```
------------------------------------------------------------
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:  186
        Match Percentage:  83 %
        Begins at (166,112) and Ends at (201,147)

      0     .    : USF.    :    .    :Sp1 .
    166 GACCACGTGGGCGCGGGGGCGACGGCCGGGCCGGGG
        |||||||| |:||||||||||:||   |||||||
    112 GACCACGTGTGTGCGGGGGCGACAGCGCCGCCGGGG
               USF, Myc/Max        CUP/Sp1

        Local Alignment Number 2
        Similarity Score:  176
        Match Percentage:  86 %
        Begins at (237,183) and Ends at (265,211)

      0     .    :    .    :Sp1 .
    237 GCGCTGGAGGCGGTGGGCGTTGCGCCGCG
        |||| |||| |:|||||||||||||:||
    183 GCGCAGGAGTCAGTGGGCGTTGCGCCACG
                      Sp1, C/EBP

        Local Alignment Number 3
        Similarity Score:  940
        Match Percentage:  86 %
        Begins at (408,360) and Ends at (553,511)

      0 TATA.    :    .    :    .    :|->+1    :    .    :    .    :
    408 TATAAAAGCTGGGCCGGCGCGGGCCGGGCCATTCGCGACCCGGAGGTGCGCGGGCGCGGG
        |||||||| |  || ||||||||| |||||||||||||||:|| ||||||||||||:|
    360 TATAAAAGCGGTCCCCGCGCGGGCCTGGCCATTCGCGACCCGAAGCTGCGCGGGCGCGAG
        TATA                            |->+1
     60     .    :    .    :    .    :    .    :    .    :    .    :
    468 CGAGCAGGGTCTCCGGGTGGGCGGCGGCGAC      GCCCCGCGCAGGCTGGAGGCCGC
        | ||: ||| | |:||||||||||||||||||------||| ||||||||||||||||||
    420 CCAGTTGGGGCACTGGGTGGGCGGCGGCGACAGCGGCGCCACGCGCAGGCTGGAGGCCGC

    120     .    :    .    :    .    :
    522 CGAGGCTCGCCATGCCGGGAGAACTCTAACTC
        ||||||||||||||||||||||||||||||||
    480 CGAGGCTCGCCATGCCGGGAGAACTCTAACTC
```