

Fig. S2

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GaculDIA1 1 MDRFLPL--KLGRLYRCLKLLLVVGLFVILLMNHHS-----LFASFQKNELTDRRFINLN
OlatiDIA1 1 MDRFLPL--KLGRLYRCLKLLLVVGLFVILLMNTHN-----LFASFQKNELTDRRFINLN
TnigrDIA1 1 MDRFLPL--KLGRLYRCLKLLLVVGLFVILLMNTHN-----LFASFQKNELTDRRFINLN
TrubrDIA1 1 MDRFLPL--KLGRLYRCLKLLLVVGLFVILLMNTHN-----LFASFQKNELTDRRFINLN
DreriDIA1b 1 MDRFLPL--KLGRLYRCLKLLLVGLFVILLMNTHN-----LFASFQKNELTDRRFINLN
DreriDIA1a 1 MDRILSL--KFGRYRCGKFLFIVALFVILLMNTHN-----LFASFQKNELTDRRFIQLN
BtaurDIA1 1 MWRLVPP--KLGRLSRSLKLAALGSLLVLMVLHSPS-----LLASWQRNELADRRFLQLN
PpymDIA1 1 MWRLVPP--KLGRLSRSLKLAALGSLLVLMVLHSPS-----LLASWQRNELADRRFLQLN
CfamiDIA1 1 MWRLVPP--KLGRLSRSLKLAALGSLLVLMVLHSPS-----LLASWQRNELADRRFLQLN
PtrogDIA1 1 MWRLVPP--KLGRLSRSLKLAALGSLLVLMVLHSPS-----LLASWQRNELADRRFLQLN
TtrunDIA1 1 MWRLVPP--KLGRLSRSLKLAALGSLLVLMVLHSPS-----LLASWQRNELADRRFLQLN
HsapiDIA1 1 MWRLVPP--KLGRLSRSLKLAALGSLLVLMVLHSPS-----LLASWQRNELADRRFLQLN
MmulaDIA1 1 MWRLVPP--KLGRLSRSLKLAALGSLLVLMVLHSPS-----LLASWQRNELADRRFLQLN
PvampDIA1 1 MWRLVPP--KLGRLSRSLKLAALGSLLVLMVLHSPS-----LLASWQRNELADRRFLQLN
MmuscDIA1 1 MWRLVPL--KLGRLSRALKLAALGSLLVLMMLHSPS-----LLASWQRNELADRRFLQLN
RnorvDIA1 1 MWRLVPL--KLGRLSRALKLAALGSLLVLMMLHSPS-----LLASWQRNELADRRFLQLN
MdomeDIA1 1 MWRLVPP--KLGRLSRSLKLAALGSLLVLMVLHSPS-----LLASWQRNELADRRFLQLN
GgallDIA1 1 MLRLVSL--KLGRLYRYVKLAVLGLSAAAIVLNTHS-----LLASLQRNELADRRFLQLN
XtropDIA1 1 MLRLASL--KFGRLFRYAKVLFASLLVVMMLNTHS-----LLSSFQKNELTDRRFINLN
BflorDIA1 1 -MRLVRLR-QFRRFSGWRVRRRCGFFFFVFFYCF-----VFQPFSSYNQLDTDFLGED
SpurpDIA1 1 MRRYFNQFTNRFCTSTQQLWLVVLSMCLFVYYQ-----LYLHF TANHLENEYFTEAT
NvectDIA1 1 -MHFGGILRKRRIQRLVLLLVIIISFSDLLWLSYQDGRAIKWDFSSGHKLTFOEIGLN
NvitrDIA1 1 -----MLVTKASVSEFIALLLILGIYIN-----R----FNLKVAEITERY
AaegyDIA1 1 -----MSQ--HRIILTKLHVALFLWIVMKYQPE---ERASSLKSLVQQCQYDITI
CpipiDIA1 1 -----MSSGFORILVNHILALLFCVIFEFQPK---EPESLTELIVNQCBEYEQH
AgambDIA1 1 -----MQS----S-RLPYFVTLFIAVVLQYLPN---EKSTSKRPLENVCDYDRNI
DyakuDIA1 1 -----MHLSPGQLKVVILILALLQE---LQVKPQREVFQELFEKDLR
DerecDIA1 1 -----MHLSPGQLKVVILILALLQE---LQVKPQREVFQELFEKDLR
DmelaDIA1 1 -----MHLSHGQLKVVILILALLQE---LQVKPQREVFQELFEKDLR
DsechDIA1 1 -----MHLSYGQLKVVILILALLQE---LQVKTQREVFQELFEKDLR
DananDIA1 1 -----MHLMSGQLRIVLVLALLQD---LQVKPQKIDIFQEHFESDLR
DpersDIA1 1 -----MHLSPGHLRIVLILALLQD---LQVKPQKIDIFRAHLERDLQ
DpseuDIA1 1 -----MHLSPGHLRIVLILALLQD---LQVKPQKIDIFRAHLERDLQ
DwillDIA1 1 -----MHLLYGQLKVVILVLLALLQE---LDVRTQKIDIFRKHFNMDDL
CinteDIA1 1 MLLKMKRYLTVWENGKRYIVFIFLITLLEVMYHNRSQGSTRVMLEAKLLSDKWSATSP
consensus 1 m r l klgrl r lkll vg l villl t l asfqnel drrfi ln

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GaculDIA1 54 KCP--ACFGT--SWCRKFMNGQVSFET-----WGRL-RLDVFNVKNVYFAQYGEPRE
OlatiDIA1 54 KCP--ACFGT--SWCRKFMNGQVSFET-----WGRL-RLDVFNVKNVYFAQYGEPRE
TnigrDIA1 54 KCP--ACFGT--SWCRKFMNGQVSFET-----WGRL-RLDVFNVKNVYFAQYGEPRE
