# SUPPLEMENTARY INFORMATION

## Olfactory function in the trace amine-associated receptor family (TAARs) evolved twice independently

Milan Dieris[1], Daniel Kowatschew[1], and Sigrun I. Korsching[1]*

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SI File 1: Treefile for phylogenetic tree shown in Figure 1

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# SUPPLEMENTARY INFORMATION
SI File 2: Amino acid sequences used in phylogenetic trees

# Olfactory function in the trace amine-associated receptor family (TAARs) evolved twice independently

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# Amino acid sequences of *taar* and *taar*-like genes (*tarl*) from jawless, cartilaginous and bony fish (for full species names see SI Table 1)

## Table of Contents

Most *taar* and *tarl* genes are monoexonic. Intron gains occurred rarely, and are indicated here by alternating blue and black color for the exons, with amino acids from codons spanning two exons in red. Frame shifts and stop codons are indicated by exclamation marks and asterisks, respectively.

# TAAR-like receptors (TARL)

## Jawless fish TARL

### *Lethenteron camtschaticum*

>Lec-tarl1a

MDTPTSSVAAPSSPASSNSSWEAPPPLPHCALVQGSFSCPGSALSSAQRAAWLATMSIAVASAVLGN
LLVVASVLHFRRLQTRTNAFAASLAVADLLVGLLVMPFKMTRSAYGCWFYGTAFCAAHTCLDIALCT
ASILHLACIAFDRHVAVCDPLRYAQRVTARHVTAMVALSWCCAAVISVVPVSLGWNVIGVPDEVVAA
SCADSCDFLLGAPYAVGSSVISFFGPAAFVVVAYARILREARRQGRAIACEQRRHQRQQEKQQQNED
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AGKSIWAGRAADAKSERNATKTLSIVVGVFLASWLPFFLVNVSDPLLGYSIDPRVWEAVTWLGYANS
AANPVIYGIFSPNFRAAFRAIAARSAFRAGSRDAQLGF*

>Lec-tarl1b

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>Lec-tarl1c

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>Lec-tarl2a

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RAAFSRIFCRGKGNAAVVVMVAAAWRDRRRPRPPPPACLEEESDS*

>Lec-tarl2b

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### >Lec-tarl3a

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### >Lec-tarl3b

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### >Lec-tarl3c

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### >Lec-tarl4a

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RNAIRIIFSRRLLQPGIRSAEL*

### >Lec-tarl4b

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HLCCIAYDRYLAICDPMHYRERFTWKTAALLLAAAWLGSLLYVVPVMLGWIVIGIEDMMASRTCPDN
CVFYMNKVFSSCGAFFSFVVPMTIMTLAYVKIYRVARKQARSISVQQQGSQGKSGFNKQQWAAMKRE
HNATKTVSIILGVFMFCWAPFFSTIVNDPWIDFKTNSIFWDIVNWFGHVNSAINPYLYGGFNRTFRN
AIRIMFSRKFWQPGSRSAEL*

### >Lec-tarl4c

MNSSLALGLMGGDPDHNASNVEPLICLIRESGLRCRPARMSARIANIVLIIMIVTTVLNVLGNMTII
MAISYFKQLQVLPNTFTFSLAVADIMVGVVVMPFYTTQCVYDCWFFGQKFCKVHHFLDAFMCTASTW
HLCCIAYERYLAICDPMHYRQRFTWKTAALLLATAWLGTVLYVVPVMLGWIVIGIEDMMASRTCTDN
CIFYMNKPFSSCGAVITFMVPTTVMTLAYAKIYRVARKQARSISIQQQGSQGKSGFNKQQWAAMKRE

HNATKTVSIILGVFIFCYAPFFYTIVKDAWIDFRTNSFTWDMVNFFGHVNSAINPYLYGGFNRAFRN
AIRIMFSRKFWQPGSRSAEL*

### >Lec-tarl4d

MNSSLALGLMDGDPDHNASNVEPLICLIRESGLLCRPARMSARIANIILLIMIVTMVLNVLGNMTII
MAISYFKQLQVLPNTFTLSLAVADIMVGVVVMPFYTTQCVYDCWFYGQTFCKVHHFLDAFVCTASTW
HLCCIAYERYLAICDPMHYRERFTWKTAALLLVTIWLGTVFQVVPVMLGWIVIGIEDLMASRICKNN
CIFYMNKTLSSCGAFLTFVVPVTVMTLAYAKIYRVARKQARSISIQQQGSQGKSGFNKQQWAAMKRE
HNATKTVSIILGVFIFCYAPFFYTIVKDPWIDFRTNSFTWDMVNWFGHVNSAINPYLYGGFNRAFRN
AIRIMFSRKFWQPGSRSAEL*

### >Lec-tarl4e

MAVWLATSSVLHLSSIAYDRYVAICQPLRHAERASRGRTAVMPLGRWFVVMHHNAPIVMGLMPPDIE
DAVASASCPDKCVVHMNANFGVSDALYCFVATMSVMGVARRRARSVHGAATSKSCGPKASGGTITVQ
WASLKREHNATKTLAIYIFWLPYFSVGTVEPFKDFTMNANTWELVVWPSYTNSTINPLLYA

### >Lec-tarl5a

MNSTLIKCIITYYNLNCTTPHLSYTHGLAVQGVLLFFIISTILGNMLVIASIMYFKQLQSHTNSLTL
SLAAADLLVGLVVMPFSMMRTVHSCWFYGALFCKLHCSLDYIFSTVSILHLSCVAFDRYIAICDPLH
YTSRVTNNTVAFMLIICWTCPLVYFAPFLLGWNIIGIEEMVQSRICADTCAIVKNVWFAYVDTCCAF
ITPMAIMITTYAKIYRVARRQARQVSAASVALQLNGHERQHQWALMKREHNATKTLGIIMGGFLFFW
LPNFVASLIDPVNDFQTDPLVWNIVVWLGYINSTINPLLYASFNRPFRKAFKIMFSLEITHLSTRNK
DLD*

### >Lec-tarl5b

MAQSVLKLNSTNLTNVSSNRCVLNAFQLLCPPLDLSYASSVLVQTALVICIVAIAVGNTLVIVSIAY
FRKLQSRMNVFTLSLALTDFLVGVLIMPFSMLKTVHNNCWFFARWFCKIHTSLDYVICTVSILHISC
IAYDRYNAICHPLCYTQRVNRAKVVVVLGGCWVAPVIYVAPIMLGWNIIGIEQIVASMTCPDSCVMF
KNIPFMVMDTVCAVILPMILMGVAYAKIYRVVRDHSRRIHSQHQQQVDGNALKREHNATKTLGLIMG
AFCVCWLPYCVVNVVDVFNNYQTSRWVWSVVTWLGYINSGFNPVLYALFSRPFRRAFAIVFSKRIFT
SDTRNMDLFRED*

### >Lec-tarl5c

MAQSTMEPNFTNIANLTNTSSGSCVLNAFQLMCPPPEMSYASSVIVQTALVICIVAIAVGNTLVIAS
IAYFRELQSRMNVFTLSLALADFLVGVLIMPFSMLKTVHNCWFFGRWFCKIHTSLDYIFSTASIVHI
SCIAYDRYNAICHPLCYTQRVNRVKVVVMLGGCWVAPVIYVAPIMLGWNIIGIEEIVASMTCPDSCV
MFKNTTFVILDTVCAFMVPMSIMGVAYGKIYKVARDQSRRVHSQHQQQVDGNALKREHNATKTLGLI
MGAFFLCWLLYIVVSLVDVFVHFQTSGEVWSVVVWLGYINSGFNPVLYALFNRPFRRAFAIIISKRI
FTSDKRNMDLSRED*

### >Lec-tarl5d

ATSVALQVLFVLFMAGTVVGNALVIAAVSLFGHLRTRTNAFTLSLAAVDALIALVVMPFSSTRTVRG
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QIHASRAQVTVRGWVSG*

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>Lec-tarl6a
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DPLRYSQRVTNHTVVIMLLISWFAPALFSSPILVNFNPEWSRDIIEIISCPNQCLFFVSTWLVSVVG
VCPYVLSLLTMSYVYARIYVVARRQGHQISSVSLQVHAQQQQQQQVEHTNFRQKSTAMKREHSAAKT
LGSIIGFYLLSWLPFYMVVLFFPNFKNSSAAVRITTWIGYISSAINPVLYASLNRPFRSAFVAVISC
KVLSSSRARTMDLSGVK*

>Lec-tarl6b
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DPLRYSQRVTNHTVVTMLLISWFGPALFSSPILVNFNPEWSRGIIEIISCPNQCLFFVSTWLVSVVG
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SCKVLSSTRARTMDLSGVK*

>Lec-tarl6c
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IGALVMPLRMVGTVYNCWYYDYSFCNVFYFVDYTLCNSSIFHLSCIAYDRYVAICDPLRYTQRVTDR
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AVYARIYHVARRQARQIAASSSTKVQQSGGDGNEQQRVSNMRREHNATVTLGSIIAVFFLSWLPFFI
IVLVFPFVGNFDVEYEVATWMGYISSAVNPLLYASFNRQFRGAFRKILSLTMFRAGARNAKLSE*

>Lec-tarl6d
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RYAQRVTKRTLVAMLLICWFGAALFTSPSLLSFSPQLAPSSIERVGCPDDCLFNVDIALHFFYGAFP
YFLTMLVITAMYARIYHVARTQARQIKAATTKVQSQGQQRVRNMRREHNATVTLGSIIVSFFLSWMP
FFIIVLVFPFVGNCDVEYEVATWMGYISSAVNPLLYASFNRQFRGAFRKILSLRIFRAGERNFKLSE
*

>Lec-tarl6e
MANTTKTLQCIDYHGYNCSGPSLPEKSRPIILIIISFLIVVTIFSNMLIISSVIIFRQLQTHTNILA
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RYAQRVTKRTLVAMLLICWFGAALFTSPSLLSFSPQLVPSAIKRVGCPDDCLFSVDVSLHFFYGACP
YFLTMLVITAMYARIYHVARTQARQIKAATTKVQSQGLQRVSNMRREHNATVTLGSIIVAFFLSWMP
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*

>Lec-tarl6f
VLYFVDYTLCTSSIFHLSCIAFDRYVAICDPLRYAQRITKRTLVAMLLICWFGAALFTSPSLLSFSP
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QGQQRVSNMRREHNATVTLGSIIGAFFLSWLPFYIIVLVFPFVGNCDVEYEVATWMGYISSAINPLL
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>Lec-tarl6g
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RYAQRITKRTLVAMLLICWFGAALFTSPSLLSFSPQLIPSAIKRVGCPDDCLFSVDITLHFFYGACP
YFLTMLVITAMYARIYHVARTQARQIKAATTKVQSQGQQRVSNIRREHNATVTLGSIIGAFFLSWLP
FYIIVLVFPFVGDCDVEYEVATWMGYISSAVNPLLYASFNRQFRGAFRKILSLRIFRAGERNFKLSE
*

>Lec-tarl6h
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LRYPTRVTDRTVAVMLALCWLGAAIFTTPALLSLSPTLSRGTIERGGCPDNCMFIVNLGLHFAYGMC
PYFLSMFIILLIYSKIYRVARRQARKVIAGAPTESQRTEVANGGSSGGGGGDEAAKRWKSRMKREH
NAAKTLGSIIACFMLSWLPYDILVIVFPFYKNTSVAYEVVCWIGYISSTVNPILYASINRPFRTAFG
RILRLDFFSAEVRHLELSNH*

>Lec-tarl6i
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LRYPTRVTDRTVAVMLALCWLGAAIFTTPTLLSLSPTLSRGTIERGGCPDSCMFTVDLGLHFAYGMC
PYFLSMFIILLIYAKIYRVARRQARRVTAGVPIHAQRVEVANGGSSGGGHDGDEAAKRWKSTMKREH
NAAKTLGSIIGCFMLSWLPYYILVIVFPFYKNTSTAYEVVSWIGYISSTVNPILYASINRPFRTAFG
RILRLDFFSAEARHLELSNH*

>Lec-tarl6j
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LRYRTRVTNRTVAVMLVLCWIGAAILTTPTLLSLSPTLSRGTIERGGCPDSCMFTVDVGLHFAYGIC
PYFLSMFIILLIYAKIYRVARRQARRVTAGMPIHAQTVEVANGGSSGGSDGDELARRWKSTMKREHN
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ILYLDVFSSDARHLELFEH*

>Lec-tarl6k
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RYGARVTRKTMAAMLLLCWLGSALFSSPSLVSLLSKAVSGGLIQRVRCPDDCVFSVYIGIQAVIGIS
PYFISLVVIVLVYGRIYSIARRQAQKVNSEGSRRRGQEAAASTDTLHKWRAMRREHNATKTLGVIIF
FFLLSWLPYNVTVIVFEFVAYASDVYQVTLWIGYISSAFNPILYACFNRPFRTAFHRILRLKVFTLA
ERDFALSTVQDGGH*
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## >Lec-tarl6l

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DPLRYESRVTRRTLVVMLVTCWLGSAVSSSPILLSLSPTLSVGTIERISCPNDCVFDINIGIMVVIG
YCPYFASLVVIVCIYGKIYRIARAQVIKIRAQQGGGGGGGSHRTDNDNAEALVKLRTMKREHSATKT
LGVIIGFFLISWLPYYVIVLASLALTDTLFAYRVALWIGYISSAFNPILYAAFNRPFRNAFRLMFRL
KVFGEGARDTDLSGRLK*

## >Lec-tarl6m

MANLTDTHASPGCIHYLDAFNCTGPTMSLPALSASLAIISFFVVATVLGNLLIMSTIAFFKQLQTST
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SDPMHYATRMTSRSLAAIIGFCWLGSAVFSSPILLSLSPALSEQTVARKSCADNCLFYVHMGIMFVV
GYCPYFASLLVIVCVYAKIYRIARNQMRKIRSVACKVEETTRQVIKREHNATKTLGVIIFFFLLSWL
PYYLIVLSSMAVKNTMSAYRVALWAGYISSAFNPLLYAFFNLHFRNAFKMMLGCKIFAPGARHTDLN
FLNKATNDRN*

## >Lec-tarl6n

MDNSSLASSPSCVISFSNLNCTPTSLKSKHDRAVAVFTISLFIVITILSNLLIVSAVALFRQLQTQA
NALALSLAVSDLLVGVVIMPLSLTKSVYKCWFYAPLLCHVHFFCDYWFTTASVLHLSCIAYDRYVAI
CDPLRYQQRMNRRALVVMLLFCWLCSALLSTPILLSLSPTLSQGTIAKNGCPDDCRFFISVGILFAI
GMWPYFTSVLLVVLMYGRIYRVARGQARKIAAMDRASSGLGGGDEAGRAAASRWASMKREHSAAKTL
GAILAAFIISWLPYYIIAIMLTVDESVILPYKVSVWLGYMNSAINPILYAAFNTQFRRAFKAILTFN
TYPSRAADDEMSSTKN*

## >Lec-tarl6o

MENTTSTSTSKCVISYYGLNCTKMDFSKSESALIVGVMSFFIGTTILSNLLIISAVAFFRQLQTRTN
TLALSLAVSDLLVGVVIMPLAMIKAIYKCWFYVQWFCNVQFFCDYWFTTASVLHLSCIAYDRYVAIC
DPLRYAQRVTRRTLTFMLLFCWIVSAIISTPILLSMSPTLAKGRIEMVGCPNDCRFLISVGILFTIG
MVPYFTSVLLIMLMYGRIYQVARSQARKIGTQSHGLPGVASETTSRWTNMKREHNATKTLGSIIAAF
IISWLPFYILAIVFTMYQDIFLPYKISFWIGYMNSTINPILYAVFNKQFRHAFKTMLSFKVFSSAAR
DKEMN*

## >Lec-tarl6p

MAENSSSSSSSNSGAEGLSECVVSYYGLNCTKMNFSKSESALIVGIMSFFIAVTILSNLLIISAVAF
FRQLQTRANALALSLAFSDLLVGVVIMPLAMVKSVYKCWFYARWLCNVQFFWDYWFTTASVLHMSCI
AYDRYVAICDPLRYQQRVTRRTLTFMLFFCWIASALLSTPILLSMSPTLSKGRIETVGCPDDCSFLI
SVGILFAIGMWPYFMSVLLIVLMYGRIYRVARGQARKIAAMDRASSVLGGGEEAGRAAASRWASMKR
EHNATKTLGAIIVAFIISWLPFYINAVIFTMDESVLLAVWIGYMNSAINPILYATFNKQFRHAFKEI
LSLNVFLSPADRNKEMQ*

## >Lec-tarl6q

MAENSSSSSSSNSGAEGLSECVVSYYGLNCTEMNFSKSESALIVGIMSFFIAVTILSNLLIISAVAF
FRQLQTRANALALSLAFSDLLVGVVIMPLAMVKSVYKCWFYARWLCNVQFFWDYWFTTASVLHLSCI
AYDRYVAICDPLRYQQRMNRRALVVMLLFCWIASALLSTPILLSMSPTLSKGRIETVGCPDDCRFLI
SVGILFAIGMWPYFTSVLLIVLMYGRIYRVARGQARKIAAMDRASSGLGGGEEAGRAAASRWASMKR

EHNATKTLGAIIAAFIISWLPFYIIAVIFTMDESVLLAYKVAVWIGYMNSAINPILYATFNKQFRHA
FKEILSLNVFLSPADRNKEMQ*

## >Lec-tarl6r

MQNTSVPQVHKECVIFADFNCTGPTQVREVRLVLLVVFAIFITATILGNLLIITAIASFTKLQTHAN
FLALSLAVSDLLVGVFIMPLSMMKTVYDCWFYASVLCNAHYFLDYTLTTATILHITCIAYDRYVAIC
DPLRYPTRVTVRTIAGLLVLCWLGAAIFSSPILLSFSPTLSRGNIERASCPDDCVFSVSFGILVTIG
MGPYFTAIHVVLLMYAVIYRVARRQSRKVAAEAASSSAADSSAVKNMKREHSAAKTLGAIIGTFMLS
WLPYYVVAMMSFTVDGLFIPYRVAMWIGYCSSAINPLLYASFNRPFRTAFRDIFRLRVFSGVVRRDS
GLSERSHGQPMAR*

## >Lec-tarl6s

MPNDSDDAASSTCVSFNHLNCTGPSLPPLSRHLVLALLLIFIAATILGNLLIIAAIASFRQLQTRAN
ALALSLAVSDLLVGVLCMPSSTLKTIYNCWFFPDVLCHWHFFADYMFTTASVLHVTCIAFDRYVAIT
DPLRYAARVTPRTLVAMLVFCWLGSALVSSPILLSLSNGDALSGPTIHRILCPNDCFFYISIGIMLV
IGMGPYFASMLVVVAVYARIYAVARGQARKIAASASGSQMRGHADESANSASVKSMKREHNATKTLG
AIICSFLLSWLPFYIITIISMFVNDMFLSYRITLWLGYISSIVNPFLYALLNRQFRAAFRTLLSVKV
FSVLGSRGADLMGVKKS*

## >Lec-tarl6t

MANSSCTISFYDLNCTGPSLSVRDRAIVLTLVALVNATTVAGNLLLIATVSFFRRLRSWPNVMALSL
AVSDLLVGTLVMPLATVKAVYSCWFYADLLCHWHFFLDFALTTCSILHVACIAYDRYVAVCDPLRYA
ARVTERTVGAMLALCWLGSALVSAPILFSLSPALSPNTIHRILCPDDCFFYVHGLIIFVIQMGPYIV
SVAFVVALYGQIYRAARLQARRIGGVGGGGKSSSAEATAAARSEHKATKQLGIIIGCFLLSCLPFYL
VDVVSLVDEALFVPFRITVLSGYISSALNPLLFAKFNRQLRAGFAMVLRAQLFRPGARDTDFSGGGR
RGE*

## >Lec-tarl6u

MTYSSLNNTTGHCVELFENQICSKPKLSYEDRIVAIAVLSFFISATIFGNCLIITAIAFFRQLQTNT
NALALSLAVSDLLVGAIIMPFSVNRSVYQCWFHGRVFCKVHFFLDYAICNASILCLGCIAFDRHVAI
CDPLRYAQRVTRGTLASMIVLIWVGAALLSAPILLSLSETWAKGIIEITGCLDGCHFAVHVILTLVV
GILPYFIIMLLMLLVYGRIYGVARRQSRQINNSSGSRASDADSRSKWAAMRREHNATLTLGMIVGFY
LVSWLPYFTASVLEMAFGISTSALVWATVTWFGYANSVVNPVLYATFNRPFRTAFRIIFSSELFAPG
ARRTDLHGLKVAGG*

## >Lec-tarl6v

MTYTSSNNTTGHCVESFENLICSKPKLSDEDRIVAMAVLSFLISATIFGNCLIITTIAFFRQLQTNT
NALALSLAVSDLLVGAIVMPFSALRSVHQCWLHGHIFCRVHYYLDYTFCNASILCLGCIAFDRHVAI
CDPLRYTQRVTRGTLAFMLALIWAGAALLSAPTLVSLDETWARGLMEIAGCPDGCHFAMHVGLTLVV
GILPYFIIMLLMLLVYGRIYGVARRQSRQINNSSGSRASDADSRSKWVAMRREHNATLTLGMIVGFY
LVSWLPYFTASVLEMAFGVTASALVWSTVMWFGYANSVVNPILYATFNRPFRTAFRIIFSSELFAPG
ARDADLYGLKVTGG*

>Lec-tarl6w

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PLRYQQRVTNRTVALMLLMCWLCSALFSAPILVSLSDVLSNGVMDRTSCPDECVFIVNLGLTFVIGI
CPYFLSFIILSLAYAKIFRVARAQASQIHAAGKHGADSSSSASIVGDANSKRTWLAMKREHNATKTL
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CRAFAVGARNKDLFGS*

>Lec-tarl6x

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PLRYQQRVTNRTVALMLLMCWLCSALFSAPILVSLSDVLSRGVIERTSCPDECVFIVNFGLMFMIGI
CPYFLSLIILSLAYAKIFRVARAQASQIHAAGKHGADSSSSASIVGDANSKRTRLAMKREHNATKTL
GMIIGFFLLSWLPFYIISVMDVIIDYQTDAVMWGTVTWIGYFSSAVNPILYASFNRPFRNAFLDIVS
CRAFTCRRGT*

>Lec-tarl7a

MFWLHLRTSMDNQSDVEAPGLLCVNSYNNLSCSSPRLPATQRTLALVVLISFSACTVVGNSLIVLSI
LYFRQLQTRTNAFTLSLALADMLVGLLVMPYSMMRAVYSCWFYGSFFCKVHTWFDFTFTSSSVIHLS
CISIDRYIAISDPLRYPKRLGPP**KV**ALMLVVCWSTTLAYGLPFFSGWTVLGIEEVIARGSCRDACPV
VGNMAFAFTNAFFAYLIPLCIMVTSYAKIFRIAREQAHKIRANSAHDPGVESSSSSARQQWAAMKRE
HNATKTLGIIMGVFLLFWLPYCSVAVIDPIIGYQTSATSWDVANWIAYVNSAINPVLFASFNRSFRG
AFRLIFTCRVSSSTYRNADLFNLNDSAN*

>Lec-tarl7b

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RYVAVADPLRYPQRVTRRAVALLLLCCWLSVPVYSWPVMSGWYSVGVPDGPGAFAGCREVCPVSVSA
TFGLANMLCAYAAPMLLMSLTYAKIYRLARAQARKIDAATAGLRRRGPADGAADGADGDGRRWKAAM
RREHNATKTLGVIAGVFVLCWVPYFVLSATDSLLDDATRRAAADISNWLTYVNSTLNPVLIVALNRS
FRNAFRATVACRVFAPGFRATDLFNYDDSER*

>Lec-tarl7c

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LAILITLAGNLLIIASIAFFRQLQTRSNVLVASLAAADLLVGSLIMPFSAMRTADNCWPYGDLFCRL
HTWLDFSATCSSIINLACISAERYISVSDPLRYRQRVTPRVLIAMLTLSWSGLAVYGATFLAGWNVA
GMEGVIAAESCPHSCRVFMNAATTFANVGAYVAPMLVMAAANVKTYGVARDQARKVHASGPLDAHGR
SRWEAMKREHNATKTMGIIMGVFILLWLPYILLASTEPMLGYGTTPATWEAVNWLPYINSTVNPVLL
ASFNRSFNGAFRVILGGKATRPGARGTDLYNLRDRVG*

>Lec-tarl7d

MPFSAARTAYNCWFYGDLFCRLHTWLDFSTCTSSIANLACISLERYASIAEPLRYRQMVTPRVLAAM
LLLSWSGLPLYGATFMLGWNLVGIKRQVAESSCRHDCRVYMNPASTATNVLVAYVMPMLLMIVANAK
IHRLARAQARRIEGSAMVSGRDDRASTKREHNATRTLGIITGAFILLWMPYFILVASEPLLGYGTSR
AAWEVVCWLPYLNSAVNPVLLMVFNRSFNGAFRLALKGRVLKSGCRGIDLFNFRDGNM*

>Lec-tarl7e

MNESGSNDSSRRCVWTFHQFSCTSSDLSAAERATLLAILLSISAITVAGNLLTITSILYFRQLQTRT
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SDPLRYGDRITHAALAAMLALSWISFPIDGLVFMLQWNLVGMEEETRRSCPDDCKVILNLPYAVANT
ACAFVLPMLLMALAYGRIYRLARVQSRKINSLGAQVQKMSGDAECLSKWNAMKRDHNATITLGIIIG
MFIAIWMPYFVVSATEPMVGYQAGPVAWEVINWFTYLNSTVNPILFAAFNRSFRWAFRLLVTCSAFR
PGIRSADLFNFKEGPA*

>Lec-tarl7f

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SDPLRYEQRVTRRACARMLVCSWLCLLVYGLAFMLEWNLVGLEEEVAHVCPDDCPVLLNLPFAMANT
IFACVVPMMLMTLAYGRIYQLARQQARKITSAAMGSNADSARSSLRREHSATITMGIIVGVFISLWI
PYFVVSVTEPIFGYQAGSVTWEVINWFTYINSTANPILFAAFNRPFRNAFYLILSGRMFASSCRGVD
LFDVPRALAKARG*

>Lec-tarl7g

METLNESIRNSSLLCVEVFHNFHCTSNDISEAERATLITIIIPAIAITIFGNLLTVVSILYFRQLQT
RTNVLTLFLAVADLLVGLLIMPFSAMRSVYNCWFYGWTFCKMHSWFDYTLCTLSVLLLSCISFDRYV
AISDPLRYHQRITNRTCALMLLFCWLCLPFYGVVFMMEWNLVGLEEEVAQICPDDCPVLLNLPFAMA
NTIFGCVVPMMLMTLAYGRIYQLARQQARKIASTAMGSNADSARSSLRREHSATITMGIIVGVFISL
WMPYFVVSTTESIFGYQASSLAWEFINWFTYINSTVNPILFAAFNRPFRNAFYLILSGRIFSSSYRG
VDLFNVQQGSKVNQGAKRCVSTLIGKKSDR*

>Lec-tarl7h

MLQETVQKVVTCNVSFYNLNCTLSELTQPQRVALICVFTIIITITVVGNILTIVSILYFRQLQTRTN
VLALSLALADFLVGCLIMPFSVMRTAYSCWFYGQLMCRIHTWLDYTFTTCSIFNLACISIDRYVAIS
DPLRYDQRVTYRILAVMLTICWSNIIPYGVSYMLKLNINGIESVVAAKSCPDNCYVFMNVPFGLANS
MGAYVLPMLFIMAAYSRIYVMARNQAKRISSLGDQVRASNASDLTMQSKWNAMKRDHNATKTLGMIM
VVLFIVWLPFIVVVAMEPVIGYRMDSTVWDVANWFTYFNSTMNPILFASFNNSFRNAFYLIMSGKIL
RGSYRGTDLFNFRRLEK*

>Lec-tarl7i

MKTHNATNTSVAPVCVVTFFNFNCSPPDLGDGERDILIGGFSLVIATTALGNILTITSILYFRQLQT
RTNAFAISLATADLLVGVMVMPYAVTRTAYTCWFYGKTFCKMHTWFDYTLTTSSILHLACISIDRYV
AISDPLRYEQRVTKKLVGRMLVFCWTSFIIYGLSYMLEWNIAGIEDIVASSTCPHNCPVFMNVQFAL
TNTLCAYVTPMLLMLAAYAKVYVMARAQARKISIAMLQTRSADAAVRSRWSAMKREHSATKTLGIIM
GAFVIFWVPFFFVAASEPLLGYASDPLVWDVANWFTYINSTMNPILFAAFNRSFRNAFYLIVSGKIL
RGSYRGTDLFSFKRGGGVAEMA*

>Lec-tarl7j

MSLHNESFPSVLCVVTFATFNCTPSPMTHVERALLMGTFTIAVAMTITGNMLTISSILYFRQLQTRT
NVLALSLALADLLVGLLVMPFASTRTAYGCWFYGRTFCKVHTWFDYTLCTSSILNLMCISLERYVAI
CDPLRYARRVTGATLAAMLVLCWSGVVAYGLTYLLEWNITGIEDSVQRTTCPDNCPVFMNVQFALTN

TLCAYVTPMLLMLAAYAKVYAMARAQARKISIAMLQTRSADAAVRSRWSAMKREHSATKTLGIIMGA
FVIFWVPFFVVAASEPLLGYASDPLVWEVANWFTYINSTMNPILFAAFNRSFRNAFYLIVSGNILRG
SYRGTDLFSFNDLVK*

### ***Lampetra fluviatilis***

>Laf-tarl4a

VMPFYMTQCVYDCWFYSHAFCKVHHFLDAFISTASTMHLCCIAYDRYLAICDPMHYRERFTWKTAAL
LLAAAWLGSLLYVVPVMLGWIVIGIEDMMESRTCPDNCVFYMNKVFSSCGAFFSFVVPMTIMTLAYA
KIYRVARKQARSISVQQQGGQGKSGFNKQQWAAMKREHNATKTVSIILGVFMFCWAPFFSTIVNDPW
IDFKTNSIFWDIVNWFGHVNSAINPYLYGGFNRTFRNAIRIMFSRKFWQPGSRSAEL

>Laf-tarl6a

MANRTVGPYDHCIDSFYHLNCSSPTFSMSERTAALSAITTLILATVLGNLLIITSIAYFRQLQTRTN
IMALSLAVADLLVGLTVMPYSMMKAVYKCWFYGQFFCNLQYFLDYMLTNSSIMHLGCIAYDRYVAIC
DPLRYPQRVTNHTVVTMLLISWFGPALFSSPILVNFNPEWSRGNIEIISCPNQCLFFVSTWLVSVVG
VCPYVLSLLTMSYVYARIYIVARRQGRQISSVSLQVHAQQQQQQQQAEPTNIRQKWTAMKREHSAAK
TLGSIIGVYLLSWLPFYMVVLFFPNFQNSSAAVRITTWIGYISSAINPVLYATLNRPFRSAFVAVIS
CKVLSSTRARTMDLSGVK

>Laf-tarl6b

FFCYLHYFLDYTLTTSSIIHLGCIAYDRYVAICDPLRYPTRVTDRTVAVMLALCWLGAAIFTTPTLL
SLSPTLSRGTIERGGCPDSCMFTVDLGLHFAYGMCPYFLSMFIILLIYAKIYRVARKQARRVTVGVP
IHAQRVEVANGGSSGGGHDGDEAAKRWKSTMKREHNAAKTLGSIIGCFMLSWLPYYILVIVFPFYKN
TSTAYEVVSWIGYISSTVNPILYASINRPFRTAFGRILRLDFFSAEARHLELSNH

>Laf-tarl6c

ICDPLRTAQRITKRTFVAMLFICWFGAAFFTSPSLLSFSPQLVPSAIKRVGCPDDCIFSVDVTLHFF
YGACPYFLTMLVITAMYARIYHVARTQARQIKAATTKVQSQGQQRVSNMRREHNATVTLGSIIGAFF
LSWLPFYIIVLVFPFVADCDVEYEVATWMGYISSAV

>Laf-tarl6d

ISDPLRYESRVTRRTLVVMLVTCWLGSAVSSSPILLSLSPTLSVGTIERISCPNDCVFDINIGIMVV
IGYCPYFVSLVVIVCIYGKIYRIARAQVIKIRAQQGGGGGGGGHRTDNDNAEALVKLRTMKREHSAT
KTLGVIIGFFLISWLPYCVIVLASLALTDTLLAYRVALWIGYISSAF

>Laf-tarl6e

MQNTSVPQVHKECVIFADFNCTGPTQVREVRLVLLIVFAFFITATILGNLLIITAIASFTKLQTHAN
FLALSLAVSDLLVGVFIMPLSMMKTVYDCWFYASVLCNAHYFLDYTLTTATILHITCIAYDRYVAIC
DPLRYATRVTVRTIAALLVLCWLGAAIFSSPILLSFSPTLSRGNIERASCPDDCVFSVSFGILVTIG
MGPYFTAIHVVLLMYAVIYRVARRQSRKVAADSSAVKNMKREHSAAKTLGAIIGTFMLSWLPYYVVA
MMSFTVDGLFIPYRVAMWIGYCSSAINPLLYASFNRPFRTAFRDIFRLRVFSGVVRRDSGLSERSHG
KAMAR

```
>Laf-tarl6f
ICDPLRYAQRVTRRTLTFMLLFCWIVSAIISTPILLSMSPTLAKGRIEMVGCPNDCRFLISVGILFT
IGMVPYFTSVLLIMLMYGRIYQVARSQARKIGTQSHGLPGVASETTSRWTNMKREHSATKTLGSIIA
AFIISWLPFYILAIVFTMYQDIFLPYKISFWIGYMNSTI
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```
>Laf-tarl6g
ICDPLRYAQRVTRGTLASMIVVIWVGAALLSAPILLSLSETWAKGIIEITGCPDGCHFAVHVILTLV
VGILPYFIIMLLMLLVYGRIYGVARRQSRQINNSSGSRASDADSRSKWAAMRREHSATLTLGMIVGF
FLVSWLPYFTASVLEMAFGISTSAFVWATETWFGYANSVV
```

```
>Laf-tarl7a
MLQETVQKVVTCNVSFYNFKCTLSELTQPQRVVLIWVFTIIITITVVGNILTIVSILYFRQLQTRTN
VLALSLALADFLVGCLIMPFSVMRTAYSCWFYGQLMCRIHTWLDYTFTTCSIFNLACISIDRYVAIS
DPLRYDQRVTYRILAVMLTICWGNIIPYGVSYMLKLNINGIESVVAAKSCPDNCSVFMNVPFGLANS
MGAYVLPMLFIMAAYSRIYVMARNQAKRISSLGDQVRASNASDLTMQSKWNAMKRDHNATKTLGMIM
VVLFIVWLPFIVVVATEPVIGYRMDSTVWDVANWFTYFNSRMNPILFASFNNSFRSAFYLIMSGKIL
RGSYRGTDLFNFRRLEK
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## ***Petromyzon marinus***

```
>Pm-tarl1a
MDPPSSSVAAPSSPASSNSSWAAPPPLPHCALVQGSFSCPGSALSSAQRAAWLAMMSVAMASAVLGN
LLVVASVLHFRRLQTRTNAFTASLAVVDLLVGLLVMPFKMTRSAYGCWFYGTAFCAAHTCLDIALCT
ASILHLACIAFDRHVAVCDPLRYAQRVTARHVAAMVALSWCCGAVISVVTVSLGWNVVGVPDEVVAA
SCADSCDFLLGAPYAVGSSVCSFFGPAAFVVVAYARILREARRQGRAIACEQWRHQRQQEKQQQQNE
DQQQGRQEDGVGEGGRGGARGEMTGNGGVVGKRYEIGGGRAEGLGTVGKIGSVLEGGRLTTAPAGKA
TQAVGRAADAKSERNATKMLSIVVGIFLASWLPFFLMNVSDPLLGYSIDPRAWEAVTWLGYANSAAN
PVIYGIFSPNFRAAFRVIAARSAFRAGSRDVQLGF*
```

```
>Pm-tarl2a
QVTFRAMALLTATWNATSPNDVLARYYGRTFCKAHTCLEYVFTTASILHLGAIAFDRHTAICDPLRY
RQRITPRRVAHLLAASWLLPFLYVPPVSLGWNVVGVEAAARRLSCPDSCVVLKNVGFALVDTCCAFF
APTALMLVAYAKIYRVARRQARQIAASSTGTASVVTASVKQQQQQQNHLQEQGNEQQATFRRTMKR
EHSATKTLAIILGAFVVCWCPYFVASAVDPFVGFSTEPALLSATLWLCYANSALNPVLYAAFNRRFR
AAFSRIFCRGKGNAAVVVMVAAAWRDRRRPRPPPPASPEEESDS*
```

