

Supplementary Materials: An Insight into the Triabin Protein Family of American Hematophagous Reduviids: Functional, Structural and Phylogenetic Analysis

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Table S1. Primary structures of proteins obtained from the transcriptome analysis of the salivary glands from *T. pallidipennis*.

ID	Protein Sequences
Q27042	EECELMPPGDNFDLEKYFSIPHVYVTHSRNGPKQVCREYKTTKNSDGTTTTLVTSYDKT GGKPYHSELKCTNTPKSGVKQGFVCEVPNGNGGKKKIHVETSVIATDYKNYALLQSC TKTESGIADDDVLLLQTKKEGVDPGVTSVLKSVNWSLDDWFSRSKVNCDNMK *
CAA56540.1	AEGDDCSIEKAMGDFKPEEFFNGTWYLAHGPVTSAPVCQKFTTSGSKGFTQIVEIGYNK FESNVKFQCNQVDNKNGEQYSFKCKSSDNTEFEADFTFISVSYDNFALVCRSITFTSQPKE DDYLVLERKSDTDPDAKEIC *
22480c0seq1	PASPGIDKCRVETPASNFASSKFFTGTWYVTQAKNISTSVCHQFSTTLAGTTINVKADGFY EIGRKRSFYNVPCSGQKSENGKFTLTCQPKRSDTTRSTITVQVEVTVMDDNNKYAVIYR CATSGPHKDDNYLVLRNKDEVISNLNTILKNKGVSGKLITRKESTHVCPQAQ *
26220c3seq6	QSVQTCTTPVMDNFKAPKFHNGTWYVTHVKYVTIPTTECRTLTWQEGDMSFVEHEF TKDGLKGNLRCEAKAEAAKRLSFTCTFNESIDKTIFIVMASDYNDYALYYICSAITGAN ADRKPGDTVENYLVARRTSGNTEIPAQLQSLTNGMNLQKCS *
26220c3s4.2	QSVQTCTTPVMDNFKAPKFHNGTWYVTHVKYVTIPTTECRTLTWQEGDMSFVQHDF TKDGKDGNLRCQAQAEAKRLSFTCKFNQESIDKTIFIVMDTDYSDYALYYICSAITGAN ADRKAGQIVDNYLIARRTSGNTEIPDKLKSLEGMNLQKCS *
25921c0s2	QVRSGQCQNYSPMQNFDPSQFFLGSWFVTHAKNGPEFAACRTYQTSVNGKNINFGND GYYGDKQKNSYYQVRCTGPKNSGGTGKFSLSLQSLSNSATRQNIASNLELTIIKTDY SQYAIYRCAKYSTVQVTKDNLMLHRDQNSLAPNIANTFQQATSMPLSGLPFTRQSTT CKKFDNHITDDLIDELLY *
25921c0s1.4	QVRSGQCQNYSPMQNFDPSQFFLGSWFVTHAKNGPEFSVCRTYQTKVSGRDINFNADG YYGDTKANSYYKVRCTGPKDSGKKGRFSLSCNLNSLNSASPTQKSITFNLDLTIIKTDYS QYAIYRCAWYSTLQVTTDNLMLHRDKNALAPNIANNFQQATRMSLSGLPYTRQRTT CKQMDNHITDDLIDELLY
26887c0s1.4	SYQPYISEKQDVKAMSNFQPTRFFSGTWYVTHAKNGTAATVCHKYKTKKEQNGKFSF DYGYNNNGNEEPFFQVHCAETKRIKNKPFsfYCKLIKGQESSNFKQYNVDLTFIGTDYESFAI FYRCVPIGTGLGYADNLFVLHRTKAISSTYAKAKNVLEKQGLFLDSFLNRKNSNCKNNPKF *
27479c2s12	WYVTNAKHGSNSTVCREYNGKRENGNPVLNGDGYSHGNLKIYFEVRCDKQSDTNYK LTFSTQKGPAGTNMNFQFQLEVTVLSTDYDDFAIMYRCVKFPPQLGSRIEDNVLVLHR KDCKTEDKDRVEETLKKNGWSLDSFKSRKGVNCPPEPPQK *
27479c2s11.5	WYVTNAKHGSNSTVCREYKGRQNGIRQLIADGYYSYGQDQATAYFNVLCHKQSDRNY KLTFNCTQRGSITDDQKVIIQFQLEITVLLTDYDDFAIMYRCVKFPPQLGSRIEDNVLVLRR NPNTDNKNPLIETTLKSQDLSLDTFSRKGVTCPKLPQK *
27479c2s8.5	WYVTNAKHGSNSTVCREYNGKRENGNPVLNGDGYYSFRNLKIYFEVRCDKQSDTNYKL TFSTQKGPAGTNMNFQFQLEVTVLSTDYDDFAIMYRCVKFPPQLGSRIEDNVLVLHRD ATKTNDKNPQIEDILKKQDWSLDTFNSRDGVECPLPPQK *
27479c2s9.5	WYVTNAKHGSNSTVCREYKGRQNGIRQLIADGYYSVGSGQKIYFEVRCDKQSDKNYKL TFSTQKGPAGSKMNFQFQLEVTVLSTDYDDFAIMYRCVKFPPQLGSRIEDNVLVLRRNP NTDNKNPLIETTLKSQDLSLDTFSRKGVTCPKLPQK *
27479c2s14	WYVTNAKHGSNSTVCREYKGRQNGIRQLIADGYYSYGQDQATAYFNVLCHKQSDRNY KLTFNCTQRGSITDDQKVIIQFQLEITVLLTDYDDFAIYRCGKIPSSSGSRIEDNVLVLHRK DCKTEDKDRVEETLKKNGWSLDSFKSRKGVNCPPEPPQK *
21634c0s2	QSRLGAKQDLIIQDFFKGSWFVTHIDGVNEATCREYITKIENDAIKLNAVGEHKLTKEQE KNSTTYCSSSKGKALKPEGPFVLQCRHIYGDNERTTFFGLTFSVIETDYTDYALVHRCTKY NNMNFITGNLLLLHRSKTS DSGSKATTSLKHSLSLQQFQKTGC *

21634c0s1.4	QSRLGAKQDLIIQDFFKGSWFVTHIDGVNEATCREYKSNIENGTIKLNAFGEHKLFEQYE YSTTNCSSSTKGKQLNQAGPFALQCRHTYGDNDYTYNNYYGLSFSVIETDYTDYALVHRC TKYNNMNFITGNLLLLHRSKTS DSGSKATTSL EKHSLSLQQFQKTGC *
22866c0s1	ATKFFSGTWYVTHVQKVPSPNVCHTFAVNQKDGKFIFGLGKDGENQVQCESKREEDK ITFSCQSVTGNFTFQSVFIVMGASYDDYAVLYNCVTVSRFKADNYVVLRSKSDKEEIPAEA KSLTNELNLRKCTDIRKSVN *
26508c1s3	SQCQNTLRTKQDLNIQSFFKGSWYVTHIKDGGDEASCREYKTSLDGIQNLIKLDADGQY KFKGQTKFYTTKCSSVSGTPLNPPTGKYVLKCRHTYGGTENIFFDLKLSIIETDYSNYALVY RCTKYDDSSLNLKYGNLLLLQRSKTANGSKATASLQKNQSSLKQFKKTA *
26508c1s1.3	QKAKCQSDLEAKKDLDIQKFFKGSWYVTHIKDGGDEASCREYKTSLDGIQNLIKLDADG QYKFKGQTKFYTTKCSSVSGTPLNPPTGKYVLKCRHTYGGTENIFFDLMLSVIETDYSNYA LVYRCTKYDDPSLNLQYGTLLLLHRSKTS DSGSKATTSLQKHRLSLQQFQKTAGC *
26220c3s3	QSVQCTCTPTPVMDFNFKAPKFHNGTWYVTHVKYVTIPECTRLTTSKDGKNKYIVEHDF KNGVKGRHLHCEASPEAEKLTFTCTFNAGESIDKTIFIVMDTDYSDYALYYICSAITGANAD RKP GDTV DNYLVARRTSGNTEIPDKLKS LTGEMDFKKCT *
26220c3s5	EVGSLSECENPTAMEGFSATKFHSGTWYVTHVTKVTEPTCRTLTTSKDGKNKYIVEHDF KNGVKGRHLHCEASPEAEKLTFTCTFNAGESIDKTIFIVMDTDYSDYALYYICSAITGANAD RKAGQIVDNYLIARRTSGNTEIPDKLKS LTEGMNLQKCS *
27168c1s1	EEPSNNNECNRAAMTNFDSTRYLQINRAFVTHSREGTGAIICRLYKTQKSGDKTDEVDIN IYEFKERRDIYSETHCNTTLARIEKGT FVSSCKEVM L TARRSDTTMKPKPRIIEVYTSVID TDYDKYIIHYRCVKT SKIIDNIEVLQTNKNAGDEPIKQALEKNGLELED FIAHG NKPEEC ENIDNGKKELL * *
27168c1s14	YDAMANFDSTKYLQIAPLYSTYEKNAKYFTYCRVYKSNTKSDDKINMNIWGYQSEKN HYEIVCSTKEQNFKTGQYWAECNVVKDSNYEDTSISEPFKLYMSVIDTDYDNYAILYLCI SDELGFEDNVEVLQKNP *
27168c1s3	EEPSKTCNYQAMANFDSTKYLQIAPLYSTYEKNAKYFTYCRVYKSNTKSDDKINMNIWG YYQSEKNHYEIVCSTKEQNFKTGQYWAECNIVK DTHYTEPIKPYQLYLSVIDTDYQNY AILYNCNSNVTHFRDNIEVLQKDPGTDDNLVKA ALET KGMNLENFIQRNFTTV CQEN KKKEEK *
27168c1s8	EEPSNNNECNRAAMTNFDSTRYLQMTPLYSTYAMYGNLTVCRVFQSITKSGDEVNINIH GYYQESGQIYNYEMSCNTNEENFKTGQYRAECNVK DTHYTEPIKPYQVYLSVIDTDYQN YAILYNCNSNETHFRANIEVLQKDPGTDDNLVKA ALET KDMKLEKFIQRNFTTV CQEN KKKEEK *
27168c1s10.6	TPNNKKCGYKPMENFDSTRYLQITTPLYLTHTKLESNYSVCREFKSIKSGD TVDINIHGY QDSGKIYNYELLCS TAESFNKGQYLSVCEILK DTHDEEPLTSM SFEQHMSVIDTDYD SYAI LYTCFNDES GFEE NVVVLK KDPGGSDEAVTTALKNH EMDLKKFFPWNYAYCQNHKA *
27168c1s12.6	EQTYNPEYPSNNLEC NNQAMANFDSTKYLQTPLYSTYARDSL NITVCRAF KPITKSGDQV NININGYYQDSGKIYNYELLCS TAESFNKGQYLSVCEILK DTHDEEPLTSM SFEQHMSVI DTDYD SYAILYTCFNDES GFEE NVVVLK KDPGGSDEAVTTALKNH EMDLKKFFPWNYA YCQNHKA *
27168c1s13	EQTYNPEYPSNNLEC NNQAMANFDSTKYLQINRAFVTHSREGTGAIICRLYKTQKSGDK TDKININIIYEFPRRDIYSETHCNTTLARIEKGT FVSSCKEVM L TARRSDTTMKPKPTIIE VYTSVIDTDYDKYIIHYKCTKTSGIIDNIEVLQTNKNAGGEPIKQALEKNGLELED FIAHE NKHKECENIDNGKKELL * *
27479c2s3	EECELTPPEDNFDLEKYFSIPHVYVTHSRNGPKEQVCREYKTTKNSDGT TTTTLVTS DYKT GGKPYHSQLKCTNTPKNGGKGQFSVECEVPNGNGGKKI HVETSVIATDYKNYALLQS CTKTESGIADDVLLLQTKKEGVDPGVTSVLKSVNWSL DKWISRTEVNCDNIQN *
27479c2s7 (Fraction 22)	KECELMPPASNFDSEKYFDIPHVYVTHSRNGPKEQVCREYNTTKIQGDTTPYTVVTS DYKI RGETHHSQLKCTNTPKNGGKGQFSVECEISNGNGGNKKKVQFETS VFATDYKNYALLQ SCTKTESGIADDVLLLQTKKEGVDPGVTSVLKSVNWSL DDWFSRSKVNCDNMK *
25439c1s1	EKCTLLPAMDKFDSDRYFSVLHLFVTHSKNEPKQQVCREYETIKKNRDGTSTTRMLEVY KIGGKQHKT VLD CINTPKSGSVGQFSVDCQVKVAENVSTKNKNQLEISIIATDYKN *
27479c2s4	KECELMPPASNFDSEKYFDIPHVYVTHSRNGPKENVCREYKTTKNTDGTTHTEVIVKTGG KQRTVLNCINTVKNIPGHYFLECEAPNGDNQKIQLE *
27479c2s13	KECELMPPASNFDSEKYFDIPHVYVTHSRNGPKENVCREYKTTKNTDGTTHTEVIVKTGG KQRTVLNCINTQKNGKPGQYSVECEVPNGNGGNQKIQLETSVFATDNEKYALLQSCNK DGESEDDIFVLQTNKDPVEQGVTSVLKSVNWSLNDWFSRSKVNCDNMK *

