

Additional file 3, content:

Part 1	Ray-finned fish ORA protein sequences.	2
Part 2	African coelacanth V1R protein sequences.	14
Part 3	Elephant shark ORA protein sequences.	17
Part 4	Teleost and African coelacanth T2R protein sequences.	18
Part 5	Tree file in Newick format for sequences shown in Figure 1.	21
Part 6	References	24

All parts: Species are indicated by the initials of their Latin names, for full names (Latin and vernacular) see Table 1.

Part 1 Ray-finned fish ORA protein sequences.

Novel sequences reported in this study are marked **cyan**, corrected sequences are marked **yellow**. Published sequences for zebrafish, *Danio rerio*, stickleback, *Gasterosteus aculeatus*, Lake Victoria cichlid, *Haplochromis chilotes*, medaka, *Oryzias latipes*, Nile tilapia, *Oreochromis niloticus*, Atlantic salmon, *Salmo salar*, spotted green pufferfish, *Tetraodon nigroviridis*, Japanese pufferfish, *Takifugu rubripes*, and rockfish, *Sebastus caurinus* and *Sebastus ruberrimus* are from [1-5] and marked **gray**.

>Am-ORA1

MDLCITIKGVSFLLQTGLGIMGNMLVLAAYGHIALVEPRLQPVQIMAHLAFANLMMLLLTRGVPQTMTVFGLRHL
LND SGCKVVIYTYRITRALSVCFTCMLSVFQALTIAPAGGPRLARLKARLPQLVAPTFAGLWLLNMAVCIAAPFF
SVAPRNGTVPPFTLNLGFCHVDFRDNLSYVINGAAVSARDFSFVGLMLGSSGYILVLLHKHSRQVRAIRRSQGG
MEMRAAKTVVMLVVLVYAVFFGIDNVIWIYMLTVAQVPAVVADMRVFFSSCYATLSPFLMISSNKKLKERMVCAAG
GEQKQDAAEDTDKTNIK

>Fh-ORA1

MDLCVTIKGVSFLLQTGMGILGNGVLLAYASIICTEPKLLPVD MILCHLAFANLMMLLLTRCVPQTMTVFGLKGL
LNDPGCKVVIYAYRVGRALSVCITCMLSVFQAATIAPAGPRLSRLKPTLPSLVLP TFAMLWFLNMAICVAAPLFS
MAPRNGTVPAFTLNLGFCHVDFRDNLSYVNVGVAVSGRDFAFVALMVGSSGYILLLLHRHSEQVRGIRRSHGSGA
ETRAAKTVVTLVVLVYVVFVGIDNVIWIYMLTVSKVSPVVADMRVFFSSCYASLSPYFIISSNKKVKRKIVCAA EH
DQPLVDTQESNEK

>Gm-ORA1

MDLCVTIKGVSFLLQTGLGV LGNALVLLAYVHIAHGADHKLLPTDLILCHLAFSNLVLLLTRCVPQTMTVFGLHD
LLDDAGCKVVIYLYRITRALSVCITCMLSVFQAATLAPDAPRLKAALPALVLP SFAGLWLLNMAVCIAAPFFSIA
PRNGTVPAFTLNLGFCHVDFRDYLSYVINGVAVSVRDFAFVLLMLLSSGYILLILHRHSRQVRSMRRGAAQGVET
RAAKTVVTLVVLVYAVFFGIDNVIWIYMLTVAKVSPVVADMRVFFSSSYAFLSPYFIISSNKKRIKGLVCAVEQQQ
SPVETQTSNEK

>Pf-ORA1

MDLCVTIKGVSFLLQTGLGILGNVVLLAYASIICTEPKLLPVD MILCHLAFANLMMLLLTRCVPQTMTVFGLKDL
LNDPGCKVVIYAYRIGRALSVCITCMLSVFQAMTIAPAGPRLSKLKPVLP SLVLP TFALWLLNMAICIAAPFFS
MAPRNGTIPAFSTLNLGFCHVDFRDNMSYVINGVAVSGRDFAFVALMLGSSGYILLLLHRHSEQVKGIRRSHGSRA
ETRAAKTVVILVVLVYVVFVGIDNVIWIYMLTVSKVSPVVADMRVFFSSCYASLSPFFIISSNKKVKRKIVCAA EH
DQPLVDTQESNEK

>Xm-ORA1

MDLCVTIKGVSFLLQTGLGILGNAVLLAYASIICTEPKLLPVD MILCHLAFANLMMLLLTRCVPQTMTVFGLKDL
LNDPGCKAVIYAYRIGRALSVCITCMLSVFQAMTIAPAGPKLSKLKPMPLSLVLP TFALWLLNMAICIAAPFFS
MAPRNGTIPAFSTLNLGFCHVDFRDNMSYVINGVAVSGRDFAFVALMLGSSGYILLLLHRHSEQVKGIRRSHGSRS
ETRAAKIVVTLVVLVYVVFVGIDNVIWIYMLTVSKVSPVVADMRVFFSSCYASLSPYFIISSNKKVKRKIVCVA EH
DQPLVDTQESNEK

>Dr-ORA1

MDLCVTIKGVSFLLQAGLGILANALVLLAYAHIRLAEARLQPVDA I LCHLALVDLLLLL TRGVPQTMTVF GMRNL
LDDTGCKVVIYTYRIARALSVCITCMLSVFQAVTVAPAAGPLL SGVKARLPQLLAPTFAALWF INMAVCIAAPFF
SVAPRNGTVPPFTLNLGFCHVDFHDNLSYVLNGVAVSVRDFAFVGAM LASSGFILLLLHRHRRQVRVRRSQGST
METRAARTVLMVLVILYSVFFGIDNVIWIYMLTVAQVPPVVAHMRVFFSSCYASLSPFLI I SSNRKLKARMVCATS
EQERQAEDGKNSSGKN

>Ga-ORA1

MDLCVTIKGVSFLLQTGMGILGNTVVLLAYAQLIYAEPKLLPVD MILCHLAFANLMMLLLTRCVPQTMSVFGLRDL
LGDPGCKVVIYAYRIGRALSVCVTCLMSVFQAVTLAPAGPRLSRLKPALPSLVLP TSAGLWLLNMAVCVAAPLFS

MAPRNGTAPAFITLNLGFCHVDFRDNL SYVINGVAVSVRDFAFVALMLGSSGYILLLLHRHSRRVRGIRRSQGGGA
ETRAAKTVITLVVLYAVXFGIDNAIWIYMLTVAKVSPVVADMRVFFSSCYASLSPYFIISSNKKVKAKILCAAEQ
DQPSVDNQETSDK

>Hc-ORA1

MDLCVTIKGVSFLLQTGMGVLGNTVVLLAYTHIVCTGPKLLPVDMLCHLAFITNLLLLLTRSVPPSMTVFGLKAL
LNDPGCKVVIYAYRIGRALSVCITCMLSVFQAVTITPTGPYLSRLKPSLPSLVIPTFAGLWLFNMAICISTPLFS
MAPRNGTVSAFTLNLGFCLVDFRDNL SYVINGVAISGRDFAFVALMVGSSGYILLLLHRHSHQMKGIHRSQGGGA
ETRAAKAVLTLVLYVVFVFGIENVIWIYMLTVEKVSPVVADMRVFFSSCYASLSPYFIISSNKKVKAKIVCTAEH
EQPSADTQDSNDK

>Ol-ORA1

MDLCVTIKGVSFLLQTGLGILGNSVLLVYSHIMCTGPKLLPVDMLCHLAFANLILLLLTRCVPQTMTVFGLKDL
LNDPGCKVVIYAYRIGRALSVCITCMLSVFQAVTIAPAGPFLSRLKLALSSLVFPTFVGLWLLNMAVCIAAPFFS
MAPRNGTVLPFTLNLGFCHVDFRDNL SYVINGVAVSVRDFAFVALMVGSSGYILLLLHRHSHQVRKIRRSHSSGA
ETRAAKTVLILVILYVVFVFGIDNVIWIYMLTVSNVSPVVADMRVFFSSCYASLSPYFIISSNKKVKRKIVCAAEQ
DQPSVETQESNDK

>On-ORA1

MDLCVTIKGVSFLLQTGMGILGNTVVLLAYTHIVCTGPKLLPVDMLCHLAFANLILLLLTRCVPQTMTVFGLKDL
LNDPGCKVVIYAYRIGRALSVCITCMLSVFQAVTITPTGPYLSRLKPSLPSLVLPTFAGLWLFNMAICIAAPLFS
MAPRNGTVPAFTLNLGFCHVDFRDNL SYVINGVAVSGRDFAFVALMVGSSGYILLLLHRHSHQVKGIRRSQGGGA
ETRAAKTVLTLVLYVVFVFGIDNVIWIYMLTVAKVSPVVADMRVFFSSCYASLSPYFIISSNKKVKAKIVCAAEH
EQPSADTQDSNDK

>Ss-ORA1

MLDLCVTIKGMSFLLQTGLGFLGNTLVLLAYTQVVCSECRLOPVDIILCQLAFVDLILILTRCIPQTMTVFGLRD
LLNDPGCKVVVYSYRIARALSVCITCMLSVFQAVTIAPAGGPCLSRKLAQLPSLIVPTIAGLWLFNMAVCLAAPL
FSIAPRNGTVPAFTLNLGFCHVDFRDRLSYKINGVVVSTRDFAFVGLMLWSSGYILLLLHRHSHQVRSIRRSSQG
GGAETRAAKTVITLVVLYAVFFGIDNIIWVYMLTVDKVSPVVNDMRVFFSCCYACLSPFFIISSNKKVKSKLVCV
AADQEOPSVNTQDSNDKM

>Sc-ORA1

CITCMLSVFQAVTIAPAGPRLSRLKPALPSLVLPTFALLWFLNMAVCIAAPFFSMAPRNGTVPAFTLNLGFCHVD
SRDHL SYVINGVAVSTRDFAFVALMLGSSGYILLLLHRHSRQVRGIRRSQGGGAETRAAKTVITLVVLYVVFVFGI
DNVIWIYMLTVPQVP

>Sr-ORA1

CITCMLSVFQAVTIDPAGPRLSRLKPALPSLVLPTFALLWFLNMAVCIAAPFFSMAPRNGTVPAFTLNLGFCHVD
FRDHL SYVINGVAVSTRDFAFVALMLGSSGYILLLLHRHSRQVRGIRRSQGGGAETRAAKTVITLVVLYVVFVFGI
DNVIWIYMLTVPQV

>Lo-ORA1

MDLCITIKGVSFLLQTGLGILGNLLVLLAYAHACSDGRVQPVDKILCHLAFANLILLLLTRCVPQTMTVFGLKDL
LNDSGCKAVIYAYRIARALSVCITSMLSVFQSI I IAPASSRWVGLKVRVSQLLFPSFAALWLINMAVCIAAPFFS
IAPRNGTVPEFTLNLGFCHVDFRDSL SY I IINGVAVSGRDFIFVGLMVCSSGYILLLLHRHGKQVRQIRSPDQHSS
RNAAETRAAKTVVTLVTLYVVFVFGIDNIIWIYMLTVAQVPPVIADMRVFFSSCYASLSPFLMITSNKKIKNKLSC
AAANPEQMSLNTEDSTRI

>Am-ORA2

MDLYFLTRGLLYLFLPVFGVPGNCAVIWAFLLALRQEGTLLPADAIVLHLACANLLVVSCRCVFEVFANFQVFNG
FNDPGCKGIYFIYRTFRGLSIWLTFTLSSYQCLSIAPPGSHWATLRS LFGRYLWLIIFLLWIINTSASAPTLVFA
VAARND SKLLENSINIQCFINFPSVFAKDANGALQVVRDVIPMSLMTTASF I IILVFLYRHSRQVSNLRS GTGTG
GGGASAERRAAISVVVLVTFFYVLMYGVDNGLWVYTLTVKQTLSSALISDLRIFFSMLFAAISPI I IITNMKVKK
QLL

>Fh-ORA2

MRGNHCLSGTRSASELPAFLPSAMP SDKLVRGWLFLSLAVVGIPGNIAVIVAFLLILQECFLLAADAIVLHLAF

ANLLVVLVRCILLEALASFHLANVFGDVGCKAVIFIYRTSRALSIWLTFLLSAYQCLSIAPPGSSWASARVLVAQN
LPAVFFILWVLHTSMSVGVAVLFSVSSRNYTAMTTSAVNAEFCYVNFPSDVLKEAYGAIQVSRDVVPMALMTLTS
VILVLLYKHSQHLKGLRGAGSAGAGSCGAEQRAAKVVVVLVTYVVLVYGVNDGFWVYTLTVRNTLSSSLISDLRV
FFASLYAALSPLVIIASNRKVNRLRCVAQERPLLGKTARLRSI

>Gm-ORA2

MPSEELIRAMLYLTTLTVVGVPGNLAVIWAFLALHQERRLLPADTILLHLASVNLLVVGVRCLLETLASFRLASV
FGDTGCKSVIFVYRTARSLSIWLTFLVLSAYQCLSIAPPGSRWAAARALAARYMAAIFLALWLNTCMSSAAVLFS
VGAGNGNGSSSLGSNGINVQFCVVRFPTRLKSDANGAVQVARDVVPMLMATASLVILVFLYRHSRQVKGLRSGG
GGGRDGAERRAAKAVVALVTLYVGLYGVNDGLWVHTLTVRRTMGSSSLVSDLRIFSSSLYAALSPAVIIATNRKVQ
RRLRCGRGEKHRGESATEATAVSTM

>Pf-ORA2

MIFYLYLLFSLSAGMPSNVNVRGMLFSLTVVGVPGNMAVIVAFLLLVQLQESWLLAADAIVLHLSCTNLLVVLVR
CLMETLASFHLANVFGDVGCKAVIFIYRTSRALSIWLTFLLSAYQCLSIAPPGSKWASVRILVAQNLPVFLFLW
VLHTSTSAGAILFSVSSKNGTAVTTSAVNLEFCYVNFPSDIIKEVYGAIQVSRDVVPMALMTLTSIIILVLLYKH
SQHLKGLRGAGHAGSGTCGSKQRAAKVVVVLVTIYVVLVYGVNDGLWVYTLTVRHTMSSSLISDLRVFFASLYAAL
SPLVIIASNRKVNSRLRCVAQEKPLLGKTAHLRSI

