

(19) World Intellectual Property  
Organization  
International Bureau



(43) International Publication Date  
5 August 2004 (05.08.2004)

PCT

(10) International Publication Number  
**WO 2004/065415 A2**

- (51) International Patent Classification<sup>7</sup>: **C07K 14/435** (74) Agents: **WEICKMANN & WEICKMANN** et al.; Postfach 860 820, 81635 München (DE).
- (21) International Application Number: PCT/EP2004/000423 (81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.
- (22) International Filing Date: 20 January 2004 (20.01.2004)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:  
03001232.2 20 January 2003 (20.01.2003) EP  
03026613.4 19 November 2003 (19.11.2003) EP
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- (84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).
- Published:  
— without international search report and to be republished upon receipt of that report
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: L-AMINO ACID OXIDASE WITH CYTOTOXIC ACTIVITY FROM *APLYSIA PUNCTATA*

(57) Abstract: The present invention relates to a cytotoxic polypeptide which is an L-amino acid oxidase isolated from the ink of the sea hare *Aplysia punctata*.

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**L-amino acid oxidase with cytotoxic activity from *Aplysia punctata*****Description**

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The present invention relates to a cytotoxic polypeptide which is an L-amino acid oxidase isolated from the ink of the sea hare *Aplysia punctata*.

10 The sea hare *Aplysia* produces a pink-coloured ink, which has cytotoxic activity towards several eukaryotic cell lines. WO97/16457 discloses a partial sequence from an *Aplysia* protein, which allegedly has anti-tumor activity. Cyplasin L (558 aa, NCBI accession number 11967690) and cyplasin S (421 aa, 11967688; Petzelt and Werner, 2001, Cell Biology  
15 International, 25(2):A23) both include parts of sequences disclosed in WO 97/16457. Cyplasin S exhibits 95% sequence identity to cyplasin L. Cyplasin L is produced in the nidamental gland but neither in the ink gland (including the mantle region) nor in the opaline gland of *Aplysia punctata*. Thus, it is concluded that cyplasin is not a component of *Aplysia* ink and is  
20 not responsible for the cytotoxic activity of the *Aplysia* ink. A detailed description of *Aplysia* anatomy and a dissection guide can be found in the internet in Richard Fox, Invertebrate anatomy (1994, <http://www.science.lander.edu/rsfox/>).

25 The overall aim in tumor therapy is the selective eradication of transformed cells without harming healthy cells. Several glycoproteins isolated from sea hares (*Aplysia* species) have attracted attention because of their anti-tumor activity, e.g. aplysianin A from *Aplysia kurodai*, or cyplasins. The underlying mechanism for such activity has however not been elucidated  
30 so far. Recombinant intracellular cyplasins seem to be non-toxic, whereas the extracellular cyplasin is cytotoxic (Petzelt et al., Neoplasia, 4:49-59, 2002).

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WO 03/057726 discloses a cyplasin which is devoid of a functional secretory signal sequence. Since cyplasin only causes eukaryotic cell death from outside, the cyplasin of WO 03/057726 can thus be functionally expressed in eukaryotic cells without killing these cells. When acting from  
5 outside, cyplasin induced cell death is accompanied by fast depolymerization of the actin filaments. Expression of bioactive cyplasin S and L in prokaryotic host cells is not possible.

WO 02/31144 discloses a further cytotoxic factor isolated from the ink of  
10 *Aplysia punctata*. Fragments of the amino acid sequence of the factor are disclosed. No data were presented demonstrating that this factor has any oxidase function or has any properties related to an oxidase.

At least two main phenotypes of cell death are described: apoptosis, a  
15 genetically fixed physiological form of cell death, is accompanied by shrinkage, membrane blebbing, nuclear fragmentation, and final disintegration into so-called apoptotic bodies. In contrast, necrosis is a pathological process characterized by membrane disruption and cell swelling. Cell death induced by reactive oxygen and nitrogen species  
20 (ROS/NOS) might lead to apoptosis and necrosis but also to other forms of cell death, which cannot be clearly assigned to one of these main forms of cell death.

The cytotoxic factors derived from the sea hares so far have several  
25 disadvantages which might hamper its application. The biological function and the nature of the cytotoxic activity, which are prerequisites for the development of a lead compound, are not known so far. Aplysianin A contains a dinucleotide binding fold and the so-called "GG motif" which are found in many flavoproteins. The GG motif has also been described in  
30 cyplasins (Petzelt et al., supra). Based on this knowledge, the factors can be applied in its entirety only, because the domains relevant for proper function and cellular receptors are unknown. The administration of an

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entire non-self protein to an animal or a human might cause severe immunologic complications.

5 The dinucleotide binding fold and the GG motif are found e.g. within the N-terminal domain of FAD containing enzymes (e.g. reductases, dehydrogenases, hydroxylases, peroxidases, and oxidases). FAD containing enzymes can be classified into five groups GR1, GR2, FR, PCMH, and PO according to the sequences of their FAD binding domains and additional conserved sequence motifs (Dym and Eisenberg, Protein Science, 10:1712-1728, 2001). The consensus sequence of GR1 and GR2 is GxGxxG. The GG motif RhGGRhxxT/S is commonly found in oxidases, e.g. L-amino acid oxidases, monoamino oxidases, polyamine oxidases, and putrescine oxidases, wherein x describes any amino acid, and h describes a hydrophobic amino acid.

15 L-amino acid oxidases catalyse the formation of  $H_2O_2$ , ammonia, and an alpha keto acid from an amino acid in the presence of oxygen and  $H_2O$  (Geyer et al, 2001, Eur. J. Biochem. 268, 4044-4053). An L-lysine alpha oxidase (EC 1.4.3.14) for instance can be obtained from the fungus Trichoderma spec. (Kusakabe et al., J. Biol. Chem. 10:976-981, 1980) which shows antimetastatic effects (Umanskii et al., Biull Eksp Biol Med. 109:458-9, 1990, Khaduev et al., Biull Eksp Biol Med. 112:419-22, 1991). The Trichoderma L-lysine oxidase is a dimer with a molecular weight of 112-119 kDa. A further L-lysine oxidase obtained from the fish Chub mackerel is a dimer and has a molecular weight of 135 kDa (Jung et al., J. Immunol. 165:1491-1497, 2000) and induces apoptosis. Apoxin is an L-leucin oxidase from the rattlesnake (Crotalus atrox) venom which induces apoptosis in tumor cells and vascular endothelial cells in vitro (Torii et al., J. Biol. Chem. 272:9539-9542, 1997). A cytotoxic L-lysine alpha oxidase is described in the art which penetrates into Jurkat cells and there activates oxidative deamination of L-lysine and correspondingly the peroxide formation. Conjugates of the enzyme with monoclonal antibodies

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against the CD5 receptor cannot penetrate into the cells and are assumed to produce toxic  $H_2O_2$  outside the cells. The conjugates have a reduced cytotoxic effect, although the effect of conjugation upon enzymatic activity is negligible (Zhukova et al., Vopr Med Khim 2001, 47:588-592). Another

5 L-lysine oxidase obtained from the snail *Achatina fulica* and producing  $H_2O_2$  is found to have an antimicrobial effect. This oxidase might be useful as an agent against pathogenic bacteria (Ehare et al., 2002, FEBS Letters, 531:509-512).

10 Most known alpha amino acid oxidases which produce  $H_2O_2$  possess a broad substrate specificity. The L-lysine alpha oxidase from *Trichoderma viride* (EC 1.4.3.14, Kusakabe et al., supra) is specific for lysine, but also oxidizes L-ornithine, L-phenylalanine, L-tyrosine, L-arginine, and L-histidine to a lesser extent. The L-lysine oxidase of Chub mackerel (EMBL,

15 AJ400781; Jung et al., supra) is specific for lysine and in addition transforms arginine, histidin, leucine, methionine, phenylalanine, and ornithine (specificity 40 fold reduced). Even if these enzymes could be cytotoxic due to their ability to produce  $H_2O_2$ , a therapeutic use is hampered because substrates of these enzymes are available in the body

20 fluid in amounts sufficient to release  $H_2O_2$  everywhere in the body. Under these conditions, possible negative side effects of  $H_2O_2$  are difficult to eliminate.

In addition to  $H_2O_2$  producing enzymes, cells possess a detoxification

25 system which eliminates reactive oxygen species (ROS), in particular  $H_2O_2$ . An important class of detoxifying peroxidases are peroxiredoxins. Peroxiredoxins comprise a class of highly conserved oxidases. In mammals, six different isoforms are known which catalyze the reduction of peroxides by using reducing equivalents that are provided by thioredoxin or

30 glutathione. During catalysis, peroxiredoxin I (Prx I) is inactivated by oxidation of the active site cysteine to cysteine sulfinic acid, a modification which is reversible upon removal of  $H_2O_2$ . Previously, overexpression of

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both Prx I and Prx II has been shown to render cells resistant to H<sub>2</sub>O<sub>2</sub> induced apoptosis.

5 The problem underlying the present invention is the provision of a means for selective generation of H<sub>2</sub>O<sub>2</sub> in target tissues, e.g. in tumor tissues with less toxic side effects upon normal cells. The solution is a cytotoxic polypeptide which can be isolated from the ink of the sea hare *Aplysia punctata* and which is a specific L-lysine and/or L-arginine oxidase producing H<sub>2</sub>O<sub>2</sub> or a fragment or derivative of said polypeptide. The activity  
10 of the enzyme can be modulated by administration of substrate. The enzyme provides a lead structure, and it can be used for target identification.

15 A first aspect of the present invention is a purified polypeptide which exhibits cytotoxic activity on tumor cells and which comprises the amino acid sequence shown in SEQ ID NO: 2, 4, or 6, or a cytotoxic fragment thereof. These sequences are derived from a cytotoxic 60 kDa protein purified from crude ink of *Aplysia punctata* via anion exchange chromatography and gel filtration (see examples 1 and 4). Thus, the  
20 polypeptide or the fragment is termed APIT (*Aplysia punctata* ink toxin). The purity of the fractions can be determined by SDS-PAGE and silver staining.

25 The cytotoxic activity of APIT or the diluted crude ink can be measured by the reduction of the metabolic activity of eukaryotic cells. A person skilled in the art knows suitable methods and cell lines. For example, the metabolic activity of Jurkat T cells can be measured by the addition of WST-1, which is a tetrazolium salt converted by cellular enzymes of viable cells, e.g. by the mitochondrial dehydrogenase, to a dark red formazan.  
30 Therefore, the amount of formazan correlates with cell vitality. Formazan can be determined photometrically at 450 nm. Further, dead eukaryotic cells killed by APIT or the diluted crude ink can be counted by adding

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propidium iodide (PI) at 1  $\mu\text{g/ml}$  in PBS and subsequent flow cytometer analysis. PI is a DNA binding dye which is taken up by dead cells with permeable membranes.

- 5 The cytotoxic activity of APIT is reduced by at least 70% after 10 min incubation at 60°C. At 70°C, the activity is almost absent, whereas 0°C to 50°C have no effect upon the activity. APIT shows a loss of activity with decrease of pH, with complete inactivation after 10 min pre-incubation at pH 3. After 30 min treatment with 6 M urea, the activity  
10 of APIT is almost unaffected. At 8M urea, the activity is reduced by about 50% (example 3).

Tumor cells treated with APIT displays a morphology which is neither typical for apoptosis nor for necrosis but rather is typical for oxidative  
15 damage induced cell death. Shrunken nuclei and lack of cell swelling are apoptotic, and early membrane permeabilization is a necrotic characteristic (example 2). The phenotype induced by APIT could be reproduced in Jurkat cells by treatment of the cells with concentrations of  $\text{H}_2\text{O}_2 > 200 \mu\text{M}$ , indicating that  $\text{H}_2\text{O}_2$  is the active compound in APIT cytotoxic effect.  
20  $\text{H}_2\text{O}_2$  concentrations  $< 100 \mu\text{M}$  induced apoptosis in Jurkat cells. In contrast to the mode of action of cyplasins, a depolymerization of the active filaments cannot be observed in APIT induced cell death, indicating that the mechanism of APIT action is distinct from that of cyplasins (Example 12).

25

By depriving possible substrates which can be converted into  $\text{H}_2\text{O}_2$  from the culture medium of the tumor cells, it can be demonstrated that no further toxic effect of APIT upon tumor cells is present. Deprivation of L-lysine and L-arginine from the medium prevents cell death completely.  
30 This phenomenon can be observed within a period of 6 to 8 hours during cultivation of tumor cells. In a detailed analysis of the enzymatic activity of APIT, media containing single amino acids (20 L-amino acids, D-lysine)

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confirmed that L-lysine and/or L-arginine is converted into  $H_2O_2$  and the respective alpha keto acid to the same extent, whereas no conversion could be measured with any other of the remaining 18 L-amino acids and D-lysine (example 7). The production of  $H_2O_2$  is independent of the  
5 presence of cells, however, the presence of cells reduces the amount of free  $H_2O_2$ , which might be due to detoxification of the medium by the cells. Catalase (a  $H_2O_2$  hydrolyzing enzyme) prevents tumor cell death induced by purified APIT and by crude ink as well, confirming the conclusion that  $H_2O_2$  is responsible for the ink mediated killing of tumor cells (example 6).

10

Anti-tumor activity also appears after long-term in vitro treatment (> 18 hours) of tumor cells by the cytotoxic factor isolated from the ink of *Aplysia punctata* in combination with an  $H_2O_2$  consuming factor, like catalase. In comparison to tumor treatment with the cytotoxic factor from  
15 *Aplysia punctata* alone, this alternative tumor treatment takes a much longer time to become effective. The interplay of both enzyme activities continuously reduces L-lysine and L-arginine in the medium which are essential for the living of tumor cells. The tumor cells die as a result.

20 In summary, the data demonstrate that the polypeptide of SEQ ID NO: 2, 4, or 6 (APIT) is an oxidase which is capable to produce  $H_2O_2$ . Particularly, the polypeptide is an alpha amino acid oxidase. More particularly, the polypeptide specifically converts L-lysine and/or L-arginine in the presence of  $O_2$  and  $H_2O$  into an alpha keto acid, ammonia, and  $H_2O_2$ . Thus, the  
25 polypeptide is preferably an L-lysine and/or L-arginine oxidase.

A characteristic feature of the active fractions containing APIT purified from crude ink were two absorption maxima at 390 nm and 470 nm, a hallmark of flavoproteins. A flavine nucleoside, particularly FAD is required  
30 as a co-factor for the anti-tumor and oxidase activity of APIT as removal of FAD inactivated APIT (example 5).

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Analysis of the sequences SEQ ID NO: 2, 4, and 6 revealed that APIT comprises a sequence similar to known dinucleotide binding folds which are characteristic for flavoproteins (Fig. 4c). The GG-motif (consensus sequence RhGGRhxT/S) is found adjacent to the dinucleotide binding fold.

5

A further aspect of the present invention is a polypeptide comprising a fragment of the polypeptides of the sequences of SEQ ID NO: 2, 4, or 6 which can be used as a lead structure for drug development. APIT can be digested by a protease without loss of activity. Digestion leaves the substrate specificity unaltered. Thus, the fragment exhibiting cytotoxic activity is an L-lysine and/or L-arginine oxidase. Preferably, proteinase K is used which is a relative unspecific protease resulting in small fragments. Other proteases which can be selected among specific or unspecific proteases known by a person skilled in the art can be used instead of proteinase K. The cytotoxic proteinase resistant domain of APIT is of particular importance for the development of a non-immunogenic, fully active small compound.

Further preferred fragments comprise partial amino acid sequences of APIT which are obtained by peptide mass fingerprinting, ESI/MS, and Edman degradation:

DG(I/V)CRNRRQ (SEQ ID NO: 46),  
DSGLDIAVFEYS DR (SEQ ID NO: 47),  
VFEYS DR (SEQ ID NO: 48),  
25 LFX YQLPNT PDVNLEI (SEQ ID NO: 49) (X=T in SEQ ID NO: 2, 4 and 6),  
VISELGLTPK (SEQ ID NO: 50),  
GDVPYDLSPEEK (SEQ ID NO: 39),  
VILAXPVYALN (SEQ ID NO: 51) (X=M in SEQ ID NO: 2, 4 and 6),  
ATQAYAAVRPI PASK (SEQ ID NO: 37),  
30 VFMTFDQP (SEQ ID NO: 52),  
SDALFFQMYD (SEQ ID NO: 53) (FFQ is FSQ in SEQ ID NO: 2, 4 and 6),  
SEASGDYILIASYADGLK (SEQ ID NO: 54),

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NQGEDIPGSDPQYNQVTEPLK (SEQ ID NO: 55) (PQY is PGY in SEQ ID NO: 2, 4 and 6)

While not wishing to be bound by theory, the FAD group which is tightly  
5 bound to the amino acid chain, e.g. by a covalent bond, might cover possible protease cleavage sites. Thus, protease treatment results in a fragment comprising the active centre of the enzyme, including the prosthetic group FAD. This conclusion is confirmed by the finding that native APIT cannot be cleaved by trypsin, but trypsin can digest  
10 denaturated APIT.

Thus, an especially preferred fragment of APIT which is an oxidase exhibiting cytotoxic activity is a sequence comprising the dinucleotide binding fold and the GG motif corresponding to amino acid residues No. 39  
15 to 77 in SEQ ID NO: 2. This sequence is identical to the sequence of amino acid residues No. 38 to 76 in SEQ ID NO: 4 and No. 21 to 59 in SEQ ID NO: 6. More preferably, the fragment has an L-lysine and/or an L-arginine oxidase activity.

20 Further, the fragment can comprise a stretch of additional amino acid residues which may be selected from SEQ ID NO: 2 or 4 from the sequences adjacent to the residues No. 39 to 77 in SEQ ID NO: 2 or No. 38 to 76 in SEQ ID NO: 4. Preferably, 1-20 additional amino acid can be present at the N-terminus and/or the C-terminus. More preferably, 1-10  
25 additional amino acid can be present at the N-terminus and/or the C-terminus. Most preferably, 1-5 additional amino acid can be present.

A further aspect are polypeptides which are homologous to the polypeptides of SEQ ID NO: 2, 4, or 6, or to fragments thereof, which have  
30 an identity of at least 70%, preferably at least 80%, more preferably at least 90%, or most preferably at least 95%. SEQ ID NO: 2, 4, or 6 describe natural variations of APIT by replacements of single amino acids

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not affecting its function. In further 11 clones, four mutations were found within the sequence comprising the dinucleotide binding fold and the GG motif (Pos. 39 to 77 in SEQ ID NO: 2, see example 4). Taking into account that a fragment obtained by proteolytic digestion is still active as a L-lysine and/or L-arginine oxidase, it can be expected that further modifications of the sequence, e.g. by amino acid substitutions, deletions and/or insertions will not substantially affect the function of APIT. A modified sequence exhibits an identity of preferably at least 70%, more preferably at least 80% and most preferably at least 90% to a reference sequence, e.g. SEQ ID NO: 2. Preferably, the sequence of Pos. 39 to 77 in SEQ ID NO: 2 has a higher degree of identity to the reference sequence than the total amino acid sequence, e.g. preferably at least 33 of 39 amino acid residues (at least about 85%), more preferably 35 of 39 residues (at least about 90%), and most preferably 37 of 39 residues (at least about 95%).

A still further aspect is a polypeptide of the present invention as described above which is a recombinant polypeptide. The recombinant polypeptide is characterized as being manufactured in a heterologous, i.e. non-*Aplysia* host cell, e.g. in a bacterial cell such as *E. coli* or *Bacillus*, in a yeast cell such as *saccharomyces cerevisiae*, in an insect cell or in a mammalian cell. The recombinant polypeptide has preferably an oxidase, or, more preferably, an L-lysine and/or an L-arginine oxidase activity. Expression of the polypeptide can be done by standard expression systems known by a person skilled in the art. For proper enzymatic function, the prosthetic group FAD may have to be introduced into the polypeptide.

The protein of the invention or a fragment thereof may be in the form of a fusion protein, i.e. fused to heterologous peptide or polypeptide sequences. Preferably fusion proteins are genetic fusions, wherein the nucleic acid sequence encoding a protein or a protein fragment as described above is fused to a nucleic acid sequence encoding a heterologous peptide or polypeptide sequence. The heterologous peptide or polypeptide sequence

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may be selected from signal sequences, which provide desired processing and/or transport in a host cell. The signal sequence is preferably located at the N- and/or C-terminus of the APIT sequence. Further examples of heterologous sequences are domains which assist expression in host cells  
5 and/or purification from cellular extracts or culture media. Still further examples of heterologous sequences are targeting sequences which may direct the APIT polypeptide to a desired target site, e.g. in an organism. Suitable targeting sequences may be e.g. single chain antibodies, which may be directed against tumor specific antigens or proteinaceous ligand  
10 sequences, which may be directed against tumor specific receptors.

A further aspect of the present invention is a nucleic acid coding for the polypeptide as described above. The total mRNA of the mantle gland, the nidamental gland, the digestive gland, and the opaline gland can be  
15 prepared by standard methods. The mRNA can be reverse transcribed using the tagged oligo dT oligonucleotide (Oligo 1, Fig. 4b). The tag is a random sequence not expected to be present within *Aplysia* mRNA to be reverse transcribed. PCR can be performed using the degenerated primer (Oligo 2) derived from the APIT peptide VFEYSDR and the specific primer  
20 (Oligo 3) directed against the tag sequence of the oligo dT primer Oligo 1. The amplified sequence can be cloned into a standard vector and can be sequenced by standard techniques. By this strategy, the 3' terminal sequence of the APIT gene can be obtained. The 5' terminal sequence can be obtained by the RACE strategy. The mRNA from selected tissues (see  
25 above) is reverse transcribed using an oligonucleotide derived from the known 3' terminal sequence (e.g. Oligo 4, or Oligo 6) and can be treated with a terminal transferase in the presence of CTP, resulting in a 3'-poly-C-sequence (at the minus strand). PCR can be performed using a tagged primer against the poly-C-sequence (Oligo 5) and a specific primer,  
30 e.g. Oligo 4, or Oligo 6. The amplified product can be cloned and sequenced by standard techniques. Finally, for obtaining full-length cDNA clones, specific primers, e.g. Oligo 8 and Oligo 9 can be used. By this

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strategy, three different clones were obtained and sequenced. The nucleotide sequences are described in SEQ. ID. No.1, 3, and 5 which are identical to 97% (1560 of 1608) of the nucleotides. 42 of 48 mutations are silent mutations which have no effect upon the amino acid sequence.

5

By this strategy, further clones of APIT can be obtained which might have a differing sequence. Since more than ten sequences of APIT are known, specific or degenerated primers may be selected from these sequences, and new clones can be obtained by a single PCR of reverse transcribed mRNA.

10

Thus, the nucleic acid encoding a polypeptide as specified above preferably comprises

- (a) a nucleotide sequence as shown in SEQ ID NO: 1, 3, or 5, or at least the polypeptide coding portion thereof, or the complement thereof, or
- (b) a nucleotide sequence corresponding to the sequence of (a) within the scope of degeneracy of the genetic code, or the complement thereof, or
- (c) a nucleotide sequence hybridizing under stringent condition with the sequence of (a) and/or (b), or
- (d) a nucleotide sequence which is homologous to the sequences of (a) and/or (b).

15

20

The nucleic acid may be a single stranded or double stranded nucleic acid (DNA or RNA). The nucleic acid is obtainable from natural sources e.g. from *Aplysia* by extraction of RNA, construction of cDNA libraries and screening of the library using degenerated oligonucleotides which were deduced from the peptide sequences described above. The nucleic acid is further obtainable by RT-PCR using RNA extracted from *Aplysia* and oligo-dT-primers or degenerated primers. On the other hand, the nucleic acid is obtainable by chemical synthesis.

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Hybridization under stringent conditions preferably means that after washing for 1 h with 1 x SSC and 0.1% SDS at 55°C, preferably at 62°C and more preferably at 68°C, particularly after washing for 1 h with 0.2 x SSC and 0.1% SDS at 55°C, preferably at 62°C and more preferably at 68°C, a hybridization signal is detected.

The degree of identity of the nucleic acid is at least 70%, preferably at least 80%, more preferably at least 90%, and most preferably at least 95% to a reference sequence, e.g. SEQ ID NO: 1, 3 or 5.

Further, the nucleic acid encoding a cytotoxic polypeptide can comprise a partial sequence of the nucleotide sequence as disclosed in SEQ ID NO: 1, 3, or 5. Preferably, the partial sequence is selected from nucleotide No. 115 to 231 in SEQ ID NO: 1, or nucleotide No. 112 to 228 in SEQ ID NO: 3, or nucleic acid residue No. 61 to 177 in SEQ ID NO: 5, or the partial sequence codes for at least one of the eleven fragments of APIT obtained by peptide mass fingerprinting, ESI/MS, and Edman degradation. Further, the partial sequence can comprise a stretch of additional nucleotides selected from the sequences adjacent to the sequence selected from SEQ ID NO: 1, 3, or 5. Preferably, 1-60 additional nucleotides can be present at the 5' and/or the 3'-terminus. More preferably, 1-30 additional nucleotides can be present at the 5' and/or the 3'-terminus. Most preferably, 1-10 additional nucleotides can be present at the 5' and/or the 3'-terminus.

Furthermore, the nucleic acid may encode a fusion polypeptide as described above.

In a preferred embodiment of the invention the nucleic acid is operatively linked to an expression control sequence, e.g. a sequence which is capable of directing expression in a suitable host cell, e.g. a prokaryotic or eukaryotic host cell. The expression control sequence usually comprises a promoter and optionally operator or enhancer sequences which enable a

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transcription of the nucleic acid operatively linked thereto. Furthermore, the expression control sequence may contain a translation signal, e.g. a ribosome binding sequence.

5 The nucleic acid of the present invention may be a recombinant vector which contains in addition usual vector sequences such as an origin of replication, a selection marker gene and/or a cloning site. Examples of suitable vectors such as plasmids, phages or viral vectors are known to the skilled person and are described e.g. in Sambrook et al., Molecular Cloning,  
10 A Laboratory Manual (2nd ed. 1998), Cold Spring Harbor, Laboratory Press.

A further aspect of the present invention is a recombinant cell transformed or transfected with a nucleic acid as described above. The recombinant cell  
15 may be a prokaryotic cell, e.g. a gram-negative prokaryotic cell such as *E. coli* or an eukaryotic cell, e.g. an insect cell or a vertebrate cell such as a mammalian cell. Techniques for transforming or transfecting host cells with nucleic acids are known to the skilled person and e.g. described in Sambrook et al., supra.

20 Still a further subject matter of the present invention is an antibody directed against the polypeptide as described above. The antibody may inhibit the cytotoxic activity of the polypeptide. The antibody may be a polyclonal or monoclonal antibody or a recombinant antibody, e.g. a  
25 chimeric antibody, a humanized antibody or a single chain antibody. Furthermore, the antibody may be an antibody fragment containing the antigen-binding site of the antibody, e.g. a Fab fragment. The antibody may be obtained by immunizing suitable experimental animals with an *Aplysia* polypeptide as described above or a partial fragment thereof or a  
30 peptide antigen optionally coupled to a suitable macromolecular carrier according to known protocols, e.g. by techniques which are described in Borrebaeck, Carl A.K. (Ed.), Antibody engineering (1992), or Clark, M.

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(Ed.), Protein engineering of antibody molecules for prophylactic and therapeutic applications in man (1993). By techniques for producing hybridoma cell lines according to Köhler and Milstein monoclonal antibodies may be obtained.

5

Methods for introducing a prosthetic group into a polypeptide are known in the art. Preferably, the FAD is introduced by a method comprising surface display of the polypeptide on a prokaryotic host, comprising the steps:

- 10 (a) providing a prokaryotic host cell transformed with a nucleic acid fusion operatively linked with an expression control sequence, said nucleic acid fusion comprising sequences necessary for displaying the protein on the outer membrane, and
- 15 (b) culturing the host cell under condition wherein the nucleic acid fusion is expressed and the expression product comprising the recombinant polypeptide is displayed on the surface of the host cell, and
- (c) contacting the recombinant polypeptide with FAD under conditions wherein FAD combines with the recombinant polypeptide and a  
20 functional recombinant polypeptide containing the prosthetic group is formed.

The nucleic acid fusion may be formed using a nucleic acid sequence as described above and further sequences necessary for surface display.  
25 Details describing the prokaryotic host cells, the sequences necessary for surface display of the polypeptide, culture conditions, and the conditions under which the recombinant polypeptide is contacted with FAD are described in WO 02/070645, which is included by reference herein.

30 A further aspect of the present invention relates to diagnostic or therapeutic applications in humans or animals. The polypeptide, and/or a nucleic acid, and/or a recombinant cell, and/or an effector, e.g. an inhibitor

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or activator of the polypeptide as described above can be used in such applications. The polypeptide as described above is able to selectively kill tumor cells. For example, T and B leukemia cell lines, a chronic myeloid leukemia cell line (K562), cells from an orphan and aggressive  
5 osteosarcoma (Ewings tumor: RDES, A673), a small cell lung cancer cell line (GLC4, GLC4/ADR), cervix cancer (Chang), and acute monocytic leukemia (THP-1) show an  $IC_{50} \leq 10$  ng/ml APIT.

Healthy human cells are resistant against APIT-induced cell death. At a  
10 concentration of 40ng/ml, APIT induces a cell death below 10% in normal HUVEC cells (Example 13). This indicates that the APIT  $IC_{50}$  values of healthy cells are at least one order of magnitude higher than the  $IC_{50}$  of tumor cells.

15 Resistance to apoptosis as well as multi drug resistance (MDR) represent severe problems in cancer therapy. It is therefore of particular interest that the polypeptide of the present invention kills apoptosis resistant cell lines as well as MDR cancer cell lines to the same extent as their non resistant counter parts. Over-expression of apoptosis inhibitors of the Bcl-2 family in  
20 cancer cell lines does not protect from APIT mediated cell death, confirming that APIT induces cell death in an apoptosis independent way. The MDR cell line GLC4/ADR possess almost the same sensitivity to APIT ( $IC_{50}$  10 ng/ml) as the parental cancer line GLC4 does ( $IC_{50}$  9 ng/ml).

25 Thus, the diagnostic or therapeutic application preferably relates to a method for diagnosis or treatment of hyperproliferative diseases, e.g. cancer. More preferably, the method is a method for diagnosis or treatment of lung cancer, breast cancer, prostate cancer, colon cancer, cervix cancer, uterus cancer, larynx cancer, stomach cancer, liver cancer, Ewings  
30 sarkoma, acute lymphoid leukemia, acute and chronic myeloid leukemia, apoptosis resistant leukemia, and/or MDR lung cancer. Moreover other tumor types can also be treated with the polypeptide, like pancreas cancer,

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gastric cancer, kidney cancer, gliomas, melanomas, chronic lymphoid leukemia, and/or lymphoma. Since all cancer cell lines tested (in total 24) were effectively killed by APIT, the polypeptide can be used for the treatment of solid tumors and leukemias in general including apoptosis  
5 resistant and multi drug resistant cancer forms.

A further aspect of the present invention is a pharmaceutical composition comprising the polypeptide of the present invention as described above, in a pharmaceutically effective amount and optionally together with suitable  
10 diluents and carriers or kit containing the composition together with other active ingredients, e.g. modulators of the polypeptide or other cytostatic or cytotoxic agents. The composition can be administered locally or systemically by any suitable means, e.g. orally, nasally or by injection (i.v., i.p., s.c., or i.m.) to a subject in need thereof. The components of a kit,  
15 which consists of at least two different compositions may be administered together or separately, e.g. at different times and/or by different routes.

In another embodiment, the pharmaceutical composition or the kit comprises a nucleic acid encoding for the polypeptide of the present  
20 invention as described above. Further, the pharmaceutical composition or kit may comprise both the polypeptide and the nucleic acid of the present invention.

From many studies it is known that tumor cells have an increased rate of  
25 metabolism compared to normal cells. A result of this high metabolic rate is a high concentration of reactive oxygen species (ROS, comprising  $H_2O_2$ ) which originate from oxidative phosphorylation reactions by the electron transport chain of the mitochondria. As a consequence ROS detoxification reactions are increased in tumor cells, and interference with detoxification  
30 has a selective toxic effect on the tumor cells but not on normal cells. Likewise, increasing the concentration of  $H_2O_2$  by administering the polypeptide of the invention in a predetermined amount may overcome the

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detoxification reactions and kill the tumor cells. The level of extra  $H_2O_2$  produced by exogenous APIT does not affect normal cells because of their higher tolerance for additional  $H_2O_2$ . An administration of the polypeptide in a varying amount, e.g. a gradually changing, e.g. increasing amount leads to the production of a defined amount of  $H_2O_2$  could thus be used for a selective killing of cancer cells.

The pharmaceutical composition or kit as described above can comprise a further component which is a substance capable of modulating the cytotoxic activity of the polypeptide, in a pharmaceutically effective amount and optionally together with suitable diluents, and carriers. In FCS (100%) at 37°C and 5%  $CO_2$  which reflect *in vivo* conditions, or in a medium containing 10% FCS (typical *in vitro* conditions) devoid of L-lysine and L-arginine, the activity of APIT (20 ng/ml) can be dose-dependently increased by the addition of L-lysine in a final concentration of 2 – 50  $\mu$ g/ml. Thus, the high specificity of APIT for L-lysine (and L-arginine) allows for modulating the enzymatic activity of APIT and thus its cytotoxic activity by providing an additional substrate *in vivo* or *in vitro*. The substance capable of modulating the cytotoxic activity of the polypeptide can be L-lysine, L-arginine, a derivative or metabolic precursor of L-lysine, or L-arginine, or a mixture thereof. A derivative is a compound which is an APIT substrate. A metabolic precursor is a compound, which can be metabolized to a compound, which is an APIT substrate. Further, the modulator may be selected from flavine nucleosides, particularly FAD, since the presence of a flavine nucleoside prosthetic group leads to a great increase in APIT activity.

The pharmaceutical composition may comprise the polypeptide and at least one modulating substance as a mixture. Preferably, the modulating substances are provided in a kit consisting of separate preparations. More preferable, the polypeptide is provided for administration before the modulating substances.

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During the passage through body fluids before reaching the tumor tissue, the cytotoxic activity of the polypeptide would be undesired, due to the toxic properties of  $H_2O_2$ . Thus, the composition may further comprise an inhibitor of the polypeptide. The inhibitor could have a short half-life time  
5 in the body fluid. A preferred inhibitor of the polypeptide is an antibody against the polypeptide (see above).

Modulating the activity of the polypeptide of the present invention can also be accomplished by modulating the product level, i.e. the  $H_2O_2$  level. The  
10 degradation of at least one of the products, namely  $H_2O_2$ , results further on in consumption of the substrates L-lysine and L-arginine by the polypeptide of the present invention. Thus, these amino acids may be deprived. Since L-lysine and L-arginine are essential for living and growing of tumor cells, deprivation of these amino acids by a combination of the polypeptide of  
15 the present invention and an  $H_2O_2$  scavenger may lead to the death of tumor cells. Thus, in another embodiment, the pharmaceutical composition may comprise the polypeptide of the present invention and an  $H_2O_2$  scavenger. A preferred  $H_2O_2$  scavenger is catalase. Preferably, a kit is provided consisting of separate preparations of the polypeptide of the  
20 present invention and catalase.

Further the polypeptide can be coupled with a substance and/or a particle which targets the polypeptide to the tumor tissue.

25 Further components of the pharmaceutical composition can be a nucleic acid coding for the polypeptide as described above, and/or a recombinant vector or cell containing the nucleic acid.

