

Additional file 1 (AF1). Deduced MHCII amino acid sequence

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Deduced amino acid sequences from *Salvelinus malma* (Saal), *Oncorhynchus nerka* (Onne), *Oncorhynchus kisutch* (Onki), *Oncorhynchus tshawytscha* (Ont), *Oncorhynchus mykiss* (Onmy), *Salmo trutta* (Satr), *Salmo salar* (Sasa) and *Esox Lucius* (Eslu) originating from the genomes described in main text Material and Methods. When available, the GenBank protein accession number and chromosomal location is provided for each sequence. Gene with internal stop codon has -ps included in gene name while partial genes containing a complete single domain or parts of domains are given a -pt extension.

AF1.0 Table of MHCII alpha and MHCII beta sequences from pike and salmonids			
MHCIIA genes	Accession #	Chr.	Genomic location
Eslu_DAA1	NP_001290803.1	chr.17	NC_047585.1:25.160.320-25.165.305
Eslu_DAA2ψ	XP_034143102.1	chr.17	NC_047585.1:25.223.821-25.225.006
Eslu_DAA3	XP_034143470.1	chr.17	NC_047585.1:25.303.871-25.315.116
Eslu_DBA1	XP_010883054.2	chr.20	NC_047588.1:30.293.930-30.298.643
Eslu_DBA2	XP_034144659.1	chr.20	NC_047588.1:30.310.087-30.314.003
Eslu_DBA3	XP_019896238.2	chr.20	NC_047588.1:30.322.856-30.325.597
Eslu_DCA	XP_019897056.2	chr.20	NC_047588.1:30.854.142-30.855.420
Eslu_DDA1	XP_028978174.2	chr.09	NC_047577.1:7.021.282-7.025.210
Eslu_DDA2	XP_028978025.2	chr.09	NC_047577.1:7.044.026-7.054.127
Eslu_DDA3	XP_019905383.2	chr.09	NC_047577.1:7.061.743-7.066.269
Eslu_DDA4	XP_010864729.3	chr.09	NC_047577.1:7.077.058-7.083.387
Onki_DAA	XP_031673251.1	chr.01	NC_034174.2:30.733.108-30.738.210
Onki_DBA	XP_020340180.1	chr.06	NC_034179.2:46.329.716-46.335.674
Onki_DCA1	XP_031675123.1		NW_022263943.1:7.643-10.265
Onki_DCA2	XP_031667867.1		NW_022261979.1:311.232-314.542
Onki_DEA	XP_031657800.1	chr.02	NC_034175.2:19.663.235-19.668.779
Onki_DFA	No	chr.13	NC_034186.2:59.583.236-
Onmy_DAA	XP_021425091.1	chr.17	NC_035093.1:49.670.799--49.671.350
Onmy_DBA	XP_021479589.1	chr.12	NC_035088.1:42.256.089-42.261.363
Onmy_DCA1	No	chr.02	NC_035078.1:949.498-1.950.031
Onmy_DCA2	XP_021419620.1	chr.02	NC_035078.1:29.471.783-29.473.031
Onmy_DCA3	XP_021450880.1		NW_018587944.1:529-1.062
Onmy_DDA	GBTD01042060.1		no genomic match
Onmy_DEA	No	chr.03	NC_035079.1:28.508.845-28.509.058
Onmy_DFA	No	chr.02	NC_035078.1:18.600.094-18.601.625
Onne_DAA	XP_029508585.1		NW_021807294.1:41.778-44.505
Onne_DBA	XP_029483109.1	chr.22	NC_042556.1:38.336.566-38.342.193
Onne_DCA	XP_029503552.1		NW_021791902.1:24-1.239
Onts_DAA	XP_024264231.1		NW_020130363.1:60.941-65.768
Onts_DBA	XP_024288155.1	chr.09	NC_037105.1:55.361.845-55.367.850
Onts_DCA1	XP_024267460.1		NW_020138771.1:20-1.199
Onts_DCA2	XP_024287887.1	chr.09	NC_037105.1:43.135.612-43.141.617
Onts_DCA3	XP_024241033.1	chr.23	NC_037119.1:991.276-992.667
Onts_DEA	No	chr.03	NC_037099.1:16.108.478-16.110.728
Onts-DFA	No	chr.23	NC_037119.1:13.088.214-13.090.095
Saal_DAA	XP_023999496.1		NW_019945608:1634-3556
Saal_DBA	XP_023866627.1	chr.20	NC_036860.1:30.150.199-30.155.979
Saal_DCA	No		NW_019944863.1:7.697-8.641
Saal_DDA	XP_023999181.1		NW_019945231:17.363-22.556
Saal_DEA	No	chr.35	NC_036874.1:9.075.676-9.078.023
Saal_DFA	No	chr.6.1	NC_036845:13.836.333-13.838.339
Sasa_DAA*0101	L77086.1	chr.12	NC_027311.1:61.701.375-61.703.967

Sasa_DBA	EG757342,EU008541	chr.13	NC_027312.1:60.436.490-60.443.021
Sasa_DCA	DW549478,DY704572	chr.02	NC_027301.1:5.092.612-5.094.817
Sasa_DDA	DW557800	chr.12	NC_027311.1:9.215.607-9.218.392
Sasa_DEA	KC316032	chr.02	NC_027301.1:25.249.180-25.251.518
Sasa_DFAps	XP_014056167.1	chr.05	NC_027304.1:55.568.279-55.570.111
Satr_DAA1	XP_029600114.1		NW_021822588.1:3.641-5.620
Satr_DAA2	XP_029591961.1	chr.36	NC_042992.1:504.310-507.170
Satr_DBA	XP_029546517.1	chr.15	NC_042971.1:21.333.634-21.340.327
Satr_DCA1	No	chr.03	NC_042959.1:66.026.793-66.028.716
Satr_DCA2	No	chr.37	NC_042993.1:6.816.058
Satr_DDA	XP_029545631.1	chr.14	NC_042970.1:79.981.941-79.984.210
Satr_DEA	No	chr.37	NC_042993.1:23.645.472-23.647.788
Satr_DFA	No	chr.03	NC_042959.1:52.808.926-52.810.975
MHCIIB genes	Accession #	chr.	Genomic location
Eslu_DAB1	XP_034143025.1	chr.17	NC_047585.1:25.147.505-25.152.712
Eslu_DAB2	XP_034143218.1	chr.17	NC_047585.1:25.335.671-25.342.225
Eslu_DBB1	NP_001290706.1	chr.20	NC_047588.1:30.301.515-30.308.996
Eslu_DBB2	XP_010883050.2	chr.20	NC_047588.1:30.314.683-30.320.727
Eslu_DCB	XP_034144799.1	chr.20	NC_047588.1:30.855.505-30.860.622
Eslu_DBB3	XP_010867200.1	chr.06	NC_047574.1:6.834.048-6.839.218
Eslu_DDB1	XP_010870891.2	chr.09	NC_047577.1:6.996.793-7.014.272
Eslu_DDB2	XP_028978022.2	chr.09	NC_047577.1:7.035.721-7.040.359
Eslu_DDB3	XP_012990668.2	chr.09	NC_047577.1:7.068.106-7.075.388
Onki_DAB	XP_031673186.1	chr.01	NC_034174.2:30.740.885-30.746.625
Onki_DBB	XP_020339901.2	chr.06	NC_034179.2:46.340.511-46.343.391
Onki_DCB1	XP_031675120.1		NW_022263943.1:2.007-7.643
Onki_DCB2	XP_031667866.1		NW_022261979.1:314.625-319.616
Onki_DDB1	XP_031676050.1		NW_022265017.1:30.916-38.225
Onki_DDB2	XP_031666909.1		NW_022261978.1:2.892.149-2.893.573
Onmy_DAB	XP_021425090.1	chr.17	NC_035093.1:49.644.190-49.668.113
Onmy_DBB	XP_021479591.1	chr.12	NC_035088.1:42.266.576-42.269.097
Onmy_DCB1	No	chr.02	NC_035078.1:1.939.969-1.940.217
Onmy_DCB2	XP_021476352.1	chr.02	NC_035078.1:1.942.531-1.943.589
Onmy_DCB3	No	chr.02	NC_035078.1:1.944.223-1.944.501
Onmy_DCB4	XP_021419604.1	chr.02	NC_035078.1:29.466.615-29.469.923
Onmy_DCB5	No		NW_018528397.1:1299-1577
Onmy_DDB1	XP_021412280.1	chr.13	NC_035089.1:5.368.697-5.370.479,
Onmy_DDB2	No	chr.17	NC_035093.1:4.571.316-4.572.534
Onmy_DEB	XP_021449969.1	chr.03	NC_035079.1:28.510.176???28.511.183,
Onne_DAB	XP_029508586.1		NW_021807294.1:46.283-52.355
Onne_DBB	XP_029483107.1	chr.22	NC_042556.1:38.326.373-38.330.559
Onne_DCB	XP_029500393.1		NW_021784836.1:4-1.153)
Onne_DDB	XP_029505744.1		NW_021797582.1:351-1498

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Onne_DEB	XP_029481671.1	chr.03	NC_042537.1:11.058.502-11.059.845
Onts_DAB	XP_024264230.1		NW_020130363.1:54.045-59.238
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Onts_DBB2	XP_024288156.1	chr.09	nNC_037105.1:55.372.711-55.376.082
Onts_DCB	XP_024241171.1	chr.23	NC_037119.1:986.253-990.499
Onts_DDB	No	chr.18	NC_037114.1:40.224.963-40.227.299
Onts_DEB	XP_024251641.1	chr.03	NC_037099.1:16.111.442-16.115.521
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Saal_DCB1	XP_023998766.1		NW_019944863.1:12.805-13.947
Saal_DCB2	XP_024000748.1		NW_019947682:21.354-23.308
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Saal_DFB	No	chr.6.1	NC_036845:13.838.788-13.839.510
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Sasa_DBB	DY726096, EU008541	chr.13	NC_027312.1:60.424.988-60.429.008
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Sasa_DCB2	XP_014028990.1	chr.02	NC_027301.1:40.319.469-40.323.752
Sasa_DDB1	No	chr.12	NC_027311.1:9.234.346-9.240.793
Sasa_DDB2	XP_014039502.1		NW_012348659.1:10.114-11.741
Sasa_DEB	KC316036	chr.02	CM003280.1:25.252.264-25.253.576
Sasa_DFBps	No	chr.05	NC_027304.1:55.566.855-55.567.573
Satr_DAB1	XP_029591960.1	chr.36	NC_042992.1:498.192-502.800
Satr_DAB2	XP_029600113.1		NW_021822588:9.176-13.055
Satr_DBB	XP_029546518.1	chr.15	NC_042971.1:21.322.740-21.326.263
Satr_DCB1	XP_029601215.1	chr.03	NC_042959.1:66.032.511-66.033.418
Satr_DCB2	XP_029594157.1	chr.37	NC_042993.1:6.809.351-6.814.933
Satr_DDB	XP_029545630.1	chr.14	NC_042970.1:79.922.139-79.957.834
Satr_DEB	XP_029593400.1	chr.37	NC_042993.1:23.647.912-23.651.646
Satr_DFB	No	chr.03	NC_042959.1:52.808.461-52.807.743

No accession number means they are manually predicted.

