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**Figure S1.** Neighbour-Joining (NJ) phylogenetic tree of the molluscan tyrosinase proteins obtained by MEGA5.2.2 under the JTT + G substitution model. The tree is rooted using the midpoint-rooted option. Statistical support for each node is indicated as percentage of 1,000 replicates.



**Figure S2.** Maximum Likelihood (ML) phylogenetic tree of molluscan tyrosinase proteins obtained by RAxMLGUI v1.3 under the PROTGAMMAWAG substitution model (final ML optimization likelihood: -7639.339332). The tree is rooted using the midpoint-rooted option. Statistical support for each node is indicated as percentage of 1,000 replicates.



**Figure S3.** Bayesian Inference (BI) phylogenetic tree of the molluscan tyrosinase proteins obtained by MrBayes v3.2 under the WAG + G substitution model. The tree is rooted using the midpoint-rooted option. Statistical support for each node is indicated as posterior probabilities after 1,500,000 generations.

Identities = 27/139 (8%), Positives = 52/319 (16%), Gaps = 204/319 (63%)



Identities = 79/292 (27%), Positives = 192/292 (44%), Gaps = 61/292 (20%)



Identities = 18/282 (6%), Positives = 36/282 (12%), Gaps = 181/282 (64%)



**Figure S4:** Sequence alignments of hypothetical proteins that belong to the microsynteny block between *C. gigas* scaffold 867 and *P. fucata* scaffolds 13287, 1286 and 19072. Amino acid similarity is shown in black (identical residues) and grey (functional equivalent residues). Hypothetical protein 1, 2 and 3 correspond to the *P. fucata* gene models pfu\_aug1.0\_1286.1\_36924.t1, pfu\_aug1.0\_19072.1\_11190.t1 and pfu\_aug1.0\_19072.1\_11188.t1, respectively.

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**Figure S5.** Quantitative PCR expression profiles of tyrosinase genes across the mantle tissue in *P. maxima* and *P. margaritifera*. (A-D) Relative expression (log scale) of tyrosinase genes in *P. maxima*. (F-I) Relative gene expression (log scale) of tyrosinase genes in *P. margaritifera*. N = 4 mantle zones/data points for four individuals of each species.

**Supplementary dataset file S1.** Tyrosinase protein sequences used in this study.

***Pinctada maxima*** (Bivalvia, Pteriidae)

>P. maxima-TyrA2 (complete)

MSKMPSLLQILYLILAVFPLCRLQQRSVNNLNPRFIMWMNSLFYIPNDRNLRVRKEYRMLSDAERRDYNRAIILLKNDRTVSPNKYDALASLHHLNSANGAHGGPGFLGWHRVYLVLFENALREKVPNVTIPYWDSTLDSDLPDPRRSIIWSPLFLGNGNGPVVNGPFRRWSTPYGPLRRDIGADRRLMNRQDIQNVFSRRWLWEITNPSARDEYNIELLHNHVHVWVGEQMSRIESSSYDPAFFAHHAFIDCLWEEFRQRQRQQGINPARDYPRIVGDQNHQPLVSMGLGRLLVIDGINDFFTRQIFRYERRPVCVRGSNTCGSPYLRCNWSTQTCLPLIMSNRGTQTRRVVQNRRQPWWRRFVNQRNTFFG\*

>P. maxima-TyrA3 (complete)

MKGLLWRFFLLVGLICVVYPDIIEIRVARELEECFEQRRFDTNQTDPRYDNIHGYCIQNFRWHLQEHYWKNITMETSNWIEELLRISNRKVRKKRQSLPVRKEYRRLTDQERADYHRAINMLKRDTTVKPNRYDALGLLHQRRGDDVHHGAGFLGFHRVLLVVYENALRQKVPTVTLPYWDSRLDQPLRDPTRSIIWSPQFLGTMRGRVINGPFAFWQTPAGPLVRNGGQEGELFTYNHIRAVMTRSHLEEISEPHAPPPFDFEIRHGDVHQMVGGIMAPAETAGYDPVFFLHHCFVDYLWEVFRRSQKEKGVDPTKDYPRRYGPAAHAPKEQMGLGRLLNEHGLSDMFTSRLYTYEPSPTCSYRRPTCGSNYLTCEFGFGRPQCVTLEMLSTTPTQSSRSNIPLQWRQFVPQLQTGVPRSPVPNQFRSALARAQARQQGNTLPNRAPNPNQFGTPRRFGRTKRQADAHAIDGGRLTQMGQNILSQFGGNQLSEFIRNKTKPLPEKAIPKLYKQRHHKRIFSK\*

>P. maxima-TyrB1.1 (complete)

MNTMTLLGKVFLLQFLIGVGFCMLMQDPKRNDTKGTYAACFRSQPQGNEPASPDCLKAFMAYAEDMKNIFHFTKEQINYLWSLERETQSLLHNHRRRKRQAVYLPVRKECRLLSELERQNLFYTVRSLKMDTSNPNEYDTLANLHRGAVQPHAHDGSNFLGWHRVYLMYYERALRRIRGDVTLCFWDTTMEFNLGMDNWEYTAVFSSDFFGNRRGQVITGPFRDWPLPPGLTESDYLYRNMTRGRGMPFDSRAASSIFYNPNTIIHSTITWEGFGFDTITNSQGQTRNITIEGEHNNVHNWVGGAMGFLDPAPQDPIFFFHHCYIDYVWERFREKMRRYFRDPTTDYPGHGNETLHDANYPMIGFEWYRNIDGYSDYFTQNVYRYESPTCQACYYSPYTVCGQGNQCIARMNYPGTEIEEGPQVPNGPVAAFSVAGGTMMMSASNGRGFIATSNSE\*

>P. maxima-TyrB1.2 (complete)

MTLLGKVFLLQFLIGVGFCMLMQDPKRNDTKSTYAACFRSQPQGNEPASPDCLKAFMAYAEDMKNIFNFTKEQINYLWSLERETQSLLHNHRRRKRQAVYLPVRKECRLLSEMERQNLFYTVRSLKMNTSNPNEYDTLANLHRGDVQPHAHQGSNFLGWHRVYLMYYERALRRIRGDVTLCFWDTTMEFNLGMDNWEYTAVFSSDLFGNRRGQVITGPFRDWPLPPGLTESDYLYRNMTRGKGIPFDSRAASSIFYNPNTRIHSTITWEGFGFDTITNSQGQTRNITIEGEHNNVHNWVGGAMEIIKPAPQDPIFFFHHCYIDYVWERFREKMRRYFRDPTTDYPGHGNETLHDANYPMIGFEWYKNIDGYSDYFTQNVYRYESPTCQACDYSPYTVCGQGNQCIARMNYPGTEIEEGPQVPNGTVAAASAAGGTMMKSASNGRGFIATSNSE\*

>P. maxima-TyrB2.1 (complete)

MMPYGLTLILLLFTLNDATLLGIKYDPIPRCAREIMADHTSPNYNSTFNNDCAEFISNSFLELKKLLNFTDDQINFIKSLDREAMSLLYGSERTKRQTRSPVRRECRTLSQNDWGRLSHAIRRLKFDPGNEYDTMAHTHTLPAVIDNSHDGSNILGWHRLFLFLFEIALRRKVPGVVLCYWDSSLDYLLRGRGQVQSAAFSHELFGNARGQVTTGPFANFPTPWGPLRRNFGGEGGSLVRPHIVDMIERDPNIRSHGQLVDGDGATGFTDPLSGERTSLEAEHNNAHVAVGALMAIIPNAAYDPLFFFHHCYIDYVWELFRRKQMRLGIDPTRDYLGHGGPAHARNAPMRGLIPGWRNIHGYSNFFSRRYRYAYHPVCGNGCSGSERFLYCPRGRRFRRCIPRTMEGRARPPQRIVGRSRGARDITFSTNYDDSTIAH\*

>P. maxima-TyrB2.2 (complete)

MTVRSLFQTHFWNLKNLLNFTDDQINFIKSLDREAMSLLYGSERTKRQTRSPVRRECRTLSQNDWGRLSHAIRRLKFDPGNEYDTMAHTHTLPAVIDNSHDGSNILGWHRLFLFLFEIALRRKVPGVVLCYWDSSLDYLLRGRGQVQSAAFSHELFGNARGQVTTGPFANFPTPWGPLRRNFGGEGGSLVRPHIVDMIERDPNIRSHGQLVDGDGATGFTDPLSGERTSLEAEHNNAHVAVGALMAIIPNAAYDPLFFFHHCYIDYVWELFRRKQMRLGIDPTRDYLGHGGPAHARNAPMRGLIPGWRNIHGYSNFFSRRYRYAYHPVCGNGCSGSERFLYCPRGRRFRRCIPRTMEGRARPPQRIVGRSRGARDITFSTNYDDSTIAH\*

>P. maxima-TyrB3.1 (complete)

MRYLKFRTSAYDFFAGLHRSLRSFRNAHIGSNFLGWHRVYLWYFERILIRVGGVPLCYWDSTLDFRIEGSGQRNTTMFTSEVVGNGIGMVINGPFRNWPIPDRNVSLRREIASFASLMRPQVVDLIMTSNLIRNHSQISNGAGSVGMIDPDQGTRTSLESEHDNTHVWVGGVMSDATIAPQDPVFWLHHTYIDYVWEKFREKIVHFRHKPSQ\*

>P. maxima-TyrB3.2 (partial)

MRYLKFRTSAYDFFAGLHRSLRSFRNAHIGSNFLGWHRVYLWYFERILIRVGGVPLCYWDSTLDFRIEGSGQRNTTMFTSEVVGNGIGMVINGPFRNWPIPDRNVSLRREIASFASLMRPQVVDLIMTSNLIRNHSQISNGAGSVGMIDPDQGTRTSLESEHDNTHVWVGGVMSDATIAPQDPVFWLHHTYIDYVWEKFREKLFTLGINPANDYPGHGGDPHAANTQMVHFYNFSNWWTNENGYTNLFTQFVYTYDEHPTCGNGCGGRGDTNLLYCPTGGTGDQRCVATVVVWSA

>P. maxima-TyrB4 (partial)

MKDGPESMYDTFARVHQNQESLDNAHGGSNFLGWHRLYVLFFENALRRIAPGLVLCYWDPTLDYMMKSTLQIHSVTFSDRLFGNGYGTVINGPFKNWQLFEPYNYRLRRNIGQEGSLTRPEVIDIITLNPKIIRSTQISSGLGAIGFKDPDTGRRHSLEQCHDNTHVYVGEVFSSLPITAQDPIFWFFHAYVDYVWELFR

>P. maxima-TyrB5 (complete)

MDRYRGLKNLLNYTEDQMNYLFSLERAMMRKHHINNKRHKRQAMMRPRQECRTLPDDARNNLFNTIVDLKASSNGMSQYDTIAGLHSLQAFPNAHQGANFLGWHRIYLNMFETALQESRSDVVLCYWDSTLDFLMPENTQLNTVTFSAELFGNGRGSVINGPFRNWRLPGGRTLQRFIAGPGSSLTRPGVVDLIATDPRINSHSQIVVGGQGFPDPDTGRPGHSLESEHDNTHVWVGGVMQNVVLSPQDPVFWFHHTYIDYVWELFRQKIGPDAREQYPADASGQHAPDAPMVGFDMVLNRDGYSDEHSKMYAIHPRCSDNCGNSRFLECLDNGPMADPNRRCVSRAVNSDMVPAAAMSAPAAAGFGFSAMSPMGAFGPAGFGPSSVGRMAPLGRAARVSLQATDTVAIRAAMSEPPLELEGPSFQSSFDDPRI\*

>P. maxima-TyrBPmaxi1 (partial)

MCALSAEEWRDLAAAIVALKRNTAVAPNLFDSLAAVHTGTAIGNAHFGPNFLGWHRIYLYYYEIALRRINPRVALCYWDSTLDFSMDSPERSVMFSSEYFGNGNGVVLEGPFRDWILPNRQPEQRLRRQINEVGSLMVYDGVREILTDPQLIRTANVSVGGIAPIQRTIEGLHNNVHVWVGQIMSGVDTAPQDPVFYFHHCYIDYFWERYREKQLASGIDPQFDYPRDMGGNAHLPGAPMAVFRWVNNERGFMNAFTRYLFRYAD

***Pinctada margaritifera*** (Bivalvia, Pteriidae)

>P. margaritifera-TyrA2 (complete)

MSKMPSLLQILYLILAIFPLCRLQQRSVNNLNPRFIMWMNSLFYIPNDRNLRVRKEYRMLSDAERRDYNRAIILLKNDRTVSPNKYDALASLHHLNSANGAHGGPGFLGWHRVYLVLFENALREKVPNVTIPYWDSTMDSDLPDPRRSIIWSPLFLGNGNGPVVNGPFRRWSTPYGPLRRDIGADRRLMNRQDIQNVFSRRWLWEITNPSARDEYNIELLHNHVHVWVGEQMSRIESSSYDPAFFAHHAFIDCLWEEFRQRQRQQGINPARDYPRIVGDQNHQPLVSMGLGRLLVIDGINDFFTRQIFRYERRPVCVRGSNTCGSPYLRCNWSTQTCLPLIMSNRGTQTRRVVQNRRQPWWRRFVNQRNTFFG\*

>P. margaritifera-TyrA3 (complete)

MKGLLWRFVLLVGLICVVYPDIIEIRVARELEECFEQRRFDTNQTDPRYDNIHGYCIQKFRWHLQEHYWKNITMETSNWIEELLRISNRKVRKKRQSLPVRKEYRRLTDQERADYHRAINMLKRDTTVKPNRYDALGLLHQRRGDDVHHGAGFLGFHRVLLVVYENALRQKVPTVTLPYWDSRLDQPLRDPTRSIIWSPQFLGTMRGRVINGPFAFWQTPAGPLVRNGGQEGELFTYNHIRAVMTRSHLEEISEPHAPPPFDFEIRHGDVHQMVGGIMAPAETAGYDPVFFLHHCFVDYLWEVFRRSQKEKGVDPTKDYPRRYGPAAHAPKEQMGLGRLLNEHGLSDMFTSRLYTYEPSPTCSYRRPTCGSNYLTCEFGFGRPQCVTLEMLSTTPTQSSRSNIPLQWRQFVPQLQTGVPRSPVPNQFRSALARARQQGNTLPNRAPNPNQFGTPRRFGRTKRQADAHAIDGGRLTQMGQNILSQFGGNQLSEFIRNKTKPLPEKSYTQAVQAAAPQTDIFQVMKDGDSELLVSPVTNICPSSSPQRVIQNLFQLNGISDSRVWVWIPIRVIYKRQPEQMTFEAFPIEAGSMMASKDIYDPTRYDGLANQFHYEFNHPRTCRDMDGIYTKIMIHSDGLNYHGTYREFALVDARQPFATSVVYIAIKSPEKWKTEVLLSGYDPCGNVCKPYCRNGKHFAPCHGAIRVTDETNQGRKRPINYGMDYGEATKMVWDLSYMYDGIPVFNDDKIFMQFVCN\*

>P. margaritifera-TyrB1 (complete)

