUAUCGCGGUUAAGGAAAUUCCAGUAUUCGUUACCCCUCCCGGAGAGCCU
* GUGCCAGUGGAGGUCCCCCCUGCGUUUAUCCUCGUAUUGGCCCCGUCAAACCUGCACGCC
* GAAUAAGCAUUAAUGGUGUAGAUUGUCGAGUUAUUCACAACGAUGCUUUGGCCAAGCUGU
* GCAGGUGCAACAGCCCAUGGCCCGGG

1.SORU C) Sıraları Protein’e çeviriniz (kodonlar kullanarak gerçekleştiriniz).Elde ettiğiniz protein sıralarını bulunuz.

(Kod içerisinde Protein\_Dosyası.fasta olarak otomatik kaydediyor. Dosya içeriği aşağıda verilmiştir.)

* >X98449.1 Feline herpesvirus type 1 gE gene [Translated Protein]
* MGLLVTILVILLIVTSSSSTIHQVTMTEGAALLVDGDGIDPPLNKTSHFLRGWTFLETPK
* GCTGEVSVLKVCIDRGVCPDDIVINKRCGHKMLETPLALAEFGISNSSLIRTKDVYFVNK
* TVFPILTPEKSGLGIQGATTNISGIYTLHEHGDNGWSHQSTFFVTVKAKHPGPSLTPAPV
* HLITPHRHGAHFHVRNYHSHVYIPGDKFLLEMHLKSDIYDPEFSATIDWYFMETDIKCPV
* FRIYETCIFHPHAASCLHPEDPSCSFTSPLRAVSLINRFYPKCDHRYADWTSRCINTPSI
* NHMPYIEQPANNVDLKFINVPTNASGLYVFILRYNGHPEEWTYTLISTGAKFLNVIRDLT
* RPRLGSHQIETDISTSSQSPTTETPRNIHITWARRYLKVIIGIICVAGILLIVISITCYI
* RFRHMRYKPYEVINPFPAVYTSIPSNDPDELYFERIASNDEESADDSFDESDEEEPLNNH
* HISTTQHTDINPEKSGSGYSVWFRDTEDTSPQPLHAPPDYSRVVKRLKSILK
* >PQ082960.1 Suid alphaherpesvirus 1 isolate HN5 gE (US8) gene, complete cds [Translated Protein]
* MRPFLLRAAQLLALLALALSTEAPSLSAETTPGPVTEVPSPSAEVWDDLSTEADDDDLNG
* DLDGDDRRAGFGSALASLREAPPAHLVNVSEGANFTLDARGDGAVLAGIWTFLPVRGCDA
* VSVTTVCFETACHPDLVLGRACVPEAPEMGIGDYLPPEVPRLRREPPIVTPERWSPHLSV
* LRATPNDTGLYTLHDASGPRAVFFVAVGDRPPAPADPVGPARHEPRFHALGFHSQLFSPG
* DTFDLMPRVVSDMGDSRENFTATLDWYYARAPPRCLLYYVYEPCIYHPRAPECLRPVDPA
* CSFTSPARARLVARRAYASCSPLLGDRWLTACPFDAFGEEVHTNATADESGLYVLVMTHN
* GHVATWDYTLVATAAEYVTVIKELTAPARAPGTPWGPGGGDDAIYVDGVTTPAPPARPWN
* PYGRTTPGRLFVLALGSFVMTCVVGGAIWLCVLCSRRRAASRPFRVPTRARTHMLSPVYT
* SLPTHEDYYDGDDDDDEEAGVIRRRPASPSGDSGYEGPYASLDPEDEFSSDEDDGLYVRP
* EEAPRSGFDVWFRDPEKPEVTNGPNYGVTANRLLMSRPA
* >AY864513.1 Drosophila simulans strain ZIM-12 hemomucin (Hum) gene, partial cds [Translated Protein]
* LQGLYVSACRSN
* >MK867787.1 Microliabum humile isolate HUM internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence [Translated Protein]
* SNPAEQNDT
* >LT717484.1 Lasianthus cyaneus chloroplast partial rbcL gene for DNA, specimen voucher USTH: 012472 [Translated Protein]
* FYVTHKQRLKQVLDSRLVLKSTN
* >LT717473.1 Lasianthus verticillatus chloroplast partial rbcL gene for DNA, specimen voucher USTH: 012464 [Translated Protein]
* ISPPNRD
* >HQ247764.1 Equid herpesvirus 2 strain BB9 glycoprotein H (gH) gene, partial cds [Translated Protein]
* FLAWWAIGGRGLATPSPSTPGFSGSSGSPGTRASVSATTRKILPTTKSVNYTEMIEKNPS
* LTIDLGNQTKYQLNWTDVVKVIPGELIEKMWEESNVTESLWFTLNKFTDVYKKDTIFKNF
* TGHFTTKYVCNVSQGEPNYNVSQREVKEIKEYDGKFGIPAPVVLS
* >NR\_152932.1 Entoloma mirum TUR K. Kokkonen 99/14 TUR ITS region; from TYPE material [Translated Protein]
* LNKLGWVAAGSQEHVHT
* >M81739.1 S.aureofaciens hydroxyurea resistance (hur) gene, complete cds [Translated Protein]
* DRRAGAGAARGGLRPGRGRGDPHGMGRGGGEGLRGDGDAGDAGGAGGREAGGGEGRVDVR
* RGRVRADPQGAGVAA
* >D00360.1 Bacteriophage phi-80 cor gene, complete cds [Translated Protein]
* LQHQYSRHTP

1.SORU D) c. Adımda bulduğunuz protein sıralarını Fasta uzantılı dosya olarak kaydediniz.

(Kod içerisinde otomatik olarak kayıt edilmiştir.)

1.SORU E) DNA sıralarının GC içeriklerini hesaplayınız.

* GC Contents:
* X98449.1: 40.71%
* PQ082960.1: 73.97%
* AY864513.1: 53.89%
* MK867787.1: 49.92%
* LT717484.1: 43.11%
* LT717473.1: 43.97%
* HQ247764.1: 43.55%
* NR\_152932.1: 43.09%
* M81739.1: 77.21%
* D00360.1: 50.32%

1.SORU F) DNA sıralarının global hizalarını bulunuz.

