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A BIFUNCTIONAL SEA ANEMONE PEPTIDE WITH KUNITZ TYPE PROTEASE AND POTASSIUM CHANNEL INHIBITING PROPERTIES.

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Abstract Sea anemone venom is a known source of interesting bioactive compounds, including peptide toxins which are invaluable tools for studying structure and function of voltage-gated potassium channels. APEKTx1 is a novel peptide isolated from the sea anemone *Anthopleura elegantissima*, containing 63 amino acids cross-linked by 3 disulfide bridges. Sequence alignment reveals that APEKTx1 is a new member of the type 2 sea anemone peptides targeting voltage-gated potassium channels (K_V's), which also include the kalicludines from *Anemonia sulcata*. Similar to the kalicludines, APEKTx1 shares structural homology with both the basic pancreatic trypsin inhibitor (BPTI), a very potent Kunitz-type protease inhibitor, and dendrotoxins which are powerful blockers of voltage-gated potassium channels. In this study, APEKTx1 has been subjected to a screening on a wide range of 23 ion channels expressed in *Xenopus leavis* oocytes: 13 cloned voltage-gated potassium channels (K_V1.1-K_V1.6, K_V1.1 triple mutant, K_V2.1, K_V3.1, K_V4.2, K_V4.3, hERG, the insect channel *Shaker* IR), 2 cloned hyperpolarization-activated cyclic nucleotide-sensitive cation non-selective channels (HCN1 and HCN2) and 8 cloned voltage-gated sodium channels (Na_V1.2-Na_V1.8 and the insect channel $DmNa_V$1). Our data shows that APEKTx1 selectively blocks K_V1.1 channels in a very potent manner with an IC_{50} value of 0.9 nM. Furthermore, we compared the trypsin inhibitory activity of this toxin with BPTI. APEKTx1 inhibits trypsin with a dissociation constant of 124 nM. In conclusion, this study demonstrates that APEKTx1 has the unique feature to combine the dual functionality of a potent and selective blocker of K_V1.1 channels with that of a competitive inhibitor of trypsin.

Keywords *Anthopleura elegantissima* · K_V channel inhibitor · sea anemone toxin · protease inhibitor ·

1. Introduction

Among ion channels, potassium channels are the most diverse class of ion channels and they are key determinants of neuronal excitability. They regulate a variety of cellular processes and functions such as heart rate, neurotransmitter release and nerve conduction, insulin secretion, blood pressure and muscle contraction [1,2] . In the mammalian genome more than 100 genes are encoding the pore forming α subunits and auxiliary β subunits of K^+ channels. Together with these numerous genes, the presence of spliced variants, association with chaperone and scaffolding molecules and the formation of heteromultimeric channels contribute greatly to the diversity of the K^+ channel family [2]. This family has been divided into 15 subfamilies of which the voltage gated potassium channels (K_V) represent one of these subfamilies [3]. They determine neuronal intrinsic electrical excitability by repolarization of the membrane after initiation of the action potential [4]. Upon depolarization of the membrane, K_V channels will open within 1 ms, allowing the flux of K^+ ions driven by their electrochemical gradient [1,2]. Functional K_V channels are formed by a complex of four pore forming α subunits associated with one or

more auxiliary β subunits. Each α subunit consists of six transmembrane spanning segments (S1-S6). The first four transmembrane segments form the voltage sensing domain with S4 serving as the voltage sensor. This S4 segment has been modeled using the crystal structure of the bacterial K_V channel K_VAP and contains 4 conserved Arg residues. These positively charged basic residues display a net movement outwards upon depolarization allowing conformational changes resulting in the opening of the pore [5,6]. The pore region of the channels is formed by the S5 and S6 segments which are connected by a re-entrant P-loop. The P-loop contains an extremely well conserved domain among the K_V channels, the so-called signature sequence (-TXGYGD-) and comprises the selectivity filter, the pore helix and the turret region [7]. The auxiliary β subunits of K_V channels (K_Vβ) are cytoplasmic proteins, capable of modifying K_V channel biophysical properties.

Since the beginning of last century sea anemones have been studied with an increasing interest. Although a number of sea anemone toxins have been isolated and characterized, these animals remain poorly studied in comparison with other venomous animals such as scorpions, spiders, cone snails or snakes. Sea anemones are a known pharmacological treasure of biological active compounds acting upon a diverse panel of ion channels such as TRPV1, voltage-gated sodium and potassium channels [8-11]. Of these different toxins those that target sodium channels are the best studied group with more then 100 known toxins [12]. In contrast, no more then 12 potassium channel toxins have been characterized to date. Based on structural differences and activity profile, these potassium channel toxins can be divided into 4 structural classes [11,13-15]. Up to date 6 toxins from *A. eleg*antissima have been isolated and characterized: APE1-1, APE1-2, APE2-2 and ApC which are type 1 sodium channel toxins; APETx1 a selective modifier of the human ether a go-go related gene K^+ channel (hERG) and APETx2 which specifically inhibits the Acid Sensing Ion Channel (ASIC3) [15-18]. In this work we present the purification, biochemical analysis and electrophysiological characterization of a very potent and selective K_V1.1 blocker which represents the newest member of the sea anemone type 2 potassium channel toxins.

2. Material and methods

2.1. Toxin purification.

The toxin APEKTx1 was purified as described previously [16,17,19]. The fraction containing APEKTx1 was further purificated by RP-HPLC with a semi preparative Vydac C18 column (4.6X250 mm). Solvent A was 0.1% TFA in water, solvent B was 0.085% TFA in acetonitrile. A linear gradient from 0 to 80% solution B was developed for 80 min at a flow rate of 1ml/min. A second purification was performed in the same conditions as described above. All final fractions were dried by speed-vac evaporation and stored at -20°C.

