

Fig. S8

SpurpDIA1	1	-----
NvectDIA1	1	-----
GaculDIA1	1	-----
OlatiDIA1	1	-----
TnigrDIA1	1	-----
TrubrDIA1	1	-----
DreriDIA1b	1	-----
DreriDIA1a	1	-----
BtaurDIA1	1	-----
PpygmDIA1	1	-----
CfamiDIA1	1	-----
PtrogDIA1	1	-----
TtrunDIA1	1	-----
HsapiDIA1	1	-----
MmulaDIA1	1	-----
PvampDIA1	1	-----
MdomeDIA1	1	-----
MmuscdIA1	1	-----
RnorvDIA1	1	-----
GgallDIA1	1	-----
XtropDIA1	1	-----
BflorDIA1	1	-----
SsalaDIA1R	1	-----
DreriDIA1R	1	-----
RnorvDIA1R	1	-----
MmuscdIA1R	1	-----
MmulaDIA1R	1	-----
HsapiDIA1R	1	-----
BtaurDIA1R	1	-----
EcabaDIA1R	1	-----
DordiDIA1R	1	-----
MdomeDIA1R	1	-----
OanatDIA1R	1	-----
GgallDIA1R	1	-----
BflorDIA1Lb	1	MASARRWCRRLLHYSGWTRVLFLLTLMIAVGF IARNYWQVEDDLEARKRISNGGDKKYAQS
BflorDIA1Lc	1	-----
AaegyDIA1	1	-----
CpipiDIA1	1	-----
DyakuDIA1	1	-----
DerecDIA1	1	-----
DmelaDIA1	1	-----
DsechDIA1	1	-----
DpersDIA1	1	-----
DpseuDIA1	1	-----
DananDIA1	1	-----
DwillDIA1	1	-----
NvitrDIA1	1	-----
SpurpDIA1L	1	-----MGPRIRKKILILGSSILFTIFTVQLTGLNSLRDDDDNNAL
BflorDIA1La	1	-----MPILVESEAGYGGRHGRAMVARRMVRKCCLP
CinteDIA1	1	-----
AgambDIA1	1	-----
consensus	1	-----

SpurpDIA1	1	-----MRRYFNQFTNRF CISTTQQI	IWL	VVLSSMCL
NvectDIA1	1	-----MHFGGILRKRRYICRLVLL	IV	ISFSDLLL
GaculDIA1	1	-----MLRFLPL-KLGRLYRCLK	LLV	VGLFVILL
OlatiDIA1	1	-----MLRFLPL-KLGRLYRCLK	LLF	VGLFVILL
TnigrDIA1	1	-----MLRFLPL-KLGRLYRCLK	LLV	VGLFVILL
TrubrDIA1	1	-----MLRFLPL-KLGRLYRCLK	LLV	VGLFVILL
DreriDIA1b	1	-----MLRFLPL-KLGRLYRCLK	LLF	LGLFVILL
DreriDIA1a	1	-----MLRILSL-KFGRVYRCGKFL	I	IVALFVILL
BtaurDIA1	1	-----MWRLVPP-KLGRLSRSLK	AA	GSLLVLMV
PpygmDIA1	1	-----MWRLVPP-KLGRLSRSLK	AA	GSLLVLMV
CfamiDIA1	1	-----MWRLVPP-KLGRLSRSLK	AA	GSLLVLMV
PtrogDIA1	1	-----MWRLVPP-KLGRLSRSLK	AA	GSLLVLMV
TtrunDIA1	1	-----MWRLVPP-KLGRLSRSLK	AA	GSLLVLMV
HsapiDIA1	1	-----MWRLVPP-KLGRLSRSLK	AA	GSLLVLMV
MmulaDIA1	1	-----MWRLVPP-KLGRLSRSLK	AA	GSLLVLMV
PvampDIA1	1	-----MWRLVPP-KLGRLSRSLK	AA	GSLLVLMV
MdomeDIA1	1	-----MWRLVPP-KLGRLSRSLK	AA	GSLLVLMV
MmuscDIA1	1	-----MWRLVPL-KLGRLSRALK	AA	GSLLVLM
RnorvDIA1	1	-----MWRLVPL-KLGRLSRALK	AA	GSLLVLM
GgallDIA1	1	-----MLRLVSL-KLGRLYRYVK	AV	GSAAALV
XtropDIA1	1	-----MLRLASL-KFGRLEFRYAK	VLF	AAASLLVVML
BflorDIA1	1	-----MRLVRLRQFRFFSGWR	VRR	MCGFFFFV
SsalaDIA1R	1	-----MPL--KRCDQRAVGSVRLT--	VCV	LSWLCVCWAPS
DreriDIA1R	1	-----MAG-----	I	WSGVWLCFILVFG
RnorvDIA1R	1	-----MELGRPGAAATAFRQRWPAWMLLW	ST	LSCSFSLPA
MmuscDIA1R	1	-----MESQWRGAAATAFHQHWLARLLW	ST	LSCSFSLPA
MmulaDIA1R	1	-----MEP-QLGPEAAALRPGWLA-LLLW	V	SALSCSFSLPA
HsapiDIA1R	1	-----MEP-QLGPEAAALRPGWLA-LLLW	V	SALSCSFSLPA
BtaurDIA1R	1	-----MEP-RLGPKAAALHLGWPF-LLLW	V	SGLSYSVSSPA
EcabaDIA1R	1	-----MEP-WLGPEAAALRPGWPA-LLLW	V	SALRCSVSSPA
DordiDIA1R	1	-----MDP-QLGPEAAALHPGWQV-LLLW	V	SVLSCFSSPA
MdomeDIA1R	1	-----MES-VIHGPLASPCLGWLT--	LLQ	LVTLSCISSTES
OanatDIA1R	1	-----MGL-RLGCRLFSAALSWMT--	LLQ	FLTRGHGPVADA
GgallDIA1R	1	-----MGR--WICCLCSRVDWLM--	LLL	VLARSSNPSAAA
BflorDIA1Lb	61	IQELLAQGIIDEKRMREALRQKAEVHRI	V	KERGEALAKEAQAKAKANVVRINIHKPEL
BflorDIA1Lc	1	-----		
AaegyDIA1	1	-----MSQHRILT	KLHL	VALFLWIVMKYQ
CpipiDIA1	1	-----MSSGFQRILVNLHI	L	ALFCVIFEFQ
DyakuDIA1	1	-----MHLSPGQLK	V	VLLALLQELQ
DerecDIA1	1	-----MHLSPGQLK	V	VLLALLQELQ
DmelaDIA1	1	-----MHLSHGQLK	V	VLLALLQELQ
DsechDIA1	1	-----MHLSYGQLK	V	VLLALLQELQ
DpersDIA1	1	-----MHLSPGHLR	I	VLLALLQDLQ
DpseuDIA1	1	-----MHLSPGHLR	I	VLLALLQDLQ
DananDIA1	1	-----MHLLSGQLR	I	VLLALLQDLQ
DwillDIA1	1	-----MHLLYGQLK	V	VLLALLQELD
NvitrDIA1	1	-----MLVTKASVSSFL	I	ALLILIL
SpurpDIA1L	40	PSTNGKFRTFVPSKGRKRNLLHAGKQK	EELG	FDSKDTRRTLQDIRTADKIGHPRIQA
BflorDIA1La	32	LLVLSATLAVLYIYLVQVQGSPVWSL	GQS	QAGNKQKKDEYIVWRGEEQKVEVQKQEEK
CinteDIA1	1	-----MLLKMKRYLTVWENGKYIV	FIF	LITLEVLL
AgambDIA1	1	-----MQSSRLPYF	V	TLFIAVVLQYL
consensus	61		1	1

