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| --- | --- | --- | --- | --- |
| ORF\* | Top-hit gene ID in BLASTX\*\* | Top-hit gene definition in BLASTX\*\* | Coverage (%) | Peptide mapping\*\*\* |
| TRINITY\_DN45806\_c0\_g1::TRINITY\_DN45806\_c0\_g1\_i1::g.104285::m.104285 | gi|958242933|gb|JAO38253.1| | ALDOA, partial [Poeciliopsis prolifica] | 95 | GRINTRARGPEGCRRRRPDLLPPSLFSQLSSQTQRVRMPHAYPFLTPEQKKELS**DIAHKIVAPG**KG**ILAADESTGSVAKRFQSIN**AENTEENRRLYR**QLLFTADDRVAPCIGGVILFHETMYQ**KADSGKTFPAHLKERHMVVG**IKVDKGVVPLAGTNGETTTQGLDGLYER**CAQYKKDGADFAKWRCVL**KITPTTPSRLAIIENANVLARYAS**ICQM**HGIVPIVE**PEILPDGDHDLKRCQ**YVTEKVLA**AVYKALSDHHVY**LEGTLLKPNMVT**AGHSCSHKYS**NQEIAMATVTALRRTVPPAVPGITFLSGGQSEEEASVNLNAMNQCPLHRP**WALTF**SYGRALQASALK**AWAGKKENGKACQEEFVKR**ALANSQACQGKYAASGASAAGGESLFVANHAY** |
| TRINITY\_DN58624\_c13\_g1::TRINITY\_DN58624\_c13\_g1\_i1::g.62013::m.62013 | gi|548512008|ref|XP\_005750706.1| | PREDICTED: myosin heavy chain, fast skeletal muscle-like [Pundamilia nyererei] | 90.8 | M**STDAEMAVYGKAAIY**LRKPERERIEAQSKPFDAKAACYVTDAKELYLKGTIIKKDGGKVTVK**VLDTQEEKTVKEDDVSQMNPPKYDKIED**MAMMTYLNEASVLYNLKERYAAWMIYTYSGLFCATVNPYKWLPVY**DSEVVNAYR**GKKRMEAPPHIFSVSDNAYQF**MLTDRENQSVLITGESGAGKTVNT**KRVIQYFATISVGGGDKKKDAAPGKMQGSLE**DQIIAANPLLEA**YGNAK**TVRNDNSSRFG**KFIRIHFG**TTGKLASADIET**YLLEKSRVTFQLPDERGYHIFYQMMTNHKPELIEMSLITTNPYDFPMCSMGQITVASIDDKEELEATDNAIDILGFTNEEKMGIYKLT**GAVLHHGNMM**FKQKQREEQAEPDGTEVADKI**AYLLGLNSADMLKAL**CFPRVKVGNEFVTKGQTVPQVKNSVTALAKSIYERMFLWMVIRINQMLDTKQQRNYFIGVLDIAGFEIFDFNTLEQLCINFTNEKLQQFFNHHMFVLEQEEYKKEGIIWEFIDFGMDLAACIELIEKPMGIFSILEEECMFPKATDTSFK**NKLYDQHLGKTKAFE**KPKPAKGKAEAHFS**LVHYAGTVDYNIG**GWL**DKNKDPLNDSVVQLYQKSPVKI**L**AALYPPVVEEVG**KKGGKKKGGSMQ**TVSSQFRENLGKLMTN**LRSTHPHFVRCL**IPNESKTPGLMENF**LVIHQLRCNGVLEGIRICRKGFPSRILYGDFKQRYKVLNA**SVIPEGQFIDN**KKASEKL**LGSIDVNHDEY**RFGHTKVFFKAGLLGVLEEMRDEKLATLVTMTQALCRGYLMRREFVKMMERRESIFTIQYNIRSFMNVKHWPWMKVYYKIKPLLKSAETEKELANMKENYDKMKTDLATALAKKKDLEEKMVSLVQEKNDLQLQVASESENLSDAEERCEGLIKSKIQMEAKLKETSERLED**EEEINAELTAK**KRKLEDECSELKKDIDDLELTLAKVEKEKHATENKVKNLTEEM**ASQDESIAKLT**KEKKALQEAHQQTLDDLQAEEDKVNTLTKAKTKLEQQVDDLEGSLEQEKKLRMDLERAKRKLEGDLKLAQESIMDLENDKQQSDEKIKKKDFETSQLL**SKIEDEQSM**SAQLQKKIKELQARIEELEEEIEAERAARAKVEKQRADLSRELEEISERLEEAGGATAAQIEMNKKREAEFQKLRRDLEESTLQHEATAAGLRKKQADSVAELGEQIDNLQRVKQKLEKEKSEYKMEIDDLS**SNMEAVAKSKGNLE**KMCR**TLEDQFSELK**TKNDEHVRQINDISGQRARLL**TENGEFGRQIEE**KEALVSQLTRGKQAFTQQIEELKRQVEEEVKAKNALAHGVQSARHDCDLLREQF**EEEQEAKAELQ**RGMSKANSEVAQWRTKYETDAIQRTEELEEAKKKLAQRLQDAEEQIEAVNSKCASLEKTKQRLQSEVEDLMIDVERANGLAANLDKKQRNFDKVLAEWKQKYEEGQAELEGAQKEARSLSTELFKMKNSYEEALDHLETMKRENKNLQQEISDLTEQMGETGKSIHELEKSKKQVETEKTEIQTALEEAEGTLEHEESKILRVQLELNQIKGEVDRKLAEKDEEMEQIKRNSQRVIDSMQGTLDSEVRSRNDALRIKKKMEGDLNEMEIQLSHANRQASESQKQLR**NVQGQFKDAQLHLDD**AVRAQEDLKEQAAMVDRRNGLMVAEIEELRAALEQTERGRKVA**EQELVDASERVGLLHSQNTSLLN**TKKKLESDLVQVQSEVDDSIQEARNAEDKAKKAITDAAMMAEELKKEQDTSAHLERMKKNLEVAVKDLQHRL**DEAENLAMKGGKKQ**LQKLESRVRELETEVEAEQRRGADAVKGVRKYERRVKELTYQTEEDKKNVARLQDLVDKLQLKVKSYKRHAEE**AEEQANVHLS**KCRKIQHELEEAEERADIAESQVNKLRAKTRDSGKGKEAAE |
| TRINITY\_DN54046\_c11\_g2::TRINITY\_DN54046\_c11\_g2\_i3::g.17254::m.17254 | gi|657594936|ref|XP\_008302105.1| | PREDICTED: creatine kinase M-type-like [Stegastes partitus] | 95.3 | M**AKNCHNDYKMK**F**TTDDEYPDLSLHNNHMAKVLT**KDIYGKLR**GKSTPSGFTVDDVIQTGVDNPGHPFIMTVGCVAGDEESYEVFK**DLLDPIISDRHGGYKPTDKHKTDLN**FENLKGGDDLDPNYVLSSRVR**TGRSIKGFTLPPHNSRGERRAIQNLSIEAL**ASLEGEFK**GKYYPLDGMTDAEQEQLIADHF**LFDKPVSPLLT**CAGMARDWPDARGIWHNDNKTFLVWVNEEDHLRVISMQKGGNMKEVFRRFCVGLQKIEEIFKKHNHGFMW**NEHLGYILTCPSNLGTGLR**GGVHVKLPKLSTHAKFEEILTRLR**LQKRGTGGVDTASVGGVFDISNADRLGSSEVYQVQ**L**VVDGVKLMVE**MEKKLE**KGESIDGMIPAQK** |
| TRINITY\_DN48833\_c4\_g9::TRINITY\_DN48833\_c4\_g9\_i1::g.72768::m.72768 | gi|1552222|dbj|BAA13446.1| | muscle actin OlMA1 [Oryzias latipes] | 98.7 | MC**DDEETTALVCDNGSGLVKAGFAGDDAPRAVFPSIVG**RPRHQGVM**VGMGQKDSYVGDEAQSKRGILT**LKYPIEHGIITNWDDMEKIWHHTFYNELR**VAPEEHPTLLTEAPLNPKANR**EKMTQIMFETFNVPAMYVAIQAVLSLYASGRTTGI**VLDAGDGVTHNVPVYE**GYALPHAIMRL**DLAGRDLTDY**LMKILTERGYSFVTTAEREIVRDIKEKLCYVALDFENE**MATAASSSSLEKS**YEL**PDGQVITIGNER**FRCPETLFQPSF**IGMESAGIHETAYN**SIMKCDIDIRKDLYANNVLSGGTTMYPGIADRMQKEITALAPSTMKIKIIAPPERKYSVWIGGSIL**ASLSTFQQM**WISKQEYD**EAGPSIVHR**KCF |
| TRINITY\_DN54808\_c0\_g1::TRINITY\_DN54808\_c0\_g1\_i1::g.84158::m.84158 | gi|657524690|ref|XP\_008277999.1| | PREDICTED: myosin-binding protein H-like isoform X1 [Stegastes partitus] | 98.2 | MPSKPAPIKKAAGKEPAKKEEKKA**PEPAPEPVPEPAPAEAAPAEAAPAEAAPAEGAPAEGAEGAPAPAEGEAAPAEDAAAAPPAE**EPKAPTPPPPDEPTSAPVELFVEDKNDTSVTIIWSQPETIGHSGLDGYTIEVCKDGTDDWKAVNEDLQKSCRYVIKNQTTGDRLKIRVVAVNAGGRSPPIALPEAVLVKEVADRPKVRLPRILKQRY**VAYVGDKINLT**IPFTGKPKPVVTWTKNGEPLDKKRVNIRSTDRDSILFIR**TSERDDSGVYEM**CVKVEDFEDKAPITLQIVELPGPPASVKIVDTWGFNVALEWTAPKDNGNTEITGYTVQKADKKTGDWFTVVEHYHRLNATISDLIMGNTYKFRVFSENKCGISESAAVSKEEAKILKTGIEYKPLEYKEHDFTEAPKFT**TSLTDRSTTVGYS**TKLLCSVRGFPKPKVIWMKNQMI**IGDDPKFR**QICVQGICSLEIRKPGNFDGGVYSCRAKNDHGEVTVSCK**LEVKQPAVADAEKK** |
| TRINITY\_DN43137\_c2\_g2::TRINITY\_DN43137\_c2\_g2\_i1::g.71288::m.71288 | gi|110808625|gb|ABG91151.1| | skeletal muscle fast troponin T isoform 2 [Hippoglossus hippoglossus] | 91.6 | MSDTEEVD**AGAVEEVVVEEVEVAPEAAPEPEAEPEPEPEPEPEPEPEVEPEPEPEPEPEPEAEP**EPEAEEEKPKFKPSAPKI**PDGEKVDFDDIQK**KRQNKDLIE**LQALIDAHFE**CRKKEEEELIALKDRIEKRRAERAEQQRVRAEKDKERQARREEERRVR**EEADATKKAAEEAKKKSA**L**SSMGSSYSSHLQ**KADSKRGGKKETEREKKKKILAARRKQLN**IDHLNEDKLKDKINELH**DWMCQ**LESEKFDHMER**LKRQKYEVTTLRKRVEELSKFSKKGAAARRRK |
| TRINITY\_DN40520\_c0\_g1::TRINITY\_DN40520\_c0\_g1\_i1::g.97405::m.97405 | gi|974115284|ref|XP\_015257043.1| | PREDICTED: beta-enolase [Cyprinodon variegatus] | 96.1 | M**SITKIHAREILDSRGNPTVEVDL**WTAKGHFR**AAVPSGASTGVHEALE**LR**DGDKARYLG**KGVLKAVDHVNKDIAPKLLEKKFSVVDQEKIDKFM**LELDGTENKSKFGAN**AILGVSLAVCKAGAKEKGVPLYRHIADLAGHKDVILPVPAFNVINGGSHAGNKLAMQEF**MILPVGASNFHEA**MRIG**AEVYHNLKNVIKAKYG**KDATNVG**DEGGFAPNILENN**EALELLKTAIEKAGYPDKIIIGM**DVAASEFYRN**GKYDLDFKSPDDPARHISGEKLGDLYRSFIKGHPVQSIEDPFDQDDWEQWAKFTASTDIQIVGDDLTVTNPKRIQQAVDKKACNCLL**LKVNQIGSVTESIQACKLA**QSSGWG**VMVSHRSGETED**CFISD**LVVGLCTGQIKTG**APCRSERLAKYNQLMRIEEELGDKAKFAGKDFRHPKIH |
| TRINITY\_DN13366\_c0\_g2::TRINITY\_DN13366\_c0\_g2\_i1::g.113635::m.113635 | gi|77799798|dbj|BAE46762.1| | white muscle parvalbumin [Trachurus japonicus] | 83.3 | GRSLQSTRDLSVSSVPYKAKTPKLTM**AFKGVLNDADVTAALDGCK**SAFDHKAFFKACGLAAKSADDIKKAF**AIIDQDKSGFIEED**ELKLFLQNFC**AGARALSDAETKAFLKAGDSDGDGKIGVDEFAAMVKH** |
| TRINITY\_DN39861\_c1\_g1::TRINITY\_DN39861\_c1\_g1\_i1::g.104849::m.104849 | gi|961866368|ref|XP\_014893949.1| | PREDICTED: triosephosphate isomerase [Poecilia latipinna] | 97.9 | MFINTPRYRFTSALLPQSRCTLVSCRYRFDSQQTHYPPKETATMSRKFFVGGNWKMNGDKKSLG**ELINTMNGAKVDPNVEVVCGAPTIYLDFVRSKLD**AK**FGVAAQNCYKVA**KGAFT**GEISPAMIH**DCGVKWVILGHSERRHVFGESDELIGQKTAHALENGLGVIACIGEKLDEREGGITEKVVFAQTKF**IADNVKDWSK**VVLAYEPVWAIGTGKTASPQQAQEVHEKLRGWMKTHVSEAVANSVR**IIYGGSVTGGTCK**ELA**SQKDVDGFLVGGASLKPEIIEIINAKA** |
| TRINITY\_DN42486\_c0\_g1::TRINITY\_DN42486\_c0\_g1\_i1::g.80855::m.80855 | gi|657590203|ref|XP\_008299528.1| | PREDICTED: sarcoplasmic/endoplasmic reticulum calcium ATPase 1 isoform X1 [Stegastes partitus] | 95.1 | **MDQAHTKNPAECLTY**F**GVNENTGLSPDQFK**KNLDKFGFNELPAEEGKSIWELIIEQFEDLLVRILLLAACISFVLAWFEEGEETVTAFVEPFVILLILIANAVVGVWQERNAEDAIEALKEYEPEMGKVYRSDRKSVQRIK**AREIVPGDIVE**VSVGDKVPADIRIVSIKSTTLRVDQSILTGESVSVIKHTEAVPDPRAVNQDKKNMLF**SGTNIAAGKAIGVA**VATGVSTEIGKIRDQMAATEQEKTPLQAKLDEFGEQLSKVITLICIAVWAINIGHFNDPVHGGSWIRGAVYYFKIAVALAVAAIPEGLPAVITTCLALGTRRMAKKNAIVRSLPSVETLGCT**SVICSDKTGTLT**TNQMCVTKMFIIKSVDGDHVDLDAFDISGSKYTPEGEVSQGGAKTNCSAYDGLVELSTICALCNDSSLDYNESKKIYEKVGEATETALCCLVEKMNVFNSNVKNLSKIERANACCAVIKQLMKKNFTLEFSRDRKSMSVYCTPGKGDGGAKMFVK**GAPEGVIER**CSYVRVGTSRVPLTGAIKEKIMAVIRDWGTGRDTLRCLALATCDSPLRPEEMNLEDSTKFANYETDLTFVGCVGMLDPPRKEVTGSIVLCREAGIRVIMITGDNKGTAIAICRRIGIFTEDEDVSGKAYTGREFD**DLPSHEQPEAVVR**ACCFARVEPSHKSKIVEFLQ**GHDDITAMTGDGVNDAPALK**KAEIGIAMGSGTAVAKSASEMVLADDNFSSIVAAVEEGRAIYNNMKQFIRYLISSNVGEVVCIFLTAALGLPEALIPVQLLWVNLVTDGLPATALGFNPPDLDIMGKPPRSPKEPLISGWLFFRYMAIGGYVGAATVGGAAWWFL**YDPTGPGVTYH**QLSHFMQCHDANEDFTGVECEIFEASPPMTMALSVLVTIEMCNALNSLSENQSLVRMPPWSNLWLAAAMTLSMSLHFMIIYVDPLPMIFKLTHLSVEQWMMVLKLSFPVILIDEVLKFFARNYVEK |
| TRINITY\_DN41606\_c6\_g1::TRINITY\_DN41606\_c6\_g1\_i1::g.74538::m.74538 | gi|281484920|gb|ADA70321.1| | parvalbumin 3 [Siniperca chuatsi] | 100 | MAFAAVLKEAEMKAALDGCAAADSFDYKKFFKACGLAGKTAEDVKKAFLIIDQDNSGFIEEEELKLFLQNFSAGARALTDKETKA**FLAAGDSDGDGKIGIDEFAALVKA** |
| TRINITY\_DN54121\_c3\_g1::TRINITY\_DN54121\_c3\_g1\_i1::g.17567::m.17567 | gi|1007754500|ref|XP\_015816723.1| | PREDICTED: phosphoglycerate kinase 1 [Nothobranchius furzeri] | 92 | RPLGVHPCCTKVTAVTRSLTNRQPKEAEDPQRGRCRKETNEASNM**SLSNKLTLDKVDVK**GKRVIMRVDFNVPMKDKHITNNQRIKAAVPTIKHCLDHGAKSVVLMSHLGRPDGNFVPDKYSLEPVAAELKTLLGKEVTFMKDCVG**KEVEAACANPAAGSVIL**LENLRFHVAEEGKGKDASGNKTKATQEQIDSFRASLSKLGDVYVNDAFGTAHRAHSSMVG**VNLPQKAAG**FLMKKELDYFAMALEKPQKPFLAILGGAKVKDKIQLINNMLDKVNEMIIGGGMAFTFLKVLNNMEIGTSLY**DEEGAGIVK**DLMAKAEKNGVKITLPVDFITADKFDEKATTGTATVAAGIPAGWMGLDCGPESSKAFSEAVGRAKQIVWNGPVGVFEWEHFAKGTKNLMDKVVEVTKTGCITIIGGGDTATCCAKWNTEDKVS**HVSTGGGASLE**L**LEGKVLPGVDALSSA** |
| TRINITY\_DN52604\_c0\_g1::TRINITY\_DN52604\_c0\_g1\_i1::g.58872::m.58872 | gi|542200547|ref|XP\_005474449.1| | PREDICTED: myozenin-1-like [Oreochromis niloticus] | 88 | M**PLGTPAPVNK**RKKPSKIIT**DLSHITQDEYE**SEPEASEFDLGTKIRTPKDIMLEELSLMKNRGSKMFKMRQQRVEKFIHE**NNPDVFSSESMD**NLQQFMGGQMGGEMINLGGHFVSKQGGLNFIGLQTAGGAPVPPPKPGS**KGAGAGGAGGAGGAGGAGG**AGGVGGGEHGKGGHHGEEGWSPLKGGGTDDASKKHIHVKIYVSPWEKAMKGDEALIATLKGGMPGPAMHKDHPHYKSFNRTAMPFGGFEKAKQFLK**FQLPEKEETKEEPEPAVVYQHEIG**CRPSFNRTPIG**WVGSSEPSSIHMENDVVPFDGETDEL** |
| TRINITY\_DN45055\_c0\_g1::TRINITY\_DN45055\_c0\_g1\_i1::g.50849::m.50849 | gi|7678748|dbj|BAA95136.1| | myosin light chain 3 [Trachurus trachurus] | 94.4 | M**AEEAAAAPAAASEFTADQMED**FKEAFGLF**DRVGDGQVAYNQVAD**IMRALGQNPGNKDVTKIL**GNPSADDMANKR**LAFDAFIPMLKQVDALQKGTYDDYVEGLRVFDKEGNGTVMGAELRIVLS**TLGEKMTEPEID**ALM**TGQEDENGSVHYEA**FVKHIMSV |
| TRINITY\_DN53071\_c2\_g2::TRINITY\_DN53071\_c2\_g2\_i2::g.16098::m.16098 | gi|657583015|ref|XP\_008295593.1| | PREDICTED: creatine kinase M-type [Stegastes partitus] | 94 | M**PFGNTHNNFK**LNYKVEEEFPDLSKH**NNHMAKVLT**KELYGKMR**DKQTPSGYTLDDVIQTGIDNPGHPFIMTVGCVAGDEESYEVFK**DLLDPVISDRHGGYKPTDKHKTDLN**FENLKGGDDLDPNYVLSSRVR**TGRSIKGFTLPPHNSRGERRHIEKLS**VEALTSLDGEFK**GKYYPLKSMTDAEQEQLIADHF**LFDKPVSPLLT**CAGMARDWPDGRGIMHNDNKTFLVWVNEEDHLRVISMQKGGNMREVFKRFCVGLQKIEAIFKKHNHGFMW**NEHLGYILTCPSNLGTGLR**GGVHVKLPKLSTHAKFEEILTRLR**LQKRGTGGVDTASVGGVFDISNADRLGSSEVDQVQLVVDGVKLMVE**MEKK |
| TRINITY\_DN49088\_c4\_g3::TRINITY\_DN49088\_c4\_g3\_i2::g.119045::m.119045 | gi|7678750|dbj|BAA95137.1| | myosin light chain 2 [Trachurus trachurus] | 95.3 | MAPKKAKRRQAAGDGGSSNVFSM**FEQSQIQEYKEAFTIIDQNRDGIIS**KDDLRDVLASMGQLNVKNEELEAM**IKEASGPINF**TVFLTMFGEKLKGADPEDVILSAFK**VLDPEGTGSIKKE**FLQELLTTQCDRFTPEEI**KNMWSAFPPDVAGNVDYKNICYVITHGEEKEE** |
| TRINITY\_DN49401\_c0\_g1::TRINITY\_DN49401\_c0\_g1\_i1::g.75819::m.75819 | gi|744782311|gb|AJD07313.1| | pyruvate kinase [Trachinotus ovatus] | 91.1 | M**SKSKDSIMH**SQQ**MHAATADTLIEH**MCL**LDIDSHPAVSRNTGIICT**IGPATRSVEKGKEMIKTGMNIARMNFSHGTHEYHAETIKNVRTATESFVPGSVEYRPVAIALDTKGPEIRTGLIK**GSGTAEVELK**KGETIKLTLDNAFMEKCDEKVLWLDYKNITKVVQAGSHIYIDDGLISLKVKEVGGDHVTCEIENGGTLGSKKGVNLPGAAVDLPAVSEKDIQDLQ**FGVEQGVDM**VFASFIRKAADVHAVRKVLGEKGKDIKIISKLENHEGVRRFDEIL**EASDGIMVARGDLG**IEIPTEKVFLAQKMMTGRCNRIGKPIVCATQMLESMTKKPRPTRAEASDVANAVLDGNDCIM**LSGETAKGDYPLE**AVRAQHLIAREAEAAMYHRQMFEELRRITPLTRDPTESVAIGAVEASFKCCASAIIVLTKTGRSAHLLSKYRPRAPIIAVTRCGQTARQAHLYRGVYPVLYTKAANDVWAEDVDLRVNFALEVGKHHKFFKSGDVAIVVSGWRPGAGYTNTMRVVLVP |
| TRINITY\_DN52779\_c3\_g17::TRINITY\_DN52779\_c3\_g17\_i1::g.123787::m.123787 | gi|295792256|gb|ADG29132.1| | troponin I [Epinephelus coioides] | 98.3 | MSHDKKMTSSRKHHLKSLMLQIAAGWIEQEKKDIAAAKVAYL**AETCPKPTISGDQAALME**ICKKIHASLDKIDEARYDAEVKVKKADKEIDDLKMKVVELAGVKKPALKRVR**MSADAMLH**ALLGGKHKVTMDLRSNLKQVKKEVKEEATEAGDWRKNIEDKADRKKMFETS |
| TRINITY\_DN44517\_c0\_g1::TRINITY\_DN44517\_c0\_g1\_i1::g.10473::m.10473 | gi|348523353|ref|XP\_003449188.1| | PREDICTED: keratin, type II cytoskeletal 8-like [Oreochromis niloticus] | 88.9 | M**SSTYRTSSYSVK**SSNAPRSF**SSSSYAGPGGITSRK**SYSVRSSF**GGSNRGYGGAGITS**SSAYGLSSSAGMGMGMGMGMGMGMGGM**GAQAPITAVTVNKSL**LAPLNLE**IDPTIQAVRTQEKE**QIKTLNNRFASFIDKVRFLEQQNKMLETKWNLLQGQTTTRSNIDAMFEAYISNLRRQLDSLGNDKMKLEADLHNMQGLVEDFKNKYEDEINKRTECENDFVLIKKDVDEAYMNKVELEAKLESLTDEINFLRSIYEEELRELQSQIKDTSVIVEMDNSRNLD**MDSIVAEVK**AQYEDIANRTRAEAETWYKTKYEEMQTSANRYGDDLRSTRTEITDLNRMIQRLTSEIDAVKGQRANLEAQIAEAEERGELAVKDAKLRIKDLEDALQRAKQDMARQIREYQDLMNVKLALDIEIATYRKLLEGEEDRLANGIKAINISQQSTSYSGFPM**DSMKSSYASTYS**SGYGSGYGSGYGSSSGGFSGGSAGGYGSAGGYGSAGGYSTTTQSKKNVVIKMIE**TKDGRVVSESSEVIED** |
| TRINITY\_DN49882\_c0\_g1::TRINITY\_DN49882\_c0\_g1\_i1::g.120111::m.120111 | gi|958229780|gb|JAO32154.1| | PYGM [Poeciliopsis prolifica] | 77.9 | M**SKPLSDHDRKKQIS**VR**GLAGVENVAELKQNFN**RHLHFTLVKDRNVATKRDYYFALAHTVRDHLMGRWIRTQQHYYEKDPKRVYYISLEFYMGRTLQNTMVNLALENACDEATYQLGLDMEELEDMEEDAGLGNGGLGRLAACFLDSMASLGLAAYGYGIRYEFGIFNQKIVNGWQVEEADDWLRYGNPWEKARPEYMRPVHFYGRTEHHPDGVKWVDSQVVLALPYDSPIPGYRNNIVNTMRLWSAKAPCDFNLKDFNVGGYIQAVLDRNLAENISRVLYPNDNFFEGKELRLKQEYFVVSATLQDIIRRFKVSKFGSRDVVRTDFNKLPEKVAIQLNDTHPAMAIPELMRVLVDEEKLLWESAWDICIRTCAYTNHTVLPEALERWPVDLFAHLLPRHLEIVYEINRRHLEKVAAKFPGDHDRMRRMS**LIEEGGQKRIN**MAHLC**IVGSHAVNGVA**QIHSDILKATIFKDFYEMEPHKFQNKTNGITPRRWLVMCNPGLAEIIAEKIGEDFIRDLDQLKGLRKFINDEAFIRDIAKVKQENKLKFSVHLEEHYKVKINPNSMFDIQVKRIHEYKRQLLNCLHIITYYNRIKKEPNKQWTPRTVMIGGKAAPGYHTAKMIIRLITAIGEVVNNDPVIGDRLKVIFLENYRVTLAEKAVPAADLSEQISTAGTEASGTGNMKFMLNGALTIGTMDGANVEMAEEAGMDNIFIFGMRVDDVDAMDRKGYHASEYYNRLPELKQAIDQIAGGFFSPNQHDLFKEIVNMLMHHDRFKVFADYEDYIKCQEKVNALYKNPKEWTKKAIHNIAGCGKFSSDRTIAQYAREIW**GMEPTLEKLPAPDDKH** |
| TRINITY\_DN49369\_c0\_g1::TRINITY\_DN49369\_c0\_g1\_i1::g.75809::m.75809 | gi|734608233|ref|XP\_010731357.1| | PREDICTED: myosin-binding protein C, fast-type-like isoform X5 [Larimichthys crocea] | 85.9 | M**PEPVPAAKPEGDDAPPPDAVEAN**HAEEEQGSTELTGLFLEKPPESVVAVTGSDVTFIAKVDSTTLTRKPVMKWLKGKWLDLGSKAGKHMQFKETYDRNTKVYTYEMKIIKVVPGDAGGYRCEVTSKDKCDSSTFEISVEAAHAEEHTDILSAFKRADAGEDEGDLDFSALLKATKKKKKPQKVEPEVDVWELLKSAHPSQYEKIAFEYGITDLRGMLKRLKKMKTVVPKHTEAFLKKLDDCYSVEKGKKIVLKCEVVDPNAQVKWLKNGQEIKPSAKYVIEAVGNVRTLTINKTTLADDAAYECVIGEDKSFTEVFVKEPPVTITKLMDDYHVVVGERVEFEIEVSEEGAHVMWFFEDIELHRDKDTKYRFKKDGKKHTLIIQEATLDDIGMYHAWTNGGHTKGELEVEEKELEVLQDIADLTVKATDQAMFKCEVSDDKVTGKWFKDGVEVLPSDRIKMSHIGRFHRLTIDDVKPEDAGDYTFIPDGYALSLSAKLNFLEIKIDYVPRQDPPKIHLDTTGSMVSQNTIIVVAGNKLRLDVEITGEPAPTVVWSKGDQPITETEGRVRVEARKDLSCFVIEGAEREDEGKYTIVVTNPAGEDKAMLFVKIVDVPDPPEHVKCTGVGEDCATITWDPPKFDGGAAIKGYLMERKKKGSSRWTKLNFDVYESTTYEAKRMIEGVLYEMRVFAVNSIGMSQPSLNSKPFMPIAPTSEPMRLTVHDVTDSTCSLKWLAPEKVGAGGLDGYVIEYCKEGDTEWVVANKDICERQGYVVRGLPVGEKINFRVVAVNIAGRSPPATLGQPVTIREIVEHPKIRLPRDLRTKYIRKVGEKINLTIPFQGKPRPVATWYKDGQPLDPKMVNVRSSNVDTILFIRSAEREHSGTYELVLQIENLEDRASINIRIIDKPGPPLNVRVTEVWGFNAALEWEPPKDDGNCDISGYTIQKSELKTKEWFTVYEHNRRTNCTASDLIMGNEYQFRVYSENLCGKSEEPRFSKNTATIVKTGLDMKANPYKEKDMNCMPKFTQPLVDRSVVAGYSTAITCSVKGFPKPKITWMKNKMIIGDDPKFLMQNNQGVLTLNIRKPSPFDGGKYSCM**AVNDLGKDEVE**CK**LDVRVATNPDKQ** |
| TRINITY\_DN47596\_c0\_g1::TRINITY\_DN47596\_c0\_g1\_i1::g.69150::m.69150 | gi|657537490|ref|XP\_008275186.1| | PREDICTED: malate dehydrogenase, mitochondrial [Stegastes partitus] | 95 | MFSRAVRPTVSLVRSLSTSSQNN**AKVAVLGASGGIGQPLSLLLKNSPLVSQ**LSLYDIAHTPGVAADLSHIETRAQVTGYMGADQLDAALKGCEVVVIPAGVPRKPGMTRDDLFNTNATIVA**ILADACARNCPEA**MICIIANPVNSTIPITSEVMKKHGVYNPNKVFGVTTLDIVRANAFVADLKGLDPARVNVPVIGGHAGKTIIPLISQCTPKVEFPADQLSALTGRIQEAGTEVVKAKAGAGSATLSMAYAGARFTFSVLDAMNGKEGVVECAYVRSEETECKYFSTPLLLGKNGIEKNLGLGKLSAFEEKLVADAIDELKGSIKKGEDFVAKMK |
| TRINITY\_DN87263\_c0\_g1::TRINITY\_DN87263\_c0\_g1\_i1::g.49173::m.49173 | gi|1007771873|ref|XP\_015824097.1| | PREDICTED: keratin, type II cytoskeletal cochleal-like [Nothobranchius furzeri] | 90.3 | GLDSPLCVLCCSARTLSLPPFLSSQKKTKPAFATMRSSMRSTRTSFTSSGGSSGGFSGGSRISMGGGGGGAVKSFSSR**SAIVSGPRISSASM**MRSSMGGGGGGAGFGMGGGFGLGGGGGGGGFSMSSYSSGGGFGGGAGGFGMGGGM**AIAPITNVQVNQSLL**APLNLDIDPTIQTVRTQEKEQIKTLNNRFASFIDKVRFLEQQNKMLETKWSLLQDQTTTRSNIDG |
| TRINITY\_DN27846\_c0\_g3::TRINITY\_DN27846\_c0\_g3\_i1::g.118352::m.118352 | gi|269306947|gb|ACZ34179.1| | glyceraldehyde-3-phosphate dehydrogenase [Rachycentron canadum] | 91.6 | M**VKVGINGFG**RIGRLVTRAAFHSKKVEIVAINDPFIDLEYMVYMFKYDSTHGRFHGEVKVEGDKLVIDGHKITVFHERDPTQIKWG**DAGAHYVVESTG**VFTTIEKASAHLKGGAKKVIISAPSADAPMFVMGVNHEKYDKSLQVVSNASCTTNCLAPLAKVINDNFHIVEGLMSTVHAITATQKTVDGPSGKLWR**DGRGASQNIIPASTGAAKAVG**KVIPELNGKLTGMAFRVPTPNVSVVDLTVRLEKPAKYDDIKKVVKAAAEGPMKGILGYTEHQVVS**TDFNGDTHSSIFD**AGAGIALNDHFVKLVTWYDNEFGYSTRVCDL**MVHMASKE** |
| TRINITY\_DN43545\_c1\_g1::TRINITY\_DN43545\_c1\_g1\_i1::g.104599::m.104599 | gi|908482009|ref|XP\_013124986.1| | PREDICTED: LIM domain-binding protein 3-like isoform X3 [Oreochromis niloticus] | 84 | MSTYTVTLNGPAPWGFRLQGGKDFNMPLTISRITPASKAAGGSLTQGDIISAIDGASTEGMTHLEAQNKIKSVTSKLVLTMQKSRRPAPVPTATPRMDSPMPVIPHQKVIANTAANVEYTPSFNPIALKDSALSTHKPIEVRGPGGKATIVHAQYNTPISMYSQDAIMDAIAGQSQAKGHDS**SSVLPVKDPVVD**CA**SPVYQAVIRPGGNQDM**SEWARRAANLQSKSFRTL**AHITGTEYMQDPDEEALQR**SREKFESEVKGPRFAKLKNWHHGLS**AQILNIQE** |
| TRINITY\_DN56725\_c6\_g7::TRINITY\_DN56725\_c6\_g7\_i1::g.108808::m.108808 | gi|499031057|ref|XP\_004566239.1| | PREDICTED: troponin I, fast skeletal muscle-like [Maylandia zebra] | 88.6 | MSEKKMTSSRRHHLKSVILQIALSW**LEQEKKDLVVAKQNY**MAE**HCPSPDASGDQAALMEL**CKKIHGIIDKIDEERYDAESKVQKADKEIEDLKIKVVDLIGVKKPALKKVRMSADTMLQALLGSKHKVTMDL |
| TRINITY\_DN56777\_c0\_g3::TRINITY\_DN56777\_c0\_g3\_i5::g.108945::m.108945 | gi|808859815|gb|KKF11904.1| | Nebulin [Larimichthys crocea] | 76.8 | TPVDMMSVVQAKHASTVQTYAGYRKIPHNYF**LLPDNLH**LQQCRNMNTIASDCDYKSDWNNCVRGLGWVPMGSIGVETAKLGGDILSEHKYRTHPSNFKYSKLMDSMDLTLATANNKIMNKQAYTSAWDKDKLTVHIMPDAPEIL**LAKANAINMSN**KLYKAGLVEMANKGHHLKADAIPILAAKSGTTIASDYKYKLAYEKAKGHHVGFR**SLQDDPLLVH**YMQVARLQSDKNYKKDYHKAKLKYHSPVDMMSMTHAKHASAVQTYAGYKQVTSRYTVLPDAMNLELARHMQIIASDNQYKSDYNNYVRGTGWVPIGSVDVELAKAAGQALSEPRYRQHPSKFNFTKDMHSMDLTLATANNHIMDKQAYFKAWENDKTSIHIMPDAMEIVLARDNKSRYSEKLYRLDNELAKKKGHHVRADAIAIQAAKACTAIASDYKYKTGYRKQVGHHIGARCIQDDPLLML**ALNSAKIASDAL**YKKDFNKSKTKFHLPVDMISFELAKKNQIQVNHANYITRLHNWTCL |
| TRINITY\_DN58690\_c14\_g50::TRINITY\_DN58690\_c14\_g50\_i3::g.63723::m.63723 | gi|768960659|ref|XP\_011618511.1| | PREDICTED: LOW QUALITY PROTEIN: uncharacterized protein LOC101065560 [Takifugu rubripes] | 88.3 | M**ADQVAKTTQSLTTAAQMRETT**MMLMQPYANWEEYLTPAPLSVAIMGEIVFISSVQDFSINKNAPKDGFKYIRYPDSFRACLMQICNSGWHAYNEAHKNMDKIRLRTATVPDHMKAVINTLFNGSDEVIENLLPNQLENIRVIADDCVALADGVEKKYSDVINLIQELLEACVNAQHFYGEELENVKMKLEESKLREKTAQLLNERSKKALEDMGKQLEETQATFKQSMDSLPSGWEMIGMDFVEGLSTAVTGILNVVTLPLKLISTIKESVTDQQSSGEINENVDEFTQMTVNSKSGEILTLVGTLKHHVSGNEIDWKNLYDQEKKCPKTNWTESQFKRIFTEVGKLPGGKASEEVLSICQKGINICKELATYTPDQKWDEATTKQLINKITELNDEALAFDSRSKKALGTPAFTPKPPMMYKEQSKSSESTSASQRAAENARFKIEQSREQLKQTREQYEKSVENMEKNEKELTDILVEMQNCKIKEIDFETTIKMLVKGLDAMGRVKEQ |
| TRINITY\_DN51492\_c0\_g6::TRINITY\_DN51492\_c0\_g6\_i1::g.126915::m.126915 | gi|808882105|gb|KKF29537.1| | Myosin heavy chain, fast skeletal muscle [Larimichthys crocea] | 89.7 | M**STDAEMEQYGPAAIY**LRKPERERIEAQNTPFDAKTAFFVIDTEEMYVKGKLTKKEGGKATVETAGGKTVTVKEDDIHPRNPPKFDKIEDMAMMTHLNEPCVLYNLKDRYASWMLYTYSGLFCVVVNPYKWLPVYDSVVVNAYRGKKRIEAPPHIFSISDNAYQSMLTDRENQSIL**ITGESGAGKTVNT**KRVIQYFATIAVVGGKKDPVPGKIQGSLE**DQIIAANPLLEA**YGNAKTIRNDNP |
| TRINITY\_DN48706\_c0\_g1::TRINITY\_DN48706\_c0\_g1\_i1::g.37279::m.37279 | gi|734608349|ref|XP\_010731423.1| | PREDICTED: glucose-6-phosphate isomerase [Larimichthys crocea] | 83.2 | M**GLTQDPNFQKLQD**W**YTAHALNLN**MRHMFETDKERFNKLSLDLKTEDGDILLDYSKNLITEDVMKMLVDLAKSRGVEAAREKMFKGDKINFTEGRAVLHVALRNRSNTPIMVDGKDVMPDVNKVLEKMKGFCHRVRSGEWKGYTGKAITDVVNVGIGGSDLGPLMVTEALKPYSKGGPRVWFVSNIDGTHIAKTLAHLNAETTLFIVASKTFTTQETITNAESAKAWFLEHAKDKAAVAKHFVALSTNGPKVKDFGIDTENMFEFWDWVGGRFSLWSAIGMSIALHIGFDNFEKLLSGAHWMDNHFRTAPLDKNAPVLLALLGIWYINFFHAETHAMLPYDQYMHRFTAYFQQGDMESNGKYITNHGARVNYHTGPIVW**GEPGTNGQHAFYQ**LIHQGTRMVPSDFLIPAQTQHPIRENLHHKILLANFLAQTEAMMKGKTTEEAKKELEASGLSGEALEKILPHKVFQGNRPTNSIIFKKLTPHTLGALIAMYEHKIFIQGVMWEINSFDQWGVELGKQLAKKIEPELKDTKEVH**SHDSSTNGLINF**LKKNFA |
| TRINITY\_DN31230\_c0\_g1::TRINITY\_DN31230\_c0\_g1\_i1::g.51888::m.51888 | gi|222087993|gb|ACM41859.1| | PDZ and LIM domain 7 [Epinephelus coioides] | 84.8 | M**SGEHTVGQEAMNVYS**ITLAGPAPWGFRLQGGKDFSMPLTVSRLTPGGKAAQAGVGVGDWVVSIGDTNAEDMTHVEAQNKIRAATDSLTLTLSKAFKTGGDQKMEALDKGEATYFDEMYLSKHGLRAENMACFIPNDRSKKRLIE**DTEDWQPRTGTT**QSRSFRIL**AQLTGTDF**MQDPDDENMKRAREKFLTEIQSPRYARLRDWHHDRSARALNIKS |
| RRRRRTRINITY\_DN55603\_c0\_g1::TRINITY\_DN55603\_c0\_g1\_i2::g.85642::m.85642 | NA | NA | 21 | AVAPEQGGAADGRTRTHLLVAQGALGAEVGGEPVVYRTGDDARQPGMTRLQENSQAVCDLSWLQYRLSKGQKALIHVERLGPVNVPCSCSTGRPLHLWPLGPDPECQNESVSGQDLGLLVGSAAAWHARHGSRQCPEHNYDEDYPILVPQGGWLHRIITAANNGSLGGSLLEAKCGCVEEALLAMYNASFMEGQATYGRSLATQVVTEMDISLQPQRLHAAMWLAVLGCQPGDQILSPMYTNVLLWQLDKRFSSDRQGLLLRAETHDGEVPTSSSAITQYLKKKRDSS**APPPPPPPPP**GPAPP**PPPPAPPPPPPP**SSLPCQVSM |
| TRINITY\_DN45055\_c2\_g5::TRINITY\_DN45055\_c2\_g5\_i1::g.50857::m.50857 | gi|7678746|dbj|BAA95135.1| | myosin light chain 1 [Trachurus trachurus] | 92.5 | RHIHTHTPLPSAIQSLPGNSVDGGQEENSLIYIRPNGDFLLRVPSTLCYTPCVDTRTGNCLCFRNTVTLLPAEMAPKKDAKAPAKKA**EPAPAPAPAPEPAPVPA**APAAVDLSAVKIEFSPDQVEDYKEAFGLF**DRVGDNKVAYNQIAD**IMRALGQNPTNKEVAKMLGTPSAEDMANKRVEFEGFLPML**QTIINSPNKAGYED**YVEGLRVFDKEGNGTVMGAELRIVLSTLGEKMTEAEIDA**LMTGQEDESGGVNYEA**FVKHIMSV |
| TRINITY\_DN58073\_c4\_g2::TRINITY\_DN58073\_c4\_g2\_i1::g.89483::m.89483 | gi|734626895|ref|XP\_010741611.1| | PREDICTED: calpastatin isoform X10 [Larimichthys crocea] | 88.4 | ESPKLRPEDIVSEGKHKKEKGVFVGEREDTLPPEYRFNKEELMKLDPPKPEPSMGTGEALDLLSGDF**MSSSKAPAVQ**APVVTPSAPPAQSKVEDLSALDLLAGDFVASTKASGVHAPIPPPTKKVPERTVCPLEKANTIDVISFKPEERPSLKKGDSLSGDALSALGDMLPAALPKPESPKLRPEDIVSEGKHKREKGVFVGEREDTLPPEYRFNKEELMKLDPPKPEPTMDTGDALDILSGDFMTSSKAPAVKAPVVTPSAPPAQSSADFALDAL**AGDFVSSSAAPTVK**SAAFVPTETQPELEAGADNALDALSDTLKDIAPAPQPVPVVPAKDMVKEKKIAEERLIKMGERDDSLPPEYQPTEEDLKKMAEAKAKAAAAPKEKTMDDLTALDLLSSDFSAAPKPAAPAASSAATTKLQPPVLDSEPLKPMAGPALDSLSGTLLPDAIKSKSDKSKGKSKSKSKSKKHHADEPSAADQLSAQLSSDVVPTSTKKGGKS |
| TRINITY\_DN33102\_c0\_g1::TRINITY\_DN33102\_c0\_g1\_i1::g.53609::m.53609 | gi|30349202|gb|AAP22041.1| | keratin 8, partial [Oreochromis mossambicus] | 93 | QNEIEAVKGQRANLEAQIAEAEERGEMAVKDAKLRIKDLEEALQRAKQDMARQVREYQELMNVKLALDIEIATYKKLLEGEESRIASGGSAATIHVQSSSSGFAAGSGGGMGMGGGMGGGFGGGMGGGYGSGMSMSMGGGMGMSSMSGGMSGL**SIGGGSSSMTKSSSIR**RF |
| TRINITY\_DN54046\_c11\_g2::TRINITY\_DN54046\_c11\_g2\_i7::g.17261::m.17261 | gi|499038049|ref|XP\_004569670.1| | PREDICTED: creatine kinase M-type [Maylandia zebra] | 96.6 | M**AKNCHNDYKMK**F**TTDDEYPDLSLHNNHMAKVLT**KDIYGKLR**GKSTPSGFTVDDVIQTGVDNPGHPFIMTVGCVAGDEESYEVFK**DLLDPIISDRHGGYKPTDKHKTDLN**FENLKGGDDLDPNYVLSSRVR**TGRSIKGFTLPPHNSRGERRAIQNLSIEAL**ASLEGEFK**GKYYPLDGMTDAEQEQLIADHF**LFDKPVSPLLT**CAGMARDWPDARGIWHNDNKTFLVWVNEEDHLRVISMQKGGNMKEVFRRFCVGLQKIEEIFKKHNHGFMW**NEHLGYILTCPSNLGTGLR**GGVHVKLPKLSTHAKFEEILTRLR**LQKRGTGGVDTASVGGVFDISNADRLGSSEVDQVQLVVDGVKLMVE**MEKKLE**KGEAIDSMIPAQK** |
| TRINITY\_DN57016\_c1\_g19::TRINITY\_DN57016\_c1\_g19\_i3::g.105518::m.105518 | gi|1007785761|ref|XP\_015829638.1| | PREDICTED: elongation factor 1-alpha [Nothobranchius furzeri] | 82.8 | KYAWVLDKLKAERERGITIDIALWKFETQRYYVTIIDAPGHRDFIKNMITGTSQADCAVLIVAAGVGEFEAGISKNGQTREHALLAYTLGVKQLIVGVNKMDSTEPPYSQKRFEEITKEVSAYIKKIGYNPATVAFVPISGWHGDNMLEASDKMGWFKGWKIERKEGGATGTTLLEALDSILPPSRPTDKPLRLPLQDVYKIGGIGTVPVGRVETGVLKPGMVVTFAPPNLTTEVKSVEMHHESLPEAVPGDNVGFNVKNVSVKEIRRGNVAGDSKN**DPPMAADNFTAQVIILNHPGQISQ**GYAPVLDCHTAHIACKFSELKEKIDRRSGKKLEDNPKALKSGDAAIINMVPGKPMCVESFSQYPPLGRFAVRDMRQTVAVGVIKSVEKKNPSGGKVTKSAQKAEKKK |
| TRINITY\_DN56391\_c1\_g18::TRINITY\_DN56391\_c1\_g18\_i2::g.87075::m.87075 | gi|734647473|ref|XP\_010752926.1| | PREDICTED: muscle-related coiled-coil protein-like [Larimichthys crocea] | 89.9 | M**TDKSGMPTGGGDDAGSIMAL**LERVAGLMDSVQTTQQRMEERQLELESTVKTIQADVVKLTSDHANTSTTVDRLLEKTRKVSRHIKDVRVRVENQNVRVKKVEATQGDLLAKNKFRVVIYQGDQEVKAVTPGNEPAEPSGSGAARAEVEPDKFELPPESDEEYMVVEEADSSAAGRVKKSGLTRIESFKATFSKQNMSKTRENLGTKVNKLGERIVTAERREKIRQSGERLKQSGERLKETITKNVPAKLKKERTVAEGQEGAEGASEGAVPVPPPKGRKGSPGAAMAADDGKAEESEVPMYDMKQLS |
| TRINITY\_DN52352\_c2\_g1::TRINITY\_DN52352\_c2\_g1\_i1::g.38561::m.38561 | gi|339896195|gb|AEK21799.1| | tropomyosin [Siniperca chuatsi] | 86.3 | **MDAIKKKMQ**MLKLDKENALDRAEQAESDKKAAEDRSKQLEDDLVALQKKLKGTEDELDKYSEALKDAQEKLELAEKKATDAEGDVASLNRRIQLVEEELDRAQERLATALTKLEEAEKAADESERGMKVIENRAMKDEEKMELQEIQLKEAKHIAEEADRKYEEVARKLVIIESDLERTEERAELSEGKCSE**LEEELKTVTN**NLKSLEAQAEKYSQKEDKYEEEIKVLTDKLKEAETRAEFAERSVAKLEKTIDDLEDELYAQKLKYKAISEELDHALNDMTSI |
| TRINITY\_DN52976\_c0\_g1::TRINITY\_DN52976\_c0\_g1\_i1::g.15659::m.15659 | gi|574588302|gb|AHG32674.1| | SET and MYND domain containing protein 1a [Siniperca chuatsi] | 56.4 | MTVGNMEAAALFDAGKKGRGLRANRDLKAGEVVFAEPSFSAVVFDSLATQVCHNCFRHQSNLHRCAQCKFAHYCDRTCQTACWDEHKRECAAIKKLVMAPSEHVRLAARVLWRIHKATGIASDSQLISVDQLEDHVSDLSEEELKKLQGDVHKFQEYWSCGRKQHSAEYISHIFGIIKCNGFTLSDQRGLQAVGVGLFPNLCLVNHDCWPNCTVILNHGNQTALSSALHSKRRIELRALEKIPEGAELTVSYVDFLNLSEDRQKKLKEHFHFDCTCDHCSQHIKDDLMMAAAESKPSADKVKEVTAFSKESLEKIETCRVEGNFQEVVKLCHECLAKQENVLADTHLYRLRVLSVASEVLSYMRKFSEAAGYAQKMVEGYIKLYHHNNAQLGMAIMRAGVTHWHAGQIEVGHGLICKAYGILIVTHGPNHSITKDLETMRAQTEVELKMYRKNKEEYHTMR**EAALLKPVTSS** |
| TRINITY\_DN43965\_c1\_g1::TRINITY\_DN43965\_c1\_g1\_i1::g.101508::m.101508 | gi|831567189|ref|XP\_012733626.1| | PREDICTED: ATP-dependent 6-phosphofructokinase, muscle type-like [Fundulus heteroclitus] | 78.2 | M**AEPHQVDPTTMGKGRAIAV**LTSGGDAQGMNAAVRATVRVGIYTGAKVYFVYEGYQGLVDGGDHIRPATWESVSMMLQLGGTVIGSARCQDFRTKEGRTKAACNLVKLGITNLCVIGGDGSLTGANQFRTEWNELLADLVRTGKITANEAKASSHLNIVGMVGSIDNDFCGTDMTIGCDSALHRIIEIVDAITTTAQSHQRTFILEVMGRHCGYLALVTALACGADWVFIPEVPPEDGWEEHLCRRLQEQRGRGSRLNIIIVAEGAMNRAGKPITCEDIKALVSKKLGFDTRTTILGHVQRGGTPSAFDRILASRMGVEAVMAL**LEATPETPACVVSLSG**NMAVRLPLMECVQVTKDVTVAMGEGRYEEAVKLRGKSFENNWNTYKMLAHVRPPDTKSNINIAILNVGAPCAGMNAAVRSAVRIGLLQGHQMLAVHDGFDGLAHGQIEPIGWSGVAGWTGKGGSLLGTKRSLPSECMEEISLSIAKFNIHALIIIGGFEAFIGGLEMVQAREKYEEVCIPIVVIPATVSNNVPGSDFSVGADTALNTITMTCDRIKQSAAGTKRRVFIVETMGGYCGYLATMAGLASGADAAYIYEDHFNIHDLEMNVEHLVEKMKTTVKRGLILRNERCNANYTTDFIFNLYSEEGKGVFDCRKNVLGHMQQGGTPSPFDRNFGTKMGIKSVLWLTDKLKDCYRHGRIFANSPDTACVLGMKKRALVFTSLEELKSETDFEHRIPKVQWWLRLVPILKILAKYKTALDTSEKAAMEHVIKKRGLVHQ |
| TRINITY\_DN24229\_c0\_g1::TRINITY\_DN24229\_c0\_g1\_i1::g.120164::m.120164 | gi|961876346|ref|XP\_014896596.1| | PREDICTED: keratin, type I cytoskeletal 18 [Poecilia latipinna] | 87.7 | MSYRRTVQQIPSSHISMTRSAPQYRAASIYGGAGGHGARISSVSSSSLR**SGAPMGSSSSSFKLS**SAL**DGGMGMGMGGRVS**MAAGGGSSSGGGGGAGILGNEKGAMQNLNDRLANYLETVRHLEKANGELE |
| TRINITY\_DN50036\_c0\_g1::TRINITY\_DN50036\_c0\_g1\_i1::g.73177::m.73177 | gi|780956767|gb|AJZ70420.1| | peroxiredoxin 5 [Oplegnathus fasciatus] | 86.4 | MLCITSASLIKSTRIVQCARLLHISPVVKM**PIQAGERLPAVEVQ**EGEPGNKVAMDQLFKGKKGVLFAVPGAFTPGCSKTHLPGFVQQAGDLKSKGIQEVACVSVNDAFVMAAWGKEHGADGKVRMLADPTGAFTKAVDLLLDNDQIVQVLGNKRSKRYSMLVEDGVVKKINVEPDGTGLTCSLATNILSEL |
| TRINITY\_DN55301\_c0\_g2::TRINITY\_DN55301\_c0\_g2\_i1::g.84690::m.84690 | gi|1012734441|gb|JAR28267.1| | Nebulin [Fundulus heteroclitus] | 77.6 | DPLLML**ALNSAKIASDAL**YKKDFNKSKTKFHLPVDMIAFELAKKCQIQVNDDRYRTRLHQWTCMPDSNDVIQARKAYDLQSDNVYKADLEWLRGCGWVAADSVDHVKVRKAQQIINERLYKKDAQDAFGKFTL**VVDRPEIL**LAKQNAANLSDLKYKETFNAEKGHYIGSEDTPQMAHSREVSKNVSEKLYKLDWDETKATGYQLDHEYIPLIMGRKGRDIASDAKYKDAHEKAKGHHMAGTLVDFPDVMRCGEQEKNKGLRLYTKDYHQTKTKTHLPPDVIANQVAKRCQDMLSDVLYRTYLHQWTCHPDQEDAIRARKTNEILSDVYYKEDLNWMRGIGCYAWDTPEIIRAKKSYELQSELKYRDEAKKEFNNYSIVTDTPVYVTAVLGHTWASELNYREAYHKEKHLYTTVLDTYDYARCHNFKYFFSNKNYTSAWDKIKAKGYQIPHDSNAMQHAKQQKVVLSNVKYKEDYEKFKSLYSLPKSLEDDPQTARCVKAGKLVLDRLYRGDYEKNKAKNHIPPDMLEIMSNRNTQSMVSGIHYRKYLHQWICLPDMQVYVQARKVNEQLSDIFYKDDLNWLRGIGCYAWDTPEILRVKHAGDLQSENKYRAKGIESFKEYSVVTDTPVYETAKQNAQNLSDLNYRYDYNVNVKGTNTAPAVTIDTERARLGNYIQSDNYYKEANKSLMPTGYSLPHDTPLIKQVKHNSIVASNVKYKEAYEMTKAKAYTLHPEGVNFVTSRKANKMINERLYRQLYHKQKDKIHTTYDTPDIRQVKMNQEHLSDLCYKEKFYNSRGQLISLPITPELLHCYHVNEITSELKYKEDLMWLRGVGCFLYDTPEMVHVRNITKQRVTYPVEAKKNLANYSVVLDTPEYKRVTELKTHMSNLIYKAHSKEEMSKVTSTLDSLDIKRVKWAQQLTNKYMYTDLAAKERAHFTPEIDTPNMGHARIMKVVYSDKKYKDQYEKMKHRYT**AIADTPILVR**SKKAYLQSSDLRYKETFELSKGHYHTVKDALDIVCHRRVTDDISEVKYREKYINSLGTWKSIPDRPEFFFSKIANDQISNIKYKEDLDWLKGIGCYVWDTPELVQAERNKTLYSERLYKASFEKNRGNFKYTCDTPFFEAVKNASVLINDRAYRANYEKSRSKFT**ITTDDPRYQLA**RANRKMSQWKYREQYERAKDKFTSILETPEYEAHKRSKKISDIIYRMEYNKTKAKGYTLPYDTPYQQHMKKVKDITSTLKYKEVYEKSKAQINIDPEARDIRAAKEAYKNISNLDYKKKYEATKNKWIWTTDRPDFLNHAKNALQQSDVEYKYDKEMMKGCVIPVVDDKLTVLCMKNAEMASDVKYKLKYEQNKGHYVPVMDTPQILHAKAVRVLASESKYKEASKKEMQSGSFTTLSQTRDTAHSKEVNKLVSGKLYKAKFEKEKGKSKYNNMIVPPDVQHAIDVAKAQSSIAYKKDAKAGLHYTTVADRPDIRKAAQASKLISNIGYRDKAREEASRGGSLAHRPDIALATEVSKLTSELKYKEKFDKEMKGKRPKYDLKESKIYKTMKEANDLASEVKYKGDLKKIHKPVTDMAESLSMQHSLSTSKLSSQVKYKEKYEREKGKPMLDFETPTYVTAKEAQHMQSQREYKKSLEQEIKGKGMLALATDTPDFMRARNATDILSQTKYKQTAEMDRASYTTVIDTPDIIHAQQMKNIVSQKKYREEAEKTMSHYVPVLDTPEMQRVRENQRNFSTVLYSDSFRKQVQGKAAFVLDTPEMRRVKETQRIISGVRYHEDFEKSKGSFTPTTSDPVTERVKKNTQDFSDINYRGIQRRVVEMERRRAIEHDQETITDLRVWRTNPGSVFDYDPAEDNIQSRSLHMMSVQAQRRSKEHSRSTSALSGMADEKSEQSQDADHHMSLYSNGFMTSSIGYQHAKTVELQQRSSSVATQQTTVSSIPSHPSTTGKTVRAMYDYGAADNDEVSFKDGDVIVNVQAIDEGWMYGTVQRTGKTGMLPANYVEAI |
| TRINITY\_DN48282\_c1\_g6::TRINITY\_DN48282\_c1\_g6\_i1::g.55915::m.55915 | gi|734625726|ref|XP\_010740972.1| | PREDICTED: guanidinoacetate N-methyltransferase [Larimichthys crocea] | 77 | M**TTAAQPIFSKGEDCK**ASWHDASAGYNETDTHLEIMGKPVMERWETPYMHSLSTVAASKGGRVLEIGFGMAIAATKIESFPIEEHWIIECNDGVFARLENWAKAQPHKVVPLKGLWEEVVPTLPDNHFDGILYDTYPLSEDTWHTHQFDFIKGHAHRMLKTGGVLTYCNLTSWGELLKTKYDNIEKMFEETQVPHLLQAGFKKEKISTTTMDIAPPSDCKYYSFKKMITPTIVKE |
| TRINITY\_DN48662\_c0\_g1::TRINITY\_DN48662\_c0\_g1\_i2::g.37167::m.37167 | gi|974084320|ref|XP\_015240095.1| | PREDICTED: phosphoglycerate mutase 2 [Cyprinodon variegatus] | 79.1 | MSKYRLVIVRHGESSWNQENRFCGWFDADLSEKGLEEAKRGAVAIKEAGMKFDVCYTSVLKRAIKTLWTIMEGTDQMWVPVIRTWRLNERHYGGLTGLNKAETAEKHGEEQVKIWRRSFDIPPPVMDKDHAYHKIISESRRYKGLK**AGELPTCESLK**DTIARALPFWNDVIAPEIKAGKNVIIAAHGNSLRGIVK**HLEGMSDA**AIME**LNLPTGIPIVYE**LDEHLKPTKPMAFLG**DAETVKKAME**AVAAQGKAKK |
| TRINITY\_DN52149\_c0\_g3::TRINITY\_DN52149\_c0\_g3\_i3::g.68962::m.68962 | gi|734634490|ref|XP\_010745783.1| | PREDICTED: alpha-actinin-3 [Larimichthys crocea] | 73.6 | M**TAVETQISYSTNSY**TITHEEAYMTQEDDWDRDLLLDPAWEKQQRKTFTAWCNSHLRKAGTQIENIEEDFRNGLKLMLLLEVISGERLPKPDKGKMRFHKIANVNKALDFICSKGVKLVSIGAEEIVDGNVKMTLGMIWTIILRFAIQDISVEETSAKEGLLLWCQRKTAPYRNVNVQNFHISWKDGLALCALIHRHRPDLIDYSKLRKDDPIGNLNTAFEVAEKFLDIPKMLDAEDIVNTPKPDEKAIMTYVSCFYHAFAGAEQAETAANRICKVLAVNQENEKLMEEYEKLASELLEWIRRTIPWLENRVAEQTMRSMQQKLEDFRDYRRIHKPPRVQEKCQLEINFNTLQTKLRLSNRPAFMPSEGKMVSDIANAWKGLEQVEKGYEEWLLTEIRRLERLDHLAEKFKQKCNMHESWTGGKEDLLSQKDYESASLMEIRALMRKHEAFESDLAAHQDRVEQIAAIAQELNELDYHDAATVNARCQGICDQWDNLGTLTQKRRDSLERVEKLWETIDQLYLEFAKRAAPFNNWMDGAMEDLQDMFIVHSIEEIQSLITAHDQFKATLPEADKERMATMGIHSEILKIAQTYGIKLSGINPYTNLSPQDISNKWDAVKHLVPLRDQMLQEEVARQQANERLRRQFAAQANIIGPWIQTKMEEISHVSVDIAGSLEEQMNSLKQYEQNIINYKSNIDKLEGDHQLSQESLIFDNKHTNYTMEHIRVGWEQLLTTIARTINEVENQILTRDAKGISQEQLNEFRASFNHFDRKRNGMMDPDDFRACLISMGYDLGEVEFARIMTLVDPNNTGVVTFQAFIDFMTRETAETDTAEQVMASFKILASDKSYITVDELRRELPPEQAEYCISRMTRYVGTDCPTGALDYISFSSALYGESDL |
| TRINITY\_DN52091\_c0\_g1::TRINITY\_DN52091\_c0\_g1\_i1::g.68197::m.68197 | gi|348537423|ref|XP\_003456194.1| | PREDICTED: apoptosis-inducing factor 1, mitochondrial [Oreochromis niloticus] | 64.2 | MLKCRTVWKKLAPLARDSSTLCRQNVKRAGLNNASAVRVPAAHM**SSGAAGGGGENKVYF**LLVGAACLGGGIYTYRTVTGDQRRYLDRMTRKSDAQISAAPSQSEPPAVPEPKPEAAPSPETEAAAPSETTEPSPVADSTPASLKVPSHAPYLLIGGGTASFAAARSIRARDPGAKVLIITDEPDLPYMRPPLSKELWFSDDPSVTETLRFKQWNGKERSIYFQPLSFYIQPDEFNSAQNGGVAVLTGKKVVHMDVRGNKVKLDDDTEISYDKCLIATGGVPRNLQAVERAGEEVMKRTTLFRKIDDFKSLDKVSRNISSITIIGGGFLGSELACALGRRSTESGLEVIQMYPEKGNMGKVLPEYLSNWTTEKVKKEGVKIISEALVKSVTYKEDKLEIKLKDGRLVKTDHIVAAVGLEPNVDLAKSAGLEVDSDFGGFRVNAELQARSNIWVAGDAACFYDIRLGRRRVEHHDHAVVSGRLAGENMTGASKPYWHQSMFWSDLGPDVGYEAIGIVDSSLPTVGVFAKATAKDTPKAATEKSGTGIRSESETEDTAVSPVASSTPAPALAPQKDNYGKGVIFYLRDKVVVGIILWNVFNRMPIARKIIKDGEEHADLNEVAKLFNIHED |
| TRINITY\_DN56176\_c2\_g3::TRINITY\_DN56176\_c2\_g3\_i1::g.86492::m.86492 | gi|554809542|ref|XP\_005915666.1| | PREDICTED: aldose reductase-like [Haplochromis burtoni] | 82 | M**ATTVTLNTGAQVPIVGLG**TWKSEPNKVLEAVKSAIAAGYRHIDGAYIYHNETEVGEGVQAMIKDGVVKREDLFIVSKVWCTFHAKSHVRKGCEKTLSDLKLDYLDLYLVHWPMGFKSGGEDFPLDSNGETINDDTYFLETWEGMEELVDAGLVKAIGVSNFNKEQIEAILNKPGLKYKPANNQVESHPYLTQDKLIDYCHSKGISVTAYSPLGSPDRPWAKPDDPSLMEDPNIKAIAEKYKKTPAQVLIRFQVQRNVIVIPKSITPHRIQENFQVFDFQLTDEEMKTILGFNRNWRVCPMQWSTKHKDYPFNAEF |
| TRINITY\_DN49364\_c0\_g1::TRINITY\_DN49364\_c0\_g1\_i1::g.75641::m.75641 | gi|808864067|gb|KKF15262.1| | Heat shock cognate protein [Larimichthys crocea] | 76.1 | M**SKGPAVGIDLGTTYSC**VGIFQHGKVEIIANDQGNRTTPSYVAFTDSERLIGDAAKNQVAMNPTNTVFDAKRLIGRKFDDPVVQSDMKHWPFKVVNDATKPKVEVEYKGEIKTFYPEEISSMVLTKMKEISEAYLGKPITNAVVTVPAYFNDSQRQATKDAGVISGLNVLRIINEPTAAAIAYGLDKKVGGERNVLIFDLGGGTFDVSILTIEDGIFEVKSTAGDTHLGGEDFDNRMVNHFIAEFKRKFKKEINNNKRAVRRLRTACERAKRTLSSSTQASIEIDSLYEGADFYTSITRARFEELNADLFRGTLEPVEKSLRDAKMDKSQIHDIVLVGGSTRIPKIQKLLQDFFNGRDLNKSINPDEAVAYGAAVQAAILAGDKSENVQDLLLLDVTPLSLGIETAGGVMTVLIKRNTTIPTKQTQTFTTYSDNQPGVLIQVYEGERAMTKDNNILGKFELTGIPPAPRGVPQIEVTFDIDANGILNVSAVDKSTGKENKITITNDKGRLSKEDIERMVQEAEQFKAEDEVQKEKVTAKNSLESLAFNMKSTVEDEKLQDKISPEDKKAIVDKCNEVIAWLDRNQTAEKDEYDHQQKELEKVCNPIISKLYQGGMPEGGPGGMPGGMPGGFPGGAGGGSSSGPTIEEVD |
| TRINITY\_DN47551\_c1\_g1::TRINITY\_DN47551\_c1\_g1\_i1::g.69020::m.69020 | gi|734630814|ref|XP\_010743767.1| | PREDICTED: proteoglycan 4-like [Larimichthys crocea] | 78 | M**AVAYGAATQPGLLS**QQYPPPLLPKPGKDNVRLQKLLKRTAKKKASAQASQSAVHFRSSLSPVNEASPDLEHSDHSTPPRTPETPFNLYSVRQPQRFSVRPLYQHVASPYPQRAAYGRATSFSPQTVAMPSYSYSQHVTTVSSYSAPAYPPGPSPASGPFAQPAVPRISVSASSVPETIPAAEVKMTSFSTTAETHAGLRPSAGAVTPQPKSLGPTPYAAAGGQALIRPLTVLTPFVKSKSPRPTFKATEPSRSPKPMFDVPQIRMYTASTSYYETSRTPPVYDTSELTAIGSTVPQVVPTETKEDLTPVFEVRGGVTQVTQHTSLATDPMRKTPTSEIKRGATPTTEISTILTPTPEVKRATPTSEVKRATPTSEVKRATP |
| TRINITY\_DN58239\_c5\_g44::TRINITY\_DN58239\_c5\_g44\_i1::g.44443::m.44443 | gi|908512265|ref|XP\_013121871.1| | PREDICTED: phosphorylase b kinase gamma catalytic chain, skeletal muscle/heart isoform [Oreochromis niloticus] | 74.4 | MTKDEEIPDWVGAQEFYDKYEPKEILGRGVSSVVRRCIDKNTSVDYAVKIIDITPSDKMTAQEIEELREATVKEIDILKKVYGQDNIIQLKDCFESKAFFFLIFDLMKRGELFDYLTEKVTLSEKETRKIMRSLMEVVQFLHNQNIVHRDLKPENILLDDDMNIKLTDFGFSVQIQPGEKLKEVCGTPGYLAPEIIECSMDAGHAGYATPVDIWSSGVIMYTLLAGSPPFWHRKQMMMLRMILAGTYDFSSPEWEDRSDTVKDLISRMLVVDPSKRFTATDVLNHSFFSQYVVHEVREFSPYRRFKVICMTVLATMRIYCNYRRAKPVTKEVIQSDPYAVKPIRKLIDACAFKIYGHWVKKGQTQNRAALFENTPKAIL**LSIAAEADEPSHS**IW |
| TRINITY\_DN46890\_c1\_g1::TRINITY\_DN46890\_c1\_g1\_i1::g.75494::m.75494 | gi|658919436|ref|XP\_008399461.1| | PREDICTED: phosphate carrier protein, mitochondrial isoform X1 [Poecilia reticulata] | 71.5 | DVTKGQIDLPRGHSASPSSRLQLSGGAILRHRQTPPAGRTPTTMYPTSLTQLARGNPFSAPLFSLQKVEEPQQSLPGQRTRKLAAA**ATADEGDSCEFGSQKY**FVLCGFGGILSCGTTHTAVVPLDLVKCRMQVNPDKYKSIGNGFSVTVREDGVRGLAKGWAPTFIGYSMQGLCKFGFYEVFKIFYSDALGEENTYLWRTSLYLAASASAEFFADIALAPMEAVKVRIQTQPGYANTLRQCVPKMFAEEGLWAFYKGVVPLWMRQIPYTMMKFACFERTVELLYKYAVPKPRSECSKGEQLVVTFVAGYIAGVFCAIVSHPADSVVSVLNKERGSTAVGVLKKLGPKGVWKGLVARIIMIGTLTALQWFIYDSVKVYFRLPRPPPPEMPESLKKKLGLVE |
