Characterisation of EST03G12 and elucidation of its role in Amoebic Gill Disease (AGD) severity

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NON TECHNICAL SUMMARY

2010/033 Characterisation of EST03G12 and elucidation of its role in Amoebic Gill Disease (AGD) severity

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OBJECTIVES:

1. Determine whether EST03G12 encodes a functional protein
2. Characterise the role of EST03G12 in AGD pathogenesis
3. Identify polymorphisms and allele frequencies of EST03G12 in Tasmanian farmed salmon
4. Determine whether different EST03G12 alleles confer resistance/susceptibility to AGD

NON TECHNICAL SUMMARY:

OUTCOMES ACHIEVED TO DATE

This project has provided evidence of specific alleles/genotypes of EST03G12 that are associated with AGD resistance. Furthermore, differences in EST03G12 genotypes may be functional as the EST potentially encodes for a novel g-type lysozyme, an innate immune molecule, in Atlantic salmon. Following presentation of the findings to the Salmonid R&D Round Table Meeting held on the 30th of November 2011 the need to look at fish health from a genomic approach/perspective was one of the three fish health R&D priorities for the TSGA.

The purpose of this project was to determine the role of the expressed sequence tag EST03G12 in AGD pathogenesis and disease severity. Central to this was to determine if the EST encoded a functional gene, to elucidate the role of that protein with regard to AGD and finally to determine at the genetic level whether there is a case for the use of EST03G12 as a marker for resistance to AGD. To that end through a number of approaches we have shown that the EST is a gene of approximately 3.9 kb in length which encodes for a mature mRNA of approximately 1.3kb.

We discovered that the EST03G12 sits either in a repetitive region of the genome and/or is close to a transposon. This position in the genome is likely to have hampered previous efforts to identify the gene, the putative promoter and the open reading frame for EST03G12. The international effort to fully sequence the geneome of the double haploid salmon, ‘Sally’, will overcome these issues and should shed additional light on what we have found here on the gene structure of EST03G12. Information from the genome sequencing effort will be available in late 2012 (W. Davidson, Simon Fraser University, pers. comm.).

Our initial bioinformatic analysis was unable to fully determine the sequence and hence the identity of the protein encoded by the EST. We were also unable to identify a protein using a high powered proteomics approach. However, by using a homology approach we obtained evidence that the EST codes for a novel g-type lysozyme in Atlantic salmon.

This finding is important as lysozyme is a key innate immune molecule responsible for fighting the initial stages of infection. Therefore, it would seem that the over expression of EST03G12 seen in AGD infected Atlantic salmon is as a result of the attempts by the fish to resolve infection.

We were also able to identify nine alleles of the EST in a relatively small sample of the Tasmanian population that segregated into 12 distinct haplotypes. One allele was dominant in the sample analysed, being present in 85% of the fish. Importantly there were a number of alleles and haplotypes that can be correlated to the development of AGD resistance.

These association results are cautionary due to the sample size. However, now that the number and identity of alleles are known an appropriate genotyping test can be designed. This test can be applied to a sub-set of the thousands of archived DNA samples from the Saltas Atlantic salmon selective breeding program for which there are also multiple phenotypic data records on their AGD status. Further work can also include functional analysis of the amoebicidal ability of the novel lysozyme gene contained within EST03G12.

KEYWORDS: amoebic gill disease, gene expression, resistance, marker assisted selection, proteomics

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2.0 BACKGROUND

In Tasmania, amoebic gill disease (AGD) is the main health concern of the Atlantic salmon mariculture industry costing >$20m p.a. to treat and in lost production. Outbreaks of AGD are most prevalent during spring/summer due to high salinity and water temperatures. Currently, freshwater bathing is used to treat AGD but this is costly, labour and time intensive and stressful to fish. Given increasing pressures for freshwater conservation and the high costs of bathing fish, it is not viewed as a sustainable long-term treatment option. As a consequence, research efforts are being directed to overcome the AGD problem through selective breeding and/or developing an effective vaccine. It is also possible that if host factors involved in susceptibility and/or resistance to AGD can be identified, that these could be targeted for disease intervention through developing drugs, or other direct treatment options such as RNAi gene silencing or for identifying markers allowing genetic selection for AGD resistance.

In the FRDC supported project 'Molecular Assessment of Resistance to Amoebic Gill Disease in Atlantic salmon' (FRDC Project #2004/218, Aquafin CRC 3.4.5) within the Aquafin CRC, CSIRO undertook two separate gene expression analyses that examined (i) fish experiencing a 'first infection' with AGD and (ii) cohorts of fish deduced to be either resistant or susceptible to AGD following multiple field infections. In both studies, expression of one gene (expressed sequence tag EST03G12) was identified to be highly (>150-fold) over expressed compared to any other genes in AGD-infected salmon.

A preliminary study to identify EST03G12 showed that it is expressed constitutively at high levels in the head kidney of salmon, moderate levels in spleen, gill, brain, liver and heart and at very low levels in skin and muscle. Closer examination using in-situ hybridisation showed EST03G12 to be expressed constitutively in epithelial pavement cells of gills, and at extremely high levels within proliferating cells associated with AGD lesions. These data suggest that EST03G12 might play a role in the gill cell hyperproliferation characteristic of AGD.

Database searches of the EST03G12 gene coding sequence showed it to possess low-level homology to an EST from *Salvalinus fontinalis* with homology to the growth factor independent zinc finger protein Gfi1. Gfi1 is an important repressor of DNA transcription that is believed to be an essential modulator preventing overshoots in inflammatory responses (reviewed by Moroy et al. 2008). In addition, Gfi1 knockout studies in mice have shown it to be involved in restricting over expression of pro-inflammatory cytokines such as tumour necrosis factor (TNF) and interlukin-1 beta (IL-1B) as well as the Toll-like receptor pathways. As such, Gfi1 can be considered a negative regulator of the innate immune response. Thus if EST03G12 is a homologue of Gfi1 with similar function, it's high level expression in fish naively challenged or susceptible to AGD may be responsible for the significant pathology and absence of a protective response in these fish. Data generated in Project #2004/218 and reported by others (Morrison et al, 2007; Young et al. 2008) suggest that the innate immune response to AGD is weak, particularly on first exposure to the amoeba. Thus if EST03G12 encodes a gene involved in the innate response to AGD, it makes it an obvious focus of research to determine its identity, function and role.

3.0 NEED

Preliminary studies of salmon EST03G12 undertaken within FRDC Project #2004/218 did not determine whether it encodes a functional protein and therefore its biological role in AGD pathology remains largely unknown. However, some evidence was obtained that it might function as either a regulator of the innate immune response or a transcriptional factor driving the hyperproliferation of gill cells observed at sites of AGD lesions. Thus it might play a significant role in the development of AGD pathology and in progress of the disease. Indeed, if EST03G12 expression impacts negatively on the innate immune response against AGD, it is an obvious target for intervention strategies. However, in order to devise such strategies there is a need to better characterise the EST to examine whether it encodes a functional protein, it's role during the progress of AGD and whether allelic differences in the gene sequence and/or its promoter amongst salmon correlate with differences in their resistance/susceptibility to AGD.

4.0 OBJECTIVES

1. Determine whether EST03G12 encodes a functional protein
2. Characterise the role of EST03G12 in AGD pathogenesis
3. Identify polymorphisms and allele frequencies of EST03G12 in Tasmanian farmed salmon
4. Determine whether different EST03G12 alleles confer resistance/susceptibility to AGD

5.0 METHODS

5.1 Northern and Southern blotting

In order to perform Northern (mRNA) and Southern (gDNA) blotting either RNA or gDNA was prepared from salmon gill tissue using the Ambion RiboPure kit (RNA) or the QIAGEN DNesay Tissue kit (gDNA) respectively.

5.1.1 Northern blotting

Eight micrograms of total RNA was added to an equal volume of 2x RNA loading dye and heated at 70°C for 10min, spun down and chilled on ice prior to loading on a 1% RNAse free agarose gel. RNA was separated at 80-100V for between 45-60min until the dye front had migrated ¾ the length of the gel. The gel was post stained with ethidium bromide (EtBr) and visualised under UV light briefly to check separation. The gel was soaked twice in 20xSSC for 15min to remove residual formaldehyde. RNA was transferred overnight to a nitrocellulose membrane using 20xSSC buffer and the RNA fixed by UV crosslinking for 3.5min. RNA was probed with a DIG labelled probe at 50°C overnight in DIG Easy Hybe buffer. Following hybridisation the membrane was washed two times for 5min each with low stringency buffer (2xSSC and 0.1%SDS) at room temperature followed by two high stringency washes (0.1xSSC with 0.1%SDS) at 50°C followed by a final wash in low stringency buffer at room temperature. For probe detection the low stringency buffer was replaced with 100ml maelic acid wash buffer and incubated for 2min on a shaker at RT. The maelic acid buffer was replaced with 100 ml blocking solution and incubated for 30min while shaking at RT. The blocking solution was discarded and replaced with 25 ml anti-body solution (anti-DIG 1:4000 in blocking solution) and incubated at room temperature for 30 mins with shaking. The membrane was washed 2 x 15 mins with 100 ml of wash buffer in a fresh tray followed by equilibration for 3 min in 20 ml detection buffer in a fresh tray. The membrane was then covered with 15 ml of colour substrate solution (NBT/BCIP) and incubated overnight in the dark at room temperature. The reaction was stopped by rinsing the membrane in 50 ml of TE buffer for 5 mins and the membrane photographed.

5.1.2 Southern blotting

In order to perform the Southern blot, 2.5µg gDNA was digested overnight at 37°C with EcoRV, StuI, DraI or PvuII restriction enzymes. Digested DNA was separated on a 1% agarose gel at 80-100V for 45-60 min. The gel was post stained with EtBr and visualised under UV light to check separation. The DNA was denatured by submerging in denaturation solution for 2 x 15 mins at RT with gentle shaking then rinsed with distilled water. The gel was neutralized by submerging in neutralization solution for 2 x 15 mins with gentle shaking. Prior to transfer the gel was equilibrated for 10 min in 20xSSC and DNA transferred to a nitrocellulose membrane overnight using 20xSSC buffer. DNA was UV crosslinked by exposure to UV for 3.5 min, following which the membrane was rinsed in distilled water and allowed to air dry. The membrane was probed as per the methods used for the Northern blotting procedure. However, probing was undertaken overnight at 38°C and high stringency washing (1xSSC and 0.1%SDS) was undertaken at 60°C. Bound probe was detected as per the method outlined for Northern blotting.

5.2 Genome walking

Genome walking, to identify the flanking regions of the known sequence of the EST, was carried out as per the instructions in the GenomeWalker Kit^{TM} (BD Biosciences). Briefly, 2.5 µg of gDNA was digested overnight with 80 units of *Dra*I, *Eco*RV, *Stu*I or *Pvu*II restriction endonucleases. The digested gDNA was cleaned up using isopropanol precipitation and 4 µl was ligated to the BD GenomeWalker adaptors overnight at 16°C in the presence of 3 units of T4 DNA ligase. The ligation reaction was stopped by incubating each of the four tubes at 70°C for 5 min followed by the addition of 72 µl of TE.

Primary walking was undertaken by PCR with the following parameters, 1 µl adaptor ligated gDNA, 40 µl ddH2O, 5 µl 10x BD Advantage 2 PCR buffer, 1 µl dNTP (10 mM ea), 1 µl each of the primer combinations listed in Table 1 and 1 µl BD Advantage 2 polymerase mix. PCR conditions consisted of 7 cycles of denaturation at 94°C for 2 sec and annealing/extension at 72°C for 3 min followed by 32 cycles of denaturation at 94°C for 2 sec and annealing/extension at 67°C for 3 min and a final extension at 67°C for 4 min. Five microlitres of each of the products were visualized on a 1.5% agarose/EtBr gel alongside a 2-log DNA ladder (New England Biosciences). One microlitre of product from each of the PCR reactions was diluted in 49 µl of dH_2O and this served as a template for the secondary nested PCR using primers listed in Table 2. Cycling conditions were 5 cycles of denaturation at 94°C for 2 sec and annealing/extension at 72°C for 3 min followed by 20 cycles of denaturation at 94°C for 2 sec and annealing/extension at 67°C for 3 min and a final extension at 67°C for 4 min and 5 µl of each product was analysed on a 1.5% agarose/EtBr gel alongside a 2-log DNA ladder. The remaining secondary PCR mix was stored at 4°C.

The remaining 45 µl of each of the four secondary PCR reactions was run on a 1.5% agarose/EtBr gel. All bands were visualized under UV light, individually excised and subjected to gel extraction purification (Gel Extraction kit, QIAGEN, The Netherlands). All bands were ligated into pGEM-Teasy (Promega, Annadale), as per the manufacturers' recommendations, and used to transform chemically competent *E. coli* (DH10B). Following incubation, 10 white colonies from each plate were selected and grown overnight at 37°C in 5 ml LB/Amp, subjected to plasmid DNA preparation (DNA Miniprep, QIAGEN, The Netherlands) and restriction digest (*Eco*RI) analysis. Positive clones were subjected to DNA sequencing using Big Dye chemistry.

Table 1. Primers used for genome walking primary PCR. Note AP1 is the universal forward primer used in combination with east of the gene specific primers (GSP1-7).

Primer	Sequence (5'-3')	Size
AP1 (Forward)	GTAATACGACTCACTATAGGGC	22-mer
GSP1	GTCTGTGTGTTCTTCCTCGATGCGAT	26-mer
GSP1A	GTTGGTATGTGAAGTGACGACAGTTGAAG	29-mer
GSP1B	GTTTTTCATGTTGGTATGTGAAGTGAC	27-mer
GSP1C	ATTCAGTAGGACATGGGGCAACACAT	26-mer
GSP3	AGGGTCTTAGCCTGAAGGTATATGCG	28-mer
GSP5	TATCTGTCTCTCCCGCTCTAATCTGT	26-mer
GSP7	CCTTACAGTGCAAGTGTAGACCCAACA	27-mer

Table 2. Primers used for genome walking secondary PCR. Note AP2 is the universal nested forward primer used in combination with each of the gene specific primers (GSP2-8).

Primer	Sequence (5'-3')	Size
AP2 (Forward)	ACTATAGGGCACGCGTGGT	19-mer
GSP2	CGCTTGAAGGTTGTAGTAATCAGGTGTT	28-mer
GSP4	GGGGACATACTGTATTAAAGGGGAAGTTTA	30-mer
GSP6	GGGACCATTCATTGCATTGTGTTAGTA	27-mer
GSP8	TAGACCCAACAGTGCAGTTCAAGAAGAG	28-mer

5.3 Gill cell lysate protein analysis

We obtained gill samples from heavily infected animals and performed a whole protein extraction using filter aided sample preparation (FASP). Briefly, gill arches from AGD infected fish were excised and stored at -80°C. Gill filaments were lysed in 150 µl lysis buffer (4% SDS, 100mM Tris/HCl pH 7.6 and 0.1M DTT) by incubating at 95°C for 3min. DNA was sheared by sonication and the lysate clarified by centrifugation at 16000 x g for 5 min. Thirty microlitres of cleared lysate was mixed with 200 µl binding buffer (8M Urea, 0.1M Tris/HCl pH 8.5) and applied to a filter unit (Microcon YM-3 (Millipore)) and centrifuged at 14000 x g for 15min. The bound proteins were washed with 200 µl binding buffer and centrifuged at 14000 x g for 15min. One hundred microlitres of 0.05M iodoacetamide was added, the filter mixed at 600 rpm in a thermo-mixer for 1min and then incubated at room temperature for 20min without mixing. The filter unit was then centrifuged at 14000 x g for 10min. The filter was washed three times with 100 µl binding buffer and centrifuged at 14000 x g for 15min followed by subsequent washing with 100 µl 0.05M NH_4HCO_3 three times and centrifugation at 14000 x g for 10min. On filter digestion was performed with 40 µl 0.05M NH_4HCO_3 containing trypsin (enzyme to protein ratio of 1:100) by mixing at 600 rpm in a thermo mixer for 1min and incubating at 37°C overnight. The filter was centrifuged at 14000 x g for 10min and the digested peptides eluted by adding 40 µl 0.05M NH_4HCO_3 and centrifuging at 14000 x g for 10min. Prior to analysis the filtrate was acidified by the addition of CF_3COOH. The filtrate was then subjected to Liquid Chromatography – Mass spectrometry (LC-MS) analysis. Resultant peptides were then run against a custom Teleosteii database and against the predicted peptides from the cDNA sequence of EST03G12.

5.4 Gene synteny searches

In order to pursue the identity of EST03G12 further we worked with Professor Willie Davidson from Simon Fraser University in Canada. The approach taken was to firstly determine which of the available Atlantic salmon Bacterial Artificial Chromosome (BAC) clones the EST is found on. From this information, to then compare these to the sequences being generated from the Atlantic salmon Genome project and map these to the Atlantic salmon physical map. Finally we used a Syntenic approach to compare the genomc information with that of a closely related and well studied species, the stickleback.

To that end, a Forward primer (5'-GCGCGCCATCGCATCGAGGAAGAACACACAGACACAGCAA-3') and a reverse primer (5'-GCGGTATGAGTGATGGTATT-3') were first designed from the EST. Filters 1-6 of the BAC library were screened and 54 BAC clones were found to be hybridization positive, mainly hitting contigs 742, 846, and 1975. Of these, 15 BAC clones were then chosen for further PCR testing. However, none of the hybridization BAC clones were positive by PCR, including the genomic DNA positive control. This observation might occur if the amplified sequence happens to be between intron-axon boundaries. A new reverse primer (5'-CCTGATTCAGTAGGACATGG-3') was designed with the predicted amplified sequence of 164 bp. This time all the hybridization BAC clones were negative but the genomic DNA was positive with an amplified sequence of around 300 bp.

New forward (5'-AAAAACTGTCGCACCCAGCATCACCATAGCCAACATAACA-3') and reverse (5'-TTGTTGAATTCGACCATACA-3') primers were made from the second half of the EST03G12 sequence. The BAC library was screened a second time using filters 1-6. Thirty nine BAC clones were hybridization positive mainly hitting contig 207, 742, and 846. Of these, 15 were picked for PCR testing. All BAC clones coming from contig 742 and 846 were PCR positive. Positive control containing the *Salmo salar* genomic DNA contained two bands, one of which had a 300 bp band and the other had a 500 bp band. All BAC clones tested from contig 742 had the 300 bp band and all the BAC clones from contig 846 had the 500 bp band.

5.5 Allele screening and correlation to resistance/susceptibility

During the 2009/10 summer, gill tissue was collected from c.a 300 fish as part of CSIRO's field work in other projects. These fish were an all-female commercial outbred population resulting from the cross of 100+ parents. The samples were taken from a number of fish presenting with various gill scores (after 3 rounds of commercial bathing). Sampling was undertaken in this way so that specific alleles from individual fish can be correlated to AGD severity. For the purposes of this work samples were selected representing the extremes in farm gill score (i.e. 0-1 and/or 4-5) resulting in a sample population of 50 fish. RNA was extracted from the gills using RNAeasy kit (Qiagen, The Netherlands) as per the manufacturer's instructions. cDNA was prepared from each of these animals and a 638 bp region of the EST amplified. The amplicon was cloned into pGEM-Teasy and 10 resultant clones picked and prepared for sequencing. Resulting sequences were sorted for each fish and the two alleles determined using BLAST and CLUSTAL analysis.

6.0 RESULTS/DISCUSSION

6.1 Northern and Southern blotting show an mRNA of approx 1kb and a gene of approx 3kb

The Northern blot produced a single discreet band at approximately 1.3kb (Figure 1) meaning that the current cDNA sequence of 673 bp represents approximately half the sequence of the mature mRNA. Given that the current cDNA sequence contains the poly-A tail then it would appear that the 5' region of the cDNA is missing.

Previous attempts to obtain more 5' sequence using RACE have only resulted in an additional 245bp being obtained. Therefore by undertaking the Northern blot it would appear that we are looking for approximately an additional 700bp of cDNA sequence. The work toward this is detailed below in section 6.2.

