

```

At1g73200      1  MVSFTGFVAVFVGLLGLAIVTAEVVGFYLLKRLNRKRDROESNSSSDPNFKSFDPROS 60 IDFSLNKQGVVWLELDENVKDWKMKELPKKQKKRV
gi|66816495   1  ----- 0-----
YOL009C      1  ----- 0-----
gi|85113864   1  ----- 0-----

At1g73200     98  DLLEVHPVRRFARIKDKHKLISD 120 SIDGPQTPITLKGCFVDAVSGSGPTRKWKAKRFPIOVESKTSVLYKGNRVFYIFLETSWEK 180 PSWCKALRL
gi|66816495   1  ----- 0-----
YOL009C      1  ----- 0-----
gi|85113864   1  ----- 0-----

At1g73200    190  AACENQERFIWSTKLKEDFRNYLASLNAAYPSFMKPSAGFSFESLDKGLKA 240 DGPSSKVRLLWKKFSSKCKSTKVNFPFSIRDKKTSSRSYQDSQST
gi|66816495   1  ----- 0-----
YOL009C      1  ----- 0-----
gi|85113864   1  ----- 0-----

At1g73200    286  GSSGKSTARRMODN 300 TPEETVQVVISRSWSHSHASDVDSSEKSFDEGTLALN 56 VVLSRLFFDVKQNTVYLNKLVRE 360 RIQRIMSNMRIPSYICG
gi|66816495   1  ----- 0-----
YOL009C      1  ----- MSFDINWSTLES-----DN---RINDLIRK 22HLNSYLQNTQITPSYVSNLRVLDLDFDLGK
gi|85113864   1  ----- 0----- MSTDLNWDVTVG-----GPDGQEAACKLRD 25FHEKFAVPLRFRFKSVTVHDFEFGS

At1g73200    378  LICCDVDIGNLFPVYIHGTRILPEMENGWVAFE----- 409-----
gi|66816495   1  ----- 0-----
YOL009C      50  VGPAAHTL----- 56-----
gi|85113864   53  IPEEHELKIDITDE-LPDFYEEQPGIDSSSEESDS 84 EEVAVENEGEYIDDPVEQYGLRGLGASASESRRRLTVNSSTGSRNCGSPNSGRVAYLPP 144

At1g73200    410  ----- 409-IDIEYTGGAQLEVEVTRVDAREEDLQKQIAEGLKIQNSAGDVPPDLLEGLADE----- 462---KQINVPGGTVDAQDVK--SGG
gi|66816495   1  ----- 0-----
YOL009C      57  ----- 56-----
gi|85113864   145 HLNPHYNGGSGNNSPPLDRDQRYR-----DPNTAGLGGPA--HGTNHHHADLGGP 194 FLGVSTPGIPGGTSLNLMHYFTSQFTAGLSGTQPL

At1g73200    482  TDKADESKGPKGT--KTGSSNGSKWKSMLKNIVEQ 514V-----SQ-----
gi|66816495   1  ----- 0-----
YOL009C      57  ----- 56-----
gi|85113864   231 AAVGAAHQRGPSWADQQQQQQ 254 QNNMLPGCAGGGCGAGGGMGGPFVAAAAAAAAAANOGLHSSSTPHLRHLPFGVGTGCKPTFC 314 EPLTCTS

At1g73200    518  517-VP-----ITLSIGVSSRLGTLCVHMKPPPSDQLWEGFTSMPDIE- 556---FNLVSSVGEHKITN---SHVAMFLVN---
gi|66816495   1  ----- 0-----
YOL009C      57  ----- 56-----
gi|85113864   323 TPLGLTGTAGGVGGIGRGMGAMGCS-M-ASMGYPPTAPVL-AITGPRHKR 371 NPSSQSLNSVGDYSPVAPAPAERQGLFSAAAAATSPPSSTPSPAV

At1g73200    580  -----RF-K-TAIRD 587VMVLPNCSVITIPWMTAEKDDWVBRNV-----APFMWLNQ--DSTS---DRE 629NLEFA
gi|66816495   1  --- 0-----MSLKIYWRVTEKHSIKLMN-----YLNBERHSGLTETYDMV 36GEMKITNLSL-GSKPPKFE-----IL---
YOL009C      57  ----- 56-----KELTDPLDEFYDSIREADQE 77TEENNDNKEDSEHICPDRT---
gi|85113864   416 GLGIGGRCIGAAGAGA 431GALATSGPRLQIPKQGLRKKHVSSTLAPNSAGTSNNRAGSAILDDDDGFLDGMHHRDHP 491AQQLEPEEDEE---

At1g73200    635  EAKSKADKPTSEMQMKTVNIPOKPRIEESVSDTAPSANSIALLVESDKS-- 686-----LEELKTPLESEKHDTIARCGSGDIIPGIG
gi|66816495   57  QISDPDALLGNKSPNGIELRAKIGYDGD 85AVTGIQAEFKVNLPTPNFISFPVNVK---VSNPIFSGIATVHYDTKVCFCFPENG 140SPDD
YOL009C      97  ---IANHEGFKDDFAPVVMPSNDIQFLLEVEKCD 130LLVTIGADLVNYPVEKFMPLPVRLS---ISDGLHSLCIVACSKQLFLSFLCDVS
gi|85113864   504  -----EEEGEERORFREPRVSDIQAVFRIKYAGD 534VKLLTADLLDYMPSEFVGLPVRLS---ITGLTFDGVGVNIRKRVHF

At1g73200    719  QS-----PSMST----- 725---VSGEEDDSNKG-KK---MGAAKARMF-----DFRKKVGEKFEKK---SHVPE 767KSROVVEKMRGP-
gi|66816495   145  -----FTPLKDVKFTQLGDS---AQOVLVDLKK 170LQNFIVDLIKTYLKKYLVFPNKMTPLESEFNN- 202
YOL009C      185  D 185PALD---DNQTVLDPKGPILAAT---KPLERISIVRSMKIETEIGEYQGGSVLRSVGE 239LEQFLFTIFKDFRRELAWPSWNLDLFDNDGD
gi|85113864   582  CFLSPEDA 589VAAVGGEENKAAGSGNCSGIGGGSDEAKTAMGGLLEIRVSEISIQRESGKQ-SLKNVVGK 648VEEFLVBOVRRIFEEEFVYPSFWT

At1g73200    780  ----- 779
gi|66816495   271  E* 271
YOL009C      673  FVV----- 675
gi|85113864

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