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# PASylated Thymosin $\alpha$ 1: A Long-Acting Immunostimulatory Peptide for Applications in Oncology and Virology

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**Abstract:** Thymosin  $\alpha$ 1 (T $\alpha$ 1) is an immunostimulatory peptide for the treatment of hepatitis B virus (HBV) and hepatitis C virus (HCV) infections and used as an immune enhancer, which also offers prospects in the context of COVID-19 infections and cancer. Manufacturing of this N-terminally acetylated 28-residue peptide is demanding, and its short plasma half-life limits in vivo efficacy and requires frequent dosing. Here, we combined the PASylation technology with enzymatic in situ N-acetylation by RimJ to produce a long-acting version of T $\alpha$ 1 in *Escherichia coli* at high yield. ESI-MS analysis of the purified fusion protein indicated the expected composition without any signs of proteolysis. SEC analysis revealed a 10-fold expanded hydrodynamic volume resulting from the fusion with a conformationally disordered Pro/Ala/Ser (PAS) polypeptide of 600 residues. This size effect led to a plasma half-life in rats extended by more than a factor 8 compared to the original synthetic peptide due to retarded kidney filtration. Our study provides the basis for therapeutic development of a next generation thymosin  $\alpha$ 1 with prolonged circulation. Generally, the strategy of producing an N-terminally protected PASylated peptide solves three major problems of peptide drugs: (i) instability in the expression host, (ii) rapid degradation by serum exopeptidases, and (iii) low bioactivity because of fast renal clearance.



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## 1. Introduction

Thymosin  $\alpha$ 1 (T $\alpha$ 1) is an immunostimulatory peptide initially isolated from calf thymus [1] and also abundant in humans. T $\alpha$ 1 is synthesized as the N-terminal moiety of the highly acidic ( $pI = 3.7$ ) prothymosin  $\alpha$  (ProT $\alpha$ ), a peculiar cytoplasmic protein due to the absence of any sulfur-containing as well as aromatic side chains and, in particular, its random coil structure under physiological conditions [2,3]. Cleaved by the lysosomal asparaginyl endopeptidase (legumain;  $\delta$ -secretase), the N-terminally acetylated 28-residue peptide T $\alpha$ 1 gets released [4]. T $\alpha$ 1 plays a significant role in activating and regulating various cells of the immune system [5], e.g., by stimulating toll-like receptor (TLR)-2 and TLR-9 on myeloid and plasmacytoid dendritic cells (DCs), which results in the secretion of immune-related cytokines [6,7]. Furthermore, T $\alpha$ 1 increases the number of activated T helper (Th) cells and provokes a shift towards the Th1 subclass, thus promoting the cell-mediated immune response. In addition, T $\alpha$ 1 was reported to reduce apoptosis of immune cells [8] and to upregulate the expression of major histocompatibility complex I (MHC I) molecules [9] as well as tumor antigens [10]. Interestingly, T $\alpha$ 1 mediates increased intracellular glutathione (GSH) levels [11], which not only inhibits the growth of certain cancer cells in vitro [7,12], but also blocks the assembly of virus particles by hindering disulfide bond formation that is required for envelope glycoprotein oligomerization [13]. These features offer a broad range of clinical applications for T $\alpha$ 1 [14].

In fact, a chemically synthesized T $\alpha$ 1 peptide drug has been marketed for more than 20 years under the trade name Zadaxin<sup>TM</sup> in more than 30 countries. Zadaxin<sup>TM</sup> is clinically approved for the treatment of chronic hepatitis B (HBV), chronic hepatitis C (HCV), as a vaccine adjuvant, and as adjuvant therapy for chemotherapy-induced immune suppression [7]. Of note, the use of T $\alpha$ 1 has recently undergone reassessment in the context of modern cancer immunotherapies, as there is indication that this peptide may support immune checkpoint inhibition. Preclinical data provide evidence that T $\alpha$ 1 transforms so called cold tumors, which poorly respond to immune checkpoint inhibitors, into highly lymphocyte-infiltrated tumors and, thus, boosts therapeutic efficacy [15]. Indeed, a retrospective study evaluating clinical phase II data reported an increase in overall survival of melanoma patients receiving sequentially T $\alpha$ 1 and the immune checkpoint inhibitor ipilimumab, a CTLA-4-blocking antibody, compared to ipilimumab therapy alone [16]. Moreover, T $\alpha$ 1 was shown to prevent intestinal toxicity in a murine model of anti-CTLA-4-induced colitis, hence contributing to an improved safety profile of immune checkpoint inhibitors [17]. Beyond that, emerging indications such as cystic fibrosis [18], multiple sclerosis [19], and sepsis [20] further emphasize the huge potential of this small therapeutic peptide. Finally, with the outbreak of the COVID-19 pandemic, T $\alpha$ 1 recently gained new attention in virology. Clinical symptoms of COVID-19 to some extent resemble a pathogen-induced sepsis, which justifies immunomodulatory T $\alpha$ 1 treatment [21]. Along these lines, Chinese medical staff members at high risk of COVID-19 infection already received a weekly T $\alpha$ 1 injection in combination with human interferon 1 (hIFN- $\alpha$ ) nasal drops as a prophylactic measure [22]. Furthermore, a recent retrospective study in treated Chinese patients revealed that T $\alpha$ 1 significantly reduced the mortality of severe COVID-19 by restoration of lymphocytopenia and reversion of exhausted T cells [23].

