Supplementary Text 1 (Text S1). Deduced MHC class II amino acid sequences of teleost fish and gar from Ensembl database[a] and matching GenBank cDNA reports[b]

[a] Deduced amino acid sequences of the MHC class II genes in the Ensembl database which were analyzed in the present study (as listed in Table S2, Fig. S2 and main text Fig. 2)

[b] Deduced amino acid sequences of GenBank cDNA reports, used for comparison and estimation whether the class II loci reported in the Ensembl database are expressed (see Table S2); not all matching cDNA reports are shown, but at least one match with above 97% constant domain sequence identity for each expressed gene and in a few cases additional matches suggestive of polymorphism

[c] For spotted gar no MHC class II cDNA reports were found in GenBank.

Zebrafish (Danio rerio) MHC class II sequences

Zebrafish Ensembl sequences:

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Zebrafish translated Genbank cDNA report sequences:

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Unnormalized (nap) Danio rerio cDNA clone nap12d02 5', mRNA sequence D8.35B3
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Stickleback (*Gasterosteus aculeatus*) MHC class II sequences

Stickleback Ensembl sequences:

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LLPSFLDPITYPGGYEVAVAEQQFCRNNLRIDLEAYKFPLERDPPSSHMIFPKDAVELGE
KNSLICHVTGFYPAPVAFSWTKNQENATEGTSRNIPFPNNDGTFNQFSTLEFTPELGDIY
SCMVEHLALDHPLVRFYDVQMSQPSIGPAVFCGVGLTVGLLGVAAGTFFLVKRNECS
>GXVIIB ENSGACG00000003680_ENSGACP00000004837_groupXVII:1117113-1119770
MSSSTFLLLLCLSSCSAADGHGYFMYADFWCNMQTARPQQVEYLVDWYFNKEFTMQYNST
VGKWTGFTAAGLVSAAVFNGNHFDVLQRKEERRLICVDNVGHALNATEDNMAAPSVRLAE
ASGSGHNTTLVCSAYDFYPRRIRLAWLRDGQEVTSGATFSEVTTNGNWTYAVHSSLSFTP
GGRDRVSCKVEHAGLQEPALRTWAAHGARDWETGFLVGGVCALLLGAACLSSGLIVHRRK
YSNIS
>GXVIIA ENSGACG00000003731_ ENSGACP00000004896_groupXVII:1163942-1165035
MAVTLMLALAAALCTSAAGSSHDFHYTYGCYESGEVRVDVLLDGDVVAYADFGREEVVFL
```

IPRLPPFLRDLKKLGYEFAKSSFTHCRSVLAKAKRASPNVTIPQDAPVLSVYSRHEGRGG
AANTLFCLADGFYPPSVNFTWTKNGARVTGGVWDLPYGHNRDGTFHRISTLSTTPREGDV
YSCSVEHRAARRPLASSWAEPKEGPSRVSPAAGFFGASLVVCLIGVASGAYFFTKQPNFG
>GXXB Gr.XX: 1081373-10814066
EPSVRLRSVHAADSRHPRMLLCTGYGFYPKQIRVMWLRNGNNVTSDVTSTEELSNGNWLY
QIHSYLEFTPRSGGEISCVVEHASLTQPKVYDW

Stickleback translated Genbank cDNA report sequences:

>DW594610 CGX114-A05.y1d-s SHGC-CGX2 Gasterosteus aculeatus cDNA clone CGX114-A05 5, mRNA sequence GXVIIB match
MSSSTFLLLLCLSSCSAADGHGYFMYADFWCNMQTARPQQVEYLVDWYFNKEFTMQYNST
VGKWTGFTAAGLVSAAVFNGNHFDVLQRKEERRLICVDNVGHALNATEDNMAAPSVRLAE
ASGSGHNTTLVCSAYDFYPGRIRLAWLRDGQEVTSGATFSEVTTNGNWTYAVHSSLSFTP
GGRDRVSCKVEHAGLQKPALRTWAAHGARDWETGFLVGGVCALLLGAACLSSGLIVHRRK
YSNIS
>DV011001 CNB266-F02.y1d-s SHGC-CNB Gasterosteus aculeatus cDNA clone CNB266-F02 5, mRNA sequence G131B1, G1313B3 and GIIIB match
MAPSFISVSLLFIGLHAADGFMEFWTDECVFNSTELKDIEFIRSYYFNKLEFTRFSSSVG
KYVGFTEYGVRNAEYWNKDASQLSAMRAQKEVYCLNNVQIDYNNILTKSAEPYVRLHSET
PPGGGPLSMLVCSVYDFYPKKIIVRWTRDGRPETTGVTSTDELADGDWYYQTHSHLEYTP
SRSGEKISCVVEHISLSKPLVTDWNPSMPESERNKVAIGASGLILGLTLSLAGFIYYKRK
ARGRILVPSH
>DW672198.1_3 CNB369-F02.y1d-s SHGC-CNB2 Gasterosteus aculeatus cDNA clone CNB369-F02 5', mRNA sequence G131A1 and G131A2 match
MKTKTMMKMMVVLVLSGVFCVSADGPHRDIAINGCSDSDGELMYGLDGEEIWYADFKHGK
GVKAQPSFVDPIEFQGAYEQAVANQQTCRSNLKNDLKAFKDVPLEKDPPSSHMIYPKDGV
ELGEKNSLICHVTGFYPAPVTFSWTKNQENVTEGSSRNVPYLNNDGTFNQFSTLEFTPKL
GDIYSCMVEHLALDHPLVKFYDVQVSQPSVGPAVFCGVGLTVGLLGVAAGTFFLIXGNEC
S

Medaka (*Oryzias latipe*s) MHC class II sequences

Medaka Ensembl sequences:

>M3A ENSORLG00000000025_ENSORLP00000000027_Chr.3:558225-564744
LLSDLKVMKVKLLLFLCEILCGILSGTAEVLHEDFGILGCSDYDQEYMYALDGEEKWYAD
YKKETGVGPQLPLGGHFINPDGYQFAKVYEQVCRRNLKALKKTTKGLQLEQDPPSNVMVY
SRDEVELGQQNTLICHVSGFYPAPVNVSWTRNGEKVPGSINVPLPSSDGTLTQISRLQFV
PQLGDIYSCSVEHPALPEVQTKIWDFEKSQPSVGPALFCGLGLVVGLLGVATGTFFLIKG
NECS
>M3B ENSORLG00000000021_ENSORLP00000000030_Chr.3:554841-556227
MDSSSLRVFLLILTLYPADGFIHYILNRCLFNSSDLKDIENIYSYYYNKEEFLRFSSSSG
KFVGYTEIGVKTAELANNDPEKMSRRRAEKETFCKPNIDNDYSTILTKSVQPRVRVQSLE
PSGGNHPAMLICSVYDFYPKKIKVSWLQDQEEVSSDVTSTAEMEDGDWFYQIHSYLEYTP
RSGGKISCRVEHISLKDPLITDWDPSMPESEKNKIAIGASGLILGLVLSLAGFVYYKRKT
RGRILVPSS
>M5A ENSORLG00000012794_ENSORLP00000016018_Chr.5:25231039-25236341
MSLTSLLLITGAVCASSTTPRHMFHFIYGCYETDEVRVDLVVDDDTIGYADFTKQEMVWC
LPYVPPSGKDLEKEAFKFAKNSIANCHSVLAKAKKADHGTPLRQEPPDLSIYTRYKAEEG
VLDTLFCSANHFYPPTINFTWTKNGAEVTEGLLNLRFSHNKDGTFRGISTLSFTPQRGDV
YSCWVSHEALERPRIITWESRRRRSPARMFFCASLILCLAGIGTGLYFFIKKPNYCCGCQ
>M5B1 ENSORLG00000012822_ENSORLP00000016051_Chr.5:25371618-25375673

