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Appendices

Appendix I: Families of Snakes and the species found within them.

Summary and excerpt copied from EMBL reptile database. http://www.embl-heidelberg.de/~uetz/LivingReptiles.html

Family Elapidae (Cobras, Kraits, Coral Snakes) (including Hydrophiidae, (Sea Snakes))

(Non marine forms: Africa, Southern Asia; North, Central, and South America. Marine forms: all continents except Europe) *Micrurus fulvius, Micrurus spixii, Micrurus sp.,* ***Acanthophis*** *antarticus (*Common Death Adder), *Naja* (Cobra, Central Asia), *Hydrophis klossi,* *Laticauda* (false sea snake, Asian), ***Bungarus*** (Krait) *Demansia* (Whip snake),

Australian: *Pseudechis* (Black snake), *Pseudechis australis* (King Brown snake), *Pseudonaja* (Brown Snake), *Oxyuranus* (Taipan + PNG), *Notechis* (Tiger snake), *Pseudonaja inframacula* (Peninsula Brown Snake), *Austrelaps* (copperhead)

Colubridae Colubridae. (Colubrids) --(Worldwide; Colubrinae and Natricinae most widespread, but neither in Madagascar)

- **Natricinae** (In US: *Clonophis, Nerodia, Regina, Seminatrix, Storeria, Thamnophis, Tropidoclonion.*) *Nerodia erythrogaster, Nerodia harteri, Thamnophis proximus, Thamnophis marcianus, Storeria dekayi*
- ***Xenodontinae*** *(in US: Carphophis, Contia, Diadophis, Farancia, Heterodon, Hypsiglena, Coniophanes, Rhadinaea, Tantilla, Trimorphodon) Heterodon platyrhinos, Diadophis punctatus, Tantilla gracilis, Hypsiglena torquata, Leimadophis epinephalus, Ninia psephota, Leptodeira annulata, Imantodes inornatus*
- ***Colubrinae*** *(in US: Arizona, Coluber, Drymarchon, Drymobius, Elaphe, Masticophis, Opheodrys, Pituophis, Salvadora, Cemophora, Lampropeltis, Rhinocheilus, Stilosoma, Chilomeniscus, Chionactis, Conopsis, Ficimia, Gyalopion, Sonora, Stenorrhina) Arizona elegans, Rhinocheilus lecontei, Elaphe guttata,* ***Elaphe obsoleta****, Pituophis melanoleucus, Lampropeltis triangulum, Lampropeltis getulus, Coluber mentovarius, Masticophis flagellum, Salvadora grahamiae, Ficimia streckeri, Sonora semiannulata, Chrysopelea paradisi,*
- ***Homalopsinae*** (Rear-fanged watersnakes; Asia) *Enhydris polylepis*

Lycodontinae (Africa, Asia) *Psammophis sp.*

Viperidae (Vipers and Pit Vipers)

- **Viperinae** (Non-pit vipers) (Europe, Africa, East Asia, Southern Asia) *Bitis gabonica*
- **Crotalinae** (Pit vipers) (East Asia, Southern Asia, North, Central, and South America) ***Agkistrodon*** *contortrix,* ***Bothrops*** *nasuta, Bothrops lateralis, Sistrurus catenatus, Crotalus atrox*

The Caenophidia are considered the most "advanced" snakes. Within the colubroids, the Viperidae and Elapidae are two generally accepted, well-supported groups. Relationships with the Colubridae are a mess. Many characters used at family/subfamily level are derived from maxilla and hemipenis. A recent molecular study does support the scolecophidians as most basal; booids intermediately placed but paraphyletic; colubroids monophyletic except that *Acrochordus* is within booids; *Atractaspis* is within Elapidae; colubrids not obviously monophyletic. (Heise *et al.*, 1995).

Appendix II; Summary of common and scientific names of Australian snakes.

Australian snakes	
Common name	**Scientific name**
Inland taipan	*Oxyuranus microlepidotus*
Common brown snake	*Pseudonaja textilis*
Taipan	*Oxyuranus scutellatus*
Reevesby Is. tiger snake	*Notechis ater niger*
Common tiger snake	*Notechis scutatus*
Western tiger snake	*Notechis ater occidentalis*
Beaked sea snake	*Enhydrina schistosa*
Chappell Is. tiger snake	*Notechis ater serventyi*
Common death adder	*Acanthophis antarcticus*
Western brown snake	*Pseudonaja nuchalis*
Lowland copperhead	*Austrelaps superbus*
Dugite	*Pseudonaja affinis*
Stephens banded snake	*Hoplocephalus stephensi*
Rough scaled snake	*Tropidechis carinatus*
Spotted black snake	*Pseudechis guttatus*
King brown snake	*Pseudechis australis*
Colletts snake	*Pseudechis colletti*
Red bellied black snake	*Pseudechis porphyriacus*
Small-eyed snake	*Rhinoplocephalus nigrescens*
Black whip snake	*Demansia papuensis and Demansia vestigiata*

Appendix III; Table describing major components characterised in snake venoms and examples within *Oxyuranus*

Class of toxin			Notes
Procoagulants	Effect on factor Xa		The conversion of prothrombin to thrombin by factor Xa requires the cleavage of two peptide bonds within the prothrombin molecule. Yet, the enzyme responsible for prothrombin activation, factor Xa, is a poor activator of prothrombin, and requires cofactors. This occurs in the form of a complex consisting of factor Xa-factor Va bound to negatively charged phospholipids in the presence of calcium ions. In view of this mechanism, prothrombin activators were classified into four groups (A, B, C and D) based on the stimulation of venom prothrombin converting activity by the accessory components of the prothrombinase complex ie Ca^{2+}, negatively charged phospholipids or factor Va (Denson, 1976). The blood disruption from the venoms of the Australian elapids fall into either group C or group D (Tu and Dekker, 1991).
		Group C	The prothrombin converting activities of this group are stimulated by factor Va and acidic/negatively charged phospholipids and calcium ions. These enzymes are present in venoms of genera including *Notechis* (Tans *et al.*, 1985, Williams & White, 1989), *Austrelaps*, *Tropidechis*, *Pseudechis* and *Hoplocephalus* (Williams *et al.*, 1994). Fohlman, et al., (1979) reported *O. microlepidotus* venom contained a prothrombin activator. Although further studies have stated the activity of this venom is not medically important (Sutherland and Tibbals, 2001).
		Group D	These come from the venoms of some species of *Pseudonaja* (Masci, *et al.*, 1988, Stocker *et al.*, 1994, Williams *et al.*, 1994, Masci, *et al.*, 2000) and *Oxyuranus* (taipan) (Marsh *et al.*, 1997, Speijer, *et al.*, 1986, Walker, *et al.*, 1980). As an example, the prothrombin activator from ~~O. scutellatus~~*O. s. scutellatus* was partially characterised by Walker *et al.* (1980) and consisted of either two separate enzymes or a single enzyme with two active sites. It contained a very potent converter of prothrombin to thrombin in the absence of all other known clotting factors (Denson, 1969). A prothrombin activator from this species was further purified by Speijer *et al* (1986), named scutelarin (EC 3.4.21.60) and confirmed the prothrombin activator as having an approximate molecular mass of 300kDa. It was composed of subunits of molecular mass 110kDa and 80kDa and two disulphide linked polypeptides each of 30 kDa molecular mass. The multimeric protein consists of a factor XI like enzyme and a factor Va like cofactor. It has been demonstrated that ~~O. scutellatus~~*O. s. scutellatus* venom possesses an activator of factor VIII (Nakagaki, *et al.*, 1992).
	Effect on factor V		The proteolytic activity required in the mechanism of coagulation is augmented by cofactors: tissue factor, factor VIIIa, and factor Va. These catalyse the proteolytic activity of factor VIIa, factor IXa and factor Xa, respectively. Two of these cofactors, factor VIIIa and factor Va, circulate in plasma as procofactors with little if any activity and require proteolytic activation for the full expression of their cofactor activity. Physiologically, proteolytic activation of factor VII and factor V is mediated by low amounts of either thrombin alone or factor Xa in the presence of calcium and a negatively charged phospholipid surface. Some snake venom proteases (*Vipera russellii* (Russell's viper) and *Bothrops atrox* (fer-de-lance) have been seen to specifically activate factor V by limited proteolysis and thus contribute to hypercoagulable states after envenomation (Boffa and Boffa, 1974).
Effects on platelets			Platelets are small and numerous and the primary 'duties' of platelets are the maintenance of endothelial integrity and haemostasis (Subburaju and Kini, 1997, Singh *et al.*, 2000). Platelets may interact with prothrombin activators to increase their effectiveness

			(Furihata, *et al.*, 2001, Speijer, *et al.*, 1987) but generally direct effects of the prothrombin activators on platelets have not been reported. Platelet responses are several and it is these changes that allow for quick and conclusive assays of pharmacologic action. One of the earliest responses to stimulation is shape change and several types of 'stickiness ' responses occur -adhesion, aggregation, and agglutination (Marshall and Herrmann, 1989). Stimulators of platelets may act on receptors that are coupled to Ca^{2+} phospholipase C and inositol triphosphate (Feinstein and Helenda, 1988).
Phospholipase A_2			
	Neurotoxic		
	Type I		Isolated from *Elapidae* and *Hydrophidai* snake venoms and mammalian pancreas. They have been characterised by the presence of a disulphide bridge between cysteine residues 11 and 78.
	Type II		Present in venoms of *Crotalidae* and *Viperidae* species. These are characterised by additional amino acids residues at their carboxyl extremity and a disulphide bridge between cysteine residues characteristic of phospholipases A2 from class I (Bon, *et al.*, 1986, Fraenkel-Conrat, 1982).
	Type III		These have been isolated from lizard (Gila monster) and bee (*Apis mellifera*) venoms. Data suggests that a generalisation is not applicable to group III as this PLA_2 has been identified in human kidney, heart, liver and skeletal muscle (Valentin and Lambeau, 2000). The identification of type III PLA_2 in human tissue implies a novel physiological role for this enzyme (Arni and Ward, 1996; Kini, 1997, Kuchler, *et al.*, 1989, Sosa, *et al.*, 1986).
		Type 1 + II neurotoxins	Phospholipase A_2 enzymes are key toxins and highly abundant and is the area where the bulk of the research of Australian elapids has been concentrated (Armugam *et al.* 2000). The majority of Australian elapid PLA_2s are basic, 118 amino acids long, have seven disulphide bonds and molecular weights around 13 kDa. Despite the homology there is a wide range of enzymatic and toxic activity found in Australian elapid PLA_2 (Dunn and Broady, 2001, Brunie, *et al.*, 1985). Neurotoxins block neuromuscular nerve transmission either pre- or post-synaptically.
		Pre-synaptic Neurotoxins (β)	Beta neurotoxins keep nerve endings from liberating acetylcholine. They can cause irreversible paralysis in as little as 3 to 5 minutes. These neurotoxins are found prominently in *Acanthophis, Pseudonaja, Notechis, Oxyuranus* and *Pseudechis* species. Beta toxins are absent in the venom of *Pseudechis australis*.
			Single chain β neurotoxins are composed of a single polypeptide chain of 13-14kDa molecular mass, the amino acid sequence of which is homologous with that of other Type I and II phospholipase A_2s from mammalian pancreas and snake venoms. Two significant phospholipase A_2s from ~~*O. scutellatus*~~*O. s. scutellatus* are the toxic monochain PLA2s **OS2** and the non toxic **OS1**. OS1 binds to M-type (muscle type) neuronal PLA_2 receptors but not the N type (neurone type) receptors (Lambeau, *et al.*, 1990), whereas OS2 binds to both M and N type PLA_2 receptors.
			Larger pre-synaptic neurotoxins are made of two, three or four polypeptide subunits that are not linked by disulphide bridges and have a sequence homology with phospholipase A_2s from both type 1 and II peptides. At least one of the subunits possesses PLA_2 activity and is responsible for the enzymatic activity of the neurotoxin. The other subunits may or may not have phospholipase activity. The multi chain neurotoxic PLA_2s exist as phospholipases in *Oxyuranus* and *Pseudonaja* venoms (**taipoxin** and textilotoxin). Although it may also contain smaller peptidic components (**taicatoxin**) this peptidic component selectively and reversibly blocks high threshold calcium channels, (Lullmann-Rauch and Thesleff, 1979; Fantini, *et al.*, 1996). The phospholipase

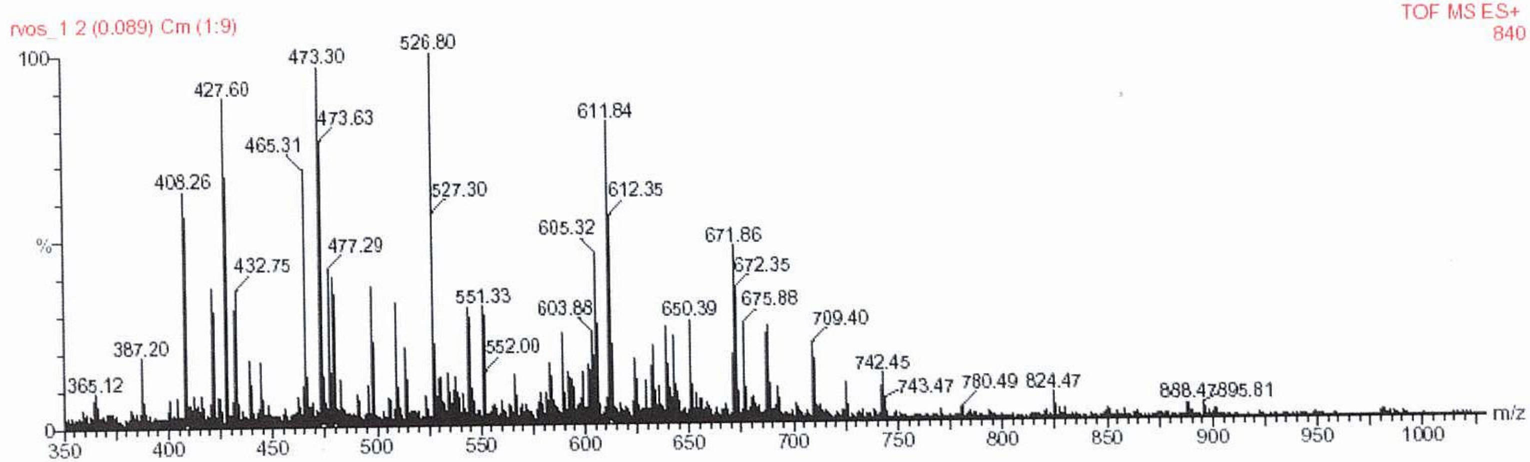
			A_2 neurotoxins, textilotoxin (*Pseudonaja*), taipoxin (*Oxyuranus*), notexin (*Notechis*) and pseudexin (*Pseudechis*) are closely related (White, 1981; Middlebrook and Kaiser, 1988; Gandolfo, *et al.*, Lambeau, *et al.*, 1990, Lambeau and Lazdunski, 1999) .
		Post-synaptic Neurotoxins (α)	The nicotinic acetylcholine receptor (AchR) plays a central role in post-synaptic neuromuscular transmission by mediating ion flux across the cell membrane in response to binding of acetylcholine (Changeux, et al., 1984, Conti-Tronconi and Raftery, 1982; Hucho, 1986, Karlin, 1980; McCarthy, *et al.*, 1986). This regulatory activity is inhibited by binding to an alpha neurotoxin (Lee, 1979) or to some anti-AchR antibodies. The receptor is a pentamer composed of four subunits (α2,β,γ,δ). Functional studies have focused mostly on the α-subunit because it is responsible for binding acetylcholine (Changeux, 1981, Moore and Raftery, 1979; Sobel, *et al.*, 1977, Tzartox and Changeux, 1983) and α-neurotoxins (Bon, *et al.*, 1979; Dufton and Hider, 1983; Endo *et al.*, 1987; Joubert and Viljoen, 1979; Lee, 1979; Noda, *et al.*, 1982, Noda, *et al.*, 1983).
			Short chain neurotoxins: The short chain neurotoxins are found in the venom of members of the genus *Acanthophis*, *Oxyuranus* and *Pseudechis*. The short chain neurotoxins isolated thus far from Australian elapids are homologous (mostly 62 amino acids), basically charged post-synaptic blockers of neuromuscular transmission with a great deal of sequence homology. Taipan **toxin 1** and **toxin 2** from OS are short chain alpha-neurotoxins that inhibit the binding of bungarotoxin to nicotinic acetylcholine receptors in skeletal muscles but not the central neuronal nicotinic receptors (Tu and Dekker, 1991). The primary structure of short neurotoxins is composed of 60, 61, or 62 amino acid residues, which are linked by disulphide bridges. Most of the invariant residues are localised in either the immediate vicinity of the disulphide bridge in the globular head or toward the distal ends of the three major loops. In contrast, the least conserved residues appear to be grouped across the loop of the globular head (Tu and Dekker, 1991).
			Long Neurotoxins : Both short and long-chain post-synaptic neurotoxins share a similar three-finger loop structure (Walkinshaw, Saenger *et al.* 1980; Yu and Dennis 1993) and show differences in their primary structure. The major variations are observed at the C-termini, as well as at the tips of loop 1 and loop 2 of these proteins (Gong, *et al.* 2001). Long-chain neurotoxins possess extra amino acids beyond the short-chain neurotoxin end point CNX (X coding N in most cases) (Tamiya, *et al.* 1985; Chang, *et al.* 1997; Fuse, *et al.*, 1990). Long chain neurotoxins are found in *Acathophis*, *Notechis*, *Pseudichis* and *Pseudonaja species*. These venoms are extensions of the short chains with about another 10 amino acids. A few other peptides found in *Oxyuranus* and *Pseudonaja* venoms inhibit the serine protease plasmin (Crachi *et al.*, 1999a). These toxins also possess a high degree of homology. Long neurotoxins generally associate and dissociate much more slowly than the short chain neurotoxins. These differing rates are reflected in major differences in the sequence between the two types of toxins. Long neurotoxins also contain four disulphide bridges of short neurotoxins, but possess an additional disulphide bond in the central loop of the molecule. Long chain neurotoxins have a longer polypeptide chain (between 65 and 74 residues) giving the characteristic COOH-terminal tail. Apparently, where there are differences in sequences or chain lengths, these alterations do not disrupt the clustering of the disulphide bridges or the three major loops. In long neurotoixns, the least conserved regions tend to be found in the COOH terminal tail and the first loop. The homologues of long neurotoxins usually lack the fifth disulfide bridge (between Cys-29 and Cys-33 in long neurotoxins) (Weber and Changeux 1974; Chicheportiche, *et al.* 1975; Pillet, *et al.*, 1993; Tremeau, *et al.*, 1995)
	Cardiotoxins		Cardiotoxins reversibly block high threshold voltage dependent calcium channels. Taicatoxin, which is different from taipoxin, has

			been isolated from ~~O. scutellatus~~O. s. scutellatus venom and is composed of three molecular entities, an ∝-neurotoxin like peptide, a 16 kDa neurotoxic phospholipase, and a 7 kDa serine protease inhibitor, linked with a stoichiometry of 1:1:4 (Lullmann-Rauch and Thesleff 1979;Brown, *et al.*, 1987; Possani, *et al.* 1992a and b). Phospholipase activities of taicatoxin have also been confirmed (Fantini, Athias *et al.* 1996). The gamma subunit of taicatoxin or the 7 kDa serine protease inhibitor is distinct from all other toxins isolated from elapids and is related (64%) to a chymotrypsin inhibitor from *Vipera ammodytes* (European long nosed viper) Willmott, *et al.*, 1995).
	Haemorrhagic		The haemotoxic PLA_2s produce haemorrhage through the blockage of factors in the coagulation cascade resulting in a disruption of haemostasis. These components themselves do not produce net anticoagulation through fibrinolysis but rather bind specifically to molecules essential to the coagulation processes (Gutierrez and Chaves 1980; Gutierrez *et al.* 1980; Condrea, *et al.*, 1981; Francischetti, *et al.*, 1997).
	Myotoxic		*Notechis* and *Pseudechis* species contain myolytic activity. Nephrotoxins causing renal failure have only been discovered in the venom of one genus, *Pseudonaja* (White, 1981). Damage is caused to the skeletal muscle after envenomation. This process, myolysis, or more specifically rhabdomyolysis, results in the release of the muscle protein myoglobin which is then excreted in the urine. If muscle damage is extensive then the resulting large quantities of myoglobin may block the kidney tubules, causing acute tubular necrosis and renal failure. As well as releasing myoglobin the damaged muscle loses enzymes, including creatine (phospho) kinase (CPK, CK). Myotoxins attack skeletal muscle and result in damage to muscle fibres. Symptoms include muscle weakness and pain upon moving (Gutierrez, *et al.*, 1995, Mebs, 1986).
	Lysophospho-lipases		Lysophospholipases hydrolyse the sn-1-acyl ester of lysophospholipids. These lipases, found in *Pseudechis australis* venom, are haemolytic (Takasaki and Tamiya, 1982), but exist in few snake venoms (Takasaki *et al* 1992; Tan and Ponnudurai, 1990; Bell, *et al.*, 1998; Bell, *et al.*, 1999).

Appendix IV: Mass Spectrometry spectra

In the upper right-hand is TOF MS ES+ or TOF MSMS XYZES+, where XYZ represents the peptide mass selected for MS/MS. The TOF MS spectra contain all of the peptides found in the mixture. Typically, doubly or triply charged ions between the m/z range 500-1000 Da are chosen for MS/MS analysis. The TOF MS/MS spectra contain two MS/MS spectra. The bottom spectrum is the raw MS/MS data collected from the instrument, whereas, the top spectrum is the MaxEnt3 deconvoluted spectra. MaxEnt3 is an algorithm that removes all multiply charged peptides so the data is compatible with sequence interpretation. Following the MS/MS spectra, the analysis of the MS/MS data is summarised. The MS/MS ions *a, b, y* and *z* (please note *y*-type ions are used for sequencing of the peptides) are shown at the top of the page along with the called sequence. The bottom of the page contains the MaxEnt3 spectra and the called sequence (reference from APAF).