Similarly to the Northern blot, the Sothern produced a single discreet band, this time at approximately 3.5kb (Figure 2). Therefore, there appears to be only one sequence with homology to EST03G12 in the salmon genome (i.e. no sequence duplication, pseudogenes or multiple copies in different genomic regions).

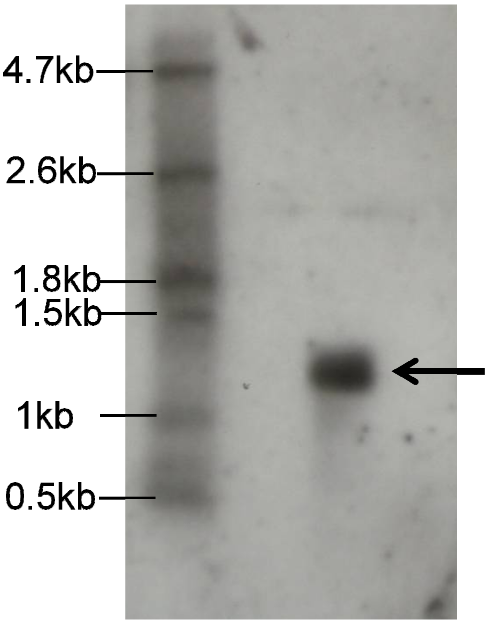

Figure 1. Northern blot of mRNA prepared from the gill tissue of a heavily infected Atlantic salmon. mRNA was detected using a DIG-labelled probe corresponding to part of the known cDNA sequence. Sizes on the left are those of a DIG-labelled RNA ladder from Roche Diagnostics. The arrow points to the positive hybridisation mRNA with an approximate size around 1.3kb.

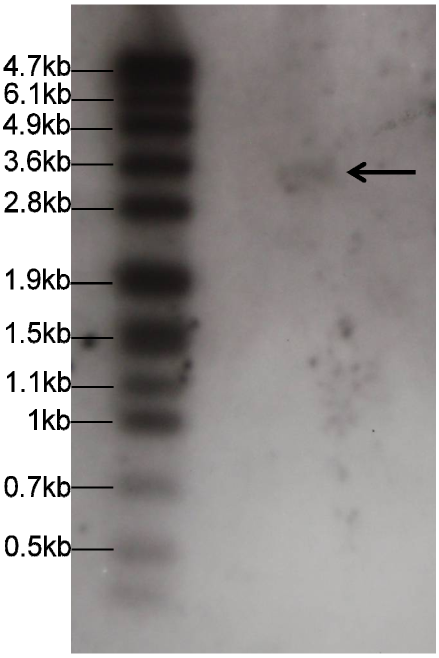

Figure 2. Southern blot of mRNA prepared from gill tissue of an AGD infected Atlantic salmon. DNA was detected using a DIG-labelled probe corresponding to part of the known cDNA sequence. Sizes on the left are those of a DIG-labelled DNA ladder from Roche Diagnostics. The arrow points to the positive hybridisation StuI cut DNA with an approximate size around 3.5kb.

6.2 EST03G12 is located in a dense region of the genome

Through an exhaustive process we were able to 'walk' approximately 2933bp upstream of the original EST sequence using 7 different combinations of primers. Sequences were filled in and verified using a number of specific primers (Appendix 3). This resulted in a total length of 3890bp which is in concordance with the Southern blot result in section 6.1. Gene structure analysis indicated that the gene encoding EST03G12 is made up of a 2157bp upstream sequence containing two putative promoters, three exons of 518bp, 416bp and 386bp encoding for a mature mRNA of 1320bp (in concordance with the Northern results obtained in section 6.1) and two introns of 122 and 291bp respectively, along with the polyA tail (Figure 3). The entire sequence obtained is presented in Appendix 4.

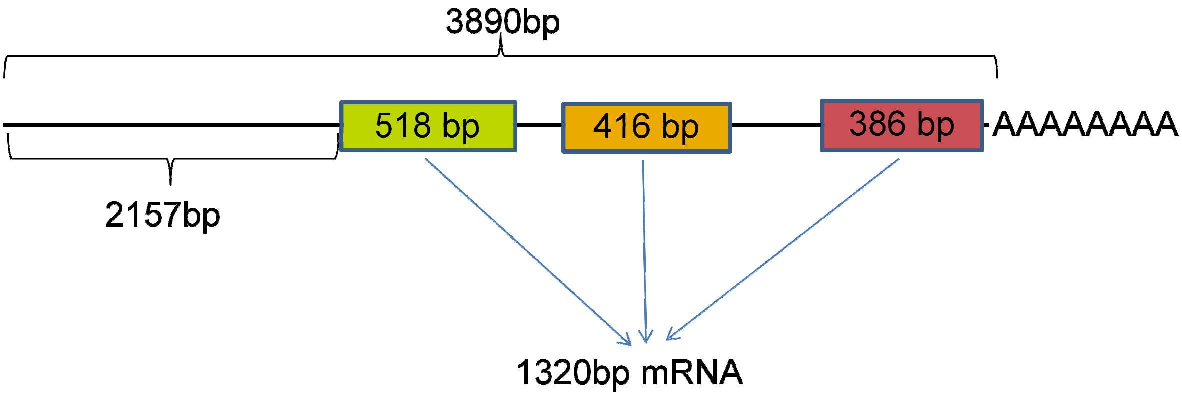

Figure 3. Diagrammatical representation of the gene encoding EST03G12. Lines indicate introns and coloured boxes indicate each of the three exons of 518, 416 and 386 bp which result in a mature mRNA of 1320 bp. The sequence obtained through our efforts and the previous work by Wynne *et al* results in a gene of approximately 3890 bp.

When trying to 'walk' upstream of EST03G12 we encountered a difficulty, in that using the same primers we obtained different sequences. Therefore we had to design and use a number of primers to sequence resultant clones and to run PCR in gDNA to verify the upstream DNA sequence. It has been estimated that the Atlantic salmon genome consists of about 30-35% repetitive DNA (Davidson et al 2010). Furthermore, 6-10% of the genome contains transposable elements of approximately 1500bp in length (de Boer et al, 2007). It is these features that led to the requirement to use Sanger based sequencing in order to produce the reference genome for Atlantic salmon. Further complicating genomic DNA studies in Atlantic salmon is the autotetraploidization of the genome resulting in pseudogene regions. It would appear from our efforts that EST03G12 sits either in a repetitive region of the genome and/or is close to a transposon. This has hampered the efforts to identify the gene, the putative promoter and the open reading frame for EST03G12. The international effort to fully sequence the genome of the double haploid salmon, 'Sally', will overcome these issues and should shed additional light on the gene structure of EST03G12. Information from the genome sequencing effort will be available in late 2012 (W. Davidson, Simon Fraser University, pers. comm.). When this is available we should be in a better position to define the true coding sequence as well as features responsible for the expression of EST03G12.

6.3 Protein lysate preparation and sequencing

Previous efforts by James Wynne and ourselves to identify the protein sequence encoded by EST03G12 using recombinant proteins and antibodies were fruitless. To that end we initially endeavoured to repeat his work using a Eukaryotic protein production system, *Picia pastoralis*. However, we were again unable to produce mature protein, presumably due to the toxic nature of the protein encoded by EST03G12.

Therefore, we embarked on a proteomics approach utilising whole protein lysates from gills of heavily infected fish. A total of 668 peptides were identified in the gill lysate mainly representing salmon peptides (Appendix 5). Of the 668 proteins present, 75% had a distinct match to known Atlantic salmon proteins, 10% to zebra fish proteins, 7% to proteins from Oncorhynchus species and the remaining 8% to unrelated species. Interestingly, five peptides showed homology to amoeba proteins, presumably as a result of amoeba being present in the gill tissue. Of particular interest is protein #661, Immuno-dominant variable surface antigen. This protein had been previously recognised in invading trophozoites of *Entamoeba histolytica* (Edman et al, 1990). This finding, despite the apparent very small contribution of amoeba to the total protein, highlights a possible powerful approach to identifying key molecules used by the amoeba to invade host tissue. Furthermore there were a number of host lectin proteins identified (e.g. protein #'s 176, 619 and 666) providing evidence toward a host-parasite lectin-sugar interaction.

None of the peptides identified showed homology to any of the predicted peptides from the cDNA sequence. We were surprised we did not have any gill lysate proteins match despite having all conceivable reading frames of the EST included in the database for the filtering of our results. It is possible that due to the small size of the predicted proteins these may not have bound to the 3KDa MW cut off filter units used or that the tryptonic digest of the proteins resulted in very small protein fragments that were filtered out in the quality control process.

We were able to identify a number of immune related proteins from the lysate. Of particular interest was the identification of both lysozyme C (protein #503 in Appendix 5) and lysosomal protective protein (protein # 614). Moreover, a number of proteins of both the innate and adaptive immune response were present including heat shock proteins, albumins, components of the complement system and stress related proteins (#'s 316, 345 and 602). Adaptive immune related proteins included MHC class I type receptors (# 599), MHC class II type receptors (#'s 290, 335 and 505) along with general immune type receptors (# 652). Other immune type proteins present were tumor associated proteins (#'s 638 and 657) and proteins indicative of an acute phase response to infection (#'s 292, 401 and 608). Previous studies, examining gene expression, indicated that there was a localised and co-ordinated down regulation of the immune response (Wynne et al 2008b, Young et al 2008). However, the data obtained here on proteins seems to be contradictory. This could in part be due to the differences in the studies. Gene expression studies compare relative abundance of mRNA for particular genes between two samples. However, one of the shortcomings is that through global gene expression analysis the biology of the condition can be overlooked. For instance, with AGD, apparent 'down-regulation' of gene expression can be an artefact of the hyperproliferation of the epithelial cells associated with the condition, something which the authors of the gene expression studies failed to consider.

Indeed it may be worth pursuing a proteomics approach toward AGD responses. This can now be easily done since we have developed the protocols for proteomics analysis of gill tissue. A logical next step would be to undertake difference gel electrophoresis (DIGE) which can be used to detect very small changes in protein abundance between two or more samples. This could be done using heavily infected versus non infected gill lysates. However, it was beyond the scope of this project due to the time consuming optimisation of protocols required.

Although we were unable to specifically identify the proteins encoded by EST03G12 we were to demonstrate the power that proteomics may offer in understanding AGD and possibly for identification of treatment options. Preoteomics is also a relatively inexpensive technology ideally suiting further investigations into AGD.

6.4 EST03G12 shares similarity with a lysozyme gene from stickleback

Following sequencing, the 300 bp amplicon from BAC contig 742 had a 97% similarity to EST03G12. The 300 bp amplicon along with the EST03G12 sequence were then blasted against scaffolds from the Atlantic salmon genome project. The scaffold 12661284 had the most significant alignment with a 67 bp identity. The scaffold was then blasted on the stickleback linkage map and a significant hit was seen on linkage group 9. This hit was interrogated and the matching DNA sequence was localised to a stickleback gene encoding a putative lysozyme.

Lysozymes are a family of enzymes that catalyze the cleavage of the β-(1,4) bond between *N*-acetyl glucosamine (GlcNAc) and *N*-acetyl muramic acid (MurNAc) in the peptidoglycan of bacterial cell walls (Prager and Jolles, 1996); in other words they are responsible for the cells digestion of waste including invading microbes. They exist ubiquitously in diverse organisms, including animals, plants, fungi, and bacteria, and within vertebrates can be classified into four major types: chicken-type (c-type), goose-type (g-type), lactalbumin and calcium-binding lysozyme. The genes encoding and proteins representative of c-type and g-type lysozymes have been described in a number of fish species. Moreover, in Atlantic salmon both c-type and g-type lysozymes have been described either at the mRNA or protein level.

The stickleback lysozyme to which EST03G12 shows homology belongs to the g-type family (http://supfam.cs.bris.ac.uk/SUPERFAMILY/cgi-bin/gene.cgi?genome=g1&seqid=ENSGACP00000025549). Interestingly, there is a 200 amino acid g-type lysozyme already reported for Atlantic salmon (Kyomuhendo et al 2007). However, this does not share homology to EST03G12 either at the mRNA or the protein level. Unlike stickleback, zebra fish are thought to have two g-type lysozyme genes (Irwin, Biegel and Stewart, 2011). Therefore it is possible that EST03G12 encodes for a 2nd g-type lysozyme gene in Atlantic salmon which is similar to the one in stickleback.

Despite obtaining further cDNA and gDNA sequence for the EST (please see section 6.2) we were unable to predict a mature peptide other than those previously identified (predicted to be either 108, 71 or 41 aa depending on the correct reading frame). It will be possible in the near future as the Salmon genome sequence becomes available, to fill in the missing parts of the sequence and decode the entire coding sequence for the EST.

From a functional viewpoint the finding that EST03G12 may represent a g-type lysozyme is interesting. As stated above, the c and g-type lysozymes are known to be bactericidal. The mechanism of action involves forming holes in the peptidoglycan walls of bacteria leading to lysis and death. Amoebae also have peptidoglycan cell walls and lysozyme may be amoebicidal. Interestingly lysozyme from humans has been shown to be amoebicidal toward *Entamoeba histolytica* (Leon-Sicairos et al 2006). If indeed EST03G12 represents a novel g-type lysozyme then the over expression observed in AGD infected fish could be as a result of trying to mount an immune response to the invading amoebae responsoible for AGD. An interesting avenue for further research would be to try and determine if EST03G12 is indeed amoebicidal to *N. Perurans*. However, this would need to come following definitive determination of the protein sequence.

6.5 Allele screening and correlation to resistance/susceptibility

In total, nine unique alleles were identified in the sample population with these combining to represent 12 unique haplotypes (Table 3). Of the population, 42% of the fish are homozygous for allele a and 82% of the total population carry the a allele. Three individuals had an allele containing a 15bp insert/repeat. Of these, two fish had the haplotype ae and both a gill score of 0 whereas the other fish (haplotype ce) had a gill score of 5. The haplotype, ai, is present in only 7% of the sample population. However all fish carrying this haplotype had a gill score of 0 at the time of measurement (after 3 rounds of commercial bathing) possibly meaning that fish with ai are more resistant to AGD. There is also a rare allele (f), for which only one individual was homozygous. This individual also had a gill score of 0.

Table 3: EST03G12 Haplotypes and corresponding GillScore for sample population used in allele screening study.

Haplotype	% of population	Average GillScore
aa	42	2.9
ab	3	5
ac	10	3.6
ad	8	3.5
ae	7	0
ah	7	2.5
ai	9	0
bc	4	1
cd	3	5
ce	3	5
ff	1	0
gg	3	1

One of the aims of the Saltas Tasmanian Atlantic salmon selective breeding program (SBP) is to breed into the population higher levels of resistance to AGD. At the moment this is based on phenotypic measurements of higher resistance to AGD in the marine growout cohort and selection of their freshwater cohort siblings. One of the ongoing aims of the R&D program is to increase the gains through genome wide selection (GWS) and/or marker assisted selection (MAS). Previous work indicated that certain alleles of the major histocompatability (MH) genes are associated with resistance to AGD (Wynne et al, 2007). Indeed a specific allele (Sasa-DAA-3UTR 239) explained some 5% of the variation. Although this is low, the authors suggested that AGD resistance, like many other diseases, is most likely polygenic. Therefore, to implement the best form of MAS a number of markers, each contributing to resistance, need to be identified. The classic or c-type lysozyme in Atlantic salmon has been implicated to be associated with resistance to a number of bacterial diseases. It should be noted that these studies were on lysozyme levels and/or activity and not on whether the resistant animals had specific alleles. However, it is possible that different alleles and/or haplotypes are responsible for increased levels and or activity. This could also be the case with EST03G12.

Previous studies have demonstrated that following a chronic infection with AGD, animals segregated into the susceptible category show over expression of genes encoding acute phase proteins (APP) (Wynne et al, 2008a). Interestingly this was in contrast to an earlier study by the same authors which showed little up-regulation of APP genes upon an acute first infection (Wynne et al, 2007). These differences could be due to the modes of infection as the Wynne et al 2008 study was performed on fish following three rounds of infection and segregation into the susceptible group was following a 100+ day exposure without intervention. Lysozyme, being a component of the innate immune system can be considered an APP. Interestingly, EST03G12 was also studied in the fish from the Wynne et al 2008 paper and its expression in ‘resistant’ and ‘susceptible’ individuals compared to naive fish. Expression in resistant fish was not significantly different from naive individuals whereas it was highly over expressed in ‘susceptible’ individuals. This together with the fact that lysozyme is an APP could mean that those individuals who develop ‘resistance’ (similar to those characterised here as 0-1 gill score) carry superior alleles of EST03G12 (with respect to AGD) and are able to mount an appropriate acute phase response leading to the development of acquired immunity and hence a resistance to AGD. However, the only way to fully test this is to perform a concurrent transcriptomics and genotype analysis.

Overall there appears from the sample population that there are certain haplotypes and alleles of the EST that are correlated to resistance to AGD. This is interesting given that EST03G12 possibly codes for an immune gene, g-type lysozyme. However, there must be a cautionary note, the sample population tested was small and that only the extremes (0-1 and 4-5) in gill score were used. Now that a number of alleles and haplotypes have been identified it would be beneficial, after designing an appropriate assay, to genotype historical samples from the SBP. These animals have multiple measurements of AGD severity allowing complex analysis with regard to EST03G12 polymorphism and disease resistance/susceptibility to be undertaken.

Of note is that the identification of nine unique alleles at this functional region of the genome in a relatively small sample size, is futher evidence of good genetic diversity in the Tasmanian population, and the opportunity for exploitation through selective breeding.

7.0 BENEFITS AND ADOPTION

In order to enhance the gains from selective breeding for AGD resistance there is a need to discover markers of ‘resistance’ that can be used as a surrogate to phenotypic studies for the selection of resistant individuals. It appears as though EST03G12 encodes for a functional immune related gene, g-type lysozyme, and therefore may be involved in an early response to AGD. Furthermore, we have shown that there appears to be ‘superior’ alleles and haplotypes present in the population that are associated with the acquisition of 'resistance' to AGD. Therefore this work potentially adds another 'marker' to the genetic toolbox to allow implementation of either a GWS or MAS approach to AGD.

8.0 FURTHER DVELOPMENT

At this time there are three pressing questions arising from this work;

a. Does EST03G12 encode a functional g-type lysozyme that plays an amoebicidal role in the response to AGD infection?

Presently, through the synteny work, we have tantalising evidence that EST03G12 encodes a previously undescribed g-type lysozyme from Atlantic salmon. Despite our best efforts in this project we were unable to deduce the definitive coding sequence for the gene and therefore were unable to undertake the functional studies originally planned. When the genome sequence for Atlantic salmon is available in late 2012, we will be a step closer to deducing the true gene sequence and its structure. This information would be invaluable in then facilitating functional studies to determine if EST03G12 is amoebicidal against *N. perurans*.

b. Are there alleles of EST03G12 that can conclusively be correlated with increased AGD resistance?

Relatively speaking, the data presented here regarding the alleles and haplotypes of EST03G12 can be considered preliminary, as the sample size is small for a population type study. However, we have identified a number of alleles and we know how these alleles differ (e.g. the SNPs etc). We are therefore in a position to design an appropriate study to rapidly screen a larger sample set to better understand the variation at this locus in the population and the relationship with AGD resistance. Through the Saltas SBP there is AGD data and accompanying DNA available on 1000's of fish from multiple year classes and with known pedigree. Therefore a logical next step would be to develop a genotyping assay and apply it to a select sample of these fish to determine the correlation between EST03G12 alleles and/or haplotypes and AGD severity. This sample set could perhaps also be examined for MH diversity and other SNP markers being discovered that are associated with AGD resistance.

c. Can a proteomics approach to AGD provide insights into the host response, differences in resistance levels and/or identify key targets in the pathogen?