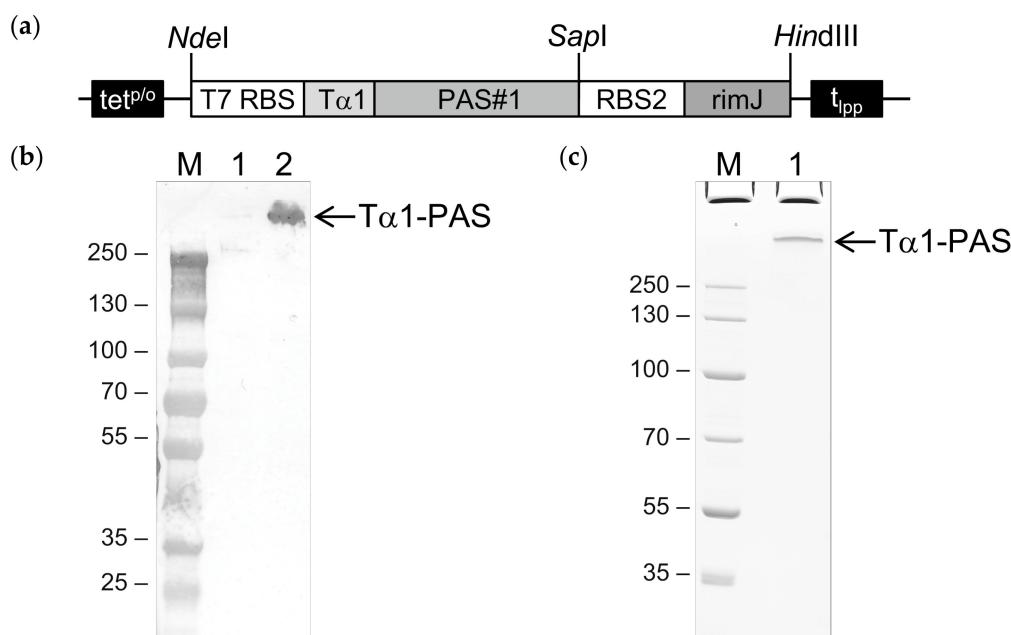
However, there are two major drawbacks of the currently marketed T $\alpha$ 1, both of which are related to its peptidic nature. First, the biopharmaceutical production of T $\alpha$ 1 is challenging. Apart from the posttranslational modification via N-terminal acetylation, chemical synthesis of T $\alpha$ 1 is complex, and obstacles comprise the large number of required protecting groups as well as the aggregation tendency of intermediates during synthesis [24]. Furthermore, the overall yield of the solid-phase synthesis is low, typically reaching only around 25% [25]. On the other hand, the biotechnological production as a recombinant peptide in an economic manner has failed so far. Short peptides, in general, are quickly degraded in the bacterial cytoplasm; thus, efficient one-step production of mature T $\alpha$ 1 in *E. coli* is not feasible. An alternative would be expression as part of a larger protein such as natural ProT $\alpha$  [26], as artificial concatamers [27], in fusion with an intein [28] or in fusion with a highly expressed bacterial protein like thioredoxin [29]. In each case, enzymatic or chemical cleavage is necessary to liberate the mature peptide, which complicates the biopharmaceutical downstream process. Second, after administration *in vivo*, the small peptide T $\alpha$ 1 is quickly eliminated via renal filtration with a terminal plasma half-life in humans of less than 3 h [30]. This limits its clinical efficacy and, to maintain viable drug levels, would require twice daily dosing.

In the present study, we applied the PASylation<sup>®</sup> technology in order to overcome both of these obstacles of the currently available T $\alpha$ 1 drug and to create a long-lasting N-terminally acetylated therapeutic peptide, also offering cheap and efficient biotechnological production in *E. coli*. To this end, we combined fusion with a 600-residue polypeptide comprising the small natural L-amino acids Pro, Ala, and Ser [31] with *in situ* N-acetylation by overexpressing the host cell N-acetyltransferase RimJ [32]. The genetically encoded uncharged “PAS” sequence is highly soluble and structurally disordered, with an expanded hydrodynamic volume, thus showing a biophysical behavior very similar to the chemical polymer polyethylene glycol (PEG), which has been utilized for plasma half-life extension of a series of other therapeutic peptides and proteins [33–35].

## 2. Results

### 2.1. Cloning and Bacterial Production of PASylated T $\alpha$ 1

To achieve C-terminal PASylation of N-terminally acetylated T $\alpha$ 1, a plasmid harboring a bicistronic operon was constructed to allow the simultaneous expression of human T $\alpha$ 1 (UniProtKB ID: P06454; residues 2–29), C-terminally fused with a PAS polypeptide comprising 601 amino acids [34], and the *E. coli* N-acetyltransferase RimJ (UniProtKB ID: P0A948) based on the vector pASK75 (Figure 1) [36]. In a parallel attempt, a plasmid encoding an N-terminally PASylated T $\alpha$ 1 was constructed, again, using plasmid pASK75 as the backbone (this time omitting the RimJ cistron, see below). Cytoplasmic gene expression was performed in both cases on a 2 L shake flask scale using the *E. coli* strain NEBExpress under control of the chemically inducible tet promoter/operator [36].



**Figure 1.** Bacterial production of N-terminally acetylated T $\alpha$ 1-PAS. (a) Expression vector for T $\alpha$ 1-PAS and the N-acetyltransferase RimJ from a bicistronic operon under control of the inducible *tet*<sup>P/O</sup>. The gene cassette cloned on pASK75 comprises the T7 phage ribosome binding site (T7 RBS) followed by the coding sequence for human T $\alpha$ 1 fused to a 601-residue PAS#1 sequence, the second RBS, the coding sequence for RimJ, and the lipoprotein terminator (*t<sub>pp</sub>*). (b) Western blot analysis after 4–12% SDS-PAGE of T $\alpha$ 1-PAS in the *E. coli* whole cell lysate using an antibody directed against the PAS#1 sequence. M, protein size standard; lane 1, whole cell extract before induction; lane 2, whole cell extract 15 h after induction. (c) 10% SDS-PAGE of purified T $\alpha$ 1-PAS. M, protein size standard; lane 1, T $\alpha$ 1-PAS after ammonium sulfate precipitation, subtractive anion exchange (AEX), cation exchange (CEX), and final AEX chromatography.

The whole cell lysate was analyzed prior to and 15 h after induction by Western blotting. Using a monoclonal antibody that recognizes an epitope of the PAS#1 sequence, a distinct band with an approximate molecular size above 250 kDa was detected (Figure 1b), which demonstrated successful bacterial expression of the full-length C-terminally PASylated T $\alpha$ 1 (T $\alpha$ 1-PAS) without signs of degradation. Of note, the unusually slow migration of T $\alpha$ 1-PAS (52.7 kD) in sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) is well known for PASylated proteins [31,37] and can be explained by the poor binding of SDS (which provides the electrophoretic driving force) to the strongly hydrophilic PAS sequence.