(Sıralama sonuçları çok uzun çıktığı için sadece 2 örnek ekledim. Örnek olarak LT717484.1’inLT717473.1 ve HQ247764.1 ile global hizalaması verilmiştir.)

**Alignment between LT717484.1 and LT717473.1: Score=421**

TTTTATGTCA-CCCACAAACAGAGACTAAAGCAAGTGTTGGATTCAAGGCTGGTGTTAAAGAGTACAAATTGACTTATTATACTCCTGAATACGAAACCAAAGATACTGATATCTTGGCAGCATTCCGAGTAACTCCTCAACCCGGAGTTCCGCCCGAAG-AAGCAGGTGCCGCGGTAGCTGCCGAATCTTCTACTGGTACATGGACAACCGTGTGGACCGATGGACTTACCAGTCTTGATCGTTACAAGGGGCGATGCTACCACATCGAGCCAGTTCCTGGAGAAGAAGATCAATATATTGCTTATGTAGCTTACCCCTTAGACCTTTTTGAAGAAGGT-TCTGTTACTAACATGTTTACTTCCATTGTAGG-TAATGTATTTGGGTTCAAAGCC-CTGCGT-GCTCTACGTCTGGAAGATT-TGCGAATCCCTATT---T-CTTATGTT-AAAACCTT-CCAAGGCCCGCCTCAC-GGCATCCAAG-TTGAGAGAGATAAATTGAACAAATACGGTCGTCCCCTG-TTGGGATGTACTA-TTAAACCTAAATTGGGT-TTATCT-GCTAAAAACTAC-GGTAGAGCGGTT-TA-TGAATGTCTTC-GCGGTGG-ACTTGATTTTACCAAA-GATGATGAA-AACGTGAACTCCCAACCA-TTTATGCGTTGGAGAGATCGATTCTTATTTGTAGCAAAAA

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----AT-T--TCCC-C---C-----C-----C------------CAA--C-----------AG-----A--G---------A---CT-AA-A-G----C----A-A--G------T-GC--C-TT----G--A----T-----C---GTT--------A-CAA--A---G--GC-G-A--T---G------CTAC-----C----AC-A-----T----CGA--G------C---C-----CGTT-------GC--TG----------GAG--A--------AG-A-AA-ATCAATATATTGCTTATGTAGCTTACCCCTTAGACCTTTTTGAAGAAGG-CTCTGTTACTAACATGTTTACTTCCATTGT-GGGTAATGTATTTGGGTTCAAAG-CTCTGCG-CGCTCTACGTCTGGAAGA-TCTGCGAATCCC----CCCTGCTTAT-TTTAAAA-CTTTCCAAGGCCCGCCTCA-TGGCATCC-AGGTTGAGAGAGATAAATTGAACAAATACGGTCGTCCCCT-ATTGGGATGTAC-AATTAAACCTAAATTGGG-GTTATC-CGCTAAAAACTA-TGGTAGAGCGG--ATAATGAATGTC-TCCGCGGT-GTACTTGATTTTA-CAAAAGATGATG-ACAACGTGAACTCCCAACC-CTTTATGCG-T-------T-G----------G-AG------

**Alignment between LT717484.1 and HQ247764.1: Score=358**

TTTTATGTCACCCACAAACAGAGACTAAA-GCAAGTGTTGG--ATTCAAGGCTGGTGTTAAAGA-GTA---CAAATTGACTTATTA-----TACTCC-TGAA-TACGAAACCAAAGATACTGA--TATCTTGGCAGCATTCCGAGTAACTCCTCAACCCGGAGT-TCCGC-CC-GAAGAAGCA-GGTGCCGC-G-GTAG-CTGCCGAATCTTCTACTGGTACATGGACAACCG-TGTG--GACCGATGGACTTACCAGTCTT---GATCGT-TACAAGGGGCG-ATG-CT-ACCACATCGAGCCAGTTCCTGGAGAAGAAGATCAATAT--ATTGCTTA-TGTAGCTT-ACCCCTTAGACCTTTT-TGAAG-AAGGTTCTGTTACT-AA-C-AT-GTT-T-A-CTTCCAT--TGT-A-GGTAAT-GTATTTGGGTTCAAAG-----CCCTGCGTGCTCT--A-C-G-TCTG-GAAGATT-TGCG-A--A-TCCCTA-T-TT-C----T-TAT-GT--TAAA--AC-CTTCCAAGGCCC--GCCTC--ACG-GCATCCAAGTTG-AG-AGA---G-ATA-AAT-TG--AACAAATACGGTCGTCCCCT--GTTGGG-ATGTACTATTAAACCTA-AA--T-TG-G-GT--T-TATCTGCTA--AA----AACTACGGTAGAGCGGTTTATGAATGTCTTCG-C-G-GTGGACTTGATTT-TACCAAAGATGATGAA--AACGTGAACTCCCAACCATTT-ATGCGTTGGAGAGATC--G--ATTCTT-A--T----TTGTA---G-CAAAAA--

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-TTT-T-T------------G-G-C---ATG---GTG--GGCTATT---GG--GG-G-----G-CG-AGGGC---TTG-C--A--ACGCCCT-CTCCCT---CTAC---ACC---G-----G-GGT-T-TT--CAG------G-GT--CT--T-----CGG-G-AT---CTCCTG--GAA-CACGG-G-CG-AGTGT-GTCTG-CG-A-C--C-AC-----CA-GGA-AA---AT-T-TTG-CC-A---AC--A--A--C--AAAGA--GTGT-CAA----C-TAT-ACTGA--A-AT---G--A--T--T---G-A-AA-A--AA-ATCCA-T-C-T-CTG-A-C--GA----TT-GA-----TCTG--GGAA---------AC-CAAACCA-AG-TATCAGC-T-CA-ACTG-GACGG--A-CG----T-GGTT--AAGGTGATCCC-G-G-G----GGAACTGAT-TGAGAAGA-TGTG-GGAGGAGT--CTAATGTTACGGAGTCT-TTGTGGT---TTACTCTT--AA----CAAG--T-TTAC-AG-AT----GTT-TA-TA-AAAAGGATACAATCT-TTAA-AAAT----T--T----TACG--GGGCA--T--T-TT--A-CTACAAAATATGTGTGTAATGT-T-T-C--CCAAGGGGAAC--C--TA-A-----TTAT-AATGT-TTC-TCAGAG-GGA---G----GT---AAA-A-GA--AATTAA-G-GAA-T-------A--TGAT--G--GGA-A-AT-TTGGGATTC--CAGCTCCAGTTGT-CCTGTC-----TG

1.SORU G) DNA sıralarının local(yerel) hizalarını bulunuz.

