

Fig. S4

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AaegyDIA1 1 -----MSQ--HRILTKLHLVALFLWIVMKYQPEERASSLKSSLVQCCQYDTT
CpipiDIA1 1 -----MSSGFQRILVNHLILALLFCVIFEFQPKPESELTELLVNQCEYETQ
AgambDIA1 1 -----MQS----S-RLPYFVTLFIAVVLQYLPNEKSTSKRPLENVCDYDRN
DyakuDIA1 1 -----MHLSPGQLKVVLILALLQELQVKPQREVFQELFEKDL
DerecDIA1 1 -----MHLSPGQLKVVLILALLQELQVKPQREVFQELYEKDL
DmelaDIA1 1 -----MHLSHGQLKVVLILALLQELQVKPQREVFQELFEKDL
DsechDIA1 1 -----MHLSYGQLKVVLILALLQELQVKTQREVFQELFEKDL
DananDIA1 1 -----MHLLSGQLRIVLVLALLQDLQVKPQDIFQEHFFESDL
DpersDIA1 1 -----MHLSPGHLRIVLILALLQDLQVKPQDIFRAHLERDL
DpseuDIA1 1 -----MHLSPGHLRIVLILALLQDLQVKPQDIFRAHLERDL
DwillDIA1 1 -----MHLLYGQLKVVLVLALLQELDVRTQDIFRKHFNMDL
GaculDIA1 1 -----MLRFLPLKLGR--LYRCLKLLLVGLFVILLMNTHSLFASFQRNELTDRRFINL
OlatiDIA1 1 -----MLRFLPLKLGR--LYRCLKLLLVGLFVILLMNTHNLFASFQRNELTDRRFINL
TnigrDIA1 1 -----MLRFLPLKLGR--LYRCLKLLLVGLFVILLMNTHNLFASFQRNELTDRRFINL
TrubrDIA1 1 -----MLRFLPLKLGR--LYRCLKLLLVGLFVILLMNTHNLFASFQRNELTDRRFINL
DreriDIA1b 1 -----MLRFLPLKLGR--LYRCLKLLLFLGLFVILLMNTHNLFASFQRNELTDRRFINL
DreriDIA1a 1 -----MLRILSLKFGR--VYRCGKFLFIVALFVILLMNTHNLFASFQRNELTDRRFIGL
BtaurDIA1 1 -----MWRLVPPKLGR--LSRSLKLAALGSLLVLMVLHSPSLLASWQRNELADRRFLQL
PpygmDIA1 1 -----MWRLVPPKLGR--LSRSLKLAALGSLLVLMVLHSPSLLASWQRNELADRRFLQL
CfamiDIA1 1 -----MWRLVPPKLGR--LSRSLKLAALGSLLVLMVLHSPSLLASWQRNELADRRFLQL
TtrunDIA1 1 -----MWRLVPPKLGR--LSRSLKLAALGSLLVLMVLHSPSLLASWQRNELADRRFLQL
PtrogDIA1 1 -----MWRLVPPKLGR--LSRSLKLAALGSLLVLMVLHSPSLLASWQRNELADRRFLQL
HsapiDIA1 1 -----MWRLVPPKLGR--LSRSLKLAALGSLLVLMVLHSPSLLASWQRNELTDRRFLQL
MmulaDIA1 1 -----MWRLVPPKLGR--LSRSLKLAALGSLLVLMVLHSPSLLASWQRNELTDRRFLQL
PvampDIA1 1 -----MWRLVPPKLGR--LSRSLKLAALGSLLVLMVLHSPSLLASWQRNELADRRFLQL
MmuscDIA1 1 -----MWRLVPLKLGR--LSRALKLAALGSLLVLMLLHSPSLLASWQRNELADRRFLQL
RnorvDIA1 1 -----MWRLVPLKLGR--LSRALKLAALGSLLVLMLLHSPSLLASWQRNELADRRFLQL
MdomeDIA1 1 -----MWRLVPPKLGR--LSRSLKLAALGSLLVLMVLHSPSLLASWQRNELADRRFLQL
GgallDIA1 1 -----MLRLVSLKLGR--LYRYVKLAVLGSLAAALVLNTHSLLASLQRNELAERFLQL
XtropDIA1 1 -----MLRLASLKFGR--LFRYAKVLFAASLLVVMLLNTHSLSSFQRNELTDRRFLSL
SpurpDIA1 1 -----MRRYFNQFTNRFCISTTQLIWLVVLSSMCLFVYYQLYLHFTANHLENEYFTEA
RnorvDIA1R 1 MELGRPGAAATAFRQRWP-AWMLLWVSTLSCSFSLPASLPPSLVPRVRSSYTLGKTFLGL
MmuscDIA1R 1 MESQWRGAAATAFHOHWL-ARLLLWVSTLSCSFSLPASLPPSLVPRVRSSYTMGKTFLGL
MmulaDIA1R 1 MEP-QLGPEAAALRPGWL-A-LLLWVSALSCSFSLPASSPSSLVSQVRTSYNFGRTFLGL
HsapiDIA1R 1 MEP-QLGPEAAALRPGWL-A-LLLWVSALSCSFSLPASSLSSLVPQVRTSYNFGRTFLGL
BtaurDIA1R 1 MEP-RLGPKAAALHIGWP-F-LLLWVSGLSYSVSSPASPSPSPVSRVRTSYNLGKTFLGL
EcabaDIA1R 1 MEP-WLGPEAAALRPGWP-A-LLLWVSALRCSVSSPASPSPSLVPRVRTSYNFGRTFLGL
DordiDIA1R 1 MDP-QLGPEAAALRPGWQ-V-LLLLVSALSCFSSPASPPSLVSRVRTSYNLGRTFLGL
MdomeDIA1R 1 MES-VIHGPLASPCLGWL-T--LLQLVTLSCLSSTESLTAPSSVPRVKSYNFGRTFLGL
OanatDIA1R 1 MGL-RLGCRLFSAALSWM-T--LLQLTRGHGPVADASPAPSLVPRVKPSYSFGRTFLGL
GgallDIA1R 1 MGR--WICCLCSRVADWL-M--LLLVLARSSNPSAAATASPS-APHVRPSYSFGRTFLGL
DreriDIA1R 1 -----MAG--TWS--G-VWILCFILVFGTADP-----SPAPQ-DKSHDRKIFLGL
SsalaDIA1R 1 MPLKRCDQRAVG-SVRLT-VCVLSWLCVCWAPSVVEPAGTPPAQ-QKALLQRAFLGL
NvitrDIA1 1 -----MLVTKASVSSFLIALLILILGIYINRFNLKVAEITER
BflorDIA1 1 -----MRLVRLQFRR-FFSGWRVRRCGFFFVVFFYCFVFQPFSYNQLIDTTFLGE
NvectDIA1 1 --MHFGGILRKRRYICRVLLLVIISFSDLLWLSYQDGRAIKWDFSQHKLTFQEIGL
CinteDIA1 1 -MLLKMKRYLTVWENCKYIVFIFILITEVLLEMYNHRSQGSTRVMLEAKLISDKWSATS
consensus 1 r kmg l lkl v llvlm sl qk ver fl l

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AaegyDIA1 94 QR---VVIKLNKEHGVEELISSICNDLKIYR---NCRLRNKEPYLR---VLRQRV
