

AT2G21770.1 AT2	1	M-----NTGGRLIAGSHNRNEFVLI
AT1G02730.1 AT1	1	MVKSAA SQSPSPVTITVTPCKGSGDRSLGLTSP IPRASVITNQNSPLSSRATRRTS ISSG
os_42915 LOC_Os	1	MA-----LSPAAAGRTG----
AT1G55850.1 AT1	1	MVN-----
AT4G23990.1 AT4	1	MYQ-----
AT2G32530.1 AT2	1	MA-----
os_25268 LOC_Os	1	MA-----
AT5G22740.1 AT5	1	M-----
AT2G24630.1 AT2	1	MAPRFDFS DLWAKETRRGTPV VVKM-----
consensus	1	*

AT2G21770.1 AT2	21	N-----
AT1G02730.1 AT1	61	NRRSNGDEGRYCSMSVEDLTAETTNS ECVLSYTVHIPP TPDHQT V FASQESE EDEMLKGN
os_42915 LOC_Os	13	-----
AT1G55850.1 AT1	4	-----
AT4G23990.1 AT4	4	-----
AT2G32530.1 AT2	3	-----
os_25268 LOC_Os	3	-----
AT5G22740.1 AT5	2	-----
AT2G24630.1 AT2	26	-----
consensus	61

AT2G21770.1 AT2	22	-----ADDTARIRSAEELSGQTC--KICRDEIELTDNGEPF
AT1G02730.1 AT1	121	SNQKSF LSGTIFTGGFKSVTRGHVIDCSMDRADPEKKSGQICWLKGCDEKV-----V
os_42915 LOC_Os	13	-----
AT1G55850.1 AT1	4	-----
AT4G23990.1 AT4	4	-----
AT2G32530.1 AT2	3	-----
os_25268 LOC_Os	3	-----
AT5G22740.1 AT5	2	-----
AT2G24630.1 AT2	26	-----
consensus	121

AT2G21770.1 AT2	56	IACNECAFPTCRPCYEYERREGNQAC PQCGTRYKRIKGS PRVEGDEEDDDIDDLEHEFYG
AT1G02730.1 AT1	173	HGRCECGFRICRDCYFDCITSGGGNC PGCKE PYRDINDDPETEEDEE DEAKPL-----
os_42915 LOC_Os	13	-----RNNNDA-----
AT1G55850.1 AT1	4	-----
AT4G23990.1 AT4	4	-----
AT2G32530.1 AT2	3	-----
os_25268 LOC_Os	3	-----
AT5G22740.1 AT5	2	-----
AT2G24630.1 AT2	26	-----
consensus	181

AT2G21770.1 AT2	116	MDPEHVTEAALY MRLNTGRGTDEVSHLYSASPGSEVPLLTYCDESDMYS DRHALIVPP
AT1G02730.1 AT1	227	-----P
os_42915 LOC_Os	20	-----
AT1G55850.1 AT1	4	-----
AT4G23990.1 AT4	4	-----
AT2G32530.1 AT2	3	-----
os_25268 LOC_Os	3	-----
AT5G22740.1 AT5	2	-----
AT2G24630.1 AT2	26	-----
consensus	241

AT2G21770.1 AT2	176	STGLGNRVHHPFTDSFASI-----HTRPMVPQKDLTVYGYG SVAW-KDRMEVWKKQQ
AT1G02730.1 AT1	228	QMGESKLDKRLSVVKS FKAQNQAGDFDHTRWLFETK--GT YGYGNAVWPKDGYGIG----
os_42915 LOC_Os	20	-----GLADPLL P AGG--G----
AT1G55850.1 AT1	4	-----
AT4G23990.1 AT4	4	-----
AT2G32530.1 AT2	3	-----
os_25268 LOC_Os	3	-----
AT5G22740.1 AT5	2	-----
AT2G24630.1 AT2	26	-----
consensus	301

AT2G21770.1 | AT2 228 IEKLQVVKNERVNDGGDGFIVDELDDPGLPMMDEG-RQP-----LSRKLPIRSSRINPY
AT1G02730.1 | AT1 282 -----SGGGNGYETPPE-----FGERS-KRP-----LTRKVSVAIAISPY
os_42915 | LOC_Os 32 -----GGGGKDKYWVPADEEEIICRGEDG-GRPPAPLLYRTFKVSGVLLHPY
AT1G55850.1 | AT1 4 -----KDDRIRPVHEAD-GEP-----LFETRRTGRVI-AY
AT4G23990.1 | AT4 4 -----VSLKQFVFLKIKSTTMEPHRKHSVGD-----TLHTCHPCRRTI-PY
AT2G32530.1 | AT2 3 -----DSSSSL-----PPLCEKISY---KNYFL
os_25268 | LOC_Os 3 -----VVA AAAATGSTTRS GGGGGEGTRS GRKKPPP PPLQERVPLGRRAAW
AT5G22740.1 | AT5 2 -----
AT2G24630.1 | AT2 26 -----ENPNYSIVEVEEPDSAFQPM EKSRGKNAKQVTWV LLLKAHKAVGCLTW
consensus 361
consensus 1 *

