4.
A.Needleman–Wunsch matrix:

	-	E	N	E	P	V	L	S	M	R	P	L	D	Y	T	R	Q
-	0	-2	-4	-6	-8	-10	-12	-14	-16	-18	-20	-22	-24	-26	-28	-30	-32
E	-2	1	-1	-3	-5	-7	-9	-11	-13	-15	-17	-19	-21	-23	-25	-27	-29
N	-4	-1	2	0	-2	-4	-6	-8	-10	-12	-14	-16	-18	-20	-22	-24	-26
E	-6	-3	0	3	1	-1	-3	-5	-7	-9	-11	-13	-15	-17	-19	-21	-23
A	-8	-5	-2	1	-1	-3	-5	-7	-9	-11	-13	-15	-17	-19	-21	-23	-25
V	-10	-7	-4	-1	-3	0	-2	-4	-6	-8	-10	-12	-14	-16	-18	-20	-22
L	-12	-9	-6	-3	-5	-2	1	-1	-3	-5	-7	-9	-11	-13	-15	-17	-19
S	-14	-11	-8	-5	-7	-4	-1	2	0	-2	-4	-6	-8	-10	-12	-14	-16
M	-16	-13	-10	-7	-9	-6	-3	0	3	1	-1	-3	-5	-7	-9	-11	-13
R	-18	-15	-12	-9	-11	-8	-5	-2	1	4	2	0	-2	-4	-6	-8	-10
P	-20	-17	-14	-11	-8	-10	-7	-4	-1	2	5	3	1	-1	-3	-5	-7
L	-22	-19	-16	-13	-10	-12	-9	-6	-3	0	3	6	4	2	0	-2	-4
D	-24	-21	-18	-15	-12	-14	-11	-8	-5	-2	1	4	7	5	3	1	-1
S	-26	-23	-20	-17	-14	-16	-13	-10	-7	-4	-1	2	5	3	1	-1	-3
D	-28	-25	-22	-19	-16	-18	-15	-12	-9	-6	-3	0	3	1	-1	-3	-5
R	-30	-27	-24	-21	-18	-20	-17	-14	-11	-8	-5	-2	1	-1	-3	0	-2

Global alignment (from backtrace):
ENEAVLSMRPLDSDR-
ENEPVLSMRPLDYTRQ

Score = −2

B.Smith–Waterman Matrix

	-	E	N	E	P	V	L	S	M	R	P	L	D	Y	T	R	Q
-	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
N	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E	0	1	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0
A	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
V	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
L	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0
S	0	0	0	0	0	0	0	3	1	0	0	0	0	0	0	0	0
M	0	0	0	0	0	0	0	1	4	2	0	0	0	0	0	0	0
R	0	0	0	0	0	0	0	0	2	5	3	1	0	0	0	1	0
P	0	0	0	0	1	0	0	0	0	3	6	4	2	0	0	0	0
L	0	0	0	0	0	0	1	0	0	1	4	7	5	3	1	0	0
D	0	0	0	0	0	0	0	0	0	0	2	5	8	6	4	2	0
S	0	0	0	0	0	0	0	1	0	0	0	3	6	4	2	0	0
D	0	0	0	0	0	0	0	0	0	0	0	1	4	2	0	0	0
R	0	0	0	0	0	0	0	0	0	1	0	0	2	0	0	1	0

Local (highest-scoring) alignment (from the cell with value 8 back to zero):

VLSMRPLD

VLSMRPLD

Score = 8 (8 matches × +1)

C. Smith–Waterman gives the longer continuous alignment because it performs *local* alignment and focuses only on the highest-scoring matching region, ignoring mismatching ends. Needleman–Wunsch forces alignment of the entire sequence, so gaps and mismatches break the continuous block.