

Additional file 4 (AF4). Deduced MHC class I amino acid sequences from selected salmonids

Deduced amino acid sequences from *Salvelinus alpinus/malma* (Saal), *Oncorhynchus nerka* (Onne), *Oncorhynchus kisutch* (Onki), *Oncorhynchus tshawytscha* (Onts), *Oncorhynchus mykiss* (Onmy), *Salmo trutta* (Satr), *Salmo salar* (Sasa) and *Esox lucius* (Eslu) originating from the NCBI genomes described in main text Material and Methods. When available, the GenBank protein accession number and chromosomal location is provided for each sequence. Pseudogenes defined as having internal stop codons are shown using a ps extension to gene name while partial gene names have been given a pt extension.

AF4.1 Deduced U lineage MHC I amino acid sequences

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AF4. Deduced amino acid sequences

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AF4. Deduced amino acid sequences

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>Satr-UGA XP_029591397.1 chr.36 NC_042992.1:32.292.855-32.301.696
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AF4. Deduced amino acid sequences

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>Satr-UHA XP_029558050.1 chr.20 NC_042976.1:8.942.111-8.953.982
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>Satr-UMAs chr.36 NC_042992:20.989.044-20.988.357
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>Sasa-UBA*0301 XP_014032819.1 chr.27 NC_027326:10.123.703-10.146.903
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>Sasa-UDA1 XP_013996967.1 chr.14 NC_027313:50.985.016-50.996.125
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>Sasa-UCA2ps chr.14 NC_027313:51.036.934-51.045.017 Pseudogene
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>Sasa-UMAs No prediction chr.14 NC_027313:71.687.592-71.688.277
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>Sasa-UGA XP_013997204.1 chr.14 NC_027313:59.499.424-59.507.750
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>Sasa-UHA2ps no gene prediction chr.21 NC_027320:48.690.859-48.692.163
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>Sasa-ULA XP_014032820.1 chr.27 NC_027326:10.049.215-10.051.213
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AF4.2 Deduced Z lineage amino acid sequences

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>Saal-ZCAa XP_023831647.1 chr.31 NC_036870:10.307.087-10.314.615
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>Saal-ZCAb XP_023830996.1 chr.30 NC_036869:17.402.402-17.403.594 dual orf
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>Onne-ZBAa XP_029514088.1 chr.4 NC_042538:45.904.746-45.954.046
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>Onne-ZCAa XP_029514085.1 chr.4 NC_042538:45.921.305-45.927.348
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AF4. Deduced amino acid sequences

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AF4. Deduced amino acid sequences

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AF4. Deduced amino acid sequences

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AF4. Deduced amino acid sequences

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 S V S K K K I P K Q D W M R E K L P A D Y W E K G T Q S R K S K E Q W F K V N V D I L M K R M R H N N T D V H V L Q W K
 V G C E I D Q Q S D G T L K F I K G I D Q Y S Y D G D D F L A F D D V T M Q W V A P V D Q A L P T K R K L D D V Q I L N
 T Y T K G Y L E K E C V D W L S K F M E Y E D K E F S W A D S A P K V Y A F A K K A K T A G H V R L T C M A T G F Y P K
 D V V M H I K K N G V P L T D R D G V Q S A G L L P N D D E T Y Q I R M S V Q I P E A D K E T Y E C Y V H H R T L E E P
 I V V K W D G K C C D C S S G G A V V I G A V V I T F I V V L I L V L G L F V L H R R G T I V I P G L R T R A N G N G A A
 A M V

>Sasa-ZBAa XP_014032768.1 chr.27 NC_027326:10.602.279-10.612.437
 M Y R P N L M F F V L Y F S L E C I C R S Q S D I Y S L N Y I Y T A L S K P V D L P G I H E F N A M G L M N N K Q I D Y
 Y D S V S K K K I P K Q N W M R E K L P A D Y W E K G T Q S R K S K E Q W F K V N V N I L M D R M R H N N T N V H I L Q
 W K H G C E I D Q Q R D G T V K F I K G I D Q Y S Y D G D D F L A F D D V T M Q W V A P V D Q A L P T K R K W D G V Q I
 L N Q Y T K G Y L E K E C V D W L S K F M E Y G D K E F S R A D S A P K V Y A F A K K A K T A G H V R L T C M A T G F Y
 P K D V E M N I K K N G V P L T K H D G V Q S A G V L P N D D E T Y Q I R M S V Q I P E A D K E T Y E C Y V H H R T L E
 E P I V I K W D G K C C D C S S F N A V V I G A V V I T F I V V L I L V L F V L H R R G T I V I H G L R T R A K D D E
 S R T S S D S G K G S Q N A G S S D S G S G E D V K K S M L P K G S V