A further aspect of the present invention is a substance modified by  
30 interaction with APIT (termed target substance of APIT). A direct interaction is a contact of APIT with this substance. In an indirect interaction, the effect upon the substance includes at least one mediator

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substance, e.g. a substance formed by APIT, or a receptor interacting with APIT and the components of the related transduction cascade.

As described above, a mediator of APIT acting on cellular polypeptides is  
5  $H_2O_2$ . Thus, preferred target substances of APIT comprise cellular polypeptides, which can be modified by  $H_2O_2$ . A major modification identified in 2-DE SDS gel patterns of cells treated with APIT was a shift of peroxiredoxin I (Prx I, Swiss-Prot No. Q06830, Genbank identifier No. 548453, SEQ ID NO: 8), which was also detected in cells treated with  
10  $H_2O_2$ . Prx I belongs to a class of peroxidases which are involved in the detoxification of ROS. Although the nature of the modification of Prx is not known, Prx I can be used as a marker for APIT anti-tumor activity.

Thus, particularly preferred substances which can be used as target  
15 substances of the polypeptide as described above are peroxidases, especially preferably peroxiredoxin I or a polypeptide having substantially the same biological activity as peroxiredoxin I. Peroxiredoxin I may comprise

- (a) the amino acid sequence shown in SEQ ID NO: 8, or/and
- 20 (b) an amino acid sequence which is homologous to the sequence of (a) with at least 70%, preferably 80%, particularly preferably 90%, especially preferably 95%, or/and
- (c) a fragment of the amino acid sequence of (a) or (b).

25 Further, peroxiredoxin I may comprise an amino acid sequence or a fragment thereof as disclosed in at least one of the Genbank entries selected from gi:4505591 (NP\_002565.1), gi:13626803 (XP\_001393.2), gi:32455264 (NP\_859047.1), gi: 32455266 (NP\_859048.1), gi: 423025 (A46711), gi: 287641 (CAA48137.1), gi: 13937907 (AAH07063.1), gi:  
30 18204954 (AHH21683.1) or gi:440306 (AAA50464.1).

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WO 02/31144 discloses proteins modified by  $H_2O_2$  which are targets of APIT: thioredoxin peroxidase 2 (Swiss Prot No. Q06830, Genbank identifier 548453), 60S ribosomal protein P0 (12654583), Hsp-60 (N-term) (14603309), stathmin (5031851), Rho GDI 2 (P52566, 1707893), 60S  
5 ribosomal protein P0(4506667), RNA binding regulatory subunit (O14805,12720028), hnRNP C1/C2 (4758544), hnRNP C1/C2 (4758544), proteasome subunit beta type 1 (P20618, 130853), pre-mRNA cleavage factor Im (5901926), proteasome subunit alpha type 7 (O14818, 12643540), U2 small nuclear ribonucleo-protein A' (P09661, 134094),  
10 GAP SH3 binding protein (5031703), DNA replication licensing factor MCM4 (P33991, 1705520), thioredoxin peroxidase 1 (P32119, 2507169), 40S ribosomal protein S21 (P35265, 464710), 40S ribosomal protein S12 (P25398, 133742), phosphoglycerate mutase 1 (P18669, 130348), HCC-1 protein (13940310), HnRNP A2/B1 (4504447/14043072), IMP dehydro-  
15 genase 2 (P12268, 124419), hnRNP A/B (14724990).

Further targets of APIT identified by 2 DE gel electrophoresis, in-gel tryptic digestion, peptide mass fingerprinting by MALDI-MS, and identification of the proteins are summarized in Table 3.

20

Still a further target of APIT is a nucleic acid. The target nucleic acid can be a DNA or an RNA, which is a mRNA. The transcription of the mRNA is up- or downregulated in the presence of APIT and/or  $H_2O_2$ . Preferably, the transcription is changed by a factor of at least 2, and more preferably, by  
25 a factor of at least 4.

By a microarray of specific 60mer oligonucleotides representing about 8500 human genes, about 70 mRNAs were identified which are targets of APIT. The information about the mRNAs are summarized in Table 4. Each  
30 mRNA is referenced by a "unigene cluster" which represents a number of nucleotide sequences belonging to the same gene or to closely related genes. Details of the nomenclature and the nucleotide sequences of the

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unigene clusters are public available under <http://www.ncbi.nlm.nih.gov/> (Homepage of the National Center for Biotechnology Information).

For most of the unigene clusters of Table 4, the gene and/or the protein is  
5 known. It is a general principle that modulation of the transcription of a messenger RNA influences the amount of protein expressed. Thus, the proteins coded by the sequences of the unigene clusters of Table 4 are also targets of APIT, because APIT may influence their expression. The  
10 sequences of the proteins and of the nucleic acids coding for these proteins are referenced by the genbank identifier, accession number and/or version number (see Table 4). The sequences are public available under <http://www.ncbi.nlm.nih.gov/>.

Additional targets of APIT (nucleic acids, proteins) obtained by microarray  
15 analysis as described above are summarized in Table 5.

A preferred substance which can be used as a target substance for the polypeptide as described above is a nucleic acid coding for a peroxidase, particularly preferably peroxiredoxin I or a polypeptide having substantially  
20 the same biological activity as peroxiredoxin I. The nucleic acid coding for peroxiredoxin I may comprise

- (a) the nucleotide sequence shown in SEQ ID NO: 7, or/and
- (b) a nucleotide sequence which corresponds to the sequence of  
25 (a) within the scope of the degeneracy of the genetic code, or/and
- (c) a nucleotide sequence hybridizing to the sequence of (a) or/and (b) under stringent conditions, or/and
- (d) a fragment of the nucleotide sequence of (a), (b) or (c).

30 SEQ ID NO: 7 is disclosed in Genbank entry gi:14721336 (XM001393).

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Preferably, the nucleic acid encoding peroxiredoxin I may comprise a nucleotide sequence which is homologous to SEQ ID NO: 7 with at least 70%, particularly preferably at least 80%, especially preferably at least 90%.

5

In further preferred embodiments, the nucleic acid encoding peroxiredoxin I may comprise a nucleotide sequence or a fragment thereof as disclosed in at least one of the Genbank entries selected from gi: 13937906 (BC007063.1, PRDX1 transcript 3), gi: 18204953 (BC021683.1, PRDX1 transcript variant 3), gi: 32455265 (NM\_181697.1, PRDX1 transcript variant 3), gi: 34528302 (AK131049.1, clone highly similar to PRDX1), gi: 287640 (X679851.1, PAG), gi: 32455263 (NM\_181696.1, PRDX1 transcript variant 2), gi: 32455267 (NM\_002574.2, PRDX1 transcript variant 2) or gi:440305, (L19184, NKEF A).

15

The target substance of the present invention (see Table 3, 4 and 5), which is identified by one of the methods as described above, may be used for the development of new pharmaceutical agents, e.g. by known high-throughput screening procedures which may be cellular screening procedures or molecular based screening procedures. These pharmaceutical agents may act upon cellular receptors and/or components of the signal transduction pathways activated or inhibited by APIT.

20

Degenerative diseases like Alzheimer's and Parkinson's disease are characterised by excessive ROS production of the affected tissue. Drugs which either activate H<sub>2</sub>O<sub>2</sub> detoxification or inhibit H<sub>2</sub>O<sub>2</sub> production may be used for therapy of degenerative diseases like Alzheimer's or Parkinson's disease. Fast growing tumor cells produce more ROS and thus require an efficient H<sub>2</sub>O<sub>2</sub> detoxification system. Drugs which either activate H<sub>2</sub>O<sub>2</sub> production or which interfere with H<sub>2</sub>O<sub>2</sub> detoxification may be used for therapy of proliferative diseases like tumors. Since e.g. thioredoxin peroxidases 1 and 2 have been shown to be overexpressed in cells at risk

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for diseases related to ROS toxicity including degenerative diseases like Alzheimer's and Parkinson's disease, and have been shown to be overexpressed in tumor cells (Butterfield et al., 1999, *Antioxidants & Redox Signalling*, 1, 385-402), the targets of Table 3 and 4 might be  
5 important targets for the development of drugs for treatment of degenerative diseases like Alzheimer's and Parkinson's disease and of proliferative diseases like tumors.

10 NK-cells have been shown to protect against malignant cells in chronic myelogenous leukemia (CML), but their number and inducibility is reduced during the progression of the disease. This reduction and dysfunction is due to the production of  $H_2O_2$  by CML-cells (Mellqvist, Blood 2000, 96, 1961-1968). NK-cells encountering  $H_2O_2$  are inhibited in their lytic activity, are made resistant to IL-2 activation and undergo apoptosis/necrosis. Any  
15 therapy providing CML-patients with ROS-hyposensitive NK-cells therefore would be of great benefit. The targets described above could be used to modulate the  $H_2O_2$  sensitivity of NK-cells or to inhibit the  $H_2O_2$  production of malignant cells, e.g. CML-cells.

20 Arteriosclerosis with its progression to heart disease, stroke and peripheral vascular disease continues to be the leading cause of death in all western civilisations. Enhanced ROS-production (via endothelial NADPH-oxidase) is required and sufficient to generate the pathologic phenotype (Meyer, FEBS Letters 2000, 472, 1-4). Therefore, targets mediating the effect of  $H_2O_2$   
25 are useful to develop new drugs for treatment of arteriosclerosis and the associated diseases like heart disease, stroke and other vascular diseases. These targets are suitable to detoxify  $H_2O_2$  and/or to block the  $H_2O_2$  induced signalling pathways.

30 Target compounds, e.g. peptides, polypeptides or low-molecular weight organic compounds, which are capable of modulating the effect of  $H_2O_2$

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may be identified in a screening system comprising the use of the APIT polypeptide as described above. Particularly, a modulation of the APIT activity, i.e. L-amino oxidase activity, may be determined.

5 Thus the present invention further relates to a pharmaceutical composition comprising as an active agent at least one of the target substances as described above.

Still a further aspect of the present invention is an inhibitor of a target as  
10 described above, in particular an inhibitor of the detoxification system of the cell which eliminates reactive oxygen species, e.g.  $H_2O_2$ . Surprisingly, it was found that the inhibition of detoxifying enzymes sensitized tumor cells to the cytotoxic activity of the polypeptide of the present invention as described above. Example 11 demonstrates that knock-down of  
15 peroxiredoxin I sensitized tumor cells for APIT-induced cell death.

Preferably, the inhibitor is an inhibitor of peroxidase, particularly of peroxiredoxin I. The inhibitor may be an antibody or a nucleic acid molecule, i.e. useful for antisense inhibition or as an siRNA molecule. It is  
20 particularly preferred that the inhibitor is an inhibitor of peroxiredoxin I activity which is an RNA molecule, particularly a double-stranded RNA molecule comprising a nucleic acid sequence of at least 15 nucleotides complementary to a peroxiredoxin I transcript. It is especially preferred that the peroxiredoxin I transcript is derived from SEQ ID NO:7.

25

The one or two strands of the RNA molecule as described above may, independently, have a length of 19 to 25 nucleotides, preferably 19 to 23 nucleotides. Especially preferred is a length of the one or two strands of 19, 20, 21, 22 or 23 nucleotides. The RNA molecule as described above  
30 may comprise at least one modified nucleotide. Preferably, modified nucleotides are selected from the group consisting of oxetane[1-(1',3'-O-anhydro- $\beta$ -D-psicofuranosyl)-nucleotides, locked nucleic acid (LNA)

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nucleotides, hexitol nucleotides, altritol nucleotides, cyclohexane nucleotides, neutral phosphate analogs.

5 The double-stranded RNA molecule as described above may have one or two 3' overhangs with, independently, a length of 1 to 5 nucleotides, preferably 1 to 3 nucleotides, particularly preferably 2 nucleotides. The one or two overhangs may consist of ribonucleotides, deoxyribonucleotides, modified nucleotides as described above or combinations thereof.

10 The double-stranded RNA molecule as described above may comprise a sequence selected from the group of sequences consisting of SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11; SEQ ID NO: 12; SEQ ID NO: 13; SEQ ID NO: 14; SEQ ID NO: 15; SEQ ID NO: 16; SEQ ID NO: 17; SEQ ID NO: 18; SEQ ID NO: 19; SEQ ID NO: 20; SEQ ID NO: 21; SEQ ID NO: 22; SEQ  
15 ID NO: 23; SEQ ID NO: 24; SEQ ID NO: 25; SEQ ID NO: 26; SEQ ID NO: 27; SEQ ID NO: 28; SEQ ID NO: 29.

Yet another aspect of the present invention is a pharmaceutical composition or kit comprising an inhibitor as described above, preferably an  
20 RNA molecule, particularly preferred a double-stranded RNA molecule, or a nucleic acid encoding such an RNA molecule. The pharmaceutical composition or kit may comprise the inhibitor as sole active agent in order to increase the amount of reactive oxygen species present in the cell due to endogenous production. More importantly, the pharmaceutical  
25 composition or kit may comprise the inhibitor and a substance capable of producing reactive oxygen species. In a preferred embodiment, the pharmaceutical composition or kit comprises as an active agent a combination of APIT and at least one inhibitor of a target substance as described in Table 3 or/and Table 4 or/and Table 5, more preferably at least  
30 one inhibitor of peroxiredoxin I. In another preferred embodiment, the pharmaceutical composition or kit comprises at least one inhibitor of a target substance as described in Table 3 or/and Table 4 or/and Table 5,

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more preferably at least one inhibitor of peroxiredoxin I, and the polypeptide of the present invention having cytotoxic activity as described above. In yet another preferred embodiment, the pharmaceutical composition or kit comprises at least one inhibitor of a target substance as described in Table 3 or/and Table 4 or/and Table 5, more preferably at least one inhibitor of peroxiredoxin I, and a cytotoxic polypeptide producing reactive oxygen species or/and a nucleic acid encoding such a cytotoxic polypeptide, wherein the cytotoxic polypeptide is selected from cytotoxic polypeptides obtainable from sea hares, e.g. Cyplasin C, Cyplasin L, Aplysianin A, Aplysianin P, Aplysianin E, Dolabellin A, Dolabellin C, Dolabellin P, Julianin G, Julianin S, or is selected from L-Lysine oxidases like EC 1.4.3.14 from *Trichoderma*, AIP from Chub mackerel (AJ400871), Apoxin from *Crotalus* (AAD45200.1), or from other L-amino acid oxidases like EC 1.4.3.2 or from other enzymes which produce H<sub>2</sub>O<sub>2</sub>. More preferably, the pharmaceutical composition or kit comprises

(I) a polypeptide obtainable from *Aplysia* comprising an amino acid sequence selected from:

- (a) D-G-E-D-A-A-V (SEQ ID NO:32) and/or
- (b) (D/Q)-G-(I/V)-C-R-N-(Q/R)-R-(Q/P) (SEQ ID NO:33),
- (c) F-A-D-S (SEQ ID NO:34),
- (d) G-P-D-G-(I/L)-V-A-D (SEQ ID NO:35),
- (e) P-G-E-V-S-(K/Q)-(I/L) (SEQ ID NO: 36),
- (f) A-T-Q-A-Y-A-A-V-R-P-I-P-A-S-K (SEQ ID NO:37),
- (g) D-S-G-L-D-I-A-V-E-Y-S-D-R (SEQ ID NO:38),
- (h) G-D-V-P-Y-D-L-S-P-E-E-K (SEQ ID NO: 39) or/and
- (i) SEQ ID NO: 41, 43, 44, 45.

or a fragment thereof wherein the polypeptide or the fragment has cytotoxic activity, or/and a nucleic acid encoding the cytotoxic polypeptide obtainable from *Aplysia* comprising

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- (i) a nucleotide sequence as shown in SEQ ID NO:40 or 42 or at least the polypeptide coding portion thereof or the complement thereof,
- (ii) a nucleotide sequence corresponding to the sequence of (a) within the scope of degeneracy of the genetic code, or the complement thereof, or/and
- (iii) a nucleotide sequence hybridizing under stringent conditions with the sequence of (a) or/and (b), and

(II) an inhibitor of a target substance as described in Table 3 or/and Table 4 or/and Table 5.

The inhibitor of the present invention may be coupled to carriers, (e.g. lipids, peptides, biodegradable polymers, dendrimers, vitamins, carbohydrate receptors) for *in vivo* targeting to predetermined tissues or/and cell types.

Delivery of the inhibitors of the present invention may be improved by linking the inhibitors with lipids, liposomes, PEG, nanoparticles or/and polymers, for example.

Yet another aspect of the present invention is a gene therapy delivery system suitable for delivery of a nucleic acid encoding an inhibitor which is an RNA molecule, preferably a double-stranded RNA molecule as described above, capable of inhibiting peroxidase, particularly peroxiredoxin I activity. Suitable delivery systems for gene therapy are commonly known in the art, for instance a recombinant adenoviral delivery system, a recombinant adenoviral-derived system or a recombinant lentiviral system. Further, the nucleic acid may be delivered by virus-like particles from *Papillomaviridae* and *Polyomaviridae*. Further, bacteria may be used as a delivery system,

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e.g. attenuated gram negative bacteria, particularly attenuated salmonella strains. The nucleic acid encoding the inhibitor is operatively linked with expression control sequences which are adapted to the host and to the delivery system. Such expression control sequences are known to a person skilled in the art. Expression of the two strands of the RNA molecule may be performed together in a self-complementary configuration which allows formation of a small hairpin RNA (shRNA) in which the two strands of the double-stranded molecule are interconnected by an additional loop, or may be performed as two separate strands which hybridize later on in the host.

10

Yet another aspect is a pharmaceutical composition or kit comprising a delivery system suitable for delivery of a nucleic acid encoding an inhibitor which is an RNA molecule, particularly a double-stranded RNA molecule preferably comprising a nucleic acid of at least 15 nucleotides complementary to a peroxiredoxin I transcript as described above, to predetermined tissues or/and cell types.

15

In yet another embodiment, the invention concerns a method for diagnosis or treatment of cancer, wherein a pharmaceutical composition as described above is administered to a subject in need thereof.

20

SEQ ID NO: 1, 3 and 5 show the APIT nucleotide sequences as shown in Fig. 4c. SEQ ID NO: 2, 4 and 6 show the amino acid sequences derived from SEQ ID NO: 1, 3 and 5, respectively. SEQ ID NO: 7 and 8 show the nucleotide sequence and the amino acid sequence of Prx I. SEQ ID NOs: 9 to 29 show the nucleotide sequences of double-stranded siRNA molecules capable of inhibiting Prx I activity. SEQ ID NOs: 30 and 31 show sequences of double stranded siRNA molecules obtained from the Lamin AC and the luciferase sequence, respectively. SEQ ID NOs: 32 to 39 show the amino acid sequences of fragments of cytotoxic *Aplysia* polypeptides. SEQ ID NO: 40 and 42 show partial sequences of nucleic acids encoding cytotoxic polypeptides of *Aplysia punctata*. SEQ ID NOs: 41, 43, 44 and

25

30

- 30 -

45 show the derived amino acid sequences of SEQ ID NOs: 40 and 42. SEQ ID NOs: 46 to 55 show the amino acid sequences of fragments of cytotoxic *Aplysia* polypeptides.

- 5 The invention is explained in more detail by the following figures, tables and examples.

### Figure 1

10 **A**, Anion exchange chromatography. Filtrated and concentrated ink was loaded onto a Source Q15 column. Proteins were eluted by a linear gradient from 0 to 800 mM NaCl, fractions were collected every minute (2 ml/min). Absorption was measured at 280 nm. Horizontal bar indicates active fractions.

15 **B**, Gelfiltration. Active fractions from the Source Q15 were pooled and concentrated and applied to a Superose 12 HR 10/30 column. Proteins were eluted with 100 mM potassium phosphate buffer (pH 7.2). Fractions were collected every minute (0.5 ml/min). Horizontal bar indicates active  
20 fractions.

### Figure 2

**A**, Phenotype of APIT-induced cell death. Jurkat cells were cultured for 7  
25 hours in the presence (APIT) or absence (medium) of APIT (30 ng/ml) and phase contrast images were recorded.

**B**, Lack of apoptotic DNA fragmentation in ink-treated cells. Jurkat cells were incubated in medium (control) or treated with cycloheximide (chx; 10  
30  $\mu$ g/ml) or ink (ink, 1/500 diluted) for 2, 4 and 6 h. Isolated DNA was visualized on a 1,6% agarose gel by ethidium bromide staining.

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C, APIT mediated loss of metabolic activity. APIT (10 ng/ml) and the tetrazolium-salt WST-1 were added simultaneously to Jurkat cells and turnover of WST-1 was measured photometrically. White circles: medium control; black circles: APIT-treated samples; mean absorbance of 8  
5 replicates  $\pm$  SD.

D, Cell death induced by ink. Jurkat cells were treated with ink (1/500 diluted) and propidium iodide (PI) uptake was measured as indicator for dead cells.  
10

### Figure 3

A, Heat sensitivity of ink. Dialysed ink was incubated for 10 min at the indicated temperatures and enzymatic activity was measured as  
15  $\text{H}_2\text{O}_2$ -production (mean of triplicates  $\pm$  SD). Blank: medium control.

B, pH-sensitivity of APIT. APIT (60 ng) was incubated for 10 min at 25 °C in 0,1 M potassium phosphate at indicated pH values. Enzymatic activity was measured as  $\text{H}_2\text{O}_2$ -production (mean of triplicates  $\pm$  SD).  
20

C, Sensitivity to increasing amounts of urea: Dialyzed ink (black bars, 1/500 diluted) and as positive control 0,625 mM  $\alpha$ -keto isocaproic acid (open bars) were treated with indicated concentrations of urea for 30 min at 25 °C. Enzymatic activity (15 min, 25 °C) was measured as  $\alpha$ -keto acid  
25 formation via MBTH.

### Figure 4

A, N-terminal and internal peptide sequences of the APIT protein.  
30

B, List of oligonucleotides used for cloning of the APIT gene.

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**C**, Nucleotide sequence of the APIT cDNA and the derived amino acid sequence. The dinucleotide binding fold (VAVVGAGPGGANSAYMLRDSGLDIAVFE) and the GG-motif (RVGGRLFT) are indicated by boxes. Consensus amino acid residues are indicated by bold letters. The  
5 N-terminal sequence of mature APIT (dashed line) and of internal peptides (solid line) derived by Edman degradation and mass finger prints are indicated. Sequence variations of the three clones are indicated by small boxes.

10 **D**, Variation of the N-terminus of APIT in 11 further clones.

### Figure 5

**A**, Anion exchange chromatography of purified APIT. Proteins were eluted  
15 by a linear gradient from 0 to 800 mM NaCl and fractions were collected every minute. Absorption was measured at 280 nm (AU: Absorption unit).

**B**, Fractions 24, 27 and 29 were separated by SDS-PAGE and tested for metabolic activity by WST-1 assay. High activity (+; + +) correlated with  
20 the presence of a prominent 60 kDa band (fractions 24 and 29). Activity is given as the dilution leading to > 85% reduction of the metabolic activity of Jurkat cells (+/- = 1:900; + = 1:2700; + + = 1:8100).

**C**, Absorption spectra of fractions 24 (black line), 27 (dashed line) and 29  
25 (dotted line).

### Figure 6

**A**, APIT induced H<sub>2</sub>O<sub>2</sub> production in medium in the absence of cells. APIT  
30 (260 ng/ml) was incubated in medium in the presence (open bar) or absence (black bar) of Jurkat cells (5x10<sup>5</sup>/ml). After 1 h of incubation at

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37°C supernatants were alkylated with N-ethylmaleimide and H<sub>2</sub>O<sub>2</sub> was measured (mean values of 3 independent experiments +/- SD).

5 **B**, Catalase inhibits ink induced cell death. Jurkat T-cells were incubated for 8 h with ink in the presence (black bars) or absence (white bars) of catalase. Cytotoxicity was measured as PI uptake (mean of triplicates ± SD).

10 **C**, Catalase protects from APIT induced loss of metabolic activity. Metabolic activity of Jurkat cells was measured after incubation with APIT (20 ng/ml) or anti-CD95 for 3h in the presence (black bars) or absence (white bars) of catalase. (mean of 5 replicates ± SD).

15 **D**, Phenotype of APIT induced cell death is mediated by hydrogen peroxide. Jurkat cells were cultured for 7 hours in the presence (APIT) or absence (medium) of APIT (60 ng/ml) or H<sub>2</sub>O<sub>2</sub> (500 µM) and were analyzed by phase contrast microscopy. Catalase was added in combination with APIT to neutralize H<sub>2</sub>O<sub>2</sub> (APIT + CAT).

20 **E**, Long-term exposure with ink from *Aplysia punctata* and catalase resulted in tumor cell death by amino acid deprivation. Metabolic activity of Jurkat T-cells was measured after overnight incubation (>18h) with ink (white bars) or H<sub>2</sub>O<sub>2</sub> (250 µM, black bars) in the presence (+) or absence (-) of catalase (2000 U/ml) (mean of triplicates ± SD).

25

### Figure 7

30 **A**, Enzymatic activity of APIT in the presence of different medium supplements. APIT (200 ng/ml) was incubated for 60 min at RT with RPMI +/- 10% FCS or KRG supplemented with different medium ingredients and H<sub>2</sub>O<sub>2</sub> production was measured. (EAA = essential amino acids, NEAA = non essential amino acids, concentrations see Table 1).

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**B**, Substrate specificity of APIT and ink. The enzymatic reaction of dialysed ink (open bars) with different L-amino acids in potassium phosphate buffer was measured as  $\text{H}_2\text{O}_2$ -production.  $50 \mu\text{M}$   $\text{H}_2\text{O}_2$  and amino acid free medium (control) were used as control. Aliquots of dialyzed ink were  
5 digested with trypsin (hatched bars) or proteinase K (black bars) at  $37^\circ\text{C}$  for 2h prior to testing the substrate specificity. Arg = L-arginine, 1mM; Lys = L-lysine, 1mM; EAA = essential amino acids, 1mM; NEAA = non essential amino acids, 1mM.

10 **C**, APIT induced cell death depends on the presence of L-lysine or L-arginine. Jurkat cells were incubated with APIT (20 ng/ml) for 6 h in the presence (white bars) or absence of L-lysine and L-arginine (black bars). Cytotoxicity was measured as PI uptake (mean of triplicates  $\pm$  SD).

15 **D**, APIT induced loss of metabolic activity depends on the presence of L-lysine or L-arginine. Jurkat cells were incubated with APIT (20 ng/ml) or anti-CD95 (150 ng/ml) in the presence (open bars) or absence (black bars) of L-lysine or L-arginine and metabolic activity was measured (mean of 5 replicates  $\pm$  SD).

20

**E**, APIT transforms L-lysine into an  $\alpha$ -keto acid. APIT was incubated with L-lysine and the formation of  $\alpha$ -keto acid was measured photometrically by its reaction with MBTH.

25 **F**, Michaelis-Menten kinetic of APIT activity with L-lysine.  $K_m$  value for L-lysine was determined as  $\text{H}_2\text{O}_2$  production.

**G**, Proposed reaction mechanism of L-amino acid oxidases according to Macheroux et al. (2001 Eur. J. Biochem. 268:1679-1686). Encircled are  
30 compounds which we demonstrated to participate in the reaction catalyzed by APIT.

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**Figure 8**

**A**, Quantification of the mRNAs of Lamin A/C and Prx I after transfection of specific siRNA (open bars) and control Luciferase siRNA (black bars) with quantitative realtime PCR. Shown are the relative mRNAs levels compared to the mRNA of GAPDH measured in the same RNA preparation.

**B**, Sensitization of HeLa cells by knock down of Prx I. Specific siRNAs directed against the mRNA of Luciferase (Luc, transfection control), Lamin A/C (control knock down) and Prx I were transfected in HeLa cells and the metabolic activity of transfectants treated in the presence (black bars) or absence of APIT (open bars) was measured. Note that the knock down of Prx I but not of the other genes sensitized cells for the cytotoxic activity of APIT.

**Figure 9**

APIT did not induce actin depolymerisation in HeLa cells. Untreated HeLa cells (A) and HeLa cells treated with Cytochalasin (B) or APIT (C) were stained with Phalloidin-TRITC for actin and Hoechst 33258 for nuclei staining. Subsequently, fluorescence microscopy was performed. Actin staining is shown in bright white, nuclei are displayed in transient grey.

**Figure 10**

HUVEC cells are resistant to the APIT induced cells death. HUVEC and Jurkat cells were incubated with APIT over night and subsequently LDH release in the culture supernatant was measure photometrically. Shown are the results of two independent experiments +/- standard deviation.

**Table 1**

Composition and concentrations of mixtures of essential and non-essential amino acids as well as single amino acids used in Fig. 7A.

5 **Table 2**

APIT kills different kinds of tumor cells. Different tumor cell lines (50,000 cells in 100  $\mu$ l) were incubated for 14 h in the presence of increasing amounts of APIT. Metabolic activity of the cells was measured via turnover of WST. The IC<sub>50</sub> values reflect the APIT concentration at which the  
10 metabolic activity is decreased to 50%. (\* stands for IC<sub>50</sub>  $\geq$  20 ng/ml at the given cell concentration of 50,000/100  $\mu$ l.)

**Table 3**

List of proteins which were changed in their expression or modified after  
15 treatment with APIT (upregulation (+), downregulation (-), or modification (m) in column "effect"). The proteins are referenced by the genbank identifier and/or accession number and/or version number.

**Table 4 and Table 5**

List of genes (referenced by unigene cluster number) and gene products  
20 (proteins) which were modulated in their expression more than 2 fold after incubation with APIT for two hours. The proteins are referenced by the genbank identifier and/or accession number. Transcription rates are indicated as increase (+, 2 to  $\leq$  4 times; ++, 4 to 6 times in Table 4 or  
25 4 to 25 times in Table 5) or decrease (-, 2 to  $\leq$  4 times; --, 4 to 6 times).

**Example 1: Purification of APIT**

*Aplysia punctata* were gained from the Station Biologique Roscoff,  
30 Bretagne, France. Crude ink was prepared by gentle squeezing the sea hares in sterile seawater. Insoluble particles were removed by

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ultracentrifugation (82,000g, 30 min, 4°C) and supernatants were stored at -70°C.

APIT was purified from crude ink via anion exchange chromatography and gelfiltration. The thawed ink was filtered through Whatman filter No. 4 under slight vacuum and subsequently through a 5 µm and 0.45 µm syringe filter. The filtrate was concentrated by using Ultrafree-15 Units (Millipore, exclusion weight 30 kDa) followed by three washing steps with 20 mM Tris HCl (pH 8.2). After centrifugation at 10.000 g for 5 min the supernatant of the concentrate (20 – 60 fold) was applied to a Source Q15 column ((10mm, length 40 mm) equilibrated with 20 mM Tris HCl, pH 8.2. Proteins were eluted by a linear gradient from 0 to 800 mM NaCl over 50 ml at a flow rate of 2 ml/min (Fig. 1A). The purity of the fractions was determined by SDS-PAGE and subsequent rapid silver staining. APIT appears as a band at 60 kDa. Cytolytic activity was measured as APIT-induced reduction of the metabolic activity of Jurkat cells via turnover of WST (see example 2). Enzymatic activity was determined as described in example 3. Fractions which show high purity and cytotoxic respectively enzymatic activity (Fig. 1A; fraction 42 to 48) were pooled, concentrated and loaded onto a Superose 12 HR 10/30 column (Pharmacia). Proteins were eluted with 100 mM potassium phosphate buffer (pH 7.2) at a flow rate of 0.5 ml/min. The first peak represents the active APIT (Fig. 2B; fraction 11 to 14).

## Example 2: Phenotype of APIT-induced cell death

The purple fluid of *Aplysia punctata* contains a cytolytic activity which induces rapid and extensive death of Jurkat T cells in culture. APIT induces cell death of tumor cells which resembles neither apoptosis nor necrosis. In order to classify the APIT-induced cell death we looked for common features of apoptosis and necrosis.

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Jurkat T cells were harvested in the log phase, centrifuged and adjusted to a density of  $5 \times 10^5/\text{ml}$  with fresh medium (RPMI supplemented with 10% FCS, 100 U/ml penicillin and 100  $\mu\text{g}/\text{ml}$  streptomycin). Cells were cultured with APIT, cycloheximide as a positive control or medium at  $37^\circ\text{C}$ , 5%  $\text{CO}_2$  and 100% humidity for the indicated times. Fragmented DNA of apoptotic cells was analyzed according to Herrmann et al. (1994, Nucleic Acid Research 22: 5506-5507). Cell vitality was determined as metabolic activity via the turnover of WST-1 (ROCHE, Mannheim) to red formazan by the mitochondrial dehydrogenase of viable cells. Absorbance of the cell suspension was measured photometrically at 450 nm (690 nm reference). Toxicity was measured by quantifying propidium iodide uptake (1  $\mu\text{g}/\text{ml}$  in PBS) by Flow Cytometry.

Morphologically, tumor cells treated with ink or APIT did not exhibit typical morphological apoptotic or necrotic signs of cell death (Fig. 2A), and neither blebbing nor swollen cells were detected when cells were treated with a lethal dose of ink. Cells did not form clusters anymore, cytoplasm became translucent and nuclei prominent (Fig. 2A). The intracellular movements of plasma and organelles stopped, detachment and formation of vacuoles were observed when adherent cells were incubated with APIT (data not shown). Consistent with the absence of apoptosis, fragmented DNA or nuclei were not detected in ink-treated tumor cells (Fig. 2 B); moreover, caspases were not activated (data not shown). Metabolic activity of tumor cells was blocked as early as 30 min after exposure to ink or APIT (Fig. 2C). Ink-treated tumor cells rapidly took up propidium iodide (PI) indicating plasma membrane permeabilization and cell death (Fig. 2D).

### Example 3: Stability of APIT

APIT was further characterized by its sensitivity to heat, low pH and high concentrations of urea.

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For determination of its heat sensitivity native ink was dialyzed against PBS at 4°C for several days to separate chromopeptides. Dialysed ink was incubated for 10 min at the indicated temperatures, and activity was measured immediately as enzymatic production of H<sub>2</sub>O<sub>2</sub>. This assay is based on the finding that APIT transforms L-lysine to H<sub>2</sub>O<sub>2</sub> and  $\alpha$ -keto acid. The production of H<sub>2</sub>O<sub>2</sub> was determined via the turnover of ABTS (2,2-Azino-bis (3-ethylbenzthiazoline-6-sulfonic acid) to a green formazan in the presence of H<sub>2</sub>O<sub>2</sub> by horseradish peroxidase. Heat-treated ink was incubated with L-lysine (1 mM) in 100  $\mu$ l 100 mM potassium phosphate buffer, pH 7.2 for 10 min at 25°C. The reaction was stopped by adding 1  $\mu$ l of 10 M phosphoric acid. To 25  $\mu$ l of this solution 1 mM ABTS and 1 Unit horseradish peroxidase was added in 225  $\mu$ l 100 mM potassium phosphate buffer, pH 5.0. Absorption was measured photometrically at 405 nm (reference 690 nm).

Purified APIT was challenged to different pH-values by adding a mixture of monobasic and dibasic potassium phosphate and phosphoric acid rendering the desired pH. After a 10 min incubation pH of samples was adjusted to pH 7.2 by adding appropriate amounts of dibasic phosphate. Afterwards enzymatic activity was measured as H<sub>2</sub>O<sub>2</sub>-production as described above.

The activity of APIT after treatment with urea was measured via the production of  $\alpha$ -keto acid, which was quantified photometrically by its reaction with the hydrazone MBTH (3-methyl-2-benzothiazolone hydrazone hydrochloride) as described by Soda (1968). Dialyzed ink was incubated with urea at indicated concentrations for 30 min. Subsequently the remaining enzymatic activity was measured without removing urea for 15 min at 25°C. As control, defined amounts of  $\alpha$ -keto isocaproic acid (Sigma; K-0629) were treated equally.

