***Milnesium tardigradum***

*>Gene.23911::GFGZ01028591.1::g.23911::m.23911 Gene.23911::GFGZ01028591.1::g.23911 ORF type:5prime\_partial len:275 (-) GFGZ01028591.1:139-963(-) (Milnesium)*

*PASGGTDIIVIGRNYVKDDSKMFIVEKNDEDEIICEREVPLLREHFHQTHLVGTVPPYRDLFITSPVELYLCVRNKSRQSEFHPFSYIPDQSIARHIASSRDRIDASVGSSAPVSPAYCGSVVGVSEQMSSEQLRMSGIQYCIQVPGQLTPIIVTIPQQMPTMSGHAQDLTATDSKMSIVKNLHQQSDTAILSINSQQKLTPFTFDLTQLPVVSIPANAPTPPLSPIQSDHSPNGSDSCADNEDELFNQLLEDIFKIQDGCQMTDNSTVNLLCE*

***Hypsibius exemplaris***

*>BV898\_00648.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein (Hypsibius exemplaris 1)*

*MNHPASSSDFTHSPDMNADLSTITSAPPPSPFLEGGLSMKMSPTTRSRLATWTASPDSGYSDATGTVKFTGGRSKRKRRANSLENQAGGLGSEELDGRMIVEQQQDALSGRMVQLEGGRREEAVETFVYPHRVGHVELVVLRQPEAQHRPRYQTEGSRGRIKDRSGSLSPAVQLKNFSGKSAILQVYVAVEEGVEALPHPLFKICKVNNKTAAPAVLRQLWGNVAVLEMAFSGKRDWTVDVDCVSLLKLRNVDCEEVPKTGTVGGETLKRIRNRRGMGGSAKIRLAFRAVLTMYDGSKQTLQVTSTPIACCSTLGTPEVNFLSHHNGPASGGLEIIVLGRSFLKNDSKLMVVERSMDEELIWEQEATQMPDKFNQVHIVARLPPYRDRDITRRVSVFLCVRNNDGKQSDLMPFTYTPDPIGAAAPTTSLSPAAADPAASQFPNSNSSDYQPASGPSILPRSEQGDPFRRQLSLNSGYAQPEQLPEQAALPRRQSAGPGGEGNFNVSHPAPAAPDGATIAHYSVELPGMTQPIIISIPVASTVSVGAVAPDGGASDCSYDLPSHHGQIQLVQQSQQQLSGGAQQDQYSDQFSQQQQQEHFSQPLQETMEHDPVSAKAFDDLLREILGPNTEDAATALGVGQGQNLSAEESWLLSVEGDQLNINDDPDADFYPR*

*>BV898\_03469.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein (Hypsibius exemplaris 2)*

*MTMWDDLMNTFNFAPDNSSNNHTSDFNNHHQQHLKLQTRAAHSSGSQPSSPCSQPGSPHVFQALQTSTYRFPAQSSMPLSASVSNGEARQQQQQPSHRHLTRSNSTKDLKREEYPSRELEAAILAPQMRQRVYTYAGATADHPSVVPVPVPAENSSLRRGIGPNKRRATCPDSMRNYPRGRGARNAAGELSAPKVVASTSAAQQKQQRNHQRNAFPKIEDVDSDISDETEAQLDFHSSGDASTASDMSYESHIGTTELCILRQPESHHRARYQKEGSRGCIKDRTGNSCPALQLRNYVGPTVVLQAFIGTENGPVRPHPLYRVCKVGGKHSTPCRERILESGITTLEMDMTRDNNYILNVDCLGIMKLRNADFEQVFEAEDLAKRRKRSPKVRLVFRAVLTLTNGKSATLQIISTPICCTPSPGVPEIHFISHPSCPAVGGTDIVVIGRNFVKDDSRLYIVEKNQDDVAVWEREVPLLQENFNQVHLVGSLPPYRDQRISKPVELSLYVRNKGGKQSEPQRLLYMPDEAQVHVLSFPPAMPPTPPQGTSQQLLCEPPTSTVTSTPYPGILNASISNMPTLPVIQLPQTNGSQEIQYCIQLPGSLQPLIITVPHAHILPSDPFIVGAQLQQSPPQETQRHRNNSQESLTDSDYGGGGAGQSGFTSNFESTSTPPNLSGGSSCRSLVLEQDLDARTLAAGMGASDEDLFDELLKEILGTGDQTALADFGLDAAGPSSSATGPFINAYHSPVQSPSTMAALSAARSFRAMDIRGSEQTLLNNNYLLEENQDDLMN*

*>BV898\_17899.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein (Hypsibius exemplaris 3)*

*MNTWGGFVQYNIKGSSPTFPSDNDQPHQPELLNQSSPEDGKHDDGDADRLATYLVLPAAEIKSGPPSTLHAVMTDACATTIPENTPLVTPHPGQRHSPGGSTDDLAGYNPDQSGRFEGAQLQQLTVQDILEFGLSESPGETASELDAYQPKQEGEFLEIPDVKGTTVSPAPRVWARGFQGDSEESFSLPSTLNPALPEEPVSRSSVRSSVSAATSPECERPPVRSSGRTQTRRSTTKRHRSTSQELQCTSSASASSPPRKHRSLSLRGADAETDESFDEMGTSNSDGSTVDLPMDTDDHSSEQTFGAQYPGQMNGLELCIVRQPEANHRARYQTEGSRGCIKDRTGLSCPTVQLKGLVGNEKVVLHVYAATEIGAVEPHHMYRVSKAGGKKATPSQEVVSEGTHMLELKMHRSDNWIAKVDCLGITKCRNTDITPPDAPKNGSPKVKMAKRSRKLRLVFQTTITSPDGRSVVLRAVSTPLSCTPLPGLPEIHHLSHREADAAGGQLLVVIGRNFVKDESKFYIIEKSDGNNDKIAWEREIPLHPEHFQTVHIVGLVPAYHNPIITQPVHVFIVVRNKGKQSEPFGFSYVPSPGLMPPVAEIANLHLDSEAVPQAEKLSFLLDPNTNVNFPMSAASYSSAPTNNSNRIQLMVRADQNNPTGHVITITVPGSNEPHAVITAPTFSTSASPALDYIHETAQTDSLPSKLHQISQQQPSQSADMTQQSTDMTQKSTDMTQKSTDMTQQSQYNTNASSDYDVGDSIASQQRFNELLRDILGSEPDHDQLGTSSGPAPDQLGTSSGTAPDQLRTSSGPSQDQLRTSS*

***Ramazzottius varieornatus***

*>RVARI.g4381.t1 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein (Ramazzottius varieornatus 1)*