MNTMALFGKVILLQFLIGVGFCMLMQDPKRNDTKSTYATCFRSQPQGNEPASPDCVKAFMAYAEDMKNIFHFTKEQINYLWSLERETQSLFHNHRRRKRQAVYLPVRKECRLLSELERQNLFYTIRSLKMDTSNPNEYDTLANLHRGAVQPHAHDGSNFLGWHRVYLMYYERALRRIRGDVTLCFWDTTMDFNLGMDNWEYTAVFSSDFFGNRRGQVITGPFRDWPLPPGLTESDYLYRNMTRGRGMPFDSRAASSIFYNPNTIIHSTVTWEGFGFDTITNSQGQTRNITIEGEHNNVHNWVGGAMGFLDPAPQDPVFFFHHCYIDYVWERFREKMRRYFRDPTTDYPGHGNETLHDANYPMIGFEWFRNIDGYSDYFIQNVYRYESPTCQACYYSPYTVCGQGNQCIARMNYPGTEIEEGPQVPNSPVVAFSVAGGTMLMSAFNGRGFIATSNSE\*

>P. margaritifera-TyrB2 (complete)

MMMPYGLTLILLLFTLSDATLLGIKYDPIPRCAREIMADHTSPNYNSTFNNDCAEFISNSFRELKKLLNFTDDQINFIKSLDREAMSLLYGSERTKRQTGLHVRRECRTLSQNDWGRLAQAIRRLKFDPGNEYDTMAHTHTLPAVIDNSHDGSNILGWHRLFLFLFEIALRRKVGGVVLCYWDSSLDYLLRGRGQVQSAAFSHELFGNARGQVTTGPFANFPTPWGPLRRNFGGEGGSLVRPHIVDMIERDPNIRRDGQLVDGDGATGFTDPLSGERTSLEAEHNNAHVAVGALMAIIPNAAYDPLFFFHHCYIDYVWELFRRKQMRLGIDPTRDYGGHGGPAHARNAPMRGLIPGWRNIHGYSNFFSRRYRYAYHPVCGNGCSGSERFLYCPRGRRFRRCIPRTMEGRARPPQRIVGRSRGASDITFSTNYDDSTIAH\*

>P. margaritifera-TyrB3 (complete)

MIQGDIFIFLACILSVSHCFNGIDTSDNLFVKCFTDETIYAFKQNNVQEIDPVCVKYFIEHIAREQKDLGVTDDQMNFLRSLERDGLGQIYERRRQKRQAGTRGRLIRRQECRALPDNRRNRLFAVMRYLKFRTGVYDFFAGLHRSLRSFRNAHIGSNFLGWHRVYLWYFERILIRVGGVPLCYWDSTLDYLIEGSGQRNTTMFTSEVVGNGIGMVINGPFRNWPIPERNVSLRREIASFASLMRPQVVDLIMTSNLIRNHSQISNGEGSVGMIDPDQGTRTSLESEHDNTHVWVGGVMSDATIAPQDPVFWLHHTYIDYVWEKFREKLFTLGINPANDYPGHGGDPHAADTQMEHFYNFSTWWTNANGYTNLFTQFVYTYDDHPTCGNGCGRRGDTNLLYCPTGGTGNQRCVATTAETDVSMFGGRSGTGQSVKVMAEQAALSEGRLNKIMPFRANFRDRRIGAP\*

>P. margaritifera-TyrB4.1 (complete)

MQLLTVIVLSPLLVASVLTINVRLRNLMETQDFKTCFGLNTTLYNLYGLDYRVPECTEIFMSTVKFSNLTKKDVHLMDSLGREVLSELQDSSRNKRYIKPLRIRRECRTLSDKARNRIFDAIVKMKEGSENMYDVFARIHLSPETLDNAHGGSNFPGWHRLYVLFFENALRRIAPGVVLCYWDPTLDFIMKSTLQIHSVTFSDRLFGNGYGTVINGPFKNWQLFEPYNFRLRRNIGQEGSLTRPKVVDIISLNPKIIRSTQILTGSGAIGFKDPDTGRRHSLEQCHDNTHVYIGGVFRSLPVTAQDPIFWFFHAYIDFVWELFRTKQKKHGIDPSKDYPEHGGEDQRALHRMVPFFAFKNIDGYGNMFTEKIYRYAPSPVCGNRCGGASKELLYCPRGGHRRSRCVSRARNVDFVPNRTLKEIHNAYLEKFVRGNKVSKGILCGISLEVAKMDGKVNLPFPLFKAPFDDPRVFVGKGYEENWRKYGG\*

>P. margaritifera-TyrB4.2 (complete)

MYDVFARIHLSPETLDNAHGGSNFPGWHRLYVLFFENALRRIAPGVVLCYWDPTLDFIMKSTLQIHSVTFSDRLFGNGYGTVINGPFKNWQLFEPYNFRLRRNIGQEGSLTRPKVVDIISLNPKIIRSTQILTGSGAIGFKDPDTGRRHSLEQCHDNTHVYIGGVFRSLPVTAQDPIFWFFHAYIDFVWELFRTKQKKAWDKSL\*

>P. margaritifera-TyrB5.1 (complete)

MDKMRTLQSLIVKLTLLYGALCMLQTENVKEINKQECIQNAVYNFNTTDSKYLDPKCVTIFMDQYRGLKNLLNYTEDQMNYIFSLERAMMRKHHINDKRHKRQAMTRPRQECRTLTDDARNNLFNTIVDLKAPSNGMSRYDTIAGLHRQAIANAHMGANFLGWHRLYLDMFEMALQETRSDVVLCYWDSTLDFLMERNTQLNTVSFSAELFGNGRGSVINGAFRNWRLPGGRTLQRFIARPGSSLTRPGVVDLIATDPRINTNSQIVFRGQGFPDPDTGRPGHSWEDEHNNTHVWVGGVMQNVVSSPQDPVFWFHHTYVDYVWELFRQKIGPGAREQYPADASGPHAPDAPMIGFDMLQNRDGYSDEHSRMYAIHPRCSNNCGNSRFLLCPDNGPMADPNRRCVSRAVNSDMVPAAAISAPEAAGFSAMSPMGAFGPAAIGPSSVGRMASLSGAARVSLQATDTVAIRAAMSEPPLQLEGPSFQSSFDDPRI\*

P. margaritifera-TyrB5.2 (complete)

>gi|391359337|sp|H2A0L0.1|TYRO1\_PINMG RecName: Full=Tyrosinase-like protein 1; AltName: Full=Tyrosinase 1; Flags: Precursor

MDKMRTLQSLIVKLTLLYGALCMLQTENVKEINKQECIQNAVYNFNTTDSKYLDPKCVTIFMDQYRGLKNLLNYTEDQMNYIFSLERAMMRKHHINDKRHKRQAMTRPRQECRTLTDDARNNLFNTIVDLKAPSNGMSRYDTIAGLHRQAIANAHMGANFLGWHRLYLDMFEMALQETRSDVVLCYWDSTLDFLMPGTSQVNTVSFSAELFGNGRGVVINGPFRFWRLPGGRTLQRFIARPGSSLTRPGVVDLIATDPRINTNSQIVFRGQGFPDPDTGRPGHSWEDEHNNTHVWVGGVMQNVVSSPQDPVFWFHHTYVDYVWELFRQKIGPGAREQYPADASGPHAPDAPMIGFDMLQNRDGYSDEHSRMYAMHPRCSNNCGNSRFLLCPNNGPMADPNRRCVSRAVNSDMVPAAAISAPEAAGFSAMSPMGAFGPAAVGPSSVGRMASRSGAARVSLQATDTVAIRAAMSEPPLQLEGPSFTSSFDDPRI\*

>P. margaritifera-TyrB5.3 (complete)

MDKMKTLQSLIVKLTLLYGVHCMLQTETVKEINKQECIQNAVYNFNTTDSKYLDPKCVTIFMDQYRGLQNLLNYTDDQMNYLFSLERAMMRKHHIKRHKRQAMMMPRQECRTLTDNARNNLFNTIVDLKFPTFGMSRYDTLAGLHSLQAFPNAHGGANFLGWHRIYLNMFEMALQETRSDVVLCYWDSTLDFLMPGTSQVNTVSFSAELFGNGRGVVINGPFRFWRLPGGRTLQRFIARPGSSLTRPGVVDLIATDPRINTNSQIVFRGQGFPDPDTGRPGHSWEDEHNNTHVWVGGVMQNVVSSPQDPVFWFHHTYVDYVWELFRQKIGPGAREQYPADASGPHAPDAPMIGFDMLQNRDGYSDEHSRMYAMHPRCSNNCGNSRFLLCPNNGPMADPNRRCVSRAVNSDMVPAAAISAPEAAGFSAMSPMGAFGPAAVGPSSVGRMASRSGAARVSLQATDTVAIRAAMSEPPLQLEGPSFTSSFDDPRI\*

***Pinctada fucata*** (Bivalvia, Pteriidae)

P. fucata-TyrA1 (partial)

>pfu\_aug1.0\_2016.1\_58739.t1

IEDLIQRKLRNILQHTFTSMENHKSYSFSMEGAWNNLFARTECCGIESIKDFHAITSNQILGPVLANIPVYCCTTNPFSELYHGQDTKCTVNLEKDLRFNTSVQPNLYDAICNLHPNVRAPNAHYGPAFLGYHRVLLWFFEKQLQRKVPGVYLPFWDSTKDSLMANPTASVIFSQAFAGTGNGVVNNGPFANFRHPAVGVLVRNLEAGGDLMTRRDIANIVRQTRTADMMTPYASSENNLELCHAKVHAWIGGTLDNLNYSPADPLFWMHHCYVDYIWELQRQNERRGGRDPDTDYPSMDDGHNADGIMYPFTNLRNKDGFNRGWIDTYYGYEDAPVRCRRDDSCRSTYYKCTRGLCCSRTIGEVYGVGQQQTFGRKKRSAPTKKSSTYSGKASSLVKKAPVVTKPVTDIQTHLKSYFPYLAKLGDSAGTFYKFKHGQSPAIKPGPEKVQDLSFEDLDLHTTGLYHSFQNSFTLDGVEDTKNWVYLPVIVYYRRPAEVKYDAHPIRNGKVMANMDVYSTTRADKYHLGKPVKTATSSTCKHIGSGAFKVYVKAYGLSYDGVFTDYAVVDERQPLSFALTQVGVQNPRMKNTTVYVTAYDSCNRQCKARCLIPGSKPARYKPCSGTIRVTPDAPFMYSSDIADAHLHTYDYNTIPPCLSYDKIFLVFYCDQKDSWPWQQSMGPAHVSSARTAGGGYTPPSMPRYAPQRMPVHVQAHRFASQHNFGFRPPQNFAAFHGKFLKY

>P. fucata-TyrA2.1 (complete)

MSKMPSLLHILLLIIAICPLCRLQQRSVNNLNHRFVTWMNSLFYIPNDRNLRVRKEYRMLSDTERRDYNRAILLLKNDRTVSPNKYDALASLHHLNSANGAHGGPGFLGWHRVYLVLFENALREKVPNITIPYWDSTMDSDLPDPRRSIIWSPLFLGNGNGPVMNGPFRRWSTPYGPLRRDIGADRRLMTRQDVQNVFSRRWLWEITNPSARDEYNIELLHNHVHVWVGEQMSRIESSSYDPAFFAHHAFIDCLWEEFRQRQRQQGINPARDYPRIVGDQNHQPLVSMGLGRLLVIDGINDFFTRQILLDMNVVQLCKGVHTCGSPLPEM\*

P. fucata-TyrA2.2 (complete)

>pfu\_aug1.0\_1286.1\_36925.t1

MPSLLHILLLIIAICPLCRLQQRSVNNLNHRFVTWMNSLFYIPNDRNLRVRKEYRMLSDTERRDYNRAILLLKNDRTVSPNKYDALASLHHLNSANGAHGGPGFLGWHRVYLVLFENALREKVPNITIPYWDSTMDSDLPDPRRSIIWSPLFLGNGNGPVMNGPFRRWSTPYGPLRRDIGADRRLMTRQDVQNVFSRRWLWEITNPSARDEYNIELLHNHVHVWVGEQMSRIESSSYDPAFFAHHAFIDCLWEEFRQRQRQQGINPARDYPRIVGDQNHQPLVSMGLGRLLVIDGINDFFTRQIFRYERRPTCVRGSNTCGSPYLRCNWSTQTCLPLIMSNRGTQTTRRVVQNRRQPWWRRFVNQRQTFFG\*

>P. fucata-TyrA3.1 (partial)

MMTDRERADFFRAIQMLKADTSIRPNRYDFLGLVHFRMVDNIHHGAAFLPWHRVFITIFENALRQKVPTVTLPYWDSTMDEAMIDSTQSNLWTPEFIGNGNGIVNNGPFAFWQTPNGPLIRNIGNAGGELFSRDAIFSILSRNRMAQITEPAAPDQFNIENYHGNVHTWLGGQMEPMETSAFDPVFYLHHAFVDYVYELFRQRQIAQGIDPTQDYPANYGAETHAPLTPTGFGNLPNAFGMNPLFTSDIYIYQPNPTCSYQNPNCGSRHLTCDISTGVPQ

>P. fucata-TyrA3.2 (complete)

>pfu\_aug1.0\_7981.1\_45772.t1

MIPILHAIAIVICTCATLSSGLIKYRELPDRLAVCYNQHYKACSTQTKVGLSILHRCMSEYHWKSGPQRDYPGRTPTPAATRYVNTLTRDFQPGGATRFRGKRQSRSRVRKEYRMLTNDERGRFHRALQALKQVSSGEDQSRFDMIASFHTTAETNAHGGCNFPGWHRYYLLLFERALQSVDPSVNLPYWDSTLDQYMDESAQSLIWSEDFLGNGDGAVTSGPFANWETSEGPLVRNIGVPDTQLYTHEQIFNTTRSTRMSQICNGQTDSEVDPLVNTGLEWHHGDVHVWMGGQMSMLTTSSYDPVFFMHHAFVDLIWEEFRQNSRRAGVDINRDYPTANYGEHDFHGPDAPLGLTTNLTVAEAIDDENIPPQVRYRYERRPSCGRNRDCGSDKLRCVQRGRNYICISKTLVEYQTDLQIEQATNGGNVNPNNGNTVIIRRPDPSPNNPNRGNRGPTFINPRRNRMINRIRGSTRWTFRDRLMRFGIRNTVAVIDQCPVPEHEHKPIQNTFCANGNSDITRWVYIPVRVLAQRAPGFQKVRIVPDS\*

P. fucata-TyrB1.1 (complete)

>pfu\_aug1.0\_8995.1\_60538.t1

MYLSDLCFRNWVFRCFATSGHVSISERVLDTSKDPQRIKDTYRLSRCLLNYGISYRQSLSCKWQFKLSEQRLKDTVGLEREEIELLWDLGAEILREKRDKRQPYGYSPGGGYGDNMGIRQECRAMSDWKRRQLFDAINYLKKNTSNPNVYLTMAKLHRGNQVFRHAHGGSNFLGWHRLYLLLYRFFSFERALQRVNRNVALCYWDSSIDFRLGKDDWVYTTAFSDSVFGSGEGEVKDGPFTDWYLPPPNRDLLLRRDIRIGKAIPIDARAVDLILRSPKLLSHTSITVGGSGFQTITDHNGDRRDVTIEGEHNNVHVFVGALMSNSDMAPLDPVFFFHHCYIDYLWEGFRKKMKRKGFDPTSDYPGHGQRESNAANYSMIGFNWYKNIDGYSEVFTSDLYTYEVTPSCKGYSPSCRYSNFMKCNKANECVATTRPPSVDRIGTSAALTPLVFTGKTFKANTNSD\*

