```
------------------------------------------------------------------
Seq1 = ">gi|807209|gb|S75265.1 C/EBP alpha"
Seq2 = ">gi|192381|gb|M62362.1|MUSCATENBP Mouse CCAAT/EBP gene"

        Local Alignment Number 1
        Similarity Score:  1540
        Match Percentage:  64 %
        Begins at (55,2) and Ends at (553,511)

      0 Sp1 .    :    .    :    .    :    .    :    .    :    .    :
     55 CGCCCTCCGCCCCCCACCCCTACCCCGTGCAGCCTCGGGATACTCCTGGGCTCCCGGCCG
        |||:|:||: ||:|||||:|:-||:||: |:|||||  : ||:||||:|||||||| : :|
      2 CGCTCCCCAACCTCCACCTCC CCTCGCTCGGCCTCTATATGCTCCCGGGCTCCCTAGTG

     60     .    :    .    :    .    :    .    :    .    :    .    :
    115 T GGCTGGATACGGGCGCCTAGGGCAGGCAGG     AGGAGGGGGCCCCCGCTACCGAC
        |-||||||| ::|||:| || :|------|||-----||||||||  ||: :|:|| |||
     61 TTGGCTGGAAGTGGGTGACTTAG      AGGCTTAAAGGAGGGGCGCCTAACCACGGAC
             NF-1/NF-Y
    120  USF.    :    .    :    .   :  Sp1    :    .    :    .    :
    169 CACGTGGGCGCGGGGGCGACGGCCGGGCCGGGGGCGGAGTTGGAGCGAGCGCCGCGGCTC
        |||||| |:||||||||||:||   |||||||  ||: | :| || :  : |  ||:||
    115 CACGTGTGTGCGGGGGCGACAGCGCCGCCGGGGTGGGGCTGAGCGCTGCAAGCCGGGTTC
         USF, Myc/Max               CUP/Sp1
    180     .    :    .    :    . Sp1:    .    :    .    :    .    :
    229 TGCTGGGCGCGCTGGAGGCGGTGGGCGTTGCGCCGCGGCCTGCCTGGGGAGCGCGGCGCT
          || |  |||| |||| |:|||||||||||||||:||::|| :|| ------------|
    175 GCCTTGCAGCGCAGGAGTCAGTGGGCGTTGCGCCACGATCTCTCTC            CA
                           Sp1, C/EBP
    240     .    :    .  Sp1    .    :    .    :    .    :    .    :
    289 GTNCCGCGCTGGTTCGCCGCCCCATGCCGGC                    CGCGCNCT
         |  |:|  || |:|  | || | ::||| |---------------------|| || ||
    223 CTAGCACTATGCTCCCGCCCCACTCACCGCCTTGGAAAGTCACAGGAGAAGGCGGGCTCT
                                        NF-kappaB
    300     .    :    .    :    .    :    .    :    .    :    .    :
    328 AGGACCCAGCAGGCGCCGCNCCGCCGCAGCCCGGGGACAGAGGCCCCCTCGGACTCTAGG
        |:|||||||||||:||:: |::|:|  |||:  |: | |||:||| :|:|||| |:|||
    283 AAGACCCAGCAGGCACCATCCTACTGGCGCCTTCGATCCGAGACCCGTTTGGACACCAGG
                                                          BTE
    360     .    :    .   :TATA.    :    .    :    .    :|->+1    :
    388 GGGCGACGCGGCCTGCCGGGTATAAAAGCTGGGCCGGCGCGGGCCGGGCCATTCGCGACC
        ||||||:|| | |: :|---|||||||| |  || ||||||||| ||||||||||||||
    343 GGGCGATGCCGACCCTC  TATAAAAGCGGTCCCCGCGCGGGCCTGGCCATTCGCGACC
                          TATA                          |->+1
    420     .    :    .    :    .    :    .    :    .    :    .    :
    448 CGGAGGTGCGCGGGCGCGGGCGAGCAGGGTCTCCGGGTGGGCGGCGGCGA      CGCC
        ||:|| |||||||||||:|| ||: ||| | |:|||||||||||||||------||||
    400 CGAAGCTGCGCGGGCGCGAGCCAGTTGGGGCACTGGGTGGGCGGCGGCGACAGCGGCGCC

    480     .    :    .    :    .    :    .    :    .    :
    502 CCGCGCAGGCTGGAGGCCGCCGAGGCTCGCCATGCCGGGAGAACTCTAACTC
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
    460 ACGCGCAGGCTGGAGGCCGCCGAGGCTCGCCATGCCGGGAGAACTCTAACTC
```