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(54) Title: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM ANTIMICROBIAL PEPTIDES FROM BONY FISH

(57) Abstract: There is provided a method of identifying candidate nucleic acid sequences encoding antimicrobial peptides. The method comprises: identifying an initial peptide of interest; identifying genomic DNA encoding the initial peptide; identifying a flanking sequence on each side of the initial peptide; obtaining primers complementary to the flanking sequences; and, screening a wide range of nucleic acid sequences to identify candidate sequences capable of being amplified using the primers from step e). In some instances the antimicrobial peptide is a hepcidin or a pleurocidin.

WO 2004/018706 A2

## A Genomic Approach to Identification of Novel Broad-spectrum Antimicrobial Peptides From Bony Fish

### 5 **BACKGROUND OF THE INVENTION**

Antimicrobial peptides have been isolated from a wide variety of plants and animals, and play an important role in defense against microbial invasion. They fall into three main classes based on secondary structure and amino acid sequence similarities:  $\alpha$ -helical structures, highly disulphide-bonded (cysteine-rich)  $\beta$ -sheets and those with a high percentage of single amino acids such as proline or arginine. Most molecules are amphiphilic and contain both cationic and hydrophobic surfaces, enabling them to insert into biological membranes. Although one of the modes of action of antimicrobial peptides has been described as lysis of pathogens, they may also exert their effects by binding to intracellular targets. They have also been reported to exert a number of effects such as mediating inflammation and modulating the immune response.

A small number of natural antimicrobial peptides have been isolated from teleosts including the pleurocidin, from the skin of winter flounder (Cole, Weis et al. 1997), pardaxin from Red Sea Moses sole (Oren and Shai 1996), misgurnin from loach (Park, Lee et al. 1997), HFA-1 from hagfish (Hwang, Seo et al. 1999), piscidins from hybrid striped bass eosinophilic granule cells (Silphaduang and Noga 2001), moronecidins from hybrid striped bass (Lauth, Shike et al. 2002), parasin, a cleavage product of histone 2A from catfish (Park, Park et al. 1998) and some uncharacterized mucous secretions from carp (LeMaitre, Orange et al. 1996) and trout (Smith, Fernandes et al. 2000). In addition, a cationic steroidal antibiotic, squalamine, has been isolated from the shark, *Squalus acanthias* (Moore, Wehrli et al. 1993).

Cysteine-rich antimicrobial peptides of the defensin family have been detected in the fat body of insects and the hemolymph of molluscs and crustaceans. They have also been isolated from various epithelia of mammals as well as circulating cells such as neutrophils and macrophages. Recently, small cysteine-rich peptides exhibiting

antimicrobial activity against various fungi, Gram positive and Gram negative bacteria have been isolated from blood ultrafiltrate (Krause, Neitz et al. 2000), the human urinary tract (Park, Valore et al. 2001), and the gill of bacterially challenged hybrid striped bass (Shike et al. 2002). These peptides, referred to as hepcidin or LEAP-1 (liver-expressed antimicrobial peptide), have been proposed to be the vertebrate counterpart of insect peptides induced in the fat body in response to infection (Park, Valore et al. 2001).

Antimicrobial peptides have a variety of potential uses. (see for example US 6,288,212 of Hancock)

The conventional approach to identifying antimicrobial peptides involves biochemical purification from tissues or secretions. Fractions are tested for antimicrobial activity, and the purified peptides that exhibit activity are then sequenced. This approach is costly, time consuming, and not well suited to the identification of low abundance or difficult-to-purify antimicrobial peptides.

Thus, it is an object of the invention to provide a method for identifying potential antimicrobial peptides.

### ***SUMMARY OF THE INVENTION***

In one aspect of the invention there is provided a method of identifying candidate nucleic acid sequences encoding antimicrobial peptides, said method comprising:

- (a) identifying an initial peptide of interest;
- (b) identifying genomic DNA encoding the initial peptide;
- (c) identifying a flanking sequence on each side of the initial peptide;
- (d) obtaining primers complementary to the flanking sequences; and,
- (e) screening a wide range of nucleic acid sequences to identify candidate sequences capable of being amplified using the primers from step d).

According to one aspect of the invention the nucleotide and deduced amino acid sequences of hepcidin-like peptides are provided.

According to another aspect of the invention, the nucleotide and deduced amino acid sequences of pleurocidin – like peptides are provided.

According to another aspect of the invention primers suitable for use in the  
5 identification, isolation and/or amplification of nucleic acid sequences encoding novel microbial peptides are provided.

According to another aspect of the invention there is provided a method for the  
10 identification of families of nucleic acid sequences encoding antimicrobial peptides.

### ***BRIEF DESCRIPTION OF THE DRAWINGS***

*Figure 1* is a textual and graphical depiction of pleurocidin WF2 cDNA from winter  
flounder (A), a graphical depiction of a predicted hydrophobicity plot of  
peptide WF2 (B), and a diagrammatic depiction of a predicted helical structure  
15 of WF2 (C).

*Figure 2* is a pictorial depiction of results of amplification of certain hepcidin-like  
cDNAs.

*Figure 3* is a depiction of certain aligned pleurocidin –like peptide sequences.

*Figure 4* is a pictorial depiction of the results of PCR amplification of certain  
20 pleurocidin-like genomic sequences.

*Figure 5* is a depiction of an extended genomic sequence of WF4.

*Figure 6* is a depiction of an alignment of certain pleurocidin-like polypeptide  
sequences.

*Figure 7* is a pictorial depiction of the results of expression of certain pleurocidin-like  
25 genes in different winter flounder tissues.

*Figure 8* is a pictorial depiction of the results of RTPCR of expression of certain  
pleurocidins during winter flounder development.

*Figure 9* is a pictorial depiction of the results of a study of the expression of certain  
pleurocidin-like genes during winter flounder development.

*Figure 10* is a pictorial depiction of the results of a Southern analysis of certain pleurocidin genes of winter flounder.

*Figure 11* is a schematic depiction of the genomic organization of certain pleurocidin genes from winter flounder.

5 *Figure 12* is a schematic depiction of certain transcription factor binding sites located upstream from pleurocidin genes from winter flounder.

*Figure 13* is a graphical depiction of results showing the impact of peptide NRC-15 on bacterial survival.

10 *Figure 14* is a graphical depiction of results showing the impact of peptide NRC-13 on bacterial survival.

*Figure 15* is a graphical depiction of results showing the impact of peptide NRC-12 on yeast survival.

15 *Figure 16* is a depiction of nucleotide sequences of an unspliced (A) and partially spliced (B) cDNA encoding a type I hepcidin and a schematic depiction of intron/exon structure of a hepcidin gene in human, mouse and salmon (C).

*Figure 17* is a depiction of certain hepcidin sequences from different species shown in alignment.

20 *Figure 18* is a depiction of certain aligned 3' untranslated regions of hepcidin genes from winter flounder (A) and Atlantic salmon (B).

*Figure 19* is a pictorial depiction of the results of Southern hybridization analysis of certain hepcidins from different fish species.

*Figure 20* is a pictorial depiction of the results of an assay of the expression of certain hepcidin and actin genes in various tissues of winter flounder.

25 *Figure 21* is a pictorial depiction of the results of an assay of the expression of certain Type I (A) and Type 2 (B) hepcidin and actin genes in various tissues of control and infected salmon.

*Figure 22* is a pictorial depiction of the results of an assay of expression of certain Type I (A), Type II (B) and Type III (C) hepcidin and actin genes in developing winter flounder larvae.

5 *Figure 23* is a schematic depiction of steps taken in an embodiment of the method for identifying pleurocidins.

*Figure 24* is a schematic depiction of steps taken in an embodiment of the method for identifying hepcidins.

*Figure 25* is a graphical depiction of experimental results using antimicrobial peptide NRC-13 in the presence of 150 mM NaCl.

## 10 ***DETAILED DESCRIPTION OF THE INVENTION***

The method of the invention builds on the surprising discovery that the flanking sequences around antimicrobial peptides, including without limitation pleurocidins and hepcidins, are conserved. The method of the invention provides a means of identifying nucleotide sequences encoding pleurocidins and hepcidins, and identifying  
15 the encoded polypeptide sequences.

In one embodiment, the method provides, generally, a way of identifying members of a family of antimicrobial peptides once a single family member has been identified. The initial family member may be an initial peptide of interest. Initial peptides of  
20 interest can be identified based on either known or reported antimicrobial activity or based on sequence similarity to other known antimicrobial peptides. Once an initial peptide has been identified, the genomic DNA encoding it is identified and its flanking sequences are determined.

25 As used herein, the term “flanking sequences” refers to nucleic acid sequences appearing at or near one or both ends of a target nucleic acid sequence encoding an antimicrobial peptide.

As used herein a nucleic acid sequence is “at or near” the end of a target  
30 sequence if a portion of the sequence is within 50 nucleic acids of the end of the gene (whether within the coding region or outside it).

When an initial peptide of interest is identified based on sequence similarity to another peptide with known antimicrobial activity, the initial peptide preferably has an amphipathic structure and a net charge. In some instances the charge will preferably be a net positive charge of at least 2. In some instances, the peptide is at least 75 %, 85% or 95 % identical in sequence to the peptide having known antimicrobial activity. In some instances the sequence similarity identified may relate to similarity between nucleic acid sequences encoding the known peptide and encoding the peptide of interest. In such instances, the predicted peptide for the peptide of interest will be considered with respect to predicted charge and amphipathic structure.

For example, the prepro-sequences of pleurocidins and hepcidins tend to be conserved. Thus, by employing nucleic acid primers specific for such sequences, one can identify potential pleurocidin- and hepcidin- encoding sequences. Alternatively or additionally, known gene sequences of other classes of antimicrobial peptides can be examined to identify regions which appear to encode conserved prepro-sequences and a similar strategy used to identify other members of this family of peptides. The corresponding antimicrobial peptide encoded by such sequences can be predicted using the general features found in most pleurocidins and hepcidins, such as, for example, a net positive charge of at least 2 and an amphipathic structure.

As used herein with respect to pre-, pro- and prepro sequences of antimicrobial peptides, "pre" and "pro" have the following meaning: "Pre" refers to the signal peptide portion (or a functional portion thereof) of the peptide. "Pro" refers to the propiece. In pleurocidins the propiece is the anionic region at the carboxy terminus. In hepcidins the propiece is the region upstream of the mature peptide. In the non-limiting examples disclosed herein pleurocidin primers were designed based on the pre and pro regions, and hepcidin primers were designed based on the pre region and the 3' untranslated region (UTR).

PCR can be used to amplify nucleic acid sequences encoding potential pleurocidins or hepcidins. This can be conveniently accomplished by using a pair of PCR primers, one of which recognises a nucleic acid sequence complementary to a polynucleotide sequence encoding an amino-terminal prepro-sequence conserved in

the peptide type of interest, and the other complementary to a 3' conserved region in the nucleotide encoding the peptide-type of interest. It will be appreciated that other prepro-sequences may exist and are specifically contemplated. For example, redundancy in the genetic code allows for multiple nucleic acid sequences encoding a particular amino acid sequence. As discussed with respect to 5' prepro-sequences, other 3' conserved sequences may exist and are specifically contemplated. When designing primers it is useful to have reference to known codon usage information for the species in which sequence amplification is sought.

10 In an embodiment of the invention there is provided the use of signal sequence I or a nucleic acid sequence encoding same in identifying or amplifying potential pleurocidins.

#### Signal Sequence I

15 MKFTATFL (X)<sub>n</sub> (L)<sub>o</sub> (F)<sub>p</sub> I (F)<sub>q</sub> (X)<sub>y</sub> VLM (X)<sub>z</sub> (V)<sub>r</sub> (E)<sub>s</sub> (D)<sub>t</sub> (P)<sub>u</sub> (L)<sub>v</sub> G E (C)<sub>w</sub> (G)<sub>x</sub>

Wherein:

n is 1 to 3	u is 0 or 1
o is 0 to 2	v is 0 or 1
p is 0 or 1	w is 0 or 1
20 r is 0 or 1	
s is 0 or 1	x is 0 or 1
t is 0 or 1	y is 0 or 1
	z is 0 or 1

with the restriction that:

25  $x + o + p = 3,$   $s + t = 1,$   
 $u + v = 1,$   $w + x = 1,$  and  
 $q = 1.$

In an embodiment of the invention there is provided the use of one or both sequence PL1 or PL2 or a nucleic acid sequence encoding same in identifying or amplifying potential pleurocidins.

PL1 GCCCACTTTGTATTCGCAAG  
 PL2 CTGAAGGCTCCTTCAAGGCG

In an embodiment of the invention there is provided the use of an acidic sequence I or a nucleic acid sequence encoding same in identifying or amplifying potential pleurocidins.

#### Acidic Sequence I

$(Y)_a(X)_b(X)_c(E)_d(X)_e(Q)_f(E)_g L(N/D) KR(A/S) V D(D/E)$

wherein:

10

a is 0 or 1	e is 1 to 3
b is 0 or 1	f is 0 or 1
c is 1 or 2	g is 0 or 1
d is 0 or 1	

15

with the restriction that

a + b = 1,  
c + d = 2, and  
e + f + g = 3.

20

As used in the sequences herein "X" refers to any amino acid. Nucleic acid sequences encoding signal sequence I and acidic sequence I are specifically contemplated, as are nucleic acid sequences complementary to such nucleic acid sequences.

25

In an embodiment of the invention there is provided the use of signal peptide II, III, IV, V or a nucleic acid encoding same, in the identification or amplification of hepcidins.

30 Signal Peptide II

MKXXXXAXXVXXVL

Signal Peptide III

MKTFSVAV

Signal Peptide IV

MKTFSVAVTVAVVLXFICIQSSA

5 Signal Peptide V

MKTFSVAVAV (T/V) (L/V) VLA (F)<sub>n</sub>(V/C) (C/M) (I/F) (Q/I) X (X)<sub>m</sub> S (S/T) AV P  
F XXV,

Wherein n is 0 or 1 and m is 0 or 1.

10 In an embodiment of the invention there is provided the use of prosequence I,  
Prosequence II or a nucleotide sequence encoding same or complementary to one  
encoding same in the identification or amplification of hepcidins.

Prosequence I

15 PEVQXLEEAXSXDNAAAEHQE

Prosequence II

PFX XVX(X)<sub>n</sub> (L/T) EEV (E/G) (G/S) XD (T/S) PV (A/G) XHQ,

Wherein n is 0 or 1,

20

In an embodiment of the invention there is provided the use of HcPA3b3' and/or  
HcSal3' or a nucleotide sequence encoding same or complementary to one encoding  
same in the identification or amplification of hepcidins.

25

HcPa3b 3' 3'ACAACCTCGTCCTTAGG5'

HcSal 3' 3'ACGCCCGTCCAGGAAT5'

### Non-limiting Examples Of Uses

30 Antimicrobial peptides are useful in the treatment and/or prevention of infection  
in a variety of subjects, including fish, reptiles, birds, mammals, amphibians and  
insects.

Antimicrobial peptides are also useful for reducing bacterial growth and/or accumulation on surfaces. This is of particular benefit in the food industry where antimicrobial peptides can be used for coating surfaces used in the processing, preparation, and/or packaging of food.

5

Antimicrobial peptides disclosed herein can be administered in a variety of ways. In some instances, oral administration will be desirable. Some types of oral administration will be improved by encapsulation of the peptides so as to allow their preferential release at a particular stage in digestion. In some instances it will be desirable to include pre and/or pro sequences in the administered peptide (for example to improve stability or modulate activity). The pre and/or pro sequences can be cleaved off by endogenous proteases at the appropriate stage. Peptides may be administered by inhalation where the subject breathes air or by addition to water for gilled subjects. Administration by injection will in some cases be desirable. Peptides may be injected into any number of sites. In some cases intravenous injection will be desired. In some instances injection directly into or adjacent to the site of infection or potential infection will be desired. In some instances topical administration will be desired. Where the presence of the antimicrobial peptide is desired at a remote and specific site, or where the peptide will be desired for a prolonged period of time, gene therapy may be used to provide expression of one or more antibacterial peptides in the tissue(s) of concern.

Where the subject is a cultured or domesticated creature such as a fish, bird or non-human mammal, production of a transgenic variety which expresses one or more antibacterial peptides may be desired. Methods for producing transgenic animals are well known. (See for example Mar.Biotechnol.4: 338,2002).

A variety of antimicrobial peptides are contemplated and fall within the scope of the invention. By way of non-limiting example, peptides comprising the following amino acid sequences or a sequence at least 80% or 90% homologous thereto, and nucleic acid sequences encoding them are specifically contemplated:

- i) GW(G/K)XXFXK
- ii) GXXXXXXXXHXGXXIH
- iii) FKCKFCCGCCXXGVCGXCC

- iv) CXXCCNCC (K/H) XKGCGFCCCKF
- v) FKCKFCCGCRGXXCGLCCKF
- vi) XXXCXXCCNXXGCGXCCKX

5 Other specific, non-limiting examples of antimicrobial sequences of interest can be found in Tables 4 and 11.

Antimicrobial peptides of the invention may be modified. Such modifications may in some instances improve the peptides' stability or activity. Examples of modifications specifically contemplated include:

- 10 - conservative amino acid substitutions (acidic with acidic, basic with basic, neutral with neutral, polar with polar, hydrophobic with hydrophobic, etc.)
- addition of positively charged amino acids (lysine, arginine, histidine) at either or both ends
- replacement of amino acids with others unlikely to result in structural
- 15 changes including D-amino acids and peptidomimetics
- deletion of one or more amino acids
- modifications at C-terminal or N-terminal ends, including methyl esters and amidates
- cyclised versions of the peptides (which may result in increased stability
- 20 without adversely affecting activity)

### Examples – Methods

#### **Fish Rearing**

Winter flounder larvae were reared as described (Douglas, Gawlicka et al. 25 1999), the disclosure of which is incorporated herein by reference. Saint John River stock Atlantic salmon (*Salmo salar* L.) were maintained in single-pass, heated, dechlorinated fresh water at 12°C in the Dalhousie University Aquatron facility in Halifax, Nova Scotia. All fish were euthanised with an overdose of tricaine methanesulfonate (MS 222, 0.1 g L<sup>-1</sup>, Argent Chemical Laboratories, Inc., Redmond, 30 WA, USA) prior to sampling. All animal procedures were approved by the Dalhousie University Committee for Laboratory Animals and the National Research Council - Halifax Local Animal Care Committee.

### Bacterial Challenge

*Aeromonas salmonicida* subsp *salmonicida* strain A449 (Trust et al. 1983) was cultured to mid-logarithmic growth in Tryptic Soy Broth (TSB) at 17°C. The absorbance at 600nm of the bacterial suspension was determined and the bacteria were resuspended to approximately  $5 \times 10^7$  cfu mL<sup>-1</sup> in sterile Hanks Balanced Salt Solution (HBSS). Three salmon (200g each) were anaesthetised with 50 mg L<sup>-1</sup> TMS, injected intraperitoneally with  $2.5 \times 10^6$  cfu bacteria in 50 µL HBSS and allowed to recover in fresh water. Uninjected fish from the same cohort were maintained in separate tanks as controls. Three days post-injection, control and infected salmon were euthanised as described above and samples of tissues removed. Blood was drawn from the caudal vein into a heparinised container. To confirm that the fish were positive for *A. salmonicida*, the posterior kidney of both infected and control fish were swabbed and used to inoculate tryptic soy agar (TSA) that was incubated at room temperature overnight. Atlantic halibut tissue samples were obtained from a bacterial challenge study performed at Bedford Institute of Oceanography, Dartmouth, Nova Scotia.

### Sampling

Tissues (oesophagus, stomach, pyloric caecae, liver, spleen, intestine, anterior kidney, posterior kidney, gill, skin, ovary, rectum, heart, muscle and brain) were removed into RNALater (Ambion, Austin, TX, USA) and kept at -80° C until used. Samples of winter flounder larvae at different stages and juveniles were rinsed in RNALater (Ambion, Austin, TX, USA), transferred into 1.5 ml Eppendorf tubes containing 0.5-1.25 ml RNALater, and kept at -80° C until used.

### Pleurocidins

The general approach followed is shown in Figure 24

### Isolation of pleurocidin cDNA

A cDNA library constructed from winter flounder skin (Gong et al 1996) was screened using degenerate oligonucleotides (PleuroA, PleuroB; Table 1). The library was plated at 80,000 phage/plate and duplicate lifts to HyBond filters were made of each of eight plates. A mixture of radioactively end-labelled PleuroA and PleuroB

probes was hybridised with the filters at 50° C using standard procedures, and the filters were washed in 1X SSC/0.1% SDS at 50° C for 45 min. Plaques that showed matching hybridization signals on both duplicate filters were picked and the library rescreened until 100% purity of the recombinant plaques was obtained. Two recombinants were completely sequenced using an ABI373 stretch automated sequencer and the AmpliTaqFS Dye Terminator Cycle Sequencing Ready Reaction kit (Perkin-Elmer, Foster City, CA, USA). Sequence data were analyzed using Sequencher (Gene Codes, Inc., Ann Arbor, MI, USA) and DNA Strider. The amino-terminal signal sequence was predicted using SignalP (http://www.cbs.dtu.dk/services/SignalP). The Helical Wheel routine of the GCG package (http://www.gcg.com) was used to model the helical structure of the predicted antimicrobial peptide sequences.

#### **Genomic PCR**

Genomic sequences were amplified using two sets of primers specific to the winter flounder pleurocidin cDNA (PL1/PL2 and PL5'/PL3'; Table 1; Fig. 1). The amplification conditions were: 1 min at 94° C; 35 cycles of 30 s at 94° C; 30 s at 52° C, 90 s at 72° C; and 2 min at 72° C, and products were resolved on a 1% agarose gel. Bands were excised from the gel, extracted using Gene-Clean (Bio101, La Jolla, CA, USA) and cloned into the Topo TA2.1 vector (Invitrogen, Carlsbad, CA, USA) as recommended by the manufacturers. Several isolates from each transformation were sequenced and analyzed as described above. Intron positions were identified by comparison with the cDNA sequence.

#### **25 Identification of additional winter flounder pleurocidin-like sequences by RT-PCR**

Total RNA was isolated from winter flounder skin and intestines substantially as described in Douglas, Gawlicka *et al* (1999). Reverse transcription of 2 µg of total RNA was performed using the RETROScript kit (Ambion, Austin, TX, USA) according to the manufacturer's recommendation. PCR was performed using PL3' and a primer corresponding to the amino terminus of the precursor polypeptide (PL5'; Table 1). The amplification conditions were: 1 min at 94° C; 32 cycles of 30 s at 94°

C, 30 s at 50° C, 90 s at 72° C; and 2 min at 72° C and products were resolved on a 2% NuSeive gel. Bands were excised, cloned and sequenced as described above.

#### **Identification of additional pleurocidin-like sequences from different tissues**

5 Tissue-specific expression of pleurocidin was investigated by northern analysis using polyadenylated RNA (500 ng) from adult skin, liver, ovary, muscle, spleen, pyloric caeca, stomach and intestine. The entire insert from the cDNA clone corresponding to WF2 was radioactively labelled and incubated with the blot overnight at 60° C in UltraHyb hybridisation solution (Ambion, Austin, TX, USA).  
10 The blot was washed to a stringency of 50° C in 1X SSC/0.1% SDS for 1 h before exposure to X-ray film. RT-PCR was also employed using primers specific to WF1, WF1a, WF2, WF3, WF4, WFYT and WFX (Table 2) to assay expression of the different pleurocidin-like variants in various tissues. The conditions used were as described in the preceding paragraph except that the annealing temperature was 52 °  
15 C.

#### **Identification of additional pleurocidin-like sequences from different developmental stages**

Two larval time series were used to assess developmental expression of  
20 pleurocidin-like genes. In the first, RNA was isolated from pooled samples of twenty whole larvae (5 and 13 dph), ten whole metamorphosing larvae (20 dph) and newly metamorphosed larvae (27 dph), gut tissue of two juveniles (41 dph), skin from the upper and lower side of adult fish and tissue from adult upper and lower intestine. RNA was isolated as described (Douglas, Gawlicka et al. 1999), the disclosure of  
25 which is incorporated herein by reference, and the assays were performed using the primers PL5' and PL2 and conditions described above for RT-PCR. Amplification of the actin mRNA was performed as previously described (Douglas, Bullerwell et al. 1999), the disclosure of which is incorporated herein by reference, to confirm the steady level of expression of a housekeeping gene and to provide an internal control  
30 for pleurocidin expression. In the second larval time series, RNA was isolated from pooled samples of twenty whole larvae (hatch, 5 and 9 dph), ten whole larvae (15, 20, 25, 30 and 36 dph) and gut tissue of two juveniles (41 dph). Assays were performed using primers specific to WF1, WF1a, WF2, WF3, WF4, WFYT and WFX (Table 2)

to determine expression of the different pleurocidin-like variants at different stages of development. The conditions used were as described in the preceding paragraph.

### **Southern analysis**

5 Southern analysis of *Bam*HI- and *Sst*I-digested genomic DNA from winter flounder, three other flatfish (American plaice *Hippoglossoides platessoides* Fabricius, Atlantic halibut *Hippoglossus hippoglossus* L. and yellowtail flounder *Pleuronectes ferruginea* Storer), haddock (*Melanogrammus aeglefinus* L.), pollock (*Pollachius virens* L.) and smelt (*Osmerus mordax* Mitchill) was performed  
10 sequentially using the entire inserts from genomic clones corresponding to WF1, WF2, WF3 and WF4 as probes. Hybridisations were performed overnight at 65° C as previously described (Douglas, Gallant et al. 1998), the disclosure of which is incorporated herein by reference, and the blots were washed at 65° C in 0.5X SSC/0.1% SDS for 1 h and exposed to X-ray film. Blots were stripped by incubating  
15 twice in boiling 0.5% SDS and checked for residual signal by exposure to X-ray film overnight.

### **Identification of additional pleurocidin-like sequences from other fish species**

Total RNA was isolated from skin and intestine of yellowtail flounder, witch  
20 flounder and Atlantic halibut and reverse-transcribed as described above (RT-PCR analysis). Total genomic DNA was isolated from milt of yellowtail flounder, witch flounder, American plaice, Atlantic halibut and tissue samples of Petrale sole, C-O sole, English sole, Starry flounder, European plaice, Greenland halibut and Pacific halibut. Two sets of primers specific to the winter flounder pleurocidin cDNA  
25 (PL1/PL2 and PL5' /PL3'; Table 1; Fig. 1) were used and the amplification conditions were: 1 min at 94° C, 32 cycles of 30 s at 94° C; 30 s at 50° C, 90 s at 72° C; and 2 min at 72° C. Products were resolved on a 2% NuSeive gel, bands excised, cloned and sequenced as described above.

30 Figure 1 is a textual and graphical depiction of WF2 pleurocidin from winter flounder A. Nucleotide sequence of cDNA for pleurocidin from winter flounder isolated from the skin library. The positions of primers used for PCR are underlined and the deduced amino acid sequence is shown in upper case letters below the

nucleotide sequence. Arrows indicate the mature 5' and 3' termini of the pleurocidin peptide and diamonds indicate the positions of introns. The single *SstI* restriction endonuclease site (GAGCTC) and the putative polyadenylation site (aataaa) are indicated in boldface. *B.* Hydrophobicity plot of predicted pleurocidin polypeptide  
5 WF2 constructed using the Kyte-Doolittle option of DNA Strider (Marck 1992). The borders of the mature pleurocidin are indicated by vertical arrows. *C.* Diagrammatic representation of helical structure of predicted pleurocidin polypeptide WF2 constructed using the Helical Wheel routine of GCG. Hydrophobic residues and glycines are boxed and polar residues are not. The first amino acid (G) of the mature  
10 polypeptide is found at the top of the wheel.

### **Identification of pleurocidin-like sequences in the winter flounder genome**

A winter flounder genomic  $\lambda$ -GEM library was screened using a radioactively labeled probe for pleurocidin (WF2; Douglas et al., 2001). Four clones were picked  
15 and replated until 100% purity was achieved. The clones were mapped using *BamHI*, *SstI*, *XhoI* and *EcoRI* and two clones ( $\lambda$ 1.1 and  $\lambda$ 5.1) that differed in restriction pattern were selected for sequencing. Both clones were completely sequenced using an ABI373 stretch automated sequencer and the AmpliTaqFS Dye Terminator Cycle Sequencing Ready Reaction kit (Perkin Elmer, Foster City, CA, USA. Transcription  
20 factor binding sites were identified using WWW Signal Scan (<http://bimas.dcrn.nih.gov/molbio/signal/>) with the TransFac and TFD databases and promoters were detected using the eukaryotic promoter prediction by neural network software available at the Baylor College of Medicine (<http://searchlauncher.bcm.tmc.edu/seq-search/gene-search.html>).

### **25 Hepcidins**

The general approach followed is depicted in Figure 24

#### **Molecular Characterisation of Hepcidin cDNAs**

Eight ESTs showing high similarity to human hepcidin were identified from  
30 the winter flounder EST database (Douglas, Gallant et al. 1999) and four from the Atlantic salmon database (Douglas, Tsoi et al. 2002). Using these sequences to screen dbEST, BLASTX analysis revealed two related sequences from Japanese flounder (C23298.1 and C23432.1), one sequence from rainbow trout (AF281354\_1) and five

identical sequences from medaka (AU178966, AU179222, AU179314, AU179768 and AU180044). Sequence data were analyzed using Sequencher (Gene Codes, Inc., Ann Arbor, MI, USA) and DNA Strider (Marck 1992). Alignments and similarity matrices were calculated using ClustalW (Thompson, Higgins et al. 1994) and graphically visualised using SeqVu (Garvan 1996). The on-line servers PSORT (5 <http://PSORT.nibb.ac.jp>), Compute pI ([http://expasy.hcuge.ch/cgi-bin/pi\\_tool](http://expasy.hcuge.ch/cgi-bin/pi_tool)), and Network Protein Sequence @analysis ([http://npsa-pbil.ibcp.fr/cgi-bin/secpred\\_consensus.pl](http://npsa-pbil.ibcp.fr/cgi-bin/secpred_consensus.pl)) were used to predict N-terminal signal sequences, pI and secondary structure, respectively. The secondary structure prediction program utilized 10 seven different algorithms (for details, see web site) and provided a consensus prediction based on these results.

### **Southern Hybridisation**

Total genomic DNA was prepared from winter flounder (*Pleuronectes americanus*), yellowtail flounder (*Pleuronectes ferruginea*), witch flounder (*Glyptocephalus cynoglossus*), Japanese flounder (*Paralichthys olivaceus*), American plaice (*Hippoglossoides platessoides*), Atlantic salmon (*Salmo salar*), haddock (*Melanogrammus aeglefinus*), smelt (*Osmerus mordax*), hagfish (*Eptatretus burgeri*), tiger shark (*Scyliorhinus torazame*) and white sturgeon (*Acipenser transmontanus*) as 15 previously described (Douglas, Bullerwell et al. 1999), the disclosure of which is incorporated herein by reference. DNA (7.5  $\mu$ g) was digested with *SstI* according to the manufacturer's recommendations and the fragments resolved on a 1% agarose gel. A 104 bp probe corresponding to amino acid residues WMENPT. . . .GCGFCC of Type I winter flounder hepcidin was labeled using the DIG Labelling Kit (Roche 20 Applied Science, Laval, PQ, Canada) and hybridized to the membrane for 2h at 42 °C using the Easy Hyb kit (Roche Applied Science, Laval, PQ, Canada). The membrane was washed in 0.2X SSC at 65 °C and signal detected using the DIG Luminescent Detection Kit (Roche Applied Science, Laval, PQ, Canada).

### **30 Identification of additional hepcidin-like sequences by RT-PCR**

Primers were designed based on the cDNA sequences determined in this study (Table 3). Amplification of actin mRNA was performed to confirm the steady-state level of expression of a housekeeping gene and provide an internal control for the hepcidin gene expression analyses. Controls were performed using single primers to

eliminate single primer artifacts and without reverse transcription to eliminate amplification products arising from contaminating genomic DNA.

Total RNA was isolated from tissues of uninfected adult winter flounder and uninfected and infected adult salmon and halibut using the RNAWiz Kit (Ambion, Austin, TX, USA) according to the manufacturer's recommendations. Tissues were  
5 homogenized using a 7mm generator on a Polytron standard rotor stator homogenizer (Kinematica). In addition, RNA was isolated from pooled samples of twenty whole larvae (hatch, 5 and 9 dph), ten whole larvae (15, 20, 25, 30 and 36 dph), gut tissue of two juveniles (41 dph) and adult winter flounder liver. To eliminate contaminating  
10 DNA, the Ambion DNA-free™ protocol was used as directed. Briefly, 4 units of DNase 1 was added to the resuspended RNA and incubated for 1 hour at 37C. After incubation, DNase Inactivation Reagent was added to remove the enzyme and RNA concentrations were determined using a Beckman DU-64 Spectrophotometer.

15 First strand cDNA was synthesized from 1 µg of total RNA using the RetroScript kit (Ambion, Austin, TX, USA) and aliquots of the reaction products were subjected to PCR using rTaq polymerase (Amersham Pharmacia Biotech AB, Uppsala, Sweden) or the Advantage2 PCR kit (Clontech, Palo Alto, CA, USA). The primers and annealing temperatures are listed in Table 3. The amplification conditions  
20 were: 1 min at 95° C; 32 cycles of 15 s at 95° C; 30 s at the annealing temperature, 30 s at 68° C; hold at 4° C. Amplification products were resolved on a 2% NuSieve agarose gel with a 100 bp ladder as a marker (Gibco BRL, Gaithersburg, MD, USA) and the amount of each product was quantified using a GelDoc 1000 video gel documentation system (BioRad, Mississauga, Ont., Canada) with the Multianalyst  
25 software.

#### **Identification of additional hepcidin-like sequences from other fish species**

Total RNA was isolated from liver and spleen of bacterially challenged Atlantic halibut and Atlantic salmon and reverse-transcribed as described above (RT-  
30 PCR analysis). Two sets of primers were used (see legend, Fig. 2) and the amplification conditions were: 2 min at 94° C; 32 cycles of 30 s at 94° C; 30 s at 52° C, 30 s at 72° C; and 2 min at 72° C. Products were resolved on a 2% NuSeive gel, bands excised, cloned and sequenced as described above.

### Prediction of active cationic peptide sequences

The mature peptide sequences from Figure 3 (pleurocidin-like peptide sequences deduced from nucleotide sequences of genes and PCR products amplified from fish tissues) constituted the basis of sequence selection. Generally, upon extensive sequence analysis, those peptides that possessed a net positive charge and had their hydrophilic and hydrophobic residues well-separated in models were produced. Also, generally those peptide genes that were likely to be expressed (possessed promoters) were used, although pseudogenes were also included in the panel. The exact start/end residues were decided upon based on several factors listed below. In most cases the N-terminus of the mature peptide was well defined, since it followed directly the conserved signal peptide region, and aligned well with other mature peptides. Wherever a straightforward determination on the N-terminal amino acid was not possible, an attempt was made to preserve GW or GF at the N-terminus, as this is frequently encountered among cationic peptides. In addition, two versions of WF1a (NRC-2 and NRC-3) were produced: one contained N-terminal GRRKRK, and the other did not. In some cases the C-terminus of the mature peptide was also well defined, since it was followed directly by a conserved acidic propiece. However significant ambiguity as to the C-terminal amino acid existed among many peptides. Generally, two rules were followed in deciding upon C-terminal amino acids: (1) wherever glycine appeared at or near the C-terminus, it was considered to be a precursor for carboxy-terminus amidation; (2) large numbers of negatively charged amino acids near the C-terminus were generally considered to be a part of the propiece and not the mature active peptide, and were not included in the sequence.

25

All antimicrobial peptides used in this study were synthesized by N-(9-fluorenyl) methoxy carbonyl (Fmoc) chemistry at the Nucleic Acid Protein Service (NAPS) unit at the University of British Columbia. Peptide sequences are shown in Table 4. Peptide purity was confirmed by HPLC and mass spectrometry analysis in each case. In the case of NRC-7 further purification by RP-HPLC was performed until homogeneity of the sample was obtained.

30

### Bacterial Strains and *Candida albicans*

All strains used in this study are listed in Table 5. Most non-fish bacterial strains as well as *Candida albicans* were grown at 37°C in Mueller-Hinton Broth (MHB; Difco Laboratories, Detroit), while the fish bacteria were maintained at 16°C  
5 in Tryptic Soy Broth (TSB; Difco, 5g/l NaCl). All strains were stored at -70°C until they were thawed for use and sub-cultured daily. The following strains, *Pseudomonas aeruginosa* K799 (parent of Z61), *Pseudomonas aeruginosa* Z61 (antibiotic supersusceptible), *Salmonella typhimurium* 14028s (parent of MS7953s), *Salmonella typhimurium* MS7953s (defensin supersusceptible), as well as *Staphylococcus epidermidis* (human clinical isolates) and methicillin-resistant *Staphylococcus aureus* (MRSA; isolated by Dr. A. Chow, University of British Columbia) have been kindly  
10 donated by Prof R.E.W. Hancock, University of British Columbia.

*Escherichia coli* strain CGSC 4908 (*his-67*, *thyA43*, *pyr-37*), auxotrophic for thymidine, uridine, and L-histidine (Cohen *et al.*, 1963) was kindly supplied, free of  
15 charge, by the *E.coli* Genetic Stock Centre (Yale University, New Haven, CT). MHB supplemented with 5 mg/L thymidine, 10 mg/L uridine and 20 mg/L L-histidine (Sigma Chemical Co., St. Louis, MO), was used to grow *E.coli* CGSC 4908 unless otherwise specified.

Two field isolates of the salmonid pathogen *Aeromonas salmonicida* are from  
20 the IMB strain collection.

### Minimum Inhibitory Concentrations

The activities of the antimicrobial peptides were determined as minimal inhibitory concentrations (MICs) using the microtitre broth dilution method of  
25 Amsterdam (Amsterdam, 1996), as modified by Wu and Hancock (1999). Serial dilutions of the peptide were made in water in 96-well polypropylene (Costar, Corning Incorporated, Corning, New York) microtiter plates. Bacteria or *C. albicans* were grown overnight to mid-logarithmic phase as described above, and diluted to give a final inoculum size of 10<sup>6</sup> cfu/ml. A suspension of bacteria or yeast was added  
30 to each well of a 96 well plate and incubated overnight at the appropriate temperature. In the case of *E. coli* CGSC 4908, supplemented MHB was used. Inhibition was defined as growth lesser or equal to one-half of the growth observed in control wells,

where no peptide was added. Three repeats of each MIC determination were performed.

### **Killing assays**

5 Survival of bacteria and *C. albicans* upon exposure to selected peptides applied at their minimal inhibitory concentrations (MICs) and ten times their MICs was measured using standard methodology. The test organisms were grown in MHB and exposed to the peptides. At the specified time intervals equal aliquots were removed from the cultures, plated on MHB plates, and the resulting colonies were  
10 counted. Percentage survival was plotted against time on a logarithmic scale. Two repeats of each experiment were performed.

### **Preparation of a Synthetic Antimicrobial Peptide**

Prediction of active cationic peptide sequences.

15

The mature peptide sequences from Figure 3 (pleurocidin-like peptide sequences deduced from nucleotide sequences of genes and PCR products amplified from fish tissues) constituted the basis of sequence selection.

Sequences were selected for peptides that possessed a net positive charge and  
20 had their hydrophilic and hydrophobic residues well separated spatially in models that were produced specifically:

- a) In order to estimate the net charge K and R were assumed to have the value of +1, H of +1/2, D and E of -1, and C-terminal amidation was  
25 counted as an additional +1.
- b) The EMBOSS Pepwheel and Pepnet internet tools available through an NRC mirror site (<http://bioinfo.pbi.nrc.ca:8090/EMBOSS/index.html>) were used to analyse the separation of hydrophilic and hydrophobic residues in helical wheel and helical net models.

30

Also, generally those peptide genes that were likely to be expressed (possessed promoters, were transcribed, etc.) were produced, although pseudogenes were also included in the panel.

The exact start/end residues were decided upon based on several factors:

- a) In most cases the N-terminus of the mature peptide was well-defined, since it followed directly the conserved signal peptide region, and aligned well with other mature peptides.
- 5 b) Wherever a straightforward determination on the N-terminal amino acid was not possible, an attempt was made to preserve GW or GF at the N-terminus, as this is frequently encountered among cationic peptides.
- c) In addition, two versions of WF1a (NRC-2 and NRC-3) were  
10 produced: one contained N-terminal GRRKRK, and the other did not; this was done because it was hypothesized that the presence of the highly positively charged GRRKRK would improve activity.
- d) Although in some cases the C-terminus of the mature peptide was also  
15 well defined, since it was followed directly by a conserved acidic propiece, significant ambiguity as to the C-terminal amino acid existed among many peptides. Generally, two rules were followed in deciding upon C-terminal amino acids:
1. wherever glycine appeared at or near the C-terminus, it was considered to be a precursor for  
20 carboxy – terminus amidation;
  2. large numbers of negatively charged amino acids near the C-terminus were generally considered to be a part of the propiece and not mature active peptide and were not included in the sequence.

25 Peptides produced according to the above steps are screened for antimicrobial activity *in vitro* by standard means. Those peptides showing *in vitro* antimicrobial activity are useful as antimicrobial peptides for use *in vivo* and for the treatment of surface, etc.

### Examples - Results

#### **Pleurocidins**

##### 30 **cDNA sequence**

The two clones isolated from the skin cDNA library were identical in sequence to each other and to the genomic PCR product WF2 after introns were removed (see

below). They contain 356 bp and encode an open reading frame of 68 amino acids (Fig. 1A). There is a 5'-untranslated region of 26 bp and a 3'-untranslated region of 84 bp, excluding the polyA tail. A canonical polyadenylation signal AATAAA is found 22 bp upstream of the polyA tail. The first 22 amino acids of the open reading  
5 frame form a highly hydrophobic domain (Fig. 1B) predicted to be a signal peptide with a cleavage site that precisely matches the amino terminus of the mature pleurocidin. The predicted amino acid sequence of residues 23-47 exactly matches the published amino acid sequence of mature pleurocidin (arrows, Fig. 1A). The mature peptide can assume an amphipathic helix that contains a predominance of positively  
10 charged amino acids on one face and hydrophobic amino acids on the other (Fig. 1C). The carboxy-terminal 21 amino acids form a negatively charged domain that is not present in the mature pleurocidin, confirming the recent report of Cole et al. (2000).

### Genomic PCR

15 Four distinct bands (WF1-4) were amplified using primers PL5' and PL3' (Fig. 4). Sequence analysis of each product was consistent with the sizes of the bands and verified that each amplification product was different (Table 6). Two distinct bands were amplified using primers PL1 and PL2 that corresponded to WF2 and WF4 containing additional upstream and downstream sequence (data not shown). When the  
20 intron sequences were removed, the sequence of WF2 exactly matched that of the pleurocidin cDNA clone isolated from the skin library (Fig. 1A).

Figure 4 is a depiction of the results of PCR amplification of pleurocidin-like sequences from winter flounder genomic DNA. Amplification products (P) were  
25 resolved on a 1 % agarose gel using the 100 bp ladder as molecular weight markers (M). Products visible as distinct bands are labeled WF1 (00 bp), WF2 (810 bp), WF3 (650 bp) and WF4 (510 bp).

All four of the pleurocidin-like genes contained two introns within the coding  
30 sequence and three of the genes showed identical intron locations (WF1, WF2 and WF4). However, the position of the second intron in WF3 occurred upstream of those of the other genes, resulting in a shorter second exon and longer third exon. The sizes and sequences of the introns varied among the four pleurocidin genes (Table 6). Evidence from the two more extensive genomic sequences of WF2 and WF4 obtained

using primers PL1 and PL2 indicates that a third intron immediately upstream of the initiation codon is also a feature of this gene family (Fig. 5). This was also noted for the genomic sequence reported by Cole et al (Cole, Darouiche et al. 2000).

5 An alignment of the predicted amino acid sequences is shown in Fig. 6. The positions of the introns (indicated by vertical arrows) were determined by comparison with the corresponding RT-PCR and cDNA-derived sequences. The positions of the mature peptide were determined by comparison with the published amino acid sequence of pleurocidin (Cole, Weis et al. 1997). All of the predicted mature  
10 polypeptides could assume amphipathic  $\alpha$ -helical structures similar to that shown in Fig. 1C, although the positively charged portions were not as striking in WF1 and WF3 as in WF2 and WF4 (data not shown).

Figure 5 describes extended genomic sequence of WF4 obtained by PCR using  
15 primers PL1/PL2. Introns are indicated in lower case and coding sequence in upper case. The positions of the primers PL1 and PL2 used for PCR are underlined.