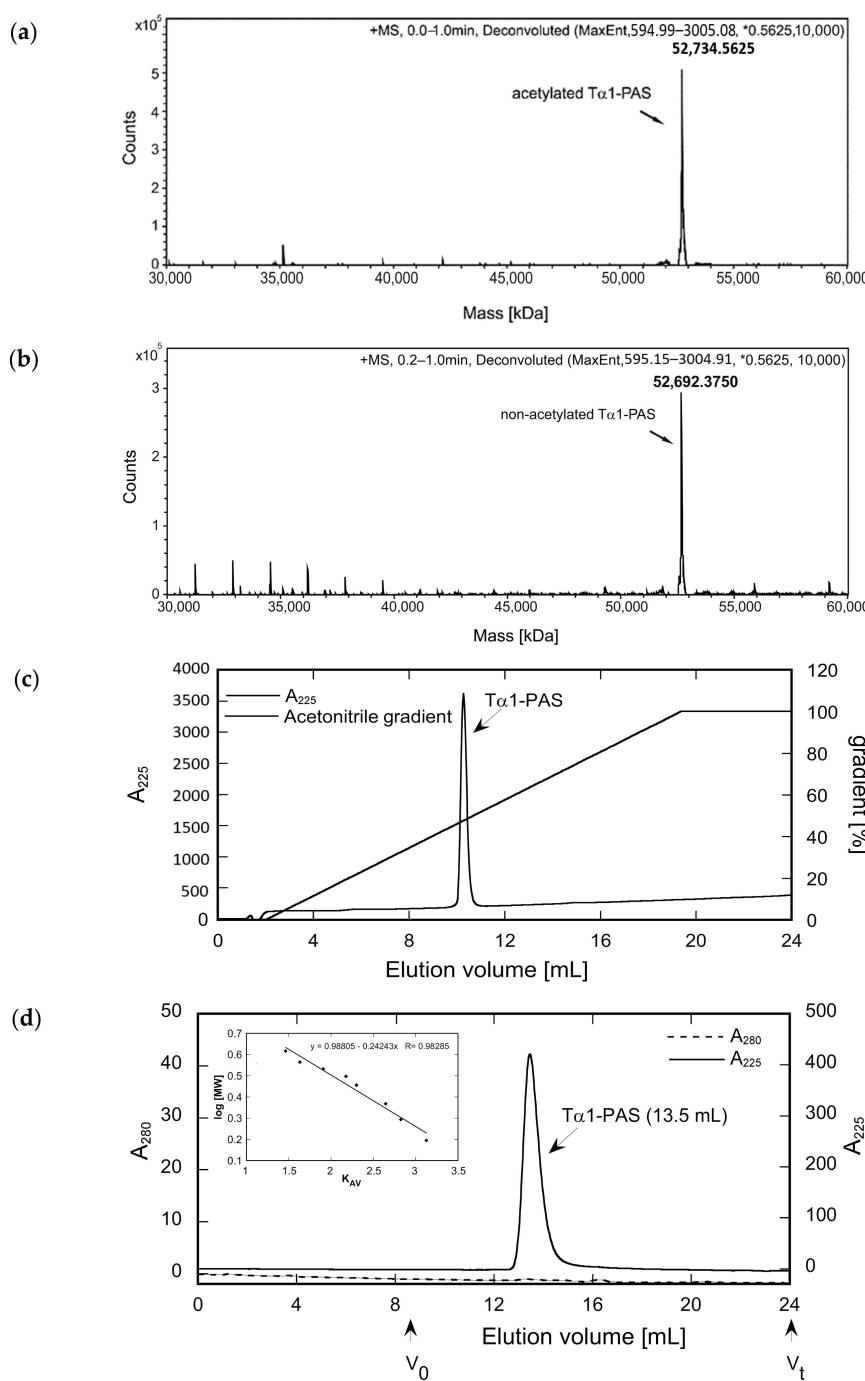
### 2.2. Purification and In Vitro Characterization of PASylated T $\alpha$ 1

The uncharged PAS moiety, which does not alter the isoelectric point of the target peptide, facilitates classical protein precipitation by ammonium sulfate, thus providing an

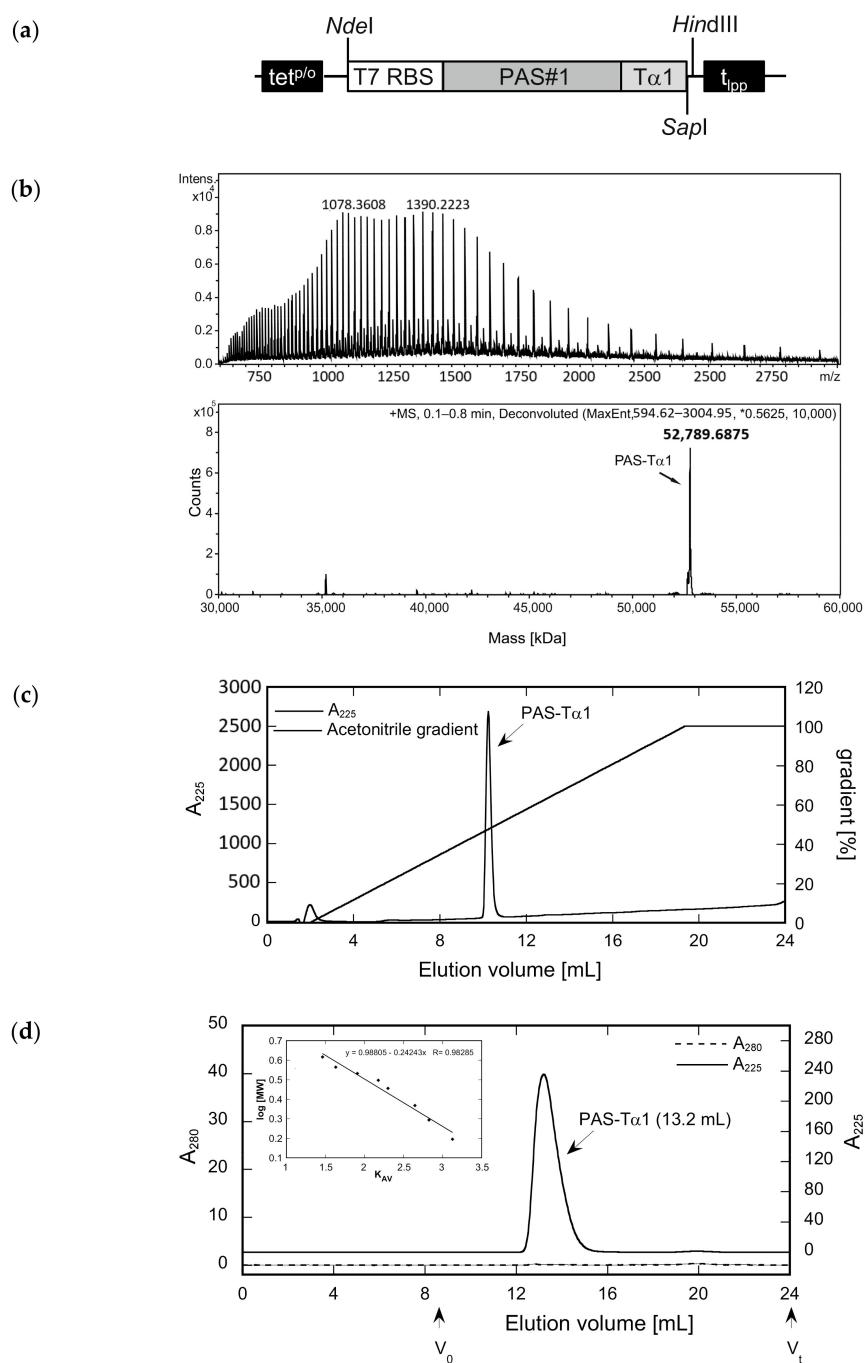
efficient and inexpensive purification step. After adjusting the cleared whole cell extract prepared by mechanical cell lysis to 30% ammonium sulfate saturation, most of the host cell proteins remained in solution while both PAS-T $\alpha$ 1 and PAS-T $\alpha$ 1 were selectively recovered as a precipitate. To remove residual *E. coli* proteins, the redissolved precipitate was subjected to ion exchange chromatography on a salt-tolerant anion exchange (AEX) resin at pH 8.5. Even though the PASylated T $\alpha$ 1 peptide with a calculated pI of 4.3 [38] for both versions should be negatively charged under these conditions and, hence, is expected to adsorb to the resin, the recombinant fusion proteins were quantitatively found in the flow-through. Possibly, the voluminous PAS polymer partially shields the small peptide from ionic interactions with the chromatography matrix. Nevertheless, this step resulted in efficient depletion both of residual host cell proteins and of bacterial endotoxins.