>Xm-ORA2

MPSNEDIRGMLFSLTVVGVPGNMAVIVAFLLLVQLQESCLLAADAIVLHLSCTNLVVVLVRCMETLASFHLANV
FGDIGCKGVIFIYRTSRALSIWLTFLLSAYQCLSIAPPGSKWASRLTLVAQSLPIVFVFLWVLHSSLSAGAILFS
VSSKNVTAVATSAVNVEFCYVNFPSDILKKVYGAIQVSRDVVPMALMTLTSIIILVLLYKHSQHLKGLRGAGHAG
SGTGGSQRAAKVVVVLVTIYVVLVYGVNDCLWVYTLTLRHTMSSSLISDLRVFFASLYAALSPLVIIIVSNRKVNS
RLRCVAQEKPLLGKTAHLHSI

>Dr-ORA2

MIAEAVIRGLLFLSLVLVGVPGNATVIVICGFILLVRREGRLSPADAIVLHLCANLVVVSVRCLLEVLTATFRIHNV
FDDAGCRAVIFLHRTARSLSIWLTFLLTALQCLSVAPPGSRRAAARALLARSLPAIFLALWLINTSMSVASLLYS
IGARNDSRLLQNAINVEFCFLSFPSRLARDANGAAQVARDVVPMLMAAGSLVLLVYLVRQRRRVQGLRGTAGGA
AERRAAVTVVTLVSLYLLVFGLDNGLWVYTLTVSHTLSSALITDLRLFFTSLYTAVSPLLIIVSNTRLRCGKQPE
TMH

>Ga-ORA2

MPSEMFVRGMLYLSLTVLGVPGNATVIVAFLLLVQLQERRLLPSDAIVLHLAFVNLLVVAARCLPETLASFRLSGI
FGDVGCKAVIFVYRTSRSLSIWLTFLVLSAYQCLSIAPPGSRWAHLRVLLAQYGLVFLILWLLNTCMSSAGILFS
FGTKNVTNLTNFDINVQFCYVNFPSKLSIQANGASQVGRDVVPMALMTLDSLIILVFLYKHSQQAKDLRGSRGGG
AERRAAKVVVALVTLYVVLVYGVNDGLWVYTLTSRKAMESSSLISDLRVFFASLYAALSPAVVIASNRKVNSRLRCD
VKRKPVEEKDTCLSTV

>Hc-ORA2

MASEVFVRGMLFSLTVVGIPGNATVIVAFLLLVQLQEKRLLAADSILLHLACVNLLVVVVVRALTETLASFRLADI
FGDTGCKSVIFIYRATRGLSIWLTFLSTYQCLSIAPPGSSWASVRALLGHYLAFLVFLWVLNACMTTAAILFS
FSTKNETSPIDNGINVQFCYLNFPKLSRDANGAIQVGRDVVPMALMTLASLIILVFLYKHSQQVKGLRSSGGGG
AGNSGAEQRAAKAVVALVTLYVVFYGDNGLWVYTLTVKKTMSSSLISDLRLFFGSLYAALSPLVIIASNRKVNS
RLGCVAHEKSAVEKIKNLSSM

>Ol-ORA2

MAHSFVFLEPFFCAGMPSDDLVRRGLYASLTIVGVPGNILVIMAFLLLVSYEENRLLAAEAIVLHLTCANLLVVVV
RCLTETLASFHVNVVFGDAGCKGVIFIYRTSRGLSIWLTFLSTYQCLSVSPPGSYWASVRVLLAQNLVVFVFLFL
WVLNTTMSGAILFSLSSKNDSSPINNAVNFECFVSFPSDLSKEIFGAVQVSRDVVPMALMTLTSVIIILVLLYQ
HNQHMNDLHRNSNASGGRCGAKRRAAKVVVVLVTLYLGLYGVDCGLWVYTLTVKKTMSSSLISDLRVFFASMYAA
LSPLVIIIVSNRKVNSRLMCISQKLA

>On-ORA2

MASEVFVRGMLYLSLTVGIPGNATVIVAFLLLVQLQEKRLLAADAILHLACVNLLVVVVVRALTETLASFRLADI
FGDTGCKSVIFIYRTTRALSILWLTFLSTYQCLSIAPPGSSWASVRALLGHYLAFLVFLWVLNACMTTAAILFS
FSTKNETSPIDNGINVQFCYVNFPSMLSRDANGAVQVGRDVVPMALMTLASLIILVFLYKHSQQVKGLRSSGGGG

AGNGGAEQRAAKAVVALVTLYVVFYGVNDVLWVYTLTVKKTMSSSLISDLRIFFGSLYAALSPLVIIASNKRVNS
RLGCV AHEKSAVEKTKNLSSM

>Ss-ORA2

MQSEEVVRGMLYLSLTVVGVPGNTAVIVAFLLALYQEHQLLPADAIVLHLACANLLVVGVRCLLETLATFRLVNI
FGDTGCQGVIFVYRTSRSLSIWLTFVLSAYQCLSIATPGSRWASIRVLVARYLAVIFLTLWVINTSMSSAAIAFS
LGSRNDSVNMQHSINVQFCYVRFPMTQSKQVNGAVQVGRDVVPMGMMTLASLVILVFLYRYSQQVKGLRSSSGAS
GGAERRAAKAVVVLVTLYVVLYGVDNGLWVYTLTVRKTMSSSLISDLRIFFSSLYAALSPLVIIATNRKVN SRLR
CVVQERPVDKATTLSTV

>Tn-ORA2

MIVVTIILRDLLSISPGMQSTEFVRGILYLSLAVVGAPGNTCVILAYFILLYQEKRLLPADVIIHLHLACANLLVV
VARCFLEFLASFRLALIFGDVGCKSVIFVYRTSRSLSIWLTFILSAYQCLCIAPLGSQATLRMIVAKYLFYVFF
FLWLLTTTMTSTAAILFSFSTQNGTNLVNNSINVQFCYVQFPSKLSKDANGAAQVGRDVVPMTLMTLASLIILAF
YKNSQQVKGLRSSSSDRAEKRAAKAVVTLVSLYVLLYGVDNGLWVYTLTVREAMASSLISEMRIFSSMYAALSP
IVIIIVSNRKVN NILRCAGQEKHVQEKTT

>Tr-ORA2

MKDYGGIILRDLFSISTGMQSVEFVRGILYLSLTVVGAPGNICLILAYLILLHQENRLLPADVIIHLHLSCVNLLV
VVARCLLEFLASFHLAIIFGDVGCKSVIFVYRTSRSLSIWLTFILSAYQCLCIAPPGSQWTTLRIVFASYLFYV
FFLWLLTTSMSSAAVLFSFGTQNDTNLINHSVNQFCFVHFPSKMSRDANGAAQVGRDVVPMALMTLASLIILAF
LYKNSQQVKGLRSRDGSGRAERRAAKAVVTLVTLYVLLYGVDNGLWVYTLTVREAMRSSLISDLRVFFSSLYAA
LSPIVIIISNRKVN SILRCAEQQKHVQ

>Lo-ORA2

MDPQVVIRGMLYFLVVGVPGNLAVIWAFFCHIMRSEKRLMPADAIVLHLAAVNLLVAAVRCSEALAAFGVLYV
FNNTGCKTIIIFIYRTSRSLSIWLTFVLSTFQCISIVPPGSRGYSIKSHAPRYLGGVFVFLWILNSWLSSAALAF
VSSGDNSTRTOYGINIEFCIVNFPSSSTWKNAGAVQVARDAPIFLMVAASLFILLFLYRHSQQVKGLRS AKRTQ
KESAESRAAKTVVTLVTLYVLFYIDNGLWVYTLTVTQTLSTSLISDLRIFFASLYAAVSPPLVIIASNKKVKSQ
L GCMKTEKGPVSVDTVSTV

>Am-ORA3

MWVNGTVTIIKATGGQLSSVPMALYMILVLLGIFGNAIVISVVGESILREPGGGRNSDMILVNMAFSNLMVSMTR
NMLLVISDTGLEVLPGKDWQCILMGVWVWLRSVNVWSTFFLSAFHFHTLRRTAPPITSLSGPRGLPRGILTGFGL
IWSSNLLYSVPAFIYSTSGGKNATETLMLVSSTTRPLLGCWDFPSVYSGLAFAFATTSMTVIHEIIPIVLMSVTNLG
SLTLYAHGSKLHATNKSQQDPTMNRVPAERRAAKVILALILLFIVSWGASVISVNYFNYNRGASSTYLLVLARF
FNSLFIALSPLILAVGHRRLRQFFKSIISH

>Fh-ORA3

MGLRTPVSPAQSAFYIILVALGIVGNAIVIGVIGKSVMDHGGGHNSDIIINLAVSNFMVSVVRNVLLIVSDLG
IQMYSSKGWCQFLMGVWVWLRSVNVWSTFFLSAFHLHTLKRVAPTIGNIQGPWSTYRTLLLSLGVIIWILNLLYSI
PAHIFSTSGNENTTETLMLVSSTTRPLLGCWVNFPSNYSGLAYATTSMAIHEIFPIILMAVTNMTSLYTLYTHGR
SRSSVQDAPVIKRVPAERRAAKVILALVMLFIVSWGTSIISVNYFNYNRGSSAEYLLVIARFANIIFIAMSPVVL
AFGHRRLRSCMKSSVSD

>Gm-ORA3

MSEAEAEELVGMGLRTDASPQVQTFYILLVLF GIVGNTTVIGVIGHSVLMNPGVGRNSDIIINMAVSNLMVSVLR
NALLVISDIGIALYSSKECCQFLMGVWVWLRSVNVWSTLLLSAFHFHTLRVAPPLGNLHGPRGLPKLLLLGLGL
IWVNLFLYSIPAHVFSINGNQNSTETLMLVSSTTRPLLGCWVNFPLKNGLLYATISMVIHETLPIVLMAFTNAGS
LYSLYAHSKMRSMVNDVHVIKKVPAERRAAKVILALIMLFIASWGTSIISVNYFNYNRGQSAEFLLVIA RFANIF
FIAMSPIILSIGHRRLRSFFTSLV

>Pf-ORA3

MQQESTTKLLGMGLRTGVSPAQSAFYIILVALGIVGNSIVIGVIGKSVLMDRGP GHNSDIIIVNLAVSNLMVSI
VNALLVISDIGIALYSSKGWCQFLMGVWVWLRSVNVWSTFFLSAFHLHTLKRVAPTIGHLQGPWSTYRTLLLSLA
IMWILNLLYSIPAHIFSTSGNENTTETLMLVSSTTRPLLGCWVNFPSNYSGLAYATTSMAIHEIFPIILMAVTNM
TSLYTLYTHGRSRSSVQDAPVLKRVPAERRAAKVILALVLLFIVSWGTSIISVNYFNYNRGSSAEFLLVIA RFAN
IIFITMSPVVLAIHGHRRLRSCMKSSVSD

>Xm-ORA3

MEQETTTKLVGMGFRTAVSPAESDFYIILVALGIVGNSIVIGVIGKNVMMDRGPGHNSDIIIVNLAVSNLMVSIM
RNLLLIISDLGFKLYSSKGWCQFLMGVWVWLRSVNVWSTFFLSAFHLHTLKRVTPTIGDLQGPRSTYRTLLLSLA
IIWILNFLYSIPAHIFSTSGNENTTETLMLVSSTTRPLLGCVWNFPNYSGLAYATTSMMVHEIFPIILMVVTNM
MSLYILNTYGRSRGSVDVPVLKRVP AEKRAAKVILALVMLFIVSWGTSIIISINYFNYNRGSSAEFLLVVARFGN
SIFITMSPVVLAIGHRRLRSCMKSSVSD

>Dr-ORA3a

MAPQKKPVNISQRITSSPFYIMLYVVLVLLGNAGNTTVIAVVGQSLLOETGTVRSSDVILVNMAFSNLMVSLLRN
TVLMVSDLGVEIFLSRDMCQFMMGLWVWVRSANVWSTFFLSAFHFQTLRRVAPPVINLHGPRGPPLSLILGFCL
WSLNLIYSIPAFIFSKNGNENSTETLMLVSSTTRPLLGCWDFPSAYSGLAFATSSMILHESIPICLMNITNLGS
LCTLYAHGHKRTVASQGEDAPVVSRI PAERRAAKVILALNILFISSWGTNVISVNYFNYNRGQSTEFLLIIARFV
NMSFIAFSP IILAVGHRKLRAF IKSVL SHMI

>Dr-ORA3b

MATTAKPLTVSQRALSSPLYIAFYVILVLLGNLGNLSLVIGVVGEGLLREPGVARSSDIIILVNMAFSNLMVSLTRN
SLLVISDMGVQVFLNRNWC RFMMGIWVWVRSANVWSTFFLSAFHFQTLRRVAPPVSNVHGHGPPRSLIFGLCLI
WSLNLIYSIPAFIFSKNGDANSTETLMLVSSTTRPLLGCWDFPSAYSGLAFATSSMILHESIPICLMSITNMGS
LLALYAHGEARRAAKSSDAPVVSRI PAERRAAKVILALNILFISSWGTNVISVNYFNYNRGSSDWDLLIARIG
NITFIALSP IIVLAVGHRRLRAFLASILTHSIALCRHLWTYKLOK

>Ga-ORA3

MAEHIGEDGESTLIGMLRVSVSPVQTAFYIMLVTLGILGNFTVVGVIKSIATDHVGGGRNSDIIINMALSSLL
VSVMRNIPLVISDIGLELYSSKEWCQVLMGLWVWLRSVNVWSTLFLSAFHLQTLRRVAPTAVSRNGPRGLPKTLL
LSLTLIWLNLVYSIPAHIFSTSGDVNSTETLMLVSSTTRPLLGCVWNFPSSYSGLAYATTSMVIHETIPIILMA
ITNLGSLYTLYTHSRVRSTDAPVIKRVPAERRAAKVILTILMFISSWGTSIISVNYFNYNRGSSAEYLLIIARF
ANIIFIAMSP IIVLTFGHRRLRSFVKSTLSH

>Hc-ORA3

MSSLSQDKDLAGMRMHIFVSPAQTAFYIILVIMGILGNTTVILVIGKSIILEHNWGRNSDIIIVNMAMSNLLVS
LLRNTLLIISEFGLQIYTAKGFCQLLMGMSVWLRSVNAWSTLFLSAFHLQTLKRVAPGATNGPRGAPKTLLMCLG
LIWIGNLIYSIPAHIFSSNGNKNNTTETLMLVSSTTRPLLGCVWNFPSTIGLAYATTSLVIHEMIP IILMAITNLT
SLYTLYTHGRNPQKDAPVLKRVP AEKRAAKVILTILFISSWGTNVISVNYFNYNRGSSADYLMVIARFANIIF
IALSPVILAVGHRQLRSCIKSTLVH