>Sasa-ZCAa XP_014032767.1 chr.27 NC_027326:10.620.148-10.627.552
 M S A F K M Y V V A L L L L F A T L S T E D T V E T W S L N Y I Y T A L S K P V E L P G I H E F T A M G L M N D K Q I D
 Y Y D S V A K K K I P K Q D W M R E K L P A D Y W E K G T Q S R K S K E Q W F K V N V N I L M D R M R H N N T D V H I L
 Q W K H G C E I N Q Q S D G T L K F I K G T D Q Y S Y D G D D F L A F D D V T M Q W V A P V D Q A L P T K R K W D G V Q
 I L N Q Y T K G Y L E K E C V D W L S T F M E Y G K K H L R M D D S A P K V Y A F A K K A K T A G H V R L T C M A T G F
 Y P K D V M H I K K N G V P L T K H D G V Q S A G V L P N D D E S Y Q I R M S V Q I P E A D K E T Y E C Y V Y H R T L
 E E P I V E K W D G K F Y D C N Q V T G V I I G V V A V V L L F I V V T P L L V L W K K G K I F A G K K G A P P P T G I
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>Sasa-ZDAa XP_014032770.1 chr.27 NC_027326:10.648.408-10.655.356
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 Y D S V S K K K I P K Q D W M R E K L P A D Y W E K G T Q S R K S K E Q W F K V N V N I L M D R M R H N N T D V H I L Q
 W K H G C E I D Q Q S D G T L K F I K G T D Q Y S Y D G D D F L A F D D V T M Q W V A P V D Q A L P T K R K W D G V Q I
 L N Q Y T K G Y L E K E C V D W L S K F M E Y G E K E F S R P D S A P K V Y A F A K K A K T A G H V R L T C M A T G F Y
 P K D V M H I K K N G V P L T D R D G V Q S A G V L P N D D E T Y Q I R M S V Q I P E A D K E T Y E C Y V H H R T L E
 K P I V I K W D G I C C D C S S F N A V V I G A V V I T F I V V L I L V V L F V L H R R G T I V I P G L R T T A T G N G
 V A F S G V N T S

>Sasa-ZBAb XP_013997187.1 chr.14 NC_027313:59.698.589-59.724.523
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 S V D K K K I P K Q D W M R E K L P A D Y W E K G T Q S R K R K E Q W F K V N V N I L M E R M R H N N T D V H V L Q W R
 H G C E V D K Q P D G T L K F M K G I D Q Y S Y D G D D F L A F D D V T M Q W V A P V D Q A L P T K R K W D G V Q I L N
 Q Y T K G Y L E K E C V D W L S K F M E Y G E K H F S S T D S P P N I Y V F T K K A K P A G N V H L T C M V T G F Y P K
 D V I I H F K K N G V Q L T E D D G V L S T G A R P N N D D T Y Q I R I S V Q I P E A D K D M Y E C S V S H A M L K E P
 I V E K W G A N T G A P P P T G I Q A S L I G N G N G A T N L N L T T P I G E D G G S S N S S D S G K G S Q K E R S
 S D G A S E E E V K T P M L L N

>Sasa-ZCAB XP_013997181.1 chr.14 NC_027313:59.735.522-59.758.314
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 S V D K K K I P K Q D W M R D K L P A D Y W E K G T Q S R K S K E Q W F K V N V N I L M E R M R H N N T G V R I L Q W K
 H G C E V D K Q P D G T L K F I K G T D Q Y S Y D G D D F L A F D D V T M Q W V A P V D Q A L P T K R K W D G V Q I L N
 Q Y T K G Y L E K E C V D W L S K F M E Y G E K H F S S A D S P P D I N V F A N K A K T A G N V H L T C M A T G F Y P K
 D V I I H F K K N G V Q L T E D D G V L S T G A R P N N D D T Y Q I R I S V Q I P E A D K Q T Y E C S V S H I T L V Q P
 I V V K W D G T C R D F S Q S T V P I I A I I I I G G S V A I G I I I V L F L S K K G K I C A G N T G A P P P T G I Q A

