**Figure 6 – source data 3**: Echinoderm PMC-specific Ig-domain protein sequences from used for tree construction. *Strongylocentrotus purpuratus* (Sp), *Lytechinus variegatus* (Lv), *Eucidaris tribuloides (Et), Parastichopus parvimensis (Pp), Patiria miniata (Pm), Acanthaster planci (Aplc), Ophionereis fasciata (Of), and Anneissia japonica (Aj)*

>Sp\_KirrelL

MNHICWIPVLLCAVVLTRYARAGFIVEPFSTEGIQSETVVLPCTILNEPGAIVVWYRNKAQLSIDKTLVESLDSDVQARFSVVGNQTFGEFNLQITNVKPADESQYYCSFISRFGGASSVVATLTVLIPPSEGYPRCSVTAETHRILRMPSGQVKWLLLTCESLGGDPAANLTWYRKNWTVSHATKHTNVYRRILTPGDNGVTFICEATSSALREPRRCEVTPMSIPPEVHVRPLTNSVPFGTNATFHCEVSAITRVQEYNWFIEGTLLTPETPGIVFGNNGKVLVIANVQMEHDSKPVECEAVIKNRLVARASTTVVVIPPRKTSPPLPSNPTEKVTIIQVEKSEVPTSHPILSANMNLIIVIVSGSLIVLLLLIAIIMGCWVFGFRKPRRPHTRVNIDYGEVPVDMPLDGISHYSVPAALFSTEIPDSRLNESFHQPRHYDENTSGYISALYATLDKNKRYPPKMTSSTSLPEKPVAQITPTAGRNVVPHFAAASTIDKRKSTGAIAYSDLKDLDNDPDFKKGCSCDCKADDSGKEDPETEQ

>Lv\_KirrelL

MNHICCIPVLLCAVVWTHYARAGFIVEPSSIEGIQSETVVLPCTIRNEPGAIVVWYRNKAQLSIDNNLVNSLDPDVRARFSVVGNGTSGEFNLQIVNVKPADESQYYCSFISRSGGASSAVATLTVLIPPSEGYPKCSVTAETPQNTKNAFWPGEVALLSCESMGGDPAANLTWYRKNWTMSHAAKHTNIYRRILTPGDNGVTFICEATSSALREPRRCEVTPMSIPPEVHVRPLTNSVQFGTNATFHCEVSAITRVQEYNWFIEGNLLTPETPGVVFGNNGKVLVIANVQMEHDSKPVECEAVIKNRLVARAGTTVVVIPPRKTAPPIPSRPTEKVTIIQVEKSEVPTSHPILSANMNLIIVIVSGSLIVLLLLIAIIMGCWVFGFRKPRRPNTRVNIDYGEVPAEMPLDGISHYSVPAALFSTEIPDSRLNESFHQPRHFDENASGYISALYATLDKNKRYPPKTNSASSLPEKPVAQITPTAGRVVPHFAAASTIDKRKSTGAIAYSDLKDLDNDPDFKKGCSCDCKSADYDDNEDPATEQ

>Et\_KirrelL

MKVQALFYAIWAAVLTGSVRAAFMVQPESTAGIKSETVTLKCQITNESGAIVVWYKNKAQLSIDRNLVDSLDHDVRSRYSVVGNRNEGEFNLQILNVKPSDEGQYYCSYISRAGGGTSAIGTITVLIPPSDGYPRCTVYAETPQNGETSFWPGEKASLSCQSAGGDPSANLTWYRKNWTVSEPTKRRNVYRRILSPGDNGITFVCEATSPALREPRRCTVTPMSIPPEVHVRPLSASVLVGDNVTFHCEVSAITRVQEYNWYIKGTLVSAETNGINFTSNGKMMVISDVQMNLNRKPVECEAVIENDLRSRARTNVEVIPPKKTPPPASTPTQKVTVGEVEVDETEIPTSSGGPLFTADMNLIIVVVSGSLIVLLLLIAIIMGCWVFGFRQPRRPNTRVNIDYGEVPADMSLDGISHYSMAAMFSTELPESHNNDVIRNPGNIDENAPGFISALYATLDKNKKYPVKMTSASSLPEKPIAQITPTSSKAAISHFASASGLEKRKSTGGAIALSDLKDSVDDPSFVKGCSCKDELEKEDPNTEQ

