

YAL010C
gi|164424184|ref|XP_962945.2|

1 MLPYMDQVLRAFYQSTHWSTQNSYEDITATSR-----LLD 36FRIPSA
1 MREFMNYITNAFYGATGWNEEDNKYNELNATSRGAILTVSVDLLQWYLETNTKTHELELD 60EPLPRG

YAL010C
gi|164424184|ref|XP_962945.2|

54 NTFNSLDFSTRSRINGSLSYLYSDAQOLEKFMRNSTDIPLQDA 96TETYRQLQPNLN----FSVSSAN
78 HFATSYQLGSGVVDGSTSYLHSSIP-LTHIAAQSDKIPLPAL 119LRCYRRLHDLRSPGQOHYILDA

YAL010C
gi|164424184|ref|XP_962945.2|

120 -----D----NTVDNDKLLH 132DSKFKKSLYYGRMYFPSSDTEAMITKRLSPQTQFMLKG
153 SARALLGAASDAAVAGGAL-DGGNTDQ 178DLGIYTHSLLYGRLLPKSLLEGMTIKRFTQALQVQVR

YAL010C
gi|164424184|ref|XP_962945.2|

182 LTCYFQRDSE 191ENLQEWIFSTSDLLCGYRVLHNFLTTPSK-----FNST-----
228 TILGLVQYDKG 238KYGLEGLYSTDGGLLGFRLYNGGDASSSSTCDPWTPTPGENNNNNNNNNNNNN

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gi|164424184|ref|XP_962945.2|

225 LYNNSSLSLGAEFWLGLVSLSPGCSTTLRYYTHSTNTGRPLTLLTSLWNPLFGHISSTY 282SAKTGTN
300 KERIYGRFSGGELYGTLNKSGGMSLGFATLPAHRGTPLTATLTINPLMGNINATK 358NDEYKG

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gi|164424184|ref|XP_962945.2|

301 YSTESNLSFGCEFWQKKHLLLETNKNNDKLEPISDELVDIN 342ENSRATKLLHENVPDLNSAVNDI
370 ---LDNNLRMGL-LWEGRAKSLIFSIGTGIDLHKLGEPPFRSLG 408LEVQ-----

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gi|164424184|ref|XP_962945.2|

377 KLLNDLTYAFSSSLRKIDEERSTIEK 402FDNKINSSIFTSVWKLSTSLRDKTLKLLWEGKWRGFLIS
413 -----YSS----- 415-----

YAL010C
gi|164424184|ref|XP_962945.2|

453 QESLSDDEKN 462DNAISISATDTENGNIPVFPKFGIQFOYST* 493
416 ----- 415----- 415