Cloning and functional expression of rat kidney dipeptidyl peptidase II

Kayoko M. FUKASAWA*[1], Katsuhiko FUKASAWA*, Koichi HIGAKI†, Naoki SHIINA†, Michiaki OHNO†, Shigeki ITO†, Junichi OTOGOTO† and Norio OTA†

*Department of Oral Biochemistry, Matsumoto Dental University, Shiojiri, Nagano 399-0781, Japan, and †Department of Periodontology, Matsumoto Dental University, Shiojiri, Nagano 399-0781, Japan

Dipeptidyl peptidase II (DPP II; EC 3.4.14.2) from rat kidney was purified to a specific activity of 65.4 μmol/min per mg of protein for Lys-Ala-β-naphthylamide. The N-terminal and partial amino acid sequences of the enzyme were determined. The peptide sequences were used to identify expressed sequence tag (EST) clones. By using the cDNA fragment of one of the EST clones as a probe, we isolated a cDNA clone with 1710 bp encoding DPP II from a rat kidney cDNA library. The cDNA of rat DPP II contained an open reading frame of 1500 bp, coding for a protein of 500 amino acids. The first 10 residues of the purified enzyme matched the deduced protein sequence starting with residue 37, suggesting the presence of a signal peptide. The mature enzyme (464 residues) had a calculated molecular mass of 51400 Da, which was lower than the value (about 60000 Da) determined by SDS/PAGE; and the deduced amino acid sequence showed six potential N-glycosylation sites. The deduced amino acid sequence of rat DPP II shared high similarity with quiescent-cell proline dipeptidase (78% identity) and prolyl carboxypeptidase (38% identity) and bore the putative catalytic triad (Ser, Asp, His) conserved in serine peptidase families. We transiently transfected COS-7 cells with pcDNA3.1 containing the cloned cDNA and obtained the overexpression of an immunoreactive protein (of about 60000 Da). The transfected cells showed Lys-Ala-methylcoumarinamide-hydrolysing activity that was 50 times higher than the control cells.

Key words: lysosomal peptidase, pH profile, serine enzyme, signal peptide.

INTRODUCTION

Mammalian dipeptidyl peptidases (DPPs) sequentially release dipeptides from polypeptides, except those with a proline or hydroxyproline at the third position (P1′) from their N-terminus. Among those enzymes, DPP II and DPP IV willingly cause the release of the dipeptide containing a penultimate proline or alanine residue. They are different with respect to their pH profiles based on their locations in the cell [1]. DPP II, first identified in bovine anterior pituitary extracts by McDonald et al. [2,3], is a serine-class enzyme and exists in the lysosomal fraction obtained by sucrose-density centrifugation. Histochemical [4–7] and immunohistochemical [8] studies on DPP II also showed it to be found exclusively within lysosomes. Its activity is affected by cations such as Tris and puromycin [2,3,9] and by anions [10].

The possible function of DPP II was proposed to be tripeptidyl peptidase I (EC 3.4.14.9)-coupled degradation of collagen in reproductive organs [11]. On the other hand, rat brain DPP II also hydrolysed the Pro–Pro bond of Xaa-Pro-Pro and released N-terminal Xaa-Pro dipeptides from casomorphin and substance P. So, this enzyme is also involved in the degradation of proline-containing neuropeptides [12]. However, the physiological function of DPP II has been obscure for a long time. In 1992, based on the results of a cytochemical study, Smid et al. [13] proposed that DPP II may have a role in programmed cell death in rat incisor tooth ameloblasts. There are several reports on mammalian enzymes having DPP activities [14–19], but they have not been classified by the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology.

Huang et al. [20] determined the amino acid sequence of the first 41 residues of the enzyme from pig seminal plasma and concluded that DPP II is related to granzymes. On the basis of the N-terminal amino acid sequence from pig seminal plasma and a number of biochemical similarities between both enzymes, Rawlings and Barrett [21] showed that DPP II is homologous with lysosomal Pro-X-carboxypeptidase [22], and thus belongs to peptidase family S 28 of the clan SC [23]. For verification of the above prediction, we cloned the enzyme from rat kidney. During the course of our experiments, Underwood et al. [24] isolated and cloned an enzyme (quiescent-cell proline dipeptidase, QPP) related to the cell death of quiescent lymphocytes, and showed it to belong to family S 28 of the clan SC. However, the pH profile of QPP covered a broad pH range, from acidic to neutral pH.

Here, we describe for the first time the full-length cDNA of DPP II cloned from rat kidney and expression of the enzyme in COS-7 cells. Moreover, we discuss the similarity in pH profile between rat DPP II and QPP.

EXPERIMENTAL PROCEDURES

Materials

Ala-β-naphthylamide (-NA), Pro-NA, Lys-Ala-NA, bestatin and Fast Garnet GBC were obtained from Sigma (St. Louis, MO, U.S.A.); Arg-methylcoumarinamide (-MCA), Gly-Pro-MCA and Lys-Ala-MCA were from Peptide Institute (Osaka, Japan); Gly-Pro-NA and benzyloxycarbonyl (Cbz)-Gly-Pro-NA were from Bachem Biosocience (Philadelphia, PA, U.S.A.); and Gly-NA and Lys-NA were from Koch–Light (Colnbrook, Bucks., U.K.). Polybuffer exchanger 94 was from Amersham Pharmacia Biotech (Little Chalfont, Bucks., U.K.). Restriction and modifying enzymes were purchased from New England Biolabs (Beverly, MA, U.S.A.) or Toyobo Co. (Osaka, Japan). Medium,

Abbreviations used: NA, β-naphthylamide; MCA, methylcoumarinamide; DPP, dipeptidyl peptidase; QPP, quiescent-cell proline dipeptidase; PCP, prolyl carboxypeptidase; Cbz, benzyloxycarbonyl; EST, expressed sequence tag.

[1] To whom correspondence should be addressed (e-mail kmf@po.mdu.ac.jp).

The nucleotide sequence data in this paper will appear in the DDBJ/EMBL/GenBank nucleotide sequence databases under the accession number AB038232.

buffers and several reagents for cell culture were purchased from Life Technologies (Gaithersburg, MD, U.S.A.).

Protein and enzyme assays, purification of the enzyme from rat kidney

Protein content was determined according to Bradford with BSA as the standard [25]. Enzyme assays and purification procedure were performed as described previously [9,26,27] except that polybuffer exchanger 94 (the isoelectric point of DPP II, pH 4.76) was added to the purification steps (see Table 1 below). The concanavalin A–Sepharose column fraction was dialysed against 25 mM imidazole/HCl buffer, pH 7.4 (start buffer), and applied on to the polybuffer exchanger 94 column (0.9 cm × 16 cm). After the column had been washed with 25.5 ml of the start buffer, the elution was carried out with 117.3 ml of the gradient buffer (polybuffer 74/HCl, pH 4.0).