From the very limited proteomics analysis carried out in this project we were able to identify a number of key proteins involved in the immune response as well as those responsible for a possible lectin-sugar interaction between the amoebae and host tissue. A logical extension is to use a DIGE based approach to look at protein differences between resistant and susceptible fish. There is also the possibility of using a similar approach to identify those factors which make *N. perurans* infective compared to, for example, *N. pemaquidensis*. Finally, the data produced by this study can be utilised to build a picture of what is happening at the protein (and hence effector) level in the host tissue.

9.0 PLANNED OUTCOMES

This project has provided the possible identity of the protein encoded by EST03G12, a novel g-type lysozyme in Atlantic salmon. This finding is of a functional importance as lysozymes are a family of proteins involved in innate immunity. It is most likely that the over expression of EST03G12 observed during AGD pathology is as a result of the fish attempting to fight the amoeba infection. We have identified a number of alleles and corresponding haplotypes in a small sample population. Some of these can be correlated to increased AGD resistance in certain individuals. This provides a basis for the design of an appropriate study using archival data and DNA to better determine the relationship between this, and other genome regions, and AGD resistance.

10.0 CONCLUSION

The massive over expression of EST03G12 in AGD infected salmon has lead to debate over both its role in AGD and whether it can be used as a marker of susceptibility and/or resistance. Therefore the aim of this project was to identify EST03G12, to determine its role in AGD and to see if it can be used as a marker of resistance. To that end through a number of approaches we were able to provide evidence that the EST encodes what appears to be a novel g-type lysozyme. G-type lysozymes are part of the innate immune system of vertebrates. Therefore it would appear that the over expression could be as a result of trying to mount a defensive response to AGD. However, there is further work required to provide true functional evidence of this.

We have provided some evidence that there are certain alleles and/or haplotypes that are associated with AGD resistance in the Tasmanian population. This can be considered preliminary as the sample size for our study was small. However, there is the possibility, following the design and testing of an appropriate genotyping test, to screen a large cohort of fish from the Saltas Atlantic salmon selective breeding population for which historical AGD scores are known. This together with the possibility that EST03G12 serves a functional role in AGD resistance makes its use as a marker for selection an attractive proposition.

The proteomics analysis, although not providing the identity of the protein encoded by EST03G12, provided insights into the power of this approach for AGD research. As we only looked at gill tissue from one infected fish the data needs to be treated with some caution. However, it did show that there are a number of immune related proteins expressed in the gill. This is in contrast to the data generated on gene expression. It also provided evidence of a lectin sugar relationship between the pathogen and host tissue. Proteins are the effector molecules; therefore it appears as though a proteomics approach to examine both basic and applied aspects of AGD seems warranted. In particular, we were able to identify pathogen specific proteins in the analysis. This is interesting given their low abundance in the protein preparation. A logical approach would be to combine proteomics and transcriptomics to examine the differences between the infective and non-infective Neoparamoeba species. This is now a possibility given the existence of an infective cultured strain of *N. perurans*.

11.0 REFERENCES

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APPENDIX 1: INTELLECTUAL PROPERTY

The valuable information arising from this research are:

1. DNA sequences for the gene encoding EST03G12 and each of the 10 alleles.
2. PCR amplification primers used.
3. List of proteins identified in the crude gill lysate.
4. Copyright in this report.

APPENDIX 2: STAFF

Staff engaged on the project:

Principal investigator

Dr Mathew Cook	CSIRO Marine and Atmospheric Research

Co-Principal Investigators

Dr Nick Elliott	CSIRO Marine and Atmospheric Research
Dr Ben Maynard	CSIRO Marine and Atmospheric Research

Research Assistants

Ms Natasha Botwright	CSIRO Livestock industries
Mrs Leanne Dierens	CSIRO Livestock Industries

APPENDIX 3: LIST OF PRIMERS USED TO DERIVE THE SEQUENCE OF THE 3.9KB GENE SEQUENCE ENCODING EST03G12

Primer	Sequence	Length
ATG1.F	ATGTCCCCTCTGCCCTCCTATTCC	24
ATG2.F	ATGTGTGCCTGGTGTGTGG	19
ATG3.F	ATGTTTTAATTTTTAGTCTGA	21
ATG4.F	ATGGTACTTTGAGATAAAATGTAG	24
ATG5.F	ATGAAATCCTTCTCTTCAGTTCTCTGG	27
ORF111.R	CTATGGTGATGCTGGGTGC	19
EST_998.R	GTTTGTTAAGCGGTATGAGTGATG	24
EST_95.F	CCCTTTAATACAGTATGTCCCCTCT	25
EST_27.F	TTCCTGGCTCATAGACTACTTTCA	24
EST_17.F	GTGTTAGTTTTTCCTGGCTCATAGA	25
EST_1173.R	AAGAGGGGTCTTCTTAAAGGTGTT	24
ESTWalk_GSP6_2.F	GCAGAAATTGGACAAACTGAC	21
ESTWalk_1A_6_full.R	TGAATTCGACCATACAATCAAA	22
ESTWalk_1A_2.F	GAGCTATTACTCGCCTGAGGT	21
ESTJames_cDNA.F	TCACTTCACATACCAACAGCA	21
EST_Walk5'_GSP2	CGACAGTTTTTCTGGGAGTCGTTTGTTA	28
EST_Walk5'_GSP1	TGTAGTAGAGACCCACTTTGCCACCTGT	28
EST_WalkF_GSP1	ACTAGAACACCTGATTACTACAACCTT	27
EST_Walk_GSP2	CATCGAGGAAGAACACACAGACACAG	26
3.3_1.F	TTAATAAGCAAGCGAACAACAG	22
2.2_1.F	GCTATTACTACCTCCTGGGAAAA	23
2.2_2.F	TGTGCTCGATTTTATACACCTG	22
2.2_3.F	AAATGATGAACCAGCGATAC	20
2.2_4.F	CAACCAACCCTACCACTGAC	20
C2.2-1.R	GCTGGTAGCAGGGTCGTAGA	20
C2.2_2.R	GTAGGGTTGGTTGCCACTGT	20
Clone2.2_FL_5'	ATGCAATGAATGGTCCCTAGT	21
Clone2.2_FL_3'	TTGGAAGCCAGTGACATAGAG	21
EST03G12_cDNA_5'	ACTTCACCTCTGCTTTCCTATCC	23
EST03G12_cDNA_3'	TTCTACTTGGAAGCCAGTGACAT	23
5'-EST03G12-71-FAM	5ATGGATTGTGCTTCAACTGTC	22
3'-EST03G12-71	TTAAGCGGTATGAGTGATGGT	21

APPENDIX 4: SEQUENCE OF THE GENE ENCODING EST03G12

>EST03G12_Contig
CGACGGCCCGGGCTGGCAAGAGATTGTTTCTCGCTTACGGCCATACCAGCCTGGGTACGCCCGATCTCGTCTGATCTCGGAAG
CTAAGCAGGGTCGGGCCTGGTTAGTACTTGGATGGGAGACCGCCTGGGAATACCAGGTGCTGTAAGCATTTTGTCCACGAGGG
GGTGCTCTTGCACTATTTCATCAGCAACACTGCCTTGTATTAAGCATTTAATGATGAATTGACTAAATGTCTGTTTTATCATC
GAGTGGTTTCAACTCCTGAAGGGCCACTCCATACTCATCCTGGAAGGCACCTTTAAGAAGAGCCTTCTCCCTAAGAGCATCTA
TGTTACTGGAAAGTGACAATACACATAGCTGCCCTGAGGAATCCCCACTTCATGGGCTGGACAACCTCCTGGCAGAGTATGCT
GAGGGTCACCCCAAGTCCTACATCCTGACTGTCGACAAAGAAGTGAAGTTAGCTGAAACAGGAAAGATCTGGGTGGATCACAA
CCCCAAAATGAAACGGCACCAGGGAACCTCCTGTATCTTAACACTGTTTGTTAATTACAGATGAAGCTATATAACAATTATTA
CAGATACAAAATATTTCATTAAAATATTAAATAATTAAACGACACTCTAGACAACTACTTTCATGCCACCTGGTTCTGTCCAC
CCACCCTACAATTCTGGAAAGAAACTATATAAAAACAATCCATCCTTTTTGAATGTGATAACCCAATAAATAAAATGTCCCAC
AAAATATGAAGCCAATATAGTATGCTATGTTCTCGTGTTTCAGGAGCGTACAGATAAGGTGTGTACGTAAGGTGTGTTGGAAA
GTGTTCAAGCGCTCTTGCGCACCTGCTAATCTAATTTCACCAGAAGTCTGACATGAAGAAACACATCTTCATTCATACAGGTG
AGTCATCATGTATTCTATGGGAATAGAGATCTTGTCTTTGTCAAGGTCACAGTCGAAATGTGTTATTAATTTTCCATAAGGCC
ATACTATTCCAAGGTTATTATAGTAAAGGAAAATTGAAACTAAAATTCTAATTCAAATTTGAAAAACAATTTAGAAAACTGAA
ATAAAAAAGTAATCAATATTGAAACGATTGTCTTTGACTGAAAAAACAAAATTGAAACCAAGTATATGTTTAGTTTTAGTTTT
TTTCTAAACTTTAGACAAAAGTCTAATGGGGTTTTTGAGCTTCTGAATCTGGCAGGTAAATGCTGTCAGTAGATGCTGATGTT
TCAAATAGGCCTATCTTGTGCATCACTATCACTAGCTATTACTACCTCCTGGGAAAACTCTAGTTTTGATTTACATTTGGTTG
GAATCCAAAAAACACATGTCTCCGTATCATTTAGTTTATTTGGTAAATATTTTCTTAACTCTTCTTGAACTGCACTGTTGGGT
CTACACTTGCACTGTAAGGTCTACACTTGTTCTATTCGGTGTATGTGACAAATACAGTTTGGTTTGATTTGACTTACAGTTGA
CTGGGGCAGGGGCAGAAATTGGACAAACTGACTTGTTGTATAAGTGGCATTCTATGATGGTGCCACGTTGAAAGTCACTGAGC
TCTTCAGTGAGGTCATTCTACTGCCCATGTTTGTCTATGGAGATTGTATGGCTGTGTGCTCGATTTTATACACCTGTCAGCAA
TGGGTGTGACTGAAATAGCTAAATCCACTAATTGGAAGGAGTGTCCACATAGTTTTGTATATATAGTGTGTATGTAGCTTTAG
AAATCAATGACTTGCTAACATCATGTCGTGTCTTGGCTATCATTAATGTGATGACGATTGTTTTATCAAATCGATTAACTATG
TTTAATTATTACGATGATTAAATTAATCCTGTAACAATTAACTCATTTGCAATCTCAGGGCACCACGGAAGAGTTTATTTAAC
GAGTTACCGTTTTCCGAATTAACTATTAAAGATATAAATATCTCTTACATTTCAGTCATTAATTAATTGTTTACCTTCTATCA
GTCTCAATCTGAATGTCGCAAAATCCTTAGATATCTGCACGAACCCAAGCATAAATGATGAACCAGCGATACACAAATTGGCT
TAATTATTTATTTACTAACTAACTAAATAATCACACAGAATTACATAAACACACAAATAGTTGGTTATTGGTTACTAACACA**A**
TGCAATGAATGGTCCCTAGTGGACTAAAGCGATATGACGTCTTGGTAGACAAAGGAAAGGGGTGGGGACAGATTAGAGCGGGA
GAGACAGATATTGGGCTTATTGTACATACATGTGGAAAACACCGCCATCGTCAATATGGATATTTAACACCCTAACAACCGCA
CTGCCCCTTTAACTTATAAAATAGTGAACTTCACCTCTGCTTTCCTATCCCAGGTGAGAAGCCCAATGTGTGCCAGGTGTGTG
GCAAAGCCTTCAGCCAGAGCTCCAACTCATCACTTGCAGCTATCAGCACAGTGGCAACCAACCCTACCACTGACCCCGCTGCC
TCTTCGGCTTCCAACGCAAACAGGAGAACCACTGCACATACTTTCAGTCTACGACCCTGCTACCAGCTGATCTGAGATCAGTT
TTAATAAGCAAGCGAACAACAGCAAATAGATAGCAACTCAGAGGCTCTCACATGGTTGCTAATGTTTGCATTCCCAGGCTAAT
CATTGTTTTATTATTTTAGGT*GATCAAACTCCCTTGATTGTCAGTGATTTACCTGTAAGGGTGTAGTTAAAGATATGGCCCTT*
*TGAGATATAATACGTTTTAGTGCTTGACAAATATATTTCTCTTGTGACACCCATGT***AGCTTCTCCGGAACTGAGTCATCCTCT**
TCAGTTCTCTAGAAAATAAACATTTAGCTGGAATGGATTGGGCTGAGAACTCCCCACCCTCCCTCTCTGTCAGCGTTACCCTA
TAAAAGCAGAGCCATCTCTCCGCTCTGCACTAGAACACCTGATTACTACAACCTTCAAGCGCGCCATCGCATCGAGGAAGAAC
ACACAGACACAGCAATGGATTGTGCTTCAACTGTCGTCACTTCACATACCAACAGCAAAAACGACTGCAATAAAAAAAAATGT
GTTGCCCCATGTCCTACTGAATCAGGCAAAAACATATCAGGTCAAAACATATCAGGCCAAAACATATCAGGCCAAAACATATC
AGGCAGTGTGGGCGGAAGTATTTCCATTGGCAACCAGGACAATACCATCACTCATACCGGT*ATGTAACCCTATCCAGCGGGAG*
GGAATCTTCATATGAATGAATAAATACATCAATTCATATTTTATTGTTTTGTGGCCATCCAACATGGGAATATAACACACATT
GATATTAGACATTTCAAAGCATAAAGCAATTACATGTCCATACACATACACATTTCACAGCTCAGTTCCAGAACCAGCATAAA
AAATGGTTTATTGTTGCACATAGCAGGGTTCTATGCAAACTCCTAATACTGACAACCACATTTATTTCAGCACTGTCAATGAC
*TCTCTCTCGTTCTCTT***AGCTTAACAAACGACTCCCAGAAAAACTGTCGCACCCAGCATCACCATAGCCAACATAACAGGTGGC**
AAAGTGGGTCTCTACTACAAGGCAGAGAAGATGGCTCTCTGTGACCTCATCGAAGGAAGTCAACTCAGGAAGGGCCACTCCAT
TCTCATCCTGGAAAACACCTTTAAGAAGACCCCTCTTCCTCCTCTATGTCACTGGCTTCCAAGTAGAAAGTGACAATACATAC
AGATTAAACTACATACAAATTATTGATTAAAAATAAAGAGAGAATACATCTCAGATAAGTGAAAAAGTGCTACAAGATATACT
TTGATTGTATGGTCGAATTCAACAATGTAATCAATGTAGGTTTTTGACAAAAAAATAAATGGTACCAAACTGAAAAAAAAAAA
AAAAAA

Features:
Underlined text is the two putative promoters
Bold text is the Exons
Italicised text is the introns

APPENDIX 5: LIST OF PROTEINS IDENTIFIED FROM GILL CELL LYSATE PREPARATIONS

N	Swissprot Accession #	Name
1	tr|B5X851|B5X851_SALSA	Histone H2A OS=Salmo salar GN=H2A PE=2 SV=1
2	tr|B5X872|B5X872_SALSA	Actin, cytoplasmic 1 OS=Salmo salar GN=ACTB PE=2 SV=1
3	tr|B9EMG4|B9EMG4_SALSA	Hemoglobin subunit beta OS=Salmo salar GN=HBB PE=2 SV=1
4	tr|C0H8L6|C0H8L6_SALSA	Hemoglobin subunit alpha OS=Salmo salar GN=HBA PE=2 SV=1
5	tr|C0PU42|C0PU42_SALSA	Myeloperoxidase (Fragment) OS=Salmo salar GN=PERM PE=2 SV=1
6	sp|P11251|HBA_SALSA	Hemoglobin subunit alpha OS=Salmo salar GN=hba PE=2 SV=2
7	tr|Q9I8X4|Q9I8X4_ONCMY	Beta-actin OS=Oncorhynchus mykiss PE=2 SV=1
8	tr|C0H8A6|C0H8A6_SALSA	Tubulin beta-2C chain OS=Salmo salar GN=TBB2C PE=2 SV=1
9	tr|C0HBD9|C0HBD9_SALSA	Elongation factor 2 OS=Salmo salar GN=EF2 PE=2 SV=1
10	tr|C0H808|C0H808_SALSA	Tubulin beta-1 chain OS=Salmo salar GN=TBB1 PE=2 SV=1
11	tr|B5X320|B5X320_SALSA	Keratin, type II cytoskeletal 8 OS=Salmo salar GN=K2C8 PE=2 SV=1
12	tr|Q8JFG4|Q8JFG4_ONCMY	Type II keratin E3 OS=Oncorhynchus mykiss GN=E3 PE=2 SV=1
13	tr|C0H8U1|C0H8U1_SALSA	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Salmo salar GN=AT1A1 PE=2 SV=1
14	tr|Q90YH3|Q90YH3_ONCMY	Simple type II keratin K8a (S1) OS=Oncorhynchus mykiss GN=S1 PE=2 SV=1
15	tr|Q90W76|Q90W76_ONCMY	Type II keratin E1 OS=Oncorhynchus mykiss GN=E1 PE=2 SV=1
16	tr|B5X0U5|B5X0U5_SALSA	Tubulin beta chain OS=Salmo salar GN=TBB5 PE=2 SV=1
17	tr|Q9W6K6|Q9W6K6_SALSA	Heat shock protein hsp90 beta OS=Salmo salar GN=hsp90 beta PE=2 SV=1
18	sp|O57607|K1C18_ONCMY	Keratin, type I cytoskeletal 18 OS=Oncorhynchus mykiss GN=krt18 PE=1 SV=1
19	tr|C0H824|C0H824_SALSA	Hemoglobin subunit beta-1 OS=Salmo salar GN=HBB1 PE=2 SV=1
20	tr|Q6PE34|Q6PE34_DANRE	Novel protein (Zgc:65894) OS=Danio rerio GN=zgc:65894 PE=2 SV=1
21	tr|B5X746|B5X746_SALSA	Hemoglobin subunit alpha-4 OS=Salmo salar GN=HBA4 PE=2 SV=1
22	tr|Q7SYE2|Q7SYE2_DANRE	Actinin, alpha 4 OS=Danio rerio GN=actn4 PE=2 SV=1
23	tr|C0HAL2|C0HAL2_SALSA	Elongation factor 1-alpha OS=Salmo salar GN=EF1A2 PE=2 SV=1
24	tr|Q91471|Q91471_SALSA	Beta globin OS=Salmo salar PE=2 SV=1