```
ILSSLIYFYLLFLTSYYSKDQHGYFMFSDFFCYIPSRNPKEVQYLIDWYFNMELTMQYNS
SVGGWTGFTPAGLITAAKFNADKYDVVQRILERELVCQRSVEMVYNGTEEAKVEPNVSLQ
TVEDNDSTLECSALDFYPKHIRLTWFSNGQEVTEGVTFSDVLPNGDWTYQAHTYLTLTPG
KQDHISCMVQHTSLKEPKIYNWEPSMNQTDRDYIIGGVCALLLGAVFLCVGLIHYKQK
>M5B2 modified from ENSORLG00000012826_ENSORLP00000016062_Chr5:25378453-
25379616
YSKDQHGYFMFSDFLCYLPSRNPKEVQYLIDWYFNMELTMQYNSSVGGWTGFTPAGLITA
AKFNADKHDVVQRILERELVCQRSVEIIYETTETAKVEPNVSLQTVEDNDSTLECSALDF
YPKHIRLTWFSNGQEVTEGVTFSDVLPNGDWTYQAHTYLTLTPGKQDHISCMVQHTSLKE
PKIYNWVCALLLGAVFLCGGLIHYK
>M16B ENSORLG00000009164_ENSORLP00000011497_16:14786594-14792142
TGKSQNCSLGFLPLFLLFSSTNAFYGHGTLKCQFTSSHDLVYLEQVYFNKRLMVQYNSTL
GKYEGYTKKAKDLADGFSKSKPFLEQAVKNREKCRTHMDLVFELQSHPVEPSVRVTPVVR
QGSSHQAMLACSAYNFYPKQIRLTWLRNGEKVINYVTSTEELPDGNWLYQIHSYLEYTPS
PREEITCMVEHASPKEPKLYNWEVLSPPMFGAVRNKIAVGTALLFGSFVFVAGLFFYKRT
T
>M16A ENSORLG00000009164_ENSORLP00000011499_16: 14790903-14792142
SRKQEGFKCSLIHFKTSFFCFVFSVEHEISYFIGCFAEGSTEVLLEFDSEEILYVDFEKE
AVVFTGPSFFKANLSERIQGLTTYKNGKKNRIWCQLADQYFTAETEERDKDPPGEVLIYT
SAEVQPGVENTIICFVNGFYPPSIKVSWTKNGNPVSEGVSHSRYYPNKDQTFHQFSTLSF
TPSWTDVYSCTVEHPALESPKTVLWEPEFHHQHPNLDVFLAASLGLGLLGFAVGTCLIII
ALKRS
>M615B ENSORLG00000019376_ENSORLP00000024128_scf.615:38464-43568
TDMDFSSLCLLFLTLYSADGFLEYDMHRCLFNSSDMKDIEYIYSKHYNKEEVIRFSSSLG
KYVGYTKFGVMAAGYWNKDLEGLRERRADKERLCKTNIDLDYLNILTKSVKPSVMIESVT
SSGGHHPAMLVCSVYDFYPKYIKVSWLRDQEEVSSDVTSTTELEDGDWYYQIHSHLEYTP
RSGEKISCRVEHASLKDPLITDWDPSMPESEKNKLAIGASGLILGLVLSLAGFIYYKRKA
LGRSSLNRF
>M615A ENSORLG00000019409_ENSORLP00000024163_scf.615:87448-89094
FLLPLSLIKVMKIKLLLFLCGILSGTAEVFHEDFQITGCSDYDEEFMVNLDGEEIVYTDF
KKGTEVDAQPSFVGHITYAGGYGATVLELQGCRNDLEVIRRFTKDLPLKQDPPSNVVVYS
RNKVELGQQNTLICHVSGFYPAPVNVSWTRNGEKVSGSINVPRPSSDGTFSQISRLQFVP
QLGDIYSCSVEHPALPEVQTMIWDVEKSQPGIGPAVFCGLGLVVGLLGVATGTFFLIKGN
ECS
>M873B ENSORLG00000018856_ENSORLP00000023542_scf.873:60767-63324
MDSSSLCLLFLTMCSADAFLRYDVDRCVFNSTDLKDIEYIYSMYYNKKEFTRFSSSLGKY
VGYTEYGVKTAERANKDTSELSARKAQKETYCKHNIDNWYKNMLSKSVQPRVRVQSLAPS
GGHHPAMLVCSVYDFYPKTIRVSWLRGKEEVSSDVTSTAEMEDGDWYYQIHSHLEYTPRS
GEKISCKVEHASLKDPLVTEWDPSMPESERNKVAIGASGLILGLVLSLAGFIYYKRKARG
RILVPSS
>M873A ENSORLG00000018887_ENSORLP00000023574_scf.873:65205-67367
MKMKLLLFVCGILSGTAAVFHEDLAITGCSDSDGEDMYALDGEEVWYADFKKQTGVEPQP
PFVDHVSYPGGYEQAVANQQICRSNLKISRIAMKDLPLERDPPSNVVVYSRDEVELGEQN
TLICHVSGFYPAPVNVSWTKNGERVSGSINIPFPSSDGTFTQISRLPFVPQLGDIYSCSV
EHPALTEVQTKIWDVEKTQPGVGPAVFCGVGLAVGLLGVAAGTFFLIKGNECS
```

Medaka translated Genbank cDNA report sequences:

```
>FS518487.1_2 FS518487 OLTE Oryzias latipes cDNA clone olte28i23 5', mRNA
sequence M873B match
SLTANTDMDSSSLCLLFLTMCSADAFLRYDVDRCVFNSTDLKDIEYIYSMYYNKKEFTRF
SSSLGKYVGYTEYGVKTAERANKDTSELSARKAQKETYCKHNIDNWYKNMLSKSVQPRVR
VQSLAPSGGHHPAMLVCSVYDFYPKTIRVSWLRGKEEVSSDVTSTAEMEDGDWYYQIHSH
LEYTPRSGEKISCKVEHASLKDPLVTEWGPVHAR
>BJ883759.1 BJ883759 MF01ASD cDNA Oryzias latipes cDNA clone MF01ASD033f06 5',
mRNA sequence M873A match
```

```
MKMKLLLFVCGILSGTAAVFHEDLAITGCSDSDGEDMYALDGEEVWYADFKKQTGVEPQPPFVDHVSYPGGYEQAVAN
QQICRSNLKISRIAMKDLPLERDPPSNVVVYSRDEVELGEQNTLICHVSGFYPAPVNVSWTKNGERVSGSINIPFPSS
DGTFTQISRLPFVPQLGDIYSCSVEHPALTEVQTKIW
>BJ877464 MF01ASD cDNA Oryzias latipes cDNA clone MF01ASD014g19 5, mRNA
sequence M5A match
ADSLVQLLTVLGFKMSLTSLLLITGAVCASSTTPRHMFHFIYGCYETDEVRVDLVVDDDT
IGYADFTKQEMVWCLPYVPPSGKDLEKEAFKFAKNSIANCHSVLAKAKKADHGTPLRQEP
PDLSIYTRYKAEEGVLDTLFCSANHFYPPTINFTWTKNGAEVTEGLLNLRFSHNKDGTFR
GISTLSFTPQRGDVYSCWVSHEALERPRIITWESR
>BJ891116 MF01ASD cDNA Oryzias latipes cDNA clone MF01ASD014g19 3, mRNA M5A
match
DDDTIGYADFTKQEMVWCLPYVPPSGKDLEKEAFKFAKNSIANCHSVLAKAKKADHGTPL
RQEPPDLSIYTRYKAEEGVLDTLFCSANHFYPPTINFTWTKNGAEVTEGLLNLRFSHNKD
GTFRGISTLSFTPQRGDVYSCWVSHEALERPRIITWESRRRRSPARMFFCASLILCLAGI
GTGLYFFIKKPNYCCGCQ
```

Fugu (*Takifugu rubripes*) MHC class II sequences

Fugu Ensembl sequences:

