

# Purification and characterization of leukotriene A<sub>4</sub> hydrolase from *Xenopus laevis* oocytes

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**Abstract** In mammals, leukotriene A<sub>4</sub> hydrolase converts leukotriene A<sub>4</sub> into the proinflammatory mediator leukotriene B<sub>4</sub>. We have purified and characterized a non-mammalian leukotriene A<sub>4</sub> hydrolase from *Xenopus laevis* oocytes. This enzyme contains one zinc atom and catalyzes an anion-dependent peptidase activity, two key features of the mammalian enzymes. The amino acid sequence of an internal segment is 60% identical with human leukotriene A<sub>4</sub> hydrolase but only 27% identical with rat aminopeptidase B. The *Xenopus laevis* enzyme is catalytically very efficient and, unlike the human enzyme, converts leukotriene A<sub>4</sub> into two enzymatic metabolites, viz. leukotriene B<sub>4</sub> and  $\Delta^6$ -*trans*- $\Delta^8$ -*cis*-leukotriene B<sub>4</sub>.

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**Key words:** Leukotriene A<sub>4</sub> hydrolase; Leukotriene B<sub>4</sub>; Aminopeptidase; Inflammation; *Xenopus laevis*

## 1. Introduction

Leukotriene (LT) A<sub>4</sub> hydrolase catalyzes the final step in the biosynthesis of LTB<sub>4</sub>, a potent chemotaxin and leukocyte activating agent [1]. The mammalian LTA<sub>4</sub> hydrolase is a soluble monomeric metalloenzyme with a molecular mass of about 69 kDa containing one catalytic zinc [2–4]. In addition to the epoxide hydrolase activity, i.e. the hydrolysis of LTA<sub>4</sub> into LTB<sub>4</sub>, the enzyme also possesses an anion-dependent peptidase activity, the physiological role of which is still unknown [4–7]. The primary structure of LTA<sub>4</sub> hydrolase is 33% identical to that of aminopeptidase B, which has also been reported to possess LTA<sub>4</sub> hydrolase activity [8].

In a recent study we found that organ extracts of the African claw toad *Xenopus laevis* converted LTA<sub>4</sub>, not only into LTB<sub>4</sub>, but also into a novel biologically active metabolite, structurally identified as 5*S*,12*R*-dihydroxy-6,10-*trans*-8,14-*cis*-eicosatetraenoic acid ( $\Delta^6$ -*trans*- $\Delta^8$ -*cis*-LTB<sub>4</sub>) [9]. We also discovered that the reproduction organs, i.e. oocytes and testes, are very rich in LTA<sub>4</sub> hydrolase activity, a circumstance which has now enabled us to purify and characterize the enzyme from a non-mammalian source. In the present report we show that the *Xenopus laevis* protein is a bifunctional zinc metalloenzyme which is structurally distinct from

aminopeptidase B and exhibits high catalytic efficiencies as well as the ability to convert LTA<sub>4</sub> into  $\Delta^6$ -*trans*- $\Delta^8$ -*cis*-LTB<sub>4</sub>.

## 2. Materials and methods

### 2.1. Preparation of oocytes

Female *Xenopus laevis* toads, 60–90 g (Blades Biological, UK), were decapitated and the oocytes were removed and kept on ice prior to homogenization in one part (mass/vol.) 50 mM Tris-HCl buffer, pH 8, and 2 mM EDTA, utilizing a Potter-Elvehjem homogenizer. The 10 000×g supernatants of the homogenates are referred to as cytosol.

### 2.2. Protein purification

Nucleic acids were removed from cytosol by streptomycin sulfate precipitation followed by centrifugation (10 000×g; 15 min; 4°C). The supernatant was subjected to ammonium sulfate precipitation on ice. After removal of the 0–35% precipitate, the solution was saturated to 80%. Proteins were pelleted by centrifugation and dissolved in 10 mM Tris-HCl, pH 8.

