

Figure S1. The prediction results of O-glycosylation (A) and N-glycosylation (B) of cAlyM. The glycosylation sites were predicted using the website (<http://www.cbs.dtu.dk/services/NetNGlyc/>, <http://www.cbs.dtu.dk/services/YinOYang/>).

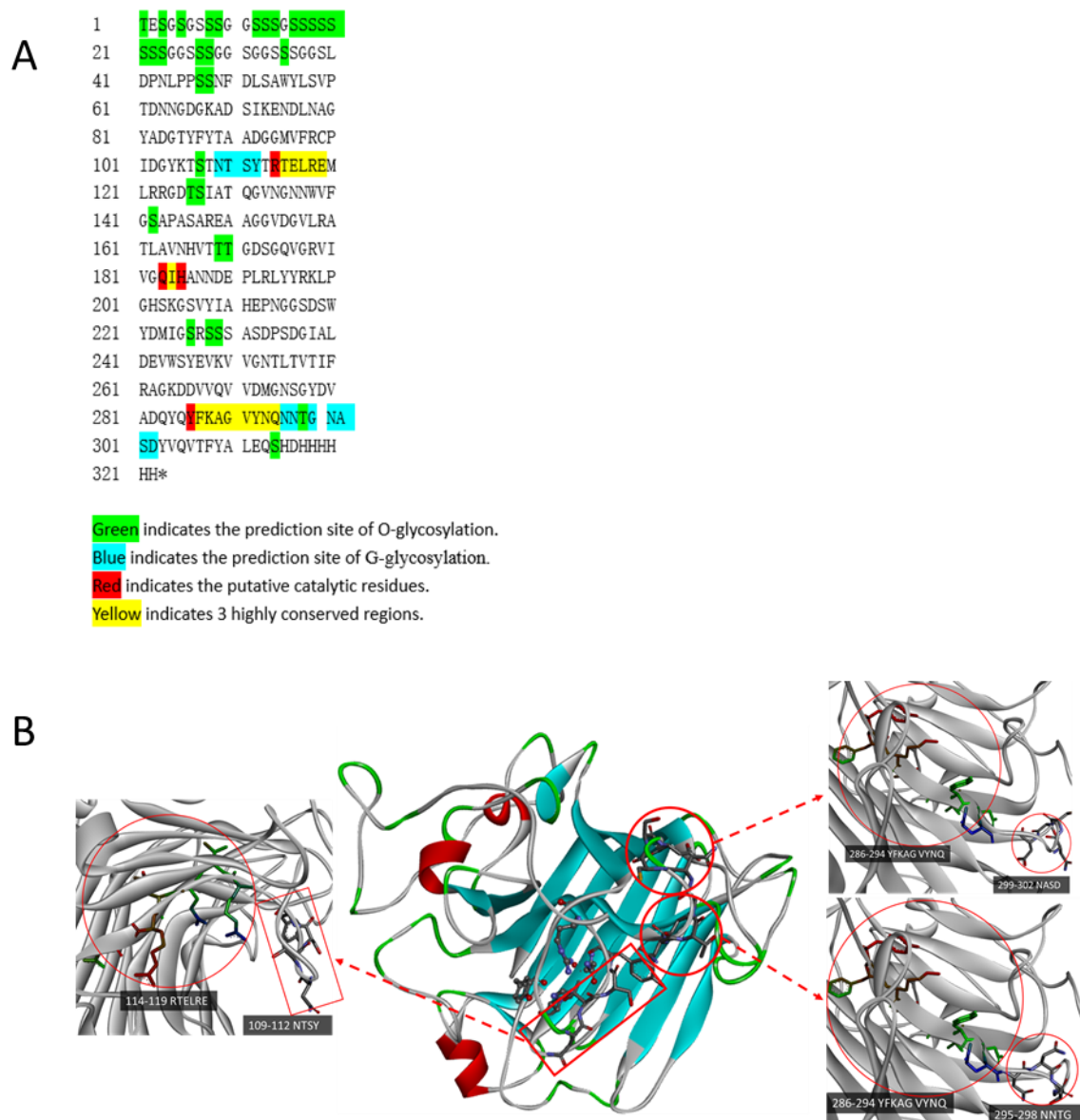


Figure S2. The predicted glycosylation sites in the gene sequence of cAlyM (A). The predicted N-glycosylation sites in the three-dimensional model of cAlyM (B). A: Green indicates the prediction site of O-glycosylation. Blue indicates the prediction site of G-glycosylation. Red indicates the putative catalytic residues. Yellow indicates 3 highly conserved regions. B: The arrows point to the magnified structures of the mutation sites.