CpipiDIA1 96 QK---VVIKTLNKNRAVEALRDAVCDELGLTQS---NCKFKSDENTLK---VLRKRV
AgambDIA1 91 KL---AVMKHLNRDNTIEKLLQEYCDAYSITKQ---NCRWAQHHDGSVDR-AKEFITTSI
DyakuDIA1 90 Q-----VVAKRKIIDAQNOQ-IKDVKKAF-----YE-----
DerecDIA1 90 Q-----VVAKRKIIDARNHK-AENVEKAF-----YE-----
DmelaDIA1 90 QE---V-Q-LVAKRKIIDAQSNQ-INKVKKDF-----YE-----
DsechDIA1 90 QA---V-Q-LVAKRKIINAHSYQ-MKNVKRAF-----YE-----
DananDIA1 90 EK---SSQ-LVAKRKSIVASHQS-LSSLQEEF-----LN-----
DpersDIA1 90 QA---A-Q-LVAKRDAIGGHSYRNMGILREAF-----LE-----
DpseuDIA1 90 QA---A-Q-LVAKRDAIGGHSYRNMGILGEAF-----LE-----
DwillDIA1 90 EN---VK-CLAKRKMTRKISKD-----
GaculDIA1 101 EGTRR-VVLKRLGSNQELAEIDQKICKRATGRPR-CDLIQAMYKTEFARINGDVRLLTPE
OlatiDIA1 101 EGTRR-VVLKRLGSNQELAEIDQKICKRATGRPR-CDLVQAMYKTEFARINGDVRLLTPE
TnigrDIA1 101 EGTRR-VVLKRLGSNQELADIDQKICKRATGRPR-CDLIQAMYKTEFARINGDVRLLTPE
TrubrDIA1 101 EGTRR-VVLKRLGSNQELADIDQKICKRATGRPR-CDLIQAMYKTEFARINGDVRLLTPE
DreriDIA1b 101 EGTRR-IVLKRLGSNQELADIDQKICKRATGRPR-CDLIQAMYKTEFARINGDVRLLTPE
DreriDIA1a 101 EGTRR-VVLKRLGSNQELAEIDQKICKRATGRPR-CDLIQSMYKTEFARINGDVRLLTPE
BtaurDIA1 101 EGGRRRVVLKRLGSOELAQLDOSICKRATGRPR-CDLLQAMPRTFARINGDVRLLTPE
PpygmDIA1 101 EGGRRRVVLKRLGSOELAQLDOSICKRATGRPR-CDLLQAMPRTFARINGDVRLLTPE
CfamiDIA1 101 EGGRRRVVLKRLGSOELAQLDOSICKRATGRPR-CDLLQAMPRTFARINGDVRLLTPE
TtrunDIA1 101 EGGRRRVVLKRLGSOELAQLDOSICKRATGRPR-CDLLQAMPRTFARINGDVRLLTPE
PtrogDIA1 101 EGGRRRVVLKRLGSOELAQLDOSICKRATGRPR-CDLLQAMPRTFARINGDVRLLTPE
HsapiDIA1 101 EGGRRRVVLKRLGSOELAQLDOSICKRATGRPR-CDLLQAMPRTFARINGDVRLLTPE
MmulaDIA1 101 EGGRRRVVLKRLGSOELAQLDOSICKRATGRPR-CDLLQAMPRTFARINGDVRLLTPE
PvampDIA1 101 EGGRRRVVLKRLGSOELAQLDOSICKRATGRPR-CDLLQAMPRTFARINGDVRLLTPE
MmuscDIA1 101 EGGRRRVVLKRLGSOELAQLDOSICKRATGRPR-CDLLQAMPRTFARINGDVRLLTPE
RnorvDIA1 101 EGGRRRVVLKRLGSOELAQLDOSICKRATGRPR-CDLLQAMPRTFARINGDVRLLTPE
MdomeDIA1 101 EGGRRRVVLKRLGSOELAQLDOSICKRATGRPR-CDLLQAMPRTFARINGDVRLLTPE
GgallDIA1 101 EGSRR-VVLKRLGSAQELADIDAKICRRATGRGR-CDLLQALHATEFASLNGDVRLLTPE
XtropDIA1 101 EGSRR-VVLKRLGSHNELSELDQRIKCKATGRPR-CDLVQAMYKTEFARINGDVRLLTPE
SpurpDIA1 99 -LDQKPVVMKRLGHNSEHNQFDKDLCTNAESGLRGCDVSQQIYKSKLSDIMYAEERLEEKD
RnorvDIA1R 107 SKTWRPVEISRLVSKYQSEISDKRICASASGPKT-CSTIERILRKTGRFQKWLQAKRLTPD
MmuscDIA1R 107 SKTWRPVEISQLVSRYOIEISDRRICASVSAPKT-CSTIERILQKTGRFQKWLQAKRLTPD
MmulaDIA1R 105 SKIWRPVEIFRLVSNYQNEISDRRICASASAPRT-CSTIERVLRKTERFQKWLQAKRLTPD
HsapiDIA1R 105 SKIWRPVEIFRLVSKYQNEISDRRICASASAPKT-CSTIERVLRKTERFQKWLQAKRLTPD
BtaurDIA1R 105 FKTWRPVEISRLVSKQQNKISDGRICASAAAPKT-CSTIERVLRKTERFQKWLQAKRLTPD
EcabaDIA1R 105 SKTWRPVEISRLVSKQQNEISDRRICAFAAAPKT-CSTIERVLRKTRRFQKWLQAKRLTPD
DordiDIA1R 105 SKTWRPVEIFRLVSKQNEISDRRICAFASAPKT-CSTIERILRKTGRFQKWLQAKRLTPD
MdomeDIA1R 104 TKSWRPVEISRLVSKYQHELSDRRICASASGSKT-CSTIERVLRKTERVKKWLKAKRLTPD
OanatDIA1R 104 SKSWRLVEISRLIGKDQNELSDOKICTSVSLVKT-CSTIERVLRKTERFQKWLKARRLTPA
GgallDIA1R 102 AQSWMVDITRLTKYQHADRADQHICTSLLKTKT-CSLERALRRTHRFQKWLAKRLTPD
DreriDIA1R 88 TAGWRPVVVSRLMSPHLHQLSDNSICTSAGKGS-CSIEGVLRSRFRQTVVHNSNLLLP
SsalaDIA1R 105 SLSWRPVVLSFLSPLCHSSDRSICRSVGRQGP-CSIEAVLRVTFRQSLNQSHELLLPH
NvitrDIA1 85 ----KKVIMKLAQSEIKTFDEMICSDELHEL-CYQSESRSKQDSKTNFYKLVESELAN
BflorDIA1 99 ----MEVALKRLGHNSEFDQLDRWICETKEGPQ-CHIPSVTYYSNFSRVYEG--LSPK
NvectDIA1 106 QR---VVLKTLGTSSSELTAFDNEICRGVGKDSN-CKISQEAWDSVVLVP-----KP
CinteDIA1 118 PCNGETCSVQIETSVLSGNVNVKWCDFKFKPTN-CDTGKVFKSWRAMNKITSAGRLDLP
consensus 121 r vvikrlas v ldq ick asg c l m kte rlltpe

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AaegyDIA1 141 LNDNQLEGAILCPLMDE--EALKRFLFEID-----E-----NDLNKILLMRINAQPLIL
