

**Fig. S9**

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	-----MRRYFNQFTNRFCSSTQQIWLVLSSMCL
NvectDIA1	1	-----MHFGGILRKRRYICRLVLLIVLISFSDLLL
GaculDIA1	1	-----MLRFLPL-KLGRLYRCLKLLLVVGLFVILL
OlatiDIA1	1	-----MLRFLPL-KLGRLYRCLKLLLVVGLFVILL
TnigrDIA1	1	-----MLRFLPL-KLGRLYRCLKLLLVVGLFVILL
TrubrDIA1	1	-----MLRFLPL-KLGRLYRCLKLLLVVGLFVILL
DreriDIA1b	1	-----MLRFLPL-KLGRLYRCLKLLFLLGLFVILL
DreriDIA1a	1	-----MLRILSL-KFGRVYRCGKFLFIVALFVILL
BtaurDIA1	1	-----MWRLVPP-KLGRLSRSLKLAALGSLLVLMV
PpygmDIA1	1	-----MWRLVPP-KLGRLSRSLKLAALGSLLVLMV
CfamiDIA1	1	-----MWRLVPP-KLGRLSRSLKLAALGSLLVLMV
PtrogDIA1	1	-----MWRLVPP-KLGRLSRSLKLAALGSLLVLMV
TtrunDIA1	1	-----MWRLVPP-KLGRLSRSLKLAALGSLLVLMV
HsapiDIA1	1	-----MWRLVPP-KLGRLSRSLKLAALGSLLVLMV
MmulaDIA1	1	-----MWRLVPP-KLGRLSRSLKLAALGSLLVLMV
PvampDIA1	1	-----MWRLVPP-KLGRLSRSLKLAALGSLLVLMV
MdomeDIA1	1	-----MWRLVPP-KLGRLSRSLKLAALGSLLVLMV
MmuscDIA1	1	-----MWRLVPL-KLGRLSRALKLAALGSLLVLMV
RnorvDIA1	1	-----MWRLVPL-KLGRLSRALKLAALGSLLVLMV
GgallDIA1	1	-----MLRLVSL-KLGRLYRYVKLAVLGSAAALV
XtropDIA1	1	-----MLRLASL-KFGRIFRYAKVLFASLLVVMV
BflorDIA1	1	-----MRLVRLRQFRFFSGWVRRMCGFFFFVV
SsalaDIA1R	1	-----MPL--KRCDQRAVGSVRLT--VCVLSWLLCVCWAPS
DreriDIA1R	1	-----MAG-----IWSGVWILCFILVFG
RnorvDIA1R	1	-----MELGRPGAAATAFRQRWPAWMLLWVSTLSCSFSLPA
MmuscDIA1R	1	-----MESQWRGAAATAFHQHWLARLLWVSTLSCSFSLPA
MmulaDIA1R	1	-----MEP-QLGPEAAALRPGWLA-LLLVVVSALSCSFSLPA
HsapiDIA1R	1	-----MEP-QLGPEAAALRPGWLA-LLLVVVSALSCSFSLPA
BtaurDIA1R	1	-----MEP-RLGPKAAALHLGWPF-LLLVVSGLSYSVSSPA
EcabaDIA1R	1	-----MEP-WLGPEAAALRPGWPA-LLLVVVSALRCSVSSPA
DordiDIA1R	1	-----MDP-QLGPEAAALHPGWQV-LLLVVVSVLSCFSSPA
MdomeDIA1R	1	-----MES-VIHGPLASPCLGWLT--LLQLVTLSCISSTES
OanatDIA1R	1	-----MGL-RLGCRLFSAALSWMT--LLQFLTRGHGPVADA
GgallDIA1R	1	-----MGR--WICCLCSRVDWLV--LLLVVLARSSNPSAAA
BflorDIA1Lb	61	IQELLAQGIDEKRMREALRQKAEVHRIVKERGEALAKEAQAKAKANVVRINLHKPEL
BflorDIA1Lc	1	-----
AaegyDIA1	1	-----MSQHRIITKLHLVALFLWIVVMKYQ
CpipiDIA1	1	-----MSSGFQRIIVNLHILALIFCVIFEFQ
DyakuDIA1	1	-----MHLSPGQLKVVVILALLQELQ
DerecDIA1	1	-----MHLSPGQLKVVVILALLQELQ
DmelaDIA1	1	-----MHLSHGQLKVVVILALLQELQ
DsechDIA1	1	-----MHLSYGQLKVVVILALLQELQ
DpersDIA1	1	-----MHLSPGHLRIVLILALLQDLQ
DpseuDIA1	1	-----MHLSPGHLRIVLILALLQDLQ
DananDIA1	1	-----MHLISGQLRIVLILALLQDLQ
DwillDIA1	1	-----MHLLYGQLKVVVILALLQELD
NvitrDIA1	1	-----MLVTKASVSSFLIALLLILIL
SpurpDIA1L	40	PSTNGKFRTFVPSKGRKRNLLHAGKQKKEELGFDSKDTRRTLQDIRTADEIKGHPRIQA
BflorDIA1La	32	LLVLSATLAVLYIYLVQVQGSPWVSLGQSQAGNKQKKDEYIIVWRGEEQKVEVQKQEEK
CinteDIA1	1	-----MLLKMKRYLTVWENGKYIVFIFILITLLEVLL
AgambDIA1	1	-----MQSSRLPYFVTLFIAVVVLYL
consensus	61	1 i 1k1 1 1l m1l