The protein solutions were dialyzed against a citrate buffer at pH 3.0 and subsequently applied to a strong cation exchange (CEX) column, which resulted in a bound fraction for PAS-T $\alpha$ 1, whereas both a flow-through fraction and a bound fraction were observed for T $\alpha$ 1-PAS (Figure 2). Electrospray ionization mass spectrometry (ESI-MS) analysis of T $\alpha$ 1-PAS in the flow-through revealed a molecular mass of 52,734.56 Da (Figure 2a), which exactly matches the calculated mass for the N-terminally acetylated gene product (52,734.56 Da). In this case, the start methionine of T $\alpha$ 1-PAS (followed by a Ser residue) was fully processed, presumably by the bacterial methionine aminopeptidase [39], then followed by N-terminal acetylation via RimJ. In contrast, the column-bound peptide fraction, which was eluted using a salt concentration gradient, showed a molecular mass of 52,692.38 Da (Figure 2b), which corresponds to the calculated mass for the non-acetylated processed polypeptide (52,692.54 Da) accompanied by some minor peaks below 40 kDa, most likely due to residual host cell impurities. Accordingly, this CEX step enabled separation of the desired N-acetylated T $\alpha$ 1-PAS from its non-acetylated precursor as a result of a single charge difference. In comparison, the fully column-bound non-acetylated PAS-T $\alpha$ 1 showed a single molecular mass of 52,789.8 Da (Figure 3) corresponding to the intact peptide, again, lacking the start methionine.

Both PASylated peptide preparations had a purity > 96% as indicated by reverse-phase chromatography (Figures 2c and 3c). For T $\alpha$ 1-PAS, we performed a final AEX polishing step, which also allowed concentration of the peptide. At pH 10, the acetylated T $\alpha$ 1-PAS bound to a strong AEX resin and eluted as a homogenous peak in a salt concentration gradient. The endotoxin content of this fraction was very low, with < 0.1 EU/mg, and the final yield was 15 mg acetylated T $\alpha$ 1-PAS per 1 L bacterial culture. In comparison, the final yield of the fully column-bound (non-acetylated) PAS-T $\alpha$ 1 reached 50 mg per 1 L bacterial culture after CEX chromatography and, again, the endotoxin content was below 0.1 EU/mg. Analytical size exclusion chromatography (SEC) of both PASylated peptide versions revealed a single symmetric peak without any signs of aggregation or truncation (Figures 2d and 3d). The N-terminally acetylated T $\alpha$ 1-PAS eluted at 13.5 mL (bed volume: 24 mL), whereas PAS-T $\alpha$ 1 eluted at 13.2 mL, thus indicating apparent molecular sizes of 557 kDa and 665 kDa, respectively. This is more than 10 times (T $\alpha$ 1-PAS) or even 12 times (PAS-T $\alpha$ 1) larger than the true molecular mass of both PASylated peptides (52.7 kDa), which demonstrates the huge expansion of the hydrodynamic molecular volume caused by the random-coil structure of the PAS polymer, in line with previous observations [35].



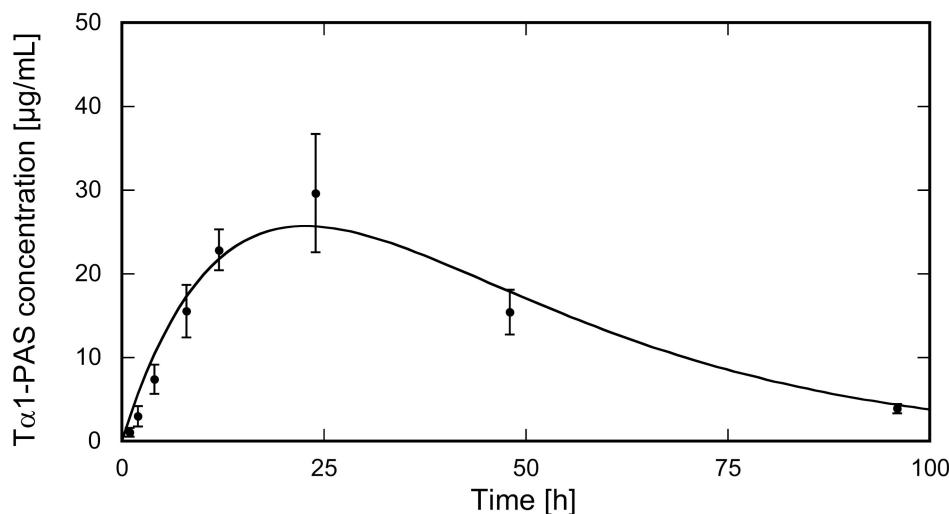
**Figure 2.** Analysis of T $\alpha$ 1-PAS N-acetylation, peptide purity, and hydrodynamic volume. **(a)** The deconvoluted ESI-MS spectrum of the T $\alpha$ 1-PAS flow-through fraction after the subtractive AEX step (see text) shows a molecular mass of 52,734.56 Da, corresponding to N-acetylated T $\alpha$ 1-PAS (calc. mass: 52,734.56 Da). **(b)** ESI-MS analysis of the bound and eluted peptide fraction from the same chromatography reveals a molecular mass of 52,692.37 Da, which matches the calculated mass of non-acetylated T $\alpha$ 1-PAS (52,692.54 Da). **(c)** Reverse-phase chromatography of the flow-through fraction indicates a purity > 96% for N-acetylated T $\alpha$ 1-PAS. **(d)** Analytical SEC of the finally purified T $\alpha$ 1-PAS in the presence of phosphate-buffered saline (PBS) results in a single peak with an elution volume of 13.5 mL. Comparison with a half-logarithmic calibration curve (inset) indicates an expanded hydrodynamic volume with an apparent molecular size of 557 kDa.



**Figure 3.** Preparation of an N-terminally PASylated version of the T $\alpha$ 1 peptide and analysis of its integrity, purity, and hydrodynamic volume. (a) Expression vector for the bacterial production of PAS-T $\alpha$ 1. The gene cassette cloned on pASK75 comprises the T7 RBS, the coding region for a 601-residue PAS#1 sequence preceded by a start methionine and a proline codon, the human T $\alpha$ 1 sequence, and, finally, t<sub>pp</sub>. (b) The deconvoluted ESI-MS spectrum of PAS-T $\alpha$ 1 purified from the *E. coli* cell extract by subtractive AEX and CEX (see text) reveals a molecular mass of 52,789.69 Da, which matches the calculated mass for PAS-T $\alpha$ 1 with a fully processed start methionine (52,789.66 Da). (c) Reverse-phase chromatography indicates a purity > 96% for PAS-T $\alpha$ 1. (d) Analytical SEC of the purified PAS-T $\alpha$ 1 in PBS results in a single peak with an elution volume of 13.2 mL. Comparison with a half-logarithmic calibration curve (inset) indicates a strongly expanded hydrodynamic volume with an apparent molecular size of 665 kDa.

