

A Query sequence GSS1 (length 510 amino acids):
MAILHQAVVL LGAALCVSAA TKPHVIMIMA DDMGWDDTST HGSKSVLTPN LDVLTRSGVS
LHRYYTHALC SPARTAVLTG KYAHTVGMQG MPLSNAEERG IPLEERLISQ YLQDAGYRTQ
MVGKWHVGHHA FFEQLPTYRG FENHFGVRGG FIDYYEYNAQ EQLDGRPVTG LCLFDDLQPD
WTTEGYITDV YTEKSTTIE NHNVSEPLYL LLTHHAPHNG NEDASLQAPP EEVRAQRHVE
LHPRRIFAAM VKKLDDSIGE IVATLEKKGM LENTIIITFST DNGAPTIVGLG ANSGSNYPLR
GVKKSPEWEGG IRGNAMIWAG PEVAPGNAWR GKVYDGNMHA ADWVPTLLEA IGEKIPAGLD
GIPMWSHIEE NKPSRTEIF EIDDYFNHSS VTLGRHKLVK GTIDESLSKH YGEDLRGIIG
TPPDYKQKLR DSKAWESLET IGIPLDADVM ADRDEAIVTC GNVVVKPCSP SAESWCPLYDI
IEDP**C**ELRDL SEELPQLAQI LLYRLEQEEA

The site with the best score is shown in black.

Prediction of potential C-terminal GPI-Modification Sites

Use of the prediction function for METAZOA

None potential GPI-modification site was found.
Among all positions checked, sequence position 485 had the best score.

B Query sequence GSS2 (length 510 amino acids):
MAILHQVVVI LGAALCVSAA TKPHVIMIMA DDMGWDDTST HGSKSVLTPN LDVLTRSGVS
LHRYYTHAVC SPARTAVLTG KYAHTLGMQG MPLSNAEERG IPLEERLISQ YLQDAGYRTQ
MVGKWHVGHHA FFEQLPTYRG FENHFGVRGG FIDYYEYNAQ SRLDGKPVTVG LCLFDDLKPD
WTTEGYITDV YTEKSTTIE NHNVSEPLYL LLTHHAPHNG NEDASLQAPP EEVRAQRHVE
LHPRRIFAAM VKKLDDSIGE IVATLEKKAM LENTIIITFST DNGAPTIVGLG ANSGSNYPLR
GVKKSPEWEGG IRGNAMIWAG PEVAPGNAWR GNVYDGNMHA ADWVPTLLEA IGEKIPAGLD
GIPMWSHIEE NKPSRTEIF EIDDYFNHSS VTLGRHKLIK GTIEESLSKH YGEDLRGIIG
TPPDYKQKLR DSKAWESLET IGISLDADVM ADRDEAIVTC GDVVPKPCSP TAESWCPLYDI
IADP**C**ELRDL SEELPQLAQI LLYRLEQEEA

The site with the best score is shown in black.

Prediction of potential C-terminal GPI-Modification Sites

Use of the prediction function for METAZOA

None potential GPI-modification site was found.
Among all positions checked, sequence position 485 had the best score.

Supplemental Fig 5. GPI-anchor sites of GSS1 (A) and GSS2 (B) predicted by GPI Modification Site Prediction [40].