 CpipiDIA1 144 L-EQELEGCIICPSKDE--KALNRLLNEVE-----G-----TELLQILLLKVNVOPLILL
 AgambDIA1 143 LDSARVEGCIFCPATNNR-QSLQRFLSLFDS----TD-----NEIWNLLAVRTNVEPLLI
 DyakuDIA1 115 -LGERPGGFHLCRTPSRKPRFVSYLEQRGH----A-----SASVWFYMMHYVSPLLM
 DerecDIA1 115 -QEEQPGGFHLCRTPSRKPPRFVSYLEQRGH----A-----SASVWFYMMHYVSPLLM
 DmelaDIA1 118 -LEERPGGFHLCRTLAREP-RFVSYLEQRGH----A-----AASVWFYMMHYVSPLLM
 DsechDIA1 118 -LEERPGGFHLCRTLAREP-RFVSYLEQRGH----VY-----GSTSVWFYMMHYVSPLLM
 DananDIA1 119 -LEERPGGFHLCRTAQKSS-PFINYLNRGY----D-----SSSYFYMLHNI SPLLM
 DpersDIA1 119 -MEERPGGFQLCRSGFRTP-RFVSYLEQRGH----E-----AATWYWMHSITPLLM
 DpseuDIA1 119 -MEERPGGFQLCRSGFRTP-RFVSYLEQRGH----E-----AATWYWMHSITPLLM
 DwillDIA1 108 -LHFNPGGFQMCRNSTR---FLAYLEERGY----L-----PATIGYLIHHSISPLLM
 GaculDIA1 159 VVEGWSDLVH-CPSQRLLDRLVRRYAETKDSGSFLLRNLKDTERMQLLMTLAFNPEPLVL
 OlatiDIA1 159 VVEGWSDLVH-CPSQRLLDRLVRRYAETKDSGSFLLRNLKDTERMQLLMTLAFNPEPLVL
 TnigrDIA1 159 VVEGWSDLVH-CPSQRLLDRLVRRYAETKDSGSFLLRNLKDTERMQLLMTLAFNPEPLVL
 TrubrDIA1 159 VVEGWSDLVH-CPSQRLLDRLVRRYAETKDSGSFLLRNLKDTERMQLLMTLAFNPEPLVL
 DreriDIA1b 159 VVEGWSDLVH-CPSQRLLDRLVRRYAETKDSGSFLLRNLKDTERMQLLMTLAFNPEPLVL
 DreriDIA1a 159 VVEGWSDLVH-CPSQRLLDRLVRRYAETKDSGSFLLRNLKDTERMQLLMTLAFNPEPLVL
 BtaurDIA1 160 AVEGWSDLVH-CPSQRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVL
 PpygmDIA1 160 AVEGWSDLVH-CPSQRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVL
 CfamiDIA1 160 AVEGWSDLVH-CPSQRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVL
 TtrunDIA1 160 AVEGWSDLVH-CPSQRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVL
 PtrogDIA1 160 AVEGWSDLVH-CPSQRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVL
 HsapiDIA1 160 AVEGWSDLVH-CPSQRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVL
 MmulaDIA1 160 AVEGWSDLVH-CPSQRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVL
 PvampDIA1 160 AVEGWSDLVH-CPSQRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVL
 MmuscDIA1 160 AVEGWSDLVH-CPSQRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVL
 RnorvDIA1 160 AVEGWSDLVH-CPSQRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVL
 MdomeDIA1 160 AVEGWSDLVH-CPSQRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVL
 GgallDIA1 159 AVEGWSDLVH-CPSQRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVL
 XtropDIA1 159 VVEGWSDLVH-CPSQRLLDRLVRRYAETKDSGSFLLRNLKDTERMQLLMTLAFNPEPLVL
 SpurpDIA1 158 -VMGLSDIVR-CPSRRLLDRIWDTFGERQ---FD-KSLARDHKLMATTI AFNPEPLIL
 RnorvDIA1R 166 LVQGLPSPFLHCPQSRLLDRLVRRYAETVVDAGSIFMDHFTDRDKLRLLYTLAVNAHPIL
 MmuscDIA1R 166 LVQGLPSPFLRCPQSRLLDRLVRRYAETVVDAGSIFMDHFTAGDKLRLLYTLAVNAHPIL
 MmulaDIA1R 164 LVQGLASPLLRCPQSRLLDRLVRRYAETVVDAGSIFMDHFTDRDKLRLLYTLAVNSHPILL
 HsapiDIA1R 164 LVQGLASPLLRCPQSRLLDRLVRRYAETVVDAGSIFMDHFTDRDKLRLLYTLAVNSHPILL
 BtaurDIA1R 164 LVRGLSSPLLRCPQSRLLDRLVRRYAETVVDAGSIFMDHFTDRDKLRLLYTLAVNTHPVLL
 EcabaDIA1R 164 LVRGLPSPFLRCPQSRLLDRLVRRYAETVVDAGSIFMDHFTDRDKLRLLYTLAVNAHPIL
 DordiDIA1R 164 LVQGLPSPFLRCPQSRLLDRLVRRYAETVVDAGSIFMDHFTDRDKLRLLYTLAVNAHPIFL
 MdomeDIA1R 163 LVQGLPSPMLRCPQSRLLDRLVRRYAETVVDAGSVFMDHFTDRDKLRLLYTLAVNSHPIML
 OanatDIA1R 163 LVQGLPSPMLRCPQSRLLDRLVRRYAETVVDAGSVYMDHFTDRDKLRLLYTLAVNSHPVLL
 GgallDIA1R 161 LVQGLSSPMLRCPQSRLLDRLVRRYAETVVDAGSIYMDHLTDQDKLRLLYTLAVNSHPILL
 DreriDIA1R 147 MVKGLVTPMLRCPQSRLLDRLVRRYFEVTDVGSVQMKHFNEKDKLRLLYTLAVNQOPLIL
 SsalaDIA1R 164 IVKGLAPPLRCPQSRLLDRLVRRYAETVVDVGSVQMKHFSEKDKLRLLYTLAVNQOPLIL
 NvitrDIA1 140 VGGDINNMRLCPTTTKLEKLFVNKVFQSHAE-----NEDYFKYLWSTIKINPEPLIL
 BflorDIA1 152 SLGDMSDMVR-CPSQRLLDRLVLEKFAEHLG---KETEELSYQEKLHFLSTLKFNPPEPLML
