ABSTRACT
Using computational methods, the structure of Eukaryotic cap MTase was predicted to be reconstructed using evolutionary relationships. The identification of novel cap (cap) metabolites suggests candidates for cloning and biochemical characterization, while the structural model will be useful in designing new experiments to understand the molecular function of cap caps.

INTRODUCTION
The MRC Genome Biology Network (MGBN) is the largest collection of sequenced genomes globally and contains the largest set of human sequences ever assembled. The MGBN's high-resolution sequence data is in the form of a database, the genome, and from the MGBN, the genome is used to generate a set of reference genomes.

The MGBN has a highly dynamic, dynamic and dynamic-based pipeline for the annotation and sequence analysis of the MRC Genome Data. As a result, the sequence information generated by the MGBN has been used to generate a vast amount of novel information for the study of human evolution, including human genomic information, population genetics Transcripts produced by RNA polymerase II are modified at their 5' end by adding a methylated 5’-terminal cap structure m7G(5')ppp(25').This modification directs pre-mRNA to processing and transport pathways in the cell nucleus and regulates both rRNA turnover and translation. Mutations in this yeast capping apparatus that inhibit any of these activities are deadly in vivo. Fungi, metazoans, protozoa and viruses differ significantly in terms of the inhibitors Several important aspects have been discussed regarding the mechanisms and structures of cellular and viral capping enzymes: the crystal structures (GTase) of the Chlorella virus PBVCV-1, and the TPases (transferasite complex protein ßAT-1) of yeast have also been solved as guides for large-scale site-directed mutagenesis experiments, but their actual function remains unclear; in contrast, there are still many undiscovered details about the structure of cap MTasaurus, which is an enzyme that drives the mechanism to achieve this. The Cap MTase is a member of the AdoMet-dependent superfamily, which includes several remotely related families of DNA, RNA, protein and small molecule-modifying enzymes. To date, more than twelve METases have been identified with three-dimensional structures, and the catalytic domain has accumulated despite low sequence similarity (reviewed in) and is located at different locations within the primary structure of most individual MRAS (but not shown to be independent gene fusions). The prolonged absence of its atomic structure led us to predict its structure and construct a three-dimensional model, which is accompanied by an evolutionary study. The findings from this report should assist in the interpretation and design of mutagenesis experiments, as they do not directly identify the substrate-binding site and instead rely on sequence analysis and resend endogenous results.

CONCLUSION
Remarkable conclusions By using computational methods, we have inferred evolutionary relationships and predicted the structure of cap MTase. Furthermore, a tertiary model for the Eukaryotic enzyme has been constructed to interpret the available mutation data and guide comparative sequence analysis. We believe that cap MTSses share similar catalytic domains with glycine N-MTains, suggesting that these two families are likely closely related. Additionally, our analysis of the AdoMet-binding site

and the identification of guanine binding sites may provide information about other members of this same