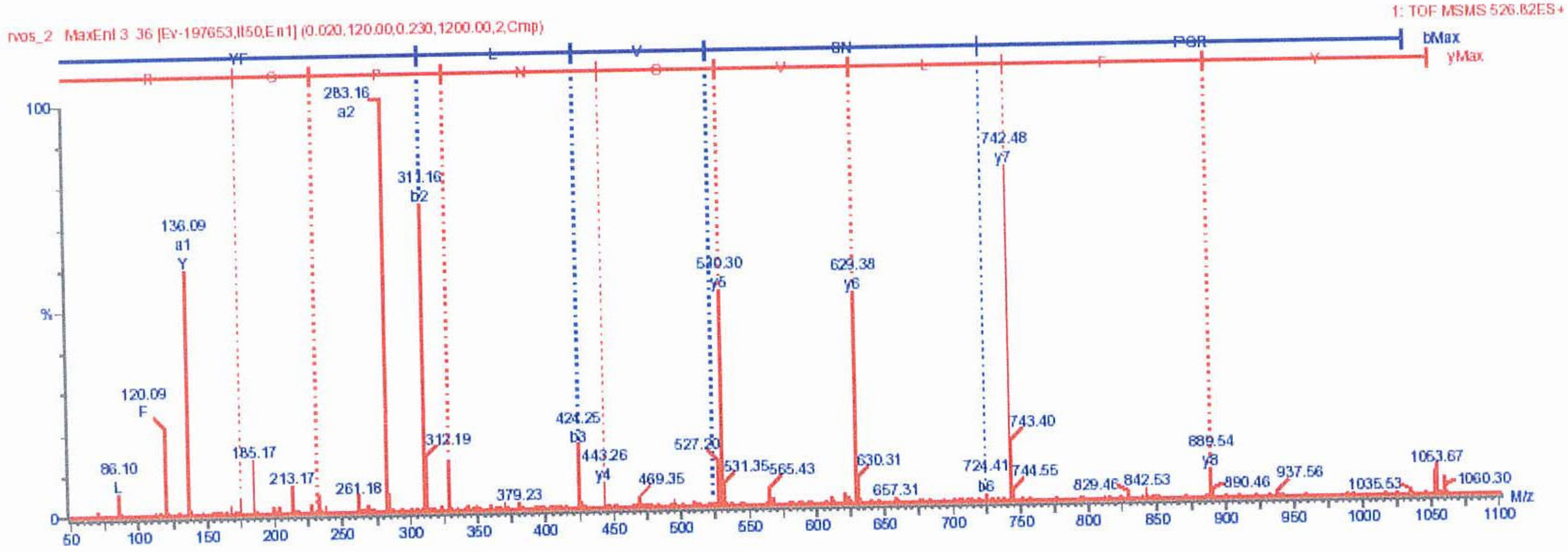
MS TOF SCAN


rvos_1 2 (0.089) Cm (1:9)
TOF MS ES+
840
100
%
0
365.12
387.20
408.26
427.60
432.75
465.31
473.30
473.63
477.29
526.80
527.30
551.33
552.00
603.88
605.32
611.84
612.35
650.39
671.86
672.35
675.88
709.40
742.45
743.47
780.49
824.47
888.47
895.81
350
400
450
500
550
600
650
700
750
800
850
900
950
1000
m/z

Peptide sequence: YF[L/I]VSNPGR

Observed MW: 1051.6244 Precursor ion charge state: 1
M/z tolerance: 0.30 Intensity threshold: 26 (0.350%)
Modifications: Methionine Sulfoxide (+/-) Cysteine acrylamide (+/-)

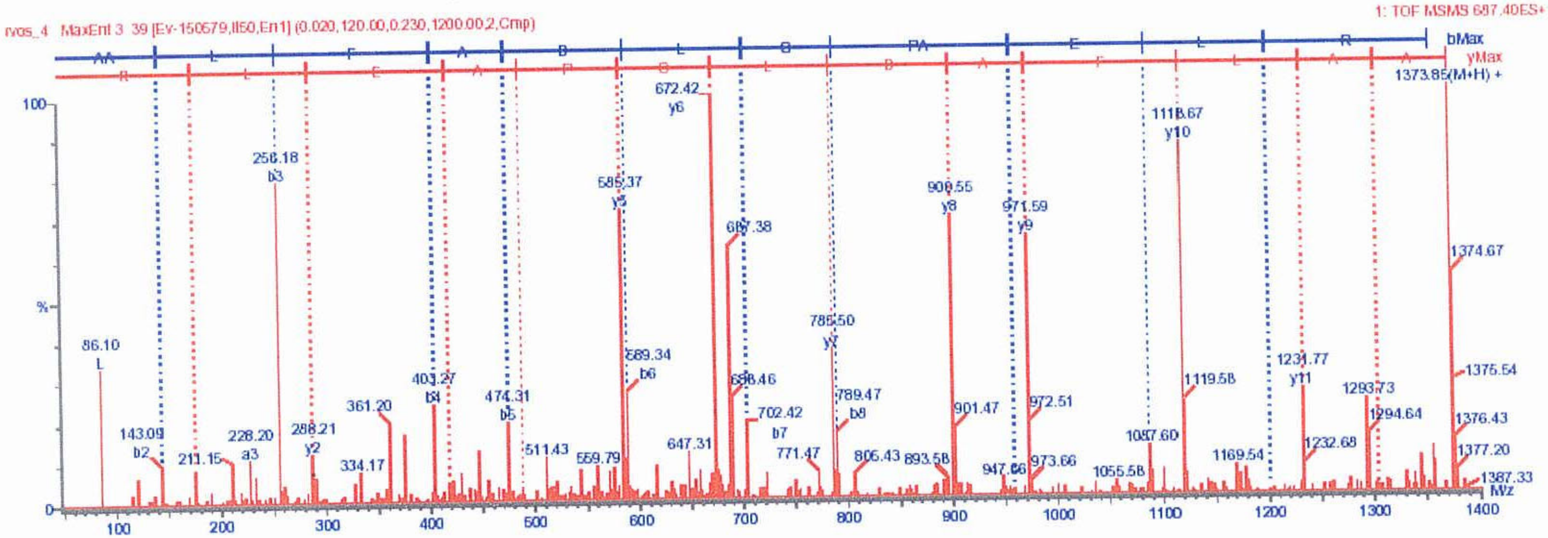
a	136.08 -0.01	283.14 -0.02	396.23 -0.01	495.30 -0.02	582.33 -0.07	696.37 ---	793.42 ---	850.45 ---	1006.55 ---
b	164.07 ---	311.14 -0.02	424.22 -0.03	523.29 -0.04	610.32 ---	724.37 -0.05	821.42 ---	878.44 ---	1034.54 ---
	Tyr	Phe	Leu	Val	Ser	Asn	Pro	Gly	Arg
y	1052.55 ---	889.49 -0.05	742.42 -0.05	629.34 -0.04	530.27 -0.03	443.24 -0.03	329.19 -0.02	232.14 -0.01	175.12 -0.01
z	1035.52 ---	872.46 ---	725.39 -0.08	612.31 -0.01	513.24 -0.05	426.21 -0.02	312.16 -0.03	215.11 ---	158.09 -0.01



Peptide sequence: AA[L/I]FAD[L/I]SPAE[L/I]R

Observed MW: 1372.7844 Precursor ion charge state: 1
M/z tolerance: 0.30 Intensity threshold: 2 (0.250%)
Modifications: Cysteine acrylamide (+/-) Methionine Sulfoxide (+/-)

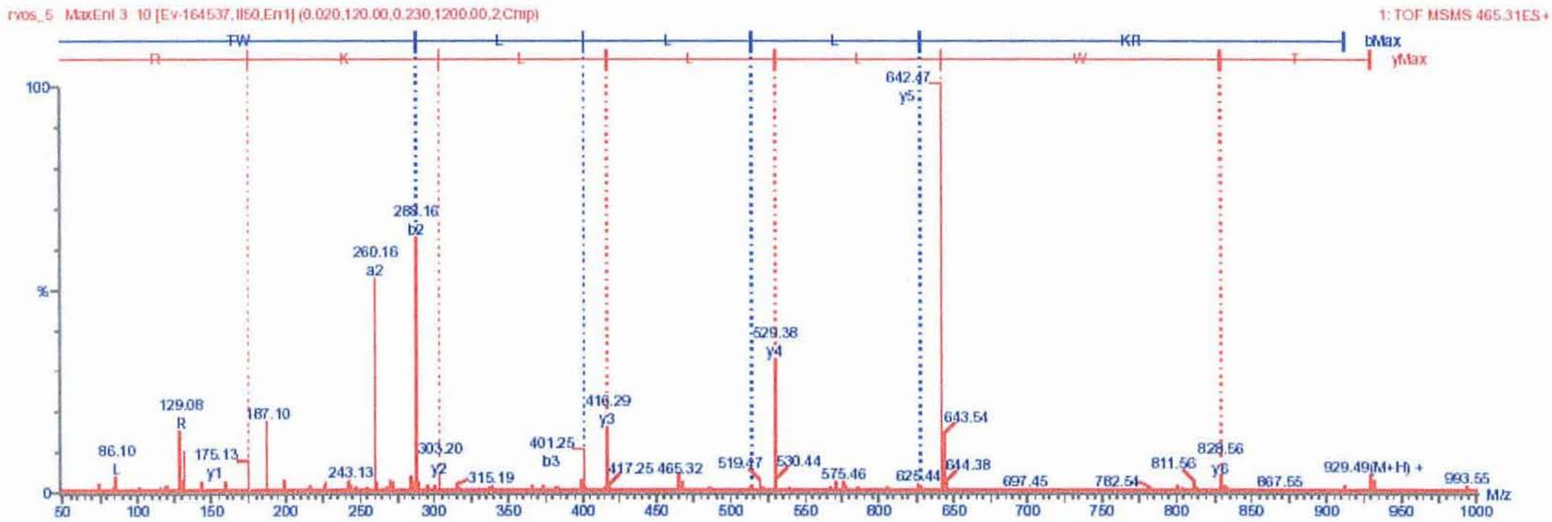
a	44.05	115.09	228.17	375.24	446.28	561.30	674.39	761.42	858.47	929.51	1058.55	1171.64	1327.74
	---	-0.01	-0.02	-0.02	-0.04	-0.03	-0.09	-0.07	---	---	---	0.01	---
b	72.04	143.08	256.17	403.23	474.27	589.30	702.38	789.41	886.47	957.50	1086.55	1199.63	1355.73
	---	-0.01	-0.02	-0.03	-0.04	-0.04	-0.04	-0.05	---	-0.02	0.10	0.01	---
	Ala	Ala	Leu	Phe	Ala	Asp	Leu	Ser	Pro	Ala	Glu	Leu	Arg
y	1373.74	1302.71	1231.67	1118.58	971.52	900.48	785.45	672.37	585.34	488.28	417.25	288.20	175.12
	---	-0.13	-0.10	-0.08	-0.07	-0.07	-0.05	-0.05	-0.03	-0.03	-0.02	-0.01	-0.01
z	1356.71	1285.68	1214.64	1101.55	954.49	883.45	768.42	655.34	568.31	471.25	400.22	271.17	158.09
	---	---	---	0.01	0.00	-0.14	---	-0.03	-0.06	-0.06	---	0.02	---



Peptide Sequence: TW[L/I][L/I][L/I][Q/K]R

Observed MW: 928.6044 Precursor ion charge state: 1
M/z tolerance: 0.30 Intensity threshold: 20 (0.250%)
Modifications: Cysteine acrylamide (+/-) Methionine Sulfoxide (+/-)

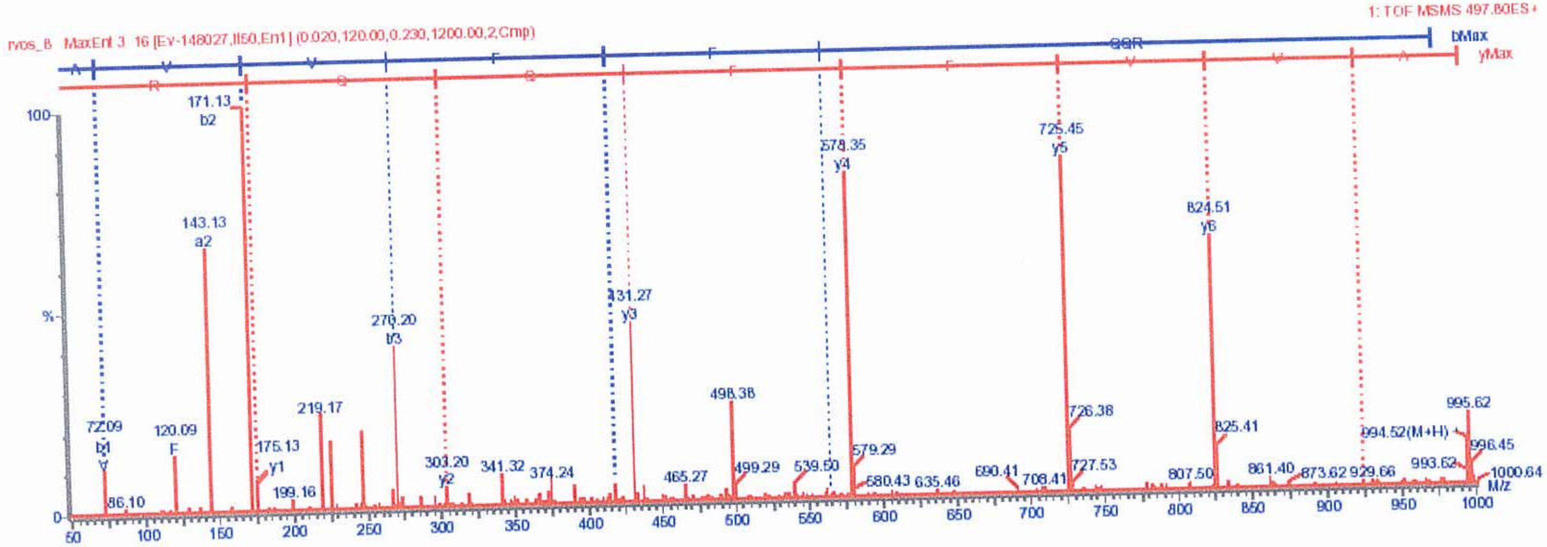
a	74.06	260.14	373.22	486.31	599.39	727.49	883.59
	-0.00	-0.02	-0.05	---	-0.07	---	---
b	102.06	288.13	401.22	514.30	627.39	755.48	911.58
	---	-0.02	-0.03	-0.04	0.01	---	---
	Thr	Trp	Leu	Leu	Leu	Lys	Arg
y	929.59	828.55	642.47	529.38	416.30	303.21	175.12
	---	-0.02	-0.00	0.00	0.01	0.01	-0.01
z	912.56	811.52	625.44	512.35	399.27	286.18	158.09
	---	-0.04	-0.00	-0.01	0.00	0.02	---



Peptide Sequence: AV[F/M][F/M]Q[Q/K]R --AVFFQ[Q/K]R

Observed MW: 993.5844 Precursor ion charge state: 1
M/z tolerance: 0.30 Intensity threshold: 8 (0.250%)
Modifications: Cysteine acrylamide (+/-) Methionine Sulfoxide (+/-)

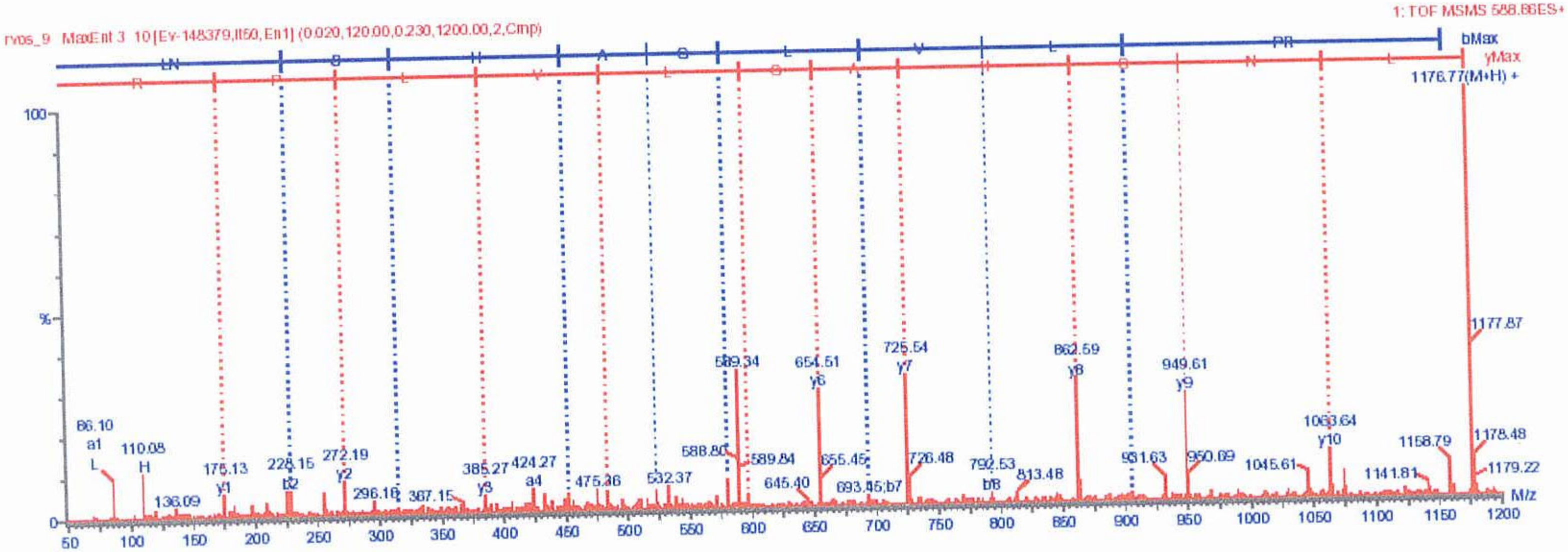
a	44.05 ---	143.12 -0.01	242.19 -0.00	389.26 -0.03	536.32 -0.02	664.38 ---	792.44 ---	948.54 ---
b	72.04 -0.04	171.11 -0.01	270.18 -0.02	417.25 -0.05	564.32 -0.06	692.38 ---	820.44 ---	976.54 ---
	Ala	Val	Val	Phe	Phe	Gln	Gln	Arg
y	994.55 ---	923.51 -0.03	824.44 -0.06	725.37 -0.08	578.31 -0.05	431.24 -0.03	303.18 -0.03	175.12 -0.02
z	977.52 ---	906.48 ---	807.41 -0.08	708.34 -0.07	561.27 -0.03	414.21 -0.04	286.15 -0.02	158.09 -0.02



Peptide Sequence:[L/I]NSHAG[L/I]V[L/I]PR

Observed MW: 1175.7043 Precursor ion charge state: 1
M/z tolerance: 0.30 Intensity threshold: 6 (0.250%)
Modifications: Cysteine acrylamide (+/-) Methionine Sulfoxide (+/-)

	Leu	Asn	Ser	His	Ala	Gly	Leu	Val	Leu	Pro	Arg
a	86.10 -0.01	200.14 -0.02	287.17 -0.02	424.23 -0.04	495.27 0.00	552.29 ---	665.37 -0.04	764.44 -0.03	877.53 ---	974.58 ---	1130.68 ---
b	114.09 ---	228.13 -0.01	315.17 -0.03	452.23 -0.04	523.26 -0.09	580.28 -0.08	693.37 -0.08	792.44 -0.09	905.52 -0.08	1002.57 ---	1158.67 ---
y	1176.69 ---	1063.60 -0.04	949.56 -0.06	862.53 -0.06	725.47 -0.07	654.43 -0.08	597.41 -0.04	484.32 -0.05	385.26 -0.02	272.17 -0.02	175.12 -0.01
z	1159.66 ---	1046.57 -0.14	932.53 -0.18	845.50 ---	708.44 ---	637.40 ---	580.38 0.01	467.29 0.02	368.23 -0.03	255.14 -0.03	158.09 -0.03



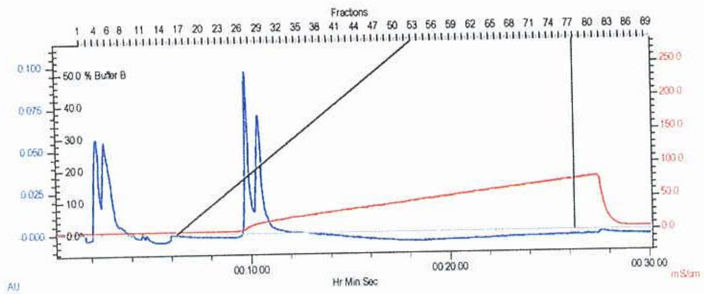
Appendix V: OS, OSC and OM whole venom fractionated via anion exchange.

Whole venom from OS, OSC and OM eluted from a Uno Q (BioRad) anion exchange column. The column was equilibrated with 50mM HEPES (pH 8.0) + 20mM NaCl. Three to five milligrams of protein was loaded in a total volume of 1ml with the same buffer. Samples were run at 3ml/min with a linear salt gradient from 0 to 100% Buffer B (1M NaCl) over 10 column volumes at 4°C. Note the differing absorbance scales (A_{280}) on the right in blue. Scales were manipulated to show the greatest resolution of the profiles.

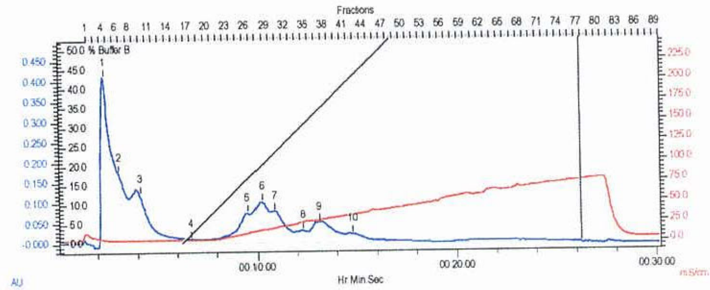
Comparison of *Oxyuranus* venom and anion exchange marker.
Whole venom from OS, OSC and OM were separated through anion exchange and the traces overlayed.

OS   OSC   OM   M

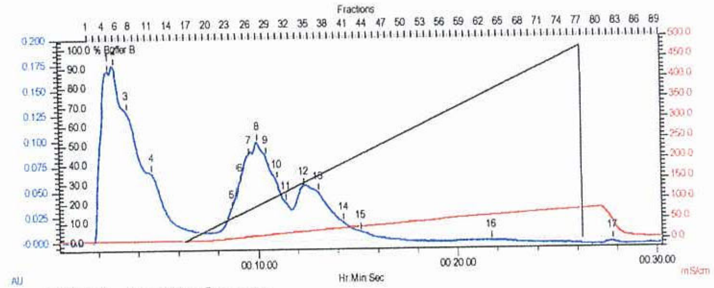
BioRad Anion Exchange Standard.; From the left peak is seen:, equine myoglobin 17 000, pI 6.9, conalbumin 77 000, pI 4.9, chicken ovalbumin 45 000, pI 4.6, soybean trypsin inhibitor 15 500, pI 4.5



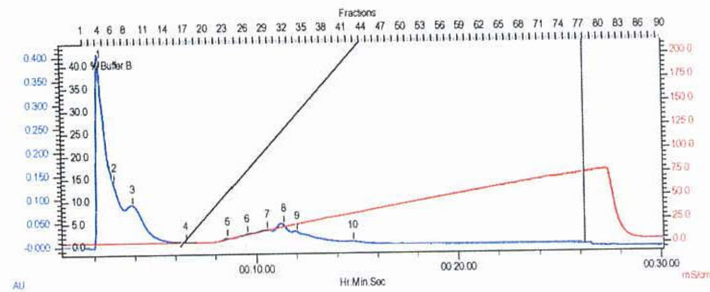
OS Anion exchange



OSC Anion Exchange



OM Anion Exchange



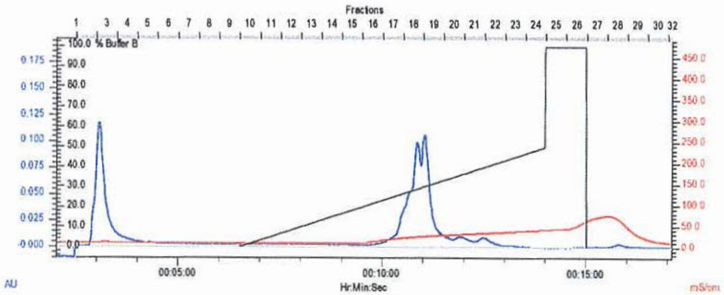
Appendix VI: OS, OSC and OM whole venom fractionated via cation exchange.

Whole venom from OS, OSC and OM on a Uno S (BioRad) cation exchange column. 3-5ug of protein loaded onto static loop in a volume of 250ul using 50mM MES (pH 6.0) + 20mM NaCl. Samples run at 2ml/min using 0 to 50% Buffer B (1M NaCl) for 8 column volumes.. Samples were run at 3ml/min with a linear salt gradient from 0-100% Buffer B (1M NaCl) over 10 column volumes at 4°C. Note the differing absorbance scales (A280) on the right in blue. Scales were manipulated to show the greatest resolution of the profiles.

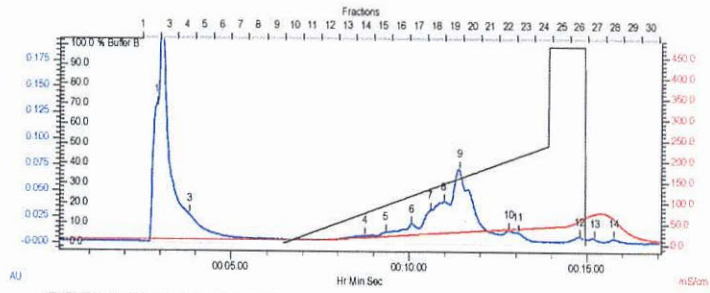
BioRaad Uno S Cation exchange standard.

Starting from the first peak on the left;

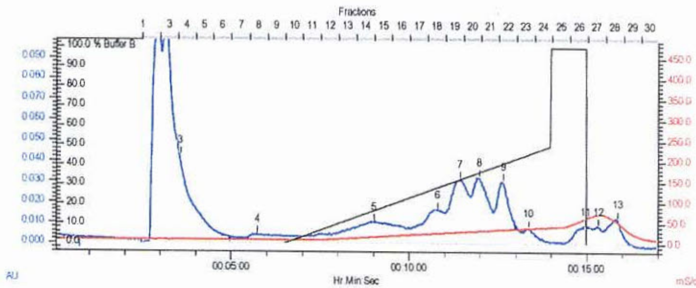
Equine myoglobin	17 000 Da, pI 6.9
Ribonuclease A	13 500 Da, pI 8.7
Cytochrome C	12 000, pI 10.7



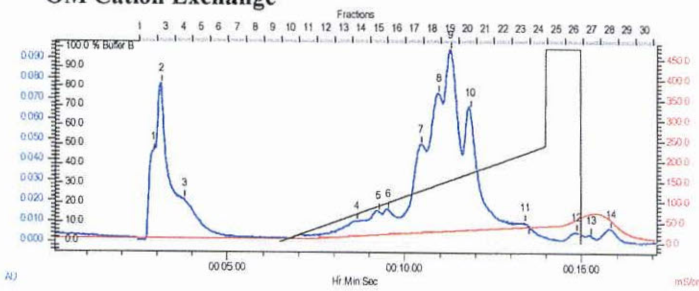
OS Cation exchange.



OSC Cation exchange

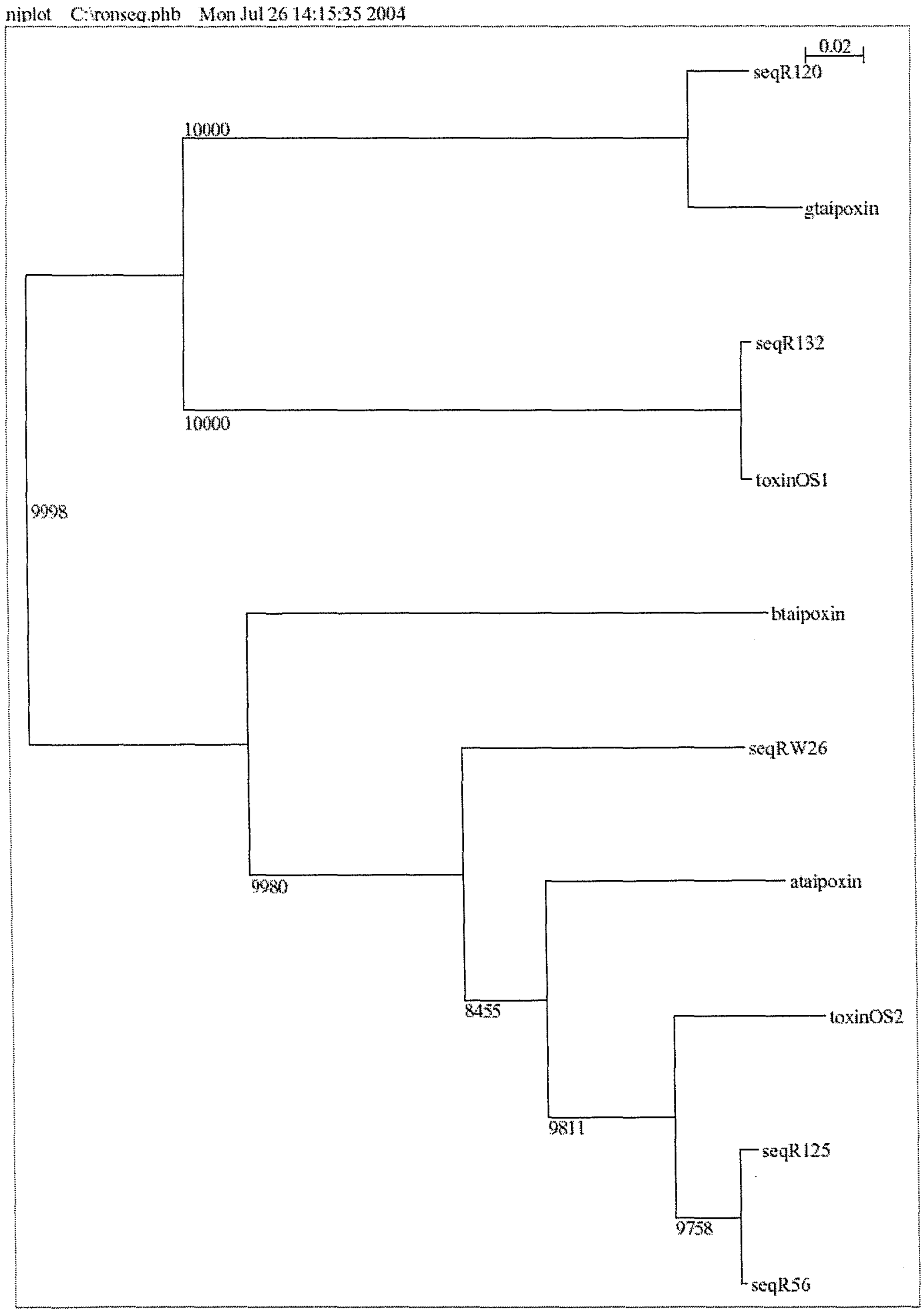


OM Cation Exchange



Appendix VII. Phylogram of a neighbour joining distance tree for *Oxyuranus* putative and peptide sequences.