Signal
peptide

SpurpDIA1	32	FVYYQ----	LYLHFTANHLENEYFTEAT-----	KCPACFGT--	SLCKRFSRGD
NvectDIA1	32	WLSYQDGRAIKWDFSSQHKLTFQETIGLN-----	KCPACFGINLSICHKLLGGG		
GaculDIA1	30	MNTHS----	LFASFQKNELTDRRFINLN-----	KCPACFGT--	SWCRKFMNGQ
OlatiDIA1	30	MNTHN----	LFASFQKNELTDRRFINLN-----	KCPACFGT--	SWCRKFMNGQ
TnigrDIA1	30	MNTHN----	LFASFQKNELTDRRFINLN-----	KCPACFGT--	SWCRKFMNGQ
TrubrDIA1	30	MNTHN----	LFASFQKNELTDRRFINLN-----	KCPACFGT--	SWCRKFMNGQ
DreriDIA1b	30	MNTHN----	LFASFQKNELTDRRFINLN-----	KCPACFGT--	SWCRKFMNGQ
DreriDIA1a	30	MNTHN----	LFASFQKNELTDRRFINLN-----	KCPACFGT--	SWCRKFMNGQ
BtaurDIA1	30	LHSPS----	LLASWQRNELADRRFLQLN-----	KCPACFGT--	SWCRRFLNGQ
PpygmDIA1	30	LHSPS----	LLASWQRNELADRRFLQLN-----	KCPACFGT--	SWCRRFLNGQ
CfamiDIA1	30	LHSPS----	LLASWQRNELADRRFLQLN-----	KCPACFGT--	SWCRRFLNGQ
PtrogDIA1	30	LHSPS----	LLASWQRNELADRRFLQLN-----	KCPACFGT--	SWCRRFLNGQ
TtrunDIA1	30	LHSPS----	LLASWQRNELADRRFLQLN-----	KCPACFGT--	SWCRRFLNGQ
HsapiDIA1	30	LHSPS----	LLASWQRNELTDRRFQLN-----	KCPACFGT--	SWCRRFLNGQ
MmulaDIA1	30	LHSPS----	LLASWQRNELTDRRFQLN-----	KCPACFGT--	SWCRRFLNGQ
PvampDIA1	30	LHSPS----	LLASWQRNELADRRFLQLN-----	KCPACFGT--	SWCRRFLNGQ
MdomeDIA1	30	LHSPS----	LLASWQRNELADRRFLQLN-----	KCPACFGT--	SWCRRFLNGQ
MmuscdIA1	30	LHSPS----	LLASWQRNELADRRFLQLN-----	KCPACFGT--	SWCRRFLNGQ
RnorvDIA1	30	LHSPS----	LLASWQRNELADRRFLQLN-----	KCPACFGT--	SWCRRFLNGQ
GgallDIA1	30	LNTHS----	LLASLQRNELAERRFLQLN-----	KCPACWGT--	SWCRKFLNGQ
XtropDIA1	30	LNTHS----	LLSSFQRNELTDRRFSLN-----	KCPACFGT--	SWCRKFMNGQ
BflorDIA1	30	FFYCF----	VFQPFYSYNQLTDTTFLGED-----	KCPACFGT--	DLCEEFENGK
SsalaDIA1R	33	VVEPAGT--	PPAPQKALILQRAFLGLD-----	KCNACVGT--	SICKKLLKDQ
DreriDIA1R	19	TADPS----	PAPQDKSHDFRKIFLGLD-----	KCNACVGT--	SICKKFFKDE
RnorvDIA1R	37	SLPPSL----	VPRVRSYTLGKTFGLD-----	KCNACVGT--	SICKKFFKKE
MmuscdIA1R	37	SLPPSL----	VPRVRSYTMGKTFGLD-----	KCNACVGT--	SICKKFFKKE
MmulaDIA1R	35	SSPSSL----	VSQVRTSYNFGRTFLGLD-----	KCNACVGT--	SICKKFFKKE
HsapiDIA1R	35	SSLSSL----	VPQVRTSYNFGRTFLGLD-----	KCNACVGT--	SICKKFFKKE
BtaurDIA1R	35	SPSPSP----	VSRVRTSYNLGKTFGLD-----	KCNACVGT--	SICKKFFKKE
EcabaDIA1R	35	SPSPSL----	VPRVRTSYNFGRTFLGLD-----	KCNACVGT--	SICKKFFKKE
DordiDIA1R	35	SPPPSL----	VSRVRTSYNLGRTFLGLD-----	KCNACVGT--	SICKKFFKKE
MdomeDIA1R	34	LTAPSS----	VPRVKSSYNFGRTFLGLD-----	KCNACVGT--	SICKKFFKKE
OanatDIA1R	34	SPAPSL----	VPRVKPSYSFGRTFLGLD-----	KCNACVGT--	SICKKFFKKE
GgallDIA1R	33	TASPS----	APHVRPSYSFGRTFLGLD-----	KCNACVGT--	SICKKFFKKE
BflorDIA1Lb	121	NPENQHSWKAIEKMAAHDEIEDHKKQPEQYMTFKRLMDAKKCPACYGES--	LCEQAEVG-		
BflorDIA1Lc	1	-----	MVIADGDNDIDISWAEPE-----	KCPACFGD--	KCELLRRGH
AaegyDIA1	25	PEERA-----	SSLKSLVQQCOYDTTI-----	LCPACFPRP--	VNCSFFENLK
CpipiDIA1	27	PKEPE-----	SLTELLVNQCEYETQH-----	LCPACFVSP--	VNCGHLANFV
DyakuDIA1	22	VKPQ-----	REVFQELFEKDLR-----	LCPNCFVQREL--	CGEIFQKI
DerecDIA1	22	VKPQ-----	REVFQELFEKDLR-----	LCPNCFVQSEL--	CGEIFQKI
DmelaDIA1	22	VKPQ-----	REVFQELFEKDLR-----	LCPNCFVQSEPC--	CGEIFQKI
DsechDIA1	22	VKTQ-----	REVFQELFEKDLR-----	LCPNCFVQKEQC--	CGEIFQKI
DpersDIA1	22	VKPQ-----	KDIFRAHLERDLQ-----	LCPACFAGQRWQ--	CEEIFEAI
DpseuDIA1	22	VKPQ-----	KDIFRAHLERDLQ-----	LCPACFAGQRWQ--	CEEIFEAI
DananDIA1	22	VKPQ-----	KDIFQEHFESDLR-----	LCPACFSAQREQ--	CEEVFRAI
DwillDIA1	22	VRTQ-----	KDIFRKHFNDL-----	ECPQCFVQREQ--	CEKFFDTI
NvitrDIA1	21	GIYI-----	NRFNLKVAEITER-----	YKCPACFGD--	SMCQVIDSNE
SpurpDIA1L	100	GDETALTQDGVQGMKNATVVMTTTRIQFEN--	LFPSLLEEERCPLCYGT--	TNCDQIYAGN	
BflorDIA1La	92	KHPAEEP--	KEKPRQDKSAVTERKPKGVPRLLRN----	APCPACVGD--	NLCEEFEDGM
CinteDIA1	32	EMYNHRSQGSTRVMLEAKLLSDKWSATSP-----	TCGNFSCFGT--	SLCKNRNRVG	
AgambDIA1	22	PNEKS-----	TSKRPLENVCDYDRN-----	ILCPACVSSG--	LECNKFDLDF
consensus	121		f l l	c a c g	C