27479c2s6	KECQLMPATDDYNADQYFSIPRVYAIYSKNGPEENVCREYETKKKTDGTIVTTVSGDKK NRGQQQTVLACTNREKSGSKGQFFVECEVPGKNGGNMKIQVETSVLATDN *
24967c0s3	FEAPKYHTGKWYVTHVKESPNDQCILRTSQNGETSIVEHDFIHNGKSGQQHCEALPETE KRLTFTCMFGDVSIDKTIQIVMATDYENYSLYLCSTFASGPDKGKTVDNYLLASRKNID AEIPDKLK *
24967c0s1.5	CTIPTKVMMDNYQAPKYHTGEWYVTHVQKSPNDQCILTTSQDGDTSIVEHDFTYNGKAG KQHCEALPETEKRLTFTCMFGDVSIDKTIQIVMATDYENYSLYLCSTFASGPDKGKTVD NYLLASRKGITAEIPKELESLSKLNLLQKCNYS *
26220c3s7	CAYSQFVQQCATPTTVMQNFEAPKFHNGTWYVTHVKYVTIPTECRTLTSKDGKNKYIVE HDFTKNGVKGRHLHCEASPEAEKKLTFTCTFNAGESIDKTIFIVTDTDYDDYALYYICSAITG ANADRPKPGDTVENYLVARRTSGNTEIPAQLQSLTNGMNLQKCS *
24967c0s2	CTIPTKVMMDNYQAPKYHTGEWYVTHVQKSPNDQCILTTSQDGDTSIVEHDFIHNGKSGQ QHCEALPETEKRLTFTCMFGDESIDKTIVQIVMDTDYNDYSLYLCSTFTSGPNKGKTVDN YLLASRKNIDAEIPDKLK *
21465c0s1	FAPPEYPPDTTECLDFEDYENFNTAKFLKGIWYVTHARYGSNSTVCREYKTRLRKNIGINI VADGYYNFGGQPPRYRVRCEGTKEEENGKLSLNCKQQSRGKVNKIIFNYQLDLSVIETDY DKFAVIYTCAKFPASNELSVEDNILILHRDKDNDNSGVETILQQHESSLQEFLSRKDSTCL PSPVKN *
24572c0s1	AEGDDCSLEKAMGDFKPEEFFNGTWYLAHGPDVTSPAVCQKFTTSGSKGFTQIVEIGYN KFESNVKFQCNQVDNKNDEQYSFKCKGSDNTEFEADFTFISVSYDNFALVCRSITFTSQPK EDDYLVLERTKSDTDPDANEIC *
24833c0s3	DTIKYGGKSCQPIPTMENFDAARFFSGSWSLTHSTPSARVTPSTICRDYELKVHENGTFGV TYGYFENSGRTNRYDIHCIGTKSNQPGLSSFDCYLTNARGEKTHTHIDAYFIAADYENYC LVYRCVTSDATFEDNVFLLYRNKDYIPSDDEEVKNIIQPFGLGLEQFISRKDATCTNK *
24833c0s1 (Fraction 22, 23 and 24)	DTIKYGGQTCQQQVPIMKDFDVERFFSGSWSLTHSTRSPRVTESTICRDYELKVHENGTFG VTYGYFENSGRNNRYDINCLGTRSDQPGLSYFDCYLTNARGEKTHTRIDGYFVTTDYDN YCLVYRCVTSDDKFEDNVFVLYRNKNYIPKDEEVKKIIEPYGLGLEQFISRKDATCTNK *
24833c0s2 (Fraction 22)	EKLEYGKGVCQNNKLDGLVNLNAQKFFSGTWYLTHATKSTRVTLSTICRDFEPKQKEDG TFEVTYGYENGKGQNHVDVSCSGTQDKTRLDIFNFDCKSNNERGETTSFHIDGSFLATD YDSYGVVYRCVTTGTLTEDNVFLIHRQKNPSDEEVTKILTHYGLSLGDVISRKDATCTNK *
23242c0s1.5	NFAGIRECQQVTAMNGFDSNKFRTGWHMTNVQNGLFSIVCQDLETENKNGKLITKYN NKNNGKEHTVQCESNGQGKNGEIPFDCEIKSRFFKFLNKVTKFQANFKIMTTDYNDYALL YKCVTLKSGTKADNYVVLNRNKNKYKIPGSAQSLLQINGVSLKKCSELVKADDINSEV *
23242c0s2	GITSINECQKVTAMQNFSTKFFRGTWYMTNVMNGLFSIVCQELETTKDGAQLFIDYNN KNGKENYVRCEKSGQEKNGQIPFDCKIEKSLFNFFSKSKKFQANFTIMTTDYNDYALFYK CVTLQSGVKADNYAVLRRSKNDYNIPGSVQSFLQINGVSMKKCSELVNADDINREVI *

Table S2. Amino acid sequence identification (ID) of the species used for the phylogenetic analysis.

Specie	No. Secs	ID
<i>Rhodnius prolixus</i>	33	AAS94228.1, AAC26160.1, 1U0X_A, 4NP1_A, AAB09090.1, AAB41587.1, Q7YSY5, Q7YT08, Q7YSZ9, Q7YT10, Q7YT05, Q7YSY9, Q94732, Q7YT07, Q7YT06, Q7YT02, Q94731, Q7YT03, Q7YT04, Q7YT09, Q7YT14, Q86PT9, Q26239, Q26241, Q7YT13, Q7YT15, Q9TY55, Q94733, Q7YT12, Q7YT11, Q6PQK2, O77000, Q94734
<i>Triatoma matogrossensis</i>	68	A6YPR4, E2J702, E2J703, E2J704, E2J705, E2J706, E2J707, E2J708, E2J709, E2J710, E2J711, E2J712, E2J713, E2J715, E2J716, E2J717, E2J718, E2J720, E2J721, E2J722, E2J723, E2J724, E2J725, E2J726, E2J727, E2J728, E2J729, E2J730, E2J731, E2J732, E2J733, E2J734, E2J735, E2J736, E2J737, E2J739, E2J740, E2J741, E2J743, E2J744, E2J745, E2J746, E2J747, E2J748, E2J749, E2J750, E2J751, E2J752, E2J753, E2J754, E2J755, E2J756, E2J757, E2J758, E2J759, E2J760, E2J762, E2J763, E2J765, E2J766, E2J767, E2J768, E2J769, E2J770, E2J7H8, E2J7H9, E2J7I1, E2J701
<i>Triatoma protracta</i>	1	Q9U6R6
<i>Triatoma rubida</i>	34	G8JKC6, G8JKC7, G8JKC8, G8JKC9, G8JKD0, G8JKD1, G8JKD2, G8JKD3, G8JKD4, G8JKD5, G8JKD6, G8JKD7, G8JKE5, G8JKE6, G8JKF6, G8JKF7, G8JKF8, G8JKF9, G8JKG0, G8JKG2, G8JKG3, G8JKG4, G8JKG5, G8JKG8, G8JKG9, G8JKH3, G8JKH5, G8JKI0, G8JKI1, G8JKI2, G8JKI4, G8JKI5, G8JKI6, G8JKI8
<i>Dipetalogaster maxima</i>	33	G3CJM3, G3CJM4, G3CJM8, G3CJM9, G3CJN0, G3CJN2, G3CJN3, G3CJN4, G3CJN5, G3CJN6, G3CJN7, G3CJN8, G3CJP0, G3CJP1, G3CJP4, G3CJP5, G3CJP6, G3CJP8, G3CJP9, G3CJQ2, G3CJQ3, G3CJQ4, G3CJQ5, G3CJQ6, G3CJR4, G3CJR5, G3CJR6, G3CJR7, G3CJR8, G3CJS0, G3CJS2, G3CJS5, G8JKH9
<i>Triatoma infestans</i>	60	A6YPC8, A6YPC9, A6YPD5, A6YPD6, A6YPE4, A6YPE5, A6YPE6, A6YPE8, A6YPE9, A6YPF0, A6YPF2, A6YPF4, A6YPF6, A6YPF8, A6YPG0, A6YPG3, A6YPG6, A6YPH0, A6YPH2, A6YPH4, A6YPH5, A6YPH8, A6YPI0, A6YPI6, A6YPK7, A6YPL3, A6YPL6, A6YPL7, A6YPM0, A6YPM1, A6YPM4, A6YPN1, A6YPN2, A6YPN3, A6YPN6, A6YPN9, A6YPP0, A6YPP6, A6YPP8, A6YPQ0, A6YPQ1, A6YPR3, A6YPR5, A6YPR6, A6YPR8, A6YPR9, A6YPS0, A6YPS5, A6YPS9, A6YPT2, A6YPU1, A7BJ45, A7BJ46, Q18NS6, Q18NS7, Q45KX1, Q6UN98, Q6UN99, Q6UNA0, Q6UNA1
<i>Triatoma brasiliensis</i>	23	A0MK83, A0MK85, A0MK87, A0MK88, A0MK92, A0MK94, Q0MTC5, Q0MTC6, Q0MTC9, Q0MTD0, Q0MTD2, Q0MTD3, Q0MTD4, Q0MTD7, Q0MTD8, Q0MTD9, Q0MTE1, Q0MTE3, Q0MTE4, Q0MTE7, Q0MTE8, Q0MTE9, Q0MTF1
<i>Triatoma pallidipennis</i>	44	See Table 1
<i>Triatoma dimidiata</i>	43	D1MWA7, D1MWA8, D1MWA9, D1MWB0, D1MWB1, D1MWB2, D1MWB3, D1MWB4, D1MWB5, D1MWB6, D1MWB7, D1MWB8, D1MWB9, D1MWC0, D1MWC2, D1MWC3, D1MWC4, D1MWC6, D1MWC7, D1MWC8, D1MWC9, D1MWD0, D1MWD1, D1MWD2, D1MWD3, D1MWD4, D1MWD5, D1MWD6, D1MWD8, D1MWD9, D1MWE0, D1MWE1, D1MWE2, D1MWE3, D1MWE4, D1MWE5, D1MWE6, D1MWE7, D1MWF0, D1MWF1, D1MWF2, D1MWF4, D1MX91
<i>Blattella germanica</i>	6	A9XFW8, B7TYB1, B7TYB2, C3RWZ4, C3RWZ5, P54962
<i>Naegleria gruberi</i>	1	D2UZV1
<i>Human</i>	3	gi 313856, gi 7245434, gi 308387777

Table S3. Amino acid sequences of proteins of each representative clade.

ID	Amino Acid Sequences
<i>Nitrophorin and amine binding protein subfamily</i>	
>AAS94228.1_NP-7	--LPGECSVNVIPKKNLDKAKFFSG-TWYETHYLDMDP--QATEKFCFSFAPRES-GGTV KEALYHFNVDSKVSFYNTGTGPL---ESNGAKYTAKFNTVDKKGKEIKPADEKYSYTVTV IEAA-KQSALIHICLQEDGKDIDGLYSVLNRNKN--ALPNKKIKKALNKVSLVLTkFVVt KDL--DCKYDDKFLSSWQK-----
>Q6PQK2_Nitro	--PGECSVNVIPKKNLDKAKFFSG-TWYETHYLDMDP--QATEKFCFSFAPRES-GGTV KEALYHFNVDSKVSFYNTGTGPL---ESNGAKYTAKFNTVDKKGKEIKPADEKYSYTVTV IEAA-KQSALIHICLQEDGKDIDGLYSVLNRNKN--ALPNKKIKKALNKVSLVLTkFVVt KDL--DCKYDDKFLSSWQK-----
>Q7YT13_Nitro	---SEDCSVNIIPKQRLAKAKFFSG-TWYETHYLDTNP--EVTDKFRFSFAPRQS-GGTV KEAFYHFSSK----- ----- -----
>AAC26160.1_NP-3	----DCSTNISPKKGLDKAKYFSG-TWYVTHYLDKDP--QVTDPCSSFTPKEs-GGTV KEALYHFNSKKKTSFYNIgEGKL---GSAGVQYTAKYNTVDKKRKEIEPADPKDSYTLTV LEAD-DSSALVHICLREGPKDLGDLYTVLSHQKT--GEPsATVKNAVAQAGLKLNDfVDT KTL--SCTYDDQFTSM-----
>O77000_Nitro	---SGDCSTNISPKKGLDKAKYFSG-TWYVTHYLDKDP--QVTDPCSSFTPKEs-GGTV KEALYHFNSKKKTSFYNIgEGKL---GSAGVQYTAKYNTVDKKRKEIEPADPKDSYTLTV LEAD-DSSALVHICLREGPKDLGDLYTVLSHQKT--GEPsATVKNAVAQAGLKLNDfVDT KTL--SCTYDDQFTSM-----
>Q94733_Nitro	---SGDCSTNISPKKGLDKAKYFSG-TWYVTHYLDKDP--QVTDPCSSFTPKEs-GGTV KEALYHFNSKKKTSFYNIgEGKL---GSSGVQYTAKYNTVDKKRKEIEPADPKDSYTLTV LEAD-DSSALVHICLREGPKDLGDLYTVLSHQKT--GEPsATVKNAVAQAGLKLNDfVDT KTL--SCTYDDQFTSM-----
>Q9TY55_Nitro	---SGDCSTNISPKKGLDKAKYFSG-TWYVTHYLDKDP--QVTDPCSSFTPKEs-GGTV KEALYHFNSKKKTSFYNIgEGKL---GSPGVQYTAKYNTVDKKRKEIEPADPKDSYTLTV LEAD-DSSALVHICLREGPKDLGDLYTVLSHQKT--GEPsATVKNAVAQAGLKLNDfVDT KTL--SCTYDDQFTSM-----