 NvectDIA1 153 PLQDAVRKYFDCPSTRFLEKIESVYQETPG-----QLSLVETIHLITGLHLNPEPLILL
 CinteDIA1 177 NLLKDISPPLQCPSTRFADRLVRRYVANKQGG--VLIIRDLSYTEKKRLIFTCCKMSPGSSVQ
 consensus 181 veg e vh Cpsqrlldrvvrryae rd gs v l d erl ll tla npeplll

AaegyDIA1	188	KLL-----QERNFPVPKLIFQGGFTLVESYEG-EALAKYYDRPLN--VRLLIANELIKAS
CpipiDIA1	190	ELF-----DGRGFPVPKLIFQGGFQLFESFDG-DALVNFYDSSLN--IRLRIAKELIQAS
AgambDIA1	193	KLLTVNYHDEPPLYVPKLILHTFGFSIIETVEG-KTLEHYDYDFPFV--TRMRIAAELIRAG
DyakuDIA1	162	QEL-----YLQGFVPTTYASCGLTHFQSYAG-RTLITNYFEGEED--LRVELALQLMQLS
DerecDIA1	163	QEL-----HLQGFVPTTYASCGLTHFQAYAG-RTLITNYFEAEEG--LRMELALQLIQLS
DmelaDIA1	165	QEL-----HLQGFVPTTYASCGLTHFQSNAG-RTLAHYVDAEEG--LRVELALQLIQLS
DsechDIA1	167	QEL-----HLQGFVPTTYASCGLTHFQSYAG-RTLAHYVNAEEG--LRLELALQLIQLS
DananDIA1	166	QEL-----QNLDFPVNTYAIICGLTHFQAYAG-RTLNHYTEAAED--LRREIARQLIHLS
DpersDIA1	166	QEL-----FLRGFPVPRSYAACGLTHFQAYAG-RTLTVHYATAGEN--LRLEMARQLLQLS
DpseuDIA1	166	QEL-----FLRGFPVPRSYAACGLTHFQAYAG-RTLTVHYATAGEN--LRLEMARQLLQLS
DwillDIA1	152	QEL-----WIMDFPVPFSFAACGLTHFQAYAG-STLSNYLKPAPID--LRLEMAKQLQLA
GaculDIA1	218	CSFP----SDEGWPFKYLGACGRMVAVNYVG-EELWSFYFNAPWE--KRVDLARQLMDIA
OlatiDIA1	218	CSFP----SDEGWPFKYLGACGRMVAVNYVG-EELWNFYFNAPWE--KRVDLARQLMDIA
TnigrDIA1	218	CSFP----SDEGWPFKYLGACGRVAVNYVG-EELWSFYFNAPWE--KRVDLARQLMDIA
TrubrDIA1	218	CSFP----SDEGWPFKYLGACGRVAVNYVG-EELWSFYFNAPWE--KRVDLARQLMDIA
DreriDIA1b	218	CSFP----SDEGWPFKYLGACGRMVAVNYVG-EELWSFFNAPWE--KRVDLAKQLMDIA
DreriDIA1a	218	CSFP----SDEGWPFKYLGACGRMVAVNYVG-EELWSFYFNAPWE--KRVDLAKQLMDIA
BtaurDIA1	219	CSFP----SDEGWPFKYLGACGRMVAVNYVG-EELWSFYFNAPWE--KRVDLAWQLMEIA
PpygmDIA1	219	CSFP----SDEGWPFKYLGACGRMVAVNYVG-EELWSFYFNAPWE--KRVDLAWQLMEIA
CfamiDIA1	219	CSFP----SDEGWPFKYLGACGRMVAVNYVG-EELWSFYFNAPWE--KRVDLAWQLMEIA
TtrunDIA1	219	CSFP----SDEGWPFKYLGACGRMVAVNYVG-EELWSFYFNAPWE--KRVDLAWQLMEIA
PtrogDIA1	219	CSFP----SDEGWPFKYLGACGRMVAVNYVG-EELWSFYFNAPWE--KRVDLAWQLMEIA
HsapiDIA1	219	CSFP----SDEGWPFKYLGACGRMVAVNYVG-EELWSFYFNAPWE--KRVDLAWQLMEIA
MmulaDIA1	219	CSFP----SDEGWPFKYLGACGRMVAVNYVG-EELWSFYFNAPWE--KRVDLAWQLMEIA
PvampDIA1	219	CSFP----SDEGWPFKYLGACGRMVAVNYVG-EELWSFFNAPWE--KRVDLAWQLMEIA
MmuscDIA1	219	CSFP----SDEGWPFKYLGACGRMVAVNYVG-EELWSFYFNAPWE--KRVDLAWQLMEIA
RnorvDIA1	219	CSFP----SDEGWPFKYLGACGRMVAVNYVG-EELWSFYFNAPWE--KRVDLAWQLMEIA
MdomeDIA1	219	CSFP----SDEGWPFKYLGACGRMVAVNYVG-EELWSFYFNAPWE--KRVDLAWQLMEIA
GgallDIA1	218	CSFP----SDEGWPFKYLGACGRMVAVNYVG-EELWSFYFNAPWE--KRVDLAWQLMEIA
XtropDIA1	218	CSFP----SDEGWPFKYLGACGRMVAVNYVG-EELWSFYFNAPWE--KRVDLAWQLMEIA
SpurpDIA1	211	CAFP----NRKGWPFKYLGACGRFTVQEYSG-HLSLYFYKFKFG--VRAALAVQALKIA
RnorvDIA1R	226	QIFP----GAEGWPMFKYLGSCGRFLVSTST--RPLQEFYDAPPE--QAADLAWQLLGVL
MmuscDIA1R	226	QIFP----GAEGWPMFKYLGSCGRFLVSTST--RPLQEFYDASPE--QAADLAWQLLRVL
MmulaDIA1R	224	QIFP----GAEGWPLPKYLGSCGRFLVSTST--RPLQEFYDAPPD--QAADLAWQLLGVL
HsapiDIA1R	224	QIFP----GAEGWPLPKYLGSCGRFLVSTST--RPLQEFYDAPPD--QAADLAWQLLGVL
BtaurDIA1R	224	QIFP----GAEGWPLPKYLGSCGRFLVSTST--SPLQEFYDAPPD--QAADLAWQLLGVL
EcabaDIA1R	224	QIFP----GAEGWPLPKYLGSCGRFLVSTST--SPLQEFYDAPPD--QAADLAWQLLGVL
DordiDIA1R	224	QIFP----GAEGWPLPKYLGSCGRFFVSTST--RPLQEFYDAPPD--EAADLAWQLLGVL
MdomeDIA1R	223	QIFP----GAEGWPLPKYLGSCGRFLVSTST--QPLEEFYSSPAD--QAADLAWQLLGVL
OanatDIA1R	223	QVFP----GAEGWPMFKYLGSCGRLLVSTST--TPLLELSSGPPD--RAADLAWQLLGVI
GgallDIA1R	221	QIFP----DVEGWPMFKYLGSCGRLLVVSAST--RPLRDFFRAPPE--VAADLAWQLLAVL
DreriDIA1R	207	QMFP----GTEGWPMFKYLGSCGRLLVWVAAS--RALRTLFSPPLE--RRADLAWQLLHIT