For anion-exchange chromatography on FPLC (Pharmacia), a column packed with Q Sepharose Fast Flow (Pharmacia) was equilibrated with 10 mM Tris-HCl, pH 8. The 35–80% ammonium sulfate fraction was dialyzed against the equilibration buffer, treated with dithiothreitol (2 mM, 30 min), and applied to the column. Adsorbed proteins were eluted with a gradient of KCl (0–500 mM) and the enzyme activity was recovered between 140 and 190 mM. Active fractions were supplemented with 20% (mass/vol.) ammonium sulfate and applied to a phenyl Superose, HR 5/5 (Pharmacia) column preequilibrated in 20 mM Tris-HCl buffer, pH 8, containing 150 mM ammonium sulfate. A linear gradient of ammonium sulfate (150–0 mM) was applied and the enzyme activity was eluted between 67 and 45 mM. For hydroxyapatite chromatography, a TSKgel HA-1000 column (Tosoh) was equilibrated in 10 mM potassium phosphate buffer, pH 7.1, supplemented with 0.2 mM CaCl<sub>2</sub>. Pooled fractions from the hydrophobic interaction chromatography were applied in the equilibration buffer. The column was eluted with a gradient of potassium phosphate (10–400 mM) and active fractions were eluted between 150 and 190 mM. The final purification was achieved by chromatofocusing on a MonoP column HR 5/20 (Pharmacia) preequilibrated with 25 mM Bis-Tris, pH adjusted to 7.1 with iminodiacetic acid. Active fractions from the hydroxyapatite column, in 10 mM Tris-HCl, pH 8.0, were applied to the column which was then eluted with a pH gradient (7.1–4.5). LTA<sub>4</sub> hydrolase eluted at a pH = pI of about 6.1. For buffer exchange, a final chromatographic step was performed on a MonoQ HR 5/5 column (Pharmacia). LTA<sub>4</sub> hydrolase was also purified from isolated human leukocytes, essentially as described [10].

### 2.3. Determinations of enzyme activities and protein concentrations

The epoxide hydrolase activity was determined as described [9]. Briefly, aliquots of the enzyme pools (1% by vol.) in 100 µl, 10 mM Tris-HCl, pH 8, were incubated with 25 µM LTA<sub>4</sub> for 10 s at room temperature. Formation of LTB<sub>4</sub> was analyzed by reverse-phase HPLC at 270 nm, using prostaglandin B<sub>1</sub> as the internal standard. The column (Nova-Pak C<sub>18</sub>, 4 µm Radial-Pak cartridge, 5×100 mm, Waters) was eluted with a mixture of acetonitrile/methanol/water/acet-ic acid (30:35:35:0.01, v/v) at 1.0 ml/min.

The peptidase activity was determined, essentially as described [10]. Alanine-4-nitroanilide was dissolved to a concentration of 1 mM in 50 mM Tris-HCl, pH 7.5, containing 100 mM KCl or, in some experiments, KSCN, NaBr, NaCl, NaF, NaI, NaNO<sub>3</sub> or NaSCN between

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**Abbreviations:** LTA<sub>4</sub>, leukotriene A<sub>4</sub>; 5*S*-*trans*-5,6-oxido-7,9-*trans*-11,14-*cis*-eicosatetraenoic acid; LTB<sub>4</sub>, leukotriene B<sub>4</sub>; 5*S*, 12*R*-dihydroxy-6,14-*cis*-8,10-*trans*-eicosatetraenoic acid;  $\Delta^6$ -*trans*- $\Delta^8$ -*cis*-LTB<sub>4</sub>, 5*S*,12*R*-diHETE, 5*S*, 12*R*-dihydroxy-6,10-*trans*-8,14-*cis*-eicosatetraenoic acid; FPLC, fast protein liquid chromatography

12.5 and 800 mM. The product (4-nitroaniline) was measured spectrophotometrically at 405 nm.

Protein concentrations were determined according to Bradford [11], using the Bio-Rad protein assay reagent and bovine serum albumin as standard.

