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#=====
#
# Aligned_sequences: 2
# 1: SPPV_02
# 2: 02
# Matrix: /ca.virology/services/needle/matrices/EBLOSUM65
# Gap_penalty: 10.0
# Extend_penalty: 0.05
#
# Length: 311
# Identity:      240/311 (77.2%)
# Similarity:    240/311 (77.2%)
# Gaps:          71/311 (22.8%)
# Score: 1283.0
#
#=====
SPPV_02          1  MITSSTKNLFFFVNINSLDKRKRSFSFLSYVKILERKKRFVFKFLVNNRK      50
02              1                                           0
SPPV_02          51  KSSVVSRRWFVSTIRHKKQPTNMSSLTFFIFCLQLFIFTSTVSGISIKRCT      100
02              1                      MSSLTFFIFCLQLFIFTSTVSGISIKRCT      29
SPPV_02          101 EEENNTWEIEVGLCIQTENFRAIKTGCYKIQGPGLLTEGNGFKIFAHDD      150
02              30 EEENNTWEIEVGLCIQTENFRAIKTGCYKIQGPGLLTEGNGFKIFAHDD      79
SPPV_02          151 CSKEKTQNNFILDVNEAVYALGKYVYMEISTSNITTLNSLPQCAKRISL      200
02              80 CSKEKTQNNFILDVNEAVYALGKYVYMEISTSNITTLNSLPQCAKRISL      129
SPPV_02          201 SISCDQVTTEMKSYVESVSFKDYDLEFVITTDISCVKHVSSSVIVRNECE      250
02              130 SISCDQVTTEMKSYVESVSFKDYDLEFVITTDISCVKHVSSSVIVRNECE      179
SPPV_02          251 KKYISTGKKIFGFNNKIDCSAVKVFSEHVNYLKTCSVGKFDRKKYYEHQHN      300
02              180 KKYISTGKKIFGFNNKIDCSAVKVFSEHVNYLKTCSVGKFDRKKYYEHQHN      229
SPPV_02          301 YIKKIFHHNEL          311
02              230 YIKKIFHHNEL          240
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