>Q26241_NitroNP-2	-----DCSTNISPKQGLDKAKYFSG-KWYVTHFLDKDP--QVTDQYCSSFTPRES-DGTV KEALYHYNANKKTSFYNIGEGKL---ESSGLQYTAKYKTVDKKKAVLKEADEKNSYTLTV LEAD-DSSALVHICLREGSKDLGDLYTVLTHQKD--AEPSAKVKSAVTQAGLQLSQFVGT KDL--GCQYDDQFTSL-----
>AAB41587.1_NitroProlixin-s	-----DCSTNISPKQGLDKAKYFSG-KWYVTHFLDKDP--QVTDQYCSSFTPRES-DGTV KEALYHYNANKKTSFYNIGEGKL---ESSGLQYTAKYKTVDKKKAVLKEADEKNSYTLTV LEAD-DSSALVHICLREGSKDLGDLYTVLTHQKD--AEPSAKVKSAVTQAGLQLSQFVGT KDL--GCQYDDQFTSL-----
>Q7YT14_Nitro	---SGDCSTNISPKQGLDKAKYFSG-KWYVTHFLDKDP--QVTDQYCSSFTPRES-DGTV KEALYHYNANKKTSFYNIGEGKL---ESSGLQYTAKYKTVEKKKKK----- -----KKKNFLAPPRAPHT----- -----
>1U0X_A_NP-4	-----ACTKNAIAQTGFNKDKYFNGDVWYVTDYLDLEPD-DVPKRYCAALAAGTA-SGKL KEALYHYDPKTQDTFYDVSELQV---ESLG-KYTANFKKVDKNGNVKVAVTAGNYTFTV MYAD-DSSALIHTCLHKGNDLGDLYAVLNRNKD--AAAGDKVKSAVSAATLEFSKFIST KEN--NCAYDNDSLKSLLTK-----
>Q94734_Nitro	-----ACTKNAIAQTGFNKDKYFNGDVWYVTDYLDLEPD-DVPKRYCAALAAGTA-SGKL KEALYHYDPKTQDTFYDVSELQV---ESLG-KYTANFKKVDKNGNVKVAVTAGNYTFTV MYAD-DSSALIHTCLHKGNDLGDLYAVLNRNKD--AAAGDKVKSAVSAATLEFSKFIST KEN--NCAYDNDSLKSLLTK-----
>Q7YT15_Nitro	---SGKCTQNAIAQTGFNKDKYFNGDVWYVTDYLDLEPD-DVPKRYCAALAAGTA-SGKL KEALYHYDPVSKDTFYDVSELTQ---ESSG-KYTANFKKVDKNGNVKVDVTAGNYTFTV MYAD-DSSALIHTCLHKGNDLGDLYAVLNRNKD--AAAGDKVKSAVSAATLEFSKFIST KEN--NCAYDNDSLKSLLTK-----
>4NP1_A_NP1	-----KCTKNALAQTGFNKDKYFNGDVWYVTDYLDLEPD-DVPKRYCAALAAGTA-SGKL KEALYHYDPKTQDTFYDVSELQE---ESPG-KYTANFKKVEKNGNVKVDVTSGNYTFTV MYAD-DSSALIHTCLHKGNDLGDLYAVLNRNKD--TNAGDKVKGAVTAASLKFSDFIST KDN--KCEYDNVSLKSLLTK-----
>Q26239_Nitro	---SGKCTKNALAQTGFNKDKYFNGDVWYVTDYLDLEPD-DVPKRYCAALAAGTA-SGKL KEALYHYDPKTQDTFYDVSELQE---ESPG-KYTANFKKVEKNGNVKVDVTSGNYTFTV MYAD-DSSALIHTCLHKGNDLGDLYAVLNRNKD--TNAGDKVKGAVTAASLKFSDFIST KDN--KCEYDNVSLKSLLTK-----

>Q86PT9_NitroABP	---ASGCS-TVDTVKDFNKNDFFTG-SWYITHYKLG DSTLEVGDKNCTKFLHQKTADGKI KEVFSNYPNPAKTYSYDISFAKVSDFDGNNNGKYTAKNVIVEKDGRKIDE----RTLQVSY IDTDYSKYSVVHVC--DPAAPDYLYAVQSR TENVKEDVKS KVEAALGKVGLKLSGLFDA TTLGNKCCQYDDETLQKLLKQSFNYPEK-
>Q7YT11_Nitro	---ASGCL-TVDTVKDFNKNDFFTG-SWYITHYKLG GGT LQDIDKNCTKFLHKKTNDGKI REVFSNYPNPGGTYSYDISFASVKTFDGNNNGKYTAKNVIVNQDGTKIDD----RKLQVSY IDTDYSKYSVVYVC--DPSAPEYYLYAVQSRNENI-NGVKDKVETALGKVNLKLKDLFDA TTL-SSCKYDEDTLKKLWDRSYPEYEKE
>Q7YT12_Nitro	SGADKRCD-NPEPMTFPDVKFFKD-AWYITHYKFGADTGSNNDKYCTKILQKIE-NDNI KEVFSIDNTTTEAYSYYLSFSKSSFDTTYGKYTAKHIQVDKVGKELEE----HSITVTY LDTDYDSYSVVYVC-GEIMENLFSLYAVQSR SQTLNQDVETKVKSALNGVNLKLDKLSSI KDF--GCKYDDSTLNALLSKSFTHETK-
>E2J733_Nitro	--VNEECR-NIKTKTDFDPEKYYGR-IWYGIYILFTNVKLTSEDYACLRTKSNFLENGKV REIETVYVPKNEAYAYSESYINAVDLRGGVSKFAAIGRPIDKDG RPLLE--EFYPLQYTI VDTDYDNYAVVYMCAQIPSGQTL SIYSILNRNSGA-KDINGKVL SILDEIGVKLDDFTRI NQN--DCNDRPVVESRRLV-----
>D1MX91_Nitro	---PEECP-NIKTKTDFDPLQNF GK-TWYVTHALFTNVQLTPEDFACLNSKTNLLENGKV KEIETVYVPKNEYVFTESYLNAA DFKG GGI AKFTALSRPIDKHERPLMK--QFYPIKINI VDTDYDDYAVVYSRAHAPNGQIISIYTIANRGSGV-KRENETVSSILDEIGVKLDDFTQI NQD--KCPRLTSCWK-----
<i>Rhodnius prolixus aggregation inhibitor-1 subfamily</i>	
>Q94731	----ANPPKMPTGCKDLNSKAVKDFKYNDFFKDKWILTHAE-RVTHPDACETF--TVNGN -KITFSLG-GKEVSCTLVKVEGAK-FTKFNC-ELQ-GKKFTAY-----LSVLATDYKNY ALVYRCGSHE SPT-KDNFLVAQRRKQSTFPSALESQVSKVG FGLKKDSFKKFNC-
>AAB09090.1_RPAI-1	----ANPPKMPTGCKDLNSKAVKDFKYNDFFKDKWILTHAE-RVTHPDACETF--TVNGN -KITFSLG-GKEVSCTLVKVEGAK-FTKFNC-ELQ-GKKFTAY-----LSVLATDYKNY ALVYRCGSHE SPT-KDNFLVAQRRKQSTFPSALESQVSKVG FGLKKDSFKKFNC-
>Q7YSY9_RPAI-7	----ATVPKMPSGCADVHNKAVSDFNFDKFFKGQWHLTHAKLRVTTAKTCETF--TVNGD -ELTFTLN-QQSVSCKLEKVTGAR-FTKFNC-QMG-QAKFTSY-----VSVLATDYDNY VLVYRCGSHEGPT-KDNYLVGQRKKVQHFLPD-----
>Q7YT10	QY--GGPPKMSRGCKDIYNRGVDNLNYKQFFTQWFLTHGE---RVSSKCDTV--SVNGD -KITFKLR-GAQINCQLENV PDAK-FTKFNC-KKSVSKTFSTE-----ISVLATDNNNY ALVYRCGVLEDDNYKDNTVVMQRQKQAPFP PALESEVGKFGHGLKKDSFKVLNC-

>Q94732	AAGASATTTMPKECLELKGDIKPGFDANQFFTGDWYWTHAR-DPKHPKLCQKY--QATSD LRLKFNGNSGSDVTCQGAKVIGKEGFYSFQC-TTS-GVTFTSF-----MAVVETDYNNY ALLYRCGRYGSSAVEDNFLVFNRQSSGGIPGGLTTKLSQLD--LTPTSFTKLGCT
>Q7YT09	----AEVTSIPTGCNALSGKIMSGFDANRFFTGDWYLTHSR-DSEVPVRCEKY--QTGSN LQLNFNGKNG-DVKCSGSTVSGNQGFYSFQCTTTS-GGSFTSY-----MAVVETDYANY ALLYRCGLYGSTTPKDNFLLFNRQSSGEIPAGLSTKLNQLE--L--TSLNKLGC
>Q7YT07_RPAI-6	----KRVPTPEGCRDVYNEADPNFKLKKFFNGSWYLTHAK-HQNHSVLCTKFGMTMKPL -EIKYEMG-GVNVTCCKGKIKGTR-RTEYVC-EGN-RGTPTPYTNYGATMSVIDTDYTN ATVYVCKKNGKH--EDNVFVLSRIRTGEPPEAAKQSLQKLR-----
<i>Triafestin subfamily</i>	
>E2J7H8_triafes-2Like	---IFLGILAFVVADYPP-IEKCSHPSSMAYFNQKKFLAGKWCVTAKHGSNSTVCRQYK GKFNDEKQQFIGDGYYNFK-CQTTYFTVRCRVP--NTNVQQPLQFICTQKKP--DQKDI QFQFQLEVTVLDTDYATYAGMYRCVQLPQEL-GSMFEDNTLLIQRNANLEV DEN-KIEKA LR---LSFDSFSRNDVKGGCPELPSK-NKNKKPKT---
>E2J741_triafestinlike	-----DYPP-IEKCNHPSAMANFNQKKFLSGKWYVTKAKHGSDSTVCRQYK GKFNDEKQQFIGDGYYNFK-CQTAYFTVRCRVP--NTNVQQPLQFICTQKKP--DQKDI QFQFQLEVTVLDTDYATYAVMYRCVQFPQEL-GSMFEDNTLLIQRNANLEV DEN-KIEKA LR---LSFDSFSRNDVKGGCPELPSK-NKNKKPKT---
>E2J729_triafestinlike	-----DYPP-IEKCNHPSAMANFNQKKFLKGKWFVTAKHGSDSTVCRQYK GKFNNQKQQFIGDGYYNFK-CHTAYFTVRCRVP--NTNVQQPLQFICTQKKP--DQKDI QFQFQLEVTVLDTDYATYAVMYRCVQFPQEL-GSMFEDNTLLLQRDVNKGVDEN-KIESK LN---LSFDSFSRNDVVGCCRKLPSK-KEYIVINLVL
>E2J710_triafestinlike	-----DYPP-IAKCNHPSAMANFNQKKFLSGKWYVTKAEHGSDSTVCRQYK GKFNNQKQQFIGDGYTTFQ-NQTFYFTVRCRVP--NTDGQPPMKFICTQKNP--DIAQM TFQFQLEVTVRD TDYRTYAVMYRCVQFPQEL-GSHFEDNTLLIQRNANLEV DEN-KIEKT LS---LSFDSFSRNDVNGGCPELPSK-KKNKKPKT---
>A6YPF2_triafeslike	-----DYP- IENCTHPPAMANFNPKKFLEGKWYVTKAKHGSNSTVCREYR AKTKDKDQILVGDGYYSFN-GGTFYFTVRCKRLP--NNEVQKPLQFTCTQKSP--DVASM QFQFQLEVTILDTDYKNYAVMYRCVQFPEKL-GAHFEDNTLLLHRNPEQLVDEN-LIESK LR---MSFDSFSRREDVVDGCPKLPSK-KKNKAS----