P. fucata-TyrB1.2 (complete)

>pfu\_aug1.0\_16905.1\_25558.t1

MLIQDTNKNDTKSTYAACFRSQSQNSEPTTPDCVKAFIMYAQDLAKIFNFKEEEINYLWSLERETQSMFYNHHRRKRQAVFLPVRKECRLLSQYERQNLFYAIRSLKMDTSNPNEYDTLANLHRGDSFQPHAHDGSNFLGWHRVYLMYYERALRRRRAGVTLCFWDTTMEFNLGMENWAETAVFSSDFFGNRRQIVTTGPFRDWPLPPGLDFAFLTRNLSIQGGMPFDSRAAYSIFYNPNTIIHSTVTDQGFGFDTITNRLGETRNVTIEGEHNNVHNWVGGVMGILDPAPQDPIFFFHHCYIDYAWERFREKMKRYGRDPTTDYPGHGVEADLHDANYPMIGFEWYRNIDGYSDFFTQNVYRYESPTCQACYNSPYTVCGPENQCIARMNYPGMEIDQGPPSQSAPYVALSAQAGATAFASSSGRRFVATXKFGINTLKSY\*

P. fucata-TyrB1.3 (partial)

>pfu\_aug1.0\_12145.1\_17832.t1

NEYDTLANLHRGDSFQPHAHDGSNFLGWHRVYLMYYERALRRRRAGVTLCFWDTTMEFNLGMENWAETAVFSSDFFGNRREIVTTGPFRDWPLPPGLDFAFLTRNLSIQGGMPFDSRAAYSIFYNPNTIIHSTVTAQGFGFDTITNRLGETRNVTIEGEHNNVHNWVGGVMGLLDPAPQDPIFFFHHCYIDYAWERFREKMKRYGRDPTTDYPGHGLDADLHDANYPMIGFEWYRNIDGYSDFFTQNVYRYESPTCQACYNSPYTVCGPENQCIARMNYPGMEIDQGPPSQSAPYVALSAQAGATAFASSSGRRF

P. fucata-TyrB2 (complete)

>gi|72132971|gb|AAZ66340.1| tyrosinase [Pinctada fucata]

MKMNLSNREVVIFLLLAACTSAALLGDKYNVPPECMEEVIFDYDSPKDNSTLNKDCVKFVSDSYRKLQQLINGTDDDINYIRSLTREGMALLYPGSGREKRQAALRARRECRSLTSEEWRRLANAIRRLKFDPGNRFDTMARIHAMPAVIANAHDGSSILGWHRVFLYLFENALRRKVPGVVLCYWDSTIDYLIPGPGQAQSSSFSHNMFGNSRGLVRTGPFANFPTPWGPLRRNFGGEGGSLMRPHVVDMIASDPRIRSHGQIVDGQGATGFIDSMTGQRTSLEAEHNNAHVAVGALMAVIPNAAWDPLFYFHHCYIDYVWQLFRRKLRNRLGIDPARDYLGHGGPAHAPNAPLLGLIPGWRNVHGYSNVFTQRVYRYHFHPVCGNGCSGSTRRLLYCPGGGSRYRRCVSNTMPGRAQPPALSIAGRSAEEKFKTVYDDPDIAS\*

P. fucata-TyrB3 (complete)

>pfu\_aug1.0\_4.1\_57868.t1

MIQTEHGVLLLSLLTIVYLYSASAIDTSNELFWKCFTDESIQAFKQNNFQEIDPVCVQYFIEQIAKEQKGLGISEERMNYLRAVERDGMGQIYERKRVKRQTRGRGGGGNRRIPLLRRKECRALENNERNRLFNSMRYLKFNTRPNVFDFFAGLHRSLRSFLNAHIGSNFLGWHRVYLWLFERVLLRVGGQPLCYWDSTLDYQIPGTGQRNTTMFTSQMVGNGRGMVINGPFRNWPIPERNVTLRRDIASFASLMRPDVVDSIMTNLSIRSHSQISNGDGAVGMEVPSDSSQRTSLESDHDNTHVWVGGVMSDATIAPQDPVFWLHHTFIDYCWEKFREKLSWRLGIDPANDYPAHGGDPHAPEEPMVHFYNYSRFWINRNGYTNLFTQLVYSYDDHPTCGNRCGGRGNTNLLYCPQEGRSGNQDVRCVATIVNRDNLSMFGGRSANGRSQEDEGPQRAAAEGPMSILRSFRANAVDRRIA\*

P. fucata-TyrB4.1 (complete)

>pfu\_aug1.0\_1032.1\_29546.t1

MEFRCLTEVRSLFVRVQQVKVFFETHDFSRCYGTDQHLPECAKLFREAVNITHFSKKEIEIVNSLTNEVIAETSLSSRGKRNIKRLRIRRECRTLSEKSRNRIFQAMVQMKQGPENMYDVFAKIHLNPESLENAHIGSNFAGWHRIYVLFFENALRRIAPGLVLCYWDPTLDYLMPGTQQVHSVTFSDKLFGNGYGTVINGPFRNWKLFQPYNYRLRRNIGQEGSLTRPEVVDLIAFNPKIIRTTQIVAGSGAQGFDDPDTGMRHSLERCHDNTHVYIGGVFTSLKVTAQDPVFWFFHAYIDYVWELFRQKQRKHGIDPSKDYPEHGGEDHKAIRTMVPFFAFRNIDGYSNMFTEKIYRYAPHPTCGNRCGGASKKFLYCPRRHHRRTRCVSRSSNVDIVPDKTLKEIENPVLEKFVRGNLASRAIVNAISLEVAKKDGKVELPDPRFSAAFNDDRVVVDQKDPYFKNGVH\*

P. fucata-TyrB4.2 (complete)

>pfu\_aug1.0\_1032.1\_29544.t1

MNIEFLKLMKTQDFQRCIGYNSTLNNLDHLSPLCNKLFLETVKVSNIEGRDINFMFSLGRQIQGEIEATRDKRYIRPLRIRRECRTLSEKQRTRIFSAIVQMKEGPENMYDVFARIHLNTQVLENAHVGSNFPGWHRIFVLFFENALRRIDPGVVLCYWDPTLDFVMPSTLQLHSVTFSDRLFGNGYATVINGPFRNWRLIKPYDYRLRRNIGQEGSLTRPKVADLISFNPKIIRTTQILTGSGALGFKDPDTGRRHSLEQCHDLTHVYVGGVFSSLPVTAQDPLFWFFHAYTDYLWELFRQKQRSHGIDPSKDYPEHGGEDHRALRNMVPFFAFRNIDGYSNSFTEKIYRYAPSPTCGNRCGGASKEFLYCPRGGHRRTRCVSQARNVDIVPDKTLMEIKNPILEEFVVGNEASKAIVNGYSFKAAVRDGRVNLPKPFFKANFNDPRVFVALIWKKCKIFPSSVPIFHNYRFYAVSTDFELTEMI\*

P. fucata-TyrB4.3 (complete)

>pfu\_aug1.0\_1032.1\_29545.t1

MYDVFARIHLNSQVLENAHVGSNFPGWHRIFVLFFENALRRIDPGVVLCYWDPTLDFVMPSTLQLHSVTFSDRLFGNGYATVINGPFRNWRLIKPYDYRLRRNIGQEGSLTRPKVADLIGFNPKIIRSTQILTGSGALGFKDPDTGRRHSLEQCHDLTHVYVGGVFKSLPVAAQEPIFWFFHAYTDYIWELFRQKQQRHGIDPSKDYPEHGGEDHRALRNMVPFFAFRNIDGAEVEQVKCLNFANPANGNRPPFDFQAIKMIALDLCFDVWVTITKISNVYRRWRPTIGGIVRCDKSKRLLF\*

P. fucata-TyrB4.4 (complete)

>pfu\_aug1.0\_20693.1\_11329.t1

MPVFSDEVRGSSVDNIYDVLAKIHLSVQTLANAHVGSNFPGWHRLYVYFFENALRRFYPTGALCYWDPTLDYLMPGTEQLNSVTFTDQLFGNGYGTVINGPYRNWELVVPYNYRLRRNIGQAGSLTRPQVVDIIAYDRRVKRSTQILTGSGSVGFLDPDTGRKHSLEQCHDNTHVYVGELFSSLPVTAQDPLFWHFHSYFDYVWELFRIKQSKMGINPAKDYPEHGGEDHRADKRMVPFFNFRNIDGYSNIFTDRIYRKEGISNQTRMQYLQMCEKEPKHP\*

P. fucata-TyrBPfuca1 (complete)

>pfu\_aug1.0\_7279.1\_31368.t1

MMRKQHMQDMHSKRHKRQAFFRPRQECRTLSDPARTALFGAIVILKQRVNGMSRYETLAALHNLQAFGNAHNGPNFLGWHRVYLNMYEEALQRIRPGVALCYWDSTLDYLMPGDSQRRTVAFSDELFGNGQGAVINSQFANWRLSDDTPLIREIGRVNTSLTRPGIVDLILTDPRINRHRWIVNAGTQTNQNPRFGFIDPDSGRRHSLEREHDNAHVWVGGIMVNVARSPEDPVFWFHHCFVDYVWELFRRKIDPFDRFDLRNDYPFDSLNEEHRAYERMAGFPAYVNIDGYHRFLRRRYAPHPRCSNNCGGSRFLRCNNIGPMGNPYRRCVSLEIDSDVVPAAAADSPAMEGFVGFRSPAMMATGAAAARVSIQATYQVAIQATIGQRRTFFNGPNFTPSYNDFRL\*

P. fucata-TyrBPfuca2 (complete)

>gi|119852229|dbj|BAF42772.1| tyrosinase-like protein 2 [Pinctada fucata]

MKKLWALAASLPLLLCVHCIKEKEILKESYKQKCMKNAVYDFNSTNPTTLEPKCATLFGHEYSDIKNFLKFDDQQMNYILSLERAMMRTQHRNNKRHKRQAMMRPRQECRTLSDPDRNALFGAIVTLKQPFSGMSRYNTLAAMHNLQAFGNAHNGPNFLGWHRVYLNMYEEALQEIRPGVALCYWDSTLDYLMPGDSQRRTVAFSDELFGNGRGAVINSQFANWRLSDNTPLRRMIGENNSSLTRPGIVDLILTDPRINRHRWIVNEGSRFNQSPRFGFIDPDSGMRHSWEREHDNTHVWVGGIMVNVERSPEDPVFWFHHLYIDYVWELFRRKIDPMDRFDLRTDYPMDSVNEQHRAFQTMAGFPAYRNIDGYHNFFRRMYAPHPRCSNNCGGSRFLRCPDIGPMGNPDRRCVSLAIDSDVVPAAAASPAAAMAGFGASRAGFAAFGGPAAMASGGAARVSLQATDEVAMRAAMSAPQTVVQGPNFTSSRADSRLL\*

P. fucata-TyrBPfuca3 (complete)

>pfu\_aug1.0\_10251.1\_39018.t1

MHSFAAYRYAHLGPSFLGWHRVYLIMYEEALQEIRSDVVLCYWDSTLDFLMPGSTQRFTVAFSADLFGNGRGNVINGAFANWQLPGGGTLRRNIAADRFPGPPPSLTRPGIVDLIATDPSITSHTQIVRGGTGFTDPDTGRVHTWEQEHDNTHVWVGEIMQDVVAAPGDPVFFFHHTFIDYGWELFRQKINPNGNIDLRNDYPNVGGFHAPDAPMFGFQGITNRDGYSDEYTRMYAPHPTCSNGCGGSTQFLYCPDGGPMANPNRRCISRDINSDLVPAAAVAPAAAMQAMASGPEATMARFGPAATMGMFGPAATRAGFSPAATMSMFGPAASRALFGPAAMTRAVPAVGSARVSVEATDAVAVRSALSEPPPPVSGISFESSFSDSRL\*

P. fucata-TyrBPfuca4 (complete)

MKTDFMQMIPNVRIIGGQHVSYVSECKIELRCESRYDTIAGMHSFAAYRYAHLGPSFLGWHRVYLIMYEEALQEIRSDVVLCYWDSTLDFLMPGSTQRFTVAFSADLFGNGRGNVINGAFANWQLPGGGTLRRDIARAQFPNPPPSLTRPGIVDLIATDPSITSHTQIVRGGTGFTDPDTGRVHTWEQEHDNTHVWVGEIMRDVVAAPGDPVFFFHHTFIDYGWELFRQKINPNGNIDLRNDYPNVGGFHAPDAPMFGFQGITNRDGYSDEYTRMYAPHPTCSNGCGGSTQFLYCPDGGPMANPNRRCISREINSDLVPAAAVAPAAAMQAMTFGPEATMARFGPAATMGMSGPAATRAGFSPAAVSMFGPAASRALFGPAAMTRAVPAVGSARVSVEATDAVAVRSALSEPPPPVSGISFESSFSDSRL\*

P. fucata-TyrBPfuca5 (complete)

>gi|154127070|dbj|BAF74507.1| tyrosinase-like protein [Pinctada fucata]

MTSLLTLFVHACILIGVNSMLQPKRVKDTYENSCLHNAVFNFNSSSTNYLEPKCQTLFMDKYTEMKNFLNYTDMQMNYLYSLERAVLRKYEKKQNGRHKRQTGMMARQECRTLSDGARGALFGAIVDLKTPTGGMSRYDTIAGMHSFAAYRYAHLGPSFLGWHRVYLIMYEEALQEIRSDVVLCYWDSTLDFLMPGSTQRFTVAFSADLFGNGRGNVINGAFANWQLPGGGTLRRDIARAQFPNPPPSLTRPGIVDLIATDPSITSHTQIVRGGTGFTDPDTGRVHTWEQEHDNTHVWVGEIMRDVVAAPGDPVFFFHHTFIDYGWELFRQKINPNGNIDLRNDYPNVFRQKINPNGNIDLRNDYPNVGGFHAPDAPMFGFQGITNRDGYSDEYTRMSHLIQLVVTGVVDQHNSFTV\*

***Crassostrea gigas*** (Bivalvia, Ostreoidae)

C. gigas-TyrA1.1 (complete)

>CGI\_10009045

MEPSTSDTFADNITYFSHNSGSFVYDTFGINGGYEPYGTDSICNRHSKHDYEIPEQVCQAKMFFFTLMLIVINARFEIAYSKMYEEPLPQEFKDCLNMILPNSDLKRDPAYIIDYACANKFLTSTPNKRWAPEKDEEEFTLITNKINKLDIHTSSENVRYEKRSIQNHLDNRHKKRSAVNPTIRRKEYRRMSPAERTDFHRALQLLKDDAERTKFNLYDILCNFHHASRAPHAHFGPAFLSWHRVSLYIFEQALRSKVPGVSLPFWDSRLEAALENPSATSLFTDELMGPGNGVVKTGHFANWSHPFAGDLVRNVGNLGEPIQRRDIERLLKARYTKEFMFPSAYPHMNLELIHGKVHMWVSGTMNNLNYSPADPIFWMHHCFIDYVWEKIRQRQKERGVDPSYDYPMNGGIGHRPYDTMKPFDLKNRDGYLIDWSKVYQYETSPVDSKCRSDSDCGPEYYVCANGNCRAKTAEEVLFDRRSRRRRSIADLGTSDLLSKDHYNDLQTSTDAQTTPVFHSMQNTFMIDGREDSKSWVDLPLIVYSKRPDHLVFSAHPYRRGEANFTADIFQPTLKEENVLPRSGNPAIKQKCKHMGSGVSKVYIRSIGVNYEGDYTSEAIIDERQALTITLIQIAVQNPYKKYTKSYISAYDQCGRMCSPYCLTGRDGTYKKCSGNIGVDSRIPRMYNTDAAGTILQMFDFKSFPPKLDQSNIFLIFYCGQEEKWPWEINKEEK\*