AF1.1 Atlantic salmon (*Salmo salar*; Sasa)MHCI sequences

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>Sasa-DAA*0101 chr.12 NC_027311.1:61.701.375-61.703.967 AAL40122.1
MKTSVIVLILCWQVYAEHKVLHIDLVTGCSDSGLDMYGLDGEEMWYADFNKQEGVVAL
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>Sasa-DAB1*0101 chr.12 NC_027311.1:61.693.947-61.699.457 XP_013988542
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>Sasa-DBB2 NW_012348659.1:10.114-11.741 corrected XP_014039502.1
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KAEQFNADPVVLASFQTP LHFCKYYGALAYKAGLNSNVENKRILSHRSMTPHSDRHP SML
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>Sasa-DEA chr.02 NC_027301.1:25.249.180-25.251.518 No pred.
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SGWALRT

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LTKPSRYGELSMLECSVLGTFYPQEVRSWLRDGLTTAVTSTDTLANGDWSYQLHSYLE
FRPQRGESVSCMVEHPSLDEPLEVVDTSGLDAKWFKMAIGVCSLFIGVAMAIGGGVYYW
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>Sasa-DFaps chr.05 NC_027304.1:55.568.279-55.570.111 XP_014056167.1
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>Sasa-DFBps chr.05 5 NC_027304.1:55.566.855-55.567.573 No pred.
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GIRNADHYNSQAWKMAIRKA*VETICPY SARFFKLSTLERIVPPTVKVCLTKTSRYGELS
MLEDTSGLHTKWFKMAIGVCSLFIGVAMAIGGGVYYWKNR

AF1.2 Brown trout (*Salmo trutta*; Satr)MHCII sequences

>Satr-DAA1 NW_021822588.1:3.641-5.620 XP_029600114.1
MKTSVIVLVLCWQVYAEHKVLHKDLYISGCSDSGLDMYGLDGEELWYADFIKGEVVAL
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TVEHKGLAEPLTRIWEPEVTQPSVGPAVFCGVGLTLGLLG VATGTFFLIKGNQCN

>Satr-DAB1 NW_021822588.9.176-13.055 XP_029600113.1
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TWLRDGGVEKSDVTSTEELANGDWYYQIHSLEYTPRSGEKISCMVEHISLTPMVYDWD
PSLPEAERNKIAIGASGLVLGAILALAGLIYYKKKSSGVL

>Satr-DAA2 chr.36 NC_042992.1:504.310-507.170 XP_029591961.1
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VELGVENTLICHVSGFFPPPVRVRWTRNNQNVTEGVRLSTPYPNADVTFNQFSSLPFTPE
EGDIYSCTVEHKGLTETLTRIWEPEVSQPSVGPAVFCGVGLTLGLLG VATGTFFLIKGNQ
CN

>Satr-DAB2 chr.36 NC_042992.1:498.192-502.800 XP_029591960.1
MSIPIAFYICLTFLSIFYGIDGYFYHRVSECYSSKDLQGI EYIDSFYFNQAEHVRFNS
TVGKYVGYTEYGVKSADAWNKDYLQELGALESYCKYNAAIYYGAILDKTVAPHVRLSSV
TPPSGRHPAMLMCSAYDFYKPIRV TWLRDGREVKSDVISTEELANGDWYYQIHSLEYT
PRSGEKISCMVEHISLSEPMYHCDPSLPEAERNKIAIGASGLVLGAILALAGLIYYKKK
SAGEVISV

>Satr-DBA chr.15 NC_042971.1:21.333.634-21.340.327 XP_029546517.1
MSLEMNYSVIIILITGAVCTSAEIHHEIHFIYGC FESSDPAVGLEIDGDEVFYGDFNKNS
NTCLIADVAFTLPKFISITPEDKERACEYATISRVWCKDCIAWGKQSEPKIPKIKDAPES
TIYPRDEVELGVENTLICFVNDFPPPVKVNWTKNGMEVTEGLSLSRYYPNKDGTFFHQFS
SLSFTPQKEDVYICAVAHTALKDPKTREYKVS GSSAGPAPVFCGVGLTLGLLG VATGIF
LIYKGRATESQEYSWEVRHWTREI

>Satr-DBB chr.15 NC_042971.1:21.322.740-21.326.263 XP_029546518.1
MYVLNFFSIHLLLLFSSLS EVDSSDEDFAHDDAWCRFSSRDLHNMEYILEHHFNKIMVA
QYNSTTERWTGYTAWGVISA EKWNEDPDEIPRRRTDMDVLC KPYANRIYNATEMFMVEPN
VTLRLEGPSDDSSLVCSVHFFYPKHIRVTWLRNGEEVTS DVTSTDLVLANGLWSYQIQSYL
KYTPTTGERITCMVEHISQTEPKLYYWDPSLPKSEKNKIVIGVCGLLLG VVVFVAGLIYW
TKSTGRLLGLIGERDYGTC

>Satr-DCA1 chr.3 No pred. NC_042959.1:66.026.793-66.028.716
MNLSVAIVVLTAVVCTSAEVP HETVYVVLGCLEKTKVEAEAEQLDGE EVVYAEFQSGQEV
WTLPEFLGPFSSSTVRNFKNAVKGRRLCRDALALWIFEEKSPPEVKDAPESTIYPRAEEE
LGVENTLICFANHFYPPPVKVNWTKNGLEVTEGTSLSRYPNEDGTFFHQFSSLSFTPQEG
DVGCTVEHTALEDPKTRFW EYEVREVSGSSAGPAVFCGVGLTLGLLG VAIGTFLYVKGQ
QFN

>Satr-DCA2 chr.37 NC_042993.1:6.816.058-6.815.141
MNLSVTIVVLTAVVCTSAEVP HETVYVVLGCLEKTKVEAEAEQLDGE EVVYADFQSGQEVWT
LPEFLGPFSSSTRKLFYKNAVKGRLLCRDALALWILEENC PPEVKDAPESTIYPRAEEE
LGVENTLICFANHFYPPPVKVNWTKNGLEVTEGASLSRYPNEDGTFFHQFSSLSFTPQEG
DVGCTVEHTALEDPKTRFW

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>Satr-DCB1 chr.03 NC_042959.1:66.032.511-66.033.418 corr. XP_029601215.1
DGYFGHFEMRCWFSSSEDPRDIEYLLQVYGNKKLMGQYNSTTEKCTVYTQWMKNFTETACK
GRAFLADRREEMKKYCSSNVPVVGYYLLDKAVEPYIRLRPVEPFSTRHPAMLVCSAYDFY
PKPIRVTWLRDQGEVTSNVTSTEELVNGDWTYQIHSLEYTPTPGERIPCMVEHFSLTEP
KLHDWDPSLPGPERNKMVIGACGLLLGVVFIAAGLIYYRKSTEGQVLVPTMALPESYGT
I
>Satr-DCB2 chr.37 NC_042993.1:6.809.351-6.814.933 XP_029594157.1
MSVLNLSSIHLLLLFSSLSGVDGYFGHFEMRCRFSSSEDQDIEYLLQVYGNKKLLGQYNS
TTEKCTVYTQWMKNFTETACKGPAFLAERREEMKKYCSSNVPVVGYYLLDKAVEPYIRLR
PVEPFSTRHPAMLVCSAYDFYPKPIRVTWLRDQGEVTSNVTSTEELVNGDWTYQIHSLEY
YTPTPGERITCMVEHFSLTEPKLYDWDPSLPGPERNKMVIGACGLLLGVVFIAAGLIYYR
KKSTEGQVLVPTMALPESYGTI
>Satr-DDA chr.14 NC_042970.1:79.981.941-79.984.210 XP_029545631.1
MMMALVFMILLFMSVSTQGEQHVFNVINARSETEEFNMTIVVDDNEYLHVYLNKEGVV
TLPEWVNYVDCPICVRVAESRRADLNNDIKLFSLETPEAKVPPEIKLYAKDEVKLGINNS
LVCVFNFFPPPVQVKWTKNDENIPKGVKVGQYATNSDYTFYRFSTLTTFEPQEGDIYTCI
VDHTALDEPLTRTWEFEVPPRASVGPVFCGLGLTLGLLG VATGTFFLVKGTQCQ
>Satr-DEB chr.14 NC_042970.1:79.922.139-79.957.834 XP_029545630.1
MMACLQSYLLFVVMFSFFTPTDGHFITTLDLCYRGEDEPHDVEYIWRASDMVKVMEYNS
TLNRF TGYP TPGKHAEQFNADPVVLASFQTPLHFFCKYYGALAYKAGLNSNVEPSVHLR
SMTPHSDRHP SMLTCSAYKFYPKQIRVTWLRNGQEVTSNM TSSEELANGDWHYQIHSYLE
YTPTPG EKISCMVEHASFTEPKILHWDMSLPESGRNKIAIGASGLVLGVVF AAAGLLYYN
RRKTTGGGGRELVP TSHPSQ
>Satr-DEA chr.37 NC_042993.1:23.645.472-23.647.788 No pred.
MGC RVFLAFILGVCLLSHCQSKHLLRFLTFCQKNVPSDEEYDVEFGDEL FYVDPITYQV
ERRLSEFAQQWTPDPGLPHEVYVSLGTCQYNNPRCIVGEKSPPEAIEVPTSHIYSQREVE
LGV PNTLICRVSDFHPTPVDVTWTRNEQPVAERTIIQTQYYSNEDFSFRIFSYLSITPQD
GGEVEVHTDHQTVETAVCVGCVTLGVVG VATGVVFIKKAKRS AW A
>Satr-DEB LG37 NC_042993.1:23.647.912-23.651.646 XP_029593400.1
MALC WVYWMAGLSVIQTWATPAGGYQFQGVIVDCEYDDTIDNMIYFVKNI FNQKLTTIYDS
RVQKYVGFEFEGIRNADRYNSQAWKMAIRKAEVETICRY SARFFKLSTLERIVPPIVKVR
LTKPSRYGEPSMLECSVLGFYPQEV RVSWLRDGLETTTAVTSTDTLANGDWSYQLHSYLE
FRPRRGESVSCMVEHPSLDEPLEVVWDTSGLD AKLFKMAIGVCSVFIGVAMAIGGGVYYW
WKNRSGFRVRNR
>satrDFA chr.3 NC_042959.1:52.808.926-52.810.975 No pred.
MGC RVFLALILGVCLLSHCQSKFAAVFDLLPKKHHSYKEYDVEFEDEL FYVDPMTYRVER
RLPAFAQQWTPDPGLPHEVNVSLGTCQYNI PCCIVGENGAPNRGSHLPHILPERGDFHPT
SVDVTWTRNEQPVGEGTVS QIQYHSNENFSFRIFSYLSITPQEGDIYSCSVGHVSLQEPL
TRIWEVEVYMDHQTVETAVCVGGVTLGVVG VASGLWFIKKAKRSGWALRT
>Satr-DFB chr.03 NC_042959.1:52.808.461-52.807.743 no pred.
SGGYQFQGVIVDCEYDTIDNMIYFVKNI FNQKLTIYGARVQKYMFGGEYAIRNADHYNSQA
WKMAIRKAEVETICPY SARFFKLSTLERIVPPTVKVCLTKTSRYGELSMLEGS DTSGLHT
KWFKMAIGVCSLFIGVAMAIGGVYYW WKNR

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AF1.3 Rainbow trout (*Oncorhynchus mykiss*; Onmy) MHCII sequences

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>Onmy-DAA Chr.17 NC_035093.1:49.670.799 -49.671.350, corr XP_021425091.1
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KEGVVALPPFADQMTFPGFYEQAVGELEIMKGNLAKCIKAYKNPPEAIDPPHSSIYPRDD
VELGVENTLICHVSGFFPPPVRVRWTRNNQNVTEGGRI STPYNTDVTFNQFSSLSFTPE
EGDIYGCTVEHKGLTEPLTRIWEPEV SQSPVGPVFCGVGLTLGLLG VATGTFFFLIKGNQ
CN
>Onmy-DAB Chr.17 NC_035093.1:49.644.190-49.668.113 XP_021425090.1
MSMPIAFYICLT LILFIFSGTDGYFYHRLAQCRYSSKDLHGMEHIDSYVFNKA EYVRFNS
TVGRFVGYTEHGLKNAEAWNSDAGILGQEQAELERFCKHNADIYSAIRDKTVEPHVRLS
SVTPPSGRHPAML MCSAYDFYPKQIRVTWLRDGREVKSDVTSTEELANGD WYYQIHSLEY
YTPKSGEKISCMVEHISLTEPMMYHWDPSLPEAERNKIAIGASGLVLGTILALAGLIYYK
KKSSGVL
>Onmy-DBA Chr.12 NC_035088.1:42.256.089-42.261.363 XP_021479589.1
MSFEMNYSVIIILITGAVCTSAEIHHEIHFIYGC FESSDPAVGLEIDGDEVFYGDFSKNS