Signal  
peptide

SpurpDIA1	32	FVYYQ----	LYLHFTANHL	ENEYF	TEAT-----	KCPACFGT	SLCKRFSR	GD							
NvectDIA1	32	WLSYQDGRAIKWDF	SSQHKLTFQEI	IGLN-----	KCPACFGT	NLSICHKLL	GGG								
GaculDIA1	30	MNTHS----	LFASFQKNE	LTD	RRFINLN-----	KCPACFGT	SWCRKFM	NGQ							
OlatiDIA1	30	MNTHN----	LFASFQKNE	LTD	RRFINLN-----	KCPACFGT	SWCRKFM	NGQ							
TnigrDIA1	30	MNTHN----	LFASFQKNE	LTD	RRFINLN-----	KCPACFGT	SWCRKFM	NGQ							
TrubrDIA1	30	MNTHN----	LFASFQKNE	LTD	RRFINLN-----	KCPACFGT	SWCRKFM	NGQ							
DreriDIA1b	30	MNTHN----	LFASFQKNE	LTD	RRFINLN-----	KCPACFGT	SWCRKFM	NGQ							
DreriDIA1a	30	MNTHN----	LFASFQ	RNE	LTD	RRFIGLN-----	KCPACFGT	SWCRKFM	NGQ						
BtaurDIA1	30	LHSPS----	LLASWQ	RNE	LADR	RRFLQLN-----	KCPACFGT	SWCRRFL	NGQ						
PpygmDIA1	30	LHSPS----	LLASWQ	RNE	LADR	RRFLQLN-----	KCPACFGT	SWCRRFL	NGQ						
CfamiDIA1	30	LHSPS----	LLASWQ	RNE	LADR	RRFLQLN-----	KCPACFGT	SWCRRFL	NGQ						
PtrogDIA1	30	LHSPS----	LLASWQ	RNE	LADR	RRFLQLN-----	KCPACFGT	SWCRRFL	NGQ						
TtrunDIA1	30	LHSPS----	LLASWQ	RNE	LADR	RRFLQLN-----	KCPACFGT	SWCRRFL	NGQ						
HsapiDIA1	30	LHSPS----	LLASWQ	RNE	LADR	RRFLQLN-----	KCPACFGT	SWCRRFL	NGQ						
MmulaDIA1	30	LHSPS----	LLASWQ	RNE	LADR	RRFLQLN-----	KCPACFGT	SWCRRFL	NGQ						
PvampDIA1	30	LHSPS----	LLASWQ	RNE	LADR	RRFLQLN-----	KCPACFGT	SWCRRFL	NGQ						
MdomeDIA1	30	LHSPS----	LLASWQ	RNE	LADR	RRFLQLN-----	KCPACFGT	SWCRRFL	NGQ						
MmuscDIA1	30	LHSPS----	LLASWQ	RNE	LADR	RRFLQLN-----	KCPACFGT	SWCRRFL	NGQ						
RnorvDIA1	30	LHSPS----	LLASWQ	RNE	LADR	RRFLQLN-----	KCPACFGT	SWCRRFL	NGQ						
GgallDIA1	30	LNTHS----	LLASQ	RNE	LA	ERFLQLN-----	KCPACFGT	SWCRKFL	NGQ						
XtropDIA1	30	LNTHS----	LLSSFQ	RNE	LTD	RRFLSLN-----	KCPACFGT	SWCRKFM	NGQ						
BflorDIA1	30	FFYCF----	VFQPF	SYN	QLT	DTTFLGED-----	KCPACFGT	DLCEEF	ENGK						
SsalaDIA1R	33	VVEPAGT--	PPAPQ	QKAL	ILQ	RAFLGLD-----	KCNACVGT	SICKKLL	KDQ						
DreriDIA1R	19	TADPS----	PAPQD	KSH	DFR	KIFLGLD-----	KCNACVGT	SICKKFF	KDE						
RnorvDIA1R	37	SLPPSL----	VPRVR	SSYT	LGK	TFLGLD-----	KCNACVGT	SICKKFF	KEE						
MmuscDIA1R	37	SLPPSL----	VPRVR	SSYT	MGK	TFLGLD-----	KCNACVGT	SICKKFF	KEE						
MmulaDIA1R	35	SSPSSL----	VSQVR	TSYN	FGRT	FGLD-----	KCNACVGT	SICKKFF	KEE						
HsapiDIA1R	35	SSLSSL----	VPQVR	TSYN	FGRT	FGLD-----	KCNACVGT	SICKKFF	KEE						
BtaurDIA1R	35	SPSPSP----	VSRVR	TSYN	LGK	TFLGLD-----	KCNACVGT	SICKKFF	KEE						
EcabaDIA1R	35	SPSPSL----	VPRVR	TSYN	FGRT	FGLD-----	KCNACVGT	SICKKFF	KEE						
DordiDIA1R	35	SPPPSL----	VSRVR	TSYN	LGRT	FGLD-----	KCNACVGT	SICKKFF	KEE						
MdomeDIA1R	34	LTAPSS----	VPRVK	SSYN	FGRT	FGLD-----	KCNACVGT	SICKKFF	KEE						
OanatDIA1R	34	SPAPSL----	VPRVK	PSYS	FGRT	FGLD-----	KCNACVGT	SICKKFF	KEE						
GgallDIA1R	33	TASPS----	APHVR	PSYS	FGRT	FGLD-----	KCNACVGT	SICKKFF	KEE						
BflorDIA1Lb	121	NPENQHSWKA	IEKMAAH	DEI	EDHKK	QPEQYMTFKRLMDAKK	KCPACVGS	LCEQAE	VG-						
BflorDIA1Lc	1	-----	MVIAD	GDND	IDI	SWAEP	-----	KCPACFGD	KCELLRR	GH					
AaegyDIA1	25	PEERA-----	SSLK	SLV	QQC	QYDTTI-----	LCPCCF	FRP-VN	C	SFFENLK					
CpipiDIA1	27	PKEPE-----	SLTELL	VNQ	CEY	ETQH-----	LCPEC	CFV	SPTVNC	GHLANFV					
DyakuDIA1	22	VKPQ-----	-----	REVF	QEL	FEKDLR-----	LCPNCF	FGORE	LCGEI	FQKI					
DerecDIA1	22	VKPQ-----	-----	REVF	QEL	FEKDLR-----	LCPD	CFV	QSE	LCVGI	FQKI				
DmelaDIA1	22	VKPQ-----	-----	REVF	QEL	FEKDLR-----	LCPD	CFV	QSE	PCGEI	FQKI				
DsechDIA1	22	VKTQ-----	-----	REVF	QEL	FEKDLR-----	LCPD	CFV	QKE	QCGEI	FQKI				
DpersDIA1	22	VKPQ-----	-----	KDIF	RAH	LERDLQ-----	LCPAC	FAG	QRW	QCEEI	FEAI				
DpseuDIA1	22	VKPQ-----	-----	KDIF	RAH	LERDLQ-----	LCPAC	FAG	QRW	QCEEI	FEAI				
DananDIA1	22	VKPQ-----	-----	KDIF	QEH	FESDLR-----	LCPAC	FSA	QRE	QCEEV	FRAI				
DwillDIA1	22	VRTQ-----	-----	KDIF	RKHF	NMDLL-----	ECPC	CF	LG	QRE	QCEK	FDTI			
NvitrDIA1	21	GIYI-----	-----	NRFNL	KVA	EITER-----	YKCPAC	FGD	-----	SMC	QVIDS	NE			
SpurpDIA1L	100	GDETALTQD	GVQGMKNAT	VVMT	TR	LQFEN--	LFPSL	LEEER	CPL	CGT	-----	TNCDQ	IYAGN		
BflorDIA1La	92	KHPAEEP-KEK	PRQDK	SAV	TER	KPKG	VPR	SLLRN----	APCPAC	LG	-----	NLCEEF	EDGM		
CinteDIA1	32	EMYNHRSQ	GSTRVM	LEAK	L	SDK	WS	SATSP-----	TCGNF	S	CFGT	-----	SLCKNR	NRNVG	
AgambDIA1	22	PNEKS-----	TSKR	PL	EN	VCDY	DRN-----	ILCP	EC	VSS	-----	LEC	NK	FDDLF	
consensus	121	m s		k	l	dr	fl	l		kcpa	Cfgt		s	Ckrf	ng