2.2. Biochemical characterization of toxins.

The mass of the intact toxin was measured by MALDI-TOF (4800 Analyzer, Applied Biosystems, USA) as well as by ESI-QUAD analysis (4000QTRAP, Applied Biosystems, USA).

The toxin peptide was subjected to Edman degradation on an Applied Biosystems Procise instrument. The toxin was digested with legumain (R&D Systems, USA). A MALDI TOF/TOF instrument (4800 Analyzer, Applied Biosystems, USA) was used for *de novo* sequencing analysis of the obtained fragments. These fragments were subjected to MS/MS analysis and the spectra were manually interpreted.

2.3. Expression of voltage-gated ion channels in Xenopus laevis oocytes.

For the expression of the VGPCs (rK_V1.1 (Accesion number: NM173095), rK_V1.2 (NM012970), hK_V1.3 (L23499), rK_V1.4 (NM012971), rK_V1.5 (NM012972), rK_V1.6 (NM575671), Shaker IR (CG12348), rK_V2.1 (NM013186), hK_V3.1 (NM004976), rK_V4.2 (NM031730), rK_V4.3 (NM031739), hERG (NM000238), mHCN 1 (NM010408), mHCN 2 (NM008226) and the VGSCs (rNa_V1.2 (NM012647),

rNa$_V$1.3 (NM012647), rNa$_V$1.4 (M26643), hNa$_V$1.5 (NM198056), mNa$_V$1.6 (L39018), rNa$_V$1.7 (AF000368), rNa$_V$1.8 (NM017247), rβ1 (NM017288), hβ1 (NM001037) and the insect channel DmNa$_V$1 (NC004354)) in *Xenopus* oocytes, the linearized plasmids were transcribed using the T7 or SP6 mMESSAGE-mMACHINE transcription kit (Ambion, USA). The harvesting of stage V-VI oocytes from anaesthetized female *Xenopus laevis* frog was previously described [20]. Oocytes were injected with 50 nl of cRNA at a concentration of 1 ng/nl using a micro-injector (Drummond Scientific, USA). The oocytes were incubated in a solution containing (in mM): NaCl, 96; KCl, 2; $CaCl_2$, 1.8; $MgCl_2$, 2 and HEPES, 5 (pH 7.4), supplemented with 50 mg/l gentamycin sulfate.

2.4. Electrophysiological recordings.

Two-electrode voltage-clamp recordings were performed at room temperature (18-22°C) using a Geneclamp 500 amplifier (Molecular Devices, USA) controlled by a pClamp data acquisition system (Axon Instruments, USA). Whole cell currents from oocytes were recorded 1-4 days after injection. Bath solution composition was ND96 (in mM): NaCl, 96; KCl, 2; $CaCl_2$, 1.8; $MgCl_2$, 2 and HEPES, 5 (pH 7.4) or HK (in mM): NaCl, 2; KCl, 96; $CaCl_2$, 1.8; $MgCl_2$, 2 and HEPES, 5 (pH 7.4). Voltage and current electrodes were filled with 3M KCl. Resistances of both electrodes were kept between 0.5-1.5 MΩ. The elicited currents were filtered at 1 kHz and sampled at 0.5 kHz (for potassium currents) or at 20 kHz (for sodium currents) using a four-pole low-pass Bessel filter. Leak subtraction was performed using a -P/4 protocol. K$_V$1.1-K$_V$1.6 and *Shaker* currents were evoked by 500 ms depolarizations to 0 mV followed by a 500 ms pulse to -50 mV, from a holding potential of -90 mV. Current traces of hERG channels were elicited by applying a +40 mV prepulse for 2 s followed by a step to -120 mV for 2 s. K$_V$2.1, K$_V$3.1 and K$_V$4.2, K$_V$4.3 currents were elicited by 500 ms pulses to +20mV from a holding potential of -90 mV. Sodium current traces were, from a holding potential of -90 mV, evoked by 100 ms depolariarions to V_{max} (the voltage corresponding to maximal sodium current in control conditions). In order to investigate the current-voltage relationship, current traces were evoked by 10 mV depolarization steps from a holding potential of -90 mV. gV curves were calculated from IV relationships as follows: $g_K=I_K/(E_m - E_K)$ with $E_k= (RT/zF)\ln[K\ \#0]_o/[K\ \#0]_i$. In these equations g_K represents the conductance, I_K the potassium current, E_m the membrane potential, E_K the reversal potential, R the gas constant (8.31 J/K.mol), T the temperature, z the charge of the ion (for K^+ ions: z = 1), F the Faraday's constant (96.500 C/mol), $[K\ \#0]_o$ and $[K\ \#0]_I$ respectively are the extracellular and intracellular K^+ ion concentrations. The values of I_K or g_K were plotted as function of voltage and fitted using the Boltzmann equation: $g_K/g_{max} = [1 + (\exp(Vg - V)/k]^{-1}$, were gmax represents maximal gK, Vg is the voltage corresponding to half-maximal conductance, and k is the slope factor. To assess the concentration dependency of the APEKTx1 induced inhibitory effects, a concentration-response curve was constructed, in which the percentage of current inhibition was plotted as a function of toxin concentration. Data were fitted with the Hill equation: $y = 100/[1 +(IC_{50}/[toxin])^h]$, were y is the amplitude of the toxin-induced effect, IC_{50} is the toxin concentration at half-maximal efficacy, [toxin] is the toxin concentration, and h is the Hill coefficient. To investigate the bimolecular kinetics of toxin inhibition, oocytes expressing wild type K$_V$1.1 channels were depolarized to o mV for 0.5 s from a holding potential of -90 mV every 5 s, both in the absence and presence of different concentrations of toxin. The obtained current values were plotted as a function of time. Data were fitted with the following exponential equation: $y = Ae^{-t/\tau}$, where t represents the time, A is the amplitude of the current and τ is the time constant for toxin binding (τ_{on}) or toxin unbinding (τ_{off}). The first-order association rate constant (k_{on}) was calculated using following equation: $\tau_{on} = (k_{on} + k_{off})^{-1}$. The first-order dissociation constant (k_{off}) was calculated using the equation: $\tau_{off} = k_{off}^{-1}$. Comparison of two sample means was made using a paired Student's t test ($p < 0.05$). All data represent at least 3 independent experiments ($n \geq 3$) and are presented as mean ± standard error.

