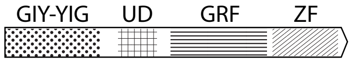
Additional file 6

PGv-1-2p
(291-aa)



GIY-YIG

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                       *              * *         *   *
PGv-1-2p               MRWIYILKC-----ED-NYFYVGETAR-LYRRFWEHTAGIGGLNTQIFKPEEIVAIY--KVDTIGKFLEYN
AACY021487243.1      MPCTWLYVLTS-----NDGDYVYVGMTHR-LITRLNEHMEGKGAVATSRRIYNTVQCVY--KIDTVEQHNHAL
AACY022610711.1        MHWVYILKC-----NN-NNLYVGETKT-LYKRLNQHVNKKGSKHTCDGTLESLNALY--KVQSLYRYLMYC
AACY023304359.1       MVHWIYVLEC-----SD-RNIYVGETTR-LYSRFSEHIGGRGSVNTSSHSPRKLIGLY--KVDDNHSFFKYR
1YWL                 MENKKSHYFYVLLC-----QD-GSFYGGYTTE-PERRLTEHNSGTGAKYTRLAKRRPVIMIHTEKFETRSEATKAE
YP_003786767.1        MENEFYYVYILLC-----ED-GSYYTGVTNN-LKERFIKHSKGKGAKYTKTHKPIKFLSAW--RVENISIALKIE
Penelope-5_NV_1p     -TCNTKNVIYMIQC-----NRCNLQYIGETKRKLKERFNDHRRTVDSQSRSIPT---HAAEH--FLKPNHSASDIE
Penelope-1_OL_1p     -SYKQSNVVYSIHC----KENCNEQYIGETKQPLHKRLYQHRRANPSG------PESAVHLH--LKATNHSFEDSE
Neptune2_Ren_2p      -TCTSSNVIYLITC-----LKCQKQYVGKTSKTLRERICHHRSSINNNEPR------YISKH--FNLPGHQLSHLK
Penelope2_Dw_1p      -TMDKSNVVYKIPCNGTNEESCDKMYIGTTKSRLKTRLSQHRSDYKLRQHSNIQ-KTALMAH--CAASGHSPNFDE
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UD

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PGv-1-2p             CAKYKDYFDKLEAENNIAECM---------------MIHNKDNWEKIRGGKYTKFNC
AACY023304359.1      GEGSGN----LDIENHITELYFHLRNKEDDIEGVSSFRYNDGMTNKVNGGKYTKMFN
AACY022610711.1      VWNNKD--WAIKVENFITEYL----------------LEE---NISVNGGKYVNDNK
AACY022686916.1      IWNNKQ--YALEIENFITECI----------------LST---NENTFGGKYVNSNR
AACY020070058.1      MEGSKD--KAEEIENYVTEFI----------------MSSVDDNKMVRGGKYMKGEK
AACY021487243.1      ---------NHALENELTLKIM---------------RSRGGAWWKVRGGKWCGMTK
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GRF

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PGv-1-2p                    PINNNIKELP-MCKCGVPCD--IKKNDDKNY--LFFRCAKKNM-WENFKDDFDI--EDEPCNFFMEYITDIEFRIDE
AACY023293758.1             PNNQLAKELP-NCNCGFPCD--VKQNEENNY--LYFRCAKKNM-WDKMREEFGI--ADEPCKFFMKYTNDNKYKIEY
AACY023304359.1             VDNDYILDRP-CCDCMFPCE--VKISKDKKT--IYFVCSVKNI-WDDFDSKGLQ--IEGPCDFYKVYTEDTYIKKAY
AACY023344224.1             IPETSIVDRP-LCKCLLPSE--VKLSKDKTK--IYFVCALKNV-WGDFFAD-LQ--IDEPCDFWQMYTEDNAAKAEY
AACY022610711.1             LKKV-----P-LCKCGLPAE--IKCVKNSKYYKLYFTCCIKNV-WSKMSSEFKKINIHNPCNYYFECMDGLEFRMIM
AACY022686916.1             NKKKSINNRP-ICKCGLPCE--VKIIKPGKYYKIYYVCSKKNI-WEHMRERFNHLNIPKCCNFYCEYLDDLEYRVKL
AACY020070058.1             GEKKEDDGRP-MCECGIPCE--IVKRQTKRKINFYYVCPLKNV-WDEMRKEFKMIEIEKPCKYFEEYMDDVEKRVMY
AACY021487243.1             PELRAIQGFPEMCLCHYPVD--VMVA---KNGRKFATCACKNTDWLRGKVNVGYEIAGSTCNYFRWTDGND------
XP_002428087.1-1GRF finger  SSSNNDLSIP-KCFCQLPAISRVVTKLGQNHGKLFYTCNNQNI--------------SNKCNFFQWALPDGQTGNHA
XP_002428087.1-2GRF finger  VSKTKDTNVV-KCHCSVSTKKCVVNKEGPNKGKSFFVCGNKNI--------------DGKCNFFKWA----------
XP_394050.4, 1GRF finger    WGDIDENSVI-LCNCNENAIQLIVRKEGPNHGRAFYKCA-KPM--------------NNRCDFFIWAPDNMSGHIQN
XP_394050.4, 2GRF finger    -NNYNVATIV-KCNCNQLATTRIVKKDGPNKGRSFYTCP-KNM--------------NESCKFFQWADENVEATCNN
EFN81542.1 1GRF finger      WGNIDNNAVI-MCNCHETAIQLTVRKEGPNIGRLFYKCA-KPQ--------------GSGCHFFLWASDSDESQANT
EFN81542.1 2GRF finger      WGSDASSNDV-ICQCNQPARKLTVHKEGPNKGRQFYGCP-KGI--------------NSSCNFFQWADENTDQSSFS
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ZF

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PGv-1-2p             KKSFWLNNVECEIDDECPE-CVSCNKYVWCDKNGEFKNNGIEYGNERRLLCRDCFVNKNEELSQKYSL---TGKCLIKL
AACY023293758.1      SKSHWLKELSGGQYEHCVGGC----------GKEYDQNNTIRYLRKAINLCFDCFIDKNEELAKKYNQNNPVGKCLIQLKHLM
AACY023304359.1      LKESWLSNIPVSLYKIHPEPCVMCKKTNYL---------AIFAFTKVRRICQECMINKYDELKKDYSSS--PGRCLMVD
AACY023344224.1      SRENWVLNIPSSRYKIHPDPCISCSKTDYL---------AIYN-NGIRRLCQSCIIKKYNDLKEKYDKS-----CLIKDT
```