>A7BJ46_triafestin-2	-----DYPS-IENCTHPPAMANFNQKKFLEGKWYVTKAKHGSNSTVCREYR AKTKGNDQILVGDGYYSFN-GGTFYFTVRCKRLP--NKEVQKPLQFTCTQKST--DDPSK MFKFQLEVITLTDYANYAVMYRCVQFPEQL-GSHFEDNTLLLHRNPDQLVDEN-QVERK LN---LSFDSFRSREDVVDGCPKLPK-KKNKAS-----
>A7BJ45_riafestin-1	-----DYPS-IPKCTHPPAMANFNQKKFLEGKWYVTKAKHGSNSTVCREYR AKTKGNDQILVGDGYYSFN-GGTFYFTVRCKRLP--NKEVQKPLQFTCTQKSP--DDPSK MFKFQLEVITLTDYANYAVMYRCVQFPEEL-GSHFEDNTLLLHRKLDQLVDEN-LIERK LK---LSLPSFKSRDDVVEGCRELPK-KKKTKP-----
>A6YPF6_triafes2like	-----DYPP-IEKCNHPPAMTKLNQKKFLNGTWYVTKAKHGSNSTVCRQYK AKFNDKKQQFIGDGYTTFQ-NQTAYFTVRCTRQPRNNKNTKKRMQFICTQKNP--DDERM QFRFQLEVTVLGTDYANYAVMYRCVQFPPEL-GSQFEDNTLLLHRNPEQLVDEN-QVERK LN---LSFDSFRSREDVVDGCPNLPK-KKNKAS-----
>A6YPF4_triafetinlike	-----DYPP-IEKCNHPPAMTNLNQKKFLNGTWYVTKAEHGSNSTVCRQYK AKFNDKKQQFIGDGYTTFQ-NQTAYFTVRCSRQPRNNKNTKKRMQFICTQKNP--AVESM IITFQLEVTVLTDYANYAVMYRCVQFPKQL-GSHFEDNTLLLHRNPDQLADEN-LIESK LS---MSFDSFRSREDVVDGCPKLPK-KKNKAS-----
>A6YPR8_triafestinlike	-----DYPTGLTECKHPIAMANFNPKFLHGKWFVTNAKHGSNSTVCREYK AKQNGRNQELIGDGYYSFS-GQTIYFTVRCKRLPNKKQQKQQPLKFTCTQKNP--NVKSM KILFQLEVTVLHTDYANYAIMYRCVKFPPEL-QSLIEDNTLVLQRKANKPVDEDSCHIKI LKQQDLLLESFBSRKGVK--CLKPPKK-KKN-----
>A6YPR9_triafeslike	-----DYPTGLTECKHPIAMANFNPKFLDGKWFVTNAKHGSNSTVCREYK AKSKGNNQELIGDGYYSFS-DQTVYFTVRCKRLPKEKKQKQQPLKFTCTQKNP--TDKKL KIPFQLEVTVLHTDYADYAIMYRCVKFPPEL-KSLIEDNTLVLQRKANKPVEKDSCVDKI LKKQGLSLESFBSRKGVV--CTPPPKK-KKV-----
>E2J709_triafestinlike	-----QYEK-IPNCNPPEATKNLDTESFLGKGYVTNAKQGSNSTVCREYR TKNKDGKQVLVGDGYTTFN-GQKPYFKVRCKRQS---PT--ELSYTCTQTMP--GNKEL KNQFQLQLTILHTDYTNSAVMYRCVQFPPEL-GSHFEDNILVLRDPSITNDNDNAVRNA LKSQGLQLNSLKSREGVV--CPEPPPK-IKE-----
>E2J753_triafeslike	-----EYAQ-IPNCTPPEAMANLDTARFLEGKWYVTNAKQGSNSTVCREYR TKTN--KEVLVGDGYTFM-NQRLYFKVRCKKQS---QT--ELSYTCKQTMP--DNSEM KNQFQLQLTILHTDYTNSAVMYRCVQFPPEL-GSNFEDNILVLRDPSITNDNDNAVRNA LKSQGLQLNSLKSREGVV--CPEPPPKRIKI-----

>E2J717_triafeslike	-----EYAQ-IPNCTPPEAMANLDTARFLEGKWYVTNAKQGSNSTVCREYR TKTN--KEVLVG DGYYTFM-NQKLYFKVRCCKQS---QT--ELSYTCKQTMP--DNSEM KNQFQLQLTILHTDYTNSAVMYRCVQFPPEL-GSNFEDNILVLHRDPSITNDNDNAVRNA LKSQGLQLNSLKSREGVV--CPEPPPKRIKI-----
>D1MWC9	-----DYPK-LDNCNPPEAMKGLDSGKFLKGTWYVTNAQCGSNSTVCREYK GKRENGNSVLNGNGYYSG-SQKVYFEVRCNKQS---NSNYKLTFDCTQKGP--AGSGK NFQLQLEVTVLTYDSDLAIMYRCVKFPPQL-GSLIEGNVLVLRRDASKTNDKNPKIEET LKKQGWSLDTFNSREGVT--CPEPPQK-----
>D1MWD0	-----DYPK-LEKCNPPEAMEGLDSGKFLKGTWYVTNAQYGSNSTVCREYK GKRENGNPVLNGDGYYSFG-SQKFYFEVSCKKQS---NRNYKLTFGCTQNGP--KDSGM NFQLQLEVTVLTYDSDLAIMYRCVKFPREL-GSLIEGNVLVLRRDASKTNDKNPKIEET LKKQGWSLNTFNSREGVT--CPEPPQK-----
>27479c2s12	-----WYVTNAKHGSNSTVCREYN GKRENGNPVLNGDGYYSHG-NLKIYFEVRCDKQS---DTNYKLTFSCCTQKGP--AGTNM NFQFQLEVTVLSTDYDDFAIMYRCVKFPPQL-GSRIEDNVLVLHRKDCKTEDKD-RVEET LKKNGWSLDSFKSRKGVN--CPEPPQK-----
>27479c2s8.5	-----WYVTNAKHGSNSTVCREYN GKRENGNPVLNGDGYYSFR-NLKIYFEVRCDKQS---DTNYKLTFSCCTQKGP--AGTNM NFQFQLEVTVLSTDYDDFAIMYRCVKFPPQL-GSRIEDNVLVLHRDATKTNDKNPQIEDI LKKQDWSLDTFNSRDGVE--CPLPPQK-----
>27479c2s9.5	-----WYVTNAKHGSNSTVCREYK GKRENGNPVLNGDGYYSVG-SQKIYFEVRCDKQS---DKNYKLTFSCCTQKGP--AGSKM NFQFQLEVTVLSTDYDDFAIMYRCVKFPPQL-GSRIEDNVLVLRRNPNTDNKNP-LIETT LKSQDLSLDTFKSRKGVN--CPKLPQK-----
>27479c2s11.5	-----WYVTNAKHGSNSTVCREYK GKRQNGIRQLIADGYYSYGQDQTAYFNVLCHKQS---DRNYKLTFNCTQRGSITDDQKV IIQFQLEITVLLTDYDDFAIMYRCVKFPPQL-GSRIEDNVLVLRRNPNTDNKNP-LIETT LKSQDLSLDTFKSRKGVN--CPKLPQK-----
>27479c2s14	-----WYVTNAKHGSNSTVCREYK GKRQNGIRQLIADGYYSYGQDQTAYFNVLCHKQS---DRNYKLTFNCTQRGSITDDQKV IIQFQLEITVLLTDYDDFAILYRCGKIPSSS-GSRIEDNVLVLHRKDCKTEDKD-RVEET LKKNGWSLDSFKSRKGVN--CPEPPQK-----

>G8JXH9_triafestinlike	RGSKFFGIVTFAFADYTK-IQNCEQPEAMQNFDANKFLKGTWYVTNAKQGSESTVCREYK AGME--MTNL TETDTTAFK-VKKT YFQVSCKKKS---ENKGKLT FQCTQRGTV-SGQMM SIQFDLDVTIVSTDYNSYAVMYRCAKFPKEL-QSRIEDNV LILRRDAKQTEIEQ-SIKTT LQNQGWPSPDKFISRKHGT--CPTPPQK-----
>G8JKI0_Triafestin2Like	-----GGDGYYSFQ-GQKTYFQVSCKKKS---ENNGKLT FQCTQSGTV-SGNEM NFQFQLEVTIVSTDYNNYAVTYRCVKLPTEL-GGGYEDNV LILRRNAKQTEIEQ-SIKTT LQNQRWPSPDKFISRKDGT--CQKPPQK-----
>G8JKI1	-----RGKKKS---ESNGKLT FQCTQSGTI-SGKTM SIQFDLDVTIVSTDYNSYAVMYRCVKFPEEL-GSRIEDNV LILRRDAKQTEVE--SIKAT VKNQEWTLDFISRKDDT--CSKLSQK-----
>G8JKD7_Triafestinlike	-----DYTK-IQNCEQPEAMQNFDANKFLKGTWYVTNAKQGSESTVCREYK AGNE--NGELNGDGYYNFK-GQKTYFQVSCKKTS---ENKGKMT FQCTQRGTV-SGNEM NFQFQLEVTIVSTDYNSYAVMYRCVKLPTEL-GGGYEDNV LILRRDAKQTEVE--SIKAT VKNQEWTLDFISRKDDT--CSKLSQK-----
>G8JKI2_triafestinLike	-----TAGATDLTVCREYK ASQN-ENGELIGDGYYNFN-GQKTYFEVRCKKKS---ESNGKLT FQCTQSGTI-SGQKM SIQFDLDVTIVSTDYNNYAIMYRCVKLPTEG-GGGYEDNV LVLHRDSSKTDDNV-NVEQT LKSKGWQFSSFISRKGRN--CQ-----
>G3CJN2_triafestinlike	-----INNNSLSRP-GQPSYFQVRCKDPS---NNNGKLT FSCCKQSGTV-GSKKM DIPFQLEVTILSTDYNDFAVMYRCAKLPSSTGGTHFEDNV LVLHRVSTKTEDKR-NVGET LKKQGWSLDDFNSRKGVD--CPAPP-----
<i>Triatin subfamily</i>	
>E2J756	SEEIQPKQKL VYGQDKCQGYGGMKDLDTEKFFKGNWSLIYSTPSPRLSHSNMCRDYKIT PYKNDTVEVTY EYDENRCGNHYVAKCYGNQNSTRIDQFDFDCYLNHNEREELTSTHVNAYF LATDYDSYSVAYRCVQNE DHF-EDNVFILFRPGKTDEDYTKTIAEHYGLTMGDFLARKDA TC---
>E2J758_triatinlike	SEEIQPKQKL VYGQDKCQGYGGMKDLDTEKFFKGNWSLIYSTPSPRLSHSNMCRDYKIT PYKNDTVEVTY EYDENRCGNHYVAKCYGNQNSTRIDQFDFDCYLNHNEREELTSTHVNAYF LATDYDSYSVAYRCVQNE DHF-E-----GKTDEDYAKTIAEHYGLTMGDFLARKDA TC---

>E2J757_triadinlike	SEEIQQPKQKL VYGQDKCQGYGGMKDLDT EKFFQGNWSLIYSTRSPRLSHSNMCRDYKIT PFGNGTVEVTY EYDENRCGNHYVAKCYGNQNSTRIDQFDFDCYLHNEREELTSTHVNAYF LATDYDSYSVAYRCVQNE DHF-EDNVFILFRPGKTDE DYAKTIAEHYGLTMSDFLARKDA TC---
>A6YPQ0_triadinlike	SEEITQTKQKL VYGQNKCCQGYGGMINLDPKRFFKGNWSLIYSTPSSRLSHSNMCRDYKIT PYENRTVEVTY EYDENRCGNHYVAKCYGNQNSTREDQFDFDCYLHNEREELTSTHVNAYF LATDYDNFSVAYRCVQSK DHF-EDNIFILFRPKTDE DYANTIAEHYGLTMDDFLARKDA PC---
>A6YPQ1_triadinlike	SEEITQTKQKL VYGQNKCCQGYGGMINLDPKRFFKGNWSLIYSTPSSRLSHSNMCRDYKIT PYQNGTVEVTY EYDENRCGNHYVAKCYGNQNSTREDQFDFDCYLHNEREELTSTHVNAYF LATDYDNFSVAYRCVQSK DHF-EDNIFILFRPKTNE DYAKTIAEHYGLTMCDFLARKDA TC---
>E2J720_triadin	----SEQKQKLEYGQG SCKRYGGIADFDPKKFFSGNWSLTHATRSTRVTDSTVCRDYDLK MHDNGTIEAMYGY NENRCGNPYDVHCYGTQNSSRKDEFNFDCHLHNDREEKMDTHIDAYF LATDYDTYCVVYRCVTTTEYF-EDNLFILFRPGKTDE SYAKILVENYGLTMNDILARKDA TCAKS
>E2J7I1_triadinLike	-----KKFFSGNWSLTHATRSTRVTDSTVCRDYDLK MHDNGTIEAMYGY NENRCGNPYDVHCYGTQNSSRKDEFNFDCHLHNDREEKMDTHIDAYF LATDYDTFCVVYRCVTTKEYF-EDNLFILFRPNKTDE DYAKVLVENYGLTMDDILARKDA TCAKS
>A6YPP0_triadinlike	----SEEKQRIQYQGNNCQGYRSMQNFTQTQFFQGIWSLTHSTPSTRVTASTICRDYEVT VHQNGTIQVTYGY NENECGNHYDVHCNGTENS DTKGVFNFDC HLYNGMEESQNT HIDVAF LATDYET YCVVYRCVKIDENFVEDNVFILYRPDKTNE DYAKTLAEHYGLSIDD FISRKNA SCTTR
>A6YPN9_triadinlike	----SEEKQKIQYQSN CQGYRSMQNFTQTQFFQGKWSLTHSTPSTRVTASTICRDYEVT VHQNGTIQVTYGY NENECGNHYDVHCNGTENS DTKGVFNFDC HLYNGMEESQNT HIDVAF LATDYDNYC VVYRCVKIDENFVEDNVFILYRPDKTNE DYAKTLAEHYGLTIDN FISRKNA SCTSR
>E2J768_triadinlike	----SVEKPKIQYKQGYCQGYRSFNDFDPKRFFKGNWSLTHSTPSNRVTASTICRDYELK EHENGTIQATYGY NENECGNRYDVHCNGTENS KLLGEFNFDCHLYNGEEES-KTHIDAAF IATDYEKYCVVYRCVTIDGQFAEDNIFILFRPKTDE ELAKKIAEHYGLTIDDFISRKNA TCTNK