C. gigas-TyrA1.2 (complete)

>CGI\_10014286

MTSYYDDVIIAMSHNVTCTLTSFDNEVDPDLSRAALATCALYASLQRPVTTASSCPATTCPNGWTRYQTSCYLVVTYELETWSGAQAKCVAENSGLVEIETEAENNFLKDVAAKTFLNGQFWTGGNDIDVEGQWRWVTSGNPFTFTDWGPGEPNDTGGNEDCMLLLSNTGYTWNDLPCSTNSLYICEKPRSIDKLALMVKPTKTISSCVCVPCCKMVEKISTRMGTGGGWIQYLLVYLYITAPCHALVYEEKMPHLLRNCLERTSHKKGNVTRDTAESIDYMCTKEYLFKTPEERWHPDLDQVINTKTLKKFASLFKELDIGETRSHKIRYRYSSIKRHFVRVRRATPIVRKEIRMLSEEERQKFLKALVAMKADTSDPQRQPNVYDWFCNLHPNKVAPNAHYGPAFFGFHRIYLYLQQQLRTYEPDTFLPFWDSTYESLLGTPTSSVLFTEDFLGGGTGTVTDGPFKNWKHDKVGVLIRNTANSGQLFQRETIDKIMMKMFMSDISNPDAEFDVNLEAKHGQVHAWIGGAMDNLDYSPADPIFYMHHCFVDAIWERFRDNQVKRGMDPTSYPDVTEGHAANKPMKPFYLEVKNGKKIYLKNKDGYALKWSQLVRYVYPKRGCKRNSDCQSDVMVCREEQCMTMTAHEYEASKAAPPPPPPPPPAPPKRRHSSSVYKAPINKVPITAAFITTTPAPTRGVDDLPGWDNWFMWRKKRSVSYVHTRYPYPYHYIRRHLYYLTRRYRKKSRQQRREKIGEVGIKYKYSDEKTSPIYHSLQNTFTIDGVEDIDNWVYIPIIVYYRRPNEVHYDAHPISHGHPIMNKDVFNQYHDAKYITHKVGNPAKNANCYHIGSGATKVYVKATGMNYNGFYTDYALVDERQPLSFGLTEVGVKKPVGKTPSKVYISAHDPCGRSCKARCLVAGSNPPRYRPCSGTIGVTSKGPLMYSSNIGDAHLNTYDFSTLPPTLSSKKIFLVFYCDQSEVWPWDA\*

C. gigas-TyrA1.3 (complete)

>CGI\_10006802

MSNTELNYLRSLFNKSKNHRKKRATQNKRKRKEYRSLTEKERKVFHDAVLALKAKSTSNYETIANYHQANAGQSAHGGPNFPGWHRVFLLIYEEALIEASNGKLSGIPYIDWRLDYRLSSPGSSILWTNEYLGNGDGRVRNGPFENWVINRTTLVRNVGTTQRDPTNEDSVAELFAITSARSFADQLENVHNIGHIYVGGLMNSLRYATYDPVFFMHHCWIDYLWWRYQCPNGRCRDDRFVYPGTNRDGDHAPTEPMDNLVYKGELLTKDGYDRRWLDNVEYEISPADCNENCNSRYATNGLECVSSRCLSATSGNFSPFEKRKKRSANRRNRHLRKRKREVLSYPVQNIFRVDCESDTTLWGYIPVKVVYVRCTDERVYNSFTVKNGTVLSSTAYDFYDNRPEIQKIDRLTLTGHPSHFKNCTADESGAFKINVNSYGLNYRGNYEEYAIVDDRIPLSSAMAYIAVKRPTKRRSSKVYLTAFDGCGRYCTPECLVPGSKPPRYEPCTGAIEIDAKRPKGYANTFDDAVLMYFNFRKPGSFPTFNERSVP

IVFYCKRNEKWIPAP\*

C. gigas-TyrA2.1 (complete)

>CGI\_10009468

MFATSDPRFEFPLTEADVTWLNSLFSLPEEGETRERKEYRLLTEEEREYFHRAVNMLKNDTTVSLNKYDLLANIHSRSSSNTAAHGGPGFLGWHRVFLLLFENALRQMIPTATLPYWDCTLDQPLSHPSESVIWSDLFLGNGDGEVNTGPFRGWNTQFGFGLLHRQVSSLRHLMSVHDLRNILEEDFLGNISYPDTKSSKNLEQLHNNVHVWVGGLMRKIEIGAFDPVFYVLHTFIDKVWEDFRVHQRSKEIDPTKDYPEFYGRRNHASFAPMGLGNLVVIDGISDVWNKNVVYRQPSCGNSGQNECGSKFLRCDHSTWTCVSKTKDEVTKSINKDKHKDTTLSRTLNSGLKELDNLYIPSLLNSGISHSVYSDFLYPLKDRQSTAMYSENVSQSSALQKAKEIYMSHLN\*

C. gigas-TyrA2.2 (complete)

>CGI\_10026230

MTRKKPDIRLSKPVVVHRETTELSKMCPVLKVSGRMFPVEIEWMKTSYGSEIADEYEIKAIEKAAEIHGREPPGDILVFLTSQLEIEQCAKKLEILLRGMKDYWILPLHGKLQTDEQKLVFKDSPIGRRKIVLATNVAETSVTIPGIKYVVDTGAVKELSYDPRKKEYVYKDFKFQTMPSLMSVLHVLVLFLAIFPISRLQIRTQTNANSRFVQWMNGLFYLPRGNELRVRKEYRLLSDEERRSYHQAILLLKNDRTVLPNKFDAIASLHHLNTASGAHGGPGFLGWHRIYLTLFENALREKVPNVTIPYWDNTLDAELPDPRRSIMWSPLFFGNGNGAVVTGPFRRFTTPYGPLRRDIGADRRLMSKTDLENVFSRRWMWEISNPSAEDRYNLELLHNHVHVWIGEQMSRIESSSYDPAFFSHHAFVDCLWEEFRQRQRQHGINPGRDYPRIVGDQGHQPLVSMGLGRLLVVDGINDIFTQRIYSCQRRPECVPGTNHCGSPYIRCNWSTRTCLPLIMSNRPNNPVAQGPAQQQVPWWARLMQRNGLFG\*

C. gigas-TyrA3.1 (complete)

>CGI\_10028079

MKISWIYSLLTISTVFLSQMKKHLCIVFTFIVLVGAYIEEIDLPESFTECLEKQRIKNLGAASGEAMSKWCMNSHRMKLTGDKFKYSNVSEDTVSWINELLRMSNVDMKLDLSSTNKLSHSVKKRQASLDTPSLYPNVQFPPQPIIDSDSSDSSNIQNSQGPEYMSETLQSFSNQHTGSGQAQRFQPGQARPFPIIGGENQAPAAQKPGQQQTVFQQPSQQINNFVAAQQQPTFAQGQQQNFQSMNAFQPQLQPQPTVMSPNMNTAQPVSGIPVVQRPQLRIRKEYRTMTEQERANFHRAILLLKQDTTIRPNRYDALGLVHFRMVDNIHHGGAFLAWHRLFITIFENALRQKVPDVTLPYWDSTMDEAMIDPTQSVTWSPQFLGNGDGLVTTGPFAFWQTPNGPLIRNVGQDGQLLSRQAIMRVLSRTRMAEITEPGAPDQYNIENYHGDAHTWIGGQMEPMETSAFDPVFYLHHAFVDYVWEIFRQQQRAMGIDPTQDYPQNFGPQSHAPFTPTGFGNLPNVFGISDMFTTQVYTYQPHPTCSFQNSNCGSPFLTCDISAGVPQCIPIGAGPPAPPRAAAMRGVPGVMGAGGPGPLLGGMPRLPFGRKKRATTANKASDKSTTADSYHQVMVKQLQCSNAWVSFSSQNTFEINNEGDTRNWVFIPVRVVNKRSPEHRKFKAYAIINGKPSVKADIYDPEQYEEIKPYFSEELMPSSAKCDAVSGDRTIGRIHIRSDGLNYQGNYDEYVIVDLRQAFTESTTYIGLRRPGKNDTEVLLTAYDSCGRKCKAFCRSRNAKSHDYHPCSGALRVNSNSPWEYGKNYGDAVRMSWDLNDLYTIPKLQDQSVFIQFFCDHR\*

>C. gigas-TyrA3.2 (partial)

MKKHLCIVFTFIVLVGAYIEEIDLPESFTECLEKQRIKNLGAASGEAMSKWCMNSHRMKLTGDKFKYSNVSEDTVSWINELLRMSNVDMKLDLSSTNKLSHSVKKRQASLDTPSLYPNVQFPPQPIIDSDSSDSSNIQNSQGPEYMSETLQSFSNQHTGSGQAQRFQPGQARPFPIIGGENQAPAAQQPGVQTQQLGAAIPQTQQFGAAIPQTQQFGAAVPQQTFSSSSNQPIPAQVPQTQINPVQTQFSQQQQQQTVFQQPSQQINNFVAAQQQPTFAQGQQQNFQSMNAFQPQLQPQPTVMSPNMNTAQPVSGIPVVQRPQLRIRKEYRTMTEQERANFHRAILLLKQDTTIRPNRYDALGLVHFRMVDNIHHGGAFLAWHRLFITIFENALRQKVPDVTLPYWDSTMDEAMIDPTQSVTWSPQFLGNGDGLVTTGPFAFWQTPNGPLIRNVGQDGQLLSRQAIMRVLSRTRMAEITEPGAPDQYNIENYHGDAHTWIGGQMEPMETSAFDPVFYLHHAFVDYVWEIFRQQQRAMGIDPTQDYPQNFGPQSHAPFTPTGFGNLPNVFGISDMFTTQVYTYQPHPTCSFQNSNCGSPFLTCDISAGVPQCIPIGAGPPAPPRAAAMRGVPGVMGA

C. gigas-TyrA3.3 (complete)

>CGI\_10026226

MIDCLTNLLLLMSTMGALLRLALAATLCYVVYSKMTIIDTPEELKTCFDQPRFNTKETDPRLDNIHQYCIQKFRWHLQNNNPNITHETTHWIDELLRMANKEARKKRQAGAERRRKEIRRATDKERTDFFRAINLLKRDTDVKPNRFDALGLLHQQRGDDVHHGAAFLSFHRVLLLIFENALRQKVPGVALLYFDSRLDQPLRDPTRSIIWSPQFLGTVKGRVTDGPFRFWQTPAGPLVRAGGHEGEYFTYRHIRAVMTRSRLEEISEPHAPPPFDFEIRHGDVHQHIGGIMAPAETAGFDPVFYMHHCFVDYLWEVFRRSQKEKGVDPTRDYPNRYGTAAHAPNALMGLGRLRNLHGMSDMYTTRMYTYEPSPTCSYRSPSCGSRYLTCEFRFGRPQCVTLEMITPTTPTAPFGSATNGQPQQPQRQRTPGFPNFPGSTFPGFPPTRRFTGRKKRQASRGNGRGRGNGVIDGSLMSNHGQNVLSQFGQNGFTQFAQNKTREMRQKKHEVRMGFNPHYENNMDVFQKITTEDEKEIILSPMTNMCPPTVPTNTIQNLFQMNGISDSRIWVYIPVQVIYKRQREQMVFESFPIEEGQLDVGKDIYDPTRYQSLKDNFIFNVNYSRSCRDMDGIFTKIMVHSDGLNYHGSFREFAVVDARQPYTSSTIYMAVKSPEKYHTEAIFQAYDPCGNVCKPYCKRFGHFQPCDGSLKLDNSPPKLYGMDYGEAIQLVWGITNEGIPKFRPDNIQLQFVCN\*

C. gigas-TyrA3.4 (complete)

>CGI\_10026227

MHKWFNYNVTSNTNVWYSRLLVFPNRRSLTNTGTGRVRKEIRMMSDFERQKFFTAIQMLKADKSIHPNKYDSLAALHQGITETAAHGGPNFLGWHRVFLIMFENALREKIPDVTLPYWDSTIDEAMANSVASAIWSDRFLGNGNGLVTNGPFADWMTPAGPLIRNIANTGQLFRRNVIQNILTRKRLSEITEPHAFTQFNLEFHHGEVHMWVDGQMGELTTAAMDPVFFLHHAYIDYVWEKFRAQQRLNGIDPARDYPSVVNHTLHLPTAMLGLGNFRNIDSFSEYIVKGIYKYDETPSCSAFNRNCGSPYLQCMNRNSEWICVSIDQAHMPPMQRRPVMANNMRIQMQQQQQQQQQQMLQQQMQNQQMQKQQMKTMQQNNAWLNKFNIPNMNVNMQRIGPNTMQNSRPAVVPQLGRNMLMSVRRDRANPMGFEIFNVPSPTMPQPNQMQQMNANMPRIRGTGSDVNRMIQGMIQNKVQNSMLPPTHSPTMSSQETCPVIPVNRPYQNSFNINGVSDMRLWVYLPVDVVYRRPPEYERYNAFPVMNGRPMKQTDIYEPDAYKSLKAPLATGRPASYASCNTGQFGAGAVFIQSNGINYVGTYKEYAIVDHRQAISSSTAFVAIKDPGYGATDVMLSAYDSCGRICRPYCKIPNSQKGESQPCSGLLRVTSTYPKLYAKDYGEAVFNTWNLRKNCPQKDGGQVYMTFYCDYEEDWPMPGIVPVVVPTPPPMPILLIPSPQPQSTESTCEIGNGCVLPGECRFCFVGTVQRCEKSCDQYARCVYGQYIPEKCPPGTMYDAAQHLCIPGTCSDETEIKHKSLVVDTDL\*

C. gigas-TyrA3.5 (complete)

>CGI\_10009318

MRNVFENTPYSIGTVPRNEFDGLMRRKSEYRSLHRPSLKLEVRMAVPKCLISVLFLGLLPVTLALIENLEYPTPYAQCLYSMWKKSRGIKEEVALSIYHQCISNYRWKTSRFRNFAAKNVTGATVQYTGSLIRSALGRVAHGQRRRRQGLDLRRERIEYRMMTDDQRNRYHSALNRLKYDEKIEGESKYDVLASFHSGATQYTAHGGCNFLGFHRLYTLMYEEALTQVDPEVTLPYLDSTLDFNMGLENSANSMIWHDDFLGTKEGFVTSGPFANWNTTVGQLFRNVGISGRPMDDEEIKNVTSRTRMSEICGDDASTWHDLEFVHGPFHLFVDGVMGIIEIASEEPVFWMHHAFIDYVWELQRENAKNKGVDVTADYPAQFGDVFHGPEEPLGDMMEGLTVMDGLSDAYIRDIYKYAPRPTCSAEKPYCGSPYLLCVQNERAEYKCRSMSIEEYEDFKANGGGHTGITTTTTTTTTTTTTTTPKPTTTPEPCPTLSPPYPPPPKNKGGDLHKPIQNSFCVNGQKNVNEWIYIPVRVTIRRPVDFGKYQSYPVVNGKPMKNTDIYASSGYSNLNRYMRGSPKPADYGSCKSTYSGAGEIYIQTDGLNYDGSYKEFAIVDHRLAVSVSIAYVAIKNPGSGQADVLISAYDSCGRVCRPSCLVPGSTNLYRPCSGALRVNTKQPLMFGNNFGDAVLGVWDFNSEKSCPQFSTDQIYVSFYCDYSDRWPWPTVFSQPGAKDPPTPPAGVQISRNTMKPSPLQNLMSPPAEAFKPIPPIIEATTEPAIQLKKCPITNKDCTILMSDCNAPCETGKSYQCVDSCNRFAKCWAGYYFVQLCYKSHYDPVSGKCQQGKGHCTNEEWNGLPQARQSRRKFSGVRGFGIVVLFIVALAIYLPTAGTLLSKINWPIFDAAFYDR\*

