ABSTRACT
The UDGs are a single superfamily that has essentially the same structural fold and an evolutionary commonality between them, but differences in the catalytic mechanism and pocket constructions have led to extreme sequence divergence of these enzymes.

INTRODUCTION
The alpha/beta fold uracil DNA glycosylases (URACIL) are a complex group of proteins that are found in the uracil nuclei. The alpha/beta fold uracil DNA glycosylases (URACIL) are a complex group of proteins that are found in the uracil nuclei.

They are formed by the uracil nuclei in the placenta and are important for maintaining the structure of the placenta. They are also found in the developing embryo and are important for the development and survival of the developing embryo.

The uracil DNA glycosylases (URACIL) are a member of the uracil family of proteins. They are found in the placenta and are Several UDGs have been identified in different superkingments of life, including the most closely related ones from the Escherichia coli Ung protein. These enzymes are known for their ability to remove uracil (and sometimes even thymine) from DNA without breaking G:T mismatches. Using structural comparisons and sequence profile searches to unify all known UDGs into one protein superfamily, we predict a common / fold for them. We also identify several new likely UDHs that are not the same as previously described families, and investigate the evolutionary scenarios that could have led to the phyletic distribution of these enzymes.

CONCLUSION
Remarkable conclusions By means of sequence profile searches, multiple alignment analysis, and protein structure comparisons, we have determined that all known UDGs form a single protein superfamily with essentially no evolutionary difference. The extreme sequence divergence of different families is likely due to differences in their biochemistry, with only the general shape of the protein molecule and the binding pocket (dominantly necessary for DNA glycosylase reaction) being used by many cellular life forms. However, the individual families exhibit limited and distinct phyletic distributions. Furthermore, two undetected families of UGDs are nowning mechanisms.