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NTCLIADVFTLPKFISITPEDKERACEYATISRVWCKDCIAWGKQSVPKIPKIKDAPES
 TIYPRDEVELGVENTLICFVNDFPPPVKVNWTKNGMEVTEGLSLSHYYPNKDGTFHQFS
 SLSFTPQKEDVYICTVAHTALKYPKTREYKVS GSSVGPAPAFICGVLTLGLLG VATGIF
 FIYKGRATESQE
 >Onmy-DBB chr.12 NC_035088.1:42.266.576-42.269.097 XP_021479591.1
 MYVLNCFPIHLLLLFSSSLSEVVDSSDEDFAHDDAWCRFSSRDLDMEYILEHHFNKIMVA
 QYNSTTERWTGYTAWGVISA EKWNEDPDEIPRRRSDMDVLCKPYANRIYNTTEMFMVEPN
 VTLRLEGPSDDSSLVCSVHFFYPKHIRVTWLRNGEEVTS DVTSTDVLANGLWSYQIQSYL
 KYTPTTGERITCMVEHISQTEPKLYYWDPSLPKSEKNKIVIGVCGLLLG VVVFV VAGLIYW
 KKSTGRLLGLIG
 >Onmy-DCA1 Chr.2 NC_035078.1:1.949.498-1.950.031 No pred.
 MNLSVAIVVLTAVVCTSAEVP HETVYVQG CLENTKVEAEAE LQVDGEEVVYADFQSGREV
 WTLPEFLGPFPSSTVRNFYKNAVKGRRLCQDALALWILEEKCPPEVK
 >Onmy-DCA2 Chr.2 NC_035078.1:29.471.783-29.473.031 XP_021419620.1
 MNLSVAIVVLTAVVCTSAEIP HETVYVQG CLENTKVEAEAE LQVDGEEVVYADFQSGQEV
 WTLPEFLGPFPSSTVRNFYKNAVKGRRLCQDALALWILEEKCPPEVKDAPESTIYPRAEE
 VLGVENTLICFANHFFYP PVPKVNWTKNGLEVTEGASLSRYYPNKDGTFHQFSSLSFTP
 GDVYACTVEHTALEDPKTRFWEYKIEHVS GSSAGPAVFCGVLTLGLLG VATGTFLYVKG
 QQFN
 >Onmy-DCA3ps NW_018587944.1:529-1.062 XP_021450880.1
 ICFANHFFYP PVPKVNWTKNGLEVTEGASLSRYYPNKDGTFHQFSSLSFTPQEGDVYACTV
 EHTALEDPKTRFWEYKIEHVS GSSAGPAVFCGVLTLGLLG VATGTFLYVKGQQFN
 >Onmy-DCB1ps chr.2 NC_035078.1:1.939.969-1.940.217 No pred.
 DGYFGHFEMRCRFSSEEPRDIEFLLQVYGNKKLLGQYNSTTEKCTVYTQWMKNFTETACK
 GPAFLAARRDEMKKYCS
 >Onmy-DCB2 chr.2 NC_035078.1:1.942.531-1.943.589 XP_021476352.1
 MSVLNLSIIHLLLLFSSSLSGVDGYFGHFEMRCRFSSEEPRDIEFLLQVYGNKKLLGQYNS
 TTEKCTVYTQWMKNFTETACK GPAFLAARRDEMKKYCSNVPVYGYLLDKAVEPYVRLR
 SVEPFSTRHLAMLVCSAYDFY PKPIRV TWLRD GQEVTSNVTSTEELVNGDWTYQIHSLE
 YTPTPGERIACMVEHFSLTEPKLYDWDPSMPGPEKNKMVIGACGLLLGVVFIAAGLIYYR
 KKSTEGRVLVPTMALPEIYGTI
 >Onmy-DCB3ps chr.2 NC_035078.1:1.944.223-1.944.501 No pred.
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 >Onmy-DCB4 chr.2 NC_035078.1:29.466.615-29.469.923 XP_021419604.1
 DGYFGHFEMRCRFSSEEPRDIEFLLQVYGNKKLLGQYNSTTEKCTVYTQWMKNFTETACK
 GPAFLAARRDEMKKYCSNVPVYGYLLDKAVEPYVRLRSVEPFSTRHLAMLVCSAYDFY
 PKPIRV TWLRD GQEVTSNVTSTEELVNGDWTYQIHSLEYTPTPGERIACMVEHFSLTEP
 KLYDWDPSMPGPEKNKMVIGACGLLLGVVFIAAGLIYYRKKSTEGRVLVPTMALPEIYGT
 I
 >OnmyDCB5ps NW_018528397.1:1299-1577 No pred.
 DGYFGHFEMRCRFSSEEPRDIEFLLQVYGNKKLLGQYNSTTEKCTVYTQWMKNFTETACK
 GPAFLAARRDEMKKYCSNVPVYGYLLDKAGE
 >Onmy-DDA GBTD01042060.1 TSA: no genomic match
 MMMALVFMIVLFTVSSTQGQAHVFTVIGARSETEEFNMTIVADGNEYLHVYLKNKEDVVT
 LPEWINDVDCPICVRIAESRRAGLSNYIKLFSLETPEAKVPPEIKLYAKEEVKLGINNSL
 VCFINNFPPPVQVKWTKNDENVPKGVKVGQYATNSDYTFYRSTLTTFEPQEGDIYTCIV
 DHMALDEPLTRTWEFEVPPHPSVGPAVFCGLGLTLGLLG VATGIFFLVKGTQRQ
 >Onmy-DDB1 chr.13 NC_035089.1:5.368.697-5.370.479, XP_021412280.1 corr.
 MMACLSYLLFVVMFSFFTPTDGHFITILDLCYRGEDPHDVEYIWR AISDMVKVMEYNS
 SLNRLTGYTPIG IHKAEQFNADPVVLASFQTPLNFLCKRYGAVAYEAGVNNNVEPSVHLK
 SMTAHGDRHPSMLTCSAYKFYPKQIRVTWLRNGQEVTSNM TSSEELANGDWHYQIHSYLQ
 YTPTPG EKISCMVEHASFTEPKILHWDMSLPESERSKIAIGPSGLVLGVVFAAAGLLYYN
 RRKTTGGDVSISHDGA AVTLRPTI
 >Onmy-DDB2 Chr.17 NC_035093.1:4.571.316-4.572.534 No pred.
 DMSLPESERSKIAIGPSGLVLGVVFAAAGLLYYNRRKTTGGDVSISHDGA AVTLRPTI
 >Onmy-DEAps Chr.3 NC_035079.1:28.508.845-28.509.058 No pred.
 KHLRLFLTFCQKNVTSDEEYDVEFDGDELFPYPAVDPM TWSLMEMSSSTQQWTPDPGLPHD
 VYVSLGTCQCNVTRCIVGEKSPPEAIGG
 >Onmy-DEBps Chr.3 NC_035079.1:28.510.176-28.511.183, XP_021449969.1
 MALCWVYVWAGLSAIQTRATPAGGG*QFQGILDCEYDDTTDNMIYFVKNIFNQKLTIIYD

SRVQKYVGFGEFGIRNADHYNSQAWEMAIRKAEVETICRYSAFYFKLSTLERIVPPIVKA
 RLTKPSRYAELSMLECSVLGFYPQEVVSVWLRDRLETTIAVTSTDTLANGDWSYQLHSYL
 EFRPQRGESVSCMVEHPSLDEPLEVVW
 >Onmy-DFaps Chr 2 NC_035078.1: 18.600.094-18.601.625 No pred.
 NHLLQFLTFCQKNITSDKEYEVEFEFDGDELFIYVDPMTYRVEQ*LSEFAQ*WTPDPGLPH*V
 YVSLGTCKYNIPHICIVGENEHYPHSGVNNRASHI*SQRKVELGVPNTLICLVINFHPTPV
 HVTWTINEQPVGERTVSQTQYYSNEDFSFRIFSYLSITPQEGDIYSCSVGHVSLQEPFTR
 NWEVEVHTAHQTAVCVGSVTLGVVGVATGVWFIKKAKRSGWA

AF1.4 Sockeye salmon (*Oncorhynchus nerka*; Onne)MHCII sequences

>Onne-DAA NW_021807294.1:41.778-44.505 XP_029508585.1
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 KEGVVALPPFADQITFPGFYEQAVGNQGVCKANLATSİKAYKNPPETIDPPHSSIIYPRDD
 VELGVENTLICHVSGFFPPPVRVRWTRNNQNVTEGGRISTPYNTDVTFNQFSSLSFTPE
 EGDYIGCTVEHKALTEPLTRIWEPEVSPSVGPAVFCGVGLTLGLLG VATGTFFLIKGNQ
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 >Onne-DAB NW_021807294.1:46.283-52.355 XP_029508586.1
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 TVGRYVGYTEYGVKNAKAWNSDAGILGQEQAE LERVCKTGAAIDYSNILDKTVEPHVRLS
 SVTPPSGRHPAMLMCSAYDFYPKPIRVTWLRDGREVKSDVTSTEELANGDWYQIHSLE
 YTPKSGEKISCMVEHISLTEPMMYHWDPSLPEAERNKIAIGALVWCWEPs
 >Onne-DBA chr.22 NC_042556.1:38.336.566-38.342.193 XP_029483109.1
 MSFEMNYSEIVLILTGAICTSAEIHHEIHFIYGC FESSDPAVGLEIDGDEVFYGDFNKNs
 NTCLIADVFTLPKISITPEDKERACEYATISRVWCKNCIAWGKQSEPKIPKIKDAPES
 TIYPRDEVELGVENTLICFVNDFPPPVKVNWTKNGMEVTEGLSLSRYYPNKDGTTFHQFS
 SLSFTFPQKEDVYICAVAHTALKDPKTREYKVS GSSVGPAPVFCGVGLTLGLLG VATGMF
 FIYK GK RAT
 >Onne-DBB chr.22 NC_042556.1:38.326.373-38.330.559 XP_029483107.1
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 QYNSTTERWTGYTAWGVISA EKWNEDPDEIPRRRSDMDVLCKPYANRIYNTTEMFMVEPN
 VTLRLEGTSSDSSLVCSVHFFYPKHIRVTWLRNGEEVTS DVTSTDVLANGLWSYQIQSYL
 KYTPTTGERITCMVEHISQTEPKLHYWDP SLPKSEKNKIVIGVCGLLLG VVVFV VAGLIYW
 KKSTGRLLDLIGELDYGTCD
 >Onne-DCA1 NW_021791902.1:24-1.239 XP_029503552.1
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 WTLPEFLGPFPSSTVRNFYKNAVKGRRLCQDALALWILEEKFPPEVKDAPESTIYPRAEE
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 >Onne-DCA2ps NW_021792314.1:276 XP_029503714.1
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 KDGTTFHQFSSLSFTPQEGDVYACTVEHTALEDPKTRFW EIHEVSGSSAGPAVFCGVGLTL
 GLLGVATGTFLYVKGQQFN
 >Onne-DCBps NW_021784836.1:4-1.153 XP_029500393.1
 LDKAVEPYIRLSVEPFSTRHLAMLVCSAYDFYPKPIRVTWLRDQEVTSNVTSTEELVN
 GDWTYQIHSHLEYTPTPGERIACMVEHFSLTEPKLYDWDP SPMGPPEKNKMVIGACGLLLG
 VVFIAAGLIYYRKKSTEGRVLVPTMALPESYGTI
 >Onne-DEB NW_021797582.1:351-1498 corr XP_029505744.1
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 IHKAEQCNADPVVLASFQTPLLSFCKHYGAVAYEAGVNNNHPSMLMCSAYKFYPKQIRVT
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 DMSLPESERSKIGLVLG VVFAAGLYYNNRRKTTGGDGE
 >Onne-DEB chr.03 NC_042537.1:11.058.502-11.059.845 corr. XP_029481671.1
 MALCWVYWVAGLSAIQTRATPAGGYQFQ GIVDCEYDDTTDNMIYFVKNI FNQKLTTIYDS
 RVQKYVGFGEFGICNADHYNSQAWKMAIRKAEVETICRYSAFFKLSTLERIVPPIVKAR
 LTKPSRYGELSMLECSVLGFYPQEVVSVWLRDWLETTTAVISTDTLANGWSYQLDSYLE
 FRPQRGERVSCMVEHPSLDEPLEVVDTSGLD AKWFKMAIGLCSLFNGVAMAIGGGVYYWW
 KNR
 >Onne-DEA chr.03 NC_042537:11.054.824-11.056.805 No pred.
 MGC RVFLAFIRGVCLLSHCQSKHLLRFLTFCQKNGTSDEEYDVEFDGDELFIYGLPHDVYV

SLGTCQYNIPRCIVGEKSPPEAIEVPTSHIYFQREVELGVPNTLICQVSDFHSTPVDVTW
 TRNEQPVGERTVIQTQYYSNKDIFRIFSYLSITPQEGDIYSCSVGNVSLQEPLTRIW
 >Onne-DFaps Chr.14 NC_042548.1:12.356.454-12.358.337 No pred.
 MGC RVFLALILGVCLLSHRQSKHFLRFLTFCQNNITSDKEYDVEFDGDELFFVDPMIYVW
 EQRLSEFAQ*WTPDPGLPH*VYVSLGTCQYNIPHCIVGEHYPHSGVNNRASHI*SQRKVE
 LGVPNTLICQVINFHPTPVDVTWTINEQPVGERTVSHTQYYSNEDFSFRIFSYLSITPQE
 GDIYSCSVGHISLQEPFTRNWEVEVHTTHQTVERAVCVGSVTLGVVGVATGVWFIKKAKR
 SGWALRT