AT2G21770.1 | AT2 282 RMLIFCRFAILGLFFHYRILHPVND AF-----GLWLTSV ICEIWF AVSWILDQFPKWYPIE
AT1G02730.1 | AT1 318 RLLIALRLVALGLFLTWRVRHPNREAM-----WLWGMSTTCELWFALS WLLDQLPKLCPVN
os_42915 | LOC_Os 79 RLLTLVRLIAVVLFLAWRLKHRDSAM-----WLWWSIAGDFWFVGTWLLNQASKLNPKV
AT1G55850.1 | AT1 33 RFFSASVFCICLIWFYRIGEIGDNRTVLDRLIWFVFMFIVEIWFGLYVVTQSSRWNPVW
AT4G23990.1 | AT4 46 RIYAVFHTCGIIALMYHHVHSLLTANTT---LITSLLLLSDIVLAFMWATTSLRYPKVR
AT2G32530.1 | AT2 23 RVVDLTIAGFLFSLLLYRILLMN-----QNN SVVVVAF LCE SFFSFIWLLITSIKWSPAS
os_25268 | LOC_Os 51 RLAGLAVTLLLALLALRLLRHGGAG-GDGGVWRVALVCEAWFAALCALNVSAKWSVPR
AT5G22740.1 | AT5 2 -----DG-----
AT2G24630.1 | AT2 74 VATVFWSLTIGSVKRRLSFTHPLGSERLGRDGLFSAIKLFLVASLAILAFELVAYVRGWH
consensus 421 ..
consensus 61

AT2G21770.1 | AT2 338 RETYLDRL-----SLRYEKEG-----KPSELAPVDV-FVSTVDPLKEPPLITANT
AT1G02730.1 | AT1 374 RLTDLGVL-----KERFESP NLRNPKGRSDLP GIDV-FVSTADPEKEPPLVTANT
os_42915 | LOC_Os 135 RVPDLSLL-----RRRFDD-----GGLP GIDV-FINTVDPVEDEPMLYTMNS
AT1G55850.1 | AT1 93 RFPFSDRL-----SRRY-----GSDLPRLDV-FVCTADPVIEPPLLVVNT
AT4G23990.1 | AT4 103 RTEYPEKY-----AAE-----PEDFPKLDV-FICTADPYKEPPMMVVNT
AT2G32530.1 | AT2 78 YKSYPERL-----DERV-----HDTSPVDM-FVTTADPVREPPLLVANT
os_25268 | LOC_Os 110 FVTRPENLVAEGRTPSTTAAEY-----GELPAVDM-LVTTADPALEPPLVTVNT
AT5G22740.1 | AT5 4 --VSPKFVLPETFDGVRMEIT-----GOLGMI--WELVKAPVIVPPLQLAVY
AT2G24630.1 | AT2 134 YFKNPNLHIPTS---KLEIQ-----SLHLFYVGVLSLRADYIAPPKALSK
consensus 481 *
consensus 121

AT2G21770.1 | AT2 382 VLSILAVDYP--VEKVACYVSDDGAA MLTFEALS YTAEFARKWVP-FCKKFSIEPRAP EW
AT1G02730.1 | AT1 423 ILSILAVDYP--VEKLACYLSDDGALLTFEALSAQTASFASTWVP-FCKRKHNI EPRNPEA
os_42915 | LOC_Os 175 ILSILATDYP--ADRHAAYLSDDGASLAHYEGLIETARFAALWVP-FCKRHRVEPRAPES
AT1G55850.1 | AT1 132 VLSVTAADYP--PEKLAVYLSDDGGSELTFYALTEAAEF AKTWVP-FCKKFNVEPTSPAA
AT4G23990.1 | AT4 141 ALSVMAYEYP--SDKISVYVSDDGSSLTFLALMEAAKFSKHWLP-FCKKNNVQDRSPEV
AT2G32530.1 | AT2 116 LLSLILAVNYP--ANKLACYVSDDGCSPLTYFSLKEASKFAKIWVP-FCKKYNIKVRAPFR
os_25268 | LOC_Os 158 VLSLILADYPRAGERLACYVSDDGCSPLTCHALREAAGFAAAWVP-FCRRYGVAVRAPFR
AT5G22740.1 | AT5 47 ICLLMSVMLL--CERVYMG I-----VIVLVKLFWKK--PDKRYKFE
AT2G24630.1 | AT2 178 FCIVLFFVQS--VDRLILCL-----GCLWIK--FKK--TKPRIDEE
consensus 541
consensus 181