Motif 1

Motif 2

SpurpDIA1	74	YRFHSYSSIR-----LFDYVN-VKNVYFATYLD----QKP-VVMKKLGHNSEHNQFDK
NvectDIA1	80	VTVKSN---T-----PWSEER-IKGVSYGLWGA----VKQRVVLKTLGTSSSELTAFDN
GaculDIA1	72	VSFETWGRRLR-----FLDVFN-VKNVYFAQYGEPEGTRR-VVLKRLGNSQELAEIDQ
OlatiDIA1	72	VSFETWGRRLR-----FLDVFN-VKNVYFAQYGEPEGTRR-VVLKRLGNSQELAEIDQ
TnigrDIA1	72	VSFETWGRRLR-----FLDVFN-VKNVYFAQYGEPEGTRR-VVLKRLGNSQELADIDQ
TrubrDIA1	72	VSFETWGRRLR-----FLDVFN-VKNVYFAQYGEPEGTRR-VVLKRLGNSQELADIDQ
DreriDIA1b	72	ISFETWGRRLR-----FLDVFN-VKNVYFAQYGEPEGTRR-IVLKRLGNSQELADIDQ
DreriDIA1a	72	VTFEMWGRRLR-----FLDFFN-VKNVYFAQYGEPEGTRR-VVLKRLGNSQELAEIDQ
BtaurDIA1	72	VVFEAWGRRLR-----LLDFFN-VKNVYFAQYGEPEGTRR-VVLKRLGNSQELAEIDQ
PpygmDIA1	72	VVFEAWGRRLR-----LLDFFN-VKNVYFAQYGEPEGTRR-VVLKRLGNSQELAEIDQ
CfamiDIA1	72	VVFEAWGRRLR-----LLDFFN-VKNVYFAQYGEPEGTRR-VVLKRLGNSQELAEIDQ
PtrogDIA1	72	VVFEAWGRRLR-----LLDFFN-VKNVYFAQYGEPEGTRR-VVLKRLGNSQELAEIDQ
TtrunDIA1	72	VVFEAWGRRLR-----LLDFFN-VKNVYFAQYGEPEGTRR-VVLKRLGNSQELAEIDQ
HsapiDIA1	72	VVFEAWGRRLR-----LLDFFN-VKNVYFAQYGEPEGTRR-VVLKRLGNSQELAEIDQ
MmulaDIA1	72	VVFEAWGRRLR-----LLDFFN-VKNVYFAQYGEPEGTRR-VVLKRLGNSQELAEIDQ
PvampDIA1	72	VVFEAWGRRLR-----LLDFFN-VKNVYFAQYGEPEGTRR-VVLKRLGNSQELAEIDQ
MdomeDIA1	72	VAFEAWGRRLR-----LLDFFN-VKNVYFAQYGEPEGTRR-VVLKRLGNSQELAEIDQ
MmuscdIA1	72	VGFEAWGRRLR-----LLDFFN-VKNVYFAQYGEPEGTRR-VVLKRLGNSQELAEIDQ
RnorvDIA1	72	VGFEAWGRRLR-----LLDFFN-VKNVYFAQYGEPEGTRR-VVLKRLGNSQELAEIDQ
GgallDIA1	72	LRLESWGRRLR-----LFDFFN-VKNVYFAQYGEPEGTRR-VVLKRLGNSQELAEIDQ
XtropDIA1	72	LSFEGWGRRLR-----LLDFFN-VKNVYFAQYGEPEGTRR-VVLKRLGNSQELAEIDQ
BflorDIA1	72	ILFKYSSRLR-----ILDIFN-IKNVYFAIY----EGME--VALKRLGHNSEHFDQLDR
SsalaDIA1R	77	IRFDWWMSPD-----TTLPLA-EKQSFPCNLTDDSLSWRP-VVLSFLSSPCLHSSSDR
DreriDIA1R	60	IRFERRLTAQ-----SNLSSA-DVRSYECNYTDSTAGWRP-VVVSRLMSPHLHQLSDN
RnorvDIA1R	79	IRLDNSLVSH-----LGLPSQ-DLLSYAANYSDDSKTWRP-VEISRLVSKYQSEISDK
MmuscdIA1R	79	IRFDNSLASH-----LGLPPQ-DLHSYAANYSDDSKTWRP-VEISRLVSKYQSEISDR
MmulaDIA1R	77	IRSDNWLASH-----LGLPPD-FLLSYAANYSDDSKIWRP-VEIFRLVSNYQNEISDR
HsapiDIA1R	77	IRSDNWLASH-----LGLPPD-SLLSYAANYSDDSKIWRP-VEIFRLVSKYQNEISDR
BtaurDIA1R	77	IRFDNGLALH-----LGPDPD-DLPSYAANYSDDFKTWRP-VEISRLVSKQONKISDG
EcabaDIA1R	77	IRFDNRLASH-----LGLPSG-YLPSYAANYSDDSKTWRP-VEVSRLVSKQNEISDR
DordiDIA1R	77	IRFDNSLASH-----LGLPSG-YLPSYAANYSDDSKTWRP-VEVSRLVSKQNEISDR
MdomeDIA1R	76	IRFDNWLASH-----LKLPPD-YFSTYPAANYSDDTKSWRP-VEISRLISKYQHELSDR
OanatDIA1R	76	IRFDNWPASH-----LKLPPD-HFPGYSAANYTDDSKSWRL-VEISRLIGKDQNELSDQ
GgallDIA1R	74	IRFDTWLSSH-----LKLPPS-YLLSYLGNYTDDAQSWRM-VDITRLITTKYQHADRADQ
BflorDIA1Lb	178	LITMDVADKT-----LEHKG--VYFGHFRNT-----E----VVAKRLVGGKDGWTRFDE
BflorDIA1Lc	36	FVKVDSESDR-----YMKKGI-VSTGRICGV-----K----VIAKSMNEAGAWQRYER
AaegyDIA1	65	SIDS----NE-----LFEELL-THFNQHCVRYGTLGSGSEQRVVIKLNKEHGVEELIS
CpipiDIA1	68	TIDS----SN-----PWNQLT-CRYNPHCVSYG-LLGSGQKVVIKTLNKNRAVEALRD
DyakuDIA1	59	AEPSDW--SK-----LLKAIS-LLVDRRAIYFLRFLKQDQ-----VVAKRKIIDAQNQ
DerecDIA1	59	AEPSDW--SK-----LLKAIS-LIVDRRAIYFLRFLKQDQ-----VVAKRKIIDARNH
DmelaDIA1	59	AEPSDW--SR-----LVKAIS-LLVDRRAIYFLRFLKDRDQEV-Q-LVAKRKIIDAQSN
DsechDIA1	59	AEPSDW--SR-----LVKAIS-LLVDRRAIHYLRLKQDQAV-Q-LVAKRKIIDAHSY
DpersDIA1	59	AEPSDW--SK-----LLKGIA-LLIDREIYFLQLNERHQAA-Q-LVAKRDAIGGHSY
DpseuDIA1	59	AEPSDW--SK-----LLKGIA-LLIDREIYFLQLNERHQAA-Q-LVAKRDAIGGHSY
DananDIA1	59	REPSDL--SK-----LWKAVT-LLFDRREIYFLWLEIGPSQEKSSQ-LLAKRKSIVASHQ
DwillDIA1	59	EPAKL--DR-----LWKDLT-LLVDPREIYFLWLELNENREN-VK-CLAKRKMTRKISK
NvitrDIA1	57	ISFEYTDYFS-----IFNNLFSVKNVYCYKYKD-----KKVIMKKLAQSEELKTFDE
SpurpDIA1L	156	ISFHVGS--S-----VNLSEP---HAIRCTWGD-----RRIVGKRLVSRVFERLEK
BflorDIA1La	144	IDLG-----SEVTSWKVKAYCTWD-----KVEVMVTQCASEERLERFEE
CinteDIA1	81	LSEDVPTLRSGWLSIYGELVDLHRVKNLVTYKLPSTLPCNGETCSVQIETSVLSGNNVNK
AgambDIA1	62	TLQDDN-----VFNIIN-NIFNSHTTRIGTIVQENKLAVMKHLNRDNTIEKLLQ
consensus	181	a y l

