

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

	1	TE <mark>S</mark> G <mark>S</mark> GS <mark>SS</mark> G	G <mark>SSS</mark> G <mark>SSSSS</mark>
Α	21	<mark>SSS</mark> GGS <mark>SS</mark> GG	SGGS <mark>S</mark> SGGSL
	41	DPNLPP <mark>SS</mark> NF	DLSAWYLSVP
	61	TDNNGDGKAD	SIKENDLNAG
	81	YADGTYFYTA	ADGGMVFRCP
	101	IDGYKT <mark>S</mark> T <mark>NT</mark>	SYT <mark>RTELRE</mark> M
	121	LRRGD <mark>TS</mark> IAT	QGVNGNNWVF
	141	G <mark>S</mark> APASAREA	AGGVDGVLRA
	161	TLAVNHVT <mark>TT</mark>	GDSGQVGRVI
	181	VG <mark>QIH</mark> ANNDE	PLRLYYRKLP
	201	GHSKGSVYIA	HEPNGGSDSW
	221	YDMIG <mark>S</mark> R <mark>SS</mark> S	ASDPSDGIAL
	241	DEVWSYEVKV	VGNTLTVTIF
	261	RAGKDDVVQV	VDMGNSGYDV
	281	ADQYQ <mark>Y</mark> FKAG	VYNQNN <mark>T</mark> G NA
	301	<mark>SD</mark> YVQVTFYA	LEQ <mark>S</mark> HDHHHH
	321	HH*	—

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.

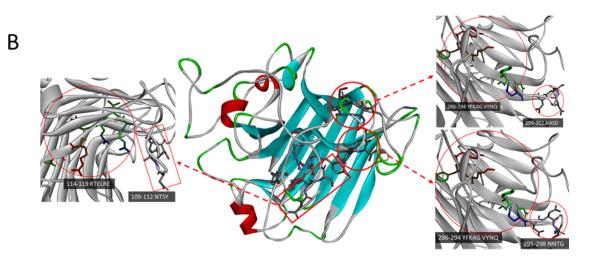


Figure S2. The predicted glycosylation sites in the gene sequence of cAlyM (A). The predicted N-glycosylation sites in the three-dimensional model of cAlyM (B). A: Green indicates the prediction site of O-glycosylation. Blue indicates the prediction site of G-glycosylation. Red indicates the putative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