Последовательности используемые в качестве образца для поиска элементов *L31.*

```
Mariner-31_CGi (транспозаза)
MENRNKLGRXYVNGKELSEDLRRIVIDNLVEGGANVSDLQLPRGLRQRVSKKFGISANCISSIWKRYVTVGTVRRRPRRGG
PSKIVQQEDVDHIAVLKTINPTMSLKSVKDNILQYSNTLQNISLPTVSNIIRKDLHMTLKRVTFCHGNRFTLPNLQYTQRF
LQYVNNEDPFALKFMDEMGFVVCDGNKXYGHSAKGTPCVAVAKFNAKIHFTISLIVGVSGVKFVKIVEGSSNSIEFLHFLG
EAGNVATDEGERVLQRGDSLIVDNAPTHRNMSEVVLRNWLPTIGVQYIFLPTYSPDLNPAELCFRKVKILLKTEKYTALLA
QNIKVALYSAFSEITVHDTLSFFRATDYIDV
```

```
Mariner-31_CGi (OPC2)
MAVFEESVREVFLKIHHECNGVKRVSPVSVEFSELTSFIGLKSAIYAEIKAIGLMSSPILAYRDEEGDYVDLTGKHYNRFL
KFVSSTDSNINIKVIDGGSEPVMQKTPQSMPETQIYVQEKAPDIFQNYTYQTPIEHSMNNLKQEILELEVQSESALEHLQN
LKDKFYHNSRQCRLEKCVSSQQCGDINKHQEEKALVESANDVLRKIQKELKTKTVEYETKFKASESVKNSFSEKXRCHLIN
SNKQKYLVQVSDGNFLPRSGIVNCDIAKLEKYYQGKCPDNLDIASNFFGNIISNFDREHAQFSRNTGSNSAKRILEENTIF
PVKFPRRLPVSTHPNPDSTYQNKVAAPHLPLKKR
```