Figure 6 describes Alignment of predicted polypeptide sequences of five winter flounder pleurocidin family members. Large vertical arrows indicate the positions  
20 where introns were found in the genomic sequences. The second intron of WF3, indicated by a small vertical arrow, is found more upstream than those of the other genes. The predicted polypeptide sequences of dermaseptin B1 (Amiche et al. 1994) and ceratotoxin B (Marchini et al. 1995) are shown below the pleurocidin family members. Boxed amino acids are shared by half of the sequences.

25

#### **Identification of additional pleurocidin-like sequences from different tissues**

Northern analysis was only able to detect pleurocidin transcripts in skin (data not shown). However, the more sensitive RT-PCR assay indicated that pleurocidin was also expressed in other tissues, particularly gill and gut. Using primers PL5' and  
30 PL3', two bands were obtained from winter flounder skin (265 and 175 bp) and two from intestine (215 and 175 bp). Sequence analysis of several clones of each size showed that the 265 bp winter flounder skin clones corresponded to the genomic sequence of WF1 when intron sequences were removed (Table 7). Five of the 175 bp clones from skin and two of the 175 bp clones from intestine corresponded to the

genomic sequence of WF2. This is consistent with results of northern analysis using the cDNA clone corresponding to the WF2 probe that showed hybridisation only to 200-nucleotide mRNA from the skin (data not shown). On the other hand, nine of the 175 bp clones from intestine and four of the 175 bp clones from skin corresponded to the genomic sequence of WF3. No RT-PCR products were obtained that corresponded to WF4. All seven of the 215 bp intestine clones corresponded to a novel family member (WF1a) not represented by any of the winter flounder genomic sequences determined in this study.

Using primers specific to each of the pleurocidin-like variants reported above, as well as to additional pleurocidin-like variants identified on Lambda clones, we were able to demonstrate that different variants were expressed in different tissues (Fig. 7). WF2, WF3 and WFYT showed the expression in the widest distribution of tissues, whereas WF1 and WF4 were expressed in mainly in the gill and skin, and WFX was only expressed in the skin. Transcripts of WF1a could not be detected in any tissue.

Figure 7 describes the expression of specific pleurocidin-like genes in different tissues of winter flounder. Tissues were esophagus (E), pyloric stomach (PS), cardiac stomach (CS), pyloric caeca (PC), liver (L), spleen (SP), intestine (I), rectum (R), gill (G), brain (B) and skin (SK). Markers (M) were the 100 bp ladder. Primers were specific to each pleurocidin variant (Table 2)

#### **Identification of additional pleurocidin-like sequences from different developmental stages**

Using primers PL5' and PL2 (Table 1) from highly conserved regions of the pleurocidin-like peptides, low levels of transcripts were evident at 5 dph and increased during development (Fig. 8). Strong signals were obtained from adult skin and weak signals from intestinal tissue. Expression of the housekeeping gene, actin, was relatively constant throughout development.

Using primers specific to each of the pleurocidin-like variants reported above, as well as to additional pleurocidin-like variants identified on Lambda clones, it was demonstrated that different variants were expressed at different times during development (Fig. 9). WFX transcripts were only detectable at 20 dph, and WF2,

WF3 and WFYT were detectable in premetamorphic larvae and metamorphic juveniles. No expression of WF1 and WF4 was detectable at any stage of development.

5 Figure 8 describes Reverse transcription-polymerase chain reaction assay of pleurocidin expression. Samples are from larvae (5 and 13 dph), metamorphosing larvae (20 dph), newly metamorphosed larvae (27 dph), juveniles (41 dph), skin from the lower (LS) and upper side (US) of the fish and tissue from the lower (LI) and upper (UI) intestine. Primers specific for pleurocidin (panel A) and actin (panel B)  
10 were used.

Figure 9 describes Expression of specific pleurocidin-like genes during winter flounder larval development. Samples are from larvae (5, 9 and 15 dph), metamorphosing larvae (20 dph), newly metamorphosed larvae (25, 30 and 36 dph)  
15 and juveniles (41 dph). Controls using the 5' or 3' primers alone and with no template (NT) are also shown. Primers were specific to each pleurocidin variant (Table 2).

### Southern analysis

Positive signals were specific to flatfish DNA using the WF1, WF2, WF3 and  
20 WF4 genomic probes (Fig. 10). No signals were detected with haddock, pollock or smelt DNA (data not shown). All four probes showed hybridisation to common *SstI* and *BamHI* bands from the DNAs of all four flatfish, indicating that the genes are clustered on these genomes. The sizes of the hybridising fragments from the winter flounder digest are given in Table 8.

25

Figure 10 describes Southern analysis of pleurocidin genes of winter flounder (WF), yellowtail flounder (YF), American plaice (AP) and Atlantic halibut (AH). Total genomic DNA (7.5 µg) was digested with *BamHI* (B) or *SstI* (S) and the fragments resolved on a 1.0% agarose gel. The blot was hybridized successively with  
30 probes corresponding to WF1, WF2, WF3, and WF4. Markers (M) are lambda DNA digested with *StyI* (24.0, 7.7, 6.2, 3.4, 2.7, 1.9, 1.4, 0.9 Kb).

**Identification of additional pleurocidin-like sequences from other fish species**

An alignment of the deduced amino acid sequences of pleurocidin-like peptides from American plaice, yellowtail flounder, witch flounder and Atlantic halibut is shown in Fig. 3. Sequences were obtained from genomic DNA of Petrale sole, C-O sole, English sole, starry flounder, European plaice, Greenland halibut and Pacific halibut. High conservation is present in the signal peptide and acidic propiece regions, whereas the portion corresponding to the mature peptide shows much more variability.

10 Figure 3 describes Alignment of pleurocidin-like peptide sequences deduced from nucleotide sequences of genes and PCR products amplified from skin and/or intestine of the following species: winter flounder (WF), yellowtail flounder (YF), witch flounder (GC), American plaice (AP) and Atlantic halibut (AH). Specific non-limiting examples of pleurocidin-like sequences identified are shown in Table 4.  
15 Non-limiting examples of cDNA and/or genomic sequences are provided in Appendix I.

**Identification of pleurocidin-like sequences in the winter flounder genome**

Two clones containing fragments of 12.5 and 15.6 kb, respectively, were isolated from a genomic library from winter flounder. The 12.5 kb fragment encoded the gene corresponding to WF2 and two pseudogenes. The 15.6 kb fragment encoded the gene corresponding to WF1, one pseudogene and two previously undescribed pleurocidin-like sequences referred to as WFX and WFYT. A schematic of the gene arrangement is shown in Fig. 11. Scanning of the sequences upstream of the coding sequence revealed a canonical eukaryotic promoter, TATA and CAAT boxes as well as highly conserved sites for several transcriptions factors including NF-IL6, AP1 and  $\alpha$ -interferon (Fig. 12). No promoter sequences were identified upstream of pseudogenes.

30 Figure 12 describes Locations of transcription factor binding sites upstream of pleurocidin genes and pseudogenes. Promoters are indicated by hatched boxes, introns by solid boxes and genes and exons by stippled boxes.

### Prediction and assessment of antimicrobially active peptide sequences

The minimal inhibitory concentrations of the chemically produced peptides against a wide range of bacterial pathogens and *C. albicans* were determined and are shown in Table 9. Generally speaking many peptides showed the ability to inhibit the growth of a broad spectrum of bacterial pathogens and *C. albicans*. Particularly good examples of peptides with a broad spectrum of antimicrobial activity are the three peptides derived from American plaice (NRC-11, NRC-12, and NRC-13) and three peptides derived from witch flounder (NRC-15, NRC-16, and NRC-17). Of those, NRC-15, NRC-13, and NRC-12 showed ability to kill methicillin-resistant *S. aureus* (Fig. 13), *P. aeruginosa* (Fig. 14) and *C. albicans* (Fig. 15), respectively.

Figure 13 describes Survival of a Gram-positive bacterium (methicillin-resistant *Staphylococcus aureus* - MRSA) upon exposure to NRC-15 at its minimal inhibitory concentration (MIC) and ten times its MIC. *S. aureus* was grown in Mueller-Hinton broth and exposed to NRC-15 at its MIC and ten times its MIC. At the specified intervals equal aliquots were removed from the culture, plated on MHB plates, and the resulting colonies were counted.

Figure 14 describes Survival of a Gram-negative bacterium (*Pseudomonas aeruginosa*) upon exposure to NRC-13 at its minimal inhibitory concentration (MIC) and ten times its MIC. *P. aeruginosa* was grown in Mueller-Hinton broth and exposed to NRC-13 at its MIC and ten times its MIC. At the specified intervals equal aliquots were removed from the culture, plated on MHB plates, and the resulting colonies were counted.

Figure 15 describes Survival of a yeast (*Candida albicans*) upon exposure to NRC-12 at its minimal inhibitory concentration (MIC) and ten times its MIC. *C. albicans* was grown in Mueller-Hinton broth and exposed to NRC-12 at its MIC and ten times its MIC. At the specified intervals equal aliquots were removed from the culture, plated on MHB plates, and the resulting colonies were counted.

In addition to demonstrating that pleurocidin-like peptides are active against a wide range of bacteria as well as *C. albicans*, the results indicate which factors should

preferably be considered in selecting antimicrobially active peptides from genomic sequences.

5 Firstly, a notable group of peptides with poor or no observed activities were peptides derived from pseudogenes (NRC-8, NRC-9, NRC-10). These results indicate that peptides capable of being expressed in the host organism may be better candidates for antimicrobials.

10 Secondly, the previously described N-terminal GRRKRK in WF1a (Fig. 2) proved to be a determinant of antimicrobial activity in NRC-3 as shown by the fact NRC-2 (identical to NRC-3 but missing the aforementioned fragment) was only marginally active (Table 9). This result stresses the importance of carefully selecting the start/end residues in the mature peptide, wherever these are not apparent in the original pre-pro-sequence.

15

Thus in an embodiment of the invention there is provided a group of pleurocidin-related antimicrobial peptides having the amino acid sequence GRRKRK. It will be appreciated that pleurocidin-like antimicrobial peptides lacking this sequence also exist and are specifically contemplated herein.

20

The previously described principles of: selecting positively charged peptides with good separation of hydrophilic and hydrophobic residues in helical wheel models, preserving GW or GF at the N-terminus, amidating the C-terminus where glycine was present, and cropping off clusters of acidic C-terminal amino acids were 25 successful in selecting antimicrobially active peptides.

Peptides of the invention can be used at a range of pH's, salt concentrations, and temperatures. These peptides are useful against pathogens grown in biofilms or under any other conditions for pathogen growth or culture. See for example Figure 25 in 30 which the ability of NRC-13 to kill *P. aeruginosa* K799 in 50 mM NaCl is shown. NRC-13 was added to a culture of *P. aeruginosa* supplemented with 150 mM NaCl to a final concentration of 4µg/ml (□) or 40 µg/ml (Δ), representing the MIC and 10X MIC, respectively. A control with no peptide added is also shown (♦).

Peptides may be used alone or in combination with one or both of their pre-and pro- sequences.

Peptides of the invention have many uses, including as antibacterial, antifungal, antiviral, anti-cancer, and antiparasitic agents, including in combination with other antibiotics, anti-infectives, and chemotherapeutants as well as with each other.

Peptides can be used as immunomodulatory agents such as for wound healing, tissue regeneration, anti-sepsis, immune promoters, etc. including in combination with other agents.

The peptides can be delivered topically (including e.g., aerosols-especially for respiratory tract infections in CF patients, ointments, lotions, rinses, eyewashes, etc.), systemically (including e.g. IV, IP, IM, subcutaneously, intracavity or transdermally) and, orally (e.g. pills, liquid medication, capsules, etc.).

Delivery via encapsulation, including in liposomes, proteinoids is contemplated, as is delivery in transgenic systems involving agricultural animals and/or plants.

Peptides can be used as protective coatings on medical devices (including catheters, etc, food preparation machinery and packaging.

Examples of antibiotics which can be used together with peptides disclosed herein in aquaculture operations include: Terramycin Aqua (oxytetracycline), Romet (sulfadimethoxine and ormetoprim), and Tribriksen (trimethoprim and sulfadiazine). In the hatchery, dipping in formaldehyde can be used together with peptides disclosed herein. Peptides can be used in combination with each other and/or in combination with conventional antibiotics for any of the uses described herein.

### **Hepcidins**

Specific non-limiting examples of hepcidin sequences identified are shown in Table 11. Examples of cDNA or genomic sequences are shown in Appendix II.

### Bacterial Challenge

Three days post-injection, the infected Atlantic salmon were lethargic and anorexic. On sampling, the posterior kidneys of the injected fish were positive for *A. salmonicida* whereas those of the control fish were not.

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### Molecular Characterisation of Hecpidin cDNAs

Although the winter flounder EST database contains sequences from liver, ovary, stomach, intestine, spleen and pyloric caecae cDNA libraries and the Atlantic salmon EST database contains sequences from liver, head kidney and spleen, hecpidin-like sequences were only detected in spleen and liver cDNA libraries of both fish. Four of 10 135 ESTs (3.0%) in the winter flounder liver library and two of 281 ESTs (0.7%) in the winter flounder spleen library encoded hecpidins. Three of 982 (0.3%) ESTs in the Atlantic salmon liver library encoded hecpidins. Five hecpidin sequences were also found in subtracted spleen (1.8%) and three in subtracted liver (0.6%) Atlantic 15 salmon cDNA libraries that were enriched in transcripts up-regulated during infection with *Aeromonas salmonicida*. Unfortunately, since these are subtracted libraries, the inserts are only portions of the complete transcripts.

Analysis of the nucleotide sequences of Atlantic salmon hecpidin cDNAs 20 revealed that one salmon EST (SL1-0412) was approximately 300 nucleotides longer than the other two. Furthermore, the hecpidin coding sequence was incomplete. Complete sequencing of this clone revealed the presence of two introns with standard GT/AG splice junctions (Fig. 16A). When removed, an open reading frame encoding a complete hecpidin-like peptide was obtained. Similarly, an incompletely spliced 25 halibut transcript was amplified that still retained the second intron (Fig. 16B). Compared to mammals, the introns of salmon and probably halibut are in similar locations but of shorter length (Fig. 16C). In addition to these incompletely spliced cDNAs, we identified a winter flounder EST (WF4) that contains a large deletion relative to the other sequences that corresponded closely to the second exon of salmon and human hecpidin. Assuming the intron positions are conserved among vertebrates, 30 this deletion could correspond to the removal of exon 2, and resulted in a peptide that differed from WF3a and WF3b in only five amino acid positions of the remaining peptide.

Figure 16 describes a Nucleotide sequence of unspliced liver cDNA encoding Type I salmonid hepcidin. Exon sequences are indicated in upper case letters and the deduced amino acid sequence is shown below the nucleotide sequence. The *gt/ag* intron/exon boundaries are highlighted in boldface and the polyadenylation signal (aataaa) is underlined. B. Nucleotide sequence of partially spliced cDNA from halibut spleen encoding Type I salmonid hepcidin. C. Comparison of intron/exon structure in human, mouse and salmon. Exons are represented by hatched boxes and introns by a single line (sizes in bp shown beneath).

10 The deduced amino acid sequences of five different winter flounder hepcidin cDNAs and two different Atlantic salmon hepcidins were aligned for comparison purposes with those extracted from dbEST corresponding to Japanese flounder (two), medaka (one) and rainbow trout (one), as well as the recently reported hepcidin from hybrid striped bass (Shike et al. 2002) and two from Atlantic halibut (Hb 17 and Hb 15 357). The sequences obtained from spleen and liver of Atlantic salmon (Sal2.1 and Sal8.6) and Atlantic halibut (Hb1.1, Hb5.3 and Hb7.5) by PCR are also included (Fig. 17). Human hepcidin was included as a representative of the mammals. The position of cleavage by signal peptidase was predicted by PSORT and the RX(K/R) motif typical of propeptide convertases (Nakayama 1997) was identified (vertical arrows; 20 Fig. 17). The signal peptide sequence is 22-24 amino acids and is highly conserved among all of the fish sequences. The anionic propiece is 38-40 amino acids, depending on the particular hepcidin variant. The processed hepcidins contain 19-27 amino acids and all are positively charged at neutral pH except WF2 (Table 10). Types I and III hepcidin from flatfish as well as salmon type hepcidin contain eight 25 cysteine residues in the mature peptide, which have been proposed to form four disulphide bonds. Type II winter flounder hepcidin is missing two cysteine residues, indicating that a maximum of three disulphide bonds could form. Hb357 contains only five cysteine residues and is quite different from the remaining hepcidin-like sequences. Results of secondary structure prediction methods indicated that the 30 consensus structure of fish hepcidins was mostly random coil, although short stretches of extended strand were predicted by some methods.

Figure 17 describes Alignment of winter flounder (WF1, WF2, WF3a, WF3b, WF4), Atlantic halibut (Hb1.1, Hb5.3, Hb7.5, Hb17, Hb357) and Atlantic salmon

(Sal1, Sal2, Sal2.1, Sal8.6) hepcidins with those of Japanese flounder (JFL4, JFL6), medaka, hybrid striped bass and human. A partial sequence from rainbow trout (GenBank accession AF281354\_1) is also shown. The predicted positions of signal peptidase and pre-protein cleavages are indicated by arrows.

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From Figure 17, it is apparent that all of the flatfish-type hepcidins have very similar signal peptides, which differ somewhat from the salmonid type and human hepcidin. Other novel features identified included different groups of hepcidins based on (1) number of cysteines, (2) unique insertion FKC in flatfish Type III, (3) two other locations that may contain unique insertions (4) a truncated version (Flatfish Type IV), (5) longer versions at the amino terminus.

Based on the alignment, it is apparent that there are at least three different groups of flatfish hepcidins distinguishable by shared insertions and deletions. WF2 and JFL6 (Flatfish Type II) share a deletion of seven amino acids near the KR cleavage site resulting in a processed peptide of 19 amino acids, whereas WF3a, WF3b, WF4, Hb1.1, Hb17, Hb5.3 and Sal8.6 (Flatfish Type III) exhibit a deletion of only four amino acids (excluding the portion corresponding to the missing exon of WF4) resulting in processed peptides of 22 amino acids. WF1 and JFL4 (Flatfish Type I) do not contain this deletion but do contain an insertion relative to all other reported hepcidins at a position adjacent to the signal peptidase cleavage site. In addition, WF1, bass and medaka share an insertion of one amino acid within the mature peptide relative to all other reported hepcidins, giving a peptide of 26-27 amino acids. WF3a and WF3b differ from each other by only one amino acid although they contain several silent substitutions and differences in the 5' and 3' untranslated regions. Hb357 represents a possible fourth class of flatfish hepcidins. The 3' untranslated regions of WF2 and WF1 are very different from those of the other hepcidin transcripts, WF2 containing a long additional portion relative to the others and WF1 being shorter and less highly conserved (Fig. 18A).

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The salmonid hepcidin-like peptides fall into one group; the four reported sequences all share two deletions and differ from each other by four amino acids in the mature peptide and four amino acids in the upstream pre-protein portion. The 3'

untranslated regions of the salmon hepcidins are only moderately conserved (Fig. 18B).

Figure 18 describes Alignment of 3' untranslated regions of (A) winter flounder (WF1, WF2, WF3a, WF3b, WF4) and (B) Atlantic salmon (Sal1, Sal2) hepcidin cDNAs. Conserved nucleotides are boxed. The positions of the primers used to amplify hepcidin homologs from halibut and salmon are indicated by arrows.

### Genomic Organisation of Winter Flounder Hepcidin Genes

Southern hybridization analysis of genomic DNA from a wide variety of fish with a probe corresponding to Type I hepcidin identified bands in all flatfish tested but none of the other fish species (Fig. 19). In winter flounder, two fragments of 4.3 and 4.5 kb hybridized with the probe. Two fragments of yellowtail flounder of identical size hybridized (4.3 kb) and two fragments of witch flounder genomic DNA also hybridized (4.3 and 20 kb), whereas only one fragment (4.3 kb) of the American plaice and one fragment (5.5kb) of the Japanese flounder genomic DNA hybridized.

Figure 19 describes Southern hybridization analysis of hepcidin in different fish species. *SstI* digests of genomic DNA (7.5 µg) from hagfish (Hg), shark (Sh), white sturgeon (St), winter flounder (WF), yellowtail flounder (YF), American plaice (AP), witch flounder (Wi), Japanese flounder (JF), Atlantic salmon (AS), smelt (Sm) and haddock (Hd) were hybridized with Type I hepcidin from winter flounder. Size markers (M) are Lambda DNA digested with *StyI*.

### Identification of Hepcidin-like sequences by RT-PCR

Figure 2 describes amplification of hepcidin cDNAs from halibut and salmon liver and spleen. RNA was prepared from tissues of fish infected with a bacterial pathogen to induce expression of antimicrobial peptide genes, reverse-transcribed and subjected to PCR using the primers listed below. Actin was run as a control to show expression of a house-keeping gene. The labelling on the figure is as follows: HL - halibut liver; SL - salmon liver; HS - halibut spleen; SS - salmon spleen; M - markers. For the primers 5'U is the Universal 5' primer used in all reactions, Sal is Hc Sal (below) and WF is HcPA3b (below).

HepUniversal 5': AAGATGAAGACATTCAGTGTTGCA  
HcPA3 3'B2: GTTGTTGGAGCAGGAATCC  
Hc Sal: TGCTGGCAGGTCCTCAGAATTTGC

5 The results of RT-PCR assays of tissue-specific expression of the three winter flounder hepcidins are shown in Fig. 20. Type I hepcidin was abundantly expressed in the liver and, to a lesser extent, in the cardiac stomach. Type II hepcidin could not be detected in any tissues, whereas Type III hepcidin was moderately expressed in the esophagus, cardiac stomach, and liver.

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In uninfected Atlantic salmon, Type I hepcidin was expressed at quite high levels in the liver, blood and muscle, at low levels in gill and skin, and at barely detectable levels in anterior and posterior kidney (Fig. 21A, Table 10). Type II hepcidin was expressed at barely detectable levels in the gill and skin only (Fig. 21B). However, 15 fish infected with *Aeromonas salmonicida* showed expression of both types of hepcidin in most tissues tested (see below).

RT-PCR analysis of hepcidin gene expression in winter flounder larvae of different ages is shown in Fig. 22. Transcripts of Type II hepcidins could not be detected at any 20 stage of development, whereas Type I and Type III hepcidins were detectable in pre-metamorphic larvae. Type I hepcidin was more abundantly expressed than Type II hepcidin and was also expressed at an earlier time (5 dph vs. 9 dph.).

Figure 20 describes Reverse transcription-PCR assay of hepcidin and actin gene expression in different tissues of winter flounder. Amplification products from adult 25 winter flounder were amplified using gene-specific primers for Flatfish Type I (panel A), Type II (panel B) and Type III (panel C) hepcidins and for actin (310 bp) and resolved by electrophoresis on a 2% agarose gel. Markers (M) are the 100 bp ladder (BRL)

30 Figure 21 describes Reverse transcription-PCR assay of hepcidin and actin gene expression in different tissues of control Atlantic salmon (C) and those infected with *Aeromonas salmonicida* (I). Amplification products from reactions using gene-specific primers for Salmonid Type I (panel A) and Type II (panel B) hepcidins (163

bp) and for actin (400 bp) were resolved by electrophoresis on a 2% agarose gel. Markers (M) are the 100 bp ladder (BRL).

Figure 22 describes Reverse transcription-PCR assay of hepcidin and actin expression in developing winter flounder larvae. Samples were larvae at 5 dph (lane 1), 12 dph (lane 2), 19 dph (lane 3), 27 dph (lane 4), 41 dph (lane 5) and adult (lane 6). Amplification products from reactions using gene-specific primers for Flatfish Type I (panel A), Type II (panel B) and Type III (panel C) hepcidins and for actin (400 bp) were resolved by electrophoresis on a 2% agarose gel using a 100 bp ladder (Pharmacia) as markers (lane M).

### **Identification of additional hepcidin-like sequences from other fish species**

Using a primer based on highly conserved sequences in the signal peptide of all reported hepcidins (Hep Universal 5') in combination with primers based on highly conserved sequences in the 3' UTR of salmon (HcSal 3') and flatfish (HcPA3b 3'), it was possible to amplify hepcidin-like sequences from the liver and spleen of halibut and salmon (Fig. 2). An alignment of the deduced amino acid sequences of hepcidin-like peptides from winter flounder, Atlantic halibut and Atlantic salmon is shown in Fig. 17. Interestingly, flatfish-type hepcidin could be amplified from salmon (S8.6) and salmon-type hepcidin could also be amplified from a flatfish (Hb7.5). Additional sequences were obtained from genomic DNA of Petrale sole, C-O sole, English sole, starry flounder, European plaice, Greenland halibut and Pacific halibut.

Figure 17 depicts an alignment of certain winter flounder (WF1, WF2, WF3a, WF3b, WF4) Atlantic halibut (Hb1.1, Hb5.3, Hb7.5, Hb17, Hb357) and Atlantic salmon (Sal1, Sal2, Sal2.1, Sal8.6) hepcidins with those of Japanese flounder (JFL4, JFL6, medaka, hybrid striped bass and human. A partial sequence from rainbow trout (Genbank Accession AF281354\_1) is also shown. The predicted positions of signal peptidase and pre-protein cleavages are indicated by arrows.

## DISCUSSION

### Pleurocidins

Most antimicrobial peptides, including cecropins and dermaseptins, are encoded by multigene families that have probably arisen by sequential gene duplications. We have demonstrated that the winter flounder, and probably other flatfish, possess a gene family encoding antimicrobial compounds similar to pleurocidin. Comparison of the genomic amplification products obtained using PL1/2 with the cDNA sequence (Fig. 1A) showed that WF2 and WF4 contain three introns, the first of which occurs only 1 bp upstream from the initiator methionine. The second and third introns both occur within the mature peptide. The genes for GLa, xenopsin, levitide and caerulein – all skin peptides from *Xenopus laevis* – also contain an intron 1 bp upstream from the initiator methionine (Kuchler et al 1989). The intron positions are conserved in all but WF3 (Fig. 6), but they differ dramatically in size (Table 5), indicating that a considerable period of evolutionary time has elapsed since the duplication events occurred, or that the intron sequences are relatively free to drift.

Southern analysis shows that WF1-4 probes hybridise to other flatfish DNAs, including yellowtail flounder, Atlantic halibut and American plaice, but not to haddock, smelt or pollock. This hybridisation could be due to the highly conserved signal sequence and anionic portion which we have shown to be conserved in sequences isolated from these flatfish. Flatfish may provide a rich reservoir of potential therapeutants for the aquaculture industry. The probes for the different pleurocidin family members often recognise the same restriction fragments in winter flounder DNA, indicating that they may be clustered at a single locus on the genome. Complete sequencing of two Lambda clones hybridizing to pleurocidin confirms that such clustering does in fact occur (Fig. 11). Clustering of antimicrobial peptide genes has also been noted for insect cecropins (Gudmundson et al. 1991) and apidaecins (Casteels-Jossen et al. 1993), among others.

Figure 11 describes an embodiment of a Schematic of genomic organization of pleurocidin-like genes and pseudogenes ( $\psi$ ) from winter flounder. Introns are represented by solid boxes and exons by stippled boxes.

All of the members of the pleurocidin family are encoded as prepropeptides consisting of an amino-terminal signal sequence followed by the active peptide and ending with an acidic portion. The deduced amino acid sequences of the signal and acidic sequences are very highly conserved whereas those of the predicted mature antimicrobial peptides are more variable (Fig. 6). All, however, appear to fold into amphipathic  $\alpha$ -helices. This sequence conservation has allowed us to use a genomic approach to identify many different members of the pleurocidin gene family, not only from winter flounder but also from a variety of other flatfish (Fig. 3, Table 4, Appendix I).

The structure of the pleurocidin prepro polypeptides bears certain resemblances to the frog dermaseptin precursors, which also contain a signal sequence of similar length (22 amino acids) and an acidic portion of 16-25 amino acids. From the full-length cDNA clone (Fig. 1A), the acidic portion of pleurocidin was shown to contain 21 residues. A major difference between the pleurocidin and dermaseptin prepropeptides is the position of the acidic portion – downstream of the mature peptide in pleurocidin and upstream of the mature peptide in dermaseptins. The acidic propeptides of defensins have been proposed to prevent interaction of the antimicrobial peptide with the membrane by neutralising the cationic charges (Valore et al. 1996) and this may also be its function in pleurocidin. This feature can be of practical significance for delivering peptides that are inactive until specifically cleaved.

The signal sequences and acidic carboxy-terminal sequences of the pleurocidin family members are extremely highly conserved. The former, and possibly the latter, are presumed to target the precursor molecules to the cell membrane for secretion. Gene families for antimicrobial peptides that contain highly conserved signal peptides (often encoded by the first exon) followed by end products with different biological activities have been described from the dermaseptin family (Valore et al. 1996) and the GLa, xenopsin, levitide and caerulein, all of which are skin peptides from *Xenopus laevis* (Kuchler et al. 1989). These authors proposed that this modular gene structure allows targeting for secretion to be achieved for markedly different peptides using a common pathway. In the pleurocidin gene family, a modular structure is also present with exon 2 encoding the signal sequence and first

half of the antimicrobial peptide, exon 3 encoding the next ten amino acids of the antimicrobial peptide, and exon 4 encoding the last three amino acids of the antimicrobial peptide and the acidic carboxy terminus.

5           The mature peptides encoded by WF2 and WF4 are 60% identical to each other (Fig. 6) and somewhat less similar to dermaseptin B1 and ceratotoxin B (Cole et al. 1997). WF1 is 64% identical to WF1a but contains a remarkably cationic stretch of 18 amino acids between the signal sequence and the mature peptide that is not present  
10 pleurocidin WF1 processing occurs remains to be determined. Both WF1 and WF1a contain an additional 10-11 amino acids relative WF2, WF3 and WF4 between the mature peptide and the acidic carboxy terminus. WF3 shares similarities with both WF2/4 and WF1/1a. Synthetic pleurocidin identical to the central portion of WF2 has been shown to protect Coho salmon against infection by *Vibrio anguillarum*, as have  
15 hybrid peptides based on pleurocidin, dermaseptin and ceratotoxin (Jia et al. 2000).

          The tissue-specific expression of the pleurocidin genes was assessed using northern blot analysis and RT-PCR. Northern analysis proved to be not sufficiently sensitive for detecting the low level of transcripts present in winter flounder mRNA. Transcripts were present only in skin in sufficient quantities to be detected by this  
20 method, so the more sensitive RT-PCR assay was used. Pleurocidin transcripts were found in both skin and intestine using this method, in agreement with the recently reported ultrastructural localisation of pleurocidin in these tissues (Cole, Darouiche et al. 2000) and supporting the role of pleurocidin in mucosal immunity. The transcript size (approximately 200 bp) is consistent with the size of products obtained by RT-  
25 PCR (Table 7), showing that the pleurocidin genes are transcribed separately.

          RT-PCR analysis showed that the genes for the different pleurocidin-like peptides are expressed in a tissue-specific manner with WF2 being expressed predominantly in the skin and gill and to a lesser extent in the muscle, intestine,  
30 stomach and liver whereas WF1 and WF4 are detected predominantly in the gill and skin (Fig. 7). WF3 and WFYT are expressed in most of the tissues sampled, WFX is detected solely in the skin and WF1a was not expressed in any of the tissues sampled. Possibly, the different antimicrobial peptides are required to control the growth of different bacterial populations in the two tissues. Since no RT-PCR products were

detected for WF4, it is possible that this gene is expressed only at low levels in adult skin or intestine or that it is expressed at a different life stage or in a different tissue.

Using primers that did not discriminate between the transcripts of the various pleurocidin-like genes, expression was first detected at 5 dph and showed a progressive increase towards adulthood. However, recent experiments using primers specific for WF1, WF1a, WF2, WF3, WF4, WFX and WFYT, transcripts were detected at different developmental stages (Fig. 9). WFX was only detectable at 20 dph, whereas WFYT, WF3 and WF2 were detectable at 5 dph and at higher levels between 25-36 dph. Interestingly, WF1 was not detectable at any larval stage and may only be expressed under specific environmental conditions in response to specific bacterial pathogens, as has been shown for *Drosophila* (Rivas and Ganz 1999). This is the first demonstration of developmental expression of an antimicrobial peptide in fish and shows that at least this component of innate immunity is present in early larval stages of winter flounder. Larval mortality prior to metamorphosis is of great concern and although the reasons for such mortality are not yet known, high bacterial load in the gut has been proposed (Padros, Minkoff et al. 1993). The adaptive immune systems of flatfish have been shown to develop later than those of other teleosts (Padros, Sala et al. 1991). Thus, the ability of larvae to produce antimicrobial peptides during this period may be crucial to survival, and the identification of factors that increase the production of such compounds would be of great benefit to aquaculturalists.

These results of testing synthetic peptides against a variety of bacterial pathogens as well as the fungal pathogen, *Candida albicans*, show promising candidates with broad-spectrum antimicrobial activities. Of particular interest is the ability of the peptides NRC-13 and NRC-15 to inhibit the growth of methicillin-resistant *S. aureus* at concentrations as low as 4 µg/ml. NRC-13 is also capable of inhibiting the growth of *C. albicans* at 4 µg/ml, *P. aeruginosa* at 1 µg/ml (and killing *P. aeruginosa* at this concentration), and *A. salmonicida* at 2 µg/ml. This means that NRC-13 is highly active against a fish pathogen, a Gram-negative human bacterium, a drug-resistant Gram-positive human bacterium, and a yeast. The example of NRC-13 demonstrates the range of potential targets and applications for cationic antimicrobial peptides.

These results also validate the process we used for selecting antimicrobially active peptides from a large amount of sequence data. The ability to accurately predict which peptides are likely to be active is a crucial link between genomics and therapeutics. While much work remains to be done in this area, we have clearly demonstrated that judicious application of the principles described earlier will aid in selecting active peptides.

Thus, a variety of cDNA and genomic sequences encoding the precursors of antimicrobial peptides identical to or similar to pleurocidin from a variety of flatfish species have been isolated. Northern hybridisation and sequence analysis of RT-PCR products showed that expression was tissue-specific. Most importantly, the timing of expression of different pleurocidin variants in developing larval winter flounder was determined, allowing an estimate of the onset of the innate immune system in this fish. These assays of pleurocidin expression are useful in directing the screening strategy for isolating novel peptide sequences expressed during specific tissues and/or developmental stages. Environmental parameters affecting the production of pleurocidin can also be assayed.

This work paves the way to further studies aimed at the over-expression of pleurocidin as a therapeutant for aquacultured fish and the production of disease-resistant fish through transgenic technology as has been demonstrated in transgenic tobacco expressing antimicrobial peptides (Jach et al. 1995) and proposed for fish (Jia et al. 2000). Furthermore, because many fish live in a saline environment, the properties of their antimicrobial peptides may be different from those produced by terrestrial animals and have application in unique situations. For instance, the pulmonary mucosa of patients with cystic fibrosis contain elevated NaCl concentrations, which inhibit the natural cationic peptides secreted by the lung (Goldman et al. 1997). Salt-adapted cationic peptides from marine fish may have application in the treatment of lung infections in these patients.

## Hepcidins

Sequence analysis of one salmon EST (SL1-0412) and one halibut clone (Hb7.5), revealed the presence of unspliced transcripts and allowed the positions of some of the introns to be determined (Fig. 16). Similar to mouse, human and hybrid striped bass, the salmon hepcidin is composed of three exons and two introns (Park, Valore et al. 2001; Shike et al. 2002; Pigeon, Ilyin et al. 2001). The position of the first intron of salmon and bass are identical and correspond to a position two amino acids 5' to those of mouse and human. However, the second salmon intron and the second halibut intron of Hb7.5 correspond to a position two amino acids 3' to those of mouse and human and several amino acids 5' to that of the bass. This is probably due to "intron sliding" whereby the positions of introns have shifted by several nucleotides over the course of evolution. Interestingly, the deletion in WF4 corresponds precisely to the position of the first salmon intron and the second mouse/human intron, indicating an intermediate intron/exon structure.

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Mouse contains two hepcidin genes that are clustered on the genome (Pigeon, Ilyin et al. 2001) but in human (Park, Valore et al. 2001) and striped bass (Shike et al. 2002) only one hepcidin gene has been identified. Although the number of hepcidin genes in winter flounder and Atlantic salmon remains to be determined, there are at least five in winter flounder, five in Atlantic halibut and four in Atlantic salmon. Since there are no *Sst*I sites within the hepcidin probe used in the Southern hybridization analysis, it is highly probable that the five winter flounder hepcidin genes reported here are clustered on two genomic fragments. Multiple genes for pleurocidin also exist (Douglas, Gallant et al. 2001) and are clustered on the genome (Fig. 11). Interestingly, all of the small flounders tested from the Atlantic exhibited a similar hybridizing band of 4.3 kb, indicating that they share similarity at the genomic level. Japanese flounder, found in the Pacific, exhibited a single hybridizing band of 5.5 kb.

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The deduced amino acid sequences of the fish prepro-hepcidins can be aligned with those from mammals throughout their length but only show high similarity in the portion corresponding to the processed peptides (Fig. 17). However, within the fish, the signal peptide and the propeptide are also very highly conserved. Conservation of

these segments has also been noted in the pleurocidin family (Douglas, Gallant et al. 2001). The amino-termini of the processed peptides were assigned based on the amino acid sequence of human hepcidin (Krause, Neitz et al. 2000; Park, Valore et al. 2001) and the proximity to the RX(K/R)R motif characteristic of processing sites  
5 (Nakayama 1997). The molecular weights of the processed hepcidins from winter flounder and Atlantic salmon range from 1992 Da (WF2) to 3066 (WF1), comparable to hepcidins isolated from mouse, human and bass. With the exception of WF2, which has an acidic pI (5.54), the pIs of hepcidins are between 7.73 and 8.76.

10 Like pleurocidins, the amino acid sequences of the hepcidin variants are highly similar within species, suggesting relatively recent duplication of an ancestral gene. It is possible that the aquatic environment in which fish live necessitates the existence of a more diverse suite of antimicrobial peptides than in terrestrial mammals. In addition, this component of the innate immune system plays a more  
15 major role in fish than in mammals, which have a more highly evolved adaptive immune system.

The human hepcidin molecule has been proposed to form a secondary structure containing a series of  $\beta$ -turns, loops and distorted  $\beta$ -sheets (Park, Valore et al. 2001). Consensus secondary structure prediction of fish hepcidins show that they  
20 contain mostly random coil structure with some extended strand structure. With the exception of WF2, JFL6 and Hb357, all hepcidins reported thus far contain eight cysteine residues which are proposed to form four disulphide bonds (Krause, Neitz et al. 2000; Park, Valore et al. 2001) in the following linkage pattern: 1-4, 2-8, 3-7, 5-6  
25 (Park, Valore et al. 2001). The loss of cysteine residues 1 and 3 from WF2 suggests that at least one disulphide bond cannot form.

Using gene-specific primers, we were able to demonstrate that different hepcidin genes are expressed in different tissues of both winter flounder (Fig. 20) and  
30 Atlantic salmon (Fig. 21). In Atlantic salmon, hepcidin was detectable in normal uninfected fish predominantly in liver, blood and muscle (Type I) and to a lesser extent in gill and skin (both types). This is consistent with the presence of three ESTs for Type I hepcidin in cDNA libraries constructed from uninfected livers, and the absence of ESTs for Type II hepcidin in cDNA libraries constructed from uninfected

liver, spleen and head kidney. Type II hepcidin expression appears to be confined to external epithelial surfaces in contact with the aqueous environment, whereas Type I hepcidin expression is more widespread, being expressed in liver, blood and muscle as well as external epithelial surfaces. In uninfected winter flounder, no transcripts of Type II hepcidin could be detected in any tissue but transcripts of Types I and III hepcidin were present in the liver and cardiac stomach. Type III hepcidin transcripts were also present in the esophagus.

Mouse hepcidin was also reported to be predominantly expressed in liver, and weakly in stomach, intestine, colon, lungs, heart and thymus by Northern analysis using one of the mouse hepcidin sequences as probe (Pigeon, Ilyin et al. 2001). However, this study did not discriminate between the two hepcidin genes and it is not known whether or not the two mouse genes are differentially expressed in tissues of mouse. Similarly, dot-blot analysis of human tissues and cell lines using the human hepcidin cDNA as probe revealed strong expression in adult and fetal liver and weaker expression in adult heart, fetal heart and adult spinal cord (Pigeon, Ilyin et al. 2001). An earlier study using RealTime quantitative RT-PCR (Krause, Neitz et al. 2000) revealed strong expression of hepcidin in human liver, heart and brain and weak expression in a variety of other tissues. Interestingly, we could not detect either Type I or Type II hepcidin expression in the brain of normal Atlantic salmon or winter flounder, or heart of normal Atlantic salmon. However, in infected animals, Type II hepcidin was expressed in both tissues, indicating that this form is the predominant one produced under conditions of stress.

It is intriguing that we detected transcripts of Type I hepcidin that were constitutively expressed in blood cells of Atlantic salmon. Constitutively expressed non-enzymic antimicrobial molecules have been reported only rarely in blood of fish; a small hydrophobic cationic peptide was found in mucus of rainbow trout (Smith et al., 2000) and moronecidin, an antimicrobial peptide from bass, was expressed in blood of uninfected animals (Lauth et al. 2002). Interestingly, expression of neither hepcidin increased in blood of infected salmon relative to the uninfected control animals. Possibly, hepcidin is fulfilling a role in iron homeostasis in control animals as well as an antimicrobial role. Its presence in circulating blood cells of uninfected animals may be a precautionary measure against impending infection.

Type I and II hepcidins from Atlantic salmon were up-regulated during infection with *Aeromonas salmonicida*, but to different extents in various tissues. While Type I hepcidin was noticeably up-regulated in the esophagus, stomach, pyloric caecae, liver, spleen, intestine, posterior kidney, rectum and muscle and to a lesser extent in anterior kidney and skin, Type II hepcidin showed a more dramatic increase in stomach, pyloric caecae, liver, spleen, intestine, brain, heart and muscle. Weaker up-regulation was present in esophagus, anterior and posterior kidney, skin and rectum. These results are consistent with those reported for bacterially challenged hybrid striped bass where up-regulation was most dramatic in liver, but was also demonstrated in skin, gill, intestine, spleen, anterior kidney and blood (Shike et al. 2002). It is not known whether there are multiple hepcidins in hybrid striped bass and, if so, whether they are differentially expressed as in Atlantic salmon and winter flounder.

Studies with mice have shown a 4.3-fold increase in hepcidin expression in livers of mice injected with LPS and a 7-fold increase in primary hepatocytes exposed to LPS (Pigeon, Ilyin et al. 2001). These studies were based on Northern analysis using only one of the mouse hepcidin sequences as probe, and were therefore unable to distinguish possible differential expression of the two mouse variants. Similar increases were noted in livers of mice subjected to iron overload, but not for primary hepatocytes exposed to iron citrate, possibly due to the differentiation status of the cultured hepatocytes. The fact that both iron overload and LPS exposure increase hepcidin expression indicates the importance of these two factors in the host response to pathogens.

During infection, iron is removed from the system by various mechanisms so that it is unavailable for use by invading pathogens. It has been proposed that recently discovered transferrin receptor2 mediates iron uptake by hepatocytes and increases their expression of hepcidin (Fleming and Sly 2001; Nicolas, Bennoun et al. 2001). Hepcidin, in turn, increases iron accumulation in macrophages and increases dietary iron absorption in duodenal crypt cells via  $\beta$ 2 microglobulin, HFE and transferrin receptor1. These crypt cells differentiate into enterocytes with reduced amounts of iron transport proteins, thereby decreasing dietary iron uptake. Hepcidin thus appears to play a crucial role in iron homeostasis during inflammation as well as acting as an

antimicrobial peptide. It is also possible that hepcidin could modulate expression of liver-derived acute phase proteins and exhibit synergistic effects with other components of the immune system.

5 Antimicrobial peptides have been shown to modulate gene expression in mouse macrophages (Scott, Rosenberger et al. 2000), and it is possible that they may exert similar effects in fish macrophages or hepatocytes. The presence of a functional nuclear localization signal (four K/R residues in a row) within prohepcidin of mouse and human indicates that hepcidin could act as a signaling molecule involved in  
10 maintenance of iron homeostasis in these organisms (Pigeon, Ilyin et al. 2001). Interestingly, the nuclear localization signal also contains the recognition signal for processing of prohepcidin, indicating that nuclear localization would occur only prior to removal of the propeptide, or that the propeptide itself is localized to the nucleus. Teleost hepcidins contain only 3 out of 4 K/R residues, which may not be sufficient  
15 for nuclear localization; a role for hepcidin in intracellular signaling awaits testing with synthetic or *in vitro*-expressed peptide.