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 >Sasa-ZDAb XP_013997179.1 chr.14 NC_027313:59.767.933-59.779.225
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 KKKIKPKQDWMREKLPADYWEKGTQSRKSKEQWFKVNVNILMERMRHNNTDVHILQWRHGC
 EVDTQPDGTLKFMKGTQDQYSYDGDFFLAFDDVTMQWVAVPDQALPTKRKWDGVQILNQYT
 KGYLEKEKCVDWLSKFMAYRDKFIRADSPPKVYAFAKKAKTAGHIRLTCMATGFYPKDVL
 MHIKKNGVQLTKQDGVQSDGVLPNDDSYQIRMSVQIPEADKETYECYVSHRTLKEPIEV
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 >Eslu-ZAA XP_010898810.3 chr.10 NC_025977:19.692.986-19.710.404
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 QWKHGCEVDKQSDGTLKFIKGTQDQYSYDGDFFLAFDDVTSQWVAVPDQALPTKRKWDGVQ
 ILNQYTKGYLEKEKCVDWLSKFMFSYEHTEFSSTDAPPKVFVAFKAKTEGHVRLTCMATGF
 YPKDQVQIMKNGVPLTEHDGVYSEGVLPNDDTYQIRKSVQIPEADTNDYEVCHVDHRTL
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 >Eslu-ZBA XP_028978590.1 chr.10 NC_025977:19.050.846-19.111.940
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 YYDSQVQKIPRQDWMKEKLPDPDYWEKGTQSRKSKEQWFKVNVNILMERMKHNNTDVHIL
 QWKHGCEVDKQSDGTLKFIKGTQDQYSYDGDFFLAFDDVTSQWVAVPDQALPTKRKWDGVQ
 ILNQYTKGYLEKEKCVDWLSKFMVSYGHTEFSSADNPPKIYGFVAFKAKTKGQLQTCMATGF
 YPKDQVQIRKNGVPLTKYDGVYSEGVLPNDDTYQIRKSVQIPEADTHDYEVCHVDHRTL
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 >Eslu-ZCA XP_028978597.1 chr.10 NC_025977:19.042.390-19.048.486
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 GCEIDEQNGTMRFIKGTQDQYSYDGDFFLAFDDVTSQWVAVPDQALPTKRKWDGVQILNQ
 YTKGYLEKEKCVDWLSKFMVSYGHEQELKASPPKVYAFAKKARTEGHVRLTCMATGFYPKD
 VEMQIRKNGVPLTKDGVHSEGVLPNDDTYQIRKSVQIPEADTNDYEVCHVDHRTLTEPQV
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 >Eslu-ZDA XP_028978589.1 chr.10 NC_025977:19.031.923-19.039.410
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 EVYKQNDGTFQFIKGTQDQYSYDGDFFLAFDDVTSQWVAVPDQALPTKRKWDGVQILNQYT
 KGYLEKEKCVDWLSKFMVSYGDELKASPPKVYAFAKKARNEGHRVRLTCMATGFYPKDVE
 MQIRKNGVPLTKDGVHSEGVLPNDDTYQIRKSVQIPEADTNDYEVCHVDHRTLTEPQV
 WDKCCDCSSSIGVIGSTVGVVLLVLLIILIVVLWKRNRVMTMNCSSSTSSSESGNGSK
 VSLETEAILTNAVNDVSTSTDSGQASNERLEMLRN
 >Eslu-ZEA XP_028978588.1 chr.10 NC_025977:19.020.042-19.028.369
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 KQKIPRQGWMEKLPDPDYWEKGTQSRKSKEQWFKVNVNILMERMKHNNTDVHILQWKHGC
 EVDKQNDGTLRFIKGTQDQYSYDGDFFLAFDDVTSQWVAVPDQALPTKRKWDGVQILNQYT
 KGYLEKEKCVDWLSKFMVSYGHQEFSSVDSPPKVYAFAKKARTEGHVRLTCMATGFYPKDVE
 MQIRKNGVPLTKDGVHSEGVLPNDDTYQIRMTVQIPEADTNDYEVCHVDHRTLTEPQV
 KWDGKCCDCSQSTVVIIGAVVCVVVLLAIFIAFLVFLWKKGIIGGFRLY

AF4.3 Deduced L lineage amino acid sequences

>Saal-LLaps No prediction NW_019943469:81.560-81.919 pseudogene
 IKTFLEKEKKCIMHKVXPRVRLIQKAMSGAIQQVSCLAFGFYPRHINLTLRDSQPIAEQ
 ALSGGQLLPNGDGTYLKRSLEVSTEELXERHNYTCTASHLSLDNKLDVSWVPESGADRS
 >Saal-LCA XP_023998402.1 NW_019944620:29.783-37.832
 MDKLSVFLFVLSFCTIVNAGSGSHSLWALATYIRGETPFPEFTVVVMLDDVQVAYYDSNM
 KHFIYRGHNTSDKIHDDDEAKNGGFVGVMYHHMKERYFHLKHHNLTEGVQVQORMAGCE
 MLDNGEPALIVTKNIVNAVVDHAIYYNMTHFTYDAGKLLQGWGMRQAQEKFLYENVLL
 PLCIRTLKTIKREKNVVMKVPVPRRLINKELSGGLQVSCLAFGFYPRHINLTLXDGQ
 PVTEQELTGGEVLPSPDGTQYLRKSLEVSTEELKRRHNYTCTASHLSLDNKLDVSWESGA
 ERVHLSTLSVLLVMLLIVILLGIFIVKRRRSN
 >Saal-LGA2pt XP_023998403.1 NW_019944620:41.294-41.896
 MMQEYERKVVENVCLPICIKTMKTFKREKNIVMCKVPPRLRLIKKEVSGGLQVSCLAFG