Motif 1

Motif 2

SpurpDIA1	74	YRFHSYSSIR	-----	LFDYVN	VKNVYFATYLD	----	QKP	VVMKRLGHNSEHNQFDK
NvectDIA1	80	VTVKSN	---T	-----	PWSEER	IKGVSYGLWGA	----	VKQRVVLKTLGTSSELTAFDN
GaculDIA1	72	VSFETWGRLR	-----	FLDVFN	VKNVYFAOYGE	PREGTRR	VVLKRLG	SNQELAEIDQ
OlatiDIA1	72	VSFETWGRLR	-----	FLDVFN	VKNVYFAOYGE	PREGTRR	VVLKRLG	SNQELAEIDQ
TnigrDIA1	72	VSFETWGRLR	-----	FLDVFN	VKNVYFAOYGE	PREGTRR	VVLKRLG	SNQELADIDQ
TrubrDIA1	72	VSFETWGRLR	-----	FLDVFN	VKNVYFAOYGE	PREGTRR	VVLKRLG	SNQELADIDQ
DreriDIA1b	72	ISFETWGRLR	-----	FLDVFN	VKNVYFAOYGE	PREGTRR	VVLKRLG	SNQELADIDQ
DreriDIA1a	72	VTFEMWGRLR	-----	FLDFFN	VKNVYFAOYGE	PREGTRR	VVLKRLG	SNQELAEIDQ
BtaurDIA1	72	VVFEAWGRLR	-----	LLDFFN	VKNVYFAOYGE	PREGTRR	VVLKRLG	SORELAQLDQ
PpygmDIA1	72	VVFEAWGRLR	-----	LLDFFN	VKNVYFAOYGE	PREGTRR	VVLKRLG	SORELAQLDQ
CfamiDIA1	72	VVFEAWGRLR	-----	LLDFFN	VKNVYFAOYGE	PREGTRR	VVLKRLG	SORELAQLDQ
PtrogDIA1	72	VVFEAWGRLR	-----	LLDFFN	VKNVYFAOYGE	PREGTRR	VVLKRLG	SORELAQLDQ
TtrunDIA1	72	VVFEAWGRLR	-----	LLDFFN	VKNVYFAOYGE	PREGTRR	VVLKRLG	SORELAQLDQ
HsapiDIA1	72	VVFEAWGRLR	-----	LLDFFN	VKNVYFAOYGE	PREGTRR	VVLKRLG	SORELAQLDQ
MmulaDIA1	72	VVFEAWGRLR	-----	LLDFFN	VKNVYFAOYGE	PREGTRR	VVLKRLG	SORELAQLDQ
PvampDIA1	72	VVFEAWGRLR	-----	LLDFFN	VKNVYFAOYGE	PREGTRR	VVLKRLG	SORELAQLDQ
MdomeDIA1	72	VAFEAWGRLR	-----	LLDFFN	VKNVYFAOYGE	PREGTRR	VVLKRLG	SORELAQLDQ
MmuscdIA1	72	VGFEAWGRLR	-----	LLDFFN	VKNVYFAOYGE	PREGTRR	VVLKRLG	SORELAQLDQ
RnorvDIA1	72	VGFEAWGRLR	-----	LLDFFN	VKNVYFAOYGE	PREGTRR	VVLKRLG	SORELAQLDQ
GgallDIA1	72	LRLESWGRLR	-----	LDFFN	VKNVYFAOYGE	PREGTRR	VVLKRLG	SAQELADIDA
XtropDIA1	72	LSFEGWGRLR	-----	LDFFN	VKNVYFAOYGE	PREGTRR	VVLKRLG	SNHELSELDQ
BflorDIA1	72	ILFKYSSRLR	-----	LDFFN	VKNVYFAOYGE	PREGTRR	VVLKRLG	HNSEFDQLDR
SsalaDIA1R	77	IRFDWWMSPD	-----	TTLPLA	EKQSEPGNLT	DDSLWRP	VVLSFL	SSPCLHSSSDR
DreriDIA1R	60	IRFERRLTAQ	-----	SNLSSA	DVRSYEGNYTD	STAGWRP	VVVSRL	MSPHLHQLSDN
RnorvDIA1R	79	IRLDNSLVSH	-----	LGLPSQ	DLLSYAANYSD	DDSKTWRP	VEISRL	VSKYQSEISDK
MmuscdIA1R	79	IRFDNSLASH	-----	LGLPPQ	DLHSYAANYSD	DDSKTWRP	VEISQL	VSRYPQIEISDR
MmulaDIA1R	77	IRSDNWLASH	-----	LGLPPD	FLLSYFANYSD	DDSKIWRP	VEIFRL	VSNYQNEISDR
HsapiDIA1R	77	IRSDNWLASH	-----	LGLPPD	SLLSYFANYSD	DDSKIWRP	VEIFRL	VSKYQNEISDR
BtaurDIA1R	77	IRFDNGLALH	-----	LGPDP	DLPSYFANYSD	DDFKTWRP	VEISRL	VSKQQNKISDG
EcabaDIA1R	77	IRFDNRLASH	-----	LGLPSG	YLPSSYANYSD	DDSKTWRP	VEVSR	VLSKQNEISDR
DordiDIA1R	77	IRFDNSLASH	-----	LELASD	YLPSSYANYSD	DDSKTWRP	VEIFRL	VSKQNEISDR
MdomeDIA1R	76	IRFDNWLASH	-----	LKLPPD	YFSTYFANYSD	DDTKSWRP	VEISRL	VSKYQHELSDR
OanatDIA1R	76	IRFDNWPASH	-----	LKPPPD	HFPGYSANYTD	DDSKSWRL	VEISRL	IGKQDQNELSDQ
GgallDIA1R	74	IRFDTWLSSH	-----	LKLPPS	YLLSYLGNYTDD	AQSWRM	VDITRL	ITKYQHADRADQ
BflorDIA1Lb	178	LITMDVADKT	-----	LEHKG	---VYFGHFRNT	-----	E---	VVAKRLVGGKDGWTRFDE
BflorDIA1Lc	36	FVKVDSESDR	-----	YMKKGI	VSTGRICGV	-----	K---	VVAKSMNEAGAWQRYER
AaegyDIA1	65	SIDS	---NE	-----	LFEELL	THFNQHC	VRYGTL	SGSEQRVVIKLN
CpipiDIA1	68	TIDS	---SN	-----	PWNQLT	CRYNPHCVSYG	LLGSGQ	KVVIKTLNKNRAVEALRD
DyakuDIA1	59	AEPSDW	--SK	-----	LLKAIS	LLVDRRVIY	FLRFK	QDQ-----VVAKRKIIDAQNQ
DerecDIA1	59	AEPSDW	--SK	-----	LLKAIS	LLVDRRAIY	FLRLK	DQAQ-----VVAKRKIIDARNH
DmelaDIA1	59	AEPSDW	--SR	-----	LVKAIS	LLVDRRAIY	FLRLK	DRDQEV-Q-LVAKRKIIDAQSN
DsechDIA1	59	AEPSDW	--SR	-----	LVKAIS	LLVDRRAIY	FLRLK	DQDQAV-Q-LVAKRKIINAHSY
DpersDIA1	59	AEPSDW	--SK	-----	LLKGIA	LLIDREIY	FLQLNER	HQAA-Q-LVAKRDAIGGHSY
DpseuDIA1	59	AEPSDW	--SK	-----	LLKGIA	LLIDREIY	FLQLNER	HQAA-Q-LVAKRDAIGGHSY
DananDIA1	59	REPSDL	--SK	-----	LWKAVT	LLFDRREI	FWLEIG	PSQEKSSQ-LLAKRKSIVASHQ
DwillDIA1	59	EPAKL	--DR	-----	LWKDLT	LLVDPREI	WLELNEN	REN-VK-CLAKRKMTRKISK
NvitrDIA1	57	ISFEYTDYFS	-----	IFNNL	FSVKNVYCKYKD	-----	KKVIM	KLAQSEIKTFDE
SpurpDIA1L	156	ISFHVG	---S	-----	VNLSEP	---HAIRGTWGD	-----	RRIVGKRLVSRVFERLEK
BflorDIA1La	144	IDLG	-----	-----	SEVTSWKVKA	YTC	TWD-----	KVEVMVTQCASEERLERFEE
CinteDIA1	81	LSEDPVTLRSGWLSIY	YGE	LVDLHR	VKLNVTYKLPSTL	PCNGETCS	VQIETS	VLSGNNVNK
AgambDIA1	62	TLODDN	-----	VFNI	IIN-NIFNSHT	TRIGTIVQEN	KLAVMKHL	NRDNTIEKLLQ
consensus	181	v f e w r		l l	v v k	y a q y d	r v v m k r l g s	l i d n