In conclusion, the sequences of new hepcidin-like peptides from different fish species and the presence of related sequences in several flatfish species by Southern  
20 hybridization have been determined. Furthermore, it has been shown that the various types of fish hepcidins are differentially expressed in a tissue-specific manner in normal fish, as a result of bacterial infection, and during larval development, thus providing a strategy for identifying additional sequences for novel peptides. Apparently in fish, different tissues produce hepcidins in a constitutive or inducible  
25 manner, indicating that hepcidin variants may have different functions under different circumstances. Given their role in iron homeostasis in mammals, it is possible that fish hepcidin variants may fulfill this role as well as that of killing specific pathogens. *In vitro* expression of hepcidin variants will allow their spectrum of antimicrobial activity to be determined as well as their effect on the innate immune response.

30 Thus, there has been provided a method for identifying potential antimicrobial peptides.

## Tables

- Table 1. Nucleotide sequences of oligonucleotides used for isolating pleurocidin-like sequences
- 5 Table 2. Nucleotide sequences of oligonucleotides used for assay of pleurocidin-like gene expression in different tissues and at different stages of development of winter flounder
- Table 3. Nucleotide sequences of primers used in RT-PCR assays to analyse hepcidin gene expression. The amino acid sequence on which the 5' primer was based is
- 10 shown. The 3' primers were within the 3' untranslated region (3' UTR). The annealing temperatures used in the PCR reactions and the sizes of the amplification products are listed.
- Table 4. One-letter amino acid sequences for pleurocidins based on genomic and expression data
- 15 Table 4a. Bacterial and *Candida* strains used in this study
- Table 5. Sizes of introns (in bp) in genomic sequences amplified using primers PL5' and PL3'
- Table 6. RT-PCR products from skin and intestine corresponding to different pleurocidin genes
- 20 Table 7. Sizes of bands (in kb) hybridising to pleurocidin probes in *Bam*HI and *Sst*I digests of winter flounder DNA
- Table 8. Minimal inhibitory concentrations of pleurocidin-like cationic antimicrobial peptides against a wide spectrum of bacterial pathogens and *Candida albicans*.
- Table 9. Characteristics of winter flounder and Atlantic salmon hepcidin-like peptides
- 25 Table 10. Results of PCR analysis of hepcidin expression
- Table 11. One-letter amino acid sequences for certain hepcidins based on genomic and expression data, including NRC reference numbers
- Table 12. Nucleotide sequences corresponding to amino acid sequences listed in Tables 11 and 13
- 30 Table 13 One-letter amino acid sequences for certain hepcidins based on genomic and expression data, including clone names

## *Appendices*

### APPENDIX I. NUCLEOTIDE SEQUENCES OF PLEUROCIDIN-LIKE GENES AND CDNAS REFERRED TO IN TABLE 4.

Appendix II. Nucleotide sequences of hepcidin-like genes and cDNAs referred to in  
5 Table 11.

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The mention of a reference is not an admission or suggestion that it is relevant to the patentability of anything disclosed herein.

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Table 1. Nucleotide sequences of oligonucleotides used for isolating pleurocidin-like sequences

Primer	Amino Acid Sequence	Nucleotide Sequence (5' ⇒ 3')
<i>Screening cDNA library</i>		
PleuroA	FFKKAHVGHK	TTCTTCAAGAAGGCGCYCAYGT[C/G]GG [C/A]AAGCA
PleuroB	HVGKAALTHYL <sup>1</sup>	CAYGT[C/G]GG[C/A]AAGGCGCYCT[C/G] AA[C/T/A]CAYTACCT
<i>Genomic PCR and RT-PCR</i>		
PL1	5' untranslated	GCCCACTTTGTATTCGCAAG
PL2	3' untranslated	CTGAAGGCTCCTTCAAGGCG
PL5'	MKFTATF	ATGAAGTTCCTGACCCTTC
PL3'	KRAVDE <sup>1</sup>	TCATCGACTGCGCGCTT

<sup>1</sup>complement

Table 2. Nucleotide sequences of oligonucleotides used for assay of pleurocidin-like gene expression in different tissues and at different stages of development of winter flounder

Gene	Primer	Amino Acid Sequence	Nucleotide Sequence (5' ⇒ 3')
WF1	RTWF1	KGRWLER	AAGGGCAGGTGGTTGGAAAGG
	RTWF1/3'	YQEGEE <sup>1</sup>	CCCTCCCCCTCCTGGTA
WF1a	RTWF1a	RKRKWLK	CGTAAGAGAAAGTGGTTGAGA
	RTWF1a/3'	YQEGEE <sup>1</sup>	CCCTCCCCCTCCTGGTA
WF2	RTWF2	KAAHVG	AAGGCTGCTCACGTTGGC
	PL2	3' untranslated	CTGAAGGCTCCTTCAAGGCG
WF3	RTWF3	FLGALIK	TTCTTAGGAGCCCTTATCAAA
	RTWF3/3'	YDEQQE <sup>1</sup>	CTCCTGCTGCTCGTCATA
WF4	RTWF4	HGRHAA	CATGGTCGTCATGCTGCC
	PL2	3' untranslated	CTGAAGGCTCCTTCAAGGCG
WFYT	RTWFYT	GFLFHG	GGGATTTCTTTTTCATGG
	RTWFYT/3'	SFDDNP <sup>1</sup>	GGGTTGTCATCGAATGAG
WFX	RTWFX	RSTEDI	CGTTCTACAGAGGACATC
	RTWFX/3'	DDDDSP <sup>1</sup>	GGGGCTGTCATCATCATC

Table 3. Nucleotide sequences of primers used in RT-PCR assays to analyse hepcidin gene expression. The amino acid sequence on which the 5' primer was based is shown. The 3' primers were within the 3' untranslated region (3' UTR). The annealing temperatures used in the PCR reactions and the sizes of the amplification products are listed.

Type	Primer Product	Amino acid sequence	Nucleotide sequence (5'⇒3')	Annealing temperature	size
<i>Winter flounder</i>					
Type I	HcPA1 5' 137 HcPA1b 3'	WMENPT 3'UTR	TGGATGGAGAATCCCACC GTGAGGTTGTGTTGCGGG	50°C	
Type II	HcPA2 5' 180 HcPA2b 3'	GMMPNN 3' UTR	GGGATGATGCCAAACAAC ACTTGGACTATGGGCTGAG	50°C	
Type III	HcPA3 5' 118 HcPA3b 3'	WMMPNN 3' UTR	TGGATGATGCCATACAAC GTTGTTGGAGCAGGAATCC	50°C	
Actin	ActF (WF) 312	AALVVD	TCGCTGCCCTCGTTGTTGAC	50°C	
	ActR (WF)*	VLLTEAP*	GGAGCCTCGGTCAGCAGGA		
	ActinF1 194 Actin R1	VFPSIV HTFYNEL	GTGTTCCATCCATCGTC GAGCTCGTTGTAGAAGGTGT	50°C	
<i>Atlantic salmon</i>					
Type I	HCSS 5' 163 Hep Liv R	MHLPEP 3' UTR	ATGCATCTGCCGGAGCCT CATTGCAAACATGTACAAACTAG	55°C	
Type II	Hep Sp F 163 Hep Sp R	MNLPMH 3' UTR	ATGAATCTGCCGATGCA GGGCAAATTAAGGCG	52°C	
Actin	Act400F 400	IVGRPRHQ	TCGTCCGGTCGTCCCAGGCATCAG	52°C	
	Act400R	GYALPHAI	ATGGCGTGGGGCAGAGCGTAACC		

\* complement

Table 4. Sequences of pleurocidin-like peptides used for activity testing. Final peptide sequences and patterns of C-terminal amidation were selected based on the analysis of translated nucleotide sequences and on principles described in the text.

Origin	Amino acid sequence	Code
Winter Flounder (1)	GKGRWLERIGKAGGIIIGGALDHL-NH <sub>2</sub>	NRC-01 <sup>a</sup>
Winter Flounder (1a)	WLRRIIGKGVKIIGGAALDHL-NH <sub>2</sub>	NRC-02 <sup>a,d</sup>
Winter Flounder (1a-l)	GRRKRKWLRRIGKGVKIIGGAALDHL-NH <sub>2</sub>	NRC-03 <sup>a,d</sup>
Winter Flounder (2) 2.1	GWGSFFKKAHVGVKGVKAAALHLYL-NH <sub>2</sub>	NRC-04 <sup>a</sup>
Winter Flounder (3)	FLGALIKGAIHGGRFIHGMIQNHH-NH <sub>2</sub>	NRC-05 <sup>a</sup>
Winter Flounder (4) 1.1	GWGSIFKHGRHAAKHI GHAAVNHYL-NH <sub>2</sub>	NRC-06 <sup>a</sup>
Yellowtail Flounder YT2	RWGKWFKKATHVGVKGVKAAALHLYL-NH <sub>2</sub>	NRC-07 <sup>b</sup>
Winter Flounder X	RSTEDIKSI SGGFLNAMNA-NH <sub>2</sub>	NRC-08 <sup>b,c</sup>
Winter Flounder Y	FFRLLFHGVHGGYLNAA-NH <sub>2</sub>	NRC-09 <sup>b,c</sup>
Winter Flounder Z	FFRLLFHGVHGVKIKPRA-NH <sub>2</sub>	NRC-10 <sup>b,c</sup>
American Plaice AP1	GWKSVFRKAKKVKTVGGLALDHYL-NH <sub>2</sub>	NRC-11 <sup>b</sup>
American Plaice AP2	GWKKWFNRKAKKVKTVGGLAVDHYL-NH <sub>2</sub>	NRC-12 <sup>b</sup>
American Plaice AP3	GWRTLLKKAQEVKTVGKLALKHYL-NH <sub>2</sub>	NRC-13 <sup>b</sup>
Witch Flounder GcSc4C5	AGWGSIFKHI FKAGKFIHGAI QAHND-NH <sub>2</sub>	NRC-14 <sup>b</sup>
Witch Flounder GcSc4B7	GFWGLFELGLHGI GLLHLL-NH <sub>2</sub>	NRC-15 <sup>b</sup>
Witch Flounder GC3.8-t	GWKKWLRKGAKHLGQAAIK-NH <sub>2</sub>	NRC-16 <sup>b</sup>
Witch Flounder GC3.8	GWKKWLRKGAKHLGQAAIKGLIAS	NRC-17 <sup>b</sup>
Witch Flounder GC3.2	GWKKWFTKGERLSQRHFA	NRC-18 <sup>b</sup>
Halibut Hb26	FLGLLFHGVHVVGVKWIHGLIHGHH-NH <sub>2</sub>	NRC-19 <sup>b</sup>
Halibut Hb18	GFLGILFHGVHVGKRLHMHNSERRS	NRC-20 <sup>b</sup>

<sup>a</sup> Peptide predicted from expressed tag and/or expression confirmed by RT-PCR and/or by *in situ* hybridization.

<sup>b</sup> Peptide predicted from genomic sequence

<sup>c</sup> Pseudogenes

<sup>d</sup> NRC-2 and NRC-3 are both derived from the same sequences with the latter including an additional N-terminal fragment.

Table 4a. Bacterial and *Candida* strains used in this study.

Species	Code ID	Comments
<i>Escherichia coli</i>	C498, UB1005	Parent of DC2
<i>Escherichia coli</i>	C500, DC2	Outer membrane-permeable mutant
<i>Escherichia coli</i>	C786, CGSC4908	Triple auxotroph (thy, uri, L-his)
<i>Salmonella enterica</i> s. Typhimurium	C587, 14028S	Parent of C610
<i>Salmonella enterica</i> s. Typhimurium	C610, MS4252S	Supersusceptible strain
<i>Pseudomonas aeruginosa</i>	H187, K799	Parent of H188
<i>Pseudomonas aeruginosa</i>	H188, Z61	Supersusceptible strain
<i>Enterococcus faecalis</i>	C625, ATCC29212	Standard strain (ATCC)
<i>Staphylococcus aureus</i>	C622, ATCC25923	Standard strain (ATCC)
<i>Staphylococcus aureus</i>	C623, SAP017	<u>MRSA</u> clinical isolate (from Tony Chow – VGH)
<i>Staphylococcus epidermidis</i>	C960, ATCC14990	Standard strain (ATCC)
<i>Staphylococcus epidermidis</i>	C621	Clinical isolate (from David Speert – Children's)
<i>Bacillus subtilis</i>	C971, ATCC6633	Standard strain (ATCC)
<i>Aeromonas salmonicida</i>	99-1, A449	Field isolate being sequenced at IMB
<i>Aeromonas salmonicida</i>	<u>97-4</u>	Field isolate
<i>Candida albicans</i>	C627, CALB105	Yeast test strain

Table 5. Sizes of introns (in bp) in genomic sequences amplified using primers PL5' and PL3'

Gene	Exon 1 Total	Intron 1	Exon 2	Intron 2	Exon3	
WF1	154	539	31	95	82	901
WF1a <sup>1</sup>	103	?	31	?	82	?
WF2 <sup>2</sup>	100	525	31	108	49	813
WF3	100	374	19	97	64	654
WF4 <sup>2</sup>	100	230	31	101	49	
	511					

<sup>1</sup>Intron sizes could not be determined as this sequence is only represented by an RT-PCR product

<sup>2</sup>Sequences were also amplified using primer PL1 and PL2

Table 6. RT-PCR products from skin and intestine corresponding to different pleurocidin genes

Skin Band	Intestine	Size	
4	n/d <sup>1</sup>	265bp	
WF1			
5	2	175bp	
WF2			
4	9	175bp	
WF3			
n/d <sup>1</sup>	n/d <sup>1</sup>	-	
WF4			
n/d <sup>1</sup>	7	215bp	n/d <sup>2</sup>

<sup>1</sup>not detected

<sup>2</sup>not detected by genomic PCR (corresponds to WF1a)

Table 7. Sizes of bands (in kb) hybridising to pleurocidin probes in *Bam*HI and *Sst*I digests of winter flounder DNA

Probe	<i>Bam</i> HI	<i>Sst</i> I
WF1	>24, 6	19, 17, 4.5, 4.4, 3.0, 2.9, 2.2, 1.3,
	x	
WF2	6	19, 17, 4.5, 4.4, 2.9, x 1.3,
	x	
WF3	>24	19, 17, 4.5, x 2.9, x 2.2, 1.3, x
WF4	17, 6	19, 17, 4.5, 4.4, 2.9, x 2.2, 1.3, 1.2

x=no hybridising band evident

Table 8. Minimal inhibitory concentrations of pleurocidin-like cationic antimicrobial peptides against a wide spectrum of bacterial pathogen and *Candida albicans*. Pathogens were grown in Mueller-Hinton broth and exposed to a range of concentrations of the

	<i>A.sal</i> 99-1	<i>A.sal</i> 97-4	<i>S.typh</i> MS4252	<i>S.typh</i> 14028s	<i>P.aeru</i> K799	<i>P.aeru</i> Z61	<i>E.coli</i> C786	<i>E.coli</i> UB1005	<i>E.coli</i> DC2	<i>S.epi</i> C621	MRSA C623	C.alb C627
NRC-1	64	64	16	>64	>64	32	32	32	32	>64	>64	64
NRC-2	>128	128	64	>64	64	32	64	64	64	>64	>64	>64
NRC-3	2	4	2	8	2	1	2	8	2	8	8	4
NRC-4	2	2	2	16	8	4	2	4	2	8	8	8
NRC-5	>64	>64	64	>64	>64	32	64	64	>64	32	32	>64
NRC-6	4	4	4	64	16	4	4	4	2	>64	32	32
NRC-7	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
NRC-8	>64	>64	>64	>64	>64	>64	>64	>64	>64	>64	>64	>64
NRC-9	>64	>64	64	>64	>64	64	64	>64	>64	>64	>64	>64
NRC-10	>64	32	16	>64	32	8	32	32	32	32	64	>64
NRC-11	8	8	4	32	32	4	4	16	4	64	>64	32
NRC-12	2	2	2	8	4	1	2	8	2	8	16	4
NRC-13	4	2	2	8	4	1	2	4	2	4	4	4
NRC-14	32	16	16	>64	32	8	16	16	16	16	16	>64
NRC-15	8	16	4	16	8	4	8	8	8	4	4	16
NRC-16	2	1	0.5	16	4	1	1	2	0.5	16	32	8
NRC-17	2	1	1	8	4	2	1	4	1	32	16	8
NRC-18	>64	128	32	>64	>64	64	64	64	64	>64	>64	>64
NRC-19	64	>64	16	64	32	8	32	16	32	8	8	64
NRC-20	>64	>64	>64	>64	>64	64	>64	>64	>64	>64	>64	>64

specified peptide. The lowest peptide concentration which inhibited bacterial growth by at least 50% was recorded as the minimal inhibitory concentration.

Table 9. Characteristics of winter flounder and Atlantic salmon hepcidin-like peptides

Name	Total Amino Acids	Total Cysteines	Molecular Weight	pI
WF1	27 8.75	8	3066	
WF2	19	6	1992	5.54
WF3	22	8	2367	8.74
WF4	22	8	2256	8.52
Hb5.3	22	8	2363	8.75
Sal8.6	22	8	2331	8.76
Hb17	22	8	2391	8.76
Hb1.1	22	8	2391	8.76
Hb357	22	5	2397	7.84
Hb7.5	25	8	2881	8.53
Sal2.1	25	7	2925	8.60
Sal1	25	8	2720	7.73
Sal2	25 8.53	8	2881	

Table 10. Semi-quantitative RT-PCR analysis of hepcidin expression in Atlantic salmon during bacterial challenge

Tissue	Type I Hepcidin			Type II Hepcidin		
	Control	Infected	Ratio	Control	Infected	Ratio
Esophagus	nd	0.08	↑	nd	0.09	↑
Stomach	nd	0.09	↑	nd	0.27	↑↑
Pyloric caecae	nd	0.14	↑	nd	0.37	↑↑
Liver	1.19	2.36	2	nd	1.45	↑↑↑
Spleen	nd	0.18	↑	nd	0.41	↑↑
Intestine	nd	0.21	↑	nd	0.33	↑↑
Brain	nd	nd	0	nd	0.50	↑↑
Blood	0.82	0.84	1	nd	nd	~
Anterior kidney	0.06	0.07	1.2	nd	0.08	↑
Posterior kidney	0.07	0.14	2	nd	0.11	↑
Gill	0.13	0.12	1	0.08	0.07	1
Skin	0.14	0.18	1.3	0.07	0.09	1.3
Ovary	nd	nd	0	nd	nd	0
Rectum	0.07	0.13	2	nd	0.08	↑
Heart	nd	nd	0	nd	0.43	↑↑
Muscle	0.38	0.8	2.1	nd	0.60	↑↑

Pixel densities obtained by densitometry are expressed relative to the actin signal. The ratio of infected:control was calculated where numerical values were obtained for both conditions. nd, not detected; ↑ weakly up-regulated; ↑↑ strongly up-regulated.

Table 11. One-letter amino acid sequences for hepcidins based on genomic and expression data

Signal peptide	Anionic propiece	Mature peptide	NRC Code
<----->	<----->	<----->	
MKTFSAVAVVVLACMFILESTAVPFSEVTEEVESIDSPVGEHQQPGGTSMNLPMHFRFKR-QSHLSLCRWCCNCCCHN-KGGGFCCKF			NRC201 <sup>b</sup>
MKTFSAVAVVVLACMFILESTAVPFSEVTEEVESIDSPVGEHQQPGGTSMNLPMHFRFKR-QSHLSLCRWCCNCCCHN-KGGGFCCKF			NRC202 <sup>a</sup>
MKAFSAVAVV--LVIAACMFILESTAVPFSEVTEEVGSDSPVGEHQQPGGESHMLPEPFRFKR-QIHLSLGLCCNCCCHN-IGGGFCCKF			NRC203 <sup>a</sup>
-----RTEEVESIDSPVGEHQQPGGTSMNLPMHFRFKR-QSHLSLCRWCCNCCCHN-KGGGFCCKF			NRC204 <sup>a</sup>
MKTFSAVAVV--PVIACMFILESTAVPFSEVTEEVGSDSPVGEHQQPGGTSMNLPMHFRFKR-QSHLSLCRWCCNCCCHN-KGGGFCCKF			NRC205 <sup>a</sup>
MKQFSVAVV--LVMACMFILESTAVPFSEVTEEVGSDSPVGEHQQPGGESHMLPEPFRFKR-QIHLSLGLCCNCCCHN-IGGGFCCKF			NRC206 <sup>a</sup>
MKAFSIAVAVTLVAFVCIQSSAVPFGVQVQEEAAGNDTPVAHQVMSMESWMEPTROKRHI SHISLRCWCCNCCKANKGGGFCCKF			NRC207 <sup>a</sup>
MKTFSAVAVTLVAFVCIQSSAVPFGVQVQEEAAGNDTPVAHQVMSMESWMEPTROKRHI SHISLRCWCCNCCCKA-KGGGFCCKF			NRC208 <sup>b</sup>
MKTFSAVAVTLVAFVCIQSSSGTFFVQVQEEAAVSNDNAAAEHQETPVDSSWMPYN-RQKR----AFKCKFCGCGCRA-GVCGLCCKF			NRC209 <sup>b</sup>
MKTFSAVAVTLVAFVCIQSSASFFPEAQEEAAVSNDNAAAEHQETPVDSSWMPYN-RQKR----SFKCKFCGCGCRA-GVCGLCCKF			NRC210 <sup>a</sup>
MKTFSAVAVTLVAFVCIQSSASFFPEAQEEAAVSNDNAAAEHQETPVDSSWMPNN-RQKR----GFKCKFCGCGCRA-GVCGLCCKF			NRC211 <sup>a</sup>
MKTFSAVAVTLVAFVCIQSSATFPE-----MPYN-RQKR----GFKCKFCGCGCRA-GVCGMCCCKF			NRC212 <sup>a</sup>
MKTFSAVAVTLVAFVCIQSSASFFPEAQEEAAVSNDNAAAEHQETPVDSSWMPNN-RQKR----SFKCKFCGCGCRA-GVCGLCCKF			NRC213 <sup>b</sup>
MKTFSAVAVTLVAFVCIQSSASFFPEAQEEAAVSNDNAAAEHQETPVDSSWMPNN-RQKR----SFKCKFCGCGCRA-GVCGLCCKF			NRC214 <sup>b</sup>
MKTFSAVAVTLVAFVCIQSSASFFPEAQEEAAVSNDNAAAEHQETPVDSSWMPYN-RQKR----SFKCKFCGCGCRA-GVCGLCCKF			NRC215 <sup>b</sup>
MKTFSGAVTVAVVLFVCIQSSASFFPEAQEEAAVSNDNAAAEHQETPVDSSWMPNN-RQKR----GFKCKFCGCGCRA-GVCGLCCKF			NRC216 <sup>b</sup>
MKTFSAVAVTLVAFVCIQSSATFPEAQEEAAVSNDNAAAEHQETPVDSSWMPYN-RPKR----SFKCKFCGCGCRA-GVCGLCCKF			NRC217 <sup>b</sup>
MKTFVAVTVAVVLFVCIQSSATFPEAQEEAAVSNDNAAAEHQETPVDSSWMPYN-RPKR----SFKCKFCGCGCRA-GVCGLCCKF			NRC218 <sup>b</sup>
MKTFVAVTVAVVLFVCIQSSATFPEAQEEAAVSNDNAAAEHQETPVDSSWMPYN-RQKR----SFKCKFCGCGCRA-GVCGLCCKF			NRC219 <sup>b</sup>
MKTFVAVTVAVVLFVCIQSSATFPEAQEEAAVSNDNAAAEHQETPVDSSWMPYN-RQKR----SFKCKFCGCGCRA-GVCGLCCKF			NRC220 <sup>b</sup>
MKTFSAVAVTLVAFVCIQSSATFPEAQEEAAVSNDNAAAEHQETPVDLWMPYN-RQKR----GFKCKFCGCGCSP-GVCGLCCKF			NRC221 <sup>b</sup>
MKTFSAVAVVAVVLFVCIQSSATFPEAQEEAAVSNDNAAAEHQETPVDLWMPYPN-RQKR----GFKCKFCGCGCRA-GVCGLCCKF			NRC222 <sup>b</sup>
MKTFSAVAVTVAVVLFVCIQSSATFPEAQEEAAVSNDNAAAEHQETPVDLWMPYPN-RHKKR----SFKCKFCGCGCRA-GVCGLCCKF			NRC223 <sup>b</sup>

Table 11 (Cont.)

Signal peptide	Anionic propiece	Mature peptide	NRC Code
MKTFSAVTVAVVLFVFCIQSSATFPEVQELGEAVSNDNAAAEHQETSVDSSWMPYIN-RPKR	-----><-----	-----><-----	NRC224 <sup>b</sup>
MKTFSAVTVAVVLFVFCIQSSATFPEVQELGEAVSNDNAAAEHQETSVDSSWMPYIN-RQKR	-----><-----	-----><-----	NRC225 <sup>a</sup>
MKTFSAVTVAVVLFVFCIQSSATFPEVQELGEAVSNDNAAAEHQETSVDLWMPYIN-RQKR	-----><-----	-----><-----	NRC226 <sup>b</sup>
MKTFSAVTVAVVLFVFCIQSSATFPEVQELGEAVSNDNAAAEHQETSVDLWMPYIN-RQKR	-----><-----	-----><-----	NRC227 <sup>b</sup>
MKTFSAVTVAVVLFVFCIQSSATFPEVQELGEAVSNDNAAAEHQETSVDLWMPYIN-RQKR	-----><-----	-----><-----	NRC228 <sup>b</sup>
MKTFSAVTVAVVLFVFCIQSSATFPEVQELGEAVSNDNAAAEHQETSVDSSWMPYIN-RQKR	-----><-----	-----><-----	NRC229 <sup>b</sup>
MKTFSAVTVAVVLFVFCIQSSATFPEVQELGEAVSNDNAAAEHQETSVDSSWMPYIN-RQKR	-----><-----	-----><-----	NRC230 <sup>a</sup>
MKTFSAVTVAVVLFVFCIQSSATFPEVQELGEAVSNDNAAAEHQETSVDSSWMPYIN-RQKR	-----><-----	-----><-----	NRC231 <sup>a</sup>
MKTFSAVTVAVVLFVFCIQSSATFPEVQELGEAVSNDNAAAEHQETSVDSSWMPYIN-RQKR	-----><-----	-----><-----	NRC232 <sup>b</sup>
MKTFSAVTVAVVLFVFCIQSSATFPEVQELGEAVSNDNAAAEHQETSVDSSWMPYIN-RQKR	-----><-----	-----><-----	NRC233 <sup>b</sup>
MKTFSAVTVAVVLFVFCIQSSATFPEVQELGEAVSNDNAAAEHQETSVDSSWMPYIN-RQKR	-----><-----	-----><-----	NRC234 <sup>b</sup>
MKTFSAVTVAVVLFVFCIQSSATFPEVQELGEAVSNDNAAAEHQETSVDSSWMPYIN-RQKR	-----><-----	-----><-----	NRC235 <sup>b</sup>
MKTFSAVTVAVVLFVFCIQSSATFPEVQELGEAVSNDNAAAEHQETSVDSSWMPYIN-RQKR	-----><-----	-----><-----	NRC236 <sup>a</sup>
MKTFSAVTVAVVLFVFCIQSSATFPEVQELGEAVSNDNAAAEHQETSVDSSWMPYIN-RQKR	-----><-----	-----><-----	NRC237 <sup>b</sup>
MKTFSAVTVAVVLFVFCIQSSATFPEVQELGEAVSNDNAAAEHQETSVDSSWMPYIN-RQKR	-----><-----	-----><-----	NRC238 <sup>b</sup>
MKTFSAVTVAVVLFVFCIQSSATFPEVQELGEAVSNDNAAAEHQETSVDSSWMPYIN-RQKR	-----><-----	-----><-----	NRC239 <sup>b</sup>

<sup>a</sup> Peptide predicted from expressed tag and/or RT-PCR product  
<sup>b</sup> Peptide predicted from genomic sequence  
 - deletions introduced to clarify alignment  
 conserved cysteines are shaded

Table 12. Nucleotide sequences of pleurocidin-like genes and cDNAs referred to in Table 11.

Winter Flounder WF1

ATGAAGTTCACCTGCCACCTTCCTCCTGTTGTTTCATCTTCGTCCTCATGGTTGATCTCGGAGAGGGTTCGTCGTAAGAAAAAGGGGTC
GAAGAGAAAGGGTCCAAGGGAAAGGGTCCAAGGGAAAGGGCAGGTGGTTGGAAAGGATTGGTAAAGGTAGAGTCACGGGAATTAA
TTTGCTTTTACATTGCAAATATTTTCATATAACATTGCTGGAAAATCACAAAAATAAGTAGTCAATATATTTGGCCAAATAGAA
TCACCTTTGATTTCAATAATAATCAAATAACAACCTAAAAGGCCCTTTGATFAGCATGTTCCCTCAATGAAATGGACATTGTAATTT
ACTTTGATTTCTACATGCTACGACCTGCTGCAGCAACATTTGAAAATAAATTTGTCCAGAAAGATTTTAAAGTACATTGTTATAGG
CGATTTATCTTTCTATTACTCAGATATTTGTTCAAACCAATAGAATAACTGGATCTCTATGCTAAAATAATAAAAACACACATTGAG
ATGTTACCAGTCAAGATTGAACGCTGTTTAAAAGTAAAGTATGAAACATCCTCTGTATGTATAATTTGTTTAACTGGTAACTTATAGT
CCTAATAAATTGCGTTATGGAAATGTATTAATGTTCATTTAATATAAATTTGCTGGAATTTATCAGTGTGTGTTTTGTTTTGTTTTTA
CACAGCTGGCGGATATATATCGGGGGGCCCTTGAGTAAGGACTTCTACCATCATTACTGTGTAATATTTATAGTTATGATCAGT
ACAGTTATTAACAACCTCTCTGTCTCGCTGAACTTCTCCATCAGTCACTCGGGCAGGGGCAGGTGCAGGGGCCGGATTACGACT
ACCAGGAGGGGGAGGAGCTCAACAAGCGCGCAGTCCGATGAA

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Winter Flounder WF1A

ATGAAGTTCACCTGCCACCTTCCTCCTGTTGTTTCATCTTCGTCCTCATGGTTGATCTCGGAGAGGGTTCGTCGTAAGAGAAAGTGGTT
GAGAAGGATTGGTAAAGGTGTCAAGATAATTGGCGGGGGCCCTTGATCACCTCGGGCAGGGGCAGGTGCAGGGGCAGGATTACG
ACTACCAGGAGGGGCAGGAGCTCAACAAGCGCGCAGTCCGATGAAA

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Winter Flounder WF2

GCCCACTTTGTATTTCGCAAGGTAATATTGATATTTTTTCATATTCATTTAGACAAATGTGCTCAGCTTGTACTGTATAATGCAAAA
GTTAATGATCTTTATTTTTCTGTTTTTTTTTTGTAGAATGAAGTTCACCTGCCACCTTCCTCATGATFGCCATCTTCGTCCTCATGGT
TGAACCTGGAGAGTGTGGCTGGGGAAAGCTTTTTTAAAAGGCTGCTCACGGTAGAGTACAGAAATTAATTAGCTTTTTGCTTTTGCA
AATATTTTTTTATAACAGCTGGAAAATCACAAAAATAAATAGTATATATATTTGGCCAATAAAAATCACTTTGATTTCAATAATAA
TCTAAATAACCAACCTAAAAGGCCCTTGATTAGCATGTTCCCTCAATGAAATGTACGTTGAGGTTTATTTTGATTTCTCAAGCAC
CAACCTGCTGCGTCAACAATTGAATCAAATTTGTCCCAAAGGAATTCAAAAGTAAATTTTTCTAGGCGATTAAATCTTTCCATTAC
TCTGATTTGTTTTTAAAATATAGAAATAACTCAATCTCTATGATAAAAACAATTACACATACATTGAGATTTTTATAGGACAAGATTG
AAAACTTCTTACAAGTATGTATAAAAACATCATCTGTATGTATAATTGTTTAAACATGTAACAACACTAGTCTACTAATTTGTGTTAAAT
TGTCAATTAATATCAATGCTTGAGTTTATCATATATGTTTTGTTTTTTTTTACACAGTTGGCAAGCATGTTGGCAAGGGCGGCC
TTACGTAAGGACTTCTACCATTTTACTGTATAATTTTGATAGTGTATCACCAGTACTGTTTTTTGACAACCTCTCTATCTCTGCTG
ACTCTCTCCATCCGACTCATCCGAGTCACTTACCTTGGCGATAAGCAGGAGCTCAACAAGCGTGCAGTCCGATGAAGACCCAAATGT
TATTGTTTTTGAATGAAGAAAT

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Winter Flounder WF3

ATGAAGTTCACCTGCCACCTTCCTGGTGTGTCCTTGGTCCCTAATGGCTGAGCCTGGAGAGTGTCTTCTAGGAGCCCTTATCAA
AGGGCCATACATGGTAGAGTCAAGGAATTAATFAGATTTTTACATGTCAAATAATGTAGTAGAACATATATAAGTAGTCAATATA
TTGACCAAGTAGAATCAATTTGATTTCAATAATAATCAAATAACAATFCCAGGCGATTAAATATTTGCAATAAATGGATTTTA
TAGAATACGGAACAACCTGGATCTTAATGCTAAAATAATCAAACATCACTCTGATTTTGGCAGGCAAAAATTAACAACACTACTTTAAA
GTATGTATAAAAACATAAATCTGTATGTTATAACAATACTCCAAGCAATGTGTGATGGAAATGTATTCATTGTCAATTTAATATAAT
TTGCTTGAGTTTATCATCTGTGTTTTGTTTTGTTTTTTTACAGGTTGGCAGGTTTATCCATGGGTAAGGACTTCTACCATCATGAC
TGTGTATTTTTAATATTTATCATCAGTACTGTTATTGACAACCTTCACTTGTCTCGCTGACTCTCTCCATCAGAATGATCCAAA
CCATCACGGTTATGACGAGCAGCAGGAGCTCAACAAGCGCGCAGTCCGATGAAA

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Winter Flounder WF4

GCCCACTTTGTATTTCGCAAGGTAATATCAATATTTTTCAAATTCATTTAGACGAGACCAACCTTTTGGGAAATCTGCTCAGCTTAT
TACTGTATAATGCAAAATGTTAATGATCTTTATTTTTCTGTTTTTTTTTTGTAGAATGAAGTTCACCTGCCACCTTCCTCATGATGTT
CATCTTCGTCCTCATGGTTGAACCTGGAGAGTGTGGTTGGGGAAAGCATTTTTAAAGCATGGTCTCATGGTAAAGTCAAGGAATTAA
TTAGCTTTTAACTTTGCAAAATATGTTTTTTTTTTTTTAAACAGCTGGAAAATCACAAAAATAAATAGCCGATATATTTGGCCAAATAT
AATCACTTTGATCTAAATAACAACCTAAAAGGCCCTTGATTAGCATGTTTCTTCAATAAAAATGATTGAACACTACTTAAAGGTATG
TATAAAAACATCATCATGTGTTTTTTGTTTTGTTTTTTTACACAGCTGCAAGCATATTTGGCCATGCAGCCGTTAAGTAAGGACTTCTACC
ATTATFACGTATAAATTTTGATAGTATTATCACCAGTATTGTTATTGACAACCTTCTCTTTTTCTGCTGATCCGACTCATCCGAG
TCATTACCTTTGGCGAGCAGCAAGATCTCGACAAGCGCGCAGTCCGATGAAGACCCAAATGTTATTGTTTTTTGAATGAAGAAAT

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Yellowtail Flounder YT2

ATGAAGTTCACCTGCCACCTTCCTCATGATGTGCATCTTCGTCCTCATGGTTGAACCTGGAGAGTGTCTGTTGGGGAAATGGTTTAA
AAAGGCCACACCGGTAGAGTCAAGAAATTAATFAGCTTTTTGCTTTGCAAAATATTTTTTTATAACAGCTGGAAAATCACAAAAAT
AAATAGTCTATATATTTGGCCAAATFAGAATCACTTTGCTTTCAATAAAAATCTAAATAACAACCTAAAAGTCCCTTTGATTAGCATT
TTCCATCAATGAAATGGACGTTGAGGTTTTATTTGATTTCTCACATGCACCGACTGCTATGTCAACAATGAAATACAAATTTGTCC
CAGAGGAATTCAAAGGAAATTTTCTAGGCGATCTAATCTTTCCATFACCTCGGATTTGTTTTTAAATATATAGAAATAACTCAATCT
CTATGATAAAAATAAACAACATACGTAAGATTTTTCAAGACAAGATTGAAAACCTTCTTAAAAGTACGTATAAAAACATCATCTGT
ATTTATAAATGTTTAACTTTAAACAATAGCCCTACTAATTTGTGTTATGGAATGTATAAATGTCAATTTAAACATAACTTGTTTGA

GTTTATCATTATTTGTTTTGTTTTGTTTTTACACAGTTGGCAAGCATGTTGGCAAGCGGCCCTTACGTAAGGACTTCTACCATCA  
TTACTGTATAATTTTGAATAGTATTATCACCAGTACTGTTATTGACAACTTCTCTTGTCTGCTGACTCTCTCCATCCGACTCATCC  
ATAGTGCTTACCTTGGCGACAAGCAAGAACTCGACAAGCGCGCAGTCGATGA

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Winter Flounder WFX

TAATAAACTAATGTGTAAGTCTTCCACTTTTTTACTGTAATTTACTTTAAACAGAAAATATTCTCAGGATTCGGAGCTGCAGC  
CACTAAGTGTGCTTTCATGAAGTGAATACACAATTTGTTCTAACCAACCCTCACCCAATTAACCAGAACTTACAAGTGAGGAAGTG  
AGAGGAGTCGTCCTGTGTTTTCAAATTTTTGAATGATCTACCCTATGTGAGCTCCTCCTGTTATAGCTCTAAATGTTACACAAT  
GAATGTGAAGTCAGTTCTGTGTATATAAAGAGTTGCCTCTGTAGAGCATAACAAGATTTACCTTTGAATCTCACAACCTCACT  
TTGTATTTCGACAGGTAAGATCGATATTTTTCAAATCATTAGACGAGACCAAGTATTTGGGAAATGTGCTCAGCTTGTCAATGTA  
TAATGCAAAATGTTAACAAATCGTTTTGTTCTTATGTTGTGTTTGTAGGATGAAGTTGCTACTGCCTTCTGATGTTGTCCATGGTC  
GTCCTCATGGCTGAACCTGGAGAGTGTGTTCTACAGAGGCATCATCAAGTCTATCTCGGGTAGAGTCCAGGAATTAATTTATAT  
CAATAACAATGAAATAACAACCAAAAGGCCTCTGATTAGCATGTTCTTCAATGAAATGGTCTGTTTTTATCTATTTTGATTTCTCA  
CATGCAACGACCTGCTGCGGCAACATTTGAAAATCAATCTTTTTACACAAATTTCAAAGTACATTGATTTATTGATTTAATCTTA  
ACATTAATCGATTTGTTTTGTTTTAAATATATCGAATAACTGGATCTCTATGATAAAATAATTAACAATACATTCTTATTTTACC  
AATCAAGATTGAACACTTCTTAAAAGTACGTATAAAACATCATCTGTATGTATAATTTGTTGATTGTTAAGTAATATTTCCAATAA  
TTGTGTAATGAAATGTATTAATTTGTCATTTAATATAATTTGCTTGAATTTATCACCATGTGTTTTTGTGTTTTTAAACAGGT  
GGAGTTTTCTCAATGCGTAAGGACTTCTATCATCATTACTGTGTAATTTTATAGTATTATCATCAGTACTGTTATTAACAGCTT  
CTCTTGTCTCACTGACTCTCTCCATCAGAATGAACGCGGTTACAATGAGCAGCAGGAGCTCAACAAGCGCTCAGATGATGATGAC  
AGCCCCAGTCTTATTGTTTTGACTGAAGAAGTCGCCCTGAAGGAGCCTTCAGATGATATATTATGCTTCTTGTCTCTTCAATGAAA  
TAATCAAC

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Winter Flounder WFY and WFZ (alternative splice products from the same pseudogene)

GAGCTCGATCAAACAGACAAAGTTGCTTCCCTTCAACAATAGAGTGGAGAGAAAACAGGAGAGGACTTGTATCCTCCTGATG  
CTGAGAAGAAATAAGAAAGACTTGCAGCATTGATACTTTACTTATACAGAAAACCTATAAACATGACGGGAGCATAAGTTAA  
AGTCACAATACAGAGAGAAACAGAAAGCCAACTGCAGCAAAATTTACTGGTATTCATATGATAAGAAAGTATGAAATAAAAAA  
CTCAGCAGCAGTGAACCAAGAGTTTAACTGTACTTGTGTCCAGGTTGAATGAAAGTATGAAATAAAAAAACCAGACAGAACAT  
GCATATTTTTTTGGAATGGAATATAAGTCAAGGAGAAATATGTTGTTGTTGTTGGCAGGATCCATCACTCTGTCAAGTTAACACA  
AACTTTTTAGAAACATAGATACGATCTCAAGTAACTTCCATTACTATTTGACTTTTTTAAATACTTACAAATATATTTTTAAAA  
AGCAACAATAAATCAGAGATAACTTCATGGAGAAGTCTATATTCATATTTGTGAGCTGAACATTCAATGCTGCCTGTTCTATCA  
CTGAGTGTGGAGGCCACTGACGTTTTACTGACCTCAACGCTTACCGCTCAATGCAATTTGGAGTTAAAGGTAAGCATTTGTTTAT  
GTCTTCACTGTATTGATACTAAATATACAGGGTTACAAATACAGTTAAACCAAGAGAGACGAGGTTGTCGAAAGCTTCAGCATCA  
GTGCTGATCGCTGATAGCTGATCTTACCCGACACCCTGACATGGCATAAAAATGACCACCTCTTTTTTCTTCTTTTTTTTGTGTA  
GGACGAAGTTCGCTGAGCTTCCCTCGTGTGTTGTTGATGTTTACATGCCAAATATTTAATGAAACATACCTTATGAGTAGTTG  
CACGGGGTCCACCATGGTAGGGTCCCGAAGTAAATTTGATTATACATGCCAAATATTTAATGAAACATACCTTATGAGTAGTTG  
TATATTTGGACAAGTAGAATCTCTATGATTTCAAGTAGAATTAGAATAACAATCAAAAAGGCCTTTGATTAGCATGTTCTTCAA  
TGAATGGACATTTAGGTTTTATTTGATTCTCACATGCTACAGCAAAATGAAATCAAAATTTTTCGCAGAAGAACTTAATTAAC  
ATTTGTTGTCGAATAGTGTCTAAAAGTGTACCAATGGAATGGTGTGCGTTTAGGCCTCAATAAAATTTGGTTATCAAATTAAT  
AAAAAATTAATATTTAAAATATTAATTAATTAATCAACTTTTAAATGTTTTAAAGTTCTCGCGGGGAACACCCTTCTTCTGAAGG  
TAAAGGATAGCCAAATTTATTTGATTAAAGATCAGTCTCATTAGATCTAGTTCAAATAGAATCTCAATATTTACCATCGAAGATTT  
TATAATGAACAGTGAAGTTATGGAGTTCTAAACAGTGTAAACAGTTGGCAAAGTTCACTATTGCAATATTAATGACAGACCATTTG  
TGAAAGAAGAACATTTATATGAGCATAATAAAGTATGAAAGCACGAATTAACAATCAAAGCTAACTAACAAAGGACGTGTGT  
GGTGTGTGTGTAATGTAATAAGGGGGGGCTCAAACCTGTTGGCCTACAAGAAGAGCCTTAAGATAGCAACCACAAGGCTGTA  
CCATAAATGTTGTAGTAAAAGAGTTATTAATGAGTTAGAATAACTAAGTAAATAGTAACTAATAGTAACTAATAGTAACTAATA  
CAACTAACAAATAACAAGGAAGTGTGTGTGAGTGTGTTGTTGTTAATGTTAATTTAGGGCTCTCAAACCTGGTGTCTTACCAGAAG  
AGTAAAGATAACAATTTCCCCCTTCTTCTGAGGTTGTTTTACGACTGTTGCTTTATGGCCGTGAGGGAAGGTTAACTCGGTGACA  
TGCTATACGTTCTGTGTAGATGTTAATCAGAGAATGCCAGAGTCAGAGAGACCTACGGAGGAAGTCTGTGAAGGGCCTATCTAAC  
ATTAGCTTTCCCTTAACTTATAACACAATATCAGAAACACATATCAACCTTATAAACACACACAGAAATCAAATAAACAGTCTTGCT  
TAGCATGTATAATATTAAGCCAGATTTATGTTACCAGTCCGAGGGAAAGAGTTCAAGTTGCAAGTTCTGTGACGTTCTCTGGCTTG  
TGGTCTGAGAGTTCTGCATTCGCGATTCTGTGAGCCGTGTCTCAGATGCAGGTTGAAGTTCTCTGAGGACATCGCGTCTGCTG  
CGAGGATTTGTAGAGCTTGAAGGGCGAGGAGATTTCCCTTGAGTGGTGAAGCTGGACCTCTGACCTCTGGTTGTTGGTTG  
GAAGAGAAGAAAGCTGGAGCCGCTGTTCTCCCTTAGCCGATGCAGGAGGAGAAGCCGGCAGCCCCACTCTTGAAGAGTTGT  
GGAGAGAGATGGGAGCAAAGAGCTAGATTTGGGGAGACCTTCTCTTATATTTGGCCCGATGACCTCACAGGCTTGGAAACGGAGT  
GACCAATAGGAGTTGACCTGGTAATTTGACACCTTTGTGGGACATTTGCAAGACCCCAAGGACATGCAGCATCTGTTACAAATC  
TGGGAGACGGAGTTCTTACTGTCTCAGAACAAATGAGAACCTTGGGATTTGGGGATTTGAGTCCACTCGAGCAGATGCGGCAT  
GTTTTTCCAAGTTTGAAGTGAAGGAGGCTGTGTTTTGCACAAAACCAATGTTCCCAACAACATTTCTAGGCAATTAATCTTTA  
CAAGATTTGAACACTTAATGAAAAGTACCTATAAAACATAATCTGTATGTATAGTTGTTGACTGTTAAATAGTAGTCTAACAAATG  
TGTAAATGAAATGTATTCAATGTTCTTTAATACTATTTGCTTATCATAATGTGTTGTTGTTTTTTAGCAGGTTGGAGTTATCTC  
AATGCGTAAGGACTTCTACCATCATTACTGTGTAATTTGATTTAGTTTATCATCAGTACTGTTATTGACAACGTTCTTGTCTTGC  
TGACTTGACTCTCTTATCAGATTAACCCAGGGCCGTTACAATGAGCAGCAGGAGCTCGACAAGCGCGCAGTGCATGACACCT  
CAGTGTATTGTTTTTACTGAAGAAGTCGACCTGAAGAATCTTTGAAATGATATGAAATGTTGCTTTCAATGAAATAAATCA  
AACATGACTGGATATTTGTTCTTTGCAATGATGTAATGTTGAGTGACAGTTGAATAATTTTGGAAAACCTTATAACAGATCTCAAT

