

TMHMM result

```
# WEBSEQUENCE Length: 432
# WEBSEQUENCE Number of predicted TMHs: 0
# WEBSEQUENCE Exp number of AAs in TMHs: 0.0252
# WEBSEQUENCE Exp number, first 60 AAs: 0
# WEBSEQUENCE Total prob of N-in: 0.00259
WEBSEQUENCE TMHMM2.0 outside 1 432
```

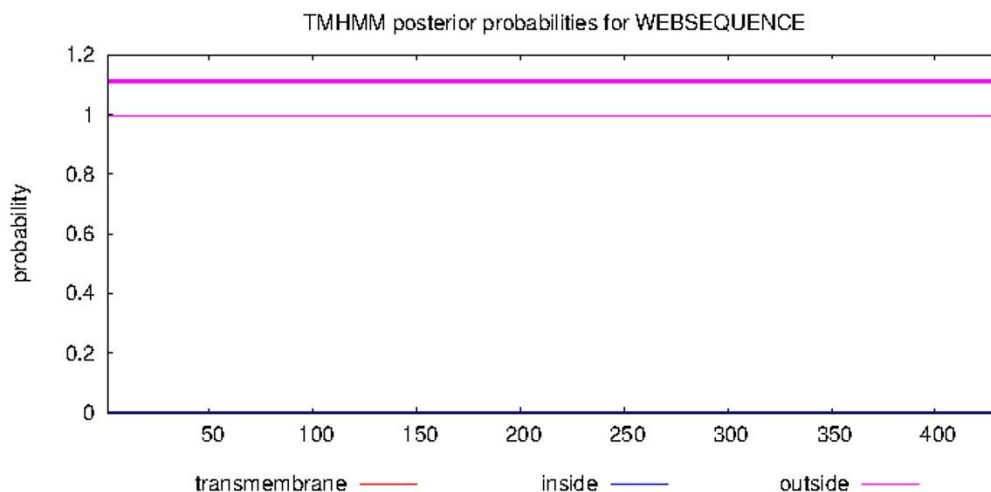


Figure S1. Transmembrane structure prediction using TMHMM Server v.2.0. The amino acid sequences of HcGOB (NCBI accession numbers: HF967182.1) was analyzed to predict transmembrane structures using TMHMM Server v.2.0. There were no transmembrane domains was predicted in this protein structure. <http://www.cbs.dtu.dk/services/TMHMM/>.

Predictions list. Use the [help page](#) for more detailed description of the output page.

Predicted proteins

Sequence

Prediction: Other

Protein type	Signal Peptide (Sec/SPI)	Other
Likelihood	0.0012	0.9988

Download: [PNG](#) / [EPS](#) / [Tabular](#)

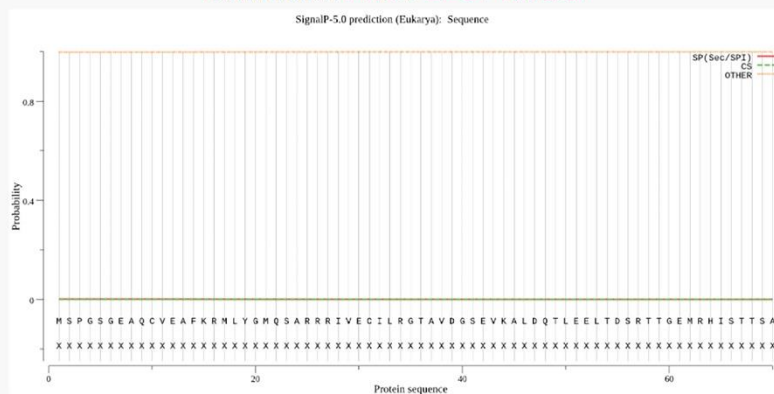


Figure S2. Signal peptide prediction. The amino acid sequences of HcGOB (NCBI accession numbers: HF967182.1) was used to predict Signal peptides by SignalP 4.1Server. There were no Signal peptides was predicted in this protein structure. <http://www.cbs.dtu.dk/services/SignalP/>.



NetNGlyc 1.0 Server - prediction results

Technical University of Denmark

Asn-Xaa-Ser/Thr sequons in the sequence output below are highlighted in **blue**.
Asparagines predicted to be N-glycosylated are highlighted in **red**.

Output for 'Sequence'

#####

Warning: This sequence may not contain a signal peptide!!

Proteins without signal peptides are unlikely to be exposed to the N-glycosylation machinery and thus may not be glycosylated (in vivo) even though they contain potential motifs.

SignalP-HM euk predictions are as follows:

#	name	Caax	pos	?	Ymax	pos	?	Snax	pos	?	Smean	?	D	?	SignalP-noTM
Sequence		0.108	12		0.118	12		0.143	1		0.113		0.115	N	0.450

SignalP output is explained at <http://www.cbs.dtu.dk/services/SignalP/output.html>

#####

Name: Sequence Length: 432

MSPGSGEAQCVEAFKRMLYGMSARRRIVECILRGTAVDGSEVKALDQTLLEELDSRTTIGEMRHISITTSADFPINIRDEI	80
RGLRKDCFLHRLSQHESGTIEHILEGLSLETILAPYHPNGPEKFHEELLNAEQFLMGFVDSADTGKPLLVTDVWGTMK	160
DYCSQYATNLQPVYSAVYMGFAELFTRATAVLTAGPLRGPGILDLTALPINGPVMFSGSWGKRWLGRKRVVHDDGISE	240
EGFDAIGRLSDENTDLLANGVFQFALVGSQVQRKVDRLTLGVQTVFGHVPLELVVRYIEAYKERIHRVDPNNTSLVLET	320
SSPLEIEVCVHNSGAVVHNGDGVAAALIESLHDTLKNKGLVAGDITSDLPMLQHAYSEKRGAMALFVAGDSLRESVRS	400
IVGDDSRICFVSCFDVVHAAFAKILAAKVELD	432

..... 80
..... 160
..... 240
..... 320
..... 400
..... 432

(Threshold=0.5)

SeqName	Position	Potential	Jury agreement	N-Glyc result
Sequence	312	0.4667	(7/9)	-
Sequence	313	0.4421	(7/9)	-
Sequence	379	0.5062	(4/9)	+

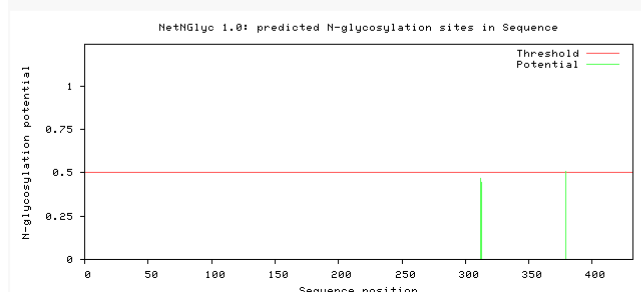


Figure S3. N-glycosylation site prediction. The amino acid sequences of HcGOB (NCBI accession numbers: HF967182.1) was used to predict N-glycosylation site by NetNGlyc 4.1 Server. The predicted results showed the presence of an N-glycosylation site in the protein structure. http://www.cbs.dtu.dk/services/NetNGlyc/#opennewwindow_