

Needleman–Wunsch Alignment Report

Match	1
Mismatch	-1
Gap penalty	-2

Sequence 1: seq1: ACGTACGT

Sequence 2: seq2: GATTACA

Path 1

ACGTACGT
GATTAC-A

Length	8
Matches	3 (37.50%)
Gaps	1

Path 2

ACGTACGT
GATTACA-

Length	8
Matches	3 (37.50%)
Gaps	1

Score Matrix Heatmap