Motif 3

SpurpDIA1	121	DLCTNAES-GLRG	CDVSQQIYKSKLS-----DIMYAERLEEKDVMG---L-SDIVRCP
NvectDIA1	125	EICRGVVGK-DSN	CKISQEAWDS-----DVLVPKPPLQDAVR-----KYFDCPS
GaculDIA1	123	KICKRATG-RPR	CDLIQAMYKTEFA-----RINGDVRLLTPEVVEG--W-SDLVHCPS
OlatiDIA1	123	KICKRATG-RPR	CDLVQAMYKTEFA-----RINGDVRLLTDPVVEG--W-SDLVHCPS
TnigrDIA1	123	KICKRATG-RPR	CDLIQAMYKTEFA-----RINGDVRLLTDPVVEG--W-SDLVHCPS
TrubrDIA1	123	KICKRATG-RPR	CDLIQAMYKTEFA-----RINGDVRLLTPEVVEG--W-SDLVHCPS
DreriDIA1b	123	KICKRATG-RPR	CDLIQAMYKTEFA-----RLNGDVRLLTDPVVEG--W-SDLVHCPS
DreriDIA1a	123	KICKRATG-RPR	CDLIQSMYKTEFA-----RLNGDVRLLTPEVVEG--W-SDLVHCPS
BtaurDIA1	124	SICKRATG-RPR	CDLLQAMPRTTEFA-----RLNGDVRLLTPEAVEG--W-SDLVHCPS
PpygmDIA1	124	SICKRATG-RPR	CDLLQAMPRTTEFA-----RLNGDVRLLTPEAVEG--W-SDLVHCPS
CfamiDIA1	124	SICKRATG-RPR	CDLLQAMPRTTEFA-----RLNGDVRLLTPEAVEG--W-SDLVHCPS
PtrogDIA1	124	SICKRATG-RPR	CDLLQAMPRTTEFA-----RLNGDVRLLTPEAVEG--W-SDLVHCPS
TtrunDIA1	124	SICKRATG-RPR	CDLLQAMPRTTEFA-----RLNGDVRLLTPEAVEG--W-SDLVHCPS
HsapiDIA1	124	SICKRATG-RPR	CDLLQAMPRTTEFA-----RLNGDVRLLTPEAVEG--W-SDLVHCPS
MmulaDIA1	124	SICKRATG-RPR	CDLLQAMPRTTEFA-----RLNGDVRLLTPEAVEG--W-SDLVHCPS
PvampDIA1	124	SICKRATG-RPR	CDLLQAMPRTTEFA-----RLNGDVRLLTPEAVEG--W-SDLVHCPS
MdomeDIA1	124	SICKRATG-RPR	CDLLQAMPKTEFA-----RLNGDVRLLTPEAVEG--W-SDLVHCPS
MmuscDIA1	124	SICKRATG-RPR	CDLLQAMPRTTEFA-----RLNGDVRLLTPEAVEG--W-SDLVHCPS
RnorvDIA1	124	SICKRATG-RPR	CDLLQAMPRTTEFA-----RLNGDVRLLTPEAVEG--W-SDLVHCPS
GgallDIA1	123	KICRRATG-RGR	CDLLQALHATEFA-----SLNGDVRLLTPEAVEG--W-SDLVHCPS
XtropDIA1	123	RICKKATG-RPR	CDLVQAMYKTDFEFA-----RLNGDVRLLTDPVVEG--W-SDLVHCPS
BflorDIA1	118	WICETGKE-GPQ	CHIPSVTYYSNFS-----RVIYEG--LSPKSLGD--M-SDMVRCP
SsalaDIA1R	128	SICRSVGR-QGP	CSIEAVLRVTPRF-----QSLNQSHLLLPHIVKG--LAPPLLRCP
DreriDIA1R	111	SICTSAGK-GKS	CSIEGVLRSRFR-----QTWVHSNLLLPSMKVKG--LVTPLMRCP
RnorvDIA1R	130	RICASASG-PKT	CSIERILRKTGRF-----QKWLQAKRLTPDLVQG--LPSPFLHCP
MmuscDIA1R	130	RICASVSA-PKT	CSIERILQKTGRF-----QKWLQAKRLTPDLVQG--LPSPFLRCP
MmulaDIA1R	128	RICASASA-PRT	CSIERVLRKTERF-----QKWLQAKRLTPDLVQG--LASPLLRCP
HsapiDIA1R	128	RICASASA-PKT	CSIERVLRKTERF-----QKWLQAKRLTPDLVQG--LASPLLRCP
BtaurDIA1R	128	RICASAAA-PKT	CSIERVLRKTGRF-----QKWLQAKRLTPDLVQG--LSSPLLRCP
EcabaDIA1R	128	RICAFAAA-PKT	CSIERVLRKTRRF-----QKWLQAKRLTPDLVQG--LPSPLLRCP
DordiDIA1R	128	RICAFASA-PKT	CSIERILRKTGRF-----QKWLQAKRLTPDLVQG--LPSPFLRCP
MdomeDIA1R	127	RICASASG-SKT	CSIERVLRKTERV-----KKWLKAKRLTPDLVQG--LPSPLMRCP
OanatDIA1R	127	KICTSVSL-VKT	CSIERVLRKTERF-----QKWLKARRLTPALVQG--LPSLLRCPT
GgallDIA1R	125	HICTSLLK-TKT	CSLERALRRTHRF-----QKWLRAKRLTPDLVQG--LSSPLMRCP
BflorDIA1Lb	220	FICQNASL-PKD	CDVSHMISDTVLVTDNVLQVSFLQDAWRIAHTRS---I--AMEACMT
BflorDIA1Lc	79	FICRSSSR-PHV	CNASSFILETMLVTDVALKVPWLREAWKICHLEKS----ALSCLVS
AaegyDIA1	113	SICNDLKI-YR-NC	RLRNKEPYLRVL-----RQRVLNDN--QLEGAILCPL
CpipiDIA1	115	AVCDELGL-TQSN	CKFKSDENTLKVLE-----RRKVL-EQ--ELEGICICPS
DyakuDIA1	104	Q-IKDVKK-AF	-----YELGE--RPGGFHLCRT
DerecDIA1	104	K-AENVEK-AF	-----YEQEE--RPGGFHLCRT
DmelaDIA1	107	Q-IKNVKK-DF	-----YELVEE--RPGGFHLCRT
DsechDIA1	107	Q-MKNVKK-AF	-----YELVEE--RPGGFHLCRT
DpersDIA1	107	RNMGILRE-AF	-----LEMEE--RPGGFQLCRS
DpseuDIA1	107	RNMGILGE-AF	-----LEMEE--RPGGFQLCRS
DananDIA1	108	S-LSSLQE-EF	-----LNLEE--RPGGFHLCRT
DwillDIA1	107	D-----	-----LHF--NPGGFQMCRN
NvitrDIA1	104	MICSDDEL-HEL	CYQSESRKQDSKTN-----FYKLVESELANVGGD--INNMKRLCPT
SpurpDIA1L	197	IICNQSQVDPKRS	CEVNAAATNSWMSKS----SALNRVHKLHQEVYESQLIAISATTCAS
BflorDIA1La	184	FVCRNLSETATS	CDPGKVLLQEDLK-----ERLQP----AHLKSLR
CinteDIA1	141	WICDKFKKPTN	---CDTGKVFKSWRAMN-----KITSAGRRLDPNLKLD--I-SPPLQCP
AgambDIA1	110	EYCDAYS�TKQN	---CRWAQHDSVDR-----AKEFITTSILDS-ARVEGCIFCPA
consensus	241	ic	c v c s

Motif 4

Motif 5 ...