TrubrDIA1 54 KCP--ACFGT--SWCRKFMNGQVSFET-----WGRL-RLDVFNVKNVYFAQYGEPRE
DreriDIA1b 54 KCP--ACFGT--SWCRKFMNGQVSFET-----WGRL-RLDVFNVKNVYFAQYGEPRE
DreriDIA1a 54 KCP--ACFGT--SWCRKFMNGQVTFEM-----WGRL-RLDFFNVKNVYFAQYGEPRE
BtaurDIA1 54 KCP--ACFGT--SWCRRFLNGQVVFEE-----WGRL-RLDFFLNKNVYFAQYGEPRE
PpymDIA1 54 KCP--ACFGT--SWCRRFLNGQVVFEE-----WGRL-RLDFFLNKNVYFAQYGEPRE
CfamiDIA1 54 KCP--ACFGT--SWCRRFLNGQVVFEE-----WGRL-RLDFFLNKNVYFAQYGEPRE
PtrogDIA1 54 KCP--ACFGT--SWCRRFLNGQVVFEE-----WGRL-RLDFFLNKNVYFAQYGEPRE
TtrunDIA1 54 KCP--ACFGT--SWCRRFLNGQVVFEE-----WGRL-RLDFFLNKNVYFAQYGEPRE
HsapiDIA1 54 KCP--ACFGT--SWCRRFLNGQVVFEE-----WGRL-RLDFFLNKNVYFAQYGEPRE
MmulaDIA1 54 KCP--ACFGT--SWCRRFLNGQVVFEE-----WGRL-RLDFFLNKNVYFAQYGEPRE
PvampDIA1 54 KCP--ACFGT--SWCRRFLNGQVVFEE-----WGRL-RLDFFLNKNVYFAQYGEPRE
MmuscDIA1 54 KCP--ACFGT--SWCRRFLNGQVGFET-----WGRL-RLDFFLNKNVYFAQYGEPRE
RnorvDIA1 54 KCP--ACFGT--SWCRRFLNGQVGFET-----WGRL-RLDFFLNKNVYFAQYGEPRE
MdomeDIA1 54 KCP--ACFGT--SWCRRFLNGQVAFEE-----WGRL-RLDFFLNKNVYFAQYGEPRE
GgallDIA1 54 KCP--ACFGT--SWCRKFLNGQLRLES-----WGRL-RLDFFNVKNVYFAQYGEPRE
XtropDIA1 54 KCP--ACFGT--SWCRKFMNGQLSFEG-----WGRL-RLDFFNVKNVYFAQYGEPRE
BflorDIA1 54 KCP--ACFGT--DLCEEFENGKILFKY-----SSRL-RLDIFNKNVYFATY----E
SpurpDIA1 56 KCP--ACFGT--SLCKRFSRGDYRFHS-----YSSI-RLFDYVNVKNVYFATYLD---
NvectDIA1 60 KCP--ACFGINLSICHKLLGGVTVKVS-----N---TPWSEERIKGVSYGLNG---
NvitrDIA1 39 KCP--ACFGD--SMCQVIDSNEISFEY-----TDFYSIFNNLFSVKNVYVYGRK----
AaegyDIA1 46 LCP--GCFPRP-VNCSFFENLKSIDS-----NELEFELLTHFNQHGVRYGTL
CpipiDIA1 48 LCP--ECFVSPVTNCGHLANFVTIDS-----SNPWNQLTCHYNPHGVSYG-LL
AgambDIA1 43 LCP--ECVSSG-LECNKFDLTLQD-----DNVFNININIFNSHTTRIGTIV
DyakuDIA1 39 LCP--NCFFGQRELCEEIFOKIAEPSD-----W---SKLLKAISLIVDRRAIVFLRFK
DerecDIA1 39 LCP--DCFVGQSELCVGFIFOKIAEPSD-----W---SKLLKAISLIVDRRAIVYFLRLK
DmelaDIA1 39 LCP--DCFVGQSEPCGEIFOKIAEPSD-----W---SRLVKAISLIVDRRAIVYFLRLK
DsechDIA1 39 LCP--DCFVGQKEQCGEIFOKIAEPSD-----W---SRLVKAISLIVDRRAIHYFLRLK
DananDIA1 39 LCP--ACFSAQREQCEEVFRAIPEPSD-----L---SKLWKAIVTLFDRREIIFWLEIG
DpersDIA1 39 LCP--ACFAGQRWQCEEIFEIAIPEPSD-----W---SKLLKGIALLIDRREIYFLQLN
DpseuDIA1 39 LCP--ACFAGQRWQCEEIFEIAIPEPSD-----W---SKLLKGIALLIDRREIYFLQLN
DwillDIA1 39 ECP--QCFLGQREQCEKFFDITIEPAK-----L---DRLWKDLTLVDPREIYWLELN
CinteDIA1 61 TCGNFSFCFGT--SLCKNRNRVGVSEIVPTLRSGWLSIYGLVLDLHRVKNVYTKLPSTLP
consensus 61 kCp aCfGt swCrkfmngqv fe wgrl rlld lnvknvyfaqygepre

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GaculDIA1 102 GTRR-VVLKRLGNSQELAEIDQKICKRATGRPR-CDLIQAMYKTEFA-RINGDVRLLTPE
OlatiDIA1 102 GTRR-VVLKRLGNSQELAEIDQKICKRATGRPR-CDLVQAMYKTEFA-RINGDVRLLTPE
TnigrDIA1 102 GTRR-VVLKRLGNSQELADIDQKICKRATGRPR-CDLIQAMYKTEFA-RINGDVRLLTPE
TrubrDIA1 102 GTRR-VVLKRLGNSQELADIDQKICKRATGRPR-CDLIQAMYKTEFA-RINGDVRLLTPE
DreriDIA1b 102 GTRR-VVLKRLGNSQELAEIDQKICKRATGRPR-CDLIQAMYKTEFA-RINGDVRLLTPE
DreriDIA1a 102 GTRR-VVLKRLGNSQELAEIDQKICKRATGRPR-CDLIQAMYKTEFA-RINGDVRLLTPE