#### 2.4. SDS-PAGE, Western blot, and isoelectric focusing

Aliquots of purified protein (2–4 µg) were subjected to SDS-PAGE (stacking gel 5%; separating gel 10%) on a Mini-Protein II (Bio-Rad) apparatus [12] or on a PhastSystem (Pharmacia) using PhastGels, gradient 10–15%. The gels were stained with Coomassie brilliant blue or AgNO<sub>3</sub>. Western blot analysis was carried out with an affinity-purified polyclonal antiserum against human LTA<sub>4</sub> hydrolase, as described [9]. For isoelectric focusing, PhastGels IEF 3–9 were used and stained with Coomassie brilliant blue.

#### 2.5. Amino acid sequence analysis

LTA<sub>4</sub> hydrolase (40 µg; 570 pmol) in 10 mM Tris-HCl, pH 8, was digested with Lys-C protease (4 µg, at 37°C, 18 h). Peptides were separated by HPLC on a Vydac C<sub>8</sub> column (2.1×150 mm), eluted with a gradient of acetonitrile (5–80%) in 0.1% trifluoroacetic acid. Peptides were sequenced on an Applied Biosystems instrument model 477A or 494.

#### 2.6. Metal analyses

Zinc was measured by graphite furnace atomic absorption spectrophotometry using a Perkin-Elmer 5000 Zeeman instrument with an electrothermal atomization unit (HGA-500). Zinc was analyzed at 213.9 nm using an EDL lamp. Mixed zinc standards (British Drug House, UK) were prepared in 0.03 M HNO<sub>3</sub> (10–200 ng/ml) and diluted 1:1 in the sample cups with deionized water (Elgastat Spectrum R.O.1, ELGA, UK) prior to analysis. Samples of LTA<sub>4</sub> hydrolase were mixed with an equal volume of 0.03 or 0.1 M HNO<sub>3</sub>. Standards and unknowns were analyzed in duplicate.

### 3. Results

#### 3.1. Purification and physicochemical properties of *Xenopus laevis* LTA<sub>4</sub> hydrolase

LTA<sub>4</sub> hydrolase was isolated from *Xenopus laevis* oocytes. Typically, the overall purification was about 8000-fold with a recovery of 30% (Table 1), resulting in an apparently homogeneous preparation (SDS-PAGE with silver staining). From SDS-PAGE, the *M<sub>r</sub>* of the *Xenopus laevis* LTA<sub>4</sub> hydrolase was estimated to 69 000 and the isoelectric point was found to be 6.1, as judged by isoelectric focusing (PhastGel) and chromatofocusing (MonoP column). Atomic absorption spectrometry revealed the presence of 0.8 mol zinc per mol enzyme. The amphibian enzyme was not recognized by an antiserum against human LTA<sub>4</sub> hydrolase in Western blot analysis and attempts to determine the N-terminal amino acid sequence did not yield any result, indicating the presence of a blocked N-terminus. To make possible an evaluation of the structure, the *Xenopus laevis* enzyme was therefore digested with Lys-C protease and seven internal peptides, varying in length between 5 and 15 amino acid residues, were sequenced. Altogether, these peptides contained 62 residues

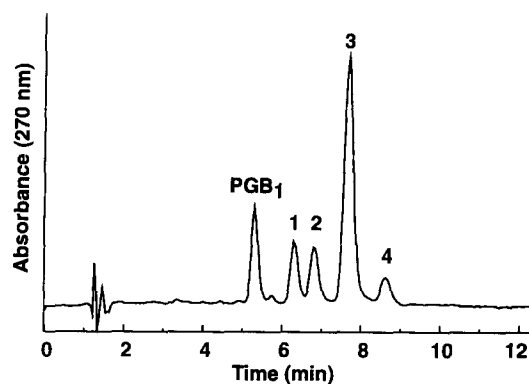


Fig. 1. Reverse-phase HPLC profile of the products formed in incubations of purified LTA<sub>4</sub> hydrolase from *Xenopus laevis* oocytes with LTA<sub>4</sub>. The reverse-phase HPLC analysis was performed as described in Section 2. PGB<sub>1</sub> denotes the internal standard prostaglandin B<sub>1</sub>. Peaks 1 and 2 elute with two non-enzymatic hydrolysis products of LTA<sub>4</sub>. Peaks 3 and 4 have the same retention times as LTB<sub>4</sub> and  $\Delta^6$ -trans- $\Delta^8$ -cis-LTB<sub>4</sub>, respectively.