| TRINITY\_DN48193\_c0\_g2::TRINITY\_DN48193\_c0\_g2\_i2::g.13059::m.13059 | gi|657539597|ref|XP\_008275951.1| | PREDICTED: myozenin-2-like isoform X1 [Stegastes partitus] | 70 | MMMMMQASQNDMTKQRMFQAKALAKEARGGGLNLGKKISVPKDVMMEELNLPSNRGSRMFQERQKRVERYTVENAANAAYDTSNVYLEATHPPQVIPGPQTGKENQAFSIPGKHSLVMNLQKTVAKKGSPEVLAPGYSGPLRGVPHEKFNTTVIPKSYCSPWSEALGNNEELLNALNTQL**PELPQTLQSANYR**CFNRSARPFGGTMASKRVIPVMSFEAVESQNLPGIALDRICKRPNFNRAPRGWGADYSPESNEL |
| TRINITY\_DN56108\_c2\_g2::TRINITY\_DN56108\_c2\_g2\_i2::g.120873::m.120873 | gi|584022108|ref|XP\_006805711.1| | PREDICTED: putative peptidyl-tRNA hydrolase PTRHD1-like [Neolamprologus brichardi] | 95.3 | M**AASGAAAGAPSRLVQY**VVVRSDLVHKLSWPLGAVITQACHAATAAVHLHYGDPDTQRYLSELDSMHKVVLGAPDEAALSALSENLTQAGVSHKLWIEQPENVPTCLALKPYPKETVQPLLRKFKLFK |
| TRINITY\_DN15360\_c0\_g1::TRINITY\_DN15360\_c0\_g1\_i1::g.127661::m.127661 | gi|734613026|ref|XP\_010733999.1| | PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial [Larimichthys crocea] | 75.9 | WEVQAVVNMAAAVGRLLSFSKNAKVLVSPLRLSAVPAHRYSVEVSSTGEAITHTGQVYDEKDPRRARFVGRQKEVNKNFAINL**VAEEPVTDVEARVVS**CDGGGGALGHPKVYINLDKDTKVGTCGYCGLQFKQKHHH |
| TRINITY\_DN43816\_c0\_g1::TRINITY\_DN43816\_c0\_g1\_i1::g.107385::m.107385 | gi|410929655|ref|XP\_003978215.1| | PREDICTED: troponin C, skeletal muscle-like [Takifugu rubripes] | 61 | TDAQSDARSFLTEEMIAEFKAAFDMFD**TDGGGDISTKELGQ**V**MRMLGQNPSRE**ELDAIIEEVDEDGSGTIDFEEFLVMMVQQLKEDQAGRSEEELSECFRIFDKNGDGFVDREEFGVILHMTGEQVTEEDIDEMFGESDNNKDGRIDFDEFLKMMESVQ |
| TRINITY\_DN87925\_c0\_g1::TRINITY\_DN87925\_c0\_g1\_i1::g.27020::m.27020 | gi|1007773964|ref|XP\_015824921.1| | PREDICTED: cofilin-2 [Nothobranchius furzeri] | 56 | M**ASGVTVNDEVIR**VFNDMKVRKSSGQDEVRKRKKAVLFCLSEDRKKIVVEEGKQILVGDIGETVDDPYACFVKLLPLNDCRYGLYDATYETKESKKEDLVFIFWAPEGAPLKSKMIYASSKDAIKKKFTGIKHEWQVNGLDDIQDRTTLAEKLGGN**VVVSLEGKPL** |
| TRINITY\_DN57646\_c0\_g1::TRINITY\_DN57646\_c0\_g1\_i2::g.61044::m.61044 | gi|734628705|ref|XP\_010742601.1| | PREDICTED: uncharacterized protein LOC104929717 [Larimichthys crocea] | 65.3 | M**SSEKGPEVVGCDASIMM**NVWEIRLREHHQKLQLEHERLEKSALPTINKDWANRSTAKMGNYKRVERKAKPAETHTDNDNVWKSKRPQAPPTLPRGAGPGPHGRPGAQSGGFSPQASNKKEGQHNNYNNRLQLLMFLTQTQPSAMVWGKSWKYSKSLPSPAEGTAISDWGQCWMFATQQPYCEAGKPWANGPNMINPCSLHLWKRPDRNVEDSQELNLGLSTEEWHMSWRKPSNNNNKKEGTSSMNGENTGCFTLLMETQRLNEALCSSEWSESWRCTKHASEQEHGGLMDESVDKQDKLKEMSSKWEECWRFVNHHGCSQVPQFQGSENPECANWTAAMMIFNKHWNSDPSLKPHPDNAYNDFSEWDKSWQVTKNMSKPCEEIEKVLKALPPKMEMEAEKLEVKPKGQCSPSNEADLLYEKLKHDVIYWPKKESNQYKLPLLKQVENNLFSSEWSDSWKTLKNRLRMERRRVRPFRMSENRGDMKSTNTEWKDSWKFTCLSRLQEPELWQQDWVTTPQPRVDRARDQNYFGEFSKNVEESWEKSWRFSRGQHRSETSQGGSSTVCHHSDDSLVQKKCVRSVADWQAAWMVSESQFHHDKPSLMQWREAWKWSVFHTEKWFEKMIQDNRMEHGMEIQTLKEKIYLQTAKAKMIQSFVNQMVTERHPEENWRDSWKAGSLLNHQTNHYESHGKKINSTNQQLHPIASEHGSKWGRSFRLANPMPHVEQPWVESTPNPCHYTVMWSRESNIHNRINTSFSNNPAILRLWGNSHQFLQDGGVKSKGMGSTKAPVDPMVITTKTKIKRNLYGNINTDKQSGRKWAGCHLLGKTQPRPKRGSPSGKKLMLVEDETKAKFFEEWAESWKLLIQPGSLKKTPMKSLAGWAESWKFLLPPYQPMNVSKAK |
| TRINITY\_DN58429\_c0\_g15::TRINITY\_DN58429\_c0\_g15\_i3::g.90372::m.90372 | gi|657565229|ref|XP\_008285902.1| | PREDICTED: myomesin-1-like isoform X3 [Stegastes partitus] | 60 | IDRCEVGTHHWAQCNDSPVKYARFPVTGLVEGRSYVFRVRALNKAGVSRPSRVSEPVVAMDPSDRARLRAGPSAPWTGMIKFTEEDSTAGVIPGDPTDVVVTEATKSYVVLAWKPPLQRGHEGVMYYIEKCISGTDTWQRVNTGMPVKSPRFALFDLAEGKSYSFRVRCCNSAGVGEPSVSTGDITVGDKLDLPSTPGSPVVTRNTDTSVVVSWAASKEVKHLVGYYIECTVVGTDVWMPCNNKPVKQTRFVCHGLATGANYVFRVKAVNAAGYSQSSSDSDAVVVQAAISVPGKPTGVKLLEAVKDYMMLGWNEPSKNGGADVRGYFVDYRTVKGDVVGKWHEMNHQALTTTSYKAENLKEDIFYQFQVRAMNMAGVSEASLPSKSLECKEWTLTVPGAPVGLHVLEVRDTTVVVLWEPPAFDGRSPVNGYYLDHKVASAGEAGWKAGHEKANKKKYMKVTGLKAGTSYVFRVRAQNLAGVGKTSAVLGPVLAQTR**PGTKEIYVDVDD**DGVISMMFECSEMNESSEFVWSKNYKAITDTSRLTIVSEKGKTRAIFNSPSLEDLGIFSCVVTNTDGISSSYTLTEEGLKRLLDISHEHKFPVIPFKNEMAMELLEKGRVRFWTQVEKWTADCHVEYVFNDVIVTEGKKYSMNFDKSTGIIEMFMDSLEVTDEGTFTFNLVDGKAKGTTSLVLIGDEFRELQKKSEFERAEWVRKQGPHFVEYLDFAVTPECDVLLKCKLGNIKAETEITWSKDSIEIREDDEDAQKIEKKDGDMTFNIGKWIIKQEKRKEGKKAPADEVPPPPRPKISKSDAGIYEVFLKDERGKDKSTFNLTDAGYQAVMNELFRVIANSSSEVKVTSTEHGIILYSTVTYYNEDLRVGWLHKDAKIAASERVKAGVTGEQLWLKINEPTEKDKGKYAMDIFDGKDGVKRAFDLSGQVWEEAFEEFQRLKAAAIAERNRARVVGGLPDVVAIQEGKSLNLTGNVWGEPTPEVSWTKNERELTSDDRYKLKFEHGKFASITIAAVTTADSGKYALVVKNKYGTEAGEFTVSVYNPEEDEHKEEKKD |
| TRINITY\_DN48852\_c2\_g4::TRINITY\_DN48852\_c2\_g4\_i1::g.72745::m.72745 | gi|110808625|gb|ABG91151.1| | skeletal muscle fast troponin T isoform 2 [Hippoglossus hippoglossus] | 89.5 | M**SDTEEVDAGEEKPKFKPS**APKI**PDGEKVDFDDIQK**KRQNKDLIE**LQALIDAHFE**CRKKEEEELIALKDRIEKRRAERAEQQRVRAEKDKERQARREEERRVR**EEADATKKAAEEAKKKSA**L**SSMGSSYSSHLQ**KADSKRGGKKETEREKKKKILAARRKQLN**IDHLNEDKLKDKINELH**DWMCQ**LESEKFDHMER**LKRQKYEVTTLRKRVEELSKFSKKGAAARRRK |
| TRINITY\_DN54997\_c0\_g3::TRINITY\_DN54997\_c0\_g3\_i1::g.60110::m.60110 | gi|734636214|ref|XP\_010746735.1| | PREDICTED: protein S100-A14 [Larimichthys crocea] | 29.1 | M**PQYSDLEKAIST**LVTQFHSASADNGPTLKTDEFKGLLSSQMPNLVKGIGSEQGLGEIMRKMGVGDGEGVSFKHFWSLIQSLATTQHGLLASNTSSPCSCMVL |
| TRINITY\_DN49794\_c1\_g1::TRINITY\_DN49794\_c1\_g1\_i1::g.57338::m.57338 | gi|583995636|ref|XP\_006792942.1| | PREDICTED: myc box-dependent-interacting protein 1-like isoform X1 [Neolamprologus brichardi] | 66.4 | SGIRVTSRETSQERERERERRGGGEEGGVGGGFYAPSVSRRHFSLQSRPDSNRRHRAAM**AEMGKGVTAGKLAIN**VQKRLTRAQEKVLQKLGKADETRDAAFEEMVANFNKQMTEGSKLQKDLKAYVLAVKTLHDASRRLQDCLADMYEPEWFGKEEMDTMVEDTDTLWLDFHQNITDKSLMSVDTYLNQFPEIKARIAKRDRKMVDFDSARHHFASLQKGKKKDEAKIAKAEEDLGRAQKIFEELNVELQDELPALWDNRVGVYVNTFQSLAGQQEKFHKEMSKLSQNLNDIMTKLEEQRLLKKGGTAAAKTEDGAKSEEANHSESASSAPKSSVTNGAGGDLPPGFLYKVKAVHEYAATDGDELELEIGDTVLVVAFDNPDEQDDGWLMGLKESQWMQKKDFSAKGVFPENFTQKI |
| TRINITY\_DN58608\_c3\_g1::TRINITY\_DN58608\_c3\_g1\_i1::g.62351::m.62351 | gi|657583703|ref|XP\_008295972.1| | PREDICTED: titin-like isoform X11 [Stegastes partitus] | 67.8 | DGGAPILGYSVKYRDFIRKPEPEVEEEEEEYEDEEEEEEEPESPEELARWVEAIPLTKSLEFTIKGLKTDAEYEFCVKTINKIGSSVRSLYSDAAAAMDRTSEPSFDVDIEMRKVHLVKHNTAFTLSVPFKGKPVPSVEWTKEGVDLKVRGTIEATDISTSLTVEKATRNDSGEYSVTIESPLGKATLPMVVKVLDSPGPPVNVKVSAVTRDSATLIWEPPENDGGDAVKAYHVEKREASKKAWVCVTSNCHALSYKVEDLQEGAIYYLRVIGENEYGVGVPQEAKAGTKITEVPSAPMKLGVANVTKDCVTIAWTRPEYDGGSRVTGYLIDALEKGQTKWVKCATVRTMTHTIKSLREGAEYFFRVRAENHAGLSEPKEMIVPVIVKEIQEAPEFDLKNYPKNTVYVKAGSNLTFEIPLTGRPMPKVTMSKNNVVIKGSKRLLTEVTPDSLIITLNESIASDAGKYDVTASNAGGTTKIFIIFVVMDRPGPPVGPVEIGEVGETTVCLKWAPPEYDGGSPVTNYVVLKRETSTPTWAEVSTNIARSAIKVTKLTKGEEYQFRIKAQNRYGLGDHIDSKSVMIKLPYTIPGPPSTPWVSFVSRESLTVCWNEPVNDGGNPVIGYHLQMKERSSILWQKVNKTAIPGNQWRITNICPGLFYEFKVAAENAAGIGKLSKTSEEVLAIDACEPPANVHVTEVTKNSVSLAWQRPPYDGGSKITGYSVERRDAPNGRWVKANFTNIIEMGFTVSGLSQDESYEFRVYARNAVGSVSNPSLIVGPVTCIDACGAPAIDLPPEYLDVVQYKAGTSVKLRIGIIAKPLPTIEWLKNGKELVATSTVSIENSTDSSAVLIKDATRHDTGSYEVKIKNVLGSASATIRIEILDKPGPPTGNINFNLITADRILFCWEPVPESDQGGSSLTHYIVERRETSRVVWSTISDKHSTDQTHVSVSKLMRGNEYVFRVMAVNKFGVGEPLESEPVIAKNAFVSPGQPHTPEVNIITKSTMVVEWDKPGVDGGSAVTGYYLERRDKKSSRWIRVYKDPISELKKTVYHLTEGNEYQYRVCAINKAGEGPFSDGSDYYKAAD**PVDPPDEPCKL**KVVDSTKTSITMGWSKPEWDGGSEVISYMLEKLVEGEEEWAMITSKGEVKTTEYTVHDLKPDVNYFFRVSAVNCAGRGEPLEMTEPVQAKDILEEAQIDSDVAMRTHYIVKAGKDVELTVPLKGRPSPTASWSKGEECIDRNPQYEFHHSDTTTVLVMREVTRLDTGKYTVKIENGVGEPKTLTLSVKVQDSPAQCRNLVLKEVTRGKVILCWEPPLLDGGAEITNYIVEKRDSSKRSFSAVTSKCTDTTYTIEDLSEKTSYFFRVLAENENGVGDPCDTPEPVKATETPGPVKEVSMKDSSKTSVTLQWLKPDYDGGSIISDYVIEKKLKDEEWSLGGTSRQCEFEVKKLKEHSDMFFRVASRNEKGQGDFVEIGPIKVIDYIITPEACLAEYPGGSISVRLGHNVHIELPYKGKPRPATLWLKDNLPLKESDQIRFKKTENKATLMIKNVKKENEGKYTLTLDNKVNRRSFHIHVITLGPPSKPVGPIRLDEVRAENIMISWDEPNDDGGGDITCYTVEKRDTSQNVWKMACSSVQDTQFRVPNLIKGLQYQFRVCAENRYGASEPLISQMVVAKHQFRPPGPPGKPVVYNITNDGMTIRWEQPIYDGGTPIQGFHVEKKEKNSVMWQKVNTMLVKENDFRILELIEGLEYSFRVYAQNDAGFSRMSDESKPAMAVSPVDPPGQPDYTDVTIDSVALKWDAPKRDGGSKITGYTIEKRQGHGRWFKANLTDVHECEYTVSGLATNERYEFRVIARNAIGVVSPPSNSSGLIVVRSENACPNIEFGPEYFEGLTVKAGDNIRLKVTITGRPVPKIVWFRDGVEVTKKMMDIINVAGSSTLFVRDADRTHSGLYTVEATNGSGSKKENILVQVQDTPGEPVGPITFSHISEGKCTLSWSPPVNDGCSEISHYIIEKRETAKISWALVSDECTECTFDASKLIKTNEYQFRVSAVNKFGVGRPLESTPIIAQMQYTTPDAPGTPDATEVTGESITLSWAPPTSDGGNPIQYYIVEKREKKTVRFYKVITKKPIEECGHKVIHLTEDMEYEFRVLAVNDAGVGTPSNISMPIKAAEPKDIPCAPSVVCVSDSTNTSISLEWSRPADDGGMEILGYIVEMVKGEDEEWKRVNEELIPETHYTVAGLETGSEYSFRVAAVNHIGRGEEKETPEPAQAVDRLTPPQVDIDASFRQTHIVKAGGSVCLGIHFRGKPVPTATWVKEEGELSVLSEITTTDGYTSLSIENCSRTDTGKYTVNLENASGSKDVTFTVKVMDTPGPPQDVSFMEVARGTVTLTWKPPLNDGGARIHHYVVERREASRRTWQQSGGKCTKHVLK**IEDLLEGVP**YFFRVSAENQHGMGEAFELTEPVTATAEPAPPKRMDILDTTDSSVVLGWLKPEHDGGSRIQGYVIEAKPKGTDKWVVVGNTKNLTYTIDKLNKGDEYDIRVKAKNEAGNSRPRETVAPVLIKEPHIEPAADLSEITNQLVTCRSGSTFIIEVPISGRPAPKVSWKLEEMRLKSSDRVTIKVTKDRTTISVKEAMRGDGGKYYLTLENVAGTKTFTIEVNVTGRPSPPSGPIEITSITSESCIVNWQPPEDDGGTDITNYIVEKRESGSTAWQLINSSVKRTTLHVSHLTKYMQYTFRISAENRFGVSKA |
| TRINITY\_DN52732\_c0\_g1::TRINITY\_DN52732\_c0\_g1\_i1::g.123903::m.123903 | gi|1737228|gb|AAB38887.1| | lactate dehydrogenase-A [Sphyraena idiastes] | 58.1 | MTTKEKLITHVMKEEPIGTRNKVTVVGVGMVGMASAVSILLKDLCDELALVDVMEDKLKGEVMDLQHGSLFLKTHKIVGDKDYS**VTANSRVVVVT**AGARQQEGESRLNLVQRNVNIFKFIIPNIVKYSPNAIL**LVVSNPVDILT**YVAWKLSGFPRHRVIGSGTNLDSARFRHIMGEKLHLHPSSCHGWIIG**EHGDSSVPVWSG**VNIAGVSLQSLNPKMG**AEGDTENWK**GVHKMVVDGAYDVIKLKGYTSWAIGMSVADLVESITKNLHKVHPVSTLVQGMHGVKDEVFLSVPCVLGNSGLTDVIHMTLKPEEEKQLVKSAETLWGVQKELTL |
| TRINITY\_DN53297\_c2\_g13::TRINITY\_DN53297\_c2\_g13\_i1::g.16570::m.16570 | gi|734605520|ref|XP\_010729866.1| | PREDICTED: AMP deaminase 1 isoform X1 [Larimichthys crocea] | 83.9 | MPKVIVPEGGSHQKTDDKMRAFAEEVF**ASETKDENVRDEIS**MF**DVAEDCPIFH**HELAHHLHADDDHEKRKRLQRSRTM**AVPAAAASAPVVSLK**VETPTYLEVPDFQRVAIIGDYASGVTLDDFELSCKGLYRALTIREKYMRLAYQRYPRTTSQYLRDIEGESFKPEDQLQPVFTTPPKNGEDPFDPKDLPKNLGYVARMKDGVIYVYNDAAAADKHQPKDMPCPDYNTFIDDMNFLIALIAQGPTKTYTHRRLKFLTSKF |
| TRINITY\_DN36664\_c0\_g3::TRINITY\_DN36664\_c0\_g3\_i1::g.7820::m.7820 | gi|6138950|gb|AAF04404.1|AF051370\_1 | AF051370\_1 cytochrome c oxidase subunit VIa precursor [Thunnus obesus] | 55.3 | MFATPVASAARRVLAAASHSSHEGKAKTWKILSFVLAIPGVSVCWLNAYMKGQAHSHEQPEFIPYPHLRLRTKKFPWGDGNHSLFH**NPHTNALPTGYESSSHH** |
| TRINITY\_DN58819\_c1\_g4::TRINITY\_DN58819\_c1\_g4\_i3::g.92778::m.92778 | gi|657592091|ref|XP\_008300557.1| | PREDICTED: calpain-3-like isoform X1 [Stegastes partitus] | 68 | FGLFCKFTLCFCTHKKKRGRTPLHKLPSETGM**SKAAAGTDNMGDNTGKVPVVEE**IQVKVLYETEAS**FEPDDKSDYSPTGAN**SIYSAILSRNEAVKDAKRLKTFLELRDKYVKKNVLFEDPLFPADESSLFYSQKPAMKFEWKRPSEICENPEFIIDGAKRTDICQGELGDCWLLAAIACLTLNEKLLYRVIPPDQSFTENYAGIFHFQFWRYGEWVDVVVDDRIPTCKNQLVFTKSFRQNEFWSALLEKAYAKLHGSYEALKGGNTLEAMEDFTGGVTEFFDLDEAPKELYKIMRKALERGSLMGCSIDAFSPSEMETRIEQGLVRGHAYSITGLEECNEVDKDTKVHLIRLRNPWGWVLWKGPWCANSKEWSTISVGDKTNLQKQTVETSEFWMCFDDFKKYYTKLEMCNLTPDTLQGDERHSWSVSVNQGRWVRGSSAGGCRNFPDTFWTNPQYRLQLYEEDDDPEDEKLTCTVVVALMQKGRRMQRHQGAKFLTIGFSIYEVPKEMRGQNQHLQKDFFLYTASKAKCKTYINLREVTARFRLPPGEYVIIPTTFQQHQDGEFILRVFSEKRNTSEEAESTIDPGQAQQDKKTKGKPIVFVSDRARANKEIEHDGILGEKKKKKRKMLEPEEETEEEKQFRAIYEKIAGEDMQICANELKTVMKNVLAKHSEIKTTEGFSLETCRSMIALMDTDGTGKLNLQEFKHLWKKIKEWQLIFKRYDKDKSSSISSFEMRNAVHDAGFHLNKQLYDILAMRYADEHLNIDFDSYICCFVRLEGMFRAFNAFDKDGDGLIKLNVLEWLQLTMYS |
| TRINITY\_DN99034\_c0\_g1::TRINITY\_DN99034\_c0\_g1\_i1::g.27726::m.27726 | gi|1012819516|gb|JAR66467.1| | 40S ribosomal protein S19 [Fundulus heteroclitus] | 63.5 | ARFNTSWKPRSTLFPSLSTSKM**PGVTVKDVNQQE**FVRALAAFLKKSGKLKVPDWVDLVKLGKHKELAPSDENWFYIRAASTVRHLYLRGGAGVGSMTKIYGSRQRNGVCPAHYSVGSKNVARKVLQALELLKMIEKDPNGGRRLTSQGTRDLDRIAGQVAAANKKTV |
| TRINITY\_DN47410\_c0\_g1::TRINITY\_DN47410\_c0\_g1\_i1::g.12333::m.12333 | gi|657585462|ref|XP\_008296929.1| | PREDICTED: peptidyl-prolyl cis-trans isomerase A-like [Stegastes partitus] | 57 | LTFSKRRDFSLLAVPTSADQLSHITFANMLLLSNRIKFCSLAFTAARLY**SSGPAAANLNPTVY**FDIAADNEPLGRVTFELNAEVVPKTAENFRALCTGEHGFGYKGSTFHRVIPQFMCQGGDFTNHNGTGGKSIYGWKFPDENFKLKHTGAGILS**MANAGPNTNGSQF**FICTAKTEWLDGRHVVFGSVKEGLDVVKKVETFGSRSGRTSKRITITDCGELK |
| TRINITY\_DN38261\_c0\_g1::TRINITY\_DN38261\_c0\_g1\_i1::g.102034::m.102034 | gi|736178360|ref|XP\_010767913.1| | PREDICTED: collagen alpha-1(I) chain-like [Notothenia coriiceps] | 82.6 | AGPPGPAGPTGAPGPQGPLGNTGAKGARGPAGPPGATGFPGAAGRVGPPGPSGNSGPPGPTGPAGKEGPKGNRGETGPAGRAGEIGNAGPPGAPGEKGNPGAEGAPGSAGIPGPQGIAGLRGIVGLPGQRGERGFPGLPGSLGEPGKQGSAGPGGERGPPGPMGPPGLAGAPGEAGREGTPGNEGSAGRDGPAGPKGDRGESGPAGASGAPGPPGAPGPVGPAGKSGDRGETGPAGIAGPAGPAGPRGPAGALGLRGDKGESGEAGERGMKGHRGFTGMQGPPGPSGPSGEQGPAGTAGPAGARGPAGSSGAAGKDGMSGLPGPTGPPGPRGRSGEMGPAGPPGPPGPPGAPGAPGGGFDLG**FIAQPQEKAPDPFR**MFRADDANVLRDRDLEVDTTLKSLSQQIEQIRSPDGTRKNPARTCRDLKMCHPDWKSGEYWIDPDQGCTQDAIKVYCNMETGETCVTPTQPEVAKKNWYVSKNIREKKHVWFGEAMNDGFQFEYGSEGSQPEDVNIQLTFLRLMSTEASQNITYHCKNSVAYMDATAGNLKKALLLQGSNEIEIRAEGNSRFTYSVLEDGCTSHTGTWGKTVIDYKTSKTSRLPIIDIAPMDVG |
| TRINITY\_DN48192\_c0\_g3::TRINITY\_DN48192\_c0\_g3\_i1::g.12991::m.12991 | gi|14194770|sp|O13164.2|HBB\_DECMA | HBB\_DECMA RecName: Full=Hemoglobin subunit beta; AltName: Full=Beta-globin; AltName: Full=Hemoglobin beta chain | 77 | M**VDWTDAERSAIS**ALWGKIDVGEIGPQALARLLIVYPWTQRHFSTFGNLSTNAAILGNPKVAAHGKTVMGGLELAIKNMDNIKGAYKSLSEKHSQVIHVDPDNFRLLAEITTICLAAKFGPSVFTPDFQEAWQKFENAVVAALARQYH |
| TRINITY\_DN5454\_c0\_g1::TRINITY\_DN5454\_c0\_g1\_i1::g.1153::m.1153 | gi|734603098|ref|XP\_010728538.1| | PREDICTED: 14 kDa phosphohistidine phosphatase-like [Larimichthys crocea] | 63.2 | DRDRTMLLSVVGTGRLAVYGLRRTVSGVLTKATM**ADALAKIPDVE**IDPEGTFKYILVRVKVKDGDAHKDIVRGTKSAEYHNHIFE**KVSPAVEALG**MECKCLGGGKIEHNSQEKKLRVFGESTGFGKADHSVSVEKLKSAY**SNYEITCSDDKK** |
| TRINITY\_DN9484\_c0\_g1::TRINITY\_DN9484\_c0\_g1\_i1::g.1675::m.1675 | gi|734595174|ref|XP\_010730128.1| | PREDICTED: lactoylglutathione lyase-like [Larimichthys crocea] | 68.9 | M**SDKGLSDEAAAAACKD**GDPVTKDFMMQQTMLRVKDPVKSLDFYTRILGMTLLQKFDFPSMRFSLFFLGYEDKKEIPADVKEKTAWTFSRRATIELTHNWGSESDESQSYHNGNSDPRGFGHIGIAVPDVYAACKLFEEQGVTFVKKPDDGKMKGLAFIQDPDGYW**IEILSPNNMVSITS** |
| TRINITY\_DN49860\_c0\_g1::TRINITY\_DN49860\_c0\_g1\_i1::g.120076::m.120076 | gi|348515631|ref|XP\_003445343.1| | PREDICTED: desmin-like [Oreochromis niloticus] | 66 | M**SKSYSSSAQSASSYR**RTFGSGVGSTPMSSLFSSGGGRSSSSSHMASRVYEVKSSPSFSSYRLSSGAGGAGYGSSTAMRAYSGEKLDFNLADAMNQDFLNTRTNEKAELQHLNDRFASYIEKVRFLEQQNAALTVEIEKLRGREGPGRVAELYEEEMRELRRQIEAISNQRARVEVERDNLADDLQKIKLRLQEEIHQKEEAENNLSAFRADVDNATLARLDLERRIESLQEEIAFLKKIHEEEIRELQSQMQDTQIQVQMDMSKPDLTAALRDIRVQYEGIAAKNIAEAEDWYKSKVSDLNQAVNKNNDALRQSKQESMEYRHQIQSYTCEIDSLKGTNESLLRQMRDMEDRMTREASGFQDTISRLEEDIAKMKDDMARHLREYQDLLNVKMALDIEIATYRKLLEGEESRITTNVPVQAAYSSIGFRETSPESQHQRSSEVHSKKTVLIKTIE**TRDGEVVSESTQHQQDIM** |
| TRINITY\_DN49056\_c0\_g1::TRINITY\_DN49056\_c0\_g1\_i1::g.118941::m.118941 | gi|551509463|ref|XP\_005806258.1| | PREDICTED: keratin, type I cytoskeletal 18-like [Xiphophorus maculatus] | 66.1 | **MKSSKQTTYS**MRSSTSSRAPAISISRTSVPVYKAPSIHGGAGGDRISISSSYRSGLGSGMGMGMGSMKAGGFSGGIQVTTSGNSADIMGNEKFAMQNLNDRLANYLETVRTLEAANHKLEVKIKEALEKSGPDFRDYSKYQAILDDLRRKVFDATVDNARLVLNIDNARLAADDFRVKFESELAIRQSVEADIVGLRKLIDDTNMGRMNLESEIESLKEELIHLKKNHENEVMEMRNQIAQSGVHVDVDAPKGQDLSQIMAEIRAKYEKMALKNQEELKAWHESQITEVQTQVSQSTEALKGAQTEVNDLRRQLQTLEIELESQRSLKGSLEGTLRDTEMRYNMEIESLNNVLLGLEAELTQLRNNIQLQTQEYEALLNMKMKLEAEIATYRRLLDGEDFTLQDALEEQKTVKKTKVMTVTQTL**VDGKVVSSSTETKQL** |
| TRINITY\_DN115797\_c0\_g1::TRINITY\_DN115797\_c0\_g1\_i1::g.133756::m.133756 | gi|736155087|ref|XP\_010769179.1| | PREDICTED: patellin-2-like [Notothenia coriiceps] | 79.7 | MEAAIQTLVKVFLKSAKGKENLGKKEFQSLVKSQLSNILSDTDSKEAVNNMGQGLDANQDGKVGFEEYMKLVGYLAVSLSEQRDLAKEEPAQNDASGQAAQSAPAKEEEKPEANLEAKEEAKPEA**SEEPKAEAVAEVK**VESNAEGEVEVKVEVKAEGETQPEAAKEEPAAAAVAEATAAAVPAAAET |
| TRINITY\_DN20884\_c0\_g1::TRINITY\_DN20884\_c0\_g1\_i1::g.28864::m.28864 | NA | NA | 93.9 | MPGKPAPIKKSPAKKAVEKAPEPAPAPEPEPAPAEAPP**APAEAAPAEAPAPAEAAAAPAEGEAAPAAPAEDTPAAEE**SAPAAPAEAAVVEEPPKAPTPP |
| TRINITY\_DN57974\_c2\_g3::TRINITY\_DN57974\_c2\_g3\_i1::g.44135::m.44135 | gi|657574681|ref|XP\_008291057.1| | PREDICTED: titin [Stegastes partitus] | 63.8 | LLKGNEYLFRVRAVNKYGEGETLESEPIRAMDPFTIPSAPTDVEVTSATSDCMTICWKRPASDGGSRISGYVIEKREKQGVRWVRVNKKPIYDSRVKASGLHEGCEYEFRVFAENIAGLSPSSKTSECYVARDPCDPPGKPEAVVITRENITLEWAKPKYDGGSTITGYVVEKRELPDGRWMKANFTNVIENQFAVTGLTEGESYEFRVTAKNGAGVWSAPSESVKITAQDVIEGPTAFIDQKFKSVTGVQAGETFVIEADYFGKPLPDVTWLKDGKEIDKATMRMEIKNTLTHTTLTVRDSTRADGGHFVLILSNTGGTTSVPVNVRVLDRPGPPDGPLRVKFVSAERCNLNWNPPVNDGGACVSQYIIEKRETSRVTWTGVDTQVEAVSYKVSKLVPGKEYIFRVAGVNKFGVGEFLESDPIIAQNPFKTPSAPSTPMASAVTGDSIALTWERPESDGGSEIDGYILEKRDKEGVRWTKCNKRRLNDLRFRCTGLTEGHYYQFRVMAENAAGAGAPSEPSEYIKVCEATYPPGPPTNPKVTDYSSSTVSLTWSKPIYDGGAAINGFVVECKETDEDEWTVCTPSAGVAETNYAVKRLKENAEYNFRICAMNAAGIGEYVDLPGSVKAAEKLEAPEIELDSALRKIVNVRACSTLHLSVNIKGRPEPEVKWSKEGGALSERAQIEVTNSYTALLIENVNRNDTGKYVLTAENCNGTKSAFINVRVLDSPSAPTNLEVKEVKKDSVTISWETPLIDGGTKISHYIVEKREEARKAFTSVCSTCVRNSYKIDNLQEGSFYYFRVLAVNEFGAGLPVETTEPVKVSEAPLPPGKITLSDVTSNTVKLSWEKPDHDGGSKITRYIVEMQAKGDDTWTICAESKALEVTATGLTRGKEYFFRVSAVNEKGRSEPKSLLAPVAVKDTSAGPIINLLSNTFSVKAGNDLKIEVPFKGVPPPTVAWKKDGNILKETSRVNVQTSDSASQIMIKEATRVDVGVYEVTLSNSVGITSAEILVNVFERPGPPCDLSVDEVSADFVSLSWQPPHYTGGSEITNYVVKKRDTGSTAWQTVSATIARTSIKISRLTQGTEYQFCVAAENRYGKSQFVEFEPVVAQYPFKSPGPPVNLHVVQASKSVMVIAWSKPDSDGGSPIIGYHIECKDQSSILWTKLNRNPVTENQFKVTSVEEGLIYEFRVYAENMAGVGPCSTASDPAAARDQCDPPCNLTVTNITNSSVSLSWDKPEYDGGAKITGYIVERKELPENCWLKCNFTNLLDTFLEVTSLTEGEQYDFRVIAKNSADLLSAPSETTGPVTVQPDVEPPKIILEDKLRQVVIVKAGDFLKMDADISGRPNPTVFWLKNGRNIGTKGRIEVTATKSHTSLLIRESVRKDSGQYTLTLQNTGGTTSKVITIKVLDRPGPPAGPLEVSGLSAEKCTLSWGPPNETGGAEIMYYIVEKCETSRVSWTLMYDDMMATTCKITKLLKGNEYIFRVRGVNKYGDGEALESEPATAMDPFTVSAAPTNVQVTAVTSEAMTICWERPVSDGGSSIAGYVIEKREKTGLRWCRVNKKPVYDLRVKASRLRDGCEYEYRVFAENAAGLSAPSNPCPLTKAEDPQFLPSPPAKPKIIDSTKTTVTLSWNKPLFDGGAPVTGYRVEYRKSLDDEWFVGVQKTKNTEFTVVGLTPGAEYVFVVKSINKIGVSEPSPESDRQIAKEREDEPVFDISNEMRKTLIVKDGSSFTMTVPFRGKPIPSVSWTKPDVDLRVRAVIDTTDTFTSITLEKATRNDSGKYTVTLSNVAGTSSLTLSVRVLDSPGPPTHIEVKDVTKTSATVTWDTPENEGGGPVKNYVVDIREASKKGWTRLTDTCHRLTYKLTDLQEGEVYYFRVTGENEYGVGVPAETKEGTKITEKPTPPPKLGVTDVSKESVSLAWAKPEHDGGSRITSYLVEARENGQEKWVRCGVTKSIHLTVSGLRENAEYFFRVRAENHAGFSEAKEMLNPVLLKDQLESPEINMKDFPHNTVYVRAGSTLKCEIPLTGKPLPKVSLSKDNVLLKSTMRFNSEVTPDSIKITLRESIAGDSGRYDITASNSSGTTKSYVNIVVLDRPSAPVGPVELYDITEDSVSLKWLPPAYEGGSPITNYIIQKRETTTANWMDVSSAVARCTMKIMKLTTGLEYQFRIKAENRYGISEHIDSPTISVNLPYTIPEAPFTPEITAVTRETITVAWKEPKADGGSHVFGYHLQMKDRNSILWQRVNKMVIRATHFKVTNINAGLIYEFKVAAENAAGMSAFSKVSDAVLAIDACEPPINLRISDITKTSISLAWQKPNFDGGSPVTGYIIEKREGVSARWSKANLTNVTGTRFTVTGLTQDETYEFRVMAKNAVGSVSNPSMTAGPATCVDTYGAPEVEIPQEYLNEVKHKAGSNVELKFNITAKPAPTIEWFKDGRELEPTSQLSFKHTFEHTSLFLKETTRLNSGTYEVKVKNSLGSACGVVRLLIQDKPGPPAGEIQFKKVTADNVTIMWSPPADEGGAMVSHYIVEKRETSRVMWSIVSEKLVDCIVNVPRLIQGNEYIFRIRGINKFGIGDPLESAPVIARNAFVPPSEPSKPKVTMITKSTMTVIWERPALDGGSDIDGYYLEKREKKSLQWFKVVKGTIRDTRQKVSNLVENNEYQYRVCAVNKAGAGNYSEASDLYNAYDPIDLPGEPSKLRVVDSTKTSITLGWEKPVYDGGSKITHYILDQLNSEEREWVTINPQVKTCEYVVSHLKPGSYYFFRVYAVNCKGKGEDIKMYQPVQAKDILEEADLDLDVPMTTQYTAKAGRDVEVFIPLKGRPAPNVTWRRGDRNIAGDNRFTITSTERATTLLIPKVTRDDCGKYLLEIENGVGEPKIITVSLKVLDSPSTCQKLMIKNVTRGKLTLSWEAPRIDGGSPVTNYIVEKKASTMKAFQVITAECANTTYKVSGLEEDVAYFFRVSAENEYGVGDTCETTEPVRATETPGAVKQLVMVDSTKSSVTLQWARPDHDGGSHITEYIIEKSTKEDPTWTLGATCKRCSCEVTGLKENAVMDFKVFAKNEKGRSDFSQIGPITVMDFIIPPEANLIDYPSGELAVRIGQNIHIELPFKGKPRPVISWLKDNLPLKESEKVRFR**TTDNKTAITVR**GAKKEHAGQYTLVLDNRVVKNYFDINVITLGPPTAPVGPIRFDEIKAQSIIISWDEPKEDGGGEITCYSVEKRETSQANWKMVCSSVVRTTFKIPNLVKGTQYQFRVRAENKYGVSESLNSTDVVAQHQYKPPGAPGKPVAFNVTSDGMTIKWEAPGFDGGSPIVGYHVEKKDRNSLLWQKVNSTIISNKEYRIIGLMEGLEYSFRVYAENNAGLSPVSEQSKHALAISPVDPPGTPVCIDVTRDSVTLQWAIPKKDGGSKIVAYSVERRQGRGKWLRCNFTDVCETQFTVTGLSPGDRFEFRVIARNAVGTVSPPSNSSGYIMTKDESIAPEIEWSPDQVATLRAGENVRLGCSITGRPVPQVVWYKDGKEIDKRTMIDIEITTGIGTSSVFVRDADRNHRGIYTVEAKNSSGTKRADVNVRVQDTPGPVEGPIRFTGITAEKCTVWWNPPENDGCAAISHYVVEKRETSRISWAMVTSKCEACSYNATNLIKGNEYQFRISAVNKFGVGKPLDSDPIIAQMQYTVPDAPGTPDATHITGDSITLGWTRPRTDGGNEIKHYILERREKKSLRWVKVSSKRPITELRHRATRLTEGYEYEFRVMAENGAGVGPASSTSRLFKCREPTCTPSAPSMIKVIDSTKSSVTLEWTKPVFDGGLEIIGYNIDMCKASLLEWHRVNSQICIHTRYTAKGLVPGELYKFKISAVNGSGEGEASEMASAVQALDRLTSPEIDIDANFKQTHIVKNGGMVTLHIAFRGKPAPLATWSRADGELPIMADVNTTESFSTLTIEGCTRYEAGKYTLSLENNSGRKSITFTVKVLDTPGPPGAITFKDVTRGALTMMWDAPTNDGGARIHHYIVDRREASRLAWQEVSTKCSRQMIRVTGLDIGIPYLFRVIAVNQYGQGEPHELTEPVIATEEPAPPKRLDVVDTSSSTASLVWLKPEHDGGSRIRGYIVEFRIKGTDRWVVYGESKSQKMLVEGLIENTEYDFRVKAKNDAGISHPQGTHGSVVIKEPRIEPTADLSSISKQLITCKTSNTFTIDIPISGRPAPKVTWKLEEMKLKETDRVSIKTTKERTTLVVKDSKRSDSGKYYLTLDNAAGVKTFTVTVVVVGRPTPPTGPVEISGVSSESCTLSWSEPADDGGTDISNYIVEKRESGSASWQVVNSSVKRTTIKVTHLTKYMEYTFRVCAENKFGVSKSIESAAVVIEHPFVPPSPPSRPDVVSVSANAISIKWDLPYADGGSQVTGYWIEKKERNTILWVRENKLPCLECHYKVSSLIEGLEYQFRVYAMNIAGLSKASEASRPVMALNPVDPPGKPEVTDISRSSVSLCWTVPFNDGGSKIVGYIVEKKVYSTDEWDDNRWLKCNYTTITENYFTVTNLGEGETLEYRIIAKNAAGVHSAPSESTGPVTCKDEYSPPKAELDSKLARETVIVSAGSDLVLDGAVGGKPEPTVHWSKGEKILELGEKYSLTYTATKAMAVIKSCDRYDTGRYILTVKNASGTKTAAVNVKVLDTPGAPADKIVITRVTEEKCTVSWKIPLEDGGDSVTHYIVERRETSRLNWVIMETECKTLSCVSSRLIKNNEYIFRVRGVNKFGPGVALESDPIIARNAYTIPSPPSTPEVTAVGKEHVIIEWMKPESDGGSEIKNYIVEKREKSSTRWTRVNRTYTIYDTRLKITGLLEGSEYQFRVTAVNAAGDSHPSDTSPYILCKDPTYTPAPPSMPRITDTTKHSISMIWTRPMYDGGSDVTGYVVEILEEGSEQWYRATTKALKTNEYVAAGLAANKKYRFRVAAINNNGTGEFSDPSAEVEPLERIEMPDLELADDLKKTVCLRAGGTLRLFVSVTGRPTPVVAWRKTGVELQSRGFIETTDSYTSLIVEKVDRYDSGKYVLEAENPSGKKTVTILVKVYDTPGPPGSVKVKDYTKESVVITWDVPSIDGGAHVSNYIIEKRDANMKSYKTVTTECRKTLFRITGLEEGMHYFFRVLPENIYGIGEPCETAEAVLVCEVPSVPLNLHVIDVTKSSVTLHWERP**LHEGGSRLT**GYTIEACKVGTDRWSTVATVKSSVSQHTIQPLMENDQYLFRLRATNSRGASEPMDTVTPVTIQDIKVMPKIDMTNIPQKIVHVHRGKPIDLNIPIKAKPHPECSWSFAGVKLKDSLDRIKIDSNGKYTHLVIRETTINDTGDYTLEVKNAIGMATEVIKVIILDKPGIPVGPMKIEDTDGVSVTVSWEPPEKDGGANVGGYVVEQRDAHRPGWITISESVTRPCFKFTRLTEGTEYVFRAAAMNRFGVGGFLQSEVVECKSPKTIPGPPSRPEVLDVTHEGMTLTWQPPEDNGGSTIAGYIIERKEAHSDRWMKINKNPVTMTRYRSSGLIEGLEYEHRITAINSRGAGKPSESSEITVAMDPIEPPGCPVEPRVTDTTRTSVSLAWLPPEEEGGAVITGYLIEMQKVDQVEWTLCNTTPTKMCEYTLTHMPQGAEYKFRVIACNAGGAGEPAEIPGVVKVQEMLGYPDYELDHKYEEGYVVRQGGVIHLSVPIKGKPIPTCKWTKDGRDISHRAMIATHDDITELVIKEAHKDDTGTYDLVLENKCGRKAVYIKVKVIGRPDVPEGPLEFDDIQARSVRVSWRSPSDDGGSDILGYIVERREVPKAAWCTVDARVTETSLVVKGLKENVQYHFKISAENQFGVSRSLKSDEAVTPKTPLCPPEPPSNPPEIMEVTKTTVALSWARPRDDGGSRVTGYYVERREVSTEKWVRHNKTHITTTMYNVTGLIPDAEYMFRVVAQNDIGQSEPGPASESVVCKDPFDKPSQPGEIDIISVTKDCITIHWLRPEHDGGKEILGYWIEFRQAGESAWKKSNKERSKDRQFTMGGLMEATEYEFRIFAENETGLSRPRRTPMGIKTKLSVGEAPALKEDIKDVTTKLGESGTMTCGIIGRPLPEIKWYRYGKELIQSRKYKMSSDGRNHSLSVLTEEQEDEGVYTCRAINEAGEIETSGKLRLQAAPQFHPGFPLKDKYFAGAGTSLRLHVVYIGRPIPQIMWFYGKKPLNVSENVIIENTESYTHLVVRNVQRKTNAGRYKVQLSNKFGTVDTSLRVEIQDKPCTPEGPMVVEGLLKSSVIISWKPPKDDGGSMITNYIVEKREAKEGELWHLVSSSVSGNTCRVPNLTESAGYYFRVSAQNQYGVSEPLEIPSVLIIKSPFEKPGIPQQPFIMSSTNDSCVVCWKPPSSDGGAKITGYYLEKREKKQNKWMSVTTKKIAETNYEIKGLIEGFEYEFRVKCENMGGESDWSEISAPIIPKSEQAPRAPAFREEIRDMTVKYQANATFVTKVVGYPKPVVKWYRGGKEILADGTKIKAQEFKGGYYQLVIAAANENDATVYQVRATNSTGSISTTANLDVEVPAKIYLPKELQGMGAVHAARGDHITVKIPISGKPEPAVTWQKGQEILSNSAHHQVITTRSFTSLVFHKGVQRKDTGYYVITAKNRFGMDKQTIEVNVADIPDVPKALVVSNIGRDSITLTWEPPANDGGSDIIGYIVEKCPTTADRWIRAGQTTDCSITIINIFGKTKYQFRVIAENQFGLSHPSHPTEPITTKEDTSVIRNYDEEVDETREITKEEALFYKVKELSSKYTISEELARCQFGAVHRCVEIATKKTFMAKFIKVRGTDRELVLREIEALNVARHKNIIYLHEYFESMEEIILIFEFISGVDIFERLGTSNFELTEQEIVRYLRQVCSSLKFLHSHNYGHFDVRPDNIVYTTRKSTIIKIIEMGQARLLVPGENIRMLFTAPEYCAPEVHRHDLVTTATDMWSVGVMAYVLLSGLNPFAAESITKMIENISSCEYIFDSEAFKDISLEAMDFVDRLLVKDRKLRMTAHEALEHPWLRMKIELVSNKAIRTLRHRRYYQYLAKRIDTIVSSARIAYGGAFKNQRGLAVGKVKIGTEYQGLRAGPVMHGSAEEGGHVRFTCSISNYDKSTQVSWYFGNRQLHPSPKYEITYSNGFASIYVKDIEESDDGVYRCKVVSDDGEDSAYGELFVETVRSIRQHYISRSIKKLRRRVDKTKILQRPPEFTLPLYNRAAYIGEDVRFGVTITVHPEPQVAWLKNGERIKPGDDDSKYTFTSDKGLYQLMIHNLDMSDDAEYTVMAHNKFGEDSCQARLTVTPHPVSEETMRPMFKRLLANVDCTEGHSVRFELRVSGIPAPTLKWQKDGQPLQFGPKVVVIQEDVDYHVLHIRETLLEDSGVYKVTATNSTGSVSCQATLKVDRLTYTRREYKTEEEKYRHIQKQIEKTNKMAEHIAATEELVPLNPTAQEAIKFAAEMYKPAVSTKNVEGEFDITVHKSETKKLEEERRIFMPYEIPEPLHHDPTVLDEDKTIKQFVPLSDMKWYKKLRDQYEIPERMERIVQKRQRRIRLSRWEQFYVMPLPRITDQYRPRWRIPKLSLDDLETVRPARRSPSPESEVSFRSRRRSLGDLSDEELLVPVDDYLSRRRASAEKMMLEDELELGFSASPAISPVRIERRAVEHEERRHEVRHEAVEVSATKKKRTVSQFMRRRRSLSPTYIELMRPVSELIRPSRARPSVEVEVEGEIVERRSPTPERTRPRSPSPIRSVERSSRSSSRFERSARFDIMSRYEARKASLKAERKYQVVSQTPFSLDHAPRVTVRMRSHRIPLGQDTKFTLNIQTKPEAEIQWFHNGTVISESSEKYIFSNLSGVLSITILECQEEDSGTYRCVCSNSKGEASDYATLDVSGGGYTTFSSRRRDEDVPKAHVPEVTRIDHYHTTHFKAGYASQTHFEVEETKSKLTETREVVTRERYAASSERYSSAERYDSSVKYASTEYLSSGSSYSSDKFSLTGKHATSETKVKSSAAAVAEEVSVHKVKPSLSARILTKPQSVTVSEGETARFSCDIDGEPAPTVTWVHESRTLVSSHHVQVTTTQYKSSLEISSVTSSHEGSYTVIVENSAGRQEAHFTLTIRRAAPKEEVKAVKSPEPSVKSPTPSVKSPEPSVTSPTPSITSPVPSVKSPEPSIKSPEPSIKSPTPSVKSPEPSVTSPVPSVKSPTPSIKSPEPEGIKSPRSVKSPEPTSPAPGLKSPAPGVKSPEPEGIKSPRGFKSPEPRLKSPPPIKSPDRVKSPEPEGVKSPRGLKSPEPAGLKTPRGLKSPEPVGIKTPRGIKSPEPSGIKSPRALKSPEPEGLKSPPRMKSPPPIMSPKRVVSPPTVKSPIPKPPKVLSQVTAEAHEGSVRMSCVCESSVREVVWFVNGRRLSQSSHFEMHYSEGSCSLLIHDLADSDQGEYTCEMTSEGGVSKSSFSFTGQVFQSIRMKVTAYREQQLAVKGSMMMSHKEASSAMSSSMMMKKEVHTMEEASSFSSSSQQAMMSSMMESSSFSSMAAEMKFETMSMSSMSSMASESYAMSSSSLTEMASHMEGSSFRAIGSAPRIEALPEDISIEPGKVLTVACAFSGDAKHIEWSRGGRTIEVTAGGRFHIETTEDLTTLIITGVKEEDAGTYTLKLSNELGSDTAIVHISIRSV |
| TRINITY\_DN55820\_c0\_g1::TRINITY\_DN55820\_c0\_g1\_i1::g.20194::m.20194 | gi|923780003|ref|XP\_013763892.1| | PREDICTED: neurofilament heavy polypeptide-like isoform X5 [Pundamilia nyererei] | 71.1 | MAEADTSAAPSSSADGSNGAAAPQTTSPKSKGLGLLGKVKVSVELLIALAALLSWVVVGVVMFDFVEYKAVPDIQQIITDPVQAVNDAVDEVSSLLNKFQECAPDLSDPMSAATYAAEEISIAKDGFVQYFSDEEGNFYLSYIDPVVIGRQAFHSTNDFMGGVMGSFRDTLCAIVDTVLDTISDINKGIIDL**SYIDPVVIGRG**VFSVTNGTVGGIVGYIQDILCAILDSILDIVKGTTDISFIDPVVIGRNVFNVTNDFVSGVAGYVKDVLCAILDVIMDTVKGIQNAVGFNPMTVLQRTVEITTEQISMLVSYVSTTLFGEQGIVPEVPIDPMKVVEDAVLEFTDKKDLFVAYMSSM**IVGDQGEPAMPVVN**IVTEKDEAVASPSDVTLVRRKGEFLPPFEKDLKAAETRKEEKKEKEAKPEKTIEIKLKEEKLQTKTKPEAKPLEEKPKEEEVVKKLPKEKKEVRKPSKDEKKVKKPLKEEKVVTKLPKDKKEVKKPPKEEDDIKKPPKALKEAKKPPKDDKEVKKPSKDKKEVKKPPKEEKEIKKLPKEEKEVKKPPKEEKEIKKLPKEEKEVKKPPKE |
| TRINITY\_DN31950\_c0\_g1::TRINITY\_DN31950\_c0\_g1\_i1::g.6433::m.6433 | gi|221158258|gb|ACM07327.1| | troponin I [Siniperca chuatsi] | 77.3 | MSHDKKMTSSRKHHLKSVMLAIAAGWLAQEKKDIAAAKQAYMAE**SCPAPSLGGDQATL**METCKKLHALIDKVDESRYDLQIKIGKGDKEIEDLRIKVVDLAGVKKPALKKVR**MSADAMLK**ALLGSKHTVNMDLRSNLKQVKKEVKEEPAEAVGDWRKNIEDKADRKKMFETS |
| TRINITY\_DN58952\_c4\_g30::TRINITY\_DN58952\_c4\_g30\_i2::g.114965::m.114965 | gi|657574621|ref|XP\_008291025.1| | PREDICTED: dehydrogenase/reductase SDR family member 7C-A-like [Stegastes partitus] | 68.8 | MALPFVVVLPLLIVVAAGVYYIYNEVMRFMSKSLVRNKVVVITDAVSGVGTECARLFHKGGARLILCGPSWDKLESLFDSLTSDADPKETFAPKLVILDFSDMDSMEDVVSEVLECYGGVDVLICNSSMKLKAPVQSVSLEADRNIMDVNYFGPSTLAKGVLPMMTSRRSGHIVLVNSIQGRLAVPFRSSYAASKHAAQAFFDCLRAEVEEFGIVVSTISHTFINASEPEPLAAAGPGPKPNFLAEFIVRQLTHGVRPSVLANEILQTVNRKRKEVVLAHPIPRVALCLRSFCPPFLFAVL**AAGVKDSVLAEQM** |
| TRINITY\_DN50013\_c0\_g1::TRINITY\_DN50013\_c0\_g1\_i1::g.117766::m.117766 | gi|958304908|gb|JAO51287.1| | RS2, partial [Poeciliopsis prolifica] | 50.5 | SCYNDHQMADDAGGRGGFRGGFGAGGRGGRGRGRGRGRGRGRGARGGKSEDKEWVPVTKLGRLVKDMKIKSLEEIYLYSLPIKESEIIDFFLGSGLKDEVLKIMPVQKQTRAGQRTRFKAFVAIGDYNGHVGLGVKCSKEVATAIRGAIILAKLSIVPVRRGYWGNKIGKPHTVPCKVTGRCGSVLVRLIPAPRGTGIVSAPVPKKLLMMAGIDDCYTSARGCTATLGNFAKATFDAISKTYSYLTPDLWKETVFTKSPYQEFTDHLAKTHTRVS**VQRGQAVQAATS** |
| TRINITY\_DN58121\_c0\_g3::TRINITY\_DN58121\_c0\_g3\_i1::g.89912::m.89912 | gi|657583721|ref|XP\_008295981.1| | PREDICTED: titin-like isoform X20 [Stegastes partitus] | 61.5 | GCMITNYIVEKRESGSTAWQLINSSVKRTTLHVSHLTKYMQYTFRISAENRFGVSKSTESETIVAEHPFTPPGPPTKPSVFNVTANTMTLKWEEPYHDGGSKVTGYWIEKKERNNILWVRENKIPCFECYHKVEALVEGLEYQFRVYAMNSAGLSKASEASKGAVAQNPVDPPSKPEVTNVTRTTVSLKWSAPLNDGGSPIVGYIIERKPYTLTGEGRWLKCNYTNVTDQFYTVTALGEGEPYEFRVIAKNTNQVFSLPSESTGSVQCKTDFEPPKAQLDSKLMSETVMVRAGSDLVLDAAVGGRPDPKASWSKGNRDLELCEKYHLQYTSTKAMAIIKFCDRDDTGKYILTVRNVSGTKTAEVNVKVLDTPGVCEGSIEISKITEESCTLSWKPPVEDGGDDISHYIVERRDTNRLNWVIMNAECKELTCNISGLFKNTEYLFRVRGVNKYGPGVHLQSGPMIARNTFTVPTPPGAPEILASGKDFATIEWLKPESDGGSPLIHYLVERRERKSARWVKVNRDGAHLDSTLKVSGLTEGNIYQFRVTAINKAGESEASEVSLYVVCRVPTCTPAPPSIPRITDTHADSISLAWSRPVEDGGSDVMGYILEMQEAGAEEWSKAHEKTLR**TTEHVVTGLS**AGKKYCFRVAGININGTGDFSEPCAETEPVERIEPPDFELHDDLKKTICLRAGGSLRMFVHVTGRPTPAITWSKPGVDLHTRGFIEVNSSSTTLIIDKVHRYDAGKYTLVAENSAGKQEVNILVKVYDTPGPTGPLKIKELTKDSATISWEAPAVDGGAPVNNFIIERREASMRAYKTVTAKCSKTSYKIDGLMEGMLYYFRVLPENIYGIGEPSETPDVILVCEVPLPPNKLEVIDVTKSTVSLGWEKPEHDGGSRLTGYVIEACKFGTDKWMKVATLKLTDFEYTIEKLNEKEQYLFRIKAVNSRGASEPKELVTAITVQEQRVMPMVDFSSIPQKVVNVLAGKTLELDLPIIGRPPPVCSWYFHENKLKVTDRVKIKSTGKFSKLTMSDTTINDTGDYSLEVKNAVGVITEVIKVVVLSKPDEPSGPFRLDEIDATCVTCSWDPPARDGGAPISGYVVEQRDAHRPGWVPVSDSVSRPTFKFVNLIEGDEYVFRAAAVNRYGTGDFLQSEIVTCKSLKNVPGPPGRPVVFDVSRDGMTVAWEPPEEDGGLDISGYIIERKEVRSDRWVRANKNPVTMTRYRSTELIEGLEYEHRITAINARGQSKPSLCSKPAVATDPIDPPGCPQNPRITDTTKSSVSLAWSPPDDEGDARVDGYLIEMQKVGTMAWIKCNTTPSLICEYTLTKMPQGEEFKFRVMACNAGGSGEPAEVPGTVTVTEMLESPDYDLELKYKDVYVVRHGGVVRLSVPIKGKPHPTCKWLK**DSGAVSTKAMIA**STEDASELVIKGAERSDSGMYDLLLENRVGKKKAQIKVKVIGRPNAPEGPMVFEDIQANSVKVCWKAPTEDGGSEILGYIVERREATRNAWYTVDSRVTDTHLVVKGLREGTEYHFKVTAENSFGVSASLKSEEPLMAKTPLCPPEPSSTTPEIMDVTKSSVALAWSRPKDDGGSAITGYFVEYKLVSSETWSRYETKISSTMFTLPGLTPDAEYQFRIVAVNDIGESEAGPVSDPVTCKDPFEKPSQPGEIDTVNVTNNLIAIRWQAPECDGGKEVLGYWVEYRKSVESTWKKCNRDRLKQMEFTMRGLAEATEYEFRVFAENETGMSRPRRTVTCIKTKLSVETKPSLRKEMDEVTTKLGQPAVMKCQIIGRPVPEIKWYHAGKEIVESRKYEMSSDGRNHSLSIMTDQQEDEGEYTCKAINDAGDAETSGVLVLEAAPSFHPDYPLKDIYYAGLGTTLRIHAAYIGRPEPKIMWLHGAKTLENTDDISIETTEHYTHLVIKNVQRRVHGGKYRIRLHNHFGRADTPFTVEIYDKPDVPQGPIVLDALLKNSVIISWKPPKDDGGCMITNYIVEKREDKEGTEWELVSSSINGTSCRVPNLIDSAGYFFRVYAQNRYGNSEPLELTSPILIKSQLEKPSPPQSPVVSGITKDSCVVSWKPPLSDGGSKIKSYCLEKKHKKDKKEWTEWTPVTTDEIKQTVFSVKRLTEGVEHIFRVKCENLGGQSDYSEETTPMIPATAVDVRAPAFKEELRNMSVKYKSNATLVCKITGQPKPVIKWFRRGKEIHSDGKKIKIQEFKGGYHQLVITEADEEDSTVYQIRATNQGGSICATVSLDVEVPAKIHLPKNLKDKEAIPALRGEVVNIKIPFSGKPDPVITWQKGQDLIDSNGHYQVIVTRSFTALVFPNGVEKKDAGFYIVCAKNRFGIDQQTVELDVADVPDPPRGIKASDVSRDSVTLNWVAPANDGGSRVISYIIEKCPTTAERWERVAQSRDTRYTVINLFGGTSYQFRAIAENKFGQSAPSETSGPVMTKEDKSRVLLYDREVDDTGHVRKGKAPNSEAKNLHNKYAIAEELGRGQFGIVHRCVDISSEKTYMAKFVKVRGADQAIVKKEIATLNLAKHTSFLLLHESFDSPEELVMIYDFISGGDIFERLSSAEFELNEREVANYIRQICSALEFLHTQSYGHFDIRPENIVYTTRTSSNVKIIELGQSRHLTPGDQIKVQYTTAEYAAPEIHQCDMVSTVTDMWSVGVLAYVLLSGLNPFTAETNQQMIDNISNAAYSYDDESFTHVSVEALDFTDRLMTKDRKHRMSAAEALAHPWLTKPVEEISGRAIPTGRHKRYYQSMVRKEWSTVISAARVACGGSIRSQRGVFVAKVKIAPFEHGPLAGQVTHAVANEGDNVKFICNIDNYDSTTEVTWYCGVRQLEAGNKYEIDYEDGLAVITVSKVTRADDGTYRCKVVNEYGEDSAYAELFINGVRKYRDFFTTRVVKRTKRRVDTARMLQKPPEFTLPLVNRTAYIGEDVRFGVTITVHPEPRVMWHKSGQKLIPGQDDKKYTFITDKGLYQLIIHDLDKEDDAEYSVVARNRYGDDSCKSRLTVVPRPKPADLTLRPMFKRLLANVECREGQKVRFEIRVSGHPTLKWEKDGTPLAFGPSIEVVHEGLDYYILHVRDTLPEDSGVYRVTATNSAGSASCQATLKVERVAHVKKEYEPSQKEKEKAAKKEELDKKVRLSQILSGTVITPLPPAAVQAVREAATMFKPAVTTKKGEKTEAEIKKEQEERKKRADEKRLRMPYDVPAPRVINPAVLEEDVEIKHFKPFSDMKWYKKLRDQYEFPEPMDKIKQKRMKRIRLSRWEQFYEVPIRIKDQYKPKWRISSMTQDDLETVRPARHRTPSPEIDAYHRIRRRSLGDLSDEELLLPVDEYLSMKRTEEERLRLEEELELGYSASPPSLSPVRFELSALRPSSPRRAYSDDEEGEEVHRYDSYRIPSKYEAGPSFIDLRQRHDKTTHRPPREKQRVYAEREDQELLRPHKTAQRISSYKSELKRMEFEEKTRTTKQKSTVTVTAYSEGVESEHLTAFTSEYIPKPIKKLPTPEPERRRSPTPERAVKTDIVYPKVDFASRYEERKQALRSERRSVERKFEVVTQAPFSLDHAPRITIRLRSHRVPYGTNTRFTLNVQAKPEPEVKWFHNGKEIHQSHKYHMTNISGVLTLQIINCVTEDGGTYRVVCKSAKGETSDYATLDVAGEEYAAFSSLRRDEEPPSSHLPEMTRTEVYHVSSSKTTVRESVKETVKETTTVVERPRETPSVPAKILTKPLSLTVEEGDLARFECDVAGEPAPCITWMHEGAVIGSSARHHIVSTQYNSSFEISAVEMSDEGSYTLEVENAGGKQEAHFTLSIRKSESKEKVVAPQRVTSPEAKSPLAKSPEPVKSPQRVKSPEPVKSPQRVKSPVSPKSPTPKSPTPKSPTPKSPTPSEKERVTSPIKSPKRVMSPTIERKPTFSVGLSDVTANSDSIVKLSVKVTGEPRPTITWLKNGKALSQGGKYEIFEESGSVHLEIYESEVSDSGEYRCTAANSSGAVSTTCTVTVRASKISEEVVKQEMVHKEVVSSHSQMSITQGQSLTSDPAKRSDAPHFLLQPRSQIVDEGQNVIFTCEVAGEPSPEVEWLKDNVTISATSNIRLSCSQHVYTLEIREATVADTGKYTIKAKNQFGQCSATTSLNVISSPPKIEALPHDVSIEPGKSLKVEGLFSGDPAPSVEWVRSGRILPNGDERYRVENTSDLSTLVISAVKEDDAGAYTLRLNNELGSDSATVNIHIRSM |
| TRINITY\_DN5796\_c0\_g1::TRINITY\_DN5796\_c0\_g1\_i1::g.101435::m.101435 | gi|6230879|dbj|BAA86218.1| | alpha hemoglobin A [Seriola quinqueradiata] | 57.3 | MSLSGKDKSIVKSFWDKVGGKAADIGADALGRML**VVFPQTKTY**FAHWADVGPDSAQVKKHGATIMAAVGDAVGKMDDLTGGLSALSELHAFKLRVDPANFRILAHNMLLVLAMYFPADFTPEVHTACDKFLQNLALALAERYR |
| TRINITY\_DN3078\_c0\_g1::TRINITY\_DN3078\_c0\_g1\_i1::g.463::m.463 | gi|961956273|ref|XP\_014869118.1| | PREDICTED: guanine nucleotide-binding protein subunit beta-2-like 1 [Poecilia mexicana] | 65.3 | M**TEQMTVRGTLKG**HSGWVTQIATTPQYPDMILSASRDKSIIMWKLTRDETNYGIPQRSLKGHSHFVSDVVISSDGQFALSGAWDGTLRLWDLTTGATTRQFVGHTKDVLSVAFSADNRQIVSGSRDKTIKLWNTLGVCKYTIQDEGHSEWVSCVRFSPNSSNPIIVSCGWDKMVKVWNLANCKLKTNHIGHTGYLNTVTVSPDGSLCASGGKDGQAMLWDLNEGKHLYTLDSGDTINALCFSPNRYWLCAATGPSIKIWDLEGKIIVDELRQEVISTNSKAEPPQCTSLAWSADGQTLFAGYTDNLIRVWQVTIGTR |
| TRINITY\_DN57995\_c0\_g4::TRINITY\_DN57995\_c0\_g4\_i1::g.44197::m.44197 | gi|657548411|ref|XP\_008279112.1| | PREDICTED: mitochondrial inner membrane protein isoform X2 [Stegastes partitus] | 63.7 | RGRSGATRASKRSKLRRRGRGSEGRKRKTRGERSQSVSQCSVCAGSSDHQCLKPPQRPRTMLRACLRGANATARKHCGRVPLNNLQHSRHYTTGGSSGGAAKVVVAGLLTVGGGVGGTIIYAKWDHKFRAAVESNVPYSDWVLGLALGPPSQDAGLPFKKQLEKAQPPSMLEKQMKAKAKSEKKAAEAAESSPVPTQPALS**LEEASTEATHIIS**AISEVPTVPAPCDTEAAAVKEECKECHDHTEAPVSAAVQPDPESAAAEPLRERPVEEVTARLAQQDLEEQDVVAAVSEGLEDSLSSSAKATLQAIGAQEAALQAITRHTLKLKEAMEAEVPPQEKSDQWKDLEAALTDRTSAVNDAQSALTKANEALDSLKSVIDKSKGLKVSAVRPLVLAAEENLHNMVVDLDKVITKVQSAESESKIVSQYSELVNEAKLQFQREVSSLTPEIQANWKGLTGKLSPDDLNALIAHAHRRIDQLNRELAEQRVREQIHMDGALEQQRLEDQKAQEKAVATALQHYKEDSRLEQERKLSELREVMEAEMRTQLRRQAAAHTDHVQDVLKVQEQELKSEAEQVLSSKMLEQETRYRQLSQEQLDNFTLDMNTAYARLKGVEEAIDSHVVAEEEARKAHQLWLSVEALNYALKTAEAGSPTAPLEGAAQ |
| TRINITY\_DN47624\_c2\_g4::TRINITY\_DN47624\_c2\_g4\_i2::g.12600::m.12600 | gi|657554793|ref|XP\_008281877.1| | PREDICTED: nascent polypeptide-associated complex subunit alpha isoform X1 [Stegastes partitus] | 85.5 | M**PGEATETVPVTE**QEMQQPQVETASSQQPQAASGPAKPKGKGAKNAQGSSAPKAVPGRRKRSSMSASSSSPTSPKSTPSTPLTPVISPLASSPASSSAQQANRSAPKVVKAGKQGKAKKGEEFVPAPTPQECKVTVAAEKPVEASPKQTVVEAKPAPAETKKPSPAAFKVTSKPAVAAPVSFSETLATSPPKSHVEVKVASPKAVAADDELPPLIPPEKPLKMPEIVPPAKVEVAVEAPKPAVEAKAAPKAKQEAAKPAVEVAKPAVEVAKPAVEVAKPVVEAKLAPVEAPKAKQEAAKPAVEVAKPAVEVAKPVVEAKLAPVEAPKAKQEA |
| TRINITY\_DN46549\_c6\_g3::TRINITY\_DN46549\_c6\_g3\_i1::g.96573::m.96573 | gi|379998736|gb|AET79258.2| | parvalbumin 1 [Siniperca chuatsi] | 95.4 | MAFASILKDADITAALAACQAADSFKYKEFFAKVGMAAKSADDIKKAF**AIIDQDKSGFIEED**ELKLFLQNFC**AGARALSDAETKAFLKAGDSDGDGKIGVDEFAAMVKA** |
| TRINITY\_DN29852\_c0\_g3::TRINITY\_DN29852\_c0\_g3\_i1::g.5844::m.5844 | gi|657528877|ref|XP\_008292573.1| | PREDICTED: proteasome subunit alpha type-1 [Stegastes partitus] | 58.9 | MFRNQYDNDVTVWSPQGRIHQIEYAMEAVKQGSATVGLKSKTHAVLVALKRAQSELAAHQKKILNVDNHIGISIAGLTADARLLCNFMRQECLDSRFVFDRPLPTSRLVSLVGSKTQIPTQRYGRRPYGVGLLIAGFDDMGPHIFQTCPSANYFDCKAMSIGARSQSARTYLERCMDKFSDCNLNDLVQHGLRALRETLPTEQDLTTKNVSIGIVGKEMEFTIYDDDDVAPFLEGLEERPQRKVAQPADEPAGD**AAPAPDEPMEH** |
| TRINITY\_DN51108\_c0\_g7::TRINITY\_DN51108\_c0\_g7\_i1::g.82614::m.82614 | gi|657588840|ref|XP\_008298779.1| | PREDICTED: creatine kinase S-type, mitochondrial [Stegastes partitus] | 81.3 | RDWPDARGIWHNNEKTFLIWINEEDHTRVISMEKGGNMKRVFDRFCKGLKQVEHLIQERGWEFMWNEHLGYV**LTCPSNLGTGLR**AGVHVRLPKLSKDPRFPKILDNLRLQKRGTGGVDTAAVGDTFDISNNDRLGKSEVELVQM**VVDGVNYL**IECEKRLEKGQDIKVPAPVSQFRK |
| TRINITY\_DN48294\_c0\_g1::TRINITY\_DN48294\_c0\_g1\_i1::g.55880::m.55880 | gi|584018877|ref|XP\_006804149.1| | PREDICTED: ATP synthase subunit beta, mitochondrial-like [Neolamprologus brichardi] | 69.3 | MLGAVGRCCTGALQALKPGVQPLKALVGSPAVLSRRDY**VAPAAAASVANGRIVA**VIGAVVDVQFDEGLPPILNALEVKGRESRLVLEVAQHLGENTVRTIAMDGTEGLVRGQKVLDTGAPIRIPVGPETLGRIMNVIGEPIDERGPISTKQTAPIHAEAPEFTDMSVEQEILVTGIKVVDLLAPYAKGGKIGLFGGAGVGKTVLIMELINNVAKAHGGYSVFAGVGERTREGNDLYHEMIESGVINLKDTTSKVALVYGQMNEPPGARARVALTGLTVAEYFRDQEGQDVLLFIDNIFRFTQAGSEVSALLGRIPSAVGYQPTLATDMGTMQERITTTKKGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSRAIAELGIYPAVDPLDSTSRIMDPNIVGSEHYDVARGVQKILQDYKSLQDIIAILGMDELSEEDKLTVARARKIQRFLSQPFQVAEVFTGHMGKLVPLKETISGFQSILGGEYDALPEQAFYMVGAIEEVVQKAEKLAEEHS |