### 2.3. PASylation Strongly Prolongs T $\alpha$ 1 Pharmacokinetics in Rats

To mimic the clinically approved route of Zadaxin™ administration, the N-acetylated T $\alpha$ 1-PAS was injected subcutaneously into the dorsal area of rats ( $N = 5$ ). The injected dose of 3.4 mg/kg T $\alpha$ 1-PAS was well tolerated without any drug-related adverse events or significant changes in body weight. The T $\alpha$ 1-PAS plasma levels at various sampling times were analyzed using a quantitative sandwich ELISA developed to detect only T $\alpha$ 1-PAS and no endogenous rat T $\alpha$ 1, which shares 100% sequence identity with the human peptide. The pharmacokinetic (PK) profile of T $\alpha$ 1-PAS (Figure 4) exhibited a typical curve according to the Bateman function [40], with a  $C_{\max}$  of  $25.6 \pm 4.4$  mg/L at  $t_{\max} = 22.7 \pm 1.1$  h. Curve fitting with the WinNonlin software revealed a drastically extended terminal half-life of  $15.9 \pm 0.9$  h, which is more than 8-fold longer than the one for the native peptide ( $\tau_{1/2} = 1.9$  h) published for rats [41]. The strong impact of PASylation on the PK profile is also reflected by other parameters such as the large area under the curve (AUC) and slow clearance (CL) (Table 1).



**Figure 4.** PK study of N-acetylated T $\alpha$ 1-PAS in rats. T $\alpha$ 1-PAS was subcutaneously injected at a dose of 3.4 mg/kg b.w. into female Wistar rats ( $N = 5$ ). The concentration of the fusion protein in plasma was quantified using sandwich ELISA. Data were plotted against the sampling time post injection (p.i.) and fitted using a one-compartment model. The PK profile shows distinct absorption and elimination phases (for PK parameters, see Table 1).

**Table 1.** Pharmacokinetic properties of T $\alpha$ 1-PAS in rats.

Parameter	T $\alpha$ 1-PAS
$C_{\max}$ (mg/L)	$25.6 \pm 4.4$
$t_{\max}$ (h)	$22.7 \pm 1.1$
$AUC_{0-\infty}$ (h $\mu$ g/mL)	$1586.7 \pm 295.1$
$\tau_{1/2\alpha}$ (h)	$15.7 \pm 0.8$
$\tau_{1/2\beta}$ (h)	$15.9 \pm 0.9$
CL (mL/h/kg)	$2.2 \pm 0.4$

### 3. Discussion

The present data demonstrate that the PASylation technology can solve two major problems of a peptide drug: (i) instability in the expression host and (ii) low bioactivity due to fast renal clearance. Typically, small peptides, if expressed in a soluble state in *E. coli*, are quickly degraded by host cell proteases [42] and, thus, require production as larger fusion proteins as well as subsequent release by site-specific cleavage in vitro. Here, fusion with a random-coil forming PAS sequence of ~600 amino acids prevented proteolytic degradation

and allowed cost-efficient one-step production of the intact fusion protein in *E. coli* without the need of additional processing steps.

Of note, in contrast to classical approaches, which involve the use of an insoluble fusion partner, for example, an  $\alpha$ -galactosidase fragment in the case of insulin [43], to provoke formation of inclusion bodies and protect the gene product from intracellular proteolysis, the PASylated T $\alpha$ 1 peptide was recovered as a soluble fusion protein, thus allowing direct purification from the cell extract without solubilization steps. Furthermore, the C-terminally attached PAS moiety was compatible with N-terminal acetylation by RimJ as confirmed by ESI-MS. Yields of our expression study at the research scale reached 15 mg purified acetylated T $\alpha$ 1-PAS and even 50 mg PAS-T $\alpha$ 1 per 1 L bacterial culture (at an optical density (OD) of 3), which surpasses the reported yield of a bacterially produced (yet probably non-acetylated and non-glycosylated) T $\alpha$ 1-Fc fusion protein (16 mg/L) [44].

Still, there is considerable opportunity of improvement for both versions of the PASylated peptide by optimizing the expression plasmid and the production process, including high cell density fermentation under controlled feeding conditions. Apart from that, the absence of a prominent band for the co-expressed enzyme RimJ in SDS-PAGE despite approximately 50% N-terminal acetylation of T $\alpha$ 1-PAS also indicates room for amelioration. Optimization of the ribosome-binding site preceding the RimJ cistron or changing the order within the bicistronic operon should boost biosynthesis of the enzyme and result in increased yield of the N-terminally acetylated T $\alpha$ 1-PAS. Finally, the use of a high-efficiency secretory bacterial expression system such as ESETEC [45] or CORYNEX [46,47] should lead to higher product titers as previously demonstrated for other PASylated fusion proteins such as PASylated human growth hormone (hGH) [48]. The yield of functional PAS-hGH was more than 100-fold higher with the ESETEC system than in a conventional laboratory strain of *E. coli*, reaching several grams per liter culture.

Attachment of the PAS sequence at either end of the T $\alpha$ 1 peptide increased the hydrodynamic volume by more than an order of magnitude as shown by SEC. This strongly expanded molecular size resulted in a plasma half-life in rats of around 16 h after a subcutaneous injection of T $\alpha$ 1-PAS, which is more than an 8-fold increase compared to the unmodified peptide drug (1.9 h) [41]. Based on in vitro cell culture assays with human serum albumin fusion proteins [49], both the C-terminus and the N-terminus of T $\alpha$ 1 should be permissible to modification while retaining bioactivity. This was also shown in animal tumor models for C-terminal fusion with an immunoglobulin Fc fragment [41], an internalizing arginylglycylaspartic acid peptide iRGD [50], and thymopentin [51]. However, in the case of T $\alpha$ 1, some caution is appropriate regarding the significance of in vitro cell culture assays as its mode of action is complex and involves different receptors provoking multiple biological effects on various cell types [52]. Second, a prolonged circulation in the body as demonstrated here via application of the PASylation technology influences both binding kinetics and bioactivity, which is not reflected in vitro. While attachment of large macromolecules, such as PAS polypeptides or albumin, but also PEG [53], can lead to lower receptor association rates for bioactive peptides or proteins, this is usually overcompensated by the drastically prolonged in vivo half-life, which results in a strongly enhanced bioactivity as demonstrated for multiple PASylated biopharmaceuticals [37,54]. In the case of T $\alpha$ 1, superior effects in preclinical cancer models due to prolonged circulation were recently demonstrated for a T $\alpha$ 1-Fc fusion protein [41,44]. Such studies would be the obvious next step to investigate enhanced in vivo bioactivity of PASylated T $\alpha$ 1, and it will be interesting to see whether its N-terminally or C-terminally PASylated version performs better.