(Sıralama sonuçları çok uzun çıktığı için sadece 2 örnek ekledim. Örnek olarak MK867787.1’nin LT717473.1 ve HQ247764.1 ile local hizalaması verilmiştir.)

**Local Alignment between MK867787.1 and LT717473.1: Score=331**

1 T--CGAACCCTGCAGAGCAGAATGACACGTGAACATGTA--CTTGGAATCGGACGCCAAACGTGACTAACCATTGTTATGATCGTAGGTGTCCCC-CAAT-GTGCGAT-CATGATTCCTTTTACAG--G-GCACCATGAATGTATGT-TGGTTATAAACA-AACCCCCGGCACAACACGTGCCAAGGATAACAAAACTAAAAAGTGC-GCGTC-ATGT-G-T-ACCTCCGTTT-G-CGGTG-TGTGCACTGTTCGT--GTCAA--CT-T-TATAATCATAAAC--G---ACTCTCGGCAAC--G-G---A-T--ATCTC-GGC-T-CAC--GCATCGATGAAGAACGCAGCAAAATGCGATACTTGGTG-TG-AA--T-TGCAGAATCCCGTGAACCATCGA-G-TT-TTTG-AACGCAAG-TTGCGC-CCAAAG-CCATCTGGT--TG-AG-GGCACGTCTGCCT-GG--GC-GTCACGCATCGTATCGCCCCCCACCA-T-GA-CATGGTG--TCGGGGG-CGGAGTTTGGCC-TCCCGTACGTATGTTGCGGT-TGGCTTA-AAC--AGAAGTCTCTT---TTGGTCG---A-C-GC-ACGG----CTAGTGGT-G-GTT-G-ATAA-GACCT-TCGTCTGGCGAC-CGTT-TGT-CTA-GA----ACCATAA-G-TGAGCGCTTCTT-A-AA-G--A-C-CCCAATGTGTCATCT-TGTGATGATGC-TTCG-A

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2 TTTC---CCC--C----C-------C-C---AACA-G-AGAC-T--AA----A-G-C-AA-GTG-----CC-----T-TGATC----GT-T----ACAA-AG-GCGATGC-T-A--CC----ACA-TCGAGC-CC------GT-TG-CTGG--------AGAA------G-A-AA-A--T--C-A--AT------A-T----A-T--TGC-T-TATGTAGCTTACC-CC--TTAGAC----CT-T----T-TT-G-AAG--AAGGCTCTGT-T-A-C-T-AACATGTTTACT-TC--C-A-TTGTGGGTAATGTAT-T-TGG-GTTCA-AAGC-TC--T---G--CGC-GC----T-C--TAC---GT-CTGGAAGATCTGC-GAATCCC-----CC--C--TGCTTATTT-TAA---AA-CTT----TCC-AAGGCC--C--G-CCT-CA-TGGCA----T-CC-AGGTTG-AG--A-G-A--G-AT--------A--AATTGAACA-----AAT------AC-G-G--T---CGTCCC---C-TA--TTG-GG-AT-G--TACAA-TTA-AA--C-C-TAAATTGG--GGTTATCCGCTA---AAAACTA-TGGTAGAG--CGGATAATGA---AT-GTCT--C--CGCG--GTGTACT-TGATTTTA-CA-AAAGATGA--------TGACAACGTGAACTCCCAA-----C--C-CT-T--T-ATGCGTT-GGA

**Local Alignment between MK867787.1 and HQ247764.1:** Score=338

1 TCGAACCCTGCA---GAGCAGAATGACACGTGAACATG--TACTTGGAATCGGACGC-CAA-ACGTGA-CT---AAC-CA--T-TG---T-TATG-ATC-GTAGGTGTCCCC---CAATGTGCGATCAT--G--AT-TCCTTTT--A-CA-GGGCACCATGAATGTATGTTGGTTA-TAAA-CAA-ACCC-CC-GGCACAACACGT---GCCAAGGATAACAAAACTAAAA-AGTGCGCGTCATGTGTACCTCCGTTTGCGGTGTGTGCACTGTT-CGTGTCAAC-T--TT-ATAATCATAAA-CGAC-TCTCG-GCAACGGAT--ATCTCGGCTCACGCATCGATGA--AGAACGCA-GC-A--A----AA-TGCGAT---ACT-TGGTGTGAATTGCAGA--ATCCCGTG---AACCATCGAGTTTTTGAACGCAAG-T-TGCGCCCAA-AGCC-A-TCTG---GTTGAG-GGCACGTCTGCCTG-G-GCGTC--ACGCATCGTATCGCCCCCCACCATGACATG-GTGTCGGGGG--CG-GA-GTTT-------GGCC-TCC-CGTA--CGT--A----TGTTG--CGGTTGGC-TTA--A--ACAGAAG-TC-TC-T-T-T--TGGT--CGACGCACGGCTAGTGGTGG----T--TG-ATAA-GACCTTCGTCT--G-GCG-ACCGTTTGTCTAGAACCAT-AAGTGAGCGCTTCTTAAAG-ACCCCA-ATG-TGTC--A--TCTTGTG-AT----G----A-T-G-C-T-TC-G