>O1-ORA3a

MSALQAVFYAILVVLGVLGNTTVIVVVGKSVIQDRRAHNSNIIINMAASNLMVSVMRNILLVMSDFGIQLFLS
RERCQFLMGVWVWLRSVNVWSTFYLSVFHLQTLRRVAPSVGNLQASRGVPKTLLNLLSIWILNLLYSIPAHIFS
TNGNANSTETLMLISSTTRPLLGCVWNFPSSYSGLAYATTSMVIHETLP IIVLMTVTNLSSLYTLHTYGRTRKSVQ
DAPVVKRVPAEKRAAKVILILVLLFTVSWGTSVISVNYFNYNRGTSSEFLLVIARFAQILFIALSPAVLAVGHRG
LRSCIKSSLT Y

>O1-ORA3b

MSAVSRMKTQLDLRPADEAAAKIKDFVGPEGRDENPKHVIGIGLQVPVSDVQIVCHVIMVVLAILGNATVIVVIGK
SVIQDRRAHNSNIIINMAVSNLMVSIMRNILLIVSDFGIQLFLSRERCQFLMGVWVWLRSVNVWSTFYLSVFH
LQTLRRVAPSVGNLQASRGVPKTLLNLLSIWLLNLLYSIPAHIFSTNGNANSTETLMLISTTTRPLLGCVWNFP
SSHSGLAYATTSMVIHEALPILLMTATNLSSLYMLHTYSRTRTRTSIQHAPVIRGVPAERRAARVILILVLLFVV
SWGTSVISVNYFNYNRGTSSEFLLVIARFAQILFIALSPAVLAVGHRGLRSCIKSSLT Y

>On-ORA3

MSSLSQDKEPDLAGMGRIFVSPAQTAFYIILVIMGILGNTTVILVIGKSIILEHNWGRNSDIIIVNMAMSNLL
VSLRNTLLIISEIGLQIYTTKGFCQLLMGMSVWLRSVNAWSTLFLSAFHLQTLKRVAPGATNGPRGVPKTLLVC
LGLIWIGNLIYSIPAHIFSSNGNKNATETLMLVSSTTRPLLGCVWNFPSTSGLAYATTSLVIHEMIP IILMAVTN
LTSLYTLYTHGRNPRKDAPVLKRVP AEKRAAKVILTILFISSWGTNVISVNYFNYNRGSSADYLLVIARFANI
FIALSPVVLAVGHRQLRSCIRSTLVH

>Ss-ORA3a

METPMPELKELEPVGVGLRVTTSPQTTFYIILVLLGIVGNTTVIGVMLDSVFKDPSGVRNSDIILNMALSNLL
VSVLRNVLLVISDLGLELNTSRDGGCHVLMGVVWVLRSVNVWSTLFLSAFHFTLRRVAPPPGTVHGPRRPPKTL
ISLGLIWFLNLIYAVPAHIYSTKGKNSTEILPIILMAITNLGSLYTLTYTHGRTHNPAHMTQDAPVIKRIPAER
AAKVILALIVLFIGSWGTSIISINYFNYNRGLSAGFLLVIARFANTIFIAISPIVLALGHRRLRAVIKYFLTH

>Ss-ORA3b

METPMPELKELEPVGVGLGVNRYPFQNALYIIFVLLGIVGNATVVGVISES VFKDPSGGRNSDIILINMALSNLL
LSLLRNILLVISDLGLELNTSRDGGCHVLMGVVWVLRSVNVWSTLFLSAFHFTLRRVAPPSTVHGPRRPPKTL
ISLGLIWFLNLIYAVPAHIYSTKGKNSTETLMLVSSTTRPLLGCVWNFPSSYDTLAYTTTSMVIHEILPVILMA
ITNLGSLYTLTYTHGRTRNPAHMTQDAPVIKRIPAERRAAKVILALITLFIIVSWGTSIISINYLNYYKGSSATFLP
VIARFANSIFIAISPIVLALGHRRLRAVIKSFLTH

>Tn-ORA3

MAANTEDDTEVVGMLRVSVSPVQTASYIFLVLLGILGNTTVVGVIKSIIMDRGGGRNSDIIIVNMALSNLLVS
LMRNTLLIILSDIGLEMYSSKEWCFLMGVWVLRSVNVWSTLFLSAFHFTLRRVAPVAGPVQGARGAPKILLIN
LFLIWFNLIYSIPAHIFSTSGNINSTETLMLVSSTTRPLLGCINWFPSRYSGLAYATTSMVLHETVPIVLMALT
NLGSLYTLTYTHNGMRSSVQEVPIKKRVAERRAAKVILALIMLFIISWGTSVISVNYFNYNQGSSAEFLLVIA
RANIIFIALSPVVLAVGHRGLRSFFKSLLAH

>Tr-ORA3

MAVNSMDEDDMELVGMLRVSVSPFQTAFYIFLVLMGILGNATVVGVIKSIIMDRGGGRNSDIIIVNMALSNLL
VSLMRNMLLILSDIGLEMYSSKEWCQFLMGVWVLRSVNVWSTLFLSAFHFTLRRVAPMAVNTGSRGAPKILL
MNMFLIWFNLIYSIPAHVFSTSGNINSTETLMLVSSTTRPLLGCINWFPTRFSGLAYATTSMVLHETVPIVLM
LTNLGSLYTLTYTHNGMQSSVQDAPVIKRVPAERRAAKVILALIMLFIASWGTSIISVNYFNYNQGSSAEFLLVIA
RFANIIFIAMSPAVLAVGHRGLRTFFKSLLSH

>Lo-ORA3

MGEQTNKVVTVLLKAAIPAQNALYGLLVMLGIVGNGLVMGVVGRGLVKEGLARQHSDIILLNLVLSNLLVSVLRN
IPLLLADVGLQLFTSPGCCQFLMFMWVLRSVNVWMTMCLSAFHFTLRLGPVVPAGPHGPRASLQRLLLVLAL
IWSLNLLYSFPGFFFSTQGGRNSTEELMLVSSTTRPLLGCVWSFPSRRGGLAYATTSLVLHELLPILLMVATNLG
TLHTLARHGSRQAGETTTLTRRIPAERRAAKVVLVLMFLFIISWGASVLSVNYNRYNRPSTEFLLVMARFTNSL
FIAFSPLVLLAGHSRLKAIFRVIADHVHSFCFSQRCLKKSC

>Am-ORA4

MELLTIEAILFGFLVFSGILGNMLVIYAVFQCALDNPSHHLSPSDIILLNISMNLLTSMFRTIPIFISDLGLKV
SLDTNWCRCVFMLLWVWRAVGCWATLTLSAFHYATLKRKRVTSTCPQALRKDRRLTWGALGLVWGTNLLFSIPASV
FTSHVHG NATTEVMVISCTTRPLLGC MWNFPTREQGYAFAAASMALNEVLPLVLMVGTNLATLHTLAKHIRAVAA
GPEMASGHSNSEKKAGHVIMSLVTLFVVCWVLQVAAVTYYNYER GKHTD SLLTVSQFSSSLFVGFS PMVVALGHG
KMRKKIMGMLQRWLRLKALCRDAEEHKRAPEISSTINSTITQKQTHH

>Fh-ORA4

MSEILTVDAILFGLLVFSGILGNILVIHVVFQSALES PSRRLPSPDTILVHLSLANLLTSLFRTVPIFVSDLGLD
VSLSAGWCRLFMLLWVWRAVGCWVTLTLSFFHCATLRRHHVSLGPLTLQRRRRVWVVLALVWGANLAFSVPAL
LYTTHVQSNATVELMVISCTTRPLLGCVWEFPSSQQGS AFASASLALNEVLPLVLMVCTNLATLHSLAKHIRAVT
DSGSHGELDKHVSTERKAAHVIMSLVSLFVVCWVLQVAAVTYYNHDRGHHAEGLLTVAHFASL FVGFSPLVVAL
GHGKLRRKIKSMILMWTGPRGPESRSVSASPTTKGKQTCFEAQKEIQVIKVKAKVKSQR

>Gm-Ora4

MAEVLTVDAILFGLLVFTGIMGNIMVMHTVCQSAMQSQRMPASDTILVHLSLANLLTSLFRTVPIFISDLGLE
VTLSPGWCRVFMLLWVWRAVGCWVTLALS AFHCSTLRRQHVAFGPLAVQKERRRVW GALGLVWGVNLVLSLPAL
VYTTHVHG NATVELMVISCTTRPLLGC IWEFP SREQGEAFAS TSLVLNEVLPLVLMICTNLATLHALAKHIRAVT
AAGGDSGDMDRHLASERKAGHVIMSLVSLFVVCWVLQVAAVTYYNH DGGHHAEGLLTVAHFAASL FVGFS PMVVA
LGHGKLRKRIVGKLVGCSNVVRCRGHEGEDDGAAGAAQQKEKGKTVFVQKEAASTKEKTMSKK

>Pf-ORA4

MSEILTVDAILFGLFVFSGILGNILVIHVVFQSALES PSRRLPSPDTILVHLSLANLLTSLFRTVPIFMSDLGLD
VSLSPGWCRIFMLLWVWRAVGCWVTLTLSIFHCATLRRQHVTFGPLTLQRRRRVWVVLGLVWGANLAFSIPAL
LFTTHIESNATMELMVISCTTRPLLGCVWKFPSDRQGLAFAS TSLALNEILPLVVMVFTNLATLHSLAKHIRAVT

SESGSHGELDKHVSTERKAAHVIMCLVSLFVVCWVLQVAAVTTYNHDDGGQHAEGLLTVAHFSASLFVGFSPPLVVALGHGKLRRKIRSMILVWTVNPLSQEAESGRKSPKTSKGQISFVAQKEVKVKVKDKVIPRR

>Xm-ORA4

MAEVLTVETAILFGLLVFSGILGNILVIHVVFQTALESPPSRRLSPSDTILVHLSLANLLTSLFRTVPIFVSDLGDLMSLSPVWCRIFFMLLWVWRAVGCWVTTLTSLIFHCTTLRRQHVTFGPLTLQERERRRVWVVLGLVWGANLVFSIPALLFTTRVESNATVELMVISCTTRPLLGCWKFPSDQOGSAFASTSLALNEVLPLVLMVFTNLLILHSLVKHIRAVTSESGSHGELDKQVSTERKAAHVIVSLVSLFVICWVLQVAAVTTYNYDGGRAEGLLTVAHFSASLFVGFSPPLVVALGHGKLRRKIRSLILMWTNVPHSQETESGKSLKTSKGKPSFVAKKEVKVKMVKDKVMPHR

>Dr-ORA4

MSEVLTVDAVLFGLLVFSGIIGNIMVFDCAKLCASRHLPPSDTILVHLCANLLTSVFRTVPIFVSDLGDLQVWLTAGWCRVFMMLLWVWRAVGCWVTTLALSFAHFCATLRRQHVSMLGHSRERRRVWVVLAVVWAANLLFSPLPALVYTTQVRGNATVELMVISCTTRPLLGCWVEFPTFQOGYAFASSSLALNEVLPLVLMVGTNLATLQALGKHIRTVRAGGSTGAELDRHVSSERKAGHVIMALVALFVGCWVLQVAAVTTYNNHNRGAHAEGLLTVAHFSASLFVGFSPPLVVALGHGKLRRRISGILQSCMHLKQTQDKPAEITEKDGRTTQSAMK

>Ga-ORA4

MSTRSNLHALRRSLMFSDAQNRNCGKCLRLHVFQSAFESPPSRRLPPSDTILVHLSLANLLTSLFRTVPIFVSDLGDLVSLSLGWCRIFMMLLWVWRAVGCWVTTLALSIFHCTVLRQHVCAGPLAQERERRHVWIALGLVWGANLAFSIPALVYSTHVHGNATVELMVISCTTRPLLGCWVEFPNQQGSASFASASLALNEVLPLVLMVCTNLATLHALAKHIRAVAAGAHPGETQKELDKHVSTERKAAHVIVSLVSLFVVCWALQVAAVTTYNHDDGDHAEGLLTVAHFSASLFVGFSPMVVALGHGKLRRRIMMILMWSEVLKCRKENSEERIKSPKAKGRGRKRSVFIVQEERMVVQVKGNAQADK

>Hc-ORA4

MSKVLTVEAILFGVLVFSGILGNILVIYVVFQSVTKTPPRRLPPSDLILVHLSLANLLSSLFRTVPIFVSDLGDLYLSSGWCRVFMMLLWVWRAVGCWVTTLTSAFQCTTLRRQNVAFGPLTVQERERRLWVVLGVVWGANLAFSVPALVYSTHVKGATVELMVISSTTRPLLGCWVEFPSEEQGTVFASSTLAVNEVLPLVLMVCTNVATLHALAKHIRAVASGGTHTELDKHLSSERKAAQVIMSLVLLFVVCWVLQVAAVTTYNNHNRGHHAEGLLTVSHFSSSLFVGFSPPLVVALGHGKLRRKIMSMMLG

>Ol-ORA4

MSKVLTLDAILFGLLVFSGLLGNTLVIYAVFQSAFETPPGRLSPSDTILVHLSLANLLTSLFRTVPIFVSDLGDLVSLSPGWCRVFMMLLWVWRAVGCWVTTLTSLIFHCTTLKRHHVSLGPLVLQKEKRRVWIIILGLVWGANLAFSIPALVYSTHVYSNATVDLMVISSTTRPLLGCWVEFPPTQOGSAFAFTSLALNEVFPVLVLMICTNVSTLHALAKHIRAVTSSMESGGSHGEVNKLSTERKAAHVIMLLVALFVVCWVLQVAAVTTYNNHNRGLHAEGLLTVAHFSASTFVGFSPMVVALGHGKLRRKIMGMILVWTKAFHCSSKDTGRKRPSPKKKKLKVFVDVQEEMRVINIRECKALNDRRE

>On-ORA4

MSEVFTVEAILFGLLVFSGILGNILVIYVVFQSVTKTPPRRLPPSDLILVHLSLANLLSSLFRTVPIFVSDLGDLLSLSSGWCRVFMMLLWVWRAVGCWVTTLTSLVFQCTTLRRQNVAFGPITVQERERRRLWVVLGVVWGANLAFSVPALVYSTHVKGATVELMVISSTTRPLLGCWVEFPSEEQGLVFTSTSLAVNEVLPLVLMVCTNVATLHALAKHIRAVASGGIHTELDKHLSSERKAAVVIISLVLLFVVCWVLQVAAVTTYNNHNRGHHVEGLLTVSHFSSSLFVGFSPPLVVALGHGKLRRKIIISMMLG