```
>F402A ENSTRUG00000004342_ENSTRUP00000010322_scaffold_402:55188-57563
MMKMLLLILCCVVGASADSQHEDIRILGCSDLDGEFMYGLDSEEVWYADFSKGEGVDINP
PFIDPITYEEGAYSSAVADLQTCKTSLDITRKSLKDMPPERVAPTSPVIYTKEEVQLSQQ
NTLICFVTGFYPAPVNVSWTRNGEHVTQGTSINVPYPNKEGTFTQISRLAFVPQQGDIYS
CRVQHPALSGQDTRMWTVEVQQPGVGPAVFCGLGLTLGLLGVAAGTFFLIKGNECR
>F713A fuguDAA_scf 713:89-334
QHKDINIVGCSDLDGEFMYGLDSEELWYADFSKGEGVYGTPPFIDPFRYEEGVYSQAVTE
LQTCKTNLDSERKAYKDMPPET
>F7533B ENSTRUG00000017449_ENSTRUP00000044727_scaffold_7533:2656-4187
SRMSSSSLRVFLLFISLYTAAGGFQSYVVDSCDFNSTDLKDIEYTRSLYYNRVMYARFSS
RVGKFEGYTKYGLFQADYWNNQSSILEGLRETKESICQPNIKIDYSNILSKSVEPTVRVH
SVVPPAGGHPAMLVCSVYDFYPRYIKVSWQRDGEEVSQDVTSTDELADGDWFYQLHSHLE
YTPRSGEKISCVVEHASLKTPLVKDWGNHLSVCS
>F7533A ENSTRUG00000017444_ENSTRUP00000044708_scaffold_7533:430-1814
MMKMLLLILCCVLGVSADSQHKDIGIVGCSDLDGEFMYGLDSEELWYADFSKGEGVYGTP
PFIDPFRPTAAAVADLQTCKYNLDVDRKGNKDMPTETVAPTSPVIYTKEEVQLSQQNTLI
CFVTGFYPAPVNVSWTRNGEHVTQGTSINVPYPNKEGTFTQISRLAFVPQQGDIYSCRVQ
HPALSGLDTRMWTVEVQQPGVGPAVFCGLGLTLGLLGVAAGTFFLIKGNECR
>F7721A ENSTRUG00000000833_ENSTRUP00000002005_scaffold_7721:158-1461
MKMLLLILCCVLGVSADSQHKDIRITGCSDLDGEDMFGLDSEELWYADFSKGEGVDGTPP
FIDPVRFEGFYSTAVTNLQICKSNMDVVRKGNKDMPPETVAPTSPVIYTKEEVQLSQQNT
LVCFVTGFYPAPVNVSWTRNGEHVTQGTSINVPYPNKEGTFTQISRLAFVPQQGDIYSCR
VQHPALSGQDTRMWSRQADRQADRQAGR
>F7721B fuguDAB_Scf 7721:2626-3027_no enstrug name
MSSSSLRVFLLFISLYTAGGFQSYRVDRCDFNSTDLKDIEYSRSHYYNKLMYVRFRSSVG
KFEGYTKDGLIQADYWNNISSYLEQMRDEKERYCEPNIKVWYSNILSKS
>F8524B ENSTRUG00000002062_ENSTRUP00000004737_scaffold_8524:1050-3165
MSSSSLRVFLLFISLYTAGGFQSYRVDRCDFNSTDLKDIEYSRSHYYNKLMYVRFRSSVG
KFEGYTKDGLIQADYWNNISSYLEQMRDEKERYCEPNIKVWYSNILSKSVEPTVRVHSVV
PPAGGHPAMLVCSVYDFYPRYIKVSWQRDGEEVSQDVTSTDELADGDWFYQLHSHLEYLP
ACLSALLSVCLSETHLSVPTCLPSDPSMPESERNQIAIGASGLILGLILSLAGFIYFKRK
SRGRILVPNN
```

Fugu translated Genbank cDNA report sequences:

```
>CA846190 haa10g02.y5 Fugu UT11 adult fin Takifugu rubripes cDNA clone
IMAGE:6343467 5 similar to TR:Q31462 Q31462 MHC CLASS II PROTEIN.mRNA F7533B
match
MSSSSLRVFLLFISLYTAGGFQYYVVSRCSFNSTDLKDIEYSRSVYYNKLMYARFSSSVG
KFEGYTKYGLFQADYWNNQSSILEQVRDNKERYCQHNIKNWYSNILSKSVEPEVIVHSVV
PPAGGHPAMLVCSVYDFYPRYIKVSWQRDGEEVSQDVTSTDELADGDWFYQLHSHLEYTP
RSGEKISCVVEHASLKTPLVKDWDPSMPESERNQIAIGASGLILGLILSLAGFIYFKRKS
RGRILVPNN
>CA846902 hab89d12.y1 Fugu hgmpC adult gill Takifugu rubripes cDNA clone
IMAGE:6355654 5 similar to TR:Q31465 Q31465 MHC CLASS II ALPHA. contains MSR1
repetitive element; mRNA sequence. F402A and F7533A match
RYEEGVYSQAVTELQTCKTNLDSERKAYKDMPPETVAPTSPMIYTKEEVQLSQQNTLICF
VTGFYPAPVNVSWTRNGEHVTQGTSINVPYPNKEGTFTQISRLAFVPQQGDIYSCRVQHP
ALSGLDTRMWTVEVQQPGVGPAVFCGLGLTLGLLGVAAGTFFLIKGNECR
>AB453019 Takifugu rubripes mRNA for MHC class II alpha chain, complete cds
F7533A match
MMKMLLLILCCVVGASADSQHEDIRILGCSDLDGEFMYGLDSEEVWYADFSKGEGVDINP
PFIDPITYEEGAYSSAVADLQTCKTSLDITRKSLKDMPPERVAPTSPVIYTKEEVQLSQQ
NTLICFVTGFYPAPVNVSWTRNGEHVTQGTSINVPHPNKEGTFTQISRLAFVPQQGDIYS
CRVQHPALSGQDTRMWTVEVQQPGVGPAVFCGLGLTLGLLGVAAGTFFLIKGNECR
```

Tetraodon (*Tetraodon nigroviridis*) MHC class II sequences

Tetraodon Ensembl sequences:

```
>T19A ENSTNIG00000005593_ENSTNIP00000008293_Un_random:19583822-19591157
MKMLLLILCCILGVSADGQHEDIRIVGCSDFDGEYMHGLDGEELWYADFRRGEGVYAQPD
FIDPIKYEGFYSTAVAVLQICKFNLGIFRKGYKDMPRELDPPTSPMVYTRNEVQLTEPNT
LVCLVTGFYPAPVNVSWTRNGEEVTQGTSINVPYPNNEGTFTQISRLDFVPQQGDIYSCR
VQHPALSEADTRMW
>T19B ENSTNIG00000005592_ENSTNIP00000008294_Un_random:19597929-19598797
MASSALRVSLLFLGLSAAGAFEHYGLRRCDFTSAEPKDMEYSLSVYYNKHLMARFSSSVG
KFVGYDKYGQYQADYWNNQSSFLEAMRSSKQRLCQHNIPLWYSHILSKSVLKDVFVYSVA
PPAGGHPAMLVCSVYDFYPKKIKVSWRRDGQEVSHDVTSTDELADGDWFYQLHSHLEYTP
RSGEKISCVVEHASLKTPLVKDWDPSMPEAERNQIAIGASGLILGLILSLAGFIYFQRKS
RGRILVPTN
>T48B ENSTNIT00000004743_ENSTNIP00000004600_Un_random: 48,695,828-48,696,540
VLVYSVAPPAGGHAAMLVCSVYDFYPKKIKVSGRRDGQEVSHDVTSTDELADGDWFYQLH
SHLEYTPRSGEKISCVVEHASLKTPLVRDWDPSMPEAERNQYAIGASGLILGLILSLAGF
IYFQRKSRGRILVPTN
>T55A ENSTNIG00000000926_ ENSTNIP00000001278_Un_random:55779303-55780575
MKMLLLILCCVLGVSADGQHEDIRIVGCSDFDGEYMYGLDGEELWYADFRRGEGVYAQPD
FIDPLKYAEDPYSLAVATLQMCKFNLGIFRKGYKDMPRELVPPTSPMVYTRSEVQLTEPN
TLVCLVTGFYPAPVNVSWTRNGEEVTQGTSINVPYPNNEGTFTQISRLDFVPQQGDIYSC
RVQHPALSEADTRMWTVEVKQPGVGPAVFCGVGLTLGLLGVAAGTFFLIKVNQCR
>T61A ENSTNIG00000003745_ENSTNIP00000001966_Un_random:61621456-61622716
MKMLLLILCCVLGVSADGRHEDVHIRGCSDFDGEDMYGLDGEERWYADFKRGEGVYALPD
FVDPLKFPEGTYSQAVADQQICKINLGISRKGNKDMPRELVPPTSPMVYPSSEVQLTEPN
TLVCLVTGFYPAPVNVSWTRNGEVTQGTSINVPYPNNEGTFTQISRLDFVPQQGDIYSCR
```