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1 T-------T---TTTG-GC---ATG----GTG-----GGCTA-TTGG----GG--G-GC--GA-G-G-GCTTGCAACGC-CCTCT-CCCTCTA--CA-CCG--GG-GT----TTTC-A-G-G-G-TC-TTCGGGATCTCC---TGGAACACGGG---C--G-A-G--TG-T-G-T-CT---GC--GA-CCACCAGG-A-AA-A--TTTTGCC------AAC--AAC--AAAGAGT----GTCA-----A----------C------T--A----TAC-TG--AA-ATGATTGA-AA--A-AAATC--CATCTC-TG--AC-GATTGATCT-GG-----G-A---A--ACCA-AAC-CAAG-TATCAGCTCAACTG-GA-CGGAC-GTGGT-T-AA--G--G-TGATCCCG-GGGGAA-C-T-GA----TTG-A-G-AAGATGTG-G-----GAG--GAGTCT-AATGTT-A-CGG-A-GTCT---T-TGTG-GT-TTA--C-TC-T-T-----------A--ACA--AGT-T------TAC-AGATGTTTATAAAAAGG--AT--AC--AATC-TTTAAAAAT-TT-TACGG--GGCATT-TTACTACA-AA-AT-AT-GTGTGTAAT-GTTTC--C-CA-----A--GG-GGAACCTAAT-TATAATG---TT--TCTCAGAG-GGA--G---G--TA-AA--A-GAA---A-------TT-AAGGA----ATATGATG--GGAAAT-TTG-GGATTCCAGCTCCAGTTGTCCTGTCTG

1.SORU H )Pozisyon Sıklık Matrislerini (PFM) bulunuz.

(Pozisyon 1’den pozisyon 1954’e kadar devam ediyor. Çok uzun olduğu için bir kısmı yazıldı)

**Position Frequency Matrix (PFM):**

* Position 1: A=3, C=2, G=1, T=4, Gap=0
* Position 2: A=1, C=1, G=0, T=8, Gap=0
* Position 3: A=0, C=0, G=5, T=5, Gap=0
* Position 4: A=2, C=4, G=1, T=3, Gap=0
* Position 5: A=5, C=1, G=3, T=1, Gap=0
* Position 6: A=2, C=3, G=3, T=2, Gap=0
* Position 7: A=1, C=6, G=3, T=0, Gap=0
* Position 8: A=2, C=4, G=2, T=2, Gap=0
* Position 9: A=4, C=4, G=1, T=1, Gap=0
* Position 10: A=1, C=5, G=2, T=2, Gap=0
* Position 11: A=1, C=4, G=1, T=4, Gap=0

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* Position 1951: A=0, C=0, G=1, T=0, Gap=9
* Position 1952: A=0, C=1, G=0, T=0, Gap=9
* Position 1953: A=0, C=0, G=1, T=0, Gap=9
* Position 1954: A=0, C=1, G=0, T=0, Gap=9

1.SORU İ) Pozisyon Olasılık Matrisleri (Position Probability Matrix) bulunuz (Pozisyon 1’den pozisyon 1954’e kadar devam ediyor. Çok uzun olduğu için bir kısmı yazıldı)

**Position Probability Matrix (PPM):**

* Position 1: A=0.300, C=0.200, G=0.100, T=0.400
* Position 2: A=0.100, C=0.100, G=0.000, T=0.800
* Position 3: A=0.000, C=0.000, G=0.500, T=0.500
* Position 4: A=0.200, C=0.400, G=0.100, T=0.300
* Position 5: A=0.500, C=0.100, G=0.300, T=0.100
* Position 6: A=0.200, C=0.300, G=0.300, T=0.200
* Position 7: A=0.100, C=0.600, G=0.300, T=0.000
* Position 8: A=0.200, C=0.400, G=0.200, T=0.200
* Position 9: A=0.400, C=0.400, G=0.100, T=0.100
* Position 10: A=0.100, C=0.500, G=0.200, T=0.200
* Position 11: A=0.100, C=0.400, G=0.100, T=0.400
* Position 12: A=0.300, C=0.200, G=0.200, T=0.300

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* Position 1951: A=0.000, C=0.000, G=0.100, T=0.000
* Position 1952: A=0.000, C=0.100, G=0.000, T=0.000
* Position 1953: A=0.000, C=0.000, G=0.100, T=0.000
* Position 1954: A=0.000, C=0.100, G=0.000, T=0.000

1.SORU J) Pozisyon-Ağırlık Matrisleri (Position Weight Matrix)

(Pozisyon 1’den pozisyon 1954’e kadar devam ediyor. Çok uzun olduğu için bir kısmı yazıldı)

**Position Weight Matrix (PWM):**

* Position 1: A=0.263, C=-0.322, G=-1.322, T=0.678
* Position 2: A=-1.322, C=-1.322, G=-inf, T=1.678
* Position 3: A=-inf, C=-inf, G=1.000, T=1.000
* Position 4: A=-0.322, C=0.678, G=-1.322, T=0.263
* Position 5: A=1.000, C=-1.322, G=0.263, T=-1.322
* Position 6: A=-0.322, C=0.263, G=0.263, T=-0.322
* Position 7: A=-1.322, C=1.263, G=0.263, T=-inf
* Position 8: A=-0.322, C=0.678, G=-0.322, T=-0.322
* Position 9: A=0.678, C=0.678, G=-1.322, T=-1.322
* Position 10: A=-1.322, C=1.000, G=-0.322, T=-0.322
* Position 11: A=-1.322, C=0.678, G=-1.322, T=0.678

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* Position 1951: A=-inf, C=-inf, G=-1.322, T=-inf
* Position 1952: A=-inf, C=-1.322, G=-inf, T=-inf
* Position 1953: A=-inf, C=-inf, G=-1.322, T=-inf
* Position 1954: A=-inf, C=-1.322, G=-inf, T=-inf

NCBI veritabanından 10 adet Protein sırası indiriniz. (Protein.fasta)

2. SORU A) Protein sıranızda 5 uzunluklu bir motif arayınız.

(Motiflerin çıktısı çok uzun olduğu için 10 ayrı ID’den ilk 51 pozisyon yazılmıştır. )

**Protein ID: sp|P0A8V0.1|RBN\_ECOLI**

**Motif matches found:**

* Position: 1, Motif: MELIF
* Position: 6, Motif: LGTSA
* Position: 11, Motif: GVPTR
* Position: 16, Motif: TRNVT
* Position: 21, Motif: AILLN
* Position: 26, Motif: LQHPT
* Position: 31, Motif: QSGLW
* Position: 36, Motif: LFDCG
* Position: 41, Motif: EGTQH
* Position: 46, Motif: QLLHT
* Position: 51, Motif: AFNPG

