

A

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      10      20      30      40      50      60      70      80
DBL1α R29  -----MTPKRTSRTVNNLSATDVLEKIATGIYNQEKVKVYPYENELKGI LSNAI FVDQLRKELNI-ESPGPSDSCSLD
DBL1α VarO  MGSSHSTNDTKSPTLSESHKSARNVLENIIGIKIYNQEKIKKNPYEQQLKGTLSRAQFVDALSSRYGY-VRNSDGNNSCLND
DBL1α FCR3S1.2 -----MAPKGRSTNEIELSARDVLENIIGIYNQEKIKKNPYEQQLKGTLSNARFHDGLHKAADLGVIPGPSHFSQLY

      90      100     110     120     130     140     150     160
DBL1α R29  HKFHTNINTEYTEGRKPCYERNEKRF SNEGEAKCGSDKIRDYGIKSAGGACAPFRRQNLCDRNLEYLINKNTNTTHDLLG
DBL1α VarO  HLFHTNIKTGYNEGRKPCYGREQNRFDENAEAYCNSDKIRGNENNSNGTACAPRRRHICDQNFLEFLDNKNTNTTHDLLG
DBL1α FCR3S1.2 YKKHTNNTKYYKDDRHPCHGRQGKRFDEGQKFECCGNDKIIIGNSDKYG--SCAPRRRHICDQNFLEFLDNNTHTDTHDVLG

      170     180     190     200     210     220     230     240
DBL1α R29  NVLVTAKYEGDSIVNNHPDKNSSGNKSSICTALARSFADIGDIVRGRDMFKPNADKVEKGLQVVFVKIYNLSPSPAQKH
DBL1α VarO  NVLVTAKYEGNYIVNDHPDKNSNGKSGICTSLARSFADIGDIVRGRDMFLPNKDDKVQKGLQVVFVKIYKSLTPEARKH
DBL1α FCR3S1.2 NVLVTAKYEGESIVNDHPDKNNGKSGICTSLARSFADIGDIVRGRDMFKPNKDAVRHGLKVVFKKIYDKLSPKVQEH

      250     260     270     280     290     300     310     320
DBL1α R29  YAHDDGSGNYKLRDWWAINRKEVWKAITCRAPNEANFRNISGNMKAFTSQGYCGHSETNVPTNLDYVVPQFLRWFEW
DBL1α VarO  YAHGDGSGNYSKLRDWWTINREQIWKALTC SAPYYADYFRKGS DGTLHFSSHGKCGHNEGAPPTYLDYVVPQFLRWFEW
DBL1α FCR3S1.2 YKDV DGS GNYKLRDWWTANRDQVWKAITYKAPQDANYFRNVSGTTMAFTSAGKCRHNDNSVPTNLDYVVPQFLRWYDEW

      330     340     350     360     370     380     390     400
DBL1α R29  AEEFCRIRKIKLENVKKECRDEPN---NKYCSGDGHDCRRTY LKDNTIFIDLNCPRCENACSNYTKWIEIQRKQFDKQKR
DBL1α VarO  SEEF CR I R K I K I D K V K K E C R D E Q N ---K Y C S G D G H D C T Q T N L S H N Q I F V D L D C P R C Q D Q C I K Y N E W I V K K L E E F Y K Q N L
DBL1α FCR3S1.2 A D D F C R I R N H K I Q K V K D T C Q G Y N N S G Y R I Y C S G D G E D C T N I L K Q N F N I V S D F F C P S C K T E C T N Y K K W I N K K Q G E F N K Q K K

      ..
DBL1α R29  KY
DBL1α VarO  KY
DBL1α FCR3S1.2 KY

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