>Pm\_KirrelL

MTMWSPRAWFVSAVAVIVLSQETQAIFTVLPANISAIAGDTVTFRCTALSSLDTFLYWSKGNTHLSLGGKLLHSLDNDLRERYSLGGNQSIGEYDLRIENVKKTDAGDYQCSYIGSAGGRASPPATMTVYVPPLAKYPLCKVRTQSQTSETTGTMWPGDGAEFTCQSSGGDPPALLQWQRINNTILEPQPSHIVYARILLPEDNGVRFTCVATGPALREPRRCSVMPMRILPVVQVRPLTRMIIPGDNATFHCEGSAIPHVASYSWQVAGNHISDSQAGFSFANQKQLLTIHDVKQSHDQIEVACEASTPTGIAESASVKMVVTPIYVPPTLPSEGTPIDFIPSAPAGPDDTSVDEEEPGIIDGDLFMITLTIFGALVILLLVVAVVMGCWALHAKGKRPQTLKRPRVEYQESTATTIDLEPLPLPTQLAYEPPTTVSSDPMAIPAPPYTADKENAPGYISQLYSTLDSSRLPARPAFSGFPEKPVASITPTQGVASTLPRPGKIDKPCGTGKPTVKECPASFSIPEEKVTSQEDKMNEENEDRKNGN

>Aplc\_KirrelL

MTVTMSLPELQLIFAVVAIVLTPKTEAMFTVLPANISAIAGDTVTFRCTAHSTLDTLQYWSKGNTHLSFGGDLADSLDNDTRSRYSLSGNQSVGEYDLTIANVKKEDGGHYRCSYIGLAGGKSSPPATMTVYVPPPARYPLCNVRAESKSSKAASTLWPGDGAEFTCQSSGGDPPALLQWLRTNRTILEPQPSNIVYPRILLPEDNGVRFTCVATSPALREPRRCSVMPMRILPVVQVRPLTRMIIPGDNATFHCEGSAIPHVASYSWRVAGKHISEGQAGISFANQRQLLTIHDVKQAHNQIEVSCEASTSTGIAESASVQMVVTPIYVPPTVSTEGIRIDFIPSVPALPDGPEVKEEVPSILKSDLFLIILTVFGALVVLLLVVAVVMGCWALNAKGKRPQTQRRPRVEYQESTTTALDMEPLPLPTQLAYEPPTTVSSDPMAIPTTPSTEDREHAPGYLSQLLDSTRLPARTAFGGSLDKPVASVTPTPGVASTLPRTGKVDKPCGMTKPTIKECPASFSIPEEKEKGYKVSDGNDKNNGH

>Pp\_KirrelL

MSEVYLILLSVTVTQLFTSCLGNFLIQPEDSTSVVGEVVIFKCSVNRTDLDSTLLYWSKDKHHLSVNERLVESLDRGVKSRLSVVGNRTLGEYNLQIENIRRTDVGSYVCSYIGLSGGQTSRVASLTVLIPPRKEFPLCFILAQTLRTTGQVDTFWPGQTARLRCVSVGGEPAATLVWKRKNATISSTKTSESIHERVLTPSDNGVAFTCEASSPALKVPKKCEVVPLKLLPSVQIRLMTREVIEGSNATYHCEASAIPKISLISWSFAGREVGFNESERVVVSEDKQFITIIDIRADEDQTSIDCVVSISTGLQSRDTMKMLVTRKPIIATNHPATASPDDRLQNADNFPWNSQLHVIVIMVAGSCVGVLIFVFSILICWGFSRAKKPRRPNTRLQVDHVNPSSNELGLEPLTYPGQIVYNTLPDCDTLPRRGGDSFRNSLHDENSTGYLSSLYASIDRRGGYTPRFGSLRGDEKPVAQITPTTSLKRPIIPYSAQPLIEQDKDSYKDSSSRDSVSSAGETEIF

>Aj\_kirrelL

MDMLTKLLCLAVLPLLAQAKFHQTPQSQVVILGETVTLRCAVTYIPELVIYWKKGPAHISIGRNILADIGVENIRRYSIVGDELSGEYFLKIVDVKVEDAGDYKCAYVSKTSGATSLPAKVDIIIPPKADFPVCLSTPDPGAHKPGSTVELNCISLGGIPRANLTWTREGVILGNVTSNNNKVTRVLTPKDNGVYFTCSATSPALRKHRKCTIMPMKIPPSPMVKVSANVSLVGDNITASCHSEGIPAIGSYTWFIDGRPIDFVIPRFSAINHHLKIRNLRMNDNNAILTCMVTTTLGLTGNYSTLLKVELPTTTVLPTTSMTPTKNTDTATELFSIIDDENNAGTGVNTKNDIDTSVTRYNMKLILALIFGMLIFIFIIVLMTLTYFFASHTTRPRQKKSSYEDSTLGPVSHRNSFIYMPALHQGENGQIFQQSLANDENSSGYISQLYASLEKPKHHMSKSQSVSALHNKHMKSVLSPSPSVVTLPVNTPCGGRKDFRNFNKVHYTKQPLRYTTHVDAPFTIPDDGMVTFHPLRRNTMDNFASTSNVANRGAYAIRRGSGYENVRLHDNFGHAEMNYAPNEDIYVNRSIDEYRNNEISDDFPPPPPYVAEDQSEPNPFLPD