**Protein ID: CAL8870498.1**

**Motif matches found:**

* Position: 1, Motif: MQVMA
* Position: 6, Motif: PRTLL
* Position: 11, Motif: LLLSG
* Position: 16, Motif: ALALT
* Position: 21, Motif: ETWAG
* Position: 26, Motif: SHSMR
* Position: 31, Motif: YFHTA
* Position: 36, Motif: VSRPG
* Position: 41, Motif: RGQPR
* Position: 46, Motif: FIYVG
* Position: 51, Motif: YVDDT

**Protein ID: ADD78563.1**

**Motif matches found:**

* Position: 1, Motif: MEGAE
* Position: 6, Motif: MSDIV
* Position: 11, Motif: PIPVP
* Position: 16, Motif: LRVAP
* Position: 21, Motif: TPDFT
* Position: 26, Motif: IKIET
* Position: 31, Motif: KDKTE
* Position: 36, Motif: DIRPR
* Position: 41, Motif: LISLK
* Position: 46, Motif: LTDNR
* Position: 51, Motif: GLEVD

**Protein ID: CAE7436266.1**

**Motif matches found:**

* Position: 1, Motif: MGKEL
* Position: 6, Motif: ALSLV
* Position: 11, Motif: IGATM
* Position: 16, Motif: GAGFK
* Position: 21, Motif: AATGQ
* Position: 26, Motif: SVKQI
* Position: 31, Motif: GKIGE
* Position: 36, Motif: AAAAT
* Position: 41, Motif: KKALS
* Position: 46, Motif: RIEKF
* Position: 51, Motif: RELKR

**Protein ID: XP\_017105059.2**

**Motif matches found:**

* Position: 1, Motif: MLGEN
* Position: 6, Motif: LETGK
* Position: 11, Motif: TDTTK
* Position: 16, Motif: TQELR
* Position: 21, Motif: CNIPR
* Position: 26, Motif: CPYRT
* Position: 31, Motif: NRAYN
* Position: 36, Motif: LWRHE
* Position: 41, Motif: ERHTL
* Position: 46, Motif: PLETK
* Position: 51, Motif: LLSCP

**Protein ID: AKN77479.1**

**Motif matches found:**

* Position: 1, Motif: MTTAT
* Position: 6, Motif: KGLAA
* Position: 11, Motif: ELKES
* Position: 16, Motif: TAKAH
* Position: 21, Motif: ADAEH
* Position: 26, Motif: SSFMS
* Position: 31, Motif: DLIEG
* Position: 36, Motif: RLDAE
* Position: 41, Motif: AFIRL
* Position: 46, Motif: QEQAW
* Position: 51, Motif: LFYTA

**Protein ID: AAB59857.1**

**Motif matches found:**

* Position: 1, Motif: MSKNK
* Position: 6, Motif: DQRTA
* Position: 11, Motif: KTLER
* Position: 16, Motif: TWDTL
* Position: 21, Motif: NHLLF
* Position: 26, Motif: ISSCL
* Position: 31, Motif: YKLNL
* Position: 36, Motif: KSVAQ
* Position: 41, Motif: ITLSI
* Position: 46, Motif: LAMII
* Position: 51, Motif: STSLI

**Protein ID: ARE59518.1**

**Motif matches found:**

* Position: 1, Motif: MSSKS
* Position: 6, Motif: STRIP
* Position: 11, Motif: APLML
* Position: 16, Motif: IARIT
* Position: 21, Motif: LILSC
* Position: 26, Motif: IRLTG
* Position: 31, Motif: SLDGR
* Position: 36, Motif: PLAAA
* Position: 41, Motif: GIVVT
* Position: 46, Motif: GDKAV
* Position: 51, Motif: NIYTS

**Protein ID: NP\_001091056.1**

**Motif matches found:**

* Position: 1, Motif: MTTHV
* Position: 6, Motif: TLEDA
* Position: 11, Motif: LSNVD
* Position: 16, Motif: LLEEL
* Position: 21, Motif: PLPDQ
* Position: 26, Motif: QPCIE
* Position: 31, Motif: PPPSS
* Position: 36, Motif: IMYQA
* Position: 41, Motif: NFDTN
* Position: 46, Motif: FEDRN
* Position: 51, Motif: AFVTG

**Protein ID: OAO94121.1**

**Motif matches found:**

* Position: 1, Motif: MNEKA
* Position: 6, Motif: NVSKE
* Position: 11, Motif: LNARH
* Position: 16, Motif: RKILE
* Position: 21, Motif: GLLKH
* Position: 26, Motif: PENRE
* Position: 31, Motif: CADCK
* Position: 36, Motif: TKGPR
* Position: 41, Motif: WASVN
* Position: 46, Motif: LGIFI
* Position: 51, Motif: CMQCS

2. SORU B) Protein sıralarının global hizalarını bulunuz. (Sıralamalar çok sayfa tuttuğu için global ve lokal için 2’şer örnekler ekledim.)

**Global Alignment between sp|P0A8V0.1|RBN\_ECOLI and CAL8870498.1: Score=120**

MELIFLGTSAG-V--PTRTRNVTAILLNLQHPTQSGLWLFDCGE-GTQHQ-L-LHT---AFNPGKLDKIFISHLHGDHL----FGL------PGLLCSRSMSGIIQPLT--IY-GP-----QGIREFVETALRISG--SWTDYPLEIVEIGAGEILDDGL---R-KVT--AYPL--EHPL-ECYG--YRI-EEHDKPGALNAQ---ALKA-AG----VPP--GP-LF-----Q-ELKAGK---TIT-------LE--DGRQIN---G----A-D---Y--L--------AAP-VPGKALAIFGD--T-------GPCDAA------LD----L----------------A---KG--V------DVMVHEATLDITME---AK-----ANS-------R-GHSS---TRQAA-T-LAR-EA---GVGKLII--TH------VS---S----RYDDKG-C--QH--L---L--R-ECR-S----IFP-----ATE-LANDFTV----F---------------------------N-------V----

| | | | | || | | | | | | | | | | | | || | | || || | | || | | | | | | | | | | | | || | | || | | | | | | | || | ||| | | | | | || | | | | | || | | | | | | ||||| | | | | | | | | | | | | | | || | || | | | | | | | | || | | | |