TTTAGGATGTCAAATCATTCTCTGTGTCTTATTCAAATATGAGATTTAACAATGACAAT

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American plaice AP1

GCCCACTTTGTATTTCGCAAGGTAAGATCAATATTTTTCAAATTCATTTAGACGAGACCAACCGTTTGGCAAATGTGCTCAGCTTGT
TATGTATAATAACAAAGTTAACGATCTTTATTTTTCTGTTTTTTGTAGAATGAAGTTCACCTGCCACCTTCCTGATGTTGTTTCAT
CTTCGTCCTCATGGTTGAACCTGGAGAGTGTGGATGGAAAAAGTGTGTTTTCTGTAAGGCTAAGAAAGGTAGAGTCACGGAATTAATTA
GCTTTTTACATTGCAAAATAGATTTTTTATAACAGCTGGAAAATCACAAAAATAAATAGTCGATATATTTGGCCAATTAGAATCACCT
TTAATTTCAATAATAATCTAAATAACAACCTAAAAGGCCCTTTGATTAGCATGTTTCTTCAATGAAATGGACATTGAGGTTTATTTT
GATTCTCACATGCACCGACCTGTGCGGCAACCATTGAATTCAGATTTGTCCAGAAGAATTCAAAGTACATTTTTCCAGGCGATTAA
AATCTTTCCATTACTCAGATTCAAAAATAAATAAATGGAATAATGAAGCACTATGATAAAAAATAATTACACATTCCTCTGACTTT
ACAAGTCAAGATTGAACACTATTAAAAAGTGTGTATAAAAAACAACATCTGTATGCATAAATGTTTAACTGTTAATAGTCCTAATAAT
TGTTTTATGGAATGTATTAAATTTACATTTAATATTTTGTCTGAGTTTTACCATCATGTGTTTTTGTGTTTTTACACAGTTGG
CAAGACTGTTGGCGCTTGGCCCTTGAGTAAGGACTTCTACCATCATTACTGTATAATTTTGATAGTATTATCACCAGTACTGTATA
TTAACTACTTCTCTGTCTGCTGACTCTCTCCATCCGACTCATCTGCAGTCATTACCTTGGCGAGCAGCAGGAGCTTGACAGCGCG
CAGTCGATGAGGACCCAGTGTCTATTGTCTTTGACTGAAGAAGTCGCCCTTGAAGGAG

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American plaice AP2

ACTTTGTATTTCGCAAGGTAAGATCAATATTTTTCAAATTCATTTAGACGAGACCAACCGTTGCGCAAATGTGCTCAACTTGTATT
GTATAATAACAAAGTTAACGATCTTTATTTTTCTGTTTTTTGTAGAATGAAGTTCACCTGCCACCTTCCTGATGTTGTTTCATCTTC
GTCCTCATGGTTGAACCTGGAGAGTGTGGATGGAAAAATGGTTAATAGGGCTAAGAAAGGTAGAGTCACGGAATTAATTAGCTT
TTTACATTGCAAAATAGATTTTTTATAACAGCTGGAAAATCACAAAAATAAATAGTCGATATATTTGGCCAATTAGAATCACCTTTAA
TTTTCAATAATCTAAATAACAACCTAAAAGGCCCTTTGATTAGCATGTTTCTTCAATGAAATGGACATTGAGGTTTATTTTGATTCTC
ACATGCACCGACCTGTGCGGCAACCATTGAATTCAGATTTGTCCAGAAGAATTCAAAGTACATTTTTCCAGGCGATTAAATCTTT
CCATTACTCAGATTCAAAAATAAATAAATAGAATAATGAAGCACTATGATAAAAAATAATTACACATTCCTCTGATTTTACAAGTC
AAGATTGAACACTATTAAAACTGTGTATAGAACATCATCTGTATGTATAATGTTTAACTGTTAATAGTCCTAATAAATGTTTTTA
TGGAATGTATTAAATTTACATTTAATAATTTTGTCTGAGTTTTACCATCATGTGTTTTTGTGTTTTTACACAGTTGGCAAGACT
GTTGGCGCTTGGCCGTTGAGTAAGGACTTCTACCATCATTACTGTATAATTTTGATAGTATTATCACCAGTACTGTTATTAACTA
CTTCTCTGTCTCGCTGACTCTCTCCATCCGACTCCTCTGCAGTCATTACCTTGGCAAGCAGCCGGAGCTCGACAAGCGCGCAGTC
GATGAGGACCCAGTGTCTATTGTCTTTGACTGAAGAAGTCGCCCTTGAAGGAGCCTTCAGAA

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American plaice AP3

TTGCCCACTTTGTATTTCGCAAGGTAAGATCAATATTTTTCAAATTCATTTAGACGAGACCAACCATTTGGGAAATGTGCTCAGCTT
GTTACTGTATAATGCAAAAGTTAAGTATCTTTATTTTTCTGTTTTTTTTTTGTAGAATGAAGTTCACIGCCAACCTTCCTCATGTTGT
TCATCTTCGTCCTCATGTTTGAACCTGGAGAGTGTGGTTGGCGAACATTGCTTAAAAAAGCTGGTTCACGGAATTAATAACGCTTTTT
ACATTGCAAAATAGATTTTTTATAACAGCTGGAAAATGACAAAAATAAATAGTCGATATATTTGGCCAATTAGAATTTATTTTGATT
CAATAATAATCTAAATAACAACCTAAAAGGCTTTGATTAGCATGTTTCTTCAATGAAATGGACATTGAGGTTTATTTTGATTCTC
ACATGACCGACCTGTGCGGCAACAATGAATTCAGATTTGTCCAGAAGAATTCAAAGTAAATTTCCAGGGGATTAATCTTTTC
CATTACTCGGATTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
AAGATTGAACACTACTTAAAAGTATGTATAAAAACATCATCTGTATGTATAATGTTTAACTGTTAACAATAAGTCCAAATAATGTT
GTTATGGAATGTATTAAATGTCATTAAATATAATTTGCTTGGTTTATCATCATGTGTTTTTTTTTTTTTTTACACAGAGGTTA
AGACTGTTGGCAAGTTGGCCCTTAAGTAAGGACTTCTACCATCATTACTGTATAATTTTGATAGTATTATCACCAGTACTGTATGTA
CTGCAACTTCTCTCTCCACCAACTCATCCGAGACATTACCTTGGCAAGCAGCCGGAGCTCGACAAGCGCGCAATGATGACGA
CCCCAGTATTATTGTTTTTGAAGTGAAGAAGTCGCCCTTGAAGGAGCCTTCAGAA

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Witch Flounder GcSc4C5

ATGAAGTTCACCTGCCACCTTCCTCATGATGTTTATGTTTCTGCTTCTCATGGCTGAACCCGGAGAGGCTGGTTGGGGAAAGTATTTCAA
ACATAATTTCAAAGCTGGAAAGTTCATCCATGGTGCATCCAGGCACACAATGACGGCGAGGAGCAGGATCTCGACAAGCGCGCAG
TCGATGA

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Witch Flounder GcSc4B7

ATGAAGTTCACCTGCCACCTTCCTGGTGTGTTTATGTTTCTGCTTCTCATGGCTGAACCTGGAGAGGTTTTTTGGGGAAAGCTTTTGAA
ATTGGGCATGCATGGAATCGGGCTGCTCCATCAGCATTGGGTGCTGACGAGCAGCAGGAGCTCGACGAGCGCTCAGAGGAGGACC
AGCCCAATGTTATTGTTTTTGAATGAAGAAGTCGCATTGAAGGAGCCTTCAG

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Witch Flounder GC3.8

ATGAAGTTCACCTGCCACCTTCCTGGTGTGTTTATGTTTCTGCTTCTCATGGCTGGATCCGGAGAGTGTGGTTGGAAAAAGTGGCTCCG
TAAAGGTAGAGTCAATGGATTTAATTTGCTTTTTACATGCAAACTTTAATATAACATAGTTGGAAAAACCACAAAAATAAGTAGT
CGATATATTTGGCCATATAGAATCACTTTGATTTCAATAATAATCAAAACAACCAATCAAAAAGCCCATTTGATTAGCATGTCCCTTC
ACTAAAATGGACATTGTAATTTATTTGATTTCTCACAGGCACCAACCTGCTGCGGCAACAATGAAATCAAATTTGTCTCAGAAGA
ATTCAAAGTACATTTGTTCTAGGCGATTTAATCTTTCCATTATCATGGATCTGTTTTTAAAAATATAGAATAACTGGATCTCTATGTT
AAAATAATAAACACACATTTCTGATTTTACCTGTCAAGATTGAACACGACTTAAAGTATGTATAAAAACATCATCTGTATGTATAA
TTGTTTTAACTGTCAACTAATAGTCCAAATAATTTGTTTATGGAATGTATTCAATGTCATATAAATATCATTTGCTTGAATTTATCA
CCATGTGTTTTTGTGTTTTTACACAGGTGCCAAGCACCTTGGCCAGGCGGCCATTAGTAAGGACTTCTACCATCATTACTGTT



AAAAACATCATCTGTATGTATAATTAATACTTGTCCAGATAAFTGTGTTGTGGAAATGTGTTAATTGACATATATCATTTGCTT  
GAATTTATCATTAATCTGCTTTGTTTGTGTTTTACACAGGTATCAAGGCGATCCATGGGTAAGGACTTCTACCTTCATGACTGTGTAT  
TTTTAATAGTATTATATTCAGTACTGTTATTGAAAACCTCTCTTGTCTCGCTGACTCTCTCCATCAGAATGATCCATGGTAACAGT  
TTAGACGAGATGCAGGAGCTCGACAAGCGCTCATTGATGACAACCCCAACGCAATTGTTTTTACTGAAAGTGCCTCGCCCTGAAGG  
AGCCTTCAGATGATATATAATGCTTCTTGTCTTTCAATGAAATAAATTGAATAATTACCCGCAACAGC

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Winter Flounder WF1-like

TACTTTTATCTACCCTATGTGAGCTCCTCCTGTTATAACTCTAATGTTACACAATGAAGATGAGGTCATTTCTGTGTATATAAA  
GAGTTCCTCTGTATAGTAGACAACATATTTCACTTTGAATCCACAAAGCTCACTTTGTAAGGTAAGATCGATATTTA  
AAAATAAATTTAGACGAAACCAAGCATTTTGGGGAATTTGCTCAACTTCTAATGTATGATACAAATGTTAACATCTTTTATTTT  
TGTTGTTGTTTTTTGTAGGATGAAGTTCCTGCCACCCTCCTCCGTTGTTTCATCTTCGTCCTCATGGTTGATCTCGGAGAGGGTC  
GTCGTAAGAAAAGGGGTCGAAGAGAAAGGGGTCGAAGGAAAGGGGTCGAAGGAAAGGGGTCGAAGGAAAGGGGTCGAAGGAAAGGGGTC  
GGTAGAGTACCGAATTAATTTGCTTTTACATTGCAAATATTTTCATATAACATTGCTGGAAAATCACAATAAAGTAGTCAA  
TATATTTGGCCAAATAGAATCACTTTGATTTCAATAATAATCAAATAACAACCTAAAAGGCTTTGATTAGCATGTTCTTCAAT  
GAAATGGACATTTGTAATTTACTTTGATTTCTCACATGCTACGACCTGCTGCAGCAACATTTGAAAATAAATTTGTCGAGAAGATTT  
TAAAGTACATTTGTTATAGGCGATTTATCTTTCTATTACTCAGATATTTGTTCAAACCAATAGAAATAACTGGATCTCTATGCTAAA  
TAATAAACACACATTGAGATGTTACCAGTCAAGATTGAACGCTGTTTAAAAGTAAAGTATGAAACATCCTCTGTATGTATAATTGT  
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GTGTTTTGTTGTTTTTACACAGCTGGCGGGATAATATCGGGGGGCCCTTGAGTAAGGACTTCTACCATCATTACTGTGTAAT  
ATTTATAGTTATGATCAGTACAGTTATFAACAACCTCTCTGTCTCGCTGAACTTCTCCATCAGTCACTCGGGCAGGGGCAGGGT  
CAGGGCCGGATACGACTACCAGGAGGGGGAGGAGCTCAACAAGCGCTCAGACGATGATGACAGCCAGTCTTATTTTTTTTGA  
CTGAAGAAGTCGCCCTGAAGGAGCTTCAGATGATATATAATGCTTCTGGCTTTTCATGAAATAAATAACGTTTACCTGCAAC  
AGCAACCATG

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Halibut Hb29

TTATGAAGTTCCTGCCACCTTCTGGTGTGTTTCATGGTTCCTCATGGCTGAACCTGGAGAGGGTTTGGGAAATGGATGGGG  
CCCATAATCAGCGGTAGAGTACCGAATTAATTTGCTTTTCCATTGCAAATATTTAATATGCAATAGCTGGAAAATCAGGAAAT  
AAGTAGTCGATATATTTGGCCAAATAGAATCACTTTGATTTCAATAATAATCAAATAACAATCAAATAAGGCTTTGATFAGCATG  
TTCCTTCAATAAAATGGACATTTGAAGTTTATTTGATGCTCACATGCACCGACCTGCTGCGGCAACAATGAAATCAAATTTGTCT  
CAGAATTTAAGTACATTTTCTAGGTGATTTAATCTTCCATTAACCTGATTTGTTTTATAAATAAGAAATAACFGGATCTTTA  
TGCCAAAATAAATAAACACACATTTCTGATTTTACCAGTCAAGATTGAACACTACTTAAAAGTAAATAAACAATCATCTGTATGTA  
TAATTTGTTAACTGTTAAACAAAAGTCCAAATAATTGTTGTTATGAAATGATTAATTTGTCATTTAATATCATTTGCTTGAATTCAT  
CACCATGTTGTTTTTGTGTTTTTACACAGGTGAAAAGAAGGCTTGCAGTAAGGACTTCTACCATCATTACTTTGTAATTTTTA  
TAGTATTATCATCAGTACTGTTATGACAACCTCTCTGTCTCGCTGACTCTCTCCATCAGGATGAACCTCAGAGCGTCCAGTTC  
GACGAGCGGCAGCAGCAGCAGCAGGAGCTCGACAAGCGCGCAGTCCGATGA

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Halibut HbSc1A13

ATGAAGTTCCTGCCACCTTCTGGTGTGTTTCATGGTTCCTCATGGCTGAACCTGGAGAGGGTTTGGGAAATGGATCGTGCG  
CCCTATCGGAGGTGAAAAGAAGGCTTGCAGATGAACCTCAGAGCGTCCGAGTTACGACGAGCGGCAGCAGCAGCAGCAGGAGCTCG  
ACAAGCGCGCAGTCCGATGAAA

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Halibut HbSc1A24

ATGAAGTTCCTGCCACCTTCTGGTGTGTTTCATGGTTCCTCATGGCTGAACCTGGAGAGAGTCTTTTGGAAAGTTCCTCAA  
GAAAGTTGTCATGCTGGCAGTCAATTTGGCGAGACAGCCTTGCATGTCGCGGAGAGCATCAGGGGCTTCATGCGCATCAGGGT  
GTCACGGGCGTACGGGGGTACAGGCGTACGGGGGTACAGGCGTACGGGCGTACGGGCGTACGGGCGTACGGGCGTACGGGCGTACGGGCGT  
CTCGACAAGCGCGCATTCGATGA

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Halibut HbSc1B34

TATGAAGTTCCTGCCACCTTCTGGTGTGTTTCATGGTTCCTCATGGCTGAACCTGGAGAGGGTTTGGGAAATGGATGGGGC  
CCCATAATCAGCGGTAGAAAAGAAGGCTTGCACATGAACCTCAGAGCGTCCGAGTTACGACGAGCGGCAGCAGCAGCAGCAGGAGCTC  
GACAAGCGCGCAGTCCGATGAAA

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Halibut Hb17

ATGAAGTTCCTGCCACCTTCTGGTGTGTTTCATGGTTCCTCATGGCTGAACCTGGAGAGTGTTTTTTGGGATTGCTTTTTTCA  
CGGGTCCACCATGGTAGGGTACGGAAGTAATTCGATTTTTACATGGCAAATATTTAAGATAACACACCATATGAGTAGTCGAT  
ATATTTGGCCAAATAGAATCACTTTGATTTCAATAATAATCAAATAACAATCTCAGGCGATTTAATATTTGCATTAATTTGGATT  
TGTTTTTAAAATAAGAAATAACTGGATCTTTATGGTAAAATAATTAACATACATTCTGATTTTACCAGTCAAGATTGAACACTA  
CTTAGAAGTATGTATAAAACATCATCTGTATGTATAATTTGTTAACTGTTAAACGAATAGTCCAAATAATTTGTGTTATGGAAATGTA  
TTAATTTGTCATTTAATATCATTTGCTTGAATTTATCACCATGTTGTTTTGTTGTTTTTACACAGTTGAAAGTTGATCCATGGGT  
AAGGACTTCTACCATCATTACTGTGATTTTTAATAGTATTATCATCAGTACTATTATGACAACCTCTCTGTCTCGCTGACTCT  
CTCCATCAGACTCATCCATGGCGTTACGACGAGCAGCAGGAGCTCGACAAGCGCGCAGTCCGATGAAA

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Witch Flounder GC1.2

GCCCACCTTTGTATTGCGCAAGGTAAGAGCGATATATTTCAAATTCATTCCGGATGAGACCAAGCATTTGGGAAATGTGCTCAGCTTGT  
TACTGTTAATGCAAATGTTAACAAATATCCTTTTTCTGTTGTTTTGTAGAATGAAGTTCGCTGCCGCTTCCCTCATGATGTTTCAT  
GGTCGTCCTCATGGCTGAACCCGGAGAGGCTCGTTGGGGAACGTTCTTCAAACATATTTCAAAGGTAGAGTACAGAAATTAATTT  
GCTTTTTACATTGCAAATATTTTATATAACATAGCTGGAAATCACAAAATAAGGGCTTGATATATTTGGCAAAGTAGAATCCC  
TTTGATTTCAATAAATAATCAAAAATAAAAATCAGAAAGGCCCTTGATTAGCATGTTCCCTTCAATAAAAATGGACATTGTAGTTATTT  
TGATTTCAAATGCACCAACCTGCTGCGGCAACAATTGAAATCAAATTTGCTCCGAAACATTTAAAGTACATTTTTCGAGGCAAT  
TTAATCTTTCTTTGATCGAATTCGTTTTTAAAAATATAGAATAACTGGATCTTTATGCTAAAAATAATAAATCATAACATCTGATT  
TTACCAGTCAAGATGGAACGCTACTTAAAAGTATGTATAAAAACATCATCTGTATGTATAATTTAATTTAACTAATAGTCCT  
AATAATTTGTTTATGGAATGTATTCAATGTCATTTAATATCATTGCTTGAATTTATCACCATGTGTTTTGTTTTGTTTTTACAC  
AGCTGGAAGGTTTCCATCCATGGTAAGGACTTCTACCATCATCTACTGTGTTATTTAATAGTATTATCATCAGTACTGTTATTGATA  
ACTTCTCTGTCTCGCTGACTCTCTCCATCAGTGCATCCAGGCACACAATGACCGCGCAGCAGGATCTCGACAAGCGCTCAGT  
GGATGATGAGCCAGTGTATTGTTTTTGAATGAAGAAGTCGCTTGAAGGAGCCTTCAG

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Witch Flounder GC1.3

GCCCACCTTTGTATTGCGCAAGGTAAGAGCAATATATTTCAAATTCATTAGACGAGACCAAGCATTTGGGATCTGTGCTCAACTTGT  
AATGTTATAATGCAAATGTTAACAAATATCTTTTTCTGTTGTTTTGTAGAATGAAGTTCGCTGCCGCTTCCCTCATGATGTTTCAT  
GGTCGTCCTCATGGCTGAACCCGGAGAGGGTGTCTGGATACCTGCCCTTGAATAGGATCTATCATGGTAGAGTACAGAGTTAATTT  
GCTTTTTACATTGCAAATATTTAATATAACATGGCTGGAAAATCACAAAATGAGTACTCGATATATTTGGCAAAGTAGAATCCC  
TTTGATTTCAATAAATAATCAAAAACACAATCAAAAAGGCCATTGATTAGCATGTTCCCTTCAATGAAATGGACATTGTAGTTTATTT  
TGATTTGACATGCACCAACTTGTGCTGCGGCAACAATTGAATTTCAATTTGCTCAGAAAAATTTAAAGTACATTTTTCTTTCCATT  
AGTCCGATTTGTTTTAAAAAATACAGAATAACTGGATCTTTATGCTAAAAATAATAAATCATAACATTTCTGATTTTACCAGTCAAGAT  
TGAACGCTACTTAAAAGTATGTATAAAAACATCATCTGTATTGATAAATTTGTTAACTTTTAACTAATAGTCCATAAATTTGTTAT  
GGAAATGTATTCAATGTCATTTAATATCATTGCTTGAATTTATCACCATGTGTTTTGTTTTGTTTTTACACAGCTTACTGAGGA  
TCAATCGGTAAGGACTTCTACCATCATTACTGTGTAATTTAATAGTATTATCATCAGTACTGTTATTGATAAATTTCTTTGCTTT  
GCTGGCTCTCTCCATCAGCCAAATGGTGTATTATCGTCCGCACTGGCACGGTGACGTCGAGCAGCAGGCTCTCGACAAGCGCTCAG  
TGGAGGACCAGCCAGTTCATTGCTTCTGCCTGAAGAAGTCGCTTGAAGGAGCCTTCAG

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Witch Flounder GC1.4

GCCCACCTTTGTATTGCGCAAGGTAAGAGCAATATATTTCAAATTCATTAGACGAGACCAAGCATTTGGGATCTGTGCTCAACTTGT  
AATGTTATAATGCAAATGTTAACAAATATCTTTCTGTTGTTTTGTAGAATGAAGTTCGCTGCCGCTTCCCTCATGATGTTTCAT  
GGTCGTCCTCATGGCTGAACCCGGAGAGGGTGTCTGGATGCTGCCCTTGAATAGGATCTATCATGGTAGAGTACAGAGTTAATTT  
GCTTTTTACATTGCAAATATTTAATATAACATGGCTGGAAAATCACAAAATGAGTACTCGATATATTTGGCAAAGTAGAATCCC  
TTTGATTTCAATAAATAATCAAAAACACAATCAAAAAGGCCATTGATTAGCATGTTCCCTTCAATGAAATGGACATTGTAGTTTATTT  
TGATTTGACATGCACCAACTTGTGCTGCGGCAACAATTGAATTTCAATTTGCTCAGAAAAATTTAAAGTACATTTTTCTTTCCATT  
AATCGGATTTGTTTTAAAAAATACAGAATAACTGGATCTTTATGCTAAAAATAATAAATCATAACATTTGATTTTACCAGTCAAGAT  
TGAACGCTACTTAAAAGTATGTATAAAAACATCATCTGTATTGATAAATTTGTTAACTTTTAACTAATAGTCCATAAATTTGTTAT  
GGAAATGTATTCAATGTCATTTAATATCATTGCTTGAATTTATCACCATGTGTTTTGTTTTGTTTTTACACAGCTTACTGAGGA  
TCAATCGGTAAGGACTTCTACCATCATTACTGTGTAATTTAATAGTATTATCATCAGTACTGTTATTGATAAATTTCTTTGCTTT  
GCTGACTCTCTCCATCAGCCAAATGGTGTATTATCGTAGGCACTGGCACGGTGACGTCGAGCAGCAGGCTCTCGACAAGCGCTCAG  
TGGAGGACCAGCCAGTTCATTGCTTCTGCCTGAAGAAGTCGCTTGAAGGAGCCTTCAG

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Witch Flounder GcSc4B35

ATGAAGTTCACGACCCTTCCCTGGTGTGTTTATGTTGCTCCTCATGGCTGGATCCGGAGAGTGTGGTTGGAAAAAGTGGTTTAC  
TAAAGGTGCCAAGCACCTTGGCCAGGCGGCCATTACGGTTTGGCTCTTGGCAAGAGCAGCAAGAGCTCGACAAGCGCTCAGAGG  
ATGACGAGCCAGTGTATTGTTTTTGA

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Witch Flounder GC3.6

ATGAAGTTCACGACCCTTCCCTGGTGTGTTTATGTTGCTCCTCATGGCTGGATCCGGAGAGTGTGGTTGGAAAAAGTGGCTCCG  
TAAAGGTAGAGTCAATGATTTAATTTGCTTTTTACATTGCAAATACTTTAATATAACATAGTTGGAAAAATCACAAAATAAGTAGT  
CGATATATTTGGCCATATAGAATCACITTTGATTTCAATAAATAAACAACAATCAAAAAGGCCATTGATTAGCATGTTCCCTTC  
ACTAAAATGGACATTGTCAATTTATTTGATTCTCACAGGCACCAACCTGCTCGGCAACAATGAAATCAAATTTGCTCAGAGA  
ATTCAAAAGTACATTTGTTCTFAGGCGATTTAATCTTTCCATTATCGGATTTGTTTTTAAAAATATAGAATAACTGGATCTCTATGTT  
AAAATAAATAAACACACATTTCTGATTTTACCTGTCAAGATTGAACACGACTTAAAAGTATGTATAAAAACATCATCTGTATGTATAA  
TTGTTTAACTGTCAACTAATAGTCAAATAAATGTGTTATGGAATGTATTCAATGTCATATAAATATCATTTGCTTGAATTTATCA  
CCATGTGTTTTGTTTTGTTTTTACACAGGTGCCAAGCACCTTGGCCAGGCGGCCATTAAAGTAAGGACTTCTACCATCATTACTGTG  
TAATTTTAAAGTATTATCATCAGTACTGTTATTGACAACACTACTTGTCTCTGTGACTCTCTCCAGGGGTTTGGCTCTTGGCAA  
GAGCAGCAGGAGCTCGACAAGCGCTCAATGGATGACGAGCCAGTGTATTGTTTTGACTGAAGAAGTCGCTTGAAGGAGCCTTC  
AG

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Witch Flounder GC2.2

GCCCACCTTTGTATTGCGCAAGGTAAGAGCGATATATTTCAAATTCATTAGACGAGACCAAGCATTTGGGAAATGTGCTCAGCTTGT  
TACTGTTATAATGCAAATGTTAACAAATGTTTTGTTCTGTTGTTTTGCAGAAATGAAGCTCGCTGCCCTTCCCTGTTGTTGTTTCAT  
GGTCGTCCTCATGGCTGAACATGGAGAGGGTTTTGGGATTTCTATATGAAGCCTGGTAGAGTACAGGAATTAATTCGATTTTAACT

ATGGCAAATATTTTACTATAACATACCATATGAGTAGTFCGATTAATTAATTTGGATTGTTTTTAAAAATATAGAATAAATTGGATCT  
TTATGCTAAAATAAATAAACATACATTTCTGATTTTTACCAGTTAAGATTGAACGCTACTTAAAAGTAGTATAAAACATCATCTGTA  
CATATAAATTGTTAACTGTTAACCAATAGTCCAAATAATTGTGTTGTGGAAATGTATTAAATTGTCATTAATATCATTTGCTTGAA  
TTTGTCCACATGTGTTGTTGTTTTGTTTTTACACAGGTAGAAAGATTCCCATGGGTAAGGACTTCTACCATCATTAAGTGTGTTAT  
TTAGCAGTATATCATCAGTACTGTTATGATAACTTCTCTTGTCTCGCTGACTCTCTACAGGTACATCAGAAGTCTTTATGGTTA  
CGACGAGCAGCAGGAGGTCGACAAGCGCTCAGTCGATGACAACCCAGTGCCATTGCTTCTGACTGAAGAAGTCGCCTTGAAGGAG  
CCTTCAGA

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Witch Flounder GcSc4B28

ATGAAGTTCACTGCCACCTTCCTGGTGTGTTTCATGGTCTGCTCATGGCTGAACCTGGCGAGGGTTATTGGCGCTTCCGCAACCA  
CCGTGGTGAAGGTTATCCAGAGGCATTTCCGTCGACGTCGAGCAGCAGGAGCTCGACAAGCGCTCAGTGGATGACGAGCCAGTT  
CTATTGCTTTTGA

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Witch Flounder GC3.7

ATGAAGTTCACTGCCACCTTCCTCGTGTGTTTCATCGTCACTGTTTGAACCTGGAGAGTGTTTTTGGAATGCTTTTTACCAGGGTCC  
ACCATGGTCGGGTCCCGAAGTAGTTCGATTTTTACATGGCAAATATTTAAATGAAACATACCATATGAGTAGTTCGATATATTTGG  
CCAAGTAGAATCACTTTGACTTCAATAATAATCAAAAACATAATCAAAAAGCCATTGATTAGCATGTTCTTCAATGAAATGGAC  
ATTGAGTTTATTTGATTTCTCACAGGCACCAACCTGCTGGCGCAACAATTGCATTCAAATTTGCCAAAGAACTTAATTAACA  
TTTTTCGGCGATTTAATCTTTGCATAAAATTGGATTTGTTTTTAAAAATATAGAATAAAGTGGATCTTTATGCTCAAAATAATTAATCA  
TACATTTCTTATTTTATCAGTCAAGATTGAACGCTACTTAAAAGTAGTATAAAAACATCATCTGTATGTATAAATTGTTTTAACTTTTA  
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TTGGTTTTTACACAGCTGGAAGGTTGATCCATAGGTAAGGACTTCTACCATCATTAAGTGTATAAATTGTTAATAATAGCATTATCATC  
AGTACTGTTATTGATAAATCTCTCTTGTCTCGCTGACTCTCTCCATCAGATTATCAAACGTCACGGGTGACCTCGAGCAGCAGGAGC  
TCGACAAGCGCTCAGTGGATGACGAGCCAGTTCTATTGCTTTTGCCTGAAGAAGTCGCCTTG

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Witch Flounder GC3.1

ATGAAGTTCACTGCCACCTTCCTGGTGTGTTTCATGGTCTGCTCATGGCTGAACCTGGAGACTGTATTTTTGGATTGATTGCGAC  
TGCGGTCCACAATGTTAAGTCAAGGAATTAATTCGATTTTTACGTTGGCAAATATTTAGTATAACATACCTTATGAGTAGTTCGATA  
TATTTGACCAAGTAGAATCATTTTGAATTTCAATAATAATCAAAAATAACAATCTCTAGGCAATTTAATAATTTGCATTAATTTGGATTT  
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TCATTTGCATATAATATCATTTGCTTGAATTTATCACCATGTGTTTTTGTGTTTTTACACAGCTGGAAGGTTGATCCATAGGTA  
AGGACTTCTACCATCATTAAGTGTATAAATTTAAGAGCATTATCATCAGTACTGTTATTGATAAATCTCTCTTGTCTCGCTGACTCTC  
TCCATCAGACTACTCGGCTTTTCATCATGGGCTCCCGGTTCTGGCACGGTGACCTCGAGCAGCAGGAGCTCGACAAGCGCTCAGT  
GGATGAGGAGCCAGTTCTATTGCTTTTGAATGAAGAAGTCGCCTTGAAGGAGCCTTCAG

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Witch Flounder GC4.1

ATGAAGTTCACTGCCACCTTCCTGGTGTGTTTCATGGTCTGCTCATGGCTGAACCTGGAGACTGTATTTTTGGATTGATTGCGAC  
TGCGGTCCACAATGTTAAGTCAAGGAATTAATTCGATTTTTACTTGGCAAATATTTAGTATAACATACCTTATGAGTAGTTCGATA  
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TCCATCAGACTACTCGGCTTTTCATCATGGGCTCCCGGTTCTGGCACGGTGACCTCGAGCAGCAGGAGCTCGACAAGCGCTCAGT  
GGATGAGGAGCCAGTTCTATTGCTTTTGAATGAAGAAGTCGCCTTGAAGGAGCCTTCAG

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Witch Flounder GC4.4

ATGAAGTTCACTGCCACCTTCCTGGTGTGTTTCATGGTCTGCTCATGGCTGAACCTGGAGACTGTATTTTTGGATTGATTGCGAC  
TGCGGTCCACAATGTTAAGTCAAGGAATTAATTCGATTTTTACTTGGCAAATATTTAGTATAACATACCTTATGAGTAGTTCGATA  
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TCCATCAGACTACTCGGCTTTTCATCATGGGCTCCAGGTTCTGGCACGGTGACCTCGAGCAGCAGGAGCTCGACAAGCGCTCAGT  
GGATGAGGAGCCAGTTCTATTGCTTTTGAATGAAGAAGTCGCCTTGAAGGAGCCTTCAG

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Petrale sole 02A(3)

ATGAAGTTCACTGCCACCTTCCTGGTGTGTTTCATGGTCTGCTCATGGCTGAACCTGGAGAGTGTTTTTTGGAAATGCGTTTTTCA  
CGGGTCCACCATGGTAGGGTCAAAAAGTGAATTTGATTATTACATGCCAAATATGTTAATGAAACATACCATATGAGCAGTTCGTA  
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TGTTTGTGTTTTTTAGCAGGTGGAGTTTTCTCAATGCGCAAGGACTTCTACCATCATTACTGTGTAATTTAATAGPATTATC  
ATCAGTACTCTTATGACAACGTCCTTGTCTCGCTGACTCTCTCTATCAGATTAACCCAGGGTATCGCGGTTACGACGAGCAGC  
AGGAGCTCGACAAGCGCGCAGTCGATGA

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Petrale sole 02B

ATGAAGTTCACCTGCCACCTTCCCTGGTGTGCTTGGTCTGCTCATGGCTGAACCTGGAGAGGGTTTTCTTTGGAGCCCTTCTCAA  
AGGTAGAGTCACCGAATTAATTTGATTGTTACATGGCAAATAATTTGTATAACATATCATATGAGCAGTCGATGATTTGACCAA  
GAAGAATCATTTTGATTTCAATAATAATCAAATAACAATCTCTTGGAGATTATATATTTGCAATAAATTGGATTTTATAAAATATA  
GAACAACCTGGATCTTAATGCTAAAATAAATAACATACATTTCTGATTTTACCAGTCAAATAAACCCTACTTTAAAGTATGTATA  
AAACATCATCTGTATGTTAATTTGTTTAACTTTTAAACAAATAGTCCAAATAATTTGTTAATGGAAATGTATTCATTGTCATATAAT  
ATAGTTTGGCTTACTTTATCACCCTGTGTTTTGTTTTGTTTTTCAACAGGTGCCAGGCTCCATGGGTAAGGACTTCTACCATC  
ATGACTGTGTAAGTTTAAATAATATATCATCAGTACTGTTATTAACGACTTCTCTTGTCTCGCTGACTCTCTCCATCAGAATCATC  
CACAATGCTCGTACCGTTACGACGAGCAGCAGGAACCTCAACAAGCGCGCAGTCGATGA

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Petrale sole PL1/2/2.1

GCCCACCTTTGTATTCGCAAGGTAAGATCAATATTTTTCAAATTCATTTAGACGAGACCAACCGTTTGGCAAATGTGCTCAGCTTGT  
TATTTGATAATAACAAAGTTAACGATCTTTATTTTTCTGTTTTTTTTGTAGAATGAAGTTCACCTGCCACCTTCTCGATGTTGTTCA  
CTTCGTCCTCATGGTTGAACCTGGAGAGTGTGGTTGGAAAGATTGGTTTTCGTAAGGCTAAGAAAGGTAGAAATCACGGAATTAATTA  
GCTTTTTACATTCAAATAGATTTTTTATAACAGCTGGAATCACAAAAATAAATAGTCGATATATTTGGCCAATTAGAATCACCTT  
TAATTTCAATAATAATCTAAATAACAACCTAAAAGGCCCTTTGATTAGCATGTTCTTCAATGAAAAGGACATTTGAGGTTTTATTTTG  
ATTCFCACATGCACCGACCTGTGCGGCAACAATTGAATTCAGATTTGTCCAGAAAGAAATTCAAAGTACATTTTTCCAGGCGATTAA  
ATCTTCCATTACTCGGATTTAAAATAAATAAATAGAAATACTGAAGCGCTATGATAAAAATAATTACACATTCATTCTGATTTTA  
CAAGTCAAGATTGAACACTATTAATAAAGTGTGATAAAAACATCATCTGTATGTATAAATGTTTAACTGTTAATAGTCTTAATAAT  
GTGTTATGGAAATGATTAATTTACATTTAATATCATTTGCTTGAGTTTACCATCATGTGTTTTGTTTTGTTTTTACACAGTTGGC  
AAGACTGTGGCGGCTTGGCCCTTAAGTAAAGAACTTACCATCATTTACTGTATAAATTTGATAGTATTTACCAGTACTGTTAT  
TAACTACTTCTCTGTCTCGCTGACTCTCTCCATCCGACTCATCCGAGTCATTAACCTTGGCGAGCAGCAGGAGCTTGCCAAGCGC  
GCAGTCGATGACGACCCAGTGTATTGTCTTTGACTGAAGAAGTCGCTTGAAGGAGCCTTCAG

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English sole 05A

ATGAAGTTCACCTGCCACCTTCCCTCATGATTTAATCTTCGCTCCTCATGGTGAACCTGGAGAGTGTGGTATTAGGAAATGGTTTTAA  
AAAGGCTGCTCACGGTAAAGTCAAGGAATTAATTTGCTTTTTGCTTTTACAAATATTTTTTTATAGCAGCTGGAAAATCACAAAAAT  
AAATAGTCGATGATTTTGGCCAATTAGAATCACTTTGATTTCAAATAATAATCTAAATAGCAACCTAAAAGGCCCTTTGATTAGCAT  
GTTCTTCAATGAAATGGATGTTGAGGTTTTATTTGATTTCTCACATGCACCGACCTGCTGCGGCAACAATTTGAATCAAATTTGTC  
CCAAAGGAATCAAAGTAACTTTTTCTAGATGATTTAATCTTTCCATAACTCGGCTTTGTTTTTAAAAATATATAATAACTCAATC  
ACTATGATAAAAATAAACAACATACATTTGATTTATAACAAGACAAGATTGAAAACCTTTTAAAAGTATGTATAAAAACATCATCTG  
TTGTATAAATGTTTTATCATTTCAAAAAGTCCAACTAATTTGTTTATGGAAATTTGATAAATTTGCTATTAATAATAATTTTTTTG  
AGTTTATCAATATGTTTTTTTTTTTTTACACAGTTGGCAAGGAAGTTGGCAAGGTGGCCCTTAAGTAAAGGACTTCTACCATTA  
TTACTGTATAAATTTGATAGTATTATCACCCGACTGTTATTGACAACCTTCTTTTTCTGCTGACTCTCTCCATCTGACTCATCT  
GCAGTCTTGCCTTGACAAGCAGCAGCAGCTCGACAAGCGCGCAGTCGATGA

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English sole PL1/2/5

GCCCACCTTTGTATTCGCAAGGTAATATCGATATTTTTCAAACCTCAATTTAGACGAGACCAAGCATTGGGAAATGTGCTAAGGTTGT  
TACTGTATAAATGAAAATTAATGATCTTTATTTTTCTGTTTTTTTTTTCAGAAATGAAGTTCACCTGCCACCTTCTCATGATTTTAA  
TCTTCGCTCCTCATGGTTCGAACCTGGAGAGTGTGGTTGAAGAAATGGTTTTAAAAGGCTGTTACCGGTAGAGTCACGGAATTAATTT  
TGCTTTTTGCTTTACAAATAATTTTTTATAGCAGCTGGAAAATCACAAAAATAAATAGTCGATGATTTGGCCAATTAGAATCACCT  
TTGATTTCAATAATAATCTAATAGCAACCTAAAAGGCCCTTTGATTAGCATGTTCTTCAATGAAATGGATGTTGAGGTTTTATTTT  
GATTTCTCACATGCACCGACCTGCTGCGGCAACAATTGAATTTCAATTTGTCCCAAAGGAATTCAAAGTAAACTTTTTTAGGCGATT  
ATACAAGACAAGATTGAAAACCTTTTGAAGTATGTATCAAACATCATCTGTTTGTATAAATGTTTTAACAGTTTCAAAAAGTCCA  
ACTAATTTGTTTATGGAATTTGATAAATTTGTCATTTAATAATAATTTTTTTGAGTTTATCAATATGTGTTTTTTGTTTTGTTTTACACA  
GTTGGCAAGAAAGTTGGCAAGGTGGCCCTTAAGTAAAGGACTTCTACCATTACTGTGTAATTTTGTATAGTATTATCACCAGTAC  
TGTATTGACAACCTTCTTTTTCTGCTGACTCTCTCCATCCGACTCATCTGCAAGTGTACCTTGGCGAGCAGCAGCAGCTCGAC  
AAGCGTGCAGTCGATGAAGAGCCAGTGTATTGCTTTTTGACTGAAGAAGTCGCTTGAAGGAGCCTTCAG

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Starry flounder 09A

ATGAAGTTCACCTGCCACCTTCCCTCATGATGTTATCTTCGCTCCTCATGGTGAACCTGGAGAGTGTGGTTFGGAGGAAATGGATTAA  
AAAGGCTACTCACGGTAAAGTCAAGGAATTAATTCGTTTTTTGCTTTTGCAAATATTTTTTTTATAACAGCTGGAAAGTCAAAAA  
TAAATAGTCAATATATTTGGCCAATTAGAATCACTTTGAGTTCAATAATAATCTAAATAACAACCAAAAAGGCCCTTCTTTAATG  
AAATGTACGTTGAAGTTTATTTGAATCTCACATGCACCGACCTGCTGCGGCAACAATTTGAATTCAAATTTCTCCAGAGGAATTC  
AAAGTAAATTTTTCTAGGCGAATTAATCTTTCCATTACTCTGATTTGTTTTAAATATATAAGAATGACTCAATTTGCTATGATAAAAT

AATAAGCCATACATTCTGATTTTTACAAGACAAGATTGAAAACCTCTTAAAAGTACGTATAAAACATCATCTGTATTATAATTGT  
TTAACATTTAACAAATGTCCTACTAATTGTGTTATGGAAATGTATAAATGTCATTTAATATCATTTGCTTGAGTTTATCATTAT  
TTGTTTTGTTTTGTTTTTACACAGTTGGCAAGCATAITGGCAAGGCGGCCCTTGAGTAAGAACTTCTACCATCATACTGTATAAT<sup>c</sup>  
TTTGATAGTATTATCACCAGTACTGTTATTGACAACCTCTCTGTCTGATGACTCTGTTTCATCCAACCTCATCTGCAGTGCCTACA  
TTGGCGGGAAGCAAGAATTCGACAAGCGCGCAGTCCGATGA