SpurpDIA1	221	FPAYMGACGRFTVQEYSG-HSLSYFYKFK--FGVRAALAVQALKIAEQISENRDEFALYL
NvectDIA1	217	FPRFYGVCGRIMVVEDSG-PPISSFLEES--WDVRAQIAVNLIITLAHQISSALDDWALYI
GaculDIA1	228	FAKYLGACGRMVAVNYVG-EELWSFYFNAP--WEKRVDLARQLMDIAEQITNNDFFDFALYL
OlatiDIA1	228	FAKYLGACGRMVAVNYVG-EELWNFYFNAP--WEKRVDLARQLMDIAEQITNNDFFDFALYL
TnigrDIA1	228	FAKYLGACGRMVAVNYVG-EELWSFYFNAP--WEKRVDLARQLMDIAEQITNNDFFDFALYL
TrubrDIA1	228	FAKYLGACGRMVAVNYVG-EELWSFYFNAP--WEKRVDLARQLMDIAEQITNNDFFDFALYL
DreriDIA1b	228	FAKYLGACGRMVAVNYVG-EELWSFYFNAP--WEKRVDLAKQLMDIAEQITNNDFFDFALYL
DreriDIA1a	228	FAKYLGACGRMVAVNYVG-EELWSFYFNAP--WEKRVDLAKQLMDIAEQITNNDFFDFALYL
BtaurDIA1	229	FAKYLGACGRMVAVNYVG-EELWSFYFNAP--WEKRVDLAWQLMEIAEQITNNDFFDFALYL
PpygmDIA1	229	FAKYLGACGRMVAVNYVG-EELWSFYFNAP--WEKRVDLAWQLMEIAEQITNNDFFDFALYL
CfamIDIA1	229	FAKYLGACGRMVAVNYVG-EELWSFYFNAP--WEKRVDLAWQLMEIAEQITNNDFFDFALYL
PtrogDIA1	229	FAKYLGACGRMVAVNYVG-EELWSFYFNAP--WEKRVDLAWQLMEIAEQITNNDFFDFALYL
TtrunDIA1	229	FAKYLGACGRMVAVNYVG-EELWSFYFNAP--WEKRVDLAWQLMEIAEQITNNDFFDFALYL
HsapiDIA1	229	FAKYLGACGRMVAVNYVG-EELWSFYFNAP--WEKRVDLAWQLMEIAEQITNNDFFDFALYL
MmulaDIA1	229	FAKYLGACGRMVAVNYVG-EELWSFYFNAP--WEKRVDLAWQLMEIAEQITNNDFFDFALYL
PvampDIA1	229	FAKYLGACGRMVAVNYVG-EELWSFYFNAP--WEKRVDLAWQLMEIAEQITNNDFFDFALYL
MdomeDIA1	229	FAKYLGACGRMVAVNYVG-EELWSFYFNAP--WEKRVDLAWQLMEIAEQITNNDFFDFALYL
MmuscDIA1	229	FAKYLGACGRMVAVNYVG-EELWSFYFNAP--WEKRVDLAWQLMEIAEQITNNDFFDFALYL
RnorvDIA1	229	FAKYLGACGRMVAVNYVG-EELWSFYFNAP--WEKRVDLAWQLMEIAEQITNNDFFDFALYL
GgallDIA1	228	FAKYLGACGRMVAVNYVG-EELWSFYFNAP--WEKRVDLAWQLMEIAEQITNNDFFDFALYL
XtropDIA1	228	FAKYLGACGRMVAVNYVG-EELWSFYFNAP--WEKRVDLAWQLMEIAEQITNNDFFDFALYL
BflorDIA1	218	FPFYFGACGRLLTVVQKCD-KTLASYYSAP--WLKRVELSLQMMKIAEYLTNNEADFGLYL
SsalaDIA1R	234	FPRYQGS CGRLMVWASS--RPLWGLYGS SREFVQRVDVAYQLLHITQGLGHNSLGFLLYY
DreriDIA1R	217	FLRYHGS CGRLMVWAAS--RALRTLFS SP--LERRADLAYQLLHITQSLSANS LRFRLFY
RnorvDIA1R	236	MPKYLGS CGRFLVSTST--RPLQEFYDAP--PEQAADLAYQLLGVLES LRSNDLN YFFYF
MmuscDIA1R	236	MPRYLGS CGRFLVSTST--RPLQEFYDAS--PEQAADLAYQLLRVLES LRSNDLN YFFYF
MmulaDIA1R	234	LPQYLGSCGRFLVSTST--RPLQEFYDAP--PDQAADLAYQLLGVLES LRSNDLN YFFYF
HsapiDIA1R	234	LPKYLGS CGRFLVSTST--RPLQEFYDAP--PDQAADLAYQLLGVLES LRSNDLN YFFYF
BtaurDIA1R	234	LPQYLGSCGRFLVSTST--SPLQEFYDAP--PDQAADLAYQLLGVLES LRSNDLN YFFYF
EcabaDIA1R	234	LPRYLGSCGRFLVSTST--SPLQEFYDAP--PDQAADLAYQLLGVLES LRSNDLN YFFYF
DordiDIA1R	234	LPKYLGS CGRFFVSTST--RPLQEFYDAP--PDEAADLAYQLLGVLES LRSNDLN YFFYF
MdomeDIA1R	233	LPRYLGSCGRFLVSTST--QPLEEFYSSP--ADQAADLAYQLLGLDLS LRNDLN YFFYF
OanatDIA1R	233	FPKYLGS CGRFLVSTST--TPLLELSSGP--PDRAADLGHQLLGVIEFLRHNDWN YFFYF
GgallDIA1R	231	FPRYLGSCGRLLVVSAST--RPLRDFRFAA--PEVAADLALQLLAVLHSMGTNDLN YFFYF
BflorDIA1Lb	326	FPKYLGACGRVLLVESGG-KLLGSAIESP--WKERANIALQLLEMDKFRNGDPKVVVIF
BflorDIA1Lc	187	FPKFYACGRVTVVEHAG-RTLDTFMESS--WEVRADIALQLLQVDAIREKDPD VWLFF
AaegyDIA1	197	VPKLIFQGGFTLVESYEG-EALAKYDRP--LNVRLLIANELIKASLNF TAGVDNFRFYL
CpipiDIA1	199	VPKVFQGGFQLFESFDG-DALVNFYDSS--LNIRLRIAKELIQASFLETEGVNGFRFYL
DyakuDIA1	171	VPTTYASCGLTHFQSYAG-RTL TN YFEGE--EDLRVELALQLMQLSLKLTFGFSDFRIML
DerecDIA1	172	VPTTYASCGLTHFQAYAG-RTL TN YFEAE--EGLRMELALQLIQLSLKLTFGFSDFRIFL
DmelaDIA1	174	VPTTYASCGLTHFQSNAG-RTLAHYVDAE--EGLRVELALQLIQLSLKLTFGFADFRIFL
DsechDIA1	176	VPTPYASCGLTHFQSYAG-RTLAHYVNAE--EGLRLELALQLIQLSLKLTFGFADFRIFL
DpersDIA1	175	VPRSYAACGLTHFQAYAG-RTL VHYATAG--ENLRLEMARQLLQLSLKLTFGFADFRIFL
DpseuDIA1	175	VPRSYAACGLTHFQAYAG-RTL VHYATAG--ENLRLEMARQLLQLSLKLTFGFADFRIFL
DananDIA1	175	VPNTYAI CGLTHFQAYAG-RTL NHYTEAA--EDLRREIARQLIHL SLKLTFGFADFRIFL
DwillDIA1	161	VPRSFVAVCGSTLVFQAYAG-STLSNYLKAP--IDLRLMAKQLLQALKLSAGFKGFRIFL
NvitrDIA1	203	TPKYFGACGRLLVEEYIG-LPLSSFIDEP--WIRRAKIASLLQAADTLMSKNSEFAFYL
SpurpDIA1L	306	FTEYLGECGRVLLTEPSG-KPLSSYLKAS--WKDRVDISLKIQLMIEDFDHSSDKWLVL
BflorDIA1La	272	IPAFLGACGNLVATETAG-KPLSMYLEVKGPWQVRANLSLQLLQMLDDFQNKDPDWLLMF
CinteDIA1	245	FQRTVGS CGALMVHGRSIVTSLYELYDAP--WKVRLDVAIQLLDLAEHFTYNDLN YMFAL
AgambDIA1	207	VPKLLHTFGFSIETYEG-KTLEHYDFP--FVTRMRIAELIRAGFKFTEGIHGFRVFL
consensus	361	g c G m l y r dla qlm i l f ly

... Motif 7

Motif 8

Motif 9

Motif 10 ...