SsalaDIA1R	224	QMFP----GTEGWPMFKYLGSCGRLLVWVASS--RPLWGLYGSSRFVQRVDVAYQLLHIT
NvitrDIA1	193	QILP----AKEGWPMFKYLGSCGRLLVVEEYIG-LPLSSFIDEPWIR--RAKLASSLLQAA
BflorDIA1	208	QIFP----ITEGWPMFKYLGSCGRLLVVKCD-KTLASYSAPWL--KRVELSLQMMKIA
NvectDIA1	207	QIFR----QEGWPMFKYLGSCGRLLVVEDSG-PPISSFLEESWD--VRAQIAVNLITLA
CinteDIA1	235	SMFP----PYEGWPMFKYLGSCGRLLVHGRSIVTSLYELYDAPWK--VRDLVAIQLLDLA
consensus	241	q fp egwpmfkylgacGrml y g l yy apfe rldla qli ia

AaegyDIA1	240	LNF	TAGVDNFR	YLT	DISP	DNIVV	SMSSEE	-EIKV	TFV	DLN	NVI	I	ILD	SHSK	R	LKP	---	SK																																					
CpipiDIA1	242	FLF	TEGVNGFR	YLT	DNPN	DNIAV	QAQPSG	-SFQV	SFID	LDN	VII	I	ILDS	QSKR	L	DRR	--	SK																																					
AgambDIA1	250	FKF	TEGIHGFR	VFL	T	INPD	DNVVV	NLKN	DNKQ	VYVS	I	V	DL	DN	V	I	ILDS	WA	EV	FLT	---	KN																																	
DyakuDIA1	214	LKL	TGFSDFR	I	ML	T	DFTG	DNFAY	DEHT	TK	---	V	YL	I	D	L	D	S	V	V	L	D	---	ASSAT	--	GQ																													
DerecDIA1	215	LKL	TGFSDFR	I	F	L	T	DFTG	DNFAY	DEDS	KR	---	V	YL	I	D	L	D	S	V	V	L	D	---	ASSAA	--	GQ																												
DmelaDIA1	217	LKL	TGFAFDR	I	L	T	DFT	A	D	N	L	A	D	E	D	E	T	K	---	V	YL	I	D	L	D	S	V	V	L	D	---	AS	FAA	--	GH																				
DsechDIA1	219	LKL	TGFAFDR	I	L	T	DFT	A	D	N	L	A	D	E	E	T	K	---	V	YL	I	D	L	D	S	V	V	L	D	---	ASS	MA	--	GQ																					
DananDIA1	218	LKL	TGFAFDR	I	F	L	T	DFT	S	D	N	L	T	F	D	E	D	T	R	---	V	L	I	D	L	D	S	V	V	M	D	---	A	A	S	T	S	--	GQ																
DpersDIA1	218	LKL	TGFAFDR	I	F	L	T	DFT	A	D	N	L	A	F	D	E	A	S	Q	---	V	I	L	I	D	L	D	S	V	V	L	D	---	A	A	V	P	L	--	GD															
DpseuDIA1	218	LKL	TGFAFDR	I	F	L	T	DFT	A	D	N	L	A	F	D	E	A	S	Q	---	V	I	L	I	D	L	D	S	V	V	L	D	---	A	A	V	P	L	--	GD															
DwillDIA1	204	LKL	SAGFKGR	I	Y	L	T	DFT	A	D	N	F	A	Y	N	E	A	N	G	---	V	L	L	I	D	M	D	T	M	V	L	V	E	S	N	D	E	A	E	S	E	S	--	QL											
GaculDIA1	271	EQL	TN	N	D	F	F	A	L	Y	L	D	V	S	F	D	N	F	A	V	G	P	R	D	G	---	V	I	V	D	A	E	N	V	L	V	A	D	K	R	L	I	K	Q	N	K	-	P	E	S	F				
OlatiDIA1	271	EQL	TN	N	D	F	F	A	L	Y	L	D	V	S	F	D	N	F	A	V	G	P	R	D	G	---	V	I	V	D	A	E	N	V	L	V	A	D	K	R	L	I	K	Q	N	K	-	P	E	S	Y				
TnigrDIA1	271	EQL	TN	N	D	F	F	A	L	Y	L	D	V	S	F	D	N	F	A	V	G	P	R	D	G	---	V	I	I	V	D	A	E	N	V	L	V	A	D	K	R	L	I	K	Q	N	K	-	P	E	N	F			
TrubrDIA1	271	EQL	TN	N	D	F	F	A	L	Y	L	D	V	S	F	D	N	F	A	V	G	P	R	D	G	---	V	I	I	V	D	A	E	N	V	L	V	A	D	K	R	L	I	K	Q	N	K	-	P	E	N	Y			
DreriDIA1b	271	EQL	TN	N	D	F	F	A	L	Y	L	D	V	S	F	D	N	F	A	V	G	P	R	D	G	---	V	I	V	D	A	E	N	V	V	A	D	K	R	L	I	K	Q	N	K	-	P	E	S	Y					
DreriDIA1a	271	EQL	TN	N	D	F	F	A	L	Y	L	D	V	S	F	D	N	F	A	V	G	P	R	D	G	---	V	I	V	I	D	A	E	N	V	I	V	A	D	K	R	L	V	K	Q	N	K	-	P	E	S	Y			
BtaurDIA1	272	EQL	TN	N	D	F	F	A	L	Y	L	D	V	S	F	D	N	F	A	V	G	P	R	D	G	---	V	I	I	V	D	A	E	N	V	L	V	A	D	K	R	L	I	R	Q	N	K	-	P	E	N	W			
PpygmDIA1	272	EQL	TN	N	D	F	F	A	L	Y	L	D	V	S	F	D	N	F	A	V	G	P	R	D	G	---	V	I	I	V	D	A	E	N	V	L	V	A	D	K	R	L	I	R	Q	N	K	-	P	E	N	W			
CfamiDIA1	272	EQL	TN	N	D	F	F	A	L	Y	L	D	V	S	F	D	N	F	A	V	G	P	R	D	G	---	V	I	I	V	D	A	E	N	V	L	V	A	D	K	R	L	I	R	Q	N	K	-	P	E	N	W			
TtrunDIA1	272	EQL	TN	N	D	F	F	A	L	Y	L	D	V	S	F	D	N	F	A	V	G	P	R	D	G	---	V	I	I	V	D	A	E	N	V	L	V	A	D	K	R	L	I	R	Q	N	K	-	P	E	N	W			
PtrogDIA1	272	EQL	TN	N	D	F	F	A	L	Y	L	D	V	S	F	D	N	F	A	V	G	P	R	D	G	---	V	I	I	V	D	A	E	N	V	L	V	A	D	K	R	L	I	R	Q	N	K	-	P	E	N	W			
HsapiDIA1	272	EQL	TN	N	D	F	F	A	L	Y	L	D	V	S	F	D	N	F	A	V	G	P	R	D	G	---	V	I	I	V	D	A	E	N	V	L	V	A	D	K	R	L	I	R	Q	N	K	-	P	E	N	W			
MmulaDIA1	272	EQL	TN	N	D	F	F	A	L	Y	L	D	V	S	F	D	N	F	A	V	G	P	R	D	G	---	V	I	I	V	D	A	E	N	V	L	V	A	D	K	R	L	I	R	Q	N	K	-	P	E	N	W			