```
VQHPALSEADARMWTVEVKQPGVGPAVFCGVGLTLGLLGVAAGTFFLIKGNQCR
>T61B ENSTNIG00000000531_ENSTNIP00000006345_Un_random:61617277-61620814
MASSALRVSLLFLGLSAAGGFEHYEVDLCDFTSAELKDIEYSRSLYYNKHLYARFSSSVG
TFVGFTKYGLHQADYWNNQSSYLDRLKEEKQRYCHRNIQNWYSHILSKSSHDVTSTDELA
DGDWFYQLHSHLEYTPRSGEKISCVVEHASLKTPLVKDWDPSMPEAERNQIAIGASGLIL
GLILSLAGFIYFQRKSRGRILVPTN
>T70B ENSTNIG00000004611_ENSTNIP00000007260_Un_random: 70,836,268-70,837,419
LKDPTVRVHLVAPPAGGHAAMLVCSVYDFYPKKIKVSWRRDGQEVSHDVTSTDELAD
GDWFYQLHSHLEYTPRSGEKISCVVEHASLKTPLVKDWDPSMPEAERNQIAIGASGLILG
LILSLAGFIYFQRKSRGRILVPTN
```

Tetraodon translated Genbank cDNA report sequences:

```
>CR731060.2 Tetraodon nigroviridis full-length cDNA T19A+T55A match
MKMLLLILCYVLGVSADGQHQDIKISGCSDFDGEFMYGLDGEELWYADFRRGEGVYPLPD
FIDPFRYDEGVYSLAVATLQVCKFNLGLFRKGYKDMPRELDPPTSPMVYTRNEVQLTEPN
TLVCLVTGFYPAPVNVSWTRNGEEVTQGTSINVPYPNNEGTFTQISRLDFVPQQGDIYSC
RVQHPALSEADTRMWTVEVKQPGVGPAVFCGVGLTLGLLGVAAGTFFLIKGNRSR
>CR732064.2 Tetraodon nigroviridis full-length cDNA T19A+T55A match
MKMLLLILCCVLGVSADGQHQDIKISGCSDFDGEFMYGLDGEELWYADFRRGEGVYPLPD
FIDPFRYDEGVYSLAVATLQVCKFNLGLFRKGYKDMPRELDPPTSPMVYTRNEVQLTEPN
TLVCLVTGFYPAPVNVSWTRNGEEVTQGTSINVPYPNNEGTFTQISRLDFVPQQGDIYSC
RVQHPALSEADTRMWTVEVKQPGVGPAVFCGVGLTLGLLGVAAGTFFLIKGNQSR
>CR682088.2 Tetraodon nigroviridis full-length cDNA T61A match
MKMLLLILCCVLGVSADGQHEDVHIKGCSDFGGEDMYGLDGEERWYADFKRGDGVYALPD
FVDPLKFVEGTYSQAVADQQVCKINLGISRKGNKDMPRELVPPTSPMVYPSSEVQLTEPN
TLVCLVTGFYPAPVNVSWTRNGEVTQGASINVPYPNNEGTFTQISRLDFVPQQGDIYSCR
VQHPALSEADTRMWTVEVKQPGVGPAVFCGVGLTLGLLGVAAGTFFLIKGNQCR
>CR727057.1 Tetraodon nigroviridis full-length cDNA T19B match
MASSALRVSLLFLGLSAAGAFKHYEVDLCDFTSAELKDIEFSRSVYYNKHLYARFSSSLG
KFVGFTKWGLRVADYWNNQSSYLDQLRGEKQRFCLHNIQVWYSNILSKSVLKDVLVYSVA
PPAGGHAAMLVCSVYDFYPKKIKVSWRRDGQEVSHDVTSTDELADGDWFYQLHSHLEYTP
RSGEKISCVVEHASLKTPLVKDWDPSMPEAERNQIAIGASGLILGLILSLAGFIYFQRKF
RGRILVPTN
>CR697461.3 Tetraodon nigroviridis full-length cDNA T19B match
MASSALRVSLLFLGLSAAGAFEHYWVSRCDFTSAELKDIEFSRSFYYNKHLNVRFSSSLG
KFVGYDKFGQHQADYWNNQTSFLEAMRDSKQRYCQHNIQNWYSNILTKSVLKDVLVYSVA
PPAGGHAAMLVCSVYDFYPKKIKVSWRRDGQEVSHDVTSTDELADGDWFYQLHSHLEYTP
RSGEKISCVVEHASLKTPLVKDWEPSMPEAERNQIAIGASGLILGLILSLAGFIYFQRKS
RGRILVPTN
>CR726114.2 Tetraodon nigroviridis full-length cDNA T19B match
MASSALRVSLPFLGLSAAGAFKEYTVDRCDFTSAELKDIEFTRSEYYNQHLVVRFSSSLG
KFVGFDKYGQYQADYYNNQSSILEAMRGEKQRYCLNHIPVWYSNILSKSVLKDVLVHSVA
PPAGGHAAMLVCSVYDFYPKKIKVSWRRDGQEVSHDVTSTDELADGDWFYQLHSHLEYTP
RSGEKISCVVEHASLKTPLVKDWDPSMPEAERNQYAIGASGLILGLNLFLAGFIYFQRKS
RGRILVPTN
```

Tilapia (*Oreochromis niloticus*) MHC class II sequences

Tilapia Ensembl sequences:

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>O1A ENSONIG00000006325  GL831301.1: 1,431,629-1,433,771