### Motif 3



SpurpDIA1 170 RRLDDRIVWDTFGEERQFDKS-----LARDHKLMLATTTIAFNPEPLVLLQAF-----NRKGWP  
 NvectDIA1 167 TRFLEKIESVYGCQETPGQ-----LSLVEITHLITGLHLNPEPLVLLQIFR-----QEGWGP  
 GaculDIA1 172 QRLDDRIVRRYAEKDSGSFLLKNLKDTERMQLLMTLAFNPEPLVLLQSF-----SDEGWGP  
 OlatiDIA1 172 QRLDDRIVRRYAEKDSGSFLLKNLKDTERMQLLMTLAFNPEPLVLLQSF-----SDEGWGP  
 TnigrDIA1 172 QRLDDRIVRRYAEKDSGSFLLKNLKDTERMQLLMTLAFNPEPLVLLQSF-----SDEGWGP  
 TrubrDIA1 172 QRLDDRIVRRYAEKDSGSFLLKNLKDTERMQLLMTLAFNPEPLVLLQSF-----SDEGWGP  
 DreriDIA1b 172 QRLDDRIVRRYAEKDSGSFLLKNLKDTERMQLLMTLAFNPEPLVLLQSF-----SDEGWGP  
 DreriDIA1a 172 QRLDDRIVRRYAEKDSGSFLLKNLKDTERMQLLMTLAFNPEPLVLLQSF-----SDEGWGP  
 BtaurDIA1 173 QRLDRLVRRYAEKDSGSFLLRNLKDSERMQLLLTLAFNPEPLVLLQSF-----SDEGWGP  
 PpygmDIA1 173 QRLDRLVRRYAEKDSGSFLLRNLKDSERMQLLLTLAFNPEPLVLLQSF-----SDEGWGP  
 CfamiDIA1 173 QRLDRLVRRYAEKDSGSFLLRNLKDSERMQLLLTLAFNPEPLVLLQSF-----SDEGWGP  
 PtrogDIA1 173 QRLDRLVRRYAEKDSGSFLLRNLKDSERMQLLLTLAFNPEPLVLLQSF-----SDEGWGP  
 TtrunDIA1 173 QRLDRLVRRYAEKDSGSFLLRNLKDSERMQLLLTLAFNPEPLVLLQSF-----SDEGWGP  
 HsapiDIA1 173 QRLDRLVRRYAEKDSGSFLLRNLKDSERMQLLLTLAFNPEPLVLLQSF-----SDEGWGP  
 MmulaDIA1 173 QRLDRLVRRYAEKDSGSFLLRNLKDSERMQLLLTLAFNPEPLVLLQSF-----SDEGWGP  
 PvampDIA1 173 QRLDRLVRRYAEKDSGSFLLRNLKDSERMQLLLTLAFNPEPLVLLQSF-----SDEGWGP  
 MdomeDIA1 173 QRLDRLVRRYAEKDSGSFLLRNLKDSERMQLLLTLAFNPEPLVLLQSF-----SDEGWGP  
 MmuscdIA1 173 QRLDRLVRRYAEKDSGSFLLRNLKDSERMQLLLTLAFNPEPLVLLQSF-----SDEGWGP  
 RnorvDIA1 173 QRLDRLVRRYAEKDSGSFLLRNLKDSERMQLLLTLAFNPEPLVLLQSF-----SDEGWGP  
 GgallDIA1 172 QRLDRLVRRYAEKDSGSFLLRNLKDSERMQLLLTLAFNPEPLVLLQSF-----SDEGWGP  
 XtropDIA1 172 QRLDRLVRRYAEKDSGSFLLRNLKDSERMQLLLTLAFNPEPLVLLQSF-----SDEGWGP  
 BflorDIA1 165 QRLIDRVLKFAEHLGKET---EELSYQEKLHFLSTLKFNPEPLVLLQIFP-----ITEGWGP  
 SsalaDIA1R 178 QRLDDRIVRRYAEVVDVGSVQMKHFSEKDKLRLLYTLAVNQOPLIILQMF-----GTEGWGP  
 DreriDIA1R 161 QRLDDRIVRRYAEVVDVGSVQMKHFNEKDKLRLLYTLAVNQOPLIILQMF-----GTEGWGP  
 RnorvDIA1R 180 QRLDDRIVRRYAEVVDAGSIFMDHFTDRDKLRLLYTLAVNAHPILLOIFP-----GAEGWGP  
 MmuscdIA1R 180 QRLDDRIVRRYAEVVDAGSIFMDHFTAGDKLRLLYTLAVNAHPILLOIFP-----GAEGWGP  
 MmulaDIA1R 178 QRLDDRIVRRYAEVADAGSIFMDHFTDRDKLRLLYTLAVNSHPILLOIFP-----GAEGWGP  
 HsapiDIA1R 178 QRLDDRIVRRYAEVADAGSIFMDHFTDRDKLRLLYTLAVNSHPILLOIFP-----GAEGWGP  
 BtaurDIA1R 178 QRLDDRIVRRYAEVADAGSIFMDHFTDRDKLRLLYTLAVNTHPVLLQIFP-----GAEGWGP  
 EcabaDIA1R 178 QRLDDRIVRRYAEVADAGSIFMDHFTDRDKLRLLYTLAVNAHPILLOIFP-----GAEGWGP  
 DordiDIA1R 178 QRLDDRIVRRYAEVADAGSIFMDHFTDRDKLRLLYTLAVNAHPILLOIFP-----GAEGWGP  
 MdomeDIA1R 177 QRLDDRIVRRYAEVADAGSVFMDHFTDRDKLRLLYTLAVNAHPILLOIFP-----GAEGWGP  
 OanatDIA1R 177 QRLDDRIVRRYAEVADAGSVYMDHFTDRDKLRLLYTLAVNAHPVLLQVFP-----GAEGWGP  
 GgallDIA1R 175 QRLDDRIVRRYAEVADAGSIYMDHFTDRDKLRLLYTLAVNSHPILLOIFP-----DVEGWGP  
 BflorDIA1Lb 274 DRLIELIKTAYDENVNGKLSK-----TERAYMITALLLNPEAALLKHETS--RAEYWP  
 BflorDIA1Lc 132 DRFLEDVRLYVDEGGTDMTKE---GDTGRAFLSTSLLLNEEAVLLRYETT--KSTTPWP  
 AaegyDIA1 155 MDEE--ALKRFLFETDEN-----DINKILLMRINAQPLLLKLLQ-----ERNFPP  
 CpipiDIA1 157 KDEK--ALNRLNEVEGT-----ELLQILLKVNVOPLLELFD-----GRGFPP  
 DyakuDIA1 128 PSRKP-RFVSYLQORGH-----SASVWFYMMHYVSPLLMQELY-----LQGFPP  
 DerecdIA1 128 PSRKP-RFVSYLQORGH-----SASVWFYMMHYVSPLLMQELH-----LQGFPP  
 DmelaDIA1 131 LAREP-RFVSYLQORGH-----AASVWFYMMHYVSPLLMQELH-----LQGFPP  
 DsechDIA1 131 LAREP-RFVSYLQORGHVY-----GSTSVWFYMMHYVSPLLMQELH-----LQGFPP  
 DpersDIA1 132 GFRTF-RFVSYLQORGE-----AATIWYMMHSITPLLMQELF-----LRGFPP  
 DpseuDIA1 132 GFRTF-RFVSYLQORGE-----AATIWYMMHSITPLLMQELF-----LRGFPP  
 DananDIA1 132 AQKSS-PFINYLNRQGYD-----SSSIYFYMLHNI SPLLMQELQ-----NLDFPP  
 DwillDIA1 121 STR---FLAYLERGYL-----PATIGYYIHHSISPLLMQELW-----IMDFPP  
 NvitrDIA1 154 TTKLEKLFVNVKFQSHAEN-----EDYFKYLWSTIKINPEPLVLLQILP-----AKEGWGP  
 SpurpDIA1L 253 PDFFEELKQLYRVSRWGTG-----IASTMAILATTMALNPEPALIKFERN--IPSLRPY  
 BflorDIA1La 222 EVFHPNTTSSLQATTCMS-----KPFLLKLLQKTFDDNGNKRNRLEQA--IPRKKLP  
 CinteDIA1 191 TRIADRIVRRYANKQGGVLLR--DLSYTEKRLIFTCKMSPGSVVQSMFP-----PYEGWLP  
 AgambDIA1 157 TNNRQ-SLQRLSLFDSTDN-----EILWNLAVRTNVEPLLLKLLTVNYHDEPPLY  
 consensus 301 qrlldrivrryae kd gs 1 d ekl ll tla npeplvlq fp egwp

... Motif 5

Motif 6

Motif 7 ...

