Problem 1:

Match score is 7. When we look at the 5th row - 3rd column we see that M's are matched and score increases by 7. Since gap score is negative value, this increase is due to match score. When we continue to the next cell in the same row (4th column) we see a decrease in the score. So this should be either gap or mismatch value. However when we look at mismatch value, it should be 3 in this cell that is not the case. That's why the decrease is because of the gap and the score is - 4.(37) Then, let us look at the 5th row- 7th column that's G-M pair. In this example, we see that either the gap value is -2 or mismatch value is -6. Since we have already found the gap value as -4, we can conclude that mismatch value is -6. To summarize, we have found matching score as 7, gap score as -4 and mismatch value as -6.

	-	М	ı	М	Α	G	E	D	ı	L
-	0	0	0	0	0	0	0	0	0	0
G	0	0	0	0	0	7	3	0	0	0
Α	0	0	0	0	7	3	1	0	0	0
M	0	7	3	7	3	1	0	0	0	0
Α	0	3	1	3	14	10	6	2	0	0
E	0	0	0	0	10	8	17	13	9	5
D	0	0	0	0	6	4	13	24	20	16
К	0	0	0	0	2	0	9	20	18	14

Sequences:

Sequence 1:	М	А	G	E	D
Sequence 2:	М	А	-	Е	D
Scores:	7	7	-4	7	7

When we add the scores, we get 7 + 7 + (-4) + 7 + 7 = 24. This result matches with the result in the table.

Filled table using the Needleman-Wunsch dynamic programming global alignment algorithm is:

	ı	M	С	G	М	G	С	М	E	L
-	0	-4	-8	-12	-16	-20	-24	-28	-32	-36
G	-4	-3	-7	-2	-6	-10	-14	-18	-22	-26
M	-8	1	-3	-6	3	-1	-5	-9	-13	-17
С	-12	-3	10	6	2	0	8	4	0	-4
M	-16	-7	6	7	11	7	4	13	9	5
E	-20	-11	2	4	7	9	5	9	18	14
D	-24	-15	-2	1	3	6	6	5	14	14
L	-28	-19	-6	-3	3	2	5	8	10	18

The best alignment of these two sequences:

Problem 2:

Sequence 1:	М	С	G	М	G	С	М	E	_	L
Sequence 2:	ı	_	G	М	_	С	М	E	D	L