AF4. Deduced amino acid sequences

FYPRHINLTLRDLGQVPAEQELTGGQVLPSPGDGNYQLRKSLEVSTEELKRRHNYTCTASH
 LSLDNKLDVSWESGAERVHLSTLSVLLVMLLIVILLGIFICVKRRRSNTASQLKLANVDA
 NVSEEMILSSTSED

>Saal-LEA XP_023998401.1 NW_019944620:51.869-53.649
 MGKLSVLLFVLSFSTIVNAGSGSHSLWALATYISGETPFPEFTVVVMLDDVQVAYYDSNI
 KHFIYRVNNTPNKIHNEAQDGAYILGMMYNNMKERSFNLKHHFKFTQVQVQRMMSGCE
 ILDNGEPVVMFVKDTFNAIYTDQMVYNNMTHFIYDAGKLLGSDGIRQAFERVLFFENVHL
 PICIRTLKTIKREKNIVMRKVPPRLRLINKEVSGGFQVSCLVFGFHRHINLTLRDSQ
 PVAEQELTGGEVLPSPGDGTYQLRKSLEVSTEELKRRHNYTCTASHLSLDNKLDVSWESGA
 ERVHLSTLSVLLVMLPIVILLGIFICVKRRWRCTASQSKLTNVDANVSEEINLSSDSET

>Saal-LHA1ps No prediction NW_019945788:11.961-12.656 pseudogene
 HILCGTCNIYSGETPFPEFTVVVMLDDVQVAYYGLHMENFIYRATHQTKRG**EAQDGAH
 VFVDMYQSMRQII*TKAPL*SSGRQVQKQKMACCEMLDNANQPWFMSKDTTNGISADMH
 YITT*HIYIRCWDTT*DGWHNASIWKDTLENYIIPFASEH*RNISEERKNVCA*SSSQ
 TQVDKERGFRCRAGELPGVCFPLPHIQPDLRDLRGGQVTEQS*QGGQVLPSPGE

>Saal-LHA2ps No prediction NW_019946183:39.211-39.759 pseudogene
 GVQVQRMAGCEMLDNGEPAMIMSKNTFNAIYTDRT*FSTQHIYI*CWETTRMGWDEQAF
 QNTFD*WLLPCIKH*KTFLKREKNCDA*SSSQTQVDKRGFWRAPGELPGVWFLPPPHQP
 DPAERRPASGRGTGADRGGVLPSPGDGTYQLRKSLEVSTEELKRRNSYCTASHLSLDTKLD
 VRW

>Saal-LBAs No prediction NW_019946183:39345-40.025 pseudogene
 SGSGSHSLWALATBIXGETPFPEFTVVVDFDDVQVGYDSNMKEFIYSGLNPTDKIHDDV
 AQDGAIVFVGTIVPRYKERLQKHHCNLTVFKFSKEWLAVRCWTMVNQ*SCQRTLSMPF
 IQIERNFQHNFTTYD-AGKLLGWDGMSKHFRLLINGYFHASNTEKHS*RERRIVMRKVP
 PRLRLIKKEVSGGLQVSCLAFGFYPRHINLTLRDLGQVPAEQELTGGE

>Saal-LNapt No prediction NW_019946183:48.240-48.899
 SGPGSHSLWALATYIIGETPFPEFTSVGLLDDVQVGYDSKDKLSVYRGLNPTDKMYDDL
 AQEGDRVFETMYQDMKERAFLKHHFNLTGGVQVQRMAGCEMLDNGEPAMIMYKETFNA
 IYTDQTVISNTHFTYDAGKLLGWDGMMQDFKRTLYINVHLPRCIRTLKFLKREKKVV
 MRKVPPRLRLIKKEVSGGLQVSCLAFGFYPRHINLTLRDL

>Saal-LDA XP_023853355.1 chr.1 NC_036838.1:57.299.152-57.301.114
 MGKLSIFLFLVLSFYTIVNAGSGSHSLWALATYIIGETPFPEFTVVVMLDDVQIGYYDSNI
 KQSVYRGYHITDKMNEAQDGTIVLGTMYHHMKERSFRLKHHNLTEGVHVQQRIGGCEI
 LHNGEPALIMTKNSFNAI FADYAVYNNMTHFTYDSGKLLGYNWMRQATERTLYANVWIN
 TLKHTICINTLKKCLNRENFVMRRVPPRLRLIKKEVSGDLQVICLAFGFYPRHINLTLR
 DGHVPAEQELTGGEVLPSPGDGTYQLRKSIVSTEELRERHNYTCTASHLSLNNKLDVSWE
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>Saal-LAA1ps No prediction chr.17 NC_036857:19.496.374-19.499.780 pseudogene
 IITGIFVHQRRIGCELVDNEKQGLMIKEVFNGIDGGVLFNFKLQYNYHPMWPELEFNQ
 RTQYVQMGDLKVFYFPCIK*LKDYLKKEEKLVMRKVSPRVRFI*KETQILKGPRTPAWPV
 YHRHINLTLRDLGQVPAEHELKGRQLLPN*DWTYQLRKSILTITVQEL*ERHNYTCTASPV
 YMDNKLDVSWPDTSPDSASIIIPVVLVMAVVLILIGSLVVFGMWVKHAGFPFSGHIYSV
 AKDTETEQSNSSELETESTDS