| TRINITY\_DN50937\_c0\_g6::TRINITY\_DN50937\_c0\_g6\_i1::g.37905::m.37905 | gi|974096226|ref|XP\_015246606.1| | PREDICTED: glycogen [starch] synthase, muscle-like [Cyprinodon variegatus] | 48.5 | MPLARSLSVTSLSGLEEWDEEFDLEDAVLFEIAWEVANKVGGIYTVIQTKARLTSEEWGENYFLVGPYVESNVRTQVELIEPTNPVLKRTIDKMNSSGCKVYFGRWLIEGSPYVVLIDVGFTAWSLDQWKKELWDLCDIGVPWFDREANDAVLFGFLTAWLLGEYAAQCEEPPHIVAHFHEWLAGLGLVLCRHRQLPIATIFTTHATLLGRYLCAGNVDFYNKLSEFNVDKEAGDRQIYHRYCLERAAAHCTHVFTTVSQITAIEAEHLLKRKPDIITPNGLNVKKFSAMHEFQNLHAQSKNRIQEFIRGHFYGHLDFNLDKCLFLFIAGRYEFSNKGADVFLEALARLNYLLRVNHSDVTVIAFFIMPARTNNFNVETLKGQAVRKQLWDTAHTVKERFGKKLYESLLVGQLPDVSKMLDKEDFTIMKRAIFATQRQCQPPICTHNMLEDSSDPILNCVRRIGLFNSSADRVKIIFHPEFLSSTSPLLPMDYEEFVRGCHLGVFPSYYEPWGYTPAECTVMGIPSVSTNLSGFGCFMEEHIADPSAYGIYILDRRDRAVDESCNQLTSFLFQFCKQSRRQRIIQRNRTERLSDLLDWRYLGRYYIAARHMALAKAFPDTYLYEPHEPSSASGFRYPRPASVPPSPALSRHSSPHHSEAEDDVDEDEDERYDEDLEAEKDRVNIRQPYTPPYKNKSLLG**ANGNGVISEKN** |
| TRINITY\_DN49351\_c1\_g1::TRINITY\_DN49351\_c1\_g1\_i1::g.75759::m.75759 | gi|657554845|ref|XP\_008281906.1| | PREDICTED: poly(rC)-binding protein 2-like isoform X2 [Stegastes partitus] | 79.3 | MDSSMVEGGLNVTLTIRLLMHGKEVGSIIGKKGESVKKMREESGARINISEGNCPERIITLAGPTTSIFKAFSMIIEKLEEDISTSMTNSTATSKPPVTMRLVVPASQCGSLIGKGGCKIKEIRESAGAQVQVAGDMLPNSTERAITVAGTPQSIIECVKQICVVMLESPPKGVTIPYRPKPSGSPVIFAGGQAYAVQGQHAIPQPDLTKLHQLAMQQSPFPIAHSNQGFQAGMDASAQTGSHELTIPNDLIGCIIGRQGAKINEIRQMSGAQIKIANPVEGSTDRQVTITGSHASISLAEYLINA**RLSSEATGLAAN** |
| TRINITY\_DN51688\_c1\_g1::TRINITY\_DN51688\_c1\_g1\_i1::g.38040::m.38040 | gi|657588631|ref|XP\_008298664.1| | PREDICTED: retinal dehydrogenase 2 [Stegastes partitus] | 62.9 | M**TSSKIEIPGEVK**SDPAALMASLQLMPSPVPNPEIKYTKIFINNEWQDSVSGKVFPAYNPATGEQICEVQEAEKADVDKAVQAARLAFSLGSVWRRMDASERGRLLSKLADLVERDSVYLATIESLNSGKPFLPTLFVDLQGTIKTLRYFAGYADKIHGTSIPMDGEYLTFTRYEPIGVCGQIIPWNFPLMMTAWKLGPALACGNTVVLKPAEQTPLTCLYMAALIKEAGFPPGVINILPGFGPTAGAAIASHMGIDKVAFTGSTEVGKLIQEAAGKSNLKRVTLELGGKNPNIIFADADLDLAVEQAHQGVFFNAGQCCTAGSRIYVEEPIYDEFVRRSVERAKRRIVGSPFDPTTEQGPQISREQQNRVLEFIQSGISEGAKLECGGKALGLKGFYIEPTVFSNVGDDMRIAREEIFGPVQQLMKFKTIEEVIERANNTDYGLVAAVFTNDINKAMTISTAMQAGTVWINCFNALSTQCPFGGYKMSGNGRELGESGLKEYSEVKTITMKMVAKNS |
| TRINITY\_DN58283\_c0\_g37::TRINITY\_DN58283\_c0\_g37\_i1::g.44842::m.44842 | gi|734645632|ref|XP\_010751918.1| | PREDICTED: methionine aminopeptidase 2 [Larimichthys crocea] | 66.9 | FPAASAIM**ADVVAEQAAEQK**AAPDRDREQLNGEAEDREEADPVETAKKRKKKKKKKSAATTGAEPEADGVGEVTKQLEKQAIEDKEKEEDGEEDGDDGENSAGKKKKKKKKKKGPKSQTDPPSVPICDLYPTGVFPIGQECEYPASQDGRSAAWRTTHEEKRVLDKANEEVWNDFRQAAEAHRQVRQHVRSFMKPGMTMIEICERLEDCSRKLIKENGLNAGLAFPTGCSLNHCAAHYTPNAGDTTVLQYDDVCKIDFGTHINGRIIDCAFTVTFNPKYDKLLEAVRDATNTGIKNAGIDVRLCDVGESIQEVMESYEVELDGKTYQVKPIRNLNGHSIGQYRIHAGKTVPIVKGGEATRMEEGEVYAIETFGSTGKGVVHDDMECSHYMKNFDVGHVPIRLPRAKHLLNVVNENFGTLAFCRRWLDRLGESKYLMALKNLCDLGIVDPYPPLCDTKGCYTAQFEHTILLRPTCKEVVSRGDDY |
| TRINITY\_DN5925\_c0\_g1::TRINITY\_DN5925\_c0\_g1\_i1::g.71521::m.71521 | gi|56565283|dbj|BAD77969.1| | type 1 collagen alpha 2 [Paralichthys olivaceus] | 89.8 | MLSFVDTRILLLLAVTSYLASCQYSGPRGDKGPRGDMGPKGPDGKDGKPGLPGPAGPPGPPGLGGNFAA**QYDGVKAPDPGPGPMG**LMGPRGPPGPPGPPGPQGHTGHAGEPGEPGQTGALGPRGPSGPPGKSGEDGNNGRPGKPGDRGTPGPQGARGFPGTPGLPGMKGHRGYTGLDGRKGEPGQTG |
| TRINITY\_DN50943\_c0\_g1::TRINITY\_DN50943\_c0\_g1\_i1::g.37726::m.37726 | gi|617417706|ref|XP\_007557445.1| | PREDICTED: 60S ribosomal protein L3-like [Poecilia formosa] | 49.8 | MSHRKFHAPRHGHLGFLPHKRSKKHRGKVRTWPKDDPSKPVHLTAFPGYKAGMTHTLREVHRTGLKQSKREDVEAVTIIETPPVIVVGIVGYIHTIRGLRSLKTIFAEHLSDECKRRFYKSWYKSKKKAFTKYSKKWQDEAGKKQLDKDFTMLKKYCSTIRVIVHSQMRLLPIKQKKAHIMEVQLNGGSISDKVDWAREHLEQAVPISSVFYQDEMIDVIGVSRGHGFKGVTSRWHTKKLPRKTHKGLRKVACIGAWHPARVAFTIARAGQKGYNHRTELNKKIYRIGRGVHIQDGKVIRNNASTSYDTSQKTITPMGGFPQYGDVNNDFVMVKGCVVGTTKRVLTLRKSLLVHTSRKSKETIELKFIDTTSKFGHGRFQTAQEKRAFMGPLKKDVK**KTLPEPLSEDV** |
| TRINITY\_DN36769\_c1\_g1::TRINITY\_DN36769\_c1\_g1\_i1::g.32743::m.32743 | gi|765111561|ref|XP\_011473251.1| | PREDICTED: 60S ribosomal protein L9 isoform X1 [Oryzias latipes] | 80 | RHVRALQQRRDVLPSSFPLLPARMKTILSSQTVDIPDNVEIRLKGRTVIVKGPRGKLVREFNHINLELSLLGKKQKKLRVDKWWGNRKELATVRTICSHVQNMIKGVTLGFRYKMRSVYAHFPINVVIQENGTLVEIRNFLGEKYIRRVRMRTGVVCTVSAAQKDELVLEGNDVELVSNSSALIQQATTVKNKDIRKFLDGIY**VSEKGTVVEGDQ** |
| TRINITY\_DN32831\_c0\_g4::TRINITY\_DN32831\_c0\_g4\_i1::g.31895::m.31895 | gi|974097077|ref|XP\_015247066.1| | PREDICTED: ATP synthase subunit delta, mitochondrial [Cyprinodon variegatus] | 73.1 | MMAARFLRRALPVVRHARSY**AEAASGAPQMSFT**FASPTQVFFKEASVKQVDVPTLTGAFGILPAHVPTLQVLRPGVVTVFSDDGSAAKYFVSSGSVTVNADSSVQLLAEEAVPLDQLDVAAAKANLEKAQSELAGASDEAARAAVQISIEANEAIVKALE |
| TRINITY\_DN54863\_c2\_g1::TRINITY\_DN54863\_c2\_g1\_i1::g.41310::m.41310 | gi|657558875|ref|XP\_008283410.1| | PREDICTED: reticulon-3-like isoform X1 [Stegastes partitus] | 69.1 | **MDPMTQSAQISSSQGLADGQN**SAAKESKLSDSFLSSSPVSLIQSPQVKDLIHWRDPKKSGLVFGVSMLMLLSLAAFSVISVVSYLLLALLCVTITFRIYKSVVQAVQKSNEGHPFKTLIDKDVSIPPETFRKHVDASLTYINRALKQMSRLFLVEDLVDSLKLAVVMWLLTYVGAVFNGITILILADILLFALPPVYEKNKTQIDQYIDVARTQVNTTMAKLQEKLPGAVKRSKTEM**GDPATLVEPTTPAVVT**AIPTAVAGETQDGNKTQSANKNGKKADSGSSGSFFNWFIVLALLGVWTSVAVVYFDLVDYQGVLGKLVAYDTDGDGDFDVEDAKVLLDEKPGDAARGGAKREIFPKDASKNLREALKQQLAIIHERVEAKKLAKLALAEVRQLLAKEEEEKALELGRQEIRGRVQDRVAARLKEEEEKIEKEEMEKAVEKLRKEKAKQQDQQKEESEEEEEKSKKGEKKVEGEGKKAQEDKGRGKETTKEKKKKSKAEKSDKGKK |
| TRINITY\_DN53268\_c1\_g1::TRINITY\_DN53268\_c1\_g1\_i5::g.16444::m.16444 | gi|930771688|ref|XP\_005950973.2| | PREDICTED: fibrous sheath CABYR-binding protein-like [Haplochromis burtoni] | 62.5 | M**GDPATLVEPTTPAVVT**AIPTAVAGETQDGNKTQSANKNGKKADSGSSGSFFNWFIVLALLGVWTSVAVVYFDLVDYQGVLGKLVAYDTDGDGDFDVEDAKVLLDEKPGDAARGGAKREIFPKDASKNLREALKQQLAIIHERVEAKKLAKLALAEVRQLLAKEEEEKALELGRQEIRGRVQDRVAARLKEEEEKIEKEEMEKAVEKLRKEKAKQQDQQKEESEEEEEKSKKGEKKVEGEGKKAQEDKGRGKETTKEKKKKSKAEKSDKGKK |
| TRINITY\_DN99037\_c0\_g1::TRINITY\_DN99037\_c0\_g1\_i1::g.27711::m.27711 | gi|657534560|ref|XP\_008274138.1| | PREDICTED: 40S ribosomal protein S25 [Stegastes partitus] | 78.1 | MPPKQDKKKDTGKSKKDKDPVNKSGGKAKKKKWSKGKVRDKLNNLVLFDKATYDKLYKEVPNYKLITPAVVSERLKIRGSLARNALQELLAKGMIKLVSKHRAQLIY**TRNTKGGDEEAAAEKA** |
| TRINITY\_DN51612\_c0\_g2::TRINITY\_DN51612\_c0\_g2\_i1::g.58145::m.58145 | gi|974088169|ref|XP\_015242208.1| | PREDICTED: cold-inducible RNA-binding protein isoform X4 [Cyprinodon variegatus] | 57.6 | MSDEGKLFIGGLSFETNEESLAAAFGKYGTIEKVDVIRDKETGRSRGFGFVKYDNAEDAKDALDAMNGKTLDGRAIRVDEAGKGGRSRGGFGSGPRGGRFSGSRGRGGRGYSRDFGGGGYNGDRGYGDRSYGDRSFGGGERSFGGGGGGGYRSGGYSSGGGGGYRENRGQGGYGDRSGSYR**DGYDSYATHE** |
| TRINITY\_DN98383\_c0\_g1::TRINITY\_DN98383\_c0\_g1\_i1::g.110710::m.110710 | gi|765133271|ref|XP\_011478710.1| | PREDICTED: rho guanine nucleotide exchange factor 9 isoform X3 [Oryzias latipes] | 8 | LGSPLQNRDQMRANVINEIMSTERHYIKHLKDICEGYLRQCRKRVDMFNDDQLKVIFGNIEDIYRFQMGFVRDLEKQYNTEEPHLSEIGPCFLEHQDGFWIYSEYCNNHLDACMELSKLMRDGRYQHFFEACRLLQQMIDIA**IDGFLLTPV**QKICKYPLQLAELLKYTAQEHSDYRYVAAALAVMRNVTQQINERKRRLENIDKIAQWQASVLDWEGDDILDRSSELIYTGELSWIYQPYGRSQQRVFFLFDHQLVLCKKDLIRRDILYYKGRIDMDRYEVRDAIDGRDDDFNVSVKNAFKLCNKDSEEIHIFLAKKPEEKIRWLRAFHEERKMVQEDEKIGFEISEYQKRQAAMTVRKVTKQKGEATRRYQV |
| TRINITY\_DN51167\_c0\_g5::TRINITY\_DN51167\_c0\_g5\_i1::g.70931::m.70931 | gi|658878547|ref|XP\_008422265.1| | PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 [Poecilia reticulata] | 16 | M**PTTVEAPTLQEL**KVDEVNVSSAVLKAAAHHYGSQCDKPNKEFMLCRWEEKDPRKCLEEGRKVNECALNFFRQIKGNCAESFTDYWTCLDYSNLGELRHC |
| TRINITY\_DN57119\_c1\_g11::TRINITY\_DN57119\_c1\_g11\_i1::g.125802::m.125802 | NA | NA | 17 | MMSYRCGCCVSFRFMSMSSPSGVKPWRRRRWRTASLRTVKTLRVNPHQSDCTTTLTVSVSVAVVVR**LCVAAVVVVVSDDDVVVRR**TKARQTLLSFRLDRSVWTVRCYGFRVV |
| TRINITY\_DN55199\_c5\_g1::TRINITY\_DN55199\_c5\_g1\_i1::g.18894::m.18894 | gi|548429331|ref|XP\_005743648.1| | PREDICTED: ankyrin repeat domain-containing protein 1 [Pundamilia nyererei] | 35.5 | MGLHSVEELVTGKRPEGKESEDFKGGVYEAAVSQEKRDDITGVGGALAEEEVSVAALNTDKSGRLKLETVDDLFNILQLKKRRRERKSPVHKKQQQQPEPLPETVDEQSFLTAAMENKLPVVEKYLRDGGKADTADHFQRTALHKASFRGHLEVMRRLLEAGAAIDKKDKLEATAVHWACRGGSLPALQLLLDQGAKFTSRDKLLSSPLHVAVRTGHCECAEHLIHCGADVNAKDRDGDTPMHDAVRINRFKMIKLLMMYGASLTTKNSDGKTPLETLNSWQNGAKSL**LCNFSEEKTNQ** |
| TRINITY\_DN46381\_c0\_g4::TRINITY\_DN46381\_c0\_g4\_i1::g.81824::m.81824 | gi|583989691|ref|XP\_006790048.1| | PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial-like [Neolamprologus brichardi] | 76.6 | LFLRGSRTSLLTTVMASSMSLLGLGRLTVINAASKALLNPIRSTSTSTLRL**AEKPGQDTQL**ITVDEKLDITPVTGVPEEHIKTRKVHIFVPAKTAMQSGVNSTKKWKMDFDTRERWENPLMGWASTGDPLSNMLLSFSTKEDAIAFAEKNGWSYDVTDKRSSKPRVKSYGANFSWNKRTRRSAK |
| TRINITY\_DN6726\_c0\_g1::TRINITY\_DN6726\_c0\_g1\_i1::g.100649::m.100649 | NA | NA | 59.8 | IIIII**IIIIIIIMI**SPAELLMKIFSMMQMKTVDRCELSHFKSQCRSLNSTPNAVFPCSSSSESSAAVQPVKLCTALRPDHSVCSAAILTRLSSRVMKQLLFSPTSTSPKPMSEVRTLMGPIAPFMWT |
| TRINITY\_DN47499\_c0\_g3::TRINITY\_DN47499\_c0\_g3\_i1::g.36137::m.36137 | gi|657524951|ref|XP\_008278859.1| | PREDICTED: dnaJ homolog subfamily C member 8 [Stegastes partitus] | 38.6 | M**AAAGGESSQPVSDEL**FQNFYTEVKQIEKRDSVLTSKQQIDRLLRPGASYFNLNPFEVLQIDPEATDDELKKRFRALSILVHPDKNQDDPDRAQKAFEAVDKAYKLLLDPEQKKRALDVIHAGKEYIEHMVKEKRKQLKKEGKMIDVEEDDPEMFKQAVYKQTMKLFAELEIKRKEREAKDMHERKRAREEEIEQAEKAKRDREWQKNFEETRDGRVDSWRTFQAKGKTKEKKNRSFLKPPKVKMEQRE |
| TRINITY\_DN54183\_c0\_g3::TRINITY\_DN54183\_c0\_g3\_i5::g.59066::m.59066 | gi|657737581|ref|XP\_008324265.1| | PREDICTED: mucin-5AC-like [Cynoglossus semilaevis] | 52.9 | QACTHWLPCAGLQPALTHPLHVRKGSQSISSPSLSKGSAKISISSGARTPFPFATQSKSEGEVRRVHSHRIIMKTNRVLLLLLLAFTPVSPSASDESTLPTSSVSPNNGAAPQLPSVSPNNGTASPATQDGTTQTAPSNKGTVRPTILATLPATTQVGATSSNNKSAESTQTPPVGTAPTPVNQTNKDESIDPQGNRPSNNPTAVNTTSSTIPGTVKANPTGNATPGTGTKQSPPVKENDAGSQTGGDKPAEPKPGNKLLWILLPVTLLAAAAVGFYLKFKSKRVNDCTETIDTGTENASFQSRPESTKDGVMLL**GVKSSGAEENAAAR** |
| TRINITY\_DN47384\_c0\_g1::TRINITY\_DN47384\_c0\_g1\_i1::g.12259::m.12259 | gi|410904401|ref|XP\_003965680.1| | PREDICTED: electron transfer flavoprotein subunit beta [Takifugu rubripes] | 63.8 | YHPKNRPTSPPWVKVHCGDCVTSTSGKLNVSSTMSGRVLVGVKRVIDYAVKIRVKPDKSGVVTDGVKHSMNPFCEIAVEEAVKLKEKKLIKEVVAVSCGPQQAQETIRTALAMGADRGIHVEVTGKDYDTLGPLQVSKIMAALAKKEEAQLVIL**GKQAIDDDCNQTGQMTA**ALLDWPQGTFASEVAMEGDKVKVVREIDGGLETIKINTPAVVTADLRLNTPRYATLPNIMKAKKKKIANVKPADLGVDLTSRLEVLRVDEPPQRQAGVKVETVDDLVGKLRETGRI |
| TRINITY\_DN1904\_c0\_g1::TRINITY\_DN1904\_c0\_g1\_i1::g.68284::m.68284 | gi|736253243|ref|XP\_010788812.1| | PREDICTED: sodium-dependent multivitamin transporter [Notothenia coriiceps] | 35.8 | ATFQSAVAILGAPSEIYTFGTQYWFLGCSYFLGLLIPAHIFIPVFYRLRLSSAYEYLELRFNKTVRICGTVTFIFQMVIYMGVVLYAPALALNAVTGFDLWGAVLAMGLVCTLYTALGGLKAVMWTDVFQTVVMFAGQLAVIVVGASQ**AGGMGEVWRKAI**NG |
| TRINITY\_DN38385\_c0\_g1::TRINITY\_DN38385\_c0\_g1\_i1::g.67027::m.67027 | gi|657530103|ref|XP\_008296779.1| | PREDICTED: succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial [Stegastes partitus] | 71 | MSHSRLFARLLLQQSGVRHCYTGSRKHLYITQNTKVICQGFTGKQGTFHSQQSIDYGSQLVGGVSPGKGGKTHLGLPVFNSVKEAREGTGADATVIYVPPPFAAAAIIE**AIDAEMPLVVC**ITEGIPQQDMVRVKHKLLRQGTTRLIGPNCPGVINPGECKIGIMPGHIHKKGRIGIVSRSGTLTYEAVHQTTQVGLGQSLCIGIGGDPFNGTNFIDCLEVFLQDPKTEGIILIGEIGGNAEENAAEYLKQHNSGANSKPVVSFIAGLTAPPGRRMGHAGAIIAGGKGGAKEKIAALQSAGVVVSMSPAQLGSTMFKEFEKRKML |
| TRINITY\_DN58865\_c0\_g4::TRINITY\_DN58865\_c0\_g4\_i1::g.24111::m.24111 | NA | NA | 81.7 | AV**TRLLHAENPPD**PRHHLVGRRVGRFVQVDDARPDVVADVPLQRVAAVGQRRVVSRPHVQFVEVLEEEGPLGRIQGNDLRLRLDEEVAALLQLPDFFITRPFRLFLLLC |
| TRINITY\_DN44769\_c0\_g1::TRINITY\_DN44769\_c0\_g1\_i1::g.69910::m.69910 | gi|348534170|ref|XP\_003454576.1| | PREDICTED: protein deglycase DJ-1 [Oreochromis niloticus] | 85.2 | MAGKKALVILSKGAEEMETVIPVDVMRRAGIAVTVAGLTGKEPVQCSRNVVICPDSSLEEASKQGPYDVVLLPGGMPGAQNLAESPAVKEVLKDQDGRKGLIAAICAGPTALLAHGIGYGSTVTTHPAMKEKMMAGDHYKYSEARVQKDGHYITSRGPGTSFEFALTIVEELLG**AEVAAQVKAPLVM**KD |
| TRINITY\_DN55256\_c0\_g1::TRINITY\_DN55256\_c0\_g1\_i1::g.84956::m.84956 | gi|657558036|ref|XP\_008283118.1| | PREDICTED: voltage-dependent anion-selective channel protein 3 isoform X2 [Stegastes partitus] | 79.8 | M**AEKEVRNMVQ**QEKTGKVKQAENKDCCVSCHHVPKGHGTMAVPPSYSDLGKSAKDIFNKGFGYGVLKLDVKTKSQSGVEFTTSGSNNTDTGKSGGHLETKYKVKELGLSFNQKWNTDNTLTTEVTMEDQLAKGLKLSLDTSFVPNTGKKSAKLKTGYKREFVNMGCDLDFDMAGPTVHAAAVLGYEGWLAGYQLAFDTAKSKLTQNNFALGYKAGDFQLHTNVNDGTEFGGSIYQKVDSNLETAVHLAWTAGSNNTRFGIGAKYQLDKDASLSAKVNNACLVGVGYTQTLRPGVKLTLSGLIDGKNVNGGGHKVGMGFELEA |
| TRINITY\_DN50560\_c0\_g3::TRINITY\_DN50560\_c0\_g3\_i1::g.58047::m.58047 | gi|734632941|ref|XP\_010744930.1| | PREDICTED: NADH dehydrogenase [ubiquinone] iron-sulfur protein 5 [Larimichthys crocea] | 39.6 | M**PFVDVQSRLG**INLDRWLLLQSGEQPNKRASRCHAFEKDWVECSHGIGQTRAKKECRLEFEDFYECMHRQKTHERLHAIRKQRDKMVKEGTYTPPACHSGKEDQSP |
| TRINITY\_DN56216\_c0\_g3::TRINITY\_DN56216\_c0\_g3\_i1::g.86577::m.86577 | gi|734602928|ref|XP\_010728444.1| | PREDICTED: myelin basic protein-like isoform X2 [Larimichthys crocea] | 47.2 | M**ASASSAQTTFGLG**RRKKNPGLLDQIGKFFGGDKKRKSKGSFRGALSPAPQKASATSPRKRAGENAVVHFFRTIGDQKSKKASGDGKGTLTRIFKMGSRSASPAKR |
| TRINITY\_DN38699\_c0\_g1::TRINITY\_DN38699\_c0\_g1\_i1::g.56447::m.56447 | gi|908504578|ref|XP\_013127347.1| | PREDICTED: PDZ and LIM domain protein 5 isoform X4 [Oreochromis niloticus] | 62.9 | M**SSNYSVTLK**GPAPWGFRLQGGKDFNMPLTLSRLTDGGKATKAGMAVGDMVLSIDGIATDGMNHLEAQNKIKSCTDNLTLTLQKASSVPKPPPVAPKTAAHHQVTKVPRKHVVETD |
| RRRRRTRINITY\_DN6653\_c0\_g1::TRINITY\_DN6653\_c0\_g1\_i1::g.127620::m.127620 | NA | NA | 15.5 | LDRWLTSSQTLSISLRPSSPRGEIKPPEPLPLSKVSTISGTHGLSHPHPVPPIPPLPRRAPPPSPAPSSTNDECVSLVDSRSQRLIEFNQAAESYQQYLQAANFFRSNRKRREITDLVNRLEVEGWSKSRDDEEETTSFIRTRRDRAVGEQDEVEVLEEGRRRRETTKRIGRRRMRA**EPGLDRFSC**TSMLTGSGVPREAVKGGERSDAELEEGEEAVRGVEVAADRDDPEGGQREEESEGVIEEEEQSEGERSPTDSDYNLIPCSNPKYLTNSVSLYMEVEKQGSVEKE**IESLTIENGG**EESVRIEADAKELHLHDPPETEKDTSHEEQGETDLPTDAHTHTPTDGHMATCQDAHMDAQNQGMGRLGVVVLPEEDELEPESHQEDS |
| RRRRRTRINITY\_DN44929\_c0\_g1::TRINITY\_DN44929\_c0\_g1\_i1::g.10843::m.10843 | NA | NA | 17.9 | AAAAAATAASKKDDEESDSGGSSSGDSAATPPKKGEGVPWAGPCAGGADSKEHNQKAQKDTAGSASDVPSSCRPNTETGSFPQFETFNAWGSGQTEAGGGASSDWGAQTQSSATGGSERFNATWGPGTESTNQESDEDEDSESGRDQERGGNEMSSRSSGESTQSVGFRTRSKAQTAYNIEKEEWIDEEEEADDFQRIREKCCAEFAAANASNDDADLNFNIEAIRDFTANINEDHESFEEDNFGFQDVFNATMQQIQYDSFAQQLSLDNPFPSEMDDDESSSHMNHTSVLEVTNRRNTERLTEDVFSEWRGRCDEPLEKILDSIQAQVPGKELNQ**VVMNAIRT**LHGMNGRRTGGESQIRDNEEWADLIRQVLRCKQFLHAVLANHISTQPDTTRGTEVAEAQGESGSAAPKGDHNQLGPSPREESSPHNLIAAVCLEVQFHLFNNWSYKFFLDLLLDMTALNCLEQCISPANTQLLAAVLRAVHLRANGLPQELVGVTTLIASKKPPDLLLQQFDKLHPEIANLISSNVTYSREYGQSYLDMLGELGSRRTELLTLLVQTGNVISAESREGEFLNKLLGAVSEQSELVALLPDAEVNEQMQNAQDRSLRIIDCLTQSANSQREEDKGTHILETLRQVLKEENLWHLVEQRLPAPEVCSILRLLLDMMASADIHKLVLGIFGEKKKLFTIVQETKRAILNGITKSFFSALLPNLPPDQELFHYLMELLSDDAGLKDNIISVDSTLLECAINPFKFRSREELDAPPETTILSVLEQMCHDQSLFLLLRRNQAKCEQLVDDEEMLERLTVDERDLLQDIHSTTHLDFKWFM |
| TRINITY\_DN54181\_c0\_g1::TRINITY\_DN54181\_c0\_g1\_i1::g.59189::m.59189 | gi|657578396|ref|XP\_008293067.1| | PREDICTED: aspartyl aminopeptidase isoform X1 [Stegastes partitus] | 61.2 | MQSVIMKSSREAVQSAAKEFLHFVNRGVSPYHVVDECRQRLLAAGFIELKETEQWDIKPASKYFVTRNFSSLIAFAVGGRFLPGNGFSMIGAHTDSPCLRVKPRSKRTKQGCLQVGVECYGGGIWNTWFDRDLTIAGRVMVKSGGRLLHRLVHVPRPLLRVPHLAIHLQRDINDSFGPNKENHLVPIIATVVQEELETGSSSSGDASTATTTAEKHHPALVKILCSELKVEPEELMDFELCLTDTQPAALGGVYEEFIYSPRLDNLHSCYCALKALVDSCAGDTLSKDPNVRMITLYDNEEVGSESAQGAQSNLTELILTRLSASASNLTAFQQAAPLSFMISADMAHAIHPNYQEKHEENHRPSFHKGPVIKFNSNQRYATTAVTASVVREVASQVDVPLQDVMVRNDSPCGTTIGPILAARLGVPVVDIGAPQLSMHSIREMCCTSSVLQSTTLFKGFFELF**PAVRSSLVVD** |
| TRINITY\_DN34974\_c0\_g2::TRINITY\_DN34974\_c0\_g2\_i1::g.49976::m.49976 | gi|734631191|ref|XP\_010743973.1| | PREDICTED: plasminogen activator inhibitor 1 RNA-binding protein-like isoform X1 [Larimichthys crocea] | 54.9 | M**PGQMQEGFG**CAITNRFDQLFDDESDPFELLKQAEVKKKKEAAAPGAAKTAAQAAKQPKKESQKDRKVPLTDKKEETQAPVPLKKDGPGMRRMGRKPEGGDGPRPQGGQGDGRPPTDRRPADRRPPRRFERPAGDAGDKPEGGEFSVEKPIGDRPMRGRGGPRGGGRGGRGRGMGRSDGFDSRGKREFDRHSGSDRSSLKGEEKRGGSGSHNWGTVKDELNELDQSNNTEETPEGEEHPPADSENKENEVEEVKEEGPKEMTLDEWKAMQDKERAKVEFNIRKANEGADWNKGFVLHKSKAEVKKDDLIDPEVEEPKGDDEHHFRKPANDITSQLEINFGDMARPGRGRGGPRGGRGGRGRGAAGGGGPGAGAGGGEATRPVRTGGRPDKSSASVPNVDDPEAFPALA |
| TRINITY\_DN20883\_c0\_g1::TRINITY\_DN20883\_c0\_g1\_i1::g.28839::m.28839 | gi|542220597|ref|XP\_003440913.2| | PREDICTED: ATP synthase-coupling factor 6, mitochondrial [Oreochromis niloticus] | 77.7 | FYRPRTSRLHVPTIHRGSSTFGILFCLSVKPKMALHRLFKLSSVLRSAVSLTLRRNIGISAVVFNRAKELDPVQKLFLDKIRDYNTKSKSSGGIVDAGPAYQKNVSEEVTKLQRLYGGGDFNKFPDFK**FTEPKFEEGTK** |
| TRINITY\_DN40464\_c0\_g6::TRINITY\_DN40464\_c0\_g6\_i1::g.97446::m.97446 | gi|734616970|ref|XP\_010736155.1| | PREDICTED: 60S ribosomal protein L28 isoform X1 [Larimichthys crocea] | 17.5 | MSSHLQWMVIRNCSSFLIK**RNGQTYSTEPNNLK**SRNSFRFNGLVHKKTVGVQPAADGKGVVVVMKKRAGQHKPAGSYEKITINKNSRATLNSLRHIISKNKYRKDLRMAALRRASAILKSQKPVVVKKKRTRAAKTA |
| TRINITY\_DN104026\_c0\_g1::TRINITY\_DN104026\_c0\_g1\_i1::g.132918::m.132918 | NA | NA | 69.9 | CVCACACVYVCVDTSRSPWSQSLSLSLI**SSFLPPSSSMSLLPR**TARSPRVRFPVVGPAVPPLPDLLEMFPLLVGRADSRAQRRDVLPWGGKLLVLVGGPVLSRPHLLTDLVDG |
| RRRRRTRINITY\_DN59229\_c15\_g167::TRINITY\_DN59229\_c15\_g167\_i1::g.98304::m.98304 | NA | NA | 80.2 | SCSQDLDGSTLGDTREGGRAEVRHH**EPEPEPEPEPEPEPEPEPEPEAAH**HDTGHQERPQPEEAAAARRGPQSEAHQPAAHPAARPAAAAAARLLVRGGHARAAGRH |
| TRINITY\_DN57762\_c0\_g1::TRINITY\_DN57762\_c0\_g1\_i1::g.113136::m.113136 | NA | NA | 49.2 | SSSQSAPIAIWSSPVCIALDSISLHLILIESEVPGARGKVLINELAVTSVGSLLLLELLLELLSS**FASGLPSEGET**TGVVCSFLFSSEGLSPPPGSSKSFFHDLIKDFARDVTSSSVLCLRMALTDIPILVD |
| TRINITY\_DN55400\_c0\_g5::TRINITY\_DN55400\_c0\_g5\_i2::g.41863::m.41863 | gi|432912307|ref|XP\_004078866.1| | PREDICTED: muscle-related coiled-coil protein-like [Oryzias latipes] | 54.4 | GVSPSPFSPSSDLSLGVSGCWVLPLSLLSPCWLPPTALVPLSPKLKHPFFKQLFLKFKGFETFETEKNSAMDQHKYRTAGVQEKLEIVGVEDESGNPISALTILSLLERVAGIIDNVQSCQQRMEERQLELESNIKTIQGDVLKLAKDHTDTSGTVEKLLQKTRKVSANVKEVRTRVEKQNVRVKKVESTQDELLTRNKFRVVIYQGETEIPSVAVTKSPKGTGLDGLELEPDAYDLPADLSSDEEYLSVEETDSSRAARLKKSVAKSTEHLKAAFSKENMSKRKDNLGTKFHHLGEKVMPAERREKMHQAGERLKQSGERLKENIAKKAPSKEAFRIKLKKERAVAEGQEGAEGETDAKESPVPPSAAGVAYTEVGPETKR**EGPVEESSATRIG** |
| TRINITY\_DN86998\_c0\_g1::TRINITY\_DN86998\_c0\_g1\_i1::g.26747::m.26747 | gi|734626328|ref|XP\_010741301.1| | PREDICTED: M-phase phosphoprotein 8 isoform X1 [Larimichthys crocea] | 16.8 | RTPTDDRRKRREDSEPKLFMACDDNQDNQEPPEGADKSDRGQATLSLGMDLNLDWMSLDDFQKHLNGEDEILSGPPLSPSELRDAVKSGDYMAVKLALNSKEDYNLDQEDVSGMSLSMLAAAGGQDDILRLLIKKGVRVNGRQKNGTTALMHAAEKNFLTTVAILLEAGSYLNAQTLSGETALMKACKRGNADVVRLLLEYGADCNILSKHKHTAMYFAKLSNNLVVCDLIRDHISVLSSVAEETIRAYFESRLVLLEPVFPLACHRLCEGPDFSMEFAFKSQPQPEGSGILLFIFHANFLNEITARLCGPCSVHAVVLNDKFQ**LPIFLDSH**FIYSFSPIPGINRLFIRLSEAPTAKVKLLICAYRVQLQ |
| TRINITY\_DN104049\_c0\_g1::TRINITY\_DN104049\_c0\_g1\_i1::g.132930::m.132930 | gi|734631009|ref|XP\_010743873.1| | PREDICTED: filamin-B, partial [Larimichthys crocea] | 41.7 | EPCLLKRMANNHIGISFIPREVGEHRVSILKNGRHVANS**PITIMVVQ**SEIGDAGRVKVHGDGLIQGTTFTNSSFVVDTREAGYGGLALAIEGPSKVDIQTEDMDDGTCGVTYCPTEPGNYIVSIRFAEEHVPGSPFTVRVTGEGRIRESITRRQKAASVASVGSVCDLSLKIPAIDMKDVTAEVTSP |
| RRRRRTRINITY\_DN40270\_c0\_g1::TRINITY\_DN40270\_c0\_g1\_i1::g.8496::m.8496 | NA | NA | 14.1 | HSLMESLTGGGGKQRFDEPWTSS**SLAAGSASFFTSGS**FSFRRFSYVMWCCEPMGWFLVYALKSRKAWTTSSMLRISVPSDSTAPDWWARWPSRSASSEM |
| TRINITY\_DN51648\_c0\_g1::TRINITY\_DN51648\_c0\_g1\_i2::g.38095::m.38095 | gi|348519606|ref|XP\_003447321.1| | PREDICTED: nudC domain-containing protein 1 [Oreochromis niloticus] | 11.6 | VSHVQDGVHSLDVLLLRVQTDPQEEEEEEAKGSGFSVALEWITVGNAAAHGEERKYEVRKRRLLRGKSVPHYAALEPRGRGLVVASEKPFVFTHVDGQKVEQQEAQPMEVEKTDPVYFWQQTPDDITVSVRLPEGVTKDDVRFRLTADSVSVAVRDFPPLLQGQMFAAVDPEASAWTFTDD**NKSLELTLQ**KRSAGAVWSELVLGDRRGEHVMSEEQAALIHQRLNHLTADDLGGPDGDKPPCNSQELEDCDGFPEDSSSLTRFDGETLRPTQVVNLSSHQYLFTVQVNPSEMPCLCLRHDVDALVWQPRPQEPGAMWEHVATFNALGYVQASKRDRKFATCAPNFSYASLCECLRRAFIYRQPSPVETVLFNRKQGRQVGQVAKQQVASLDSDKAILGFRATNERLFVLTSSHLFILKVNND |
| RRRRRTRINITY\_DN5942\_c0\_g1::TRINITY\_DN5942\_c0\_g1\_i1::g.71498::m.71498 | NA | NA | 15.6 | QEPQSTFYDDTRFVSPVERRQHPAPRRPSAPKNLFGPVSMTRLIKKFAGPLTGLEGE**AQTVQEEMASVNAGV**MKVFAELKDIRRYIQRMEDSKQQIQPLNENVIQSTDNRIMDLMGVFEDVRTLMEELSKELCLIEEGATARIYSSYSLATHRLDEDDQEPDHQDTGPQRDAEEPSPPDV |
| TRINITY\_DN56407\_c1\_g6::TRINITY\_DN56407\_c1\_g6\_i1::g.87323::m.87323 | gi|657545575|ref|XP\_008278096.1| | PREDICTED: phosphatidylethanolamine-binding protein 1 [Stegastes partitus] | 30.5 | MPVDLSQWSGSLELQEVEEQPTQPLTVKYDSVEIDELGKVLTPTQVQNRPTCVEWAGCDPSKLYTLALTDPDAPSRKDPKFREWHHFLVVNMKGNDVSSGCVMSDYVGSGPPKGTGLHRYVWLVYEQPGSLSCSEAVLTNRSGDGRGKFKLQSFRKKYNLGAPVAGTCYQAEWDDYVPRL**YEQLAGK** |
| TRINITY\_DN57096\_c0\_g2::TRINITY\_DN57096\_c0\_g2\_i1::g.125565::m.125565 | gi|657586840|ref|XP\_008297684.1| | PREDICTED: glutamate dehydrogenase, mitochondrial [Stegastes partitus] | 50.4 | MYRYFGELLSRSAGSALASGCVDSALPASSSLMRVRHY**ADAADKPDDPNF**FRMVEGFFDRGATIVEDKLVEDLRTRESPEQKRNRVRGILRIIKPCNHVLSVSFPIKRDNGEWEVVEGYRAQHSQHRTPCKGGIRYSTDVSVDEVKALASLMTYKCAVVDVPFGGAKAGVKINPRNYTDNELEKITRRFTIELAKKGFIGPGIDVPAPDMSTGEREMSWIADTYANTIAHTDINAHACVTGKPISQGGIHGRISATGRGVFHGIENFINEASYMSMLGLTPGFQDKTFIVQGFGNVGLHSMRYLHRFGAKCVGVGEIDGSIYNPEGIDPKQLEDYKLQHGTIVGFPGAKPYEGSILEANCHILIPAAGEKQLTRLNAPKIKAKIIAEGANGPTTPDADKVFLENNVMVIPDMYLNAGGVTVSYFEWLKNLNHVSYGRLTFKYERDSNYHLLMSVQESLERKFGKQGGPIPIVPTADFQARVAGASEKDIVHSGLAYTMERSARQIMRTASKYNLGLDLRTAAYVNAIEKVFKVYNEAGLTFT |
| TRINITY\_DN52217\_c0\_g1::TRINITY\_DN52217\_c0\_g1\_i1::g.68870::m.68870 | NA | NA | 36.5 | MGSGLTHYLEGLFGPFSQRFDVSSRFPPRQDVSLRVSSQNISGQTEHKALDELGLLVFSKDALFLSELSRDQCPEVD**VGFPACDDVGAV**AWVKLHRKHGLVGALDLCVLGGLVAVPHRQHVFVGVVDHTQERPGVRNREGHGSHSSLEGAEADLLQRDQGGGVPDVNTRLQGLPVFVHTRCLTRRHSHFVRMEGETANAVCVFAVVTLCSVVDVVEHDDAGDEVHRLARRQEVQVGPAVAPPVTVDPVQLQTLRGRLHLQVVVVLDVGGDVHGDGPAADEHLDRLSLAVGSSPGPRRPCGGDQLLGSVLQARGAREEVGRGRRLLIQTLPLPIR |
| TRINITY\_DN44215\_c0\_g1::TRINITY\_DN44215\_c0\_g1\_i1::g.79637::m.79637 | gi|831579180|ref|XP\_012737738.1| | PREDICTED: hematological and neurological expressed 1-like protein [Fundulus heteroclitus] | 40.8 | QQQQQQQQQQELAGRPVGKLTKLSSGNLKAQKQKTTMTSTNMFQGLETSSKPSSRVLRPPGGGSSNLFGGYEDDAAATRRPNKMASKVFSPAEEPQSVPRRSNPPGGKSSGIFGECEPPAQPQRPIPPGGSTSNIFGSAESAPVQSPLRSHPNKPKDNLSVGPESKPEPPAPKVKVSQPEVKEVAAPPAPAP**APAPAAAPAPAPA**AAPAPAPVPAKEEPAAVSAPPEPEATPPPSSSSSSSPPPDDMKKHEPHLGPKPRSHN |
| TRINITY\_DN58685\_c1\_g7::TRINITY\_DN58685\_c1\_g7\_i2::g.63594::m.63594 | NA | NA | 49.7 | WASCSSRSMRTTSTRCFMTKRPFRWKTGMSQRYRANHTSLPGRPMSTCCSTNLCLIGSRA**SFASSHRGQGSL**VNRVRVGGALVEKGRSSRRGQVLRKDICFVSVPVPWVQRLPERSREVRSSRSLEQRLRVSCSFLLLLLFLLLLLLLL |
| TRINITY\_DN40476\_c0\_g1::TRINITY\_DN40476\_c0\_g1\_i1::g.97533::m.97533 | gi|734611971|ref|XP\_010733416.1| | PREDICTED: 60S ribosomal protein L4-B isoform X1 [Larimichthys crocea] | 31.2 | PTSFLLWPPYRQERGSRRAEKLFTKMACARPLISVYSEKGESSGKNVVMPAVFK**APIRPDVVN**FVHTNMRKNSRQPYAVSELAGHQTSAESWGTGRAVARIPRVRGGGTHRSGQGAFGNMCRGGRMFAPTKTWRRWHRRINTTQKRYAICSALAASAIPALVMSKGHRIEEIPEVPLVVDDKVEGYKKTKEAVLLLKKLKAWNDIKKVYASQRMRAGKGKMRNRRRIQRRGPCIIYNQDAGVTKAFRNIPGITLQNVNKLNLLRLAPGGHVGRFCIWTESAFRKLDELYGTWRKSASLKVDYNLPMHKMTNTDLSRILKSEEIQKSLRAPNKKINRRVLKKNPLKNLRIMLKLNPYAKTARRHAILQHDPSIKAKMLKPKKKPGKKGAPAKPKA |
| RRRRRTRINITY\_DN44176\_c0\_g1::TRINITY\_DN44176\_c0\_g1\_i2::g.79581::m.79581 | NA | NA | 14.7 | RERLPLNPNSLFSLQQELSCVRFALYCSSLILLIILLTFFKLLQYEMQGLEAVPESLLGRDTQLAREELLQESKFPTDTASLSSTSNGLLDPLSSSVSVVSPKRRWKLVSPFE**DVVPFEDPTP**FEDLSLTPEEMFQKLSLSKGNVQLHTCIRRLVDYVSDRSLLSVFVYKQGTDTTIALGNPVLGATKHKKVLRVSAVPIAVKIDKGFLNACFCLWNRSIYLRGQLLIDRLLACSYVKMLIEDKPVCQFLKHYQSNYKSVTSGRYCKKVDEYSLDEILQFRFHGHTDDDKSPDLDQTSLLGTEESQEQQETM |
| TRINITY\_DN48778\_c0\_g2::TRINITY\_DN48778\_c0\_g2\_i2::g.83449::m.83449 | gi|348527198|ref|XP\_003451106.1| | PREDICTED: 28S ribosomal protein S36, mitochondrial [Oreochromis niloticus] | 26.6 | MGSKVSSKMAAPAARVIQAVRPHMPLIKFPNRHDVPKPNAQEALKTLAVNLPQHGTSPLAAAPPPISRTLTPISGTPDTLASIQLLPARYRRRAVAVDEME**FIQRGGPE** |
| RRRRRTRINITY\_DN54808\_c0\_g1::TRINITY\_DN54808\_c0\_g1\_i1::g.84158::m.84158 | NA | NA | 91 | KKEADAVAPQKVELKCSVTVEGHDNKARCSYVGGDFNGPKRIELSCIGQVCIQRFKPDDGIIMQNKMWIVKPKPFGRVSCLLKTSYGVTTSRDTLSTTFKPAETFDHEKYELPKYEIGTKLIKAEEKSVAASESIGCKNESFVRFKYTNGMILDSITANLRHYHEVVTFWDGTKKDAKQVTYGTIETNGNDKPATWELAVNFGWTDVIKVSAPPGPLEVIQLTIPAKDEFDEVKVCMEYVGSDDRESTRIFLISDRDTSRINVRKKDLPEGNKTWTVVPKPKGTFPITLNIKDGVYAVYRQKLIRPLRVKPRDAVEKVLVAEPLAIPPSRGGANVAVVRIKLRDGTTQNKIVYRCSKQLDENVAKWDDTGDKCVEITYGDLGSHGITEPQSWIITVSTDNKDEVFLEVPASTPEDPPPPTPAKPEEAPPAAAADEAPAAE**GEAPAPAGEAGEA**PAGEAPAAEAPAAEAPAAEAPAPEPVPEPAPEPAKKEEKKAPEKGAAKKIPAPKSPM |
| TRINITY\_DN33878\_c0\_g1::TRINITY\_DN33878\_c0\_g1\_i1::g.66530::m.66530 | gi|300677970|gb|ADK27292.1| | ubiquitin [Siniperca chuatsi] | 28.9 | MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKESTLHLVLRLRGG**IIEPSLRQ**LAQKYNCDKMICRKCYARLHPRAVNCRKKKCGHTNNLRPKKKLK |
| RRRRRTRINITY\_DN3449\_c0\_g1::TRINITY\_DN3449\_c0\_g1\_i1::g.104468::m.104468 | NA | NA | 7.5 | KDLYVPLFTLVWIELNVASCFRSTQPKYWEVCFFSLDIQVHVNRFMVFFGMQVVTLDVPFSIVRSVQLLANGGTCAFCLMYSASVTLWDQRHSIIIKRK**AFVFFFSLFV**FFLSLISVVKDHFGGSFLGPNRMM |
| TRINITY\_DN55094\_c3\_g4::TRINITY\_DN55094\_c3\_g4\_i3::g.60959::m.60959 | gi|734596849|ref|XP\_010739068.1| | PREDICTED: synaptophysin-like protein 1 [Larimichthys crocea] | 19.6 | MDSVAQKVLTSGFTLDLGPLKEPLAFIRLLEWLFSIFAFATTCGYSGTTSFNIICQGQPSREIHAVFNYPFRLMDHPYDVPDCKVNQTTTTPTFLTGDHASSAQFYVCIGVLAFLYSTATLVLYLGYQHVYRESSRGPIVDLLVTGALTFLWLASSSAWAKGLTDVKWATSPATIVSVLPVCHGGTGNTCTPGAVPHMGRLNASVIF**GFLNLILWGG**NCWFIYKETPFHKEAHPPADVEGGVRPS |
| TRINITY\_DN50583\_c0\_g3::TRINITY\_DN50583\_c0\_g3\_i1::g.57916::m.57916 | NA | NA | 40.4 | MGVHLRLDVVILTLPGFFVHRLVLCSGGELSNQRVVDGYCVVQTALPVPCGILLPRIKAGIGYLPDVHKPADEIGVCEEHLEHFAGTDVEDLVYVDSTLHLGL**SHLLLHFFN**AV |
| TRINITY\_DN7343\_c0\_g1::TRINITY\_DN7343\_c0\_g1\_i1::g.1594::m.1594 | gi|828407500|gb|AKK51793.1| | peroxiredoxin 1 [Trachinotus ovatus] | 24.9 | MSSGNAKIGQPAPNFKATAVVNGQFKDIQLSDYKGKYVVFFFYPLDFTFVCPTEIVAFSDRAEEFRKINCEVIGCSIDSHFSHLAWINTPRKQGGLGNMNIPLVADLTKTISTDYGVLKADDGIAYRGLFVIDDKGVLRQ**ITINDLPV**GRSVDETLRLVQAFQHTDKYGEVCPAGWKPGSDTIVPDVEKSKEFFSKQ |
| TRINITY\_DN36846\_c0\_g1::TRINITY\_DN36846\_c0\_g1\_i3::g.73667::m.73667 | NA | NA | 42.6 | YSGTAILFVTGKPYYFEQPLQSFCSPRQTCYAVQSRKQRVVPLSISLHLGFKRVERLHRRQGRPSQLKCSKINE**STSLPFVLRT**VFSPCVNRNLRSLLLFT |
| TRINITY\_DN40727\_c0\_g1::TRINITY\_DN40727\_c0\_g1\_i1::g.117819::m.117819 | gi|583984960|ref|XP\_006787734.1| | PREDICTED: collagen alpha-2(I) chain-like isoform X1 [Neolamprologus brichardi] | 70.9 ||
| RRRRRTRINITY\_DN38469\_c0\_g1::TRINITY\_DN38469\_c0\_g1\_i1::g.76300::m.76300 | NA | NA | 14.6 | LGCGQLSMSSLRSPLTHPSSSNEDKLEHSRQQFFDCPRFPFHTESQLTSATATTQSVRLDPGSWEPFGIATHKTSEHVCVCRLFCCFLLLLLLSRSKPVISVLCHECHRSVMWVCVCVRVFVCVCKKIWLSVFGRLCRFSFCFLVCHLLRFVCFKL**DLLSKSKQP**IRLLSLSHTHTKSHTHTHTH |
| RRRRRTRINITY\_DN55744\_c0\_g3::TRINITY\_DN55744\_c0\_g3\_i2::g.19917::m.19917 | NA | NA | 15.2 | FYDRRRSDDSIFSPNWQAPYICSHRSGPLGTFPYLGNRELDSNRLAPSYY**IDTMQLLNKT**SGNEQMEITERGWEMSIRNNKPFDAYPSMQLDGSKFIIKNIDNKDKKCCTVILAIILILLLAGGAPSVVVAILKYFNGCNFGGFGFMCPVCTGNELKYGDGCELCSLDDPNHKYYGQLCQCYATGNTDTCTSRETDCQTKQAVCLSEVHYTLQYRLVMRCHSSCNRLFMQISNNVEASTVDTSISFMNIALILFGNEEKKSLTSRSYGQYVSLSANLLQIIERQIEHMIASKSIVSDNPPRKVSFTGLFTKARTCTRGDELDFGLPCECSFSGHTNVCRSGQPCPDRECEDRDQNCNPGTWAQQCLCTYEPGENSVCMGGNMCPNSVCPNGPPPLPTPAMTPQIDTPSTTVVLETTGRETQKGTTHLVETSRTPTSPTYTTTVDHSDAGPTGTTEIQMTTVKTPTAIHTSPGQ |
| RRRRRTRINITY\_DN59368\_c0\_g1::TRINITY\_DN59368\_c0\_g1\_i1::g.92804::m.92804 | NA | NA | 23.4 | LLVVL**LETQLHDPGS**VIVAEDGREEERLLRTTRSQSQSSKIHLQCLHLVRNGLLGDTQHPHLEPFRGDLFDVSVFRRVLRDGVLQPPRHPFVVQGLPPQQPDDCLSLLVQLVPGVPVQLLQLRV |
| RRRRRTRINITY\_DN51887\_c3\_g3::TRINITY\_DN51887\_c3\_g3\_i5::g.14682::m.14682 | NA | NA | 17.9 | GSGSGSGSGSGSGTSSEAGAHGGSNHEENHIKKHTTPSGKESPCPSPTPNCSESGILQTMYICYDLLTRTKMAGPLDQLEETSEKVADGGPLTEAKNEEGSVSSKAGSASLFHQFWEEKERGTRGFLYLTVPLQHDPLAHIETKEEEEQGEVLSEEGVEGEALTICIPYKKNWVRKRALGPPLLSVKCNSLQYTCSRLFVADRPSEDFAAWRPINARPQALRLRSGELTVYVSHTISPHFTEPDYGHTENMWGELIEPDTLKDDLPCMSSKFRSGKNSRTNSRQPAFMFLVVLGLMFGCAVGVSLGTLYPPLPLVFFGYALLGVPVLWHFPLSSGPVIGRPQAYTKRRTGRSRNQLEVVQLVDGYTQIEYHSDRSHTHHDASGSSKLLSGKQLRRLPTEFVGRHESDTRRFCKFEADEGSMERGCSGQSAPSDGAGSARGQKPSGSSEDGMIKSLMSLPDQMAESFKRRTDELEAILSSGRPETPSMSGTSPPSAWDDNEILGGTEPRAELIRPQTLQKWPHLHLKSDSKSLNVEPEVRRSIETSLSKVLSLLPKSRLSSSERPELDTSSSKVLNTTVLLGA**SSSSLDALSGP**SSPSHPLFPQSRHGQSLDLDIGLSLDPQSERAQSKDKSFAVTPGEDHHDLSFILKSEEM |
| RRRRRTRINITY\_DN43189\_c0\_g2::TRINITY\_DN43189\_c0\_g2\_i1::g.71184::m.71184 | NA | NA | 16.4 | VTSENVTGGRQTQHGETDGVDGAYSRERRREDDDANMMMMLMLMARKLDLGTSSLQYCVCVASLVMIAEMVCDDSGSMGSLWLSLQSASSEAASTYQWFDPQSRAMSVAQLFNRN**DPPPPPPPPPPP**P |
| RRRRRTRINITY\_DN96081\_c0\_g1::TRINITY\_DN96081\_c0\_g1\_i1::g.110591::m.110591 | NA | NA | 27.3 | YFSHQLLKSNVTAVLQKYFRNKKGCDPLFTVLSGLGSTWNVTPCLDKSL**LVLNLVLSGT**HSSAKVKGMWLGLVWSNSTSTFSALCSHESPVNVTGRLRRSSASSMVSFWC |
| RRRRRTRINITY\_DN57181\_c0\_g5::TRINITY\_DN57181\_c0\_g5\_i2::g.21369::m.21369 | NA | NA | 20.6 | VSRTTTLCQNVVELLSSNE**LAAAVREK**DALQKNVAEESAHTGPTIHVDIKFRNPLSRLLKVKISLGILTAMSCHPITPTFEIGVFNEADNVNVRIQEVVNLEELSLPHEPDNISRILDFIERDDIPDHVDEDEDAATMLRDGSRQFIVPNANELRTGGSM |
| RRRRRTRINITY\_DN49247\_c0\_g2::TRINITY\_DN49247\_c0\_g2\_i2::g.37590::m.37590 | NA | NA | 12.2 | TSKIGQFGCFNWRKELSAGVGTLEQKFTCPLRSLLAEVESPNIKTDLRQLYSCIYEISAGFPHVHLFTSIIGVLLAERESHVPSPPNKETPGEKEQSCSVVTTETNQNASEENGRD**NQELQMVHT**NQLNQLGEKLTQVQNKLQQKDDLSKELDAERQKLEERMKLLQKQMGQLAQQLFSLQQSHTSDEESRMPQNKGQEQKLLEVENRYADLQCRLSDNEEKLAEAQSVGSDESDKSDPTDEMDDDSMEMEEERRIGMLQENHMNRIEEAQKHWMDLNKRQAKSFHDWAKQKSAAQFVSVIQEFQGLIGSLATKFKEKAEEMEKEHQSKESMLRRIHSNSSQIMSYFNNANRRNVEGRELWTLLVRVAEAFKGDDKIKDGLQSCEHESYHVIPPPSPPRLRDEEMKRRHREERALMRQHCEWEYLDDRAQAFDVHLRGTDKKDTSSGLRIRYGSLFLAKDVTFEEAFRIHCFNKKSKRIATIDGCQGFVEMILQENANEPLGGVFVTKCGPPRDRTAPPPLNPNPPFLTCSKCHIIEKITPIDQSLPAPVIGLGPMMPNMPTIGAMMSLNPDFDPMLPQGTMGMPPMGLNNMATAWANPDSMPMTISNSDMTMNCIGEPPLVTRKRKKSNEAANELPPCESVLPGSSGNFQLPDNNTAPDFPLANLGTYQLLFM |
| TRINITY\_DN20986\_c0\_g2::TRINITY\_DN20986\_c0\_g2\_i1::g.83723::m.83723 | gi|734598400|ref|XP\_010747287.1| | PREDICTED: ataxin-10 [Larimichthys crocea] | 33.3 | MAADTNSNLDLLASIADILNENHCPEHLQALKTFTTALRDRQYRDAVEVQAFSRLHEVLTRLSDDLQTADGDDESAALQLQLIAECFRAQRNSCVQSTRNQTLLRELGFVDVSLKI**LSFLLNTN**MESRDAVYEPLRCGIQFLGNLAVGNQLCKDDIWQLSFPNLLLQLLSSDDEKTVNYASMVLHTCLDEAKVEELSEPSKIELALKVMELCRTQPDLDWTVLIATQHFLKSSALVESMYSGMSHHERLTLLELLFAQLREDDSEECGIPSSVARFLANSFQKGCGAVLSLATGSASNDEVLQEALTVISALDVLCEMTSDHRQFMFLQDHPDLLVTTVELL |
| TRINITY\_DN46695\_c0\_g2::TRINITY\_DN46695\_c0\_g2\_i1::g.11770::m.11770 | gi|657583353|ref|XP\_008295780.1| | PREDICTED: glutamate--cysteine ligase catalytic subunit [Stegastes partitus] | 45 | DSSSLRVWFCFVFLHLTSLSCAMGLLSQGSPLNWEETKKYADHIRKHGIIQFLNIYNKVKDRQRDVLKWGDEVEYMLVELDDKDEKVRLVLNGGDV**LETLQDQGEKIT**PITPRSGDQSTA |
| TRINITY\_DN57931\_c14\_g2::TRINITY\_DN57931\_c14\_g2\_i1::g.43259::m.43259 | gi|736294681|ref|XP\_010790936.1| | PREDICTED: centromere protein V [Notothenia coriiceps] | 45.7 | MDLVKHTGGCHCGAVRFEVLNSPDLHVFHCNCSICTKKQHHHFIVPKMNFTLLQGSENLTTYTFNTHVAKHPFCKTCGVQSFSIPRSNPDGYGVAPHCLDPGTVRSVTVDNFDGEKWEEAMEAHKTIR**DMSRPASDTA** |
| TRINITY\_DN79260\_c0\_g1::TRINITY\_DN79260\_c0\_g1\_i1::g.26210::m.26210 | NA | NA | 32.2 | LLLRWDVADVPQTSLVAPQRVLGVFSVSDHHVDRLQLLQVDGGEAVDLLHLPQRDVQLGAQQRGGAGLLRRRQHLLRLLS**DGAQVLLQPLQ**LRLHLHLLGRLHGDGLQRLLVDRLAETSHRAVLTSLQTQTQLLDLRQVALTHRLVLLT |
| RRRRRTRINITY\_DN18123\_c0\_g1::TRINITY\_DN18123\_c0\_g1\_i1::g.118198::m.118198 | NA | NA | 15.1 | NAKHHKKKNKVLIKGMLEMPSPLPAGSELPYKELPETLLADGFISRCYEAMKAQQKPSDVHNEFSLIVPFPSTKFACEAIAEIVEKFSIETTITFGHTIVPEEETTRGKWCDL**EICRCGSLLV**QKYMEVSSNGALQGATLYTNHSSNIFYHSLPLTMDESQDLKEPPIISNEEGNLYRAFGEMSIQGKQALSANPEYKDVLLQVQEPKLPPYLIENLRPDRQKNNIFDTMQEVTLYPRSKAGVDSFIHDLEPRSCINNLFMSYVDPTFDEQPISDNRGSPLGCNELATEVRKRDASFMRFINKVPIRGEPNLQLKLRTYGKELCAERSMNQVFLNSALTFLEEAWEKATEEQFAMFNL |
| RRRRRTRINITY\_DN52684\_c0\_g1::TRINITY\_DN52684\_c0\_g1\_i1::g.110226::m.110226 | NA | NA | 19.6 | SSDLFAKLLSEAASPCASPSVRLCSLSSVRSRNSTSFSSSTCIPIFCSISSDMFISSFSTQSFCSARTSSLCCSSSRRVMLWCSLW**LDCLTSALE**LCFLSMM |
| TRINITY\_DN58269\_c3\_g135::TRINITY\_DN58269\_c3\_g135\_i2::g.44917::m.44917 | gi|1012730222|gb|JAR26581.1| | Myomesin-2 [Fundulus heteroclitus] | 16.3 | M**ASKDIHWH**MKKHVSHVKTDYAYHHKHAVKHHSERKSSSKSASQVQARATEVMAEPAYTIPVFRQRTAEETEEYQRVSTNVGKGLAVIQEELHRMRIATKAQVDSLEIQREVRGMMSRRGDLLDDIPKMPDFLVALRPHTVWEKTPVKLFCTVQGHPRPIVKWYKGGMPVDPLSAPGKYKIENKYGVHSLIISRCVVSDTAEYSAVATNQHGTASSKAMVTVKRPSGTGESCQLGLVPHLTEIHPSKLEVTLLDRFSVSFGVEGGAISLVATMVVVPDLPNVPPLAQWYRDDHLLKPSKLAEMKVGGGAARLTLPHLAKDDEGLYTLRIFTKDGTAEHSAYLFVSDAAPSAPGAPGAPMSLKAFDVNSDYVMVAWKPPNTVNEAPITGYFVDRREAGSDAWVQCNDAPVKVCKYPVHGLSKGHSYHFRVRAVNSAGMSRPSRKTEKVIAMSADEHERLLGTDEGVPSAPGQVVATRNSKSSVFVQWDPPKHPNHLIGYYIDGRAAGSKDWFPCNHKPFRHTRFVVHGLIPGETYVFRVQAVNIFGLSEESQESSPISVEPALATPSAPFGITMLSCDGSSMTVAWKSPKHCGGSKVNAYYIDKRDADSHLWQEVNTSAVKERICTIEHLTEGTFYEFKVQAGNMAGVG**LASAPSAPMK**CSAWTMDEPGPAYDLSFSEVRGHSLVVLWKAPVYTGASAVTGYFVDMAKKGSKEFVTVNEEAVHHRYLQVKGLEEGHSYVFRVRAVNASGTGKASQVSEPVCAKALPGTKEIEAGVDEETGDIYLSLEACEICETSKFVWSKNYKPIGDCPRVAVTTHGRTSRLTFTNPDKDDLGRYSVVVTDTDGVSGSHTLTEDALNTMLELSHAIRNPIIPLKHGLNYEILEKGHVRFWLQAVKLSSAVSYRFIVNDKEVTSGEGHKISHDVATGIIQMTVDHFTRANEGTYTVQIHDGKAKAQTSLVLVGDVFKAALKEAEFQRKEHIRKQGPHFSEYLYFTVTEDCTVLLTCKVANVKKETTFHWYKEDDEIVPETPPNVMSGACALPLPLFSRKDHGVFKAVLGDDRGKDTSTIDISGQVFDDIINAIAKIAGASASDLVLQCTPEGIRLQCYMSYYTEEMKTVWKHKESKIASSEKMRIGGTAEMAWMQICDPSDKEKGHYSIEISDGVQTHTRTFDLSGQAYTDAYEEYLRLKAAAFAEKNRGRVVGGLPDVVTIMEQKSLSLTCTVWGEPTPEVTWFKNEQEVTSSEHTKVTFEGGKFASLVITKVTPDDSGKYSINVRNKYGGEFVEITVSVYKHGEQIPEPKLGQPRMAATPASTPATTPMPPKSPAPHSKTPTPTPSKSHTPAPSLKSPTPASTPIPKSPTPTPRSPTPKSPPSTPRSVRSPTPPRFMKSPTPPRK |
| TRINITY\_DN58644\_c1\_g1::TRINITY\_DN58644\_c1\_g1\_i2::g.64019::m.64019 | gi|657548070|ref|XP\_008278992.1| | PREDICTED: unconventional myosin-XVIIIb isoform X1 [Stegastes partitus] | 12.9 | GGGGGGGRGGAATESELVLQLECSQTEVEFVRRRLKQTEEKLETERETRQQLDSKVSALQAQLEQARRSVTELKRHGRRVTSDLQDARVLTDSLQGRMHELERKQRRFDSELTQALEEADSEREQKDKSFLENTALGAEIYKLRRDLQESRAEAERLQKQKEELCAQIRDLSRPVDLTCESLPDLKKQLRLLETQSSERSEEIRQLTARIQQQQQIHMRFEMEMERMKQMHQKELEDKEEELEDVHKSSQRRLRQLEMQLEQEYEEKQMVIHEKHDLEGLIATLCDQVGHRDFDVEKKLRRDLKRTHALLADAQLLLSTVDSPGLHLPNGSKDQIERLHCQLEESEASRVEAESVQTTLSQELENTQIELENICKQKSLVDEQLSMLQHEKLDLLKRLEEDQEDLNELMKKHKALIAQSSSDIAQIKELQAELEEAKKQRHSLQEELQQSVSRVQFLESSTVGRSIVSKQEARVCDLENKLEFQRGQVKRFEVLVLRLRDSVVRLGEELEQSAAAEARERDNAKYYLQRLQDMKLEMEDLIQREGDSGRRRMELEMQVEELSAVRQALQADL**ETSIRRIVDL**QAALEEVESSDESDSESVQTAVESLTRKKDLDSVSSVGSIGTEDVGEGIRHWLG |
| TRINITY\_DN81987\_c0\_g1::TRINITY\_DN81987\_c0\_g1\_i1::g.26352::m.26352 | gi|958665750|gb|JAO66309.1| | RN213, partial [Poeciliopsis prolifica] | 26 | DLDVFTY**QGVEGSHVE**CLQMLLMYCGITDPSWAELRNFAWFLNLQLQDCESSDFCNDTLTEDTGLTGFKTFVVDFMILMAKDFATPSLSISDQSPGRLQMDLTGVRDEDLAPFKIRKRWETEPHPYIFFNDDHVSMTFIGFHLEPNEQNFVDAIDPTSGRVIKKNVMTRALYEGLRLQRVPFNMDFDRLPRGEKIE |
| TRINITY\_DN53568\_c0\_g5::TRINITY\_DN53568\_c0\_g5\_i1::g.39152::m.39152 | gi|498999453|ref|XP\_004554488.1| | PREDICTED: myozenin-2 [Maylandia zebra] | 36.5 | MSRFSTMTTQERKMQAAAICREVQAQEDLEMDLGKKMCVPKDIMLEELSLASNRGSRLFKMRQRRSEKYTFENIQNENNKQLNDAVVSQTENE**NAVDGHGGQNNTGVEQPSD**APETAVVPNPDSIAPGYGGPLKDIPAEKFNCTAVPKSYHSPWEQAIISDPALADTIVTHLPEPEPRADLPGFKSFNRVATPFGGFSKTPRPAPIKPVQVEPLPDFPELQAETTVDRPSFNRAALGWVSTGGPLTLPTVPLEPMFIPESEDL |
| RRRRRTRINITY\_DN45575\_c0\_g1::TRINITY\_DN45575\_c0\_g1\_i4::g.34400::m.34400 | NA | NA | 16.1 | STSLDELTGEPDLGSPIQEESTSMWITRSGLVGSALTTWTTRGACSAGLGVRSVLGGLAWFFLEAWVTITFMTSFGDLETNEGGLRLSGKELDSLSKTFWSLDRAMN**LSSELDAPDL**FLSCTPRGPGLFFARIDRVRESKRVR |
| TRINITY\_DN123084\_c0\_g1::TRINITY\_DN123084\_c0\_g1\_i1::g.136278::m.136278 | NA | NA | 37.8 | GVCGWRSGVGLCPLDHQGAGSD**GSAGGGVLPPL**ATLLDPAQSLSPLLLKHVSLVLGEVKALALQHLLLLSDLLHHLLLVLLLLAALPLLFLLVESYQFLDDGRVGLGGGGGRSGDGTLRHCCWACFL |
| TRINITY\_DN54879\_c0\_g1::TRINITY\_DN54879\_c0\_g1\_i1::g.40787::m.40787 | gi|657739072|ref|XP\_008332233.1| | PREDICTED: probable rRNA-processing protein EBP2 [Cynoglossus semilaevis] | 21.5 | MVIDGMSMESVEEEEQLGLESEEENSELSDNELQEAFAKGLLKPGMNVLVNKAKKFVNNVEGMKHCLADLRRDLPWVERLDLTN**LPAEDIISKAE**GKIPNKTNGDVNADDDFQREMFFYRQAQATVLEALPLLSKYDIATKRPDDYFAEMAKSDQHMQKIRKKLISKQMILEKSEKAKKLREQRKFGKKVQVEVIQKRQKEKKAMMTAVKKYQKGMTDKLDFLEGDQKAGKGSAQASKKEQNKKGPNAKRKFKDQRFGFGGKKSGKKWNTKESYNDVSSFRAKVANAKGGKGGKKGKGGKQNKRPGKSVRRKMKGRS |