In comparison with other published approaches to prolong the circulation of T $\alpha$ 1, the measured terminal half-life of T $\alpha$ 1-PAS is even longer than the value of around 8.2 h reported for a corresponding PEGylated peptide after an intravenous injection into the tail vein of Sprague–Dawley rats [55]. This modified T $\alpha$ 1 was prepared by chemically coupling a 5 kDa methoxypolyethylene glycol maleimide via an engineered N-terminal Cys residue. Of note, according to the rules of allometric scaling, a much longer half-life in

the range of several days can be expected for T $\alpha$ 1-PAS in humans [56,57], which would allow weekly dosing while achieving a lasting pharmacological effect. According to the prescription information for Zadaxin<sup>TM</sup> to treat chronic hepatitis B, the recommended dose for the monotherapy, or the combination therapy with interferon, is a 1.6 mg subcutaneous injection twice weekly over 6 months (52 doses). Consequently, weekly or biweekly injections would considerably decrease patient burden and improve compliance.

Moreover, a more continuous plasma level above the minimum effective dose due to slower clearance, as illustrated by the drastically increased AUC, should boost in vivo efficacy and open new treatment perspectives. Especially in preclinical animal models, which typically suffer from a much quicker drug clearance compared to humans [37] owing to their smaller body size, a long-acting T $\alpha$ 1 should lead to more convincing pharmacodynamic (PD) effects and pave the way for biopharmaceutical development for novel indications such as cystic fibrosis [18], HIV-1 infection [58], sepsis [20], or cancer [59]. For example, cancer studies have demonstrated that high doses of the conventional peptide are required to achieve antitumor activity [60].

The beneficial application of the PASylation technology demonstrated in this work can be transferred to other peptides. There are more than 7000 naturally occurring peptides covering a wide range of physiological functions [61], including many peptides with proven therapeutic potential, which could profit from the presented approach. Examples are therapeutically active peptides such as thymosin beta 4 [62,63], the C-type natriuretic peptide (CNP) [64], human parathyroid hormone (PTH) [65], relaxin [66], or glucagon-like peptide-1 (GLP-1) and its analogs [67]. Today, it is generally recognized that intrinsic weaknesses of this drug class, such as poor stability and short circulating plasma half-life, need to be addressed in order to transform peptides into efficacious medicines [61]. The approach described here, N- or C-terminal PASylation, optionally combined with acetylation, solves both. On the one hand, N-terminal acetylation protects peptides from proteolytic degradation by exoproteases, for example, dipeptidyl peptidase-4 (DPP-IV), as shown for N-terminally acetylated GLP-1 [68]. On the other hand, PASylation increases the hydrodynamic volume of the peptide above the pore size of the glomerular basement membrane, hence retarding kidney filtration and prolonging the pharmacodynamic effect of its fusion partner [31].

Furthermore, PASylation can serve as a linker to join two peptides [69]. This is of particular interest if both entities act synergistically, for example, GLP-1 and GIP [70] or T $\alpha$ 1 and GM-CSF [71]. Alternatively, the biologically active protein/peptide can be linked via the PAS sequence to a targeting domain such as the arginylglycylaspartic acid peptide RGD peptide which binds to integrins  $\alpha$ V $\beta$ 3 and  $\alpha$ V $\beta$ 5 in order to enhance tumor penetration and accumulation. In fact, fusion of the short-acting T $\alpha$ 1 with the tumor-targeting iRGD peptide using a Gly<sub>4</sub> linker has recently demonstrated enhanced antitumor activity [50]. In contrast to synthetic PEG linkers, which are commonly used for bioconjugations, the recombinant PAS sequence exhibits a precisely defined size and is biodegradable [72]. The PAS polypeptide itself is stable in blood plasma but quickly degraded by intracellular enzymes, thus avoiding organ accumulation [31], a well-known effect for PEGylation [73]. Moreover, PAS sequences are non-immunogenic in animals [31,74] and offer a one-step production of PASylated peptides in various commercially scalable expression systems including bacteria, yeasts, or mammalian cells [35,48], which would even allow the preparation of peptides carrying posttranslational modifications.

## 4. Materials and Methods

### 4.1. Construction of the Expression Plasmid

A bicistronic operon for the simultaneous expression of human T $\alpha$ 1 (UniProt P06454, residues 2–29) and the *E. coli* N-acetyltransferase RimJ (UniProt P0A948) flanked by the restriction sites *Nde*I and *Hind*III was prepared using gene synthesis (Thermofisher Scientific, Regensburg, Germany). To this end, the coding sequence of human T $\alpha$ 1 was codon-optimized for expression in *E. coli* and linked to the RimJ structural gene via the nu-

codon sequence GCCTGAAGAGCAGAAAATAAA comprising a “GCC” alanine codon, the opal stop codon “TGA”, a *SapI* restriction site for insertion of the PAS gene cassette, and a ribosome-binding site (RBS). The entire gene fragment was subcloned via *NdeI* and *HindIII* on a derivative of pASK75 [36] for cytoplasmic expression under control of the tetracycline promoter/operator (*tet*<sup>P/O</sup>). Subsequently, a substantially non-repetitive sequence-verified PAS gene cassette [34] encoding a PAS#1 polypeptide of 601 amino acids was inserted via the *SapI* restriction site to create the expression vector for the C-terminally PASylated thymosin  $\alpha$ 1 (T $\alpha$ 1-PAS), pASK75-T $\alpha$ 1-PAS#1(600)/RimJ. To construct a plasmid for the bacterial production of an N-terminally PASylated T $\alpha$ 1 (PAS-T $\alpha$ 1), the synthetic gene of human T $\alpha$ 1 was amplified via PCR using the primers THY-For (5'-AGCTCTCTGCCAGTGATGCAGCAGTTGATACC) and THY-Rev (5'-GCTCAAGCTTAG TTCTCGGCTTCCAC). The PCR product was digested with *SapI* and *HindIII* and inserted via these restriction sites downstream of the PAS#1(600) sequence preceded by Met and Pro encoded on a suitable pASK75 plasmid derivative.