>Ss-ORA4

MSEVLTVDAILFGFLVFSGILGNILVIHVVFQSAIESLSRRLPPSDTILVNLSLANLLTSLFRTVPIFVSDLGDLVSLSQGWCRFLFMFLWVWRAVSCWVTTLTSAFHCATLKRQHVAMGPLAQEHERRKVWVALGLVWGLNLAFSPLPALVYTHVQGNATVELMVISCTTRPLLGCWVEFPSEEQGSASFASSTLALNEVPLVLMVGTNLATLHSLAKHIRAVTSAGEAGGGTHGELDRHVASERKASHVIMLLVMLFVVCWVLQVAAVTTYNNHNRGNHAEELLTVAHFSASVFGFSPMVVALGHGKLRRRIMRMIAGCADRVKCQOEKIIDESKAPDKRERTAKQTVFTIQKEREVIK

>Tn-ORA4

MSEVLTVDAILFGLLVFSGILGNILVIHVVLQAAFQGTSGRLPLSDTILVHLSLANLLTSLSRTVPIFVSDLGDLVSLSAGWCRVFMMLLWVWRAVGCWVTTLVLSVFHCTTLKRQRLYIGPNAQRRERRRLWVILGLVWGLNLAFSTPALIYSTHVHGNATVELMVISCTTRPLLGCWVEFPTAQOGSAFASASLALNEVLPLVLMVCTNLATLHALAKHIRAVVSSQSGGSQGELDKHLSTERKAAHLIMLLVSLFVTCWVLQVAAVTTYNNHNRGHHAEGLLTVAHFSASLFVGFSPPLVVALGHGKLRRRISKVMLSWCRRRLKGSNTKLMQIVFFVPQKQ

>Tr-ORA4

MSEVLTVDAILFGLLVFSGILGNFLVIHVVLQAAFQASARRPLPLSDTILVHLSLANLLTSLFRTVPIFVSDLGSD
VSLSPGWCQVFMLLWVWRAVGCWLTALSLIFHCTTLKRQRLYMGPDMQRRERRRMWVILGLVWGLNLAFSIPAL
IYSTHVHGNAVELMVISCTTRPLLGCWEFPTAQQGSASFASASLALNEVLPLVLMVCTNLATLHALAKHIRAVM
SSGQPGGSHVELDKHLSTERKAAQVIMLLVSLFVVCWVLQVAAVTYYNHDGGHHAEGLLTVAHFSASLFGFSPM
VVALGHSKLRRRISSMMLGWCQCFKGRSEDDPPNTRAAKIIISFVQHKQ

>Lo-ORA4

MAQVLPVDAILFGVLVLSGIVGNVLVICAVVQSVLQNSLLRIPPSDLILANLSLANLLTSFFRTVPIFVSDLGLE
VSLAPGWCRLFMFLWVWRAVGCWATLGLSLFHWAMLRHSFMSGLOAHRAELRRVCVALALVWALNFAYSIPAL
VYSTHSRGNTTVELMVISCTTRPLLGCWVEFPSEVQGIATASLVVNELVPLVLMVGTNLASLCLVLRRIHTVA
GANMELQGHMASERRASHVILVLVTLFVTCWGLQVTAVTHYNYNRGRQAEITLLTVSHFAASVFGFSPLVVALGH
SKLRGRLRRMLRLHCGRREGPGGEDVGDREDRDREAATKTPTTTRTCRDKS

>Am-ORA5a

MNAKEWIKSTIRGFMVSGILGNNWLGFCSLPKRSRQLRTNNILFINLAISNLITNYMVDLPDTLELVKRWPVGR
MYCSAFNFFSDLSETSSIFTTTFITVFWHQKLVGSLKHGGAPVQMDNTRLVMALLAGSWTVSVVFSPLPHLFFTS
NIQNQSSEECLEYFPSQEVKQTYEMVFLMLANVPIVIGIVFASIQTITVTLQSQKRIKNISSRAGPRGDDQKAA
SNELSSKDYISNATSANAPNTIQKVQKSQDRSNSSSGSSQVRAAKSVVAVATVFVICWLTHLLLSITSTIHDSIV
IHEMTSYIGALYTCTIIPYIYLYGVKKLTCLTCSSID

>Am-ORA5b

MDAEGWIKSVIRGLMCVSGIIGNHWLGFSAALPKSRAHLKTNDILFVNLAASSNLITNYLVLDLPDMMDFTYNFLMGQ
MYCSVFNFCSLSETSSIFTTTFITVFWHQKLVGSLKRGAPVQMDNIRLVAALLAGSWIVAIAFSLPHIFLASK
NNGNNTYFECLEDYPSLKAKQAYDLMYLVFANIIPYIIGIFFASIQTITVTLQNKRIKINSNTTAVTTGAKNTKITP
AEPVSHSNQSSQEAVSYSNAVVPNPGQARSSSSGSLRAAKSVVTVATIFLICWVVHVILRLISTIQESSLIME
LASYIGAAYTCTIIPYIYLYGVKKFSCTCRG

>Fh-ORA5

MDADELIESIIRALMFIAGILGNNWLAIITSLPKRRSDIRTNEILLVNLAVSNLITNCLVDAPDTMADFAGRWFLG
ATFCGIFRFSADLSETSSLFTTLFICAFWHQKLVGSLKRGAPVQLENLRLVGCLLAGSWILSTVFSIPHFFVVS
LEGTNGSREDCIDVFPDALSSQIYEIFFLVLANALPVAGIMVASVQIVVTLLQNKRIQSRSSDPAKGAIKENHP
ERSVSSVSVPDHCKDLKGPSSPAHSGKTGHKADSGVEAQANSSRPSQMPKQSTSAHSQVRAAKSVVAVATVVL
CWVTHLLLRISNNIQTSSLMMELASYIGASYTCTIIPYIFLHGLKKLSCCRKS

>Gm-ORA5

MDVDDIIESAVRALMFLGMLGNNWLAVRSIPRSLALRTNELFLNLAVSNLITNYLVLDLPDTMADIAGGWFLG
DGYCGVFRFCADLSETSSIFSTLFIISVYWYQKLVGSLKRGGPVQLDSLRLVGGLLAGSWGVAVVFSIPHFFVT
VEGENSSLECNDFPSEEAKQTYEALYLTANALPVAGIVYATARIVVTLMQSQKRIQGHGGNQAASEEGRAAP
AAAASIKAAAGGAEGGGVAGGGEVRGAKPAPKPSGSSNQVRAAKSVVAVASIFVVCWVTHLLLRISNNIQTSP
IVVEVASIYAASYTCTIIPYIFLYGVKKLSCSCCGAKQ

>Pf-ORA5

MDADKLVESIVRILMFIAGILGNNWLAIASLPRKKSEIRTNEILLINLAVSNLITNYLVDPVTMEDFAGQWLLG
LTFCGIFRFSADLSETSSLFTTIIICVFWHQKLVGSLKRGAPVQLDNLRLGCLLVGSWTSLSVLSMPRLFFVS
LEVNTNESLEHCVDVFPNVLRSQTYEVFFLSLANALPIAGIWWASIQIVLALLQHKRIQSASSHRVNVKQDKSER
SVSSVSVDQSHKDLKESSSPAERVSSCPNGECLGKSPQSSPLANKTDSRAEAQPNHKSQIPSKQSNNTSSQVR
AAKSVVAVATVVLCCWMTLILRISNSIQDSSLMMELASYIGAAYTCTIIPYIFLHGVKKLSCSCK

>Xm-ORA5

MDADKLIQSIIVRILMFIAGILGNNLLVIASLPRKKSEIRTNEILLINLAVSNLITNYLVDPVTMEDFAGRWFLG
LSFCGIFHFSSDLSETSSLFTTLIIICIFWHQKLVGSLKRGAPVQLDNLHLLGCLLAGSWTSLAIFSMPLRFFVS
QEVKNESHENCIDVFPDVLRSRETYEVIFLSLANALPVAGIWWASIQIVLTLQHRKRIQSVSSHRVKVKQDKSER
SVSSVSVDQSHKDLKESSSPTEHVSSCPNGKCLGKSPRSSPLANKTDSRAEAQPNHSCQSSQIPSKQSNASSQ
VRAAKSVVAVATVVLCCWLTHLILRISNSMQDSPLMMELASYIGAAYTCTIIPYIFLHGVKKLSRLCK

>Dr-ORA5

MQLQDWVESSIRAFFCVTGITGNFWLALRSLPRSRSLRPNDVLFINLAVSNLITNCMVLDLPDTLAQFLNSWLLS
RNYCSVLQFSSDLSETSSIFSTMFITLYWHQKLVGSLKRGGAPVQLDNLRLVLWLLLGSMVALTFSVPHFFIAE
HDGNDTLEVCEEKFTPAEKKTFDGLYLIVANVPLVGITYASVQIVVTLLIQSQKRVDHSGGSEQKTEVRSSGN
PSSGTHVRAAKSVVAVASIFIFCWFihlVLRIYSGFRNSILVVKLTNFIGATYTCFVPYVYLHG VKKLNCSCCW

>Ga-ORA5

MDAEGWIESLIRALMFLAGILGNNWLAI RSLPGHKSSIRTNEVLFINLAVSNLITNYLVDLPD TVADFAGHWFLG
ETFCAAFRFCADLSETSSIFTTFISVFWHQKLVGSLKRGGAPVQLDRLCLVGCLLAGSWTVAAVFSIPHVFFVA
VEGRNGSKVDCVDVFP SAVA RQTYEIFYLTLANALPLAGLVFASAQIVVTLLRNKQRVQGHSSGASEEGENKSGG
GRDGGVAGTASGPGPTEDPKDPSSLTDIYTGV PASARPTGGSPGHAGTLVGDTYSGGGAPEGPGRPSQTRAKTSS
GTQVRAAKSVVAVAVFLVCWLTHLLLRI SNNIHTSSMLVEVASYIAASYTCIIPYIFLYGVKKLGCP CR

>Hc-ORA5

MEGLIEAIIRALMFIAGILGNNWLAICSLPRHKSSIRTNEVLFINLAISNLITNYLVDLPD TMADFAGRWFLGKT
YCGVFCFCAGLSETSSIFTTFISVFWHQKLVGSLKRGGAPVQMDSLCLVGWLLAGSWTVAVVFSVPHYFFFTLE
VANDSHEDCIEIFPNPNARQIYEAIYLTLANALPMAGIVFASAQIVITLLQNHQIRSHNSDQTKEMVKEERKRS
ESKR NKASVSIISGPTTSKDLRSTSTNHIYTGV PAPSSPNRQPSGHS LHNAPQNC SVGAQPNLSRPSQIPSKPH
PNSSTQVRAAKSVVAVASVVLVCWLTHLLLHITNNIHTSSIVVEVSSYIAASYTCIIPYIFLHG VKKLTCSSKR

>Ol-ORA5

MELNKPIASVISALMFLASILGNNWLAVASLPKDRSAIRTNEVLFINLAVSNLITNYV VNLPE TMADIADNWFLG
ETFCCVFLFSIDFSETSSLFSTFLISAFWHQKLVGSLKRGGAPVQLDNLCLVGFLLAGSWTVCAVFSIH HFFLAS
VEGINGSHRYCVD AFPSALAEQTFDIIFLTVANVFPLVGIIVASFQIVVTLLQS QKRIGGHTSVSPKEMIREDKS
SQSKKQVMGPLKGLKVVRTYKSEPVTSSVTLPQTSSQNKTG S NCSLGAPANHSKPSKANPNSSTQVRAAKSVVA
VGSVVLVCWLTHLLLHITNTVHSSQSTLEVAGYITASYS CIIPYILLHG VKKLTC SHKR

>On-ORA5

MEELIESIIRGLMFIAGILGNNWLAICSLPRHKSSIRTNEVLFINLAISNLITNYLVDLPD TMADFAGRWFLGET
YCGVFCFCAGLSETSSIFTTFISVFWHQKLVGSLKRGGAPVQMDSLCLVGCLLAGSWTVAVVFSVPHFFFTLE
GANDSHEDCIEIFPNPNARQTYEAIYLTLANALPMAGIVFASAQIVITLLQNHQIRSHNSDQTKEMVKEERKRF
ESKR NKASVSIISGPTSSKDLRSTSTNHIYTGV PAPSSPNRQPSGHS LRNAPQNC SVGAQPNLSRPSQIPSKPH
PNSSTQVRAAKSVVAVASVVLVCWLTHLLLHITNNIHTSSIVVEVSSYIAASYTCIIPYIFLHG VKKLTCSSKR

>Ss-ORA5a

MDATEWIEAFIRGLMCLLGILGNNWLCLRSLPGPKSSLRTNEVLFINLAVSNLITNYLVDLPD TMADFVGHWFLG
EAYCCVVQFCSDLSETSSVFSTLFISVFWYQKLVGSLKRGGAPVQLDSLRLVACLLVGSWTVAVVFSVPQLFFVR
MESGNESHDDCIEIFPSQTARQTYEPLYLTFANALPIAGIAFASIQIVITLLRNQTRIQGLTSDHHKGTANSLPN
NGPSVVHSSISSPLYQVDIGDNIVRAPADLKRSSQPPAKPSPGSGTQVRAAKSVVAVATVFVVCWVTHLLLMMAS
NIHTSSLVLELASIYGSSYTCIIPYIFLYGVKKLSCSCRG

>Ss-ORA5b

MDAKDWIEALIRGLMCLVGILGNNWLGLRSLPGPKSHLRTNELLFINLAVSNLITNYLVDLPD TMADFAGRWFLG
EAYCGVFRFCSDLSETSSIFSTLFISVFWYQKLVGSLKRGGAPVQLDSLRLVAYLLAGSWTVAGVFSVPHFFFFVQ
VDSGNESHKDCIEVFPSQTARRTYETLYLTLANALPIAGIVFSSIQIVITLLRNQMRIKGLTSDHHKGTDKALPN
KREKMDVSEKYDETGIKTS DKEADLPIVASPDPQSCRNQRISDIRPNLPGVSCSVLPCAGPSVVHSSISSPLYQ
VEVGDCRVRASPD LQRTS QPPAKLSPGSGTQVRAAKSVVAVATVFVVCWVTHLLLRISSNIHTSSVVVEVASYIA
SSYTCIIPYIFLYGVKKLSCSCRR