*MLDKSKLSTADGVETSCSGQDDAHSGPAEDSAPSTSATHGSIKRPIFGECDRNILASSPVVLDRSLGTVQKSAKVSWKTNASPDDDPQYSDDARLLLPLTTTIPAKYNGMELVIERQPERHHRARYQKEGSRGCIRDESGNSCPAVRLKGIEHASLLQIFVATESGKVCPHPMYRLCKAGGNNSTPCRHRTIDGIDVLEIDINPEQKGFVTVDCMAIIKLRNADLEASGQVEGGGGGGRKKRQSGVRLVFRAITRCGKSQAALTLQVCSTPVSCAPLPGVPEIHRLSHQESPASGGLGLIILGRNFLKNDTRMFVQEVSDKNAEEVIWQREVTLERELFHVAHMVAVIPPYHKLLITQPVTVQIIVQNRAKVSEPHPFTYVPDEAVKRLLQHRPVSHLSSVPEQPEAVSAGNRSLAEVRPRCSTIGSFPDYAMASQDGNRLWDSGSSMEQISYSQQTTTGDQPIFLTIPSTTASPAQCQNDMVNGSQLVITYDDMAASTSAYYPASHQAGPDFLQSVEQNELGSIDVSQLMEEAPLSAAQAAFTSDELFDELVKEIMDWKRDC*

*>RVARI.g1792.t1 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein (Ramazzottius varieornatus 2)*

*MTQKSALRDLLRVIKKNGTDRLFVVADAGMKRNSPSMASLPAIRDRASRSGVVRSRAGTIDSDSGYSELVPSVPSTPPVRGSTKRPSSGNSNNSHHNDDVFPVTIPYGSRSSGRKAAKISRDNASPDERFDDMGLLTPLTKTIPAKYGVLELVVERQPEGHHRARYQKEGSRGCIKDRTGNSCPAVQLKGIEHASILQIFVATESGKVRPHPLYRACKVGGKNSTPCRDRTIQNINVLEMDIKPENDGFVNIDCMGILKLRNADLEATAEADDTAGRRKKREPGVRLVFRAITRYGETPVTLQVCSIPVCCTPTPGVPEIHRISHKECLASGGLELIILGRNFVKDDTKMFIQEVTDKTEEEVVWQREVTLQREFFHAAHMVAAIPPYHNLLISQPVNVQIVIKNKAKVSEPYPFSYSPDEAVERLLQQNHLSRIPGVVEDERKSECRSMMSSASRSPSSTIPAPNFTDGEDAADVRPRSITMASTTVSNHSMESGHTASFPPIGRVETLVPITPAGGSMGQISYYLQAPGGNQPIFITIPNINQQQPQTPAQMQNSMMNMIIGNLQAQMARAEASSSPFTPQPTQAPYYPSPDTPTNQPSYDAQQMKKFLQSFNTGELRTMDVTQMNEDPFTAANAETAADELFAQLLSDIMDA*

*>RVARI.g6386.t1 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein (Ramazzottius varieornatus 3)*

*MSIPPLTDALPSRHGNLELVINRQPRSYHRARYEKEGSRGSIKDATGNSCPAIRLKGLKGTKGATSILHVFVAAKSDPIGPHPLYRIHAVFGKNCIPCDERQIDGIPVVEVPIRNDNDGVVNLNCMGITKLRNADLETAPGARKISRRNVPDSSVRLVFRAITSVRGRDGFCQTTILQTCSDPICCTSLPGVPEVLQLSHEQWPVTGGLRIIILGRNFIKDECRAIVQETKGKGDETVIWQHELFIQRENFLTVHLVALMVPYVKLLITRPVQCQLIIQQKGQTSEPYYFTYIPSVQPLWPPPQIQPSPLLRRALCTSYSACSSPTDEPALEHSLGSMGSSSSAYTPFSQTSNEDVQDAYPVPRHCLHEPSPSWNNTLEVDHSSAVVTNVSGRRDLLALHTEQPQALHHSFPGAGQHQIAGKKRNHPEHDEVSWPLPPRDGTLSSAIDDITVDEYLASLGSEEMMNAANALFAEVFDEIMNCP*

*>RVARI.g913.t1 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein (Ramazzottius varieornatus 4)*

*MSTSMEELLQHFQQQRQESLNISNISCSMAHAVAPTTLSDVLPPSSPASQQQQQLFLVGNLAQTQRPRLATWTFSPADSGYAESVASPGTCSLPGCKKRFSASLDDISDSSGSGNKIHRQESIAEIEGSDLENSFFRLDFSQEYPSRTGCTELLILRQPEAQHRPRYETEGSRGRIKDRSGSMCPAVQLRNFHGQSAVLQVYVAVERGLPKPHPLFRVCKVNSKRTAPAILRSQPEDNCTILEIPFSAKDDWTIDIDCCSLVKLRNSDCDALKKASGSASALSDGKVDPSKRPKRMGCPKVRLGFRAILTMLDGSILVLQTTSSTISCSSTLGVPEVHFVSHKSCPASGGLDIVVIGRGFVRNESHLFVIERDQDDNTLWEAELDIAWDKFNQVHLVGTLPAYRDPSVSHPVLVYLSVRNNDGKKSDLQPLIYTPVDSVEIAHTVTVVTREEPVKELSHSSVKIDPYPIQPKSPDSPVLIASQPPVGVLADGNIHYLIQLPGTAQPIIITVPQPNNVVTQELPQFAVETVSPAVEQKPFPLPQSPTSYDQPVLESHVCPAEETCSVVAERSNYINSTESGLPSGSDGGKEDCENAASQLDQLLREIFGFDILPEAYPQVLAGAAQQQQDNQQHQQCYQAYDMDLGNAEAWLMEVEQENSAGYADYESSGRQ*

*>RVARI.g2858.t2 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein (Ramazzottius varieornatus 5)*