BtaurDIA1 102 GRRRVVLKRLGNSQELAQLDQSIKCRATGRPR-CDLQAMPRTTEFA-RINGDVRLLTPE
PpygmDIA1 102 GRRRVVLKRLGNSQELAQLDQSIKCRATGRPR-CDLQAMPRTTEFA-RINGDVRLLTPE
CfamiDIA1 102 GRRRVVLKRLGNSQELAQLDQSIKCRATGRPR-CDLQAMPRTTEFA-RINGDVRLLTPE
PtrogDIA1 102 GRRRVVLKRLGNSQELAQLDQSIKCRATGRPR-CDLQAMPRTTEFA-RINGDVRLLTPE
TtrunDIA1 102 GRRRVVLKRLGNSQELAQLDQSIKCRATGRPR-CDLQAMPRTTEFA-RINGDVRLLTPE
HsapiDIA1 102 GRRRVVLKRLGNSQELAQLDQSIKCRATGRPR-CDLQAMPRTTEFA-RINGDVRLLTPE
MmulaDIA1 102 GRRRVVLKRLGNSQELAQLDQSIKCRATGRPR-CDLQAMPRTTEFA-RINGDVRLLTPE
PvampDIA1 102 GRRRVVLKRLGNSQELAQLDQSIKCRATGRPR-CDLQAMPRTTEFA-RINGDVRLLTPE
MmuscDIA1 102 GRRRVVLKRLGNSQELAQLDQSIKCRATGRPR-CDLQAMPRTTEFA-RINGDVRLLTPE
RnorvDIA1 102 GRRRVVLKRLGNSQELAQLDQSIKCRATGRPR-CDLQAMPRTTEFA-RINGDVRLLTPE
MdomeDIA1 102 GRRRVVLKRLGNSQELAQLDQSIKCRATGRPR-CDLQAMPRTTEFA-RINGDVRLLTPE
GgallDIA1 102 GSRR-VVLKRLGSAQELADIDAKICRRATGRGR-CDLQALHATEFA-SINGDVRLLTPE
XtropDIA1 102 GSRR-VVLKRLGNSHELSELDQRIKCRATGRPR-CDLVQAMYKTEFA-RINGDVRLLTPE
BflorDIA1 98 GMEV--ALKRLGHNSSEFDQLDRWICETKEGEQ-CHIPSVTYYSNFS-RVIYEG--LSPK
SpurDIA1 101 --QKPVVVKLGHNSSEHNQFDKDLCTNAESGLRGCDVSOQYKSKLS-DIMYAEF--LEEK
NvectDIA1 103 AVKQRVVLKTLGTSSELTAFDNEICRGVGVKDSN-CKLSQEAWSDV-LVPPKQO-----
NvitrDIA1 84 --DKKVIKMLAQESSELKTFDEMICSDELHELQYSESRSKQDSKTN-FYKLVESELANV
AaegyDIA1 91 GSEQRVVKLNLNKEHGEVELISSICNDLKIYR-NQRLRNKEPYLR-----VLRQVVL---
CpipiDIA1 93 GSGQKVVKTLNKNRAVEALRDVACDELGLTQSNCKFKSDENTLK-----VLRKVVL---
AgambDIA1 88 QENKLAVMKHLNRDNTTEKLLCEYCDAYSLTKQNCRWACHDGSVDRA-KEFITTSIL---
DyakuDIA1 87 DQDQ----VVAKRKIIDAQNOQ-IKDVKKAF-----YE-----
DerecDIA1 87 DQAQ----VVAKRKIIDARNHK-AENVEKAF-----YE-----
DmelaDIA1 87 DRDQEV-Q-LVAKRKIIDAQSNQ-IKNVKKDF-----YE-----
DsechDIA1 87 DQDQAV-Q-LVAKRKIINAHSYQ-MKNVKRAF-----YE-----
DananDIA1 87 PSQEKSSQ-LLAKRKSIVASHQS-LSSLQEEF-----LN-----
DpersDIA1 87 ERHQAA-Q-LVAKRDAIGGHSYRNMGI LREAF-----LE-----
DpseudDIA1 87 ERHQAA-Q-LVAKRDAIGGHSYRNMGI LGEAF-----LE-----
DwillDIA1 87 ENREN-VK-CLAKRMTRKISKD-----
CinteDIA1 119 CNGETCSVQIETSVLSGNNVNWIKCDKFKKPTN-CDTGKVFKSWRAMNKITSAGRLDPE
consensus 121 g rr vvlkrlgnsrela idq ickratgrpr cdliqam ktefa ringdvrltpe

GaculDIA1 159 VVEGWSDLVHCPQSRLLDRLVRRYAETKDSGSFLLKLNKDKTERMQLLMTLAFNPEPLVLQ
OlatiDIA1 159 VVEGWSDLVHCPQSRLLDRLVRRYAETKDSGSFLLKLNKDKTERMQLLMTLAFNPEPLVLQ
TnigrDIA1 159 VVEGWSDLVHCPQSRLLDRLVRRYAETKDSGSFLLKLNKDKTERMQLLMTLAFNPEPLVLQ
TrubrDIA1 159 VVEGWSDLVHCPQSRLLDRLVRRYAETKDSGSFLLKLNKDKTERMQLLMTLAFNPEPLVLQ
DreriDIA1b 159 VVEGWSDLVHCPQSRLLDRLVRRYAETKDSGSFLLKLNKDKTERMQLLMTLAFNPEPLVLQ
DreriDIA1a 159 VVEGWSDLVHCPQSRLLDRLVRRYAETKDSGSFLLKLNKDKTERMQLLMTLAFNPEPLVLQ
BtaurDIA1 160 AVEGWSDLVHCPQSRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVLQ
PpygmDIA1 160 AVEGWSDLVHCPQSRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVLQ
CfamiDIA1 160 AVEGWSDLVHCPQSRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVLQ
PtrogDIA1 160 AVEGWSDLVHCPQSRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVLQ
TtrunDIA1 160 AVEGWSDLVHCPQSRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVLQ
HsapiDIA1 160 AVEGWSDLVHCPQSRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVLQ
MmulaDIA1 160 AVEGWSDLVHCPQSRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVLQ
PvampDIA1 160 AVEGWSDLVHCPQSRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVLQ
MmuscDIA1 160 AVEGWSDLVHCPQSRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVLQ
RnorvDIA1 160 AVEGWSDLVHCPQSRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVLQ
MdomeDIA1 160 AVEGWSDLVHCPQSRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVLQ
GgallDIA1 159 AVEGWSDLVHCPQSRLLDRLVRRYAETKDSGSFLLRNLKDSERMQLLMTLAFNPEPLVLQ
XtropDIA1 159 VVEGWSDLVHCPQSRLLDRLVRRYAETKDSGSFLLRNLKDKTERMQLLMTLAFNPEPLVLQ
BflorDIA1 152 SEGDMSDVRCPQSRLLDRLVLEKFAEHLGKET---EELSYQEKLHFLSTLKFNPPEPLMLQ
SpurDIA1 157 DVMGLSDIVRCPQSRLLDRLVDTFGERQFDKS-----LARDHKLMLATTLAFNPEPLILQ
NvectDIA1 156 --DAVRKYFDCPSTRLEKIESVYQETPGQLS-----LVETIHLTGLHLNPEPLLLQ
NvitrDIA1 141 GGFINNKMLRCPPTTTKLEKLFVNVKFSHAEN-----EDYFKYLWSTIKINPEPLILQ
AaegyDIA1 142 NDNQLEGAFLCPLMDE--EALKRFLFEIDEND-----LNKILLMRINAQPLLLK
CpipiDIA1 145 -EQELEGCHICPSKDE--KALNRLNEVVGTE-----LLQLLKLKVNQPLLLK
AgambDIA1 144 DSARVEGCHFCPATNNR-QSLQRFSLSEFSDTD-----NELWNLAVRTNVEPLLIK
DyakuDIA1 115 LGERPGGFHLCRTPSRKP-RFVSYLEQRGHA-----SASVWFYMMHYVSPLLMQ
DerecDIA1 115 QEBQPPGGFHLCRTPSRKP-RFVSYLEQRGHA-----SASVWFYMMHYVSPLLMQ
DmelaDIA1 118 LBERPGGFHLCRTLAREP-RFVSYLEQRGHA-----AASVWFYMMHYVSPLLMQ
DsechDIA1 118 LBERPGGFHLCRTLAREP-RFVSYLEQRGHVY-----GSTSVWFYMMHYVSPLLMQ
DananDIA1 119 LBERPGGFHLCRTAQKSS-PFINYLNRQGYD-----SSSIYFYMLHNSPLLMQ
DpersDIA1 119 MBERPGGFQLCRSGFRTP-RFVSYLEQRGHE-----AATIWFYMMHSITPLLMQ
DpseudDIA1 119 MBERPGGFQLCRSGFRTP-RFVSYLEQRGHE-----AATIWFYMMHSITPLLMQ
DwillDIA1 108 LHFNPPGGFQMCORNSTR---FLAYLEERGYL-----PATIGYYTHHSISPLLMQ
CinteDIA1 178 LKDI SPPVQCPSTRADRI VRRVANKQGGVLLR--DLSYTEKRLFFCTKMSGSSVVS
consensus 181 vegwsdlvhCpsqrlldrvvrryaetkdsGSfllknkdktermqlllmtlafnpeplvlq

GaculDIA1	219	SFP----	SDEGWPF	AKYLGACGRM	VAVN--	YVGEEL	WSFY	NAPWEK	RVDLAR	QQLMD	IAEQ
OlatiDIA1	219	SFP----	SDEGWPF	AKYLGACGRM	VAVN--	YVGEEL	WNFY	NAPWEK	RVDLAR	QQLMD	IAEQ
TnigrDIA1	219	SFP----	SDEGWPF	AKYLGACGRV	VAVN--	YVGEEL	WSFY	NAPWEK	RVDLAR	QQLMD	IAEQ
TrubrDIA1	219	SFP----	SDEGWPF	AKYLGACGRV	VAVN--	YVGEEL	WSFY	NAPWEK	RVDLAR	QQLMD	IAEQ
DreridIA1b	219	SFP----	SDEGWPF	AKYLGACGRM	VAVN--	YVGEEL	WSFF	NAPWEK	RVDLAR	QQLMD	IAEQ
DreridIA1a	219	SFP----	SDEGWPF	AKYLGACGRM	VAVN--	YVGEEL	WSFY	NAPWEK	RVDLAR	QQLMD	IAEQ
BtaurDIA1	220	SFP----	SDEGWPF	AKYLGACGRM	VAVN--	YVGEEL	WSFY	NAPWEK	RVDLAR	QQLME	IAEQ
PpygmDIA1	220	SFP----	SDEGWPF	AKYLGACGRM	VAVN--	YVGEEL	WSFY	NAPWEK	RVDLAR	QQLME	IAEQ
CfamiDIA1	220	SFP----	SDEGWPF	AKYLGACGRM	VAVN--	YVGEEL	WSFY	NAPWEK	RVDLAR	QQLME	IAEQ
PtrogDIA1	220	SFP----	SDEGWPF	AKYLGACGRM	VAVN--	YVGEEL	WSFY	NAPWEK	RVDLAR	QQLME	IAEQ