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APIT was characterized by its heat sensitivity and was found to exhibit a high and constant activity after pre-incubation for 10 min at 0°C to 50°C. Activity was clearly reduced at 60°C and absent at temperatures of 70°C or higher (Fig. 3A). APIT also shows a loss of activity with decreasing pH, with complete inactivation after a 10 min pre-incubation at pH 3 or lower (Fig. 3B). An outstanding feature of APIT is its resistance to urea (Fig. 3C). After 30 min treatment with 6 M urea, the activity of APIT was almost unaffected. At 8 M urea, the activity was reduced by about 50%.

#### 10 **Example 4: Sequencing and cloning of APIT**

In order to clone the cDNA of APIT N-terminal and internal peptide sequences were identified by PMF (peptide mass fingerprint), ESI/MS and Edman degradation (Fig. 4A). A suitable internal peptide sequence was used to design a degenerated primer for PCR (Fig. 4A, underlined sequence) with reverse transcribed mRNA, prepared from *Aplysia punctata* tissues. Subsequent 5'-RACE yielded the full length cDNA which was cloned and analyzed.

20 **Amino acid sequencing by peptide mass fingerprint (PMF), ESI/MS and Edman degradation.** Purified APIT was separated by SDS PAGE and 2 DE gel electrophoresis (Thiede et al., 2001, J. Biol. Chem. 276: 26044-26050). The N-terminus of APIT was identified from a single band/spot of a PVDF blot by Edmann degradation. For the identification of internal peptide sequences a single band/spot was punched from the gel, digested with trypsin and dissolved in aqueous trifluoroacetic acid (Thiede et al., 2001, J. Biol. Chem. 276:26044-26050). Tryptic peptides were separated using a Smart-HPLC system with a column of 2.1 mm inner diameter and 10 cm length ( $\mu$ RPC C2/C18 SC 2.1/10, Smart System, Pharmacia Biotech, Freiburg, Germany) and an acetonitrile gradient in 0.1% (v/v) trifluoroacetic acid at a flow rate of 100  $\mu$ l/min at room temperature. The peptide fractions were dried, dissolved in 6  $\mu$ l 0.3% (v/v) aqueous trifluoroacetic

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acid/acetonitrile (2:1) and analyzed by MALDI-MS. The mass spectra were recorded by using a time-of-flight delayed extraction MALDI mass spectrometer (Voyager-Elite, Perseptive Biosystems, Framingham, MA, USA) as previously described (Thiede et al., 2001, J. Biol. Chem. 276:26044-26050). Briefly, fifty mg/ml 2,5-dihydroxybenzoic acid in 0.3% (v/v) aqueous trifluoroacetic acid/acetonitrile (2:1) was used as matrix and 0.3  $\mu$ l of the sample and 0.3  $\mu$ l of the matrix were mixed and applied to a gold-plated sample holder and introduced into the mass spectrometer after drying. The spectra were obtained in the reflectron mode by summing 50-150 laser shots. For N-terminal sequencing peptide fractions containing single masses were loaded onto a Biobrene-coated glass fiber filter, transferred to a PVDF membrane and excised. Sequencing was performed using a Procise sequencer (Applied Biosystems, Weiterstadt, Germany).

**Cloning of the APIT gene.** In order to dissect mantle gland, nidamental gland, digestive gland and opaline gland some animals were relaxed by injection of 5 – 10 ml sterile  $MgCl_2$  solution (380 mM). Isolated tissues were frozen immediately in liquid nitrogen. Total RNA was prepared from these tissues using the „peq gold TRIfast“ reagent (Pqlab). mRNA was reverse transcribed using the tagged oligo dT oligonucleotide 5'-tcc taa cgt agg tct aga cct gtt gca  $t_{(18)}$ -3' (Fig. 4B, oligo 1) and the Superscript II polymerase (LIFE) at 42 °C. In order to amplify a fragment of the APIT gene the degenerated primer 5'-tc gtg ttc gar tac tci gay cg-3' derived from the APIT peptide VFEYSDR (Fig. 4B, oligo 2) and the specific primer 5'- ctg tag gtc tag acc tgt tgc a-3' (Fig. 4B, oligo 3) directed against the tag sequence of the oligo dT-primer was used. PCR was performed with the „expand long template“ system (ROCHE, Mannheim) at 68 °C and the product was cloned into the pCMV-vector (Stratgene) and sequenced. The 5' terminal cDNA of APIT was cloned using the 5' RACE System (LIFE) according to the manufacturers instructions. Primers 5'-ccg tgt aga tct cac tgc cat a-3' (Fig. 4B, oligo 4) or 5'-ccg ttg agt tgt aga cct-3 (Fig. 4B, oligo 6) were combined with the primers 5'-ggc cac gcg tcg act agt acg ggi igg gii ggg

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iig-3' (Fig. 4B, oligo 5) or 5'-aatt ggc cac gcg tcg act agt ac-3' (Fig. 4B, oligo 7) to yield a product which was cloned into the pCDNA3-vector (Invitrogen) and sequenced. Finally, full length APIT cDNA was obtained by amplifying the APIT using the specific primers 5' – aa ttc tcg tct gct gtg  
5 ctt ctc ct (Fig. 4B, oligo 8) and 5' – gac tta gag gaa gta gtc gtt ga (Fig. 4B, oligo 9) and cloned into the pGEX-4T3 Vector (Amersham). DNA from 3 clones of transfected E.coli was prepared and sequenced.

The identity of the isolated gene was confirmed by comparing the  
10 computed translational product (Fig. 4C) with the amino acid sequences of the tryptic peptides (Fig. 4A) and the peptide mass fingerprint. It consisted of 1608 bp coding for a protein of 535 amino acids (Fig. 4C) with the predicted mass of 60,167 dalton and a pI of 4.59. The N-terminal 18 amino acids of APIT comprised a putative secretion signal sequence which  
15 was absent from the mature protein, most likely due to posttranslational modification during secretion. Furthermore, APIT exhibited homology to FAD-binding oxidoreductases with a conserved dinucleotide binding fold around amino acids 39 to 66 followed by a so-called GG-motif typical for certain oxidases like LAAO, MAO (Fig. 4C) (Dailey et al., 1998, J.Biol.  
20 Chem. 273:13658-13662; Vallon et al., 2000, Proteins 38:95-114; Macheroux et al., 2001 Eur. J. Biochem. 268:1679-1686). The highest degree of homology existed to the Cyplasin from *A. punctata*, the Aplysianin from *A. kurodai* and the mucus-toxin of the giant African snail *Achatina fulica*.

25

Comparing the 3 derived DNA-sequences we often found differences in the third position of coding triplets which nevertheless only seldom produced changes in the amino acid sequence of APIT (Fig. 4C).

30 By the method described above, further 11 clones were isolated from *Aplysia punctata* which have a homology to the sequences described in Fig. 4 of at least 95%. Several mutations of the amino acid sequence were

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found in the domain comprising the dinucleotide binding fold and the GG motif, which probably have no effect upon the function (Fig. 4D). In Pos. 22 of SEQ ID NO: 2, C is replaced by S in two clones. In Pos. 52, A is replaced by T in one clone. In Pos. 60, L is replaced by Q in 7 clones. In  
5 Pos. 69, D is replaced by H in one clone. In Pos. 77, T is replaced by S in one clone.

#### Example 5: FAD association

10 The toxic and enzymatic activity of APIT is due to the presence of an attached FAD.

In order to purify the tumor lytic activity, ink from *A. punctata* was subjected to different purification protocols and afterwards each fraction  
15 was tested for its toxic activity (see example 1). Activity always correlated with the presence of a protein of approximately 60 kDa (Fig. 5 A and B). Moreover, APIT was found to contain carbohydrate residues using the DIG Glycan/Protein double labeling method (Roche; data not shown). Furthermore, all spectra of the highly active fractions exhibited a double  
20 peak at 390/470 nm (Fig. 5C) which is characteristic for protein bound flavines (Massey et al., 2000, Biochem Soc. Trans. 28:283-96). Heating of APIT for 10 min to 60°C, which is accompanied by a substantial loss of activity also results in loss of detectable FAD-absorption, as is the case with lowering the pH to inactivating values around pH 3. Heating and  
25 pH-challenge of APIT was performed as described in example 3 (data not shown).

Consistently, APIT contained the conserved dinucleotide binding fold involved in pyrophosphate binding (Wierenga et al., 1986, J. Mol. Biol.,  
30 187:101-107) which is found in many flavoproteins (Fig. 4B; example 4). Moreover, in APIT like in many oxidases a so-called GG-motif is found adjacent to the dinucleotide binding fold (Dailey et al., 1998, J. Biol.

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Chem. 273:13658-13662, Vallon et al., 2000, Proteins, 38:95-114). Based on the structure of the dinucleotide binding fold and conserved sequence motifs, FAD containing proteins are ordered into 4 families (Dym et al., 2001, Protein Sci. 10:1712-28). According to this classification and  
5 based on homology APIT belongs to the Glutathione reductase 2 family (GR2) (Dym et al., 2001, Protein Sci. 10:1712-28). The data show that FAD is a necessary prosthetic group for toxic and enzymatic activity of APIT.

10 **Example 6: Cell-death is mediated via H<sub>2</sub>O<sub>2</sub>**

Proteome analysis revealed that thioredoxin peroxidase II is involved in the APIT mediated tumor cell death. Thioredoxinperoxidase II is involved in detoxification of reactive oxygen species (ROS) by reducing hydrogen  
15 peroxides as well as other peroxides. We therefore tested whether H<sub>2</sub>O<sub>2</sub> is produced during APIT incubation and found that H<sub>2</sub>O<sub>2</sub> is the mediator of APIT-induced cell death. Scavenging this toxic compound by catalase over a certain period of time (6-8 hours) results in survival of APIT treated cells. Notable long-term exposure of tumor cells (> 18 hours) with APIT and  
20 catalase causes the death of tumor cells by the deprivation of L-lysine and L-arginine.

H<sub>2</sub>O<sub>2</sub> production was measured after incubation of APIT in medium alone and in cell suspension as described in example 3. Toxicity was measured  
25 by quantifying propidium iodide uptake (1  $\mu$ g/ml in PBS) by Flow Cytometry. Cell vitality was determined as metabolic activity via the turnover of WST-1 (ROCHE, Mannheim) to red formazan by the mitochondrial dehydrogenase of viable cells. Absorbance of the cell suspension was measured photometrically at 450 nm (690 nm reference).

30

As shown in Fig. 6A, APIT induced the production of H<sub>2</sub>O<sub>2</sub> in the presence (167  $\mu$ M) as well as in absence of cells (280  $\mu$ M). This strongly argues for

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an enzymatic activity of APIT which transforms medium ingredients under the production of hydrogen peroxide. In the presence of cells the measured  $H_2O_2$  amount is somewhat lower which might be explained by cellular consumption and degradation of  $H_2O_2$ . In the absence of APIT  $H_2O_2$  was not detectable. To investigate whether the APIT-induced cell death is mediated by  $H_2O_2$ , cells were treated with APIT in the presence of the  $H_2O_2$  degrading enzyme catalase and then stained with PI. Catalase completely abolished the ink-induced increase of PI stained cells (Fig. 6B). Degradation of  $H_2O_2$  by catalase also inhibited the rapid break-down of metabolic activity induced by APIT (Fig. 6C) but, as expected, was ineffective in blocking CD95 (Fas/Apo-1)-induced cell death in the same assay (Fig. 6C). In the presence of catalase APIT no longer induced morphological changes of tumor cells as judged by microscopic investigation (Fig. 6D). The highly efficient inhibition by catalase in particular suggested that no other substance than  $H_2O_2$  elicits the toxic effect observed in APIT-treated samples. Consistently,  $H_2O_2$  induced the phenotype typical for APIT-treated cells (Fig. 6D). Furthermore, proteome analyses revealed changes in  $H_2O_2$  treated cells which were characteristic of APIT-treated cells. These data together clearly demonstrated that the cytotoxic activity depended on the  $H_2O_2$  producing enzymatic activity of APIT.

Long-term exposure of Jurkat cells to ink from *Aplysia punctata* in combination with catalase resulted in metabolic activity being decreased to 20% (Fig. 6 E, right panel, white bar). The same result is achieved by treatment with purified APIT in combination with catalase (not shown). Since catalase was effective in inhibiting the  $H_2O_2$ -induced loss of metabolic activity completely (Fig. 6E, right panel, black bar), it was concluded that long-term treatment with APIT in the presence of an  $H_2O_2$  scavenger, such as catalase, kills tumor cells not by the remaining low  $H_2O_2$  concentrations but by the deprivation of L-lysine and L-arginine.

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**Example 7: APIT is a L-lysine/L-arginine  $\alpha$ -oxidase. Enzymatic activity is a prerequisite for toxicity**

APIT produced  $H_2O_2$  in RPMI medium in the absence of cells. In order to  
5 identify the substrates in cell culture medium which are converted to  $H_2O_2$   
by APIT, we prepared different media with defined amino acid composition  
by supplementing HEPES buffered modified Krebs Ringer medium (KRG: 25  
mM HEPES pH 7.4, 125 mM NaCl, 5 mM KCl, 1.2 mM  $KH_2PO_4$ , 5 mM  
NaHCO<sub>3</sub>, 6 mM glucose, 1.2 mM MgSO<sub>4</sub>, 1 mM CaCl<sub>2</sub>) with 10% FCS, 2  
10 mM glutamine, essential and non-essential amino acids (Invitrogen), or  
single essential amino acids in concentrations equivalent to RPMI medium  
(Invitrogen). Media were adjusted to pH 7.4 and filter sterilized. After  
incubation of these media with purified APIT the enzymatic activity was  
measured as  $H_2O_2$  production via turnover of ABTS (2,2-Azino-bis  
15 (3-ethylbenzthiazoline-6-sulfonic acid) to a green formazan in the presence  
of  $H_2O_2$  and horseradish peroxidase (Fig. 7A and Table 1).

In a next step we checked whether the substrate specificity could be  
impaired by digest of APIT. For proteolytic digest aliquots of dialysed ink  
20 were treated for 2 h with proteinase K (0,05 mg/ml final) in PBS at 37 °C.  
Reaction was stopped by adding aprotinin (1  $\mu$ g/ml final) or PEFA ([4-(2-  
aminoethyl)-benzolsulfonyl fluoride-hydrochloride]-hydrochloride; 0,25  
mg/ml final), and digest was checked on a 15% SDS-PAGE. After  
incubation of digested ink with different amino acid compositions in  
25 potassium phosphate buffer the enzymatic activity was measured as  $H_2O_2$   
production (Fig. 7B).

In order to test whether withdrawal of L-lysine and L-arginine results in  
rescue of APIT-treated cells we incubated Jurkat cells in medium lacking  
30 L-lysine and L-arginine. Control cells were cultured in a medium containing  
L-lysine(HCl (40 mg/l) and L-arginine(HCl (240 mg/l). Toxicity was

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measured by quantifying propidium iodide uptake (1  $\mu$ g/ml in PBS) by Flow Cytometry (Fig. 7C).

5 Cell vitality was determined as metabolic activity via the turnover of WST-1 (ROCHE, Mannheim) to red formazan by the mitochondrial dehydrogenase of viable cells. Absorbance of the cell suspension was measured photometrically at 450 nm (690 nm reference). As control tumor cells were killed by anti-CD95 treatment (Fig. 7D).

10  $\alpha$ -Keto acids were quantified photometrically by their reaction with the hydrazone MBTH (3-methyl-2-benzothiazolone hydrazone hydrochloride) as described (Soda et al., 1968, Anal. Biochem. 25:228-235) (Fig. 7E).

15 The  $K_m$  value for L-lysine was determined as  $H_2O_2$  production and calculated according to Michaelis Menten with the GraphPad Prism 3.0 software (GraphPad Software, San Diego California USA) using non linear regression (Fig. 7F).

20 Surprisingly, from all amino acids tested only L-lysine and L-arginine served as substrates for APIT to produce hydrogen peroxide (Fig. 7A). Moreover, the restricted substrate specificity was even maintained when APIT was digested with protease K suggesting that the protease resistant fragment of APIT contains both, the active domain and the domain which determines the substrate specificity (Fig. 7B). These data were confirmed by functional  
25 analyses which showed that APIT was unable to induce cell death (Fig. 7C) or reduce metabolic activity (Fig. 7D) in tumor cells incubated in medium lacking L-lysine and L-arginine, indicating that the enzymatic activity of APIT is the prerequisite for its toxicity. L-lysine and L-arginine deprivation had no influence on the metabolic activity of tumor cells under the  
30 experimental conditions (Fig. 7D). Activation of CD95(Fas/Apo-1) efficiently impaired cell vitality irrespective of the presence of L-lysine or

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L-arginine (Fig. 7D), demonstrating that cell death can be induced under L-lysine and L-arginine limited conditions.

5 As shown in the reaction scheme in figure 7G,  $\alpha$ -keto derivatives are produced by amino acid oxidases and these could indeed be demonstrated when L-lysine was used as substrate for APIT (Fig. 7E). These results suggested that APIT catalyses the formation of  $H_2O_2$  by the reaction outlined in figure 7G. Kinetic studies analyzed according to Michaelis-Menten revealed a  $K_m$  of 0.182 mM for L-lysine (Fig. 7F).

10

By adding L-lysine (2-50  $\mu$ g/ml) to tumor cells which are cultured with APIT (20 ng/ml) in medium depleted of L-lysine and L-arginine or in pure FCS, the metabolic activity of the tumor cells can be reduced down to 16% respectively 50% of the control cells without additional L-lysine. This shows that the tumorolytic effect of APIT can be manipulated by changing the amount of available substrate which is of significance for *in vivo* studies and/or for application of APIT in pharmaceutical compositions and/or methods for treatment of cancer.

15

20 **Example 8: Sensitivity of different tumor cell lines to APIT induced cell death.**

25

Tumor cells were harvested in the log phase. Triplicates of each 50,000 cells were cultured in a flat bottomed 96-well-plate in 100  $\mu$ l medium with increasing concentrations of APIT. After 14 hours the metabolic activity of the cells was determined by addition of 10  $\mu$ l WST-1 per well (ROCHE, Mannheim). The yellow tetrazolium salt is cleaved to red formazan by cellular enzymes of viable cells. The metabolic activity correlates with cell vitality and was quantified by measuring the absorbance of the dye solution with a spectrophotometer at 450 nm (reference 650 nm).

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APIT is able to kill different tumor cells. T and B cell leukemia cell lines (Jurkat neo, CEM neo, SKW neo), a chronic myelogenous leukemia cell line (K562), and cells from an orphan and aggressive osteosarcoma (Ewings tumor: RDES, A673) showed the highest sensitivity to the APIT induced cell death ( $IC_{50} \leq 5.6$  ng/ml), followed by cells derived from small cell lung cancer (GLC4, GLC4/ADR), cervix cancer (Chang) and acute monocytic leukemia (THP-1) ( $IC_{50} \leq 10$  ng/ml). Most of the adherent growing cells of solid tumors (breast cancer: MCF-7, SK-BR-3; prostate cancer: PC3, DU-145; colon cancer: HT-29; cervix cancer: HeLa; uterus cancer: Hec-1-B; larynx cancer HEP-2; stomach cancer: AGS; liver cancer: Hep G2) and the monocyte leukemia cell line MonoMac 6 are less sensitive at the indicated cell concentration ( $IC_{50} \leq 20$  ng/ml), but become more sensitive when lower cell concentrations were used ( $IC_{50}$  5 - 10 ng/ml).

Resistance to apoptosis as well as multi drug resistance (MDR) represent severe problems in cancer therapy. It is therefore of particular interest that APIT kills apoptosis resistant cell lines as well as MDR cancer cell lines equally efficient as their non resistant counter parts (Tab. 2): Over-expression of apoptosis inhibitors of the Bcl-2 family in acute lymphoblastic leukemia cell lines (CEM Bcl-X<sub>L</sub>, Jurkat Bcl-2) as well as in B cell leukemia (SKW Bcl-2) (Tab. 2; 4th row) does not protect from APIT mediated cell death and results in  $IC_{50}$  values of  $\leq 6$  ng/ml, similar to the non-transfected parental cell lines, confirming that APIT induce cell death in an apoptosis independent way. The MDR cell line GLC4/ADR (Tab. 2, 5th row) was generated by selection with doxorubicin (Zijlstra et al., 1987, Cancer Res. 47:1780-1784). Its multifactorial MDR is caused by over-expression of MRP-1 and a decreased activity of the DNA topoisomerase II. GLC4/ADR cells possess almost the same sensitivity to APIT ( $IC_{50}$  10 ng/ml) as the parental line GLC4 does ( $IC_{50}$  9 ng/ml).

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**Example 9: Proteome analysis: change in protein expression pattern in Jurkat T cells after treatment with APIT**

**Treatment with APIT.** Jurkat T cells ( $5 \times 10^5$  /ml) were incubated with  
5 APIT (20 ng/ml) for 8 h at 37 °C in 5.0% CO<sub>2</sub> in the presence of 1 µg/ml cycloheximide. Controls were performed without APIT.

**Total cell lysate.** The Jurkat T cells were solubilized in 5 volumes of a buffer containing 9 M urea, 25 mM Tris/HCl, pH 7.1, 50 mM KCl, 3 mM  
10 EDTA, 70 mM DTT, 2.9 mM benzamidine, 2.1 µM leupeptin, 0.1 µM pepstatin, 1 mM PMSF, and 2% carrier ampholytes (Servalyte pH 2-4, Serva, Heidelberg, Germany). After 30 minutes of gentle stirring at room temperature, the samples were centrifuged at 100000 g (Ultracentrifuge Optima TLX, Beckman, München, Germany) for 30 minutes with a  
15 TLA120.2 rotor, which were kept at room temperature before centrifugation. The clear supernatant was frozen at -70 °C.

**Proteomics.** The methods of preparing 2-DE gels, staining with Coomassie Blue G-250, staining with silver nitrate, in-gel tryptic digestion, peptide  
20 mass fingerprinting by MALDI-MS, and identification of the proteins are described in Jungblut et al., Molecular Microbiology, 2000, 36, 710-725.

Identification was performed using the peptide mass fingerprinting analysis software MS-Fit (<http://prospector.ucsf.edu/ucsfhtml3.2/msfit.htm>) or  
25 ProFound (<http://canada.proteometrics.com/prowl-cgi/ProFound.exe?FORM=1>). Searches were performed in the databases NCBI nr and SwissProt. The proteins are referenced by the genbank identifier, accession number and/or version number.

30 **Results.** APIT induces either upregulation, downregulation, or modification of the proteins. Modification in the context of this example is a change in the apparent mass and/or the apparent pI value of the protein. By

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comparison of 2-DE patterns of APIT-treated whole cell lysates with the corresponding patterns of untreated cells, the proteins as described in Table 3 were identified to be affected by APIT.

5     **Example 10:           Transcriptome analysis**

The influence of APIT on the gene expression of tumor cells was investigated by Microarray technology.

10     ***In situ* Oligonucleotide Arrays.** A custom oligonucleotide glass array of specific 60mer oligonucleotides representing the mRNA of about 8500 human genes was designed based on human Unigene clusters (Unigene build No. 148) including positive and negative control oligonucleotides (*Homo sapiens* house keeping genes and *Arabidopsis thaliana* genes  
15     respectively). The probe design included a base composition filter and a homology search to minimise cross-hybridisation.

**RNA isolation, labelling and hybridisation to arrays.** Jurkat neo cells ( $1 \times 10^7$  in 20 ml) were cultured for 2 hours in medium (RPMI + 10 % FCS) in the  
20     presence or absence of APIT (10 ng/ml) at 37°C, 5% CO<sub>2</sub>. Cells were harvested and the pellet was dissolved in 2 ml Trizol (Life Technologies). Total RNA was extracted after addition of chloroform and subsequent centrifugation and precipitated with isopropanol. After washing the pellet with 75% ethanol it was briefly air-dried. Quality control of the RNA  
25     included exclusion of genomic DNA by PCR and "Lab on a chip technology" (Bioanalyser). RNA (5 µg) from each pool was amplified using a reverse transcriptase/T7 polymerase. 1.5 µg of test cRNAs labelled either with Cy3 or Cy5 were hybridised for 16 hours at 65°C to arrays. Each sample was also labelled and hybridised with the reverse fluorophore to  
30     obviate possible dye bias. Slides were scanned using a Microarray scanner. Background signal was determined using negative control spots and

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subtracted, data were normalised relative to non-regulated genes. Data from duplicate hybridizations were combined.

**Results.** Tables 4 and 5 summarize the genes with increased or decreased transcription rate of treated cells compared with untreated cells, indicating these genes and/or its gene products (proteins) to be targets of APIT and/or H<sub>2</sub>O<sub>2</sub>.

**Example 11: Knock down of Prx I sensitized tumor cells for APIT induced cell death**

Peroxiredoxin I (Prx I) exhibited the most significant modification observed in 2-DE protein patterns of APIT treated cells in comparison to untreated Jurkat cells (Table 3). The modification of Prx I which is observed in 2-DE gel analysis of APIT treated cells resembles that described for the oxidized and inactivated Prx I, indicating that APIT inactivates this detoxification system. In order to investigate the role of Prx I for the APIT induced cell death we performed knock down of Prx I expression by RNA interference (RNAi). If Prx I was involved in the detoxification of H<sub>2</sub>O<sub>2</sub> produced by APIT, we expected to observe a sensitization in cells in which Prx I expression is decreased.

Therefore, 20.000 HeLa cells/well were seeded in a 96 well plate one day prior to transfection. Transfection was performed with 0.25 µg siRNA directed against

Prx I having the sequence (SEQ ID NO: 9):

5' -GGCUGAUGAAGGCAUCUCGdTdT-3'  
3' -dTdTCCGACUACUCCGUAGAGC-5' ,

Lamin A/C having the sequence (SEQ ID NO: 30):

5' -CUGGACUCCAGAAGAACAAdTdT  
3' -dTdTGACCUGAAGGUCUUCUUGU-5' ,

and Luciferase having the sequence (SEQ ID NO: 31):

5' -CUUACGCUGAGUACUUCGAdTdT-3'  
3' -dTdTGAAUGCGACUCAUGAAGCU-5' ,

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as control and 2  $\mu$ l transmessenger per well using the transmessenger transfection kit (Qiagen, Hilden, Germany) according to manufacturers instructions. For APIT treatment (40ng/ml) transfections were conducted in triplicates. 24 h after transfection cells were splitted and grown for additional 48 h before fresh medium with or without APIT was added for 6h. Assay conditions which led to a 50 to 70 % reduction of the metabolic activity of treated cells were chosen for RNAi experiments. Metabolic activity was determined as described in Example 2. In parallel, RNA from about 50.000 cells was isolated using the RNeasy 96 BioRobot 8000 system (Qiagen) 48 h after transfection. The relative amount of mRNA was determined by realtime PCR using Quantitect<sup>TM</sup> SYBR Green RT-PCR Kit from Qiagen following manufacturers instructions. The expression level of Prx I mRNA was normalised against the internal standard GAPDH. The following primers were used: Prx I 5': CTGTTATGCCAGATGGTCAG, Prx I 3': GATACCAAAGGAATGTTCATG,  
Lamin A/C 5':CAAGAAGGAGGGTGACCTGA,  
Lamin A/C 3':GCATCTCATCCTGAAGTTGCTT,  
GAPDH 5':GGTATCGTGGAAGGACTCATGAC,  
GAPDH 3':ATGCCAGTGAGCTTCCCGTTCAG.

20

To measure sensitization, conditions were chosen under which the reduction of metabolic activity of treated cells was 50 % or less of the untreated cells. siRNAs were transfected into HeLa cells and after 72 h cells were treated with APIT for 6 h and metabolic activity was determined. In parallel, cells were harvested for quantitative analysis of the respective mRNAs by realtime PCR (Fig. 8 A). The mRNA of Prx I was reduced by more than 90 % compared to the mRNA level of GAPDH. Interestingly, this reduction of Prx I expression significantly sensitized the cells for killing by APIT whereas control siRNA directed against Luciferase and Lamin A/C had no effect (Fig. 8 B). Our data show that knock down of Prx I by RNAi rendered the cells hypersensitive for APIT suggesting that Prx I is part of an H<sub>2</sub>O<sub>2</sub> detoxifying pathway which is modulated by APIT.

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In summary, we identified the modification of Prx I, as an important step in the APIT of this detoxification system. The fact that the knock down of Prx I expression by RNAi increased the sensitivity of tumor cells for the cytolytic activity of APIT underlines the impact of Prx 1 RNA interference  
5 for cancer therapy.

**Example 12: APIT does not induce actin depolymerisation**

Cyplasin S and L, proteins from *Aplysia punctata* which induce cell death  
10 of tumor cells were described to cause fast actin depolymerisation in human tumor cells (see WO 03/057726). The influence of APIT treatment on actin filaments by fluorescence staining of actin by Phalloidin-TRITC (Tetramethylrhodamin- isothiocyanat) is investigated.

15 HeLa cells (1.5 x 10<sup>5</sup> cells/well/ml) were cultured over night on cover slips in 12 well plates. Subsequently, cells were incubated in the presence or absence of APIT (40 ng/ml) for 6 h or Cytochalasin D (1  $\mu$ M; Sigma 8273) for 30 min. After washing in PBS, cells on cover slips were fixed for 10 min in 3,7 % PFA (paraformaldehyde), washed again and finally  
20 permeabilized by a 1 min incubation in 0,5 % Triton X-100. Blocking of unspecific binding sites by incubation in PBS, 1% FCS, 0,05 % Tween 20 was followed by actin staining with Phalloidin-TRITC in blocking puffer for 15 min and 3 fold washing. Nuclei were stained by the presence of Hoechst 33258 in the last washing step. Cover slips were investigated by  
25 fluorescence microscopy.

As shown in Fig. 9 untreated cells (A) possess a typical actin cytoskeleton. Incubation in the presence of Cytochalasin (B), an inducer of rapid actin depolymerisation, resulted in a massive loss of actin filaments and an  
30 accumulation of actin in clumps. In contrast, APIT(C) did not induce actin depolymerisation in HeLa cells. APIT treated cells remain their actin filaments, even after 6 h when the plasma membrane was already

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disrupted (see example 2, Fig. 2D). This clearly differentiates APIT induced cell death from that induced by Cyplasins.

**Example 13:        Healthy human cells are resistant against the APIT-induced cell death**

5

To analyze the specificity of APIT for tumor cells, normal human umbilical vein endothelial cells (HUVEC) and tumor cells (Jurkat cells) were incubated with increasing amounts of purified APIT and analyzed for lactate dehydrogenase (LDH) release (Fig. 10).

10

HUVEC and Jurkat cells (50,000 cells/100  $\mu$ l/wells) were treated with increasing amounts of APIT in a 96 well plate. After over night incubation half of the culture supernatants (50  $\mu$ l) were transferred in fresh wells and mixed with 50  $\mu$ l reagent of Cytotoxicity Detection Kit-LDH according to the manufacturers instruction (Roche 1644793). Release of LDH in the supernatant is found only, when cells were killed by APIT. LDH release was calculated as the ratio of LDH activity of APIT treated cells relative to the LDH activity of Triton X 100 lysed cells.

15

20

Jurkat cells showed a dramatic release of LDH upon incubation with APIT (Fig. 10). In contrast, even at the highest APIT concentrations used in this experiments (40 ng/ml), APIT treated HUVEC cells only showed a minor LDH release below 10 %, indicating a strong resistance of these normal cells against the cytolytic activity of APIT. As several tumor cell lines showed a similar APIT sensitivity as the Jurkat cells (Table 2), the data suggest the toxic effect induced by APIT is tumor specific.

25

**Claims**

1. A polypeptide comprising the amino acid sequence shown in SEQ ID  
5 NO: 2, 4, or 6.
2. A polypeptide claimed in Claim 1 which is an oxidase which is  
capable to produce H<sub>2</sub>O<sub>2</sub>.
- 10 3. A polypeptide as claimed in any one of the Claims 1 to 2 which is  
an alpha amino acid oxidase.
4. A polypeptide as claimed in Claim 3 which is a L-lysine and/or L  
arginine oxidase.
- 15 5. A polypeptide comprising a fragment of the polypeptide as claimed  
in any one of the Claims 1 to 4.
6. A polypeptide as claimed in Claim 5 which is obtained by protease  
20 digestion of the polypeptide as claimed in any of the Claims 1 to 4.
7. A polypeptide as claimed in Claim 6 which is obtained by proteinase  
K digestion.
- 25 8. A polypeptide as claimed in Claim 5 comprising the sequence  
selected from amino acid residue No. 39 to 77 in SEQ ID NO: 2.
9. A polypeptide as claimed in Claim 8 comprising 1 to 20 additional  
amino acid residues at the N-terminus and/or the C-terminus  
30 selected from the sequences of SEQ ID NO: 2 or SEQ ID NO: 4  
adjacent to the sequence selected in claim 8.

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10. A polypeptide as claimed in Claim 8 comprising 1 to 10 additional amino acid residues at the N-terminus and/or the C-terminus selected from the sequences of SEQ ID NO: 2 adjacent to the sequence selected in claim 8.
- 5 11. A polypeptide as claimed in Claim 8 comprising 1 to 5 additional amino acid residues at the N-terminus and/or the C-terminus selected from the sequences of SEQ ID NO: 2 adjacent to the sequence selected in claim 8.
- 10 12. A polypeptide as claimed in any one of the Claims 2 to 11, wherein the H<sub>2</sub>O<sub>2</sub> producing activity can be regulated by the addition or removal of an L-amino acid.
- 15 13. A polypeptide as claimed in Claim 12 which is regulated by L-lysine, L-arginine, a derivative or precursor of L-lysine, a derivative or a precursor of L-arginine, or a mixture thereof.
- 20 14. A polypeptide which has an identity to the polypeptides of any of the claims 1 to 13 of at least 70%.
15. A polypeptide as claimed in any one of the claims 1 to 14 which is a recombinant polypeptide.
- 25 16. The polypeptide as claimed in claim 15, which is a fusion polypeptide.
17. A nucleic acid encoding a polypeptide of any of the Claims 1 to 16.
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18. The nucleic acid of Claim 17 comprising
- (a) a nucleotide sequence as shown in SEQ ID NO: 1, 3, or 5, or at least the polypeptide coding portion thereof, or the complement thereof, or
  - 5 (b) a nucleotide sequence corresponding to the sequence of (a) within the scope of degeneracy of the genetic code, or the complement thereof, or
  - (c) a nucleotide sequence hybridizing under stringent condition with the sequence of (a) and/or (b), or
  - 10 (d) a nucleotide sequence which has a homology of at least 70% to the sequences of (a) and/or (b).
19. The nucleic acid of claim 17 or 18 operatively linked to an expression control sequence.
- 15 20. The nucleic acid of any one of claims 17 to 19 which is a recombinant vector.
21. A recombinant cell comprising the nucleic acid of any one of the Claims 17 to 20.
- 20 22. An antibody directed against a polypeptide of any one of the Claims 1 to 16.
- 25 23. A pharmaceutical composition or a kit of pharmaceutical compositions comprising the polypeptide as claimed in any of the Claims 1 to 16, in a pharmaceutically effective amount and optionally together with suitable diluents, carriers and/or adjuvants.
- 30 24. The pharmaceutical composition or kit of Claim 23 comprising at least one further component which is a substance capable of modulating the cytotoxic activity of the polypeptide.