AT2G21770.1 | AT2 439 YFSQKMD-YLKHKVDPAFVMERRAMKRDIYEFKVKINALVSVSOK-----
AT1G02730.1 | AT1 480 YFGQKRNF LKNKVR LDFVRERRRKRREYDEFKVRINSLPEAIRRRSDAYNVHEELRAKK
os_42915 | LOC_Os 232 YFAAKAAPYAGPALPEEFFGDRRLVRRREYEFKARLDALFTDIPORSEA-----
AT1G55850.1 | AT1 189 YLSSKAN-CLDSAA-----EEVAKLYREMAARTETAARLGRIPEEA-----
AT4G23990.1 | AT4 198 YFSSKLR-SRSDEA-----ENIKMMYEDMKSRVEHVVESGKV-ETA-----
AT2G32530.1 | AT2 173 YFLNPPAATESS---EFSKDWEITKREYEFKLSRRVEDATGDSHWLDJAE-----
os_25268 | LOC_Os 217 YFSSSSSPESGGPADRKFLDDWTFMKDEYDKLVRRTKNTDERSLLRHGG-----
AT5G22740.1 | AT5 84 PIHDDE--ELGS-SNFPVVLVQIPMFNEREVYKLSIGAACGLSWPSDRL-----
AT2G24630.1 | AT2 213 HFRNDD--FEGSGSEYPMVLVQIPMCNEREVYEQSISAVCQLDWPKDRL-----
consensus 601
consensus 241

AT2G21770.1 | AT2 483 -----VPEDGWTMQDGPWPG-----NNVRDHPGMIQVFLGHSGVC
AT1G02730.1 | AT1 539 KQMEMMMGN NPQETVIVPKATW-MSDGSHPGTWSSGETDNSRGDHAGIQAMLAPPNAE
os_42915 | LOC_Os 281 -----SVGNANTKGA---KATL-MADGTPWPGTWTEPAENHKKGHAGIVKVMLSHPGEE
AT1G55850.1 | AT1 229 -----RV-----KYGDGFSQWDADATRRNHGTILOVIV-----
AT4G23990.1 | AT4 237 -----FITCDQFRGVFDLWTDKFRHDHPTIIQVQLQSEN--
AT2G32530.1 | AT2 218 -----DD-FEDFSNTKPNHSTIVKVVWENKG--
os_25268 | LOC_Os 266 -----GEFFAEFLNVERRNHPTIVK-----
AT5G22740.1 | AT5 130 -----VIOVLLDDSTDPT
AT2G24630.1 | AT2 260 -----LVQVLLDDSDDES
consensus 661
consensus 301

AT2G21770.1 | AT2 519 DMDGNE-----LRLVYVSRERKRPGF DHHK KAGAMNSLIRVSAVLSNAPY
AT1G02730.1 | AT1 598 PVYGAEDAENLIDTTDVIDRLPMLVYVSRERKRPGYDHNKKAGAMNALVRTSAIMSNPFF
os_42915 | LOC_Os 332 PQLGMPASSGHPLDFS AVDVR LPLVYIAREKRPQYDQHKKAGAMNAQLRVSSALLSNAPF
AT1G55850.1 | AT1 257 --DGREGNT-----IAIPTLVYLSREKRPQH HNF KAGAMNALLRVSSKITCGKI
AT4G23990.1 | AT4 272 --DMDDTK-----YIMPNIYVSR EKSKVSSHFFKAGALNTLLRVSGVMTNSPI
AT2G32530.1 | AT2 244 -----G VGVENEVPHFVYISREKRPNV LHHYKAGAMNFLV RVSGLMTNAPY
os_25268 | LOC_Os 286 -----TRVSAVMTNAPI
AT5G22740.1 | AT5 142 VKOMVEVEC-----ORWASKGINIRYQIRENRVGY----KAGALKEGLKRSYV-KHCEY
AT2G24630.1 | AT2 272 IQELIRDEV-----TKWSQKGVNIYRHR LVRTGY----KAGNLKSAMSCDYV-EAYEF
consensus 721 *
consensus 1 *