PvampDIA1	272	EQL	TN	N	D	F	F	A	L	Y	L	D	V	S	F	D	N	F	A	V	G	P	R	D	G	---	V	I	I	V	D	A	E	N	V	L	V	A	D	K	R	L	I	R	Q	N	K	-	P	E	N	W			
MmuscDIA1	272	EQL	TN	N	D	F	F	A	L	Y	L	D	V	S	F	D	N	F	A	V	G	P	R	D	G	---	V	I	I	V	D	A	E	N	V	L	V	A	D	K	R	L	I	R	Q	N	K	-	P	E	N	W			
RnorvDIA1	272	EQL	TN	N	D	F	F	A	L	Y	L	D	V	S	F	D	N	F	A	V	G	P	R	D	G	---	V	I	I	V	D	A	E	N	V	L	V	A	D	K	R	L	I	R	Q	N	K	-	P	E	N	W			
MdomeDIA1	272	EQL	TN	N	D	F	F	A	L	Y	L	D	V	S	F	D	N	F	A	V	G	P	R	D	G	---	V	I	I	V	D	A	E	N	V	L	V	A	D	K	K	L	I	R	Q	N	K	-	P	E	N	W			
GgallDIA1	271	EQL	TN	N	D	F	F	A	L	Y	L	D	V	S	F	D	N	F	A	V	G	P	R	D	G	---	V	I	I	V	D	A	E	N	V	L	V	A	D	K	R	L	I	R	Q	N	K	-	P	E	N	W			
XtropDIA1	271	EQL	TN	N	D	F	F	A	L	Y	L	D	V	S	F	D	N	F	A	V	G	P	R	D	G	---	V	I	I	V	D	A	E	N	V	L	V	A	D	K	K	L	I	K	Q	N	K	-	P	E	N	W			
SpurpDIA1	264	EQL	SEN	R	D	E	F	A	L	Y	L	T	D	V	S	E	D	N	L	A	V	N	-	N	G	E	---	V	L	V	I	D	A	E	N	I	V	V	D	K	K	I	K	E	D	A	-	N	P	G	W				
RnorvDIA1R	278	ESL	R	S	N	D	L	N	Y	F	F	Y	F	T	H	V	D	A	G	M	F	G	I	F	D	-	N	G	H	---	L	F	I	R	D	A	S	A	L	G	I	I	D	K	Q	E	A	S	Q	A	---	A	D	R	
MmuscDIA1R	278	ESL	R	S	N	D	L	N	Y	F	F	Y	F	T	H	V	D	A	G	M	F	G	I	F	D	-	N	G	H	---	L	F	I	R	D	A	S	A	L	G	I	I	D	K	Q	E	G	S	Q	A	---	A	A	R	
MmulaDIA1R	276	ESL	R	S	N	D	L	N	Y	F	F	Y	F	T	H	I	D	A	G	M	F	G	V	F	N	-	N	G	H	---	L	F	I	R	D	A	S	A	V	G	V	I	D	K	Q	E	G	S	Q	E	---	A	T	R	
HsapiDIA1R	276	ESL	R	S	N	D	L	N	Y	F	F	Y	F	T	H	I	D	A	G	M	F	G	V	F	N	-	N	G	H	---	L	F	I	R	D	A	S	A	V	G	V	I	D	K	Q	E	G	S	Q	E	---	A	N	R	
BtaurDIA1R	276	ESL	R	S	N	D	L	N	Y	F	F	Y	F	T	H	V	D	A	D	M	F	G	I	F	N	-	N	G	H	---	L	F	I	R	D	A	S	A	L	G	V	I	D	R	Q	E	G	S	Q	A	---	A	S	G	
EcabaDIA1R	276	ESL	R	S	N	D	L	N	Y	F	F	Y	F	T	H	V	D	A	G	M	F	G	I	F	N	-	N	G	H	---	L	F	I	R	D	A	S	T	L	G	V	I	D	R	Q	E	G	S	Q	A	---	A	A	R	
DordiDIA1R	276	ESL	R	S	N	D	L	N	Y	F	F	Y	F	T	H	V	D	A	A	M	F	G	I	F	S	-	N	G	H	---	L	F	I	R	D	A	S	A	L	G	V	I	D	K	Q	E	G	S	Q	A	---	A	P	K	
MdomeDIA1R	275	D	S	L	R	N	D	L	N	Y	F	F	Y	F	T	R	I	D	A	G	T	F	G	I	F	D	-	N	G	H	---	L	F	I	R	D	A	S	T	V	G	V	I	D	K	Q	R	G	S	L	T	---	L	D	R
OanatDIA1R	275	E	F	L	R	H	N	D	W	N	Y	F	F	Y	F	T	R	I	H	A	G	T	F	G	V	F	D	-	N	G	H	---	L	F	I	R	D	A	S	S	L	G	V	I	D	R	Q	E	G	K	R	P	---		

AaegyDIA1 296 QKHVHSRIDCDGC-----FAYIQEDICVHQISDINLFQAVCOLLENLNGDSKRGFLHSLG
 CpipiDIA1 299 ARNIHSRIPCDGC-----FAYVQEDLCSYQHS DINQFAICQLLYENLNGDREGGFLHIQP
 AgambDIA1 307 THHVHSKIIECNGC-----FAYVQEDVCRYQNSDINLEATCQLLENLNGHYAKGLLHYDR
 DyakuDIA1 264 AEKYEP-LPGE-----FTFDVSAFCSGHQLDANIYQACLLLRDYLLKLNLN-----
 DerecDIA1 265 AEKYVP-LPGE-----FTFDVSAFCSGHQLDANIYQACLLLRDFLLKLNLDN-----
 DmelaDIA1 267 AEKYEP-LTGE-----FTFDVSAFCSGHQLDANIYQACLLLRDYLLKLNLDN-----
 DsechDIA1 269 AEKYEP-LAGE-----FTFDVSAFCSGHQLDANIYQACLLLRDSLLKLNLDN-----
 DananDIA1 268 AEKYEP-LPGE-----FTFDVSAFCSGRQLDANVYQACLLLRDFLLKDLDN-----
 DpersDIA1 268 AQKYEP-LPGDG-----FTFDVKSFCGGQQLDANVYQACLLLRKDFLLRDLAN-----
 DpseuDIA1 268 AQKYEP-LPGDG-----FTFDVKSFCGGQQLDANVYQACLLLRKDFLLRDLAN-----
 DwillDIA1 258 SKKYKP-FPGE-----FTYDVNAFCDNQDLANIYQVCLLRDQLLPDVKN-----
 GaculDIA1 326 DVWYESRFEECD--REACLSFSKESLCSRVTVDHNYAVCQNLRSRYATWRGTT-----
 OlatiDIA1 326 DVWYESRFEECD--REACLSFSKDSLCSRVTVDHNYAVCQNLRSRYATWRGTT-----
 TnigrDIA1 326 DVWYESRFEECD--REACLSFSKDSLCSRVTVDHNYAVCQNLRSRYATWRGTT-----
 TrubrDIA1 326 DVWYESRFEECD--REACLSFSKDSLCSRVTVDHNYAVCQNLRSRYATWRGTT-----
 DreriDIA1b 326 DVWYESRFEECD--KEACLSFSKMDLCSRVTVDHNYAICQNLRSRYATWRGSS-----
 DreriDIA1a 326 DVWYESRYEED--KEACLSFSKDI LCSRVTVDHNYAVCQDLRSRFSWRGST-----
 BtaurDIA1 327 DVWYESKFDDCD--KEACLSFSKEILCARATVDHNYAVCQNLRSRHATWRGTS-----
 PpygmDIA1 327 DVWYESKFDDCD--KEACLSFSKEILCARATVDHNYAVCQNLRSRHATWRGTS-----
 CfamiDIA1 327 DVWYESKFDDCD--KEACLSFSKEILCARATVDHNYAVCQNLRSRHATWRGTS-----