*MSSFPCQKMSMWDDLMSSLNNAENPSAQVMVRSHQQNGHGGSHHPALAPSHLSLKLSPRSSSFPSNLSSTSPPYFYDNISPSTPNAPSFPIPSSSTTPFVPSEYPPHPAFLDFAHNTPLKQRMSLPHSSPNYPYPLPQVASSKSIKQEEHYYHFQDSDHLSPTSFQQARVFNWADMNGKDSTSHTSGNASPFPNIERLDQEAFSPDQLRSLLQAINDGSISLPTSPLMTPSTTSSTRPTPRSRHFTTGGLTAGTVSPLPTTSRKPQLASTSSSRSSEENKQVKPPPGPPEHKKRRYTLPDSLRAYQRSLEDDTLDGQVNQLASNRQNSVSVTSKGKPPLTIVKRQFPKIEDVESDVSDYGNEGGPSNTSSSVAGDQDSEMQVDKSSKRTSGPSVPRNRAQNAASHPSTSHPSVDTHSCKVGGVELAIVRQPESHHRARYQKEGSRGCIKDRTGSSCPSIQLKGYNGKNLLLHAYIGTETDPIRPHPLYRVCKVGGKHSTPCREKVLDDGITCLEMDMTREKDYTLNIDCLGILKLRNADFDPTVVDSEEMTKRRKRSPKVRLVMRCPDVQLADGSTKTLQVISSPISCTPSPGVPEIHFISHNSCPASGDMDVVVIGRNFVKDDSRLFIAEKNNAGLNHSDSGEGENVNTPSAWEQELNLLQEHFSPVHLVGTIPPYCDKEITEPVEVLVFVRNKGGKTSEGFPFRYTPVERGEEARQSRSPSTTKSRPSVSTAPSALLELVEPHSSEEPMNVAADGDALPAVTAVSQPVPIQPRPQSEQAVYSLQEPLIVTTPSSMTSQAVEGGQMQYCIQLPGIVQPIIITIPQSPLQEQSVVGQPTIGVQSVMPPPAYNTLPVSNQAAYNQQQLPLMGNPQDVQPYQTAQQYPPNKVELLDTVVASSSMMRPETSNVNPSAVGPRDEDLFDELLKEILGPDSDMSEMMALMQQEGYLAAAGGGTNPNRNVNPADALNSFLTMNISKQRQHNPDGSL*

***Mesobiotus philippinicus***

*>TRINITY\_DN10528\_c0\_g1::TRINITY\_DN10528\_c0\_g1\_i1::g.32484::m.32484 TRINITY\_DN10528\_c0\_g1::TRINITY\_DN10528\_c0\_g1\_i1::g.32484 ORF type:complete len:684 (-) TRINITY\_DN10528\_c0\_g1\_i1:444-2495(-) (Mesobiotus philippinicus 1)*

*MEPGGQSSSSSEPLKAYLILTTETLDTTTINAPSASMIILDQAQQPQRTFRQRSMTATSQGNSPGSSPPLPLPSVSRPRLQTWTFSPADSGYSDYVASPTQPDSPHPLFGGTLKRRANSTEEIFPSDHCNKILRQYELTEHSEEGAGADLEPGPSKKANIIPTRRPKAWPQFPPNVGNTELVIVLQPEAQHRPRYETEGSRGRIKDRSGSSTPLVQLKNFSGSSAFMHVFIGEEKDPIVPHPLYRVCKINSKNSSPALIRTLEDHTTVLEMPFSEKDKWTLAVDCVSIMKIRNADYEEKVEGGGETVKKSRKRLGSPKVRLIFRAFITSKKGKTDVLQVASMPIACCATPGIPEITFISHKSCPAYGSTEIVIIGKNFIKNDTTVIVVEKNKDDDILWEAVVELKKDKMAPVHLVATMPAYRNLVTSVPVDVYLIVRNTDGKQSDPYKFQYTPNPKVLEALQAMETECTPVSTPVPLIRANSPISSPATPLPSSPLFQSDVQAAPAQESCVHYHFKLPGTNQDMYISIPQSQAIPGQHPVVTPVVPAPQMDIDFNNQILQEPYQPPSDEFVVNVMDFLQQDQPPVASDLEYTEDTFAPRQRTRQFTTDSSTSDDVKKFDQDDAFEQLLRDILGTSSDSQPPLPFDEQSLDVLLPNVSAGTDAPWSEEAPSDNNPDLNMGDQCR*

*>TRINITY\_DN12085\_c0\_g1::TRINITY\_DN12085\_c0\_g1\_i2::g.40947::m.40947 TRINITY\_DN12085\_c0\_g1::TRINITY\_DN12085\_c0\_g1\_i2::g.40947 ORF type:complete len:567 (+) TRINITY\_DN12085\_c0\_g1\_i2:237-1937(+) (Mesobiotus philippinicus 2)*

*MRAYQRKSTSSATHVKRQCPKISDVESDISDEVENGSADASMDVDAVRSQSATASSTCLVPGPMGVMEFTILRQPESHHRARYQKEGSRGCIKDRTGNSCPAVQLKGFSGVSAVVQAFIGTESGPIRPHPLYRVCKVGGKHSTPCRERLLEPSIYAFEMDLLRDSGYILNVDCLGIMKLRNADFEQLTDAEELAKRRKRSPKVRLVFRCICKMNDGSMQTMQVVSTPICCTPSPGVPEIHFVSHLSAPASGGVDIVIIGRNFVKDDSKIFIVEKNDDDEIRWERELALLTENFNQVHLVGTVPPYRDLLITRPIENVFLYVRNKGGKQSEPCAFKYTPDETVLRQIQTRPTANPASVSTASPQKAGMPSPLSSTSHRSSITPKEMLRSTVSSPSLPVCASTAPPSPPVQQPGTALQYCIQLPGSNQPIFITIPQTQQSQSAPENQGQNEVITVDFSQLPIQGLNDPFLGTANGMPSPASFFSQDSNSKMETEMETNQNLNGEASSSAMNDEDLFNELLRDILGPSGDDSMTSIGFPNDYAASAAASSLSALDINFDSNSMDDYGRL*

*>TRINITY\_DN299\_c0\_g2::TRINITY\_DN299\_c0\_g2\_i1::g.27145::m.27145 TRINITY\_DN299\_c0\_g2::TRINITY\_DN299\_c0\_g2\_i1::g.27145 ORF type:5prime\_partial len:846 (-) TRINITY\_DN299\_c0\_g2\_i1:414-2951(-) (Mesobiotus philippinicus 3)*

*ASESSSEQVAFNPRKYLMKRKYFNPESEGEIRCSAVVEREEEAERVRVEGREDASSYSGSYAYPAGYPSVHSAYPGAGVNDASFREGFPSDRMGANSPVRSASWSSSHQHREMDELAGRDRSKTLPEQSKRARLAATTGSGRVESVIQSTPPVAEYLRVHSPVPVPGRRQDDISLYLSRKPSDFPSTGWSSQQTSSIPTTVEEDRERERFPRHPSAEILSRMSSVSSTSSLGTRRTSPQAPPQRSLSQLERPLNVMDEDEGELVGEREVLRREYSRSESTGLTGRPLSCPSAQLTSGRLTNQSPAAERGRSGLAEFSTSFSRSGSSRSMESCQSQRSPPGSSEPDYPPSQRRSCSNERDKCKESDVVKVNVNTDGELAEGNCVTIDTENADGAGITLKIIRQPESHYRPRYQKEGSRGCVKDSTGRFPLSVQLINWDGEHQKGGKAVLQVYIGSETDPVRVHPWYRVCIVGGRTGNQARIVNIDPGTTALELDIPPGAKGLVNVNCLGIVKLRNSDLEQTGGAQKKDQMNRRKWTADVRLVFRAFLTDAQGKAKIIQAVSTVISCTPSSGVPQIQYTSLQQAPATGGVEIVVIGRNLIKGTTKLLMQESVENNGRERIVWQESVALLPNFFAQVHLVAKIPAYPNVNIDEPIQVSLVLKNNKKCSQPYPFLYIPVSQSYTQGDQTTKIFRHAGVQCSFLLAPDSPWPTLAMPIPPSGLTSAIFPPPSLPVTFPRELLVSPTSSTLSISSADYFRTKTLDGDEEPLRRLSKDTSGTPASLFPLSPHDHAFLEQCGLVVDASVKDADAPPVAQELNIANVHGTVRVRPQSALAFQWAKARLPKKRRL*

