Both global and local alignments achieved the same score of 1810, when using the BLOSUM62 matrix, and using the parameter dx.
But when the parameter for both local and global is set to ds with open and extend gap penalties equal to -4, then the local alignment does a better job since it gave a score of 133, while global alignment gave a score of -241.

The Accession Number for seq1.txt is NP_001341538. The organism is human (homo sapiens). It is the sequence for serine/threonine-protein kinase B-raf isoform 2.

The Accession Number for seq2.txt is NP_659542. The organism is a house mouse. Its the protein sequence for a protein called transcription intermediary factor 1-alpha isoform 1.

After experimenting with *penalize_extend_when_opening* and *penalize_end_gaps,* I still got the same global alignment score of 1810 when the parameter is set to dx.

When the parameter is set to ds, with both open and extend gap penalties equal to -4, then:
1. When *penalize_extend_when_opening* = True and *penalize_end_gaps = (False, False), the score = 10*

2. When *penalize_extend_when_opening* = True and *penalize_end_gaps = (True, True), the score = -780*

3. When *penalize_extend_when_opening* = True and *penalize_end_gaps = (True, False), the score = -775*

4. When *penalize_extend_when_opening* = True and *penalize_end_gaps = (False, True), the score = -186*

5. When *penalize_extend_when_opening* = False and *penalize_end_gaps = (False, False), the score = 108*

6. When *penalize_extend_when_opening* = False and *penalize_end_gaps = (True, True), the score = -241*

7. When *penalize_extend_when_opening = False* and *penalize_end_gaps =
   (True, False), the score = -240*

8. When *penalize_extend_when_opening = False* and *penalize_end_gaps =
   (False, True), the score = 104*