>Sp\_Kirrel2L MACCWNLYIVILTLMMMQWKLILGGIFKHGPSDTVLVQGKTAVLRCAVKTQGNEVVYWFHVDSGQYISYDENIYSFVMEDRYSIIGNHKKGEYYLTIRSARKSDKGEYRCVYGNQFISARMVVLVPPNDGSPACEVLPAADTTSIGNVAQLSCTSQGGDPPAELSWYREDKLIAGPTVHANSVQRLVKQEDNGVLFTCSATTPALTYPRTCTVMVLKNPPMVTVTPPEVNIKHGETAQFTCRGTGETNVTGYRWFINYVVVGSKVSSPRYTLDPTNTTLTIHNVQAWENGVIVSCEANIQSGLKGRGSANLAVILPPNFKTASPPISNNGNKGNGTRLSPKGLHPQPFMTTNIAAIAGASAGALVLLIVVSTLAACCAKGKHKYPAGKNIPGSLRYKTSQQILIEEDFPIYAKPMKVKRLNCGVKEPSRPNSNSTTAESALTGVILDVGQGVAIPLCLRPPSLKRLGRKITSNYEKIGFDGPLPLTRPEPMGSEDKDSVPVEGAARPTEICRSQNNATNGDLRNGTSKPGELVYADLDLKENNNDSSAKQTQSDGVAYAKLRL

>Lv\_Kirrel2L MASCWNLWFVAVILMVNQWKLSLGGIFRHGPSDTVLVQGKTAVLRCAVKTQGSEVVYWFHVDSGQYISYDENIYSFVMEDRYSIIGNHKKGEYYLTIRNARKSDKGEYRCVYGNQFASARMVVLVPPNDGSPACEALPAADSTSIGNVAQLSCTSQGGDPPAELSWYRQDKLIAGPAVHANSIQRLVKTEDNGVIFTCSATTPALTYPRTCSVMILKNPPMVTVTPPEVNIKHGQTAQFSCQGIAESNVTGYRWFVNYVVVGSKVSSPRYTLDPTNTTLTIHNVQAWENGVIVSCEANIQSGLKGRGSANLGVKLPPNFRTASPPISNNGNNSNGTGLSPKGLHPQPFITTNIAAIAGASAGALVLLIVVSTLAACCAKGKSHKYPAGKNMPGSLRYKTSQQVLIEEDFPIYAKPMKVKRHNCEVTESSRPNSISKASTAESALTGVGSDAGHGVAIPLCLRPPSLKRLGRKITSNYEKIGFDGPLPLTRPEPMGSEDKDSAPVENPLRQTELCRSQNNATNGELRNGTSKPGELVYADLDLAENNNDSSTKQTQPNSKASDAVAYAKLRL

>Et\_Kirrel2L

MNLLLPLICFSVFTLNTCHARRPTFRYGPTDTVLVEGKTAVLRCAIRTQANEVVYWFHVDTGQYLSYDHNIYSFVMEDRYSIIGNHKKAGEYFLTIRNTRKSDKGEYRCVYGNQFRSARLVVLVPPDGGSPACEVMPAADSTSPGNVAQLTCTAHGGDPPAELSWYRNDKKIAGPSVHSNSLQRLVTEDDNGVLFTCSASTPALTYPRTCSVMVLNKPPVAKITPKDVTVKHGRTATFTCSGTGVPSVTLYRWFVNYVIVGSKVSSPRYNLDLTNTTLTINNVQSWENGVVVTCEVSIASGLKGRASANLVVQLPPNFRTNPPPVPDWNQGGGNNTKLTPRGLEPRPVMTPNMAAIAGASAGALALLIIVILLAVYCARGKSTKYQPNKNIPGPQLRYRKSQQMLIEDDFPIYAKPIKIKRSNIEVKDSSRPSSDSTTASTAESALTGESSVRSDHVNVVAIPLCLRPPSLKRFGRKTTSNYEKIGLDGVLPLTRPEPMGSESKDSVTRESSTRQNPLGTKVSATSDTGDKPNVEGLVYADLDLVENNNETSSKQTQTSLKHTDGVAYAKLRL