***Paramacrobiotus richtersi***

*>Gene.25851::GFGY01006732.1::g.25851::m.25851 Gene.25851::GFGY01006732.1::g.25851 ORF type:complete len:562 (+) GFGY01006732.1:374-2059(+) (Paramacrobiotus richtersi 1)*

*MASNGSKSSYPYKTDHPLDNFMRPRFNTWDSTDSGCTEASTVSGQSAKSDGSNESRATIKRRCSSPEGVSKARRYVQQLQLDRGGSDEDTVELERTKVTPPALTEVSSLTKAHPARAGGLELVIVRQPEGHHRARYQKEGSRGCIKDRTGNTCPAVQLKGCTGPAVLQVFIATEAGKVRPHHLYRACRVGGKNCTPCRDRTVEKTTVLEMDILPENNWMVNMDCLGILKLRNADLDQGVEAETRKKKKTPQIRIAFRAVVPGDRGAVRTLQAISTPVCCTPSPGMPEVHRTSHSSCPVTGGIEMIIIGRNFIKDETKIFITETNETDDVVWEGEIQVVKEYFHTVHLVTMLPAYKDLDVTKPVNVNIIVKNKNKTSEPYPFLFTPVREASDGFRSRLASTSSSIQSVTSNMFHEDSGLNTMPTSPISEDLSYQASCSSLDNLSLAPSAASAANQFLSYSCGFDNTSGSYQYHIQPPGVDYPIIITIPQLDAGGASRMPSVDLGTPGRVEPNGFCGIAFPTAQVVGIPSNSSMDGAVEDDMFNTILRDLLADPELIQKNLQL*

*>Gene.21762::GFGY01005291.1::g.21762::m.21762 Gene.21762::GFGY01005291.1::g.21762 ORF type:complete len:675 (-) GFGY01005291.1:411-2435(-) (Paramacrobiotus richtersi 2)*

*MESFAPSHKNEPTNTYLILTTPGIPFDQAMTGSQSGVIFVDPVPPGPPSPQTASSATVTPGSSSPPLPPIPRARLATWTFSPDSGYSDQLASPTGPDSPSQIGAAAYKRKFNSTENLNLKSSTAKTVRQYTLPDIDIDGPGFVESEICSPAKLANLFSPTGKRWPQFPSRLGGTEIVIVRQPEAQHRPRYETEGSRGRIKDRTGTASPSVQLKGFTGNSAILHVFIGEEKDPVAPHPLYKVCKVNNKHSAPASIRKLDTRTTVMEMAFNAKDNWTLSVDCVSIMKMRNADFEEMTTDPEDLKKTKRKAGSPKVRLIFRAIIADKSGQIQVLQVASTSISCCATPGLPEITFVSHKTCPVLGGIDVVVIGKNFIKNDTRLFVTERNNDDDVIWQSEATLRKDKFNPVHLVASIPAYKDLLITKPLDVCLIVKNGDGKQSEPHKFQYVPDDSLMREPSPSVSPSVLPSSSPVMPVNLAVAPLPVPVPADQVIYQPSVPVSTPMGMNNCIHYCLQLPGSLQPLIITIPSAGVTAAHPPIVSAILPSHMALDSPTEDERNFVLPSTSTVDGPGREYPLPLPVGTPTINLVDYLQTSPDESLRDYSSAQPTYSQNVGEEPAPGSEEAIFEELLRDILGPDQTSNAQALDALLPNVAAWSTGNEPERDETMDTSDYSPWN*

*>Gene.14629::GFGY01003065.1::g.14629::m.14629 Gene.14629::GFGY01003065.1::g.14629 ORF type:complete len:769 (-) GFGY01003065.1:345-2651(-) (Paramacrobiotus richtersi 3)*

*MPSWTPQSTGGVTSSVPLTFIISGNNVPDQNIKMSTWDELFQSLQSPTVPPSSHPGKSSVSGVAMTNGLLPSSSSAPTFVNIPIPAVFARYQPGGLLNGHNPAGGSKDTDDLPEDNLAPFMRPRLSTWGSTISDSSCSGMSGVSGSAVPTSRRGRGKATPHQVPVERTVSSPSTAPPLSKRRFTCPSSAFKRHCQKISDVESDISDNESEFPTRETPMDTDTTPTANNTAVCAKATRIGQLELKIVRQPENHHRARYQKEGSRGCIKDRTGNSCPAVQLTGYTGGGAIIQAFIGTESGPVRPHPLYRVCKVGGKHSTPCRERNLEGNIYALEMDLLRENGYLLSVDCLGIMKLRNADFEQIADAEELAKRRKRSPKVRLVFRCVVKLPDGTSESLQVASTPICCTPSPGVPEIHFISHTAAPVSGGVDIVIIGRNFVKDDSKIWIMEKSEDEGVVWEREVPLLMENFNQVHLVGSIPPYKDLTVTKPVENISLVVRNKGGKQSEAQSFRYTPDESIMRHFSRSRSVPGPVPAPLNLASSSSSMSSASLASLETKESVCTTPTPYMHQNGLVHSPPVRPPQPTTAPQPTPPPGSANSFQYCIQLPGSNQPIFITIPQTTGQGTPMTESYHNVQAGRAGTSVTHSTNHSPPHNTNHHHNNVITVDLSQLPMHTNDPMLSTACAQSPPSFYSDPMTGMSPGMGDNGTAMSDEDLFNELLRDILGPSEDAEMGGLGESNEQAAMAAASSLSALDINYNGQYRHAGHREGKPY*

***Richtersius coronifer***

*>TRINITY\_DN26792\_c0\_g1\_i15.p1 TRINITY\_DN26792\_c0\_g1~~TRINITY\_DN26792\_c0\_g1\_i15.p1 ORF type:complete len:747 (+),score=92.09 TRINITY\_DN26792\_c0\_g1\_i15:4146-6386(+) (Richtersius coronifer 1)*