| TRINITY\_DN116106\_c0\_g1::TRINITY\_DN116106\_c0\_g1\_i1::g.130398::m.130398 | gi|808876634|gb|KKF25251.1| | Titin [Larimichthys crocea] | 20.7 | DDEGEYTAVVGDDKCAAELIISEAPTDFSVSLKDQTITEFEDAEFSCKLTKEKAEVKWYRNGREIREGPRYTFEKNGKFCTLRIKECRPDDECEYACGVDDKRSRARLFVEEI**PVEIIRPP**QDVFEAPGSDVVFEVELNKDRVEVKWLRNNMTVVQGDKYQMMS |
| RRRRRTRINITY\_DN67429\_c0\_g1::TRINITY\_DN67429\_c0\_g1\_i1::g.64638::m.64638 | NA | NA | 9.1 | CFAVSPAFFGHSRALEASL**DITELTRGT**PLPLSVSENSRSLIFCSIKSSTNRSNCLTFSSIMSAMLCSSLRTLVVYDRLAVGRCSGGKRVMAGAAAATA |
| TRINITY\_DN58243\_c0\_g1::TRINITY\_DN58243\_c0\_g1\_i1::g.44626::m.44626 | gi|734610466|ref|XP\_010732594.1| | PREDICTED: collagen alpha-2(V) chain [Larimichthys crocea] | 39.3 | MMSFVHLRTFLFLVVSVAQVLIVTCQDGTSGDDMSCTADGQVYTNRDIWKPEPCRICVCDNGQVLCDEIQCDELSNCEKMVIPEGECCPICQTESPSTGGTDTFGGGGRIYKGQKGEPGDVPLVTGIRGRPGPMGPPGSPGDRGQRGNKGRPGLRGPAGYDGEPGVPGQPGEAGPPGHPTHPGGLEAQMASGFDGKTGPQAMLSGSRGESGTRGPPGPNGVPGHAGPQGPPGEVGDPGHMGSSGQRGPEGPPGKPGEDGEAGKSGNSGEVGFPGSAGSRGFPGTPGPPGLKGHRGHGGPLGQKGETGALGSKGATGPPGPMGGPGPMGPAGMPGERGRPGPGGIAGKRGSQGNIGKHGPMGPLGINGPPGYPGTPGMKGQPGPTGVRGPEGPQGQRGETGHLGRAGPVGLRGPGGTDGGPGSKGPVGHLGPQGAGGHPGPSGPPGPQGSTGQPGIKGQLGDVGVPGFKGEAGPKGEPGPPGSQGVIGPQGEEGKRGPRGDSGSVGPHGPVGERGAPGNRGFPGADGLPGPKGAQGDRGTGGPGGPKGSLGDPGRTGEPGLPGARGLTGTPGVQGAEGKPGPSGAPGEDGRPGPAGSIGNRGPAGTMGVLGPKGFSGDPGKTGEQGSAGVPGQRGPPGKDGEVGPAGSQGPSGSAGDRGEQGPPGVNGFQGLPGNQGPPGESGKPGDQGIPGELGAVGQIGPRGERGIPGERGELGANGLQGPKGIPGAPGPDGPKGSPGPPGALGDVGPPGLQGMPGERGISGPPGPKGDRGAIGEKGSEGTPGNDGARGAPGPVGPLGPAGPSGEKGEPGPKGPAGPAGSRGVPGARGEPGPIGAVGFSGPPGPDGQPGVKGEPGEQGQKGDAGLPGPQGLAGAHGPPGPVGVAGLKGGRGTQGAPGPTGFPGSAGRVGPPGPTGPVGEPGPLGPPGKEGPLGLRGDHGSPGRQGERGPAGPPGSPGDKGDSGEDGPTGPD**GPPGPAGTTG**QRGIVGLPGQRGERGMPGLPGPAGPPGKQGTTGSSGDKGPPGPVGTPGANGPRGDPGPDGPAGSDGPPGKDGVLGQRGARGDPGPEGLVGPQGLPGTPGPVGIPGDAGKRGEAGSRGPVGPPGSAGKRGLVGPQGPRGDKGDLGDHGERGQKGHRGFTGLQGLPGPPGTTGEQGTPGIVGPGGPRGPPGPIGPHGKEGYVGQPGPMGPPGTRGLSGEIGPEGPPGEAGPPGPPGPPGPPIAAMDDLFGGGPQDYDSGPPPPPEFSEDEAMPNSNSSTIVPVDPSVQATLKALSSQIDSMKSPDGSRKHPARTCDDLKRCYPMKKSGEFWVDPNQGSAEDAIKVHCNMDTGETCISANPDSIPRKVWWSSSRNKPVWFGADINRGTHFTYGNKDQPANSITVQMTFIRLLSKEASQTITYHCKNSVGYKDERNSNLKKAVVLKGSNDLELKAEGNSRFRYTVVEDSCSRATGNWGKTVFEYRTQKTARLPIVDIAPVDIGGPDQEFGVDIGPVCFL |
| RRRRRTRINITY\_DN53035\_c0\_g1::TRINITY\_DN53035\_c0\_g1\_i1::g.16041::m.16041 | NA | NA | 19.7 | IESLAEIPQNSSHLTNVPTGKDEFAVRTGDSSGDCNILVQNCDEAEMLPRTKSHVNLDILEEFSWQNSKGNLGSVLGVKASDQENLFESGEVLHGKPAPSVAQTEETSIGNNNEKDDTEPKGNVADLPEEEQLEPEGSALDDSACEDKDAETTIDDGQANTECSMEGGDEDGNEPSKDDDRKGDPGDGKRTRKMIEEIRKKREMREQQNQQMIRDREQRVREAEELAKAEAEEREKQLEAQRVAEEEAMKVREEEAMRAEEEERVKREEALKKEEEVRKLRAEEELRKEEEKRLREEEERQVRLQEEKEKQERMLRRNEALIKA**AEAASNTGTAGKPD**DKEKTKSSDSSQPATAQVPCLEKSKSDRKRLTPPGTPTLAPKQIPPPKTSAPQPSPPRQKMAGPSPPRTRSGQKATGPSPTRKP |
| TRINITY\_DN55183\_c0\_g5::TRINITY\_DN55183\_c0\_g5\_i4::g.18913::m.18913 | NA | NA | 48 | PRRGESVLQEAAAALAWRLEQLDVATQPGHKGPNHHVRHLWQLVVQQGGGGVVRYLLEDLVLGLGPDVQ**LSVLVVNVLVE**SADDGPVDEQRAHHDDGLQHLA |
| TRINITY\_DN51608\_c0\_g1::TRINITY\_DN51608\_c0\_g1\_i1::g.58214::m.58214 | NA | NA | 19.1 | MVGTELDVVKTSR**ALICDLIISA**IDMTFDTGFGISVNSIICSDVFMFSGLFIKCGMAASNSFDFKFCNSDLLSTFDIVVFFSLQDASTVIISASLSTTSLVFSILVCSTIPKAIVSVSISTTFSFWASTNNSATLLLSTSSSTCISVPSTVFIAVSTWLCGVVGGETLHPGEFSAPPGLSTGDFCRSVKRTAGL |
| RRRRRTRINITY\_DN51160\_c0\_g1::TRINITY\_DN51160\_c0\_g1\_i1::g.70811::m.70811 | NA | NA | 18.7 | GYLDDDAEENFVPGSGTGGSGHSPGSGGTASSPFRFSGFGRSQQLTQAFMEYKRIDNDSVSRRAFRMAEEFHDKRIEPVPDDEEVEMASPNTQRERERRIENEISERIALKCARQCIETLDAGSFGNTMKALFDLDVDKSIPSKRLNAKLISMRSKEDPLPIYILQDLRGPRLIAPDIIDPRNTAGIIFVNKKSSMGDMETLIQNIVRDAAGGGDGVNGGRAKAISDLEDFFLVCPAAQRAKDFIERVNAESEGFWMTLLEPGKISIFNAQCENAIAKALLTKGCGPPGYFLVGKSPTMGFKLFKDPHEVPYQVLEQLERKVDELGGIDEWTINPVEVVTERLASPNSQSLAWKFDDMTVALSNMVEADITEDELDILDMKKRIAQ**LAAESCLAAL**DAGVHGHTENAVQELDVDDALKMNKTHIQLIELRGTADPIGIDVERDFRGFRRLAPDISNPRNTAAMVIVHARQKLGDMLTLLQSVIRREVEGHTKERKPAIADLEDIFIIAPANKEAEEFAKRLNSESEGALKSMIEPGNILFFFAGTENAVARAILTKGTGPPGYLLIGRPPKVGIAKFLAPHRLPLEVMEKIQALQKRVGGIDDYGVENLSEEEDERRIPEGECHIVTDPAVICYPSPDTEVVKFEVARMGGRVLFIDGKRIPRYAELFYPKLYVEFLNGTIGEVTDDIPLVHIRKGYKVDPCPQISIVDGLRVRLNNRVVRNMRVKEDSCTDDSLVICVTERRKKGKMLVTDGRFLQLEDMKTQSLSVVSNDENISEDVILRNPRNKQKLIATALDDNKSEGGSAM |
| TRINITY\_DN54347\_c0\_g5::TRINITY\_DN54347\_c0\_g5\_i1::g.17703::m.17703 | gi|734609199|ref|XP\_010731893.1| | PREDICTED: SH3 domain-binding glutamic acid-rich protein isoform X2 [Larimichthys crocea] | 23 | M**VIKVFLAS**SSGSTAIKKKQQDVVGFLEALKVDYTQLDIACNEENRLWMRKNVPEERKPANGIPLPPQIFNEESYCGDYDTFFDAKEDNLVYSFLGLPPPPGSKEAAEADKADIVENGTHGEETNAEGNLDESIEARAQEEGEQEEADDDREEEEAEAQEEEAAE |
| RRRRRTRINITY\_DN54000\_c1\_g1::TRINITY\_DN54000\_c1\_g1\_i1::g.79990::m.79990 | NA | NA | 25.7 | DLHAEEPEEDHHEHSCQQAPDVDLLEVSEEESGSAAGEAALAGSDNDATSEDAASAQLLLDVPSPCPPDEAQVPPEAPPDHSDVPLPSDGMPPSPSESSETPFSQPDTSEAPLQHPEAPPFGSDSFIDTSALASALDMTVQSSLEQSENQDEASSSLLVSDELEEVGSIEGEREEHMALSTNTMDISSMSLDLRDAVDAAEPNMVAVESDSFGPDMVRHVPPPLPAEQISVQEVDLVEESQSSPAMLPAETFGHTPLTPSPEEEPEPTPPKPTPVSPNVPIRHLYGYGIGCGLSGEGGWAGNPTVVVERCGDTQINYVLLKLPKGEHAEVLSFFDESDQLVQDAGVIYDTHPQLGALAAP**SSAEVDLVH**WVNESAGQYSCFRVSAGLLGQGGWMTSPVVELERVRTSKTSYVEMRVAKEMNAKLIEKLLENEENLRKSDLSLIFDFFPQLGAKEAPSNPQVGHVHYGYTGGESAESSQSLGM |
| TRINITY\_DN56228\_c0\_g1::TRINITY\_DN56228\_c0\_g1\_i1::g.20225::m.20225 | gi|657570952|ref|XP\_008289022.1| | PREDICTED: vacuolar protein sorting-associated protein 41 homolog [Stegastes partitus] | 12.9 | MAEVEEGRKSSEEFTDE**SEEEDSEEE**PKLKYERLSNGVTEILQKDAASCMTVHDKFLALGTHFGKVFLLDIQGNVTQKFEISSVKINQISLDESGEHVGICSEDGKVQVFGLYTREGFHENFDCPIKVVALHPQFTRSNYKQFVTGGNKLLLYERNWLNRWKTSLLHEGEGSITNIKWRANLIAWANNVGVKIYDISTKQRITNVLRDNVSLRPDMYPCSLCWKDNTTLIVGWGTSIKMCVVKERNPTEMRDLPSRYVEIVSAFETEFFISGLAPLADQLVTLFFVKENSDQMDEEFRARPRLDIIQPLPESCEEISSDALTVRNFQDNECRDYRLEHSEGESLFYIISPKDIVVAKERDQDDHIDWLLEKKKYEEALMAAEISFKNIKRHDVQKIGMAYINHLVEKGDYDSAARKCQKVLGKNMELWENEVYRFKTIGQLKAISQYLPRGDLRLRPAIYEMILHEFLRTDYEGFATLIREWPGELYNNMAIVQAVTDHLKRDPTNSTLLTTLAELYTYDQRYDRALEIYLRLRHKDVYQLIHKHNLFSSIEDKIVLLMDFDKEKAVDMLLDNEDKISTDRVVEELADRPELLHVYLHKLFKRDHHKGQKYHERQIGLYAEYDRPNLLPFLRDSTHCPLEKALEICQQRNFVEETVFLLSRMGNCRRALQMIMEELEDVDKAIEFAKEQDDAELWEDLISYSIDKPPFITGLLNNIGTHVDPILLIHRIKEGMEIPNLRDSLVKILQDYNLQILLREGCKKILVADSLSLLQKMHRTQMRGVRVDEENICESCHTTILPSDMAKPFGVVVFHCRHMFHKECLPSPGTIHGVQFCNICSAKRRGPGSGILEMKK |
| TRINITY\_DN40649\_c2\_g1::TRINITY\_DN40649\_c2\_g1\_i1::g.8817::m.8817 | gi|657574681|ref|XP\_008291057.1| | PREDICTED: titin [Stegastes partitus] | 19.7 | VASAIQKTTMRVIRLHDGVEYIFRVFAENKYGVGEYLRSDPVIAQHPFNVPEAPAPPEIVSIRHESAILTWADPKDTGGSPITGYHVEFKERNSLMWKRATKTPLRVKECRVTGLVEGLEYEFRVMAMNMAGLGKASRVTEAVVALDPIDPPGKPDVINVTRNTVTLIWTAPKYDGGYKLIGYMVEKLEAGGKAWMKANHVNVQGCAFTVPDLTEGSQYQFRIRAKNSAGAISVPSESTDLLTCKDEYEPPSITIDPDMKDGVSVRAGDTIVVSASKIVGKPPPTSFWSKGGRELKSSDIVTITSTPTSSTLSIKYASRKNTGEYTITASNPFGIKEEHVKVKVLDVPGPPGPIEASNISAEKCTLTWLPPDEDGGCSIKSYILEKRETSRLQWTKLAENVIDCRYVASKLIKGNEYIFRVSAVNQYGTGDSSQSGPVKMVDSYRPPGPPSIPEIDNVTRTSVTISWKRPVQDGGSDIRGYCVERKERRGMRWVRACKRTVPDLRFKVQGLSEGVEYEFRVTAENKAGFGEPSEPSSPVMTKDIVYPPGPPSNPRITDTTKTTASFAWGRPFYDGGLPVEGYIVEYKKDGHDDWETETQYPLKVTEHVIGKLQKRGKYHFRVSAVNSEGVGEPAEVEKVTELVDQEALPDFELDAELRRTLVVRCRASIRMFVPIRGRPVPEVTWSKDDTNLKQRAHIDTTESYTLLVIPDCTRYDAGKYNLCLENVAGKKTGFVNVKVLDTPGPPVHLKPREITKNSITLQWEIPIIDGGSKIHNYVIEKRDATKKAYTVLTTTWQKCSFKFTDLEEGAYYYFRVSAENDLGVGEPAETPEPIRVSQAPSAPENLYVTDVTADSASLAWVKPLHDGGSLITGYVIEAQKKDTDQWVHVGTIKALDYTVTDLIEGAEYTFRIMAVNASGRSDPRESRPAVIREQTSAPSFDLRGVYQKTVIAKAGDRVKVEIPVLGKPRPVVSWKKGDVSLKETQRINTETTPTSTILNIGEIKRTDGGQYSMTGKNMLGTVTETITVLVHDIPGPPTGPIKLDEVSCDYVLMSWEAPENDGGVPINNYIVEMRETTGTSWLELAATVIRTTFKAARLNTGTQYQFRVRAQNRYGIGPCIVSESVVAAYPFDVPGQPGTPVVTSFNKDAMTLSWNEPSSDGGSAILGYHVDRKEKNSILWQRISKALVVGNIFKSTGLVDGIAYEHRVTAENMAGLSKPSKPSETMYALD**PVDPPGRP**VALNITRHEVTVSWTKPEGDGGFSITGYTVERREMPNGRWLKANFNNILETIYTVSGLIEDATYEFRVFARNSAGAVSAPSQSSEAITCRDDIEEPRLDVDASYSSNVVVMAGEVFKLEANVTGRPIPSLVWTKEGKELEDTGKLEIKTSDFHTTLVNKDSLRRDGGAFTLTASNPGGFAKFTFNVKVLDRPGPPDSLTVTDVTAEKCVLNWLHPTHDGGAKIEYFIIQRRETSRLAWTNVATDLQANRFKVTKLLKGNEYIFRVMAVNKYGIGEPLESEPVVCANPYVPSDAPQQPEVTTITKDSMVVCWERPEHDGGSRINTYVIERRDKTGLRWVKCNKRTVTDLRFKASGLTPGHEYEFRVLAENNAGLSAPSPSSPFYKAVDTIFQPGPPGNPRVLDTTKSSITLAWNKPVYDGGSEITGYVVETCLPEEDEWTIQTPKKGWTATSFTITNLKENQEYKINICATNCEGVGEPAAVPGTPKAEDRLLPPEIELGAELRKVVCIRACGTLRLFVPIKGRPAPEVKWSREHGESLDKAIIEITSSFTTLQIENVDRFDGGKYMVTVENASGSRTAFVNVRVLDTPGAPQNLIVKEVTRDSVSLVWDAPLIDGGSRVRNYIVEKRESARKAYSTVCASCHKSSWKIGELEEGKM |
| TRINITY\_DN51668\_c0\_g2::TRINITY\_DN51668\_c0\_g2\_i1::g.38123::m.38123 | gi|657559650|ref|XP\_008283695.1| | PREDICTED: methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial-like [Stegastes partitus] | 14.2 | LINSNPYGNGTAIFTTNGATARKYTHEVDVGQIGVNVPIPVPLPMFSFTGSRGSFRGDTNFYGKQGIQFYTQIKTVTSQWKAEDATVTSPAVTMPTMGR |
| TRINITY\_DN52590\_c0\_g1::TRINITY\_DN52590\_c0\_g1\_i1::g.58894::m.58894 | gi|734640681|ref|XP\_010749192.1| | PREDICTED: dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase [Larimichthys crocea] | 13 | RSPRRLYAAEMAGGVRRKSPGSPSPLWGKLHSLWQDKHLVLFKTEYTLLVVSVLWFLEIGINVWVIQKVAYTEIDWKAYMDEVEGVINGTYDYTQLKGDTGPLVYPAGFVY**IFTALYYIT**GHGVNIRLGQYIFAVFYLITLLLVFRIYHRTKKVPPYVFFFVCCASYRIHSIFVLRLFNDPVAMMLLFAAVNLFMDGHWTLGCGLYSLAVSVKMNVLLFAPGLLFLLLSEFGFIRTIPKLSLCAVIQLLLGLPFLLDNPIGYLSRAFDLGRQFMFKWTVNWRFLPEWLFLNRYFHLVLLAAHLLTLLLFAFRRWKRPGESIFELLKDPGKRKTPPQKSTVDQIVLILFTSNFIGMCFSRSLHYQFYVWYFHTLPYLLWSGGVKKLAHLLRVLILGLIELSWNTYPSTNSSSTALHVCHLIILLCLWLAPPLPSAPAETQHTPVKDKRQ |
| RRRRRTRINITY\_DN55561\_c0\_g2::TRINITY\_DN55561\_c0\_g2\_i1::g.85617::m.85617 | NA | NA | 35.1 | IRGGAFSRRGTLQSRLQHGLNVLSQPFKWHSMTLGTEGATFAYQSSCSTGLYFEENAAAATEEEETDAHDDDKLDGLTVIDSHDSSSLLSVHGKGEAGDGAESVCLTEDVTREGLTDDLSDGAREEVCGASASARTDQLEAEEVPPR**ELLEAGYEVA**AELGLTEIDSGENSIITWGCSSEADSSTESM |
| TRINITY\_DN77549\_c0\_g1::TRINITY\_DN77549\_c0\_g1\_i1::g.94567::m.94567 | gi|1012643614|gb|JAQ86588.1| | RT pepA17: Reverse transcriptase (RTs) in retrotransposons domain-containing protein [Fundulus heteroclitus] | 20 | CAEDNKSSFDAAVVDTVLCNFYVDDCLRSVASEQEAVKLYQDLKAICLTGGFRLTKWMTNDRDVLSSIPPEDRATEVKNLDFDQELLAIERALGVQWCIRSDQFKFHVNIQQRPLTRRGILSMMSSV**YDPLGMLSPV**ILPAKNILQELCRLRTGWDDAVPDHLAQQWSRWMEELQQLTDVGVDRCFKPPD |
| TRINITY\_DN49024\_c0\_g2::TRINITY\_DN49024\_c0\_g2\_i2::g.118898::m.118898 | NA | NA | 9 | MDNVLMAHEGCHVDGCQARLSDSLDRCSMFKQQLHHFDSVLLAGDVKWSE**AIQGLGVGVGL**LVNDELGHLVVTTVGGDVQRRQVVVGDVVHGHVVLEQKLDAVQVVPLSGHVERRQAVLGLG |
| TRINITY\_DN53285\_c0\_g1::TRINITY\_DN53285\_c0\_g1\_i1::g.16306::m.16306 | gi|657563859|ref|XP\_008285221.1| | PREDICTED: myeloid leukemia factor 1 isoform X1 [Stegastes partitus] | 28.2 | MFNSNIRDSDDDAFFSDPFRAHREHMRQMMRSFSEPFGGSIMPSSIMDGRSRGGHNMLEHPNSSVGLRDEHRDMSR**SLLPFGST**DSTDMMRNPFGMFDNIMANMRNRMQDMHQNFETMPSNSNTHSFSSSSVMTYSKVGNEPPKVFQATSSTRRAPGGITETRRAVKDSESGMEKMAIGHHIQDRGHVVEKKFNKKTGEKEFIQDFQNLDESEAQSFDDEWQEEVSKFQPSGPMSRLEEAPPSRTVRWAALTGPEQAQRDQSKGTAEGEGNIKGSGSTKQ |
| TRINITY\_DN49335\_c1\_g4::TRINITY\_DN49335\_c1\_g4\_i1::g.75727::m.75727 | gi|734603445|ref|XP\_010728732.1| | PREDICTED: LOW QUALITY PROTEIN: myosin heavy chain, fast skeletal muscle-like [Larimichthys crocea] | 61.7 | FKNKLH**DQHLGKTKAFE**KPKPAKGKAEAHFS**LVHYAGTVDYN**ITGWL**DKNKDPLNDSVVQLYQ**KSSNKLLALLYAAHAGADEAAGGGKKKKKGGSFQTVSALFR**ENLGKLMTN**LRSTHPHFVRCL**IPNETKTPGLM**ENHLVIHQLRCNGVLEGIRICRKGFPSRILYGDFKQRYKVLNA**SVIPEGQFIDN**KKASEKLLGSIDVDHTQYKFGHTKVFFKAGLLGTLEEMRDEKLAELVTMTQALARGYLMRKEFVKMMERRESIFTVQYNIRSFMNVKNWPWMNLYFKIKPLLKSAETEKELMNMKDNY |
| TRINITY\_DN49996\_c0\_g2::TRINITY\_DN49996\_c0\_g2\_i1::g.117709::m.117709 | gi|657588925|ref|XP\_008298825.1| | PREDICTED: CDK5 regulatory subunit-associated protein 2 isoform X3 [Stegastes partitus] | 18.6 | NNLMELLDMAEKALMSSDGQDENPELSDVCSRIKDTLQQVNALSNSESPSGVFGRRDSAAMQELQRHTDSLQEALWEQNRLNAELQEKLRDSGKAADAPAQQGLTGVSAGQDGECSTQRGAEKESDDHHGATGSSDDTGSNQEMTKALLNCLSATESAIASLAEHCTNPSSSASTRCSEISTNLQTHLDKLQRALQERKELEEATQPATKSSSSESTAAAAGTKGNQNLHLHQNLSLLYKVFNDLSHRISEMQASLQEERGRKEESEAHRAVQDGKGLPRSVQVQLEALHKALREKKKACKNLEEKLATALTETPSPETARRALEQDDKGVQVDLQDLGYETSGK**SENDREES**SSTDLEVGVNPSCSASSLPSLLKHEQATFSSTENLDSTSSTPYPSS |
| TRINITY\_DN9426\_c0\_g1::TRINITY\_DN9426\_c0\_g1\_i1::g.1683::m.1683 | gi|958809503|gb|JAO83317.1| | SMO, partial [Poeciliopsis prolifica] | 26 | KNYRYRAGFVL**APIGVVLVVGG**YFLIRGVMTLFSIKSNHPGLLSEKAASKINETMLRLGIFGFLAFGFVLITFGCHFYDFFNQAEWERSFREYVLCEANVTIASQTNKPIPECTIKNRPSLMV |
| RRRRRTRINITY\_DN22864\_c0\_g3::TRINITY\_DN22864\_c0\_g3\_i1::g.80412::m.80412 | NA | NA | 35.5 | FAGIETGWPRYPKSL**TSSPSVASLATP**SVLPFASFSLPFASLSSLSSLLPPSLKSTQVPLNLPLSGNPSVRLSETPPMVNLRSTGSAESTSSSSTPSSSSSSSSSSPPSS |
| RRRRRTRINITY\_DN128253\_c0\_g1::TRINITY\_DN128253\_c0\_g1\_i1::g.138880::m.138880 | NA | NA | 14.8 | EFWLTLNTTHRIMRLLNPSNKEKDEKTWVSGVLESPRVARY**LESELLTL**QRAIEIPHLTMLEFSDVQGARCIHWEIPPPPSEFTINHSVGNSQTQLKRKIIKNISEVWKRMSKGRLQIKSTIYEELRSRLELDNEFDYFHHEVWQRFVNLVRLQVPQVYEKRFRQLEAAMPQDGNWLAQRDEETPEPEPIEIRDILLTLLEQPKCFSRYTTLFTRVFNPDAYMHYTLREILKGVTGAKIIPIGTKSQVKDEFVINEESDQVAFR |
| RRRRRTRINITY\_DN9842\_c0\_g1::TRINITY\_DN9842\_c0\_g1\_i1::g.66836::m.66836 | NA | NA | 4 | ENEGEEPGELEAAHQREEEEEEEEEDTLGERKLADMDDSGDDSEATCIGYCMLSIVGLPLGFLFCGLLPSSRFVSMITSKADFAVRKIRQIIGDGGYAQASGNLVSSIFQVLQEMTEIPEGPLFYQENSTNLIIVSPVTVEGMILSNIYDNGDMHGFQFDRNFHERYEKAVRQILSKLRGSKETPDKEDIVAIAVLKGTEGLEYLTFGDIQLYGQFREKNVWSSLSGDEYEDYTFFGGDKFVVVAPLEPLTVSEPLVEESASFFYTYVILESAVDNYKEKLPSEGGIYLFLVDHRKMMHEFMHKSPLARVAPGSVRNAFEVIDDKTRPGKYNYALDGKLLKITPYGRVGFESAMGSYATADMKGVRVPSGSSKLEMGVDMWVPELKKCYGCWPAYFDVLWVDNVRTDKFTDDLDEVFALVASS**LFAAVVASI**LSAKVEAMAELQFVLCSI |
| RRRRRTRINITY\_DN31503\_c0\_g1::TRINITY\_DN31503\_c0\_g1\_i1::g.107836::m.107836 | NA | NA | 4.1 | SCQLIIPTEVRESRGVH**WGRKCIRT**LYDTFDPRAIHLLFHPLDPLNNLAVIVNGHVCLEGANNDSRNALEAARHVVLVLQQPTIDVEQLDDLEPEREHVLVSVIGGARRRPLEVEFEVECFVHVRLVGYVQELVGAELKFLVFFFSDVRQVESLQEHRGTQNQTFVDLPERKVAAVVKTVQHLEQCVSSERLLFVV |
| TRINITY\_DN58875\_c0\_g2::TRINITY\_DN58875\_c0\_g2\_i1::g.23877::m.23877 | gi|657577209|ref|XP\_008292423.1| | PREDICTED: ATP-binding cassette sub-family A member 1-like isoform X2 [Stegastes partitus] | 13.3 | RDLCNATPLEEFVHIADRNVSRMTQEIICKSSSDWLDQAQSHFLSNLDFLKPIRRDVRSDPKVVQDVSAATDSLLESLGALAVELSSMNSWKDMRKEILYLTANATSSPNQMYQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALFGNHGNDSESEPLSAYDNSSTPYCNNMMRSLESSPISRMIWRALKPLLMGKILYTPDTPATQRIIHEVNKTFQELGVLRDLGGMWEEMRPKIWSFMENSEEMDMVRTLLQNNASAAFLNSQLSETEWHVSDVFDFLSKASEDHRPAGSTYTWREVFNETDQAIQTISRFMECVNLDKLEPVANEERLVNKSMGLLDNQKFWAGIVFPDIAHSNSTDLPPNVNYKIRMDIDNVERTNKIKDGYWDPGPRADPFEDLRYIWGGFSYLQDVIEHGIIRAITGSKEKTGIYIQQMPYPCYVDDIFLRVMSRSMPLFMTLAWMYSVAIIIKGVVYEKEARLKETMRIMGLNNGTLWLSWFISSLIPLLISAGLLVMLLKMGNLLPYSDPGVVFLFLGSFGVVTIMQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFGAKVIVSLLSPVAFGFGCEYFALFEEQGVGIQWSNLLASPLEEDSYNLTTSICLMLFDAVLYGIMTWYIEAVFPGQYGIPRPWYFPFTRTYWCGEKENKNLSTPLSKKGNAEAVCIEEEPGHIDPGVYIENLVKVYSHGNKLAVDGLSLRFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYILGKDIRNELSTIRQNLGVCPQHNVLFSMLTVEEHIWFYARLKGLPEEKVKAEMEQIVNDVGLPHKRKSRTSTLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYARRGIWDLLLKYRQGRTIILSTHHMDEADILGDRIAIISHGKLCCVGSSLFLKTQLGTGYYLTLVKRDYDLTLQSCRNSASTVCYSKKTEKEDSVSESSSDAGLGSEPESETTTIDVSLISNVIFKHVPEARLVEDLGHEITYVLPYQSAKDGAFVELFHELDDRLTDLAISSYGISDTTLEEIFLKVAEDSGVDAVELSDGVVPTRTRRRHAFGDHQSCLKPFTEDDFDFNDSEESRETDWLSGTDGKGSYQVKGWSLKRQQFVALLWKRFLYARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSLALDPSMYGEQFTFISNDMPEDPHTNKLLGALTEKPGFGTRCMEGEPIPDTPCSAVQDEWSVPEVSQSVKDLFDEGNWTMEDPSPLCECSCGGRKRMLPECPAGAGGLPPPQTKISDTDTLQNLTGRNISDYLVKTYAQIIGKSLKNKIWVNEFRYGGFSLGARNSHMLSNRDEIDDAIAELRRRFRLERGTAADRFFGSLSSFIQGLDTKNNVKIWFNNKGWHSIGSFLNVMNNGILRASLPTGKDATKFGITAYNHPLNLTKEQLSQVALMTTSVDVLVSICVIFAMSFVPASFVVFLIQERVNKAKHMQFISGVQPFLYWLANFVWDMCNYIVPATLVIIIFVCFQQDAYVSSTNLPVLALLLLLYGWSITPLMYPASFFFKIPSTAYVVLTSVNILIGINGSVSTFVLELFGSNEIGGINDILKNVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFRSPLAWDMVGKNLFAMAIEGVIFFCITVLIQYRFCIKARSSTSHLKPIGEEDEDVARERQRILSGGGHTDILELRQLTKIYKRKQKPAVDRLCVGIPPGECFGLLGVNGAGKTSTFKMLTGDSDVTGGEAYLAGKSVNSEIDEVHQNMGYCPQFDAINDLLTGREHLEFYAILRGVPEKEVCEVAEWGIRKLGLVKYVDKSAGSYSGGNMRKLSTAIALIGGPP**VVFLDEPT**TGMDPKARRALWNAILSIIKEGRSVVLTSHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIILRVAGPDPDLRPVMDFIEHELPGSTLKEKHRNMLQYQLPSSLTSLARIFSLLSKNKEALSIEDYSVSQTTLDQVFVNFAKDQSDEDHLKDVHLNKRDAVVVDFSQLNSFLTDNKTRESCV |
| TRINITY\_DN86307\_c0\_g1::TRINITY\_DN86307\_c0\_g1\_i1::g.26593::m.26593 | gi|657595654|ref|XP\_008302497.1| | PREDICTED: 40S ribosomal protein S11 [Stegastes partitus] | 90.2 | RACIGLFTTLLAKM**ADAQTERAYQKQPTIFQ**NKKRVLVADGGKEAKEKLPRYHKSVGLGFKTPREAIDGTYIDKKCPFTGNVSIRGRILSGVVTKMKMQRTIVIRRDYLHYIRKYNRFEKRHKNLSVHLSPCFRDVTVGDIVTVGECRPLSKTVRFNVLKVTKAAGAKKQFQKF |
| TRINITY\_DN58867\_c1\_g3::TRINITY\_DN58867\_c1\_g3\_i1::g.23632::m.23632 | gi|923867160|ref|XP\_013770704.1| | PREDICTED: dysferlin [Pundamilia nyererei] | 16 | LSTVMEQAEDWAGRLRTMSEEPQNSLPDIVIWMLQGDRRVAYHRIPAHTVIFSQEHCGKHCGQLQTVFLKPPQSSGAEAKLPGQLRVKVWFGLAADVKHFNQYAEGKLSVFAETYENQTRLALVGSWGTTGLTYPKFSDVTGRVKLPKESFKPSPGWSWAGDWYISPEKTLLFDVDAGHMTFTEEVFENQMRLPGGQWIGMPEGYTDVNGEKAVPKDEVECPPGWAWEEVEWSEDLNRAVDDQGWEYGITIPPDRRPKSWVPAEKMYHTNRRRRWIRMRRRDQQKMEALRKQRPDEAEREGWEYASLFGWRFHLKPRKTDSFRRRRWRCRMEPLEKTGPAAIFALECSLSSIEDKNDDKSVTTTFGVNRPTISCFFDRGTRYHLRCYLYQARDLPPMDKDSFSDAYAVVSFLHQSQRTVTVRNTLNPCWDQTLIFYELEIFGDAEATTSSPPNVVVELYDQDTYGADEFMGRCVCQPTFTPSPRLAWFPIRRGDKSAGELLAAFELIQREKPSIHHIPGQEGDIMTTTHVLDELMFSGFLSENLQQWPDESDLPYPPPQREPNVFMVPQGIKPVLQRTAIEILAWGVRNLKSFQMSSVTSPSLQVECGGATIQSCVIRSVKKKPNFDVNTLVLDVRLPREELYMPPIVIKVIDNRQFGRKPVVGQCTIRSLEDYRCDPEAEGATVEEDEEGWRREMPHYSGEVFIDIDDELPLVTDQEEEFMDWWSKFYASTGEKNKCGTYLERGFDTLKVYDQELEKVEGFGGLSDFCQTFKLYRGKTQDEGEDPSVVGEFKGMFKIYPLPDDPSAPVPQRQFRKLPPNGIEECLVRVYIIQAHSLQPKDTNGKCDPYVKITLGKKTITDHDNYIPCTLEPVFGKMFELTCSLPLEKDLKVTLYDHDLLSKDEKIGETVIDLENRFLSRYGALCGLPQSYCVSGVNQWRDQLSPSRLLNRLCERRNLKKPVYQDDVVHFRGDQHTAADLEDKHESKRHLGPIRERLSLHVLRKLGLVPEHVETRRLFSPLQPDIEQGRLMMWVDLFPKSLGPPGPPFNVTPRRAKKFFLRCVIWNTSDVILDDVSLSGERMSDIYVKGWLDGHEHIKQKTDVHYRSLGGEGNFNFRFLFPFHYLPAEQLCVVDRKAHFWSVDKSETKLPPKLTIQIWDNDKFSFDDYLGHLVLDLNRMLRPAKSPQKCDVDLLQQPPEKLVSLFEQKTVKGWWPCTSEQDGHKSLAGKVEMSLEIVSEQEQDERPAGVGRDEPNMNPHLEEPQRPETSFLWFSSPYKTLKFILWRRFKWFIVLFIILFFILLFLGVFLYSFPNYAAMKM**VGPFGPATKQ** |
| RRRRRTRINITY\_DN112158\_c0\_g1::TRINITY\_DN112158\_c0\_g1\_i1::g.135108::m.135108 | NA | NA | 6.2 | SVNLLASIGIADLVEKKSAHLASGLYLFPLIEVPGGQDHHPTGCSSCASDISSQSNLSPLSKTKLCFEPYESFFRDYGGKLLYIRTGSSD**RSLANLVL**TVTSDEKVSDSDQTREDYLVVASYMGSRFRGR |
| TRINITY\_DN53068\_c0\_g1::TRINITY\_DN53068\_c0\_g1\_i2::g.16031::m.16031 | gi|548525400|ref|XP\_005751719.1| | PREDICTED: T-complex protein 1 subunit delta [Pundamilia nyererei] | 38.7 | M**PEAMMAPKLS**VAGGRHKGGAYVDRDKPAQIRFSNISAAKAVADAIRTSLGPKGMDKMIQDEKGDVTITNDGATILKQMQVLHPAAKMLVELSKAQDIEAGDGTTSVVVIAGALLDACSKLLQRGIHPTTISESFQKAVDKGVEVLTSMSRPVLLSDRDTLLNSATTSLSSKVVSQYSGLLAPMSVDAVMRVIDPATATGVDLQDIKVTKKLGGTIDDCELVDGLVLTQRVANSGVSRVEKAKIGLIQFCLSPPKTDMDNQIVVSDYAQMDRVLREERAYILNLVKQIKKAGCNVLLIQKSILRDALSDLALHFLNKMKIMVVKEIEREDIEFICKTLGTRPIAHIDHFSPEMLGSAELAEEVNLDGSGKLVKITGCTSPGKTVSLVVRGSNKLVLEEAERSIHDALCVIRCLVKKRALIAGGGAPEIELAVRLAEYSRTLAGMEAYCVRAYADALEVIPSTLAENAGLNPISTVTELRNRHAQGDKVAGINVRKGGISNILEELVVQPLLVSISALTLATETVRSILKIDDVVNTR |
| RRRRRTRINITY\_DN34201\_c0\_g1::TRINITY\_DN34201\_c0\_g1\_i1::g.112708::m.112708 | NA | NA | 55.4 | SFLFIKFTHMLLSLKADDPTAGTEVTATDGTGAATTATVRGTKVEVAAGPAAEATDATAVDTVGGGATVRGVAAGAGTGARAPAGAATATGGAAT**TVTAGGTAAPAG**EGGAATATPAGGGGGATPAEREIPATRSGQESGATDAGRWRKEGERGAKKGTRGEEGKRQQETKVRCMVM |
| RRRRRTRINITY\_DN28079\_c0\_g1::TRINITY\_DN28079\_c0\_g1\_i1::g.5639::m.5639 | NA | NA | 23 | TQEVGWHVYDSSPQCRVAAAAAARKQPTKYGDAPSSTAELPRKRNEMNVPCVSQSVPAEEPPPSSSLFSLLPSLPSS**LSSLSLGALSLGG**PNGGRRRRSSSVASRYSQVFVSPLFQGPKTNE |
| RRRRRTRINITY\_DN100510\_c0\_g1::TRINITY\_DN100510\_c0\_g1\_i1::g.132784::m.132784 | NA | NA | 21.4 | PSSDLLQQLQPQILNLFPKYGLCDTSAWSDVALLGNRVSQVTEQPVEPSDLFGIVQKIVNADRLILGIVVCWELCGAEMFVHLLYRLQVQSKHPGKNALEMSIHELEAQSLSLTSSNEDVMTWD**GDVVSSTET**LDTASGISYEEVKNTLLSLFADHTQPSHQNSHASSATDMDKARQGLRDLWNHNT |
| RRRRRTRINITY\_DN57018\_c0\_g1::TRINITY\_DN57018\_c0\_g1\_i1::g.105264::m.105264 | NA | NA | 8.6 | TVGPKRFVRLAICGLFVAILGFFICGSISLLVRRKLLLNKTKFHDSNKSYLPREDRVGCCTYSSQKPDNQPTVFHKKSMGDIPQDEKFWTYNWTMNKSEVMMVECTLVLSDTSFVESWGTLLVIKAQPREEVNLQRVKSQDSHF**VEKTGRKV**KCSYLGTNATVVSSITHNNGSETLQTNDKYWLYEWGSSINFHCTFSVSDGTHMDEHEPNQVLTVNPKDDYVSLTLESSIISNVHRTKLKASCSYQGRHSASASSISLFRQDSDFSVAKGPQVKQGDKYWTYKWNTSGDNWCEMQMSESPFVDLWQTVKKLSPVPIELIRLYRGSPEASYESKDRKAVCKYTGSDSSSANHIPFDHNNPLPVEDKYWQYKWGSSVGVSCEFFVTEGEYMTNVDPNQTILAKPKEGQVQLQIAQSSDTHFVQNRGRKAQCTYLGSDATVVSNVSYMRDSAGLRNSDKYWLYEWGSSVNIHCSFSVSEGPYMVSYEPDQTLILRPKEGYVTLTLPNSSSSQVSRG |
| RRRRRTRINITY\_DN56638\_c1\_g1::TRINITY\_DN56638\_c1\_g1\_i1::g.124257::m.124257 | NA | NA | 43.6 | GHGFRGLHRHPSGRHRPPLHLLLGDQLGAQHTPEASVASVVPHGGDGGGLRAGGGGAGHSEKKEEQIEEGSSQGHLEAPREHH**GAAGRAGQVPAH**RGVPLAAPLRREGSDPREKGEEESKGGVGVHQGLGTEARPHPAPQEPCMKAPQAPSPRVPGPPLDVHHRRGDCGSCAEPQCARGRGLGRQPAPPAHVHPPWLFLLRASRQHQRGAPRLAEGEDRRHRGLGKQHQLVRPFVCVQSRGHHPGGAEEGPPQRHHLHASRRDVEEPPFHLEGEAPTRGPQREAQSHQLGAAPGAAAAPVHEEALGRLRAARRAPPAAGGAVGVAG |
| TRINITY\_DN108373\_c0\_g1::TRINITY\_DN108373\_c0\_g1\_i1::g.134391::m.134391 | gi|734650230|ref|XP\_010754438.1| | PREDICTED: protocadherin gamma-A4-like [Larimichthys crocea] | 24.1 | YRRIHSELLLQFLLGGKTVYIVISSPYDIRKLKMDSKMSWVQMCSICFLLLFFNVAHGDMSYSFPEEMKRGSVIGNIAK**DLGLETGVLSKRRAR**IDTDGTDKRYCDINLNNGELIVADRIDREGLCGKKASCILKHELVLENPLELHRISLHVQDIND |
| TRINITY\_DN9128\_c0\_g1::TRINITY\_DN9128\_c0\_g1\_i1::g.78330::m.78330 | gi|657581759|ref|XP\_008294911.1| | PREDICTED: tectonin beta-propeller repeat-containing protein 2 [Stegastes partitus] | 17.2 | YSSPGPGGGVASHSGPANQTERTTDRQDDPDRDTHKPDQLAESWM**GYSGPGCGIL**SLQVTDRYVWCLDFKGGLFCSPLPETGLSWQRFEDNVHQVALSPTGNLLWKVEQKSMTAFACAKVAAKGKRHWYKAAEQTAFVALSDDSAWIIRTNGDLYLQTGLSVERPCARSVKVDAPCVFSQVCVRGGVVWALSEHKAVFYREGLSSFCSE |
| RRRRRTRINITY\_DN134767\_c0\_g1::TRINITY\_DN134767\_c0\_g1\_i1::g.141463::m.141463 | NA | NA | 21.2 | IPGQNSHPWYSFIKLKDKVSALKFRCFNNGPDNIRTLDIQEFLFKLTKFFRNRFSQSSAVVFSLFFANN**SIFTTLDT**AYSFTHPTMFSFGAQINYSACM |
| TRINITY\_DN43403\_c0\_g1::TRINITY\_DN43403\_c0\_g1\_i1::g.70386::m.70386 | NA | NA | 13.3 | QRRGSLIHNGRHDGAGVLCPEQRQHDPLSLFRGAHRGVLTEGASGAGVRVQQPSVGAAASRRAPLRVLSDHQHAH**AGQHISHLRT**QEELRPEEAARRLREDPGRPPQPGGLGPQLPPGGDTLPAPRLLSQGLPQPDPAESYNAQSGFLHPRRQEPAAHHRPREDRHRGRQAGARRRPPPAQPHRSLLCLSGRRNLDSHLPPSL |
| TRINITY\_DN49775\_c0\_g1::TRINITY\_DN49775\_c0\_g1\_i1::g.57280::m.57280 | gi|657557850|ref|XP\_008283049.1| | PREDICTED: 26S proteasome non-ATPase regulatory subunit 14 [Stegastes partitus] | 17.1 | MDRLLRLGGGMPGLGQGPPTDAPAVDTAEQVYISSLALLKMLKHGRAGVPMEVMGLMLGEFVDDYTVRVIDVFAMPQSGTGVSVEAVDPVFQAKMLDMLKQTGRPEMVVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVAVVVDPIQSVKGKVVIDAFRLINANMMVLGHEPRQTTSNLGHLNKPSIQALIHGLNRHYYSITINYRKNELEQKMLLNLHKKSWMEGLTLQDYSEHCKLNETIVKEMLELAKNYNKAVEEEDKMTPEQLAIKNVGKQDPKRHLEEHVDVLMTSNIVQCL**AAMLDTVVFQ** |
| RRRRRTRINITY\_DN58559\_c1\_g2::TRINITY\_DN58559\_c1\_g2\_i2::g.62478::m.62478 | NA | NA | 16.7 | VEVTVTPGNSTDELPTTETPASSEKAAEEKKDGDAVLPTNEAAGQQESSTTSAPQEAKEEAKEEAKVEAPQEAVKTENVIQVSDAAAAQATKVEGNQVPFLGELADYLFQYQELSTVMNQREKRLSKVVQFVDVLKETKASDLLNWMACFIGSRSSGDNCHVVATQSKSHKIEKMMDTLDQAKEPVESKGWKLFQFQKVSRSDKRKVHRILMNRCIFSPTIETSEVEVEFDGFTKKEKDWYACDSEQDEESCDSLMVITTARKQYVMLLFDSMTDPLPTQAAIFARQGWYGHIYSANIYKTADEDEEDSSEEEEDEDPESDRSHGEDVKLLVRNYDYPMVASTRNKKKNEETVGTNSTRWNKYSPLREFEDEMLTPEDSKQKLTSLTSHLESLSIETEGFQNHEVLAQHILIYQAEVQVMLCRQRRLRVVY**GYVDVRGEAELGE**MMADIGIYTGTRGVGASCHVVIPGSFFNKFANVRRRLKLLLHPEGPVGHDPWSMFQIHTVERETSKERKNILTLHRITYDPCHDESTLKVIFEEFIETERDPSPWYQACKVRNGEECRTVMVIISSQQEWVMRWFDGVTEEKPGQAAIYKKAEKYGDIYSANIYDCGPDGNGTSLQVRNYDYPLIDVYRNKPANYTKKAEKVTFRSFIRPVSQFEALFLRGEDALKRKYAELLAEAAIPEVPMLNEEDNATSILMMNETLDHSQRRKLIFIKYIVFLLAVTTLIILFVLFGIVAKDNYFTTVDKEAPESELRGNFVTVQVKYTTSYSLDKFEFKCKHNEKEKKVKGGLLLKARFKREPGNFPGHYECSVDITNHEPQPTKVKGNQVPEPKGIGTRERLETQTADREMDKYRPRVKCTYETFPNLGTVDCTGGPQHNRPTVTGTSHRKPHHLEDCSCDYSLNGLVPHCKQSTTDWTFQISTSTKDQLRNSITFDCDIRV |
| TRINITY\_DN38010\_c0\_g1::TRINITY\_DN38010\_c0\_g1\_i2::g.125166::m.125166 | gi|734610060|ref|XP\_010732368.1| | PREDICTED: A-kinase anchor protein 13 isoform X1 [Larimichthys crocea] | 14.4 | VDSKVNEHEKRRRLKEFHSRMDSKSIMMMKSGQIFAREDLLRRRLIHEGALQLKNSQGRLKDIHALLLSDIFVFLQEKDQKYVFAMLDQRSTVMSLQKLIVREVANEERGLFLITAGIEKPEMMEVLASSKEERNTWMQLIQEAMQSMEKDEDEGIPSETEDDKRQLETKAKEMRDLLRQKDTEIMSLLEEKVRLFRGMWEGLSPGEEACQQVEPFFRSTCSLEPPRGATIMNDALLEVETLQALVNGSLGGAMASVQEEGGVGPVCLPRRAETFGGFDSHQMHSNKSGDKEEGEDTVGDLRRTESDSVLKKGGNANLLLLLKRNSEQVLHSVSNLHLLLNTLQAVVVQQDSFIEDQRQALSERSSSCTSLSRPSSRPNSLIEQEKQRSLEKQRQELTSLQRQQAAHAEEKRRREKDWELREHHLTEREMLVNMQEEDVLKQHKELEWEKQELQSKKEEYQKDLERLRDAQRKLERDREAVQRQLDKMEELRLAERTPSTTSDESQFPGSSQSLELDPMELSSSSHASLPRLLPQQSKPKGKGLNPFTSSSTNANLKGSDSNSQISKSLLQLAKSKSKEGKEKKKKKGKGGSAQTADPQHRPEPPLDGEIFFC |
| RRRRRTRINITY\_DN40656\_c0\_g1::TRINITY\_DN40656\_c0\_g1\_i1::g.8890::m.8890 | NA | NA | 15.1 | CFQMGAVRGNKMIVDRPSLFPLFECKEEKALEMEEPVARINTFGKRFCVFVRKAGCRLASTACDFATDGAGLVIVVGRIEPLAARCQCMGKKSASAVLPLFDKSTFFGQDMTLGQFIKARNAQPLGIGIFVAKFGEQRLSMLTMGNVGLGKECVVKVGLDKMLDIEFQVVEYPLRFQPIEATSLGGTYKQREFVTINDYGLRALFTACSISAPGCGILAIPTHYSEPMESPPPLEPNRVQAIGMKSFVETAFQQLGGINIPGEESAYLNCGGVCLDSTPCVMGCTLGLPNDSLISRAAGYYNKNAISTIFSKIDLNTPCSKQCPADACKLCRMAERLAGRESLTTHKIDDFNNELKVCSDCSREPNRKWHKKEKKKNATSVIQAHTKVRPNLALISEIDPLDKSLM |
| TRINITY\_DN51738\_c0\_g5::TRINITY\_DN51738\_c0\_g5\_i1::g.58543::m.58543 | gi|1007710542|ref|XP\_015825806.1| | PREDICTED: keratin, type I cytoskeletal 19-like isoform X1 [Nothobranchius furzeri] | 33.5 | MGMGGGAAFDLSGALDQSTVHLNEKATMQNLNDRLASYLEKVRSLEAANAKLEKQIREYYEQKGPAAERDYSKYWAIINDLKDKIAGATIGNANILLQIDNSKLAADDFRTKFEHELMMRQSVEADIANLRRLLDQTTLTKADLEMQIEGLQDELAYLKKNHAEELEAMRAQLTGTINVEVDAAPQQDLNKVL**EEIRAQYEGITD**KHRRDQESW**FNEKSATLS**KEVAMSTETIQTSKTEINDLRRSLQGLEIELQSQLSMKGALENTLAETEARYSSMLAGYQNTINMLEQDLANVRASIEQQGHDFKMLMDIKTRLEQEIATYRSLLETEESRPISTGGGKTTITTTT |
| TRINITY\_DN60889\_c0\_g1::TRINITY\_DN60889\_c0\_g1\_i1::g.48167::m.48167 | gi|962014024|ref|XP\_014832040.1| | PREDICTED: DEP domain-containing protein 5-like isoform X4 [Poecilia mexicana] | 18.2 | NQKTLEEQQQQQQAKPSAAVSEPSNITTAPTYVDSPRKDAAFILDFIRSPRSSYIYHSQLPVEANEAADKGV**QSGASGGAAAAQPAG**ESVASSSTDTSGLSAAGVLSLSSSSTPHELLEAIKHPTTGVQLLPEQKGLPFNCFISAEVVHWLVNSVEGVATQGMAVDIMQKMLDEGLVAHASGDAMRTFVYGFYFYRIVGEKDGQTSQLT |
| TRINITY\_DN88439\_c0\_g1::TRINITY\_DN88439\_c0\_g1\_i1::g.27095::m.27095 | NA | NA | 30.3 | LGVDPEVLAGRPV**SCRVVAPDLN**EVMGVWLHSLQPGVVLLAGHHHLLSPTLTVFLIPPVLHLVSINIALCEGQPPHDGLCGGESFSVNTCRSFRWSILC |
| TRINITY\_DN99402\_c0\_g1::TRINITY\_DN99402\_c0\_g1\_i1::g.66290::m.66290 | gi|1007706830|ref|XP\_015807780.1| | PREDICTED: nuclear factor NF-kappa-B p105 subunit [Nothobranchius furzeri] | 9 | GSVKLTAL**LMAAGADPHRENF**EPLFFREEEEEEEEEEDEGYIPGTTPLNMAATAQVLELLSGKEYEAQSAAPVSTPPGDLSSLAVEVKQEVSRALESEGCWESLAHSLGLGILNTAFRLSPSPAKTLLDSYEVSHTHTHTHIRSL |
| TRINITY\_DN57246\_c0\_g1::TRINITY\_DN57246\_c0\_g1\_i1::g.21598::m.21598 | gi|734640730|ref|XP\_010749218.1| | PREDICTED: vacuolar protein sorting-associated protein 11 homolog [Larimichthys crocea] | 12.7 | MAAFLQWRKFVFFDKDTVKDPGDNGKNFALPLGISACDSGRGHIVLGDMDGKIWLMTRSLQLSCFQAYKLRVTHLYQLKQHSILVSVGQDEQGINPLVKVWNLDKRDSGNPLCTRIFPAIPGNKPTEVSCLSVHENLNFMAIGFTDGSVVLTKGDITRDRHSKTLTLHEGSSPVTGLAFRQVAKVTHLFVATLEKVHCYTLSIKEYPKIELDTHGCGLRCSSLADPSQDSQFIVAGDDCVYLYQPDERGPCFAFDGHKMLAHWHRGYLFLLIRDAKSPNKTGFASRESSPSDKQLLTIYDLDNKFIAYSASFDDVIDVVAEWGSFYILTREGKMFVLQEKDTQTKLEMLFKKNLFVMAINLAKSQHLDSDGLSEIFRQYGDHLYLKGDHDGAIQQYIRTIGKLEPSYVIRKFLDAQRIHNLTAYLQALHRQSLAN**ADHTTLLLN**CYTKLKDSSKLEEFIKCSESEVHFDVEIAIKVLRQAGYHSHAVFLAEKHMHHEWYLKIQLEDLKNYQEGLRYIGRLPFEQAESTMKHYGKTLMHHVPEGTTLLLKGLCTNYHPSGDTAERDSPERSRVNKANSEEFIPIFANNPRELKAFLEHMIKVDPRSPQGVYDTLLELRLQDWAHERDPQRKKVLQGEAVSLLRSDNTVFDKALVLCQMHNFKEGVLYLYEKGKLYQQIMHYHMQNEEYGKVVEACKRYGDQESCLWEQALGYFARKEEDCKAYISEVLQHIDQNNLMPPLLVVQTLAHNSTATLSVIKDYLINKLQRESQQIEDDERKIHQYREETAHLRSEIQELKTSAKIFQKTKCNMCNSPLELPSVHFLCSHSFHQHCFESYAESEAECPTCTPENRKVMDMLRAQDQKRDLHDHFNRQLRCSNDGFSVVADYFGRGVFNKLTLVTDLPGNKTVGSLEVNLQRDLLIHTKRNC |
| TRINITY\_DN58520\_c0\_g5::TRINITY\_DN58520\_c0\_g5\_i9::g.90647::m.90647 | gi|548380238|ref|XP\_005734223.1| | PREDICTED: histone H1.10-like [Pundamilia nyererei] | 52 | M**AEVAPAAPAAPA**AAAPAKAAKKKPAAAKPSKKSGPSVSELILKTVAASKERKGLSTVALKKALKAAGYDVEHNGAHVRRAIKSLVAKGSLVQTKGTGASGSFKAGKSAEKPAKKKAVTAAKKKPAAAKSTPKKAKKPAAAAKKAAAKKPAAAKKPKAAKTTPKKAKKPAAKKPAAAAAKKTGKSPKKAAVKKAAAPKKAAAAKKVAKPKAAKPKKAAAKKTGKK |
| TRINITY\_DN35879\_c0\_g1::TRINITY\_DN35879\_c0\_g1\_i1::g.32401::m.32401 | gi|734629481|ref|XP\_010743032.1| | PREDICTED: PDZ and LIM domain protein 7-like isoform X2 [Larimichthys crocea] | 41.8 | TNAEDMTHVEAQNKIRAATDSLTLTLSKAFKTGGDQKDSLAEASVQPKYSFAPSTTINKMARPFTAGGGSANSGP**VIKPVAYS**PKLNTPSSQGRASMQQPQNG |
| TRINITY\_DN46987\_c0\_g1::TRINITY\_DN46987\_c0\_g1\_i1::g.98828::m.98828 | gi|47218682|emb|CAG12406.1| | unnamed protein product [Tetraodon nigroviridis] | 18.6 | M**ADKIKDAKII**FVVGGPGSGKGTQCEKVVTKYGYTHLSSGDLLRAEVSSGSERGKQLQAIMQKGELVPLDTVLDMIKDAMIAKADVSKGFLIDGYPREVKQGEEFEKKIGKPCLLLYIDAKAETMVKRLLKRGETSGRSDDNEETIKKRLDLY**YKATEPVIA**FYESRGIVRKIDSELPVDEVFGHVAKAIDALK |
| TRINITY\_DN49859\_c0\_g1::TRINITY\_DN49859\_c0\_g1\_i1::g.119995::m.119995 | gi|808861831|gb|KKF13621.1| | Protein IMPACT-B [Larimichthys crocea] | 3.1 | MADIITQENEGDLQAQIEEVEALSSIYGDEWCVIDEASRIFCIKISNDLDKPKLTACLQIILPPDYP**SAAPPIYQIN**AAWLRGPERAKLANSLEDLYVEHMGESILYLWVEKIREFLVEKSQSSETVDQPEKVNLTAEEEVDDDDDDEDIPDFRALKLNTENAHLFMDHANGEELPPIKHGNPITDRRSTFQPHLAPVVTPRQVKMVLENLYENKKIASATHNIYAYRIYCEDKHSFLQDCEDDGETAAGGRLLHLLQILDVRNVMVVVSRWYGGILLGPDRFKHINNCARNILVEEGYTASSDESARAGGKTKKPKSKKTK |
| RRRRRTRINITY\_DN54223\_c0\_g1::TRINITY\_DN54223\_c0\_g1\_i2::g.59145::m.59145 | NA | NA | 15.5 | EPQPQKELMSKLKKFKNKGMRNKNQPKMKKAKTKKEFRSGEKKGAKSAKTEEATKVAPKKAEAGKVTEGEMKAMKAKKPGTSSNKKGKSKVNAKDKAAKGNTQAKEKLGGAKGPVTKKAKDGKSPKEQPSET**VTEPAEPAE**SSEEAKGAPTTPIVNSFKKLKAVFFGDMNHSHPYFRRTLRLSPHFRREKFRTFGEKGFDLGTPVLKVNRKKLAYDVVWENEEVMISCTCYVLYGGSPSEANVSDIASLILEKQLHASRQIDAEDKSTKVAPDKAIVGTGSCPADLLVRDFGGMVKPFQRGDYNCVVTNTVGLRHINGVVSKLRDANADNAVITGTNRMLQAVYTTKGGPASSMDLVLEGEQPSLAMVPLFSSAGQLMYQGALYEPTAGIPVSSDYIVLGVKSWKGLPDLNVGRNILAQALDRRRTKLTNTRITVPRHIENAELFDVLESLPFLDILKEILFNNYSYYMCLDKKLLSIYEAREKGEERKTSFNCLVDINDKIRQYITKLDLPLVGEKEAEEAGPLRFKDMDDINAQVTDEEDMDADSKDEDDDDDDEEEE |
| TRINITY\_DN9126\_c0\_g2::TRINITY\_DN9126\_c0\_g2\_i1::g.78281::m.78281 | NA | NA | 11.2 | ARLYRSSTAAAVYQLWKSHKRRTTSSRLCSAGPVELYHVSMVSVVVIVTHRLRQPISAERQATDGRRLGISHLALVCIDLVICKLVERTFSEQFNDQW**EWIINCIFT**IIYKIILNIQYIYTWEMN |
| TRINITY\_DN54984\_c1\_g1::TRINITY\_DN54984\_c1\_g1\_i2::g.60393::m.60393 | NA | NA | 6.3 | LLLRPPRHRLLTKDAAGRSDGPRSSPGTGVAEVIRLSVVVVVGPQRAGVK**WTPPPTH**RHLLPGPRSPLSLSLTPENHSRLVFTDKTSGQDGSVGVSGGARPALQEEEEEEED |
| TRINITY\_DN53776\_c0\_g1::TRINITY\_DN53776\_c0\_g1\_i1::g.76810::m.76810 | gi|226524991|gb|ACO70859.1| | glycerol-3-phosphate dehydrogenase [Rachycentron canadum] | 75.9 | MM**AAPKKVCVIGSGN**WGSAIAKIVGANAAKYDKFDTTVNMWVFEETVNGRKLTEIINTDHENVKYLPGHKLPPNVLAVPDLAESVKGADILIFVVPHQFIVRVCDTIKDHIKKDTIGMSLIKGVDAGPEGLKLISEVIRAKLGITMTVLMGANIANEVADEKFCETTIGCKDATHGPLLKDLMQTTNFRVTVVPESDVVEICGALKNIVAVGAGFCDGLGFGDNTKAAVIRLGLMEMIAFAKFFCTNCPVSPATFLESCGIADLITTCYGGRNRKIGEAFAKTGKTIEQLENELLNGQKLQGPATATEVHQILKQKNMVEKFPLFTEVYQICFNNHPVKEFIKCLQNHPEHM |
| RRRRRTRINITY\_DN49506\_c0\_g1::TRINITY\_DN49506\_c0\_g1\_i1::g.76464::m.76464 | NA | NA | 16.4 | VGGADSYPQGALECCLRTSTLETVSVYFFFFFFVQQTLPLRNRRTVDPGGCGGPNYIRCPHRFLGRELRLLVRYSLLTPRDSSCCDHCWSSCLLPNQLTQICSLDHDPVSAKDEGQLLSAVHLSPRPCRFSSGLVRFCHPLQVPLEQSCAGIDHLR**ESEVGTVVFQ**HVSAVSLAEGPLLYVFRSTVQGALHGVLTISQHGSSDRLGGRVEAALTLIVNLGDELLLELDEDLFVYVEQDCLVELVHFLSLPCDLSQLGGALWHSRSHANSRVSVQVADARSVTSDSQDFSSSLNHANVAVEVWLGTHLSDLHHLLSHVLGPKLSVVHALRQGVVGRVAVALTEDVQWLEGETQLRPDQGSPVHLFIGTFRVVNPDTVDAAATSKFGIVDTGQSLLQRRLPAGQWSTRLLMAGPATAQLHVCLRPDSCPGTTVVPLCQLRRRTTREAGGHGCRVAPADGFAVRVQHLLLLGGGLLLQLSEKVLGVFAVSSRRRRRHM |
| RRRRRTRINITY\_DN89913\_c0\_g1::TRINITY\_DN89913\_c0\_g1\_i1::g.108349::m.108349 | NA | NA | 7.3 | YCNAPVVSVIAAQTTPTKTMPADPATPPASTSTQLTEQSDSFCFAGFLRDPNAPWKVLGTKNKGCNMDPTLRPIVAVGEAIWGYKCTELEQQLAEQMQEKTAMTARVSQCA**DRAATFNLTYDDGE**ILLFVGAPRHGKPIQVLESESAPFLAAFCLLLFQTFCWVAAMNYNLHTYSSSAFRFFCMLHICLIFI |
| RRRRRTRINITY\_DN42315\_c0\_g1::TRINITY\_DN42315\_c0\_g1\_i1::g.33740::m.33740 | NA | NA | 31.9 | LKGLKTEMPLIQSSQRTNHTKHTQEPRLSHIELKKHTPTHESTTKPEPLLLLLLLLLVLPPTFSSPPLLVGVPGAAQLLAVNGPVVLLEPHVEQASRREPGGDGVVEEEPVSSSLDRPLVEDVVVQGLSRHVPQ**LDDVLSVDL**DHESGPLRRHVPLVDPEVDAAHVRKLPVQLRSLVLQADLSLVPQRHDVGGLAVAGEQEAHEGGHQDDAEQ |
| TRINITY\_DN46704\_c0\_g1::TRINITY\_DN46704\_c0\_g1\_i1::g.11750::m.11750 | gi|808861050|gb|KKF12953.1| | Stromal interaction molecule 2 [Larimichthys crocea] | 19.4 | MSYIHKVVNVLLRGLVIYAVLGSQCTTHSNDLPDHSSDAANVATTDPCLTVMPPCIGEADRFSLEALRHIHKQLDDDNDGGIEVNESVEFIIEDMKQQQTNKHSNLHREDQHITVEELWKGWKTSEVHNWTMDDTVQWLKESVELPQYEKNFRDFRVTGNTLPRIAANEPSFMSMQLKILDQRHKQKLNLKALDAVLFGPPLRPQHNWMKDFVLMVSIVIGVGGCWFAYVQNKSSKVHISQMMKDLESLQTAEQSLLDLQSRLEKAQEENRTVAVEKQNLEQKMRDEITGAKKEAHRLRELREGAECELSRLKYAEEELVQVRKALKRAEKEMQSERSVPEALQKWLQLTHEVEVQYYNIKKQSAEFQLCVAKDEAEKIKKKRSSVFGTLHVAHSSSLDEVDHKILEAKKALSEVTACLRERLHRWQPIEKLCGFPVVNNSGLPSLTASLYSDHSWVVMPRVSVPPYPIAGG**VDDLDEDTPP**IIPQFTSATMIRPSLTRSSSLCRSRRSLLSSPQSSLMSPDPDLLSMASSSLSYHPEADDEHIMFSSDRRGEPAQDGSSDTDSLNSSMGRKQMHNPGSETPYRKISREELLLFSQSSELPASASSAATHSSSSSGSLRDSTPP |
| TRINITY\_DN52135\_c0\_g1::TRINITY\_DN52135\_c0\_g1\_i1::g.68639::m.68639 | gi|657544995|ref|XP\_008277879.1| | PREDICTED: transcription factor BTF3 homolog 4 isoform X2 [Stegastes partitus] | 29 | VCCIAAGLSCAAASHSPAARTFPRAVSEFPHQKNT**MNQEKLAKLQ**AQVRIGGKGTARRKKKVVHKTATADDKKLQGSLKKLAVNNIAGIEEVNMIKDDGTVIHFNNPKVQASLSANTFAITGHAETKQLTEMLPGILSQLGADSLSSLRKLAEQFPRQSMDMKAVKEETAEEEDDDVPDLVENFDEASKNEAN |
| TRINITY\_DN33998\_c0\_g1::TRINITY\_DN33998\_c0\_g1\_i1::g.6993::m.6993 | gi|542227779|ref|XP\_005452844.1| | PREDICTED: eyes absent homolog 3-like isoform X2 [Oreochromis niloticus] | 18.1 | VGKAKGKGKKSEGSAPSDTDLERIFLWDLDETIIIFHSLLTGSYAQKFGKDPATVLNLGLQMEELIFELADTHLFFNDLEECDQVHVEDVASDDNGQDLGNYNFLADGFSGPSGGGGASGATAGVQGGVEWMRKLAFRYRRLKEIYNSYKGNVGSLLNPMKRDLLVRLQSEIEGVTDSWLSTALKSLLLIQSRGKCM**NVLVTTTQLVPA**LAKVLLYGLGDVFPIENIYSATKIGKESCFERIVSRFGKKVTYVVIGDGRDEEFAAKQHNMPFWRISTHGDLVSLHQALELDFL |
| TRINITY\_DN31463\_c0\_g3::TRINITY\_DN31463\_c0\_g3\_i1::g.107825::m.107825 | NA | NA | 55 | MFSPTVTSPEWGFSVKSPVRSCLVSGGCPSSTTG**GASCAGAAVSSPAGA**GAGAGGAESGCGSSLDLAGGSSLDLAGGSPLDLAGGSPLDLAGSLALAAFLTGSGILNGLLSSTIVCDSLF |
| TRINITY\_DN58798\_c0\_g5::TRINITY\_DN58798\_c0\_g5\_i6::g.92290::m.92290 | NA | NA | 14.6 | MRDDDGDFTLHELIEHFHGLTGLALICLDEVFQGDYQTWDDRVHLVLLFCADEGSYGCEGQNAIIQGCWV**AVVLQYSAQQLQ**QLAVVRLEGLRVGIHHFIQQQEANLSVIRIATLGGLTEEMQEGGPAVRCLMFDHHCTQLGQGVLHCVLCFLHEGLQHHLLEALSVVRAYLLPMFLYSHSQHHCSRLADLWVLGATHDSTQGWNNGWVFKSLFQLGCGLLNNRVVRLCHLQQDLLQFGCHLDSSAATLPAASSDDPCDR |
| RRRRRTRINITY\_DN57902\_c3\_g6::TRINITY\_DN57902\_c3\_g6\_i3::g.128457::m.128457 | NA | NA | 10.8 | KKPRSGGGKEKEFQAIQNFINLLNAPLDKKPTAG**TALTVSRP**NGATVSRERIEDEERRKRGEKERKEGGVESLEERGRNEYRGGDFSNRKSRKSVSASNASYESRVSSRRSYESDASSCSVKRRRNDDLSRRRKSDSHSRKDEKGRERNKERRERSRSRREERDPSVSSRRRKARSEEGDGGKRERRSSDSEENESAASLSYLQCIRREEEADEEDREGFGPGGKQNLFTASTNPPAPYWEVEEEEEEDKEKRDRESKGEESRRSERSSIRRQRKGGRESRRRKKKKKKSRRRSSSSSSSASSSRTSTSSSSSSSASRKRKKKM |