>Of\_kirrel2L

MALSQLFQIGIFFQAIFLSCALIFRYGPTDTTMAVGKTAVLQCAVVLQSNNEKVSWFHVESNQILSHDENILTLEDRYSIIGNREGKGEYYLTIRNVQRFDEGEYRCISGSDFRSATLKVIVPPPQDYPVCDVSPAPAGNQPGLLTQLTCTSDGGDPPARLTWKRHGIIISPTVSHANQLQRVVYEEDNGVPYTCFASSAALEYPRSCTVMVLNIPPRAEIKPMEQEVRAGDTATFECFGYGIPEVTSYQWLVNYAPVSEERNPRYSVDKTNRTLRISNVRRWEHGSLIICEVSIESGLKGRANARLLVHSPPVTVAKGSGPIVTLAPTAHPNMHPNPEQPKGRFHITGHAGALIGSIIGTLLLLTIVLVLTCLVLRAKLSQMGVDIIPFCKEKDKSPNGDNFPIYAKPNKIRNDAPPLPDAPRPDRSTLTRMATLPRAADDLEKKPKRKIKKHFSNYERIDLVPRQVSFLETKNDLDQETDLTLVTSTPNAEGIVYADLELNKGGIPAPDVVSSNRPDMVAYAQLRL

>Pm\_Kirrel2L

MSCRKRGLVVLALRTLLFSLSSAAVVFRDSPEDLVLAAGNTAVLRCSIQAGGGERDTVKWMHLESDQVLSKNEAGVRPASGEYRITSNRRGGEYHLRIIGVQLTDRGEYRCMCGSEYRSAILTVVVPPDTGYPLCHVQPNPTQQQPGRIAELTCNSHGGTPPAALIWHRKGEPISEVTTHSNALKSLVTAEDNGVVFTCFAQSKAASLPVRRCEVMVLDTPPTGSINPDLHVVYPGDSASYTCTGAGIPKVIRYRWLVNSIDVTRAENRGQRYEVLDNSRTLRITDVRSWEDGAVIACEVSIASGLTGRARAKLSIALQPVTSAANEANPGALFPINDRVPTENDKKTGPTGLKPQGNTATAGVVAGATMATVGIILALVAIAILLLKIKASGHFSMANANEKKCFPDKLDLSTGTIKKVDECPIYAKPNKLRKGPAPAPPGAAAAVLAACDLAMQKKQLRKNHHSYEKVEILGCSSPGQTYTLPVRLQARAPTTPKTRRSDTLRCIKAQAPLPPNLPPLPRSPLPPLPQKSPLPTPTPSDWPTGDLVYADLDLPAKTETVNQSHPSFVGVDYAMLQGRNSGSSGGYDWGTS

>Aplc\_Kirrel2L

MSARRVATPVVLQTILAAVSAAVVFLDSPEDLVLAAGNTAVLRCSVEPQGTEREPVKWVHLESNRILSEDSVVMGPTRDKYSVVRNHGGGEYTLKISAIQLGDEGEYRCMCGSEYRSAVLTVVVPPDAGYPLCHVQPNPTKQRPGGTAELSCTSHGGTPPADLVWHRGDLLISDVTTQANALQHMVTASDNGVRFTCFAKSKAPSLPVRKCETMVLNIPPEASISPQLHVVQPGESVTYTCAGAGIPAVTGYRWLVNYIDVTGEENRGQRYKLLDDNRTLRITDARSWEDGALIACEVSTHSGLIGRAWAKLSINSPPVMSTTKEVNPGLLLPTTDNVPIENDKKKIGPTVLKPQTNSATAGVVAGAILATVGIILALVVIAILLTKTKASGQFSMATANKKKCFEDKPGLSTGTIKKMDECPIYAKPDKLRKGPAPVPPSAAAPAPECALATQKKKARKNHHSYEKVDILGCSLPGQAYTLPVRLQSKAPATPTTRRSDTSRLLKAQAPPPPGFPLPPLPRKSPVPTPQHPPNNELLYADLDLPATRETINQSHNSTAGVDYAILPVHNSVNSGGYDWGTS