>Tn-ORA5

MDTKELAESIIRGMMFLAGILGNNYLAARSFPTQRTSIRTNEVLFINLAVSNLITNYLVDLPD TMADFAGRWFLG
ETYCGIFRFCADLSETSSIFTTLFISVFWHQKLVGSLRRGGAPVQMDNLCLVACLLAGSWTVAAVFSVPHFFFFVK
VEATNESSEDCIDVFPNKLAQTYEIIYLTLANIFPVAGIVFASMQIVVTLLQNQRRIQSHSSNPTQT TNRTE DR
SSCTSGKDSTLTSPVYTGVPPVSADGGALAQSSGEPQPGGTARSHQECPRPGQAPT KPTLASGSQVRAAKSVVAV
ASVFLVCWLTHLLLRI SNNVHTSSVVVEVASYIAASYTCIIPYIFLHG VKKLYC SCKR

>Tr-ORA5

MDAEELVESIVRGLMFLAGVLGNNWLAVRSFPTQRSSVRTNEVLFLNLALSNLITNYLVDLPD TVADFAGRWFLG
ETYCGIFRFCADLSETSSIFTTLFISVFWHQKLVGSLKRGGSPVQMDSLCLVACLLAGSWTVAVVFSIPHFFFFVK

VEGSNESSEDCIDVFPNKAAKQTYEIIYLTLANAVPVAGIVFASVQIVITLLRNHRRIRSHGPDPTKISNEPKDR
SSDPGPTPPSQVYTGVPSPGGAVAQSSREPQPGGTDRTPEGGPRPSQAPAKPTMASSSQVRAAKSVVGVASVFLV
CWLTHLLLRLITNSVHTSSLVVEVASIAASYTCIIPYIFLHG VKKLHCCKR

>Lo-ORA5

MDTVGVIESTVRASMCFLGIMGNSMLVLHSLPSKRSHLKTSEVLFINLAASNLTNCLVDLPDTLADIAGRWFLG
EAYCGIFLFCSDLSETSSVLTLLISVFWYQKLVGSLKRGNA PVKLD SLGLSCGLLAASWGAALVFSVPLLSFVT
VGSNRSASQDCQAHFPTHASKQTYEATYLTLANAVPVA FMVFTNLQIVITLLTQRKRIEALKKEARLOPAAERAQ
PTSTGPDSPREFSSVSTPAGNQNPSSQALADPAGKGRDLALAAAAVAPPRSRNAPRQHPGAQVRAAMSVVAVAS
VFLVCWVTHLLLRIASNVNESSAIVEIASIAASYTCIIPFIFLHG VKKLSCRCWK

>Am-ORA6

MESFIFGLLVLRIMLSVIGVLGNTVLIVSILQMTRLKTFEVFLLGLAVSNLEEIMIVDIYDMIVLRSTHSISILS
CGVLKFM TLSGEVASIFFTVLISIYRYQKLHNAAMRIITPIFMDSMKIGVGLSLLCVLVAVLASVPTYIINLDSW
HHMYNSTITDCPADFFQCPRDNCPILNNIYRFLFIFFCYLIPLVIVTGTSSLIIRILMIQQKVAELHHNSEPATI
AANNDDHHHHHHHHHHHDNHHHHHDHHDHHTNVFHRSTIGILAAMMIFQVYCILYLARHLAFNLYDFPAWSELE
FFIATFYTALIPYVYGMGHNFSLKHFRRO

>Fh-ORA6

MCHLSVYLFLGLKTFISCIGFVGNIFLIVSIFQTAVSHVKPFELFLLGLASANLEEIVIVNIYDVHVLEVFSATAG
SWRCRLIGFMTVFGEIASILFTVVICIFRYQKLRDINHRGSLPIWLD SITSAGMMSGVCVTLSTLVSLPVFFTLO
ESVKNTTVNSGGCPSDLFQCGENYCPTLNRVYKYLMMILCHLLPLIIVTVTSCLTITVLLRQIYSVTPANDARCP
DHPSGKSHGLQRTACTQVGRCEHGGVALGLHLPVCVYVRGNLPRLVSA AETPRNSWSFAADVIATACPCGTRRRD
GAAR

>Gm-ORA6

MAKVEYKTMITLVTIRFVMSLIGIMGNMFLVFVIFQTKISRIKSFEV FLLGLAVSNLEELVVVD FYEVIMLIGHI
QNSLLCRTMKFLNLLGEVSSILFTVLICVFRYQKLRDAEKRGNAPIFLDSRKS AWVVSGLCMLLSVMLGLPVYFV
RIDTHVEADNGTSCSPDFFQCHEHFCPLNRFYKYLFLVSCNLLPLLAVTVSSSLIVKVLLGQKRVPAPALGASG
PPGKKSKGPRLQRSTVGILTAMGVFQIDWTMYLVFHLAFSPVNVPLWGDIEFFITTSYTTLSPPYVYGIGYDLFSL
RYFIKR

>Pf-ORA6

MSDLSVDLQGLRMFVSCVGLVGNIFLILSIFQTRVSNIKSFELFLLGLASVNLEEIVIINVYDVIILDTVSTTTG
AWWCRLKFM TTFGEIASILFTVVIICIFRYQKLRD VDHGRGSLPICLDSIASAWMLSGVCVTLSTLLSLPMFAVTF
QGSVENVTENRGGCPTDFFQCGENYCPIFN RVYKYLIMLLCHLLPLIIVTVTSCLTIVVLLGRNTVTPANDIIS
PNHHHGKSHSLFRSTVAVVAAMGLFQVDWTLYLILQWTFSPSDCPIWIEIEFFISTSYMSISPPYVYGIGGHLFSL
ENCKHLLKR

>Xm-ORA6

MSHLSVDLLGLRLFVSCVGLVGNIFLILFIFQTRVSHIKSFELFLLGLASFNLEEIVSINVYHVIILDTVFTTTG
AWWCRLKFM TTFGEIASILFTVVICIFRYQKLRD VDHGRGSLPICLDSIASAWTMSGVCVTL SALLSLPMFAIAF
RGSVENVTENREGCPTDFFQCGENYCPI LNCVYKYLIMLLCHLLPLIIVTVTSCLTIVVLLGRNTVTPANDIIS
PDHHPGKSHGFYRSTVAVVAAMGLFQVDWTLYLILQWTFSPSDCPIWVEIEFFISASYMSISPPYVYGIGGHLFSL
ENCKHLLKR

>Dr-ORA6

MEQIQVNLLSLRLFISIIIGVVGNTLLLVSI LHTHTHLKSFELFLLALCSANLQQLVMVDVYDVLLLCSPSCIGVC
SCRALRFLTVFGEVCSVLFTALISIRHQKLHDVFSHVNV PVLLDSLRWAVCMCVLCVCVALAFGLPTLLVNTHW
SVSNSSLERCPVDFQCPSSSPCLTHIYKYVFLVCVPLPLLVTVTSVLMVRVLLAQQRVVRVREAEPPHPHH
HSSLLRSTLAILAAMLLFLLDWSVYLLHLAFDPYSFPLWAEVEFFITTIYTALSPYVYGIGNDLFSIKRLYC

>Ga-ORA6

MVGLSVDLLGLKVFI LCVGLMGNVFLMVAVAQTKFPRVKS FELFLLGLAAANLEEIAITTVFDVDFLQASSRGVD
TWSCRSLKFLSKFGEVASIFFTVLISVFRQQKLSDA AKRANLP IYLD SIGSARMASGVCVLLATLLSLPVFAIEP
KEPAGNATGNATGNATGNAIGCPPDFFQCSKSRCPALNGLYKHVFILVCNLLPLAVVTVTGCLILAVLLGQRSTV
TPASVGSRSGGSTLRRSSVAVLAAMGLFQVEWTLYLILQLTAVYVDFAFRAEAELLISFSYTCISPPYVYGIGNDL
FSLKNFKRN

>Hc-ORA6

MAELSVNLLGLRLVFSSIGLMGNTVLIASIIKINFFHIKSFEIFLFGGLAAANLWEIVIINIYDIIILQTPSTATG
TWSCYLLEFVTVIGEINSIFFTVLICIFRYQKLRDLNTRVNFPLFLDNIRSAWTVSGISVMLS SVLLSVPMFVIDQ
ESKAENVTRNSSMCPDFFHCTQNHCPVFNRIYKYLFI V SCHLLPLIIVTVTSCLILTVLLSQRKTVTPAVNETG
SSQFSRKS KDTKIQWSTIAVLGAMGLFQVDWTTYLIFQLAFNPYEF PFWSEAQFFITISYTSISP MYMIGHNMI
PPHSCKKG

>Ol-ORA6

MEGIYVNLLGLRIA VSFTGLVGNVCLILSIIHV KWSHIKSFEV FLLGLAAANLEEIVILNVYDAFMLQTSSSDTW
WCRFLKFMTMFGETASIFFTVIIISIFRYQKLGVSLSVHPDRIGVAQLLSGVCVMFSFLLSFPVVAIKPAALTESA
ANNSGGGCPADSFHCGKNYCPAPNRAYKYLFI LVS YLLPLIVITVTNCLILAVLLVQRRITITPEISVHQSNHSHT
NGRDLRFQHSMMAVVAAMGLFLVNWTFYLLFLFLLKPNNLPSWREIEFFTLTSYSCFSPYVYGIGHNLF SLENFK
IIRNKF

>On-ORA6

MAELSVNLLGLRLVFSSVGLMGNTILIASIIKINFFHIKSFEIFLFGGLAAANLWEIVITNIYDIIILQTSSTATG
TWSCYLLEFMTVIGEINSIFFTVLICIFRYQKLRDVNTRVNFPLFLDNIRSAWMVSGISVMLS SVLLSVPMFVIDQ
ESKAENVTRNSSVCPDFFHCTQNHCPVFN SIYKYLFI V LCHLLPLIIVTVTSCLILAVLLSQRKTVTPAVNETG
SSQFSRKS KDTKIQWSTIAVLGAMGLFQVDWTIYLIFQLAFNPYEF LFWSEVQFFITISYTSISP MYMIGHNMI
PLHSCKKGSFKGTVSDFVEVI

>Ss-ORA6

MVDTELLLVFRIFISTVGIVGYVVLILSLIKNQISCLKTFEV FLLGLAASN LVAPNHN VHPHHLVLPAPQVLHNG
LAFLGQWWAISRLLLVLVS YTAEGYMSLRPGQAEIKLCVWLYLFGMLVFGKIASILFTVLFSIFRYQKR

>Tn-ORA6

MLALSVQLLATRIIISCIGIFGNVFLIISVVQTKFSRIKSFEFLFLELAAANLEEIVNVYDIILLCTSYATVG
TWSCTRLKFLTSLGETASILITVLISIFRYQKLRDASRRVPIYLD SIRS AWTVSGILLMFTVLLASPIFVLNIKE
MSQNVTINGSGCPPDFFQCNKDNCPELNGIYKYLFI LLFNLLPLIIVTVTSCLII MVLLSQRKTVAPVVNASSQT
AQRSKCQKFQ RSTIAVL TAMGLFQVDWTLNLIFQLTSSPGAFTSGAEIKFFISSYTAISP YVYGIGNNLFSLKK
FRKT

>Tr-ORA6

MLGLSVQLLATRIIISCIGIFGNVFLIVSVVQNKFSQIKSFEFLFLELAAANLEEILIVNIYDMIILQTSFATVG
TWSRLLKFLTMLGENASILVTVLISIFRYQKLRDASRRVNLPIYLD SIRS VWT VSGILTVFTILLSSPIFVLNI
KETSQNFTNNGSGCPPDFFQCNKEDCPELNGIYKYLFI LLFNLLPLIIVTVTSCLII AVLLSQRKTVTPVESGSS
QISRKSKGLKFQ RSTIAVL TAMGLFQVDWTVYLIFQLTISP GDSSSWAEIKFFISTSYTSISP YVYGIGNNLFSL
KKLRKN

>Lo-ORA6

MDLMNPVLLVLRYLISIVGIIGNITLVVSILSHSHMKTFEIFLLGLSFSNLEGIFLV SIFDITTRLALQSLEEWS
FKILRFMASLGETATIFFTVLISVFRYQKLRHAEARGNLPTS WDNTSTAWALSGMSLFLSFCFCLPGYFIESDER
VDNHTSRNFLTDPFQCPRINCPAINLIYKTLFLLFSNLIPLLIITATSGLILKVLLHRRKTVSDVYDSSHHHQ
NLYFSKSTKTVLAAMCIFO LDWIMYLV LHAFDSSKMDNWSEIEFFIVTTYTTISP YVYGIGTNIFSCRQIVKVL
SCLSFSAAGLYRQHSMCAKWNQ

>Lo-ORA7

MDLQNLAKAVATLLQNMVGIPANLTVLGVFVHVARTERRLLPTDAIVSHLVSVNLLLILTRGIPQSL S ALDYRGF
YDSATCKFLIFTYRTTRAMSISLTFVL SAYQCITIAPASSRLSRLKPWLYRCLLPLNLFFWLLNGGTTYTSILYT
SQVRNTTLSTNTNLGYCLVFPSEESYFANGVMYLTRDLFFVILMV LASFYILLLLYRHQRRVKGLQSSNMSG
SRAETRAAKTVVTLVTLVYLVFFGIDNLIWAYTLTTEKVP LLMNDVRVFFSSLYASVCPVVIVSNRKVNRRLS
KLA

>Lo-ORA8a

GLNAVVCQASLLYSSAPTNSLSEYTLNLEFCIVAFPSFEAYMGNGVMHIVRDFV FVGMMASAGGYIVVILYRHR
KQTRGLOGAARMQRKTVEASKAVLTLIAMYVILFGLDNVWVIYTL CVSRVHPIASDTRVFFASCYSALSPIFIIT
TNKKIVASLSCCKGKDQKHLIAESTVSHLSPGQ

>Lo-ORA8b

VMYIVRDFV FVGMMASAGGYIVVILYRHRRTGLQGADRMQRKTVEASKAVLT
LIAMYVILFSLDNVMWIYPLC
VSHVHPIVSDIRVFFASCYSALSPVFIITTNKKIAASLSCCKGKDQKHLIAESTVSHLSPGQ

Part 2 African coelacanth V1R protein sequences.