SpurpDIA1	278	TDVSEDNLAVND-NG----	EVLVIDAENIIVVDRKKIKEDANPGWDVKH----	QSEHEG
NvectDIA1	274	ADPAPGNFVSD-SG----	KVTLLDLEHLVVVDLSEVQMEENDKPKPS-----	D
GaculDIA1	285	LDVSFDNFVAVGPRDG----	KVIIVVDAENVLVADKRLIKQNKPEFVWY-----	ESRFEE
OlatiDIA1	285	LDVSFDNFVAVGPRDG----	KVIIVVDAENVLVADKRLIKQNKPEYDVWY-----	ESRFEE
TnigrDIA1	285	LDVSFDNFVAVGPRDG----	KVIIVVDAENVLVADKRLIKQNKPENFVWY-----	ESRFEE
TrubrDIA1	285	LDVSFDNFVAVGPRDG----	KVIIVVDAENVLVADKRLIKQNKPENYDVWY-----	ESRFEE
DreriDIA1b	285	LDVSFDNFVAVGPRDG----	KVIIVVDAENVLVADKRLIKQNKPEYDVWY-----	ESRFEE
DreriDIA1a	285	LDVSFDNFVAVGPRDG----	KVIIVVDAENVLVADKRLVQNKPEYDVWY-----	ESRYEE
BtaurDIA1	286	LDVSFDNFVAVGPRDG----	KVIIVVDAENVLVADKRLIRQNKPENWDVWY-----	ESKFDD
PpygmDIA1	286	LDVSFDNFVAVGPRDG----	KVIIVVDAENVLVADKRLIRQNKPENWDVWY-----	ESKFDD
CfamIDIA1	286	LDVSFDNFVAVGPRDG----	KVIIVVDAENVLVADKRLIRQNKPENWDVWY-----	ESKFDD
PtrogDIA1	286	LDVSFDNFVAVGPRDG----	KVIIVVDAENVLVADKRLIRQNKPENWDVWY-----	ESKFDD
TtrunDIA1	286	LDVSFDNFVAVGPRDG----	KVIIVVDAENVLVADKRLIRQNKPENWDVWY-----	ESKFDD
HsapiDIA1	286	LDVSFDNFVAVGPRDG----	KVIIVVDAENVLVADKRLIRQNKPENWDVWY-----	ESKFDD
MmulaDIA1	286	LDVSFDNFVAVGPRDG----	KVIIVVDAENVLVADKRLIRQNKPENWDVWY-----	ESKFDD
PvampDIA1	286	LDVSFDNFVAVGPRDG----	KVIIVVDAENVLVADKRLIRQNKPENWDVWY-----	ESKFDD
MdomeDIA1	286	LDVSFDNFVAVGPRDG----	KVIIVVDAENVLVADKRLIRQNKPENWDVWY-----	ESKFDD
MmuscDIA1	286	LDVSFDNFVAVGPRDG----	KVIIVVDAENVLVADKRLIRQNKPENWDVWY-----	ESKFDD
RnorvDIA1	286	LDVSFDNFVAVGPRDG----	KVIIVVDAENVLVADKRLIRQNKPENWDVWY-----	ESKFDD
GgallDIA1	285	LDVSFDNFVAVGPRDG----	KVIIVVDAENVLVADKRLIRQNKPENWDVWY-----	ESKFDD
XtropDIA1	285	LDVSFDNFVAVGPRDG----	KVIIVVDAENVLVADKRLIKQNKPENWDVWY-----	ESKFDD
BflorDIA1	275	TDISYENFVTS-DG----	NLFVIDVENVVVDKQKIKADKPRNWEARY-----	QSHFDE
SsalaDIA1R	292	TRLGEDMFGILD-DQ----	RVFITDASSIGVIDLEQGFPPDPPS-QTGS-----	DGDIFS
DreriDIA1R	273	TRIPEDMFGILE-DN----	KVFIVDTSTIGVIDLQEGHPPDK-D-LLPE-----	ELDVFS
RnorvDIA1R	292	THVDAGMFGIFD-NG----	HLFIRDASALGVIDKQEASQAAD---RTGE-----	NEDIFS
MmuscDIA1R	292	THVDAGMFGIFD-NG----	HLFIRDASALGVIDKQEGSQAAA---RTGE-----	NEDIFS
MmulaDIA1R	290	THIDAGMFGVFN-NG----	HLFIRDASAVGVIDKQEGSQEAT---RAGE-----	NKDIFS
HsapiDIA1R	290	THIDAGMFGVFN-NG----	HLFIRDASAVGVIDKQEGSQEAN---RAGE-----	NKDIFS
BtaurDIA1R	290	THVDADMFGIFN-NG----	HLFIRDASALGVIDRQEGSQAAS---GAGD-----	NKDIFS
EcabaDIA1R	290	THVDAGMFGIFN-NG----	HLFIRDASTLGVIDRQEGSQAAA---RAGE-----	NKDIFS
DordiDIA1R	290	THVDAAMFGIFS-NG----	HLFIRDASALGVIDKQEGSQAAP---KAGE-----	NQDIFS
MdomeDIA1R	289	TRIDAGTFGIFD-NG----	HLFIRDASTVGVIDKQRGSLTLD---RQEE-----	SKDIFS
OanatDIA1R	289	TRIHAGTFGVFD-NG----	HLFIRDASSLGVIDRQEGKRPAR---SSPE-----	PRDIFS
GgallDIA1R	287	TRVDVGTFGVFS-NG----	HLFIRDASTLGVIDKEEGSQPID---GQQE-----	YKDIFS
BflorDIA1Lb	383	VDFSFNFAVNN-YG----	RLTLIDFDVMLIDREEFVGENK--TEPCD-----	LKCFKT
BflorDIA1Lc	244	LDVSFQNFVAVDS-RG----	WVRLIDLDDVMVIDRRTVVVNQEQ--TEMCN-----	EQCYTD
AaegyDIA1	254	TDISPDNIVSMSSEEE-I	KVTFVLDLNNVILDSHSHKRLKP-----	SK-----QKHVHS
CpipiDIA1	256	TDINPDNIAVQAQPSGS-F	QVSFIDLNNVILDSQSKRLDRR-----	SK-----ARNIHS
DyakuDIA1	228	TDFTGDNFAVDEHTK----	KVYLIDLDSVVLVD-----	ASSAT-----GQ-----AEKYEP
DerecDIA1	229	TDFTGDNFAVDEDSK----	RVYLIDLDSVVLVD-----	ASSAA-----GQ-----AEKYVP
DmelaDIA1	231	TDFTADNLAVDEDTK----	KVYLIDLDSVVLVD-----	ASFAA-----GH-----AEKYEP
DsechDIA1	233	TDFTADNLAVDEETK----	KVYLIDLDSVVLVD-----	ASSMA-----GQ-----AEKYEP
DpersDIA1	232	TDFTADNLAVDEASQ----	SVILIDLDSVVLVD-----	AAVPL-----GD-----AQKYEP
DpseuDIA1	232	TDFTADNLAVDEASQ----	SVILIDLDSVVLVD-----	AAVPL-----GD-----AQKYEP
DananDIA1	232	TDFTSDNLTFDEDTR----	RVLLIDLDSVVMVD-----	AASTS-----GQ-----AEKYEP
DwillDIA1	218	TDFTADNLAVNEANG----	TVLLIDMDTVMVLSNDEAESES-----	QL-----SKKYKP
NvitrDIA1	260	TDISMDNIAVNNEDK----	AIFVDLENIIVEKPNPEKALVGIESWNE-----	TYTNAV
SpurpDIA1L	363	LDFGYENFVMTS-EG----	QLKVVNLGGVIVDKDQTSTTPDMNPHLNNRTELCNEDCLN	
BflorDIA1La	331	VEVNIENFVSS-DG----	RLILTDLGNMTIINKHDLDKNSTKKRSSVC-----	NEACFK
CinteDIA1	303	HRLTPRDIIVGSD-TG----	KLRIKNAENVILID-----	NNSKN-----DKGLYE
AgambDIA1	264	TDINPDNVVNLKNDNKQVYS	IVDLNVIILDSWAEVFLTKN-----	THVHS
consensus	421	d fav	kv i d e i v d	

