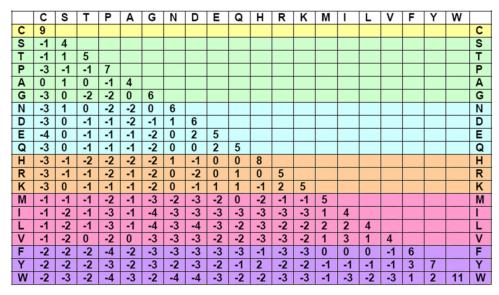
Homework

We have talked about pairwise DNA sequence alignment in the class. Pairwise protein sequence alignment will follow the same principles. Can you implement a dynamic programming algorithm for pairwise protein sequence alignment? Please use -2 for the gap penalty and the BLOSUM62 substitution matrix for the cost of mismatch and reward of match (download link on next page).



The BLOSUM 62 substitution matrix