AF1.5 Coho salmon (*Oncorhynchus kisutch*; Onki)MHCII sequences

>Onki-DAA chr.01 NC_034174.2:30.733.108-30.738.210 XP_031673251.1
 MSLCCLNMKTSMIVLILCCQVYAEDKVLHIDIYITGCSDSGDVMDYGLDGEELWYADFNK
 KEGVVALPPFADQISFPGFYELAVGNQGVCKANLATFIKAYKNPPETIDPPHSSIIYPRDD
 VELGVENTLICHVSGFHPAPVRVRWTRNNQNVTEGVRISTPYNTDFTLNQFSSLSFTPE
 EGDIYGCTVEHKALTEPLTRIWEPEVSQPSVGPVAVFCGVGLTLGLLGVATGTFFLIKGNQ
 CN
 >Onki-DAB chr.01 NC_034174.2:30.740.885-30.746.625 XP_031673186.1
 MSMPIAFYICLTLLWSIFSGTDGYFHVVSQCRYSSKDLHGIEFIDSYVFNVRVEHIRFNS
 TVGRYVGYTELGLKNAEAWNKGQQLGQEQGELERFCKRNADLHYRAILDKTVEPHVRLSS
 VTPPSGRHPAMLMCSAYDFYPKQIRVTWLRDGREVKSDVTSTEELANGDWYYQIHSHLEY
 TPKSGEKISCMVEHISLTEPMMYHWDPSLPEAERNKIAIGASGLVLGTILALAGLIYYKK
 KSSGVL
 >Onki-DBA chr.06 NC_034179.2:46.329.716-46.335.674 XP_020340180.1
 MSFEMNYSVIIILITGAAC TSAETHHEIHFI FGC FESSDPAVGLEIDGDEVFYGDFNKN
 NTCLIADVFTLPKFVSITPEDKERACEYATISRVWCKDGIAGWKKSEPKIPKIDAPES
 TIYPRDEVELGVENTLICFVNDFPPPPVKVNWTKNGMEVTEGLSLSRYYPNKDGTFHQFS
 SLSFTFPQKEDVYICAVVHTALKDPKTREYKVS GSSVGPVAVFCGVGLTLGLLGVATGIS
 FIYKGRATESQE
 >Onki-DBB chr.06 NC_034179.2:46.340.511-46.343.391 XP_020339901.2
 LQIRLLKNTFTCPFSVIIIVDSSDEDFAHNDAWCRFSSSDLHMEYILEHHFNKIMVAQYN
 STTERWTGYTAWGVISA EKWNEDPDEIPRRRSDMDVLCKPYANRIYNTTEMFMVEPNVT
 RLEGPSDSSSLVCSVHFFYPKHIRVTWLRNGEEVTS DVTSTDVLANGLXSYQIQSYLKYT
 PTTGERITCMVEHISQTEPKLYYWDPSLPKSEKNKIVIGVCGLLLG VV FV VAGLIYWKKS
 TGRLLDLIGELDYGTCD
 >Onki-DCA1 NW_022263943.1:7.643-10.265 XP_031675123.1
 MNLSVAIVVLTAVVCTSAEIPHETVYVQGCLEKTKVEAEAEQVDGEEVVYADFQSGQEV
 WTLPEFLGPFPSSTVHNFKYNAVKGRRLCQDALALWILEEKFPPEVKDAPESTIYPRAEE
 VLGLENTLICFANHFPYPPPVKVNWTKNGLEVTEGASLSRYYPNKDGTFHQFSSLSFTPQE
 GDVYACTVEHTALEDPKTRFWEIHEVSGSSAGPAVFCGVGLTLGLLGVATGTFLYVKGQQ
 FN
 >Onki-DCB1 NW_022263943.1:2.007-7.643 XP_031675120.1
 MSVLNLSSIHLLLLFSSLSGVDGYFGHFEMRCRFSSEEPRIEFLLQVYGNKLLGQYNS
 TTEKCTVYTQWMKNFTETACKGPAFLAARREEMKKYCSSNVPVVFYGLLDKAVEPYIRLR
 SVEPFSTRHLAMLVCSAYDFYPKPIRVTWLRDQEVTSNVTSTEELVNGDWTYQIHSHLE
 YTPTPGERIACMVEHFSLTEPKLYDWDPSMPGPEKNKMVIGACGLLLGVVFIAAGLIYYR
 KKSTEGRLVPTMALPESYGTI
 >Onki-DCA2 NW_022261979.1:311.232-314.542 XP_031667867.1
 MNLSVAIVVLTAVVCTSAEIPHETVYVQGCLEKTKVEAEAEQVDGEEVVYADFQSGQEV
 WTLPEFLGPFPSSTVHNFKYNAVKGRRLCQDALALWILEEKFPPEVKDAPESTIYPRAEE
 VLGLENTLICFANHFPYPPPVKVNWTKNGLEVTEGASLSRYYPNKDGTFHQFSSLSFTPQE
 GDVYACTVEHTALEDPKTRFWEIHEVSGSSAGPAVFCGVGLTLGLLGVATGTFLYVKGQQ
 FN
 >Onki-DCB2 NW_022261979.1:314.625-319.616 XP_031667866.1
 MSVLNLSSIHLLLLVSSLSGVDGYFGHFEMRCRFSSEEPRIEFLLQVYGNKLLGQYNS
 TTEKCTVYTQWMKNFTETACKGPAFLAARREEMKKYCSSNVPVVFYGLLDKAVEPYIRLR
 SVEPFSTRHLAMLVCSAYDFYPKPIRVTWLRDQEVTSNVTSTEELVNGDWTYQIHSHLE
 YTPTPGERIACMVEHFSLTEPKLYDWDPSMPGPEKNKMVIGACGLLLGVVFIAAGLIYYR
 KKSTEGRLVPTMALPESYGTI
 >Onki-DBB1 NW_022265017.1:30.916-38.225 XP_031676050.1
 MDGSHPGGPQLLQSNYTDQQCHGDDPDGHFITILDLCYSRGEDPHDVEDIWR AISDLVKV

MEYNSSLNRFTGYTPIGIHTAEQLNADPVVLASFQTPPLHFFCKHYGAVAYEAGLNNNVEP
SVHLSMTPHGDRHPSMLTCSAYKFYPKQIRVTWLRNGQEVPSNMTSSEELANGDWHYQIH
SYLEYTPTPGKISCMVEHTSFTEPKILHWDMSLPESERSKIAIGASGLVLGVVFAVAGL
LYYNRRKTTGGDGEYKMFYCIHRIHGLMMVSILEMCKECLLLF
>Onki-DDB2 NW_022261978.1:2.892.149-2.893.573 XP_031666909.1
VHSCFFSPDGHFITILDLCYYRGEDPHDVEDIWRASDMVKVMEYNSPVVLASFQTPPLHF
FCKHYGAVAYEAGLNNNHLSTPHGDRHPSMLTCSAYKFYPKQIRVTWLRNGQEVPSNMT
SSEELANGDWHYQIHSYLEYTPTPGKISCMVEHTSFTEPKILHWDMSLPESERSKIAIG
ASGLVLGVVFAVAGLLYYNRRKTTGGDGE
>Onki-DEA 1 chr.02 NC_034175.2:19.663.235-19.668.779 XP_031657800.
MGC RVFLAFILSVCLLSHCQTLLPSRGQLTQGLPHDVVSLGTCQYNIPRCIVGEKSPPE
AIEVPTSHIYSQREVELGVPNTLICQVSDFHPTPVDVTWTRNKQPVGERTVIQTQYLSNK
DFSFRNFSYLSITPQEGDIYSCSVGHVSLQEPLTRIWEVEVDTDHQTIVETAVCVGGVTLG
VVGVASPGRSGATSSTPT
>Onki-DFaps chr.13 NC_034186.2:59.583.236- 59.585.022 No pred.
MGGRVFLALILGVCLLSHHQSGNHLRLFTFCQNNITSDKEYDVEFDGDELFYVDPMTYW
VDQRLSEFAQ*WTPDPGLPRVYVSLGTCQYNIPHCIVGEHYPHSGVNNRASHI*SQRKVD
LGVPNTLICQVINFHSTPVDVTWTINEQPVGERTVSQTQYYSNEDFSFRIFSYSITPQE
GGDIYSCSVGHISLQEPFTRNWEVEVHTAHQTIVETAVRVGVSVTLEVVGVATGVWFIKKAK
RSGWALRT

AF1.6 Chinook salmon (*Oncorhynchus tshawytscha*) MHCII sequences

>Onts_DAA NW_020130363.1:60.941-65.768 XP_024264231.1
MSLCCLNMKTSMIVLILCCQVYAEDKVLHIDISINGCSDSDGVGMVGLDGEELWYADFNK
KEGVMLPPFADQMTFPGFYEQAVGNQGVCKANLATSIAKYNPPETIDPPHSSIIYPRDD
VKLGVENTLICHVSGFFPPPVRVRWTRNNQNVTEGGRISTPYPNTDVTFNQFSSLSFTPE
EGDIYGCTVEHKGLTEPLTRIWEPEVSQPSVGPVAVFCGVGLTLGLMGVATGTFFLIKGNQ
CN
>Onts-DAB NW_020130363.1:54.045-59.238 XP_024264230.1
MSMPIAFYICLTLLIFISGTDGYFHHRLVQCRYSSKDLHGIEFIDSYVFNKAIEYIRFNS
TVGRYVGYTELGVKNAEAWNKGPQLGQEQAELERFCKPNAALHYRAILDKTVEPHVRLSS
VTPPSGRHPAMLMCSAYDFYPKQIRVTWLRDGREVKSDVTSTEELANGDWYYQIHSHLEY
TPKSGEKISCMVEHISLTEPMYHWDPSLXELNRNKIAIGAXGLWLGTILALAGLIYYRK
KSSGVL
>Onts-DBA1 chr.09 NC_037105.1:43.135.612-43.141.617 XP_024287887.1
MSFEMNYSVIIILITGAVYTSAEIHHEIHFIYGC FESSDPAVGLEIDGDEVFYGDFNKNS
NTCLIADVFTLPKFISITPEDKERACEYATISRVWCKDCIAWGKQSKPKIPKIKDAPES
TIYPRDEVELGVENTLICFVNDFPPPVKVNWTKNGMEVTEGLSLSRYYPNKDGTTFHQFS
SLSFTPQKEDVYICAVAHTALKDPKTREYKVSRSVGPVAVFCGVGLTLGLLG VATGIF
FIYKGRATESQE
>Onts-DBB1 chr.09 NC_037105.1:43.147.513-43.149.018 No pred.
AHDDAWCRFSSRDLHMEYILEHHFNKIMVAQYNSTTERWTGYTAWGVISAEKWNEPDPE
IPRRSDMDVLCKPYANRIYNTTEMFMVEPNVTLRLEGPSDSSLVCSVHFFYPKHIRT
WLRNGEVTSDVTSTDVLANGLWSYQIQSYLKYTPTTGERITCMVEHISQTEPKLYYWDPS
LSKSEKNKIVIGVCGLLLGVVFFVAGLIYWKSTGEE
>Onts-DBA2 chr.09 NC_037105.1:55.361.845-55.367.850 XP_024288155.1
MSFEMNYSVIIILITGAVYTSAEIHHEIHFIYGC FESSDPAVGLEIDGDEVFYGDFNKNS
NTCLIADVFTLPKFISITPEDKERACEYATISRVWCKDCIAWGKQSKPKIPKIKDAPES
TIYPRDEVELGVENTLICFVNDFPPPVKVNWTKNGMEVTEGLSLSRYYPNKDGTTFHQFS
SLSFTPQKEDVYICAVAHTALKDPKTREYKVSRSVGPVAVFCGVGLTLGLLG VATGIF
FIYKGRATESQE
>Onts-DBB2 chr.09 nNC_037105.1:55.372.711-55.376.082 XP_024288156.1
MYVLNCFSIHLLLLFSSSLSEVVDSSDEDFAHDDAWCRFSSRDLHMEYILEHHFNKIMVA
QYNSTTERWTGYTAWGVISAEKWNEPDPEIPRRSDMDVLCKPYANRIYNTTEMFMVEPN
VTLRLEGPSDSSLVCSVHFFYPKHIRTWLRNGEVTSDVTSTDVLANGLWSYQIQSYL
KYTPTTGERITCMVEHISQTEPKLYYWDPSLSKSEKNKIVIGVCGLLLGVVFFVAGLIYW
KKSTGRLLGLIGELDYGTCD
>Onts-DCA1 chr.23 NC_037119.1:991.276-992.667 XP_024241033.1
YADFQSGQEVWTLPEFLGPFPSSTVRNFYKNAVKGRRLCQDALALWILEEKFPPEVKDAP
ESTIYPRAEEVLGVENTLICFAIXFYPPPVNVNWTNGLEVTEGVSLSRYYPNKDGTTFHQ

FSSLSFTPQEGDVXSLHVEHTALEDPKTRFWEIHGVSGSSAGPAVFCGVGLTLGLLGVAT
GTFLYVKGQQFN

>Onts-DCB chr.23 NC_037119.1:986.253-990.499 XP_024241171.1
MRCRFSSEEPDIEFLQVYGNKLLGQYNSTTEKCTVYTQWMKNFTETACKGPAFLAAR
RDEMKKYCSSNPVYGYLLDKAVEPYIRLSRVEPFSTRHLAMLVCSAYDFYPKPIRVTW
LRDGGQEVTSNVTSTEELVNGDWTYQIHSHLEYTPTPGERIACMVEHFSLTEPKLYDWDP
MPGPEKNKMVIGACGLLLGVVFIAAGLIYYRKKCNEGRVLXPTMALPESYGTI

>Onts-DCA2 NW_020138771.1:20-1.199 XP_024267460.1
MNLSVAIVVLTAVVCTSAEIPHETVYVQGCLEKTKVEAEAEELQVDGEEVVYADFQSGQEV
WTLPEFLGPFPSSTVRNFYKNVAVKGRRLCQDALALWILEEKFPPEVKDAPESTIYPRAE
VLGVENTLICFANHFFYPVNVNWTNKGLEVTGVSLSRYYPNKDGTTFHQFSSLSFTPQE
GDVYACTVEHTALEDPKTRFWEIHEVSGSSAGPAVFCGVGLTLGLLGVATGTFLYVKGQQ
FN