```
>Pm-tarl2b
*RSLCESMALCVTLYESMALHVSMSLWTCSAKPPSLSLSRRYTARVTPGAVAAMLVACWLGPLLYVA
PIMLGLQSVGAEASLALACPDDCPFVMSATFSLAATSCSFVAPMIIMLAAYARIYRVARRHARSIAS
RPPAPPGGGDGAKGMAAASSS!
SAPRRWRQEYNATKTLGVILGAFFALWLPFFSAAVADGLPGGPRVDGTTWHCVTWLGYVNSAVNPVL
YASLNRAFRRAFGILFSPRELAKGRRDAEFTD*
```

>Pm-tarl2c

MDKHQTNHAAVAADMVYTNSTATPVDAEPGPTCVVLQGAFNCTGPGPLLPPLPSPLAALALAAALL!
LSAAAVLGNALVVLAVAYFARLR!
PTNALALSLAVADLLVGAVVVPFSATRAVRGCWLHGATFCQLHTCLDVMLSTASIVHLSCIAFDRYV
AICDPL**R**YTARVTPGAVAAMLVACWLGPLLYVAPIMLGLQSVGAEASLALACPDDCPFVMSATFSLA
ATSCSFVAPMIIMLAAYARIYRVARRHARSIASRPP!TPWWRRRGQGDGSG!
RLSSAPRRWRQEYNATKTLGVILGAFFALWLPFFSAAVADGLPGGPRVDGTTWHCVTWLGYVNSAVN
PVLYASLNRAFRRAFGILFSPRELAKGRRDAEFTD*

>pm-tarl3a

LLPSRLSTGRQLQTRTNAFTLSLAVADLLVGLLVMPFSATRSLYGCWFFGRTFCKVHTCLDVLLSTA
SIAHLGAIAFDRHTAICDPLRYDQRLTAGRAAALVAICWVGSALLAVGPILLGWNTVGIEELVASSC
PDACVLLMNAPFAIAGSTCSFFVPSFVMVVTYLRIYRVALHQARAVRNVVSVSSVAWEHCDINSRPE
KRTDQRRDRSATKTLGIIMVAFVTCWLPYFSLTLLDPFTGFLAEPWVWESTAWLAYMNSALNPILYP
AFNQAFRQAFRLVFTCAWRLRNVRRANLA*

>Pm-tarl4a

MYMGKYASPALALNSSIQNGTFQSHCVLTQFNLVCRQPTVPPEYAEVILIAMIMSIILNMFGNALII
AAILYFTSSLSVADILVGVVVMPFYMN*CVYNCWFYGHAFCKVHHFLHAFLPTASTMHFCCIGYDRY
LAICDPFHYQERFTRRTAVIALAATWLGSLLYVVPIMLDWIDIEEMVAERTCPDNCIFFTNKVFSSC
GAFFSFVLPMGIMTVTYAKIYRIARKQARSIGAQQHGMLGQTALGFNKQQWAAMKREHNATKTVSII
LGIFICWAPFFGTIVIDPYLNYTTKPVVWEMLNWIGHVNSAINPFLYGCFNRTFRNAICIIFSRRLL
QPGIRSAEL*

>Pm-tarl4b

MYMGKYASPALALNSSVQNGTFQSHCVLTQFNLVCRQPTVPPEYAEIILIAMIMSIILNMFGNALII
AAILYFKQLQVLPNVFTFSLSVADILVGVVVMPFYMNQCVYNCWFYGHAFCKVHHFLHAFLPTASTM
HLCCIGYDRCLAICDPFHYQERFTRRTAVIALAATWLGSLLYVVPIMLDWIVIGIKEMVAERTCPDN
CIFFTNKVFLSCGAFFSFVLPMGIMTVTYAKIYRIARKQAHSIGAQQHGMLGQTALGFNKQQWAAMK
REHNATKTVSIILGIFMICWAPFFGTIVIDPYLNYTTKPVVWEMLNWIGHVNSAINPFLYGGFNRTF
RNAICIIFSRRLLQPGIRSAEL*

>pm-tarl5a

MNSTLIKCIITYYNLNCTTPHLSYTHGLVVQGVLLFFIISTILGNMLVIASIIYFKQLQSHTNSLTL
SLAAADLLVGLVVMPFSMMRTVHSCWFYGKLLCKLHCSLDYIFSTVSILHLSCVAFDRYVAICDPLH
YTSRVTNNTVAFMLILCWTCPLVYFAPFLLSWNIIGIEEMVQSRICADTCAIVKNVWFAYVDTCCAF
ITPMAIMITTYVKIYRVARRQARQVSAASVALQLNRDERQNQWALMKREHNATKTLGIIMGGFLFFW
LPNFVASLIDPVNDFQTDPLVWNIVVWLGYINSTINPLLYASFNRPFRKAFKIMFSLEITHLSTRNK
DLD*

>Pm-tarl5b

MAQSVLKLNLTNLTNVSSNSCVLNAFQLLCPPPEMSYASSVLVQTALVICIVAIAVGNTLVIASIAY
FRELQSRMNVFTLSLALADFLVGVLIMPFSMLKTVHNCWFFGRWFCKIHTSLDYIFSTASIVHISCI
AYDRYNAICHPLCYTQRVNRAKVVVMLGGCWVAPVIYVAPIMLGWNIIGIEEVVASMTCPDSCVMFK
NTTFVLLDTVCAFMVPMSIMGVAYGKIYRVARDQSRRVHSQHQQQVDGNALKREYNATKTLGLIMGA

FCVCWLPYCVVNVVDVFNNDQTSRWVWSVVAWLGYINSGFNPVLYGLFNRPFRRAFAIVLSKRIFTS
DTRNVDLFRED*

## >Pm-tarl5c

MAQSVLKLNLTNLTNVSSNSCVLNAFQLLCPPPEMSYASSVLVQTALVICIVAIAVGNTLVIASIAY
FRELQSRMNVFTLSLALADFLVGVLIMPFSMLKTVHNCWFFGRWFCKIHTSLDYIFSTASILHLSCI
AYDRYNAICHPLCYTQRVNRAKVVVMLGGCWVAPVIYVAPIMLGWNIIGIEEVVASMTCPDSCVMFK
NTTFVLLDTVCAFMVPMSIMGVAYGKIYKVARDQSRRVHSQHQQQVDGNALKREHNATKTLGLIMGA
FCVCWLPYCVVSLVDVFVHFQTSGVVWSVVAWLGYINSGFNPVLYGLFNRPFRRAFAIVLSKRIFTS
DTRNVDLFRED*

## >Pm-tarl5d

MEPNFTKIANLTNSSSGSCVLNAFQLLCPPPEMSYASSVLVQTALVICIVAIAVGNTLVIASIAYFR
ELQSRMNVFTLSLALADFLVGVLIMPFSMLKTVHNCWFFGRWFCKIHTSLDYIFSTASIVHISCIAY
DRYNAICHPLCYTQRVNRAKVVVMLG

## >Pm-tarl6a

MENRTVGPYDHCVDSFYHLNCSSPTFSMSERTAALSAITTLILATVLGNLLIITSIAYFRQLQTRTN
IMALSLAVADLLVGLTVMPYSMMKAVYKCWFYGQFFCNLQYFLDYMLTNSSIMHLGCIAYDRYVAIC
DPLRYSQRVTNHTVATMLLISWFGPALFSSPILVNFNPEWSRGIIEIISCPNQCLFFVSTWLVSVVG
VCPYVLSLLTMSYVYARIYVVARRQGRQISSVSLQVHAQQQQQQVEHTNTRQKWTAMKREYSAAKT
LGSIIGFYLLSWLPFYMVVLFFPNFQNSSAAVRITTWIGYISSAINPVLYATLNRPFRSAFVAVISC
KMLSSTRARTMDLSGVK*

## >Pm-tarl6b

MANTTKTLQCIDYHGYNCSGPSLPEKSQPIILIIISFFIVVTILSNLLIISSVIIFRQLQTHTNILA
MSLAVSDFSLGSMVMPLRMMGTVYNCWYYDYSFCNVLYFVDYTLCTSSIFHLSCIAYDRYVAICDPL
RYAQRVTKRAIVAMLLISWLGAALFTSPSLLSFSPQLAPGAIEREGCPDDCLFSVDVSLHFFYGACP
YFITMLVIMAVYARIYHVARRQARQIKAATTKVQSQGQQRVSSMRREHNATVTLGSIIAAFFLSWLP
FYIIVLVFPFVSNFDVEYEVATWMGYISSAVNPLLYASFNRQFRGAFRKILSLRIFRAGERNFRLSE
*

## >Pm-tarl6c

MFCGLVFLALDNSTTMDNSTTGSLCSLHYENYNCTGPSLSEEDRILTLAIIIFFIIATILGNLLIIV
AIAFFRQLQTHANILALSLAVSDFFIGLLIMPFRMMHAVYQCWFYASFFCHLHYFLDYTLTTSSIIH
LSCIAYDRYVAICDPLRYPTRVTDRTVAVMLALCWIGAAIFTTPALLSLSPTLSRGTIERGGCPDNC
MFIVNLGLHFAYGMCPYFLSMFIILLIYSKIYRVARRQARRVTADVPMEAQRTEVANGGSSGGSGGG
DEAAKRWKSTMKREHNAAKTLGSIIGCFMLSWLPYDILVIIFPFYKNTSVAYEVVCWIGYISSTVNP
ILYASINRPFRMAFGRILRLDFFSAEARHLELSKH*

## >Pm-tarl6d

MDNSTTGSPCSLHYEYYNCTGPSLSEEDRALTLAIIIFFIIATILGNLLIIVAIAFFRQLQTHANTL
ALSLAVSDLLIGLLIMPFSMMHAVYECWFYASFFCHLHYFLDYTLTTSSIIHLGCIAYDRYVAICDP
LRYPTRVTDRTVAVMLALCWIGAAIFTTPTLLSLSPTLSRGTIERGGCPDSCMFTVDLGLHFAYGMC
PYFLSMFIILLIYSKIYRVARRQARRVTAGVPIHAQRVEVANGASSGGGRDGDEAAKRWKSTMKREH

NAAKTLGSIIGCFMLSWLPYYILVIVFPFYKNTSTAYEVVCWIGYISSTVNPILYASINRPFRTAFG
RILRLDFFSAEARHLELSKH*

### >Pm-tarl6e

MDNSTTGSPCSLHYEYYNCTGPSLSEEERTLTLAIIIFFIIATILGNLLIIVAIGFFRQLQTHANIL
ALSLAVSDLLIGLLIMPFSMMHAVYECWFYASFFCHLHYFLDYTLTTSSTIHLGCIAYDRYVAICDP
LRYPTRVTDRTVAVMLALCWLGAAILTTPTLFSLSPTLSRGTIERGGCPDSCMFTVDVGLHFAYGMC
PYFLAMFIILLIYARIYRVARRQARRVTAGMPIHSQRGEVANGGSSGGSDGDEAARRWKLTMKREHN
AAKTLGSIIACFMLSWLPYDIMVMVFPFYKNTSAVYEVMSWIGYISSTINPILYASINRPFRIAFGR
ILYLDVFSSEARHLELFQH*

### >Pm-tarl6f

MYNNTSNPCAALYHGYNCTGPSLPPTNLCAVVVLLSSFIAATVLGNLLIICSIAFFKQLQTFPTTLA
LSLALSDFLVGLVIMPFAVMKTAYRCWFCASAFCNAHHFLDYMFTNSSIFHITCIAFERYVAISDPL
RYRARVTRKTMAAMLLLCWLGSALFSSPSLVSLMSKSASGGLIQRVRCPNDCVFSVYIGIQAVIGIS
PYFISLVVIVLVYGRIYSIARRQAQKINSEGSRRRGQDAAAASAACTDALHKWKAMRREHNATKTLG
VIIFFFLLSWLPYNVTVIVFEFVAYASDVYQVTLWIGYISSAFNPILYACFNRPFRTAFHRILRLKV
FTLADRDFAFSTAQDGGH*

### >Pm-tarl6g

MNHTSAPSTRNPCVTFRSFNCTGPSLPENYRALLLAILAFFTLATILGNLLIISSIAFFRQLQSFPN
VLALSLAFSDFLVGLVIMPLAVTKVIYNCWFYARLYCNVHYFLDFTFTNCSILHLCSIALNRYVAIT
DPLRYESRVTRRTLVVMLVTCWLGSAVSSSPILLSLSPTLSVGTIKRISCPDDCVFDINIGIMVVIG
YCPYFASLVVIVCIYGKIYRIARAQVTKIRAQQGGGAGGGAGAGGGGGPRTDKDNAEALLKLRTMKR
EHSATKTLGVIIGFFLISWLPYYVIVLASLALADTLLAYRVALWIGYISSAFNPILYAAFNRPFRNA
FRLMFRLKVFGEGARDTDLSGRLK*

### >Pm-tarl6h

MANLTDTHASAGCILYMDAFNCTGPTMPLPARSASLAVISLFVVTTVLGNLLIISTIAFFKQLQTST
NVLALSLAVTDFLIGLIIMPMAMTKEMFNCWFYGDVFCNVHFFIDYMLTNCSMLHLGSIALQRYVAI
SDPLHYATRMTRRSLAAIIGFCWLGSAVFSSPILLSFSSALSEQTVARKSCADNCLFYVHMGIMFVV
GYCPYFASLLVIVCVYAKIYRIARNQMRKIRSVACKVEETTLQVIKREHNATKTLGVIIFFFLVSWL
PYYLIVLSSMAVKNTMSVYRVALWAGYISSAFNPLLYASFNLHFRNAFKMMLSCKIFAPGARHTNLN
YLNKATNDHN*

### >Pm-tarl6i

MDNSSLASSPSCVISFSNLNCTPTSLNSKHDRAVAVFTISLFIAVTILSNLLIVSAVALFRQLQTRA
NALALSLAVSDLLVGVVIMPLSLTKSVYKCWFYAPLLCHVHFFCDYWFTTASVLHLSCIAYDRYVAI
CDPLRYQQRINRRTLVFMLLFCWLCSALLSTPILLSLSPTLSQGTIAKNGCPDDCRFFISVGILFAI
GMWPYFTSVLLVVLMYGRIYRVARGQARKIAALSRASSGLGGGEEAGRAAASRWASMRREHSAAKTL
GAIIAAFIISWLPYYIIAIVLTVDESVILPYKVSVWFGYMNSAINPILYATFNKQFRRAFKAILTFN
TFPSRAADDEMSSTKN*

### >Pm-tarl6j

MENTTSTSASKCVVSYYGLNCTKMDFSKSETALIVGIMSFFIATTILSNLLIISAVAFFRQLQTRTN
TLALSLAVSDLLVGVVIMPLAMIKSVYKCWFYVQWFCNVQFFCDYWFTTASVLHLSCIAYDRYVAIC
DPLRYAQRVTRRTLTFMLLFCWIASAIISTPILLSMSPTLAKGRIEMVGCPNDCRFLISVGILFTIG
MVPYFTSVLLIMLMYGRIYHVARSQARKIGTQSHGLPGVSSEATSRWANMKREHNATKTLGSIIAAF
IISWLPFYILAIVFTMYEDIFLPYKISFWIGYMNSTINPILYAVFNKQFRHAFKTMLSFKVFSSTAR
DKEMN*

### >Pm-tarl6k

MAENSSSSSSSNSGSGAEGSSECVVSYYGLNCTQMDFSKSESALIVGIMSFFITVTIISNLLIISAV
VFFRQLQTRANALALSLAVSDLLVGVVIMPLAMVKSVYKCWFYARWLCNVQFFWDYWFTTASVLHLS
CIAYDRYVAICDPLRYAQRVTRRTLTFMLLFCWIASALLSTPILLSMSPTLSKGRIETVGCPDDCRF
LISVGILFTIGMWPYFTSVLLIMLMYGRIYRVARGQARKIAAMDRTSSGLGGGEEAGRVAASRWASM
RREHSATKTLGAIIAAFIISWLPFYIIAVIFTMDESVLLAYKVAVWIGYMNSAINPILYATFNKQFR
HAFKEILTLNVFLSPADRNKEMQ*

### >Pm-tarl6l

MTYSSSNNTTGHCVELFENQICSKPKLSYEDRIVAMAVLSFFISATIFGNCLIITAIAFFRQLQTNT
NALALSLAVSDLLVGAIIMPFSVNRSVYQCWFHGRVFCKVHFFLDYAICNASILCLGCIAFDRHVAI
CDPLRYAQRVTRGTLASMIVLIWVGAALLSAPILLSLSETWAKGIIEITGCPDGCHFAVHVILTLVV
GILPYFIIMLLMLLVYGRIYGVARRQSRQINNSRGSRASDADSRSKWVAMRREHSATLTLGMIVGFY
LVSWLPYFTASVLEMAFGISTSALVWATVTWFGYANSVVNPILYATFNRPFRTAFRIIFSSEMFAPG
ARGADLHGLKVAGG*

### >Pm-tarl6m

MTYTSSNNTTGHCVESFENLICSKPKLSDKDRIAAMAVLSFLISATIFGNCLIITTIAFFRQLQTNT
NTLALSLAVSDLLVGAIVMPFSASRSIHQCWFHGRTFCRVHYYLDYTFCNASILCLGCIAFDRHVAI
CDPLRYAQRVTRGTLASMLALIWVGAALLSAPTLVSLDEAWARGLMEIAGCPDGCHFAVHVGLTLVV
GILPYFIIMLLMLLVYGRIY

### >Pm-tarl6n

MMEANSTLGECHVPFLEFNCTGPGLEPTDQALVLSILILFIAATIIGNLLIVCAVLRFRQLQTRTNA
VTTSLAVADLMVGAVIIPCSMTHEVYRCWFFGQTFCRIHYFMDYWFTNASILHLGCIAFDRYVAICD
PLRYQQRVTNHTVVLMLLMCWLCSALFSAPILISLSDVLSNGVMDRTSCPDECVFIVNLGLTFLIGI
CPYFLSLFILSLAYAKIFRVARVQASQIHAAGKHGADSSSSASIVGDANSKRTWLAMKREHNAAKTL
GMIIGFFLLSWLPFYVISVVDVIIDYQTNAVLRRTVTWVGYFSSAVNPVLYASFNRPFRNAFRDIVS
CRAFAVGARNKDLFGS*

### >Pm-tarl6o

MPETNSTLGKCAAPFLQLNCTGPGLEPTNQAFVLSIIILLIVVTIIGNLLVACAVLRFRQLQTRTNA
VTTSLAVADLMVGAVIIPCSMTQEVYRCWFFGQTFCRIHYFMDYWFTNASILHLGCIAFDRYVAICD
PLRYQQRVTNRTVVLMLLMCWLCSALFSAPILISLSDVLSRGVMERTSCPDECVFIVNFGLMFIIGI
CPYFLSLITLSLAYAKIFSVARVQASQIHAAGKHGADSSSSASIVGDANSKRTWLAMKREHNATKTL
GMIIGFFLLSWLPFYIISVVDVIIHYQIDAVMWGTVTWIGYFSSAVNPILYASFNRPFRNAFRDIVS
CRAFTSRRGT*

### >Pm-tarl7a

MFWLHIRTSMDNQSDVEAPRLLCVNSYNNLSCSSPRLPAPQRTLALVVLISFSACTVVGNSLIVLSI
LYFRQLQTRTNAFTLSLALADMLVGLLVMPYSMMRAVYSCWFYGSLFCKVHTWFDFTFTSSSVIHLS
CISIDRYIAVSDPLRYPKRLGPS**KV**ALMLVVCWSTTLAYGLPFFSGWTVLGIEQVIARGSCRDACPV
VGNMAFAFTNAFFAYLIPLCIMVTSYAKIFRIAREQVNKIRANSAHVPGVEFSSSSTRQQWAAMRRE
HNATKTLGIIMGVFLIFWLPYCSVAVIDPIIGYQTSATSWDVANWIAYVNSAINPVLFASFNRSFRG
AFRLIFTCRVSSSTYRNADLFNLKDSAN*

### >Pm-tarl7b

PRSSRGTIAGNLMVMAFIAYFRHLQTRTNALALSLALADFLVGLLIMPYSTMRSVDRCWPYGGGVFC
RVHTWLDFSLTTSSVVHLCCISYDRYVAVADPLRYPQRVTRRAVALLLLCCWLSVPVYSWPIMSGWY
SVGVPDGPGAFPGCREVCPVSVNATFGLANMLCAYAAPMLLMSLTYAKIYRLARAQARKIDAATAGL
RRLGPADGAADDGDGGRWKAAMRREHNATKTLGVIAGVFVLCWVPYFVLSASDSLLDDATRRAAADI
SNWLTYVNSTLNPVLVVALNRSFRNAFRATVACRVFAPGFRTADLFNYDGSER*

### >Pm-tarl7c

*VYRSLCESRQLQSRSNVLVASLAVADLLVGLLIMPFSAARTAYNCWFYGDLFCHLHTWLDFSTCTS
SIANLACISLERYASIAEPLRYRQMVTPRVLAAMLLLSWSGLPLYGATFMLGWNLVGIKRQVTESSC
RHDCRVYMNPASTATNVLVAYVTPMLLMIVANAKIHRLARAQVRRIEGSAMVSGRDDRASTKREHNA
TQTLGIITGTFILLWMPYFILVASEPLLGYGTSRAAWEVVCWLPYLNSAVNPVLLMVFNRSFNGAFR
LALKGGVLKSKCRGIDLFNFRDGNM*

### >Pm-tarl7d

MNESGSIDSSRRCVWTFHQVSCTSSDLSAAERATLLAILLSISAITIAGNILTIASILYFRQLQTRP
NVLTLSLAVADLLVGLLIMPFNAMSSMHNCLFYGRVSCRVHTWLDYIFCTSSIVHLSCISFDRYVAI
SDPLRYSDSVTHAALAAMLALSWFSFPIDGLVFMMQWNLVGLEEETRRSCPDDCEVILNLPYAVAIT
TCAFVLTMLLMALAYDRIYRLARVQSREINSLGAQVQKASSDGECLSKWNAMKRDHNATITLGIIIG
IFIVIWMPYFVVSATEPMVGYQAGPVAWEVINWFTYLNSMANPILFAAFNMSYRWAFRLLVMCSAFR
PGIRGVDLFNFMERPA*

### >Pm-tarl7e

METLNESIRNSSLLCVEAFHNFHCTYNDVSEAERAILIAIIIPAIAITIFGNLLTVVSILYFRQLQT
RTNVLTLFLAVADLLVGLLIMPFSAMRSVYNCWFYGWTFCKIHSWFDYTLCTLSVLLLSCISFDRYV
AISDPLRYHQRITNRTCALMLLFCWLCLPFYGLVFMLEWNLVGLEEELAQICPDDCPVLLNLPFAMA
NTIFGCVVPMILMTLAYGRIYQLARQQARKITSTAMGSNVDSARSSLRREHSATITMGIIVGVFISL
WMPYFVVSTTESIFGYQASSLAWEFINWFTYINSTVNPILFAAFNRPFRNAFYLILSGRIFSSSYRG
VDLFNVQHGSKVNQGAKRCVSTLISKESDR*

### >Pm-tarl7f

MPLHNESFPSVLCVVTFATFNCTPSQMTNVERALLMGAFTIAVATTITGNMLTISSILYFRQLQTRT
NVLALSLALADLLVGLLVMPFASTRTAYGCWFYGRTFCKVHTWFDYTLCTSSILNLMCISLERYVAI
CDPLRYARRVTGATLVAMLVLCWSGVVAYGLAYLLEWNIAGIEDSVQQTTCPDNCPVFMNVQFALTN
TLCAYVTPMLLMLAAYANVYAMARAQARKISIAMLQARSADAAVRSRWSAMKREHSATKTLGIIMGA

FVVFWVPFFVVAASEPLLGYASDPVVWEVANWFTYINSTMNPILFAAFNRSFRNAFYLIVSGKIMRG
SYRGTDLFSFNGSGK*

## Cartilaginous fish and tetrapod TARL

### >Cm-tarl2

MDTSHSPPFNYTLSCNSSESVPYTARQVIQCVTTLSVLTIITLLTVLGNVLVIASIAYFTKLQTPTN
AFILSLATADILVGLVVMPFSMVKAVFGWYFGRIFCKIHSIMDVMLCTSSIVNLSCIAFDRYFAVCY
PLKYRFTMSRKRVTFLLLICWILPALVSIVPLVLDLHVIGLEDSFEQLDSQDCVFVVNIPYSVTASI
IAFYLPMPVILVAYAKIFLVATNQVREIAARQQGMNLEMIQQNSSIRKERKAAKTLGIIIGCFLLCW
VPFFTLNIIDPLLGYQADSILIEVFLWLGYLNSGLNPFLYAFFNKSFRRAFSMIISCKIITKDCHYN
SLAGSTKLNTRLKTISRQFTLTSELFDEEE*

### >Le-tarl2

MLSAVIICPTSQVVNVLIYNCSAHRNSSAIVPRATWQIIEQVFILTVLTI!
ILGAFLGNLLVIVSIIYFTKLRTVTNAFLLSLAVADFLVGIIVMPFSMIKVMFGWYFGKAFCTIHTV
MDVMLCTSSIMNLSCIAFDRYYAV*YPLRYRFRVSQKRVTTLLLVCWVLPGLVSFVPLLLGLHLTGL
ETIHSQLDPHDCVFIVNIPYALCASVIS!YLPMLVMLAAYGKIFQV!
IQARQIYTMENGSHEMDATRFHHSTSTKKERKAAKTLGVIIGCFLFCWLPFFTANIANALLGYQVHH
IVLEVFVWLGYVNSALNPLLYALFNKSFRRAFGLIL

### >Rt-tarl1

MQNTSGLFKVSTSSGWRMADRCLSSIGSPAVRTGLYLFIMVIMAATLAGNFLVVLAVVYFKQLRSAT
NAFVLSLSIADFFVGIMVMPYSMSRTIEGCWHFGPTFCQIHSSLDVMFCTASILHLSCIALDRYYAI
CDPLVYRCKMSPSRVVVLLLACWVVPAAISVIPIMLQLHRLGVDPDLLTNRSCVLMVNQTYAIWASL
ISFYLPMVVMLVAYWKIYQAARKQAIQINAMDNQVQGYASGLATAHVRKQSNKRERKAAKTLGIIIG
IFLSSWLPFFMANIVDPFLGYKIDRGTWEVLVWLGYSNSSMNPILYGVVNRSFRRAFLIIISCKICV
SRSLQKHRLIQQ*

### >Rt-tarl2

MFSAIIISTSSQEMNTTPFNNWTTHSNSSGKASSATWQVIDQVVVFSVLTVIIAGTIFGNLLVIASI
AYFTKLRTPTNAFIVSLAVADFLVGIIVMPFSMAKLVFGWYFGKAFCKIHTIMDVMLCTSSIMNLSC
IAFDRFYAVCYPLKYRFRMSQKRVTVLLLICWFVPALMSFVPLLLDVHLRGLEAILLPFDPHSCVFM
VNIPYAVSASVIAFYFPMLVMLVAYGKIFLVARIQARQVYTIENGLEGRNTLTRCQNSSMKKERKAA
KTLGIIMGCFLICWLPFFTTNIVNPLLGYPAHHILLEVFLWLGYVNSTLNPLLYAFFNQSFRRAFYM
VIGCKILASDCQNNNLSDSIRQNTQLATLSR*

### >Xl-tarl1

MLNTSKWLQNASRSTNSPDESCSSVVSSSTFKLILYSLTGGLIVTTFLGNILVITSIAYFKHLHSPT
NSFVLSLAVADFLVGGLVMPFSMIRTIEGCWYFGSVLCRLHSSLDVMLCSASILHLSCIAFDRYYAV
CNPLLYSYKMSTRRVSVLICTCWVIPMLISFAPIMLGLHLLGMEHLLQEGTCLFVVNHIYSVSASLI
TFYCPMTIMFVAYCKIYRAARKQALQIHDMKRNVTTQYGGDCSMKKRKYSLKRERKAAKTLGVIMGL

FLFFWSPFFTANIVDPLIGYKMGMVGWEVFLWLGYVNSALNPFLYGLLHKSYRRAFFMIIGCKTCYS
ATSLNIDLSSTKQEKVKRKTTDLH*

### >Xt-tarl1

MAVASTTASSPMDSCSSVVSSSTSKLILYLLTSGLIMTTFLGNILVISSIVYFKQLRSPTNSFVLSL
AVADFLVGVMVMPYSMVRSIEGCWYFGSGFCRLHSSLDVMLCSASILHLSCIAFDRYYAVCNPLLYG
YKMSTRRVSILICTCWFIPVLISFAPIMLGLHLLGMEHLWQEGACLFVVNQIYSVCASLIAFYCPMI
IMLVAYCRIYRAARNQALRIHAMERNVSSGNASDGPMKKRKYSLKRERKAAKTLGVIMGLFLLFWTP
FFTANIVDPLIGYKMGTVEWEVCLWLGYVNSALNPFLYGLFHKSYRRAFFMIVGCQTCYSGTSQNIE
LSTAKQEKVRRQMNVLH*

## Bony fish TARL

### >Aa-tarl1

MANTSAAANVSVDTGGDSTPCVPWRSQGSRVALYMFIMAGIACTVVGNFLVVLAIAYFKRLQSPTNS
FVMSLAVADFLVGLIVMPYSMVRTVEGCWYFGPTFCEVHSSLDVMLCTASIFHLSCIAFDRYYAVCN
PLVYAFKMSRVRVGLLIVVCWVVPLLISFGPIMLGLHKVGIDIQLPEGICAFLVNRVYAVMASLVAF
YLPMVIMLVAYWKIYKAAKRQAMQISAMEHQMTVHGLNSAGRKQKQRQNCMRRERKAAKTLGIIMGA
FLLFWLPFFTTNVVDPFIEYRTAGVVWDVFLWLGYVNSSLNPFLYAFFNRSFRRAFFMIMGCRICLP
GSPASIDLSLTKRDANEHIEN*

### >Ac-tarl1

MDNSTLGWLGDDNTSLQLELQPCALLRHQVSRIFLYAFLSFGIICTVVGNFLVVLSIAYFKQLQSPT
NCFVMSLAVADCLVGLVVMPYSMIRTVEGCWYFGSLFCQIHSSLDVMLCTASIFHLSCIAFDRYYAV
CNPLVYSLKMSHKRVALFIAVCWVVPILISFGPIMLDLHTAGVNILIPKDLCVFLVNRIYAVMASLV
AFYLPMAIMLVAYWKIFKAAKRQARQISAMESQMAAGVGKDSSKKKRHRNAMKRERKAAKTLGIIMG
VFLIFWMPFFTVNIVDPFIEYSTEVIVWDLFLWLGYINSSLNPFLYGLFNRSFRRAFLMFMGCRVCL
PGSSSGMELSHTRKEANECADQS*

### >Af-tarl1

MDNGSLGLLGDANTSLQNELQSCITLRNQVSRIFLYAFLSVGIVCTVVGNFLVVLSIAYFKQLQSPT
NSFVMSLAVADCLVGLVVMPYSMIRTVEGCWYFGVQLCKLHSSLDVMLCTASIFHLSCIAFDRYYAV
CNPLVYSLKMSRSRVALLIVICWAVPTLISFGPIMLDLHIADVDILLPKNVCVFLVNRIYAVMASLV
AFYLPMAVMLIAYWKIFKAAKRQARQISAMESQMAAGVGKDSSKKQRHRNTMKRERKAAKTLGIIMG
VFLIFWMPFFTVNIVDPFIEYSTEVVVWDIFLWLGYINSSLNPFLYGFFNRSFRRAFLMFIGCRVCL
PGSSPGMELSHTKERGK*

### >Aj-tarl1a

MANTSAAANVSVDTGGDSTPCVPWRSQGSRVALYMFIMAGIACTVVGNFLVVLAIAYFKRLQSPTNS
FVMSLAVADFLVGLIVMPYSMVRTVEGCWYFGPTFCEVHSSLDVMLCTASIFHLSCIAFDRYYAVCN
PLVYAFKMSRVRVGLLIVVCWVVPLLISFGPIMLGLHKVGIDIQLPEGICAFLVNRVYAIMASLVAF
YLPMVIMLVAYWKIYKAAKRQAMQISAMEHQMTVHGLNSAGRKQKQRQNCMRRERKAAKTLGIIMGA

FLLFWLPFFTTNVVDPFIEYRTAGVVWDVFLWLGYVNSSLNPFLYAFFNRSFRRAFFMIMGCRICLP
GSPASIDLSLTKRDANEHIEN*

### >Aj-tarl1b

MPCVSAFIFPAAERSHNHTETGFSNCSAGDHDSMESMKVLLLFLLLPIIVFAILGNLFIVLSVAYFR
QLQTSTNAFIVSLATADFLVGALVMPFSLVRSVDRWRFGQLFCTAHFLLDVILCTASIFNLSCVALD
RYLAVCDPLRYPARMSAARVAKLLLLSWLIPVSGSCLLVVADLHTQSGEGVLTGRGGEECFPEMRAP
YGVMASVLSFFLPMAFVVAAYGRIFQEAQRQARQIQAAEAHVRQSHPAQSPSVPQATPGIAARKAGK
ATRTLGILLGGFLLCWLPFFSVNVGHPLCGRPVGRQVQECVLWLGYANSALNPVLYAFVNRAFRRSF
VILLACGILGRRLQDGPLDPGASRNTGPELGSVAR*

### >Al-tarl1

MDNISLEWTREANTSLQTEMSCATLRNQVSHIFLYTFLSAGIVSTVVGNFLVVLSIAYFKQLQSPTN
CFVMSLAVADCLVGLLVMPYSMIRTVEGCWYFGSLFCKLHSSLDVMLCTASIFHLSCIAFDRYYAVC
NPLVYSLKMSPNRVALLIAVCWAVPMLISFGPIMLDLHIADIDIPIPEDMCVFLVSRIYAVMASLVA
FYLPMAVMLVAYWKIFKAAKRQAQQINAMESQMAAGVGKDSSKKKRHRNTMKREGKAAKTLGIIMGV
FLIFWMPFFTINIMDPFINYSTEVVVWDVFLWLGYINSSLNPFLYVYFNRCFRRAFLMFIGCKVCLP
GISPGMELSHSKKEAN*

### >Am-tarl1

MANSSDWLEDSNASLVGDLEACTTVRSPGSRIALYIFIIIGIFCTVVGNFLVVLAIAYFKQLQSHTN
SFVMSLAVADFLVGLVVMPYSMVRTVEGCWHFGATFCHLHSSLDVMLCTASIFHLSCIAFDRYYAVC
NPLVYSFKMSRSRVALLIVVCWAVPLLISFGPILLGLHKLGVNVSLPENVCVFLVNRVYAVIASLVA
FYLPMATMLFAYWKIYKAAKRQAMQISAMEAQMAAGVGKDSSKKQKHRNSMRRERKAAKTLGIIMGV
FLLFWLPFFTVNIVDPFIDYSTAGVIWDVFLWLGYVNSSLNPFLYGFFNRSFRRAFLMIMGCRICLP
GSAPGMDLSLSRKDANERTENQ*

### >Ar-tarl1

MQCFFFGRFQEAMANTSAAANVSVDTGGDSTPCVPWRSQGSRVALYMFIMAGIACTVVGNFLVVLAI
AYFKRLQSPTNSFVMSLAVADFLVGLIVMPYSMVRTVEGCWYFGPTFCEVHSSLDVMLCTASIFHLS
CIAFDRYYAVCNPLVYAFKMSRVRVGLLIVVCWVVPLLISFGPIMLGLHKVGIDIQLPEGICAFLVN
RIYAVMASLVAFYLPMVIMLVAYWKIYKAAKRQAMQISAMEHQMTVHGLNSAGRKQKQRQNCMRRER
KAAKTLGIIMGAFLLFWLPFFTTNVVDPFIEYRTAGVVWDVFLWLGYVNSSLNPFLYAFFNRSFRRA
FFMIMGCRICLPGSPASIDLSLTKRDANEHIEN*

### >Ar-tarl2

MPCVSASIFPAAEQSHNHTETGFSNCSAGNHDSTESMKVLLLFLLLPIIVFAILGNLFIVVSVAYFR
QLQTSTNAFIVSLATADFLVGALVMPVSLVRSVDRWRFGRLFCTAHFLLDVILCTASIFNLSCVALD
RYLAVCDPLRYPARMSAARVTKLLLLSWLIPVSGSCLLVVADLHTQSGEGVLTGRGGEECFPEMRAP
YGVMASVLSFFLPMAFVVAAYGRIFQEAQRQARQIQAAEAHVRQSHPAQSPSVPQATPGIAARKAGK
ATRTLGILLGGFLLCWLPFFSVNAGHPLCGRPVGRQVQECVLWLGYANSALNPVLYAFVNRAFRRSF
VILLACGILGRRLQDGPLDPGASRNTGPELGSVAR*

>Bp-tarl1

MANHTSETPASFNFTDVLELDCSILRNQTSQVFLYIFLSLVIICTVVGNSLVVLSIAYFKRLQSATN
FFVLSLAVADCLVGLIVMPYSMVRTIEGCWIFGPLFCQIHSSLDVMLCTSSIFHLSCIAFDRYYAVC
NPLCYSLKMSNNRVVFLIILCWGVSSLISFGPVMLELHVANTDIEIPKDSCVFVVNQIYAVLASVVS
FYLPMLTMLLAYWKIYKVARKQARQISAMESQMGKDTSKKKRHRNAMKREGKAAKILGIVMGVFLLF
WMPFFTINVVDPFIGYRTEAVVWDVFLWLGYLNSSLNPLLYGFFNRSFRRAFLMFIGCRVCLHQPLS
WVELSQTKKDVQNEQRN*

>Cc-tarl1a

MENSSEWSNISLDSDFEPCATLRSSGSRVALYVFIIAGIVCTVVGNFLVVLAIAYFKQLQCPTNSFV
MSLAVADFLVGLVVMPYSMVRTVEGCWYFGPTFCHLHSSLDVMLCTASIFHLSCIAFDRYYAVCNPL
VYSFKMSRKRVGLLIVVCWAIPFLISFGPILLGLHKLGMDVPLTENMCIFLVNRVYAVMASLVAFYL
PMVTMLVAYWKIYKAAKRQAMQISAMEAQMAAGVGKDSSKKQKHRNSIRRERKAAKTLGIIMG!
FLLFWLPFFTVNIVDPFIEYGTAAVIWDVFLWLGYVNSSLNPFLYGFFNRSFRRAFLMIMGCRICLH
GTAQGMDLSHSKRDANERTDNQ*

>Cc-tarl1b

MENSSEWINISLDSEFEPCATVRSSSSRVALYIFIITGITCTVIGNFLVVLAIAYFKQLQCPTNSFV
MSLAVADFLVGLVVMPYSMVRTVEGCWYFGPTFCHIHSSLDVML*TASIFHLSCIAFDRYYAVCNPL
VYLFKMSRKRVGLLIVVCWAIPFLISFGPILLGLHKLGMDVPLPANVCIFLVNRVYAVMASLVAFYL
PMVTMSVAYWKIYKAAKRQAMQISAMEAQMAEGVGKDSSKKQKHSNSIRRERKAAKTLGIIMGGFLL
FWLPFFTVNIVDPFIEYGTAAVIWDVFLWLGYVNSSLNPFLYGFFNRSFRRAFLMIMGCRICLHGTT
QGIDLSNSKRDASEHTDKK*

>Ch-tarl1

MNASWLDESNASVTGVIESCAILRNPGTRVALYTFFLAGIVCTVVGNFLVVLAIAYFKQLQSPTNCF
VMSLAVADFLVGLVVMPYSMVRTVEGCWHFSATFCQLHSSLDVMLCTASIFHLSCIAFDRYYAVCNP
LVYSFKMSRARVALLIVVCWAVPLLISFGPILLGLHKAGVAIPLPENMCVFLVNRIYAVMASMVAFY
LPMAIMLVAYWKIYKAAKRQAMQISAMESQMAAGVGKDSSKKQRHRNSLRRERKAAKTLGIIMGVFL
LFWLPFFTVNIVDPFIDYSTAGEVWDVFLWLGYVNSSLNPFLYGLFNRSFRRAFFLIMGCRICLPGS
NPSMDLSHSKRDGNDN*

>Cn-tarl1

MENGSREWPGNSNASVQIELLACVTMRSHISRIFLYTFLSVGIVCTVVGNFLVVLSISYFKQLQSPT
NSFVLSLAVADCLVGLLVMPFSMIRTVEGCWYFGSLFCKFHSSLDVMLCTASIFHLSCIAFDRYYAV
CNPLVYSLKMSNSNVALLIAICWTVPMLISFGPIMLDLHIANVDILIPSDLCVFLVSRVYAVMASLV
AFYLPMAVMLVAYWKIYKAAKRQSKQISAMESQMAAGVGKDSSKKKRHRNTMKREGKAAKTLGIIMG
VFLVFWMPFFTVNIVDPFIEYSTEVVVWDVFLWLGYINSSLNPFLYGFFNHCFRRAFIMFIGCRVCL
PGISPGMELSHSKKVKN*

>Cr-tarl1

MCFDRLNLTMDNSSLGLLGDANTSLQIELESCITLRNQVSRIFLYVFLSVGIVCTVVGNFLVVLSIA
YFKQLQSPTNSFVMSLAVADCLVGLVVMPYSMIRTVEGCWYFGVLLCQLHSSLDVMLCTASIFHLSC
IAFDRYYAVCNPLVYSLKMSHSRVALLIVICWAVPTLISFGPIMLDLHIAGVDILLPKDVCVFLVNR
IYAVMASLVAFYLPMAIMLIAYWKIFKAAKRQAMQISAMESQMAAGVGKDSSKKRRHRNTMKRERKA

AKTLGIIMGVFLIFWMPFFTVNIVDPFIEYSTEVIAWDIFLWLGYINSSLNPFLYGLFNRSFRRAFQ
MFMGCRVCLPGSSPGMELSHTKKEANERAD*

>Cs-tarl1

MDYGSLGLSRDYNRSFQIEIESCPAPRSQASRVLLYAVFFAVITCTVFGNFLVVLSIAYFKQLQSPT
NSFVMSLAVADCLVGLIVMPYSMVRTVDRCWYFGALFCRIHSSLDVMLCTASIFHLSSIAFDRYYAV
CNPLIYSLKMSRSRVALLIVACWVVPMFISFAPIMLDLHVAGVNVYLPEELCLFLVNRIYAVMASVV
AFYLPMVIMLAAYWSIFKAARRQAQQISVIESQMAAGVGKDTSRKRRHRNTIKRERKAAKTLGIIMG
VFLIFWMPFFTVNILDPFIDYSTEVVVWDVSLWLGYINSSLNPFLYGFFNRSFRRAFLMFLGCKVCL
PGTSSGMELSQTRKEPSGRTDKA*

>Cv-tarl1

MENGSREWPGNSNASVQIELLACVTMRSHISRIFLYTFLSVGIVCTVVGNFLVVLSISYFKQLQSPT
NSFVLSLAVADCLVGLLVMPFSMIRTVEGCWYFGSLFCKFHSSLDVMLCTASIFHLSCIAFDRYYAV
CNPLVYSLKMSNSNVAMLIAICWTVPMLISFGPIMLDLHIANVDILIPSDLCVFLVSRVYAVMASLV
AFYLPMAVMLVAYWKIYKAAKRQSKQISAMESQMAAGVGKDSSKKKRHRNTMKREGKAAKTLGIIMG
VFLIFWMPFFTVNIVDPFIEYSTEVVVWDVFLWLGYINSSLNPFLYGFFNHCFRRAFIMFISCRVCL
PGISPGMELSHSKKEKN*

>Dl-tarl1

MDNSSLGLLGDVNTSLKTEIQSCTTLRNQASRIFLYAFLSVGIVCTVVGNFLVVLSITYFKQLQSPT
NSFVMSLAVADCLVGLLVMPYSMIRTIEGCWYFGVLFCRLHSSLDVMLCTASIFHLSCIAFDRYYAV
CNPLLYSLKMSRSRVALLIVVCWAVPMLISFGPIMLDLHIAGVDVLLPEDVCVFLVNRIYAVMASLV
AFYLPMAIMLVAYWKIFKAAKRQARQISAMESQMAAGVGKDSSKKQRHRNTMKRERKAAKTLGIIMG
VFLIFWMPFFTVNIVDPFIEYSTEVVVWDIFLWLGYINSSLNPFLYGLFNRSFRRAFLMFMGCRVCL
PGSSPGMELSHTRKEANERADQP*

>Dr-tarl1

MENTSEWSNNSLDSDFEACATLRSFGSRVALYLFIITGILCTVVGNFLVVLAIAYFKQLQCPTNSFV
MSLAVADFLVGLVVMPYSMVRTVEGCWYFGPTFCHLHSSLDVMLCTASIFHLSCIAFDRYYAVCNPL
VYSFKMSRKRVGLLIVVCWAIPFLISFGPILFGLHKLGVDIPLPENMCVFLVNRIYAVMASLVAFYL
PMVTMLVAYWKIYKAAKRQAMQISAMEAQMAAGVGKDSSKKQKHRNSIRRERKAAKTLGIIMGVFLL
FWLPFFTVNIIDPFIEYGTAVVIWDVFLWLGYINSSLNPFLYGFFNRSFRRAFLMIMGCRICLHGSA
QGMDLSHSKRDGNERTDN*

>El-tarl1

MDNSSLGWSADIDVVSNTSSSPRGSVEDLCATSARRRASRVTLYAFLTAGIVCTVVGNFLVVLAIAY
FKQLQSPTNSFVTSLAVADCLVGLVVMPYSMVRTAEGCWLFGTVFCRIHSSLDVMLCTASIFHLSCI
AFDRYYAVCNPLVYHQKMSQGRVALLIVACWAVPLFISFGPIMLGLHEAVAPAAPDNTCVFLVNRIY
AVAASLVAFYLPMGVMLAAYWKIYRAAKRQAMQISAMESQFSAGVGKDSSKEQRHRNAMRRERKAAQ
TLGIIMGVFLLFWLPFFTVNIVDPFVDHGTAAEVWEVFLWLGYVNSSLNPFLYGLFNRSFRRAFVMI
MGCRICAQSLSPGMDLSKEGNEHTNK*

>El-tarl2

MMFLASNRSTTDSCVNLSAPGGHSESTSGTLQSTTVKVCVVCILLPIPVLAILGNILIWASVVRFRS
LQTPTNSFIVSLATADFLVAVLVMPFSLVGSVGTWCFGQNFCVAHFLLDLTLCTTSIFNLSCVALDR
YVAVCDPLHYPARMSTRRVTLLLFLSWLIPLLVSSLCVSLGTYSLNAPSGHRGAQQESQTCVAQFHT
PYAVAVSTVCFFIPVLFMLFAYGKIFMAAQRQARWIHAIENQVRQLHTAQNPSRDDPNQPHPARRVG
ARVGGFSIRKEKKAARTLGLIMGVFLLCWLPHFSVNIAFSLWGTRISPVVLDAFMWLGYANSSLNPF
IYASFNKDFRHAFAAILGFRILGRRIRGCLVATQEVSRRVQTGVTMETISK*

>Fh-tarl1

MENSSLAWPGNDSTSLQIELPSCATLRSQISRILLYAFLSAGVVCTVVGNFLVVLSISYFKQLQSPT
NSFVLSLAVADCLVGLLVMPFSMIRTVEGCWYFGPLFCKFHSSLDVMLCTASIFHLSCIAFDRYYAV
CNPLVYSLKMSNSHVAQLIAICWTVPMLISFGPIMLDLHIAYVDIFIPSDVCVFLVNRIYAVMASLV
AFYLPMAIMLVAYWKIFKAAKRQAKQISAMESQMASGVGKDSSKKKRHRNTMKREGKAAKTLGIIMG
VFLIFWMPFFTVNIVDPFIEYSTEVVVWDVFLWLGYINSSLNPFLYGFFNRCFRRAFLMFLGCRVCL
PGISPGMELSHSKKGIN*

>Ga-tarl1

MENISLDLLGEGNTSLQNELYSCLTLRNQVSRIFLYAFLSVGIVCTVVGNCLVVLSIAYFKQLQSPT
NSFVMSLAVADCLVGLLVMPYSMIRTMEGCWYFGVLLCQLHSSLDVMLCTASIFHLSCIAFDRYYAV
CNPLLYSLKITRGRVALLIVICWAVPTLISFGPIMLDLHIAGVDIPLPGDVCVFLVNRIYAVMASLV
AFYLPMAIMLIAYWKIFKAAKRQAVQISAMESQMAAGVGKDSSKKQRHRNAMKRERKAAKTLGIIMG
VFLIFWMPFFTVNIVDPFIEYTTEVVVWDTFLWLGYINSSLNPFLYGFFNRSFRRAFLMFMGCRVCL
PGTSPGMELSHTRKEANEHSDQP*

>Gm-tarl1a

MDNSSLDPRTPEPSDTSLHGTAPPCTTERHQASRLLLYSLLSAAVVCTVVGNLLVVLSIAYFKQLQS
PTNCFVMSLAVADSLVGLVVMPFSMLRTLDGCWRLGALFCRLHSSLDVMLCSASIFHLSCIAFDRYY
AVCNPLLYSLVMSRDRVAALIVGCWAIPMLISFGPIMGGLHAVGVDVPLPPDVCVLLVNRAYAVTAS
LVAFYLPMAVMLVAYWKIYKAAKRQAMQISAMESQMAAGVGKDSSKKQRHRNAMRRERKAAKTLGII
MGVFLLFWMPFFTVNIVDPFIEHSTHALVWDVFLWLGYINSSLNPFLYGLFNRSFRRAFLMIMGCRI
CLPGASPRIDLSQSQEGAERTDQQ*

>Gm-tarl1b

MFERPPRHRPPATRSGTPGPPPARSTASPAPPWSAPWVGNLLVVLSIAYFKQLQSPPTASSCPLAVA
DSLVGLVVDALQQLRTWTALRAARAPLLPPCHPAWKSCCAAASISTSAASPSTATTPLSTPLPLLAG
DVAGPRGRRLIVGCWAIPMLISFGPIQWGASTRSAWMSPAPDVCVLLVNRAYAVTASLVAFYLPMAV
MLVAYWKIYKAAKRQAMQISAMESQMAAGVGKDSSKKQRHRNAMRRERKAAKTLGIIMGVFLLFWMP
FFTVNIVDPFIEHSTHALVWDVFLWLGYINSSLNPFLYGLFNRSFRRAFLMIMGCRICLPGASPRIV
DLSQSQEGC*

>Hb-tarl1

MDNSTLGWLGDDNTSLQLELQSCTLLRHRVSRIFLYAFLSVGIICTVVGNFLVVLSIAYFKQLQSPT
NCFVMSLAVADCLVGLVVMPYSMIRTVEGCWYFGSLFCRIHSSLDVMLCTASIFHLSCIAFDRYYAV
CNPLVYSLKMSHRRVALLIAVCWLVPILISFGPIMLDLHVAGVDMVIPKDLCVFLVSRIYAVMASLV
AFYLPMAIMLVAYWKIFKAAKRQARQISAMESQMAAGVGKDSSKKKRHRNAMKRERKAAKTLGIIMG

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>Hc-tarl1

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>Ip-tarl1

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GSAPIMDLSQSKKDTNERTEKQ*

>Km-tarl1

MDNSSLEWSGDGNASLRTELQSCATLRNQVSRIFLYAFLSAGIVSTVVGNFLVVLSIAYFKQLQSPT
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>Lac-tarl1

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CNPLVYSLKMSRNRVALLIVICWAVPMLISFGPIMLDLHIAGVDILLPKDMCLFLVNRIYAIMASLV
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>Lac-tarl2

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ASPSACTPRHLLLC*AAACSRIFRPAWPHFMSPLPLQPQLSPPFPWVSCCLRVWEHFHGSHKQARWI
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>Lb-tarl1
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>Lc-tarl1
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>Lo-tarl1
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>Lw-tarl1
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SFRRAFLMIMGCRICLFGTAQGMDLSHSKRVPVSAQTTSRL*
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>Mc-tarl1
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>Mim-tarl1
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>Moa-tarl1
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VFLIFWMPFFTVNIVDPFIEYSTEGIVWDIFLWLGYMNSSLNPFLYGFFNRSFHKAFLMFMGCRVCL
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>Mom-tarl1
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MQISAMESQMAAGVGKDSSKKQRHRNTMKRERKAAKTLGIIMGVFLIFWMPFFTINIVDPFIDYSTE
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>Ms-tarl1
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>Mz-tarl1
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>Nb-tarl1
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>Nf-tarl1
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>Ol-tarl1
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>On-tarl1
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PGSSPGMELSHTRKEANECAEQS*

>Pa-tarl1
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>Pem-tarl1
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VQIPKDSCVFMVNQIYAVLASVVSFYLPMLTMLLAYWKIYKVARRQARQISAMEGQMGKDTSKKQRH
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>Pf-tarl1
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AFYLPMAVMLVAYWKIFKAAKRQAKQISAMESQMAAGVGKDSSKKKRHRNTMKREGKAAKTLGIIMG
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PGISSGMELSHSKKEKN*
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>Pl-tarl1
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CNPLVYSLKMSNSHVALLIAICWTVPMLISFGPIMLDLHVADVDIFIPSDVCVFLVSRVYAVMASLV
AFYLPMAVMLVAYWKIFKAAKRQAKQISAMESQMAAGVGKDSSKKKRHRNTMKREGKAAKTLGIIMG
VFLIFWMPFFTVNIVDPFIEYTTEGVVWDVFLWLGYINSSLNPFLYGFFNRCFRRAFLMFLSCRVCL
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>Po-tarl1
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VFLIFWMPFFTVNIVDPFIGYSTEVVVWDVFLWLGYINSSLNPFLYGFFNRSFRRAFLMFIGCRVCL
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>Pom-tarl1
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CNPLVYSLKMSNSHVALLIAICWTVPMLISFGPIMLDLHVADVDIFIPSDVCVFLVSRVYAVMASLV
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VFLIFWMPFFTVNIVDPFIEYTTEGVVWDVFLWLGYINSSLNPFLYGFFNRCFRRAFLMFLSCRVCL
PGISSGMELSHSKKEKN*
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>Pp-tarl1
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QGMDLSHSKRDASERTENQ*
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>Pr-tarl1
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CNPLVYSLKMSNSHVALLIAICWTVPMLISFGPIMLDLHVADVDIFIPSDLCVFLVSRIYAVMASLV
AFYLPMAIMLVAYWKIFKAAKRQAKQISAMESQMAAGVGKDSSKKKRHRNTMKREGKAAKTLGIIMG
VFLIFWMPFFTVNIVDPFIEYTTEGVVWDVFLWLGYINSSLNPFLYGFFNRCFRRAFLMFLSCRVCL
PGISSGMELSHSKKEKN*
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>Ps-tarl1
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CNPLCYSLKMSNNRVVFLIMICWVISLLISFGPVMLELHVASTDVQIPKDSCVFMVNQIYAVLASVV
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SWVELSQTRRDLPNERRN*

>Pun-tarl1

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VFLIFWMPFFTVNIVDPFIEYSTEVVLWDLFLWLGYINSSLNPFLYGLFNRSFRRAFLMFMGCRVCL
PGSSPGMELSHTRKEANECAEQS*

>Py-tarl1

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PGSSPGMELSHTRKEANERAHQP*

>Pyn-tarl1

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>Sa-tarl1a

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QGMDLSHSKRDANERTDNQ*

>Sa-tarl1b

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PIVTMLVAYWKIYKAAKRQVMQISAMEAQMAADVGKDSSKKQKHRNSIRRERKAAKTLGIIMGVFLL
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>Sea-tarl1

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>Sem-tarl1
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>Ser-tarl1
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>Ses-tarl1
MDNGTLGLLGDANTSLHIESCTTLRNQVSRIFLYAFLSVGIVCTVVGNFLVVLSIAYFKQLQSPTNS
FVMSLAVADCLVGLVVMPYSMIRTVEGCWFFGVLFCQLHSSLDVMLCTASIFHLSCIAFDRYYAVCN
PLVYSLKMSRSRVALLIVVCWAVPMLISFGPIMLDLHVAGVDILLPKDVCVFLVNRIYAVMASMVAF
YLPMAIMLIAYWKIFKAAKRQAMQISAMESQMAAGVGKDSSKKKRHRNTMKRERKAAKTLGIIMGVF
LLFWMPFFTVNIVDPFIEYSTEVVVWDIFLWLGYINSSLNPFLYGFFNRYFRRAFLMFMGCRVCLPG
TSPGMELSHTRKEANERADQP*
```

```
>Sf-tarl1
MANSSQWWAASEGPNASLHGDVEPCVPWRSPGSRVVLYALLAAGIVSTVVGNFLVVLAIAYFKQLQS
PTNSFVLSLAVADFLVGLVVMPYSMVRTVEGCWYFGSVFCEVHSSLDVMLCTTSIFHLSCIAFDRYY
AVCNPLVYALKMSRTRVALLIVTCWVLPMLISFGPIMLGLHKANMEVVPPEDSCSFLVNRVYAVTAS
LVAFYLPMATMLVAYWKIYKAARRQAMQISAMESQMTTSQGTDAGRKQKQRNSMRRERKAAKTLGFI
MGAFLLFWLPFFTTNIIDPFIEYCTAGVIWDIFLWLGYANSSLNPFLYGFFNRSFRRAFFMIMGCRI
CLPGSPPSADLSYTKRDGQDHPEN*
```

```
>Sf-tarl2
NLTEDNFSNCTARHCNSTAMKVCLLLVLVFIAISATLGNLLAVVPVAYFRPLHTPTNVFIVSLAVAD
FLVGALVIPLSLVRSVARWMFRRPFRTAHVLLDVTFCSASIFDLCCIALDRYLAVRNPLRYVLVSVL
VVTLGLRAHTLSEKPGAQAPATCTLMVNPPPTARLPLTPSFILPTSVMVTAYWKIFRAAQKQAQRIS
TMENQVRQMDQDQNRSEAQTSLSARLEMKAVKTLGIIMGAYLLCWLPFFSTNTVYPLHGYHVSSWTI
ELVLRLGYANSALNPILYAFFKTTFRQAFAIILGCGSHGLEQQNSNLSP*
```

```
>Sg-tarl1
MENSSEWSNISLNTDFEPCATLRSSGSRVALYVFIIAGIVCTVVGNFLVVLAIAYFKQLRCPTNSFV
MSLAVADFLVGLVVMPYSMVRTVEGCWYFGPNFCHLHSSLDVMLCTASIFHLSCIAFDRYYAVCNPL
VYSFKMSRKRVGLLIVVCWAIPFLISFGPILLGLHKLGMDIPLPENMCIFLVNRVYAVMASLVAFYL
PMVTMLVAYWKIYKAAKRQAMQISAMEAQMAAGVGKDSSKKQKHRNSIRRERKAAKTLGIIMGVFLL
FWLPFFTVNIVDPFIEYGTAAVIWDVFLWLGYVNSSLNPFLYGFFNRSFRRAFLMIMGCRICLHGTA
QGMDLSHSKRDANERTDNQ*
```

```
>Sh-tarl1
MANRTMEIPGPFNSTDLLELDCSMLRNYTSQIFLYVFLSFVIVCTVVGNSLVVLSIGYFKRLQSPTN
FFVLSLAVADCLVGLIVMPYSMVRTIEGCWLFGPLFCQIHSSLDVMLCTSSIFHLSCIAFDRYYAVC
NPLCYSLKMSNGRVIFLIISCWGVSSLISFGPVMLELHVAASADIEIPKDSCVFVVNPIYAVLASVV
SFYLPMLTMLLAYWKIYKVARKQARQISAMESQMGKDTSKKQRHRNAMKREGKAAKILGIVMGVFLL
FWMPFFTTNVVDPFIGYRTEAVVWDVFLWLGYLNSSLNPLLYGLFNRSFRRAFLMFIGCRVCLHQPL
SWVELSQTKKDVQNERRN*
```

```
>Sn-tarl1
MDNGTLGLLGDANTSLHIESCTTLRNQVSRIFLYAFLSVGIVCTVVGNFLVVLSIAYFKQLQSPTNS
FVMSLAVADCLVGLVVMPYSMIRTVEGCWFFGVLFCQLHSSLDVMLCTASIFHLSCIAFDRYYAVCN
PLVYSLKMSRSRVALLIVVCWAVPMLISFGPIMLDLHVAGVDILLPKDVCVFLVNRIYAVMASMVAF
YLPMAIMLIAYWKIFKAAKRQAMQISAMESQMAAGVGKDSSKKKRHRNTMKRERKAAKTLGIIMGVF
LLFWMPFFTVNIVDPFIEYSTEVVVWDIFLWLGYINSSLNPFLYGFFNRYFRRAFLMFMGCRVCLPG
TSPGMELSHTRKEANERADQP*
```

```
>Sr-tarl1a
MENSSEWSNISLDSDFEPCATLRSSGSRVALYVFIIAGIVCTVVGNFLVVLAIAYFKQLQCPTNSFV
MSLAVADFLVGLVVMPYSMVRTVEGCWYFGPNFCHLHSSLDVMLCTASIFHLSCIAFDRYYAVCNPL
VYSFKMSRKRVGLLIVVCWAIPFLISFGPILLGLHKLGMDVPLPENMCIFLVNRVYAVMASLVAFYL
PMVTMLVAYWKIYKAAKRQAMQISAMEAQMAAGVGKDSSKKQKHRNSIRRERKAAKTLGIIMGVFLL
FWLPFFTVNIVDPFIEYGTAAVIWDVFLWLGYVNSSLNPFLYGFFNRSFRRAFLMIMGCRICLHGTA
QGMDLSHSKRDANERTDNQ*
```

```
>Sr-tarl1b
MENSSEWSNISLDSDFEPCATLRSSGSRVALYVFIITGIVCTVVGNFLVVLAIAYFKQLQCPTNSFI
MSLAVADFLVGLVVMPYSMVRTVEGCWYFGPTFCHLHSSLDVMLCTASIFHLSCIAFDRYYAVCNPL
VYSFKMSRERVGLLIVVCWAIPFLISFGPILLGLHKLGMDVPVPENVCIFLVNRVYAVMASLVAFYL
PMVTMLVAYWKIYKAAKRQAMQISAMEAQMAAGVGKDSSKKQKHRNSIRRESKAAKTLGIIMGVFLL
FWLPFFTVNIVDPFIEYGTAAVIWDVFLWLGYVNSSLNPFLYGFFNRSFRRAFLMIMGCRICLHGTA
QGIDLSHSKRDANERTDNQ*
```

```
>Ss-tarl1a
MLTGAICSVLEMSHHTAKSCQNVHIMDVVCILTEQDQAMNNTSLGWPEDLDGDANLSSLHGDLEDFC
ATSSRHQASRVILYAFFTAGILCTVVGNFLVVLAIAYYKQLQSPTNSFVMSLAVADCLVGLVVMPYS
MVRTVEGCWLFGALFCRVHSSLDVMLCTASIFHLSCIAFDRYYAVCNPLVYHLKMSQGRVAFLIVVC
WAVPLLISFGPIMLGLHKAGVNMVPMPPEDACVFLVNRVYAVMASLVAFYLPMGVMLAAYWKIYKAA
```

```
KRQAMQISAMESQFSAGVGKDSSKKQRHRNAMRRERKAAKTLGIIMGVFLLFWLPFFTVNIVDPFID
YSTAVEVWEFFLWLGYVNSSLNPFLYGFFNRSFRRAFMMIMGCRICLSSSSPGMDLSKESNERKVNQ
*
```

>Ss-tarl1b

```
MLCVFLTEHDQAMDNTSLGWPEDLDGDVNLSSF*GDLEDFCATSSRHQASRVILYAFFTAGIVCTVV
DNFLVVLAIVYCKQLQSPTNSFVMSLAVADCLVGLVIMPYSMVCTVEGCWFFGALFCQVHSSLDIML
CTASIFHLSCIPFNRYYAMCNPLVYHLKMSQGRVAFLIVVCWAVPLLISFGPIMLGLHKAGVDMVPM
PPEDTCVFLVNRVYTVMASLVAFYLPMGIMLAAYWKIYKAAKRQAMQISAMESQFSAGVGKDSSKKQ
RHRNAMRRERKAAKTLGIIMGVFLLFWLPFFIVNIVDPFIDYSIVVEVWEFFLWLGYVNSSLNPFLY
GFFNRSFRRAFMMVMGCRICLSSSSPGLDLPKESNERKVNQ*
```

>Ss-tarl2

```
MWMAGVLSHGVLLSGSNSSTTDYINLTDTGGHNESTSALLRSTAFKVCVLCVLIPIPVFAILGNLLI
VASVGRFRNIQMPTNSFIVSLAMADLLVAVLVMPFSLVRSVDTWWFGRNFCVAHFLLDMTLCTSSIF
NLSCVALDRYVAVCDPLHYPTRMSPRRVTMLLLLSWLLPLLISSLCVSLSMYYLTPPTGYRGTQQES
PTCVAQIHTPYAVADSTVCFFIPVVFMLFAYGRIFMVAQRQARWIHAMENHSGQLHMDQNPTREDPA
RPDPARPDPARSDPARRVQARLGGFSIRKENKAARTLGLIMGVFLMCWLPYFSINIAFPLWGDRISP
IVLEASMWLGYANSSLNPFIYAFFNKDFRHAFVAILGCEILGRQIRGCLVSTQEISRQVHTVVTLET
ISK*
```

>Stp-tarl1

```
MDNSSLGWLEDANTSLQIELQPCSTLRNQISRIFLYAFLSVGIVCTVVGNFLVVLSIAYFKQLQSPT
NSFVMSLAVADCLVGLVVMPYSMIRTVEGCWFFGSLFCQLHSSLDVMLCTASIFHLSCIAFDRYYAV
CNPLVYSLKMSSSRVALLIAICWAVPMLISFGPIMLDLHVADVDILLPKDVCVFLVSRIYAVMASLV
AFYLPMAIMLVAYWKIFKAAKRQARQISAMESQMAAGVGKDSSKKKRHRNTMKRERKAAKTLGIIMG
VFLLFWMPFFTVNIVDPFIDYSTEVVVWDIFLWLGYINSSLNPFLYGFFNRSFRRAFLMFMGCRVCM
PGSSPGMELSHTRKEANECADQP*
```

>Tn-tarl1

```
MDNSSFELFGVTNSSLLSETPSCVTLRHLVSRIFLYTFFSFGIVCTVVGNFLVVLSIAYFKQLQSPT
NTFVMSLAVADCLVGLLVMPYSMIRTMEGCWYFGLLFCRLHSSLDVMLCTASIFHLSCIAFDRYYAV
CNPLLYSLKMSHGRVALLIFVCWSVPMLISFGPIMLDLHVSGVDIELPIDVCVFLVNRVYAVTASVV
AFYLPSVIMLIAYWKIFKAAKRQAMQISAMESQMAAGVGKDSSKKRRHRNNMKRERKAAKTLGIIMG
VFLIFWMPFFTINIVDPFIEYSTDGVVWDIFLWLGYINSSLNPFLYGFFNRSFRKAFLMLIGCRVCL
PGSSPGMELSHTRREAN*
```

>To-tarl1

```
MDNSSLGFHYDANTSLQIELQSCTTLRNQASRIFLYGFFSIGIVCTVVGNFLVVLSIAYFKQLQSPT
NSFVMSLAVADCLVGLVVMPYSMIRTVEGCWYFGDLFCQLHSSLDVMLCTASIFHLSCIAFDRYYAV
CNPLVYSLKMSRNRVALLIVICWAVPMLISFGPIMLDLHIAGVDILLPNNVCIFLVNRIYAVMASLV
AFYLPMAIMLVAYWKIFKAAKRQARQISAMESQMAAGVGKDSSKKQRHRNTMKREGKAAKTLGIIMG
VFLIFWMPFFTVNIVDPFIEYSTEVVVWDIFLWLGYINSSLNPFLYGFFYRSFRRAFLMFMGCKVCL
PGSSPGMDLSHTKKEENEHADQP*
```

>To-tarl2

```
MIHIPGVNTSDNNSLTTDGSDSALFHSNTIKVCVLCLLLPIPIFAIMGNLLIMAAVARFQSLRTPTN
AFVVSLAVADFLVAVLVMPFSLVRSIDGWYFGHCFCQAHFLLDMSFCTSSIFNLSCVALDRYIAVCD
PLHYLSRMSPKRVALLLLLCWILPLIISCLCVSFGMYTQSPPAAESSVTQQDTQTCQASFHIPYAFA
TSAISFFIPTGFMLFAYGKIFMAAQRQARWIHAIEHHTGQLQMNQSSMRTDPTRRVHVERYSLKKER
KAAKTLGLIMGVFLLCWLPFFCVNVVHPLKGYSINPLVLEASMWLGYANSSLNPFLYALFNKNYRHA
FVTMLGCGSLGRHLRAGLEYSHFFRQTHTVVTLETISR*
```

>Tr-tarl1

```
MNNSSFESSPSETESCLTLRHPASRILLYTFFSVGIICTVVGNLLVVLSIAYFKQLQSPTNTFVMSL
AVADCLVGLLVMPYSMIRTVEGCWYLGLLFCRLHSSLDVMLCTASIFHLSCIAFDRYYAVCNPLLYS
LRMSHSRVALLIFVCWSVPMLISFGPIMLELHIAGVDIQLPKDVCMFLVNQVYAVTASVVAFYFPSA
IMLIAYWKIFKAAKRQAMQISAMESQMAAGVGKDTSRKWQHRNNMRRERKAAKTLGIIMGVFLIFWM
PFFTTNIVDPFIEYGTEGVVWDVFLWLGYINSSLNPFLYGFFNRSFRKAFLMLMGCRVCLTGSSAGM
ELSHTPREAN*
```

>Xc-tarl1

```
MENSSLAWPGNDNASLHIELPSCATLRSQISRIFLYAFLSVGTGCTVVGNFLVVLSISYFKQLQSPT
NSFVLSLAVADCLVGLLVMPFSMIRTVEGCWYFGSLFCRLHSSLDVMLCTASIFHLSCIAFDRYYAV
CNPLVYSLKMSNSHVALLIAICWTVPMLISFGPIMLDLHVADVDIFIPSDLCVFLVSRVYAVMASLV
AFYLPMAIMLVAYWKIFKAAKRQAKQISAMESQMAAGVGKDSSKKKRHRNTMKREGKAAKTLGIIMG
VFLIFWMPFFTVNIVDPFIEYTTEGVVWDVFLWLGYINSSLNPFLYGFFNRCFRRAFLMFLSCKVCL
PEISSGMELSHSKKEKN*
```

>Xm-tarl1

```
MENSSLAWPGNDNTSLHIELPSCATLRSQISRIFLYAFLSVGTGCTVVGNFLVVLSISYFKQLQSPT
NSFVLSLAVADCLVGLLVMPFSMIRTVEGCWYFGSLFCRLHSSLDVMLCTASIFHLSCIAFDRYYAV
CNPLVYSLKMSNSHVALLIAICWTVPMLISFGPIMLDLHVADVDIFIPSDLCVFLVSRVYAVMASLV
AFYLPMVIMLVAYWKIFKAAKRQAKQISAMESQMAAGVGKDSSKKKRHRNTMKREGKAAKTLGIIMG
VFLIFWMPFFTVNIVDPFIEYTTEGVVWDVFLWLGYINSSLNPFLYGFFNRCFRRAFLMFLSCKVCL
PEISSGMELSHSKKEKN*
```

# TAAR receptors class II from bony fish and cartilaginous fish species

## Cartilaginous fish class II TAAR

### *Callorhinchus milii*

>Cm-taarIIa

MINSTSGEKVENVQYCFEFVNDSCPKAIRFIPTCTMLYIFMV!
SIVITVLGNQMVTISISHFRQLHTPTNCLVLSLAIADFLVGLLVMPYSMLRLIETC*YFGNLFCK
IHSSLDMMMSTASIFHLFCIAIDCYYAVFDPLLYTTKITPPVITTFVAVSWVVPTIFAFGVVFSE
INLAGIENLLETSSCMGSCALLFNELSVSSGNRVFIPSIIMLGIYIKRFLVARKHARAIEGVTEK
NNEGKTNRISRNKEHKPAKTLGLVMGIFLIYWVPFFITTIIDPIINFSTPPIIFDTFVWFGYFNS
AFNPILYAFFYPWFHKALKLILSCRLFDSDSSTINLFPK*

>Cm-taarIIb

MQFCFEFVNTSCPKVIRSAAIYTVTYAVIIISTIITIVGNLEVIISIAHFKQLQTPTNYFILLLA
TTHFLIGLIILPYSMVRSVETCWYFGYVFCKIHSSLGMMLTTA*IFHLCFIAVDRYNAMCDPLLY
ITKITLPVLSMFITISWALPRVFAFGIVFSEINLKGMEDYFAAISCHGM!
VLIFNKQWGLLDPVIAFFAPSLVLVGMNIKIFLVARKHSRVTGNKSNKIHSTKENNTRISCRKEH
KNTKTLGIVMGVFLICWLPFFIDTIIDAYIKFTTPPVLVDAFVWFGF!
NSPLNPMIFCFFYPWFRKALKLILSFKIFNIDSFVSNLFPE*

>Cm-taarIIc

MNSINLENSEDLQYCFEFNMSCPKSIRSTTTTVTMYIFITISIVITILGNSVVMISILHFKQLQT
PTNYLVLSLAFVDFLMGFFVLPFSMVRSVETCWYFGDTFCDIHSTLDVVLTTVSIYNLCFIAIDR
YYAVCEPLLYSIKMTLPMTALIITLNWLFAIIYGSCVFLSEFTKKASGHYRTTISCKGSCIEYRF
GGHMDALIVLFIPTFIILGIYLKIYFVQRKHARKIGNMPNNINSKEEINVRVLQTKEKTAAKNQG
VVMGIFVLSWLPFYLSSIINPYLNFATPPILFEAFTWFGFFNSAFNPVLYAFFYPWFRTALKSIL
TCQILRPESSIMNLFPE*

### *Leucoraja erinacea*

>Le-taarIIa

MNLTYLENSEDVQYCFQYVNASCPRVTRPIAIKATLYLIISLSIFISILGNLVVIASVLHFKQLQ
TPTNYLVLSLAVVDFLVASIVLPYSMIRSIETCWYFGHVFCKIHSVLEIVLTIVSIYNVCFIAID
RYYAICDPLLYSIKITVPVTFIILSLIWLFAIYYGFNVVFLDFSKKILSDYVPTMACEGSCIAYA
KFEGHMDSLIIFFIPILIIILGVNIKIFFVVKCKRGRKIGNLPNNDTGEINKETLHNKEQIAVKNQ
SAIMGIFTFSWLPFYVNSILNPYFDSLIPTPLDDVITWFGFFNSTLNPMLYAFLYPWYRRVLKLT
FSCQI

### *Rhincodon typus*

>Rt-taarIIa

MNSTQIQDKADTEDCFEFVNTSCRKNSQSTAVHVALYMIFVIIVLITIISNLLVIISILHFRKLQ
TETNFLVLSLAVTDFLVGLVVLPYSTIRSVDTCWYFESIFCKIHSGLDMVLTITSI!
FIAIDRYYAVCKPLLYPTKITLPVIGLFVTFSCMFSIVYGFALIFSDANVYGIEDYISAISCHGS
CALIFNKLWGHLDPLIAVFVPVSVIVYIYLKIYFVARKHFRAIGNITHRLNSKQQNNTGGFQKKE
FKAAVKLGDVIGIFIICWLPFFIITIVDPYIGFSTPPALFEVFVWLGYFNSTCNPILYGFFYLWF
HKALKMIISCKIFDEHSPMMNVYLE*

>Rt-taarIIb

MQNPICAALVGNLQ*CFKFVNDSCSRAVMFTVTQVTMYIVLITSILITVFGNLMVIISISHFRQF
QTPTM!
FSSAATDFLVGFSVIPYSMVRSIETYWYFGSTFCKIHSSLDMMSTASIFHLCFITIDLYCAVCDP
LHYLTPLVNAIFTTVSW!
IPALFAFGVVFSEMNLWGIQDVIISNSRVGSCVHVFNHQWGILAPTIAFCIPGVIMLGIYINIYF
VARKHAKANENTNKRTNCAEENKRQRSRSKEVKTAKSLGIVIGICWTCWIPFFITPVIDPMINFS
TLPIIFDAFVWFGHFNSAFNPILCALLHPWF*RSLKLMLTWKILDFNSSTINLFLDWLPSEPCKK
NE

>Rt-taarIIc

SLSLILVTVLGNLLVIISISHFKQLHTPTYYLVLSLAVADLLLGLVVLPNCMGYSVETCWYVGNI
LCDVHIRLSVTLALVSINLLGFIAVSHYYAVCDPLLYTTKITLPAIITIIIFIWVFSIIYGFGLV
CSKIIRKGIEDYIRTVSCHGSCILAFNKLWGHLNPLIGFLGPSLTIFDIYIRIFIIARRHARVIR
NMTRKAQSEEEYSNLDFAGKEHNAAMKLSIVIVVYIICWLPYCMIIVVDPYINYSTSRVLFSATL
WFGFINSAFNPILYAFFYPWFCKAVKRILSCKILNLDSSTINLFPDN*

>Rt-taarIId

MNLSDHENSDNVQYCFEFVNTSCARVTRSIAINVALYIFIITSILITIFGNLVVIISVLHFKQLQ
TPTNFLLSSLAVVDFLVGFIVLPYSMVRSVEKCWYFGEVFCKIHSITEIVLTVVSIYTLCFIAID
RYYAMCDPLFYSVKITLPVTVMTIILIWLFAVFYGLSVFLLDFSKKSVDDYVAVRSCEGSCIAYH
KFEGHIDALIVFFIPIFIILGIYVKIFFVTRCKRCRKIENMPNDSHCTEENNVTIMHKKDQIVVR
KQDILIGIFTFSWLPFYVNSILNPYFDFLIPPVLDSVFAWFGFFNSTLNPLLYAFLYPWFRKSLK
LILSCQIFNTDPSTVNFLSE*

## Bony fish class II TAAR

### *TAAR 12*

### ***Anguilla anguilla***

```
>Aa-taar12a
MKSLGINLTGDSAETQYCFPYLKGSCPRSQTLIIIKAAMYMFMAFTILLTVCGNLLVIISISHFR
QLHSPTNLLILSLACIDCCLGSFIMPYSMIRSVENCWYFGEIICKMHACFDMMMSIASILHLCLI
SVDRYWAICKPLQYKSLVSMQKVACLIAIIWIFSFGFGFGVLLSKVHLAGMEEFIMMNSCAGTCF
VILNKEWGVVAALVAFFIPGTVMTSLYLKIFYVARSHARKINDSLAVTAEINNHKNRMSEQREKK
AAKTLGIVMGVFLLCWLPFFTTIVVDPFINFSTPNSVFDALVWLGYFNSTCNPLIYGLFYPWFQK
VFKIILSGQVFHRGSSSLNICSEM
```

```
>Aa-taar12b
MDSLGINMTGDSAETLYCFPHLERSCPRSQTFIIIKAAMYMFMAFSILMTVCGNLLVIISISHFR
QLHSPTNLIILSLAxSKRPSCIDWFLGAVIMPGSMIRTVENCWYYGEAACIILSSFDMMMSIASI
LHLCLISVDRYCAICKPFWYRSSVTMQKVACVIVIIWTFSFGFGFGVFLSNFPLADLEEFVMASP
CVGNCVLVIKGEWGVGSAVLSFFVPGIVMTSLYLKIFYVARSHARKINDSLALTGAVYNHKDHMS
EQREKKAAKTLGIVMGVFLLCWLPFFLTVIIETLHHFPNIFFVLDLLLWLGYLNSTCNPLIYGFF
YSWFQTVFKMIISGKVFHSGSSSFNIGTDHFK
```

```
>Aa-taar12c
MEILALNWTGDSAGTQYCFPHLKGSCLRSQTPIIIKVVMYMLMAVTILLTVCGNLLVIIVISHFR
QLHSPTNLLILSLACIDWFLGAFIMPYSMIRSVENCWYFGETFCKIHSSLDIMMTVASLLHLGLI
SVDRYLSICKPLQYSTSVTTRNVAALVVITWMFSFAFGFGVIHSNINRVGMEKLLMNNSCTGNCT
FFFNKEGGMMAIILGFFIPGSVMIALYMKIFCVAKEQARKIDCSLAMTRARCDKKCPSEHRERKA
AKTLAIALGVFLLCWLPLVMALIIDPFFDFSAPVVLFDAFLWLGYFNSTCNPVIYGFFFSCFQKV
FKIILSGKIFQNGSALLNIYEENY
```

```
>Aa-taar12d
VAALIGITWMFSFAFGFGVILSKVNLVGVEELFINSCTGTCILFFNKEGGMMAAFVGFFIPGSVM
IALYMKIFYVAKVQARKIKCSLAITRAQCDKKCTSEHRERKAAKTLAIVLGAFLLCWFPFVMVLI
IDPFFDFSTPAVVYDALVWLGYFNSTCNPLIYGFFYPWFQRVFKIIISGKVFQNGSSLLNIYSEN
Y*
```

```
>Aa-taar12e
LAFGFGVILSKVNLVGVEELFIDPCTGSCILFFSKERGMMAAFVAFFIPGTVMIALYMKIFYVAK
VQARKIKCSLAMTRAQCNKNGTSEQTERKAAKTLAIVLGVFLLCCLPFTMLLVVNSFLDYSAPTV
VFDALGWLTYINSTCNPLIYGFFYPWFKRVFKIILSGKVFQNGSSLLNIYEERN*
```

```
>Aa-taar12f
MEVLGRNLTGDSAETPYCFPKVKGSCLRSQTLILIKVAVYIFVAFIILMTVCGNLLVIISISHFR
QLHSPTNLLILSLAFTDWFLGGFVMPCSLIRSVENCWYFGETFCKIHSSLDITLGIASLLHLGLI
SVDRYLAICKPLQYRTSVTMHKVAALVGITWMFSFAXXFGVILSEINLVGIEELFINSCTGTCFY
VFNKQGGVIASFVTFFIPGTVMTGLYMKIFHVAKLQARKINCSMAMTRALHEKKDCTSEQKERKA
AKTLSIVLGVFLLCWLPFFLVLIVDPFLDFSTPAVVFDALSWLAYFNSTCNPLIYGFFYPWFRKV
FKMFLSGQIFQNGSSLLNIYAENKL
```

>Aa-taar12g

LLILSLACIDCCLGSFVMPYSMIRSVESCWYFGEIACKMHSAFDMTMSTASILHLCLISIDRYFA
ICKPLWYRSSVTMNKVTCLIVITWLFSFGFSFGVVFSMVNLVGMEELITMNSCTGNCLLIFNKQW
GVVAALVAFFIPGTVMTSLYLKIFYVARSHAKKINDSLSAPRAVTDKKNHSFEQREKKAAKTLAF
VMGVFVLCWLPFFVTLIVDPFINFSTPLSVADALIWLGYFNSTCNPLIYGFFYPWFQKVFKIIIS
GKVFQNGSSLLSIYIENV

### *Anguilla japonica*

>Aj-taar12a

MKSLGINLTGDSAETQYCFPYLKGSCPRSQTLIIIKAAMYMFMAFTILLTVCGNLLVIISISHFR
QLHSPTNLLILSLACIDCCLGSFIMPYSMIRSVENCWYFGEIICKMHSSFDMMMSIASILHLCLI
SVDRYWAICKPLQYKSLVSMQKVAWLIAIIWIFSFGFGFGVLLSKVHLAGMEEFIMMNSCAGTCF
VILNKEWGVVAALVAFFIPGTVMTSLYLKIFYVARSHARKINDSLAVTAEINNHKNRMSEQREKK
AAKTLGIVMGVFLLCWLPFFTTIVVDPFINFSTPNSVFDALMWLGYFNSTCNPLIYGFFYPWFQK
VFKIILSGQVFHRGSSSLNICSEM*

>Aj-taar12b

MDSLSINMTGDSAETQYCFPHLERSCPRSQTFIITKVAMYMFMAFSILMTVCGNLLVIISISHFK
QLHSPTNLLVLSLACIDWFLGAVIMPGSMIRTVENCWYYGEAACIILSSFDMMMSIASILHLCLI
SVDRYCAICKPFWYRSSVTMQKVACVIVIIWTFSFGFGFVVFLSNFPLADLEKSVMASPCVGNCV
LVIKGEWGVGSAVLSFFVPGIVMTLLYLKIFYVARSHARKINDSLALTGAVYNHKDHMSEQREKK
AAKTLGIVMGVFLLCWLPFFITVIIETLHHFPNIFFVLDLLLWLGYLNSTCNPLIYGFFYSWFQT
VFKMIISGKVFHIGSSSFNIGTDHFK*

>Aj-taar12c

MEILSLNWTGDSAETQYCFPHLKGSCLRSQTPIIIKAVMYMLMAVTILMTVCGNLLVIIAISHFR
QLHSPTNLLILSLAFIDWFLGAFIMPYSMIRSVENCWYFGETFCKIHSSLDIMMTVASLLHLGLI
SVDRYLSICKPLQYSTSVTTRNVAALVVITWMFSFAFGFGVIHSNINRVGMEKLLMKNSCTGNCT
FFFNKEGGMMAIILGFFIPGTVMTALYMKIFCVAKEQARKIDCSLAMTRARCDKKCPSEHRERKA
AKTLAIALGVFLLCWLPLVMALIIDPFLDFSAPVVLFDAFLWLGYFNSTCNPVIYGFFFSCFQKV
YKIILSGKIFQNGSSLLHIYEENY*

>Aj-taar12d

MGSLGRNLTGDSAGTQYCFPHLKGSCPRSQTLILIKAAMYMFMAFTILMTVCGNLLVIISISHFR
QLHSPTNLIILSLAFIDWFLGTFIMPYSMIRSVENCWYFGETFCKIHSSIDIMMSIASLLHLGLI
SVDRYLAICKPLQYRASVTMHKVAALIGITWMFSFAFGFGVILSKVNLVGVEELFINSCAGTCIL
FFNKEGGMMAAFVGFFIPGSVMIALYMKIFYVAKVQARKIKCSLAITRAQCDKKCTSEHRERKAA
KTLAIVLGAFLLCWFPFVMVLIIDPFFDFSTPAVVYDALVWLGYFNSTCNPLIYGFFYPWFQRVF
KIIISGKVFQNGSSLLNIYSENY*

>Aj-taar12e

MEILARNSTGDSEETQYCFPNLQGSCLRSQKLIFIKAAMYICMGFIILMTVCGNLLVIISISHFR
QLHSPTNLIILSLAFIDWFVGAFVMPYSMIESVENCWYFGETFCKIHSSIDIMMSIASLLHLGLI

SVDRYLAICKPLQYRTSVTMHKVATLIGITWMFSFAFGFGVILSKVNLVGVEELFINSCTGTCIV
FFNKEGGMMAAFVGFFIPGSVMIALYMNIFYVAKVQAWKINCSLAMTRARCDKKCTSEHTDRKAA
KTLAIVLGVFLLCWLPFSMVLVLDPFFDYSTPAVVFDALGWLGYFNSTCNPLIYGLFYPWFRRVF
KIILSGNVFQNGSSLLNIYVERN*

### >Aj-taar12f

MKFLSINLTGDSEETKYCFPNLKGSCLRSQKLILIKVAMYFCMAFIILMTICGNLLVIISISHFR
QLHSPTNLIILSLAFIDWFLGAVLMPCSMIRSVEDCWYFGETFCKIHSSVDIMVSIASLLHLGLI
SVDRYLAICQPLQYRTSVTMHKVAALIGIIWMFSFAFGFGVILSKVNLVGVEELFINSCTGTCIV
FFNKEGGMMAAFVAFFIPGIVMIALYMNIFYVAKVQARKIKCSLAMTRARCDKNGTSEQTERKAA
KTLAIVLGVFLLCCLPFSMVLVLGPVFDYSTPAVVFDAVGWLGYFNSTCNPLIYGLFYPWFRRVF
KMILSGKVFQNGSSLLNIYVERN*

### >Aj-taar12g

MENMGLNLTGVSAETQYCFPHLNGSCQRSQTLTIIKAAMYMFMACTILMTVFGNLLVIIGISHFR
QLHSPTNLLILSLACIDCCLGSFVMPYSMIRSVESCWYFGEIACKMHSAFDMTMSTASILHLCLI
SIDRYFAICKPLWYRSSVTINKVTCLIVITWLFSFGFSFGVVFSMVNLVGMEELITMNSCTGNCL
LIFNKQWGVVAALVAFFIPGTVMTSLYLKIFYVARSHAKKINDSLSAPRAVTDKKNHSFEQREKK
AAKTLAFVMGVFVLCWLPFFVTLIVDPFINFSTPLSVADALIWLGYFNSTCNPLIYGFFYPWFQK
VFKIIISGKVFQNGSSLLSIYIENV*

### >Aj-taar12h

MKIIMQIFVCCRYYLEVSAKMEILALNLTGDSVETQYCFPHLKGSCLRSQTLILIKAAMYMFMAF
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IHYSTDVMMSTASLLHLGLISVDRYLAICKPLQYRTSVTMHKVAALVGITWMFSFAFGFGVILSK
INLVGVDELLINPCAGTCIMFVNREWGMTAAFVGFFIPGTIMVALYMKIFYVAKIQARKINCSLG
VTRAEQDKKDYSSEQREKKAAKTLGFVLGVYGLCWLPFVMTLVINPSFDLSTSAVVFDALGWLGY
FNSTCNPLIYGFFYPWFQRVFRIILSGKVFQNGSSLLNIYAENNL*

### >Aj-taar12i

MEILVHNMTGDSAEMQYCVPHQKGSCLRSQTLIIIKVAMYICMGFIILMTVCGNLLVIISISHFR
QLHSPTNLIMLSLAFIDWFLGAFIMPCSMIRSVENCWYFGETFCKIHSSVDIMMSIASLLHLGLI
SVDRYLAICKPLQYRTSVTMHKVAALIGITWMFSFAFGFGVILSKMNLVGVEELFINACTGTCYL
FFNKQGGLVVAFLGFIMPCTVMVVLYMKILYVAKVQARKINCSLTMTGAKQDKKNCAPEQREKKA
AKTLAIVLGVFLLCWLPIMMVLIVDPFFNFSTPVVVFDGLMWLAYFNSSCNPLIYGYFYPWFRRV
FKIIISGKVFQNGSSLLNIYAENKR*

## ***Astyanax mexicanus***

### >Am-taar12a

MNLTDAAADNVLLCFPHLPDSCPREHRFLVLKVVMYFLTLGTILMTVLGNLLVIITISYFKQLQS
PTNLIILSMALVDCMLGCLIMPFSLVRWLERCWFLGEIFCQIHSGLDMTLSIASILHLCLVSVDR
YMAICDPLSYKMNVTNFSAAVCIAVIWLFSVTFSFGVVLSKINIVGLEELLMQAACVGSCALIFN
RQWGVIVSLVAFFGPGAVMSALYLKIFHVARKQAKIMSERSTVRQTNSETKAHSSEHRERKAAKT

LGIVMGIFLLCWLPFFIVTITDPFLNFSTPIDVFDALVWFGYLNSTFNPLIYGFFYPRFQRAFKI
IISKVLHLNNANNLLL*

### >Am-taar12b

MDSLIMNMTAAENVLLCFPHLPDSCPRAHRFLAFKVIMYFLMMASILMTVFGNLLVIITISYFKQ
LQSPTNLIILSLALVDCLLGCMVMPFSLVRWLERCWFLGEIFCQIHSGLDMTLSIVSILHLCLVS
VDRYMAICKPLSYRMKVTNGSVSVCIAVIWLFSLTYSFGVVLSKVNVIGLENLLVQAPCVGNCAL
IFNLQSGISLALVGFFVPGAVMTTLYLKIFQVARKQAKIMSERATVRQTNSETAVHSSEHRERKA
AKTLGIIMGIFLLCWLPFFLVTLTDPLLGFPTPLDVFDALVWFGYLNSTFNPLIYGFFHPRFQRA
FKIIISKVLHLNNANNLLL*