	<i>Dipetalodipin and pallidipin</i>
>G3CJP9_pallidipin2	RAINAAILLGILMHAFSEECTLKSPAENFDADKYFDVPHVYVTHSKSGPKEKVCREYNTT KNSDKTTSTTVVTL--KTGGT-QSIILSCTNTPKTGKNGQYSMDCKAPNSKDG--KNIQL ESSIIATDNQNYALIHFCPETPSGTITEDILVVQTNKDGVNEGVTSAIKNYGWSIENWIS RKDAGCQ----
>G3CJM8_PallidipinLike	-----NGPKEKVCREYNTT KNSDKTTSTTVVTL--KTGGT-QSIILSCTNTPKTGKNGQYSMDCKAPNSKDG--KNIQL ESSIIATDNQNYALIHFCPETPSGTITEDILVVQTNKDGVNEGVTSAIKNYGWSIENWIS RKDAGCQ----
>G3CJP8_pallidipin2	-----KEKVCREYNTT RNSNKTSTTVVTL--KTGGT-QSIILSCTNTPKTGKNGRYSMDCKAPNSKDG--KNIQL ESSIIATDNQNYALIHFCPETPSGTITEDILVVQTNKDGVNEGVTSAIKNYGWSIENWIS RKDAGCQ----
>G3CJM9_pallidipin2	-----ERVCREYNTT KNSGGPTSTTKVIS--KTGGT-QSIILSCTNTPKTGKNGQYSMDCKAPNSKDG--KNIQL ESSIIATDNQNYALIHFCPETPSGTITEDILVVQTNKDGVNEGVTSAIKNYGWSIENWIS RKDAGCQ----
>G3CJN5	-----GQRKKXCREYNTT KNSDKTTSTTKVTS--KTGGT-QSIVLSCNNSPKSGVKQYFMDQCQVPGGTGG--NNIQL ESSIIATDNKNYALVHFCPITGRGVVTE DIVVLQTNKDNVDPGVTSAFRTNGWSLQEWTS RKDVTCK----
>G3CJS0_dipetalodipin	-----KECTLMAAASNFNNSDKYFDVPHVYVTHSKNGPKEKVCREYNTT KNSDKTTSTTVVTL--KTGGT-QSIVLSCNNSPKSGVKQYFMDQCQVPGGTGG--INIQL ESSIIATDNKNYALVHFCPITGRG-VTEDIVVLQTNKDNVDPGVTSAIKNYGWSLENWKS RKDAGCQ----
>G3CJP1_pallidipin2	-----HSRNGTNEEVCREYNTT KNSDKTTSTTVVTL--KTGG--QGQKLSCNTNPKTGSAGQFSVECQGDG-----TNIQL ETSVIATDYQKYALLQTCLKSGSGAITDDILVLQTKKDGVDPGVTSVFTTNRWSIETWHS RAKANCD----
>D1MWE1_pallidipin2like	-----KECELMPPAENFSDKYFNIPHVYVTYSKNGPQEKVCREYKTT KNSDGTNTTEVIV---KTGGQQQKTVLCTCTNKEKNGKPGQYSVECEVPNG----NHKIQL ETSVFATDNKNYALLQSCNKDGKS--DYDIFVLQTNKDVVDPGVTSAFNLAKWSLKDWS RSNVDCNNIQN

>D1MWE0_pallidipinLike	-----ECELMPPASNFD SKKYFNIPHVYVTHSKNGPDKKVCREYKTT KNSNGTTNTEVTV---KTGGK-EQTLLKCINKEKNGKAGQYSVECEVPNG---NHKIQL ETSVFATDNKNYALLQSCNKGKN--DFDIFVLQTNKDG-DPGVTA VFDLTKWPLDKWVS RSNVNC-----
>27479c2s4_pallidipinlike	-----KECELMPPASNFDSEKYFDIPHVYVTHSRNGPKENVCREYKTT KSTGGLTLTDVIV---NTGGK-QRTVLNCINTVKNIPGHYFLECEAPNGD---NQKIQL E----- -----
>27479c2s13_pallidipinlike	-----KECELMPPASNFDSEKYFDIPHVYVTHSRNGPKENVCREYKTT KNTDGTTHTEVIV---KTGGK-QRTVLNCINTQKNGKPGQYSVECEVPNGNGG-NQKIQL ETSVFATDNEKYALLQSCNKDGES--EDDIFVLQTNKDPVEQGVTSVLKSVNWSLNDWFS RSKVNCDNMK-
>27479c2s3_pallidipinlike	-----EECELTPPEDNFDLEKYFSIPHVYVTHSRNGPKQVCREYKTT KNSDGT TTTTLVTSDYKTGGKPYHSQKCTNTPKNGGKGQFSVECEVPNGNGG-KKKIHV ETSVIATDYKNYALLQSCTKTESG-IADDVLLLQTKKEGVDPGVT SVLKSVNWSLDKWIS RTEVNCDNIQN
>Q27042_pallidipin	-----EECELMPPGDNFDLEKYFSIPHVYVTHSRNGPKQVCREYKTT KNSDG-TTTTLVTSDYKTGGKPYHSELKCTNTPKSGVKGQFSVECEVPNGNGG-KKKIHV ETSVIATDYKNYALLQSCTKTESG-IADDVLLLQTKKEGVDPGVT SVLKSVNWSLDDWFS RSKVNCDNMK-
>27479c2s7_pallidipinlike	-----KECELMPPASNFDSEKYFDIPHVYVTHSRNGPKQVCREYNTT KIQGD TTPYTVVTSDYKIRGETHHSQKCTNTPKNGGKGQFSVECEISNGNGGNKKKVQF ETSVFATDYKNYALLQSCTKTESG-IADDVLLLQTKKEGVDPGVT SVLKSVNWSLDDWFS RSKVNCDNMK-
>27479c2s6_pallidipinlike	-----KECQLMPATDDYNADQYFSIPRVYAIYSKNGPEENVCREYETK KKT DGTIVTTVSGD-KKNRGQ-QQTVLACTNREKSGSKGQFFVECEVPGKNGG-NMKIQV ETSVLATDN----- -----
>G8JKI8_pallidipin2Like	-----P-----GVPQVYMTLSKNGPKEKLCREYKTT ESS--TTVNNLVIL--EKRGN-EQTQLNCIETLKSDRKGQFSVECELPNGSG---KKVQF ESSVIATDNKNYAILQTCPKTESSIVTEDIVVLQTN EEGVEEGVTNYFTSQGWSLDTWHS RKKVKC-----

	<i>Triplatin and infestilin subfamily</i>
>A6YPE4_triplatinlike	----ETCTLIDAA-PNFDADKYFKISHAYATYSQNREPETTVCREYSTT-TRDGKIITTF TID--DRTLRT--NVECTNTPI-TGKNGQFTSNCRLSAGNTITVTSSILATDNKSYAILQ RC-----SQNGPGNILVLQTNKDGGVPQGVTDYFKGKGWDINKWISRKEANCR----
>Q6UN99_triplatinlike	----ETCTLIDAA-PNFDADKYFKISHAYATHSQNREPETTVCREYSTT-TRGGKIITTF TIN--DRTLRT--DVECTNTPI-TGKKGQFTSNCRLSAGNTITVTSSILATDNKSYAILQ RC-----SQNGPGNILVLQTNKDGGVPKGVTDYFKGKGWDINKWISRKEANCR----
>Q18NS6_triplatin-2	EVNSETCTLMEEA-KNFDENKYFNIPLAYATHSKNREPETNVCREYSTARGPDGKTVTTF TIK--DKTLTS--AVKCTNTPI-PGSNGQFSSDCELSAGNRITVTSSILATDNEKYAILQ RC-----PTSGPGNILVLQTNKNGVEQ-GVQNYFNQKGWDISTWLSRTTVGC-----
>A6YPH4_triplatinlike	----EECVLKPGA-SNFDSKKYFDIPLAYVTHSQN-DPETNVCRDYQSSRRADGKPVTSF TIT--DRSYPTGAKVTCVNNI-KGEKGHFTSVCELPAGNKYEKSSILATDNESYAVLQ RC-----GTSGPGNILVLQTKKNGVNP-AVTKYLNANGWDITKWISRQTVRC-----
>Q45KX1_infestilin	EVNSETCTLMEEA-KNFDENKYFSIPLAYATHSQNREPETTVCRDYRTT-KTDGKIVTTF TIN--DKIAPKDTQVSCINTPT---SKGQFSSECTLPAGTKIKVTTSILATDNANYAVFR D-----ALRVDQ-----VIFWYYRKIKMAP----
>Q18NS7Triplatin-1	----EECRLMQPA-ANFDAATYFSIPHVYVTHSKN-EPKTDVCREYDTSKT-DGGSTTVI TSNYKIKGQAVNNKVTCTSTGLKNGQTGQFSVVCQPPTGAAVTLTTSVLATDNQNYAILQ RC-----PTSGQGNILVLQTAKEGVNP-GVKDFFQKKGWNIDSWFSRTNVNCENIQS
>A6YPS0_pallidipinlike	----QECQLMQPA-ANFDAPTYFSIPHVYVTHSKN-EPKTDVCREYDTSKT-DGGSTTVI TSYYKIKGQAVNNKVTCTSTGLKNGQTGQFSVVCQPPTGTAVTLTTSVLATDNQNYAILQ RC-----PTSGQGNILVLQTTKEGVNT-RVTDFFKKQSWNIHSWISRTKVNENIES
>Q6UNA0_pallidipinlike	----EECRLMQPA-ANFDAATYFS-PHVWVTHSKN-EPKTDVCREYDTSKNGDGSTTTVI TSNYISRGVAVNNKVTCTSTGL-SGQKGQFSVVCQPPTGTAITLTTSVLATDNQNYAILQ RC-----PKSGQGNILVLQTTESGVNP-GVKRYFDDNGWSIGSWFSRTNVNCKNIEN
>E2J754_pallidipinlike	----ENCCLKQPV-ANFDSEKYFSISRSFVTYSKN--DQKPVCREYLTRNTDGTTKTVY TIR--DRTAPSDVEVNCINKPK-SGSNGQFSVSCTLPAGNTFQLTTSVVDTDYNKYVILQ SC-----PDSGPGDILVFQTDKNEIP-AVTNYIAQQG---GQWYSRINDRC-----
>Q0MTD7_pallidipin2like	----EDCVLKPTCRQTFNSEQYFAIRHSYVTYSKN-GPETKVCREYVTTKNTNGTTTTVY TIK--DQTNPSGSNATCINTPK-TGSNGQFSVTCTLSAGNEFQLTTSVVDTDHKTIVILQ VCLNSGPGITDSGPGDILVLQTDKNVEIP-AVTKYIQGNT---GQWYSRKNSRC-----

	<i>Dimiconin and triabin subfamily</i>
>E2J756	SEEIQQPKQKL VYGQDKCQGYGGMKDLDTEKFFKGNWSLIYSTPSPRLSHSNMCRDYKIT PYKNDTVEVTY EYDENRCGNHYVAKCYGNQNSTRIDQFDFDCYLHNEREELTSTHVNAYF LATDYDSYSVAYRCVQNE DHF-EDNVFILFRPGKTDEDYTKTIAEHYGLTMGDFLARKDA TC---
>E2J758_triadinlike	SEEIQQPKQKL VYGQDKCQGYGGMKDLDTEKFFKGNWSLIYSTPSPRLSHSNMCRDYKIT PYKNDTVEVTY EYDENRCGNHYVAKCYGNQNSTRIDQFDFDCYLHNEREELTSTHVNAYF LATDYDSYSVAYRCVQNE DHF-E-----GKTDEDYAKTIAEHYGLTMGDFLARKDA TC---
>E2J757_triadinlike	SEEIQQPKQKL VYGQDKCQGYGGMKDLDTEKFFQGNWSLIYSTRSPRLSHSNMCRDYKIT PFGNGTVEVTY EYDENRCGNHYVAKCYGNQNSTRIDQFDFDCYLHNEREELTSTHVNAYF LATDYDSYSVAYRCVQNE DHF-EDNVFILFRPGKTDEDYAKTIAEHYGLTMSDFLARKDA TC---
>A6YPQ0_triadinlike	SEEIQTQKQKL VYGQNKCCQGYGGMINLDPKRFFKGNWSLIYSTPSSRLSHSNMCRDYKIT PYENRTVEVTY EYDENRCGNHYVAKCYGNQNSTRIDQFDFDCYLHNEREELTSTHVNAYF LATDYDNFSVAYRCVQSK DHF-EDNIFILFRPKTDEDYANTIAEHYGLTMDDFLARKDA PC---
>A6YPQ1_triadinlike	SEEIQTQKQKL VYGQNKCCQGYGGMINLDPKRFFKGNWSLIYSTPSSRLSHSNMCRDYKIT PYQNGTVEVTY EYDENRCGNHYVAKCYGNQNSTRIDQFDFDCYLHNEREELTSTHVNAYF LATDYDNFSVAYRCVQSK DHF-EDNIFILFRPKTNEDYAKTIAEHYGLTMCDFLARKDA TC---
>E2J720_triadin	---SEQKQKLEYGQG SCKRYGGIADFDPKKFFSGNWSLTHATRSTRVTDSTVCRDYDLK MHDNGTIEAMYGYNENRCGNPYDVH CYGTQNSSRKDEFNFDCHLHNDREEKMDTHIDAYF LATDYDTYCVVYRCVTTTEYF-EDNLFILFRPGKTDESYAKILVENYGLTMNDILARKDA TCAKS
>E2J7I1_TriadinLike	-----KKFFSGNWSLTHATRSTRVTDSTVCRDYDLK MHDNGTIEAMYGYNENRCGNPYDVH CYGTQNSSRKDEFNFDCHLHNDREEKMDTHIDAYF LATDYDTFCVVYRCVTTKEYF-EDNLFILFRPNKTDEDYAKVLVENYGLTMDDILARKDA TCAKS
>A6YPP0_triadinlike	---SEEKQRIQYGQNNCQGYRSMQNFTQTQFFQGIWSLTHSTPSTRVTASTICRDYEV VHQNGTIQVTYGYNENECGNHYDVHCNGTENS DTKG VFNFDCHLYNGMEESQNT HIDVAF LATDYET YCVVYRCVKIDENFVEDNVFILYRPDKTNEDYAKTLAEHYGLSIDD FISRKNA SCTTR