>Onts-DEB chr.03 NC_037099.1:16.108.478-16.110.728 No pred.
MGRVFLAFILGVCLLSHCQSKHLLRFLTFCQKNVTSDEEYDVEFDGDELPHYGLPHDVYV
SLGTCQYNIPRCIVGEKSSPEAIEVPTSDIYSQREVELGVPNTLICQVSDFHPTPVDVTW
TRNEQPVGERTVIQTQYYSNKDFSFRIFYLSITPQEGDIYSCSVGHVSLQELPRSWEVEV
DTDH*TVETAVCVGGVTLGVVGVASGVWFIKAKRSGWALRT

>Onts-DEA chr.03 NC_037099.1:16.111.442-16.115.521 XP_024251641.1
MHGSLGLLGGWTFHSDPGNTSRAQKYVGFGEFGIRNADHYSQAWKMAIRKAEVETI
CRYSARFFKLSTLERIVPPIVKVRLTKPSSYGELSMLECSVLGFYPQEVVRVSWLRDGLT
HSXVTSTDTLANGDWSYPLHSYLEFRPQRGESVSCMVEHPSLDEPLEVWGERPGEGLV
WSGVRAGGRGGNVGERGTERGNILLIAVFS

>Onts-DEA chr.23 NC_037119.1:13.088.214-13.090.095 No pred.
MGRVFLALILGVCLLSHRQSKHLLRFLTFCQKNITSDKEYEVEFDGDELPHYVDPMTYRV
EQ*LSEFAQ*WTPDPGLPH*VYVSLRTCQYNIPHCIVAEHYPHSGVNNRASHI*SQRKVE
L*VPNTLICQVINFHSTPVDVTWTINEQPVGERTISQTQYYSNEDFSFRIFSYSITPQE
GDIYSCSVGHISLQEPFTRNWEVEVHTAHQTVETAVCVGSVTLGVVGVATGVWFIKAKR
SGWALRT

AF1.7 Charr (*Salvelinus alpinus/malma*)MHCII sequences

>Saal-DAA NW_019945608:1634-3556 corr. XP_023999496.1
MSLCCCLNMKTSVIVLILCCQVYAEDKLLHIDLYIAGCSDSDGVDMYGLDGEELLYADFKK
GEVVMPLPPFADPFTYPGAYEQAVGNQGACKANLATSIAKYNPPETIDPPHSSIIYPRDD
VELGVENTLICHVSGFHPAPVRVRWTRNNQNVTEGVRTSTPYNTDFTLNQFSSLTFTPE
EEDIYGCTVEHKGLTEPLTRIWEPAVWSAVFCGVGLTLGLLGVATGTFFLIKGN

>Saal-DAB NW_019945608:6748-11843 XP_023999497.1
YSSKDLHGAEFIDSYVFNKAEYVRFNSTVGKYVGYTEHGVYNAKTWNKGSELVRELGELE
RFCKHNADIHYSAILDKTVEPHVRLSSVTPSSGRHPAMLMCSAYDFYPKPIRVTWLRDGH
EVKSDVTSTEELANGDWYYQIHSHLEYTPKSGEKISCMVEHISLTPEMMYHWDPSLPEAE
RNKIAIGASGLVLGAVLALAGLIYYKKKSSGVL

>Saal-DBA chr.20 NC_036860.1:30.150.199-30.155.979 XP_023866627.1
MSFEMNYSVIIILITGAVCTSAEIHHEIHFIYGCFFESSDPAVGLEIDGDEVJYGFNKN
NTCLIADVFTLPKFISITPEDKEXACEYATISRVWCKNCVWAGKQSEPKIPKIKDAPES
TIYPRDEVELGWENTLICFVNDFFPPVKVNWTKNGMEVTEGLSLSRYYPNKDGTTFHQFS
RLSFTPQKEDGYICAVVHTALKDPKTREYKVSAGGPAVFCRVGLTLGLLGVATGIF
FIYKGRATESQE

>Saal-DBB chr.20 NC_036860.1:30.142.406-30.145.022 XP_023868529.1
MYVLNCFSIHLLLLFSFLSEVVHSSDEDFAYNDVWCRFSSRDLDMEYILEHHFNKIMVA
QYNSTTERWTGYTALGVISA EKWNEDPDEIPRRRTDMDVLCKPYATRIYNTVEMFMVEPN
VTLRLEGPSDDSSLVCSVHFFYPKHIRVTWLRNGEEVTS DVTSTDILANGLWSYQIQSYL
KYTPTTGERIICMVEHISQTEPKLYHWDPSLPKSEKNKIVIGVCGLLLGVVFFVAGLIYW
KKSTGRSLGLIGECGYGTC

>Saal-DCAps NW_019944863.1:7.697-8.641 No pred.

MNFCVAIVVLTAVVCTSAESHETVYVLGCKLEKTKVEAEALQVDGEK*YMLTSRVVTGSLD
IA*VLGPFFQALLSVTSYKNAVKGRRLCRDALALWILEEKGPPEVKVENTLICFANHFFYP
PVKVNWTKNGLEVTEGASLSRYYPNEDGTFHQLSLSLSTPQEGDVYACTVEHTALEDPKT
RFW
>Saal-DCB1ps? NW_019944863.1:12.805-13.947 pseudogene
MKNFTETACKGPAFLAARREEMKKYCSSNVPVVGYYLLDKAVEPYIRLRSVEPFSTRHLA
MLVCSAYDFYFKPIRVTWLRDGEVTSNVTSTEELVNGDWTYQIHSHLEYTPTLERESPV
WWSTSASLSPNCMTGTPPCLVLRGIRW
>Saal-DCB2 NW_019947682:21.354-23.308 XP_024000748.1
DGYFGRFEMRCRFSSSEDPRIEFLQVYGNKKLLGQYNSTTEKCTVYTQWMKNFTETACKG
PAFLAARREEMKKYCSSNVPVVGYYLLDKAVEPYIRLRSVEPFSTRHLAMLVCSAYDFYF
KPIRVTWLRDGEVTSNVTSTEELVNGDWTYQIHSHLEYTPTGERITCMVEHFSLTEPK
LYDWDPSMPGPERNKMVIGACGLLLGVVFIAAGLIYYRKKSTEGRVLVPTMALLESYGTI
>Saal-DDAps NW_019945231:17.363-22.556 XP_023999181.1 corr.
HVFNVINARSETEEFNMTVVXDGNELHVVYLNKEDVVTREPWGNIDCPICVRFAERQR
AGLNNSIKVLSLETPEAKVPPEIKLYAKEEVNLGINNSLXCFVNXXFPPPVQVKWTKNDE
NVPKGVKAGQYATNSDYTFYHFSTLTTFEPQEGDIYTCIVDHTALDEPLTRTWEFEVPPP*
GPAVFCGLGLTLGLLGVATGTFFLVKGTQCQ
>Saal-DDB1 NW_019945231:30.347-33.914 No pred.
FFSPDVHFVTTLELCYRGEDPQHVSSESINMVTVAEYNSAFNRYTGYTVGIYHAEIQ
NKDLFFYCKDDGELVYKAGFNKVEPSIHLRSMTPHPSKLTCCSSYKFNPKQIRVTXWRDQ
EVTSDATSPEDLANGNGYHQIHTYLEYTPPIPERISCMVKHASFTEPKSLHWSGLVLGVFF
GAVGLDYNNRRKTTTCG
>Saal-DDB2ps NW_019952256:1.709-3.388 XP_024001573.1
NSTLNRFM*GYTPFGIHTRAI*EQFNADPVVL*ASFQTPHFFCKHYGALSTKVEPSVHL
RSMTXHSDRHPMSMLTCSAYKFYFKQIRVTWWRDGEVTSNMTSSEELSNGDWHYQIHSYL
EYTPTPGEKISCMVEHASFTEPKILHWDMSLPGSERSKIAIGASGLVLGLVFAAAGLLYY
NGRKTGTGGDRELVPSTHPSQ
>Saal-DDB3 NW_019944305.1:90.396-105.291 no pred.
MVACLQSYLLFVVMFSFFTPTDGHFMTSLDLCYRGEDPHDVEYVWRAISDMVKVMEYNS
TLNRFYGYTPFGIHIAEQFNADPVVLASFQTPHFFCKHYGALVYEAGINNNVEPSVIWR
SMTPHSDRHPMLTCSAYKFYFKQIRVTWWRDGEVTSNMTSSEELSNGDWHYQIHSYLE
YTPTPGEKISCMVRHASFTEPKILHWDMSLPGSERSKIAIGASGLVLGLVFAAAGLLYYN
GRKTGTG
>Saal-DEA chr.35 NC_036874.1: 9.075.676-9.078.023 No pred.
MGCVRFLAFILGVCLLSHCQSGKHLRLFLTFCQKNIPSDDEYDVEFDGDELFIYVDPITYR
VERRLSEFAQQWTPDPGLPHEVYVSLGTCQYNIPRCIVGEKSPPEAIIHYSQREVELGVP
NTLICRVSDFHPTPVDVTWTRNEQPVGERTIIQTQYYSNKDFSFRIFSYSITPQEGDIY
SCSVGHVSLQEPLTRIWEVEVHTDHQTVETAVCVGGVTLGVVG VATGVWFIKKAKRSGWA
LRT
>Saal-DEBps chr.35 NC_036874.1:9.078.877-9.079.056 No pred.
VSPSVKVRILTTPSRYGELSMLECSVLGFYPQEVVRVSWLGDGLETTTAVTSTDTLANGDWS
>Saal-DFA chr.6.1 NC_036845: 13.836.333- 13.838.339 No pred.
MGCVRFLALILGVCLLSYCSKHLFLIFCQKNITSNKEYDVEFAGDELFIYVDPMTYRV
EQRLEFAQQWTPDPGLPQEVYVSLGTCQYNIPHCIVGENSHIYSQRKVEXGVPNTLICR
VINFHPTPVDVTWTRIEQPVGERTVXQTQYYSNEDFRIFSYSITPQEGDIYSCSVGHVS
LQEPLTRIWEVEVHTDHQTVTTAVCVGSVTLGVVG VVTGVWFIKKAKRSGWALRT
>Saal-DFBps chr.6.1 NC_036845: 13.838.788-13.839.510 No pred.
SGGYQFQGIVDEYDDTIDDMYFV*KNIFNQKLTIIYGSRVQKYMGEYGCNADHYSQ
AWKME*VETICPY SARFFKLSTLERIKVCLTKPSR*GELSMLEGS*VINFHPTPVDVTWT
RIEQPVGERTVXQTQYYSNEDFRIFSYSITPQEGDIYSCSVGHVSLQEPLTRIWDTSCL
DTKWFKMAIVVCSLFIGVAVAIGGFYSWWKNR

AF1.8 Northern pike (*Esox Lucius*) MHCII sequences

>Eslu-DAB1 XP_034143025.1 chr.17 NC_047585.1:25.147.505-25.152.712
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FNMVEDVRFNSSVGEYVGYTELGVKNAKAWNSDPGELAGIRAQLDSYCRNNAGIHYSAVL
DKTAKPYVRMSSVTPPSGRHTAMLCSAYDFYFKQIRVTWQRDGEIKSDVTSTEELADG
DWYYQIHSHLEYTPKSGEKISCMVEHSSLPEPMVYDWDPSMPESERNKIAIGASGLVLGA
IIALAGLVYKKKSAGVL