and were 60–100% (mean value 74%) identical to human LTA<sub>4</sub> hydrolase and 17–50% (mean value 32%) identical to rat aminopeptidase B. The longest 15 residue peptide (ELLEPSVYEFAETEK) exhibited 60% identity to the corresponding segment of human LTA<sub>4</sub> hydrolase (residues 225–239) but only 27% identity to rat aminopeptidase B (residues 252–267).

#### 3.2. Catalytic properties

The purified *Xenopus laevis* LTA<sub>4</sub> hydrolase (0.2 µg) efficiently converted LTA<sub>4</sub> into LTB<sub>4</sub> at a pH optimum of 8.5 (Tris-HCl or phosphate buffer). The specific epoxide hydrolase activity was  $6.7 \pm 1.6$  µmol/mg/min (mean  $\pm$  S.D., *n* = 8) as compared to only  $0.95 \pm 0.3$  µmol/mg/min (mean  $\pm$  S.D., *n* = 4) for the human LTA<sub>4</sub> hydrolase (1 µg). Multiple exposures (4 times) to LTA<sub>4</sub> (25 µM, 30 min) led to a partial inactivation of the *Xenopus laevis* enzyme, suggesting that it was susceptible to suicide inactivation.

The *Xenopus laevis* enzyme also produced a second enzymatic metabolite of LTA<sub>4</sub>. Thus, reverse-phase HPLC analysis of enzyme samples incubated with LTA<sub>4</sub> revealed four peaks (Fig. 1). Peaks 1 and 2 cochromatographed with the two non-enzymatic hydrolysis products of LTA<sub>4</sub>. The third peak (3) eluted with synthetic LTB<sub>4</sub> whereas the fourth peak (4) had the same HPLC retention time and UV spectrum (in MeOH) as a recently identified enzymatic product of LTA<sub>4</sub>, viz. 5*S*,12*R*-dihydroxy-8,14-*cis*-6,10-*trans* eicosatetraenoic acid, also termed  $\Delta^6$ -trans- $\Delta^8$ -cis-LTB<sub>4</sub> or 5*S*-12*R*-dihETE [9]. The formation of  $\Delta^6$ -trans- $\Delta^8$ -cis-LTB<sub>4</sub> appeared at all stages of purification and always in the ratio 1:10,

Table 1  
Purification of LTA<sub>4</sub> hydrolase from *Xenopus laevis* oocytes

Step	Total protein (mg)	Total activity (nmol/mg)	Specific activity (nmol/mg/min)	Yield (%)	Purification (-fold)
Dialysis	1650	2018	1.2	100	1
Q Sepharose	9.5	1900	202	95	168
Phenyl Sepharose	1.5	1627	1085	80	904
Hydroxyapatite	0.3	882	3095	44	2580
MonoP	0.07	486	6480	24	5400
MonoQ	0.071	704	9850	30	8200

relative to LTB<sub>4</sub>. Incubations of the human leukocyte LTA<sub>4</sub> hydrolase with LTA<sub>4</sub> generated no other product than LTB<sub>4</sub>, as judged by reverse-phase HPLC.

When the *Xenopus laevis* LTA<sub>4</sub> hydrolase (0.2 µg) was incubated in 50 mM Tris-HCl (pH 7.5), with 100 mM KCl, hydrolysis of the synthetic peptidase substrate alanine-4-nitroanilide (1 mM) into alanine and 4-nitroaniline was observed. The pH optimum for this peptidase activity (Tris-HCl or phosphate buffer) was determined to 7.5. The specific activity was calculated to 581 ± 213 nmol/mg/min (mean ± S.D., *n* = 5). Under the same conditions, the human leukocyte enzyme (0.2 µg) exhibited a specific activity of 209 ± 99 nmol/mg/min (mean ± S.D., *n* = 4).