>A6YPN9_triatinlike	----SEEKQKIQYQGSNCQGYRSMQNFTQTQFFQGWSLTHSTPSTRVTASTICRDYEVT VHQNGTIQVTYGYNENECGNHYDVHCNGTENS DTKGVFNF DCHLYNGMEESQNT HIDVAF LATDYDNYCVVYRCVKIDENFVEDNVFILYRPGKTNEDYAKTLAEHYGLTIDNFISRKNA SCTSR
>E2J768_triatinlike	---SVEKPKIQYKQGYCQGYRSFNDFDPKRFFKGNWSLTHSTPSNRVTASTICRDYELK EHENGTIQATYGYNENECGNRYDVHCNGTENS KLLGEFNFDCHLYNGEEES-KTHIDAAF IATDYEKYCVVYRCVTIDGQFAEDNIFILFRPKTDEELAKKIAEHYGLTIDDFISRKNA TCTNK
	<i>Procalin subfamily</i>
>G3CJS2	V-TGSECNMPSPMAGFEKSKFFTGMWYVTHETNVTTPSECNTLTTRLENNKVFEHKYVK DGKTGTLVCEGQEDGQNMFPLNCKFNGVTMEEVTRIVMDTDYNDYALYYLCTAYKSGVNT GKKA EHYIISRREP KDDIPEKLRQAATLQLQKCGKVAS
>G3CJR6_Procalinlike	QNVQNGCKMPTPMANLDATKFFQGTWHVTHETNVTIPSECNTLTTSKKGDKVVVEHKYTK DGKEGR LICEGQEDGQNMFPLNCKFEGETLEEVT RIVMNTDYNDYALYYLCTTYKSGVNA GKKA EHYIISRRDPNKEIPDHLQSKVKELNLQKCGQNTG
>Q9U6R6_procalinTriatoma protracta	----DECENPEPMQGFSA SQFYQGXWYVTHETSAXTLSECNILTTSNDNGKFTVKHKYTK DGXVGELICEGQASANNKFTYDCKFXGZTMEQVTRTAMDTDYNDYALYYLCTTYKXGPNA GKKEGHYILSRRQPNT EIPDALKTKTKDLNLKLCG----
	Proteins without biological function
	<i>T. matogrossensis</i>
>E2J750	-----ATTGISECKTVTPMDRFSATRFFQRTWYVSHVQKKSNTVCQTFKTSSPSDG VYAI EYTF----GDNNVRCEATREKEKKLTFTCKNGDTTIFTALFVIMDTDYENYALFYR CVTM-TGGYKDDNYLVLSSTSGDQQIPTSLTSLTSSLNLLWCKDIRASVV
>E2J746	-----ATTGISECKTVTPMDRFSATRFFQRTWYVSHVQKKSNTVCQTFKTSSPSDG VYVIEYTF----GDNNVRCEATREKEKKLTFTCKNGDTTIFTALFVIMDTDYENYALFYR CVTM-TGGYKDDNYLVLSSTSGDQQIPTSLTSLTSSLNLLWCKDIRASVV
>E2J751	-----ATTGISECKTVTPMDRFSATRFFQRTWYASHVQKKSNTVCQTFKTSSPSDG VYVIEYTF----GDNNVRCEATREKEKKLTFTCKNGDTTIFTALFVIMDTDYENYALFYR CVTM-TGGYKDDNYLVLSSTSGDQQIPTSLTSLTSSLNLLWCKDIRASVV
>E2J752	-----ATTGISECQSVTPMENFSATKFFQRTWYVSHVQKKSNTVCQTFKTSSPSDG VYVIEYTF----GDNNVRCEATREKEKKLTFTCKNGDTTIFTALFVIMDTDYENYALFYR CVTM-TGGYKDDNYLVLSSTSGDQQIPTSLTSLTSSLNLLWCKDIRASVV

>E2J7H9	GILTYAYGATSGISECKTATPMDRFTATRFFPRTWYVSHVQKKSNTVCQTFKTSSPSDG VYVIEYTF----GDNNVRCETTREKEKKLTFTCKNGDTTIFTALFVIMDTDYENYALFYR CVTM-TGGYKDDNYLVLSSTSGDQQIPTSLTSLTSSLNLLWCKDIRASVV
>E2J749	-----ATTGISECKTVTPMDRFSATRFFQRTWYVSHVQKKSNTVCQTFKTSSPSDG VYVIEYTF----GDNNVRCETTREKEKKLTFTCKNGDTTIFTALFVIMDTDYENYALFYR CVTM-TGGYKDDNYLVLSSTSGDQAIPASLTSLTSSLGLKSCEEIKTMVY
>E2J747	-----ATTGISECKTVTPMDGFSATRFFTRTWYVTHVQKKSNTVCQFTASKPSNT TYAVDYTFTGDNGENNVHCVATRTEKKLTFNCKNGDTPIFDAVFVIMATDYNMYALFYR CVTMKSSRVKDDNFLVLSSTSGDQAIPASLTSLTSSLGLKSCEEIKTMVY
>E2J716	-----ATTGISECKTVTPMDGFSATRFFTRTWYVTHVQKKSNTVCQFTASKPSNT TYAVDYTFTGDNGENNVHCVATRTEKKLTFNCKNGDTPIFDAVFVIMATDYNMYALFYR CVTMKSSGVKDDNFLVLSSTSGDQAIPASLTSLTSSLGLKSCEEIKTMVY
>E2J748	-----ATTVISECKTVTPMDGFSATRFFTRTWYATHVQKKSNTVCQFTASKPSNT TYAVDYTFTGDNGENNVHCVATRTEKKLTFNCKNGDTPIFDAVFVIMATDYNMYALFYR CVTMKSSGVKDDNFLVLSSTSGDQAIPASLTSLTSSLGLKSCEEIKTMVY
>E2J711	-----ATTGISECKTVTPMDRFSATRFFTGTWYVTHVQKQTSQTVQCQFTASKPSNT TYAVDYTFTGDNGENNVHCEATRTEKKLTFNCKNGDTPIFTAVFVVMATDYTDYALFYR CVTM-TSGYKDDNYLVLSRTSGNQEIPTSLTSLTSDLNLLSCADISTPVV
>E2J760	-----DSSGISQCKTVEAKTDFRATNFFTGTWYVTHVQKKSNTVCQFTASKISNT TYVVEYTFDNNQNNIRCEAERGEHQMTFTCKNGGNTIFTAVFVVMATDYTDYALFYR CVTMTSTGNKDDNYLVLSRTNGDQAIPASLTDLTSSLNLRSCADLRTRVV
>E2J726	-----TSSGISECKTVDAKTDFSGTQFFTGTWYVTHVQKKSNTVCQTFASKPSNT TYVVDYTFDNDNGKNNIRCEAERGEHQMTFICKNGDTPIFTAIFVVMATDYTDYALFYR CVTMLSTGNKDDNYLVLSRKSGNEALPTSLTSLTSDLNLLSCQTI-----
<i>T. rubida</i>	
>G8JKC7	E---MVTVAECGGAQVNAMEADNYRAPDYHKEKWYVTHVTKVTEPTECRTLTATTKSDGKTF TVEHPFGDGGSQTLHCEAQAEAAKRLTFTCKVGDQVVDKTIFITVDTDYNDYSLYYLCIA PTGGTPHDTYLIARRKAG-DNIPPQLESFTQGMDFKK-----C-----
>G8JKC9	E---MVTVAECGGAQVNAMEADNYRAPDYHKEKWYVTHVTKVTEPTECRTLTATTKSDGKTF TVEHPFGDGGSQTLHCEAQAEAAKRLTFTCKVGDQVVDKTIFITVDTDYNDYSLYYLCIA PTGGTPHDTYLIARRKAG-DNIPPQLESFTQGMFEKK-----C-----

>G8JKD2	E---MVTVAECGGAQVNAMDNYRAPDYHKEKWYVTHVTKVTEPTECRTLTATTKSDGKTF TVEHPFGDGGSQLHCEAQAEAAKRLTFTCKVGDQVVDKTIFITVDTDYNDYSLYYLCIA PTGGTPHDTYLIARRKAG-DNIPPQLESFTQGMDFFKMLVILQNECPKTFVV
>G8JKE5	E---MVTVAECGGAQVNAMDNYRAPDYHKEKWYVTHVTKVTEPTECRTLTATTKSDGKTF TVEHPFGEGGSQTLHCEAQAEAAKRLTFTCKVGDQVVDKTIFITVNTDYNDYALYYLCTA PTGGTPHDTYLIARRKPG-DNIPPQLESFTQGMFEFK-----C-----
>G8JKD0	E---MVTVAECGGAQVNAMDNYHASDFHKEKWYVTHVTKVTEPTECRTVTATTKSDGKTF TVEHPFGEGGSQTLHCEAQAEAAKRLTFTCKVGDQVVDKTIFITVNTDYNDYALYYLCTA PTGGTPHDTYLIARRKAG-DNIPPQLESFTQGMDFFK-----C-----
>G8JKC6	E---MVTVAECGGAQVNAMDNYHASDFHKEKWYVTHVTKVTEPTECRTVTATTKSDGKTF TVEHPFGEGGSQTLHCEAQAEAAKRLTFTCKVGDQVVDKTIFITVNTDYNDYALYYLCTA PTGGTPHDTYLIARRKPG-DNIPPQLESFTQGMFEFK-----C-----
>G8JKG0	G-----AECGGAQVNAMDNYHASDFHKEKWYVTHVTKVTEPTECRTVTATTKSDGKTF TVEHPFGEGGSQTLHCEAQAEAAKRLTFTCKVGDQVVDKTIFITVNTDYNDYALYYLCTA PTGGTPHDTYLIARRKPG-DNIPPQLESLEGMDFKK-----C-----
>G8JKC8	E---MVTVAECGGAQVNAMDNYRAPDYHKEKWYVTHVTKVTEPTECRTLTATTKSDGKTF TVEHPFGDGGSQLHCEAQAEAAKRLTFTCKVGDQVVDKTIFITVNTDYNDYSLYYLCIA PTGGTPHDTYLIARRKPGDDNIPPQLESLEGMDFKK-----C-----
>G8JKD3	E---MVTVAECGGAQVNAMDNYRAPDYHKEKWYVTHVTKVTEPTECRTLTATTKSDGKTF TVEHPFGDGGSQLHCEAQAEAAKRLTFTCKVGDQVVDKTIFITVDTDYNDYSLYYLCIA PTGGTPHDTYLIARRKPD-DNIPATLKELTSKGDFKK-----CSDLTK-
>G8JKF7	-----KVNAMDNYHAPDFHKDKWYVTHVSKVTDPTTECRTLTATNSADGKTF TVENSVGEEEGQKSTCVGHHEEAANKLSFTCKVGNQVVAKSILITVATDYKDYALIYICST PTGRSPMNPYLIARRKPD-DNIPEALKELTKGKDFKK-----CSDLTK-
>G8JKF6	-----KVNAMDNYHAPDFHKDKWYVTHVSKVTDPTTECRTLTATNSADGKTF TVENSVGEEESQKSTCVGHHEEAANKLSFTCKVGNQVVAKSILITVATDYKDYALIYICST PTGRSPMNPYLIARRKPD-DNIPEALKELTKGKDFKK-----CSDLTK-
>G8JKF8	-----TVNAMDNYHAPDFHKDKWYVTHVSKVTDPTTECRTLTATNSADGKTF TVENSVGEGESQKSTCVGHHEEAANKLSFTCKVGNQVVAKSILITVATDYKDYALIYICST PTGRSPMNPYLIARRKPD-DNVPEALKELTKGKDFKK-----CSDLTK-
>G8JKG5	-----TVAECGGEQVNAMDNYRAPDFHKDKWYVTHVSKVTDPTTECRTLTATNSADGKTF TVENSVGEEESQKNTCVGHHEEAANKLSFTCKVGNQVVAKSILITVATDYKDYALIYICST PTGRSPMNPYLIARRKPD-DNIPEALKELTKGKDFKK-----CSDLTK-