... Motif 10

Motif 11

SpurpDIA1	328	CGSRRECIMFSHTDL	CNHYYSDHNY	YAVCQGLF	GKDSPHGD	-----	GGLHSIP
NvectDIA1	318	CS-QPDCLSFSPSDMC	SGGSRDHNY	YAVCQGL	LAGSSRRQ	-----	GLLHNPP
GaculDIA1	336	CD-REACLSFSKESLC	SRVTVDHNY	YAVCQNLL	SRyatWRGTT	-----	GLLHDPP
OlatiDIA1	336	CD-REACLSFSKDSL	SRVTVDHNY	YAVCQNLL	SRyatWRGTT	-----	GLLHDPP
TnigrDIA1	336	CD-REACLSFSKDSL	SRVTVDHNY	YAVCQNLL	SRyatWRGTT	-----	GLLHDPP
TrubrDIA1	336	CD-REACLSFSKDSL	SRVTVDHNY	YAVCQNLL	SRyatWRGTT	-----	GLLHDPP
DreriDIALb	336	CD-KEACLSFSKMDL	SRVTVDHNY	YAVCQNLL	SRyatWRGSS	-----	GLLHDPP
DreriDIALa	336	CD-KEACLSFSKDIL	SRVTVDHNY	YAVCQDLL	SRFSSWRGST	-----	GLLHDPP
BtaurDIA1	337	CD-KEACLSFSKEIL	CARATVDHNY	YAVCQNLL	SRHATWRGTS	-----	GLLHDPP
PpygmDIA1	337	CD-KEACLSFSKEIL	CARATVDHNY	YAVCQNLL	SRHATWRGTS	-----	GLLHDPP
CfamIDIA1	337	CD-KEACLSFSKEIL	CARATVDHNY	YAVCQNLL	SRHATWRGTS	-----	GLLHDPP
PtrogDIA1	337	CD-KEACLSFSKEIL	CARATVDHNY	YAVCQNLL	SRHATWRGTS	-----	GLLHDPP
TtrunDIA1	337	CD-KEACLSFSKEIL	CARATVDHNY	YAVCQNLL	SRHATWRGTS	-----	GLLHDPP
HsapiDIA1	337	CD-KEACLSFSKEIL	CARATVDHNY	YAVCQNLL	SRHATWRGTS	-----	GLLHDPP
MmulaDIA1	337	CD-KEACLSFSKEIL	CARATVDHNY	YAVCQNLL	SRHATWRGTS	-----	GLLHDPP
PvampDIA1	337	CD-KEACLSFSKEIL	CARVTVDHNY	YAVCQNLL	FRHATWRGTS	-----	GLLHDPP
MdomeDIA1	337	CD-KEACLSFSKEIL	CSRATVDHNY	YAVCQNLL	SRHATWRGTS	-----	GLLHDPP
MmuscDIA1	337	CD-KEACLSFSKEIL	CARVTVDHNY	YAVCQNLL	SRHATWRGTS	-----	GLLHDPP
RnorvDIA1	337	CD-KEACLSFSKEIL	CARVTVDHNY	YAVCQNLL	SRHATWRGTS	-----	GLLHDPP
GgallDIA1	336	CD-KEACLSFSKEIL	CARVTVDHNY	YAVCQNLL	SRHATWRGTS	-----	GLLHDPP
XtropDIA1	336	CD-KEACLSFSKEIL	CSRATVDHNY	YAVCQNLL	SRHATWRGTS	-----	GLLHDPP
BflorDIA1	325	CPGMSNCLSFVSA	LCRYLHTDHNY	YAVCRNML	SEYASEMGKP	-----	GLLHDPP
SsalaDIA1R	341	CLGQGTSPCHR-SPP	CSVVRPTQSLTLL	CTALLP	RRLLLTERGAQT	TRLPMEGEAEAGRLA	
DreriDIA1R	321	CL--SGS	CVR--PPP	ETVREAQSF	ILLCKYILN	-NLLTSN	-----DKQSG-LP
RnorvDIA1R	339	CL-VSGCQVQ--	MSSCDTVPEKQ	NLVLCQQLLP	-QLLRG	-----	KFPSPVQ
MmuscDIA1R	339	CL-VSDCQIQ--	LSSCDTVPEKQ	SLVLCQQLLP	-QLLQG	-----	KFPSPVQ
MmulaDIA1R	337	CL-VSGCQAQ--	LPSCESVSEKQ	SLVLCQQLLP	-RLLQG	-----	RFPSPVQ
HsapiDIA1R	337	CL-VSGCQAQ--	LPSCESISEKQ	SLVLCQQLLP	-RLLQG	-----	RFPSPVQ
BtaurDIA1R	337	CL-VSGCQTK--	LPSCDTIPEKQ	NLVLCQQLLP	-LLLQA	-----	KFPSPVQ
EcabaDIA1R	337	CL-LSDCQAE--	LPSCDTVPEKQ	SLVLCQQLLP	-RLLQG	-----	KFPSPVQ
DordiDIA1R	337	CL-VSGCQAQL-	LPSCDNIPDKQ	SVVLCQQLLP	-QLLQG	-----	KFPSPVQ
MdomeDIA1R	336	CL-VLDCQSP--	FPS	CSVKEKQSWMAC	QQLLP-QLLKE	-----	KFPQPIQ
OanatDIA1R	336	CL-AADCQSD--	LPS	CNTVQEHQSLVLC	RELLP-KLLEG	-----	KFPKPVQ
GgallDIA1R	334	CL-TVDCQSA--	FVSCNS	SIREKQSLVMVC	QELLP-KLLRG	-----	KFLPPVQ
BflorDIALb	431	FISQIEAMNSYDSC	SAMPQYSQMMYAL	ACVRLLSHL	PEHLSEP--	NPMDPKPKHRP	DSE
BflorDIALc	292	FQKKLYS-DEYH-	CDDIFKYAPMMYAS	ICARLLSNLQKHP	PERRKWEIREYQE	GQSI	ELD
AaegyDIA1	302	RIDCDGCFAYIQEDI	CVHQISDINL	FAVCQLLEN	LNNGDSKR	-----	GFLHSLG
CpipiDIA1	305	RIPCDGCFAYVQEDL	CSYQHS	DINQFAICQLLY	ENLNQDREG	-----	GFLHIQ
DyakuDIA1	270	-LPGEG-FTFDVSAF	CSGHQLDANIY	QACLLLRDYL	LKLNLDN	-----	
DerecDIA1	271	-LPGEG-FTFDVSAF	CSGHQLDANIY	QACLLLRDYL	LKLNLDN	-----	
DmelaDIA1	273	-LTGEG-FTFDVSAF	CSGHQLDANIY	QACLLLRDYL	LKLNLDN	-----	
DsechDIA1	275	-LAGEG-FTFDVSAF	CSGHQLDANIY	QACLLLRDYL	LKLNLDN	-----	
DpersDIA1	274	-LPGDG-FTFDVKS	FCGGQQLDANVY	QACLLLKDF	LRLDLAN	-----	
DpseuDIA1	274	-LPGDG-FTFDVKS	FCGGQQLDANVY	QACLLLKDF	LRLDLAN	-----	
DananDIA1	274	-LPGEG-FTFDVSAF	CSGRQLDANVY	QACLLLRDYL	LKDLDN	-----	
DwillDIA1	264	-FPGEG-FTYDVNAF	CDNQDL	DANIYQVCLLRDQL	LPDVKN	-----	
NvitrDIA1	310	DLDCQDCVVFSPNDIC	SHKVS	DHNFYAVICQHLL	TQALGAVFHN	-----	QGLHDPP
SpurpDIALl	418	TFVKQLQTEPDTH	CREVPRHVEL	MYMMACHSLL	SDLMTTKYER	-----	FFQPLDTPR
BflorDIALa	381	RFTRNLSHRPETS	CRQAGRYSQLMY	ARACQRLG	CGWQTERSGE	-----	GRVVLSSSKDAS
CinteDIA1	342	VRYKQEKVDITEENL	CDHSENDVNY	YVICRHF	LGGTWK	KERKGGK	-----KYPGGLLDHPK
AgambDIA1	313	KIECN	CFAYVQEDV	CRYQNSDLNLE	FATCQLLEN	LNNGHYAK	-----GLLHYDR
consensus	481	c	ac	c	dnyCll		g lh

Motif 12

Motif 13

Motif 14 ...