### >Am-taar12c

MDTLFMNKTDVDNVLLCFPNQLDSCPRLQRFSVLKGAMYGFMLVAILMTVFGNLLVIFSISHFKQ
LQSPTNFIILSMALVDCLLGCLVMPFSMVRWVEGCWFLGDFFCQIHSSLDMTLSIASILHLCLVS
VDRYMAICDPLSYRMKVTNGSVAVWIVVTWLFSCLFSFGIVFSKVNLIGLDEQMLNSCVGNCVLI
FNKEWGVIAPLLNFYIPGTIMSCLYLKIFHVARKQAKMISDRTAVGLAGEKNQVSEQRERKAAKT
LGIVMGVFLLCWLPFFLTTVIDPFLGFSTPVDVFDALIWFGYFNSMFNPLIYGFFYPRFQKAFRI
IILRYVCRFTNSSNLVLQ*

## ***Anguilla rostrata***

### >Ar-taar12a

MKSLGINLTGDSAETQYCFPYLKGSCPRSQTLIIIKAAMYMFMAFTILLTVCGNLLVIISISHFR
QLHSPTNLLILSLACIDCCLGSFIMPYSMIRSVENCWYFGEIICKMHSSFDMMMSIASILHLCLI
SVDRYWAICKPLQYKSLVSMQKVACLIAIIWIFSFGFGFGVLLSKVHLAGMEEFIMMNSCAGTCF
VILNKEWGVVAALVAFFIPGTVMTSLYLKIFYVARSHARKINDSLAVTAEINNHKNRMSEQREKK
AAKTLGIVMGVFLLCWLPFFTTIVVDPFINFSTPNSVFDALMWLGYFNSTCNPLIYGLFYPWFQK
VFKIILSGQVFHRGSSSLNICSEM*

### >Ar-taar12b

MDSLGINMTGDSAGTQYCFPHLERSCPRSQTFIIIKAAMYMFMAFSILMTVCGNLLVIISISHFK
QLHSPTNLLVLSLACIDWFLGAVIMPGSMIRTVENCWYYGEAACIIFSSFDMMMSIASILHLCLI
SVDRYCAICKPFWYRSSVTMQKVACVIVIIWTFSFGFGFGVFLSNFPLADLEEFVMASPCVGNCV
LVIKGEWGVGSAVLSFFVPGIVMTSLYLKIFYVARSHARKINDSLALTGAVYNHKDRMSEQREKK
AAKTLGIVMGVFLLCWLPFFLTVIIETLHHFPNIFFVLDLLLWLGYLNSTCNPLIYGFFYSWFQT
VFKMIISGKVFHSGSSSFNIGTDHFK*

### >Ar-taar12c

MEILAFNWTGDSAETQYCFPHLKGSCLRSQTPIIIKVVMYMLMAVTILLTVCGNLLVIIAISHFR
QLHSPTNLLILSLACIDWFLGAFIMPYSMIRSVENCWYFGETFCKIHSSLDIMMTVASLLHLGLI
SVDRYLSICKPLQYSTSVTTRNVAALVVITWMFSFAFGFGVIHSNINRVGMEKLLMKNYCTGNCT
FFFNKEGGMMAIILGFFIPGTVMTALYMKIFCVAKEQARKIDCSLAMTRARCDKKCPSEHRERKA
AKTLAIALGVFLLCWLPLVMALIIDPFLDFSAPVVLFDAFLWLGYFNSTCNPVIYGFFFSCFQKV
FKIILSGKIFQNGSSLLNIYEENY*

>Ar-taar12d

SMIRSVENCWYFGETFCKIHSSIDIMMSIASLLHLGLISVDRYLAICKPLQYRTSVTMHKVAALI
GITWMFSFAFGFGVILSKVNLVGVEELFINSCTGTCILFFNKEGGMMAAFVGFFIPGSVMIALYM
KIFYVAKVQARKIKCSLAITTAQCDKKCTSEHRERKAAKTLAIVLGAFLLCWFPFVMVLIIDPFF
DFSTPAVVYDALVWLGYFNSTCNPLIYGFFYPWFQRVFKIIISGKVFQNGSSLLNIYSENY*

>Ar-taar12e

MEILALNLTGDSAETQYCFPHQKGSCLRNQTLILLKVVMYICMAFIILMTVFGNLLVIISISHFR
QLHSPTNLIILSLAFIDWFVGAFVMPCSMIRSVEDCWYFGETFCKIHSSIDIMMSAASLLHLGLI
SVDRYLAICKPLQYRTSVTMHKVAALIGITWMFSFAFGFGVILSKVNLVGVEELFINSCTGTCIV
FFNKEAGMMAAFVAFFIPGTVMIALYMKIFYVAKVQARKINCSLAMTRAQCNKKCTSEQTERKVA
KTLAIVLGVFLLCWLPFSMMLIVDPFFDYSTPAVVFEAFGWLGYFNSTCNPLIYGFFYPWFKRVF
KIILSGKVFQNGSSLLNIY*

>Ar-taar12f

MEILALNFTEDSEETQYCFPNLKGSCLRSQTLILIKVAMYICMGFIILMTVCGNLLVIISISHFR
QLHSPTNLIILSLAFADWFLGAFVMPYTMITYVENCWYFGETFCKIHTSTDITLCVASLLHLGFI
SVDRYLAICKPLQYRTSVTMHKVAALIGIIWMFSFAFGFGVILSQVNLVSGEELFINYCTGSCIL
FFSKEKAMVAVFVAFFIPGSVMLALYMKIFYVAKVQARKINFSLAMTRAQCDKKCTSEHRERKAA
KTLAIVLGAFLLCWFPFVMVLVVDPFFDYSTPTVVFEAFGWLGGFNSTCNPLIYGFFYPWFRRVF
KIIISGKVFQNGSSLLNIYAERN*

>Ar-taar12g1

MEILARNLTGDSEETQYCFPNLQGSCLRSQKLIFIKVAMYICMASISLMTVCGNLLVIISISHFR
QLHSPTNLIILSLAFIDWFLGTFLMPCSMIRSVEDCWYFGETFCKIHTSTDIMLCVASLLHLGLI
SVDRYLAICKPLQYRTSVTMHKVATLIGITWMFSFAFGFGVILSKVNLVGVEELFINSCTGTCIL
FFNKEGGMMAAFVGFFIPGTVMIALYMKIFYVAKVQARKINCSLAMTRARCDKKCTSEHTDRKAA
KTLAIVLGVFLLCWLPFSMVLVLDPFFDYSTPAVVFDALGWLGYFNSTCNPLIYGLFYPWFRRVF
KIILSGKVFQNGSSLLNIYVERN*

>Ar-taar12g2

CWYFGETFCKIHTSTDIMLCVASLLHLGLISVDRYLAICKPLQYRTSVTMHKVAALIGITWMFSF
AFGFGVILSKVNLVGVEELFINSCTGTCIVFFNKEGGMMAAFVAFFIPGSVMIALYMKIFYVAKV
QARKINCSLAMTRARCDKKCTSEQTERKAAKTLAIVLGAFLLCWLPFSMVLVLDPFFDYSTPAVV
FDALGWLGCFNSTCNPLIYGLFYPWFRRAFKIILSGKVFQNGSSLLNIYEERN*

>Ar-taar12h

MKIIMQIFLCCRYYLEVSAKMKILALNLTGDSVETQYCFPHQKGSCLRSQTLILIKAAMYMFMAF
IILMTVCGNLLVIISISHFRQLHSPTNLIILSLACIDWFLGAVVMPGSMIKSVENCWYFGETFCK
IHYSTDVMMSTASLLHLGLISVDRYLAICKPLQYRTSVTMHKVAALIGITWMFSFAFGFGVILSK
INLVGVDELLINPCAGTCIMFVNKEWGMTAAFVGFFIPGTIMVALYIKIFYVAKIQARKINCSLG
VTRAEQDKKDYSSGQREKKAAKTLGIVLGVYGLCWLPFVMTLVINPSFDLSTSAVVFDALGWLGY
FNSTCNPLIYGFFYPWFQRVFRIILSGKVFQNGSSLLNIYAENNL*

### >Ar-taar12i

MEILAHNMTGDSAEMQYCVPHQKGSCLRSQTLIIIKVAMYICMGFIILMTVC**GN**LLVIISISHFR
QLHSPTNLIMLSLAFIDWFLGAFIMPCSMIRSVENCWYFGETFCKIHSSVDIMMSIASLLHLGLI
SV**DRYLAICKPL**QYRTSVTMHKVAALIGITWMFSFAFGFGVILSKMNLVGVEELFINACTGTCYL
FFNKQGGLVVAFLGFIMPCTVMVVLYMKILYVANVQARKINCSLTMTGAKQDKKNCAPEQREKKA
AKTLAIVLGVFLLCWLPIMMVLIVDPFFNFSTPVVVFDGLMWLAYFNSSCNPLIYGYFYPWFRRV
FKIIISGKVFQNGSSLLNIYAENKR*

### >Ar-taar12j

MEVLGRNFTGDSAETLYCFPQVKGSCLRSQTLILIKVVVYIFVTFIILMTICGNLLVIIAISHFR
QLHSPTNLLILSLAFTEWFLGGFVMPYSMIRSVENCWYFGETFCKIHSSLDITLGIASLLHLGLI
SVDRYLAICKPLQYRTSVTMHKVAALVGITWMFSFASGFGVILSEINLVGIEELFINSCTGTCFY
VFNKQGGVIASFVTFFIPGTVMTGLYMKIFHVAKLQARKINCSMAMTRALHEKKDCTSEQKERKA
AKTLSIVLGVFLLCWLPFFLVLIVDPFLDFSTPAVVFDALSWLAYFNSTCNPLIYGFFYPWFRKV
FKMFLSGQIFQNGSSLLNIYAENK*

### >Ar-taar12k

MEIPAPNLTRDSAEIQYCFPNQKGSCLRSQTLILIKVTMYICMAFIILITVCGNLLVIISISHFR
QLHSPTNLIIILSLAFTDWFLGAFIMPCSMIRSVENCWYFGETFCKIHSSVDIMMSIASLLHLGLI
SVDRYLAICKPLQYRTSVTMHKVAALIGITWMFSFAFGFGVILSKVNLIGVEELFINSCTGTCIL
FFNKQGGLMAAFLGFIMPCTVMVVLYMHIFYVAKVQARKINCSLTMTGAKQDKKNCASEQREKKA
AKTLAIVLGVFLLCWLPFVMVLIVDPFFKFSTPAVVFDGLMWLAYLNSSCNPLIYGYFYPWFQRV
FKIIISGKVFQNGSSLLNIYAESK*

### >Ar-taar12l

MGSLGLNLTGDSVETQYCFPHQKGSCPRSQTLILIKAAMYMFMAFTILMTVFGNLLVIISISHFR
QLHSPTNLIIILSLAFIDWFLGTFIMPYSMIRSVENCWYFGETFCKIHSSIDIMMSIASLLHLGLI
SVDRYLAICKPLQYRTSVTMHKVAALIGITWMFSFAFGFGVILSKMNLVGVEELFINACTGTCYL
FFNKQGGLVVAFLGFIMPCTVMVVLYMKILYVANVQARKINCSLTMTGAKQDKKNCAPEQREKKA
AKTLAIVLGVFLLCWLPIMMVLIVDPFFNFSTPVVVFDGLMWLAYFNSSCNPLIYGYFYPWFRRV
FKIIISGKVFQNGSSLLNIYAE

## ***Cyprinus carpio***

### >Cc-taar12a

MIANETDIENVFLCYPLRPDSCPSAHRLTVLKVVMYVFMLLMILTTVFGNLLIIISISHFKQLQS
PTHLIVQSLAACDCLLGSLVMPYSMVRSVEGCWYLGDVVCKVHSSLDMTFSISSILHLSLIAIDR
YWAICDPLRYRMRVTNNTVTVFITFTWLFSFVYSFSVVFTGVNNVGLEELILQISCFGGCVLFFN
KEWGLICALFVFLIPGTIMSSLYMSIFNVVKKHVKVLSEKVSVAPTVGSNCQTSSQRESKAAKTL
AIVMGVFYLCWLPFFTATAIDPFLNFVTPVDVFDALVWFGYFNSTCNPLIYGFFYPRFQKAFKIL
ISTYICGISKSHTLTFQ*

### >Cc-taar12b

MTLNETGIYPENVFLCYPLLPDSCPRAHRLPALKVAMYVFMVLMILTTVFGNLLIIISISQFKQL
QSPTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGDVVCKVHSSLDMTFSISSLIHLSLISV

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DRYMAICDPLRYKMRVTNNIVSVFTTFTWLFSFLYSFSIVFSGVNKIGLESFIMQVYCVGSCVLF
FNKQWGLICSLLTFFLPGTIMSSLYMEIFHVARKHAKVMSERVTVMATGGLKIQSSTEREGKAAK
TLAIVMGVFYFCWLPFFTATAVDPFLNFVTPGDVFDALVWFGYFNSTCNPLIYGFFYPRFQKAFK
ILISTYICGCNDSSTLILE*

>Cc-taar12c
MCISFFGYWSLTNCTIFIILSLFMITKKIFLASRSNVMTLNKTDIYFENMFLCYPLLPNSCPKLH
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RSVEGCWYLGDVVCTVHSSLDMSFCISSLLHLSLVSVDRYMAICDPLRYRMRVTNNTVTAFITFI
WLFSIFYSFFIVFSGVNKIGLESFIMQVYCVGSCVLFFNKQWGIICPILTFFLPGTIMSSLYMKI
FYVAQKHAKVMSERVTVMAAVELKSQSSVHRERKAAKTLAIVMGVFLFCWLPIFIATIIDSFLNF
VTPASVFDALVWFGYFNSTCNPLIYGFFYSRFQKAFKILISSCIYGFSDSITLTFE*

>Cc-taar12d
MTSNETDIVNMLLFYPLWSDSCLKLHHLAVVKVAMYVLIVLMILTTVFGTC*SLISISHFK!
TSFKCHPTHHRMYRLSELPATVSSVEGCWNLGDVVCKVHSSLDMSFCISSLLHLSLISVDRYTAI
CDPLRYKMRIKNNKVTALISFIWVFSLVYSFYVVFSGINRIGLESFFIQVYCMGSCVLFLNKEWG
IMRPILVFILPKTIMNSLYIKIFHVARKHTKVMSERVTGRLKSQSSAHRERNAAKALAIVIGVFC
SAGFLFFFYCYCTYFFTPAVVKVILWVRLPFH*

>Cc-taar12e
MTSNETQTENILLCYPLRPDSCPKLHCLTVVKVAMYVLMLLMILTTVFGNLLIIISISHFKQLQS
PTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGDFVCKVHSSLDMSFCISSLLHLSLISVDR
YWAICDPLRYKMRVTNNTVTVFTTFIWLFSFLYSFYVVFSGVNTIGLELFIMQVYCVGSCVLFFN
KQWGLICPILTFFLPGTIMSSLYLKIFHVARKHAKVMSESVTGGLKSQSSAHRERKAAKTLAIVM
CVFLFCWLPYFTVTALDPFFNFFTPAVVFDALIWFAYLNSTCNPLIYGFFYPCFQSAFKILISTY
ICGNKDPNTTTFK*

>Cc-taar12f
MTSNETDTQIVFLCYPLRPDSCLKVPRYVMVKVAMYAFLVLMILTTVFGNLLIIISISHFKQLQS
PTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGDFVCEVHSSLDMTFCISSILHLSLISVDR
YWAIFDPLRYKIRVTNNTVTVFTTFICLFSFLYSFSIVFSGVNKIGLESFIMQFYCVGSCVLVFN
KQWGIICPILTFLLPGMIMSSLYIKIFYVARKHAKVMSERVTGGLKSQSSAHRERKAAKTLAIVM
CVFLFCWLPNFTAAALDPFFNLWTPAAVFDALFWFAYFNSTCNPLIYGFFYPCFQKAFKILISTY
ICGIKHSNTLIF

>Cc-taar12g
MTSNDNQTENMFLCFPLRPDSCLKLHRLTVVKGAMYVLMVLMILTTVFGNLLIIISISYFKQLQS
PTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGDFVCEVHSSLDMSFCISSILHLSLISVDR
YMAICDPLRYRMRVTNNTVTAFIIFIWLFSFVYSFSVVFSGITADGLEMLILQTYCVGSCVVFFN
KQWGIVCPILTFFLPGMIMSSLYLKIFYVAQKHAKVMSERVTGGMKSQSSAHRERKAAKTLAIVM
GVFLLCWLPYFTAAALDPFLNFWTPAVVFDALFWFAYFNSTCNPLIYGFFYPCFQKAFKILISTY
ICGNKHSNTLIFE*
```

```
>Cc-taar12h
MTSNKTQTENMFLCYPLRPNSCPKLHRLTVVKVAMYSFLVLMILTTVFGNLLIIISISQFKQLQS
PTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGEFLCKVHSSLDMTFCMSSLLHLSLISVDR
YWAICDPLRYRMRVTNNTVTVFITFIWLFSFVYSFSVVFSGISAVGIEMVILQSYCVGNCVVFFN
KEWSIICPVLVFFLPGMIMSSLYVKIFYVARKHAKVMSERVTGGLKSQSSAHRERKAAKTLAIVI
GVYLFCWLPYFTAAVLDPFFYFWTPAVVFDALFWFAYFNSTCNPLIYGFFYPCFQKAFKILISTY
ICGIKHSNTLTFE*
```

```
>Cc-taar12i
MTSNLTQTENMFLCFPLRPNSCPKLHRLTVVKVAMYAFFVLMILTTVFGNLLIIISISHFKQLQSPTHLIV
RSLAASDCLLGSLVMPYSMVRSVEGCWYLGEFLCKVHTNLDMTFSMSSLLHLSLISVDRYWAICDPLRYKM
RVTNNTVTVFIAFIWLFSFVYSFSIVFSGISAVGIEMVILQSYCVGNCVMFFNKEWSIICPVLVFFLPGTI
MSSLYVKIFYVARKHAKVMSERVTGGLKSQSSAHRERKAAKTLAIVMGVYLFCCLPYFTASVLDPFFNYWT
PAVVFDALFWFAYFNTTCDPLIYGFFYPCFQKAFKILISTYFCGIKHLNTLIFVMNTALTLISGITINIYF
HVILFFSYMLKPFCKRVLLEAVLIFLLI*
```

```
>Cc-taar12j
MMTSNKTQTENMFLCYPLRPNSCPKLHHLTVVKVAMYAFFVLMILTTVFGNLLIIISISHFKQLQ
SPTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGEFLCKVHSSLDMTFSMSSLLHLSLISVD
RYWAICDPLRYKMSVTNNTVTVFITFIWLFSFVYSFSVVFSGIGAVGLEMLILQSYCVGNCVVLF
NKEWSIICPVLVFFLLGMIMSSLYVKIFYVAQKHAKVMSERVTGGLKSQKSSV*
```

```
>Cc-taar12k
MTSNKTQTENMFLCYPLRPNSCPKTTRLTVVKVAMYAFFVLMILTTVFGNLLIIISISQFKQLQS
PTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGEFLCKVHSSLDMTFCMSSLLHLSLISVDR
YWAICDPLRYKMRVTNNTVTVFITFIWLFSFVYSFSVVFSGINTVGLEMVILQSYCVGNCVVFFN
KEWSIICPVLVFFLPGTIMSSLYVKIFYVAQKHAKVMSERVTGGLKSQSSAHRERKAAKTLAIVM
GVFLFCWLPFFTASVLDTFLNFWTPAVVFDALFWFAYFNSTCNPLIYGFFYPCFQKAFKILISTY
ICGIKQSNTLIFE*
```

```
>Cc-taar12l
MMTSNKTQTENMFLCYPLRPNSCLKLHRLTVVKVAMYAFFVLMILTTVFGNLLIIISISQFKQLQ
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RYWAICDPLRYKMRITNNTVTVFTTFIWLFSFVYSFSVVFSGISAVGLEMVILQRYCVGSCVVLF
NKEWSIICPVLIFFLPGTIMSSLYVKIFYVAQKHAKVMSERVTGGLKSQSSAHRERKAAKTLAIV
MGVFLFCWLPFFTASVLDTFLNFWTPAVVFDALFWFAYFNSTCNPLIYGFFYPCFQKAFKILIST
YICGIKQSNTLIFE*
```

```
>Cc-taar12m
MTSNKTQTENMFLCYPLRPNSCPKLHRLTVVKVAMYAFFVLMILTTVFGNLLIIISISQFKQLQS
PTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGDFLCKVNSSLDMTFCMSSLLHLSLISVDR
YWAICDPLRYKMRITNNTVTVFTTFIWLFSFVYSFSVVFSGISAVGLEMVILQRYCVGSCVVLFN
KEWSIICPVLIFFLPGTIMSSLYVKIFYVAQKHAKVMSERVTGGLKSQSSAHRERKAAKTLAIVM
GVYLFCWLPYFTAAVLDPFFNYWTPAVVFDALFWFAYFNSACNPLIYGLFYSCFQKAFKILISTY
FCGIKHSNTFIFE*
```

>Cc-taar12n

MTSNETNTQIVFLCYPLWPDSCLKVQRNVVVKVAMYVFLLLMILTTVFGNLLIIISISHFKQLQS
PTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGEFLCKVHSSLDMTFCMSSLLHLSLISVDR
YWAICDPLRYKMRVTNNTVTVFTTFIWLISFLYSFTVVFSGISAVGLEMLILQTYCVGNCVVFSN
KQWGLICPIFTFFLPGMIMSSLYMKIFHVARKHAKVMSERVTGGLKSQSSAHRERKAAKTLAIVM
GVYLFCWLPYFTAAVLDPFFNYWTPAVVFDALFWFAYFNSACNPLIYGLFYSCFQKAFKILISTY
ICGIKHSNTLIFKRILLSHLFQASQ*

>Cc-taar12o

MISKKMISVSGADVMTSNETQTENILLCYPFQSDSCPKLHRLTVVKVAMYVFMVLMILTTVFGNL
LIIISISHFKQLQSPTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGDFLCKVHSSLDMTFC
ISSLLHLSLISVDRYWAICDPLRYKMRVTNNTVTVFTTFIWLISFLYSFTVVFSGISAVGLEMLI
LQTYCVGNCVVFSNKQWGLICPIFTFFLPGMIMSSLYMKIFHVARKHAKVMSERVTGGLKSQSSA
HRERKAAKTLAIVIGVYLCL*

### *Ictalurus punctatus*

>Ip-taar12a

MEWIGSLITNATHANVDTALLCFPHEPDSCLRTARFVVIRFVMYILMLPTILMTVFGNMLVIITI
SYFKQLHSPTNFIILSLAVVDCLLGSMIMPFSMVRWVEGCWFLGEIFCKIHSSLDMTLSIVSILH
LCLVSIDRYMAITDPLSYKMKVTNDRVVVGIAVIWLFSFSFSFGVVLSNVNLDGLEDLLMLSSCV
GNCALIFNRQWGVIAALVAFFVPGTIMSCLYLKIFHVARKQAKVMAERTTIGNCETKNRSSEQRE
RKAAKTLGIVMGIFLLCWLPFFIMTIADPFLNFSTPVDVFDVLVWFGYLNSTCNPLVYGFFYPRF
QKAFKMIISKYVFHLNDSGNLTL*

>Ip-taar12b

MGTLFMNNTDVEILLLCFPHQPDSCLKTTRFFVIRVIMYFLTLTAIVMTVFGNLLVIITISYFKQ
LHSPTNFIILSLAFVDFMLGCLVMPFSMVRWVEGCWFLGDLFCQIHSSLDMTLSISSILHLCLVS
IDRYMAITDPLGYKLKVTNGNTAVCIAVVWIFSGMFSFGIVFSKINIAGLDEQMLNTCVGNCVLI
FNKEWGIIAPLLNFYIPGAIMTCLYLKIFHVARKHARLISDRTAGLTSGETKKQVSDQRERKAAK
TLGIVMGVFLLCWLPFFLITVIDPFLNFSTPLDVFDALIWFGYFNSMFNPLIYGFFYPRFQKAFK
IIIVRYLFHLKSSSNLVLQ*

### *Lepisosteus oculatus*

>Lo-taar12a

MNSTEVIEEMQYCFQHLKGSCPKVRRLAVIKVAMYVFMAGTIFVAVCGNCMVIISISHFKQLHSP
SNFLILSLGCVDCLLGSLIMPYSMIRSVESCWYFGEIFCAIHSSLDMMMSIASILHLGFIAADRY
FAICDPLRYRNKMTMFNITLFIVISWLFSFAFGFGVVLSKVNLAGIEEFVVSSSCVGACIVILNK
EWGMLSASVAFIIPGTVMISLYIKIFFVARRHARVINAAAPVDDKSSIADKREKKAAKTLGIVIG
VFLLCWLPFFITIIIDPFIDFSTPVIVFDTLMWLGYFNSACNPMIYGFFYPWFQKAFKIVVTGKV
FCVGSSSINIFTDKY*

>Lo-taar12b

MNSTTEFEEMQYCFQYLEGSCPKAHRTAVIKVAMYIFMVGTMLATVSGNLMVIISIAHFKQLHSP
TNFLTLSLGCADCLLGAFVMPYSMVRSVETCWYFGDLFCKIHSSLDMTISVASILHLTFIAVDRY
VAICDPLRYRSKITTFVVAIFIGISWIYSLGLGFGVVFSKINLTGIEEFVILNSCVGTCFLIFNK
HWGVLAALLAFLIPGTVMISLYVKIFMVASRHVRVLNDTSGKICARNDHKRKIVENRERKAAKTL
GIVMGVFLICWLPFFMATIIDPFIGFSTPVILFDALVWFGYFNSTCNPVIYGFFYPWFQKAFKII
ITGKVFCYNSSSTHLFTDKH*

>Lo-taar12c

MEFLVDHGLKRFIMNSTNEEMEYCFQHVKGSCLKARRLAAIKGAIYTFVLGTILVTVCGNLMVII
SIAHFKQLHSPTNFLILSLGCVDCLLGVLVMPYSMVRSVETCWYFGDLFCKIHSSLDMTISVASI
LHLNCIAVDRYFAICNPLRYQNIITTLVVAIFIGIVWLYSLLFGFGLVFFKGRLASTDELIISNS
CVGSCFIQFDKHWAVLGPLLVFFLPAVVMISLYVKILIVASRQAKVIKEISGTVVYQNGNKNKIK
ANRERKAVKTLSIVMGIYLLCYVPFSVTTVTDLFLIFSPPVVIFDTLIWLGYFNSTCNPIIYAFF
YPWFQKAFKIIITGNVFHFGSSSINLFSDKY*

### *Leuciscus waleckii*

>Lw-taar12a

MGMYYIYVNLSLDIGLYQPIIYTIILLILCLITIKEMISASGVDVMMSNVTDSENVFLCYPLRLD
SCPKVHRLTVVKVAMYVFMVLMILTTVFGNLLIIISISH!
KHLQSPTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGDFVCKVHSSLDLTFCISSI!
HLSLISIDRYWAICDPLRYKMRVTNNTVTVFTTFTWLFSFVYSFSIVFTGINAVGLEMLILQVYC
VGSCVLFFNKQWGLIAPILTFFLPGAIMSSLYMKIFHVARKHAKVMSERVTVAAAGGLKSQSSAQ
RERKAAKTLAIVMGVFLFCWLPFFTVAALSSFFTLLTPADFFDALVWFAYFNSTCNPLIYGFFYP
CFQNAFKILISVASSIQTP*

### *Pimephales promelas*

>Pp-taar12a

VAMYVFMVLMILTTVFGNLLIIISISHFKHLQSPTHMIVQSLAACDCLLGSLVMPYSMVRSVEGC
WYLGDFVCKVHSSLDMTFSISSILHLSLVSIDRYWAICDPLRYKMRVTNNTVAVFITFTWLFSFV
YSFSVVFTGVNNVGLEELLLQISCFGGCFLLFNREWGLICALFVFLIPGTIMSSLYLSIFNVVKK
HAKVMSEKVSVAPTVGGNCQTSSQRERKAAKTLAIVMGVFYLCWLPFFTATAVDPFLNFVTPGDV
FDALVWFGYFNSTCNPLIYGFFYPRFQKAFKILISTYICGISESHILTFE*

>Pp-taar12b

DCLLGSLVMPYSMVRSVEGCWYLGDFVCKVHSSLDMTFSISSKIHLCLISVDRYWAICDPLMYKM
RVTNNIVTVFTTFTWLFSFLYSFSIVFSGVNTIGLESFIMQVYCVGSCVLFFNKQWGLICSLLTF
FLPVATMSSLYMKIFHVARRHAKVMSERVTVVTVGGLKSQSSAQREGKAAKTLAIVMGVFCICWL
PFFTATAVDPFLNFVTPVDVFDALVWFGYFNSTCNPLIYGFFYPRFQKAFKILISTYICGFKSSN
ALILE*

### >Pp-taar12c

MITKKIILGFGTNVMTSNITDTKNMFLCYPLLLNSCAKSHRLTVVRVAMYVFMVLMILTTVFGNL
LIIISISHFKHLQSPTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGDFVCKVHSSLDMTFC
ISSILHLSLVSIDRYWAICDPLRYKMRVTNNSVAVFITFTWLFSFLYSFSIVFSGVNKIGLESFI
MQVYCVGSCVLFFNKQWGLICPILTFFLPGMIMSSLYMKIFHVARKHAKVMSERVTVVTAGGLKS
QSSAQREGKAAKTLAIVMGVFYLCWLPIFIATIIDSSLNFVTPASVFDALVWFGYFNSTCNPLIY
GFFYSRFQKAFMILISSRIYGFSDSRTLTFE*

### >Pp-taar12d

MYYINVNLSLDIGFYQAIVYKIILLILCLIKMKETISAYGADVMTSNETDSENMFLCYPLLPDSC
PKVHRLTVVRVAMYVFMVLMILTTVFGNLLIIISISHFKHLQSPTHLIVRSLAASDCLLGSLVMP
YSMVRSVEGCWYLGDFVCKVHSSLDMTFCISSILHLSLVSIDRYWAICDPLRYKMRVTNNIVTVF
TTFTWLFSFVYSFYVVFSGINAVGLEMLILQIYCVGSCVLFFNKQWSLTCSILTFFLPGTIMSSL
YMKIFHVARKHAKVMSERGLKSQRSAQREGKAAKTLAIVIGVFYVCWLPYFTVTAVDPFYNYLTP
ADVFDVVIWFAYFNSTCNPLIYGFFYPCFQNAFKTLISTYVCGVNDSNTLTLNE*

### >Pp-taar12e

MYYINVNLSLDIGLYQAIIYKIILLILCLIKIISAYGADLITSNETDSENMFLCYPLLPDSCPKVHRLTVV
KVAMYVFMVLMILTTVFGNLLIIISISHFKHLQSPTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGD
FVCKLHFSLDMTFCISSILHLSLVSIDRYWAICDPLRYKLRVTNNIVTIFTTFTWLFSFVYSFYVVFSGIN
AVGKMLILQISCVGSCVLFFNKQWGLICTVLLFFLPGMIMSSLYMKIFHVARRHAKVMSERVTVVTAGGLK
SQRSAHRERKAAKTLAIVMGVFYFCWLPYFTVTALDPFFNYLTPVDVFDALVWFAYFNSTCNPLIYGFFYP
CFQNAFKILISTYVCGINDSNTLTLNK*

## *Pygocentrus nattereri*

### >Pyn-taar12a

MNVLNENMTEADVENVLLCFPHQPDSCPRAHRFLALKVPMYFLMLASILMTVFGNLLVIITISHF
KQLHSPTNLIVLSLALVDCLLGCLVMPFSMVRWLERCWFLGDVFCKIHSSLDMTLSIVSILHLSL
VSIDRYLAICEPLSYRMRVTNGTVAVCIAFIWLFSLTFSFGVVLSEVNITGLENLLMLNSCGGNC
ALIFNKQWGVIAALVAFFIPGTIMSSLYLKIFHVARKQAKVMSERATVRRTSCEMNVQSSEQRER
KAAKTLGIVMGIFLLCWLPFFIATIIDPFLDFSTPVDVFDALVWFGYLNSTFNPLVYGFFYPRFQ
SAFKIIISKYVLHLRNASQLVL*

### >Pyn-taar12b

MNVLNENMTEADVENVLLCFPHQPDSCPRAHRFLALKVAVYVLLLATILMTVFGNLLVIITISHF
KQLHSPTNLIVLSLALVDCLLGCLIMPFSMVRWLERCWFLGDVFCKIHSSLDMTLSIVSILHLSL
VSIDRYLAICEPLSYRMRVTNGTVAICIAFIWLFSLTFSFGVILSEVNITGLENLLILSSCVGNC
ALIYNKESGFILSFVAFFIPGAIMISLYLKIFHVVRQQAKVMSERATVRRTSCEMNVQSSEQRER
KAAKTLGIIMGIFLLCWLPFFIVTLTDPFQNFSTPLDVFDALVWFGYLNSTLNPLVYGFFYPRFQ
SAFKIIISKYVLRLSNANRLVL*

### >Pyn-taar12c

MNVLNENMTEADVENVLLCFPHQPDSCPRAHRFLALKVAVYVLLLATILMTVFGNLLVIITISHF
KQLHSPTNLIVLSLALVDCLLGCLVMPFSMVRWLERCWFLGDVFCKIHSSLDMTLSIVSILHLSL
VSIDRYLAICEPLSYRMRVTNGTVAICIAFIWLFSLAYSFGVILSEVNITGLENLLILSSCVGNC

VLIFNKENAFILSFVLFFIPGTIMSSLYLKIFHVVRQQAKVMSERATVRRTSCEMNVQSSDHRER
KAAKTLGIIMGIFLLCWLPFFIVTLSDPFRNFSTPLDVFDALVWFGYLNSTLNPLVYGFFYPRFQ
RAFKIIISKYVLHLGNASQLVL*

### >Pyn-taar12d

MDSFIANMTEADVKDVLLCFPHQPDSCPRVHRFSVLKFMMYAFMLVTIFMTVFGNLLVIITISHF
KQLHSPTNLIILSLALVDCMMGCLVMPFTMVRWVEGCWFLGDFLCQIHSSLDMTISIASILHLCL
VSVDRYVAICEPLQYRMKVTNSKIAVCLATIWLFSLSFGFGIVLSKVNALGLDTVVTPCVGYCAL
TFNKEWSVIGSLLNFFIPGTIMSCLYLKIFCVARKQAKVMSERTAVVKPCETSHSSEQRERKAAK
TLGIVMGFFLLCWLPFFMANLIDPFLNFMTPVDVFDALIWLAYFNSMCNPLIYGFFYPRFQRAFK
IIISRYVLRLSDANNLIL*

### >Pyn-taar12e

MDMLFVNKTDVENVLLCFPHQPDSCAGKHRFLVLRVAMYVCMLLAILMTVFGNLLVIVSISHFKQ
LHSPTNFIILSLAWVDSLLGCLVMPFSMVRWVEGCWLLGELFCQIHSSLDMTLSIASILHLCLVS
IDRFVAICEPLSYRMKVTNANVAVCIAVIWLFSCVFSFGIVFSKVNVMDLDEHMLNPCVGNCALV
FNKEWGVIAPLLNFYIPGTIMSCLYLKIFYVARRQAKVISVGTAVTSGEKSQVSEQRERKAAKTL
GIVMGVFLLCWLPFFLTTVIDPFLGFSTPVEVFDALVWFGYFNSMFNPLIYGFFYPRFQKAFKII
ISRSVCRSTNSNFVLQ*

## ***Sinocyclocheilus anshuiensis***

### >Sa-taar12a

MTSNETDIYPENVFFCYPLLPDSCPRAHRLPALKVAMYVLMVLMILTTVFGNLLIIISISHFKQL
QSPTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGDFVCKVHSSLDMTFSISSLIHLSLISV
DRYWAICDPLRYKMRVTNNIVTVFTTFTWLFSFLYSFSIVFSGINKIGLESFIMQVYCVGSCVLF
FNKQWGLICSLLTFFLPGTIMSSLYMNIFYVARKHAKVMSERVTGGLKSQGSAQREGKAAKTLAI
VMGVFYLCWLPFFTATAVDPFLNFVTPGDVFDALVWFGYFNSTCNPLIYGFFYPRFQKAFKILIS
TYTCGCNDSSTLILE*

### >Sa-taar12b

MNLVNVITVDFQKLSG**I**TVVFFCYPLLPDSCPRAHRLPALKVAMYVLMVLMILTTVFGNLLIIIS
ISHFKQLQSPTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGDFVCKVHSSLDMTFSISSLI
HLSLISVDRYWAICDPLRYKMRVTNNIVTVFTTFTWLFSFLYSFSIVFSGINKIGLESFIMQVYC
VGSCVLFFNKQWGLICSLLTFFLPGTIMSSLYMNIFYVARKHAKVMSERVTGGLKSQGSAQREGK
AAKTLAIVMGVFYLCWLPFFTATAVDPFLNFVTPGDVFDALVWFGYFNSTCNPLIYGFFYPRFQK
AFKILISTYTCGCNDSSTLILE*

### >Sa-taar12c

MTLNKTDIYFENMFLCYPLLPNSCPKLHRLTVVKVAIYILMVLMILTTVFGNLLIIISISHFKQL
QSPTHLIVRSLASSDCLLGSLVMPYSMVRSVEGCWYLGDFVCKVHSSLDMRFCISSILHLSLISV
DRYMAICDPLRYRMRVTDKTVAVFITFIWLFSILYSFFIVFSGVNKMGLESFILQVYCVGSCVLF
FNKQWGIICPILTFFLPGTIMSSLYMKIFYVAQKHAKMMSERVTVMAAGGLKSQSSVHRERKAAK
TLAIVMGVFLFYWLPIFIATIIDSFLNL!
TPASVFDALVWFGYFNSTCNPLIYGFFYSRFQKAFKILISSSIYGFIDSSTFT

>Sa-taar12d

MTSNETNTQIVFLCYPLRPDSCLKVQRYVVVKVAMYVFLVLMILTTVFGNLLIIISISHFKQLQS
PTHLIVRSLASSDCLLGSLVMPYSMVRSVEGCWYLGDFVCKVHSSLDMSFCISSILHLSLISVDR
YMAICDPLRYIMRVTNNTVTAFIIFIWLFSFVYSFSVVFSGINAVGLEMLILQTHCVGSCVLFFN
KQWGIICPILTFFLPGSIMSSLYMKIFYVAQKHAKVMSERVTGRLKSQSSAHRERKAAKTLAFVM
GVFLFCWLPFFTVTALDPFFNFFTPAIVFDAVIWFAYLNSTCNPLIYGFFYPCFQSAFKILISTY
ICGNKDCNTLVFE*

***Sinocyclocheilus grahami***

>Sg-taar12a

MTSNETDIYPENVFFCYPLLPDSCPRAHRLPALKVAMYVLMVLMILTTVFGNLLIIISISHFKQL
QSPTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGDFVCKVHSSLDMTFSISSLIHLSLISV
DRYWAICDPLRYKMRVTNNIVTVFTTFTWLFSFLYSFSIVFSGINKIGLESFIMQVYCVGSCVLF
FNKQWGLICSLLTFFLPGTIMSSLYMIIFYVARKHAKVMSERVTGGLKSQGSAQREGKAAKTLAI
VMGVFYLCWLPFFTATAVDPFLNFVTPVDVFDALVWFGYFNSTCNPLIYGLFYPRFQKAFKILIS
TYICGCNDSSTLILELI*

>Sg-taar12b

MTSNETDIYPENVFFCYPLLPDSCPRAHRLPALKVAMYVLMVLMILTTVFGNLLIIISISHFKQL
QSPTHLIVYSLAASDCLLGALVMPYSMVRSVEGCWYLGDFVCKVHSSLDMTFSISSKIHLGLISV
DRYWAICDPLRYKMRVTNNIVTVFSTFAWLFSFLYSFSIVFSGINIIGLESFIMQVYCVGSCVLF
FNKQWGLICSLLTFFLPGTIMSSLYMKIFYVARKHAKAMSERVTGGLKSQGSAQREGKAAKTLAI
VMGVFYLCWLPFFTATAVDPFLNFVTPVDVFDALVWFGYFNSTCNPLIYGLFYPRFQKAFKILIS
TYICGCNDSSTLILELI*

>Sg-taar12c

MTLNKTDIYFENMFLCYPLLPDSCPKLHRLTVVKVAIYILMVLMILTTVFGNLLIIISISHFKQL
QSPTHLIVRSLASSDCLLGSLVMPYSMVRSVEGCWYLGDFVCKVHSSLDMSFCISSILHLSLISV
DRYMAICDPLRYRMRVTNNTVTVFITFIWLFSILYSFFIVFSGVNKIGLESFILQVYCVGSCVLF
FNKQWGIICPILTFFLPGTIMSSLYMKIFYVAQKHAKIMSERVTVMAARGLKSQSSVHRERKAAK
TLAIVMGVFLFCWLPIFISTIIDSFLNFVTPASVFDALVWFGYFNSTCNPLIYGFFYSRFQKAFK
ILISSCIYGFIDSSTFTFE*

>Sg-taar12d

MTSNETYTQIVFHCYPLRPDSCLKVQRYVVVKVAMYVFLVLMILTTVFGNLLIIISISHFKQLQS
PTHLIVRSLASSDCLLGSLVMPYSMVRSVEGCWYLGDFVCKVHSSLDTSFCISSLLHLSLISVDR
YMAICDPLRYRMRVTNNTVTAFIIFIWLFSFVFSFSVVFSGINAVGLEMLILQTHCVGSCVLFFN
KQWGIICPILTFFLPGTIMCSLYMKIFYVAQKHAKVMSERMTGGMKSQSSAHRERKAAKTLAIVM
GVFLFCWLPFFTVTALDPFFNFFTPAVVFDAVIWFAYLNSTCNPLIYGFFYPCFQSAFKILISTY
ICGNKDCNTLVFE*

### >Sg-taar12e

MTSNETQTENMFLCYPLRLDSCLKPHRLTVVKVAMYTLMVLMILTTVFGNLLIIISISHFKQLQS
PTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGDFVCKVHSSLDMSFCISSILHLSLISVDR
YMAICDPLRYGMRVTNNTVTVFIIFIWLFSFVYSFSVVFSGITAVGLEMLILQTYCVGSCAVFFN
KEWGIICSVLTLFLPGTIMSSLYLKIFYVARKHAKVMSERMTGGMKSQSSVHRERKAAKTLAIVM
GVFLLCWLPYFTAALLDPFFNFWTPAVVFDAVIWFAYFNSTCNPLIYGFFYPYFQKAFKILISTY
ICGIKHSNTLIFE*

### >Sg-taar12f

MIANETDIESVFLCYPLRPDSCLRAHRLTVLKVAMYVFMVLMILTTVFGNLLVIISISHFKQLQS
PTHMIVQSLAACDCLLGSLVMPYSMVRSVEGCWYLGDVVCKVHSSLDMTFSISSILHLSLIAIDR
YWAICDPLRYKMRVTNNTVTVFITFTWLFSFVYSFSVVFTGVNNVGLEELILQISCFGGCVLFFN
KEWGLICALFVFLIPGTIMSSLYMSIFNVVKKHAKVLSEKVSVAPTVGGNCQTSSQRERKAAKTL
AIVMGVFYLCWLPFFTATAIDPFLNFVTPVDVFDALVWFGYFNSTCNPLIYGFFYPRFQKAFKIL
ISTYICGISESHTLTFE*

## *Sinocyclocheilus rhinocerous*

### >Sr-taar12a

MTSNETDIYPENVFFCYPLLPDSCPRAHRLPALKVAMYVLMVLMILTTVFGNLLIIISISHFKQL
QSPTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGDFVCKVHSSLDMTFSISSLIHLSLISI
DRYWAICDPLRYKMRVTNNIVTVFTTFTWLFSFLYSFSIVFSGINKIGLESFIMQVYCVGSCVLF
FNKQWGLICSLLTFFLPGTIMSSLYMNIFYVARKHAKVMSERVTGGLKSQGSAQREGKAAKTLAI
VMGVFYLCWLPFFTATAVDPFLNFVTPGDVFDALVWFGYFNSTCNPLIYGFFYPRFQKAFKILIS
TYICGCNDSSTLILE*

### >Sr-taar12b

MTSNETDIYPENVFFCYPLLPDSCPRAHRLPALKVAMYVLMVLMILTTVFGNLLIIISISHFKQL
QSPTHLIVCSLTASDCLLGSLVMPYSMVRSVEGCWYLGDFVCKVHSSLDMTFSISSLIHLSLISI
DRYWAICDPLRYKMRVTNNIVTVFTTFTWLFSFLYSFSIVFSGINKIGLESFIMQVYCVGSCVLF
FNKQWGLICSLLTFFLPGTIMSSLYMNIFYVARKHAKVMSERVTGGLKSQGSAQREGKAAKTLAI
VMGVFYLCWLPFFTATAVDPFLNFVTPGDVFDALVWFGYFNSTCNPLIYGFFYPRFQKAFKILIS
TYICGCNDSSTLILE*

### >Sr-taar12c

MTLNKTDIYFENMFLCYPLLPNSCPKLHRLTVVKVAMYVLMVLMILTTVFGNLLIIISISHFKQL
QSPTHLIVRSLASSDCLLGSLVMPYSMVRSVEGCWYLGDFVCKVHSSLDMSFCISSILHLSLISV
DRYMAICDPLRYRMRVTNKTVAVCITFIWLFSILYSFFIVFSGVNKISLESFILQVYCVGSCVLF
FNKQWGIICPILTFFFPGTIMSSLYMKIFYVAQKHAKIMSERVTVMAAGGLKSQSSVHRERKAAK
TLAIVMGVFLFCWLPIFIATIIDSFLNFVTPASVFDALVWFGYFNSTCNPLIYGFFYSRFQKAFK
ILISSCIYGFIDSSTFIFE*

### >Sr-taar12d

MTSNETNTQIVFLCYPLRPDSCLKVQRYVVVKVAMYVFLVLMILTTVFGNLLIIISISHFKQLQS
PTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGDFVCKVHSSLDTSFCMSSLLHLSLISVDR

YMASCDPLRYRMRVTNNTVTAFIIFIWLFSFVYSFSVVFSGINAVGLEMLILQTHCVGSCVLFFN
KQWGIICPILTFFLPGTIMSSLYMKIFYVAQKHAKVMSERMTGRLKSQSSAHRERKAAKTLAFVM
GVFLFCWLPFFTVTALDPFFNFFTPAVVCCQVHSPDT*

#### >Sr-taar12e

MTSNETQTENMFLCYPLRPDSCLKVHRLTVIKVAMYVLVVLMILTTVFGNLLIIISISHFKQLQS
PTHLIVRSLASSDCLLGSLVMPYSMVRSVEGCWYLGDFVCKVHSSLDMSFCISSLLHLSLISVDS
YWAICDPLSQVRMRVTNNTVTVFITFIWLFSFVYSFSVVFSGITAVGLEMLILQTYCVGSCVVFF
NKQWGIVCPILTFFLPGTIMSSLYLKIFYVARKHAKVMSERMTGGMKNQSSAHRERKAAKTLAIV
MGVFLLCWLPYFTATVLDPFFSFWTPAVVFDALFWFAYFNSTCNPLIYGFFYPYFQKAFKILIST
YICGIKHSNTLIFE*

#### >Sr-taar12f

YSMVRSVEGCWYLGDVVCKVHSSLDMTFSISSILHLSLIAIDRYWAICDPLRYKMRVTNNTVTVF
ITFTWLFSFVYSFSVVFTGVNNVGLEELILQISCFGGCVLFFNKEWGLICALFVFLIPGTIMSSL
YMSIFNVVKKHAKVLSEKVSVAPTVGGNCQTSSQRERKAAKTLAIVMGVFYLCWLPFFTATAIDP
FLNFVTPVDVFDALVWFGYFNSTCNPLIYGFFYPRFQKAFKILISTYICGI

#### >Sr-taar12g

MYCIYINLSLHICLYHVIIYEIILGTIWSIFEWLFTFTKQTLCFSLAYQSLFEAHVMIANETDIE
NVFLCYPLRPDSCPRAHRLTILKVAMYVFMVLMILTTVFGNLLVIISISHFKQLQSPTHMIVQSL
AACDCLLGSLVMPYSMVRSVEGCWYLGDFVCKVHSSLDMTFSISSKIHLGLISVDRYWAICDPLR
YKMRVTNNIVTVFTTFTWLFSFLYSFSIVFSGINKIGLESFIMQVYCVGSCVLFFNKQWGLICSL
LTFFLPGTIMSSLYMNIFYVARKHAKVMSERVTGGLKSQGSAQREGKAAKTLAIVMGVFYLCWLP
FFTATAVDPFLNFVTPGDVFDALVWFGYFNSTCNPLIYGFFYPRFQKALTVNHSATLFHKPG*

## ***TAAR 13***

### ***Anguilla anguilla***

#### >Aa-taar13a

MDILKHQELNASQLCYPSVNGSCIKINQTWAAQFISYIFLVAGMIFTILGNLVVIISIAHFKQLH
TPTNILVMSLAAADLLLGIVVIPFSMIRSVDGCWYFGDAFCLLHSSFDLFLTCASLFHLIFIAID
RYQAVCNPLHYSTRITIPIAWLMSALSWVIAGVYSYGLLYSKANVKGLEEHIASIYCFGSCILLF
NSLWGVLDTLIAFFLPCCIMMGLYAKIFFVXPSSSNMNLFIER

#### >Aa-taar13b

MDILKHQDLNAPQFCFPSVNGSCIKISQTWAAQFILYIFFVAGMIFTILGNLVVIISIAHFKQLH
TPTNILVMSLAVADLLLGMVVMPFSMIRSVEGCWYFGDAFCLLHSSFDMFLTCASLFHLIFIAID
RYQAVCNPLHYSTRITIPIAWLMSALSWVIAGVYSYGLLYSKANVKGLEAHIASIYCLGSCILLF
NSLWGVLDTLIAFFLPCSIMMGFYVKIFFVAREHVRKIGDMNHQKQLNEENKNKLSRSSERKAAK
TLGIVMGVFILCWMPFFVNMIIDPYTNFSTPVIIFDVLVWLGYFNSTLNPIIYSLFYPWFQKTFK
IIVSLKILTPNSSNINLFTER

>Aa-taar13c

HSSFDMFLTSVSIFHLISIAIDRYQAVCNPLHYSTRITIPIAWLMSALSWVIAAAYSYGLLYSKA
NVKGLEDYIASIYCLGDCVLLFNALWGALDTLIAFFLPCFVMMGLYTKIFLVAREHARKIEDMKH
KITVNEENRNKPSQRSEQKAAKTLGIVVGVFIICWLPFFVNSLIDPYTNFATPAIVFDVFVWLGY
FNSTLNPIIYALFYPWFQKTLKLIVTFKIFTPHSSNINVFPER

>Aa-taar13d

MDDLVHQEPDAQEYYYPSTNGSCIKGNQSIAAQVMLYIFFVTGMIFTILGNLVVIISIAHFKQLH
SPTNILVMSLAVVDLLLGMVVMPFSMIRSVEGFWYFGDAFCLLHSSFDMFLTCASIFHLIVIAID
RYQAVCNPLHYSTRITIPIAFLMSALSWIIAAAYSYALLYSKANVKGVEDDVASINCLGGCVLLF
NAVWGPLDTMIEFFVPCFVMMGLYTKIILVAREHARK

>Aa-taar13e

DAQQYCYPAINGSCIKGNHTIAAQVILYIFFVAGIIFTVLGNLVVIISITHFKRLHTPTNILVMS
LAVADMLLGMLVMPFSMVRSVAGCWYFGEVFCQLHSSFDMFLATVSIFHLICIAIDRHEAVCNPL
HYSRRITIPIAFLMSTLSWSIAAAYSYGLLYSKADEKGVEDYIASIHCLGSCFPFVLSFNALWGV
LDSLIAFFVPCVIMMGLYAKIYLVAREHARKIEGMNNKRPVNEENRNKLSQGSEQKAAKTLGIVV
SAFIVCWLPFFINSLIDPYTTFSTNSPVLSDAFVWLGYFNSGLNPIIYGLFYPWFQKTLKLIITF
KIFTPHSSNINVFSER

***Anoplopoma fimbria***

>Af-taar13a

MMSRGLSQEQYCFPGSNASCVTAQFSMGTEVALYLLFSLGILITILGNSVVIVSIGHFKQLHNPT
NVLILSLALADLLVGVIVMPFSAIRTIHGCWFYGDDFCLLHSSFDMFLTSVSIFQLICIAVDRQQ
AICNPLHYSRNITMSVAWIMVCASWSLAAVYSYGLLYSKANVAGIEDYMSSINCLGSCNLVFNHI
WGILDGVTAFFFPCTVMVCLYTKIFIVAKDHVRKIGDMSKGSNNRGRGGLIKQSEHKAAKTLGIV
LGAFIFCWMPFFINSIIDAYTGFSTPASVFEAFVWLGYFNSTLNPIIYALFY

>Af-taar13b

IVSIGHFKQLHNPTNVLILSLALVDLLVGVIVMPFSAIRTIHGCWFYGDDFCLLHSCLDVFLTTL
SIFHLISIAIDRQQAICNPLHYSRNITXSVAWIMVCASWSLAAVYSXGLLYSKANVAGIEDYMSS
INCLGSCNLVFNHIWGILDGVTAFFFPCTVMVCLYTKIFIVAKDHVRKIGDMSKGSNNRGRGGLI
KQSEHKAAKTLGIVLGAFIFCWMPFFINSIIDAYTGFSTPASVFEAFVWLGYFNSTLNPIIYALF
Y

***Anguilla japonica***

>Aj-taar13a

MDILKHQELNAPQFCYPSVNGSCIKINQTWAAQFISYIFLVAGMIFTILGNLVVIISIAHFKQLH
TPTNILVMSLAAADLLLGIVVIPFSMIRSVDGCWYFGDAFCLLHSSFDLFLTCASLFHLIFIAID
RYQAVCNPLHYSTRITIPIAWLMSALSWVIAGVYSYGLLYSKANVKGMEEHIASIYCFGSCILLF
NSLWGVLDTLIAFFLPCCIMMGLYAKIFFVAREHVRKIGDMNHRKHLNEENKNKLSRSSERKAAK
TLGIVMGVFILCWMPFFVNMIIDLYTNLSTPFIIVEVLFWLGYFNSTLNPIIYSLFYPWFQKTFK
LIVSLKILNPNSSNMNLFTER*

>Aj-taar13b1

MDILKHQELNAPQFCFPSVNGSCIKISQTWAAQFILYIFFVAGMIFTILGNLVVIISIAHFKQLH
TPTNILVMSLAVADLLLGMVVMPFSIIRSVEGCWYFGDAFCLLHSSFDMFLTCASLFHLIFIAID
RYQAVCNPLHYSTRITIPIAWLMSALSWVIAGVYSYGLLYSKANVKGLEAHIASMYCLGSCILLF
NSLWGVLDTLIAFFLPCSIMMGF!
YVKIFFVAREHVRKIGDMNHQKHLNEENKNKLSRSSERKAAKTLGIVMGVFILCWMPFFVNMIID
PYTNFSTPLIVFDVLVWLGYFNSTLNPIIYSLFYPWFQKALKLIVSLKILTPSSSNMNLFIER*

>Aj-taar13b2

MDILKHQELNAPQFCYPSVNGSCIKISQTWPAQFILYIFFVAGMIFTILGNLVVIISIAHFKQLH
TPTNILLMSLAAADLLLGMVVMPFSMIRSVEGCWYFGDDFCLLHSSFDMFLTCASLFHLIFIAID
RYQAVCNPLHYSTRITIPIAWLMSALSWVIANVYSYGLLYSKANVKGLEDHIASMYCLGNCILLV
NSLWGVLDSLIAFFLPCSIMMGFYAKIFFVAREHVRKIGDMNHQKHLNEENKNKLSRSSERKAAK
TLGIVMGVFILCWMPFFVNLIIDPYINFSTPVIVFDVLVWLGYFNSTLNPIIYSLFYPWFQKTFK
IIVSLKILNPNSSNMNLFPER*

>Aj-taar13c

MEALVHQEPDAQQYCYPSTNGSCIKGNQPIAAQVILYIFFVTGMIITILGNLVVIISIAHFKQLH
TPTNILVMSLAVADLLLGMSVMPFSMIRSVEGCWYFGDAFCLLHSSFDMFLTSVSIFHLISIAID
RYQAVCNPLHYSTRITIPIAWLMSALSWIIAAAYSYGLLYSKANVKGLKDYIASIYCLGDCVLLF
NALWGALDTLIAFFLPCFVMMG

>Aj-taar13d1

MHRNTIIPQLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXGMVVMPFTMIRSVEGFWYFGDAFCLLHSSFDMFLTCASIFHLIFIAIDRYQAVC
NPLHYSTRITIPIAFLMSALSWIIAAAYSYGLLYSKANVKGVEDDVASINCLGGCVLLFNALWGP
LDTFIEFFVPCFVMMGLYTKIFLVAREHARKIEDMKHKITVNEENRNKPSQRSEQKAAKTLGIVV
GVFIICWLPFFVNSLIDPYTNFATPAIVFDVFVWLGYFNSTLNPIIYALFYPWFQKTLKLIVTFK
IFAPHSSNINVFPER*

>Aj-taar13d2

DLVHQEPDAQEYYYPSTNGSCIKGNQSIAAQVTLYIFFVAGMILTILGNLVVIISIVHFKQLHTP
TNVLVMSLAVVDLLLGMVVMPFSMIRSVEGFWYFGDAFCLLHSSFDMFLTCASIFHLIFIAIDRI
AIDRYQAVCNPLHYSTRITIPIAFLMSALSWIIAAAYSYALLYSKANVKGVEDDVASIYCLGGCV
LLFNAVWGPLDTMIEFFVPCFVMMGLYTKIILVAREHARKIEDMKHKITVNEENRNKLSQRSEQK
AAKTLGIVVSAFIICWFPFFSNSLIDPYTDFATPPIVFDAFVWLGYFNSTLNPIIYGLFYPWFQK
TLKLIITLKIFTPHSSNINVFS

>Aj-taar13e

MDALVHQEPDAQQYCYPAINGSCIKGNHTIAAQVILYIFFVAGIIFTVLGNLVVIISITHFKQLH
TPTNILVMSLAAADMLLGMLVMPFSMVRSVAGCWYFGEVFCQLHSSFDMFLATVSIFHLICIAID
RHEAVCNPLHYSARITIPIAFLMSALSWSIAAAYSYGLLYSKADEKGVEDYIASIHCLGSCFPFV
LSFNALWGVLDSLIAFFVPCVIMMGLYAKIYLVAREHARKIEGMNRKRPVNEENKHKLSQGSEQK

AAKTLGIVVSAFIVCWLPFFINSLIDPYTTFSTNSPVLSDAFVWLGYFNSGLNPIIYGLFYPWFQ
KTLKLIITFKIFTPHSSNINVFSER

>Aj-taar13f

MDALVLQKPDAQQYCYPSTNGSCFKGNQPIAAQVILYIFFVTGMIITILGNLVVIISIAHFKQLH
TPTNILVMSLAVADLLLGMLVMPFSMIRSVDGCWYFGDAFCLLHSSYDMFLATASIFHLIFIAID
RHEAVCNPLHYSTRITIPIAFLMSALSWIIAAAYSYGLLYSKADVKGLEDYIASLHCLGRCVHFV
LSLNALWGVLDTLIAFFVPCFVMMGLYAKIYLVAREHARKIGGMNHKRPVNEENKHKLSQGSEQK
AAKX

>Aj-taar13g

MEALVHQEPDAQQYCYPSTNGSCFKGNQPIAAQVILYIFFVTGMIITILGNLVVIISIAHFKQLH
TPTNILVMSLAVADLLLGMLVMPFSMVRSVDGCWYFGDAFCLLHSSYDMFLATASIFHLIFIAID
RHQAVCNPLYYSTRITIPIAFLMSALSWSIAAAYSYGLLYSKADVKGLEDYIASIHCFGGCVHFV
LSFNALWGVLDTLIAFFVPCFVMMSLYAKIFLVAREHARKIGGINHKIPVNEENKHKLSQGSEQK
AAKTLGIVMSVFLICWLPCFVNSLIDPYTTFSANHVVSDAFVWLGYFNSTLNPIIYGLFYPWFQK
TLKLXKVIVCKVVLQANFTISKNAVL*

***Astyanax mexicanus***

>Am-taar13a

MESYLTEEADLSQYCYPESNASCVKSFYSVGAKSVLYFLLILAMAVTVLGNFVVIVSIAHFKQLH
TPTNILVMSLALADLFVGMIVMPFSTIRSVDGCWYFGQGFCLLHSSFDMLLTSASIFHLVCIATD
RYQAVCHPLHYPTRITIPTAWLMVALSWTTAAVYSYGLMYSKANVANLEEYMESIFCVGSCDLLF
NALWGALDTLIGFLLPCSVMGCLYAKIFLVSKKHATKIEGKKQCKKGTSMNMVSQSVKHENKAAK
TLGIVVGAFILCWMPFFVNSIVDPYINFSTPAVLFEVLVWLGYLNSTLNPIIYGLFYPWFRKSLY
LIVTLRIFTPHSSDTNIFLA*

***Anguilla rostrata***

>Ar-taar13a

MDILKHQELNASQFCYPSVNGSCIKINQTWAAQFISYIFLVAGMIFTILGNLVVIISIAHFKQLH
TPTNILVMSLAAADLLLGIVVIPFSMIRSVDGCWYFGDAFCLLHSSFDLFLTCASLFHLIFIAID
RYQAVCNPLHYSTRITIPIAWLMSALSWVIAGVYSYGLLYSKANVKGLEEHIASIYCFGSCILLF
NSLWGVLDTLIAFFLPCCIMMGLYAKIFFVAREHVRKIGDMNHRKHLNEENKNKLSRSSERKAAK
TLGIVMGVFILCWMPFFVNMIIDLYTNLSTPFIIVEVLFWLGYFNSTLNPIIYSLFYPWFQKTFK
LIVSLKILNPSSSNMNLFIER*

>Ar-taar13b1

MDILKHQELNAPQFCYPSVNGSCIKISQTWAAQFILYIFFVAGMIFTILGNLVVIISIAHFKQLH
TPTNILLMSLAAADLLLGMVVMPFSMIRSVEGCWYFGDAFCLLHSSFDMFLTCASLFHLIFIAID
RYQAVCNPLHYSTRITIPIAWLMSALSWVIAGVYSYGLLYSKANVKGLEAHIASIYCLGNCILLV
NSLWGVLDSLIAFFLPCSIMMGFYAKIFFVAREHVRKIGDMNHQKHLNEENKNKLSRSSERKAAK
TLGIVMGVFILCWMPFFVNLIIDPYINFSTPVIIFDVLVWLGYFNSTLNPIIYSLFYPWFQKTFK
IIVSLKILTPSSSNINLFIER*

>Ar-taar13b2

MDILKHQDLNAPQFCFPSVNGSCIKISQTWAAQFILYIFFVAGMIFTILGNLVVIISIAHFKQLH
TPTNILVMSLAVADLLLGMVVMPFSMIRSVEGCWYFGDAFCLLHSSFDMFLTCASLFHLIFIAID
RYQAVCNPLHYSTRITIPIAWLMSALSWVIAGVYSYGLLYSKANVEGLEAHIASIYCLGSCILLF
NSLWGVLDTLIAFFLPCSIMMGFYVKIFFVAREHVRKIGDMNHQKQLNEENKNKLSRSSERKAAK
TLGIVMGVFILCWMPFFVNMIIDPYTNFSTPVIIFDVLVWLGYFNSTLNPIIYSLFYPWFQKALK
LIVSLKILTPSSSNMNLFIER*

>Ar-taar13c

MDALVHQEPDAQQYCYPSTNGSCFKGNQPIAAQVILYIFFVTGMIITIFGNLVVIISIAHFKQLH
TPTNILVMSLAVADLLLGMSVMPFSMIRSVEGCWYFGDAFCLLHSSFDMFLTSVSIFHLISIAID
RYQAVCNPLHYSTRITIPIAWLMSALSWIIAAAYSYGLLYSKANVKGLEDYIASIYCLGDCVLLF
NAVWGALDTLIAFFLPCFVMMGLYTKIFLVAREHARKIEDMKHKITVNEENRNKPSQRSEQKAAK
TLGIVVGVFIICWLPFFVNSLIDPYTNFATPAIVFDVFVWLGYFNSTLNPIIYALFYPWFQKTLK
LIVTFKIFTPHSSNINVFPER*

>Ar-taar13d1

MDDLVHQEPDAQEYYYPSTNGSCIKGNQSIAAQVMLYIFFVTGMIFTILGNLVVIISIAHFKQLH
TPTNILVMSLAVVDLLLGMVVMPFSMIRSVEGFWYFGDAFCLLHSSFDMFLTCASIFHLIVIAID
RYQAVCNPLHYSRRITIPIAFLMSALSWVIAAAYSYALLYSKANVKGVEDDVASIYCLGGCVLLF
NAVWGPLDTMIEFFVPCFVMMGLYTKIILVAREHARKIEDMKHKITVNEENRNKLSQRSERKAAK
TLGIVVSVFIICWLPFFSNSLIDPYTDFGTSPIVFDAFVWLGYFNSTLNPIIYGLFYPWFQKTLK
LIITLKIFTPHSSNINVFSER*

>Ar-taar13d2

MDDLVHQEPDAQEYYYPSTNGSCIKGNQTIAAQVTLYIFFVTGMIFTILGNLVVIISIAHFKQLH
TPTNILVMSLAVVDLLLGMVVMPFTMIRSVEGFWYFGDAFCLLHSSFDMFLTCASIFHLIFIAID
RYQAVCNPLHYSTRITIPIAFLMSALSWIIAAAYSYALLYSKANVKGVEDDVASINCLGGCVLLF
NAVWGPLDTMIEFFVPCFVMMGLYTKIFLVAREHARKIEDMKHKIPVNEENRNKLSQRSEQKAAK
TLGIVVSAFIICWLPFFSNSLIDPYTNFATPPIVFDAFGWLGYFNSTLNPIIYGLFYPWFQKTLK
LIITLKIFTPHSSNINVFS*

>Ar-taar13e

MDALVHQEPDAQQYCYPAINGSCIKGNHTIAAQVILYIFFVAGIIFTVLGNLVVIISITHFKRLH
TPTNILVMSLAVADMLLGMLVMPFSMVRSVAGCWYFGEVFCQLHSSFDMFLATVSIFHLICIAID
RHEAVCNPLHYSRRITIPIAFLMSTLSWSIAAAYSYGLLYSKADEKGVEDYIASIHCLGSCFPFV
LSFNALWGVLDSLIAFFVPCVIMMGLYAKIYLVAREHARKIEGMNNKRPVNEENRNKLSQGSEQK
AAKTLGIVVSAFIVCWLPFFINSLIDPYTTFSTNSPVLSDAFVWLGYFNSGLNPIIYGLFYPWFQ
KTLKLIITFKIFTPHSSNINVFSER*

>Ar-taar13f

MDALVHQEPDAQQYCYPSTNGSCFKGNQPIAAQVILYIFFVTGMIITILGNLVVIISIAHFKQLH
TPTNILVMSLAVADLLLGMLVMPFSMIRSVDGCWYFGDAFCLLHSSYDMFLATASIFHLIFIAID