>G8JKD1	E---MITVAECGGEQVNAMDNYHAPDFHKDKWYVTHVTKVTEPTECRTLTATNSEDGKTF TVENSVGEGESQKSTCVGHEEAANKLSFTCKVGNQVVAKSILITVATDYKDYALIYICST PTGRSPMNTYLIARRKAG-DNIPPQLESFTQGMEFKK-----C-----
>G8JKF9	-----TVNAMDNHAPDFHKDKWYVTHVTKVIEPTECRTLTATNSEDGKTF TVENSVGEGESQKSTCVGHEEAANKLSFTCKVGNQVVAKSILITVATDYKDYALIYICST PTGRSPMNTYLIARRKAG-DNIPPQLESFTQGMEFKK-----C-----
>G8JKE6	E---MITVAECGGEQVNAMDNYHAPDFHKDKWYVTHVTKVTEPTECRTLTATNSEDGKTF TVENSVGEGESQKSTCVGHEEAANKLSFTCKVGNQVVAKSILITVATDYKDYALIYICST PTGGTPHDTYLIARRKPG-DNIPPQLESFTQGMEFKK-----C-----
>G8JKG3	-----QVNAMDNYHAPDFHKDKWYVTHVTKVTEPTECRTLTATNSADGKTF TVENSVGEGESQKSTCVGHEEAANKLSFTCKVGNQVVAKSILITVATDYKDYALIYICST PTGRSPMNTYLIARRKAG-DNIPPQLESFTQGMEFKKMLVKNKNECPKTFVV
>G8JKG4	-----QVNAMDNYHAPDFHKDKWYVTHVTKVTEPTECRTLTATNSADGKTF TVENSVGEGESQKSTCVGHEEAANKLTFTCKVGDQVVDKTIFITVNTDYNDYALYYLCTA PTGGTPHDTYLIARRKAG-DNIPPQLESFTQGMEFKK-----C-----
>G8JKG9	RAYSEDPFSKC-SKPKTVMDDYDATKWHSGKWYVTHVQKESTPTDCRTL--TTSQDGDVS IVQHPY-ETGNGTLYCQGKKQEDNSLIFDCKSGEESMDKTIYIAVDTDYTDYALYYLCTS PTKGDLYENYLVARREKQKDIPQQLQSSTSSLNLKQ-----CK-----
>G8JKD5	---EDPFSKC-SKPKTVMDDYDATKWHSGKWYVTHVQKESTPTDCRTL--TTSQDGDVS IVQHPY-ETGNGTLYCQGKKQEDNSLIFGCKSGEESMDKTIYIAVDTDYTDYALYYLCTS PTKGDLYENYLVARREKQKDIPQQLQSSTSSLNLKQ-----CK-----
>G8JKG8	-----DDYDATKWHSGTWYVTHVQKESTPTDCRTL--TTSQDGDVS IVQHPY-ESGNGTLYCQGKKQEDNSLIFDCKSGDESMKTIYIAVATDYNNAALYYLCTS PTTGDLYENYLVARREKQKDIPQQLQSSTSSLNLKQ-----CK-----
>G8JKD4	----DQFSAC-KKPTTVMG DYDATKWHTGTWYVTHVQKESTPTDCRTL--TTSQDGDVS IVQHPY-ETGNGTLYCQGKKQEDNSLIFDCKSGDESMKTIYIAVATDYNNAALYYLCTS PTTGDLYENYLVARRDGQKDIPKQLQSSTSSLNLKQ-----C-----
<i>D. maxima</i>	
>G3CJQ3	-----DFKATQFHSGTWYVTHVANETEPTDCRTLS MSTTTSG-NSKTFVVQHPYGECDKDKLHCTAQPETEKRLTFTCKNGGKVTDTTIFIAMVT DYNDYALYYLCTTVKSGSNEGKVYDNYLVARRDGSKKDIPAALKTYTNLGLKSC-

>G3CJQ4	TFIALTFIGILTYA-HGA-SECKTPTPVVPDFKATQFHSGTWYVTHVANETEPTDCRCLS MSTTTSG-NSKTFVVQHPYGECDKDKLHCTAQPETEKRLTFTCKSGGKVTDTTIFIAMVT DYNDYALYYLCTTVKSGSNEGKVYDNYLVARRDGSKKDIPAALKTYTNNLGLKSC-
>G3CJP4	-----AGDFHSGTWYVTHVANETEPTDCRCLS MSTTTSG-NSKTFVVQHPYGECDKDKLHCTAQPETEKRLTFTCKSGGKVTDTTIFIAMVT DYNDYALYYLCTTVKSGSNEGKVYDNYLVARRDGSKKDIPAALKTYTNNLGLKSC-
>G3CJR4	-----A-SECKTPTPVVQDFKATDFHSGTWYVTHVANETEPTDCRCLS MSTTTSG-NSKTFVVQHPYGECDKDKLHCTAQPETEKRLTFTCKSGGKVTDTTIFIAMVT DYNDYALYYLCTTVKSGSNEGKVYDNYLVARRDGSKKDIPAALKTYTNNLGLKSC-
>G3CJQ2	TFIALTFIGILTYA-HGA-SECKTPTPVVQDFKATDFLSGTWYVTHVANQTDPTDCRCLS MSTTGSG-NSKTFVVQHPYGECDKDKLHCTAQPETEKRLTFTCKSGGKVTDTTIFIAMVT DYNDYALYYLCTTVKSGSNEGKVYDNYLVARRDGSKKDIPAALKTYTNNLGLKSC-
>G3CJN4	-----ATDFHSGTWYVTHVANQTDPTDCRCLS MSTTGSG-NSKTFVVQHPYGECDKDKLHCTAKPETEKRLTFTCKSGGKVTDTTIFIAMVT DYNDYALYYLCTTVESGSSKGQIYDNYLVARRDGSKKDIPAALKTYTNNLGLKSC-
>G3CJM4	---ITFIGILTYA-HGA-SECKTPTPVVQDFKATDFHSGTWYVTHVANQTDPTDCRCLS MSTTGSG-NSKTFVVQHPYGECDKDKLHCTAKPETEKRLTFTCKSGGKVTDTTIFIAMVT DYNDYALYYLCTTVESGSSKGQIYDNYLVARRNGSKKDIPAALKTYTNNLGLKSC-
>G3CJP0	-----DFKATDFHSGTWYVTHVANETEPTDCRCLS MSTTTSG-NSKTFVVQHPYGECDKDKLHCTAQPETEKRLTFTCKSGGKVTDTTIFIAMVT DYNDYALYYLCTTVKSGSNEGKVYDNYVVARRSQT-KEIPEKLSSTKDLDMPKC-
>G3CJQ5	-----A-GGSISECKTPASVVDDFSATKFHGGTWYVTHVANQTDPTTECRCLT TSTTGSG-KDKTYVVQHPFGDGDKETLRCTAQPEQQKRLTFTCKNGETVTDTTIFIAMVT DYNDYALYYLCTTVKSGSNEGKVYDNYLVARRDGSKKDIPAALKTYTNNLGLKSC-
>G3CJR5	-----SISECKTPASVVDDFSATKFHGGTWYVTHVANQTDPTTECRCLT TSTTGSG-KDKTYVVQHPFGDGDKETLRCTAQPEQQKRLTFTCKNGETVTDTTIFIAMET DYNDYALYYLCTTVKAGDKNGQIYDNYVVARRSKT-NEIPDKLKSSTKDLDMPKC-
>G3CJS5	-----GSISECKKPQP-MNGFSGTQFHGGVWYVTHVSNVTDPTTECRCLT TSKVG-----EKYIVEHPFESGD-GKLRCEATGEAEKRLTFTCKTGGTVTDSTIFIAMDT DYNDYALYYLCTTVKAGDKMGEIYDNYVVARRSQT-KEIPEKLSSTKDLDMPKC-
>G3CJN7	-----YAYAGSISECKKPQP-MNGFSGTQFRGGVWYATHVSNVTDPTTECRCLT TSKVG-----EKYIVEHPFESGD-GKLRCEATGEAEKRLTFTCKTGGTVTDSTIFIAMDT DYNDYALYYLCTTVKAGDKMGEIYDNYVVARRSQT-KEIPEKLSSTKDLDMPKC-

>G3CJM3	-----GILTYVYAGSISECKTPKP-MDDFSGTKFHGGIWHVTHVANVTDPTTECRTLT TSKVG-----EKYIVEHPFESSD-GTLRCEATGEAEQKLTFTCKTGSTVTDTTIFIAMET DYEDYALYYLCTTVKSS---GDMYDNYVVARRSPS-KEIPGKLKSLTKDLGLEPCS
>G3CJR7	-----GSISECKQPTPVVDGFKATEFHTGTWYVTHVANKTEPTDCRTLS TSTRNPGTNDKTYIVEHPYEVGNEKKLHCEAKPEAQKRLTFACKTDGKDTDSTIFIAMAT DYKDYALYYLCTTVLSGSDKGQKYDNFLVARRSPS-NEIPGKLQDLTKNLNLQRCS
<i>T. brasiliensis</i>	
>Q0MTD4	YAYAATTGISQCQTVTPMEGFSATSFFTGTWYVTHVQKNTSATVCQTFTTKDENRTLVE YSF-NDGQQKNVRCEG-QRGEEKKVAFNCKVNEAPMFDVDFIVLATDYDDYALFYRCITF TSSGDKNDNYLVLRSSGDQEIPASLRDLTSSNLQSCQNLRASVL
>Q0MTC6	----ATTGISECQNVTPMERFSATQFFTGTWYVTHVQKNTSATVCQTFTTKDENRTLVE YSF-NDGQENNVRCCEGQQRRRKKKLHFKCKVNDVPKFDADFIILDTDYNDYALFYRCITF TSSGSKNDNYLVLRSSGDQDIPTSLASLSKLGLLAC-----
>Q0MTD9	----ATTGISECQNVTPMERFSATQFFTGTWYVTHVQKNTSATVCQTFTTKDENRTLVE YSF-NDGQENNVRCCEG-QRGEEKKVAFKCKVNDVPKFDADFIILDTDYNDYALFYRCITF TSSGSKNDNYLVLRSSGDQDIPTSLASLSKLGLLACKDIRPPVA
>Q0MTE9	----ATTGISECQNVTPMERFSATQFFTGTWYVTHVQKNTSATVCQTFTTKDENRTLVE YSF-NDGQENSVRCEG-QRGEEKKVAFKCKVNDVPKFDADFIILDTDYNDYALFYRCITF TSSGSKNDNYLVLRSSGDQDIPTSLASLSKLGLLACKDIRPPVA
>Q0MTC9	-----CQTVTPMDGFTATRFFTGTWYVTHVQKNTSATVCQTFTTKDENRTLVE YSFNNNGQENKVRCEG-QRGVEKKVAFNCKVNGAHTFDADFIILDTDYTDYALFYRCVTF T-SGSKDDNHLVLRSPGIQQIPESLTSLSGLGLMSCE-----

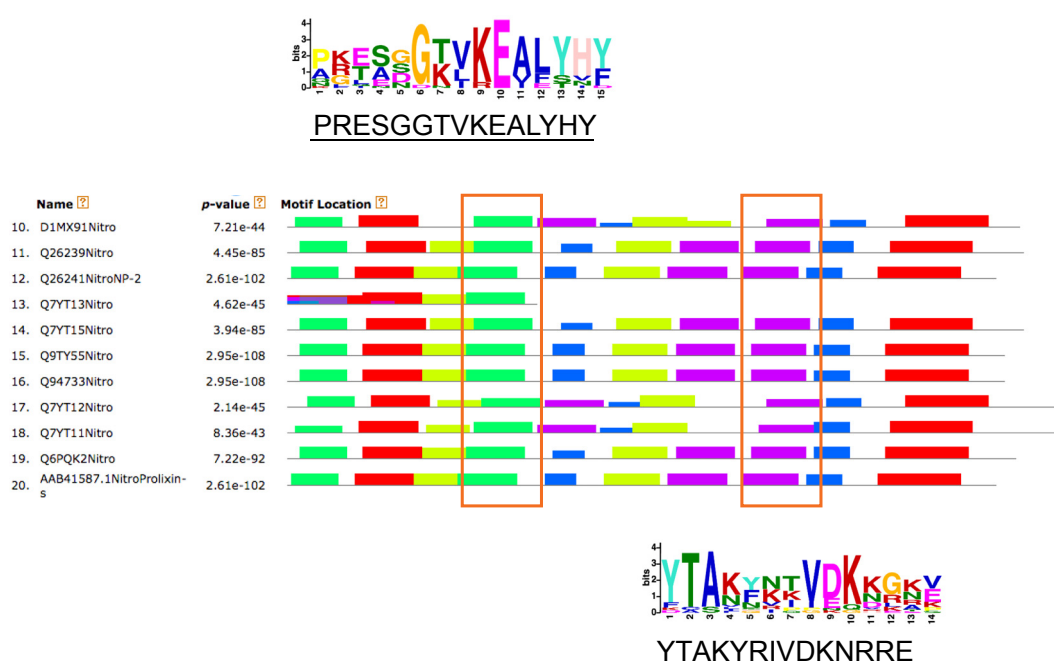


Figure S1. Representative amino acid sequence alignment of nitrophorins and amine binding proteins. The sequence alignments were performed with the MEME software, and they show the sequence motif detected and their position within the protein sequence (The amino acid sequences in FASTA format are part of the supplementary data, see Table S3).