2.5. Kunitz-type inhibition activity.

The possible trypsin inhibition activity of APEKTx1 was measured spectrophotometrically as described previosly [21]. Briefly, aliquots containing a final concentration of 3 µM trypsin (from bovine pancreas, TPCK treated, Sigma-Aldrich, USA) were incubated with various concentrations of peptides in 5 mM $CaCl_2$ and 50 nM Tris-HCl, pH 7.8. After incubation for 3 h at 25°C the remaining trypsin activity was determined by addition of 5 µl of a 5 mM Nα-benzoyl-DL-arginine p-nitroanilide (BAPNA, Sigma-Aldrich,USA). Paranitroanaline release was measured at 405 nm.

2.6. Molecular modeling.

APEKTx1 was modeled using the publicly available program MODELLER9v8 (http://www.salilab.org/modeller) using textilinin-1, a Kunitz-type serine protease inhibitor from the venom of the Australian common brown snake *Pseudonaja textilis* (PDB code 3BYB; http://www.pdb.org/pdb) as template.

3. Results

3.1. Purification of APEKTx1.

The screening of fractions obtained from the sea anemone A. *elegantissima*, after anion and cation exchange and gel filtration, yielded one fraction which was able to fully block $K_V1.1$ channels. This fraction was further purified in 2 steps using reversed-phase HPLC. A linear gradient from 0 to 80% solution B was developed for 80 min at a flow rate of 1ml/min. A second purification was performed in the same conditions as described above (fig.1).

3.2. Biochemical properties.

With MALDI analysis in the linear mode, a broad mass peak with an apex mass of 7468.8 Da was measured. This experimental mass of 7475 Da corresponds well with the theoretical mass of 7468.5 Da. During ESI analysis, a mass of 7484.8 Da was observed, suggesting an oxidation of Met32. The intact toxin was subjected to Edman degradation. Since only the 20 first N-terminal amino acids could be reliably sequenced, we subjected the toxin to a proteolytic treatment in order to obtain fragments amenable to *de novo* sequencing analysis by MALDI TOF/TOF instrument. Digestion of the toxin by trypsin, gluC, thermolysin turned out to be unsuccessful. Finally, an asparaginylendopeptidase was found to cut the toxin peptide into smaller fragments. The digestion was executed according to the protocol of the manufacturer. After digestion, the resulting peptides were separated and desalted by HPLC. The HPLC fractions were dried by speed-vac evaporation and resolubilized in alfa-cyano 4-hydrocinnamic acid matrix solution before analysis by MALDI TOF/TOF. The protein sequence data reported in this paper will appear in the UniProt Knowledgebase under the accession number P86862.

3.3. Electrophysiological experiments.

Sequence alignment (fig. 2A) indicated that APEKTx1 is a new member of the type 2 sea anemone peptides directing against voltage-gated potassium channels, which also include the kalicludines from *A. sulcata* and SHTX II from *Stichodactyla haddoni* [21,22]. From figure 2B it can be seen that APEKTx1 also shares homology with protease inhibitors from other sea anemones and with the potent Kunitz-type protease inhibitor Bovine Pancreatic Trypsin Inhibitor (BPTI). Previous electrophysiological experiments in *Xenopus leavis* oocytes have shown that the kalicludines block $K_V1.2$ channels with IC_{50} values around 1 µM. SHTX II was reported to inhibit the binding of ^{125}I-α-DTX to synaptosomal membranes with an Kd value of 650 nM [21,22]. As shown in figure 3A, the pure peptide APEKTx1 was subject of a wide screening on 23 ion channels: 12 cloned voltage-gated potassium channels ($K_V1.1$-$K_V1.6$, $K_V1.1$ mutant, $K_V2.1$, $K_V3.1$, $K_V4.2$, $K_V4.3$, hERG, the insect channel Shaker IR); 2 cloned hyperpolarization-activated

cyclic nucleotide-sensitive cation non-selective channels (HCN1 and HCN2) and 8 cloned voltage-gated sodium channels ($Na_V1.2$-$Na_V1.8$ and the insect channel $DmNa_V1$). Surprisingly, at concentrations up to 1 µM, no significant effect could be observed on the other ion channel isoforms tested. Figure 3B shows original traces for wild type $K_V1.1$ channels with application of 0.3, 1 and 3 nM APEKTx1 and for mutant $K_V1.1$ channels with application of 100 µM APEKTx1. A concentration response curve was constructed in order to determine the concentration at which half of the channels were blocked by APEKTx1. The IC_{50} value yielded 0.9 ± 0.1 nM (fig. 4A). Thus APEKTx1 inhibits $K_V1.1$ channels with the same potency as DTX I and α-DTX and is approximately 700 to 3000 times more potent than other known 2 sea anemone peptides directed against K_V channels. Moreover, this also means that at concentrations which are a 1000-fold the IC_{50} value of APETx1 on $K_V1.1$, this toxin still discriminates between subtype isoforms.

