

10	20	30	40	*	50	*	60
MLPARLIVML	LGITLATSFQ	YGYHSAVINQ	PLHFIADFIG	NISESRYGVS	NESYKTTVAS		
I							
70	80	90	100	110	120		
ICVTSFIVGG	LVGALSSGTI	SNKLGRKKSI	LFLTIPCLLG	TVLIMLDYLT	RSFETIIIGR		
II				III			
130	140	150	160	170	180		
FLIGCSCGAY	TAVAPIYLSE	VTPVSLRGMG	GVLNQVMIVI	SVVVSQILGL	PSIMNTDVLW		
IV				V			
190	200	210	220	230	240		
PYLLGINVVP	CVVGAICLFF	CPESPRYLYL	AKKDITSAAS	ALKSLRNNPE	DVVKELDELA		
VI							
250	260	270	280	290	300		
KELDVTSQKV	SQITEPHNFR	KAGVLDILRV	PHLRLALLIA	LAAHCGQQLS	GMNGLLFYSV		
VII							
310	320	330	340	350	360		
ELFKSNGLSA	AAANYATTGI	GCVLLGVTII	SIFVIDRVGR	RVLLIWGLCV	VLTSLLIFTL		
VIII				IX			
370	380	390	400	410	420		
RMIKDAAHM	SWLVNVAMAS	IYVFVCGFGV	GAGSIPWFLV	VEMFSQEYRD	TATAIGVAVN		
X							
430	440	450	460	470	480		
WTCIIIIGLG	FIQLIKYFGV	YAFLPSACIE	AIVILVLYKY	MPETMGRTPM	SIEAELKRKV		
XI				XII			
490	500	510	520	524			
AVNRASHNEP	QVQDMLLKQH	EAEVQLEE	DVTGVFNSEQ	KCST			

Supplementary Fig. S2. Amino acid sequence analysis of CsGTP5. The deduced amino acid sequence of CsGTP5 is shown. Asterisks indicate predicted N-glycosylation sites. Red letters indicate putative glucose-binding residues predicted by molecular docking analysis.