Последовательности *ITm*-транспозаз, которые были использованы для филогенетического анализа.

```
>Famar1_Forficula_auricularia_(AAO12863)
MENQKEHFRHILLFYFRKGKNASQAHKKLCAVYGDEAFKERQCQNWFAKFRSGDFSLKDEKRSGRPVEVDDDLIKAIIDSD
RHSTTREIAEKLHVSHTCIENHLKQLGYVQKLDTWVPHELKETHLTQRINSCDLLKKRNENDPFLKRLITGDEKWVVYNNI
KRKRSWSRPGEPAQTTSKAGIHQKKVLLSVWWDYKGIVYFELLPPNRTINSVVYIEQLTKLNNAVEEKRAELTNRKGVVFH
HDNARPHTSLVTRQKLLELGWDVLPHPPYSPDLAPSDYFLFRSLQNSLNGKNFNNDDDVKSYLIQFFANKNQKFYERGIMM
LPERWQKVIDQNGQYITE
```

```
>Dmmar1_Drosophila_mauritiana_(AAA28678)
MSSFVPNKEQTRTVLIFCFHLKKTAAESHRMLVEAFGEQVPTVKKCERWFQRFKSGDFDVDDKEHGKPPKRYEDAELQALL
DEDDAQTQKQLAEQLEVSQQAVSNRLREMGKIQKVGRWVPHELNERQMERRKNTCEILLSRYKRKSFLHRIVTGDEKWIFF
VSPKRKKSYVDPGQPATSTARPNRFGKKTMLCVWWDQSGVIYYELLKRGETVNTARYQQQLINLNRALQRKRPEYQKRQHR
VIFLHDNAPSHTARAVRDTLETLNWEVLPHAAYSPDLAPSDYHLFASMGHALAEQRFDSYESVKKWLDEWFAAKDDEFYWR
GIHKLPERWEKCVASDGKYLE
```

```
>Tvmar1_Trichomonas_vaginalis_(AAP45328)
MYMMSMLYFGAMPGYKMNFETRGGFAGNFGGIFFIFLMNHKENILALAKKCKDCKKIYETLVKCFGMDAPSYSTVTYHVRM
YHFMNKKAPIIKIDKKSPDQRKIKAILQALDEDPRASLRRIEEMTKIPRTTVSYYLHNYLNYKLAYTRWVPHNLNSVQKKS
RVQSSKELLSILGAYQSKKFRFLVTGDESWFQYATEAKIMWIPKDENPQTFPKKKIDTPMMMLSVFWGVNGIIAIDILQKP
NTMNAQYLIDNVLTQIINSDEFEKSKQQKQKFAIHFDNSRVHKSHKVMNYLVENNVKVVPNPIYSPDIAPSDFYLFGTLKK
RAEGREFASPDDLENFVREQFEQFSHDDLKRVFQAWIDRCERVIESNGDYI
```

```
>Hsmar1_Homo_sapiens_(AAC52010)
MEMMLDKKQIRAIFLFEFKMGRKAAETTRNINNAFGPGTANERTVQWWFKKFCKGDESLEDEERSGRPSEVDNDQLRAIIE
ADPLTTTREVAEELNVDHSTVVRHLKQIGKVKKLDKWVPHELSENQKNRRFEVSSSLILRNNNEPFLDRIVTCDEKWILYD
NRRRPAQWLDREEAPKHFPKPNLHQKKVMVTVWWSAAGLIHYSFLNPGETITSEKYAQQIDEMHRKLQRLQPALVNRKGPI
LLHDNARPHVAQPTLQKLNELGYEVLPHPPYSPDLSPTDYHFFKHLDNFLQGKRFHNQQDAENAFQEFVESRSTDFYATGI
NKLISRWQKCVDCNGSYFD
```

```
>Bytmar1_Bythograea_thermydron_(CAD45367)
MGKIEYHAVIKFLTKVGKNAKEIHDRLVAVYNDTASSYATVTRWHKEFRHGRESLEDDSRVGRTFEATSEDTVDRVEAMIM
ENRRVKVEEISLEIRISHGSVCTIINHHLGMSKVSARWVPRNLSLHDRLQGQTSSEELLTLYNAYPAGFKSRVMTGDETWV
HHWDPETKLESMAWKQKGSPTPLKFWTQPLAGKIMATIFWDAGGVLLVDVLPRGSTITGKYYAGVLGRLRDSIRQKRRGKL
TRGVLLLLLHDNAPVHKAHHAQAALRDCGFEQFNHPSYSPDLAPNDYFLFRQLKSSLRGRRFDDNDEVKEAVMMWLEEQLES
FWLAGIQSPSRQVVQMYSIKGNYIEK
```

```
>Quetzal_(AAB02109)
MTREELSVSKRQDIIRLHGAQGKSYTEIAMLTNINRNTVARVIQRYKYEGRVSNLPRKGRPSVCTDRMRRAIKRLVDAEPE
ISAQSVAIVLNERHGIAISCETVRRYIHKFGYKAYNRRKKPQISPINRKRRLEFAKKYVNHPPEFWKKVLFTDESKFNIFG
WDGTIKVWRPPGEGLNPKYTAKTVKHNGGGVLVWGCMAANGVGNLQVIDGIMDQYVYINILKQNLGPSLEKLGMSQDYWFQ
QDNDPKHTAFNSRLFLLYNTPHQLKSPPQSPDLNPIEHAWELLERKIRQTRIKNRVDLENKLKEAWITISEDYTQNLVNSM
PRRLAEVIKMKGYATRY
```

```
>Mariner-14_CGi_(Repbase)
MGRKGSELCASEKESILSLSKANIKLKEISEITGRPISTICSFLKRQERRGITENKNRSGRPRKCSVQGERQLIRLVKNNR
RRTLTELTNVSNENGASRLSESTVKRILRKGGYRRRLVKKKLRIREVNKKKRVNWCKQYRHKTVDDFWNNIIFSDECKVMI
DGEQRVYVWRKDGEEWDPPCVAPPPGRRLDLMVWGCITAHGVGTLCIVDGNINAEKYIEIIDSNLWPVVAMHFPNNQYIFQ
DDNAPVHRARVVKDFVTREGITTLEWPAQSPDLNIIENCWKKMKHEINRNVHNLRTNDDLAAAVRQAWENIPLQFIQRLYQ
SIPRRIQAVIKSKGCLTKY

>SsTRT_[41]
MGQKRDLTDSEKSKILKSISEECSTLEIAKILGRDHRTIKRFVANSQQGRKNRVEKKRRKLTAKDLRRIKREATRNPLSSS
AVIFQNCNLPGVPRSTRCSVLRDMAKVRKAETRPPLNKTHKLKRQDWAKKYLKTDFSKVLWTDEMRVTLDGPDGWARGWIS
NGHGAPLRLRRQQGGGGVLVWGGIIKDELVGPFRVEDGLKLNSQTYCQFLEDTFFKQWYRKKSASFKKTMIFMQDNAPSHA
SKYSTAWLASKGLKDERIMTWPPSSPDLNPIENLWSLLKRTIYGEGKQYTSLTSVWEAVVAAAQKVDGQQIKKLTDSMDGR
LMTVIEKKGGYIGHRFFF

>An-gambiae1_(AF378002)
MEAERREKIVHNYLENPLWSASRLAKKLKFPRNTVWRVIKRYKEILTTIRKPQANRRSGTVDQNLRSKILKTIKGNPNLSD
RDLARKFGATHSTVRRTRLREGIKSYRASKQSNRTIKQNSLIKTRARKLYDQVLTKFDGCLLMDDETYVKADFGQIPGQTF
YLATGRGDVPAKFKFVFADKFARKFMIWQGICSCGKKTKVFVTNKTMTSELYQKECLQKRILPFIRSHDHPVMFWPDLASC
HYSKVVREWYAEKGVLFVPKNLNPPNCPQFRPIEKYWAIMKRRLKAKGKVVKDINQMTTWWNKIAKTMDEEDVRRLMSRVK
GKNREFLRNREE

>Guest_Ca-sativa_(XP010462775)
MTDGERLKVYHALLERSNNGTLKRTHTREVANLLSVPLLTVQRIWKLAKDIPNGEVVDVSHKRKGKCGGKNIVFDLDRIVD
IPFNRRKTLRSLAAALKISRTTLWRCLKRGLIKRHSNAIKPRLTENNMRARLQFCLSMLDRTTLLGHPKFVDMHNVVHIDE
KWFYMTKRSENYYLHPSEEEPYRTCQSKNYIGKVMFLAAMARPRFDNNGNETFSGKIGVFPFVTMQPAQRHSRNREAGTLE
LKPMTSIKRENINDFLIGKVLPRIRERWPQEDFEKTIFIQQDNARTHVDPRDEDFRAASSHHGFDIRLMCQPPNSPDLNIL
DLGFFNAIQTLQHEVCPKTIEELVSAVEVMFDEYPPYLVNRIFVTLQSCMQEIMKV

>Guest_Soymar1_(AF078934)
MQRKVKMLSNEERITIYQLLLQKSVDGKLPQGVKESVASSFSVCRKTIDRIWKRAKESETHDVSHKKTKNSGRKRVEIDLS
QLREIPLSQRTTVRTLAVAMKTNTSAMYRLIQSGAIKRHSSAIKPQLTEEGKRLRLEFCLSMLEGIPHDPMFQSMYNIIHI
DEKWFYMTKKSERYYLLPDEDKPHRSCKSKNFVPKVMFLTAVARPRFDSEKNVTFSGKIGIFLFVTQEPAKRTSVNRVAGT
METKAITSINRDLIRSVFIEKVLPATKEVWPRDELGSTIFIQQDNARTHINPDDPEFVQAATQDGFDIRLMCQPPNSPDFN
VLDLGFFSAIQSLHYKEAPKTIDELVNAVVKSFENYCVVKSNFIFLSLQLCMIETMKAKGSNRYTSQHMQKEKLETEEQLP
IQLKCDPILVQETLDYLNNN

>Guest_Br-oleracea_(XP013589454)
MTDEERVEVYHALLERSNNGKLLKNSTREVSGLLDVPLQTVQNIWKRAKNTGYGEVVDVSHRRKGKCGRKKKQIDWLKVVD
IPLHRRTTIRSLAAALGMSPTVVFRSLKEGQLRRHSNAIKPLIKEDNKKTRVKFCLSMLNKNALPHQPKFVDMYNVVHIDE
KWFYMTKKTQTYYLLPSEEDPLRTCQSKNYISKVMFLAAMARPRYDGEGNETFSGKIGIFPFVTLQKAQRRSCNREAGTME
LKPMVSIKREDIKHFLIEKVLPRIYERWPAEDFGKTIFIQQDNAKTHVTVNDEEFQVAALQHGLDIQLMCQPPNSPDLNIF
DLGYFRAIQALQHHVCPKTVEDLVTAVEEAYDEYPPNLVNRVFLTLQSCMIEIMKIGGGNNYKIPHLKKDTLEREGLLPVQ
MDCDPNLVEEAMNYVAC

>Guest_Phyllostachys_edulis_(ADP24264)
MANLDLNQPIHWEEIEDYDGPVIDLNFDLVFHDSDEGEDGGPTHGEEDGTLAHGEEDGGAPSHGEEDGAPAHGEEDGAPAP
NAYETISTNKAKNCGRKWVAFDPEAIKDVPLSSRTTIRDLAGALNISKSTLFRRMKEGKFRRHTNDIKFTLTEDNKRARVK
FCLSMLDKLSMPQEPTFEGMYNIVYIDEKWFYRTRKCQNYYLALDEDKPERTTKSKNFIEKVMLLAAIARPRFDGDGNVTF
SGKIGIFPFTFVEPAKRSSANRPAGTLVTKAMTSVTKETSREYLVNKVLPAIKQKWPAEEVGTPIFIQQDNARTHIAINDD
EFCRAASADGFDISLMCQPPNSPDLNVLDLGFFAAIQSMFQKSSPSNVEDIVAKVIQAFDEYPVDRSNRIFLTHQSCMREI
LRQKGGQHYAIPHLKKQSLERNGVLPVSLQCDPEVVNEAIVYIN

>Guest_Pisum_sativum_(AAX51974)
MYIYHELLQKSVDGKLRKGATNEVASSNSVPLRTVQRIWKRAKESETRDVSHRKTKNCGRKRISIDENQIRELPFSQRTNI
RSLAFALKTNPTSVFRLIKSGAIRRNSNAIKPLLKEENKISRLEFCLSMLEGTPHDPMFKSMHNIIHIDEKWFYMTKKSEK
YYLLPDEDEPYRTCKSKNFIAKVMFLVAQTRPRFDSEENETFSGKIGVFPFVTHEPAIRSSINRVAGTMVTKAITTVNRDV
VRSFLIDKVLPAIREKWPRDEFESTIFIQQDNARTHINHDDPLFREAATKDGFDIRLMCQPANSPDLNILDLGFFSAIQSL
QYKEAPKTIDELISAVVKSFENFPSIKSNRIFVSLQLCMIEIMKEKGSNKYKIPHVNKERLERVGQLPIQIKCDPILVQEV
KNYLNME

>pogoR11_(S20478)
MGKTKRVVGLTLKEKLQIIELVTNKVDKKEICAKFKCDRSTVNRILQKTNEIHEAVAASGLKRKRQRKGAHDLVEEALYIW
```

```
FGQQESKNVILDRHVILAKAKEFCQKFNDAFEPDASWLWRWRKRHNIKYGKIHGETATNDSVSANEYKNDILPGLLKGYNP
EDIFNADETALFYKAMPNATFFTCGKQLNGQKSQRVRLTLLFICNATGTYKKTFVIGRSKSPRCFKNANVPIPYYANKKAW
MTKDLWRKIMTGFDEEMKKQNRKILLFIDNATSHTTVKDFENIKLCFMPPNATALLQPLDQGIIHSFKLEYRRILVKQQLI
AVNCGKSTVEFLKSLSLLDALYFVNQGWKNVKMLTIQNCFKKAGFKFSFENEDTIAEKDKQCVEVDIVSNINWNEYANVDA
DEACHGQLDDDEIVRSLVQDAKTSDNEESHSDEDVDDTERPTFKDGFAAIKALKSIFMRNNNDEFLQNLNSMEDKLFNLHI
NSAVLQKKITDYF

>Tigger1_(U49973)
MASKCSSERKSRTSLTLNQKLEMIKLSEEGMSKAEIGRKLGLLRQTVSQVVNAKEKFLKEIKSATPVNTRMIRKRNSLIAD
MEKVLVVWIEDQTSHNIPLSQSLIQSKALTLFNSMKAERGEEAAEEKLEASRGWFMRFKERSRLHNIKVQGEAASADGEAA
ASYPEDLAKIIDEGGYTKQQIFNVDETAFYWKKMPSRTFIAREEKSMPGFKASKDRLTLLLGANAAGDFKLKPMLIYHSEN
PRALKNYAKSTLPVLYKWNNKAWMTAHLFTAWFTEYFKPTVETYCSEKKISFKILLLIDNAPGHPRALMEMYKEINVVFMP
ANTTSILQPMDQGVISTFKSYYLRNTFRKAIAAIDSDSSDGSGQSKLKTFWKGFTILDAIKNIRDSWEEVKISTLTGVWKK
LIPTLMDDFEGFKTSVEEVTADVVEIARELELEVEPEDVTELLQSHDKT

>Fot1_(Q00832)
MPVYSADDLENAIADFKNGVSLKTAAKKNGLPPSTLRGRLTGAQSRQVARQEQLRLTTDQEDDLERWILRQEKLGHAPTHA
QVRTIVRSVLARHGDHAPLGRKWTTRFVERHPALKTKLGRRTDWERVNAATPANIKRLFDVYETVDWIPPERRYNADEGGI
MEGQGVNGLVIGSSQESPNAVPVKTATVRTWTSIIECISAVGVVLHPLVIFKAKTIQEQWFRREFLQKHLGWQVTFSKNGW
TSNSIALEWLEKVFLPQTAPADPADARLLIVDGHGSHATEQFMAKCYLNNVYLLFLPAHCSHVLQPLDLGCFSSLKAAYRT
LVGEHTALTDSTRVGKQRFLDFYARAREIGFRKVNIRSGWRAAGLWPVNINKPLASRWVMVLTKSALPPSETLDIATPKRG
GDVVKLFSAKSSSPSSRLSIRKAAAALDKVAIELAMKDREIERLRAQLEAAQPKKKRKIRQDPNECFISLAQILAEANREP
DQRVIQSQKGDLDCIVVDGKSSSESEEDPAPVRRSTRVRRATKMYIRQDLSSEESD

>Tan1_(U58946)
MPPKASIPSKSQVEREGRILLAIEAIRKGQITSIREAARVYDVARTTLQARLSGRVFAKNMTNARQKLSNNEEESLVKWIL
SLDKRGASPRPLDIRDMANLIISKRGYSTVEQVGINWAYSFVKRHESLRTRFARRLNYQRAKMEDPEVIKDWFKRVQEVIQ
EYGISSDDIYNFDETGFAMGMIATYKVVTSSQRAGRPSLVQPGNREWVTAIECIRSNGEVLPSTLIFKGKTHLKAWYEGQS
IPPTWRFEVSDNGWTTDKIGLRWLQKHFIPLIRGKSVGKYSLLVLDGHGSHLTPEFDQSCAENEVIPICMPAHSSHLLQPL
DVGCFSVLKRTYGGMVQKQMQYGRNHIDKLDFLEVYPKAHQCALSKSNIISGFRATGLVPLDPDQVLSRLHIRLKTPPTPD
SQSSGSVLQTPHNIKHLLKHPKSVERLLRKRQASPTSPTNSTLRQLLKGCELAITNSIILAKENAELRASHEKQLPKRKRS
RKQVIYTEGTTVEEAQRAIQEVEEVQNDEDIEVEPQSQYTETPSRAPPRCSNCFNIGHRRTQCSKPPTN

>Pot2_(Z33638)
MKQYTEKQLISAINDVNNGNPIAKTSRKWGIPRSTLQSRLKGSQPYKKAQSPFQRLSTEQEKHLADWVLTQTALGLPPTHQ
ELRFFAERILQAAGETKGLGKRWITRFLARYPILKTQRPRRIDNARVNGATTEVIKSWWLYITNPVINAIKPENRWNMDET
GIMEGKGSNGLVLGLNGIRPLQRKEPGTRGWTTIIECISATGVALPPLVIFKGKNVQQQWFPTDLSPFDNWQFHATENGWT
NNQTAIEWLKKVFIPYTQPLTPEKRLLVLDGHGSHITDEFMLLCLQNNIQLLYLPPHSSHVLQPLDLSVFGPLKEAYRRQL