C. gigas-TyrA3.6 (complete)

>CGI\_10009319

MTYVSVCLLALCVLFMKTDGLLQSRDLPIEMAKCLNRFYSSCTIEEEVGLSILHNCIQEYKWKPNRERQYPEKRLSPEGQRYLEGLTRKVRSLHTSRGKRQAAVRRRKEYRMLSANERARYHNAVRRLKQSTGGEPSRYDTISSFHTGDIEQTAHFGCHFAGFHREYLKVYEMALQEIDPTVTLPYWDSLLDQYMDDSASSLMFSPQFMGNGNGEVTSGPAANWQTETGPLRRNVGVEGELYLYEEIQNITTRTRFVEICGMTRDMENHGLEFHHGDIHLWVGGNMAELNTAADDPLFWMHHASVDRIWELQRQNALRAGVDIDNDYPTNPEDYGNEFHAPDAEFGLLRPDLTVRDGVRRNMMDGLYMYEPSPTCSARSMDCGSNQLRCVQLNGNYICISKTLREYQRDLEEERNGQRPGTNNNNNGGVSRRPTFPWVNTRWFNRNNRIPSPPQLVNPEAPEQLTYPLIDQCSAFEYKPIQNSFCANGRKDIKEWVYIPVRVITQRDPSFTKYDSYPVRSGNIRSGSDIYSLNTYTKLKSALNPGRPDCYQKCKSSQTGAGEVFVRTDGISYSGTYQEYAIVDQRLPVSVSVAYVAVKTPIRGKTSAVVSAYDSCGRVCRPSCLNLRTKKYEPCSGAIDITTKLPHLYAYSLGDSIMKLYELDGFPQFNENEIFLSFFCDYSNKWPWQTVINQHIPQQSFSWTRPTYPGIEGPRRNAQQTSPVRTKFNGATSFAGTLNKCDLGNGCIIQKTGPCTSPCSENQIYECTNSCNKFARCTMGKYFVEEAVGVECPEICNGVQGDIIGGGTPVVHSWGK\*

C. gigas-TyrACgiga1 (complete)

>CGI\_10007793

MRKGQLNFIVCFLATVVLPTSFGLIEEIQTPRDILECLIYKSQNSTIGEVSGRTIQDFCIRKYTLDTQSGKENFAKNISTEGVQYLKSLFRQLESEVHDQKRGKRQAGTWRVRREIRTLSDAERNNVFQCLRRLKGDYSIDPRMSTYDLIASLHSGQAARMMHNGPAFLPRHMVYLLVMETACRVPMPYWDMTTDSEMMDPTTSIVWSDLFFGPGNGPVLTGPFGRFRTPTGTPIIRNIGSGGASLARKAGIRALLSRRRTFEISEPQPAQSIFSIEVHHNGVHNYIDGYMSGLNTASWDPVFWFIHSFFQLLWVAFRNGQRANGINPERDYPRGVRVPAGHEFYQRMNFMPFMRRITNLEGLSNRYDRIVQYAPMPRCPACGGSPFLVCLRGVCVSRSSRRAPVFFRGKRSAGTSGDQLADENVNPNTTNLIQSNEAALSTLNKPYQNTFMIDGKIDEDAWAYIPIRVLYERPKGFNFHTTSPGATKRDMYDPENFKNEAKRIGLHNEVQYKQQCTPSGSGAAKVFVQSNGLNYAGKYKDYAIVDERQPVTSAITYVGFKKPSTSDSEVILTAYDTCGRICRPACPVYGHHRESYRACSGSFRISSKSPLTFSQNYGSAVSSTWNVREMEPGCKSSQSLPITFVCDHQNSWPWESKL\*

C. gigas-TyrACgiga2 (complete)

>CGI\_10007753

MSITPSTKITKSIAHGSGVPGPKMSRERTAMFAVAFALVALPTISGLITKIPTPKELYECYLYKSLNASISETPAKVIQEFCISKYIVQHMDETIYTHNITKEGVNYLNAMSRELNQEITAMEKLQKKPRHKRQAFGTWRIRKEIRTLTRQEFQALVNCFNRLKNDYSIDSSMSTYDLIGSMHTGRAARSMHNGPGFFPRHMLMMLIMETACHSPMHYWDMTMDSDMIVPTDSIMFSEEFYGNGDGIVRTGPFAHWRTPIGTPIIRNIGSGGESLAGKQGIRAMLSRRRLAEISEPQVGHAAYSVEVHHNGVHNWIDGHMARLNTAWFDPIFYGIHSFFTLIWIAFKGLQRNRGIDPQRDYPLGPNVPSGHEFFQRADFRPFLRQISNLDALADTYDRMVTYMPMPRCPSCDNSPYLVCQRQVCVSRARPRMRQNMFMFGRKKRSANVNPTPSVYGTQKPLSDSDSLADDNVDNKTINILQSSETALSTLDQPYQNTFLIDGKSDLNQWVWLNIKILFERPKGFNFHTNLPGQNNTVDMYDTSNFERIAEKIGIHNQITYKKQCSSSGSGAAKVFVQSDGLNYAGRYKDYAIVDERQPIYSSVSYIAVKKPTTAKTTKVLLTAFDTCGRSCRAACPVPGTNGNSYEPCKGAFEITSEYPLMYSTSYGGAVSAAFSVHLESKGPMYRVNNHPITFVCDHQNKWPWE\*

C. gigas-TyrACgiga3 (complete)

>CGI\_10021076

MYNKKYYLFSAALAVCLPFIFGIVQEKPTPTELQECFFLKSLNTSVAEVPGKLIEDFCLRKYSLSQFEGKTQKNISVEGVRYLESLFRQIDAETQLTRKKRQATATWRVRSEIRTLSAAQRNRIFGCLNRLKRDYTIDRNTNTYDLIGSLHSGQSAQLMHNGPGFLGRHALYVLAMETACRTPIPYWDFMMDGALNNPTSSAIWSNTFFGNGNGAVRTGFCGNWVTPQNTPIIRNVGAGGVRLPRRDALRAILSRTTTREITEPLPTMSMFSIEVHHNAVHNYVDGHFSALDTSTFDPVFWFLHSMFHYMWYMFKNNQRARGVDPQRDYPRGPNVPQGHEYFQRVNFMPFVRPMTNLETFANRYDNIVRYTSLPRCPDCGGSQYLVCIQGECIARSVRTTRNPARISRRPGVLPVRQFVRGKRSTETDNFSLTQNHAELLSVLDRSYTNTLVINGHYTPKDWVYLNVRVIYERPKGNMFNSTGSVNGRDMYDPSSFHDGGKEIGIKNQVFYKQRCVPSGSGATKVFVQSDGLNYHGKYKEYAIIDERQAVSSAILQVAVRKPSDENTETYLSAYDSCGRVCRPICPMKEGSLLAYKACSGSFKITNEYPLMYSNSYEGAISSLWHLSLDGKGPLFKSTFSPITFVCDHQNVWPWSQK\*

>C. gigas-TyrACgiga4 (complete)

MKNPNHQIISLVLAVCLPSVYGIVQKIPTPTDVLECFFYKSLNTSVAEVPGKLIEDFCLRKYSLSQFERNTQKNISVEGVQYLKSLFRQIDAEAQEARNKRQVTATWRVRSEIRTLSAAQRNRIFGCLNRLKRDFTIDPNTNTYDLIGSLHSGQAAQLMHNGPGFLGRHSLYVLAMETACRTPIPYWDFMMDGAMTDPTSSAIWSNTFFGNGNGPVRTGFCGNWVTPQNTPIIRNVGAGGLQLPRRDVLRAILSRTRTSEITEPQPAMSVFSIEVHHNAVHNHIDGHFSALDTSTFDPVFWFLHSMFHYMWYMFKNNQRSRGVDPQRDYPRGPNVPQGHEFFQRVNFMPFVRPMTNLETFADRYDRIVSYTPLPRCPTCGGSPFLVCLQGTCVARSVRRTGRIPAIARRPVGLPITPFIRGKRSVDGNNNAGLLKNHEETLAALDRSYTNTFVIDGHFAPENWVYLNVRVIYERPKGDVFNSTGSADGHDMYDPSSFSDGGKEIGVENRVLYKQRCAPSGSGATKIYVQSDGLNYHGKYKEYAILDERQAVSSAILQIAVRKPSDKYTETYLSAYNSCGRVCRPVCSIGEGSSSIYKACSGSFKVTNEFPLMYSNSYEGAISSLWHLSLDGKGPLFRNTFSPITFICDHQNAWPWSQN\*

C. gigas-TyrACgiga5 (complete)

>CGI\_10017214

MVRDQPYFENYILVSEIMILNQKMSRHYSYRFLLGLALCLPFIFGKVQEIQTPIELQECFFYKSLNTSVAEVPGKLIEDFCLRKYSLSQYEENTQKNISAEGVRYLESLYRQIDAETQLTRKKRQTTATWRVRSEIRTLSAAQRNRIFGCLNRLKRDFTIDRTRSIYDLIGSLHSGQAAQLMHNGPGFLGRHTLYVLALETACRTPIPYWDFMMDGAMNDPTSSAVWSNTFFGNGNGPVRTGFCGNWVTPQNTPIIRNVGAGGVRLPRRDALRALMSRTRTSEITEPQPAMSVFSIEVHHNAVHNHIDGHFSALDTSPFDPVFWFLHSMFHYMWYMFKNNQRARGVDPQRDYPRGPNVPQGHEFFQRVNFMPFVRPMTNLETFSDRYDRIVRYTPLPRCPTCGGSRYLVCLQGVCVARSRGTGNIPGLVRRPTGLRRVRTIVRGKRSANIDNNSVLLQSHAEALSALDRSYTNTLMINGHYTPKDWVYLNVRVIYERPKSDVFNSTVDGRDMYDPSSFYDGGKELGINNRVLYKQRCEPSGSGATKVFVQSDGLNYHGRYKEFAILDERQAVSSAIVQVAVRKPSDENSNAYLSAYDSCGRVCRPVCSVQKGSSSAYKACSGSFKITNEYPLMYSNSYESAISSLWHLSLDGKGPLFTNHFSAITFICDHQNLWPWSKY\*

C. gigas-TyrACgiga6 (complete)

>CGI\_10011912

MAIVWTKAVSVFCLVLSLLKLSSALLEPNPFPKTLKECYDFRSYNMTPSDEVALMIQNHCFKNYQYKQIADGKIWTAPNITQEGMNYINSLFRKLFGEIVASSKSKHQKRQAAVRFRREVRSPGAFAPFVECIRRLYNTQVSANMNEYQAIASLHTGQALQSAHDGAAFLPWHRIYLLLLETACRGVPVPYWDSTVDHVMPDPTRSIVWSEQFFGNGDGQVLTGPFRNFQTTVPGDSITREIGTSRNALFTKEGLAAVLSRTRYSEIVEPKRGREYVYSLEGHHNGPHNWVGGHLPLPWVAAFDPVFFMHHAYVDAVWEVFRAQQIRNGIDPGRDYPLQNEPGHGPFDIIDFRPYFPPIRNIDAMSQAVARLVRYEPFPSCQNNCNSSPHLTCVGGVCMSRARPAASPIESFGGAAAFGPSAQDVPSQSRVLAQARGPIPGGERFRSSPFMDTRNRPNTIGNAPVAPELEAASFQARTAGMRSKRDASKILHYNVSSNAHVQSVSSLERSYTNTFIMDGVIDVKRWVYVPVRVVYNRTNANGNDPTFKANILKENLNEMCRAVGSGASKVYVASNGLDYFGTYKEFAIIDERQPISETTAAVGIKNPDYGAGEVMFSAYDSCGRPCRPFCLTSIQGKQKYRPCSGVFKISSAEXQRCVCP\*

C. gigas-TyrACgiga7 (complete)

>CGI\_10011913

MPGLLFVSLCVGFLGLSLALLEPIPFPASLQECYEYRSYNMTPSFEAAHQIQQYCYRNFEYQQIASGKVWSGTNITIQGINYIDSLFRQIFREVEEMERQNKNGRRTKRQTIGRRYRREVRSPGAYQPFADCIVRLQNQFVEDPSTGRNTYQTLAAFHSGQALRTAHGGPGFAPWHRIYLLLLETACGAPIPYWESGLDHDMEDPTASILWSDDFFGNGNGVVTTGPFRSMRTILGGPIIRNYGTGEGALFTKTGYNAVLSRTRYDDISEPKQGAAYFFTLEGHHNGPHTWTGGHLARPNSAPYDPVFYMHHSYVDAVYEAFRQRQRQNGINPETDYPVNTPPGHGFDDLIDFRPYINQITNRYAMSDAVANLVTYEPFANCRNRCNGSPHLYCQNGVCVSRNRPTAAPSGTFAFGDSDGAFRRNQERMRFAEAAGPIPAGEKFRTAPLRDIRNQEDRLGIAPVAPEIQAASMQVREVQARFRRDVSHLSKNESLHHGSHQSISSIGRSYTNSFILDGVVDQKRWVYVPVRIVYTRSPNVKGTDPTLLGNSELQNDVCQTAHSGASKVFVASDGLDYYGNYKEFAIIDERQPVSVTTTAVGIKNPEFGEGEVLFTSYDSCGRPCRPLCLTSVNGQQKYKACSGAFKISSAAPTLYRNSYKEAISVSLSSYNLVDSSLDDASPPVTFVCGNDNAWPWVY\*

>C. gigas-TyrACgiga8 (complete)

MMLGLLFVSLCVGFLGLSLALLEPIPFPASLQECYEYRSYNMTPSFEAAHQIQQYCYRNFEYQQIASGKVWSGTNITIQGINYIDSLFRQIFREVEEMERQNKNGRRTKRQTIGRRYRREVRSPGAYQPFADCIVRLQNQFVEDPSTGRNTYQTLAAFHSGQALQTAHGGPGFAPWHRIYLLLLETACGAPIPYWESGLDHDMEDPTESILWSDDFFGNGNGVVTTGPFRSMRTILGGPIIRNYGTGEGALFTKTGYNAVLSRTRYDDISEPKQGAAYFFTLEGHHNGPHTWTGGHLARPNSAPYDPVFYMHHSYVDAVYEAFRQRQRQNGINPETDYPVNTPPGHGFDDLIDFRPYINQITNRYAMSDAVANLVTYEPFANCRNRCNGSPHLYCQNGVCVSRNRPTAAPSGAFVFGDSDRAFRRNQERMRFAEAAGPIPAGEKFRTAPLRDIRNQEDRLGIAPVAPEIQAASMQVREVQARFRRDVTHLSKNESLHHGSHQSISSIGRSYTNSFILDGVVDQKRWVYVPVRIVYTRSPNVKGTDPTLLGNSELQNDVCQTAHSGASKVFVASDGLDYYGNYKEFAIIDERQPVSVTTTAVGIKNPEFGEGEVLFTSYDSCGRPCRPLCLTSVNGQQKYKACSGAFKISSTAPTMYRNSYKEAIAANLLEELNMVDSGSDASSPPVTFVCGNSNTWPWSY\*