>Saal-LAA2ps No prediction chr.7 NC_036847:21.281.746-21.283.178 pseudogene
 VLSILDHVQMGYYDSNAWICISKTGNSDEAFEGVAQITLWDVFLIMRGIQVFNQRLCGCE
 LMDNXKQGIIMIKESFNGFDGALNFKLQYHPKWPPELAFNQHRPQYIQMGLGKVLHPICI
 KTLKDYLLKKGEMLMRAFGFYPCINLTLRNGQPVAEHLDTGGQLLPNGDRL*QLRMNL
 TINAQELRERGRDIITPVLPLICLDNKLVSW

>Saal-LIAs No prediction chr.36 NC_036875:17.167.958-17.168.785 pseudogene
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 GHMFLSMKRRLSDLRYRFNSTGNIDVQQRMTGCEMLETGEPLILSTDAFNAI FADLIYY
 NMTHYSYNSGNLLSPWSEMHQTYAKWRYQTIYLPICIKTLKLYE*LKNFVMRKVPRV
 LIQKAMSGGARVSCLAFGFYPRHINLTLRDLGQVIVEQEMTGGQLLPNGDGTYQLRKSLE
 VNTEELRERHNYTCTSHLSLDNKLDVSWIPESGID

>Saal-LJAs No prediction chr.2 NC_036839:31.412.441-31.413.246 pseudogene
 TYIIGDTPFPEYTVVLMDDIEVGYEWSNVLQHERQII*LKQRFNFTEGIHVQQRMAGC
 EMLDNKMLVTLRSRSTFNKTVDAGMCMYNTQNTYYTGNPQLAWDEVKLEYVKMLYAHVYL
 TLCIKTLKIFLERENNLMRKVRPRVRLIKKAKSGGLQVSCLAFGFYPRHINVTLLRDLGQ
 PIAEKELTGGQLLPNGDGTYQLRKSLEIIAEDLRERHNYTCTVSHLSLDNKLDASWVPEP
 GRD

>Onne-LAA1pt XP_029477974.1 chr.20 NC_042554.1:16.723.950-16.727.606
 HVLGETEFPEFCVLWMLDDVQVGYDSKSWRFISRTDGNIDEEYSRTVQGASWDVYLSMR
 KWSSLLQHRFNSTGIFVHQRLIGCELVDNEKQGLMIKEAFNGIDGGVLFNFKLQYNYH

AF4. Deduced amino acid sequences

PKWPELEFNQQRQTQYVQMGLDKVYLPICIKSLKDYLLKKEEELVMRKVRPRVRLISKESTD
TAGAKITCLAFGFYPRHINLTLRRDQGPVAEHELKGGGAIATEGDWTYQLRKSLLTITIQE
LRERPNTCTANHISMDNKLDSVSWGVPTFSGHIYSAKVTEQSNSSLETEPTDS
>Onne-LAA2ps No prediction chr.7 NC_042541:47.191.684-47.192.995 pseudogene
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HHFNNGIFVNLRRCGCELLDNNKQKIMIKESFNGFDGALNFKLQYHPKWPELAFNQHL
ENLHLPICIKTLKDYLTGKEMLMRVRV*KKTLGIQQEQIYSGSIDTHQAFGFYPCINLT
LLRNGQPVAEHDLTGGQ
>Onne-LJApS No prediction chr.3 NC_042537:50.850.799-50.851.083 pseudogene
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AITEELRERHNYTCTVSHLSLDNKLDSWEPDPR
>Onne-LIA XP_029493803.1 chr.1 NC_042535:19.342.746-19.344.526
MVKLCFFWLFLSLYTIINAGSHSLAFATCISGEAPFPECSVVLMDQDIQVGYFDSNTEQ
FIHKGPYAPDETEVDLAQDAANVFGHMFLSMKRRLLDLRYRFNSTGNIDVQQRMAGCEML
DTGEPGLILSTDAFNAILADLIYYNMTHYSYNSGNLLSPWSEVHQTYAKWRYQTIYLPIC
IKTLKFLERLKNFVMRKVRPRVRLTQKAMSGGARVSVCLAFGFYPRHINLTLRRDQGPV
EQDITGGQLLPPNGDGTYQLRKSLEVNTTEELRERHNYTCTTSHLSLDNKLDSWIPESGID
RVGLYVKSGLMVAIIILLSIFVCRRRNAAGSQTLSQLSNANDAQVAEQMSLSSHSET
>Onne-LGA2 XP_029512659.1 NW_021815573:18.384-20.495
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KQSVYRGQHINDKAEDEEVQDQALVFGDMYQSMKNRFLKFKHFNLTQVQVQKRIAGCE
MLDNAGEPALVMFKNVFNVTVDYAIYYNMTHFTYDAGQLLQGWGDKRKEVEINNLMEVYL
PICIKSLKRFLKREKNIVMRKVPPRLRLIKKEVSGGFQVSVCLAFGFYPRHINMTLLRDGQ
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ERVHLSTL
>Onne-LNAPS No prediction NW_021815399:7.214-7.912
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NMTHFTYDAGKLRPGYDGRREYLRTLFGNVFLPICIRTLKTLKREKNVVMRKVPPQTQ
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LSVLLVMLLILLLGIFICVKRRRTASQT*SQLATVDAKVEG*INLSSDSKT
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TLCIRTLKTLKREKNVVMRKVPPRLRLIKKEVSGRFQMSCLAFGFYPRHINMTLLRDGQ
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MRGYTIKIMGKLSVFLFVLSFYTIIVNAGPVSHSLWALATYITGETPFPEFTVVMLDDVQ
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AF4. Deduced amino acid sequences