25	tr|Q6IQL9|Q6IQL9_DANRE	Novel actin protein OS=Danio rerio GN=RP71-1C22.1 PE=2 SV=1
26	tr|Q92025|Q92025_SALSA	Beta-globin (Fragment) OS=Salmo salar PE=3 SV=1
27	tr|Q90W75|Q90W75_ONCMY	Type II keratin E2 OS=Oncorhynchus mykiss GN=E2 PE=2 SV=1
28	tr|B5X2B3|B5X2B3_SALSA	Serotransferrin-1 OS=Salmo salar GN=TRF1 PE=2 SV=1
29	tr|C0HBL4|C0HBL4_SALSA	Tubulin beta-2A chain OS=Salmo salar GN=TBB2A PE=2 SV=1
30	tr|B5DFX7|B5DFX7_SALSA	Heat shock cognate 70 kDa protein OS=Salmo salar GN=hspa8 PE=2 SV=1
31	tr|Q8JFQ5|Q8JFQ5_ONCMY	Keratin 12 (Fragment) OS=Oncorhynchus mykiss GN=k12 PE=2 SV=1
32	tr|B5DH02|B5DH02_SALSA	Tubulin, alpha 8 like 3-2 OS=Salmo salar PE=2 SV=1
33	tr|Q6DHS1|Q6DHS1_DANRE	Actin, alpha 2, smooth muscle, aorta OS=Danio rerio GN=acta2 PE=2 SV=1
34	tr|Q92015|Q92015_SALSA	Alpha-globin OS=Salmo salar GN=HBA PE=2 SV=1
35	tr|B5XFF2|B5XFF2_SALSA	Apolipoprotein A-I-1 OS=Salmo salar GN=APA11 PE=2 SV=1
36	tr|B5DGE8|B5DGE8_SALSA	Tubulin alpha chain OS=Salmo salar GN=tuba8l2 PE=2 SV=1
37	sp|Q03156|ALBU2_SALSA	Serum albumin 2 OS=Salmo salar GN=alb2 PE=2 SV=1
38	tr|F6KMH7|F6KMH7_EPICO	Keratin type II E3 (Fragment) OS=Epinephelus coioides PE=2 SV=1
39	tr|C0H9I5|C0H9I5_SALSA	Alpha-actinin-1 OS=Salmo salar GN=ACTN1 PE=2 SV=1
40	tr|C0PU67|C0PU67_SALSA	Gelsolin (Fragment) OS=Salmo salar GN=GELS PE=2 SV=1
41	tr|Q6R4A2|Q6R4A2_ONCMY	Cytoplasmic carbonic anhydrase OS=Oncorhynchus mykiss GN=CA2 PE=2 SV=1
42	sp|Q8JFQ6|K1C13_ONCMY	Keratin, type I cytoskeletal 13 OS=Oncorhynchus mykiss GN=krt13 PE=2 SV=1
43	tr|B5X4R7|B5X4R7_SALSA	Transketolase OS=Salmo salar GN=TKT PE=2 SV=1
44	sp|P21848|ALBU1_SALSA	Serum albumin 1 OS=Salmo salar GN=alb1 PE=2 SV=1
45	tr|B5DGS2|B5DGS2_SALSA	Isocitrate dehydrogenase [NADP] OS=Salmo salar GN=IDHP PE=2 SV=1
46	tr|B5X3K2|B5X3K2_SALSA	Glyceraldehyde-3-phosphate dehydrogenase OS=Salmo salar GN=G3P PE=2 SV=1
47	tr|C0PUK9|C0PUK9_SALSA	Pyruvate kinase (Fragment) OS=Salmo salar GN=KPYK PE=2 SV=1
48	tr|C0HB50|C0HB50_SALSA	Probable ATP-dependent RNA helicase DDX5 OS=Salmo salar GN=DDX5 PE=2 SV=1
49	tr|Q4U0S2|Q4U0S2_DANRE	Smooth muscle myosin heavy chain OS=Danio rerio GN=myh11 PE=2 SV=1
50	tr|A4IEA9|A4IEA9_ONCMY	Lymphocyte cytosolic protein 1 (Fragment) OS=Oncorhynchus mykiss GN=lcp1 PE=2 SV=1
51	tr|B5X3I8|B5X3I8_SALSA	Carbonic anhydrase OS=Salmo salar GN=CAHZ PE=2 SV=1
52	tr|B5X3Q6|B5X3Q6_SALSA	60S ribosomal protein L4-A OS=Salmo salar GN=RL4A PE=2 SV=1
53	tr|C0PUT2|C0PUT2_SALSA	Filamin-A (Fragment) OS=Salmo salar GN=FLNA PE=2 SV=1
54	tr|B5DGS4|B5DGS4_SALSA	Malate dehydrogenase OS=Salmo salar PE=2 SV=1

55	tr|Q8UUJ3|Q8UUJ3_ONCKE	Type I collagen alpha 2 chain (Fragment) OS=Oncorhynchus keta GN=col1a2.2 PE=2 SV=1
56	tr|B5X8C1|B5X8C1_SALSA	ADP/ATP translocase 2 OS=Salmo salar GN=ADT2 PE=2 SV=1
57	tr|B5X2E1|B5X2E1_SALSA	Adenylyl cyclase-associated protein OS=Salmo salar GN=CAP1 PE=2 SV=1
58	tr|B5X4L1|B5X4L1_SALSA	Junction plakoglobin OS=Salmo salar GN=PLAK PE=2 SV=1
59	tr|B5DGC7|B5DGC7_SALSA	60S acidic ribosomal protein P0 OS=Salmo salar GN=arbp PE=2 SV=1
60	sp|O93484|CO1A2_ONCMY	Collagen alpha-2(I) chain OS=Oncorhynchus mykiss GN=col1a2 PE=2 SV=2
61	tr|C0PUM3|C0PUM3_SALSA	ATP-dependent RNA helicase DDX39 (Fragment) OS=Salmo salar GN=DDX39 PE=2 SV=1
62	tr|B5XCU8|B5XCU8_SALSA	Annexin A1 OS=Salmo salar GN=ANXA1 PE=2 SV=1
63	tr|B5XCJ8|B5XCJ8_SALSA	Nucleoside diphosphate kinase OS=Salmo salar GN=NDKA PE=2 SV=1
64	tr|C0PUM7|C0PUM7_SALSA	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform (Fragment) OS=Salmo salar
65	tr|B5XGV3|B5XGV3_SALSA	Deoxyribonuclease OS=Salmo salar GN=DNSL3 PE=2 SV=1
66	tr|B5X1G7|B5X1G7_SALSA	60 kDa heat shock protein, mitochondrial OS=Salmo salar GN=CH60 PE=2 SV=1
67	tr|B5X1B5|B5X1B5_SALSA	Enolase OS=Salmo salar GN=ENOA PE=2 SV=1
68	tr|B9ENC8|B9ENC8_SALSA	Transgelin OS=Salmo salar GN=TAGL PE=2 SV=1
69	tr|C0H815|C0H815_SALSA	Annexin A5 OS=Salmo salar GN=ANXA5 PE=2 SV=1
70	tr|B5X397|B5X397_SALSA	78 kDa glucose-regulated protein OS=Salmo salar GN=GRP78 PE=2 SV=1
71	tr|B5XBH3|B5XBH3_SALSA	Apolipoprotein A-I OS=Salmo salar GN=APOA1 PE=2 SV=1
72	tr|Q7ZU67|Q7ZU67_DANRE	Eukaryotic translation initiation factor 4A isoform 1B OS=Danio rerio GN=eif4a1b PE=2 SV=1
73	tr|B5X1K8|B5X1K8_SALSA	Myosin regulatory light chain 2, smooth muscle isoform OS=Salmo salar GN=MLRN PE=2 SV=1
74	tr|C1BLG8|C1BLG8_OSMMO	Glyceraldehyde-3-phosphate dehydrogenase OS=Osmerus mordax GN=G3P PE=2 SV=1
75	tr|E0R838|E0R838_SALSA	40S ribosomal protein SA OS=Salmo salar GN=RSSA PE=2 SV=1
76	tr|Q0ZHF2|Q0ZHF2_SALSA	Decorin OS=Salmo salar PE=2 SV=1
77	tr|Q90W73|Q90W73_ONCMY	Type I keratin S8 OS=Oncorhynchus mykiss GN=S8 PE=2 SV=1
78	sp|P84234|H32_ONCMY	Histone H3.2 OS=Oncorhynchus mykiss PE=1 SV=2
79	tr|B5X1Q8|B5X1Q8_SALSA	Leukocyte elastase inhibitor OS=Salmo salar GN=ILEU PE=2 SV=1
80	sp|P69069|H2B_ONCMY	Histone H2B OS=Oncorhynchus mykiss PE=1 SV=2
81	tr|B5XFJ3|B5XFJ3_SALSA	Ictacalcin OS=Salmo salar GN=S10I PE=4 SV=1
82	tr|Q642H5|Q642H5_DANRE	Protein phosphatase 2 (Formerly 2A), regulatory subunit A, beta isoform OS=Danio rerio GN=ppp2r1b PE=2 SV=1
83	tr|B5X1Z2|B5X1Z2_SALSA	T-complex protein 1 subunit delta OS=Salmo salar GN=TCPD PE=2 SV=1
84	tr|B5XDR4|B5XDR4_SALSA	Myosin light polypeptide 6 OS=Salmo salar GN=MYL6 PE=2 SV=1

85	tr|Q910C0|Q910C0_ONCMY	Collagen a1(I) OS=Oncorhynchus mykiss GN=COL1A1 PE=2 SV=1
86	tr|B5X8A9|B5X8A9_SALSA	40S ribosomal protein S3 OS=Salmo salar GN=RS3 PE=2 SV=1
87	tr|Q91452|Q91452_ONCMY	Anion exchanger OS=Oncorhynchus mykiss PE=2 SV=1
88	tr|C0HBE5|C0HBE5_SALSA	Actin-related protein 3 OS=Salmo salar GN=ARP3 PE=2 SV=1
89	tr|B5X4K4|B5X4K4_SALSA	L-lactate dehydrogenase OS=Salmo salar GN=LDHB PE=2 SV=1
90	tr|B5DGB9|B5DGB9_SALSA	14-3-3 protein beta/alpha-2 OS=Salmo salar GN=ywhab2 PE=2 SV=1
91	tr|C0H7L6|C0H7L6_SALSA	60S ribosomal protein L7 OS=Salmo salar GN=RL7 PE=2 SV=1
92	tr|D9UB75|D9UB75_ONCMY	94 kD glucose-regulated protein OS=Oncorhynchus mykiss GN=grp94 PE=2 SV=1
93	tr|C0HA51|C0HA51_SALSA	Glutamate dehydrogenase 1, mitochondrial OS=Salmo salar GN=DHE3 PE=2 SV=1
94	tr|Q499B6|Q499B6_DANRE	Poly A binding protein, cytoplasmic 1 a OS=Danio rerio GN=pabpc1a PE=2 SV=1
95	sp|P32847|B3AT_ONCMY	Band 3 anion exchange protein OS=Oncorhynchus mykiss GN=slc4a1 PE=2 SV=2
96	tr|C0H8K4|C0H8K4_SALSA	Calmodulin OS=Salmo salar GN=CALM PE=2 SV=1
97	tr|B5X1U5|B5X1U5_SALSA	Tropomyosin-1 alpha chain OS=Salmo salar GN=TPM1 PE=2 SV=1
98	tr|Q64HW4|Q64HW4_ONCMY	Leukocyte elastase inhibitor OS=Oncorhynchus mykiss PE=2 SV=1
99	tr|B5XEI6|B5XEI6_SALSA	Annexin A4 OS=Salmo salar GN=ANXA4 PE=2 SV=1
100	tr|B9ENT8|B9ENT8_SALSA	Histone H3 OS=Salmo salar GN=H33 PE=2 SV=1
101	tr|B5DGE0|B5DGE0_SALSA	Adenosylhomocysteinase OS=Salmo salar GN=ahcy PE=2 SV=1
102	tr|B5DGA8|B5DGA8_SALSA	40S ribosomal protein S2 OS=Salmo salar GN=rps2 PE=2 SV=1
103	tr|B5X7S6|B5X7S6_SALSA	High choriolytic enzyme 1 OS=Salmo salar GN=HCE1 PE=2 SV=1
104	tr|C0H9U3|C0H9U3_SALSA	6-phosphogluconate dehydrogenase, decarboxylating OS=Salmo salar GN=6PGD PE=2 SV=1
105	tr|B5XC25|B5XC25_SALSA	Cofilin-2 OS=Salmo salar GN=COF2 PE=2 SV=1
106	tr|C0HA30|C0HA30_SALSA	T-complex protein 1 subunit alpha OS=Salmo salar GN=TCPA PE=2 SV=1
107	tr|B5X1S6|B5X1S6_SALSA	Rab GDP dissociation inhibitor beta OS=Salmo salar GN=GDIB PE=2 SV=1
108	tr|B5X4M2|B5X4M2_SALSA	T-complex protein 1 subunit theta OS=Salmo salar GN=TCPQ PE=2 SV=1
109	tr|C0H734|C0H734_SALSA	40S ribosomal protein S4 OS=Salmo salar GN=RS4 PE=2 SV=1
110	tr|C0H8G4|C0H8G4_SALSA	60S ribosomal protein L7a OS=Salmo salar GN=RL7A PE=2 SV=1
111	tr|B5X3E2|B5X3E2_SALSA	ADP-ribosylation factor 1 OS=Salmo salar GN=ARF1 PE=2 SV=1
112	tr|Q5IRA1|Q5IRA1_SALSA	Na,K-ATPase alpha subunit isoform 1b/i (Fragment) OS=Salmo salar GN=ATP1A1B/i PE=4 SV=1
113	tr|C4B4C5|C4B4C5_ONCMY	Apolipoprotein A-II OS=Oncorhynchus mykiss GN=apoa2 PE=2 SV=1
114	tr|B5DGK7|B5DGK7_SALSA	40S ribosomal protein S8 OS=Salmo salar GN=rps8 PE=2 SV=1

115	tr|C0PUL2|C0PUL2_SALSA	Lysyl-tRNA synthetase (Fragment) OS=Salmo salar GN=SYK PE=2 SV=1
116	tr|C0H9I1|C0H9I1_SALSA	Fructose-bisphosphate aldolase OS=Salmo salar GN=ALDOA PE=2 SV=1
117	tr|B5DGL3|B5DGL3_SALSA	Triosephosphate isomerase OS=Salmo salar GN=tpi1b PE=2 SV=1
118	tr|C0HAH7|C0HAH7_SALSA	Sodium/potassium-transporting ATPase subunit beta-233 OS=Salmo salar GN=AT233 PE=2 SV=1
119	tr|B5X5I8|B5X5I8_SALSA	Profilin OS=Salmo salar GN=PROF2 PE=2 SV=1
120	tr|B5DFX3|B5DFX3_SALSA	Guanine nucleotide binding protein (G protein) beta polypeptide 2-like 1 OS=Salmo salar GN=gnb2l1 PE=2 SV=1
121	tr|C0PU50|C0PU50_SALSA	Myosin-9 (Fragment) OS=Salmo salar GN=MYH9 PE=2 SV=1
122	tr|B9ELU2|B9ELU2_SALSA	GTP-binding nuclear protein Ran OS=Salmo salar GN=RAN PE=2 SV=1
123	tr|Q90W74|Q90W74_ONCMY	Type I keratin E7 OS=Oncorhynchus mykiss GN=E7 PE=2 SV=1
124	tr|B9EM96|B9EM96_SALSA	Glutathione S-transferase A OS=Salmo salar GN=GSTA PE=2 SV=1
125	tr|B5X1F9|B5X1F9_SALSA	Protein-glutamine gamma-glutamyltransferase 2 OS=Salmo salar GN=TGM2 PE=2 SV=1
126	tr|B5DGV2|B5DGV2_SALSA	Ribosomal protein OS=Salmo salar GN=RL10A PE=2 SV=1
127	tr|B5XAI3|B5XAI3_SALSA	ATP synthase subunit b, mitochondrial OS=Salmo salar GN=AT5F1 PE=2 SV=1
128	tr|B5DG94|B5DG94_SALSA	Peptidyl-prolyl cis-trans isomerase OS=Salmo salar GN=ppia1 PE=2 SV=1
129	tr|Q4QZ25|Q4QZ25_ONCMY	Complement component C9 OS=Oncorhynchus mykiss PE=2 SV=1
130	tr|Q910B9|Q910B9_ONCMY	Collagen a3(I) OS=Oncorhynchus mykiss GN=COL1A3 PE=2 SV=1
131	tr|B5X2S2|B5X2S2_SALSA	Tropomyosin alpha-4 chain OS=Salmo salar GN=TPM4 PE=2 SV=1
132	tr|B5XGZ2|B5XGZ2_SALSA	Glutathione S-transferase P OS=Salmo salar GN=GSTP1 PE=2 SV=1
133	tr|Q6DG81|Q6DG81_DANRE	Plastin 3 (T isoform) OS=Danio rerio GN=pls3 PE=2 SV=1
134	tr|B5XDE4|B5XDE4_SALSA	14-3-3 protein beta/alpha OS=Salmo salar GN=1433B PE=2 SV=1
135	tr|E0R869|E0R869_SALSA	40S ribosomal protein S3a OS=Salmo salar GN=RS3A PE=2 SV=1
136	tr|B5X4L8|B5X4L8_SALSA	14-3-3 protein epsilon OS=Salmo salar GN=1433E PE=2 SV=1
137	tr|B5XCY4|B5XCY4_SALSA	14-3-3 protein beta/alpha-1 OS=Salmo salar GN=143B1 PE=2 SV=1
138	tr|Q508P8|Q508P8_DANRE	Slow myosin heavy chain 1 OS=Danio rerio GN=smyhc1 PE=2 SV=1
139	tr|B5XF17|B5XF17_SALSA	Transforming protein RhoA OS=Salmo salar GN=RHOA PE=2 SV=1
140	tr|B5X229|B5X229_SALSA	Rho-related GTP-binding protein RhoC OS=Salmo salar GN=RHOC PE=2 SV=1
141	tr|A9YVA1|A9YVA1_ONCMA	Alpha-globin I OS=Oncorhynchus masou formosanus GN=hbaa1 PE=2 SV=1
142	tr|B5DFX8|B5DFX8_SALSA	Phosphoglycerate kinase OS=Salmo salar GN=pgk1 PE=2 SV=1
143	tr|Q7T1N7|Q7T1N7_SALSA	Glutamate dehydrogenase (Fragment) OS=Salmo salar GN=gdh1 PE=2 SV=1
144	tr|C0HB84|C0HB84_SALSA	Moesin OS=Salmo salar GN=MOES PE=2 SV=1

145	tr|B5X300|B5X300_SALSA	rRNA 2-O-methyltransferase fibrillarin OS=Salmo salar GN=FBRL PE=2 SV=1
146	tr|B5X0W2|B5X0W2_SALSA	Rho GDP-dissociation inhibitor 1 OS=Salmo salar GN=GDIR PE=2 SV=1
147	tr|B5DGC6|B5DGC6_SALSA	Nucleoside diphosphate kinase OS=Salmo salar GN=nme1 PE=2 SV=1
148	tr|C0H9C0|C0H9C0_SALSA	Tropomyosin alpha-3 chain OS=Salmo salar GN=TPM3 PE=2 SV=1
149	tr|C0H7C4|C0H7C4_SALSA	40S ribosomal protein S19 OS=Salmo salar GN=RS19 PE=2 SV=1
150	tr|B9EPW1|B9EPW1_SALSA	Proteasome activator complex subunit 1 OS=Salmo salar GN=PSME1 PE=2 SV=1
151	tr|B9ELV5|B9ELV5_SALSA	ADP-ribosylation factor 4 OS=Salmo salar GN=ARF4 PE=2 SV=1
152	tr|B5X1W1|B5X1W1_SALSA	Histone H1-beta, late embryonic OS=Salmo salar GN=H1B PE=2 SV=1
153	tr|B5DG02|B5DG02_SALSA	60S ribosomal protein L9 OS=Salmo salar GN=rpl9 PE=2 SV=1
154	tr|B5XE91|B5XE91_SALSA	Actin-related protein 2/3 complex subunit 4 OS=Salmo salar GN=ARPC4 PE=2 SV=1
155	tr|Q9PVF8|Q9PVF8_DANRE	Catenin (Cadherin-associated protein), alpha OS=Danio rerio GN=ctnna PE=2 SV=1
156	tr|C0HAV1|C0HAV1_SALSA	Catalase OS=Salmo salar GN=CATA PE=2 SV=1
157	tr|Q4LAN6|Q4LAN6_ONCMY	C-type MBL-2 protein OS=Oncorhynchus mykiss GN=mbl PE=2 SV=1
158	tr|B5RIB1|B5RIB1_SALSA	ATP synthase H+ transporting mitochondrial F1 complex O subunit (Fragment) OS=Salmo salar GN=atp5o PE=2 SV=1
159	tr|B5X5B0|B5X5B0_SALSA	ATP synthase subunit O, mitochondrial OS=Salmo salar GN=ATPO PE=2 SV=1
160	tr|C0H844|C0H844_SALSA	Heterogeneous nuclear ribonucleoprotein A/B OS=Salmo salar GN=ROAA PE=2 SV=1
161	tr|B5XFC3|B5XFC3_SALSA	Tumor-associated calcium signal transducer 2 OS=Salmo salar GN=TACD2 PE=2 SV=1
162	tr|B5X1W5|B5X1W5_SALSA	Annexin A11 OS=Salmo salar GN=ANX11 PE=2 SV=1
163	tr|C0PUI7|C0PUI7_SALSA	Transketolase-like protein 2 (Fragment) OS=Salmo salar GN=TKTL2 PE=2 SV=1
164	tr|Q5U7N6|Q5U7N6_DANRE	Talin 1 OS=Danio rerio GN=tln1 PE=2 SV=1
165	tr|A9NJG3|A9NJG3_SALSA	Na/K/2Cl co-transporter OS=Salmo salar GN=NKCC1a PE=2 SV=1
166	tr|B5X340|B5X340_SALSA	Asparaginyl-tRNA synthetase, cytoplasmic OS=Salmo salar GN=SYNC PE=2 SV=1
167	tr|B5X7X7|B5X7X7_SALSA	Peroxiredoxin-1 OS=Salmo salar GN=PRDX1 PE=2 SV=1
168	tr|B5X865|B5X865_SALSA	Annexin A2-A OS=Salmo salar GN=ANX2A PE=2 SV=1
169	tr|C0H7M0|C0H7M0_SALSA	60S ribosomal protein L6 OS=Salmo salar GN=RL6 PE=2 SV=1
170	tr|C0H959|C0H959_SALSA	Coronin-1A OS=Salmo salar GN=COR1A PE=2 SV=1
171	tr|C0H9Z9|C0H9Z9_SALSA	Coagulation factor XIII A chain OS=Salmo salar GN=F13A PE=2 SV=1
172	tr|B5DGJ4|B5DGJ4_SALSA	Ribosomal protein L6 OS=Salmo salar GN=rpl6 PE=2 SV=1
173	tr|C0H7V4|C0H7V4_SALSA	Elongation factor 1-gamma OS=Salmo salar GN=EF1G PE=2 SV=1
174	tr|B5DG32|B5DG32_SALSA	GDP dissociation inhibitor 2 OS=Salmo salar GN=gdi2 PE=2 SV=1