>Eslu-DAA1 NP_001290803.1 chr.17 NC_047585.1:25.160.320-25.165.305
MKSSVIFLILSSVYAEIKVLHIDLYTDGCSDSGDVMDYGLDGEEKWYADFNKQKGV EPL
PPFADPLTYPGGYEQAVANQQICKQNLATSIKANKNPEEKIVPPHSSIIYPRDDVVLGVKN
TLICHVSGFHPPAPVRVRWTRNNQIVTEGVRMSTPYPNQDFSHNQFSSLTFTPEEGDIYSC
TVEHQGLSEPLTRIWEPEVTQPSVGPVFCGVGLTLGLLG VATGTFFLIKGNECN
>Eslu-DAA2ps XP_034143102.1 chr.17 NC_047585.1:25.223.821-25.225.006
MFGLDGEEKWYAILSPTLEANLQPCXGNLAVDIKAYKNPEEKIVSPHSSIIYPRDDVVLGV
ENTLICHVTGFIPPPVRVRWTRNNQTVTEGVHMSTPYPNQDFSHKQSPXLTFTPEDRDIY
SCTVVHQGLSEPPQTRIWKP KVTQPSVDPVFCGVGLTVGLLG VATGTFFLIKGNERLRLQ
LQSIMVKSV
>Eslu-DAA3 chr.17 XP_034143470.1 NC_047585.1:25.303.871-25.315.116
MICCCCLNMKTPMIFVFLASVYTEGKFLHIDLSIDGCSDSRVTIGEDGDELWFADFNK
HQGVGALPPFADPISFQGLYERAVSSQICKHNLVVD SKAFNKPEEKIVPPHSSIIYHRDD
VILGLENTLICHVSGFHPPPVRIRWTRNNQNVTEGIRISNPYPNQDFSYSQFSSLTFTPE
EGDIYSCTVDHKGISEPQTRIWEPEGTHPSVGPTVFCGVGLTLGLLG VATGTFFLIKGNR
>Eslu-DAB2 XP_034143218.1 chr.17 NC_047585.1:25.335.671-25.342.225
MGLININMFLIGILSISHRTDGYFEQLIDQCRFISKDLQDMEFIRSEVFNQVEIIRFNST
VGEFVGYTEYGFSAIKRMNSDTAYLAAIQAERDSVCKPNAWNHYRSIMDKTVKPTLR LRS
VTPPSDRHPAMLICSAYSFYKPI SVSWLRDGH EIKSDVISTEELADRDWYYQIHSHLEY
TPKSGEKISCMVEHISLPEPMVYDWDPSMPESERNKIAIGASGLVLGAI IALAGLVYYKK
KSAGVLP
>Eslu-DBA1 Chr.20 XP_010883054.2 NC_047588.1:30.293.930-30.298.643
MRMNIFVIIILISGTVCTSAQDHELFATLTCFEP SHPELVVMVDGDEVGYTDFQKDEPVM
LLPTPADIHIFPSIVNAYAQLSEMWCKERIAW GELATPSIPQVKDAPESTIYTRNEVELG
VNNTLICFFYNFFPPA IKVNWTKNGMEVTTGGASLSRYHPNKDGT FHLFSTLSFTPLEGDI
YACTVEHTALEEPKTRSWEPVSEFSAGPTIFCGVCLTLGLLG VATGTFFLLTKRKPCFKY
FYTQTGRTGISFDLQGV SANL
>Eslu-DBB1 NP_001290706.1 chr.20 NC_047588.1:30.301.515-30.308.996
MCVLYFWSLHLLFFCVVHSSDGVFAEHNARCHFRKVDEIEYTEDIYFNKEVLLWYNGSTG
IWKGDTSKKNILASYFNNDPNDHFSRRRAIKDVLCLLNAKALYENLKNYTVKPNVRLKSVE
HSSHRHSAMLVCSAYDFYPKTIMITWLRNGQTVNSDVTSIEEMSNGDRSYQIHSYLEYTP
TAGEIITCMVEHYSLLPQLHDWDPSMPKSEMNIKIVIGISGLLLGLVFLAAGLIYNRKN S
TVLIPVRTSDDMG PSSG
>Eslu-DBA2 XP_034144659.1 Chr.20 NC_047588.1:30.310.087-30.314.003
MNFSVIIILISGLIICSFADVEHEVIGAVGCFESGDTKVVVMLDGD EMMFFSNYEKEMVETK
MPGSLSGIESPSVQYQYAKLSIRRCKERLEWGRNAVPSIPQVKDAPKSSIIYTRNEVELGK
NNTLICFVNGFFPPP INVNWTNGKDVTEEAALSSYPNTDGT FHFQSTLSFTPKDGDLY
ACTVKHTALEEHQTRTWETEVSERGGPAIFCGVGLTLGLLG FSTGTFFLLIKGKMKF
>Eslu-DBB2 XP_010883050.2 chr.20 NC_047588.1:30.314.683-30.320.727
MSVLKFLSLHLVLLFSVHAVVFPTDGNFAELHARCRFRKKYDIEYIEENYFNKKKMLFYN
TTKDYWIGYTPSGTDLANIFNKDPYHKDAKRAAKDILCAHADPLYN FLQNYTLTPHIRL
RSVKPTGTRHSAMLVCSAYDFYPKTIIMTWLKNKRAVTS DVIESTEEMSNGDWSYQIHLYL
EYTPTAGEIITCMVEHITLTEPQLYDWDPSMPKSERNEIVIGVFGLLLGVVSVAMGLIYY
KKKSTGLMLVPTGYDMDPSSG
>Eslu-DBA3 XP_019896238.2 chr.20 NC_047588.1:30.322.856-30.325.597
MFHHEIHFIYGC FESGDPEVGMMVDGDEVFYGFFNSNVVDV VWTLPKYPPIKMNQIQKLL
ALEYVTNSEPWCKENLAWGQMAQPKIPKVK EAPESTIYPREHVKLGENNTLICFVN NFFP
PPVKMYWKKN GMEVTKGTSLSRYYPNKDGT FHFQSTLSFTPEEGDIYACTVEHTSLEDPE
SYFWEHEVSEVIVSSAGYSVFCGMGLSLGLLG VATGTFLMVKRSKSN
>Eslu-DBB3 chr.06 XP_010867200.1 NC_047574.1:6.834.048-6.839.218
MSKLINYYIDMLLFFCLTELVDSSDEDFGYVDAWC RIRSRDLHDLEYILEHHINKQ MVA
QYNSTTERWKGYTEYGEMSAKLWNNDPDEIPRRTLEKNVLCRLNAPVIYDNVEAFMDPPN
VTLRQDGPPSNPTLVCSVRYFYPKDITVTWLRNGQEVTS DVTTTGQLANGFWSYQIHSHW
KYTPTAGDRITCMVEHFSLSEPKLYDWDPSLPESERRKIVIGACVLM LGSVFLAAGLVFR
NRSTEWPMETTGA VNYATISG
>Eslu-DCA chr.20 XP_019897056.2 NC_047588.1:30.854.142-30.855.420
MVRNNAQKSRLIRPGNIPVFNCPIFVPHEAIYVFGCREEGDDEAEIQ LDGNEIVHAD FQ
RREVVMMLPGDTEFSFN VYFTHGIFLRDAFRNIQTCDVLKIWTAEERSPPEVKEAPEST
IYSREDVKLGENNTLICFGNNFFPPPVKMYWKKN GMEVTEGTSLSQYYPNKDGT FHFQST
LRFTPEEGDIYACTVEHTALNKPQTRFW EYKNSEMNGSSAGSAVFCGLGLVLGLLG VASG
IFLYVKGQQFN

>Eslu-DCB XP_034144799.1 chr.20 NC_047588.1:30.855.505-30.860.622
 MSGNLNLSIIHLLLLFSLSGVVSFYFGHIQMKCQFNSKDLRDTLVNLNINKGLVAEYNSS
 TNRFTANTEWVKKLVDSDNDEPDSRHKIQFYFDQYCRRNIPLMYEYIMNKTLKPQVRLSL
 AEPSGTRHSAMLVCSAYRFYPKDIIIVTWLKNQKVTSDVSSTEQLADSDWSYQIHSYLEY
 TPTAGEIITCMVEHYSLTEPQLHDWDSSIPWSENNIVIGASVLLLGAHSVAMGLIYYRK
 KSTANRTGPI

>Eslu-DDB1 XP_010870891.2 chr.09 NC_047577.1:6.996.793-7.014.272
 MMASLQSYLLFVCLFSFFIQTGFFLTIQHLCYFRGEDPLDVEYVFRIYSNRVNALEYNS
 TLNRFSGYTPYGESSASHINQDPLSLTKQKAVLDLYCKHYGPLVYDAVLLKMWQPYVRLS
 VEKHPSDRHTPTMLKCSAYKFYPRKIRVTWLRDQGEVPMSSTEELANGDWYYQIHSYLEFT
 PTPGEKISCMVEHPSLTEPMILHWDESLPESGRSDLVVGVSGLVLGVIFAAAGLIFYHNR
 RKTSGDNSM

>Eslu-DDA1 XP_028978174.2 chr.09 NC_047577.1:7.021.282-7.025.210
 MCTVFVILHLGVISALVQAQHVFNVMIKRSKTEEFKMTACADGEEYLYVDLDNRKVVITA
 PEFGEEIECPICSLAAENGRIYTKELSNIFGLDTPEDKVPPDVMLYPKEEVKQGVNNSLV
 CFVNNFFPPPQVQKWTKNVDNITKEVKLSPIFFNTDITFYHFSTLTDFDPEDGDLYTCTVE
 HPALDEPLTRKWEFLTDHFLPWYKKKNRAFRSKTIFMHDNAPSHAAENTSVSLAAMGIKG
 GTLMVWPPSSPDLPNFENLWSILKQTI

>Eslu-DDB2 XP_028978022.2 chr.09 NC_047577.1:7.035.721-7.040.359
 MTHLNTENLLVTMLLPMVFSVITIRCLFCHFHSVHGCTVMMACLRSYLLSIGMISIFTP
 NDGHFFTIHHLCFRGEETEYILREISDMTKVLEYNSTLKRFTGFTRLGIYNAERFNKDP
 LLLALLEAVLNIFYCKDYRTNISKLDESHVEPSVHLRSMKPKQSSTHTTMLKCSAYKFFPKK
 IRVTWLRDQGEVPLNMTSTEELANGDWFYQIHSYLLFTPTPGDKISCMVEHPSLTEPMIL
 HWDASLPESERNKIMIGVSGVLVLGVIFTAAGLIHYHNGRKYSGAIPVTTQ

>Eslu-DDA2 XP_028978025.2 chr.09 NC_047577.1:7.044.026-7.054.127
 MSIDGMMSSVFVILLGLVISAQEPVHVYDVIAKACSETEQFNMIILVDDEEYGYVDLKKN
 ATVTTLPDFATPVDCPICLTAYAEQESQRAEREISIFSKEQAEKVRPDVMLYPKEEVAQG
 TRNSLTFVFNFFPPPQVQKWTKNDENITERAEAGRYATNSDNTFYHFSTLTFTPEEGDI
 YTCTVEHPALDNPLTKIWDFFEMPPGTSGLPAVFCGLGLTLGILGIATGTFFYVKGNGRQI

>Eslu-DDA3 XP_019905383.2 chr.09 NC_047577.1:7.061.743-7.066.269
 MCTVFVILHLGVISALVQAQHVFNVMVLRSETEEFEMTACADGEEYLYVDLDNQKVVITA
 PEFKQIECPVCLNVAEGYIPVGKKHFSDLAFDSPEAKVPPDVMLYPKEEVKQGVNNYLV
 CYINFFPPPQVQKWTKNVDKITKGVKASHYLFNNDITFYHFSTLTDFDPEDGDIYTCTVE
 HPALDEPVTRKWEFEVPPGPSLDPVVFGLGLTLGILGIATGMFFFCVKGMQLTNVL

>Eslu-DDB3 XP_012990668.2 chr.09 NC_047577.1:7.068.106-7.075.388
 MASLQCYLLFVCLLSFFIQTGDFITIQNLQCYFRGEDPLDVEFVYRIYANRVKSFEYNST
 LDRFTGYTPNGIDKARILNYDPASLENKRRRLDYCKDYQLGYNAVLLKTVKPYARLRT
 EKHPSDRHRIMLKCSAYKFYPRKIRVTWFRDQGEVPMNMTSTEELANGDWYYQIHSYLEF
 TPTPGEKISCMKLKHASLIEPMILHWDEPLPGSGRSKIAMGASGLVLGLVFAAAGLIYYYY
 CRLKATGHYHNR

>Eslu-DDA4 XP_010864729.3 chr.09 NC_047577.1:7.077.058-7.083.387
 MSTLLAILYLEVISAYIQAQHVFNVMVLRSDTEGFEMTGDADGEECFYVDVDNQKVVITA
 PEFGEQIECPICLNVAERYIPAGKKHFSDLAFDTPAEKVPDVMLYPKEEVKQGVNNSLV
 CFVNNFFPPPQVQKWTKNVDNITKGVKASHYLFNNDITFYHFSTLTDFDPEEGDIYTCTVE
 HPALDEPVTRKWEFEVPPGPSLDPVVFGLGLTLGILGLGTGMFFFCVKGKQLTNVL

AF1.9 Deduced amino acid sequences from other species used in phylogenies

Spotted gar (*Lepisosteus oculatus*; Leoc-) MHC class II Ensembl sequences (Main text ref. Dijkstra et al.2013):

>Leoc-501A1 MHCIIA JH591501: 64.610-66.685
 MSVGWKCLGLLVVMQGAATVAVEHTYEVAYFCQSENKRKGSRNEVFDDDEMFIHDPDRKVD
 EPRLPEFEKAWNDSSLIQALANLGICENHLKGVMKAIPDEPAVKVPPKPAVFPEEPVE
 LGWPNTLICALNDFTPTTAQLRWLKNQPVTSVSDYIPLSSNKFAMFSYLSFTPOEG
 DIYTCHVEHTALSEPVSFVWDAEVPTDSDASETAFAIGLALGILGVVLGTVFLIKAIF
 HS

>Leoc-501B1 MHCII B JH591501: 70.640-74.060
 MRLVLLCSALVLCCLTSLGADDFVYFFRSECHFSASDLRDLVYVRSMTFNGKERVRFNSTV
 GKYVGFDTWGEKQANYWNGQKDYIARLSADKDRFCKYNVQLMASGMQDRKIKPEVKIYPA

