

Practice example for global alignment of amino acid sequences
(based on Simplified Needleman-Wunsch algorithm)

Scheme used for scoring in this example:

matches: 1 point
mismatches: -1 point
gaps: -1 point

	gaps	S	A	G	P	T
gaps	0	-2	-4			
S	-2	¹ -2 1	⁻³ -1 -1			
V	-4	⁻³ -6 -1	⁰ -3 0			
G						
G						
P						
T						