AT2G21770.1 | AT2 564 LLNVDCDHYINNSKAIREAMCFMMDPQ-SGKKICYVQFPQRF DGDIDRH--DRYSNRNVVF
AT1G02730.1 | AT1 658 ILNLDCDHYIYNSMALREGMCFMLD-R-GGDRICYVQFPQRFEGIDPN--DRYANHNTVF
os_42915 | LOC_Os 392 IFNFDG DHYINNSQAFRAALCFMLDCR-HGDDTAFVQFPQRFDDVDPT--DRYCNHNRVF
AT1G55850.1 | AT1 305 ILNLDCDMYANNSKSTRDALCILLDEK-EGKEIAFVQFPQCFDNDVTRN--DLYGSMRNVF
AT4G23990.1 | AT4 320 ILTLDCDMYSNDPATPVRALCYLTDPK-IKTGLGFVQFPQTFQGISKN--DIYACAYKRL
AT2G32530.1 | AT2 290 MLNVDCDMYANEADVVRQAMCIFLQKSMNSNHCAFVQFPQEFYDSNAD--EL--TVLQSY
os_25268 | LOC_Os 298 MLNMDCDMFVNNPQAVLHAMCLLLGFD-DEASSGFVQAPQRFYDALKD--DPFGNQMECF
AT5G22740.1 | AT5 191 VVIFDAD-FQPEPDFLRRSIPFLM---HNPNIALVQARWRVNSDECLLTRMQEMSLDY
AT2G24630.1 | AT2 321 VAIFDAD-FQPN SDFLKLTVPHFK---EKPELGLVQARWAVNKDENLLTRLQNI LCF
consensus 781 . * * * * *
consensus 61

AT2G21770.1 | AT2 621 FDINMKGLDGIQGP I--YVGTGCVFRROALYGF DAPKKKQPPGRTCN CWPKWCC LCCGMR
AT1G02730.1 | AT1 714 FDVSMRALDGLQGP M--YVGTGCI FRRTALYGFSP PRATEHHG-----W-----LGRR
os_42915 | LOC_Os 449 FDATELLGLNGVQGPS--YVGTGCMFRVALY GADPPR-----W-----
AT1G55850.1 | AT1 362 IDVEFLGLDGNNGPL--YIGTGCFHRRDVICGRKY-----
AT4G23990.1 | AT4 377 FEINMIGFDGLMGN--HVGTGCFHRRRGFYGAPS-----
AT2G32530.1 | AT2 346 LGR---GIAGIQGPT--YAGSGCFHRRRV MYGL-----
os_25268 | LOC_Os 355 FKR F ISGVQGVQGA F--YAGTGCFHRRKAVYGVPP-----
AT5G22740.1 | AT5 246 HFTVEQEVGSS THAFFG FNGTAGIWR IAAI-----
AT2G24630.1 | AT2 376 HFEVEQQVNGVFLNFFGFNGTAGVWR IKA L-----
consensus 841 *
consensus 121

AT2G21770.1 | AT2 679 KKKTKGVKDNQRKKPKETSQIHALEHIEEGLQVTNAENNS ETAQLKLEKKFGQSPVLVA
AT1G02730.1 | AT1 760 KVKI-----SLRRPKAMMKK DDEVSLPINGEYNEE EDDGDIESLLLPKRFGNSNSFVA
os_42915 | LOC_Os 485 -----RP-----EDD KALGCPGRYGN SMPFIN
AT1G55850.1 | AT1 395 -----G-----EEEEEEE
AT4G23990.1 | AT4 410 -----NLILP-----EIDELKP
AT2G32530.1 | AT2 374 -----SIDDLEDDGSLSSLATRKYLAEENLAREFGNSNEMVT
os_25268 | LOC_Os 388 -----NFNGAEREDTIGSSSYKE-----LHTRFGNSEELNE
AT5G22740.1 | AT5 276 -----NEA
AT2G24630.1 | AT2 406 -----EES
consensus 901
consensus 181

AT2G21770.1 | AT2 739 STILL-----LNG-----GVPSNVN PASLLRESIQVISCGYEEKTEWGKE
AT1G02730.1 | AT1 814 SIPVAEYQGR LIQDLQKGKNSRPAGSLAVPREPLDAATVAE AISVSCFYEDKTEWGKR
os_42915 | LOC_Os 509 TIPAAASQERSIA-----SPAAASLD-----ETAAMAEVEVMTCAYEDGTEWGDG
AT1G55850.1 | AT1 403 -----SERIHENLEPEMIKAL---ASCTYEENTQWGKE
AT4G23990.1 | AT4 422 -----NRIVDKPINAQDVLALAH RVAGCIYELNTNWGSK
AT2G32530.1 | AT2 411 SVVEAL-----QRKPNPONTLANSLEAAQEVGHCFEYQTSWGKT
os_25268 | LOC_Os 419 SARNIIW-----DLSSKPMVDISSRIEVAKAVSACNYDIGTCWGQE
AT5G22740.1 | AT5 276 -----NEA
AT2G24630.1 | AT2 406 -----EES
consensus 961
consensus 241