>Sp\_Hypp1164

MAWLSVTILLVTLMFSGALGLSFRNQPDTVTVYAGDTIYMRCDLNLDGVAGSSVSVTWIKSDNTNPQTQYISIRGHVVHTYTRFSIAGDSNLGEHDLMIRNVDYEDAGMYWCQASGAGGVIESVAGRLTVRVPIPIPTCSMTPPQPSVGQRVTVICSQQMHPSVNYEALNWWNETSRSKIRTQGRYSDGSIFFTRLLSDTDQGQQFVCSQSSVFVEGERNCTVVPLPAIEVSTIANPLETIVMNPTVKYVTEGSSAMFGCQSRAGPVARWVFGYGSRASKIRQTRGRFLVSADRSEFTVIRTALNDNGTAVRCIVILPSGVKLIGESTLKVLPADTQPAAVNPRKPPPPPPVSTRQTFRTEQPPIIPTRKPSTDQEPSTDGTSHGASNAANTETDSHPNLSGGKTIVNGQTTTKMPTATSKTTTKAAETSTRRDVVQIGANTDIDSGVIATEANVNLNHAGAPKIQTGGGYRQGGGNTHQVSNKDLPDQESNGSGIAGAIIGSLLIIALIVLIIFLIKTKRYPKSVPTWIPPHVVAALKRPIDMVKKSGSAGGQSGSSVKSSKRNAQMRMKEIEVVVNPPPPEWQFRLKDVESNSGGQVGGYALTPRQSHMMDGPVYANITPDLSKAPPGQDEHDLDDDDLDDDSVFSSDFDDDLDLEGEIAAELVARSCESEGNTDEFIEERKSKNVEGLVYAQLDMGPNAVKRSTVFIEGEKTQYAHIKVGNSAKAK

>Lv\_Hypp1164

MERTILLFTLMFSAALGLSFRNQPDTVTAYAGDTIYMRCDLNLGEVAGSSVHVTWIKSDNKNPTTYISIRGHFVHSFIGRFSIAGDTTRGEHDLMIQDVQYEDAGLYYCQVSGPGGTVITSVMGRLTVRVPIPIPTCSMTPSSPRVGQRVTFICRQQMHPSVDYEVLNWWNETSRSRIQQQGRYSDGSIFFTRLLSDSDQGQQFVCSQSQVFVEGERNCTVVPLPAAEVSTIANPLETIVINPTVKYVAEGSSATFGCQSRAAPVSRWVFGYGSKASKVRQSRGRFLVSADRSEFTVIRTTSNDNHTAVRCIVLLPSGEKLVAESTLKVLPSDTQPSAGNSRLPPPPPIITTQATTTERPSTRPTRMTSNGPTGHRDTPTVNDPSIGQGTSNKANTGLGLQPDFSDGKSVSNVQTTPTKAEVTTKVTSKPAETSTRRDVVQIGANTDIDPGVLATDANVNQNRAEAPKIQTGGGYRVIDGGNTHQVSNKERPDQGSSSSGIVGAVMGSLLIIALIVLIIFLIKTKRYPKSVPTWIPPHVVAALKRPIDMVKKSSSDAGQGGGSEKSFKGNAPMRMKQIEVVVNPPPPEWQFRLKDVESNSGQVGTYAVTPRESHMLDGPVYANITPDLSKTQTHAVQDDHELDDDDDDSLFSSDFDDDLDLEGEIAAELVARSCESGGNTEDSIEQKKSKNVEGLVYAQLDLGPDAEKRSTVFIEGEKTQYAHIKVGNPVKPRSQRH

>Et\_Hypp1164

MAPLRAVDVIFTVFISAILITCALGLRFRNEPGTVTVYAGETVYFRCDVYTNQGAPPANLRVTWMKADSRNARKIISVSGVIVSAFADPNRFSQVGDPELGEHDLMITNVQYEDAGMYWCQVSTSGQYLESRMGRLTVQVPVPIPVCSVDQPTPTVGQRVTFNCQQQMHPEVNYEALNWWDETTRRKVVTQRRYSDGSISFVRVLTESDRNRKFVCIQGLSFVEGQRNCSVLPLPAPQISTPANLAQTIIMNPEVKYVTEGSSATFGCTSSAGPVSRWIFGYGSSSTKIRQTYDRFLVSSDRSELTIIRTTLRDNGRAVRCVVLTSTGDKLIGQSVLNVLAPGTEPAATIPKIPPPPPSTSRPTTPTKPPTTKAETTQNDTPKQSTSHTQNTETVSQTTTTNTGNKGNTETNVNATTNQEPSTRRDAGQIGASNPDVITDAETKTPPNTEQNNANAPKIQSGGVYRSSNPHQVSSDNNGNQRDSSAAIVGAVLGSLLLIALVVLAVFLVKTKRYPKTMPVWFPPALLAVLKRPSKKQDGATGNENGPEVITSGKQSIRLKRIEVVVNPPPPDWQFRLKDVEGGDGKSVAPLNNYETHEGPVYANLTPELTKACPEEDPDDDDNDSLFSSDFDDDMDLEGEISATLAQMAANPEPIYENRMSLGPLPVMTSVPATAPVPAPAPSPNERKSKNVEGLVYAQLDLGPDAVKRSTIFIEGEKTQYAHIQHGNSAKRK