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AF4. Deduced amino acid sequences

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AF4. Deduced amino acid sequences

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>Onmy-LDA XP_021425739.1 chr.17 NC_035093:67.362.765-67.364.428
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>Onmy-LGA XP_021442415.1 chr.26 NC_035102:33.996.968-34.014.691
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AF4. Deduced amino acid sequences

PVAEQDLTGGEVLPSPGDGTYQLRKSLEVSTEELKRRHNYTCTAFHLSLDNKLDVSWEFGA
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>Satr-LAA2pt no prediction chr.28 NC_042984:22.516.693-22.518.122
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>Satr-LNaps no prediction chr.12 NC_042968.1:35.027.883-35.028.903
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>Satr-LGA2.3 No prediction chr.12 NC_042968.1:35.639.205-35.640.653
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GCEMMDNGEPGLAMFKNIFNGISEDYAMYNTTHVYTNAGKILLGWDWKMAYNINKFEN

AF4. Deduced amino acid sequences

YYLPICIKHLKTLKREKNIVMRKVPPRLRLIKKEVSGGFQVSCLAFGFYPRHINLTLLR
 DGQPVAEQELTGGEVLPSPGDGTYQLRKSLEVSTEELKRRHNYTCTASHLSLDNKLDVSWE
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 >Satr-LMA4 No prediction chr.12 NC_042968.1:35.712.951-35.713.960
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 >Satr-LMA6 No prediction chr.12 NC_042968.1:35.745.282-35.746.293
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 KVPRLRLIKKEVSGGFQVSCLAFGFYPRHINLTLLRDGQPVAEQELTGGEVLPSPGDGTY
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AF4. Deduced amino acid sequences

>Satr-LCA2 XP_029622515.1 chr.12 NC_042968.1:35.752.335-35.758.141
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>Satr-LCA1 XP_029623986.1 chr.12 NC_042968.1:35.796.559-35.799.118
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>Satr-LDA XP_029630277.1 chr.14 NC_042970.1:10.704.457-10.706.122
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>Satr-LIA XP_029558880.1 chr.20 NC_042976:33.824.877-33.826.457
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>Satr-LJaps No prediction chr.24 NC_042980:29.522.035-29.522.883
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>Satr-LLaps No prediction chr.24 NC_042980:40.874.193-40.876.693
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IQKDLSSGGVQMQSCLPFGFYPRHINLTLRRDGRPIAEQVNLGGQLLHNGDGTIYQLRKSIV
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>Satr-LGA1.1pt XP_029576636.1 chr.29 NC_042985.1:9.493.218.-9.494.900
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>Satr-LHA XP_029576650.1 chr.29 NC_042985.1:10.157.491-10.162.043

AF4. Deduced amino acid sequences

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 >Satr-LMA1 No prediction NW_021823199:19.749-20.758
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 EGAYLLGKMYHHMKERSFNLKHHFNLTQVQVQQRMSGCEMLDNGEPLIMVKDTFNAIY
 TDQMVYYNMTHFIYDAGKLLLGWDGMRQAYERVLFFENVHLPICIRTOKTLKREKNVVR
 KVPRRLRLIKKEVSGGFQVSCLAFGFYPRHINLTLRRDQGPVAEQELTGGEVLPSPGDGT
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 >Satr-LGA2.2ps No prediction NW_021823199:33.983-35.055
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 >Sasa-LFA XP_014031975.1 chr.26 NC_027325.1:38.686.632-38.689.189
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 LDNGEPALIMFKETFNGIFVDHAIYNSMTHFTYDSGTLGYYGIRQAYEKALFENVLLP
 ICIKNLKTLKREKNVVRKVPRLRLIKKEVSGGLQVSCLAFGFYPRHINLTLRRDQGP
 VAEQELTGGEVLPSPGDGTQYLRKSLEVSTEELKRRHNYTCTASHLSLDNKLDVSWESEAE
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 >Sasa-LGA XP_014031973.1 chr.26 NC_027325.1:38.706.031-38.709.086
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AF4. Deduced amino acid sequences