M----------QVMAP---R--T--LL-L-------L-L-----SG----ALAL-TETWA---G-------S-----H-SMRYF--HTAVSRPG----R---G--QP--RFIYVG-YVDDTQ----FV----R---FDS--D---------A--------ASPRMK--PRA-P-WME---QE--GPEY--WEE---------QTRKA-KANA-QTDRV--DLG-TL-LRYYNQSE---G-GSHTI-QKMYGCDL-GPDGR---LLRGYHQHAYDGKDYFALNEDLRSWTAA-DV---A-A----QNTQRKWEAAG---AAEQVRAYL-EGECLEWLRRYLENGKETLQRAERPK-THVTHHPISD---HEATL-----RCWA-LGFYPA--EITLTWQRDG---EEQT-Q--DTEL--VE-TRPG-G----DGT-FQKWGAV-VVPSGEEQRY----TCHVQHEGLPEPLTLRWE--PSSQSTI-PIVGIVA--GLA----VLGAVFIGAVVAAVMWRRKSSGGKGGSYSQAASNDSAQGSDVSLTA

**Global Alignment between sp|P0A8V0.1|RBN\_ECOLI and ADD78563.1: Score=132**

MELIFLGTSAG-----VPTRT-----RNVTAILLNLQHPTQSGLWLF-DCGEG-TQHQLLH----TAFNPGKLDK---IF----ISHLHGDH-LF----GLPG----L-LCSR----S-----MS---G--I---I----QPLT------I-----YGPQG----IREFVET--ALRIS----GSW-----TD-YPLEI---V-E----IGA---GEILD--DGLRKVTAY-PLE-------HPLECYGYRIE----EH-DKPGA-----LNAQA-LKAA-G-V-----------PPGPLFQELKAGK-T-----IT-LEDG----RQIN-GAD-YLAAPVPG--KALAIFG--DTGPCDA-----AL---DL---A--KG--VD---------VM--VHE-A-----TLDI-------TMEA------KA-----NSRG-H-SSTRQ--A--A-------------TL----AR----E--------A-G---VG----K-LIITH--VS-SRYD-DKGCQHLLRECRSI-FPAT-----ELA---N-DFT-VFN-V-----

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ME----G--A-EMSDIVP---IPVPLR-V-A-------PT-------PD----FT------IKIET-----K-DKTEDI-RPRLIS-L----KL-TDNRGL--EVDQLDL---VLDDSDGQLVM-PPFGAKIVLEIGWKGQPL-ADKGSYIIDQVTY--QGAPDTI-----TVVA-R-SADFSGS-LDVKITDSYP---DMTVGEVVDKI-AKRNG--L-TSD----V---RP-EIAKKKIKH--------I-DQTQE-TD--G-TFITRL---AML---VGAVAAIKDKTLLFFPPG---Q----G-VTVSGKPI-PL---LNLNRQ--DG-DKY-------EYK-L--F-KRD----D-YSGVEA-KWYD-QKKAQQKGITV-NTIPPATPAV-NPVH-PAAKNIPT--IGQQDPGKT---YVFGSNK-KLFVLN---THFSS--QEEAEEAAKAKWQELQRNRATLKILLA-LGAAELIPETPVKAQGFKSV-IDNQKWL-IT-NIV-HS---LDK----------S-GF--TTMLYLEL-MVENVD--YV--LVEKQAG

2.SORU C) Protein sıralarının local(yerel) hizalarını bulunuz.

**Local Alignment between sp|P0A8V0.1|RBN\_ECOLI and CAE7436266.1:**  **Score=242**

1 M--EL-----I-------FL----G---------------T----S--------------A--------------GV--------PTR--TRNV------------------------------------------------T---AIL------L---------------NL--QH-------------P--------------T---------Q------S-----G-LW-----------------------L--F--DC----G---E--G-------T---------QH-Q--L-------LH---------------T-A------F----N--------------P------G------KLD----KI----F------I--SH---------------LH--------------G---DHLFGLP-----------GL------LCSR---S--------M-----------------S-G-I----IQ-------P---L------------T------------------------I------Y------GPQG--I--------RE---------F----------VE-------T-ALR----I------------------S------G---SW-TDY-----------------PLE--I-------VE--------IG-A--------GE---------------------------------------------------I------------L-D--DG--LRK------------V--T-A--Y--P-LEH---------P-----L--------ECY---G---------------Y---RIEEHD------K---P------------G---ALN-AQA--LKA--A--G---VPPGP-----L---------------F-QE-------L----KAG-----------------------K-----TI---T--L------------------E-------------------D----------G---------R----Q-------------IN-----GA------------------------------D----------Y-------------------------L-------AA-----P-V-----------------------------------P-G-------K----------------A---LAI-----------F------------G-D---T-G---PCD--------A-ALD----------L-A-K-G---------V---D--------VM--V--------------H-----------EA-T--------------L-D-------I-------------------T----M-E------AK-----------------AN-------------S---------R-------------GHS----ST--R--------------Q---A--------AT--L-----A-----RE-A-------G--V-----------------GKL----II-----------TH--V-------------S---------S----------------------------R-YD------------------------D-----------------------K------GCQ-----------------H-L------------LR-------EC------R--S----I-------F---------------------P--------A--------T------------------------------E-L----A-------------------N-----D-------------FT-----V------------F----N-----------------------------------V

| || | | | | | | | ||| || | | | | || | | | | | | | | | | | | | | | | | | | | | | | | || | | | | | | | |||| || | | | | | | | | | | | | | | | | | | | || | | | || | || | || || | | | | | | || | | | | | || | | | | | |||| | | | || | | | | | | | | | | | ||| | || | | | | | | | | || | | | || | | | | | | || | | | | | | | | | | | | | | | | | || | | | | | | | | | | | || | | | | | | | | | | | ||| || | | | | | | | | | | | || | | | | | | | | | | | | | | | | | |