The peptidase activity of the *Xenopus laevis* LTA<sub>4</sub> hydrolase towards alanine-4-nitroanilide was dose dependently stimulated by a number of monovalent anions added as potassium and/or sodium salts. The choice of cation did not influence the effect of the anion. Among the anions tested, thiocyanate was found to be the most effective activator followed by bromide and chloride ( $\text{SCN}^- \gg \text{Br}^- > \text{Cl}^- \approx \text{I}^- \approx \text{NO}_3^- \gg \text{F}^-$ ). For chloride ions, the pattern of stimulation seemed to obey saturation kinetics and from Eadie-Hofstee plots of the kinetic data, an apparent affinity constant ( $K_A$ ) for chloride was calculated to 80 mM. Bromide or thiocyanate caused a similar activation, but concentrations exceeding 200 mM suppressed the enzyme activity. A value of  $K_A$  for thiocyanate (0–100 mM) was estimated to 30 mM. Chloride (150–600 mM KCl) did not stimulate the epoxide hydrolase activity.

### 3.3. Apparent kinetic constants

Apparent kinetic constants for the two activities were determined for both the *Xenopus laevis* and the human LTA<sub>4</sub> hydrolase. Values of  $K_m$  and  $V_{max}$  were calculated from Eadie-Hofstee plots of the kinetic data.

For the epoxide hydrolase activity, 0.3 µg of the amphibian enzyme or 1 µg of the human enzyme were incubated with varying amounts of LTA<sub>4</sub> (5–90 µM). In a typical experiment with the *Xenopus laevis* enzyme, the  $K_m$  and  $V_{max}$  for LTA<sub>4</sub> were calculated to 20 µM and 12.0 µmol/mg/min, respectively (mean of duplicates). Corresponding values for the human enzyme were 2.7 µM and 1.3 µmol/mg/min (mean of duplicates), respectively (Table 2).

For the peptidase activity, 0.25 µg each of *Xenopus laevis* and human LTA<sub>4</sub> hydrolase were incubated with varying amounts of alanine-4-nitroanilide (0.125–16 mM). The values of  $K_m$  and  $V_{max}$  were determined to 2.4 mM and 1800 nmol/mg/min (mean of triplicates), respectively, for the *Xenopus laevis* enzyme. For the human enzyme the values were 0.7 mM and 470 nmol/mg/min (mean of triplicates), respectively (Table 2).

## 4. Discussion

### 4.1. General properties of *Xenopus laevis* LTA<sub>4</sub> hydrolase

In the present study we purified LTA<sub>4</sub> hydrolase to apparent homogeneity from a non-mammalian species, i.e. the African claw toad *Xenopus laevis* (Table 1), making possible metal analysis and assay for a peptidase activity. The amphibian enzyme contained one zinc atom per enzyme molecule and displayed a peptide cleaving activity against the synthetic substrate alanine-4-nitroanilide. Hence, *Xenopus laevis* LTA<sub>4</sub> hydrolase is a bifunctional zinc metalloenzyme, key properties of the mammalian counterparts [4,5].

The peptidase activity of the *Xenopus laevis* LTA<sub>4</sub> hydrolase was greatly stimulated by monovalent anions. For chloride, the physiologically most relevant anion, an apparent affinity constant ( $K_A$ ) was calculated to be 80 mM, in good agreement with the value of 100 mM previously obtained with the human enzyme [6]. The profound and selective effects of chloride suggests that the peptidase activity may be regulated by the steady-state levels or fluxes of this electrolyte. Moreover, further studies are warranted to clarify the function of this peptide cleaving activity and explain the presence of the enzyme in the reproduction organs of *Xenopus laevis*.

