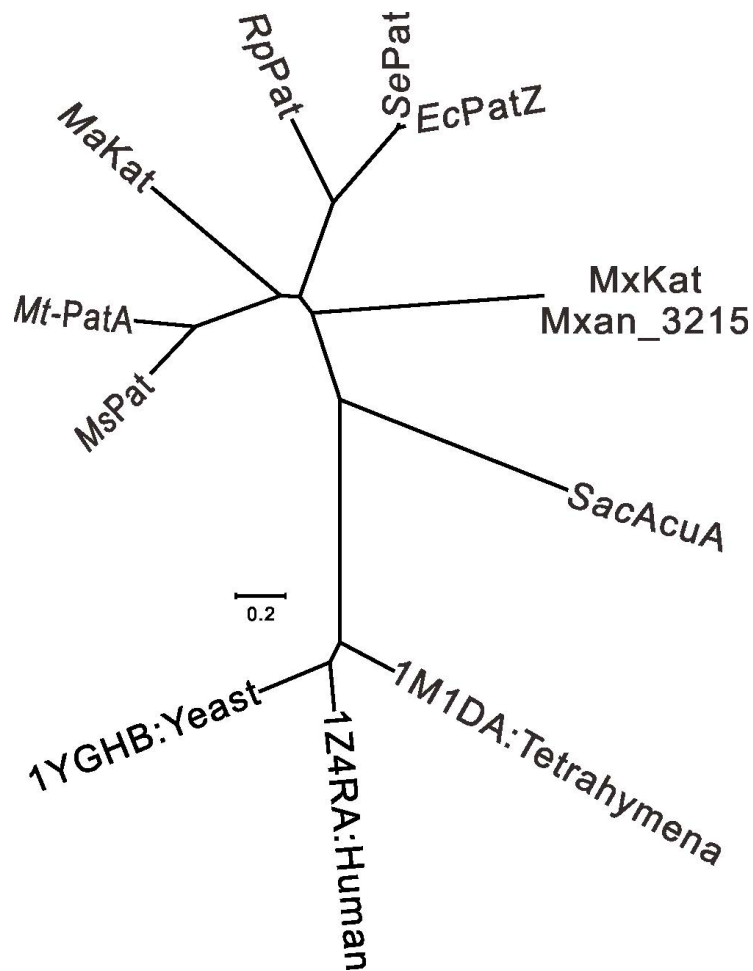
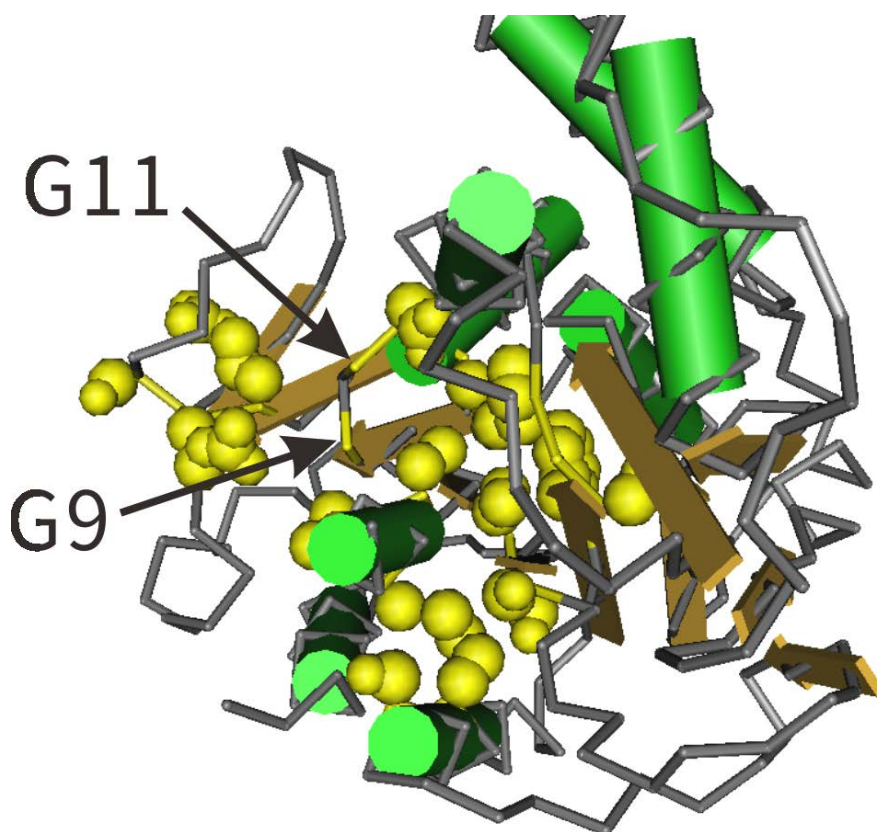


**Figure S1. Illustration of the three-dimensional model of the GNAT domain.** SWISS-MODEL (<http://swissmodel.expasy.org/interactive>) was used to build a three-dimensional model of the GNAT domain of MxKat with default parameters, and then the position of the important amino acids was marked manually. The active sites (R366, G369, and G371) of the R/Q-X-X-G-X-G/A motif are indicated.



**Figure S2. Phylogenetic analysis.** A phylogenetic tree was constructed using MEGA software according to the sequence of GNAT domains in the acetyltransferases of different species.



**Figure S3. Three-dimensional model of the NADP<sup>+</sup>-binding domain.** A three-dimensional model constructed in Conserved Domain Database (CDD) (<http://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi>), and then the predicted important amino acids were marked manually. The candidate residues of MxKat that interact with NADP<sup>+</sup> are shown.