>C. gigas-TyrACgiga9 (complete)

MMLGLLFVSLCVGFLGLSLALLEPIPFPASLQECYEYRSYNMTPSFEAAHQIQQYCYRNFEYQQIASGKVWSGTNITIQGINYIDSLFRQIFREVEEMERQNKNGRRTKRQTIGRRYRREVRSPGAYQPFADCIVRLQNQFVEDPSTGRNTYQTLAAFHSGQALQTAHGGPGFAPWHRIYLLLLETACGAPIPYWESGLDHDMEDPTESILWSDDFFGNGNGVVTTGPFRSMRTILGGPIIRNYGTGEGALFTKTGYNAVLSRTRYDDISEPKQGAAYFFTLEGHHNGPHTWTGGHLARPNSAPYDPVFYMHHSYVDAVYEAFRQRQRQNGINPETDYPVNTPPGHGFDDLIDFRPYINQITNRYAMSDAVANLVTYEPFANCRNRCNGSPHLYCQNGVCVSRNRPTAAPSGAFVFGDSDRAFRRNQERMRFAEAAGPIPAGEKFRTAPLRDIRNQEDRLGIAPVAPEIQAASMQVREVQARFRRDVTHLSKNESLHHGSHQSISSIGRSYTNSFILDGVVDQKRWVYVPVRIVYTRSPNVKGTDPTLLGNSELQNDVCQTAHSGASKVFVASDGLDYYGNYKEFAIIDERQPVSVTTTAVGIKNPEFGEGEVLFTSYDSCGRPCRPLCLTSVNGQQKYKACSGAFKISSTAPTLYRNSYKEAISVSLSSLNLVDSSLDDASPPVTFVCGNDNAWPWVY\*

>C. gigas-TyrACgiga10 (complete)

MRCFMEYTSRFMKMPRLSNLFAKLFSIMIIQRAFFEKFSNKYQLDRTNKIRIRNKKMIDTYLYAVWIGLIGLSSALLEPTPFPAELQECYEYRAYNMTPSFKAAMHIQNICFRNYQYNQFAAGKVWSGPNITQEGVNYIESLFRQILLEAKHVEKYNKHGGRQKRQAFPGRFRREVRSPGAFQPYANCIQRLQSESVEPATAGRNTYQTMAVFHTGETLRYAHGGPAFAPWHRIYLLLLETACRAPIPYWDSGLDHDMTDPTMSILWSNQFFGNGDGEVMNGPFRDMRTILGTPVIRNYGTGDSALFTKEGLRAVLSQRNYADIAEPLFGDAFMNSLEGHHNGPHVWVGGHISALNSAPWDPVFYMHHAYVDAVWERFREQQVTNGINPETDYPRTPPPPEGHAANDRIDFRPYINPITNIFAMRNLVANLVRYEPFPTCENTCNSSPHLSCDRARRICVSRERPVAQGNIVSASSSSSSVAMGASRGSAFRVESRSQARAEARGPLPVGQKFRSSPMQDPRNGADTIGTGPAAAQIRQASVQVRASATSQSQSSTQTRVRRDVFQNTTAHSNHQSVSSLERSFTNTFVLDGVVDLKRWVYVPVRIVYTRSPNVQGVDPTLLGNAELANDVCQTAHSGASKVFVASNGLNYYGNYKEFAIIDERQPVSITTTAVGIKNPEFGEGEVLFTSYDSCGRPCRPLCLTSVNGQQKYKACSGAFKISSTAPTLYRNSYKEAISVSLSSLNLVDSSLDDASPPVTFVCGNDNAWPWVY\*

>C. gigas-TyrACgiga11 (complete)

MRCFMEYTSRFMKMPRLSNLFAKLFSIMIIQRAFFEKFSNKYQLDRTNKIRIRNKKMIDTYLYAVWIGLIGLSSALLEPTPFPAELQECYEYRAYNMTPSFKAAMHIQNICFRNYQYNQFAAGKVWSGPNITQEGVNYIESLFRQILLEAKHVEKYNKHGGRQKRQAFPGRFRREVRSPGAFQPYANCIQRLQSESVEPATAGRNTYQTMAVFHTGETLRYAHGGPAFAPWHRIYLLLLETACRAPIPYWDSGLDHDMTDPTMSILWSNQFFGNGDGEVMNGPFRDMRTILGTPVIRNYGTGDSALFTKEGLRAVLSQRNYADIAEPLFGDAFMNSLEGHHNGPHVWVGGHISALNSAPWDPVFYMHHAYVDAVWERFREQQVTNGINPETDYPRTPPPPEGHAANDRIDFRPYINPITNIFAMRNLVANLVRYEPFPTCENTCNSSPHLSCDRARRICVSRERPVAQGNIVSASSSSSSVAMGASRGSAFRVESRSQARAEARGPLPVGQKFRSSPMQDPRNGADTIGTGPAAAQIRQASVQVRASATSQSQSSTQTRVRRDVFQNTTAHSNHQSVSSLERSFTNTFVLDGVVDLKRWVYVPVRIVYTRSPNVQGVDPTLLGNAELANDVCQTAHSGASKVFVASNGLNYYGNYKEFAIIDERQPVSITTTAVGIKNPEFGEGEVLFTSYDSCGRPCRPLCLTSVNGQQKYKACSGAFKISSTAPTMYRNSYKEAIAANLLEELNMVDSGSDASSPPVTFVCGNSNTWPWSY\*

C. gigas-TyrACgiga12 (complete)

>CGI\_10011916

MIIQRAFFEKFSNKYQLDRTNKIRIRNKKSVEPATAGRNTYQTMAVFHTGETLRYAHGGPAFAPWHRIYLLLLETACRAPIPYWDSGLDHDMTDPTMSILWSNQFFGNGDGEVMNGPFRDMRTILGTPVIRNYGTGDSALFTKEGLRAVLSQRNYADIAEPLFGDAFMNSLEGHHNGPHVWVGGHISALNSAPWDPVFYMHHAYVDAVWERFREQQVTNGINPETDYPRTPPPPEGHAANDRIDFRPYINPITNIFAMRNLIANLVRYEPFPTCENTCNSSPHLSCDRARRICVSRERPVAQGNIVSASSSSSSVAMGASRGSAFRVESRSQARAEARGPLPVGQKFRSSPVQDPRNGADTIGTGPAAAQIRQASVQVRASATSQSQSSTQTRVRRDVFQNTTAHGSHQSVSSLERSFTNTFVLDGVVDLKRWVYVPVRIVYTRSPNVQGVDPTLLGNAELANDVCQTAHSGASKVFVASNGLNYYGNYKEFAIIDERQPVSITTTAVGIKNPEFGEGEVLFTSYDSCGRPCRPLCLTSVNGQQKYKACSGAFKISSAAPTMYRNSYKEAIAANLLEELNMVDSGSDASSPPVTFVCGNSNTWPWSY\*

C. gigas-TyrB6 (complete)

>CGI\_10026225

MYSLVALCGILTFHFGYSMIEEMTTPGDIEDCFDGYYRKTSLQRSIGSKIYWKCMQRAACNRAMLNLGSNMTLEERHYIESLLPPPEVFYGNGAKGFHPNSEHRWRKEYRMMTEKERQAYHFAVNKLKRLRLGTSNRYDVIAALHEGAIVNAAHEGPNFMGWHRIYLIVYENALRQIVPGVTIPYFAGDLDEPLRDSTQSVLFCERFFGNGNGVVTSGPYANWSTPSGPLVRNYGDDGELWTREGLQRILNKTRNAEIIAPNAEEEDNLEDQHGAIHNWIGGGNGQIGELQTSSQDPAFFSLHAYVDYIWEEFRKRQASLGINPAKDYPVDYGPEEHHPLRLAGFATLRNIDGYSHGLASLVSYKPKPTCSKDRPFCGSPFLRCDKKSNPPRCVSKTIASFYRSNDPDDDSECNRTRTDNAVQNRFSCNGAQDIRQWVYIPVEIICVRPPEKKIYGSYPVFNGNLYRRGDIYSPKTYGIDDVLKTDILAKYSRCKDDTDRNSGRVTIQSRGLNYRGTYAEFALMDTRLAMANSMAYVAVKNPEHGVSEVMLSARDSCGRICKAYCKNNAPGSSDYRPCNGIIRVTSRTPKLYGRHYGENVYDMWNLPLGENCPSIKKTQVSVKFFCDFKNEWPWHSDFVLQQRQRGHFHGRRVTGNGPVRQMIMPSMVRGIVQENRIPSLQQEFISGNRKLPGCFLGHNCLVPGPCKPCQNGQKLQCLNTHISFAVCNNGAYVIRQCIGRSHINGHSLMCMGDVFRKPFLYR\*

C. gigas-TyrBCgiga1 (complete)

>CGI\_10008737

MVDYSSWVISELIQLRLADQESVEHSRAFPDNIVKPSAMSERSRICNERNQLGDKLKNGLDEDALHKMRWASYYAIFLVVLETHAAVWECKLPGLFKECYDFYSRMARVQDTPAYSIQSRCINSYLWKTSFVRYHVSLSTSDINYIRSLQREMESKRRYKRYKRQAATPVAVRREFRTLSDAEREAFFNAVNAMKNDGRYDALANMHTGIALQSGHEGPGFLAWHREYLTAFETALRRVDPSVSLPYWDSSKDFVMDNPALTSFFSSALVGNGDGIVVNGPFAGWPARPDGQRLSRDIGVIGSLFTPEGLDLFLNDPTVNLTRQIVLGTNEMLANTLEGQHNNVHNWVGGDMSRLNTAAHDPVFFMYHAHVDYVWERFREKQIALGSANPEADYPIINSPLHQPDRAMDGFPNVTNLEGFSNRYTSELYTYANSPECADGCGGSRFLRCSTTINRCVALTAAEVGGTADTNQNPVVDMGDFQFFNTFNDPRTRFARSTEHIRHKRDNAYIQTLLPKYALNLSHKPTSIANPFTKYGFNNHKTTITHKPKYASKTAVIHGTTPVLERGRQNLFSLDGVCDVSRWAYIPVKIINERDVSGPGFNSPIIVRDQFIPGVDIYNPLVYTALRPLFYQTRGQVVAKFPTCKKVNSGVKKVYIRSDGLTYDGHFIEHAVMDERQPISETTAYVAVKHPKLGPGKAILTAYDSSGRVCEPKCLIPGSYPPSYRTCSGVINISNLPPKMYGDDYGQAVRSQWNFVPGGCPSQQRSPIYLVFYCSPSVQWPWKKCLT\*

>C. gigas-TyrBCgiga2 (partial)

MAATCVLKVFLGLVLFAFRTHSIMWEADMPSLLKKCYEEHTRGLTVSDIASHDIQSYCLGSYIWQIPHIQRQVNMTESQINYIKSVYREYQHKMYSARRQKRQAPQRALRRELRVLSDAERQRFFDALNALKADGSYDAWANVHANMMVIRSGHEGPNFLGFHRVYLLFFEFALQRIDSSVSLCYWDSTMDNDMAEPQETAMFTSQLVGNGNGPVVNGPFSNWEEDDGPLTRNIATVRSSLMVKTALNRFFEGNAATTHRDVVVGFGVNLANTIEGQHNNVHNWVGGTMADAVTTAYDPVFILHHTFIDYVWERFRQKIRQQGTDPTDYPWPMQNADWNTNFLHYTNRPMDLYENFTNADGYSDIFTQDFYQYEDMPSCATNCGNSRFLTCQGGVCVGLTASDIGEDSSAQVMGQTAFLGRAAAEMEERPVVAPFQTSFVDPRTGNGNGNGGNLAAPASRSPVGFSPFQSSMNDPRTGNGNGWNGIRQQSRGSPAGSLQGMQRFNAGVGPMQLNRAPIAANLRNPAGIGIRNVGGMFRPNSPNTLARFGSLVTPNNPIRHLWDQSVRRNSFQRSNLARSHLHSSGLLNADDIRRMVHLRDLPIQNTFTMDGVSDARRWVYLPVRIVYMRPPGQFFGSRMVYNSQFVRASDMYAPQIYPEFNNISPKIAPATYPNCLKNLGGSSKVFVQSNGFSYKGKYLDYAVLDERQPVSESIAYVAVKNPDLGAAQCYLTAFDSCGRVCQPRCLIPGSNPPAYRPCSGVVNVSNRLPRMYGRTYGEAVKSRWSFSDKNCPSSFQGEIFMTFYCDYENVWPWKGCNGGTTRRKSYAGWWSIDIK

***Azumapecten farreri*** (Bivalvia, Pectinidae)

A. farreri-TyrB7 (complete)

>gi|193878323|gb|ACF25906.1| tyrosinase [Azumapecten farreri]

MKIKQTTTSFVLYSITLNLLLNIVKVTGQRILTNPAINCEQYRDNRGQLEITGNDDSLYCLHEHLYKSALSSPPNNAPDVYVNELLQKALTRCSFKKTQSSELSKTEKKTCKSRKCKKLRYHGRRRKRFARKSKSNRGRRYKAEHNECNWERKEVRMLSRSEWNQFTKRINILKKPIALPGGGSFIPYDVISNVHRGRRSLEAAHRGSNFPSWHRIYLLVMEAAIGIPIPYWDHRMDYDMDEPIDSIVWTDEFFGPGIGEVKSGPFANWTTAHNEPLSRNIGLTGSLISECMVKGLLRYKSHDPIIYPTIKSYSLEDIHNGPHRWVAGQLSVLRKSPQDPIFFLHHSFVDYLWYLFRKSTRETGNIDPSTDYPDKGPASQGRYEYMIPFSKLRNIHGYSDFIEGLSSFKPPPKCPHCGGSDYLECDAQISRCKSKASKAVVPDIQFLRRQAMNIVIRGTKFVSPITDIRTSGVALSFLQLANNTLG\*

***Perna viridis*** (Bivalvia, Mytilidae)

P. viridis-TyrA1 (complete)

>gi|556912021|gb|AGZ84287.1| tyrosinase 5 [Perna viridis]