KTASQGHTHMLVCHAHGFYPRQIAVSWLRNGQPVSSDLTSMFASDGDWTYQTLLEYLEFT
PQGGETFECAVDHVALDGTCLKLRWDPAAREAKRNKVIMGASGLVLGLVFAVIGVVYWKRK
TKGHHRLVSSERLVSCVGQVFSGGLVSCPGCALPCAQCILG
>Leoc-501A2 MHCIIA JH591501: 82.102-84.669
TSHIDINVIGCKSDDPVAQDEAQLDGDDEMFYADFDKKEMILTLPAFADSFVDPGWVQGA
IANRQICINNLEVAIKAENNPENTDAPVNTIYPRDEVELGKPNLTICLANNFFPPPVKV
RWTKNDDVDVSEQATLSRYYPNSDATFYQFSTLSFTPLQGDVYSCSVEHKALPEPKTRIWG
EERSALTSDAN
>Leoc-501B2 MHCIIA JH591501: 95.883-99.847
MLMCSALGFYPKQIKVSWLRDGTQTVTSDVTSTEELADGDWYYQIHSHLEYTPRAGESIVC
RVEHSSFATPKELTWDPSMPEADRNKIIIGASGLVLGLVIAAAGGIYYKKKSG
>Leoc-501A3 MHCIIA JH591501: 120.683-125.781
MHGIAVGSIACREISEWKPRGPCQGGDRDRAALGWIFRQDGDAPTAMVYPRDSVELGKPN
LICSVTDHFPMGIGVTWTHNDRPVTEGVTQTTPLSGRDFSFKVFSFLPFTPRLGDVYSCQ
VQHSALPEPLARLW
>Leoc-615A MHCIIA JH591615: 5.333-9.156
MLCAFLTAVLLGASGVLSQAQIRHLDRLLTFCVSNSTEAEELEKEHDEDEIFYVDLETQKS
VQRLPEFAEKWHVGPWPFFAQQEVETCRLLYLAAGGEGFPEEKLDPPISRLYSENEVELG
VPNALICFITDFHPAPVKVSWTRNTEPVTQGFNVTQYYSNKDYSRLFSYLSFTPLQAGDV
YSCSVEHRALEPLTRLWEVEVQSDSEAAETAVCGVGLTLGLLGVAAGTFFLIKGNKCN
>Leoc-615B MHCIIA JH591615: 11.335-16.190
MDSPLHRLAVAVLVLGCTGSRRSVDGNMYQFVHDCEYNDHLEDFLYTRRDIFNKIEILRY
DSNIQTFTVGYTPLGIKYAERFNQDKEYLAGLKDDLNYCKHNAGVYKSTMTDRKVPSPVK
VSATKLLSSKHPTMLVCHVTGFYFQIRITVTWLRDGLIKTDVTSTDLLANGDWTYQVHSH
LELTFRAGETVACRVEHSSLERPLEVTWDPSPMPESKKNKIVIGVSGILGLIITAAGVIY
YKKKSSGRILVPSD

**Tetraodon (*Tetraodon nigroviridis*; Teni-) MHC class II
Ensembl sequences (Main text ref. Dijkstra et al.2013):**

>T19A ENSTNIG00000005593_ENSTNIP00000008293_Un_random:19583822-19591157
MKMLLLILCCILGVSAADGQHEDIRIVGCSDFDGEYMHGLDGEELWYADFRRGEGVYAQPD
FIDPIKYEFGYSTAVAVLQICKFNLGIFRKGKYMPELDPPTSPMVYTRNEVQLTEPNT
LVCLVTGFYPAPVNV
>T19B ENSTNIG00000005592_ENSTNIP00000008294_Un_random:19597929-19598797
MASSALRVSLFLGLSAAGAFEHYGLRRCDFTSAEPKDMEYSLSVYYNKHLMARFSSSVG
KFVGDKYQYQADYWNQSSFLEAMRSSKQRLCQHNIPLWYSHILSKSVLKDVVYSVA
PPAGGHPAMLVCSVYDFYPKKIKVSWRRDGEVSHDVTSTDELADGDWYQLHSHLEYTP
RSGEKISCVEHASLKTPLVKDWDPSMPEARNQIAIGASGLILGLILSLAGFIYFQRKS
RGRILVPTN

**Fugu (*Takifugu rubripes*; Taru-) MHC class II sequences Ensembl
sequences (Main text ref. Dijkstra et al.2013):**

>F402A ENSTRUG00000004342_ENSTRUP00000010322_scaffold_402:55188-57563
MMKMLLLILCCVVGASADSQHEDIRILGCSLDLGEFMYGLDSEEVWYADFSKGEVDINP
PFIDPITYEYGAYSSAVADLQCTCKTSLDITRSLKDMPPERVAPTSPVIYTKKEVQLSQQ
NTLICFVTGFYPAPVNVSWTRNGEHVTQGT SINVPYPNKEGTFTQISRLAFVPQQGDIYS
CRVQHPALSGQDTRMWTVEVQQPGVGPVFCGLGLTLGLLGVAAGTFFLIKNECR
>F7533B ENSTRUG00000017449_ENSTRUP00000044727_scaffold_7533:2656-4187
SRMSSSLRVFLLFISLYTAAGGFQSYVVDSCDFNSTDLKDIEYTRSLYNNRVMYARFSS
RVGKFEGYTKYGLFQADYWNQSSILEGLRETKEISICQPNIKIDYSNLSKSVEPTVRVH
SVVPPAGGHPAMLVCSVYDFYPRIKVSQRDGEVSVQDVTSTDELADGDWYQLHSHLE
YTPRSGEKISCVEHASLKTPLVKDWGNHLSVCS
>F7533A ENSTRUG00000017444_ENSTRUP00000044708_scaffold_7533:430-1814
MMKMLLLILCCVLGVSAADSQHKDIGIVGCSDLDGEFMYGLDSEELWYADFSKGEVYGT
PFIDPFRPTAAVADLQCTCKYNLDVDRKGNKDMPTETVAPTSPVIYTKKEVQLSQQNTLI
CFVTGFYPAPVNVSWTRNGEHVTQGT SINVPYPNKEGTFTQISRLAFVPQQGDIYSCRQ

HPALSGLDTRMWTVEVQQPGVGPAVFCGLGLTLGLLGVAAGTFFFLIKGNECR

**Medaka (*Oryzias latipes*; Orla-) MHC class II sequences
(Main text ref. Dijkstra et al.2013 and Bannai & Nonaka 2013):**

>Orla-DAB*21 AGA53814.1 Main text ref. Bannai & Nonaka 2013
MDSSSLCLLFLTMCSADAFRLRYDVDRCVFNSTDLKDIEYIYSMYYNKKEFTRFSSSLGKY
VGYTEYGVKTAERANKDTSELSARKAQKETYCKHNIDNWKYKMLSKSVQPRVRVQSLAPS
GGHHFAMLVCSVYDFYPKTIRVSWLRGKEEVSSDVTSTAEMEDGDWYYQIHSLEYTPRS
GEKISCKVEHASLKDPLVTEWDPSMPESERNKVAIGASGLILGLVLSLAGFIYYKRKARG
RILVPSS

>Orla-DAA*21 AGA53805.1 Main text ref. Bannai & Nonaka 2013
MKMKLLLFVCGILSGTAAVFHEDLAITGCSDSDGEDMYALDGEVWYADFKKQGTGVEPQP
PFVDHVSYPGGYEQAVANQQICRSNLKISRIAMKDLPLERDPPSNVYVYSRDEVELGEQN
TLICHVSGFYPAVNVSWTKNGERVSGSINIPFPSSDGTFTQISRLPFVPQLGDIYSCSV
EHPALTEVQTKIWDVEKTQPGVGPAVFCGVLAVGLLGVAAGTFFFLIKGNECS

>Orla-DCB*21 AGA53816.1 Main text ref. Bannai & Nonaka 2013
MDSSSLRVFLLILTLPADGFIHYILNRCLFNSSDLKDIEYIYSYYNKEEFRLFSSSSSG
KFGVGYTEIGVKTAELANNDPEKMSRRRAEKETFCKPNIDNDYSTILTKSVQPRVRVQSLE
PSGGNHFAMLVCSVYDFYPKKIKVSWLQDQEEVSSDVTSTAEMEDGDWYQIHSLEYTP
RSGGKISCRVEHISLKDPLITDWDPSMPESEKNKIAIGASGLILGLVLSLAGFVYYKRKT
RGRILVPSS

>Orla-DDA ENSORLP00000016018 Main text Dijkstra et al.2013 Orla-M5A
MSLTSLLLITGAVCASSTTPRHMFFHIYGCYETDEVVRDLVDDDTIGYADFTKQEMVWC
LPYVPPSGKDLEKEAFKFAKNSIANCHSVLAKAKKADHGTPLRQEPDLISYTRYKAEEG
VLDTLFCSANHFYPPTINFRTWTKNGAEVTEGLLNLRFSHNKDGTFRGISTLSFTFPQRGDV
YSCWVSHEALERPRIITWESRRRRSPARMFFCASILCLAGIGTGLYFFIKKPNYCCGCGQ

>Orla-DEB ENSORLP00000016051 Main text Dijkstra et al.2013 Orla-M5B1
ILSSLIYFYLLFLTSSYYSKDQHGFMFSDFFCYIPSRNPKEVQYLIDWYFNMELTMQYNS
SVGGWTGFTPAGLITAAKFANADKYDVVQRILRELVCQRSVEMVYNGTEEAKVEPNVSLQ
TVEDNDSTLECSALDFYPKHIRTWFSNGQEVTEGVTFSDVLPNGDWTYQAHTYLTLP
KQDHISCMVQHTSLKEPKIYNWEPSPMNQTDRTDIIIGVVCALLLGAVFLCVGLIHYKQK

>Orla-DEA ENSORLP00000011499 Main text Dijkstra et al.2013 Orla-M16A
SRKQEGFKCSLIHFKTSFFCFVFSVEHEISYFIGCFAEGSTEVLLFEFDSEEILYVDFEKE
AVVFTGPSFFKANLSERIQLTTYKNGKKNRIWCQLADQYFTAETEERDKDPPGEVLIYT
SAEVQPGVENTIICFVNGFYPPSIKVSWTKNNGNPVSEGVSHSRYPNPKDQTFHQFSTLSF
TPSWTDVYSCTVEHPALES PKTVLWEPEFHQHHPNLDVFLAASLGLGLLGFAVGTCLIII
ALKRS

>Orla-DEB ENSORLP00000011497 Main text Dijkstra et al.2013 Orla-M16B
TGKSQNCSLGFLPLFLFSSTNAFYGHGTLKQFTSSHDLVYLEQVYFNKRLMVQYNSTL
GKYEGYTKKADLADGFSKSKPFLEQAVKNREKCRTHMDLVFELQSHPVPEPSVRVTPVVR
QGSSHQAMLACSAYNFYPKQIRLTWLRNGEKVINYVTSTEELPDGNWLYQIHSLEYTPS
PREEITCMVEHASPKPKLYNWEVLSPPMFGAVRNKIAVGTALLFGSFVFAVGLFFYKRT
T

**Stickleback (*Gasterosteus aculeatus*; Gaac-) MHC class II Ensembl
sequences (Main text ref. Dijkstra et al.2013):**

>Gaac-G131A1 ENSGACG00000000330_ENSGACP00000000421_scf_131:52153-54217
MKTKTMMKMMVVLVLSGVFCVSADGPHKDIAIVGCSDSDEEMYGLDGEVWYADFKHGK
GVRPQPSFVDPIDYREGTYETAVGNQQICRNNLKIDLKAFKDFPLEKDPSSHMIYPKDG
VELGEKNSLICHVTGFYPAPVTFSWTKNQDNVTEGSSRNVPYLNNDGTFTNQFSTLEFTPK
LGDIYSCMVEHLALDHPLVKFYDVQVSQPSVGPAVFCGVLTVGLLGVAAGTFFFLIKGNE
CS

>Gaac-G131B1 ENSGACG00000000336_ENSGACP00000000425_scf_131:56853-59742
MAPSFISVSLFLIGLHAADGFMEFVATECVFNSTELKDIEYIQSYYNKLEYTRFSSSVG
KFGVFTERGKNAANNNPSYLSRAKAQKEVYCLNHVPVYYNNMLTKSAEPYVRLHSET

