

Ali_1

$s(a, a) = +1$, $s(a, b) = -1$, $s(gap, a) = s(gap, a) = s(gap) = -2$; Hierbei ist *gap* das Symbol für die Lücke

		D		C		D		D		E		G	
	0	-2	-4	-6	-8	-10	-12						
F	-2	-1	-4	-3	-6	-5	-8	-7	-10	-9	-12	-11	-14
		-4	-1	-3	-3	-5	-5	-7	-7	-9	-9	-11	-11
C	-4	-3	-3	0	-5	-4	-7	-6	-9	-8	-11	-10	-13
		-6	-3	-5	0	-2	-2	-4	-4	-6	-6	-8	-8
D	-6	-3	-5	-4	-2	1	-4	-1	-6	-5	-8	-7	-10
		-8	-3	-5	-2	-4	1	-1	-1	-3	-3	-5	-5
E	-8	-7	-5	-4	-4	-3	-1	0	-3	0	-5	-4	-7
		-10	-5	-7	-4	-6	-1	-3	0	-2	0	-2	-2
G	-10	-9	-7	-6	-6	-5	-3	-2	-2	-1	-2	1	-4
		-12	-7	-9	-6	-8	-3	-5	-2	-4	-1	-3	1

Alignment:	D	C	D	D	E	G
	F	C	-	D	E	G
	-1	1	-2	1	1	1

=1

Ali_2

$$S_{i,j} = \max(0, S_{i-1,j} + s(a_i, \varepsilon), S_{i-1,j-1} + s(a_i, b_j), S_{i,j-1} + s(\varepsilon, b_j))$$

		D	V	Y	W	A	R	D	G
	0	0	0	0	0	0	0	0	0
A	0	-2 -2 -2 0	0 -2 -2 0	-2 -2 -2 0	-3 -2 -2 0	4 -2 -2 4	-1 -2 2 2	-2 -2 0 0	0 -2 -2 0
R	0	-2 -2 -2 0	-3 -2 -2 0	-2 -2 -2 0	-3 -2 -2 0	-1 2 -2 2	9 0 0 9	0 -2 7 7	-2 -2 5 5
Y	0	-2 -2 -2 0	-1 -2 -2 0	7 -2 -2 7	2 -2 5 5	-2 0 3 3	0 7 1 7	6 5 5 6	4 3 4 4
W	0	-4 -2 -2 0	-3 -2 -2 0	2 5 -2 5	18 3 3 18	2 1 16 16	0 5 14 14	3 4 12 12	4 2 10 10
C	0	-3 -2 -2 0	-1 -2 -2 0	-2 3 -2 3	3 16 1 16	18 14 14 18	13 12 16 16	11 10 14 14	9 8 12 12
Q	0	0 -2 -2 0	-2 -2 -2 0	-1 1 -2 1	1 14 -1 14	15 16 12 16	19 14 14 19	16 12 17 17	14 10 15 15
L	0	-4 -2 -2 0	1 -2 -2 1	-1 -1 -1 0	-1 12 -2 12	13 14 10 14	14 17 12 17	15 15 15 15	13 13 13 13
I	0	-3 -2 -2 0	3 -1 -2 3	0 -2 1 1	-3 10 -1 10	11 12 8 12	11 15 10 15	14 13 13 14	11 11 12 12

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A	Ala	4																			
R	Arg	-1	5																		
N	Asn	-2	0	6																	
D	Asp	-2	-2	1	6																
C	Cys	0	-3	-3	-3	9															
Q	Gln	-1	1	0	0	-3	5														
E	Glu	-1	0	0	2	-4	2	5													
G	Gly	0	-2	0	-1	-3	-2	-2	6												
H	His	-2	0	1	-1	-3	0	0	-2	8											
I	Ile	-1	-3	-3	-3	-1	-3	-3	-4	-3	4										
L	Leu	-1	-2	-3	-4	-1	-2	-3	-4	-3	2	4									
K	Lys	-1	2	0	-1	-3	1	1	-2	-1	-3	-2	5								
M	Met	-1	-1	-2	-3	-1	0	-2	-3	-2	1	2	-1	5							
F	Phe	-2	-3	-3	-3	-2	-3	-3	-3	-1	0	0	-3	0	6						
P	Pro	-1	-2	-2	-1	-3	-1	-1	-2	-2	-3	-3	-1	-2	-4	7					
S	Ser	1	-1	1	0	-1	0	0	0	-1	-2	-2	0	-1	-2	-1	4				
T	Thr	0	-1	0	-1	-1	-1	-1	-2	-2	-1	-1	-1	-1	-2	-1	1	5			
W	Trp	-3	-3	-4	-4	-2	-2	-3	-2	-2	-3	-2	-3	-1	1	-4	-3	-2	11		
Y	Tyr	-2	-2	-2	-3	-2	-1	-2	-3	2	-1	-1	-2	-1	3	-3	-2	-2	2	7	
V	Val	0	-3	-3	-3	-1	-2	-2	-3	-3	3	1	-2	1	-1	-2	-2	0	-3	-1	4
	Ala	Arg	Asn	Asp	Cys	Gln	Glu	Gly	His	Ile	Leu	Lys	Met	Phe	Pro	Ser	Thr	Trp	Tyr	Val	
	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V	