MLKILVCLVALNSFCGVKCLISQIDMPPYLKDCIKLKTSKHDPTQSPSEDVCNTCVTRYVWIKGPNLKKCSHQQDNTTMADISRFFGKVICDHYNYRQKRQARTHMRQEIRMMSPQRRKNLRAAWKKAYDDGYFGWLARFHNDQIRDSAHAGPAFPGYHRFFLLMLESVLKHYDKDITMPYWDSTKEANMENPANSVLWTDDYLGEMNGVVNSGMCGGFRDLRGNPIMRNGGNAGSLFTSYDTRFVINIPNIERLTEPSPYVTLESAHDNVHNWVGGTMAPIELAPWDCIFWMHHAYVDYLWEVWRYNHNYDMKYPYKAGLPGHGPNTPMKNMPYMRFLGRVPTNKDGYSARLAKLAYYQLSPTCSAQNTYCGSPDLQCKIGRYASECVSVDVRFRRETQPFRQANNRGGNVNFKVNRAGRKKRRADHQGYYEDYEFSVPADQIDNIHIPIEREPCMGRPIQNNFIADCSSDAKQWVYLPVKVVHLRPQEVVFKASGHDYGQPSRYDMYDEHNYAKLNQYVKPGNPAVYEDCMEDESGAFKVRLKSSGLSYFGSYTDYVFVDNRLPVSSHIGYIAVQKPTPYKPTDVLITASDACGRLCKATCRKQVGNHVYYEPCKGTIRVTPDMPLMYGNDFGEAVLSIWEFNGKFTPTESEHNIYLEFYCDYSNKWIWDECPHSKQG\*

P. viridis-TyrB7.1 (complete)

>gi|556912023|gb|AGZ84288.1| tyrosinase 3 [Perna viridis]

MGLIHLLFLTFAGCGIHGYMWKDWLPGDLEDCLLNQCKQADLSKLTMYNIEYMCLNKHMAKLNAHKDMITPLTDSQKEYLLHLGRKFKGIEYAYRRRKRSTRLPAHFLHKRQEIRVMPEKQRKAYFNALNKLKTRGFYDAISNLHQQTAIQGAHFGCGFLGWHRVFLLILQLAVWDINPTVMLPYCDTRLDYNMNNPRDTILSSQKYFGNFNGIVKSGPFKNWTTPTNVKLQRNGFNGGSFITDENIRQTMAKRHTREVCAVPGIFNIEHYHNSVHVIIGGLMGDLNWAPCDPIFFCHHNFIDYVWEQFRIHQRKDEGIDPGNDYPNTNDNWHKPDAKMEMIDRYLNLNLTHKHGYDNMFSDEIMIAWEKSPSYPNCGNSPDIIKDDTRQVCHSISLTVDEKKNHTWFGVMRSPKKDEFKVTNAFKAASHDRRLKKNIKKRSVSYRRRDKKTWNVPARSSPLDYTVENTFKLNDKVTAKAWGFIPVRIVYKRRPGAHFDVETAKYQRVLEEVAENKPQESLSIADKDLYDPQNYPRLWKKIKEGKPASYGKIRAAGSGAYKIMVKSTGFSYNGKYTDYAIVDERQALSEAVAYVAIKRPVGNETVKSFVMAYDPAGNVCEARCKVPGSKPPKYERCSGVIKVNSKTPKMYGENLGDAYLMRYRFQGDDLPSNHDGDIFLMFFCKYSNECPWTESYTKKK\*

P. viridis-TyrB7.2 (complete)

>gi|556912019|gb|AGZ84286.1| tyrosinase 1 [Perna viridis]

MVAFIYTLLISLVTISVALITEQPMPQLLCNCFNRELSASKDEPGAMIIYTCVNKYLAITWRDRYYQKMSNDPEVINWFKSLYRKNKSLEYHSRLKRQTGSLLHGTRQEIRTLSNAQRRRFITAVQRLKTTRVGSTNRYDAIAAAHDGPALENAHFGPNFLGWHREYLLLFETALRQIDSRVVLPYWDTRLEYNLRNELESNIWDLSFMGDSQGVVSYGPFARWRQPNGAFLERSAGADGSYIPPVGIQRVLSRQSNIQISEPWAADRFSLENYHNAVHMRVGGSMTGLNTAPADPIFFLHHAFIDCVWEDFRRQQTYPERDYPWNNQARRSQRPSERMINLESNKRNIEGYSNEYTQRYYRCARSPQTCRECRNRRNLRCGTWNPGLCAAGRQSRRTSTRARNALQDEPKNKPLGISQSFRSTIIDKRKNNRGKRSIPAADFSMNFTKMFSHEDYPEKIPKTWRPSESELESPIQNSFVIDGVPDIKRWVFIPVIVKHKRPPGLYFNSKVIVHGDIQAGVDVYSYAMILNDTKTNRDQATFPNRNIPSKVGFDKVFVQVDGLSYSGKYKDYAVVDSRLPISESVTFVGVKSPKLNNSRSYVSAYDSHGRLCHAYCLVYGSNPPEYKKCSGVIDLTTTSPFMYGDSIGESNGLLYRKLKSVNHVRSYENVFLTFHCDYDDTPWSQCK\*

P. viridis-TyrBPviri1 (complete)

>gi|556912025|gb|AGZ84289.1| tyrosinase 2 [Perna viridis]

MVEFSAFMPDMNHVLPLLVILLYHQYDVTMSKVISEGFPGEIADCRYVERSELYTCIRSKFDNPDWIPDSGPKLQLRLRQDFYWHPTKRIRRECRAIPREEWHALCDAINKLKKDKTFAPNVYDNFADYHTNEAVNSIHFGPNFFGWHRIFILVFEELLRKVNPNVTLCYWDSRLDHNMKHPEKSIMFTKEFFGNTKGPVVTGPFAGWKTIRNIPLRRNSAQEGELISTAAFDKVLSKHYHVQITTPTADDDSNVESLHNGVHAYIGGQMNDFNTSSQDICFWFHHAFIDSVWEKFCSKLRNKGLDPQEDYVIIDERLHRPRRLMDHFFPFKNIDGYSDYFPRNIYKYEEYATCPDCLNSPYLKCNNVTNKCYSIQENEPKRLVFKPLKKIETNHLSAPKDEFKIISGKENLESMVFVPVKVVFRDAVHKSIRKQYIAGCEYQKKDIDVCKKSVAIVESHGMSYHGKYRNYVINDACVPQWVYAFVGVRDPALGDSMSFISVTDKLGNHCFAYCLDLEAKKYRSCSGVIKLTTDTPRMYSKSLDDAKASGFPFSPLEADTLDPRIQLSFLCY\*

P. viridis-TyrBPviri2 (complete)

>gi|556912027|gb|AGZ84290.1| tyrosinase 4, partial [Perna viridis]

MQVKTFVYFYICLSVHLANGNISPDIEQQCKDVQDSHMCFFNLLKNNTEINRTTLIIQEEYFWHPVKRKRKDCRALSEKERNDLFSAINALRKDKSKTPNVYDNYAAFHTQRTLKSVHHGPNFFGWHRIYLLRFEELLRKVNPSVTLCFWESPLNYYMKNPLDFVMFTDDFLGNGRGTVTTGPFANWTTMDNRPLRRRLGKHRDGRLLAPFEIKYVLSKNRHSQITHPNADFGSDLEMMHNVVHILVGGQMGDLKTSTQDPFFWFHHAYLDSVWEQFCAKIRQNGIDPKDDYVKVKNKLHHPKRRMDRLFPFRNEDGYSDYFTKYVYEYDEHAKCPYCSYSPYLDCNKKKNVCYALSSRDKTRNITMPFHDFAPTGPGHKISILSGQENAKRLIFLPIKIIFEDALKKNLHMKKIAGCQFEQRSR\*

***Hyriopsis cumingii*** (Bivalvia, Unionidae)

>H. cumingii-TyrA1 (partial)

MVWLFSLPVIMFSLVPYVKATVEQTDVPEELTWNFHVAQKKTSMSNTPASAIQSWCTNVYKWQYDSIVHGGRNASTGTRQLVNYLSNQVNLSVRRTGLVKRQVAPSGPKRRRKEIRMMSEKELDLYFRAVRAAKANTTTAPNVYEALAEFHTGITSISAHGGCNFFGWHRVYLLMYENMLRDQGPEFAEVTIPYWDSRLEARMDQPTSTVLFTDRLLGTGSGEASGGILGSGWSTSAGPLIRNIGADGPPMTDEAIVNVTRMTRMREICGADSSIESDLEFHHNGIHRWVDGQMAMLQTSALDPAFWSHHTFIDFVWEAFRKNSTEKWSEY

>H. cumingii-TyrA2 (partial)

MPSIAVFLILLFAVIPYSDLQAQVTSNRSLDPSFLRWLNSLFYLPPEGELRVRKEYRMLTDIERNNFHHAMRLLKMDTSVPPNKFDALASLHHMNTAEAAHGGPNFLGWHRVYLVLCENALREKIANVTIPYWDNTLEEALPDPRQSILFSPLFMGSASGQVVTGPFSYWSTVGYGQLARDVGNSRRLMNPGDLTAIFSRRLIADISNPNAPESSNLEELHNDVHVYVGEQMSRIESASYDPLFYIHHAFIDCVWEEFRNLQRLSGVDPARDFPRIVGEQAHQPLAAMGLGRLLVIDGINNIFTQRIYRCESRPACIMNSNTCGSPYLRCDWTRQRCMPLIMSSGPGMFARSQWTFPGFFAG

>H. cumingii-TyrAHcum1 (complete)

MHYLKFLKRRIFDNHFRAKRQSDINPSPPSGFRVRKEYRRLTDSERTAYHSVLNVMKRNGEYDTFARIHSGPNLGQFHDGPNFLGWHRIYLAYFEEAVRRYDNSLSLPFWDYTLDFPLSDPTQSVLWSATFLGNGDGVVWSGPFSGWVVNGSPLIRNTGHQGALMSKQDVDTVLTRCDTSEITFPRETGTYNLEIYHNRVHNWVGGNMELLDTAAFDPAFFLHHAFVDYVWELFRLRQLTVCGINPEANYPNVVGDHAPQREMHAFPQHRASDGYANYWTDSWYTYEMSPSCSRVRPDCGSLYLKCDIDRDICVSKTRSEIKTSRTSSTERRKRSALVLETPSSCTGTISGTMQNTYLINGNNDIDSWVYIPIQIAYIRPSGYHFHSYPIQDGKVQYVQDVYSPFLYPNLHSYVKSEDLKAYPNCGLDPSGAGQIYVRSDGLTYYGTYVDYVLSDVRQPYGSTVVYIGVKNPGSGISEAILSAHDKCGRPCSVTCDQTKYRSAILQEMFWCHSSVRASSANVWFKLWRCSAQCLGSAWNGT\*

>H. cumingii-TyrAHcum2 (partial)

MSPITLLLFVTALPLLVTADLQYMSWPDHLFSCLDSFQKVTDITEEVGEHIFRHCIDVQNIKNSKLSWTWVNITGVGDQPRAKRQATTPVTSPPSGYRTRKEYRTLTDDERNRFHAALNAMRRTGEFQRFASYHRNIPGRNVLQEFHNGPAFLGWHRVYLARFEEALRRYDNTVSLPYWNSSLDFYMTGDPANSVLWSDLFLGTRSGFVTSGPFAGWPGGANSILTRDVMLNRRGLLISNDDVNNVLRLCSTADVSFPPRRPLNSIIEFHHNRPHTFVGGNTGDMSTLPNAAFDPAFFLHHAYVDYIWELFRTRQRSACNVDPTTDYPNTVPIPICNLHMHDGERKLDR

>H. cumingii-TyrAHcum3 (partial)

MLSDTERNNFHQALNMLKADTSIPPNRFDSLGLLHQTQGIRSHDGPNFLGWHRLFLIMAENALREKIPTVTIPYWDSTLDAALPDPRASVFFSPEFMGDAIGAVDTGPFSGWRTPIGPLIRHFGQDGYLMNWTSIRDVFTRSRLEEITAPHAVSKYNIEQHHAGPHLWVGGYMSPQALAGYDPIFYLHHSFVDLIWELFRNIQRRGGVDPTTDYPTNITIEGQGGQDQNGFNTLTNRDALSDYYTTTIYSYQLPPTCTTEQPDCGSPYLHCDTAGSSPRCVSVTIFDPKPSDLMHENGLPMNGSPRRNRVTKRSANQTGNGHRNTLEEGTLCKGKNWDQQYTNNYFIDGLIDKKLWAYIPVGIIFKNDDHTFLTHQNSSVLAVYSKCIDGVPISPHVTIESNGLNYEGMYKEITPVDKDLPIFSTTTFIGVKSPDTNGSEVLISAYDACGRVCQAFCRDTSSKSASLDMPCSGAIRITRDSPLLYGRSASEVAENLFKTPEAGAFPEFQRNEMFLQFYCKQEDWPWKSKFSHL

>H. cumingii-TyrAHcum4 (partial)

MTGKLVRATFVALIGVVLVSGLIEEIPMPPELQSCLKDFHTKTNITDTVGEKIFSYCLNSFLWKTETTNWGEFNITQADLEYFHRLVDQLITRHVPSRGKRQALGPVLFPPTGFRIRREYRRLNGMERDAFHRAVIELKRRGEYDLFARMHQDIVIQSAHNGPNFLGWHRVYITMYEEALRRIIPMVVLPYWDSTLDFHMDEPTESVIWTPLFMGDGSGVVNTGPFTSWSTPIGPLRRNIGVQSRLISRQNVIDILSRCRHAEITFPAALPQFNLEFIHGGPHGWVGGHMAGLNTAAFDPIFFLHHAF

***Laternula elliptica*** (Bivalvia, Laternulidae)

>L. elliptica-TyrALelli1 (partial)

MGRLVLLVTQLVLLYMSMSTAQPANQMCLLIPPDIQTCYRAYQNTTISSLAAQVACLKKLLWRFSPDSSLTNEDITNIRTTGGAAGFSASFATSDPFPETGFRTRKEFRSLTTNERTRLFRALRQLHTNGVIRSYARLHLQANRNIHNGAAFLPWHRAFLSYFEEDLRKIDPTVSLPYWDSTIDVEMSSPALSRLWEEGLFANGVGEVVTYPFDRWTTDSGWLERDVGRRGVLISKQNVARVLTKCTLGEISEPTRVQRRDSWEFYHNGVHNFVGGDMVSWLSPYDPVFFFHHAFIDYVWELFRERQRSTCGVDPTTDYPATSGGHGPNSVMPGYPHLRNIDGC

>L. elliptica-TyrB6 (complete)

MSAGFLTRQGVIMRLTYTLALLCSLQIKTSRARVESIELPPDLESYFYDYQSRTDLTQASGDTIFWNCMQKYITKFTKTTFSGATLSQINFMQENIRSMMQSLLSESNGKRKKRQSRGRRIRKELRMMTTLERNNYFRAVNELKMDTRVGPNVYDFLASFHSTRDNLRRAHFGPGFPGWHRVYLWIYENFLRQKVPTVTVPYWASVLDNDLPDARDTVIFSDTFFGNGVGEVNRGPFANWSQINPDNIITRNIGSGNLYTYEQIAAFMSKRNNAQILIPSSDPDSNFEIMHGGVHGWTGGVMNRLDSAPQDPVFYSHHAYVDKLWEDFRMQQRRNGINPQNDYPFIFNNASWPDEHRPDAPMGFAHPNITVRDVQQRVGYLNVFSALVRYEGIPTCTARRPDCGSIYLRCNSQFTPPRCMARTTAEVPQTNYVNDPKPPRT\*

***Patella vulgata*** (Gastropoda, Patellidae)

>P. vulgata-TyrA1.1 (partial)