Antibody production

The purified DPP II (200 μg) was emulsified with an equal volume of complete Freund's adjuvant and injected subcutanously into a 2 kg male rabbit. After 10 days, 100 μg of the antigen was injected three times at 2 week intervals in the same manner. After the last injection (10 days), the animal was bled from the carotid artery. The selective reactivity between the enzyme and the antiserum was verified by Western-blot analysis. The antiserum was stored at 4 °C.

SDS/PAGE and immunoblotting

Electrophoresis of proteins was performed under denaturing and reducing conditions on either 5.0 % (w/v) polyacrylamide gels for determination of molecular mass or on 10 % (w/v) gels for other purposes by the method of Laemmli [28]. The proteins were stained with Coomassie Brilliant Blue R-250 and blotted on to nitrocellulose membranes (Bio-Rad, Hercules, CA, U.S.A.) in a Bio-Rad apparatus (1.5 h, 40 V). The membranes were blocked at room temperature in Tris-buffered saline [TBS, 50 mM Tris/HCl buffer (pH 8.0)/0.15 M NaCl] containing 3.0 % (w/v) BSA and 0.05 % Tween-20. Rabbit anti-rat DPP II antiserum (described above) for detection of the purified enzyme or the protein expressed in COS-7 cells was diluted 1:3000 with the same buffer, and the membranes were incubated in it for 1 h at room temperature. The membranes were then washed twice with TBS containing 0.05 % Tween-20 and incubated for 1 h at room temperature with alkaline phosphatase-conjugated goat anti-rabbit IgG (Bio-Rad), diluted 1:2000 with blocking solution. After the membranes had been washed twice with TBS containing 0.05 % Tween-20, the bands were visualized by use of an alkaline phosphatase colour development kit (Bio-Rad). For determination of molecular mass, the following marker proteins were used: myosin (200000 Da), *Escherichia coli* β-galactosidase (116250 Da), rabbit muscle phosphorylase *b* (97400 Da), BSA (66200 Da), hen egg-white ovalbumin (45000 Da) and bovine carbonic anhydrase (31000 Da). SDS/PAGE for molecular-mass determination was done five times for the purified enzyme, and the molecular-mass value was calculated by a logarithmic regression program (mean ± S.D.).

Protein sequencing

To obtain the N-terminal amino acid sequence of the enzyme, we resolved the purified protein by SDS/PAGE on a 10 % gel (described in the previous section), blotted it on to a PVDF membrane (Bio-Rad), visualized it by Coomassie Brilliant Blue R-250 staining and excised the band. For determination of the partial amino acid sequence, the purified enzyme (200 μg) was digested with 2 % (w/w) trypsin in 100 mM ammonium bicarbonate buffer, pH 8.0, for 16 h at 37 °C. The digested material was fractionated on a cation-exchange HPLC column (Pepkat 300; 5 μm, 4.0 mm × 125 mm) and also on a reversed-phase HPLC column (Shim-pack CLC-ODS; 6.0 mm × 150 mm). The preparation conditions were performed as described previously [27]. The protein and the purified peptides were sequenced by Edman degradation using an Applied Biosystems Procise Sequencer (PROCISE-cLC).

Enzyme kinetics

For curve fitting by non-linear regression and calculation of V_{max} and K_m, the program KaleidoGraph (Hulinks, Tokyo, Japan) was used. The amounts of substrates used in these kinetic studies ranged from 0.1 to 1.0 mM for Lys-Ala-NA, from 0.05 to 0.4 mM for Gly-Pro-NA, from 0.025 to 0.4 mM for Lys-Ala-MCA and from 0.00625 to 0.1 mM for Gly-Pro-MCA. Concentrations of enzyme tested were 0.0267 μg/ml for Lys-Ala-NA, 0.2177 μg/ml for Gly-Pro-NA, 0.0964 μg/ml for Lys-Ala-MCA and 0.0653 μg/ml for Gly-Pro-MCA. The k_{cat} values were calculated based on a molecular mass of 120000 Da determined by Sephadex G-150 superfine column chromatography according to the methods described previously [9].

pH profile

The following buffers substituted for the standard assay buffer for determination of the purified enzyme's pH activity profile: 170 mM cacodylate buffer (pH range 4.0–7.0, increments of 0.5) and 50 mM Hepes (pH range 7.0–8.5, increments of 0.5). Results are expressed as a percentage of the maximum activity.

Datebase searches

The sequences of the three tryptic peptides of the enzyme were compared with those of the predicted translation products from the expressed sequence tag (EST) databases by use of the BLAST program at DDBJ. The search detected a rat clone encoding a sequence containing the peptide 3 sequence (accession number AI716264).

Cloning and sequencing of rat DPP II cDNA

For isolation of the rat kidney cDNA, mRNA from female Wistar rat kidney was obtained by use of a mRNA isolation kit (Stratagene, La Jolla, CA, U.S.A.). The cDNA was constructed and ligated into λ ZAP II vector digested with *Eco*RI/*Xho*I by use of a Uni-Zap synthesis kit from Stratagene.

Double-stranded cDNA was amplified by PCR using the two primers based on the nucleotide sequence of the rat EST clone (accession number AI716264). The sequence of the 5′-oligomer was 5′-GCAACATCATTTTCTCCAACGG-3′, and that of the 3′-oligomer was 5′-TGTCACACGCGGCTCACATAG-3′. The reaction was carried out on a Quick Thermo Personal cycler (Nippon Genetics, Tokyo, Japan). The following amplification protocol was employed: 30 cycles of denaturing at 94 °C (1 min), primer annealing at 58.5 °C (1 min) and primer extension at 72 °C (1 min). Initial amplification of the cDNA revealed the presence of a 300 bp amplified product. This PCR product was sequenced and used as a probe to screen the rat kidney cDNA library. pBluescript phagemids containing DPP II cDNA were excised from the Uni-Zap clones by use of ExAssist helper phage for subcloning the cDNA.

Table 1 Purification of DPP II from rat kidney (244 g, wet weight)

ND, not determined.