*MSVFATEWEELMKSLAVPSDYVSKQSSDTPPRRSSPGLAWKQTASWEMKPSLSGDAGIDSLPVPTRFSRDYPLARNTQTRSPCSKMKEAEDLPVVDTLSPIKRSRVFTWGSTMSDSGCSEISTVSFNNAICPTSIPVCSVDECRDDGSSGFEEYKERPVRHIRGSAAARRRFTCPRAMRSFNRRKDNDAGSKGLEQLILDEMESDISDDVQGKDTLWESPMESDCSSVAFSRISSSIELLILRQPESHHRARYQKEGSRGCIKDRTGNSCPCIQLKGYNGPSAVLQVFIGTETGPMRPHPLYRVCKVGGKHCTPCRERFIEPNIHSFEMDFLRETGYIINVDCLGIMKLRNADFELMSDAENLSKRRKQSPKVRLVFRAIFQQMDGCAETLQVVSSPISCTPSPGMPEIHFISHSSCSSNGGLNIALIGRNFVKDDSRIFVMEKDLDDEVIWELEVKPLPENFNQVHLVGTMPPYRDPSITQPAENVFLYVRNRSGKRSELYPFRYTPDETTARLLTPPPYTSPPPILKRSRHGGSTSSLSTMDSSDQNFPYNTPSHSPSPYETNGKPTTTTTSCPHHTILPTPTSANNNSFQYHIGLPGSDQPLIITVSSGNQTATGSTVVQSVQNIPPGTITVDLRQIPPVKHEEPSGKSGTGKQEEASICSPPYSPPSASAPIVPGLDDTEGGATDDDVFNDLLKEILGMEDSAMDGLGYSMDYAASLAASSMSALDINLETFLNRPNNGSGR*

*>TRINITY\_DN29007\_c0\_g1\_i2.p1 TRINITY\_DN29007\_c0\_g1~~TRINITY\_DN29007\_c0\_g1\_i2.p1 ORF type:complete len:696 (-),score=111.21 TRINITY\_DN29007\_c0\_g1\_i2:505-2592(-) (Richtersius coronifer 2)*

*MEQIHQNGSLQPTDTYLILSSNLTFDCISNNHNDVFCYGTASPEHATLVTATTPGASPPLPPLPRPRLATWAFSPDSGYSDYNPSPVAVDYHIPVPTNLKRRANSTEDLTFGDIQNGKVSCNFVEDIDAEETGQQAEGEQGFSKIDITFPKPAKGWRQFPCRIGGTEICILRQPESQHRPRYETEGSRGRIKDRTGSSSPAVQLKGFTGRSAILHVFIGEEKDPVGPHALYRVCKVNNKYAAPAIIRRLEDGTTVLEMAFTAKEDWTIAVDCVSIMKLRNADFEDSTQDPEDLKKTKRKSTGSRKIRLIFRAIITAKTGKTQVIQVASSLISCCATPGLPEISFVSHDSCPVSGGTDVVIIGRNFVKNDSKLLVFEKNSNDEVIWQREAAMRMDKFNQVHLVAGIPAYDNLVVKEPVEVFLIVKNTDGKQSDPQKFYYTPNPLLLEDPRSRSARHSPSPLLIPSAPSPLREPPAATQLVNALMAPSSVSSHDSNLTDSVTTSTPSPDTSIPSSSSQPLFAANSSAVPNCIHYCIQIPGYHQPLIITVPQFNSAQPTTTVSCAQEIDGSEQEFVQTTRDDFGQSNSETGRLENDMDYGQYCPLKPSEEDQQMRDVSSEIPKDSDGPTVCPTDDVYDSEKPCTEQDRLIFEELLREILEAENDPSLSTEAVGFGLDMSLLPNVAPGTWFNENDNMQE*

*>TRINITY\_DN27634\_c0\_g5\_i1.p1 TRINITY\_DN27634\_c0\_g5~~TRINITY\_DN27634\_c0\_g5\_i1.p1 ORF type:complete len:482 (-),score=57.41 TRINITY\_DN27634\_c0\_g5\_i1:1635-3080(-) (Richtersius coronifer 3)*

*MMQSGQQPRCLFEDGLAFDFDRSRLDALSVDYSNSGFSGISTPVSEMSDVSTTEFRGTLKRRRSTPEVPQKPRRSLLKNKKKVPVEHHVKTGGVCESRECPPLAKTFPTRLGAIELVILRQPEGHHRARYQKEGSRGCIKDTTGNTCPALQIRGYAGPGVIQAFIATENGKVRPHTLYRACRVGGKHCTQSKEYVVGSTNVLEMDLLPHNNGTINVDCLGILKLRNVDLDQVSDSESRRRKQAPSVRVVFRAILRSENGTKILQTVSTPICCTPSPGMPEIQRISHPECPVTGGEMIVVGRNFVKDESKLYVVEYEDESQQQVSWEAQVPLAREYFHAVHLVATLPPYKDVNVSKEITIYLIVKNKNKTSEPYELKYVPRPERKETAGISLPASTSSPGTAMTNINNGASHLSAPAGTIKVLGTFCEIRTMKLDQCSQPALSMATSGETFCRFGLAVSVLSCPRRYFAESHHVVVRGTGDA*

*>TRINITY\_DN24759\_c0\_g1\_i10.p1 TRINITY\_DN24759\_c0\_g1~~TRINITY\_DN24759\_c0\_g1\_i10.p1 ORF type:complete len:537 (+),score=70.24 TRINITY\_DN24759\_c0\_g1\_i10:140-1750(+) (Richtersius coronifer 4)*

*MMQSGQQPRCLFEDGLAFDFDRSRLDALSVDYSNSGFSGISTPVSEMSDVSTTEFRGTLKRRRSTPEVPQKPRRSLLKNKKKVPVEHHVKTGGVCESRECPPLAKTFPTRLGAIELVILRQPEGHHRARYQKEGSRGCIKDTTGNTCPALQIRGYAGPGVIQAFIATENGKVRPHTLYRACRVGGKHCTQSKEYVVGSTNVLEMDLLPHNNGTINVDCLGILKLRNVDLDQVSDSESRRRKQAPSVRVVFRAILRSENGTKILQTVSTPICCTPSPGMPEIQRISHPECPVTGGEMIVVGRNFVKDESKLYVVEYEDESQQQVSWEAQVPLAREYFHAVHLVATLPPYKDVNVSKEITIYLIVKNKNKTSEPYELKYVPRPERKETAGISLPASTSSPGTAMTNINNGASHLSAPDLHGVQGYQYCIQPPGSSQPIIITIPQITPWQSGHPSIEGVKVPAPTQIASAYAGQDLVPRPVVESRTTGELMKLDEPKVPARLGLLDCMMQPTEEELFDQILRDILDNPERLQGIASSHL*