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25. The pharmaceutical composition or kit of Claim 24, wherein the polypeptide and the modulating substances are provided as separate preparations.
- 5 26. The pharmaceutical composition or kit of Claim 25, wherein the polypeptide is provided for administration before the modulating substances.
- 10 27. The pharmaceutical composition or kit of any one of the Claims 24 to 26, wherein the modulating substance selected from (i) L-lysine, L-arginine, a derivative or precursor of L-lysine, a derivative or precursor of L-arginine, or a mixture thereof, and/or (ii) a flavine nucleoside.
- 15 28. The pharmaceutical composition or kit of any one of the Claims 24 to 27, further comprising a nucleic acid, and/or a recombinant cell, and/or an APIT inhibitor.
- 20 29. The pharmaceutical composition or kit of Claim 28, wherein the inhibitor is an antibody against the polypeptide.
30. A polypeptide, and/or a nucleic acid, and/or a recombinant cell, and/or an inhibitor as claimed in any one of the Claims 1 to 22, for use in a diagnostic or therapeutic method in humans or animals.
- 25 31. A polypeptide, and/or a nucleic acid, and/or a recombinant cell, and/or an inhibitor as claimed in Claim 30 for diagnosis or treatment of cancer.
- 30

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32. A polypeptide, and/or a nucleic acid, and/or a recombinant cell, and/or an inhibitor as claimed in Claim 30 or 31 for diagnosis or treatment of lung cancer, breast cancer, prostate cancer, colon cancer, cervix cancer, uterus cancer, larynx cancer, stomach cancer, liver cancer, Ewings sarkoma, acute lymphoid leukemia, chronic myeloid leukemia, apoptosis resistant leukemia, MDR lung cancer, pancreas cancer, gastric cancer, kidney cancer, gliomas, melanomas, chronic lymphoid leukemia, and/or lymphoma.
33. Use of a substance as described in Table 3 or/and Table 4 or/and Table 5 as target substance for a polypeptide of any one of Claim 1-16.
34. Use of claim 33 in which the target substance is a protein.
35. Use of claim 34 in which the target substance is a peroxidase, particularly peroxiredoxin I.
36. Use of claim 35 in which the target substance comprises
- (a) the amino acid sequence shown in SEQ ID NO: 8, or/and
  - (b) an amino acid sequence which is homologous to the sequence of (a) with at least 70%, or/and
  - (c) a fragment of the amino acid sequence of (a) or (b).
37. Use of claim 33 in which the target substance is a nucleic acid.
38. Use of claim 37 in which the target substance codes for a peroxidase, particularly peroxiredoxin I.

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39. Use of claim 38 in which the target substance comprises
- (a) the nucleotide sequence shown in SEQ ID NO: 7, or/and
  - (b) a nucleotide sequence which corresponds to the sequence of (a) within the scope of the degeneracy of the genetic code, or/and
  - (c) a nucleotide sequence hybridizing to the sequence of (a) or/and (b) under stringent conditions, or/and
  - (d) a fragment of the nucleotide sequence of (a), (b) or (c).
40. Use of a substance of any one of the claims 33 to 39 for the identification of new pharmaceutical agents, particularly in a screening method.
41. A pharmaceutical composition or kit comprising as an active agent a combination of APIT and at least one inhibitor of a substance of any one of claims 33 to 39.
42. An inhibitor of peroxiredoxin I activity which is an RNA molecule, particularly a double stranded RNA molecule comprising a nucleic acid of at least 15 nucleotides complementary to a peroxiredoxin I transcript.
43. An inhibitor as claimed in claim 42, wherein the peroxiredoxin I transcript is derived from the sequence of SEQ ID NO: 7.
44. An inhibitor as claimed in claims 42 or 43, wherein the one or two strands independently have a length of 19 to 25 nucleotides, preferably 19 to 23 nucleotides.

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45. An inhibitor as claimed in any of the claims 42 to 44 which is a double-stranded RNA molecule having a sequence selected from the group of sequences consisting of SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11; SEQ ID NO: 12; SEQ ID NO: 13; SEQ ID NO: 14; SEQ ID NO: 15; SEQ ID NO: 16; SEQ ID NO: 17; SEQ ID NO: 18; SEQ ID NO: 19; SEQ ID NO: 20; SEQ ID NO: 21; SEQ ID NO: 22; SEQ ID NO: 23; SEQ ID NO: 24; SEQ ID NO: 25; SEQ ID NO: 26; SEQ ID NO: 27; SEQ ID NO: 28; SEQ ID NO: 29, optionally with one or two 3' overhangs and optionally one or more modified nucleotides.
46. A pharmaceutical composition or kit comprising an inhibitor or a nucleic acid encoding an inhibitor as claimed in any one of the claims 42 to 45.
47. A pharmaceutical composition as claimed in claim 46, comprising a gene therapy delivery system suitable for the delivery of a nucleic acid encoding the inhibitor as claimed in any of the claims 42 to 45 to predetermined tissues or/and cell types.
48. Use of an inhibitor as claimed in any of the claims 42 to 45 for the manufacture of a medicament for the diagnosis or/and treatment of cancer.
49. A pharmaceutical composition or kit comprising
- (I) a polypeptide obtainable from *Aplysia*, comprising an amino acid sequence selected from:
    - (a) D-G-E-D-A-A-V (SEQ ID NO:32) and/or
    - (b) (D/Q)-G-(I/V)-C-R-N-(Q/R)-R-(Q/P) (SEQ ID NO:33),
    - (c) F-A-D-S (SEQ ID NO:34),
    - (d) G-P-D-G-(I/L)-V-A-D (SEQ ID NO:35),
    - (e) P-G-E-V-S-(K/Q)-(I/L) (SEQ ID NO: 36),

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- (f) A-T-Q-A-Y-A-A-V-R-P-I-P-A-S-K (SEQ ID NO:37),
- (g) D-S-G-L-D-I-A-V-E-Y-S-D-R (SEQ ID NO:38),
- (h) G-D-V-P-Y-D-L-S-P-E-E-K (SEQ ID NO: 39) or/and
- (i) SEQ ID NO: 41, 43, 44, 45.

5 or a fragment thereof,

wherein the polypeptide or fragment has cytotoxic activity,  
or/and a nucleic acid comprising

- (i) a nucleotide sequence as shown in SEQ ID NO: 40 or  
42 or at least the polypeptide coding portion thereof or  
10 the complement thereof,

- (ii) a nucleotide sequence corresponding to the sequence  
of (i) within the scope of degeneracy of the genetic  
code, or the complement thereof, or/and

- (iii) a nucleotide sequence hybridizing under stringent  
15 conditions with the sequence of (i) or/and (ii), and

- (II) an inhibitor of a target substance as described in Table 3  
or/and Table 4 or/and Table 5.

- 50. A method for the diagnosis or treatment of cancer, wherein the  
20 pharmaceutical composition or kit as claimed in claims 41, 46, 47 or  
49 is administered to a subject in need thereof.

Table 1

| <b>EAA</b><br>(essential amino acids) |            | <b>NEAA</b><br>(non-essential amino acids) |           |
|---------------------------------------|------------|--------------------------------------------|-----------|
| L-arginine·HCl                        | 126.4 mg/l | L-alanine                                  | 8.9 mg/l  |
| L-cystine                             | 24.02 mg/l | L-asparagine                               | 13.2 mg/l |
| L-histidine·HCl·H <sub>2</sub> O      | 41.92 mg/l | L-aspartic-acid                            | 13.3 mg/l |
| L-isoleucine                          | 52.46 mg/l | L-glutamic acid                            | 14.7 mg/l |
| L-leucine                             | 52.46 mg/l | glycine                                    | 7.5 mg/l  |
| L-lysine·HCl                          | 73.06 mg/l | L-prolin                                   | 11.5 mg/l |
| L-methionine                          | 14.92 mg/l | L-serine                                   | 10.5 mg/l |
| L-phenylalanine                       | 33.02 mg/l |                                            |           |
| L-threonine                           | 47.64 mg/l |                                            |           |
| L-tryptophane                         | 10.2 mg/l  |                                            |           |
| L-tyrosine                            | 36.22 mg/l |                                            |           |
| L-valine                              | 46.86 mg/l |                                            |           |

| <b>Single amino acids</b>      |          |
|--------------------------------|----------|
| histidine·HCl·H <sub>2</sub> O | 20 mg/l  |
| isoleucine                     | 50 mg/l  |
| leucine                        | 50 mg/l  |
| methionine                     | 15 mg/l  |
| phenylalanine                  | 15 mg/l  |
| threonine                      | 20 mg/l  |
| tyrosine                       | 20 mg/l  |
| arginine·HCl                   | 240 mg/l |
| lysine                         | 40 mg/l  |
| D-lysine                       | 40 mg/l  |
| cystine                        | 50 mg/l  |
| tryptophane                    | 5 mg/l   |
| valine                         | 20 mg/l  |
| glutamine                      | 300 mg/l |

Table 2. APIT kills different tumor cell lines

| models for                    | kind of tumor           | tumor cell line        | IC50 (ng/ml) |
|-------------------------------|-------------------------|------------------------|--------------|
| 1. solid tumors               | lung cancer             | GLC4                   | 9.           |
|                               | breast cancer           | MCF-7, SK-BR-3         | *            |
|                               | prostate cancer         | PC3, DU145             | *            |
|                               | colon cancer            | HT-29                  | 20           |
|                               | cervix cancer           | HeLa, Chang            | *, 10        |
|                               | uterus carcinoma        | Hec-1-B                | *            |
|                               | larynx cancer           | HEp-2                  | *            |
|                               | stomach cancer          | AGS                    | *            |
|                               | liver cancer            | Hep G2                 | *            |
| 2. leukemia                   | T cell leukemia (ALL)   | Jurkat neo             | 3.2          |
|                               | T cell leukemia (ALL)   | CEM neo                | 5.6          |
|                               | B cell leukemia         | SKW neo                | 3            |
|                               | Monocyte leukemia (AML) | Mono Mac 6             | *            |
|                               | Monocyte leukemia (AML) | THP-1                  | 10           |
| 3. "orphan" tumors            | Ewings sarcoma          | RDES                   | 4.5          |
|                               |                         | A673                   | 5            |
| 4. apoptosis resistant tumors | (CML)                   | K562                   | 4.25         |
|                               | T cell leukemia (ALL)   | Jurkat Bcl-2           | 2.7          |
|                               | T cell leukemia (ALL)   | CEM Bcl-X <sub>L</sub> | 4.0          |
|                               | B cell leukemia         | SKW Bcl-2              | 5.5          |
| 5. MDR tumors                 | Lung cancer             | GLC4-ADR               | 10           |

Table 3. Proteome analysis

| Description                                                                               | gi                  | NCBI                | NCBI version          | swissprot   | effect |
|-------------------------------------------------------------------------------------------|---------------------|---------------------|-----------------------|-------------|--------|
| Aldolase A (E.C.4.1.2.13)                                                                 | 229674              | 1ALD                | 1ALD                  | P04075      | -      |
| 26S proteasome regulatory chain 12                                                        | 2134660             | S65491              | S65491                | -           | -      |
| 3-Hydroxyacyl-CoA dehydrogenase                                                           | 2078327             | AAB54008            | AAB54008.1            | Q16836      | -      |
| C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase)                              | 115206              | P11586              | P11586                | P11586      | -      |
| Chain A, Structure Of Human Glutamate Dehydrogenase-Apo Form or Glutamate dehydrogenase 1 | 20151189<br>4885281 | 1L1F_A<br>NP_005262 | 1L1F_A<br>NP_005262.1 | -<br>P00367 | m      |
| Cleavage and polyadenylation specific factor 5, 25 kD subunit                             | 5901926             | NP_008937           | NP_008937.1           | -           | +      |
| Cofilin 1                                                                                 | 5031635             | NP_005498           | NP_005498.1           | P23528      | -      |
| Coronin, actin binding protein, 1A                                                        | 5902134             | NP_009005           | NP_009005.1           | P31146      | +      |
| Dihydrolipoamide dehydrogenase precursor; E3 component of pyruvate dehydrogenase          | 4557525             | NP_000099           | NP_000099.1           | P09622      | -      |
| dJ553F4.4 (Novel protein similar to Drosophila CG8055 protein)                            | 12314022            | CAC14088            | CAC14088.1            | -           | +      |
| DNA replication licensing factor MCM4                                                     | 1705520             | -                   | -                     | P33991      | +      |
| Elongation factor1-delta (EF-1-delta)                                                     | 20141357            | P29692              | P29692                | P29692      | -      |
| Enolase 1, alpha; phosphopyruvate hydratase                                               | 4503571             | NP_001419           | NP_001419.1           | Q05524      | +      |
| Glyceraldehyde-3-phosphate dehydrogenase                                                  | 31645               | CAA25833            | CAA25833.1            | P04406*     | +      |
| or uracil DNAGlycosylase                                                                  | 35053               | CAA37794            | CAA37794.1            | P04406*     | -      |
| Heat shock 60kD protein 1 (chaperonin)                                                    | 14603309            | AAH10112            | AAH10112.1            | Q96FZ6      | -      |
| Heat shock 60kDa protein 1 (chaperonin)                                                   | 4504521             | NP_002147           | NP_002147.1           | P10809      | -      |
| Heat shock 70kD protein 9B (mortalin-2)                                                   | 4758570             | NP_004125           | NP_004125.1           | Q8N1C8      | -      |
| Heterogeneous nuclear ribonucleoprotein C, isoform b                                      | 4758544             | NP_004491           | NP_004491.1           | P07910      | m      |
| Hspc117                                                                                   | 6841456             | AAF29081            | AAF29081.1            | Q9P037      | m      |
| Inosine-5'-monophosphate dehydrogenase 2 (IMP dehydrogenase 2)                            | 124419              | P12268              | P12268                | P12268      | +      |
| Isocitrate dehydrogenase 3 (NAD+) alpha                                                   | 5031777             | NP_005521           | NP_005521.1           | P50213      | -      |
| KH-type splicing regulatory protein (FUSE binding protein 2)                              | 4504865             | NP_003676           | NP_003676.1           | -           | -      |
| Nuclear matrix protein NMP200 related to splicing factor PRP19                            | 7657381             | NP_055317           | NP_055317.1           | Q9UMS4      | -      |
| Nucleobindin 2                                                                            | 4826870             | NP_005004           | NP_005004.1           | P80303      | -      |
| 54 kDa nuclear RNA- and DNA-binding protein (p54(nrb)) (p54nrb)                           | 13124797            | Q15233              | Q15233                | Q15233      | +      |
| Peroxisome oxidin 1 (Thioredoxin peroxidase 2)                                            | 548453              | Q06830              | Q06830                | Q06830      | m      |
| Peroxisome oxidin 1; Proliferation-associated gene A; proliferation-associated gene A     | 4505591             | NP_002565.1         | NP_002565.1           | Q06830      | m      |

Table 3. Continuation I

| Description                                                                                                  | gi                  | NCBI                   | NCBI version               | swissprot        | effect |
|--------------------------------------------------------------------------------------------------------------|---------------------|------------------------|----------------------------|------------------|--------|
| Peroxioredoxin 2 (Thioredoxin peroxidase 1)                                                                  | 2507169             | P32119                 | P32119                     | P32119           | +      |
| Peroxioredoxin 3; antioxidant protein 1; thioredoxin-dependent peroxide reductase precursor                  | 5802974             | NP_006784              | NP_006784.1                | P30048           | -      |
| 2-phosphopyruvate-hydratase alpha-enolase; carbonate dehydratase                                             | 693933              | CAA59331               | CAA59331.1                 | P06733           | +      |
| Proteasome subunit alpha type 7                                                                              | 12643540            | O14818                 | O14818                     | O14818           | +      |
| Proteasome subunit beta type 1 (Proteasome component C5) (Macropain subunit C5)                              | 130853              | P20618                 | P20618                     | P20618           | +      |
| Ras-GTPase-activating protein SH3-domain-binding protein; GAP binding protein                                | 5031703             | NP_005745.1            | NP_005745.1                | Q13283           | m      |
| Replication protein A2, 32kDa                                                                                | 4506585             | NP_002937              | NP_002937.1                | P15927           | -      |
| Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (Ly-GDI)                                         | 1707893             | P52566                 | P52566                     | P52566           | -      |
| Ribosomal protein P0; 60S acidic ribosomal protein P0 or similar BLOCK 23                                    | 4506667<br>20536934 | NP_000993<br>XP_165448 | NP_000993.1<br>XP_165448.1 | P05388<br>Q8NHW5 | -      |
| Ribosomal protein, large, P0                                                                                 | 12654583            | AAH01127               | AAH01127.1                 | P05388           | -      |
| RNA-binding protein regulatory subunit                                                                       | 6005749             | NP_009193              | NP_009193.1                | O14805           | +      |
| RNA-binding protein regulatory subunit                                                                       | 12720028            | XP_001707              | XP_001707.2                | O14805           | +      |
| Semenogelin I; Semenogelin                                                                                   | 4506883             | NP_002998              | NP_002998.1                | P04279           | -      |
| Similar to villin 2 (ezrin)                                                                                  | 15530243            | AAH13903               | AAH13903.1                 | P15311           | -      |
| Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)                     | 4826998             | NP_005057              | NP_005057.1                | P23246           | -      |
| Stathmin 1; metablastin; prosolin; oncoprotein 18; phosphoprotein 19; leukemia-associated phosphoprotein p18 | 5031851             | NP_005554              | NP_005554.1                |                  | -      |
| U2 small nuclear ribonucleoprotein A' (U2 snRNP-A')                                                          | 134094              | P09661                 | P09661                     | P09661           | +      |
| Vimentin                                                                                                     | 4507895             | NP_003371              | NP_003371.1                | P08670           | -      |
| Voltage-dependent anion-selective channel protein 2 (VDAC-2) (hVDAC2)                                        | 1172554             | P45880                 | P45880                     | P45880           | -      |

Table 4. Transcriptome analysis

| Unigene cluster | Description                                                                            | GENE     | gi       | pir/NCBI/swissprot | effect |
|-----------------|----------------------------------------------------------------------------------------|----------|----------|--------------------|--------|
| Hs.3833         | 3'-phosphoadenosine 5'-phosphosulfate synthase 1                                       | PAPSS1   | 4885537  | NP_005434.1        | -      |
| Hs.166563       | replication factor C (activator 1) 1, 145kDa                                           | RFC1     | 15011931 | ref:NP_002904.2    | -      |
| Hs.78991        | DNA segment, numerous copies, expressed probes (GS1 gene)                              | DXF68S1E | 6912346  | ref:NP_036212.1    | -      |
| Hs.326035       | early growth response 1                                                                | EGR1     | 119242   | sp:P18146          | ++     |
| Hs.108885       | collagen, type VI, alpha 1                                                             | COL6A1   | 15011913 | ref:NP_001839.1    | ++     |
| Hs.78944        | regulator of G-protein signalling 2, 24kDa                                             | RGS2     | 2135146  | pir:I53020         | ++     |
| Hs.110571       | growth arrest and DNA-damage-inducible, beta                                           | GADD45B  | 9945332  | ref:NP_056490.1    | ++     |
| Hs.78465        | v-jun sarcoma virus 17 oncogene homolog (avian)                                        | JUN      | 135298   | sp:P05412          | +      |
| Hs.82646        | DnaJ (Hsp40) homolog, subfamily B, member 1                                            | DNAJB1   | 1706473  | sp:P25685          | +      |
| Hs.169840       | TTK protein kinase                                                                     | TTK      | 346403   | pir:A42861         | +      |
| Hs.211601       | mitogen-activated protein kinase kinase kinase 12                                      | MAP3K12  | 18202489 | sp:Q12852          | +      |
| Hs.345728       | suppressor of cytokine signaling 3                                                     | SSI-3    | 4507235  | ref:NP_003946.1    | +      |
| Hs.3776         | zinc finger protein 216                                                                | ZNF216   | 5174755  | ref:NP_005998.1    | +      |
| Hs.73037        | cannabinoid receptor 2 (macrophage)                                                    | CNR2     | 450068   | prf:1920360A       | +      |
| Hs.167578       | EST, FLJ25357 hypothetical protein FLJ25357                                            |          | 740170   | 2004399A           | +      |
| Hs.8715         | hypothetical protein MGC3232                                                           | MGC3232  | 3024681  | sp:O00268          | +      |
| Hs.74520        | spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1) | SCA1     | 1082237  | pir:S46268         | +      |
| Hs.6151         | pumilio homolog 2 (Drosophila)                                                         | PUM2     | 14277945 | pdb:1IB3           | +      |
| Hs.8026         | EST, Highly similar to SES2_HUMAN Sestrin 2 [H.sapiens]                                |          | 13633882 | sp:P58004          | +      |
| Hs.82173        | TGFB inducible early growth response                                                   | TIEG     | 11387050 | sp:Q13118          | +      |
| Hs.198307       | von Hippel-Lindau binding protein 1                                                    | VBP1     | 4507873  | ref:NP_003363.1    | +      |
| Hs.179982       | tumor protein p53-binding protein                                                      | TP53BPL  | 5032191  | ref:NP_005793.1    | +      |
| Hs.2549         | adrenergic, beta-3-, receptor                                                          | ADRB3    | 1070630  | pir:QRHUBE         | +      |
| Hs.2128         | dual specificity phosphatase 5                                                         | DUSP5    | 12707566 | ref:NP_004410.2    | +      |
| Hs.36927        | heat shock 105kD                                                                       | HSP105B  | 5729879  | ref:NP_006635.1    | +      |
| Hs.77558        | high mobility group nucleosomal binding domain 3                                       | HMGN3    | 2495254  | sp:Q15651          | +      |
| Hs.460          | activating transcription factor 3                                                      | ATF3     | 88875    | pir:C34223         | +      |
| Hs.104125       | adenylyl cyclase-associated protein                                                    | CAP      | 399184   | sp:Q01518          | +      |
| Hs.24719        | modulator of apoptosis 1                                                               | MAP-1    | 11545896 | ref:NP_071434.1    | +      |
| Hs.8257         | cytokine inducible SH2-containing protein                                              | CISH     | 13124022 | sp:Q9NSE2          | +      |
| Hs.101383       | ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal - human (fragments)       |          | 2135765  | pir:A43932         | +      |

Table 4. Continuation I

| Unigene cluster | Description                                                                                                                                                      | GENE         | gi       | pir/NCBI/swissprot | effect |
|-----------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------|----------|--------------------|--------|
| Hs.276770       | CDW52 antigen (CAMPATH-1 antigen)                                                                                                                                | CDW52        | 4502761  | ref:NP_001794.1    | +      |
| Hs.8084         | hypothetical protein dJ465N24.2.1                                                                                                                                | DJ465N24.2.1 | 10092679 | ref:NP_064713.1    | +      |
| Hs.78829        | ubiquitin specific protease 10                                                                                                                                   | USP10        | 11360280 | pir:T47164         | +      |
| Hs.889          | Charot-Leyden crystal protein                                                                                                                                    | CLC          | 1942631  | pdb:1LCL           | +      |
| Hs.277401       | bromodomain adjacent to zinc finger domain, 2A                                                                                                                   | BAZ2A        | 7304921  | ref:NP_038477.1    | +      |
| Hs.300863       | lethal (3) malignant brain tumor (3)mbt protein (Drosophila) homolog                                                                                             | H-L(3)MBT    | 14141728 | ref:NP_056293.2    | +      |
| Hs.4552         | ubiquitin 2                                                                                                                                                      | UBQLN2       | 16753207 | ref:NP_038472.2    | +      |
| Hs.151903       | GrpE-like protein cochaperone                                                                                                                                    | HMGE         | 18202951 | sp:Q9HAV7          | +      |
| Hs.36606        | EST, Weakly similar to T29982 hypothetical protein F11G11.12 - [C. elegans]                                                                                      |              |          |                    | +      |
| Hs.85302        | adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)                                                                                                         | ADARB1       | 2829669  | sp:P78563          | +      |
| Hs.113823       | ClpX caseinolytic protease X homolog (E. coli)                                                                                                                   | CLPX         | 14916956 | sp:O76031          | +      |
| Hs.25911        | HLA-B associated transcript 2                                                                                                                                    | BAT2         | 18375626 | ref:NP_542417.1    | +      |
| Hs.95821        | osteoclast stimulating factor 1                                                                                                                                  | OSTF1        | 11134088 | sp:Q92882          | +      |
| Hs.11217        | KIAA0877 protein                                                                                                                                                 | KIAA0877     |          |                    | +      |
| Hs.301064       | arfaptin 1                                                                                                                                                       | HSU52521     | 1703203  | sp:P53367          | +      |
| Hs.276238       | EST, Moderately similar to kinase suppressor of ras [Mus musculus]                                                                                               |              |          |                    | +      |
| Hs.211569       | G protein-coupled receptor kinase 5                                                                                                                              | GPRK5        | 2135145  | pir:A48277         | +      |
| Hs.25524        | protein tyrosine phosphatase, non-receptor type 23                                                                                                               | PTPN23       | 7512735  | pir:T14756         | +      |
| Hs.94498        | leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2                                                                                   | LILRA2       | 5803068  | ref:NP_006857.1    | +      |
| Hs.24427        | DKFZP566O1646 protein                                                                                                                                            | DC8          | 7512839  | pir:T08737         | +      |
| Hs.46           | platelet-activating factor receptor                                                                                                                              | PTAFR        | 107346   | pir:A40191         | +      |
| Hs.90800        | EST, Highly similar to matrix metalloproteinase 16, isoform 1; membrane-type matrix metalloproteinase 3; membrane-type-3 matrix metalloproteinase [Homo sapiens] |              | 13027802 | ref:NP_005932.2    | +      |
| Hs.81648        | hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4                                                                                 | FLJ11021     | 2833266  | sp:Q15696          | +      |
| Hs.80338        | Bcl-2-associated transcription factor                                                                                                                            | BTF          | 7661958  | ref:NP_055554.1    | +      |
| Hs.238407       | EST, Weakly similar to hypothetical protein FLJ20489 [Homo sapiens] [H.sapiens]                                                                                  |              | 8923452  | ref:NP_060312.1    | +      |
| Hs.154668       | KIAA0391 gene product                                                                                                                                            | KIAA0391     | 3024899  | sp:O15091          | +      |
| Hs.76666        | chromosome 9 open reading frame 10                                                                                                                               | C9orf10      | 13431358 | sp:Q9NZB2          | +      |
| Hs.9701         | growth arrest and DNA-damage-inducible, gamma                                                                                                                    | GADD45G      | 5729836  | ref:NP_006696.1    | +      |
| Hs.100527       | connector enhancer of KSR2                                                                                                                                       | CNK2         | 7662368  | ref:NP_055742.1    | +      |
| Hs.77274        | plasminogen activator, urokinase                                                                                                                                 | PLAU         | 224665   | prf:1110198A       | +      |

Table 4. Continuation II

| Unigene cluster | Description                                                                    | GENE    | gi      | pir/NCBI/swissprot | effect |
|-----------------|--------------------------------------------------------------------------------|---------|---------|--------------------|--------|
| Hs.93516        | ESTs                                                                           |         |         |                    | +      |
| Hs.376709       | Homo sapiens cDNA FLJ33768 fis, clone BRHIP2000021                             |         |         |                    | +      |
| Hs.110299       | mitogen-activated protein kinase 7                                             |         |         |                    | +      |
| Hs.31396        | ESTs, Weakly similar to S2807 collagen alpha 1(X) chain precursor [M.musculus] | MAP2K7  | 4826946 | ref:NP_005034.1    | +      |
| Hs.129715       | gonadotropin-releasing hormone 2                                               |         |         |                    | +      |
| Hs.169370       | FYN oncogene related to SRC, FGR, YES                                          | GNRH2   | 3913735 | sp:O43555          | +      |
| Hs.82007        | methionyl aminopeptidase 1                                                     | FYN     | 125370  | sp:P06241          | +      |
| Hs.239018       | RAB11B, member RAS oncogene family                                             | METAP1  | 1703270 | sp:P53582          | +      |
| Hs.126852       | solute carrier family 6 (neurotransmitter transporter, GABA), member 13        | RAB11B  | 1082426 | pir:JC2487         | +      |
|                 |                                                                                | SLC6A13 | 7705539 | ref:NP_057699.1    | +      |

Table 5. Transcriptome analysis

| GENBANK   | GENENAME                                                                 | SYMBOL    | EFFECT |
|-----------|--------------------------------------------------------------------------|-----------|--------|
| NM_005252 | v-fos FBJ murine osteosarcoma viral oncogene homolog                     | FOS       | ++     |
| NM_006705 | growth arrest and DNA-damage-inducible, gamma                            | GADD45G * | ++     |
| NM_001964 | early growth response 1                                                  | EGR1 *    | ++     |
| NM_002228 | v-jun sarcoma virus 17 oncogene homolog (avian)                          | JUN *     | ++     |
| NM_015675 | growth arrest and DNA-damage-inducible, beta                             | GADD45B * | ++     |
| NM_001124 | adrenomedullin                                                           | ADM       | ++     |
| NM_005346 | heat shock 70kDa protein 1B                                              | HSPA1B    | ++     |
| NM_002166 | inhibitor of DNA binding 2, dominant negative helix-loop-helix protein   | ID2       | ++     |
| NM_004417 | dual specificity phosphatase 1                                           | DUSP1     | ++     |
| NM_003745 | suppressor of cytokine signaling 1                                       | Socs1     | ++     |
| NM_002923 | regulator of G-protein signaling 2, 24kDa                                | RGS2 *    | ++     |
| NM_005627 | serum/glucocorticoid regulated kinase                                    | SGK       | ++     |
| BC012321  | activity-regulated cytoskeleton-associated protein                       | ARC       | ++     |
| NM_025195 | phosphoprotein regulated by mitogenic pathways                           | C8FW      | +      |
| NM_030751 | transcription factor 8 (represses interleukin 2 expression)              | TCF8      | +      |
| NM_014330 | protein phosphatase 1, regulatory (inhibitor) subunit 15A                | PPP1R15A  | +      |
| NM_004083 | DNA-damage-inducible transcript 3                                        | DDIT3     | +      |
| NM_001841 | cannabinoid receptor 2 (macrophage)                                      | CNR2 *    | +      |
| NM_004024 | activating transcription factor 3                                        | ATF3 *    | +      |
| NM_001706 | B-cell CLL/lymphoma 6 (zinc finger protein 51)                           | BCL6      | +      |
| NM_004428 | ephrin-A1                                                                | EFNA1 *   | +      |
| NM_004419 | dual specificity phosphatase 5                                           | DUSP5 *   | +      |
| NM_003088 | fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus) | FSCN1     | +      |
| AB014566  | dishevelled associated activator of morphogenesis 1                      | DAAM1     | +      |
| NM_006145 | DnaJ (Hsp40) homolog, subfamily B, member 1                              | DNAJB1 *  | +      |
| NM_004962 | growth differentiation factor 10                                         | GDF10     | +      |
| D79994    | kidney ankyrin repeat-containing protein                                 | KANK      | +      |
| NM_006301 | mitogen-activated protein kinase kinase kinase 12                        | MAP3K12 * | +      |
| NM_002928 | regulator of G-protein signaling 16                                      | RGS16     | +      |
| NM_003955 | suppressor of cytokine signaling 3                                       | Socs3     | +      |
| NM_004430 | early growth response 3                                                  | EGR3      | +      |
| NM_001731 | B-cell translocation gene 1, anti-proliferative                          | BTG1      | +      |
| NM_012342 | putative transmembrane protein                                           | NMA       | +      |
| NM_002262 | killer cell lectin-like receptor subfamily D, member 1                   | KLRD1     | +      |
| NM_006007 | zinc finger protein 216                                                  | ZNF216 *  | +      |
| NM_000905 | neuropeptide Y                                                           | NPY       | +      |

| Table 5. (continued) Transcriptome analysis |                                                                                   |  |  |               |        |   |
|---------------------------------------------|-----------------------------------------------------------------------------------|--|--|---------------|--------|---|
| GENBANK                                     | GENENAME                                                                          |  |  | SYMBOL        | EFFECT |   |
| NM_004418                                   | dual specificity phosphatase 2                                                    |  |  | DUSP2         | +      |   |
| NM_031459                                   | sestrin 2                                                                         |  |  | SES2          | +      |   |
| AF332558                                    | BCL2 binding component 3                                                          |  |  | BBC3          | +      |   |
| NM_006000                                   | tubulin, alpha 1 (testis specific)                                                |  |  | TUBA1         | +      |   |
| NM_006644                                   | heat shock 105kDa/110kDa protein 1                                                |  |  | HSPH1         | +      |   |
| L24498                                      | growth arrest and DNA-damage-inducible, alpha                                     |  |  | GADD45A       | +      |   |
| AK024029                                    | modulator of apoptosis 1                                                          |  |  | MOAP1         | +      |   |
| NM_005409                                   | chemokine (C-X-C motif) ligand 11                                                 |  |  | CXCL11        | +      |   |
| NM_003383                                   | very low density lipoprotein receptor                                             |  |  | VLDLR         | +      |   |
| AF267856                                    | hypothetical protein dJ465N24.2.1                                                 |  |  | DJ465N24.2.1* | +      |   |
| NM_002450                                   | metallothionein 1L                                                                |  |  | MT1L          | +      |   |
| NM_001828                                   | Charot-Leyden crystal protein                                                     |  |  | CLC           | *      | + |
| NM_013370                                   | pregnancy-induced growth inhibitor                                                |  |  | OKL38         | +      |   |
| AB014581                                    | l(3)mbt-like (Drosophila)                                                         |  |  | L3MBTL        | +      |   |
| NM_006875                                   | pim-2 oncogene                                                                    |  |  | PIM2          | +      |   |
| AL031665                                    | actin, gamma pseudogene 3                                                         |  |  | ACTGP3        | +      |   |
| AI985514                                    | ribosomal protein S19                                                             |  |  | RPS19         | +      |   |
| NM_080686                                   | HLA-B associated transcript 2                                                     |  |  | BAT2          | +      |   |
| NM_021184                                   | chromosome 6 open reading frame 47                                                |  |  | C6orf47       | +      |   |
| NM_015471                                   | DKFZP566O1646 protein                                                             |  |  | DC8           | *      | + |
| NM_000952                                   | platelet-activating factor receptor                                               |  |  | PTAFR         | +      |   |
| BC012625                                    | protein phosphatase 1, regulatory (inhibitor) subunit 3C                          |  |  | PPP1R3C       | +      |   |
| NM_023012                                   | hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4. |  |  | FLJ11021      | *      | + |
| AK024358                                    | macrophage expressed gene 1                                                       |  |  | LOC219972     | +      |   |
| NM_002658                                   | plasminogen activator, urokinase                                                  |  |  | PLAU          | *      | + |
| U12767                                      | nuclear receptor subfamily 4, group A, member 3                                   |  |  | NR4A3         | +      |   |
| NM_016615                                   | solute carrier family 6 (neurotransmitter transporter, GABA), member 13           |  |  | SLC6A13       | +      |   |
| NM_002135                                   | nuclear receptor subfamily 4, group A, member 1                                   |  |  | NR4A1         | +      |   |
| AJ251595                                    | CD44 antigen (homing function and Indian blood group system)                      |  |  | CD44          | -      |   |
| NM_005433                                   | v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1                                |  |  | YES1          | -      |   |
| NM_006325                                   | RAN, member RAS oncogene family                                                   |  |  | RAN           | -      |   |
| NM_004775                                   | UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6                 |  |  | B4GALT6       | -      |   |
| AK056671                                    | upstream regulatory element binding protein 1                                     |  |  | UREB1         | -      |   |
| NM_022817                                   | period homolog 2 (Drosophila)                                                     |  |  | PER2          | -      |   |
| L07044                                      | calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma                 |  |  | CAMK2G        | --     |   |
| NM_014890                                   | downregulated in ovarian cancer 1                                                 |  |  | DOC1          | --     |   |