#### 4.2. Bacterial Production of Recombinant PASylated T $\alpha$ 1

The BL21 derivative *E. coli* strain NEBexpress® (New England Biolabs, Frankfurt am Main, Germany) was transformed with the plasmids pASK75-T $\alpha$ 1-PAS#1(600)/RimJ or pASK75-MP-PAS#1(600)-T $\alpha$ 1 from above. Two milliliters of Terrific Broth supplemented with 100  $\mu$ g/mL ampicillin (TB<sub>amp</sub>) was inoculated with a single colony and grown overnight at 37 °C, 170 rpm. This overnight culture was used to inoculate a 50 mL preculture, which was grown under the same conditions until OD<sub>550</sub> = 1.1 was reached. Subsequently, the 50 mL preculture was transferred into 2 L TB<sub>amp</sub> and incubated in a 5 L baffled flask at 37 °C and 100 rpm. After reaching OD<sub>550</sub> = 0.6, the temperature was decreased to 26 °C and the cells were subsequently induced at OD<sub>550</sub> = 1 with 200  $\mu$ g/mL aTc for 15 h.

#### 4.3. Purification of PASylated T $\alpha$ 1

Bacteria were harvested by centrifugation and disrupted in the presence of 100 mM citric acid using an EmuliFlex C5 cell homogenizer (Avestin, Mannheim, Germany). After centrifugation for 20 min (39,200  $\times$  g) at 16 °C, the supernatant was filter-sterilized using a 0.45  $\mu$ m syringe filter (Sartorius, Göttingen, Germany). The clear filtrate was adjusted with ammonium sulfate to 30% saturation, stirred for 30 min at RT, and centrifuged for 30 min (39,200  $\times$  g) at RT. The precipitate was solubilized in subtractive AEX buffer (sAEX; 20 mM Tris/HCl, 1 mM EDTA, pH 8.5), filter-sterilized, and dialyzed twice against a 100-fold volume of sAEX buffer at 4 °C. Subsequent chromatography steps were performed on an ÄKTA Explorer 100 system (GE Healthcare, Freiburg, Germany) operated at a flow rate of 5 mL/min. The dialyzed sample (T $\alpha$ 1-PAS or PAS-T $\alpha$ 1) was first applied to a 5 mL TOYOPEARL NH2-750F column (Tosoh Bioscience, Griesheim, Germany) equilibrated with the sAEX buffer. The flow-through containing the PASylated T $\alpha$ 1 was collected and dialyzed twice against a 100-fold volume of the CEX buffer (20 mM Na-citrate, pH 3.0) at 4 °C. The protein solution was then applied to an 85 mL TOYOPEARL Sulfate-650F column (Tosoh Bioscience) equilibrated with the CEX buffer. PAS-T $\alpha$ 1 quantitatively bound to the column and the pure protein was eluted using a NaCl concentration gradient (0–250 mM over 2 column volumes). In the case of T $\alpha$ 1-PAS, the CEX flow-through fraction contained the N-terminally acetylated protein, whereas the non-acetylated T $\alpha$ 1-PAS stayed bound to the column and could again be eluted in a NaCl concentration gradient. The acetylated T $\alpha$ 1-PAS fraction from the flow-through was dialyzed twice against AEX buffer (20 mM ethanolamine/HCl, pH 10) and then applied to a 100 mL Fractogel® EMD TMAE (M)strong anion exchanger (Merck Millipore, Burlington, MA, USA) equilibrated with the AEX buffer. This time, highly pure acetylated T $\alpha$ 1-PAS was eluted using a NaCl concentration gradient (0–200 mM over 2 column volumes) in the AEX buffer. Both purified PASylated peptides were dialyzed 5 times against a 200-fold volume of water, lyophilized, and stored at –20 °C until further use.

#### 4.4. Analytical Size Exclusion Chromatography

Analytical SEC was performed on a 24 mL Superose<sup>®</sup> 6 10/300 GL column (GE Healthcare) using an AKTA Explorer 10 system operated at a flow rate of 0.5 mL/min with PBS as the running buffer. To determine the apparent molecular size, purified PAS-T $\alpha$ 1 or PAS-T $\alpha$ 1 (100  $\mu$ L) was applied to the column and the elution volume was used for linear interpolation from a half-logarithmic calibration line obtained using the reference proteins thyroglobulin (octamer), thyroglobulin (tetramer), apoferritin,  $\beta$ -amylase, alcohol dehydrogenase (tetramer), transferrin, ovalbumin, and carboanhydrase as well as blue dextran (all from Merck, Darmstadt, Germany).

#### 4.5. Endotoxin Quantification

T $\alpha$ 1-PAS samples were diluted to 1 mg/mL in endotoxin-free water (Veolia Water Technologies, Celle, Germany), heated to 90 °C for 5 min, and, after cooling down to RT, bacterial endotoxins were quantified using an Endosafe<sup>®</sup> system (Charles River Laboratories, Wilmington, MA, USA) with an FDA-licensed PTS<sup>TM</sup> cartridge (10–0.1 EU/mL sensitivity).

#### 4.6. Western Blot Analysis

The whole cell protein extract was applied to a 4–12% SurePAGE<sup>TM</sup> Bis–Tris gradient gel (Genscript, Piscataway, NJ, USA) with 3-(N-morpholino)propanesulfonic acid (MOPS) as running buffer and electrotransferred onto a nitrocellulose membrane using an iBlot 1 dry blotting system (ThermoFisher, Waltham, MA, USA). After washing 3 times with PBS supplemented with 0.1% v/v Tween 20 (PBS/T), the membrane was incubated with 1  $\mu$ g/mL anti-PAS antibody in PBS/T for 1 h at RT. The membrane was washed 3 times with PBS/T and incubated with a 1:5000 dilution of a goat anti-mouse IgG (Fc-specific) alkaline phosphatase (AP) conjugate (Merck) for 1 h. After washing twice with PBS/T and twice with PBS, the blot was developed by a chromogenic reaction using BCIP (37.5  $\mu$ g/mL) and NBT (150  $\mu$ g/mL) in alkaline phosphatase buffer (100 mM Tris/HCl, pH 8.8, 100 mM NaCl, 5 mM MgCl<sub>2</sub>).

#### 4.7. Reverse-Phase Chromatography (RPC) and ESI Mass Spectrometry

Directly after the CEX chromatography, a 200  $\mu$ L sample of PAS-T $\alpha$ 1 or PAS-T $\alpha$ 1 was adjusted to 2% v/v acetonitrile, 0.1% v/v formic acid and applied to a Resource RPC 1 mL column (GE Healthcare) equilibrated with 2% v/v acetonitrile, 0.1% v/v formic acid. The protein was eluted using a concentration gradient of up to 80% v/v acetonitrile, 0.1% v/v formic acid over 20 column volumes at a flow rate of 2 mL/min while spectrophotometrically monitoring protein elution at 225 nm. The eluted protein fraction was directly injected into a maXis quadrupole time of flight (Q-TOF) instrument (Bruker Daltonics, Bremen, Germany) operated in the positive ion mode. Raw data was deconvoluted using the MaxEntX algorithm (Bruker Daltonics).