*>TRINITY\_DN28405\_c1\_g1\_i2.p1 TRINITY\_DN28405\_c1\_g1~~TRINITY\_DN28405\_c1\_g1\_i2.p1 ORF type:complete len:584 (-),score=93.56 TRINITY\_DN28405\_c1\_g1\_i2:495-2246(-) (Richtersius coronifer 5)*

*MMMPYDYLQSSSRASAMSSPSKRRNTCPPSTRPPRPKRRNVPRPRSQGQEDLSATDSTDSLDESTTASSASHGPMVTDATAVVYPSRIGNVEVVILRQPESHHRARYQKEGSRGCLKDQSCNSCPAIQLRGYDGLSAIVQIFIATESGKIRTHPLYRVCKVGGKHCTPCRERQLDPVTYALEMDLTKEMNFVLNVDCLGIMKLRNRDFELSSDAQRLAKVVKRSPGVRVVFRVIYKTPDDRTETLQISSTPICCTPSPGLPEIKFISHPSCPASGGVNLVVIGRNFVKDDSKVFIAEQSEDGQQEDWKQEMTVLEENFHQVHLVVSVPPYRNPFIMKPVEDVCIYVLNKNGKRSEPFAFQYTPDPPISRPASEPSSPSPSSIGLRSISDATVTCSEISIPQSVYTAGGSNFAYLQPSLSSGSSLRNDSSLEYHIPVPGSQQSIIITLPPMNKPIPAPPAVQYEPLSPAASGSAPRTVAPLGYSPIGQQNTDDPMLQSLANSPYMWNAESGGSGSLPAGPTPPARVVDDDLEIFEQLLKEVVGQDGMVDGLGYSTDYSGALTASSLRALNLFGPSSGNQNPSNK*

*>TRINITY\_DN14469\_c0\_g1\_i1.p1 TRINITY\_DN14469\_c0\_g1~~TRINITY\_DN14469\_c0\_g1\_i1.p1 ORF type:5prime\_partial len:435 (-),score=57.83 TRINITY\_DN14469\_c0\_g1\_i1:368-1672(-) (Richtersius coronifer 6)*

*ILRQPEQHYRPRYQKEGSRGCVKDTTGRFPLSVQLKNWDGEERGGKGVIQVFIGSEDDPVRIHPWYRICIVGGRSGNHARIATLDDSTSALELDIPSGAKGVVNINCLGIVKLRNSDLEHSGSSGAGSHKRDSSNKSKWTADVRLVFRAIMKEPGVPVKTAQAVSTVISCTPSSGVPQIHFISLTQSPAYGGVEIVLLGRNLVKDSTRLYVQETVENSSEDVRVVWQEAATLLPSFFTQVHMLARIPPYRDPHIAFPVAVSLILKNNKKCSVPFPFEYVPVSSPPGNTGAQRAPIEKRDAIIQCTLSTSPIVPFTRGHTHKCPSVNPPSASSPDPQQGGSMDFQRISQYYLARRKKSKPPSLFRLSPHDLSFLESCGLSIDPRVSNQEDTSAEVWNVGVLSGGVVPQSSLAYQWAKGREEATSPEHPLMVDHIG*

***Epiperipatus sp.***

*>TRINITY\_DN3720\_c0\_g1::TRINITY\_DN3720\_c0\_g1\_i1::g.18::m.18 TRINITY\_DN3720\_c0\_g1::TRINITY\_DN3720\_c0\_g1\_i1::g.18 ORF type:3prime\_partial len:196 (+) TRINITY\_DN3720\_c0\_g1\_i1:68-652(+) (Epiperipatus sp 1)*

*MASSSETFLYVRNTSNLWTPSDFNLTDELINSSNGDMSIETAFTSETNLLTCEPYLQIIEQPRARGLRFRYECEGPRAGSLLGENTTAETKTYPKVQIKNYRGPAVIVGSCVTKEPPHQPHPHSLVGKDCVNGVCTVKVDSSSDTDPAEDMQVRFPQLGIQCAKKKDIEEALRVRERIRVDPFNTGFQHQAGSLD*

*>TRINITY\_DN66394\_c3\_g2::TRINITY\_DN66394\_c3\_g2\_i3::g.28933::m.28933 TRINITY\_DN66394\_c3\_g2::TRINITY\_DN66394\_c3\_g2\_i3::g.28933 ORF type:3prime\_partial len:410 (+) TRINITY\_DN66394\_c3\_g2\_i3:162-1388(+) (Epiperipatus sp 2)*

*MSDISELFDNLLSRSPEELLGLTCNGQLKPTVVIVEQPQSQGFRFRYKSETGSHGGLQGESSSKKHKTFPKIKVENCSAYPVKVQAMLYTNESKPRLHVHKLMGSDCDNDGIWQKTFDASVWQQDHIALQGFSILHASKRDIVSILYEREKKDKKISKTLLGAQRVLPSDVVLTKEEDDYIKKLADSKAKEFNDHLNSVKLGFTAECNGIRGPVCFTTPIFDCKSPSTCKLKICRIDHSSGSCEGGQEIFLLCEKVQKENIEVIFFEKSGDEISWSSKGIFGLHDVHKQFAIVFKTPPYERTDIEREVEVFLQLVRPSDKATSDPLHYTYTPKEDDYDQVQRKKRKKLPGIDDNFSYLLSNYASTSTMYDDTAASAQMSYLLPEHIGSLISRDASLSEDPGLCKDDSLL*

*>TRINITY\_DN68614\_c4\_g3::TRINITY\_DN68614\_c4\_g3\_i7::g.20071::m.20071 TRINITY\_DN68614\_c4\_g3::TRINITY\_DN68614\_c4\_g3\_i7::g.20071 ORF type:complete len:522 (+) TRINITY\_DN68614\_c4\_g3\_i7:2-1567(+) (Epiperipatus sp 3)*

*MLLLLIMLFVVVFVSILLLLVTFVFSENLLTNINYTMVNHDKSKNKSASNDNSYKGSRQTKIPSPVGSSQDEYSHHSSSSDSSSDTTSEQPIFDTESESLQSVTNLLNHWHSDSQPESDVKPRKAQKTSIRDFPTCSPINNEQCFNADSAASSSYFAFKQFGKSNQTFGDSNERVNSNGVTSSPSSPSEQVSTTATRGSTRLTHLSRKNIKQPSLVNSYPSKDNGFELCILAQPEEQHRARYMTEGSRGSVKDKNNDGYPTVKLFGYNQPAVLQVFVGNDFGRVRPHGFYQACKVSGKNATSCKEKEIDGTTVIEINMLPENDMTISCDCVGILKLRNADVERRMKFVRGKKKSVHARLVFRVTLLKPDGSPLTLQCASTPILCTQPPGIPEICKKSLSSCSVVGGQELFIIGKNFAKGSKVLFQLLSESGNIVWEAFGDIDQEYFQQSHIVCKVPPYNSQLITKPVTVTLIVQSNDRNSDSHLFTYEPETGAKQVKKILCRLLHINYAYSHPWLCFVHIM*