Step	Total activity (units)	Protein (mg)	Specific activity (units/mg of protein)	Recovery (%)	Purification (-fold)
$(NH_4)_2SO_4$ fraction (40–70%)	440	15172	0.029	100	1
DEAE-TOYO	365	2807	0.13	82.9	4.48
Concanavalin A–Sepharose	117	20	5.85	26.5	202
Polybuffer exchanger 94	75.7	ND	ND	17.2	ND
Phenyl-Sepharose	70.3	1.3	54.0	15.9	1862
Sephadex G-150 Superfine	65.4	1.0	65.4	14.8	2255

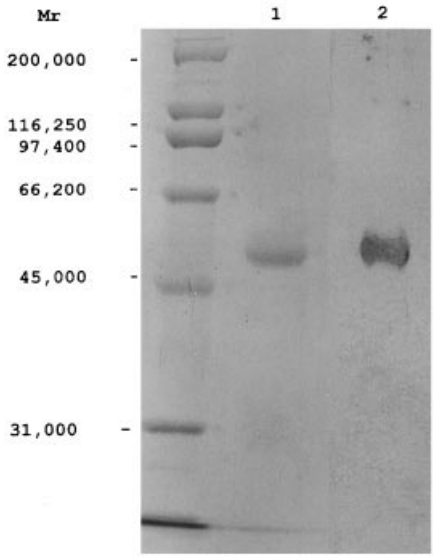

Figure 1 SDS/PAGE of purified rat kidney DPP II

A 5 μg amount of enzyme purified from rat kidney (lane 1) was loaded on to a standard 10% gel and stained with Coomassie Brilliant Blue following electrophoresis. Western-blot analysis of the purified enzyme was also done (lane 2, 0.5 μg).

The nucleotide sequence was determined by the dideoxynucleotide chain-termination method [29] using the single-stranded pBluescript SK(−) phagemid excised from the Uni-Zap DPP II clone by use of VCSM13 helper phage. Appropriate nucleotide oligomers were synthesized by Sawaday Co. (Tokyo, Japan) for sequencing primers.

Functional expression of DPP II in COS-7 cells

A DNA fragment containing the entire coding region of the rat DPP II was inserted at an *Eco*RI/*Xho*I site into pcDNA3.1/HisA (Invitrogen, SanDiego, CA, U.S.A.). The constructed plasmid, named pcDrdpII, was purified by using a Qiagen plasmid-purification kit and used for transfection of COS-7 cells (obtained from Riken Cell Bank, Tsukuba, Japan) with LIPOFECTAMINE™ (Life Technologies, Gaithersburg, MD, U.S.A.). COS-7 cells (2×10^5 cells/35 mm dish) grown in Dulbecco's modified Eagle medium (DMEM) containing 10% fetal calf serum were washed twice with serum-free DMEM, and transfection medium containing 1.5 μg of pcDrdp II and 12.5 μl of LIPOFECTAMINE™ in 1 ml of serum-free DMEM was then added. A negative control was performed under the same conditions with 1.5 μg of pcDNA3.1/HisA vector (control cells). After incubation for 5 h, 1 ml of DMEM containing 20% fetal calf serum was added, and the cells were incubated for a further 48 h. The cells were collected, washed with PBS (1.06 mM KH_2PO_4/2.97 mM Na_2HPO_4/0.9% NaCl, pH 7.4), and resuspended in 1 ml of PBS. The suspension was then sonicated with three 10 s bursts on ice and subsequently subjected to three cycles of freezing (in liquid nitrogen) and thawing (at 37 °C). The crude lysate was assayed for protein contents and Lys-Ala-MCA cleaving activity. For the latter, 0.02 μmol of each of *o*-phenanthroline and bestatin were preincubated at 37 °C for 10 min with the cell lysate. The reaction was initiated by the addition of 0.02 μmol of Lys-Ala-MCA. The recombinant protein was partially purified from the

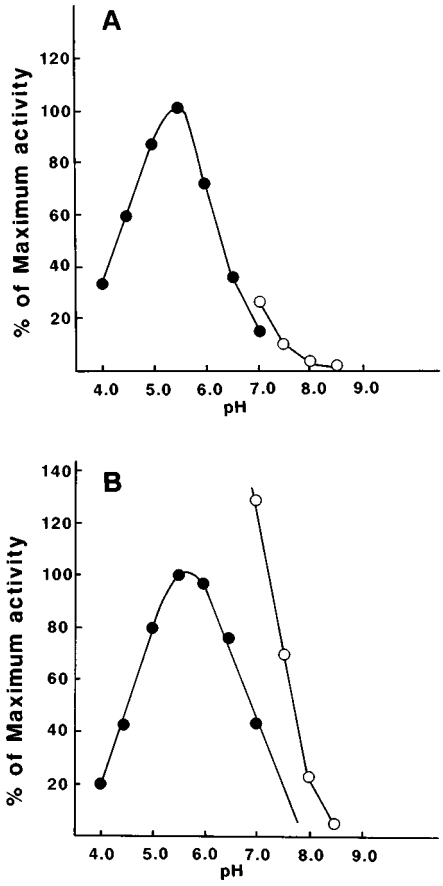

Figure 2 pH profile of purified rat kidney DPP II

(**A**) Lys-Ala-NA-cleaving activity. (**B**) Gly-Pro-NA-cleaving activity. ●, 170 mM cacodylate buffer; ○, 50 mM Hepes buffer. Results are mean values of three determinations.

lysate according to the same purification procedures used for the rat kidney DPP II.

RESULTS

Purification and properties of the purified enzyme

The purification was 2255-fold, and the yield was 14.8% with respect to the total activity of the $(NH_4)_2SO_4$ fraction (Table 1). SDS/PAGE and Western-blot analysis of the purified enzyme are shown in Figure 1. The DPP II activity during purification (steps 1–3 as listed in Table 1) was assayed in the presence of 0.02 μmol of bestatin to inhibit the aminopeptidase activity. The rat kidney enzyme (1 mg/ml in 10 mM sodium phosphate buffer, pH 7.6, containing 0.15 M NaCl and 2 mM mercaptoethanol) was stable at −20 °C for 3 months without loss of activity, but after 1 year the activity had dropped to 70% of the original activity.