SpurpDIA1	221	FPAYMGACGRFTVQEYSG--HLSYFYKFK--FGVRAALAVQALKIABOLSENRFDEFALYL
NvectDIA1	217	FPRFYGVCGRIMVVEDSG--PPISSFLEES--WDVRAQIAVNLIITLAHQSSALDDWALYI
GaculDIA1	228	FAKYLGACGRMVAVNYVG--EELWSFYNAP--WEKRVDLARQLMDIAEQLTNNDFDFALYL
OlatiDIA1	228	FAKYLGACGRMVAVNYVG--EELWNFYNAP--WEKRVDLARQLMDIAEQLTNNDFDFALYL
TnigrDIA1	228	FAKYLGACGRMVAVNYVG--EELWSFYNAP--WEKRVDLARQLMDIAEQLTNNDFDFALYL
TrubrDIA1	228	FAKYLGACGRMVAVNYVG--EELWSFYNAP--WEKRVDLARQLMDIAEQLTNNDFDFALYL
DreriDIA1b	228	FAKYLGACGRMVAVNYVG--EELWSFFNAP--WEKRVDLAKQLMDIAEQLTNNDFDFALYL
DreriDIA1a	228	FAKYLGACGRMVAVNYVG--EELWSFYNAP--WEKRVDLAKQLMDIAEQLTNNDFDFALYL
BtaurDIA1	229	FAKYLGACGRMVAVNYVG--EELWSYFNAP--WEKRVDLAWQLMEIAEQLTNNDFDFALYL
PpygmDIA1	229	FAKYLGACGRMVAVNYVG--EELWSYFNAP--WEKRVDLAWQLMEIAEQLTNNDFDFALYL
CfamiDIA1	229	FAKYLGACGRMVAVNYVG--EELWSYFNAP--WEKRVDLAWQLMEIAEQLTNNDFDFALYL
PtrogDIA1	229	FAKYLGACGRMVAVNYVG--EELWSYFNAP--WEKRVDLAWQLMEIAEQLTNNDFDFALYL
TtrunDIA1	229	FAKYLGACGRMVAVNYVG--EELWSYFNAP--WEKRVDLAWQLMEIAEQLTNNDFDFALYL
HsapiDIA1	229	FAKYLGACGRMVAVNYVG--EELWSYFNAP--WEKRVDLAWQLMEIAEQLTNNDFDFALYL
MmulaDIA1	229	FAKYLGACGRMVAVNYVG--EELWSYFNAP--WEKRVDLAWQLMEIAEQLTNNDFDFALYL
PvampDIA1	229	FAKYLGACGRMVAVNYVG--EELWSFFNAP--WEKRVDLAWQLMEIAEQLTNNDFDFALYL
MdomeDIA1	229	FAKYLGACGRMVAVNYVG--EELWSYFNAP--WEKRVDLAWQLMEIAEQLTNNDFDFALYL
MmuscdIA1	229	FAKYLGACGRMVAVNYVG--EELWSYFNAP--WEKRVDLAWQLMEIAEQLTNNDFDFALYL
RnorvDIA1	229	FAKYLGACGRMVAVNYVG--EELWSYFNAP--WEKRVDLAWQLMEIAEQLTNNDFDFALYL
GgallDIA1	228	FAKYLGACGRMVAVNYVG--EELWSYFNAP--WEKRVDLAWQLMEIAEQLTNNDFDFALYL
XtropDIA1	228	FAKYLGACGRMVAVNYVG--EELWSYFNAP--WEKRVDLAWQLMEIAEQLTNNDFDFALYL
BflorDIA1	218	FPFYFGACGRITVVQKCD--KTLASYYSAP--WLKRVELSLQMMKIAEYLTNNEADFGLYL
SsalaDIA1R	234	FPRYQGS CGRLMVWASS--RPLWGLY GSSRE FVQRVDVAYQLLHITQGLGHNSLGFLLYY
DreriDIA1R	217	FLRYHGS CGRLMVWAAS--RALRTL FSSP --LERRADLAYQLLHITQSLANSLSRFLRY
RnorvDIA1R	236	MPKYLGS CGRFLVSTST--RPLQEFYDAP--PEQAADIAYQLLGVLESLRSNDLNYFFFYF
MmuscdIA1R	236	MPRYLGSCGRFLVSTST--RPLQEFYDAS--PEQAADLAYQLLRVLESLRSNDLNYFFFYF
MmulaDIA1R	234	LPQYLGSCGRFLVSTST--RPLQEFYDAP--PDQAADLAYQLLGVLESLRSNDLNYFFFYF
HsapiDIA1R	234	LPKYLGS CGRFLVSTST--RPLQEFYDAP--PDQAADLAYQLLGVLESLRSNDLNYFFFYF
BtaurDIA1R	234	LPQYLGSCGRFLVSTST--SPLQEFYDAP--PDQAADLAYQLLGVLESLRSNDLNYFFFYF
EcabaDIA1R	234	LPRYLGSCGRFLVSTST--SPLQEFYSAP--PDQAADLAYQLLGVLESLRSNDLNYFFFYF
DordiDIA1R	234	LPKYLGS CGRFFVSTST--RPLQEFYDAP--PDEAADLAYQLLGVLESLRSNDLNYFFFYF
MdomeDIA1R	233	LPRYLGSCGRFLVSTST--QPLEEFYSSP--ADQAADLAYQLLGVLESLRNNDLNYFFFYF
OanatDIA1R	233	FPKYLGS CGRLVSTST--TPLLELSSGP--PDRAADLGHQLLGVLEFLRHNDWNYFFFYF
GgallDIA1R	231	FPRYLGSCGRLVVSAST--RPLRDFFRAA--PEVAADLALQLLAVLHSMGTNDLNYFFFYF
BflorDIA1Lb	326	FPKYLGACGRVILVESGG--KLLGSAIESP--WKERANTIALQLLEMDKFRNGDPKVVVIF
BflorDIA1Lc	187	FPKFYGACGRVIVVEHAG--RTLDTFMESS--WEVRADIALQLLQLVDAIREKDPDWVLF
AaegyDIA1	197	VPKLI FQGGFTLVESYEG--EALAKYYDRP--LNVRLLIANELIKASLNF TAGVDNFRFYL
CpipiDIA1	199	VPKVI FQGGFQLFESEFDG--DALVNFYDSS--LNIRLRIAKELIQASFLETEGVNGFRFYL
DyakuDIA1	171	VPTTYASCGLTHFQSYAG--RTL TN YFEGE--EDLRVELALQLMQLSLKLTFGFSDFRIFL
DerecDIA1	172	VPTTYASCGLTHFQAYAG--RTL TN YFEAE--EGLRMELALQLIQLSLKLTFGFSDFRIFL
DmelaDIA1	174	VPTTYASCGLTHFQSNAG--RTLAHYVDAE--EGLRVELALQLIQLSLKLTFGFADFRIIL
DsechDIA1	176	VPTPYASCGLTHFQSYAG--RTLAHYVNAE--EGLRLELALQLIQLSLKLTFGFADFRIIL
DpersDIA1	175	VPRSYAACGLTHFQAYAG--RTL VHYATAG--ENLRLEMARQLLQLSLKLTFGFADFRIFL
DpseuDIA1	175	VPRSYAACGLTHFQAYAG--RTL VHYATAG--ENLRLEMARQLLQLSLKLTFGFADFRIFL
DananDIA1	175	VPNTYAI CGLTHFQAYAG--RTL NHYTEAA--EDLRREIARQLIHLISLKLTFGFADFRIFL
DwillDIA1	161	VPRSFVAVCGSTL FQAYAG--STLSNYLKAP--IDLRLMAKQLLQLALKLSAGFKGFRFYL
NvitrDIA1	203	TPKYFGACGRLIVEBYIG--LPLSSFIDEP--WIRRAKIASSLLQAADTLMSKNSEFAFYL
SpurpDIA1L	306	FTEYLGECGRVILTEPSG--KPLSSYLKAS--WKDRVDISLKIQLMLED FHDSSDKWLVL
BflorDIA1La	272	IPAF LGACGNLVATETAG--KPLSMYLEVKGPWQVRANLSLQLIQMLDDFONKDPDWLLMF
CinteDIA1	245	FQRTVGS CGALMVHGRSIVTSLYELYDAP--WKVRLDVAIQLLDLAEHFYNDLNYMFAL
AgambDIA1	207	VPKLLHTFGFSIETVEG--KTL EHYDFP--FVTRMRIAELIRACFKFTEGIHGFRVFL
consensus	361	fpylgacGrim y g l fy ap wd rvdla qll iae lt nd ef lyl

... Motif 7

Motif 8

Motif 9

Motif 10 ...