***Opisthopatus kwazululandi***

*>TRINITY\_DN107889\_c1\_g1::TRINITY\_DN107889\_c1\_g1\_i7::g.43688::m.43688 TRINITY\_DN107889\_c1\_g1::TRINITY\_DN107889\_c1\_g1\_i7::g.43688 ORF type:internal len:399 (+) TRINITY\_DN107889\_c1\_g1\_i7:2-1195(+) (Opisthopatus kwazululandi 1)*

*LNMASNSEDDTNLQEFLDFNSPALAVNNSSPYIKIIEQPRSRGLRFRYECEGPRAGSLLGAQSTSETRTCPRIQIMNYNGPALVLVSCVTKEKPHRPHPHSLVGKDCKDGICKIPIDERNCENMVVKFPQLGIQCAKKKDIVEALSLRKSLGVDPFQVGFQYESGSLDLTVVCLCFQVLILNSDRSMYISVGTPVVSEPIFDKKALSELVICRIDKHAAPCCGGQEMFLLCDKITKDDIEIRFFEETGDGQLTWEGFGDFSPSDVHKQVAIVFKIPQYKTLTINGPVSVMVQLRRPSDKETSDPKPFQYLPLDPDPDGIERKRKKGLNTSMLNYIEDLGFKRSSSPSQSSTLPTINVFQNRTIRQPLHKIKAETATPDNCTLSSASKSFSSPISNIFS*

*>TRINITY\_DN114213\_c2\_g1::TRINITY\_DN114213\_c2\_g1\_i2::g.47695::m.47695 TRINITY\_DN114213\_c2\_g1::TRINITY\_DN114213\_c2\_g1\_i2::g.47695 ORF type:3prime\_partial len:151 (+) TRINITY\_DN114213\_c2\_g1\_i2:106-555(+) (Opisthopatus kwazululandi 2)*

*MMAYNSIINQNPSMLMGLYSYEQIQPKIVILEQPMAQGFRFRYRSETGSHGGLQGASSNKGNKTYPKIKIENCSANEVIIRAMLYTNEEIPRLHVHQLLGTKCLNGIWECKVGPREHWIANLSGVGILHAAKKDITNILCERAIQELKEI*

*>TRINITY\_DN117724\_c0\_g4::TRINITY\_DN117724\_c0\_g4\_i3::g.95004::m.95004 TRINITY\_DN117724\_c0\_g4::TRINITY\_DN117724\_c0\_g4\_i3::g.95004 ORF type:internal len:255 (+) TRINITY\_DN117724\_c0\_g4\_i3:1-762(+) (Opisthopatus kwazululandi 3)*

*YPASVNNKMAEENIPSEILVITNLENAIPQLEASLHPIAPKVSYSSSNLKSDHLRYIHGGFNKKDYPKPPGVKINNFSGQIKVRISCVTESYPHHPHSFGVACNPSNTSGYIEHVQEIYNSGDIWFPKLAIIKYSKKNTGTLALRQERGIDPCGAGFTDGQRFSSNVRLAFELFIIENNLVKYVGTLKSDVIKNIKQNMSLKICELDPYANCVSCLSTVFLTTGDLPNNLDIWIEIKNMENEQLFECFKAKKHS*

***Paragordius varius***

*>TRINITY\_DN36908\_c1\_g1::TRINITY\_DN36908\_c1\_g1\_i1::g.18815::m.18815 TRINITY\_DN36908\_c1\_g1::TRINITY\_DN36908\_c1\_g1\_i1::g.18815 ORF type:3prime\_partial len:833 (-) TRINITY\_DN36908\_c1\_g1\_i1:1-2496(-) (Paragordius varius)*

*MRHGSGYPQPFIRILEQPLERGFRFRYKSEAGAHGGLPAESSQRNSKKYPTIKIENYIGPARIEVTLMTNEPEPRLHVHKLVGKNCEDGVCHVRVNPENDMIVSFQNLGVLHVPKKEVAQIMHERLEEEYRIQRMMNNDSDSDNYEFTEVEKQMLRHNAEESAKSMELNVVRLCFQAYIIDAGGNEIPIPPVLSNPVYDSKSPNTAALKICRMDKQAGFCVGNEEIFLLCERVQKDDVSVRFFELDESGKEVWHDYGKFSIHDVHKQYAIVFRTPAFRFQNITKPAKVFIQLQKKKDGLTSEPKPFTFKPLPCYEEIGRKRQKSILNLADVEILNDALNMIHKSSSDSNIPTNSPSGLANSQHPKERCNNIVGKNNHPQVSQVLEERSMPHHRHEKVYPESMAYEKTFVIGELFPQNRVSKLYPVTRENEGVPQQEHHKQSLQYGSSKERSNPNNININYHHYQQQHFYHPSFITGPLAPPNYETQAHHPPPSHSHEHSKDSTIHEHPKFYNSRGRSAGNVNANDMHVRERMHTKNFSENDVQSSVPCNGVEHDELEYVKTKSREISNERALKESQITANNYKMSQGEVYSSGGVSSGGDNDSSIRCNSYISDGSSPQSTPPSFVRYNNPAGTGLVEGQRKCSQDDDSNNPASMINGYDDVYNHRGVPTKEDYHTSPTSYNYNVGAQHFNVTMSPNTLPYYVSNGRNEIWSRDYDQYEHTESEEVCAEAPRMLQMSQIDRDKHLYQHQPTGNMENSIRHTVHPYNLNQYDQAMEESNKRSQDLIPMLIARGHELKKPSETSLEVKTVGKVYPMLKMTGDKANSTLENIGEEF*

***Priapulus caudatus***

*>XP\_014663067.1 PREDICTED: embryonic polarity protein dorsal-like [Priapulus caudatus] (Priapulus caudatus 1)*

*MEQWPPYSVHQDVMTQRPGDHQWRPPLDDNANSNSPGESQEPVVIITEHPASKLRFRYECEGRAAGSIPGEHSIPEKKTFPAIQVRNVSRPFKVIVSCVSHEKPPAKPRSHPHSLVGKNCQDGVCVVSVTNPRDGRIEFPGVGIQCAKIKDRKDQLAKRQKMKIDPYKVGFTHSDQSLDVSVVRLCFQLFIPTVMDPETNQWSYAQETWKAIRPVCSQPIYDKRAVAQLNISRIDRISGPACGGQEVWLLCDKVTRDGIEVRFFEEKNGQTVWQEKAQIVLVHKQVAIVVKTPPYRDPDITSITMVKVALHRPTDMEISPAIGYKYYPSNNGEDRELAGQFPAMAPPVMMLDHLLLKQDKQHSQVHEPFRSAMIKQEIVKPVTNCPATLPGSAMAISAATAAMPPPLHPFAVSYAIEHPLVFMQDMHPAAAAAAAAACDDSNADTHMTSLASQFNSSLSFSSLSSLSELICTGDITMAPPISNSSEVEWLLKNITDMQQ*