175	tr|A4UYK4|A4UYK4_SOLSE	Type I keratin isoform 2 OS=Solea senegalensis GN=sseKer2 PE=2 SV=1
176	tr|B5X9U1|B5X9U1_SALSA	Mannose-specific lectin OS=Salmo salar GN=ASAL PE=4 SV=1
177	tr|C0H9M4|C0H9M4_SALSA	Glucose-6-phosphate isomerase OS=Salmo salar GN=G6PI PE=2 SV=1
178	tr|B5XDI6|B5XDI6_SALSA	Plastin-2 OS=Salmo salar GN=PLSL PE=2 SV=1
179	tr|B5X0R4|B5X0R4_SALSA	Epidermis-type lipoxygenase 3 OS=Salmo salar GN=LOXE3 PE=2 SV=1
180	tr|C0HAC2|C0HAC2_SALSA	Nucleolar protein 5A OS=Salmo salar GN=NOL5A PE=2 SV=1
181	tr|B5X3M6|B5X3M6_SALSA	Epoxide hydrolase 2 OS=Salmo salar GN=HYES PE=2 SV=1
182	tr|Q7ZZW1|Q7ZZW1_ONCMY	Alpha-1-antiproteinase-like protein OS=Oncorhynchus mykiss GN=antiprot1 PE=2 SV=1
183	tr|B9ELQ2|B9ELQ2_SALSA	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Salmo salar GN=AN32B PE=2 SV=1
184	tr|C1BF87|C1BF87_ONCMY	Transitional endoplasmic reticulum ATPase OS=Oncorhynchus mykiss GN=TERA PE=2 SV=1
185	tr|C0H9H2|C0H9H2_SALSA	Actin-related protein 2-A OS=Salmo salar GN=ARP2A PE=2 SV=1
186	tr|B5AJV0|B5AJV0_9TELE	Complement component C3 (Fragment) OS=Salmo marmoratus PE=2 SV=1
187	tr|Q2V6Q8|Q2V6Q8_SALSA	Anterior gradient protein 2 homolog OS=Salmo salar GN=AGR2 PE=2 SV=1
188	tr|P79825|P79825_ONCMY	Hemopexin-like protein (Fragment) OS=Oncorhynchus mykiss PE=2 SV=1
189	tr|C0H8N3|C0H8N3_SALSA	Heterogeneous nuclear ribonucleoprotein A1 OS=Salmo salar GN=ROA1 PE=2 SV=1
190	tr|C0H764|C0H764_SALSA	Coactosin-like protein OS=Salmo salar GN=COTL1 PE=2 SV=1
191	tr|C0HA52|C0HA52_SALSA	Major vault protein OS=Salmo salar GN=MVP PE=2 SV=1
192	tr|C0H7L1|C0H7L1_SALSA	60S ribosomal protein L10 OS=Salmo salar GN=RL10 PE=2 SV=1
193	tr|B5X369|B5X369_SALSA	60S ribosomal protein L17 OS=Salmo salar GN=RL17 PE=2 SV=1
194	tr|C0HBC4|C0HBC4_SALSA	Myelin expression factor 2 OS=Salmo salar GN=MYEF2 PE=2 SV=1
195	tr|B5DFV7|B5DFV7_SALSA	SET translocation (Myeloid leukemia-associated) B OS=Salmo salar GN=setb PE=2 SV=1
196	tr|B9EM17|B9EM17_SALSA	Transaldolase OS=Salmo salar GN=TALDO PE=2 SV=1
197	tr|B5XDB6|B5XDB6_SALSA	Elongation factor 1-beta OS=Salmo salar GN=EF1B PE=2 SV=1
198	tr|B5X8D6|B5X8D6_SALSA	60S ribosomal protein L3 OS=Salmo salar GN=RL3 PE=2 SV=1
199	tr|C1BXM3|C1BXM3_ESOLU	40S ribosomal protein S8 OS=Esox lucius GN=RS8 PE=2 SV=1
200	tr|D0QEL0|D0QEL0_SALSA	Protein disulfide isomerase associated 3 OS=Salmo salar PE=2 SV=1
201	tr|Q15AR5|Q15AR5_9PERC	Histone H3 (Fragment) OS=Trachinus collignoni GN=H3 PE=3 SV=1
202	tr|C0H7E7|C0H7E7_SALSA	40S ribosomal protein S14 OS=Salmo salar GN=RS14 PE=2 SV=1
203	tr|Q9I9I1|Q9I9I1_ONCMY	Nucleolin (Fragment) OS=Oncorhynchus mykiss PE=2 SV=1
204	tr|E6ZHG1|E6ZHG1_DICLA	Vinculin OS=Dicentrarchus labrax GN=VCL PE=4 SV=1

205	tr|B5DGX3|B5DGX3_SALSA	40S ribosomal protein S15a OS=Salmo salar GN=RS15A PE=2 SV=1
206	tr|C0H987|C0H987_SALSA	Malic enzyme OS=Salmo salar GN=MAON PE=2 SV=1
207	tr|B5XE01|B5XE01_SALSA	Proteasome activator complex subunit 2 OS=Salmo salar GN=PSME2 PE=2 SV=1
208	tr|B5RI17|B5RI17_SALSA	Chaperonin containing TCP1, subunit 3 (Fragment) OS=Salmo salar GN=cct3 PE=2 SV=1
209	tr|C0HAL3|C0HAL3_SALSA	Prohibitin-2 OS=Salmo salar GN=PHB2 PE=2 SV=1
210	tr|B5XFH3|B5XFH3_SALSA	40S ribosomal protein S25 OS=Salmo salar GN=RS25 PE=2 SV=1
211	tr|C0H7R0|C0H7R0_SALSA	FK506-binding protein 1A OS=Salmo salar GN=FKB1A PE=3 SV=1
212	tr|B5X293|B5X293_SALSA	Lumican OS=Salmo salar GN=LUM PE=2 SV=1
213	tr|B5DGU8|B5DGU8_SALSA	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 13 OS=Salmo salar PE=2 SV=1
214	tr|B5X5Q6|B5X5Q6_SALSA	Peroxiredoxin-5, mitochondrial OS=Salmo salar GN=PRDX5 PE=2 SV=1
215	tr|Q4T382|Q4T382_TETNG	Adenylyl cyclase-associated protein (Fragment) OS=Tetraodon nigroviridis GN=GSTENG00007962001 PE=3 SV=1
216	tr|B5XDU3|B5XDU3_SALSA	14-3-3 protein zeta OS=Salmo salar GN=1433Z PE=2 SV=1
217	tr|B5DGG8|B5DGG8_SALSA	40S ribosomal protein S12 OS=Salmo salar GN=rps12 PE=2 SV=1
218	sp|Q5QT17|CF058_ONCMY	UPF0762 protein C6orf58 homolog OS=Oncorhynchus mykiss PE=2 SV=1
219	tr|B5X9V9|B5X9V9_SALSA	60S ribosomal protein L27 OS=Salmo salar GN=RL17 PE=2 SV=1
220	tr|B9EPZ9|B9EPZ9_SALSA	Thioredoxin OS=Salmo salar GN=THIO PE=2 SV=1
221	tr|B5X748|B5X748_SALSA	60S ribosomal protein L24 OS=Salmo salar GN=RL24 PE=2 SV=1
222	tr|B5X9C6|B5X9C6_SALSA	Aldose reductase OS=Salmo salar GN=ALDR PE=2 SV=1
223	tr|C0HAZ8|C0HAZ8_SALSA	Heterogeneous nuclear ribonucleoprotein Q OS=Salmo salar GN=HNRPQ PE=2 SV=1
224	tr|B5X3Z1|B5X3Z1_SALSA	Aspartate aminotransferase OS=Salmo salar GN=AATM PE=2 SV=1
225	tr|B5X8X7|B5X8X7_SALSA	40S ribosomal protein S9 OS=Salmo salar GN=RS9 PE=2 SV=1
226	tr|C0H8V2|C0H8V2_SALSA	26S proteasome non-ATPase regulatory subunit 2 OS=Salmo salar GN=PSMD2 PE=2 SV=1
227	tr|Q7T023|Q7T023_DANRE	Novel protein similar to human non-muscle myosin, heavy polypeptide 10 (MYH10) (Fragment) OS=Danio rerio
228	tr|B5DH07|B5DH07_SALSA	Voltage-dependent anion channel 2-3 OS=Salmo salar GN=VDAC2 PE=2 SV=1
229	tr|C0H7Q4|C0H7Q4_SALSA	40S ribosomal protein S16 OS=Salmo salar GN=RS16 PE=2 SV=1
230	tr|B9EQF7|B9EQF7_SALSA	Histone H1 OS=Salmo salar GN=H1 PE=2 SV=1
231	tr|Q6ZM60|Q6ZM60_DANRE	Novel protein similar to vertebrate ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 (ATP2A2) OS=Danio rerio
232	tr|Q7ZW18|Q7ZW18_DANRE	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2a OS=Danio rerio GN=atp2a2a PE=2 SV=1
233	tr|C0H8L1|C0H8L1_SALSA	60S ribosomal protein L13a OS=Salmo salar GN=RL13A PE=2 SV=1
234	tr|C0HBJ4|C0HBJ4_SALSA	Ras-related protein Rab-1A OS=Salmo salar GN=RAB1A PE=2 SV=1

235	tr|C0H753|C0H753_SALSA	40S ribosomal protein S13 OS=Salmo salar GN=RS13 PE=2 SV=1
236	tr|B9EPL7|B9EPL7_SALSA	High mobility group protein B2 OS=Salmo salar GN=HMGB2 PE=2 SV=1
237	tr|Q90XD7|Q90XD7_DANRE	Nuclear lamin A OS=Danio rerio GN=lmna PE=2 SV=1
238	tr|B5XCE5|B5XCE5_SALSA	F-actin-capping protein subunit beta OS=Salmo salar GN=CAPZB PE=2 SV=1
239	tr|B9EQK6|B9EQK6_SALSA	Actin-related protein 2/3 complex subunit 3 OS=Salmo salar GN=ARPC3 PE=2 SV=1
240	tr|B9EMV4|B9EMV4_SALSA	Eukaryotic translation initiation factor 5A-1 OS=Salmo salar GN=IF5A1 PE=2 SV=1
241	tr|B5XFD5|B5XFD5_SALSA	Proteasome subunit alpha type OS=Salmo salar GN=PSA2 PE=2 SV=1
242	tr|Q9YGQ0|Q9YGQ0_SALSA	Ribosomal protein S15 OS=Salmo salar GN=rig PE=2 SV=1
243	tr|C0H8V9|C0H8V9_SALSA	40S ribosomal protein S24 OS=Salmo salar GN=RS24 PE=2 SV=1
244	tr|B5XCY0|B5XCY0_SALSA	Ribosomal protein L18 OS=Salmo salar GN=RL18 PE=2 SV=1
245	tr|B5XEL8|B5XEL8_SALSA	Nascent polypeptide-associated complex subunit alpha OS=Salmo salar GN=NACA PE=2 SV=1
246	tr|B5X4Q7|B5X4Q7_SALSA	Voltage-dependent anion-selective channel protein 1 OS=Salmo salar GN=VDAC1 PE=2 SV=1
247	tr|Q3ZLR1|Q3ZLR1_SALSA	Superoxide dismutase [Cu-Zn] OS=Salmo salar GN=SOD1 PE=2 SV=1
248	tr|B5X8X3|B5X8X3_SALSA	40S ribosomal protein S7 OS=Salmo salar GN=RS7 PE=2 SV=1
249	tr|C0HBR6|C0HBR6_SALSA	Actin-related protein 2/3 complex subunit 1B OS=Salmo salar GN=ARC1B PE=2 SV=1
250	tr|C0H785|C0H785_SALSA	60S ribosomal protein L22 OS=Salmo salar GN=RL22 PE=2 SV=1
251	tr|B5XEB4|B5XEB4_SALSA	60S acidic ribosomal protein P2 OS=Salmo salar GN=RLA2 PE=2 SV=1
252	tr|B5XDV1|B5XDV1_SALSA	S100-A16 OS=Salmo salar GN=S10AG PE=4 SV=1
253	tr|B5XDH2|B5XDH2_SALSA	S100-A13 OS=Salmo salar GN=S10AD PE=4 SV=1
254	tr|Q6PBB2|Q6PBB2_DANRE	Pl10 OS=Danio rerio GN=pl10 PE=2 SV=1
255	tr|C0HAM4|C0HAM4_SALSA	Elongation factor 1-delta OS=Salmo salar GN=EF1D PE=2 SV=1
256	tr|B9ELM7|B9ELM7_SALSA	Ras-related protein Rab-10 OS=Salmo salar GN=RAB10 PE=2 SV=1
257	tr|B5DGJ5|B5DGJ5_SALSA	Calpain small subunit 1 OS=Salmo salar GN=capns1 PE=2 SV=1
258	tr|Q804G3|Q804G3_DANRE	Annexin 11b OS=Danio rerio GN=anxa11b PE=2 SV=1
259	tr|Q6TGW7|Q6TGW7_DANRE	NS1-associated protein 1 OS=Danio rerio GN=syncripl PE=2 SV=1
260	tr|Q802X5|Q802X5_DANRE	Synaptotagmin binding, cytoplasmic RNA interacting protein, like OS=Danio rerio GN=syncripl PE=2 SV=1
261	tr|C0H9B8|C0H9B8_SALSA	Trifunctional enzyme subunit beta, mitochondrial OS=Salmo salar GN=ECHB PE=2 SV=1
262	tr|C0HA68|C0HA68_SALSA	Heterogeneous nuclear ribonucleoprotein R OS=Salmo salar GN=HNRPR PE=2 SV=1
263	tr|C0PUU6|C0PUU6_SALSA	Ras GTPase-activating-like protein IQGAP1 (Fragment) OS=Salmo salar GN=IQGA1 PE=2 SV=1
264	tr|C0H9H1|C0H9H1_SALSA	Phosphorylase OS=Salmo salar GN=PYGB PE=2 SV=1

265	tr|Q0KFS8|Q0KFS8_SALSA	Ubiquitin/ribosomal fusion protein homologue (Fragment) OS=Salmo salar GN=ufph PE=2 SV=1
266	tr|C0H7M7|C0H7M7_SALSA	60S ribosomal protein L23 OS=Salmo salar GN=RL23 PE=2 SV=1
267	tr|Q6P406|Q6P406_DANRE	Plastin 1 (I isoform) OS=Danio rerio GN=pls1 PE=2 SV=1
268	tr|B5DH21|B5DH21_SALSA	60S acidic ribosomal protein P1 OS=Salmo salar GN=RLA1 PE=4 SV=1
269	tr|B5XGP0|B5XGP0_SALSA	40S ribosomal protein S18 OS=Salmo salar GN=RS18 PE=2 SV=1
270	tr|C0PU77|C0PU77_SALSA	Trifunctional enzyme subunit alpha, mitochondrial (Fragment) OS=Salmo salar GN=ECHA PE=2 SV=1
271	tr|C0H8X4|C0H8X4_SALSA	Polypyrimidine tract-binding protein 1 OS=Salmo salar GN=PTBP1 PE=2 SV=1
272	tr|B3DKJ0|B3DKJ0_DANRE	Chaperonin containing TCP1, subunit 7 (Eta) OS=Danio rerio GN=cct7 PE=2 SV=1
273	tr|C0H7H1|C0H7H1_SALSA	40S ribosomal protein S6 OS=Salmo salar GN=RS6 PE=2 SV=1
274	tr|B5X361|B5X361_SALSA	Coatomer subunit gamma OS=Salmo salar GN=COPG2 PE=2 SV=1
275	tr|Q803M8|Q803M8_DANRE	Tryosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide OS=Danio rerio
276	tr|B5X3W0|B5X3W0_SALSA	GTP-binding protein SAR1a OS=Salmo salar GN=SAR1A PE=2 SV=1
277	tr|B5XC82|B5XC82_SALSA	40S ribosomal protein S5 OS=Salmo salar GN=RS5 PE=2 SV=1
278	tr|B5X2M2|B5X2M2_SALSA	Prohibitin OS=Salmo salar GN=PHB PE=2 SV=1
279	tr|E2JDK6|E2JDK6_SALSA	Cytochrome c oxidase subunit 2 (Fragment) OS=Salmo salar GN=COII PE=3 SV=1
280	tr|B5X5I0|B5X5I0_SALSA	26S protease regulatory subunit 6A OS=Salmo salar GN=PRS6A PE=2 SV=1
281	tr|Q5IR98|Q5IR98_SALSA	Na,K-ATPase alpha subunit isoform 1c/i (Fragment) OS=Salmo salar GN=ATP1A1C/ii PE=4 SV=1
282	tr|Q8JIP5|Q8JIP5_ONCKE	Myosin heavy chain OS=Oncorhynchus keta PE=2 SV=1
283	tr|B5X330|B5X330_SALSA	14-3-3 protein eta OS=Salmo salar GN=1433F PE=2 SV=1
284	tr|B5X2M8|B5X2M8_SALSA	T-complex protein 1 subunit beta OS=Salmo salar GN=TCPB PE=2 SV=1
285	tr|B5XCZ3|B5XCZ3_SALSA	60S ribosomal protein L36 OS=Salmo salar GN=RL36 PE=2 SV=1
286	tr|B5X0V1|B5X0V1_SALSA	Voltage-dependent anion-selective channel protein 2 OS=Salmo salar GN=VDAC2 PE=2 SV=1
287	tr|Q6PFJ6|Q6PFJ6_DANRE	Glutathione S-transferase M OS=Danio rerio GN=gstm PE=2 SV=1
288	tr|B5DGI1|B5DGI1_SALSA	Ribosomal protein L28 OS=Salmo salar GN=rpl28 PE=2 SV=1
289	tr|C0H9S0|C0H9S0_SALSA	Eukaryotic translation initiation factor 3 subunit A OS=Salmo salar GN=EIF3A PE=2 SV=1
290	tr|Q5ZQM7|Q5ZQM7_SALSA	MHC class II antigen alpha chain (Fragment) OS=Salmo salar GN=DAA PE=2 SV=1
291	tr|B5XE05|B5XE05_SALSA	60S ribosomal protein L11 OS=Salmo salar GN=RL11 PE=2 SV=1
292	tr|B5XD52|B5XD52_SALSA	Proliferation-associated protein 2G4 OS=Salmo salar GN=PA2G4 PE=2 SV=1
293	tr|C0H8L4|C0H8L4_SALSA	60S ribosomal protein L28 OS=Salmo salar GN=RL28 PE=2 SV=1
294	tr|Q9DF27|Q9DF27_SALSA	40S ribosomal protein S11 OS=Salmo salar GN=RS11 PE=2 SV=1

