```
            1        10        20        30        40        50        60        70        80        90       100       110       120       130
            |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
ScGsy1      MARDLQNHLLFEVATEVTNRVGGIYSVLKSKAPYTVAQYGDNYTLLGPLNKATYESEVEKLDWEDESIFPEELLPIQKTLMSMREKGVNFVYGNWLIEGAPRVILFELDSYRHFLNEWKADLWSLVGIPS
ScGsy2      MSRDLQNHLLFETATEVANRVGGIYSVLKSKAPITVAQYKDHYHLIGPLNKATYQNEVDILDWKKPEAFSDEMRPVQHALQTMESRGVHFVYGRWLIEGAPKVILFDLDSYRGYSNEWKGDLWSLVGIPS
KpGsy1      MGKDITNHLLFEIATEVANRVGGIYSVLKSKAPVTVAEYKDRYTLIGPLNANSANVEVEELPYLDPV--------LKRTLDSMSGRGIRYLYGRWLIEGAPRVILFDIGSAAGYLNEWKSDLWNIAGVPT
Consensus   M.rDlqNHLLFE.ATEVaNRVGGIYSVLKSKAP!TVA#YkD.YtLiGPLNkaty#.EV#.Ldw.dp..f..e..p.q.tL.sM..rG!.%vYGrWLIEGAPrVILF#ldSvrg%lNEWK.DLWslvG!Ps

            131      140       150       160       170       180       190       200       210       220       230       240       250       260
            |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
ScGsy1      PEHDHETNDAILLGYVYVWFLGEVSKLDS-SHAIIGHFHEWLAGVALPLCRKKRIDVYTIFTTHATLLGRYLCAAGDVDFYNNLQYFDVDQEAGKRGIYHRYCIERAAAHTADVFTTVSQITALEAEHLL
ScGsy2      PENDFETNDAILLGYTVAWFLGEVAHLDS-QHAIVAHFHEWLAGVALPLCRKRRIDVYTIFTTHATLLGRYLCASGSFDFYNCLESVDVDHEAGRFGIYHRYCIERAAAHSADVFTTVSQITAFEAEHLL
KpGsy1      PEHDVETNDAILLGYLVAWFLGELVHNDGHKRAIICHAHEWLAAVCLPLCRKRKIDVTTVFTTHATLLGRYLCA-GSVDFYNNLDKFDVDAEAGKRGIYHRYCIERAAAHSADVFTTVSHITAYEAEHLL
Consensus   PEHd.ETNDAILLGY.VaWFLGEv.hlDs..hAI!.HfHEWLAgVaLPLCRKrrIDVvT!FTTHATLLGRYLCA.GsvDFYNnL#.fDVD.EAGkrGIYHRYCIERAAAHsADVFTTVSqITA.EAEHLL

            261      270       280       290       300       310       320       330       340       350       360       370       380       390
            |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
ScGsy1      KRKPDGILPNGLNVVKFQAVHEFQNLHALKKDKINDFVRGHFHGCFDFDLDNTVYFFIAGRYEYKNKGADMFIESLARLNYRLKVSGSKKTVVAFLIMPAKTNSFTVEALKSQAIVKSLENTVNEVTASI
ScGsy2      KRKPDGILPNGLNVIKFQRFHEFQNLHALKKEKINDFVRGHFHGCFDFDLDNTLYFFIAGRYEYKNKGADMFIEALARLNYRLKVSGSKKTVVAFIVMPAKNNSFTVEALKGQAEVRALENTVHEVTTSI
KpGsy1      KRKPDGVLPNGLNVIKFQAVHEFQNLHAEKKEKINEFIRGHFYGQLDFKLNNTLYFFIAGRYEYRNKGVDFFIESLARLNHRLKASNSNMTVVAFIIMPAKTNSYTVETLKGQAVIKQLENTINDIEALV
Consensus   KRKPDG!LPNGLNV!KFQAvHEFQNLHAlKK#KIN#F!RGHFhGcfDFdL#NTlYFFIAGRYEYkNKGaDmFIEsLARLNyRLKvSgSkkTVVAFi!MPAKtNS%TVEaLKgQA.!k.LENT!n#!tas!

