

gi|66826855|ref|XP_646782.1| 1 -----MSLKLKINKI-----AKKS 135TLLKSSLSLQKTKFNHINRSSSR--SNENNYKRY-----SS
YKR016W 1 -----MMLRWTSRRIVLR-----RGL
gi|85115071|ref|XP_964810.1| 1 MLRRTSLRSVRALGSRFSAAVAGRQWQAVVVRRAAVSQQRHAFADDKRPVVPFESQPAVMPA 60SPLTSPPLPPASPQVEPTSTVPPETPLPPTPPEATVIPPVAEPP

gi|66826855|ref|XP_646782.1| 54 FSKKEDPEPESHPF 66GF-----KPLHALVLVGGHSAYLKAAWNQDEMESSKLPYORBEVEKFKKIMKEI 116HQDSQRENLNIEKESKESKESDQOQHQQO
YKR016W 18 ASINUGIIVASW 29NASHKFNNTLWTIAMSATAFYAGGI-IVSQKNDKFGDFPSNNVFFAEDLETYEHYHDR- 87-----PTLF-----LE
gi|85115071|ref|XP_964810.1| 108 VVPPHLEFPRK 1ZOGFFRLRNFFLSLHLGATAFGGV-YMSRINDAFHFFETIYIPYQAVLYLEEDFKK 179RF---PDVVV-RVTGRPRDSGEVKVPA

gi|66826855|ref|XP_646782.1| 147 PQQHHQQEKEEKEKVGVENTHLE-----171-----DNIEESIKNHHEEMK-NELVSLIESVQDKVAHSNDDLEHNDEREMDSETGV 221STSEISKLEE
YKR016W 94 PSWDGLKAKSNDLLSGLTSSQRR---118-----SNR-----NIEV-----126-----KK-----
gi|85115071|ref|XP_964810.1| 204 VSGASWRVASGG---EPACRQSESISKAGAA 231AQDVPKSEPAVVAAREETAELKTEATTTATPAEP-----APAPAAADASG 280PV---KPKF

gi|66826855|ref|XP_646782.1| 234 HKQNEPELPLDLE---DVNYGVL-SIMPEAVKSAEETVENAKKFT 275HSNDDDDTTTTSTINTS-----DELKWHNINIENGNEES---LVSDLVNY
YKR016W 129 ---ILGPEFNIEFENSDDPKKIGS---LNDVNSLN 161GSLIPESEFENSIKKSNQMLTNISQVNETLKEALSNY-----M-----IQRSE
gi|85115071|ref|XP_964810.1| 288 APEVDEPFRWPPASLIDPLV-NGATDPVQDLVKM---ADVITVIN 331HDNANEKKA--PTCKA-KNE---SKVAHKINEKAKVEADAAKQVAVRVDGDKA

gi|66826855|ref|XP_646782.1| 321 NV 322LSIPEKVRSEKVKVNVLKKFPE-----QYLEKVEKLI-----356-----SENMKLVDFDKLINGDDEBLKRVVEEIRK
YKR016W 208 207--VITE---LNTQYENSAREFEKNLQKNLLQVDFPENLTKQKLEPKKAGNELL 261QAHANEVGLSITQVKEFNKIKDKI-----EK
gi|85115071|ref|XP_964810.1| 383 ANE 385--LVSRVSEMAAQRAAWKREFEETR---LKSVDREVMHQDR-----EHQQA 431LEKLNNELEQAQLQRFTENIKHHV-----E

gi|66826855|ref|XP_646782.1| 388 YRSSLDAAEELNKDLDEK 407KQMDQFIRSKVFD-NQAVLQETL--EROKSNLNFKQQAESIKQSELEKRAITQLTQCI 464VDLQK---LLHDKSAID----
YKR016W 293 NGRLAHLEETINSEVNDLS 310KSIDRS--SRILSKNEALVQITFQVDEIIS-----RINNNLPDVNIDKELSR 357KLSNLSLNFNKKSCDDGDCQCC
gi|85115071|ref|XP_964810.1| 460 QERDGRGKLNELHKAVAE 480RLTSGL--NEVVDTNLRVQLHVAVDVRA-----SLEDHHPNPFKE 526KE

gi|66826855|ref|XP_646782.1| 479 ---GANCKGLLVRFSKNTLDLSNYQLIKELLSLPE 512GFEXKPVHLDLNNQFDIAKLRKSQLDHNDNSLLGKAVBELASLFIPEKGMVQ-G 571NLYD
YKR016W 382 KKGKNEGKREKISCKCKPKTNPPLLSVALDELES 417GSGKKILSNQIYNRWLLADDFKASLLPP-NSGILQLAKVFLFLFKTKGNPSNA 476HDDSV
gi|85115071|ref|XP_964810.1| 529 -----IAADDPVDAATASINP 545TAYQRCPTTAEIDRFRRVATEVRKASLLPE-DAGVASHASYVLSKLMFKREGLA-G 603DDV

gi|66826855|ref|XP_646782.1| 576 AILARAEDHLRKNLSSAIKEMESIQOQSSKSSNTDNHHLSEKLTSNWIKQAKERD 631DLENISKLELLEKLELHKQOQKKEEQQ 660
YKR016W 483 YARVGDNLRVSNLNAVEEVVSLKWP-----HKVCSWIEDARRKL 524VQRLVEHOCERTL*-----540
gi|85115071|ref|XP_964810.1| 607 ESILTRTQTYLEGGDLDNAAREMNLKQWA-----KTLSRDWLGEVRKVI 651EVQALDVIQAEARLQSLRVE-----672