AT2G21770.1 | AT2 778 IGVIIYGSVTE DILTGFKMECHGWRSVYCM PKRAAFKGSAPINLS DRLHQVLRWALGSVEI
AT1G02730.1 | AT1 874 VGVIIYGSVTE DVVVTG YRMRHNGWRSIYCVTKRDAFRGTAPINL TDRLHQVLRWATGSVEI
os_42915 | LOC_Os 555 VGVVYDIATEDVVTGFR LHRKGWRSMYCAMEPDAFRGTAPINLTERLYQILRWATGSLEM
AT1G55850.1 | AT1 433 MGVKYGCPVEDVITGLTIQCRGWKSAYLNPEKQAF LGVAPTNLHQMLVQORRWSE GDFQI
AT4G23990.1 | AT4 456 IGF RYGS LVEDY YTG YRLHCEGWRSVFCRPKRAAF CGDSPKSLIDVVSQOKRWAI G LLEV
AT2G32530.1 | AT2 451 IGVLYESTAE DANTSIGIHSRGWTS SVISPKPPAFLGAMP PGGPEAMLQORRWATGLLEV
os_25268 | LOC_Os 460 VGVVYGS LTEDILTGORIHAMGWRSVLMVTEPPAFMGSAPIGGPACLTQFKRWATGQSEI
AT5G22740.1 | AT5 279 GGWKDR TTVEDMDLAVRASLRGWKFLYLG DLO--VKSELPSTFRFRFQOHRWSCGPANL
AT2G24630.1 | AT2 409 GGWLER TTVEDMDI AVRAHLHGWKFIYLN DVK--VLCVPESEYEAYKKQOHRWHS GPMQL
consensus 1021 * . . * * . . * * . . * * . . * * . . * * . . * * . .
consensus 301

AT2G21770.1 | AT2 838 F-----LSRHCPINWYGYGGGLKWLERFSYINSVVYPWTSPLPLLVYCSLPAICL-LTG
AT1G02730.1 | AT1 934 F-----FSRNNAI F--ATRRMKFLORVAYFNVGMYPFTSLFLVIVY CILPAISL-FSG
os_42915 | LOC_Os 615 F-----FSRNCPLL--AGCRLRPMQRVAYANMTAYPVSALFMVYD LLPVIVLWLSHG
AT1G55850.1 | AT1 493 M-----LSKYSVPWY-GKGKISLGLILGYCCYCLWAPSSLPVLIYSVLTSLCL-FKG
AT4G23990.1 | AT4 516 A-----ISRYSPTY-GVKS MGLVTGVGYCYACWAFWSLPLIVYGF LPLQAL-LYQ
AT2G32530.1 | AT2 511 L-----FNKQSPLIGMFCRKRIRFRQSLAYLYIFTWGLRSIPELIYCLLPAYCL-LHN
os_25268 | LOC_Os 520 I-----ISRNNPILATMFKRLKFRQCLAYLIVLWGLRPAFELCYGLLGPYCI-LTN
AT5G22740.1 | AT5 337 FRKMVMEIVRNKKVRFW---KKVYVYIYSFFFVVKIHAHWVTF--CFYCVVLP LTI-LVP
AT2G24630.1 | AT2 467 FR-LCLRSILTSKIAMW---KKANLILLFFLLRKLILPFYFSF--TLCVILPITM-FVP
consensus 1081
consensus 1 *

AT2G21770.1 | AT2 889 KFIVPEI-SNYAGILFLLMFMSIAVTGILEMOWGKIGIDDWWRNEQFVWIGGVSSHFLFAL
AT1G02730.1 | AT1 983 QFIVQSLDITFLIYLLSITLT-LCMLSLEIKWSGITLHEWWRNEQFVWIGGTSAPAAV
os_42915 | LOC_Os 665 EFHIQKPFSTYVAYLVAVIAM-IEVIGLVEIKWAGLTLLDWRNEQFYMIGATGVYLAAV
AT1G55850.1 | AT1 543 IPLFPKV-SSSWFIPFGYVTVAAATAYSLAEFLWCGGTFRGWVNEQRMWLYRRTSSFLFGF
AT4G23990.1 | AT4 566 SSVFPKS-SDPWFVLYIVLFLGAYGQDLLDFVLEGGTYGGWVNDQRMWSIRGFSSHLFGF
AT2G32530.1 | AT2 562 AALFPKG-VYLGIVVTLVGM--HCLYSLWEFMSLGFVSVQSWFASQSFWRIKTTC SWLFSI
os_25268 | LOC_Os 571 QSFLPKA-SEDGFSVPLAIFISYNTYNFMEYMACGLSARAWVNNHRMQRISVSAWTLAF
AT5G22740.1 | AT5 390 EVKVPPIW-GSVYIPSIITILNSVGTPRSIIHLF-----YWILFENVMSLHRTKATLIGL
AT2G24630.1 | AT2 519 EAELPIW-VICYVPITFMSILNIIPAPKSPFPFIV-----PVLLFENTMSVTKFNAMVSGL
consensus 1141
consensus 61