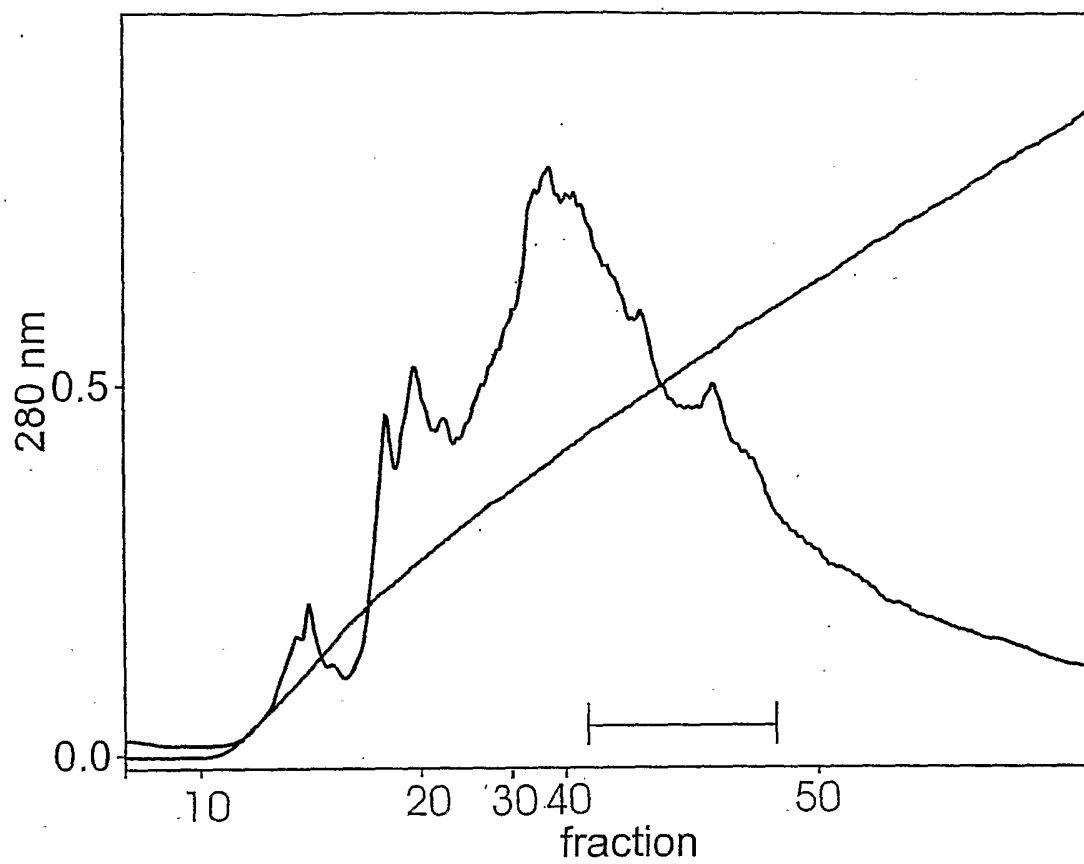
| Table 5. (continued) Transcriptome analysis |                                                                                                                          |          |        |
|---------------------------------------------|--------------------------------------------------------------------------------------------------------------------------|----------|--------|
| GENBANK                                     | GENENAME                                                                                                                 | SYMBOL   | EFFECT |
| NM_001782                                   | CD72 antigen                                                                                                             | CD72     | -      |
| NM_005766                                   | FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)                                              | FARP1    | -      |
| NM_000566                                   | Fc fragment of IgG, high affinity Ia, receptor for (CD64)                                                                | FCGR1A   | -      |
| NM_003036                                   | v-ski sarcoma viral oncogene homolog (avian)                                                                             | SKI      | -      |
| NM_001713                                   | betaine-homocysteine methyltransferase                                                                                   | BHMT     | -      |
| NM_001682                                   | ATPase, Ca++ transporting, plasma membrane 1                                                                             | ATP2B1   | -      |
| NM_003985                                   | tyrosine kinase, non-receptor, 1                                                                                         | TNK1     | -      |
| NM_004752                                   | glial cells missing homolog 2 (Drosophila)                                                                               | GCM2     | -      |
| BC001619                                    | aldehyde dehydrogenase 1 family, member B1                                                                               | ALDH1B1  | -      |
| NM_002422                                   | matrix metalloproteinase 3 (stromelysin 1, progelatinase)                                                                | MMP3     | -      |
| NM_003024                                   | intersectin 1 (SH3 domain protein)                                                                                       | ITSN1    | -      |
| NM_002613                                   | 3-phosphoinositide dependent protein kinase-1                                                                            | PDPK1    | -      |
| NM_000098                                   | carnitine palmitoyltransferase II                                                                                        | CPT2     | -      |
| BC002712                                    | v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)                                             | MYCN     | -      |
| NM_003112                                   | Sp4 transcription factor                                                                                                 | SP4      | -      |
| NM_012062                                   | dynamitin 1-like                                                                                                         | DNM1L    | -      |
| NM_000880                                   | interleukin 7                                                                                                            | IL7      | -      |
| NM_004564                                   | PET112-like (yeast)                                                                                                      | PET112L  | -      |
| NM_001771                                   | CD22 antigen                                                                                                             | CD22     | -      |
| AA904067                                    | protein phosphatase 1, regulatory (inhibitor) subunit 12B                                                                | PPP1R12B | -      |
| NM_001633                                   | alpha-1-microglobulin/bikunin precursor                                                                                  | AMBP     | -      |
| NM_007216                                   | Hermansky-Pudlak syndrome 5                                                                                              | HPS5     | -      |
| AV708310                                    | protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform                                                    | PPP2CA   | -      |
| AF296765                                    | cerebral cavernous malformations 1                                                                                       | CCM1     | -      |
| AF155117                                    | kinesin family member 21A                                                                                                | KIF21A   | -      |
| NM_002006                                   | fibroblast growth factor 2 (basic)                                                                                       | FGF2     | -      |
| NM_004362                                   | calmeglin                                                                                                                | CLGN     | -      |
| NM_021221                                   | lymphocyte antigen 6 complex, locus G5B                                                                                  | LY6G5B   | -      |
| AK001541                                    | secretory carrier membrane protein 1                                                                                     | SCAMP1   | -      |
| H08291                                      | acid phosphatase 1, soluble                                                                                              | ACP1     | -      |
| NM_014636                                   | Ral guanine nucleotide exchange factor RalGPS1A                                                                          | RALGPS1A | -      |
| NM_053006                                   | serine/threonine kinase 22B (spermiogenesis associated)                                                                  | STK22B   | -      |
| NM_000220                                   | potassium inwardly-rectifying channel, subfamily J, member 1                                                             | KCNJ1    | -      |
| NM_000633                                   | B-cell CLL/lymphoma 2                                                                                                    | BCL2     | -      |
| NM_003605                                   | O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase) | OGT      | -      |

Table 5. (continued) Transcriptome analysis

| GENBANK   | GENENAME                                                            | SYMBOL    | EFFECT |
|-----------|---------------------------------------------------------------------|-----------|--------|
| NM_006114 | translocase of outer mitochondrial membrane 40 homolog (yeast)      | TOMM40    | -      |
| NM_013404 | mesothelin                                                          | MSLN      | -      |
| NM_020974 | signal peptide, CUB domain, EGF-like 2                              | SCUBE2    | -      |
| NM_000439 | proprotein convertase subtilisin/kexin type 1                       | PCSK1     | -      |
| NM_002035 | follicular lymphoma variant translocation 1                         | FVT1      | -      |
| AL136924  | Ras and Rab interactor 2                                            | RIN2      | -      |
| NM_006020 | alkB, alkylation repair homolog (E. coli)                           | ALKBH     | -      |
| NM_005433 | v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1                  | YES1      | -      |
| NM_003423 | zinc finger protein 43 (HTF6)                                       | ZNF43     | -      |
| AF056490  | phosphodiesterase 8A                                                | PDE8A     | -      |
| NM_033480 | F-box only protein 9                                                | FBXO9     | -      |
| NM_022789 | interleukin 17E                                                     | IL17E     | -      |
| NM_007150 | zinc finger protein 185 (LIM domain)                                | ZNF185    | -      |
| NM_017450 | BAI1-associated protein 2                                           | BAIAP2    | -      |
| AB037762  | myelin expression factor 2                                          | MYEF2     | -      |
| NM_003263 | toll-like receptor 1                                                | TLR1      | -      |
| NM_001089 | ATP-binding cassette, sub-family A (ABC1), member 3                 | ABCA3     | -      |
| NM_018240 | kin of IRRE like (Drosophila)                                       | KIRREL    | -      |
| NM_003827 | N-ethylmaleimide-sensitive factor attachment protein, alpha         | NAPA      | -      |
| NM_003569 | syntaxin 7                                                          | STX7      | -      |
| AB046797  | KIAA1577 protein                                                    | KIAA1577  | -      |
| AV723914  | hypothetical protein LOC164729                                      | LOC164729 | -      |
| NM_015967 | protein tyrosine phosphatase, non-receptor type 22 (lymphoid)       | PTPN22    | -      |
| AB007892  | CDC5 cell division cycle 5-like (S. pombe)                          | CDC5L     | -      |
| NM_022907 | hypothetical protein FLJ23053                                       | FLJ23053  | -      |
| NM_004379 | cAMP responsive element binding protein 1                           | CREB1     | -      |
| AB023198  | KIAA0981 protein                                                    | KIAA0981  | -      |
| NM_024958 | chromosome 20 open reading frame 98                                 | C20orf98  | -      |
| NM_001186 | BTB and CNC homology 1, basic leucine zipper transcription factor 1 | BACH1     | -      |
| NM_014639 | KIAA0372 gene product                                               | KIAA0372  | -      |
| NM_024641 | mannosidase, endo-alpha                                             | MANEA     | -      |
| AK056671  | upstream regulatory element binding protein 1                       | UREB1     | -      |
| NM_003618 | mitogen-activated protein kinase kinase kinase 3                    | MAP4K3    | -      |
| NM_005443 | 3'-phosphoadenosine 5'-phosphosulfate synthase 1                    | PAPSS1    | *      |
| NM_022781 | ring finger protein 38                                              | RNF38     | -      |
| NM_003874 | CD84 antigen (leukocyte antigen)                                    | CD84      | -      |

Table 5. (continued) Transcriptome analysis

| <i>GENBANK</i> | <i>GENENAME</i>                                        | <i>SYMBOL</i> | <i>EFFECT</i> |
|----------------|--------------------------------------------------------|---------------|---------------|
| NM_000091      | collagen, type IV, alpha 3 (Goodpasture antigen)       | COL4A3        | -             |
| NM_000160      | glucagon receptor                                      | GCGR          | -             |
| NM_005019      | phosphodiesterase 1A, calmodulin-dependent             | PDE1A         | -             |
| NM_012080      | family with sequence similarity 16, member A, X-linked | FAM16AX       | -             |

Fig.  
1A

1B

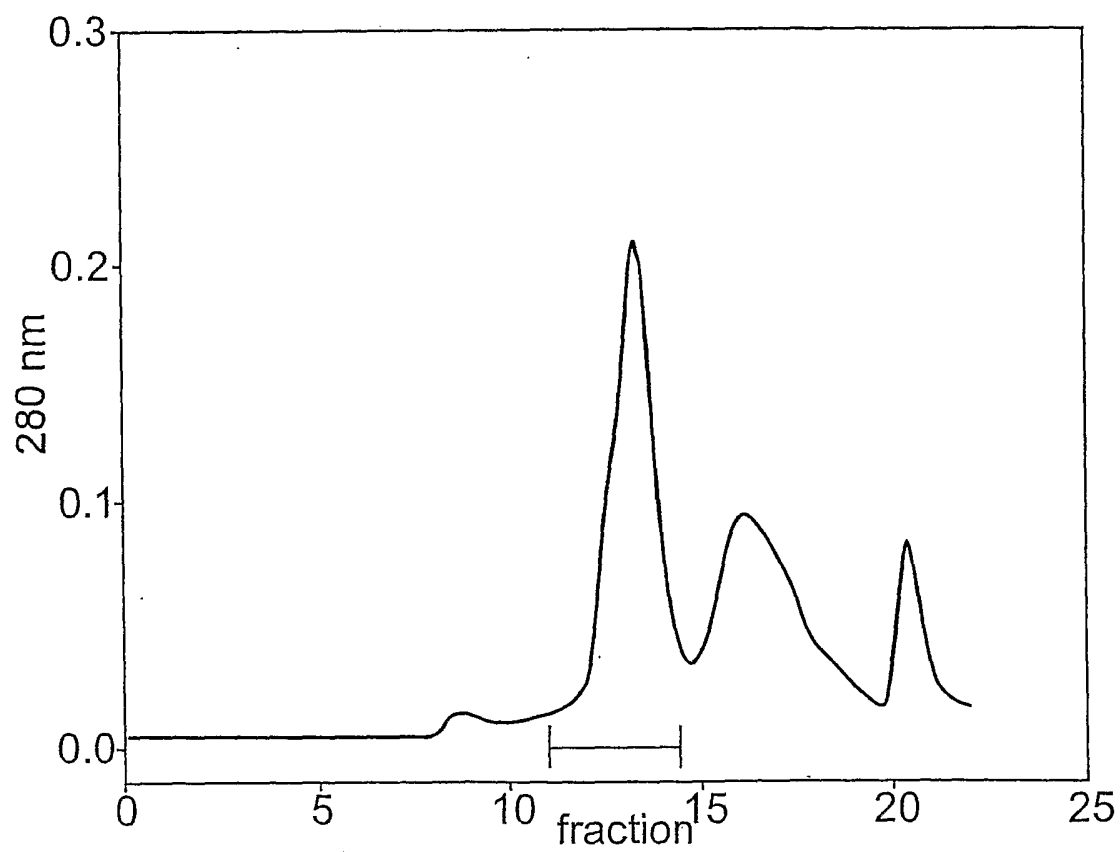


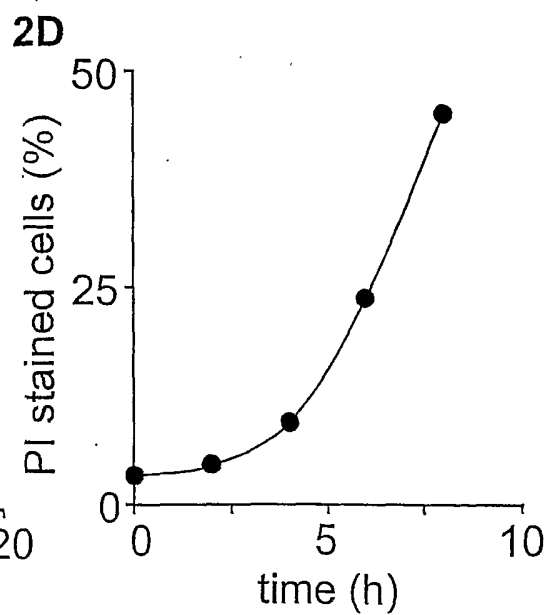
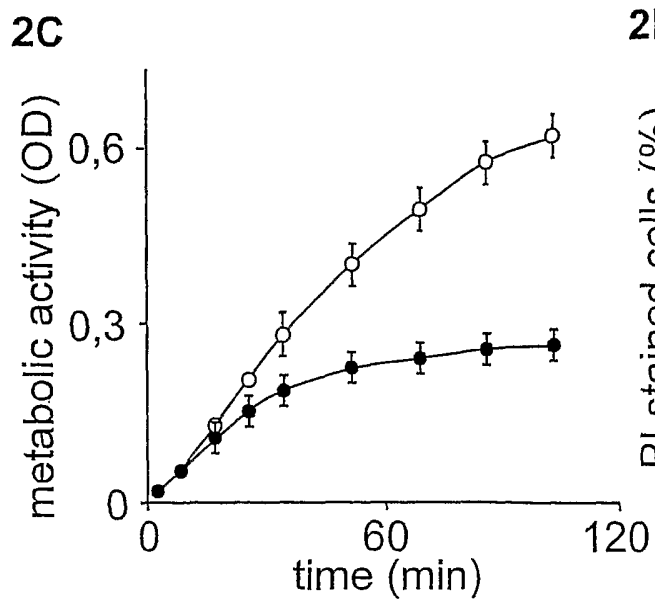
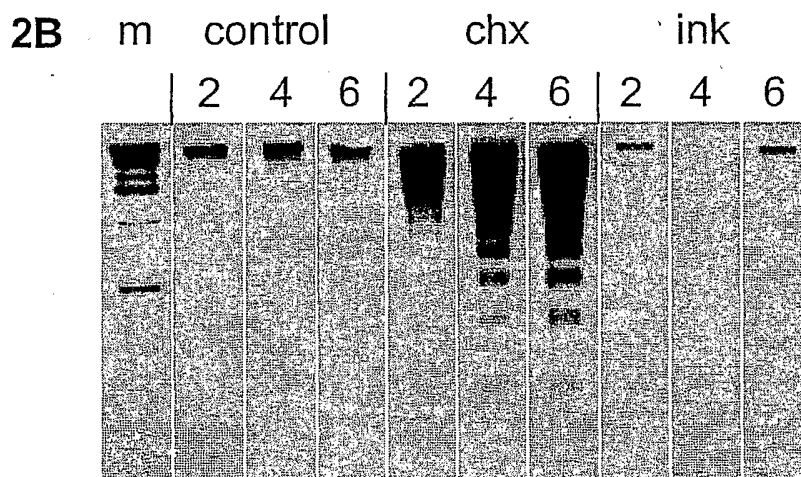
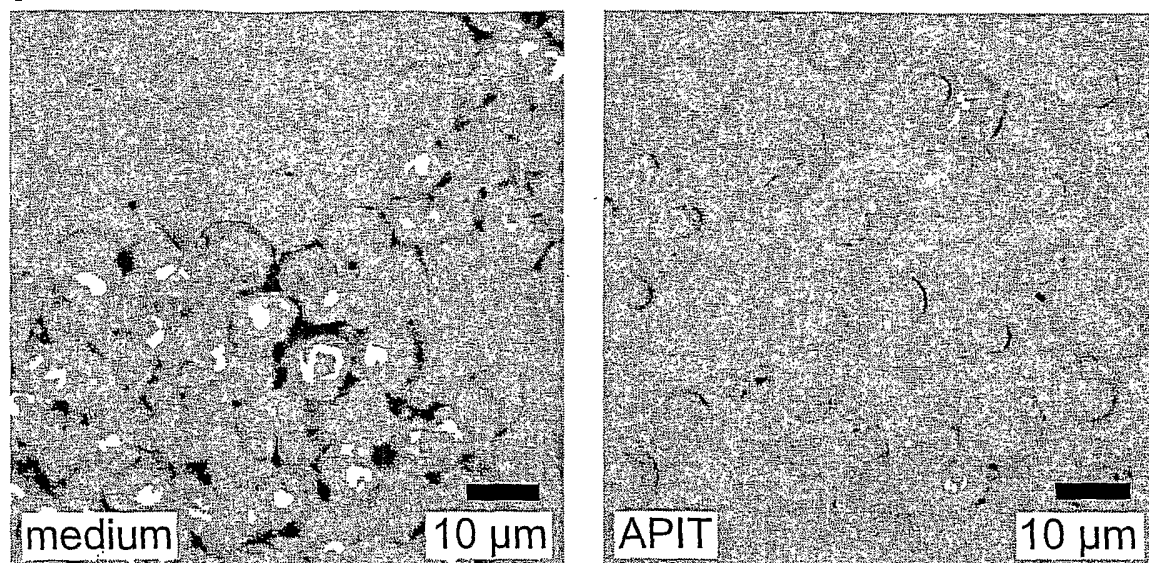
Fig.  
2A

Fig.

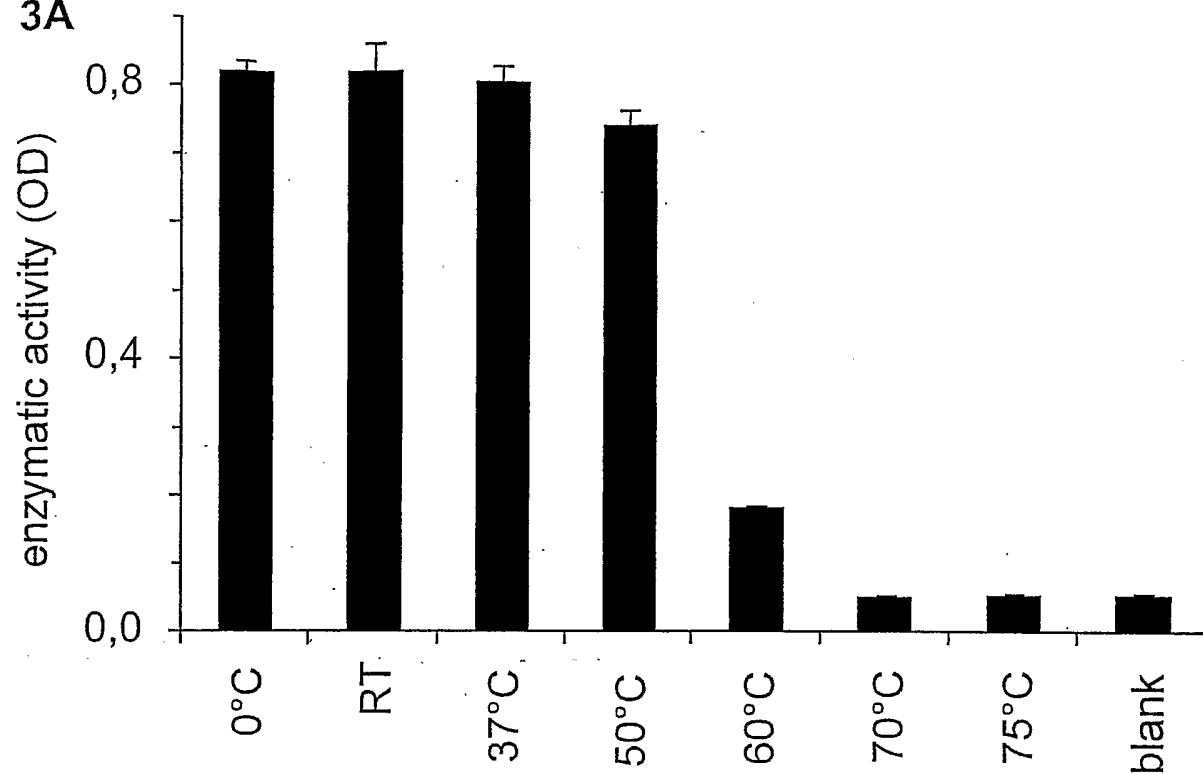
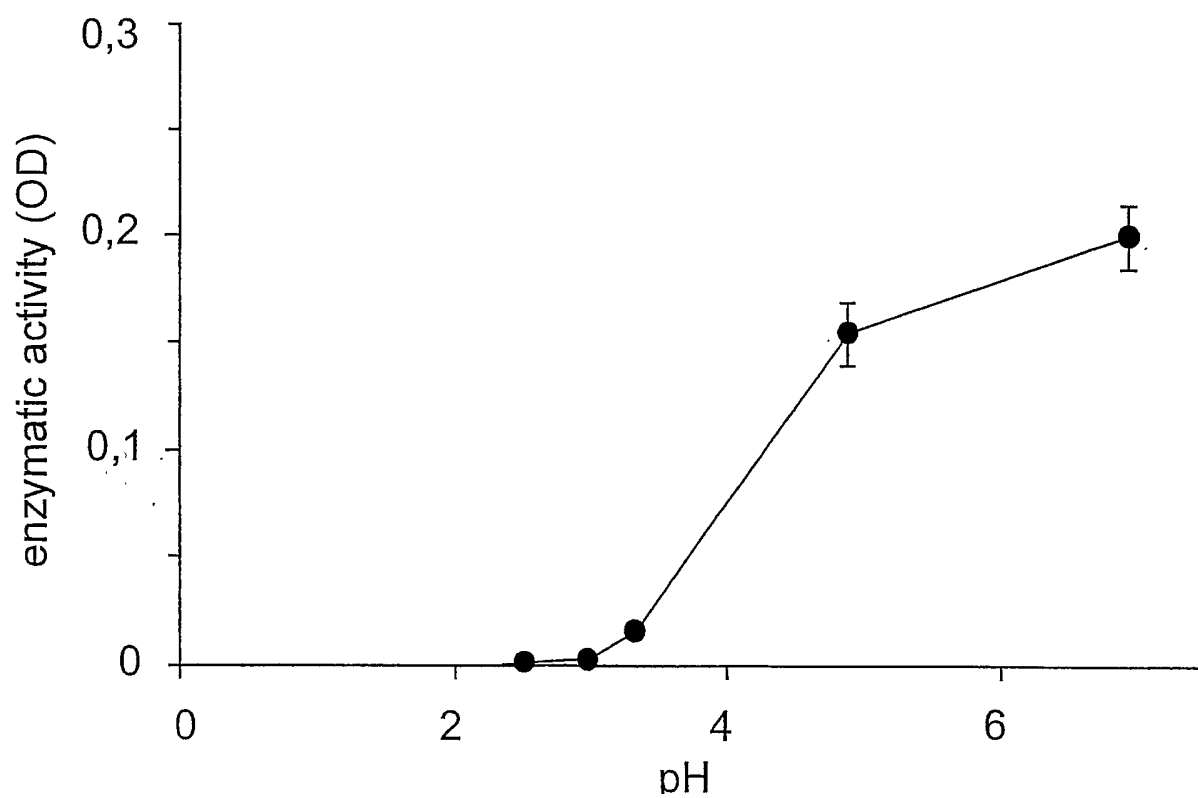
**3A****3B**

Fig.

3C

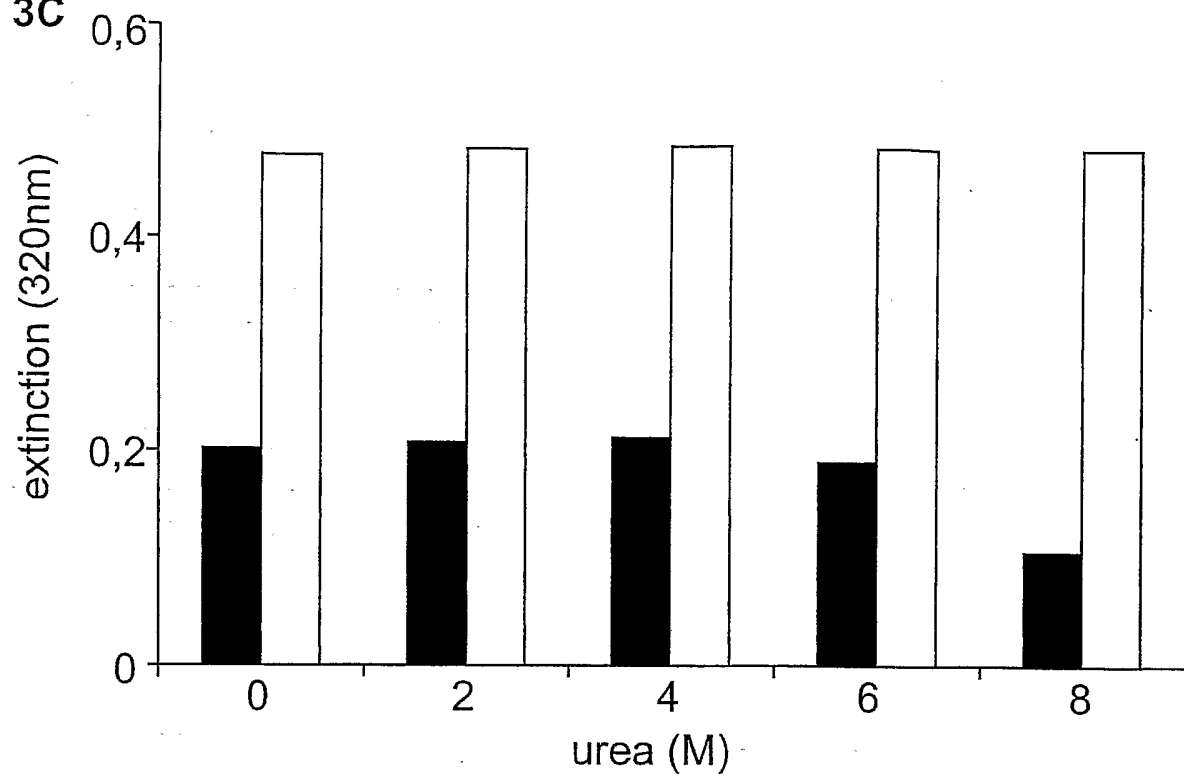


Fig.  
**4A**

**N-terminal sequence:**

D-G-I-C-R-N-Q-R-Q  
Q V R P

**Internal peptide sequences**

|           | <b>Sequence</b>                  |
|-----------|----------------------------------|
| <b>1</b>  | <b>DSGLDIAVFEYSDR</b>            |
| <b>2</b>  | <b>LFXYQLPNTPDVNLEI</b>          |
| <b>3</b>  | <b>VISELGLTPK</b>                |
| <b>4</b>  | <b>XGDVPYDLSPEEK</b>             |
| <b>5</b>  | <b>VILAXPVYALN</b>               |
| <b>6</b>  | <b>ATQAYAAVRPIPASK</b>           |
| <b>7</b>  | <b>VFMTFDQP</b>                  |
| <b>8</b>  | <b>SDALFFQMYD</b>                |
| <b>9</b>  | <b>SEASGDYILIASYADGLK</b>        |
| <b>10</b> | <b>NQGEDIPGSDPQYNQVTEP(L)(K)</b> |

X = not determinable

underlined: primer sequence for RT-PCR

Fig.

**4B**

|   |                              |                                                                |
|---|------------------------------|----------------------------------------------------------------|
| 1 | Oligo-dT<br>DBuTag1          | tcc taa cgt agg tct aga cct gtt gca ttt ttt<br>ttt ttt ttt ttt |
| 2 | V-Fey 3 DTS 5'               | tc gtg ttc gar tac tci gay cg                                  |
| 3 | DBuTag1 DTS 3'               | ctg tag gtc tag acc tgt tgc a                                  |
| 4 | ATF Race 3' 660              | ccg tgt aga tct cac tgc cat a                                  |
| 5 | Abrided Anchor<br>Primer     | ggc cac gcg tcg act agt acg ggi igg gii<br>ggg iig             |
| 6 | ATF Race 3' 436              | ccg ttg agt tgt aga cct                                        |
| 7 | AUAP-EcoRI                   | aatt ggc cac gcg tcg act agt ac                                |
| 8 | ATF 5' Sign Eco<br>RI GEX/ET | aa ttc tcg tct gct gtg ctt ctc ct                              |
| 9 | ATF 3' XhoI                  | gac tta gag gaa gta gtc gtt ga                                 |

Fig.

4C

M S S A V L L L A C A L V I S V H A D G IV C  
ATGTCGTCTGCTGTGCTTCTCCTGGCTTGTGCGTTGGTCATCTCTGTCCACGCCGACGGTATCTGC  
...TCGTCTGCTGTGCTTCTCCTGGCTTGTGCGTTGGTCATCTCTGTCCACGCCGACGGTGTCTGC  
.....GACGGTATCTGC

R N R R Q C N R E V C G S T Y D V A V V G A  
AGAAACAGACGTCAATGTAACAGAGAGGTGTGCGGTTCTACCTACGATGTGGCCGTCGTGGGGGCG  
AGAAACAGACGTCAATGTAACAGAGAGGTGTGCGGTTCTACCTACGATGTGGCCGTCGTGGGGGCG  
AGAAACAGACGTCAATGTAACAGAGAGGTGTGCGGTTCTACCTACGATGTGGCTGTCTGTGGGGGCG

G P G G A N S A Y M L R D S G L D I A V F E  
GGGCCTGGGGGAGCTAACTCCGCCTACATGCTGAGGGACTCCGGCCTGGACATCGCTGTGTTTCGAG  
GGGCCTGGGGGAGCTAACTCCGCCTACATGCTGAGGGACTCCGGCCTGGACATCGCTGTGTTTCGAG  
GGGCCTGGGGGAGCTAACTCCGCCTACATGCTGAGGGACTCCGGCCTGGACATCGCTGTGTTTCGAG

Y S D R V G G R L F T Y O L P N T P D V N L  
TACTCGACCCGAGTGGGCGGCCGGCTGTTACCTACCAGCTGCCCAACACACCCGACGTAACTCT  
TACTCAGACCCGAGTGGGCGGCCGGCTGTTACCTACCAGCTGCCCAACACACCCGACGTAACTCT  
TACTCAGACCCGAGTGGGCGGCCGGCTGTTACCTACCAGCTGCCCAACACACCCGACGTAACTCT

E I G G M R F I E G A M H R L W R V I S E L  
GAGATTGGCGGCATGAGGTTTCATCGAAGGCGCCATGCACAGGCTCTGGAGGGTCATTTTCAGAACTC  
GAGATTGGCGGCATGAGGTTTCATCGAAGGCGCCATGCACAGGCTCTGGAGGGTCATTTTCAGAACTC  
GAGATTGGCGGCATGAGGTTTCATCGAAGGCGCCATGCACAGGCTCTGGAGGGTCATTTTCAGAACTC

G L T P K V F K E G F G K E G R Q R F Y L R  
GGCCTAACCCCCAAGGTGTTCAAGGAAGGTTTCGGCAAGGAGGGCAGACAAGATTTCCTGCGG  
GGCCTAACCCCCAAGGTGTTCAAGGAAGGTTTCGGAAAGGAGGGCAGACAGAGATTTTCCTGCGG  
GGCCTAACCCCCAAGGTGTTCAAGGAAGGTTTCGGAAAGGAGGGCAGACAGAGATTTTCCTGCGG

G Q S L T K K Q V K S G D V P Y D L S P E E  
GGACAGAGCCTGACCAAGAAACAGGTCAAGAGTGGGGACGTACCCTATGACCTCAGCCCGGAGGAG  
GGACAGAGCCTGACCAAGAAACAGGTCAAGAGTGGGGACGTACCCTATGACCTCAGCCCGGAGGAG  
GGACAGAGCCTGACCAAGAAACAGGTCAAGAGTGGGGACGTACCCTATGACCTCAGCCCGGAGGAG

K E N Q G N L V E Y Y L E K L T G L QK L N G  
AAAGAAAACCAGGGAAATCTGGTCAATACTACCTGGAGAACTGACAGGTCTACAACTCAACGGC  
AAAGAAAACCAGGGAAATCTGGTCAATACTACCTGGAGAACTGACAGGTCTACAACTCAATGGT  
AAAGAAAACCAGGGAAATCTGGTCAATACTACCTGGAGAACTGACAGGTCTAACTCAACGGC

EG P L K R E V A L K L T V P D G R F L Y D L  
GACCGCTCAAACGTGAGGTTGCGCTTAACTAACCGTGCCGGACGGCAGATTTCCTCTATGACCTC  
GAACCGCTCAAACGTGAGGTTGCGCTTAACTAACCGTGCCGGACGGCAGATTTCCTCTATGACCTC  
GACCGCTCAAACGTGAGGTTGCGCTTAACTAACCGTGCCGGACGGCAGATTTCCTCTATGACCTC

S F D E A M D L V A S P E G K E F T R D T H  
TCGTTTGACGAAGCCATGGATCTGGTTGCCTCCCCTGAGGGCAAAGAGTTACCCGAGACACGCAC  
TCGTTTGACGAAGCCATGGATCTGGTTGCCTCCCCTGAGGGCAAAGAGTTACCCGAGACACGCAC  
TCGTTTGACGAAGCCATGGACTGGTTGCCTCCCCTGAGGGCAAAGAGTTACCCGAGACACGCAC

Fig.