```
RHQAVCNPLHYSTRITIPIAFLMSTLSWIIAAAYSYGLLYSKADVKGLEDYIASIHCLGGCVHFV
LSFNALWGVLDTLIAFFVPCFVMMSLYAKIFLVAREHARKIGGMNRKIPVNAENKHKLSQGSEQK
AAKTLGIVMSVFIICWLPCFVNSLIDPYTTFSANHVVSDAFVWLGYFNSTLNPIIYGLFYPWFQK
TLKLIITFKIFTPHSSNINVFSER*
```

## *Cyprinus carpio*

### >Cc-taar13a

```
MDLSSQEYDSTQFCYPAVNKSCLKGTHHVSTQTVVYLLLVLAMIVTILGNLVVIISIAHFKQLQT
PTNILVMSLALADLLLGLVVMPFSMIRSVDGCWYYGDAFCLLHSTFDLFLTSVSIFHLIFIAIDR
HQAAVCYPLQYPTRITISVAWVMVMISWSMAALYSYGLVYSKANVEGLEEYIESIYCMGSCTLLF
NALWGAIDTLVAFLLPCSVMVGLYARIFVIAKQHARKLCEANQQENENMFKSSRRSERKAAKTLG
VVVGAFIICWLPFFINSLIDPYINFSTPIALFEVFVWLGYINSTINPIIYGLFYPWFRKTLSLII
TMRIFEPNSSDINVFTV*
```

### >Cc-taar13b

```
MDLSSQEYDPTQFCYSAVNNSCLKGTHHVSTQTAVYLLLVLAMIVTILGNLVVIISIAHFKQLQT
PTNILVMSLALADLLLGLVVMPFSMIRSVDGCWYYGDAFCLLHSSFDLFLTSVSIFHLIFIAIDR
HEAVCYPLQYPTRITISVAWIMVMISWSMAALYSYGLVYSKANLEGLEEYIESIYCMGSCTLLFN
ALWSVLDTLLTFFLPCSVMIGLYARIFVVARKHIRTIGEANHHENESTFKSSRRSERKAAKTLGV
VVGAFIICWLPFFINSLIDPYISFSTPFALFEAFVWLGYINSTINPIIYGLFYPWFRKTLSLIIR
LKIFEPNSSDISVFTV*
```

### >Cc-taar13c

```
MDLSSQEYSPTQFCFPAVNNSCLKGTHHVSTQTVVYLLLVSAMIVTILGNSVVIISIAHFKQLQT
PTNILVMSLALADLLLGLVVMPFSMIRSVDGCWYYGDAFCLLHSSFDLFLTSVSIFHLIFIAIDR
HQAVCYPLQYPTRITIPVAWVMVMISWSMAALYSYGLVYSKANVEGLEEYSESIYCMGSCTLLFN
SLWSVLDTLLTFFLPCSVMIGLYARIFVVAKKHIRTIGEASQHENENMFKSSRRSERKAAKTLGV
VVGAFIICWLPFFINSLMDPYINFSTPFVLFDAFGWFGYINSTINPIIYGLFYPWFRKSLSLIIT
MRIFEPNSSDINVFTV*
```

### >Cc-taar13d

```
MDLSSQQYDPTQFCFPAVNNSCLKGTHHVSTQTVVYLLLVSAMIVTILGNSVVIISIAHFKQLQT
PTNILVMSLALADLLLGLVVMPFSMIRSVDGCWYYGDAFCLLHSTFDLFLTSVSILHLVCIAIDR
HQAVCYPLQYPTRITIPVAWVMVMISWAMIAVYSYGLLYSKANVEGLEEYIESIYCIGHCSLLFS
NLWSVLDTLITFFFPCSVMFGLYVRIFVVAKKHVRTISEANQHENENVFKSSRRSERKAAKTLGV
VVLPFFINSVMDPYINFSTPLALFEVFVWLGYINSTINPIIYGFFYPWFRKTLSLIVTRRIFEPN
SSDINVFTV*
```

### >Cc-taar13e

```
KKQHFIGSSFLKLRGFKGTHHVSTQTVVYLLLVSAMIVTILGNSVVIISIAHFKQLQTPTNILVM
SLALADLLLGLVVMPFSMIRSVDGCWYYGDAFLFAAIPPLTLFLASVFYFPFLFVLLLSIAIDRH
QAVCYPLQYPTRITIPVAWVMVMISWAMIAVYSYGLLYSKANVEGLEEYIESIYCIGHCSLLFSN
LWSVLDTLITFFFPCSVMFGLYVRIFVVAKKHVRTISEANQHENENVFKSSRRSERKAAKTLGVV
```

VGAFIICWLPFFINSVMDPYINFSTPLALFEVFVWLGYINSTINPIIYGFFYPWFRKTLSLIVTR
RIFEPNSSDINVFTV*

### *Clupea harengus*

>Ch-taar13a

MDTGISSDQYCFPSVNGSCMKGTYNQGTQVVLYIMFWTSMVITILGNLVVIISIMHFKQLHTPTN
LLVMSLALADLLLGLTVMPFSIVRSVDGCWYYGNAFCLLHSSFDMFLTSASIFHLISIAIDRHQA
VCYPLLYPTSITIPVAWLMIAVSWAIAAAYSFGLLYSRANVAGLDDFLKSIYCIGSCNLLFNALW
GALDTLIAFFLPCTIMVGLYAKIFSVAKGHIKKIEDVNRELNLKNEHVQSSERKAAKTLGIVVGA
FIFCWMPFFVNSIVDPYTNFSTPAILFEIFTWLGYFNSTLNPIIYGLFYPWFRKSLYLIVTLKIF
SPHSSDINIFPS*

### *Dicentrarchus labrax*

>Dl-taar13a

MMTGSLSQEQYCFPGSNASCVMAQLRMGTKFALYLLFALGMLVTILGNSVVIVSISHFKQLHNPT
NMLILSLALVDLLVGVIVMPFSAFRTIHGCWFYGDAFCLLHSSFDVFFTTLSIFHLICIAVDRQQ
AICNPLHYSRKITMPVAWFMICVSWTLAAVYSYGLLYSKANIEGLEDYILSINCLGSCFLLFNPL
WGVLDSVICFFFPCTVMVCLYTKIFIVAKEHVRQIGDMSNFSIDRGKGGLIKQSEHKAAKTLGIV
LGAFIFCWMPFFITSVTDAFTGFSTPVAIFEAFVWLGYLNSTLNPIIYALFYPCFKKCFYCIATL
KIFSSNSSTMNVSVN*

>Dl-taar13b

MMTGSLSQELYCFPGSNASCVIAQFGVGTKATLTLLFAFGMLVTILGNSVVIVSISHFKQLHNPT
NMFILSLALADLLVGVIVMPFSAFRTIHGCWFYGDAFCLLHSSFDMFLTSVSIFHLICIAVDRQQ
AICNPLHYSRKITMPVAWFMICVSWTLAAVYSYGLLYSKANIEGLEDYILSINCLGSCNLLFNPL
WGVLDSITAFFFPCTVMVCLYTKIFIVAKEHVRKIGDMNNCSNDRGKGGLIKQSEHKAAKTLGIV
LGAFIFCWMPFFINSIIDAFTGFSTPVAIFEASVWLGYFNSTLNPIIYALFYPWFKKCFYLIVNL
KIFNPHSSTIKVHVLTHL*

### *Esox Lucius*

>El-taar13a

MSHTCSCDYVAKISSNFECVLFMAMDVPPQPLDPKLFCYPETNASCTREILNEGAQIALYLLFVL
GILVTILGNGVVIISIAHIKQLHTPTNMLIMSLALADLLIGVTVMPFSSIRAVEGCWYFGEVFCL
LHSSFDMFLTSVSIFHLVFIAIDRYLAVCNPLRYTTNITLPTAWLMVLGSWCLSALYSYGLLYSK
AHVRGQDESIASVYCLGSCDLFFNALWGALDTLIAFFFPCSVMVGLYTKIFFVAKEHVRKIEDRQ
KKLVGGGVVSKRSERKAAKTLGIVVGVFIFCWLPFFVNSIVDPYTNFSHNDFTPDTVFEMFLWLG
YFNSTVNPIIYALFYPWFRKCLNVIVTLKIFNKNSSYINVFAAT*

### *Gasterosteus aculeatus*

>Ga-taar13a

MSLGLSQEQYCFSGSNSSCFRAQFSVETKVTLQLIFSLGMLITILGNSVVIVSIGHFKQLHNPTN
VLIVSLAYADLLVGVTVMPFSAIRTIHGCWFYGEDLCLLHSSFDMFLTTVSIFHLICIAIDRQQA

ICNPLHYSRNITISVAWIMVCASWALAAIYSHGLIYSKANVAGIE!
LLDNIFCFFFPCILMVCLYTKVFIVAKEHVRKIEDMSKSSMNKESGGLIKQSEHKAAKTLGIVLG
GFIFCWMPFFLNSIIDAYTGFSTSAFVFEALVWLGYFNSTLNPIIYALFYPCFKKCFCLIVNLKI
FNSQSSTIKVHILTHV*

### *Gadus morhua*

#### >Gm-taar13a

MLIMTDIINQVEQQLCYPGSNTSCPRAEFHLGAQVALYTLFVLGMLVTVVGNAVVIVSIAHFKQL
HSPTNVLVLSLALADLLLGVTVMPFSTVRAVQGCWFYGDTFCLLHSAFDMFLTSVSIFHLICIAV
DRHEAVCKPLHYSRNITMTVAWLMVSASWALAALYSYCLMYSKANIRGLEDYLASIYCLGSCNLL
FNKLWGTLDTIIAFFFPCTIMVGLYAKIFLVAREHARKIDDMGGHGGTLNGKGAGGQTKRSEHKA
AKTLGIVVGAFIFCWMPFFLNSIADAYTGFSTPEAVFEVFVWLGYFNSTLNPVIYALNYPWFRKT
SRLIFTLKIFTSGSSSMNVTVN*

#### >Gm-taar13b

MRVCVYLCMLIMIDRIYQIEQQLCYPGSNTSCPRAEFHLGAQVALYTLFVLGMLATVVGNAVVIV
SIAHFQQLHSPTNVLVLSLALADLLLGVTVMPLSTVRAVQGCWFYGDTFCLLHSAFDMFLTSVSI
FHLICIAVDRHEAVCKPLHYSRNITMTVAWLMVSASWALAALYSYCLIYSKANIRGLEDYLASMY
CLGSCNMLFNKLWGTLDTIIAFFFPCTVMVGLYAKIFLVAREHARKIDDMGGHGGTLNGKGAGGQ
TKRSEHKAAKTLGIVVVAFIFCWMPFFLNSIVDAYTGFSTPAAVFEVFSWLSYFNSILNPVIYSL
NYPWFRKTSRLIFTLKIFTSDSSSINVTVN*

#### >Gm-taar13c

MLCEAYTRCCAQIPCRAGISDCVCLCMLIMTDIINQVEQQLCYPGSNTSCPRADFHLGAQVALYT
LFVLGMLVTVVGNAIVIVSIAHFKQLHSPTNVLVLSLALADLLLGLTVMPFSTLRAVQGCWFYGD
TFCLLHSAFDMLLTCNSIFHLICIAVDRHEAVCKPLHYSRNITMTVAWLMVSASWALATLYSYCL
IYSKANIRGLEDYLASIYCLGSCNLLFNKLWGTLDTIIAFFFPCTIMVGLYAKIFLVAREHARKI
DDMGGHGGTLNGKGASGQTKRSEHKAAKTLGIVVGAFIFCWMPFFLNSIADAYTGFSTPAAVFEV
FVWLGYFNSTLNPAIYALNYPWFRKTSRLIFT*

### *Ictalurus punctatus*

#### >Ip-taar13a

MPEVLNPSLLEGAHLEEYCFPDSNVSCLKASYHMAAQTAIYFLLLLATTITILGNSVVIISIAHF
KQLHTPTNILVMSLGLADLIVGVIVMPFSMIRSVDGCWYFGEEFCLWHSSFDVFLTTASVFHLVC
IAVDRYEAVSYPLQYPTRVTMPVAWFMVTVSWTAAALYSFGLLLSKANVENLDEYIASTYCLGYC
NILFNELWSVLDTCVCFLLPCSVMICLYAKIFLISKKHARKVDCARQGKNDVTKFSQKVKHENKA
AKTLGIVVGAFNLCWMPFYINSILDPYINFSTPLVLFDIFVWLGYINSTLNPIIYGLFYPWFRKT
LYLMVTLKIFAPDSSDIKVYAA*

#### >Ip-taar13b

MPEALNSSLPEEVDLKTYCFPDSNVSCVKASYNIASKTVLYFILVFAMTITILGNSVVIISIAHF
KQLHTPTNILVMSLALVDLLLGLTVMPFSMIRSVDGCWYYGEEFCFIHSSFDMCLTTASIFHLIS
IATDRYEAVCHPLQYPSRVTIPVAWLMVALSWTAAAVYSYGLLCSKANVEKLDEYIASISCLGYC

GLLFNALWAALDACICFFLPCSVMFCLYAQIFFISKKHARKIEGVKPGRNDMNLTKFSQRVKHEN
KAAKTLGIVVGAFICCWMPFFVTSLLDPYINFATPLIIFDVFVWLGYINSALNPIIYGLFYPWFR
KTLHLIVTLKIFAPHSSDIKVYAA*

### >Ip-taar13c

MPEALNSSLLEEVDLKTYCFPDSNVSCVKASYNVASKTVLYFILVFAMTITILGNSVVIISIAHF
KQLHTPTNILVMSLALVDLLLGLTVMPFSMIRSVDGCWYYGEEFCFLHSSFDMCLTGASIFHLIS
IAIDRYQAVSYPLQYPSRVTIPVAWFMAVTSWTASVVYSYTLLCSKANVEKLDEYIASISCLGYC
GLLFNALWAALDACICFFLPCSVMFCLYAQIFFISKKHARKIEGVKPGRNDMNLTKFSQRVKHEN
KAAKTLGIVVGAFICCWMPFFVTSLLDPFINFATPLVLYDVFIWLGYINSTLNPIIYGLFYPWFR
KTLHLIVTLKIFCSHSSDMKLYAS*

### >Ip-taar13d

MPDAPNSSLLEEAHLEEYCYPDSNVSCLKMSYHMTTKTVLYFILVFAMTITIIGNFFVIISIAHF
KQLQTPTNILVMSLALVDLLLGITVMPFSMIRSVDGCWYYSKEFCFLHSSFDMCLTGASIFHLIS
IAIDRYQAVCYPLQYPTRVTKPVAWFMVAVSWTVAVVYSYSLLLTKASVDNGFADCLGSCSLFLN
ELWAILSIVTGFILPCCVMIGLYAKIFFISKKHARKIEGVKQGRTDMALTKFSQRVKHENKAAKT
LGIVVGAFNFCWMPFFLTSLLDPFINFATPLLLYDVFVWLGYINSTLNPIIYGFFYPWFRKTLYV
IVTLKIFAPHSSDMKVYTS*

### >Ip-taar13e

MPGSLSYLQEEADFKVYCFPDYNASCLKNPHNVATQTVLYFILVFAMTITIIGNSFVIISIAHFK
QLQTPTNILVMSLALVDLLLGITVMPFSMIRSVDGCWYYSKEFCFLHSSFDMCLTGASIFHLISI
AIDRYQAVCYPLQYPTRVTKPVAWFMVAVSWTVAVVYSYSLLLTKASVDNEFADCLGSCSLFMNA
LWAILSIVTGFFLPCSAMIGLYAKIFFISNKHARKIEGVKQGRTDMALTKFSQRVKHENKAVKTL
GIVVGAFNFCWLPYFLTSLLDPFINFATPILLYDVFVWLGYINSTLNPIIYGFFYPWFRKTLYLI
VTLKIFAPHSSDMKVYTS*

### >Ip-taar13f

MLDAPNSSLLEAADLREYCYPESNVSCVKISQNVVARTVLYSLLVFATVITILGNSMVIISIAHF
KQLHTPTNILVMSLALVDLLLGLTVMPFSMVRSVDGCWYFSEEFCFWHSSFDFLFTGASIFHLIF
IAVDRYQAVCHPLQYPTRVTKRVAWLMAALSWTIAAGYSYSLLLTKANVENLDDYAASINCLGSC
IFLINALCAVLSTFIGLILPCSFMICLYAQIYLISTRHAIKIGATKQSRHNRTIKVSQRVKHENK
AAKTLGIVVSAFHFCWMPYFITSVVDPFLNFTTPPSLYEVFVWLGYINSTLNPIIYGLFYPWFRK
ALYLILTLKIFARNSSDIKVYAT*

### >Ip-taar13g

MVEAQNSAVLEVEDFIEYCYPESNVSCVKMSHNVVAKTVLYSILVFAMAITIVGNFVVIISIAHF
KQLHTPTNILVMSLALVDLLLGITVMPFSMVRTVDGCWYFGKEFCYWHSTFDFLFTGASIFHLIS
IATDRYQAVCYPLQYPTRITLPVAGFMAALSWILATVYAFSTVGSKANEANLQDYIASIECFGNC
FFLVNAICASISTSLFFILPVCIMIGLYAQIFLVSEKHARKMEGTKQNRTDMTSNKIFQKVKHEK
KAAKTLGIVVGAFNLCWMPYFITSVVDPLYNFTTPAIVYELFVWLGYINSTFNPIIYGLFYPWFR
KTLYLIVTLKIFAPNSSDIKVYAA*

>Ip-taar13h

```
MEAQNSAVLEVEDFIEYCYPESNVSCVKMSHNVVAKTVLYSILVFVLAITIVGNFVVIISIAHFK
QLHTPTNILVMSLALVDLLLGVTIMPFSMVRTVDGCWYFGKEFCYWHSTFDFLFTGASIFHLISI
ATDRYQAVCYPLQYPTRITLPVAGFMAALSWILATVYAFSTVGSKANEANLQDHIASIDCFGKCF
LLVNAVCASICASLFFILPVCIMIGLYAQIFLVSEKHARKMEGTKQNRTDMTSNKIFQKVKHEKK
AAKTLGIVVGAFNLCWMPYFITSVVDPLYNFTTPAIVYELFVWLGYINSTFNPIIYGLFYPWFRK
TLYLIVTLKIFAPNSSDVKVYAA*
```

### *Lates calcarifer*

>Lac-taar13a

```
MTGGLSPEQYCFPDSNASCVMAQFSVGTKVALYLLFALGMLVTILGNSVVIVSIAHFTQLQNPTN
VLVLSLALADLLVGVVVMPFSAIRTVHGCWFYGDAFCLLHSSFDMFLTSVSIFHLICIAVDRHQA
ICNPLHYSRKITISVACFMVCVSWALAALYSYGLLYSKANIAGLEDYIASIYCLGSCNLLFNQLW
GVLDSITAFFFPCTVMVCLYTQIFIVAKEHVRKIGDMNNSSNDRGRGGLIKQSEHKAAKTLGIVL
GAFIFCWMPFFITSITDAYTGFITPAAIFEAFVWLGYFNSTLNPVIYAFFYPWFKKCFYLIVSLK
IFNPNSSTIKVNIRTHS*
```

>Lac-taar13b

```
MTGGLSPEQYCFPDSNASCVMAQFSVGTKVALYLLFALGMLVTILGNFVVIVSIAHFTQLQNPTN
VLVLSLALVDLLVGVVVMPFSAIRTVHGCWFYGDAFCLLHSSFDVFFTTLSIFHLICIAVDRHQA
ICNPLHYSRKISISVACFMVCVSWALAALYSYGLLYSKANIAGLEDYIASIYCLGSCNLLFNQLW
GVLDSIICFFFPCTVMVCLYTQIFIVAKEHVRKIGDMNNSSNDRGRGGLIKQSEHKAAKTLGIVL
GAFIFCWMPFFITSITDAYTGFITPAAIFEAFVWLGYFNSTLNPVIYALFYPCFKNCFYCIVTLK
IFSSNSSNMHISLK*
```

### *Labrus bergylta*

>Lb-taar13a

```
MMVVGFSQEQFCFPESNASCVLTQFSVGTKFILYLLFSLGMLITILGNTVVIVSISHFKQLHNST
NVLILSLALVDLLVGVIVMPFSAIRTVHGCWFYGEVFCQLHSSFDMFLTSVSIFHLICIAIDRHE
AICDPLHYSMKITMPVAWIMVCCSWALAAVYSFGLLYSKANVAGLEDYIESIYCLGSCNLLFNHL
WGILDSIIAFFFPCIVMVCLYTKIFIVARDHVRKIGDMKSSSNERGKIGFIKQSEHKAAKTLGIV
LGSFIFCWMPFFLNSIADAYTGFSTPVAVFEAFVWLGYFNSTLNPIIYALFYPWFRKCFYLIINL
KIFSPNSSSIKVHTLTQL*
```

>Lb-taar13b

```
MMVVGFSQEQFCFPESNASCVLTQFSVGTKFILYLLFSLGMLITILGNTVVIVSISHFKQLHNST
SVLILSLALVDLLVGVIVMPFSAIGTVHGCWFYGEVFCQLHSSFDMFLTSVSIFHLICIAIDRHE
AICDPLHYSMKITMPVAWIMVCCSWALAAVYSFGLLYSKANVAGLEDYIESINCLGSCNLLFNHL
WEILDSIIVFFFPCIVMVCLYTQIFIVAKEHLQKIGDVKHSSKDRGRIWVIKQSEHKAAKTLGIV
LLLLDAIFL!
NSVGDAYNGFSTPVAVFETFVWLGYFNSTLNPIIYALFYPCFKKCFYRIITLKIFSPNSSTMNVS
LK*
```

>Lb-taar13c

MMTGGLSEEHYCFPGFNVSCVRTQFSVGTKFALFMLFALSMGLTILGNTVVIVSISHFKQLHNPT
NVLILSLALVDLLVGVIVMPFSAIRTVHGCWFYGEVFCQLHSSFDMFLTTLSIFHLICIAVDRQQ
AICDPLHYSMKITMPVAWIMVCCSWALAAVFSFGLLYSKANVAGLEDYIESINCLGSCYLLFNHL
WGILDSIIVFFFPCIVMVCLYTQIFIVAKEHLQKIGDVKHSSKDRGRIWVIKQSEHKAAKTLGIV
LGAFIFCWMPFFLNSVGDAYNGFSTPVAVFETFVWLGYFNSTLNPIIYALFYPCFKKCFYCIITL
KIFSPNSSTMNVSLK*

>Lb-taar13d

MMTGGLSEEHYCFPGFNVSCVRTQFSVGTKFALFMLFALSMGITILGNTVVIVSISHFKQLHNPT
NVLILSLALVDLLVGVIVMPFSAIRTVHGCWFYGEVFCQLHSSFDMFLTTLSIFHLICIAVDRHE
AICDPMHYSMKITMPVAWIMVCCSWALAAVYCFGLLYSKASVAGLEDYIESIYCLGSCYLLFNHL
WGILDSILSFFFSCTVMIFLYTKIFIVAKAHAQKIGDVKKGTNEKGRAGLLKQSEHKAAKTLSIV
LGAFIFCWMPFFTISLFEMILGFSTPVAVFEAFFWLGYFNSTLNPIIYALFYPCFKKCFYCIITL
KIFSPSSSTMNVAFK*

***Larimichthys crocea***

>Lc-taar13a

MMTGGLSQEQYCFPGYNASCVRTQFSVGTKFALSLLFTIGMLITILGNSVVIVSIRHFKQLHNPT
NLLILSLALADFLVGVIVMPFSADRTINGCWFYGEAFCLLHSSFDMFLTSVSIFHLICIAVDRQQ
AICNPLHYYRKITMSVAWIMVCGSWALAAIYSYGLLYSKANIVGLEDYILSINCLGSCNLLFNPL
WGILDSITAFFFPCTVMVCLYAKIFITAREHVRKIETSNDRERGGLIKQSEHKAAKTLGIVLGAF
ILCWMPFFINSIIDAFTGFSTPAAVFEAFVWLGYFNSTLNPIIYAFFYPWFKKCFYLIVNLKIFQ
PNSSTINVHVLTQV*

>Lc-taar13b

MMTGGLSQEQYCFPGYNASCVRTQFSVGTKFALSLLFTIGMLITILGNSVVIVSIRHFKQLHNPT
NLLILSLALADFLVGVIVMPFSADRTINGCWFYGEAFCLLHSSFDMFLTSVSIFHLICIAVDRQQ
AICNPLHYYRKITMSVAWIMICGSWALAALFSYGLLYSKANIVGLEDYILSINCLGSCNLLFNPL
WGILDSITAFFFPCTVMVCLYAKIFITAREHVRKIETSNDRERGGLIKQSEHKAAKTLGIVLGAY
IVCWMPFFINSIIDAFTGFITPAAIFESFVWLGYFNSTLNPIIYAFFYPWFKKCFYLIVNLKIFQ
PKSSTIKVHVLTHS*

>Lc-taar13c

MFWHIFRLMMTAGLSQEQYCFPGYNASCVRTQFSVGIKFALSLLFALGILVTILGNSVVIVSICH
FKQLHNPTNLLILSLALADFLVGVIVMPFSADRTINGCWFYGEAFCLLHSCLDMSLTTVSIFHLI
CIAVDRQQAICNPLHYYRKITMSVAWIMICGSWALAALFSYGLLYSKANIVGLEDYILSINCLGS
CYLLFNPLWGIVDSITCFFFPCTVMVCLYAKIFITAREHVRKIGDMNCSNDRERGGLIKQSEHKA
AKTLGIVLGAYIVCWMPFFINSIIDAFTGFITPAAIFESFVWLGYFNSTLNPIIYAFFYPWFKKC
FYLIVNLKIFQPKSSTIKVHVLTHS*

### *Lepisosteus oculatus*

>Lo-taar13a

MDVSMLQELRKENFCYPTINGSCTREVRSLTTYILLYILLSTGMIITIFGNLVVMISITYFKQLH
TPTNMLVLSLALADFLLGMSVMPFSMIRSVETCWYYGDMFCQLHSSFDMFLTTVSIFHLIFIALD
RYQAVCNPLHYYSKITNRVAWLMIGVSWGVAAIYTYGLLYSRGNAEGLNEYVSSTYCLGSCVLFY
NALWGSLDTLIAFFLPCCIMVGLYTKIFFIARKHVVQIGTKTDQEKKDRFSEKSEWKAAKTLGIV
VGVFILCWMPFFVNSIIDPFTNFSTPAILFELFVWLGYFNSTLNPIIYAFFYPWFQKSLKLIVTF
RIFTKHSSSTKLFSEQI*

>Lo-taar5-like

MKSTDLEINLLEYCFENMTLSCIKVVRSPAIKVILYCVFLLTVLITIFGNLVVIISISHFRQLHL
PSNLLILSLATADFLLGLFVLPFSMIRTVESCWYMGSFFCKLHTSIDLLLCLASVFHVFFIAFYR
YYAVCHPLHYTSKMTTQVTFRFIVVGWVFPTICSIAFISFHYQDKETENTGSKVGCEGSCILLFN
EIFNFMDSLTFYVACLITLLMYARIFTIARKQANHISMEARTTYLEHNKIHFKGGNDRKAVKTLG
IVVGCFLFCWLPFITDKTVDPYVNFDTPAVVYDSFIWLAYFNSTFNPFIYAFFFPWFRKALKIIA
TCKIFRPNSSRIQIYTE*

### *Leuciscus waleckii*

>Lw-taar13a

MDLSSQEYDPTELCFPAVNNSCLKGTHLVSTQTVFYLILVSAMTVTILGNSVVIISIAHFKQLQT
PTNILVMSLALADLLLGLVVMPFSMIRSVNGCWYYGDTFCLLHSSFDLFLTSVSIFHLIFIAIDR
HQAVCYPLQYPTRITIPVAWVMVMISWSMAALYSYGLVYSKANVEGLEEFIESIYCMGSCTLLFN
ALWSVLDTLLTFFLPCSVMVGLYARIFVIARKHIRKIGDANQHENESTFKSSRRSERKAAKTLGV
VVGAFILCWLPFFINSIMDPYINFSTPVALFEAFVWLGYINSTINPIIYGLFYPWF!
KTLSLIITMRIFEPNSSDITVFTV*

>Lw-taar13b

MDLSSQEYDPTELCFPAVNNSCVKGTHLVSTQTVLYLILVSAMTVTILGNSVVIISIAHFKQLQT
PTNILVMSLALADLLLGLVVMPFSMIRSVNGCWYYGDTFCLLHSSFDLFLTSVSIFHLIFIAIDR
HQAVCYPLQYPTRITIPVAWVMVMISWSMAALYSYGLVYSKANVEGLEEFIASIYCMGSCSLLFN
ALWGALDTLIGFFLPCSVMVGLYARIFVIAKKHARKLDDANQHEKENVFKSSRRSERKAAKTLGV
VVGAFIICWLRFLL!
SMLDPYINFSTPVSLFEVFVWLGYINSTIKPIIYGLFYPWFRKTLSLILTMRIFEPNSSDINVFT
V*

### *Morone saxatilis*

>Ms-taar13a

MMTGDFSQDLYCFPGSNASCVIAQFGVGTKFALYLLFALGMLVTILGNSVIVSISHFKQLHNPTN
MLILSLALVDLLVGVIVMPFSAFWTIHGCWFYGDAFCLLHSSFDVFLTTLSIFHLICIAVDRQQA
ICNPLHYSRKITMPVAWFMICVSWTLAAVYSYGLFSKANIFNPLWGVLDSVICFFFPCTVMVCLY
TKIFIVVKEVKELKRHL

## *Pimephales promelas*

### >Pp-taar13a

```
MDLSSQEYDLTEFCFPAVNNSCLKGTHLVSTQTVLYLILVLAMTVTILGNSVVIISIAHFKQLQT
PTNILVMSLALADLLLGLVVMPFSMIRSVDGCWYYGDAFCLLHSTFDLFLTSVSIFHLIFIAIDR
HQAVCYPLQYPRRITMSVAWVMVLISWSMAALYSYGLLYSKANVEGMEEFIASTYCLGSCTLFFN
ALWSVLDTLLTFFLPCSVMVGLYARIFVIARKHIRTIGDAKQHENETTFKSSRRSERKAAKTLGV
VVGAFIVCWLPFFINSMMDPYINFSTPVALFEAFVWLGYINSTINPIIYGLFYPWFRKTLSLIIT
MKIFEPNSSDITVFTV*
```

### >Pp-taar13b

```
MDLSSQEYDLTEFCFPAVNNSCLKGTHLVSTQTVLYLILVLAMTVTILGNSVVIISIAHFKQLQT
PTNILVMSLALADLLLGLVVMPFSMIRSADGCWYYGDAFCLLHSTFDLFLTSVSIFHLIFIAIDR
HQAVCYPLQYPRRITISVAWVMVLISWSMAALYSYGLVYSKANVEGLEEFIASTYCLGSCTLFFN
ALWGALDTLIGFFLPCSVMVGLYARIFVIAKKHARKVDNANQHEKENVFKSSRRSERKAAKTLGV
VVGAFIICWLPFFINSMIDPYINFSTPVALFEVFVWLGYINSTINPIIYGLFYPWFRKTLSLIIT
MKIFEPNSCDINVFTV*
```

## *Pygocentrus nattereri*

### >Pyn-taar13a

```
MLQATNSSFLVEADLKEYCYPESNVSCVRSFYSVAARSVLYVLLVLAMSVTILGNSVVIISIAHF
KQLHTPTNMLVMSLALADLLLGVIVMPFSMIRSVDGCWYFGEAFCLLHSSFDMLLTTASIFHLMC
VATDRYQAVCHPLQYPTRITIPTAWLMVAVSWITAAGYSYGLMYSKANVEKLDEYIESISCMGSC
NLVFNALWGALDTLIGFLLPCTVMFCLYAQIFLVSKRHARKIEGTKQSRNETSLNKVSQSMKREN
KAAKTLGIVVGAFIFCWIPFFINSLIDPYINFSTPVVLFEVFVWLGYINSTLNPIIYGLFYPWFR
KCLNLIVTLRIFAPHSSDTNVFAA*
```

### >Pyn-taar13b

```
MLQATNSSFLVEADLKEYCYPESNVSCVRSFYSVAAQSVLYVLLVLAMSVTILGNSVVIISIAHF
KQLHTPTNMLVMSLALADLLLGVIVMPFSMIRSVDGCWYFGEAFCLLHSSFDMLLTTASIFHLIC
ISVDRYQAVCHPLQYPTRITIPTAWLMVAVSWITAAGYSYGLMYSKANVENLDEYIESISCMGSC
NILFNTLWGPLDVLLCFLLPCTVMFCLYAQIFLVSKRHARKIEGTKQSKTETSLNNISQSMKREN
KAAKTLGIVVGTFIFCWIPFFINSIIDPYINFSTPVVLFEVFVWLSYINSTLNPIIYGRFSPWFR
KCLYLIVTLRIFAPHSSDTNVFAA*
```

### >Pyn-taar13c

```
MLQATNSSFLVEADLKEYCYPESNVSCVRSFYSVAAQSVLYVLLVLAMSVTILGNSVVIISIAHF
KQLHTPTNMLVMSLALADLLLGVIVMPFSMIRSVDGCWYFGEAFCLLHSSFDIFLTSASTFHLMC
VAIDRYQAVCHPLQYPTRITIPTAWVMVAVSWITAAGYSYGLMYSKANVVNLDEYIESISCMGSC
NLVFNALWGPLDALLCFLSPCTVMFCLYAQIFLVSKRHARKIEGTKQSRNETSLNKVSQSMKREN
KAAKTLGIVVGTFIFCWMPFYVNSLMEPHINFSTPVELFEVFVWLGYINSTLNPLIYGLFYPWFR
KCLYLIVTLRIFAPHSSDTNVFAA*
```

#### >Pyn-taar13d

MLQATNSSFLVEADLKEYCYPESNMSCVRSFYSVVARSVLYVLLVLAMSVTILGNSVVIISIAHF
KQLHTPTNMLVMSLALADLLLGVIVMPFSMIRSVDGCWYFGEAFCLLHSSIDIFLTSASTFHLMC
VATDRYQAVCHPLQYPTRITIPTAWVMVAVSWITAAGYSYGLMYSKANVVNLDEYIESISCMGSC
NLVFNALWGPLDVLLCFLSPCTVMFCLYAQIFLVSKRHARKIEGTKQSRNELSLNKVSQSMKREN
KAAKTLGIVVGTFIFCWMPYYINSLTNPYINFSTPVELFEVFVWLGYINSTLNPIIYGLFYPWFR
KCLYLIVTLRIFAPHSSDTNVFAA*

### ***Sinocyclocheilus anshuiensis***

#### >Sa-taar13a

MDLSSQEYDPTQFCFPAVNNSCLKGTHHVSTQTVVYLLLVLAMTVTILGNLVVIISIAHFKQLQT
PTNILVMSLALADLLLGLVVMPFSMIRSVGGCWYYGDAFCLLHSTFDLFLTSVSIFHLIFIAIDR
HQAVCYPLQYPARITIPVAWVMVMISWCMAALYSYGLVYSKANVEGLEEYIESIYCMGSCTLLFN
ALWGAIDTLIAFLLPCSVMVGLYARIFVIAKQHARKLCETNQHEKENMFKSSRRSERKAAKTLGV
VVGAFIICWLPFFINSLIDPYINFSTPIALFEVFVWLGYINSTINPIIYGLFYPWFRKTLSLIIT
RRIFEPNSSDINVFTV*

#### >Sa-taar13b

KFCSLLYPTRITIPVAWVMVMISWSMAALYSYGLVYSKANVEGLEEYIESIYCMGSCTLLFNALW
SV*THYLTFFLPCSVMIGLYARIFVVAKKHIRTIGEANQQENVSTFKSSRRSERKAAKTLGVVVG
AFIICWLPFFINSMDPYINFSTPFVLFEAFVWLGYINSTINPIIYDLFYPWFRKTFLSL

#### >Sa-taar13c

MDLSQEYDLTQFCFPAVNNSCLRGTHHVSTQTVVYLLLVSAMTVTILGNSVVIISIAHFKQLQTP
TNILVMSLALADLLLGLVVMPFSMIRSVDGCWYYGDAFCLLHSSFDLFLTSVSIFHLIFIAIDRH
QAVCYPLQYPTRITIPVAWVMVMISWSIAALYSYGLVYSKANVEGLEEYSDSMYCMGSCTLLFNA
LWSVLDTLLTFFLPCSVMIGLYARIFVVAKKHIRTIGEANQYENENMFKTSRRSERKAAKTLGVV
VGAFIICWLPFFINSLMDPYINFSTPFVLFDTFGWLGYINSTINPIIYGLFYPWFRKSLSLIVTM
RIFEPNSSDISVFTV*

#### >Sa-taar13d

MDLSSQEYDPTQFCFPAVNNSCLKGTHHVSTQTVVYLLLVLAMTVTILGNLVVIISIAHFKQLQT
PTNILVMSLALADLLLGLVVMPFSMIRSVIGCWYYGDAFCLLHSTFDLFLTSVSILHLVCIAIDR
HQAVCYPLQYPTRITIPVAWVMVMISWALIAVYSYGLLYSEANVEGLEEYIESIYCIGRCSLLFS
KLWSVLDTLITFFFPCSVMIGLYVRIFVVAKKHVRIISEANQHEIQNVFKSSRRSERKAAKTLGV
VVGAFIICWLPFFINSVMDPYINFSTPLALFEVFVWLGYINSTINPIIYGFFYPWFRKTLSLIIT
RRIFEPNSSDINVFTV*

#### >Sa-taar13e

MDLSSQEYDPTQFCFPAVNNSCLKGTHHVSTQTVVYLLLVLAMTVTILGNLVVIISIAHFKQLQT
PTNILVMSLALADLLLGLVVMPFSMIRSVGGCWYFGDAFCLLHSSFDLFLTSVSIFHLIFIAIDR
HQAVCYPLLYPTKITIPVAWVMVMISWCMAALYSYGLVYSKANVEGLEEYIESIYCMGSCTLLFN
ALWSVLDTLLTFFLPCSVMIGLYARIFVVAKKHIRTIGEANHHENESTFKSSRRSERKAAKTLGV

VVGAFIICWLPFFINSLIDPYINFSTPFALFEAFVWLGYINSTINPIIYGLFYPWFRKTLSLIIT
LKIFEPNSSDISVFTV*

### *Sebastes aleutianus*

>Sea-taar13a

MDLSLFGFFWVISEVLAYVFELMMSFDLSQEQYCFPGSNTSCVRAHFSVGTKVALYLLFALGMLV
TILGNSVVIVSIGHFKQLHNPTNVLIVSLALVDLLVGVTVMPFSTIRTIDGCWFYGDDFCLLHSS
FDVFFTTLSIFHLICIAVDRQQAICNPLHYSRNITMSVAWIMVCASWALAAVYSYGLLYSKANVA
GLEDYMASIDCLGSCYLLFNPLWGXLDSIVCFFFPCTVMVCLYTKIFIVAKEHVRKIGDMHNRSN
DRVGGGLIKQSEHKAAKTLGIVLGAYIFCWMPFFINSIIDVYIGFSTPVAIFEAFVWLGYFNSTL
NPIIYAFFYPCFKKCLYCIVTLKAFPSNP*

>Sea-taar13b

MSLDLSQEQYCFPGSNASCVRAHFSIGTKVALYLLFTLGMLVTILGNSVVIVSIGHFKQLHNPTN
VLIVSLALADLLVGLTVVPFSTIRTIHGCWFYGDDFCMLHSCFDMFLTTVSIFHLICIAVDRQQA
ICNPLHYSSNITMSVAWIMVCASWALAAVYSYGLLYSKANVAGLEDYIASIDCLGSCNILFNSLW
GILDSIASFFFPCTVMVCL

>Sea-taar13c

MTFGLSEEXYCFPGSNALCVREQFSVGAKVALYLLFT!
RMLVTILGNSVVIVSIGHFKQLHNPTNVLIVSLALVDLLVGVTVMPFSTIRTIHGCWFYGDDFCM
LHSSFDMFLTTVSIFHLICIAVDRQQAICNPL!
YSSNITMSVAWIMVCASWALAAVYTYGLLYSKANVAGLEDYMASIDCLGSCNLLFNSLWGILDS

### *Sebastes minor*

>Sem-taar13a

ILGNSVVIVSIGHFKQLHNPTNVLIVSLALVDLLVGVTVMPFSTIRTIHGCWFYGDDFCLLHSSF
DVFFTTLSIFHLICIAVDRQQAICNPLHYSRNITISVAWIMVCASWALAAVYSYGLLYSKANVAG
LEDYMASIDCLGSCYLLFNPLWGVLDSIVCFFFPCTVMVCLYTKIFIVAKEHVRKIGDMHNxxxK
QSEHKAAKTLGIVLGAYIFCWMPFFINSIIDVYIGFSTPVAIFEAxxxLGYFNSTLNPIIYAFFY
PCFKKCLYCIVTLKAFPSNP*

>Sem-taar13b

VTILGNSVVIVSIGHFKQLHNPTNVLILSLALADLLVGLTVVPFSTIRTIHGCWFYGDDFCMLHS
SFDMFLTTVSIFHLICIAVDRQQAICNPLHYSSxxxSVAWIMVCASWALAAVYSYGLLYS

### *Sebastes nigrocinctus*

>Sn-taar13a

MDLSLFGFCWVICEVLVYLFELMMSFDLSQEQYCFPGSNASCVRAHFSVGTKVALYLLFTLGMLV
TILGNSVVIVSIGHFKQLHNPTNVLIVSLALVDLLVGVTVMPFSTIRTIHGCWFYGDDFCLLHSS
FDVFFTTLSIFHLICIAVDRQQAICNPLHYSRNITMSVAWIMVCASWALAAVYSYGLLYSKANVA
GLEDYMASIDCLGSCYLLFNPLWGVLDSIVCFFFPCTVMVCLYTKIFIVAKEHVRKIGDMHNRSN

```
VREGGGLIKQSEHKAAKTLGIVLGAYIFCWMPFFINSIIDVYIGFSTPVAIFEAFVWLGYFNSTL
NPIIYAFFYPCFKKCLYCIVTLKAYPSNP*
```

### *Sebastes rubrivinctus*

```
>Ser-taar13a
MDLSLFGFCWVICEVLVYLFELMMSFDLSQEQYCFPGSNASCVRAHFSVGAKVALYLLFTLGMLV
TILGNSVVIVSIGHFKQLHNPTNVLIVSLALVDLLVGVTVMPFSTIRTIHGCWFYGDDFCLLHSS
FDVFFTTLSIFHLICIAVDRQQAICNPLHYSRNITMSVAWIMVCASWALAAVYSYGLLYSKANVA
GLEDYMASIDCLGSCYLLFNPLWGVLDSIVCFFFPCTVMVCLYTKIFIVAKEHVRKIGDMHNRSN
VREGGGLIKQSEHKAAKTLGIVLGAFIFCWMPFFINSIIDVYIGFSTPVAIFEAFVWLGYFNSTL
NPIIYAFFYPCFKKCLYCIVTLKAYPSNP*
```

```
>Ser-taar13b
MMSFVLSQEQYCFPGSNASCVREQFSVGTKVALYLLFTLGMLVTILGNSVVIVSIGHFKQLHNPT
NVLILSLALSDLLVGVTVMPFSTIRTIHGCWFYGTKVALYLLFTLGMLVTILGNSVVIVSIGHFK
QLHNPTNVLILSLALSDLLVGLTVMPFSTIRTIHGCWFYSDDFCLLHSSFDMFLTSVSIFHLICI
AVDRQQAICNPLHYSRNITMSVAWIMVCASWALAAVYSYGLLYSKANVAGLEDYIASIDCLGSCN
LLFNSLWGILDSITAFFFPCTVMVCLYTKIFFVAKEHVRKIGX
```

### *Sebastes steindachneri*

```
>Ses-taar13a
NPTNVLIVSLALVDLLVGVTVMPFSTIRTIHGCWFYGDDFCMLHSSFDVFFTTLSIFHLICIAVD
RQQAICNPLHYSRNITMSVAWxxxKANVAGLEDYIASIDCLGSCYLLFNPLWGVLDSIVCFFFPC
TVMVCLYTKIFIVAKEHVRKIGDMHNRSNDRVGGGLIKQSEHKAxxxIFCWMPFFINSIIDVYIG
FSTPVAIFEAFVWLGYF
```

### *Scleropages formosus*

```
>Sf-taar13a
MNISREPDAEQYCYPASNRTCTKYIHSAAAYAALYAFFALGSAVTVTGNLVVLVSIAHFRQLHTP
ANMLIMSLAMADLLVGILVMPFSAIRTIEGCWYFGEAFCLLHSTFDLFLTSVSIFHLISIAIDRY
QAVCNPLRYPTTITIPVVWLMIFLSWGAAAAYSYSLLYTKANVAGLEEYIALINCLGSCNLLFNA
LWGALDSLVGFFLPCSVMMGLYAKIFLVARQHVRRLGDNSHQAHMNTENTIRKNHSSERKAARTL
GIVLGVFFLCWMPFFINSVIDPYINFGTPSIVFELLVWLAYFNSTLNPIIYALFYPWFQKSLKFI
VTMKIFTPHSSDFNVFPER*
```

```
>Sf-taar13b
MNISREPDAEQQYCYPAPNRTCTKYIHSAAAYAALYAFFALGSAVTVTGNLVVLVSIAHFRQLHT
PANMLIMSLAMADLLVGILVMPFSAIRTIEGCWYFGEAFCLLHSTFDLFLTSVSIFHLISIAIDR
YQAVCNPLRYPTTVTIPKAWLMVFLSWVAAAAYSYSLLYTKANVAGLGGYIALIKFF!
LGSCNLLFNALWGALDSLVGFFLPCSVMMGLYAKIFLVARQHVRRLGDNSHQAHMNMENTIRKNH
SSERKAARTLGIVMGAFFLCWMPIFINSIIDPYINFGTPSIVFELLVWLAYFNSTLNPIIYALFY
PWFQKSLKFIVTMKIFTPHSSDFNVFPER*
```

>Sf-taar13c

MNISREPDAEQYCYPASNRTCTKYIHSAAAYAALYAFFALGSAVTVTGNLVVLVSIAHFRQLHTP
ANMLIMSLAMADLLVGILVMPFSAIRTIEGCWYFGEAFCLLHSTFDLFLTSVSIFHLISIAIDRY
QAVCNPLRYPTTITIPVAWLMIFLSWGVAAAYSYSLLYTKANVAGLEEYIALINCLGSCNLLFNA
LWAALDSTTEFFLSFSVMMGVYAKIFLVARQHVRRLGDNSHQAHMNTENTIRKNHSSERKAARTL
GIVMGAFFLCWMPFFINSVIDPYINFGTPSIVFEVLVWLGYFNSTLNPIIYALFYPWFQKSLKFI
VTLKIFTPHSSDFNVFPER*

>Sf-taar13d

MNISREPDAEQYCYPASNRTCTKYIHSAAAYAALYAFFALGSAVTVTGNLVVLVSIAHFRQLHTP
ANMLIMSLAMADLLVGILVMPFSAIRTIEGCWYFG!
AWLMVFLSWGAAAAYSYSLLYTKANVAGLEEYIALINCLGSCNLLFNALWAALDTLAEFFLSCCV
MIGVYAKIFLVARQHVRRLGDNSHQAHMNTENTIRKNHSSERKAARTLGIVMGAFFLCWMPFFIN
SIIDPYINFGTPSIVFEVLVWLGYFNSTLNPIIYALFYPWFQKSLKFIVTMKIFTPHSSDFNVFP
ER*

### *Sinocyclocheilus grahami*

>Sg-taar13a

MDLSSKEYDPTQFCYPAVNNSCLKGTHHVSTQTVVYLLLVLAMTVTILGNLVVIISIAHFKQLQT
PTNILVMSLALADLLLGLVVMPFSMIRSVGGCWYYGDAFCLLHSTFDLFLTSVSIFHLIFIAIDR
HQAVCYPLQYPARITIPVAWVMVMISWSMAALYSYGLVYSNANVEGLEEYIESIYCMGSCTLLFN
ALWGAIDTLIAFLLPCSVMVGLYARIFVIAKQHARKLCETNQHENENMFKSSRRSERKAAKTLGV
VVGAFIICWLPFFINSLIDPYINFSTPIALFEVFVWLGYINSTINPIIYGLFYPWFRKTLYLIIT
RRIFEPNSSDINVFTV*

>Sg-taar13b

FHLKGILKFCSLLYPTRITIPVAWVMVMISWSMAALYSYGLVYSKANLEGLEEYSDSIYCMGSCT
LLFNALWSVLDTL!TFFLPCSVMIGLYARIFVV!
KKHIRTIGEANQNENVSTFKSSRWSECKAAKTLGVVVGAFIICWLPFFINSMDPYINLSTPFVLF
EAFVWLGYINSTINPIIYGLFYPWFRKNLSVIITMKIFEPNSSDISVFTV*

>Sg-taar13c

MDLSQEYDLTQFCFPAVNNSCLRGTHHVSTQTVVYLLLVSAMTVTILGNSVVIISIAHFKQLQTP
TNILVMSLALADLLLGLVVMPFSMIRSVDGCWYYGDAFCLLHSSFDLFLTSVSIFHLIFIAIDRH
QAVCYPLQYPTRITIPVAWVMVMISWSIAALYSYGLVYSKANVEGLEEYSDSIYCMGSCTLLFNA
LWSVLDTLLTFFLPCSVMIGLYARIFVVAKKHIRTIGEANQHENENMFKTSRRSERKAAKTLGVV
VGAFIICWLPFFINSLMDPYINFSTPFVLFDTFGWLGYINSTINPIIYGLFYPWFRKSLSLIITM
RIFEPNSSDISVFTV*

>Sg-taar13d

MDLSSQEYDPTQFCFPAVNNSCLKGTHHVSTQTVVYLLLVLAMTVTILGNLVVIISIAHFKQLQT
PTNILVMSLALADLLLGLVVMPFSMIRSVGGCWYYGDAFCLLHSTFDLFLTSVSILHLVCIAIDR
HQAVCYPLQYPARITIPVAWVMVMISWALIAIYSYSLLYSEANVEGLEEYIESIYCIGHCSLLFS
KLWSVLDTLITFFFPCSVMIGLYVRIFVVAKKHVRIISEANQHEIENVFKSSRRSERKAAKTLGV

```
VVGAFIICWLPFFINSVMDPYINFSTPLALFEVFVWLGYINSTINPIIYGFFYPWFRKTLSLIIT
KRIFEPNSSDINVFTV*
```

```
>Sg-taar13e
MDLSSQEYDPTQFCFPAVNNSCLKGTHHVSTQTVVYLLLVLAMTVTILGNLVVIISIAHFKQLQT
PTNILVMSLALADLLLGLVVMPFSMIRSVGGCWYYGDAFCLLHSSFDLFLTSVSIFHLIFIAIDR
HQAVCYPLLYPTKITIPVAWVMVMISWCMAALYSYGLVYSKANVEGLEEYIESIYCMGSCTLLFN
ALWSVLDTLLTFFLPCSVMIGLYAIIFVVARKHIRTIGEANHHENESTFKSSRRSERKAAKTLGV
VVGAFIICWLPFFINSLIDPYINFSTPFALFETFVWLGYINSTINPIIYGLFYPWFRKTLSLIIT
LKIFEPNSSDISVFTV*
```

## *Sinocyclocheilus rhinocerous*

```
>Sr-taar13a1
MDLSSQEYDPTQFCYPAVNNSCLKGTHHVSTQTVVYLLLVLAMTVTILGNLVVIISIAHFKQLQT
PTNILVMSLALADLLLGLVVMPFSMIRSVGGCWYYGNAFCLLHSTFDLFLTSVSIFHLIFIAIDR
HQAVCYPLQYPARITIPVAWVMVMISWSMAALYSYGLVYSKANVEGLEEYIESIYCMGSCTLLFN
ALWGAIDTLIAFLLPCSVMIGLYARIFVIAKQHARKLCETNQHENENMFKSSRRSERKAAKTLGV
VVGAFIICWLPFFINSLIDPYINFSTPIALFEVFVWLGYINSTINPIIYGLFYPWFRKTLSLIIT
RRIFEPNSSDINVFTV*
```

```
>Sr-taar13a2
SEANVEGLEEYIESMYCKGSCTLLFNVVWGAIDT*IAFLLPCSVMVGLYARIFVIVKQHARKLCK
DKNENMFKSS*RSEHKAAKTLSVVVGAFIICWLPFFINSLIDPYINFSTPLVLFEVFVWLGYINS
TINPIIYGFFWYRKTLSLIITSNKFITSSSDINVFTV*
```

```
>Sr-taar13b
KFCSLLYPTRITIPVAWVMVMVSWSMAALYSYGLVYSKANVEGLEEYIESIYCMGSCTLLFNALW
SVLDTL!
TFFLPCSVMIGLYARIFVVAKQHIRTIGEANQHENVSTFKSSRQSECKAAKSLGVVMGAFIICWL
PFFINSMDPYINFSTPFALFEAFVWLGYINSTINHIIYGLFYPWFKKNLSVIITLKIFEPNSSDI
SVFTV*
```

```
>Sr-taar13c1
FWNPVCYPLQYPTRITIPVAWVMVMISWSMAALYSYGLVYSKANVEGLEEYSDSIYCMGSCTLLF
NALWSVLDTLLTFFLPCSVMIGLYARIFVVAKKHIRTIGEANQHENENMFKTSRRSERKAAKTLG
VVVGAFIICWLPFFINSLMDPYINFSTPFVLFDTFGWLGYINSTINPIIYGLFYPWFRKSLSLII
TMRIFEPNSSDISVFTV*
```

```
>Sr-taar13c2
MDLSQEYDLTQFCFPAVNNSCLRGTHHVSTQTVVYLLLVSAMTVTILGNSVVIISIAHFKQLQTP
TNILVMSLALADLLLGLVVMPFSMIRSVDGCWYYGDAFCLLHSSFDLFLTSVSIFHLICIAIDRH
QAVCYPLQYPTRITIPVAWVMV
```

```
>Sr-taar13d
MDLSSQEYDPTQFCFPAVNNSCLKGTHHVSTQTVVYLLLVLAMTVTILGNLVVIISIAHFKQLQT
PTNILVMSLALADLLLGLVVMPFSMIRSVGGCWYYGDAFCLLHSTFDLFLTSVSILHLVCIAIDR
HQAVCYPLQYPTRITIPVAWVMVMISWALIAVYSYGLLYSEANVEGLEEYIESIYCIGRCSLLFS
KLWSVLDTLITFFFPCSVMIGLYVRIFVVAKKHVRIISEANHHETENVFKSSRRSERKAAKTLGV
VVGAFIICWLPFFINSVMDPYINFSTPLALFEVFVWLGYINSTINPIIYGFFYPWFRKTLSLIIT
RRIFEPNSSDINVFTV*
```

```
>Sr-taar13e
MSLFGKDATSSSHLALGILCHSSLQILSSSVRLDGKRWWTAIFRSLQRCSIGFNGDAFCLLHSSF
DLFLTSVSIFHLIFIAIDRHQAVCYPLLYPTKITIPVAWVMVMISWCMAALYSYGLVYSKANVEG
LEEYIESIYCMGSCTLLFNALWSVLDTLLTFFLPCSVMIGLYARIFVVARKHIRTIGEANHHENE
STFKSSRRSERKAAKTLGVVVGTFIICWLPFFINSLIDPYINFSTPFALFEAFVWLGYINSTINP
IIYGLFYPWFRKTLSLIITLKIFEPNSSDISVFTV*
```

### *Salmo salar*

```
>Ss-taar13a
MDISSHQHLDPKMFCYPESNASCTRDIFSGGVQIALYFLFVSGMLVTILGNGVVIISIAHIKQLH
TPTNMLIMSLAVADLLLGVTVMPFSTMRAVEGCWYFGDAFCLLHSSFDMFLTSVSIFHLVFIAID
RYEAVCNPLRYSTKITIPIAWLMVLASWAVAALYSYCLLYSKANVRGLDEFIASIYCLGSCNLVF
NALWGALDTLIAFFFPCSVMVGLYTKIFLVAKEHLRKIEDSQKNSNERDKGVVSQRSERKAAKTL
GIVVGVFIFCWLPFFVNSIVDPYTNFSTPPILFEVFIWLGYFNSTANPIIYGLFYPWFRKCLNLI
VTLKIFNRNSSYINVFATT*
```

```
>Ss-taar13b
MNISSHQHLDPKMFCYPESNASCTRDIFSGGVQIALYFLFVSGMLVTILGNSVVIISIAHIKQLH
TPTNMLIMSLAVADLLLGVTVMPFSTMRPVEGCCYFGDAFCLLHSDMFLTSVSIFHLVFIAIDRY
EAVCNPLRYSTKITIPIAWLMVLASWAVAALYSYCLLYSKANVRGLDEFIASIYCLGSCNIVFNA
LWGTLDTLIAFFFPCSVMVGLYTKILLVAKEHLRKIDDSQKNSNERDKGVVSQRSERKAAKTLGI
VVGVFIFCWLPFFVNSIVDPYTNFST!
YSLFEVFIWLGYFNSTANPIIYALFYPWFRKCLNLIVTLKIFNRNSSYINVFAT
```

```
>Ss-taar13c
MDISSHQHLDPKLFCYPESNASCTREIVS*GVQIALYFLFVSGMLVTILGNSVVIISIAHIKQLH
TPTNMLIMSLAVADLLLGVTVMPFSTMRPVEGCCYFGDAFCLLHSDMFLTSVSIFHLVFIAIDRY
EAVCNPLHYSTKITIPIAWLMVFASWAVAALYSYCLLYSKANVRGLDEFIASIYCLGSCNIVFNA
LWGALDTLIAFFFPCSVMVGLYTKILLVAKEHLRKIEDSQKNSNERDKGVVSQRSERKAAKTLGI
VVGVFIFCWLPFFVNFIVDPYTNFSTPPILFEVFIWLGNFNSTANPIIYALFYPWFRKCLNLIVT
FYLFLIIYLFHLYLTR*
```

# Reference TAAR sequences from all classes (class I, II, III) in several bony vertebrate species (zebrafish, stickleback, fugu and mouse)

Amino acid sequences were taken from Hussain et al., 2009, see also Suppl. Table 1.

>Mm-taar1

```
MHLCHAITNISHRNSDWSREVQASLYSLMSLIILATLVGNLIVIISISHFKQLHTPTNWLLHSMA
IVDFLLGCLIMPCSMVRTVERCWYFGEILCKVHTSTDIMLSSASIFHLAFISIDRYCAVCDPLRY
KAKINISTILVMILVSWSLPAVYAFGMIFLELNLKGVEELYRSQVSDLGGCSPFFSKVSGVLAFM
TSFYIPGSVMLFVYYRIYFIAKGQARSINRTNVQVGLEGKSQAPQSKETKAAKTLGIMVGVFLVC
WCPFFLCTVLDPFLGYVIPPSLNDALYWFGYLNSALNPMVYAFFYPWFRRALKMVLLGKIFQKDS
SRSKLFL
```

>Mm-taar2

```
MASFEAQQETFDCSEYGNGSCPENERSLGVRAAMYSLMACAIFITIFGNLAMIISISYFKQLHTP
TNLLILSMAVTDFLLGFTIMPYSMVRSVENCWYFGLTFCKIHYSFDLMLSITSIFHLCSVAVDRF
YAICHPLHYCTKMTIPVVRRLLLVCWSVPGAFAFGVVFSEAYADGIEGYDILVACSSSCPVMFNK
LWGTTLFVAGFFTPSSMMVGIYGKIFAVSKKHARVIDNLPENQNNQMRKDKKAAKTLGIVMGVFL
LCWFPCFFTILLDPFLNFSTPAVLFDALTWFGYFNSTCNPLIYGFFYPWFRRALKYILLGKIFSS
HFHNTNLFTQKETE
```

>Mm-taar3

```
MDLIYIPEDLSSCPKFGNKSCPPTNRSFRVRMIMYLFMTGAMVITIFGNLVIIISISHFKQLHSP
TNFLILSMATTDFLLGFVIMPYSMVRSVESCWYFGDSFCKFHASFDMMLSLTSIFHLCSIAIDRF
YAVCDPLHYTTTMTVSMIKRLLAFCWAAPALFSFGLVLSEANVSGMQSYEILVACFNFCALTFNK
FWGTILFTTCFFTPGSIMVGIYGKIFIVSRRHARALSDMPANTKGAVGKNLSKKKDRKAAKTLGI
VMGVFLACWLPCFLAVLIDPYLDYSTPIIVLDLLVWLGYFNSTCNPLIHGFFYPWFRKALQFIVS
GKIFRSNSDTANLFPEAH
```

>Mm-taar4

```
MNTPDPWSSPEVQFCFAAANSSCPRKARPALVVCAMYLIMIGAIVMTMLGNMAVIISIAHFKQLH
SPTNFLILSMATTDFLLSCVVMPFSMIRSIESCWYFGDLFCKVHSCCDIMLCTTSIFHLCFISVD
RHYAVCDPLHYVTQITTRVVGVFLLISWSVPIFFAFGLVFSELNLIGAEDFVAAIDCTGLCVLIF
NKLWGVLASFIAFFLPGTVMVGIYIHIFTVAQKHARQIGTGPRTKQALSESKMKATSKKESKATK
TLSIVMGVFVLCWLPFFVLTITDPFIDFTTPEDLYNVFLWLGYFNSTFNPIIYGMFYPWFRKALR
MIVTGTIFRSDSSTSSLHPAHP
```

>Mm-taar5