The inhibition of $K_V1.1$ channels by APEKTx1 was not voltage-dependent as in a range of test potentials from -30 mV to +40 mV no difference in the degree of APEKTx1 induced block could be observed (n=8) (fig. 4B).

In order to investigate if the observed current inhibition is due to pore blockage or rather to altered channel gating upon APEKTx1 binding, the *IV* and *gV* curves in ND96 and HK solution were constructed (fig. 4C and D). Application of 10 nM APEKTX1 caused 80.45 ± 2.23% and 84.21 ± 3.74% inhibition of the potassium current in ND96 and HK, respectively (n=10). In ND96, the g_{max} curve in control and in the presence of 10 nM toxin was characterized by a $V_{1/2}$ value of -15.7 ± 1.23 mV and -12.71 ± 0.5 mV (n=8) respectively. In HK, the $V_{1/2}$ was respectively, -25.84 ± 2.53 mV and -19.89 ± 3.2 mV (n=8). It can be concluded that in both solutions no significant difference in $V_{1/2}$ values occurred (P>0.05). Furthermore, the *IV* relationship in HK solution shows that the reversal potential, E_K is not significantly influenced by APEKTx1 (P>0.05; n=8). E_K values yielded -7.56 +/- 2.45 mV in control and -7.96 +/- 1.92 mV after application of toxin. All together, these experiments imply that current inhibition upon APEKTx1 binding does not result from changes in the voltage-dependence of channel gating. Presumably, APEKTx1 acts by blocking the pore in the open state of the K_V channel.

Blockage of $K_V1.1$ channels occurred rapidly and its binding was reversible since the current recovered quickly and completely upon washout (n=10) (fig. 4E). Both characteristics suggest an extracellular site of action. The reversibility of current inhibition is in contrast with DTX K binding. Toxin K binding is reversible at low concentrations but becomes irreversibly at concentrations higher than its IC_{50} value. However, alanine substitution of the Lys3 or Lys26 rendered DTX K binding reversible, possibly explaining the reversible binding of APEKTx1 since this toxin also possess neutral residues at these positions. Another observed difference between both toxins is that DTX K cannot fully inhibit the potassium current, even at very high concentrations. APEKTx1 however, is able to completely inhibit the current.

Because APEKTx1 did not alter channel gating and binding was reversible we investigated whether APEKTx1 blockage followed the kinetic behavior of a bimolecular reaction [23]. Figure 4F shows the effects of increasing concentrations APEKTx1 on a $K_V1.1$ channel. The apparent first order association rate constant k_{on} (open circles) increased linearly with toxin concentration, while the second order dissociation constant k_{off} (closed circles) remained constant. Both values are in concordance with the scheme of a bimolecular reaction. The influence on toxin-channel binding by through-space electrostatic forces between charged residues of the $K_V1.1$ channel and of APEKTx1 was also examined. This was done by measuring the effectiveness of APEKTx1 binding on $K_V1.1$ channels in solutions of different ionic strength. As described above, the IC_{50} value of APEKTx1 for $K_V1.1$ homomeric channels was 0.9 ± 0.1 nM. However, when using an iso-osmotic solution with a 48 mM NaCl concentration (sucrose substitution) the obtained IC_{50} value was 0.43 ± 0.07 nM. This 2 fold increase in APEKTx1 potency underlines that through-space electrostatic interaction is involved in APEKTx1 binding. These results are in corroboration with previously described similar observations for charybdotoxin binding to Shaker channels and for α-DTX binding to $K_V1.1$ channels [23-25].

In order to define the α-dendrotoxin footprint on mammalian potassium channels, 3 mutations (A352P, E353S and Y379H) were introduced in the dendrotoxin binding site, located in the H5 loop between the

transmembrane domains S5 and S6 of $K_V1.1$ subunits (fig. 5). By mutating these 3 particular residues, the pore region of the $K_V1.1$ triple mutant closely resembles this one of $K_V1.3$ channels [23,24]. We investigated whether the sensitivity of APEKTx1 for $K_V1.1$ could be affected by mutating these 3 critical residues. Interestingly, even at extreme high concentrations, APEKTx1 was unable to induce full blockage of current through these mutated $K_V1.1$ channels. Application of 100 µM APEKTx1 caused only 53 % inhibition (n=4) and the obtained IC_{50} yielded 10.8 ± 0.6 µM (fig. 4 A and Fig. 3B). This dramatic loss of affinity underlines the crucial interaction of these mutated residues with the toxin. Since it was reported that DTX K only needs one $K_V1.1$ subunit to cause inhibition of the potassium current through wild type heteromultimeric channels [26], we investigated also if DTX K could block the triple mutant. Concentration response curves were constructed for both $K_V1.1$ wild type and triple mutant channels (fig. 4A). The observed IC_{50} value for wild type channels was 0.51 ± 0.064 nM which is in good accordance with previous reported values [27]. For mutant channels the IC_{50} was 5.28 ± 0.23 nM. This means a 10-fold decrease in sensitivity compared to wild type channels.