AT2G21770.1 | AT2 948 FQGLLKVLAVS-TNFTVT-----SKAAD-----D-----GEFSELY---IFKW---
AT1G02730.1 | AT1 1042 LQGLLKVIAGVD-ISFTLT-----SKSSAPEDGD-----DEFADLY---VVKW---
os_42915 | LOC_Os 724 LHIVLKRLLGLKGRVFKLT-----AKOLA-GGAR-----ERFAELY---DVHW---
AT1G55850.1 | AT1 602 MDTIKKLLGVSE-SAFVIT-----AKVA-----E-----EEAERYKKEVMEFGVE
AT4G23990.1 | AT4 625 IEFTLKTNLNST-HGFNVT-----SKAND-----D-----EEQSKRYEKEIF EFGPS
AT2G32530.1 | AT2 619 PDIILKLLGISK-TVFIVTKKTMPTMSGSGSEKSO-R-----EVDCPNQDSGKFEF-DG
os_25268 | LOC_Os 630 LTVLLKSLGLSE-TVFEVT-----GKDKMSD-D-----DDNTDGADPGRFTF-DS
AT5G22740.1 | AT5 443 FE-----AGRA-NEWVVT-----AKLGSGQSAK
AT2G24630.1 | AT2 572 FQ-----LGSS-YEWIVT-----KKAGRSES DLLALTDKESKMPNQILRGVSD
consensus 1201
consensus 121

AT2G21770.1 | AT2 983 TSLI-----IPPTLLIINLVGVIVGVSDAINNGY--DSWGPLFGRLFFALWVIV
AT1G02730.1 | AT1 1081 SFLM-----VPPLTIMMVNMI AIVGLARTLYSPF--PQWSKLVGGVFFSFWVLC
os_42915 | LOC_Os 763 SPLL-----APTVMVAVNVTAIGAAGKAVVGGWTPAQVAAGSAGLVFNWVWLV
AT1G55850.1 | AT1 642 SPMF-----LVLGTLGMLNLFCAA AVARIVS-GD-----GGDLKTMGMQFVIT
AT4G23990.1 | AT4 666 SSMF-----LPLTTVAIVNLLAFVWGLYGLFAWGE-----GLVLELMLASFAVV
AT2G32530.1 | AT2 671 SLYF-----LPGTFILLVNLA--LAGCSVGLQRHRG--GGSGLAEACGCILVVI
os_25268 | LOC_Os 673 LPVF-----IPVTALAMLNTVAVTVGACRVAFGTAEGVPCAPGIGEFMCCGWLVI
AT5G22740.1 | AT5 465 -----GNTKGIKRFPRIFKLPDR LNTLELGF AAF LFVCGCYDFVHGKNFYIYLFLOTM
AT2G24630.1 | AT2 616 SELLEISQVEEQKQPVSVKTKNKIFHKE LALAFLLLTAAVRSLLASQGVHFYLLFOGT
consensus 1261
consensus 181

AT2G21770.1 | AT2 1031 HLY-----PFLKGLLGKQD--RVPTIILVW-----SILLASILTLL-----WV-
AT1G02730.1 | AT1 1129 HLY-----PFAKGLMGRRG--RVPTIVFVW-----SGLLSIIVSLL-----WV-
os_42915 | LOC_Os 813 LLY-----PFALGIMGRWS--KRPCALFALLVAACA AAVAGFVAVHAVLAAGSAAPS WL G
AT1G55850.1 | AT1 685 GVLVVINWPLYKGM LLRQDKGKMPMSVTVK-----SVVLALS-ACT-----
AT4G23990.1 | AT4 710 NCL-----PIYEA MVLRI DDGKLPKRVCFV-----AGLTFVLIVS-----
AT2G32530.1 | AT2 717 LFL-----PFLKGM-FEKGKYGIPWSTLSK-----AAFLAVL FV VFSVGN-----
os_25268 | LOC_Os 723 CFF-----PFV RGI VWGKGSY GIPWSVKLK-----ASLLVAMFVTFCKRN-----
AT5G22740.1 | AT5 519 SFF-----ISGL-----GWIGTYVPS-----
AT2G24630.1 | AT2 676 TFL-----LVGL-----DLIGEOM-S-----
consensus 1321
consensus 241