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Greenland halibut 12B

ATGAAGTTCACGACCCTTCTCTGGTGTGTTTCATGGTCTGCTCATGGCTGAACCTGGAGAGGGTTTTTTCCGATTGCTTTTTCA  
CGGGATCCACCATGGTAGGGTACGGAATTAATTAGATGTTTACATGGCAAATATTTTAAAGATAACACACCATATGAGTAGTCGAT  
ATATTTGACCAATTAGAATCACTTTAATTTCAATAATAATCACATAACAATCTCTAGGCCATTTAATCTTTCCATTAATCGGATT  
TGTTTTTTTAAATATAGAATAACTGGATCTTTATGCTAAAATAATGAAACATAACATTCTGATTTTACCAGTCAAGATTGAACGTTA  
CTTAAAAGTATGTTTTAAAACATCATCTGTATGTATAAATGTTTGTAGCTGTAAACAAATAGTCCAAATAAATGTGTTTATGGAAATGTA  
TTAATTTGTCATATAATAAATTTGCTTGAATTTATCACCATGTTTTTTGTTTTGTTTTTTTAAACACAGCTGGAAAGTTGATCCATGG  
GTAAGGACTTCTACCATCATACTGTGTATTTTAATAGTATTATCATCAGTACTGTTTATTAACAACCTCTCTTCTATCGCTGACT  
CTCTCCATCAGACTCATCCATCATGGTTACGACGAGCAGCAGGAGCTCGACAAGCGCGCAGTCCGATGA

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Pacific halibut 15A

ATGAAGTTCACGACCCTTCTCTGGTGTGTTTCATGGTCTGCTCATGGCTGAACCTGGAGAGGGTTTTGGGAAATGGATGGGGCC  
CCATATCAGCGGTAGAGTACGGAATTAATTTGCTTTTTCCATTGCAAATATTTAATATGTCATAGCTGGAAAATCACGAAATAA  
GTAGTCGATATATTTGGCCAAATAGAATAACTTTGATTTCAATAATAATCAAATAATCAATCAAAAAGGCCCTTTGATTAGCATGTT  
CCTTCAATAAAAATGGACATTTGAAGTTTTATTTGATGCTCACAATGACCGACCTGCTGCGGCAACAAATGAAATCAAATTTGCTCA  
GAATTTAAAGTACATTTTTCTAGGTGATTTAATCTTTCCATTCACTGATTTATTTTAAATATAGAATAACGATCTTTCTGC  
TAAAATAATAAAACACACATCTGATTTTACCAGTCAAGATTGAACACTACTTAAAAGTATGTATAAAACATCATCTGTATGTATA  
ATTGTTTAACTGTTAAACAATAGTCCAAATAAATGTTGTTAAGGAAATGTATTAATTTGTCATTTAATATCATTTGCTTGAATTTATCA  
CCATGAGTTTTTTGTTTTGTTTTTACACAGGTAGAAGAAGGCCCTGTCAGTAAAGGACTTCTACCATCATACTTTGTAATTTTTATA  
GTATTATCATCAGTACTGTTATTGACAACCTCTCTTGTCTCGCTGACTCTCTCCATCAGGATGAACCTCAGAGCGTCCGAGTTACGA  
CGAGTAGCAGCAGAAGCTCGACAAGCGCGCAGTCCGATGA

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Pacific halibut 15B

ATGAAGTTCACGACCCTTCTCTGGTGTGTTTCATGGTCTGCTCATGGCTGAACCTGGAGAGTGTTTTTTGGGATTGCTTTTTCA  
CGGGTCCACCATGGTAGGGTACGGAAGTAATTCGATTTTTACATGGCAAATATTTTAAAGATAACACACCATATGAGTAGTCGAT  
ATATTTGATATATAGAATCACTTTGATTTCAATAATAATCAAATAACAATCTCTAGGCCATTTAATATTTGCTTTAATTTGGATT  
TGTTTTTAAAATAGAATAACTGGATCTTTATGTTAAAATAATTAACATAACATTCTGATTTTACCAGTCAAGATTGAACACTA  
CTTAGAAGTATGTATAAAACATCATCTGTATGTATAAATGTTTAACTGTTAACTAATAGTCCAAATAAATGTGTTTATGGAAATGTA  
TTAATTTGTCATTTAATATCATTTGCTTGAATTTATCACCATGTTTTTTGTTTTGTTTTTACACAGTTGGAAATTTGATCCATGGGT  
AAGGACTTCTACCATCATACTGTGTATTTTAATAGTATTATCATCAGTACTGTTATTGACAACCTCTCTTGTCTCGCTGACTCT  
CTCCATCAGACTCATCCATCAGGTTACGACGAGCAGCAGGAGCTCGACAAGCGCGCAGTCCGATGA

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C-0 sole PL1/2/6

GCCCACTTTGTATTTCGCAAGGTAATATCGATATTTTTCAAACCTCAITTAGACGAGACCAGGCATTTGGGAAACGTTGCTAAGGTGTTACTG  
TATAATGCAAAATTAATGATCTTTATTTTTCTGTTTTTTTTGCGAATGAAGTTCACTGCCACCTTCTCATGATTTAATCTTCGTCT  
CATGGTCGAACCTGGAGAGTGTGGTATTAGGAAATGGTTTTAAAAGGGCTGCTCACGGTAAAGTACGGAATTAATTTGCTTTTTGCTTTAC  
AAATATTTTTTACAGCAGCTGGAAAATCAAAAATAAATAGTCGATGTATTTGGCCAAATAGAATCACTTTGATTTCAATAATAATCTA  
AATAGCAACCTAAAAGGCCCTTTGATTAGCATGTTCCCTTCAATGAATGGGTGTTGAGGTTTATTTTTGATTTCTCACATGCACCGACCTGCTG  
CGGCAACAATGAATTCAAATTTGCTCCAAAGGAATTCAAAGTAAACTTTTTCTAGGCGATTTAATCTTTCCATAACTCGGCTTTGTTTTTA  
AAAATATATAATAACTCAATCGCTATGATAAAAATAAACAACATACATTCTGATTTATACAAGACAAGATTGAAAACCTCTTGAAGTATG  
TATCAAAACATCATCTGTTTATATAATTGTTTAAACATTTCAAAAAGTCCAACCTAATTTGTTTATGGAATTTGATAAATTTGTCATTTAATA  
TAAATTTTTGAGTTTATCAATATGTTTTTTGTTTTGTTTTTACACAGTTGGCAAGAAAGTTGGCAAGGTTGGCCCTTAAGTAAGGACTTCTA  
CCATTAATFACTGTATAATTTGATAGTATTATCACCAGTACTGTTATTGACAACCTCTCTTTCTGCTGACTCTCTCCATCCGACTCATC  
TGCAGTGTCTTACCTTTGGCGAGCAGCAGCAGCTCGACAAGCGGTGCACTGATGAAGAGCCAGTGTATTGCTTTTTGACTGAAGGAGTCCGC  
TTGAAGGAGCCCTC

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Table 13

Clone Name	Signal peptide	Anionic propiece	Mature peptide
Hal7.5	MKTFSAVAVVVLACMFI	ESTAVPFSEV	TEEVESIDSPVGEHQPGFTSMNLP
Sa14.1	MKTFSAVAVVVLACMFI	ESTAVPFSEV	TEEVESIDSPVGEHQPGFTSMNLP
Sa11	MKAFSAVV - LVIA	CMFIIESTAVPFSEV	TEEVESIDSPVGEHQPGFTSMNLP
Sa12	-----	-----	-----
Sa12.1	MKTFSAVV - PVIA	CMFIIESTAVPFSEV	TEEVESIDSPVGEHQPGFTSMNLP
Sa12.4	MKQFSVAVV - LVMA	CMFIVESTAVPFSEV	TEEVESIDSPVGEHQPGFTSMNLP
WF1	MKAFLAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
JapF2.4	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
WF3a	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
WF3b	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
WF4	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
WFD1.1	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
WFD1.4	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
AP5.1	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
AP5.3	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
AP5.4	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
AP5.5	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
AP6.1	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
AP6.2	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
AP6.4	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
AP6.3	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
Sa18.6	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
Hal7.1	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
Hal7.4	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
Hal8.2	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
Hal8.3	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
Hal15.3	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
Hal11.1	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
WF2	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
YT11.1	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
YT12.1	MKTFSAVAVTLVAFVCI	QSSAVPFQGVQ	EEAAGNDTPVAEHQVMSBESWME
GC9.3	-----	-----	-----

Appendix I. Nucleotide sequences of pleurocidin-like genes and cDNAs referred to in Table 4.

NRC-01

ATGAAGTTCACCTGCCACCTTCCCTCCTGTTGTTTCATCTTCGTCCTCATGGTTGATCTCGGAGAGGGTTCGTCGTAAGAAAAAGGGGTCG
AAGAGAAAGGGGTCCAAGGGAAAGGGGTCCAAGGGAAAGGGCAGGTGGTTGGAAAGGATTGGTAAAGGTAGAGTCACGGAATTAATT
TGCTTTTACATTTGCAAATATTTTCATATAACATTGCTGGAAAAATCAAAAAATAAGTAGTCAATATATTTGGCCAAATAGAATCA
CTTTGATTTCAATAATAATAAATAAACAACCTAAAAGGCCTTTGATTAGCATGTTCTTCAATGAAATGGACATTGTAATTTACTT
TGATTTCCACATGCTACGACCTGCTGCAGCAACATTTGAAAAATAAATTTGTCCCAGAAAGATTTTAAAGTACATTGTTATAGGCGATT
TATCTTTCTATTACTCAGATATTTGTTCAAACCAATAGAATAACTGGATCTCTATGCTAAAATAAATAAAACACACATTGATGTTA
CCAGTCAAGATTGAAAGCTGTTTAAAAGTAAAGTATGAAACATCCTCTGTATGTATAATTTGTTAACTGGTAACTTATAGTCCTAATA
ATTGCGTTATGGAATGTATTAATTTGTCATTTAATAATAAATTTGCTGGAATTTATCACCTGTGTGTTTTGTTTTGTTTTACACAGCTG
GCGGGATAATATCGGGGGGGCCCTTGAGTAAGGACTTCCACCATCATTAAGTGTGTAATATTTATAGTTATGATCAGTACAGTTATT
AACAACTTCTCTGTCTCGCTGAACTTCTCCATCAGTCACCTCGGGCAGGGGCAGGTGCAGGGGCCGATTACGACTACCAGGAGGG
GGAGGAGCTCAACAAGCGCGCAGTCGATGAA

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NRC-02 and NRC-03

ATGAAGTTCACCTGCCACCTTCCCTCCTGTTGTTTCATCTTCGTCCTCATGGTTGATCTCGGAGAGGGTTCGTCGTAAGAAAGTGGTTG
AGAAGGATTGGTAAAGGTGTCAAGATAAATGGCGGGGGCGCCCTTGATCACCTCGGGCAGGGGCAGGTGCAGGGGCAGGATTACGAC
TACCAGGAGGGGCAGGAGCTCAACAAGCGCGCAGTCGATGAA

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NRC-04

GCCACCTTTGATTCGCAAGTAATATTGATAATTTTTCATATTCATTTAGACAAATGTGCTCAGCTTGTACTGTATAATGCAAAAG
TTAATGATCTTTATTTTCTGTTTTTTTTGTTAGAAATGAAGTTCACCTGCCACCTTCCCTCATGATTGCCATCTTCGTCCTCATGGTTG
AACCTGGAGAGTGTGGCTGGGGAAGCTTTTTTAAAAAGGCTGCTCACGGTAGAGTCACAGAATTAATAGCTTTTTGCTTTGCAAAAT
ATTTTTTTTATAACAGCTGGAAAATCAAAAAATAAATAGTATATATATTTGGCCAAATAAATCACTTTGATTTCAATAATAATCTA
AATAACCAACCTAAAAGGCCTTTGATTAGCATGTTCTTCAATGAAATGTACGTTGAGGTTATTTTGTATCTCACAAAGCACCAC
TGCTGCGTCAACAATGAATTTCAAATTTGTCCAAAGGAATTCAAAGTAAATTTTTCTAGGCGATTAACTCTTCCATTACTCTGAT
TTGTTTTTAAAAATAAGAATAACTCAATCTCTATGATAAAACAATACACATACATTGATTTTTATAGGACAAGATTGAAAACCTT
CTTACAAGTATGTATAAAACATCATCTGTATGTATAAATGTTTAAACATGTAACAACACTAGTCTACTAATTTGTTAAATTTGTCATTT
AATATCAATTTGCTTGTGTTTATCATTTATGTTGTTTTGTTTTTTTACACAGTTGGCAAGCATGTTGGCAAGCGCCCTTACGTAAG
GACTTCTACCAATTTTACGTATAAATTTGATAGTGTATCACAGTACTGTTTTTTGACAACTTCTCTATTTCTGCTGACTCTCTCCA
TCCGACTCATCCGCGAGTCATTACCTTGGCGATAAGCAGGAGCTCAACAAGCGTGCAGTCGATGAAGACCCAAATGTTATGTTTTT
AATGAAGAAAT

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NRC-05

ATGAAGTTCACCTGCCACCTTCCCTGCTGTCCTCGTCCATATGGCTGAGCCTGGAGAGTGTTCCTTAGGAGCCCTTATCAAA
GGGGCCATACATGGTAGAGTCAAGGAATTAATAGATTTTTTACATGTCAAATAATGTAGTAGAACAATATAAAGTAGTCAATATAT
TGACCAAGTAGAATCATTTTGTATTTCAATAATAAATAAATAAACAATCTCCAGCGGATTAAATATTTGCAATAATTTGATTTATAG
AATACGGAACAACCTGGATCTTAATGCTAAAATAAATAAACAATACATTTCTGATTTTGGCAGGCAAAATTAACACTACTTTAAAGTAT
GTATAAAACATAATCTGTATGTTATAACAATACTCCAAGCAATTTGTGTGATGAAAATGTATTCATTGTCATTTAATAATAATTTGCT
TGAGTTTATCATCTTGTGTTTTGTTTTGTTTTTCAAGGTTGGCAGGTTTATCCATGGGTAAGGACTTCTACCATCATGACTGTGTA
TTTTAATAATTAATCATCAGTACTGTTATTTGACAACTTCCCTTCTCGTACTCTCTCCATCAGAATGATCCAAAACCATCAC
GTTTATGACGAGCAGGAGCTCAACAAGCGCGCAGTCGATGAA

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NRC-06

GCCACCTTTGATTCGCAAGTAATATCAATATTTTTCAAATTCATTTAGACGAGACCAACCTTTTGGGAAATCTGCTCAGCTTATT
ACTGTATAATGCAAAATGTTAATGATCTTTATTTTTCTGTTTTTTTTTTGTTAGAAATGAAGTTCACCTGCCACCTTCCCTCATGATGTTCA
TCTTCGTCCTCATGGTTGAACTGGAGAGTGTGGTTGGGGAAGCAATTTTAAAGCATGGTTCGTCATGGTAAAGTCACGGAATTAATTA
GCTTTTAACTTTGCAAAATATTGTTTTTTTTTAAACAGCTGGAAACTCACAAAAATAAATAGCCGATATAATTTGGCCAAATATAATC
ACTTTGATCTAAATAACAACCTAAAAGGCCTTTGATTAGCATGTTTCTTCAATAAATAAATGATTGAACACTACTTAAAGGTATGTATAA
AACATCATCATGTGTTTTGTTTTGTTTTTACACAGCTGCCAAGCAATTTGGCCATGCAGCCGTTAAGTAAGGACTTCTACCATTATT
ACTGTATAATTTGATAGTATTTATCACAGTATTGTTATTTGACAACTTCTCTTTTTTCTGCTGATCCGACTCATCCGAGTCATTAC
CTTTGGCGAGCAGCAAGATCTCGACAAGCGCGCAGTCGATGAAGACCCAAATGTTATGTTTTTGAATGAAGAAAT

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NRC-07

ATGAAGTTCACCTGCCACCTTCCCTCATGATGTGCATCTTCGTCCTCATGGTTGAACTGGAGAGTGTGCTTGGGGGAAATGTTTTAAA
AAGGCCACACACGGTAGAGTCAAGAATTAATAGCTTTTGTCTTTGCAAAATATTTTTTATAACAGCTGGAAAATCAAAAAATAA
ATAGTCTATATAATTTGGCCAAATTAGAATCACTTTGCTTTCAATAAAAAATCTAAAATAACAACCTAAAAGTCTTTGATTAGCATTTTC
CATCAATGAAATGGACGTTGAGGTTTATTTGATTCTCATATGCACCGACCTGCTATGTCAACAATTTGAATACAAATTTGTCCCAGA
GGAATTCAAAGGAAATTTTTCTAGGCGATCAATCTTCCATTACTCGGATTTGTTTTTAAATAATAAGAATAACTCAATCTCTATG
ATAAATAATAACAATACGTAAGGATTTTTTCAAGACAAGATTGAAACTTCTTAAAAGTACGTATAAAAAATCATCATCTGTATTTAT
AATTGTTTTAACATTTAAACAAATAGCCCTACTAATTTGTTTATGAAATGTATAAATTTGTCATTTAACATAACTTTGTTGAGTTTATC
ATTAATTTGTTTTGTTTTGTTTTTACACAGTTGGCAAGCATGTTGGCAAGGCGCCCTTACGTAAGGACTTCTACCATCATTAAGTATC
TAATTTTGATAGTATTTATCACAGTACTGTTATTTGACAACTTCTCTTGTCTGCTGACTCTCTCCATCCGACTCATCCATAGTGCTT
ACCTTTGGCGACAAGCAAGAATCTGACAAGCGCGCAGTCGATGAA

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NRC-08

TAATAAAAATAATGTGTAAGTCTTCCACTTTTTTACTGTATTTACTTAAACAGAAAATATTCTCACGATTCTGGAGCTGCAGCC
ACTAAGTGTTCCTTCATGAAGTGAATACACAATGTTCTTAAACAACCTCACCCAAATTAACCAGAATCTCAAAAGTGAGGAAGTGA
AGGAGTCTGCTGTTGTTTTCAAATTTTTTGAATGATCTACCACATATGTGAGCTCCTCCTGTTATAGCTCTAAATGTTACACAATGAA
TGTGAAGTCAGTTCTGTGTATAAAGAGTTGCCCTCTGTAGAGCATACAACAGATTTTCACTTTGAAATCTCACAAACCTCACTTTGT
ATTCGACAGGTAAGATCGATAATTTTTCAAACCTCATTTAGACGAGACCAAGTATTTGGGAAATGTGCTCAGCTTGTCAATGTATAATG
CAAATGTAAACAATCGTTTTGTTTTCTTATGTTGTTTTGTTAGGATGAAGTTTCGCTACTGCCTTCCGATGTTGTTCCATGGTCTGCTC
ATGGCTGAACCTGGAGAGTGTGCTTCTACAGAGGACATCATCAAGTCTATCTCGGGTAGAGTCCAGGAATTAATTTATTAATAAC
AATGAAATAACAACAAAAGGCCTCTGATTAGCATGTTCTTCAATGAAATGGTTCGTTTTTATCTATTTGATTCTCACATGCAAC
GACCTGCTGCGGCAACATTTGAAAATCAATCTTTTTTACACAAATTCAAAGTACATTTGATTTATTCGATTTAATCTTAAACATTAATC





TTACACAGGTATCAGGGCGATCCATCAGTAAGGACTTCTACCATCATGACTGTGTATTTTAAATAGTATTATCATCAGTACTTTTAT  
TAAACAACCTCTCTTGTCTCGTCTGACTCTCTCCATCAGTCTCATCCATGGTCAAAGATACGACGAGCAGCAGGAGCTTGACAAGCGCT  
CAGTCGATGACAACCCCGGTGCTATTGTTTTGACTGAAGACGTGCGCTTGAAGGAGCCTTCAG

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NRC-102

ATGAAGTTCACTGCCACCTTCTGGTGTGTCCATGGTCTCATGGCTGAACCTGGAGAGGGTTTCTTTGGAGCCCTTATCAA  
GGGGCCATCCATGGTGGCAAGTTGCTCCATAAACTCATCAAAAAAACAATGAACATCACGGTTATGGCAAGCATTTGGGGCTTGAC  
AAGCGCGCAGTCGATGA

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NRC-103

TTGAAAGTGAGGAAGTGAGAGGAGGACTAGGTCCTGTGTTTTAGTCTGTTGTAATATCTAACACTATCTGAGCCCCCTCCTGCAATAA  
CTCTAAATGTTACACAGTACTAGGAAAGTCACTCTGTGTATATAAAGAGTTGCATCTGTTGTTATCAGTAGACAACAGATTACACC  
TTGAAATCTCAAAGCTCATTGTTGTTTTCGACAGGTAAGATCGATATGTTTTCAAACCTCATTTAGATGAGACCAAGCATTTGGGAAA  
TGTGCTCAGCTTCTAACGTATGATGCAAAATGTTAAACAATCTTTTTGTTCTGTGTTTTGTAGGATGAAGTTGGCTGCCGCCCTTCT  
GGTGTCTGTTCTGGTCTGCTCATGGCTGAACCTGGAGAGAGTTTTTTGGGATTTCTTTTTCATGGTATCCGCCATGGTAGGGTAC  
TGAATTGATACATTTTTACATGGCAAATATTTGAATGTAACATACTATATGAGTTGTCAATATATGTGGCCAAAGTAGAAGCCTTTG  
ATTTCAAGTAATAAATAAATAAACAATCACTAGGCCATTTAAATAATGTCATTAATAACACTTGTTTTTATATAGAAATATAGAACT  
GGATCTTTATGCTAAAAATAAACAATGAATTCAGATTTTAAAGATTTTTCAAGATTGAAAACACTTTAAAAGTATGTAATAAACA  
TCATCTGTATGTATAAATAAATACTTGTCCAGATAATTTGTGTTGTGGAAATGTGTTAATTGACATATATCATTTGCTTGAATTTATC  
ATTATCTGCTTTGTTGTTTTTACACAGGTATCAAGCGATCCAAGGTAAGGACTTCTACCTTATGACTGTGATTTTTTAAATAGT  
ATATATCTCAGTACTGTTATTTGAAAACCTTCTTGTCTCGTCTGACTCTCTCCATCAGAATGATCCATGGTAAACAGTTTAGACGAGAT  
GCAGGAGCTCGACAAGCGCTCATTGATGACAACCCCAAGCAATGTTTTGACTGAAGAGTCTGCCCTGAAGGAGCCTTCAGATG  
ATATATAATGCTTCTTGTCTTTCAATGAAAATAAATGAATAATTACCCGCAACAGC

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NRC-104

TACTTTTATCTACCACATATGTGAGCTCCTCCTGTTAFAACTCTAAATGTTACACAATGAAGATGAGGTCATTTCTGTGTATATAAAG  
AGTTGCTCTGTATAGTAGACAACATATTTCACTTTGAAATCCCAAAAGCTCACTTTGTACTCAACAGGTAAGATCGATATTTAAA  
AACTAATTTAGACGAAACCAAGCATTGTTGGGAAATTTGCTCAACTTCTAAATGTATGATACAAATGTTAAACAATCTTTTTATTTCTGT  
TGTGTTTTTTGTAGGATGAAGTTCACTGCCACCCCTCCTCCTGTTGTTTCTCTCGTCTCATGTTGATCTCGGAGAGGGTCTGTCG  
TAAGAAAAGGGGTGAAAGGAAAGGGTCCAAGGGAAAGGGTCCAAGGGAAAGGGCAGGTGTTGAGCAGGATTTGTTAAAGGTAG  
AGTCACGGAATTAATTTGCTTTTTACATTTGCAAATATTTTTCATATAACATTTGCTGGAAAATCAAAAAATAAGTAGTCAATATATT  
TGGCCAAATAGAACTTTGATTTCAATAATAAATAAATAAACAACCTAAAAGGCTTTGATTTAGCATGTTTCTTCAATGAAATGG  
ACATTTGTAATTTACTTTGATTTCTCACATGCTACGACCTGCTGCAGCAACATTTGAAAATAAATTTGTCCCAGAAGATTTTAAAGTAC  
ATTTGTTATAGGCGATTTATCTTTCTAATTTACTCAGATATTTGTTCAAACCAATAGAAATAAAGTGGATCTCTATGCTAAAAATAA  
ACACATTTAGATGTTACCAGTCAAGATTGAAACGCTGTTTAAAAGTAAGTATGAAACATCCTCTGTATGTAATAATTTGTTAACTGGTA  
ACTTATAGTCCATAAATTTGCTTTATGGAATGTAATAATTTGCTGGAATTTATCACTGTGTGTTTTGTT  
TGTTTTTACACAGCTGGCGGATAAATATCGGGGGGCCCTTGAGTAAGGACTTCTACCATCATTACTGTGTAATATTTATAGTTAT  
GATCAGTACAGTTAATAACAATTTCTTTGCTCTCGTGAACCTTCTCCATCAGTCACTCGGGCAGGGGCGAGTGCAGGGGCGGAT  
ACGACTACCAGGAGGGGAGGAGCTCAACAAGCGCTCAGACGATGATGACAGCCCAAGCTTTAATTTTTGACTGAGAAAGTCTGCC  
CTGAAGGAGCCTTCAGATGATATATAATGCTTCTGGCTTTTCTGAAATAAATAACGTTTACTTGAACAGCAACCATG

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NRC-105

TTATGAAGTTCACTGCCACCTTCTGGTGTGTTTTCATGGTCTGCTCCTCATGGCTGAACCTGGAGAGGGTTTTGGGAAATGGATGGGG  
CCCATATCAGCGGTAGAGTACCGAATTAATTTGCTTTTTCCATTTGCAAATATTTTAAATATTGCATAGCTGGAAAATCACGAAATAA  
GTAGTCGATATATTTGGCCAAATAGAACTCACTTTGATTTCAATAATAATCAAAAATAACAATCAAAAAGGCCTTTGATTTAGCATGTT  
CTTCAATAAAAATGACATTTGAAGTTTATTTGATGCTCACATGCACCGACCTGCTGCGGCAACAAATGAAATCAAATTTGTTCTCAGA  
ATTTAAAGTACATTTTTCTAGGTGATTTAACTTTCCATTAACCTGATTTGTTTTTATAAATAAATAAATAAATAAATAAATAAATAA  
AAATAAATAAACAACATTTCTGATTTTACCAGTCAAGATTGAACACTACTTAAAAGTAATATAAACAATCATCTGTATGTATAAATTG  
TTTTAACTGTTAAACAAGTCCAAATAATTTGTTTATGGAATGTAATAATTTGCTAATTAATAATCATTTGCTTGAATTTATCACCATG  
TGTTTTTTGTTTTTTTTACACAGGTGAAAAGAAGCCCTTGACGTAAGGACTTCTACCATCATTACTTTGTAATTTTATAGTATTA  
TCATCAGTACTGTTATTTGACAACCTTCTTGTCTCGTGACTCTCTCCATCAGGATGAACTCAGAGCGTTCAGAGTTACGACGAGCGG  
CAGCAGCAGCAGCAGGAGCTCGACAAGCGCGCAGTCGATGA

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NRC-106

ATGAAGTTCACTGCCACCTTCTGGTGTGTTTTCATGGTCTGCTCCTCATGGCTGAACCTGGAGAGGGTTTTGGGAAATTTGGATCGTGCGC  
CCTATCGGAGGTGAAAAGAAGGCCTTGCAGATGAACTCAGAGCGTTCGAGTTACGACGAGCGGCAGCAGCAGCAGCAGGAGCTCGAC  
AAGCGCGCAGTCGATGAAA

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NRC-107

ATGAAGTTCACTGCCACCTTCTGGTGTGTTTTCATGGTCTGCTCCTCATAGCTGAACCTGGAGAGAGTCTTTTTGGAAAAGTTTCTCAAG  
AAAGTTGTCATGCTGGCAGTCAATTTGGCGAGACAGCCTTGCATGTCGCGCAGAGCATCACGGGCTTATCGCGCATCACGGGTGT  
CACGGGCGTCACGGGGTCAAGCGCTCACGGGGTCAAGCGCTCACGGGCGTTCGCGGTTACGACGAGCAGCAGCAGGAGGAGCTC  
GACAAGCGCGCATTCGATGA

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NRC-108

TATGAAGTTCACTGCCACCTTCTGGTGTGTTTTCATGGTCTGCTCCTCATGGCTGAACCTGGAGAGGGTTTTGGGAAATTTGGATGGGGC  
CCATATCAGCGGTAGAAAAGAAGGCCTTGCACATGAACTCAGAGCGTTCGAGTTACGACGAGCGGCAGCAGCAGCAGCAGGAGCTCGA  
CAAGCGCGCAGTCGATGAAA

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NRC-109

ATGAAGTTCACTGCCACCTTCTGGTGTGTTTTCATGGTCTGCTCCTCATGGCTGAACCTGGAGAGGTTTTTTGGGATTTGCTTTTTTAC  
GGGGTCCACCATGTTAGGGTCAAGGAAATTCGATTTTTTACATGGCAAATATTTTAAAGATAACACACCATATGAGTAGTCGATAT  
ATTTGGCCAATTAGAATCACTTTGATTTCAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA  
TTTTAAAATAA  
GAAGTATGTAATAAACAATCATCTGTATGTATAAATTTGTTAACTGTTAACGAATAGTCCAAATAAATTTGTTTATGGAATGTAATAA  
TGTCATTTAATAATCATTTGCTTGAATTTATCACCATGTTTTTTGTTTTTTTTTACACAGTTGGAAAGTTGATCCATGGGTAAGGAC  
TTCTACCATCATTACTGTGATTTTTTAAATAGTATTATCATCAGTACTAATTTGACAACCTTCTCTTGTCTCGTGACTCTCTCCATC

AGACTCATCCATGGCGGTTACGACGAGCAGCAGGAGCTCGACAAGCGCGCAGTCGATGAA

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NRC-110

GCCCACTTTGTATTGCGCAAGGTAAGAGCGGATATATTTCAAATTCATTCGGATGAGACCAAGCATTGGGAAATGTGCTCAGCTTGT  
ACTGTTAATGCAAATGTTAAACAATATCCTTTTTCTGTTGTTTTTGTAGAATGAAGTTCCGCTGCCGCTTCCTCATGATGTTCAATGG  
TCGTCCTCATGGCTGAACCCGGAGAGGCTCGTTGGGGAACGTTCTTCAAACATATTTTCAAAGGTAGAGTACAGAAATTAATTTGCT  
TTTTACATTGCAAATATTTTCATATAACATAGCTGGAAAAACAAAAATAAGGGCTTGATATATTTGGCAAAGTAGAATCCCTTTG  
ATTTCAATAATAATCAAATAAAAAATCAGAAAGGCCTTTGATTAGCATGTTCTTCAATAAAATGGACATGTAGTTTATTTTGAT  
CTCAAATGCAACCACTGCTGCGCAACAATGAAATCAAATTTGCTCCGAAACATTTAAAGTACATTTTCGAGGCAATTTAATC  
TTTTCTTTGATCGAATTCGTTTTTAAAAATATAGAATAACTGGATCTTTATGCTAAAAATAATAATCATACATTCTGATTTTACCAG  
TCAAGATTGAACGCTACTTAAAGTATGTATAAAACATCATCTGTATGTATAAATTTGTTAACTTTTAACTAATAGTCTAATAATTTG  
TGTTATGGAAATGTATTCTATTGTCATTTAATATCATTTGCTTGAATTTTACCATGTGTTTTTGTGTTTACACAGCTGGAAG  
GTTTATCCATGGGTAAGGACTTCTACCATCATTTACTGTGTATTTTAAATAGTATTATCATCAGTACTGTTATTGATAACTTCTCTTG  
TCTCGCTGACTCTCTCCATCAGTGGATCCAGGCACAAATGACGGCGAGCAGCAGGATCTCGACAAGCGCTCAGTGGATGATGAGC  
CCAGTGTATTGTTTTTGAATGAAGAAGTGCCTTGAAGGAGCCTTCAG

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NRC-111

GCCCACTTTGTATTGCGCAAGGTAAGAGCAATATATTTCAAATTCATTTAGACGAGACCAAGCATTGGGATCTGTGCTCAACTTGTA  
ACTGTATAATGCAAATGTTAAACAATATCCTTTTTCTGTTGTTTTTGTAGAATGAAGTTCCGCTGCCGCTTCCTCATGATGTTCAATGG  
TCGTCCTCATGGCTGAACCCGGAGAGGGTGGATGCTGGATACCTGCCCTTGAATAGGATCTATCATGGTAGAGTACAGAGTTAATTTGCT  
TTTTACATTGCAAATATTTTAAATAAACATGGCTGGAAAAACAAAAATGAGTACTCGATATATTTGGCAAAGTAGAATCCCTTTG  
ATTTCAATAATAATCAAACAACAATCAAAGGCATTGATTAGCATGTTCTTCAATGAAATGGACATTTGATGTTTATTTTGATT  
CTGACATGCACCAACTTGTCTGCGGCAACAATGAAATTTCAATTTGCTCAGAAAAATTTAAAGTACATTTTCTTTCCATTTAGTCGG  
ATTTGTTTTAAAAATAACAGAAATAACTGGATCTTTATGCTAAAAATAAAATCATAATTCTGATTTTACCAGTCAAGATTGAACGC  
TACTTAAAGTATGTATAAAAACATCATCTGTATTGATAAATTTGTTAACTTTTAACTAATAGTCTAATAAATTTGTTTATGGAAATGT  
ATTCATTGTCATTTAATAATCATTTGCTTGAATTTTACCATGTGTTTTGTTTGTGTTTTTACACAGCTCTACTGAGGATCAATCGGT  
AAGGACTTCTACCATCATTACTGTGTAATTTAATAGTATTATCATCAGTACTGTTATTGATAACTTCTCTTGTCTTGTCTGGCTCTC  
TCCATCAGCCAAATGGTGTATTATCGTGGCACTGGCAGGTCAGCTCGAGCAGCAGGCTCTCGACAAGCGCTCAGTGGAGGACCAG  
CCAGTTCATTGCTTCTGCTGAAGAAGTGCCTTGAAGGAGCCTTCAG

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NRC-112

GCCCACTTTGTATTGCGCAAGGTAAGAGCAATATATTTCAAATTCATTTAGACGAGACCAAGCATTGGGATCTGTGCTCAACTTGTA  
ACTGTATAATGCAAATGTTAAACAATATCCTTTCTGTTGTTTTTGTAGAATGAAGTTCCGCTGCCGCTTCCTCATGATGTTCAATGG  
TCGTCCTCATGGCTGAACCCGGAGAGGGTGGATGCTGGATGCTGCCCTTGAATAGGATCTATCATGGTAGAGTACAGAGTTAATTTGCT  
TTTTACATTGCAAATATTTTAAATAAACATGGCTGGAAAAACAAAAATGAGTACTCGATATATTTGGCAAAGTAGAATCCCTTTG  
ATTTCAATAATAATCAAACAACAATCAAAGGCATTGATTAGCATGTTCTTCAATGAAATGGACATTTGATGTTTATTTTGATT  
CTGACATGCACCAACTTGTCTGCGGCAACAATGAAATTTCAATTTGCTCAGAAAAATTTAAAGTACATTTTCTTTCCATTTAATCGG  
ATTTGTTTTAAAAATAACAGAAATAACTGGATCTTTATGCTAAAAATAAAATCATAATTCTGATTTTACCAGTCAAGATTGAACGC  
TACTTAAAGTATGTATAAAAACATCATCTGTATTGATAAATTTGTTAACTTTTAACTAATAGTCTAATAAATTTGTTTATGGAAATGT  
ATTCATTGTCATTTAATAATCATTTGCTTGAATTTTACCATGTGTTTTGTTTGTGTTTTTACACAGCTCTACTGAGGATCAATCGGT  
AAGGACTTCTACCATCATTACTGTGTAATTTAATAGTATTATCATCAGTACTGTTATTGATAACTTCTCTTGTCTTGTCTGGCTCTC  
TCCATCAGCCAAATGGTGTATTATCGTAGGCACCTGGCAGGTCAGCTCGAGCAGCAGGCTCTCGACAAGCGCTCAGTGGAGGACCAG  
CCAGTTCATTGCTTCTGCTGAAGAAGTGCCTTGAAGGAGCCTTCAG

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NRC-113

ATGAAGTTCACTGCCACCTTCTGGTGTGTTGTTTATGTTGCTTCTCATGGCTGATCCGGAGAGTGTGGTTGGAAAAAGTGGTTCACT  
AAAGTGCCAAAGCACCTTGGCCAGGCGCCATTAACGGTTTTGGCCTTCTTGGCAAGAGCAGCAAGAGCTCGACAAGCGCTCAGAGGAT  
GACGAGCCAGTGCTATTGTTTTTTGAA

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NRC-114

ATGAAGTTCACTGCCACCTTCTGGTGTGTTGTTTATGTTGCTTCTCATGGCTGATCCGGAGAGTGTGGTTGGAAAAAGTGGCTCCGT  
AAAGGTAGAGTCATGGATTTAATTTGCTTTTTACATTGCAAATACTTTAAATAACAATAGTTGGAAAAACAAAAATAAGTAGTCTG  
ATATATTTGGCCATATAGAATCACTTTGATTTCAATAATAATCAAACAACAATCAAAGGCCATTGATTAGCATGTTCTTCACT  
AAAATGGACATTTGTCATTTATTTGATTCTCAGGCAACCACTGCTGGCGCAACAATGAAATCAAATTTGCTCAGAAGAAATC  
AAAGTACATTTGTTCTAGGCGATTTAATCTTTCCATTCACTGGATTTGTTTTTAAAAATAAGAATAACTGGATCTCTATGTTAAAAT  
AATAAAAACACATTTCTGATTTTACCTGTCAAGATTGAACACGACTTAAAGTATGTATAAAACATCATCTGTATGTATAAATTTGTT  
AACTGTCAACTAATAGTCCAAATAAATTTGTTTATGGAATGTATTCTTGTATATAAATATCATTTGCTTGAATTTTACCATGTTG  
TTTTTGTGTTTTTACACAGGTTGCCAAGCACTTGGCCAGGCGGCCATTAAGTAAGGACTTCTACCATCATTACTGTGTAATTTTA  
ACAGTATTATCATCAGTACTGTTATTGACAATACTCTTGTCTCTGTGACTCTCTCCAGGGTTTTGGCCTCTTGGCAAGAGCAGCAG  
GAGCTCGACAAGCGCTCAATGGATGACGAGCCAGTGTATTGTTTTTGAAGTGAAGAAGTGCCTTGAAGGAGCCTTCAG

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NRC-115

GCCCACTTTGTATTGCGCAAGGTAAGAGCGGATATATTTCAAATTCATATAGACGAGACCAAGCATTGGGAAATGTGCTCAGCTTGT  
ACTGTATAATGCAAATGTTAAACAATGTTTTGTTCTGTTGTTTTTGCAGAATGAAGTCCGCTGCCGCTTCCTGGTGTGTTTCAATGG  
TCGTCCTCATGGCTGAACATGGAGAGGGTTTTGGGATTTCTATATGAAGCCTGGTAGAGTACAGGAATTAATTCGATTTTAAACATG  
GCAAAATATTTTAACTAATAACATACCATATAGTAGTCGATTAATTAATTTGATTTGTTTTTAAAAATAAGAATAAATTTGATCTTTAT  
GCTAAAAATAATTAACATACATTTCTGATTTTACCAGTTAAGATTGAACGCTACTTAAAGTATGTATAAAACATCATCTGTACATAT  
AATGTTTTAACTGTTAAACCAATAGTCCAAATAAATTTGTTTGGAAATTTATTAATTTGCTTAAATATCATTTGCTTGAATTTGCT  
ACCATGTGTTGTTGTTTTTACACAGGTTAGAAAGATTTCCATGGTGAAGGACTTCTACCATCATTACTGTATTATTTTACGAG  
TATTATCATCAGTACTGTTATTGATAAATACTCTTGTCTCTGTGACTCTCTCCAGGGTTTTGGCCTCTTGGCAAGAGCAGCAG  
AGCAGGAGGTCGACAAGCGCTCAGTGGATGACAAACCCAGTGCATTTGCTTCTGACTGAAGAAGTGCCTTGAAGGAGCCTTCAG

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NRC-116

ATGAAGTTCACTGCCACCTTCTGGTGTGTTGTTTATGTTGCTTCTCATGGCTGAACTTGGCGAGGGTTATTGGCGCTTCCGCAACCAC  
CGTGGTGAAGGTTATCCAGAGGCATTTCTGCTGACGTCGAGCAGCAGGAGCTCGACAAGCGCTCAGTGGATGACGAGCCAGTCT  
ATTGCTTTTTGA

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NRC-117

ATGAAGTTCAGTCCACCTTCCTCGTGTGTTTCATCGTCACTGTTTGAACCTGGAGAGTGTGTTTTGGAAATGCTTTTTACCGGGTCCA  
CCATGGTCCGGTACGGAAGTAGTTCGATTTTTACATGGCAAATATTTAAATGAAACATACCATATGAGTAGTCGATATATTTGGCC  
AAGTAGAATCACTTTGACTTCAATAATAATCAAAAACATAATCAAAAAGCCATTGATAGCATGTTCTTCAATGAAATGGACAT  
GAGGTTTTATTTGATCTCACAGGCACCAACCTGCTGCGGCAACAATTGCATTCAAAATTTGTCCCAAAGAACTTAAATTAACATTT  
CTGGCCGATTTAATCTTTGCAAAAATGGATTTGTTTTAAAAATATAGAATAAAGTGGATCTTTATGCTCAAATAATTAATCATA  
TCTTATTTTATCAGTCAAGATTGAACGCTACTTAAAAGTATGTATAAAACATCATCTGTATGTATAAATGTTTAACTTTAACTAAA  
AGTCCATAAATATGTTGTTATGAAATGTATTAATTTGTCATTTAATATCATTTTCTTGAATTTATCACCATGTGTTTTGTTGGTTT  
TTACACAGCTGGAAGTTGATCCATAGGTAAGGACTTCTACCATCATTTACTGTATAAATGTTAATAATAGCATTATCATCAGTACTGT  
TATTGATAACTTCTCTTGTCTCGTCTGACTCTCTCCATCAGATTATCAACCGTACGGTGACGTCGAGCAGCAGGAGCTCGACAAGC  
GCTCAGTGGATGACGAGCCAGTTCTATTGCTTTTGCCTGAAGAAGTCCGCTTG

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NRC-118

ATGAAGTTCAGTCCACCTTCCTGGTGTGTTTCATGGTCTGCTCATGGCTGAACCTGGAGACTGTATTTTTGGATTGATTGCGACT  
GCGGTCCACAATGGTAAGTCAAGGAATTAATTCGATTTTTACTTGGCAAATATTTAGTATAACATACCTTATGAGTAGTCGATATA  
TTTGACCAAGTAGAATCACTTTGACTTCAATAATAATCAAAAATAACAATCTCTAGGCAATTTAATATTTGCATTAATTTGATTGTT  
TTTAAAAATATAGAATAAAGTGGATCTTAAATGCTAAAATAATTAACATACATTTCTGATATTACCAGTCAAGATTGAACGCTACTTAA  
AAGTATGTATAAAACATCATCTGTATGTATAAATGTTTAACTGTGACTAATAGTCCATAAATTTGTGTTATGAAATGTATTCAAT  
GTCATATAAATATCACTTTGCTTGAATTTATCACCATGTGTTTTGTTGTTTTTACACAGCTGGAAGTTGATCCATAGGTAAGGACT  
TCTACCATCACTACTGTATAAATTTAAGAGCATTATCATCAGTACTGTTATTGATAAATCTCTTGTCTCGCTGACTCTCTCCATCA  
GACTACTCGGCTTTTATCATGAGGCTCCCGGGTCTGGCACGGTGACGTCGAGCAGCAGGAGCTCGACAAGCGCTCAGTGGATGAGG  
AGCCAGTTCTATTGCTTTTACTGAAAGAAGTCCGCTTGAAGGAGCCTTCAG