SpurpDIA1	278	TDVSEDNLAVND-NG	----EVLVIDAENIIVVDR	KKIKEDANPGWDVKH	----QSEH	EG
NvectDIA1	274	ADPAPGNFVSD-SG	----KVTLLDLEHLVVVDL	SEVQMEEANDKPKPS	-----D	
GaculDIA1	285	LDVSFDNFVAVGPRDG	----KVIIVDAENVLVADKRLIK	QNKPKESFDVWY	----ESRFEE	
OlatiDIA1	285	LDVSFDNFVAVGPRDG	----KVIIVDAENVLVADKRLIK	QNKPKESYDVWY	----ESRFEE	
TnigrDIA1	285	LDVSFDNFVAVGPRDG	----KVIIVDAENVLVADKRLIK	QNKPENFDVWY	----ESRFEE	
TrubrDIA1	285	LDVSFDNFVAVGPRDG	----KVIIVDAENVLVADKRLIK	QNKPENYDVWY	----ESRFEE	
DreriDIA1b	285	LDVSFDNFVAVGPRDG	----KVIIVDAENVVVDKRLIK	QNKPKESYDVWY	----ESRFEE	
DreriDIA1a	285	LDVSFDNFVAVGPRDG	----KVIIVDAENVIVVDKRLV	KQNKPKESYDVWY	----ESRYEE	
BtaurDIA1	286	LDVSFDNFVAVGPRDG	----KVIIVDAENVLVADKRLIR	QNKPENWDVWY	----ESKFDD	
PpygmDIA1	286	LDVSFDNFVAVGPRDG	----KVIIVDAENVLVADKRLIR	QNKPENWDVWY	----ESKFDD	
CfamiDIA1	286	LDVSFDNFVAVGPRDG	----KVIIVDAENVLVADKRLIR	QNKPENWDVWY	----ESKFDD	
PtrogDIA1	286	LDVSFDNFVAVGPRDG	----KVIIVDAENVLVADKRLIR	QNKPENWDVWY	----ESKFDD	
TtrunDIA1	286	LDVSFDNFVAVGPRDG	----KVIIVDAENVLVADKRLIR	QNKPENWDVWY	----ESKFDD	
HsapiDIA1	286	LDVSFDNFVAVGPRDG	----KVIIVDAENVLVADKRLIR	QNKPENWDVWY	----ESKFDD	
MmulaDIA1	286	LDVSFDNFVAVGPRDG	----KVIIVDAENVLVADKRLIR	QNKPENWDVWY	----ESKFDD	
PvampDIA1	286	LDVSFDNFVAVGPRDG	----KVIIVDAENVLVADKRLIR	QNKPENWDVWY	----ESKFDD	
MdomeDIA1	286	LDVSFDNFVAVGPRDG	----KVIIVDAENVLVADKRLIR	QNKPENWDVWY	----ESKFDD	
MmuscdIA1	286	LDVSFDNFVAVGPRDG	----KVIIVDAENVLVADKRLIR	QNKPENWDVWY	----ESKFDD	
RnorvDIA1	286	LDVSFDNFVAVGPRDG	----KVIIVDAENVLVADKRLIR	QNKPENWDVWY	----ESKFDD	
GgallDIA1	285	LDVSFDNFVAVGPRDG	----KVIIVDAENVLVADKRLIR	QNKPENWDVWY	----ESKFDD	
XtropDIA1	285	LDVSFDNFVAVGPRDG	----KVIIVDAENVLVADKRLIK	QNKPENWDVWY	----ESKFDD	
BflorDIA1	275	TDISYENFVTS-DG	----NLFVIDVENVIVVDK	QKIKADKPRNWEARY	----QSHFDE	
SsalaDIA1R	292	TRLGEDMFGILD-DQ	----RVFITDASSIGVID	LEQGFPPDPPS-QTGS	----DGDIFS	
DreriDIA1R	273	TRIPEDMFGILE-DN	----KVFIVDTSTIGI	DLQEGHPPDK-D-LLPE	----ELDVFS	
RnorvDIA1R	292	THVDAGMFGIFD-NG	----HLFIRDASALGIDK	QEASQAAD---RTGE	----NEDIFS	
MmuscdIA1R	292	THVDAGMFGIFD-NG	----HLFIRDASALGIDK	QEGSQAAA---RTGE	----NEDIFS	
MmulaDIA1R	290	THIDAGMFGVFN-NG	----HLFIRDASAVGVIDK	QEGSQEAT---RAGE	----NKDIFS	
HsapiDIA1R	290	THIDAGMFGVFN-NG	----HLFIRDASAVGVIDK	QEGSQEAN---RAGE	----NKDIFS	
BtaurDIA1R	290	THVDADMFGIFN-NG	----HLFIRDASALGVIDR	QEGSQAAS---GAGD	----NKDIFS	
EcabaDIA1R	290	THVDAGMFGIFN-NG	----HLFIRDASTLGVIDR	QEGSQAAA---RAGE	----NKDIFS	
DordiDIA1R	290	THVDAAMFGIFS-NG	----HLFIRDASALGVIDK	QEGSQAAP---KAGE	----NQDIFS	
MdomeDIA1R	289	TRIDAGTFGIFD-NG	----HLFIRDASTVGVIDK	QRGSLTLD---RQEE	----SKDIFS	
OanatDIA1R	289	TRIHAGTFGVFD-NG	----HLFIRDASSIGVIDR	QEGKRPAR---SSPE	----PRDIFS	
GgallDIA1R	287	TRVDVGTFGVFS-NG	----HLFIRDASTLGLIDK	EEGSOPID---GQQE	----YKDIFS	
BflorDIA1Lb	383	VDFSFNFAVNN-YG	----RLTLIDFDVMLIDR	EEFVGENK--TEPCD	----LKCFKT	
BflorDIA1Lc	244	LDVSFQNFVAVDS-RG	----WVRLIDLDDVMVIDR	RTVVNQEQ--TEMCN	----EQCYTD	
AaegyDIA1	254	TDISPDNIVSMSSEEE-I	KVTFVDLNNVILDS	SHSKRLKP-----SK	----QKHVHS	
CpipiDIA1	256	TDINPDNIAVQAQPSGS-F	QVSFIDLDNVILDS	QSKRLDRR-----SK	----ARNIHS	
DyakuDIA1	228	TDFTGDNFAYDEHTK	----KVYLIDLDSVVLVD	----ASSAT	----GQ	----AEKYEP
DerecdIA1	229	TDFTGDNFAYDEDSK	----RVYLIDLDSVVLVD	----ASSAA	----GQ	----AEKYVP
DmelaDIA1	231	TDFTADNLAYDEDTK	----KVYLIDLDSVVLVD	----ASFAA	----GH	----AEKYEP
DsechDIA1	233	TDFTADNLAYDEETK	----KVYLIDLDSVVLVD	----ASSMA	----GQ	----AEKYEP
DpersDIA1	232	TDFTADNLAFDEASQ	----SVILIDLDSVVLVD	----AAVPL	----GD	----AQKYEP
DpseuDIA1	232	TDFTADNLAFDEASQ	----SVILIDLDSVVLVD	----AAVPL	----GD	----AQKYEP
DananDIA1	232	TDFTSDNLTFDEDTR	----RVLLIDLDSVVMVD	----AASTS	----GQ	----AEKYEP
DwillDIA1	218	TDFTADNFAYNEANG	----TVLLIDMDTIVLVE	SNDEAESES----QL	----SKKYKP	
NvitrDIA1	260	TDISMDNIAVNNEK	----AIFVDLENIIVE	KNPPEKALVGIESWNE	----TYTNAV	
SpurpDIA1L	363	LDFGYENFVTS-EG	----QLKVVNLGGMVLVDK	DQTSTTPDMNPHLNNRTELC	NEDCLN	
BflorDIA1La	331	VEVNIENFSVSS-DG	----RLILTDLGNMTI	INKHDLKDNSTKKRSSVC	----NEACFK	
CinteDIA1	303	HRLTPRDIIGISD-TG	----KLRIKNADNVILID	----NNSKN	-----DKGLYE	
AgambDIA1	264	TDINPDNVVNLKNDNKQVY	VSIVDLDNVILLD	SWAEVFLTKN-----TH	HVHS	
consensus	421	tdvs dnfav g	kvliidaenvivvdk	q		rfe