In contrast to mammalian forms of LTA<sub>4</sub> hydrolase, the N-terminus of the *Xenopus laevis* enzyme appeared to be blocked. Furthermore, the amphibian protein was not detected in Western blots, using a probe for the human protein. To get an estimate of the structural conservation of the *Xenopus laevis* enzyme, several internal peptides were isolated and sequenced. Thus, seven peptides, encompassing 62 amino acid residues, were ~70% identical to the corresponding segments of human LTA<sub>4</sub> hydrolase and their sequences clearly distinguished the toad enzyme from aminopeptidase B (~30% identity), an enzyme which has also been shown to possess LTA<sub>4</sub> hydrolase activity [8].

### 4.2. The *Xenopus laevis* LTA<sub>4</sub> hydrolase displays a high catalytic efficiency

The apparent kinetic constants for the epoxide hydrolase and peptidase activities differed considerably between the *Xenopus laevis* and human LTA<sub>4</sub> hydrolase (Table 2). Thus, the value of  $V_{max}$  for the epoxide hydrolase activity of the *Xenopus laevis* enzyme was approximately 9-fold higher as compared to the human enzyme. On the other hand, it displayed a 7-fold higher  $K_m$  for LTA<sub>4</sub> and therefore, the specificity constants ( $k_{cat}/K_m$ ) for LTA<sub>4</sub> were almost the same for the two species, suggesting that the two active sites are equally well adapted to process the substrate LTA<sub>4</sub>. Of note, due to the instability of LTA<sub>4</sub> we consider the differences in substrate turnover ( $k_{cat}$ ) more significant than those of the Michaelis

Table 2

Apparent kinetic constants for the epoxide hydrolase and peptidase activity of LTA<sub>4</sub> hydrolase from *Xenopus laevis* oocytes and human leukocytes

	Epoxide hydrolase activity		Peptidase activity	
	<i>Xenopus laevis</i>	Human	<i>Xenopus laevis</i>	Human
$K_m$ (µM)	20	2.7	2400	700
$V_{max}$ (µmol/mg/min)	12	1.3	1.8	0.5
$k_{cat}$ (s <sup>-1</sup> )	14	1.5	2.1	0.5
$k_{cat}/K_m$ (s <sup>-1</sup> M <sup>-1</sup> )	$6.9 \times 10^5$	$5.5 \times 10^5$	860	770

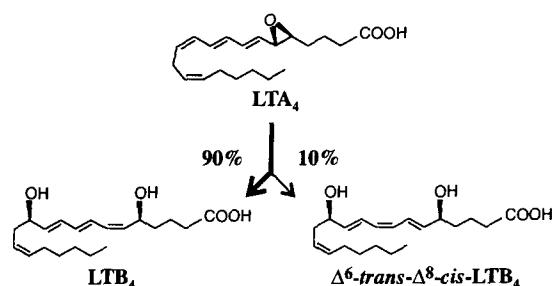


Fig. 2. Structure and formation of the enzymatic metabolites of  $\text{LTA}_4$  generated by *Xenopus laevis*  $\text{LTA}_4$  hydrolase.

constant. When comparing the peptidase activities, the values of both  $V_{\max}$  and  $K_m$  were again higher (approx. 3.5-fold for both parameters) for the *Xenopus laevis* enzyme. As for the epoxide hydrolase activity, the specificity constants ( $k_{\text{cat}}/K_m$ ) were almost the same for the two species.

#### 4.3. The *Xenopus laevis* $\text{LTA}_4$ hydrolase can form a second enzymatic metabolite of $\text{LTA}_4$

In a recent study, we found that organs of *Xenopus laevis* contained an enzyme activity which converted  $\text{LTA}_4$  into a novel, biologically active, product identified as  $\Delta^6$ -trans- $\Delta^8$ -cis- $\text{LTB}_4$  [9]. The relative formation of  $\Delta^6$ -trans- $\Delta^8$ -cis- $\text{LTB}_4$  versus  $\text{LTB}_4$  was always about 1:10. The *Xenopus laevis*  $\text{LTA}_4$  hydrolase that was purified in the present study has the ability to convert  $\text{LTA}_4$  into both  $\Delta^6$ -trans- $\Delta^8$ -cis- $\text{LTB}_4$  and  $\text{LTB}_4$  in a ratio of about 1:10 (Fig. 1) and can account for both of the enzyme activities observed in the organ extracts (Fig. 2).