AT2G21770.1 | AT2 1067 -----RVNPFVSKDGPVLEICGLDCLK---AAFKGSAPINLSDR LHQVLRWALGSVEI
AT1G02730.1 | AT1 1165 -----YINPPSGKQ-----DYMQFQFPDAFRGTAPINLTDRLHQVLRWATGSVEI
os_42915 | LOC_Os 866 WSRGATAILPSSWR-----LKRGF-DAFRGTAPINLTERLYQILRWSGGSLEM
AT1G55850.1 | AT1 725 -----CLAFL-----QAF LGVAPTNLHQMLVQORRWSE GDFQI
AT4G23990.1 | AT4 746 -----GYVFLK---AAFCGDSPKSLIDVVSQOKRWAI G LLEV
AT2G32530.1 | AT2 -----PAFLGAMP PGGPEAMLQORRWATGLLEV
os_25268 | LOC_Os -----PAFMGSAPIGGPACLTQFKRWATGQSEI
AT5G22740.1 | AT5 -----VKSEL PSTFRAF RFQOHRWSCGPANL
AT2G24630.1 | AT2 -----VLCEVPESEYAYKKOQRWHS GPMQL
consensus 1381
consensus 301

AT2G21770.1 | AT2 838 F-----LSRHCPINWYGYGGGLKWLERFSYINSVVYPWTSPLPLLVYCSLPATCL-LTG
AT1G02730.1 | AT1 934 F-----FSRNNAI F--ATRRMKFLORVAYFNVGMYPFTSLFLVIVYCLIPATSL-FSG
os_42915 | LOC_Os 615 F-----FSRNCPLL--AGCRLRPMQRVAYANMTAYPVSALFMVYDLPVIVLWLSHG
AT1G55850.1 | AT1 493 M-----LSKYSVPWY-GKGKISLGLILGYCCYCLWAPSSLPVLIYSVLTSLCL-FKG
AT4G23990.1 | AT4 516 A-----ISRYSPTY-GVKS MGLVTGVGYCYACWAFWSLPLIVYGFPLQAL-LYQ
AT2G32530.1 | AT2 511 L-----FNKQSPLIGMFCRKRIRFRQSLAYLYIFTWGLRSIPELIYCLLPAYCL-LHN
os_25268 | LOC_Os 520 I-----ISRNNPILATMFKRRLKFRQCLAYLIVLWGLPLRAPFELCYGLLGPYCI-LTN
AT5G22740.1 | AT5 337 FRKMVMEIVRNKKVRFW----KKVYVYIYSFFFVVKIHAHWVTF--CFYCVVLPITI-LVP
AT2G24630.1 | AT2 467 FR-LCLRSILTSKIAMW----KKANLILLFFLLRKLILPFYFSF--TLFCVILPITM-FVP
consensus 1081
consensus 1 *

AT2G21770.1 | AT2 889 KFIVPEI-SNYAGILFLLMFMSIAVTGILEMOWGKIGIDDWWRNEQFVWIGGVSSHFLFAL
AT1G02730.1 | AT1 983 QFIVQSLDITFLIYLLSITLT-LCMLSLEIKWSGITLHEWWRNEQFVWIGGSAHPAAV
os_42915 | LOC_Os 665 EFHIQKPFSTYVAYLVAVIAM-IEVIGLVEIKWAGLTLLDWRNEQFYMIGATGVYLAAV
AT1G55850.1 | AT1 543 IPLFPKV-SSSWFIPFGYVTVAAATAYSLAEFLWCGGTFRGWNEQRMWLYRRTSSFLFGF
AT4G23990.1 | AT4 566 SSVFPKS-SDPWFVLYIVLFLGAYGQDLLDFVLEGGTYGGWWDORMWSIRGFSSHLFGF
AT2G32530.1 | AT2 562 AALFPKG-VYLGIVVTLVGM--HCLYSLWEFMSLGFVSQSWFASQSFWRIKTTCSWLFSI
os_25268 | LOC_Os 571 QSFLPKA-SEDGFSVPLAIFISYNTYNFMEYMACGLSARAWWNNHRMORIISVSAWTLAF
AT5G22740.1 | AT5 390 EVKVPPIW-GSVYIPSIITILNSVGTPRSIIHLF-----YWILFENVMSLHRTKATLIGL
AT2G24630.1 | AT2 519 EAELPIW-VICYVPITFMSILNIIPAPKSPFPFIV-----PVLLFENTMSVTKFNAMVSGL
consensus 1141
consensus 61