Mono-amino-acid-NA and Cbz-Gly-Pro-NA were not hydrolysed at all, even if 100 times more purified enzyme and reaction times longer than those used for the assay with Lys-Ala-NA as the substrate were employed. K_m values for Lys-Ala-MCA were the same as those of pig seminal plasma and human kidney enzymes [20,30]. Di-isopropyl fluorophosphate (1 mM) and 50 mM Tris caused 88 and 65% inhibition, respectively, of the control enzyme activity. On the other hand, 1 mM *o*-phenanthroline, 1 mM E-64 [(L-3-*trans*-carboxyoxiran-2-carbonyl)-L-

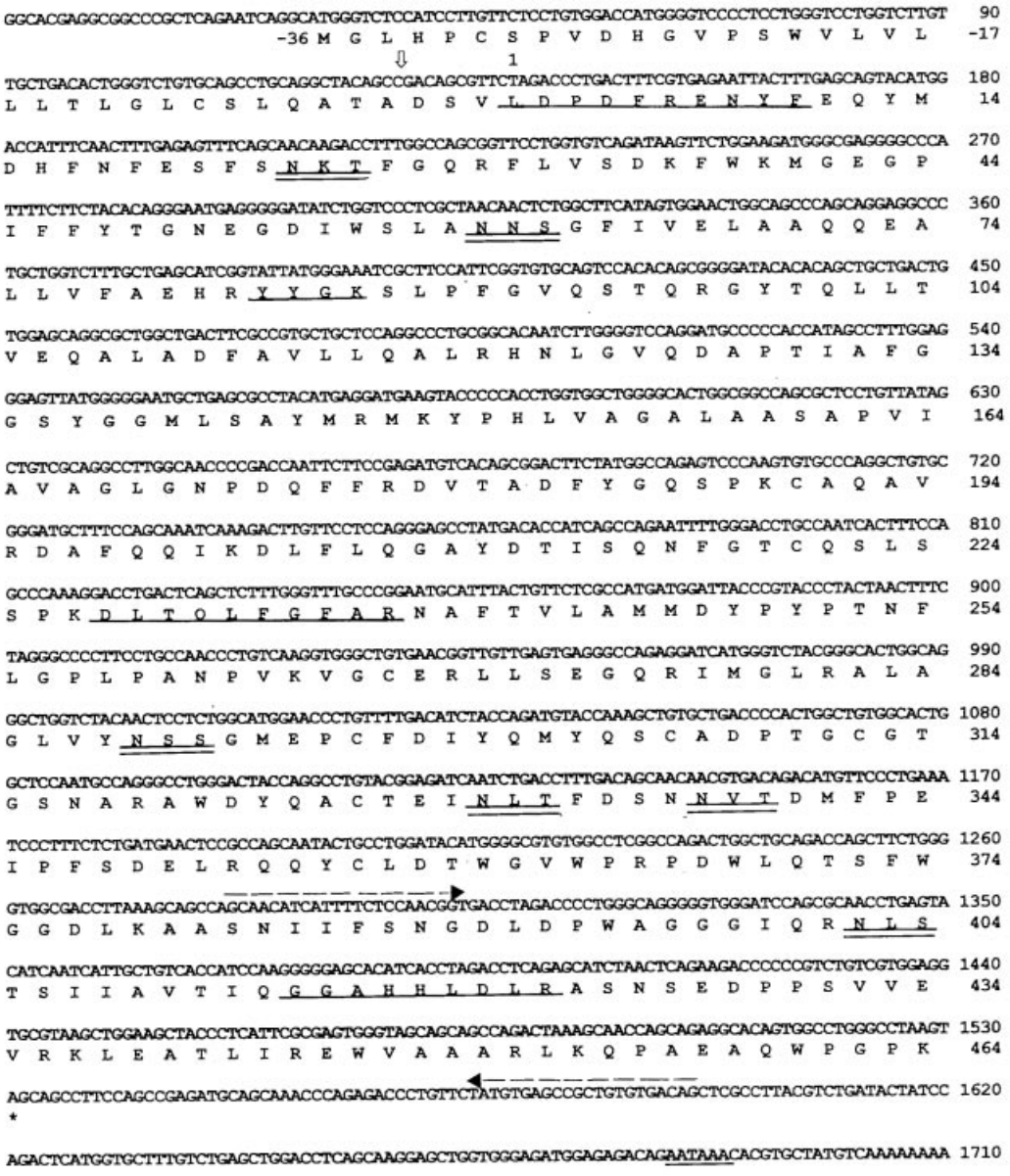

Figure 3 Nucleotide and deduced amino acid sequences of rat kidney DPP II

Nucleotides and amino acid residues are numbered on the right. The amino acid sequence is numbered with respect to the N-terminal Leu of the mature protein. The asterisk indicates the termination codon. The potential signal peptide cleavage site is shown by the open arrow. The sequences of the three tryptic peptides obtained by automated Edman degradation are underlined. Six potential N-linked glycosylation sites are double-underlined. The positions of the two PCR primers are shown with two dashed arrows above the nucleotide residues. The polyadenylation sequence near the 3′ end is also underlined.