```
MRAVLLPGSGEQPTAFCYQVNGSCPRTVHPLAIQVVIYLACAVGVLITVLGNLFVVFAVSYFKVL
HTPTNFLLLSLALADMLLGLLVLPLSTVRSVESCWFFGDFLCRLHTYLDTLFCLTSIFHLCFISI
DRHCAICDPLLYPSKFTVRTALRYIVAGWGIPAAYTAFFLYTDVVERALSQWLEEMPCVGSCQLL
FNKFWGWLNFPAFFVPCLIMISLYLKIFVVATRQAQQIRTLSQSLAGAVKRERKAAKTLGIAVGI
```

YLVCWLPFTVDTLVDSLLNFITPPLVFDIFIWFAYFNSACNPIIYVFSYRWFRKALKLLLSREIF
SPRTPTVDLYHD

>Mm-taar6

MGSNSSPPTVLQLCYENVTGSCVKTPYSPGSRVILYAVFGFGAVLAVFGNLMVMISILHFKQLHS
PTNFLIASLACADFGVGISVMPFSMVRSIESCWYFGRSFCTFHTCCDVAFCYSSLFHLSFISIDR
YIAVTDPLVYPTKFTVSVSGICIGVSWILPLVYSGAVFYTGVYDDGLEELSSALNCVGGCQVVVN
QNWVLIDFLSFLIPTLVMIILYGNIFLVARQQAKKIENIGSKTESSSESYKARVARRERKAAKTL
GITVVAFMISWLPYSIDSLVDAFMGFITPAYIYEICVWCAYYNSAMNPLIYALFYPWFKKAIKVI
MSGQVFKNSSATMNLFSEQI

>Mm-taar8a

MTSNFSQPALQLCYENTNGSCIKTPYSPGPRVILYMVYGFGAVLAVCGNLLVVISVLHFKQLHSP
ANFLIASLASADFLVGISVMPFSMVRSIESCWYFGDAFCSLHSCCDVAFCYSSVLHLCFISVDRY
IAVTDPLVYPTKFTVSVSGICISISWILPLVYSSAVFYTGISAKGIESLVSALNCVGGCQIVINQ
DFVLISFLLFFIPTLVMIILYSKIFLVAKQQAVKIETSVSGNRGESSSESHKARVAKRERKAAKT
LGVTVVAFMVSWLPYTIDALVDAFMGFITPAYVYEICCWGTYYNSAMNPLIYAFFFPWFKKAIKL
ILSGEILKGHSSTANLFSE

>Mm-taar9

MTSDFSPEPPMELCYENVNGSCIKSSYAPWPRAILYGVLGLGALLAVFGNLLVIIAILHFKQLHT
PTNFLVASLACADFLVGVTVMPFSTVRSVESCWYFGESYCKFHTCFDTSFCFASLFHLCCISIDR
YIAVTDPLTYPTKFTVSVSGLCIALSWFFSVTYSFSIFYTGANEEGIEELVVALTCVGGCQAPLN
QNWVLLCFLLFFLPTVVMVFLYGRIFLVAKYQARKIEGTANQAQASSESYKERVAKRERKAAKTL
GIAMAAFLVSWLPYIIDAVIDAYMNFITPAYVYEILVWCVYYNSAMNPLIYAFFYPWFRKAIKLI
VSGKVFRADSSTTNLFSEEAGAG

>Dr-taar1b

MDLCYEAMNGSCWKYVRPHAIHVPMLIAIMLIISMTFIGNLLVIISIGHFRQLHTPTNQLILSLA
LCDFLIGLFVMPLSAVRSMQGCWYFGEFLCKLHTCIDITLSTSSIFHLVSVSAERFCAVCGPLRY
RSCFGLSTVLLMISISWLIPGIFAYVMTFLEINIHGGKDFYDAHVRCVGGCHVFFSHGPAVFTSV
FSFYIPGFIIVVIYSRIYMVARNQERSIRLQLNQLRRVYPSRDVQLQTRKATVTIAIVVGAFLVC
WTPFFLCNILNPFIGYATPPMLIDVLMWFGYANSTLNPFIYAFMHSWCRKAVRIIVTGEIFKNNS
SRKDLYT

>Dr-taar10a

MDDHINISQTESWEKPLLCYEFSNRSCQKFVYPLDTRILLYMLFSISSIITIIGNLLVIITVVHF
RQLHTPTNYLILSLAVADLLVGGVVMPPSMLRSIETCWYLGDLFCKIHSSLDVTLCTASILNLCI
ISLDRYYAICHPFQYHSKMTSLATLIMIIICWTVSAVLGFGMIFMELNILGVEDFYYENIRCDGG
CFVFQSKTGGTVFSLICFYIPAFVMLGVYLKILHEAQRQVQAIQSVNSELKKEGKATKTLAIIMG
VFLTFWIPFFLCNLIDPLIGYSVPSLVFDLFLWVGYYNSTCNPIVYAFFYSWFRHAFRVILSKRV
FQTNSSRTILM

### >Dr-taar11

MMNQSHQWSAETFSLCFESINDSCVKTVYSPVFRAPLYLLFIIAIILIVFGNLWVICTISFFQQL
HTPTNYLILSMAVSDLLLGSFVMPPSMLRSLETCWYFGDFFCKFHSATDFTLCNASVLHLVFISI
DRYYAVCQPFHYQSRMTTRVSVFMILISWSFSAFFGFGIIFSELKIEKKRTEELHVACKGGCLAL
HGREIGVTYSLVFYFLPMFIIVSLYSRVFIIALKHVRVINSAASSLSATKMDLKATKTLAIIIGV
FMSCWTPYFMCNIIDPIVNHTIPALLYEVLMWVAYLNAVFNPLVYAFFYSWFRDKSKLLLEKLYK
LC

### >Dr-taar12a

MIKKKIIQDVMTSNQTQTENILLCYPLLSNSCPKLHRLAVVQVGLYVFLLLMILTTVFGNLMIII
SISHFKHLQSPTHLIVQSLAACDCLMGSLVMPYSMVRSVEGCWYLGDVVCKVHFSFDVTFCISSL
LHLCLISVDRYLAICDPLRYKIRVTNTTMTVFIIFIWLFSVVYSFSIVFSGITAVGLEMLILQTY
CVGSCVLFFNKEWAVYPFLTFFITGAIMSSLYMKIFHVARKHAKVMSERVKGGLKSQRSAQRERK
AAKTLAIVMGVFMFCWLPYCAFTALYPFFTFLNSAEVFDVLFWFAYFNSSCNPLIYGFFYPCFQK
AFKILIFLWSQKCKHFSF

### >Dr-taar12b

MTSNETQTDNILLCYPLLSNSCPKLHRLAVVQVGLYVCLLLMILTTVFGNLLIIISISHFKHLQS
PTHLIVQSLAACDCLMGSLVMPYSMVRSVEGCWYLGDVVCKVHSSLDMTFCMSSLLHLGLISVDR
YWAICDPLRYRLRVTNTTVTVFIIVIWLFSFIYNFSIVFSGITAVGLEMLILQTYCVGSCIVLFN
KEWAVYPFLTFFITGAIMSSLYMKIFHVAQKHAKVMSERVTGGLKSQSSAQRERKAAKTLAIVMG
VFMFCWLPYCAFTALYPFFTFLNSAEVFDVLFWFAYFNSSCNPVIYGFFYPCFQKAFKILISTYI
FGIRNANTSTYE

### >Dr-taar12c

MTSNETQTDNVHLCFPLLPNSCSKLHHFVVVKVAMYVCLLLMILTTVFGNLLIIISISHFKHLQS
PTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGDVVCKVHSSLDMTFCISSLLHLGLISVDR
YWAICDPLRYRLRVTNTTVTVFTVFIWLFAFVYSFSVVFSGIAAVGLEMLILQTYCVGSCVLFFN
KEWGLICPILTFFLPGAIMSFLYMKIFHVARKHAKVMSERVTGGLKSQSSAQRERKAAKTLAIVM
GVFMFCWLPYFTVTILGPFFNFATPADVFDALVWFAYLNSTCNPLIYGFFYPCFQKAFHILISTY
ICGVRNSDTLIYE

### >Dr-taar12d

MTSNETQTDNVHLCFPLLPNSCSKLHHFVVVKVAMYVCLLLMILTTVFGNLLIIISISHFKHLQS
PTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGDVVCKVHSSLDMTFCISSLLHLGLISVDR
YWAICDPLRYRLRVTNTTVTVFTVFIWLFAFVYSFSVVFSGIAAVGLEMLILQTYCVGSCVLFFN
KEWGLICPILTFFLPGAIMSFLYMKIFHVARKHAKVMSERVKGGLKSQSSAQRERKAAKTLAIVM
GVFMFCWLPYCAFTALYPFFTFLNSAEVFDVLFWFAYFNSSCNPLIYGFFYPCFQKAFKILIFLW
SQKCKHFSF

### >Dr-taar12e

MMSLNETQTENILLCYPLLSNSCPKLHRLAVVQVGLYVFLLLMILTTVFGNLLIIISISHFKHLQ
SPTHLIVRSLAACDCLLGLLVMPYSMVRSVEGCWYLGDVVCKVHSSLDMTFCISSLLHLGLISVD
RYWAICDPLRYRLRVTNITVTVFIVFIWLFSFVYSFYVVFSGVNTVGLETFIMQVYCVGSCVLYF
NKQWGLICPILVFFLPGAIMSSLYMKIFHVARKHAKVMSERVTGGLKSQSSAQRERKAAKILAIV

MGVFLFCWLPFFTVNALDPFFNFFTPADIFDAVIWFAYLNSTCNPLIYGFFYPCFQKAFKILIFT
YICGVRNLDTFA

### >Dr-taar12f

MKPSNETQTENILLCYPLLSNSCPKLHRLAVVQVGLYVFLLLMILTTVFGNLLIIISISHFKHLQ
SPTHLIVRSLAACDCLLGSLVMPYSMVRSVEGCWYLGDVVCKVHSSLDMTFCISSLLHLGLISVD
RYWAICDPLRYRLRVTNTTVTVFIVFIWLFSFVYSFYVVFSGVNTVGLETFIMQVYCVGNCVLYF
NKQWGLICPILTFFLPGTIMSSLYMKIFHVARKHAKVMSERVTGGLKSQSSAQRERKAAKILAIV
MGVFLFCWLPFFTVNALDPFFNFFTPADIFDAVIWFAYLNSTCNPLIYGLFYPCFQKAFKILIST
YLCGVRNLDTFA

### >Dr-taar12g

MTSNESENIQLCYPLLSNSCPKLHRLAVVQVGLYICLLLMILTTVFGNLLIIISISHFKHLQSPT
HLIVRSLAACDCLLGSLVMPNSMVRSVEGCWYLGDVVCKVHSSLDMTLCISSLLHLGLISVDRYL
AICDPLRYRIRVTNTTVTVFTVFIWLFSVVYSFYVKFSGITAVGLEMLILQTYCVGRCVVFFNKQ
WGLICPVLAFFLPGAIMSSLYMKIFHVARKQAKVISERVTGGLKSQSSAQRERKAAKTLAIVMGV
FLFCWMPFFTLTALDPFFNFLSSADVFDALFWFAYLNSACNPLIYGFFYPCFQKAFKILIFTYIC
GVKKANTLTFE

### >Dr-taar12h

MILNDTDIYSENVLLCYPLLPDSCPRTQRLPALKVAMYAVMVLMILTTVFGNLLVIISISHFKQL
QSPTHLIVQSLAACDCLLGSLVMPYSMVRSVEGCWYLGTVVCKVHSSLDMTFSISSILHLSLIAI
DRFWAISDPLRYKMRVTNTTVAGFITFTWLFSFVYSFSVVFTGVNNVGLEELILQISCFGGCVLF
FNKEWGLICALFVFLIPGTIMSSLYMSIFNVVKRHAKVMSEKVSAAATAGSHFQTSSHRERKAAK
TLAIVMGVFYLCWLPFFTATAVDPFLNFSTPGDVFDALVWFGYFNSTCNPLIYGFFYPRFQKAFK
ILISTYICGSSDSHTLTFE

### >Dr-taar12i

MTSNETQTDNVHLCFPLLPNSCSKLHHFVVVKVAMYVCLLLMILTTVFGNLLIIISISHFKHLQS
PTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGDVVCKVHSSLDMTFCISSLLHLGLVSIDR
YWAICDPLRYRIRVTNTTVTLYTIFIWLFSFLYSFVIVFSGVNRIGLETFIMQVYCVGSCVLFFN
KEWGLICPVLTFFIPGAIMSSLYMKIFHVARKHAKVMSERVTGGLKSQSSAQRERKAAKTLAIVM
GVFLLCWTPIFIASIIDSFLNFVTPAGVFDALIWFGYFNSTCNPLIYGFFYSCFQKAFKILLSSL
FLGFGNSSTLTFE

### >Dr-taar12j

MTSNDTDVHSENVLLCYPLLSDSCPRTQRLTALTVTMYAFMVLMILTTVFGNLLIIISISHFKQL
QSPTHLIVRSLAASDCLLGSLVMPYSMVRSVEGCWYLGDVVCKVHSSLDMTFSISSLIHLSLVSV
DRYWAICDPLRYRMRVTNNTVIVFTVFTWLFSFVYSFSVVFSGVNRIGLETFIMQVYCVGSCVLF
FNKQWGLICSLLTFFLPCTIMSSLYMKIFHVARKHAKVMSERVTGGLKSQSSAQREGKAAKTLAI
VMGVFYLCWLPFFTATAVDPFLNFSTPVHVFDALVWFGYFNSTCNPLIYGFFYPRFQKAFNILIS
TYICGSSDSHTLIPE

```
>Dr-taar12k
MTSNQTQTENILLCYPLLSNSCPKLHRLAVVQVGLYVFLLLMILTTVFGNLMIIISISHFKHLQS
PTHLIVQSLAACDCLMGSLVMPYSMVRSVEGCWYLGDVVCKVHFSFDVTFCISSLLHLCLIAIDR
FWAISDPLRYKMRVTNTTVAGFITFTWLFSFVYSFSVVFTGVNNVGLEELILQISCFGGCVLFFN
KEWGLICALFVFLIPGTIMSSLYMSIFNVVKRHAKVMSEKVSAAATAGSHFQTSSHRERKAAKTL
AIVMGVFYLCWLPFFTATAVDPFLNFSTPGDVFDALVWFGYFNSTCNPLIYGFFYPRFQKAFKIL
ISTYICGSSDSHTLTFE
```

```
>Dr-taar12m
MAANETDVYAENVFLCFPLRLDSCLSAQRLTTVKVAMYILMLLIIFLTVFGNLLVVVSISYFKHL
QSPTHLIVQSLAACDCLLGSLVMPYSMVRSIEGCWYLGDVICKVHSSLDMTLSISSKMHLSLISV
DRYWAICDPLMYRTRVTNYSITVFIMCAWLFAFVYSFSIVFSEVNLIGLEVLVLQISCLGSCVLL
FNKPSALICSILTFFLPGAIMSSLYVKIFRVASKHAKVLSERVSVLEIKSQTYAQRERKAAKIVA
IVVGAFLLCWLPFFVATALDPFLDFWTPADVFDALVWFGYFNSTCNPLIYGFFYPRFQKAFKILM
STVMCGSSSSRTLAFG
```

```
>Dr-taar13a
MDLSSQEYDPSQFCFPAVNNSCLKGTHHVSTQTVVYLILASAMTVTILGNSVVIISIAHFKQLQT
PTNILVMSLALADLLLGLVVMPFSMIRSVDGCWYYGETFCMLHSTFDLFLTSVSILHLVCIAVDR
HQAVCYPLQYPTRITISVAWVMVMISWTLIAIYSYGLVYSKANVEGLEEYIESIYCMGHCSLLFS
KLWSVLDTFITFFFPSCIMVGLYIRIFVVANKHARVITEANPNENENVFKSSRRSERKAAKTLGI
VVGAFIICWLPFFINSLMDPYINFSTPVALFDAFVWLGYINSTINPIIYGFFYPWFRKTLYLIIT
RRIFEPNSSDINVFTV
```

```
>Dr-taar13b
MDLSSQEYDPSQFCFPAVNNSCLKGTHHVSTQTVVYLVLASAMTVTVLGNSVVIISIAHFKQLQT
PTNILVMSLALADLLLGLVVMPFSMIRSVDGCWYYGETFCLLHSTFDLFLTSVSILHLVCIAVDR
HQAVCYPLQYPTRITISVAWVMVMISWAVIAIFSYSLMYSKANMEGLEEYIESIYCMGHCSLLMN
KLWSVLDTFITFFFPSFVMVGLYIRIFVVAKKHARVITEANPNENENLFKSSRRSERKAAKTLGI
VVGAFIMCWLPFFINSTLDAYINFSTPVALFDALVWLGYVNSTINPIIYGFFYPWFRKTLSLIVS
LKIFEPNSSDINVFTV
```

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>Dr-taar13c
MDLSSQEYDPSQFCFPAVNNSCLKGTHHVSTQTVVYLILASAMTVTVLGNSVVIISIAHFKQLQT
PTNILVMSLALADLLLGLVVMPFSMIRSVDGCWYYGETFCLLHTGFDLFLTSVSIFHLIFIAVDR
HQAVCFPLQYPTRITIPVAWVMVMISWSMAAFYSYGVVYSKANLEGLEEYIASVYCMGGCTLYFN
ALWSVLDTLLTFFLPCSVMVGLYARIFVVAKKHIKSITEANQNENENVFKNPRRSERKAAKTLGI
VVGAFILCWLPFFINSLVDPYINFSTPYALFDAFGWLGYTNSTLNPIIYGLFYPWFRKTLSLIVT
LRIFEPNSSDINLFTV
```

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>Dr-taar13d
MDLSSQEYDPSQFCFPAVNNSCLKGTHHVSTQTVVYLILASAMTVTILGNSVVIISIAHFKQLQT
TTNILVMSLALADLLLGLVVMPFSMIRSVDGCWYYGETFCMLHSSFDLFLTSVSIFHLIFIAVDR
HQAVCFPLQYPTMITIPVAWVMVMISWSMAALYSYGLVYSKANMEGLDEYIQSMYCVGGCTLYFN
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ALWSVLDTLITFFLPCSVMIGLYARIFVVAKKHARIINEANQNEIDGTFKSSRRSEQKAAKTLGI
VVGAFIMCWLPFFINSLMDPYINFSTPVALFEAFVWLGYINSTMNPIIYGFFYPWFRKTLYLIIT
RRIFEPNSSDINIFTL

>Dr-taar13e

MDLSAQEYDASQFCFPAVNNSCLKGTHHVSTQTVVYLVLASAMTVTILGNSVVIISIAHFKQLQT
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HQAVCFPLQYPTMITIPVAWVMVIISWSMAAFYSYGLVYSKANVEGLEEYIESIYCMGGCTLLFN
ALWGAIDTLVAFFLPCFVMIGLYARIFMIAKKHARKLGEANQHDNENLFKSSRRSERKAAKTLGI
VVGAFVICWLPFFINSMMDPYINFSTPGVLFEAFVWLGYMNSAINPIIYGLFYPWFRKTLYLIIT
LRMFEPNSSDINVFTV

>Dr-taar14f

MNLTAVNQTDMCEDYSCPERSVSLSVYVILYVAAAAVALLTVCGNLLVIISVSHFKQLHTPANIL
ILSLAASDLLVGVFVIPLHLSWVIESCWISGPVVCLVFKLVNYQATSVSVHTVALIAVDRFLALS
FPFFYSEKISLTVVCTAALLNWLFSLIYNFTLFYVNENFTVVVCPGVCFHHLDGISSLIDLLIVF
VMPCTLIIILYTHVFVIAKKHATAIRALQVHNSTESSKNKISDKSERKAAMLLGILVFVFLLCLL
PYYITFLVIPYGSIIYMYVINVAVIFFFLNSTINPIIYALFYSWFKKSLKLIFTFKVFHKDSSLM
NVM

>Dr-taar15a

MEFQEHHCLSHWNTSCSLDFHLSYVNVFLFLYISAISVLTVCGNLLVIVSIAVFKQLHTPTNLLI
LSLAISDLLVGICLMPVESIRSINSCFYMGKSHCHIFHSIMSIVGSASLMNIMLVAIDRYFAVCN
PLLYMSKMTIRKALICVGLGWTVSICYNLVPVNLGNSDPTGAVVVCLRECAVAFSNSWGPADLIV
TFIAPCITLLILYIRILTVALKQAKAISNMTKKNGSQPSRKSEVKATKTLSTIVFVYLICWIPWY
ASMLNMEQFNKSPVSLTALLCLFYTNSCINPFIYAISYPWFKRSVKLVVSLRILQTATNQLNLFA
EDC

>Dr-taar16a

MKDKNLEIQFCFPNNNLSCFKEIKPQTDYVVLYIFIFLASVVTVFLNLLVIISISHFRQLHTPTN
LLILSLAVADLIVGLIVIPFMGIRFIDSCWYYGETFCSVFLFITFAVVSGSLGNLVLISLDRYIA
VSDPLRYTVKITTDRIVICIVVNWLCSSIYSFIFLYNSVFYPETQNGCYGDCRVSFKFEHFVTDL
LVTFVAPSCVIMSIYVKIFCVAKHQAKVVNSVTGVSKSQRKAGKTLGIVVMVFFMCWIPYYIVIL
IEGNELTESVEFNVTCWIVYMNSCMNPLIYSLFYKWFRISAKHILTLNILKLSSEYFNLFPEDK

>Dr-taar17a

NKLLTGAESLMAYETEETQYCYPAFNSSCVKGKRSNYESNILYVFFSLLSAWTVFLNLLVIFSIS
HFKKLHTPTNMIILSLSVADLLVGLIVMPIEATELIETCWYFGDTLCNLFLILMGLLTSTSLCSL
VLIAVDRYVAVCHPLMYPQTITMNRTLIIVCFSWFFSSAYNIILSITHTSDGCYGECNVQLTFEW
KATDLVLSFLLPCTVIITLHLRIFYVVHQQVKVINSQMKSEKCVMEGSVKRKSESKAALILGIIV
AIHLICFITYYILTLTDSMAIPPTVLSCLICFLYINSSLDPLLYALFYTWFRKSIKHILTLKIFQ
PESSQVNILTNH

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>Dr-taar18a
MKGQKGEQNKLLTGGDSLMAYETEDQETQYCFPDINSSCVKENRSKHEYNIMYVFFSLLSAWTVF
LNLLVIISISHFKKLHTPTNMIILSLAVNDLLLGLIVMPVDAVKLIETCWYFGDILCDLYMIIMG
LLLSASLSNLILIAVDRYVAICHPLLYPQKITMTRTLISIFVCWFVCLTNNIAFLVSSRHFDILQ
KTNMCHGQCTLIVSFSWTFTDLFLSFLVPCTLIITLYLRIFYVAYQQVKVINAIIKGGKCAVEGS
VKRKSERKAALTLGIVVTVYLLCYIPYYILSVIGTTVISSTMKILIWSLYINSCLNPLIYALFYR
WFKISVKCVLTLKILEPASSLLDIFKDNS

>Dr-taar19a
NKLLTGGDLLMAYETEDQETQYCFPDINSSCVKGRHSSHGYIIIYLFVSLLSVWTVFLNLLVIIS
ISHFKKLHTPTNMIILSLAVNDLIIGLFVIPIQAIKLIETCWYFGDTFCGLYLFLIFELLSASLS
NLVLIAVDRYVAVCHPLLYPQKITITKTLMSICLSWVCYSAYNTALIINNRYSETSHRTDECYGR
CFIVMSFSWLVADLVMSFIFPCLIMITLYLMIFYVVHQQVKVMNSLMKGGKCVTEGSVKRKSESK
AALTLGIIVTIYLLCYIPYYICSLVVNSSTAIHVMSWTVYVNSGMNPLVYALFYPWFKKTAKIIF
TLKIFQPASSLINIFTE

>Dr-tar20a
MKGQKGEQNKLLTGGDSLMAYETEDQETQYCFPDINSSCVKEQHSSHGYIIIHLFVSLLSAWTVF
LNLLVIISISHFKKLHTPTNMIILSLAVNDLFIGIAMPVEAIRLIETCWYFGDTFCVLYLFFVAL
LLSPSLGNLFLIAVDRYVAVCHPLLYTQKTTIAKIFCLSICLSCVCFSAYFTALVNVNNQDFDTS
QRTDVCYGQCLVMITFSWIVIDLFVSFIFPCTLIMMFYLRIFYVVHQQVKVINSLMKGGKCVTEG
SVKRKSESKAALTLGIIVSVYLLCYIPYYICSLTVNSSTAINVLVWLVYSNSGMNPLVYAIFYPW
FKKTAKLILTLKIFQPASSLINIFTEL

>Ga-taar21a
MEPEETDNGFNAVSDLHPCYESDNGTYSFTSNFSISCVSLYVFLGGLSVVTICGNLLVIISVSYF
KQLHVATNFLILSLAVADLLVGVVVFPFSMVFTVTSCWHHEGLFCKVRGGFDVTLSTASILHLCC
ISIDRYYAVCQPLSYKSKVNDRVTGMMILMSWAVPLLIGICIIIAGFNQGKCEESCLIDALISTT
LACIFSFYIPVIIMLSIYLKIFLVAKRQAISIQITTGLTKKSGTTVSKRERKATKTLAIVLGVFL
LCWAPYFLCMIFQPITYNVTPIAVIETLNWLTLSNSMLNPFIYAFFYSWFRSAFKMIISGKVFWG
NLENSKLL

>Ga-taar22a
MDGMEGAQLCFPQLLNSSCRGLLRPRTESVLLYTLLSSMAVLTVLLNLLVIISISHFAQLHTPTN
LLLLSLAISDLLVGLLVMPSEMVSVIETCWLLGDLLCTLSTMMGSTLVSASVGNMVLISIDRYVA
ICYPLQYPIQITRSRISVLYNGLILKDRLRQPDRDNSCDGECKVVINNVSGAIDLVFTFFAPCSV
IVVLYVRVFTVAVSQARVGSHFTAVGAVKITAKKSERKAARTLGMVILVFLISFCPFYYPALAGQ
EISNNASSWVIVSWLLFFNSCLNPLIYALFYPWFRKAVKLIVTLKILEQNSSQENII

>Ga-taar23
MAEHASQLCFPQLLNVSCRKPSVLWNDAVLSLALMSVSALTVALNLVVIISVSLFRHLHTPTNIL
IVSLAVSDLFVGLLVMPVEILFRVSCWFLGDLVCALFNYVFFIITSVSVGTMVLISLDRYLSICE
PLHYATRVTVKRVRCSVCTCWLCSVCYSGVLASDGVTPSGRYSSCHGECLIVIDYVTVTVDLVVT
FGVPVSVIVVLYMRVFAVAASQARSLRSHVLVVTHQLPVGQRAKKSELKAARTLGVLVVLFLICF
CPYYIVSLVGYSQLSNLYMSFVLYLFYLNSCLNPLIYALFYPWFRKAVKRIVTLQTGS
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>Ga-taar24

METLPGDYLCFPQLNSSCKKPAHPHTEAMLVYVLLSSISLITVVLNVLVIISISHFRQLHSPTNL
LILSLAVSDLLVGLLLMPVEIIYIEACWFLGDILCTTYYLVDYVITSASVANMVLISVDRYIAIC
EPLHYPTKVTKRRVQNCVCFCWIWSAIFRIFLLYDHLEKPGSSNSCLGECVVIINYAAGVADLVF
TFIIPILCIIVLYLRVFVVALSQARAMRSRVAASTTRRSGATTVKKTEMKAARTLGLVILVFLFC
FCPYYYPALAGKDTSIDASSAAFEIWLAHFNSCLNPVIYAFFYPWFRKSIQLILTLQILKPGSCD
ANVL

>Ga-taar25a

MKSLEEDELCFPHLLNSSCRKAMHPHFVSMLTYILLSSISLLTVTLNLLVIISISHFRQLHTPTN
LLLLSLAVSDFFVGFIVFFQIVVIEGCWFLGDLMCILYIFLDYIITSASVGTMVLISVDRYVAIC
EPLHYSNKVTQKRVKISVCLCWTCSAFLQTLLLKDNLEEPGRYNSCFGECVVVINYIAGLADLFF
TFIGPVTVIIVLYMRVFVVAVTQARVMRSHVAVLPHKFSMNITAKKSEMKAARTLGVVIVVFLLC
VCPYYCVLLSAQDTLFNISSAAFVTCVFYFNSCLNPLIYAFFYPWFTKSMKLIVTLEILQPGSCE
RNLL

>Ga-taar26a

METLVGTELCFPQLINTSCRKPIRPHLEAMLIYILLSSISLLTLALNLLVIISISHFKQLHTPTN
LILLSLAVSDFFVGLFVIFQIMIIEGCWLLGDLMCSLWLILSSIIMSSSIGTMVLISVDRYVAIC
YPLHYFTKVKPKRIRVCVCLCWMFAALFNSLLLKNNLQHPGRYNSCIGECVIEMNYIANVFDLIL
SFFFPITVIVILYIRIFGVVVYQARAMRPHIAVVTMKVAVKKSEMKAARNLGVVVVVFLICVCPY
YCFTLTSQNNLYTSLSVTILVWLFQFNSCLNPLIYATLYPWFRKSIKVIVTLQILKPGSYRTNML

>Ga-taar27

MEPVLCYESRNGSCLRTIYSLPIQITVYMILGVIVVLTVFGNLLVTVSIAYFKQLHTPTNYLISS
LAVCDLLLGLLVMFPSMVQCVESCWYFGDVFCKVYMSSDVMLCTTSILNLLFISIDRHYAICQPL
RYREKISVNVVLIMILLSWTISGLIGFGMIFLKLNFWGIEEFYSNHIVCEGECILFQTGLSSIMS
SVLSFYIPGIILLSVYLKIFLVARRQYSIQIASRTCSEGISNTSQKKATKTLAIIMGAFLSFWTP
FFVCNIVDPFISYSTPPALFKTLVWLGYFNSTVNPLIYAFFYSWFRKALKLFTSGIMFKADISET
TLFTL

>Tr-taar28a

MIYVFRHFQTTTNLLLLSMAVSDLLVGLAVMPLMIVTLDSCRCISSYLCFLFHLLSFVLTSASVG
NMVLISVDRYVAICYPLRYSSITPNTVKICVSVCWTSSIIYNLVLLKDNILYIDFFSSCNKKCPL
YINYILAIADIIITFYGPLTVIIVLYTRVFVVAVTQARAMRSQVSTTGSKAVSAMKSEMRAARTL
GIVILFFLICFFPYYISSLTGQGISNEDSTGQLFLFFSNSTINPIIYAFFYPWFRKTVKLFLSCQ
FCKL

## Aminergic receptors used as outgroup (species names, gene IDs: Suppl. Table 1)

### *Adrenergic receptors*

>Bbe-adra1a

MAGLPLELDNFTLDDNNGTWNVTEADHPSQILGLRMSLPASLLVGAVLSCICILTIAGNVLVVLA
VCLERSLRTNIGYFYINLAAADLLLGCLVLPFSATRELLNYWPFGEALCELWAAVDVLCCTASIF
SLCVISLDRYIGVTRPLHHNMIVTKRRVVLILFAVWATSAAISVGPLFGWKHPKSYQNMQCNINS
SPSYIIFSVVGSFYVPAFVVLYVYRQVYRAAVRETSKLMITLKAQEDRNQTPVESVRIHRGKASV
TAEKRLSPPRLSPNSSKPRMAREALSSVKNRIEKFTKEKKAAKTVGIIVGVFLVCWLPFFVMYPI
DSMIAKVPELLITMAFWLGYCNSFLNPIIYACSNGHFRRAFRRFLLCGKRQGRFPTMRTEDYTLS
SRSSFRRVHSSCSSRDGSRRQQLKIQLQELTVS

>Cm-adra1a

RAHKVIWLVLGSFILFALLGNILVILSVASHRHLHTATHYFIVNLAIADLLLSSTVLPFSALLEI
LGRWVFGRLFCNIWAAMDVLCSTASIMSLCVISIDRYIGVSYPLRHPAIMTEKRGVLTLVAVWLL
ALVISVGPLFGWKEPEPEDESVCKITEVPGYVLFSAFGSFYVPLAIILLMYCQVYVVAKRETRSL
MAGEKREGSDTNKVTLRIHRKNVGGDVSPRSGEHHSRGKGHHLKTHFSVQLLKFTRQKKAAKTLG
IVVGGFILCWLPFFVVLPLGSCFPAYRPPETVFKVTFWLGYFNSCLNPVIYRCFSQEFKRAFRNV
LRGECHRRKPPVNQGSSLSSSSAHSGAERPKEVVRTQVGTNEAFLGIARPQAPSQWSLLPARPDH
RTARSPRQPPRALLGSCCGGVVVVELQ

>Lec-adra1a

MFVTHENSTSHLNGTSEGISVSNETSPTVEPRRAVTLALVLGAFIIFAIAGNILVVLSVVCNKHL
RTVTNYFIINLASADLLLSTTVLPFSATFEILGYWVFGRIFCDIWAALDVLCCTASIMSLCAISI
DRYIGVSYPLRYPTIMTERRVLLILIAVWVLAIVISVGPLLGWKEPAPPDETVCEITEVPGYALF
SAMGSFYIPLVILLAMYCRVYVAARRQTKSLEEGIKRERSSSSEEVTLRIHRRTIAPGEYSLRDT
SKGPHFRSSLSVRFMKFSREKKAAKTLGIVVGVFILCWLPFFIALPIGSFFPSVRPSQTVFKVVF
WLGYFNSCINPLIYPCSSQEFKRAFLRALRCHCREGQRRRRQPWGLHHASSTGSSYSGGRKGSSH
LSQLHEVHGGCSPDGLCERSRSPDEPSPVSQDSLRGWRLLSTSKALSGTALILERANSPQPET*

>Mm-adra1a

MVLLSENASEGSNCTHPPAQVNISKAILLGVILGGLIIFGVLGNILVILSVACHRHLHSVTHYYI
VNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAAVDVLCCTASIMGLCIISIDRYIGVSY
PLRYPTIVTQRRGVRALLCVWALSLVISIGPLFGWRQQAPEDETICQINEEPGYVLFSALGSFYV
PLTIILVMYCRVYVVAKRESRGLKSGLKTDKSDSEQVTLRIHRKNVPAEGSGVSSAKNKTHFSVR
LLKFSREKKAAKTLGIVVGCFVLCWLPFFLVMPIGSFFPNFKPPETVFKIVFWLGYLNSCINPII
YPCSSQEFKKAFQNVLRIQCLRRRQSSKHALGYTLHPPSQAVEGQHRGMVRIPVGSGETFYKISK
TDGVREWKFFSSMPQGSARITMPKDQSACTTARGFYP

>Mm-adra1b

MNPDLDTGHNTSAPAHWGELKDANFTGPNQTSSNSTLPQLDVTRAISVGLVLGAFILFAIVGNIL
VILSVACNRHLRTPTNYFIVNLAIADLLLSFTVLPFSATLEVLGYWVLGRIFCDIWAAVDVLCCT

ASILSLCAISIDRYIGVRYSLQYPTLVTRRKAILALLSVWVLSTVISIGPLLGWKEPAPNDDKEC
GVTEEPFYALFSSLGSFYIPLAVILVMYCRVYIVAKRTTKNLEAGVMKEMSNSKELTLRIHSKNF
HEDTLSSTKAKGHNPRSSIAVKLFKFSREKKAAKTLGIVVGMFILCWLPFFIALPLGSLFSTLKP
PDAVFKVVFWLGYFNSCLNPIIYPCSSKEFKRAFMRILGCQCRGGRRRRRRRLGGCAYTYRPWT
RGGSLERSQSRKDSLDDSGSCMSGSQRTLPSASPSPGYLGRGTQPPVELCAFPEWKPGALLSLPE
PPGRRGRLDSGPLFTFKLLGEPESPGTEGDASNGGCDTTTDLANGQPGFKSNMPLAPGHF

>Le-adra1b

MTFAEFTNESLDGNCSNASALSYAVFPNDSVTANRSGNSEGLDVNQAVALGVILGAFILFAIVGN
IMVILSVACNRHLQTVTNYFIINLAIADLLLSTIILPFSASLEIFGYWAFGRIFCDVWAAVDVLC
CTASIMSLCVISIDRYIGVRYSLRYPTIMTEVKAVWILIVLWVTSIVVSVGPLLGWKEPAPADDT
MCSITEEPGYALFSSLFSFYLPLMVILVMYFRIYVVARRTTKSLEAGVKRERSKTMEVVLRIHCR
SVLDDSHSNFKNKGHHLRSSLSMRLLKFSREKKAAQTLGIVVGVFILCWLPFFTILPLGR*

>Bfl-adra2

QAMKGVQNLFLVSLACSDVTVGTLVMPFKLANELMGYWYFGQTWCDIYLALDVFACTASIFNLCA
ISIDRYWAITKPIKYLSMRTRRRVGIMIAIVWMSSALVCLPPLFGWKSGDDSGDEQEASETPGCQ
LNSSPGYVVFSSVSSFYIPLGVLIFVYTSIIRAVRKRFKFRNKNGEWKQICNVRLKDSYDVPGYV
RSRGAISSPGKKSRGHSQCGDTLQRPEKELQVLEALQPLKSPGFSPRGPYFDGKMVVLPTKTTPI
VDNVRKVREKLRAAQQKERKSLSIIFCVVSVFLICWLPFFVCYLVVTLCESCWVPPPLFMFVEWM
GYGNSALNPVIYALFNKEFRDGVKMLFRRNNYSIPLANT

>Cin-adra2

SSILYSEEQVVIFSALTSILCIIGLFGNLTVIVVIRRDRVIYKHRQNLYLLSLAVADVSLVVLVV
PFSITNELLGYWPFGTVYCRIYLSVDILLCTASIWNICMIGLDRYISVKYPMTYRKFRTMPKIRL
FIVSIWLFAAVVSLLPFVSEIETINSERGCFINASSWYIVVSCSLSFFIPSCIIWPVYIRIYMIG
NHIQMNMLIRRSDPKQDSTSKFETKVRRLSRTSRSLENLMTLLVVPNSTNNSRSVTSATTDQRQM
NRSQSFTECLNSGREDGNLLSSVAYDVTSQKSTRSDIYYISRSSSQSQQSSCTTAMSRRERRFVC
IISIITGCFMACWMPFFLTYMIYAVCRACCINNTLFKVFFWLGYLNSALNPVLYTAFNKDFRSAF
QRLFHLSGRRTIC

>Lec-adra2

MQNMSDPAAARSTLLSPYAAFNFTLAEPENVTGGTNSLNGTDEKLGWEYSVLAGLGLSSLVLILV
FATVFGNCLVIIAVLTRPSLKAPQNLFLVSLATADILVATLVIPFSLFNELMGYWYFGRVWCEIY
LALDVLFCTSSIVHLCAISLDRYWSVSQAVEYNIKRTPRRMKRIIVIVWFIAIAISLPPLISMNQ
KNRQQQEELGRPNCELNTNTWYILGSCIGSFFAPCLIMVLVYARIYHLVKWRAAKLRRDKEAPIT
SCRPMESIRMSEVNGNGGGGGGGEGNGNGEKNCNGAGNKSRHHHHPPHHQHPPSHHHPEVDVEE
TSVSSDKNERRRDDASAGAKASRKPCSPTKDDYNPEMEILERQNKARERRKIAQARERRFTFVLS
VMIGVFVICWFPFFFTYSLSALCSPEFCVIPETLFKFFFWFGYCNSCLNPVIYTVFNRDFRRAFK
KILCMQFNTSF*

>Mm-adra2a

MFRQEQPLAEGSFAPMGSLQPDAGNSSWNGTEAPGGGTRATPYSLQVTLTLVCLAGLLMLFTVFG
NVLVIIAVFTSRALKAPQNLFLVSLASADILVATLVIPFSLANEVMGYWYFGKVWCEIYLALDVL
FCTSSIVHLCAISLDRYWSITQAIEYNLKRTPRRIKAIIVTVWVISAVISFPPLISIEKKGAGGG

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QQPAEPSCKINDQKWYVISSSIGSFFAPCLIMILVYVRIYQIAKRRTRVPPSRRGPDACSAPPGG
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PDRGPRAKGKTRASQVKPGDSLPRRGPGAAGPGASGSGHGEERGGGAKASRWRGRQNREKRFTFV
LAVVIGVFVVCWFPFFFTYTLIAVGCPVPSQLFNFFFWFGYCNSSLNPVIYTIFNHDFRRAFKKI
LCRGDRKRIV

>Rt-adra2a
NKDLGGDNMLVENIGGGIAVCKDSRARAGHGGAGSRARGLSVRGRGRGRLRERLGAPRLLMALTI
FGNVLVIIAVFTSRALRAPQNLFLVSLATADILVATLVIPFSLAKELMGYWYFGRLWCQVHLAID
VLFCTASIAHLCAISLDRYWSISQAIEYNLKRTPRRIKGIIVIVWVIAAAISCPPLITNISTNQS
QEPGTCHINDQVWYIISSCIGSFFAPCIIMILVYIRIYQIAKLRSRGRPGDIPNGLNQPPSPPGA
PEPGQHNGGDEQGVLAEVEDSSSSEQPPCPALAPSPSPAAHRQHCHPPQPQHTAPNPAKATGQVR
CVDGRPVTSLAPRSRWKGRQNREKRFTFVLAVVIGVFVLCWFPFFFTYSLTAICPKLCPVPEKLF
KFFFWMGYCNSSVNPLIYTVFNQDFRKAFKKILCRGQRRGQKL

>Mm-adrB1
MGAGALALGASEPCNLSSAAPLPDGAATAARLLVLASPPASLLPPASEGSAPLSQQWTAGMGLLL
ALIVLLIVVGNVLVIVAIAKTPRLQTLTNLFIMSLASADLVMGLLVVPFGATIVVWGRWEYGSFF
CELWTSVDVLCVTASIETLCVIALDRYLAITSPFRYQSLLTRARARALVCTVWAISALVSFLPIL
MHWWRAESDEARRCYNDPKCCDFVTNRAYAIASSVVSFYVPLCIMAFVYLRVFREAQKQVKKIDS
CERRFLGGPARPPSPEPSPSPGPPRPADSLANGRSSKRRPSRLVALREQKALKTLGIIMGVFTLC
WLPFFLANVVKAFHRDLVPDRLFVFFNWLGYANSAFNPIIYCRSPDFRKAFQRLLCCARRAACRR
RAAHGDRPRASGCLARAGPPPSPGAPSDDDDDDAGTTPPARLLEPWTGCNGGTTTVDSDSSLDEP
GRQGFSSESKV

>Rat-adrB
MEPHGNDSDFLLAPNGSRAPGHDITQERDEAWVVGMAILMSVIVLAIVFGNVLVITAIAKFERLQ
TVTNYFITSLACADLVMGLAVVPFGASHILMKMWNFGNFWCEFWTSIDVLCVTASIETLCVIAVD
RYVAITSPFKYQSLLTKNKARVVILMVWIVSGLTSFLPIQMHWYRATHKQAIDCYAKETCCDFFT
NQAYAIASSIVSFYVPLVVMVFVYSRVFQVAKRQLQKIDKSEGRFHAQNLSQVEQDGRSGHGLRR
SSKFCLKEHKALKTLGIIMGTFTLCWLPFFIVNIVHVIRANLIPKEVYILLNWLGYVNSAFNPLI
YCRSPDFRIAFQELLCLRRSSSKTYGNGYSSNSNGRTDYTGEQSAYQLGQEKENELLCEEAPGME
GFVNCQGTVPSLSIDSQGRNCNTNDSPL

>Alu-adrb
MSANTTVSPTQTTAILTTNSTDSPVGSCFAPNPYSAGVQAVLGFITVILILLTVVGNLLVILAVT
CHRKLRTVTNFFIISLACADLSVGITVLPFAATNDILGYWPFGGYCDVWVSFDVLNSTASILNLC
VIAFDRFLAITAPFTYHTRMTERTAGILIASVWGIAVVVSFLPVQAGWYRDNQSTEALAIYADPC
LCIFAASTAYTIVSSLISFYIPLVIMLVFYGYVFKAARDQARKINALEGRIEQENNRHGKKISLA
KEKKAAKTLGIIMGVFILCWLPFFVVNIVNPFCNRCVPPAGFIALTWLGWINSCFNPIIYAFNKE
FRKVFVKMICCYKCRGVTVGPNMADLTYDPVAMRLKKKGDNLNSSANGKANGNLDQVAGEGTSDS
*
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>Cin-adrb

GLSILLGSICTVTVLGNLIVIFTAILFRQLRTIPNMFIISLASADLLMGTIVLPMWSHYVIGDFK
WSLGFFWCDVWTSIDVLSVTASIGTLCAISLDRFVAITMPFKYATKMTRPRARFIIGFIWMVSGT
IAFVPINLGWWKTNKPEDLECYDSPTCCEFRPNVIYAVVSSCISFYIPLIIMICAYSVVFKSKAI
FTHFTIVISTTVAIQKRGVLPWEKREHRAVITMGIIMGTFVVCWLPFFIVNIAQVFCQCVASTPF
LMVNCLGYTNSLFNPIIYCRSEEFRKAFKRVLMCGLC

>Cm-adrb1

MGDGMDCNSSSSSHHHHHNNNNNRSATLVSANSANGVSPNGPEQSSSEHQWVIVMGVIMAVIVLI
IVVGNLLVVLAIARNQRLQTLTNLFIVSLACADLVMGLLVVPFGATLVVRGTWLYGSFFCEFWTS
VDVLCVTASIETLCVIAIDRYIAITSPFRYQHLLTKTRARGIVCVVWAISALISFLPIMMHWWRD
ENPDAIVCYNDPCCCDFLTNKAYALASSIISFYLPLLIMIFVYARVFQEAKKQMQKIIKCEGRFY
SSYFIPNGRSARRRPSKTIAIKDQKALKTLGIIMGTFTLCWLPFFLVNVAKAFRSEIVDDKLFLF
LNWLGYVNSAFNPIIYCRSPDFRKAFKRLLFCPRRPGSRLDLDSGGFSRCSGMFGNTLDPRNLEM
WSDWNMALQSSSEGQGVGMGQGMGQGMGAGDGAGDGAGDGDGEGDGEGDGEGEGDSPGIAVINSA
FFFSLQRSKRD

>Csa-adrb

MFAFKKKNLKQQLNGLAEHSTGYRKLNGRRNRKLWFYFFGLIVLIHLFAIPVHASDTTQSFTPTP
NLTSNKFTDLRHSGITIPEYENQGLNAPLKAGLYFILSCVCIFTVIGNVMVILTATIFRKLRTIP
NMFIISLASADLTIGTVVLPMWSHYVIGGKWDLGAFWCDIWTSVDVLSVTASIGTLCAISLDRFV
AITMPFKYSTKMTRLRARFIIGFIWIVSAAIAFIPINLGLWKTNEPDDQKFYDDVTNCEFKPNTV
YAVVSSCISFYIPLIIMVCAYSIVFKIAIQKGSKIRNREGVYRRASMPGSRTLLWGKREYRAVFT
MGIIMGTFVICWLPFFIANIVQVFCEGCISAPAFMMINCLGYINSFFNPIIYCHSLEFRRAFKRL
LLCGLCRDGRYKANKFYSFLFNTLSLKMTV*

>Lec-adrb

MLNFQVIPHEDATPPCVVGNSSAWNDSDPATSVGVNCSSEGTGQKPAEMEWMVGLGMLMSLIVLF
IVFGNVLVITAVAKFRRLQTQTNYFVVSLACADLLMGLIVVPFGATPVVSGTWTWYFGPRFCSFW
TAVDIMCVTASIDTLCVIAVDRYIAVARPLRYETLMNKRRARFIIVAVWLVSALISFLPIEMGWW
KSEAAAAANNTAEDVCEFNISLEYAVASSSVSFYLPLTVMIILYSKVFREARKQMEKINTSEGRF
YNNANDSATIKNPARKLSRFLSRKEHRALKTLGLIMGTFTLCWLPFFVVNIVQVVWNCVPTGVFV
SLNWLGYINSAFNPIIYCRSPDFRSAFERLLCCGRLVGRRRRRRGRGRKDNNELGQCTSWPICPD
SGSTQGYVERCSETGTTLCGASTSSQGSSNSEQSLDTNGNSHGLLSAL*

>Rt-adrb-like

MGDRLSSEDCHTNKSSTILFVNPANGVSPHVPQQEFSEQWVIGMGTVMASIVLIIVLGNLLVVFA
IARNQRLQTLTNVFIVSLACADLIMGLLVVPFGATLVVRGNWLYGSVFCEIWTSVDVLCVTASIE
TLCVIAIDRYVAITSPFRYQSLLTKARARAIVCVVWLISGLISLLPIMMHWWRDDQPDAIRCYND
PCCCDFVTNKAYALASSIISFYLPLLIMIFVYARVFQEAKKQMKKIDKCEGRFYTSHFIPNGRSA
RRRPSKIIAIKDHKALKTLGIIMGTFTLCWLPFFLANVAKAFRTDIVPGKLFLFFNWLGYVNSAF
NPIIYCKSPDFRAAFKRLLFCPGQADSNRLCSGSGEFSRCSGMFGNTLDPRSLETWSEWNRSQEA
NGGGLDRHMGENPEDQESQF

### *Dopaminergic receptors*

>Pm-drd1-like

MLMVVVAMMEEKGFKAEPACAAGNEDEDDTRRVMLNLTADEALGCEPGKGLSFRILAGCLLSLLI
LSTLFGNTLVCAAVIKFRHLRSKVTNYFVISLAVSDLFVALLVMPWKAITEVAGFWPFGAFCNVW
VAFDIMCSTASILNLCVISVDRYWAISSPFRYERKMTQRVAFVMISVAWTLSVLISFIPVQLNWH
KAQHVQQTWEFHNASGGADADASVPENCDSSLNRTYAISSSLISFYIPVAIMIVTYTKIYRIAQR
QIRRIASLERAAEHAHNCQLNPNDCPNEMSFKTSFKKETKVLKTLSVIMGVFVFCWLPFFILNCV
VPFCDSAGVEGDDEQQQQHHPLCVSETTFSIFVWFGWANSSLNPIIYAFNADFRKAFSTLLGCN
TLCASTPVETVNLSNEVASYPHDVTSNHKDGGANYVQFIPHVVIVNDESDGDFDKVPEESRSMRE
DRSGIDHRLDCDEDVSLETITPFTPNGVHET

>Mm-drd1a

MAPNTSTMDETGLPVERDFSFRILTACFLSLLILSTLLGNTLVCAAVIRFRHLRSKVTNFFVISL
AVSDLLVAVLVMPWKAVAEIAGFWPFGSFCNIWVAFDIMCSTASILNLCVISVDRYWAISSPFQY
ERKMTPKAAFILISVAWTLSVLISFIPVQLSWHKAKPTWPLDGNFTSLEDAEDDNCDTRLSRTYA
ISSSLISFYIPVAIMIVTYTSIYRIAQKQIRRISALERAAVHAKNCQTTTGNGNPVECSQSESSF
KMSFKRETKVLKTLSVIMGVFVCCWLPFFISNCMVPFCGSEETQPFCIDSITFDVFVWFGWANSS
LNPIIYAFNADFQKAFSTLLGCYRLCPTTNNAIETVSINNNGAVMFSSHHEPRGSISKDCNLVYL
IPHAVGSSEDLKREEAGGIPKPLEKLSPALSVILDYDTDVSLEKIQPVTHSGQHST

>Cm-drd1

MDGRSVTTKDKDSSFRILTACFLSLLILSTLLGNTLVCVAVVRFRHLRSKVTNFFVISLAVSDLL
VAVLVMPWKAVSGVAGYWPFGSFCTIWVAFDIMCSTASILNLCVISVDRYWAISSPFRYERKMTP
KVAFIMIGVAWTLSVLISFIPVQLDWHKAKATSTLLDYNVSYQGQGRVDNCDSSLNRTYAISSSL
ISFYIPVAIMLVTYTRIYRIAQKQIRRISALERAAVHAKNCQTSCESGSLDGQQQQQQQSESSF
KMSFKRETKVLKTLSVIMGVFVCCWLPFFILNCIVPFCEHPGRVSTKDQLPCISDTTFDIFVWFG
WANSSLNPIIYAFNADFRKAFSTLLGCHRLCSGNAVETVTIHNNGVTGCNPEPSGQQQQQVLGNC
VYLIPHPVSCEAGNAPDPHHCCPRKLSPASLHGAVSLQSGYNTDCEADVSLEKITPITQNGQHNT

>Rt-drd1

MRLNTTTMDGSSLAAEQDSSFRVLTGCFLSLLILSTLLGNTLVCVAVIRFRHLRTKVTNFFVISL
AVSDLLVAVLVMPWKAVSEIAGFWPFGPFCNVWVAFDIMCSTASILNLCVISVDRYWAISSPFRY
ERKMTPKVAFVMISAAWSLSLLISFIPVQLDWHKARAPNGLHGNASSQRLGDNCDSSLNRTYAIS
SSLISFYIPVAIMIVTYTRIYRIAQKQIRRISALERAAVHAKNCQSNRSSASTTDIQSESSFKLS
FKRETKVLKTLSVIMGVFVCCWLPFFILNCMVPFCESHASPPPLPCVSGSTFDVFVWFGWANSSL
NPIIYAFNADFRKAFSTLLGCDTLCASNAVETVTIHNGVSSYHPGPSLDKAENSVYLIPHSVPCP
PETPTDPNHCAKLSPISQHGAVSLLSSNGDYETDVSLEKIIPITQNGQHNT*

>Alu-drd1,5

MAAANNSTNSTDMVQVWDDLDGLDLLRVVGIGGILYLIVLMTILGNLIVLTAVMKYPHLRTKVTN
YFICSLAVSDLMVGFLVLPWAAAQELLGYWPFGQFCSTFVSLDVMCCTASILNLCVISVDRYWAI
SDPFKYERDMTCCRAALMIGLAWCLSAMISFIPIGLGFHHIGETITVTQRQCESNMNQVYAITSS
FVSFYIPVIIMVMAYSKIMQIARRKYEDIVALHRSVNQNTKSVQESRTALRRETRIFKTLACILG

VFIVCWLPFFILNCLVPFCPLKTGGKANFTCVSDTVFTVFEWLGWVNSTLNPVIYAFNNDFRKAF
WRMLCRRVPFSRTEAAATSCPCCPAEAYEMAEYKTSNRSPKSV*

>Bfl-drd1,5

MTMVAVNNSTNSSDMFQGWEDLDGVDLLRVVGVGGTLYLIVLLTILGNLMVLTAVMKYPHLRSKV
TNYFICSLAVSDLMVGFLVLPWAAAQELLGYWPFGQFCSTFVSLDVMCCTASILNLCVISVDRYW
AISDPFKYERDMTCCRAAIMIGLAWCLSAMISLIPIGLGFHHIGETITVTQRQCESNMNEIYAIT
SSFVSFYIPVIIMVLAYSKIMQIARRKYEDIAALHRSVNQNTKSVQESRTALRRETRIFKTLACI
LGVFIVCWLPFFILNCLLPFCPLRTGGKANFTCIDHTVFTVFEWLGWANSMLNPIIYAFNNDFRK
AFWRMLCRRVAYRGSDTAVNFPCCPADTYEMAEYRTSNRAPRSV*

>Mm-drd2

MDPLNLSWYDDDLERQNWSRPFNGSEGKPDRPHYNYYAMLLTLLIFIIVFGNVLVCMAVSREKAL
QTTTNYLIVSLAVADLLVATLVMPWVVYLEVVGEWKFSRIHCDIFVTLDVMMCTASILNLCAISI
DRYTAVAMPMLYNTRYSSKRRVTVMIAIVWVLSFTISCPLLFGLNNTDQNECIIANPAFVVYSSI
VSFYVPFIVTLLVYIKIYIVLRKRRKRVNTKRSSRAFRANLKTPLKGNCTHPEDMKLCTVIMKSN
GSFPVNRRRMDAARRAQELEMEMLSSTSPPERTRYSPIPPSHHQLTLPDPSHHGLHSNPDSPAKP
EKNGHAKIVNPRIAKFFEIQTMPNGKTRTSLKTMSRRKLSQQKEKKATQMLAIVLGVFIICWLPF
FITHILNIHCDCNIPPVLYSAFTWLGYVNSAVNPIIYTTFNIEFRKAFMKILHC

>Dr-drd2

MEVFTAYAFNESFFENASRDFNATEQGGRHQYNYYAMLLTLLIFVIVFGNVLVCMAVSREKALQT
TTNYLIVSLAVADLLVATLVMPWVVYLEVVGEWRFSTIHCDIFVTLDVMMCTASILNLCAISIDR
YTAVAMPMLYNTRYSSKRRVTVMISVVWILSFAISCPLLFGLNNTVTHDDALCVIANPAFVVYSS
IVSFYVPFIITLLVYVQIYVVLRKRRKRVNTKRTCPVTDMDMSSTIKKCTHPDDVKLCTVIVKSS
GNCPVNNKNVIFIKEVVNNGDDIQMDEITNRNPSRQRKQDQSGGSQQNSRLVNSNLRETDISPPS
PEAGVKPERNGNTSSITKGAKAFEIQVSPTGKTQTSVKTLNKRKISQQKEKKATQMLAIVLGVFI
ICWLPFFITHIVNTYCQVPPELYTAFTWLGYVNSAVNPIIYTTFNIEFRKAFIKILHC

>Dr-drd3

MGFCFGSSLEKLNRSSTLMAMFSSGEWLWNDSEHSFTPGGNYSPASGVEEAKRNYYAMLYSLLIL
AIVFGNVLVCIAVLRERALQTTTNYLVVSLAVADLLVASLVMPWAVYLEVVGGAWLFSRLYCNVF
VTLDVMMCTASILNLCAISIDRYTAVVMPVLYNTTHSSRKRVSVMIATVWVLAFAVSCPLLFGFN
TTDDPAVCSISNPDFVIYSSVVSFYLPFAVTLLVYVRIYIFLRRRRKKITFRQGSGKVQPASAPP
SVEMCLQDDAHKEKRDLSPIRINVITESKEQVIRPRLLANCLRRKRPQTAPAENSLLPPVITLNY
CSISQASFARTEQDANREEEEGGDEEQVAVRSCEVKKLANGRTHTSLRPPRAAHAMVCPSQARCR
SMHSKEKKATQMLAIVLGVFLICWLPFFVTHILNTHCRACHIPPEVYSAFTWLGYVNSALNPVIY
TTFNIEFRRAFIKILSC

>Mm-drd3

MAPLSQISSHINSTCGAENSTGVNRARPHAYYALSYCALILAIIFGNGLVCAAVLRERALQTTTN
YLVVSLAVADLLVATLVMPWVVYLEVTGGVWNFSRICCDVFVTLDVMMCTASILNLCAISIDRYT
AVVMPVHYQHGTGQSSCRRVALMITAVWVLAFAVSCPLLFGFNTTGDPSICSISNPDFVIYSSVV
SFYVPFGVTVLVYARIYMVLRQRRRKRILTRQNSQCISIRPGFPQQSSCLRLHPIRQFSIRARFL
SDATGQMEHIEDKPYPQKCQDPLLSHLQPLSPGQTHGELKRYYSICQDTALRHPNFEGGGGMSQV

ERTRNSLSPTMAPKLSLEVRKLSNGRLSTSLKLGPLQPRGVPLREKKATQMVVIVLGAFIVCWLP
FFLTHVLNTHCQACHVSPELYRATTWLGYVNSALNPVIYTTFNIEFRKAFLKILSC

### >Mm-drd4

MGNSSATEDGGLLAGRGPESLGTGAGLGGAGAAALVGGVLLIGLVLAGNSLVCVSVASERTLQTP
TNYFIVSLAAADLLLAVLVLPLFVYSEVQGGVWLLSPRLCDTLMAMDVMLCTASIFNLCAISVDR
FVAVTVPLRYNQQGQCQLLLIAATWLLSAAVASPVVCGLNDVPGRDPAVCCLENRDYVVYSSVCS
FFLPCPLMLLLYWATFRGLRRWEAARHTKLHSRAPRRPSGPGPPVSDPTQGPFFPDCPPPLPSLR
TSPSDSSRPESELSQRPCSPGCLLADAALPQPPEPSSRRRRGAKITGRERKAMRVLPVVVGAFLV
CWTPFFVVHITRALCPACFVSPRLVSAVTWLGYVNSALNPIIYTIFNAEFRSVFRKTLRLRC

### >Dr-drd4a

MPANLTISTHTTNYNFPALIFGILLIIIIICGNVLVCLSVYTEKALKTTTNYFIVSLAVADLLLA
VLVLPLFVYAEFQDGVWSLNMTVCDGLMTMDVMLCTASIFNLCAISIDRFIAVSIPLNYNRKHVD
QRQIVLLSATWILALAVASPVMFGINNVPNRDHSECKLEDNNYVIYSSVCSFFVPCPIMLLLYCG
MFRGLRNWEEARKAKLRSNMEACRKLQEAAASLQPLSGLPPPLPPVIEKDITLEELDQDHYPDPD
SPDPVSMLAYPGGGYNQDQNQNRQRKRAKINGRERKAMRVLPVVVGAFLFCWTPFFVVHTMRALC
EDCEIPGSVTSIVTWLGYVNSAINPIIYTVFNTEFRKFFRKFLPTLPGCC

### >Bfl-drd4

MLCTASIFNLVAISIDRFYAVTWPVRYSKHKSNTRLAITITLVWTLSFVICAPLLFGSNYPAKGE
RTPEMCGIFNNNYMIYSSMCSFFIPCTAMLVLYYKILKKIKERSKKMAKKMPKSTSAGMICGDTV
IANTTTSSGIALKENGASKKTLSTPVLDGHAGHAVSAVDANSRPSSECAKLPKTRLDAIKIKLKG
KVKDEFPNKREQKAINVMKIVIGVFLICWTPFFVTNVVRACSTCTIPDVLFSIVTWLGYLNSGMN
PIIYTIFNQEFRSAFRKLLCKTH

### >Mm-drd5

MLPPGRNGTAHRARLGLQRQLAQVDAPGGSAAPLGPAQVVTAGLLTLLIVWTLLGNVLVCAAIVR
SRHLRAKMTNIFIVSLAVSDLFVALLVMPWKAVAEVAGYWPFGAFCDIWVAFDIMCSTASILNLC
IISVDRYWAISRPFRYERKMTQRVALVMVALAWTLSILISFIPVQLNWHRDKAGSQGREGLLSNE
TPWEEGWELDGRTENCDSSLNRTYAISSSLISFYIPVAIMIVTYTRIYRIAQVQIRRISSLERAA
EHAQSCRSRGACEPDPSLRASIKKETKVFKTLSVIMGVFVCCWLPFFILNCMVPFCSSGDAQGPR
TGFPCVSETTFDIFVWFGWANSSLNPIIYAFNADFRKVFAQLLGCSHLCFRTPVQTVNISNELIS
YNQDTVFHREIAAAYVHMIPNAVSSGDREVGEEEEAEEEGPFDHMSQISPTTPDGDLAAESVWEL
DCEEEVSLGKISPLTPNCFHKTA

### >Rt-drd5

MRNGSLWKEPGGDKVLAGRVLTGALLSALILFTLLGNALVCVAVLRYHNLRAKVTNLFIVSLALS
DLLLAVLVMPWKAAAEVASGWPFGPFCKVWLAFDIMCSTASILNLCVISVDRYWAIASPFRYERR
MSRRLALLVVGLTWALAVLVSFVPVQLDWHTAPAARSSSAPRPPPRGQRPPANCDSSLNRAYAIS
SSLISFYIPVAIMLVTYDRIYRIARVQIRRIAALERAAQHARSCRQEQHRSLRSSFYKETKVLKT
LSVIMGVFVCCWLPFFVLNCLVPFCDRRSPSPPCVSETTFDVFVWFGWANSALNPVVYAFNAEFR
QAFSGLLGCTRVCCAPTAGRVHSANISNELVSYHQETALQREVACADMIPNAVQRAPAAFDSMSQ
ISAAADEDDEEEEPASDSAAELGLTFCKITPFTPNGVH*