... Motif 10

Motif 11



SpurpDIA1	328	CGSRRECIMFSHTDLCNHYYS	DHNYAVCQGLFGKDSPHGD	-----GGLHSIP
NvectDIA1	318	CS-QPDCLSFSPSDMCSGGS	RDHNYAICQGLLAGSSRRQ	-----GLLHNPP
GaculDIA1	336	CD-REACLSFSKESLCSRVT	VDHNYAVCONLLSRYATWRGTT	-----GLLHDPP
OlatiDIA1	336	CD-REACLSFSKDSLCSRVT	VDHNYAVCONLLSRYATWRGTT	-----GLLHDPP
TnigrDIA1	336	CD-REACLSFSKDSLCSRVT	VDHNYAVCONLLSRYATWRGTT	-----GLLHDPP
TrubrDIA1	336	CD-REACLSFSKDSLCSRVT	VDHNYAVCONLLSRYATWRGTT	-----GLLHDPP
DreriDIA1b	336	CD-KEACLSFSKMDLCSRVT	VDHNYAICONLLSRYATWRGSS	-----GLLHDPP
DreriDIA1a	336	CD-KEACLSFSKDILCSRVT	VDHNYAVCDLLSRFSSWRGST	-----GLLHDPP
BtaurDIA1	337	CD-KEACLSFSKEILCARAT	VDHNYAVCONLLSRHATWRGTS	-----GLLHDPP
PpygmDIA1	337	CD-KEACLSFSKEILCARAT	VDHNYAVCONLLSRHATWRGTS	-----GLLHDPP
CfamIDIA1	337	CD-KEACLSFSKEILCARAT	VDHNYAVCONLLSRHATWRGTS	-----GLLHDPP
PtrogDIA1	337	CD-KEACLSFSKEILCARAT	VDHNYAVCONLLSRHATWRGTS	-----GLLHDPP
TtrunDIA1	337	CD-KEACLSFSKEILCARAT	VDHNYAVCONLLSRHATWRGTS	-----GLLHDPP
HsapiDIA1	337	CD-KEACLSFSKEILCARAT	VDHNYAVCONLLSRHATWRGTS	-----GLLHDPP
MmulaDIA1	337	CD-KEACLSFSKEILCARAT	VDHNYAVCONLLSRHATWRGTS	-----GLLHDPP
PvampDIA1	337	CD-KEACLSFSKEILCARVT	VDHNYAVCONLLFRHATWRGTS	-----GLLHDPP
MdomeDIA1	337	CD-KEACLSFSKEILCSRAT	VDHNYAICONLLSRHATWRGTS	-----GLLHDPP
MmuscDIA1	337	CD-KEACLSFSKEILCARVT	VDHNYAVCONLLSRHATWRGTS	-----GLLHDPP
RnorvDIA1	337	CD-KEACLSFSKEILCARVT	VDHNYAVCONLLSRHATWRGTS	-----GLLHDPP
GgallDIA1	336	CD-KEACLSFSKEILCARVT	VDHNYAVCONLLSRHATWRGTS	-----GLLHDPP
XtropDIA1	336	CD-KEACLSFSKEILCSRAT	VDHNYAICONLLSRHATWRGTS	-----GLLHDPP
BflorDIA1	325	CPGMSNCLSFVDSALCRYLHT	DHNYAVCRNMLSEYASEMGKP	-----GLLHDPP
SsalaDIA1R	341	CLGQGTSPCHR-SPPCSSVRPT	QSLTLLCTALLPRLLLTERGAQT	TRLPMEGEAEAGRLA
DreriDIA1R	321	CL--SGSCVR--PPPETVREAQ	SFILCKYILN-NLLTSN	-----DKQSG-LP
RnorvDIA1R	339	CL-VSGCQVQ--MSSCDTVPEK	QNLVLCQQLLP-QLLRG	-----KFPSPVQ
MmuscDIA1R	339	CL-VSDCQIQ--LSSCDTVPEK	QSLVLCQQLLP-QLLQG	-----KFPSPVQ
MmulaDIA1R	337	CL-VSGCQAQ--LPSCEVSEK	QSLVLCQQLLP-RLLQG	-----RFPSPVQ
HsapiDIA1R	337	CL-VSGCQAQ--LPSCEVSEK	QSLVLCQQLLP-RLLQG	-----RFPSPVQ
BtaurDIA1R	337	CL-VSGCQIK--LPSCDTIPEK	QNLVLCQQLLP-LLLQA	-----KFPSPVQ
EcabaDIA1R	337	CL-LSDCQAE--LPSCDTVPEK	QSLVLCQQLLP-RLLQG	-----KFPSPVQ
DordiDIA1R	337	CL-VSGCQAQL-LPSCDNIPDK	QSVLVCQQLLP-QLLQG	-----KFPSPVQ
MdomeDIA1R	336	CL-VLDCQSP--FPSCSSVKEK	QSMVMAQQQLLP-QLLKE	-----KFPQPIQ
OanatDIA1R	336	CL-AADCQSD--LPSCNTVQEH	QSLVLCRELLP-KLLEG	-----KFPKPVQ
GgallDIA1R	334	CL-TVDCQSA--FVSCNSIREK	QSLVMCQQLLP-KLLRG	-----KFLPPVQ
BflorDIA1Lb	431	FISQIEAMNSYDSCSAMPQYS	QMMYALACVRLLSHLPEHLSEP	--NPMDPKPKHRPDS
BflorDIA1Lc	292	FQKKLYS-DEYH-CDDIFKYAP	MMYASICARLLSNLQKHPERR	KWGEIREYQEQSIELD
AaegyDIA1	302	RIDCDGCFAYIQEDICVHQIS	DINLFAVCQLLENLNGDSKR	-----GFLHSLG
CpipiDIA1	305	RIPCDGCFAYVQEDICSYQHS	DINQFAICQLLYENLNGDREG	-----GFLHIQP
DyakuDIA1	270	-LPGEG-FTFDVSAFCSGHQL	DANIYQACLLLRDYLLKLNLDN	-----
DerecDIA1	271	-LPGEG-FTFDVSAFCSGHQL	DANIYQACLLLRDFLLKLNLDN	-----
DmelaDIA1	273	-LTGEG-FTFDVSAFCSGHQL	DANIYQACLLLRDYLLKLNLDN	-----
DsechDIA1	275	-LAGEG-FTFDVSAFCSGHQL	DANIYQACLLLRDSLLKLNLDN	-----
DpersDIA1	274	-LPGDG-FTFDVKSFCGGQQL	DANVYQACLLKDFLLRDLAN	-----
DpseuDIA1	274	-LPGDG-FTFDVKSFCGGQQL	DANVYQACLLKDFLLRDLAN	-----
DananDIA1	274	-LPGEG-FTFDVSAFCSGRQL	DANVYQACLLLRDFLLKDLDN	-----
DwillDIA1	264	-FPGEG-FTYDVNAFCDNQDL	DANIYQVCLLRDQLLPDVKN	-----
NvitrDIA1	310	DLDCQDCFVFSFNDICSHKVS	DHNYAICQHLLTQALGAVFHN	-----QGLHDPP
SpurpDIA1L	418	TFVKQLQTEPDTHCREVPRH	VELMYMMACHSLLSDLMTTKYER	-----FFQPLDTPR
BflorDIA1La	381	RFTRNLSHRPETS	CRQAGRYSQLMYARACRILG	CWQTERSGE-----GRVVLSSSKDAS
CinteDIA1	342	VRYKQEKVDITEENLCDHSE	NDVNYVICRHFLLGGTWKERK	GK-----KYPGGLLHDPK
AgambDIA1	313	KIECNCFAYVQEDVCRYQNS	DLNLEATCOLLENLNGHYAK	-----GLLHYDR
consensus	481	c eac sf lc vd nyavCq ll		g lh

Motif 12

Motif 13

Motif 14 ...