African coelacanth V1R sequences were taken from [6].

>Lc-V1R01

MDLCITIKGVSFLLQTGLGVLANLIVLLAYTHIAYS DHKLVAVDMILFHLAFVNMMSSLTRGIPLTMTIFGLRHI
LNDAGCVLVVFIYRVVRALSVCITCLLSWFQAITIVPATSKLSRFKIKVPNYIIPSFVVLWLINIFIYSGVPYYT
TAPTKNSSVPKYTMSTGFCYVIFPNQMSFSLYGVVITSRD LIFVILMILASGYILLILYRHRQQVKALRNPEYST
KSTAESKAAKIVLTLVLFYIAVFGIENIIGLYVTSLSQVHEYIIDLRVVFVSSSYASFSPFLIILNFNKKIKSRLRC
AFLE

>Lc-V1R01a

RMDLCTMIKGVSFLLLETGLGTLGNFLILLAYAYIVFREHKLS PVD MIFCHLAFANMMVLLTRGVPQTMTVFGLCN
LLNDVECKIIVIYTYRIVRALSVCITCLLSMFQAITVAPVTSTWASIKMKAPNNIIPSFALWLINMAVCIAAPFS
SKAPRNGTVPEYTLNLGFC HVDFKDQVSYVINGIAVTMRDCIFVILMVVASCYILLLLHRHSQVKKSIRSSDRNQ
KTTAETRAAKIVIMLVLLYVVFVGIDNIIWIAMLTIAKVSPVIADMRVFFSSCYAALSPFLIISNKKIKAVLRC
NSQQREPRDQATDISYVTT

>Lc-V1R07

MDLRAIMKATSFVLTVIGIPGNFTVLAVFSHIAFTEYKLLPTDIIVTNLALVNFILVISRGFPQILTAFQLRNL
FDTFGCKLIIFAFRIARALSISMTFLLSASQSVTISPATSRLSFLKQRLPKYLWPLIVFFWLLSGATSVTSILYS
TADPNSTASQFTFNLEYCYVAFPGKDAYEGNGTMYVSRDLTFVILMALASIYILFVLYRHSQQVKSI RNP NRNQ
TSAESRAAKTVVTLVALYVIFFGVDNLIWIYSISISRVSPMISDIRVFFSSLYATVSPIVIICSNKKIINKLYCT
RRNQVSQAVEIIFTTV

>Lc-V1R11

SMDAYSFLKGVLFLLLAVIGIPC NF AILGAFGKMIYLGKNLFPVEGIIICLLALVNTMMILTRGVPHILFVFEIRR
LYSQHGCAVIIMARVSRAMAICLTCLLSCSQFLSITPPPSKWISLKAILSKTKNLALIVVCLLFLNLGLCVCSV
LYAMPETNSTNLNFTYNLGYCIVKFPNRHAYLGFGLSLLARDLTFVTSMVIASIAIVMTLLRHRQQVSSIRRSSQ
SHEATVETQAAKS VVTLVTLYVLF FGIENTIFLYTMTGHQVNSVLS D V R F F F S T C Y A S V F P I V A I V A S S K I R E Q L
KCFTQSKE

>Lc-V1R12

MNLYNLMKGLIFLLMGIIAIFGNLIIMVLFHIVYVEGKLPTEFILLNLAWTNMQMVASRGIPQSLYVFG LKKL
FNDSGCRAIIYSARISRAMVICLTCHLS CFQCVTIATSNPKWILVKTKMQKYL VHTIFSLWVFNMFCISRI LFT
FSPFNSTSPENTFN LGYCVVFPDPKVSFEVNGYILFTRDIVFVALMALASACILFLLHRHKRQM QS VRRSGRNQE
SNAENQAAKIVVTLVSLYVFFFGIETTISLYQTTIPASVVSIVSDVRYFFSICYCTIFPFILCRFNQKIKNKLKS
SVGETEKKQIKAFFCN

>Lc-V1R13

MELYNLMKGIIF FIVAIIGTVGNLVVLALFLHIA YQHKLTAERLLLNLAWSNSIMLLTRGVPHSLFVFG LRD L F
SDIGCKIVVYLSRVSRAMSICLT CFLSCLQCIT IATSTLKWVYIKVKMQKYVIPITV FVCLLNMIICIGSVIFS
ISGTNSNYTQFAFNLGYCIVNFPDKLTLHFNGFAPFARDIVFVAMALASAYILLILYRHGKKVKGIRNSEHSHE
STAEGQATKT VVTLVTLYIIFFGIDNTIFVYQIAVSKEVHTIVSDIRFFLSICYGLVFPFIIIGFNSKIRTKLKP
SSSEQQTEVQEVS SI

>Lc-V1R14

MDLYNLVKGIIIFILTAIVGVSGNLVILVSFYHIALQERKFVTAQVILLNLAWANMIMALTRGVPHSLFIFGLRFL
FDDIGCKIVVFASRVSRAMSICLTCLLS CFQ CITITKSTLKWLSLKGRMQKYVILIIIGLCVMNMLVCIAAVLFS
VSSTNTTNLEYTFNLGYCLVTFPDQLSFQVNGFAIFARDIIFVVLMA LASAYILLVLF RHGRQVKGIRSSDRNNV
TTAEGQATKT VVTLVTLYVLF FGI DNTIWFYQITVSKEVHSIVSDIRFFF SVCYASICPIVIIMFNPQIRNKLKA
SSSEQETQVQEISSTQ

>Lc-V1R15

RVIFILITLIGTAGNLVILVSLTHIAYQEHKLLAIEKIVFNLSGANLVISLVRGIPHNLF LF GFRNLYSDVGCKI

TGYVHITFRAVAIVLTCLLSCFQCATIARGRSQWTFVKLNLOKHLEWIIIFGLYLFCMISTIDVIPFSISGQNVN
LKFAVSLGYCFVVPDNIMFQLVGYGIFARDFLVFLMTLASSYILLILYKHKQVQGIRSTERNHETTAEGQAA
KTVVTLVSFYVSVFGLDNTIWFYIEIVSKIMFPVAFDIRNLFSCMCYASFFPIVIITFNKKIRHQLKCPRGEQKQI
ACLSS

>Lc-V1R16

VMDLYEILRRVIFILITLIGTAGNLVILVSLTHIAYQEHKLLAIEKIVFNLSGANLVISLVRGIPHNLFLLFGFRN
LYSDVGCKITGYVHITFRAVAIVLTCLLSCFQCATIARGGPQWTFIKLSLQKHLEWIIIFGLYLFCMITTIDVIPL
SISGQNVNFKFAVSLGYCFVVPDNIMFQLVGYVIFTRDFLFMILMTLASSYILLVLYRHGKQVQGIRSTERNH
EPTAEGQAAKTVVTLVSFYVSVFGLDNTIWFYIEIVSKRMFPVAFDIRNLFSCMCYASFFPIVIITFNKKIRHQLK
PRGEQK

>Lc-V1R17

KMDPEIVNGAVHFVISIIGIAGNIVILASFSHITYHKRKIMAVEKILVNLSGANLIILVSRGLPLSLYAFGLRNL
FNDFCCQFIGYVHITFRALSVALTCLLSCFQSIMLAKNSPKTAKLKLKLQTHIVPILSLLCIFSMLCSVDVIVFS
VSSYNVTVPQYTAAMGYCLVVPNIVTFHLVGYGIFTRDFLVFLMALASSYILLVLYRHGKQVQGIRSMERNHE
STAEGQAAKTVVTLVSFYVTLFGIDNTIWFYQIISKGLISKVFDIRTLISILYAVVFPFVIIAFNKKIRSKLKCF
TSEQKSEISIIIEEMKHIQ

>Lc-V1R18

SMDPETVRGAGYFVITIIGIIGNVVILTTSFSHIAYQERKIMAVEKILVNLSGANLIILVTRGLPLSLYAFGLRNL
FNDLCKKIISFVHISFRALSVALTCLLSCFQSIMLAKNSPKTAKLKVKLQAHIVPILSLLFIFCILCSVDMIVFC
ISSYNVTVLEYTDTMGYCLEVYPNAVMFHLVGYGIFARDFLVFLMALASSYILLVLYRHGKQVQGIRSAEQNRE
STAEGQAAKMVVTLV

TFYATLFGIDNIVWFYQTISEHMISQEFDRTLISLLYAAVFPLVIVFNKKIQNKIKYF

VSLQKSELSLTE

>Lc-V1R19

MVSVTGRGAVYFVITIIGIIGNVVTLTSFSHIAYQERKIMAVEKILVNLSGANLILLMTEGLPMSMYSFGLRHCF
NDACHEFIYYVKMTFRGLSVVLTCLLSCFQSIMLAPNGPKTAKLKMKLQVHIVPILSLLFIFCILFNVDMSVFCI
SSYNITVLEYTDTTEYCFAVMFDFLMGYGVFARDSLVFLMALASFYILLVLYRHGKQVQGIRSAEQNRKSTAEGQ
AAKMVVTLVSFYVTLFGIDNIVWFYKTFAYQLISQEFDIRMLTSLLYVTLFPFVIVFNKKIQNKIKYFVSLQKS
ELSLTE

>Lc-V1R08

MEVRLIFKAAGSIFLEALGIPGNALILATFVFIGISNRKLLPADILLMKLAFVNLIIVMLTFNIPTTVSAFGVRKL
FNDDGCKTVIFLFRVSRALSICMTALLSCYQSIVLAPSSKRWRILKQKMPQKLLLIVIIIFWCVNMLIYSWTLIFS
AEQSFAKSNYSIPMAYCVVSFSPSYTFFAVLGMVFIVRDLLFIAIMVVSSSCIVFILYKHKQVKGIRSSAKNHGR
TAETQAAKAVVMLVILYVFLFGLDNIWAYSLSNLSVLVPEITDVRHFLASCFPSISPIIIITTNKKLQNKLRFIS
QRKKLQNAETVVSINVHTISE

>Lc-V1R09

MDIQVIFKVISFLLLVLVIGIPGNITVMAAFVHLRLSDSKLMPPDIILTKLAFVNLLVVFTRGVPQVLTALGIKKL
FNNNGCRAIIFLFRVSRALSICMTALLSCYQSIVLAPSSKRWRILKQKMPQKLLLIVIIIFWCVNMLIYSWTLIFS
YGPLNSTTEYTLNLEFCFVVPPTFAFYIGNGTLYLFRDFLVGLMVLASGYIVFILYQHRKQVKGIRSSDRGQEN
TAETRAAKAVVMLVALYVILFGLDNIWIYTLQVSKVATVVSARVFFASCYSALSPILIIATNKKIQMKLKSLG
QNQHQTTPETSVSHVQVEI

>Lc-V1R10

MNIRVTLKAIGFFLMVVIGIPGNFTILAVFALIKLSNGKLLSTDIIILTKLAFVNLLIVLVKGIPQAFTAIGIRKL
FNDNGCRAVLLLYRVSRAALSICMTALLSCYQSIIIPSSNRWRALKQKMPQKLVFIMIILWCNIFIYSWTLIFS
FAQLNSTTTEYTLNLEFCFVVPSPFQFYIGNGTLYLFRDFLVGLMVLASGYIVFILYQHRKQVKGIRSSDRGQE
TRAETRAAKAVVMLVALYVILFGLDNIWIYTLQLSKVAPEISDARVFFASCYSALSPILIIATNKKIQMKLKYL
GQKHHHQTPETTISHVQMEM

>Lc-V1R05

MVLSASISEWITYMVFTFIGIVGNSILIHGILTCPTGRLRPSFLLLFSLAAVHMARNVVVNLLSIIYSAGGVSVF

GSAGCKVFKFASALTGTLGIWFTLYTVVFYSVKLEQAVHPLNCAVNTNWRGYHLAGIFVLWVAGLVVCCPIAVFA
EKAKVQVVGNVTHPYRSSVYVGCRCNYPAPEVALIYGTLALTAIDLVPVLAIFSIRIMLLLRKRTGVQFGDIW
IGERTETDVFRAAKCALLLVLLVTALWVSHFTILQCLRRLDEYYFIPTVLAVLSSGYATLSPYLLMIINYRIRAN
L

>Lc-V1R02

TMGTWSIIKGTAFILTVIGMPGNLIIVYAFSYAAYS DHKLM PADIIVLNLALVNLMMVVLVRCIPEMLAAYGINE
LFSDSGCKIVICIYRTRTRALS IWLTFLLSGFQCISIAPITTKWAAF KLQAPGHLFGVLAFLWVFNVGFSIPALLY
GISSSGNSTGNGFSINLEYCFVKFPSQYVKITVGNLQISRDIIPIFLMIFASVYILLILYHHSQQVKHLQSSNRK
RGSSAEIRAAKAVITLVLLYVIFFGIDNVLWVYTLTIKAMTTSVISDLRVFFSSLYAAVSPIVIIIVSNKKVQKRL
KCEREQQGSLAPETVTSTVRM

>Lc-V1R03

MRFSADNVFYGILVLLGIVGNLLVVVTITVAGYEVGTILASDFILANLAIVNFLISTIRNVPLFISDLGLKIYLS
RDYCKIFMFLWVWLRVS SIWATFCISFFHFLVIRRHHSVLRKGKELRNIIITTSVIWIGNFFYAFPTCFYSTRA
YGNETDTIQLLSATRPFLGCIWKFPSLYSGVAYATASLVIHEVFIPLMVVINLGTLYIILYRHSRAVGVETLVT
RVASERRAAKVILILVTLFVICWVTNVLMMVNYNHNTSEKIRVFM LANFGASLFIGFSPVVL MVGHSKLRKKLMN
FTLYLNGIKQKRGKRLTTGKC

>Lc-V1R04

MSQGEHPVQLFFYTMLVALGIVGNSLVIWIVLDTARAANTIPSSDFILLNIAVNNLLISLTRNTLLLALDIGYTF
SMSDGACRILMCIWVWFRCVGVWVTLCLSFHF MVIRSSHSALGKINERRNVIVIVAVLWALNNLLYSSTALALTS
NTSTNISSLVVISSTIRPLLGCWIFSTDTAALFYGILSFIVHEIIPIFLMVITNCGTLFLLYKHHRQVHRADIA
ITRVESEWKA AKTILALILLFVFCWGTHIVSVNYYNFYSSSSSTRYMLIIARFSASGFLGFYPLVVTFGH SKLRK
FHS AVLFWRKQNEVS

>Lc-V1R06

MELTRIIIFLVIRILVCLFGMTGNVAILSVLIKRAFTFRLKTFEMLLVGLTASNFTQELLVDVPEIMKELSGVTIH
RWFCKTLKFTFTFGRANSII FTILICIFRYQKLRHAVSRVNLPVPLDNVKIIHVISASVLAFTFLFSVPVLLHET
NVEMTLKNQTSCPALFFDCPKINCEVSYMAYKLIYLACIDILPILIIILVITTHLLRILYKNYKLVSVTLDGFSPN
KSKIKDSKVRFWKSTKAVLAALLLFQISWTMQLII EFAVSSKKFDYWSETDFLIVALYTSLSPPYVFGIGNNILT

Part 3 Elephant shark ORA protein sequences.