#### >Le-drd5

MDGAPGVKSELATRILTGLLLSLLILFTLLGNALVCVAVVHFRHLRSKVTNVFIVSLALSDLLVA
VLVMPWKAVAEVAAYWPFGRRFCSVWVASDIMCSTASILNLCVISVDRYWAISSPFRYQRKMTHR
AALVMIAVAWAFSLLISFIPVQLSWHSIREPAGAGHSNNSSAAFAHPPESCDSSLNRTYAISSSL
VSFYIPVAIMLVTYTRIYRIARIQIRRIASLERAAEHAQSCRRRRLEPRQQQQPMHHHSALERSF
KKETKVLKTLSIIMGVFVCCWLPFFVLNCMVPFCDRSSPAAAARLPCVSDTTFDIFVWFGWANST
LNPVVYAFNAEFRKAFSSLLGCQDFCSGNQVETVNISNELVSYNQDTVFHREIVTAYVTMIPNVM
GCMEDDQIFDRMSQILATNEQATETASEMEGDADLSLGKITPCTPNGLH*

### *Histaminergic receptors*

#### >Mm-hrh1

MSLPNTSSASEDKMCEGNRTAMASPQLLPLVVVLSSISLVTVGLNLLVLYAVRSERKLHTVGNLY
IVSLSVADLIVGAVVMPMNILYLIMTKWSLGRPLCLFWLSMDYVASTASIFSVFILCIDRYRSVQ
QPLRYLRYRTKTRASATILGAWFLSFLWVIPILGWHHFTPLAPELREDKCETDFYNVTWFKIMTA
IINFYLPTLLMLWFYVKIYKAVRRHCQHRQLTNGSLPTFLEIKLRSEDAKEGAKKPGKESPWGVQ
KRPSRDPTGGLDQKSTSEDPKVTSPTVFSQEGERETVTRPCFRLDVMQTQPVPEGDARGSKANDQ
TLSQPKMDEQSLSTCRRISETSEDQTLVDRQSFSRTTDSDTSIEPGLGKVKARSRSNSGLDYIKV
TWKRLRSHSRQYVSGLHLNRERKAAKQLGCIMAAFILCWIPYFIFFMVIAFCNSCCSEPVHMFTI
WLGYINSTLNPLIYPLCNENFKKTFKKILHIRS

#### >Dr-hrh1

MCFLTTLTSCDTLERPMESTTTLTTANSQFKRIDNTTLLIPSAPLHHHINNAVLGIFLGMLSLLT
VIMNLLVLFAVRKERTLHTVGNLYIVSLSIADLIVGATVMPLNLVYLLEDQWKLGHVVCQFWLVM
DYVASTASIFSLFILCLDRYRSVRHPLQYLKYRTRGRATLLICSAWLLSMTWTIPILGWRMFASV
DKKTELENQCDTDFRFVTWFKVLTAILNFYIPSFLMLVFYSQIFIAVRDHYREWENFAGPALKTD
ATDTLTNGLQLQITKASEKESLALNAYSQNEGLLDQYSLEQPYNSRENTEEMISEPKRKMCYKKK
AIFNLSKRMRKSVPDSEISFQSDDGETVAEGRPSLSLAFLQSENTAQPQTFINVSDCNVLVPNSV
GNICESTPTVDIHNYTAVLCTPPSPPSPWAENSPPLDASIALPAKQSWQKLCEQSKQSIHSMRIR
KERKAARQLGFIIGVFMVCWIPYFITFMVMALCETCVHHDLHMFTIWLGYINSTLNPFIYPLCNE
NFKRVFKKIFHMSR

#### >Dr-hrh2b

MTIRALCWVVLVAFIALTICGNILVCMAVATSRRLHQLSSCFILSLAVTDLLLGLLVLPLSAMLE
LRNGKWPLGGVFCNIYISMDVMLSSASILTLLAISVDRYLAISNPLFYPRRVTPRRVAIALTAIW
TCSLAVSFVSINLGWNSPDFRVQNLDWSMWDEGEEGRTCRYEWNNNYVLLKAFGIFYLPLLVMCG
MYHRIFCVAREQVRRIRAATPSSAQVANAAATAREHKATVTLAAVLGAFIICWFPYFTYFTYMGM
WAIHPNKLTHSIVLWLGYLNSALNPILYPALNRDFRQACGQLLCRCGKRGDFNTSRRKTFIALGT
IKVIKGSLAH

#### >Rat-hrh2

MEPNGTVHSCCLDSMALKVTISVVLTTLILITIAGNVVVCLAVSLNRRLRSLTNCFIVSLAATDL
LLGLLVLPFSAIYQLSFTWSFGHVFCNIYTSLDVMLCTASILNLFMISLDRYCAVTDPLRYPVLV

TPVRVAISLVFIWVISITLSFLSIHLGWNSRNGTRGGNDTFKCKVQVNEVYGLVDGLVTFYLPLL
IMCVTYYRIFKIAREQAKRINHISSWKAATIREHKATVTLAAVMGAFIICWFPYFTAFVYRGLRG
DDAINEAVEGIVLWLGYANSALNPILYAALNRDFRTAYQQLFHCKFASHNSHKTSLRLNNSLLPR
SQSREGRWQEEKPLKLQVWSGTELTHPQGNPIR

>Dr-hrh2

MTSQIALAVTLSVLILLTVSGNILVCLAVYATRRLRNVTNCFIVSLAVTDFLLGALVLPFSTLYQ
VTGDWPLGAHFCNIYISLDVMLCTASILNLFAISLDRYFAVTAPLRYPMLVLPWRVGAILATIWL
VSVGVSFVPIHLGWNTRDLSVQNIREGDHARDCRFELNPTYAIVDAFSTFYLPLLAMCWSYHRVF
RIARMRAKRIISTRRGSTSSQGVTILTLREHKATVTLAVVLGAFVVCWFPYFTFFTIMGIRNEEN
PPQTAQSVVLWLGYANSALNPVLYATLNRDFRSAYAKLLCGGRRCKTETTIPIAATAAGTMTGHA
HSSKGAGFLPRTCVLLKDSENRMLDDNSATNGATVTVVANGSKR

>Le-hrh2

MENGQNITSECESRSVLSTVLVGLVMGMITLITIFGNVLVCLVVGLNRKLQSHTNSLIVSLAATD
LLLGLLVMPFSTTLQLLNSEWPFGPTFCNIYTSMDVMLSTASILNLFAISLERYLAVTAPLRYNI
VITPNRVIVSLVFIWCISIMFSFLPINLGWNSKDALTQSSNETNQCHLEMNPSYAIVDAFITFYI
PLAIMCLTYYKIFKIAREQAKRISSATRSTLPGLKEHKATVTLATVMGVFIICWFPYFTVFLHAG
ISGIQSDKTVFAVVLWLGYVNSALNPIVYAALNREFRMAYQKLLFCRKRNACNRGSSINYQVGRL
RNEQCHQLVRILDDNEPSSDNTITKDICLCTEDSER*

>Rt-hrh2

MEVEGSQNATTSSENRTVLSTVLIGLVLGVIVIITIFGNVLVCL
AVGLNRKLQNHTNCFIVSLAATDLLLGLLVLPFSAISELFEWPFGDTFCNIYTSLDVMLCTASIL
NLFMISLDRYYAVTAPLRYAVFITRNRVVISLGLIWCISIMVSFLPINLGWNTKDLSVQSLANTN
QCHLELNKVYALIDAFITFYIPLPIMCLTYYRIFKIAREQAKRINTVTGCTALNRSLPTVKEHKA
TVTLAIVMGVFIICWFPYFTVFTHEGISGRQANKTVFAVVLWLGYVNSALNPILYATLNRDFRKA
YEKLLCCKKRNSYHKDPPDKPLSCRPLHNGDPRNERCHQLGPDMEENELTSEDRNGENVATYKED
SERSLDGIVHSREVFLEGETNTPQ

>Alu-hrh2

MCLLPHPDRAAGGSMDNLSTTTVTDNATLLPETTRAPYGGKTLFAAVVLGTVLGLITLGTVVGNV
LVCLAAVVNRRLRNITNYFVVSLAVADLLVGVLVLPFSTIFEVTRYWNFGLILCNMWVSTDVLCC
TASILNLFAISLDRYYAITRPFTYSNKMCRRKAFMAIAIVWTVSLLVSFLPIWVGWNTQDGRLQN
IDDPTKCNFDNTNVPYIMIVAFGTYYIPLIIMCVTYFRIFLIAKEQASRINALQPEVRDANRRQN
QNLANEHKATRTLAAVLGAFIICWTPYFTVFTITPLCGCTIPHQLYSVVLWLGYVNSLINPCVYA
FMNKEFRRAFKKLLCFQTNSICFFSNPRNRRLDTPTTSTAHRN*

>Bfl-hrh2

MENVSVAVTDNATLLPGGGVDARAPYGGKTLFAAVLVGTFLGIITLGTIIGNVLVCLAAVVNRRL
RNITNYFVVSLAVADLLVGVLVLPFSTIFEVTRYWNFGLIMCNLWVSLDVLCCTASILNLFAISL
DRYYAITRPFTYSNKMCRQKAFMAIAVVWIVSLLVSFLPIWVGWNTQDGRLQNVDDPTQCSFNNT
NVPYIMIVAFGTYYIPLIIMCVTYFRIFLIAKEQANRINALQPEVRDANRRQNQNLANEHKATRT
LAAVLGAFIICWTPYFTVFTITPLCGCTIPEQLYSVVLWLGYINSLLNPCVYAFMNKEFRRAFKK
LLCFQTGNTVCFCGNPRNWAQDEPTTSTAPRQS*

>Dr-hrh3

MQSSLLSVAHSPGIPTAVSLMWKSGNHQSSNWSGMERENATSLADLDTFENRRAQYGQFSPSTSI
FLTVLMTLLVFATVLGNALVILAFVVEKSLRTQGNFFFLNLAIADFLVGGFCIPVYIPYVLTGEW
RLGRGLCKLWLVVDYMLCTASVFNIVLISFDRFQSVTKAVSYRCQKGITKDAVLKMLCVWLAAFL
LYGPAIISWEHITGGSVVPDGECYAEFYFNWYFLMTASTVEFFTPFISVTYFNLSIYINIRNRCA
MREEQPTYVRLRSFKMKPLGAGDVQRVFFVRPVEESRVADLASRSRCCRLASTAKVSAAEFGNGR
QSKRRDSTLADLPPLQVEERILAASEAQFHYVDHSAGPHRHRPDMVASLANRFRLSRDKKVAKSL
AVIVCVFGLCWAPYTLLMIIRAACHGQCVQHYLYEISFWLLWINSSINPILYPLCHSSFKRAFSK
LLCPSKTKIQPQNIDQKY

>Rt-hrh3 _

MAKLGTLRAIAWTAPLLCASLGAEVNSSQRSLPNLAQSTGCLPFHQFSATSAGLLITLMVLLVII
TVLASVIPAFVVDKSLRSQNNFFLYFLVGAFCIPLYVPXALASRWMLGKTLCKFXLVMNYLLCTS
SVFNTVLISYVRFDCVARPFSYQAQQWKRRNAAIKIMLVRLTAFLLYGPAITAWEXVIGRNIVLV
GECYAEFYNNWYFLITASTVEFFVPFISVMYFNLSIYLNLQQRTRSQSNSFWNTKSKSSLEHLEA
GSNLACSLKICKSDQKTKLIKSTVCDLTTMSSEIKIKVERSETLDHLKRRNDLGRTIPSSEVKCL
MKEEISQSQLFSKRKIKLISQNVVQHFRLLRDKRTAKSLAVIVCVFGICWAPYTLLLVVRAGCQG
HYMAYDWYEASFWFLWINSAINPILYPLCHKNFKRAFMKLLCPTKLKMRPRSSRQ

>Dr-hrh4

MKTLLSSSAAGKASHDDFRPVAASPNVLDLTMVTCFNTSGSNGTTVSPAEAPFPGYTMVILAILM
ATLVVVVVVGNALVILAFVVDKSLRNQCNYFFLNLAISDFLVGAFCIPLYMPYILTGRWMLGRGL
CKLWLVMDYLLCTASVFNIVLISYDRFLSVTRAVRYRAQQGVTRLAVLKMLAVWVSAFLLYGPAI
IFWELLVGESIVPEDECFAEFYCTWYFLLSASTFEFFSPFISVAFFNFSIYLNIQRRNRSRMAHV
EAEKEDGWRVIDGQTSSVFFVKTRKVSSSEPAAVSAVIEDDEEVSPSSSGDPSSTHSVSLTMKTT
IKKRGLFGGWVRTRIIRAQEVTNPCAPCRSGGHARLSRDKKIAKSLAVIVCVFGVCWAPYTLLMI
IRAACSGSCVEHHWYEVTFWLLWLNSAINPFLYPLCHSSFRRAFAKILCPKRQSVQPHEESPSCP

### *Muscarinergic acetylcholine receptors*

>Mm-chrm1

MNTSVPPAVSPNITVLAPGKGPWQVAFIGITTGLLSLATVTGNLLVLISFKVNTELKTVNNYFLL
SLACADLIIGTFSMNLYTTYLLMGHWALGTLACDLWLALDYVASNASVMNLLLISFDRYFSVTRP
LSYRAKRTPRRAALMIGLAWLVSFVLWAPAILFWQYLVGERTVLAGQCYIQFLSQPIITFGTAMA
AFYLPVTVMCTLYWRIYRETENRARELAALQGSETPGKGGGSSSSERSQPGAEGSPESPPGRCC
RCCRAPRLLQAYSWKEEEEEDEGSMESLTSSEGEEPGSEVVIKMPMVDPEAQAPTKQPPKSSPNT
VKRPTKKGRDRGGKGQKPRGKEQLAKRKTFSLVKEKKAARTLSAILLAFILTWTPYNIMVLVSTF
CKDCVPETLWELGYWLCYVNSTVNPMCYALCNKAFRDTFRLLLLCRWDKRRWRKIPKRPGSVHRT
PSRQC

>Dr-chrm2a

MDTINFTFWNASDGNETMETADESPYKTVEVVFIVLVAGSLSLVTVIGNILVMLSIKVNRSLQTV
NNYFLFSLACADLIIGLCSMNLYTVYIVIGYWPLGPVVCDLWLALDYVVSNASVMNLLIISFDRY

```
FCVTKPLSYPVKRTTKMAGMMIAAAWVLSFILWAPAILFWQFIVGGRTVPEKECYIQFFSNAAVT
FGTAIAAFYLPVIIMMVLYWQVSRASKSRVKKDNRKPSGGNLDVASSNQIRENSANKPTNNNLTA
EETDRGQTQLTDDTINQHDAKLQNGKAPSTASGEAEEAGQANCIPAEEKESSNDSTSGSGAVTNQ
KEEAAPPSSAAANDSQTSTRHRAKAGGSKLTCIKIITKSPKGDCYAPSNATVEIVPAVERQNHVA
RKIVKMTKQPPKKKKAPSSREKKVTRTIMAILVAFVATWTPYNVMVLINTFCSSCIPNTVWTIGY
WLCYINSTINPACYALCNITFKKTFKQLLLCQYKNIRSTR
```

>Dr-chrm3b

```
MNLTLSAEPGLFLTNSSPGMRANPVTAFMSHDLHPANDSLHNITQIPSVLSDPLGGHSVLQVVMI
ALLCGSISLLTIIGNTLVLLSFKLNKQLKTVNNYYLLSLAFADLIIGVLSMNLYTTYIIMDQWAL
GNFACDLWLAIDYVASNASVMNLLVISFDRYFSVTRPLTYRAKRTTKRAMTMIGLAWSISFILWA
PAILFWQYFVGERTVEPDKCYIQFISEPITTFCTAIAAFYLPVTIMTVLYWRIYKETENRSRELA
GLKASGNVEEESVVVVPQTGSSRSHSSYELQPAAPMRKTKTRRLWFWSRGDVERSSSDSWNNNET
AISIDQSDDDEEEDAEHIYTIEKQDLEAKPSKFGVSKSSTLDSKDQPVKSARKTNKRKKLSLVKE
KKAAQTLSAILLAFIITWTPYNIMVLLNAFCDGCIPETLWALGYWLCYVNSTVNPMCYALCNKAF
RTTFRSILLCQWRKKKLNKAQIQKRAPAATYRKHTQSLD
```

>Bbe-chrm

```
MAFPTIPPPGPDYTTLLYGTEVVPVVYDAVNGTPVWSTSGTFNISCGNESTTLPAECNVTTAPPL
DPLGGHQVWEVVLICLLTCSLSIMTVGGNILVFVSFRVNRQLHTVNNYFLLSLAVADTLIGLLSM
NLYTVYMVMGRWALGPAICDLYLTVDYVSSNASVMNLCVISFDRYFSITRPLTYRAKRTPKRAAW
LIALAWVTSVLVWAPLIVGWQYIVGGRNVPENECYIHPEQPAKPLPSAAALAASRPKLSAAQLWK
RAAENTTRTKLKSDRARKISMVLKEKKAAKMLSAILLAFIITWLPYSVTVLFKPFYKVPTTVWNV
GYWLCYVNSTINPWCYALCNRTFRKTFKDILVCRVKKQNFRQLQSKRLY*
```

>Cin-chrm1-5

```
LLICILAGACSLLTIVGNVVVIVSFFINKSLRNFSNYLILSLAISDLTIGAFSMNVYTSYNVKNE
WILGEVMCKAWLAVDYTASNASVMNLLVICVDRYLAITKPVKYRKWCTPQRAAIAIAGVWILSFL
MWCPAIVLWDLFSTDTKMPTNDCYIPFMKDNAWVTVATIVGAFYIPATAMCALYYQVISKLRKRR
LKCFYREPQRVVRERRVTVLLKFILTCFIVLWLPYSLIIILVTSFWPSCMVPIYIWNLSYWLCYLN
STVNPFCYGFCNENFRQTFKVIIT
```

>Csa-chrm

```
VTICFLSALASILTIGGNVMVIVSFVINRALRTVNNYLILSLAAADLVIGVVSMNLFTVFIVSGS
WKLGAVLCDVWLALDYVASNASVMNLLIICLDRYYSVTKPVEYRNQRTPKRFITAIIGAWSISFI
LWAPWVLFWQFIVNKRTVPENASQTGADSPRSRTNSGRLLFIRRQIKKAPDTDSNLDSGGIIKVT
ERLKLQVVKKKLQSLNKETKAARLLASILAAFILLWLPYNIMALVEAFCPLAEKCIPDLAWNFGY
WFCYLNSTLNPVCYAMCNKNFQQTFKFLLS
```

>Csa-chrm1-5

```
AISIMAVILMVVTVTGNFLVIASYRSNRNLRTINNMFLVSLACSDLVIGVVSMTLYPIYMISRKW
MLGPILCDIWLCIDYTLSMASVANLMLICLDRYFSVTRPFTYRDSRTRYKTRVFILMAWVFSMLL
WSPAIVIWPIVRGRTVPDDQCQIQFFEDATITLVTAILAFYLPVLVMTVLYALIYRETRKCSQYL
EYLRNYGKSRSNTSSSPKAARTLSAILLAFIVTWLPYNVCAVYKSFCGEECVPSAAWDAAYYLCY
INSTVNPFCFALCNKTFRETFVKLLCGRKRGKLDDLPRSKRKCKSMKLQPSTS
```

### >Mm-chrm4

MANFTPVNGSSANQSVRLVTTAHNHLETVEMVFIATVTGSLSLVTVVGNILVMLSIKVNRQLQTV
NNYFLFSLACADLIIGAFSMNLYTLYIIKGYWPLGAVVCDLWLALDYVVSNASVMNLLIISFDRY
FCVTKPLTYPARRTTKMAGLMIAAAWVLSFVLWAPAILFWQFVVGKRTVPDNQCFIQFLSNPAVT
FGTAIAAFYLPVVIMTVLYIHISLASRSRVHKHRPEGPKEKKAKTLAFLKSPLMKPSIKKPPPGG
ASREELRNGKLEEAPPPALPPPPRPVADKDTSNESSSGSATQNTKERPPTELSTTEAATTPALPA
PTLQPRTLNPASKWSKIQIVTKQTGSECVTAIEIVPATPAGMRPAANVARKFASIARNQVRKKRQ
MAARERKVTRTIFAILLAFILTWTPYNVMVLVNTFCQSCIPERVWSIGYWLCYVNSTINPACYAL
CNATFKKTFRHLLLCQYRNIGTAR

### >Rt-chrm

MIPDYNSTASPFFFNSSFSWNHDSQTQVVLGSRPVDRSANGLFRSAVLSPTTSLGANGSLLSNST
TDPLGGHTVWQVVLIAFFTGILSLVTIIGNILVIVAFKVNKQLKTVNNYFLLSLAFADVIIGVIS
MNLYTTYIIMDRWALGNVACDLWLAIDYVASNASVMNLLVISFDRYLSITRPLTYRAKRTPKRAG
IMIGLAWIVSFVLWAPAILFWQYFVGERTVPPNECFIQFLSEPIITFGTAIAAFYLPVTIMTILY
WRIYKETEKRTKELAALQASTTDMETIHFVHQTGSSRSCSSNELQQAGMKEQRRLRRCRFWANSK
TWKSSTEGEQEGSSSDSWNNNDGGGSLDHSASSDEDDVVSETRAIYSIVLNLPGLKTAASLSRST
NANNIDLCSDELAKADNSVKERKFRSQEFKDPDEQGNSFHQHFAKLPVQSLPSIHPSKTSGGIAS
LAKSSTSMSLRETTVAKAFASKARTQITKRKRMSLVKEKKAAQTLSAILLAFIITWTPYNIMVLV
NTFCDKCIRDSLWQLGYWLCYVNSTVNPMCYALCNKTFRNTFKMLLLCHFEKRKKRRQQYQPKQA
VIFHKRIPCEPS*

### >Pm-chrm

MEGINIQDEGIVWSPTSQNPSAPLTLNSSAADDPLAGEQNVAQVVVIAVVAAMFSLITVVGNTLV
MLSFRVSRQLKTVSNYFLLSLAAADLIVGLFSMNLYTAYILTGRWAMGAVMCDLWLTLDYVASNA
SVMNLLAISFDRYFSITRPLKYKAKRTKRRASIMIGLAWAVSLVLWAPAILFWQHMVGKRTVPQD
QCYIQFLSEPIITFGTAIAAFYLPITIMMVLYWRIYRETRRRSRQFATLQGSESKSRSHVPTGTR
GCLTFLKDDDCDDDYDEDCGARAHDGIRSPKSKTSQGSQPWKCSLQSCEGHVETTHEEEEDDDEE
EEEEAVSLGCAISSDDDEQEPANERADSCAKPAAAATDGSSPRPSAPSDVPDDPVAAADSVVGNG
GETCAEPQHARISSTVRGRDLGRNNCVTLADMRIEESLLPRDAERESPREDEPAADKIVLRGRSH
RGRCKGGKAHSSTARRHCSLLARDNKAVRILCAILLAFIVTWTPYNIMVLVSTFCDDCVPKKLWH
LGYWLCYVNSTVNPMCYALCNMHFRKTFKTILSCKWNAVT*

## *Serotonergic receptors*

### >Pm-htr1A

AAVTAMEAHNITGSAPALAVSAAQGNSSEPSSVAYTVISSLCLTALILCAIFGNSCVIAAIALER
TLQNVANYLIGSLAVTDLLVSILVLPMAALYQVLDRWTLGQVVCDIFIALDVLCCTSSILHLCVI
ALDRYWAITNPIDYVNKRTPRRAVIMISLTWLVGFSISIPPMLGWRTPEDRADPNACKISQDHGY
TIYSTFGAFYIPLILMLVLYSRIFRAARFRIRKNVKKATEKKSFDAPFAISNRAEMPSAAAEAET
AAPPSPAPCNGDSKQRSHRDLALPEAVGARSPSSLAHSSARPHLSPAMMPTQQQHGNGTGADAC
RRKTALLISPFCGERCHLPPGVFAVINWLGYSNSLLNPIIYAYFNKDFQNAFKKIIKCKFCRQ

```
>Dr-htr1a
MESYNNTTESQDWSGNATSVSEVALSYQIIGSLFLAALILFAILGNACVIAAIALERSLQNVANY
LIGSLAVTDLMVSVLVLPMAALYQVLNKWTLGQEMCDIFISLDVLCCTSSILHLCAIALDRYWAI
TDPIDYVNKRTPRRAAILISLTWLIGFSISIPPMLGWRKPEDRADPDACTISQDHGYTIYSTFGA
FYIPLILMLVLYGRIFRAARFRIRKTVKKTEKAKIADKCLAVSPALFPRKANGEVGKTWRRSVEP
CANGALKNSDDGESFEITEVQSISKNHLSLPNNPQPCFENRNEKNTEAKRKVALARERKTVKTLG
IIMGTFIFCWLPFFIVALVLPFCQDCFMPEWLGAVINWLGYSNSLLNPVIYAYFNKDFQNAFKKI
LKCKCIRQ
```

```
>Dr-htr1fb
MDPINCTSVDLSDVLASKMSPSKILLSLTLSFLAVATTAINSLVITAILITRKLHQPANYLICSL
AVTDLLVAVLVMPVSIVYIAEETWVLGPIVCHLWLGVDVTCCTCSILHLAAIALDRYRAITDAVA
YSQKRTYKRVIVTILSLWTLSILVSLPPLVWRKFPKVEFKDGKREPMDCLIEHDHVAFTVYSTFG
AFYIPLALILVLYYKIYKAAEMLRNRRGSSRLVKQTVSSVMLPGMSSDKDIALSPDSFCPIEKSF
SDPSTDGERVRITSSSGNLIRVRRNPGARERRAALTLGLILGAFVVCWLPFFLKEVIVNICPTCT
TSAVLADFLTWLGYLNSLINPLIYTIFNEDFKKAFKKLLPLCCSTVL
```

```
>Mm-htr1b
MEEQGIQCAPPPPAASQTGVPLTNLSHNCSADGYIYQDSIALPWKVLLVALLALITLATTLSNAF
VIATVYRTRKLHTPANYLIASLAVTDLLVSILVMPISTMYTVTGRWTLGQVVCDFWLSSDITCCT
ASIMHLCVIALDRYWAITDAVEYSAKRTPKRAAIMIVLVWVFSISISLPPFFWRQAKAEEEMLDC
FVNTDHVLYTVYSTVGAFYLPTLLLIALYGRIYVEARSRILKQTPNKTGKRLTRAQLITDSPGST
SSVTSINSRAPDVPSESGSPVYVNQVKVRVSDALLEKKKLMAARERKATKTLGIILGAFIVCWLP
FFIISLVMPICKDACWFHMAIFDFFNWLGYLNSLINPIIYTMSNEDFKQAFHKLIRFKCAG
```

```
>Rt-htr1
MNFSNCTNESCQGQSKTLTERTAIALILSLIAIMTTLLNSAVMVAICITKKLHQPANYLICSLAL
TDLLVAILVMPISITYITTDAWVLGYIVCEAWLSLDMTFCTCSILHLCVIALDRYWAITDAVEYT
PKRTAKRAGVMILTVWTISVFISMPPLFWRSHNVNSTGEKCIIQHDHVIYTIYSTFGAFYVPSAL
ILILYYRIYHAAKNLYQKRGSSRHFTGRKSESQISTCMNYKLTQTFCVSNLHSCEPVLKFHSDHR
TCRVPTLENRQGSTEERQQNSNSRERNAARILGLILGTFVFCWLPFFIKELCVGLHLWVASQVVT
DFLAWLGYINSLINPLLYTSFNEDFKLAFRKLIRCKTHG*
```

```
>Le-htr1
MNITDCPRGSGPERTKSFAEKTAVALTLSLVMILTVVLNGVVIAAISLTKKLHQPANYLICSLAL
TDLLVALTVMPLSILYISAETWLLGQAFCQAWLSLDMTFCTCSILHLSAIALDRYWAITDAVQYS
RRRTGRRVAGMILAAWVLSVSISMPPLFWRSRMVNGTMGQQCTIRHDHAIYTIYSTFGAFYAPLG
LILILYYRIYRAARTLHRRRASSCKLAHTSCPSEAPRPGSQLGREKGIGEQPVSMGRERRAARVL
GLILGAFVLCWLPFFVKELLAGMQVWAASPTLGDLLTWLGYLNSLVNPLLYTSFNQDFVTAFRRV
ASCGRYG*
```

```
>Rt-htr1b
MMNQSAECLAPNSVELQANSKHVNCSTKVNPPGGAGITAWGISASVFLCLITLATVLSNGFVIAT
IYQARKLHTPANILIASLAITDLLVSILVMPLSIVYTVSGTWSLGQVVCDIWLSSDITCCTASIL
HLCVIALDRYWAITDAVEYSMKRTPERAAGMIVTVWVISICISIPPLFWRQAKAGELMHCTVNTD
```

```
QIFYTIYSTFGAFYIPTLLLIALYGRIYVEARSRILKQTPKQTGKRLTKAQLVTHSSGSSSLSSV
NSRVNEFPTETGSPVNLNHVKVKVSDVLLEKKRISAARERKATKTLGIILGAFIVCWLPFFIITL
VLPICKEACWFHHAIFDFFNWLGYLNSLINPIIYTMSNEDFKQAFHKLTRCR*
```

```
>Cm-htr1
MMNRSIQCLEPNADQLQTNSKSTNCSTKLSTQEQESQITALGISLSVFLSLITLAIVLSNAFVVI
TISRTRKLQTPANILIASLAVTDLLVSILVLPISIVYTVSGTWTLGQIVCDIWLSSDITCCTASI
LHLCVIALDRYWAITDAVEYSSKRTPKRAAGMIVTVWVISICISMPPMFWRQSKAGELTHCVVNT
DQIFYTIYSTFGAFYIPTLLLIALYGRIYVEARSRILKQSPKRTGKRLTTAQLITNSPGSSSVSS
VNSRVNENSGETGSPVVLNHVKVKVSDTLLERKKILAARERKATKTLGIILGAFIVCWLPFFIIS
LVVPICKEACWFHPAIFDFFTWLGYLNSLINPIIYTMSNDDFKQAFQKLIRFRYFTS
```

```
>Cm-htr1
MDQQNFSTAASEYNTMSSAWDLLGLKVSLSVVMAVITLATILSNLFVIVAVCLTRKLHTPANYLI
ASLAVTDLLVALLVMPISIAFTMQRTWVLGQVMCNIWVLLDVTLCTVSILHLCIIALDRYWAITH
ALKYTKHRTPFRAGLMIAAAWGIAVCISTSPLFWISSRTQEKQDECVFNENVFYCIFATCVSFYI
PSLVLVFLYAKIYLAARSRILRAPSTKDSNIQHPEPTSSSQCSVNYNSQDMLNYYVEQPDRLIHI
KMSSNFLQKKNISAAKERKATKTLGLILGAFIFCWLPFFTTTLVITICQEACWSNPVLIDFFTWL
GFVNSLINPVIYTIFNKNFKRAFRKLVLSRLC
```

```
>Dr-htr2b
MANVRQTDSVDWPSHWAALLILLVIVPTIGGNILVILAVSLERKLQNATNFFLMSLAVADLLVGL
LVMPIALVTVLYNSTWPLADFLCPIWLFLDVLFSTASIMHLCAISLDRYIAIKKPIQHSQFKSRA
KVLAKIALVWLISIGIAIPIPIKGLQFFDHPNITFNKNHTCLLSPEGFRDFKVYGSLVAFFIPLA
IMMIIYLLTIQVLRKKAYLLRSRAARPSISTVFQQELSVLASPEKMVISNGIKRDRTLNPVNPIT
GDEVPLRRMSTIGKRSMQNLTNEQRASKVLGIVFMLFVVMWCPFFITNVTSVLCERCNGNLVDQL
LDIFQWVGYVSSGINPLVYTLFNRTFRLAFRRYITCNYKSVRTPKLQRRSKISFRSSVTENSKRF
MKHGMKNGISPVGYQSPIRHRSTQLQTSANIMLDTLLLTDNEDCKPDEHVSHV
```

```
>Csa-htr2b
WFMLFLIPIIVLVALGNVLVIISVCLDRRLRSSTNYFLTSLAVADLLVALVVMPPSLGMIMNNYK
WPFSDELCGVWAMLDVFFSTSSILHLCMISLDRYIALSRYRNYDKLPVAKSVAIRICTVWTMAIG
IAIPLPVLGAQDRSNLFIGDTCAINVREFAIFGSLVAFLLPLIIMFVTYTLTILTLRKQAREISA
AMDRPQGGTLRTARNVEQDGDGRSLLLTRQHSHVSGKEWKCSEVITPDYSALTKALRQVQALFGF
GVIIPTSDVKSPNTNRTRERNNNFASKISLQQTRSSTRRMSGSFKQRVMTSITNEQRASKVGFQV
LGLIFVLFCVFWCPFFITNVVSHLCDSCDQDLMGSFMNWFVWVGYVSSGVNPCVYTLFSKRFRET
FFNVLRGRF
```

```
>Rat-htr2A
MEILCEDNISLSSIPNSLMQLGDGPRLYHNDFNSRDANTSEASNWTIDAENRTNLSCEGYLPPTC
LSILHLQEKNWSALLTTVVIILTIAGNILVIMAVSLEKKLQNATNYFLMSLAIADMLLGFLVMPV
SMLTILYGYRWPLPSKLCAIWIYLDVLFSTASIMHLCAISLDRYVAIQNPIHHSRFNSRTKAFLK
IIAVWTISVGISMPIPVFGLQDDSKVFKEGSCLLADDNFVLIGSFVAFFIPLTIMVITYFLTIKS
LQKEATLCVSDLSTRAKLASFSFLPQSSLSSEKLFQRSIHREPGSYAGRRTMQSISNEQKACKVL
GIVFFLFVVMWCPFFITNIMAVICKESCNENVIGALLNVFVWIGYLSSAVNPLVYTLFNKTYRSA
```

```
FSRYIQCQYKENRKPLQLILVNTIPALAYKSSQLQVGQKKNSQEDAEQTVDDCSMVTLGKQQSEE
NCTDNIETVNEKVSCV

>Aj-htr4-like
RKKKTNYFIVSLAFADLLVALVVMPFAAIELTTGRWSYGETFCLVRTSLDVLLTTASILHLCCIA
LDRYYAICCQPLVYRNKMTPMRVALMLGGCWVIPTFISFLPIMQGWNSIGINHLIEERKFSGVAN
ETNCVFLVNRPYALICSAVAFYVPLGLMVLAYQRIYVTAMEHARQIGTLQRAGSAPDSYFGPDHQ
GSSRMKIETKAAKTLAVIMGCFCLCWAPFFITNVVDPFIRYRVPWQVWTAWLWLGYINSGLNPFL
YAFLNRAFRRAFLMILCCGDDRYTRHGSFSPSRPYSASVNGTSIALR

>Cm-htr4
MWPLTLMRSYFSLAFSASKSEPHDLTGLSMLQKTVLITFLAAVMMMTVLGNLLVMVAVCKDRQLR
KIKTNYFIVSLAFADLLVSVMVMPFGAIELIENNWAYGNTFCLVRTSLDVLLTTASILHLCCISL
DRYYAICCQPLVYSNKMTPIRVTIMLGGCWFIPLFISFLPIMKGWNSVGIQELIEDRKFRNDTKH
CVFMVNKPYAITCSVVAFYIPLVLMVLAYQRIYVTAREHVRQIDILKRAGASIDNGQQADQQGHH
RMKTETKAAKTLCIIMGCFCLCWAPFFITNVVDPFINYSVPDQLWTAFLWLGYINSGLNPFLYAF
LNKSFRCAFLTILCCGNRRYRRASFLGQTIPSSSTAINGSTQVLR

>Cm-htr4-like
MMTILGNLLVMVALCMDKQLRKIKTNYFIVSLAFTDLLVAILVMPFGTIETVQEHWTYGETFCLV
RTSLDVLLTTASILHLCCIALDRYYAICCKPLVYRNKMTPWRVALMLGGCWVIPCFISFLPILQG
WNTIGITETIEERKFNRAINETYCVFMVNKTYAITCSAVAFYIPLILMVLAYQRIYVTAMEHARR
IGNLQRAGAATDTDSTEHQGSSVMKRETKAAKTLGIIMGCFCLCWAPFFITNIVDPFIEYSTPMQ
LWNACLWLGYINSGLNPFLYAFLNKSFRRAFLIIILCCGDHRYGRGAGYGATYTTSVNRTTVILR*

>Dr-htr4-like
MATASDSAEDSVDEVVSKHTSRITLSIVLVTIIIMTALGNLLVMVALCKDRQLRKKKTNFFIVSL
AFADLLVALVVMPLAAIELTTGKWNYGETFCLVRTSLDVLLTTASILHLCCIALDRYYAICCQPL
VYNNKMTPVRVSLMLVGCWVIPFFISFLPIMQSWNTIGIESFIEQRKLNSSRNSTCVFMVNQPYA
LVCSAVAFYVPLVLMVLAYQRIYVTAMGHARRIGSLHRAGSAPTSTYPNNDQHGSSRIKNETKAA
KTLAVIMGCFCLCWAPFFVTNVVDPFINYSVPWQMWTAWLWLGYINSGLNPFLYAFLNRAFRRAF
LMILCCGDERYARQGGFSPSRQCSESVNGTSISLRLSFLQSRRYSDNSNRFLSCELESQESAIAS

>Dr-htr4
MQGCEFPQEDLKSCHGFDPRAPHRNGPLRIDGYMNLSSTGQMPEMEEVDTNESNGLAKRVALISF
LSLVMLMSVLGNLLVMVAVCKDRQLRKIKTNYFIVSLAFADLLVSVLVMPFGAIELIHQNWIYGE
TFCLVRTSLDVLLTTASILHLCCISLDRYYAICCQPLVYRNKMTPLRVTLMIGGCWIIPTVISFL
PIMQGWNSIGIKDLIDKRKISGNSTVCVFMVNKPYALTCSVVAFYLPLVLMVLAYQRIYVTAREH
ARQISMLQRAGGAGNADSADHQRNHRMRTETKAAKTLCIIMGCFCLCWAPFFITNVVDPFIDYSV
PEQLWAACLWLGYINSMLNPILYAFLNKSFRRAFLIIILCCGHKRYRRPSILGPGTTCTATQINGS
THVLKYAVLHNGNHNEQEKLSIQNDTESQESCF

>Ga-htr4
RKIKTNYFIVSLAFADLLVSVLVMPFGAIELVHQHWIYGETFCLVRTSLDVLLTTASILHLCCIA
LDRYYAICCQPLVYQNKMTPMRVALMMGGCWVIPTFISFLPIMLGWNSIGIDHLIEERRYSEGTN
```

```
STSCVFMVNKPYALTCSVVAFYIPLVLMVLAYQRIYVTARAHALQISVLQRAGGAGVGADSADHQ
RNHRMRTETKAAKTLCIIMGCFCLCWAPFFITNVVDPFIDYTVPDKLWVACLWLGYINSMLNPIL
YAFLNKSFRRAFLIILCCGRKRYRR

>Ga-htr4-like
LRKKKTNYFIVSLAFADLLVALLVMPFAAIELTTGEWRYGEIFCLVRTSLDVLLTTASILHLCCI
ALDRYYAICCQPLVYRHKMTPLRVAGMLSGCWLIPTFISFLPIMQSWNAIGIEDIIEDRRSSGGS
NDTSCVFLVNRPYALICSTVAFYVPLALMVLAYQRIYVTAMTHVRQIETLQRAGSAPVFGTTPVV
TVRSSTSSDPTDQYHLRTAASSSSSEHAPIANSRMRIETKAAKTLAVIMGCFCLCWAPFFITNVV
DPFIHYSVPWQLWTAWLWLGYINSGLNPFLYAFLNRAFRRAFLVILCCGDERYARQGSCSYGHTQ
RAYSAGSVNGTSMALR

>Lec-htr4
VPLCSCHPVSDDTSSQAEKYILAGIFSIIIAVTILGNLLVVVAVCKDRHLRKIKTNYFIVSLAVA
DLLVAILVMPFGAVERVQNDWPYGDKFCIIRTSFDVMFTTASIMHLCCIALDRFYAICCKPLVYQ
NKMTPLRVGLMLGACWVVPSLISFIPIANGWNIIGIEQQLELRLGQAKEANQTHCIFMVNKVYAV
ACSLVAFYIPLGLMAAAYQRIYVTARAHARQIGSLQRAVSKDTTGDEVTMVTSGAASPLRAQHLV
PVAQATMVQTQSTRFRHETKAAKTLAIIMGCFCLCWAPFFINNVIDPFVNYDTPPQLWDAWLWLG
YANSALNPLLYAFLNRSFRRAFLAILCCWDAARYRRSSFSGHSVRYSVSTNGSTVQPVP

>Le-htr4
FAFSARSDGKPHEIPGFSMVQKTILITFLSSIIIMTILGNLLVMVAVCKDRQLRKIKTNYFIVSL
AFADLLVSVMVMPFGAIELIQQNWIYGDTFCLVRTSLDVLLTTASILHLCCIALDRYYAICCQPL
VYRNKMTRSRVIIMLGGCWIIPSFISFLPIMQGWNSIGIQELVEIRKFQNDTNTTYCVFMVNKPY
AITCSVVAFYIPLILMVLAYQRIYVTARAHARQIEMLKRAGTSNESGQHADHHSNHRMKTETKAA
KTLCIIMGCFCLCWAPFFITNIVDPFIKYSVPDKIWTAFLWLGYINSGLNPFLYAYLNKSFRRAF
LTILCCGERYRRSSLLGQTIPCSTATINGSTHVLR

>Lo-htr4
MPVMEEADVNESTPEATPQALSSYSVVERIVLITFLSLVMLMTVLGNLLVMVAVCKDRQLRKIKT
NYFIVSLAFADLLVSVLVMPFGAIELIHQNWIYGETFCLVRTSLDVLLTTASILHLCCISLDRYY
AICCQPLVYRNKMTPMRVALMLGGCWVIPTFISFLPIMQGWNSIGINDLIEQRKFSGEANATLCV
FMVNKPYALTCSVVAFYIPLGLMVLAYQRIYVTAREHARQIGMLQRAGGANSGASDSADHQRNHR
MRTETKAAKTLCIIMGCFCLCWAPFFITNVVDPFIDYTVPEKLWTACLWLGYINSMLNPFLYAFL
NKSFRRAFLIILCCGQERYRRPSILGPSAPCTSTQINGSTHVLSGCSSASKLLLWFCNTRPVPV

>Lo-htr4-like
RKKKTNYFIVSLAFADLLVAVVVMPFAAIELSKGYWEYGETFCLVRTSLDVMLTTASILHLCCIA
LDRYYAICCQPLVYRNKMTPLRVALMLGGCWVISFFISFLPIMQSWNAIGIEKIIEERKFNNSTN
ETYCVFLVNRPYAIICSAVAFYIPLVLMVLAYQRIYITAMEHVRQIGTLQRAGSAPEAYDGSDHQ
GSSRMKIETKAAKTLAVIMGCFCLCWAPFFITNIIDPFIDYSVPWELWTAWLWLGYVNSGLNPFL
YAFLNRAFRRAFLMILCCGNERYVRPGSFGPSRHYTTSVNGTSIALRYFFKCF*
```

>Mm-htr4

```
MDKLDANVSSNEGFRSVEKVVLLTFLAVVILMAILGNLLVMVAVCRDRQLRKIKTNYFIVSLAFA
DLLVSVLVMPFGAIELVQDIWAYGEMFCLVRTSLDVLLTTASIFHLCCISLDRYYAICCQPLVYR
NKMTPLRIALMLGGCWVLPMFISFLPIMQGWNNIGIVDVIEKRKFSHNSNSTWCVFMVNKPYAIT
CSVVAFYIPFLLMVLAYYRIYVTAKEHAQQIQMLQRAGATSESRPQPADQHSTHRMRTETKAAKT
LCVIMGCFCFCWAPFFVTNIVDPFIDYTVPEQVWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLI
ILCCDDERYKRPPILGQTVPCSTTTINGSTHVLRDTVECGGQWESRCHLTATSPLVAAQPSDT
```

>Np-htr4

```
MEELDSNVRPHEGFGVGEKIVLITFISAVILMTTLGNLLVMVAVCRDRQLRKIKTNYFIVSLAFA
DLLVSVLVMPFGAIELIQDKWIYGEMFCLVRTSLDVLLTTASILHLCCISLDRYYAICCQPLVYR
NKMTPLRIALMLGGCWIIPTFISFLPIMQGWNSIGILDLIEKRKFSKDSNSTYCIFMVNKPYAIT
CSVVAFYIPLFLMVLAYYRIYVTAREHARQIGVLQRAGAPADHRHQHPDQHTTHRMKTETKAAKT
LCIIMGCFCLCWAPFFITNVIDPFIDYSVPGQLWTAFLWLGYINSGFNPFLYAFLNKSFRRAFLI
ILCCGDEKYRRPSILGQTVPCSTTTINGSTHVLRYTVLYNGHHQEQDKLPIQIDPESQESCF
```

>Pm-htr4

```
MYGNNTTFNNDETSSQAEKYILAGIFSIIIAVTILGNLLVVVAVCKDRHLRKIKTNYFIVSLAVA
DLLVAILVMPFGAVERVQNDWPYGDKFCIIRTSFDVMFTTASIMHLCCIALDRFYAICCKPLVYQ
NKMTPLRVGLMLGACWVVPSLISFIPIANGWNIIGIEQQLELRLGQAKEANQTHCIFMVNKVYAV
ACSLVAFYIPLGLMAAAYQRIYVTARAHARQIGSLQRAVSKDTTGDEVTMVTSGAASPLRAQQLV
PVAQATMVQTQSTRFRHETKAAKTLAIIMGCFCLCWAPFFINNVIDPFVNYDTPQQLWDAWLWLG
YANSALNPLLYAFLNRSFRRAFLAILCCWDAARYRRSSFSSHSVRYSVSTNGSAVQPVPSARVRA
RARLPSRPRTRAAACPAVSKLVTHFCGAPSPV
```

>Rt-htr4

```
MDEADVNESTSDGEPHEIPGFSILQKTVLITFLSAIMVMTILGNLLVMVAVCKDRQLRKIKTNYF
IVSLAFADLLVSVMVMPFGAIELIQQNWIYGDRFCLVRTSLDVLLTTASILHLCCISLDRYYAIC
CQPLVYRNKMTPLRITIMLGGCWIIPSFISFLPIMQGWNIIGIQELVEERKSSNDTNITKCVFMV
NKPFAITCSVVAFYVPLLLMVLAYQRIYVTAREHARQIEMLKRAGTSTDSGQQADHSGNHRMKTE
TKAAKTLCIIMGCFCLCWAPFFITNIVDPFINYSVPEQLWTACLWLGYINSGFNPFLYAYLNKSF
RRAFLRILCCGDRYRRSSLLGQTIPCSATTINGSAHVLR
```

>Xt-htr4 _

```
MAHNINVTSNEGYGVAARIVLISFISAVILMTILGNLLVMVAVCRDRQLRKIKTNYFIVSLAFAD
LLVSVLVMPFGAIELVQEKWIYGEMFCLVRTSLDVLLTTASILHLCCISLDRYYAICCQPLVYRN
KMTPLRITLMLSGCWIIPTFISFLPIMQGWNSIGILDLIETRKYNKSSNSTNCIFMVNKPYAITC
SVVAFYIPFFLMVLAYYRIYITAREHARQIGVLQRAGAPADHRHQHPDQHTTHRMKTETKAAKTL
CIIMGCFCLCWAPFFITNVVDPFINYSVPVELWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLII
LCCGDEKYRRPSILGQTVPCSTTTINGSTHVLRYTVLYNGHQQEHDTLPIHIDPESQESCF
```

>Xl-htr4.S _

```
MLCSEKSLVSMDICIYFIGPIFYRSNEGYGVAARIVLISFISAVILMTILGNLLVMVAVCRDRQL
RKIKTNYFIVSLAFADLLVSVLVMPFGAIELVQEKWIYGEMFCLVRTSLDVLLTTASILHLCCIS
```

```
LDRYYAICCQPLVYRNKMTPLRIALMLSGCWIIPTFISFLPIMQGWNSIGILDLIETRKYNKSSN
STNCIFMVNKPYAITCSVVAFYIPFLLMVLAYYRIYITAREHARQIGVLQRAGAPVDHRHQHPDQ
HTTHRMKTETKAAKTLCIIMGCFCLCWAPFFITNVVDPFINYSVPVELWTAFLWLGYINSGLNPF
LYAFLNKSFRRAFLIILCCGDEKYRRPSILGQTVPCSTTTINGSTHVLRYTVLYNGHHQEHDTLP
IHIDPESQESCF

>Mm-htr5A
MDLPVNLTSFSLSTPSSLEPNRSLDTEVLRPSRPFLSAFRVLVLTLLGFLAAATFTWNLLVLATI
LKVRTFHRVPHNLVASMAISDVLVAVLVMPLSLVHELSGRRWQLGRRLCQLWIACDVLCCTASIW
NVTAIALDRYWSITRHLEYTLRTRKRVSNVMILLTWALSTVISLAPLLFGWGETYSEPSEECQVS
REPSYTVFSTVGAFYLPLCVVLFVYWKIYRAAKFRMGSRKTNSVSPVPEAVEVKNATQHPQMVFT
VRHATVTFQTEGDTWREQKEQRAALMVGILIGVFVLCWFPFFVTELISPLCSWDVPAIWKSIFLW
LGYSNSFFNPLIYTAFNRSYSSAFKVFFSKQQ

>Dr-htr5ab
MTQPNVTALSANISGGSESGNLYRPFSVFSVLTLTLLAMLVVATFVWNLLVLVTILRVRTFHRVP
HNLVASMAISDVMVAGLVMPLSLVRELYGRRWILGRALCQVWISCDVLCCTASIWNVTAIALDRY
WSITRHLEYTLKTRKRISNVMIGLTWLLSSVISLSPLFGWGETYSEDSLACQVSQEPSYTVFSTF
GAFYLPLCVVLFVYWKIYKAAKFRIGSRKTNTITPMAEVIEVKEAERQPQMAFTVRHATVSFQTD
GETWREQKERRAALMVGILIGVFVLCWIPFFLAELIIPLCSCDIPPVWKSVFLWLGYSNSFFNPL
IYTAFNKNYNNAFRNLFSRQR

>Lec-htr5
MDGNRHSDDLSPNMSTWPMNGSDPWPDHNVSDQPQPFSFFSILTFTLLAILILATFAWNVLVIVT
ILRVKTFHCVPHNLVASMAVSDVLVAALVMPLSLVSELHRRRWRLGPVMCDVWISCDVLCCTASI
WNVTAVALDRFWSITRHLEYTIRVRKCISNLMIALTWLLSATISLSPLFGWGEGYYSDKSQHCHF
SQGPLYTVFSTVGAFYLPLCVVLFVYWKIYKATKFCFGSHKANSVMPISDEIEVRR

>csa-htr5
ALAILLVVIIVGSIFGNILVVAAVKSERNLQTTANFLICSLAITDFMVACLVMPFSALYEILGTW
VFGDILCQFWTAIDIACCTASILHLCAIAFERHRSITGAVRYFSQGRRRTRTQTTVGRVRFVDQG
NIACYPSGSNAVNGGIVPLVKRTQDTLQYRRIPSFEAQQKSTPRIAGIFNCCHKYSDRKQQRRLV
DQRRSSIMLAHSLSLRAKIKLLKTREVRAIKTLGTIVGAFVICWLPFFAVTLAAAFCDCEIPRSL
RSIVLWLGYCNSLVNPILYGAFNRDFHSAFKKLLTSHFYKIRCR*

>Cin-htr5
ALAILLAIIIIGSMFGNILVVIAVRSERNLQTTANFLICSLAITDFLVACLVMPFSALYEISGTW
VFGDILCQTWTAIDIACCTASILHLCAIAFERHRSITSAVRYFSQGRRHTVAPKIVLVWVLAICI
SIPPILGWKPSSQQQTQVNNVTTAASTVQRCEVGHYREYTLYATLGSFYIPLALLLTAYVRIYRR
LLNQRRSSIMLAHSLSLRAKVKLLKAREVRAIKTLGTIVGAFVICWLPFFAVTLAAAFCNCKMPH
TLTSIVLWLGYCNSLVNPILYGAFNRDFYAAFKKL

>Dr-htr6
MMSGSPPIPRVEAASDLWKIHRSFNDSSTISDGWSIGGSGPWLLAVMLSLIILVTACGNILLIAL
VFAHRSLRCTSNCFLVSLFLSDLMVALVVMPPAMLNVLCGTWVLAPGFCPVWLCFDVMCCSASIL
```

NLCVISLDRYLLIISPLRYKQHMTPPRALLLVGGAWGLAALTSFLPIKMDWHSLGRMQELTEDDP
GNATHLNSFYPSSYFQLSSSGMPSTQCRLRVTLPFALVATFLTFFLPSTAICFTYCRILLAARRQ
ARQVEALTHPAYPQHSLGEPSRPPSPGHAIQDGDDYSHQEPPGLRHAPLSVNSERRLAHRQRKRA
LKASLTLGVLLGLFFSAWLPFFITNMAQAVCECVPPSFFDAITWLGYCNSTMNPIIYPMFMRDFK
RALARLLPCCSSSQAPRRPSLPLSLSLRNSGEPQLPSEPPSLVSDPPQLPATATDAVNLLDAEHA
GIDLPLLLPNQVDTLDD

### >Mm-htr6

MVPEPGPVNSSTPAWGPGPPPAPGGSGWVAAALCVVIVLTAAANSLLIALICTQPALRNTSNFFL
VSLFTSDLMVGLVVMPPAMLNALYGRWVLARGLCLLWTAFDVMCCSASILNLCLISLDRYLLILS
PLRYKLRMTAPRALALILGAWSLAALASFLPLLLGWHELGKARTSAPGQCRLLASLPYVLVASGV
TFFLPSGAICFTYCRILLAARKQAVQVASLTTGTATAGQALETLQVPRTPRPGMESADSRRLTTK
HSRKALKASLTLGILLSMFFVTWLPFFVASIAQAVCDCISPGLFDVLTWLGYCNSTMNPIIYPLF
MRDFKRALGRFVPCVHCPPEHRASPASPSMWTSHSGARPGLSLQQVLPLPLPPNSDSDSASGGTS
GLQLTAQLLLPGEATRDPPPPTRAPTVVNFFVTDSVEPEIRQHPLGSPMN*

### >Rt-htr6

MDNGLWAEGKGPELGQGAAPEGRQWIAAFLCLIIILTTAGNSLLILLIFTQRSLRNTSNYFLVSL
FMSDLMVGLVVMPPAMLNELYGRWVLESELCSIWYSFDVMCCSASILNLCVISLDRYFLIISPLK
YKLRMTSCRALFLIFTTWTLAALASFLPIEMGWHEMDFDAQALNSTLELPEEAAQCRFLVSLPYA
LIASSLTFFLPSVAISFTYCRILLAAKKQAVQVASLTTNVATTSDEPVQVKLPLSQNPSARTSDS
RKFTKHSKKALKASLTLGVLLGMFFVAWLPFFVANVTQAVCECVPALLFDVLTWLGYCNSTMNPI
IYPLFMRDFKRAMAKYLPCCHRWWERRPTVVSLSMKNSNSGRRLGLSLPNMLTLPPQTGSGDSVI
QVNEHILLAASKDQQLTKDQQLEDSLQLFELEQTDQEFQGNPLNTPMD*

### >Mm-htr7

MMDVNSSGRPDLYGHLRSLILPEVGRRLQDLSPDGGAHSVVSSWMPHLLSGFPEVTASPAPTWDA
PPDNVSGCGEQINYGRVEKVVIGSILTLITLLTIAGNCLVVISVCFVKKLRQPSNYLIVSLALAD
LSVAVAVMPFVSVTDLIGGKWIFGHFFCNVFIAMDVMCCTASIMTLCVISIDRYLGITRPLTYPV
RQNGKCMAKMILSVWLLSASITLPPLFGWAQNVNDDKVCLISQDFGYTIYSTAVAFYIPMSVMLF
MYYQIYKAARKSAAKHKFSGFPRVQPESVISLNGVVKLQKEVEECANLSRLLKHERKNISIFKRE
QKAATTLGIIVGAFTVCWLPFFLLSTARPFICGTSCSCIPLWVERTCLWLGYANSLINPFIYAFF
NRDLRTTYRSLLQCQYRNINRKLSAAGMHEALKLAERPERSEFVLQNCDHCGKKGHDT

### >Dr-htr7

MISALTKDRVQSIVNSLTSEVMDVSFLNKIHDTTTTLPTPSFMDNGTRCGVPILSYGHVEKVLIG
GVLTMLTFLTVCGNLLVVISVCFVKKLKQPSNYLIVSLAVADLSVAVVVMPFVSITDLIGGQWIF
GRVFCNVFIAMDVMCCTASIMTLCVISIDRYLGITKPLTYPVRQSGKCMAKIVLSVWLLSASITL
PPLFGWAQNVNDDNVCLISQDLGYTIYSTAVAFYIPMSVMLIMYYRIYRVAKDSAAKHTIAGFPK
AEDEESMNCVTAALKLQREVEECVSFSRLLKSDRKNISIFKREQKAAATLGIVVGAFAVCWMPFF
LLSTARPFICGLQCSCVPLWVERTLLWLGYANSLINPFIYAFFNRDLRTTYHNLIRCRYRNINRK
LSAASMHEALKLAERPDLVL

>Cin-htr7

```
MSNLSFCPEDGNTTSAEGDAMLTTALIAALTSLLSLLIVVGNGLIIVSVALVKKLRQPANYLIVS
LALSDFLVGLVVLPLTIVYDIMGEWVFGPNVCDVHVSFDVICCTASIMNLCMISIDRYLMITQPM
TYPKRRTGKLMLLLIATAWVLSCLVIIPALFGFTKNVKDGKVHSFAINQTAGYENPMLGEFQVFG
IKKYGKACLISQERWFTIYSTLGAFYLPLAVMLCMYWKIYLEASRFNARHRLRSYSTTGSQDSTN
GNAVNLIRSSSGVVCGLGMKNGFPRNGTTRHNGMEWRFPTISEVDILTSLNEEGEQTNKETETET
INGKINEEYRARTLYTRASANSLLATEKTPKLVGKPSPRSRLFMLYGKPRLLRATSTPCPTTTNK
PNTQHTRKSSFRTLRQNSEITFPCNRRPTVFNQIRRRVSLATSRDRMRNVKATRTLGIVVGAFTF
CWLPFFIVTFLRPFACPIPESQDCIPLWLVRFVLWLGYLNSALNPLIYIGFSPDLRETFRFLICC
KCTNVDRRLAQIELRQAIAVERKASMASRSYAPESIV*
```

>csa-htr7

```
ALIAALTSLLSLLIVVGNGLIIVSVALVKKLRQPANYLIVSLALSDFLVGLVVLPLTIVYDIMGE
WVFGPNVCDVHVSFDVICCTASIMNLCMISIDRYLMITQPMTYPKRRTGKLMLLLIATAWLLSCL
VIIPALFGFTKNVKDGKRAIFEINKTAGFENPSLGEFQVFGIKKYGKTCLISQERWFTIYSTLGA
FYLPLAVMLCMYWKIYLEASRFNSRHRLRSYSTSGSQRANGVNGVELIRCESGIALEERNGASRH
QRANGVEWRFPTISKVNILTSLDENGEETIKRTITSPCDAQQQNGKFFSEYQARTLYTRASAQSL
IAAEQSLISSGKNGKIPDKTHSRSKLSLLYGQARCCRPRLLRTTSSPAQSPSNGSKLSSANVRKA
SFRTVRQNSEITFPCQRRPTVFNQIRRRVSLATSRDRMRNVKATRTLGIVVGAFTFCWLPFFIVT
FLRPFACPIPEAQDCIPLWLVRFVLWLGYLNSALNPLIYIGFSPDLRETFRFLICCKCTNVDRRL
AQIELRQAIAHERRNSVASRSYAAESIV
```

### ***Unclassified aminergic receptors***

>Cin-AmR

```
MIMESTNLVTALPEQNMSLFEVSMSTNTNSTYEPPFDSIGIAISAVIIFTFLVLGVVGNSLTLAV
ILTYKELNNNLFMRFIFSLCISDLLSALISWLFLYRRTWGFDVWDPIPAVFCKFYWATDIMTSYA
TALHVLSFAIVRFISVQYPVQYNKMKLIHANIWIVGIWVACIISGFIPSMFIFGAKARDRESSSP
DSRWPSCTANLADLDKYILYQKVAYPLFLYIPTIGVVITCILIAVTLKKRSGSANLNKKEERRLR
KERQAVLQLILIIISFLLGYIPFTAYEFWGANTHPRERYYFLVDNWFGMIEYFCLRFSECLNPVF
YNLGSTKMRTYTKMFLKKKVFCCIEWQPTTPMSPTSNTRGNKSGVNTIANSVDATLENTNHHNV
```

>Csa-AmR1

```
MANLALAVIYFTVFFFGIIGNAIVLFVLLRQRRGWSVTTAYLFNLALSDVLFLCVLPFWGHQYLN
GLDWAFGLGWCKIVGSVTSINMYASVFFLTAMSADRYMAVVHATSVNVVRSSYIARWVCVAVWFA
ALLLSLPQLIHQTLHPIFYVQTNSTNASQVSTPGESPMLRDVTSAMAEAPRSYAAPESPIACTFY
IPAGSSKALRMGLVEFTRSMLGFVVPMIVISVCYAKIVITVKKKVIGKRVRKDRVAKLAALVVLA
FFFCWLPMQIMKLFSALGGWWKLRVFEFDEDLYNTVYPFMVALAYSNSCINPVVYAFTTTNFQEN
IKDICGSDKAARPYKMTLSPQQGHNGDPKTGFVTKTEALNMYSPCPKRNMTAYSPAVQVHAAEVS
TIAQYIELFCRSITPVYVRPVSLVVKCVAF*
```

### >Csa-AmR2

MREILTNIFSLTTLSLREMNSSILNQVLNEKNECKLLSVIYTQSDLQGVPEFLMNCTSIERLDIS
SNLISRILEHDFRRLTELKHLNLHNNRLQRIERGSFSSLVKLETVDISENKDVLYDNSLFSSQSK
LINVLGNDFIICCLARKTSSTSLRFCSPVDAISSCERLIAKDYIRALIWIQALIAIIGNVLVAIL
RAKEYPKQESRGGKLNSSFVGVLSIADLLMGLFLLIIAIVDSVYRVEFYKIAKTWRLDSALCRFC
GFLSLFSAEASVFTLLVITFTRMVSIVSPIYYLRANLHIFRFAMLIAWTVALSISVVPLFRFRTF
FSKTSLCLPAFYSSTSDDDWIYSIFVIILNLVAFLAMMTSYLVIIVATRRSQTRSEERRSSNPRP
KAKLGKRVLLIVATDFFCWMPVCMLGFVSIASDGLNFYNDIYPWTAVILLPINSSMNPLIYTFLT
RGTICQTITQMRSESKSGSRTASSTAK*

## Deuterostome serotonergic receptor 4

### >alu-htr4

MTTIVTMSGYNTTQALGIPGTDLTRTVQPVTNWTNGSLGCTETYIGPQYSLTV**QV**LLSSFLALVI
LLTIVGNILVISTVALFRSLRSLTNYF**VV**SLAVADLLVGVIVMTLGTQYEVSGRWRHGEIFCLVF
TSMDVSLTTCSIMHLSCIAFDRYYAICHPFKYPTKMTHRKMRVMIAMCWVVPVIIAWVPIMNGWN
TLNIAxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxAVLMILAYYQVYRVARRQMQRI
ISVEGAAPNNENTRREKKAAKTLGIIMGCFLVCWMPFFVTNIIDPLCGYCIAQSCELCLKFFLWL
GYINSTLNPMIYAFFNRSFRRAFKRILSCSSCCDLDKRDFDPAVSTALQGRTRSRRRPNGDVVNN
S*

### >Bbe-htr4

MTTIVSMSDYNTTQALLVPETHDVRTVQPGTNDTNGSSGCTEAYLGSQYSLVI**QI**LLSCFLALVI
LLTIVGNILVISTVALFRSLRSLTNYF**VV**SLAVADLLVGVIVMTLGTQYEVSGRWRHGEIFCLVF
TSMDISLTTCSIMHLSCIAFDRYYAICHPFKYPTKMSHRK**MV**LMIALCWIVPVIMAYVPIMNRWN
TIGIEPVVEDTKCALGPDSCVFLVNKEFSLIASTLSFYLPAVMMTLAYYQVYRAARRQMQQIISL
ERAMNNNENMRREKKAAKTLGIIMGCFLVCWTPFFVANIVEPLCGYCITNSCELCLKFFLWLGYI
NSTLNPMIYAFFNRSFRRAFKRILSCWSCCDVDNRDFDPAVSTALQTRTSRRHQNGEVVNNT*

### >Bfl-htr4

MTTIVSMSDYNTTQALAVPETHHVRTVQPGANGTNGSSGCTEAYLGPQYSLEI**QV**LLSSFLALVI
LLTIVGNILVISTVALFRSLRSLTNYF**VV**SLAVADLLVGVIVMTLGTQYEVSGRWRHGEIFCLIF
TSMDISLTTCSIMHLSCIAFDRYYAICHPFKYPTKMSHRKMVLMIAMCWVVPVIMAYVPIMNRWN
TIGIEPVVEDTKCALGPESCVFLVNKEFSLIASTLSFYLPAVMMTLAYYQVYRAARRQMQQIISL
ERSMNNNENMRREKKAAKTLGIIMGCFLVCWMPFFVANIVEPLCGYCITRSCDLCLKFFLWLGYI
NSTLNPMIYAFFNRSFRRAFKRILSCSSCCDLDNRDFDPAVSTALQRRTSTRHQNGEAVNNT*

### >Bla-htr4

MTTIVSMSDFNTTQALVVPETHPLRTAPPVTNHTNGSTGCTESYLGPQYSLVI**QI**LLSCFLALVI
LLTIVGNILVISTVALFRSLRSLTNYF**VV**SLAVADLLVGVIVMTLGTQYEVSGRWRHGEIFCLVF
TSMDISLTTCSIMHLSCIAFDRYYAICHPFKYPTKMSHRKMVLMIAMCWVVPVIMAYVPIMNRWN
TIGIEPVVEDTKCELGPDSCVFLVNKEFSLIASTLSFYLPAIMMTLAYYQVYRAARRQMQQIISL
ERAMNNNENMRREKKAAKTLGIIMGCFLVCWMPFFVANIVEPLCGYCITRSCALCSKFFLWLGYI
NSTLNPMIYAFFNRSFRRAFKRILSCSSCCDVDNRDFDPAVSTALQGRSSRRHQNGEVVNNT*

```
>Ptfl-htr4
MSTNNIHGLPYVFESSDTPATSAVFVVELETTRQPFLITNDNASTWAVSGGVQPGSFNVAERIVI
GFILSLIILTTIVGNILVCTSIIIFPSLRTLTNYFVFSLAIADVLVACLVMAISTIYIVTETWMY
GDTFCLVFISFDIAFCTASIMHLSCIAYDRYSAICNPFQYPIKMTSRRVAVMLAACWVVPMLISF
IPILLGWNTLGIENVIAEVKQHTGPNSCVFLVNRPYAAVASTIAFYIPCILMASAYLFIFRAARK
QAAQIKSLERATANWNNARNGESGGRGSVSLAAEKKAAKTLGIIMGCFTVCWCPFFVLNIIDPFC
DFCISPKVWPPITWLGYTNSMLNPILYAFFNRTFRRAFSRLLRCHVCKGSAAEFDPTITSHERRS
*
```

```
>Sako-htr4
MESGITSSTDAISYHSFALDKTSRVYVLEVFTDTGEPIVGAVNDNSTGLSGNVLQYGLAERIIIG
FVLTVIIILTIAGNILVCASIFIFPSLRTLTNYFVFSLAIADILVACLVMTFSTINVVTETWIYG
DTFCLIFISFDISFCTASIMHLSCIAFDRYSAICNPFQYPLKMTSRRVTIMLASCWVVPMFISFI
PILLQWNTIGIENVIADVKNFAGPYSCIFLVNKPYAVIASTIAFYMPCILMATAYFFIFRAARKQ
AQQIKSLERATMNWNNTRNGPGDGHPHHHGRRVSLAAEKKAAKTLGIIMGCFTICWCPFFVFNIV
DPFCDFCIDPGAWPPVTWLGYINSMLNPLLYAFFNRSFRRAFIRLLRCHVCKGTTAEFDPTISSR
ER*
```

SUPPLEMENTARY INFORMATION
SI Figure 1: Phylogenetic tree for htr4 indeuterostomes and inferred gene gain/loss events

# Olfactory function in the trace amine-associated receptor family (TAARs) evolved twice independently

Milan Dieris[1], Daniel Kowatschew[1], and Sigrun I. Korsching[1]*

[1]Institute for Genetics, University at Cologne, Germany
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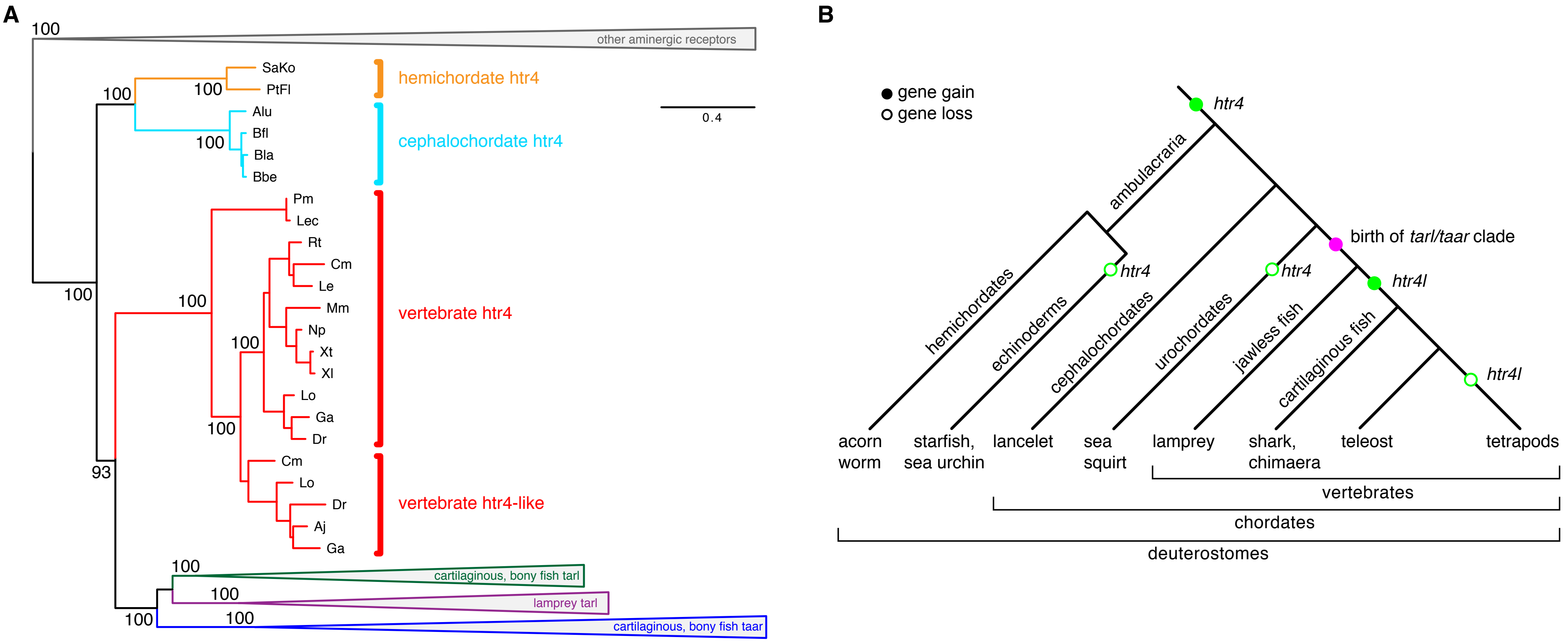

*SI Figure 1 Phylogenetic tree for HTR4 in deuterostomes and inferred gene gain/loss events*

A) A phylogenetic tree of deuterostome *htr4* genes was constructed using MAFFT for alignment and maximum likelihood algoritm PhyML-aLRT. For details see Methods. Representative *taar* and *tarl* genes are added as reference. Clades are collapsed as indicated.