 TtrunDIA1 327 DVWYESKFDDCD--KEACLSFSKEILCARATVDHNYAVCQNLRSRHATWRGTS-----
 PtrogDIA1 327 DVWYESKFDDCD--KEACLSFSKEILCARATVDHNYAVCQNLRSRHATWRGTS-----
 HsapiDIA1 327 DVWYESKFDDCD--KEACLSFSKEILCARATVDHNYAVCQNLRSRHATWRGTS-----
 MmulaDIA1 327 DVWYESKFDDCD--KEACLSFSKEILCARATVDHNYAVCQNLRSRHATWRGTS-----
 PvampDIA1 327 DVWYESKFDDCD--KEACLSFSKEILCARVTVDHNYAVCQNLRSRHATWRGTS-----
 MmuscDIA1 327 DVWYESKFDDCD--KEACLSFSKEILCARVTVDHNYAVCQNLRSRHATWRGTS-----
 RnorvDIA1 327 DVWYESKFDDCD--KEACLSFSKEILCARVTVDHNYAVCQNLRSRHATWRGTS-----
 MdomeDIA1 327 DVWYESKFDDCD--KEACLSFSKEILCSRATVDHNYAICQNLRSRHATWRGTS-----
 GgallDIA1 326 DVWYESKFDDCD--KEACLSFSKEILCARVTVDHNYAVCQNLRSRHATWRGTS-----
 XtropDIA1 326 DVWYESKFDDCD--KEACLSFSKEILCSRATVDHNYAICQNLRSRHATWRGTS-----
 SpurpDIA1 318 DVKHQSEHEGCGS--RRECIMFSHTDL CNHYSDHNYAVCQGLFGKDSPHG--D-----
 RnorvDIA1R 330 TGENEDIF SCL---VSGCQVQ--MSSCDTVPEKQNLVLCQQLLPQLLRG-----
 MmuscDIA1R 330 TGENEDIF SCL---VSDCQIQ--LSSCDTVPEKQSLVLCQQLLPQLLQG-----
 MmulaDIA1R 328 AGENKDI F SCL---VSGCQAQ--LPSCE SVSEKQSLVLCQKLLPRL LQG-----
 HsapiDIA1R 328 AGENKDI F SCL---VSGCQAQ--LPSCE SISEKQSLVLCQKLLPRL LQG-----
 BtaurDIA1R 328 AGDNKDI F SCL---VSGCQTK--LPSCDTIPEKQNLVLCQSVLP LLLQA-----
 EcabaDIA1R 328 AGENKDI F SCL---LSDCQAE--LPSCDTVPEKQSLVLCQROVLP RLLQG-----
 DordiDIA1R 328 AGENQDI F SCL---VSGCQAQL-LPSCDNIPDKQSVVLCQQLLPQLLQG-----
 MdomeDIA1R 327 QEESKDI F SCL---VLDCQSP--FPSCSSVKEKQSVVMACQQLLPQLLKE-----
 OanatDIA1R 327 SPEPRDI F SCL---AADCQSD--LPSCNTVQEHQSLVLCRELLPK LLEG-----
 GgallDIA1R 325 QQEYKDI F SCL---TVDCQSA--FVSCNSIREKQSLVMVCQELLPK LLRG-----
 DreriDIA1R 312 LPEELDV F SCL---SGSCVRP---PPCETVREAQSE ILLCKYILNLLTSN-----
 SsalaDIA1R 332 TGSDDI F SCLGQGTSPGCHRS---PPCSSVRPTQSLTLLCTALLP RLLTERGA-----
 NvitrDIA1 299 ESWNETY TNVAVDLCQDC FVFPNDICSHKVS DHNYAICQHIL TQALGAVFHN-----
 BflorDIA1 315 EARYSHF DECPG--MSNCLSF DVSALCRYLHTDHNYAVCRNMLSEYASEMGKP-----
 NvectDIA1 311 N--DKPKP SDCS--QPDCLSFSPSDMCSGGSRDHNYAICQGVLAGSSRQ-----
 CinteDIA1 340 Y--EVRYKQEK-----VDITEENL CDHSENDVNYVICRHFLGGTWKERK GK-----
 consensus 361 yesrf aclsf ic ld nyavCqnll r

AaegyDIA1	351	TDS---KLEAFRKLH-----QCVCQPPYCED-----RQEVLRQIMEI
CpipiDIA1	354	NDDSQPRLSEIRQLLH-----HCVCVFPDCRD-----ROGLLQQVQEI
AgambDIA1	362	DAEAFPVLGEASKMLQN-----LLSECVYQPEDCQN-----RSHILKDMLEHI
DyakuDIA1	310	-----ERLQLLLE-----QCVCQDDFCDM-----RFQHAYDLIKM
DerecDIA1	311	-----ERLQLLLE-----QCVCQDDFCDM-----RFQHAYDLIKV
DmelaDIA1	313	-----EKLQLLLE-----QCVCQDDFCDM-----RFQHAYDLIKV
DsechDIA1	315	-----EKLQLLLE-----QCVCQDDFCDM-----RFQHAYDLIKE
DananDIA1	314	-----ERLQLLLE-----KCVQCQDDLCDM-----RFQYAYDLIKL
DpersDIA1	314	-----GRLEMLLE-----QCVCDDATCDM-----RFQQAAYDLIKL
DpseuDIA1	314	-----GRLEMLLE-----QCVCDDATCDM-----RFQQAAYDLIKL
DwillDIA1	304	-----HRLKEMLN-----DCVQCEDDKCDI-----RFKYANNLIDL
GaculDIA1	378	---GGLLHDPPAHTAK---DGQLLTLLEDECTREPKKRY-G-----RFQAAKELREY
OlatiDIA1	378	---GGLLHDPPAHTAK---DGQLEALLDECTREPKKRY-G-----RFQAAKELREY
TnigrDIA1	378	---GGLLHDPPAHTAK---DGQLEALLDECTKPKKRY-G-----RFQAAKELREY
TrubrDIA1	378	---GGLLHDPPAHTAK---DGQLEALLDECTKPKKRF-G-----RFQAAKELREY
DreriDIA1b	378	---GGLLHDPPEHTAK---DGQLEALLEECANPKKRY-G-----RFQAAKELRDY
DreriDIA1a	378	---GGLLHDPPEVVK---DGRLEALLDECTREPKKRY-G-----RFQAAKELREF
BtaurDIA1	379	---GGLLHDPPEHTAK---DGRLEALLDECANPKKRY-G-----RFQAAKELREY
PpygmDIA1	379	---GGLLHDPPEHTAK---DGRLEALLDECANPKKRY-G-----RFQAAKELREY
CfamiDIA1	379	---GGLLHDPPEHTAK---DGRLEALLDECANPKKRY-G-----RFQAAKELREY
TtrunDIA1	379	---GGLLHDPPEHTAK---DGRLEALLDECANPKKRY-G-----RFQAAKELREY