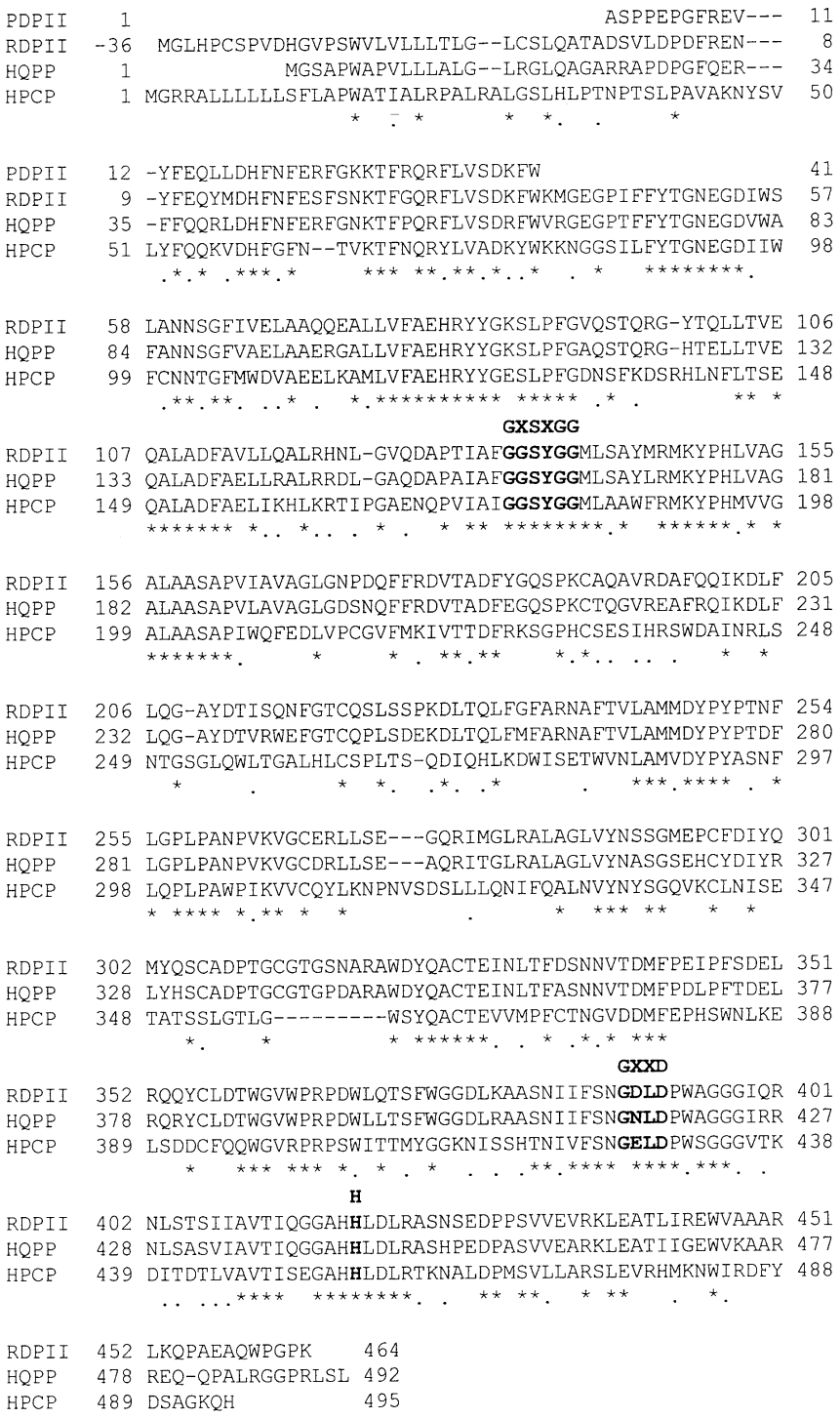

Figure 4 Alignment of the deduced amino acid sequence of rat DPP II with those sequences of porcine DPP II, human QPP and human PCP

Identical residues are shown with asterisks. Dashes are gaps introduced to maximize alignment. Consensus sequences (GXSXGG and GXXD) and potential active residue (H) of serine proteases are indicated above these amino acid residues. PDPII, porcine DPP II; RDPII, rat DPP II; HQPP, human QPP; HPCP, human PCP.

Leu-agmatin] or 0.1 mM diprotin A (DPP IV inhibitor) did not inhibit it significantly, as was reported previously [9].

The optimum pH of rat kidney DPP II in 170 mM cacodylate buffer with Lys-Ala-NA used as the substrate was pH 5.5, the same as found when universal buffer (0.0286 M citric acid/KH_2PO_4/H_3BO_3/barbital buffer, pH 3.0–10.0) was used, as described previously [9]. The activity of the enzyme at pH 7.0 in 50 mM Hepes buffer was only 25.6% (31.9 nmol/min per mg of protein) of that observed at pH 5.5 in cacodylate buffer (124.4 nmol/min per mg of protein, Figure 2A). However, the activity with Gly-Pro-NA as the substrate became 129% (12.75 versus 9.88 nmol/min per mg of protein, Figure 2B).

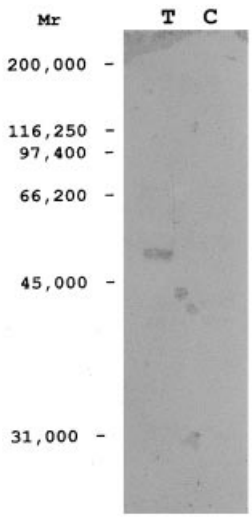

Figure 5 Western-blot analysis of the lysates from control and DPP II cDNA-transfected COS-7 cells

C, control lysate; T, DPP II cDNA-transfected lysate (20 μl each).

Isolation and sequencing of cDNA encoding rat DPP II

Three peptides from the trypsin digest of the purified enzyme were successfully isolated and sequenced. The amino acid sequences of the three peptides and the retention times (in min) of each peptide on each column (Pepkat, Shim-pack, respectively) were as follows: peptide 1, YYGK (7.3, 13.3); peptide 2, DLTQLFGFAR (8.1, 15.0); and peptide 3, GGAHHLDLR (9.5, 16.6). The peptide sequences were used as probes to search for translation products in the rat EST database. Several EST clones were identified, and the largest clone (AI716264) contained 435 bases of sequence, including a polyadenylation signal and poly(A)$^+$ tail, and encoded peptide 3, GGAHHLDLR. A rat kidney cDNA was amplified by PCR using two primers based on the nucleotide sequence of the EST clone (AI716264), for screening the rat kidney cDNA library. Four positive clones were isolated from the library. Three of these clones had the same molecular mass as the insert cDNA, and the 5′ regions of these insert cDNAs also had the same nucleotide sequence, indicating that the three clones were identical. The cDNA was 1710 bp long with an open reading frame of 1500 bp encoding a protein of 500 amino acid residues (Figure 3). A potential initiation codon (ATG) was found beginning at nucleotide 30, and the nucleotide sequence surrounding this codon (GGCATGG) obeyed Kozak's rule [31]. In the 3′ non-coding region, a polyadenylation signal and poly(A)$^+$ tail were found, so the cDNA contained the complete open reading frame.

The N-terminal 10 amino acids derived from protein-sequencing analysis of the purified enzyme matched perfectly residues 37–46 of the deduced sequence, and the peptide sequences analysed also matched the three portions of the molecule, indicating that the cDNA encoded the entire mature protein (Figure 3). The mature protein had 464 amino acid residues with a theoretical molecular mass of 51400 Da. On the other hand the molecular mass of DPP II purified from rat kidney was estimated to be 60000$\pm$2800 Da by SDS/PAGE. The predicted primary structure of the protein contained six potential N-glycosylation sites distributed throughout the molecule (Figure 3), which might account for the difference between the theoretical molecular mass and that estimated by SDS/PAGE, as in the case of prolyl carboxypeptidase (PCP) [22]. The mature protein is thought to contain carbohydrate.

Table 2 Kinetic parameters of the purified enzyme

In the calculation of k_{cat}, the apparent molecular mass of the purified enzyme was taken as 120000 Da.