*>XP\_014679732.1 PREDICTED: uncharacterized protein LOC106819641, partial [Priapulus caudatus] (Priapulus caudatus 2)*

*MSQLPSPAQAYVNPRSNESGDSGFGSNPRSNDPPIQDCLSPISKTSEDTGIGSNPGSNNPTQHCFSPMSNTFGDTGIGSNPGSNNPPTQDDCFSHMSNTSGDLSSVGDNVMWNHGTVSCNDVSNSIQFVGNLGSNNPVSFANSAGSSAVAYTNTGHCDPASYENFGANIPVAHAVTGQSNPASMSWSPDTAVAYTNNTETSNPASYPNFNLETLDVLLASIRRDEELASAPEVTDNMMHLEMPRNVTPNLFELQVGSNSQMTDVMQSASPMQVQPYLKILRQPQRNGHRFRYTSERGSHGTLEAERMSRDQKKKEYVSVKLVGYGPRAKIVVSLVTNDSQRESHIHRLVSKKSDLSANVWSHPELQVDMACEMTATFSDIAVTVVPQKMLTDMHFKEHISAEKGKSRSVPINSAVRKKLDEELKSKNKRLKKFDGQHIVVLKFEAYSLNGDGSTGPQLCSPVFSSEVINQRSTQNGELRISKISKSSESCKGGHSRENDTQMLMFTSKVKKG*

*>XP\_014675484.1 PREDICTED: uncharacterized protein LOC106815532 isoform X1 [Priapulus caudatus] (Priapulus caudatus 3)*

*MINIYIFTDSRRLSTSCLFHTMSQWPSPGSHAQAYANPRSNESGDTGFGSNPGSNNPTQDRFSPMSNTSGDSSSVGDYAMWNQVTVPGNAVSNSFPAVSSAVAYISTGHSDPASYENFGANIPVAHAVTGQSNPASMSWSPDTAVSYTTNTETSNPASYGNFNLETLNDLMATIRDEEFASAPEGTDTLMHLEMPINVTPNFLGSQVGSNSQMTVVMQSASPMQPYLKILRQPQRNGHRFRYTSERGSHGTLEADRMSGDQKKKEYVSVKLVGYRPRAKIVASLVTNDSQRESHIHRLVPKKFDLSANEWSHPEIQVNMACDMTATFNDIAVAVFPQKMLTDMHIKEHICAEKRKSRSVSINPAVRRKLDEELKSKIKRLKKFDGQHIVVLKFEAYSLNEDGLTGPQLCSPVFSSEVINQRSTQNGELRIYKIGKSAESCQGGQSRENDTEMLMFTSKVKKGGKKCIGLPVNVCYL*

*>XP\_014681174.1 PREDICTED: nuclear factor NF-kappa-B p110 subunit-like isoform X1 [Priapulus caudatus] (Priapulus caudatus 4)*

*MHTKSNWEPPQAFLNKSNDMTAVFNDISIVILTSHALVEMSLKMDKLEPENPKVSISSTEREKHQEYVKKRLNEFRGSDRRHVAVIKFQAFQLNGDGSIGHELCYPAYSNKVVNQRSTQHGELKIIRISRSLESCRGGKSRLIDRELLLFTSKIKKGVNVRFYDHEGWAKDVEPSLIHEQTAVSVLVPPYKCQDLKEEVQVHIRLVRQHTSMQDEELCGEDVSEPVTMKYQPVDVDVGVEAYRVGVKRCKLET*

*>XP\_014681175.1 PREDICTED: uncharacterized protein LOC106821049 isoform X2 [Priapulus caudatus] (Priapulus caudatus 5)*

*MHTKSNWEPPQAFLNKSNDMTAVFNDISIVILTSHALVEMSLKMDKLEPENPKVSISSTEREKHQEYVKKRLNEFRGSDRRHVAVIKFQAFQLNGDGSIGHELCYPAYSNKVVNQSVNVRFYDHEGWAKDVEPSLIHEQTAVSVLVPPYKCQDLKEEVQVHIRLVRQHTSMQDEELCGEDVSEPVTMKYQPVDVDVGVEAYRVGVKRCKLET*

*>XP\_014679270.1 PREDICTED: nuclear factor of activated T-cells 5-like [Priapulus caudatus] (Priapulus caudatus 6)*

*MSEGEDEEGRRGAGVRLPFNADSARPPTTQFVFQKFGQEGGREKEEEEKEKTPDAGERGGAARAGKRYGEYGVGGAEETGLAAGWGSSSSHEPPLTTQLPSRCGDVELKITAQPESNHRARYLTEGSRGAVKDRAQKGHPAVKLFGYSKPAKLQVFVGSDAAKVRPHGYYQACEVQGKNSCPCEKRQQEGTHIIELELSPESNMTAVLDCVGILKLRNADVEHRLGVARSRKKSTKARLIFRVTLPRQDGSSYTLQTASMPILCTQPPGQPEICRMSLTESPPEGGHDLFIIGKNFLKGTHIVFIEKDTYGEDIWQAEAAIEKEYFQTTHLICAIPPYKDVDITEPVELFVSVRCVDRCGDLQPFTYIPKPKEVKPDPLLVDVTTNLSSGMSRATLEINRRFQISEGQSPFAVNVTVVSPLQRQPPPPPQTHADLPLAAATTATTVAPSDFVGMLMGDSAIQSLGGGGSAMAPLSASAMAPLSATTMAPPSAHQVAPVEHMDASSAAVGATYQLDKPPALPMDTSPAVAMETTPRPAAAALDDAAGATYRLPSVASLLPAAPSGEASVAEGRRTRRRRRRRHGATRTPAAGGC*

*>XP\_014677631.1 PREDICTED: uncharacterized protein LOC106817480 [Priapulus caudatus] (Priapulus caudatus 7)*

*MIGDQKKKEYVRVKLVGYGSRAKIVVSLVTKECESHIHRLVSKKSDLSANEWSHPEIQVDMASEMTATFSDIAVTVVPQKMLTDMHIKEHICAEKGKSRSVPISAAVRKKLDEELKLKIKRLKKFDGQHIVVLKFEAYLLNDDGSTGPQLCSPVFSSEVINQRSTQNGELRISKIGKSSESCKGGHSREKDNEMLMFTSKVKRGVQWSPVSFVGMNGHIT*