MKMKELLLFLSCVLCVSANFLHEDIHIVGCSESNGEVMFGLDGEELWYADFENKIGVSPQ
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PSFVDPISFGDGAYETAVINLYICKTNMQVSQEGMKDYPLNHDAPSGVMIYTRNEVELRV
TNTLICHVTGFYPGPVKVSWTKNGQKLTEGFSINVPYPNKDGTFKQIARLQFIPQQGDIY
SCTVEHLALKEPLTKIYNVEAPEKPKPSVGPAVFCGLGVIIGLLSAAGGTFFILKANKCT
>O1B ENSONIG00000006327 GL831301.1: 1,435,653-1,439,547
MASSFLCFTLLFISIHNADGFLEYIVDRCDFNSTELENMEYIYSHYYNKMEYIRFSSNVG
QYVGFTDFGVRLAEVWNNDTADLNLMRLKIATYCHHNIDINDRAILTKSVQPSVRIKSMT
PPSGQHPAMLVCSVYDFFPSKIKVSWLRDGQAVSSDITSTEEMPNGDWYYQTHSQLEYTP
RSGEKISCVVEHASLKEPLITDWDPSSDKSTSESTTLIAIGASILTLGLILLLAGFIFYR
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Tilapia translated Genbank cDNA report sequences:

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antigen, A-B alpha chain in Mus musculus (P14434), mRNA sequence O29A3 match
MMSHHTTDMKHAPLLILILNNFCVFSQIPHEMTYVVGCFVQGLTEVQFEFDGEEFLYADF
PKEEIVYTVPKFIFPDPSHVLVGLSILKDALDNRDWCLIITKIAAMEEKYPPEEKDPPEI
VLFSSDKVELGVENSLICLVNHFYPPSINVTWTKNGHPVSTGVSLSRYFPNKDQTFHQLS
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TLTFTPSEGDFYSCTVEHSALETPQTRIWEAEVTNSDQ
>GR671091 IIA cNOnOE1_014_G17.ab1_c Tilapia adult olfactory epithelium library
Oreochromis niloticus cDNA 5 similar to HLA class II histocompatibility
antigen, DP alpha chain in Homo sapiens (P20036), mRNA sequence O79A3 match
MKMKLWVLLLVLSSVLCVSADALHGDNWISGCSDTDGEAVLILDDEAVWYADFNKQEGIY
PLPPFVDPTTFPGQYGQAVADQQVCRANLKVTRQAMKDVPKELDPPSSLIIYTVLNVELG
VPNILICHVTGFYPAPVNVTWTKNEQKVTEGTSISVPFPNKDGSFKQTSRLNFIPKQGDV
YSCTVEHVALTQPMTKFYAVENSDLILGPAM
>GR702301.1_1 cNOnTE2014_G22.ab1_c Tilapia adult testis library Oreochromis
niloticus cDNA 5' similar to RT1 class II histocompatibility antigen, A beta
chain in Rattus norvegicus (P06341), mRNA sequence O80B match
GGKREARGETRSGRRSACQVN*TSARPTVKLHSTTPLSSHHPAMLVCSVYDFFPSKIKVS
WHRDGQEVTSDVTSTEEMEDGDWYYQTHCYLEYTPRSGEKISCVVEHASLEKPLITNWIP
PHPHSCLRQRGTSLPSAPQD
>GR627548 cNOn16-40D022_P07.ab1_c Tilapia juveniles 16-40 days post-
fertilization library Oreochromis niloticus cDNA 5 similar to HLA class II
histocompatibility antigen, DQ(W1.1) beta chain in Homo sapiens (P01919), mRNA
sequence O57B match
XGGNMRIQNFYFYMFLSLFGLVSSDEDYFQSRACCTFKGPHFEDMEYTRIISLNKIAVLE
YNHTRGSWIGFTPYTIEIAKFWNLNPFGTSEAKALCSTNLGYIQILSNVTDIPTIRVKSV
KQHSGGHPAMLVCSAFNFYPKQIRMIWLRNQKEVTTGVSYSEVMPDGDWYYQIHSYLEYT
PTHGEKITCVVEHLSVSEPILAIWDPTLPVAARNKIIVGICGLLLGFV
>FF281534 AQAH-SP-0931 Spleen of Oreochromis niloticus infected with
Streptococcus agalactiae Oreochromis niloticus cDNA clone SP1179 5 similar to
MHC class II beta chain, mRNA sequence O79B2 match
MASKFLCFTLLFINICTADGYELYSSTRCLFNSTELKDIEFIRSYYYNRMELIRFDSDVG
