ABSTRACT
By means of sequence profile searches, we reveal that 2OG-Fe(II) oxygenase fold is present in multiple protein families that were previously unknown to us, enabling us to predict the catalytic activity of various biologically relevant proteins from eukaryotes and bacteria.

INTRODUCTION
A number of DNA-repair proteins have been identified, mainly with regard to the ability to repair DNA damage. AlkB is a type of protein found in the nucleus of living cells capable of cleaving DNA molecules, making them safe for DNA repair and DNA replication. EGL-9 is an enzyme from the yeast genome and is known to be important in the formation of DNA. Leprecan is a member of the genus Alcespora and is recognized as a potential repair protein. Leprecan is a member of the genus Alcespora, and is known to be important in the formation of DNA. Leprecan is a member of the genus Alcespora, and is known to be important in the The catalytic mechanism of dioxygenases, which are found in eukaryotes and bacteria, involves oxidation of an organic substrate by a small amount of ATP. One well-studied example is the hydroxylation of proline and lysine sidechains in collagen and other animal glycoproteins by enzymes of the 2-OH receptor family, while others play cyclization and desaturation steps in the biosynthesis of antibiotics such as penicillin and cephalin. By using sequence profile analysis, we reveal that the DNA-repair protein AlkB, the extracellular matrix protein leprecan and the disease-related protein EGL-9 define new families of the 2OG-Fe(II) dioxygenase superfamily. AlckB is a significant counterweight to the toxic DNA modifications caused by alkylating agents in bacteria and eukaryotes. Our research indicates that AlcB plays disproportionate roles in DNA repair process, while our findings suggest that itbatorligatant genes indicate that

CONCLUSION
Remarkable conclusions Prior to this study, the structure determination, biochemical studies, and sequence comparisons of 2OG-Fe(II) dioxygenases had provided an explanation for their structural fold, active-site residues, or reaction mechanism. However, our research reveals that other protein families have the same structural pattern and are expected to adopt the identical fold. Our approach allows us to predict the catalytic activity of various functionally important proteins from eukaryotes and bacteria by using sequence profile searches to identify their common architecture and activation mechanisms.