GFVSQFCCSTVIGKRNFLLCYRKARLKAFIAKTIQSGWRTTGLWPVNLVKPLLSPFLLENSNANVIKDKNNGLQRDKTPES
PAQKINDPSLLIWKTPKTTRDIRLQLQKLSQSNKTNATSRLLFAKVQKSFEAKDTLLASAQQKISLLEAQLEAIRPVKRRR
VVPDPNELLVNKQNIIGLQENDIENLEPLADEEEVNEPEKRENDCIFVR

>In_Rhinella_marina_[42]
MGKKGDLSAFKRGMVVGARRAGLSISETADLLGFSRTTISRVYREWSEKEKTSSERQFCGRKCLVDARGQRRMGRLVRADR
KATVTQIATRYNQGRQKSISERTVRRTLRQMGYSSRRPHRVPLLSAKNRKLRLQFAQAHRNWTVEDWKNVAWSDESRFLLR
HSDGRVRIWRQQHESMDPSCLVSTVQAGGGGVMVWGIFSWHSLGPLVPIEHRCNATAYLSIVADHVHPFMTTMYPTSDGYF
QQDNAPCHKAGIISDCFLEHDNEFTVLKWPPQSPDLNPIEHLWDVVEREIRIMDVQPTNLRQLCDAIMSIWTKISEECFQH
LVESMPRRIEAVLKAKGGPTRY

>DD35E_TR-Xihe_[43]
MVISKETRAVIIALHKNGLTGKRIAARKIAPQSTIYRIIKNFKERGSIVAKKAPGRPRKTSKRQDRLLKVFQLRDRATSSA
ELAQEWQQAGVSASARTVRRRLLEQGLVSRRAAKKPLLSRKNIRDRLIFCKRYREWTAEDWGKVIFSDESPFRLFGTSGKQ
LVRRRQGERYHQSCLMPTVKHPETIHVWGCFSAKGVGSLTVLPKNTAMNKEWYQNVLREQLLPTVQEQFGDEQCLFQHDGA
PCHKAKVISNWLREQNIEILGPWPGNSPDLNPIENL

>DD38E_IT_At_[44]
MGKTKEHSQETRGIIIGLHKSGKSNREISRLQKMPRQTVDYIVKKFASEGTVCNNRRPGRPRATTSSEDLNIVIKSKRNRR
LTAPEIAAHFNMGRDKPVSVSTVKRRLLDAGLKGCIAVSKPLLKTINKKKRLNWAREHKNWITEDWKKVLWTDESKFEIFG
SKRRVFVRRQSNERVIDACTVASVKHGGGSVMVWGCFGGSAVGDLVRIEGILKKEGYKTILENSAVPSGTRLIGPGFVFQH
DNDPKHTSKLCKDFLKGKEQQNVLKLMMWPPQSPDLNPIELLWDQLDRQIRNRCPTSQEDLWRKLQDEWQKISKTTLDKLV
ARMPKLCEAVIKNKGGHIDESKI

>TLEWI-1_BPl_[45]
```

```
MAMGKVNRLSISTRHLIIEYSKKGLSAVHIQRLLHRKYNITTTRQSIFMFVKRYSSTGVLAPATRRDNKFPRKLTDFQRRC
IDMWLRHNSELTSQALVDRLFRVFDVRVKTSYMSKVRKALGWCTRTLQYCQLISHTNKLCRLQWSLDALRSKETFDNVIFT
DETSVEMGADGGAFFYKRTSDLDFLPAKKMKPKHAYKVHV*SGISYRGRTSICIFSGIMDSVIFQNILQSNLLPFVEHQFP
DGFRLYQDNDSKHVSKSTKKWMEEHGILDKVMTTPASSPDINPIENLWSALKGHLLKEVKPKTKDELIGGIRTFWESLTKE
KCCSYIDHIHRVIPFVILNGGGPSDF

>pogo-5_PBac_[49]
MPSRGRSRPLYQRAKKPRKTTRQSWTVENMSLAIQAVKSGQHGYLAAANKYGVPRSTLERRVKDRNKIATGTKKMLGNSLS
VLPPDLELKLVDYVKTMEERLFGLTANDLRRLAYQLAERNNLTHMFNKEEGMAGYHWMHGFLNRHPELSLRKPENVSANRS
RSFNAANVKKFFDILVKVQEEHGFGPYDIYNADEKGLSTVPNYPPRILALKGKKQVGTLASAERGVNTTVLLCGNAAGEFV
PPFYIFPRKKQNLELLRGASAGSKHFNVPSGWMTNEAFYAWLEHFIGHIKCSNEKKALLILDGHVTHVKSLPPLELAKANG
LIILCLPPHCTHKMQPLDVCVMSPLETGFAKYCKDWMRNNPGDVITIKNVAELFTNAYKAVVQSPSMASGFEKTGIWPLQP
SRFDDQFTSAHQKSCTVSDTPAAEPSTPTSPQVDANSSNQSIATNPEDVIPIPVIEYKDKKKKKDRSGKTAIVTSSPYLKE
LRLETENKELKEQVKLLKRENKALKKGTVVQKKQEKKKNAKKRGKKREPSLSPISEPPTPRDPDDTTPNGPRRRICITNSR
ASSQVRINRIRKYRSLIG

>pogo-2_BOva_[49]
MAKSPVKRARKRTRGEGYCYKRKSSTRQSWNGTDMRKAISAVRNKECGYELASKTYLVPKTTLVRRVKGKNKVVLGSEKGM
GHRTVLPIELEKRLVQHILRMEEALFGLTYTDVRKLAYELAEQNGIANNFNRTAKTAGYYWLYGFLRRNPEITLREPENTS
IARSRSFNKTNVDRFFELYQKLLDEHNFTPNRIFNCDEKGVTTVPNNPPKILARSGKKQVGTVGSGEKGVNTTVLLCACAD
GNLLPPMFVFPRVKDNPDLLRGAPVGSIQANNKSGWVVQDSFIQWLKHFIKCSSSSISNPCLLILDGHSEHIKSIEAINIA
RDNGVHILCLPPHCTHRMQPLDVTCMKPLSSALAREVQLWHRDNPSNTLKINHIAEIFCNAYKGSIGPAVVLSGFAKCGIF
PLQPHVFDDCFTSAHQTSTNAPGDDPPNATHSNEPTTIILDEVQKACTTAGVSPQADVVIDKHSPSGSDLDSSFKILPEDI
IPVPKVIYKDNEGATKKPGKAKGATNIVTSSPYLKKLTIEEENKKLKEDVKNFSREIKALKKALKSKDAGKDSTAKADVRR
ELFSEKGKSKKKKKNKVLNIENDEVPKVISSVVRTPSTLDCSNLAPGQFVLVSFNDFGVCDLTADNPTSSKESKPVFYAGF
IKRLCSKTDVETKFLRRSDLKKGNQIKFIYPEEEDLCTHPIDNIVLLLPKPKTAVGKSKRLGSILEFEDERLLDFSPIM

>VS-Maze_[46]
MSKRLTREERIEIVLISGERSNRVIAADFNARHPTRPPISHATVSKLLAKFRETGSVLDLPKCGRMKTVTNEETSVAVLAS
FSKSPQRSTRRMSLESGISRTSLRRILATHKWHPYKLQLLQHLNEDDPDRRTEFAEWAKQKLEQDPQFTQKILFSDEANFY
VNGEVNKQNHLYWSDTNPHWMDPSKTVGTTKVMVWCGIWGTTIVGPFFINGNLKATGYLKLLHDDVFPSLCTEAGTFPEFF
QQDGAPPHYGCQVRAFLDEQFPGKWIGRRGPVEWPPRSPDLTPLDFYLWGHLKAIVYGVKIRDVQHLKLRILDACAGISPA
VLLSVCEEWEKRVALTIQHNGQHIEHIL

>Gambol_(AAAB01008815)
MADSNVPGVDVPNETNSRDNPTDGNNPDEVNVPGTSRLNRKHKTTSNEDRERIIAANENGYSTTLIAEMLSINRSTVYSIL
KKYWKTGEIEAQRRGGVKQKKLTNAAVIHIQSWIDEDCSISLKKLKSKVLERHGIEVSTSTIARAIKGFNYSFKRVKLLPA
RRNNSNTVAERKEYALSYNRCTQRLPQASIIFIDEVGFNVSMRTMMGRSEVGTAATKVVPQLRSRNISIVCAMNRTGILHY
ISRNRAINQEVFVDFIRQLKENLNGDNIGHPPLLIMDNVAFHKCTAVREAIIEEGCEVKYLPPYSPFLNPIENLFSKWKTI
VKRANPQNEGELMTAIQQGASLITSQDCDGYFCNMYRYIEKCVLGEEITD

>Gambol_(AAAB01008960)
MLNLHRATVYSIIKKFQKTWNVEAAKRGGNRAKLLPEEAVQSIRTWIDEDCTVTLKALAEKVHERYSVRVSTSTIARQIKG
FNYTFKRIHNLPERRNTSSTIEERKSYATMFYQLSVENSNTGIVFLDEVGFNLSMRTSQGRSQKGTIPTLVVPQLRSRNIS
IICAMDKNGIVHYHSHNRAVNRELFKQFILQLKEKLRTRGIDESYLIMDNVAFHKCIEVKEAIGNEEDKPLYLPPYSPFLN
PIENMFSKWKNLVKRSNAQNEEELMAAIADSSTFITSQDCEGYFRNMTAYLARCFRGEVIED

>Gambol_(AAAB01008968)
MLNMNRGTVYSIIKKFQNTWEVAAAKRGGNRAKLLSEEAAQSIRAWIDEDCTVTLKALVEKVYERFNVRVSTTTVAREIKG
FNYSFKRIHNLPERRNTDSTIEERRSYASMFYQISMENPDTDIVFLDEVGFKVSMRTSKGRSLKGTTPTIVVPQLRSRNIS
IVCAMNKSGIVHYLSHNRAINRELFTQFIYELKEKLRMREIHRTFMVMDNVAFHKSSEVKEAKGYDEDKPVYLPPYSPFLN
PIENLFSKWKNLVKRANAQNEQELMEAITNCANLVTSQDCEEYFRNMGAYLARCLRGEVIED

>Gambol_(AAAB01016702)
MDIDNSEQEESVQTPKRNNRTTTIEDRKRIITAYEKGVSIANICTSFDMNRNTVYTILRKVKLTGDIEPGKRGGKKPKKLS
DEAICSIKQWIDEDCTLSLRKIRQKLEAEHNIVVSITSIGRAIEGFNYSFKRVHRQPEKRNALSNIQIRKEYAIQIMALPR
QMSEFNIIYIDEVGMNVSMRASMGRSAVGKPAVVVVPQLRNRNISIACAMTRQGILHYEAKTTAINRISFKKFLTELQEKM
VEKGIHAAVMVMDNVAFHKCQEIKELVTQQNNKLLYLPPYSPFLNPIENMFSKWKNTVKRANPQNEMQLMTAIENGASLIT
QEDCDGYVRNMWSYVERCIREEEITD

>Gambol_(AAAB01006894)
MLNIKRPTVYGIINKYNATWQIAAAKRGGTCKKKLSQDAVESIRAWIDEDCAITLKSLAQKVFERHGVHVSISTIAREVKG
FNYSFKMLQKIPERRNTTATIEERTTYARNFYQITRAFPVSGLIYLDEVGFNVSMRTSKGRSQKGTPAVTVVPQIRTRNIS
```

```
IVCAMNSNGIVHYVTHNQPVNRELFTNFIYELKDILRSKNINRSYLIMDNVAFHKSQSVQEAIGTVIDKPLYLPPYSPFLN
PIENMFSKWKNYVKRSNCTNHDQLMEAICNGANYVTAEDCEGFINNMWNYMSRCLSGEEILD

>Gambol_(AAAB01006919)
MFGLNRFTVYSILRKVRLTGVVEARKRGGTKPKKLSNDVIDSIKRWIDQDCTISLRKMQQKLEQEHNIQASITTITRAIEG
FHYSFKRVNRHPERRNAPSNIEERRKYAVEFMSLPREYSERNIIYIDEVGMNVSMRATMGRSAVGKPAVVVVPQLRSRNIS
IVCAMARHGIVHYVAKTTAIERVSFKDFILQLKGKLEEVGIFEPVLVMDNVAFHKCNEVKECITQHINARLLYLPPYSPFL
NPIENMFSKWKNIVRRANPENENDLMTAIENGASLITFQDCEGYVRNMWEYINRSLSGEQILD

>Gambol_(AAAB01008879)
MLNIKRPTVYGIINKYNATWQIAAAKRGGTCKKKLSQDAVESIRAWIDEDCAITLKSLAQKVFERHGVHVSISTIAREVKG
FNYSFKMLQKIPERRNTTATIEERTTYARNFYQITRAFPVSGLIYLDEVGFNVSMRTSKGRSQKGTPAVTVVPQIRTRNIS
IVCAMNSNGIVHYVTHNQPVNRELFTNFIYELKDILRSKNINRSYLIMDNVAFHKSQSVQEAIGTVIDKPLYLPPYSPFLN
PIENMFSKWKNYVKRSNCTNHDQLMEAICNGANYVTAEDCEGFINNMWNYMSRCLSGEEILD

>Gambol_(AAAB01008849)
MLNMKRQTVAGIIKKFNETSVIEAGLRGGTRAKKLSTEQEEQIRAWIDEDCSISLKKLAAKVHEAFQITVSKTTIAKVIEG
FNYTLKRVHKVPVRRNVDETIESRRQYAVEYTTLGGRYPQYEVIFIDEVGFNVSMRDTRGRALAGKPAVKELPALRARNIS
VVCAMSRNGIVHYVSRTRAINKEFFVSFIDELHDKLEEKLITNAILILDNVAFHKSYEVKQKIESYGYKIMYLPPYSPFLN
PIENMFAQWKQITKRANPNNETELMHTIETGATLITSADCENYYKHMWTYLPLCLNGERI

>Gambol_(AAAB01008958)
MLNIKLGTVYGIIKQYKATWKVTAKKRGGHNAKLLTQEAVDRIQRWIDEDCTVSLKVLAEKVFQEYGIRVSTSTVAREVKG
FNYSYKMIQRIPERRNAAANIEERTTYAAEFYTLTRDFPVNGLIYLDEVGFNVSMRTSKGRSAKGTPATTIVPQLRTRNIS
IICAMNASGIVLYTVHNQAVNREKFIELILELKATLRAKAIARSYFIMDNVAFHKCSSVKEAIGNNEDKPLYLPPYSPFLN
PIENLFSQWKNHVKRAKPNNQEELMEAISNGASYVTAEDCESYIRNMWFYMARCLRGEIILD

>L18-1_HVul_[47]
MGKVIGKSNLAASLKKRIAELGKLGKSKAEVAAAIGCSEKSIQRYWRKPVNTNFNEKKRCGRPTVLSPASKNLITSEMKDK
WGSSTRSCAKKLNFSERYITRKKQISRSTVQRFVQHQPWGKVAYHKPIKPLLTEKNQNDRLKFRDWLEQNGYLQDEHVGRQ
KRGHVLWTDESPVELFPVPNRQNMRIWTDDKSKITPAVCPKFGLKIMVCGGMSRYGLTELVVVPEKQTVDADYYINHILPK
YVEATTRNHQGDTADKRKMFFNQDMILFQQDGAPAHSAKIVQQFCAKNFPSMIPKELWPGNSPDINVIEHLWNFLQQSVFE
APKPKNRVELVERVKDKWSSVTGDYLCLLVKSLPKRVQEIRAANGGHSSY

>Z-1_POch_[47]
AWNVEGISNREIARRLGVPEGTVRYNLRKQRETGSMDPRPKSGRLRATLPREDRHLMQTCRRNRFLCAPELAMDLARTSGV
EVHRSTVSRRLADAGLHGRVARHRHKPRLTPIHKQRRLAWARDHLTWTADDWSRVLRSDESRFQLYQSDGRVYVRRTVGEE
FAENCVVPSVKHGGSGIMVWGCMCSAGVGVLARVEGNINAVAYIDILRDHMLPSAHRLIGHEFLFQHDNAPPHTARITQEF
IADPTPDFIREMGGSWEFEVMVWPAQSPDLNPIENLWNELGRRVQRENRPRNQGELYQILNRVWEGLDLNVITSLLASMPR
RCQDVIDAAEAFTPY

>Bmmar1_[48]
MEWGDKENRIAVIALHKVGMEPNAIFKTLHTLGISKMFVYRAINRCNETSSVCDRKRSGRPRSVRTKKVVKAVRERIRRNP
VRKQKILSREMKIAPRTMSRILKDDLGLAAYKRRTGHFLTDNLKENRVVKSKQLLKRYAKGGHRKILFTDENFFTIEQHFN
KQNDRIYAQSSKEASQLVDRVQRGHYPTSVMVWWGISYEGVTEPYFCEKGIKTSAQVYQDTILEKVVKPLNNTMFNNQEWS
FQQDSAPGHKARSTQSWLETNVSDFIRAEDWPSSSPDLNPLDYDLWSVLESTACSKRHDNLESLKQSVRLAVKIFPMERVR
ASIDNWPQRLKDCIAANGDHFE

>IS630Ss_(X05955)
MPIIAPISRDERRLMQKAIHKTHDKNYARRLTAMLMLHRGDRVSDVARTLCCARSSVGRWINWFTQSGVEGLKSLPAGRAR
RWPFEHICTLLRELVKHSPGDFGYQRSRWSTELLAIKINEITGCQLNAGTVRRWLPSAGIVWRRAAPTLRIRDPHKDEKMA
AIHKALDECSAEHPVFYEDEVDIHLNPKIGADWQLRGQQKRVVTPGQNEKYYLAGALHSGTGKVSCVGGNSKSSALFISLL
KRLKATYRRAKTITLIVDNYIIHKSRETQSWLKENPKFRVIYQPVYSPWVNHVERLWQALHDTITRNHQCSSMWQLLKKVR
HFMETVSPFPGGKHGLAKV

>IS630Se_(NP_073225)
MPIIAAIPDEERQLMRKEAQQTHDKNHARRLIAMLMLHQGMTVTDVARLLCAARSSVGRWINWFTLHGVEGLKSLRPGRAP
RWPVADILQLLPLLVQRSPKDFGWLRSRWSTELLALVINRLFDVTLHRSTLHRYLRQADMVWRRAAPTLKIKDPHYEEKRL
VIDQALAQEQTAHPVFYQDEVDIDLNPKIGADWMPKGQQKRIATPGQNQKHYLAGALHSGTGRVHYVSGSSKSSDLFISLL
ETLRRTYRRAKTITLVADNYIIHKSRKVERWLEENPKFRLLFLPMYSPWLNPIERLWLSLHETITRNHQCRYMWQLLKQVA