3.4. Trypsin inhibition activity.

As all members of the type 2 sea anemone toxins APEKTx1 share sequence homology with the well characterized and potent Kunitz-type protease inhibitor BPTI, we also investigated if APEKTx1 could block trypsin activity. In order to do this, trypsin was incubated with different concentrations of APEKTx1 at room temperature for 3 hours to reach equilibrium. In the same conditions, trypsin was also incubated with DTX I, DTX K or BPTI. The protease inhibition activity was determined spectrophotomatrically after incubation by measuring the ability of the remaining free trypsin to release paranitroaniline from BAPNA. It has been shown before that the kalicludines have a very similar inhibition profile as BPTI [21]. Figure 6 shows that APEKTx1 is a trypsin inhibitor with a K_d = 124 nM. Presumably, APEKTx1 is a competitive trypsin inhibitor. A 3-fold molecular excess of APEKTx1 over trypsin completely inhibited the paranitroanaline release. However, this is almost 3 times the amount of BPTI or the kalicludines necessary to reach total inhibition of trypsin activity. The same figure also indicates that DTX I and DTX K, could not inhibit the trypsin activity, even at a 6:1 ratio of toxin over trypsin.

4. Discussion

The unique feature of a dual functionality within one molecule is intriguing. However, since the production of toxins is an energy demanding task for an organism, the dual effects contained within one molecule can be seen as an efficient and economic manner to save energy with a maximal pharmacological output. Furthermore, the dual effect has clearly advantages for the sea anemone in both an offensive and defensive point of view: the presence of a trypsin inhibitor will prolong the half-life of the peptides in the venom and therefore optimize the strategy of the venom.

APEKTx1 is the newest member of the type 2 sea anemone toxins directed towards voltage-gated potassium channels. To date, this family exists of only 4 other toxins, 3 kalicludines and SHTX II. Although it is known that these toxins are effective on K_V channels, little is known about their subtype selectivity. Here we report for the first time a screening of a type 2 toxin on a wide range of 23 different ion channels. This broad screening not only reveals a potent activity against $K_V1.1$ (IC_{50} = 0.9 ± 0.1 nM) but also points out an impressive selectivity for these channels over the other isoforms tested. Even at concentrations 1000-fold higher than the IC_{50} value for $K_V1.1$ channels, APEKTx1 has the ability to selectively inhibit this isoform subtype over others within the K_V1 family. Moreover, A352P, E353S and Y379H substitutions in the $K_V1.1$ subunit made these channels insensitive for APEKTx1 indicating that these 3 residues are critical for the toxin-channel interaction. Further electrophysiological characterization showed that this toxin does not modulate the voltage dependence of gating of K_V channels. The IV relationship in HK solution showed that ion selectivity was not changed after toxin binding. The observation that there is no difference in the percentage induced block either in ND96 or HK leads to the

conclusion that channel blockage is independent of the direction of the potassium current flux and is not influenced by the extracellular concentration of K^+ ions. Moreover, APEKTx1 did not show voltage dependence in its blockage of channels in a wide voltage range. The site of toxin binding is presumably located at the extracellular side since the inhibition of current through $K_V1.1$ channels occurred rapidly and binding was reversible upon washout. We have shown that APEKTx1 shares not only sequence and structure homology with dendrotoxins (fig. 7) but also a similar activity profile with a comparable potency as these snake toxins. The APEKTx1 blockage followed the kinetic behavior of a bimolecular reaction as previously described for α-DTX. The dendrotoxins have been extensively studied. The X-ray structure of α-DTX and the NMR structure of DTX K have been reported [28,29]. They both possess structures which resemble very well the Kunitz-type serine protease inhibitors such as BPTI. The dendrotoxins have an N-terminal 3_{10}-helix, a β hairpin and a C-terminal α-helix. The residues important for their potent K_V blocking activity have been characterized. For DTX K, site-directed mutagenesis studies have shown that Lys3, Tyr4, Lys6, Pro8, Arg10, Trp25, Lys26 and Lys28 are the main residues involved in the interaction with the $K_V1.1$ channels [30-32]. Among these, the basic residues in the 3_{10}-helix, Lys3 and Lys6, have been pointed out as the key residues for toxin binding since mutation to an alanine led to an dramatically decrease in the ability to inhibit the K^+ current [33]. Mutating the Pro8 and the Arg10 caused a 50- and 140-fold increase in IC_{50} value, respectively. The dramatic loss of affinity observed for DTX K binding to synaptic membranes when Trp25 and Lys26 were mutated to a alanine underlines that these residues are critical in recognition of $K_V1.1$ channels [33,34]. Among these key residues, Pro8, Arg10 and Arg28 are conserved in APEKTx1.

For α-DTX a mutational approach based on site-directed mutagenesis and chemical synthesis in which 31 out of 59 amino acids were mutated, revealed that Arg1, Arg2, Lys3, Leu4, Ile6, Leu7 were crucial for channel blockage activity of this toxin. Substituting Arg1 by alanine resulted in a less than 10-fold decreased affinity, whereas Arg2, Leu4 and Ile6 substitution lowered the affinity 10 to 30 times. The Lys3 and Leu6 seem to be the most critical residues since mutating these amino acids resulted in a thousand times less potent toxins [30,31,35,36]. Of these residues critical for α-DTX binding, the leu4 and Ile6 are replaced by a homologous residue in APEKTx1.

