Fig 1: Seq ID no 1

KEACPTGLYTHSGECCKACNLGEGVAQPCGANQTVCEPCLDSVTFSDVVSATEPCK
PCTECVGLQSMSAPCVEADDAVCRCAYGYYQDETTGRCEACRVCEAGSGLVFSCQ
DKQNTVCEECPDGTYSDEANHVDPCLPCTVCEDTERQLRECTRWADAECEEIPGRW
ITRSTPPEGSDSTAPSTQEPEAPPEQDLIASTVAGVVTTVMGGGG*EPKSSDKTHTCPPC*
PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

Fig 2 Table 2

Amino Acid Sequence Indicating Glycosylation Sites / Post-Translational Modifications

KEACPTGLYT_HSGECCKACN_LGEGVAQPCG_ANQTVCEPCL_DSVTFSDVVS_ATEPCKPC
TE 60
CVGLQSMSAP_CVEADDAVCR_CAYGYYQDET_TGRCEACRVC_EAGSGLVFSC_QDKQNT
VCEE 120
CPDGTYSDEA_NHVDPCLPCT_VCEDTERQLR_ECTRWADAEC_EEIPGRWITR_*ST*PPEGSD*S*
T 180
AP*ST*QEPEAP_PEQDLIA*ST*V_AGVV*TT*VMGG_GGEPK*SS*DK*T*_H*T*CPPCPAPE_LLGGPSVFLF
240
PPKPKDTLMI_SRTPEVTCVV_VDVSHEDPEV_KFNWYVDGVE_VHNAKTKPRE_EQYNSTY
RVV 300
SVLTVLHQDW_LNGKEYKCKV_SNKALPAPIE_KTISKAKGQP_REPQVYTLPP_SRDELTKN
QV_360
SLTCLVKGFY_PSDIAVEWES_NGQPENNYKT_TPPVLDSDGS_FFLYSKLTV_DKSRWQQGN
V_420
FSCSVMHEAL_HNHYTQKSL_SLSPG

N linked glyosylation sites shown in bold
O linked glycosylation sites shown in italics+underlined

Fig 3

Seq ID no 2:

KEACPTGLYTHSGECCKACNLGEGVAQPCGANQTVCEPCLDSVTFSDVVSATEPCKPCTECV
GLQSMSAPCVEADDAVCRCAYGYYQDETTGRCEACRVCEAGSLGLVFSCQDKQNTVCEEC
PDGTYDEANHVDPCLPCTVCEDTERQLFECTRWADAECEEIPGGGGEPKSDKTHTCPPCPAP
ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCVMHEALHNHYTQKSLLSLSPG

Fig 4

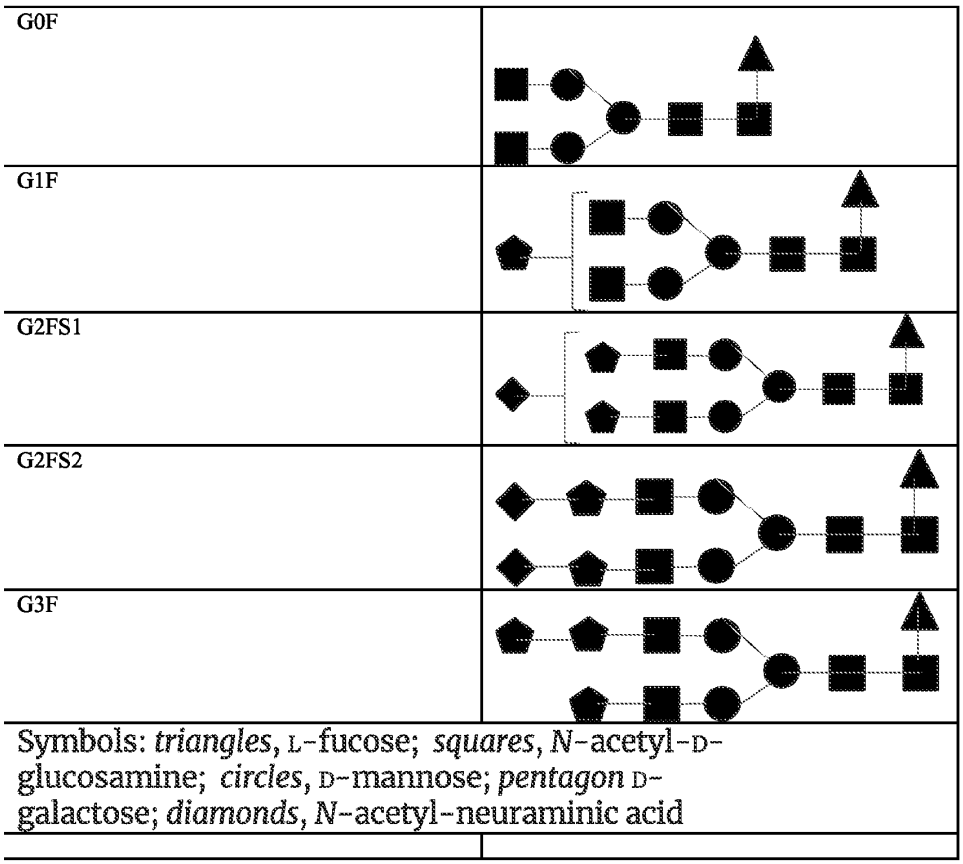

Fig 5

Seq ID No 3

KEACPTGLYTHSGECCKACNLGEGVAQPCGANQTVCEPCLDSVTFSDVVSATEPCK
PCTECVGLQSMSAPCVEADDAVCRCAYGYYQDETTGRCEACRVCEAGSGLVFSCQ
DKQNTVCEECPDGTYSDEANHVDPCLPCTVCEDTERQLRECTRWADAECEEIPGRW
ITRSTPPEGSDSTAPSTQEPEAPPEQDLIASTVAGVVTTVMG