1 MGKELALSLVIGATMGAGF-KAATGQSVKQIGKIGEAAAATKKALSRIEKFRELKRGLGEAKRSFEQAERQAESLG-REFHQTQKPTRDLTR--RFEEAKRAAASARKAYYSQAEQLQQLRRDADAAGQSFRGLSQQQKQLRTVGMA-LGSAQRDLAAIGTQHDALMQRRANLRGQ-LTDVVALGLALGAPVKAAIGFESAMADVTKALNDISPDQIKELRKSILDMSGDL-GMAADQIADITAAAGRAGIPVGELQQFTAD-AIKMGVAFEIVGEQAGGAMTGIRNIFKLTQ-DQTVLTGDAINAL-GNSMDAREAEILNILTRAGATADMFGLTSNQTAALGATFLQLKTPVAVASTGINAMLNKL-VNSEK-QTGAFQEGLEAIGLS-ASEMRRMIEEDAQAAL-LTFLDAVSTADDVQGTLFD-LFGL-EYADDITKLVSGLDQYKAAL---ATVSDETKIAGGMNDEYQKKLATTERQLQNSKGKIAAMAI-VLGSRLLPAVKLAGSVVGGLAGGVTWLAETFPGFTTVVVGATAGLMALKITTIGLGYAWTFVAG--GALIVKKALVLLR-VAALLTNGAFFKLALGAIPAV-VAGMKAMTLAL-MANPIGLVVGGIALGAAAIIANWSTVKQWFGDFWSWMT--GGTGSAWEAIKTVMSFSPL-GLIMKAWGPAVEFLSGVMDTIGRAVSAATSFFG-DDTAAAVSQPGATRRGRGRAAGAAVAASLAVAPAAASAAPSTTVNDSSTTTITIVQQPGEDAEALADKVD-KELR-RQHEWRWPSQERVGRTPALQYTGPGLE-RVELNGVIYPHYKGGLGQIDSMRAE--ADEGTPLILVDGRGRVWGKYAITRIEE--TQAVLAKDGGPRRQTFMLELAAYGEDDAL-CA-AVGL--VCALKGDDCV--G-QTRRSLDSTDASVMAVEINTSFCQ-KATGFSCLTFNEKAGLGRSNAVLRRFDGAISRRCLAVDKSVFVKTIIDLTIRLMPCGVCAAIRKGADALAVEEQLKFTHGLMLRALVTPGNDNSQPNHLVANGSDITPLIADRLISLQVTDEAGDESDAAVI-TLDDRGAGLALLPTGAKLSISIGLKETGLTSLGLYTVDELELSGPPDTYVIRAKAADMRDAMKAPRTRTWHDTTLGTIVGNIAADNGLTPRVAAALASVAIAHEDQTEESDLHLLRRLAKEHDAISKPAGGHLLFLPKGQSTTVSGRQLPTVTIARKELA-DWRMVAAKRGRFQSVEAVWRDKEAGSDEVVTAGSGNP--VKRLRRTYANA--ERAKQAAAAELRASKRGEATLELTMAVGRADLFAEAKLSV-AGVRTGINGAWTITRVEHSVNSSGWITRVEAETPTGHSMKHSRKNTPLPDWHGRHFPIHSRRPDAEYLERWRDYIKKTGRPEMFEGVSTTPA-PPEFPLELLSIEIPVPIA-KREDQDKVPCPVCSPDSPKFTKGRMAYFPMEKVVRFIGH-KCAAS-HFRDGHYRMAEEEYRREQQRIACQEFLRKNA-GKLPEIVSAGKSLLR-IAHNAKQVHGHMVRHRDLAQFLRNKIRVDDGKLSVFEIIPEFARANPMDRT-REVTFGYLRGKPAVANSFDAPVKIANSIKALDDFLPLAGEDVATKIDTMPEAAQDRAY-TAILSNYNVLARQAQKLAEFVSFFDGNNIRALSRLTLSNTSLEPVVPAKPVAPYIG--GKKNLATRLVARIETIPHDLYAEPFVGMGGVFLRRKSAPRAE-VINDVNREVSNFFRILQRHYVAFLQMMQYQLTTRAEFERLSRVDPNTLTDLERAARFLYLQRTAFGGLVRKQSFGVSPDRPGRFNVTRLAPMLEDLHTRLAGVVIECLSWEVFLARYDRPNALFYLDPPYWGSERDYGDAF-GREDFVRLAEVLRGLKGRFLMSLNDHPGVRETFHDFHFEEVQVARTVGRSASSRKSVGEV

**Local Alignment between sp|P0A8V0.1|RBN\_ECOLI and XP\_017105059.2: Score=138**

1 MELIFLG----TSAGVP-TR-T------R-NV-------T--AILL-NLQ--HP----TQSGLW-LFDCGEGTQHQ-LLHTAFN--PGKLDKIF-I-SH------L--H-GD--HLFGLPGLLCSRS-M-------SGI--IQPLTIYGPQGIREFVETALRISGSWTDYP----LEIVEIGAG---EIL-----D----------------DG----L------RKVTAYP-LE--HPL-ECYGY-R---IEEHD--KPG-A--LNA---------QA---LK---AAGVPPGP------LF-------Q-------E--LKA----GK------TI-TL---ED---GR----Q-I--N--GADY-LAA-------PVP-GKA---L--AIFG--------DTGPCDA--ALD-LAKGV--DV---MVH-EATL---D--ITM-EA--KAN---SR-----G-HS--STRQAATLAREAGVGK-L------I--ITH-----V---S----SRYD-----DK-GCQH------------L------------LR-----------EC-R--SIFPATE--------L-AN----------DF------T

| || | | | | | | | | || | | | | | | || | | | | | | | | | | | || || || | || | | | | | | | | | | | || | | | | | | | | | | | || | || | || | | ||| | || | | || | | | | | | | | | | | | | || || | | | | | | | || | | | | | | | | | | | | | | | | | || | | | | | | | |

1 M----LGENLET--G--KT-DTTKTQELRCN-IPRCPYRTNRA---YNL-WRH-EERHT---L-PL----E-T---KLL-----SCP------FCIYS-TDKVSNLKRHIG-IRH----P------STMDDPDDPESG-KMIQ--TI--P------VE---R---S-T---KVHCL--V-I--GCKYE--TNRPYDMKRHMMVHNNREKSHRD-YKCSLCMYSSDRK--A--NL-KRH--HE----LRHSGI-E-DAIK--TADEL--EYEERLLEEQAQEQL-DQVAA-----PAKSMKHLFSSFEDDIQDNSSAVQEEELKADYIYG-ENAPLITIST-GKSE-ILQGRRIEKQVIAVNVNG---EL--RWFQSIDP-PPG-ASNKLQLA---MQEEQEQLD----D-ELAL-SLA---EED-QKSM--ME--LLPEDEPI--KE-EPKA-VVWS-WSTPNGIH-HFS-----T------V--DLETPTTEIQKI--DDLEEVLLDSKVTPS--DFPAWWD-DG-Q-YTKMQKNQTFRDLRTKPSQASVQRILRIIYDIYYKPFKE-KRKRS-----EVFQIKDSWLCA-TRMSRMQIIKD-MYSKQGT

2.SORU D) b ve c şıkları için ayrı ayrı kendiniz belirlediğiniz farklı match, mismatch ve gap skorları için yeniden hizalamaları yapınız.