This tree represents the relationship of *O. scutellatus* pre-synaptic neurotoxin sequences. Alignment was conducted using NJTree and TreeView. These sequences were subjected to bootstrapping x 10,000. Bootstrap values (x 10,000) are displayed at the nodes and indicate how robust the clusters are. The clone numbers and characterised *Oxyuranus* peptides are discussed in Chapter 5.



Appendix VIII Summary of clones from cDNA library

The majority of nucleotide sequences from the ~~*O. scutellatus*~~*O. s. scutellatus* cDNA library were isolated using binding studies, with a small percentage isolated using mass excision as indicated. All sequences are displayed using either their putative peptide name, as identified from sequence homology using BLAST or, if no conclusive match was found, the clone number was used (see Table 5.1). These sequences are followed by their GenBank accession number, if submitted, clone number and nucleotide sequence. The abundant HSP and PDI nucleotide sequences are displayed with their putative translated sequences (MacVector) aligned. Translation of some nucleotide sequences using vertebrate mitochondrial codons resulted in an ORF for all cytochrome C and NADH dehydrogenase sequences. A small number of sequences, which shared low homology with characterised peptide toxins, did not contain an ORF regardless of the codons used for translation.

For reference, all clones were sequences from the 5'-end (T3primer) and some complete protein matches were achieved using BLAST without the complete sequence of the clone required. GenBank sequences not matching characterised toxins are to be released immediately. Sequences sharing homology with characterised toxins are to be released on October 22nd 2005 or until publication of this thesis.

Complete sequences of clones aligning with areas of serpente nucleotide sequences
This group of nucleotide sequences were isolated through binding studies using taipan monovalent antivenom (CSL). These clones, which produced an antigenic protein, did not code for an ORF using either universal or mitochondrial codon usage.

R 5
The nucleotide sequence was very clean from 1 to 2,000 bp with no ORF found. Within the sequence (between nucleotide 2,000 to 3,000) clean sequence was difficult to obtain suggesting there is possibly a secondary structure in this region. The nucleotide sequence matched the C-terminus of *Homo sapiens* PHD finger protein (GenBank accession no. NM024517) 5238 bp; with 129/134 matches (96%), *Gallus gallus* (GenBank accession no. CR406187) 931 bp, 107/112 matches (95%), *Bungarus multisinctus* (GenBank accession no. AJ421675) Exon 1-3 2358 bp, 57/58 matches (87%) and Gamma bungarotoxin, GenBank accession no. AJ416991, 2448 bp; 41/47 bp (87%), *Naja atra* gene for cobrotoxin (GenBank accession no. YI3399) 2386 bp; 49/46 base pairs (87%).

R5 nucleotide sequence

CTTAGTGAACAATACCAGTTAACTTTTTGCCACCACTTTAATAAATTCTTTTTAACTTTCGGCAGTTAAAACCTGTACAGATACTGCT
ATAAATATTTTTTAATATAGATGTCCTTTCTCAAATTGCTGAGAGTGACTAGTTCGCAAAAAGTTAATTCTCCAAGACACTGAGGATC
ATTCCAGTTTTAGGAAAGTATCCATTTAACTTGTTTATAAGTGAGGAAAAAGTTGTTTTTAAGAGTATGCACATTCATTTCAATTATG
CTTCTTTTATCAAATTTGAACCAATTTTAAAGAGTTATCTGGTTAAAAGGCAGAGTTTAAAAAAAAGTTTCTCAAATTGACTTGTAGA
CAAGGGAAAGAAATTTATGCCATGACTGTTTGAGATACAATACATGCATGAAACAATATGCATAAAAATTAATTAGTTTTCTTTATCT
GGCTCATGATAAATATGTTTTATTCAGAAGAGAAGTTAAAATTGCACTTCAGCACTGCTAAAACTTTCCCTATAACCAGACATTGGAG
AACTATGGATGACTTAATTTATTTTATGTGCAATGCAAGATGATTTTTTAAAAACATTATGGATTACAAATCCAATTTAATTGGTTAA
TGATTTGGATATAGGTAATTAATGAACTGGTGCAGTTCTTTGGACATCAAATGGGGTTTTTTAATTAGCTTTGGTTGGTGTTGGTTTG
CATCTCTTTTCGTTGATAAATTTTTAGCACTCCCACTGTTTCTTATATATATATTGTTTTAACTTTGGTCCCATGGTATGTTTTCCAT
GCTCAATGTCTTTGTTCTCATAATTGAATATCATTGAGTGATAGGAATTAAAGATCAGCAAACAGAAAGAACCTTTCTCTCCCTGCTA
AACTTTCACAATTATGTGTAATTGAGTAAAACATTACAAATCAATTGGTACCTCAAAGTCAAAATCTGAGAACATTGACTCTTGACTG
TACTTATATGACATGGTTTACAGGCCTACAGGGGCTAAAGCAAAATCAAATCAATTGTACTATATCTTAGTATGTTAGCGTAGGGCCA
TTATTTTAAACTGTCATTGTTTGCTTTGGCTTCTTATGTGAATAGAGCCTCTGTGTATTTTGTAAACCATAATTAATGGATTAATGTG
TTTACATCCAGTCTGAATTTGATGGTTTTTTTCTCTCTCTCTCACCTGTTCTAGCTAAAATTTGTTTACATGACCATGGAAACTGGAA
GTATTCCTTCCCCCATGCCCATATATTTTTAATTTGGCGTTGCAGTTTTGAAATTATATCCTCATTAATTTAATTTCACGGCTAGGGT
TAGGGTTAGGGTGGAATCAGACATTAACTTGATGATAGTATTGTAGCTTCTGCTTGGATGGTCATAATGTATTGATAACATGTGACAT
TGGAGAATATGTAAGAAAAAAGATGCCAGGTTCATCCCTAGATGCTGCTGCCAAGAATGCCAGTGACAAAATGCCAGTTTTCTTTGTG
CGGCCTGAGTGGGTAGCAGGCATATCACAATCATTAGAGAGGGCTGTAAAACACTGTGAAGCAGTATATAAGTCTAAGTGCTATTGCT
ATTGCTGTCTTATAAAATGGCATCTTTAGTCAAATATCTCTTTCCTTATTTTTTTGAAGGAACTTTTAATCTCCCTCTAGCAATTCTA
AACTCTAAAGTTCATGACTGATGATTTACCTCATAAATCACTTACGTTATCTTGAGATGAAAGAGAGAAAGACAATGGTTCTTTTTTC
ACTTCCATTTCCCCGGATCATGGATTAATCCCTGCATCATGTAAACAAATCAAGCAAAGAAGCTCCTGTCCTGGGACTCCAAGCACTT
ATTTTCTGATCTATAACCAAACCCTTTCCTTGAGCTGCATATCAGGAGAAAAAAATGCACCAAACAAGATTATTTCACCCACCCACCC
CCAAAGGAACACACACCAACCTTTTAGAGCTTATGAATCCATTTAATAATATTATAGATCAGCTGTTTATATAAACCTCAGTTGCAAG
CCTGTAATTAGGTAGAAAGAATGTGCAGCCCTATTGGAGAAGGATTCTGACAATTCGAATGTATGCTGTATCTCAAAGCAACTTCCAC
TTGTCAAGAGTATGCTTGTCTGTAAGGATACAAGGGCTGTGCTCACCTAAGGGTTAGGCCAGGTGAGTAGCCAAGCTTATCGTACTAG
TTTAACTGGTATACTTGTTGTTTGAACTCTTTAGTGTTTGGTGTAGAATGCATTATATTTACATTAAATAGCTTGTCTGCATATAAAC
ACTTAGAGCTACAATCCTATGCTATGTTTACTCAGTATATCAAACCTGTTGTGTTCCATGGAACTTACTCTCTATGTATAGAGTACTA
TGTACAGGATTGTAGCCTTAAGGTGTGCATTTGTTTTCAGGCAATTCCAGATTTTCATTTATAGATACTTGTCTGAAAGCATATTTTT
TCATAGAATCTAGCCTGTAAATAGCTTTTTAAAGTACCTTCTTTTTTATAAGATCAAAGTATCTTTAGACATTTCTTTCTATAGATAG
TTCATTTAACCTTTTATACAATTTTTTTGCTGAGTATTTTGCCCCGAGTATTTTTAAGTTTCTGACTCTGAATGGGATACTCTGTTTT
TGTCCTGATTTAATCCTTTTTCTCCCCTTTTTTAATTTGGCCATTGCCCTGGAAAAACAAGTAAAACTTTGTGCAGCCTTATACAGAA
TCAATAATAGTACAAAATTATCTATTTAAGATACAATATGAAGAAGAATCTTTGACTTTATAATACCAGCTCCTTGTCTCTAATTCTT
GTATTATGAGGGGATACAATTATTTTATTAGCACCTTGTGAAGTGTTTCTGTGTTTTGTGATGATGTAATTTATTAATGTTTGTAGCT
TTTTATATTTGTACATTTCTTATGAGCTTTGTTTATATACACATTACCTGGATGTGATGTCCATGAGGAAAAAATAAAACAGCTATAG
AAAACAACTGAGGCCTTATTAACTGACCTTTCTAGTTATGGTGAGCGACTGGTTCTGAATTCTCGGCATCAAAAATATTAGTTGAATA
GGGCCCCAGAGTTAAGCAAGTTTTTTAAAGCTTCCCTAGTATACTGTTATTGTCAAGCATTTATATAACGCAGACATCATGCTGGTTT
TATTATTATGTTTATGTTTATGATTATTATTTTCACAACATGTACATTTCTAACAAAGTTTATTGTGGCTATCTATTACAGTGTTTTA
TTTACCAATTCATATCAAATGCTCTTGTATCAAGTCCATGAAATCTAAGTAAACTTAGATC

R8

The R8 nucleotide sequence matched with *Elaph Obsoleta microsatellie* Eobms sequence (GenBank accession no. AF544661); 41/46 matches (89%) and *Atractospis microlepidota* andersoni partial 469 bp GenBank accession no. D13322, 31/33 matches (93%).

R8 Nucleotide sequence

ATAAAATACAGTTAAAGAGAAGGTTTCCTTTAAGGAAATTACTCCTTTTGTTTTCATTTAATAATGCATCATTGCTGCTGCTGCGTTC
ATGTTTTCCCAAAATAATTACATGCTGGATTTGCAGTAGCTGGAGAATAAAAGTTAAAATTTTAAATTACATTTTCCACACTGAAGTA
CTGAAAATACATTTACCAGAGAGTAAATCTCTAGTGATATTAGTCACTATTAACTGATCAATTTTGGCACAACTTAATTGTAAGATTG
TATAATTGTACAAAATCCTTATTGAATCTCATAGGAATTTCATATTCGTAGTTGTATGCCATGTTAGAGCCAACATGGGCATATATAC
CAAGACAAATTCTTTATGTGTCTCACCACACTTGGCCAATAAAACATTCATTCACATGTCGGAAGCATTTCCAAAGATTTTTTATCAG
AAATACTACATAAGTACCATGTTGTTTTAAAGAAGTTGCATGGGCAAAGATGCATTTCTGGTTTTGTGGTATGTTTCATTTCATGAGC
AGATGTTTTATTCCCAAAGTGCTAGAAATATTCTTCCTAATAGAAAAAAGAAGGAGCTGTATATTCCATTGTGTATATTCCACTTCCT
CTTTCCACAAATTGAAACTGGCAGCAAAGTAGACAGCACAATTTAAAATTTAAAATAAAAATATCTTCTTCTAGTACAGGAGTCTCCA
ACCTTGGCACTTTAAGACTAGCAGACTTCAAACTCCTTGAATTTCCCAGCTAATGGCTAATTCCCCAGCAGGAGAATTCTGGGAGTTG
AATCCATCAGGCTTGGAGTTGCCAAGGTTGGAGACCCCTGTTCTGGTACAAATAGCAACATTCAGGTGAGCTTCTCTGGTGAAAGAAC
ATCAGAAACTGAGAAGGGGCTTTTTTCAGTTACCACCCATCTCATATCTATCAGTGCAGACACCTGAATGAGGGGCTCAGATTGCTTC
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AGCCTTCATACAATATTAATTTGTAGTGTATGGTATGTTATATAACAGAATATGATTAAACTATTTCCAGTGTGAAAATTAAATTAAA
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TTAATATTATGTAAATGTCTTAGATTTTGTTGAAAAAAAATCTTCATGGGCACTGGATATTTTTATTTATCTTCATTGACCACTGAAA
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AGAGTCAGCACAGTATCAATTTTGTACCTATCTTATAAATATTGATTATTTAAACTGCTGATGCAGTACTTAGCATTTTTCAGAATCT
GAAAATAAACTGTATCTAGTTTTCTAAGCTCCTTCTTTGTGAGCAGATGTCTTTCATTTTCTGAATATTAACAATTGTCAGGAAATCT
TCTTTGACTGGGAGAAAGAGTTTTCTTGAAACCAATATAAATGGTTAAAGCAACGGATATCTTCCTTGCCTTTGGACTTTTATTTCCC
CCCATAATAACCCTCATGGGAGATAGGTTAGGTTGCAAAAGAATGGTTGGTCCAGAATCACCTGGAGCGCTTTCAGGGCTAACAGCTG
ATCCAGCCCTAGTCCTATATGTGAAATAAATGTATTTTGGTGCATAACAGTTGAACAATAAAATATAAACAGTTTATTAT

R 11

This sequence aligns with a small area of *Trimeresurus flavoviridis* (crotalid, GenBank accession no. D31777), D13384 gene for PLA_2, *Trimeresurus gramineus* (GenBank accession no. D31782) TATA box binding prot and *Laticauda semifasciata* gene for PLA_2 (GenBank accession no. AB111959).

R11 Nucleotide sequence

AATTCGGCACGAGGGTCAAATACTACCTGTATAGCAAACTGGCTCATGATATGGCATAACGCTGCAATACATAGTTTATATTGTTAAT
TTATGGTTCATCGTGTAGTGGGAGCACAGTCCATTGGACTCATTCAGATAGTCATAATTAGTTAATTCTGGTATGGGCTTTGAATGGT
TTCAAGCAAACCTTTTGGAAACTTCTGATCCAAAGTTCTGTAAAAGATTTGGGATGCCCTTATCAAGATCATATGAAGTGTTAATATC
ACTTTATAATGCCTTGTTAAGGCCATATACTATATTGGAATACTGTATTCAGTTTTGGTTGCCACGATGTAAAGAAGATGTTGAGGCT
CTAGAAGGACTGGAGAGAAGAGCAACAAAGATGATTAGGGGGCTGGAGGCTAAAACATGAAGAACGGTTGCAGGATCTGGGTATGTCT
AGTCTAATGAAAAGAAGGACTGGGGAGACATGATAGTAGTTTTCCAATATCTCAGGGGTTGCCACAAAGAAGAGGGAGTCAAGCTATT
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CCACCTGTTCCCTGAGCCTACCAATTTATAACAAATTCTTCCATAGTCCTGCCTGATTTCAATTTGTCTTGCTGACTTGGATTGAGAG
TTCCTTATTTTTTTAGCACATATACATTGTTACTTTCATCTGAGTGTGTTTTACCAAAATTCAGAATTGCCTCAGTATTACTTGGGAA
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AACATCCAGGAAGCTAAAATCCTAAACACTTTGAGGTAAAAAGAAGTACTGTTGAACTAAGAGTAGTTGGGGTCAGTCTAAACTATAT
GTGTGTGATGTCTGTATCAGACACAATTCAACAAGATTTTATTAATTTGCTTTAGATAGATTTGTATATAGCAACAAAACGTATTTCT
GTGTTCTCCGATCTTCAAATAATGTTTTAAAACTGACTTTAGAAAAAGATAATGTAGGAACTGCATTTTTTATTTTTCAATGTCTTGT
CAAAATACTGAAACAGACAGTAGAGGGTGCAGTATTCATTCTTTGTAAATCAATCTGTCTGATTTGAATGGTGAATGCAAATTATATT
GGAGGCAATTTTAAAAAAGTATTACCTTTTGTGTTATAAAATTAGTTAAATATAAAATTAGAAATACTTCCGTGTAAAAAAAAAAAAA
AAAAA

R51

This clone was isolated using mass excision. The sequence aligned with a small area of *Naja naja* genomic DNA (GenBank accession no. AF236683)and *Elaphe bimaculata* 12S ribosomal gene (GenBank accession no. AF236671).

R 51 nucleotide sequence

AATTCGGCACGAGGCATACATGCAAGCCTCAACACAACAGTGAAAAAGCCCACCATAACAACTTCTTGGAGACTGGTATCAGGCTAAT
AGCCCATAACACCAAGCAAACAAGCCACTACCCCCTACGGGCCCGCAGCACGTACTTAATATTGGGCCATAAGCGCAAGCTTGACCCA
ATAATGGGGTTCACAGGGCCGGTTAATCTCGTGCCAGCGACCGCGGTTATACGACAGACCCAAGATATACACCACCGGCGTAAAGCAC
GACTAAAAATTTAAAGTCCAATTGTTAAGGATGACGACAAGCTGGGCTGTAAAAAGCCATAAGCAATACTAAACATAACCCTTAACAT
CCATACAACTTTAACTCGTGAAAGCTAGGGTACAAACTAAGATTAGATACCTTACTATGCCTAACCTTAAAAAAACAATCAAACAACC
AATTGTTCGCCAAATAACTACGAGTAAAAACTTAAATTTAAAAGACTTGACGGTACTTCACCCCGACCTAGAGGAGCCTGTCTAATAA
CCGATAACCCACGATTAACCCAACCAACTCTAGCCTAACAGTCTATATACCGCCGTCGCCAGCTTACCTTGTGAAAGAATAAAGTAAG
CTCAATAAACCCATAATACGACAGTCGAAAAAAAAAAAAAA

R 65

No ORF was contained in this sequence, yet it aligned with a small area of *Elaph quadrivirgata* mRNA PLA_2 inhibitor (GenBank accession no. AB060638), *Vipera ammodytes* genomic DNA (GenBank accession no. AF332697), Bov B, *Bungarus multisinctus* (GenBank accession no. AF251222), *Laticauda colubrina* PLA_2 gene (GenBank accession no. AB062448) gene LcPLA2PC20.

Nucleotide sequence of R65

ACTGGCCATGCCTGCAAATAAATCACACAAATAATTAGCTTTCAAACCTTCAGTGCAGCCCTGGTAAACAGGCCCTTCCCGGAAAACA
GTTGAAAGAAGACATATTGACTCAGATGGCGCTGAATGTTCAATAGTAGATTTCAGCAGGCCTCTAATGAGCAGAATAACAGAGCTGG
AAGGGACCTTGGAGGTCTTGTAGTCCAACCACTCTTGTTGTGGTTAGCCAGCAGCAGGTGTGGATGGCTGAGGAGAGCGAGGACTCAG
GTGAAGGGCCAGGACCATTGGGGAGTGGACTGCTGCCTTCAGAGATTGTGGGGGCTGGCAGCAGTGATGAGGAGGTTCCCGAGGAGCC
TGTGCCAAGTGCGCGTGCGTGCAGGATTGCTCAGAGGAAAGAGCAGTTACAACAGCATGGGCAACTCGGGATAAGGCTGCAAGGTAAT
GGCCCCTCCTTCAAGAAGATAAAAGCCAGCTGTGAAGCGAATGTTCTTTGTAGGAAGCAAAGACGTTTTGAAACTCAGCCTCATGGAC
ATTACAGTTGATATTATCTTGTATTGTAAACTATTTCTTATCTGTTATTTTTTGGCAGCCTTGCAAAAACTTGGAAGGCTCTTTCTTT
CAGAGCTAATTAGTTGGAAGCAGTGAAGAAACAGGATTCATAGATGAAACATTAAAAGGTTATGCTGCTGCCTTTGTCTTATGTTTGC
TCTCTTGGAACCAGGTTTGGCTCAGGCAGGAAACTTGTCTCCTGGTTTCTAACCTGCTGCCTTAATCACTACTAGGCCCAAACTGGCT
CTTTGCCACCATCTTGAGGTCACTTTGATTTTTGCAGCCAGGTCTGACAGCCCATCCTGATCAGCAACCCAGGAGAAGGAGTCTCAAG
ATGTAACTAAATGCTGAATGGGTGAACGAAACAACCCCCCTCAAGAAGAGAATCATCTTTACGTCAGCACAATTCAAAAGCAGGTCAC
AGAAAAAAGAAAAGAAAAAAAAAACAGCTCAGCACGGCGAACGGAAGGCTGCATCAACACATTCAACATCTGCTTTAATTCCGCCTCA
GGAAAAGTTGCAATTAGAAGTAAAGAAATGGAGTAAATGAAGTCAGAAGTATCAGGGGAGAATGGGAACTGAAGCAAAACACAGAACT
GAAATGCAGCTGAGCACCAAGGAAAAGAAACGTCCCCGAGGAAGGTTTCAAGCTATATAATTCCCTAGGAATGAGTGCAGGGTACAGG
CTTCTCCCCGCTCCCCTC

Sequences of clones aligning with complete proteins after BLAST matches

Natriuretic peptide (GenBank accession No. AY691663).
Alignment of R27 shared homology with the partial characterised natriuretic peptides from *Oxyuranus scutellatus* (100%)(natriuretic peptide, GenBank Accession no. P83225), *Oxyuranus microlepidotus* (100%)(GenBank Accession no. P83224), and full sequences from *Micurus corallinus* (GenBank Accession no. AAC60341.1), *Bothrops insularis*; bradykinin potentiating protein (75%) (GenBank Accession no. AAMO9692) and *Bothrops jaracara* Bradykinin potentiating protein 75% (GenBank Accession no. BAA12879, Murayama 1997).