Typically,  $\text{LTA}_4$  hydrolase becomes suicide inactivated and covalently modified by its lipid substrate  $\text{LTA}_4$  [13]. In this process, Tyr-378 is a primary site for covalent binding of  $\text{LTA}_4$  since exchange of this residue for a phenylalanine resulted in a recombinant enzyme that was protected from suicide inactivation [14]. Interestingly, this mutant, [Y378F] $\text{LTA}_4$  hydrolase, exhibited an increased turnover of  $\text{LTA}_4$  together with an increased  $K_m$  and converted  $\text{LTA}_4$  into both  $\text{LTB}_4$  and  $\Delta^6$ -trans- $\Delta^8$ -cis- $\text{LTB}_4$  and thus shares several catalytic properties with the *Xenopus laevis* enzyme. However, the latter enzyme is catalytically even more efficient

and, in contrast to [Y378F] $\text{LTA}_4$  hydrolase, appears to be suicide inactivated by the substrate  $\text{LTA}_4$ . Nevertheless, it is tempting to speculate that Tyr-378 is located in a segment of  $\text{LTA}_4$  hydrolase which may determine some of the catalytic differences between the human and of the *Xenopus laevis* enzyme.

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#### References

- [1] Ford-Hutchinson, A.W. (1990) Crit. Rev. Immunol. 10, 1–12.
- [2] Malfroy, B., Kado-Fong, H., Gros, C., Giros, B., Schwartz, J.-C. and Hellmiss, R. (1989) Biochem. Biophys. Res. Commun. 161, 236–241.
- [3] Haeggström, J.Z., Wetterholm, A., Shapiro, R., Vallee, B.L. and Samuelsson, B. (1990) Biochem. Biophys. Res. Commun. 172, 965–970.
- [4] Minami, M., Ohishi, N., Mutoh, H., Izumi, T., Bito, H., Wada, H., Seyama, Y., Toh, H. and Shimizu, T. (1990) Biochem. Biophys. Res. Commun. 173, 620–626.
- [5] Haeggström, J.Z., Wetterholm, A., Vallee, B.L. and Samuelsson, B. (1990) Biochem. Biophys. Res. Commun. 173, 431–437.
- [6] Wetterholm, A. and Haeggström, J.Z. (1992) Biochim. Biophys. Acta 1123, 275–281.
- [7] Örning, L. and Fitzpatrick, F.A. (1992) Biochemistry 31, 4218–4223.
- [8] Cadet, S., Foulon, T., Viron, A., Balogh, A., Midolmonnet, S., Noel, N. and Cohen, P. (1997) Proc. Natl. Acad. Sci. USA 94, 2963–2968.
- [9] Strömberg, F., Hamberg, M., Rosenqvist, U., Dahlén, S.E. and Haeggström, J.Z. (1996) Eur. J. Biochem. 238, 599–605.
- [10] Wetterholm, A., Medina, J.F., Rådmark, O., Shapiro, R., Haeggström, J.Z., Vallee, B.L. and Samuelsson, B. (1991) Biochim. Biophys. Acta 1080, 96–102.
- [11] Bradford, M.M. (1976) Anal. Biochem. 72, 248–254.
- [12] Laemmli, U.K. (1970) Nature 227, 680–685.
- [13] Evans, J.F., Nathaniel, D.J., Zamboni, R.J. and Ford-Hutchinson, A.W. (1985) J. Biol. Chem. 260, 10966–10970.
- [14] Mueller, M.J., Blomster, M., Oppermann, U.C., Jörnvall, H., Samuelsson, B. and Haeggström, J.Z. (1996) Proc. Natl. Acad. Sci. USA 93, 5931–5935.