S3 Figure. Multiple sequence alignment of RulB homologs from *Pseudomonas fluorescens* PC20, PC24; *Pseudomonas putida* plasmid pWW0 RulB (Q8VMP6) and *E. coli* K-12 UmuC (P04152). Black boxes indicate the putative active site residues according to NCBI Conserved Protein Domain Family database (source cd00424; superfamily cl12025; PolY_Pol_V_uムC). [1] Residues surrounded by pink boxes have been shown to be important in the UmuDC mediated mutagenesis [2-10]. Sequences were aligned with ClustalX2 and domains were marked according to Protein sequence analysis and classification portal Interpro ([http://www.ebi.ac.uk/interpro/](http://www.ebi.ac.uk/interpro/)) based on the sequence of UmuC (P04152).