B) A deuterostome species tree with predicted gene gain and loss events for *htr4* and the birth of the *taar/tarl* clade.

# SUPPLEMENTARY INFORMATION

SI Figure 2: No correlation between genomic coverage and detection of *taar* genes

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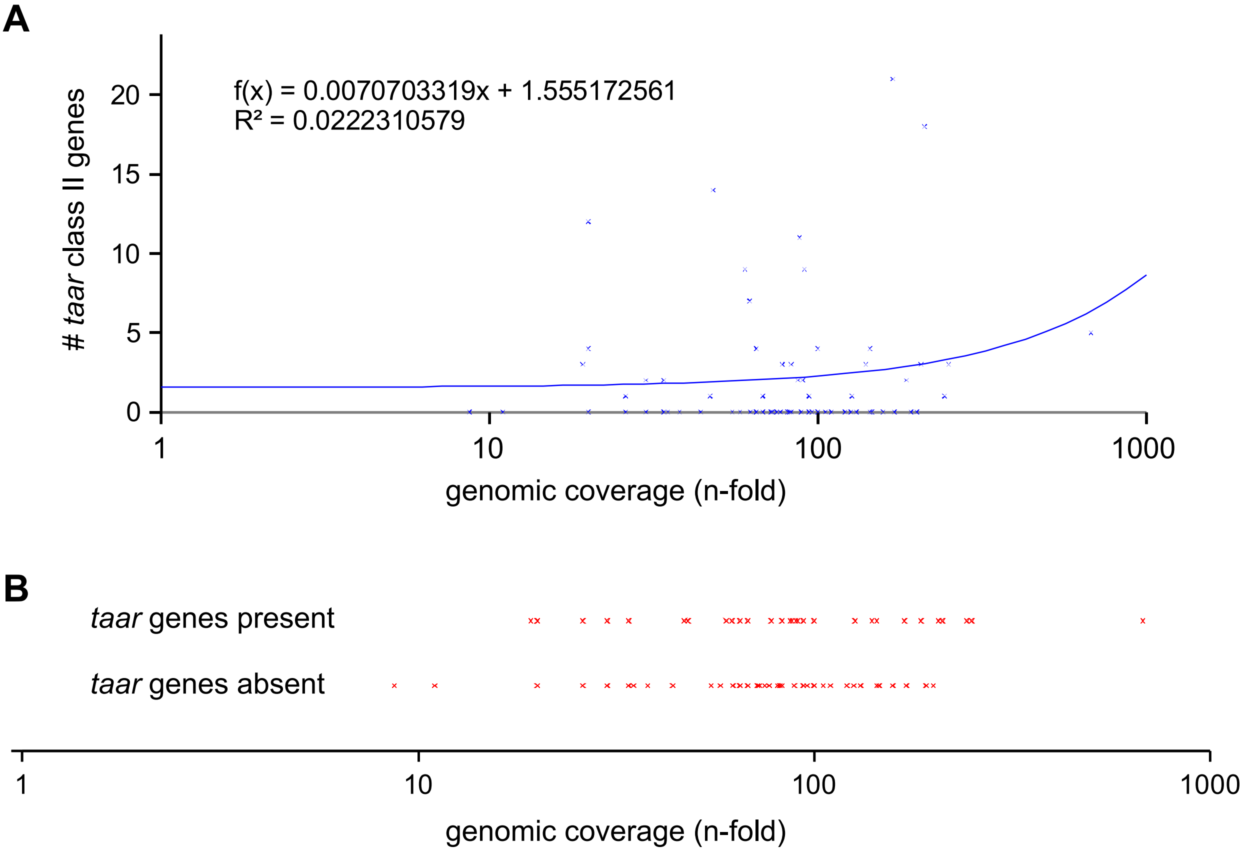

*SI Figure 2   No correlation between genomic coverage and detection of taar genes*

A) Number of *taar* genes is shown for 69 cartilaginous and bony fish species. Each blue cross represents one species. Linear regression and correlation coefficient R as indicated.

B) Presence respectively absence of *taar* genes is shown for 69 cartilaginous and bony fish species. Each red cross represents one species.

SUPPLEMENTARY INFORMATION
SI Table 1: Genomic location of all genes analysed

# Olfactory function in the trace amine-associated receptor family (TAARs) evolved twice independently

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# SUPPLEMENTARY INFORMATION

Table of Contents for SI Table 1: Genomic location of all genes analysed

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**SI table 1 consists of seven sheets:**

| | |
|---|---|
| Sheet 1 | Overview: Presence of *htr4, taar* and *tarl* genes in non-vertebrate deuterostomes<br>*htr4* genes in chordates and hemichordates |
| Sheet 2 | Overview: Number of *taar* and *tarl* genes in aquatic vertebrates |
| Sheet 3 | *tarl* genes of jawless vertebrates identified in this study |
| Sheet 4 | *tarl* genes of jawed vertebrates identified in this study |
| Sheet 5 | *taar* genes of jawed vertebrates identified in this study |
| Sheet 6 | Representative reference TAAR sequences |
| Sheet 7 | Aminergic receptors used as outgroup in phylogenetic analysis |

**Overview: Presence of *htr4*, *taar* and *tarl* genes in non-vertebrate deuterostomes (chordates, hemichordates and echinoderms)**

| Belongs to taxonomical group | Abbre-viation | Latin species name | Vernacular name | htr4 | taar | tarl |
|---|---|---|---|---|---|---|
| echinoderm | AcPl | *Acanthaster planci* | Crown-of-thorns starfish | - | - | - |
| cephalochordate | Alu | *Asymmetron lucayanum* | Sharptail lancelet | + | - | - |
| echinoderm | ApPa | *Apostichopus parvimensis* | Warty sea cucumber | - | - | - |
| echinoderm | ApJa | *Apostichopus japonicus* | Japanese spiky sea cucumber | - | - | - |
| cephalochordate | Bbe | *Branchiostoma belcheri* | Chinese amphioxus | + | - | - |
| cephalochordate | Bfl | *Branchiostoma floridae* | Florida lancelet | + | - | - |
| cephalochordate | Bla | *Branchiostoma lanceolatum* | European lancelet | + | - | - |
| urochordate | Cin | *Ciona intestinalis* | Vase tunicate | - | - | - |
| urochordate | Csa | *Ciona savignyi* | Pacific transparent seq squirt | - | - | - |
| echinoderm | EuTr | *Eucidaris tribuloides* | Slate pencil urchin | - | - | - |
| echinoderm | HePu | *Hemicentrotus pulcherrimus* | a sea urchin | - | - | - |
| echinoderm | LyVa | *Lytechinus variegatus* | Green sea urchin | - | - | - |
| echinoderm | OpFa | *Ophionereis fasciata* | Mottled brittle star | - | - | - |
| echinoderm | OpSp | *Ophiothrix spiculata* | Spiny brittle star | - | - | - |
| echinoderm | PaMi | *Patiria miniata* | Bat star | - | - | - |
| echinoderm | PaRe | *Patiriella regularis* | Common cushion star | - | - | - |
| hemichordate | PtFl | *Ptychodera flava* | Hawaiian acorn worm | + | - | - |
| hemichordate | SaKo | *Saccoglossus kowalevskii* | Acorn worm | + | - | - |
| echinoderm | StPu | *Strongylocentrotus purpuratus* | Purple sea urchin | - | - | - |

***htr4* genes in cephalochordates and hemichordates**

| | Abbre-viation | Latin species name | Vernacular name | Gene name | Accession | length (full, partial) | Pseudo-gene (Ψ) | # exons | Database incl. Version number | chr | contig | location in contig (bp) | Strand (+/-) | Comments |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Cephalochordates** | | | | | | | | | | | | | | |
| | Alu | *Asymmetron lucayanum* | Sharptail lancelet | *htr4* | - | partial | - | 3 | GCA_001663935.1 | - | LZCU01069842.1,<br>LZCU01138971.1 | 2645-4248, 3-464 | +, + | 2nd exon in two contigs, 35aa missing in between |
| | Bbe | *Branchiostoma belcheri* | Chinese amphioxus | *htr4* | GeneID:109485254 | full | - | 4 | GCF_001625305.1 | - | NW_017804398.1 | 521476-519001 | - | annotated as 5-hydroxytryptamine receptor 4-like |
| | Bfl | *Branchiostoma floridae* | Florida lancelet | *htr4* | GeneID:118414956 | full | - | 3 | GCF_000003815.2 | 4 | NC_049982.1 | 14530149-14532452 | + | annotated as 5-hydroxytryptamine receptor 4-like |
| | Bla | *Branchiostoma lanceolatum* | European lancelet | *htr4* | - | full | - | 3 | GCA_900088365.1 | - | FLLO01000036.1 | 925959-928070 | + | |
| **Hemichordates** | | | | | | | | | | | | | | |
| | PtFl | *Ptychodera flava* | Hawaiian acorn worm | *htr4* | - | full | - | 1 | GCA_001465055.1 | - | LD352455.1 | 57543-56371 | - | |
| | SaKo | *Saccoglossus kowalevskii* | Acorn worm | *htr4* | GeneID:100374682 | full | - | 1 | GCF_000003605.2 | - | NW_003129357.1 | 24544-25722 | + | annotated as 5-hydroxytryptamine receptor 4-like |

**Overview: Number of *taar* and *tarl* genes in aquatic vertebrates**

| | | | | Class II taar genes | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| Abbre-viation | Latin species name | Vernacular name | *tarl* | *taar12* | *taar13* | Other class II *taars* | genome | fold coverage | Database for species without *taar* and *tarl* genes |
| Aa | *Anguilla anguilla* | European eel | 1 | 7 | 5 | 0 | full | 20.0x | |
| Ac | *Amphilophus citrinellus* | Midas cichlid | 1 | 0 | 0 | 0 | full | 89.0x | |
| Af | *Anoplopoma fimbria* | Sablefish | 1 | 0 | 2 | 0 | full | 186.0x | |
| Aj | *Anguilla japonica* | Japanese eel | 2 | 9 | 9 | 0 | full | 211.0x | |
| Al | *Austrofundulus limnaeus* | Järvikilli | 1 | 0 | 0 | 0 | full | 94.0x | |
| Am | *Astyanax mexicanus* | Mexican cavefish | 1 | 3 | 1 | 0 | full | 65x | |
| Ar | *Anguilla rostrata* | American eel | 2 | 13 | 8 | 0 | full | 169x | |
| Bp | *Boleophthalmus pectinirostris* | Giant blue-spotted mudskipper | 1 | 0 | 0 | 0 | full | 144x | |
| Cc | *Cyprinus carpio* | Common carp | 2 | 15 | 5 | 0 | full | n/a | |
| Ch | *Clupea harengus* | Herring | 1 | 0 | 1 | 0 | full | 127x | |
| Cm | *Callorhinchus milii* | Elephant shark | 1 | 0 | 0 | 3 | full | 19.25x | |
| Cs | *Cynoglossus semilaevis* | Tongue sole | 1 | 0 | 0 | 0 | full | 117x/94x | |
| Cn | *Cyprinodon nevadensis* | Amargosa pupfish | 1 | 0 | 0 | 0 | full | 26.0x | |
| Cr | *Cottus rhenanus* | Rheingroppe | 1 | 0 | 0 | 0 | full | 11.0x | |
| Cv | *Cyprinodon variegatus* | Sheepshead pupfish | 1 | 0 | 0 | 0 | full | 81x | |
| Dr | *Danio rerio* | Zebrafish | 1 | 12 | 5 | 0 | full | n/a | |
| Dl | *Dicentrarchus labrax* | European seebass | 1 | 0 | 2 | 0 | full | 30x | |
| El | *Esox Lucius* | Northern pike | 2 | 0 | 1 | 0 | full | 243.0x | |
| Fh | *Fundulus heteroclitus* | Mummichog | 1 | 0 | 0 | 0 | full | 75x | |
| Gm | *Gadus morhua* | Atlantic cod | 2 | 0 | 3 | 0 | full | 83x | |
| Ga | *Gasterosteus aculeatus* | Three-spined stickleback | 1 | 0 | 1 | 0 | full | n/a | |
| Hb | *Haplochromis burtoni* | Burton's mouth-breeder | 1 | 0 | 0 | 0 | full | 131x | |
| Hc | *Hippocampus comes* | Tiger tail seahorse | 1 | 0 | 0 | 0 | full | 192x | |
| Ip | *Ictalurus punctatus* | Channel catfish | 1 | 2 | 8 | 0 | full | n/a | |
| Km | *Kryptolebias marmoratus* | Mangrove killifish | 1 | 0 | 0 | 0 | full | 72.75x | |
| Lb | *Labrus bergylta* | Ballan wrasse | 1 | 0 | 4 | 0 | full | 144x | |
| Lc | *Larimichthys crocea* | Yellow croaker | 1 | 0 | 3 | 0 | full | 140x | |
| Lac | *Lates calcarifer* | Asian sea bass | 2 | 0 | 2 | 0 | full | 90.0x | |
| Lo | *Lepisosteus oculatus* | Spotted gar | 1 | 3 | 1 | 1 *taar5*-like | full | 677.5x | |
| Lec | *Lethenteron camtschaticum* | Arctic lamprey | 51 | 0 | 0 | 0 | full | 20.0x | |
| Lw | *Leuciscus waleckii* | Amur ide | 1 | 1 | 2 | 0 | full | 250x | |
| Le | *Leucoraja erinacea* | Little skate | 1 | 0 | 0 | 1 | full | 26.x | |
| Mz | *Maylandia zebra* | Zebra mbuna | 1 | 0 | 0 | 0 | full | 65x | |
| Mc | *Mchenga conophoros* | Happy | 1 | 0 | 0 | 0 | full | n/a | |
| Mim | *Miichthys miiuy* | Mi-iuy croaker | 1 | 0 | 0 | 0 | full | 158x | |
| Mom | *Mola mola* | Ocean sunfish | 1 | 0 | 0 | 0 | full | 96x | |
| Moa | *Monopterus albus* | Asian swamp eel | 1 | 0 | 0 | 0 | full | 146x | |
| Ms | *Morone saxatilis* | Striped bass | 1 | 0 | 1 | 0 | full | 68.0x | |
| Nb | *Neolamprologus brichardi* | Lyretail cichlid | 1 | 0 | 0 | 0 | full | 171x | |
| Nf | *Nothobranchius furzeri* | Turquoise killifish | 1 | 0 | 0 | 0 | full | 100x | |
| Nc | *Notothenia coriiceps* | Black rockcod | 0 | 0 | 0 | 0 | full | 38x | GCF_000735185.1 |
| On | *Oreochromis niloticus* | Nile tilapia | 1 | 0 | 0 | 0 | full | 44.0x | |
| Ol | *Oryzias latipes* | Medaka | 1 | 0 | 0 | 0 | full | 99% | |
| Po | *Paralichthys olivaceus* | Bastard halibut, japanese flounder | 1 | 0 | 0 | 0 | full | 100.0x | |
| Pa | *Pampus argenteus* | Silver pomfret | 1 | 0 | 0 | 0 | full | 58.0x | |
| Ps | *Periophthalmodon schlosseri* | Giant mudskipper | 1 | 0 | 0 | 0 | full | 65x | |
| Pem | *Periophthalmus magnuspinnatus* | Giant-fin mudskipper | 1 | 0 | 0 | 0 | full | 77x | |
| Pm | *Petromyzon marinus* | Marine lamprey | 32 | 0 | 0 | 0 | full | 62.36x | |
| Pp | *Pimephales promelas* | Fathead minnow | 1 | 5 | 2 | 0 | full | 62.0x | |
| Pf | *Poecilia Formosa* | Amazon molly | 1 | 0 | 0 | 0 | full | 82x | |
| Pl | *Poecilia latipinna* | Sailfin molly | 1 | 0 | 0 | 0 | full | 34x | |
| Pom | *Poecilia Mexicana* | Shortfin molly | 1 | 0 | 0 | 0 | full | 30x | |
| Pr | *Poecilia reticulata* | Guppy | 1 | 0 | 0 | 0 | full | 110.0x | |
| Py | *Pseudopleuronectes yokohamae* | Marbled flounder | 1 | 0 | 0 | 0 | full | 35x | |
| Pun | *Pundamilia nyererei* | Nyereres Viktoriabuntbarsch | 1 | 0 | 0 | 0 | full | 126x | |
| Pyn | *Pygocentrus nattereri* | Red-bellied piranha | 1 | 5 | 4 | 0 | full | 91x | |
| Rt | *Rhincodon typus* | Whale shark | 2 | 0 | 0 | 4 | full | 20.0x | |
| Ss | *Salmo salar* | Atlantic salmon | 3 | 0 | 3 | 0 | full | 206.0x | |
| Sh | *Scartelaos histophorus* | Blue mudskipper, walking goby | 1 | 0 | 0 | 0 | full | 72x | |
| Sf | *Scleropages formosus* | Dragonfish, Asian bonytongue | 2 | 0 | 4 | 0 | full | 100x | |
| Sea | *Sebastes aleutianus* | Rougheye rockfish | 1 | 0 | 3 | 0 | full | 78.0x | |
| Sem | *Sebastes minor* | Akagaya | 1 | 0 | 2 | 0 | full | 34.0x | |
| Ses | *Sebastes steindachneri* | Yanaginomai | 1 | 0 | 1 | 0 | full | 47.0x | |
| Sn | *Sebastes nigrocinctus* | Tiger rockfish | 1 | 0 | 1 | 0 | full | 94.0x | |
| Ser | *Sebastes rubrivinctus* | Flag rockfish | 1 | 0 | 2 | 0 | full | 87.0x | |
| Sa | *Sinocyclocheilus anshuiensis* | Anshui sõõrhuul | 2 | 4 | 5 | 0 | full | 60x | |
| Sg | *Sinocyclocheilus grahami* | Golden-line barbel | 1 | 6 | 5 | 0 | full | 88x | |
| Sr | *Sinocyclocheilus rhinocerous* | Ninasarv-sõõrhuul | 2 | 7 | 7 | 0 | full | 48x | |
| Stp | *Stegastes partitus* | Bicolor damselfish | 1 | 0 | 0 | 0 | full | 121x | |
| Tf | *Takifugu flavidus* | Yellowbelly pufferfish | 0 | 0 | 0 | 0 | full | 200x | GCA_003711565.2 |
| Tr | *Takifugu rubripes* | Japanese pufferfish, torafugu | 1 | 0 | 0 | 0 | full | 8.7x | |
| Tn | *Tetraodon nigroviridis* | Spotted green pufferfish | 1 | 0 | 0 | 0 | full | n/a | |
| To | *Thunnus orientalis* | Pacific bluefin tuna | 2 | 0 | 0 | 0 | full | 54.9x | |
| Xl | *Xenopus laevis* | African clawed frog | 1 | n.d. | n.d. | n.d. | full | 30x | |
| Xt | *Xenopus tropicalis* | Western clawed frog | 1 | 4* | 0 | 0 | full | 7.6x | * Syed et al., 2015 – DOI 10.1038/srep13935 |
| Xc | *Xiphophorus couchianus* | Monterrey platyfish | 1 | 0 | 0 | 0 | full | 77x | |
| Xh | *Xiphophorus hellerii* | Green swordtail | 0 | 0 | 0 | 0 | full | 68x | GCA_003331165.2 |
| Xm | *Xiphophorus maculatus* | Southern platyfish | 1 | 0 | 0 | 0 | full | 83x | |

***tarl* genes of jawless vertebrates identified in this study**

| Species (Latin name and abbreviation) | Gene name | synonyms | Accession | length (full, partial) | Pseudo-gene (Ψ) | *, stop; !, frameshift | # exons | Database incl. Version number | chr | contig | location in contig (bp) | Strand (+/-) | Comments |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Jawless vertebrates** | | | | | | | | | | | | | |
| *Lethenteron camtschaticum (Lec)* | *tarl1a* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE994369.1 | 40635-41954 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl1b* | - | - | full | Ψ | 1! | 1 | GCA_000466285.1 | - | APJL01100547.1 | 1474-2801 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl1c* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE994369.1 | 23941-25266 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl2a* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE994369.1 | 162-1100 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl2b* | - | - | partial | - | - | 1 | GCA_000466285.1 | - | KE994480.1 | 13204-13944 | - | |
| *Lethenteron camtschaticum (Lec)* | *tarl3a* | - | - | full | - | - | 2 | GCA_000466285.1 | - | KE994369.1 | 8911-10535 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl3b* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE994369.1 | 49915-50784 | - | |
| *Lethenteron camtschaticum (Lec)* | *tarl3c* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE994369.1 | 66652-67515 | - | |
| *Lethenteron camtschaticum (Lec)* | *tarl4a* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 1364576-1365646 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl4b* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 1544889-1545953 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl4c* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 1436910-1437974 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl4d* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 1393333-1394397 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl4e* | - | - | partial | - | - | 1 | GCA_000466285.1 | - | KE993829.1 | 1308332-1308916 | - | |
| *Lethenteron camtschaticum (Lec)* | *tarl5a* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993679.1 | 5764171-5765184 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl5b* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993688.1 | 1032661-1033701 | - | |
| *Lethenteron camtschaticum (Lec)* | *tarl5c* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993688.1 | 1019923-1020969 | - | |
| *Lethenteron camtschaticum (Lec)* | *tarl5d* | - | - | partial | Ψ | 1* | 2 | GCA_000466285.1 | - | KE997555.1 | 6843-5134 | - | |
| *Lethenteron camtschaticum (Lec)* | *tarl6a* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 473955-475010 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl6b* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 486091-487152 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl6c* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE994203.1 | 259736-260932 | - | |
| *Lethenteron camtschaticum (Lec)* | *tarl6d* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE994203.1 | 296524-297528 | - | |
| *Lethenteron camtschaticum (Lec)* | *tarl6e* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE994203.1 | 278253-279257 | - | |
| *Lethenteron camtschaticum (Lec)* | *tarl6f* | - | - | partial | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 14829-15527 | - | |
| *Lethenteron camtschaticum (Lec)* | *tarl6g* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 14829-15833 | - | |
| *Lethenteron camtschaticum (Lec)* | *tarl6h* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 344070-345134 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl6i* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 357384-358448 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl6j* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 327596-328657 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl6k* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE994615.1 | 4070-5116 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl6l* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE994615.1 | 62137-63192 | - | |
| *Lethenteron camtschaticum (Lec)* | *tarl6m* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE994615.1 | 51233-52267 | - | |
| *Lethenteron camtschaticum (Lec)* | *tarl6n* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 440758-441810 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl6o* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 406856-407875 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl6p* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 419329-420384 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl6q* | - | - | full | - | - | 1 | GCA_000466285.1 | - | APJL01103800.1 | 1115-45 | - | |
| *Lethenteron camtschaticum (Lec)* | *tarl6r* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 380880-381923 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl6s* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 218537-219592 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl6t* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 204658-205671 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl6u* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 279150-280196 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl6v* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 303451-304497 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl6w* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 452976-454028 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl6x* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 465265-466299 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl7a* | - | - | full | - | - | 2 | GCA_000466285.1 | - | KE993775.1 | 570318-572603 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl7b* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE994615.1 | 10587-11681 | - | |
| *Lethenteron camtschaticum (Lec)* | *tarl7c* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993904.1 | 434011-435126 | - | |
| *Lethenteron camtschaticum (Lec)* | *tarl7d* | - | - | partial | - | - | 1 | GCA_000466285.1 | - | APJL01179032.1 | 171-950 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl7e* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 520997-522049 | - | |
| *Lethenteron camtschaticum (Lec)* | *tarl7f* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 494975-496018 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl7g* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 504937-506031 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl7h* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 552562-553617 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl7i* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 559513-560583 | + | |
| *Lethenteron camtschaticum (Lec)* | *tarl7j* | - | - | full | - | - | 1 | GCA_000466285.1 | - | KE993775.1 | 537538-538587 | + | |
| *Lampetra fluviatilis (Laf)* | *tarl4a* | LOR12 | AAC82384.1 | partial | - | - | 1 | n.a. | - | AF069549.1 | 1-774 | n.a. | |
| *Lampetra fluviatilis (Laf)* | *tarl6a* | LOR4 | AAC82382.1 | partial | - | - | 1 | n.a. | - | AF069547.1 | 1-1059 | n.a. | |
| *Lampetra fluviatilis (Laf)* | *tarl6b* | LOR22 | AAC82385.1 | partial | - | - | 1 | n.a. | - | AF069550.1 | 1-768 | n.a. | |
| *Lampetra fluviatilis (Laf)* | *tarl6c* | LOR6 | AAC82388.1 | partial | - | - | 1 | n.a. | - | AF069553.1 | 1-510 | n.a. | |
| *Lampetra fluviatilis (Laf)* | *tarl6d* | LOR20 | AAC82387.1 | partial | - | - | 1 | n.a. | - | AF069552.1 | 1-543 | n.a. | |
| *Lampetra fluviatilis (Laf)* | *tarl6e* | LOR14 | AAC82383.1 | partial | - | - | 1 | n.a. | - | AF069548.1 | 1-1020 | n.a. | |
| *Lampetra fluviatilis (Laf)* | *tarl6f* | LOR25 | AAC82386.1 | partial | - | - | 1 | n.a. | - | AF069551.1 | 1-519 | n.a. | |
| *Lampetra fluviatilis (Laf)* | *tarl6g* | LOR16 | AAC82389.1 | partial | - | - | 1 | n.a. | - | AF069554.1 | 1-522 | n.a. | |
| *Lampetra fluviatilis (Laf)* | *tarl7a* | LOR3 | AAC82381.1 | partial | - | - | 1 | n.a. | - | AF069546.1 | 1-1056 | n.a. | |
| *Petromyzon marinus (Pm)* | *tarl1a* | - | - | full | - | - | 1 | GCA_002833325.1 | - | PIZI01000032.1 | 6275329-6276639 | + | |
| *Petromyzon marinus (Pm)* | *tarl2a* | - | - | partial | - | - | 1 | GCA_002833325.1 | - | PIZI01000032.1 | 6253583-6254518 | + | |
| *Petromyzon marinus (Pm)* | *tarl2b* | - | - | partial | Ψ | 1* 1! | 1 | GCA_002833325.1 | - | PIZI01000103.1 | 284940-285702 | + | |
| *Petromyzon marinus (Pm)* | *tarl2c* | - | - | full | Ψ | 4! | 2 | GCA_002833325.1 | - | PIZI01000103.1 | 284148-285702 | + | |
| *Petromyzon marinus (Pm)* | *tarl3a* | - | - | partial | - | - | 1 | GCA_002833325.1 | - | PIZI01000032.1 | 6299113-6300003 | - | |
| *Petromyzon marinus (Pm)* | *tarl4a* | - | - | full | Ψ | 1* | 1 | WGS_VDB://AEFG01 | - | AEFG01051656.1 | 3845-2811 | - | WGS, not found in genome assembly |
| *Petromyzon marinus (Pm)* | *tarl4b* | - | - | full | - | - | 1 | WGS_VDB://AEFG01 | - | AEFG01045923.1 | 3064-4137 | + | WGS, not found in genome assembly |
| *Petromyzon marinus (Pm)* | *tarl5a* | # | | full | - | - | 1 | GCA_002833325.1 | - | PIZI01001092.1 | 11747-12763 | + | |
| *Petromyzon marinus (Pm)* | *tarl5b* | # | | full | - | - | 1 | WGS_VDB://AEFG01 | - | AEFG01032376.1 | 5123-6163 | + | WGS, in genome assembly incomplete |
| *Petromyzon marinus (Pm)* | *tarl5c* | # | | full | - | - | 1 | WGS_VDB://AEFG01 | - | AEFG01032376.1 | 2293-3333 | + | WGS, frame shift in genome assembly |
| *Petromyzon marinus (Pm)* | *tarl5d* | - | - | partial | - | - | 1 | WGS_VDB://AEFG01 | - | PIZI01000009.1 | 10839713-10840192 | - | |
| *Petromyzon marinus (Pm)* | *tarl6a* | #, TAAR353* | | full | - | - | 1 | WGS_VDB://AEFG01 | - | AEFG01071253.1 | 6274-7332 | - | WGS, not found in genome assembly |
| *Petromyzon marinus (Pm)* | *tarl6b* | TAAR335* | | full | - | - | 1 | GCA_002833325.1 | - | PIZI01005860.1 | 3568-4575 | - | |
| *Petromyzon marinus (Pm)* | *tarl6c* | #, TAAR355b* | | full | - | - | 1 | WGS_VDB://AEFG01 | - | AEFG01071256.1 | 5671-6783 | - | WGS, 2 frame shifts in genome assembly |
| *Petromyzon marinus (Pm)* | *tarl6d* | #, TAAR355a* | | full | - | - | 1 | WGS_VDB://AEFG01 | - | AEFG01071255.1 | 1898-2965 | - | WGS, not found in genome assembly |
| *Petromyzon marinus (Pm)* | *tarl6e* | #, TAAR354* | | full | - | - | 1 | WGS_VDB://AEFG01 | - | AEFG01071258.1 | 13628-14692 | - | WGS, frame shift in genome assembly |
| *Petromyzon marinus (Pm)* | *tarl6f* | TAAR353* | | full | - | - | 1 | WGS_VDB://AEFG01 | | AEFG01041529.1 | 3108-4169 | - | WGS, not found in genome assembly |
| *Petromyzon marinus (Pm)* | *tarl6g* | TAAR360* | | full | - | - | 1 | WGS_VDB://AEFG01 | - | AEFG01028932.1 | 1473-2552 | - | WGS, frame shift in genome assembly |
| *Petromyzon marinus (Pm)* | *tarl6h* | #, TAAR345* | | full | - | - | 1 | GCA_002833325.1 | - | PIZI01000032.1 | 322327-323364 | - | |
| *Petromyzon marinus (Pm)* | *tarl6i* | TAAR351* | | full | - | - | 1 | GCA_002833325.1 | - | PIZI01000032.1 | 4902127-4903182 | + | |
| *Petromyzon marinus (Pm)* | *tarl6j* | #, TAAR340* | | full | - | - | 1 | WGS_VDB://AEFG01 | - | AEFG01025162.1 | 5312-6334 | - | WGS, frame shift in genome assembly |
| *Petromyzon marinus (Pm)* | *tarl6k* | #, TAAR358* | | full | - | - | 1 | GCA_002833325.1 | - | AEFG01025161.1 | 2059-3069 | - | WGS, 2 frame shifts in genome assembly |
| *Petromyzon marinus (Pm)* | *tarl6l* | TAAR349a* | | full | - | - | 1 | GCA_002833325.1 | - | PIZI01000032.1 | 4747149-4748162 | + | |
| *Petromyzon marinus (Pm)* | *tarl6m* | TAAR349b* | | partial | - | - | 1 | WGS_VDB://AEFG01 | - | AEFG01019733.1 | 1 – 663 | - | WGS, frame shift in genome assembly |
| *Petromyzon marinus (Pm)* | *tarl6n* | #, TAAR351* | | full | - | - | 1 | WGS_VDB://AEFG01 | - | AEFG01033136.1 | 2692-3747 | - | WGS, 2 frame shifts in genome assembly |
| *Petromyzon marinus (Pm)* | *tarl6o* | #, TAAR345* | | full | - | - | 1 | WGS_VDB://AEFG01 | - | AEFG01033134.1 | 1788-2825 | - | WGS, frame shift in genome assembly |
| *Petromyzon marinus (Pm)* | *tarl7a* | - | - | full | - | - | 2 | GCA_002833325.1 | - | PIZI01000586.1 | 41436-43748 | - | |
| *Petromyzon marinus (Pm)* | *tarl7b* | # | | partial | - | - | 1 | WGS_VDB://AEFG01 | | AEFG01041527.1 | 651-1601 | + | WGS, not found in genome assembly |
| *Petromyzon marinus (Pm)* | *tarl7c* | - | - | partial | - | - | 1 | WGS_VDB://AEFG01 | - | AEFG01042991.1 | 2131-3012 | + | WGS, 2 frame shifts in genome assembly |
| *Petromyzon marinus (Pm)* | *tarl7d* | #, TAAR351* | | full | - | - | 1 | GCA_002833325.1 | - | PIZI01000032.1 | 5000570-5001625 | + | |
| *Petromyzon marinus (Pm)* | *tarl7e* | #, TAAR365* | | full | - | - | 1 | GCA_002833325.1 | - | PIZI01000032.1 | 4990958-4992055 | + | |
| *Petromyzon marinus (Pm)* | *tarl7f* | # | | full | - | - | 1 | GCA_002833325.1 | - | PIZI01000032.1 | 5008987-5010039 | + | |

#, described, but not named in Hashiguchi and Nishida, 2007

*, described in Libants et al., 2009

**_tarl_ genes of jawed vertebrates identified in this study**

| Species (Latin name and abbreviation) | Gene name | automatted annotation | Accession | length (full, partial) | Pseudo-gene (Ψ) | *, stop; !, frameshift | # exons | Database incl. Version number | chr | contig | location in contig (bp) | Strand (+/-) | Comments |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***Cartilaginous fish*** | | | | | | | | | | | | | |
| *Callorhinchus milii (Cm)* | *tarl2* | 5-HTR4-like | LOC103186492 | full | - | - | 1 | GCF_000165045.1 | - | NW_006890197.1 | 1614139-1615236 | + | |
| *Leucoraja erinacea (Le)* | *tarl2* | - | - | full | Ψ | 1* 3! | 1 | WGS_VDB://AESE01 | - | AESE010035790.1;<br>AESE010257460.1 | 124-760;4-312 | +, - | |
| *Rhincodon typus (Rt)* | *tarl1* | - | LOC109911122 | full | - | - | 1 | GCF_001642345.1 | - | NW_018030254.1 | 4655-5698 | + | |
| *Rhincodon typus (Rt)* | *tarl2* | 5-HTR4-like | LOC109915544 | full | - | - | 1 | GCF_001642345.1 | - | NW_018027816.1 | 181321-182421 | - | |
| ***Amphibians*** | | | | | | | | | | | | | |
| *Xenopus laevis (Xl)* | *tarl1* | TAAR1-like | LOC108719346 | full | - | - | 1 | GCF_001663975.1 | 1L | NC_030724.1 | 2828991-2830067 | - | |
| *Xenopus tropicalis (Xt)* | *tarl1* | TAAR1 | LOC100496115 | full | - | - | 1 | GCF_000004195.3 | 1 | NC_030677.1 | 5537899-5538957 | + | all five *taar* genes on chromosome 5, *htr4* on chromosome 3 |
| **Bony fish** | | | | | | | | | | | | | |
| *Anguilla anguilla (Aa)* | *tarl1* | - | - | full | - | - | 1 | GCA_000695075.1 | - | AZBK01800005.1 | 9-1076 | + | |
| *Anguilla japonica (Aj)* | *tarl1a* | - | - | full | - | - | 1 | GCA_003597225.1 | - | BEWY01000002.1 | 9612299-9613369 | - | |
| *Anguilla japonica (Aj)* | *tarl1b* | - | - | full | - | - | 1 | GCA_003597225.1 | - | BEWY01000015.1 | 12067318-12068430 | + | |
| *Anguilla rostrata (Ar)* | *tarl1* | - | - | full | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01002349.1 | 67811-68917 | + | GCA_001606085.1 |
| *Anguilla rostrata (Ar)* | *tarl2* | - | - | full | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01004196.1 | 172162-173274 | - | GCA_001606085.1 |
| *Anoplopoma fimbria (Af)* | *tarl1* | - | - | full | - | - | 1 | GCA_000499045.1 | - | AWGY01160213.1 | 10245-11303 | - | |
| *Amphilophus citrinellus (Ac)* | *tarl1* | - | - | full | - | - | 2 | GCA_013435755.1 | | CM024197.1 | 22725795-22724719 | - | |
| *Astyanax mexicanus (Am)* | *tarl1* | - | LOC103027537 | full | - | - | 1 | GCF_000372685.2 | - | NW_019172941.1 | 420606-421679 | - | |
| *Austrofundulus limnaeus (Al)* | *tarl1* | 5-HTR4-like | XP_013863315.1 | full | - | - | 1 | GCF_001266775.1 | - | XM_014007861.1 | 225-1280 | + | |
| *Boleophthalmus pectinirostris (Bp)* | *tarl1* | 5-HTR4-like | XP_020786106.1 | full | - | - | 1 | GCF_000788275.1 | - | NW_018356255.1 | 3197207-3198265 | + | |
| *Clupea harengus (Ch)* | *tarl1* | - | LOC105903878 | full | - | - | 1 | GCF_000966335.1 | - | NW_012221853.1 | 1367956-1369011 | - | |
| *Cottus rhenanus (Cr)* | *tarl1* | - | - | full | - | - | 1 | GCA_001455555.1 | - | LKTN01076329.1 | 4308-5405 | + | |
| *Cynoglossus semilaevis (Cs)* | *tarl1* | 5-HTR4-like | XP_008315345.1 | full | - | - | 1 | GCF_000523025.1 | 9 | NC_024315.1 | 9847779-9848852 | + | |
| *Cyprinodon nevadensis pectoralis (Cn)* | *tarl1* | - | - | full | - | - | 1 | GCA_000776015.1 | - | JSUU01003036.1 | 31440-32498 | - | |
| *Cyprinodon variegatus (Cv)* | *tarl1* | 5-HTR4-like | XP_015228425.1 | full | - | - | 1 | GCF_000732505.1 | - | NW_015150531.1 | 763289-764344 | - | |
| *Cyprinus carpio (Cc)* | *tarl1a* | - | LOC109066000;<br>LOC109065999 | full | Ψ | 1! | 1 | GCF_000951615.1 | - | NW_017538292.1 | 209579-210642 | - | |
| *Cyprinus carpio (Cc)* | *tarl1b* | - | LOC109061621 | full | Ψ | 1* | 1 | GCF_000951615.1 | - | NW_017538179.2 | 182099-183163 | - | |
| *Danio rerio (Dr)* | *tarl1* | 5-HTR4-like | XP_001337671.1 | full | - | - | 1 | GCF_000002035.6 | 1 | NC_007112.7 | 41949321-41950379 | + | |
| *Dicentrarchus labrax (Dl)* | *tarl1* | - | - | full | - | - | 1 | GCA_000689215.1 | - | HG916847.1 | 18587864-18588940 | + | |
| *Esox lucius (El)* | *tarl1* | - | LOC105021074 | full | - | - | 1 | GCF_000721915.3 | - | NC_025992.3 | 3614001-3615086 | - | |
| *Esox lucius (El)* | *tarl2* | 5-HTR4-like | XP_010900554.1 | full | - | - | 1 | GCF_000721915.3 | - | NC_025971.3 | 13319582-13320742 | + | |
| *Fundulus heteroclitus (Fh)* | *tarl1* | TAAR3-like | XP_012733128.2 | full | - | - | 1 | GCF_000826765.1 | - | NW_012234461.1 | 109571-110629 | - | |
| *Gadus morhua (Gm)* | *tarl1a* | - | - | full | - | - | 1 | GCF_902167405.1 | 3 | NC_044050.1 | 10445555-10444476 | - | |
| *Gadus morhua (Gm)* | *tarl1b* | - | - | full | - | - | 1 | WGS_VDB://CAEA02 | - | CAEA020003354.1 | 429215-428181 | - | not in GCF_902167405.1 |
| *Gasterosteus aculeatus (Ga)* | *tarl1* | - | - | full | - | - | 1 | GCA_000180675.1 | - | AANH01003210.1 | 55276-56352 | + | |
| *Haplochromis burtoni (Hb)* | *tarl1* | 5-HTR4-like | XP_005928396.2 | full | - | - | 1 | GCF_000239415.1 | - | NW_005179495.1 | 110901-111977 | - | |
| *Hippocampus comes (Hc)* | *tarl1* | 5-HTR4-like | XP_019732039.1 | full | - | - | 1 | GCF_001891065.1 | - | NW_017805497.1 | 3571388-3572455 | - | |
| *Ictalurus punctatus (Ip)* | *tarl1* | - | LOC108260501 | full | - | - | 1 | GCF_001660625.1 | 29 | NC_030444.1 | 13728150-13729223 | + | |
| *Kryptolebias marmoratus (Km)* | *tarl1* | - | - | full | - | - | 1 | ASM164957v1 | - | NW_016094240.1 | 1908256-1909314 | + | |
| *Labrus bergylta (Lb)* | *tarl1* | - | LOC109994121 | full | - | - | 1 | GCF_900080235.1 | - | NW_018114694.1 | 280280-281356 | + | |
| *Larimichthys crocea (Lc)* | *tarl1* | 5-HTR4 | XP_027138281.1 | full | - | - | 1 | GCF_000972845.2 | X | NC_040020.1 | 2591785-2592858 | - | |
| *Lates calcarifer (Lac)* | *tarl1* | 5-HTR4-like | XP_018551385.1 | full | - | - | 1 | GCF_001640805.1 | - | NW_017365769.1 | 1510510-1511586 | + | |
| *Lates calcarifer (Lac)* | *tarl2* | - | - | full | Ψ | 1 * | 1 | GCF_001640805.1 | - | NW_017363881.1 | 4502697-4503698 | - | |
| *Lepisosteus oculatus (Lo)* | *tarl1* | - | - | full | - | - | 1 | GCF_000242695.1 | LG4 | NC_023182.1 | 5406278-5407351 | + | |
| *Leuciscus waleckii (Lw)* | *tarl1* | - | - | full | Ψ | 1! | 1 | GCA_900092035.1 | - | FLSR01004869.1 | 10142941-10144067 | - | |
| *Maylandia zebra (Mz)* | *tarl1* | - | - | full | - | - | 1 | GCF_000238955.4 | | NC_036785 | 19082571-19083644 | - | |
| *Mchenga conophoros (Mc)* | *tarl1* | - | - | partial | Ψ | - | n.d. | GCA_000150855.1 | - | ABPJ01069830.1,<br>ABPJ01067448.1 | 456-773, 726-604 | +,- | |
| *Miichthys miiuy (Mim)* | *tarl1* | - | - | full | - | - | 1 | GCA_001593715.1 | - | JXSJ01001024.1 | 6749-7822 | + | |
| *Mola mola (Mom)* | *tarl1* | - | - | full | - | - | 1 | GCA_001698575.1 | - | KV751317.1 | 19347442-19348629 | - | |
| *Monopterus albus (Moa)* | *tarl1* | 5-HTR4-like | XP_020457684.1 | full | - | - | 1 | GCF_001952655.1 | - | NW_018127934.1 | 1776181-1777257 | - | |
| *Morone saxatilis (Ms)* | *tarl1* | - | - | full | - | - | 1 | GCA_001663605.1 | - | JTCL01023305.1 | 2572-3654 | + | |
| *Neolamprologus brichardi (Nb)* | *tarl1* | 5-HTR4-like | XP_006787601.1 | full | - | - | 1 | GCF_000239395.1 | - | NW_006272012.1 | 3793196-3794272 | - | |
| *Nothobranchius furzeri (Nf)* | *tarl1* | - | - | full | - | - | 1 | GCF_001465895.1 | sgr02 | NC_029650.1 | 83794088-83795149 | + | |
| *Oreochromis niloticus (On)* | *tarl1* | 5-HTR4-like | XP_025764064.1 | full | - | - | 1 | GCF_001858045.2 | - | NC_031971.2 | 20801250-20802326 | - | |
| *Oryzias latipes (Ol)* | *tarl1* | TAAR1-like | XP_004085557.3 | full | - | - | 1 | GCF_002234675.1 | 1 | NC_019859.2 | 14263830-14264918 | + | |
| *Pampus argenteus (Pa)* | *tarl1* | - | - | full | - | - | 1 | GCA_000697985.1 | - | JHEK01029396.1 | 391-1470 | - | |
| *Paralichtys olivaceus (Po)* | *tarl1* | - | - | full | - | - | 1 | GCF_001970005.1 | - | NW_017859678.1 | 2600450-2601526 | + | |
| *Periophthalmodon schlosseri (Ps)* | *tarl1* | - | - | full | - | - | 1 | GCA_000787095.1 | - | JACM01022706.1 | 42492-41431 | - | |
| *Periophthalmus magnuspinnatus (Pem)* | *tarl1* | - | - | full | - | - | 1 | GCA_000787105.1 | - | KN462927.1 | 37253-38383 | + | |
| *Pimephales promelas (Pp)* | *tarl1* | - | - | full | - | - | 1 | GCA_000700825.1 | - | JNCD01012483.1 | 34693-35757 | - | |
| *Poecilia formosa (Pf)* | *tarl1* | 5-HTR4-like | XP_016526920.1 | full | - | - | 1 | GCF_000485575.1 | - | NW_006799983.1 | 1413491-1414549 | - | |
| *Poecilia latipinna (Pl)* | *tarl1* | 5-HTR4-like | XP_014889534.1 | full | - | - | 1 | GCF_001443285.1 | - | NW_015112902.1 | 147239-148297 | - | |
| *Poecilia mexicana (Pom)* | *tarl1* | 5-HTR4-like | XM_015004974.1 | full | - | - | 1 | GCF_001443325.1 | - | NW_015095551.1 | 360810-361865 | - | |
| *Poecilia reticulata (Pr)* | *tarl1* | - | GeneID:103467537 | full | - | - | 1 | GCF_000633615.1 | - | NC_024331.1 | 20413752-20414810 | + | |
| *Pseudopleuronectes yokohamae (Py)* | *tarl1* | - | - | full | - | - | 1 | GCA_000787555.1 | - | BBOV01036133.1 | 602-1678 | - | |
| *Pundamilia nyererei (Pun)* | *tarl1* | 5-HTR4-like | XP_005741265.2 | full | - | - | 1 | GCF_000239375.1 | - | NW_005187508.1 | 23053-24129 | - | |
| *Pygocentrus nattereri (Pyn)* | *tarl1* | - | LOC108434381 | full | - | - | 1 | GCF_001682695.1 | - | NW_016243911.1 | 1365121-1366194 | - | |
| *Salmo salar (Ss)* | *tarl1a* | - | - | full | - | - | 1 | GCF_000233375.1 | ssa04 | NC_027303.1 | 20922696-20923904 | + | |
| *Salmo salar (Ss)* | *tarl1b* | - | - | full | Ψ | 1* | 1 | GCF_000233375.1 | ssa08 | NC_027307.1 | 4286494-4287624 | + | |
| *Salmo salar (Ss)* | *tarl2* | - | - | full | - | - | 1 | GCF_000233375.1 | ssa09 | NC_027308.1 | 70306722-70307939 | + | |
| *Scartelaos histophorus (Sh)* | *tarl1* | - | - | full | - | - | 1 | GCA_000787155.1 | - | KN487589.1 | 9394 -10455 | + | |
| *Scleropages formosus (Sf)* | *tarl1* | - | LOC108924382 | full | - | - | 1 | GCF_001624265.1 | - | NW_017371553.1 | 5548625-5549701 | + | |
| *Scleropages formosus (Sf)* | *tarl2* | TAAR9-like | XP_018607201.1 | partial | - | - | 1 | GCF_001624265.1 | - | NW_017371831.1 | 4523316-4524268 | - | |
| *Sebastes aleutianus (Sea)* | *tarl1* | - | - | full | - | - | 1 | GCA_001910805.2 | - | LHVS01034712.1 | 8104-9174 | + | |
| *Sebastes minor(Sem)* | *tarl1* | - | - | full | - | - | 1 | GCA_001910765.2 | - | LHCJ01538447.1 | 456-1526 | - | |
| *Sebastes nigrocinctus (Sn)* | *tarl1* | - | - | full | - | - | 1 | GCA_000475235.3 | - | AUPR02010153.1 | 9020-10090 | - | |
| *Sebastes rubrivinctus (Ser)* | *tarl1* | - | - | full | - | - | 1 | GCA_000475215.1 | - | KI455860.1 | 2786-3856 | + | |
| *Sebastes steindachneri (Ses)* | *tarl1* | - | - | full | - | - | 1 | GCA_001910785.2 | - | LCWK010689365.1 | 647-1717 | + | |
| *Sinocyclocheilus anshuiensis (Sa)* | *tarl1a* | 5-HTR4-like | XP_016342958.1 | full | - | - | 1 | GCF_001515605.1 | - | NW_015540933.1 | 270706-271770 | + | |
| *Sinocyclocheilus anshuiensis (Sa)* | *tarl1b* | 5-HTR4-like | XP_016334547.1 | full | - | - | 1 | GCF_001515605.1 | - | NW_015619744.1 | 1-879 | - | |
| *Sinocyclocheilus rhinocerous (Sr)* | *tarl1a* | - | LOC107719773 | full | - | - | 1 | GCF_001515625.1 | - | NW_015656168.1 | 47289-48353 | - | |
| *Sinocyclocheilus rhinocerous (Sr)* | *tarl1b* | - | LOC107711518 | full | - | - | 1 | GCF_001515625.1 | - | NW_015650091.1 | 727057-728118 | - | |
| *Sinocyclocheilus grahami (Sg)* | *tarl1* | 5-HTR4.ps | Gene ID:107552355 | full | - | - | 1 | GCF_001515645.1 | - | NW_015505196.1 | 5614517-5615581 | - | |
| *Stegastes partitus (Stp)* | *tarl1* | 5-HTR4-like | XP_008296907.1 | full | - | - | 1 | GCF_000690725.1 | - | NW_007577760.1 | 271701-272777 | + | |
| *Takifugu rubripes (Tr)* | *tarl1* | 5-HTR4-like | XP_003976403.1 | full | - | - | 1 | GCF_000180615.1 | - | NW_004071248.1 | 83330-84367 | - | |
| *Tetraodon nigroviridis (Tn)* | *tarl1* | - | CAF93600.1 | full | - | - | 1 | GCA_000180735.1 | - | CAAE01011002.1 | 7437-8495 | - | |
| *Thunnus orientalis (To)* | *tarl1* | - | - | full | - | - | 1 | GCA_000418415.1 | - | BADN01004245.1 | 4208-5284 | - | |
| *Thunnus orientalis (To)* | *tarl2* | - | - | full | - | - | 1 | GCA_000418415.1 | - | BADN01043078.1 | 6332-7453 | + | |
| *Xiphophorus couchianus (Xc)* | *tarl1* | - | - | full | - | - | 1 | GCA_001444195.3 | 5 | CM010730.1 | 15290538-15291596 | + | |
| *Xiphophorus maculatus (Xm)* | *tarl1* | - | - | full | - | - | 1 | GCF_002775205.1 | 5 | NC_036447.1 | 14312375-14313433 | + | |