KYVGYTEFGVKNAEMWNNDPGQLAAMRAQKETYCQYNVGIWYADVLSKSVTPSVRLHSTM
APGCHHPAMLVCSVYDFYPKWIKVSWVRNGQEITSDITSTEEFANGDWLYQVHSHLEYMP
RSGEKISCVVEHASLEKPLIINWVPPMPETERLIIVGAVGLILGLILFLAGVIYRRKSGD
TSLACRFSEKQAEDWDKDAAALSLWKPQKEMFFKPGSELCFTNVLLKSV
>GR679428.1 cNOnOV1024_K05.ab1_c Tilapia adult ovary library Oreochromis
niloticus cDNA 5' similar to HLA class II histocompatibility antigen, DQ(6)
alpha chain in Homo sapiens (P01906), mRNA sequence O97A match disrupted orf
MALSVIALILSAGAACGYIQTQSHNFHYIYGCYESDDVRVDAVVDDDVVAYADFNKEEVV
WVLPHLPQPAKDFKKMAYGVAKASTAHCHSVLGKAKKC*
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Spotted gar (*Lepisosteus oculatus*) MHC class II sequences:

Spotted gar PreEnsembl sequences:

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>501A1 MHCIIA   JH591501: 64.610-66.685
MSVGWKCLGLLVVMQGAATVAVEHTYEVAYFCQSENRKGSRNEVFDDDEMFHIDPDRKVD
EPRLPEFEKWAWNDSSLIQGALANLGICENHLKGVMKAIPDEPAVKVPPKPAVFPEEPVE
LGWPNTLICALNDFTPPTAQLRWLKNGQPVTSDVSSTDYIPLSSNKFAMFSYLSFTPQEG
DIYTCHVEHTALSEPVSVFWDAEVPTDSDASETAFCAIGLALGILGVVLGTVFLIKAIKF
HS
>501B1 MHCIIB   JH591501: 70.640-74.060
MRLVLLCSALVLCLTLSGADDFVYFFRSECHFSASDLRDLVYVRSMTFNGKERVRFNSTV
GKYVGFDTWGEKQANYWNGQKDYIARLSADKDRFCKYNVQLMASGMQDRKIKPEVKIYPA
KTASQGHTHMLVCHAHGFYPRQIAVSWLRNGQPVSSDLTSMSFASDGDWTYQTLLYLEFT
PQGGETFECAVDHVALDGTLKLRWDPAAREAKRNKVIMGASGLVLGLVFAVIGVVYWKRK
TKGHHRLVSSERLVSCVGQVFSGGLVSCPGCALPCAQCLLG
>501A2 MHCIIA  JH591501:  82.102-84.669
TSHIDINVIGCKSDDPVAQDEAQLDGDEMFYADFDKKEMILTLPAFADSFGVDPGWVQGA
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IANRQICINNLEVAIKAENNPPENTDAPVNTIYPRDEVELGKPNTLICLANNFFPPPVKV
RWTKNDVDVSEQATLSRYYPNSDATFYQFSTLSFTPQLGDVYSCSVEHKALPEPKTRIWG
EERSALTSDAN
>501B2 MHCIIB   JH591501:  95.883-99.847
MLMCSALGFYPKQIKVSWLRDGQTVTSDVTSTEELADGDWYYQIHSHLEYTPRAGESIVC
RVEHSSFATPKELTWDPSMPEADRNKIIIGASGLVLGLVIAAAGGIYYKKKSG
>501A3 MHCIIA   JH591501:  120.683-125.781
MHGIAVGSIACREISEWKPGRPCQGGRDRAALGWIFRQDGDAPTAMVYPRDSVELGKPNT
LICSVTDFHPMGIGVTWTHNDRPVTEGVTQTTPLSGRDFSFKVFSFLPFTPRLGDVYSCQ
VQHSALPEPLARLW
>615A MHCIIA JH591615:  5.333-9.156
MLCAFLTAVLLGASGVLSQAQIRHLDRLLTFCVSNSTEAELEKEHDEDEIFYVDLETKQS
VQRLPEFAEKWHVGPEWPPFAQQEVETCRLYLAAKGEGFPEEKLDPPISRLYSENEVELG
VPNALICFITDFHPAPVKVSWTRNTEPVTQGFNVTQYYSNKDYSLRLFSYLSFTPQAGDV
YSCSVEHRALQEPLTRLWEVEVQSDSEAAETAVCGVGLTLGLLGVAAGTFFLIKGNKCN
>615B MHCIIB JH591615: 11.335-16.190
MDSPLHRLAVAVLVLGCTGSRRSVDGNMYQFVHDCEYNDHLEDFLYTRRDIFNKIEILRY
DSNIQTFVGYTPLGIKYAERFNQDKEYLAGLKDDLDNYCKHNAGVYKSTMTDRKVPPSVK
VSATKLLSSKHPTMLVCHVTGFYPQRITVTWLRDGLEIKTDVTSTDLLANGDWTYQVHSH
LELTPRAGETVACRVEHSSLERPLEVTWDPSMPESKKNKIVIGVSGLILGLIITAAGVIY
YKKKSSGRILVPSD
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For spotted gar MHC class II we could not find cDNA reports in GenBank.