Substrate	Concentration (mM)	K_m (mM)	k_{cat} (s^{-1})	k_{cat}/K_m ($mM^{-1} \cdot s^{-1}$)
Lys-Ala-NA	0.1–1	0.763$\pm$0.068	656	859
Gly-Pro-NA	0.05–0.4	0.192$\pm$0.05	46.7	243
Lys-Ala-MCA	0.025–0.4	0.26$\pm$0.02	54.8	211
Gly-Pro-MCA	0.00625–0.1	0.072$\pm$0.002	73.6	1022

The 36-amino acid peptide upstream from the N-terminal Leu of the mature protein most probably contains a signal peptide and a propeptide. An Internet-based analysis employing the signal-prediction server SignalP V1.1 (http://genome.cbs.dtu.dk/services/SignlP/index.html/) predicted this stretch to represent a typical N-terminal signal sequence: a positively charged N-terminal region (Met^{-36}–Trp^{-21}), a central hydrophobic region (Val^{-20}–Leu^{-11}) and a polar C-terminal region (Cys^{-10}–Ala^{-4}) [32,33]. The presence of Ala at the -4 and -6 positions is consistent with a signal-peptidase-cleavage site at Ala^{-4}–Asp^{-3} [34] and the remaining three residues are thought to comprise a propeptide (Asp^{-3}–Val^{-1}). However, experiments to determine whether DPP II is initially synthesized as an inactive proenzyme have not yet been performed.

A search of the National Biomedical Research Foundation-The Protein Information Resource (NBRF-PIR) protein sequence database with the primary structure of rat DPP II showed that it had highly significant similarity to human N-terminal proline-specific dipeptidase (QPP, 78 % identity [24]) and human lysosomal PCP (38 % identity). Furthermore, the deduced amino acid sequence of DPP II contained the consensus sequences GXSXGG, for the active-site serine residue, and GXXD, for the aspartic acid residue of serine-type proteases, such as are found in prolyl oligopeptidases [23], PCP and QPP (Figure 4).

Functional expression of DPP II in COS-7 cells

To determine whether the cDNA encoded an active DPP II, we transfected COS-7 cells with the cDNA cloned into the pcDNA3.1/HisA expression vector. The protein content of the cell lysate was 674.5$\pm$88 μg/ml for the control cells ($n = 6$) and 723.7$\pm$107 μg/ml for the transfected cells ($n = 4$), and the corresponding Lys-Ala-MCA-cleaving activity was 211$\pm$24 and 9985.2$\pm$1400 pmol/min per ml. Thus transfected COS-7 cells showed 50 times higher Lys-Ala-MCA-hydrolysing activity than the control COS-7 cells. Figure 5 shows the existence of expressed DPP II in transfected-cell lysate. The activity with Gly-Pro-MCA as the substrate was about 120 times higher than that of the control cells (results not shown). The partial purified recombinant enzyme showed the same properties as the native enzyme with respect to gel filtration, immunoblotting and pH profile (results not shown). The K_m values for Lys-Ala-MCA and Gly-Pro-MCA were 0.26 and 0.07 mM, respectively (Table 2).

DISCUSSION

The molecular mass of rat DPP II was about 60000 Da by SDS/PAGE and 120000 Da by gel filtration (results not shown). These findings suggest that the rat DPP II is composed of two

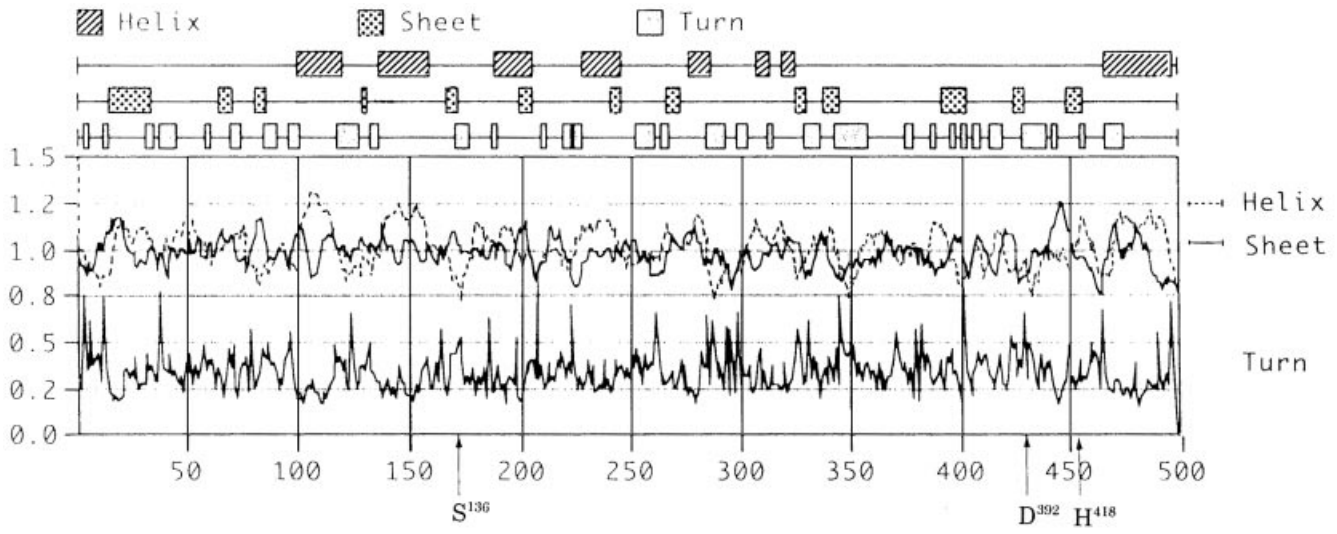

Figure 6 Schematic representation of secondary-structure predictions for rat DPP II

Calculations were made by using the Chou and Fasman algorithm with Macintosh sequence-analysis software. The positions of the potential active amino acid residues (S^{136}, D^{392} and H^{418}) are indicated by arrows.

identical subunits. The results were the same for the molecular masses of bovine pituitary and guinea pig testis enzymes [35,36]. The predicted primary structure of the protein contained six potential N-glycosylation sites (Figure 3), which might account for the difference between the theoretical molecular mass and that estimated by SDS/PAGE, as in the case of PCP [22]. The mature protein is thought to contain about 14% carbohydrate. From our study, we can conclude that DPP II belongs to the family S 28 of the clan SC, as was predicted previously by Rawlings and Barrett [21].