TtrunDIA1	220	SFP----	SDEGWPF	AKYLGACGRM	VAVN--	YVGEEL	WSFY	NAPWEK	RVDLAR	QQLME	IAEQ
HsapiDIA1	220	SFP----	SDEGWPF	AKYLGACGRM	VAVN--	YVGEEL	WSFY	NAPWEK	RVDLAR	QQLME	IAEQ
MmulaDIA1	220	SFP----	SDEGWPF	AKYLGACGRM	VAVN--	YVGEEL	WSFY	NAPWEK	RVDLAR	QQLME	IAEQ
PvampDIA1	220	SFP----	SDEGWPF	AKYLGACGRM	VAVN--	YVGEEL	WSFF	NAPWEK	RVDLAR	QQLME	IAEQ
MmuscDIA1	220	SFP----	SDEGWPF	AKYLGACGRM	VAVN--	YVGEEL	WSFY	NAPWEK	RVDLAR	QQLME	IAEQ
RnorvDIA1	220	SFP----	SDEGWPF	AKYLGACGRM	VAVN--	YVGEEL	WSFY	NAPWEK	RVDLAR	QQLME	IAEQ
MdomeDIA1	220	SFP----	SDEGWPF	AKYLGACGRM	VAVN--	YVGEEL	WSFY	NAPWEK	RVDLAR	QQLME	IAEQ
GgallDIA1	219	SFP----	SDEGWPF	AKYLGACGRM	VAVN--	YVGEEL	WSFY	NAPWEK	RVDLAR	QQLME	IAEQ
XtropDIA1	219	SFP----	SDEGWPF	AKYLGACGRM	VAVN--	YVGEEL	WSFY	NAPWEK	RVDLAR	QQLME	IAEQ
BflorDIA1	209	TFP----	ITEGWPF	PFYFGACGR	LTIVC-	KCDKTL	ASYS	SAPWL	KRVLEL	SLOMK	IAEYL
SpurpDIA1	212	AFP----	NRKGWPF	PAYMGACGR	FTVQE-	YSGHSL	SYFY	KFKG	GVRAAL	AVQAL	KIAEQ
NvectDIA1	208	IFR----	QTEGWPF	PREYGVCGR	IMVVE-	DSGPPH	SSFL	EESSW	DVRAQ	IAVNL	ITLAHQ
NvitrDIA1	194	ILP----	AKEGWPT	KYFGACGR	LIVEE-	YIGLPL	SSFI	DEBP	WIRRAK	IASSL	IQAADL
AeegyDIA1	189	LL-----	QRNFVVP	KLIFQGGFT	LIVES-	YEGEAL	AKYY	DRPL	NVRL	LITANEL	IKASLN
CpipiDIA1	191	LF-----	DGRGFVP	PKVIFQGGF	QLFES-	FDGDAL	VNFY	DSSLN	IRLRL	AKELI	QASFLF
AgambDIA1	194	LLTVNYHD	PPLYVVP	KLLHTFGFS	LIET-	YEGKTL	EHYY	DFPF	VTRMR	IAAEL	IACFKF
DyakuDIA1	163	EL-----	YLQGFVP	PTYASCGLT	HFQS-	YAGRTL	TNYFE	EEED	LRLV	LALQL	QLSLKL
DerecDIA1	164	EL-----	HLQGFVP	PTYASCGLT	HFQA-	YAGRTL	TNYFE	EEED	LRLV	LALQL	QLSLKL
DmelaDIA1	166	EL-----	HLQGFVP	PTYASCGLT	HFQS-	NAGRTL	LAHYV	DAEGL	RVEL	LALQL	QLSLKL
DsechDIA1	168	EL-----	HLQGFVP	PTYASCGLT	HFQS-	YAGRTL	LAHYV	NAEGL	RLEL	LALQL	QLSLKL
DananDIA1	167	EL-----	QNLDFVP	PNTYAI	CGLTHFQA-	YAGRTL	NHYTE	AAED	LRRE	IARQL	IHL
DpersDIA1	167	EL-----	FLRGFVP	PSYAACGLT	HFQA-	YAGRTL	VHYAT	AGENL	RLEMA	RQLL	QLSLKL
DpseuDIA1	167	EL-----	FLRGFVP	PSYAACGLT	HFQA-	YAGRTL	VHYAT	AGENL	RLEMA	RQLL	QLSLKL
DwillDIA1	153	EL-----	WIMDFVP	RSFVACG	STLFA-	YAGSTL	SNYLK	APIDL	RLEMA	QQLI	QLALKL
CinteDIA1	236	MFP----	PYEGWLF	QSTVGS	CGALMVHGRS	IVTSLM	ELYL	DAPWK	VRLD	VAIQL	LDLDAEHF
consensus	241	sfp	sdegw	pfakylgac	grmvavn	yvgeel	wsyyn	apwek	rvdla	qlmdia	aeql

GaculDIA1	274	TNND	DFALYLL	DVSFDNF	AVGPRD	GK----	VIIVDA	ENVL	VADKRL	IKONK	PESE	YDVWY								
OlatiDIA1	274	TNND	DFALYLL	DVSFDNF	AVGPRD	GK----	VIIVDA	ENVL	VADKRL	IKONK	PESE	YDVWY								
TnigrDIA1	274	TNND	DFALYLL	DVSFDNF	AVGPRD	GK----	VIIVDA	ENVL	VADKRL	IKONK	PENF	YDVWY								
TrubrDIA1	274	TNND	DFALYLL	DVSFDNF	AVGPRD	GK----	VIIVDA	ENVL	VADKRL	IKONK	PENY	YDVWY								
DreridIA1b	274	TNND	DFALYLL	DVSFDNF	AVGPRD	GK----	VIIVDA	ENVL	VADKRL	IKONK	PESE	YDVWY								
DreridIA1a	274	TNND	DFALYLL	DVSFDNF	AVGPRD	GK----	VIIVDA	ENVI	VADKRL	IKONK	PESE	YDVWY								
BtaurDIA1	275	TNND	DFALYLL	DVSFDNF	AVGPRD	GK----	VIIVDA	ENVL	VADKRL	IKONK	PENW	YDVWY								
