

Computation of alignment scores:

In the table below, the two amino acid sequences **KNAAWPG** and **KQWAALSPG** are aligned in two different ways.

Compute alignment scores for alignment 1 and 2 using both substitution matrices BLOSUM-50 and ID-6,3 (next page). In both cases gaps are penalized using the affine gap penalties indicated at the bottom of this page.

	Alignment 1:	Alignment 2:
	KNAAW----PG : : :: KQ--WAALSPG	KN-AAW-PG : :: :: KQWAALSPG
Score, BLOSUM-50		
Score, ID-6,3		

Affine gap penalties:

Gap opening: -10

Gap elongation: -1