P83228 sdpkigdgcf glpldhigsv sglgcnrpvq nrpkk

Nucleotide and deduced amino acid sequence of R27 in two reading frames.

```
1     AATTCGGCACGAGGAGACGCTCCTGCAGCCACAGTACCCGGCTTGGCTCTCTTCGGCTCAGCAGTCTGC  69

70    GCCCTTGAGGATTCCTCGCTCTCTCTCTCTCATCCACCCGGGGAAA ATG GTC GGC CTC TCC CGT 133
 1                                                    M   V   G   L   S   R    6

134   CTG GCG GGA GGC GGG CTG CTG CTG CTG CTG CTG CTG GCC CTG CTG CCT CTC GCC 187
  7    L   A   G   G   G   L   L   L   L   L   L   L   A   L   L   P   L   A   24

188   CTC GAC GGG AAG CCG GCG CCG CTG CCT CAG GCG CTG CCC GAG GCT CTG GCG GGC 241
 25    L   D   G   K   P   A   P   L   P   Q   A   L   P   E   A   L   A   G   42

242   GGC ACG ACG GCG TTG CGG CGG GAC GTG ACG GAG GAG CAG CAG CAG CAG CTG GTG 295
 43    G   T   T   A   L   R   R   D   V   T   E   E   Q   Q   Q   Q   L   V   60

296   GCG GAG GAG TCC TCG GGT CCC GCG GCT GGG CGC AGC GAC CCC AAG ATA GGG GAT 349
 61    A   E   E   S   S   G   P   A   A   G   R   S   D   P   K   I   G   D   78

350   GGC TGC TTC GGC CTC CCG CTC GAC CAC ATC GGC AGT GTA AGC GGC CTG GGC TGC 403
 79    G   C   F   G   L   P   L   D   H   I   G   S   V   S   G   L   G   C   96

404   AAC AGA CCC GTC CAA AAC CGC CCG AAA CAA ATA CCT GGC GGA TCC TAAATAATTGG 459
 97    N   R   P   V   Q   N   R   P   K   Q   I   P   G   G   S   *          112

450   CTTTATTTTAGTTTTACTTCTTTAGATTGTTTAGTATATATCGGCTTAGAGAAAATTAAGGATCATAATGAT 531

532   GTGTCATGTAAAATGAAATAGGGGGTAAGCTGAAAAATGGAAATAAAAGGGGATAAAGAATTGAAACCTATG 603

604   TCTGGATGAAATGATATTGATATTGAATTCATGAATTGAAACAGGAAATGCAAATTTACTTACAGATGAGTG 675

676   AAATGGATAATGATATGAGATGATATTATATAAGATTAATGGAAATGAAAGTATGATTATGTACAAGTGTTA 747

748   TAATCCGAAATCATGTTGCTCACGTGAAGAGATGTGTAAAAATTTTTTAAAAATAAAAAACTTTTACATCTT 819

      AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
```

HSP 70 (GenBank accession No. AY691667).
The deduced amino acid sequence is shown below the nucleotide sequence.

```
        10        20        30        40        50        60        70
AATTCGGCACGAGGGTTGTTCGTTGTTGGTGTTTAACTGTCAGCTTCGGAAAACTTTCATTTTAATCCTC

        80        90       100       110       120       130       140
GAAGTTTTAGAGGGATATCTTGATCGCGTTACTGCAACCATGTCGGCCAAAGCGCCTGCCATAGGCATTG
                                        M  S  A  K  A  P  A  I  G  I>

       150       160       170       180       190       200       210
ACTTGGGCACCACGTACTCCTGCGTCGGAGTTTTCCAGCACGGGAAAGTGGAGATTATCGCCAACGACCA
D  L  G  T  T  Y  S  C  V  G  V  F  Q  H  G  K  V  E  I  I  A  N  D  Q>

       220       230       240       250       260       270       280
AGGCAACCGCACTACACCGAGCTACGTTGCCTTTACGGACACTGAACGGCTTATCGGAGATGCAGCCAAG
  G  N  R  T  T  P  S  Y  V  A  F  T  D  T  E  R  L  I  G  D  A  A  K>

       290       300       310       320       330       340       350
AATCAAGTGGCTATGAATCCTAACAATACCATCTTTGATGCCAAGCGTCTCATTGGCCGCAAATTCGATG
 N  Q  V  A  M  N  P  N  N  T  I  F  D  A  K  R  L  I  G  R  K  F  D>

       360       370       380       390       400       410       420
ACCCTACGGTGCAGTCCGATATGAAGCACTGGCCTTTCCGTGTGGTGAGTGAAGCCGGGAAGCCCAAAGT
D  P  T  V  Q  S  D  M  K  H  W  P  F  R  V  V  S  E  A  G  K  P  K  V>

       430       440       450       460       470       480       490
GCAAGTCGAGTACAAGGGTGACACCAAGAACTTCTTTCCTGAAGAAATTTCCTCGATGGTATTGACCAAA
  Q  V  E  Y  K  G  D  T  K  N  F  F  P  E  E  I  S  S  M  V  L  T  K>

       500       510       520       530       540       550       560
ATGAAGGAAATAGCCGAGGCTTACCTGGGTCGCAAAGTCCAGAGTGCTGTGATTACTGTACCTGCATATT
 M  K  E  I  A  E  A  Y  L  G  R  K  V  Q  S  A  V  I  T  V  P  A  Y>

       570       580       590       600       610       620       630
TCAATGACTCCCAACGCCAAGCCACCAAAGATGCAGGTACCATTACAGGTCTCAACGTATTGCGCATCAT
F  N  D  S  Q  R  Q  A  T  K  D  A  G  T  I  T  G  L  N  V  L  R  I  I>

       640       650       660       670       680       690       700
TAATGAGCCCACGGCTGCTGCCATTGCCTATGGTTTGGATAAAAAAGGGAGCAGAGCAGGTGAGAAGAAT
  N  E  P  T  A  A  A  I  A  Y  G  L  D  K  K  G  S  R  A  G  E  K  N>

       710       720       730       740       750       760       770
GTACTGATCTTTGACTTGGGTGGTGGCACATTTGATGTTTCCATTTTGACCATTGAAGATGGCATCTTTG
 V  L  I  F  D  L  G  G  G  T  F  D  V  S  I  L  T  I  E  D  G  I  F>

       780       790       800       810       820       830       840
AAGTGAAATCTACTGCTGGAGATACCCACTTGGGTGGGGAGGACTTTGACAATCGCATGGTGAGTCACTT
E  V  K  S  T  A  G  D  T  H  L  G  G  E  D  F  D  N  R  M  V  S  H  F>

       850       860       870       880       890       900       910
TGTGGAGGAATTCAAGCGCAAGCATAAGCGTGACATTGCTGGCAATAAGCGAGCAGTTCGACGGCTCCGC
  V  E  E  F  K  R  K  H  K  R  D  I  A  G  N  K  R  A  V  R  R  L  R>

       920       930       940       950       960       970       980
ACAGCCTGTGAGAGAGCCAAACGTACCCTGAGTTCCTCCACCCAGGCTTCTATTGAGATTGACTCCTTAT
 T  A  C  E  R  A  K  R  T  L  S  S  S  T  Q  A  S  I  E  I  D  S  L>

       990      1000      1010      1020      1030      1040      1050
TTGATGGCMTTGATTTCTATACATCCATTACTCGTGCTCGCTTTGAGGAGCTCAATGCTGATCTCTTCCG
F  D  G  X  D  F  Y  T  S  I  T  R  A  R  F  E  E  L  N  A  D  L  F  R>

      1060      1070      1080      1090      1100      1110      1120
TGGTACTCTTGAACCTGTGGAGAAGGCTCTTCGTGATGCTAAGCTAGACAAAGGACAGATTAATGAAATT
  G  T  L  E  P  V  E  K  A  L  R  D  A  K  L  D  K  G  Q  I  N  E  I>

      1130      1140      1150      1160      1170      1180      1190
GTTCTGGTTGGTGGCTCAACTCGTATTCCCAAGATCCAAAAGTTGCTCCAAGATTTCTTTAATGGAAAAG
 V  L  V  G  G  S  T  R  I  P  K  I  Q  K  L  L  Q  D  F  F  N  G  K>

      1200      1210      1220      1230      1240      1250      1260
AGCTAAACAAAAGCATAAATCCTGATGAAGCTGTGGCGTATGGTGCTGCTGTGCAGGCTGCTATTCTGAT
```

```
 E  L  N  K  S  I  N  P  D  E  A  V  A  Y  G  A  A  V  Q  A  A  I  L  M>

      1270       1280       1290       1300       1310       1320       1330
GGGTGACAAGTCAGAAAATGTGCAAGACCTGCTGCTGCTTGATGTAGCACCACTTTCTCTGGGTATTGAG
  G  D  K  S  E  N  V  Q  D  L  L  L  L  D  V  A  P  L  S  L  G  I  E>

      1340       1350       1360       1370       1380       1390       1400
ACTGCTGGTGGTGTGATGACTGCCTTAATCAAGCGCAACACAACTATTCCAACCAAGCAAACCCAGACCT
 T  A  G  G  V  M  T  A  L  I  K  R  N  T  T  I  P  T  K  Q  T  Q  T>

      1410       1420       1430       1440       1450       1460       1470
TCACTACCTATTCAGACAACCAGAGTAGTGTGCTGGTACAAGTGTATGAAGGTGAGAGAGCCATGACCAA
F  T  T  Y  S  D  N  Q  S  S  V  L  V  Q  V  Y  E  G  E  R  A  M  T  K>

      1480       1490       1500       1510       1520       1530       1540
GGACAACAATCTGCTGGGCAAGTTTGACCTGACAGGTATTCCACCTGCACCTCGTGGTGTGCCCCAAATT
  D  N  N  L  L  G  K  F  D  L  T  G  I  P  P  A  P  R  G  V  P  Q  I>

      1550       1560       1570       1580       1590       1600       1610
GAGGTGACATTCGACATAGATGCAAATGGTATTCTCAATGTCACTGCAGTGGACAAGAGCACCGGAAAAG
 E  V  T  F  D  I  D  A  N  G  I  L  N  V  T  A  V  D  K  S  T  G  K>

      1620       1630       1640       1650       1660       1670       1680
AGAACAAGATTACAATAACTAATGACAAAGGCCGCCTCAGCAAAGATGACATTGATCGCATGGTGCAAGA
E  N  K  I  T  I  T  N  D  K  G  R  L  S  K  D  D  I  D  R  M  V  Q  E>

      1690       1700       1710       1720       1730       1740       1750
AGCAGAGCGTTATAAGGTAGAGGATGAGGCTAACCGAGAACGAGTAGTCTCCAAAAATGCCCTGGAATCC
  A  E  R  Y  K  V  E  D  E  A  N  R  E  R  V  V  S  K  N  A  L  E  S>

      1760       1770       1780       1790       1800       1810       1820
TATGCATACAACATTAAGCAGACTGTGGAGGATGACAAGCTGAAAGGCAAGATTAGTGAGCAAGACAAGC
 Y  A  Y  N  I  K  Q  T  V  E  D  D  K  L  K  G  K  I  S  E  Q  D  K>

      1830       1840       1850       1860       1870       1880       1890
AGAGGGTGCTTGAAAAGTGCCAGGAGGTGATCAATTGGCTCGACCGAAACCAGATGGCTGAGAAAGAAGA
Q  R  V  L  E  K  C  Q  E  V  I  N  W  L  D  R  N  Q  M  A  E  K  E  E>

      1900       1910       1920       1930       1940       1950       1960
ATTTGAGCATAAGCAGAAGGAGCTAGAGAAGCTTTGTAACCCCATCATTGCCAAATTGTACCAGGGTGCA
  F  E  H  K  Q  K  E  L  E  K  L  C  N  P  I  I  A  K  L  Y  Q  G  A>

      1970       1980       1990       2000       2010       2020       2030
GGAGCTGCAGGTGCTGGTGCTCCAGGTGGTGGTCCCACTATTGAAGAAGTAGATTAAGATACCATGGACT
 G  A  A  G  A  G  A  P  G  G  G  P  T  I  E  E  V  D  *

      2040       2050       2060       2070       2080       2090       2100
AGACTGTATGAGCAATTGCCATCTGCTCTACTCTTTCCCCGTGGCGTCTGGGGTGTGTAAGGGAGGAGGT

      2110       2120       2130       2140       2150       2160       2170
ATTATCTTGCTCTACTTTATTGGAAAGCATTGCCAGCTCATTTTGTTGCAGATGTTTGCCTTAGTATTAA

      2180       2190       2200       2210       2220       2230       2240
GATGTCTATGCTAATTGGTGGATATTTGGTTTTTATGTTCAATGTTGTAAATATCTACTTGAGCATTACA

      2250       2260       2270       2280       2290       2300       2310
ATTGAGGGAAGAACATTTCAAAAGAGTTAAACATTTTAAAAAAAAGCTTTATGTTTTTTGGCAACTTTTT

      2320       2330       2340       2350
TGGTCTGATTATTTTGAGAATTTTGGTAATAAAAGTTATTTGAAAAAAAAAAAAAAA
```

PDI (GenBank accession No. AY691666).
The deduced amino acid sequence is shown below the nucleotide sequence. A potential C-terminal tetrapeptide is underlined.

```
        10        20        30        40        50        60        70
GCTGAAGATCCTGTCGTCGTCGTCGTCGTCTTCGCTGCTGCCGCCATGAAGCTCCCCCGTTTCTTCGCTC
                                              M  K  L  P  R  F  F  A>

        80        90       100       110       120       130       140
CGGCGCTGTGTTTGCTTTGGCTGGGTCAAGCCTGCCTCGCCGTCGACATCGAGGAAGAGGAAGGCGTGCT
P  A  L  C  L  L  W  L  G  Q  A  C  L  A  V  D  I  E  E  E  E  G  V  L>

       150       160       170       180       190       200       210
GGTGCTGAAGTCTGCCAACTTCGACCAAGCGCTGGAGCAATACCCGAATATCCTGGTGGAGTTCTATGCA
  V  L  K  S  A  N  F  D  Q  A  L  E  Q  Y  P  N  I  L  V  E  F  Y  A>

       220       230       240       250       260       270       280
CCATGGTGTGGTCACTGTAAAGCTCTGGCACCTGAATATGTGAAAGCAGCAGCAACGTTGAAAACTGAAA
 P  W  C  G  H  C  K  A  L  A  P  E  Y  V  K  A  A  A  T  L  K  T  E>

       290       300       310       320       330       340       350
ATTCTGAAATCAGATTGGCTAAGGTAGATGCTACAGAAGAATCTGAACTCGCCCAACAATTTGGTGTTCG
N  S  E  I  R  L  A  K  V  D  A  T  E  E  S  E  L  A  Q  Q  F  G  V  R>

       360       370       380       390       400       410       420
AGGTTATCCTACTATCAAATTCTTCAAGAATGGAGATAAGTCTGCTCCCAAAGAATACACAGCTGGCAGA
  G  Y  P  T  I  K  F  F  K  N  G  D  K  S  A  P  K  E  Y  T  A  G  R>

       430       440       450       460       470       480       490
GAAGCAAATGACATTCTAAATTGGTTAAAGAAACGCACAGGACCTGCAGCCACTACCYTGGCAGATGTAG
 E  A  N  D  I  L  N  W  L  K  K  R  T  G  P  A  A  T  T  L  A  D  V>

       500       510       520       530       540       550       560
CTGCTGTGGAAGAGCTAGTGGAATCCAATGAAGTTGCTGTGATTGGATTCTTTAAGGATGCAGAATCTGA
A  A  V  E  E  L  V  E  S  N  E  V  A  V  I  G  F  F  K  D  A  E  S  D>

       570       580       590       600       610       620       630
TGTGGCCAAAGAGTTTCTGTTGGCAGCAGAAGCCACTGATGACATTCCTTTCGGGATCACTTCCAAAAGT
  V  A  K  E  F  L  L  A  A  E  A  T  D  D  I  P  F  G  I  T  S  K  S>

       640       650       660       670       680       690       700
GATGTATTTGCCAAATACCAGCTCAAAAAAGATGGAGTTGTTCTTTTTAAGAAGTTTGATGAAGGTCGTA
 D  V  F  A  K  Y  Q  L  K  K  D  G  V  V  L  F  K  K  F  D  E  G  R>

       710       720       730       740       750       760       770
ACAATTTTGATGGGGAAATAACAAAGGAAAACCTGCTGAATTTCATCAAATCAAACCAGTTACCCTTAGT
N  N  F  D  G  E  I  T  K  E  N  L  L  N  F  I  K  S  N  Q  L  P  L  V>

       780       790       800       810       820       830       840
GATTGAATTTACCGAACAGACTGCACCTAAAATTTTTGGCGGAGAGATTAAGACACACATCCTGTTATTC
  I  E  F  T  E  Q  T  A  P  K  I  F  G  G  E  I  K  T  H  I  L  L  F>

       850       860       870       880       890       900       910
TTGCCTAAGAGTGTTGAGGAATACCAGAGTAAACTGGATAACTTCAAAACAGCAGCTGAAGATTTCAGAG
 L  P  K  S  V  E  E  Y  Q  S  K  L  D  N  F  K  T  A  A  E  D  F  R>

       920       930       940       950       960       970       980
GAAAGATCTTGTTCATTTACATCGACAGCGACCATAGTGACAACCAGAGGATCTTGGAGTTCTTTGGTCT
G  K  I  L  F  I  Y  I  D  S  D  H  S  D  N  Q  R  I  L  E  F  F  G  L>

       990      1000      1010      1020      1030      1040      1050
CAAAAAGGAGGAATGCCCTGCCATACGCCTTATTACTCTGGAGGAAGAAATGACCAAGTACAAACCAGAA
  K  K  E  E  C  P  A  I  R  L  I  T  L  E  E  E  M  T  K  Y  K  P  E>

      1060      1070      1080      1090      1100      1110      1120
TCCAATGATCTGAGTCCAGAGAATATCAGGGACTTCTGCCACAAGTTCTTGGATGGCAAAGTTAAGCCCC
 S  N  D  L  S  P  E  N  I  R  D  F  C  H  K  F  L  D  G  K  V  K  P>

      1130      1140      1150      1160      1170      1180      1190
ACTTGATGAGCCAAGAGATTTCTGATGAGTGGGACAAGCAGCCTGTCAAAGTTCTGGTTGGAAAGAACTT
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H  L  M  S  Q  E  I  S  D  E  W  D  K  Q  P  V  K  V  L  V  G  K  N  F>

      1200       1210       1220       1230       1240       1250       1260
CGAAGAGGTGGCTTTTGATGAAAATAAGAATGTCTTTGTGGAATTCTATGCTCCCTGGTGTGGCCACTGC
  E  E  V  A  F  D  E  N  K  N  V  F  V  E  F  Y  A  P  W  C  G  H  C>

      1270       1280       1290       1300       1310       1320       1330
AAACAGTTAGCTCCTATTTGGGATAAACTTGGAGAAACTTACAAGGACCATGAAAACATCATTATTGCTA
 K  Q  L  A  P  I  W  D  K  L  G  E  T  Y  K  D  H  E  N  I  I  I  A>

      1340       1350       1360       1370       1380       1390       1400
AGATGGACTCCACAGCGAATGAAGTTGACATTGTGAAGGTCCACAGTTTCCCTACCCTCAAGTATTTTCC
K  M  D  S  T  A  N  E  V  D  I  V  K  V  H  S  F  P  T  L  K  Y  F  P>

      1410       1420       1430       1440       1450       1460       1470
TGCTGGCCCTGATAGAACGGTTGTAGATTACAATGGAGAGAGGACATTGGAAGGTTTTAAGAAATTCCTA
  A  G  P  D  R  T  V  V  D  Y  N  G  E  R  T  L  E  G  F  K  K  F  L>

      1480       1490       1500       1510       1520       1530       1540
GAAAGTGGTGGAAAAGATGGTGGTGTAGATGAGAACGATCTGGAAGATCTAGAGGATGCAGAAGAGGAGC
 E  S  G  G  K  D  G  G  V  D  E  N  D  L  E  D  L  E  D  A  E  E  E>

      1550       1560       1570       1580       1590       1600       1610
CAGATTTTGAAGAGGAAGAAGAACCTGCACCTAAAAAAGATGAACTGTAAACAGAAGTCCAATCTGCATA
P  D  F  E  E  E  E  E  P  A  P  K  K  D  E  L  *

      1620       1630       1640       1650       1660       1670       1680
TCCCCAGACACTGTGCTGTGGCTGCCAACTCAAGCAAGTCAGCAAATCAACTCTAAACAGAAGACTGAAA

      1690       1700       1710       1720       1730       1740       1750
CTGGTTGGGAGTCCAGGGAAATTAACCCATTCCTCTAACCTGTCAAACAAATCTAGTTTTATTCTATGCT

      1760       1770       1780       1790       1800       1810       1820
GAAGAAGGATCTGACTAGTTGGCAAACTGCTGGGTCTTTTTTCTTGTCTTTTTTCTCTTCTTTCATTTGC

      1830       1840       1850       1860       1870       1880       1890
AAACTGTGATGTACATTTCCTTAGAGTATTGCGGCCTGGGTAGAAGCACATTGAAATGATAATATGTCCT

      1900       1910       1920       1930       1940       1950       1960
ATTGCCTAACTAACTTGGGAATTTCATGAGTAAGGCATCCTTAAACATTAATAACACTTTGTCTAAATGA

      1970       1980       1990       2000       2010       2020       2030
CATATGCTGCTGTTGACCCAGCAGGCTCTTGGATATTGTCCCAGCTTTTTTTCCTTATGCTTTTGATTGT

      2040       2050       2060       2070       2080       2090       2100
TGTTGTTTTTTTCTTACCCCGGACCATTCCAGTGTGGAGGAAATCACTAGGCTGACCAAGGGAATAAGTG

      2110       2120       2130       2140       2150       2160       2170
GGGTATAGTAGGTCCTCTTAACTATTTGCATAGTCTCATGTCCTCTTTATATACTGTACAATTGATTTCT

      2180       2190       2200       2210       2220       2230       2240
GTCATCCAAAGATCTGGAAGGGTAGGAAACCATTGCTGAGGAATGAGAGTCCAATTGCCTTCTTACCTAA

      2250       2260       2270       2280       2290       2300       2310
AGCGAAATCAAACTTGAGTTGCTATCTCACCTGCAATGAAACAAAAGCCTTGCTATCTACACGTTATTTT

      2320       2330       2340       2350       2360       2370       2380
GCAATGGGTTTTCTGGGAACTGTTGGGAAATAACTTCTCTGAATCTAACAAAAAGGACACTTGATAACTA

      2390       2400       2410       2420       2430       2440       2450
AGGAGTTTTGTGGGGATACTTGAGAGCCATGGAAAGTCTGTATTACAAAGAGGATGAATTCATTTTAAGC

                 2460       2470       2480       2490
ATCCATGATGCTCAGAGGAATGGAACTCATTGGCCAAATAAAAGTAAAAAAAAAAAAA
```

Elongation factor 2 (GenBank accession No. AY691668).

<u>R14 nucleotide sequence using T3 primer</u>

GAATTCGGCACGAGGCTCATGATGGGACGCTACGTGGAGCCCATTGAAGATGTGCCTTGCGGTAACATCGTAGGCCTGGTTGGCGTCG
ACCAATTCCTGGTCAAGACGGGCACCATCACCACCTTTGAACACGCCCACAATATGCGCGTCATGAAGTTCAGCGTCAGCCCCGTCGT
GCGTGTGGCGGTGGAGGCCAAGAACCCAGCCGACCTGCCCAAACTGGTCGAGGGCTTGAAGAGGTTGGCCAAGTCTGACCCTATGGTG
CAGTGTATCATTGAGGAATCTGGAGAGCACATCATAGCCGGAGCCGGAGAACTGCATTTGGAGATCTGCCTGAAGGATCTGGAGGAGG
ATCACGCCTGCATTCCCATCAAGAAATCCGATCCCGTCGTGTCTTACCGGGAGACTGTTAGTGAGGAGTCGGGAACGTTGTGCCTTTC
CAAATCGCCCAACAAACACAACCGCCTGTACATGAAAGCCCGCCCCTTCCCGGATGGCCTGGCCGAAGACATCGACAAGGGGGATGTC
TCAGCCCGCCAGGAGCTGAAGCAGCGGGCCAGGTACCTGGCCGAGAAATACGAGTGGGACGTGGCTGAAGCCCGTAAGATCTGGTGCT
TCGGCCCCGACGGCACCGGTCCCAACATCCTGACCGATATCACCAAAGGAGTGCAGTACCTCAACGAGATCAAGGACAGCGTGGTGGC
CGGCTTCCAATGGGCCACAAAGGAGGGGGCCCTCTGCGAGGAGAACCTGCGTGGGGTCCGCTTTGACGTGCACGACGTCACCCTGCAC
GCCGACGCCATCCACCGTGGGGGCGGCCAGATCATCCCCACAGCCCGGCGATGCCTCTACGCCTGCATGCTGACCGCTCAGCCCCGCC
TCATGGAGCCAATCTATCTGGTGGAGATCCAGTGCCCTGAACAAGTTGTGGGTGGCATTTATGGCGTGCTGAACAGGAAACGAGGCCA
CGTCTTTGAAGAGTCCCAGGTGGCTGGCACCCCCATGTTCGTGGTCAAGGCTTACCTGCCTGTGAACGAATCTTTTGGTTTCACGGCC
GACTTGAGATCCAACACCGGAGGCCAGGCTTTCCCACAGTGCGTGTTTGATCACTGGCAGATCCTCCCCGGGGATCCCTTCGACAGCA
CCAGCCGCCCTTCTCAAGTGGTCAGTGAGACACGGAAACGCAAAGGGCTGAAAGAGGGCATCCCCGCGCTGGATAACTTCCTGGATAA
ATTGTAAAGCCGATCGAATGAAATAATAACCGAGTCAGATCTTAAAAACAAACAAAAAGAATAAATTTTAAAAATGGCTGTTG

CGI protein (GenBank accession No.AY691669).

<u>R9 nucleotide sequence using T3 primer</u>

CGATAATGCCACGCAGTGCTTCTATGAGGAGATCGTGCAGGGCACTAAGTGTACCCTGGAATTTCAGGTGATTACTGGAGGACACTAT
GATGTTGATTGCCGCTTAGAAGATCCAGATGGGGCTGTGCTATATAAAGAAATGAAGAAACAGTATGATACTTTTACCTTTACTGCAT
CTAGAAATGGAACATATAAGTTTTGTTTCAGCAATGAGTTTTCAACTTTTACACACAAAACAGTATACTTTGACTTCCAAGTTGGGGA
TGATCCACCTCTCTTTCCTAGTGAAAACAGAGTCACTGCACTTACTCAGATGGAGTCAGCATGTGTTTCAATTCATGAAGCTCTAAAG
TCTGTCATTGATTATCAGACACATTTTCGACTGAGGGAAGCACAAGGCCGTAGCAGAGCAGAAGACTTAAACCCCCGAGTGGCTTATT
GGTCAATAGGCGAAGCCATCATTCTACTTGTAGTTAGCATTGGGCAGGTATTTCTTCTCAAAAGCTTCTTCTCTGACAAAAGAACCAC
TACAACACGCGTTGGATCATAACAGTCTTTAAATCCATTGTTTGAAAAATATATTATTATTTGAATGATTCTAGTTAAAGACATTCAG
TACAGGGACTTTTAATCCTTTAGCCTCTCCTTCAAGTTCTGAAATCATATTTCGAAAGCTGTCCAGAAAAAAAAA

Gene 2.19 (GenBank accession No. AY691670).