QFMNAASLFPGNQQGLAKVER

>IS630_Citrobacter_braakii_(STH95988)
```

```
MPIIAPIPRGERRLMQKAIHKTRDKNHARRLTAMLMLHRGERVSDVARTLCCARSSVGRWINWFTHSGIEGLKSLPAGRSR
RWPFEHICTLLRELIKHSPGDFGYQRSRWSTELLAIKINEITGCQLHAGTVRRWLPSAGLVWRRAAPTLRIRDPHKDEKMA
VIHKALDECSAEHPVFYEDEVDIHLNPKIGADWQLRGQQKRVVTPGQNEKYYLAGALHSGTGKVSYVGGNSKSSALFIALL
KHLKATYRRAKTITLIVDNYIIHKSRETQRWLKANPKFRVIYQPVYSPWVNHVERLWQALHDTITRNHQCRSMWQLLKKVR
HFMETASPFPGGKHGQAKV

>IS630_Escherichia_coli_(GDW80866)
MPIIAPIPRTQRRLMQKTIHKTKDKNHARRLTAMLMLHRGDTVSYVARTLCCARSSIGRWINWSTLSGVEGLKSLPSGRGS
RWPFEHICALLRELVKHSPGDFGYQRSRWSTELLAIKIRDVTGCPLHASTIRRWLPAAGLVWRRAAPTLRIRDPHKEEKMA
AIHEALAKCSAENPVFYEDEVDIHLNPKIGADWQLRGQQKRVVTPGQNEKYYLAGALHSGTGKVSYIGGNSKGSSLFIRLL
KHLKATYRRAKTITLIVDNYIIHKSRETLRWLKANPKFRVIYQPVYSPWVNHVERLWQALHETITRNQQCRLMWQLLKKVR
HFMDTGSPFPGGKHGLAKV

>IS630_Shigella_dysenteriae_(VDG84061)
MPIIAPISRDERRLMQKAIHKTHDKNYARRLTAMLMLHRGDRVSDVARTLCCARSSVGRWINWFTQSGVEGLKSLPAGRAR
RWPFEHICTLLRELVKHSPGDFGYQRSRWSTELLAIKINEITGCQLNAGTVRRWLPSAGIVWRRAAPTLRIRDPHKDEKMA
AIHKALDECSAEHPVFYEDEVDIHLHPKIGADWQLRGQQKRVVTPGQNEKYYLAGALHSGTGKVSYVGGNSKSSALFISLL
KRLKATYRRAKTITLIVDNYIIHKSRETQSWLKENPKFRGIYQPVYSPWVNHVERLWQALHDTITRNHQCRSMWQLLKKVR
HFMETVSPFPGGKHGLAKV

>IS630_Shigella_flexneri_(SRR10263
MPIIAPISRDERRLMQKAIHKTHDKNYARRLTAMLMLHRGDRVSDVARTLCCARSSVGRWINWFTQSGVEGLKSLPAGRAR
RWPFEHICTLLRELVKHSPGDFGYQRSRWSTELLAIKINEITGCQLNAGTVRRWLPSAGIVWRRAAPTLRIRDPHKDEKMA
AIHKALDECSAEHPVFYEDEVDIHLHPKIGADWQLRGQQKRVVTPGQNEKYYLAGALHSGTGKVSYVGGNSKSSALFISLL
KRLKATYRRAKTITLIVDNYIIHKSRETQSWLKENPKFRGIYQPVYSPWVNHVERLWQALHDTITRNHQCRSMWQLLKKVR
HFMETVSPFPGGKHGLAKV

>TBE_AAA18578_Oxytricha_fallax_[30]
ADEAVFTFSTFIQKSWYKRNSNIEVYDQKVKVQTMAILGGISEDAGLETYIIHPRSIKTEQYIKFLEQLREKYPEQEIILF
VDNLSVHKTKETKKSYEQLRITPVFNVPYSPQFNGIEFYWGI

>TBE_AAB42017_Oxytricha_fallax_[30]
ADEAVFTFNTFIQKSWYKRNSNIEVYDQKVKVQTMAILGGISEDAGLETYVIHPRSIKTEQYIKFLEQLREKYPEQEIILF
VDNLSVHKTKETRKSYEQLSITPVFNVPYSPQFNGIEFYWGI

>TBE_AAB42032_Oxytricha_fallax_[30]
SDEAVFTFNTFIQKSWYKRNSNIEVYDQKVKVQTMAILGGISEDAGLETYIIHPRSIKTEQYIKFLEQLREKYPEQEIILF
VDNLSVHKTKETRKSYEQLGITPVFNVPYSPQFNGIEFYWGI

>TBE_AAB49643_Oxytricha_fallax_[30]
ADEAVFTFNTFIQKSWYKRNSNIEVYDQKVKVQTMAILGGISEDAGLETYXIHPRSIKTEQYIKFLEQLREKYPEQEIILF
VDNLSVHKTKETRKSYEQLXITPVFNVPYSPQFNGIEFYWGI

>TBE_AAB49646_Oxytricha_fallax_[30]
ADEAVFTFNTFIQKSWYKRHSNIEVYDQKVKVQTMAILGGISEDXGLETYXIHPRSIKTEQYIKFLEQLREKYPEQEIILF
VDNLSVHKTKXTRKSYEQLRITPVFNVPYSPQFNGIEFYWGI

>TBE_AAB58026_Oxytricha_fallax_[30]
ADEAVFTFNTFIQKSWYKRNSNIEVYDQKVKVQTMAILGGVSEDAGLETYIIHPRSIKTEQYIKFLEQLREKYPEQEIILF
VDNLSVHKTKETRKSYEQLGITPVFNVPYSPQFNGIEFYWGI

>TBE_AAB58028_Oxytricha_fallax_[30]
ADEAVFTFNTFIQKSWYKRNSNREVYDQKVKVQTMAILGGISEDAGLETYVIHPRSIKTEQYIKFLEQLREKYPEQEIILF
VDNLSVHKTKETRKSYEQLSITPVFNVPYSPQFNGIEFYWGI

>TBE_AAB58030_Oxytricha_fallax_[30]
AXEAVFTFNTFIQKSWYKRNSNIEVYDQKVKVQTMAILGGISEDAGLETYVIHPRSIKTEQYIKFLEQLREKYPEQEIILF
VDNLSVHKTKETRKSYEQLSITPVFNVPYSPQFNGIEFYWGI

>TBE_AAB58032_Oxytricha_fallax_[30]
ADEAVFTFNTFIQKSWYKRNSNIEVYDQKVKVQTMAILGGVSEDAGLETYIIHPRSIKTEQYIKFLEQLREKYPEQEIILF
VDNLSVHKTKETRKSYEQLGITPVFNVPYSPQFNGIEFYWGI
```

```
>TBE_AAB58034_Oxytricha_fallax_[30]
ADEAVFTFNTFIQKSWYKRNSNIEVYDQKVKVQTMAILGGISEDAGLETYVIHPRSIKTEQYIKFLEQLREKYPEQEIILF
VDNLSVHKTKETRKSYEQLRITPVFNVPYSPQFNGIEFYWGI

>TBE_AAB58036_Oxytricha_fallax_[30]
ADEAVFTFNTFIQKSWYKRNSNIEVYDQKVKVQTMAILGGISEDAGLETYIIHPRSIKTEQYIKFLEQLREKYPEQEIILF
VDNLSVHKTKETRKSYEQLRITPVFNVPYSPQFNGIEFYWGI

>TBE_AAB58377_Oxytricha_fallax_[30]
ADEAVFTFNTFIQKSWYKRNSNIEVYDQKVKVQTMAILXGISEDAGLETYIIHPRSIKTEQYIKFLEQLREKYPEQEIILF
VDNLSVHKTKETRKSYEQLRITPVFNVPYSPQFNGIEFYWGI

>TBE_TBE1_Oxytricha_fallax_[30]
SDEAVFTFNTFIQKSWYKRNSNIEVYDQKVKVQTMAILGGISEDAGLETYIIHPRSIKTEQYIKFLEQLREKYPEQEIILF
VDNLSVHKTKETRKSYEQLGITPVFNVPYSPQFNGIEFYWGIL

>TBE_AAB42034_Oxytricha_trifallax_[30]
ADEAVFTFNTFIQKSWYKRHSNIEVYDQKVKVQTMAILGGISEDAGLETYVIHPRSIKTEQYIKFLEQLREKYPEQEIILF
VDNLSVHKTKETRKSYEQLRITPVFNVPYSPQFNGIEFYWGI

>TBE_EJY78953_Oxytricha_trifallax_[30]
ADEAVFTFNTFIQKSWYKRHSNIEVYDQKVKVQTMAILGGISEDAGLETYVIHPRSIKTEQYIKFLEQLREKYPEQEIILF
VDNLSVHKTKRNKE

>TBE_EJY85485_Oxytricha_trifallax_[30]
ADEAVFTFNTFINKSWYKKYDNIEVYDQKVKVVTHAILAGISEDSGLESYVIHPRSIKREQYIEFLHKLREKYSNQQIILF
VDNLSVHKTKESKKAYEELNITPVYN

>HvSm_XP_004209659_Hydra_vulgaris_[30]
IFFIDEVGVSLSMQVRRGRSLAGKRATQTLTNIRSRNISVCCAMNKNGILKFKAQTKAFNTESVLDFIRLVLAQLAVNEVV
GAILILDNVRFHKTAVVHNEIVCAGHSLIFLPPYSPFLNPIENMFSEWKQ

>HvSm_XP_004212365_Hydra_vulgaris_[30]
IFFIDEAGFSLSMQVRRGRSLAGKRATQTVTNIRSRNISVCYAMNKNGILKYEAQTRAFNTESFFDFIRLVLAQLAVNEVV
GSILILDNVQFHKTDVVHNEIVRAGHSLIFLPPYSPFLNPIENMFSEWKQ

>HvSm_XP_012557766_Hydra_vulgaris_[30]
IFFIDEVGFSLSMRVRRGRSLAGKRVTQTVTNIRLRNISVCCAMNKNGILKYEAQTRAFNTESFLDFIRLVLAQLAVNEVV
RAILILDNVRFHKTAVVHNEIVRAGHSLIFLPPYSPFLNPIENMFSEWKQ

>HvSm_M-6_SM_Schmidtea_mediterranea_[30]
FIDEVGFKVSTRVSRGRSLVGTPAVAIVPTIRSRNIICCAMTRAGIVHYQTQTTPFNTACFMAFINGLIVRLRETNVQSAI
FIMDNVAFHRTNAVRDLIIAEGFSYDFLPPYSPFLNPIENMFSKWKE

>Tec_AAA62601_Moneuplotes_crassus_[30]
VVYIDECSFNRSALPLYTWHAKGTEAPKLIRSSNQRYNCIAAQVCNHKLFHVKQDTTKEDSFIEFLENLHDKLRTILSKRQ
LSKRTIYVFDNASIHLTQKVVKCVTDRKMVCFTIPPYCPELNKVEHTFGLLKN

>Tec_AAA91339_Moneuplotes_crassus_[30]
IVYIDECSFNASALPLYTWNKIGDEPVKLIRSTNQRFNCIAAQVEQHKIFHIKTETTKDQNFITFLEKLNSLLKTMIAKKQ
LMKRTVYVFDNASIHSTEKVVKAITGMKMVCFTIPPYSPELNKIEHTFGTLKR

>Tec_AAM80490_Moneuplotes_crassus_[30]
VVYIDECSFNASALPLYTWHAKGTEAPKLIRSSIQRYNCIAAQVCNHKLFHIKQDTTKEDSFIEFLENLHDKLRTILSKRQ
LTKRTIYVFDNASIHLTKKVVKCVTDRKMVCFTIPPYCPELNKVEHTFGLLKN

>Tec_Tec1_Euplotes_crassus_[30]
YIDECSFNASALPLYTWNKIGDEPVKLIRSTNQRFNCIAAQVEQHKIFHIKTETTKDQNFITFLEKLNSLLKTMIAKKQLM
KRTVYVFDNASIHSTEKVVKAITGMKMVCFTIPPYSPELNKIEHTFGTLKR

>Sailor_Mo_Batpla_[29]
YVDETWVNENDSPFKKWTSPQGETSNPPPSGKGKRLIILHEGSADSGFIDGYELVFKAKKGEGDYHAEMNTTVFMDWFTNT
LIPALDSPSVIVIDNAVYHNKITEQSQSPVSSHRKGEMIGWLELQGINVDPKLIKSEIYQIVRQHKPNPKYVTDEIAMENG
```

```
HFVLRTPIRHCELNAIELIW

>Sailor_Mo_Cepnem_[29]
YLDETWINAHHTSEKEWQSMDGKIKRYVPSSKGQRLVIAHAGSTHNGLLQNAGLVFVSKHTDNRDYHNEMNGNVFRDWLEN
TVLPSLDRPSCLIMDNASYHNVVAQEDKIPTASSAKEAIKIWLRRENIPFPETYFKLQLLSLVKQAQKSKKFQIDKLIEEH
GHRCLRLPPYHSHLNPIELVW

>Sailor_Mo_Cragig_[29]
YLDETWLNTNHVARGDWVDCPRTSTSAFESHRGGHGRFVPSGKGSRLIIVDAGSSAVGMIPGSALIFESKTGNQDYHDEMN
SENFTKWFTEQLLPNLPANSVIVMDNASYHSHLDPESRCPTSSAPKAEIQSWLDRKGIHYNPRMIKAELVTLVKQHKPRPK
YVIDDLASQSGHTVLRLPPYHCELNPIELVW

>Sailor_Mo_Cycsin_[29]
YVDETWVNANHCVKGEWSDSSVNDMSRLLGNEKGACEFIPSGKGKRLIVLDAGCRNVGLIPGVGEVFVAQNESGDYHNEMN
HEHFFNWWKNTLIPALPGPSTIVVDNASYHSVLTDDTRSPTTATRKDDIKVWLQERHIHFTDDMVKAELLEIVRRSKPRPK
FVIDEYAMESCQKVLRLPPRHCELNPIELVW

>Sailor_Mo_Hallae_[29]
YTDETWVNKNHSTDRMWLSCDMSSAPKIPSGKGKRLIILHAGRRECGLIPGCDLVFEVNSSEGDYHKEMNSQVFMEWLEHQ
XXXXXHNPSVIVLDNASYHNVKVESTVSPSMASKMCVMQSWFKDHDVSFHAKDIKPKRPEQIKVNKPKPQYQTDALAGSQG
HDVLRAPARHCELSPIELIW

>Sailor_Mo_Halrub_[29]
YLDETWVNANHTAARQWLPTDPSDGRKIPTGKGERLIVLHAGSHRGFLPGCDLVFRSKSTDGRDYHTEMNSTVFTQYVEEQ
LLPALPYKSLVVMDNAPYHSVRDPNNRCPTSNTKKSDMQQWLTNNNIQFSIKATKPQLYSLIKPNKPPPTYNIDNMLRQHG
HKVLRLPPYHCDLNPIELIW

>Sailor_Mo_Halruf_[29]
FLDETWVNASHTASSQWVPSGDCKESGRKLPMGKGERLIVLHAGSASQGFLPDCDLVFRAKAKDNRDYHTEMNGNVFLEWV
KDKLVPALPTKSLIVMDNAPYHSVQDPESKTPTSNNRKGDMVTWLQRRNITFPSRATKPQLYEIIKTMKPDPVYKVDSYIK
GQGHAVLRLPPYHCDLNPIELVW

>Sailor_Mo_Limfor_[29]
YLDETWLNTNHVVKGDWLDHPSTSMSVFEPPCKGCGRVLPTGKGTRMIILDAGSSQQGLIPGCGLIFESKTSSSDYHDEMN
SEHFTEWFRDKLIPRLLPRSIIVMDNAPYHSHLVPDSKVPNTGSRKSEISAWLERNDVQYDKEMVKAELLDLVKQHKPRPR
YVIDELASDHGHEVLRLPPHHCELNPIEMVW

>Sailor_Mo_Mermer_[29]
YLDETWIDTSHTAKYCWRSVEERGVAAPFSKGQRLIVVHAGGQNGFVPGAELVFKANCATGDYHHEMNGPNFEKWLKEKLL
PNLRVKCVIIMDNASYHSVQSEKTPSSSTRKADIQEWLRNRDIPFGEKLTRPELLNIVKMYKPKEKVYRIDSLIKERGHEV
LRLPPYHCEFNPIELIW

>Sailor_Mo_Modphi_[29]
YTDETWIDTSYTAKFCWQSTEESGVLLPISRGKRLIEVHAGGNKGFVPGALLVSKATSNTGDYHKEMNGENFKKWFTEKLL
DNLHEKSIVVMDNALCHSVKSEKCPTSSTRKADIQAWLTKHGIRFDSKMLRPQLLALAKSHKVDPQYVIDDIAKDRGHIIL
RLPPYHPDLNPIELVW

>Sailor_Mo_Mytcor_[29]
YLDETWLNTNHVVKGDWLDVPSTSMSVFEPHCKGTHRKVPSGKGTRLIIILDVGSSQQGLIPGCGLIFESKTNSSDYHDEMN
KEHFTEWFRDTLIPKLPPQSVIVMDNAPYHSHLDPDSRVPNTNSNKSEISAWLEKSNVHYDKKMKKTELLDLVKQKKPQPR
YIIDDLASANGHEILRTPPYHCELNPIEMVW

>Sailor_Mo_Pinimb_[29]
YLDETWVNKNHSTDFMWLPSDSSDAPKIPSGKGKRLIVLHAGTAKEGLIKGCDLVFVAKTKDGDYHNEMNSEVFLDWFENQ
LLPALKAPSVIVLDNASYHNTKTEQTTTPNMNNRKAVMQEWLKQHHITFAQSDTKPVLYEKIKRHKPQIVYQTDELAHQNG
HVVLRTPVRHCELNPIELIW

>Sailor_Mo_Rudphi_[29]
YTDETFLHTSHTVAKSWQSTFVGLKSPLNKGDRLIVVHAGNENGFIEGASLVFKSKSSTGDYHSEMNGENFLKWVREKLVP
NLPARSVLIVDNAPYHNLQTDKCPTQANRKAEIQDWLRRHGIVFEDNMLKAQLLQLCKSNKPAPRYVLDSLLKDHGHEVLR
LPAYHADLNAIELVW

>Sailor_Mo_Sacglo_[29]
```