| RRRRRTRINITY\_DN13697\_c0\_g1::TRINITY\_DN13697\_c0\_g1\_i1::g.127795::m.127795 | NA | NA | 8 | PRRLSKLFERTIFGSGYAVLLGDKNMSSALMAFLAEYVGYKLLTVQDNLDLSSFGPVSKAFETLETVTEVSTCQCVHFIRVEADRDKLVG**AAGVMKAVL**TQEALQLTEMDHVVFPPTSTKGTLITRAKAKNMNFNKLYAEYIQRALTKQDAIQPDEVERDGTVMEAKLKLKESQPMRGFRIANHSMGVSLCKQFRCYQCKNRNKKQIKCRRECKDYELKLRITRRFFGKCGECAHVGYHYGSARDACVRCELNLSSSSSSFEDQGAAVGYIVSSPSSAPTLADLVTSGESGNSSSQYEPVDLSSLADNDISQSIDHLEEMGGMFDDDACLPSDLLPDELPSPPHYHSEMDVM |
| RRRRRTRINITY\_DN128386\_c0\_g1::TRINITY\_DN128386\_c0\_g1\_i1::g.139519::m.139519 | NA | NA | 23.1 | VSRLPHLNGGLARQTGGLLNQTPTPYIEGVKLLSPLGTTLRGQSTNCWLSWPGVPPVQTKPTKATTRYLHQRGMIPTITLTPITTTT**TTPAQPIVA**ELPLKLRPCAQITGTGCTSRRITPAPTAGLQPGM |
| TRINITY\_DN67053\_c0\_g1::TRINITY\_DN67053\_c0\_g1\_i1::g.64593::m.64593 | NA | NA | 18.6 | MLAGTHKTMYSKTLVVPLTGPHFCTKRLHQLHIQITKLPSTT**IARVCSCLLLT**HIIPMSLPCESSFLCTVIGVDGRYKWQQPVISDRQVGLFLFPLSSSLSS |
| RRRRRTRINITY\_DN28317\_c0\_g2::TRINITY\_DN28317\_c0\_g2\_i1::g.5714::m.5714 | NA | NA | 8.9 | WCRQMVKYVDDPCRQPCAMRYGKEVQERAQQNTMGPYPCVGLSFTEWLLIGYSWVDSESSYRGYNLAEPATWKIPIQKLGSSSYVGDDEQRSMGFDSIKLVSGEGVLCNRAA**LDRLCVSPSPP** |
| TRINITY\_DN59203\_c0\_g1::TRINITY\_DN59203\_c0\_g1\_i2::g.117000::m.117000 | gi|657556149|ref|XP\_008282392.1| | PREDICTED: translational activator GCN1 [Stegastes partitus] | 19.7 | VPTVFSAPEKREGPVWKKMVEVQSLLVAEVVGGAKTIAHKSIVKNLNHLWEQHPGLVDQYISTLLSLDQSPTTLAMLGVCLDFCTAQKDKATIEKHKSALLDLYIKSVLMSKTKPQQHILDKSGSLLRHVSHSEFKELLLPTLQKTMLRSPENAMQTVSYMLSSVTLDLSQYAMDIGKAIASQLKANNAQLMEEAVQAMQNLAQQCSDPTAVQDIVTHLFKILGGSEGKLTVVAQKMSVLSGISSCSHHAVSGTSSQTLSSAVTVMFIPYLQQEVHEGTLVHAVSVLSQWSSRLTVEVPKALSDWLKKAFTLKTSTSLVRHAYLQAMVGAFKGDTLAQASDLVPLLLQTVEKAVAQNSQHALLAEGVAASVLLSRLALLDTQTEAKFTTFWNVILDEKKPLFTTEKFLSQASEETLLTELLLCERLFLDHAHRLNTSKSQMYHHATVAVLLSRSWRVRKRAQQTIKKLLSSLGGSSLAHGLLKELCVVINKHKVLPQDVLVSESGELTELGRSYVPPRVLLDALCVVCSSASQWSDPAEAENLAMEILIVTHHPSIVEARRGLWPVLLSSMNIKAEEFLEKNLEAVLPHLLEVKANNQAVKNAVGALSGLSPNKLLPRVISHVTEGLSQPALLQVTREEYAIMLTPDGELYDNSIIQSAQKESTKKVNMKRENKAYSYKEQIIELELQEELKKKKGIKEEVQLTSKQKEMLQIQLDKETSIRKRLQALDAELQSVVGLVEATLIEKPAQITRELPSVLQSLLPLLQSPLAAPRIQQVFLDIGVCLMPKPLHSLAVLVGHVTLRMLKPECDLDEAWELEDLDTAAERTVGLLHNHTVPQRESKAGDVAPLSAPAFSFCFPLLNAMLRESSDSTEETENMMTRALQVVNEHSQLRASTESDDIVIDENGPELLPRVTMLLLLTRIISTATPRLQVLASQCLTALCASAGGDMGCTVAEQPEIDVLLNALLSPCFSVRDAALRGLLEMEFALPTDSTEASGLSLLRRLWVARFDVEEEGRALAEKLWESLGLELVPELCTLLIGDVTHHEEAVRTAAAEALSTAVSEYRDQSPAVLGKLTELYHQKLYRPPPVLDALGRVISEAPPDQWEARCGIALALNKLSQYLDEAQVTPLFLFFVPDALNDRHTEVRRCMLDAALSALNTHGKDNVSSLLPVFEEFLKNAPQDASYDSVRQSVVILMGSLAKHLDKNDPKVK**PIVAKLIT**ALSTPSQQVQESVASCLPPLVPAIKEDAAGIVRNLLQLLLESDKYAERKGAAYGLAGLVKGLGILALKQQDIMTTLTDAIQDKKNFRRREGALFAFEMLCNMLGKLFEPYVVHVLPHLLLCFGDGNQYVREAADDCAKAVMRNLSAHGVKLVLPSLLVALEEESWRTKAGSVELLGAMAFCAPKQLSSCLPSIVPKLTEVLTDSHVKVQKAGQQALRQIGSVIRNPEILAITPILLDALTDPSRRTQTCLQTLLDTKFVHFIDAASLALIMPIVQRAFQDRSTDTRKMAAQIIGNMYSLTDQKDLSPYLPSVIPGLKTSLLDPVPEVRTVSAKALGAMVKGMGESCFDDLLPWLMETLASEQSSVDRSGAAQGLAEVMAGLGVEKLDKLMPDVVQTASKIDIASHVRDGYIMMFIYLPLTFGDKFTPYVGPIIPCILKALADENEYVRDTALRAGQRIISMYAETAIALLLPELEQGLFDDLWRIRFSSVQLLGDLLFHISGVTGKMTTETACEDDNFGTAASNKAIISSLGAERRNRVLSGLYMGRSDTQLVVRQASLHVWKIVVSNTPRTLREILPTLFTLLLGFLASTCPDKRTIAARTLGDLVRKLGEKILPEIIPILEEGLRSDKSDERQGVCIGLSEIMKSTSKDAVLVFSESLVPTVRKALCDPLEEVREAAAKTFEQLHATIGHQALDDILPTLLKQLDDEDTAEFALDGLKQVMAVKSRSVLPYLVPKLTAPPVNTRVLAFLSAVAGDALTRHLGVILPALLSSLKGKLGTEDEAQELCSCQTVILSVEDEVGQRIIIEDLLEATRGADPGLRQAAVTILNAYFARTRLDYSNHTRTLLSGLIRLLNDSNPDVLAQSWDTINSITKKLDASSQLALIDDLHRDIRSAAADVKGQHLPGFCLPKKGVTCILPVLREGVLTGSPEQKEEAAKALGGVIKLTSPEALRPSVVNITGPLIRILGDRFAWTVKTALLETLTLLLAKVGIALKPFLPQLQTTFLKALQDSSRAVRLRAAEALGQLVSIHTKVDPLFTEQLSAIRNAEDSGVRETMLQALRFVIQGAGSKVDPTIRKNITTTLLGMLGHDEDATRMASAGCVGELCAFLSEEELKSVLLQHVLADVSGVDWMVRHGRSLALAIAVKSAPEKLCGKDYYDTVTETVLTNATADRIPIATSGIRAMGYLMRHNLRTEGGGSISQRIITQLVKCLQNQSSDIRLVSERVLWWVFKESATPLMETSLIKPVLKSLLDNTKDKNTSVRAQSDYTIVNLLRLREGEETMQSFTAILDTASNDLLAECHRRSLKKIASLPDSNEEIDDTILT |
| RRRRRTRINITY\_DN21715\_c0\_g1::TRINITY\_DN21715\_c0\_g1\_i1::g.51539::m.51539 | NA | NA | 20.1 | PKTWQIVIIDKTVHIAEPIGPPDCPDRAVCGESVKSCRGIGVINEAYVRYEYEISEELPHSKFTTDHILTKNIKVWLISNREKRELHYGLVPSGGDTVPEHWEVVQHDRSLSAIFPTGPPGPERYPYQAVVASSDLGHSKGYRNQAIIRFQYEAGTKLRHVKITTRACNITVNEWTATTTDRKQVIYNSIQCGGNHKPPDWSLTVSQTTVENFRVPGSPPGPKELVIVEVTTDKKGASNTVHISYMGGDDGAAEKISLTTHTRTNLINVRTTFKLPAGDKSWAVTPKPRGFVPIDINMDKGVHVSYSSFAPRVDPEFVLDKTMVPGALVKPDSKGKDNMATIRFLYEEGPNLNSVTAEMTKFTNVGSWKDQGKLQVELLYQIVRSGGDYEPKEWALSISTKTQDTVILNKPSQPVESVKLPDVITAPLGVGHGNEALVRFYYSCGEQLPDIKWSLAHCNTVVAAFTKRTSERKEVIYNKIKSGGDLLPPEWALTVSQNTIEKVKLNVPASPTDLVRVVVFASKTGSSNEATVTYKGSDNRSMKDIVLSTYSSTVEVQATEKLAAEDKDWKITPTPRGKIPIFLRLSAGAKITVIKRLEADIDLDPEEPRDQAVVAGSVDAHEGVGVKNIACVRFKYAQNEKLNPVEFKTKKVGTPPTCMIWEEAPAATAAADEAQAEAPAEVPEASMTTTCCEVIYGQIECGGDCMVKSWSLFVSSKTTDTVKPNLPPGPRFIPDLAKFFVTPSTPEGVGVANDAAVRFEYLHSELLGTVKFTLDTVTQRNCRTWRVGEKDHKEIIYGTIPSGGDESPAEWTLVMSDKKIHSVELSKPPGPTLYPDKIIVAASELPAGVGFQNVARVRFIYENGELLKTVKLCINEVKLDVVTWVLRSTERREVTYHSIKSGGDQIPPKWAISCRDKTVGTIILPGQPEGPKDLVVVNVQVAKEGGPNKLLLTYEGGDSLKAEKVSIYAKTPTNKIERHITNGLEQEGKMWHISPLPKGHVDADIKFNDGSNIVITQTYEPDISIRPPEIEDRATIPGTSYSPLSFVGAANRAIVRFEYQNDMVLGTAVYETEIINTFNAKQWRGEPLEKKEVIYGTVKAGGDYEPKTWIITVSDKSIKSAEPTGPPDCPDRAIHGESVKSMKGIGVINEAYVRYEYEMGPELGTTKFTQDTIISKNLKVWLISNREKRELHYGLIQSGGDNVPENWAVVMSDKTWAAISPTGPPGPLKYPYQAVICASVLVPGKGYRNEATIRFQYESGTKLRGAKIKTRALNPSVVMWTTTSTDRKEVIYNKITCGGDYEPRNWSITVSDSTVEEVKVPGGPQGPKDLVVIGINATTAGATNTLTILYQGVDDRTAEKISLNLMKDTAGFNVRTTRKLPQGDKVWSVAAKPRAVYPVEVTLDEGALVSFTNFLMKAVPAIVLDKVIVPVGIQRPDSAGKENKAAVRFMYEEGANLGSITAETEKVICSQSWKDVGKPQIEVVYCGIRSGGDHEPKEWSLTVSNKTVDKLTIKGPPQPKESVKISEGTEIPLGIGYENEALVRFYYNCGELLQSVTFTNHHCLANVTAYAKRTSERKEVIYNKIKVGGDNVPPDWTLTVAEKTVATIKLNQPASPTDLVRVQVTVTKSGSSNEVTLNYKGSDFRNVNEIVLLTYSTTTDITAREVPEGDGKTWKAQPTPRGRIPVFLRLSCCARLSVVKRLEADLDLEPPLLRDEAKTNDPVSVAEGIGENNVASINIKYEQNEK**LNIITFST**ALFGEKPTVITWEEEEEKELPICTEVIYGTIDSGGDYVPKNWAVTISSKTTDLIRPNCPAGPKYLGDTAKYFPSSVSPAGVGAANEAIVRFEYEHGVVLGTAKFQLDKVKRKNCKVWRLGIRDKREINYNTIPTGGDSKPAQWMLVMSDKTIATVEPNEPPDPVVYPNDAITPDSELSEGLGYKNVAMVRFIYENGKLL |
| TRINITY\_DN42432\_c0\_g1::TRINITY\_DN42432\_c0\_g1\_i1::g.80733::m.80733 | NA | NA | 16 | SDGRSSPERLPELRRRLPPLSLSQTPRLRSRSYPPSRRVYRWTVFCWDGPAVPSPLGVRLRLLCSSFGKQIPLFWLNSRSLHEHFSPFLLYRFSTLYLLRNPLYSLCLQTVVFHRLSHRLPLFLFPYQRPFDSLLTDALPPFVPTPFPPLSLFFSSFSFAFSAG**LDGLSFPSE**ALSVFSTEFTSAVLSSCVFVGSCLTASASSGPGVLSPVLVASRFVSSSQLTLSFISSGFSVFSEGVLVSSGVVSVAAGLEASDSSSTFLTSEDSVLFLLSDVFSDFSTCEGWSAFLMTEEVLMICELSVLPPSFTFSVDLITDGDSVFLGLSDFSGGTSLTGGDFTPGFFSCAESSRCSTLVLDVSVSLASLSPASGFSFCIVLVSAA |
| RRRRRTRINITY\_DN47500\_c1\_g1::TRINITY\_DN47500\_c1\_g1\_i1::g.36205::m.36205 | NA | NA | 21.8 | VGVYSFVDKILDNTRLPQQLVLGTQQHGMPQAVQGLHVQDQDHHLPLHRLHARVLLEHGCLSGERLEQPRVGGHVLSVIIFNWPASASSCLVAAYSSQSATRDDATLGLQGLGALLALVLVHLGLVRLDALQHLGVLGVHSPDLQRHEAGVQLG**DADKQGEDAQQ**QEQGM |
| TRINITY\_DN96891\_c0\_g1::TRINITY\_DN96891\_c0\_g1\_i1::g.95900::m.95900 | gi|734624149|ref|XP\_010740109.1| | PREDICTED: protocadherin-18-like isoform X2 [Larimichthys crocea] | 13.6 | GESTFDTSLIII**ISLGAICAVLMV**IMVVFAAHCNREKKENRHSYNCRVAESTHQHHPKKPSRQIHKGDITLVPTVNGTLPIRSHHRSPSATPPMDRAQMGSRQNHHSRQSLNSLVTISSNHIPESFALELAHATPPVEGQYQPRPRF |
| RRRRRTRINITY\_DN88459\_c0\_g1::TRINITY\_DN88459\_c0\_g1\_i1::g.27092::m.27092 | NA | NA | 12.6 | ARALPSFFLQLPFQLFPPEQLFLLFSTRTSASSSSFPAVCSALESSARISDLLSSSSDPRCSSFFGPKTTSMSSRPLMMFLTLFALLLSSLRPSPWIT**FTDLIFPT**FFISSSSSLRSIIVGARLSASVFCPYLSM |
| TRINITY\_DN43983\_c1\_g1::TRINITY\_DN43983\_c1\_g1\_i1::g.101609::m.101609 | gi|657542915|ref|XP\_008277143.1| | PREDICTED: tetraspanin-18 [Stegastes partitus] | 20.5 | MGQGEASARGTTMEGDCLSCIKYLMFVFNFLIFLGGSFLLGVGVWVLVDPTGFREIVAANPLLFTGVYIILGMGGMLFLLGFLGCCGAIRENKCLLLFF**FMLILLIF**LAELAAAILAFIFREHLTREYFTKELKRHYQGYNNTDVFTSTWNAIMTTFDCCGVNSPEDFKDSLFRLINPNHMVPEACCQHASQAGELAHISQEQCLSGSMMFRNNKGCYSAVVDYFELYIYVAGALAIVVLTIELFAMVFAMCLFRGIQ |
| TRINITY\_DN56039\_c0\_g2::TRINITY\_DN56039\_c0\_g2\_i2::g.121118::m.121118 | gi|657581962|ref|XP\_008295020.1| | PREDICTED: vacuolar protein sorting-associated protein 4A [Stegastes partitus] | 9.9 | MTTSTLQKAIDLVTKATEEDKAKNYEEALRLYQHAVEYFLHAIKYEAHSDKAKESIRAKCMQYLDRAEKLKDYLKNKDKQGKKPVKEAQSNDKSDSDSEGENPEKKKLQEQLMGAIVMEKPNVRWNDVAGLEGAKEALKEAVILPIKFPHLFTGKRTPWRGILLFGPPGTGKSYLAKAVATEANNSTFFSVSSSDLMSKWLGESEKLVKNLFDLARQHKPSIIFIDEVDSLCGSRNENESEAARRIKTEFLVQMQGV**GNNNDGILVL**GATNIPWVLDAAIRRRFEKRIYIPLPEEPARAQMFRLHLGNTPHSLSEADLRQLARKTDGYSGADISIIVRDALMQPVRKVQSATHFKKVRGPSRSNNQVMVDDLLTPCSPGDPAAIEMTWMDVPSDKLLEPIVCMSDMLRSLSTTRPTVNTEDLLKVKKFTEDFGMEG |
| TRINITY\_DN55015\_c0\_g1::TRINITY\_DN55015\_c0\_g1\_i1::g.60336::m.60336 | gi|734647663|ref|XP\_010753031.1| | PREDICTED: asparagine--tRNA ligase, cytoplasmic [Larimichthys crocea] | 6.5 | M**AEITKGVEQVSVG**ELYVSDKCGNDQDGDGTEQKPFKTPLKALIFAGKEPFPTIYVESQKEGERWAVISKTQMKNAKKAFNREQMKSDVKDKKEAEDNERREKNLEEAKKITIEKDPSLPEPESVKINFLEPKRGQRVKVFGWVHRLRRQGKNLMFIVLRDGTGFLQCVLSDKLCQCYNALLLSTESTVALYGTVTPVPEGKQAPGGHELHCDFWELVGLAPAGGADNLLNEESDVDVQLNNRHMLIRGENVSKVLRVRSAVTQCFRDHFFSQGYCEITPPTLVQTQVEGGSTLFNLNYFGEQAYLTQSSQLYLETCIPALGDTFCISQSYRAEQSRTRRHLSEYTHVEAECPFISFDDLLNRLENLVCDVVDRVLKSPAGQLLYDINPNFKPPKRPFKRMNYTDAIEWLREHDIKKDDGTYYEFGEDIPEAPERLMTDSINETILLCRFPTEIKSFYMQRCPEDRRLTESVDVLMPNVGEIVGGSMRIWDAEELLEGYKREGIDPTPYYWYTDQRKYGTCPHGGYGLGLERFLTWLLNRHHIRDVCLYPRFIQRCRP |
| TRINITY\_DN24643\_c0\_g1::TRINITY\_DN24643\_c0\_g1\_i1::g.51455::m.51455 | gi|584022063|ref|XP\_006805690.1| | PREDICTED: DENN domain-containing protein 4B-like [Neolamprologus brichardi] | 23.5 | SSAVRVRLLWDTLTPDTDQWPPLYILWRIHSGVPMRSYGWRRHNHPFTLSFLEEVLRWVGMNEVHKAVTLL**LDTLAKQP**GSPRIQRSLYREFLFLTLAAMGKDHVAAFDKKYKAAYSRLSSSLGRDELRRKRVQPPSPKAIDCRRSFHPPLEC |
| RRRRRTRINITY\_DN73312\_c0\_g1::TRINITY\_DN73312\_c0\_g1\_i1::g.64936::m.64936 | NA | NA | 8.9 | SDISHRLSDATSPRSGSRTPPRSNYRSPPLSGGKQKSLPYERDRNVEGGQSGPRYDATNIIRHSSPTVPRQLPED**VSPQPLLT**PKRKLKAMNTMIGLYETTLLSEGSLERPQPQLVEEKDLDTEMLDEDNDDEEEEDDSEPAEEEASNLQKIIFEIQRNLDPNDEKSYCRLIEEVSMERAEQRVSPICLISYLAGNVYPRVEHNEHGLLDTLVKLVHKANEACKRKGKTRLCLNMLLAASYELTYDTLCDSDQLEDVLWGILDDAIMATQQSRRLSLKQLAVLVNERALSDNEERRLAETLLKLLVPIQSLYV |
| TRINITY\_DN101316\_c0\_g1::TRINITY\_DN101316\_c0\_g1\_i1::g.139505::m.139505 | gi|1012671156|gb|JAR00360.1| | Reverse transcriptase [Fundulus heteroclitus] | 15.8 | ASLQNLSLETLRSTWETDIGEAISPEQWGSALDGVHSSSICARHGVIQFKVIHRLHFSKVKLSKIFPDVDPTCNRCKRSPASLAHSFWQCSSLSTYWNSIFKTLS**DVFQLTIR**P |
| TRINITY\_DN45220\_c0\_g1::TRINITY\_DN45220\_c0\_g1\_i1::g.73436::m.73436 | NA | NA | 12.4 | MLSVCVLYSMMVLGGRLRTLRRVSRMRAVVAWSLAVLFQMEMMSSWNRTDTTAPQISSPTMNCSPSIARIRFSQQ**RDARPFLS**RMIHFPPILLASSSHIGLIPSLKRWKSLWPVKSPGRIM |
| RRRRRTRINITY\_DN56705\_c0\_g1::TRINITY\_DN56705\_c0\_g1\_i3::g.124552::m.124552 | NA | NA | 16.6 | TTIKAIVGQNVPAPKGCAKVCLEHTDFRNKNGGCGGYWFRTCAKSHADYHWKLVFKACTGEEKPLQCIDVATLAVPVPLMEVQEGQQVQQQVQQQPEPETEPKDLPTTNVTSIGQNVRKHEAAKTTVIGKRTSVTQGEATHASVVVHYTQASELNDVALETSSVNTKLVLTHDVLRTVTVEFYVFLKPDPSSWRLKLGSSTINFVHLEDADKQKRQHVAQHNEHHKQHNEQQQSSSFPNKLPQDSQFWKCNKSVEPSMYFANEISIYKPLLQSFTQLHKDYFQSLSDLRKFFVDSPESAMRSLVRSDGATLRNGVGMIVLFYGRCKVETAIRVLQEGEEEVGGTVFLILVKRDRPLPAQEFVLEVTSEIAAALARGGELQPTKDLLFRVIDQASHHETLGIDVHIPSGTQNHLYEYPAQQIVSVRAHHLSSTPNSSVHLHEVIQAIYRKIETFVTPYTSESSDVVFAMDIDVDTTFSRRDRTSLPPVYDCMQDPSCFDFCIHCNMVKQIVSNYQASGPSPLVIVQAMATNNIQLARTLAREERSVLFLTAIGADHLRLAANTVAQVQGLQEGVFFIAVKRVLFGSRVRKFTNQALFSMATELNRSKNTSLTQLGELRQVLARKRLADAFRVETVVESNYLTLAVRAGRPCNSEAITIDKVLRLATERMRSFAQRNVQKSADLAIALETPYLPCELKGYCCPCNDRIKKVLDCQVVGPGRPGKDGYPGAYGVEGKQGPTGINGSVGRQGRNGGPGPGGQTGPDGAAGKPGPFGPFGEDGKRGKPGVVGFGDRGDEGPEGRPGLPGVVGKPGPEGPEGKRGISGRRGKEGIPGSDGGPGRPGPNGDEGRPGPAGNPGTQGRSGGIGPEGPEGAGGPK**GANGPQGPPGRR**GNAGPRGLEGPGGKKGDQGPDGAPGADGAEGKPGARNNDQGSTGPDGRIGKEGSDGAQGKTGKPGRRGPNGRDGPPGAVGSKGEEGNIGDLGIEGFEGKEGSYGRSGKVGRQGPCGQFGQTGNVGPPGREGPGGEDGPHGQSGPLGPNGKSGPLGVAGRDGRNGICKCPVGCCQREAINDLEEVLEYDLDMINVRLPRTYRFGRGYELMLAEEFKNVRELGVLIFSNVGSQQLEVVRRKMEAYPADLGDTLHIVVKVADDQRTKFRNNYASITKGNLLFPGRNRLARFGEFLEDANNTFDLQAPESASDMALMGVQVSPIQGSSCSIPAMKSIRQLIAGMKSQLNTQSSFINQGSVDFGVLVEVNCTKPTDQVGVCLKGKVEDDLTELIQENLESLELFTSARAVTSSESAINELENGTNGVGVAFVRVGKSKLGLAATKSDDASRGGTVVMLIQPTGDDMRSGKERTFHVDQVHRIAAGINIKRGGKYETREIADIIEQKNKFTNLYFADTVDAAFHALSFQLNDRDNYFLDILNIIFSMVEKFNERGLNISGDVLFVIDAKKSPIGTDIDVTPPEVPITGHLRAVVKDQLASLGPFTPVQLVDDSTTAIQSLQRTDASGAGVGICSVRSSKLLPGYISVDQSSRGGTLVVLHQSAETPRVGASPRLENQMVYNIADALDSSRGGMQRLRKIASIVAPKNNHSNLSFETKVRDAYQVVAVRVQDPQVDLQQVLQLIFDRIHAIGGAGTNDSGDILFIIDKKGLHIPDIEVPTYSAIIDATSMTKVSDILQSEVRPLQQFNDVTYVLEPKLSIQKLEDPDANRSGIALPAVQGRKLQDAPGSVDDASKGGTVLILFQPVGDEIRSGASRQYINKSVWELARGTNLRNGGKSRIRMVAQRVEEKTSYENLLFELNPDDSYQVVAIRVKQMGVDLKDVVRRIMERISPFESRMATTGDILFVVDRKEGGTSTPTIVDPTPFVPRMNQIADDSLETITTILNDQVTHLSPLDDVTFVFNPVYSVVRLETPNVDRTGISLPIVRSQKLSSAPRSIDDTSSGSSISIVFQPVGEQKRSGRAATLVDQSVFQLAQGLNRQRGGRQRIARVSNLVGEKTTFSNLYMDAHASDGYQVVGIRIKNEGVNLSEVVRRIFERIVPFDRGVGDSGDVLFVIDKRPGVAEAKELVEILQQKPLVLINNLRSPITSLETFEKVNFAFSPNHSIDQIQKPDANKVGVGFPIVGDTKLAGAPEKVNDRSRSGALIITFQPVKLAARGGNRELFITDKMFRLAGGTNLSRGGAPSMTNVARLVEDKTQYTNFFFVPTPKESHQVVAVRVKDTGIDLPELIKIIFRRIHEFEGRVNDTGDILIAVDREAGSVVKEEPLAMDTDGVVTILKPMVVEAMAPINSFSVDHYALDPVFAVTRLLAEDAQGSSVVFTLVQNVALEDAIKKVEDQPPGGTILVLVQQVGQRRRSGTSSQFMTDLAHRMAAGTNLVSGGMLRLQSIRDVVDQRNNFQNLYFEINPYEAFQLLGIQVRDPRVDLQNVVNIMFDRVYPLNTSGVYNSGDVLFVIDRVVRQTQVTTIEVVPETPGETVIVGALTSLADVIARPNRNLARFDKLMFVVSDAFAIQKLEQENAAKSGVALTLVGMRHLSTAPTEVNDSSKKSTLVLLLQPVQQQIRSGKEPRLMNTRVFDLAAGINVSSGQRPKIAGLAATLAESSGHSNLDIELRPTNGFQAVGVQVQDPGIPMTDVFRKIFERVSNILTSGMTSDILFIIDRKGVTLVEQADLKPLLGAFLVGLLACLPLLRHRRM |
| TRINITY\_DN51815\_c0\_g1::TRINITY\_DN51815\_c0\_g1\_i1::g.58500::m.58500 | gi|734601409|ref|XP\_010727607.1| | PREDICTED: EGF, latrophilin and seven transmembrane domain-containing protein 1 [Larimichthys crocea] | 18 | LKVKSRLSASMESLLKSPMKLVLLTAWLSSLMDPCSLSDICAHPCHKLASCKTINGSNSACFCDHGYTGDGTTFCDDDDECRNVTNICGDRGTCTNTEGSYFCTCVSGYTSTGKDQFQPNDGTECHDIDECQKVDVCGPNSKCHNTIGSYNCTCQRDYVPSSGAKHFHPESGVRCKEHPQKYCHDNIGCITQTVNKTLEYMSNLTEPQSLLKEIAKQTSGELTSVEVIAYVEALCRSTSTLAAGEKDYTVKPSVINSTLSKLVKAVNNLVEKDELMAWSRIKEERREHTITKLLHAVEESALTLANNYKTPAELEIKASEMEMKVFTFDARHTKAKLSASMGGDRIDLTPKLRPEEDRNGSVSVVFVRYDSIGGILKPSSDPGVTDYSRYAETGEIIVNSQVIAAAVKPADVYQLDHVTFTLRHNEPIDTKADVTKCAFWEYEPDSLQGHWATHGCKTVHVTSNTTTCSCNHLTHFAILMSSGRANLVAHYTILTRITQLGMIISLICLSMCIFTFWFFSEIQSTRTTIHKNLCC**SLFMAEFI**FLVGINMKTHKLFCSVIAGLLHYFFLAAFAWMCIEGIHLYLIVVGVIYNKGFLHRNFYIFGYGSPAVVVAISATLGSRYYGTDKVCWLSTENHFIWSFIGPACLIILVNLLAFGVIIYKVYRHTAVKKPEISHYENIRSCARGALALLFVLGATWTFGVLHILHETTLTAYLFTIANTFQGMFIFIFLCVLSRKIQEEYYRLFKNVPCCFECLR |
| RRRRRTRINITY\_DN62702\_c0\_g1::TRINITY\_DN62702\_c0\_g1\_i1::g.93291::m.93291 | NA | NA | 34.4 | Q**LTASASPIQ**PHQGGLWLGGLSLSALATPDLLSPLGGTSSLLQLLQEQNMFPFAEALPLPAPSDGVASHTPPNHDVLRSSLPGPSTAALPKTVTSVKPNVCGSQDAGTFHNEQSSMEVDTTRESASGEGQPLTSSAALLALVHNSLDLPKPSTSIAMSVNGQSHSLDVSTSIGNGSLEMAVTGEPAAEQ |
| RRRRRTRINITY\_DN101993\_c0\_g1::TRINITY\_DN101993\_c0\_g1\_i1::g.134716::m.134716 | NA | NA | 14.8 | SSLSKKVKKATPLVT**EGVAAAPVASAPT**SVASATIEGGAVLHEMEAAASTKMFDIREEKTYAMKFRPDLLTAMDLLKETTDDDYKESLYKIIGEKITKTLPSDDEQSKLIEHKFIHLVPKVYSVSVYN |
| RRRRRTRINITY\_DN99536\_c0\_g1::TRINITY\_DN99536\_c0\_g1\_i1::g.27938::m.27938 | NA | NA | 8.4 | FLVCVVAHLVVNFLHYSAATLESFLYNMRFTLVTLPRYSKHSREEAMPTGWFDNLFLNRLPTSPRLDKNDLIASVDDFVFGCSLSNWYCG**VVLGTLLLI**EKWSVVAM |
| RRRRRTRINITY\_DN55782\_c1\_g2::TRINITY\_DN55782\_c1\_g2\_i2::g.20017::m.20017 | NA | NA | 16.4 | SPSSSSSSSSQPLFISRDYTGASPISTVRPPSEVRKRRMTPTVSGPRSKSDRLRLTSSDGAVPPHLQLQHREEVLRKILQDRESLREQLRGLQLDDCRPERRRCREERERLENELAVIRAQLHTQASSYESVLSQMEKKHERRIKEVEERRKDEEREKKKEEDEEEEKVDEEKREEWHKQSEELKEMEVRLKEVEEKLRQAEEELQADRKKRLEVTEEEKEETEVNKQISKEKLQKKLTANERQLELMACRSEDLQREFVQNQNQQKLDQQLAMMQTHAQLQAQLDEIQQMHRQTMQRSWETHQQTLEARQKDLELHHMTLLRNRESLVDEKAKKELTQLAMTHSHREEALSQSQPEQLLDRLKKNIEKTEQVEKRLRDIEPNGHCDDGQCAKKEEVEDLQGQLESMQTQMEQERNQWRQESEAVAANMEIRFEARLRDECEARIRDETHRQSQELLSRETNLRSQELVKEELRHKDARLSAIERQQRDWQKEADEQVRALRSRTQHLEEELRSCHPGCSAAAEPAAKDKKEQQQIASELRCIENTADKLKTRLEEREKELENRLEEGARREEELRTCVEQNTKKESSLAEQVSHLEAAHRRMVEEIAKRVQEKLRKRDEEAKEVLRKKEEELKQQVNAREAEVQEINKDLQSRVRVREVELEKRQRELEEEKERRLREKIEEVEKHLGEKEEERERRLTNRDKEFQDRERQLSEREKDIEKQLKDREDDAHKQIRRLEETQARVMESRLSSLAEAHQRIQRAHDSNRGSSQLELERNRSQLRSAQSRLEEVESCVCVECGGRNLLEEARSQLEDEQLLLREKAVALEEEARKAVGEAESVRRRDLELEEELDQIREQLKVTNRKSEALRELHSEVEAEARKVRERLASHMGKKEEEEREEWRQREERWEAEMKKRVDENEESLNNVKQEWQEREEKVAQRKREEARDREEKLAKVELLLAKVRELDKREETQKEEEDKKNDKDERQREEEKREKDEDAAKQLEDCKADLTQIQEKAKELEMSLRLSEEQTASNQARAEQLEEEAAQLREEFRKRLEVETEREREEALIRFCEFDAQVQAGVRQQEDLSVQLELLRTRLVTGEGEHCTDMLIRHLEEHHAQSLALLAAEQEENKMNLSYIVKTLQAIKKCMKSHMQYDYLEQEINPF**EAATGNVSSGPG**PPQAAKGAGSAMIFGGGGGGGGGW |
| RRRRRTRINITY\_DN52665\_c1\_g2::TRINITY\_DN52665\_c1\_g2\_i1::g.110264::m.110264 | NA | NA | 12.3 | RGVPPHCECAQRIACLMIEVLATEQRDTLAEEGAMPEDLLLSIMTEWDKLLESACEWLSDVLYAGHEHLESELFFFVTTKILSGNLSQRGRRPLGEEEPGRHSFLKKFLFEGASVAIPRHASYVLHYVSECDEATLVEDSSQLVLTLLKVAQVAVDYEKDLTMSVIRDKFRSTFLELRTCLERNYFLGQLATLCKLRVEGQKDHMTWGVYKLYSDNLFADSYLKMWVGIEEICIARIEAIADRYRHVFVGKFIANMMNEIEDQNEQLEKRKQLLLELRDNARKPVAKNREAEYQRQTNDMNISLNLAVNVLATMLKMAALTSTHRFARVQSDSLGTLLSIVTDMMYEDYIISYQCQRVLVSIFECFSSKFKKWQPGAITLPYDGSDEDFEETMRRIIESNQMNRFMEGSVVGKCGSCQIFFNILDLLAVDRDHKYSEIWDDVVSQMASRGLKVVEFLMMNEMGNEQHHGNLRGAGKG |
| RRRRRTRINITY\_DN42608\_c0\_g2::TRINITY\_DN42608\_c0\_g2\_i1::g.82791::m.82791 | NA | NA | 14.8 | KWNFTRGVLEFFKKNPEHFFQYLKQLIAPAVHPHARGKSDHLCRERGHDRLCYFGKTKNFYFNSANIQPELKLFREVKKMEPFPDRILEDGDVVHISELPFYQLWNQMHMYYLSRNLAKYGLNIEGDKVLISEIPQYRKHKQLRNYFVQTYDSLVRETPDRLILLLKIDPNMQHIRKPVKSATFYAPTKEVTLQDPYAYPMQSLYWPLGKTFHSEWDFFHVENQAAAVSSHL**SLMEILARTGG**KRVGIIIIQPLQQLTGNPHTTTGNDTPSSTPPSPPGEEVMPRSPIPPSQIAFLLLGLLLAAM |
| TRINITY\_DN37519\_c0\_g1::TRINITY\_DN37519\_c0\_g1\_i1::g.127159::m.127159 | gi|348527560|ref|XP\_003451287.1| | PREDICTED: metaxin-1-like [Oreochromis niloticus] | 13.7 | LFRGEGFTSGRKMAAPDELFCWEGDWGLPSVSTDCLVVLAYAQFAGAPLKLRKICNPWRSPSGALPALRTNQKETLSRVSDIIIHLRKQKYNADYDLSAKEGADSLAFISLMEEKLVPALIYTFWVEPKNYVEVTRRWFAEHMPFPLNLFLPGRMRGVQLEKLRLLRGDEGLEAGDELEKELYR**DAAECMNLL**SQRLGSHKFFFGDSPSSLDAYVFGHLAPVLRSKLPNMKLQQHLKSLENLNLFCSNILQLYFPRDGRESGG |
| RRRRRTRINITY\_DN112831\_c0\_g1::TRINITY\_DN112831\_c0\_g1\_i1::g.140067::m.140067 | NA | NA | 22.2 | QKS**QTYCSILY**KEWDSDQKRMQLQVTSRKVLGINKLKNHKAHGNQALRLSLSAGRRMAGLKGKELFLEVTVKSGQPYLRAYLTRNHVMAKFWGVAEESWDRGNVPTVNALSVQVAQLPLAAMDPTLEKINLLSLCATGGHDLMRVEVKISTEREADTSNNDGSVGCIKTVQARCWQEHQPFWGMVQTGIDPICNQEAYSCSAKWRDTVLAQLKTHS |
| TRINITY\_DN91867\_c0\_g1::TRINITY\_DN91867\_c0\_g1\_i1::g.95589::m.95589 | NA | NA | 8.9 | MSVRRLGCCFKSDLKNEWKTIFGLPHFPFETTFRLIEFSNSFNCLETSRATLKSQIFQFYVIV**DRRVGLSSF**FHFYTSSLSFVVIQIFIKLLKQTKSLPEI |
| TRINITY\_DN23576\_c0\_g1::TRINITY\_DN23576\_c0\_g1\_i1::g.68493::m.68493 | NA | NA | 10 | MLPGDQTWLLGKRLKMCPPPDRDHRFPSLFPLWSGHESPEFLQKTPHWALEDRGSH**FRHTLAVYPLE**SGHLEHLGWENLCPSAQHIWGYACSRSRAHNSHSESPSDCHES |
| TRINITY\_DN56777\_c0\_g3::TRINITY\_DN56777\_c0\_g3\_i3::g.108931::m.108931 | gi|1012854798|gb|JAR72817.1| | Nebulin [Fundulus heteroclitus] | 62.6 | MTTVVEEYVEYEEEEEEEGEEIVQESGLPTRKVRKKVKVDTSKFMTPYLAHSQKMLDQFSHNKYRHAYDMSRGQPPAITTESPEMIRIRKAQEQLSEVKYRMEGNKARTGSMYDGEAREIAHVKHVSELISKVLYRQKWDETKDRYLLPPDAPELVLAVKNAANYSKKLYTEAWDEEKTMCYPYSDSPELRRVAKAQEVLSDIIYKKGHHERKAKYTSLADPPEVELARKVDKQRSDLKYKEDYNKNVRGQWCETPYFDVATARVAMDNLSNRKYTQHHEDTKDQIYFMQTTTPVYDANKKARIAASEVQYKKEYEKSKAQCDYNTLPATENPLLRQLRYAGTILSDKVYKANYEKSRGSSINYCDTPKFQMDSVLKQFSDAHYKEKYDNEVKGHYIGSYEDVYMLHCQKVEEMKSEQAYKADYEDIKTRCFYPQTITPEYEVSKKLQQCNDKVYRQHPDKVKFTQVVDSPVQVQAAINAKQLSDLNYKAKYEEIKFKNTLPPDYPFFIQSRVNAFNLSDNCYKYDWEKDKDKKFEVKGDAISILAARAHTNIASDVKYKKEYEKNKGQMVGALSINDDPKIMHSVHVAKIQSSREYKKDYEKIKTKYHTPLDMLSVTTAKKSQAIASMAGYRSISNKFFLPYDSVLLDLAKKANIIQSDNEYKSDYNNLTKGTPWVPFGSIEVEKAKKAGEILSERKYRQHPDTVPFTPIADHPVMMQAKVNQLQRSDLFYKRGLEEVLQKYSLPPDAPEFLQARCNSYNVSEKNYKLAWQELIAKGYDLQPDAISVKAAKAARHAASDVQYKKAYEKDKGHHVGFR**SLQDDPLLVH**YMQVAKLQSDKNYKKDYHKAKLKYHSPVDMMSMTHAKHASAVQTYAGYKKIPHNYF**LLPDNLH**LQLCRNMNTNASDFNYKQDYENSVKGSGWIPIGSLDVERAKTAAAALDETKYRQHPDTIKFTSVTDSMNMELAKANAKIMNMKEYKASGEKFVHTYHLPPDVPELMQARYNAVNISQNYYTYAHRQDILKGHHVKEDAISIVAAKSSRDIASNYRYKLAYEKAKGHHVGFR**SLQDDPLLVH**YMEVAKLQSDKNYKKDYHKAKLKYHSPVDMMSMTHAKHASAVQTYAGYRKIPHNY**FLLPDNMH**LQLCRNMMEIQSDNHYKSDYDACVKGSGWVPIGSIDVELAKAAKAALDETNYRQHPSTLKFTSKSDSMNMALALANSKTLDHAAYKASGEKFVHTYNLPADCPEFLQAKFNAQTLSESHYKQKWLEDIAKGYDMKPDAISILHAKHGRHIASDVQYKKAYEKDKGHHVGFR**SLQDDPLLVH**YMQVAKLQSDKNYKKDYHKAKLKYHTPVDMMSVVQAKHASTVQTYAGYRKIPHNYF**LLPDNLH**LQQCRNMNTIASDCDYKSDWNNCVRGLGWVPMGSIGVETAKLGGDILSEHKYRTHPSNFKYSKLMDSMDLTLATANNKIMNKQAYTSAWDKDKLTVHIMPDAP |
| TRINITY\_DN58414\_c0\_g1::TRINITY\_DN58414\_c0\_g1\_i3::g.45922::m.45922 | gi|958219378|gb|JAO26969.1| | ACON, partial [Poeciliopsis prolifica] | 14.8 | YNCVTSPPSSTSLSVNKMATYCLTVARLQLALGHGARRLHVSAAYRAK**AQVSMSRFEPTS**FVNYQKLQSNVDIVRKRLSRPLTLSEKIVYGHLDDPHNQDIDRGRTYLRLRPDRVAMQDATAQMAMLQFISSGLPKVAVPSTIHCDHLIEAQTGGVKDLARAKDINQEVYNFLASAGAKYGVGFWKPGSGIIHQIILENYAYPGVMLIGTDSHTPNGGGLGAICIGVGGADAVDVMAGIPWELKCPKVIGVKLTGSLSGWTSPKDVILKVAGILTVKGGTGAIVEYHGPGVDSISCTGMATICNMGAEIGATTSVFPYNHRMKTYLEKTGRGQIALLADAYSDLLVPDKGCEYDELIELNLDELKPHINGPFTPDLAHPVADVGAVAEKSGWPLEVKVGLIGSCTNSSYEDMGRAASLAKQALDKGLKCKAQFTVTPGSEQIRATIERDGYAKILSDVGGVVLANACGPCIGQWDRKDVKKGEKNTIVTSFNRNFTARNDANPATHAFVTSPEIVTAMALAGTLNFNPETDFLTAPNGDKFKLEPPTGDELPSRDFDPGQDTYQHPPTEGGSVKVDVSPSSNRLQLLEPFDKWNGKDLENMRVLIKVKGKCTTDHISAAGPWLKFRGHLDNISNNLLIGAVNIENDAVNKVKNQLTGEYGGVPDVARDYKAKGVNWVVVGDENYGEGSSREHAALEPRHLGGRAIIVKSFARIHETNLKKQGLLPLTFADPADYDKIRPDDKISITGLNSLGPGKPLTAVIQHSDGSQQSISLNHTFNETQIEWFQAGSALNRMKQLQH |
| RRRRRTRINITY\_DN33412\_c0\_g1::TRINITY\_DN33412\_c0\_g1\_i3::g.51737::m.51737 | NA | NA | 13.8 | LHFTKALAKLEPAPLLDLAEELDGLDKETELFGNKVLEQAVPELDSSIEEYDLKNVQLWKLKRQFLRVYLKQGMVSLREFAHVPSMDDQNFLARDDENELVAQLVTRFNRLYYPLRPPHFGEVTQEGGTQQAGFEPLSDSNIVAD**SIESIEESSL**LPDGSSTSPIETERQEAVATEAVTKNKSSSLEVPERSEEFKAKKRFGATKGTSPTQKKRKALKSSTPRLTPADVRLLTEPKQTKQKLDRGKESNLLDAVAAPTEAETATLDIVTVSDTKNESSEILVNEKQSSSLTEPPDTEKEPLEPAHKGDTQTRECPKHYKRSLKSSLSGLDITRVVTKSHIERPAPPQQNNNKKFYPSTKTEKVDEEKRRDREPSKTPDKRPSLQISPVVSNSASAASSDGREFNQCQLDIHENIKFKPVLHGCLPCALKSPPQSSFFSSIPTVTAASASMGATVSGKKKSKSLSLSRRPKGTDDRQTM |
| RRRRRTRINITY\_DN47660\_c0\_g1::TRINITY\_DN47660\_c0\_g1\_i1::g.12525::m.12525 | NA | NA | 37.1 | FVRARNCISNHSDLFLDAAFIWRGFMDTLVSLPIFSGPLTFRHAAATLVLASTFVGADTGFSLTEMVVLDAAGRTGAVVATLAALLLSVR**VHTLAVHAVP**QRRVPHGTLIHVLALLLIQASTLTLLTNVGRPLMLTVASM |
| TRINITY\_DN76281\_c0\_g1::TRINITY\_DN76281\_c0\_g1\_i1::g.94487::m.94487 | gi|808866658|gb|KKF17335.1| | Cysteine-rich motor neuron 1 protein, partial [Larimichthys crocea] | 17.5 | WHDGCRDCYCHSGREMCVLISCPVPSCSHPLVRPDQCCPTCEDESGSGQPEGMDMVVCRAPGGE**FYVEGET**WNLDECTRCTCRKGRVLCDTEVCPPALCQTPIRNKDTCCHICQEETLSPLLPVNTSQQEYCITSDGDVLLAGDSWKAN |
| TRINITY\_DN55676\_c0\_g1::TRINITY\_DN55676\_c0\_g1\_i1::g.19098::m.19098 | NA | NA | 28 | LLFCGSCVRPRIATAATNGSGCKLRCPGCLH**PSKPQFFSTDSVR**WRPKHAPRSPSTSSKPTCLQKSIQSKVSRSPARARSCSAGVFRRSRSYRLCHKHRN |
| RRRRRTRINITY\_DN44675\_c0\_g2::TRINITY\_DN44675\_c0\_g2\_i1::g.10722::m.10722 | NA | NA | 18.3 | RQAAGPRLLPAAAGAVPSGPLLLLLLLFLRLVDGPPLGLVGHHLNSVGPHDAEGCSDDGEDQGLPLHVFVSQLLELDSLPHFIRVFAVI**FAAAVVAVCLPG**VHVLLPQPHSYHSA |
| RRRRRTRINITY\_DN51685\_c0\_g1::TRINITY\_DN51685\_c0\_g1\_i1::g.38236::m.38236 | NA | NA | 17 | VQGDQIRVRADGRVGPLVGVHALSGCPHLRTFLTAAFAVALALSH**AGLFLLPL**GYGGGAVEQLGLLMLFLASDMGRRMIFVSSAVAGEGAQGVTGNGAMHGGGGMM |
| RRRRRTRINITY\_DN30597\_c0\_g3::TRINITY\_DN30597\_c0\_g3\_i1::g.118032::m.118032 | NA | NA | 14 | SPISSPPRPAALQVLKMDAVTFFSSSVMTASCMLSSLRPSMSESLPIFSPASLFLPLS**ASLSSWPEAS**PQLSAPGREGRGGGEPRSGGGGGGASRSGGEEEEQEEEDEDDEFFVLNRGGGSLFVGSEMS |
| TRINITY\_DN56105\_c0\_g1::TRINITY\_DN56105\_c0\_g1\_i2::g.121309::m.121309 | gi|583989866|ref|XP\_006790134.1| | PREDICTED: PDZ and LIM domain protein 5-like [Neolamprologus brichardi] | 42.2 | RLQGGKDFNMPLTLSRLTDGGKATKAGMAVGDMVLSIDGIATDGMNHLEAQNKIKSCTDNLTLTLQKASSVPKPPPVAPKTAAHHQVTKVPRKHVVETDIHFYHVPTHADASRKRIMEDTEDWRPRTGTTQSRSFKILAQITGTENAQEEEAEKAKKTKVNKTTTRMVIGPKYNELRDSHHRVS**ARTLNVVQ** |
| TRINITY\_DN46814\_c0\_g1::TRINITY\_DN46814\_c0\_g1\_i1::g.12144::m.12144 | gi|734611888|ref|XP\_010733370.1| | PREDICTED: peroxisome proliferator-activated receptor gamma coactivator-related protein 1-like [Larimichthys crocea] | 11.1 | SRSESLDVDPRLHSTAHFESIQQESSAASPQRPASPSSSSSPTTEPKPPVS**LANQTHTAPLQ**EINKKFTEIASDVSRRPPALCPPSTRPEPASGCSRPPPQQHTTSPTTGTQLEPRALQSPGPDPARHVKCPSSTPRSAQTPPAPDAHVALKEEVAPRSISSPQEPPSPLQVGCGGQRAASDSGIEAPDLTSLLEQFEETQAKEERVDDNDSTAAPPSNVEVPGNCVGSEKTSGSPPTPSVGPVKPVGVPEARPQLQTSEPVDIPEPLATEIVLSTPARRKPPPSKAIQIIDPRPLPPKKTHIGLSEPPAAHSSPHMYSAVSCDHDYCAPVDQSLTRVKPSLPKDSPKPTNDLQATAVDSSAAAAPAARTTQSASQHQSEKPRTNLPADTDRALQFSGRSVAMGDAGAGEAETAPCSLPTPPPSPVRGRQKRRYRRRSPRSDSSSSCSSSSSSSSSSSSSSSSSSASRSPKRQKLHRRRSESSSCSSS |
| TRINITY\_DN7657\_c0\_g1::TRINITY\_DN7657\_c0\_g1\_i1::g.52125::m.52125 | gi|657793852|ref|XP\_008323851.1| | PREDICTED: tyrosine-protein phosphatase non-receptor type 11 isoform X1 [Cynoglossus semilaevis] | 11.3 | PEPEPKPSAAKPRKSYIATQGCLQNTVSDFWRMVFQENSRVIVMTTKEVERGKSKCVKYWPDVSALKEYGAMRVRNVRETAAHDYILRELKLSKVGQGNTERTVWQYHFRAWPDHGVPTDPGGVLDFLEEVNLKQESILEAGPIAVHCSAGI**GRTGTFIVIDILI**DVIREKGVDCDIDVPKTIQMVRSQRSGMVQTEAQYRFIYMAVQHYIETLQRRIEEEQ |
| TRINITY\_DN30026\_c0\_g2::TRINITY\_DN30026\_c0\_g2\_i1::g.6026::m.6026 | NA | NA | 18 | PLSAHPLLPPTRQPFCSQCPFFCFVFPC**GVCPLSTYV**DASFDIYPTLVKPRQTFSSPITMAKVTFGTDERASVVNKRPGRRTLLQAISVQSINFQDVRQK |
| RRRRRTRINITY\_DN44142\_c1\_g1::TRINITY\_DN44142\_c1\_g1\_i2::g.79405::m.79405 | NA | NA | 16.9 | HN**AAASTPRPLN**QETIPQVRFRRSQLEAASFEEWWCSCTIRILPNLSSSASSSGQSAGHSRFASPWHFRPLMLFPLQQHFHHGSSPDTGIRCCPLIVRIPLVLHDHKRQQHSARFFSLCHRGAM |
| TRINITY\_DN50163\_c0\_g1::TRINITY\_DN50163\_c0\_g1\_i1::g.57559::m.57559 | NA | NA | 8.5 | PPFPSPLPQPWLWENE**ISATSDKDAEL**CNNDSRTNTRRWGADGRARSGRGEIRVRSHPTDHSALLCSPQLTHSHSSSPGTLLHHHTDRTRYPPRAKKAACVCVNCPPNTHTHTVAYISILAARLGWLSP |
| TRINITY\_DN49475\_c0\_g2::TRINITY\_DN49475\_c0\_g2\_i1::g.76360::m.76360 | NA | NA | 9.8 | IRFRPWSK**LASADSKLLAT**TRMKPQRPWLWSGGIVRVSGMAVQRRCTVGQVPPGNSALDVCPWMCLAPLYSGPGSKAMSLLCGVNELTSLTVTGSSDVACRTNKTSITIRLG |
| TRINITY\_DN50542\_c0\_g8::TRINITY\_DN50542\_c0\_g8\_i2::g.57896::m.57896 | NA | NA | 63.3 | RGEGRPAAAQRAHLAAHAAGAAAHAAERHRADDQRQLQDQLLTAGDVQVDHEGVVHLDDVTAHQRGLQSGDADHLPLPHVAHPRDDVVPSDRRQLLAQHLGAAVGHVAVLGDDGGLGHH**DPGAGVLEL**GVDVDVLALAEALPVDLSADGHLAVRDEQT |
| TRINITY\_DN54679\_c1\_g2::TRINITY\_DN54679\_c1\_g2\_i7::g.18160::m.18160 | gi|734624466|ref|XP\_010740284.1| | PREDICTED: transcription factor SOX-6-like [Larimichthys crocea] | 7.6 | MMSSMRATPPFHPPSEEEEAISQDNAAWAKEEREREGPKETASPSSHDQPHPDELQPVRDKLKDIEWDIVGPAAMDNESSKGCSVYSYRTNSTSPHKPEECSRDRGEPMIGLTFGTPERRKGSLADVVDTLKQKKLVELTKTEQDEPSCMERLLSKDWKEHVDRLNANELLGEVKGTPESLEEKERQLSTMIGQLINLREQLLAAHDEQKKMAASQLEKQRQQMELARQQQEQIARQQQQLLQQQQKINILQQQIQVQGHMPPLMIPVFPHDQRSLAAAAAAQQGFLFPPGMSYKPAGENYPMQFIPSTMAAAAASGLSPLQLQQLYAAQLASMQISPGAKMAPLPQAPNSSDPLSPSALKSEKR**ACSPVAQIK**EEGSTQPLNLSARPKTAEALHSPTSPTHSLFSGNKTSPSGMGKGRIPSPLPSLGRNTSLDILSSLNSTALFGDQDAVMKAIQEARSMREQIQREQLHQQQQSGHHSLEAKLSALSGMTLNNGNKERLHYETLSQHLGKLGEDAGKMVHRVIDLTRPEDLDGNNITEARVFREARGRNNNEPHIKRPMNAFMVWAKDERRKILQTFPDMHNSNISKILGSRWKSMTNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKRTCIIDGKKLRIGEYKQMMRSRRQEMRQFFVGPQPPIPLGSSPGGVGVYPGAITMATTATPSPHLTSDCSSNSASPEPATAVIQSTYGVKTEP |
| TRINITY\_DN114298\_c0\_g1::TRINITY\_DN114298\_c0\_g1\_i1::g.141192::m.141192 | gi|657800553|ref|XP\_008327408.1| | PREDICTED: periplakin [Cynoglossus semilaevis] | 18.2 | VIKYKTDPATERELERLRNEIVDKSHQTEKSEMEIRQLRDDIQRWKDTKPQVQTKEVVNEVLQYREDPKTKEEVEVLKRKLADEQKKRLDLERDRSSQEEKIRVRKIDLSQVREKIVQQEVVKMEEDPLLRSECDTF**SLNISTEQRNRD**GLKTELSQLQRQKADLDLQLEELERERRSRRDAELEIQRLRVRLSELEIRDKDNREKVTVKQKVVLQQDPQQEKEHSILRLQLDEEKHKRTLLEKELSALVQQQHALERMDVKERVVRTEKVQVERDPEAEIEIENLRRTLEEEKRR |
| RRRRRTRINITY\_DN53829\_c0\_g1::TRINITY\_DN53829\_c0\_g1\_i1::g.16745::m.16745 | NA | NA | 16.1 | LNCAVGALACFVGEYTACFLAHAVVLGLEAHLEWDRPLHVQPRVFVARPFGAEEVPDVGAELPVFVVLRMVVEVVRRGLDDLSVLEVDEVWVQDVFAGGRLIEELGTGVVLVKTNQPEVGARGVLVDGELDHVPLPLVRVSVTEATLKGVPDELQPEVELSVAVPSLLGRELISWSGRQQTKLWVCHITKTTCDNKYQNT**GAVILILN**NCSWIQVTTQFIFQLATQFNCM |
| TRINITY\_DN48163\_c0\_g1::TRINITY\_DN48163\_c0\_g1\_i1::g.13080::m.13080 | NA | NA | 20.8 | SILSDGTDRSAISSSNSSSSRSSSSLSSSSSSSSSSSPSFSAA**LSLAGFSLLAW**LCAFFLLLSLRCWTNFIRSAGSVMILKLNFSSSPSSMTSLSVSESSP |
| RRRRRTRINITY\_DN53574\_c0\_g2::TRINITY\_DN53574\_c0\_g2\_i2::g.39036::m.39036 | NA | NA | 4.7 | LYIVFGPLKGVPGSHTGADHISSGINALLDPIQLSAAMQQHGCRASQHVHHLPALNSQVVAVVQDQILCITHQVHAEFRLDSADHFLVGHWMFANPLSHHETSGEGFLDLDQGPIEQLLINEQGHAPHAGGRLVDSLLHHPHLLAVLPGEEQVQEASCALVRQSQHKHLGLFTCVGQLV**EQVSLAIGA**GTDM |
| RRRRRTRINITY\_DN42507\_c0\_g3::TRINITY\_DN42507\_c0\_g3\_i2::g.80811::m.80811 | NA | NA | 4.5 | GCTDLVAKQTSLNQRGDDHPSPFAQPSNDAQSSSIATNFPLLEAKFSLSNIIAVSFDDGSSSKNPEQVILQELMIVTCLVTYKLLRIAALQLDFRVDGKVEVDARCGTPVPSQKVLGAALRPVFDLAMLRQKLVGLLALEAGFHLVTFAGDWHLRTSNHGGPIADLMSLPQSG**HAATILDQT**PVDQAELPRQKGMEQM |
| TRINITY\_DN52412\_c0\_g1::TRINITY\_DN52412\_c0\_g1\_i1::g.38550::m.38550 | gi|734603309|ref|XP\_010728656.1| | PREDICTED: collagen alpha-3(V) chain [Larimichthys crocea] | 36.7 | MDHLVRTRSRRRISLFICILLHVTATQAADIIDVLRELEVSENMEGVSLEAGLCSSRRGTEEADLAYKIDKKIQLSAPTKQFFPDSKFPENFSLMATLRAKKGSQFFLLSVYDDQGVQQLGLEVGRSPVFLYEDQHGQPAPEMYPTFKKINLADGKWHRIAYSVQDKSVTLYLDCQKVETLDLLRGDDAVVSTEGVTVFGTRLLDEDVFEGDIQQLLILEDAQAAASYCVNYIPDCDSALPYSSHIPDLQENARLGSDALMQSDQPDEPEEAPKKDRKGKKNKKKRDKGSKGKRKGKGKGKKGSRKKKHQEEGLEDGFLRVSTKLPEYLSQEPFLTTELPEIKTTKETAIPAEVLDELLMEMPTHEPDSTTEASALVPSAVPESVVTEEEDKPVKKPVVEEYEDDLYKDLYEDLSVSTVTVGPNVTEYELVQYEDYKNDTEYEEYEAYTDGFD**FAERDRAET**WDGQGSVRGEKGQKGEPAIIEPDSLAAGPPGLPGPEGLTGPAGPTGPPGPRGDPGELGPPGRPGLAGVDGIPGPPGTLLMLPFQYGGDSQKGPVVSPQEAQAQAILQQAQLSMKGPPGPMGLTGRPGPLGIPGPSGLKGDSGVSGHSGPRGLPGPPGINGKPGKRGRAGVDGGRGAPGETGTKGDRGFDGLPGLPGNKGHRGDRGKPGPHGPVGESGEKGSDGPVGPRGQPGEPGTRGLVGPRGPPGPPGQPGIQGTDGAQGQKGNLGPAGEIGPPGQQGNPGVQGLPGPQGPIGLPGEKGPQGKQGMLGLPGIDGPPGHPGREGPPGEKGIQGLLGAQGPVGYPGTRGVKGADGVRGLKGSKGEKGEDGFPGFKGDMGIKGDRGDNGAPGGRGEDGPEGAKGQGGLIGDAGPLGIAGEKGKLGVPGLPGYPGRQGSKGSLGFPGMAGAPGEKGRRGPAGQQGPVGQRGPNGARGGRGVNGPGGKPGEKGSSGQDGPPGSPGEQGPGGAQGRHGEPGPRGPNGQPGKDGIPGHPGQRGEPGFQGKNGLPGPTGVVGPQGKSGETGPTGDRGHPGSPGPPGEHGLPGVAGKEGAKGDPGPPGASGKSGPAGLQGFRGSRGTPGAMGPAGLKGGEGLPGVAGAIGATGERGPSGSAGAIGQPGRPGGVGPAGPMGEKGEPGEKGPVGPAGHDGEMG |
| RRRRRTRINITY\_DN58155\_c0\_g3::TRINITY\_DN58155\_c0\_g3\_i1::g.22324::m.22324 | NA | NA | 12.9 | KSLGEEEEKPVSSPLDPQSPTKDKKGRSLGWRDWRSRRDGESAKESHVSSASEISEKSAAAGTQKALQNEPIGMGKLGRGESQSHRHRTFLPTRKGETDEKREESQSRIKTSIEAVKNEFKHRMALVPSDAVKKSEKQVLEKQSGGVDKEKREESQTRIKASIGAVKSEFKRRMASVSSEDAKRQEREEPQKPTTTDLSKSRGIAWSVRKSAAPEQQKEEKGKEGKKDVSTSRKNRLSLRGIIGFGTEKDEGRLDQVSKSKEQLGKSVVELPAGRAGPRYVEESGEGAKRSLVPSKEESKNRTLKRLGRTLSSERKKFRAEFVEESDIDKIDTRLVPQRPAAPLDPNSSTSVSAPSRDATAVKAFVAPHQPLTPSDTGKTQAKDSSKVPGSAAQIVRSTKAAERKVDKENIHLQQHEKREEEEDDEEIVIIPTIVSPSRSESEVTDTQTKTRKEKDEHVKVNNQKQQQDVGPTPLVFSTRKTPSTSTSEMTTQETLASMSTAEQLKKGEMSESGVSPIELPAGFRRHLPMPESDGQTFSASKRFVKTKPTDEGPSDSSAARTMTPPGARSRRLNRDLSGTQREDEMGLTEFLPGRLGSMKKDMSGGRLLRQRMLELKLAYDEQSLKAAGPSPSRNPLEMSVAKKLSKSSTESAEAGKGEEPDIHLLLASDASSGRRMTARRAKTESEDAEVSSGKKLPVRKTKEAKEGSPTEEENESRKGAGEGEGTGAVETNKRTGDALVGPWGPGDEDGPIENLSVRSGSFVMSLPMPIFPLEDVDADSDSSSSLQPSGEKLHRAVAISVHSSSDN**LLEPISR**MIMKAKYSILSRQWRRRSLVQKLMATSISKNTPSKFWPHRLCEVASPRLRDVVLLKIVFGKAEKCLDAFMSEEFAVNYNRINLATARDNEGAFPSVGTLCLYTIVGVPWIDTATSVPTQNVIEPAVYEPTGYKCYYGESTELRVANGFDCIRIQDSGPSAMLINEPKIDLHAINKQHLYRLGELVQQISCRIELEMATTKKAMRELFEEHCLETILVVVDKKEFADHFYLVRENDLESLLEMERLALAKRKGRASTFKAAFEAKGKKEKVRKVYSFAGRGIEKHIDYYDTLRRMKRLITGEDEMPEPAEKRETHVTLEAKCSNSGALNKATCTYVGSHEPRANLVVLSYEPDDYVFTFHSSESLLVDDKYWLIDPDPKGEVVVALRCTESIHVDVDEMITEFKPPVALALQLTCLDSGFQNSATVVLQGIDTGRIRQLKLTHQDDDPMSMECTG |
| TRINITY\_DN52552\_c0\_g1::TRINITY\_DN52552\_c0\_g1\_i2::g.58836::m.58836 | gi|734633780|ref|XP\_010745392.1| | PREDICTED: signal transducer and activator of transcription 2 isoform X2 [Larimichthys crocea] | 15.2 | MAQWEKLCQLPTVYGQQLHELYDRDALPMDVRHYLSAWIEKQEWQRAARDHDLAVVLLQVLLENLDIQHSRFVQEESFLMQHNIRRYKQNFQRYLEEPCALASTILWFLEKENEILQSADLAEQVQFLQVQQETMETSSQQDLERKMAGLRNEVQCMEHTIICLEEQQDEFDFKYQTHKMEAVADEATKRDQVKVLQQLVNRLNDCRKRTLSDLTKLLDRAEDLIGTLVQKELVEWQRRQQKACIGAPDDVGLDQLENWFSCVAVCLFQVREFISKLEELVGKVSYDNDPVKAQRPALQKRADTLLKDLLKSSFVVETQPSMPQGKGPLVLRTNVQFSVKTRLLVKFPELNHSMKVNVSMEREIPQIKGYRRFNVLGTKSKALNMAESHNGGMVADFRHLTLKEQKSGGGGKGGSDIPLTVTEELHIIVFDTVFEMKGLSVELQASSLPVVIISNSSQQQSAWASILWFNMISLDTKDIMFFAN**SPAATWPQ**FGEMLSWQFLSATKRGLNDDQLEMIAHRVFGKHQNYDACKVAWSKFSKENTPDTFWVWFDGILVMVKTFLEDLWRDGLIMGFVSKGKEKSLLKKKQRGTFLLRFSESVIGGITFSWVEITATGEPEVKTVQPFTKVDLIQIPFQEIIRNYQILEAENIPENPLLYLYPNIPKDEAFGKYYSTKTGDDNPYIKYIKTKLMFVSKENTLEAKSPMSCDMTQGEGLEPFTGLCGEAAGESGSPCCPNQLL |
| TRINITY\_DN46052\_c0\_g2::TRINITY\_DN46052\_c0\_g2\_i2::g.34840::m.34840 | gi|657578826|ref|XP\_008293302.1| | PREDICTED: asparagine synthetase domain-containing protein 1 [Stegastes partitus] | 14.4 | MCGIFCLLSRSPAHFEWDKTVHEHLRRRGPNSSQDLTVTGGSPPRYQCLFSAHVLHLRGRLTPQPVQDDAGNVLVWNGEVFGGLPVTPAENDTAVVSEKLSSCSSPSQILSVLSSIRGPWGFVYYQKAGDYLWFGRDFFGRRSLLWKPEAEVLTLTSVAAHASDSDPSAWKEVPAVGVYRIDLKTMAETSNMMLEVFPWASAGNDASSACIEPPLESLPHGCTAVMNQSGLVLTSPVCPLNMSIPASLNETEMNPNSHSSVSDLEQLLASREKDDEVKCLIEVLSEAVRRRVQSLPFEDEDSSLSNNQARVAILFSGGIDSMILAALADRHIPAHLPIDLLNVAFKLQEPKKQQESAKKKHKNKAAIDSKTTEAGSRTSGPFDVPDRITGKAGLKELRHLSPERRWN**FVEINVT**QEELQRTRQGRICHLVHPLDTVLDDSIGCAVWFAARGTGFITEDNDQRPFTSPAKVILTGIGADEQLAGYSRHRVRYKMSGHQGLIQELAMELGRISSRNLGRDDRVIGDHGKEARFPFLDEDVVSYLNSLPVWEKADLSLPRGVGEKLLLRLTAKQLGLGQSAVLPKRAMQFGSRIAKMEDSHEKASDKCTRLLTG |
| TRINITY\_DN54034\_c0\_g1::TRINITY\_DN54034\_c0\_g1\_i1::g.17270::m.17270 | gi|734608814|ref|XP\_010731681.1| | PREDICTED: dipeptidyl peptidase 9 [Larimichthys crocea] | 8.5 | MHRVKRVKLCDTKEGIWKSCVTVSMTAVDGLSHSTE**VVEMEDVP**SQYFVEKHSWEGLRDIIHCSRKYSGMIANKAPHDFQFVQKKDENGPHSHRLYYLGMPYGSRENSLLYSEIPKKIRKEALLVLSWKQMLDHFQATPHQGAYSREEELLRERKRLGAFGITSYDYHAQTGLFLFQASNSLFYCQDGGNNGFIQSAPVKPVEIKTQCSGTRMDPKVCPGDPDFIAFINNNDLWITSIKTGEERRLTYCHKGVDNVKEDPKSAGVATFVIQEEFDRFTGYWWSPSAVKDPDGGKTVYLLYEEVDETEVEIIHVPSPALEERKADAYRYPRTGSKNPQATLKLAEIKTDHQGRIVSTQDKELVVPFTSLFPGTEYIARVGWTSDGKYGWAVLLDRSQRRLQLVLLPPALFIPVTDDPAQRQESVEAVPTNTQPYIIYEETTDVWINVHDIFYPFIQTTEDEFSFIWVNESKTGFSHLYKITSLLQPGCYHWTEDYQHIEGDFKCAIKEEITLTTGEWEVLARHGSKIWVNEATKSVYFQGTRDTPLEHHLYVVSYDSPGDVVRLTKPGFSHSCSVSQNFDFFVSHYSNVSTPPCVHVYRLTSSEGDPLHMIPEFWASMMESPGCPGDYSPPEIFDFPGKSGFQLYGMVYKPHNLQPGRKHPTVLFVYGGPQVQLVNNSFKGMKYLRLNTLASLGYAVVVIDGRGSCQRGLEFEGALKNKMGQVEIEDQVEGLQYVAEKFNFVDLSRVAIHGWSYGGFLSLMGLIQRPNVFKLAIAGAPVTVWMAYDTGYTERYMDVPENNQQGYEEGSVALHVDKLPSEPNRLLILHGFLDENVHFFHTNFLVSQIIRAGKPYQLQVYPNERHSIRCPESGEHYEIMLLHFLQQYL |
| RRRRRTRINITY\_DN5241\_c0\_g1::TRINITY\_DN5241\_c0\_g1\_i1::g.77170::m.77170 | NA | NA | 14.5 | SLIKDRANQIVLQPFNEDVAEEPQPEASVGSVATASRSPCSAASLGGGGRKRPTDWKRRGPSMPGPNLRNECVNIHVPSERPINLLRSGDHILGSGSSLRTHLATYSVPTSHSLMCHSTQAPSFTSNAESVTSCVVAGASAITLVR**QRAMNALGI**RTRTRQCASIAPSNQLSKIQNLTFDLKKWLSTMVAPVEPCTEKAKAAVYENLITTLGKGFISLVCAPITGDATTHEAYEKLNPSEHIFAQSTATLGEEQLYGLVLRAVDSPLLM |
| TRINITY\_DN48713\_c0\_g1::TRINITY\_DN48713\_c0\_g1\_i2::g.37266::m.37266 | gi|734610615|ref|XP\_010732676.1| | PREDICTED: mediator of RNA polymerase II transcription subunit 8 isoform X2 [Larimichthys crocea] | 9.1 | PEVHLSRAIQSLKFFSLASISTMQQREEKQLEASVESLISRVAHVKNALHNFIYKLENEYERLTWPSVLDNFALLSGQLNTINKLLKNEKTPSFRNQVIIPLLLSPDRDEDLAKLTEQRVPVFSHEIVPDYLRTKPDPEVEEQEKLLSAEAARIGPEVAQKQIQTLNKLCSNLLEKLSNP**RDERDAET**AAMRQNKPSFNPADTNALVGAVAFGKGLSKCRPPGPVAQGPMMSGGPTLQQVTIGGGSSQQAGMGGPVPPQQQGQPGKMPSSIKTNIKSASNSMHPYNR |
| RRRRRTRINITY\_DN49611\_c0\_g1::TRINITY\_DN49611\_c0\_g1\_i4::g.101150::m.101150 | NA | NA | 16.2 | LCGGFQRRS**SLPCGSLSDL**LLALMCRKQLCLWCLRPRPLPCLLPGHLRISYSPMSSPLISSPNLTKTKTKVYSIHRLQPLSLFVFSFAFLFVCFKRFISLFFVCIVTLDMKRGQVTGNFLIGPAIELVACPEPETRLLTAGCKALHCHFFFLYTHEKGARSDDHTNM |
| RRRRRTRINITY\_DN46075\_c0\_g1::TRINITY\_DN46075\_c0\_g1\_i2::g.35014::m.35014 | NA | NA | 26.6 | **LQESGLTVLGG**AVGEAVAVETQSSSPVGVVVGTQVDVRQDWCAAWGVVLLCAVVWQGEGSVSVETGGGEWRYGAVEELSATEGQSAGQEWMQFGRKSGWLLSRPLSYFALPFPMNSCHWSWLTM |