## 4C (continued)

V F T G E V T L DG A S A V S L F D D H L G E  
GTCTTCACAGGAGAGGTCACCCCTGGACGCGTCGGCTGTCTCCCTCTTCGACGACCACCTGGGAGAG  
GTCTTCACCGGAGAGGTCACCCCTGGCGCGTCGGCTGTCTCCCTCTTCGACGACCACCTGGGAGAG  
GTGTTACCGGAGAAGTCACCCCTGGACGCGTCGGCTGTCTCCCTCTTCGACGACCACCTGGGAGAG

D Y Y G S E I Y T L K E G L S S V P Q G L L  
GACTACTATGGCAGTGAGATCTACACCCTAAAGGAAGGACTGTCTTCCGTCCCACAAGGGCTCCTA  
GACTACTACGGCAGTGAGATCTACACCCTCAAGGAAGGACTGTCTTCCGTCCCCAAGGGCTCCTA  
GACTACTATGGCAGTGAGATCTACACCCTAAAGGAAGGACTGTCTTCCGTCCCACAAGGGCTCCTA

Q AT F L D A A D S N E F Y P N S H L K A L R  
CAGGCTTTTCTGGACGCCGCAGACTCCAACGAGTTCTATCCCAACAGCCACCTGAAGGCCCTGAGA  
CAGGCTTTTCTGGACGCCGCAGACTCCAACGAGTTCTATCCCAACAGCCACCTGAAGGCCCTGAGA  
CAGACTTTTCTGGACGCCGCAGACTCCAACGAGTTCTATCCCAACAGCCACCTGAAGGCCCTGAGA

R K T N G Q Y V L Y F E P T T S K D G Q T T  
CGTAAGACCAACGGTCAGTATGTTCTTTACTTTGAGCCCACCACCTCCAAGGATGGACAAACCACA  
CGTAAGACCAACGGTCAGTATGTTCTTTACTTTGAGCCCACCACCTCCAAGGATGGACAAACCACA  
CGTAAGACCAACGGTCAGTATGTTCTTTACTTTGAGCCCACCACCTCCAAGGATGGACAAACCACA

I N Y L E P L Q V V C A Q R V I L A M P V Y  
ATCAACTATCTGGAACCCCTGCAGGTTGTGTGTGCACAAAGAGTCATCCTGGCCATGCCGGTATAC  
ATCAACTATCTGGAACCCCTGCAGGTTGTGTGTGCACAGAGAGTCATTCTGGCCATGCCGGTCTAC  
ATCAACTATCTGGAACCCCTGCAGGTTGTGTGTGCACAGAGAGTCATCCTGGCCATGCCGGTCTAC

A L N Q L D W N Q L R N D R A T O A Y A A V  
GCTCTGAACCAACTAGACTGGAATCAGCTCAGAAATGACCGAGCCACCCAAGCGTACGCTGCCGTT  
GCTCTCAACCAGTGGATTGGAATCAGCTCAGAAATGACCGAGCCACCCAAGCGTACGCTGCCGTG  
GCTCTCAACCAACTGGATGGAATCAGCTCAGAAATGACCGAGCCACCCAAGCGTACGCTGCCGTG

R P I P A S K V F M TS F D Q P W W L E N E R  
CGCCCGATTCTGCAAGTAAGGTGTTATGTCCTTTGATCAGCCCTGGTGGTTGGAGAACGAGAGG  
CGCCCGATTCTGCAAGTAAGGTGTTATGACCTTTGATCAGCCCTGGTGGTTGGAGAACGAGAGG  
CGCCCGATTCTGCAAGTAAAGTGTTATGACCTTTGATCAGCCCTGGTGGTTGGAGAACGAGAGG

K S W V T K S D A L F S O M Y D W Q K S E A  
AAATCCTGGGTACCAAGTCGGACGCGCTTTTCAGCCAAATGTACGACTGGCAGAAGTCTGAGGCG  
AAATCCTGGGTACCAAGTCGGACGCGCTTTTCAGTCAAATGTACGACTGGCAGAAGTCTGAGGCG  
AAATCCTGGGTACCAAGTCGGACGCGCTTTTCAGCCAAATGTACGACTGGCAGAAGTCTGAGGCG

S G D Y I L I A S Y A D G L K A Q Y L R E L  
TCCGGAGACTACATCCTGATCGCCAGCTACGCCGACGGCCTCAAAGCCCAGTACCTGCGGGAGCTG  
TCCGGAGACTACATCCTGATCGCCAGCTACGCCGACGGCCTCAAAGCCCAGTACCTGCGGGAGCTG  
TCCGGAGACTACATCCTGATCGCCAGCTACGCCGACGGCCTCAAAGCCCAGTACCTGCGGGAGCTG

K N O G E D I P G S D P G Y N Q V T E P L K  
AAGAATCAGGGAGAGGACATCCCAGGCTCTGACCCAGGCTACAACCAGGTTACCGAACCCCTCAAG  
AAGAATCAGGGAGAGGACATCCCAGGCTCTGACCCAGGCTACAACCAGGTACCGAACCCCTCAAG  
AAGAATCAGGGAGAGGACATCCCAGGCTCTGACCCAGGCTACAACCAGGTACCGAACCCCTCAAG

Fig.

## 4C (continued)

D T I L D H L T E A Y G V E R D S I PR E P V  
 GACACCATTTCTTGACCACCTCACTGAGGCTTATGGCGTGGAGCGAGACTCGATCCCGGAACCCGTG  
 GACACCATTTCTTGACCACCTCACTGAGGCCTATGGCGTGGAGCGAGACTCGATCCCGGAACCCGTG  
 GACACCATTTCTTGACCACCTCACTGAGGCTTATGGCGTGGAACGAGACTCGATCCCGGAACCCGTG

T A A S Q F W T D Y P F G C G W I T W R A G  
 ACCGCCGCTTCCCAGTTCTGGACAGACTACCCGTTTGGCTGTGGATGGATCACCTGGAGGGCCGGC  
 ACCGCCGCTTCCCAGTTCTGGACAGACTACCCGTTTGGCTGTGGATGGATCACCTGGAGGGCCGGC  
 ACCGCCGCTTCCCAGTTCTGGACCGACTACCCGTTGGCTGTGGATGGATCACCTGGAGGGCAGGC

F H F D D V I S T M R R P S L K D E V Y V V  
 TTCCATTTTCGATGACGTCATCAGCACCATGCGTCGCCCGTCACTGAAAGATGAGGTATACGTGGTG  
 TTCCATTTTCGATGACGTCATCAGCACCATGCGTCGCCCGTCACTGAAAGATGAGGTCTACGTGGTG  
 TTCCATTTTCGATGACGTCATCAGCACCATGCGTCGCCCGTCACTGAAAGATGAGGTCTACGTGGTG

G A D Y S W G L I S S W I E G A L E T S E N  
 GGAGCCGACTACTCCTGGGGACTTATCTCCTCCTGGATAGAGGGCGCTCTGGAGACCTCGGAAAAC  
 GGAGCCGATTACTCCTGGGGACTTATCTCCTCCTGGATAGAGGGCGCTCTGGAGACCTCAGAAAAC  
 GGAGCCGATTACTCCTGGGGACTTATCTCCTCCTGGATAGAGGGCGCTCTGGAGACCTCGGAAAAC

V I N D Y F L -  
 GTCATCAACGACTACTTCCTCTAA  
 GTCATCAACGACTACTTCCTCTAA  
 GTCATCAACGACTACTTCCTCTAA

## 4D

VS

MSSAVLLLLACALVISVHADGICRNRQCNREVCGSTYDVAVVGA

10 20 30 40

T Q H S  
GPGGANSAYMLRDSGLDIAVFEYSDRVGGRLFTYQLPNTPDVNL

50 60 70 80

Fig.

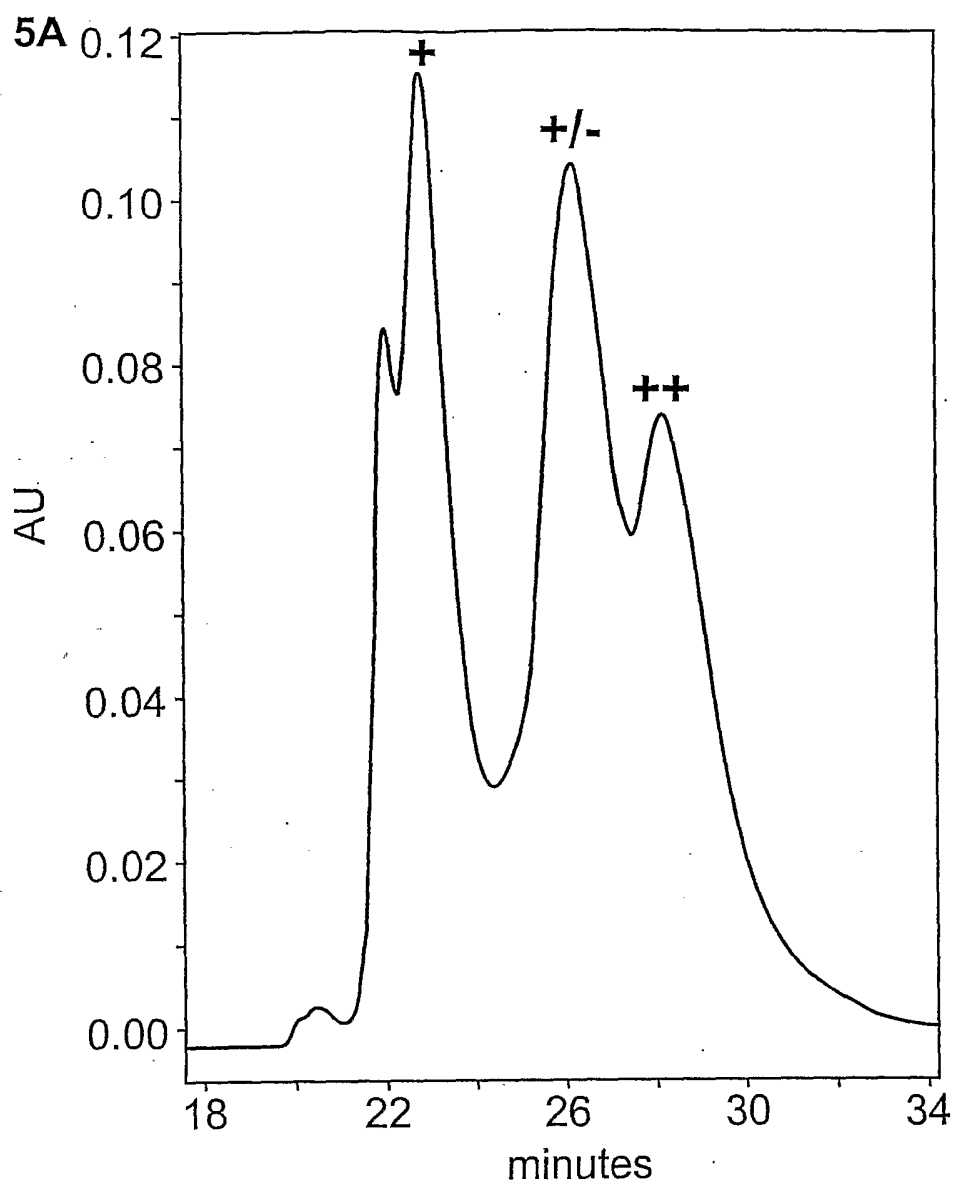
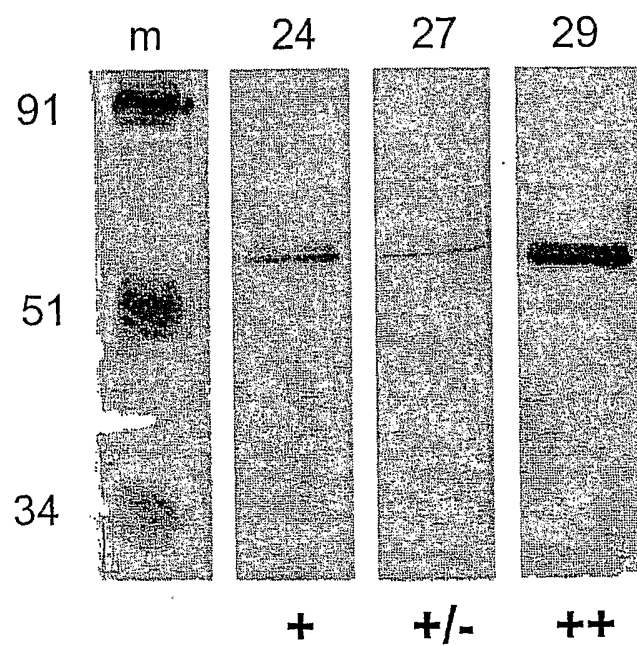
**5B**

Fig.

5 C

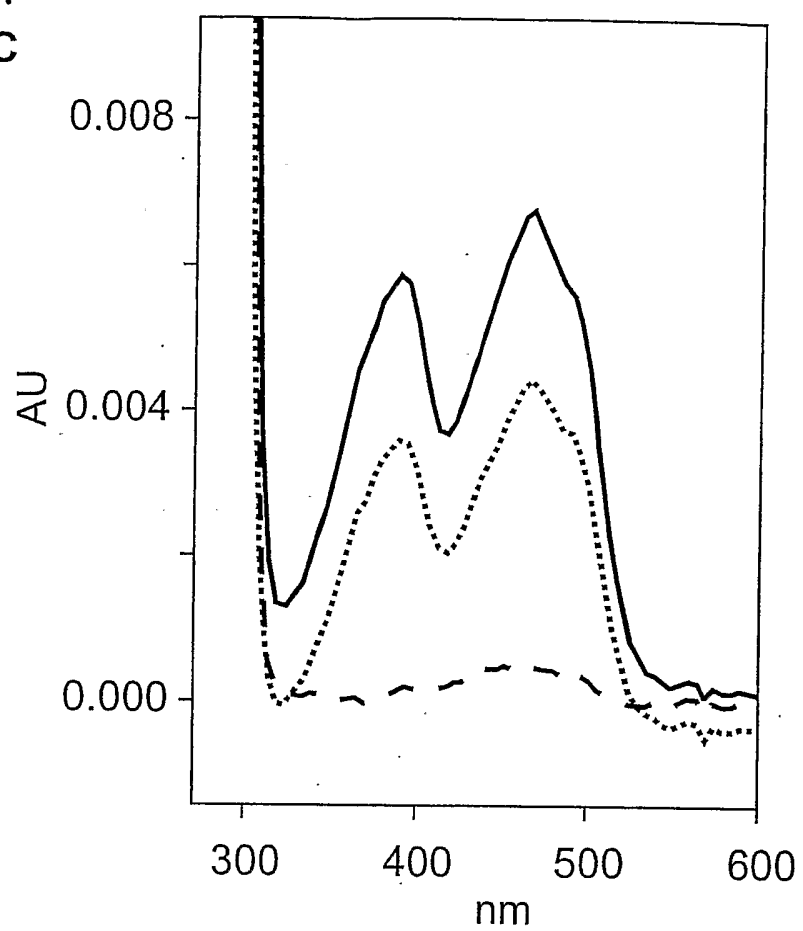


Fig.

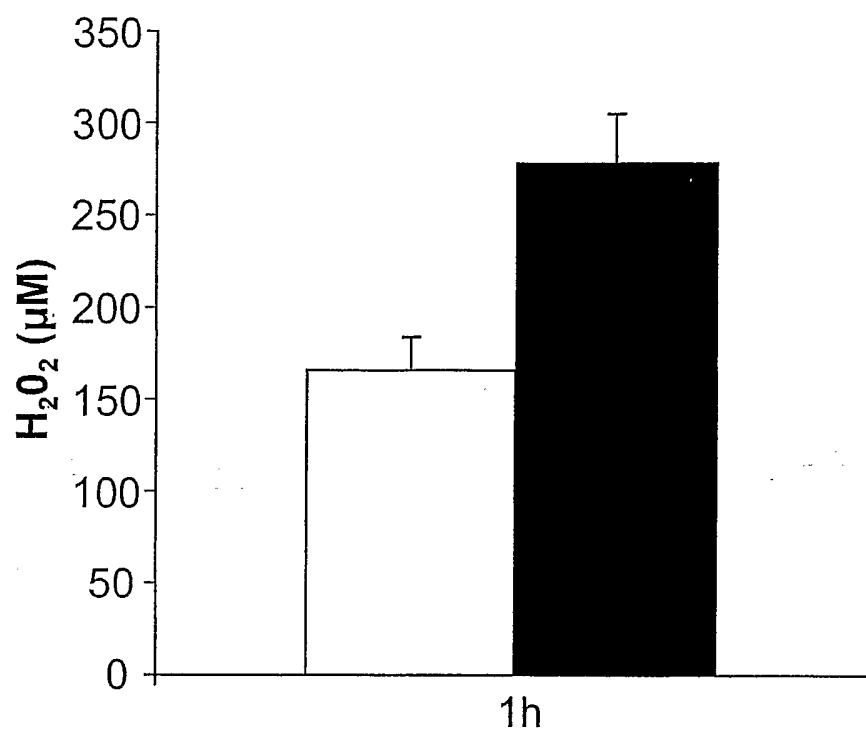
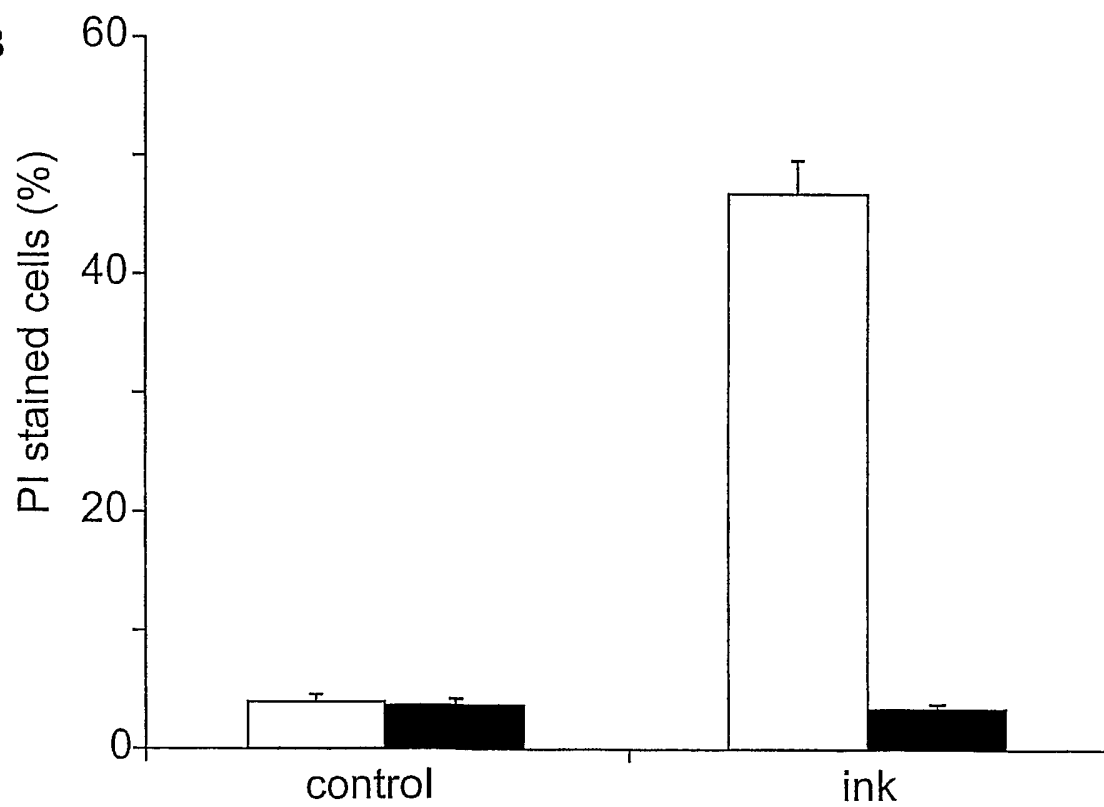
**6A****6B**

Fig.

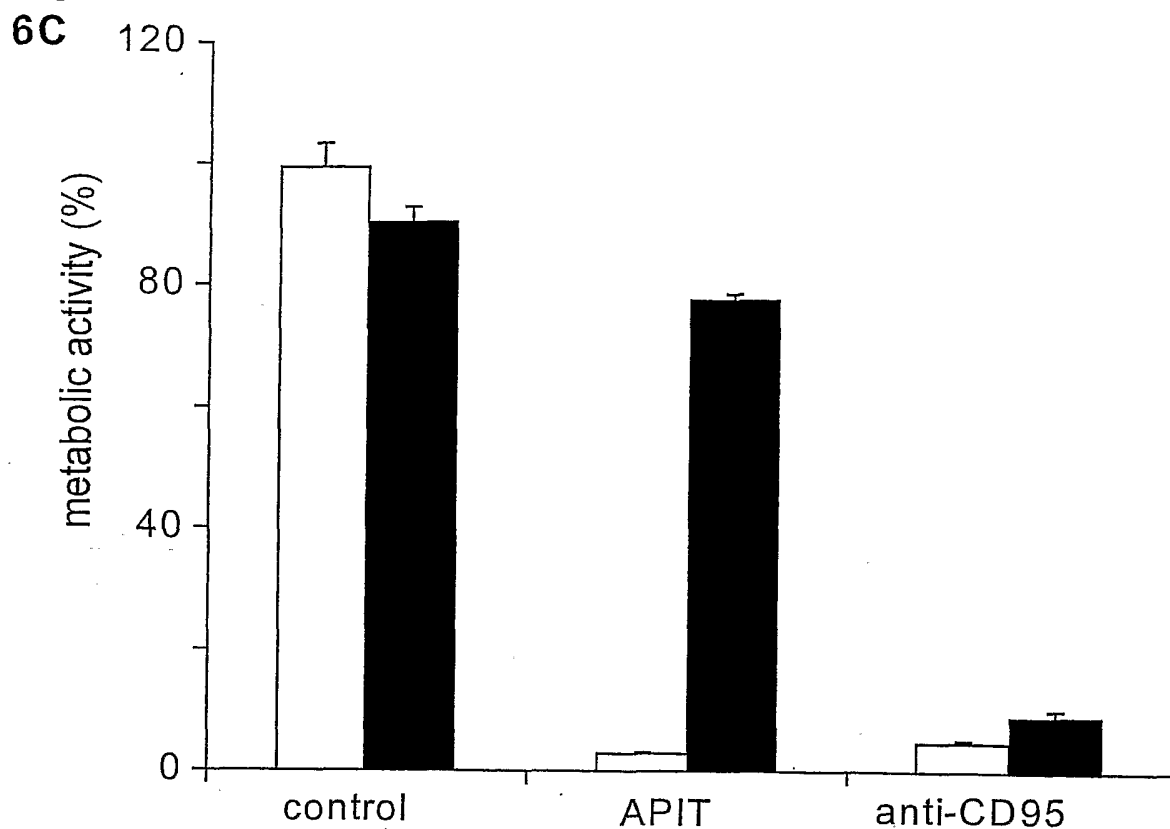
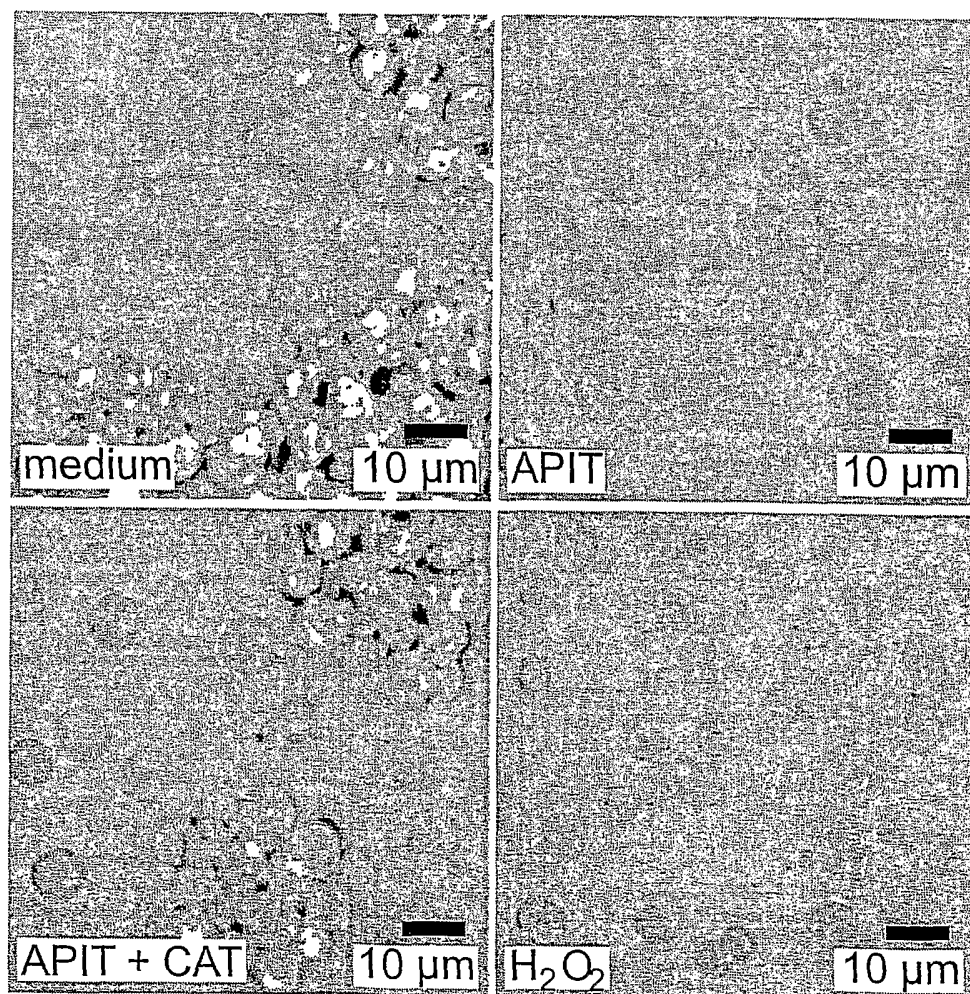
**6D**

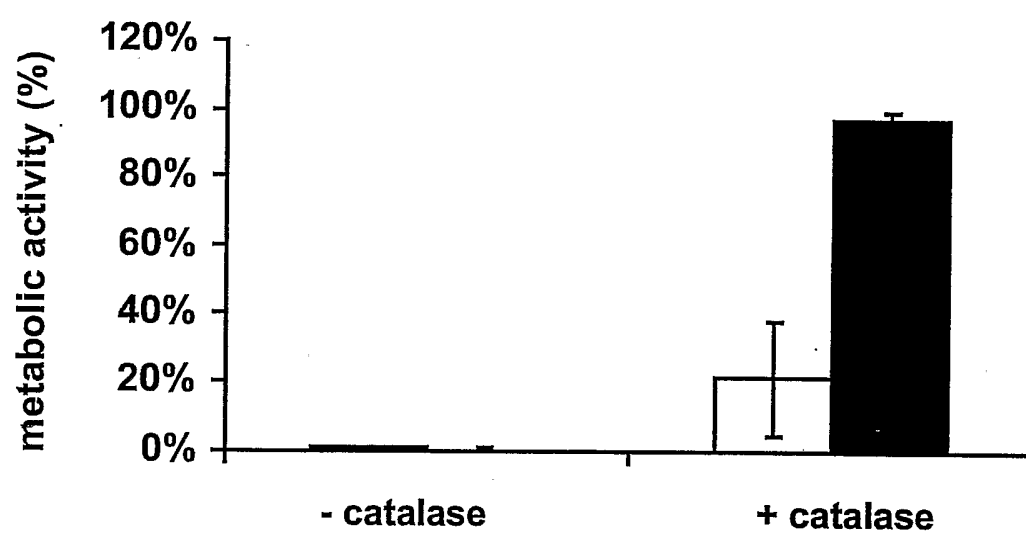
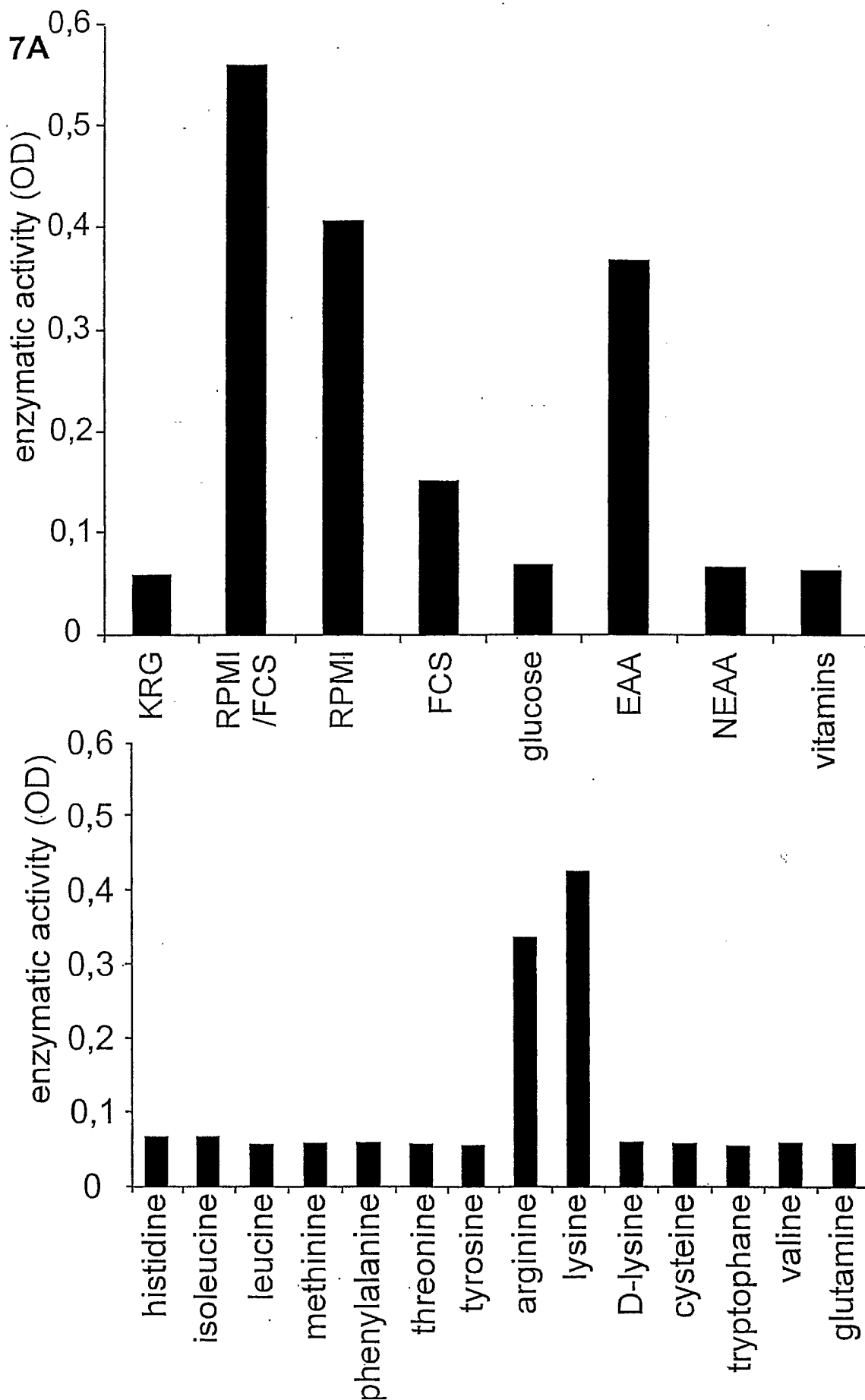
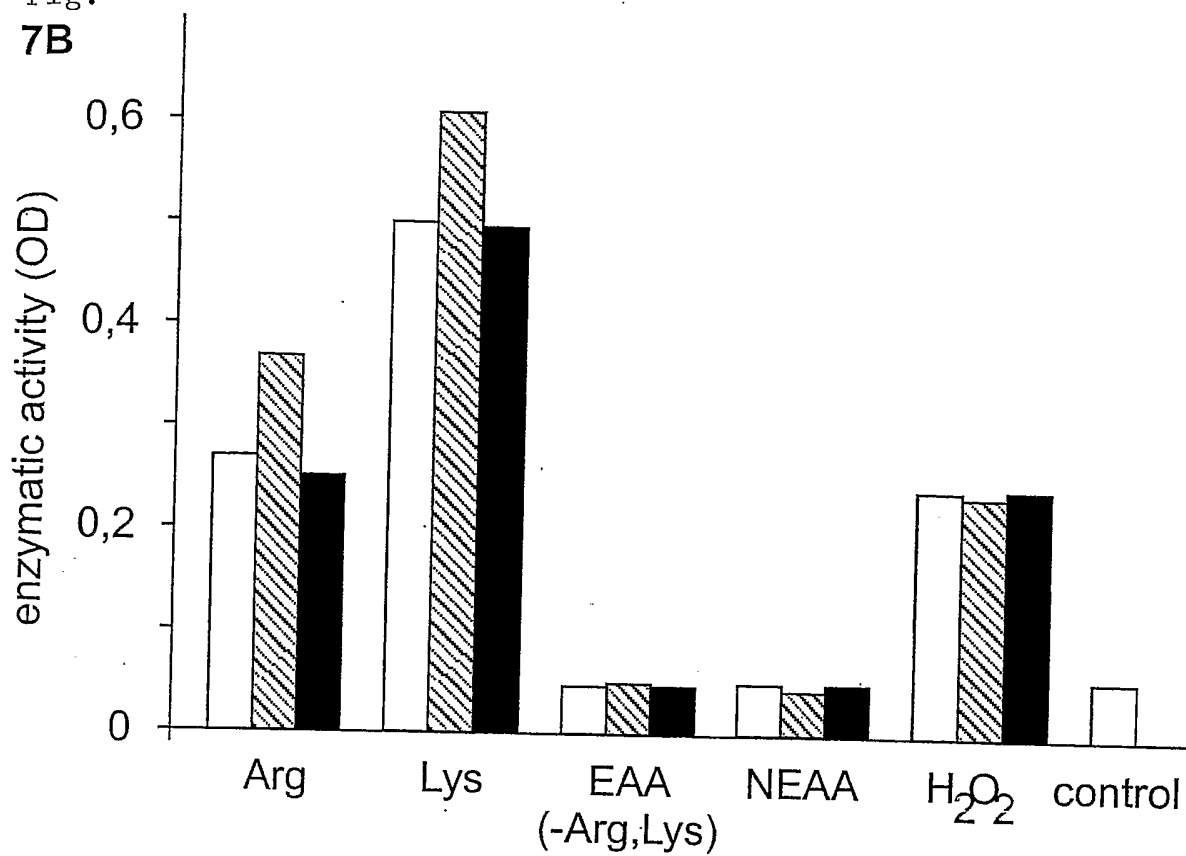
**Fig. 6E**

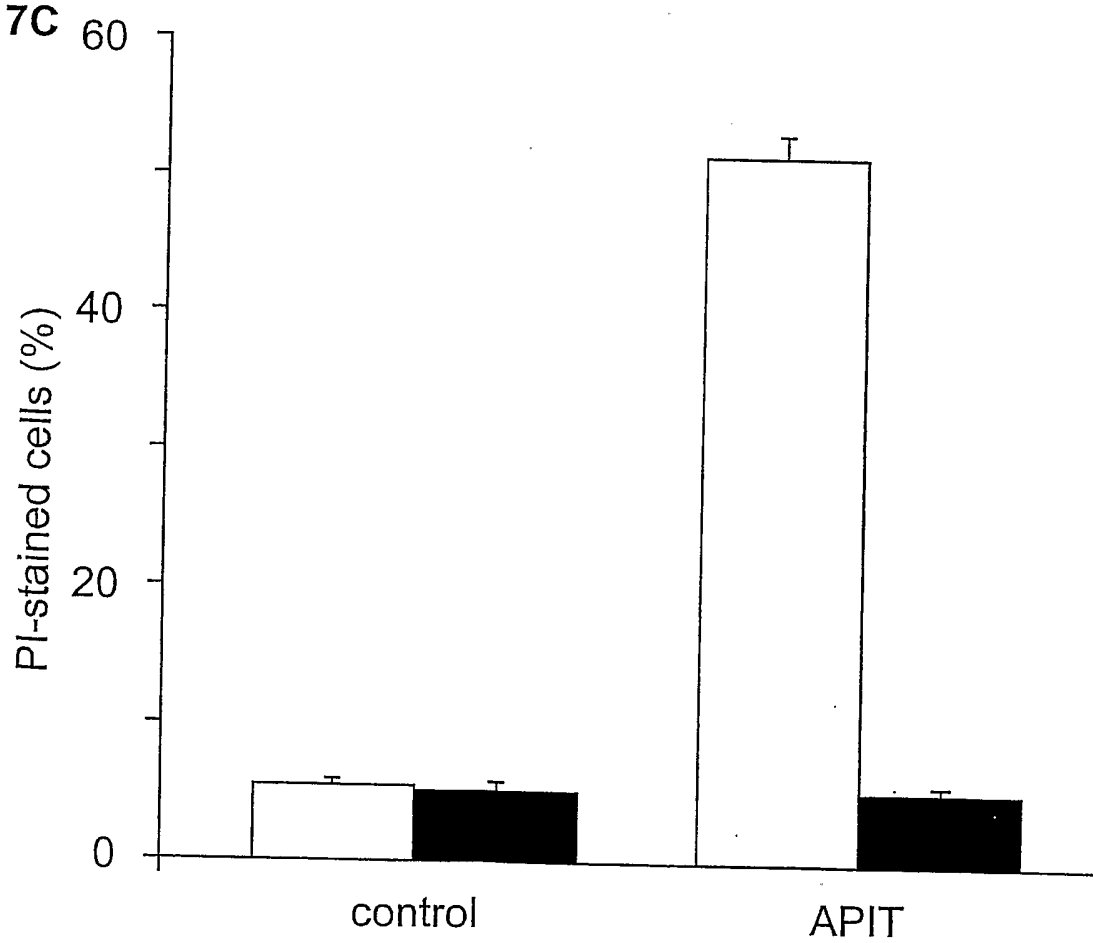
Fig.