AT2G21770.1 | AT2 948 FQGLLKVLAVS-TNFTVT-----SKAAD-----D-----GEFSELY---IFKW---
AT1G02730.1 | AT1 1042 LQGLLKVIAGVD-ISFTLT-----SKSSAPEDGD-----DEFADLY---VVKW---
os_42915 | LOC_Os 724 LHIVLKRLLGLKGRVFKLT-----AKOLA-GGAR-----ERFAELY---DVHW---
AT1G55850.1 | AT1 602 MDTIKKLLGVSE-SAFVIT-----AKVA-----E-----EEAERYKKEVMEFGVE
AT4G23990.1 | AT4 625 IEFTLKTNLNST-HGFNVT-----SKAND-----D-----EEQSKRYEKEIFEFGPS
AT2G32530.1 | AT2 619 PDIILKLLGISK-TVFIVTKKTMPTMSGSGSEKSO-R-----EVDCPNQDSGKFEF-DG
os_25268 | LOC_Os 630 LTVLLKSLGLSE-TVFEVT-----GKDKMSD-D-----DDNTDGADPGRFTF-DS
AT5G22740.1 | AT5 443 FE-----AGRA-NEWVVT-----AKLGSGQSAK-----
AT2G24630.1 | AT2 572 FQ-----LGSS-YEWIVT-----KKAGRSES DLLALTDKESKMPNQILRGVSD
consensus 1201
consensus 121

AT2G21770.1 | AT2 983 TSLI-----IPPTLLIINLVGVIVGVSDAINNGY--DSWGPLFGRLFFALWVIV
AT1G02730.1 | AT1 1081 SFLM-----VPPLTIMMVNMIAMVGLARTLYSPF--PQWSKLVGGVFFSFWVLC
os_42915 | LOC_Os 763 SPLL-----APTVMVAVNVTAIGAAGKAVVGGWTPAQVAAGSAGLVFNWVWLV
AT1G55850.1 | AT1 642 SPMF-----LVLGTLGMLNLFCAAARIVS-GD-----GGDLKTMGMQFVIT
AT4G23990.1 | AT4 666 SSMF-----LPLTTVAIVNLLAFVWGLYGLFAWGE-----GLVLELMLASFAVV
AT2G32530.1 | AT2 671 SLYF-----LPGTFILLVNLA--LAGCSVGLQRHRG--GGSGLAEACGCILVVI
os_25268 | LOC_Os 673 LPVF-----IPVTALAMLNTVAVTVGACRVAFGTAEGVPCAPGIGEFMCCGWLVI
AT5G22740.1 | AT5 465 -----GNTKGIKRFPRIFKLPDRNLNLELGFAAFVFCVGCYDFVHGKNFYIYLFLOTM
AT2G24630.1 | AT2 616 SELLEISQVEEQKQPVSVKTKNKIFHKEALAFLLTAAVRSLLASQGVHFYFLFOGT
consensus 1261
consensus 181

AT2G21770.1 | AT2 1031 HLY-----PFLKGLLGKQD--RVPTIILVW-----SILLASILTLL-----WV-
AT1G02730.1 | AT1 1129 HLY-----PFAKGLMGRRG--RVPTIVFVW-----SGLLSIIVSLL-----WV-
os_42915 | LOC_Os 813 LLY-----PFALGIMGRWS--KRPCALFALLVAACAAVAAGFVAVHAVLAAGSAAPSWLG
AT1G55850.1 | AT1 685 GVLVVINWPLYKGMLLRQDKGKMPMSVTVK-----SVVLALS-ACT-----
AT4G23990.1 | AT4 710 NCL-----PIYEA MVLRIIDGKLPKRVCFV-----AGLTFVLIVS-----
AT2G32530.1 | AT2 717 LFL-----PFLKGM-FEKGKYGIPWSTLSK-----AAFLAVLFFVFSVGN-----
os_25268 | LOC_Os 723 CFF-----PFVRGIVWGKGSYGIPWSVKLK-----ASLLVAMFVTFCKRN-----
AT5G22740.1 | AT5 519 SFF-----ISGL-----GWIGTYVPS-----
AT2G24630.1 | AT2 676 TFL-----LVGL-----DLIGEOM-S-----
consensus 1321
consensus 241

AT2G21770.1 | AT2 1067 -----RVNPFVSKDGPVLEICGLDCLK---AAFKGSAPINLSDRLHQVLRWALGSVEI
AT1G02730.1 | AT1 1165 -----YINPPSGKQ-----DYMQFQFPDAFRGTAPINLTDRLHQVLRWATGSVEI
os_42915 | LOC_Os 866 WSRGATAILPSSWR-----LKRGF-DAFRGTAPINLTERLYQILRWSSGGSLEM
AT1G55850.1 | AT1 725 -----CLAFL-----QAFLLGVAPTNLHQMLVQORRWSEGDFQI
AT4G23990.1 | AT4 746 -----GYVFLK---AAF CGDSPKSLIDVVSQOKRWAI G LLEV
AT2G32530.1 | AT2 -----PAFLGAMP PGGPEAMLQORRWATGLLEV
os_25268 | LOC_Os -----PAFMGSAPIGGPACLTQFKRWATGQSEI
AT5G22740.1 | AT5 -----VKSEL PSTFRAFRFQOHRWSSG PANL
AT2G24630.1 | AT2 -----VLCEVPESEYAYKKOQRWSSGPMQL
consensus 1381
consensus 301