| RRRRRTRINITY\_DN26193\_c0\_g2::TRINITY\_DN26193\_c0\_g2\_i1::g.100351::m.100351 | NA | NA | 34.3 | SLCWFLDQTLAPSFSCAQCISCLWPSGC**PSLFLGASLCVC**VCVSLPLPLPSLRSTFFVSFFYTFVSTFPFFLPLSSCTRSLSSTQMSFVVSTYWHNLLVPIFLFP |
| RRRRRTRINITY\_DN7208\_c0\_g1::TRINITY\_DN7208\_c0\_g1\_i1::g.96807::m.96807 | NA | NA | 16.9 | LSVTDSRLLLFSPSSLSFSLSLLSTLFSPSSKPLFSSLLSL**FLQPSSLFSHILSST**LFIFSASSLHCSFFCSLPHYFFFFILNFLSPHLLALLFVLHPRPPLFLFFIFPPSLFLPLSPSKPLRTFNFHSRTLIFSSSSILLFLPIPSFFSQHPLFSSPLSLSLQPFFSLFFSLFFSLFFSLFFS |
| TRINITY\_DN58750\_c0\_g2::TRINITY\_DN58750\_c0\_g2\_i1::g.92144::m.92144 | gi|808880847|gb|KKF28558.1| | Kinase D-interacting substrate [Larimichthys crocea] | 14.5 | MDTTTSLKMTSLAVQSLFSYVEEENLAAIKAHLDKFKDVDSRSDNGQTPLMVAAEQGNLEIVQELIRRGANVNLDDVDCWTALISAAKEGHIEVVRELLENNANLEHRDMGGWTAVMWASYKGCTDVAQL**LLEKGANPN**ITGQYSVYPIIWAAGRGHAEIVHLLLQYGAKVNCSDKYGTTPLIWASRKGHYECVMHLLANGADVDQEGANSMTALIVGVKGGYTEVVKELLKRNPNVNMTDKDGNTALAIAAKDGHTEIVQDLLDAGTYVNIPDRSGETVLIGAVRGGHVEIVRALLNKYADIDVRGQDGKTALYWAVEKGNATMVRDILQCNPDTESCTKEGETPLIKATKMRNIEVVELLLDRGAKVSAVDKKGDTPLHIAIRGRSRKLAELLLRNPKDGRLLYRPNKAGETPYNIDCSHQKSILTQIFGAKHLSPSESDGDMLGYDLYSSALADILSEPTMQPPICVGLYAQWGSGKSFLLKKLEDEMKTFAGQQIEPLFQFSWLVVFLTLLLCGSVAVVLGFTVDPKLAIAVSLSLLALLYIFFVLVYFGSRRERESWNWAWVISTRLARQVGYLELLLKLMFVNPPELPEQTTRALPVRFLFTDYNRLSSVGGETSMAEMIATLSDACEREFGFMATRLFRVFKNDEVQGKKWKKTCCVPSFVLFSLTLGCLITGMALLAIFKVDGKNLTVNAVLIAMASVVGLALLLNCRTWWQVADSVLNSQRKRLHSAANNLHKLKSEGFMKVLKNEVELMSKMAKTIDGFTQNQTRMAVIIDGLDACEQDKVLQMLDTVRVLFSKGPFISIFASDPHIIIKAINQNLNSVLRDSNINGHDYMRNIVHLPVFLNSRGLSTAKKLCMAAPGNGEALPVEGWHEEMDRKMSQSSLGQDQAKFGSKNALNRRDTYRRRQMQRTITRQMSFDLTKLLVTEDWFSDISPQTMRRLLNIVSITGRLLRANQIIFNWDRLASWINLTEEWPYRTSWIILFLEETDGVSDQVTLKTIYERISKNIPTTKDVEPLLEIDGDIRSFEVFLSSRTPVLAARDVETFLPCTVNLDPKLREIIADVRAAREQMHLGGVTYPTLPMQEAVPRPQPGYGHHSAACSPTGSFTGSLPPQPHSSYFSGMTGPQHPFYNRPYFPHHVYHLPRHYPHHVPPSSRSSIKPSGHPQDPNGLDVIAEDARESLPSCPSEPTMVSPAVLLSSMNTDAVCERLKQMDGIDPNMLPQYTATIKKANINGRVLSQCNLDELKKEMEMNFGDWQLFRGMVMEQRHAESQALIQDESRAVSEQGSSVHHGEPSRRSAGAQRESGAFSLNLSFEELSGAGLEEPPRHSNNTHWPVANHRTSSMSSLNSQESSNDICKLTDKQQAEYRDAYREYIAQMAQVEMSGGGGERPVQPHPGQFLQAASSEDKAAKEGADQDGRKSFTKRGSKTSDATDFPSGTDAQTLDPISEEDEKLDHSSSSRTPGTRKKGAGAYYHKLPNDEDSGPEEADNTTPLLHREDEGGAPSIGLLTKPGFLNEILLDKKESSDSGMRSSDSSSDRSLEEAEGDDALKPSPIELELEGLVKKRGLLPSSLSGLQDATVARMSICSEAPSEASLMASSPDEGWPSSGVNNLNRTASNTTLNNNTSSPSDTTTNTNTNNSQQQQQQQQQQQ |
| TRINITY\_DN53354\_c0\_g1::TRINITY\_DN53354\_c0\_g1\_i7::g.72043::m.72043 | gi|657577699|ref|XP\_008292691.1| | PREDICTED: transcription factor E2-alpha-like isoform X1 [Stegastes partitus] | 34.6 | MAAVETDKELSDLLDFSAMFEPPVSNGKNRPTTLGSSQFGGSGIDDRSGSSPWGPGGHHSPSFNQGRGYGEEGLYSQHEGMASAPIFGSGIVGKAERGPFSSFAAQPGFMPSEIPMPSPDPLSPPGLKSNSQFYSSYEGSNPRRRPAQDPIEPQPKKIRKVPPGLPSSVYAHASGEDYNRDNAGYSASKAGNVYPPPFYMQEGLHPPSDPWGSAGSMAQPGFSSMLGNSPHLNQHGPFTAINPHDRLKRQPLPLSPQNYPLHGSEVNGAHHAGFHSGSSSFGVANHTPPIAGTDTIMANRGAVPGSSGDEIGKALASIYPSDPNSNAFPPSPSTPSGSPQAVSGSGSQWTRSSGQATPSPNFEGGIQSMSKMEDRLDEAINVLQRHASVQGGPGLAEIHSLLASGLGLPPGFSSAALGLASRLPGLMSSHHEDSAGLPSSGGILHSHHGPTSGSQPEGFSGLPGSLNRSSVTDIKQEGKEDDENCSITDKSEDDRKEMKIRPRTSLDDDDEDGDEGPVEFKAEREKVRRLANNARERLRVRDINEAFKELGHMVQLHMSNEKPQTKLIILQQ**AVNIILNLEQ**QVRERNLNPKAACLKRREEEKVSSMDPQMQLGGGHHGLGGDGHNPVSHM |
| TRINITY\_DN63012\_c0\_g1::TRINITY\_DN63012\_c0\_g1\_i1::g.64465::m.64465 | NA | NA | 86.5 | MSFPAPTASLFRMRLIFKLFPNSRSAVSTPMWMKLLPVVLYGRAFIVADACLSGGIPGSAVFAVTVRL**APPATVLTVTF**AMPLGPVMPGTFPGCKRTSIPFAGV |
| TRINITY\_DN21806\_c0\_g3::TRINITY\_DN21806\_c0\_g3\_i1::g.51629::m.51629 | gi|1007788934|ref|XP\_015830866.1| | PREDICTED: small G protein signaling modulator 3 [Nothobranchius furzeri] | 20.8 | MSGTYTPAPGGPFSALTPSMWPQDILAKYHQKDSSEQPELLYDEFGFRVDLEDGEEPKSWLGTEGSPQREDPQQRLRWQAHLEFTHNHTVGDLTWELIDPVLSRSERLRSLVLGGIPHSMRPQLWMRLSGALQKKRTSEISYREIIKNSSNEESTTAKQIEKDLLRTMPTNACFCSLTSVGVPRLRRVLKGLAWLYPDIGYCQGTGMVVSCLLLFLEEEDVLWMMCALIEDLLPPSYFSSTLLGVQTDQRVLRQLIVQYLPALDRLLQEHDIELSLITLHWFLTSFAS**VVDIRLLL**RIWDLLFYQGSLVLFQITLGMLKIKEEELVTSENSASIFNTLSDLPSQLRDGPAVLGEAMRLAGTLSQDTLEAHRHKHLAYILNEQAQLNNGNNTALNTNLNKVVRRQSLRRKSTLSSLLFGEDEAEALKSKNIKQTELVAALREAIARTAEHFHCL |
| TRINITY\_DN55488\_c1\_g1::TRINITY\_DN55488\_c1\_g1\_i2::g.119369::m.119369 | gi|657581304|ref|XP\_008294660.1| | PREDICTED: glycerol-3-phosphate acyltransferase 1, mitochondrial [Stegastes partitus] | 12.4 | MEMSDGLLLQVNNGEQWCNRWKHPNDDSDRSTSPSVLRCVTSTWKEGLLNRKRPFVGRCCHSCTPQSWEKLFNPSIPSLGLRNVIYINETHTRQRGWLARRLSYVLFVMERDVNKDMFTRNVVDNVLNNSRVETAIEQVATDLDAAASQSGQEHKAVSKVKQKARAFLQEMVANISPAFIRMTGWVLLRLFNGFFWSIQIHKGQLEMVKKAATEQNVPMVFLPVHKSHIDYLLITLILFCHNIKAPHIAAGNNLSIPILSTLIRKLGGFFIRRRMEETGDGKKDVLY**RSLLHAYTEE**LLRQQQFLEVYLEGTRSRSGKPSTARAGMLSIVVDTLRTGSIPDVLVVPVGISYDRIIEGNYNSEQLGKPKKNESLWGIACGVFRMLRKNYGCVRVDFNQPFSLKEYLGTQRSRHIPPPESLEHTLMPTIISAQPDAQLFEGQEEQMNRELPEDIFRRQLINNLAKHVLFTANKSSAIMSTHIVACLLLYRHRQGVALSKLVEDFFNMKEEILSRDFDLGFSGNSEDVVMRALHLLGNCVNVTSSANRNGEFTIAPSQTVPALFELNFYSNGLFHVFISDAIIACSILSLQRELVVESESSNQSGGHSSLLLSQERLIRKAAGLSHFLINEVAVAPPCLTIYQVLHDAVTRLIQYGVLYVAEEDQEELSPSPTDEPWPKKFPEPLSWRSDEEDEDSDFGEEQRDRYLKVSVSAEHQEFFIFLQRLLSPVLEAYSGAAIFVHSLSQPMAESDYTGRLFRYLLTRTERGVAAYGESATHYLVKNTVRTFKELGVLKERRENKVTTLELSSTFLPQANRNKLLQYILGFTLL |
| TRINITY\_DN74706\_c0\_g1::TRINITY\_DN74706\_c0\_g1\_i1::g.94312::m.94312 | gi|808877379|gb|KKF25853.1| | PiggyBac transposable element-derived protein 4 [Larimichthys crocea] | 20.3 | VLCQHTNKNAERRPLTAQWKPVDTEAIMKYMSIVIYLGLVKPSAMRDLWRKDRLHSHPFPSSVMAGYRFELIG**TFLHMSD**PAADLVNDQLRGQPGYDPLCRLKPLQDQILMACKAYYHPYQNLAIDERMVASKARHGMKQYMKDKPIKWGFKLFVLADGKTGYTCNFNVYQGKAHTPSGNGLSYDAVVNLLDVPFLGTGYNVYVDNFYTSTALFLHLHQIRYGACGTIRENRLGFLNALPKTAERGDMRWLREGPLLYVKWKDTRDVTVCSSLHKAYGGDTVQRRVRNHDGSWTRRTVPVPEPVREYNKYMGGVDLSDALIKYFSVTQKT |
| TRINITY\_DN99833\_c0\_g1::TRINITY\_DN99833\_c0\_g1\_i1::g.96013::m.96013 | NA | NA | 41.7 | GANGCWLLSLAACSCSLANRCFSSRVRDILLGCEAADDAAADPFSFPLTPVLPKISSIWLTELGGLLVSSDWPPGFVMF**ILLCCSCM**TCSCSSLVLCSASMRLSMSRMTIMNELN |
| RRRRRTRINITY\_DN87172\_c0\_g1::TRINITY\_DN87172\_c0\_g1\_i1::g.26848::m.26848 | NA | NA | 30.4 | CAVSGLLMRLGRQAARMLCTFSEAGSTRSAAKSAKPVAMFTTPSFATFGKKASKSLSLSSLIFSHESFTSSGPPLFPAPPPPPPAPSLFVAA**LAGGAASAGVLDE**AGGLFVDLAAELLGDPPGGLFPLGVEAPAPFDLFPASLLSTVSVSNDVSTHSSKAAFTSGAEQRCCSSEALQFSLSALMSSNWLATSVM |
| RRRRRTRINITY\_DN57361\_c0\_g4::TRINITY\_DN57361\_c0\_g4\_i3::g.103141::m.103141 | NA | NA | 12.2 | SWETTNLRDSKVRGRCRYDGSHSSSAPSIRYEHQDPPKLSTPTEWEYTWETDGGQIECSVTITEGRYIEPWNPQLTVVARNPAINSIRISDSDESYYVPNGRGGRCRYLGGQSVSIRGSSLFVADQTTLTTYSQDGRYWSYTWDDSPNVSCTLTVSGGAPIERDDARLQAKPKSSVTKTIGESWQTSSYWDRRNRGRCKYKGSRVASTRWYNVDTQHTTSRPTTWEYWWETDGGGEIDCTLTITEGSFLQSWNPQSTLTVRNSFTIEITVESGHTYIVPDGRGGRCGYTGGQSVRIERSQDGDRRSLDEDSGSTRRRYWYYRWEAPKDVSCTLTVSDGVPITTEGALLTATPKDSVNLSVINSRKYQWHYAFCQYEGSYWTQLPLIFRKNSRYQFFGLNDKDIRYQWDTEKGEKVDCIFTVSEGTFFTSWNPELTLVVDEAHGSYLLSMLVL**ITSFFLGL**VCPSTQGM |
| RRRRRTRINITY\_DN47536\_c0\_g1::TRINITY\_DN47536\_c0\_g1\_i5::g.68992::m.68992 | NA | NA | 26.7 | VKHGGASQVFGLALEPEFHPWWGGLTPPDQPQGVGVAVAGQLLWECPHSVVQSRWGGRPGAQEAQVTRCSWQQDAGGAAPTVSAFHDAGALPEAGSEFHGAQLQGQLMRLGTQELPAEATRLKSGVMAGGESEWGALSAVGARETSLGGAAALSCSWEEVPRLEAFVPEQSH**EETLMLLAALE**PEEM |
| TRINITY\_DN87086\_c0\_g1::TRINITY\_DN87086\_c0\_g1\_i1::g.26817::m.26817 | NA | NA | 15.5 | MEVLRMLRESEEEFE**DDDSSDIDSVDS**VEEDAFEQGEDVLLDQINEDASPSCPCPVPGPSTALMQSPTIPRPPPATPPQSPSPNSQSSSPTVERPCKRAATVSTTRTPTKTPRRTPTKTPTRTPTRTPTRTPTRTPKRTPTKRPAVVPQHQDQNQ |
| TRINITY\_DN57136\_c0\_g1::TRINITY\_DN57136\_c0\_g1\_i1::g.21581::m.21581 | gi|543891010|gb|AGV76842.1| | cytochrome c oxidase subunit 5B isoform 1 [Sparus aurata] | 22.1 | ETRVMAGRLLLRAGSTTLRLRNNVALRPTYRAM**ASEKGIPTD**EEQATGLERRVMVSFKEGKDPYSIKQPKFYSGTREDPQIVPCTLDKRLVGCLCEEDNTAIVWFWLHEGKPQRCPSCGTHYKLIHHDLPH |
| TRINITY\_DN35285\_c0\_g1::TRINITY\_DN35285\_c0\_g1\_i1::g.54828::m.54828 | gi|657577590|ref|XP\_008292632.1| | PREDICTED: coiled-coil domain-containing protein 22 [Stegastes partitus] | 8.9 | VNLAAQWEKHRAPLIDEHRRLKEICGNRDMESSRKLSEIKSLHDKIRVSTEEAR**KKEEMYK**QLVTELENLPQDVSRSAYTQRILEIVSNIKKQKEEITKILSDTKELQKEINSLTGKLDRTFAVTDELIFKDAKKDESVRKSYKYLAALHENCNQLIQTIEDTGTILREIRDLEEQIETENGNKTVANLERILDDYKAIRQENSALAAKVREG |
| TRINITY\_DN3122\_c0\_g1::TRINITY\_DN3122\_c0\_g1\_i1::g.29254::m.29254 | NA | NA | 11.5 | QIICLHLLVCYEEDNYHFFYNLGFILIVLAAVSIDYNNTALHNGIVEIFVALSDLFHSQISTINLSTVSVVIDRNVGLNYVKYLKLNQSSKLLDPSRTVS**FSHVTDVH**RVLER |
| TRINITY\_DN118457\_c0\_g1::TRINITY\_DN118457\_c0\_g1\_i1::g.130681::m.130681 | NA | NA | 22.6 | FELLEVEQQEEAPLGVDGVDQVPKGALGDRGDQVRVEDLVGGAVRVVSFHQRDPVVLLGDLDELKQVIHAIVISALCDSRALTAPKHQQQKYPCQLHGA**TPTCSAACLI**KTAKEK |
| TRINITY\_DN42411\_c0\_g1::TRINITY\_DN42411\_c0\_g1\_i1::g.71640::m.71640 | gi|657558081|ref|XP\_008283134.1| | PREDICTED: phosphatidylinositol 4-kinase alpha isoform X2 [Stegastes partitus] | 14.2 | MYEQLRDISIDNICRCLKAGLTMDQVIVEAFLASLSNRLYISQENDKDAHLIPDHTIRALGHIAVALRDTPKVMEHILQILQQKFCQPPSQLDVLIIDQLGCMVITGNQYIYQEVWNLFQQISVKASSVVYSATKDYRDHGYRHCSLAVINALANIAANLQGEQLVDELMVNLLELFVQLGLEGKRASERASDKGPALKASSSAGNLGVLIPVIAVLTRRLPPIKEAKPRLQKLFRDFWLYSVVMGFAVEGSGLWPEEWYEGVCEIATKSPLLTFPSGEPLRSELQYNSALKNDTVTPAELSELRATISNLLDPSPEGSALINKLDFAMSTYLLSVYRLEYMRMLRSNDSDSFQVMFRYFEDKAIQKDKSGMMQCIICVGDKVFDVFLQMMAEKPKTKEHEEELERHAQFLLINFNHTHKRIRRVADKYLSGLAETFPHLLWSGRVLKTMLDILQTLSLSLSADIHKDQPYYDIPDTPYRITVPDTYEARESIVKDFAARCGEILKEAMKWAPSVTKSHLQEYLNKHQNWVSGLSQHTGLAMATESILHFAGYNRQSTTLGTTQLTERPACVKKDYSNFMASLNLRNRYTGEVAGMIQFSEATHSQSDLNKLMVLQMTRALDRKDPEAFTQAMFKMAALLITTKNCDPQLLHHLCWSPLKMFTEHGMETAIACWEWLLAAHNGVEVPFMREMAGAWQMTVELKMGLFSEAVVETGPLAVSEESQPAPCAPDVIPHFLWIEFLVQRFEIAKYSSADQVEIFTTILQRSLSLSVGGPKSSLNRHVAAIGPRFRLLTLGLTRLHADVVTNATIRNVLREKIYSTAFDYFST**TPKFPTQT**DKR |
| RRRRRTRINITY\_DN40086\_c0\_g4::TRINITY\_DN40086\_c0\_g4\_i1::g.125289::m.125289 | NA | NA | 18.7 | PQGSDRILFTGQ**LADSLIDHA**EEMAMPGWYYGSHQLQQYTCKVLEYEAPSSFPRLHTPWSDADAETVLQRWTEAEDRLNLKSWHLIDLQRETPEQSDAKVREPSQEPGGPEEPAESQSQTEATANQQRSQALKKELNDRVMRCHLIKKKVVQQVM |
| RRRRRTRINITY\_DN44483\_c0\_g1::TRINITY\_DN44483\_c0\_g1\_i1::g.10550::m.10550 | NA | NA | 12.9 | KIQLPQIQLIVPMGSSSAGSDASSPKEVSADKAETSSDHTPNVPTAKTESSGATSATPVTQDSYKAEPELKSESSAETSWKLGVELGLVEELGVGLGSCGERIEQKMTVVEMNEELFEEIEELTPQFGGPPEETEVNSWNLYDINEEKVPGRKAPEDRWSDCLLTSLPM**SAASGAPVSNTGGLSAQ**SLLHDLISDQSEASSNSGYSSSLVQSDPSSCSRPSSLESLDDESLPSPMVQYSGLDTVMDSLRYAAPSGGYPLFTEESVPFNDVM |
| TRINITY\_DN137400\_c0\_g1::TRINITY\_DN137400\_c0\_g1\_i1::g.137893::m.137893 | NA | NA | 14.3 | PPSSPFYNIYFFFLLNYPPSFLLSFPPFFFPLPFSPPPPLPPFFSFLPPFFLFSPPFPFPSLPSALGLCPRRFFLCLLFSSSGAGCNKSFARGLLARPARKSPLL**HSLPLSES**LLPSSS |
| TRINITY\_DN46428\_c0\_g1::TRINITY\_DN46428\_c0\_g1\_i1::g.35479::m.35479 | gi|542197803|ref|XP\_005473406.1| | PREDICTED: V-type proton ATPase 116 kDa subunit a isoform 2 [Oreochromis niloticus] | 21.5 | CISELGELGLVEFRDLNPNVNAFQRKHVNEIKKCEEMERILGYLLREIKKADISLPEGDVNPVAPLPKHVMTIMEQLQRLEVELGEVTRNKEKLQKNLLELTEYTHMLRITRNFVQRTSERETLQVQYEEFPFLEKDTMMDYNSMQRLGAKLGFISGLIQRVKIEAFERMLWRVCKGYTILSYAEVEEYLEDPDTGEPTKSVVFLISYWGEQIGQKVKKICDCYHCHLYPYPSSNEERNDVVEGLRTRIQDLHTVLHRTEDYLRQVLIKASESVYTWVIQVKKMKAIYYILNLCSFDVTNKCLIAEVWCPVNDIPNLRRALEDGSRKSGATVPSFVNRIPTNDTPPTLIRTNKFTSGFQNIVDAYGVGSYREVNPAPFTIITFPFLFAVMFGDLGHGLIMAVFAAWMVLCENNRKLKNTRNEIWNTFFEGRYIILMMGLFSIYTGLIYNDCFSKSLNIFGSGWSVKSMFKQKVWNNDVLRENRFLTLDPNVTGVFKGPYPLGIDPIWNLATNRLTFLNSYKMKMSVILGVIHMSFGVVLSTYNHLHFRKKYNLYLVFLPELLFLLCLFGYLVFMIFYKWLVFSAHNSRHAPSILIHFINMFLMQGDTIQPLYPGQTGLQVFLVVIAVLSVPVLLLGKPLYLYWLQSGRHRLGMYRGYERVRRNSEEELYLMRAHDMEEGSS**LSDLSSSGEH**QTEEFDFADEFLHQAIHTIEYCLGCISNTASYLRLWALSLAHAQLSEVLWTMVMRVGLRMDTTLGVLFLLPVFGLFAVLTVSILLVMEGLSAFLHALRLHWVEFQNKFYSGTGVKFCPFSFSLLPSSFEQDGLL |
| RRRRRTRINITY\_DN56422\_c0\_g12::TRINITY\_DN56422\_c0\_g12\_i1::g.86927::m.86927 | NA | NA | 18.3 | QEAEKEVPKPLVDESKFRLAESTHSAIIAREIFPGMDAPRHSCVDILVTQLNSLIQEKPMDLTAIKTRVFCENEVMYEHGTKFLQLMKPINTGVSGRKSKPFKKRLKNKLPVLKPLMEPVTVYFDASVEDDLIQQVLEAGGVFAAGNDQAVKVQNADETFVLVKNMETQLPHPLHVTSVFAEVRRKKELKMNLKLDVYVNQDSPTFDLLQFSKLLDLADSVDYVTRPYYRMVYVDDVPAWATRGYPKHRNTDDIVRQEKKEEKEKEQLEAAVAPVGGIGRDAEKAAMQAKVLGNKECKSKAKRDAKDKSQQEKWNSLDIILKPEYYHNVESDRWILNDLYSPSSVAKYNCTHSCQLDCYKNEHHEDGDEDPTWSREPPFLSSYDFSPEDLFKERDGDAYKRPDVQVEEEDTVDSLARPDVQVEDPDHGSHLHWDAESLQSEHYRDWTHSHSQDMLLIDDVEDEIHFPHLSVPEDLPFSYDAMYPHALAEEATLRDMPNFTLIKELFDLA**QPSVDPLL**KALPTHPKSMDNRIFVPIVSHLEQRDEERLVPISELILQMQELEHAGAFLTKGTLMEAFICGAAWMDIAKTYNNPSLLLRPSRYWKTVLGESLHGKHSYHPDMIRALGFDGIKLVLDETNVFLNAPKLDRHLVNASHIYKLGRLLQYMFLRAHGESLLGRELLQCLDTEMYEQVIYVSNVETLSVVDETLRRGNPGLTEFVKVINDHDLRRIIKIERLAHKVSQPDTLIIKKVAVRKDCDTDVASFVLGNGGYGLPKLDMYRSGLDFGHINMLSEFKEAM |
| TRINITY\_DN24534\_c0\_g2::TRINITY\_DN24534\_c0\_g2\_i1::g.54645::m.54645 | gi|657561116|ref|XP\_008284223.1| | PREDICTED: chromodomain-helicase-DNA-binding protein 8 [Stegastes partitus] | 12.2 | QLEKDKRIHQKIKRFKTKHAQMRRIFQEDEEPFNPDYMEVDRILDVSHSVDKDNGEPVIYYLVKWCSLPYEDATWELKEDVDEGKVEEFGKIQNRQPRLKRAARPASGTWKKLEETREYKNGNTLREYQLEGVNWLLFNWYNRQNCILADEMGLGKTI**QSIALLSE**VYAAGIQGPFLVIAPLSTITNWEREFSTWTHMNAIVYHGSLASRQMIQQYEMYCKDDKEHLIPGAYKFDALITTFEMVLSDCPELREISWRCVIIDEAHRLKNRNCKLLDSLKMLDLEHKVLLTGTPLQNTVEELFSLLHFLEPAQFPSETEFLRDFGDLKTEEQVQKLQAILKPMMLRRLKEDVEKNLAPKQETIIEVELTDIQKKYYRAILERNFSFLSLGANSNSNVPNLLNTMMELRKCCNHPYLINGAEEKIVAELREVYDPLAPDFHLQALIRSAGKLVLLDKLLPRLKAGGHKVLIFSQMVRCLDILEDYLINKRYLYERIDGRVRGNLRQAAIDRFSKPDSDRFVFLLCTRAGGLGINLTAADTCVIFDSDWNPQNDLQAQARCHRIGQSKAVKVYRLITRNSYEREMLDKASLKLGLDRAVLQSMSGNKESNVNGQIQQFSKKEIEDLLRKGAYAAIMDENDEGSRFCEEDIDQILQRRATTITIESEGKGSTFSKASFVASENRNDIALDDPEFWEKWAKKADIDMDTINRKNTLVIDTPRVRKQTRQYSTLRGEGGDLSDLESDDEYPPANSRQSRSSRRSDRHSGGGYGRTDCFRVEKHLLVYGWGRWKDILSHARCKRRLSERDVETICRVILVFCLLHYRGDENIKSFIW |
| TRINITY\_DN29977\_c0\_g1::TRINITY\_DN29977\_c0\_g1\_i1::g.70140::m.70140 | gi|1012781246|gb|JAR49503.1| | Thrombospondin-4, partial [Fundulus heteroclitus] | 28.2 | HLGALGTHVHQVQHRVVVKVVLTHVAHAVRVRVLLVGVDDESAVVVVVEDAVVVVVVVTVVAQAVVVRVQLGAVGDVGAVVSAVLETVAVGVLIGVTDVSHQVVVHVRLHGVTELRAAVTGVSHSVSVSVRLHRVRHLRTVVQDVGNTVPVYVLVAGVPLSVVVRVSLVA**VGDVGTVVTGVA**ERVAVRVLLVFVRDQPAVVLHVLDPVSVCVLVTLISDPVVVGVFLTRVWREHTVVLFAVLVVVQTGQRAVGVLPVVLLAVESQQHSAQ |
| RRRRRTRINITY\_DN38203\_c0\_g1::TRINITY\_DN38203\_c0\_g1\_i1::g.8029::m.8029 | NA | NA | 8.7 | TLYFARKVKEDASLDPKSRERHGGCLSSSSSSSSSSCPAAVEERQPIRFGALNLLDRIMQGKIAVDLATNSHLSPSINVELIWPKLNEDLMIDFGFLEHCSYPTKVHMKLLSNVYPESGIITKIVIDKIKEWLLTTNVGKAGLYQWLAKLAWKHGQCAKDDSNTQYESNKKNVSYNTLHMFKNGLTKMSSSYKCSAFRVLGDTFIYIRLPDYSTVYVYIRLDFKNGSILYPKHLYKQVLLPRKRPMQSWKHIVQIGIGRASAPPKIIWKQRSGGDEWAKRLLKIDQPLVFTRPFFSFEQKGYRAQMKSLNRWLRDKRGIQFTGPFHNLKQHEDLSKFGPSKMHHGWCGLWDHSKKTAKFHSRGVTHKVVNPTVPSMKWKLLRRQEVPLLEVKENATSFYLTPSIFPFLSPVLAPREERDDEAGLSMPEEVGSLLTISATSSAGNISSCDSDDDDSCANELEDPLEEEGGDVQMVCESGSAQTEGVLREETTLPSHSSNSSSSSSMSAPQGQKTLHISSIQTTVSGVSTGAPPSSVDPIIDAPAPQQQQQQSASVSASLVTPVPGSPCLSVEPPGTRRCSSL**TSEAPYQSETAQKN**VDQSAMTPAKSSTTAALVAPPGGTVQLQNNLDSIITCSNQTQCCKTAAKASQCRKTSVERATSRIEPTTSDGGPADQGLTAGRHEGPTLCLPPVSPVSCCDAAELQPM |
| RRRRRTRINITY\_DN124586\_c0\_g1::TRINITY\_DN124586\_c0\_g1\_i1::g.131171::m.131171 | NA | NA | 9.5 | ALPKVIKMSIYNPLSYLLIALFLIVITLLILVIFLCRFRRWVIFKMTKCPNTFWFFSTEPRKPPDLKPNMNPEDRGKGAPKEDVDAESVIELTMEVKGGLARQGDKEISCPWWGRVSQQAFLSKALEKKNPVGVELVDMMDLSCKDPNKAPAVLDRLDLEVTGLYDDLSFKDNDWIQVILKPPIRFESKDLSWFHEKKSVLCLQEAPLYDFEFVFRWNFNGDGDLSRYHVDTKQKDEEMGPMWGKVYIDSMNEG**TISTEDLTVD**TTNWVVARLFYKKAKRPTIDFPPGPVGISKPFVDVWMQLKGQSLNPQFSSYLTRTEVHEPVLGQKRLVHLCLRERAPGLHQHVEKNNEFQALTYDKGNFTLSNGNDETRPKSLGKLRALNELIQSPKLQDRWQNIGSICYTQPLGCYSNYRSLFRNELDIVTEGVKEDRSLLDYDCVSIKLDKDQPLFC |
| TRINITY\_DN58526\_c0\_g2::TRINITY\_DN58526\_c0\_g2\_i1::g.62059::m.62059 | NA | NA | 9 | MKVSWWALVTEPITSSSPLSDALGEDELGLVSIVTVGSGSELPSDWLERGEEEGEQEEAEPP**SSEVGSVVLAG**SGLAMGKVWLLCSWLCSWLLFIMLFIALCISSSMRCFSRLGIRPKRTESLDIPTIRHFLKRHCWQRFLLILMMGQLSFLRHFLYWMFCWMLLLKKPLQPSQAWTP |
| RRRRRTRINITY\_DN53957\_c0\_g1::TRINITY\_DN53957\_c0\_g1\_i1::g.79740::m.79740 | NA | NA | 3.9 | YRYHDPKFPGEAPLGLYKAQKDSLKTL**KVGLKDLHAA**AVQEDLKKPLFYVGLPYKSTNTWLEIQALVQNTFSNSMVFSPHGMACGLNVLRGEALIIIHRGSKMRYRDVQPKINIKEAANKTLWSMDIECDFHGINCVIADDKMNEFHHGLIIDECGTTTVFINGEKSAEDMTTVEYGEMAAQLANIPDIETVIVRAGFGRLAQVCGKGVDGYGAVVAVKGAIMVDTARKIGDILSERCGYLNDFKSKTVSDNVNIAPIKLDGKKMMKYLNHVGTTTEESVGRIGTLLKPYKQHVLNTLDGGDDLIMNLPQGDKFYITQEICWVYEEDTEGKWAYVPIGAKAIAAAAHDQTSFINCSSWQVEAGLAILTEILVATQLTMHLCGAIRAGKLPKSQGYMERMKMLGPMENEAIDIAKRGWEALSIDAVKFSLKDSM |
| TRINITY\_DN120282\_c0\_g1::TRINITY\_DN120282\_c0\_g1\_i1::g.135001::m.135001 | NA | NA | 8.1 | SGSGCVRAVCGGLYSAAGMPHYVMPCQYTLHFRTVESLHQVCLQVMLPEHSQEVQSLLSFADHCCCVGVPCQVVSHMYTTRNLK**EETLSTQTPL**SAVGRGLLSSSSSPSPSPWLFIEHHVTSSL |
| RRRRRTRINITY\_DN46169\_c0\_g1::TRINITY\_DN46169\_c0\_g1\_i1::g.77472::m.77472 | NA | NA | 25.5 | KLQLKHQSQGVWTFSNHVELSEPSTSKHRLDIIVDVHAMSCNSLTLTVPVLCLSDQVFPHTYTEPYHLNTKILQSLEASPVVVPLPVESKFKLLVMEQAEEKPTLSTAEKGITQLAVHLQGELILQKNDEVVYAKWIVIINLDLENCKKVINSIDSARDESSMSGQSKSNSTTRSSAVDVRQPESTRCCRFFFDGCPTSSSIIRENGLNLDAFTYKQVADSTAQHPKCRTARFCLKARERSTLKCDKDRSPNICKHLRWNQSSSSVQVIHFERVGSESTNINEVDIFVLTGGSGKDDLSHHPSVSSRSASAQVSLSRSACIFVTHRLVRHSIKLGKEISEYYFLFSIEHVGEQDPGRLWLPLQTSEGPQLTSGEIPIDMVSSLQSFDEASVLMESAVSGPQPMTALTKYASCSEASNPSLPTDPTTAQSGFTFFDPHTSAVRLGRLAVSSVNCFEVYAKRIEGCLLATPFQLFFVEMLPMSPTIIPDLRRDPGHRVVMKDEKTQNLRPGQIKLDQKGRVVMLSTTQQGDTGPATDGSSTEALNYVVGVINLQGTRHPLLRLRATKTEEPGMNFDLITETTVIDDKQAVGRALTEENTITEGELAEATKQNAPSAADATFRWLLSLNSLALPVKLPNRFSVEVIIPEEVVALPHRLNDTQSNLCCQTPQFTGPVTGRNAAAVLQEELHCWMTALDQDYEQDLSVHTAAQKEGEALRREHGFYVRTASSHICPLPLQPLDVENGGMVSKYVYLYERLFAAQQTATQRSDNTLIQRFAVVANEPQRLTFSQRGITFNIHDEALSWGREKYVQMAQCYCRLAHRRQGAKSFRHGALIMHFAFKRVMPNRMNIFCHAAQELLLASRLDSDESTMKILLTAADSYKAQSKLIEASLLACREALVMNKCVDRYTQIATDMYHAPYPRAAGAQLFASVAAMELAGAAYLMAQDSLFDKKATHYCSYALEYHQVLFCLDAMKRIQLEPAEPPYLLGCTSKPESISKEPGKGGGFWKKTATFLSRSLGKRSVLQDNLQRINKEIHPLLGRFTFEQIFQRIHDHDNLTLFAGHSGAGGATGEPDRTGKKMDTNVASITHLSGSGSESDLQLPHSELSNSVGDKETPHPLDVEAAGISNE**AAASNVTPDDLT**DQNQLNNRHLYQSWPDPIQEDEEPSSTRSNMKLLYCGQPGYRQKMDEYVADARQEDGESMDHLLVYYKLTNPIFWKPNTYEGSHQVRHQEQSLKLFQEVPVAETSSVVLLCALYHNLFEHESAPMTQLFNERYAEFWPTTASFNLDYDGATIVSSAA |
| RRRRRTRINITY\_DN7173\_c0\_g2::TRINITY\_DN7173\_c0\_g2\_i1::g.1539::m.1539 | NA | NA | 22.1 | RDLWCISPYRDSLTKRLQASQSKDRTEVVCEVKAKFLESKESHRRHCIDLLRVDERSLVDLLRAMDGPWEGLQVSFKSVRDDLVLARDVCQRVLELEMNASSVVVAVRKGRLEPLQGALIAALGMAGETDVTSREFEQFRLMAVLSDEESVTIVKDVLKKALQFTNIGLSHEMLDGYLKKNPNSHIDKVPNDTKLSQLLLPFGEPEVGIILTQSNLHK**IAAATGALLG**YQGAAPVVVADLKHVQEYIEMGVTGLGALYEASEDEEVYLYGNEKALHRAHNQSDRGTSGYS |
| RRRRRTRINITY\_DN58243\_c0\_g1::TRINITY\_DN58243\_c0\_g1\_i1::g.44626::m.44626 | NA | NA | 43.1 | LFCVPGIDVGFEQDPGGIDVPAIDVIPLRATKQTRYEFVTKGWNGTARSCSDEVVTYRFRSNGEAKLELDNSGKLVVAKKLNSNREDKYGVSNKCHYTITQSAEKSLLRIFTMQVTISNAPQDKNGYTFHTGRNIDAGFWVPKNRSSSWWVKRPISDPNASICTEGTDMNCHVKIADEASGQNPDVWFEGSKKMPYCRKLDDCTRAPHKRSGDPSKMSDIQSSLAKLTAQVSPDVPVITSSNSNPMAEDESFEPPPPPGSDYDQPGGGFLDDMAAIPPGPPGPPGPPGAEGPPGEPGIEGSLGRTGPPGMPGPQGVYGEKGHPGIPGPPGRPGGPGVIGPTGQEGTTGPPGPLGQLGTFGRHGKQGREGHDGLDGKDGRPGQPGVLGRKGASGPPGVPGRSGAEGRKGADGPIGVPGPTGPLGQPG**VLGEPGPDG**RAGRQGLVGDKGPPGDSGAPGDPGPDGRPGNAGPTGVPGPPGKDGSSGTTGQKGPPGAPGPLGPMGREGRQGPLGVIGRQGTTGAPGPPGDPGTPGDEGSDGKDGPSGPPGAPGREGQRGPSGHDGRLGLPGEKGPPGLPGPEGVPGTPGPPGVRGASGPFGTPGPAGQTGRGGKLGAVGVPGPPGHAGALGQPGPLGADGKQGQEGPEGKVGPQGDPGPPGSFGVAGIPGPEGRAGPVGRSGAPGAPGKPGPEGKEGSPGAPGLPGVPGPAGRAGDNGPTGESGKEGIAGRDGKPGPPGSIGREGPMGQLGPPGVDGLAGPPGPSGKPGDPGPAGPIGKPGQLGNAGLEGREGPIGREGRPGIQGVAGLEGPIGQDGPKGSEGPPGQNGPLGQFGNVGPPGQEGRDGASGSPGQSGAPGVEGDKGPPGRQGPVGASGQEGTKGPDGSFGKPGLVGMTGAPGRNGISGAPGPRGDEGPAGSPGPKGEAGQVGPTGTLGRAGPLGPEGTRGPDGLSGKPGGPGGTGRDGQAGKPGPLGDAGPFGRNGPAGREGVPGHPGVSGSDGRPGRKGEEGQPGIVGQSGPPGPEGKPGAEGKFGPVGVDGLQGKIGPQGTSGQPGPPGSPGPHGGAGQPGLHGVPGKSGPGGDTGGPGRLGVPGARGLHGTEGRQGQPGEPGRVGTPGPQGKMGPTGPYGPPGNIGLPGMPGHKGINGQSGRKGAIGGPGPRGREGPMGAPGMPGPGGMPGPPGTAGKSGLAGTEGKQGLPGGHGRHGKLGPPGPTGPFGRSGASGPFGVEGSNGSKGAEGDEGPKGPPGEPGRQGSSGMHGPDGVEGPPGQPGAHGPVGNPGPPGRTGSEGRSGSLMAQPGTKGDFGSAMQAELGGPHTPHGPPGAEGPQGPVGPEGDYGAPGRLGPRGKNGRQGRDGPSGPPGMPGPRGRIGTVLPVDGPEGKQGKYIRGGGGFTDTGGTSPSETQCIPCCEGEPIVMKECNSLEDCQIEDCLVQGNDCVCIRCPEPKWIDRNTYVQGDATCSMDDGSTGDQCTVILVQAVSVVLFLFTRLHVFSMM |
| TRINITY\_DN57514\_c0\_g1::TRINITY\_DN57514\_c0\_g1\_i2::g.122339::m.122339 | gi|554841313|ref|XP\_005931074.1| | PREDICTED: pre-rRNA processing protein FTSJ3 [Haplochromis burtoni] | 25.4 | MGKKLKVGKTRKDKFYHLAKETGYRSRSSFKLIQLNRKFMFLQKARALIDLCAAPGGWLQVASKFMPVSSLVIGVDLVPIKPIPNVVTLQEDITTEKCRQALRKELQTWKVDVVLNDGAPNVGANWQHDAFTQAHLTLMALKLACDFLTKGGTFVTKVFRSKDYQPLLWIFQQFFKKVQATKPQASRNESAEIFVICQGFLAPDKIDSKFFDSKYAFKEVEVQAKTVKELIPVKKPKAEGYTDGDLTLYHTFTATAFLKAENPVDFLSKASEITFDNADLESHPGTSLEIKECCRDIKVLGRKELRLLLNWRSKLRRFLAKKLRTEAKQLDREINLSSDENESHSEEEPEKKKEERKDGEEVEEGEEKMDTDEEEEMEKKLAELKAEEVADLRRKKKKLLKERRKQRERVELKMDLPGVSIADGNDTSMFSLATINKQKALADISKGDMKIADTLVDEDDDLHLSEDDEEDDEDADEMSLASDLDEDDMEEVEHRQKELEKKAPKKKVQFAEEEDDDDEEPEGGLLVELEGKDEKKERETNLWFSKGIFSEIDLEGDAENELQQTEWLQNKQTEKGKKRKAEEQEEEDIAQPEEEQAGPSQEAAEESDSDSDDSSD**DENEISRMKQAKGAAGK**SGEAGDDDFQVVPVESTSKKARILDAEGLALGCQIATSKKTARDLMDGSFHRFANSEEAWEVPEWFLDDERKHRKKPVPVTKEMVEEYKQKWKEIDARPIKRVAEAKARKKRRMMKKMEQAKKKAEAVVNTVDISEREKMAQLKSIYKKAGVGKEKREITYVVSKKGAGKKVRRPAGVKGVFKVVDGRMKKDMRGMQRKEQHAKGGKGRGGKGKGRPSKGGKGGMKGGKGRKGK |
| TRINITY\_DN58026\_c0\_g1::TRINITY\_DN58026\_c0\_g1\_i1::g.90009::m.90009 | gi|1041114050|ref|XP\_017280573.1| | PREDICTED: aryl hydrocarbon receptor nuclear translocator isoform X5 [Kryptolebias marmoratus] | 14.1 | MLFHTDMSSSNPELPDPNLGMGESGTQAGGRAVMPKGTNKRPAAPDFDDDDGSKLFRCDDDTGGSNNDKERFARENHSEIERRRRNKMTAYITELSDMVPTCSALARKPDKLTILRMAVSHMKSLRGSGNTNTDGSYKPSFLTDQELKHLILEAADGFLFVVSCETGRIVYVSDSLTPVLNQSQPEWLGSSLYDQLHPDDTEKLREQLSTAENNNTGRMLDLKTGTVKKESQQSSARMSMGARRSFICRMRCGTCPVEPLSMNRLNFLRNRNRNGLGPAKEGEPQYVVVHCTGYIKSWPPAGVSLTDDEADNTQGSRYCLVAIGRLQVTCCPSDTDINSISVPVEFISRHNCQGMFTFVDHRCMATVGYQPQDMLGKN**ILEFAHPE**DQGLLRDSFQQVMKLKGQVLSVMFRFRSKSREWIWMRTSSFTFQNPFSEEIEYIICTNVNVKQFQQQQQAELEGAGARDGLYEAGPITLSQMPVQPVQPVTAAGPDHSKSLEKPELYSSLFQGPDQTKAMPSTSTPSTQIYPPANNFTANRPNDAYRPVNMTPQMAQPTHSAGQMLARMSRPNGAPQSVTPSSTGSPLHGGPAGGWPGAGAGPQFNNNQQVAPQAPKTMSPSFAPMGGFGGSSSNSCGQMPTGAAPTPTSGANYPQMNARASLNTNGYNGNQSGAQFPSRAAEAVWPQWQGQQHSQSNAEQHPHAQGNQQDMFPDVLSMLDQPANFNSDDFEIPMYPSFNE |
| RRRRRTRINITY\_DN75141\_c0\_g1::TRINITY\_DN75141\_c0\_g1\_i1::g.25850::m.25850 | NA | NA | 29.7 | LLVIFGSSFGAAVTRGSPSVALSRILGASLNNYALRFEHQLGPKRPDIFRLVSDASGFVVSCHPAPMTTVATIPNKGDVAEYFRIQKGTYQDWLHVTGDCSVVEQSAELQGVYFVSKRHDSYTLRPEVEQTGDGHNYLPWLKITKDKSGSLFYDEGALPA**LCKITGSHG**LFSQLRIQHFHFHPDQQNLGIEYQWYALWNGQLSRGSRPLEQKLASDEVTPGTVWSTSFSALA |
| RRRRRTRINITY\_DN42009\_c0\_g1::TRINITY\_DN42009\_c0\_g1\_i1::g.80702::m.80702 | NA | NA | 17.6 | HPREGTHSRTHVNLHSKCSFGKGCHTCTYPLEGTHSRNHLLLEGSSLFSKG**CTTCLYN**KEGKHMQVHRTLGAKSFSKGCITCLNSPGQHLREHKQLSYKCLFGKNCQSCPFIRGRKHLRQHQYFGSPSTFGKDCLRCHYRFSHLKSHTKLQNPHEFVKDCTPCKTEEETFNKNVARTSLFRKDEGTREKRRRCKKNEVNDKKQKREQKKEVSEKQKDKKKEANLEKSKLQTKARPRKVCVKQIPASKQHERQIHEQVKRKQRHAFSCQPCIFLRSLPATEKKALWEDATVDSSQGDSDVGEVYKLAPLEQENDYVDDEESYAETFKGVTIQPPLALMSLLIDEESSSPATSLTGLQRHHLLLTTMAIPESLHQGFEESVSTTDTLSAAIQQLDPTPLLQELRSLLESVLQELKQDYASGYNAPFVEKFFSEKEFPVNLLSQVLNAFNTYSTKLIDSSAMQDASSVEISCTHIRDLHSQIAQLNAVGDDRCLELVLRARLGVVLQVRHLPSLLEPVIETVLSIFDVLKDYQMVNHQQITQWIFASMLRVPPVLLHLSSLPLPVGNSKWAM |
| TRINITY\_DN46467\_c0\_g1::TRINITY\_DN46467\_c0\_g1\_i1::g.35360::m.35360 | gi|657545506|ref|XP\_008278071.1| | PREDICTED: tyrosine-protein phosphatase non-receptor type 21 isoform X1 [Stegastes partitus] | 10.2 | MPLPFGLKLKRTRRY**TVSSKSCL**VTRIQQLNGEFVEFTLSVESTGQECLEAVAQRLELREITYFSLWYFNKQNQQRWIDLEKPLKKQLDKYGLEPTVYFGVVFYIPSVTQLQQEITRYQYYLQLKKDVLEGRISCSLDQVIRLASLAVQADFGDFNRYDSQEFLQKFVLFPIDWIQDERVLEEATQKVALLYQSFRGLSAPEAEMLYMQEVEKMEGYGQESYQAKDSTGTDVTLGSCLDGIFVKHKNGRPHILFRWDEINNMSHNRSFFALELANREESVQFQTEDMETSKYVCRMCLARLKFYKINKSSLEECDPLPSEGSQKSLLTLSFPRFPMLSRPSLPSNKGQAQPTVVNPVRRRSSTRISLPKPQAYMMPPPQMHYNGHFTEPYTSSQDNLYMNSQNGYYYHSQTSLDCSPLEYGSGGRLRNGSVYSAHSTSSLTNPQHYLQPSPMSSNPSITSDITRPDYVPSHRHSALIPPSYRATPDYETVMRQKTRGTGGGMVLSQEHRQSHSMRNLNIGNSYAYSRPDPLVYSQPEIRGEHGGAAQHHHYPFHLGSSFHSPSPYPYPTERRPVVGAVSVPELTNVQLQQAQEYPAPNIMRTQVYRPPPPYPYAHPRPANSTPDLSRHLYVSSSNPDLIITRRVHHSVQ |
| RRRRRTRINITY\_DN44194\_c0\_g1::TRINITY\_DN44194\_c0\_g1\_i1::g.79464::m.79464 | NA | NA | 19 | LKESSPIWIYPGSQEEIILKIKNYIEELSDGQVIATFFEGFDQELKVAKDFVKNAQEYTQRKNMEMLAEISK**PKIFIAIP**YLQAQQLRKIANGSVDLICHKGREAVTRVSLISTGYLNENFQGAEIFKNDQIDKEMQERSGVFHYDQGDMENERRPRTTHPVCSGFKHPFESILDDNVRDKMPGLIIVPRTYHIEQRIVPEYSLITDEQGKSSSESDSTNSTLCQESEVLEQVINEKSKYFPFKRSLNFSKKRKVKVPRNSEIMGTRAHFKVTKLRAREKKEVRKKSPIVGIQESEGHPTVLRAQWWEDDSANIVHLIDGYSFSLGQSPLCSDRTRDYDFLARVYLSRKESTRLSGSGSSMSSNMMQE |
| TRINITY\_DN59050\_c5\_g4::TRINITY\_DN59050\_c5\_g4\_i1::g.46567::m.46567 | NA | NA | 27.7 | TIFFYFKKINTLLPAEKHQKQSNSYTSKDFLFRGADPSSAELLLQLIQEILPKPPRLVAGAARPPAAGQQVSQQLDALHPRRQEVALHDAGGVRVPLLSGQLVQLHQDGGLLLQLEQQQLQSRQHGAHGLAARLLDVSAAVVAPPLCQVAQHGLRLLLLLLRLLVEERSHAR**QRDVVPLK**HTGQSLQSVRAVQQQAAHPAQRLLHGGRQVVSGPAGGRGAPVRLTQRQAAL |
| TRINITY\_DN46549\_c6\_g2::TRINITY\_DN46549\_c6\_g2\_i1::g.96570::m.96570 | NA | NA | 27.2 | MAANSSTPILPSPSESPALRK**ALVSASVRALA**PAEKFCRNSFSSSSSMKPLLSWSMMAKAFLMSSADLAAMPTLAKNSLYLKESAAWQAARAAVMSASFRIEANAIFNSGLPLRLEWIRSDEPDESAHCSEALSDSHKLIYFHSPEI |
| TRINITY\_DN44772\_c1\_g1::TRINITY\_DN44772\_c1\_g1\_i1::g.69897::m.69897 | gi|348517094|ref|XP\_003446070.1| | PREDICTED: V-type proton ATPase subunit S1 [Oreochromis niloticus] | 11.5 | KMASARAAHLRGVSAGWAAVWAAVLGLFSVLSAGSGDEQVPLLLWTSEGISLPIQSLPTAGHIVGQQQLASYLEKVLNVGPRNVVLFLQDKMSIEDFTMYGGAFGNKQDSVFPNLEGALMSSSSPLVLPAVSWPASNAVIGQLQDQLDTSPLYMDPETLSQLRLNASSPALLVFRLPYGIGADLMSAKEILSGNDEVIGQVLSIMKTQSVPYTAIYTALRPS**REAASLSMEAGVGGG**RSLLQARGGYRERERERERQRRIKERAGIYAPVEFKEGEETCILLWAKSLSVSILRSGRWEEQDLTPLTFGEGVSPKLHGSSCDKTKAKLVLNYEDVLDHRSFKLIFAMSQRHYKVSARRWFTLDAVELEYDKIKATFNGSRHVYAPAEYSYRCESVTNFRWPVLIPRSSKDPANQWRVSFEDFQIQGFNVSGTEFSYASDCAGFFSPGIWMGLMTSLLMVLVLTYGLHMIMQLRTMDRFDD |
| TRINITY\_DN17548\_c0\_g1::TRINITY\_DN17548\_c0\_g1\_i1::g.80166::m.80166 | gi|734631583|ref|XP\_010744183.1| | PREDICTED: rho-related GTP-binding protein RhoN [Larimichthys crocea] | 30.9 | MESKGLLRCKIVVVGDTQCGKTALLHVFAKDSYPENYVPTVFENYTASFEIDKQRIELNMWDTSGSAYYDNVRPLAYPDSDAVLICFDISRPETLDSVLKKWQGETQEFCPNAKVVLVGCKLDMRTDLNVLRELSKHR**LIPVTHEQGTNL**AR |
| RRRRRTRINITY\_DN44004\_c0\_g1::TRINITY\_DN44004\_c0\_g1\_i1::g.101614::m.101614 | NA | NA | 15.7 | VEMSNKFANNVIARLLLRDGIQSPGRFTFMDIARLTPHAQCLRSAAITAVNVMWAMIQGGFTNVQHNAHPPLVLEVSEVKTKEAAVANEVASTDAQQISGHSLLDRIIEDHVMRVRRREAAVSYEVHEKQTRPVIPKLIVKQGTHTRQTVFTACAHCVRWHRDSFLDECSVCIGVEMSTNFARNVKAKINVVQGVSITHEFHIDDMSATVCPSGAHREASLCATSDIWKLLQGVSLEQRHNSHCPMV**IQSMKLETP**NVSEEEEEEEEEEDKEVDGFVRSTMRSLQSRSVVIDLCTAPQRV |
| TRINITY\_DN29815\_c0\_g1::TRINITY\_DN29815\_c0\_g1\_i5::g.5823::m.5823 | NA | NA | 38.7 | MVEGAESLGSNQTLRLLLCFPAVRALLRGPAVSAPPGPPGHQGPGSSLLLLPVQLLLLHLLLLLLLLQP**ATTTAAAAAAAAAAA**PGKSCSNTAPISKCVPVKSVRVGWFSASDYPASGG |
| TRINITY\_DN10772\_c0\_g1::TRINITY\_DN10772\_c0\_g1\_i1::g.101234::m.101234 | NA | NA | 25.7 | VLLGTVAEPVAVGVMMVLVVLVLVAAVEDMLLVRAEVVGLVGVVLQLMRRLGPVLGVLLLLMVVLVLVLVDVLLLLLLVVLVVVELHFLRLLLRSLPFVRGRRQL |
| RRRRRTRINITY\_DN58174\_c0\_g1::TRINITY\_DN58174\_c0\_g1\_i1::g.23087::m.23087 | NA | NA | 11.2 | TAVSTVIQVVEGNEGQIAGQIAEKVEMDTQLAPALEAAQVAATHDPVPALQVYQVQIDPPLSSGEVATAGGDASAVAILQAGHLVQGDQGVHVQHIQLNGESDQTIQVEEGQPVQAIHLQGQPIVQVQGDEGIRHFQVQQNALTYHLTQQTATEMHATEEGMGGETVSSRPTRKSFSKVALSQGRQKRRWATRCKSDISQKIRYWDSESIGFKHFLHCRIGYIMLPDLQKKGHKGQGS**LNSMAQVE**RHFLYDLLTLAMKEATRCNTSIHLMDAPSVPCRVRMEPNNEDGLWTGEPYDDLSSPLFPEEFVAVC |
| RRRRRTRINITY\_DN43783\_c0\_g2::TRINITY\_DN43783\_c0\_g2\_i1::g.107257::m.107257 | NA | NA | 20.9 | YLCRTPRSSEAGCHGHREGTAPTAAATATATATTRPTSPWARTAMTVPAPRCVCAGGHCGPRNTCLLSRTSRRLSWRQQPTA**PASPCLLFLPPLSTQH**SSTIAVCNIVPHYTTEKKKKRHGSRWFGHLCCVLRM |
| TRINITY\_DN57301\_c3\_g3::TRINITY\_DN57301\_c3\_g3\_i1::g.21922::m.21922 | gi|584006915|ref|XP\_006798435.1| | PREDICTED: uncharacterized protein LOC102798648 isoform X1 [Neolamprologus brichardi] | 20.2 | MDKAKQLKWFLFTVLVAAPTILYITVLTPKSYTSVPTPHGPPKSCPFH**ISEETITPL**NNTKHFLVSAYMDQRVNGFDIRIISMFRKDSNQPLHCFFCCAGYTSR |
| TRINITY\_DN55754\_c7\_g2::TRINITY\_DN55754\_c7\_g2\_i2::g.19983::m.19983 | gi|734598865|ref|XP\_010749703.1| | PREDICTED: protein VPRBP [Larimichthys crocea] | 26.3 | EEEEDEEDQEDDDQEEDDDDDEDSDDDVDTDPLIAELENENGGEDEDDEEEDDGNDEFSPSDEEVARLLEEDVDVGDDDDEDDNDEDDSDNDDVDLEGDNDSSDNS**DLEDDIIL**SLNE |
| TRINITY\_DN28943\_c0\_g1::TRINITY\_DN28943\_c0\_g1\_i1::g.56623::m.56623 | NA | NA | 16.5 | QSLIKVFSSLPGLCVFTRCHIYPGFQDCPLSRAIGEFNHSVRVLPCLVISPQQPEKHPSVVKTRGRCTFTIVF**DLSIKFLYD**FSVWVCLFFLSIDKRHQRAERHIYIISYCVELY |
| TRINITY\_DN12118\_c0\_g2::TRINITY\_DN12118\_c0\_g2\_i1::g.2423::m.2423 | gi|734635644|ref|XP\_010746420.1| | PREDICTED: semaphorin-6D-like [Larimichthys crocea] | 14.5 | RELDRDHHALFVAFSSCVIRVPLSRCSDYSTCKKSCLSSRDPYCIWLKSGSCATVSPGFKGGFEQDVENGYHQ**HPDTCHDVLA**TTRKQNTALDSAYGKTTPTSASTTYHGAAFPKEAGDPERGTGPDGPPPVGEQGSPDSEPISVEMEGVRRPPELDKPNHSVHYTLLIACVLVAFVLGAFLSGFLVSCYCNHTGHKTKKLSKDPEAPIPHALSLRSLAKLNGLLDSQGKDEKMEVSSPKIYNSFFANSKEHHPPRRNGHHGMTMGDLVHPHHHHHHLHHSDLQVYTHWKVSAWSGP |
| RRRRRTRINITY\_DN23663\_c0\_g2::TRINITY\_DN23663\_c0\_g2\_i1::g.121537::m.121537 | NA | NA | 10.5 | VDPAHGHGEHLKPKHSCTPKREHDRQSKQRWDHFIWSSYLRKWGTLPIFCVPTQSFRKQSVYKTNKTLGSARVQQVRAQLLDGLTEVLNTFTPRDAPSAEWCALMTSYIEPTSYEPARMRTG**AKLRHCF**EEDIHLGPYPSAGLSFIEWLLIGYSWVDSQTTFVKDFISEPSMWKLPLRADGKRVYDPDKYIDRALGFDCIKVVKNDSLLVNRAALDRHICKRSALYEMGRAVQFSFSIL |
| RRRRRTRINITY\_DN118723\_c0\_g1::TRINITY\_DN118723\_c0\_g1\_i1::g.138488::m.138488 | NA | NA | 16 | HSTHVSWGRHLDGVFVHPEEDGVVGGVGGQVLEDLLQLFISDGGYHSHALGGVVGGQHHLLSDLNQIPREVVSSRGGVLDHVIPQVQQLQLEPLLGAAADSDVTHGSQPSSRNQDCEGQDFTP**HFIFISDL**ENSLLTSSREVALLQEVQLFITWLHAQAEFIG |
| TRINITY\_DN68349\_c0\_g1::TRINITY\_DN68349\_c0\_g1\_i1::g.104526::m.104526 | gi|657555180|ref|XP\_008282049.1| | PREDICTED: histone-lysine N-methyltransferase 2B-like isoform X2 [Stegastes partitus] | 15.8 | SRGRHLRCDRCGQSGATVGCCLATCQSNFHFMCARAQHCVFQQDRKMYCYKHRDLVSEKMVSGKGFEVSRRVY**VDFEGINFR**RKFLTGLEPETINMTIGSLQIQRLGVLSELSSNGRMLYPVGYQCSRLYWST |
| RRRRRTRINITY\_DN53650\_c0\_g7::TRINITY\_DN53650\_c0\_g7\_i1::g.39619::m.39619 | NA | NA | 19.6 | AALFADSSWISRSQLLRLSTYLPNSGSQEAASVCVCVCVCVCVCVCGFQQLLTSTLNSIFRKFSHNSKRHKISSIDCASYFRI**IMIIITILA**PTNHTHSSSLVSARM |
| TRINITY\_DN51639\_c0\_g1::TRINITY\_DN51639\_c0\_g1\_i1::g.38075::m.38075 | gi|734621434|ref|XP\_010738618.1| | PREDICTED: alpha-2-macroglobulin-like isoform X1 [Larimichthys crocea] | 75.7 | PVALQVVMEMKSVTTVVLTEVVKEDFYRCVTFQVPAVLSRTVANIKVTVQGENGAMTKTSKVAIEPPSFMHIIQTDKPIYKPGQTVQFRIVSIDTNFIPVARVYKIVELQDPNSNRIAQWLDKSIDGGILDLSHPIIPEAPQGTYQISATTDKGEQIGYSFDVKEYVLPKYEVKVHLPSVISILDKEATMQICGKYTYGKPVIGSVKAEFCRLPARFYWYSRQDMICKTYQLTTDKSGCATQIVNVTEFSPDKTMYDDNFDVTAEIEEFGTGVVLKGSAQTSFSSSIRVVTFEDVPAAYKPGIPFEGKVNVVGPGNKPVADELVYLFVGDAQNETLRTDKSGMASFSLDTSLWKSSELLRASTKKTEDFETFERNVRRPSYRSAHHHVTAFYSKSSSFLKLMQAGEISCDKDATVRAQYIIAGEELKTGQEVLDFFYLVMSRGGIVQHGRIPVTVKTGTVNTGELSVTLRQLTGLAPFAQVVVYTLMPSGEAVADSQDFPVQLCLSNKVSLKFSSVQSLPAEKTTLSLQASPRSLCSLRAIDQSVLLLQTEPEISTKQVYSDLPLQRLTGYSYDVEDSEPYPCYPVLVPVPVV**EPEPEPEPEPEPEP**KPEQCSWIITKNNKHINTVSIDLLMSVILLNLIIN |
| RRRRRTRINITY\_DN65456\_c0\_g1::TRINITY\_DN65456\_c0\_g1\_i1::g.112674::m.112674 | NA | NA | 39.8 | GLRHGTTRHAIRIESLRVVIEDLEALFDPDHRRSRLQLYKKKRKRKQRKLKDYGPCGHSRRKCKHKHKEKHGLLSSAPAAPHPRRPDPSSRAGHPSPSPSPHEMLMASHRRRGRSNLGVGPG**MASGIVGPM**LLGSGMGPPMGIGGLGGAGGAKEGRDSTSNNDTGIGSDSPVTEESHSESVPSPTAEKLESLPAPSTPHLPRPPSLKHYHYHQRYHHHHHHYGRCSKKQSAAAAMSSGLGPNRPNPASFTP |
| RRRRRTRINITY\_DN45755\_c0\_g1::TRINITY\_DN45755\_c0\_g1\_i1::g.104132::m.104132 | NA | NA | 11.8 | KMNNGIWDKFNAVHTYVTYLDPDCEGQDYGFSVLGLLRWLGKSERQGQAFGLSPNQNSTARNDTTASLVLIGGTDSPCINSSGYDPKQSACLMNDTVSVPVGNRAYQQECPVIDALQVVGVRAREDGGLSSDPLPSWGTVLGQGSTVEEAQSESLCLPLVKEGVRAKDLLKVVAMDSDLINPDYNPHVAISAVRLHQLGKSQRRDDRYHKGVVVKIKAADLPYVKGLETVCHAAVVVSRQNVLAGSCVLQWDSAEDHNGTGARGDKKLSGALSDAKTVKTEIGNTSRRYIAALWPWHAEEPREPDFTPHKGCVPSCSVHRGSWKGTKLCTRRSSGSHQYFQSACEYEIHTYLHHFGPSLQPLVPPGKTPGDSQLQRGLMSSYFKHVPTKRSPTQPPMVRQKVLESVKPERCARICLPQKGSWTGDPQCSRRTDGSLAYSHNCFFEVTQPELGPVVQHYGHYLRPLPPCSKESFSQNVEKEKEKDKEEKERELEEETKEAPDKETKDEKITAKEKPKGDDEGG**GRYLIYQTIN**VRTPIIKRGPEPSGITNNEKKTDKTDYTVTNNKTMELEFIEVTNEGESIVTRLKTDNPGVKDPDRKGNVQGEKRGQEEQGKDKIVVIETIDTKGTGVNIDPSDEKKEPPTVAEPEKKEVTNLSNDTDKSDVKDKTSGGPKESPTNIEEENRDEAVPKEPITGTYKDERDVTTTNEHETNIDKGKPSEKEGATNEQSKEKPTNIDKDSYTKTEQGSETSKAKNNEKDAETLTNNVKTCVPPIGSWTNNPLCTRQSIGSLEYPQDCLYQLAILVDNPGYVLFHNGHAPKPPLSCVREAPVCEPAPASWTGDSLCIATRYGRLEFGPDCRFTIRAGSYHFVGETSGHTPVPPRRCGLVNECRKGTYGALCACHYTYSTDLICTGDHLCPSSSCASSEQFIAFFGDFNKYGDSVFLIHLSNGSSHIPAPRNNGCFRGIVGSNINDGDRVEVYDYRCSHHHELSLMMFRLEITFPR |
| RRRRRTRINITY\_DN26775\_c0\_g1::TRINITY\_DN26775\_c0\_g1\_i1::g.5204::m.5204 | NA | NA | 6.9 | VSAIVIMLHPSISSISNLLDPALRSLHSESFECPPFIQVVYAPQNSGPNPVNIIGAAQKAQLYTIFGSKLAQTQGLVDEQDRGCPLALLLCYDNDVQRARYTTMRRAVSDLQSAELRMRQVIRLLPGGEPPPLSRQALLTNGSVFHLQVAAQDNKLALLGQWVIPYKTLLQVMDVSRHVSHDLKADPRPQLSSSPPVAPPPTPLFSPPGKQLSLDPKHTLSMPSTMPSQYSPSVT**DGAIRSIH**SLDSSTAHRLHSSEPKSDSGGGHSQSMKSRHGLDPEPPVQSSTIGQNALSHGPFQSPFGRMDRYVPFSGTGGPHMLQVGHTHPSVMVPSSAHVGRIRSESSPPHILKGELPKLSEKTSLEIAKGVIPSKSPGS |
| RRRRRTRINITY\_DN36542\_c0\_g1::TRINITY\_DN36542\_c0\_g1\_i1::g.7636::m.7636 | NA | NA | 20 | RTIASAEPTSPASPTTFPNRAVVPESELPEGVGYKNVATVRFIYENGPLLKTIKYSIAQIKPEVMTWSLRSTERKEIIYHSISAGGDHSPHNWHLYCKEATVGKVELPGDPPGPRDLVKVNIPIMKVGGVNVLKLVFHGGDVRVCDKVTLITRTLTTKVEMRQTAKDIENGEKLWVVEPLPKGTYDADIVFTEGAHVVTLDKFKSDLTAEPAEIEDKATIEGTSHSPR**SSVGAANRAI**VRFEYVCDETAGSYTFQTDIINTFSAKMWRTDPHKRREVVYGTIASGGDYQPKTWQLTVHNRTIDIAEPTGPPDCPDRAVTTESIKSAPSIGAINEAYVRFEYEIGEELETTKFRTDPILLKNLKTWLLSNKEKRELHYGLVPSGGNNTPPKWEVVMSDKVAASIIPTGPAAPESFPYQAVVAPSIIASSKGYRNEASVRFQYEVGTKLNTVKITSRAITASVIQWATTTTDRKEVIYNNIQCGGTYEPPEWSLTVYNSSVEEVKVPGTPPGPKDLIIVTLEETATGVSSTATLIYKGSDEKNADKICLKTSSQTSTVNLRTTEKLAHGDKKWEVKPVPRGIIPIEIKLDDGHLLSYTNVAIKFGPEITVDKATVPAALSRPDSRGKENFAVVRFLYEHGTSLGSVTGECTKTTTA |
| TRINITY\_DN39983\_c1\_g2::TRINITY\_DN39983\_c1\_g2\_i1::g.33393::m.33393 | gi|736153680|ref|XP\_010764284.1| | PREDICTED: receptor-type tyrosine-protein phosphatase eta-like, partial [Notothenia coriiceps] | 22.5 | ETEGDTKKLTTVTTPQPVGELSVTVFTTSSISVTWTKPEGYSFFYRVQWTNGNDSHTTNVSQTSITIPELTAGVKYAIHVTAVADDNHTEGQSVSVSHHTRPTKPGNISGQGTLNLSISWDLPGGKVDQYVVNISNIMLQDFNTINTADTKAHFNDLKPGRIYNVTVTALAGDLSNTSDLTSLATNPTPPGSLNIIERTNSSLQLNWAIPVQMENAPGISYNITYQPVVGEVQHNTALNTTVLSPLSSGIRYNITVVTVGPQDLRSTAVYASSYTLPNPVLNLRASTESTTSIKVEWQYPHGAQPYYKYLIKANSATGKPVNETTDNN**SIDLTDLEPG**SRYNISVSTIIEEESGLVSTEEETFSYTMPKAVIN |
| RRRRRTRINITY\_DN58270\_c2\_g1::TRINITY\_DN58270\_c2\_g1\_i7::g.45040::m.45040 | NA | NA | 9.6 | HPRTQTIMKLRSQDIVDLLNKADVALAHAAMLMQKKYDKQLSTMVYQQALKMKAILEALDSNLLKQAMEIERHTSAPLVPITEDVTALLTRLALGVEKVMPVYEEPAAPQIRNSMEIVAKVLGTVNEYVKDNSRDLNATPPPSIEQPQLKVGENYSDVPCLSALNTLHSPAGPRPPKKPPAVHEPKGVPQYIHQSGGPAQLTGDERDISGRSNRSEAKMFSEEQELWRQDDEMQQQQMMLREEMMAQGVCGGDEMNPSWLANHEPRHQNWSDTPPYSGGVGGVGGHASPPFHNHQPSSFFGESSRPSPYGPRSPKPPAEDSGGSDWSVTVQRRMEMRLREEQQLKEEELITSLQTKLETFRPRKSPDYSWCKTMLSYLTPPCQPPMALREGNEIRGIVDNNKVGQFPKIGYMLIEWMCVGFMWVDSASTFRRFNISEPAMWKIPLKGKSAKYYSSDEMYRSLGFDGLMVCDVSSVLVNRAAIDRHVFRKSELYALATSLQYAFLILTALDLSYKRVQLFSRLEGLTCLEMIIWVPNETIVGILKVIHPHDFQRMTLAEQLFKERVSDSTCNKCTKIAVPLGPKDPSNYVGQHVDGFQGEGICRGLEIRDRQIEYDRAEVVGYSMSPMTYTDEEDVIEAYDDTEDGSLDENPPSDSCFVFPLLFRRAKTPKPPTSTVLDSVSIARVGSRVAELKKENNSLKPISPLAREGEKQFRVIFSHTEMSILRCYGDILDALNEAMTLSATTVTLPEAAGAVNLQLMGKRDKEEMASYQISQVQNFNALHTPTSGKDTLYSIGEEPGIALEVQIVWSSGLACKFCEKDYRYIPALIELFKLICQEDNLNAVQKFTQQILKRLSKAKVSDLLDKPFFRRLGVDKELLEYNSKKDLANGRMEKFFRRIELCGLKLAVDQEVQDGIDTMYDTKVQHYFYNLTPKDETFQQVFGKPLYRIRLEYRWEENPRAQEYKERVHSVGMDPHLWHLQDRSQSNSLRLGFCSTWRVKHIDLIKQIIGRVDTADGYRINSSWCSNETNTEFHHFVKLVRDVSGAMTRDSGGASLRSKAGGLLTNNLNPDLYATAM |