<u>R 7 Nucleotide sequence using T3 primer</u>

AGAACATTCGTTTGCCTTCCGGATGACAAGCGGTGCAGCCAATGTCATTGGGCCCAAGATCTGCCTTGAAGATAAAATGCTAATGAGC
AGCATGAAGGATAATGTAGGCAGAGGACTGAACATTGCCCTGGTGAATGGTGTGAATGGAGACTTGATTGATGCTAAGTCTTTTGACA
TGTGGGCAGGAGATGTGAACGAGCTGCTAAAATTCATCCGGTCATTGCACGAAGGGACATTGGTATTTGTTGCTTCTTATGATGATCC
TGCTACAAAAATGAATGAGGAGGCCCGTAAAATCTTCACAGAATTGGGCAGCAAATTTGCTCGGGAACTGGCTTTTCGAGACAGCTGG
ATCTTCGTTGGAGCCAAAGGAGTGCAAGACAAGAGTCCCTTTGAGCAGCACATGAGAAACAGCAGGAGCTCCAACAAGTACGAGGGCT
GGCCCGAAGCCCTTGAGATGGAGGGCTGCATTCCGCAGCGAACCACTGAGGTCCTGTGAGGATCTGTTTCTTCAAAACTTGAAGTGAA
TTTTCTCATGGGAGCGGGAGAAAAAAGTCTCCAGTCTTCCACTTATTGTTGTCTACCCTTATTGTGGCAGCTGCCTTTTTTCCTTCTC
CACAGTGGCCTGTTTGGCAGTGCCTTAATAAGCTAACCAGTTGCCTTTTCAGAAAGTTTCTTGCCTGGACTTTGGGAAGGAGACGTGT
AACACTCGTATTGCAGATAGTCTCCTTCCTCCTAGGCCTACATTTCCCGGTGAAGGCTA

BET 3 (trafficking protein) (GenBank accession No. AY691670).

<u>R 140/R 141 nucleotide sequence using T3 primer</u>

ACAAAATGGCACGTCAGGGCAGCCGAGGAGGCTCCGAGAGCAAGAAAATGAGCTCGGAGCTCTTCACTTTGACGTATGGGGCTTTGGT
CACTCAGCTGTGTAAGGACTATGAGAATGATGAAGATGTGAACAAGCAGCTTGACAAAATGGGCTACAACATAGGTGTTCGACTTGTG
GAAGACTTTCTAGCACGATCCAACGTTGGGAGATGCCATGACTTTCGAGAAACAGCAGACGTAATTGCAAAGGTAGCATTTAAAATGT
ACTTGGGTATCACACCAAGCATCACAAACTGGAGTCCAGCAGGCGATGAATTCTCCCTTATCCTGGAAAACAATCCACTGGTGGATTT
TGTGGAATTACCAGACAACCATTCCTCTCTTATTTACTCTAACCTCTTATGTGGAGTGCTACGGGGAGCCCTGGAAATGGTACAGATG
GCTGTGGATGTCAGATTTCTTCTGGACACCTTGAAAGGGGATGGAGTCACAGAAATAAGGATGAAGTTTATCAGGCGGATCGAAGACA
ACCTCCCAGTTGGAGAGGAGTGAGTCTTGAGCAGCCTTCATACTGGACTGGAAGGGATGAAGTCACTGAACTGGAGCTTCATTCACAT
ATAGTACCCTATGTACTTTGAGACACTGACTGGTTAAGACGTCAATTCATTTGAAATAGTCTGTTTATTTCCACAGATTTCTATTAAA
AGCTTTTGTAGGATGCAGAACTCTTTCACATTCATCAGAAAACACCAAGGGCA

Polyposis.

<u>R117 nucleotide sequence using T3 primer</u>

GCCCTTTGCACTGAGCGGAGCCGAAGTGCAAAGCTACAGCCAGCCAAAGAGTCTCGGCAATGACGGCGTCTGGAGGGAGAGATTCGAC
AAGTTCCTGCACGAGAAGAACTGGCTGAACAATGTGCTTGGTAAAATTGAGAGCAAGACCGGCGTCAGCAGGTTCCTAACGTCTGCCA
TTCGGCCATTATTGCGTGTGCGTTGGGCTATTTACTTGGTTATTGGCTATGGAGCATCATTGCTGTGCAACCTGATCGGATTTGGTTA
TCCTGCATATATCTCCATCAAAGCCATCGAAAGCCCTAACAAAGATGATGATACACAGTGGCTGACCTACTGGGTTGTGTATGGAATC
TTCAGCATAGCAGAATTTTTCTCTGACATCTTTCTGTCTTGGTTCCCATTCTACTTTTTGATGAAGTGTGGCTTTCTGGTGTGGTGTA
TGGCCCCAAGTCCCTCAAATGGAGCAGAGTTCCTTTATCAGCAAAATTTATCCGCCCTTTCGTTCTTGAGGCATGAGGCTCAGCTGGA
CAATGTTATGAAGGAGTTTAAAGAAAAGGCTGGAGAGACAACAAGAACAACATTACAAAGGGAAGTTAAAAAAGCTGCAATAAATTTA
CTGGGTGATGAGAAGAAGAGCACCTAAAGGCATTAACTGGAAGGAAATTTCTTCCTTATCACGTANCGTTTATACAGTGGTGANGGTA
ACTGGGGACTGTGATACAGTAATTTGAAGTAATGTTGCCTTGTAACGCTTTTTGAAGTTNTAAGAAGA

Polydenylate binding protein (GenBank accession No. AY691673).

<u>R 19 nucleotide sequence</u>

CTTGTTGTGTATCCAAAGGAAGGGGGTGGCAAAGGAGAAAGGGACCTGAATAAAGAAGGGCGAGAAGCAACGGCCAGCTTGGAGCCTC
CGTGTCTGAAAGGCTGCTTACGCGAGGCTTAAGCTCAAAGGCACAACCATGAAAGATCCAAGTCGTAGGAGTACTAGTCCAAGCATTA
TCAGTGAAGATATGATCATGAATGGTCACTCTCATGAAGATGATAATCCATTTGCAGAATATATGTGGATGGAAAATGAAGAGGAATT
CAACAGGCAGATTGAAGAGGAATTGTGGGAAGAAGAATTTATAGAACGTTGCTTCCAAGAAATGCTGGAAGAAGAGGAAGAGCACGAA
TGGTTTATCCCAGCAAGAGATCTTCCGCAAACGATGGATCAAATTCAAGACCAGTTTAATGATCTTGTTATCAGTGACAGTTCGTCAC
TGGAAGATCTGGTGGTCAAGAGTAATCTGAATCCCAATGCAAAGGAGTTTGTTCCTGGGGTGAAGTACTAAATATATGAGTAGACTGG
GCCCTCTTTTGGTGGATGTAGCACAATTTCCACACTGTGAAGCCAGTATTAGAAGATTTAATTGTTAAAACGCTCTCTCTTCTTGTCA
CTGTGTTACACTTATGCATTGCCAAAGTTTTGTTAGTCTTGCATGCTTAATAAAAGTGCTGAGACTGTTATTAAGTCAACTGCTGTCA
GAGGTTAATGAATTGGAAAAGTCTAATTGGATCCAGGCTTTTTGTGAGGGAGACAATAAGGAAGGAAGCACCAGTCATGTTGAGAAAA
GTACCAAGTTTCTGAGAAACTCTTGCAATTCTGTTTTTAGAAGGATTCAGACTTTGATAAAGAGTGGTCTGTTTTACTTAAAAACTTA
TGGCGGTGTTGATATGCCCCCAATAATGCCTTAATGTGAAAATAAAAGCAAGGTTTAHCTGATTATGCAGATTAGCTGAATTTCAGTA
CTGCTATTAATTCCTCCCATTATCAAGCAAAACTTTACTCCACACTGTTCTTTTTTGAGGAAGGTGTGAATTGTAAAAATACCTGAAT
CACTTTTACAGGCCTGTATAGAATCCTTTCTCTTGGCTACAAATCTGGTTGGGGGGGGGAGGGGGGAAGAAAATTTGGCAATTGAGAT
TATATTTGCAGCAAGTTATCATGTTGGAATGTTTGTCCCACTTCTGAGTTTAACGTGATGTGAAGTTGCACATCACAGATTCTTCCAG
GAATCCAGAAACATGGCACTGCCTCTGTAAAATTTTACAATCTTAAAAATTGGATTCAATTGTAAATTTTAGCATTAGTGATTTGAGT
GGTGCTTTTCCCTTGCTTTGTTTAATCATCACTACACAATAGTCTACAGCACAGCTTTTTTTAAAAAACACCTAGTACAGTTTTGGCT
TCTTAAACTTCATATTTGGGTAGCTTACGCTGCCTTATGTGTTCAGTGTGAATAGTGTTTAAGTTGATTATAATGTAAAAAAATTATA
TTTTTTCA

RW 21. No matches

<u>RW21 nucleotide sequence</u>

TGTTGACCGGNTAACAATTCACACAGGGAAACAGCTATGACCATGATTACGCCAAGCTCGAAATTTAACCCTCACTAAAGGGAACAAA
GCTGGGAGCTCCACCGCGGTGGCGGCCGCTCTAGAACTAGTGGATCCCCCGGGCTGCAGGAATTCGGCACGAGGGGGTACCGGGCTAT
CGCGCTGCCGCCATGGCGCTCTACAACTTCAGGAAGATTATGGTGGTTCCGTCCGCGAAGGACTTCATTGATTTAACATTGTCCAAGA
CCCAGCGAAAGACTCCTACAGTCATTCATAAGCATTATCAAATCCACAGAATCCGTCATTTCTACATGAGAAAAGTAAAATATACCCA
ACAAAATTATCACGACAGGCTTACTCAGATAATTATGGATTTCCCAAAGCTTGATGATATTCATCCCTTTTATGCAGATTTGATGAAT
GTACTCTATGATAAAGATCATTACAAACTAGCTTTGGGGCAAATAAATATTGCCAAAAATCTGATTGACAATGTTGCCAAAGATTACG
TGCGTCTGATGAAATACGGGGATTCCCTCTATCGATGCAAACAGTTGAAACGTGCAGCCTTGGGACGGATGTGTACCATAATCAAAAG
ACAGAAGCAGAGCCTGGAATATTTAGAACAAGTGCGCCAGCATTTATCACGATTGCCAACCATTGATCCTAACACACGAACTCTCCTG
TTGTGTGGGTACCCCAATGTTGGGAAATCAAGTTTCATAAATAAGGTAACAAGAGCTGATGTAGATGTGCAGCCATACGCATTTACCA
CAAAATCTCTGTTTGTGGACMACATGATAACADDTMTTTGCGTTGGCAGGTCATAGATACTCCTGGTATTTTGGATCATCCTTTGGAA
GAGAGAAACACCATCGAGATGCAGGCTATAACTGCACTTGCCCATCCTCCGGTCTGCGGTGCTCTATGTCATGGATGTATCAGAACAG
TGTGGCCATAGCTTGGAAGAACAGCTGGCACTGTTTGAGAATATTAAGCCATTGTTTGCCAACAAGCCTCTAATTATTGTAGCCAATA
AATGTGATGTGAAAAGGATTTCTGAACTTTCAGAAGAGAATCAGAAAATATTTGCTGAATTAGAAGCTGATGGACTTCCTGTGATTGA
GACAAGCACTATGACAGAAGAAGRTSTTATTCGRKTTWRAMCTGAMSCTTKTKATYAGRTKRKYKGMYCWTCGCKTTASCACSAATWA
TSARASGAWWSAWAGTGMWYGRTGYACTGMACAGGYTWSWWWTARCTNCGTTGCCTCATWCMMAAAGRGACAGCAAKKWRMGGYCYYC
TTTYAYWMMGGCACAGRAGCCYTKATKCGSAGASMWGYRCATGRRMSTTGAWGTGYSCMMAAAAGAAATTGGAGAAAGACTTGGAAAT
GGAACTGGGGGATGACTATATATTGGATCTTAAGAAATATTGGGATCTGATGAATCCATCTGAAAAATACGATGTAATACCTGAGATT
TGGGAAGGTCTATAACATAGCTGATTATATTGACCCAGACATCATGATGAAATTGGAACAACTGGAGAAAGAAGAAGAGTAAAGGAWA
TAGCTGGAGAATMTGTAKAGTGWTTCAGAWRGCGAGGATGAGGAAATGATGGGAATTAGGCAGTTGGCACAACAAATTCGTGAGAAGA
AGAAAATGAAGATCCTGGAATCAAAGGAGAAGAACATACATGGGCCCAGAATGCCTAGAACAGCTAAAAAGATTCAACAAAAAACCCT
TGAACAAGAGATGACAAACCTGGGAGTTGGTCTACCTGGCAACATTGAGGGAAGGAGGTCACGCAGTGTCACCCGTAAACGTAAGCGA
GAAGATTCTGAAGAAGGTGCCTCAATGCCAGTAAGTNNNAAAGGCTCTCGTCCCCCTCGTGATGTCTCTGGTCTTCGTGATGCTAAGA
TGGTGAAAAAAGCAAAAATTATGATGAAGAATGCTCAGAAGGTAATGAATCAGATGGGCAAGAAAGGCGAGGCGGATAGAGCTGTCTT
TGACCTGAAGCCTAAACACCTGTTTTCTGGGAAGAGAAAAGCTGGTTCCACCNCCCGAAGATAGAGCAAAAAAAATAAAGATTCCTGT
GTTGNCTCT

R26. No strong matches by comparison to peptides within the BLAST database.

<u>R 26 nucleotide sequence using T3 primer</u>

ATTCAAGCCGTGAGAGAGAAAAATATTGCTTCCTTAGAGGGGGTTGTCTTTTTTTTTTAAATCAAATTCATGGTGGAATTACAATTAC
TGGAGCTTCAGTTTGATAGAAAAGACTAGTAAAATACTGGAACAAACTTACAATAATAAGATGCGGGAAATGCGTTCAAAGATTGATT
AATGCAGTCATTGGTTGCAAAGTGGGATGTTGCAAAATTTGCCTTTGTCCCACAGTATGAAAGCCAAACTTGATTAGGTTGGATGTTC
GGGTGTTGATAAACAATCTTCTATGCTTTTCTTTCAAAATAGAAGATACCACACTATCCCTTTCTACCAAACCAACTCAGAAAACTAG
AGTTGTACAAGTAAACTAAAGGCACAGATGATTTTGCACTCTTCTGGTCAAGCCTGTCTGATGGGAGTTAGACAGAAATCTTTTGCAA
ATAGAAGTATTGCAATCTCCTTTTTCGGGATAAAATAAGAGGCCCAAGATTTTGTTCTGACCATCAGAGAATGAACTGAGTGCCTTTT
GAATTCCTGACGAGATTGCCTCCACGTGTAAATACACATTTCTCTTCTTTGATCAGAAGAAAGCTCATGTTATCTGCTTTCACGCAGG
GCTGGGGAAATCATAGAANGGAAGGAACTGGAAAGAGACGTGGGGGACTATACATACTTAAATCCTATCTAATTTACCCAGCTGTTCC
AGATAGAATTAGTGGGTCTAAGCTCCTTGGCCATGATGAGTGTGAGGCTTAGAATGGGAGGCATGAACAAGAGAGACGCCTGTGGGTT
TGGATATTCTTGCCGGAAC

Peptide similar to archease.

<u>R 36 and RW 26 nucleotide sequence</u>

GGGACTACGGCCTGACCGAAGCGCAGCAAGGGGTCAAATGCCAAATACCCGGCCATCCAGAAGAAGTACGAATATCTGGATCATACGG
CTGATGTGCAGTTGCACGCTTGGGGTGATTCCTTGGAAGAGGCATTTGAACAATGTGCTATGGCCATGTTTGGGTACATGACAGACAC
GGAGACTGTTGAACCTGTTGACACTGTAGAGGTGAAAGCGGAAGGGCATGATATGCTCTCTCTCCTCTTTCATTTCCTCGATGAGTGG
CTCTATAAATTCAGCGCCGAGGAGTTTTTCATACCCAGAGAAGTGAAAGTGGTTCACATGGACCGAATACGCTTCAAGATACGATCTA
TTGGGTGGGGAGAGGAGTTCTCTTTGCAGAAGCATCCCCAGGGGACAGAAGTCAAAGCAATCACGTATTCGGCCATGCAGGTCCACGA
AGAAGGAAAACCAGAGGTTTTTGTCATCATTGATATTTTAAACGAAGCCATTCTGTTGGGTGGTTCCTCTGCGTCTGGGACAACAGGA
ATCGTTTTCAGGAGGAGCCAGAAGCCAGGAGAAAAAAGCTCTGGGTGCAGTTTCAGGCAAGCAGCCATTGAGAAGATAATTGGCCGTG

AAGCCAGAGATGAAGTTGTATTCTATTCCATGACAAGGTCCTTCATGGAAATTACCAGGATTAATACTTTCTTATTTAATTTTGCCGT
TTCTCCACTTCCCCTTTGGGGAATATGTTGTGAATATCCATTTGCTTTTGGCACCGATTGCAGCCATTCAGTTACACTGGTTCCTTCC
CCTCCCACCTACCCCTTAGGTAGCCATAGTTGGCCCTACCCGAGCCCAGGGATGCCATTCTGGCGGGTGGACAGTCGGACGGAACCTC
GCAGCAGTAATGACGATGTGCTGCTGAAGATTGGTGATGGGTGGGACGTGCTGCGCATGCGCGGCCAACAGCTGAGGTGTGGGGTTTA
ATTGTCTGTCAAATGGCGTTCTCCTTGCTTGGAGAAAGTAAATTACAGGGTGTGGTGAAGGTGGTCGTGGCTATATTGGTCGTGGGTG
GCACTCAGCCGGCAGCCCTGACAAAAAGCAAGTTTGTTGCTGGTCCCTTCGTGCTGTGTTTTTACTGCAGAGATCATTGGCAGAAGGT
TTGCTTTTTGTCTTTATTCTCTGGCGTGAATAGCGGAAGCCGACAGCCATAAGAAACCACTGGAGGATGGGGCTGTAACGCAGCCCTC
CTCCAGCCGTGCTCTCTGCGTGATAAGGTGGCCATGAAAACACAACTTACATCTTCTGTTCTCCATGATAAATTCTTTCATAACCTCA
AAAAAAAAAAAAAAAAAAAAAAAAAA

R 38. No matches.

R38 nucleotide sequence using T3 primer

AATTCGGCACGAGGCTTGTTATGTGTCTTTGTACCCATGTATCACGTAGGACTGAAACTAAAACTATAGAAGCTGTCAATTTGCACAT
TTAGAATTAATAGCAGCTGCTTCTAGAATTGAAGCATACAACCATTTCCTGCTGCTTTGTTTGTGTACATTCTGCACTTTATGTAACT
GACCCCATCTGACCGGAGCCTGATGAAGCAAAAGGACAGTGCTCCAAGGGTGGATACCAAGATAACTGGTCTAGCAGTTATGGGCTGT
GTGGGGGTTTTCAGGAAGCAAGATTGTAATTACTGCTGGCTTTCAGTCTCACATGAATAAAACTGTAAACCGTAATTGTACCTTATCC
CTCAATGCAGAATAAATATTTCTTCATGCAGCTCCCATTTATAAGCCAACATAAATTTAAATATTGTATTTATTTTTAAAGCAGTATC
ATGATCCTATGGTTGACTTAAAATAAGCTATTGCTTCTTCCTAGGCACTTGAGGACAAAAGACAGGAACATTTTTTTTTGCTTTTTTT
GTGTTCTCTAAATGACCAGAAAACTTTTATTTCAATGGGTAAATGAATATGTTAAAATTCCCTTTGAGACCACAAGCCTCTATACCCA
AACATACCTTGATTTACCTGAAATGTATTTTCTTTAAGGAAGCCTGACTTGGTGCAAGGTAGCACCAAATCCTATTATATTTACTCTT
CCATGGTCTCTATAGGGCTGCCACCATCCTGTTACGTCTTAAGGTCGTGATCTTTTCACATCGTAATCACACTAAGTCATAATGCAGT
GGTACCAGATTTGGGGTACAAAAGCCCAGATGAATGCTACAGGGAAGCAAAGATTTGCTGCCATTAAATGGAAGTCTAGATTTTTATA
ATACAGTACAGTACATAGTGGTTTGTTTATTCTTTGGTGTAGTGTATGAAGCTAAATATGCTTTTTCTGCTAGTTTCACTATGCCTCC
ACAGCTAAACACGTTTTTGATAGGTTGTCTTGAAATCAATTAATACATCTAATAATGGTTGTATTTGGAACATGCTACATTTACATTG
TCCAGATTCTCGCCAGCATCCAATTTTCAGTTATGTAGAATGAGAAACTACATCACTGTTAGAGCTATGTTGCATAGTTGTGCTGGAA
AGTGGATGCGTTTTTGAGATGGCAAATCTTCAGATAATGAAAAATCACAATAGTAAGGAAACAACCCAAGTGATACAATCCTACATGA
ACTTATGTTGATATAATTTATTTTTAATTCAGCATGTTTAAATTATAGGAAAGCAGAGAACTCTTAAGGAAAAATAAACAGAAGCAAT
GGTATCCCATAGAGGCAGAT

R 39. No matches.

R 39 nucleotide sequence using T3 primer

TCAAGGAGAGGAGCACAGAGGTCTGTTTTGGATATCTGATCGGAGCAGGTGGGTTGGGAAAGCAGGATCAGAATTTATGCTTCCAGCT
CAGTTGGACTCTTGGAAAAAGCAGGATATTCGTGCCTCAGATAATTTGGAAGAAGGGCACAACCCTTGAGAGCCTGTGTTTGGGATGA
GGTTTGAAGGGCGTCTTCCAAATTGTCATTGCCCTGTTTTGCTATTTTAGTGAGGTGTGGATAACACAAGGCTTGGCAGCTCTCTGGC
TGTGACCTCAGAATATATTGCAGCCAATCCATGCATTTAGGAAGGGCCGTGAGGGATTAGGCCAAGGCAGTCGGGGGCCAGTGGGGAT
AAGCAGATCGAAGGCTGTATGCATTAAGTGGTAATGGCTTCTGAAAGAAAAGAAAAGCCAACTGGAGTCATTTCATAATTGGCTTTTT
AAAACAATTAATGCAACACCGCTCTGTTTTGCCAATTAAGCAGATTAAAACTGTTATAATCTCAAAAAAAAAAAANAAAAAAAA

R 42. No matches.

R 42 nucleotide sequence using T3 primer

AAGACCCAGGCCCATCCCCTCTGCATCCTAGAGCATGCAGGGAGAAACGAAAAAGAGAGCAATGTGAGTTGTGTGGCTTACGGGGGAG
GAAAGGGCCTTGATTCCCTTCATTAACTGCAGCTGGGAACACGGTGTTTTAAAAGGGAAGCTGCGTGCAGCAAGCTGTTGGGAGCAAA
TCGTGAATTTATCTGGTATTGTGGCTTATCTGCGTTCCTGGCGTCTTCCCAATTGTGTGAGTTTTGCCATGCTTTCAAGGCTGAAAGT
CCTTTTCGTGCCCTGTCAAGTTTATTACTGCAGCTTGGTTTATTTGGATTTTTAGTTAGTTGTATGTCACCTTGTTCTGGACTGAATT
TTCACCAGTTAAAGGCTGTTCCTGGGAATTTTTCTCCAGCCAGAAGGTAACCTGGACGTTGGGGCAAAGTTGGAGATAATAAAGGGAC
TCTTCTTGCTTATTTGACTGTGTTGCCTTTGTGCCACGCCCCGAGTCATCACAGAAGATAACAGTATTCCGTGCACCCCGGCATATAT
ATATATGCTGGCCACATGACCACGGAAATTTTCTTTGGACAACGCTGGCTCCCTCAACTAAGAAATGGGGACGAGCTGCAACCCCTAG
AGTCCGAGACAACTGGAAAGGGGGAAACCTTTATCTTTGTTGGTAGTCATAGGAAAATAAACGTTTCCAGTACATCCTGAAGTGGCGT
TTTGTATCTGTGGTGCTGCAAAGATCTAATGTTCACTTCACCATGGATTGCTTAACTGCCAAATGCTATAAGCATTTCAGTTCACTTT
GGGATGTGTGTATTGTGAAGCCAGGATTGCAGTCAGTAAGTGACAGGTAATAGAACAATAGTTTAGTATGATGTGACAATTTGGTAAT
CATTAACTATTTGATGATGCTATTTGGATGTTTATAAGAGGGTCCATCAGCCCGAAGTAGCTATATTATAATGAAGTATGGTCCTGTG
TTTGGATGTTTTGCCTGAAATTGCTACTTTTCTAAGCATTGAAAAAAGATTTTTTTTTCTTATTATAGTATTTAGACCACCTCGAAAT
AAGAATGGGACTGCTGAAAGTAAATGAATGATACAAGATACTTGTCCACTAGAAACACCAAACCAGACCTGCCCCCCCCCCCAAAAAA
AAATCAGGAAGGCTTAAACTATAATAATAACAGAATCTTGCAAGTCTGTGTATGTTATATCTTTTCTTCCTACTTAACAGTTCAGAGA
ATTAGAAAGTTTTCTGTCTGAGCCTCTTCTGAATATTATCTGCCTGTTGCGGACGTAAAATATGTTTTACTGTTCATTGTCCTGGCAA
TGGAACTTGCAAATCCCCATCAAAGTTGTCATCTTTATTCTCTATGGTACTTTTGGGTCCTTGGTGTCAGTGCATGTGAGAATGGCCC
CTGCTGTTCTCATTAGTGGCCGTAGGCACCATATCCTATCCTGGTATTGAATTGTCCACTACTAAGCTCAGCCAAGAACCCAACAGTG
AACCCTGGAACTATGTATAAGTTCTAATATTGGAACAAGGAAATGGGGAAAAGTTTGACCTAAATTCTTTCATTATATCTATGTTGCT
GGCATAATCCTTTGTAATTTCTGTAGCTCCGACCAGATGGGGCTGGTAAATAGAATTTGTAGTGTAAAATTTCTACCCAAAATCACAT
TCTATTTTAAAAGCCTAATATTTGCCCATCCAACATTATTCTTGGCCTTTTAAATTCCTTTCACGGCCTTAGGAAAATCACTTTAAAA
ATGTGAATAATCTGGGTATTTTGTTTAACTTCTGTCTTGCAATTTCATGGTAATAAATGTGTCGGTCCTTTGTCTGTTTTTTCAAAAG
TAAAAGGCTATAAAGGCTTGCCAGATTTCTGTGAAAAGATCCACAAAGAGTAAAATGAAAAACAAGTTGTCAGTCCTTAAGCTGTACT
AATAAATGTGATGCCCACCCATCCATCTCTCTTTGTTTTACCATGCTATGCAATAATATCATTAAAACCATTGGTGT

R46, RW32. No matches.