YLDETWLNTNHVARGDWVDCPRTSTSAFESHREGHGRFVPPGKGSRLIIVDAGSSAVGMIPGSSLVFESKTGTQDYHDEMN
SGNFTRWFTEQLLPNLPGNSVIVMDNASYHSHLDPESKCPTSSARKAEIQSWLDRKGIHYTPAMIKAELLTLVKQHKPRPK
YVIDDLASQAGHTVLRLPPYHCELNPIELVW

>Sailor_Mo_Teggra_[29]
YMDETYINSSHTVPKCWQLDWNGLSVPIGAGDRLVVVDAGSEKGFVPNASLIYKAKSSTGDYHHEMNAENFTKWLREKLIP
NLEPNSVLVVDNASYHNVQEDKKPTTSWKKKDIQEWLTKHNIKFTEDMVRAQLLTICKQQIIPPSYRIDYILREHGHKILR
LPPYHTDLNPIELIW

Последовательности транспозаз *L31*-элементов двустворчатых моллюсков, которые были выявлены данном исследовании.

>L31-2a_MCor
GKTTGQDLKILIVQEMIEAGANLITGEVPRGVYTKIANKFKINRQSVTNF*YRYVTVGSISEKKKEKTLLGRRKLNEQGVR
LIEFIKKENPSITARKLKDKLLRCSPGNDNVYVFTIYRTMSRYLDFTLKRSHCLSGGYVNTGKYEIYITQAYLDFVQTKRP
HQTKFM**NE**SDFKLVTANRKYGHSQKGEQCIEIGRFIPGANFTLNFFIGFDCVSYYNFVDGPSNSERYLNFLHEASLTQDGY
SRPTFFQGDLIIV**DNCVIH**HHQAERILTNFFNMQGIDYGFLPVYSPDLNSV*MCFSKLKTVIKQERLKELISQNLKLAAI*
AIQQINKYDINGFNRHIGYFSV*

>L31-1a_MCor
TKPSIQFLNYVSNKIPFTVKFM**DE**MGVMLVDGQPVYGHSRKGTPFVEITRYDPHANFTASLNLGITGVKYVKIIEEASDSV
EYLQFIGKASQSYTND

>L31-2a_MEdu
MATKKNIYGREYLAGKATGRDMRSLIVQEMIEAGANLKTGEVPRGVYTKIADKFKINRQSVTNFWKRYVSEGTISQKKKEK
TMLGRRKLNEPDVRLIEFIKKENPSITARELKDTLLRYSPASANVDVSTIYRTMSRDLDFTFKRLHRPSGDRFTPRNMRYT
QAYLDFCQTKRPHQIKFM**DE**SGFKLVTANRNYGHSKKGEQCIEIGRFIEGANLTLNCLIGLDCVLYFNFVDGPSNSERYLN
FWHEASLSQDCYGRPTFLPGDLIIV**DNCAIH**HNQSERILNTFFNMQGIDYGFLPVYSPDLNPI**E**ICFSKIKTVIKQERFKE
LVSKNLKLAVIKAIQEINQSDIHGFYRHTGYFNV*

>L31-2b_MEdu
MERQNKYGRRFKQGFKLSDDFRTLTIDKCLEYGGNSDNQTIPRGTFSKVSEELKVTDFFVRKMWKQFCIDKEVKCKPHKGL
QPKLSNPDREYILAKKMEKPTISLSELREKLLHHSVVPNNNVSRMTICRVIKKDLNMTFKKVSRPKAERFTAANLRYTQAF
IDHIQTLDANKILFM**DE**SGYVVTVAHRTRGHSEVGTRCVEVERYHPNPNVTLNLIVGLNGRMYHNFVDGTSDTNTYLQFMG
EASHANTENGISVISPGDTIIV**DNSPLH**RNRAEVTLANFFAPMGVTLIFMPVYSPDLSAA**E**PVFMKSKIVLKQERFQTIIK
ENLKFAVSLSLGEVTTSDTREFFNGTGMFNV*

>L31-1a_MEdu
MTYKRIAHYKKNRFTVRNLQYTQQFLNYVSNKDPFTLKFM**DE**MGVKLVDGQPVYGHSRKGTPCVKLQDMTLMQISQLASDS
GEYLQFIGEASQSYTNDGESVFQPGECLVV**DNAPTH**HNMSERVLRNWLPTVGMEYLFLPAYSPDLNPA**E**HCFRKVK

>L31-1a_MGal
MKRNNSQGRQYSAGKALGDDLRGLIVHELKESGVHVGNSIPKGIAPKVAEKYKITKQTVHNIWKKYNEDLSVSRRPCAGGR
PRKYGIDEIEFVNVLKTERPSVEQNTLRDQLLQYSAISSISTSTVSRIITNDLNMTYKRTCITHYKKNRFMVRNLQYTQQF
LNYVSNKDPFTLKFM**DE**MGVKLVDGQPVYGHSGKGTPCVEITRYDPHANFTASLIIGITGVKYVKIIEGASDSGEYLQFIG
EASQSYTNDGESVFQPGECLVV**DNAPTH**HNMSERVLRNWLPTVGMEYLFLPAYSPDLNPA**E**QCFRKVKKLLKSDRFGPVLR
QDLKVAVYKAFNEITLMDTRSFFKATEYMNI*

>L31-2b_MGal
MERQNKYGRRFKQGFKLSDDFRTLTIDKCLEYGGNSDNQTIPRGTFSKVSEELKVTDFFVRKMWKQFCIDKEVKCKPHKGL
QPKLSNPDKEYILAKKMEKPTISLSELREKLLHNSVVPNNNVSRMTICRVIKKDLNMTFKKVSRPKAERFTAANLRYTQAF
IDHIQTLDANKILFM**DE**SGYVVTVANRTRGHSEVGTRCVEVERYHPNPNVTLNLIVGLNGRMYHNFVDGTSDTNTYLQFMG
EASHANTENGISVIAPGDTIIV**DNSPLH**RNRAEVTLANFFAPMGVTLIFMPVYSPDLSAA**E**PVFMKSKIVLKQERFQTIIK
ENLKFAVSLSLGEVTTSDTREFFNGTGMFNV*

>L31-2a_MGal
QRKNIYGREYLAGKATGRDMRSLIVQEMIEAGANLKTGEVPRGVYNRQSITNFWKRYVSEGSISQKKKEKTMLGRRKLNEP
DVRLIEFIKKENPSITARELKDTLLRYSPASANVDVSTIYRTMSRDLDFTFKRLHRPSGDRFTLRNMRYTQAYLDFCQTKR
PHQIKFM**DE**TGFKLVTANRNYGHSKKGEQCIEIGRFIEGANLTLNCLIGLDCVLYFNFVDGPSNSERYLNFWHEASLSQDC
YGRPTFLSGDLIIV**DNCAIH**HNQSERILNTFFNMQGIDYGFLPVYSPDLNPI**E**ICFSKIKTVIKQERFKELVSKNLKLAVI
KAIQKINQSDIQGFYRHTGYFNV*

>L31-3a_GPla
MSIPSGDRTNKFGRVYYKGASLSSDFRQLLIDNVIKNGANAVNGDVPRGLYSALGRSHGVSRTAVRSVWLKYCEDGRYEPR
PKKDVGAGSQRKLNDGALVFVQSILKEKPSTSYCEIADKLEQFSNWESVKTVPSVRNYLLSGKFSFKRITRQMGDKYNQNN
MKYYQHFVNYVSQMDPSKSKYF**DE**SGFKLTTAHRKYGHSLVEEKCVEVGRLVENPNTTLNLLVSVNGINHFNFVDGASNTN
TFVNFFFEAANSVSENGFPILEPGDLVSV**DNCPIH**RFNGEVRVSIFFFTADGSRIHFFLPRYSPELNIA**E**HCFLKMKTVLK
QERFLNTVRANLKVVIGQALQEITIHDLKEFCVATGC*