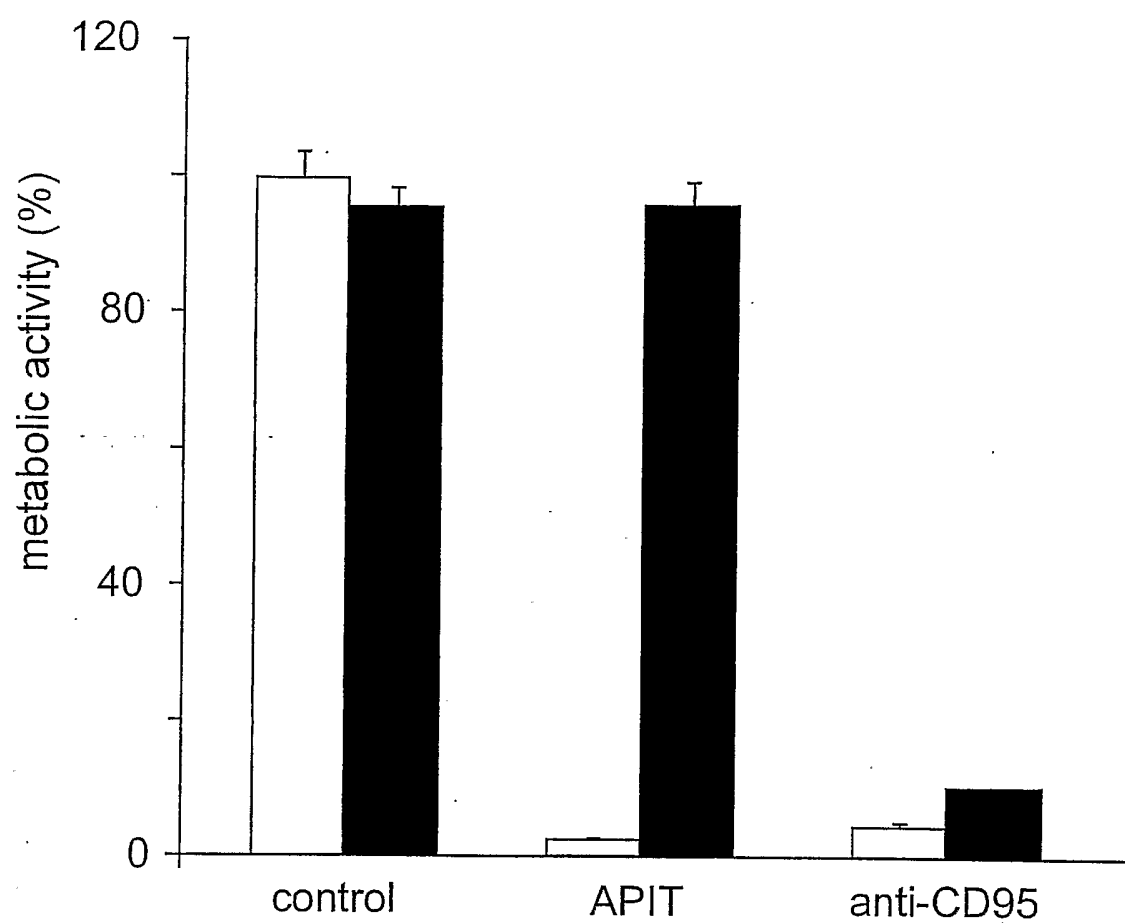
7B



7C



7D



7E

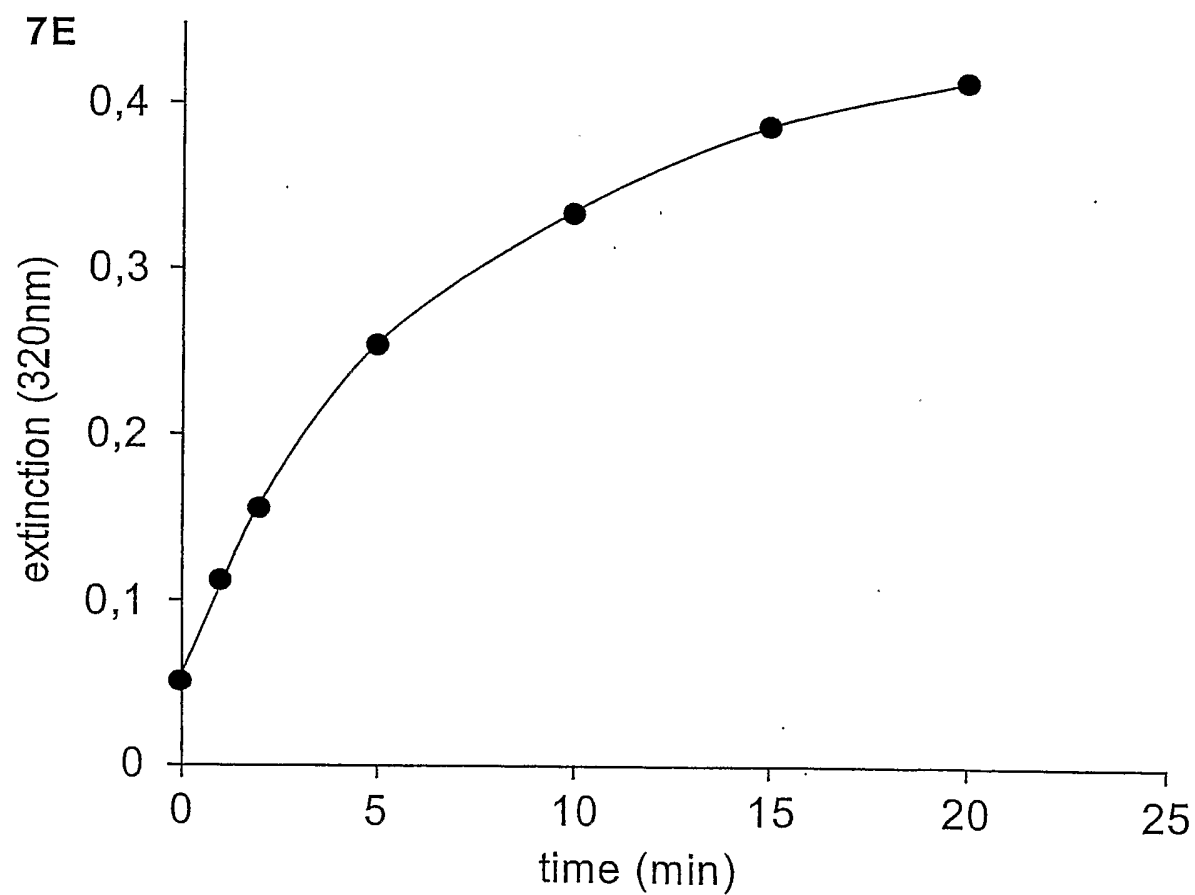
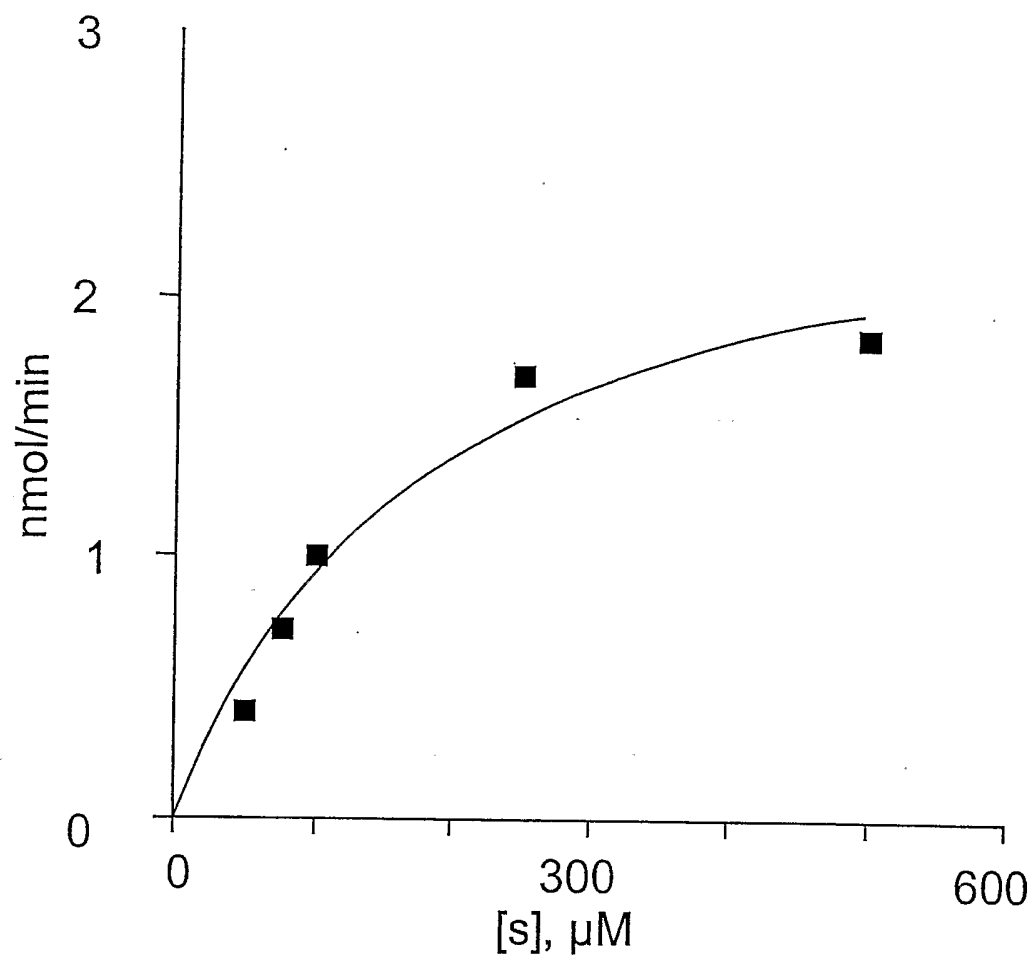


Fig.

7F



7G

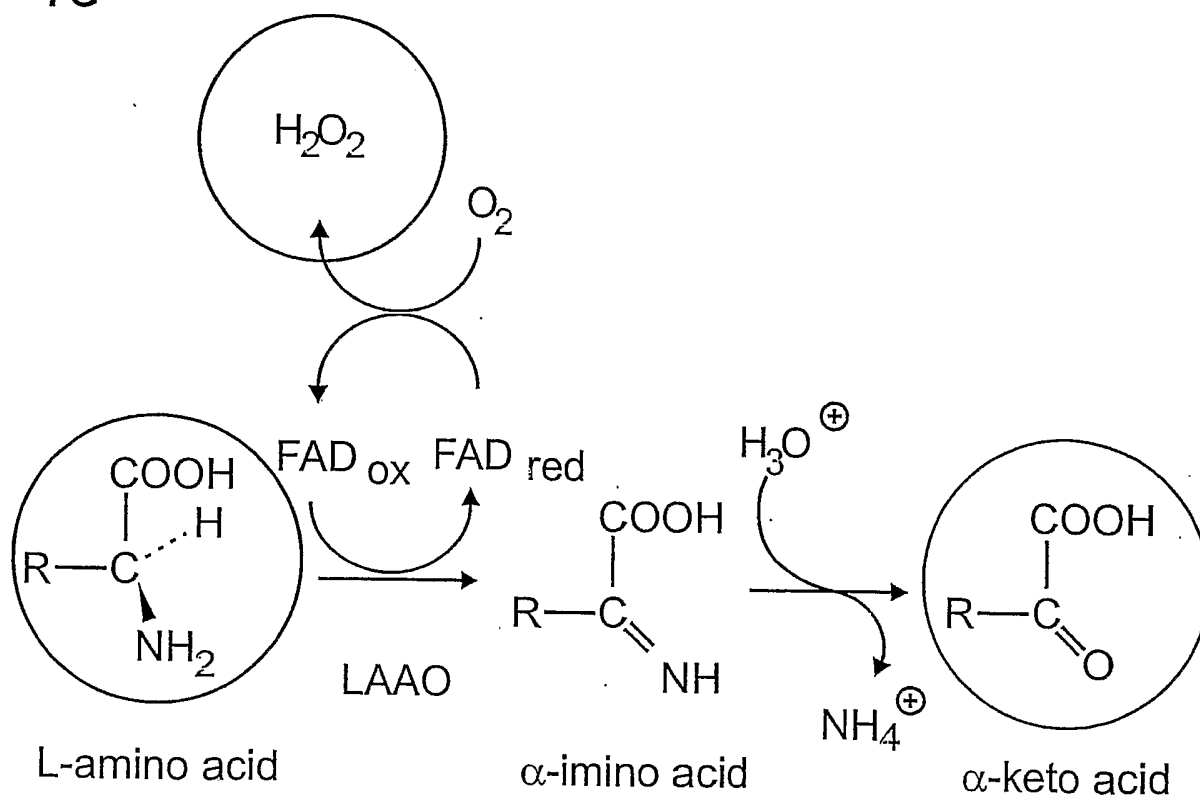
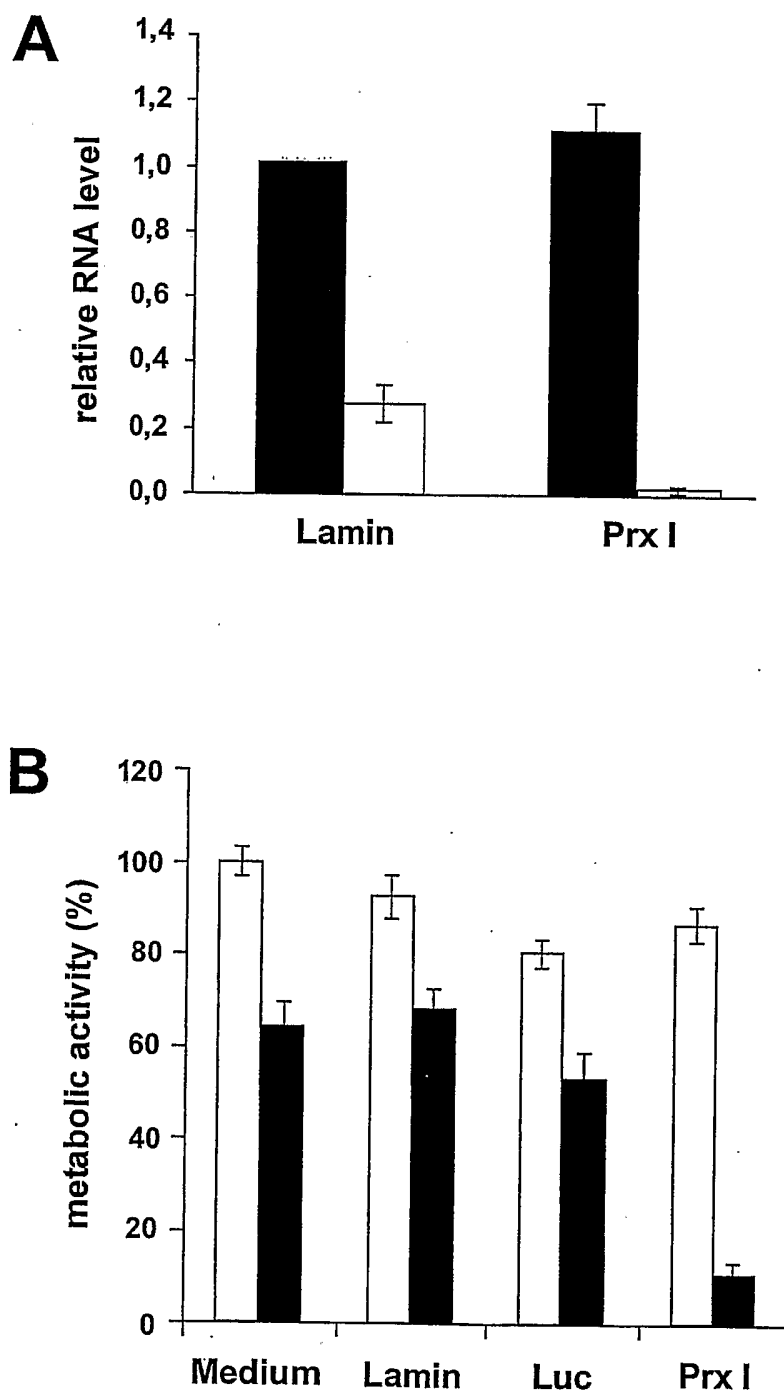


**Fig. 8**

# Fig. 9

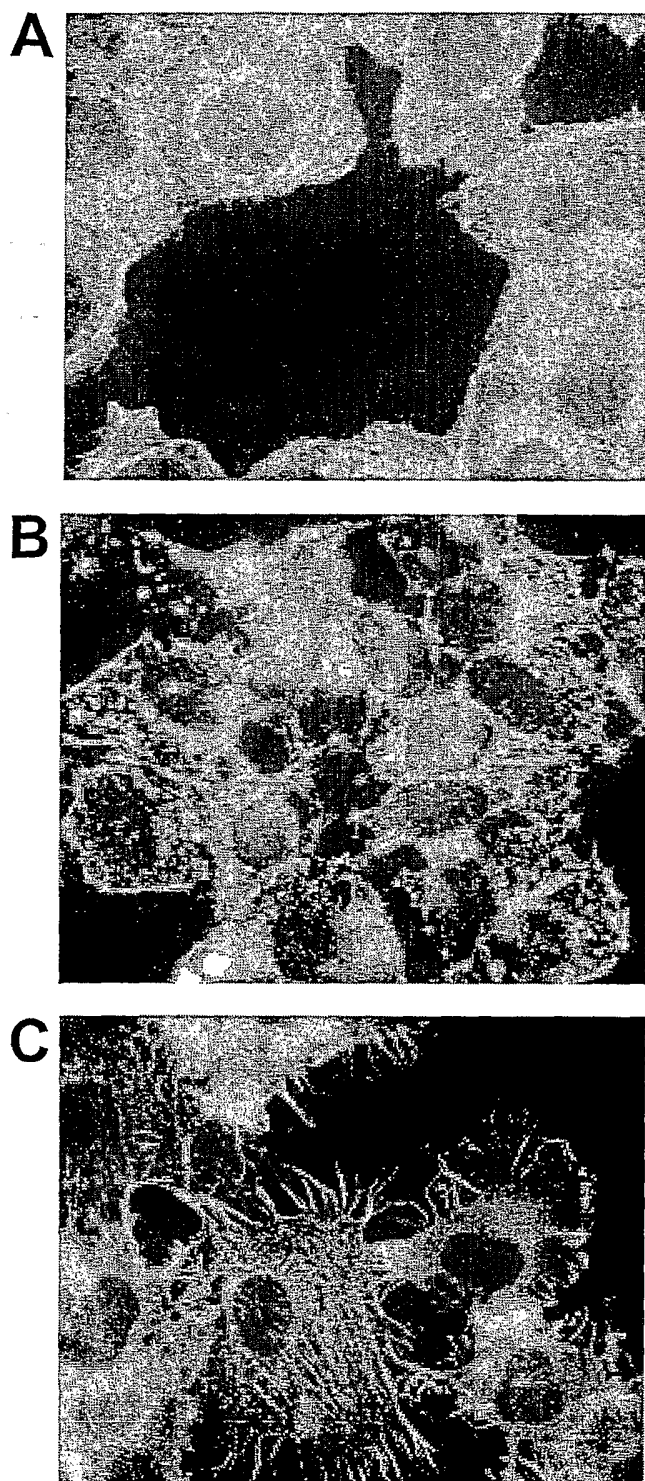
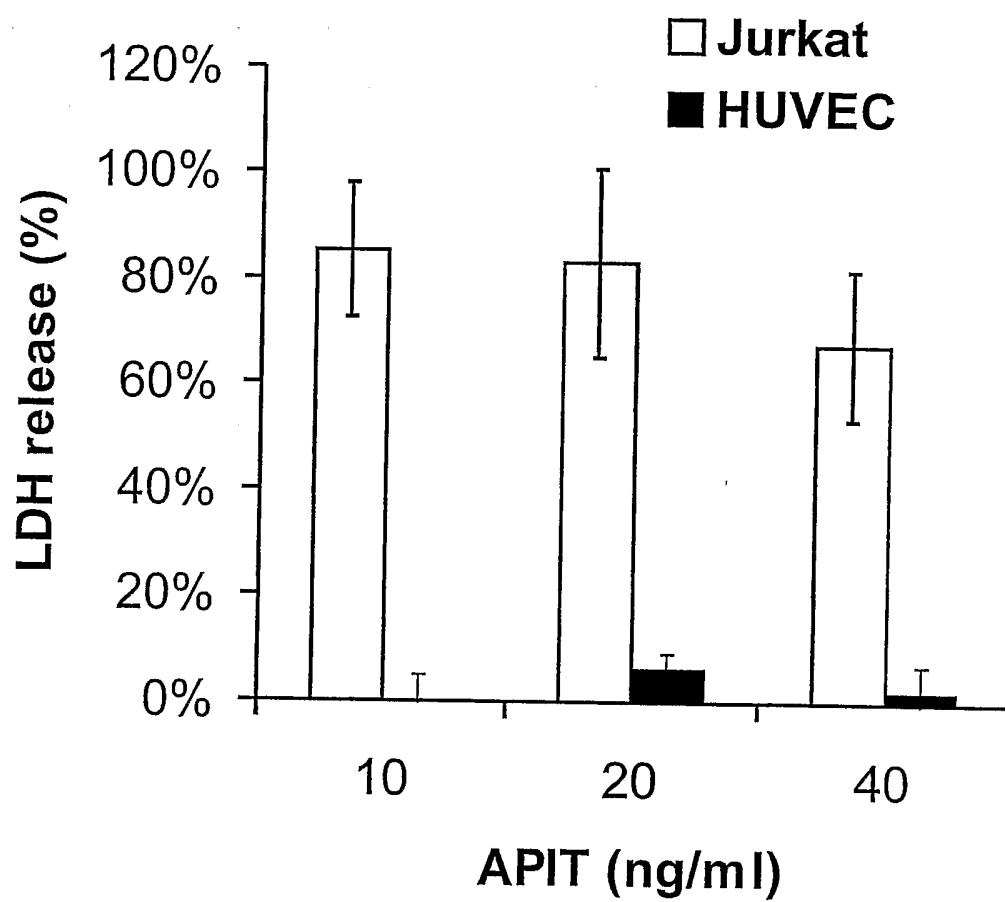


**Fig. 10**

## SEQUENCE LISTING

&lt;110&gt; Max-Planck-Gesellschaft zur Förderung der Wissensch

<120> L-amino acid oxidase with cytotoxic activity from  
Aplysia punctata

&lt;130&gt; 29644PEP-1

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 55

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 1608

&lt;212&gt; DNA

&lt;213&gt; Aplysia punctata

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1608)

&lt;400&gt; 1

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| atg | tcg | tct | gct | gtg | ctt | ctc | ctg | gct | tgt | gcg | ttg | gtc | atc | tct | gtc | 48 |
| Met | Ser | Ser | Ala | Val | Leu | Leu | Leu | Ala | Cys | Ala | Leu | Val | Ile | Ser | Val |    |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| cac | gcc | gac | ggt | atc | tgc | aga | aac | aga | cgt | caa | tgt | aac | aga | gag | gtg | 96 |
| His | Ala | Asp | Gly | Ile | Cys | Arg | Asn | Arg | Arg | Gln | Cys | Asn | Arg | Glu | Val |    |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tgc | ggt | tct | acc | tac | gat | gtg | gcc | gtc | gtg | ggg | gcg | ggg | cct | ggg | gga | 144 |
| Cys | Gly | Ser | Thr | Tyr | Asp | Val | Ala | Val | Val | Gly | Ala | Gly | Pro | Gly | Gly |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gct | aac | tcc | gcc | tac | atg | ctg | agg | gac | tcc | ggc | ctg | gac | atc | gct | gtg | 192 |
| Ala | Asn | Ser | Ala | Tyr | Met | Leu | Arg | Asp | Ser | Gly | Leu | Asp | Ile | Ala | Val |     |
|     | 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ttc | gag | tac | tcg | gac | cga | gtg | ggc | ggc | cgg | ctg | ttc | acc | tac | cag | ctg | 240 |
| Phe | Glu | Tyr | Ser | Asp | Arg | Val | Gly | Gly | Arg | Leu | Phe | Thr | Tyr | Gln | Leu |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ccc | aac | aca | ccc | gac | gtt | aac | ctg | gag | att | ggc | ggc | atg | agg | ttc | atc | 288 |
| Pro | Asn | Thr | Pro | Asp | Val | Asn | Leu | Glu | Ile | Gly | Gly | Met | Arg | Phe | Ile |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gaa | ggc | gcc | atg | cac | agg | ctc | tgg | agg | gtc | att | tca | gaa | ctc | ggc | cta | 336 |
| Glu | Gly | Ala | Met | His | Arg | Leu | Trp | Arg | Val | Ile | Ser | Glu | Leu | Gly | Leu |     |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| acc | ccc | aag | gtg | ttc | aag | gaa | ggt | ttc | ggc | aag | gag | ggc | aga | caa | aga | 384 |
| Thr | Pro | Lys | Val | Phe | Lys | Glu | Gly | Phe | Gly | Lys | Glu | Gly | Arg | Gln | Arg |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ttt | tac | ctg | cgg | gga | cag | agc | ctg | acc | aag | aaa | cag | gtc | aag | agt | ggg | 432 |
| Phe | Tyr | Leu | Arg | Gly | Gln | Ser | Leu | Thr | Lys | Lys | Gln | Val | Lys | Ser | Gly |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |

2

ttc agc caa atg tac gac tgg cag aag tct gag gcg tcc gga gac tac 1200  
 Phe Ser Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr  
 385 390 395 400  
  
 atc ctg atc gcc agc tac gcc gac ggc ctc aaa gcc cag tac ctg cgg 1248  
 Ile Leu Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg  
 405 410 415  
  
 gag ctg aag aat cag gga gag gac atc cca ggc tct gac cca ggc tac 1296  
 Glu Leu Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr  
 420 425 430  
  
 aac cag gtt acc gaa ccc ctc aag gac acc att ctt gac cac ctc act 1344  
 Asn Gln Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr  
 435 440 445  
  
 gag gct tat ggc gtg gag cga gac tcg atc ccg gaa ccc gtg acc gcc 1392  
 Glu Ala Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala  
 450 455 460  
  
 gct tcc cag ttc tgg aca gac tac ccg ttt ggc tgt gga tgg atc acc 1440  
 Ala Ser Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr  
 465 470 475 480  
  
 tgg agg gcc ggc ttc cat ttc gat gac gtc atc agc acc atg cgt cgc 1488  
 Trp Arg Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg  
 485 490 495  
  
 ccg tca ctg aaa gat gag gta tac gtg gtg gga gcc gac tac tcc tgg 1536  
 Pro Ser Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp  
 500 505 510  
  
 gga ctt atc tcc tcc tgg ata gag ggc gct ctg gag acc tcg gaa aac 1584  
 Gly Leu Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn  
 515 520 525  
  
 gtc atc aac gac tac ttc ctc taa 1608  
 Val Ile Asn Asp Tyr Phe Leu  
 530 535

&lt;210&gt; 2

&lt;211&gt; 535

&lt;212&gt; PRT

<213> *Aplysia punctata*

&lt;400&gt; 2

Met Ser Ser Ala Val Leu Leu Leu Ala Cys Ala Leu Val Ile Ser Val  
 1 5 10 15  
  
 His Ala Asp Gly Ile Cys Arg Asn Arg Arg Gln Cys Asn Arg Glu Val  
 20 25 30  
  
 Cys Gly Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly  
 35 40 45  
  
 Ala Asn Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val  
 50 55 60  
  
 Phe Glu Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu  
 65 70 75 80

4

Ile Leu Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg  
 405 410 415

Glu Leu Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr  
 420 425 430

Asn Gln Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr  
 435 440 445

Glu Ala Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala  
 450 455 460

Ala Ser Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr  
 465 470 475 480

Trp Arg Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg  
 485 490 495

Pro Ser Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp  
 500 505 510

Gly Leu Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn  
 515 520 525

Val Ile Asn Asp Tyr Phe Leu  
 530 535

<210> 3  
 <211> 1605  
 <212> DNA  
 <213> *Aplysia punctata*

<220>  
 <221> CDS  
 <222> (1)..(1605)

<220>  
 <221> sig\_peptide  
 <222> (1)..(51)  
 <223> Signal peptide not complete