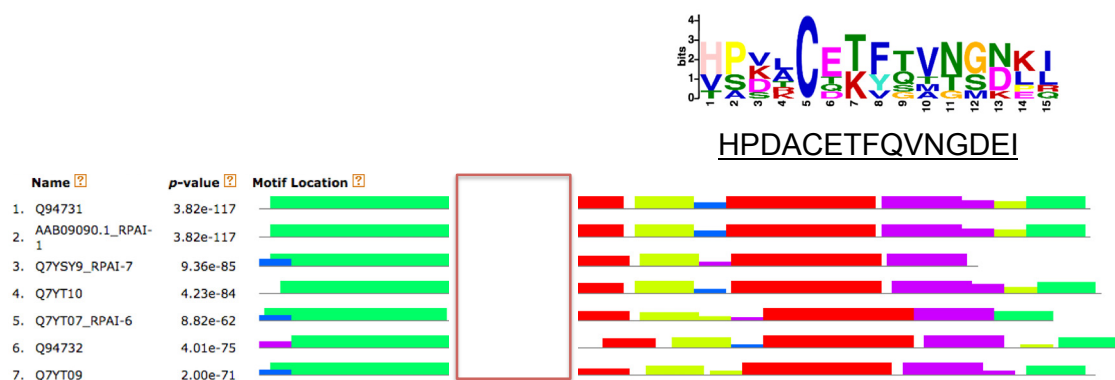


Figure S2. Representative amino acid sequence alignment of *Rhodnius prolixus* aggregation inhibitors (RPAI). The sequence alignments were performed with the MEME software, and they show the sequence motif detected and their position within the protein sequence (The amino acid sequences in FASTA format are part of the supplementary data, see Table S3).

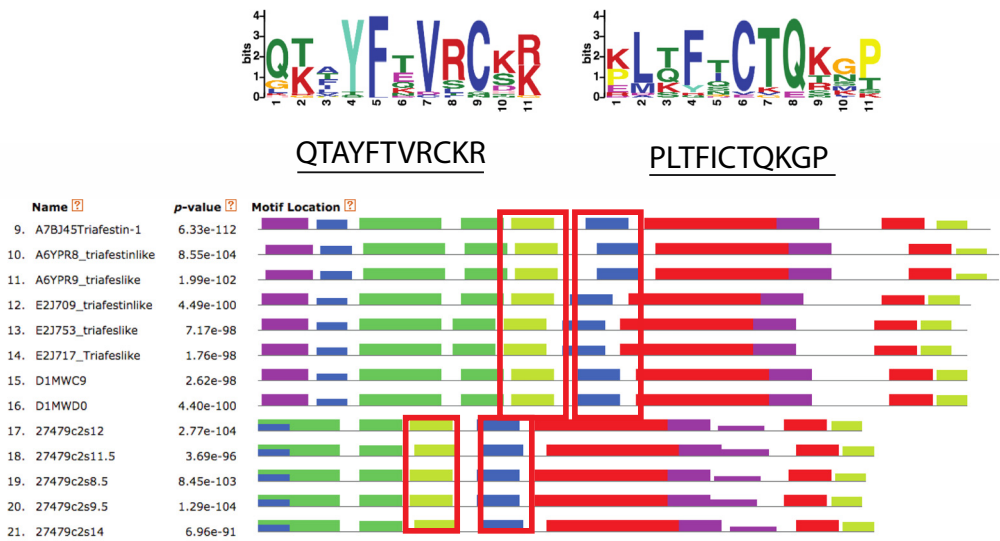


Figure S3. Representative amino acid sequence alignment of triafestins. The sequence alignments were performed with the MEME software, and they show the sequence motif detected and their position within the protein sequence (The amino acid sequences in FASTA format are part of the supplementary data, see Table S3).



Figure S4. Representative amino acid sequence alignment of triatins. The sequence alignments were performed with the MEME software, and they show the sequence motif detected and their position within the protein sequence (The amino acid sequences in FASTA format are part of the supplementary data, see Table S3).



Figure S5. Representative amino acid sequence alignment of pallidipins and dipetalodipins. The sequence alignments were performed with the MEME software. However, an exclusively sequence motif for this clade was not found (The amino acid sequences in FASTA format are part of the supplementary data, see Table S3).

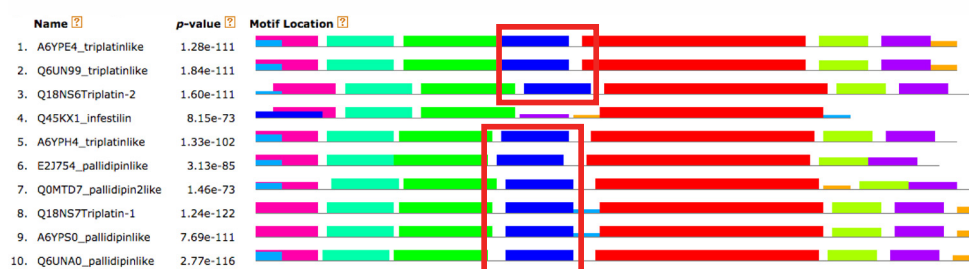
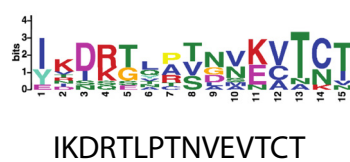


Figure S6. Representative amino acid sequence alignment of triplatin and infestilin. The sequence alignments were performed with the MEME software, and they show the sequence motif detected and their position within the protein sequence (The amino acid sequences in FASTA format are part of the supplementary data, see Table S3).

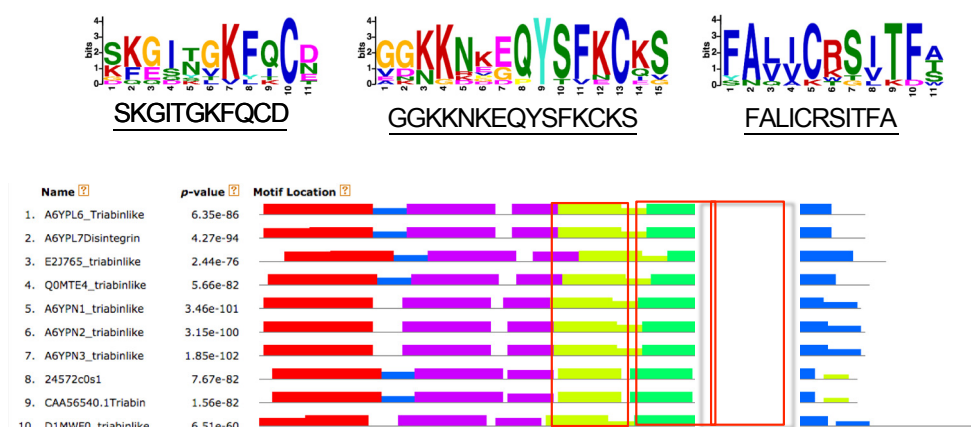


Figure S7. Representative amino acid sequence alignment of triabins and dimiconins. The sequence alignments were performed with the MEME software, and they show the sequence motif detected and their position within the protein sequence (The amino acid sequences in FASTA format are part of the supplementary data, see Table S3).



Figure S8. Representative amino acid sequence alignment of triabins from *D. maxima*. The sequence alignments were performed with the MEME software, and they show the sequences motif detected and their position within the protein sequence (The amino acid sequences in FASTA format are part of the supplementary data, see Table S3).

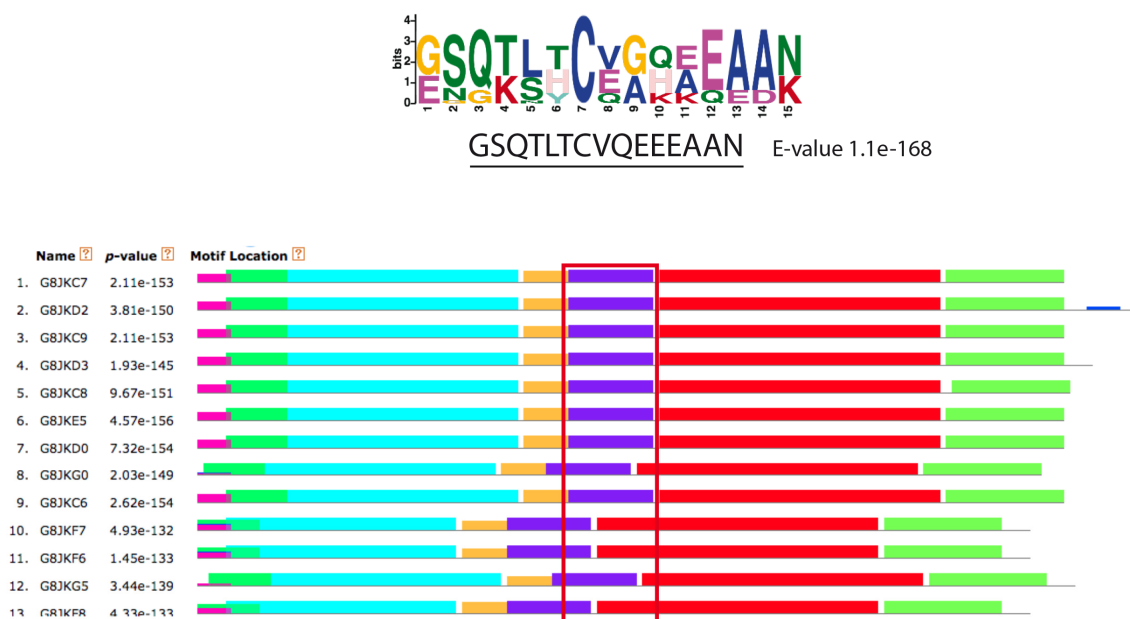


Figure S9. Representative amino acid sequence alignment of triabins from *T. rubida*. The sequence alignments were performed with the MEME software, and they show the sequence motif detected and their position within the protein sequence (The amino acid sequences in FASTA format are part of the supplementary data, see Table S3).

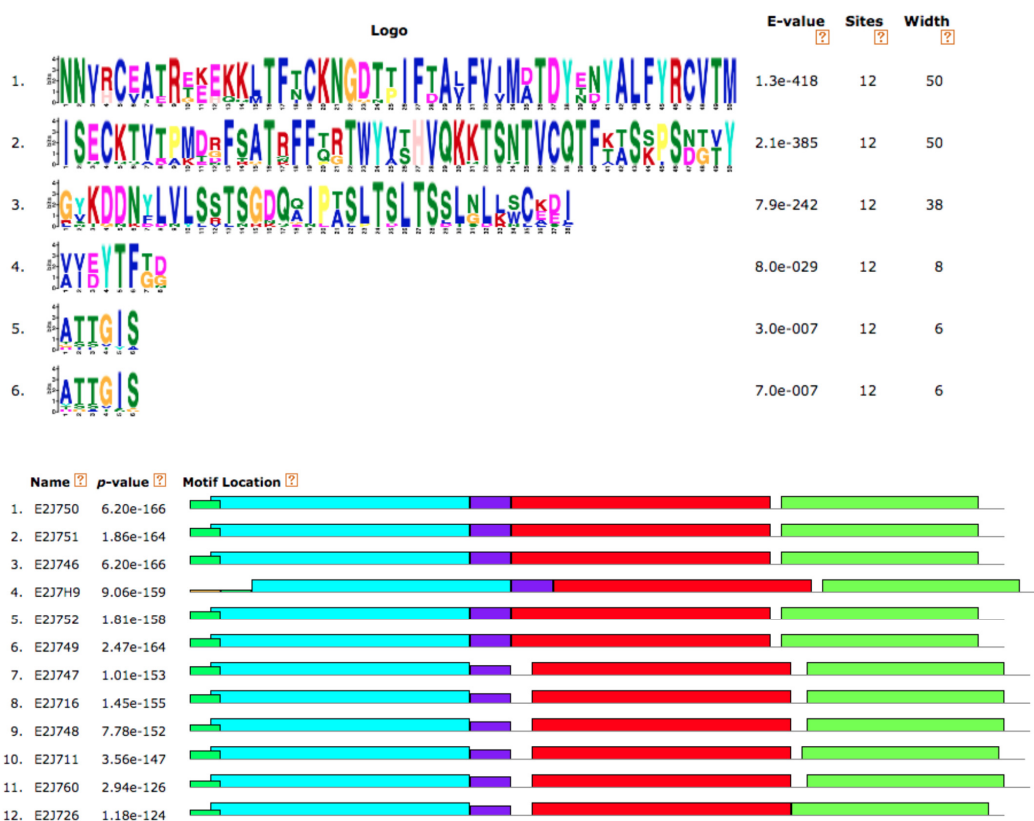


Figure S10. Representative amino acid sequence alignment of triabins from *T. matogrossensis*. The sequence alignments were performed with the MEME software. There was not a specific sequence motif, but the graphical representation of the sequence conservation (logo) is shown (The amino acid sequences in FASTA format are part of the supplementary data, see Table S3).