>L31-1a_MPhi
MEKKSISGRSYINGKALGDGLRSLIIDDLKDAGAKIGEKMPKGLVGRVAEKYKVCQTTIYRLWKKYSEDLSIKRRPYSTGR
PKKYGVEELEFVHVLKKERPSMQLKTVKDQLLQYSNIEAISYASISRMIHNDLNMTYKRVTHYKKERFTLGNLQYTQQFLN
YVHNKDPFLLKFM**DE**MGVNLTNAQPKYGHSEKGTPCVELTRYNRHSNFTVSLIVGVTGVKYVKVIEGSSDSVEFLQFIGEA
IQSYTDDGEPVFTPGQCLVV**DNAPTH**HNLSERVLRRFLPTVGLEYLFLPAYSPDLNPA**E**NCFRKVKALLQTDRYIPFVKND
LKVAVYKAFGEISLADTCSFFQATEYIDV*

>L31-1b_MPhi
IEKRNSQCRVYVQGKAMSDDLRYLILDDIKNEGAVSGQNLPKGLAGKISSKFK**IK**DDIEFVKVLKKEKPSIQYKSLKDQLL
QHSTLESISQGTLCNIVRKDLGMTYKK*QTMTKIDTL*ITCNIHNSF*ITLKIK**I**HLH*NLWILLDGQPVYGHSKKGMKCI
ELTRYDKHANLTVTLIVGVTGVKYVNIIEGSSDSVEFLSFIGEAVESYTDDGEPAFFPGDCLVV**DNAPIH**HNMSERVLRAW
LPTMGLEYLFLPSYSPDLNPA**E**QCFRKVKALLKTDKYSILMAKDLKVAVYIAFGEITLLDTRSFFSTTEYIDV*

>L31-3b_MPhi
MNQKNIFGRNYSKGKALSEDIRELIVTDLLENGANAASCHIPRGLPTKLSTKYKVSDRTVKNIWVKYCENGEVGRRPAAGG
RDRALSDGDLELIEVLLKEKPTISYANISSKLQQYSALPYALSKQRISDAVRKYLPSGKMTFKKVSRQSGDRYTQRNLNYT
QHFLTYASRANPHKLKFF**DE**SGFKITVCHRNYGHSKVGEPCIEIGRYKENRNLTLNLLVSLSGVCYYNFLDGPSNTDSSIQ
FWQEAAESVNENATSALEPGDIVIV**DNCPIH**RNNGELIVSNFLDRMGIEYMFLPIYSPDLNPA**E**S*FSQIKNILKQERFVG
MAIANLKVAIGEAIKEITGENIAGYYRATGYINV*

>L31-2b_MPhi
MESEDSCSKTNDFGRQFQKGRALSLEFRQLIVQEIKKLSGGSLLEVPFGIYSKVGRKFKIHTSSVTKIWRRFLENGCPSER
PRHGKQNVGKLTPDDFQFIEVLKREKPSICIKDIREKLYEHSDIDGGVSLSTIGRAVRNNLTGGKWTLKKLERPLGDRFSI
PNLRYTQAYLDYIFQQDVERLKFF**DE**SGFKTLTANKTRGHSLKGRRCIEVGPFRDSPNITLNLLVGIDGVKYFNFVDGASN
SAFYVNFFHEAIESVTDEGVPVLSPGDIVVV**DNAAFH**HNDSEVILSNYFSMQNIGYVFLPTYSPDMNPV**E**LCFSKIKQTLQ
NRYNYLVKDNLKLAVTLAVEDISPKDLQGFYLHTETFNM*

>L31-2a_MPhi
MATRKNSHGRECMPGKAIGQDLRQLIVQNVLESGGNASTGEVPLGTYTNIASKLKISRQSVVNIWRRFISDASVAEKKRTS
NGNPKLTEPDVRMIEFLKRETTSITAKELKEKLTRYSPVTGNVHETTVYRAINQKLNFTFKRLIRPIGDRFSAYIYMRYTQ
AFIDYCQTKQPHQIKFM**DE**SGFKVVTANRQYGHSERGKPCIEIRKYHPGPNLTLNFFISVDCVLYYNFVSGPSNTATYLNF
WHEASLSQDIFGRPLFLPGDLVIV**DNCAIH**HNQAEQVLAHFFGMRGVEYAFLPTFSPDLNPA**E**NCFLKIKTVLKQRRYSGI
VEQNLKLSIIKAISEIKQEDLIGFYRHTGYLNV*

>L31-3a_MPhi
NKFGRVYHKGASLSSDFRQLLMDNLIRNGADTVTGDVPRGYILV*SRNHRVTRTTVRSVWLKYCGKYEPRPKKGIGAGRQR
KLNDGDLVFVQSILKEKPSSSYSEIADKLEQYSATGRVSKQCLSHSVRNYLPSGKFSFKRITRQMGDKYYQNNVNYYQHFV
NYISHMDPSKCKYF**DE**SGFKITTAHRNYGHIIVGEKCVEVGRLVDNPNTTLN*LVSVNGINH*NFVDGALNTDTFVNFFFE
AANSVSENGFSALEPGDLVIV**DACPIH**RFNGEVRVSNFLQQMGVGYIFLPRYSPELNTA**E**NCFLNVKTVLKQKRFLNLVRA
NLKVAIGQTLQEITLHDLKEFIIATGCLNVQ*

>L31-4a_MPhi
MEKEKRFISQKGVSLSKDMRKLIVTKLKELGSDEESKFSPRGAFSIVRSNLNLDRRLVGRVWSEFCERRDFSTLKDKNKGG
RTTSLSNSDIGYLEFLKTSDPAISYKQMNEKLKMFSTTNVSVGKIQRAVKGKFLGGEWTYKKLTTFSKDRFTDGNIEYTES
FMELLHRADPYKLRFM**DE**SGFCTPDVGTPKYGHALKGTRGVMVNPNRKTPMTTLDLLVGLTGVMHAKTFRGSVDSFDFMDF
ITECVHSVNQFGELALQPGDILVV**DNSPLH**HSEVARSTKRWLEAQGIDVVFTPRYSPDMNPV**E**LCFSKLKKILNRPNFRSR
LVEDMPGCIYDILGELTPSDMQGFFRETGYISI*

>L31-1b_CGig
MENRNKLGRFFVNGKELSEDLRRIVIDNLVEGGANVSDLQLPRGLRQRVSKKFGISANCISSIWKRYVTVGTVRRRPRRGG
PSKTVQQEDVDHIAVLKTINPTMSLKSVKDNILQYSNTLQNISLPTVSNIIRKDLHMTLKRVTFCHGNRFTLPNLQYTQRF
LQYVNNEDPFTLKFM**DE**MGFVVCDGNKVYGHSVKGTPCVAVAKFNAKIHFTISLIVGVSGVKFVKIVEGSSNSIEFLHFLG
EAGNVATDEGERVLQRGDSLIV**DNAPTH**RNMSEVVLRNWLPTIGVQYIFLPTYSPDLNPA**E**LCFRKVKILLKTEKYTALLA
QNIKVALYSAFSEITVHDTLSFFRATDYIDV*

>L31-2a.1_CGig
MCTKRNMYGREYQQGIELSTDFRSLLIQDLIDRGCDSASGKVPWGALSATAKKFKVSVKTVNKIWRRFVEHGTCTEKMRNK
SGPRKLTEPDQRFIECLKRETPSMSCKEIQEKLRRYSPVSGEVSLPTINRCILKNLKFTYKRLKYSRIERFTNDNMIYSQA
YIDFCQTKNTRQIKFM**DE**SGFKLTNANRTYGHSRRGEPCVEIGRFVKDRNLTLNLLIGKDCVLYYNFVDGSLNMYTYLNFW
EEAAQNQDEYGRAVLIPGDFVVV**DNCPIH**RNNSERVLRHYFGMQGVQYGFLPVYSPDFNPV**E**NCFLKLKKILSQEKYLPYL
QVSLKLAITQALKEISSNDIRQFYRQTGYLNV*

>L31-1a_CVir
MAKINSAGRVYDKGTPLGIDLRRSIINYMEEQGAKFGSLQLPRGLPQKVSEIFKVSHPLVTKIWKQYCIEGIVKLPEYKGG
RKRKLDQEDVQHIHFLKETKPSMPLKSVKEEVLKYSNAVIKVSESTISRHLKNDLNMTYKRIARYSKNRFTPQNMNYTQNF
LNYVGQKDPFSLKFM**DE**MGVKLSDGQNVYGHSLKGTPCIEMTRHNPHRNVTASVIVGISGVKYVKIFDGASNGTEYTQFIA
EATQSYTDEGEPVFNPGDCLIA**DNAPIH**HNMAERELNNYLPTVGVEYVFLPTYSPDLNPA**E**QVFRKVKKILKCDRYITLLN
LDLKVAVYEAFKEISTADTLSFFRSTEYIKNP*

>L31-1d_SGlo
MEKRNKYGRVFVNGKPLSNDLRGLIVQDICEMGGVPKGVKKELAKKYKLNPDTITRVWLKHIEGEQISKKPTGRPKILDEE
DVEFISALKTARPSMQLETIRDQVIQNSNTVQNVSTSTVCRALKNDLSMTYKRITKYDKDRFTLNNLIFTQRFLNYIQNKN
PYTLKFM**DE**MGVSLSSGNPNYGHSVKGTRCVELTRYKRHTNFTVSIIVGITGVKYVSIVDGPSNTAEFLKFVGEAVNSYTD
EGEAVFSHGDCLVV**DNAPTH**HNTSERILRTFLPTMGIDYLFLPAYSPDMNPA**E**QCFRKVKTLLKRDRYIVHMEQCLKVAVF
KAFSEVSAADTRSFFHATEIVNC*

>L31-2a_SGlo
MATNKQGREYSNGVGVSKDLRALIVQEVIERGGSSVTGKVPRGVFTAVSEKFKVVVQTVSNVWKRYLSTGDLSERRRNTQG
RPKLTEPDVRMIQFLKQESPSVTGREVLDKLKKYSPVSGNVTVRTINRSLRRDLNFTFKRLKRPICDRFTQGNMFYTQAYI
NY*QTKQPHQIKFM**DE**SGFKTTCVNRNYGHSEKGTSCIEVGRYLPGRNLTLNLLVSVDCVLYYNFIDGPSNTEKYLNFWQE
ASLGQDDYGRPVFLPGDAVIV**DNCAIH**HNQAERVLSNFLGLKGIDYGFLPTYSPDFNPV**E**NCFGKIKKILSQERFHGIVGQ
NLKLAITQAIKEISQSDLIRFYRHTGYLNV*

>L31-1b_OLur
MEKQNEFGRTYKCGKELNEDMRRMVAEDGSRSSNERRSRCLNSKIAERIASIYRKEIWYFCELR*YVTLGTACRGPCRGGR
PKTVQQDDVNHVAVLEIINPTMLLKSIKDNILQYSNTLQNISLQTVSKI*I*HLNVS*CVMVTDLQYTQRFLQYVNNKDPF
SL**DE**MGFEASNGNKVYGHAIPKLHSKVHYTVSLIVGVSGVKYVKIVDGSSDSLEFLHFLGEAGHSYTNEGEKVLQGGDVSL
IV**DNASIH**HNMSEMVLRDWLPTIGVKHLFLPTYAPDLNPA**E**RCFRKVKILLKSEKYCRLLSENVKAAFYTAFNEITVHDTL
SFFRATEYIDV*

>L31-2a_CHon
MCTKRNMYGREYQQDIGLSTDFRSLLIQDLIDRGCDSASGKVPWGALSATAKKFKVSVKTVNKIWRRFVEHGTCTEKMRNK
SGPRKLTEPDQRFIECLKRETPSMSCKEIQEKLRRYSPVSGEVSLPTINRCILKNLKFTYKRLKYSRIERFTNDNMIYSQA
YIDFCQTKNTRQIKFM**DE**SGFKLTNANRTYGHSRRGEPCVEIGRFVKDRNLTLNNFVDGSSNMYTYLNFWEEAAQNQDE*G
RAVLIPGDFVVV**DNCPIH**RNNSERVLRHYFGMQGVKYGFLPVYSPDCNPV**E**NCFLKLKKILSQEKYLPYLQVSLKLAITQA
LKEISSNDIRQFYRQTGYLNV*

>L31-1a_CAri
MLSVNRRNIAGRVYEKGIPTGIDYRRSIIDYMESNGARLGEYSLPRGLQKTASQQFKVSPATITNFWTQYCNEGCVKVPVQ
TNRGRKKKLLEEDVEYVRFLKHVRPSMPLQTVRDELLKNSNSMETVGLSTISRTLKEDLNMTYKRISKINKNRFTPQNMNY
TQHFINHINQKDPFTLKFM**DE**MGIKLADGQNNYGHSVKGLPCIELSRYNPHANVTVNAIVGMSGVKYVKIFDGPSNGTEYV
QFIAEAAQSFTDEGEPVFHPGDILIA**DNAAIH**HNRAERELRNFLPTVGVEYFFLPTYSPDLNPV**E**AVFRKIKKIMKGDKYI
TLLHADLKVAVYEAFKEITSADTLSFFKNTEYINY*