PpygmDIA1	275	TNND	DFALYLL	DVSFDNF	AVGPRD	GK----	VIIVDA	ENVL	VADKRL	IKONK	PENW	YDVWY								
CfamiDIA1	275	TNND	DFALYLL	DVSFDNF	AVGPRD	GK----	VIIVDA	ENVL	VADKRL	IKONK	PENW	YDVWY								
PtrogDIA1	275	TNND	DFALYLL	DVSFDNF	AVGPRD	GK----	VIIVDA	ENVL	VADKRL	IKONK	PENW	YDVWY								
TtrunDIA1	275	TNND	DFALYLL	DVSFDNF	AVGPRD	GK----	VIIVDA	ENVL	VADKRL	IKONK	PENW	YDVWY								
HsapiDIA1	275	TNND	DFALYLL	DVSFDNF	AVGPRD	GK----	VIIVDA	ENVL	VADKRL	IKONK	PENW	YDVWY								
MmulaDIA1	275	TNND	DFALYLL	DVSFDNF	AVGPRD	GK----	VIIVDA	ENVL	VADKRL	IKONK	PENW	YDVWY								
PvampDIA1	275	TNND	DFALYLL	DVSFDNF	AVGPRD	GK----	VIIVDA	ENVL	VADKRL	IKONK	PENW	YDVWY								
MmuscDIA1	275	TNND	DFALYLL	DVSFDNF	AVGPRD	GK----	VIIVDA	ENVL	VADKRL	IKONK	PENW	YDVWY								
RnorvDIA1	275	TNND	DFALYLL	DVSFDNF	AVGPRD	GK----	VIIVDA	ENVL	VADKRL	IKONK	PENW	YDVWY								
MdomeDIA1	275	TNND	DFALYLL	DVSFDNF	AVGPRD	GK----	VIIVDA	ENVL	VADKRL	IKONK	PENW	YDVWY								
GgallDIA1	274	TNND	DFALYLL	DVSFDNF	AVGPRD	GK----	VIIVDA	ENVL	VADKRL	IKONK	PENW	YDVWY								
XtropDIA1	274	TNND	DFALYLL	DVSFDNF	AVGPRD	GK----	VIIVDA	ENVL	VADKRL	IKONK	PENW	YDVWY								
BflorDIA1	264	TNNE	ADFLYL	TDTSY	ENFV	GVTSDGN	----	LFV	IDVENV	IVV	DKQIK	KADKPNWEARY								
SpurpDIA1	267	SEN	RDFALY	LLTDV	SEDN	LAVND-NGE	----	VLV	IDAENI	IVV	DRKKI	KEDANPGWVVKH								
NvectDIA1	263	SSAL	DDWALY	IADP	APGNF	GVSD-SGK	----	VTLL	DLLEHL	VVVDL	SEVQ	MEEAN----								
NvitrDIA1	249	MSKN	SEFA	YLTDIS	MNIA	VANN-EDK	----	AIF	VDL	ENIIT	VEK	NPPEKALVG-IESWN								
AeegyDIA1	243	TEG	VDNFR	EYLT	DISP	NIIV	SMSSEE-EIK	VTF	VDL	NNVI	ILDS	SKRLKP-SKQKHVH								
CpipiDIA1	245	TEG	VNGFR	EYLT	DISP	NIIV	QAQPSG-SFQ	VST	IDL	DNVI	ILDS	SQSKLDRRSKARNIH								
AgambDIA1	253	TEGI	HGFR	VFLTD	INP	DNVV	NLKN	DNKQ	VYVSI	VDL	DNVI	ILDS	SWAEVFLT-KNTHHHV							
DyakuDIA1	217	TFG	FSDFR	MLTDF	TGDN	FAYDEHTTK	----	VYL	IDL	DSV	VLV	VD----	ASSATGQAEKYE							
DerecDIA1	218	TFG	FSDFR	MLTDF	TGDN	FAYDEDSKR	----	VYL	IDL	DSV	VLV	VD----	ASSAAGQAEKYV							
DmelaDIA1	220	TFG	FADFR	MLTDF	TADN	LAYDEDTKK	----	VYL	IDL	DSV	VLV	VD----	ASFAAGHAEKYE							
DsechDIA1	222	TFG	FADFR	MLTDF	TADN	LAYDEETKK	----	VYL	IDL	DSV	VLV	VD----	ASSMAGQAEKYE							
DananDIA1	221	TFG	FADFR	MLTDF	TSDN	LTFDEDTRE	----	VLL	IDL	DSV	V	MVD----	AASTSGQAEKYE							
DpersDIA1	221	TFG	FADFR	MLTDF	TADN	LAFDEASQS	----	VIL	IDL	DSV	V	V	VD----	AAVPLGDAQKYE						
DpseuDIA1	221	TFG	FADFR	MLTDF	TADN	LAFDEASQS	----	VIL	IDL	DSV	V	V	VD----	AAVPLGDAQKYE						
DwillDIA1	207	SAG	FKGFR	YLTDF	TADN	FAYNEANGT	----	VLL	IDM	DTM	V	LVES	ND	EASES	QLSKKYK					
CinteDIA1	292	TYND	LNYM	FALH	RLLTP	RDIG	SD-TGK	----	LR	RK	ADNV	IL	IDNN	--SK	NDKGL	YEVRY				
consensus	301	tnn	dfal	yll	dvsf	dnfavg	prdgk		viv	daen	vl	v	adk	rlik	q	kn	pen	fd	vw	y

GaculDIA1 330 ESRFEECD--REACLSFSKESLCSRVTVDHNYAVCQNLLSRYATWRGTT---GGLLHDP
 OlatiDIA1 330 ESRFEECD--REACLSFSKDSLCSRVTVDHNYAVCQNLLSRYATWRGTT---GGLLHDP