#### 4.8. Pharmacokinetic Analysis in Rats

A PK study in female Wistar rats at 8–9 weeks of age was conducted at the Aurigon Toxicological Research Center (ATRC, Dunakeszi, Hungary). Up to 3 animals per cage were housed in a controlled environment at 22 ± 3 °C with a relative humidity of 50 ± 20%, 12 h light and 12 h dark. Endotoxin-free purified T $\alpha$ 1-PAS (3.4 mg/kg) was administered subcutaneously via a single injection into the rat dorsal area. Blood samples (100  $\mu$ L) were taken from 5 animals each at various time points. Following collection in tubes containing tri-potassium ethylenediaminetetraacetic acid (K3-EDTA) (Greiner Bio-One, Frickenhausen, Germany), samples were centrifuged at room temperature for 10 min (3000× g) and the resulting plasma was stored at –15 to –30 °C. T $\alpha$ 1-PAS in these samples was quantified using sandwich ELISA (see below) and the data were analyzed using the Phoenix WinNonlin 6.3 software (Certara, Princeton, NJ, USA) using a one-compartment model assuming 1st order absorption and elimination.

#### 4.9. Quantification of Purified $T\alpha 1$ -PAS

Due to the absence of aromatic side chains, PASylated  $T\alpha 1$  does not absorb light at 280 nm. Thus, for reliable quantification via the peptide backbone absorption, an extinction coefficient at 225 nm was determined. To this end, highly pure  $T\alpha 1$ -PAS was lyophilized from water, weighed, and dissolved in a defined volume of water. The concentration of this  $T\alpha 1$ -PAS solution was additionally quantified by measuring the backbone peptide groups using UV absorption at 205 nm using a generic calculated extinction coefficient [75], which led to a fair agreement ( $\pm 6\%$ ). The absorbance at 225 nm was measured for various dilutions of the gravimetrically prepared peptide stock solution and plotted against the concentration. The linear range was fitted by a straight line, resulting in an extinction coefficient of  $253,057 \text{ M}^{-1} \cdot \text{cm}^{-1}$ . While most buffers strongly absorb light at 205 nm, such a spectral overlap is usually absent at 225 nm.

#### 4.10. ELISA Quantification of PASylated $T\alpha 1$

A 96-well Nunc Maxisorb ELISA plate (ThermoFisher) was coated with  $100 \mu\text{g}/\text{mL}$  anti-PAS antibody in PBS at  $4^\circ\text{C}$  overnight. After washing twice with PBS/T, free binding sites were blocked with  $3\% \text{ w/v}$  bovine serum albumin (BSA) in PBS/T at room temperature for 1 h. After washing 3 times with PBS/T, the rat plasma samples were applied in dilution series in PBS/T supplemented with  $0.5\% \text{ (v/v)}$  plasma from an untreated animal (to maintain a constant proportion of rat plasma constituents). In the same manner, a standard curve was prepared using dilution series of purified  $T\alpha 1$ -PAS (used for spiking rat plasma) at defined concentrations. After incubation for 1 h at RT, wells were washed 3 times with PBS/T. To detect bound  $T\alpha 1$ -PAS, wells were incubated for 1 h with  $50 \mu\text{l}$  of a  $1 \mu\text{g}/\text{mL}$  PBS/T solution of the second anti-PAS antibody conjugated with alkaline phosphatase using the Lightning-Link alkaline phosphatase antibody labeling kit (BioTechne, Wiesbaden, Germany). After washing twice with PBS/T and twice with PBS, the enzymatic activity was detected using p-nitrophenyl phosphate ( $0.5 \text{ mg}/\text{mL}$ ). To this end, the plate was incubated for 20 min at  $30^\circ\text{C}$ , the absorbance was measured at 405 nm using a SpectraMax M5e microtiter plate reader (Molecular Devices, Sunnyvale, CA, USA) and the  $T\alpha 1$ -PAS concentrations in rat plasma samples were quantified by comparison with the standard curve.

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## Abbreviations

AEX	Anion exchange
AP	Alkaline phosphatase
aTc	Anhydrotetracycline hydrochloride
AUC	Area under the curve
BCIP	5-Bromo-4-chloro-3-indoxyl phosphate
BSA	Bovine serum albumin
CEX	Cation exchange
CL	Clearance
C <sub>max</sub>	Maximum (or peak) serum concentration
CNP	C-type natriuretic peptide
CORYNEX	<i>Corynebacterium glutamicum</i> protein expression system
COVID-19	Severe acute respiratory syndrome coronavirus 2
CTLA-4	Cytotoxic T-lymphocyte-associated protein 4
CV	Column volume
DCs	Dendritic cells
DPP-IV	Dipeptidyl peptidase-4
ELISA	Enzyme-linked immunosorbent assay
ESETEC	<i>E. coli</i> secretion technology
ESI-MS	Electrospray ionization mass spectrometry
FPLC	Fast protein liquid chromatography
GCC	Glucagon
GIP	Glucose-dependent insulinotropic polypeptide
GLP-1	Glucagon-like peptide 1
GM-CSF	Granulocyte-macrophage colony-stimulating factor
GSH	γ-L-Glutamyl-L-cysteinyl-glycine
HBV	Hepatitis B virus
HCV	Hepatitis C virus
hGH	Human growth hormone
hIFN-α	Human interferon 1
HIV-1	Human immunodeficiency virus I
iRGD	Internalizing arginylglycylaspartic acid peptide
K3-EDTA	Tri-potassium ethylenediaminetetraacetic acid
MHC	Major histocompatibility complex
MOPS	3-(N-morpholino)propanesulfonic acid
NBT	Nitro blue tetrazolium
OD	Optical density at 550 nm
PAS	Proline/alanine-rich sequence
PAS-T $\alpha$ 1	N-terminally PASylated T $\alpha$ 1
PBS	Phosphate-buffered saline
PD	Pharmacodynamics
PEG	Polyethylene glycol
p.i.	Post injection
PK	Pharmacokinetics
ProT $\alpha$	Prothymosin alpha
PTH	Parathyroid hormone
Q-TOF	Quadrupole time of flight
RBS	Ribosome-binding site
RGD	Arginylglycylaspartic acid
RimJ	Ribosomal-protein-S5-alanine N-acetyltransferase
RPC	Reverse phase chromatography
RT	Room temperature
SEC	Size exclusion chromatography
SDS-PAGE	Sodium dodecyl sulfate polyacrylamide gel electrophoresis

$\tau_{1/2\alpha}$	Half-life of distribution
$\tau_{1/2\beta}$	Elimination half-life
T $\alpha$ 1	Thymosin alpha 1
T $\alpha$ 1-PAS	C-terminally PASylated Thymosin alpha 1
tet <sup>p/o</sup>	Tetracycline promoter/operator
Th	T helper cell
t <sub>lpp</sub>	Lipoprotein terminator
TLR-2	Toll-like receptor 1
TLR-9	Toll-like receptor 2
TMAE	Trimethylaminoethyl
t <sub>max</sub>	Time to reach C <sub>max</sub>

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