>L31-1c_CAri
MESLSKQGRLNINGKSLSRDMRNAVICDLVNGGASAGDLKFPRGLGANLAKKYKISKSTVSNIWRKYNENFSISPRKPMNT
KDRKIGNEDREFIKALKNERPSIQLQTIRDELLKHSNTITSISISTISNTIRKDLSMTYKKICLYNKNRFTLQNLQYTQQF
LNYVFNKDPFRLKFM**DE**MGIRLVDGQPTYGHSVKGSKCVEMTRYSRTSNYTVNLLVGITGVKYVNILDGPSDTTKYVDFVG
EAANSFTDDGERAIQVGDVLVV**DNAPIH**HHAAERILRNWLPTIRAEYLFLPTYSPDLNPA**E**QCFRKVKTLLKNDRYRVRLS
NNFKMAVLEAFGEITISDTLSFFHATECVHTG*

>L31-1c.2_CHon
MESLSKQGRLNINGKSLSRDMRNAVICDLVNGGASVGDLKFPRGLSLFL*RSGPSFERQKSIKFQNRLFQISWRNIMKTFP
FLLVNQ*TQKIGK*EIKIVNLSRH*KTKHLLFSFKQFEMNCSNILTQLQASVFQQLAKPFEKICQ*HTKKFCLYNKNIFTL
QNLQYTQQFLNYVNKDPFMLKFM**DE**MGIRLADGQPTYGHSVRGSKCVEMTRYSRTSNYTVNLLVGITGVKYFNILDGPSET
TKYVDFVGEAANSFTDDGERAIQVGDVLVV**DNVPKH**HHAAERILRNWLPTIGAEYLFLPNYSPDLNPA**E**QCFRKVKTLLKN
DWYRVRLSDNFKMAVLEAFGEITISDTMSFFHATECVHTG*

>L31-1c.1_CHon
M*DLSKQGRLNINGKSLSRDMRNAVICDLINGGALVGDLKFPRGLSANLAKKYKISKSTVSNLWAKYNETFSISPRKPMNT
KDRKIGNEDQEFIKALKNERPSIQLQTIRDELPKHSNTITSISI*TIGKTIRKDLSMTYKKKLSLQQKQINFTKSSVYPTI
FEFCFNKDPFRLKFM**DE**MGIRLADGQPTYCHSVRGSKCVEMTRYSRTFNYTVDLLVSITGVKYVNILDGPSDTTKYVDFVG
EAANSFTDDGERAIQEGDVLVV**DIAPIH**HHAAERILRN*LPAIGAEYLFLPTYSPDLNPA**E**QYFRKVKNLLKNDRYGVRLS
DNFKMAVLEAFGEITISDTLSFFHATECVHTG*

>L31-1a.1_CHon
MLSVNRRNIAGRAYEKGIPTGIDYRRSIIDYMESNGARLGEYSLPRGLRKTASQKFKVCPATITSFWTQYCNEGCVKVPVQ
TNRGRKKKLLEEDVEYVRFLKHVRPSMPLTTVRDELLKNSNSIETLGLSTISRTLKEDLNMTYKRISKINKNRFTPQNMNY
TQHYINHINQKDPFTLKFM**DE**MGIKLANYGHSLKGLPCIELTRYNPHANVTVNAIVGMSGVKYVKIFDGPSNGTEYVQFIA
EATQSFTDEGEPVFHPGDVLIA**DNAAIH**HNRAERELRNFLPTVGVEYFFLPTYSPDLNPV**E**AVFRKIKNILKGDKYITLLH
ADLKVAVYEAFEEITSADTLSFFKNTEYINY*

>L31-1a.2_CHon
MLSVNRRNIAGRAYEKGIPTGIDYRRSIIDYMESNGARLGEYSLPRGLRKTASQKFKVCPATITTFWTQYCNEGCVKVPIQ
TNRGRKKKLLEEDVEYVRFLKHVRPSMPLTTVRDELLKNSNSIETLGLSTISRTLKEDLNMTYKRISKINKNRFTPQNMNF
TQHYINHINQKDPFTLKFM**DE**MGIKLADGQNNYGHSVKGLPCIELTRYNPHANVTVNAIVGMSGVKYVKIFDGPSNGTEYV
QFIAEATQSFTDDGEPVFHPGDVLIA**DNAAIH**HNRAERELRNFLPTVGVEYFFLPTYSPDLNPV**E**AVFRKIKNILKGDKYI
TLLHADLKVAVYEAFKEITSADTLSFFKNTEYINY*

>L31-1b_CHon
MENRNKLGRFFVNGKELSEDLRRIVIDNLVEGGANVSDLQLPRGLRQRVSKKFGISANCISSIWKRYVTVGTVRRRPRREG
PSKTVQQEDVDHIAVLKTINPTMSLKSVKDNILQYSNTLQNISLPTVSNIIRKDLHMTLKRVTFCHGNRFTLPNLQYTQRF
LQYVNNEDPFTLKFM**DE**MGFVVRDGNKVYGHSVKGTPCVAVAKFNAKIHFTISLIVGVSGVKFVKIVEGSSNSIEFLHFLG
EAGNVATDEGERVLQRGDSLIV**DNAPTH**RNMSEVVLRNWLPTIGVQYIFLTTYSPDLNPA**E**LCFRKVKILIKTEKYTALLA
QNIKVALYSAFSEITVHDTLSFFRATDYIDV*

>L31-1c.3_CHon
MESLSKQGRLNINGKSPSRDMRYAVICDLVNGGASVGDLKFPRG*SANLAKKYKISKSTVSNLWAKYNENFSISPRKPMNT
RDRKIGNEDREFINALKNERPSIQLQTIRDELLKHSNTITSVSISSISRTIRKDLSMTYKKICLYNKNRFTLQNLQYTQQF
LNYVFNKDPFRLKFM**DE**MGIRRATNLWSLCKGFKVRRNDPIQQNF*

>L31-2a.2_CGig
MCTKRNMYGREYQQGIGLSTDFRSLLIQDLIDRGCDSASGKVPWGALSATAEKFKVSVKTVNKIWRRFVEHGTCTEKMRNK
SGPRKLTEPDQRFIECLKRETPSMSCKEIQEKLRRYSPVSGEVSLPTINRCILKNLKFTYKRLKYSRIERFTNDNMIYSQA
YIDFCQTKNTRQIKFM**DE**SGFKLTNANRTYGHSRRGEPCVEIGRFVKDRNLTLNLLIGKDCVLYYNFVDGSSNMYTYLNFW
EEAAQNQDEYGRAVLIPGDFVVV**DNCPIH**RNNSERVLRHYFGMQGVQYGFLPVYSPDFNPV**E**NCFLKLKKILSQEKYLPYL
QVSLKLAITQALKEISSNDIRQFYRQTGYLNV*

>L31-1a_CGig
MLSVNRRNIAGRAYEKGIPTGIDYRRSIIDYMESNGARLGEYSLPRGLRKTASQKFKVCPATITTFWTQYCNEGCVKVPVQ
TNRGRKKKLLEEDVEYVRFLKHVRPSMPLTTVRDELLKNSNSIETLGLSTISRTLKEDLNMTYKRISKINKNRFTPQNMNY
TQHYINYINQKDPFTLKFM**DE**MGIKLADGQNNYGHSVKGLPCIELTRYNPHANVTVNAIVGMSGVKYVKIFDGPSNGTEYV
QFIAEATQSFTDEGEPVFHPGDVLIA**DNAAIH**HNRAERELRNFLPTVGVEYFFLPTYSPDLNPV**E**AVFRKIKNILKGDKYI
TLLHADLKVAVYEAFKEITSADTLSFFKNTEYINY*

>L31-1c_SGlo
METVNQRGRPYVKGKALSKDMRSLLIYDLIQGGAVKGNPTIPRGLGVELMRKFKVSKSTANLWKKYNEKFSVSPRKPFHAS
TRKIGEEDCEFIKVLKTEQPSMQLKTIKNELLRHSNSITHVGIRTISNTIEDLNMTYKKMCLYHKNRFNIHNLQYTQRFLN
YVANKDPYTLKFK**DE**MGIKLVDGQPNYGHSIKGTRCVEMTRYDRTANYTVNLIVGITGVKYVSIIDGPSDTFKYVGFIGEA
ANSFTDEGERAFQLGDTLVI**DNAPIH**HHTAERILRNWLPTIGVDVLLPTYSPDLNPA**E**KYFLKVKTLIKSDRYVTALHKDM
KEAVLQAFGEITMADTLSFFHATDCIITKAYKGQIRK*

>L31-3a_SGlo
MRRSKLGREYNQGKALSDDYRASLITSLKISGARVDTGFIPRGEISNVANNFNVHPSTVKRIWKNFCKGGDVCPGVRGGKK
PRKLSEHDVVFIEACLREKPTTTYKEIVEKLKQFSPTPDVTEKDISNAVIKFLPSGRFTFKKITRMAKERFTVENMQYTQT
YIDILSQLNPRKVKFF**DE**SGFKTTVAHRHYGHSKYNERAIELGRFIPNANITLNLFVSLEGPAYFNFVDGPSNAQAFLNFW
AEAAETFTPNGVTANEPGDVIIV**DSCAIH**KYQAEIELTRFFNRMGVTYFFLPTYSPDLNPE**E**RCFNKLKLLLKQQRYHDLV
QNNLKVAVGNAIQEINADDLCLF*KCTGCLNV*

>L31-2a_AIrr
MATRKNKYGREYHNGTGISQDLRSLIIQEIIELGGNSQSGNVPRGIYVKVANTFRVDEKSVRTFWKKYISEGSMSETARHK

AGNPKLNGADVQLVSFLKRNTPSVTGNKIKRNLCKYSPVSGNVHNSTIYRAMSRELDLTYKRINRPSCDRFTQYNMQYTQA
FIDFCQTKRADQIKFM**DE**SGFKLTTTNPAYGHSKKGQACVEIGKYRPGRNLTLNLLVGLNGVLYFNFVNGASNMNTYLNFW
GEASACQDNMGCPLFKPGDVVIV**DNCSIH**HNHAERVLRQYFSMQGVQYTFLPVYSPNFNPV**E**NCFAKIKNIFTQERFQDLA
GINLKLAIGDFRKDGDDVTQRYIRALKGTTLYIYT*

>L31-5_MYes
MEVTQSGRYFTKGERITDAEKTKVIELYSAGLPYSQIAKSTGITKGCCFKITQTFTTDKPQRDPVISPKLTNEVLQFIE*Q
KIAKPSIYAKEIYVKLLETNVCTMNNIPSVRTIHHALKSILGMTHKVLQRIPSETTTDQFENKLNRFLT*LLLYTPEQLHF
F**DE**ASIVRTDGNRKRGHNYRGEKAVEIQKYASNATFTINLCTWYFGIDHFGIIEGSSNANIMLKFFDEAMQEMNIVGNPVL
ALGDCIVI**DNCGFH**HQRFGEAFLRHMLGIRGINLVFLPPYSPELNPC**E**YVFKLMRYRLRQNTALTYEYTEYAVVNAVTGI

>L31-2a_PMax
MTTRKNASGREYKKGDGISSDLRKLIVQETLHLGGNVLTGEIPRGVFNKVAEKYKVNRQTVTNFWRQYVSDGALSEKTRNT
LGRPKLNTTDIEMIHFLKKDRPSITGTELKQKLIEYSPVSGKVDTSTIYRTMSKKLDLTYKRITRPSCDRFSQHNMVYTQA
YMDFCKTVRPCQVKFM**DE**SGFKITTTNSNYGHSKKGVACVEIGKFHPGRNLTLNLVVGLNGVIYYNFVDGPSNMNTYLNFW
NEASLSQDRLGRSAFLPGDVVVV**DNCAIH**HNNAEIALSQFFQMQGVGYTFLPVYSPDLNPV**E**NCFAKIKSLMTQERFRELA
SVNLKLSIIRAIEEITPTDMKGFYRHTGCFNV*

>L31-5_AIrr
MNRNVDINVNGRVYKKGKPLDDDSRYTVICLRDSGLPYSKISKQTGVSASTCHKIATNNLTIPIRVKKKPVSVGKKITTPV
MKFIEFESVKRPSIYDREIRSKLLTSNICTAENVPSKTSINKVRHQYLDMTFKKISQIPEETTRPNHEDTVTRFIAKMTNF
TPQQMHFF**DE**ASVISTSGNRSYGHSTIGKKAYEVQRYASNKTFTVNACCGYFGLDYFDVLEGPSNAMEMLSFFEEALRQTN
DLGNRVFAMGDVVVMDNCGFHHQRAGERILRTML**DNAGVE**LVFQPPYSPQYNIAECVFHAMRCRLRDNTSFT**E**NFTELAIV
TALGDIPNRELANYFRLCGYV*