These Lys3 and Leu6 residues in α-DTX form the so-called dyad. It has been proposed that most toxins that block K_V channels possess a conserved functional core composed of a key basic residue (Lys or Arg) associated with a 6.6 ± 1 Å distant key hydrophobic residue (Leu, Tyr or Phe). Such a functional dyad can be found in a broad range of structurally unrelated peptides from various animals such as scorpions, cone snails, snakes and sea anemones [37,38]. However, it has been reported that besides this dyad, other toxin determinants are required for a high affinity interaction between the toxin and his target [39]. Known examples of toxins lacking a dyad but still capable of blocking the K_V channel (or the other way around toxins with a dyad but incapable of blocking) strongly suggest that the functional dyad on its own cannot represent the minimal pharmacophore or prerequisite for Kv1 binding [40,41]. Docking experiments with the scorpion toxin Pi1 and its homologs have highlighted that a ring of basic residues interacts with acidic residues of the K^+ channel turret located in the most extracellular part of the channel outer vestibule. Pi1 analogs, in which the basic residues from the ring were replaced by alanines, show a 50-480-fold reduction in peptide affinity for their target but were still able to block the potassium current [38]. In general, it is assumed that toxins recognize the Kv1 subtypes through the interaction of various toxin residues, among which the basic ring, with certain residues of the K_V1 channel turret. These interactions can be sufficient to inhibit the potassium current. Moreover, these specific molecular contacts determine toxin selectivity towards particular K_V1 channel isoforms. The functional dyad can then be viewed as a secondary anchoring point, providing a higher toxin affinity without altering toxin selectivity. The side chain of the basic key residue enters the ion channel pore and is surrounded by four Asp residues of the P-loop selectivity filter. This Asp residue is highly conserved among all the K_V1 channel isoforms. The carbonyl oxygen atoms of these Asp residues will form a stabilizing interaction with the side chain of the basic residue of the dyad. The key hydrophobic residue of the dyad will interact through both hydrophobic forces and hydrogen bonding with a cluster of aromatic residues in the P-loop. The specific positioning of the 2 residues from the dyad results in a physical barrier, especially because of the

positively charged side chain which is opposed to the K^+ flux [42,43]. Because of the low identity with other K_V channel toxins and because none of the key residues critical for the K_V blockage of DTX K or α-DTX are conserved in APEKTx1, we tried to hypothesize the key residues of APEKTx1 with the help of structural models. As it can be seen from figure 7, the role of a possible dyad in APEKTx1 can be fulfilled by Arg15 and Phe13, a basic and hydrophobic residues which are 6.2 Å separated. Assumably, the side chain of Arg15 enters the K_V1.1 channel pore and interacts with the carbonyl oxygen atoms of the Asp377 residues. The Phe13 will most likely interact through hydrophobic forces with the aromatic cluster formed by Phe356, Trp364, Trp365, and Tyr375. Previous work has highlighted Tyr375 in K_V1.1 as a crucial residue for the selectivity of scorpion and sea anemone toxins [44]. The amino acid at this position is highly variable between K_V1 isoforms and the nature of the side chain of this residue contributes significantly to the subtype selectivity of toxins. The observed 12000-fold decrease in affinity of APEKTx1 for mutated K_V1.1 channels can be explained partially by the Y379H mutation. The same mutation prevented the K_V1.1 binding of another sea anemone toxin BgK, which binds to wild type channels with an IC_{50} value of 0.7 nM [43-46]. The E353 also seems to be critical for interaction with APEKTx1. *Hurst et al* have shown that each of the 3 mutations on its own decreased dendrotoxin potency and that the removal of a negative charge at position 353 caused the greatest decrease in affinity [24]. However, simultaneous substitution of all 3 residues caused a much stronger decrease in DTX sensitivity than the single mutations. Further site-directed mutagenesis studies or ideally co-crystallization studies are required to elucidate if such subtle changes in sequence of the pore region are responsible for the dramatically loss of sensitivity of K_V1.1 for this toxin.

Also shown in figure 7 are the basic residues which are conserved in DTX K and α-DTX. These residues possibly contribute to the basic ring important for recognition, interaction and correct positioning of the toxin on the channel. As mentioned above, previous work has shown that mutating these conserved residues leads to affinity loss in DTX K or α-DTX [30]. However, this is only a hypothesis which requires further conformation from site-directed mutagenesis studies, docking experiments and structure analysis.

The bovine pancreatic trypsin inhibitor belongs to the Kunitz-type inhibitors and is a potent inhibitor of serine proteases. The crystal structures of BPTI with bovine trypsin and with bovine chymotrypsin have been determined [47-49]. Analysis of these complexes have shown that there are 10-13 residues on the inhibitor forming less than 4 Å contacts with 20-25 residues of the enzyme. The 13 key residues of the inhibitor form a structural epitope seen as two extended and exposed loops. The first loop which is the primary contact site is composed of the residues Thr11 to Ile19. The second loop is more C-terminal situated and is formed by residues Gly36 to Arg39 [50,51]. The Lys15 has been pinpointed as a single residue hot spot responsible for a major part of the enzyme-inhibitor contacts. The side chain of this basic amino acid penetrates deeply into the specificity binding pocket of the protease where it electrostaticly interacts with the Asp189 of the protease. This Lys15-Asp189 interaction delivers the major contribution to the association energy for the BPTI-trypsin complex. The role of Lys15 as a crucial player in the energetics of the recognition was demonstrated by substituting this residue with Gly. The point mutation reduced the total association energy with 70% leading to an association constant decreased by 9 orders of magnitude. Structure determination of α-DTX provided an explanation why this toxin and its homologue DTX I cannot inhibit proteases. The basic amino acid in BPTI has been replaced in α-DTX by a Tyr incapable of interacting effectively with binding pocket of trypsin [52-54]. Further explanation for the lack of protease inhibition by the dendrotoxins can be found in the presence of Asp17 in α-DTX, Glu17 in DTX I and Arg16 in DTX K. The existence of these longer amino acid residues in dendrotoxins instead of the smaller alanine in BPTI causes a most unfavorable complex with the trypsin binding site. Moreover, the Pro19 in DTX K and Pro21 in DTX I and α-DTX instead of the Ile19 in BPTI greatly impedes a good interaction with the side chain of the Tyr39 of trypsin. The residues essential for kunitz-type inhibition in the primary contact site (Gly12, Cys14, Lys15 and Ala16) are all conserved in APEKTx1 except for the Arg15 (fig. 7). However, previous residue-specific modification studies have shown that mutating the Lys 15 to Arg did not alter the association constant. The lower protease inhibition activity of APEKTx1 compared to BPTI (fig.5) can be explained by the presence of Phe13 and Pro19. A double BPTI mutant with a phenylalanine at position 13 and an arginine at position 15, exactly as in APEKTx1, resulted in a

100-fold decreased association constant compared to the wild type [54]. The unfavorable interaction of Pro19 with trypsin has been described above.

