Figure. Multiple sequence alignment of RulA homologs from *Pseudomonas fluorescens* PC20, PC24; *Pseudomonas putida* plasmid pWW0 RulA (Q8VMP5) and *E. coli* K-12 UmuD (P0AG11). Black boxes indicate the putative active sites residues according to NCBI Conserved Protein Domain Family database (source pfam; superfamily cl10465; Peptidase_S24_S26; [1]). Residues shaded orange represent the autocatalytic cleavage site shown to be required for posttranslational processing of UmuD/RulA homologs [2,3]. Residues surrounded by pink boxes[1] have been shown to be important in the UmuDC mediated mutagenesis [4]. Sequences were aligned with ClustalX2 and domains were marked according to Protein sequence analysis and classification portal Interpro (http://www.ebi.ac.uk/interpro/) based on the sequence of UmuD (P0AG11).