 TnigrDIA1 330 ESRFEECD--REACLSFSKDSLCSRVTVDHNYAVCQNLLSRYATWRGTT---GGLLHDP
 TrubrDIA1 330 ESRFEECD--REACLSFSKDSLCSRVTVDHNYAVCQNLLSRYATWRGTT---GGLLHDP
 DreriDIA1b 330 ESRFEECD--KEACLSFSKDLCSRVTVDHNYAVCQNLLSRYATWRGSS---GGLLHDP
 DreriDIA1a 330 ESRYEECD--KEACLSFSKDLCSRVTVDHNYAVCQDLLSRFSSWRGST---GGLLHDP
 BtaurDIA1 331 ESKFDDCD--KEACLSFSKEILCARATVDHNYAVCQNLLSRHATWRGTS---GGLLHDP
 PpymDIA1 331 ESKFDDCD--KEACLSFSKEILCARATVDHNYAVCQNLLSRHATWRGTS---GGLLHDP
 CfamiDIA1 331 ESKFDDCD--KEACLSFSKEILCARATVDHNYAVCQNLLSRHATWRGTS---GGLLHDP
 PtrogDIA1 331 ESKFDDCD--KEACLSFSKEILCARATVDHNYAVCQNLLSRHATWRGTS---GGLLHDP
 TtrunDIA1 331 ESKFDDCD--KEACLSFSKEILCARATVDHNYAVCQNLLSRHATWRGTS---GGLLHDP
 HsapiDIA1 331 ESKFDDCD--KEACLSFSKEILCARATVDHNYAVCQNLLSRHATWRGTS---GGLLHDP
 MmulaDIA1 331 ESKFDDCD--KEACLSFSKEILCARATVDHNYAVCQNLLSRHATWRGTS---GGLLHDP
 PvampDIA1 331 ESKFDDCD--KEACLSFSKEILCARVTVDHNYAVCQNLLSRHATWRGTS---GGLLHDP
 MmuscDIA1 331 ESKFDDCD--KEACLSFSKEILCARVTVDHNYAVCQNLLSRHATWRGTS---GGLLHDP
 RnorvDIA1 331 ESKFDDCD--KEACLSFSKEILCARVTVDHNYAVCQNLLSRHATWRGTS---GGLLHDP
 MdomeDIA1 331 ESKFDDCD--KEACLSFSKEILCSRATVDHNYAVCQNLLSRHATWRGTS---GGLLHDP
 GgallDIA1 330 ESKFDDCD--KEACLSFSKEILCARVTVDHNYAVCQNLLSRHATWRGTS---GGLLHDP
 XtropDIA1 330 ESKFDDCD--KEACLSFSKEILCSRATVDHNYAVCQNLLSRHATWRGTS---GGLLHDP
 BflorDIA1 319 QSHFDECPG--MSNCLSFVDSALCRYLHTDHNYAVCRNMLSEYASEMGKP---GGLLHDP
 SpurpDIA1 322 QSEHEGCGS--RRECIMFSHTDLONHYSDHNYAVCQGLFGKDSPHG--D---GGLLHDI
 NvectDIA1 313 KKPSPDCS--QPDCLSFSPSDMCGSGSRDHNYAVCQGVLAGSSRRQ-----GGLLHNP
 NvitrDIA1 303 EYITNAVLDLDCQDFVFSFNDLCSHKVSDHNFYATCQHILQALGAVFHN---QGLLHDP
 AegyDIA1 301 SRIDCGC-----FAYIQEDLCVHQISDINLFAVCQLLENLNGDSKRG-----FLHSL
 CpipiDIA1 304 SRIPCDGC-----FAYVQEDLCSYQHSINQFATCOLLYENLNGDREGG-----FLHIQ
 AgambDIA1 312 SKIECNGC-----FAYVQEDVCRYQNSDLNLEATCOLLENLNGHYAKG-----LLHYD
 DyakuDIA1 269 P-LPGE-----FTFDVSAFCSGHQLDANIYQACLLLRDYLLKLNLDN-----GGLLHDP
 DerecDIA1 270 P-LPGE-----FTFDVSAFCSGHQLDANIYQACLLLRDFLLKLNLDN-----GGLLHDP
 DmelaDIA1 272 P-LTGE-----FTFDVSAFCSGHQLDANIYQACLLLRDYLLKLNLDN-----GGLLHDP
 DsechDIA1 274 P-LAGE-----FTFDVSAFCSGHQLDANIYQACLLLRDSLLKLNLDN-----GGLLHDP
 DananDIA1 273 P-LPGE-----FTFDVSAFCSGRQLDANVYQACLLLRDFLLKDLNDN-----GGLLHDP
 DpersDIA1 273 P-LPGD-----FTFDVKSFCGGQQLDANVYQACLLLKDFLLRDLAN-----GGLLHDP
 DpseuDIA1 273 P-LPGD-----FTFDVKSFCGGQQLDANVYQACLLLKDFLLRDLAN-----GGLLHDP
 DwillDIA1 263 P-FPGE-----FTYDVNAFCQDNQDLANIYQVCLLLLRDQLLPDVKN-----GGLLHDP
 CinteDIA1 345 K--QEK-----VDITEENLDCDHSNDVNYVYVTCRHFLGGTWEKRGKGYKPGGLLHDP
 consensus 361 esrfedcd reacclsfske lC r tvDhNyyavCqnllsr atwrgtt gllhdp

GaculDIA1 385 PAHIAK--DGQLTLLDECT-----RPKKRYGRFQAAKELREYLTQLAAASSSATAR--
 OlatiDIA1 385 PAHIAK--DGQLEALLDECT-----RPKKRYGRFQAAKELREYLTQLAAASSSATSR--
 TnigrDIA1 385 PAHIAK--DGQLEALLDECT-----KPKKRYGRFQAAKELREYLTQLAAASSSLSVSAR--
 TrubrDIA1 385 PAHIAK--DGQLEALLDECT-----KPKKRYGRFQAAKELREYLTQLAAASSSLSVSAR--