5. Conclusion

We have demonstrated the unique dual function of APEKTx1, which is a competitive Kunitz-type protease inhibitor and a very potent and selective $K_V1.1$ channel blocker. Moreover, several amino acid residues have been suggested to play a functionally critical role in the high potency and unique selectivity of this toxin. Further structure-function analysis involving site-directed mutagenesis studies, docking experiments and NMR are required in order to confirm their role. Because of its high affinity and selectivity, APEKTx1 might be a very interesting probe for further characterization of the binding sites of $K_V1.1$ channels. Finally, APEKTx1 represents a valuable tool to examine the exact role of $K_V1.1$ in various channelopathies, and might serve as a lead compound in the development of novel therapeutical agents for these diseases.

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Conflict of interest The authors declare that they have no conflict of interest.

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Footnotes

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The abbreviations used are: APEKTx1, Anthopleura elegantissime potassium channel toxin 1; MALDI TOF, matrix-assisted laser desorption-ionization time of flight; RP-HPLC, reversed-phase high performance liquid chromatography; TFA, trifluoroacetic acid; K_V channel, voltage-gated potassium channel; DTX; dendrotoxin; BPTI, bovine pancreatic trypsin inhibitor.

Figure Legends

Fig. 1: Purification of APEKTx1.
A, the crude fraction found to be active in the electrophysiological screening was loaded on a C18 column with a linear gradient of 0.085% TFA in acetonitrile. Only the fraction containing the largest peak indicated by the arrow was active on K_V1.1 channels. B, this active fraction was further purified using the same conditions as in A.

Fig. 2: Alignment.
Amino acid sequence of APEKTx1 and alignment with the other members of the type 2 sea anemone toxins, dendrotoxins, protease inhibitors from sea anemones and BPTI. Amino acid residues identical with APEKTx1 are shown on grey background, cysteine residues are printed in red. Disulfide bridge pattern based on AsKC3 are indicated. AsKC1-3 from *Anemonia sulcata*, AFAPI-I and AFAPI-III from *Anthopleura fuscoviridis*, AXPI-II from *Anthopleura xanthogrammica*, DTX E from *Dendroaspis*

polylepis polylepis, SHTX III from *Stichodactyla haddoni*, DTX K from *Dendroaspis polylepis*, α-DTX from and BPTI from *Bos taurus*.

Fig. 3: Activity of APEKTx1 on K_V channels.

A, Differential effects of APEKTx1 on several cloned voltage gated potassium and sodium channel isoforms expressed in *X. laevis* oocytes. Representative whole-cell current traces in control and toxin conditions are shown. The dotted line indicates the zero-current level. The asterisk (*) marks steady-state current traces after application of 1 µM of APEKTx1. This screening on a large number of K_V channel isoforms belonging to different subfamilies of the voltage gated potassium channel family shows that APEKTx1 selectively blocks $K_V1.1$ channels at a concentration of 1 µM. Traces shown are representative traces of at least 3 independent experiments ($n \geq 3$).

B, Original traces for wild type $K_V1.1$ channels with application of 0.3, 1 and 3 nM APEKTx1. For mutant $K_V1.1$ channels original traces with application of 100 µM APEKTx1 are also shown.

Fig. 4: Effects on $K_V1.1$ channel gating.

A, dose-response curve on wild-type (closed symbols) and triple mutant (open symbols) $K_V1.1$ channels obtained by plotting the percentage blocked current as a function of increasing toxin concentrations. For APEKTx1 (triangles), IC_{50} values yielded 0.9 ± 0.1 nM and 10.8 ± 0.6 µM for wild type and mutant channels, respectively. For DTX K (squares), IC_{50} values were determined at 0.51 ± 0.064 nM and 5.28 ± 0.2 nM for wild-type and mutant channels, respectively.

B, the percentage of residual current after application of 10 nM APEKTx1 as a function of membrane potential. In a range of test potentials from -30 mV to +40 mV, no difference in the degree of APEKTx1 induced block could be observed.

C and D, show *IV* and *gV* curves in ND96 and HK respectively. APEKTx1 does not act as a gating modifier. In ND96, the $V_{1/2}$ in control (open circles) and in the presence of 10 nM APEKTx1 (closed circles) was characterized by a value of -15.7 ± 1.23 mV (n=5) and -12.71 ± 0.5 mV (n=6) respectively. In HK, the $V_{1/2}$ yielded respectively, -25.84 ± 2.53 mV and -19.89 ± 3.2 mV. No significant shift was observed. Moreover, APEKTx1 did not significantly alter the reversal potential.

E, fast kinetics of inhibition of $K_V1.1$ channels and reversibility of the inhibition upon washout. Control (open triangles), wash-in, (open triangles+ black bar), wash-out (open circles). Values for τ_{on} and τ_{off} in this experiment were 92.7 and 47s, respectively.

F, APEKTx1 blockage followed the kinetic behavior of a bimolecular reaction as proposed by Tytgat *et al*. Displayed are the effects of increasing concentrations APEKTx1 on a $K_V1.1$ channel. The apparent first order association rate constant k_{on} (open circles) increased linearly with the toxin concentration. The second order dissociation constant k_{off} (closed circles) remained constant. Both these values are in correlation with the scheme of a bimolecular reaction.

