Høst 2015
Exercise 2

You are given two protein sequences q: **MIGV** and d: **FFIGL** and the scoring matrix (excerpt from PAM250) shown at the top of the figure. The lower part of the figure shows the *matrix H,* partially filled, which is used to find the best global alignment(s) by dynamic programming. Use the information given here to answer the questions in this part of the exam (2A-2D).

4. 2A. Which gap penalty has been used in this matrix? Calculate and fill in the remaining values in the matrix *H* for the cells labelled *A, B, C, and D (give the answer as follows: A=<value>, B=<value>, etc)*. What is the score(s) for the best global alignment(s)?

Gap cost/penalty used is 2 (can also be given as -2).
The four remaining values of the matrix H are:
A=8 B=6 C=6 D=10
Since it is a global alignment, **best score** is = value in **D=10**.

5. 2B. For the sequences and the scoring matrix given in 2A, find the best global alignment(s). *(Write the alignment with one sequence above the other and with dash(es) to indicate where gaps are).*

There are two alignments with the same best score of 10:

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q: M-IGV
d: FFIGL
```

and

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q: -MIGV
d: FFIGL
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Vår 2016
Exercise 3

3	Sequence alignment by dyn.prog	130
3A	**Global alignment** (100p) Fyll ut de resterende verdiene i matrisen H for cellene merket A, B, C og D (angi svaret slik: A=<verdi>, B=<verdi> etc.). Hva er score for de(n) beste globale sammenstillingen(e)? Finn den (eller de) beste globale sammenstillingen(e), og forklar kort prosedyren. Skriv sammenstillingene med sekvensen q øverst og d nederst og bruk bindestrek for å angi hvor det skal være gap.	- Values are: A = 6, B = 12, C = 8, D = 11 and score is 11 - There are two alignments with score 11 … - *As the question is phrased, we have only asked for the procedure for backtracking*, i.e. starting from the cell with highest score and following the path(s) that gave this score, using either match or gaps. YMLQ- Y::Q YIAQI 7 1 -1 5 -1 11 YML-Q- Y : Q Y-IAQI 7 -1 2 -1 5 -1 11
3B	Global vs local alignment (30p) Forklar kort forskjellen på prosedyrene for globale og lokale sammenstillinger ved dynamisk programmering?	- Matrix is initiated differently, zeros in the cells of "first axes" - When scoring, negative values are set to zero - Backtracking starts the any cell with highest score and runs till first occurrence of zero