 DreriDIA1b 385 PPHIAK--DGQLEALLDECA-----NPKKRYGRFQAAKELREYLTQLSGSAR--
 DreriDIA1a 385 PPDVVK--DGRLEALLDECT-----RPKKRYGRFQAAKELREYLTQLTQTSNADR----
 BtaurDIA1 386 PSEIAK--DGRLEALLDECA-----NPKKRYGRFQAAKELREYLAQLSNNVR-----
 PpymDIA1 386 PSEIAK--DGRLEALLDECA-----NPKKRYGRFQAAKELREYLAQLSNNVR-----
 CfamiDIA1 386 PSEIAK--DGRLEALLDECA-----NPKKRYGRFQAAKELREYLAQLSNNVR-----
 PtrogDIA1 386 PSEIAK--DGRLEALLDECA-----NPKKRYGRFQAAKELREYLAQLSNNVR-----
 TtrunDIA1 386 PSEIAK--DGRLEALLDECA-----NPKKRYGRFQAAKELREYLAQLSNNVR-----
 HsapiDIA1 386 PSEIAK--DGRLEALLDECA-----NPKKRYGRFQAAKELREYLAQLSNNVR-----
 MmulaDIA1 386 PSEIAK--DGRLEALLDECA-----NPKKRYGRFQAAKELREYLAQLSNNVR-----
 PvampDIA1 386 PSEIAK--DGRLEALLDECA-----NPKKRYGRFQAAKELREYLAQLSNNVR-----
 MmuscDIA1 386 PSEIAK--DGRLEALLDECT-----NPKKRYGRFQAAKELRGYLAQLSHNVR-----
 RnorvDIA1 386 PSEIAK--DGRLEALLDECT-----NPKKRYGRFQAAKELRGYLAQLSHNVR-----
 MdomeDIA1 386 PGEIAK--DGRLEALLDECA-----HPKKRYGRFQAAKELREYLAQLSNNGR-----
 GgallDIA1 385 PADIAK--DGRLEALLDECA-----NPKKRYGRFQAAKELREYLAQLSNNVR-----
 XtropDIA1 385 PABIAK--DGRLEALLDECA-----NPKKRYGRFQAAKELREYLAQLSNNAR-----
 BflorDIA1 375 PETVVR--DGTLQRLLAECA-----KPRRTLYGRFQAAKELTELLGSLFKDR-----
 SpurpDIA1 376 PSDLSSYMRKVKQIAEACR-----SPSKRDGRMLVVKELKELTKMLKIT-----
 NvectDIA1 364 PVALKA---SLNQLLODCT-----AQMNRNTREETAQKSELLQGYL-----
 NvitrDIA1 360 PDYILQK--HPTLIDILLEQCA-----KPDIGYSRIDIAHKLIVLLDSVIKNA-----
 AegyDIA1 350 GTDS---KLEAFRKLHQCQV---YCPYCEDRQEVLRQIMEIHDVLEHEVV-----
 CpipiDIA1 353 PNDDSQRLSEIRQLLHHCV---YCPYCEDRQEVLRQIMEIHDVLEHEVV-----
 AgambDIA1 361 RDAEAFVPLGEASKMLQNLSECVCYCPDPCQNRSHILKDMLHIDQTIQS-----
 DyakuDIA1 310 -----ERLQILLEQCV---ACDDFCDMRFQCHAYDLIKVLDISKI-----
 DerecDIA1 311 -----ERLQILLEQCV---ACDDFCDMRFQCHAYDLIKVLDISKI-----
 DmelaDIA1 313 -----EKLQILLEQCV---ACDDFCDMRFQCHAYDLIKVLESNN-----
 DsechDIA1 315 -----EKLQILLEQCV---ACDDFCDMRFQCHAYDLIKELESKN-----
 DananDIA1 314 -----ERLQILLEKCV---ECDDLCDMRFQYAYDLIKLLDS-----
 DpersDIA1 314 -----GRLEMILLEQCV---RCDDATCDMRFQYAYDLIKLLGELLS-----
 DpseuDIA1 314 -----GRLEMILLEQCV---RCDDATCDMRFQYAYDLIKLLGELLS-----
 DwillDIA1 304 -----HRLKMLNDCV---QCEDDKCDIRFKYANNLITLLVEINNKIEIL-----
 CinteDIA1 395 KEFGVFS--SQMFVLLDICSRGKTAVAPERTLSHSIRRLAANQLRNVLERRRICSPDFK
 consensus 421 p iak dgrlealldc npkkrygrfqaakelreyl ql

GaculDIA1	-----
OlatiDIA1	-----
TnigrDIA1	-----
TrubrDIA1	-----
DreriDIA1b	-----
DreriDIA1a	-----
BtaurDIA1	-----
PpygmDIA1	-----
CfamiDIA1	-----
PtrogDIA1	-----
TtrunDIA1	-----
HsapiDIA1	-----
MmulaDIA1	-----
PvampDIA1	-----
MmuscDIA1	-----
RnorvDIA1	-----
MdomeDIA1	-----
GgallDIA1	-----
XtropDIA1	-----
BflorDIA1	-----
SpurpDIA1	-----
NvectDIA1	-----
NvitrDIA1	-----
AaegyDIA1	-----
CpipiDIA1	-----
AgambDIA1	-----
DyakuDIA1	-----
DerecDIA1	-----
DmelaDIA1	-----
DsechDIA1	-----
DananDIA1	-----
DpersDIA1	-----
DpseuDIA1	-----
DwillDIA1	-----
CinteDIA1	453 YRYPECELAEDAGINLPSIELQWLH
consensus	481