PPGGGPLSMLVCSVYDFYPKKIIVRWTRDGRPETTGVTSTDELADGDWYYQTHSHLEYTP
 SRSGEKISCVEHISLSKPLVTDWTDPSMPESERNKVAIGASGLILGLTSLAGFIYYKR
 KARGRILVPSH
 >Gaac-GVIIB ENSGACG00000019051_ENSGACP00000025189_groupVII:2444693-2447881
 MAPSFHSVSLLFIFLHAAGGFMEFVKDQCVFNSTDLKGIEFIRSTYFNKLQYTKFSSSVG
 KFGVGFTEQGMKNAASNNNNMYMASIRAAKETICQPNIQRMVDNLTLSAQPYVRLHSET
 PLGGRTSSMLVCSVYDFYPQNIIVRWTRDGRPEATGVSSTDELADGDWYYQTHSYLEYTP
 SRSGEKIAACVVEHISLSKPLVTDWTDPSMPESERNKIAIGGSGILGLTSLAGFIYYKRK
 GRGRILVPSY
 >Gaac-GVIIA ENSGACG00000019052_ENSGACP00000025193_groupVII:2449972-2451242
 MKTMKMMMIIVLVLSGVSAIVPHEAIRISGCSDSDGEEMFGLDGEELWYADFKLGKGV
 LLPSFLDPITYPGGYEVAVAEQQFCRNNLRIDLEAYKFPLERDPPSSHMIFPKDAVELGE
 KNSLICHVTGFYPAPVAFSWTKNQENATEGTSRNIPFPNDGTFNQFSTLEFTPELGDYI
 SCMVEHLALDHPLVRFYDVQMSQPSIGPAVFCGVGLTVGLLGVAAGTFFLVKRNECS
 >Gaac-GXVIIB ENSGACG00000003680_ENSGACP00000004837_groupXVII:1117113-
 1119770
 MSSSTFLLLLLCLSSCSAADGHGYFMYADFWCNMQTARPQQVEYLVDWYFNKEFTMQYNST
 VGKWTGFTAAGLVSAAVFNGNHFDVLQRKEERRLICVDNVGHALNATEDNMAAPSVRLAE
 ASGSGHNTTLVCSAYDFYPRIRLAWLRDQGEVTSATFSEVTTNGNWTYAVHSSLSFTP
 GGRDRVSCKEHAGLQEPALRTWAAHGARDWETGFLVGGVCALLLGAACLSSGLIVHRRK
 YSNIS
 >Gaac-GXVIIA ENSGACG00000003731_ENSGACP00000004896_groupXVII:1163942-
 1165035
 MAVTLMALAAALCTSAAGSSSHDFHYTYGYESGEVRVDVLLDGDVVAYADFGREEVVFL
 IPRLPFFLRDLKLGYEFAKSSFTHCRSVLAKAKRASPNTIPQDAPVLSVYSRHEGRGG
 AANTLFLCLADGFYPPSVNFTWTKNGARVTGGVWDLPGHNRDGTFFHRISTLSTTPREGDV
 YSCSVEHRAARRPLASSWAEPKEGSPSRVSPAAGFFGASLVVCLIGVASGAYFFTKQPNFG

**Zebrafish (*Danio rerio*; Dare-) MHC class II Ensembl sequences
 (Main text ref. Dijkstra et al.2013):**

>Dare-D8.35B2 ENSDARG00000053738_ENSDARP00000070311_8:35956359-35959768
 MSQKKLYSSLILILALFFVGESANVYYMYRVSRCIFSSSNISAMVYFDRTYFNKNLFIQF
 NSNLGRFEGFNEYGLKLAEFWNNGTTFVDQEKDVVEFFCKYNSQIYENSILDKAVKPKVKL
 SSVTRAGGRQSTVLMCSAYDFYPPHINVFWRNGEVMTSEVTSTMEMADGDWYYQIHSEL
 EYSPKPGERISCVIEHASSNKPMIYDWDPSLPVFERNKISIGVSALVLGIITAAAGIIYY
 KKKTTGRTSVVPSRLITLPLMFR
 >Dare-D8.35A2 ENSDARG00000055441_ENSDARP00000072260_8:36283500-36286998
 MELYITTLVLTIILSAGAKVVHEDFAIRGCSDTEKEDTYGMDEEELWHADFNQKKGVETL
 PDFGDPMTFPGFYEGSEGEMAVCKSNLALRIKGFKSPPPEMDAPQTSIYPKDDVELGVQN
 TLVCHVTGFYPPSVSVSWTKNNINVEDITLSQYRPRIDGTNIFSTLKFTPAEGDIYSC
 MVKHRAIKDQPQTKTWDVDAVLPSVGPVFCGIGLTLGLLGAVAGTFFLVKGNNCN
 >Dare-D8.45B1 ENSDARG00000041705_ENSDARP00000088910_8:45758566-45761489
 MNAKINYSAAVFLSALFETVHAYTYAQIQCHVSDSLQKIEFIFSVTYNMIELVRYNST
 EDTFFGYTAIGQKFAEEYNKDKVLLAQHDFVLNQCRELGDVILPNAVWLAVKPEVIRSV
 TEAKGNRKAVLVCSAYDFYPKGIKLTWMRDDKKVTAELTSSEVMADGHWHYQIHSYLEYF
 PQTGEKISCVDHASSLKPMIYYWDPSLPESERSKIILGAVGLLMGIFTAAAGVIYYKRK
 QTGFYRLPVCLLPMETMNDTELQ
 >Dare-D8.45A1 ENSDARG00000079593_ENSDARP00000061131_8:45768098-45769605
 MFKTFSGITFFIFCLIHTEGQSYPEFGFIETCRGSSYDKIVFILDTEEAAYKDIEKEKLV
 FTLPLDMANPQYSLNDLRLNDVGIPAFCTEIIYHKILSLNVSEDEPLEPPWTTVYSRNDVK
 LNVKNTLICHVTGFFPPVRVLWTKNNVNTDGSTISRYYPNKDGTMMNVFSRLSFIPEEG
 DVGCSVEHKALQQPQTRTWDVEVQQPSIGPSVFCGVSLALGLFGFATGVLFIAKGLCK
 >Dare-D8.45B2 DCB_ENSDARG00000088872_ENSDARP00000110668_8:45773380-45774524
 MQFSRVACLAMILSALLEKVCNGYGLQSQCRLVLSSTKKVELIFSIFFNKIEYIRYNSTD
 QKIVGYTEFGEKFVENYKNNTFVLVLAIEFGIDNCKKIAKALISDGMLNHVTVKPEVIIRS
 VTEAKGNQKAVLVCSAYDFYPKAIKLTWMRNDKKVTADVMSIEEMADGDWYYQIHSHLEY
 FPQPGEKISCVDHASFKPMIYYWDPSLPETERSKIILGAVGLLMGIFTAAAGVIYYKR
 KQTG
 >Dare-D8.45A2 ENSDARG00000086294_ENSDARP00000112102_8:45778095-45779781
 MLVYSSDHSIVELTQANMLELLCRIMLFIAWTCSEGMQDLEYGLMESCTGSPDDEIVFT

FNTELAAYLVVVDGTLVLTVPNFIKDYPGFYELPLLDASPATVGLTALCKVVYEKTLNLN
VSEPLEPPWVLLYPRNDVKLNKNTLICHVTGFFPPVRLWTKNNVNVTDGSTISRYYP
DNDRNFNVFSQLSFIPEEGDVYSCSVEHKALQQPQTRTWDEVKQPSIGPSVFCGVGLAF
GLLSFAAGIFFNAKGKKWM
>Dare-D8.46A ENSDARG00000075932_ENSDARP00000010619_8:47078720-47080882
MEALLRITLICVCVQAKDYHKYGLIGACGDADQEDFIVQFDDEQLAHVDFKEQKDVITLP
EFAGQAVLPPIYVDAKRAEFNCKAYLAVLREVIYASSPEVLEPPWSSIYPKSDPQLNLKNT
LICHVTGFFPPVRLWTKNNVNVTDGSTISRYYPNKDGTMMNVFSRSLFSFIPEEGDIYSCS
VEHKALQQPQTRTWDEVKQPSIGPSVFCGVGLALGLGFATGVFFFTAKGNCCN
>Dare-D18B ENSDARG00000056330_ENSDARP00000090055_Chr18:29872428-29875206
MFNVLVIRLALLLPFLLETAGHYGFVQFTCHMLGSLQNVETYSIYFDTTELLRFNSTE
NKAVAYTEYAMKWANDLNKQPKWLHEQVEKNIADCKLFGETYFPLVAKTVKPEVFRSLR
EASGKRALLSCSAYNFYPKHIKLTWMRDDKVVTADVMSTKVMADGDWYYQIHSLEYFP
QPGEKISCVEHASSHKPMIYYWDSFLTESNKNKIITGAAGIVLGAIMAAGGLIYYKRKH
TVKSHVHVLIY
>Dare-D18A ENSDARG00000093885_No ENSDARP_18:29867551-29868594
DYHKYGLIGASGDADQEDFIVQFDDEQLAHVDFKEQKDVITLPEFADLAVFQPLYVDAKR
AFNGKAFLAVLREVIYASSPEVLEPPWSSIYPKSDPQLNVKNTLICQVTGFFPPVRLWT
KNNVNVTDGSTISRYYPNKDGTMMNVFS*LSFIPEEGDIHSCLEVEHKALQQPQTRTW

**Sturgeon (*Acipenser dabryanus/ transmontanus*) MHCII sequences
(Main text ref. Chen et al.2020 and GenBank) :**

>Acda-1 MN249653.1 *Acipenser dabryanus* MHC class II alpha antigen (Acda-DAA) mRNA,
Acda-DAA*1201 allele, complete cds
MKSCVFLAVLLLTAVQAETVSHLYRNLIACQTNNTNTERELDQDELYYIDFDKKE
GVLRLPRFSEHWSVGGQVPRAEENREVCIHNVAGFAKCHEYPPPEQDPPRASVYTENHL
ELGKPNLTICFINGFYPAIKVSWTKNTLPVTEGVTQTDLYSNKDFTRMFYSLSFTPEL
GAMYSQCQVQHSALPETLTTFWEPDVQTDSDVGETAFCAVGLTLGLLGVAVGTFFLIKGNK
CN*
>Acda-2 MK923687.1 *Acipenser dabryanus* MHC class II alpha antigen (Acda-DAA) mRNA,
Acda-DAA*0601 allele, complete cds
MKSCVFLAALLLTAVQAETVTHLFRALVACQTNGLTPEDDYELDDDELFDHIDFDKKE
AVQRIPIQFAKYWSPPEGAPARAETDRQTCINNVAAKCHKYPPEQVSPRVTLYPEKDL
ELGKPNLTICFITDFHPAAIKVSWTKNTLPVTEGVSILTQYYSNKDFTLQMFYSLSFTPEL
GDVYSCQVQHSALPETLTTFWEPDVQTDSDVGETAYCAVGLSLGLLGVAVGTFFLIKGNK
CN*
>Acda-3 MK923706.1 *Acipenser dabryanus* MHC class II beta antigen (Acda-DAB) mRNA,
Acda-DAB*1001 allele, complete cds
MGTSLSLQISSLYTLCLRGLVLVSLMFCCSKTSFSGVEGYLMQMMRDCEYSDSSMTDMVLSW
RYVFNQEEVHYDTHKIKHVGNTACGVKNAEWNKDKDRMARLLGDVDRYCKYNMGLYRG
GTTREIIPPSVRVSSIKPFSSQHQTMLICYVIGFYPREIKVTWLRNGAKVTADVSSSELL
PDGDWTYQIHSYLELTPQSGDSYTCRVEHSSLAEEAIEEKWDPAMPESKRNKIIIGTSGIV
LGLVISAAGLIYYKKATGRILVPSD*
>Acda-4 MN249661.1 *Acipenser dabryanus* MHC class II beta antigen (Acda-DAB) mRNA,
Acda-DAB*0303 allele, complete cds
MGTSLSLQIYSLYTQCLRGLVLVSLMCSSKTSFSGVDGYLYQVMSDCEYSDSSMTDMVYSW
RYVFNQEEYVHYDSKIQLKFGVNTACGVKNAEWNKDKAQLAGLLGEVDRYCKYNAELDLS
FTADRKIPPAVRVRSIKPFSSQHQTMLVCYAFGFYPRDIKVTWLRNGVKVTADVSSSELL
HDGDWTYQIHSYLELTPQSGDSYTCRVEHSSLAEEAIEEKWDPAMPESKRNKIIIGASGIV
LGLVIAAAGLIYYKKATGRILVPSD*
>Actr-DXA White sturgeon, *Acipenser transmontanus*, DR975335
MSQVAGVCECAVTELRDQTLTLHWHKHHIWIQSGLYGVNMKSCVFLAALLLTAVQA
ETVTHLFRALVACQTNGLTPEDDYELDDDELFDHIDFDKKEAVQRIPIQFAKYWSPPEGAP
ARAETDRQTCINNVAAKCHKYPPEQVSPRVTLYPEKDLGKPNLTICFITDFHPAAI
KVTWTKNTLPVTEGVSILTQYYSNKDFTLQMFYSLSFTPELGDVYSCQVQHSALPETLTTF
WEPDVQTDSDVGETAYCAVGLXXSPHQ

Fathead minnow (*Pimephales promelas*) MHCII sequence:

>Pipr-DEB Fathead minnow, *Pimephales promelas*, DT151632
MRTFRLTLVLVGFAFCCVSSKDVYVFQNIIVECEYSKVDLSDMVYIIKLVF

AF1. Deduced amino acid sequences

NQKLLCSYDSRLGKYVGYDEFGIRNADHYNSQGWKMKQRKEELETLCRAN
ARLYVNSTRRKVPPAVTIRPTKKAHYGQLSTLVCHAYNFYPQAINITWLL
DGSEVTGDVISTEFMDNGDWRYQMHSLLDLVLRGVSVSCRVEHSGLEKP
LVVQWDSTSLDTRIAKLAVGCFSFLLG