Elephant shark sequences were taken from [7] and [8].

>Cm-ORA1

MELCTVVKGTSFLLQTAIGILGNLTILLSYAHIGYSDRKLLPVDVILTHLAFVNLMVVLTRGVPQTLVTFDVANL
LNDAGCKIVIFYAYRVVRALSV CETCLLSVFQGLTLPVTSKLANYK RKAGRSIGPLAAALWALNIALCIAAPLFS
VAVANSTVSNFTLDLGFCLVGFDPDRVS YVVNGVFISTRDFLVGLMTFASGYILLILHRHRQVRAIQ RAGSAQQ
AKAENRAAKSVISLVSLYVVF FGIDNLIWIYMLTVPLVPPDIADLRVFFSSCYASFSPLLIISSTKKIKSKLFRA
TPQIGPRPPSTEMSHVQQ

>Cm-ORA2

MEGRSAIKGTLYLLLTVLGIPGNLTIISSFVHIAQHRRRLHPADKIVGNLALVNLAVVLVRCVPETTAAFGLEQL
FDDNGCKIVIFYRTT RSLSIWLTFLLSGFQGITLAPSTPKWSIAKRLAPRCLPGALALLWLLNMCLSTSAILFS
ISSGNNSTRKKFAVNLEYCLVKFPSRAVKIAIGALQTSRDVIPIALMILASAYILLILYKHHQQVKGLRSSSKGQ
RSSAETRAAKAVLTLVTLYVLFFGIDNIMWVYTLTVAETMQTSVTS DIRVFFSSLYASVSPIVIIASNKKIQNKM
KCTKAKPEMEASETVPSHN

>Cm-ORA3

MTYQFNPHIIFYGALIFLGT LGNFLVLATILAIVLEDHSFPSSDILLTNLTIVNLLISIFWNIPEFILESGVEML
LPLSWCRLFMFIWVWLRCVSIWVTFLLSLFYFLKIKQHVRLSTKAREATFVSATLLAIWLVNFAYAI PALFYAKA
TSGNETVSLMIVSTTVKPF LGCVWNFPNAQAALAVSKSYLVIQ EILPMLLM LGTNLSTVYYLQKHMRSIGVERLH
SLQVERKAAKVIMALVTLFVLCWGTHLLAVNYYSYNRGSATSFILTLANYSASLFIGFSPLILAMGHGKLRGKIC
KILRIKLT

>Cm-ORA4

MAEHPVLVVAYGLLVSCGILGNSAVISVTMDSTCERNRLSSSDLILINI AVANLLLSLTRNTLLLTLDAGLPVSF
SSEGCR LMMFVWTWLRSTSIWVTLSLSWFHFVTVRTSRGALERLSERRRVIALMAAEWGVNLVYSGFALGYSSNS
TNSTNHLAVISSTIRPLLGC VWTFPTKQSGFIYALVSVVVHEAIPVVLMLYANAGTLLFLYQHHRKVQDSQLAGG
DRISHEWRAAKTILYLI GLFVFCWGTHVLSVNYYNFKGSPSTHYLLVIARFSASGFIGLYPLVVAMGH SKLKHRL
KNILKCLCP

Part 4 Teleost and African coelacanth T2R protein sequences.

Teleost T2R sequences were taken from [9] and [10], African coelacanth sequences were from [6].

>Dr-T2R5

MLSTQDKLVAVLLIGVLAAILTIFFNMYLLLVNYSYRKKHKLNPADFIITAIAIASISQQVLTYSWQTMVDIDTV
CQISLVEAILLVLVFSVKLIIFWSTAFITFYTGKLVVEPVHCYTRIQEAIKHHVHIVLTVIVVSGFANCVPLLS
VLTYYNGTTELGDGCSIMPSDTPGLVYVFYVVISDIIPGIVMFKCSISISYHLAKHLLDMKASSNGTHGPKLGT
QMRVIKMTLSLVFVYSCFVVVDIYTQTTVVLMRQNTLALIMLFASIYTTVSAFVLIYGKKS YWKELIASYNLFLD
EYPCLNKMKVVEVKHEPHEHSHGH

>Dr-T2R4

MEPWLYALISSPLCLIGMVFNLLFFFCLMRPVSGVTLRNPLRFLLIIVLVNSTFQYLVIAVTIIMLLFDYIFWLE
TVTRALIYQFFCGNFLCNAWISIFYYISIVPQHHAIFIWIKRNIKAILYGGFILNQIVLTFIAISTGAVTYFFLGP
VPVNFTALELNSTALAQTLADMFLFHVANFSYLLYCTCPLVTLIVSWGKTFYLRGHMKMKMGQSGESFSQPQQK
SQMRVTVTGMVQAALFLPSSLWTVAAALLYITGLFEEVDPSRFITMTFCSSLGNLLCFGFSQSVFRRGIVSVI
KKLKG

>Dr-T2R2

MSYQCRTLKRKMSTDVGDVLFLLGVGVGVSGNIFNLIFTVQQQVKTRTIQTVGLILDVISISNIILALAILSMV
VGIFLNPQIWCIPYPFDLRLEIYLMLTGCFISFWAIAWLSLFYCIKVVNFSSEIFRTLKKNISTVINTAVLLSC
LFSCFLFIPLFSLDVTVDSTEQNDNAYGNVTCMPSPFTIQMNQDAYSAAVLFLLCPIPLMIMLPTSVRMVVHLCAH
TRALQKNQTQVQGSYSYLLVCKLTISLVGVYLFNLFFVSLFILMKLIGAYITYQYLVSTFTFYCGVTSALLTASN
RYLKDKLWSLFCCKAKEPASKSHTVVTGDV

>Dr-T2R3

MGFFVYISFLAYALVNPVSIITILMNVFFVYCMFSSEKQANSVKPPLNVLLWSLIGCSLLHNIFNLLFVLYE
LVYPPVWLYIISGATILFAMRTSFTACLGLQICYFLQIVPVRWPCFIWMKKHIKLFMYVLLFLDRLYFLSQYVIR
VFLEIRRVMSFNSSSVYDNTTSQSADFGYYMFIADFWLKCCYFFICLGIMLTSGITTVVYLWKHKRMKENTSS
LSALCKRQQMRVTIMGIIQTVLFFFASGWLMTTEEFIECYFGGYDVGTHLASTVMALYSLGTTLTLGIGQSKFRLL
AKDICKKTRKPKS

>Dr-T2R1

MQSNFAYEDHSPFLHKITCILPDVIOYQRRTLKRKMSTDVGNVLFVGVGVGVSGNIFNLIFSLQQQVKTRSIQ
TVGLILDVISISNIILVLSTLAMVSVFLNAHIWCIPYPLGLRFEMYLMTCGFISFWAIAWLSLFYCIKVVNF
SSEIFRTLKKNISTVINTAVTLSCFLSFLFLPAFSLDLPDSADKNISETNITTCPOPTFTLQIDINAYAAVLL
LICPIPLMIMLPTSVRMVVHLCAHTRALQKNQTQVQGSYSYLLVCKLTISLVGVYLSLTFMVALYFIIKVLGAFM
TYQALVSAFTFYCGMTSVLLTASNRYLKDKLWSLFCCKAKEPVSKSQTVVTQDV

>Ga-T2R1

MDFQTYAALNGSLAVLNIVTIAFYIFCLVRPLHGEKIKQPLKLLWTLIGCTKTFLLSGFVSGVTDGFSFQSAVS
SKINQIFYLLMISSVSTSMTSVWLNFFYYSQIVPAHSALFIWIKNNVKSIIYGFWITERIYCLFDFTSMFLRFT
DFDLLLIRNNFTMVDDMPENNFYKEMFWIVFYTLRAHFVFCCLVMVMSSGSTVLYLCGHMRHMAANGQPASSPRF
RNQVRVTVTGLLQGVLYVFSASWIIYSFFPKNDLYIDFTMIDSTVIMSYMSATLFLNLGAGQAVFRQRAEHIWLRA
AHCFAKAPQVQQTQGA

>Ga-T2R2

MDFQTYAALNGSLAVLNTMIIAFYIFCMIRPLHGEKIKQPLKLLWTLIGCTITYLLSGVVAFFSQISAVSSKIN
QIFDLLMICSVSTSMTSVWLNFFYNSQIVPAHSALFIWIKNNVKSIIYGFWITERIYSLLDFTSMFLFTNIDV
SLISNNLTMVDDMSENNFYEEMFWIVFFTLKAHFVFCCLVMVMSSGSTVLYLCGHMRHMAANGQPASSPRFRNQV
RVTVTGLLQGVLYVFSASWTIHSTFQKDGIYIGFTMIDSTVINLYMSATLFLNLGAGQAVFRQRAEHIWLRAAQC
FKAPQVQQTQGA

>Ga-T2R3ie5

MYVMNKSTIWVLTGLLAVTTVFFNVYIFLMSLLSYRQNKWSPCETIILALSLADVAHQVCYLWMTMDEVDSKC
RIADLPYAVMLLLIFSLKFTIMWDTGFLTFFYSTKLVNAPNHCYTRIQAIVILKHVSLAVLLIPLCALGTCMPMLV
VFQSTNVTDGNKDCGLMPASTAGMVYEVYIYLLADVLPGVLMVKCCISISVHLALHLRHMKATTNGTHGPKLGS
QMRVIRMALSLVAVFVFLVIDLYVNYQITMNHESILTTLTFLFTSVYTTVTAMVLIYGKKTFWKALIEHVNVCLE
EYPCLSLKVPEHKAQTGTAKD

>Tn-T2R2

MNVDTAELIRVNLPIVILNALSNLFFVFCLMRPSQGEMLKQPLKLLWMTMVCNLSFLVMLLVRHFVNDIVTS
LIGFATFIFSLTMSLNASVWLNFFYYMQIVPSKSALFVWIKRNLKPIIYYICVAEKVQIWLIGSIIIVYNITEKN
YKLEYLNIVNTSYVASFATSSHLRTFTLTMTIFSDGVYIITLCVMMASSLCTVAYLSRHHMQMASOGLSGSRFRS
QVRVTASGVLQGALYVAIFVLTLPQFQFNILDGATAYMTLSDITMINVYMMGTSVNLGGMQIVFRQRAVDLLHRA
VRSCCTTIKAPQPQPGGS

>Tn-T2R3

MDIFLIIRINVPMVILNLLSNLFFVFCLMRPSQGETLKQPLKLLWMTIICSTLSFLVTLVLVFFMDHDIPEANLA
ICGMFLLSLSISLNASVWLNFFYYMQIVPSKSAIFVWIKRNLKLIYYIWVAEKVINGLIVWSILTFSISITNYL
NDFKFPNSTNASYVIFMPSHLVNMRSSIIATQIYILICLCIMLASSWCTVAYLSRHHMQMASOGLSGSHFRQVR
VTATGVMQGVLYMMVTMCIVSVNLLSDVLSTQASYFSLSNITMINVYMMGTSVNLGGMQIVFRQRAVDLWHRVR
SCTTIKAPQPQPGGS

>Tn-T2R4

MSVDTAELIRVNLPIVILNALSNLFFVFCLMRPSQGEMLKQPLKLLWMTMVCSTLSFLVTLVLVFLHLSFSDIVTS
FTSYGMFVITLSISMNTSVWLNFFYYMQIVPSKSAFVWIKRNLKPIIYYIWVAEKIYIGLFVSSIVLFNITVIK
YELEYLNIVNTSSVAPFETASHLRTLTITIVLSGEIYFIFNLCIMSASSWCTVVYLSRHHMQMASOGLSGSRFRS
QVRVTATGILQGVLYLVISVWTLSQFQFSDIADYAAACVSLSNITMINIYMMGTSVNLGVGQIVFRQKAVDLWHR
AVRSCCTTIKAPK

>Tn-T2R5

MNVDTAELIRVNLPIVILNALSNLFFVFCLMRPSQGETLKQPLKLLWMTMVCNLSFLVMLLVRHFVNDIVTS
LIGFATFIFSLSISLNASVWLNFFYYMQIVPSKSAFVWIKRNLKPIIYCIWVAEKVQIWLIGSIIIVYNIIEKK
YELEYLNIVNTSYVASFATSSHLRTFTLTMTIFSDGIYYIITLCVMSASSLCTVVYLSRHHMQMASOGLSGSRFRS
QVRVTASGVLQGALFVAIFVLTLPQFEFNVLDGATAYMTLSDITMISVYMMGTSVNLGGMQIVFRQRAVDLWHR
VRSCCTTIKAPQPQPGGS

>Tn-T2R6

MERCYIDLDKRTFQLIMYPLCGINLFSNFFFGYCLVSNRRRLRQPLKMLLTFLVLCTIAFVVHLIISHPLFAEMT
NNDVRHHSWMITLLIMHSSMTGAVSMSFYVQIVPSQRALLIWIKNISFIYVIFLFGEIFLAFSSFVNLS
VVLDSWVVSANNCTNNELPVVGPTATDTVVSIFVRIHILCCMAIMGVCNFSMTHYLLRHKSRTROGFAASETQM
RVAISDLIQAVFFLICGLLYSVCTFIFEYSKQFSFGPLLYLTGVLLYMTGTASLATGQAIFRQGAVDLWKVLTA
SF

>Lc-T2R01

MLPSVQFSLWIINSFIIVASIFGNLFVFLMNYRSYRRKGYFLPCELI CCALSAISGFLEVVFYLWMSMSELDRSC
LISQACYISL LLLVIFSLHSA LLWITAFLLFFYS AKIVIEPIHCYTKVQDAILKHAPT VLA AIFFFSFTFNIPLII
LSKHTANETNTQOCGNLVVRDKIIFLSIYLPITAILPAVVMVKSSISILVHLMHRLHKLANTNGFHTPKLSSQM
RVVRMTLVLTIVYLI ALITYVLCMTFAMINNNRLFEIAGTAASIYTMASSLILSYGKQSHWNE LAKLWREFVALF
PMVCSHRPFGCRRE