| TRINITY\_DN45326\_c0\_g2::TRINITY\_DN45326\_c0\_g2\_i1::g.11399::m.11399 | gi|928054232|ref|XP\_013876370.1| | PREDICTED: 26S protease regulatory subunit 4 [Austrofundulus limnaeus] | 20 | ADVTPERQATMGQSQSGGHGPGGGKKDDKDKKKKYEPPIPTRVGKKKKKTKGPDAASKLPLVTPHTQCRLKLLKQERIKDYLLMEEEFIRNQEQMKPLEEKQEEERSKVDDLRGTPMSVGTLEEIIDDNHAIVSTSVGSEHYVSILSFVDKDLLEPGCSVLLNHKVHAVIGVLMDDTDPLVTVMKVEKAPQETYADIGGLDNQIQEIKESVELPLTHPEYYEEMGIKPPKGVILYGPPGTGKTLLAKAVANQTSATFLRVVGSELIQKYLGDGPKLVRELFRVAEEHAPSIVFIDEIDAIGTKRYDSNSGGEREIQRTMLELLNQLDGFDSRGDVKVIMATNRIETLDPALIRPGRIDRKIEFPLPDEKTKRRI**FQIHTSRMT**VADDVTLDDLILAKDDLSGADIKAICTEAGLMALRERRMKVTNEDFKKSKENVLYKKQEGTPEGLYL |
| TRINITY\_DN56997\_c0\_g1::TRINITY\_DN56997\_c0\_g1\_i2::g.105558::m.105558 | gi|657564694|ref|XP\_008285610.1| | PREDICTED: protein FAM49A isoform X2 [Stegastes partitus] | 25.6 | MGNLLKVLTCTELEQGPNFFLDFENAQPTDGEREVWNQVNSVLQDSESILSGLQAYKGAGQEIRDAIQNPNDLRLQEQAWNSVCPLVIKLKKFYSFSLRLEEALQ**SLLESLTCPP**FTPTQHLEREQALAKQFAEILHFTLRFDELKMRIPAIQNDFSYYRRTISRNRINNMNLDIESEVNNEMANRMSLFYAEATPMLKTLSNATTNFVTENKTLPLENTTDCLSTMASVCKVMLETPEYSSRFSSEDTLLFCMRVMVGVIILYDHVHPNGAFNKSSKIDMKGCIKVLKDQPADNVEGLLNALKFTTKHLNDESTPKNIRTMLQ |
| TRINITY\_DN38384\_c0\_g1::TRINITY\_DN38384\_c0\_g1\_i2::g.66945::m.66945 | gi|736301518|ref|XP\_010793302.1| | PREDICTED: nexilin isoform X2 [Notothenia coriiceps] | 16.8 | KAEEEAKRRMEEERRAFAEARKSMLVDEDDEALMALLNLEGSKPGKICASFEELERQRREEEQKKAEEEAKRRLEEEKRLFAEARKSMVVDEDGEGLVKSDSQEALNPRKLE**INFEELL**KEKEKAERRRKAEERKKKMEQEKQEFEQLRQEMGEDEVNESSDVVSKEYEELTKLKRTGSIQAKNLKSKFEKIKQLTEEDIQKKVEMERARRKAIDDEIKEREAERFQEEDEERESTPVRAEESPFKQKVDMKARFEQMAKAREEEEKRRIEEQKLQRMQFEQQEIDAALQKKKEDDGEDEGSIINGSAAYEDEEDHARSGAPWFKKPLKNQSVVDSEPVRFTVKITGEPKPEVTWWFEGEMLQDCEDYQYIDRGETYCLYLPETFPEDEGEYMCKAVNSRGTAASTCILTIETYDY |
| TRINITY\_DN58549\_c0\_g4::TRINITY\_DN58549\_c0\_g4\_i1::g.62889::m.62889 | gi|657550921|ref|XP\_008280000.1| | PREDICTED: zinc finger FYVE domain-containing protein 1-like isoform X1 [Stegastes partitus] | 8.7 | MSGQGPAVDKGMNTVLVCQESYACGGTDEAAFECDECGSLQCARCELELHRQERMRNHDRVRIAPGHVPFCDSCKGDSSCSGNGGRLRAVVRCQGCKINLCLDCQKRTHSGVNKRKHPLTPYPPAKAPQENSVSAGEAEIEILKAKLEKVCSFLLVDEKEEMQVKDDDEFVGRLGCRPDELLKVVSIFGNTGEGKSHTLNHTFFLGREVFKTSPTQESCTVGVWAAMDPVHCVV**VIDTEGLLGAGA**NQGQRTRLLLKVLAVSDVVIYRTHADRLHDDLFKFLGDASDAYLKHFTRELKATTSRCGLDVPLSTLGPGVIIFHETVHTKLLGSDKPNESAERLLQERFRKLGLFPEAFSSIQYRGTRTYNPPTDFSGLLRTLEQQLDNNTTRSPRSASVIYKALQALSERFSGEITDDYMTSNSFFPDEYFTCSSLCLSCGSGCKRSMNHLKEGLDHEAKHRCRYSAQYDNRIYTCKACYEGGKEVIVVPKTTASSDSPWFGLAIYAWSGYVIECPNCAVIYRSRQYWYGNQDPVETVVRTEIQHIWPGSDGFLKDNNNAAQRLLDGVKYISQSVSELSVKPAKAVTSWLTDQIAPTYWKPNSLILQCHKCAEEFQPNDTKHHCRSCGEGFCDACSSKTRPVPERGWGLAPVRVCDACFHNRGIPTELLDAALEEEGGTLIARKVGEAVQNTLGAVVGAIDIPLGLVKDAARPTYWIPDQDITSCCECQREFAPRLSIHHCRACGQGVCDDCSQERRPVPSRGWDHPVRVCSGCNQKPGEL |
| RRRRRTRINITY\_DN57666\_c2\_g2::TRINITY\_DN57666\_c2\_g2\_i3::g.61717::m.61717 | NA | NA | 10.7 | VISKLTDLAAKPEEPECPAESDAIARHYEQLISIVLDHGFQMGDDLPTNGWRDKMHPNVKCVETLFIVAEVHGEAAAIHLATRSDYDRQEMDIASLAFRRLASVDGSYAAFMLNVVSKNPDDDSRRRPDHKKTFHRLNDYNHFNFNSVLEQCFHIGRVSNGLRDLPPSWCMMGMVNPVVLLVAGSVGSKAPLGVHFAFQGSFDYMGCSHMLSLTNRVAEASLV**REGTIPCIGG**NALTSAMVSGSECTVEISCLQFYFDLAATMDANDPFCKKEKLYYGIAYNRDGTERESQFTANSFGVFETGAMSKLFEMVYDFREAKNSHPKILSSIVIAGANVMPNHPKDEENLSLKNFKFGSPEKGVFQHVRESGLEHVAIAYELPKVCSQLCLPVKTDGVSYRQGDITCLSAGWLDSSFKALQPIYDAVQGGEQQQASDFMKDIQQTFEDFNPIIFKKRFAKTLLMINNGVCRKFFKKDMMVPGVSDRASQRMQRVCDRLRPDSTLLGTKRLASIFQSLPIMEKGETITYFLLDEMSSMLRSRNSHGQDVEPGKQHHFARHTHPSAAVWCPLPVPQQTRSLVINDAGVRASIGANKFLQLIGPNATRLSKLCHM |
| RRRRRTRINITY\_DN54378\_c0\_g1::TRINITY\_DN54378\_c0\_g1\_i1::g.17758::m.17758 | NA | NA | 11.4 | HLVRLVPDPQNLDDGLVALGQETLGVPPLHYLFHRLKPDSSSGEVARIVVP**RADLAAPLAG**REDHGDRLRRRGLAFDHQLFVVAPADLRLVDEAPHRRVHGMPDLRQTPRLLQRLLPAGVRGVRDLHEQEGAQRLRGGEEGRQGDLEGAPDLEDEHVHTVPVVVAAQHLDAHRLGGGVDELHRLAYIAIAVTRPLEQRQSGHVSEQTRDLGLHVVQEDETQDEDVQQGPHVEEDCLSCCHFSKHNQDSCQSGVVGDQQHGPKRNQSQQLQGVQVGQVAVAQLQEAVGVGGGQGAHHSGVPGEVGGVRGQEQGGVQGVAQQDVVELLLPAAAGAAALVAGGVQLPQGAQPVPVGGVQQVGDGGRQLVEGRVLRVPVFVGVQQQLAQGEGVQPQARQDVQVVDLGQGGPPEPARVCVTCSLPQQQGLVRRLWM |
| RRRRRTRINITY\_DN51640\_c0\_g1::TRINITY\_DN51640\_c0\_g1\_i3::g.38275::m.38275 | NA | NA | 49.3 | ATRVPPVTLDPLDELDLPDLPVLPDERELLELLDPCVRCALSDETDRTDEIELRVLREETERPVLPALLVVSVLLALPVLPVLLAVREVTVLRELPASVAL**PDLLVLPVLP**DLMALSVVIERPALLETAVLPVM |
| TRINITY\_DN56629\_c0\_g2::TRINITY\_DN56629\_c0\_g2\_i1::g.124889::m.124889 | gi|657582301|ref|XP\_008295204.1| | PREDICTED: uncharacterized protein LOC103368577 isoform X1 [Stegastes partitus] | 26.6 | LFSHVKDYETKTGLRVLPALHSVLQSVPSVWIINLSERKTSILLEVLKLQPEKKPVKLTGWSDEESEVRSFLQCLPYISQLSFSEEFDVSDGVKLFGNLICAAAEREHQTG**EKILEMLT**SVYRYETFPLSDRDMNDYFKRRYQCSFLLDLFSHV |
| TRINITY\_DN50020\_c0\_g1::TRINITY\_DN50020\_c0\_g1\_i2::g.117602::m.117602 | gi|734639227|ref|XP\_010748390.1| | PREDICTED: glucosamine-6-phosphate isomerase 2 [Larimichthys crocea] | 21.1 | MRLVILDDYDLASEWAAKYIRNRIIQFRPSSERYFTLGLPTGSTPFGCYKKLIEYYRNGDISFKYVKTFNMDEYVGLPRAHPESYHSYMWNNFFKHIDIDPANAHILDGNADNLEAECQVFEQKIAEAGGIELFVGGI**GPDGHIAFN**EPGSSLVSRTRVKTLAKDTIVANARFFGNDLSKVPTMALTVGVGTVMDSKEVMILITGAHKAFALYKAIEEGVNHMWTVSAFQQHPRTIFVCDEDATLELRVKTVKYFKGLMHVHNKLVDPVLSIKDQ |
| TRINITY\_DN73442\_c0\_g1::TRINITY\_DN73442\_c0\_g1\_i1::g.94183::m.94183 | NA | NA | 36.2 | MRLGSGDPCLQKQRQTRLVEPPGGLHCD**EDVLVPQL**RLGDTCALRARESTVSSTTSSTTTVIISTSRLERIVGREDGGSLLDGAVVRAGGWMVVDHPESGGVAGA |
| TRINITY\_DN56898\_c2\_g7::TRINITY\_DN56898\_c2\_g7\_i1::g.43127::m.43127 | gi|657564868|ref|XP\_008285705.1| | PREDICTED: elongation factor 1-delta-like isoform X1 [Stegastes partitus] | 21.1 | M**PKQSTNMSGVQC**LATENIWFDKHSYDEAEKRFYEGVNGPSTQQQQVKTALQQPKGRQQKRQHRNSSSHGGDQELVTRMKSLELENQTLHKVVADMRAALQKLESRVAS |
| TRINITY\_DN55970\_c0\_g1::TRINITY\_DN55970\_c0\_g1\_i2::g.86185::m.86185 | gi|657754097|ref|XP\_008312570.1| | PREDICTED: peripheral myelin protein 22 [Cynoglossus semilaevis] | 7 | MLLLLLGIILLHVAA**LVLLFVSTIVS**VWTSGETSTSDLWINCSTANGGFHCDPASTGEWIQAVQALMILSIIFSCLSLFLFFCQLFTLQKGGRFFLTGTFQILASLFVMSGAIIYTVMSPEWVPDTNAFGYSYILAWVAFPLALISGLIYVILRKRE |
| RRRRRTRINITY\_DN94585\_c0\_g1::TRINITY\_DN94585\_c0\_g1\_i1::g.95793::m.95793 | NA | NA | 17.2 | QELEAIRDEAVVLKAQLDKEATCPEVKDLLSQSVQCLLEEKAQLKQETE**ELSNGLAT**MKVLAEKLDEEKREVLREYMEKTQRIEEEKERLFQSMKQFEQTAREYSHELTYYDAEET |
| TRINITY\_DN60101\_c0\_g1::TRINITY\_DN60101\_c0\_g1\_i1::g.92996::m.92996 | gi|736230689|ref|XP\_010782413.1| | PREDICTED: chromodomain-helicase-DNA-binding protein 8-like [Notothenia coriiceps] | 13.9 | QRNVRSVACCDETGLSERGALPLGLYGDGVGSSLEDLVDVFLTEFGA**FVFFVHQSSVRSLS**QQVLNLLLGQLLDPAVGVLPSAHALQHGLVQSQLQTGLVK |
| TRINITY\_DN58729\_c0\_g1::TRINITY\_DN58729\_c0\_g1\_i1::g.92118::m.92118 | gi|734629649|ref|XP\_010743126.1| | PREDICTED: fructose-bisphosphate aldolase A-like [Larimichthys crocea] | 71.9 | QYKKDGADFAKWRCVLKITSTTPSQLAIMENANVLARYASICQM**HGIVPIVE**PEILPDGDHDLERCQ**YVTEKVLA**AVYKALSDHHVY**LEGTLLKPNMVT**AGHSCPKKYKPQQIA**MATVTALR**RSVPPAVPGVT**FLSGGQSEEEA**TLNLNAMNQCHLHRPWALTF**SYGRALQASALK**AWGGKKENGKACQEQYITRALNNSKAAVGKYVSSGDKGAAAQESL**FVADHAY** |
| RRRRRTRINITY\_DN12320\_c0\_g1::TRINITY\_DN12320\_c0\_g1\_i1::g.83169::m.83169 | NA | NA | 16.3 | LLLLFLLYPLTFPPLFPSILLPIPQT**LSILSSSF**IILLFFTHLLLFYLFQTLFLILYQSPHILLLLHFFPLTLIFQQFFFYFPHLPLYPYSP**IILLLLPF**SFSLSFSSSPFFLSLFLLFIPLFPSSISFFIRFHSSLPVLP |
| RRRRRTRINITY\_DN58368\_c2\_g9::TRINITY\_DN58368\_c2\_g9\_i1::g.45504::m.45504 | NA | NA | 37.5 | KTLLLRTYGDATEIKINSEDSLEEGDLYWQVKIPERGIYPIKFAAKQGKKVTVPTKFKELEETDFRPPDEVFIQAETKRGDAEFKYTGSSEETVKHIKLRHFTGDKTITIGDESKIEEGDKYWIGQCDERSVKCEIEAAEGVIAKCDSLAAHFHVGPDVVPEEVEVLKKKSRKGKKGTKGGDGQNTTEEDNSDGVVPEEVEVLKKKSRKGKKGTKGGDGTTEEDNSDGIVTDPVLPGDRARRRKGKGGEGGEGGEGEGELDDDSFELSDFDEDGFEGGVG**AGEGGAAGGAGAGGAGAAGDVGGA**GGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAAGAAGDAG |
| RRRRRTRINITY\_DN49208\_c0\_g1::TRINITY\_DN49208\_c0\_g1\_i1::g.56946::m.56946 | NA | NA | 21.6 | SLSGSLSTITLDRQQLEGSLKSVEKRMGEASHPQQARHLEERLKKMEAVSSDCEAKMNRLDQETQSQDARQRTVKDLKERLCALEAKLQVESTEAFHLKSATRELDLRMTEIGTSGQAAVCDELSRIVQDKDQLVQNLRAAENRLRQCELSTRRVSTDQSDLLAHLEEREGSFVQRERQHQGVCMDLPRLRQLELELEQSHLSDQIRVLQSRLSQVESCCERHEREKRCSARQSTVH**TLEETLSKNQAE**LATLQTQYQIHQQEWEACRRHYEKLKDHLQTVESLEAEKSRASSEKFQKRQLKHHYSRKLKELEECVKQLRKEYKAVLEQRDTQADEVQKHLLKIELDRREILSKSTLLEEETTKLRYGMTQIETEWERRQHNVMIDIQRMLEQLEPECSSLVSSLDPNQLSGLYAEM |
| TRINITY\_DN34194\_c0\_g1::TRINITY\_DN34194\_c0\_g1\_i1::g.112725::m.112725 | gi|734624207|ref|XP\_010740142.1| | PREDICTED: stomatin-like protein 2, mitochondrial [Larimichthys crocea] | 11.8 | MMLRTLCRAGGALLQQSQRTAPRLWVTPAQQRWASSLPMNTVVLFVPQQEAWVVERMGRFHRILEPGLNFLIPILDRIRYVQSLKEIVIDVPEQSAVSLDNVTLQIDGVLYLRILDPFKASYGVEDPEYAVTQLAQTTMRSELGKLTLDKVFRERESLNSNIVHSINQASDDWGIRCLRYEIKDIHVPPRVKESMQMQVEAERKKRATVLESEGTRESAINVAEGRKQAQILASEGQKAEQINKAAGEAQAVL**AKAEAKAKAI**RMLSDALTEQNGNAAASLSVAEQYVTAFSNLAKESNTILLPSNTGDISGMVTQAMTIYGKLAKTASPAAATATAEAVEKEMEEDQNQSTSTQ |
| TRINITY\_DN39161\_c0\_g1::TRINITY\_DN39161\_c0\_g1\_i2::g.77899::m.77899 | NA | NA | 13.5 | MRAAQPATHSRPSWARPCGTRRCPTTGTTSSWSTWIWRSSCRRTVSLPPTRPRASRLSRRRSSSSRHNNRLLRHH**RPRPLPPWST**SAAARPPRFTRAWRLRPASAAPAAQQHCQHPGTPPAPSTQSPFRCPSPTTPTRQTWLCPASPARKCSTQGNASSPQRS |
| RRRRRTRINITY\_DN55113\_c3\_g13::TRINITY\_DN55113\_c3\_g13\_i1::g.60702::m.60702 | NA | NA | 15.9 | ESATRCCGTLISVDTRQRKGKIKKYKPELSWRSRVKDDTVHRAALAASSTKGNQFSNQR**FRLLLGRAN**RASQFSETHVYVTPLLRRDCAGGGKFAPPPPQREYAGGG |
| RRRRRTRINITY\_DN57974\_c2\_g2::TRINITY\_DN57974\_c2\_g2\_i2::g.44166::m.44166 | NA | NA | 57.4 | MSRIHINVTASDSGLENNLRLTYAGADDEKVASIVLTSLDSTNEVRYREDGNPLIRGSRVWEVSPAPDGSFLGEVKLSKGPEISVDHPLAEIKPPSSIVNLSTTASCQGFQNKAKITYKGTDAVTAERIELTYVHQSCSLRINSTASITVNDKLWEVEPSPEGAVECTFIVNQGEDVIQSRPQLLFHPADSRKAPDSTLSQGQTISMQSHSSVVEKHVMEQKVVEESIKSARVTVTCTTSVAGSSNAATCRYEGSDSVESEYIELHVSGSEEFIEYKGGQSLAKGNKLWTITPRPEGTVKVSLKVISDSNATVDSLGVSFTPKREITPSMVRKPSKIPSTVREKESPTPSKPTPSKPTPSKPTPSKPSVPSKVRQPSKVPEPSKVRQPSKVPEPSKALPSKAEPSTVRQPAVVKEKSESKRISLTFHAEQKGGANEVELTYSGEDSMEVASIEFSSNYQTSVIHHRASSGIVAGEHMWTICPAPEGAVDCEFRALDGEEVTLSLPKTLIKAPVSPTERPREVVTTTEKVTEKVSERVTTKSSSVHYVETRTMEPLHSSPPEEDRRLSSFAAYEEGAVDLTAYDSTEGKASKCVVRYTGGDETVCNIIQLTLVGSINTMHYKHSQHIEKGNHFWKVEPEPKAQVNLTFRTNTGYPVRHSRLRITIRPAHDLSFPAQTVVEFKREVSRRESRLAQKREEYRSAFDVKPYVIDTKVAREPTPSRRREPEPTPLKKIPKPIYESTFATLHESEVGESYATVTVTSKQKTTRTKEEFEMRKLESKYSSIRQATKHPRLLEQDEREAYVRQKERPPRHTTKDHRQRLDIFSPGAEYKSPIRYSDYRHVEEGEEDDSYARRPSSPRLASLEFRVPSLSPPSASYGLELEEELRLREEETRKMSLYEDVPLLLEEDSLDGLSRRRIRHYADIEPSPTRHRAPRVTELDDQTMSSIRWKPKYQDKIRIPVEYFQEWRSLRIRKMRKQKIKDMPEPFEYQDRLKKYWKMDSFPKFHKIEVDEELVAPNIVRPAPVDYPMRLRKEDARKKREEQEKKIEAETKEGKKTTVAPKFMTAAERVAQVAAPPLPTIVTGSLIQSLRVKKDLEEKKAAKEKEKQSPEYEKKVHAVREVKLTAQCSASGASNTATVRYVGSDEPLTDRVHLIYYDLGEHVVEISPGFALPTGDKEWKLTPHGSVRIEFRVKQGERCEVNALLRKFMPRLTLDAPKPRPVVTLRSKCSDDGYRNRAVVSYEADDEKDLDHIILQYLGKDTIFTYKKDDQGPILKQGSKHWMVRPEPHVTITVGFRVDEGIYATRNVLPLTFEPPKQLMRATDVRRKTRKVVRTTFFDRYKRVGNIFLEAYASDEGYENVVKCRYTGDDARTVKSVTIVALGDEYDIEYKNGAELQRVGCYWTVETTSDYNDINCIFKVNDGENAVAHTVQGALPGHEFPAIKVKAVFVGRQSRISGGCAVRAASIVTSWEKRVMSQYYRKHRGTPIARGSIEEVPKTLWPHALAEAASMRHKRDKTMLRDTFDLAEVSVHTFSEDDYSYAANSINDIMQQNTEATFPNLGSLLVYALVGVSWMDTVTSVMDCQHIEPAAYEATTYQVKIQDGPTLHRSQGLEIIKVNSSTRTTYVINEPRIDFHGYSQTHLFELASCIQRIYNAVERENLEFEASSLREFIDGGSIFDYIMVLEEPSDFSEHLLLFSTHKALNLTAIEKKVIAQDAGRVKVFKAMYTKESSIDVCRHVIGFQGRGLEEAIAYKNHLNKAESNPAKGKRVHGTDDVERDYLLVRSKDEKTMVPGSTESPASQGFKNEAIARFQYSTGGFLNIVTYRTDRSQAVREWREATTPCKEIIYSIVRSGGDNAPAVWNLTVSDRSVDSAKIGRPPDPVDAVDLEVTQQDIGFRNKACVIYFGADKKEVGNPFVLATFSRTVIVQYHGNSDILDQGKQWTIVPDPKGSFPIKINVVEGRLAPIAEKDKLNKPLHIKAPVEVDLSVTACISGGQNTARIQYVTSDEEDAETIVLQHYGGKFEQIKIKKGDSHIEKGRRFWKIVPKPQGTIKCVLTANSKYKVSMNRLEEKFAPARVDVATAPIMPTTEESYDSQGGLNECKVRFIHEVGETLRKVSFVTQKIEDTTVPTWETWEKKDKKHKKELCYSKIKSGGDSLPPKWSVVCSDKTIGSVVPSQPPSPKELQSKILIPSTLELPESNGYRNQAYVRFFYGASDILNPVRCSTGNISSSVLEWETGEKDERKEVIYNTIMCGGDDKPPKWSIIVSNKLLADLVIPGQPVDPKDYIEVTFPTDARGFHNHLRIRYKGGHVRRQVNKIVLHTYHETTEISIDDTNELTKAGHLWMIKPEPRGIYAAHIRLTTGLGAYYIDKLPYDPHFSPAAELVLVGSTEADGADNIAKCTYEGEDEQQDTMISLSHNRGDSSMEYKRSEVIEKGAHYWKIEPVPRGIIQCKMVAPQGLKTTVEDMEKRLSPKTEVSLKTKICTVTRRPRSMGTENEAFVRFEYETAEALGRMTFEMQKLRDRNCKKWTSEVSKRYEVWYGLVEKGGDCEPAQWRIAILNNTVNVTDIEGPQSPKEFPDKCTVPDSVPGAESEGIDNVAVIRFQYEADPTLGPLTFMTSSIKTEYRSWTESSVLKYEVFYGTIASGGDDKPRSWALAVSSKTVDMIEPTTSSPEPPCLPTKAMLPEESKLSASVGFSNEATVKFHYETGERLGKVVLHTDTVRSDVTYWANRTAERREVIYGLIESGGDETPAKWCVKVSNAQIDEFVMPGEPANPRGIVKVKIQAKKKGVRNELLLDYMGSDSREAGKIVLESADETSAIMAKTSVAGSDKLWKCTPHPKGKIPVSLRVVGGHRVVYVDKYKLELDYDPSELMETVTVTGPVEAPEGSGGANCAMVRFKFEEGQPMKTLTYECILSPTTNCKIWAMTGVKQMEILYGDVRADGEDDPPSWALSVSSKTTDTIRPNQPCGPPDIPDTAVAPKSCLSPKSQGRANIATIRHEYELGEILETSRYRTMTVPNKNARVWRDSRVEKREIIYGSIDLGGDEEPPEWAVTMGDRSVDFVVPRGPPGPVNKLSKCTVIESQLFDGTGYRNVAAARFVYEDGEILNVFKFTPRSVSDSVPVWGPRHADRQEVVYGSIPAGGDRAPPDWSCTVCTADIEDLRFPGSPEDPKSLVVVKIVETIVGVANKVELSYDGTDNITTDSMTLKSFKGTSKIKVRDTVKLKNEHFYWSCVPPPRGIIPLDLELTKGALVNVVKQPISSFDVMPMVRQEQVTIATVLEKPESAGRSNVAKIRFLYQEKENLKEITYEFDTLKLTAVKMWKDTGFKCAEIVYGTLRSGGDHEPKEWGLSVTSKTVDIVELKNPPLPVECVLIVDPTESPEGIGYINEPLVRFYYLMGEMLGDIKYSTKSCKATVTKYARMSAERREIIFNNVPAGGDVAPAEWSITASDKTLEKIKLPGTPGPTDYVKVLINVEQKGASNEAVLTYKGADYRHVKDIILTTSSSNVEIFGRTHLDVGPKSWTIAPTPRGTVHVFMRLSGGARLCITKKLDDHLEFDPPEIREVPETEACPESFDGTGNINIGAVRFCYKKGASLGTVVHETTRLTKEHAKSWEEAGAEQMELIYGMVDSGGDEVPRSWALSISDAHTDTIRPISPPAPTCTPVRCVVYLSVESAESEGAKNIATVRFQYINGETLGSVKLTSDLHAGDRNVKVWRASKRERREVLYHILPSGGDSEPKLWEITAFDKGSALIEPAGPPTPVTFTNRAIMPGSQLHVGPGYKNVGRVRFLYETNKFLGSINCTLEKCEANMIVWNLRNTDRREVIYHSIDDGGDEVPPKWSLTCSEETIKSIEISGECVGPTDLVKVNVEATKTGSVNRVTLIYKGTDDRDCFKIIAMAKTSTYQLHYKECLELDRNGKSWSAKPDPRGGVAADLVLDSGARVMVTESMLKSDLQAKPPEFDTKCQVSGTSESPLSFVQNTNKAIVRFEYPEGEGLATVTYFQDTVNTYNCKLWRGEGTLTYPKREIIYGVIPSGGDNLPASWKLSVTTRTVNTVEPKSPPDVPNQAVAGKSAESAKSLGASNMAYVRFQYELGEVLAEVKHYCEFCPIKNERVWLINNREKKEIWYGTVKSGGDHYPEEWKLTMTNATVNFVSPKTPPGPPTFPHEAVITESETSKSVGFRNEASIRFTYQMYKTLHSVHLTTRKVSSNILQWATSGSERKEVIYNTIMCGGDDKPPKWSIIVSNKLLADLVIPGQPVDPKDYIEVTFPTDARGFHNHLRIRYKGGHVRRQVNKIVLHTYHETTEISIDDTNELTKAGHLWMIKPEPRGIYAAHIRLTTGLGAYYIDKLPYDPHFSPAAELVLVGSTEADGADNIAKCTYEGEDEQQDTMISLSHNRGDSSMEYKRSEVIEKGAHYWKIEPVPRGIIQCKMVAPQGLKTTVEDMEKRLSPKTEVSLKTKICTVTRRPRSMGTENEAFVRFEYETAEALGRMTFEMQKLRDRNCKKWTSEVSKRYEVW |
| TRINITY\_DN57211\_c0\_g5::TRINITY\_DN57211\_c0\_g5\_i5::g.21089::m.21089 | gi|542186679|ref|XP\_005469859.1| | PREDICTED: sorbin and SH3 domain-containing protein 2 isoform X12 [Oreochromis niloticus] | 18 | MNTGSDSHSSDLDSWRSRSATDGLKNGDASNSSLAAKGFRSVRPNLQDKKSPTQGQVLSHAMNGSTSHPQRPLSPPSYPPPPASLHTGLPRQSRSSEGSECVTRESVVSGHTSVCSTVPIARFSEEEKKVSVIKAPHYEGIGPVDESGIPIAIRTTVDRPKDWYKTMFKQIHKVHKADDDYSDTYNATYAVINNDDYSLSSTATMAHPPPRTHTYRPLSKSPSDNGGHLGPREPSPSPVPPPPPPMPSLLQLRARDSDRDKDSPDMNEWGPPDRKVDTRKYRAEPKSIFEYEPGKSSILEHERPTYDDIDLENEPWYKFFSELEFGRPPPKKRLDYNPDISARQRIETSLHIAPADKAPERPASAASDYRKRRKSEPSSSQVNAQSQSRSVISPKPVDAYRPSSSLKKPVIRSSPSSPSRAKDQDVSRSYSTMDGRHTPQSRRPTPDREKQPARAIYDFKAQTAKELTFKKGDAVNIIRQIDNNWYEGEHRGRVGIFPISYVEKMPSTEKQQPIRPPPPAHVREIGEGVARYNFNADTNVELSLRKGEKVIVIRQVDQNWYEGKIPDTTKQGIFPVSYVDIVKRSPSKSSAHHIDPHGHPGIRTPSSTPVKPFYHLPPPSTTRDLPSSPHPPLRRLDLLAVTDEWLSLTMVPSASTPPHSIAATPLPPTPPPLPPDLTFLQRAQERRTPSPSPAPSPAPTQRGLALLP**QTFSRTPP**LKEGRLGVGHAPPALPLSFPPSPVPSPPPPATHFSLTSSPCDSSLRDNSSWEFIETPQKLRNAKPEFFSCTAPEPIKSPTQTPQSHRSTAPVNKSHKPPDIELQVKDPYDDLLTMILDGSTSAENVDFSRWSPIDSPPAPLTHETQSSLKLKAEEPNQTEWETQVPTPAGQPAGDVRLEVQFHKPMTMEPLSITWGEQPETLNDDEAVEFEMPLSVEGKGFTELFIEEEDDDLEEKEEDIRVLSDRLSPQADVSPSALTWLSHPGLSSPSLPPPLTSTPPPPASSLSSPSSVPPPPPPPPPPP |
| TRINITY\_DN55782\_c1\_g2::TRINITY\_DN55782\_c1\_g2\_i2::g.20017::m.20017 | gi|657573930|ref|XP\_008290650.1| | PREDICTED: LOW QUALITY PROTEIN: protein FAM184B [Stegastes partitus] | 15.3 | RERDQFEKDRNTLRREREEEKEGLHKEVEEIKERLRREKEEELERQRKELEVERVRVRSQLDKNIEQVEAERANVQQKLEEEKKRLVEKAEEDRKRLKEQVRKAIEEVMRRHAAELHSVQEALSSEKKTNQEVCTRLEEERRAGEELRNELEKEREELRTKLKDATNEICRLESAIQQQEKKDKAAPEAAASCGPHCSRLEEELHQTRSRLARVQEDAEKQWDRQQREIASLRADKHRLEEKVLEQSRLNTERSLLEQSQRHTEDRIRAECEDRLRAEFRIEMNAAVAESEQRWQNREQEMQTQMSELQGQLDEVEEKKACQGDDCHGNPEIDRLRKEVQETKEINKKLRDLLQEPQSQSLAEERHSHTMALQTLEKKAKEDVLSERNRLLTMHHLELDKQRAELTQQHTEWSRQMTQRHMQQIEDLQAQLQAHTQMMALQQDLKQQNQNQVFERQLDESRCAMLELQRENATLKKQLKEKSIQKNVETEEKEEETVELRKKRDAQLEEEAQRLKEEVEKLRVEMEKLEESQKHWEERKEEDVKEEEEDEEKKKEREEDKRREEVEKIRREHKKEMQSLVSEYSSAQTHLQARIVALENELREREERCRRREPRCDDLQLGRLQERLSERDQLIKRLVEERHQLQLHPPVAGDSSTLRLRDSKSRPGSVTPTMRRKRVESPPRVTSIPSAGTYDRSIFLPQSSSSSSSSPS |
| RRRRRTRINITY\_DN57594\_c0\_g1::TRINITY\_DN57594\_c0\_g1\_i1::g.88869::m.88869 | NA | NA | 16.2 | SATDDPRKLVASYKMPAG**DAKLQVEVLT**FISIVQEVPAMEADEPIWVLTLESKKGVKRHHFSNLGAVSKCYIRKQVGYRLVLVDFSQDLVGMVMAESDLPGCEKVFVGFFLESSLEQVRKSVTKKDNCHSAQKQVQKTSLGLHPGCKLSSALLRHVIIDAYRRIPSTFHTYFPVNLAYHKFLAEDTVEGTCFYLAMQMPRSCMHTLVEKRASSYEDDGITTNLSKHLAGASSLDINIGLQDCLEQLEDVMKTKPPPHRRLLALQPFKRYIHNATAINALLMFEEVLKNSDRYQYIYCGQPMMTEKDLTFSLKLQDLRLAGGSFRQARLNKAISHLNLVAQHIEDIPHVPDVPPLEEASFMKEPAKIMSQAHDYSLKVCSRIVSRGFWESLIKGEPTIKWIVSFTLRDTLPNLSCLEECLLRPLMPIVKQVMYVSTARQSAVADLTNNEEVFYSVDAIHVGVEFNGDPLQKCSLADDLDRATAPDITFICENRLDKRQSMEEPPITWPLNKPLCDLVEDSFESFDVDYETLIGETEPEIEGAQGLTKALRGEAFNNDAPWDTIRCIFLTSAYDGPRSTFDEPCDSLPVNIRPVRHDVPSFMAFPKDPLFKLFGTAARSHKREVIYVVKATKQLIEGNPRPAPPDELQGGQETCHDEVIVDPKAAHEAKKQMKQVMHEKQAESESAGECDTDPRVVKWQEQPLVQVVVVDGNLARNRSVIGDLFIDWTDDPSPIFAEHYKKPNIRLQGQILEGRKLGHSVEESTMYPEFVQKRPGRGGKNKRKDAPSNTTSARPQQMKKDKGHPSMPRSLQTDVKTGERSKEEEPHKPLNKKKSKATKDQDQGSAGAKKPSQPRGVLMDAGKSDKNKKQQKQSKNMENPTLGALEEGSEVDGDHSTATDRRQGRRQRDPMGQKRECDQLTNRSSLKEMYLSLSTEEAKNRLSSPSFDSSDSFDNPVQDRKRQPINLRDSQAKLLTSPGNGERQCSLDKAYQELYLSFKSSRHQSLLRAYADKQPPTSSQNQSRKPERSQNAKKSQRPSDMHCGKCSAAESIGTSTTYSLQRESSFALRSVAANVEET |
| TRINITY\_DN53444\_c0\_g1::TRINITY\_DN53444\_c0\_g1\_i3::g.106400::m.106400 | gi|734642277|ref|XP\_010750064.1| | PREDICTED: lysine-specific demethylase 4C-like isoform X4 [Larimichthys crocea] | 7.7 | MAGAEVFTPANPTCKIMTFRPTMEEFRDFNQYLVYMESQGAHRAGLAKVIPPKGWKPRRTYDDIDDLMIDAPIQQMVAGQSGLFTQYNIQKKPLSVQEFRRLANSDMYCTPRYLNYEDLERKYWKNLTFVSPIYGADVSGSLYDEDIEEWNIGHLNSVLDVIEEDCGVSIQGVNTPYLYFGMWKTTFSWHTEDMDLYSINYLHFGEPKSWYAIPPEHGKRLERLATGFFPNSFKGCEAFLRHKMTLISPSILKKYGIPFDKITQEAGEFMITFPYGYHAGFNHGFNCAESTNFATLRWIDYGKVATQCTCSKDMVKISMEPFVKRFQPDRYPNWMVGKDSTPIDHTHPTPSTTPELQSWLQGRHKTKPTNKGSSHSRMRSKRLRTTEEPVGLDGSSTLSSSKRKGLGGPSGPKVRRSVTGTTCREEKEKKKEVEPKHNLNENSLQLPDPCRQMCVVKVNRVESNSLGFSNKRPSHSSSCSPSPSPASPVKNDVKAETVAHDDPQHLSGSGATSRTPEGQHPEATQMHPGINQSRCCSPDPQDLSTSQDCSGLSGVTHLEANKPNPSSHTTSTSAETEMNLCPPDCEAQTSSSSCREDTLSLTPNTDISMDTGTENYTNDTAKAEKMDTLADRKHITPHSTTEALYDLKAEPVEGDRRTSCGSFSPSGHTCSLEKSSTEENLFPPLLQRNAADMPQLTPEPADKVGICPLPPVLTQEMPSLTPADDVLTDEPKSRLRSHHVAPVLQRETPTGSVSAGGAKRGEGENELMTSKESPTVEHANNWHFDSPYNCKGAAASSLEGNTAHLAANAMHKITSGGAHKMLIMPDIAVQKGHTKL**ENLTPGQSSATS**GQLVQSGAPLTQQQSNSVELASTDDSKESKERDSTFSVSSAGSILTGASDNNPPAPSPPLCTQSDSHSALQLNHHTTFSPSHCSSQNPYMEPKSFSSSIWKNFSSQSPAVLIQSLHPELPSDFTHDPLPYTMWTEPQCKEVTDLEDPDQVLRESENQEEEGGPLTWAQLEPTSLVSVGAVEPLGLCGDYGLHRGEEEGAEGLSLCRELGRQREAGESLHSDAAVSPLGTREREQDGVSDMEIGGSDGEEAEQQSSVKGESSSDSSDEEEEEEEEENDTSNYECDESGLEPGEVCAYPALSVKRTTKSWRHPLRKPTARAVPTAVKQQATSDDEPPEASLAEEEEQEMEVWAKPLVYLWQNRKSCFTAEREYNAQAATMQPCCAVCTLFMPYYQPEDKAEDNRPATAKDTSKSSSPTEGPTRPCGGLRRTKPLIPEICFSFREQNCPPTPTNPLLQEDGTSPLLYCQGCCLQVHASCYGVAADDVSEQWSCDRCTEGSFTAECCLCNLRGGALKKTQNDKWAHVMCAIALPEARFSDEAKRSPIDTSRIPMQRYKLKCIYCRKRCSGKRQAGACIQCSCGRCPTSFHVTCAHAAGVIMEPDDWPYVVSITCHRHQSRSSSAKQRACQASISLGQTVISKHKNLRYYSSKVTQITSQVFYEVMFDDGSFSNDTYPEDIVSRDCANLGPPEVGEAVQVKWPDGLFYGAKYLGSNVSYMYQVEFEDGSQVLAKREDVYTLDEDLPKKSTASSMRFQDAFFTTQGERKRQRTPNSRFQKDYVALPGLRTTAKSTWEQRSHKGK |
| RRRRRTRINITY\_DN39870\_c0\_g2::TRINITY\_DN39870\_c0\_g2\_i1::g.104826::m.104826 | NA | NA | 31.4 | RALQLRPAPLSAHQLQKRAHKTYGTENKFNNVAQRLFKNAILNDPSVDSQKCTYCIHEESDLLATRICDDCYSNGCCPIVVADTMLDNCIPCLLEDPIPDTDDESSSQDHPVFPPREKKGQAYAEADIAPIAYEGTSTLMAGKTGPEAKVMFSQPIGKSIRVPKPGEVSKDQVMLMPCQRIYHGAKGCRFCTYHAPPPGVAKKSYHIPDYEHNSQSMMAKIKDEESANADVLNATKALQALSMSPSSDTPRSSGVVATDSRDVIFTRGAPKVG**GLPTRRVIVS**SHKPIHAEDDTYEERTQANTIQLDCDTAKLRERAMIQRKLEN |
| TRINITY\_DN112195\_c0\_g1::TRINITY\_DN112195\_c0\_g1\_i1::g.135113::m.135113 | gi|548418414|ref|XP\_005742228.1| | PREDICTED: immunoglobulin superfamily member 10 [Pundamilia nyererei] | 25.3 | GEAVMVVQLEVTSMLRRPIFRNPYNERIVSRIGKTTVLNCSADGNPMPEIIWTLPNGTRFISGLDHGSRHHLGTDGSLIIYSSHKDDSGKYRCGAKNIMGYIEKLIILDIGQKPYILTRPRGIIRSVSGEPLFLHCLSDGSPRPRIYWTIPGGHTFTRPQVLGRYQLLENGTLVVQDTTLHDRGNYICRARNDAGEALLTVPVLIIAYPPRITRGPPPSVKAVTGTPIQLHCAANGVPKPEITWELPDHSVLSTAEQGRPTGSELLHPQGTLIIQRPTVSDSGTYKC**LAKNHLGT**DSKVTYVHVL |
| TRINITY\_DN43618\_c0\_g1::TRINITY\_DN43618\_c0\_g1\_i1::g.104607::m.104607 | NA | NA | 22.3 | ALLDVEHRGSDGGHRLGRLSGWHVEDGAALVHGEHVGARADVDAGVLGLDVLDGQDAVEVHGPVGKLPVTPAGPHQGVGRGLALCSTDEADCRPHPDSLRFGLLNRHLNGFSLDACDNYLSAAPVGAALVSA**GADVDAGVTGLDVGEVQ**LCSLSASVCSAGDGPSVLSGPVEIVRRRSGHLAAQGDGAALGRQDPLWINLHHQGGCSIVRTTLLPLLWVSNVSRSTTFTVLAGVAGLAGRALVASVSEALTGGRELVVGVSVGAGAGLAILRSANSRVAEEAGGALLAEFTLSVMQAARADAGLWVAGVRVAVTFTQLTVTQV |
| TRINITY\_DN58550\_c9\_g1::TRINITY\_DN58550\_c9\_g1\_i1::g.62529::m.62529 | gi|1007751297|ref|XP\_015815187.1| | PREDICTED: protein timeless homolog [Nothobranchius furzeri] | 40.4 | EEEDGPRSPAGDPQEEDEKEEKEKEEEEKE**EVSGEQRAQ**ALRALLLARKRKQPPGSEPTAPVSDSTPSEKTHSPAERSQSRKTSAKRSRSRVLEDDDDDEEEEKEKEKEDGDSSSVMDVDGDADSDGELNTSAPVK |
| TRINITY\_DN54061\_c0\_g1::TRINITY\_DN54061\_c0\_g1\_i2::g.17164::m.17164 | gi|808865870|gb|KKF16666.1| | UPF0364 protein [Larimichthys crocea] | 18.1 | PSPSATMMAADQTVLGVPPSLSGKVVGSFAYLTIRDRLPTILTKVIDTIHRNKNKFFEEYGEEGIQAEKQTISLLSKMRNELQTDKPILPLTDALQDTESWNQYLQRHRGSHGDEESVSWFKSPWLYVECYMYRRVHEALWLNPPISDYDVFNEGKTQSFFESQQAVMTLCTYLGGINKGMEEMSKNQLLEHFNKLLLVSLWGNKCDLSISAGQDNSQKTSPIDSLSSLQPFILVDDSDMVWSTLISSQRPGQSEKITGGRVDIVLDNAGFELVTDLVLADFLVSSGLAREIHFHGKSIPWFVSDVTANDFQWTIRQVMAANHKWMSKSGFQWQNYVKEGVWSYHDHPFWTQPHEFCDMPADAPDLYATLQGADLVLF**KGDLNYRK**LTGDRDWDHTVGFDTALRGFGPAPLCSLRTLKANIQVGLQQGQGEKLSSQDPDWMTSGKYAVIQFNCRKSEQ |
| TRINITY\_DN88080\_c0\_g1::TRINITY\_DN88080\_c0\_g1\_i1::g.27057::m.27057 | gi|808858922|gb|KKF11228.1| | Tyrosine-protein phosphatase non-receptor type 13 [Larimichthys crocea] | 29.2 | SRQAWDRSVYQTPSSNLGLGHYGSTGHLDDTVHSTFYSPNQSMTRSDLSKRHPSSPVAADLESSPLPMVSSPTAPS**PDPLPPPL**PLPLNLTMAGNGQDIEEFVPEVELKVSLVKSEKGSLGFTLTKGNDHGCYIHDIVQDPAKGDGRLRPGDRMIMVNTTDVSNMGHT |
| TRINITY\_DN28035\_c0\_g1::TRINITY\_DN28035\_c0\_g1\_i1::g.5665::m.5665 | gi|583968584|ref|XP\_006779751.1| | PREDICTED: EMILIN-1-like [Neolamprologus brichardi] | 11.6 | LRPSYSLYTGGHAHSARATSRHRNWCAFVVTKTVSCVVEDGVETYVKPDYHPCNWGSGQCSRVVVYRTYMRPRYKVAYKMVTEMEWKCCHGYSGEDCTDGPVGGAGTQIASTRPQPRPGQGGGTSHGQGGGGSASGSSGGHGGGADREKMRQLEEK**IESLTKNLQD**LRSTLEQESNKPGLSGGRGGGGRNPADAAQPEIKETIHSIQAKLDQLDNRTQAHDKTLVSINNHLVNGKGNDMDRGFSGGVNSLKEEILRELERRVSLSCSSCQAGVEDLRRQQEEDRERIRALEKQLNAMDVRYLQDLGGLRRDVTRLQGCCDTVDDLQYRVTDAERKISSASENIDILQNHVDDLRGGEEGGGGRRKEGGKGGGRKRRKKEGR |
| TRINITY\_DN25797\_c0\_g1::TRINITY\_DN25797\_c0\_g1\_i1::g.108128::m.108128 | gi|808877642|gb|KKF26066.1| | A-kinase anchor protein 13 [Larimichthys crocea] | 20.6 | PDWKEGGVRGGREEEVETTYSRQNCEAADIEETGEEKPAGEERGAKGRKKRRKKKGRRGGGAEHKLSSSSSVESQSQSETLVHREPAATGLGPQSPTEPEAQDTTKREPLESEPACREEAEEEAMHLPSQTETHNRDTHGPVCDVTASESGYAGTTDHGRTDLTEASETKESSEDLSQVLNLDSASDLSQ**TVFMETET**TAGPQGGKETVESSSSPVQQAAGDKETKELAAAGEDAECVDLTGLLESECPEELPVRHSDPTGLAEERSPVEFP |
| TRINITY\_DN25047\_c0\_g1::TRINITY\_DN25047\_c0\_g1\_i1::g.29679::m.29679 | gi|808869080|gb|KKF19258.1| | Ral GTPase-activating protein subunit beta [Larimichthys crocea] | 7.8 | MSISLAALELLAGLAKVKVGVDSADRKRAVSSICGYIVYQCSRPAPLQSRDLHSMIVAAFQFLCVWLTEHPDMLDEKDCLVEVLEIVELGISGSKSRQEQEVRHKGEKEHNPASMRVKDAAEATLSCIMQVLGAFPSPSGPASTCSLLNEDTLIRYARLSATGASNFRYFVLDNSVILAMLEQPLGNEQNPSPSVTVLIRGTAGRHAWTMQLFHQPRGARANQRQVFVPEGRPMPNNDVGIKYNVKQRPFPEEVDKIPLVKADVSIPDLDDIVSKELEVQHDKLRILMHKQIEYENALERHSEEIWKSKPYPDPQTDCKPPPPSQEFQTARLFLSHFGFLSLEALKEPNNSRLPPHLIGLESSLPGFFDDISYLDLLPCRPFDTVFIFYVRAGQKSSHEILRNVESSSSVQPHFLEFLLSLGWPVDVGRHPGWTGHLDTSWSLNSCSDSNDIQQTADEATTPEDTGGSVFNGEKKVLYYADALTEIAFVVPSLTENSEESSVHSDSTVEAD**TNADIMPSL**HKQPNLTLELFPNHSENLESAKKLSPLVKTKRSSTGKSFPALGPETKVFVVWVERFDDIENFPLTDLLAETSTGLEASMSNSTSCRSGLLEKDVPLIFIHPLKTGLFRIRLHGAVGKFGMVIPLVDGMVVSRRALGFLVRQTVINVCRRKRLESDLYNPPHVRRKQKITEIVQRYRNKQLEPEFYTSL |
| RRRRRTRINITY\_DN53427\_c0\_g1::TRINITY\_DN53427\_c0\_g1\_i3::g.106537::m.106537 | NA | NA | 7.4 | SQQGGWQSDVPRRLLEEVHRAVDMTDDLDFDGDADLMSDSMSPYIGYTHPHNVPAPSAGHDMYTPNGSAPDPNATAFEPVVQKIQPKVYGDVAKSLPPTYYKSFVEDKPRDPYLFLLHNLDSIRDALSRISFDKTTYPMLNWVMREGAKNPNEAVWAITIGGIESDSFRLLFTGNPKSMLMDQAQQKNVFGLIAGDNWHPKLHKKTLEMVGDFWQWFTFNRGPLSERNFQSWTMTMNRYDDPNNSSISFAKQALFVLNEESLGRNSQVEAKYKMNIADCLQPWLVKDPVLFPVRGPEAFANDWLVTATANNDQSGHVIVVVPLSLTKVQFVLENGGVSFQSEFLITFKEETVSEAGRRDSRKIRKLSMNRFHASLTGTTQHYEMVCNNNLIEGSSDNRTNENKLLAKAQQESIITAKVQPPNMHVNLKGGVLLRVTAAFKTQTKLVQPPQKEIIFTSTVLASIIDTITSNLENLLEEIPGPIPLQQRLHEARRIQQRNQWITEALKECWSQLIDLGGEPPGGNGALQQRRKWQILEDDLIITQQKRLLQLTKQHKEALDLRYKQLTNAERTLWAEVTARKSLLAPERLQRDAPP**LTALSTLQAQ**IRLSEQYQIIFYEQNHQLKRLDNETDQTMLRLEEFAQNIQQYKQSMSDLMGGVPSSSNTAERVLRQETYLIHKICRVLELPCRDYTSKLQNAYHGLKIKLLFGDEGVQHEAKNQLEQILSDLLRKAKFEEQPNELDIVDWLQGEIWQSLYHRVEIPFHQGYLSQMQHLADGQLQQAQIWVAM |
| RRRRRTRINITY\_DN50106\_c0\_g1::TRINITY\_DN50106\_c0\_g1\_i2::g.72987::m.72987 | NA | NA | 33.5 | LGCLPGLWMPPPPFETMHPALPAPKMPMRGPGCPFFLLLPPPPAFTPPTPPPALSNFSMFAFLLFFGAPPSPGPTAAPTPPPPLPPPVPPPFAFPTLAAPPSGSLETVMDGTSERSDGCE**YVPSTDPVTD**VVAFEGGRSLLGVVLCISGGTLWMSPWCCLQTPM |
| TRINITY\_DN52923\_c0\_g1::TRINITY\_DN52923\_c0\_g1\_i2::g.15490::m.15490 | gi|499024963|ref|XP\_004563236.1| | PREDICTED: translation factor GUF1, mitochondrial isoform X1 [Maylandia zebra] | 8.2 | MSAALVLSPLLRRGLHFKMYRKKILNYSWTCTVLRHRWMKGLPVFSSGFRMVSSSTQTDKQATMDLSKFPADKIRNFCIIAHIDHGKSTLADRLLEMTGAIAKTEKNKQVLDKLQVERERGITVKAQTASLFYSHQGEQYLLNLIDTPGHVDFSYEVSRSISACQGVLLIVDANQGIQAQTVANFYLAFEAQLTIIPVINKIDLKNADPERVESQIEKVFDLPREECIRISAKQGTNVEMVLQAVVDRIPPPVASIEDPFKALVFDSNFDHYRGVVANIAVFGGRVRKGDKIVSAHLGKTYEVNELGLLRPDEHPTQKLFAGQVGYIIAGMKDVKEAQIGDTLYHQEQPVKALPGFKPAKAMVFAGMYPMDQSEYPGLRSAIERLTLNDSSVTVQRDSSLALGAGWRLGFLGLLHMEVFNQRLEQEYNASVIVTAPT**VPYKAVLS**SAKLIKEHGSEEITIVNPAQFPERSVVSQYLEPMVLGTILAPDTYTGKIMTLCLNRRAVQKNMVYIDDQRVMMKYIFPLNEIVVDFYDLLKSMSSGYASFDYENAGYQAADLIKMDILLNGRPVEELTTIVHRDRAYTSGKAMCERLKDSIPRQMFEIAVQAAIGSKVIARETIKAYRKNVLAKCYGGDITRKMKLLKRQAEGKKKMRRIGNIDVPKDAFISVLKRKDK |
| TRINITY\_DN20852\_c0\_g1::TRINITY\_DN20852\_c0\_g1\_i1::g.28843::m.28843 | gi|734596266|ref|XP\_010736015.1| | PREDICTED: general transcription factor II-I repeat domain-containing protein 1 [Larimichthys crocea] | 10.4 | FKRPCTYGVPKLKRILDERHGIRFIVKRMFDERIFTAAGKIAREEGKHDLGSTPEDSFPDNLSLPPTAAELVSNPHSSRSTSACVSPLADCEAGPSGDCIPLKRIKTEPPDGEIIQVTVPAEALSPSPASQSIRRSSEAGSLVEDIGEMILQLRRQVESLFSIKYADALGLPEPAKVPYSKFQMYPEDLYVTGLPEGISLRRPNCFGAAKLRKILTASSQIKFFIKRPELLTEQVKQEMPSIPVCDSEPDTKDAAPATEDTAAVSKRPGFSECLESKLSRIDLANTLREQVQDLFNRKYGEALGIKYPVQVPYKRIKNNPDSVIIEGLPPGIPFRKPCTFGSQNLERILAVADKISFTITRPFQGLIPKPAPRRVTLLKKAYASISDDDDINRMGEKVVLREQVKELFNKKYG**EALGLDRSVMV**PYKLIRGSPESVEVSGLPDDIPFRNPNTYDIVCLEKILQAMDKIKFNIKSQLQPFAEICSQPCNTVGTDASTNRRKRKRVQESNRAPASSDLGISTNQIPVMQWPMYMVDYSGVNVQVPGKVNY |
| TRINITY\_DN16805\_c0\_g1::TRINITY\_DN16805\_c0\_g1\_i1::g.2913::m.2913 | gi|657531755|ref|XP\_008302457.1| | PREDICTED: centromere protein F-like isoform X2 [Stegastes partitus] | 10.9 | GKESALLSQTEELQKCKQELDALRAKTEVKEREERSAETTALQPNEEKHCMTVAVCDSADQPKTVTPEAETQTPVSSEEDSELFGRPGSVDSDKTESNHDSACVLLEETECGQDGAAAAAADVVAELLALKQENQQLKQKIAGFTVGSSSLASQTVSGNQEDPFKQSQNAGSAVLPCLTEQRPTSEQSDITAEGHESRLQKERRRRDDEGEGGDLKREDKRTAGAEEELDEISQLHVSHLEEQVVALQTKVRLLSEKTQQQAEELLLWRLASQPPPTSDRSPPDRDDQDQSSAVRHTQVVQESSGNITVIREDELLLSTSSNKLQGRMLFSSLQHSNLPEPKSFHLSKKTAALQEHNQDAAKIDKESEKENQE**INVSQRSEVT**CPAHHRDKRDTELSQISSEKTSQQQQQQQHVTKDLQKVSAPNKTKTTECRPGNPEAKPNASRSTNEINTTNDSSDRPARTEMKSVCSQTEETFCSR |
| TRINITY\_DN7223\_c0\_g1::TRINITY\_DN7223\_c0\_g1\_i1::g.96790::m.96790 | gi|657566147|ref|XP\_008286402.1| | PREDICTED: lysine--tRNA ligase isoform X1 [Stegastes partitus] | 12.9 | EVFIIGKNFLKDTKVIFQENVSDEKSWKAEAEIDMELFHQNHLIVKVPPYQNQAITSAVCVGIYVVTNAGRSHDVQPFTYTPTDPVKQDVPVKKEMPSPVKTCTFDEQIKVLDGAL**MPSMLPLV**KREDVTPMEVTSNLQSAGVFKTADLCPAQQNPDMSAGHLNKSRPFSNNLSQPAGDPDKSQTPVFTNPEPLSTIQKQDIAATGSFSVPADSLLQQGSQQFLLESREGLRQERPGSGSGAVGRLCGEPPPQQQQ |
| TRINITY\_DN52558\_c0\_g1::TRINITY\_DN52558\_c0\_g1\_i1::g.58874::m.58874 | gi|1012506563|gb|JAQ20959.1| | hypothetical protein [Fundulus heteroclitus] | 25.4 | AQLAVAVLTADIPHHVSSRQHDSVLDLAVLQIHHLVEQESSARGPGEARGDELSSVGQDGVTVGAG**EEASPTDVI**QEDTPHFTDHQVKTTKRLLRSKIFTKKHRRFSPKCFYPSFGLNCRNN |
| TRINITY\_DN48857\_c0\_g1::TRINITY\_DN48857\_c0\_g1\_i1::g.72616::m.72616 | NA | NA | 39.5 | MITTRMIIPALSSSLLPSFCLGLVVAALVVLAVFVVEVWLSGGLRGVGVVKSVVGLLVVVPPPFSLVVLGDMLMLVVLILL**VERELLVLG**LALVVILEGIWSLEILSPLPPVTSDTSEY |
| TRINITY\_DN130679\_c0\_g1::TRINITY\_DN130679\_c0\_g1\_i1::g.132129::m.132129 | gi|657565866|ref|XP\_008286253.1| | PREDICTED: teneurin-3-like [Stegastes partitus] | 22.3 | LKTLTAQGQELVLFSYHGNSGLLATKSIQIGWTTFYDYDSEGRLTNVTFPTGVVTNLHGDMSSGAVAVDIETSGRDEDVSITTNL**SSVDSFYTLVQ**DQLRNSYQVGNDHSLR |
| TRINITY\_DN119168\_c0\_g1::TRINITY\_DN119168\_c0\_g1\_i1::g.135215::m.135215 | gi|657557352|ref|XP\_008282872.1| | PREDICTED: tubulin--tyrosine ligase [Stegastes partitus] | 10.4 | GIIMTAPMYTFVTRDDNSTVYAEVSKILVSTGKWKRLKRDNPRFNLMLGERNRLPFGRLGHEPGLVQLVNYYRGADKLCRKASLVKLIKTSPELSDSSNWFPESYIIYPTNLNTPVAPATNGISHLKNNPKTDEREVFLASYHSKKESGEGTVWIAKSSAGAKGAGILISHDANQLLEYIDNQGQVHVIQKYLEKPLLLEPGHRKFDIRSWVLVDHQYNIYLYREGVLRTSSEPYNSSDLQDMTSHLTNHCIQKEHSQNYGRYEEGNEMFFDEFRLYLLNTHNVTLETTILPQIKQII**KSCLSCIEPAIST**KHLSYQSFQLFGFDFMVDESFKVWLIEINGAPACAQKLYSELCQGIVEVAISSVFTLNSSSDSSSASSSPYSSSPSSTFSTNSCSSPKLRGPLHVGPFTRL |
| TRINITY\_DN112730\_c0\_g1::TRINITY\_DN112730\_c0\_g1\_i1::g.133060::m.133060 | gi|548371092|ref|XP\_005732622.1| | PREDICTED: sentrin-specific protease 1-like [Pundamilia nyererei] | 14.4 | SSRPGIQAWSLDTDLSSNRAATLTSAPSPSALQDNSSQDTQSSAHDGDSVIIVNEKKGKKKDSSRVPCFQAELWIKELTSMYDSRARERRRQIEEQEALTAQLLRQRLSEEGQRSPDVEVHVRVPLEKEVPLTPVIEEPKPVEE**KPEFPELT**EEMEADVNRVLRGGSPHEVLSEGFGLSLTRKDLHTLSNLNWLNDEVSAYY |
| RRRRRTRINITY\_DN86082\_c0\_g1::TRINITY\_DN86082\_c0\_g1\_i1::g.49114::m.49114 | NA | NA | 11.1 | KILTGDNCHWVIGEVRGDPSEQFWSCLQQFDVPPPNRIQVSGHSVLCHVPQKKSGLGYPNANVNTGILELTQEML**EALPVAAIE**LEDEGGDPRLVLAKGVEYDVVSSHWCYQKNDKEVPVWGPIHGHEDPLPRGNDHKVRHAPIWTEPVTKFDEEVNWQFGKCSRHTHQHKKFRKEAQKNPKRDLRAWL |
| RRRRRTRINITY\_DN4314\_c0\_g2::TRINITY\_DN4314\_c0\_g2\_i1::g.743::m.743 | NA | NA | 15.3 | GVGAIVVVIVVVRVCVPFADTASARRDIVSSSVGISWD**ISADGITVIN**IIISSSYVSPPLINGHLPSLSLLPLFLYLPHLHPLLLLLPPLLPHPPLLLLLSFPPPPLLHLEYVRLLLLYLINPRTTEGVGGERVRRRRADGEVGGGGEEE |
| TRINITY\_DN98793\_c0\_g1::TRINITY\_DN98793\_c0\_g1\_i1::g.27658::m.27658 | NA | NA | 24.3 | MLRQLGYPISCHPD**ISPCVSADSL**SPHDSPGWALWHPTLWHLGCQRQPEDHQNLGFSCHPWLRSLINHLIRLCLTALLNYSCVGLQWALSARLLGLAIAGFHS |
| TRINITY\_DN25823\_c0\_g1::TRINITY\_DN25823\_c0\_g1\_i1::g.67745::m.67745 | gi|736207514|ref|XP\_010776255.1| | PREDICTED: cyclin-dependent kinase-like 2, partial [Notothenia coriiceps] | 30.2 | ATFWGGSSSSINTTMERYESLGLVGEGSYGTVLKCRHRDSGRLVAIKKFMDSDDDKTVKKIAQREIKLLRQLRHGNLVNLLAVWKRRRRW**YLVFEFVE**RTLLDDLE |
| TRINITY\_DN136544\_c0\_g1::TRINITY\_DN136544\_c0\_g1\_i1::g.141709::m.141709 | NA | NA | 10.9 | DDRERREECVLVCVEP**AESVLLAPIS**TTRPGHTHTHTHTHTLIHTLIHTYTQIFKLFNERCALDLSHQTDRQTKKLKKNKPQKWTNQKQVQTSQVLLVVFGFFLFFSFLFFSFLFFSFL |
| RRRRRTRINITY\_DN58624\_c13\_g1::TRINITY\_DN58624\_c13\_g1\_i1::g.62017::m.62017 | NA | NA | 24.3 | RSVMFRSFLFRCCSIESRVSCIPS**VPLLMWS**SSFDLFCTSVSFVSIWVARSSASPVRSCSSDLIRRTWSSSLWILPSTSLFSASFSSSISCILLFLWLTISEM |
| RRRRRTRINITY\_DN56930\_c0\_g2::TRINITY\_DN56930\_c0\_g2\_i1::g.105562::m.105562 | NA | NA | 21.4 | DVNVACRSLFSLPFSSPISVTPSFMYFILCRTLYLHTLSSFSLIFSLQCITFVSIHYLIYFIVNLLIPFCFFSVLSLRSPILLPKKRCQFILASLSIVDHGELSLHVSLSHCTPVSPNLSNFILNM |
| TRINITY\_DN15796\_c0\_g1::TRINITY\_DN15796\_c0\_g1\_i1::g.30168::m.30168 | NA | NA | 14.7 | PP**ASDQPVLP**PRRDRGSGRGEREPGLPAAHLRGQGLPAAEGPPRRAVLLQGQAAQVHRDSRSDSDGRRGGRQSGAAQRGGLRPRDEPVEEHGLPALRREQTRAGGVGLHPVFSRRGVSRRLGQQGDVAL |
| RRRRRTRINITY\_DN49553\_c0\_g2::TRINITY\_DN49553\_c0\_g2\_i2::g.101002::m.101002 | NA | NA | 15.4 | SVRRASRSSANLAPSATRTGCRTRTSWTRTEQCSWRTAARAGTAMKGPAVSAVCLRAMMERVSRSVPWPS**TASPAASVT**RTGTATRITCSRQILALPADASQVPTPVSSRLASPACM |
| RRRRRTRINITY\_DN43735\_c0\_g2::TRINITY\_DN43735\_c0\_g2\_i1::g.107229::m.107229 | NA | NA | 12.3 | KYTCFFIFIVIARSDRMVCSSILFSGSFGISRSFVQGRRSLTKVVLLPRCWLGSSNARPLTGELSSCIYVHISAVRFSSVLRTFSTYGSAL**FFPVCKLK**AMTKGSGLPFVYLNFSMPLVTDPRFPASSEM |
| RRRRRTRINITY\_DN105124\_c0\_g1::TRINITY\_DN105124\_c0\_g1\_i1::g.133609::m.133609 | NA | NA | 12.9 | PGTIPPGHIATMAPAFTRYLSHNFVPSRINAMVADLLPQCLYQQKTAVPPPPPTPVAMDNKLKELAIECKQLTRLPCRT**NPDTLINLL**SKMKSLDKKRDENKDIKNIMRRLPEIYKSLQKLKEMYQQDELSTAGAPSMVSSPNGSSL |
| TRINITY\_DN6278\_c0\_g2::TRINITY\_DN6278\_c0\_g2\_i1::g.53135::m.53135 | gi|657583996|ref|XP\_008296132.1| | PREDICTED: GTPase IMAP family member 8-like [Stegastes partitus] | 9.1 | MVMVTKEMAPEVGGGSNGADNVFKNTCIKLTGPSAEKLGEAFYGPGIVVLQEIKGVEKGAAYAEDPENSKEKEKELIINRIVRGALMQPPPGCGGEQVTEREGAMAEVKP**APVPPTRIIAG** |
| TRINITY\_DN10297\_c0\_g1::TRINITY\_DN10297\_c0\_g1\_i1::g.28240::m.28240 | NA | NA | 7.9 | VGHLKSINKLVSSERGDERCRRCSSNKRAWTSQPRVIPVSRQSVPSRGPFRPVLISCFIHAVAGAQRGLSSEWRAKLS**HQQLAGTTGT**TRLTHRVRAWWWSRTVPAWSPSLIMAVLLASRRAPSPG |