R46 nucleotide sequence

CTCATGGTAAAATTGTGGTAGAAAGGAGTATTGTGTCATACTGCCTTCTGATACCCAACTTCTATTCTATTTAAAGCTGAAGCTTTAA
ATTCAGCCTTACTCTTAGCATTGCATTATGTTTGCTGTTTTTCCTGCTGTTTTCCTTATGCCATTTGTCATCTTTTTACTGGGGCTGT
GCTCTGATTTGGCGTGAACCCATTCAGATAATGAGAAATACATCATGGGCACTTACTTGTAAAGAGCCAAATCTGAAACCCCCAAGAG
CAGTTTCTACAAACTGTGACTTTATCCTCAGAATAATAGCCTTTCCCGAAAATAGAATCCTATTTTGATTAAAACAAAAAACAGGACA

AGACACTCTTGCTTATTTAGGTGTCTTCTCTTAATAACAAATGGGGAGGTTCCAAAAATGGGAATGAGTCAGTGGGCATGACATCATA
GCAATACAGGACAGACGAGACAACTTGTCTCATAACAAGCTGACCTTGTGGCCTTGAAGCATGATCCTTGCACAGCCCCATCATTTAC
AGTTTGGATTATGGCAGGTGGAAATATGAAAAATAAATACATAATAGTTGATAATTAAGTTATTGGGAACTATTTTTTAAAATGGAAA
AGAGCCATTGAAAAACTTACTCAATGAAATTAAATAGCCTTGAAGAAATATTTTTGCACGAAGGATGCAGAACATCTTTTTAACAAAT
GTGTCGTTGATTATTTCAATGGCAGGTTTTTAAATTCTGATGAATGGAATATTGAAGGAAAATGGCAGCTCTTCTTTTACTTTCTGGC
AATTTTTTTGAAGTAAAGTTTTGACTGTGTTTAATCAACTTTTGTTAAAATAACTGTTCCAATTTTAACTCTTCAGAAGCCAGTTGAA
ATATTGATCAGAAATTATGATCAAATTATGCTCAAAGGCTCAGGACAAACTTGATAAGCTATAATACTGTACAATTTAGGCAATGTAC
AATTTTTAAAATGGAAACAAGTTAATAGAGGTATACACAATGACCATGCTAAAGTTAATCAGAGCATGTCATTAATGGTGGATGTGTA
TTCTTCTTGAAATGTTACATCCTTGCTTTTTTATTATTGGGAGACTTGAAGAGTTAAAAAAATCTAAATGTGAAGTTTGTAGCTTGTT
GTATTTGACTTGTTTCTTGACAGTTAGAATTTGTCTTTATTCCAATCATATTGTTTTTAAGTCTCTTCTGTGCAAGCTTTAAAGGATG
CATTCTTGCCAACTCACGTACTGGAAGATCGCTTGTCAGATAAATACCACTTTGGACTTAAATGTCAATTATATAAACTGACAAACCT
CAGCTAATCAGTATTATCCTTGTAGATCACCATGTCTTTCACATATCAAACTTGGACCACCTCTGGGTGTCTAAAAGCATTCTTTGAG
TTTGTTTGCATTTTCTTCCGCTTGCTGGTAATTGTGTTTTTAAATGCAGATGTGATGTAATCTTATTTTCTTTGGATCAAAGCTGGAC
TGAAAATTGTATTATGTAATTATTTTTGTGCTCTTAATGTTATTTGGTACCTAAGTTGTAAATAATGTCTACTGCTGTTTATTCCAGT
TTCTACTACCTCAGGTATCCTATAGATTTTCTTCTACCAAAGTTCACTTTCACATTGAAATTATATTTGCTATGTGACTGATTCCTAA
GAGTTCCAGGGCTTAAGGGCACCTTATTGTGCAAGTAAATTTTAAAGATCTCTGGGTTAAGAAAATTTGGCTTCGATTATATTCTTTG
TTATTTTAAATATATCAAGATATTTTAATTAAAAGTTTTTACCCCTTTAAAAAAAAAAAAAAAAAAAAGAACTCGAGGGGGCCCCGAGCA
ATA

Endocrine regulating (GenBank accession No. AY02468).

R 50 nucleotide sequence

GAATTCGGCACGAGGATCTCAATGAAGATTTTCGCGAACTTGAAAGTGCTAGAAGGAAAAGAAAAGAAGAGGAACTGAGCAGAAATCT
GAGTCGGGAACTATCAGGCAATAGCTATGCGATGACTGGTTCAACTAATCCAACGAAATCTTCTGAACCTCAGTACCATTATAGACCT
GATGAGGCACCAGCAATGCCCAAAAAATCTATTTTGAAGAAACGTGTGGATGATCATCCTGTACAGCCTGAAGTCTTTTCTAGCGGTT
CTTCCTCTATTAAAGATCCCCCACTTCTTTCAAATCATTCTTTGCCCCAGCGTAGTAGCGTTGCTCCTTTTTCATTGGAGGTAGAGAA
TTTCCTCAAACAATTCAACAAAAGTGCAGTTGCAGAGTCTACCAGTAAGGAAACTCAAAGCAGTGAGCCTGACTGGAGACCATTTTCT
GGTCCACATCAAAATACACTTCCTACTGAGCAAAACTCTGAAAATTTTCTAAAACAAAAAGAGTCTCATGAGTCAACATCAGAGTCTG
TTGACCAGCCTGGTGATTTCCTGCTTCCTCATGAAAGAGCCAGCCAGGATGGAAGTGGCTTTTCACGCATTCTGGGCATTTTGGGAGT
CATGGCAGACTCTAAAGTAATATGGAAGAAGAAAAAAAAGGAACCAGGTTTCCTGAATGACTCGAGGATAGAGAGAATTCTTTATGGT
GATGATGACGACGATTGTAATACCAGCTCTCCATCTCCTCAAAAGCTAACTATGAGTGATGAGAAGGAATCTGTAGTCAAAAGTAGTA
CTCCACTCCTTACAACTGTAAACAAACATATAGAATTGAATCCAGACCAGAGTATAGAGAAGATTCATAGTTTTGCTTTAAAAACTAT
TGGTCTTGACATTGGGGTGGCCGAAATAGGTAAACTTGCTGCTCGTACTCAGGAACGTCTTCATGGGAAAAAAGTCATCTCGTATCAC
CTGATCGCTATATCAGTAAGCTATCTATCCAAACCAGAAATGTGGGAGAGGCGTCGCAATCGCAGTGAAACTTATTCTCCAGAATCAA
ACCAGAAGCACTCTCTCTCACCTACTAGTTCTTATCCATTATCTAAAGTTAGATCCTCTGTTACAAAATCTGAGCACAATACAAGCAA
AATGTTAGGACGAGATAATCCTCCTGACACAGTTGAGCAGTCTGTTCCTCCACTATCTCTAATTCCATCAGCTCCACCATCTCTTCCT
AATTTGTCACCTACACCCACCTCTGTTTCCCAATACAGACTTCCAAGCTTTTCACCTTTTCCTACACCACAGTTGCCACAAAACTATC
CTTCTCCCACAATGGCCCCTCCTGGCTACGATGCGTATGGACACTACATGGCTTATGCAGCTTCTGGCTGGCCCATGTATGCTCAGCA
GACTGACCCTGGGCTTACAGATATGCATGGACTTGTCACACTAACAGTGCCATCAAATCCAACACGGCCCAATCTTAGAGTTATTGAG
ACCGTTTCCACAGCCAAAGGGACTCCTGATACCAAAAGAGATGACTCTGTGCTTGTGCAAATCCCTACAGTAGCTTCTTATTCAAAAT
TACATCCTCAGTTCTCTCAACCTTCATTAAGAGGTTCCAAGGAAAGAATACCTGATGAAAAAAATCGAGCTTCTAGGAAACAAAAGGT
AGTAGAAGAAATTGAGAAGTTGAAAGCTGAACAGGAAGCACGGCAAAAAAAACTACATTATCTCAGAGCTGAATTAAACAGACTTTCA
AAACAACAAGGGGAATTGCTTCGGAAGAAACGGAGGGAGAAGGATGGACACAAAGACCCTTTACTAATAGAAGTCAACCGACTGCAAG
ATAACATTGCGAAGGAAATAGCTCAGCTGAAGATGAATGCTGATGCTGCAGAGAAGAAACAATCTGAACTTGACAAGGTAGCCCAGAT
CCTGGGGATTAATATTTTTGAGAAATCCCGGAAACTATCTTCAGAAAGTAAAGAGTCTTCAGAAAATGCAAGGACTCAGGAGAAAACT
TCTGATCTAGTCAAGGAACCAAAAACTAATAGTGACAGATTCAAGGAAAAGAGTCCTAAGCCTACGGAATCATCTTCACAGCCATTGC
AAGGGACCAGTATTTATGACTACTATGATACAGGGAATCATTGGTGTAAAGATTGCAATACTACCTGTGGAACTATGTTCGATTTCTT
CACACATATGCATAATAAGAAACATAGACAGACCCTGGATCCATATAATAGACCCTGGCAGCAAGACTCAAATGAAACAAAGCAGGAA
GTCACAAACGAATTGACAAAATACTGTCCAGCCAAAGTTCTGAATTCTTATCCCAGTCACTGGATACTACTGCAACTCTGCAGCGAAT
CTTTGGAGACAGATATCAGCAGAACAACATGTCAAAGTCATCTACATAATGAGAAATATAAGAAACATGTGGATGAGAATCCTCTGTA
TGAAGAAAGGCGGAATCTGGATCATCAGGCAGGATTGTCTGTGATTCAGGAAACTGAACGCAGGCTGAGACGGAAACTGTGTGAAAAA
CAAAAAGAGGAAAATGATGAGAAGACAACAAAAACAGCAAAAAAAAAAAAAAAAAAA

R 52. No matches

R 52 nucleotide sequence

TGTGAGCCAGCTTAATCTTAGGCTAATTTCAGAATTCTATGGATGTGCCTGCCGACTTTGCATGACAAAAAAAAAAAGTCAGCAGTTC
TCAAGTCTGTTGTTTTAATCAGCTTCTGTTGCTTTCCATTGCTTAGCTTAATAAAGCCCTTAAATCTTGATTTTGTTGACATTGCAAT
TTAAATGGCACTCAAGTCTTTTCCCCATTATCGAAAAGAAAATTCATCCTTAGAAAAGAACAGAAGCTGTAATCAAGAGAAAATATGC
AGAAAGGAAGATCCCAATTGCTTTTCAGCCTGTATTTGTGTTGCTGTATATCAAGATAATTCTTTAATAAACAGTCTATCAAAAAAAA
AGTGAATACTGGAAAACAGTATAACCACAGATTTTAATATACAGGAAATACACTGTACAACTTTTCTCCAGGAAGTGTTGAGGCTGTA
CTGAATTGTGCTTTCAGTTAACTGATTTCTGCCTTAGTTGAGTTCTGGACCATTCTGAGACCATATACGTAAATATAATTTCCCTTCA
GATCTCAAGCCTACAGTATATGCATGTTGAATAGAGATGGTCTTCATCTTGAGCTTTTCTCATTTCAGATAAAC

R 54 and Ron 3

R54 nucleotide sequence

GGGTTCTGCACAGCTTTCACCAGGGCCCTGCAAAACCTCATTTCCCTGGGGGACACCAGCAAGGAGTGCAGAGTGCCCCAAATATCGC
TGTGAGTGCAAGAGCCCCCAATCTGGGAGCCAGGAAGGGAGAAAAGCAAGGTGTAAGGACCCCAGCGGCCCGTATGTTGCCTTGGGCC
CCCTTAGTTCATTCCTCACTATGCCTTAAGCTCAGCTCTTCTCCAGGACCTGTGGGGGCTGCCCAGATTTTCTTGAGATTATCAGGCG
CCAACAGCTGCAGCTGTTGAGGCTCTGTCGTTGGCTGGCATGGACTATTTTCCCCCAAGCCTCCCAGACGAGGCCACCTTTGGCTCCC
AGGCCCACTGCAAACCTTCATTTCTCTGAATTGCACCGTGGGCTGTGGCTGCCAGCACTTCCACCGCATGGTTTCCTCCCTGCCGGGA
AAGGCGCTGTTTTCAAAGAGTGGCCGCTGCGGAGGCATCTCACTGAGCAAGCTTCTACATAACCAGCTTTAAATGGGTTTTTATATAT
TTTTTAAAAAACAGATCAAAACTTGATTGTATGAAATCCTGAGGGACTCTTTTAATTGTTTTTAATAATGAATGAACTCTGAATAAAG
AATACTGAAAAAAAAAAAAAAAAAAAAAAAAAAACC

Incomplete cDNA clones

HSP 90 (GenBank accession No. AY02457), missing internal sequence. Could not sequence from 790 to 993. Tried Pst 1 deletion, and used 8 different primers from different locations both plus and minus, all failed. Perhaps there is some secondary structure here that is causing a problem?

<u>(5')R 37 Nucleotide sequence from mass excision</u>
GCAGCTCTCCCTGTTGGAAGGTCACGCCGTGCTCCAGGCTCGTCTCTCCCGCCGTCGATCAAAATGCCTGAAGAAATCCAGCATGGTG
AAGAGGAGGTGGAAACATTTGCCTTCCAGGCAGAGATCGCCCAGCTTATGTCCCTGATCATCAATACCTTCTATTCCAACAAGGAAAT
CTTTATGCGGGAGTTAATTTCCAATGCCTCTGATGCTTTGGACAAGATCCGCTATGAGAGTCTAACAGATCCCTCAAAGCTGGAAAGT
GGAAAGGAGTTGAAAATAGATATCATCCCCAATCCTCATGACCGTACCCTTACATTGGTGGACACTGGCATTGGAATGACAAAGGCAG
ATCTTGTCCAATCAATTCTGGGCACTATTGCCAAGTCTGGCACAAAAGCCTTTATGGAAGCATTGCAGGCTGGCGCAGATATCTCCAT
GATTGGGCAGTTTGGTGTGGGGTTTTACTCTGCTTACCTTGTGGCTGAGAAAGTTGTGGTCATCACCAAGCACAATGACGATGAGCAA
TATGCATGGGAGTCCTCTGCAGGAGGCTCCTTCACTGTCCGGATTGATCATGGTGAACCCATTGGCCGAGGCACCAAAGTGATCTTGT
TCCTAAAGGAGGATCAGACA

T7 sequence (GenBank accession No. AY702458)
GATGAGGAGGAGGAAAGTGGCAAGAGCAAAAAGAAGACCAAGAAGATCAAAGAGAAGTATATTGACCACGAAGAGCTGAACAAGACCA
AAGCCATCTGGACCCGCAACCCTGATGATATCACCCAGGAGGAATACGGTGAATTCTACAAGAGCCTCACCAATGACTGGGAAGACCA
TTTGGCGGTCAAGCATTTCTCTGTGGAGGGGCAGCTGGAGTTCCGGGCGCTCCTCTTCATCCCCCGTCGGGCTCCATTTGACCTTTTT
GAGAACAAGAAGAAAAAGAACAACATCAAACTCTACGTCAGGAGGGTCTTTATCATGGACAGCTGTGATGAACTCATCCCAGAATATT
TGAATTTTATTCGAGGTGTGGTGGATTCTGAAGACCTGCCCTTGAACATCTCCCGTGAAATGCTACAGCAAAGCAAGATTCTCAAAGT
GATTCGCAAGAACATTGTCAAGAAATGTCTGGAACTTTTTGCAGAGTTGGCTGAAGACAAAGAGAACTATAAAAAATTCTATGAGGCC
TTTTCCAAAAATTTGAAGCTGGGGATCCATGAAGATTCTGCCAACAGGAAACGTCTCTCAGAGCTCCTGCGCTATCACACTTCTCATT
CTGGAGATGAGATGAACTCTCTAACAGAGTATGTGTCCCGAATGAAGGAGAACCAGAAGAACATTTATTATATCACAGGAGAGAGCAA
AGAACAAGTGGCCAACTCTGCTTTTGTGGAACGTGTGAGAAAGCGTGGTTTTGAGGTGATATACATGACGGAGCCCATTGATGAGTAT
AGTGTTCAACAACTGAAGGAGTTTGACGGGAAGACATTAGTATCGGTCACCAAGGAAGGCCTGGAATTGCCAGAAGATGAAGATGAAA
AGAAAAAAATGGAAGAGAACAAATCTAAATTTGAGAATCTTTGCAAATTAATGAAGGAAATCCTGGAGAAGAAAGTTGAAAAGGTGAC
AGTTTCAAACCGGCTAGTTTCTTCCCCCTGTTGTATTGTCACCAGTACCTATGGCTGGACAGCCAACATGGAACGTATCATGAAGGCC
CAGGCTTTACGAGATAACTCTACTATGGGCTACATGATGGCCAAGAAGCATCTGGAGATAAATCCTGATCACCCCATTGTAGAGACTT
TGCGTCAAAAGGCTGAGGCAGACAAAAATGACAAGGCTGTCAAGGATCTAGTGGTACTTCTCTTTGAAACAGCATTACTTTCTTCGGG
TTTCTCCTTGGAGGATCCACAGACCCACTCTAATCGGATCTATAGAATGATCAAGCTGGGATTAGGAATTGATGAAGAAGAAGTTGCT
GTTGAAGAATCCACTTCTACTGTATCTGAAGAGATCCCTCCCCTGGAAGGAGATGAGGATGCATCGCGCATGGAGGAGGTGGATTAAA
GAGCAGGAGCTGATCTTCCCTCTTTCCTACCTCCCTCTTTTTTCCCTGTGCCATCACCTTGCTCAGGAACCCTGGCAGTGCTAACTGC
ACCCTCAAAATGGTCTCTGTGTCTTTTATAAATGGTAACTAACATGGCAGGCAGCCTTCCACATTTATTTGGTCTGTCTGCTTGTTCA
AACATGCTGCTTTAGGGGAAAAGGGTCAGTCTAATTGTTCAAAGGTTTTTTGCTCTCCTGTCCATGAAGATTTTGTTGTAGTTTTAGC
TTGACCACCAAACATCCATCCCACTATAGCTGAAGTAAACACCCAGAGAATGTCCTTTCCAATAATATAGCAGTGAGACTCCTGCCCC
GCCCATCTCTCGCTGCTGTCTGTTGTCTTGAGAAAGCAGGGACTTGCAAGTCTTGTTCATGTATTTGGTTTTGTTCTACTGGAATTAA
AATAAAGAAGAATATAGAGTTACAATGTAAAAAAAAAAA

Elongation factor 1 (GenBank accession No. AY702459)
<u>R 129 T3 nucleotide sequence</u>
AGATGGCGGTGGCCGGGACTCTCTACACTTACCCCGAGAACTGGCGGGCATTCAAAGCCCTCATTGCTGCTCAATACAGCGGGGCCAA
GATCAAAGTCCTCTCCACGCCGCCCCAGTTCCACTTCGGGCAGACCAACAAGACTCCTGAATTTCTGAAAAAATTCCCAGTTGGAAAG
GTTCCGGCGTTCGAAGGAGAAGATGGATTTTGCATATTCGAGAGCAATGCCATTGCACACTACGTCAGCAACGAGGAACTACGAGGCA
CAACTCAAGAGGCCGCTTCCCAGGTCCTTCAGTGGGTGAGCTTTGCTGACAGCGACATTGTGCCTCCA
GCC

V abelson oncogene (GenBank accession No. AY702460), no internal sequence
<u>R 21 T3 nucleotide sequence</u>
DNAACGAGGCAGAGCAGCTCTGGGAAGCGCCGGGTGCGGCTTCTAAAGCGGGGTAGGGGGCGGAATGTGAGCAGGAGGAGGAGACGGA
GGGCTCTGGCGGGGGCCCAGAACGGGAGGAGAGCGGGGATGGGCCAGCAGGTGGGCCGCGTCGGCGAGCCGGGTGCCGCTGCGCTTCA
ACATCAGCCGCCACCGCCGCCGCCGCCGCCGCCGCAACAGCAGCAGCAGCAGCAGCAGCTGCTGCCTCTTTCCCAGCCACAGTCTCAA
CCCAGAGGGCTTCGTGGGAGTAATAGCAGCGGGAGTAGGCCTGCCAGCCGGAGGCGAGAAACGGCCGCTCCGCGAGCTGCCGACAGCG
GCTTCAATATCTTCACCCAGCACGAGGCTCTCCACCGCCCTTTTGGTTGTGACACTGAACCACAGGCACTGAATGAAGCCATCAGGTG
GAGTTCCAAGGAGAATCTTCTAGGAGCCACTGAGAGTGACCCCAATCTTTTTGTTGCACTTTATGATTTTGTAGCAAGTGGTGACAAC
ACACTCAGCATCACCAAAGGTGAGAAGCTACGTGTATTGGGTTACAATCAAAATGGTGAATGGAGTGAAGTACGCTCCAAAAATGGAC
AAGGATGGGTGCCAAGTAACTACATCACTCCAGTAAACAGCCTGGAGAAGCATTCCTGGTATCATGGACCAGTATCACGCAGTGCAGC
TGAATATCTGTTGAGCAGCCTCATTAATGGCAGCT

<u>Ron 6 24/5/03 T7 nucleotide sequence (</u>GenBank accession No. AY702461)
CAATCTAGTACAATTATTAGGTGTGTGCACCCTAGAACCCCCTTTTTATATAGTAACCGAATATATGCCCTATGGGAACCTGCTGGAC
TACCTACGAGAGTGCAATCGGGAAGAAGTGACTGCTGTTGTTCTGCTGTACATGGCCACCCAAATATCTTCTGCCATGGAGTACCTGG
AGAAGAAGAATTTCATTCACAGGGATCTAGCAGCTCGGAATTGTTTGGTGGGAGAAAATCATGTGGTGAAAGTAGCTGACTTTGGATT
AAGCAGACTGATGACGGGTGATACTTATACAGCTCATGCTGGAGCAAAGTTTCCTATCAAATGGACAGCACCGGAAAGTTTGGCCTAC
AACACATTTTCAATCAAATCAGATGTTTGGGCTTTTGGAGTTTTGCTGTGGGAGATTGCCACTTATGGAATGTCCCCCTATCCCGGCA
TTGACCTTTCTCAAGTTTATGATCTGTTGGAGAAAGGTTACAGGATGGAACAACCTGAAGGTTGCCCGCCAAAGGTCTATGAACTTAT
GAGAGCATGCTGGAAATGGAGTCCCCTAGATAGACCTTCATTTGCTGAAACTCACCAAGCTTTTGAAACCATGTTTCATGATTCTAGC
ATCTCTGAAGAAGTGGCAGAAGAACTTGGAAGGACCGCATCCTCTTCTTCAATAGTTCCATATTTGCCTCGGTTACCA

Lecithin Retinol or disease resistance protein (GenBank accession No. AY691672)

R20/R 31 T3 nucleotide sequence

CTTCAGGTTCTCCGGGGAAAGACTTTTATTTTCTCTCTCTCTCTCTTTCTCTCTCTCTCCCCCCCCCCTCTATCCCCCCCACACC
CAAAGACTGAATTGGGAGACTTGACGAATTAAACAAAGCAAGCCTGGCTGCCAGGAGCGATCTAAGAAAAAAGCCACAGGCTGATTGT
GAGAATGAGGGGACTGTGCACTGTGGCGTCACCCTCTCTTCCCGAATCTCAATCCTTGATGTTTTCCAGGAACTGCCCATTTTCCTGT
CTACCAATCAAAACAGACTCAGTGTGTGGGATGGCCCAACTTGCTATACTAAAAAGAGACCAAACCAGAATTAATCAGGAGCAGCTCA
TACAGCGAGAAAAAAACAACATGAAAAACCCAATGTATGAAATACCATTCCTGTTGCTGGAAAAGTTACTTCTGCTTGCCAACTTGAA
AGTTCTTCAGACAAATCCTGGTGGAGAGGAGGAGAAGGAAAAAAACCACGTTTCTTGTTATGACTCTTCCTATTTCAGACCAGGAGAT
TTGCTAGGAGGTGCCTCGCACTCTTTTCATTCATTTTGGCATTTATCTGGGAGATAACCAAGTGGCGCATCTTATGCCGGACATGCTG
CCTGCTTTCACGAATGAC

G Protein binding protein, no internal sequence

R 32 nucleotide sequence using T3 (GenBank accession No. AY702469)

AATTCGGCACGAGGGGGTACCGGGCTATCGCGCTGCCGCCATGGCGCTCTACAACTTCAGGAAGATTATGGTGGTTCCGTCCGCGAAG
GACTTCATTGATTTAACATTGTCCAAGACCCAGCGAAAGACTCCTACAGTCATTCATAAGCATTATCAAATCCACAGAATCCGTCATT
TCTACATGAGAAAAGTAAAATATACCCAACAAAATTATCACGACAGGCTTACTCAGATAATTATGGATTTCCCAAAGCTTGATGATAT
TCATCCCTTTTATGCAGATTTGATGAATGTACTCTATGATAAAGATCATTACAAACTAGCTTTGGGGCAAATAAATATTGCCAAAAAT
CTGATTGACAATGTTGCCAAAGATTACGTGCGTCTGATGAAATACGGGGATTCCCTCTATCGATGCAAACAGTTGAAACGTGCAGCCT
TGGGACGGATGTGTACCATAATCAAAAGACAGAAGCAGAGCCTGGAATATTTAGAACAAGTGCGCCAGCATTTATCACGATTGCCAAC
CATTGATCCTAACACACGAACTCTCCTGTTGTGTGGGTACCCCAATGTTGGGAAATCAAGTTTCATAAATAAGGTAACAAGAGCTGAT
GTAGATGTGCAGCC