LNNGESALVMYKDFVNAIYTDRTLYNMTHFTYDAGKLLLGWDGIRQAYERTLYENVYLP
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 >Sasa-LHA XP_014032010.1 chr.26 NC_027325.1:40.134.217-40.138.243
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 >Sasa-LJaps No prediction chr.25 NC_027324:29.534.954-29.535.742
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 CYNMTQNTYYTGNPQLAWDEVKLEYVKMLYAHVYLPICIKTLNIFLEREKNIVMRKVRPR
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 >Sasa-LLaps No prediction chr.25 NC_027324:41.418.460-41.420.842
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 VHQTYYVKGLYQTIYLNICMDTLKTFLEKEKCCIMHKVHARVRLIQKDMGGVQQMCLPF
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 >Sasa-LEA No prediction NW_012354073:3.249-4.233
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 MLDNGDPALIMMKDIFNAISVDHAFYNIHITYYDPGKLLLGWDGIRQAVERSLVENVYL
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 >Eslu-LPA XP_019909495.1 chr.15 NC_025982:6.802.982-6.806.755
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 EVPDKIDDDISQDSGRFVFGSMLNEMKARSSDLQRYFNSTDGIHVQORMAGCEMKDNGKP
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 VRLEREKSTVMRKVRPRVRLIQKAMSGGVKVSCLAFGFYPRHINLTLLRDSQPIADQDLT
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 >Eslu-LIA XP_010888243.1 chr.20 NC_025987:10.835.945-10.837.883
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 ERFVHKGHNTQNDVDMADATYVFGHMFLSLKRRLSALKYRYNSTGDIVVNQRMGTGCE

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 ICIKTLKKFLEKENNFVMRKVRPRVRLIQKAVSGGTRVSVCLAFGFYPRHINLTLQRDGGQT
 IPDQEL SAGLVLP SADGT YQLR KSLTVSAEELSEKHSYTCSTFHLSLDNKLDVSWVPRDG
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AF4.4 Deduced S lineage amino acid sequences

>Saal-SAA XP_023991886.1 NW_019942612:111.299-114.376
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 LLQFSVTFREP KVPVAVSLFERSPHGNSEVEVTCHVTGFYPRAVQVEWLGAEGLPMVDGVS
 SGEVLPNGDGSYQLR KSLTVPQEAQDTQSY SCLVLHSSKAENITVTWAPKKNL PNVLMAT
 VIIIVSVVLILT VLVFYL VWRRAVAQNPE

>Saal-SBAps LG22 No orf chr.22 NC_036862:35.259.299-35.262.616
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 RYVMDTAVRVTSEHYNH*HSGQTWAAAVFQAVHFRKCRANGAFDLES LYECIVRLK TIL
 KYAAWIHDKKS P S SACY**KRPTDTLQGGGHVTGFY P QAVQVE*LTGQGLPLVDRVSSGE
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>Onne-SAA XP_029537278.1 chr.14 NC_042548.1:49.264.637-49.267.655
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>Onne-SBAps chr.11 No prediction NC_042545:1.740.497-1.736.849
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>Onki-SAA XP_020324114.1 chr.18 NC_034191:16.365.696-16.368.709
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 LLEFSVTVREP KVPVAVSLFERPPHGNSEVEVTCHVTGFYPRAVQVEWLGAEGLPMVDGVN
 SGEVLPNGDGSYQLR KSLTVPQEAQDTQSY SCLVLHSSIAGNITVTWAPKKNLANVLMAI
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>Onki-SBAps chr.15 NC_034188:77.214.861-77.218.450 pseudogene
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 EVLPNGDGSYQLR KSPSPVQGSQDTQRYSC

>Onts-SAA XP_024301302.1 chr.14 NC_037110:47.875.406-47.879.660
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 DVSTRWTAAVSHAVFYKRKRETDLEDLVRLVIHYESGCIRWLEK LLEFSVTVREP KVPV
 VSLFERPPHGN SKVEVTCHVTGFYPRAVQVDWLGAEGLPMVDGVNSGEVLPNGDGSYQLR
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>Onts-SBAps no prediction chr.13 NC_037109:70.437.457-70.441.973 pseudogene
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>Onmy-SAA XP_021437178.1 chr.24 NC_035100:28.955.775-28.958.794
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>Onmy-SBAps no orf predicted chr.27 NC_035103:34.982.134-34.984.099 pseudogene
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AF4. Deduced amino acid sequences