<400> 3  
 tcg tct gct gtg ctt ctc ctg gct tgt gcg ttg gtc atc tct gtc cac 48  
 Ser Ser Ala Val Leu Leu Leu Ala Cys Ala Leu Val Ile Ser Val His  
 1 5 10 15

gcc gac ggt gtc tgc aga aac aga cgt caa tgt aac aga gag gtg tgc 96  
 Ala Asp Gly Val Cys Arg Asn Arg Arg Gln Cys Asn Arg Glu Val Cys  
 20 25 30

ggt tct acc tac gat gtg gcc gtc gtg ggg gcg ggg cct ggg gga gct 144  
 Gly Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala  
 35 40 45

aac tcc gcc tac atg ctg agg gac tcc ggc ctg gac atc gct gtg ttc 192  
 Asn Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe  
 50 55 60

gag tac tca gac cga gtg ggc ggc cgg ctg ttc acc tac cag ctg ccc 240

|           |     |     |     |     |           |     |     |     |     |           |     |     |     |     |           |     |
|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|
| Glu<br>65 | Tyr | Ser | Asp | Arg | Val<br>70 | Gly | Gly | Arg | Leu | Phe<br>75 | Thr | Tyr | Gln | Leu | Pro<br>80 |     |
| aac       | aca | ccc | gac | gtt | aat       | ctc | gag | att | ggc | ggc       | atg | agg | ttc | atc | gag       | 288 |
| Asn       | Thr | Pro | Asp | Val | Asn       | Leu | Glu | Ile | Gly | Gly       | Met | Arg | Phe | Ile | Glu       |     |
|           |     |     |     | 85  |           |     |     |     | 90  |           |     |     |     | 95  |           |     |
| ggc       | gcc | atg | cac | agg | ctc       | tgg | agg | gtc | att | tca       | gaa | ctc | ggc | cta | acc       | 336 |
| Gly       | Ala | Met | His | Arg | Leu       | Trp | Arg | Val | Ile | Ser       | Glu | Leu | Gly | Leu | Thr       |     |
|           |     |     | 100 |     |           |     |     | 105 |     |           |     |     | 110 |     |           |     |
| ccc       | aag | gtg | ttc | aag | gaa       | ggt | ttc | gga | aag | gag       | ggc | aga | cag | aga | ttt       | 384 |
| Pro       | Lys | Val | Phe | Lys | Glu       | Gly | Phe | Gly | Lys | Glu       | Gly | Arg | Gln | Arg | Phe       |     |
|           |     | 115 |     |     |           |     |     | 120 |     |           |     | 125 |     |     |           |     |
| tac       | ctg | cgg | gga | cag | agc       | ctg | acc | aag | aaa | cag       | gtc | aag | agt | ggg | gac       | 432 |
| Tyr       | Leu | Arg | Gly | Gln | Ser       | Leu | Thr | Lys | Lys | Gln       | Val | Lys | Ser | Gly | Asp       |     |
|           |     | 130 |     |     |           |     |     | 135 |     |           |     | 140 |     |     |           |     |
| gta       | ccc | tat | gac | ctc | agc       | ccg | gag | gag | aaa | gaa       | aac | cag | gga | aat | ctg       | 480 |
| Val       | Pro | Tyr | Asp | Leu | Ser       | Pro | Glu | Glu | Lys | Glu       | Asn | Gln | Gly | Asn | Leu       |     |
|           |     |     |     |     |           | 150 |     |     |     |           | 155 |     |     |     | 160       |     |
| gtc       | gaa | tac | tac | ctg | gag       | aaa | ctg | aca | ggt | cta       | caa | ctc | aat | ggt | gaa       | 528 |
| Val       | Glu | Tyr | Tyr | Leu | Glu       | Lys | Leu | Thr | Gly | Leu       | Gln | Leu | Asn | Gly | Glu       |     |
|           |     |     |     | 165 |           |     |     |     | 170 |           |     |     |     | 175 |           |     |
| ccg       | ctc | aaa | cgt | gag | gtt       | gcg | ctt | aaa | cta | acc       | gtg | ccg | gac | ggc | aga       | 576 |
| Pro       | Leu | Lys | Arg | Glu | Val       | Ala | Leu | Lys | Leu | Thr       | Val | Pro | Asp | Gly | Arg       |     |
|           |     |     | 180 |     |           |     |     | 185 |     |           |     |     | 190 |     |           |     |
| ttc       | ctc | tat | gac | ctc | tcg       | ttt | gac | gaa | gcc | atg       | gat | ctg | gtt | gcc | tcc       | 624 |
| Phe       | Leu | Tyr | Asp | Leu | Ser       | Phe | Asp | Glu | Ala | Met       | Asp | Leu | Val | Ala | Ser       |     |
|           |     | 195 |     |     |           |     | 200 |     |     |           |     | 205 |     |     |           |     |
| cct       | gag | ggc | aaa | gag | ttc       | acc | cga | gac | acg | cac       | gtc | ttc | acc | gga | gag       | 672 |
| Pro       | Glu | Gly | Lys | Glu | Phe       | Thr | Arg | Asp | Thr | His       | Val | Phe | Thr | Gly | Glu       |     |
|           |     | 210 |     |     |           | 215 |     |     |     |           | 220 |     |     |     |           |     |
| gtc       | acc | ctg | ggc | gcg | tcg       | gct | gtc | tcc | ctc | ttc       | gac | gac | cac | ctg | gga       | 720 |
| Val       | Thr | Leu | Gly | Ala | Ser       | Ala | Val | Ser | Leu | Phe       | Asp | Asp | His | Leu | Gly       |     |
|           |     | 225 |     |     |           | 230 |     |     |     |           | 235 |     |     |     | 240       |     |
| gag       | gac | tac | tac | ggc | agt       | gag | atc | tac | acc | ctc       | aag | gaa | gga | ctg | tct       | 768 |
| Glu       | Asp | Tyr | Tyr | Gly | Ser       | Glu | Ile | Tyr | Thr | Leu       | Lys | Glu | Gly | Leu | Ser       |     |
|           |     |     |     | 245 |           |     |     |     | 250 |           |     |     |     | 255 |           |     |
| tcc       | gtc | cct | caa | ggg | ctc       | cta | cag | gct | ttt | ctg       | gac | gcc | gca | gac | tcc       | 816 |
| Ser       | Val | Pro | Gln | Gly | Leu       | Leu | Gln | Ala | Phe | Leu       | Asp | Ala | Ala | Asp | Ser       |     |
|           |     |     | 260 |     |           |     |     | 265 |     |           |     |     | 270 |     |           |     |
| aac       | gag | ttc | tat | ccc | aac       | agc | cac | ctg | aag | gcc       | ctg | aga | cgt | aag | acc       | 864 |
| Asn       | Glu | Phe | Tyr | Pro | Asn       | Ser | His | Leu | Lys | Ala       | Leu | Arg | Arg | Lys | Thr       |     |
|           |     | 275 |     |     |           |     | 280 |     |     |           |     | 285 |     |     |           |     |
| aac       | ggt | cag | tat | gtt | ctt       | tac | ttt | gag | ccc | acc       | acc | tcc | aag | gat | gga       | 912 |
| Asn       | Gly | Gln | Tyr | Val | Leu       | Tyr | Phe | Glu | Pro | Thr       | Thr | Ser | Lys | Asp | Gly       |     |
|           |     | 290 |     |     |           | 295 |     |     |     |           | 300 |     |     |     |           |     |
| caa       | acc | aca | atc | aac | tat       | ctg | gaa | ccc | ctg | cag       | gtt | gtg | tgt | gca | cag       | 960 |
| Gln       | Thr | Thr | Ile | Asn | Tyr       | Leu | Glu | Pro | Leu | Gln       | Val | Val | Cys | Ala | Gln       |     |

| 305                                                             | 310 | 315 | 320 |      |
|-----------------------------------------------------------------|-----|-----|-----|------|
| aga gtc att ctg gcc atg ccg gtc tac gct ctc aac cag ttg gat tgg |     |     |     | 1008 |
| Arg Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp Trp |     |     |     |      |
| 325                                                             |     | 330 | 335 |      |
| aat cag ctc aga aat gac cga gcc acc caa gcg tac gct gcc gtg cgc |     |     |     | 1056 |
| Asn Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val Arg |     |     |     |      |
| 340                                                             |     | 345 | 350 |      |
| ccg att cct gca agt aag gtg ttc atg acc ttt gat cag ccc tgg tgg |     |     |     | 1104 |
| Pro Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp |     |     |     |      |
| 355                                                             |     | 360 | 365 |      |
| ttg gag aac gag agg aaa tcc tgg gtc acc aag tcg gac gcg ctt ttc |     |     |     | 1152 |
| Leu Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu Phe |     |     |     |      |
| 370                                                             |     | 375 | 380 |      |
| agt caa atg tac gac tgg cag aag tct gag gcg tcc gga gac tac atc |     |     |     | 1200 |
| Ser Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr Ile |     |     |     |      |
| 385                                                             |     | 390 | 395 | 400  |
| ctg atc gcc agc tac gcc gac ggc ctc aaa gcc cag tac ctg cgg gag |     |     |     | 1248 |
| Leu Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg Glu |     |     |     |      |
| 405                                                             |     | 410 | 415 |      |
| ctg aag aat cag gga gag gac atc cca ggc tct gac cca ggc tac aac |     |     |     | 1296 |
| Leu Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr Asn |     |     |     |      |
| 420                                                             |     | 425 | 430 |      |
| cag gtc acc gaa ccc ctc aag gac acc att ctt gac cac ctc act gag |     |     |     | 1344 |
| Gln Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr Glu |     |     |     |      |
| 435                                                             |     | 440 | 445 |      |
| gcc tat ggc gtg gag cga gac tcg atc cgg gaa ccc gtg acc gcc gct |     |     |     | 1392 |
| Ala Tyr Gly Val Glu Arg Asp Ser Ile Arg Glu Pro Val Thr Ala Ala |     |     |     |      |
| 450                                                             |     | 455 | 460 |      |
| tcc cag ttc tgg aca gac tac ccg ttt ggc tgt gga tgg atc acc tgg |     |     |     | 1440 |
| Ser Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr Trp |     |     |     |      |
| 465                                                             |     | 470 | 475 | 480  |
| agg gcc ggc ttc cat ttc gat gac gtc atc agc acc atg cgt cgc ccg |     |     |     | 1488 |
| Arg Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg Pro |     |     |     |      |
| 485                                                             |     | 490 | 495 |      |
| tca ctg aaa gat gag gtc tac gtg gtg gga gcc gat tac tcc tgg gga |     |     |     | 1536 |
| Ser Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp Gly |     |     |     |      |
| 500                                                             |     | 505 | 510 |      |
| ctt atc tcc tcc tgg ata gag ggc gct ctg gag acc tca gaa aac gtc |     |     |     | 1584 |
| Leu Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn Val |     |     |     |      |
| 515                                                             |     | 520 | 525 |      |
| atc aac gac tac ttc ctc taa                                     |     |     |     | 1605 |
| Ile Asn Asp Tyr Phe Leu                                         |     |     |     |      |
| 530                                                             |     | 535 |     |      |

&lt;210&gt; 4

&lt;211&gt; 534

&lt;212&gt; PRT

<213> *Aplysia punctata*

&lt;400&gt; 4

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Ser Ser Ala Val Leu Leu Leu Ala Cys Ala Leu Val Ile Ser Val His
 1              5              10              15

Ala Asp Gly Val Cys Arg Asn Arg Arg Gln Cys Asn Arg Glu Val Cys
      20              25              30

Gly Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala
      35              40              45

Asn Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe
      50              55              60

Glu Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu Pro
      65              70              75              80

Asn Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile Glu
      85              90              95

Gly Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu Thr
      100              105              110

Pro Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg Phe
      115              120              125

Tyr Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly Asp
      130              135              140

Val Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gln Gly Asn Leu
      145              150              155              160

Val Glu Tyr Tyr Leu Glu Lys Leu Thr Gly Leu Gln Leu Asn Gly Glu
      165              170              175

Pro Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly Arg
      180              185              190

Phe Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala Ser
      195              200              205

Pro Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly Glu
      210              215              220

Val Thr Leu Gly Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu Gly
      225              230              235              240

Glu Asp Tyr Tyr Gly Ser Glu Ile Tyr Thr Leu Lys Glu Gly Leu Ser
      245              250              255

Ser Val Pro Gln Gly Leu Leu Gln Ala Phe Leu Asp Ala Ala Asp Ser
      260              265              270

Asn Glu Phe Tyr Pro Asn Ser His Leu Lys Ala Leu Arg Arg Lys Thr
      275              280              285

Asn Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp Gly
      290              295              300

```

Gln Thr Thr Ile Asn Tyr Leu Glu Pro Leu Gln Val Val Cys Ala Gln  
 305 310 315 320  
 Arg Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp Trp  
 325 330 335  
 Asn Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val Arg  
 340 345 350  
 Pro Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp  
 355 360 365  
 Leu Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu Phe  
 370 375 380  
 Ser Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr Ile  
 385 390 395 400  
 Leu Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg Glu  
 405 410 415  
 Leu Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr Asn  
 420 425 430  
 Gln Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr Glu  
 435 440 445  
 Ala Tyr Gly Val Glu Arg Asp Ser Ile Arg Glu Pro Val Thr Ala Ala  
 450 455 460  
 Ser Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr Trp  
 465 470 475 480  
 Arg Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg Pro  
 485 490 495  
 Ser Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp Gly  
 500 505 510  
 Leu Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn Val  
 515 520 525  
 Ile Asn Asp Tyr Phe Leu  
 530

&lt;210&gt; 5

&lt;211&gt; 1554

&lt;212&gt; DNA

&lt;213&gt; Aplysia punctata

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1554)

&lt;400&gt; 5

gac ggt atc tgc aga aac aga cgt caa tgt aac aga gag gtg tgc ggt 48  
 Asp Gly Ile Cys Arg Asn Arg Arg Gln Cys Asn Arg Glu Val Cys Gly  
 1 5 10 15

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| tct acc tac gat gtg gct gtc gtg ggg gcg ggg cct ggg gga gct aac | 96  |
| Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala Asn |     |
| 20 25 30                                                        |     |
| tcc gcc tac atg ctg agg gac tcc ggc ctg gac atc gct gtg ttc gag | 144 |
| Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe Glu |     |
| 35 40 45                                                        |     |
| tac tca gac cga gtg ggc ggc cgg ctg ttc acc tac cag ctg ccc aac | 192 |
| Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu Pro Asn |     |
| 50 55 60                                                        |     |
| aca ccc gac gtt aat ctc gag att ggc ggc atg agg ttc atc gag ggc | 240 |
| Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile Glu Gly |     |
| 65 70 75 80                                                     |     |
| gcc atg cac agg ctc tgg agg gtc att tca gaa ctc ggc cta acc ccc | 288 |
| Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu Thr Pro |     |
| 85 90 95                                                        |     |
| aag gtg ttc aag gaa ggt ttc gga aag gag ggc aga cag aga ttt tac | 336 |
| Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg Phe Tyr |     |
| 100 105 110                                                     |     |
| ctg cgg gga cag agc ctg acc aag aaa cag gtc aag agt ggg gac gta | 384 |
| Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly Asp Val |     |
| 115 120 125                                                     |     |
| ccc tat gac ctc agc ccg gag gag aaa gaa aac cag gga aat ctg gtc | 432 |
| Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gln Gly Asn Leu Val |     |
| 130 135 140                                                     |     |
| gaa tac tac ctg gag aaa ctg aca ggt cta aaa ctc aac ggc gga ccg | 480 |
| Glu Tyr Tyr Leu Glu Lys Leu Thr Gly Leu Lys Leu Asn Gly Gly Pro |     |
| 145 150 155 160                                                 |     |
| ctc aaa cgt gag gtt gcg ctt aaa cta acc gtg ccg gac ggc aga ttc | 528 |
| Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly Arg Phe |     |
| 165 170 175                                                     |     |
| ctc tat gac ctc tcg ttt gac gaa gcc atg gac ctg gtt gcc tcc cct | 576 |
| Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala Ser Pro |     |
| 180 185 190                                                     |     |
| gag ggc aaa gag ttc acc cga gac acg cac gtg ttc acc gga gaa gtc | 624 |
| Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly Glu Val |     |
| 195 200 205                                                     |     |
| acc ctg gac gcg tcg gct gtc tcc ctc ttc gac gac cac ctg gga gag | 672 |
| Thr Leu Asp Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu Gly Glu |     |
| 210 215 220                                                     |     |
| gac tac tat ggc agt gag atc tac acc cta aag gaa gga ctg tct tcc | 720 |
| Asp Tyr Tyr Gly Ser Glu Ile Tyr Thr Leu Lys Glu Gly Leu Ser Ser |     |
| 225 230 235 240                                                 |     |
| gtc cca caa ggg ctc cta cag act ttt ctg gac gcc gca gac tcc aac | 768 |
| Val Pro Gln Gly Leu Leu Gln Thr Phe Leu Asp Ala Ala Asp Ser Asn |     |
| 245 250 255                                                     |     |
| gag ttc tat ccc aac agc cac ctg aag gcc ctg aga cgt aag acc aac | 816 |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| Glu Phe Tyr Pro Asn Ser His Leu Lys Ala Leu Arg Arg Lys Thr Asn |      |
| 260 265 270                                                     |      |
| ggt cag tat gtt ctt tac ttt gag ccc acc acc tcc aag gat gga caa | 864  |
| Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp Gly Gln |      |
| 275 280 285                                                     |      |
| acc aca atc aac tat ctg gaa ccc ctg cag gtt gtg tgt gca cag aga | 912  |
| Thr Thr Ile Asn Tyr Leu Glu Pro Leu Gln Val Val Cys Ala Gln Arg |      |
| 290 295 300                                                     |      |
| gtc atc ctg gcc atg ccg gtc tac gct ctc aac caa ctg gac tgg aat | 960  |
| Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp Trp Asn |      |
| 305 310 315 320                                                 |      |
| cag ctc aga aat gac cga gcc acc caa gcg tac gct gcc gtg cgc ccg | 1008 |
| Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val Arg Pro |      |
| 325 330 335                                                     |      |
| att cct gca agt aaa gtg ttc atg acc ttt gat cag ccc tgg tgg ttg | 1056 |
| Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp Leu |      |
| 340 345 350                                                     |      |
| gag aac gag agg aaa tcc tgg gtc acc aag tcg gac gcg ctt ttc agc | 1104 |
| Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu Phe Ser |      |
| 355 360 365                                                     |      |
| caa atg tac gac tgg cag aag tct gag gcg tcc gga gac tac atc ctg | 1152 |
| Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr Ile Leu |      |
| 370 375 380                                                     |      |
| atc gcc agc tac gcc gac ggc ctc aaa gcc cag tac ctg cgg gag ctg | 1200 |
| Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg Glu Leu |      |
| 385 390 395 400                                                 |      |
| aag aat cag gga gag gac atc cca ggc tct gac cca ggc tac aac cag | 1248 |
| Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr Asn Gln |      |
| 405 410 415                                                     |      |
| gtc acc gaa ccc ctc aag gac acc att ctt gac cac ctc act gag gct | 1296 |
| Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr Glu Ala |      |
| 420 425 430                                                     |      |
| tat ggc gtg gaa cga gac tcg atc ccg gaa ccc gtg acc gcc gct tcc | 1344 |
| Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala Ala Ser |      |
| 435 440 445                                                     |      |
| cag ttc tgg acc gac tac ccg ttc ggc tgt gga tgg atc acc tgg agg | 1392 |
| Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr Trp Arg |      |
| 450 455 460                                                     |      |
| gca ggc ttc cat ttt gat gac gtc atc agc acc atg cgt cgc ccg tca | 1440 |
| Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg Pro Ser |      |
| 465 470 475 480                                                 |      |
| ctg aaa gat gag gtc tac gtg gtg gga gcc gat tac tcc tgg gga ctt | 1488 |
| Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp Gly Leu |      |
| 485 490 495                                                     |      |
| atc tcc tcc tgg ata gag ggc gct ctg gag acc tcg gaa aac gtc atc | 1536 |
| Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn Val Ile |      |

500 505 510 1554

aac gac tac ttc ctc taa  
 Asn Asp Tyr Phe Leu  
 515

<210> 6  
 <211> 517  
 <212> PRT  
 <213> Aplysia punctata

<400> 6  
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 Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala Asn  
 20 25 30  
 Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe Glu  
 35 40 45  
 Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu Pro Asn  
 50 55 60  
 Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile Glu Gly  
 65 70 75 80  
 Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu Thr Pro  
 85 90 95  
 Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg Phe Tyr  
 100 105 110  
 Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly Asp Val  
 115 120 125  
 Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gln Gly Asn Leu Val  
 130 135 140  
 Glu Tyr Tyr Leu Glu Lys Leu Thr Gly Leu Lys Leu Asn Gly Gly Pro  
 145 150 155 160  
 Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly Arg Phe  
 165 170 175  
 Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala Ser Pro  
 180 185 190  
 Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly Glu Val  
 195 200 205  
 Thr Leu Asp Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu Gly Glu  
 210 215 220  
 Asp Tyr Tyr Gly Ser Glu Ile Tyr Thr Leu Lys Glu Gly Leu Ser Ser  
 225 230 235 240  
 Val Pro Gln Gly Leu Leu Gln Thr Phe Leu Asp Ala Ala Asp Ser Asn  
 245 250 255

Glu Phe Tyr Pro Asn Ser His Leu Lys Ala Leu Arg Arg Lys Thr Asn  
 260 265 270  
 Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp Gly Gln  
 275 280 285  
 Thr Thr Ile Asn Tyr Leu Glu Pro Leu Gln Val Val Cys Ala Gln Arg  
 290 295 300  
 Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp Trp Asn  
 305 310 315 320  
 Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val Arg Pro  
 325 330 335  
 Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp Leu  
 340 345 350  
 Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu Phe Ser  
 355 360 365  
 Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr Ile Leu  
 370 375 380  
 Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg Glu Leu  
 385 390 395 400  
 Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr Asn Gln  
 405 410 415  
 Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr Glu Ala  
 420 425 430  
 Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala Ala Ser  
 435 440 445  
 Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr Trp Arg  
 450 455 460  
 Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg Pro Ser  
 465 470 475 480  
 Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp Gly Leu  
 485 490 495  
 Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn Val Ile  
 500 505 510  
 Asn Asp Tyr Phe Leu  
 515

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 <211> 600  
 <212> DNA  
 <213> Human

<220>  
 <221> CDS  
 <222> (1)..(600)

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gcc aca gct gtt atg cca gat ggt cag ttt aaa gat atc agc ctg tct 96
Ala Thr Ala Val Met Pro Asp Gly Gln Phe Lys Asp Ile Ser Leu Ser
20 25 30

gac tac aaa gga aaa tat gtt gtg ttc ttc ttt tac cct ctt gac ttc 144
Asp Tyr Lys Gly Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu Asp Phe
35 40 45

acc ttt gtg tgc ccc acg gag atc att gct ttc agt gat agg gca gaa 192
Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Glu
50 55 60

gaa ttt aag aaa ctc aac tgc caa gtg att ggt gct tct gtg gat tct 240
Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser
65 70 75 80

cac ttc tgt cat cta gca tgg gtc aat aca cct aag aaa caa gga gga 288
His Phe Cys His Leu Ala Trp Val Asn Thr Pro Lys Lys Gln Gly Gly
85 90 95

ctg gga ccc atg aac att cct ttg gta tca gac ccg aag cgc acc att 336
Leu Gly Pro Met Asn Ile Pro Leu Val Ser Asp Pro Lys Arg Thr Ile
100 105 110

gct cag gat tat ggg gtc tta aag gct gat gaa ggc atc tcg ttc agg 384
Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser Phe Arg
115 120 125

ggc ctt ttt atc att gat gat aag ggt att ctt cgg cag atc act gta 432
Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Val
130 135 140

aat gac ctc cct gtt ggc cgc tct gtg gat gag act ttg aga cta gtt 480
Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Thr Leu Arg Leu Val
145 150 155 160

cag gcc ttc cag ttc act gac aaa cat ggg gaa gtg tgc cca gct ggc 528
Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly
165 170 175

tgg aaa cct ggc agt gat acc atc aag cct gat gtc caa aag agc aaa 576
Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Gln Lys Ser Lys
180 185 190

gaa tat ttc tcc aag cag aag tga 600
Glu Tyr Phe Ser Lys Gln Lys
195 200

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<210> 8
<211> 199
<212> PRT
<213> Human

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<400> 8

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Met Ser Ser Gly Asn Ala Lys Ile Gly His Pro Ala Pro Asn Phe Lys  
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 20 25 30  
 Asp Tyr Lys Gly Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu Asp Phe  
 35 40 45  
 Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Glu  
 50 55 60  
 Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser  
 65 70 75 80  
 His Phe Cys His Leu Ala Trp Val Asn Thr Pro Lys Lys Gln Gly Gly  
 85 90 95  
 Leu Gly Pro Met Asn Ile Pro Leu Val Ser Asp Pro Lys Arg Thr Ile  
 100 105 110  
 Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser Phe Arg  
 115 120 125  
 Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Val  
 130 135 140  
 Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Thr Leu Arg Leu Val  
 145 150 155 160  
 Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly  
 165 170 175  
 Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Gln Lys Ser Lys  
 180 185 190  
 Glu Tyr Phe Ser Lys Gln Lys  
 195

&lt;210&gt; 9

&lt;211&gt; 19

&lt;212&gt; RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: synthetic  
double-stranded RNA molecule

&lt;400&gt; 9

ggcugaugaa ggcaucucg

19

&lt;210&gt; 10

&lt;211&gt; 19

&lt;212&gt; RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: synthetic

double-stranded RNA molecule

<400> 10  
augcuaaaau ug'gcacccc 19

<210> 11  
<211> 19  
<212> RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: synthetic  
double-stranded RNA molecule

<400> 11  
ugcuaaaau gg'gcacccu 19

<210> 12  
<211> 19  
<212> RNA  
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<220>  
<223> Description of Artificial Sequence: synthetic  
double-stranded RNA molecule

<400> 12  
cuucaaagcc acagcuguu 19

<210> 13  
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<212> RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: synthetic  
double-stranded RNA molecule

<400> 13  
agccacagcu guuaugcca 19

<210> 14  
<211> 19  
<212> RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: synthetic  
double-stranded RNA molecule

<400> 14  
gccacagcug uuaugccag 19

<210> 15  
<211> 19  
<212> RNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic  
double-stranded RNA molecule

<400> 15

agauaucagc cugucugac

19

<210> 16

<211> 19

<212> RNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic  
double-stranded RNA molecule

<400> 16

gauaucagcc ugucugacu

19

<210> 17

<211> 19

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic  
double-stranded RNA molecule

<400> 17

gaaacucaac ugccaagug

19

<210> 18

<211> 19

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic  
double-stranded RNA molecule

<400> 18

acucaacugc caagugauu

19

<210> 19

<211> 19

<212> RNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic  
double-stranded RNA molecule

<400> 19

cucaacugcc aagugauug

19

<210> 20  
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<400> 20  
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<210> 21  
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<212> RNA  
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double-stranded RNA molecule

<400> 21  
gugauuggug cuucugugg 19

<210> 22  
<211> 19  
<212> RNA  
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<220>  
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double-stranded RNA molecule

<400> 22  
gaaacaagga ggacuggga 19

<210> 23  
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<212> RNA  
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<400> 23  
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<210> 24  
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double-stranded RNA molecule

<400> 24  
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<210> 25  
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<212> RNA  
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<220>  
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double-stranded RNA molecule

<400> 25  
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<210> 26  
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<212> RNA  
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double-stranded RNA molecule

<400> 26  
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<210> 27  
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<212> RNA  
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double-stranded RNA molecule

<400> 27  
accuggcagu gauaccauc 19

<210> 28  
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<400> 28  
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<210> 29  
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<223> Description of Artificial Sequence: synthetic  
double-stranded RNA molecule

<400> 29

gccugauguc caaaagagc

19

<210> 30

<211> 19

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic  
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<400> 30

cuggacuucc agaagaaca

19

<210> 31

<211> 19

<212> RNA

<213> Artificial Sequence

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<400> 31

cuuacgcuga guacuucga

19

<210> 32

<211> 7

<212> PRT

<213> Aplysia

<400> 32

Asp Gly Glu Asp Ala Ala Val  
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<210> 33

<211> 9

<212> PRT

<213> Aplysia

<220>

<221> MOD\_RES

<222> (1)

<223> Asp can be Asp or Gln

<220>

<221> MOD\_RES

<222> (3)

<223> Ile can be Ile or Val

<220>  
<221> MOD\_RES  
<222> (7)  
<223> Gln can be Gln or Arg  
  
<220>  
<221> MOD\_RES  
<222> (9)  
<223> Pro can be Pro or Gln  
  
<400> 33  
Asp Gly Ile Cys Arg Asn Gln Arg Pro  
1 5

<210> 34  
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<213> Aplysia

<400> 34  
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<210> 35  
<211> 8  
<212> PRT  
<213> Aplysia

<220>  
<221> MOD\_RES  
<222> (5)  
<223> Ile can be Ile or Leu

<400> 35  
Gly Pro Asp Gly Ile Val Ala Asp  
1 5

<210> 36  
<211> 7  
<212> PRT  
<213> Aplysia

<220>  
<221> MOD\_RES  
<222> (6)  
<223> Lys can be Lys or Gln

<220>  
<221> MOD\_RES  
<222> (7)  
<223> Ile can be Ile or Leu

<400> 36  
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1 5

<210> 37  
 <211> 15  
 <212> PRT  
 <213> Aplysia

<400> 37  
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<210> 38  
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 <212> PRT  
 <213> Aplysia

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 <213> Aplysia

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 <213> Aplysia

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 agcagcggca gcgttcttca cgtgctgcag tgtgccggct tcttcgaggt gtgctacgag 180  
 gagaggatca ccaccagcc agccacgact gtcgctgcag cagaggatca atgcaaaaag 240  
 ttcatcgcaa ccacaaaatt ggaggagact gttgatggaa ggatcgtcag catcgagctt 300  
 gtccagagac tgaagaaaca atccggatac ggtccaagtg gcggttctgg ttatggcaac 360  
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 agaggaggat acaaccctaa ag 442

<210> 41  
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 <212> PRT  
 <213> Aplysia

<400> 41  
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Val Leu Lys Ala Phe Gly Lys Pro Gly Tyr Gly Tyr Lys Gln Pro Ser  
                   20                                  25                                  30

Cys Lys Glu Gly Lys Asp Tyr Val Ser Ser Gly Ser Val Leu His Val  
                   35                                  40                                  45

Leu Gln Cys Ala Gly Phe Phe Glu Val Cys Tyr Glu Glu Arg Ile Thr  
                   50                                  55                                  60

Thr Gln Pro Ala Thr Thr Val Ala Ala Ala Glu Val Gln Cys Lys Lys  
                   65                                  70                                  75                                  80

Phe Ile Ala Thr His Lys Leu Glu Glu Thr Val Asp Gly Arg Ile Val  
                                   85                                  90                                  95

Ser Ile Glu Leu Val Gln Arg Leu Lys Lys Gln Ser Gly Tyr Gly Pro  
                   100                                  105                                  110

Ser Gly Gly Ser Gly Tyr Gly Asn Gly His Gly Gln Arg Pro Gly Tyr  
                   115                                  120                                  125

Gly Tyr Gly Ser Gly Ser Gly Ser Gly Tyr Ala Pro Arg Gly Gly Tyr  
                   130                                  135                                  140

Asn Pro Lys  
 145

<210> 42  
 <211> 462  
 <212> DNA  
 <213> Aplysia

<400> 42  
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 gttcaacgtg ganaagaaat tcgaagggtc cagaatcgtg agtttcaagc tcatccgcct 120  
 gttcaacagg tncaagaagt gcaagaaagn ccagtattcc gtgtctggcg atgatgagga 180  
 cncattogtt gtcagtgggt gttctggcgt gttccaggtn tgctacgaag aacaaacggc 240  
 gcccgctaca accnccacag aagcccgaa gccagagcca agaagaccca agaggaaaaa 300  
 tttcccaatc aaatttngta aacactgatg ggtaaantg acgaccagtg cgtctgcgaa 360  
 agaatcatgt tatggttcat gatgtcatgc tcttaatat ggttgtaacg tttaacgcga 420  
 tacagacatt aaaactcatt gttcaaaaaa aaaaaaaaaa aa 462

<210> 43  
 <211> 155  
 <212> PRT  
 <213> Aplysia

<220>  
 <221> MOD\_RES  
 <222> (1)..(155)  
 <223> Xaa = unknown amino acid or STOP-codon

<400> 43  
 Tyr Arg Pro Arg His His Xaa Xaa Thr Ser Arg Thr Asn Leu Arg Glu  
           1                                  5                                  10                                  15

Ala Val Arg Xaa Val Gln Arg Gly Xaa Glu Ile Arg Arg Phe Gln Asn  
                   20                                  25                                  30

Arg Glu Phe Gln Ala His Pro Pro Val Gln Gln Xaa Gln Glu Val Gln  
           35                                  40                                  45  
 Glu Xaa Pro Val Phe Arg Val Trp Arg Xaa Xaa Gly Xaa Ile Arg Cys  
           50                                  55                                  60  
 Gln Trp Leu Phe Trp Arg Val Pro Gly Xaa Leu Arg Arg Thr Asn Gly  
           65                                  70                                  75                                  80  
 Ala Arg Tyr Asn Xaa His Arg Ser Pro Glu Ala Arg Ala Lys Lys Thr  
                                   85                                  90                                  95  
 Gln Glu Glu Lys Phe Pro Asn Gln Ile Xaa Xaa Thr Leu Met Gly Xaa  
                                   100                                  105                                  110  
 Xaa Asp Asp Gln Cys Val Cys Glu Arg Ile Met Leu Trp Phe Met Met  
           115                                  120                                  125  
 Ser Cys Ser Xaa Xaa Tyr Arg Leu Xaa Arg Leu Thr Arg Tyr Arg His  
           130                                  135                                  140  
 Xaa Asn Ser Leu Phe Lys Lys Lys Lys Lys Lys  
   145                                  150                                  155

&lt;210&gt; 44

&lt;211&gt; 153

&lt;212&gt; PRT

&lt;213&gt; Aplysia

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (1)..(153)

&lt;223&gt; Xaa = unknown amino acid or STOP-codon

&lt;400&gt; 44

Thr Ala Pro Ala Thr Thr Xaa Ala Pro Ala Glu Pro Thr Cys Glu Lys  
   1                                  5                                  10                                  15  
 Leu Ser Xaa Trp Phe Asn Val Xaa Lys Lys Phe Glu Gly Ser Arg Ile  
           20                                  25                                  30  
 Val Ser Phe Lys Leu Ile Arg Leu Phe Asn Arg Xaa Lys Lys Cys Lys  
           35                                  40                                  45  
 Lys Xaa Gln Tyr Ser Val Ser Gly Asp Asp Glu Asp Xaa Phe Val Val  
           50                                  55                                  60  
 Ser Gly Cys Ser Gly Val Phe Gln Xaa Cys Tyr Glu Glu Gln Thr Ala  
           65                                  70                                  75                                  80  
 Pro Ala Thr Thr Xaa Thr Glu Ala Pro Lys Pro Glu Pro Arg Arg Pro  
                                   85                                  90                                  95  
 Lys Arg Lys Asn Phe Pro Ile Lys Phe Xaa Lys His Xaa Trp Val Asn  
           100                                  105                                  110  
 Xaa Thr Thr Ser Ala Ser Ala Lys Glu Ser Cys Tyr Gly Ser Xaa Cys  
           115                                  120                                  125

His Ala Leu Asn Ile Gly Cys Asn Val Xaa Arg Asp Thr Asp Ile Lys  
 130 135 140

Thr His Cys Ser Lys Lys Lys Lys Lys  
 145 150

<210> 45  
 <211> 153  
 <212> PRT  
 <213> Aplysia

<220>  
 <221> MOD\_RES  
 <222> (1)..(153)  
 <223> Xaa = unknown amino acid or STOP-codon

<400> 45  
 Pro Pro Pro Pro Pro Xaa Xaa His Gln Gln Asn Gln Pro Ala Arg Ser  
 1 5 10 15

Cys Pro Xaa Gly Ser Thr Trp Xaa Arg Asn Ser Lys Val Pro Glu Ser  
 20 25 30

Xaa Val Ser Ser Ser Ser Ala Cys Ser Thr Gly Xaa Arg Ser Ala Arg  
 35 40 45

Lys Xaa Ser Ile Pro Cys Leu Ala Met Met Arg Xaa His Ser Leu Ser  
 50 55 60

Val Val Val Leu Ala Cys Ser Arg Xaa Ala Thr Lys Asn Lys Arg Arg  
 65 70 75 80

Pro Leu Gln Xaa Pro Gln Lys Pro Arg Ser Gln Ser Gln Glu Asp Pro  
 85 90 95

Arg Gly Lys Ile Ser Gln Ser Asn Xaa Val Asn Thr Asp Gly Leu Xaa  
 100 105 110

Xaa Arg Pro Val Arg Leu Arg Lys Asn His Val Met Val His Asp Val  
 115 120 125

Met Leu Leu Ile Xaa Val Val Thr Phe Asn Ala Ile Gln Thr Leu Lys  
 130 135 140

Leu Ile Val Gln Lys Lys Lys Lys Lys  
 145 150

<210> 46  
 <211> 9  
 <212> PRT  
 <213> Aplysia

<220>  
 <221> MOD\_RES  
 <222> (3)  
 <223> Ile can be Ile or Val

&lt;400&gt; 46

Asp Gly Ile Cys Arg Asn Arg Arg Gln  
1 5

&lt;210&gt; 47

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Aplysia

&lt;400&gt; 47

Asp Ser Gly Leu Asp Ile Ala Val Phe Glu Tyr Ser Asp Arg  
1 5 10

&lt;210&gt; 48

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Aplysia

&lt;400&gt; 48

Val Phe Glu Tyr Ser Asp Arg  
1 5

&lt;210&gt; 49

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Aplysia

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (3)

&lt;223&gt; Xaa = any amino acid, in particular Thr

&lt;400&gt; 49

Leu Phe Xaa Tyr Gln Leu Pro Asn Thr Pro Asp Val Asn Leu Glu Ile  
1 5 10 15

&lt;210&gt; 50

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Aplysia

&lt;400&gt; 50

Val Ile Ser Glu Leu Gly Leu Thr Pro Lys  
1 5 10

&lt;210&gt; 51

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Aplysia

<220>  
<221> MOD\_RES  
<222> (5)  
<223> Xaa = any amino acid, in particular Met

<400> 51  
Val Ile Leu Ala Xaa Pro Val Tyr Ala Leu Asn  
1 5 10

<210> 52  
<211> 8  
<212> PRT  
<213> Aplysia

<400> 52  
Val Phe Met Thr Phe Asp Gln Pro  
1 5

<210> 53  
<211> 10  
<212> PRT  
<213> Aplysia

<220>  
<221> MOD\_RES  
<222> (6)  
<223> Phe can be Phe or Ser

<400> 53  
Ser Asp Ala Leu Phe Phe Gln Met Tyr Asp  
1 5 10

<210> 54  
<211> 18  
<212> PRT  
<213> Aplysia

<400> 54  
Ser Glu Ala Ser Gly Asp Tyr Ile Leu Ile Ala Ser Tyr Ala Asp Gly  
1 5 10 15

Leu Lys

<210> 55  
<211> 21  
<212> PRT  
<213> Aplysia

<220>  
<221> MOD\_RES  
<222> (12)  
<223> Gln can be Gln or Gly

&lt;400&gt; 55

Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gln Tyr Asn Gln Val  
1 5 10 15

Thr Glu Pro Leu Lys  
20