>Aplc\_Hypp1164

MVWYGGVVFVTAFLSLAAAVNFLSGPSNTVVPVGGTARLKCVADLRTVRGTVTLYWYKAQDGGGYYITGGSDIYSRNLGAERYSLETSSVNGEYSYTLKITSVEAVDSGQYQCMGVDSSGHTRSPRGSLSVVQAATDEPLTCSFYPQSPTVGQTVTFSCIAPRGIAPEMLSWWMAHSVRIQPSAHLSNNHGISFVKTLSNADNFAEFTCLVGSSFDTTNNMNCSVTPLAVPIRAEVTAETAFVVADRTATFRCRGTAIPPVTRYRWIYGSGRNTIKISTSRGRYTVINNGDSSTLTIAGITMQDNGQTVRCVVLNEVTKTIGSSTLRVTNRIQTTQKTTILTSSSTSPMYSTVLTETPTASLDPSQPTTSVRVTGDILVSTNQQIHTTNDHGDVINIVGCKDCGGKISPQQNPGDEEKSSNSTLAVALGILAICALVAGIIAYIVYTKRGRTSGRVIKRKWKNKPLQRLRSLRQSVSSSNQDVVNPNSVRLKTIEVIVNQPPPEWQLRVKDVAGEEKEPREQDLPKLGNDQSPVIQVTPDCALPENCDALYAKPDKMKKKRRHHGDEDGNDPRPVTASPTVPGQYLTADADDCFSDGVSDASTWDMSSVDSGCEEEMDEIRQDATAYAELDLTVAAERSKECTPPTETVEYANTTVTKTSLPRS

>Pm\_Hypp1164

MLCYGIVLVTIALSSVTALDFVSGPGSVIIPAGGTARLKCVADLRTVRGSLTLYWYKAQDGGGYYITGGSEVYARNLGAERYSLETSSVNGEYSYILKIAAVEAVDSGQYRCMGVDAGGSTSSPRGTLSVVQAATSEPLTCSYYPESPSLGQTVTFSCTAPRGISPEMLSWWMAGTVRIQPSANPSNNHGISFVKTLDNNDNFAEFTCLVGTSFDTANNMNCSVMPLAVPIRADVTPQTALALLGGSATFRCRGTAIPRVTRYRWIYGSGVSTAKIATSRGRFTVINNGDSSTLTIGGISMQDNDLSVRCVVMNEITKTIGSATIQVTTHIQTTRATTSLMSPSISPVGTTEKPTESLNPIQPREPMDPSQPTPSIRTTGKVLGSTNQQISTTNDNGDVINILGCGKECGEKLSPQQSPDGEEGSSNSALAAALSVLAICALATGVIVYIAYTKRGRTSGRVTKRKRKNKPLKRLRSLRLSVSNSKPELINPDSVRLKTIEVIVNSPPPEWQHRVRDVESETKEVQEQDLPRLEVTPDCDALYAKPDKTRKKRHHGDAVGDDTHPVATAPPAVPGQYLSADADDCLSDDVSDASTWDMSSVDSGCEEETDEIREDAAAYTELDLTKAGERDNKCIPLTEAIEYENTIITKASLPRN

>Of\_hypp1164

MEWSAGLFRLHRHLRVLCLTLVGIYYLVNLVESLSISEQPRNRGVQEGGTFTLNCVVESTNQAYVIWYKVESPGSSVPLSTYRTIRPEAPDSERLSIVGSGNVYNLKVINARNADESSYQCVAYSRGSSVRSEVAKVFILSVGDSVDCHLYPQHVRVGANLNYTCRAPESLPTATLTWWRGDQPMSAVETLPDGALQLRYVISEYDNFVRFTCTVGVDFTQAYGLNCSSVPLHVPLDGNLNPHLNRVSVGSNAAFRCSAVAAPPVNKIKWLVGYGSNSKISGTGGRYEVKGEPRDHTASTLIIKNIAQADNGTTVRCVVMNEIRQKDIAMAYVIVSDTNDPKVAPPPTVSPAIRTTRRPSRTNHLPTTKRTTTELTTKILTRLYQPGLKDVEISVHDGIPTRDIIPSVNNDGISEGNTENSSPSSNSNLAPTVAAICVLLVLLIAGGGIAVYFLIFRRKIVNKNKFNGEVKYRQSSDPNGGELTAEERASARMSLRLQTIEVVVNQPPPDWQCKLQDVKPNENEYTHFTSKANEIHGSPPPAYTKTPTDTERRSSRDEQDGGDKQNGSDEEKENDAIYALPAKKPSTGKRDGDTHQPAKRQISESKKRLLSQDYNDNENEEDEDIEWDQSSWDNSSFEDETETVERIQEGRMYSGPGEKIYANATEEGALNDYGPEYGNLPNLNVDETDPTYSRVASLKE