MSLAPPRIGEAIELANHLVRLPWRRPSIRKECRLLTSTELQRIFDALQAAKRDTRVRPNVLDAFAFLHSHPEINEGAHGGTAFLPFHRYYLHLYEKMLRMYEPTVSLCFWDTTLEPENYEESAMWTADIFGSPRGLITEGFAANWLTPLGPLIREVAGARGRTLNDRDIEEVLRQTRIGEISFPNGITSANVEELHNHVHLVVGGLMSQIESASYDPIFWFHHTYVDCLYERFRKKQNETGKINPQRDWPRDFGDPSNAPFVPMRLGAMMNIDGANNIFSGMITCEDVPECRTDRDCGRFMNCDRIRQRCISNTRRNSQSASMFGGMFGMSTNSFGGMFQNGLFSSQGSGGFPGFNPMSFNNNGNQAFGQMNNFGNTQGGFPGGPSNMQPGLMGNQNQNFGGPPQQFQGMQGFPGAGNQGQQNMPQFPGMPGSNNMQSFPGMANFGGMMPGMPNMGGGG

>P. vulgata-TyrA1.2 (partial)

MTFHPCQVLYIVLLVAVPVSESLITEGPLPLPLKECYERHYSKPLSQVVGKTLCWMCEAPVLRKTEGVVKQLLPAQKAYIDGLYNSVENHHRGKRQAPRCLRKEYRRLTDDERSAFHQAVNALKYDTSVTPNRYDAIASLHTGTASLVAHGGPLFPSWHRIYLLMFERALQEKVPGVCLPYIDNTIESEVDVNEISHLFSEDFAGTANGVVTSGPFANWTTPVGPLTRNVGNQAVPMSKLQLDGIMSRNSMEEINEPSENAEFSLEFNHGAFHIFIGGHMENLDRASFDPLFFLHHCYIDKVWQLFREKLRSIGVDPNIYPEMSNTPSLQIANALLGFGNVTASESYSDIFELYDYEPAPECSQINPSCGSTKYLQCNTDTWRCVPVDPNTVTGPINPGP

***Lottia gigantea*** (Gastropoda, Lottidae)

L. gigantea-TyrA1.1 (complete)

>jgi|Lotgi1|160808|fgenesh2\_pg.C\_sca\_26000106

MCQNAPNQCYFSKPFCQKMFRLIHIVIALTLFPYTQQQFRMRLDSPTIGQAVELAHVLFEDEESEGISYRRDCRLLDEDELSDLFGAVQDAKDDTTARPNVLDAFSFLHSRNEVNSGAHGGVGFLPFHRVFLYLYEKLLRQYRPGVSLCFWDPTLEPEDYEQSEIWGDRLFGTARGIVSEGFAANWMTPVGPLIREVGRTGGTGRNGRTLNEKDIENVLSKKRLGEISFPNGRLSENVEELHNHVHLYIGGLMAQIETAAYDPIFWFYHVYVDCLFEEFREKQRNNTTPPVIDPELDWPYDYAEPEHAPFGPMRLGALRNIDGQNNFFSDRIRCEKVPSCRSDRDCGRFMNCRSRKCISNRRPRNRSNNNMFGGFMNGLVGPQTSNPMIQALQGMGMMGRGGFPGMGGNMAGMFGGGGGFPGMGGGFPGMPGMGGQGMPQMGNQQGRLQGLPGMAAGGSQGFSAFGGFPGMGGSQIFSGQGFPGMGGSQGFPGMGGMGGFPGMGGMGGFSMGGQGGGGGGFPFGK\*

L. gigantea-TyrA1.2 (complete)

>jgi|Lotgi1|166196|fgenesh2\_pg.C\_sca\_56000109

MRIALSLLLLLSIVTDVEPLIREAPLPKQLKECYQKYSRKSLASVVGKSLCWYCETSLRGRMNPPAEPMVLPNRRDYRRLAEPLINRRVKRQAGGSTCIRKEYRMLTSAERDNYHNAINALKQDTTMTPNMYDAVAMFHVGDASVRAHGGPGFLGWHRMYLVMYERALQSKVPGVCIPYIDNTIEAELGDDGSYLWSDEFLGTPNGVVTSGPFANWNTPIGELTRNVGNQAFPMDKDILNDIMSRGRIEDIVSPTAELEHDIEYHHGSYHIHVGGLMESIDTASFDPVFFMHHAYIDYVWEQFRQKTLAAGGDPTRYPESNDLPLHTGDTVINVIQLPTGNVTVTQRDMYATLTDYEYQPSPECSRTNPDCGSIYLACNRTSYRCYPVNPSLQPPVNPGPPINPGPPVNPGPPVNPGPPVNPGPPVNPGPPVDPPTDPWTPVDPRPPVNPGPPINPIPPVNPRPSNCIDSNRYIKAPRTCQNTFCIDGVCDTNKWSYFPVKVISNRAPEFSGSGSYPVRNGKVMTKNDIYEPKAYTAVNQYVRPRAVEPKGYGNCQDTHGIGQIFISSQGINYEGYYSESSIIDQRLATSISIAYLAVKDIGISGKSTALLRAFDQCGRICHTACRVPGSNPAKYRPCSGVVDITPDFPKQYSSSYGESLLQVWGYKQDRECPIFEGEDFFMSFYCDYKDRLPWVESGPVYGQTQPSPLIMPIFQPKPVVPPKPKAVCKVNTKCTVEVACESRKCSTYGHIILETILALGYPRNSV\*

***Illex argentinus*** (Cephalopoda, Ommastrephidae)

I. argentinus-TyrA2.1 (complete)

>gi|34850933|dbj|BAC87844.1| tyrosinase precursor 2 [Illex argentinus]

MESYRLLVLVSAFGLCQAMVDVSQSDELQSCLDRFADDTSTFSQQEQLSLCSKYYMQKNWKSADVSKPKISTLATMSPQEYIQSLIDRFTAEARNPQGRRVRKEYRMMTNEERDNYHRAIVMLKQDTTVLPNKFEIIADLHAGSVTNSAHGGPGFLPWHRIYMMIWEEGLREQVPTVVVPYWDVTRDSAMDDPRRSIVWSPQFQGNGHGLVTVGPFADWTTGYGPLHRNYAVFTHLLTRANIQTVFTERTIAEISQLTANDQRYVFELYHNNIHDWIGGTVSVQAWASFDPAFMLIHGYVDYIWYRFQEMQLELGGIDISVDYPFTANHQILNGTAFDGEEPVGLIPGMTNREAVAEGVVYMNLMNYEEAQSDCDQQTPCPPNYECVDGFCASRAVDNDVCNQIQPLQNNFCINKECDVSLFSFLAVEIIHERMENICNMGNFPVRQWLADKTADIYRVSASVIHQGKYSNSLSDMCGRPGGCCKPVERVNIQVSGNDGDLWLYRESAFVDARLAVSHSQMFVAVRRVPIGRFLIFAADEYGNLCDAYLVDTFGNRILLRRSEGIIISEDDPRLSNTLAEAESKMFDYQNGQDLPPNVLQNQYVLSFHCRADRNLGPSVRNGNKK\*

I. argentinus-TyrA2.2 (complete)

>gi|34850931|dbj|BAC87843.1| tyrosinase precursor 1 [Illex argentinus]

MESYRLLVLVSAFGLCQAMVDVSQSDGLQSCLDRFADDTSTFSQQEQLSLCSKYYMQKNWKSADVSKPKISTLATMSPQEYIQSLIDRFTAEARNPQGRRVRKEYRMMTNEERDNYHRAIVMLKQDTTVLPNKFEIIADLHAGSVTNSAHGGPGFLPWHRIYMMIWEEGLREQVPTVVVPYWDVTRDSAMDDPRRSIVWSPQFQGNGHGLVTVGPFADWTTGYGPLHRNYAVFTHLLTRANIQTVFTERTIAEISQLTANDQRYVFELYHNNIHDWIGGTVSVQAWASFDPAFMLIHGYVDYIWYRFQEMQLELGGIDISVDYPFTANHQILNGTAFDGEEPVGLIPGMTNREAVAEGVVYMNLMNYEEAQSDCDQQTPCPPNYECVDGFCASRAVDNDVCNQIQPLQNNFCINKECDVSLFSFLAVEIIHERMENLCNMGNFPVRQWLADKTADIYRESASVIHQGKYSNSLSDMCGRPGGCCKPVERVNIQVSGNDGDLWLYRESAFVDARLAVSHSQMFVAVRRVPIGRFLIFAADEYGNLCDAYLVDTFGNKILLRRSEGIIISEDDPRLSNTLAEAESKMFDYQNGQDLPPNVLQNQYVLSFHCRADRNLGPSVRNGNKK\*

***Sepia officinalis*** (Cephalopoda, Sepiidae)

S. officinalis-TyrA2 (complete)

>gi|32452643|emb|CAC82191.1| tyrosinase [Sepia officinalis]

MSLFGICKAMVNISQSNMLQNCFDRFASDSSILTEQEQVSLCFKYYTQNNLQSADVPNSKVSPLATMTPEEYIQSLIGRFTAEARNPQNKRVHKEYRMMTNEERENYHQAIIMLKQDTTVLPNKFEVIADLHVGFITNSAHGGPGFLPWHRIYMMIWEEGLREQIPSVVVPYWDVTRDSALEDPRRSIIWSPEFQGNGHGLVTSGPFAGWLTGYGPLHRNYAVFTHLLTRENVRTVFTQKSLAQISQLTANEQRYIFELYHNNIHDWIGGTVSVQAWASFDPAFMLIHGYVDYIWYRFQEMQLEANINISEDYPMTSNHQILNGTAFDADAPIGIIAGMSNREAVAESVVYMNLIDYEEAPTDCDEETPCGSPYYECVNGFCASRIIANDVCSQTIPLQNNFCVDKICDTGLFSFLPVEVIHERLESLCDMSNFPVRQWVPDNTMDIYRESANIVHQDRYFNRPSDMCGRPGGCCKPVERVNIQVNGNDGNLWLYKESVYVDTRLAVSHSHMFVAIKRAPIGRFLIFAADEYGNLCDTYLLDTFGNRILLRRNEGIIISENDQRISSTLAEAELKMFNYVTGQSLPTVRQDQYVISFHCRADRNQN\*

**Supplementary dataset file S2.** List of *Pinctada margaritifera* reference gene sequences used for qPCR analysis.

>P. margaritifera-ferritin

TAGTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGCAATTTTTTTATTTGCTTTTTTCAGTATTTTCACAGCCCGTAAAAACAATGATAAAAGAAGTAAGTTTTTGTTTATTTTGAGAAACAAAGATTGGAGTCCAGATTATATGAATTTCACAAAGCAGTTAGTACAATTGTAATGTCCACTAAATAATGGCTGTGAGAGTGGGTGGAGTTTCAGACCCCTTTTACTCCGAAGACTGGAGCCTGAGGTCGTACTGGTACTCTCCCAGTCCTGGACCCACACGTTTCAGCTGGGTTATGTGGTCGGAGATCTCCTTTATGGCATTCACCTGTTCCTCAAGGTACTCACTCTCTATGAAATCCATCATCTGGGCATCTCCGTGGGTGTCGGCCACTTTATGAAGGTCAAGCAGGGCCTGATTGACAGACTTCTCAAGCTGCAGGGCCACCTGCATGGCTTCAAGTCCATTCCCCCAATCATCACGATCAGGCTTCTTGATGTCTTGAAGGACAATGCGCCCTCCTCTCTTGTTCTGGTACTTCATCAGCTTCTCAGCATGTTCACGCTCCTCATCAGAGGAATGCTTGAAGTACTTGGCAAATCCTGGTAGAGCAACATCATCACGATCAAAGTAGAAGGACATGGACTGGTAGGTGTAACTGGCGTACAACTCCATGTTTATCTGCCTGTTGATCCCTGCTTCACTCTCAACGTGGAAGTTCTGGCGAGGCTGACTTAGTGCCATTTTGATGTTTCAGGTATTAAAATTAAGCTGTGTGAAAAACAGTTGTTTAACTGAGATGTGGCGGAATAAGGCTAATTTGCCCGTACGTTCACTGACGCAGCAAGACAAATATCACCCGGAATCCCCGGCCGTAATGGCCACTCTGCGTTGATACCACTGCTTATTCTAGAGGCCGAGGCGGCCGACATGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATTTTTTT

>P. margaritifera-αnac

CCGGACGGCGGGTCGGACAGGTTTTTTTGTTTTTTTTTTTTTTTTTTGCTTTTGATCAGTTTTATTCCCCATGACAGGGTAGAGAACACATACATAACACAGGCGGGACGGGGGACAATCACACACACAGAGCTTTGATCTTCTGCTACATTGTTAACTCCATTATAGCATTTACGATGTCGTTACTATTATTTTTCAGTGCCTTAACCGCTTTCTGCCGCGATACATTTGCCTGTGACATTACAAGCTCGATATCCTTAGCTTCCACTCCTGTTTCATCAACCTCAGCCTCTTCTTCTGATTCCTCTTGTATAGGTTGTGACACAGGGTTGGGCACCTCTCCTCCCAAGCCCGCTGGGTTGTCTGGTGTCTTGAATTTTTTGGCTGCTTCCATCTGGGCTTGCTGACTCAGATCTTCAATCTTGGCCTCTCCAAATACTATGTATGTGTCTGAGGCAGGACTTTTATATACATCTGGTCTGTTTATCACAAAGAGAATATTTTTGGATTTACGAATGGTTACTCTGGTAACGCCTGTGACCTGTTTAAGACCTAGTTTTGACATGGCTTTTCTGGCCTTCTTTTCACTCCTGCTTTGTTTGGCCTTGCTGACAAGCTCTTCCTGTATACCTGCTGCTGCAGCTACCTGTGATGTCTGTTGGTTAACATCACCATCCTCCAAATCTGGCATGTCCTCGTCACTGTCTGTATCCGTCCCAGACCCTGAACCCTCCTCAGGTTTTGTCTCCTCCATTGGCTTTTCTACAGCTTCTGTTGGCATCTTTTGATTTTTATGGTGTGTGGAATCAGATTAAGATGGATTTTAAAGTTGTTCAGTGTTGTCGTCTGTAATGGCCACTCTGCGTTGATACCACTGCTTA

>P. margaritifera-enCoA

TGCATGTAGATTGACTTCCCAAAGTTGACCTCAAGAAAAGCATACAGATTATATTCCTTGCGTATTTATTTATGATTTGTTCACATCTAGTACACAAAGGAAAAAGATATGTCACCCCAACACTGCTGTAGCAGGTCTAATCATCATTTTATCACAGTACAGAAGTTATAGATGATGTACAGAATGTTTTACATTCTAGTACTCAGTCAATCAACACTTTTCCAGAATCACTGCAATTCCTTGTCCTCCCCCTATACAGGCTGTTCCCAAAGCAAATTGTTTGTTCTGCCTCTGAAGTTCATGTGTAAGGTGACCTGTAATTCTGGCCCCTGAAGCTGCCAATGGATGCCCTAGGGCAATGGCACCACCATTCATGTTGGTTATTTCTCTATTCAACCCAAGCTCCTTCTCTACAGCTAAGTACTGGGGTGCAAAAGCCTCATTTACCTCTACAATTTGCATGTCTTTGATATCTTTACCAGCTGCCTTCAAAGCTGCCCTGGAGGAGGGAGCTGGACCTATACCCATAATTTTAGGATCACAACCTGAAATTCCATAGGAGACTAGCCTAGCTAATGGTGTGAGATTGTGCTGTTTGACTGCTGCCTCACTGGCTATAACCAAAG