| RRRRRTRINITY\_DN57974\_c2\_g3::TRINITY\_DN57974\_c2\_g3\_i1::g.44135::m.44135 | NA | NA | 59 | VSRISIHVIATDSGLENSLKLTYTGADEEKVGTIILTTLDETTEIHFRGGATVEITRGGRSWEIHKADGSFACAVTLVKGPEISIDEPLAEIRPASGIARFSSGEMHSAMETLSSSSMAYSESAMSSMSSMSMTEFKMEAAMSSFSSSEMMSSMMAQQSSSSFSSAEEMTHVEKKMMMSSSMASSAEKHSMMMSGKVALQQERYATVKMRISQFVQGTFSFSSKSVGGESTMECTYEGQDSDALDHILLSCSGESYHMEFHSSQSLRRGNVFWVVERVSSECVCSMRVSGEHAEATVQSLVKPPKPIPSKVTPPSVVRKPSMIPPPSKMRPPSKLGEPEPSKLARPSKIGSPEPSKIGRPTKIGVPEPSKLGRPTKLGAPEPSKLGRPSKVGEPEPSKVRDPSKIPPPSKLRPEPSKFGRPSKIGEPEPSKVGPAPSKLGPAPSTPEPSKVSRPSKIGEPEPSKISPTPSKVSPVPSTVSPEPSKVSPTPSKISPEPSKISPEPSKVSPVPSTISPTPSTVSPEPSKVSPTPSKVSPEPSKVAKVEEKPAARRITLTFHAEQRGASNEVIVTYSGEHSSTVSSIELSSKYQTTTVQVHHSSVLTRSEHVWTVTPAPEGDIDCSFRATEGESVTVSQPKTLIRASLSPKVKHVSVEEAVAAASSKVKTESTAHKGTLSFKDSSYSSGSSLYETSAYKVSSDYREASSYRESSAAYRERTVVERTETLKSKTEEVEFHTQSAYGAKFHTTHYHDIRTVEPVHAKPVDEDRRRSSFTTYGGGSVDLTAYDSAEGKSNSCVCRYTGSDEEQCELITISLVGSLNSFIYKESSESIVTGNHFWQIEAEPKTQINLTFKTDQGLPIRHSRMRVTVRPAHDLSFPTQSVVQYKREAKLSAKRAEYRSMIDFRASREFRSSSRSSREVSRIPSPSRPRTREPTPSRREVIEGEVEVEVSPRARSPRILESVPRMLEIYTPSLSRRRRMFQSVTRKKKTASVEVAEHRVEHRREEHEVARREIRVPSIAPSASFGLELEDELMMKEASARRRSLYDDVPVLLEEDSLDGLSRRRSRFSVESEPSPSRRAPRVTELDDLSLKPIRWRPRYQDTIRPLPMVYFQEWRSLRIRRQRKQVIREMREPIEYQDRLKKYWKMDSLPVFQKITKDEDLVTPDHHLPEPIEYPMFIRREEELKKTESKHVTIDFEGEVNKTSVAPKYMEAAFKIAEQATPNLPVLEETAAIHEAMKNTKEIQKQIHRYKEEETKYERRTYTLRDVKLTAQCSVSGTSNTATVKYVGSDELLTERIHLVHYDVDEQIVVVKPGFQLPQGDKQWKLTPAPIGSVRLEFRVSHGETCDVNALLRKFMPRMTEESVPHPTVTLRAQCSDEGFKNHAMVTYEADDSMDLNHIMLQYLGKDSTFTYKSDDDGPKIREGNKLWAVQPEPHVTITVGFRVDEGIYAARNYLPLTFEPPRQLIKTKDVRRRLKKISRSIYHQRISRVTEVFLEGYASDEGDDSVVKCRYVGDDSEEIDKVYISAFGNSYTIEYKPSPHLQRNGFYWSVQTSKDYNSISCTFRVHGGEEASGHMVPGARLGQYETGIKVKGVALGRQNKFAGGYAIRASSVITDIRKALYQYYRRHRLTRIAKNSVLEIKMRLWPHELAEHATMRLKRDKVLLRDVFDMAELSIDKFAESDFIYECSSINEIMKTISEAAFPNLGSLLVYAMVGVSWMDTATTVLDHRHVEPACYEPATFLMRINEGPVLLRAQGMEIIKIITSKRTTYVINDPRVDFHGYNHSHLFKLSSCVQRLYRVIEQETLEFNSTGLREFIDVGSIFEFILIIEEMSEFYEHLYIINKHRAVNLAEIERLVLERDTGRVKIFKAMFTKKTAIEVCRHVAGFQCRALEESITYKSSLEKVKYFLAEEKTIERTEDVEEDYNRIVSTDEKTTIPETPHSPHSLGFQNEAIVRFQYKTKGFINIITISCDTTQGARIWRDATTPCKEVIYGIIDSGGDNAPPEWTLTISDRGINSVVLAKPVDPIDAVNVEITQKDMGFRNKATIVYYGTDKRQVGKHFVLSTFSRTTIVQHHASNSLIEQGKQWTVAPEPKGSIPIKVTIHDGRAAHVAGMGQLEKPLYIKAPVEVDLNATTSISGTSNTARVQYVTADNENAAAIVLQYYGGKFEQAKIKTGDALIEKGGRYWKVVPKPYGVVKTVFTANAQYKVTMDRIEERFAPARPAQESKPIIPASIESWDSEGGMNECKVRFEYEFGEILGKIEYNTEAIKKTTVSMWKNQKKERKELYYGTIKAGGDSSPPKWCVVCSDNTSSMIFPQQPIGPKEFPSKIILVSPIELPESVGYQNQASVRFYYGASETLNPVRCTNGSVSSSVLHWLEGEKAERKEVIYNTIMSGGDDKPPKWSIIVSSKLLGEVVMPGEPTCPKDQIEVRLSTDVTGFKNSLQVKYRGANTKRQVNRVVLHTYSETNEIIVNESVNLPKKGYFWMIQPIPRGIYVVHLRLSTGAGAFYKDKLPFGPHFQPAAQLRLKGSTEIEGAENIARCTYVGEDEQEETLVSLSHNRGDSSMKYKRSQILEKGYRYWKIEPLPRGIIGCTMTGSEGLKTTVDKIDEKLAPAEGVSLKTKIGMPTRRPRSLGTENEAFIRFEYETAEMLGGMTFQRDKSREKNSKKWASEGAQRFEIWYGLIEKGGDHEPRLWHITICDKTVSIIDIEGPQSPKDFPDKCVVSESAPGPESQGIDNQAVVRFMYEADPILGTVNYMTTTIHTKNHRVWKETSVERREVYYGTVRSGGDDRPRAWSLAVTTKTVEMIEPPNSPPEPPCLPTKPTVAEDSKLSRSVGFQNEASIKFHYQVNEKLGKVVLSTETVRADVTCWAAKPVERREVIYGLIDSGGDDSPSRWSVRVSRAQIDDFELPGEPVDPRGIVKVKIYVAKRGCKNELVLDYTGTDDKHAEKIVLETIDDHTAIMARHSIDRGDKTWKCTPIPKGKIPVSLHIVGGQRVVYGEEYKHDLEYDPYGLMEQVKVVGPIEAPEGAGGANCAIVRFKYEAGQPMHTLTYECMKTPTTNCLTWEVQDVKQMEILYGTIVAGGEEEPPLWALSVSTRTTDTVRPEVPCGPPEIPDMAVTIESSESPKGAGRSNIATIRHEYELGEILGSSRYRTMTVPNKNIKMWRDSHAEKREIIYGAITSGGNDEPPQWTLTMGEHTVDLVEPRSPPGPITKPSKCEVVESQLFGGVGFRNMAAARFVYETGETLRTFKFCPRTVSESITIWGPRHADRQEVVYGGVNAGGDKEPPEWSVTVSVGDTDEIKMPGVPIGPKDLIIVKIVETAMGIANKVELTYDGTDNITTERIVLHTYKGNSDIKIRDLSDKLKVGAFSWSCEPHPKAKIPINLDIPKGRHVHVIKQPINTMDIKPMVKIDQITVPTVTDMPESAGRSNTARLRFLYQDNEMLPQITHQSVSSKVTAVTSWRDTGVKCAEITYGTLRSGGEHLPREWHLTVSSKTVDIVHLNLPVSPVECVLVAEATECPEGIGYINEPLVRFFYHMGEELGTIRFLTKRCETTVTKYSKMNADRKEIIYNSVHAGGDISPVDWTIVVSEKTYDKVKVSGPPGPTDYVKVLITVTKKGSPNEAELVYKGSDYRDVKEVILSTYSDTTEIFGRSQLEVGTKRWAVVPTPRGTVSVFLRLTGGARLCVTKKLDDALELDPMEIRELPEVEASPDSFEGTGNNNIAAVRFRYKKNAALGAAVYENTKLAKTTARYWQESGEELIEVVYGTVDSGGDYMPRTWIMSISHKTTDTIRPMSPPAPTYTPDKCLIYPSTDSPHSDGAANVATVRFQYESGELLGTIKLRTDYITYTRNVRTWRTSSKERKEVIYNKIESGGDSEPKMWEIIVHEKGVATVEPTSPPSPITYANRAIIPDSELAVGPGFKNVGRVRFIYENNKILRSSVCSLTKCETEMIVWNLRSTERREVIYHTVSDGGDELPIKWSVTCKEETVRTIVIKDAPAGPTDLVKVNVAATKTGSANKVTLIYRGTDYRDCSKIVAMAKTATYTLSYKEGLELIKEGKSWHVTPEPKGGVAGDLVLDSGASVIVTERALKSDLEAKPPSYEDKCTVPGTSESPASHVGAANKAIIRYELTEGEGLNTVTFYNETITTYNCKLWRNDDWEDTSYVKKEVIYGVIKSGGDNFPVTWCLSVSSRSIDTVEPKGPPDVPNLAMVPRSAESAKSLGAINMAYVRFQYELGEILSSVKYHCELCPLKNERVWLITNREKKEIWYGTVQSGGDAYPLDWKISIANASVSVVDPRSPPSPPVFPHEIVVAASEISKSVGFKNEACVRFTYEMYKTLHTVKITTRKVSSNVVQWSASGSERKEVIYNSIDTGGDDAPESWSLTCSESSVGSIEVPGTPPTPRGVVVVTVTFTKVGAANDLTLYYKGSDSRKSDKVVLTTREKTTKISVRDTEKLKMEELKWTVKPAPRGSIPIDITFTNSTKCTILQKSISSLDATPEIRPEKIVVSGHTGQPHSIGADNKAKVRFDYETNEILGEVLMKQSKSEGYVVWRDTGKIRFEVIYGRIRSGGDHEPKLWVLSATSSSTDVVDLRKPPAPEETAIVPETLEHPEGQGYQNVAIVRFLYPIGIDLGTVRIMQRSCKTSVEQWALRSAERRDVIYHHIRAGGDNTPADWMMTLAGRTVDKFTIAGPPGPTDLVKVTFTISKRGSNNELSLTYKGAEYRTCGEITLTSFSETTNVDAMIPLEGDARSWTALPAPKGRFAIHLTVMGGNKVIHTQKFNADIDIEPSTLRDLAQVASAMESAEGEGSGNVASIKFKYLEGPVLGKATYRTHICIQSNVRHWELLSAKCMDINYGIIELGGDFVPKTWELTVSSKTSDIVKIMSPASPTCTPERCKFLRSTSSAPGVGAGNEAMVRFEYEYGETLRTARHRLETIPRKSSVKVWRLSKKERRELIYHKIENGGDTRPRTWGLTISDGTIHTADPTGPADPVTYQMQAIIPDSDLPKGVGFKNVASIRFQYENGKILNTANYSCAECKSTVMAWSIRSTERKEVVYHSIAACGDNEPPNWWVTCKEATIGTFRIPGEVPGPTDQVRVNVDARKTGSSNKAEVTYIGRHNRDADRVFVSSTGIGTTIEIDIMTRKDIEKGDKYWVVQPVPRGTISCGLRVNEGARLTAVQDPSWEIEPAISEDKTMIYGSSNSPPSVTGVANRAIVRFEFRDGPSLGTVTFQTECVDTFNCRLWKGRGQRREVSYAVIKSGGDKKPIAWQLTVSDRTVDICVPTGPPDVPSIALAHKSQESVPSLGANNEAYVRFSYELGEMLGIIRYEKNSIITSNVKQWLLSNRDKKEVHYGVIPSGGDFGPAEWKITMGDSTVNFAVPKGPAGPPKYQHQAVVDTSNLSESVGYKNEARVRFQYQTGKVLNPIKFTTRVVSSCVMKWNAQSTERKEVSYCTIEGGGDEKPEDWSIIISQAKIEDFRIPGVPATPPGLTIVNIDFYNKVVRNDLVLTYQGAHEKKAGRVTIATKNDTTRFRVKESEKLPLNDKLWSIVPRPKGKFPLEIHINQGIRVALEGSPYDILNAEPPIIFDMVTIPGIQSFDSRGKENKAFVKFDMVANEKLGTVECSCRKCTAGLTWTPDEKTSKEIIYETIHSGGDHDPRAWQLTVSSKTSDVMVLQKVAGPTETARVPETTECTDGVGYENEASVRFFYAVDEELGSVKYTTNACEATIVQFAKMTSAKKEVIYNTVPSGGDIRPAEWSLTLKGRTVNKIMLKQCTSPSDLVKLSVTIIKPEGVGNEIELLYKGCDDRTVKPILLTTARETSTITFRNDGAINRDGRRWTVNPAPRGKLPIFVEVDRGAKATYQTTMPVDLDLDAEELIDKAQVPQYMKIDEGKGKCNVAYVRFFYYSGPKLHSVVYECTKVQPNITVWEREESNLQDLIYHTIKSGGDYVPKEWGLTISTKTSDVVRLKSPEGPLDIPDYANYLDSAESYNGAGAKNVACVRYQYENNEVLNSVKQRTDRITGKVVKFWQLSKKERKELYYGDIDSGGDLAPREWIVTMTSKTIMTVKPKSPESPPVFANRAIVPASELPDGIGFKNIGRIRFIYENGQILRPVNVICDVLKESVISWMVRSTERKEVIYHSVMAGGEDAPPSWMITVNDATVKKFQIEGAPPGPKDQILLRVVGCASGLSNKVKVEYTGSNLRTTEKLFLSTHEFTHKFSLQSTPELERGDKFWEITPAPKATINFKLEVNSGAKHKVENLYEQPIEVEPAGYTDVCTAPGATMSPNSVSGVANKAMVRFEYTEDQTLGTVTFRTGTVNTLNAKSWRASVGERKEIIYGTVPSGGDFNPKQWALSISTKTIDSIRLNIPPECADIALVADSVKSFASMGAANEAAVKFEYILGANINTVKFHTARIVMKNVRQWLISNRDKMQLHYGFVHSGGDAKPEKWAVTITERTVATIEPTFPAEPITYPLNVSITPSDIHESIGYRNEAKIRFQYELGTTLKMIKMTCRAVASSVDMWNATTTERKQIIYNTIPSGGEYAPPLWKLSVSDETIDYLEVPGVPASPRDLVVINVYSKTTGSSNSATIDYRGSDGAISERLTIKISDPTVESNFRMTSKLLVNDKSLSVKPLPKGTLPIECKLTSGARVYVTNHPFDKMNIEPSELQDKLLVPNLMEKAESFGAHNEARVRFFYEANERLGSVTLHISKTVGCRVWKEQGNERAEVLYSTIRSGGDHEPKAWALSVSEKSVDTVGLKPPPTPKETIKTGEKTEAPVGVGYENEGTVRFYYVEGEQLDTLKYTLRHCTDTLRTWGKKSAERIDVVYNKVPGGGENEPTDWTVTASTKTVDKVEIHTPPGPSDLVRVSLTLSSTGAVNSLTVTYKGSDNRTAKELTISTFTDTTDIVARVRLDVDPKTWSVSPIPKGRFPVTMTFSSGDKVILTKRMENSIDFVPEDEREKAIQRDSEPSPESVGIKNISKVVFVYEAGPTLGVVTFETNKTKQVGVFWEDDLSKRYEVRYGTVPAGGDFLPKNWSLTVTTKTSDIIKPKAPPSPLFQPDEAKTLPCPNSPASLGAANEAFVRYEYECGDRLRSAKVRLDYVPKKNVRCWRLGTKERKEIVYG**AISSGGDSVPR**EWCITMAESTVATVQVNTPAASVTFPDMATAPESELAEGDGYKNVGRVRFIYENGKLLKTIKCTTAMMDDYMLTWSVRSTECKEVIYYMIEAGGTENPPGWSLTCKEASLGSVELPGAPPGPRDLVKITIVKSTTGGTNQLTLTYQGSDKRVSERILLSTHSKTATVEIRGKTGINRGNKLWFVTPNPRGSIDADMKLFDGAKVIVVQRLKDELIIKPPEVDPQVTVPGTTESPASLLDASNKAIVRFDYQEGETLSTVELFTDLLNTFNCKLWCNEPLEKREVIYGTIKAGGDYEPKDWSLSVSSNTINTVTLNCPPDCQDRAAAPDSATSCPGVGAMNEAYVRFEYILGEEVSTVKFQNETVPNRNLKTWLISSQDKCEIHYGIIPSGGDSDPKSWAIVMVSKSAQVVHLNVPPGPSKFPYQAVVPEFEVFQSKGYRNEAAVCFQYETGQTLRSIKISTRAITASVTQWATSGTDRKKVVYNTIESGGTYHPPQWSLSVFDASVEDVSLDCPPGPREFVNVLIEASTIGVSNSLTVEYVGVDVRTAEKIMIQSASDSTQVNVRSTEKLINGDKKWAVTPPPVGKFPVEIKLDNGAKVSFTNSLLNIIPGASTDKVAVPALLSKPESRGKENVASVRFFYEKGRTLGTATVELAKSEACITWTDDGKAQMEVIYRTIKSGGDHDPKEWSLKVTNSTVDSLTIKGPPLPAESVKVPETTEVPLGAGFENVALVRFYYFSGEQLNDIKYSNRVCTSCVSTFAKRAEERKEVIYHSIKTGGDILPTEWSITVSDKKVEKVELNTPASPSDLVRVNIFASKTGNCNEATLVYKGTDNRNVNEILLATYSNTVEIQARESLAGGEKSWKVEPEPRGKINVSLHLTSCARVNVIKRLASDLEIEPAELKEAAKVSGPLDVYEGIGAANMACIRFNYEANEKLRKVAYNTEAVGASPTCVTWEDEDTEKCEVVFGNIAAGGDYIPKSWTLSVTSSSYDTVKPNTPPGPPYTAECVKIYESPESPAGAGAANEAMVRFQYYHGETLGTCRFRLDNLRRKNCKTWRVGEKDRKELIYGDIESGGDSEPREWTLAISDGTVASAMPTSPASPTKFPNQAIIPDSELFEGVGFKNVGAVRFIYEKGPVLKSVKYSVAEVQTDVGTWTVRSTERKEIIYQSVCAGGDNVPPNWNLNCREASVFKVRLPGDPPGPRDLVRVNVPVSTTGGTNSLILVFHGGDARTSDRVTLTTHTLTNKIEMRMTAKDIEKGDKLWTVDPLPKGFYDAEIVFTEGAQVGTVSKFKQDIFATPGEIVDQATIKVSESPASWVGAGNKATVRFEYSEGETLGTVAFQNEIVNTFNAKMWRGDPLERKEVVYGTITSGGDYKPKAWELTINERTIVVAEPKGPPDCPDRAVYCESTKSSPSLGAINEAFVRFEYECGEHLGSAKVRSDYIPKKNVRVWRVGQKERKEIVYGSIRSGGDSAPRKWCITMCDSTASTVEVDTPASPITFPDMARIPESELTEGEGYKNVARVRFLYENGKLL |
| TRINITY\_DN58818\_c1\_g3::TRINITY\_DN58818\_c1\_g3\_i4::g.91903::m.91903 | gi|734595468|ref|XP\_010731667.1| | PREDICTED: microprocessor complex subunit DGCR8 [Larimichthys crocea] | 16.9 | MEIDDVLPPLPLEPPDDFGQDEGRAPPPPPLQTSSDAEVMDVSSGGDGYTYTPGDGEAPPPQPLSKGSITFCSHLSDEANPNPPCPRTARHAPPVTTFLPELKLLRDVKISVSFTESSNSKDRKVQYTGEGQEGGSDDGLDGLNGELHDWTKEQEVAESSSAAGNTGRRSEEAELDAENKVEFAVLDELDDFYDNFLDHDDGDNGGFKSEVIVQQEQADEEAGPYPYEEEFDNDVDALLEEGMPVPKKMRPAEDKYGGDSDHQSDGEGGVQPMMTKIKTVLKSRGRPPTEPLPDGWIMTFHNSGIPVYLHRETRVVTWSRPYFLGTGSIRKHDPPTSSIPCLHYKKMKEVE**EKELNGDATHN**TEESPVKPRQEANGEDGAGKSDAAAEDQDGAPPSALTDAAPDGEGAADSSQQLKESQLFEIAQGALGQVKAKVEVCKDESIELEDFRLYLEKCFDFEQVTVKKFRTWAERRQFNRDMKRKQAESERPILPANQKLITLSVQDAPTKKEFVINPNGKSEVCILHEYMQRVLKVRPVYNFFECENPSEPFGASVIIDGVTYGTGTASSKKLAKNKAARATLEILIPDFVKQTSEEKPVEGDELEYFNHISIEDSRVYELTNKAGLLSPYQILHECLKRNHGMGDTSIKFEVIPGKNQKSEYVMTCGKHTVRGWCKNKRVGKQLASQKILQMLHPHVKNWGSLLRMYGRESNKMVKKESSDKSVIELQQFAKKNKPNLHILNKLQEEMRKLATQREETRKKPKMTIMESAQPGSEPLCTVDV |
| TRINITY\_DN61040\_c0\_g1::TRINITY\_DN61040\_c0\_g1\_i1::g.64248::m.64248 | gi|808858429|gb|KKF10813.1| | Polyphosphoinositide phosphatase [Larimichthys crocea] | 16.5 | TKHRVLKIDRTEPKDLVIIDDKHVYNQQEVRELLGRLDLGNRTKIGQKGSSGLSRAVSAFGIVGFVRFLEGYYIVLITKRRKMADIGGHSIYKIEDTSMIYIPNDSVRVTHPDEARYVRIFQNVDLSSNFYFSYSYDLSHSLQYNLTLLQRPYDLWSSTASSTEEEVHTQSKQDSFDIFEDEGLPTQVVYSLQTEPYYKYVWNGKLLERVKDIVHHDWLMYIIHGFCGQSKLLIYGRPVYITLIARRSSKFAGTRFLKRGANCEGDVANEVETEQIVHDASVMSFSAGSYSSYVQVRGSVPLYWSQDISTMMPKPPIRLDQADPYAHVAALHFDQMLQRFGSPIIILNLVKKREKRKHEKILSEE**LYPAVINLN**QFLPPDHWIDYIAWDMARYTKSKLCNVLDRLSMIAENVVKRTGFYINRSNFYCHTLRPDDRWGDVGGHITASGRVQTGVLRTNCVDCLDRTNTAQFMVGKCALAYQLYALGMIDKPKLQFDTDCVRLFEELYEDHGDTLSLQYGGSQLVHRVKTYRKIAPWTQHSKDIMQT |
| TRINITY\_DN25699\_c0\_g1::TRINITY\_DN25699\_c0\_g1\_i1::g.56040::m.56040 | gi|734625846|ref|XP\_010741037.1| | PREDICTED: prolyl endopeptidase-like [Larimichthys crocea] | 10.6 | MAFKYPAARRDESKVDDYHGTKISDPYAWLEDPDSAETMVFVEEQNKLTMPYLEGCAVRAQFHQRLTDLYDYPKYSCPYKRGQRYFYFHNKGLQNQDVLYVQDSLDAPATVFFDPNKLSEDGTVALKMGRLSEECEYFAYGLSSSGSDWVTVRFMKADDLSALPDVLERVKFSCLAWTHDAKGIFYNSYPRQEGKTDGTETTCNINQKLYYHVIGTKQSEDILVAEFPDHPKWHSSVTISDDGRYAVLSITEGCEPVNQLWYCDLQQLPNGITGLLPWVKLVDNFEAQYSYITNEGTVFTFRSNLDAPRYCLINIDIQKPDRQHWTTLLPQHDKDVLGFVSCLNQHHLLVNYVHDVKDILQVYELSTGKVVRDLPLDVGTVAGVSCKKKHSEFFYKFTSFTTPGIIYHCDLSEPIPEPKVFREVEVKGIKQEDYQTTQ**VFYPSKDGT**KIPMFLVHAKGLKKDGSHPVFLYGYGGFENSIQPYYNVAYLLFVRHLGGILAVANIRGGGEYGLTWHKGGTLANKQNCFDDFQCAAEYLIQEKYTTASRIAINGASNGGLLVAACVNQRPDLYGCAVAEVGVMDMLKFHKFTIGHAWTTDYGCSEEPEQFKWLSKYSPLHNLPQPPYSGPPYPAVLLLTADHDDRVVPLHTLKYCATLQHGVGSSPLQRQPLMVRVDTRSGHGAGKPTAKAILEDAHIFSFIAETLGLSWKE |
| RRRRRTRINITY\_DN58259\_c0\_g1::TRINITY\_DN58259\_c0\_g1\_i1::g.44712::m.44712 | NA | NA | 10.9 | LQGFVEAERHSDLESFSRQNQVRFVLVFQFFAHHQTDTQTEGVQQIFVALLLLLLLVGQEDAVCYLDVLLLGGRYECRHLLLNFVHSDEQLVVILVVLLFVAVVRLLQQPFSSAARRQQGVSGSVLHRRLLLPSSVLLLQGVMQVFLGPASQRLLLSLLLNLLGSFGVHGVLVHRLHRSFFVDPLHLDEDVLLVLGDDHGDKTDGRREVDGGDLVDTHGYFS**VVGVQPDVE**VDGAARQASLFSVDEGVGVGCEDFFDRVSRGVHLSGAVRRHRGGVQLVSEADDLLHLLAVLRSLRLLLLLLADDLLVREDDVEVAAVGFEFVEVDSGVDCLLPHLARQLRVGVTEAERRDASVFHVDEVVVDFVGDELRAVPLHDDYQVEVELVGDHETLPAVRVDLEVRLDALDGRVQAFVLVHVVAVVQVRLLHLALHPVLELRRELVEDLLHLRQRFLLQLEFNGESVEPELAGGVPAGTQQLRRGAGEDVDSFPRGEHHRQVLDLEDVELADLEVQLVEVHDDHVLVVVLLDGHDVGHGDVREVGDLLPEVRTVDLVGLADLRQVPGLDHLRDDVVGLPEELLSAPREEVGLALSTASLFVRLRPLVLSEVRRRVFFLLLLFVAVFVVARLRLVRIVALRQAALLLAAFVPVLQLFLGPFRVSL |
| RRRRRTRINITY\_DN596\_c0\_g1::TRINITY\_DN596\_c0\_g1\_i1::g.135::m.135 | NA | NA | 24.3 | MDLLHPHIATHDAKLLRRETAQASEFLTTCKRYHCNYSDKDTDYLREKELRNDFLQQLPERDAWRSIVKGDVFSSFMSTELFRSLFRLHSTPQVSLFSGKDFNFTGERNSLWSDLDLASHIVFDDYRGFMAAFRGAFVERLQINLKAAKLEEDEEE**FERGLTKGGESVK**GGGCRRALAQLRELVALEEGGLNGNRRDEMLDELVLSSMRP |
| RRRRRTRINITY\_DN58944\_c0\_g3::TRINITY\_DN58944\_c0\_g3\_i5::g.113937::m.113937 | NA | NA | 20.3 | KNWKIYKKENKLGEKWFAELKPCLWLIHTHNGVHPGCNRWCKNSHTTSFKATIEPTRFFRMVVKWKFERWVNSNTVMHVETCIEEWMDHSINSNIEIEWREKVQATNNLNMSLFIQYCYSIIKKDWKKTQGVKILLEEILTPKTVKDWDKHKLLFDRLQLYRFFDTSPIKF**EESLQTFSK**FNGANHLQHLNTLGYESWKRFGTDLKSPVFDNMYGINTLASITKPLGFTSKIFTIKTWDGM |
| TRINITY\_DN54218\_c0\_g20::TRINITY\_DN54218\_c0\_g20\_i1::g.59247::m.59247 | gi|657588939|ref|XP\_008298832.1| | PREDICTED: myozenin-1-like isoform X1 [Stegastes partitus] | 24.4 | AVKEKRRKEYVRTYVSPWERAMKGNEELTATMRAAMPGPVYAHPDMPYYKSFNRMALPYGGYDKASKMLTFEI**PEINAPAEE**PEPVPNLQADIRSRPSFNRTPIGWICSEDNSHIHMDLDTMPFDGETDDL |
| RRRRRTRINITY\_DN53303\_c0\_g4::TRINITY\_DN53303\_c0\_g4\_i1::g.16365::m.16365 | NA | NA | 23.9 | INGMGGLLAGKSLRRSIYT**RLEPEAESPL**SSDILTLSFDDHSTTSDARRQNWAVNEGSAESRTGQYLYITYYCNLQVKQSYGTIEESDFDDKEEVDISDQFSSTQSTFM |
| RRRRRTRINITY\_DN22592\_c0\_g1::TRINITY\_DN22592\_c0\_g1\_i2::g.4335::m.4335 | NA | NA | 14.8 | PKVGDAVPLPVPLPVVLGARG**AVGDDVVQL**RVRRVLESDAGILVLAAAAPAFRDDVVGVHATFRWLLRELQTVRQGLGHFRVSRVSQERRTWSQVVPSSEGRWEFSGTEGSSSARWERWRLTAMVVSHRQIFSVRNSVGRHVTRGRRGG |
| RRRRRTRINITY\_DN41303\_c0\_g1::TRINITY\_DN41303\_c0\_g1\_i1::g.113707::m.113707 | NA | NA | 22.4 | SAATIETSVPEIEKVAEEIVEIVQAMVEACKGSSPKETESETEPQSAAAEEEAAPTEESVTSLKSASAPSEAKASTDEAVPGNSDFEVAAEEEVSEEVVEATQLVVQVPMHIELVKEKNEESQPKVEEAAEKVDPEQVTEEEEKSQEEKVEEPEEGTQSEAKIEVVEEVVISEESVKVEVAKKLEEEPKKEEEVAPADTTEIVEIPVNDTVEMAVHLPRPSKPAPKECIVAVPTETIVPAETTMEIEKETTATAQVPTPTTATPTDPKPPEPKEESVKDMADQIVAQAIVMSQAEIEGAEHVDEKTEEMEENAQEAVASIESEATQVIAAEVMEVVPTDCVADKVEDSIAVQDSEPSLSAVLVVTETIVPAEESPMAVPIAPEIEKTITIKATECITSSLEETVVQVVEKIPTNEETAALTETDLKVEKTEVTPESVEVSQTCIASESTPTIPNVVVAKPSNESVSTAQIVEAEQPVTNIVGAKEIEPEDSETATQVDMVESQSTEVMPELDVTEVQEAQAMTVEDEGPTAEETSAPKEEISVESSLADRVVALCEVVPVVPKELAVKAIEKTGLGTCIAMAEDQAHPQLIANEKIEATETPPEYETNETAVELPVDEVTVSTQIPIESIQAEVAAVVEEATGSQPGQPVPTTVAPTAVAVPKEEATSLRRGMRGSVKPPISTQEEAEDEAVDTDVSKPTAADAEEPIDSLQDHKEEADEVSAPIWSPSRDETSAKVQVAAPEAVVEQEAEVQEDYESMPVVAPTDSDEEGSGVETSAQKEAKKKRRGPFFKRLSFSSEDKPAESDSQVQEGGEEPKEESKAKNKSMVMRKLTDWTSEREPPSSLPEPSSAVEGDSETNQSSVIAAETKGEQEGEAAAAEEDIKTEDDDSDSTKRTRKKPGGMCMLAEWSVSTDMKRKPEETSSVLKETNETKPEEEAPKEVEADEEVSKDALAASESSPLPKAPKEGTAEDESESSRKVLKKPTVLKKFSSWAIIGEKKKEGDSTVEGEAEQNSGNQTVEVAIVHEGSEEPSSPGSDAKPAETSETSSQLQEAAQEGSETLKSEADKKTKQKKTSLKKLGAGTFLKKLPSGQPKVKEQSSLLEAESTVEVPAKEEEAGGEAKEEEKKTEETAAAAPVATEVTVEAEPTAEPKAEEPTAAAEEKPESKDEEPTAAAEEEKTEQEAEAKEEKEDVAATEETKAAEEEAAAEKDEEEKTKKISAKKRLNSFLGGSFLKRFPSLTTEQSPPAAEGDKEAEDEKVAEDTAEATTGEAPADTAEAKEDNEKTVEAEVTAAETEAEKEEATSKEEAAEEEKTPEETGSVEEGEKDKVTLLKVPDKEESKDKKLTFKFGVFRFIKKFGVESADDPKEEAAKEEVASIDNADPSEKEVKEGNVQPAVEDQITGMTEPAEEKQAVSVGDPQGVTLTITGLM |
| TRINITY\_DN58368\_c2\_g1::TRINITY\_DN58368\_c2\_g1\_i3::g.45497::m.45497 | gi|908453958|ref|XP\_013132059.1| | PREDICTED: immunoglobulin-like and fibronectin type III domain-containing protein 1 isoform X1 [Oreochromis niloticus] | 26.7 | MWKKSKVTDQTAAGQAGIKKKSKVPGVMITQFKEELPEGQSTPDFTRKPIALTIQEGKFAVFKAIVVGDPTPAVTWSRANGEIVFHPEVCQQNYDEASHEHTISFPKVTPEDADTYKCYATNEHGRAVCTVVLNVIAVGFSKEKELKKTQSGEDITDIRKQLKKRNPDGTREHGKVMEDEEKVWEILLSADKKDYEKICAEYGIKDFRGMLKRLSEMKREREEEIAEFVSHITKLKPIEVTAEDFATIELDMDLKDPNSKVFVYKDGIMVAFSKEEGEGLKHSLKQIGKKFIFTISKLGKDDAGLYSVDVEGVNVFSSDFKVPEVDFAVKIREVKAEEREDALFQCVLSAPMNEIKWFGKNAPLTNGEKHQIIVSEDMLIHKLIVRDCMPLDAGIYAAVAGIKSCNAWLVVEANKDPASKGKKAARKTTVAGGGDDEDLMRIAKEQQEKYQKEMQEKLERAKKEKEEKDAADAAAEAEALAARKEAAKAKARAKAEAKARAKRAASGKSMKSGAAGGA**DGAAGAAGAGGAGGAGGAGGAGGAG**GAGGAGGAGGAGGAGGVDGAAGAGGAGAGGAAGGEGAGVGGEFGDEDFDSLEFSDDDLEGEGEGGEGGEGGKGKRRRARDGPLVPDTVI |
| TRINITY\_DN59145\_c1\_g4::TRINITY\_DN59145\_c1\_g4\_i1::g.116184::m.116184 | gi|657536573|ref|XP\_008274854.1| | PREDICTED: protein furry homolog isoform X2 [Stegastes partitus] | 16.3 | MDGAAVCWSKASVISFIKGLASPVGNGYNKPPIPPVCCPQGEKGPPAMMPISIDPESKPGEYVLKSLFANFTTASERKIRIIMAEPLEKPLTKSLQRGEDPQFDQLISAMSSLAEYCLPSILRTLFDWYKRQNGLEEELHEYRPRANTKSKNDEQQRDYLLERRDLAIDFIFSLVLIEVLKQMPLYPVLDSLVNEVINLAFKHFRYKEGYHGPNTGNMHTVADLYAEVIGVLAQSKFPAVKKKFMTELKELRQKEQSPYVVQSTISLIMGVKFFRIKMYPVEDFEASFQFMQECAQYFLEVKDKDIKHALAGLFVEILVPVAAAVKNEVNVPCLRNFVDSLYDTTLDLSSRKKHSLAFYPLVTCLLCVSQKQFFLNRWHVFLNNCLSNLKSRDTKMARVALESLYRLLWVYMIRIKCESNTATQGRLTTIVTTLFPKGSRSVVPRDMPLNIFVKIIQFIAQERLDFAMKEIIFDLLCVGKPAKAFSLNPERMNIGLRAFLVIADKLQQKDGEPPMPNTGCTLPSGNTLRVKKTYLSKTLTDEEAKVIGMSQYYFNVRKAIDNILRHLDKEVGRCMMMTNAQMLNKEPEDMITGERKPKIDLFRTCVAAIPRILPDGMSKPELIDLLSRLTIHMDDELRLIAQNSLQSLLVDFSDWRDDVLFGFTNFLLREVQDTHQGLLDTSLKLLLQLLTQWKLTQAAPGRSYDTAKIHTAELLQTSSSMKIPPERGPHSTVLHAVEGLALVLLCSCQLSTRRLAIAILKEIRSLFMTIGQTEDDDKPMIEIMDQLSPVILESFVNVAVSDTAALPAGHHVDLQWLVEWNALLVNSHYDIRSPSHVWIFAQSVKDPWVLCVYSLLRQDNLPKHCPTALSYAWPYAFTRMQMLMPLVDPNNPVYAKKTSTSGGGDNYVTLWRNYLILCFGVAKPSIMSPGHLRASTPEIASTTPDSGGSYDNKVIGSPSVAWLLKQLVPLMRAESIELTESLVLGFGRTNSLVFRELVEELHPLMKEALERRPENKKRRERRDLLRLQLLRIFELLADAGVISDSTNGALERDTLALGALFLEYVDLTRMVLEAENDKDAEILKDIRAHFSAMVANLIQCVPVHHRRFLFPQQSLRHHLFILFSQWAGPFSIMFTPLDRYSDRNHQITRYQYCALKAMSA**VLCCGPVF**DNVGLSPDGYLYKWLDNILACQDQRVHQLGCEVVILLLELNADQVNLFNWAVDRCYTGSYQLASGCFKAIATVCGSRNYQGDIVTLLNLVLFKASDTNREIYEIAMQLMQILEAKLFVYSKRIAEQKPNNILYGTHGPLPPLYSVSLPQLSSQLARMYPELTLPLFSEVSQRFPTTHPNGRQIMLTYLLPWLGNIELVDSGLLLPVFTPCTSDYDAPSRTTSTNSSHQLRGTGWGSLQATSMVLNNLMFMTAKYGDDLPGPEMENAWNALVSNDKWSNNLRTTLQFLISLCGVSSDTTLLPYIKKVVIYLCRNNTIQTMEELIFELQQTDPVNPVVQHCDSPPFYRS |
| TRINITY\_DN59185\_c2\_g1::TRINITY\_DN59185\_c2\_g1\_i1::g.117514::m.117514 | gi|808874097|gb|KKF23281.1| | hypothetical protein EH28\_21636 [Larimichthys crocea] | 17.8 | GGGGGGGGGGGGEEVGEKGRLAKEHSSFSQPEGSVRGVSSAETETCPPTDVAESQLKSQSWREPIATITESICTEQDRLSHPCQEQHGAAISPLPTHPEPSSGNTNAGGVRADLTQNLISEEALSSGHACEESSLTETERNYSQDLDSLIQPQPLTTSQQIAVERQESNNQQVRPESSTTEARTAESAAEIQVQAQGQSNSGTMPGVGVCASRGGTNRVHFADTVKQEGSSTVAVRNKPVSPMDCASLPPLTVHENLHYPVVEASFIFPDFLSGKKPEIPINAAPSKDEAAKQSSADFPKPLKDGQLDKGGSETKSIAVDQSGNNILVTNTVDLQLASKAGTKQLPSPAEKNGTSNKECFDLSQTAGSAVASADHATVEQVSAKALKQEEEKTEKSPIKLDLSKEKELNKFHAESTDSVKSDQPQESPLISAVPEEKEGNQQPLHSRPELPADDVTCKPLNDVTALSAGTDLSLTPEAVNLTCAASLQTDTSDPSYQLPTQSDQTPPCGLVISDPMKASEGAKPTVHSADQTEDESVTSEVKPSDQSMPVIEQCASNPAFVLQPPGPMLTHLEFITDSDIRPPEQTDERRADGDSTKVSGELDGNRSGETTQMSSAQDLKQTNASVTADEADPKPEDRNYAEMSVIELEKSAIKNENILFSQEENVCAPVKLPATLAVTDNVISLSQTEPDSIAIKAVICETSIRDGLINESCPLSSDLPSNDDETNKDNMTEKQKMGDGQDGQTWMQFEEDKKQSGEATMDNEEKTEISSKLQAGKKSTAPQLSDEPDKEVAGELRDPLQPPHEHKVEKSESPVRDKTEEGEGKREIASKSETETSSLSSPTRPAGPSEDTVPTEVESGSEPPTVYDPSLSQTPTATLERSSDSNTAQDLSAALSQSQSTSDPNCFAQQQEQQQQQECLGSRHPTEELSGGCLKGVDETQTLVPGVKGVAEGWDGSIGSLQPSESRDELTCDDSGGSDGVKGLEREDREGAGAVKGADEVYVLSHVGSDLNESGKAAEQNASVDMVITTASSHVGETGQAMDEIKSLGLGFVSSDAELMPGTEFTTDMGGKGQQKSNLSAACQDQHGQPETSTNTAASVEPASQEHETSPSQISISSKANRDSQDIHAEALPSANRSEEIHQENVSVLPDPVGQAETVEKDVSVALAVKDNSSETEECEILDTVSEPLELQSPNKTSATQSSPAVQTAIKGSDVEGITREDKAALDEEKASGQGTAQTEINTVNSGATEKQGVENQILSCKDSESVVSHSSSEQTKTTKNDSGVTDSITPDVVTVPAAVLSKCPEDLASLGKPNDQASLSEPVDVIVVKPIVAASQREGKPLDEAPACVSPAEGPSVNAAAADVSDSPAPKPTAPEPDTNWIKALKEAASQSQGEPVHTAETLRPLPSLESPQLEFHTPTEEIASPLRQEEIPPPEQAAEKTTEIPPPPKKPVDLPEPL**KKLADLPEPT**QSTREELSEPTKEEEEPPRELPEPERESVTSPEIVEGPAELPEAPKSTEDL |
| TRINITY\_DN44057\_c0\_g1::TRINITY\_DN44057\_c0\_g1\_i4::g.10034::m.10034 | gi|1007764938|ref|XP\_015821192.1| | PREDICTED: calphotin-like isoform X1 [Nothobranchius furzeri] | 63.5 | MAASLLRIGRLGCVKCLQTESWITLSRAPAASAYSSKSGGNKKSSKKNSSDKNQAQTYFDIEKLVQHKPYELPKKEVSSVAAAAAAAAAQPVAEPVASAAASEAV**AAASVEEATNPVV**KATATADAVSKPDLPPEAPPVVEAPPTADAVSELAAGTEAAAVEATTEAVVEAAAAPAVEAAPAAVAVPVAEVATETVVEAAPVVEAAPAEEATPVAEAATETIVEAEAAPAVEAAPAAEAAPVVEAAPAEEAAPVAEAATETIVEAEATPAVEAAAEVIAEAVAEAAPVVEAAAEVLVEAVAEAAPVVEAAAEVLVEAVAEAAPVVEAAAEVLVEAVAEAA |
| TRINITY\_DN32908\_c0\_g1::TRINITY\_DN32908\_c0\_g1\_i1::g.32032::m.32032 | gi|734627401|ref|XP\_010741883.1| | PREDICTED: lon protease homolog 2, peroxisomal [Larimichthys crocea] | 24 | SFDGDSQEVFVCRICFPPKKTVTSENKSTMASGSGIHIPSRLPLLLTHEGVLLPGSTVRFSVDSARNMHLVSQRLLKGTSLKSTIIGVIPNTRDPEHDTDDLPTLHKIGTAGIAVQVVGSNWPKPHYTLLITGLCRFRVSSLLKERPFVLAEVEQLDKLEQYTTSSTEGVATDDAELGELSQKFYQAAVQLLGMLDTSVPVVAKFRRLLDSLPRETLPDVVASMIRTSNKEKLQVLDALSLEERFKKALPMLTRQIEGLKLLQKTRKTNPDNERVLSVRKGGVFPGRQFNLDEEDEDEDGDDMAVLERKVHGANMPEAALRVCLKELKRLKKMPQSMPEYALTRNYLDLMVELPWSKSTKDRLDIRAARTLLDNDHYAMDKLKRRVLEYLAVRQLKTSLKGPILCFVGPPGVGKTSVGRSIARTLGREFHRIALGGVCDQSDIRGHRRTYVGSMPGRIINGLKTVGVNNPVFLLDEVDK**LGKSLQGDPA**AALLEVLDPEQNHSFTDHYLNVAFDLSQVLFIATANTTATIPPALLDRMEVLQVPGYTQEEKVEIAHRHLIPNQLEQHGLTPQQLHIPQDTTQDIISRYTREAGVRSLERKIGAICRAVAVKVAEGHRVTKTDTLIPEGPVEPGDKAAPPEMPIVIDHVALKDILGHPLFEMEVSERFTLPGVALGLAWTPLGGEIMFVEASRMEGEGQLTLTGQLGDVMKESAHLAISWLRANARTYQLTNMVGAPDPLEGTDIHLHFPAGAVTKDGPSAGVTIVTCLASLFSGRLVRSDIAMTGEITLRGLVLPVGGIKDKVLAAYRAGVKCVILPKRNEKDLEELPANIRADLDFVTARNLDEVLNAAFDGGFQGTASTHTPPQLTSKL |
| TRINITY\_DN86221\_c0\_g1::TRINITY\_DN86221\_c0\_g1\_i1::g.95108::m.95108 | gi|657574681|ref|XP\_008291057.1| | PREDICTED: titin [Stegastes partitus] | 16.5 | ASISHYIIEKRETSRLSWTMVEPKIQAISYKITKLLPGNEYIFRVTAVNKYGVGEPLESEPVVARNPFTTPSAPSTPEASAITRDSMVLTWERPEDDGGAQIEGYVLEKRDKDGIRWTKCNKKRLNDIRFRCTGLTEGHSFEFRVSAENAAGVGKPSAPTHYFKACDATYPPGPPNNPKVIDHSSTTVSLSWSRPIYDGGAKISGYVVEMKETADDEWIICTPHSGVQATHYTVKKLKENAEYHFRICAVNCEGVGEHVDLPGSVIASEKLEAPEIELDADLRKMVNIRATSTLRLFVTIRGKPEPEVRWSKADGTLNERAQIEVTSSYTMLVIENVDRFDTGKYVLTLENLSGSKSAFINVRVLDSPSAPTNLEVKDVKRSSVSISWEPPLIDGGAKIAHYIVEKREQKRMAFTSVCTNCVRNSYIISDLQEGGRYYFRVLAVNELGVGLPASTEQVKVSEAPLPPGKIVLVDVTRHTVTLSWEKPDHDGGSKITKYIVEMQPKGDDKWTVCSEVKALEATIEGLLTGEEYSFRVTAVNDKGKSDAKPLAVPVVVKDITVEPTINLLFNTYSVKAGDDLKIDVPFKGRPQPEVSWKKDGHALK**QTTRVNVLN**SKTSSKIIIKDATKEDVGKYEITLTNAIGTKTAEISVIILDKPGPPSNIKMDEVSADFICLSWDPPTYDGGCQINNYVVEKRDTTTTTWQIVSATVARTSIKVTRLNQGTEYQFRIAAENRYGKSHVVDSAPVVAQYPFEPPGHPTNVHVAHATKTGMLVEWGRPASDGGSPVIGYHIECKDQSSILWTKVNRGLLAENQFKMTGIEESLLYQFRVYAENIAGIGPCSKACDPVAARDPCESPHNLRVTNITRTSVSLFWEKPEYDGGIKITGYIVERNELPNGRWLKCNFTN |
| RRRRRTRINITY\_DN55348\_c1\_g1::TRINITY\_DN55348\_c1\_g1\_i3::g.41807::m.41807 | NA | NA | 14.4 | LKAAMFNIHPKALPFLPLSRKFETMDQVLTPQPPFVCSHAPSASDVSTSQPLSPAPALNVDNQAPFEGVIPCSDMERSLVHVSVKHRKPADVMLRDRYFQMVNEKTLTKLYAVEINDRDFNYQQSIIEGWYKACEASLKKPKDLRRIALAQIHKQFAEDSMEEVAKEMTCLFAEVRSELYHPAKESQMIFRLGQVGNARRPGSFVIYGLQEKTRLTNFCPESIIQCFLELLMNDHTTQMDTQY**YIEIGCN**NHVENRQQYVYWGGDPVQVERYRILQSPLLPKTHAHEILTDEVMQMMGLASEKTINGHLLTEIHLRSLLQPIFAKLRPLTVDDLAERLEDKTWAVETMLLRLYYMAHQHPQEARFNNLSRMYAEKIIDFRREDIEFTAMKEIIKKLLIHQKDNYGKVSLLIANMGSAVGYVLGALRAAYTYEKLDDKLLRLLLYTMNCHLPDAYLYRSFFEFNLCAKPLFFKDDQKFWVKSMATDKILTPVSPSDKELPYIEFNTPIFENKMPLKFKGNLDANGWKKISEESIAEQKYQTGYWEETKDTQGEFSKSVVAVRVHEPRLKDLVMEILDPRFDELLYEAALVEELPYYHLLGAVKSTYGRPREKDKFRFAVKNLDKCEDFVWAQPGETRLKQIYQFMHFIIDEVHLLGEETLDVNIIFFMFGRAGEKQGGVLTNVWGKSKLESLLSGPGEHGILHGLYHGPNSKYYKQLDPIPFTVYLNRIDKIPVVKYFQRLHEEQFPHEPFEPIPVSKNEVEGFLNVVMATLEDLSERGLVCLGMLNSSYYTSHFTLLEQRIDVGDKSPRTELTLKNGTGFKSFPHNPNGTAKELQFLRWADNMLNKEHESDVANVERDKCSEDFLPCLFFQAFRDLAGQLHEHSVDFYYNTHEGSTFANSSGAHESLFQSYENEKPYKKTGLFLMHECFHALGSINGPDSLSGIQVDLAASSKDTTPDSILMAKLGNTFELGRYVRKDEPSRIIDSVVRDVAPDTMRLPLSSVLRFVQNFHFGTSASQIYRTHQAAQNICKFMSQVWPFCVKAKVAGDK |
| TRINITY\_DN49670\_c0\_g4::TRINITY\_DN49670\_c0\_g4\_i1::g.57146::m.57146 | gi|657591042|ref|XP\_008299984.1| | PREDICTED: peptidyl-glycine alpha-amidating monooxygenase isoform X2 [Stegastes partitus] | 16.9 | MIPGTMG**VPTLCVLVLA**FICHSHSLEMNDPLYRVKRSQENVLLDPSSCSSRTEQQIFTNRHNFSVALRMPGVVPAGSDTYLCVSFPVPTNRDAYIVDFIPHASMDTVHHMILFGCQTPVSTTNYWDCGSASGTCEDDPSIMYAWARNAPPTKLPKDVGFKVGRNSGITNFVLQIHYGDVSAFRDHHRDCSGLSLRMTTKPQPFVAGIYLLMSMDTVILPGKRVTNADIACDYSSYPIYPFGFRTHTHRLGKVVSGYRIRDGKWTLIGRQSPQLPQAFYPTSKGVDVKYGDTIAARCVFTGEGKTSKTYIGGASDDEMCNFYIMYYMDSRHAVPYMSCVDTGPKELFQHIPAEANVPITVSPDHMNMMHMGHSADQQDKKPLVDANTADQVLDQDNHLEQVSGWPQSSLQLGQVSGLALDSDSNLVIFHRGDHHWGGNSFNNQYRYQQRSLGPIQQSTILVVDPAKGNIVKASGRNMFYLPHGITTDKENNYWVTDVALHQVVKVSSDGRDKTLLALGEAFTPGSDSKHFCQPTDVAVDPETGDIFVSDGYCNARILRFTAQGQYLTEWGAGSSDRRRRIPFQVPHSLVFLPDRREVCVADRENGRIQCFIAETGEFVKEIKKEEFGGEVFAITYSPAGDGLIFAVNGESQYHSVPLKGFVINYSTKDILDTFSPNSKLQEFKMPHDIVETRDGSVFVGDAGSKTVFKFTTEKFHRSVKKAGIEVQELEEMETIIQTKLRPEHNMSKTAAVQEKQTVALQPQPQQKGKEDEEEKKKQEEEEKEEEEKKKSAAKP |
| RRRRRTRINITY\_DN58414\_c0\_g1::TRINITY\_DN58414\_c0\_g1\_i3::g.45922::m.45922 | NA | NA | 18.2 | HQLQKMRNLASGAQFWEIQTENFTHNLSISQQSGDSHQIVATLPKGPGLSNLGTISIKDDPRIKDYDAPDAFTLPLLGQKKLNTEHIRAFSKVIIARGGLHRPELAAHERSSGEGYNEDGVVVWNVGKAKYDRAVDPVGGYEGTLQNKVKNVADNEINVAGILLNNSINDLHGRFKLWPGAASIHDTTCKGKVKILVRMNELDKGNWKDFPELLQLRNSSPSVDVKVSGGETPPHQYTDQGPDFDRSPLEDGTPPELKFKDGNPATLFDTEPNFNLTGALAMATVIEPSTVFAHTAPNADNRATFNRNFSTVITNKEGKKVDKRDWQGICPGCANALVVGGVDSLIKAYGDREITARIQESGPTVTFQAKCKLGKDLAQKALSAARGMDEYSSNTCSGILGVKVELPWGSKEAVAGVDAVPHALDPTFPGNIHPKLEDLNLEILEDYECGKDPVLLDSYADALLAIQGRGTKELYTKMRHNYPFVSTTAGIEAGMNCITAMGTCSISDVGPGHYEVIAGTGGKVTLIGAVKLIVDKPSTWGSLSGTLKVGIVKPCKLEWPIGAMVDVADAGGVGICIAGLGGGNPTHSDTGILMVGPYAYNELIIQHIIGSGPKWFGVGYKAGASALFNYVEQNIDKARALDKVGGTQAEILHDCHITSPVAVKPLGSSIFQLMAMQATADQMAVRDPRLRLYTRGRDIDQNHPDDLHGYVIKESLTLPRSLRKRVIDVNSQLKQYNVFSTPEFR**SMSVQAKARYA**ASVHLRRAGHGLALQLRAVTLCYTAMKNVSLSTSSPPSTVCNY |
| RRRRRTRINITY\_DN53007\_c0\_g1::TRINITY\_DN53007\_c0\_g1\_i4::g.15702::m.15702 | NA | NA | 21.8 | ESLLLRKPKNRRAASPIPQRNQGSNASDTPDPILTPSQTPGLSPTVAPTSNLTTAPAETKTQLPADVPPREKPKRGRKKGTTAGNRVEAKIGNNELAKSKSSSVVQTAAARFWNQSHTKSIHYKVGSESSFEKQCILCTYKGLEGGGQSCNALHAKLGSVSSYVAECNENTCCIFGKEKVQNKWTELLEPSFNPLGPRTYNLRKSDPVLDDKIRRKTGWDKALEDEAIEQLHFVAVQASRRRVRGSPTREFDEGQSVNQVVKGNDREREKGKERDKERAEREKEKPHGSPAKEQWDTKDPQSQEKKGGSPSEESVVREKGTNNNPDTINDKSNNNTAASTTTTTIIPSHETRVHYDRGAKSRYTKGCHQCLFVPKEDDSLEGGCRKQHYQYGMLSSFHAS |
| RRRRRTRINITY\_DN43812\_c0\_g2::TRINITY\_DN43812\_c0\_g2\_i2::g.107305::m.107305 | NA | NA | 19.6 | GHITKNWHTKSNRYLAPFMIPLIKAANDSILSMIYENNWYYLAREAVQFHPSSVCKALQRFLPEQVKVFESPEIVDLIEELENLFMVEKPSHTKPWYKLLAMVVPETLTSDKELFQVVCYALQPHYVSLSKVKHLPLLVKLLFIKHEEKLPLAFGNIISGLIELLEAIGNHHETEYIFRYFINNIQKRIYARLGLFKGYIRHLTTKLFDRERPDESDFLELLQMVFKQDIYKKAINPQFDPSELFRLFFEYVLQLHPWAAELTPEDEEPDFEAGTPNSSPPLTRFMNVAFMHVVEPYIPETIVNRNHTIYEVMESLAARKVEKWKLDSLPDSLFDFLVCCQRLKQIFLKEQEAPAVDRFHMLAVPQFPGNSNPA**DVVMRDGSKNCT**LM |
| TRINITY\_DN43602\_c0\_g1::TRINITY\_DN43602\_c0\_g1\_i1::g.104726::m.104726 | gi|657587916|ref|XP\_008298272.1| | PREDICTED: transmembrane protein 41B [Stegastes partitus] | 24.5 | MAKKRRERRETDGLLAQEEVKAAVTDSQQLKEAQHNVGGSARMSLLILFSIFACSASVMYLVYRNFPELPDDEMEKIKIPKDMDDAKALGTVLSKYKDTYYTQVLVAYFATYIFLQTFAIPGSIFLSILSGYLYPFPLALFLVCLCSGLGASFCYMLSYLVGRPMVYKYLTERAQKWSQQVDKHRDHLINYIIFLRITPFLPNWFINITSPVINVPLGVFFIGTFLGVAPPSFVAINAGTTLYKLTTAGEAVSWNSLA**VLGVLAVLS**ILPVCFQKKLQQKLE |
| RRRRRTRINITY\_DN56848\_c0\_g1::TRINITY\_DN56848\_c0\_g1\_i1::g.42584::m.42584 | NA | NA | 20 | HQKATEQVEQEATETCVSQSLEEAQRDDKEAVTVVTKGRAHGQELKQFAQPVQTFPFQAEVVPLIKGADVLKRIEDLAPGDPAYFGWRYFVGSSIINQIAKSHLTLGAHITGDLLGMSDTNLLLPTVLTIYKAGSWPKLLGMAWDETDGGINDLILDFKEMMELQDAVDGATYDVVEDAGLGRVLGEANQSCTVTVHAGWAKLLQISFTGVGGSGGTILVRKDSSSD**RCLGGANVLA**SLATSAVYPISAAEAHSVLEPKHSVEYETLTLFEALSGQKWPPVAAWVEDGPAFHTVESGCDMVVGSVDRGLIVPFESDSDTMVSMPDKRLKLLKAGYGGRMSIDLPNLSAAHVKILVESPSSVAPVTVEDTYRLVGNTGYQDIVWASMCSQLRSPSSCVHRRCCVSCGARALAKTSGAVKSGLLCLLRASAM |
| TRINITY\_DN45645\_c0\_g1::TRINITY\_DN45645\_c0\_g1\_i1::g.97043::m.97043 | NA | NA | 36.2 | MPNTKTPPLKTPPRSLKTSTTRNQKTSASARLPVSCSSSGRSFCLRQ**VSPRSPIL**HRCCPDLQGRKRRPRPRPGSPLPPPPPAVQLKTLQPRSPRTAPNRTVTRARRPEPPPPQQPPPPPPRQTNRRPPAARSRPRGRRKK |
| RRRRRTRINITY\_DN110183\_c0\_g1::TRINITY\_DN110183\_c0\_g1\_i1::g.129779::m.129779 | NA | NA | 47 | TATTTAATAAATTATTA**ATATTTAATAAAT**TATTAATATTTAAAATAATANHTPEEQGSCGAPPKRAPAAGPGPDQLRPDSSQAAAAAGPQLCLTRPGASGHQVHQVHQVHQVHQVH |
| TRINITY\_DN50760\_c0\_g1::TRINITY\_DN50760\_c0\_g1\_i1::g.121839::m.121839 | gi|734594222|ref|XP\_010735607.1| | PREDICTED: cation transport regulator-like protein 2 [Larimichthys crocea] | 25 | MWVFGYGSLIWKVDFPYEEKRIGYIKGFSRRFWQGSTDHRGVPGKPGRVVTLVEDPEGCVWGVAYKLPTGREQEVKSYLDYREKGGYQVITVTFHPRPPLVPPPNQTLLYIGSQDNPDYLGPAPLEEIANQIVSSTGPSGQNTEYLFQLADAVRT**ILPEDLDAHL**FSLETLVRERLQSVQKHSHSQTG |
| TRINITY\_DN27493\_c0\_g1::TRINITY\_DN27493\_c0\_g1\_i1::g.5557::m.5557 | NA | NA | 25.7 | METFTDTCTCRTCTPREQTTSQAPVCQSLPVTSLAAVLSSVRWRSTNTTTTPCTDM**FAAPAVAPC**QVPGSWTFTFRSGTTLSSLSSPRGRTCTSVWWKAVDRSSGQVNTGKTI |
| RRRRRTRINITY\_DN52176\_c0\_g1::TRINITY\_DN52176\_c0\_g1\_i2::g.68765::m.68765 | NA | NA | 27.3 | RSFDCLDSEALMDLRQVGATLQQSCVFSLQHLQPLAGAVGEDVTLFCQLLKVIVDCLCLRPEMFLRLL**FAPAFGAFQL**STFGFLTQNTQKHSVFSCHHHLHVTLGVKDGTILLELLQHLVYREGRQSMLLIFTLVPRSVDLADQQSFVQVFESHTFSSRQCILHSECYTTETLVHRHLPRHRD |
| RRRRRTRINITY\_DN14691\_c0\_g2::TRINITY\_DN14691\_c0\_g2\_i1::g.71346::m.71346 | NA | NA | 24.1 | PQFAEDKSLQLHKWRRIAVKYKETGSTEGFVRRITVRMLTVTNDQNESLVLDLTDGVKVTKSKKILKRGNLRLKNDYFADEIKNRSIDLGAKMILDYRFSQVY**KEIDKYDKPQ**NPDEDGEVEYDSDEPDKEDEDEEETQQATRATGKKKSSKFRLHHVSWSRVPDRGHLVLRHCGSAPFASCGWLQRTHISRPCWETQMLGYGAALLHRSNLRGLQRMALAQVVLNQM |
| TRINITY\_DN37702\_c0\_g3::TRINITY\_DN37702\_c0\_g3\_i2::g.77697::m.77697 | NA | NA | 31.2 | VCVCVCVCVCVCVCVFTVLEQRKSKTLMFSQRYLSLSPSLPLSPSEKILSSHMKNQDEGTDVLQIVVLFFGLSGPGHVVI**VVFKQTP**SSFWRISFSWRQLEHLEHLEQVQSPPVSPLVCSSSFSLHWQRQQLSSPSSL |
| TRINITY\_DN19292\_c0\_g1::TRINITY\_DN19292\_c0\_g1\_i1::g.3547::m.3547 | NA | NA | 35.7 | MWRRRCLHCCVAAQRDAGSRRTTPRTHSPLSLTDPRPLPRLRRLRSSRCSRLLLSSRRLRPRPHRHPLPL**YTPPPPLP**PLLLLLPPLPPLHHPPASPLPLCSPGSRCLCRSL |
| TRINITY\_DN16613\_c0\_g1::TRINITY\_DN16613\_c0\_g1\_i1::g.103829::m.103829 | gi|808887656|gb|KKF33984.1| | hypothetical protein EH28\_05835 [Larimichthys crocea] | 26.6 | QMRHTAHELRVTLDHVLQGGEPSVAPPNSQDEALSFLTEPEVEMRAVHNIPEDDLNFLFLAENLRVPKNLYERISEIADYKKYTSALLMILFDRETLATHSLQGRRNTFTGEDCHKPQLPPDILRSIIDHVAAKFGVD**CSQIKTAIRT**KLNNEDKLLKKRLGVGKAENKPSADQSFCQEASLLP |
| RRRRRTRINITY\_DN54116\_c0\_g2::TRINITY\_DN54116\_c0\_g2\_i1::g.17246::m.17246 | NA | NA | 16.6 | LVVRDTPRDSSEGSHFCLLSAVVLSVTAIFSPQLWDEGTTQEERTDVSCMEYRRVAHQVHCLLISGRFTASNFPKTCIHSDLGPSRCRGSILKKRVQSSPIPAVIGGRALVPEHWPPQGQPGGGVDAEAEAGSGSAGARESLSSLSISISLSPTISGSVTSGCSMSPNSFASTVSSII**SKALSFFIS**AILARPSPSRCFARSSKESAMLSFGQTAMM |
| RRRRRTRINITY\_DN4698\_c0\_g1::TRINITY\_DN4698\_c0\_g1\_i1::g.864::m.864 | NA | NA | 14.7 | DLCVYPLINLRSEDGHPDLSICETWDYWNGKTDYCGNVGSWHQAHLRSLDQDNVERSVGPLDKAPQEAALVHTKKADKSRHDEKKLFETMFFHASPTHAGSSTLVNSQQSLYSQIIESRSLEKWDTQQFPSPPVPPNQKPQESREPEPRHEPQPRVEGDQCSDKLFSTKIQGTVPDFTLRRDKLRVPKTGDDVTQGDLNVVYDKPRYKQRKRKGTSGVAGDDELSATDSAPSATSNKKCLPRSQSDSDASWLGDTHLGQ**VCVNLAQPSP**GLGSTDVSGPRLAPSSLRPPESQAQPATQQ |
| RRRRRTRINITY\_DN20669\_c0\_g1::TRINITY\_DN20669\_c0\_g1\_i1::g.83915::m.83915 | NA | NA | 17.5 | WAQTQPQPQMQPPAYSPRMHAYGPAEVLPGTQAWQP**LAQVAPHAQSQLAQH**TEPHYPAPIPHRQQPTWVGTQTPSQTQPYGQPYLQPQAAAQPYPVSIPSSTRVQTWTQLQGQSPHGPQQVLAQAHTSYQTPAGPQVQTHHQPLPQGQSTWVMPQVQTQPHVLPQPHTQVQAMSQVQTQPHAKPQPHTQVHAMSQVQTQPHAKPQPHTQVHA |
| TRINITY\_DN97605\_c0\_g1::TRINITY\_DN97605\_c0\_g1\_i1::g.27609::m.27609 | gi|317419749|emb|CBN81785.1| | DNA-dependent protein kinase catalytic subunit [Dicentrarchus labrax] | 40.2 | LRLRRRFLKDQEKVSINYAQKEIRQQRQKKEDKADERLKKEAQVTLYRNYRVGDFPDIQIPYSSLIAPLQALAQKDPILAKQLFSSLFAGILQEVDKDKPAE |
| TRINITY\_DN58331\_c1\_g1::TRINITY\_DN58331\_c1\_g1\_i1::g.46034::m.46034 | NA | NA | 11.9 | MSVGGEDVPHAPGAAVGSEVRAPLRVLVRDSDPELRPVVHLHLPVVTTSDRDQIPQDGHTPAEGAVVEGHGADGQLLVSVEDGESVLGDGQTGMSRVLQQVEERSCCGDGDDITPVAGPADVDRPDGDEVAASGLQLDQTLTGRHGNDGLGDVALSAVGPQLAQLHCVRVHRVGVS |
| TRINITY\_DN43949\_c0\_g2::TRINITY\_DN43949\_c0\_g2\_i1::g.101517::m.101517 | NA | NA | 25.2 | MGTKEF**DVDVTAATVT**SSSSSSLFFFFLFFSPPSGVTASSSSVTAATATASSSFFFFFLFFSPPPFSSSSSGGRTTSSSSFLFFFFFFLFSSPSLFCSSSSSSGGRTTSSFSSSSSFLFFFFFFLFFSPPPFSSSSSGG |
| RRRRRTRINITY\_DN78144\_c0\_g1::TRINITY\_DN78144\_c0\_g1\_i1::g.94632::m.94632 | NA | NA | 34.3 | TVLCEHSVLVEPCAPLSLGQHHVQVELGQPNGQHCPVVPLCRGQLVLPFALPWLNVPAE**LTAQSPPL**RPGSRVVPGLLVPPCFPCFLIEQSPQALPLSP |
| RRRRRTRINITY\_DN62534\_c0\_g1::TRINITY\_DN62534\_c0\_g1\_i1::g.97702::m.97702 | NA | NA | 26.1 | KPLEDETTLRFYGSMGFRFVIDMPKDAQGAKVSQ**KPADSKIPTLTLKVE**KGRSAATIRYAESTFSVDPSKSVESKRVPGTFVVGNCMKNVYLSALHLEPGEPMKIFTHWVLFLSRQQYVQLHIVGFTCTELTCHNDQE |
| RRRRRTRINITY\_DN48872\_c0\_g1::TRINITY\_DN48872\_c0\_g1\_i1::g.72600::m.72600 | NA | NA | 13.5 | PNSSASSSSSAASSSVAQVNGYRPECYSNDDASVSLHDLFYLIVCADPNLEFWVVAARWVPYCLDHTRGVLSLVRCFDYGVQQPADLSSPRWSVAPASPTPAPLA**VPVHPGRTAQ**LLEGEGDRGHLGAEDNSFTTLRDLADALLRSGPDLQLSVRWGVGVGVDLHECDSAGRLLDVVGPLQHLLLDPSWDSRHAAWVAGRTWVSAWAWVTRRSRGSGGPSGHTWVVRPRVVLSRWPWM |
| TRINITY\_DN86315\_c0\_g1::TRINITY\_DN86315\_c0\_g1\_i1::g.26591::m.26591 | gi|734637300|ref|XP\_010747330.1| | PREDICTED: ubiquitin carboxyl-terminal hydrolase CYLD-like isoform X1 [Larimichthys crocea] | 24.3 | KFVEAPSCLLLLMPRFGKDFKMFDAILPSLS**LDITDLLD**DTLRQCSICQAVAEWECLQCYEDPDITPGRLKQYCATCNTQVHSHRKRSSHGPVKVRVPDGPWTGPLHCTRQ |
| TRINITY\_DN80726\_c0\_g1::TRINITY\_DN80726\_c0\_g1\_i1::g.98561::m.98561 | gi|657532668|ref|XP\_008305048.1| | PREDICTED: baculoviral IAP repeat-containing protein 6 isoform X7 [Stegastes partitus] | 22.5 | HEFLSRLQVHLSSTCPQMFSEFLLKLMHILSTERGPFQSGQGPLDAQV**KLLEFTLEQ**NFEVVSVATISAVIESITFLVHHYITCSDKVVSRSGSDSSVGARACFGGLFANFIRPGDAKAV |
| TRINITY\_DN78259\_c0\_g1::TRINITY\_DN78259\_c0\_g1\_i1::g.26075::m.26075 | gi|542199074|ref|XP\_005473880.1| | PREDICTED: monoacylglycerol lipase ABHD12 isoform X2 [Oreochromis niloticus] | 18.4 | MKRRAVGQTDPSPGPSEVQRAGAEDSAQGQPETESRWWLKRGLLAASVIFILVP**ISLRILPE**LIQHLVYTHRIRLPFFADLSRPADLSLNHTINMYLTSEEGISLGVWHTVPESQWKEAQGKDLAWYQNTLSDGSPVFIYLHGNTGT |
| TRINITY\_DN76008\_c0\_g1::TRINITY\_DN76008\_c0\_g1\_i1::g.94422::m.94422 | gi|657587270|ref|XP\_008297918.1| | PREDICTED: WD repeat and FYVE domain-containing protein 1 [Stegastes partitus] | 9.6 | KKKKKNTKQTMAAEIHSRPQTARPVLLNKIEGHSDAVNAAVLIPKEDGVITVSEDRTIRVWLKRDSGQYWPSIYHTVSSPCSCMSYHHDSRRIF**IGQDNGAVVE**FLISEDFNKMNHVKTYPAHQNRVSDMVFSLESEWVVSTGHDKSVSWMCTQSGSMLGRHYFTAWASCLQYDHETQHAFVGDYSGQITLLKLEKQ |
| TRINITY\_DN54250\_c0\_g1::TRINITY\_DN54250\_c0\_g1\_i1::g.39997::m.39997 | NA | NA | 17.1 | MFTGINTYLTRLHQQLQVYVL**ECVLGCVLE**CVSVCVLWSAVSAASVPAACCSANMSVSFSSRTGSLDSAAACSLAAAAPLLLRTTPSDSNTFPVSSNTVDSSTSPRRCSSENLSTNL |
| TRINITY\_DN42444\_c0\_g8::TRINITY\_DN42444\_c0\_g8\_i1::g.80898::m.80898 | NA | NA | 15.2 | SAFILKIKLFRVIAFIILYGIHSHRKIQSERSSSASVRVFFFQSFFSPKGKRRSEFSYFPQHLNAASHLNSLPPPPWSVGFGESVDACRDHQLMVPHLPLQEGLQLVDVHLRNNGPRGDEHPEHRVDPLQRHGVEVGQHGLDVGPEQLQLLLPLLRL**GGGVGVSLLVAV**DQHHSSLHLLLGRARLHHVVPP |
| TRINITY\_DN36663\_c0\_g3::TRINITY\_DN36663\_c0\_g3\_i3::g.7766::m.7766 | gi|734635203|ref|XP\_010746177.1| | PREDICTED: C-C motif chemokine 24 [Larimichthys crocea] | 13.1 | MRFCLATLVCIATWMSSVQANNGQNCRCLGVSTTRPRVQRIKNYTIQPEGLCPVKAVVFFMLSEKIVCSDPNRDWVKNAMKKVDKDTM**VPPVMEE**EEQVSTTVMQKVDTETTVPPVIEKKEEVSTTVMQKVDTETTVPPVKEEKEEVSTTVMQKVDTETTVPPVTEKKEHVSTTAMQKVDTDLVVPPVIEEKEKESSIV |
| TRINITY\_DN28462\_c0\_g2::TRINITY\_DN28462\_c0\_g2\_i1::g.70660::m.70660 | gi|1012770260|gb|JAR44010.1| | hypothetical protein [Fundulus heteroclitus] | 17.7 | SHHVLGIKHLLSELGDCKGTVLLAAPAGQWSKARHEEVQTRERHHVDSQFA**EISIELT**GEAQASGDSAHGSGHQVVKVSIGGCGQFESAEADVVQSLVVDAVGLVCVLHQLVD |
| TRINITY\_DN23496\_c0\_g1::TRINITY\_DN23496\_c0\_g1\_i1::g.4626::m.4626 | gi|657576750|ref|XP\_008292170.1| | PREDICTED: proteasome subunit beta type-5 [Stegastes partitus] | 9.6 | LGALRGPAAMTQINVPGFTRRKRLVHQTVTKMALASVLNSDCADFSFDKCQPFGFGCGAEQSGLGFDATPGDSLSFSVKNPLCAGGDDGVERKIEFLHGTTTLAFKFQHGVIVAVDSRATAGSYIASQTVKKVIEINPYLLGTMAGGAADCSFWERLLARQCRIYELRNKERISVAAASKLLANMVYQYKGMGLSMGTMVCGWDKRGPGLYYVDSEGNRVCGDLFAVGSGSMYAYGVMD**SGLRQDLSVEE**ACELGRRAIYQATYRDAYSGGQVNLYHVHSEGWTRVSQEDVLMLHQQYKDQA |
| RRRRRTRINITY\_DN57102\_c1\_g2::TRINITY\_DN57102\_c1\_g2\_i1::g.126058::m.126058 | NA | NA | 26.4 | SGGAGLGSGGGGTTIIGVGGGGTSGTAGTAGLTSTDTPQWVSYSGTKGGMCIMA**WPLPPTGPPGG**VCTLLSSLMSPLRCDSRLLSPTCVTALPTHPAQQLGMTPCTTVAM |
| RRRRRTRINITY\_DN52888\_c0\_g1::TRINITY\_DN52888\_c0\_g1\_i1::g.15129::m.15129 | NA | NA | 11.2 | LTNYNLPKWAFRQCY**FLTGCRLAT**QTDRCRYSALTCPDVVAAEQGNCLQILSCIAQPTAYSLVADMVSKSFEGIITECQDRYSSPFIHCIEELLNIVATETREKPLLDELTKVLFLCFSCQTQPSANESTGAAQLAANVFYSLMKDQKGCSGCLGIMKCVQDPKAITSIFNIALPFMKELEDKCLKATAPPGPLHDCVSELGNMIKKQIDANSLLDVLLEIIKTCDQCVDGNPRTAEPVTQLSDAHLTLANCHLGISLFLLFTLLAM |
| RRRRRTRINITY\_DN49941\_c0\_g1::TRINITY\_DN49941\_c0\_g1\_i1::g.117740::m.117740 | NA | NA | 17.9 | DLIRDGPRNWRWGELQQHETYQLRRDHFVVRIISKVMKGTIEPLEGIKRNDLMRIEYSQGQNLYTLTEDHLKVAPSTAACLVYQFPLIKNDTDPPLNSEEQKFIPLALVDSMSYAGAGLEQGIGSLSADFDQVLG**SEIVEDTLPL**KLAWAM |
| RRRRRTRINITY\_DN102801\_c0\_g1::TRINITY\_DN102801\_c0\_g1\_i1::g.139401::m.139401 | NA | NA | 26.3 | LVHAWDFYHLVWVSGEGLRGHHLASQRLLPPLQLLRSSCRLHVADGSTEVLVPDVGHGVILSPLDSGVHSTDARHGGVDRRPLSVGESPVLHRVALLRLHGDQLLSLAQGDVLQLLLG |
| TRINITY\_DN75480\_c0\_g1::TRINITY\_DN75480\_c0\_g1\_i1::g.94369::m.94369 | gi|958251808|gb|JAO40423.1| | VIGLN, partial [Poeciliopsis prolifica] | 14.7 | VAIPQRYHRAIMGPKGCRIQHITREHEVQIKFPERDDSASGQEPP**PQENGEVSP**EAEFVPRKCDIITISGRAEKCEPAKAALLALVPITEDVEVSYELHRYIIGQKGSGIRKMMEEYEVNIWVPQPEKQLDVIKVTGLVANVDRAKLGLA |
| TRINITY\_DN49988\_c0\_g1::TRINITY\_DN49988\_c0\_g1\_i1::g.117669::m.117669 | NA | NA | 13.4 | MLVWWMSRLALTNTFITFPSLKYVLRVSLKLLEYFTNSFFCCSSARLFRYWYFLKTVLTVSSSS**FMALAMSL**MVCRKRTLSLISRGMVLRMCLRARALSFSSWNSGSRLSIMNSGTSSAAMRSSDSL |
| RRRRRTRINITY\_DN89119\_c0\_g1::TRINITY\_DN89119\_c0\_g1\_i1::g.95393::m.95393 | NA | NA | 15.6 | IWPRLLILTFSVKVNFQ**EASDVGGGI**KVQFSFSVSICVKGTSSFSMVSTESLPFYVQSTIFLIVPFVDDATCSSVTVRKGSGGVGVGCGSPQEAPQMAPITIPQRTTIA |
| RRRRRTRINITY\_DN22990\_c1\_g1::TRINITY\_DN22990\_c1\_g1\_i1::g.52719::m.52719 | NA | NA | 11.3 | EVTIASAPVATYQPIYTGQM**PAAAAAPMYTGT**TGLSLHNMQQTLPAMVSSPHLSLSPEIAAAPTIVAGTPQMVYQQHPMWSTSQVQYTSVPSAAIFPTISTQAIMRNTSISYPSSYFGNQMATPDYTLAMGSEGERTWPRGNQPYKVQTQRKKQGGDAFK |

\*ORF code output from TransDecorder is shown.

\*\* The gene ID or the definition (including name of protein and specie) of top-hit gene is shown.

\*\*\*The color of character indicates the peptide confidence; green, yellow and red means the peptide confidence is ≥95%, <95% ⋏ ≥50% and <50% respectively.