INPUT:  
\*\*\*\*\*\*

>s1  
ACATGCTACACGTATCCGATACCCCGTAACCGATAACGATACACAGACCTCGTACGCTTG  
CTACAACGTACTCTATAACCGAGAACGATTGACATGCCTCGTACACATGCTACACGTACT  
CCGAT   
  
>s2  
ACATGCGACACTACTCCGATACCCCGTAACCGATAACGATACAGAGACCTCGTACGCTTG   
CTAATAACCGAGAACGATTGACATTCCTCGTACAGCTACACGTACT   
CCGAT

OUTPUT:  
\*\*\*\*\*\*\*\*

Scores:    match = 1, mismatch = -2, h =-5, g = -2

Sequence 1 = "s1", length = 125 characters  
Sequence 2 = "s2", length = 111 characters

s1 1 ACATGCTACACGTATCCGATACCCCGTAACCGATAACGATACACAGACCTCGTACGCTTG 60

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

s2 1 ACATGCGACACTACTCCGATACCCCGTAACCGATAACGATACAGAGACCTCGTACGCTTG 60

s1 61 CTACAACGTACTCTATAACCGAGAACGATTGACATGCCTCGTACACATGCTACACGTACT 120

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

s2 61 CTA-----------ATAACCGAGAACGATTGACATTCCTCGTACA---GCTACACGTACT 106

s1 121 CCGAT 125

|||||

s2 107 CCGAT 111

Report:

Global optimal score = 55

Number of:  matches = 105, mismatches = 6, gaps = 14, opening gaps = 2

 Identities = 105/125 (84%), Gaps = 14/125 (11%)