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NRC-119

ATGAAGTTCAGTCCACCTTCCTGGTGTGTTTCATGGTCTGCTCATGGCTGAACCTGGAGACTGTATTTTTGGATTGATTGCGACT  
GCGGTCCACAATGGTAAGTCAAGGAATTAATTCGATTTTTACTTGGCAAATATTTAGTATAACATACCTTATGAGTAGTCGATATA  
TTTGACCAAGTAGAATCACTTTGATTTCAATAATAATCAAAAATAACAATCTCTAGGCAATTTAATATTTGCATTAATTTGATTGTT  
TTTAAAAATATAGAATAAAGTGGATCTTAAATGCTAAAATAATTAACATACATTTCTGATATTACCAGTCAAGATTGAACGCTACTTAA  
AAGTATGTATAAAACATCATCTGTATGTATAAATGTTTAACTGTGACTAATAGTCCATAAATTTGTGTTATGAAATGTATTCAAT  
GTCATATAAATATCACTTTGCTTGAATTTATCACCATGTGTTTTGTTGTTTTTACACAGTTGGAAGTTGGTCCATGGGTAAAGGACT  
TCTACCATCACTACTGTATAAATTTAAGAGCATTATCATCAGTACTGTTATTGATAAATCTCTTGTCTCGCTGACTCTCTCCATCA  
GACTACTCGGCTTTTATCATGAGGCTCCCGGGTCTGGCACGGTGACGTCGAGCAGCAGGAGCTCGACAAGCGCTCAGTGGATGAGG  
AGCCAGTGTCTATTGTTTTTGAATGAAGAAGTCCGCTTGAAGGAGCCTTCAG

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NRC-120

ATGAAGTTCAGTCCACCTTCCTGGTGTGTTTCATGGTCTGCTCATGGCTGAACCTGGAGACTGTATTTTTGGATTGATTGCGACT  
GCGGTCCACAATGGTAAGTCAAGGAATTAATTCGATTTTTACTTGGCAAATATTTAGTATAACATACCTTATGAGTAGTCGATATA  
TTTGACCAAGTAGAATCACTTTGATTTCAATAATAATCAAAAATAACAATCTCTAGGCAATTTAATATTTGCATTAATTTGATTGTT  
TTTAAAAATATAGAATAAAGTGGATCTTAAATGCTAAAATAATTAACATACATTTCTGATATTACCAGTCAAGATTGAACGCTACTTAA  
AAGTATGTATAAAACATCATCTGTATGTATAAATGTTTAACTGTGACTAATAGTCCATAAATTTGTGTTATGAAATGTATTCAAT  
GTCATATAAATATCACTTTGCTTGAATTTATCACCATGTGTTTTGTTGTTTTTACACAGTTGGAAGTTGGTCCATGGGTAAAGGACT  
TCTACCATCACTACTGTATAAATTTAAGAGCATTATCATCAGTACTGTTATTGATAAATCTCTTGTCTCGCTGACTCTCTCCATCA  
GACTACTCGGCTTTTATCATGAGGCTCCCGGGTCTGGCACGGTGACGTCGAGCAGCAGGAGCTCGACAAGCGCTCAGTGGATGAGG  
AGCCAGTGTCTATTGTTTTTGAATGAAGAAGTCCGCTTGAAGGAGCCTTCAG

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NRC-121

ATGAAGTTCAGTCCACCTTCCTCGTGTGTTTCATGGTCACTGTTTGAACCTGGAGAGTGTGTTTTGGAAATGCGTTTTTAC  
GGGTCCACCATGGTAGGGTCAAAAAGTGAATTTGATTTATACATGCCAAATATGTTAATGAAACATACCATATGAGCAGTCTGATTT  
ATTTGGACAAGTAGAATCACTTTGATTTCAATAGTAATTAATAACAATCAAAAAGCCCTTTGATTTAGCATGTTCTTCAAATGAAA  
TGGACATTTGAGGTTTATTTGATTTCTCACCTGCATCGACCTGCTGCGGCAACTATTGAAATCAAAATTTGTCCAGAAGAACTTAAAT  
TAACATTTTCTAGGCCATCTAATCTTTGCAATGAATTTGATTTGTTTTCAAAAATAAGTGGATTTTATGCTAAAATAATA  
AAAACACACATTTCTGATTTTACCAGTCAAGATTGAACACTACTTAAAAGTACGTATAAAACATCATCTGTATGTATAAATGTTTGGAC  
TTTTAACAAATAGTCAAAATGATTTGTTATGAAATGCAATTAATTTGATTTAATATCATTTACTTGAATTTATCACCATGTGTTTGT  
TTGTTTTTTAGCAGGTGGAGGTTTTCTCAATGCGCAAGGACTTCTACCATCACTACTGTGTAATTTAATAGTATTTATCATCAGTAC  
TCTTATTTGACAACGCTCTCTTGTCTCGTCTGACTCTCTATCAGATTAAACCCAGGGTATCGCGTTACGACGAGCAGCAGGAGCTCG  
ACAAGCGCGCAGTCGATGA

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NRC-122

ATGAAGTTCAGTCCACCTTCCTGGTGTGTTGCTTGGTCTGCTCATGGCTGAACCTGGAGAGGGTTTTCTTTGGAGCCCTTCTCAA  
GGTAGAGTACGGAATTAATTTGATTTGATACATGGCAAATAATTTGTATAACATATCATATGAGCAGTCTGATTTTACCAAGA  
AGAATCATTTTTGATTTCAATAATAATCAAAAATAACAATCTCTGGAGATTATATATTTGCAATAATTTGATTTTATAAATAATAGAA  
CAACTGGATCTTAAATGCTAAAATAATTAACATACATTTCTGATTTTACCAGTCAAAAATAACCACTACTTTAAAGTATGTATAAAAC  
ATCATCTGTATGTTTAAATGTTTAACTTTTAAACAAATAGTCCAAAATAATTTGTGTAATGGAATGTATTCATTGTATATAAATAGT  
TTGCTTACTTTTACCGTGTGTTTTGTTTTGTTTTTACAGGTTGCCAGGCGCTCCATGGGTAAAGGACTTCTACCATCATGACT  
GTGTAAGTTTAAATAATATTTATCATCAGTACTGTTATTAACGACTTCTCTTGTCTCGCTGACTCTCTCCATCAGAAATCATCCCAATG  
CTGTCACGGTTACGACGAGCAGCAGGAACCTCAACAAGCGCGCAGTCTGATGA

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NRC-123

GCCCCTTTGATTTGCAAGGTAAGATCAATAATTTTTCAAATTCATTTAGACGAGACCAACCGTTTTGCGAAATGTGCTCAGCTTGT  
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TCGTCCTCATGGTTGAACCTGGAGAGTGTGGTTGAAAGATTGGTTTCGTAAGGCTAAGAAAGGTAGAATCACGGAATTAATTTAGCT  
TTTTACATTTGCAAAATAGATTTTTTATAACAGCTGGAATCAAAAAATAAATAGTTCGATATAATTTGGCCAATTAAGATCACTTTAAT  
TTCAATAATAATCTAAAATAACAACCTAAAAGGCTTTGATTTAGCATGTTCTTCAATGAAAAGGACATTTGAGGTTTTATTTGATTTCT  
CACATGCAACCGACTGTGCGGCAACAATTTGAATTTGATTTTCCAGAAAGAAATTTCAAAGTACATTTTTCCAGGCGGATTAATCTTT  
CCATTTACTCGGATTTAAAATAAATAAATAAGAACTGAAGCGCTATGATAAATAATTAACATTTCTGATTTTACAAGTCA  
AGATTGAACACTATTTAAAAGTGTGTATAAAACATCATCTGTATGTATAAATGTTTAACTGTTAATAGTCTTAATAAATTTGTTTATG  
GAAATGTATTAATTTACATTTAATATCATTTGCTTGGATTTACCATCATGTTTTTTGTTTTGTTTTTACACAGTTTGGCAAGACTGT

GGCGGCTTGGCCCTTAAGTAAGAACCTTCTACCATCACTACTGTATAATTTGATAGTATTATCACCCAGTACTGTTATTAACACTTCT  
TCTTGTCTCGCTGACTCTCTCCATCCGACTCATCCGAGTCACTTACCTTGGCGAGCAGCAGGAGCTTGCCAAGCGCGCAGTTCGATGA  
CGACCCAGTGTATTGCTTTGACTGAAGAAGTCGCTTGAAGGAGCCTTCAG

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NRC-124

ATGAAGTTCACTGCCACCTTCTCATGATTTTAACTCTCGTCTCATGGTTCGAACCTGGAGAGTGTGGTATTAGGAAATGGTTTTAA  
AAGGCTGCTCAGCGTAAAGTCACGGAATTAATTTGCTTTTGGCTTTTACAAATATTTTTTATAGCAGCTGGAAAATCACAAAAATA  
ATAGTCGATGTATTTGGCCAAATTAGAATCACTTTGATTTCAAATAAATACTAAATAGCAACCTAAAAGGCTTTGATAGCATGTT  
CCTTCAATGAAATGGATGTTGAGGTTTATTTGATTTCTACATGCACCGACCTGCTGCGGCAACAATGAATTCAAATTTGTCCAA  
AGGAATTCAAAGTAAACTTTTCTAGATGATTTAATCTTTCCATAACTCGGCTTTGTTTTTAAAAATATATAAATACTCAATCACTAT  
GATAAAATAAACAACATACATTCTGATTTATACAAGACAAGATTTGAAAACCTTCTAAAAGTATGTATAAAACATCATCTGTTTGT  
TAATTTGTTTTATCATTTTCAAAAAAGTCCAACTAATTTGTTTATGGAATTTGATAAATTTGTCATTTAATATAATTTTTTTGATTTAT  
CAATATGTGTTTTTGTGTTTTTACACAGTTGGCAAGGAAGTTGGCAAGGTGGCCCTTAAAGTAAAGACTTCTACCATTTACTGTA  
TAATTTTGATAGTATTATCACCCGACTGTTATTGACAACTTCTCTTTTCTGCTGACTCTCTCCATCTGACTCATCTGCAGTGTCT  
GCCTTGACAAGCAGCAGCAGCTCGACAAGCGCGCAGTTCGATGA

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NRC-125

GCCCACTTTGTATTTCGCAAGGTAATATCGATATTTTTCAAACCTCACTTAGACGAGACCAAGCATTTGGGAAATGTGCTAAGGTTGTT  
ACTGTATAATGCAAAATTAATGATCTTTATTTTTCTGTTTTTTTTTGCAGAAATGAAGTTCACCTGCCACCTTCTCATGATTTTAAATC  
TTGCTCTCATGGTTCGAACCTGGAGAGTGTGGTTTGAAGAAATGGTTTAAAAAGGCTGTTTACGGTAGAGTTCACGGAATTAATTTGC  
TTTTTGTCTTTTCAAAATATTTTTTATAGCAGCTGGAAAATCACAAAAATAAATAGTTCGATGTTTGGCCAAATAGAATCACTTTGA  
TTTTCAATAATACTAAATAGCAACCTAAAAGGCTTTGATTTAGCATGTTCTTCAATGAAATGGATGTTGAGGTTTTATTTGATTC  
TCACATGCACCGACCTGCTGCGGCAACAATTTGAATTTCAAATTTGTTCCAAAGGAATTTCAAAGTAAACTTTTCTAGGCGATTTAATCT  
TTCCATAACTCGGCTTTGTTTTTAAAAATATATAAATACTCAATCCCTATGATAAAAATAAACAACATACATTCTGATTTATACAAG  
ACAAGATTTGAAAATCTTCTGAAAAGTATGATCAAAACATCATCTGTTTGTATAAATTTGTTAACAGTTTCAAAAAAGTCCAACTAATTG  
TGTTATGGAATTTGATAAATTTGTCATTTAATAATAATTTTTTGGATTTATCAATATGTGTTTTTGTGTTTTTACACAGTTGGCAAG  
AAAGTTGGCAAGGTGGCCCTTAAAGTAAAGACTTCTACCATTTACTGTTGTAATTTTGATAGTATTATCACCCAGTACTGTTATTGAC  
AACTTCTTTTTCTGCTGACTCTCTCCATCCGACTCATCTGCAGTGTCTTACCTTGGCGAGCAGCAGCTCGACAAGCGCTGCAGT  
CGATGAAGAGCCAGTGTATTGCTTTTACTGACTGAAGAAGTCGCTTGAAGGAGCCTTCAG

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NRC-126

ATGAAGTTCACTGCCACCTTCTCATGATTTTCACTCTCGTCTCATGGTTCGAACCTGGAGAGTGTGGTTGGAGGAAATGGATTAAA  
AAGGCTACTCAGCGTAAAGTCACGGAATTAATTCGTTTTTGGCTTTGCAAATATTTTTTTTATAACAGCTGGAAAAGTCAAAAAATA  
AATAGTCAATATAATTTGGCCAAATAGAATCACTTTGATTTCAATAATAACTAAATAACAACCAAAAAGGCTTTCTCTTTAATGAAA  
TGTACGTTGAAGTTTATTTGAACTCTCACATGCACCGACTGCTGCGGCAACAATTTGAATTTCAAATTTCTCCAGGAAATTCAAAAG  
TAAATTTTTTCTAGGCGATTTAATCTTTCCATTTACTCTGATTTGTTTTTAAATATATAAGAATGACTCAATTTGCTATGATAAAAATAATA  
GCCATACATTCTGATTTTTTACAAGACAAGATTTGAAAACCTTCTTAAAAGTACGTATAAAAACATCATCTGATTTTATAAATTTGTTAA  
TTTTAACAAATTTGCTTACTAATTTGTTGTTATGGAATTTGATAAATTTGTCATTTAATATCATTTGCTTTGAGTTTATCATTATTTGTTTT  
TGTTTTGTTTTTACACAGTTGGCAAGCATAATTTGGCAAGCGGCCCTTGAGTAAAGAACTTCTACCATCATTTACTGTTATAAATTTGATAG  
TATTATCACAGTACTGTTATTTGACAACTTCTCTTGTCTGATGACTCTGTTTATCCAACTCATCTGCAGTGTCTTACATTGGCGGGA  
AGCAAGAACTCGACAAGCGCGCAGTTCGATGA

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NRC-127

ATGAAGTTCACTGCCACCTTCTCATGATTTTAACTCTCGTCTCATGGTTCGAACCTGGAGAGTGTGGTTGTAAGAAATG  
GTTTTAAAAGGCTGCTCAGGTAGAGTACGGAATTAATTTGCTTTTTGCTTTTACAAATATTTTTTTTATAGCAGCTGGAA  
AATCACAAAAATAAATAGTTCGATGTTTGGCCAAATAGAATCACTTTCAATTTCAATAATACTAAATAGCAACCTAAA  
AGGCTTTGATTTAGCAGTCTTCTTCAATGAAATGGATGTTGAGGTTTTATTTGATTTCTCACATGCACCGCAGCTGCTGCGG  
CAACAATTTGAATTTCAAATTTGTTCCAAAGGAATTTCAAAGTAAACTTTTCTAGGCGATTTAATCTTTCCATAACTCGGCTT  
TGTTTTTAAAAATATATAAATACTCAATCCCTATGATAAAAATAAACAACATACATTCTGATTTTATAAAGCAAGATTTG  
AAAACCTTCTGAAAAGTATGATCAAAACATCATCTGTTTGTATAAATTTGTTAACATTTCAAAAAAGTCCAACTAATTGTTG  
TTATGGAATTTGATAAATTTGTCATTTAATAATAATTTTTTTGAGTTTTATCAATATGTGTTTTTGTGTTTTTACACAGTTG  
GCAAGAACGTTGGCAAGGTGGCCCTTAAAGTAAAGACTTCTACCATTTACTGTTATAAATTTTGGATAGTATTATCACCCAGT  
ACTGTTATTGACAACCTTCTCTTTTCTGCTGACTCTCTCCATCCGACTCATCTGCAGTGTCTTACCTTGGTGGAGCAGCAG  
AGCTCGACAAGCGTGCAGTTCGATGAAGAGCCAGTGTATTGCTTTTACTGACTGAAGAAGTCGCTTGAAGGAGCCTTCAG

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NRC-128

GCCCACTTTGTATTTCGCAAGGTAATATCGATATTTTTCAAACCTCACTTAGACGAGACCAAGCATTTGGGAAACGTGCTAA  
GGTTGTTACTGTATAATGCAAAAATAATGATCTTTATTTTTCTGTTTTTTTTTGCAGAAATGAAGTTCACTGCCACCTTCC  
TCATGATTTTAACTTCTGCTCATGGTTCGAACCTGGAGAGTGTGGTATTAGGAAATGGTTTAAAAAGGCTGCTCAGGTT  
AAAGTCAAGGAAATTAATTTGCTTTTGGCTTTTACAAATATTTTTTTTATAGCAGCTGGAAAATCACAAAAATAAATAGTTC  
ATGATTTTGGCCAAATAGAATCACTTTGATTTCAAATAATACTAAATAGCAACCTAAAAGGCTTTGATTTAGCATGTTCT  
CTTCAATGAAATGGATGTTGAGGTTTATTTGATTTCTCACATGCACCGACCTGCTGCGGCAACAATTTGAATTTCAAATTTG  
TCCAAAGGAAATTCAAAGTAAACTTTTCTAGGCGATTTAATCTTTCCATAACTCGGCTTTGTTTTTAAAAATATAAATA  
AACTCAATCCCTATGATAAAAATAAACAACATACATTCTGATTTTATAACAAGCAAGATTTGAAAACCTTCTTGAAGTATGT  
ATCAAAACATCATCTGTTTGTATAAATTTGTTAACATTTCAAAAAAGTCCAACTAGTTGTTGTTATGGAATTTGATAAATTTG  
TCATTTAATAATAATTTTTTGGATTTATCAATATGTGTTTTTGTGTTTTTACACAGTTGGCAAGGAGTTGGCAAGGTTG  
GCCCTTAAAGTAAAGACTTCTACCATTTACTGTTATAAATTTTGGATAGTATTATCACCCAGTACTGTTATTGACAACCTTCTC  
TTTTCTGCTGACTCTCTCCATCCGACTCATCTGCAGTGTCTTACCTTGGCGAGCAGCAGCTCGACAAGCGTGCAGT  
GATGAAGAGCCAGTGTATTGCTTTTACTGACTGAAGAAGTCGCTTGAAGGAGCCTTCAG

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NRC-129

AATGAAGTTCACTGCCACCTTCTCATGAAATGGTTCATCTTCTGCTCAATGGGTTGAAAACCTGAAGGAGTGTGGTTGG  
AAAGAAAGTGGTTTTAAAAAGGCTACTCAGGTAAAGTCACGGAATTAATTTAGCATTTTTTCTTTGCAAAATATTTTTTTTAT  
ACAGCTGCAAAAATTCAAAAATAAATAGTTCGATATATTTGGCCAAATAGAATCACTTTGATTTCAAATAATACTAAAT  
AACAACTAAAAGGCTTTGATTTAGCATGTTCTTCAATGAAATGGAGCTTGGAGTTTTATTTGATTTCTCACATGCACCG  
ACCTGCTGCGTCAACAATTTGAATTTCAAATTTGAGAGGAAATTCAGCGTAAATTTTTTCTAGGCGATTTAATCTTTCCATTA  
TCGGATTTGTTTTTAAATATATAGAATAACTCAATTTGCTATGATAAAAATAAACAACATACATTGATTTTACAAAG

AAGATTGAAAACCTCTTAAAGGTACGTATAAAACATCATCTGTATTTATAATTGTTTTAACATTTAACAAATAATCCTACT
AATTGTGTATGGAAATGTATAAAATGTAATTTAATATAAATTTGCTTTAGTTTATCATTTATTTGTTTTGTTTTGTTTTTA
CACAGTTGGCAAGCAFTTTGGCAAGGCGGCCCTTGAGTAAGAACTTCTACCATCATTACTGTATAAATTTTGATAGTGTTA
TCACCAGTACTGTTATTTGACAACCTCTCTTGTCTCTGACTCTCTCCATCCGACTCATCCGAGTGCTTACCTCGGCCA
GAAGCAAGAACTCGACAAGCGCGCAGTCGATG

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NRC-130

ATGAAGTTCACTGCCACCTTCTGGTGTGTTTCATGGTCGTCTCATGGCTGAACCTGGAGAGGGTTTTTTTCGGATTGCTTTTTTCAC
GGGATCCACCATGGTAGGGTACGGAATTAATTAGATGTTTTACATGGCAAATATTTTAAAGATAACACACCATATGAGTAGTCGATAT
ATTTGACCAATTAGAATCACTTTAATTTCAATAATAATCACAAATAACAATCTCTAGGCCATTTAATCTTTCCATTAATCGGATTTGT
TTTTTTAAATATAGAATAACTGGATCTTTATGCTAAAATAATGAAACATACATTTCTGATTTTACCAGTCAAGATTGAACGTTACTTTA
AAAGTATGTTTTAAAACATCATCTGTATGTATAAATTGTTTAGCTGTAACAAATAGTCCAAATAATTGTGTTATGGAAATGTATTAAT
TGTCATATAATAATAAATTTGCTTGAATTTATCACCATGTGTTTTGTTTTGTTTTTTTAAACACAGCTGGAAAGTTGATCCATGGGTAAGG
ACTTCTACCATCATTACTGTGTATTTTAAATAGTATTATCATCAGTACTGTTATTAACAACCTTCTCTTCTATCGCTGACTCTCTCCA
TCAGACTCATCCATCATGGTTACGACGAGCAGCAGGAGCTCGACAAGCGCGCAGTCGATGA

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NRC-131

ATGAAGTTCACTGCCACCTTCTGGTGTGTTTCATGGTCGTCTCATGGCTGAACCTGGAGAGGGTTTTGGGAAATTGGATGGGGCCC
CATATCAGCGGTAGAGTACGGAATTAATTTGCTTTTTCCATTGCAAATATTTAATAATGTCATAGCTGGAAAATCAGGAAATAAGT
AGTCGATATATTTGGCCAAATAGAATAAATTTGATTTCAATAATAATCAAAAATACAATCAAAAAGGCCTTTGATTTAGCATGTTCCCT
TCAATAAAAATGGACATTTGAAGTTTTATTTGATGCTCACATGCACCGACCTGCTGCGGCAACAATTGAAATCAAATTTGTCTCAGAAT
TTAAAGTACATTTTTCTAGGTGATTTAATCTTTCCATTCATCTGATTTATTTTATAAATATAGAATAACTGGATCTTTCTGCTAAAA
TAATAAAACACACATTTCTGATTTTACCAGTCAAGATTGAACACTACTTAAAAGTATGTATAAAAACATCATCTGTATGTATAAATTGTT
TAACTGTTAACAATAGTCCAAATAATTGTGTTAAGGAAATGTATTAATTTGTCATTTAATATCATTGCTTGAATTTATCACCATGAG
TTTTTTTGTGTTTTTTTACACAGGTAGAAAGAAGGCCCTTGACGTAAGGACTTCTACCATCATTACTTTGTAATTTTTATAGTATTATC
ATCAGTACTGTTATTTGACAACCTTCTCTTGTCTCGCTGACTCTCTCCATCAGGATGAACCTCAGAGCGTTCGAGTTACGACGAGTAGCA
GCAGAAGCTCGACAAGCGCGCAGTCGATGA

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NRC-132

ATGAAGTTCACTGCCACCTTCTGGTGTGTTTCATGGTCGTCTCATGGCTGAACCTGGAGAGTGTTTTTTGGGATTGCTTTTTTCAC
GGGGTCCACCATGGTAGGGTACGGAAGTAATTCGATTTTTACATGGCAAATATTTAAGATAACACACCATATGAGTAGTCGATAT
ATTTGATATATAGAAATCACTTTGATTTCAATAATAATCAAAAATACAATCTCTAGGCGAATTAATATTTGCATTAATTTGGATTTGT
TTTTAAAAATATAGAATAACTGGATCTTTATGGTAAAATAATTAACATACATTTCTGATTTTACCAGTCAAGATTGAACACTACTTTA
GAAGTATGTATAAAAACATCATCTGTATGTATAAATTGTTTAACTGTTAACTAATAGTCCAAATAAATTGTGTTATGGAAATGTATTAAT
TGTCATTTAATATCATTGCTTGAATTTATCACCATGTGTTTTGTTTTGTTTTTACACAGTTGAAATTTGATCCATGGGTAAGGAC
TTCTACCATCATTACTGTGTATTTTTAATAGTATTATCATCAGTACTGTTATTTGACAACCTTCTCTTGTCTCGCTGACTCTCTCCATC
AGACTCATCCATCACGGTTACGACGAGCAGCAGGAGCTCGACAAGCGCGCAGTCGATGA

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NRC-133

GCCCACTTTGTATTTCGCAAGGTAATATCGATATTTTTCAAACCTCATTAGACGAGACCAGGCATTTGGGAAACGTGCTAAGGTTGTTACT
ATGCAAAATTAATGATCTTTATTTTTCTGTTTTTTTTTCGAGAATGAAGTTCACTGCCACCTTCTCATGATTTTAAATCTTCGTCTCTCAT
AACCTGGAGAGTGTGGTATTAGGAAATGGTTTAAAAGGCTGCTCACGGTAAAGTACGGAATTAATTTGCTTTTTGCTTTACAAATATT
ACAGCAGCTGGAAAATCACAAAATAAATAGTCGATGTATTTGGCCAATTAGAATCACTTTGATTTCAATAATAATCTAAATAGCAACCT
GCCTTTGATTAGCATGTTCCTTCAATGAAATGGGTGTTGAGGTTTATTTTGATTTCTCACATGCACCGACCTGCTGCGGCAACAATTGAAT
TTTTGCTCCAAAGGAATTCAAAGTAACTTTTCTAGGCGATTTAATCTTTCCATAACTCGGCTTTGTTTTTAAAATATATAAATAACTCAA
ATGATAAAAATAAACAATACATCTGATTTATACAAGACAAGATTGAAAACCTTCTTGAAGTATGTATCAAACATCATCTGTTTTATAE
TTTTAACATTTTCAAAAAGTCCAATAATGTGTTATGGAAATGTATAAATTTGTCATTTAATAATAAATTTTTTTGAGTTTTATCAATATGTG
GTTTTGTTTTTACACAGTTGGCAAGAAAGTTGGCAAGGTGGCCCTTAACTAAGGACTTCTACCATTATTAAGTATAAATTTTGTAGTATTAT
AGTACTGTTATTTGACAACCTTCTTTTTCTGCTGACTCTCTCCATCCGACTCATCTGAGTGCTTACCTTGGCGAGCAGCAGCAGCTCGA
GTGCACTCGATGAAGAGCCAGTGTATTGCTTTTTGACTGAAGGAGTCGCCTTGAAGGAGCCTTC

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Appendix II. Nucleotide sequences of hepcidin-like genes and cDNAs referred to in Table 11.

NRC201

CGCCCTTAAGATGAAGACATTCAGTGTTCAGTGGTTCAGTGGTTCGTCCTCGCATGTATGTTTCATCCTTGAAAGCACCGCTGTTCC  
 TTTTCTCCGAGGTGCGAACCGGAGGAGTTGAAAGCATTGACAGTCCAGTTGGGGAACATCAACAGCCGGGCGGCACGTCCATGAATCT  
 GCCGGTACGTTCAATTTAGTGAATGAATTAAGTAATTACCTTTAGCAAATTAACATCTAAGTGGTTGCGTTTACCCTTGGAATTGA  
 ATTAGCCCACTAGCGCTAGTTGTTAACCATTTGATTTGTGAGCCGGTAGAGAGGGCTTCAGGGCGAGTAGTGTGAATACTTTGTGAAGT  
 GGAGACTTGGACAAAAATACTTACCATGTGCTTGTCCACCTTTTTCATTTTCTTTTCTGGCTGAGATACAGATGCATTTCAAGT  
 TCAAGCGTCAGAGCCACCTCTCCCTGTGCCGTTGGTGTGCTGCAACTGCTGTCAACAAGGGCTGTGGCTTCTGCTGCAAAATCTGAG  
 GACCTGCCAGCAAAGGGCGAATTCGTTTAAACAC

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NRC202

AGATGAAGACATTCAGTGTTCAGTGGTTCAGTGGTGGTTCGTCCTCGCATGTATGTTTCATCCTTGAAAGCACCGCTGTTCTTTCTCCG  
 AGGTGCGAACCGGAGGAGTTGAAAGCATTGACAGTCCAGTTGGGGAACATCAACAGCCGGGCGGCACGTCCATGAATCTGCCGATGC  
 ATTTCAAGTTCAGCGTCAGAGCCACCTCTCCCTGTGCCGTTGGTGTGCTGCAACTGCTGTCAACAAGGGCTGTGGCTTCTGCTGCA  
 AATTCAGGACCTGCCAGCA

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NRC203

ACGAGGTCCCTCATCCGCTGACACCAAAGAACAATCAATCAACTTTGGACTCGTCTTAGTGCATTGAAAATTGTGCGTT  
 GGAGAGCGTTCGCTTTTTGGGAACATTGAAGAGTTCTGATCTTCCCTATAAACTGTCACTTCAATTTCAACTGATTTCAAC  
 AGGACTTTTAAATAGGCTATAAACTTCTTAAAAAACAAGAGGCTTTAGTGTTCAGTGGTACTCGTCAATTCG  
 ATGTATGTTTCATCCTTGAAAGCACCGCTGTTTCTTCTCCGAGGTGCGAACCGGAGGAGTTGGAAGCTTTGACAGTCCAG  
 TTGGGGAACATCAACAGCCGGGCGGCAGTCCATGCATCTGCCGAGCCTTTCAAGTTCAGCGTCAGATCCACCTCTCC  
 CTGTGCCGTTTGTGCTGCAACTGCTGTCAACAATTGGCTGTGGCTTCTGCTGCAAAATCTAAGGACCTGCCCGCAACAT  
 TTTCTAGTTTGTACATGTTTGAATGTTTCTTTCTGAGATGTTGTTTTGTGACTATGATAATGATTTATAAAATCACT  
 TCTTATTGTGACACTTTAAAAAATAAACACATTTCTTTGAATACAAAAAATAAAAAAAAAA

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NRC204

CGAACCGGAGGAGTTGAAAGCATTGACAGTCCAGTTGGGGAACATCAACAGCCGGGCGGCACGTCCATGAATCTGCCGAT  
 GCATTTCAAGTTCAGGTTCAACCGTCAGAGCCACCTCTCCCTGTGCCGTTGGTGTGCAACTGCTGTCAACAAGGGCTGTGGCT  
 TCTGCTGCAAAATCTGAGGACCTGCCAGCACTAAAGCCATTTTATTAACCTTATCGCCTTTAATTTGCCCTATTCTTCTA  
 TGTTTTCTTTGGACTCTGTGGAGAAGATGCAATCTCATTGACGTTTATCACATGCACAACCTCAATCTTGT

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NRC205

AAGATGAAGACATTCAGTGTTCAGTGGTACCCGTCATTGCATGTATGTTTCATCCTTGAAAGCACCGCTGTTCTTTCTCCGAGGTG  
 CGAACCGGAGGAGTTGGAAGCTTTGACAGTCCAGTTGGGGAACATCAACAGCCGGGCGGCACGTCCATGAATCTGCCGATGCATTTCT  
 AGGTTCAAGCGTCAGAGCCACCTCTCCCTGTGCCGTTGGTGTGCTTCAACTGCTGTCAACAAGGGCTGTGGCTTCTGCTGCAAAATC  
 TGAGGACCTGCCAGCA

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NRC206

TAAGATGAAGCAATTCAGTGTGGCAGTGGTACTCGTTCATGGCATGTATGTTTCATCGTGGAAAGCACCGCTGTTCTTTCTCCGAGGT  
 GCGAACCGGAGGAGTTGGAAGCTTTGACAGTCCAGTTGGGGAACATCAACAGCCGGGCGGCAGTCCATGCATCTGCCGAGCCTTT  
 CAGGTTCAAGCGTCAGATCCACCTCTCCCTGTGCCGTTTGTGCTGCAACTGCTGTCAACAATTTGGCTGTGGCTTCTGCTGCAAAAT  
 CTGAGACTGCCAGCA

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NRC207

ACGAGGCACACGCTGACCAGGGGTCACCACAACCTTCTGAAGAGACCCAGGTTCTTAGAGAGCCACTAGAGAATCACCCG  
 GGAGCCCGAAGAACAACAGGACGCTGCGGTGCTCGTGGTGGCCGGACCCATGAGACAGAAGACCTACAAGCCTCTCAG  
 CTTTCAAGAGGATTTCTGACTCAGCATCTAAAACCTCCCTCAAAATGAAGGCATTGAGCATTGCAATTTGAGTGCACACT  
 GTGCTCGCCTTTGTTTGCATTGAGTGCAGTCTGCGCTCCCATTTCAAGGGGTGCAAGGAGCTGGAGGAGGCCGGGGGCA  
 TGACACTCCAGTTGCGGAACATCAAGTGAATGCAATGGAATCCTGGAATGGAGAATCCACCAGGCAGAAAGCGCCACATCA  
 GCCACATCTCCCTGTGCCGCTGGTGTGCAACTGCTGCAAGGCCAACAAAGGGCTGTGGCTTCTGCTGCAAGTTCTGAGGA  
 TTTCCGCAACACAACCTCACAAATGATTAATTTATTAACACTTTTGTGAGAAATGTCCTTTTTCTGACCTCTTTTGT  
 ATTTTGTATAATCTTTTAAATAAAAACGGGTACGATTCATGGAATAAAACCTTTGAAATAAAATAAAAAAAAAA  
 AAAAAAC

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NRC208

AAGATGAAGACATTCAGTGTTCAGTGGTTCAGTGGTGGTTCGTCCTGCTCCTTTGTTTGCATTTCAGGACAGCTCTGCCGTCCTTCCAG  
 GGGGTAAGAACGCAACTTTAACTCGCTTCAATTTGCTTATAGCCATAAATGTTTTGTCAGGATGCTGAGACACGGCTCCTAAATGTG  
 TATAAATTCATTAACAGGTGCAGGAGCTGGAGGAGGCAGGGGGCAATGACACTCCAGTTGCGGCACATCAAATGATGTCAATGGAATC  
 GTGGATGGTATGTTCAATCTGTTCAATCGACTGGATGAATTAAGCCAAATTACTGTGAGCGCGTTAACATTTAAGTGGCTGTGTTCCA  
 GCCGGTGTGTAGGGAATAAAACCCCTCGTTCAATGTGCTTGTCCGTTCCACAGGAGAGTCCCGTCAGGCAGAAAGCGTCACATCAGC  
 CACATCTCCATGTGCCGCTGGTGTGCAACTGCTGCAAGGCCAAGGGCTGTGGCCCTGCTGCAAAATCTGAGGACCTGCCAGCA

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NRC209

AAGATGAAGACATTCAGTGTTCAGTGGTTCAGTGGTGGTTCGTCCTGCTCCTTTATTTGTATCCAGCAGAGCTCTGGCACCTTTCTGAG  
 GTAAGCTCCTGACTTCAGATCGTTTCATTTGCTTGTATCCATGAATCTCTCATCAACAGACTGAGACTTGATTCCTTCTTTATCA  
 GGTACAAGAGCTGGAGGAGGCAATGACAAATGCAACTGCACTCAGGAGACATCAGTGGACTCATGGATGGTAGGTTTC  
 AGTTCACTGAATGGATCAAAACCAATTCACATCAGACCTTTCAAGTGGAGTGAATGTTGTTTTAGTCTCAAAGGTGCCCTGAAGCTCA  
 GTTTACACAAGCAGTGAACAACAACAGAAAGTTATGATGATGCTGATGAACTTCTCCTCATGTCTCATGTCTCTCACACAGATGC  
 CATAACAAGACAGAAGCGTGCCTTCAAGTGAAGTTCTGCTGCGGCTGCTGCAAGAGCTGGTGTCTGTGGACTGTGCTGCAAGTTCT  
 GAGGATTCCTGCTCCAACAAC

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NRC210

ACGAGCTGACAGGAGCTGACAGGAGTCAACCAGCAGAGTCAAAGAACTAAACAATTAACCTCAGTCAAATCTCAAAGATG  
 AAGACATTCAGTGTTCAGTGCAGTGCAGTGGCCGTCGTCCTGCTTTTATTTGTATCCAGCAGAGCTCTGCCTCCTTCTCTGA

GGCACAAAGAGCTGGAGGAGGCAGTGCAGCAATGACAATGCAGCTGCTGAGCATCAGGAGACACCAGTGGACTCGTGGATGA  
TGCCATACAAAGAGCAGAAAGCGTAGCTTTAAGTGTAAAGTTCTGCTGCGGCTGCTGCAGAGCTGGTGTCTGTGGACTGTGC  
TGCAAGTTCTGAGGATTCTGCTCCAACAACCATCAAATATTCATTTGTTTTGCCTTTTGTCTTAAAGTTTCAATGAACTA  
TAAACATATTTCTGTTGAGCATGTGATAGTTTAAATGGTGTACTCATTTGGTTTATGGTATAGTCAAGTGTTCAGAGATG  
TGATTTGATACCCACATATTTCTCTGTTAGGTGTATTTCAATAAATGCCAATGATCCTTTGAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

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NRC211  
ACGAGCGGCACGAGGTGAAGTGCAGGAGTGCAGGAGTACCAGCAGAGTCAAAGAATAAACAACCTTAACTCAGTCA  
AACTCTCAAAGATGAAGACATTAGTGTGGCAGTACAGTGGCCGTCGTGCTCGTCTTTATTTGTATCCAGCAGAGCTCT  
GCCTCCTTTCTGAGGCACAAGAGCTGGAGGAGGCAGTGCAGCAATGACAATGCAGCTGCTGAAACATCAGGAGACACCAGT  
TGACTCGTGGATGATGCCAAACAACAGACAGAAGCGTGGCTTTAAGTGTAAAGTTCTGCTGCGGCTGCTGCAGAGCTGGTG  
TCTGTGGACTGTGCTGCAAGTTCTGAGGATTCTGCTCCAACAACCATCAAATATTCATTTGTTTTGCCTTTTGTTTTAA  
AGTTCAATGAACTATATACATATTTCTGGTAGAGCATGTGATAGTTTAAATGGTGTACTCCTTGGTTTATGGTGTAGTTA  
AGTGTTCAGAGATGTGATTGTATACCCACATATTTCTCTGTTAAGGTGTATTTTCAATAAATGTTAATGTCTCTTTGAA  
AAAAAAAAAAAAAAAAAAAAA

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NRC212  
ACGAGACTGCAGGAGTGCAGGAGTACCAGCAGAGTCAAAGAATAAACAACCTTAACTCAGTCAAACCTCTCAAAGAT  
GAAGACATTAGTGTGGCAGTACAGTGGCCGTCGTGCTCGTCTTTATTTGTATCCAGCAGAGCTCTGCCACCTTTCTG  
AGATGCCATACAAAGCAGCAAGAGCTGGAGGAGGCAGTGCAGCAATGACAATGCAGCTGCTGAAACATCAGGAGACACCAGT  
TGCTGCAAGTTCTGAGGATTCTGCTCCAACAACCATCAAATATTCATTTGTTTTGCCTTTTGTCTTAAAGTTTCAATGAA  
CTATAACAATATTTCTGTTGAGCATGTGATAGTTTAAATGGTGTACTCATTTGGTTTATGGTGTAGTCAAGTGTTCAGAG  
ATGTGATTGTATACCCACATATTTCTCTGTTAGGTGTATTTTCAATAAATGCCAATGATCCTTTGAAAAAAAAAAAAA  
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NRC213  
AAGATGAAGACATTAGTGTGGCAGTACAGTGGCCGTCGTGCTCGTCTTTATTTGTATCCAGCAGAGCTCTGCCTCCTT  
TCCTGAGGTAAGCACCTGACTTCAGATCGTTTCAATTTGCTTGTATCCATGAATCTCTCATCATCATACTGAGACTTGAT  
TCCTTCTTTATCAGGCACAAGAGCTGGAGGAGGCAGTGCAGCAATGACAATGCAGCTGCTGAGCATCAGGAGACACCAGTG  
GACTCCAGGAGTGAATGTGTTTTAGTCAAAAAGTGCCTGAAAGCTCAGTTTACACAAGCAGAGAAAACAAAACAGAGTAA  
GTTATGATGATGCTGATGAAGGTCTCCTCATGTCTCATGTCTCTCACACAGATTCCATACAAACAGACAGAAGCGTAGCTT  
TAAGTGAAGTTCTGCTGCGGCTGCTGCAGAGCTGGTGTCTGTGGACTGTGCTGCAAGTTCTGAGGATTCCTGCTCCAAC  
AAC  
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NRC214  
AGATGAAGACATGCAGTGTTCAGTGCAGTGCAGTGGCCGTCGTGCTCGTCTTTATTTGTATCCAGCAGAGCTCTGCCTCCTT  
CCTGAGGTAAGCACCTGACTTCAGATCGTTTCAATTTGCTTGTATCCATGAATCTCTCATCATCATACTGAGACTTGAT  
CCTTCTTTATCAGGTACAAGAGCTGGAGGAGGCAGTGCAGCAATGACAATGCAGCTGCTGAAACATCAGGAGACACCAGTTG  
ACTCGTGGATGGTAGGTTAGTTCAGTTCAGTGAATGGATCAATCCATTTACATCAGATCTTTTCAAGTGAAGTGAATGTGTT  
TAGTCAAAAAGTGCCTGAAAGCTCAGTTTACACAAGCAGAGAAAACAAAACAGAGTAAAGTTATGATGATGCTGATGAAG  
GTCTCCTCATGTCTCATGTCTCTCACACAGATGCCAAAACACAGACAGAAGCGTGGCTTTAAGTGAAGTTCTGCTGCGG  
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NRC215  
AAGATGAAGACAATCAGTGTTCAGTGCAGTGCAGTGGCCGTCGTGCTCGTCTTTATTTGTATCCAGCAGAGCTCTGCCTCCTT  
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TCCTTCTTTATCAGGCACAAGAGCTGGAGGAGGCAGTGCAGCAATGACAATGCAGCTGCTGAAACATCAGGAGACACCAGTG  
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GTCTCCTCATGTCTCATGTCTCTCACACAGATTCCATACAAACAGACAGAAGCGTAGCTTTAAGTGAAGTTCTGCTGCGG  
CTGCTGCAGAGCTGGTGTCTGTGGACTGTGCTGCAAAATTCAGGACCTGCCAGCA  
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NRC216  
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TCCTTCTTTATCAGGTACAAGAGCTGGAGGAGGCAGTGCAGCAATGACAATGCAGCTGCTGAAACATCAGGAGACACCAGTT  
GACTCGTGGATGGTAGGTTAGTTCAGTTCAGTGAATGGATCAATCCATTTACATCAGATCTTTTCAAGTGAAGTGAATGTGTT  
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GTCTCCTCATGTCTCATGTCTCTCACACAGATTCCATACAAACAGACAGAAGCGTAGCTTTAAGTGAAGTTCTGCTGCGG  
CTGCTGCAGAGCTGGTGTCTGTGGACTGTGCTGCAAAATTCAGGACCTGCCAGCA  
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NRC217  
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GTACAAGAGCTGGAGGAGGCAGTGCAGCAATGACAATGCAGCTGCTGCGCATCAGGAGACATCAGTGGACTCGTGGATGGTAGGTTCA  
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ATACAACAGACCGAAGCGTAGCTTTAAGTGAAGTTCTGCTGCGGCTGCTGCAGAGCTGGTGTCTGTGGACTGTGCTGCAAAATTCG  
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NRC218  
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GTACAAGAGCTGGAGGAGGCAGTGCAGCAATGACAATGCAGCTGCTGAAACATCAGGAGACATCAGTGGACTCGTGGATGGTAGGTTCA  
GTTCACTCAATGGATCAAACCAATTACATCAGATCTTTTCAAGTGAAGTGAATGTGTTTTAGTCAAGAAGTGCCTGATGCTCAG  
TTTACACAAGCAGAGAAAACAAAGCAGAGTAAAGTTATGATGATGCTGATGAACGTGTCTCATGTCTCTCACACAGATGCC  
ATACAACAGACCGAAGCGTAGCTTTAAGTGAAGTTCTGCTGCGGCTGCTGCAGAGCTGGTGTCTGTGGACTGTGCTGCAAAATTCG  
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AGGATTCCTGCTCCAACAAC

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NRC219

AAGATGAAGACATTCAGTGGTTGCAGTCAAGTGGCCGTCGTGCTCGTCTTTATTTGTATCCAGCAGAGCTCTGCCACCTTTCTGAG  
GTAAGCACCTGACTTCAGATAGCTTCATTTGCTTGTATCCATGAATCTCTCATCAACATACTGAGACTTGATTCTTTCTTTATCAG  
GTACAAGAGCTGGAGGAGGCAGTGAGCAATGACAATGCAGCCGCTGAACATCAGGAGACATCAGTGGACTCGTGGATGGTAGGTTCA  
GTTCACTCAATGGATCAAACCAATTCACATCAGATCTTTAGATGGAAGTGAAGTGTGTTTGTAGTCAAAAAGTGCCCTGATGCTCAG  
TTTACACAAGCAGAGAAAAACAAGCAGAGTAAGTTATGATGATGCTGATGAACGTCCTCATGTCTCATGTCTCTCACACAGATGCC  
ATACAACAGACAGAAGCGTAGCTTTAAGTGTAAAGTTCTGCTGCGGCTGCTGCAGAGCTGGTGTCTGTGGACTGTGCTGCAAAATTCG  
AGGATTCCTGCTCCAACAAC

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NRC220

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NRC221

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NRC222

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NRC223

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NRC224

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NRC226

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NRC227

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NRC228

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NRC229

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NRC230

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NRC231

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NRC232

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NRC233

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NRC234

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NRC235

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NRC236

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NRC237

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NRC238

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NRC239

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## We Claim:

1. A method of identifying candidate nucleic acid sequences encoding antimicrobial peptides, said method comprising:
  - a) identifying an initial peptide of interest;
  - 5 b) identifying genomic DNA encoding the initial peptide;
  - c) identifying a flanking sequence on each side of the initial peptide;
  - d) obtaining primers complementary to the flanking sequences; and,
  - e) screening a wide range of nucleic acid sequences to identify candidate sequences capable of being amplified using the primers from step d).
- 10 2. The method of claim 1 wherein the initial peptide of interest has a net positive charge of at least 2 and has an amphipathic structure.
3. The method of claim 1 wherein the initial peptide of interest is a hepcidin, a pleurocidin, a pardaxin, a misgurin, HFA-1, a piscidin, a moronecidin, a parasin, or a cleavage product of histone 2A from catfish.
- 15 4. The method of claim 1 wherein the initial peptide of interest is a hepcidin or a pleurocidin.
5. The method of claim 1, 2 or 3 comprising a further step g) of predicting the amino acid sequence encoded by the candidate sequence and selecting nucleic acid sequences which are predicted to encode peptides having an amphipathic structure  
20 and a net charge.
6. The method of claim 5 comprising a further additional steps of obtaining a peptide corresponding to the candidate nucleic acid sequence and assaying the peptide sequence for antimicrobial activity.
7. The method of claim 1 comprising a further step (a') of confirming that the initial  
25 peptide of interest has antimicrobial activity.
8. An isolated nucleic acid sequence identifiable using the method of any preceding claim.
9. An isolated polypeptide capable of being encoded by the nucleic acid sequence of claim 8.
- 30 10. An isolated nucleic acid sequence comprising a flanking sequence.