RW 24 T4 nucleotide sequence using T7 (GenBank accession no. AY702470)

ACCTGAGATTTGGGAAGGTCATAACATAGCTGATTATATTGACCCAGACATCATGATGAAATTGGAACAACTGGAGAAAGAAGAAGAG
CTAAAGGAAATAGCTGGAGAATATGATAGTGATTCAGAAAGCGAGGATGAGGAAATGATGGGAATTAGGCAGTTGGCACAACAAATTC
GTGAGAAGAAGAAAATGAAGATCCTGGAATCAAAGGAGAAGAACATACATGGGCCCAGAATGCCTAGAACAGCTAAAAAGATTCAACA
AAAAACCCTTGAACAAGAGATGACAAACCTGGGAGTTGGTCTACCTGGCAACATTGAGGGAAGGAAATCACGCAGTATCACCCGTAAA
CGTAAGCGAGAAGATTCTGAAGAAGGTGCCTCAATGCCAGTAAGTCGCAATGGCTCTCGTCCCCCTCGTGATGTCTCTGGTCTTCGTG
ATGCTAAGATGGTGAAAAAAGCAAAAATTATGATGAAGAATGCTCAGAAGGTAATGAATCAGATGGGCAAGAAAGGCGAGGCGGATAG
AGCTGTCTTTGACCTGAAGCCTAAACACCTGTTTTCTGGGAAGAGAAAAGCTGGTTCCACCACCCAAAGATAGAGCAAAAAAAATAAA
GATTCCTGTGTTGACACAAATAAATACAGGGAAAACATCANAAAAAAAAAAA

Ca ATPase (GenBank accession No. AY702462)

R122 nucleotide sequence using T3 primer

CCCATTTCATGCAATGTACAGATGACCACCCTTCCTTTGATGGCTTGGACTGTGACATCTTTGAGTCCTCTGTCCCCATGACTATGGC
TTTGTCCGTCTTGGTCACCATTGAGATGTGCAATGCGCTCAACAGCCTTTCAGAGAACCAGTCCTTGGTACGGATGCCTCCCTGGGTA
AACATCTGGCTTCTGGGATCTATCTGCCTCTCCATGTCTCTGCATTTTGTCATCCTTTACATTGACCCCCTGCCTATGATCTTCAAAC
TGACACACTTGGAGTTGCATCATTGGCTCATGGTGTTCAAGATATCCTTGCCCGTCATCTTTCTGGATGAATGTCTCAAATTCATTGC
CCGGAACTATCTGGAGCCATAAGCTCCTTCCCCCTCTATTCTCCTGTATCCTGCCTCCCAGAGAATTTAGAAGGAAAGAAGTGAACCT
TTGAGTCGTCATGGAAATAACCACATCGTTTCCCCCCAATCGTCAAGATCTGCCCATTTCCCAAACCCCACTGTCTTGTCTTCAGCCC
TGCCTCTGCTTCTCTGTCCCTCTGTTATTTAATAGTGTCACTCTTCCTCTTTATCCTCTCTGCTAGTGGGATTGCTAGTGTGGGCCAC
AGTGCTGGCATTTGCCATGCCATGTTCCCTGCCAGCTGCTTCTCTACCCAACCCACAAACCTCACCAGCGACTCGGTTTCTGTACATT
TTGAACCACCTGCCTGTCCTTGCCTTCGCACACGCAAGCTCACACACTGCACATATGCACACATACCGTCCCAAGTGCTTTCCGCATT
AGTGA

Golgi associated (GenBank accession No. AY702463)

R 62 nucleotide sequence using T3 primer

GGACCGATTACCAGAAGCAGCTTTCTTAGCACGTACATATTTGCCAAGTCAAGTTTCAAGGGTTGTAAAACTATGGAGAGAAAATCTT
TCTAAAATCAACCAGAAAGCTGCTGAATCCCTAGCTGATCCCACAGAGTATGAAAATTTGTTTCCTGGATTGAAGGAAGCGTTTGTTG
CTGAAGAATACATAAAAAATTCCCTATATACCATATCACGGCCAGCCAATGAATACCCTCTAGTTACTCCAAATGAAGAAAGAAATAT
CATGCAAGAAACCATAGATTTCACAGTGCAAAACAAAGTATCAGAGGAACCAGAAGATGAATCAGTCCCATCTCCTAGGCCTCTAATA
ATGCCTCCAGTTGCTAGAAAGGTTTCGGAGGAGATCAAAGATGAAAAGGTTTTATTGGACCTAGATGTAGATCTGGATAACTTGGAAT
TGGAGGATATTGATACCACCGATATTTTTCTGGATGAAGAAATGTCTGACTGAACTTTTAAGCTTATGCACATTCTTACACCTAGTTA
TGCTTGAGTGTAGTCTTCTTGTTGAAAAGTGGCTCTTTTTATATTTAAGGTGAAAAATAAATAGGGTCAGTCTTTTACAGTACAGATA
TAGATTTCCCCATTTGTGATGTAGGACTCCTTAGATACAGTAGCAAGCTCATATCACATGATCAAACAATTTTCTAATAAATGTCTTT
CAGATTCAAAAAAAAAAAAAAA

Carboxypepsidase (GenBank accession No. AY702464)

R 136 nucleotide sequence using T3 primer

CCCATCGCCTCTTTCTGGAACGTTCCACCATGGAGCTCATCCTGTGGTTTGCAGTTTTGCTCGGCGTCGCCTGCAGCCGGGAAACGTT
TGAAGGTGACCAGGTTCTCCACCTGAAACCGCGCAATGGGGAACAGATTGAGTTGCTGACAAAATTGGGAGGCCTGAAACATCTCCAG
CTGGATTTCTGGAGGTCTCCTTCGTACCCCAAAAAACCGGTCGATGTCAAGGTGCCCTTCACTTCCCTCCAAGCTGTCAAAGTCCTTC
TAGAGTCCCAACAGATCGATTACTCCATCCTGATTGAAGATGTGCAGGCCCTGCTGGACGAAGAATCTCGCGAGATGCAGAGTAACCG
TCAACGGGAATACAGCAACAGTAATTTCAACTATGGAGCTTACCATAACTTGGACACGATTTATCAAGCAATGGATGATATTGTGAAG
GACCATCCCCGGATCGTGAGCAAACTCCAGATTGGACGGACCTATGAAAAACGACCTCTGTTTGTCCTCAAGTTCAGCACTGGGGGAA
ACCGACGCCCTGCCATCTGGATCGATGCTGGGATTCACGCCCGAGAATGGGTGACCCAGGCCACGGCTCTCTGGACAGCTAAAAAGAT
CGCTTCTGACTTTGGGAAGGATCCTTCTGTGACCTCCCTCCTCAACAAAATGGATATTTTTCTGCTGGTGGTGGCAAACCCTGATGGA
TACGTCTACTCTCACACCAAGAATCGTATGTGGCCGAAAAA

Carboxylate (GenBank accession No. AY702465)

R 135 nucleotide sequence using T3 primer

GCTTGTGGTTTTTCATGGATGCTCTGGACCTGTACAGCATGTTCTCCAACAAATCCTTAAAGACAGAGACTGGCTGGATAATGTCTTT
TTCCCAATAAGTAAAAAAAGATTAAAAGAAGCTCAAAACATTCTCGTGGATGGTCTTGCAGAAATCGGAATACCTGTTTTAAAAAGCT
CAGGAGGGTTATATGTGTGGGCTGATTTCAGGAAGTTTTTAAAAACACAGACATTTGAAGCTGAAATCGATTTATGGATGAAGATTCT
TGATGAAAAACTTCTTATTAGTCCTGGGAAGGCCTTCTGCTGTTATGAACCTGGATGGTTTAGAGTAGTTTTCTCAGATTCTGTAGAT
AAGATCATTTTATGCATTCAGAGACTTCAACAATTGCTTTGTGATAAAATGGATGAACCTGTTAGTCTGTGTTCATGTCCTGAACGAA
ACAAATGTACTGAGTCAGATGAGAATGTTTCTGCTAATGTCATGAATACACCAGTGGATGATGTGTCAGAGGGTTATTCACAGCTGAA

GAACAATAGCTGTTTTCTAAGATCTGGACTGACAACACAAATAACCTGTTTTTATGTATCTGTGACTCCTTTTCTTTTTCTCTTTTAT
CATAATCTGAATATACCTTTTACCTTGTAGTTTGTAATGTACGGTTATTAATTTAAGAATCACAGTATTACATCTGAGAATGATTAAT
TTCCTTAATGAAGGTTTATCTTTAACTTGAAGGTTGTTTAAGGTTGGCATTGTTCGAGGGGTTAACCTTTATTACTTTGGNAAACACA
ACAAGGACAGTTATTTTTCAACTTGGTGGTACCTTTTCAGACACAAGGGTTCACAATGCTNCCTTAAGTTTGGACAAGCAATAAGTTT
NGGGACAAGGAAATATTTCCTTG

Myosin Light (GenBank accession No. AY702471)

Wel 13 nucleotide sequence using T3 primer

GGATCTCTCCAGGAAAGATGGCCAGCCGAAAAACCAAAAAGAAGGAAGGCGGTGCCAAACGTGCTCAAAGGGCTTCTTCTAATGTTTT
CTCCAACTTTGAACAGACACAGATCCAAGAGTTTAAGGAAGCTTTCACCTTAATTGATCAGAACAGAGATGGCTTCATAGACAAAGAA
GACCTAAAAGATACCTACGCATCATTGGGTAAAACCAATGTCAAAGATGATGAATTAGAGTCTATGCTTAAAGAAGCTACAGGGCCTA
TTAATTTCACCATGTTTTTGAACCTATTTGGGGAAAAGTTAAGTGGTACAGATACTGAAGAGACTATACTGAATGCATTTAAAATGTT
TGACCCAGACGCTAAAGGCAATATTAACAAGGATTATATGAAACGCTTAATGATGTCCCAAGGTGATAAGTTTACAGCAGAAGAGATA
GATCAGATGTTTCAGTGCTCCCCTATTGACTCGGCAGGAAATCTGGATTACAAAGCTCTCTGCTACACCATCACACATGGAGATGAAA
AAGAATGAAATTCATAAGCTTTAGGAAGTTGTGTAAACATCTGTCACATTAATTAAACAAAATGACAAAAAAAAAAAAAA

Myosin heavy, superfast (GenBank accession No. AY702466)

R 48 nucleotide sequence using T3 primer

CTGGATTTGATCAACAGAACACGCTGGAGGAAGACCAAACCGGCAAACGCTGACGCTCCAACGCTTGGTCTCCAAGCTCAACACCGAA
GTTACAACCTGGAGGACCAAATATGAAACCGATGCTATTCAGAGAACTGAGGAGCTGGAAGAGACTAAGAGAAAACTGACCGCCCGTC
TTCAGGAGGCGGAGGAAACGGCCGAAACGGCGCAAGCTCGGGTAGCCAGCATGGAGAAGTACAAGCAGAAGCTCCAAATGGAAGTGGA
GGATCTAACTTTGGACCTGGAAAAGGCCAATGCAGCCTGTGCAGTCCTGGATAAGAAGCAACGGGCCTTTGACAAGATGCTGTCTGAA
TGGCAGCAGAAGTGTGAGGAGCTCCAACTGGAAGTGGACAATTCCCAGAAGGAATGTCGCATGTACATGACGGAGAACTTCAAGCTCA
AGACGGCCTATGAGGAAGCCTTAGAGCAGCTGGAAGCTGTGAAGAAGGACAACAAGACTCTTCAGGAGGAAATCAAGGATCTCATTGA
CCAGTTGGGTGAGGGAGGAAGAAGTGTCCATGAGCTGCAGAAAGATGAAAAGAAGTTGGAAATCGAGAAGATGAGCTTCAGGTGGCCC
TGGAGAACCGATCTTCCTGGAGTGGAGAAGCAGCTGATTCGCATTCAG

Alpha Actin (GenBank accession No. AY702472)

R 133 nucleotide sequence using T3 primer

ATAAGCGGCAACCGGAGCTGAGAGCCAGGAACCCCCAAGAAAGCCAACATCATGTGTGATGAGGATGAGACCACTGCACTTGTGTGCG
ACAATGGCTCCGGCTTGGTGAAGGCTGGCTTTGCTGGGGATGACGCCCCTAGGGCTGTCTTTCCCTCCATTGTTGGCCGCCCACGTCA
TCAGGGTGTCATGGTGGGTATGGGTCAAAAAGACTCCTACGTAGGGGATGAAGCCCAAAGCAAAAGAGGTATCCTGACCCTGAAGTAC
CCCATTGAACATGGCATCATCACCAACTGGGATGACATGGAGAAGATCTGGCATCATACTTTCTACAATGAGCTCCGTGTTGCCCCTG
AGGAGCACCCCACCCTGCTCACTGAAGCCCCTCTTAACCCCAAGGCCAATCGTGAAAAGATGACCCAGATCATGTTTGAGACCTTCAA
CGTCCCTGCCATGTATGTGGCCATCCAGGCTGTGCTGTCCCTCTATGCCTCTGGCCGTACTACCGGTATTGTGCTGGACTCTGGCGAT
GGTGTCACCCACAATGTGCCCATCTATGAGGGTTATGCCCTGCCCCATGCCATCATGCGTTTGGACTTGGCTGGTCGGGATCTCACTG
ACTACCTGATGAAGATCCTGACTGAGAGAGGCTACTCTTTTGTCACCACAGCTGAACGTGAGATTGTCCGTGACATCAAAGAAAAGCT
GTGCTATGTGGCTCTGGACTTC

Beta actin (GenBank accession No. AY702473)

R8 23/3/03 nucleotide sequence using T3 primer

GCGCCCCCCACGGTCCTCTTTGCTCACCTGCTTTTTTTTTTTTTAAACATTTTTAATTTTGGGGGTCCCCGGTTGGATCGCTTTTGCG
CCCTCCCCAAGCCGCCCCCTCTGCCTCCAACCCGAAAGGTCTCCGCGTTTCAAGCACCGCCGAGCGCCTTCTTCCTCCGAAGCAGCAG
CAGCAGCCGCCGCCACCCAAAAGATCTGCCATGGATGATGATATTGCAGCGCTTGTGGTCGACAACGGCTCCGGCATGTGCAAAGCCG
GCTTCGCGGGAGACGATGCGCCCAGGGCCGTCTTCCCCTCCATCGTGGGTCGCCCCAGGCATCAGGGTGTGATGGTCGGGATGGGCCA
GAAAGACAGCTATGTTGGAGACGAGGCGCAGAGCAAGAGGGGCATCCTGACTCTCAAGTACCCCATCGAACATGGCATTGTCACCAAC
TGGGATGACATGGAGAAGATTTGGCATCACACCTTCTACAATGAGCTCAGAGTCGCCCCGGAAGAACATCCTGTGCTCTTGACAGAAG
CTCCCCTGAACCCCAAGGCCAACAGAGAGAAGATGACCCAGATCATGTTTGAGACCTTCAACACCCCAGCCATGTACGTTGCCATCCA
GGCTGTGCTCTCCCTGTACGCCTCTGGCCGTACCACCGGCATTGTGATGGACTCTGGTGATGGTGTCACCCACACTGTGCCCATCTAT
GAAGGTTACGCCTTGCCCCACGCAATCCTCCGTCTGGACCTGGCTGGCCGCGACTTGACCGACTACCTCATGAACTGACGAAGGGCAC
AGCT

Ribonucease HI large subunit (GenBank accession No. AY702467)

R 59 and RW 35 nucleotide sequence using T3 primer

GTAGGATGGGCCCTACACATCCTCTCCCCCAATTTCATCTCAACTAGTATGCAGAGACGGACAAAGTACAACTTGAATGCACTATCTC
ATGATACAGCCATTGGCCTAATCCAGCATGCACTAGATTCTGGAGTGCAACTTGCAGAGGTTTTTGTAGACACAGTGGGACCAGCAGA
GAAATACCAAGAAAAGCTAAAGCAGCAGTTTCCTGAGCTGGAAGTTACAGTGAGGGCCAAGGCAGACTCTCTCTTCCCTACCGTAAGC
GCAGCCAGCATTTGTGCCAAGGTAGCAAGGGACCGGATTGTGAAGAATTGGAAATTCTTGGAAAACCTGGAAGATACAGAAATGGATT
ATGGCTCGGGCTATCCCAATGATCCCAAAACTAAAGAATGGCTCGCTCAAAACCTGGACCCAATCTTTGGCTATCCACAGTTTGTACG
ATTTAGCTGGAGCACAGCTCAGCTCATTCTGGAGAGCAAAGCTGTGCCTGTTCATTGGGATGATACTGAAGATGGCCCATCCCAGCAG
AGTGCAAAGTCCTTGCTCAGCTACTTTACCCGGAAGGTTTCCCCCTCCAAGCGTACACCCCATCGCTTCTTTTATGAACGCAAACTGG
AAACTGTCACCAGCTTGTAGTTGGTGGCAGGTGGTTTTCCTCTTGTTGAAAATTATCTTATGACAGAAAACTGACATTTAGTTTTTAT
TTAATGGGCAGTCCCAAATCCTTTGCGCCATAGCTACAAAACAGCATGAAACCCAAAGGTTCAGCTGAAAGATATAAAATTAAACAGA
GAAAGAATCTGGTAAATGTTCTTCCTGGAGGCCCTCCTGCCCTTGTACTTAATTCCTTTTTAGTTAATAAATTATCAAGACCTGATAA
AAAAAAAAAAAAAAAAAAAAAAAAA

Ribophorin (GenBank accession No. AY702474)

R 45 nucleotide sequence using T3 primer

CTGGCTTTGGACCCCAGCTTGGAGGACACCAAAATCTACCTGGGGGCGCAGGTGAAAGCTGAAGAAGAAGAGGAAAATATCCTGGAGG
TAAAGGAGACAAAAGTAAAAGGTAAAAGTGGCAAATTCTTCACTGTGAAATTGCTGGCTCCTTTGCCTCCAGGTGGAAAAATTCGTTT
ATCTATTGAAACCGTTTTCACACATGTCCTGCAACCCTACCCCACNCNCATCTCTCAGGCAGAGAAGCAGTTTGTGGTTTTTGAAGGT
AATCATTATTTCTACTCTCCATATGTAACCAAGACCCAGACAACTCGTGTGAAACTGGCCTCAAGAAACATTGAAAACTACACCAAGT
TAGGCAATCCCAGCCGCTCAGAGGATATGATTGAATATGGACCCTTCAAGGATGTACCCCCATACAGTGAGGATAACCTTAAGATACA
TTATGAAAACAACAGTCCATTCCTGACGATTACCAGCATGATACGTGTCATTGAAGTGTCTCACTGGGGTAATATTGCAGTTGAAGAA
AACGTTGACTTAAAGCATACAGGAGCTGTACTCAAAGGACCCTTCTCCAGATACGACTATCAAAGACAGCCAGAA

RW31 T7 nucleotide sequence (GenBank accession No. AY702475)

AAGGTCCGCAGCAGAGCTAGGATGAAAGTTGCTTGCATTACAGAGCAAGTTCTAACTGGAGTGATAAGAGATTATGTCTTTACCGCTT
TTGATGAAGCTGTGAATAAGTACAAGCAGTCACGTGATATTTCTTACTTTCTGAATAGGGCAAAAAGTCTTCTGGAAGTTGAACATAA
AGCCTTAACAAATGAAATAGCCTCATTGCAATCCAAGTTGAAGATGGAAGGTTCTGACCTATGTGACAAAGTCAGCGAAATACAGAAG
CTGGATAGTCAAGTCAAGGAGCTGGTTGTAAAATCATCTTTGGAGGCCGAGCGTCTGGTTGTTGGCAAACTTAAGAAGGATACGTACA
TAGAGAATGATAAGATCCATTCCAGCCGGCGTCAAGAGTTGATCAGCAAAATTGACAACATTCTCGATGCACTATAAGTTAGGATTTA
AAAATTGGGGTAATGTGAGGGAAGAATGCAAGGCAATTGTATGGGTATACTGAGCCATACTAATTTAGAAAGTAAGAGAGCAGTAAAT
AAGTATGCCTGGTGTTTAACATGGGGTTGGGGAGGCTTTTTTTTTCCTTGTAAACCTGAATTTGGAATTTGAGGTTTGTTATTTTGGG
GCATGTTTGCATTGCTATGTGGAGGAGGTTGGATACTACGTTGGCTCAACACAACTTTTGTCCTCGCATAAAGTTCCAAGTGTTAATT
ATTATGACTTCCGAGTCTGTTGTAAAGTCCCCTAATCGCCAGTAGAGAAACATGCACACAGGTCCTCTTCGGACACTGGATATCTCAG
AAGACAATAAATACAAGAATTTTTCAAAAAAAAAAAAAAA

Mitochondrial DNA

Cytochrome C subunit one

R 55 nucleotide sequence, not complete, using T3 primer (GenBank accession No. AY691675)

ACCCGCCCCTATCGGGAAACTTAGTTCACTCCGGGCCATCCGTCGACTTAGCTATTTTTTCACTCCACCTAGCAGGAGCCTCCTCCAT
CCTGGGAGCAATCAACTTTATCACAACATGCATCAACATAAAACCCAAATCAATACCAATATTTAATATACCCTTGTTCGTATGGTCC
GTCCTAATCACTGCTATCATACTGCTTCTGGCTCTACCTGTGCTGGCTGCCGCAATCACAATATTACTAACAGACCGCAACCTAAACA
CATCCTTCTTTGACCCCTGCGGAGGAGGAGACCCGGTCCTATTTCAACACTTATTCTGATTCTTTGGTCACCCAGAGGTTTATATCCT
TATCCTCCCAGGCTTTGGTATTGTATCTAGCATTATTACCTTCTACACTGGAAAAAAAAACACATTTGGCTACACCAGCATAATCTGA
GCAATAATATCAATTGCCATTCTAGGCTTTGTAGTATGGGCCCACCACATATTCACCGTTGGCCTAGACATCGATAGCCGAGCCTATT
TTACAGCAGCAACAATAATCATCGCTGTTCCCACAGGAATTAAAGTCTTCGGCTGACTAGCCACACTAGCAGGAGGCCAAATTAAATG
ACAAACCCCAATCTACTGGGCCCTTGGGTTTATCTTCTTATTTACAGTTGGTGGTATAACAGGTATTATCCTAGCAAACTCATCACTA
GACATTGTCCTACATGATACTTATTACGTAGTAGCCCACA

Cytochrome C subunit 2 (GenBank accession No. AY691676)

R 61 and RW37 nucleotide sequence, complete, using T3 primer

CCCAACTCTCTCTACAAGAAGCCACAGGCCCAGCTATAGAAGAAGTTGTTTTCCTACACGACCACGTCCTTCTACTAACATGTCTCAT
ATCTCTGGTAATCCTAATGTTTGCTATTACCACAACAACATCAACCCTAACCCACAATGACCCTACAGAAGAAGCAGAGCAGCTAGAG
GCAGCATGAACAGCCGCTCCTATTATAATCCTTATCTTGACAGCCCTTCCATCCGTACGATCCCTCTACCTCATAGAAGAAGTATTTG
ACCCTTATTTAACTATTAAAACTACCGGCCACCAATGATATTGAAACTATGAATACTCAGATGGGGCCCAAGTTTCATTTGACTCTTA
CATAATCCGAACCCCTGATCTACAAAACGGGTCTCCCCGCCTATTAGAAGTAGACAACCGCATAACAATACCAATGGACTGCAAGTC
CGGATGGTAGTTACCGCAGAAGATGTGCTTCACTCATGGGCAATTCCATCATTGGGGGTTAAAGTAGATGCAGTACCAGGACGACTAA
ACCAGCTTCCTTTGGCCACATCACGAAGCGGCGTGTTCTTTGGGCAGTGTTCTGAGATCTGCGGAGCAAATCATAGCTTTATACCAAT
TGTAGTAGAGTCTATCCCTATAACCCAATTCGAACTTTGACTGACCTCCGAGCAAAAAAAAAAAAAAAA

Cytochrome C subunit three (GenBank accession No. AY691677)

R124 nucleotide sequence, incomplete, using T3 primer

ATACCATCTTGTTTGACCCAAGCCCATGGCCTCTGACAGGGGCCATGGGTTCCTTACTCCTGACCTCAGGCCTAGCGGTATGGTTCCA
CACTTCATCCACAACCCTTATAAAACTAGGCCTTCTAACCCTCATGATAACCATAATCCAGTGATGACGAGACGTGATCCGAGAAAGT
ACATACCAAGGACACCACACCTTGGGCGTACAAAAAAACATACGATATGGGATAATCTTATTTATTACTTCAGAGGTTTTCTTCTTCC
TAGGGTTCTTCTGAGCCCTATATCACGTGAGCCTAGTCCCTACCCCAGAGCTAGGAGCAGAGTGACCCCCAACTGGAATTATCCCACT
TAATCCAATAGAAGTCCCACTTCTAAACACAGCTGTACTCCTGGCCTCAGGGGCAACAATCACCTGATCCCACCACACAATAATAAAA
GGAAATAAAAAAGAAGCAACTCACGCCCTAATAATTACCATCACACTTGGAATCTATTTCACTGCCCTACAGCTGTCAGAATATAAAG
AAACTCCCTTTACTATCTCAGATAGTGTCTACGGTTCCTTGTTCTTTGTAGCCACAGGATTCCACGGACTCCACGTCATAATCGGAAC
CACCTTCTTACTAGTCTGCATACTACGACTAGTTCAATCCCATTTCACA

Cytochrome C subunit four (GenBank accession No. AY691674)

R 144 nucleotide sequence, complete, using T3 primer

TCCGGTTGTAGAGGACACGGGCCGTCTCGGGATGTTGGCTGCTAGGGCATTCAGCCTTATTGGCAGGCGGGTTTTGTCCACTTCTGTT
TGTGTAAGAGCACATGGGCACGAAGTTACAAAAGCGCCACATTATACTCAGCCCGTCTATGAGGATTACCCTCTGATTCCTTTGCCGG
ATATTCCATTTATACAAGACCTGAGCCCTGAGCAGAAAGCCCTGAAAGAAAAAGAGAAGGGGGCTTGGACCTCCCTCACCCCGGAGGA
GAAGATTGCTCTGTACCACATCAAATTTGACAAAACATTTGCTGAAATGCTGAAGCCATCGAAAGAATGGAAGACTGCGTTCGGTTTA
GCTGGCTACCTGATTGGCCTCGCGGCTTTATTTTTCATTTGGGAGGTTCTGTATGTTCTGAAACCAGCCCCCCACACTTTATCGGAGG
ATTGGAAAGCCATGGAGCTCCGGAAGCATCTGGATATGAAACCGGATCCCATTATGGGCCTTTGCTCCAAGTGGGATTATGAGAAGAA
CGAATGGAAAAAATAAATACCTTTCAGGAAATCTCCACGACTTCTCTCGGGATGTGAAAGTCTGAAACCATTTCTTCATCTCTAGGTT
TGCAGCCTGGCTTCTGCCTCGGATGAAATAGAATCGTATCCTTGGTTTAAACCATAACAGCTTTATGTACTCGGAATTGCTGAA

Dehydrogenase (GenBank accession No. AY702456)

R 40 or RW 7 nucleotide sequence, incomplete, using T3 primer

two subunits in one sequence

AACAATACTATACCTAGCCTTCATTATCACCTTAATAGGCCTGTCTATACAAAATAAACACCTTATACTAGCACTTATGTGCGTAGAA
ACAATAATACTGCTCCTCTTCACAATACTAGTAATTTTCCTTTCTTCTTCCCTCGCACTATCACAAACCCCAATACCCATTATCCTAC
TCACTTTCTCAGTTTGTGGGGCAGCAGTAGGATTAAGCCTCGTTGTTGCAATTACACGAACCCGAGGAAATGACTTCCTAAATAGCCT
CAACCTACTATAATGCTCAAACTTATTTACATAACTGTTATATTAATCCCAACGACACTGTTAACTAAACCAAAAGCCCTTATACAAA
TAACAACCGCCTACTCCTTCATTCTAGCTTTTCTCAGCCTTAACTTTTTAACCCCTAAATCTAACCTCTATCTATTTCTAGATGGTGT
CTCAGCTCCTCTACTAGTGCTCTCCTATTGACTTTTACCAATAAGAGTATTAGCCAGTCAATTCACACTATCTAAAGAACCCGTACAA
CGACAACGCACATTTCTAGCAACTATCGGCCTCCTGCAATTATTTATTGCATTAACATTTTCAGCCTACACAATAACCCTAATATATG
TAATATTGGAACTACCTAATCCCACCCCTAATATCATCACACGATGGGGGCAACAGGCCGAACGACTAACAGCAGGCACCTACT

No matches or ORF

Wel 12 nucleotide sequence, low match to centromere (38%).