>Sp\_IgTM

MMILVSCWLMLAMSKMAYAVDLLMTPPVVQVYQAQTFRVTCVVTGEYQARYHSIHILHLPPKGKETYVTNDETIARTLNQNRQLRYSIFKKTSGSGANQRWEFMLTISKATKADVGRYQCLRIERAPRTTQYSTTFSRVFVNDIIAASQVAPQCALSPANPSPGQTTTFSCFSIGEAPKLTLTWTKGKKALPSKSSNSSGKFNVVTFQHIISEWDNNATFTCTATGLALGYETRTCSVVPFVIPTNVTVTSTQRVKSGKPAEFICLAVSVPATNKYTWVITKGSGKEIVDRSSGRYVIEQGGALLRINSVTPSDNNSSVHCIASNGMDIEGTSTGTLFTEPAKPSTGPGGGGIGSRHGKGDGNFAFFGKGGGSGLTPHPGLFTPGNGRRDIGTNGFGGERPNVPLLVGGTAGFVIFMTLIVLLLAMVMRTRTKRRKTITKLDVQRRPISIISLSNAFDVEKADVALVEANTTTQEKAVPRSTSLRKSVHSVSSRKSSINQDISRNQLADKLAATLRSKSYVSLVETPIPTQPGQSDKLDDDDCVSRVSTEDSAYDELTCSVSSSVVLSSRSNSNTASQSCYGSLGSLPSSVRYSRGKDALEVFKNPNLHYAEIDWSGRMPPSGKIVDGEEKSLYAQIMKK

>Lv\_IgTM

MRVLVSCWIMLAMSRMACAVDLLMTPPLVQVYQGQTFRVTCVVTGEYQARYHSIHLLHHPRNGRETYVTNDETVARTLDPNRQIRYSIHKKTSGSGQNQRWEFILTVVKAAKADIGRFQCLRIERAPRSTQHSSTFTRVYVNDVVPASPVAPQCALSPANPLPGQRTTFSCFSIGEAPKLTLNWSRGKRRLPSKSSNSTGKFNVVTYQHVISEWDNNATFTCTATGLALSYETRTCSVVPFVINTNVTVTSTQRVKEKEPAEFICLAVSVPATSKYTWVITQGSKKEVVDRSSGRYVIEQGGALLRINSVSLEDNNSSVECIASNGMNMEGTSTGTLFTEPATTSPRPRGDGIGTRHGHGEKGDRNFVFYSNGGDPGRTPHPSSPENEIEKNGFGGRKPYIPLFVGGTTGFVIFVTLIVLLLAMVMRTRSKRQKAVITSDAQRRPISIISLTTAFDVEKPDVALVEAKTTPQSQTVLKSTAYRKSLHNLPSSSSRKSGANQDISRQHLADKLSASLRSKSYISLMETPIPTQHTLHSDDATDDDCVSRVSTEDSAYDDLTCSLGSVSALGSRSNSNATSNSQSCYGSVGSLLSTVRYSRGNDTLEVMKKRSLHYAEIDWSGRTPPSGKIVDSDEKTLYAQIRK

>Et\_IgTM

MKGDLLGFKMSLMLYLPVGIILFVGRLTLAVDLLMIPPIVHVYETQPFVVTCVVTGEYQAILHTIHIVHHAANGKETIITQDETIHSIVDAGRAQRYGVTKKTFGSGADQRWEFTLAVSRASKVDVGRYQCLRTEESSQKRQLSPTFSHVHVNVVVPAGPNVPRCSIQPAEPLPGQTATFSCYSFGEAPKLTLTWKRGPEKFSTQANSTGKFNVISFTRSLSPWDNNATFTCTARGIAIGSETRNCTIVPFKIKTNVTVTSVQKVRHGEVAEFLCLAKAIPPATKYTWIVSKGTHEVTINRSHGKYEVEQSGALLKITAAASDNNSTVRCVAHNGIGIDGMSSGTLFTEPSTSPSGPNRGGGRGGIFNKHGNGDSVFFDKDGADGTNNGSSGTSDGGSNIQNPGKNDIGSNITSGHHPNVALLVGGAFGFISFMALVVFLLAVVMRSRGRRQKHVPAIRRQSSVRSIIADNRQNAEIAMIRETSAPHEKLRGSAATYRSTLQPQGVRKSALYSEVSRTQLADKLAATLRTKSYVALLDSPLPSRPGEENLTNTDDDDCVSRESTESTFADSAYDELSCSMTSTVLTSRSNSNSSPRPKDNSSNESASLPSSIRYSRGKDQLVGTSATNSKLLYAEIDWSDRKPPSGQILSGDEKTLYAKIRKK