>Satr-SAA XP_029629540.1 chr.13 NC_042969.1:77.567.602-77.570.818
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>Satr-SAA2pt XP_029629541.1 chr.13 NC_042969.1:77.576.696-77.578.445
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>Satr-SBAps no prediction chr.26 NC_042982:33.079.931-33.082.983 pseudogene
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>Sasa-SAA1 XP_014039590.1 NW_012348808:12.841-15.855
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>Sasa-SAA2 XP_014044169.1 NW_012366222:207-2.911
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TLVLFKYLVRRAVAVGKSQS
>Sasa-SAA4 XP_014043725.1 NW_012363096:2.586-5.597
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>Sasa-SAA5pt XR_001327798.1 NW_012573932:108-952
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>Sasa-SAA6pt XR_001326745.1 NW_012361613:51-929
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>Eslu-SAA XP_010891190.1 chr.01 NC_025968.4:29.672.471-29.675.989
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ASMSHAYDGKDFVSVFVSTRTWTAAVSHAAFYKRRKRETDLEDLVRLLVIHYESGCIRWLEN
LLKFSIKVREPKEVIVFERLPHGSSEVEVTCHVTGFYPRAVQVEWIGSEGLPLVDRVI
SGEVLPNGDGSYQLRKSLTVLQGVQYNQSYTCLVHSSVTSVTSVTVWVWPKKNLNYMVI
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AF4.5 Deduced H lineage amino acid sequences

>Saa1-HAA XP_023833862.1 chr.32 NC_036871:14.212.450-14.221.846
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TLDQSTDTWTAEVPAQALSILKQLWDWDTERTRRERMQLHESCTELMELTQSEPTTNGAGTS
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AF4. Deduced amino acid sequences

XNQVL

>Saal-HBA chr.19 XP_023865004.1 NC_036859:27.504.960-27.509.583
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 L

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>Onne-HBA XP_029479749.1 chr.20 NC_042554:60.651.094-60.662.234
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>Onki-HAA XP_020322949.1 chr.30 NC_034203:14.721.044-14.737.299
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>Onki-HBA XP_031663205.1 chr.27 NC_034200:28.309.378-28.315.392
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>Onts-HAA XP_024291244.1 chr.10 NC_037106:35.188.051-35.172.011
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>Onts-HBA XP_024247562.1 chr.28 NC_037124:27.560.431-27.566.291
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>Onmy-HAA XP_021468778.1 chr.08 NC_035084:52.834.866-52.853.052
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>Onmy-HBA XR_002471367.1 chr.28 NC_035104:26.645.362-26.651.156
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>Satr-HAA XP_029560449.1 chr.21 NC_042977: 17.473.705-17.488.093
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 VLLGNDSESFQQAFAEIEENVNTNTITKNPTYQYLRVRECKLNGFRVVHLTDQLLVNGNYFL
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>Sasa-HAA XP_013995094.1 chr.14 NC_027313.1:16.479.536-16.491.787

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 >Sasa-HBAps chr.03_NC_027302.1:17.030.685-17.037.352 pseudogene
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 >Eslu-HAA XP_010881876.1 chr.03 NC_025970:32.751.310-32.757.904
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 LDRATDTWTAIEGPQALPLKHLWDRESTRTRREIMQLHESCTKLLEEITCSEPGATGGMDI
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AF4.6 Deduced P lineage amino acid sequences

>Saal-PAapt No prediction chr.03 NC_036840:4.724.783-4.724.090
 VLQRRRGCTYITNESSTGFDQWGLNGENFLTFDPTSHWTMSESPQANPIEPSWNSNKVRS
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 >Onne-PAAs No prediction chr.08 NC_042542:3.503.547-3.504.250 pseudogene
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 >Onki-PAAs No prediction chr.09 NC_034182:5.596.843-5.596.152 pseudogene
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 VEIPTGLTKT*RYRCKVQTSTSNATA
 >Onts-PAAs No prediction chr.15 NC_037111:3.386.312-3.386.578 pseudogene
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 >Onmy-PAAs No prediction chr.21 NC_035097:14.167.986-14.168.685 pseudogene
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 >Satr-PAAs No prediction chr.08 NC_042964:41.135.886-41.136.011 pseudogene
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 >Sasa-PAAs No prediction chr.07 NC_027306.1:43.236.079-43.236.783 pseudogene
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 HMFKEFLQHDVCPH*EDVSLRCHVTSTDLGSLKVHLTRDRVMTDRARVIGPLPNVDGSVL
 LRLSVEIPTGHTKS*RYHCKVQTSTSNATA