Figure 6: Clustal alignment of the gSG1/Trio family of proteins

```
GSG1A               ------------ACTLQVPETMITRLLQAD-QPAGGCAAAWDSLLSRLEQMRHNLTGCSE
SG1                 -----------EQCVIQLVRGMVTRLLGPN-QAALSCDNLWSNLLLSFNFTRQDLVACQD
SG1-LIKE-3_LONG     RGLPESSDK-LEACGQHYGALLKASTTWNE--KE--CNGST-KLAA-----------CVV
GSG1B               DGGSFLAPSGSNYCPIPLEVLEQENGTAPADWSAS-CTQRRTEDH-------------AK
SG1-2               --QQTPEQ---SACVSHAGAILTAPLIHCHPLKA--CDGEAILKP---------------
TRIO                ---EEAPKPEKEICGLKVGRLLDSVKGWLSVSQQEKCPLNKYCENK------------IQ
                                 *                       *

GSG1A               RETTNPAPPDDTRTNAPCQLLLNE---LQRKGNQ-TLLQLDKEMASKALYERIELAKVVQ
SG1                 GELLVH-PPEP--YFSDCQQRLDS---AKRDAEA-DRRAFTAEMQKKIQVNQWEADRYVQ
SG1-LIKE-3_LONG     SEHEQA-YRE---LKQRCQEAHDERT-AKVNAIYEKLPAYLSEVSARVNVLQVSLQHDLP
GSG1B               IEQAVA-------VIKDHLEKQAA----ATKPIRDELRQFGGTLLPLLNSAQ--VKTDAA
SG1-2               --YLA--------LYQQCRINASERANLRDNFLF-RLNHWHDDHPFLLETVAKAYEPLKA
TRIO                ADQYNL-------VPLTCIRWRSLNP-ASPTGSL-GGKDVVSKIDAAMSNFKTLFEPMKA

GSG1A               DQDRIQQAIETMRTEQ----RNHRQQLLLLYLDAADLRRALHQYK-LLVAQGDRHLPQQI
SG1                 ESDTIRNQLTRLRDEL----RSTYRSLVLMSVQGGASKQALKYYHYYLEGQPPGQLLSSI
SG1-LIKE-3_LONG     NLQEMVGEQRHLIEQAWQYGAQLQHELMLTSMESDRVQRALVLHSMLVNAS-----LAEM
GSG1B               ELDELR------------------MSVLVAAIEAGRIPEAMTQFLMLAGWN----RWPQI
SG1-2               ALESEQDAHRSLRLVP-----ELQRKQLIYSIEAGRLEDAHILHMTLKGQWK----PDQI
TRIO                DLAKLEEEVKRQVLDAWKALEPLQKEVYRSTLASGRIERAVFYSFMEMGDN---------
                                                .     : .     *

GSG1A               VKFVYAAPRHENRRLENLLDLVRQLPARQDQRTLYQLLQPEIMKRPTQNQSTLAMLTALE
SG1                 IAAVYSVPEHAHERFEYLLDFARKVPGNSVRLAFYHQITAELRRHPEQRDSYLAMIAALD
SG1-LIKE-3_LONG     VKESYQTHGADGRMVVRMLKFVRLLPGADERVAVYKQL-AELLKSNGQDGRFPAVIFSTD
GSG1B               VAQIYQNTRRDRQHIANLLEFIRIVPARDDRVAFYHELKKHMVASKDYESYLGAMFAADA
SG1-2               VSAIQDGYHVNPTIMEHLLEFVRAIPVRKERAAYYKAIGPVIRNFKLTLTYVTLLFAGDA
TRIO                ---VKLDNYFQPANVEELLKYAWALPMHKKQRSMYDLIGQLVQSSK---SPMLQTLHAVE
                                  .  :*.    :*  . : : *. :   :            : .

GSG1A               MG-------QVVEGNGELKKQQDAMYQLVLKRWMFLCLAGQ-YREIVQFATKHPRLFEQI
SG1                 LGKL-----AFLSQNADARQLYLGLFNPALKRLQAAVIAGS-YDEIVTFATAYPDHFEQI
SG1-LIKE-3_LONG     VR----------QLEDRYKPDHAQYEGKVVERWLAELQAGT-FHEVVEFARDYPEYFARV
GSG1B               FHVVYEADGKTPLNESDVKALYTTMLDGAGAYFQRALLTGANRYDLFLLDEHHPQLFDLL
SG1-2               TG---------VFDTRKDRDDYISQPLTVFVHMLRWQLANLEFEFHLSLAERFPRYYSLH
TRIO                LA----------TVVNPELENRENLLNDQVVQLRDNLYKNS-FATLVSIARHFPDHFDTL
                                                          .      . :   .*  :

GSG1A               GAKIATIHPKYWWKFS-FTQFVTYPNLLPLPEQRLEAFRTIMKQLKQRNG-----KFFAD
SG1                 ANQLSTLESEAWNQAN-FERLLLYPNRLPLAKQRLEAFRMMLLQINQRNK-----HDFAP
SG1-LIKE-3_LONG     EEPLYETLKQQWSAEG-LDRMVSFPNALPVGVQRVRALRALLETLLQHQGE----QNNDV
GSG1B               FDRIVNVSQANMRKFN-SWQMMGALCRVHRPMSKVLLFRKTANLLLDHFKWE---KENEY
SG1-2               IEQIFFFAPPHWQKAE-KRRLFEIASLFKAKGHRFAAIEQLLKWAHQYAPMRGGKAHLEE
TRIO                RQRLFKLPDGSKPGADTLPNIVNFIAQLPSDELRLSSVDLLLQSLTAENGT---LVQDPE
                       :               .:.     .     :.  .

GSG1A               HLAKLAPQIERCEQFLRQ-QKKELEWKDELVKLKGQFADFDR------RKDYAYYLKNS-
SG1                 RLTRVAKELDKCESFVKSGSKTQQSDLEKLVAVKRMFATRDA------NRDYDHYLQES-
SG1-LIKE-3_LONG     YLIRLAHETGRVEATVGQADAAVRQALDDVKKLFEQFKYQRG------FPDYEALYKLF-
GSG1B               YAPMLAGYFEVCLPDIRK-DPATAGLVTEVQNIFGRYKKGMN------YKSISHIIGKNI
SG1-2               ILPTLALETEKLRRTVEQTGKSS-AELVRLKKLEEKFVSKKDRWNTNTYRTYLHMIKTKG
TRIO                YVYRLSQLAHAMPSLVDV--KAHPDLQQSVDDLMAKFNTPIDGKTLQYFQNIGISPSSSV
```