***taar* genes of jawed vertebrates identified in this study**

| *Species (Latin name and abbreviation)* | Gene name | Automatted annotation | Accession | Length (full, partial) | Pseudo-gene (Ψ) | *, stop; !, frameshift | # exons | Database incl. Version number | Chromo-some | Contig | Location in contig (bp) | Strand (+/-) | Comments |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Cartilaginous fish** | | | | | | | | | | | | | |
| *Callorhinchus milii (Cm)* | *taar-IIa* | TAAR4-like | XP_007897493.1 | full | Ψ | 1! 1* | 1 | GCF_000165045.1 | - | NW_006890121.1 | 242855-243884 | + | |
| *Callorhinchus milii (Cm)* | *taar-IIb* | TAAR2-like | XP_007897495.1 | full | Ψ | 2! 1* | 1 | GCF_000165045.1 | - | NW_006890121.1 | 258544-259545 | + | |
| *Callorhinchus milii (Cm)* | *taar-IIc* | TAAR4-like | XP_007897494.1 | full | - | - | 1 | GCF_000165045.1 | - | NW_006890121.1 | 248799-249827 | + | |
| *Leucoraja erinacea (Le)* | *taar-IIa* | - | - | full | - | - | 1 | WGS_VDB://AESE01 | - | AESE011082060.1,<br>AESE010020089.1 | 1-856, 26-502 | +,+ | not present in genome assembly |
| *Rhincodon typus (Rt)* | *taar-IIa* | TAAR4-like | XP_020378973.1 | full | Ψ | 1! | 1 | GCF_001642345.1 | - | NW_018045707.1 | 45125-46162 | + | |
| *Rhincodon typus (Rt)* | *taar-IIb* | TAAR4-like | XP_020378971.1 | full | Ψ | 2! 2* | 1 | GCF_001642345.1 | - | NW_018045707.1 | 21650-22701 | + | |
| *Rhincodon typus (Rt)* | *taar-IIc* | TAAR4-like | XP_020378970.1 | 5' partial | - | - | 1 | GCF_001642345.1 | - | NW_018045707.1 | 66985-67908 | - | |
| *Rhincodon typus (Rt)* | *taar-IId* | TAAR4-like | XP_020378972.1 | full | - | - | 1 | GCF_001642345.1 | - | NW_018045707.1 | 37597_38635 | + | |
| **Bony fish** | | | | | | | | | | | | | |
| *Anguilla anguilla (Aa)* | *taar12a* | - | - | full | - | - | 1 | GCA_000695075.1 | - | AZBK01826618.1 | 794-1840 | + | |
| *Anguilla anguilla (Aa)* | *taar12b* | - | - | full | - | - | 2 | GCA_000695075.2 | - | AZBK01826619.1 | 1284-2473 | + | |
| *Anguilla anguilla (Aa)* | *taar12c* | - | - | full | - | - | 1 | GCA_000695075.3 | - | AZBK01826622.1 | 5586-6632 | + | |
| *Anguilla anguilla (Aa)* | *taar12d* | - | - | partial | - | - | 1 | GCA_000695075.4 | - | AZBK01826625.1 | 2-592 | + | |
| *Anguilla anguilla (Aa)* | *taar12e* | - | - | partial | - | - | 1 | GCA_000695075.5 | - | AZBK01503223.1 | 12-566 | - | |
| *Anguilla anguilla (Aa)* | *taar12f* | - | - | full | - | - | 1 | GCA_000695075.6 | - | AZBK01826622.1 | 1234-2283 | + | |
| *Anguilla anguilla (Aa)* | *taar12g* | - | - | partial | - | - | 1 | GCA_000695075.7 | - | AZBK01826620.1 | 2-835 | + | |
| *Anguilla anguilla (Aa)* | *taar13a* | - | - | partial | - | - | 1 | GCA_000695075.1 | - | AZBK01826618.1 | 9792-10505 | - | |
| *Anguilla anguilla (Aa)* | *taar13b* | - | - | full | - | - | 1 | GCA_000695075.1 | - | AZBK01826618.1 | 6365-7402 | - | |
| *Anguilla anguilla (Aa)* | *taar13c* | - | - | partial | - | - | 1 | GCA_000695075.1 | - | AZBK01826606.1 | 1-714 | + | |
| *Anguilla anguilla (Aa)* | *taar13d* | - | - | partial | - | - | 1 | GCA_000695075.1 | - | AZBK01826616.1 | 4358-5053 | + | |
| *Anguilla anguilla (Aa)* | *taar13e* | - | - | full | - | - | 1 | GCA_000695075.1 | - | AZBK01826603.1 | 2-1024 | + | |
| *Anoplopoma fimbria (Af)* | *taar13a* | - | - | full | - | - | 1 | GCA_000499045.1 | - | AWGY01187787.1 | 907-1842 | + | |
| *Anoplopoma fimbria (Af)* | *taar13b* | - | - | partial | - | - | 1 | GCA_000499045.1 | - | AWGY01171310.1 | 3-785 | - | |
| *Anguilla japonica (Aj)* | *taar12a* | - | - | full | - | - | 1 | GCA_003597225.1 | LG19 | BEWY01000019.1 | 10043670-10044719 | + | |
| *Anguilla japonica (Aj)* | *taar12b* | - | - | full | - | - | 1 | GCA_003597225.1 | LG19 | BEWY01000019.1 | 10038585-10039640 | + | |
| *Anguilla japonica (Aj)* | *taar12c* | - | - | full | - | - | 1 | GCA_003597225.1 | LG19 | BEWY01000019.1 | 10023900-10024949 | + | |
| *Anguilla japonica (Aj)* | *taar12d* | - | - | full | - | - | 1 | GCA_003597225.1 | LG19 | BEWY01000019.1 | 10006478-10007524 | + | |
| *Anguilla japonica (Aj)* | *taar12e* | - | - | full | - | - | 1 | GCA_003597225.1 | LG19 | BEWY01000019.1 | 9993867-9994913 | + | |
| *Anguilla japonica (Aj)* | *taar12f* | - | - | full | - | - | 1 | GCA_003597225.1 | LG19 | BEWY01000019.1 | 9986347-9987393 | + | |
| *Anguilla japonica (Aj)* | *taar12g* | - | - | full | - | - | 1 | GCA_003597225.1 | LG19 | BEWY01000019.1 | 10033303-10034355 | + | |
| *Anguilla japonica (Aj)* | *taar12h* | - | - | full | - | - | 1 | GCA_003597225.1 | LG19 | BEWY01000019.1 | 9977289-9978401 | + | genomic sequence has 1 aa difference to WGS |
| *Anguilla japonica (Aj)* | *taar12i* | - | - | full | - | - | 1 | GCA_003597225.1 | LG19 | BEWY01000019.1 | 10001006-10002058 | + | |
| *Anguilla japonica (Aj)* | *taar13a* | - | - | full | - | - | 1 | WGS_VDB://AVPY01 | - | AVPY01144813.1 | 1202-262 | - | not present in genome assembly |
| *Anguilla japonica (Aj)* | *taar13b1* | - | - | full | Ψ | 1! | 1 | GCA_003597225.1 | LG19 | BEWY01000019.1 | 10053840-10052801 | - | genomic sequence has 4 aa difference to WGS |
| *Anguilla japonica (Aj)* | *taar13b2* | - | - | full | - | - | 1 | GCA_003597225.2 | LG19 | BEWY01000019.2 | 10050453-10049413 | - | |
| *Anguilla japonica (Aj)* | *taar13c* | - | - | partial | - | - | 1 | GCA_003597225.1 | LG19 | BEWY01000019.1 | 10072929-10073579 | + | |
| *Anguilla japonica (Aj)* | *taar13d1* | - | - | partial | - | - | 1 | WGS_VDB://AVPY01 | - | AVPY01144817.1 | 3-797 | + | pseudogene  in genomic database |
| *Anguilla japonica (Aj)* | *taar13d2* | - | - | full | - | - | 1 | GCA_003597225.1 | LG19 | BEWY01000019.1 | 10063062-10064087 | + | |
| *Anguilla japonica (Aj)* | *taar13e* | - | - | full | - | - | 1 | GCA_003597225.1 | LG19 | BEWY01000019.1 | 10078261-10079310 | + | |
| *Anguilla japonica (Aj)* | *taar13f* | - | - | partial | - | - | 1 | GCA_003597225.1 | LG19 | BEWY01000019.1 | 10070326-10071114 | + | genomic sequence has 4 aa difference to WGS |
| *Anguilla japonica (Aj)* | *taar13g* | - | - | full | - | - | 1 | GCA_003597225.2 | LG19 | BEWY01000019.1 | 10066035-10067006 | + | genomic sequence has 4 aa difference to WGS |
| *Astyanax mexicanus (Am)* | *taar12a* | TAAR4-like | XP_015463987.2 | full | - | - | 1 | GCF_000372685.2 | 3 | NC_035899.1 | 39668818-39669713 | + | |
| *Astyanax mexicanus (Am)* | *taar12b* | TAAR4-like | XP_015463989.2 | full | - | - | 1 | GCF_000372685.2 | 3 | NC_035899.1 | 39667005-39665971 | - | |
| *Astyanax mexicanus (Am)* | *taar12c* | TAAR4-like | XP_007259911.2 | full | - | - | 1 | GCF_000372685.2 | 3 | NC_035899.1 | 39661121-39662152 | - | |
| *Astyanax mexicanus (Am)* | *taar13a* | TAAR13c-like | XP_015463986.2 | full | - | - | 1 | GCF_000372685.2 | 3 | NC_035899.1 | 39656351-39657388 | + | |
| *Anguilla rostrata (Ar)* | *taar12a* | - | - | full | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01001697.1 | 195538-196587 | - | |
| *Anguilla rostrata (Ar)* | *taar12b* | - | - | full | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01001697.1 | 200565-201620 | - | |
| *Anguilla rostrata (Ar)* | *taar12c* | - | - | full | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01001697.1 | 228169-229218 | - | |
| *Anguilla rostrata (Ar)* | *taar12d* | - | - | partial | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01007895.1 | 31310-32080 | + | |
| *Anguilla rostrata (Ar)* | *taar12e* | - | - | full | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01007895.1 | 15225-16259 | + | |
| *Anguilla rostrata (Ar)* | *taar12f* | - | - | full | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01007895.1 | 9659-10705 | + | |
| *Anguilla rostrata (Ar)* | *taar12g1* | - | - | full | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01007895.1 | 3930-4976 | + | |
| *Anguilla rostrata (Ar)* | *taar12g2* | - | - | partial | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01007895.1 | 3-749 | + | |
| *Anguilla rostrata (Ar)* | *taar12h* | - | - | full | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01006975.1 | 1392-2504 | - | |
| *Anguilla rostrata (Ar)* | *taar12i* | - | - | full | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01007895.1 | 19379-20431 | + | |
| *Anguilla rostrata (Ar)* | *taar12j* | - | - | full | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01001697.1 | 232505-233554 | - | |
| *Anguilla rostrata (Ar)* | *taar12k* | - | - | full | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01007895.1 | 34780-35829 | + | |
| *Anguilla rostrata (Ar)* | *taar12l* | - | - | full | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01007895.1 | 30123-31163 | + | |
| *Anguilla rostrata (Ar)* | *taar13a* | - | - | full | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01001697.1 | 184810-185850 | + | |
| *Anguilla rostrata (Ar)* | *taar13b1* | - | - | full | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01001697.1 | 190058-191098 | + | |
| *Anguilla rostrata (Ar)* | *taar13b2* | - | - | full | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01001697.1 | 181375-182415 | + | |
| *Anguilla rostrata (Ar)* | *taar13c* | - | - | full | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01001697.1 | 162511-163551 | - | |
| *Anguilla rostrata (Ar)* | *taar13d1* | - | - | full | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01001697.1 | 170738-171778 | - | |
| *Anguilla rostrata (Ar)* | *taar13d2* | - | - | full | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01001697.1 | 174330-175364 | - | |
| *Anguilla rostrata (Ar)* | *taar13e* | - | - | full | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01001697.1 | 156645-157697 | - | |
| *Anguilla rostrata (Ar)* | *taar13f* | - | - | full | - | - | 1 | WGS_VDB://LTYT01 | - | LTYT01001697.1 | 167001-168050 | - | |
| *Cyprinus carpio (Cc)* | *taar12a* | TAAR4-like | XP_018959267.1 | full | - | - | 1 | GCF_000951615.1 | 9 | NC_031705.1 | 15759047-15760075 | - | |
| *Cyprinus carpio (Cc)* | *taar12b* | TAAR4-like | XP_018959253.1 | full | - | - | 1 | GCF_000951615.1 | 9 | NC_031705.1 | 15752901-15753935 | - | |
| *Cyprinus carpio (Cc)* | *taar12c* | - | LOC109075658 | full | - | - | 1 | WGS_VDB://LHQP01 | - | LHQP01008012.1 | 15916-14771 | - | pseudogene  in genomic database |
| *Cyprinus carpio (Cc)* | *taar12d* | - | LOC109080729 | full | Ψ | 1! 1* | 1 | GCF_000951615.1 | 9 | NC_031705.1 | 15764159-15764995 | - | |
| *Cyprinus carpio (Cc)* | *taar12e* | TAAR4-like | XP_018975893.1 | full | - | - | 1 | GCF_000951615.1 | 33 | NC_031729.1 | 11068745-11069761 | - | |
| *Cyprinus carpio (Cc)* | *taar12f* | TAAR4-like | XP_018961602.1 | full | - | - | 1 | GCF_000951615.1 | 12 | NC_031708.1 | 6966749-6967759 | + | |
| *Cyprinus carpio (Cc)* | *taar12g* | TAAR4-like | XP_018946046.1 | full | - | - | 1 | WGS_VDB://LHQP01 | - | LHQP01033775.1 | 15629-16645 | + | not present in genome assembly |
| *Cyprinus carpio (Cc)* | *taar12h* | TAAR4-like | XP_018946046.1 | full | - | - | 1 | GCF_000951615.1 | - | NW_017540643.1 | 74888-75904 | + | |
| *Cyprinus carpio (Cc)* | *taar12i* | TAAR3-like | XP_018959120.1 | full | - | - | 1 | GCF_000951615.1 | - | NW_017545985.1 | 8783-9934 | + | |
| *Cyprinus carpio (Cc)* | *taar12j* | TAAR4-like | XP_018946046.1 | partial | Ψ | 1! 1* | 1 | WGS_VDB://SAUK01 | - | SAUK01000530.1 | 33619-32874 | - | not present in genome assembly |
| *Cyprinus carpio (Cc)* | *taar12k* | TAAR4-like | XP_018961608.1 | full | - | - | 1 | GCF_000951615.1 | 12 | NC_031708.1 | 6978116-6979132 | + | |
| *Cyprinus carpio (Cc)* | *taar12l* | - | - | full | - | - | 1 | WGS_VDB://LHQP01 | - | LHQP01055690.1 | 10065-11084 | + | not present in genome assembly |
| *Cyprinus carpio (Cc)* | *taar12m* | TAAR4-like | XP_018961603.1 | full | - | - | 1 | GCF_000951615.1 | 12 | NC_031708.1 | 6988431-6989447 | + | |
| *Cyprinus carpio (Cc)* | *taar12n* | TAAR4-like | XP_018941218.1 | full | - | - | 1 | GCF_000951615.1 | - | NW_017539046.1 | 750-1802 | - | |
| *Cyprinus carpio (Cc)* | *taar12o* | - | LOC109092292 | partial | - | - | 1 | GCF_000951615.1 | 12 | NC_031708.1 | 6944320-6944959 | + | |
| *Cyprinus carpio (Cc)* | *taar13a* | TAAR13c-like | XP_018959962.1 | full | - | - | 1 | GCF_000951615.1 | 2 | NC_031698.1 | 8856169-8857456 | + | |
| *Cyprinus carpio (Cc)* | *taar13b* | TAAR13c-like | XP_018959967.1 | full | - | - | 1 | GCF_000951615.1 | 2 | NC_031698.1 | 8860794-8861813 | + | |
| *Cyprinus carpio (Cc)* | *taar13c* | TAAR13c | XP_018932792.1 | full | - | - | 1 | GCF_000951615.1 | - | NW_017538119.1 | 334753-335778 | - | |
| *Cyprinus carpio (Cc)* | *taar13d* | TAAR13c-like | XP_018932791.1 | full | - | - | 1 | GCF_000951615.1 | - | NW_017538119.1 | 332109-333113 | - | |
| *Cyprinus carpio (Cc)* | *taar13e* | - | - | partial | - | - | 1 | GCF_000951615.1 | 7 | NC_031703.1 | 4705416-4706438 | + | |
| *Clupea harengus (Ch)* | *taar13a* | taar2 | XP_012683945.1 | full | - | - | 1 | GCF_000966335.1 | - | NW_012218207.1 | 76993-78006 | - | |
| *Dicentrarchus labrax (Dl)* | *taar13a* | - | - | full | - | - | 1 | GCA_000689215.1 | - | HG916851.1 | 95392926-95393909 | + | |
| *Dicentrarchus labrax (Dl)* | *taar13b* | - | - | full | - | - | 1 | GCA_000689215.1 | - | HG916851.1 | 57561723-57562754 | - | |
| *Esox Lucius (El)* | *taar13a* | TAAR13c-like | XP_012993972.2 | full | - | - | 1 | GCF_000721915.3 | - | NC_025985.3 | 16543278-16544387 | + | |
| *Gasterosteus aculeatus (Ga)* | *taar13a* | - | - | full | Ψ | 1! | 1 | GCA_000180675.1 | - | AANH01006890.1 | 20685-21651 | - | |
| *Gadus morhua (Gm)* | *taar13a* | - | - | full | - | - | 1 | GCA_000231765.1 | - | HE569769.1 | 743882-744925 | - | |
| *Gadus morhua (Gm)* | *taar13b* | - | - | full | - | - | 1 | GCA_000231765.1 | - | HE569769.1 | 720836-721903 | - | |
| *Gadus morhua (Gm)* | *taar13c* | - | - | full | - | - | 1 | GCA_000231765.1 | - | HE569769.1 | 733644-734717 | - | |
| *Ictalurus punctatus (Ip)* | *taar12a* | TAAR4-like | XP_017341644.1 | full | - | - | 1 | GCF_001660625.1 | 2 | NC_030417.1 | 36456374..36457420 | + | |
| *Ictalurus punctatus (Ip)* | *taar12b* | TAAR4-like | XP_017339448.1 | full | - | - | 1 | GCF_001660625.1 | 2 | NC_030417.1 | 36501767-36502801 | + | |
| *Ictalurus punctatus (Ip)* | *taar13a* | TAAR13c-like | XP_017341732.1 | full | - | - | 1 | GCF_001660625.1 | 2 | NC_030417.1 | 36495889-36496932 | + | |
| *Ictalurus punctatus (Ip)* | *taar13b* | TAAR13c-like | XP_017341719.1 | full | - | - | 1 | GCF_001660625.1 | 2 | NC_030417.1 | 36491561-36492610 | + | |
| *Ictalurus punctatus (Ip)* | *taar13c* | TAAR13c-like | XP_017341711.1 | full | - | - | 1 | GCF_001660625.1 | 2 | NC_030417.1 | 36488929-36489978 | + | |
| *Ictalurus punctatus (Ip)* | *taar13d* | TAAR13c-like | XP_017341696.1 | full | - | - | 1 | GCF_001660625.1 | 2 | NC_030417.1 | 36484353-36485387 | + | |
| *Ictalurus punctatus (Ip)* | *taar13e* | TAAR13c-like | XP_017341685.1 | full | - | - | 1 | GCF_001660625.1 | 2 | NC_030417.1 | 36480581-36481612 | + | |
| *Ictalurus punctatus (Ip)* | *taar13f* | TAAR13c-like | XP_017341662.1 | full | - | - | 1 | GCF_001660625.1 | 2 | NC_030417.1 | 36472284-36473330 | + | |
| *Ictalurus punctatus (Ip)* | *taar13g* | TAAR13c-like | XP_017341651.1 | full | - | - | 1 | GCF_001660625.1 | 2 | NC_030417.1 | 36464856-36465905 | + | |
| *Ictalurus punctatus (Ip)* | *taar13h* | TAAR13c-like | XP_017341672.1 | full | - | - | 1 | GCF_001660625.1 | 2 | NC_030417.1 | 36475867-36476913 | + | |
| *Lates calcarifer (Lac)* | *taar13a* | TAAR13c-like | XP_018555677.1 | full | - | - | 1 | GCF_001640805.1 | - | NW_017363841.1 | 2551627-2552655 | - | |
| *Lates calcarifer (Lac)* | *taar13b* | TAAR13c-like | XP_018555664.1 | full | - | - | 1 | GCF_001640805.1 | - | NW_017363841.1 | 2546203-2547222 | - | |
| *Labrus bergylta (Lb)* | *taar13a* | TAAR13c-like | XP_020496621.1 | full | - | - | 1 | GCF_900080235.1 | - | NW_018114570.1 | 87924-88955 | + | |
| *Labrus bergylta (Lb)* | *taar13b* | | LOC109989273 | full | Ψ | 1! | 1 | GCF_900080235.1 | - | NW_018114570.1 | 25196-26207 | - | |
| *Labrus bergylta (Lb)* | *taar13c* | TAAR13c-like | XP_020496622.1 | full | - | - | 1 | GCF_900080235.1 | - | NW_018114570.1 | 94469-95485 | + | |
| *Labrus bergylta (Lb)* | *taar13d* | TAAR13c-like | XP_020496624.1 | full | - | - | 1 | GCF_900080235.1 | - | NW_018114570.1 | 99727-100749 | + | |
| *Larimichthys crocea (Lc)* | *taar13a* | TAAR13c-like | XP_027138405.1 | full | - | - | 1 | GCF_000972845.2 | X | NC_040020.1 | 19809619-19810638 | - | |
| *Larimichthys crocea (Lc)* | *taar13b* | TAAR13c-like | XP_019117237.1 | full | - | - | 1 | GCF_000972845.1 | - | NW_017608435.1 | 1-879 | - | not in GCF_000972845.2 |
| *Larimichthys crocea (Lc)* | *taar13c* | TAAR13c-like | XP_019117238.2 | full | - | - | 1 | GCF_000972845.2 | X | NC_040020.1 | 19814894-19815943 | - | |
| *Lepisosteus oculatus (Lo)* | *taar12a* | - | - | full | - | - | 1 | GCF_000242695.1 | LG1 | NC_023179.1 | 68708840-68709862 | + | |
| *Lepisosteus oculatus (Lo)* | *taar12b* | - | - | full | - | - | 1 | GCF_000242695.1 | LG1 | NC_023179.1 | 68698466-68699503 | + | |
| *Lepisosteus oculatus (Lo)* | *taar12c* | - | - | full | - | - | 1 | GCF_000242695.1 | LG1 | NC_023179.1 | 68742836-68743906 | + | |
| *Lepisosteus oculatus (Lo)* | *taar13a* | - | - | full | - | - | 1 | GCF_000242695.1 | LG1 | NC_023179.1 | 68772650-68773678 | + | |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Lepisosteus oculatus (Lo)* | *taar5-like* | - | - | full | - | - | 1 | GCF_000242695.1 | LG1 | NC_023179.1 | 69059546-69060574 | + |
| | | | | | | | | | | | | |
| *Leuciscus waleckii (Lw)* | *taar12a* | - | - | full | Ψ | 2! | 1 | GCA_900092035.1 | - | FLSR01004880.1 | 3072502-3073642 | - |
| | | | | | | | | | | | | |
| *Leuciscus waleckii (Lw)* | *taar13a* | - | - | full | Ψ | 1! | 1 | GCA_900092035.1 | - | FLSR01000467.1 | 1995-2945 | - |
| *Leuciscus waleckii (Lw)* | *taar13b* | - | - | full | Ψ | 1! | 1 | GCA_900092035.1 | - | FLSR01000467.1 | 10828-11851 | - |
| | | | | | | | | | | | | |
| *Morone saxatilis (Ms)* | *taar13a* | - | - | partial | - | - | 1 | GCA_001663605.1 | - | JTCL01016091.1 | 18020-18655 | - |
| | | | | | | | | | | | | |
| *Pimephales promelas (Pp)* | *taar12a* | - | - | partial | - | - | 1 | GCA_000700825.1 | - | JNCD01017678.1 | 86739-87671 | - |
| *Pimephales promelas (Pp)* | *taar12b* | - | - | partial | - | - | 1 | GCA_000700825.1 | - | JNCD01002744.1 | 122449-123246 | - |
| *Pimephales promelas (Pp)* | *taar12c* | - | - | full | - | - | 1 | GCA_000700825.1 | - | JNCD01017678.1 | 29732-30802 | - |
| *Pimephales promelas (Pp)* | *taar12d* | - | - | full | - | - | 1 | GCA_000700825.1 | - | JNCD01017678.1 | 89609-90748 | - |
| *Pimephales promelas (Pp)* | *taar12e* | - | - | full | - | - | 1 | GCA_000700825.1 | - | JNCD01017678.1 | 21261-22409 | - |
| | | | | | | | | | | | | |
| *Pimephales promelas (Pp)* | *taar13a* | - | - | full | - | - | 1 | GCA_000700825.1 | - | JNCD01004450.1 | 57751-58776 | - |
| *Pimephales promelas (Pp)* | *taar13b* | - | - | full | - | - | 1 | GCA_000700825.2 | - | JNCD01017678.1 | 6857-7882 | + |
| | | | | | | | | | | | | |
| *Pygocentrus nattereri (Pyn)* | *taar12a* | TAAR4-like | XP_017562409.1 | full | - | - | 1 | GCF_001682695.1 | - | NW_016243879.1 | 1733682-1734725 | + |
| *Pygocentrus nattereri (Pyn)* | *taar12b* | TAAR4-like | XP_017562407.1 | full | - | - | 1 | GCF_001682695.1 | - | NW_016243879.1 | 1718560-1719591 | + |
| *Pygocentrus nattereri (Pyn)* | *taar12c* | TAAR4-like | XP_017562408.1 | full | - | - | 1 | GCF_001682695.1 | - | NW_016243879.1 | 1729237-1730268 | + |
| *Pygocentrus nattereri (Pyn)* | *taar12d* | TAAR3-like | XP_017562412.1 | full | - | - | 1 | GCF_001682695.1 | - | NW_016243879.1 | 1737731-1738762 | + |
| *Pygocentrus nattereri (Pyn)* | *taar12e* | TAAR4-like | XP_017562414.1 | full | - | - | 1 | GCF_001682695.1 | - | NW_016243879.1 | 1747895-1748920 | + |
| | | | | | | | | | | | | |
| *Pygocentrus nattereri (Pyn)* | *taar13a* | TAAR13c-like | XP_017562388.1 | full | - | - | 1 | GCF_001682695.1 | - | NW_016243879.1 | 1758494-1759543 | + |
| *Pygocentrus nattereri (Pyn)* | *taar13b* | TAAR13c-like | XP_017562390.1 | full | - | - | 1 | GCF_001682695.1 | - | NW_016243879.1 | 1774862-1775911 | + |
| *Pygocentrus nattereri (Pyn)* | *taar13c* | TAAR13c-like | XP_017562387.1 | full | - | - | 1 | GCF_001682695.1 | - | NW_016243879.1 | 1751534-1752583 | + |
| *Pygocentrus nattereri (Pyn)* | *taar13d* | TAAR13c-like | XP_017562389.1 | full | - | - | 1 | GCF_001682695.1 | - | NW_016243879.1 | 1766788-1767837 | + |
| | | | | | | | | | | | | |
| *Salmo salar (Ss)* | *taar13a* | - | - | full | - | - | 1 | GCF_000233375.1 | ssa15 | NC_027314.1 | 30597459-30598328 | - |
| *Salmo salar (Ss)* | *taar13b* | - | - | full | Ψ | 1! | 2 | GCF_000233375.1 | ssa15 | NC_027314.1 | 30597304-30598328 | - |
| *Salmo salar (Ss)* | *taar13c* | - | - | full | - | - | 1 | GCF_000233375.1 | ssa15 | NC_027314.1 | 30659257-30660219 | - |
| | | | | | | | | | | | | |
| *Sebastes aleutianus (Sea)* | *taar13a* | - | - | full | - | - | 1 | GCA_001910805.2 | - | LHVS01040848.1 | 11319-12383 | - |
| *Sebastes aleutianus (Sea)* | *taar13b* | - | - | partial | - | - | 1 | GCA_001910805.2 | - | LHVS01040851.1 | 3-641 | - |
| *Sebastes aleutianus (Sea)* | *taar13c* | - | - | full | Ψ | 2! | 1 | GCA_001910805.2 | - | LHVS01040852.1 | 3-602 | - |
| | | | | | | | | | | | | |
| *Sebastes minor (Sem)* | *taar13a* | - | - | full | - | - | 1 | GCA_001910765.2 | - | LHCJ01837248.1 | 2-574 | - |
| *Sebastes minor (Sem)* | *taar13b* | - | - | partial | - | - | 1 | GCA_001910765.2 | - | LHCJ01837248.1 | 203..574 | - |
| | | | | | | | | | | | | |
| *Sebastes rubrivinctus (Ser)* | *taar13a* | - | - | full | - | - | 1 | GCA_000475215.1 | - | AUPQ01075218.1 | 1668-2732 | + |
| *Sebastes rubrivinctus (Ser)* | *taar13b* | - | - | partial | - | - | 1 | GCA_000475215.1 | - | AUPQ01038002.1 | 908-3 | - |
| | | | | | | | | | | | | |
| *Sebastes nigrocinctus (Sn)* | *taar13a* | - | - | full | - | - | 1 | GCA_000475235.3 | - | AUPR02083636.1 | 12257-13321 | - |
| | | | | | | | | | | | | |
| *Sebastes steindachneri (Ses)* | *taar13a* | - | - | partial | - | - | n.d. | GCA_001910785.2 | - | LCWK010354496.1; LCW | 1-144;1-114;2-256;3-107 | + |
| | | | | | | | | | | | | |
| *Scleropages formosus (Sf)* | *taar13a* | TAAR13c-like | XP_018599052.1 | full | - | - | 1 | ASM162426v1 | - | NW_017371616.1 | 39141-40175 | + |
| *Scleropages formosus (Sf)* | *taar13b* | - | LOC108929171 | full | Ψ | 1! | 1 | ASM162426v1 | - | NW_017371616.1 | 51463-52507 | + |
| *Scleropages formosus (Sf)* | *taar13c* | TAAR13c-like | XP_018599050.1 | full | - | - | 1 | ASM162426v1 | - | NW_017371616.1 | 25892-26926 | + |
| *Scleropages formosus (Sf)* | *taar13d* | - | LOC108929166 | full | Ψ | 1! | 1 | ASM162426v1 | - | NW_017371616.1 | 18411-19305 | + |
| | | | | | | | | | | | | |
| *Sinocyclocheilus anshuiensis (Sa)* | *taar12a* | TAAR4-like | XP_016353209.1 | full | - | - | 1 | GCF_001515605.1 | - | NW_015544213.1 | 2578639-2579658 | - |
| *Sinocyclocheilus anshuiensis (Sa)* | *taar12b* | TAAR4-like | XP_016353208.1 | full | - | - | 2 | GCF_001515605.1 | - | NW_015544213.1 | 2575897-2576889 | - |
| *Sinocyclocheilus anshuiensis (Sa)* | *taar12c* | - | LOC107697102 | full | Ψ | 1! | 1 | GCF_001515605.1 | - | NW_015544213.1 | 2616124-2617023 | - |
| *Sinocyclocheilus anshuiensis (Sa)* | *taar12d* | TAAR4-like | XP_016353229.1 | full | - | - | 1 | GCF_001515605.1 | - | NW_015544213.1 | 2611370-2612386 | - |
| | | | | | | | | | | | | |
| *Sinocyclocheilus anshuiensis (Sa)* | *taar13a* | TAAR13c-like | XP_016353236.1 | full | - | - | 1 | GCF_001515605.1 | - | NW_015544213.1 | 2664594-2665619 | + |
| *Sinocyclocheilus anshuiensis (Sa)* | *taar13b* | - | LOC107685375 | partial | Ψ | 1* | 1 | GCF_001515605.1 | - | NW_015539878.1 | 409227-409793 | - |
| *Sinocyclocheilus anshuiensis (Sa)* | *taar13c* | TAAR13c | XP_016337433.1 | full | - | - | 1 | GCF_001515605.1 | - | NW_015539878.1 | 412165-413187 | - |
| *Sinocyclocheilus anshuiensis (Sa)* | *taar13d* | TAAR13c-like | XP_016353237.1 | full | - | - | 1 | GCF_001515605.1 | - | NW_015544213.1 | 2667473-2668498 | + |
| *Sinocyclocheilus anshuiensis (Sa)* | *taar13e* | TAAR13c-like | XP_016353238.1 | full | - | - | 1 | GCF_001515605.1 | - | NW_015544213.1 | 2670779-2671801 | + |
| | | | | | | | | | | | | |
| *Sinocyclocheilus grahami (Sg)* | *taar12a* | TAAR4-like | XP_016087126.1 | full | - | - | 1 | GCF_001515645.1 | - | NW_015505576.1 | 896804-897832 | + |
| *Sinocyclocheilus grahami (Sg)* | *taar12b* | TAAR4-like | XP_016087127.1 | full | - | - | 1 | GCF_001515645.1 | - | NW_015505576.1 | 902334-903362 | + |
| *Sinocyclocheilus grahami (Sg)* | *taar12c* | TAAR4-like | XP_016087138.1 | full | - | - | 1 | GCF_001515645.1 | - | NW_015505576.1 | 871953-872987 | + |
| *Sinocyclocheilus grahami (Sg)* | *taar12d* | TAAR4-like | XP_016087141.1 | full | - | - | 1 | GCF_001515645.1 | - | NW_015505576.1 | 874541-875557 | + |
| *Sinocyclocheilus grahami (Sg)* | *taar12e* | TAAR4-like | XP_016087140.1 | full | - | - | 1 | GCF_001515645.1 | - | NW_015505576.1 | 882475-883491 | + |
| *Sinocyclocheilus grahami (Sg)* | *taar12f* | TAAR4-like | XP_016087142.1 | full | - | - | 1 | GCF_001515645.1 | - | NW_015505576.1 | 891479-892504 | + |
| | | | | | | | | | | | | |
| *Sinocyclocheilus grahami (Sg)* | *taar13a* | TAAR13c-like | XP_016087134.1 | full | - | - | 1 | GCF_001515645.1 | - | NW_015505576.1 | 810574-811599 | - |
| *Sinocyclocheilus grahami (Sg)* | *taar13b* | - | LOC107593282 | partial | Ψ | 2!1* | 1 | GCF_001515645.1 | - | NW_015505347.1 | 359338-359967 | + |
| *Sinocyclocheilus grahami (Sg)* | *taar13c* | TAAR13c | XP_016138370.1 | full | - | - | 1 | GCF_001515645.1 | - | NW_015505347.1 | 354967-355989 | + |
| *Sinocyclocheilus grahami (Sg)* | *taar13d* | TAAR13c-like | XP_016087133.1 | full | - | - | 1 | GCF_001515645.1 | - | NW_015505576.1 | 805830-806855 | - |
| *Sinocyclocheilus grahami (Sg)* | *taar13e* | TAAR13c-like | XP_016087132.1 | full | - | - | 1 | GCF_001515645.1 | - | NW_015505576.1 | 800744-801769 | - |
| | | | | | | | | | | | | |
| *Sinocyclocheilus rhinocerous (Sr)* | *taar12a* | TAAR4-like | XP_016429344.1 | full | - | - | 1 | GCF_001515625.1 | - | NW_015642822.1 | 7441-8463; | + |
| *Sinocyclocheilus rhinocerous (Sr)* | *taar12b* | TAAR4-like | XP_016429345.1 | full | - | - | 1 | GCF_001515625.1 | - | NW_015642822.1 | 11768-12790 | + |
| *Sinocyclocheilus rhinocerous (Sr)* | *taar12c* | TAAR4-like | XP_016400476.1 | full | - | - | 1 | GCF_001515625.1 | - | NW_015667042.1 | 16881-17915 | + |
| *Sinocyclocheilus rhinocerous (Sr)* | *taar12d* | TAAR4-like | XP_016400475.1 | full | Ψ | 1* | 1 | GCF_001515625.1 | - | NW_015667042.1 | 21894-22787 | + |
| *Sinocyclocheilus rhinocerous (Sr)* | *taar12e* | TAAR4-like | XP_016384356.1 | full | - | - | 1 | GCF_001515625.1 | - | NW_015657344.1 | 740-1759 | - |
| *Sinocyclocheilus rhinocerous (Sr)* | *taar12f* | TAAR4-like | XP_016402534.1 | partial | - | - | 1 | GCF_001515625.1 | - | NW_015769517.1 | 2-739 | - |
| *Sinocyclocheilus rhinocerous (Sr)* | *taar12g* | TAAR4-like | XP_016429343.1 | full | - | - | 1 | GCF_001515625.1 | - | NW_015642822.1 | 2050-3213 | + |
| | | | | | | | | | | | | |
| *Sinocyclocheilus rhinocerous (Sr)* | *taar13a1* | TAAR13c | XP_016382319.1 | full | - | - | 1 | GCF_001515625.1 | - | NW_015656152.1 | 39210-40235 | + |
| *Sinocyclocheilus rhinocerous (Sr)* | *taar13a2* | - | LOC107742731 | partial | Ψ | 2* | 1 | GCF_001515625.1 | - | NW_015632707.1 | 688968-689471 | + |
| *Sinocyclocheilus rhinocerous (Sr)* | *taar13b* | TAAR13c-like | XP_016382289.1 | partial | Ψ | 1!1* | 1 | GCF_001515625.1 | - | NW_015656152.1 | 46150-46764 | + |
| *Sinocyclocheilus rhinocerous (Sr)* | *taar13c1* | TAAR13c-like | XP_016411245.1 | partial | - | - | 1 | GCF_001515625.1 | - | NW_015632707.1 | 696850-697488 | + |
| *Sinocyclocheilus rhinocerous (Sr)* | *taar13c2* | TAAR13c-like | XP_016402954.1 | partial | - | - | 1 | GCF_001515625.1 | - | NW_015779853.1 | 605-1060 | + |
| *Sinocyclocheilus rhinocerous (Sr)* | *taar13d* | TAAR13c-like | XP_016382320.1 | full | - | - | 1 | GCF_001515625.1 | - | NW_015656152.1 | 42268-43293 | + |
| *Sinocyclocheilus rhinocerous (Sr)* | *taar13e* | TAAR13c-like | XP_016382289.1 | full | - | - | 1 | GCF_001515625.1 | - | NW_015656152.1 | 45877-46764 | + |

**Representative reference TAAR sequences from all classes (class I, II, III) in several bony vertebrate species (mouse, zebrafish, stickleback, and fugu) used for phylogenetic analysis**

Amino acid sequences were taken from Hussain et al., PNAS 2009

| | Species (Latin name and abbreviation) | Gene name | Synonyms/autom. predictions | Accession No/gene ID/protein ID | chromosomal location |
|---|---|---|---|---|---|
| M | Mus musculus (Mm) | taar1 | TAAR1 | NP_444435.1 | 10 |
| o | Mus musculus (Mm) | taar2 | TAAR2 | NP_001007267.1 | 10 |
| u | Mus musculus (Mm) | taar3 | TAAR3 | NP_001008429.1 | 10 |
| s | Mus musculus (Mm) | taar4 | TAAR4 | NP_001008499.1 | 10 |
| e | Mus musculus (Mm) | taar5 | TAAR5 | NP_001009574.1 | 10 |
| | Mus musculus (Mm) | taar6 | TAAR6 | NP_001010828.1 | 10 |
| | Mus musculus (Mm) | taar8 | TAAR8a | NP_001010830.1 | 10 |
| | Mus musculus (Mm) | taar9 | TAAR9 | NP_001010831.1 | 10 |
| | | | | | |
| Z | Danio rerio (Dr) | taar1b | TAAR1 | NP_001076373.1 | 20 |
| e | Danio rerio (Dr) | taar10a | TAAR10a | NP_001076367.1 | 20 |
| b | Danio rerio (Dr) | taar11 | TAAR11 | NP_001076546.1 | 20 |
| r | Danio rerio (Dr) | taar12a | TAAR12a | NP_001076578.1 | 20 |
| a | Danio rerio (Dr) | taar12b | TAAR12b | NP_001076573.1 | 20 |
| f | Danio rerio (Dr) | taar12c | TAAR12c | NP_001076564.1 | 20 |
| I | Danio rerio (Dr) | taar12d | TAAR12c | NP_001076564.1 | 20 |
| s | Danio rerio (Dr) | taar12e | TAAR12e | NP_001076563.1 | 20 |
| h | Danio rerio (Dr) | taar12f | TAAR12f | NP_001124143.1 | 20 |
| | Danio rerio (Dr) | taar12g | TAAR12g | NP_001076377.1 | 20 |
| | Danio rerio (Dr) | taar12h | TAAR12h | NP_001076378.1 | 20 |
| | Danio rerio (Dr) | taar12i | TAAR12i | NP_001076554.1 | 20 |
| | Danio rerio (Dr) | taar12j | TAAR12j | NP_001076380.1 | 20 |
| | Danio rerio (Dr) | taar12k | TAAR12h | NP_001076378.1 | 20 |
| | Danio rerio (Dr) | taar12m | TAAR4 | XP_001920844.2 | 15 |
| | Danio rerio (Dr) | taar13a | TAAR64 | NP_001076571.1 | 20 |
| | Danio rerio (Dr) | taar13b | TAAR13b | NP_001076511.1 | 20 |
| | Danio rerio (Dr) | taar13c | TAAR13c | NP_001076509.1 | 20 |
| | Danio rerio (Dr) | taar13d | TAAR13d | NP_001076510.1 | 20 |
| | Danio rerio (Dr) | taar13e | TAAR13e | NP_001076512.1 | 20 |
| | Danio rerio (Dr) | taar14f | TAAR14f | NP_001076382.1 | 20 |
| | Danio rerio (Dr) | taar15a | TAAR13c-like | XP_009300776.1 | 20 |
| | Danio rerio (Dr) | taar16a | TAAR6-like | XP_009303909.1 | 10 |
| | Danio rerio (Dr) | taar17a | TAAR13c-like | XP_021334896.1 | 10 |
| | Danio rerio (Dr) | taar18a | TAAR13c-like | XP_021335131.1 | 10 |
| | Danio rerio (Dr) | taar19a | TAAR13c-like | XP_017213596.1 | 10 |
| | Danio rerio (Dr) | tar20a | TAAR13c-like | XP_017213576.1 | 10 |
| | | | | | |
| S | Gasterosteus aculeatus (Ga) | taar21a | - | VDFJ01000095.1 | |
| ti | Gasterosteus aculeatus (Ga) | taar22a | - | VDFJ01000016.1 | |
| ck | Gasterosteus aculeatus (Ga) | taar23 | - | VDFJ01000278.1 | |
| le | Gasterosteus aculeatus (Ga) | taar24 | - | VDFJ01000206.1 | |
| ba | Gasterosteus aculeatus (Ga) | taar25a | - | VDFJ01000180.1 | |
| ck | Gasterosteus aculeatus (Ga) | taar26a | - | VDFJ01003622.1 | |
| | Gasterosteus aculeatus (Ga) | taar27 | - | VDFJ01000276.1 | |
| | | | | | |
| F | Takifugu rubripes (Tr) | taar28a | - | GeneID:115247326 | |
| u | | | | | |
| g | | | | | |
| u | | | | | |

**Aminergic receptors used as outgroup in phylogenetic analysis**

| Species (Latin name and abbreviation) | Gene name | Accession or genomic location (in case of missing accession) | Comments |
|---|---|---|---|
| **Adrenergic receptors** | | | |
| *Branchiostoma belcheri* (Bbe) | *adra1a* | GeneID:109485326 | |
| *Callorhinchus milii (Cm)* | *adra1a* | GeneID:103191393 | |
| *Lethenteron camtschaticum (Lec)* | *adra1a* | GCA_000466285.1, contig KE993747.1, range 33178-34107 (+) | |
| *Mus musculus (Mm)* | *adra1a* | GeneID:11549 | |
| *Mus musculus (Mm)* | *adra1b* | GeneID:11548 | |
| *Leucoraja erinacea (Le)* | *adra1b* | AESE000000000.1, contig AESE012504078.1 range 1321-2283 (+) | |
| | | | |
| *Branchiostoma floridae (Bfl)* | *adra2* | Gene ID:7251580 | |
| *Ciona intestinalis (Cin)* | *adra2* | GeneID:100184338 | Annotated as htr1a |
| *Lethenteron camtschaticum (Lec)* | *adra2* | GCA_000466285.1, contig KE993680.1, range 3745198-3746598 (+) | |
| *Mus musculus (Mm)* | *adra2a* | GeneID:11551 | |
| *Rhincodon typus (Rt)* | *adra2a* | GeneID:109933335 | |
| | | | |
| *Asymmetron lucayanum (Alu)* | *adrB* | GCA_001663935.1, contig  LZCU01211521.1, range 1805-2977 (+) | |
| *Callorhinchus milii (Cm)* | *adrB1* | GeneID:103186583 | |
| *Ciona intestinalis (Cin)* | *adrB* | GeneID:100177523 | |
| *Ciona savignyi (Csa)* | *adrB* | GCA_000149265.1, contig CH002630.1, range 98843-100777 (+) | |
| *Lethenteron camtschaticum (Lec)* | *adrB* | GCA_000466285.1, contig KE993680.1, range 3147094 to 3148410(+) | |
| *Mus musculus (Mm)* | *adrB1* | GeneID:11554 | |
| *Rattus norvegicus (Rat)* | *adrB* | GeneID:24176 | |
| *Rhincodon typus (Rt)* | *adrB* | GeneID:109923571 | |
| **Dopaminergic receptors** | | | |
| *Asymmetron lucayanum (Alu)* | *drd1,5* | GCA_001663935.1, contig LZCU01179855.1, range 3013-4119 (+) | |
| *Branchiostoma floridae (Bfl)* | *drd1,5* | GCA_000003815.1, contig GG666484.1, range 3478069-3479178 (-) | |
| *Callorhinchus milii (Cm)* | *drd1* | GeneID:103187244 | |
| *Mus musculus (Mm)* | *drd1a* | GeneID:13488 | |
| *Petromyzon marinus (Pm)* | *drd1* | GCA_002833325.1, contig PIZI01000015.1, range 6404870-6406297 (-) | |
| *Rhincodon typus (Rt)* | *drd1* | GeneID:109937715 | |
| | | | |
| *Danio rerio (Dr)* | *drd2* | GeneID:282557 | |
| *Mus musculus (Mm)* | *drd2* | GRCm38.p4, contig NC_000075.6, range 49395616-49407091 (+) | |
| *Danio rerio (Dr)* | *drd3* | GRCz11, contig NC_007136.7, range 4708538-4732991 (-) | |
| *Mus musculus (Mm)* | *drd3* | GeneID:13490 | |
| | | | |
| *Branchiostoma floridae (Bfl)* | *drd4* | GeneID:7249502 | |
| *Danio rerio (Dr)* | *drd4a* | GeneID:503564 | |
| *Mus musculus (Mm)* | *drd4* | GeneID:13491 | |
| *Leucoraja erinacea (Le)* | *drd5* | WGS_VDB://AESE01, contig AESE011486231.1, range 406-1725 (+) | |
| *Mus musculus (Mm)* | *drd5* | GeneID:13492 | Synonym drd1b |
| *Rhincodon typus (Rt)* | *drd5* | GeneID:109916214 | Annotated as drd1-like |
| **Histaminergic receptors** | | | |
| *Danio rerio (Dr)* | *hrh1* | GeneID:735302 | |
| *Mus musculus (Mm)* | *hrh1* | GeneID:15465 | |
| | | | |
| *Asymmetron lucayanum (Alu)* | *hrh2* | GCA_001663935.1, contig LZCU01123976.1, range 103-1209 (-) | |
| *Branchiostoma floridae (Bfl)* | *hrh2* | GCA_000003815.1, contig GG666476.1, range 1325027-1326103 (+) | |
| *Danio rerio (Dr)* | *hrh2* | GeneID:25461 | |
| *Danio rerio (Dr)* | *hrh2b* | GeneID:100005590 | |
| *Leucoraja erinacea (Le)* | *hrh2* | WGS_VDB://AESE01, contig AESE010707911.1, range 742-1827 (-) | |
| *Rattus norvegicus (Rat)* | *hrh2* | GeneID:25461 | |
| *Rhincodon typus (Rt)* | *hrh2* | GeneID:109918887 | |
| | | | |
| *Danio rerio (Dr)* | *hrh3* | GeneID:561773 | |
| *Rhincodon typus (Rt)* | *hrh3* | GeneID:109927117 | |
| *Danio rerio (Dr)* | *hrh4* | Gene ID:100334962 | |
| **Muscarinergic acetylcholine receptors** | | | |
| *Branchiostoma belcheri* (Bbe) | *chrm* | GeneID:109479226 | |
| *Ciona intestinalis (Cin)* | *chrm1-5* | GeneID:100182166 | |
| *Ciona savignyi (Csa)* | *chrm1-5* | GCA_000149265.2, contig CH001357.1, range 38054-39553 (-) | |
| *Ciona savignyi (Csa)* | *chrm* | GCA_000149265.1, contig CH002155.1, range 846677-855548 (+) | |
| *Mus musculus (Mm)* | *chrm1* | ENSMUSG00000032773 | |
| | | | |
| *Danio rerio (Dr)* | *chrm2a* | GeneID:352938 | |
| *Danio rerio (Dr)* | *chrm3b* | GeneID:100149598 | |
| *Mus musculus (Mm)* | *chrm4* | GeneID:12672 | |
| *Petromyzon marinus (Pm)* | *chrm* | GCA_002833325.1, contig PIZI01000025.1, range 2511456-2513136 (-) | |
| *Rhincodon typus (Rt)* | chrm | GeneID:109911563 | |
| **Serotonergic receptors** | | | |
| *Callorhinchus milii (Cm)* | *htr1b* | GeneID:103175228 | |
| *Callorhinchus milii (Cm)* | *htr1d* | GeneID:103179607 | |
| *Danio rerio (Dr)* | *htr1a* | GeneID:100001828 | |
| *Danio rerio (Dr)* | *htr1fb* | GeneID:100004819 | |
| *Leucoraja erinacea (Le)* | *htr1* | WGS_VDB://AESE01, contig AESE011561756.1, range 155-1153 (+) | |
| *Mus musculus (Mm)* | *htr1b* | GeneID:319405 | |
| *Petromyzon marinus (Pm)* | *htr1a* | GCA_002833325.1, contig PIZI01000013.1, range 14953024-14954282 (+) | |
| *Rhincodon typus (Rt)* | *htr1* | GeneID:109924543 | |
| *Rhincodon typus (Rt)* | *htr1b* | GeneID:109927187 | |
| | | | |
| *Ciona savignyi (Csa)* | *htr2b* | GCA_000149265.1, contig CH003080.1, range 117045-118924 (-) | |
| *Danio rerio (Dr)* | *htr2b* | GeneID:751784 | |
| *Rattus norvegicus (Rat)* | *htr2a* | GeneID:29595 | |
| | | | |
| *Anguilla japonica (Aj)* | *htr4-like* | GCA_003597225.1, contig BEWY01000739.1, range 143720-158412 (+) | |
| *Asymmetron lucayanum (Alu)* | *htr4* | GCA_001663935.1, contigs LZCU01069842.1, LZCU01138971.1, ranges 2645-4248, 3-464 (+) | |
| *Branchiostoma belcheri (Bbe)* | *htr4* | GeneID:109485254 | |
| *Branchiostoma floridae (Bfl)* | *htr4* | GeneID:118414956 | |
| *Branchiostoma lanceolatum (Bla)* | *htr4* | GCA_900088365.1, contig FLLO01000036.1, range 925959-928070 (+) | |
| *Callorhinchus milii (Cm)* | *htr4* | GeneID:103191306 | |
| *Callorhinchus milii (Cm)* | *htr4-like* | GeneID:103185614 | |
| *Danio rerio (Dr)* | *htr4* | Gene ID:101882850, chromosome 14 | |
| *Danio rerio (Dr)* | *htr4-like* | GeneID:559089 | |
| *Gasterosteus aculeatus (Ga)* | *htr4* | GCA_000180675.1, contig AANH01006599.1, range 101622-116517 (-) | |
| *Gasterosteus aculeatus (Ga)* | *htr4-like* | GCA_000180675.1, contig AANH01004594.1, range 57696-60366 (-) | |
| *Lepisosteus oculatus (Lo)* | *htr4* | LepOcu1, LG6, contig NC_023184.1, range 37736330-37712459 (-) | |
| *Lepisosteus oculatus (Lo)* | *htr4-like* | LepOcu1, LG2, contig NC_023180.1, range 51326623-51338351 (+) | |
| *Lethenteron camtschaticum (Lec)* | *htr4* | GCA_000466285.1, contig KE993680.1, range 1331383-1338029 (-) | |
| *Leucoraja erinacea (Le)* | *htr4* | WGS_VDB://AESE01, contig AESE010074862.1;AESE011513946.1 33-236;397-960 (+-) | |
| *Mus musculus (Mm)* | *htr4* | GeneID:15562 | |
| *Nanorana parkeri (Np)* | *htr4* | GeneID:108784291 | |
| *Petromyzon marinus (Pm)* | *htr4* | XP_032806628.1 | |
| *Ptychodera flava (PtFl)* | *htr4* | GCA_001465055.1, contig LD352455.1, range 57543-56371 (-) | |
| *Rhincodon typus (Rt)* | *htr4* | GeneID:109927282 | |
| *Saccoglossus kowalevskii (SaKo)* | *htr4* | GeneID:100374682 | |
| *Xenopus tropicalis (Xt)* | *htr4* | GeneID:100493952, chromosome 3 | |
| *Xenopus laevis (Xl)* | *htr4.S* | GeneID:496394 | |
| | | | |
| *Ciona intestinalis (Cin)* | *htr5* | GeneID:104265465 | |
| *Ciona savignyi (Csa)* | *htr5* | GCA_000149265.1, contig CH003386.1, range 620733-623491 (-) | |
| *Danio rerio (Dr)* | *htr5ab* | GeneID:368475 | |
| *Lethenteron camtschaticum (Lec)* | *htr5* | GCA_000466285.1, contig KE993731.1, range 1661553-1662305 (-) | |
| *Mus musculus (Mm)* | *htr5a* | GeneID:15563 | |
| | | | |
| *Danio rerio (Dr)* | *htr6* | GeneID:568269 | |
| *Mus musculus (Mm)* | *htr6* | GeneID:15565 | |
| *Rhincodon typus (Rt)* | *htr6* | GeneID:109917804 | |
| | | | |
| *Ciona intestinalis (Cin)* | *htr7* | GCF_000224145.3, NC_020173.2, range 2187887-2192745 (-) | |
| *Ciona savignyi (Csa)* | *htr7* | GCA_000149265.1, contig CH000164.1, range 44580-52046 (-) | |
| *Danio rerio (Dr)* | *htr7* | GeneID:100536080 | |
| *Mus musculus (Mm)* | *htr7* | GeneID:15566 | |
| **Unclassified aminergic receptors (AmR)** | | | |
| *Ciona intestinalis (Cin)* | *AmR* | GeneID:101242922 | |
| *Ciona savignyi (Csa)* | *AmR1* | GCA_000149265.1, contig CH002901.1, range 1249970-1251418 (-) | |
| *Ciona savignyi (Csa)* | *AmR2* | GCA_000149265.1, contig CH000120.1, range 16409-17671 (-) | |

## SUPPLEMENTARY INFORMATION

SI Table 2: Intron position in *htr4, taar* and *tarl* genes

# Olfactory function in the trace amine-associated receptor family (TAARs) evolved twice independently

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**SI Table 2** MSA shows differentially conserved intron borders in chordate and vertebrate htr4

```
Sako-htr4  MESGITSSTDAIS-----YHSFALDKTSRVYVLEVFTDTGEPIVGAVNDNSTGLSGNVL-
PtFl-htr4  M------STNNIHGLPYVFESSDTPATSAVFVVELETTRQPFLITNDNASTWAVSGGVQP
alu-htr4   M--------------TTIVTMSGYNTTQALGIPGTDLTRTVQPVTNWTNGSLGCTETYIG
bfl-htr4   M--------------TTIVSMSDYNTTQALAVPETHHVRTVQPGANGTNGSSGCTEAYLG
Bla-htr4   M--------------TTIVSMSDFNTTQALVVPETHPLRTAPPVTNHTNGSTGCTESYLG
Pm-htr4    --------------------MYGNNTTF-------------------NNDE---------
Rt-htr4    --------------------MDEADVNE-------------------STSD---GEPHEI
Dr-htr4    MQGCEFPQEDSCHGTGQMPEMEEVDTNE-------------------SN-----------
Mm-htr4    --------------------MDKLDANV-------------------SSNE---------
Dr-tarl1   --------------------ME--NTSE------------------WSNNSLDSDFEACA
Pm-tarl1a  --------------------MDPPSSSV------------AAPSSPASSNSVQGSFSCPG
Rt-taarIId --------------------MN-LSDHE--------NSDNVQYCFEFVNTS------CAR
Dr-taar13c --------------------MD-LSSQE---------YDPSQFCFPAVNNS------CLK


Sako-htr4  -QYGLAERIIIGFVLTVIIILTIAGNILVCASIFIFPSLRTL-TNYFVFSLAIADILVAC
PtFl-htr4  GSFNVAERIVIGFILSLIILTTIVGNILVCTSIIIFPSLRTL-TNYFVFSLAIADVLVAC
alu-htr4   PQYSLTVQVLLSSFLALVILLTIVGNILVISTVALFRSLRSL-TNYFVVSLAVADLLVGV
bfl-htr4   PQYSLEIQVLLSSFLALVILLTIVGNILVISTVALFRSLRSL-TNYFVVSLAVADLLVGV
Bla-htr4   PQYSLVIQILLSCFLALVILLTIVGNILVISTVALFRSLRSL-TNYFVVSLAVADLLVGV
Pm-htr4    -TSSQAEKYILAGIFSIIIAVTILGNLLVVVAVCKDRHLRKIKTNYFIVSLAVADLLVAI
Rt-htr4    PGFSILQKTVLITFLSAIMVMTILGNLLVMVAVCKDRQLRKIKTNYFIVSLAFADLLVSV
Dr-htr4    ---GLAKRVALISFLSLVMLMSVLGNLLVMVAVCKDRQLRKIKTNYFIVSLAFADLLVSV
Mm-htr4    -GFRSVEKVVLLTFLAVVILMAILGNLLVMVAVCRDRQLRKIKTNYFIVSLAFADLLVSV
Dr-tarl1   TLRSFGSRVALYLFIITGILCTVVGNFLVVLAIAYFKQLQCP-TNSFVMSLAVADFLVGL
Pm-tarl1a  SALSSAQRAAWLAMMSVAMASAVLGNLLVVASVLHFRRLQTR-TNAFTASLAVVDLLVGL
Rt-taarIId VTRSIAINVALYIFIITSILITIFGNLVVIISVLHFKQLQTP-TNFLLSSLAVVDFLVGF
Dr-taar13c GTHHVSTQTVVYLILASAMTVTVLGNSVVIISIAHFKQLQTP-TNILVMSLALADLLLGL
                                   **  *         *    **    ***  * *

Sako-htr4  LVMTFSTINVVTETWIYGDTFCLIFISFDISFCTASIMHLSCIAFDRYSAI-CNPFQYPL
PtFl-htr4  LVMAISTIYIVTETWMYGDTFCLVFISFDIAFCTASIMHLSCIAYDRYSAI-CNPFQYPI
alu-htr4   IVMTLGTQYEVSGRWRHGEIFCLVFTSMDVSLTTCSIMHLSCIAFDRYYAI-CHPFKYPT
bfl-htr4   IVMTLGTQYEVSGRWRHGEIFCLIFTSMDISLTTCSIMHLSCIAFDRYYAI-CHPFKYPT
Bla-htr4   IVMTLGTQYEVSGRWRHGEIFCLVFTSMDISLTTCSIMHLSCIAFDRYYAI-CHPFKYPT
Pm-htr4    LVMPFGAVERVQNDWPYGDKFCIIRTSFDVMFTTASIMHLCCIALDRFYAICCKPLVYQN
Rt-htr4    MVMPFGAIELIQQNWIYGDRFCLVRTSLDVLLTTASILHLCCISLDRYYAICCQPLVYRN
Dr-htr4    LVMPFGAIELIHQNWIYGETFCLVRTSLDVLLTTASILHLCCISLDRYYAICCQPLVYRN
Mm-htr4    LVMPFGAIELVQDIWAYGEMFCLVRTSLDVLLTTASIFHLCCISLDRYYAICCQPLVYRN
Dr-tarl1   VVMPYSMVRTVEGCWYFGPTFCHLHSSLDVMLCTASIFHLSCIAFDRYYAV-CNPLVYSF
Pm-tarl1a  LVMPFKMTRSAYGCWFYGTAFCAAHTCLDIALCTASILHLACIAFDRHVAV-CDPLRYAQ
Rt-taarIId IVLPYSMVRSVEKCWYFGEVFCKIHSITEIVLTVVSIYTLCFIAIDRYYAM-CDPLFYSV
Dr-taar13c VVMPFSMIRSVDGCWYYGETFCLLHTGFDLFLTSVSIFHLIFIAVDRHQAV-CFPLQYPT
            *            *  *  **             **  *  *  **  *  * *  *

Sako-htr4  KMTSRRVTIMLASCWVVPMFISFIPILLQWNTIGIENVIADVKNF--AGPYSCIFLVNKP
PtFl-htr4  KMTSRRVAVMLAACWVVPMLISFIPILLGWNTLGIENVIAEVKQH--TGPNSCVFLVNRP
alu-htr4   KMTHRKMRVMIAMCWVVPVIIAWVPIMNGWNTLNIAXXXXXXXXX--XXXXXXXXXXXXX
bfl-htr4   KMSHRKMVLMIAMCWVVPVIMAYVPIMNRWNTIGIEPVVEDTKCA--LGPESCVFLVNKE
Bla-htr4   KMSHRKMVLMIAMCWVVPVIMAYVPIMNRWNTIGIEPVVEDTKCE--LGPDSCVFLVNKE
Pm-htr4    KMTPLRVGLMLGACWVVPSLISFIPIANGWNIIGIEQQLELRGQAKEANQTHCIFMVNKV
Rt-htr4    KMTPLRITIMLGGCWIIPSFISFLPIMQGWNIIGIQELVEERKSSNDTNITKCVFMVNKP
Dr-htr4    KMTPLRVTLMIGGCWIIPTVISFLPIMQGWNSIGIKDLIDKRKIS--GNSTVCVFMVNKP
Mm-htr4    KMTPLRIALMLGGCWVLPMFISFLPIMQGWNNIGIVDVIEKRKFSHNSNSTWCVFMVNKP
Dr-tarl1   KMSRKRVGLLIVVCWAIPFLISFGPILFGLHKLGVDIPLPE---------NMCVFLVNRI
Pm-tarl1a  RVTARHVAAMVALSWCCGAVISVVTVSLGWNVVGVPDEVVAA-----SCADSCDFLLGAP
Rt-taarIId KITLPVTVMTIILIWLFAVFYGLSVFLLDFSKKSVDDYVAVR-----SCEGSCI-AYHKF
Dr-taar13c RITIPVAWVMVMISWSMAAFYSYGVVYSKANLEGLEEYIASV-----YCMGGCTLYFNAL
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Sako-htr4  YAVIASTIAFYMPCILMATAYFFIFRAARKQAQQIKSL-ERATMNWNN-TRNGPGDGH--
PtFl-htr4  YAAVASTIAFYIPCILMASAYLFIFRAARKQAAQIKSL-ERATANWNN-ARNGESGGR--
alu-htr4   XXXXXXXXXXXXXAVLMILAYYQVYRVARRQMQRIISV-EGAAPNNEN------------
bfl-htr4   FSLIASTLSFYLPAVMMTLAYYQVYRAARRQMQQIISL-ERSMNNNEN------------
Bla-htr4   FSLIASTLSFYLPAIMMTLAYYQVYRAARRQMQQIISL-ERAMNNNEN------------
Pm-htr4    YAVACSLVAFYIPLGLMAAAYQRIYVTARAHARQIGSL-QRAVSKDTT-GDEVTMVTSGA
Rt-htr4    FAITCSVVAFYVPLLLMVLAYQRIYVTAREHARQIEML-KRAGTSTDS-GQQ--------
Dr-htr4    YALTCSVVAFYLPLVLMVLAYQRIYVTAREHARQISML-QRAGGAGNA--DS--------
Mm-htr4    YAITCSVVAFYIPFLLMVLAYYRIYVTAKEHAQQIQML-QRAGATSESRPQP--------
Dr-tarl1   YAVMASLVAFYLPMVTMLVAYWKIYKAAKRQAMQISAM-EAQMAAGVG-KDS--------
Pm-tarl1a  YAVGSSVCSFFGPAAFVVVAYARILREARRQGRAIACEQEKQQQQNEDQGRQEDGVGEGG
Rt-taarIId EGHIDALIVFFIPIFIILGIYVKIFFVTRKRCRKIENMPNDSHCTEEN------------
Dr-taar13c WSVLDTLLTFFLPCSVMVGLYARIFVVAKKHIKSIT---EANQNENEN------------
                               *             *

Sako-htr4  ---------------PHHHGRRVSLAAEKKAAKTLGIIMGCFTICWCPFFVFNIVDPFCD
PtFl-htr4  --------------------GSVSLAAEKKAAKTLGIIMGCFTVCWCPFFVLNIIDPFCD
alu-htr4   ------------------------TRREKKAAKTLGIIMGCFLVCWMPFFVTNIIDPLCG
bfl-htr4   ------------------------MRREKKAAKTLGIIMGCFLVCWMPFFVANIVEPLCG
Bla-htr4   ------------------------MRREKKAAKTLGIIMGCFLVCWMPFFVANIVEPLCG
Pm-htr4    ASPLRAQQLVPVAQATMVQTQSTRFRHETKAAKTLAIIMGCFCLCWAPFFINNVIDPFVN
Rt-htr4    ----------------ADHSGNHRMKTETKAAKTLCIIMGCFCLCWAPFFITNIVDPFIN
Dr-htr4    ----------------ADHQRNHRMRTETKAAKTLCIIMGCFCLCWAPFFITNVVDPFID
Mm-htr4    ----------------ADQHSTHRMRTETKAAKTLCVIMGCFCFCWAPFFVTNIVDPFID
Dr-tarl1   ---------------SKKQKHRNSIRRERKAAKTLGIIMGVFLLFWLPFFTVNIIDPFIE
Pm-tarl1a  RGGARGEMTAPAGKATQAVGRAADAKSERNATKMLSIVVGIFLASWLPFFLMNVSDPLLG
Rt-taarIId -------------------NVTIMHKKDQIVVRKQDILIGIFTFSWLPFYVNSILNPYFD
Dr-taar13c -------------------VFKNPRRSERKAAKTLGIVVGAFILCWLPFFINSLVDPYIN
                                                  * *   * **       *

Sako-htr4  FCIDPG---AWPPVTWLGYINSMLNPLLYAFFNRSFRRAFIRLLRC--------------
PtFl-htr4  FCISPK---VWPPITWLGYTNSMLNPILYAFFNRTFRRAFSRLLRC--------------
alu-htr4   YCIAQSCELCLKFFLWLGYINSTLNPMIYAFFNRSFRRAFKRILSCS-------------
bfl-htr4   YCITRSCDLCLKFFLWLGYINSTLNPMIYAFFNRSFRRAFKRILSCS-------------
Bla-htr4   YCITRSCALCSKFFLWLGYINSTLNPMIYAFFNRSFRRAFKRILSCS-------------
Pm-htr4    YDTPQQ---LWDAWLWLGYANSALNPLLYAFLNRSFRRAFLAILCCWDARYRRSSFSSHS
Rt-htr4    YSVPEQ---LWTACLWLGYINSGFNPFLYAYLNKSFRRAFLRILCCGD-RYRRSSLLGQT
Dr-htr4    YSVPEQ---LWAACLWLGYINSMLNPILYAFLNKSFRRAFLIILCCGHKRYRRPSILGPG
Mm-htr4    YTVPEQ---VWTAFLWLGYINSGLNPFLYAFLNKSFRRAFLIILCCDDERYKRPPILGQT
Dr-tarl1   YGTAVV---IWDVFLWLGYINSSLNPFLYGFFNRSFRRAFLMIMGCR-------------
Pm-tarl1a  YSIDPR---AWEAVTWLGYANSAANPVIYGIFSPNFRAAFRVIAAR--------------
Rt-taarIId FLIPPV---LDSVFAWFGFFNSTLNPLLYAFLYPWFRKSLKLILSC--------------
Dr-taar13c FSTPYA---LFDAFGWLGYTNSTLNPIIYGLFYPWFRKTLSLIVTL--------------
                          * *  **  **  *      **

Sako-htr4  -----HVCKGTTAEFDPTISSRER-------------------------
PtFl-htr4  -----HVCKGSAAEFDPTITSHER-RS----------------------
alu-htr4   -----SCCDLDKRDFDPAVSTALQGRTRSRRRPNGDVVN--------NS
bfl-htr4   -----SCCDLDNRDFDPAVSTALQRRTSTRHQ-NGEAVN--------NT
Bla-htr4   -----SCCDVDNRDFDPAVSTALQGRSSRRHQ-NGEVVN--------NT
Pm-htr4    VRYS-VSTNGSAVQPVPS--ARVRARARLPSRPRTRAAAPAVSKAPSPV
Rt-htr4    IPCSATTINGSAHVLR---------------------------------
Dr-htr4    TTCTATQINGSTHVLKYAVLH----NGNHNEQEKLSIQNDTESQESCF-
Mm-htr4    VPCSTTTINGSTHVLRDTVEC----GGQWESRCHLTATSPLVAAQPSDT
Dr-tarl1   -----ICLHGSAQGMDLSHSKRDG---------NERTDN----------
Pm-tarl1a  -----SAFRAGSRDVQLG--F----------------------------
Rt-taarIId -----QIFNTDPSTVNFLSE-----------------------------
Dr-taar13c -----RIFEPNSSDINLFTV-----------------------------
```

## SI Table 2 Multiple sequence alignment (MSA) of 9 HTR4, 2 TARL and 2 TAAR sequences.

Sequences are given by species abbreviation and gene name, for full species names and further details see SI Table 1. Introns were predicted with Genewise 2 (Birney et al., 2004). Note the differential conservation of intron borders in **lancelet** (alu, bfl, bla) vs. **vertebrate** (Pm, Rt, Dr, Mm) *htr4*. The MSA was generated using MAFFT v7.471, E-INS-i setting, (Katoh and Standley, 2013), and sequence positions with over 85% gaps were removed using Gapstreeze (http://hcv.lanl.gov/content/se- quence/GAPSTREEZE/gap.html).

## References

Birney E., Clamp, M. & Durbin, R. (2004) GeneWise and Genomewise. *Genome Research* **14**, 988–995.

Katoh K. & Standley D.M. (2013) MAFFT Multiple Sequence Alignment Software Version 7: Improvements in Performance and Usability. *Molecular Biology and Evolution* **30**, 772–780.