11. A kit comprising:
- a. a first nucleic acid sequence at least 95 % identical to a first flanking sequence, located at or near a 5' end of a target sequence encoding an antimicrobial peptide;
  - 5 b. a second nucleic acid sequence at least 95 % identical to a second flanking sequence located at or near a 3' end of a target sequence encoding an antimicrobial peptide; and
  - c. instructions for carrying out the method of claim 1.
12. Use of at least one of signal sequence I, acidic sequence I, signal peptide II, signal peptide III, signal peptide IV, signal peptide V, prosequence I, prosequence II, 10 nucleic acid sequences encoding them, and nucleic acid sequences substantially complementary to such encoding nucleic acids, in the identification or amplification of antimicrobial peptides.
13. An isolated antimicrobial peptide at least 80% homologous to one of peptide a, b, 15 c or d:
- Peptide a      GW(G/K)XXFXK
- Peptide b      GXXXXXXXXHXGXXIH
- Peptide c      FKCKFCCGCCXXGVCGXCC
- Peptide d      CXXCCNCC(K/H)XKGC GFCKF
- 20 Peptide e FKCKFCCGCRCGXXCGLCCKF
- Peptide f XXXCXXCCNXXGCGXCKX
14. The antimicrobial peptide of claim 13 which is at least 90% homologous to one of peptide a, b c or d.
- 25 15. The antimicrobial peptide of claim 13 which is one of peptide a, b, c or d.
16. An isolated nucleic acid sequence depicted in Appendix I or Appendix II.
17. An isolated nucleic acid sequence depicted in Table 4 or 13.
18. A method of identifying candidate nucleic acid sequences encoding antimicrobial peptides, said method comprising:
- 30 a) identifying a nucleic acid sequence encoding an initial peptide of interest;
  - b) identifying genomic DNA encoding the initial peptide;

- c) identifying a flanking sequence on each side of the initial peptide;
- d) obtaining primers complementary to the flanking sequences; and,
- e) screening a wide range of nucleic acid sequences to identify candidate sequences capable of being amplified using the primers from step d).

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2/36

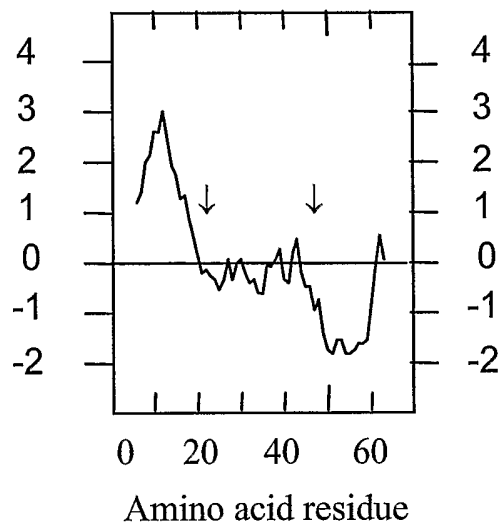


Fig. 1b

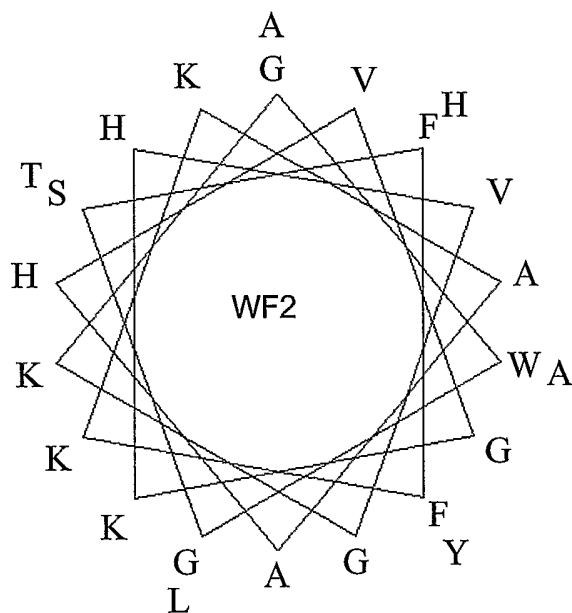


Fig. 1c

3/36

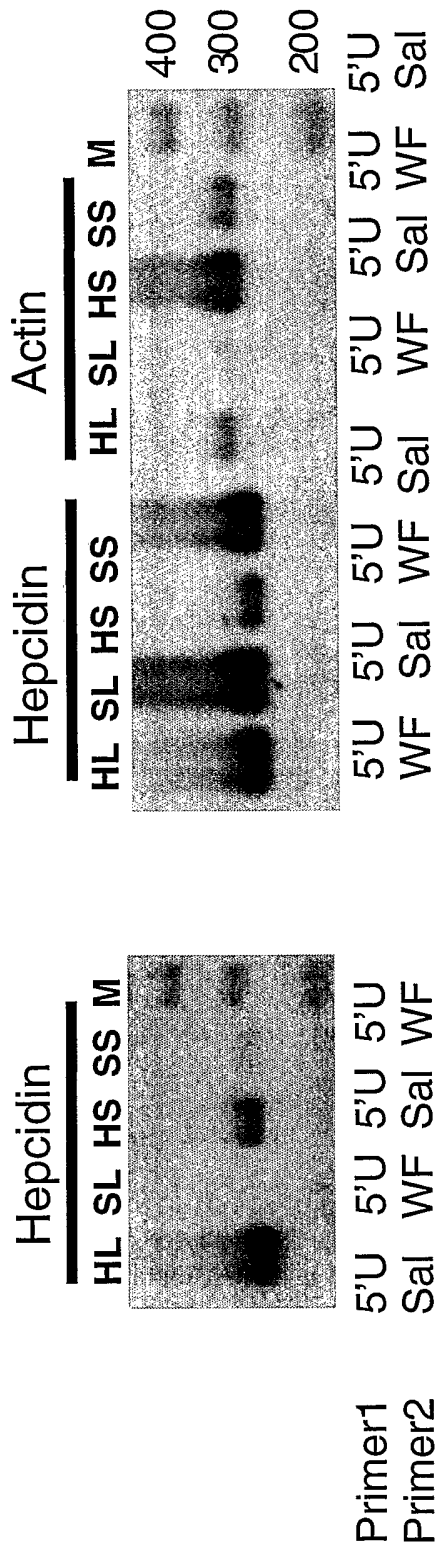


Fig. 2

4/36

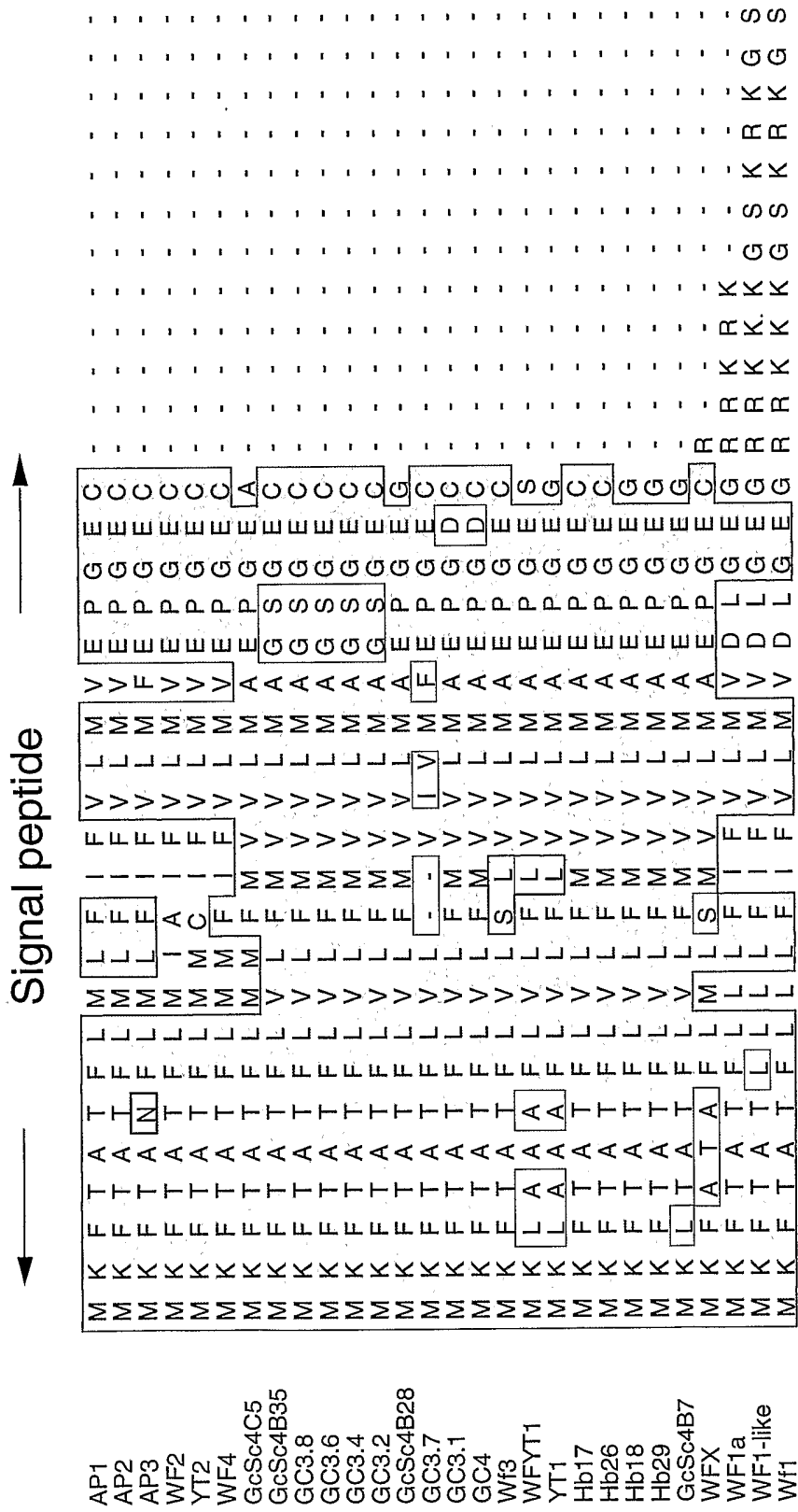


Fig. 3

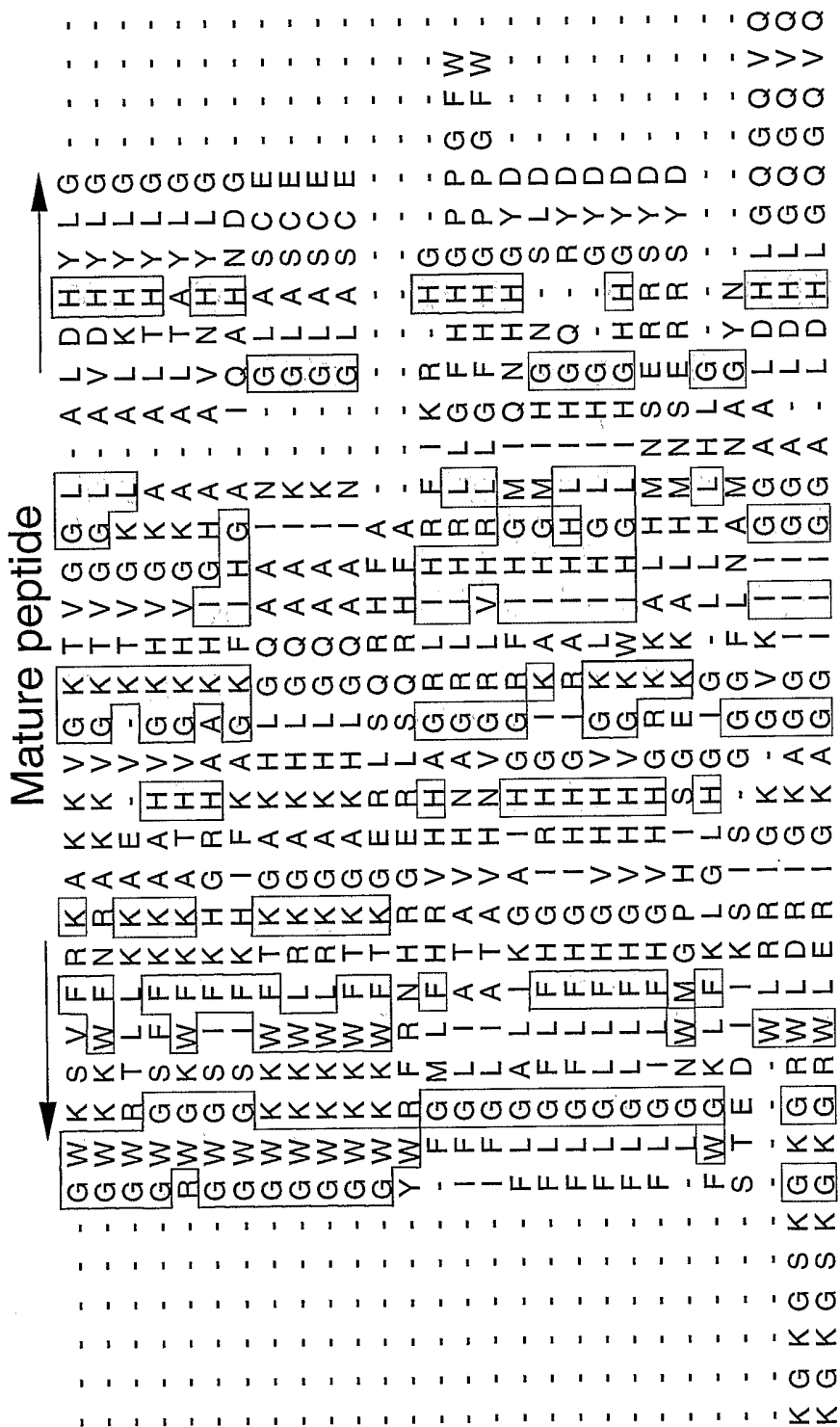


Fig. 3 (Cont.)



7/36

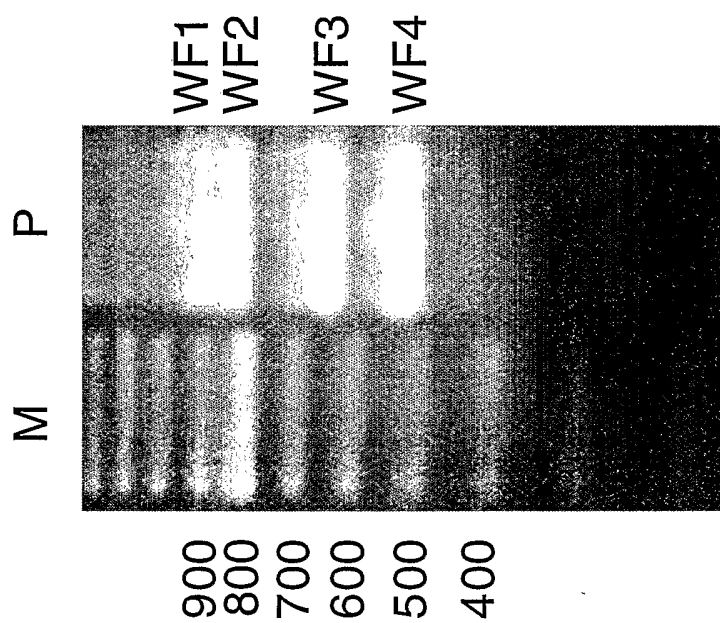


Fig. 4

8/36

Primer PL1

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 101 ctgtataatgcaaatgttaatgatctttatctgtttttttttgtaga  
 1  
 189 TTC GTC CTC ATG GTT GAA CCT GGA GAG TGT GGT TGG GGA  
 13 F V L M V E P G E C G W G  
 267 ttaattagcttttaactttgcaaattgttttttttttaacagctggaaa  
 367 atctaaataacaacctaaaaggcctttgattagcatgtttcttcaataaaat  
 467 gtttgtttttacacag CT GCC AAG CAT ATT GGC CAT GCA GCC  
 35 A K H I G H A A  
 555 ttatcaccagattgttattgacaacttctcttttttctgctgatccgactc  
 45  
 643 GAC AAG CGC GCA GTC GAT GAA GAC CCA AAT GTT ATT GTT  
 54 D K R A V D E D P N V I V

Fig. 5

aattcatttagacgagaccaaccttttgggaaatctgctcagcttatta 100  
 ATG AAG TTC ACT GCC ACC TTC CTC ATG ATG TTC ATC 188  
 M K F T A T F L M M F I 12  
 AGC ATT TTT AAG CAT GGT CGT CAT G gtaaagtcacggaa 266  
 S I F K H G R H A 34  
 ctcaaaaaataaatagccgatataatttgccaattataatcactttg 366  
 gattgaacactacttaaaggatgtataaaacatcatcatgtgttttt 466  
 GTT AA gtaaggacttctaccattattactgtataattttgatagta 554  
 V N 44  
 atccgcag T CAT TAC CTT GGC GAG CAG CAA GAT CTC 642  
 H Y L G E Q Q D L 53  
 TTT GAA TGAagaaatcgccttgaaggagccttcagaagggcgaattc 728  
 F E \* Primer PL2 68

Fig. 5 (Cont.)



10/36

M E PS CS PC L SP I R G B M SK M

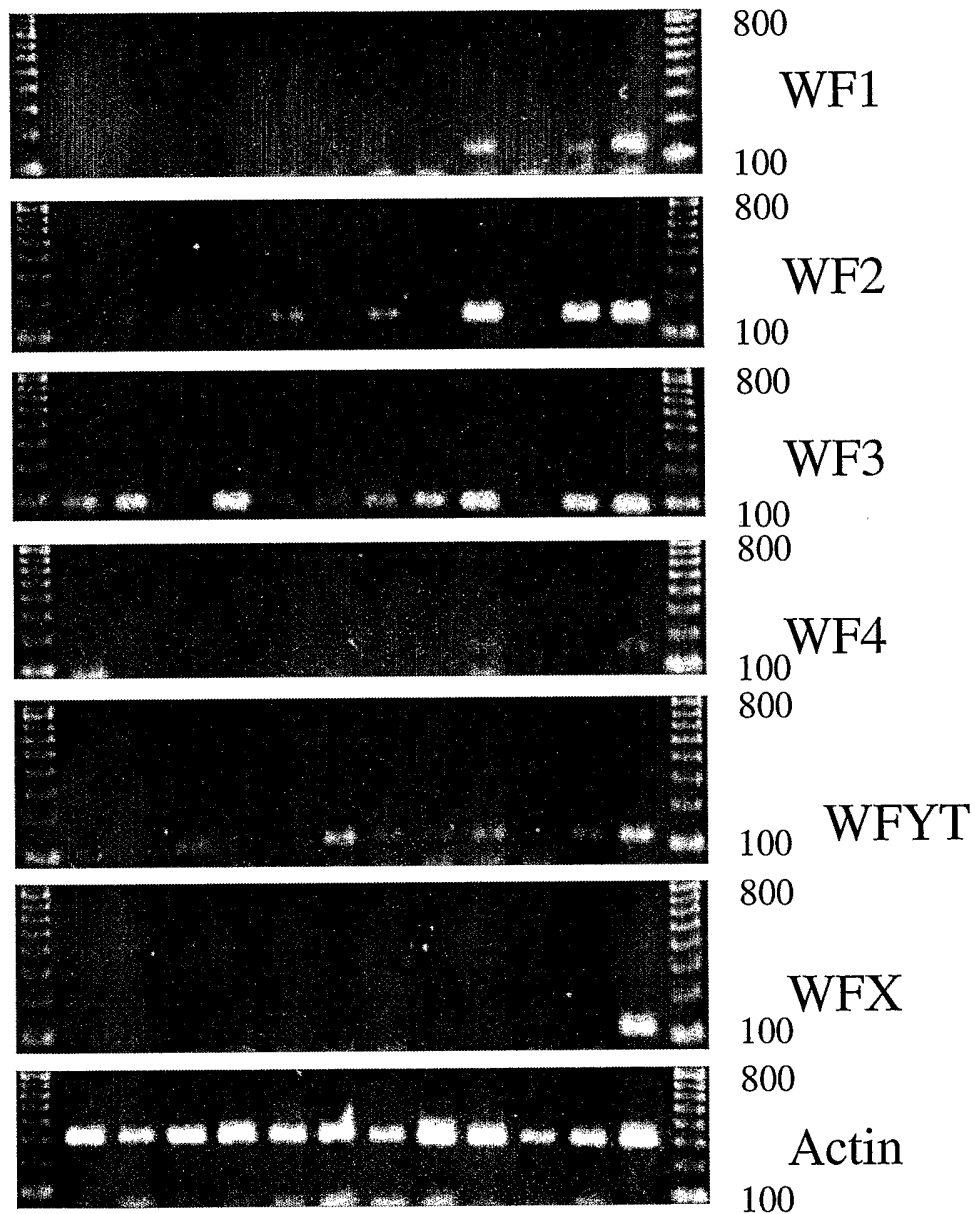


Fig. 7

11/36

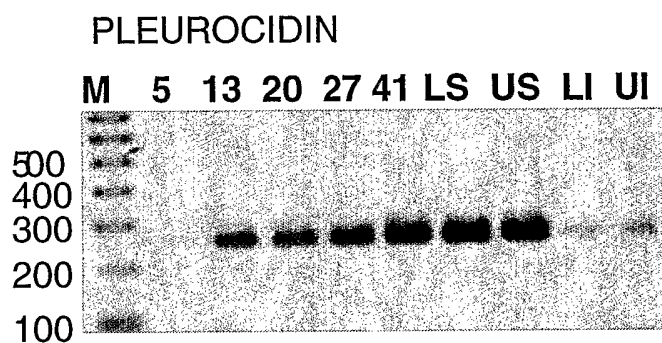


Fig. 8a

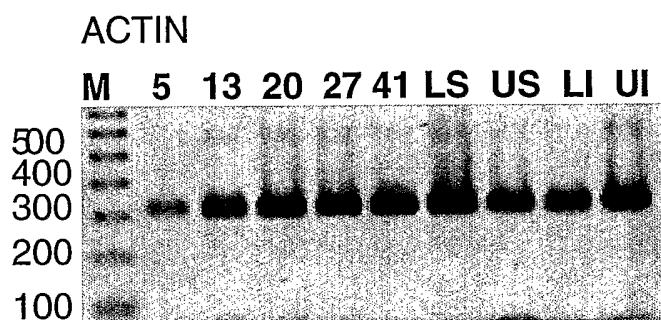


Fig. 8b

12/36

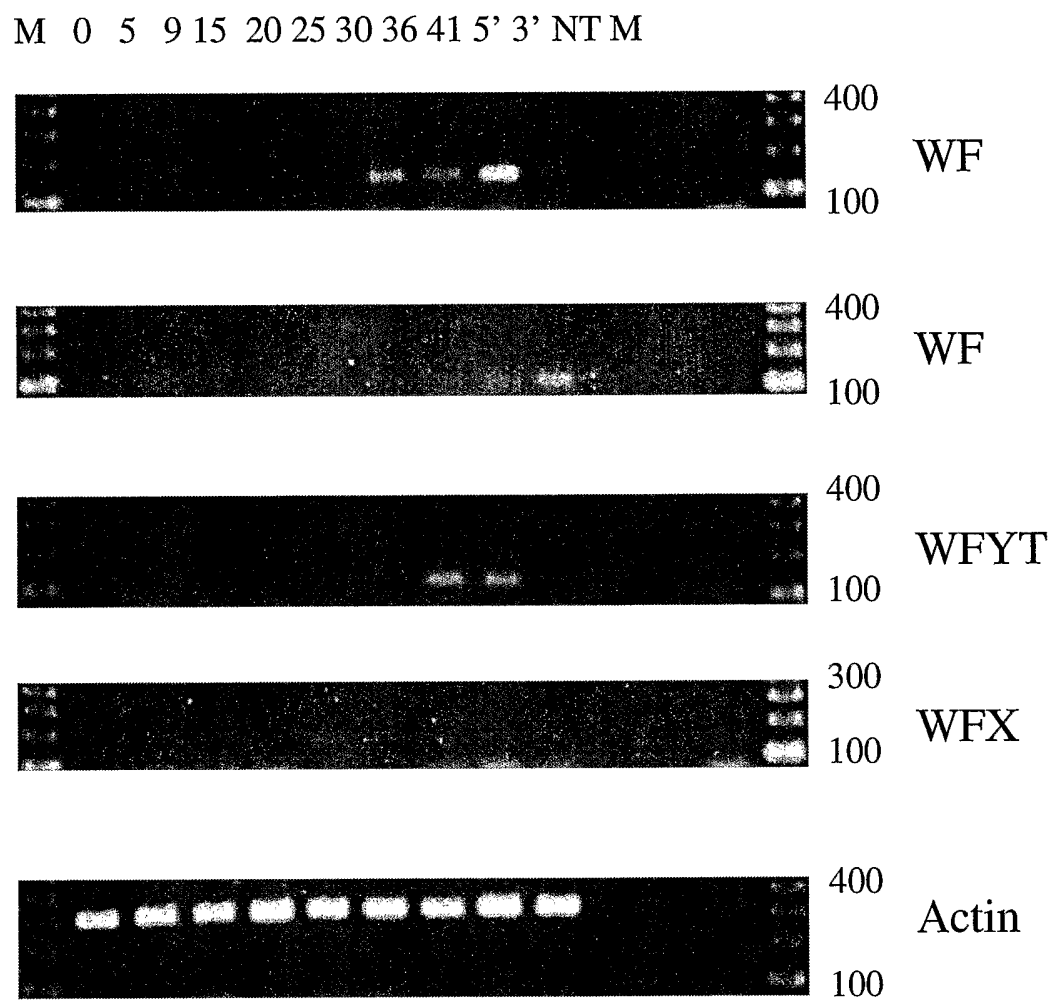


Fig. 9



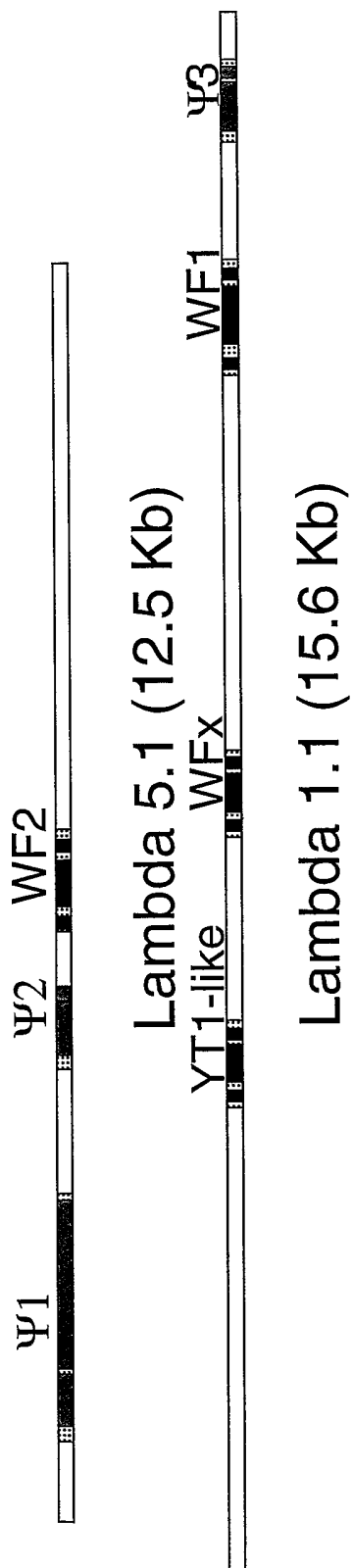


Fig. 11

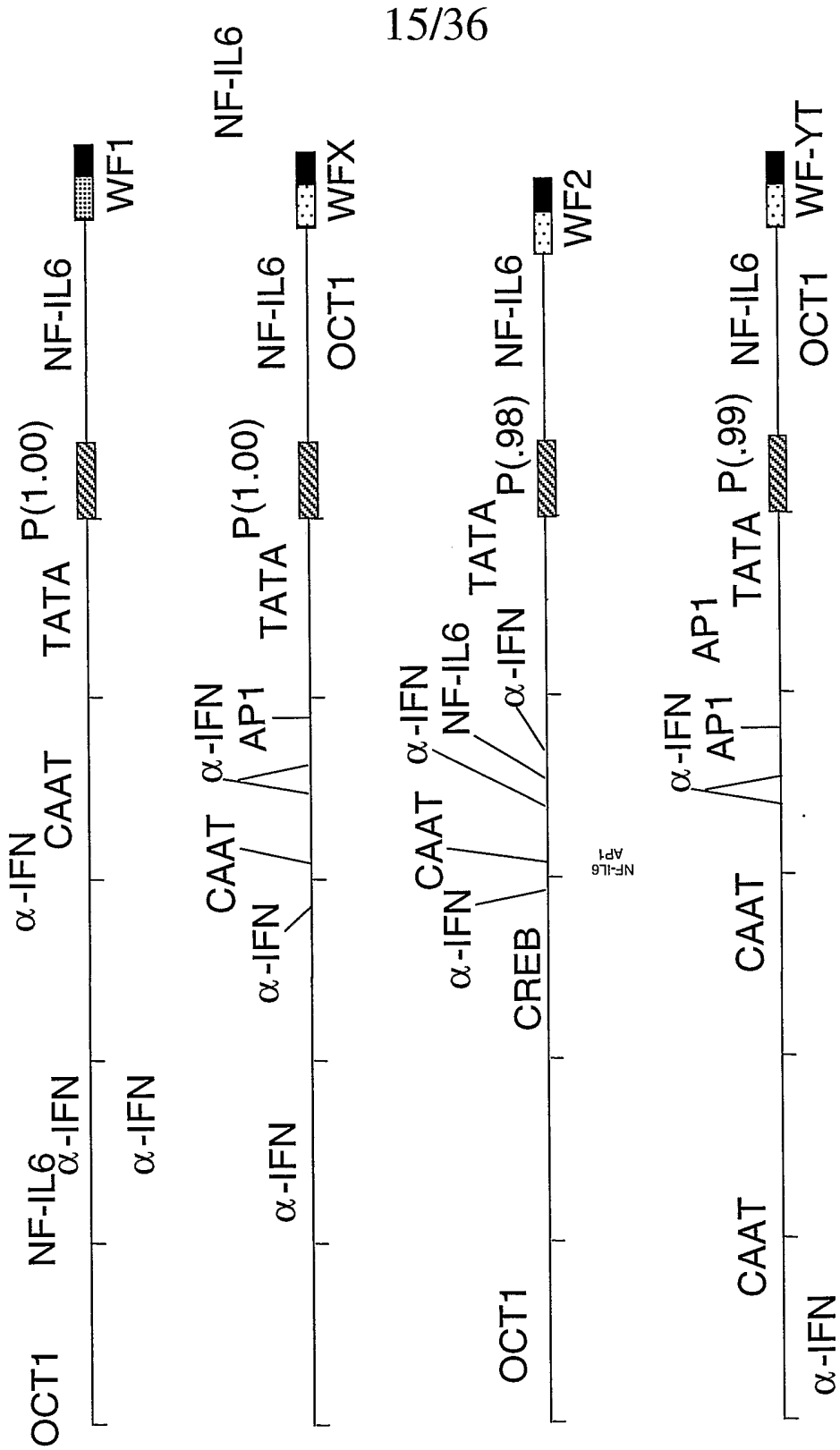


Fig. 12

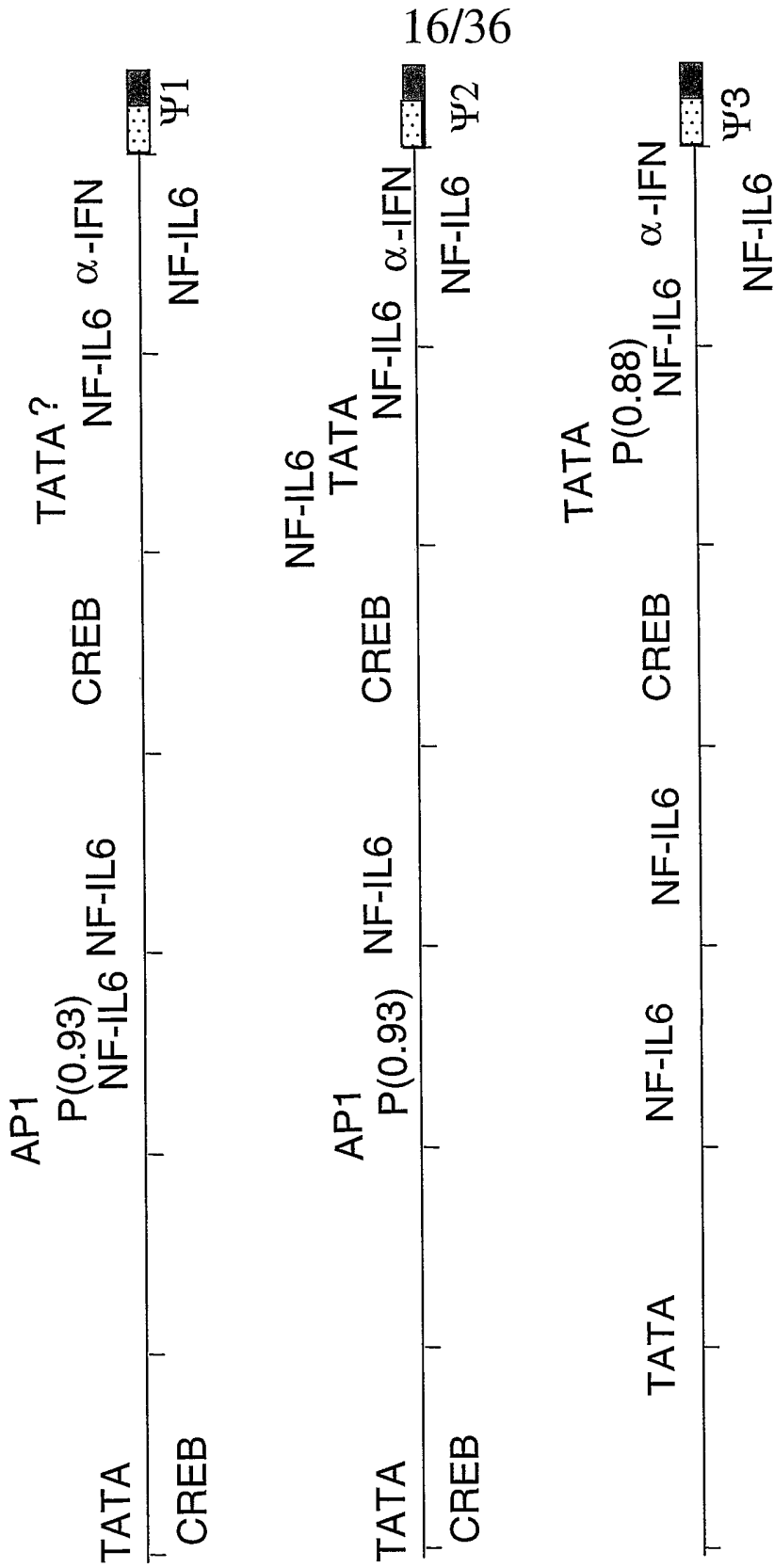


Fig. 12 (Cont.)

17/36

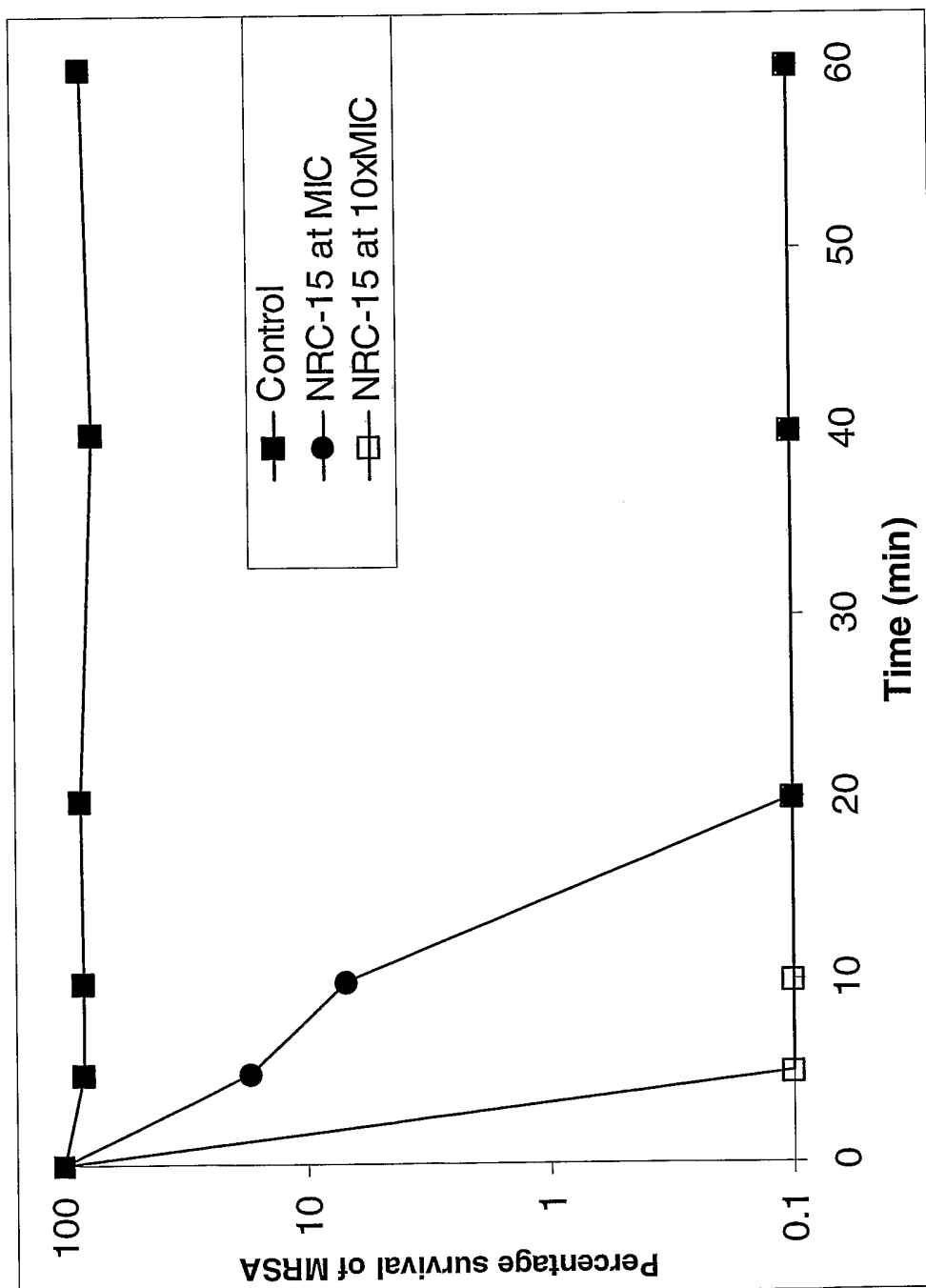


Fig. 13

18/36

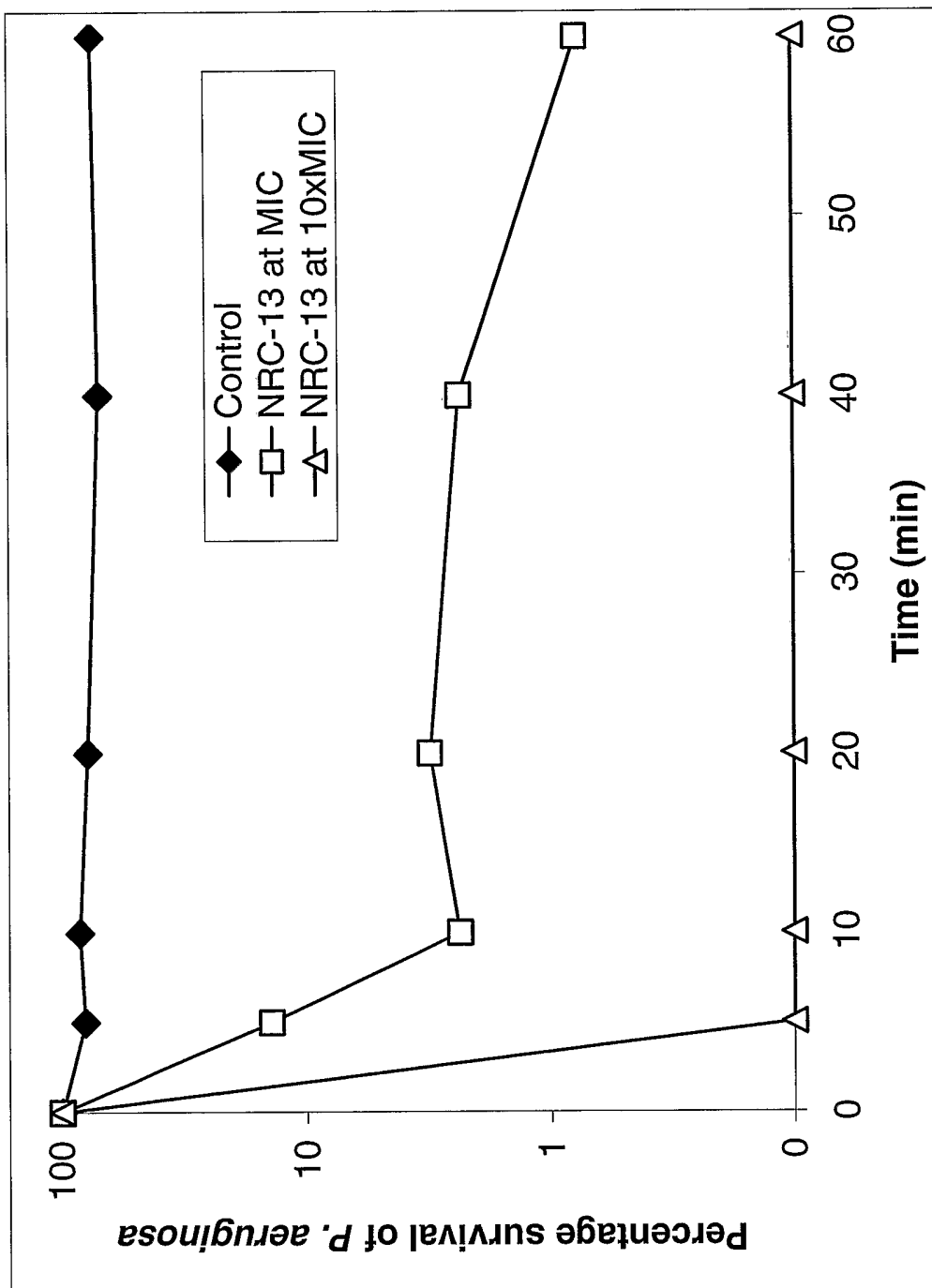


Fig. 14

19/36

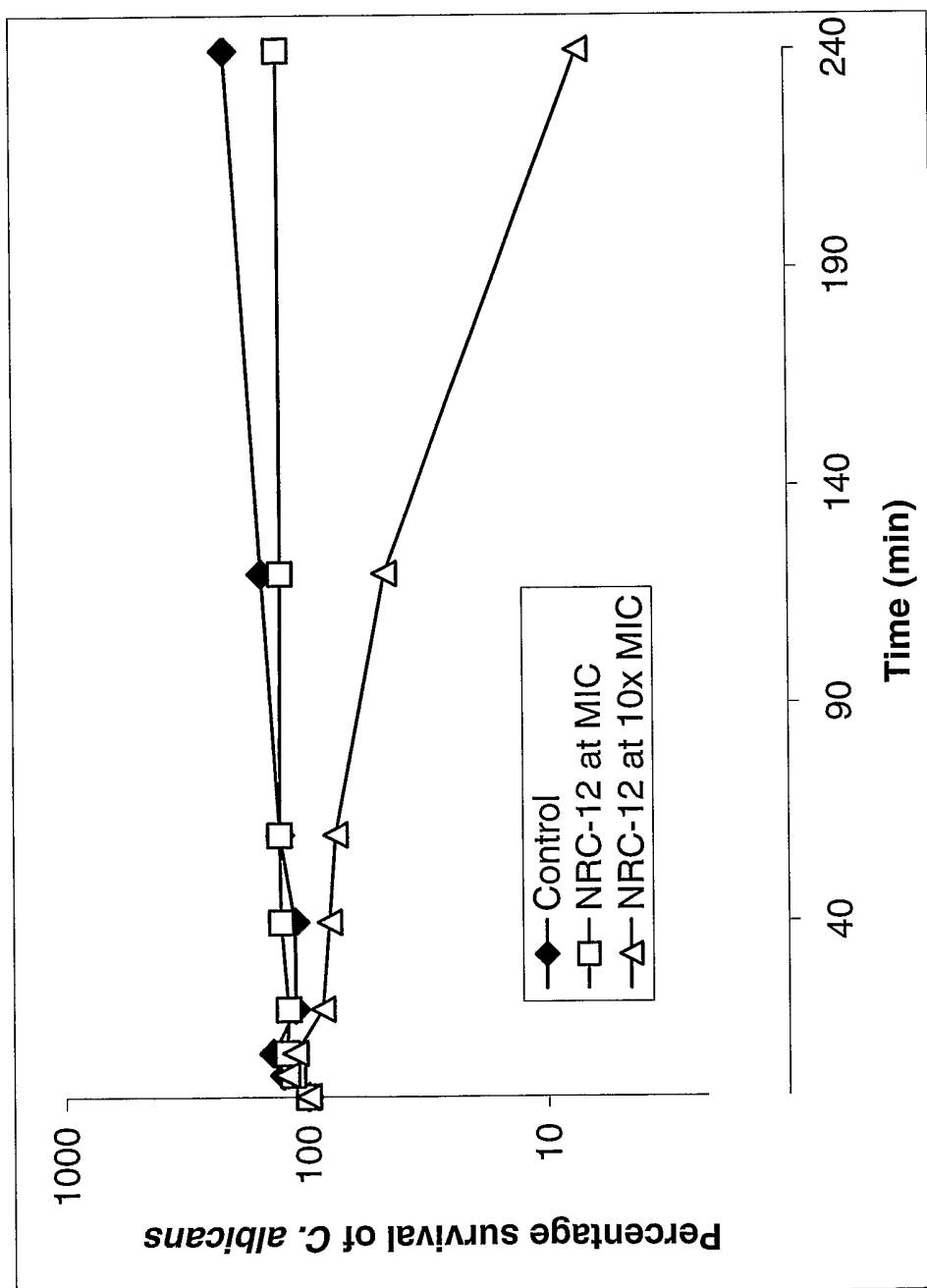


Fig. 15

20/36

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195 TTT AGT GTT GCA GTG GTA CTC GTC ATT GCA TGT ATG TTC  
F S V A V V L V I A C M F  
271 gtcaaattctccaacaccaaccactacaaacatgtgtgcatcgatttta  
367 ACG GAG GAG GTT GGA AGC TTT GAC AGT CCA GTT GGG GAA  
T E E V G S F D S P V G E  
442 gtacgttcaattgaatgaatgaattacgctaattacctttagcaaattaa  
542 tagctgttaaccatttgattgtgagccgtagagggcttcagggcgagca  
642 cttttttcatattatttttcttggcggggatacag GAG CCT TTC AGG  
E P F R  
724 TGC TGC AAC TGC TGT CAC AAC ATT GGC TGT GGC TTT TGC  
C C N C C H N I G C G F C  
807 tgtttgcaatgttttcttctgagatgttgtttttgtgactatgataatga  
907 ctttgaataacaaaaaaaaaaaaaaaaaaaa

Fig. 16a

21/36

aaaattgtgCGTTGGAGAGCGTCGCTTTTTGGGAACATTGAAGAGTTCTG  
ttaaataGGCTATAAACTTCCTAAAAAAACGAGA ATG AAG GCC  
M K A  
ATC CTT GAA AGC ACC GCT GTT CCT TTC TCC GAG gTat  
I L E S T A V P F S E  
gaggTTGGTCATGACTCATTGTGCTAATGTCTTTGCAG GTG CGA  
V R  
CAT CAA CAG CCG GGC GGC GAG TCC ATG CAT CTG CCG  
H Q Q P G G E S M H L P  
cattttagTGGTTGCGTTTTACCCTCGGAATAGAATTAGATCAGTAGCGC  
gtgtgcaacgtggTTGTGAAGTGGAGATATACTTACTTGCTTGTTCCCTC  
TTC AAG CGT CAG ATC CAC CTC TCC CTG TGC GGT TTG  
F K R Q I H L S L C G L  
TGC AAA TTC TAA ggacctgcccGCAACATTTTCTAGTTTGTACA  
C K F \*  
tttataaaatcacttcttattgtgacactttaaaaaataaacacatt

Fig. 16a (Cont.)