GGAATTTTTTTGAGGGGAGCGGGGAGAAGCCTGTACCCTGCACTCATTCCTAGGGAATTATATAGCTTGAAACCTTCCTCGGGGACG
TTTCTTTTCCTTGGTGCTCAGCTGCATTTCAGTTCTGTGTTTTGCTTCAGTTCCCATTCTCCCCTGATACTTCTGACTTCATTTACTC
CATTTCTTTACTTCTAATTGCAACTTTTCCTGAGGCGGAATTAAAGCAGATGTTGAATGTGTTGATGCAGCCTTCCGTTCGCCGTGCT
GAGCTGTTTTTTTTTTCTTTTCTTTTTTCTGTGACCTGCTTTTGAATTGTGCTGACGTAAAGATGATTCTCTTCTTGAGGGGGGTTGT
TTCGTTCACCCATTCAGCATTTAGTTACATCTTGAGACTCCTTCTCCTGGGTTGCTGATCAGGATGGGCTGTCAGACCTGGCTGCAAA
AATCAAAGTGACCTCAAGATGGTGGCAAAGAGCCAGTTTGGGCCTAGTAGTGATTAAGGCAGCAGGTTAGAAACCAGGAGACAAGTTT
CCTGCCTGAGCCAAACCTGGTTCCAAGAGAGCAACATAAGACAAAGGCAGCAGCATAACCTTTTAATGTTCATCTATGAATCCTGTTC
TTCACTGCTTCCAACTAATTAGCTCTGAAAGAAAGAGCCTTCCAAGTTTTGCAAGGCTGCCAAAAAATAACAGATAAGAAATAGTTTA
CAATACAAGATAATATCAACTGTAATGTCCATGAGGCTGAGTTTCAAAACGTCTTTGCTTCCTACAAAGAACATTCGCTTCACAGCTG
GCTTTTATCTTCTTGAAGGAGGGGCCATTACCTTGCAGCCTTATCCCGAGTTGCCCATGCTGTTGTAACTGCTCTTTCCTCTGAGCAA
TCCTGCACGCACGCGCACTTGGCACAGGCTCCTCGGGAACCTCCTCATCACTGCTGCCAGCCCCCACAATCTCTGAAGGCAGCAGTCC
ACTCCCCAATGGTCCTGGCCCTTCACCTGAGTCCTCGCTCTCCTCAGCCATCCACACCTGCTGCTGGCTAACCACAACAAGAGGGTTG
GACTACAAGACCTCCAAGGTCCCTTCCAGCTCTGTTATTCTGCTCATTAGAGGCCTGCTGAAATCTACTATTGAACATTCAGCGCCAT
CTGAGTCAATATGTCTTCTTTCAACTGTTTTCCGGGAAGGGCCTGTTTACCAGGAGATGCACTGAAGGTTTGAAAGCTAATTATTTGT
GTGATTTATTTGCAGGGGAGGCAGTAAAAAAAAAAAAAAAA

Wel 16 (T3) and R 6 (T7), no internal sequence, no match

Wel 16 nucleotide sequence, using T3 primer

TATGTAAATTTTATTTTATTGCAAGCAGATTTAAACATCTACTGCTTTATAGAGAATCTACAGAAAGTCCCAAAATATGGATATAAGA
ATTCATGTTGTCTACAGAAATGAAAGTTTAAAAACAGCACAGAAAATAAACTTCACATCAATGCACATATATATATTGTATTTATATA
TATTTATATCAACTTAATAATTGAGACTGCTTTGAACCTTTTAATGAAGTATTATAGATTAATCTAACACAGATTTTAAAGGCTGAAT
TATCAGGCAAGTGAACGTATCACTGTACCATTTACAAATACATGTCAGTATTTAGTGCTGATGATTATAGATATTTTAATGATTAATG
TTCTAATAACTACGTTCCGCTTTTCCCAAGAGCATTTTCTGCCAATTCTACTTTGCAATATAGATTGAAAGATTATTGAGAACAGTTT
GCGCATCACAGAATTTCAGACATACTTAAAATTCTGTAATTTTGACAAAGGTAAAGCTATAGAAACTGATGTGTGTAATTATACAATG
TACAATCATACACATAATTATTTCTTGTATAATACTTTTGACATGTTCTGTTAAAGCTTTCTGACATGATCTTATTGATATTACATGT
GTAATTTCTCTGATATGTATATGTATAATAACAGATCGATGCAGCAGATTAATGGTTGGTCA

R6 T7 nucleotide sequence

CGTTCCCACTCAGATCAAAAAAAATTTCCATCACCAAATGGGGGCAAGCATCGCATTGAGCTAATAACCAGTTTTACGTAATGACTGC
ATATCTCACTTATTTGGTAGAATTCAATACTGGGTGCACCAGTGTACATATATTGAGATTTTGTGCATAGGGGTTTCTACCCTAGAAT
TCTACACACCTGCCCATTTATAGAAAGGCAGTGAAGGAAAATCGAAGTTAATACCTAGATATCTTTTCCTTTTGTCATTTTCCTAAAA
TATGATTAAAACCCACCTTGTAAATGAAATGGAGCTTTTAAATTCAAAACTGTCTCCTAACTTAATGTAATGAGAGGGATGCCAGATT
TGATCATTGTTAAAGGAGACCTATTGAGTTTAATGTGAAGTCTAGAATAAGCTCCTAGAAGGAAATGGTCAGAAAAGTTTTTTTTTAA
AAAAGTCAAGAAAGTGTCAGCCATTGCATGATTAAAGCCCGGCCTCTTTTTATGTGGGTGATAAAAGGGGGCAGGGTTTTGATTGTTC
ACTCTCAGGCACTAGTTGCCTTTTTTGGACATGTGCATCACACACACACACACTGGCAGATGCCCCTTGAACTCAGTGGTTCAATGTT
TTTAATGTTTTTTTTTCCTCTACAACTACCATAANGTTCGGGGCCCGGNCA

Wel 10 24/3/03, no matches

Wel 10 Nucleotide sequence, using T3 primer

CTTAGGAACAATACCAGTTAACTTTTTGCCACCACTTTAATAAATTCTTTTTAACTTTCGGCAGTTAAAACCTGTACAGATACTGCTA
TAAATATTTTTTAATATAGATGTCCTTTCTCAAATTGCTGAGAGTGACTAGTTCGCAAAAAGTTAATTCTCCAAGACACTGAGGATCA
TTCCAGTTTTAGGAAAGTATCCATTTAACTTGTTTATAAGTGAGGAAAAAGTTGTTTTTAAGAGTATGCACATTCATTTCAATTATGC
TTCTTTTATCAAATTTGAACCAATTTTAAAGAGTTATCTGGTTAAAAGGCAGAGTTTAAAAAAAAGTTTCTCAAATTGACTTGTAGAC
AAGGGAAAGAAATTTATGCCATGACTGTTTGAGATACAATACATGCATGAAACAATATGCATAAAAATTAATTAGTTTTCTTTATCTG
GCTCATGATAAATATGTTTTATTCAGAAGAGAAGTTAAAATTGCACTTCAGCACTGCTAAAACTTTCCCTATAACCAGACATTGGAGA
ACTATGGATGACTTAATTTATTTTATGTGCAATGCAAGATGATTTTTAAAACATTATGGATTACAATCCAATTTAATTGGTTAATGAT
TTGGATATAGGTAATATGACTGGTGCAGTCTTTGGACATCAATGGGGTTTTAATAGCTTTGGTGGTGTGGTTGCATCTCTTTCGTGAT
AATTTTAGCACTCCACTGTTCTATATATATATGTTTACTT

R 138/R 139, no conclusive matches

nucleotide sequence using T3 primer

TTTTTTAGTATTAAAATTAACTTTTATTTGGCCAATGAGTTCCATTCCTCTGAGCATCATGGATGCTTAAAATGAATTCATCCTCTTT
GTAATACAGACTTTCCATGGCTCTCAAGTATCCCCACAAAACTCCTTAGTTATCAAGTGTCCTTTTTGTTAGATTCAGAGAAGTTATT
TCCCAACAGTTCCCAGAAAACCCATTGCAAAATAACGTGTAGATAGCAAGGCTTTTGTTTCATTGCAGGTGAGATAGCAACTCAAGTT
TGATTTCGCTTTAGGTAAGAAGGCAATTGGACTCTCATTCCTCAGCAATGGTTTCCTACCCTTCCAGATCTTTGGATGACAGAAATCA
ATTGTACAGTATATAAAGAGGACATGAGACTATGCAAATAGTTAAGAGGACCTACTATACCCCACTTATTCCCTTGGTCAGCCTAGTG
ATTTCCTCCACACTGGAATGGTCCGGGGTAAGAAAAAAACAACAACAATAAAAGCATAAGGAAAAAAAGCTGGGACAATATCCAAGAG
CCTGCTGGGTCAACAGCAGCATATGTCATTTAGACAAAGTGTTATTAATGTTTAAGGATGCCTTACTCATGAAATTCCCAAGTTAGTT
AGGCAATAGGACATATTATCATTTCAATGTGCTTCTACCCAGGCCGCAATACTCTAAGGAAATGTACATCACAGTTTGCAAATGAACA
GAAGAGAACACAGACAGAAAAAGACCCAGCAGG

R148, no conclusive matches

R148 nucleotide sequence using T3 primer

GTAGAGTTCAGAGGGTACTGTCACCAATTTACAGCAGTGCAGAACCACAGGAATGGGGCTGTAGCATCTGGGGAAGCAATCATCATCC
ATGTTTTGCACACAGCAGCAATCATCAATTATTTCTTCTCTTTATGGAACCAGTCTCTAGGCAAACCATTGCCCAGCCAGACCACATT
CATTTTTATTTGAAATACTGGTACTAAATCCCCAAGGAAACAAACCCATCTACTTTCCTTTCTAACTTCCAATGTTCTTCCTTAAAGC
CTAGGTTTATCCTGTACATCTTGGACAAAAAAAAAGATGCTTTATTAGTCACAGAGGCCTCAAAGTTGCCACAAGCGAGGCATGGTTTT
TCACTTTTGCAGAAGAGTGCAAAATACCTTTAAGCATATTTTGGCCACCTGATGACCTAGACCACGGGTGTCAAACTCCACCGCGTCA
TGTGCCGTATCACGATGTATCTAATATGCCTTTGTGAAGCCATGAGGTGGGCATGGCCTGCACATGACTGCATCCGGTCCACAGGCTA
GNCACTTTGATACTCCTGGCCTAGACTGATTCGTGACGGGTGATTGCAAAGGCTGAACTGTCATGGCACAATACTCTTTTACCTTGCT
TTAGGGTATNCCTTCGANAGAATTNTCATAACTG

Appendix IX: Buffers and Solutions

Buffers and solutions

All buffers used (GTE, IPTG, SSC, LB, SDS, sodium acetate, TE, TBE, Phenol:Chloroform,Western and SDS buffer solutions) were prepared as described by Sambrook, *et al.,* 1989). All other variations are listed below.

Agarose Stop mix

Combined: 0.6 ml 0.5 M EDTA pH 8.0, 50 µl 1 M TRIS pH 7.9, 1.5 ml glycerol and 0.5 mg bromophenol blue to a final volume of 5 ml with water.

SDS PAGE Solutions

SDS PAGE Gel

Recipes for SDS polyacrylamide gels used.

Resolving SDS Page Gel

Denaturing	Component Volumes (ml) for 2 Gels		
	7.50%	12%	15%
30% Bis Acrylamide (37.5:1)	3	3.6	4.5
1.5M TRIS-HCl pH 8.8	3	2.25	2.25
ddH_2O	5.5	3	2.1
10% SDS	0.090	0.0090	0.0090
TEMED	0.0036	0.0036	0.0036
10% APS	0.0036	0.0036	0.0036
Native	8%	12%	15%
30% Bis Acrylamide (37.5:1)	3.0	4.5	5.625
1.5 M TRIS-HCl pH 8.8	2.8	2.8	2.8
ddH_2O	5.25	3.75	3.0
10% Nonidet	0.003	0.003	0.003
TEMED*	0.0045	0.0045	0.0045
10% APS*	0.0045	0.0045	0.0045

Stacking Gel			
Denaturing Component Volumes (ml) for 2 Gels		Native Component Volumes (ml) for 2 Gels	
30% Bis Acrylamide	0.54	30% Bis Acrylamide	0.45
0.5 M TRIS-HCl pH 6.8	0.9	0. M TRIS-HCl pH 6.8	0.75
ddH_2O	2.1	ddH_2O	1.75
10% SDS	0.0036	10% Nonidet	0.0075
TEMED*	0.0036	TEMED*	0.003
10% APS*	0.003	10% APS*	0.0025
*Add these reagents immediately before use.			

Cracking Buffer (Stock)

Combined 350 µl TRIS 2M, 1.5 ml Loading Buffer (2X or 4X), 250 µl DTT (1mM), 250 µl 20% SDS

Silver Stain solutions
Silver stain recipe used within this project

		250 ml	1L Stock
Fixing solution:	Ethanol		400 ml
30 min	Acetic Acid		100 ml
	Stock: made up to 1.0 litre with ddH_20		
Incubation solution	Ethanol	75ml	300 ml
30 min-overnight	Sodium acetate.$3H_2O$	17.0 g (41g anhydrous)	68.0 g
	Glutaraldehyde (25% w/v)*		1.3 ml
	Sodium thiosulfate, $Na_2S_2O3.5H2O$	2.0 g	
	Stock: Make up to 250 ml with ddH2O		
Wash: 3 x 5 min	Distilled water		
Silver solution:	Silver Nitrate	0.25 g	
40 min	Formaldehyde*	50 µl	
	Made up to 250 ml with ddH_2O		
Developing solution: (anhydrous)	Sodium carbonate		25.0 g (65 g $10H_2O$)
15 min	Formaldehyde*	25 µl	
	Made up to 250 ml with distilled water ddH_20 to 1 lt		
Stop solution:	EDTA-Na.$2H_2O$		14.6 g
2 x 5-10 min	Stock: made up to 1 litre with distilled water		
Wash: 3 x 5 min	Distilled water		
Preserving solution:	Glycerol		100 ml
20 min	Stock: make up to 250 ml with distilled water		

*Note: Add these components immediately before use

Primers
Primers used for sequencing clones in Chapter 5.'
Primers were produced when deletion and religation was not possible to continue sequencing of the clone. Primers were produced from nucleotide sequences near the end of the incomplete sequence. Sequences were chosen with consideration of the most beneficial melting temperature, length, lack of hairpin production and a lack of duplication within the sequence. These sequences were sent to Proligo Australia Pty Ltd Southern Cross University, Military Road, Lismore NSW 2480 Australia for the primer production.

Stock Primers
T7 5'-TAATACGACTCACTATAGGG-3'
T3 5'-ATTAACCCTCACTAAAGGGA-3'
SP6 5'-TATTAGGTGACACTATAGAAT-3'
FUP 5'-ACTGGCCGTCGTTTTAC-3'
RUP 5'-CAGGAAACAGCTATGAC-3'

PROLIGO primers

Clone reference Number	PROLIGO primer sequence	Primer reference No.
R5	5'- CCAGACATTGGAGAACTATGG -3'	R5
	5'- AGAAACACTTCACAAGGTGC -3'	R6
R14	5'- ATCGCCCAACAAACACAACCGC -3'	R7
	5'- TTCAGCACGCCATAAATGCCACCC -3'	R8

R18	5'- TTCTGGTCAAGCCTGTCTGATGGG -3'	R9
R20	5'- TCAGACAAATCCTGGTGG -3'	R10
	5'- GTTCCCCAAAATGTATGCTG -3'	R11
R21	5'- GATGACATTCCTTTCGGG -3'	R12
	5'- TCATTTCCTCATCCTCGC -3'	R13
R36	5'- CGAATACGCTTCAAGATACG -3'	R14
	5'- CAAGGAGAACGCCATTTG -3'	R15
R 38	5'- TGCTGGCTTTCAGTCTCAC -3'	R16
	5'- TTGGATGCTGGCGAGAATCTGG -3'	R17
R 42	5'- GGTATTGTGGCTTATCTGCG -3'	R18
	5'- ATTTACCAGCCCCATCTG -3'	R19
R 46	5'- ATGGGAATGAGTCAGTGGGC -3'	R20
	5'- CAGAGGTGGTCCAAGTTTG -3'	R21
R 50	5'- ATAGACCTGATGAGGCACCAGC -3'	R22
R 60	5'- TTATTCCCTTGGTCAGCC -3'	R23
	5'- TTCATTCGCTGTGGAGTCC -3'	R24
R 65	5'- TTCGTTCACCCATTCAGC -3'	R25
	5'- GCGAATGTTCTTTGTAGGAAGC -3'	R26
R50	5'- ATGAAAGAGCCAGCCAGGATGG -3'	R27
R8	5'- CCTGATGGATTCAACTCCC -3'	R28
R8	5'- CACTGAAAACAACTGTGGC -3'	R29
R8	5'- CATCTGCTCACAAAGAAGGAG -3'	R30
R5	5'- CTTTGGTTGGTGTTGGTTTG -3'	R 31
R 27	5'- AACAGACCCGTCCAAAACCG -3'	R 32
R5	5' AACCCTTAGGTGAGCACAGC 3'	R 33
	5' AAGGGTAAGGGTGGATC 3'	R 34
R18	5'- AGACTGGGACTTGACTTGG -3'	R 35
R 21	5'- ATCTATGACCTGCCAACGC -3'	R 36
R 50	5'- AATGTGCCCTCTTCCCACGAGAAC -3'	R 37
	5'- CCAAACCAGAAATGTGGG -3'	R 38
R 65	5'- GACCTTCCACAACTTGAAC -3'	R 39
R42	5'- ACTGGAAAGGGGGAAACC -3'	R 40
	5'- ACTTTCAGCAGTCCCATTC -3'	R 41
R 46	5'- GCTCAGGACAAACTTGATAAGC -3'	R 42
R5	5'- CAGGGGCTAAAGCAAAATC -3'	R 43
R 18	5'- TCAGAGGTGGTATTGGCTGG -3'	R 44
R 21	5'- CCCAAGAGCATTTTCTGC -3'	R 45
R 42	5'- TAAGAAATGGGGACGAGC -3'	R 46
	5'- TTCAGGGTTCACTGTTGGG -3'	R 47
R 50	5'- TTGAGACCGTTTCCACAGCC -3'	R 48
R 21	5' AGTCTTTCGCTGGGTCTTGG 3'	R 49
R 50	5' CGGAATCATCTTCACAGCC 3'	R 50
R5	5' CCGACATTTTCAATCCTCCAGAAG 3'	R 51
R 15 conserved region (minus)	5'- CAGTAGCAACCGTAGT 3'	R 52
R8	5'-TGTCTCACCACACTTGGC 3'	R 53
R 17	5'- TTTGATGCCAAGCGTCTC -3'	R 54
	5'- TGTCATCCTCCACAGTCTGC -3'	R 55
R 37	5'- TACATTGGTGGACACTGGG -3'	R 56
	5'- GGAGGTAGGAAAGAGGGAAG -3'	R 57
R22	5 '- AAAGAAACGCACAGGACC -3'	R 58
	5'- CACTTATTCCCTTGGTCAGC -3'	R 59
R 17	5'-ACCCATCAGAATAGCAGCC 3'	R 60
R 22	5'-ACTTGCTTGAGTTGGCAGC 3'	R 61
	5'-TAAGCCCCACTTGATGAGCC 3'	R 62
R37	5'-TGTCCAAAGCATCAGAGGC -3'	R 63
R 37	5'-ATCACCTCAAAACCACGC-3'	R 64

AQIS

AUSTRALIAN QUARANTINE AND INSPECTION SERVICE
DEPARTMENT OF AGRICULTURE, FISHERIES AND FORESTRY

Quarantine Act 1908 Sect. 13

Phone: (02) 6272 4578
Fax: (02) 6273 2097
File Ref: 01/4475

Permit to Import Quarantine Material

Permit: 200105617 **Valid From:** 17 May 2001 **Valid To:** 17 May 2003 **Page** 1 of 6

Importer	Exporter
James Cook University Department of Biochemistry and Molecular Biology Townsville QLD 4811 Attn: Dr Subhash Vasudevan	All exporters All addresses All countries

You are authorised to import the following material under the listed conditions

Note: This permit covers AQIS quarantine requirements only.

All imports may be subject to quarantine inspection on arrival to determine compliance with the listed permit conditions and freedom from contamination. Imports not in compliance or not appropriately identified or packaged and labelled in accordance with the import conditions they represent may be subject to seizure, treatment, re-export or destruction at the importer's expense.

Additionally, all foods imported into Australia must comply with the provisions of the Imported Foods Control Act 1992, and are consequently liable for inspection and/or analysis against the requirements of the Australian Food Standards Code.

All imports containing or derived from Genetically Manipulated Material must comply with the Genetic Manipulation Advisory Committee Guidelines.

It is the importer's responsibility to be aware of and to ensure compliance with the requirements of all other regulatory organisations prior to and after importation. Examples of organisations that may impose requirements on imported products include: the Australian Customs Service, Environment Australia, State Departments of Agriculture, State Departments of Health, Therapeutic Goods Administration, Australia New Zealand Food Authority, National Registration Authority (for Agricultural and Veterinary Chemicals), Commonwealth and State Environmental Protection Authorities. PLEASE NOTE that this list is not exclusive.

Import conditions are subject to change at the discretion of the Director of Quarantine. This Permit may therefore be revoked without notice.

Commodity Name	Condition Number(s)	Country	End Use
Cell lines (Human and insect)	PC0820	All countries	In-vitro
Antibodies (Human antibodies raised against synthetic material or antigens from multicellular organisms)	PC0819	All countries	In-vitro
Antibodies (Rabbit antibodies raised against synthetic material or antigens from multicellular organisms)	PC0819	All countries	In-vitro
Antibodies (Rodent antibodies raised against synthetic material or antigens from multicellular organisms)	PC0819	All countries	In-vitro
Antibodies (Sheep	PC0600 AND PC0819	All countries	In-vitro

[illegible]

[redacted]

Authorising Officer (for Director of Quarantine)

Printed Name Narelle Clegg **Date** 17 May 2001

Stamp: DEPARTMENT OF AGRICULTURE, FISHERIES & FORESTRY QUARANTINE AUSTRALIA