Recently, an enzyme (QPP) related to the cell death of quiescent lymphocytes was isolated and cloned [24]. It had the same substrate specificity as DPP II and IV [24,37]. QPP also shared the same properties of DPP II with respect to molecular mass, lysosomal localization and serine peptidase classification, and was assigned to family S 28 of clan SC [23]. Underwood et al. [24] showed that QPP and DPP II were different with respect to their pH profiles. The optimum pH of rat kidney DPP II in 170 mM cacodylate buffer with Lys-Ala-NA as the substrate was pH 5.5, the same as in universal buffer described previously [9]. The activity of the enzyme at pH 7.0 in 50 mM Hepes buffer was only 25.6% of that observed at pH 5.5 in cacodylate buffer (Figure 2A). However, the pH profile of purified DPP II using Gly-Pro-NA as the substrate, as shown in Figure 2(B), showed the same behaviour as that of QPP. This profile was dependent on the buffers used and on the nature of the substrates' P1 and P1′ sites, because the pH profiles tended to be similar with Lys-Ala-MCA as the substrate (cacodylate buffer, pH 5.5, 100% versus Hepes buffer, pH 7.0, 45%) and with Gly-Pro-MCA as the substrate (cacodylate buffer, pH 5.5, 100% versus Hepes buffer, pH 7.0, 113%).

The amino acid homology between rat kidney DPP II and QPP showed 78% identity over 500 residues (Figure 4). Moreover, the N-terminal amino acid sequence of human placental DPP II and human QPP were consistent with 32 out of 33 residues by a search of the NBRF-PIR protein sequence database (accession no. S77568). Therefore, it is conceivable that QPP is human DPP II.

The active site of serine proteases classified as clan SC has the Ser-Asp-His triad, and it shows an α/β hydrolase fold [23]. The protein secondary structure of DPP II predicted by the Chou and Fasman algorithm used by Macintosh Vector sequence analysis software is shown in Figure 6. Ser^{136} in the GXSXGG motif and His^{418} are in the α/β hydrolase fold, but Asp^{392} in the GXXD motif is not. Especially, active-site Ser^{136} exists between the fifth β-sheet and the third α-helix region from the N-terminus, as shown in Figure 6. Its position is consistent with the results from X-ray crystallographic analysis on proline aminopeptidase [38].

It is probable that DPP II causes apoptosis in quiescent lymphocytes [37]. Moreover, the activity of this enzyme significantly increased in the gingival crevicular fluid of periodontal patients (M. Ohno, N. Ota, K. Fukasawa and K. M. Fukasawa, unpublished work). However, it remains to be explained why DPP II in various human carcinoma cells was found in a 6–24-fold higher concentration than that in normal human fibroblasts [39]. Because many cytokines have N-terminal Xaa-Pro or Xaa-Ala sequences [40], identification of endogenous substrates in each cell type remains to be accomplished for DPP II, as reported for DPP I [41].

We dedicate this paper to Dr Minoru Harada and the late Dr George G. Glenner, who encouraged K.F. and K.M.F. in this interesting research field. We are grateful to Tomoko Takei for secretarial assistance.

REFERENCES

1 McDonald, J. K. and Barrett, A. J. (1986) Dipeptidyl peptidases I-IV. In Mammalian Proteases: a Glossary and Bibliography, vol. 2, Exopeptidases (McDonald, J. K. and Barrett, A. J., eds), pp. 111–144, Academic Press, London
2 McDonald, J. K., Reilly, T. J., Zeitman, B. B. and Ellis, S. (1968) Dipeptidyl arylamidase II of the pituitary: properties of lysylalanyl-β-naphthylamide hydrolysis: inhibition by cations, distribution in tissues, and subcellular localization. J. Biol. Chem. **243**, 2028–2037
3 McDonald, J. K. and Schwabe, C. (1980) Dipeptidyl peptidase II of bovine dental pulp: initial demonstration and characterization as a fibroblastic, lysosomal peptidase of the serine class active on collagen-related peptides. Biochim. Biophys. Acta **616**, 68–81