            391      400       410       420       430       440       450       460       470       480       490       500       510       520
            |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
ScGsy1      GKRIFEHTHRYPHNGLESELPT-NLDELLKSSEKVLLKKRVLALRRPYGELPPVYTHNMCDDANDPILNQIRHVRLFNDSSDRVKVIFHPEFLNANNPILGLDYDEFVRGCHLGVFPSYYEPWGYTPAEC
ScGsy2      GKRIFDHAIRYPHNGLTTELPT-DLGELLKSSDKVMLKRRILALRRPEGQLPPIVTHNMVDDANDLILNKIRQVQLFNSPSDRVKMIFHPEFLNANNPILGLDYDEFVRGCHLGVFPSYYEPWGYTPAEC
KpGsy1      GKRLFEFCQHPATSSNSSHIEMPDIDDLLKPSDRVLLKRRMFAMKRE--GLPPIVTHNMADDSTDPILNQIRNVQLFNRPEDRVKIIFHPEFLNSNNPILSLDYDEFVRGCHLGVFPSYYEPWGYTPAEC
Consensus   GKRiF#h..ryphngl.selpt.#ld#LLKsS#kV$LKrR.lA$rRp.g.LPP!VTHNM.DDanDpILNqIR.VqLFN.psDRVK.IFHPEFLNaNNPILgLDYDEFVRGCHLGVFPSYYEPWGYTPAEC

            521      530       540       550       560       570       580       590       600       610       620       630       640       650
            |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
ScGsy1      TVMGVPSITTNVSGFGAYMEDLIETDQAKDYGIYIVDRRFKSPDESVEQLADYHEEFVNKTRRQRINQRNRTERLSDLLDWKRMGLEYYKARQLGLRRAYPEQFKQLVGETISDANMNTLAGGKKFKIAR
ScGsy2      TVMGVPSITTNVSGFGAYMEDLIETNQAKDYGIYIVDRRFKAPDESVEQLVDYMEEFVKKTRRQRINQRNRTERLSDLLDWKRMGLEYYKARQLALRRGYPDQFRELVGEELNDSNMDALAGGKKLKVAR
KpGsy1      TVMGIPSITTNLSGFGCYMEDLIEN--SSDYGIYIVDRRLKSYDESIDQLTSYHFDFVDKTRRQRINQRNRYERLSDLLDWRRMGLEYYKGRSLALRRAYPDEFKNQ-----NNEHSNPFSESNSIKITR
Consensus   TVMG!PSITTNvSGFGaYMEDLIEt.qakDYGIYIVDRRfKspDES!#QL.dYMe#FV.KTRRQRINQRNRtERLSDLLDWkRMGLEYYKaRqLaLRRaYP##Fk#lvge..n#.nm#.laggkk.K!aR

            651      660       670       680       690       700       710       721
            |--------+---------+---------+---------+---------+---------+---------+----------+|
ScGsy1      PLSVPGSPK-VRSNSTVYMTPGDLGTLQDANNADDYFNLSTNGAIDNDDDDNDTSAYYEDN
ScGsy2      PLSVPGSPRDLRSNSTVYMTPGDLGTLQEVNNADDYFSLGVNPAADDDDD----GPYADDS
KpGsy1      PLSVPGSPRDKYSSSANIMTPGDLGTLQENNSTDYISWRLGNDTEEDGLDVTLRGLSVAPSAEQSGDEFDA
Consensus   PLSVPGSPrd.rSnStvyMTPGDLGTLQ#.NnaDdyf.l..N.a.##ddD....g.y..ds..........
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Figure S1. Multiple sequence alignment of *K. phaffii* Gsy1 and its orthologues in *S. cerevisiae*. ScGsy1, *S. cerevisiae* glycogen synthase 1 (YFR015C); ScGsy2, *S. cerevisiae* glycogen synthase 2 (YLR258W); KpGsy1, *K. phaffii* glycogen synthase 1 (XP_002493014.1). Color code of amino acid residues: red – high consensus, blue – low consensus, black – neutral. The alignment was generated using MultAlin software [36]. Alignment parameters: Blosum62 – 12 – 2 (symbol comparison table – gap penalty at opening – gap penalty at extension).