295	tr|B0UXL3|B0UXL3_DANRE	Isocitrate dehydrogenase 1 (NADP+), soluble (Fragment) OS=Danio rerio GN=idh1 PE=3 SV=1
296	tr|C0H8G7|C0H8G7_SALSA	Phosphate carrier protein, mitochondrial OS=Salmo salar GN=MPCP PE=2 SV=1
297	tr|B5XD30|B5XD30_SALSA	60S ribosomal protein L13 OS=Salmo salar GN=RL13 PE=2 SV=1
298	tr|B5XDA7|B5XDA7_SALSA	60S ribosomal protein L23a OS=Salmo salar GN=RL23A PE=2 SV=1
299	tr|C0HAN7|C0HAN7_SALSA	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Salmo salar GN=ODPA PE=2 SV=1
300	tr|B5X173|B5X173_SALSA	Splicing factor, proline-and glutamine-rich OS=Salmo salar GN=SFPQ PE=2 SV=1
301	tr|B5XE59|B5XE59_SALSA	GDP-mannose 4,6 dehydratase OS=Salmo salar GN=GMDS PE=2 SV=1
302	tr|B9EP53|B9EP53_SALSA	High choriolytic enzyme 2 OS=Salmo salar GN=HCE2 PE=2 SV=1
303	tr|C0PUH3|C0PUH3_SALSA	F-actin-capping protein subunit alpha-2 (Fragment) OS=Salmo salar GN=CAZA2 PE=2 SV=1
304	tr|B5XEW1|B5XEW1_SALSA	Translationally-controlled tumor protein OS=Salmo salar GN=TCTP PE=2 SV=1
305	tr|B5XGU1|B5XGU1_SALSA	40S ribosomal protein S21 OS=Salmo salar GN=RS21 PE=4 SV=1
306	tr|B5XB94|B5XB94_SALSA	ATP synthase gamma chain OS=Salmo salar GN=ATPG PE=2 SV=1
307	tr|C0H751|C0H751_SALSA	60S ribosomal protein L12 OS=Salmo salar GN=RL12 PE=2 SV=1
308	tr|B9EMZ7|B9EMZ7_SALSA	Cytochrome c OS=Salmo salar GN=CYC PE=3 SV=1
309	tr|B5XDG0|B5XDG0_SALSA	60S ribosomal protein L30 OS=Salmo salar GN=RL30 PE=3 SV=1
310	tr|B5X4G1|B5X4G1_SALSA	Hsc70-interacting protein OS=Salmo salar GN=F10A1 PE=2 SV=1
311	tr|B5X2T3|B5X2T3_SALSA	Aldehyde dehydrogenase, mitochondrial OS=Salmo salar GN=ALDH2 PE=2 SV=1
312	tr|C0H7F7|C0H7F7_SALSA	ATP synthase subunit g, mitochondrial OS=Salmo salar GN=ATP5L PE=4 SV=1
313	tr|B5X9X0|B5X9X0_SALSA	S100-A1 OS=Salmo salar GN=S10A1 PE=4 SV=1
314	tr|B5X2U1|B5X2U1_SALSA	Heterogeneous nuclear ribonucleoprotein M OS=Salmo salar GN=HNRPM PE=2 SV=1
315	tr|Q0GMZ1|Q0GMZ1_9SMEG	Importin beta 1 subunit (Fragment) OS=Xiphophorus nigrensis GN=Kpnb1 PE=2 SV=1
316	tr|C0PU93|C0PU93_SALSA	Stress-70 protein, mitochondrial (Fragment) OS=Salmo salar GN=GRP75 PE=2 SV=1
317	tr|Q6NWE8|Q6NWE8_DANRE	Sb:cb283 protein (Fragment) OS=Danio rerio GN=alas2 PE=2 SV=1
318	sp|B5DGH9|EIF3E_SALSA	Eukaryotic translation initiation factor 3 subunit E OS=Salmo salar GN=eif3e PE=2 SV=1
319	tr|B5XGA3|B5XGA3_SALSA	17-beta-hydroxysteroid dehydrogenase 14 OS=Salmo salar GN=DHB14 PE=2 SV=1
320	tr|B5X1C7|B5X1C7_SALSA	Nuclear receptor coactivator 5 OS=Salmo salar GN=NCOA5 PE=2 SV=1
321	tr|B5X931|B5X931_SALSA	Carbonyl reductase 1 OS=Salmo salar GN=DHCA PE=2 SV=1
322	tr|B5XDN8|B5XDN8_SALSA	Ras-related protein Rab-11B OS=Salmo salar GN=RB11B PE=2 SV=1
323	tr|Q7ZYV6|Q7ZYV6_SALSA	Hyperosmotic glycine rich protein OS=Salmo salar PE=2 SV=1
324	tr|Q6NYN3|Q6NYN3_DANRE	Importin 7 OS=Danio rerio GN=ipo7 PE=2 SV=1

325	tr|B5XEN8|B5XEN8_SALSA	Complement factor D OS=Salmo salar GN=CFAD PE=2 SV=1
326	tr|C0H8F9|C0H8F9_SALSA	Ras-related protein Rap-1b OS=Salmo salar GN=RAP1B PE=2 SV=1
327	tr|B5XBB1|B5XBB1_SALSA	Small nuclear ribonucleoprotein Sm D3 OS=Salmo salar GN=SMD3 PE=2 SV=1
328	tr|C0HAU7|C0HAU7_SALSA	Lupus La protein homolog B OS=Salmo salar GN=LAB PE=2 SV=1
329	tr|C0H8S0|C0H8S0_SALSA	Eukaryotic translation initiation factor 4H OS=Salmo salar GN=IF4H PE=2 SV=1
330	tr|C0H7P0|C0H7P0_SALSA	60S ribosomal protein L14 OS=Salmo salar GN=RL14 PE=2 SV=1
331	tr|B9EQA7|B9EQA7_SALSA	Metalloproteinase inhibitor 2 OS=Salmo salar GN=TIMP2 PE=2 SV=1
332	tr|B9EQ17|B9EQ17_SALSA	THO complex subunit 4 OS=Salmo salar GN=THOC4 PE=2 SV=1
333	tr|B5XG42|B5XG42_SALSA	40S ribosomal protein S10 OS=Salmo salar GN=RS10 PE=2 SV=1
334	tr|B5X3S5|B5X3S5_SALSA	Coatomer subunit beta OS=Salmo salar GN=COPB PE=2 SV=1
335	tr|A4V838|A4V838_SALSA	MHC class II antigen (Fragment) OS=Salmo salar GN=DAB PE=2 SV=1
336	tr|Q8JHH1|Q8JHH1_DANRE	Small nuclear ribonucleoprotein D1 OS=Danio rerio GN=snrpd1 PE=2 SV=1
337	tr|B9ENL7|B9ENL7_SALSA	Ras-related protein Rab-5C OS=Salmo salar GN=RAB5C PE=2 SV=1
338	tr|C0H7D5|C0H7D5_SALSA	40S ribosomal protein S28 OS=Salmo salar GN=RS28 PE=2 SV=1
339	tr|C0H7D3|C0H7D3_SALSA	Cytochrome c oxidase subunit 5A, mitochondrial OS=Salmo salar GN=COX5A PE=2 SV=1
340	tr|C0H944|C0H944_SALSA	Obg-like ATPase 1 OS=Salmo salar GN=OLA1 PE=2 SV=1
341	tr|C0H747|C0H747_SALSA	40S ribosomal protein S17 OS=Salmo salar GN=RS17 PE=2 SV=1
342	tr|B5X8M1|B5X8M1_SALSA	26S protease regulatory subunit S10B OS=Salmo salar GN=PRS10 PE=2 SV=1
343	tr|B5XAX6|B5XAX6_SALSA	Cytochrome c oxidase subunit VIb isoform 1 OS=Salmo salar GN=CX6B1 PE=4 SV=1
344	tr|B5XAB2|B5XAB2_SALSA	26S proteasome non-ATPase regulatory subunit 8 OS=Salmo salar GN=PSD8 PE=2 SV=1
345	tr|B5XF66|B5XF66_SALSA	Cold-inducible RNA-binding protein OS=Salmo salar GN=CIRBP PE=2 SV=1
346	tr|B9EMG8|B9EMG8_SALSA	C6orf115 OS=Salmo salar GN=CF115 PE=4 SV=1
347	tr|C0HA39|C0HA39_SALSA	Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Salmo salar GN=HNRL1 PE=2 SV=1
348	tr|B9ELG2|B9ELG2_SALSA	Calponin-1 OS=Salmo salar GN=CNN1 PE=2 SV=1
349	tr|B5XEA2|B5XEA2_SALSA	S100-A11 OS=Salmo salar GN=S10AB PE=4 SV=1
350	tr|B5XB09|B5XB09_SALSA	Myosin light polypeptide 3 OS=Salmo salar GN=MYL3 PE=2 SV=1
351	tr|B5X1V8|B5X1V8_SALSA	Dihydrolipoyl dehydrogenase OS=Salmo salar GN=DLDH PE=2 SV=1
352	tr|C0H8E8|C0H8E8_SALSA	60S ribosomal protein L5 OS=Salmo salar GN=RL5 PE=2 SV=1
353	tr|B5X1T5|B5X1T5_SALSA	Beta-hexosaminidase beta chain OS=Salmo salar GN=HEXB PE=2 SV=1
354	tr|B9EN57|B9EN57_SALSA	Low choriolytic enzyme OS=Salmo salar GN=LCE PE=2 SV=1

355	tr|Q0KFS2|Q0KFS2_SALSA	S100 calcium binding protein (Fragment) OS=Salmo salar GN=s100 PE=2 SV=1
356	tr|B9V3U5|B9V3U5_EPICO	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide like OS=Epinephelus coioides
357	tr|C0IL38|C0IL38_KRYMA	Glutathione S-transferase mu OS=Kryptolebias marmoratus PE=2 SV=1
358	tr|Q6P9P3|Q6P9P3_DANRE	Ubiquitin-activating enzyme E1 OS=Danio rerio GN=uba1 PE=2 SV=1
359	tr|B5XBL8|B5XBL8_SALSA	Mimecan OS=Salmo salar GN=MIME PE=2 SV=1
360	tr|B5X0S0|B5X0S0_SALSA	Creatine kinase B-type OS=Salmo salar GN=KCRB PE=2 SV=1
361	tr|B5X0W3|B5X0W3_SALSA	Heterogeneous nuclear ribonucleoprotein K OS=Salmo salar GN=HNRPK PE=2 SV=1
362	tr|Q2L4Q6|Q2L4Q6_ONCMY	Complement factor H OS=Oncorhynchus mykiss GN=cfh PE=2 SV=1
363	tr|C0H8T1|C0H8T1_SALSA	Heterogeneous nuclear ribonucleoprotein G OS=Salmo salar GN=HNRPG PE=2 SV=1
364	tr|B5X291|B5X291_SALSA	Disulfide-isomerase A6 OS=Salmo salar GN=PDIA6 PE=2 SV=1
365	tr|C0H7K2|C0H7K2_SALSA	40S ribosomal protein S23 OS=Salmo salar GN=RS23 PE=2 SV=1
366	tr|B5XEA6|B5XEA6_SALSA	Peroxiredoxin OS=Salmo salar GN=TDX PE=2 SV=1
367	tr|C0H9A4|C0H9A4_SALSA	Myotrophin OS=Salmo salar GN=MTPN PE=4 SV=1
368	tr|C0H7R8|C0H7R8_SALSA	40S ribosomal protein S26 OS=Salmo salar GN=RS26 PE=2 SV=1
369	tr|B5XBS3|B5XBS3_SALSA	40S ribosomal protein S26 OS=Salmo salar GN=RS26 PE=4 SV=1
370	tr|B8JHR9|B8JHR9_DANRE	Novel protein similar to vertebrate importin 5 (IPO5) OS=Danio rerio GN=kpnb3 PE=4 SV=1
371	tr|B5XA45|B5XA45_SALSA	Flavin reductase OS=Salmo salar GN=BLVRB PE=2 SV=1
372	tr|Q4ZHV1|Q4ZHV1_SALSA	Caspase 6A (Fragment) OS=Salmo salar PE=3 SV=1
373	tr|B5X1J7|B5X1J7_SALSA	Ras-related protein Rab-6A OS=Salmo salar GN=RAB6A PE=2 SV=1
374	tr|C0H7F0|C0H7F0_SALSA	60S ribosomal protein L35 OS=Salmo salar GN=RL35 PE=2 SV=1
375	tr|B5X999|B5X999_SALSA	Annexin A3 OS=Salmo salar GN=ANXA3 PE=2 SV=1
376	tr|A8KC60|A8KC60_DANRE	Zgc:92586 protein OS=Danio rerio GN=tars PE=2 SV=1
377	sp|B5DG42|IF4A3_SALSA	Eukaryotic initiation factor 4A-III OS=Salmo salar GN=eif4a3 PE=2 SV=1
378	tr|B5X2K6|B5X2K6_SALSA	Interleukin enhancer-binding factor 2 homolog OS=Salmo salar GN=ILF2 PE=2 SV=1
379	tr|B5DG28|B5DG28_SALSA	APEX nuclease 1 OS=Salmo salar GN=apex1 PE=2 SV=1
380	tr|B5DGV5|B5DGV5_SALSA	60S ribosomal protein L21 OS=Salmo salar GN=RL21 PE=2 SV=1
381	tr|B5X270|B5X270_SALSA	H/ACA ribonucleoprotein complex subunit 4 OS=Salmo salar GN=DKC1 PE=2 SV=1
382	tr|C0H7F9|C0H7F9_SALSA	60S ribosomal protein L31 OS=Salmo salar GN=RL31 PE=2 SV=1
383	tr|B5X0S9|B5X0S9_SALSA	Aldehyde dehydrogenase family 7 member A1 homolog OS=Salmo salar GN=AL7A1 PE=2 SV=1
384	tr|B9EMD0|B9EMD0_SALSA	Apoptosis-associated speck-like protein containing a CARD OS=Salmo salar GN=ASC PE=2 SV=1

385	tr|C0PUD4|C0PUD4_SALSA	26S proteasome non-ATPase regulatory subunit 11 (Fragment) OS=Salmo salar GN=PSD11 PE=2 SV=1
386	tr|Q6ZZX5|Q6ZZX5_SALSA	Heterogeneous nuclear ribonucleoprotein (Fragment) OS=Salmo salar PE=2 SV=1
387	sp|Q6S9V7|CISY_KATPE	Citrate synthase, mitochondrial OS=Katsuwonus pelamis GN=cs PE=2 SV=1
388	tr|B9EPF8|B9EPF8_SALSA	26S protease regulatory subunit 6B OS=Salmo salar GN=PRS6B PE=2 SV=1
389	tr|B9EMB8|B9EMB8_SALSA	Sorcin OS=Salmo salar GN=SORCN PE=2 SV=1
390	tr|Q6P022|Q6P022_DANRE	Novel protein (Zgc:77804) OS=Danio rerio GN=u2af2b PE=2 SV=1
391	tr|Q6AZC1|Q6AZC1_DANRE	Proteasome (Prosome, macropain) 26S subunit, ATPase, 5 OS=Danio rerio GN=psmc5 PE=2 SV=1
392	tr|Q90XS7|Q90XS7_ONCMY	Complement component C5 (Fragment) OS=Oncorhynchus mykiss PE=2 SV=1
393	tr|B5X3B0|B5X3B0_SALSA	Ras-related C3 botulinum toxin substrate 1 OS=Salmo salar GN=RAC1 PE=2 SV=1
394	tr|C0H901|C0H901_SALSA	Ras-related C3 botulinum toxin substrate 2 OS=Salmo salar GN=RAC2 PE=2 SV=1
395	tr|B5XE81|B5XE81_SALSA	Cell division control protein 42 homolog OS=Salmo salar GN=CDC42 PE=2 SV=1
396	tr|B5DGD5|B5DGD5_SALSA	Actin related protein 2/3 complex subunit 2 OS=Salmo salar GN=arpc2 PE=2 SV=1
397	tr|Q4V966|Q4V966_DANRE	Sept7a protein OS=Danio rerio GN=sept7a PE=2 SV=1
398	tr|B9EPV8|B9EPV8_SALSA	Nucleosome assembly protein 1-like 1 OS=Salmo salar GN=NP1L1 PE=2 SV=1
399	tr|Q672G9|Q672G9_ONCMY	Calpain 2 catalytic subunit OS=Oncorhynchus mykiss GN=Capn2 PE=2 SV=1
400	tr|B5X4K2|B5X4K2_SALSA	Cytosolic non-specific dipeptidase OS=Salmo salar GN=CNDP2 PE=2 SV=1
401	tr|B5XGK1|B5XGK1_SALSA	Allograft inflammatory factor 1 OS=Salmo salar GN=AIF1 PE=2 SV=1
402	tr|B5X4N2|B5X4N2_SALSA	PolyrC-binding protein 2 OS=Salmo salar GN=PCBP2 PE=2 SV=1
403	tr|C0HAM9|C0HAM9_SALSA	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Salmo salar GN=RPN1 PE=2 SV=1
404	tr|C0HBT4|C0HBT4_SALSA	EF-hand domain-containing protein D2 OS=Salmo salar GN=EFHD2 PE=2 SV=1
405	tr|C0H9G6|C0H9G6_SALSA	Proactivator polypeptide OS=Salmo salar GN=SAP PE=2 SV=1
406	tr|B5X3G4|B5X3G4_SALSA	Histone-binding protein RBBP7 OS=Salmo salar GN=RBBP7 PE=2 SV=1
407	tr|C0PUV6|C0PUV6_SALSA	Spectrin alpha chain, brain (Fragment) OS=Salmo salar GN=SPTA2 PE=2 SV=1
408	tr|B5X9W9|B5X9W9_SALSA	NHP2-like protein 1 OS=Salmo salar GN=NH2L1 PE=2 SV=1
409	tr|B5XAU0|B5XAU0_SALSA	Splicing factor, arginine/serine-rich 3 OS=Salmo salar GN=SFRS3 PE=2 SV=1
410	tr|Q6YLY1|Q6YLY1_ONCMY	Guanylate-binding protein OS=Oncorhynchus mykiss PE=2 SV=1
411	tr|Q6DG67|Q6DG67_DANRE	ATP citrate lyase OS=Danio rerio GN=aclya PE=2 SV=1
412	tr|B5X1I3|B5X1I3_SALSA	Glucose-6-phosphate 1-dehydrogenase OS=Salmo salar GN=G6PD PE=2 SV=1
413	tr|C0H8I0|C0H8I0_SALSA	60S ribosomal protein L18a OS=Salmo salar GN=RL18A PE=2 SV=1
414	tr|Q70SU8|Q70SU8_SALSA	Cathepsin M OS=Salmo salar GN=salarin PE=2 SV=1