SpurpDIA1	377	SDL-----SSYMRAKVKGQIAECSRPSK--RDGRYLVVKELKETLM-----
NvectDIA1	365	-----VALKASLNQLLQDCTAQDM--RNTREETAQKLSELLQ-----
GaculDIA1	386	AH-----IAKDGQLLTLLEDECTRPKK--RYGRFOAAKELREYLT-----
OlatiDIA1	386	AH-----IAKDGQLEALLDECTRPKK--RYGRFOAAKELREYLT-----
TnigrDIA1	386	AH-----IAKDGQLEALLDECTKPKK--RYGRFOAAKELREYLT-----
TrubrDIA1	386	AH-----IAKDGQLEALLDECTKPKK--RFGRFOAAKELREYLT-----
DreriDIA1b	386	PH-----IAKDGQLEALLEECANPKK--RYGRFOAAKELRDYLT-----
DreriDIA1a	386	PD-----VVKDGRLLIALLDECTRPQK--RYGRFOAAKELREFLT-----
BtaurDIA1	387	SE-----IAKDGRLLEALLDECANPKK--RYGRFOAAKELREYLA-----
PpygmDIA1	387	SE-----IAKDGRLLEALLDECANPKK--RYGRFOAAKELREYLA-----
CfamiDIA1	387	SE-----IAKDGRLLEALLDECANPKK--RYGRFOAAKELREYLA-----
PtrogDIA1	387	SE-----IAKDGRLLEALLDECANPKK--RYGRFOAAKELREYLA-----
TtrunDIA1	387	SE-----IAKDGRLLEALLDECANPKK--RYGRFOAAKELREYLA-----
HsapiDIA1	387	SE-----IAKDGRLLEALLDECANPKK--RYGRFOAAKELREYLA-----
MmulaDIA1	387	SE-----IAKDGRLLEALLDECANPKK--RYGRFOAAKELREYLA-----
PvampDIA1	387	SE-----IAKDGRLLEALLDECANPKK--RYGRFHAAKELREYLA-----
MdomeDIA1	387	GE-----IAKDGRLLEALLDECAHPKK--RFGRFOAAKELREYLA-----
MmuscdIA1	387	SE-----IAKDGRLLEALLDECTNPKK--RYGRFOAAKELRGYLA-----
RnorvDIA1	387	SE-----IAKDGRLLEALLDECTNPKK--RYGRFOAAKELRGYLA-----
GgallDIA1	386	AD-----IAKDGRLLEALLDECANPKK--RYGRFOAAKELREYLA-----
XtropDIA1	386	AE-----IAKDGRLLEALLDECANPKK--RYGRFKSAKELREYLA-----
BflorDIA1	376	ET-----VVRDGTLQRLLAECAKPRT--LYGRFDAAKELIELLG-----
SsalaDIA1R	400	RDV-----PLLLGVCADPSQPDWRIMAA--VGSLMDLLKPMRPCNP-----
DreriDIA1R	364	RAA-----VDELLVCADPSQLDQTIIKS--VQSLKNILKTLRPCSP-----
RnorvDIA1R	382	QEI-----DSALSLSCKDASTNLEVFGA--TSLLKNILRSLRRTCDP-----
MmuscdIA1R	382	KEI-----DSALSLSCKDNSTDLEVLGA--TSWLKDILRSLRRTCDP-----
MmulaDIA1R	380	DDI-----DSALAQCGDSTRPDPEVLGA--ASWLKHILRPLRRTCDP-----
HsapiDIA1R	380	DDI-----DSILVQCGDSIRPDPEVLGA--ASQLKDILRPLRRTCDP-----
BtaurDIA1R	380	E EI-----DAELTRCADGTRPDPEVLGA--ASRLKDILRPLRRTCDP-----
EcabaDIA1R	380	E EI-----DATLTWCGEDTRPDAEVLGA--ASRLKDILRPLRRTCDP-----
DordiDIA1R	381	VEI-----DSALAQCGGIRPDSEVFGA--ASRLKDILRPLRRTCDP-----
MdomeDIA1R	379	EQI-----DSALVLCGNSSLSDQEVIEA--ASRLKAILKPLRRTCDP-----
OanatDIA1R	379	E EI-----DALLDRCGDSSLDGQTVIGG--ARRLMDILKSLRRTCDP-----
GgallDIA1R	377	EKI-----DSFLQHCAGEGLADDQVNEA--MAKLAQLLKPLRSCDS-----
BflorDIA1Lb	489	RP---RLLWGPPEQEAKVLEELLRGCVEENV--AGGRLEAVGELKTFILR-----
BflorDIA1Lc	350	EPPVKGFLHNPPDEIREALEGALTQCVHETL--PRGRLGAVLRLOEILG-----
AaegyDIA1	351	TDS-----KLEAFRKLHLHQCVYQPPYCEDRQEVLRIMEITH-----
CpipiDIA1	354	NDD-----SQPRLSEIRQLLHHCVYCVPPDCRDRQGLLQQVQEIID-----
DyakuDIA1	310	-----ERLQLLLEQCVCACQDDFCDMRFQHAYDLIKMLD-----
DerecdIA1	311	-----ERLQLLLEQCVCACQDDFCDMRFQHAYDLIKVLD-----
DmelaDIA1	313	-----EKLQLLLEQCVCACQDDFCDMRFQHAYDLIKVLE-----
DsechDIA1	315	-----EKLQLLLEQCVCACQDDFCDMRFQHAYDLIKBLE-----
DpersDIA1	314	-----GRLEMLLEQCVCRCDDATCDMRFQAYDLIKLLG-----
DpseuDIA1	314	-----GRLEMLLEQCVCRCDDATCDMRFQAYDLIKLLG-----
DananDIA1	314	-----ERLQLLLEKVCVEQDDLCDMRFQYAYDLIKLLD-----
DwillDIA1	304	-----HRLKEMLNDCVQCEDDKCDIRFKYANNLIDLLV-----
NvitrDIA1	361	D-----YILQKHPTLIDLLEQCAKPDIG--YSRIDIAHKLIVLLD-----
SpurpDIA1L	470	KHHPGMLHDAPYEVDSVLSELLYECVFEGQ--PGRRMHSVRVLRLLLT-----
BflorDIA1La	436	CAYGRGLLFGPPREAKQELLEDLLTECVEETK--AGGRITALKQIRVLLA-----
CinteDIA1	396	EFG-----VFSSQMFVLLDICSRGKTAVAPERRTLSHSIRRLAANQLRNVLERRR
AgambDIA1	362	DAEAFP----VLGEASKMLQNLLESCVYQPPDCQNRSHILKMDLHITD-----
consensus	541	d le lldec rfq akelr l

... Motif 14

Motif 15

SpurpDIA1	416	---K	LIT	-----
NvectDIA1	400	---	GYL	-----
GaculDIA1	423	---	Q	LAASSSATAR-----
OlatiDIA1	423	---	K	LAASSSATS-----
TnigrDIA1	423	---	Q	LA-----
TrubrDIA1	423	---	Q	LAASSSLVSAR-----
DreriDIA1b	423	---	Q	LSGSAR-----
DreriDIA1a	423	---	Q	LQTQTSNADR-----
BtaurDIA1	424	---	Q	LSNNVR-----
PpygmDIA1	424	---	Q	LSNNVR-----
CfamiDIA1	424	---	Q	LSNNVR-----
PtrogDIA1	424	---	Q	LSNNVR-----
TtrunDIA1	424	---	Q	LSNNVR-----
HsapiDIA1	424	---	Q	LSNNVR-----
MmulaDIA1	424	---	Q	LSNNVR-----
PvampDIA1	424	---	Q	LSNNVR-----
MdomeDIA1	424	---	Q	LSNNGR-----
MmuscDIA1	424	---	Q	LSHNVR-----
RnorvDIA1	424	---	Q	LSHNVR-----
GgallDIA1	423	---	Q	LSNNVR-----
XtropDIA1	423	---	Q	LSNNAR-----
BflorDIA1	413	---	S	FLKDR-----
SsalaDIA1R	439	---	H	YTYRYPECRYNQDY-----
DreriDIA1R	403	---	Q	YAYRYPECLYSDKF-----
RnorvDIA1R	421	---	R	FAYRYPDCKYNDRF-----
MmuscDIA1R	421	---	R	FAYRYPDCKYNDRF-----
MmulaDIA1R	419	---	R	FAYRYPDCKYNDKF-----
HsapiDIA1R	419	---	R	FAYRYPDCKYNDKF-----
BtaurDIA1R	419	---	R	FAYRYPDCKYDDKF-----
EcabaDIA1R	419	---	R	FAYRYPDCKYNDKF-----
DordiDIA1R	420	---	R	FAYRYPDCKYNDRF-----
MdomeDIA1R	418	---	R	YAYRYPDCKYSDRY-----
OanatDIA1R	418	---	R	FAYRYPDCKYSEKY-----
GgallDIA1R	416	---	R	FAYRYPDCKYSDKY-----
BflorDIA1Lb	533	---	R	NAKGEN-----
BflorDIA1Lc	397	---	T	T-----
AaegyDIA1	389	---	D	VLHEVV-----
CpipiDIA1	395	---	G	LVES-----
DyakuDIA1	343	---	S	KN-----
DerecDIA1	344	---	S	KI-----
DmelaDIA1	346	---	S	NN-----
DsechDIA1	348	---	S	KN-----
DpersDIA1	347	---	E	LGS-----
DpseuDIA1	347	---	E	LGS-----
DananDIA1	347	---	S	-----
DwillDIA1	337	---	E	INNKIEIL-----
NvitrDIA1	399	---	S	VIKNA-----
SpurpDIA1L	517	---	I	IQRGFSYKDAADRTSL-----
BflorDIA1La	483	---	A	-----
CinteDIA1	446	I	CSPDFKYRYPECELAEDAGINLPSIELQWLH	
AgambDIA1	407	---	Q	TIIQS-----
consensus	601		1	