4 Sannes, P. L., McDonald, J. K. and Spicer, S. S. (1977) Dipeptidyl aminopeptidase II in rat peritoneal wash cells: cytochemical localization and biochemical characterization. Lab. Invest. **37**, 243–253
5 Gossrau, R. and Lojda, Z. (1980) Study on dipeptidylpetidase II (DPP II). Histochemistry **70**, 53–76
6 Gorenstein, C., Tran, V. T. and Snyder, S. H. (1981) Brain peptidase with a unique neuronal localization: the histochemical distribution of dipeptidyl-aminopeptidase II. J. Neurosci. **1**, 1096–1102
7 Kugler, P. (1982) Quantitative histochemistry of the lysosomal dipeptidyl aminopeptidase II in the proximal tubule of the rat kidney. Histochemistry **76**, 557–566
8 Ito, M., Yoshida, M., Karasawa, N., Fukasawa, K., Fukasawa, K. M., Harada, M. and Nagatsu, I. (1986) Immunohistochemical distribution of dipeptidyl-aminopeptidase II and tyrosine hydroxylase in the rat brain. Biogenic Amines **3**, 267–277
9 Fukasawa, K., Fukasawa, K. M., Hiraoka, B. Y. and Harada, M. (1983) Purification and properties of dipeptidyl peptidase II from rat kidney. Biochim. Biophys. Acta **745**, 6–11
10 Stevens, B. R., Fernandez, A., Sumners, C. and Hearing, L. (1988) Neonatal rat brain astroglial dipeptidyl peptidase II activity regulation by cations and anions. Neurosci. Lett. **89**, 319–322
11 McDonald, J. K., Hoisington, A. R. and Eisenhauer, D. A. (1985) Partial purification and chracterization of an ovarian tripeptidyl peptidase: a lysosomal exopeptidase that sequentially releases collagen-related (Gly-Pro-X) triplets. Biochem. Biophys. Res. Commun. **126**, 63–71
12 Mentlein, R. and Struckhoff, G. (1989) Purification of two dipeptidyl aminopeptidases II from rat brain and their action on proline-containing neuropeptides. J. Neurochem. **52**, 1284–1293
13 Smid, J. R., Monsour, P. A., Rousseau, E. M. and Young, W. G. (1992) Cytochemical localization of dipeptidyl peptidase II activity in rat incisor tooth ameloblasts. Anat. Rec. **233**, 493–503
14 Cherot, P., Fournie-Zaluski, M. C. and Laval, J. (1986) Purification and characterization of an enkephalin-degrading dipeptidyl-aminopeptidase from porcine brain. Biochemistry **25**, 8184–8191
15 Hui, K.-S. (1988) A novel dipeptidyl aminopeptidase in rat brain membranes: its isolation, purification, and characterization. J. Biol. Chem. **263**, 6613–6618
16 Wada, K., Yokotani, N., Hunter, C., Doi, K., Wenthold, R. J. and Shimasaki, S. (1992) Differential expression of two distinct forms of mRNA encoding member of a dipeptidyl aminopeptidase family. Proc. Natl. Acad. Sci. U.S.A. **89**, 197–201
17 Duke-Cohan, J. S., Morimoto, C., Rocker, J. A. and Schlossman, S. F. (1995) A novel form of dipeptidylpeptidase IV found in human serum: isolation, characterization, and comparison with T lymphocyte membrane dipeptidylpeptidase IV (CD 26). J. Biol. Chem. **270**, 14107–14114
18 Blanco, J., Nguyen, C., Callebaut, C., Jacotot, E., Krust, B., Mazaleyrat, J.-P. and Hovanessian, A. G. (1998) Dipeptidyl-peptidase IV-β-further characterization and comparison to dipeptidyl-peptidase IV activity of CD 26. Eur. J. Biochem. **256**, 369–378
19 Park, J. E., Lenter, M. C., Zimmermann, R. N., Garin-Chesa, P., Old, L. J. and Rettig, W. J. (1999) Fibroblast activation protein, a dual specificity serine protease expressed in reactive human tumor stromal fibroblasts. J. Biol. Chem. **274**, 36505–36512
20 Huang, K., Takagaki, M., Kani, K. and Ohkubo, I. (1996) Dipeptidyl peptidase II from porcine seminal plasma: purification, characterization, and its homology to granzymes, cytotoxic cell proteinases (CCP1–4). Biochim. Biophys. Acta **1290**, 149–156
21 Rawlings, N. D. and Barrett, A. J. (1996) Dipeptidyl-peptidase II is related to lysosomal Pro-X carboxypeptidase. Biochim. Biophys. Acta **1298**, 1–3
22 Tan, F., Morris, P. W., Skidgel, R. A. and Erdös, E. G. (1993) Sequencing and cloning of human prolylcarboxypeptidase (angiotensinase C): similarity to both serine carboxypeptidase and prolylendopeptidase families. J. Biol. Chem. **268**, 16631–16638
23 Rawlings, N. D. and Barrett, A. J. (1994) Serine peptidases. Methods Enzymol. **244**, 9–61
24 Underwood, R., Chiravuri, M., Lee, H., Schmitz, T., Kabcenell, A. K., Yardley, K. and Huber, B. T. (1999) Sequence, purification, and cloning of intracellular serine protease, quiescent cell proline dipeptidase. J. Biol. Chem. **274**, 34053–34058
25 Bradford, M. M. (1976) A rapid and sensitive method for the quantitation of microgram quantities of protein utilizing the principle of protein-dye binding. Anal. Biochem. **72**, 248–254
26 Nagatsu, T., Sakai, T., Kojima, K., Araki, E., Sakakibara, S., Fukasawa, K. and Harada, M. (1985) A sensitive and specific assay for dipeptidyl-aminopeptidase II in serum and tissues by liquid chromatography-fluolometry. Anal. Biochem. **147**, 80–85
27 Fukasawa, K., Fukasawa, K. M., Kanai, M., Fujii, S., Hirose, J. and Harada, M. (1998) Dipeptidyl peptidase III is a zinc metallo-exopeptidase: molecular cloning and expression. Biochem. J. **329**, 275–282
28 Laemmli, U. K. (1970) Cleavage of structural proteins during the assembly of the head of bacteriophage T_4. Nature (London) **227**, 680–685
29 Sanger, F., Nicklen, S. and Coulson, A. R. (1977) DNA sequencing with chain-terminating inhibitors. Proc. Natl. Acad Sci. U.S.A. **74**, 5463–5467
30 Mantle, D. (1991) Characterization of dipeptidyl and tripeptidyl aminopeptidases in human kidney soluble fraction. Clin. Chim. Acta **196**, 135–142
31 Kozak, M. (1987) An analysis of 5′-noncoding sequences from 699 vertebrate messenger RNAs. Nucleic Acids Res. **15**, 8125–8148
32 Nielsen, H., Engelbrecht, J., Brunak, S. and Heijne, G. (1997) Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites. Protein Eng. **10**, 1–6
33 Nielsen, H. and Krogh, A. (1998) Prediction of signal peptides and signal anchors by a hidden Markov model. In Proceedings of the Sixth International Conference on Intelligent Systems for Molecular Biology (ISMB 6), pp. 122–130, AAAI Press, Menlo Park, CA
34 von Heijne, G. (1986) A new method for predicting signal sequence cleavage site. Nucleic Acids Res. **14**, 4683–4690
35 McDonald, J. K., Leibach, F. H., Grindeland, R. E. and Ellis, S. (1968) Purification of dipeptidyl aminopeptidase II (dipeptidyl arylamidase II) of the anterior pituitary gland: peptidase and dipeptide esterase activities. J. Biol. Chem. **243**, 4143–4150
36 DiCarlantonio, G., Talbot, P. and Dudenhausen, E. (1986) Partial purification and characterization of dipeptidylpeptidase II (DPP II) from giniea pig testes. Gamete Res. **15**, 161–175
37 Chiravuri, M., Schmitz, T., Yardley, K., Underwood, R., Dayal, Y. and Huber, B. T. (1999) A novel apoptotic pathway in quiescent lymphocytes identified by inhibition of a post-proline cleaving aminodipeptidase: a candidate target protease, quiescent cell proline dipeptidase. J. Immunol. **163**, 3092–3099
38 Medrano, F. J., Alonso, J., Garcia, J. L., Romero, A., Bode, W. and Gomis-Ruth, F. X. (1998) Structure of proline iminopeptidase from *Xanthomonas campestris* pv. *citri*: a prototype for the prolyl oligopeptidase family. EMBO J. **17**, 1–9
39 Komatsu, M., Urade, M., Yamaoka, M., Fukasawa, K. and Harada, M. (1987) Alteration in dipeptidyl peptidase activities in cultured human carcinoma cells. J. Natl. Cancer Inst. **78**, 863–868
40 Kahne, T., Lendeckel, U., Wrenger, S., Neubert, K., Ansorge, S. and Reinhold, D. (1999) Dipeptidyl peptidase IV: a cell surface peptidase involved in regulating T cell growth. Int. J. Mol. Med. **4**, 3–15
41 Pham, C. T. and Ley, T. J. (1999) Dipeptidyl peptidase I is required the processing and activation of granzymes A and B *in vivo*. Proc. Natl. Acad Sci. U.S.A. **96**, 8627–8632

Received 11 May 2000/20 September 2000; accepted 27 October 2000