>Aplc\_IgTM

MPPQMVTVGDSAEFFCLATSVPPSNRYRWFVGRGQSMTRVSKTKGRFVIANQGASLRILNITREDSGMPVRCVARNPLDMKGMDEDMLQVLIQRDPIPTTTIAPTKPPRTTTKSPPTPSPTTLPLTVLLKTSQRIRLQTLRAQATKAPSLAPPEQPTLRTASKQQPLTQSPEPKNPVTTVLVTTNKMDEPVSASPPLQDVTIPHVPPDSVLQPGPKGKGFTAGAAVGFTVLVLIVLALTGILIKIKFVDKHEKPVKRKTLRPANKPRIDKLDIVVVPNATPEEDGNTNNAQPSNNTDATPKPARSARRQSFVHPDFLEQLASTIRSKSHCSSMFKRGSFSWRKRKASTLDRPHTVKSEDPALDTEATSTVKRYSAFFNAVPQLSSDEMPVATARQVQKTESVYENTEIGLRLQQQVNRRSRDRESPYENTQCPMRDAAPLSDPDRRKSEASSLLDLVYADLDWTGFSSNQDEVNDTEEKTEYAAIRTSKVLS

>Pm\_IgTM

MESRLIFTSLVLTAVYAAELRVKPSDSTVTIGQPHTFECIIAGEYQKGKQHVYWAWTGPRNQQKFLSVDRTLYPAVDADKRSRYSITGNMNEGEFNLHISSTTADDQGQFRCIMYDSGRSARASAMLSVQEPRLPHQGYPKCSITPTNPQPGEYATFSCISAGGNPPATLSWARRKKSDIPAHHNSTGQQTGAYLHRLLTGHDNNVTFTCFSRSAHSADFGSCTVVPFEIPTHVTIMPPQMVAVGDFAEFFCLATSVPSSIKYRWFVGERQSMTKVTRTKGRFVLANEGASLRILNITQDDNGMPVQCVARNPLDIKGMDADIVRVVVQRNPIPTVTTTKPLLRSTKATPTTSTPFVPPRTSRKTWMQTFTVQATEFQTPAPPKHPPLRTAPKRVPESPKPKNSAAIIPVTTNEVDEPVSPSPPLEDDTTRQPPDSVQQPGPNSKGFTAGAAVGFTMLILIVFVLIGILIKIKIVDKQEKPAERKTLRPAYKPRIDKLDIVVLPNTAQENDSNTSDVQRSSSDDAPRSKHKQNSVKSDKSPRRSSFVHPDFLEQLASTIRSKSHCSSMFKRGSISWRKRKASTLDRPSAVKSESSLAEEATSTVKRYSAFFNAVPKVPNEEVPVASPRNIQTPESVYENTEIGLKLQEEANRFSRESPYENTQYPMNDTALSSDPDNRKSEASSLLNLVYADLDWTGFPSRHEDVNDTEERTEYAAIRTSKVL

>Of\_IgTM

MEQLATWKYLSFCFILTLISGVIEAVEIVLHPSSASGVQGSTITLRCGVNTEFRAGVHRIYWAFYGTPGQHTFLSVDRSIYSSLTSSKRNRYSIGGGVGLGQIEFNLQISNAQLEDNGVYECILYDPFTGQRVTTPDPARVVVLPLRPPDRGSPECRLSPPNPRPGVIVTFTCITSEGLPRPTLTWRKQGTILPGVLNSTDDLGLEILQFKRYISNWDNNATFTCTAASPAMPESRNCTVKPFEVPIHVSVTSLQLVKVGQSAEFYCTASGVPDVNRYRWFIGRGDTAERITRTQGRYTLSTQGTYLRINDVTEKDNGLPVRCVARNAIDLRGVDEGVLRVIVPRPTVNVVNNPTTVGILTTPLPKPVTQSRNGHDFKPAVGTNPVGTDTGRKGGGGKESGGRFGHFPERPFRPKPSASVGFFTARPNGDPTMKQRAFDKPHVTYTIQHNDIEQAHASPRLNMTFLVSGATGLLLLVLIVFLILIVVVRKSTSSKPPPVKSARNRNLRPYSTGTLSKSDIVVLPVPTSEDEEKDTTKPVGADGITTVRLISLEKAATLDKPKSYSTHQDFMAQLKGTLRSRNTYANFFENEAVTKKFDRSNSNSSDFSEGEIVRCDSAFCDDFKPGLSGSETAINDYSPEARFFKDNKTDKSNSTGNLVYVELDFGKAKPTSAVKGGDDKTHYAEIRLSKNIDL