415	tr|C0HBN0|C0HBN0_SALSA	Ras-related protein Rab-7a OS=Salmo salar GN=RAB7A PE=2 SV=1
416	tr|B5XFP5|B5XFP5_SALSA	Heterogeneous nuclear ribonucleoprotein A0 OS=Salmo salar GN=ROA0 PE=2 SV=1
417	tr|C0PUJ3|C0PUJ3_SALSA	Staphylococcal nuclease domain-containing protein 1 (Fragment) OS=Salmo salar GN=SND1 PE=2 SV=1
418	tr|B5XBH5|B5XBH5_SALSA	Disulfide-isomerase OS=Salmo salar GN=PDIA1 PE=4 SV=1
419	tr|B5X3B8|B5X3B8_SALSA	Acetyl-CoA acetyltransferase, mitochondrial OS=Salmo salar GN=THIL PE=2 SV=1
420	tr|B5XBH7|B5XBH7_SALSA	Heterogeneous nuclear ribonucleoprotein A3 homolog 2 OS=Salmo salar GN=RO32 PE=2 SV=1
421	tr|C0H9I7|C0H9I7_SALSA	Eukaryotic translation initiation factor 3 subunit C OS=Salmo salar GN=EIF3C PE=2 SV=1
422	tr|C0HBB4|C0HBB4_SALSA	T-complex protein 1 subunit epsilon OS=Salmo salar GN=TCPE PE=2 SV=1
423	tr|C0H9N7|C0H9N7_SALSA	Serine/threonine-protein phosphatase OS=Salmo salar GN=PP2AA PE=2 SV=1
424	tr|C0H7L4|C0H7L4_SALSA	60S ribosomal protein L38 OS=Salmo salar GN=RL38 PE=2 SV=1
425	tr|B5X779|B5X779_SALSA	Glutathione S-transferase OS=Salmo salar GN=GSTA3 PE=2 SV=1
426	tr|B5X1Z0|B5X1Z0_SALSA	WD repeat-containing protein 1 OS=Salmo salar GN=WDR1 PE=2 SV=1
427	tr|B9EMQ6|B9EMQ6_SALSA	Proliferating cell nuclear antigen OS=Salmo salar GN=PCNA PE=2 SV=1
428	tr|C0H715|C0H715_SALSA	ATP synthase subunit d, mitochondrial OS=Salmo salar GN=ATP5H PE=2 SV=1
429	tr|B5XGY0|B5XGY0_SALSA	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Salmo salar GN=HCDH PE=2 SV=1
430	tr|B5X3R8|B5X3R8_SALSA	Calponin-2 OS=Salmo salar GN=CNN2 PE=2 SV=1
431	tr|C0HAP3|C0HAP3_SALSA	Transport protein Sec61 subunit alpha OS=Salmo salar GN=SC61A PE=2 SV=1
432	tr|C0H958|C0H958_SALSA	Epithelial cadherin OS=Salmo salar GN=CADH1 PE=2 SV=1
433	tr|B5X1G1|B5X1G1_SALSA	Annexin A13 OS=Salmo salar GN=ANX13 PE=2 SV=1
434	tr|Q6DRC0|Q6DRC0_DANRE	Seryl-tRNA synthetase OS=Danio rerio GN=sars PE=2 SV=1
435	tr|B5X0V5|B5X0V5_SALSA	Calreticulin OS=Salmo salar GN=CALR PE=2 SV=1
436	tr|B5DGK9|B5DGK9_SALSA	40S ribosomal protein S20 OS=Salmo salar GN=rps20 PE=4 SV=1
437	tr|B6D1P3|B6D1P3_ONCMY	Rhbg2a OS=Oncorhynchus mykiss PE=2 SV=1
438	tr|B5XFV7|B5XFV7_SALSA	Eukaryotic translation initiation factor 3 subunit G OS=Salmo salar GN=EIF3G PE=2 SV=1
439	tr|B5X2W6|B5X2W6_SALSA	Eukaryotic translation initiation factor 2 subunit 1 OS=Salmo salar GN=IF2A PE=2 SV=1
440	tr|C0H9F4|C0H9F4_SALSA	2,3-cyclic-nucleotide 3-phosphodiesterase OS=Salmo salar GN=CN37 PE=2 SV=1
441	tr|B5X232|B5X232_SALSA	Polypyrimidine tract-binding protein 2 OS=Salmo salar GN=PTBP2 PE=2 SV=1
442	tr|B5XGY1|B5XGY1_SALSA	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Salmo salar GN=HCD2 PE=2 SV=1
443	tr|B5X2A5|B5X2A5_SALSA	3-ketoacyl-CoA thiolase, mitochondrial OS=Salmo salar GN=THIM PE=2 SV=1
444	tr|B5X4G9|B5X4G9_SALSA	Guanine nucleotide-binding protein GI/GS/GT subunit beta-1 OS=Salmo salar GN=GBB1 PE=2 SV=1

445	tr|C0PUI6|C0PUI6_SALSA	5-3 exoribonuclease 2 (Fragment) OS=Salmo salar GN=XRN2 PE=2 SV=1
446	tr|C0HAA7|C0HAA7_SALSA	Alpha-N-acetylgalactosaminidase OS=Salmo salar GN=NAGAB PE=2 SV=1
447	tr|C0HA95|C0HA95_SALSA	Calpastatin OS=Salmo salar GN=ICAL PE=2 SV=1
448	tr|C0H880|C0H880_SALSA	S100-A14 OS=Salmo salar GN=S10AE PE=4 SV=1
449	tr|Q7ZWI2|Q7ZWI2_DANRE	Copine I OS=Danio rerio GN=cpne1 PE=2 SV=1
450	tr|Q7SXJ5|Q7SXJ5_DANRE	Bleomycin hydrolase OS=Danio rerio GN=blmh PE=2 SV=1
451	tr|Q5R1Y9|Q5R1Y9_ONCMY	M-calpain OS=Oncorhynchus mykiss PE=2 SV=1
452	tr|A2BFE3|A2BFE3_DANRE	Novel protein similar to vertebrate spectrin, beta, non-erythrocytic 2 (SPTBN2) OS=Danio rerio
453	tr|B8JJ32|B8JJ32_DANRE	Novel protein (Zgc:158660) OS=Danio rerio GN=DKEY-250O4.3 PE=4 SV=1
454	tr|Q6R758|Q6R758_SALSA	Muscle fatty acid binding protein OS=Salmo salar PE=2 SV=1
455	tr|B5DFV6|B5DFV6_SALSA	Cathepsin D OS=Salmo salar GN=ctsd PE=2 SV=1
456	tr|B5X0X6|B5X0X6_SALSA	Succinate dehydrogenase flavoprotein subunit, mitochondrial OS=Salmo salar GN=DHSA PE=2 SV=1
457	tr|B5XG92|B5XG92_SALSA	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Salmo salar GN=ETFA PE=2 SV=1
458	tr|B9EQ40|B9EQ40_SALSA	Intracellular hyaluronan-binding protein 4 OS=Salmo salar GN=HABP4 PE=2 SV=1
459	tr|B0Z6J2|B0Z6J2_9EUKA	Alpha-tubulin (Fragment) OS=Trichosphaerium sp. ATCC 40318 PE=3 SV=1
460	tr|Q91480|Q91480_SALSA	Apolipoprotein B (Fragment) OS=Salmo salar PE=2 SV=1
461	tr|C0HBF7|C0HBF7_SALSA	Splicing factor, arginine/serine-rich 6 OS=Salmo salar GN=SFRS6 PE=2 SV=1
462	tr|B5DFU2|B5DFU2_SALSA	Hypoxanthine phosphoribosyltransferase 1 OS=Salmo salar GN=hprt1 PE=2 SV=1
463	tr|B5X4F0|B5X4F0_SALSA	Guanine nucleotide-binding protein Gi, alpha-2 subunit OS=Salmo salar GN=GNAI2 PE=2 SV=1
464	tr|C0H7F3|C0H7F3_SALSA	Ribosomal protein L19 OS=Salmo salar GN=RL19 PE=2 SV=1
465	tr|O13133|O13133_ONCMY	Stat3 OS=Oncorhynchus mykiss GN=rbtStat3 PE=2 SV=1
466	tr|C0HA19|C0HA19_SALSA	Vigilin OS=Salmo salar GN=VIGLN PE=2 SV=1
467	tr|B5X3S1|B5X3S1_SALSA	Apoptosis inhibitor 5 OS=Salmo salar GN=API5 PE=2 SV=1
468	tr|B5X386|B5X386_SALSA	26S proteasome non-ATPase regulatory subunit 12 OS=Salmo salar GN=PSD12 PE=2 SV=1
469	tr|B5X3T2|B5X3T2_SALSA	ELAV-like protein 1 OS=Salmo salar GN=ELAV1 PE=2 SV=1
470	tr|B5DH26|B5DH26_SALSA	ATP synthase subunit a OS=Salmo salar GN=ATP6 PE=2 SV=1
471	tr|Q7ZVY9|Q7ZVY9_DANRE	Karyopherin alpha 4 (Importin alpha 3) OS=Danio rerio GN=kpna4 PE=2 SV=1
472	tr|C0H9E1|C0H9E1_SALSA	Beta-centractin OS=Salmo salar GN=ACTY PE=2 SV=1
473	tr|Q7SZY1|Q7SZY1_DANRE	Novel protein similar to mouse and human host cell factor C1 (VP16-accessory protein) (HCFC1) OS=Danio rerio
474	tr|Q7SZR4|Q7SZR4_DANRE	Phosphoglycerate mutase OS=Danio rerio GN=pgam1a PE=2 SV=1

475	tr|Q6NYQ7|Q6NYQ7_DANRE	Nicotinamide nucleotide transhydrogenase OS=Danio rerio GN=nnt PE=2 SV=1
476	tr|C0H9E4|C0H9E4_SALSA	Surfeit locus protein 4 OS=Salmo salar GN=SURF4 PE=2 SV=1
477	tr|Q4V9I4|Q4V9I4_DANRE	Si:dkey-276i5.1 protein (Fragment) OS=Danio rerio GN=si:dkey-276i5.1 PE=2 SV=1
478	tr|C0HAU4|C0HAU4_SALSA	Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Salmo salar GN=AN32E PE=2 SV=1
479	tr|B5X3D1|B5X3D1_SALSA	Glucosamine--fructose-6-phosphate aminotransferase 1 OS=Salmo salar GN=GFPT1 PE=2 SV=1
480	tr|B9EMV0|B9EMV0_SALSA	Transcription factor BTF3 OS=Salmo salar GN=BTF3 PE=2 SV=1
481	tr|Q1LWT7|Q1LWT7_DANRE	Novel protein similar to vertebrate myosin V family (Myo5) (Fragment) OS=Danio rerio GN=myo5b PE=4 SV=1
482	tr|B5XFD8|B5XFD8_SALSA	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Salmo salar GN=PRDX3 PE=2 SV=1
483	tr|B9ENA6|B9ENA6_SALSA	Programmed cell death protein 5 OS=Salmo salar GN=PDCD5 PE=2 SV=1
484	tr|C1BYB2|C1BYB2_ESOLU	UMP-CMP kinase OS=Esox lucius GN=KCY PE=2 SV=1
485	tr|C0HAQ0|C0HAQ0_SALSA	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Salmo salar GN=MCCC2 PE=2 SV=1
486	tr|C0H7J1|C0H7J1_SALSA	FucU homolog OS=Salmo salar GN=CJ125 PE=2 SV=1
487	tr|B9ELK3|B9ELK3_SALSA	PRA1 family protein 3 OS=Salmo salar GN=PRAF3 PE=2 SV=1
488	tr|B5XGD5|B5XGD5_SALSA	15-hydroxyprostaglandin dehydrogenase OS=Salmo salar GN=PGDH PE=2 SV=1
489	tr|B5XG99|B5XG99_SALSA	NADH dehydrogenase iron-sulfur protein 3, mitochondrial OS=Salmo salar GN=NDUS3 PE=2 SV=1
490	tr|B5XET6|B5XET6_SALSA	CD81 antigen OS=Salmo salar GN=CD81 PE=2 SV=1
491	tr|B5XDW7|B5XDW7_SALSA	60S ribosomal protein L32 OS=Salmo salar GN=RL32 PE=4 SV=1
492	tr|B5XBQ0|B5XBQ0_SALSA	Lactoylglutathione lyase OS=Salmo salar GN=LGUL PE=2 SV=1
493	tr|B5XAP9|B5XAP9_SALSA	Argininosuccinate synthase OS=Salmo salar GN=ASSY PE=2 SV=1
494	tr|B5X588|B5X588_SALSA	Keratin, type I cytoskeletal 20 OS=Salmo salar GN=K1C20 PE=2 SV=1
495	tr|B5X4T6|B5X4T6_SALSA	Aminopeptidase B OS=Salmo salar GN=AMPB PE=2 SV=1
496	tr|B5X4P7|B5X4P7_SALSA	Collagenase 3 OS=Salmo salar GN=MMP13 PE=2 SV=1
497	tr|B5X3F7|B5X3F7_SALSA	Thymidine phosphorylase OS=Salmo salar GN=TYPH PE=2 SV=1
498	tr|C3RXC5|C3RXC5_SALSA	NADH dehydrogenase subunit 5 (Fragment) OS=Salmo salar GN=NADH-5 PE=4 SV=1
499	tr|Q9DG75|Q9DG75_ONCMY	Apolipoprotein CII OS=Oncorhynchus mykiss PE=4 SV=1
500	tr|Q9DFF7|Q9DFF7_ONCMY	Biotinidase 2 (Fragment) OS=Oncorhynchus mykiss PE=2 SV=1
501	tr|Q9DFF1|Q9DFF1_ONCMY	Hemopexin-like protein variant 1 (Fragment) OS=Oncorhynchus mykiss PE=2 SV=1
502	tr|B5XGC5|B5XGC5_SALSA	Lipocalin OS=Salmo salar GN=LIPO PE=2 SV=1
503	tr|Q9DD55|Q9DD55_SALSA	Lysozyme C (Fragment) OS=Salmo salar PE=2 SV=1
504	tr|C0H7M1|C0H7M1_SALSA	60S ribosomal protein L27a OS=Salmo salar GN=RL27A PE=2 SV=1

505	tr|Q95IS3|Q95IS3_SALSA	MHC class II beta chain (Fragment) OS=Salmo salar PE=4 SV=1
506	tr|Q91218|Q91218_ONCMY	Thrombin (Fragment) OS=Oncorhynchus mykiss GN=thrombin PE=2 SV=1
507	tr|C0H7I5|C0H7I5_SALSA	40S ribosomal protein S27 OS=Salmo salar GN=RS27 PE=3 SV=1
508	tr|B9EPK9|B9EPK9_SALSA	40S ribosomal protein S30 OS=Salmo salar GN=RS30 PE=2 SV=1
509	tr|C0H962|C0H962_SALSA	TAR DNA-binding protein 43 OS=Salmo salar GN=TADBP PE=2 SV=1
510	tr|B5X3D8|B5X3D8_SALSA	Mps one binder kinase activator-like 1A OS=Salmo salar GN=MOL1A PE=2 SV=1
511	tr|B9EP40|B9EP40_SALSA	Ubiquitin carrier protein OS=Salmo salar GN=UB2D2 PE=2 SV=1
512	tr|Q7ZUM5|Q7ZUM5_DANRE	Heat shock protein 4 OS=Danio rerio GN=hspa4 PE=2 SV=1
513	tr|Q6QZI3|Q6QZI3_PSEAM	Gamma fibrinogen (Fragment) OS=Pseudopleuronectes americanus PE=2 SV=1
514	tr|Q6P3G9|Q6P3G9_DANRE	Thioredoxin domain containing 4 (Endoplasmic reticulum) OS=Danio rerio GN=erp44 PE=2 SV=1
515	tr|B5X958|B5X958_SALSA	Osteoclast-stimulating factor 1 OS=Salmo salar GN=OSTF1 PE=2 SV=1
516	tr|B9ENB3|B9ENB3_SALSA	Small nuclear ribonucleoprotein G OS=Salmo salar GN=RUXG PE=4 SV=1
517	tr|B9EMD1|B9EMD1_SALSA	CD63 antigen OS=Salmo salar GN=CD63 PE=2 SV=1
518	tr|B5X8G3|B5X8G3_SALSA	Ribosomal protein L22-like 1 OS=Salmo salar GN=RL22L PE=2 SV=1
519	tr|B9EMK9|B9EMK9_SALSA	Cysteine and glycine-rich protein 1 OS=Salmo salar GN=CSRP1 PE=2 SV=1
520	tr|B5XD06|B5XD06_SALSA	Small nuclear ribonucleoprotein E OS=Salmo salar GN=RUXE PE=4 SV=1
521	tr|Q1L8Q2|Q1L8Q2_DANRE	Cleavage and polyadenylation specific factor 6 OS=Danio rerio GN=cpsf6 PE=2 SV=1
522	tr|B9EQF4|B9EQF4_SALSA	Cleavage and polyadenylation specificity factor subunit 5 OS=Salmo salar GN=CPSF5 PE=2 SV=1
523	tr|B5XAH1|B5XAH1_SALSA	26S proteasome non-ATPase regulatory subunit 14 OS=Salmo salar GN=PSDE PE=2 SV=1
524	tr|C0H8K8|C0H8K8_SALSA	Small ubiquitin-related modifier 3-A OS=Salmo salar GN=SMO3B PE=4 SV=1
525	tr|B5XCB0|B5XCB0_SALSA	ATP synthase subunit epsilon, mitochondrial OS=Salmo salar GN=ATP5E PE=4 SV=1
526	tr|C0HAF2|C0HAF2_SALSA	Eukaryotic translation initiation factor 3 subunit E-interacting protein OS=Salmo salar GN=IF3EI PE=2 SV=1
527	tr|A5PMS9|A5PMS9_DANRE	Novel protein similar to vertebrate adaptor-related protein complex 1, beta 1 subunit (AP1B1) OS=Danio rerio
528	tr|C0PTZ1|C0PTZ1_SALSA	Transmembrane emp24 domain-containing protein 10 (Fragment) OS=Salmo salar GN=TMEDA PE=2 SV=1
529	tr|F1C716|F1C716_PERFV	26S proteasome non-ATPase regulatory subunit 1 (Fragment) OS=Perca flavescens GN=Psmd1 PE=2 SV=1
530	tr|E6ZHC8|E6ZHC8_DICLA	Synaptic vesicle membrane protein VAT-1 homolog OS=Dicentrarchus labrax GN=VAT1 PE=4 SV=1
531	tr|D6R710|D6R710_HYPMO	Fibrinogen B beta polypeptide (Fragment) OS=Hypophthalmichthys molitrix PE=2 SV=1
532	tr|B9EMM0|B9EMM0_SALSA	Prostaglandin E synthase 3 OS=Salmo salar GN=TEBP PE=2 SV=1
533	tr|B5XET7|B5XET7_SALSA	ADP-ribosylation factor-like protein 1 OS=Salmo salar GN=ARL1 PE=2 SV=1
534	tr|C1BWL8|C1BWL8_ESOLU	Adenine phosphoribosyltransferase OS=Esox lucius GN=APT PE=2 SV=1