PtrogDIA1	379	---GGLLHDPPEHTAK---DGRLEALLDECANPKKRY-G-----RFQAAKELREY
HsapiDIA1	379	---GGLLHDPPEHTAK---DGRLEALLDECANPKKRY-G-----RFQAAKELREY
MmulaDIA1	379	---GGLLHDPPEHTAK---DGRLEALLDECANPKKRY-G-----RFQAAKELREY
PvampDIA1	379	---GGLLHDPPEHTAK---DGRLEALLDECANPKKRY-G-----RFQAAKELREY
MmuscDIA1	379	---GGLLHDPPEHTAK---DGRLEALLDECTNEPKKRY-G-----RFQAAKELRGY
RnorvDIA1	379	---GGLLHDPPEHTAK---DGRLEALLDECTNEPKKRY-G-----RFQAAKELRGY
MdomeDIA1	379	---GGLLHDPPEHTAK---DGRLEALLDECAHPKRF-G-----RFQAAKELREY
GgallDIA1	378	---GGLLHDPPEHTAK---DGRLEALLDECANPKKRY-G-----RFQAAKELREY
XtropDIA1	378	---GGLLHDPPEHTAK---DGRLEALLDECANPKKRY-G-----RFKSAKELREY
SpurpDIA1	369	---GGLLHSTPSDLSY-MRAKVKGQIAECRSESKRD-G-----RYLVVKELKET
RnorvDIA1R	375	---KFPSPVQVEIDS-----ALSLSCKDASTNLE-----VFGATSLKNI
MmuscDIA1R	375	---KFPSPVQVEIDS-----ALSLSCKDNSTDLE-----VLGATSWLKDI
MmulaDIA1R	373	---RFPSPVQDDIDS-----ALAQCQDSTRPDPE-----VLGAASWLKHI
HsapiDIA1R	373	---RFPSPVQDDIDS-----ILVQCQDSIRPDPE-----VLGAASQLKDI
BtaurDIA1R	373	---KFPSPVQVEIDA-----ELTRCADGTRPDPE-----VLGAASRLKDI
EcabaDIA1R	373	---KFPSPVQVEIDA-----TLTWCGEDTRPDAE-----VLGAASRLKDI
DordiDIA1R	374	---KFPSPVQVEIDS-----ALAQCQGIRPDSE-----VFGAASRLKDI
MdomeDIA1R	372	---KFPQPIQEIDS-----ALVLCQNSLSDQE-----VIEAASRLKAI
OanatDIA1R	372	---KFPKPVQEIDA-----LLDRCQDSSLDGQT-----VIGGARRLMDI
GgallDIA1R	370	---KFLPPVQEKIDS-----FLQHCAEGLADDQD-----VNEAMAKLAQL
DreriDIA1R	357	---DKQSGLEPRAAVD-----ELLCVCAQDFSQLDQT-----IKSVQSLKNI
SsalaDIA1R	383	---QTTRLPMEGAEAGRLARDVPLLLGVCADFSQPDWR-----IMAAVGSIMDL
NvitrDIA1	353	---QGFLHDPDYILQK---HPTLIDLLEQCAKEDIGY-S-----RIDIAHKLIVL
BflorDIA1	368	---GGLLHDPPEVVR---DGTLQRLLECAKERTLYG-----RFDAAKELIEL
NvectDIA1	358	---GGLLHNPVALKAS---LNQLLQDCTAQDMRN-T-----REETAQKLSL
CinteDIA1	385	K-YPGGLLHDPKEFGVFS---SQMFVLLDICSRGKTAVAPERRTLSHSIRRLAANQLRNV
consensus	421	gvlhe p di 1 ll Ca p k rfqaakdlrei

AaegyDIA1	387	IHDV	LHEVV-----
CpipiDIA1	393	IDG	ILVES-----
AgambDIA1	405	IDQT	I IQS-----
DyakuDIA1	341	LDSKN	-----
DerecDIA1	342	LDSKI	-----
DmelaDIA1	344	LESNN	-----
DsechDIA1	346	LESKN	-----
DananDIA1	345	LDS	-----
DpersDIA1	345	LGEL	L LGS-----
DpseuDIA1	345	LGEL	L LGS-----
DwillDIA1	335	LVE	INN KIEIL-----
GaculDIA1	421	LTQL	AAASSS ATAR-----
OlatiDIA1	421	LTKL	AAASSS ATSR-----
TnigrDIA1	421	LTQL	A-----
TrubrDIA1	421	LTQL	AASSSS LVSAR-----
DreriDIA1b	421	LTQL	SGSAR-----
DreriDIA1a	421	LTQL	TQTSNADR-----
BtaurDIA1	422	LAQL	SNNVR-----
PpygmDIA1	422	LAQL	SNNVR-----
CfamiDIA1	422	LAQL	SNNVR-----
TtrunDIA1	422	LAQL	SNNVR-----
PtrogDIA1	422	LAQL	SNNVR-----
HsapiDIA1	422	LAQL	SNNVR-----
MmulaDIA1	422	LAQL	SNNVR-----
PvampDIA1	422	LAQL	SNNVR-----
MmuscDIA1	422	LAQL	SHNVR-----
RnorvDIA1	422	LAQL	SHNVR-----
MdomeDIA1	422	LAQL	SNNGR-----
GgallDIA1	421	LAQL	SNNVR-----
XtropDIA1	421	LAQL	SNNAR-----
SpurpDIA1	414	LMKL	IT-----
RnorvDIA1R	412	LRSL	RTCDPRFAYRYP DCKYNDRF-----
MmuscDIA1R	412	LRSL	RTCDPRFAYRYP DCKYNDRF-----
MmulaDIA1R	410	LRPL	RTCDSRFAYRYP DCKYNDKF-----
HsapiDIA1R	410	LRPL	RTCDSRFAYRYP DCKYNDKF-----
BtaurDIA1R	410	LRPL	RTCDPRFAYRYP DCKYDDKF-----
EcabaDIA1R	410	LRPL	RTCDPRFAYRYP DCKYNDKF-----
DordiDIA1R	411	LRPL	RTCDPRFAYRYP DCKYNDRF-----
MdomeDIA1R	409	LKPL	RTCDPRYAYRYP DCKYSDRY-----
OanatDIA1R	409	LKSL	RTCDARFAYRYP DCKYSEKY-----
GgallDIA1R	407	LKPL	RSCDSRFAYRYP DCKYSDKY-----
DreriDIA1R	394	LKTL	RPCSPQYAYRYPECLYSDKF-----
SsalaDIA1R	430	LKPM	RPCNPHYTYRYPECRYNQDY-----
NvitrDIA1	397	LDS	VIKNA-----
BflorDIA1	411	LG	SFLKDR-----
NvectDIA1	398	LQ	GYL-----
CinteDIA1	441	LERR	ICSPDFKYRYPECELAEDAGINLPSIELQWLH
consensus	481	1	1