**GLOBAL İÇİN = match\_score=2, mismatch\_penalty=-1, gap\_open\_penalty=-2, gap\_extend\_penalty=-0.5**

**LOKAL İÇİN = match\_score=3, mismatch\_penalty=-2, gap\_open\_penalty=-5, gap\_extend\_penalty=-1**

(Global ve lokal hizalama sonuçları çok sayfa tuttuğu için her biri için 2’şer örnek ekledim.)

**GLOBAL SONUÇLARI:**

**Global Alignment between sp|P0A8V0.1|RBN\_ECOLI and CAL8870498.1: Score=-84.5**

MELIFLGTSAGVPTRTRNVTAILLNLQHPTQSG-LWLFDCGEGTQH--QLLHTAFN-PGKLDKIFISHLHG---DHLFGLPGLLCSRSMSGIIQP--------LTIYGP--------------QGIREFVETALR---IS--GSWTDYPLEIVEIGAGEILD-DGLRKVTAYPLEHPLECYGYRIEEHD-KPG-ALN------------AQ--ALK--AAG----VPPGPLFQELKAGKTITLEDGRQINGADYLAAPVPGKALAIFGDTGPCDAALDLA---KG-V------DVMVHEATL----------DITMEAKANSR-GHSSTRQAAT-L--AREAGVG---KLIITHVSS----RYDDKGC--QH------L-LR-ECRS---IFP-----ATELANDFTVF---------------------------N-------V----

| ...| | || ||.| .|| |.|.....| .| ...|||.. ||.....|| ..| |..| .|..|....| ....|| |..|....|.|| .| ||.| | ....|..|. || | | | .||.....| |.. ||| || ..| ||| | ...| | | ..||..| .|| ..|| .| |..| |. | | ||||| .|| ....| |...| | .| | .|..|.| |.....|.| || .| || | || |..| | | | .||....|| | |

M-----QVMA--P-RT------LLLL----LSGALALTETWAG-SHSMRYFHTAVSRPGRGQPRFI--YVGYVDDTQF-------VRFDSDAASPRMKPRAPWMEQEGPEYWEEQTRKAKANAQTDRVDLGTLLRYYNQSEGGSHT-----I-QKMYGCDLGPDG-R------L---L--RGYHQHAYDGKDYFALNEDLRSWTAADVAAQNTQRKWEAAGAAEQV-RAYL--E---G--ECLEWLR-----RYL---ENGK------ET------LQRAERPKTHVTHHPISD---HEATLRCWALGFYPAEIT---LTWQRDGEEQT-Q-DTELVETRPGGDGTFQKWGAVVVPSGEEQRY---TCHVQHEGLPEPLTLRWEPSSQSTI-PIVGIVA-GLAVLGAVFIGAVVAAVMWRRKSSGGKGGSYSQAASNDSAQGSDVSLTA

**Global Alignment between sp|P0A8V0.1|RBN\_ECOLI and ADD78563.1:** Score=-80.5

MELIFLG--TSAGV---------PT----------------RTRNVTAILLNLQHPT--------QSGLWLFDC-GEGTQHQLLHTAFNPGKLDKIFISHLH-GDHLFGLPGLLCSRSMSGIIQPLTIY-G-PQGIREFVETALR---ISGS----WTD-YPLEIVEIGAGEILD-----DGL----RKVTAYPLE-H---PLECYGYRIEEHDKP-GALNAQALKAAGV-PPGPLFQELKA-GKTITL-----EDG---------RQINGADY---LAAPVPGK-A--LAIFGDTGPCDA--A----LDLAK-----GV-D-----V-------MV---H-----EATLDITMEA-KANSRGHSSTRQAATL-------ARE--------A-G---V---GK-LI--ITHVSSRYDDKGCQHLLRECRSIFPATELANDFTVFNV----------

|| | .|..| || |.| .|.|.| | |..|.|.|. | ||....| | .|| .|. | ..|.| | ....|.||...| | | |..| .| .| | .||| .|| ||...| ||..| .|| |...|.... | ..|..|..|...... ||..|...|.... ||| |.... ||.|.| .|| | .|| .|.....| | ..|...|.| .| | ...|| |. | | .| | || .|| || ......|..||| |.| | | | .| || |.| | .|| |.| .|.|.....|.||

ME----GAEMSDIVPIPVPLRVAPTPDFTIKIETKDKTEDIRPR---LISLKL---TDNRGLEVDQLDLVLDDSDG-----QLVMPPF--G--AKI---VLEIG--WKGQP--L-ADKGSYIIDQVT-YQGAPDTI--TV-VA-RSADFSGSLDVKITDSYPDMTV----GEVVDKIAKRNGLTSDVRPEIAKKKIKHIDQTQETDGTFITRLAMLVGAVAAIKDKTLLFFPPG---QGVTVSGKPIPLLNLNRQDGDKYEYKLFKR----DDYSGVEAKWYDQKKAQQKGITVNTIP-PATPAVNPVHPAAKNIPTIGQQDPGKTYVFGSNKKLFVLNTHFSSQEEA-----EEAAKA--KWQELQRNRATLKILLALGAAELIPETPVKAQGFKSVIDNQKWLITNIVH-S---LDK----------SGF-TTMLYLELMVENVDYVLVEKQAG

**LOKAL SONUÇLARI:**

**Local Alignment between sp|P0A8V0.1|RBN\_ECOLI and CAL8870498.1: Score=15**

231 HEATL

|||||

221 HEATL

**Local Alignment between sp|P0A8V0.1|RBN\_ECOLI and ADD78563.1: Score=12**

23 LLNL

||||

210 LLNL