SpurpDIA1	377	SDL-----SSYMR	AKVKGQIAE	CRSPSK--	RDGRYL	VVKE	LKETLM-----
NvectDIA1	365	-----	VALKASLNQLLQD	CTAQDM--	RNTREETAQK	LSELLQ-----	
GaculDIA1	386	AH-----	IAKDGQLLTLDE	CTRPKK--	RYGRFQA	AKELREYLT-----	
OlatiDIA1	386	AH-----	IAKDGQLEALDE	CTRPKK--	RYGRFQA	AKELREYLT-----	
TnigrDIA1	386	AH-----	IAKDGQLEALDE	CTKPKK--	RYGRFQA	AKELREYLT-----	
TrubrDIA1	386	AH-----	IAKDGQLEALDE	CTKPKK--	RFGRFQA	AKELREYLT-----	
DreriDIA1b	386	PH-----	IAKDGQLEALDE	EKANPKK--	RYGRFQA	AKELRDYLT-----	
DreriDIA1a	386	PD-----	VVKDGRLIALLDE	CTRPQK--	RYGRFQA	AKELREFLT-----	
BtaurDIA1	387	SE-----	IAKDGRLEALDE	CANPKK--	RYGRFQA	AKELREYLA-----	
PpygmDIA1	387	SE-----	IAKDGRLEALDE	CANPKK--	RYGRFQA	AKELREYLA-----	
CfamiDIA1	387	SE-----	IAKDGRLEALDE	CANPKK--	RYGRFQA	AKELREYLA-----	
PtrogDIA1	387	SE-----	IAKDGRLEALDE	CANPKK--	RYGRFQA	AKELREYLA-----	
TtrunDIA1	387	SE-----	IAKDGRLEALDE	CANPKK--	RYGRFQA	AKELREYLA-----	
HsapiDIA1	387	SE-----	IAKDGRLEALDE	CANPKK--	RYGRFQA	AKELREYLA-----	
MmulaDIA1	387	SE-----	IAKDGRLEALDE	CANPKK--	RYGRFQA	AKELREYLA-----	
PvampDIA1	387	SE-----	IAKDGRLEALDE	CANPKK--	RYGRFHA	AKELREYLA-----	
MdomeDIA1	387	GE-----	IAKDGRLEALDE	CAHPKK--	RFGRFQA	AKELREYLA-----	
MmuscdIA1	387	SE-----	IAKDGRLEALDE	CTNPKK--	RYGRFQA	AKELRGYLA-----	
RnorvDIA1	387	SE-----	IAKDGRLEALDE	CTNPKK--	RYGRFQA	AKELRGYLA-----	
GgallDIA1	386	AD-----	IAKDGRLEALDE	CANPKK--	RYGRFQA	AKELREYLA-----	
XtropDIA1	386	AE-----	IAKDGRLEALDE	CANPKK--	RYGRFKA	SAKELREYLA-----	
BflorDIA1	376	ET-----	VVRDGTLQRLAE	CAKPRT--	LYGRFDA	AAKELIELLG-----	
SsalaDIA1R	400	RDV-----	PLLLGVCADPSQP	DWRIMAA--	VGSLMDLLK	PMRPCNP-----	
DreriDIA1R	364	RAA-----	VDELLVCADPSQL	DQTIIKS--	VQSLKNILK	TLRPCSP-----	
RnorvDIA1R	382	QEI-----	DSALSLSCKDASTN	LEVFGA--	TSLLKNILR	SLRTCDP-----	
MmuscdIA1R	382	KEI-----	DSALSLSCKDNST	DLEVLGA--	TSWLKDILR	SLRTCDP-----	
MmulaDIA1R	380	DDI-----	DSALAQCGDSTRP	DPEVLGA--	ASWLKHILR	PLRTCDS-----	
HsapiDIA1R	380	DDI-----	DSILVQCGDSIRP	DPEVLGA--	ASQLKDILR	PLRTCDS-----	
BtaurDIA1R	380	E EI-----	DAELTRCADGTRP	DPEVLGA--	ASRLKDILR	PLRTCDP-----	
EcabaDIA1R	380	E EI-----	DATLTWCGEDTRP	DAEVLGA--	ASRLKDILR	PLRTCDP-----	
DordiDIA1R	381	VEI-----	DSALAQCGQGIRP	DSEVFGA--	ASRLKDILR	PLRTCDP-----	
MdomeDIA1R	379	E QI-----	DSALVLCGNSSLS	DQEVIEA--	ASRLKAILK	PLRTCDP-----	
OanatDIA1R	379	E EI-----	DALLDRCGDSSLD	GGQTVIGG--	ARRLMDILK	SLRTCDA-----	
GgallDIA1R	377	E KI-----	DSFLQHCAEGLAD	DQVNEA--	MAKLAQLLK	PLRSCDS-----	
BflorDIA1Lb	489	RP---	RLWGPPEQEAKV	LEELRGC	VEENV--	AGGRLEAVGELK	TFILR-----
BflorDIA1Lc	350	E PPVKGFLHNP	PEIREALEGALT	QCVHETL--	PRGRLGAVLR	LQEIILG-----	
AaegyDIA1	351	T DS-----	KLEAFRKLHQC	VYQPPYCEDR	QEVLRIME	I IH-----	
CpipiDIA1	354	N DD-----	SQPRLSEIRQLL	HHCVCVPPDC	DRDQGLLQ	QVQEI ID-----	
DyakuDIA1	310	-----	ERLQLLLEQC	VACQDDFC	DMRFQHAYD	L IKMLD-----	
DerecdIA1	311	-----	ERLQLLLEQC	VACQDDFC	DMRFQHAYD	L IKVLD-----	
DmelaDIA1	313	-----	EKLQLLLEQC	VACQDDFC	DMRFQHAYD	L IKVLE-----	
DsechDIA1	315	-----	EKLQLLLEQC	VACQDDFC	DMRFQHAYD	L IKELE-----	
DpersDIA1	314	-----	GRLEMLLEQC	VRCDDATC	DMRFQAYD	L IKLLG-----	
DpseuDIA1	314	-----	GRLEMLLEQC	VRCDDATC	DMRFQAYD	L IKLLG-----	
DananDIA1	314	-----	ERLQLLLEK	CVQCDDLC	DMRFQYAYD	L IKLLD-----	
DwillDIA1	304	-----	HRLKEMLNDC	VQCEDDKC	DIRFKYANN	L IDLLV-----	
NvitrDIA1	361	D-----	YILQKHPTLIDL	LEQCAKPDIG--	YSRIDIAHKL	IVLLD-----	
SpurpDIA1L	470	KHHPGMLHDAP	YEVDSVLSELLY	ECVFEQG--	PGRRMH	SVRVLKRLLT-----	
BflorDIA1La	436	CAYGRGLLFG	PPREAKQELEDL	TEC	VEETK--	AGGRITALKQ	TRVLLA-----
CinteDIA1	396	EFG-----	VFSSQMFVLLD	ICSRGKTAV	APERRTL	LSHSIRRLAANQL	RNVLERRR-----
AgambDIA1	362	DAEAFP----	VLGEASKMLQNL	LS	ECVYQPPDC	QNRSHILKDM	LHI ID-----
consensus	541	e		l e		l	

... Motif 14

Motif 15

SpurpDIA1	416	----KLIT-----
NvectDIA1	400	----GYL-----
GaculDIA1	423	----QLAAASSSATAR-----
OlatiDIA1	423	----KLAAASSSATS-----
TnigrDIA1	423	----QLA-----
TrubrDIA1	423	----QLAASSSSLV SAR-----
DreriDIA1b	423	----QLSGSAR-----
DreriDIA1a	423	----QLTQTSNADR-----
BtaurDIA1	424	----QLSNNVR-----
PpygmDIA1	424	----QLSNNVR-----
CfamiDIA1	424	----QLSNNVR-----
PtrogDIA1	424	----QLSNNVR-----
TtrunDIA1	424	----QLSNNVR-----
HsapiDIA1	424	----QLSNNVR-----
MmulaDIA1	424	----QLSNNVR-----
PvampDIA1	424	----QLSNNVR-----
MdomeDIA1	424	----QLSNNGR-----
MmuscDIA1	424	----QLSHNVR-----
RnorvDIA1	424	----QLSHNVR-----
GgallDIA1	423	----QLSNNVR-----
XtropDIA1	423	----QLSNNAR-----
BflorDIA1	413	----SFLKDR-----
SsalaDIA1R	439	----HYTYRYPECRYNQDY-----
DreriDIA1R	403	----QYAYRYPECLYSDKF-----
RnorvDIA1R	421	----RFAYRYPDCKYNDRF-----
MmuscDIA1R	421	----RFAYRYPDCKYNDRF-----
MmulaDIA1R	419	----RFAYRYPDCKYNDKF-----
HsapiDIA1R	419	----RFAYRYPDCKYNDKF-----
BtaurDIA1R	419	----RFAYRYPDCKYDDKF-----
EcabaDIA1R	419	----RFAYRYPDCKYNDKF-----
DordiDIA1R	420	----RFAYRYPDCKYNDRF-----
MdomeDIA1R	418	----RYAYRYPDCKYSDRY-----
OanatDIA1R	418	----RFAYRYPDCKYSEKY-----
GgallDIA1R	416	----RFAYRYPDCKYSDKY-----
BflorDIA1Lb	533	----RNAKGEN-----
BflorDIA1Lc	397	----TT-----
AaegyDIA1	389	----DVLHEVV-----
CpipiDIA1	395	----GILVES-----
DyakuDIA1	343	----SKN-----
DerecDIA1	344	----SKI-----
DmelaDIA1	346	----SNN-----
DsechDIA1	348	----SKN-----
DpersDIA1	347	----ELLGS-----
DpseuDIA1	347	----ELLGS-----
DananDIA1	347	----S-----
DwillDIA1	337	----EINNKIEIL-----
NvitrDIA1	399	----SVIKNA-----
SpurpDIA1L	517	----I IQRGFSYKDAADRTSL-----
BflorDIA1La	483	----A-----
CinteDIA1	446	ICSPDFKYRYPECELAEDAGINLPSIELQWLH
AgambDIA1	407	----QTIIQS-----
consensus	601	