22/36

1 cgcccttaag ATG AAG ACA TTC AGT GTT GCA GTT GCA GTG  
 1 M K T F S V A V A V  
 77 ACC GCT GTT CCT TTC TCC GAG GTG CGA ACG GAG GAG  
 23 T A V P F S E V R T E E  
 152 CCG GGC GGC ACG TCC ATG AAT CTG CCGgtacgttcaattt  
 48 P G G T S M N L P  
 243 gtttcacccttggaattgaattagcccactagcgctagttgttaacca  
 343 tgaagtggagacttggacaaaaatacttaccatgtgcttgttcccacc  
 57  
 438 AAG CGT CAG AGC CAC CTC TCC CTG TGC CGT TGG TGC  
 62 K R Q S H L S L C R W C  
 513 AAA TTC TGA ggacctgccagcaaagggcgaattcgtttaaaacac  
 87 K F \*

Fig. 16b

GTG GTC GTC CTC GCA TGT ATG TTC ATC CTT GAA AGC  
 V V V L A C M F I L E S  
 GTT GAA AGC ATT GAC AGT CCA GTT GGG GAA CAT CAA CAG  
 V E S I D S P V G E H Q Q  
 agtgaatgaattaagtaattacctttagcaaattaacatctaagtggttgc  
 tttgattgtgagccggtagagagggcttcagggcgagttagtgaataacttg  
 tttttcattttcttttcttggtgagatacag ATG CAT TTC AGGTTC  
 M H F R F  
 TGC AAC TGC TGT CAC AAC AAG GGC TGT GGC TTC TGC TGC  
 C N C C H N K G C G F C C

Fig. 16b (Cont.)

23/36

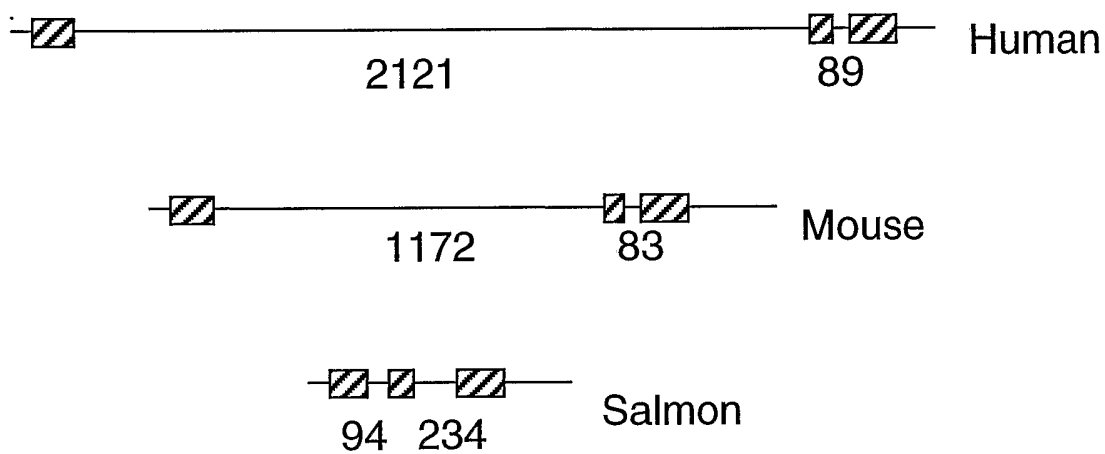


Fig. 16c

24/36 Signal Peptidase



WF2	M	K	T	F	S	V	A	V	T	V	A	V	V	L	V	F	I	C	I	Q	Q	-	S	S	A	T
JFL6	M	K	T	F	S	A	A	V	T	V	A	V	V	L	V	F	I	C	I	Q	Q	-	S	S	A	T
WF3a	M	K	T	F	S	V	A	V	T	V	A	V	V	L	V	F	I	C	I	Q	Q	-	S	S	A	S
WF3b	M	K	T	F	S	V	A	V	T	V	A	V	V	L	V	F	I	C	I	Q	Q	-	S	S	A	S
WF4	M	K	T	F	S	V	A	V	T	V	A	V	V	L	V	F	I	C	I	Q	Q	-	S	S	A	T
Hb5.3	M	K	T	F	S	V	A	V	T	V	A	V	V	L	V	F	I	C	I	Q	Q	-	S	S	A	T
Sal8.6	M	K	T	F	S	V	A	V	T	V	A	V	V	L	I	F	I	C	I	Q	Q	-	S	S	A	T
Hb17	M	K	T	F	S	V	A	V	T	V	A	V	V	L	V	F	I	C	I	Q	Q	-	S	S	A	T
Hb1.1	M	K	T	F	S	V	A	V	T	V	A	V	V	L	V	F	I	C	I	Q	Q	-	S	S	A	T
Hb357	M	K	T	C	G	F	A	A	A	V	A	V	L	L	T	F	I	C	I	Q	E	-	G	G	A	V
Bass	M	K	T	F	S	V	A	V	A	V	A	V	V	L	A	F	I	C	L	Q	E	-	S	S	A	V
Med1	M	K	A	F	S	I	A	V	A	V	T	L	V	L	A	F	I	C	I	L	Q	-	S	S	A	I
WF1	M	K	A	F	S	I	A	V	A	V	T	L	V	L	A	F	V	C	I	Q	C	-	S	S	A	V
JFL4	M	K	A	F	S	I	A	V	A	V	T	L	V	L	A	F	V	C	I	Q	D	-	S	S	A	I
Hb7.5	M	K	T	F	S	V	A	V	A	V	V	V	V	L	A	-	C	M	F	I	L	E	S	T	A	V
Sal2	M	K	T	F	S	V	A	V	A	V	V	V	V	L	A	-	C	M	F	I	L	E	S	T	A	V
Sal2.1	M	K	T	F	S	V	A	V	-	-	V	P	V	I	A	-	C	M	F	I	L	E	S	T	A	V
Trout	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Sal1	M	K	Q	F	S	V	A	V	-	-	V	L	V	M	A	-	C	M	F	I	V	E	S	T	A	V
Human	-	M	A	L	S	S	Q	I	W	A	A	C	L	L	L	L	L	L	L	A	S	L	T	S	G	S

Fig. 17a

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

Fig. 17a (Cont.)







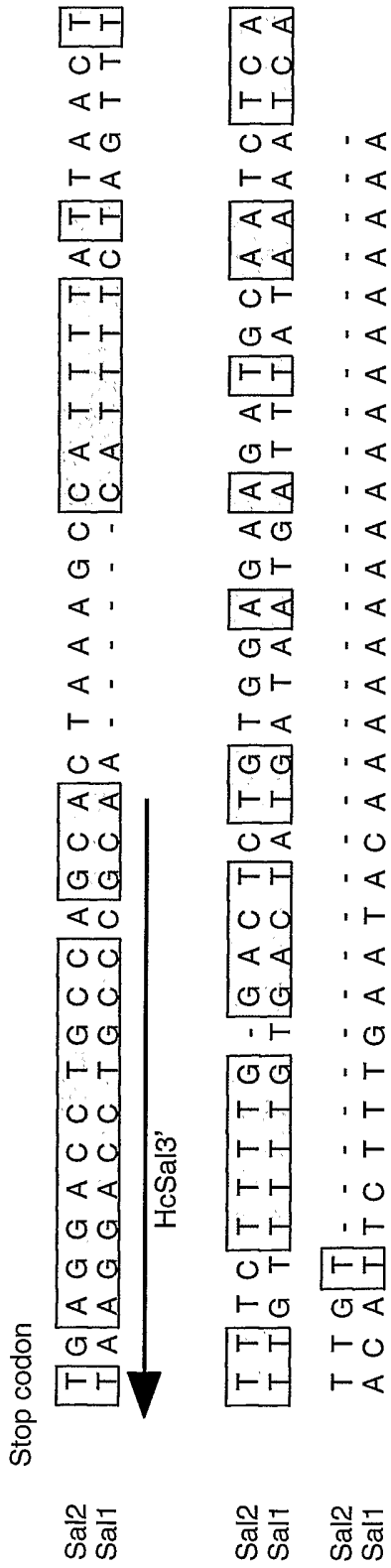


Fig. 18b

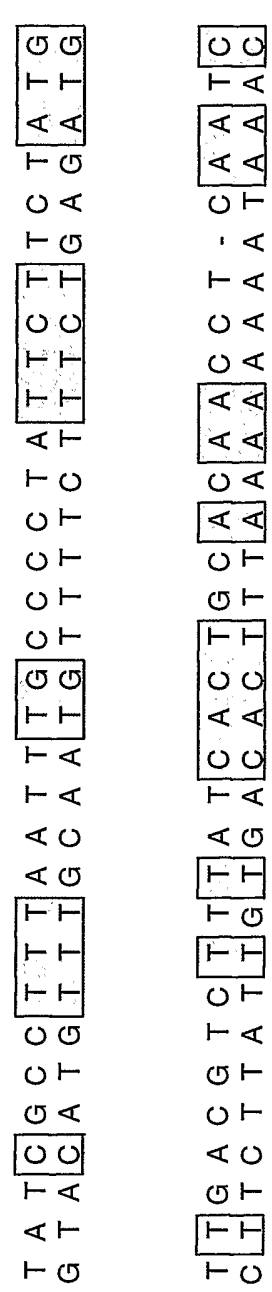


Fig. 18b (Cont.)

29/36

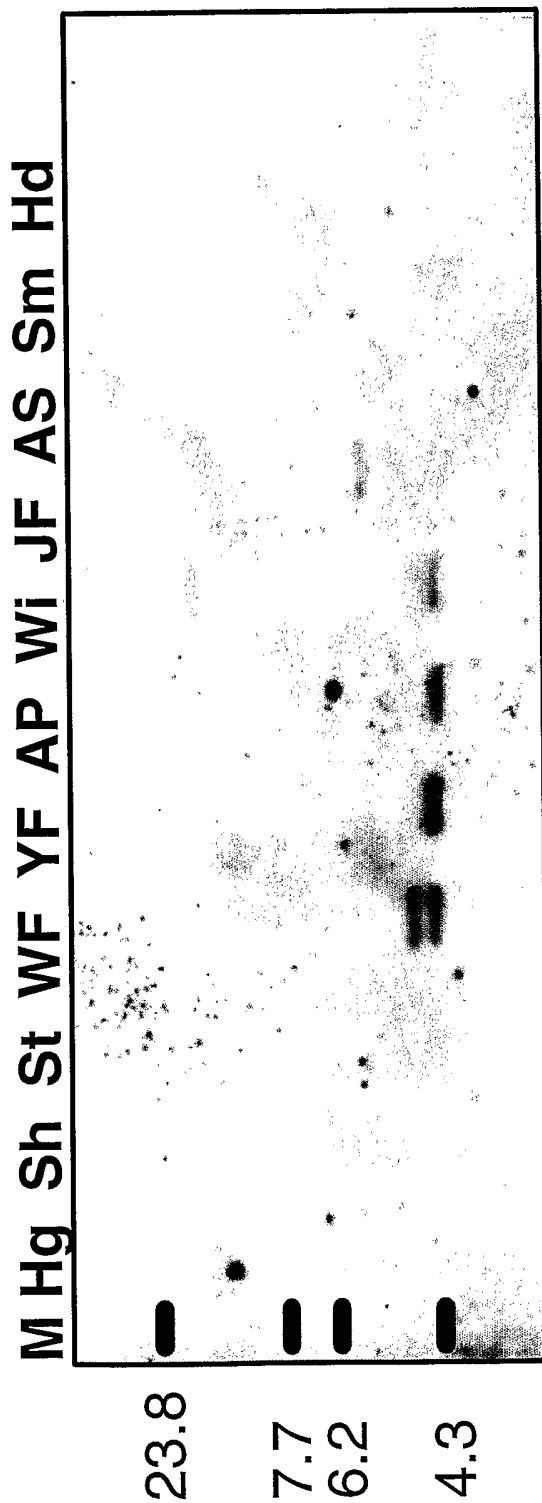


Fig. 19

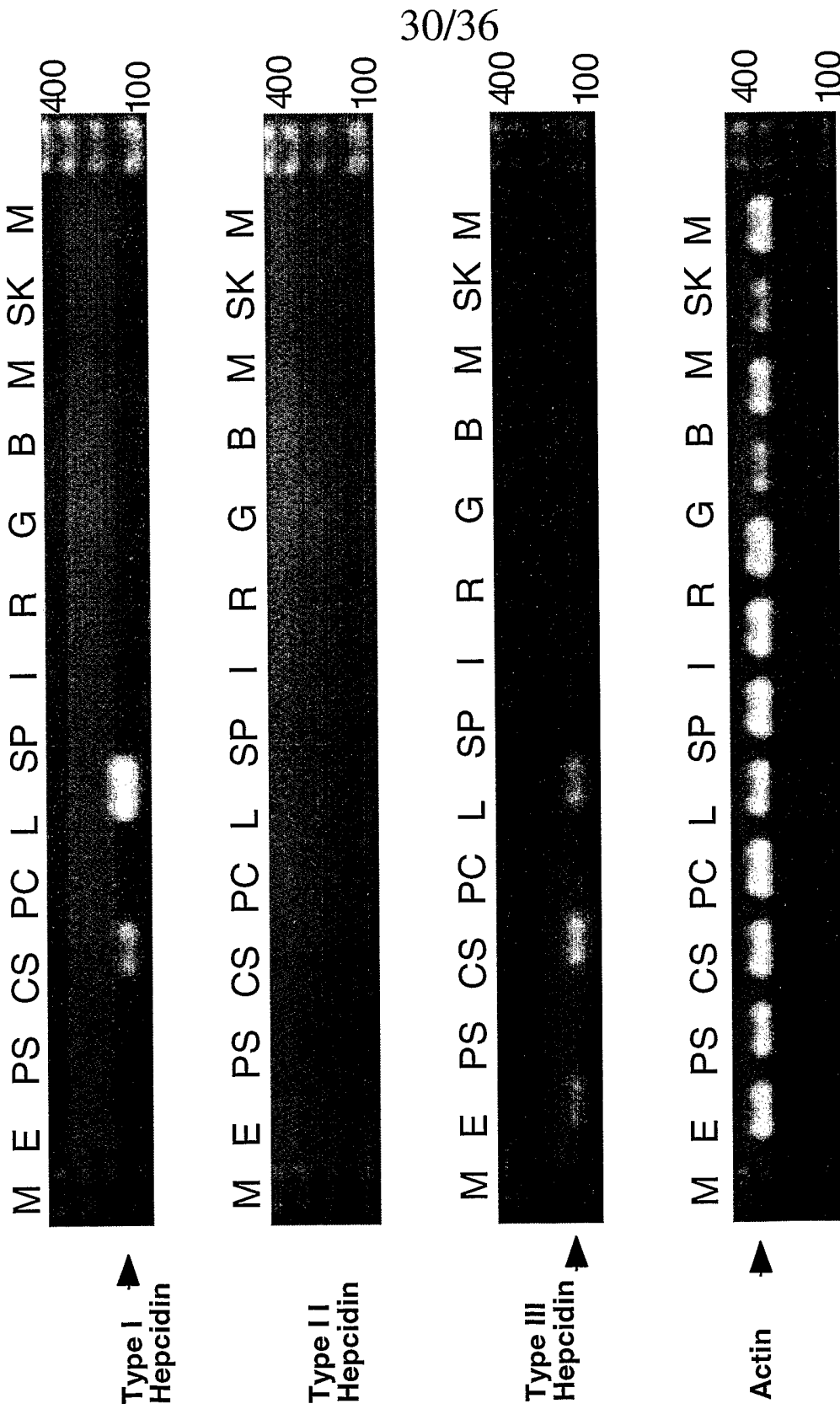


Fig. 20

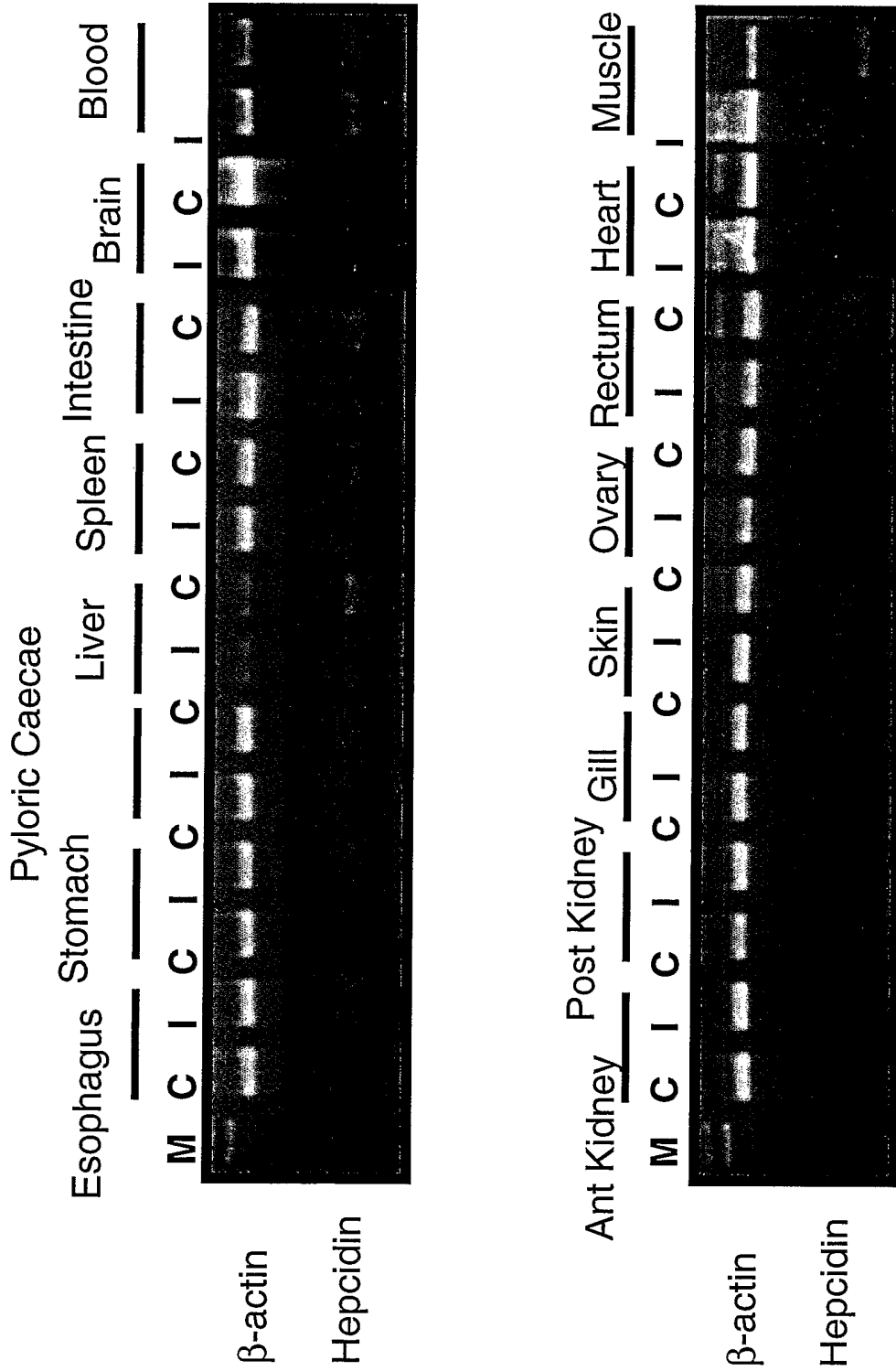


Fig. 21a

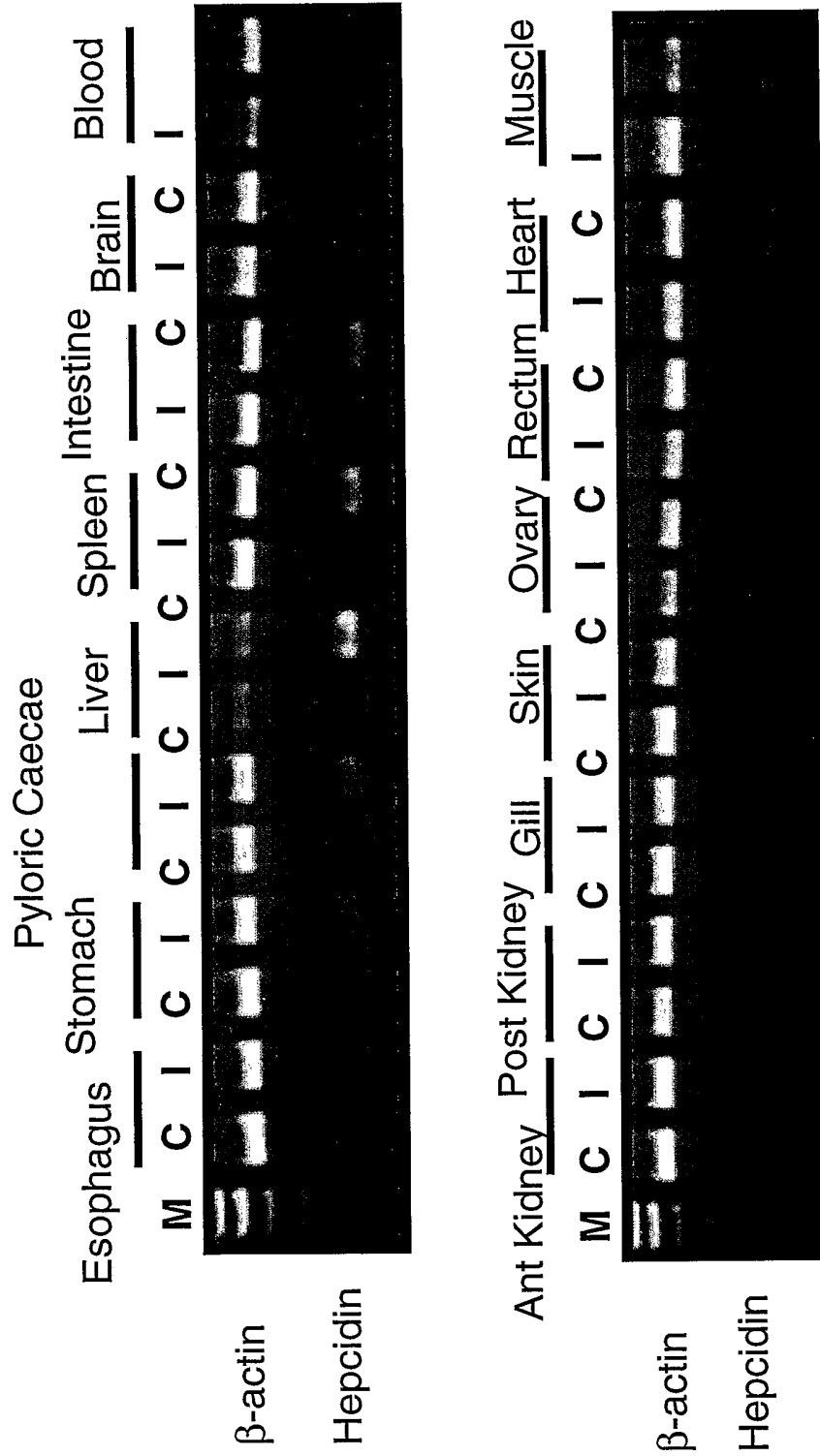


Fig. 21b

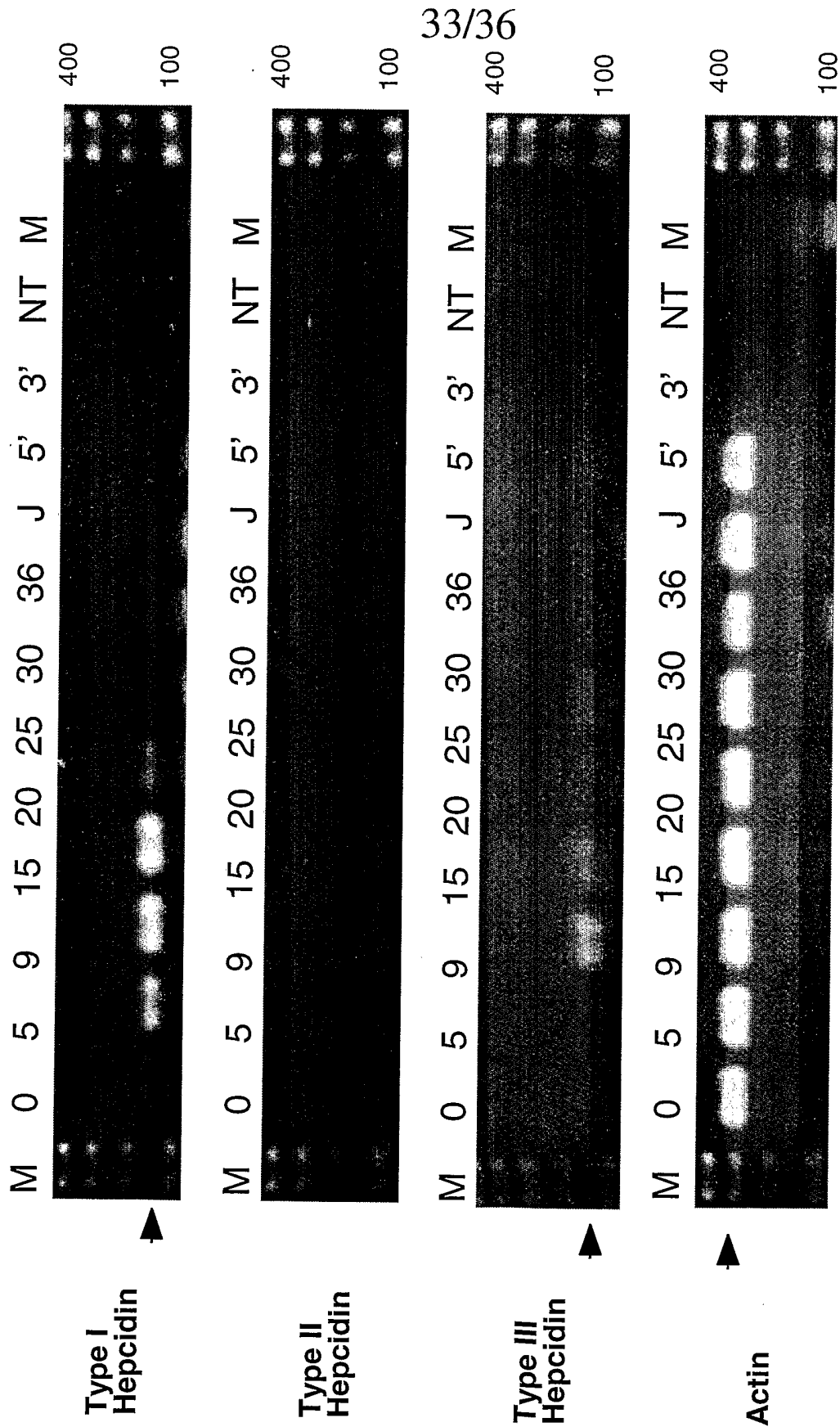


Fig. 22

# FLOWCHART FOR IDENTIFICATION OF PLEUROCIDINS

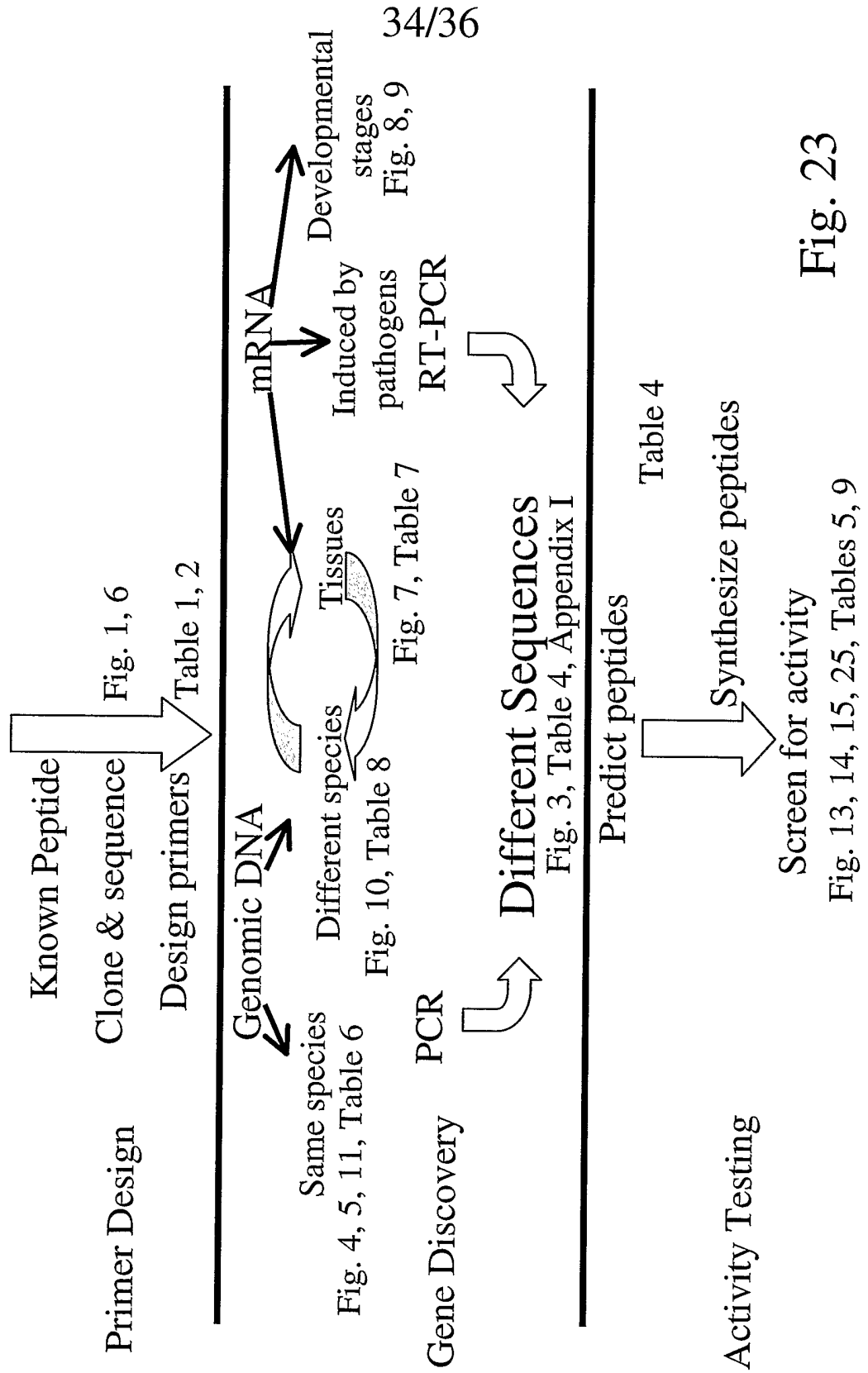
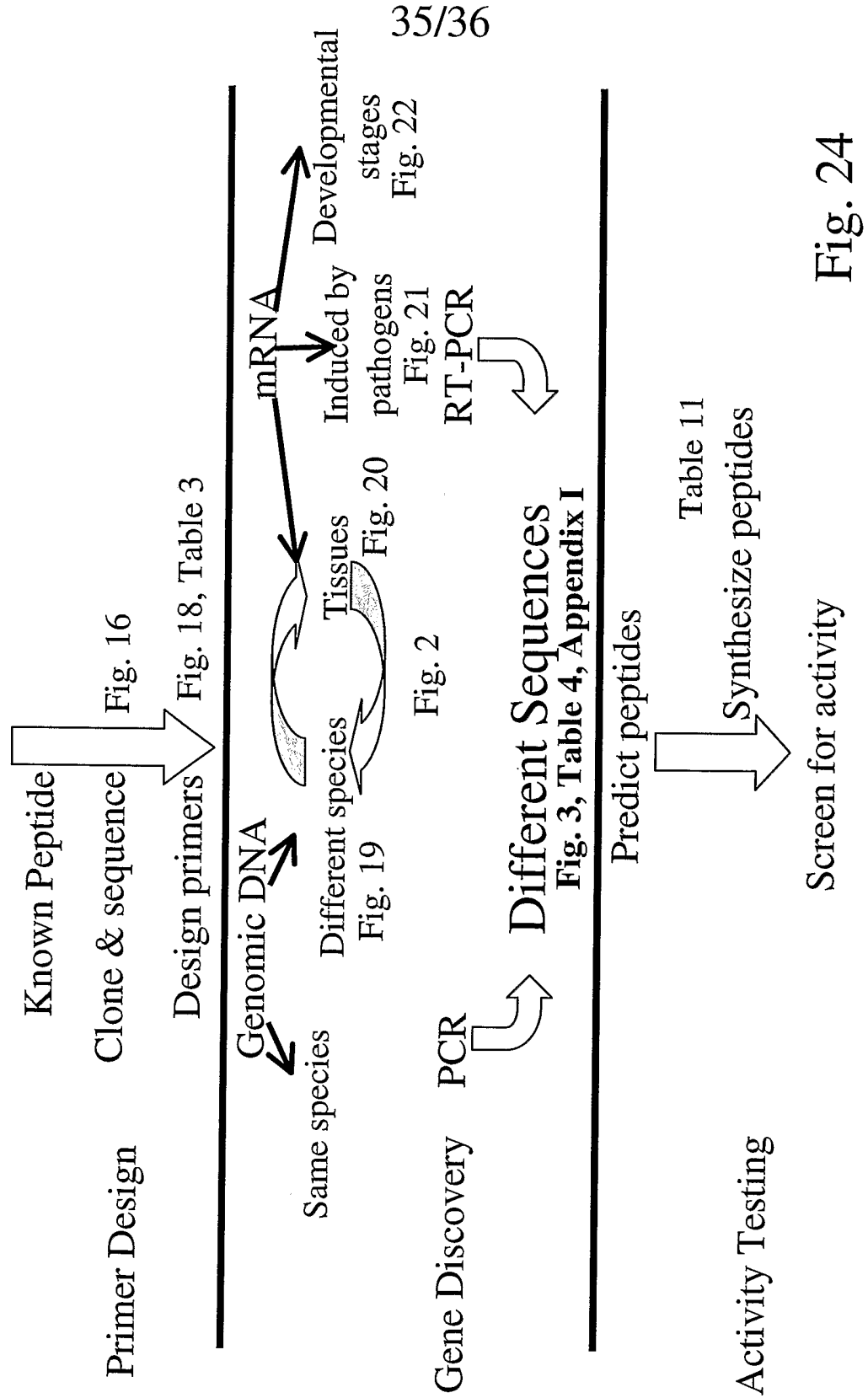


Fig. 23

# FLOWCHART FOR IDENTIFICATION OF PLEUROCIDINS



36/36

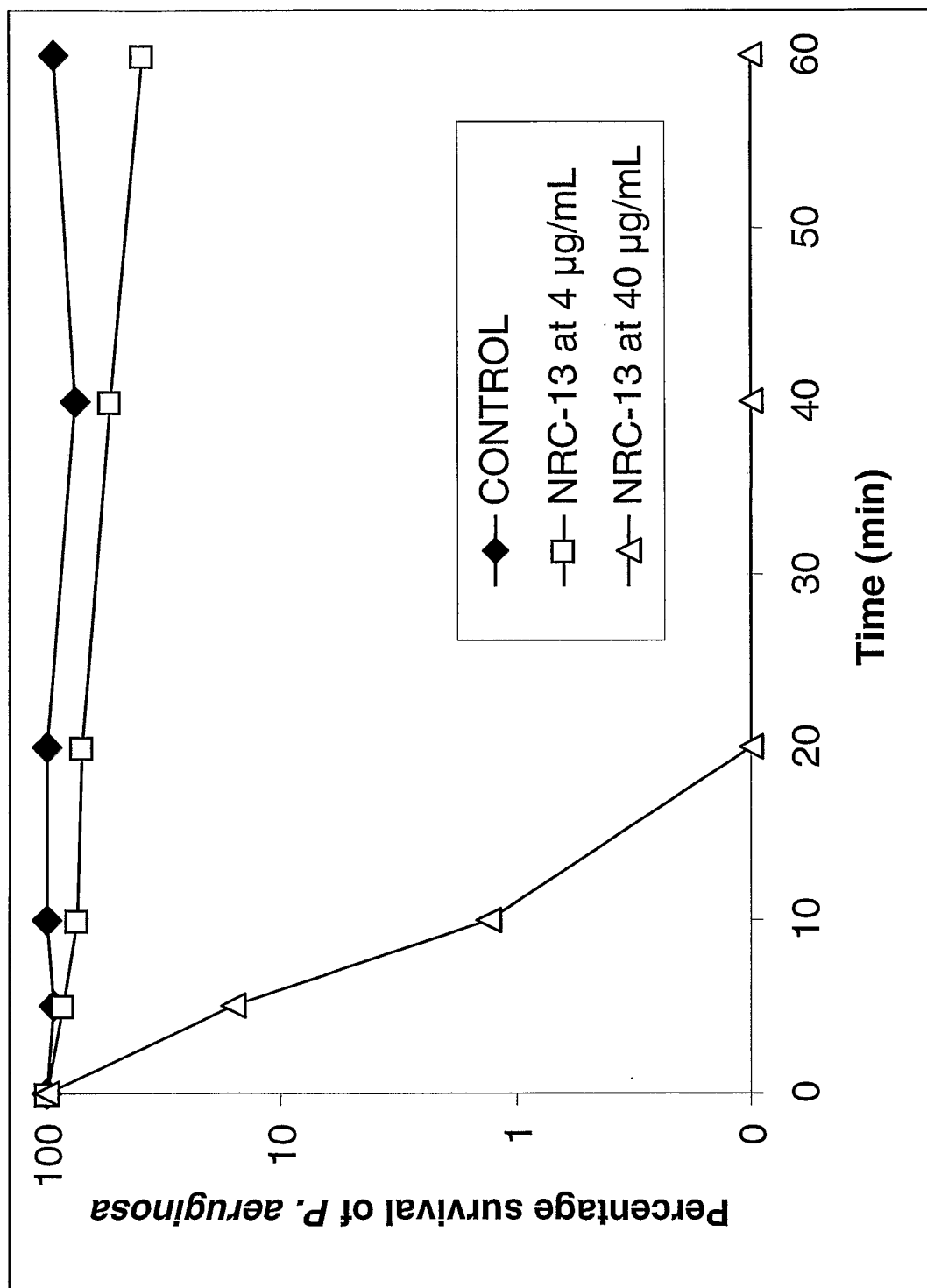


Fig. 25