>Lc-T2R02

MELSVRVSF LVAFAVAYLLALCMNLFILVRYFHAVRKGEVLQPSDLLLIGLIVCNVHHQTSILALSVLGLFHVGC
YAGGYMFKTL SLVFTSASSAQFWLMAWLCTFYCLNIVRISRFFIRM RQCVSGLVPHLLAGSVIGTF AVSLPYFV
YVPVVSNNGLANSTICLMDFRSPAPFYLSLYLTNLCLLPLVLMVASSSVIIMFLHCHVRRMEENTSGFSSPRSD
AYLRITKM LLSLVCLYISFNVATILMNLIKCNFCGLIIS SFAEVYPSLCAII IILGTSKL RQGSTPHCPRCLCL

>Lc-T2R03

MNTAYNIGILVIATALTAIGAPGNLFILAINLSTVRSQQVLPPTDLIISGLALSGIVFQTFVLVLYVMELLGMT
CQMEISTFM MIFYITDALGSVNFWFISWLCIFYCAKIVRSGSRLVIRFQQWINGAVRHLLAWSAVGSFTVPVCYYV
FSLGMNHTDILNNCTNLNIAEHKQIVDDSYCYLVLCCLLPLVIMTTSSSFILLFLRRHAMRMQRSAADGFSSP

SSEAHVRVSKMVLSLMGIYTVFDISIMIFIFTSNEILVLITILLCYLCPGVTPVI I IWGTAKLRNRLPTACWSK
>Lc-T2R04
MYFDFLIAFCVSIFVLLVIGVSGNLFILVSNLNTVRSQQGLPPSDFILTGLSTCNII FQISNGTIGVLLLLLDVIY
TMQNYAWRLYFYITELLVSI GFWFTAWLCVFYCAKII RSSSR LVIQIQQWIVGAVPHLLVWSAVGNFVVCTPKLV
LIFLRNETKTSCNSSFGHFRESKWKLDYMNTFY LALCCLSP LVIMITSSSFII LFLRRHVAKIRRN TTNGFSSPS
SEAYVRVSKMVLSLMGIYSTFDVCFMISLFTTNEVLFLIIIFLCHVYSSVTAALIILGTTKL RKR FNTVCWSKCC
NLLKIGI

Part 5 Tree file in Newick format for sequences shown in Figure 1.

```
(((((Hc_ORA5/1-292:0.025891,On_ORA5/1-292:0.000001)0.999850:0.115729,
((Tr_ORA5/1-294:0.071344,Tn_ORA5/1-294:0.068860)0.999850:0.064032,
((((((Lc_V1R05/1-292:1.555522,((((((LC_T2R04/1-291:0.319128,
LC_T2R03/1-293:0.422544)0.999850:0.301036,LC_T2R02/1-293:0.699631)
0.999850:0.352664,(Dr_T2R1/34-329:0.100066,Dr_T2R2/10-305:0.102929)
0.999850:1.516280)0.993727:0.178072,((Dr_T2R3/6-286:0.941741,
(((Tn_T2R3/1-287:0.199313,(Tn_T2R4/1-288:0.090901,(Tn_T2R5/1-289:0.022745,
Tn_T2R2/1-289:0.026171)0.999850:0.139829)0.999850:0.133825)0.999850:0.423064,
(Ga_T2R2/1-284:0.043038,Ga_T2R1/1-288:0.060334)0.999850:0.603660)
0.999850:0.220361,Tn_T2R6/6-285:1.045838)0.806714:0.066130)0.999850:0.213120,
Dr_T2R4/1-282:0.982660)0.999850:0.818057)0.744109:0.141197,
((Dr_T2R5/3-302:0.408945,Ga_T2R3ie5/2-302:0.436234)0.999850:0.389266,
LC_T2R01/2-297:0.492591)0.999850:0.812569)0.999850:0.413533,
(((((((Ss_ORA2/1-308:0.110057,(((Tr_ORA2/1-304:0.073026,Tn_ORA2/1-306:0.076923)
0.999850:0.129912,Ga_ORA2/1-306:0.146906)0.987816:0.022595,
((OI_ORA2/1-304:0.193657,((Xm_ORA2/1-309:0.061025,Pf_ORA2/15-323:0.013873)
0.999850:0.041252,Fh_ORA2/24-332:0.092193)0.999850:0.093860)0.999850:0.114349,
(Hc_ORA2/1-309:0.038427,On_ORA2/1-309:0.008698)0.999850:0.098331)
0.999850:0.044006)0.999850:0.062894)0.991100:0.056815,Gm_ORA2/1-309:0.142100)
0.974001:0.061344,(Dr_ORA2/1-298:0.332525,Am_ORA2/1-298:0.321737)
0.986950:0.064237)0.999850:0.219183,Lo_ORA2/1-309:0.172730)0.999850:0.254048,
(Cm_ORA2/1-309:0.210308,Lc_V1R02/2-310:0.300987)0.339823:0.034496)
0.445654:0.028566,((((Cm_ORA1/1-309:0.311689,(Lc_V1R01/1-304:0.405854,
(Lc_V1R01a/2-310:0.169730,(Lo_ORA1/1-309:0.124883,(((Gm_ORA1/1-303:0.153795,
(Ga_ORA1/1-306:0.056684,(((Hc_ORA1/1-306:0.059797,On_ORA1/1-306:0.000001)
```

0.999850:0.044944,(OI_ORA1/1-306:0.073734,((Xm_ORA1/1-306:0.019084,
 Pf_ORA1/1-306:0.009971)0.999850:0.028938,Fh_ORA1/1-306:0.030678)
 0.999850:0.024495)0.970784:0.015372)0.999850:0.021912,(Sr_ORA1/1-164:0.006235,
 Sc_ORA1/1-165:0.007107)0.999850:0.041703)0.889947:0.005132)0.999850:0.034255)
 0.992719:0.021645,Ss_ORA1/2-308:0.146575)0.999850:0.042882,
 (Dr_ORA1/1-306:0.142605,Am_ORA1/1-306:0.104147)0.999850:0.044504)
 0.999850:0.094573)0.999850:0.120938)0.993097:0.052023)0.996604:0.062314)
 0.999850:0.174872,(Lc_V1R11/2-305:0.578101,(Lc_V1R12/1-308:0.434657,
 ((Lc_V1R14/1-308:0.147782,Lc_V1R13/1-308:0.250696)0.994874:0.036637,
 ((Lc_V1R17/2-309:0.071693,(Lc_V1R18/2-307:0.029732,Lc_V1R19/1-301:0.187340)
 0.999850:0.117684)0.999850:0.219360,(Lc_V1R16/2-305:0.039215,
 Lc_V1R15/1-299:0.021480)0.999850:0.257617)0.999850:0.279661)0.996854:0.059526)
 0.999850:0.115290)0.999850:0.159897)0.999850:0.065054,((Lc_V1R08/1-305:0.492536,
 (Lc_V1R10/1-309:0.120550,Lc_V1R09/1-308:0.091326)0.999850:0.138687)
 0.859806:0.060401,(Lo_ORA8b/1-125:0.045014,Lo_ORA8a/1-171:0.041007)
 0.999850:0.385357)0.999850:0.151643)0.999850:0.056258,(Lc_V1R07/1-309:0.246345,
 Lo_ORA7/1-303:0.442535)0.999850:0.127521)0.999850:0.182962)0.999850:0.820478,
 (((Lc_V1R04/2-308:0.356525,Cm_ORA4/1-307:0.354635)0.999850:0.326638,
 (Lo_ORA3/13-325:0.279786,(((Dr_ORA3b/13-328:0.124232,Dr_ORA3a/13-327:0.132052)
 0.999850:0.126896,Am_ORA3/14-327:0.246275)0.898716:0.044675,
 (((((Tr_ORA3/19-329:0.046624,Tn_ORA3/17-327:0.053390)0.999850:0.089710,
 Ga_ORA3/19-328:0.094010)0.801132:0.023700,(((OI_ORA3b/44-354:0.069572,
 OI_ORA3a/1-308:0.035903)0.999850:0.165337,(Fh_ORA3/4-314:0.027247,
 (Pf_ORA3/15-325:0.013146,Xm_ORA3/15-325:0.069396)0.999850:0.033493)
 0.999850:0.108108)0.989649:0.029358,(Hc_ORA3/17-322:0.026901,
 On_ORA3/19-324:0.017972)0.999850:0.187065)0.999850:0.032602)0.926022:0.025716,

Gm_ORA3/14-321:0.193113)0.993940:0.036965,(Ss_ORA3b/19-332:0.000001,
 Ss_ORA3a/19-295:0.000001)0.999850:0.166562)0.999850:0.072961)0.999850:0.221018)
 0.999850:0.286331)0.754270:0.046175,((Cm_ORA3/1-305:0.587830,
 Lc_V1R03/1-305:0.435647)0.742873:0.075983,((Am_ORA4/1-316:0.255356,
 (Dr_ORA4/1-311:0.138997,((Ga_ORA4/1-320:0.151383,(((OI_ORA4/1-322:0.139303,
 (Tr_ORA4/1-321:0.029551,Tn_ORA4/1-320:0.057188)0.999850:0.082025)
 0.858952:0.014562,Ss_ORA4/1-322:0.115946)0.989398:0.009803,
 ((Hc_ORA4/1-312:0.013341,On_ORA4/1-312:0.028329)0.999850:0.120732,
 ((Xm_ORA4/1-319:0.062598,Pf_ORA4/1-319:0.032279)0.999850:0.030776,
 Fh_ORA4/1-318:0.042357)0.999850:0.036737)0.998859:0.020347)0.928807:0.014959)
 0.999850:0.053549,Gm_Ora4/1-319:0.133832)0.996504:0.045142)0.995019:0.058330)
 0.999850:0.205802,Lo_ORA4/1-317:0.168302)0.999850:0.386914)0.923614:0.067604)
 0.999850:0.575203)0.997764:0.172013)0.969433:0.195984)0.999850:0.327016,
 (((((Dr_ORA6/1-292:0.530390,Am_ORA6/1-294:0.437447)0.999850:0.133054,
 (Gm_ORA6/1-295:0.465359,((((Xm_ORA6/1-300:0.057075,Pf_ORA6/1-300:0.030828)
 0.999850:0.070328,Fh_ORA6/1-290:0.463988)0.999850:0.206459,
 OI_ORA6/1-294:0.426793)0.943429:0.067516,(Hc_ORA6/1-297:0.035629,
 On_ORA6/1-302:0.012507)0.999850:0.264463)0.967453:0.034732,
 (Ga_ORA6/1-300:0.362072,(Tr_ORA6/1-297:0.064267,Tn_ORA6/1-295:0.086598)
 0.999850:0.160149)0.935740:0.041535)0.995752:0.119868)0.999850:0.140737)
 0.486476:0.059750,Ss_ORA6/1-106:0.730380)0.967121:0.166329,
 Lo_ORA6/1-301:0.407695)0.999850:0.264482,Lc_V1R06/1-290:0.616847)
 0.999850:0.612092)0.999850:0.614691,Lo_ORA5/1-294:0.227177)0.999850:0.152917,
 Gm_ORA5/1-294:0.192129)0.925696:0.048964,(Ss_ORA5b/1-294:0.041105,
 Ss_ORA5a/1-294:0.101137)0.999850:0.060593)0.955185:0.030527,
 (Dr_ORA5/1-289:0.404683,(Am_ORA5b/1-293:0.250523,Am_ORA5a/1-295:0.185641)

0.995590:0.096371)0.999850:0.161105)0.999850:0.061690,Ga_ORA5/1-294:0.147018)
 0.994044:0.036586)0.998545:0.021325)0.917902:0.042847,OI_ORA5/1-292:0.294414)
 0.999850:0.090063,Fh_ORA5/1-294:0.084234)0.999850:0.119472,
 Xm_ORA5/1-293:0.068018,Pf_ORA5/1-293:0.049265);

Part 6 References

1. Saraiva LR, Korsching SI: **A novel olfactory receptor gene family in teleost fish.** *Genome Research* 2007, **17**(10):1448-1457.
2. Ota T, Nikaido M, Suzuki H, Hagino-Yamagishi K, Okada N: **Characterization of V1R receptor (ora) genes in Lake Victoria cichlids.** *Gene* 2012, **499**(2):273-279.
3. Nikaido M, Ota T, Hirata T, Suzuki H, Satta Y, Aibara M, Mzighani SI, Sturmbauer C, Hagino-Yamagishi K, Okada N: **Multiple Episodic Evolution Events in V1R Receptor Genes of East-African Cichlids.** *Genome Biology and Evolution* 2014, **6**(5):1135-1144.
4. Johnstone KA, Lubieniecki KP, Chow W, Phillips RB, Koop BF, Davidson WS: **Genomic organization and characterization of two vomeronasal 1 receptor-like genes (ora1 and ora2) in Atlantic salmon *Salmo salar*.** *Marine Genomics* 2008, **1**(1):23-31.
5. Johnstone KA, Lubieniecki KP, Koop BF, Davidson WS: **Identification of olfactory receptor genes in Atlantic salmon *Salmo salar*.** *Journal of Fish Biology* 2012, **81**(2):559-575.
6. Syed AS, Korsching SI: **Positive Darwinian selection in the singularly large taste receptor gene family of an 'ancient' fish, *Latimeria chalumnae*.** *Bmc Genomics* 2014, **15**.
7. Grus WE, Zhang J: **Origin of the Genetic Components of the Vomeronasal System in the Common Ancestor of all Extant Vertebrates.** *Molecular Biology and Evolution* 2009, **26**(2):407-419.
8. Venkatesh B, Lee AP, Ravi V, Maurya AK, Lian MM, Swann JB, Ohta Y, Flajnik MF, Sutoh Y, Kasahara M *et al*: **Elephant shark genome provides unique insights into gnathostome evolution (vol 505, pg 174, 2014).** *Nature* 2014, **513**(7519).
9. Dong D, Jones G, Zhang S: **Dynamic evolution of bitter taste receptor genes in vertebrates.** *Bmc Evolutionary Biology* 2009, **9**.
10. Oike H, Nagai T, Furuyama A, Okada S, Aihara Y, Ishimaru Y, Marui T, Matsumoto I, Misaka T, Abe K: **Characterization of ligands for fish taste receptors.** *Journal of Neuroscience* 2007, **27**(21):5584-5592.