535	tr|B5XFP1|B5XFP1_SALSA	Barrier-to-autointegration factor OS=Salmo salar GN=BAF PE=4 SV=1
536	tr|B9EPK8|B9EPK8_SALSA	Histone H1x OS=Salmo salar GN=H1X PE=2 SV=1
537	tr|C0HAC7|C0HAC7_SALSA	26S protease regulatory subunit 4 OS=Salmo salar GN=PRS4 PE=2 SV=1
538	tr|C0PTZ5|C0PTZ5_SALSA	Mitochondrial carrier homolog 2 (Fragment) OS=Salmo salar GN=MTCH2 PE=2 SV=1
539	tr|C0HAR9|C0HAR9_SALSA	Probable saccharopine dehydrogenase OS=Salmo salar GN=SCPDH PE=2 SV=1
540	tr|C0HAD3|C0HAD3_SALSA	Serine/arginine repetitive matrix protein 1 OS=Salmo salar GN=SRRM1 PE=2 SV=1
541	tr|C0H8E0|C0H8E0_SALSA	Actin-related protein 2/3 complex subunit 5 OS=Salmo salar GN=ARPC5 PE=2 SV=1
542	tr|C0H7D0|C0H7D0_SALSA	ATP synthase subunit f, mitochondrial OS=Salmo salar GN=ATPK PE=2 SV=1
543	tr|B9EPE7|B9EPE7_SALSA	SH3 domain-binding glutamic acid-rich-like protein OS=Salmo salar GN=SH3L1 PE=4 SV=1
544	tr|B9EMP7|B9EMP7_SALSA	Myosin light polypeptide 4 OS=Salmo salar GN=MYL4 PE=2 SV=1
545	tr|B8YBH8|B8YBH8_SALSA	Non-specific cytotoxic cell receptor protein-1 OS=Salmo salar GN=NCCRP-1 PE=2 SV=2
546	tr|B5X9Q1|B5X9Q1_SALSA	Peroxiredoxin-6 OS=Salmo salar GN=PRDX6 PE=2 SV=1
547	tr|B5X6Y1|B5X6Y1_SALSA	Type-4 ice-structuring protein OS=Salmo salar GN=AFP4 PE=4 SV=1
548	tr|B5X6G0|B5X6G0_SALSA	SH3 domain-binding glutamic acid-rich-like protein 3 OS=Salmo salar GN=SH3L3 PE=4 SV=1
549	tr|B5X3U1|B5X3U1_SALSA	Ganglioside GM2 activator OS=Salmo salar GN=SAP3 PE=2 SV=1
550	tr|B5X3C0|B5X3C0_SALSA	Glutathione reductase, mitochondrial OS=Salmo salar GN=GSHR PE=2 SV=1
551	tr|B5X2G1|B5X2G1_SALSA	Sialic acid synthase OS=Salmo salar GN=SIAS PE=2 SV=1
552	tr|B5X2E6|B5X2E6_SALSA	Tripeptidyl-peptidase 1 OS=Salmo salar GN=TPP1 PE=2 SV=1
553	tr|B5X1X6|B5X1X6_SALSA	Stomatin-like protein 2 OS=Salmo salar GN=STML2 PE=2 SV=1
554	sp|Q8AY73|XPO2_ORENI	Exportin-2 OS=Oreochromis niloticus GN=cse1l PE=2 SV=1
555	sp|B5X2Z0|PUA1A_SALSA	Adenylosuccinate synthetase isozyme 1 A OS=Salmo salar GN=adssl1a PE=2 SV=1
556	tr|B5XGW8|B5XGW8_SALSA	S100-A5 OS=Salmo salar GN=S10A5 PE=4 SV=1
557	tr|B5X2F6|B5X2F6_SALSA	NADH dehydrogenase flavoprotein 1, mitochondrial OS=Salmo salar GN=NDUV1 PE=2 SV=1
558	tr|B5X1I2|B5X1I2_SALSA	Natterin-like protein OS=Salmo salar GN=NATTL PE=2 SV=1
559	tr|C0H9R1|C0H9R1_SALSA	26S proteasome non-ATPase regulatory subunit 3 OS=Salmo salar GN=PSD3 PE=2 SV=1
560	tr|C0H9C5|C0H9C5_SALSA	Legumain OS=Salmo salar GN=LGMN PE=2 SV=1
561	tr|B5X373|B5X373_SALSA	Adenylosuccinate synthetase OS=Salmo salar GN=PURA2 PE=2 SV=1
562	tr|B5X858|B5X858_SALSA	NADH dehydrogenase flavoprotein 2, mitochondrial OS=Salmo salar GN=NDUV2 PE=2 SV=1
563	tr|C0H7D2|C0H7D2_SALSA	60S ribosomal protein L35a OS=Salmo salar GN=RL35A PE=4 SV=1
564	tr|B5X1V6|B5X1V6_SALSA	Cystathionine gamma-lyase OS=Salmo salar GN=CGL PE=2 SV=1

565	tr|B5DG29|B5DG29_SALSA	Acyl-Coenzyme A dehydrogenase C-4 to C-12 straight chain OS=Salmo salar GN=acadm PE=2 SV=1
566	tr|C0HAW6|C0HAW6_SALSA	3,2-trans-enoyl-CoA isomerase, mitochondrial OS=Salmo salar GN=D3D2 PE=2 SV=1
567	tr|Q6NYE1|Q6NYE1_DANRE	Fibrinogen, B beta polypeptide OS=Danio rerio GN=fgb PE=2 SV=1
568	tr|Q9PT02|Q9PT02_ONCMY	Apolipoprotein E OS=Oncorhynchus mykiss GN=apoE PE=2 SV=1
569	tr|C0H996|C0H996_SALSA	Annexin A6 OS=Salmo salar GN=ANXA6 PE=2 SV=1
570	tr|B5XBK1|B5XBK1_SALSA	Vacuolar proton pump subunit E 1 OS=Salmo salar GN=VATE1 PE=2 SV=1
571	tr|B9EPN0|B9EPN0_SALSA	6-phosphogluconolactonase OS=Salmo salar GN=6PGL PE=2 SV=1
572	tr|B9EP10|B9EP10_SALSA	Sorting nexin-12 OS=Salmo salar GN=SNX12 PE=2 SV=1
573	tr|C0H850|C0H850_SALSA	Cathepsin B OS=Salmo salar GN=CATB PE=2 SV=1
574	tr|Q6PEI6|Q6PEI6_DANRE	Aconitase 2, mitochondrial OS=Danio rerio GN=aco2 PE=2 SV=1
575	tr|C0H802|C0H802_SALSA	Mitogen-activated protein kinase 3 OS=Salmo salar GN=MK03 PE=2 SV=1
576	tr|B0S754|B0S754_DANRE	Novel protein similar to vertebrate activating signal cointegrator 1 complex subunit 3-like 1 (ASCC3L1) OS=Danio rerio
577	tr|C0HB37|C0HB37_SALSA	C-terminal-binding protein 1 OS=Salmo salar GN=CTBP1 PE=2 SV=1
578	tr|B9EN45|B9EN45_SALSA	Ubiquitin-conjugating enzyme E2 variant 1 OS=Salmo salar GN=UB2V1 PE=2 SV=1
579	tr|O93314|O93314_ONCMY	Glucokinase OS=Oncorhynchus mykiss PE=2 SV=2
580	tr|C0HAR0|C0HAR0_SALSA	Coronin-1C OS=Salmo salar GN=COR1C PE=2 SV=1
581	tr|B5XAU5|B5XAU5_SALSA	Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Salmo salar GN=C1QBP PE=2 SV=1
582	tr|C0H9Z3|C0H9Z3_SALSA	Splicing factor, arginine/serine-rich 1 OS=Salmo salar GN=SFRS1 PE=2 SV=1
583	tr|B5DGM5|B5DGM5_SALSA	Adenylate kinase OS=Salmo salar GN=KAD PE=2 SV=1
584	tr|Q6P3J7|Q6P3J7_DANRE	EH-domain containing 2 OS=Danio rerio GN=ehd2 PE=2 SV=1
585	tr|Q6GMI5|Q6GMI5_DANRE	Biglycan OS=Danio rerio GN=bgn PE=2 SV=1
586	tr|B5X1G4|B5X1G4_SALSA	Cysteinyl-tRNA synthetase, cytoplasmic OS=Salmo salar GN=SYCC PE=2 SV=1
587	tr|B9EMW8|B9EMW8_SALSA	QIL1 OS=Salmo salar GN=QIL1 PE=4 SV=1
588	tr|C0PUR6|C0PUR6_SALSA	Fatty acyl-CoA hydrolase, medium chain (Fragment) OS=Salmo salar GN=SASB PE=2 SV=1
589	tr|B5XEF8|B5XEF8_SALSA	NADH-cytochrome b5 reductase 3 OS=Salmo salar GN=NB5R3 PE=2 SV=1
590	tr|C0H7M9|C0H7M9_SALSA	60S ribosomal protein L34 OS=Salmo salar GN=RL34 PE=2 SV=1
591	tr|B5X6K3|B5X6K3_SALSA	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Salmo salar GN=AN32A PE=2 SV=1
592	tr|B5XA48|B5XA48_SALSA	60S ribosomal protein L39 OS=Salmo salar GN=RL39 PE=4 SV=1
593	tr|C0HBI8|C0HBI8_SALSA	Prolyl endopeptidase OS=Salmo salar GN=PPCE PE=2 SV=1
594	tr|B5XBE5|B5XBE5_SALSA	60S ribosomal protein L26 OS=Salmo salar GN=RL26 PE=2 SV=1

595	tr|B0Z6I3|B0Z6I3_9EUKA	Beta-tubulin (Fragment) OS=Nolandella sp. ATCC PRA-27 PE=3 SV=1
596	tr|B5X448|B5X448_SALSA	Splicing factor, arginine/serine-rich 9 OS=Salmo salar GN=SFRS9 PE=2 SV=1
597	tr|B5XE16|B5XE16_SALSA	Apolipoprotein C-I OS=Salmo salar GN=APOC1 PE=4 SV=1
598	tr|B5RI94|B5RI94_SALSA	Eukaryotic translation termination factor 1-like (Fragment) OS=Salmo salar PE=2 SV=1
599	tr|Q5IEF8|Q5IEF8_SALSA	MHC class I antigen (Fragment) OS=Salmo salar GN=Sasa-UBA PE=3 SV=1
600	tr|C0H986|C0H986_SALSA	Twinfilin-1 OS=Salmo salar GN=TWF1 PE=2 SV=1
601	tr|Q6NYF2|Q6NYF2_DANRE	Chloride intracellular channel 1 OS=Danio rerio GN=clic1 PE=2 SV=1
602	tr|Q803V0|Q803V0_DANRE	Oxidative-stress responsive 1b OS=Danio rerio GN=oxsr1b PE=2 SV=1
603	tr|B5XFL9|B5XFL9_SALSA	Transcription elongation factor B polypeptide 2 OS=Salmo salar GN=ELOB PE=4 SV=2
604	tr|Q7ZV01|Q7ZV01_DANRE	Zgc:56304 OS=Danio rerio GN=zgc:56304 PE=2 SV=1
605	tr|Q502E4|Q502E4_DANRE	NADH dehydrogenase (Ubiquinone) Fe-S protein 4, (NADH-coenzyme Q reductase) OS=Danio rerio GN=ndufs4 PE=2 SV=1
606	tr|B5XCW1|B5XCW1_SALSA	FK506-binding protein 3 OS=Salmo salar GN=FKBP3 PE=2 SV=1
607	tr|B5X2W0|B5X2W0_SALSA	U3 small nucleolar RNA-associated protein 15 homolog OS=Salmo salar GN=UTP15 PE=2 SV=1
608	tr|Q0ZBS0|Q0ZBS0_SALSA	Macrophage migration inhibitory factor OS=Salmo salar GN=mif PE=4 SV=1
609	tr|C0H991|C0H991_SALSA	Vacuolar protein sorting-associating protein 4B OS=Salmo salar GN=VPS4B PE=2 SV=1
610	tr|Q67EX5|Q67EX5_SPAAU	Alpha-2-macroglobulin (Fragment) OS=Sparus aurata PE=2 SV=1
611	tr|B5XA49|B5XA49_SALSA	Cytochrome b-c1 complex subunit 9 OS=Salmo salar GN=QCR9 PE=4 SV=1
612	tr|B5XBA6|B5XBA6_SALSA	40S ribosomal protein S29 OS=Salmo salar GN=RS29 PE=4 SV=1
613	tr|B9EM26|B9EM26_SALSA	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Salmo salar GN=COX41 PE=2 SV=1
614	tr|B5X2W5|B5X2W5_SALSA	Lysosomal protective protein OS=Salmo salar GN=PPGB PE=2 SV=1
615	tr|C0H9R4|C0H9R4_SALSA	Flotillin-1 OS=Salmo salar GN=FLOT1 PE=2 SV=1
616	tr|B0EED1|B0EED1_ENTDI	Fructokinase, putative OS=Entamoeba dispar SAW760 GN=EDI_079180 PE=4 SV=1
617	tr|Q6AZB2|Q6AZB2_DANRE	3-oxoacid CoA transferase 1 OS=Danio rerio GN=oxct1a PE=2 SV=1
618	tr|C0PU02|C0PU02_SALSA	Periostin (Fragment) OS=Salmo salar GN=POSTN PE=2 SV=1
619	tr|C0H7G5|C0H7G5_SALSA	Lectin OS=Salmo salar GN=LECA PE=2 SV=1
620	tr|B9EPC9|B9EPC9_SALSA	Zymogen granule membrane protein 16 OS=Salmo salar GN=ZG16 PE=2 SV=1
621	tr|B5X326|B5X326_SALSA	Plasminogen activator inhibitor 1 RNA-binding protein OS=Salmo salar GN=PAIRB PE=2 SV=1
622	tr|C0H868|C0H868_SALSA	Alcohol dehydrogenase class 3 OS=Salmo salar GN=ADHX PE=2 SV=1
623	tr|C0PUA8|C0PUA8_SALSA	Cytochrome b-c1 complex subunit 1, mitochondrial (Fragment) OS=Salmo salar GN=QCR1 PE=2 SV=1
624	tr|B0S542|B0S542_DANRE	Novel protein similar to H.sapiens SEPT7, septin 7 (SEPT7, zgc:153214) OS=Danio rerio GN=sept7b PE=3 SV=1

625	tr|Q6NW56|Q6NW56_DANRE	KH domain containing, RNA binding, signal transduction associated 1 OS=Danio rerio GN=khdrbs1a PE=2 SV=1
626	tr|Q7ZUF4|Q7ZUF4_DANRE	Adaptor-related protein complex 2, beta 1 subunit OS=Danio rerio GN=ap2b1 PE=2 SV=1
627	tr|F0ZVA8|F0ZVA8_DICPU	Putative uncharacterized protein (Fragment) OS=Dictyostelium purpureum GN=DICPUDRAFT_82025 PE=4 SV=1
628	tr|Q9DFD4|Q9DFD4_ONCMY	Putative hepatocyte growth factor activator/GRAAL (Fragment) OS=Oncorhynchus mykiss PE=2 SV=1
629	tr|B5X1P0|B5X1P0_SALSA	Drebrin-like protein OS=Salmo salar GN=DBNL PE=2 SV=1
630	tr|B5X0Z8|B5X0Z8_SALSA	Phenylalanyl-tRNA synthetase beta chain OS=Salmo salar GN=SYFB PE=2 SV=1
631	tr|B5X5D3|B5X5D3_SALSA	ADP-ribosylation factor-like protein 8B OS=Salmo salar GN=ARL8B PE=2 SV=1
632	tr|B5X2U4|B5X2U4_SALSA	Asparagine synthetase OS=Salmo salar GN=ASNS PE=2 SV=1
633	tr|B5X5V8|B5X5V8_SALSA	L-xylulose reductase OS=Salmo salar GN=DCXR PE=2 SV=1
634	tr|B5XB05|B5XB05_SALSA	Ribosomal protein L15 OS=Salmo salar GN=RL15 PE=2 SV=1
635	tr|B5XEH8|B5XEH8_SALSA	Mitogen-activated protein kinase 12 OS=Salmo salar GN=MK12 PE=2 SV=1
636	tr|B5X454|B5X454_SALSA	Mitogen-activated protein kinase 13 OS=Salmo salar GN=MK13 PE=2 SV=1
637	tr|B9ENX5|B9ENX5_SALSA	Glutathione transferase omega-1 OS=Salmo salar GN=GSTO1 PE=2 SV=1
638	tr|C0H8Y5|C0H8Y5_SALSA	Tumor protein D52 OS=Salmo salar GN=TPD52 PE=2 SV=1
639	tr|C0H9L8|C0H9L8_SALSA	Vacuolar protein sorting-associated protein 35 OS=Salmo salar GN=VPS35 PE=2 SV=1
640	tr|B9ELX2|B9ELX2_SALSA	NADH dehydrogenase 1 alpha subcomplex subunit 4 OS=Salmo salar GN=NDUA4 PE=4 SV=1
641	sp|Q869S8|PSMG2_DICDI	Proteasome assembly chaperone 2 OS=Dictyostelium discoideum GN=psmG2 PE=3 SV=1
642	tr|C0H9C8|C0H9C8_SALSA	Calponin-3 OS=Salmo salar GN=CNN3 PE=2 SV=1
643	tr|C0HBP8|C0HBP8_SALSA	High mobility group-T protein OS=Salmo salar GN=HMGT PE=2 SV=1
644	tr|B5X7S5|B5X7S5_SALSA	Cathepsin H OS=Salmo salar GN=CATH PE=2 SV=1
645	tr|O13169|O13169_CYPCA	Alpha-globin OS=Cyprinus carpio GN=No.3 alpha PE=3 SV=1
646	tr|O13038|O13038_ICTPU	Leukocyte DNA binding receptor OS=Ictalurus punctatus PE=2 SV=1
647	tr|B5DG69|B5DG69_SALSA	Microtubule-associated protein, RP/EB family member 1 OS=Salmo salar GN=mapre1 PE=2 SV=1
648	tr|B9ELF6|B9ELF6_SALSA	ADP-ribosylation factor-like protein 6-interacting protein 1 OS=Salmo salar GN=AR6P1 PE=2 SV=1
649	tr|Q54U88|Q54U88_DICDI	C2 domain-containing protein OS=Dictyostelium discoideum GN=DG1113 PE=4 SV=1
650	tr|B5X3P0|B5X3P0_SALSA	Bifunctional 3-phosphoadenosine 5-phosphosulfate synthetase 2 OS=Salmo salar GN=PAPS2 PE=2 SV=1
651	tr|Q5TLN1|Q5TLN1_ANGJA	Reverse transcriptase OS=Anguilla japonica PE=4 SV=1
652	tr|Q9IB04|Q9IB04_9PERC	Immune-type receptor 7 OS=Sphoeroides nephelus PE=4 SV=1
653	tr|D3BH31|D3BH31_POLPA	AB-hydrolase associated lipase region containing protein OS=Polysphondylium pallidum GN=PPL_07833 PE=4 SV=1
654	sp|Q54FN7|PKS33_DICDI	Probable polyketide synthase 33 OS=Dictyostelium discoideum GN=pks33 PE=3 SV=2

655	tr|F4Q7F7|F4Q7F7_9MYCE	LISK family protein kinase OS=Dictyostelium fasciculatum GN=kxcA PE=3 SV=1
656	tr|F2EN88|F2EN88_9PERC	NADH-ubiquinone oxidoreductase chain 2 OS=Pelagocephalus marki GN=ND2 PE=3 SV=1
657	tr|Q1LX15|Q1LX15_DANRE	Serologically defined colon cancer antigen 33 OS=Danio rerio GN=tshz1 PE=2 SV=1
658	tr|Q24806|Q24806_ENTHI	Ras family GTPase OS=Entamoeba histolytica GN=Ehras1 PE=4 SV=1
659	tr|Q6U6Z9|Q6U6Z9_DANRE	Zinc finger transcription factor Gli3 OS=Danio rerio GN=gli3 PE=2 SV=1
660	tr|Q55DZ2|Q55DZ2_DICDI	Ubiquitin domain-containing protein OS=Dictyostelium discoideum GN=DDB_0190282 PE=4 SV=2
661	tr|Q05352|Q05352_ENTHI	Immuno-dominant variable surface antigen OS=Entamoeba histolytica PE=2 SV=1
662	tr|F4PYM5|F4PYM5_9MYCE	DEAD/DEAH box helicase OS=Dictyostelium fasciculatum GN=ascc3l PE=4 SV=1
663	tr|Q9DGM6|Q9DGM6_DANRE	Beta-spectrin OS=Danio rerio GN=sptb PE=2 SV=1
664	tr|Q7T158|Q7T158_DANRE	Novel protein similar to rodent myosin Ib (MYO1B) (Fragment) OS=Danio rerio GN=myo1bl2 PE=2 SV=1
665	tr|Q6KC12|Q6KC12_TETNG	Alpha-2,8-sialyltransferase ST8Sia I (Fragment) OS=Tetraodon nigroviridis GN=siat 8A PE=2 SV=1
666	tr|B5X9R4|B5X9R4_SALSA	Galectin-9 OS=Salmo salar GN=LEG9 PE=2 SV=1
667	tr|Q55BX2|Q55BX2_DICDI	DUF255 family protein OS=Dictyostelium discoideum GN=DDB_0202012 PE=4 SV=1
668	tr|B5X9B3|B5X9B3_SALSA	Phosphopantothenate--cysteine ligase OS=Salmo salar GN=PPCS PE=2 SV=1