>L31-4b_PImb
MKKSHVNNKGRRYDWGKPLGEDLRSLIVQYLLEKGANSESRFIPRGEMAKAGERFNVSNNTIKNIWTLYCDSGDVKHRQGA
RGRPKLLDEEDFNYIAAIKKEKPFETLENIKEKLLQNANKEVTTMTISNALRKDLIGGQWTRKVLTKTATERFTPANEQYT
EAYIAEIQSKPPLRLKFM**DE**AGFALSEAVNRTRGHAPKGLRAIEAQKRMKTTNLTLNLMIGLDGTVFSTFVDGPSNRDEFL
KFIDEAATSFSDDGSPVLQPGDVLVV**DNATIH**RFEAERILRIFFNNIGVEYIFLPKYSPDMNPV**E**FSFNYIRTMLKSEIFS
ALANDNLQYAILKVLDTISQDDIAGFFSKVGYIEA*

>L31-4a.1_PImb
MSKSKKGRLYKFGTSLSADFRLNIISKLKDYGANDDTGSIPRGIKAKVSKELLIDKNCVTRAWLSWINDKNVESKPKGPTK
GSTMSLDQNDLHYIEFLKRERPSISLREIHNKLLENCNKIIHESTISHALKQNLAAGEFTRKRLCKPARERFTSDNLKYTE
ALMYYLSQKDVHRIKYF**DE**AGFNSRDCSPIYGHALRGERAVEVSSKAKSTNLTLNLMIGVNGVVHCNIVDGATDTIQYLNF
FDQAIDSYTDEGYHALVPGDIVVV**DNAPVH**RYSGGNALSVFLDQFGIEYVFTPTYSPDLNPV**E**NVFSKIRQIMQRNEFKQL
IETNLEYAIFKSVSQISPVDCKSYYTNLGYLSM*

>L31-3a_PImb
MATRMNVRGRPYTNGKAISDDLRELIVSALIENGADKETGKVPRGIFTKVSMQFKVSNSSATNIWKKNCEDGSVSRRPGGV
KPRKLSDGDIGLIQTIVSTTPSISYKKISEELEKYSSTGRVQEQLIGKAVRKYLPSGENTRKIITRQNRNRYTDGNMAYTQ
WYLNYIQQKNVRKLKFF**DE**SGFKITDANKRYGHSPIGEKCIEIGKYVATPNLTLNFMVSLDGVSYYNFVEGAADTDNFVEF
FYEAAESYTSIGMPVLEPGDVVVL**DNCPTH**KHEGERRAKDFLGRMGIELVFLPVYSPDLNPA**E**MCFSKIKTLLKDESYQNL
VPANLKVAIGMAISEISVSNVKGYYRCTEYLQV*

>L31-3b.1_PImb
KGKRCIEIGKYQGSNVTPNMIISLNGILYYNFVDGASDTEIFVNF*TEAVESLSPNDNATLQPGDIVIL**DNCPVH**KNEGER
CVSAFLASMGIELVFLPTYSPDLNVI**E**NCFGLLKSILKQDGLLQIVQENPKVCIAEAMRRISSVDTEKFYLDT

>L31-3b.2_PImb
LSEDLRTLIIRTLKDNGANDVLNTCPRGLLTTTSVQFKVSSQCVKKKSGNNTVQVVTQHARNDPKYLFSEGDLELIEALLR
EKPTMSYRKISEKLMQYSSIPKHVSKQRISDAVRKRLPSGMFTNKKVRRKQEDRFTNENIRYTKAFITYISHKNPRKLTFF
DECGVKVSSCNPTRGMSEKRKRCIEIGKYQQGSNVTFNMLISLDGILYYNFVDKASDAETFVNFWTEADATL*PGDIVIL**D**
NCPIHKNEGERRVSAFLASMGI*LIFLLTYSPDLNVI**E**NCFGLLKSILKQD

>L31-4c.1_PImb
MYQKSNSLG*TYDNGKATGSDLRSLIIDHLKNSGANVELRHLPRGLIDVKYFQSFLGICEEDMGRLL*FRFCEAITTFWRE
NRYSQSARFGILYFLKKERPSLSLKEVREKINENCGKDVSLSTISRAINTKLNEGNWSYKVLTAPSTERFSDHNVNYLDAY
IQEIRTKDPYKLKFL**DE**AGFAMSVAVNRKRERSPIGLRAIETQISK*EPNSTLNLLLGLNGEVCVDFIYGASNSAEFLRFF
HEAATTYSDDDRPYIEPGDTVVV**DNASIH**RFEAERALRIYFAGIGVEYIFLPTVSP*MNPV**E**HAFNFNRTKLQYEFSDMTK
ENLPIYAILEITKKIDLECIAGFFRPVGYILN*

>L31-4c.2_PImb
QHSGGKTDILSQQDLEYIYSL*KERPSLSLKEVREKINKNCGKAVSLSTISRAINTKLNEGNWSY*VLTTPATERFSDHNV
NYLDAYIQEIRTKDPYKLKFM**DE**AGFAMSVSINRKRGHSPIGLRAIVTQISKQEPNSTLNLLLGLNGVVCADFIYGASNSD
EFLEAATTYSDDDRPHIEPCDTVVV**DNASIH**RFDAERALRIYFAGIVVEYIFLPTYSPDMNTV**E**HAFNFIRTKLQYEFSDM
AKENHPYAIWKNIDLECIAGFFRSVGYILN*

>L31-4a.2_PImb
MSKSKKGRLYKFGTSLSADFRLNIISKLKDYGANDDTGSIPRGIKAKVSKELLIDKNCVTRAWLSWINDKNVESKPKGPTK
GSTMSLDQNDLHYIEFLKRERPSISLREIHNKLLENCNKIIHESTISRALKQNLPAGEFTRKRLCKPARERFTSDNLKYTE
ALMYYLSQKDVHRIKYF**DE**AGFNSRDCSPIYGHALRGERAVEVSSKAKSTNLTLNLMIGVNGVVHCNIVDGATDTIQYLNF
FDQAIDSYTDEGYHALVPGDIVVV**DNAPVH**RYSGGNALSVFLDQFGIEYVFTPTYSPDLNPV**E**NVFSKIRQIMQRNEFKQL
IEANLEYAIFKSVSQISPVDCKSYYTNLGYLSM*

>L31-1a_MCal
MKRINSQGRQYSAGKALGDDLRDLILHELRESGANVGNSIPKGIAPKVAEKYKINKQTVRNIWNKYNEDLSVSRRPCAGGR
PRKYGIDEIEFVNVLKTERPSVEQSTLRDQLRQYSAINNISRSTVSRIITNDLKMTYKRIAHYKKNTFTVRNLQYTQQFLN
YVSNKDPFTLKFM**DE**MGVKLVDGQPVYGHSRKGPCIEITRYDPHANFTASLILGITGVKYVKIIEGASDSVEYLQFIGEAS
QSYTNDGESVFQPGECLVV**DNAPTH**HNMSERVLRNWLPTVGMEYLFLPAYSPDLNPA**E**QCFRKVKKLLKSDRFGPVLRQDL
KVAVYKAFNEIKLMDTRSFFKATEYMNI*

>L31-2a.1_MCal
MATKKNSYGREYLVGKATGRDMRSLIVQEMIEAGANLKTGEVPRGVYTKIADKFKINRQSVTNFWKRYVSEGSISQKKKEK
TMLGKRKLNEPDVRLIEFIKKENPSITARELKDKLLRYSPANANVDVSTIYRTMSRDLDFTFKRLHRPSGDRFTPGNMRYT
QAYLDFCQTKRPHQIKFM**DE**SGFKLVTANRNYGHSQKGEQCIEIGRFIPGANLTLNFLIGLDCVLYYNFVDGPSNSERYLN
FWHEASLTQDCYGRPTFFPGDLIIV**DNCAIH**HHQSERILNNFFNMQGIDYGFLPVYSPDLNPV**E**MCFSKIKTVIKQERFKE
LVSQNLKLAVIKAIQEINQSDIKGFYRHTGYFNV*

>L31-2a.2_MCal
LNEPDVRLIEFIKKENSTITARELKDKLLRYSPANAYVDVSTSIYRTMSRDLDFTFKRLHLPTGDRFTPGNVRYTQAYLDF
CQTKRPHQIKFMDENGFKLVTANRNYGHSLKGEQCIEIGRFIPGANLTLNFLIGLHFVTVTADRPFFPGDLIIVDNCAFYH
HQSERILNNFFNMQGIDYGSLPVYSPDLNPVEMCFSKIKTVIKQERFKELVNLKLAVIKAIREINQSDIKGFYRHTGYFNV
FVFFVSLQQ*

>L31-2a.3_MCal
TQAYLDFCQTKRPHQTKFM**DE**SDFELVSANRKYGHSQKGEQCIEIGRIIPGANFTLNFLLDLTASFYNFVDGPSNSGRYLN
FCMRQV*HRTVIRPTFFPGDLIIV**DNCAFH**HYQAERILNNSFNMQGIDYGFLPVYSPDLNSI**E**MCFSKLKTVIKQERLKEL
IRQNLKLAVISAIQQINKSDINGFYRHIGYYSV*

>L31-4a_SGra
GGNQIDGTLPRGVLSRVSLCLGVNKNTAKAVWQSYCQTGGVSRPYHHGGGRSRKLTDEQERYMDFLVTETPSLSLGDIQLR
IKQMFDINIATCNISRLLNRLKTRKRIVRPAAARFDANNVAYTNVFLRTISTVDHRRLKFFDESGFSIPDICNPRYGRAPP
GERAIEVYTLNLMIGSNGVEHFNILEGPSNVETFEEFFVQAVNGTNNAGEFSLKPGDIVIMDNCPIHHGRAEVVIRHLLNT
VHVDIVFLPTYSPHLNPVELCFQHIKTVFKSNDVARRLAKDNLEFAIAHVVNSVTAENRSSYFKHVRYVNI*

>L31-4a_EMer
MATSSKPKGGRPLSSDFRNLIIKKMINFGADENLNIKPRGAYTSVARQLEIDRGTVRNIWNKYCATKNCAPSPYIRHASGK
LTDEHKQYIIFLVQQTPSLSLGSIKDKLSAMCNVDISKPAICGFLKKEMTRKILTKPAAERFNDENMMYTRAFLAVMYRTD
PKKMKFLDESGFHKPDVCNRRYGRSTKGERAIEIQTRTRTKNVTLNLLIGIDGVCHANILDGASNADTFMEFVFNALNSTT
NYGDLALRPGDFLILDNCPIHRFRAEDVLSRMLDRFGIEYILLPTYSPHLNPVELCFNHIKTLMKTEDIRSVAKDNLEYAI
MCCVNSITADDCMGYYSHVGYLRM*

>L31-4a_CSin
MKRLEKKILSEDFRLLVIRKIKDLGGDTETNTVPRGTYATVARSCGVHQTTVKNIWDKYCLTGEVKVMPKNGGRKKTFGTE
EMNFLNYLVKQKPSISLGELKDKLSEQCDLEVSTSTVSRYLTKYNTRKLLTRPAADRFTDINRIYTQAFIDALHRQDVASI
KFFDESGFALPDVANPRYGRSPRGDRAIEIHDRKRIPNKTLNLLIGINGVMFANILDGPSNTDTYVNFFLQAINATNNAGD
FALRPGDLLIVDNCPLHHHRAEEILKFFLYRHGIEYIFAPTYSPHLNPVELCFQHIKNLFKFEPVRSLAKENLQYAIMHCV
NSISSRNCEMYYRHVGYLNV*

>L31_Mariner-53_CGi_(Repbase)
MLSVNRRNIAGRAYEKGIPTGIDYRRSIIDYMESNGARLGEYSLPRGLRKTASQKFKVCPATITTFWTQYCNEGCVKVPVQ
TNRGRKKKLLEEDVEYVRFLKHVRPSMPLTTVRDELLKNSNSIETLGLSTISRTLKEDLNMTYKRISKINKNRFTPQNMNY

```
TQHYINHINQKDPFTLKFMDEMGIKLADGQNNYGHSVKGLPCIELTRYNPHANVTVNAIVGMSGVKYVKIFDGPSNGTEYV
QFIAEATQSFTDEGEPVFHPGDVLIADNAAIHHNRAERELRNFLPTVGVEYFFLPTYSPDLNPVEAVFRKIKNILKGDKYI
TLLHADLKVAVYEAFKEITSADTLSFFKNTEYINYLNKNQYCLAFVFLSLFFKCKKKNPCCRKEEASLKSGYLGRKNSXIA
CIPXRDTXYKYLLFNIFXINFRVASRLHGNK

>L31_Mariner-31_CGi_(Repbase)
MENRNKLGRXYVNGKELSEDLRRIVIDNLVEGGANVSDLQLPRGLRQRVSKKFGISANCISSIWKRYVTVGTVRRRPRRGG
PSKIVQQEDVDHIAVLKTINPTMSLKSVKDNILQYSNTLQNISLPTVSNIIRKDLHMTLKRVTFCHGNRFTLPNLQYTQRF
LQYVNNEDPFALKFMDEMGFVVCDGNKXYGHSAKGTPCVAVAKFNAKIHFTISLIVGVSGVKFVKIVEGSSNSIEFLHFLG
EAGNVATDEGERVLQRGDSLIVDNAPTHRNMSEVVLRNWLPTIGVQYIFLPTYSPDLNPAELCFRKVKILLKTEKYTALLA
QNIKVALYSAFSEITVHDTLSFFRATDYIDV
```