Fig. 5:.Alignment of the pore regions of K_V1 family.

Sequence alignment of the pore region of $K_V1.1$-$K_V1.6$ and the $K_V1.1$ mutant. The 3 mutated residues (A352P, E353S and Y379H) in the $K_V1.1$ mutant are shown in red. Asp377, important for stabilizing the side chain of the basic residue of the dyad is shown in blue while the residue from the aromatic cluster (Phe356, Trp364, Trp365, Tyr375) which interacts with the hydrophobic residue of the dyad are shown in green.

Fig. 6: Kunitz-type protease inhibition.

The figure shows the concentration dependence of trypsin inhibition by different concentrations of BPTI, closed circles; APEKTx1, open circles; DTX I, open triangles and DTX K, open squares. A 3-fold molecular excess of APEKTx1 over trypsin inhibited the paranitroanaline release completely

Fig. 7: Spatial structure models of α-DTX, DTX K, BPTI and APEKTx1.

Structural models for α-DTX (PDB accession code 1DTX), DTX K (1DTK), BPTI (1PIT) and APEKTx1. The model of APEKTx1 was built on the basis of the structure of the homologue snake protease inhibitor textilinin (3BYB). Residues known to be important for K_V channel blockade (α-DTX, DTX K, APEKTx1) are indicated in red. The model for APEKTx1 shows the residues possibly forming a dyad in red, the residues possibly contributing to the basic ring are shown in green. The residues known to be

important for protease inhibition (BPTI and APEKTx1) are colored in blue (primary contact site) and in yellow (secondary contact site).

Figure 1

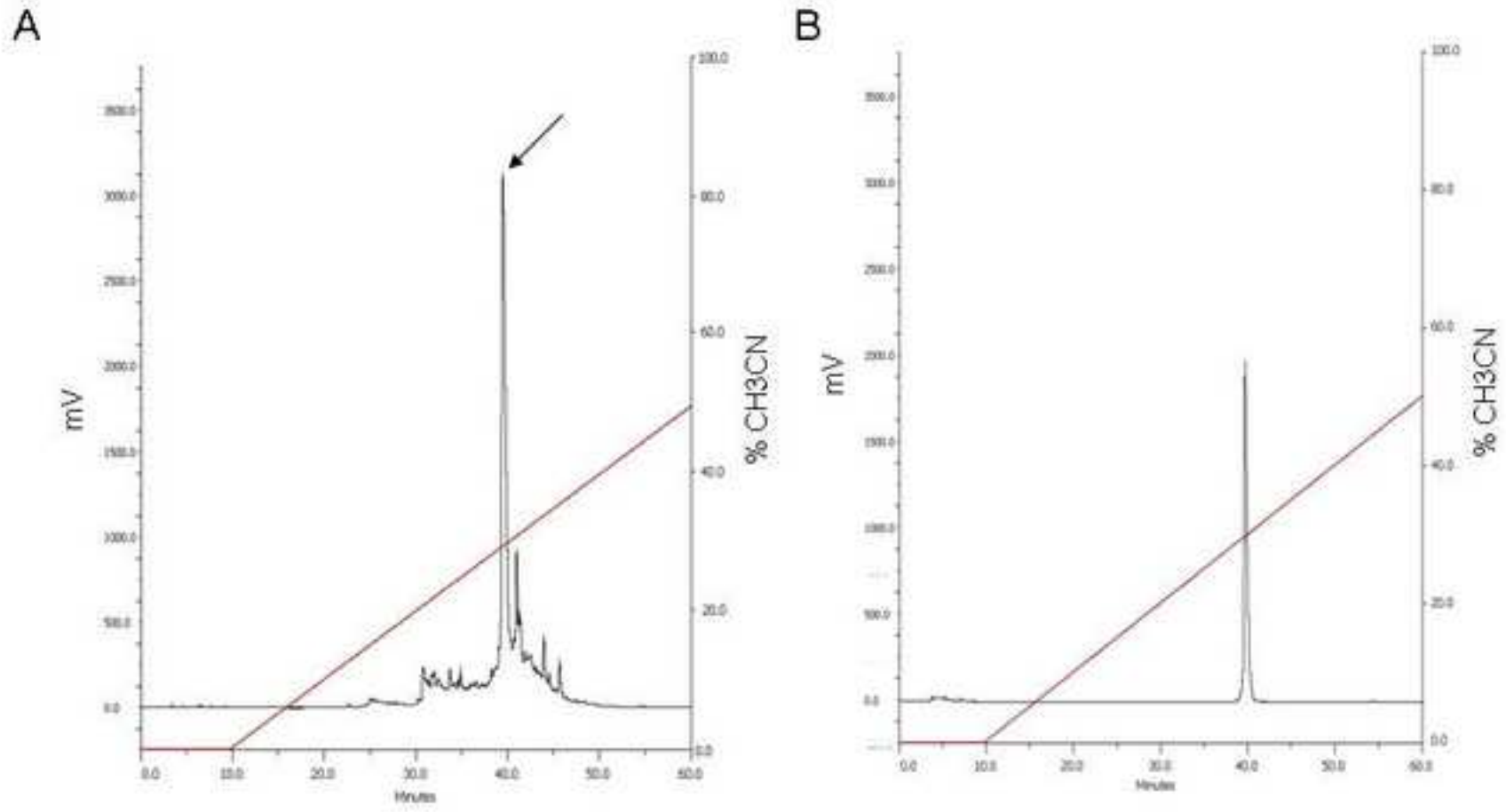


Figure 2

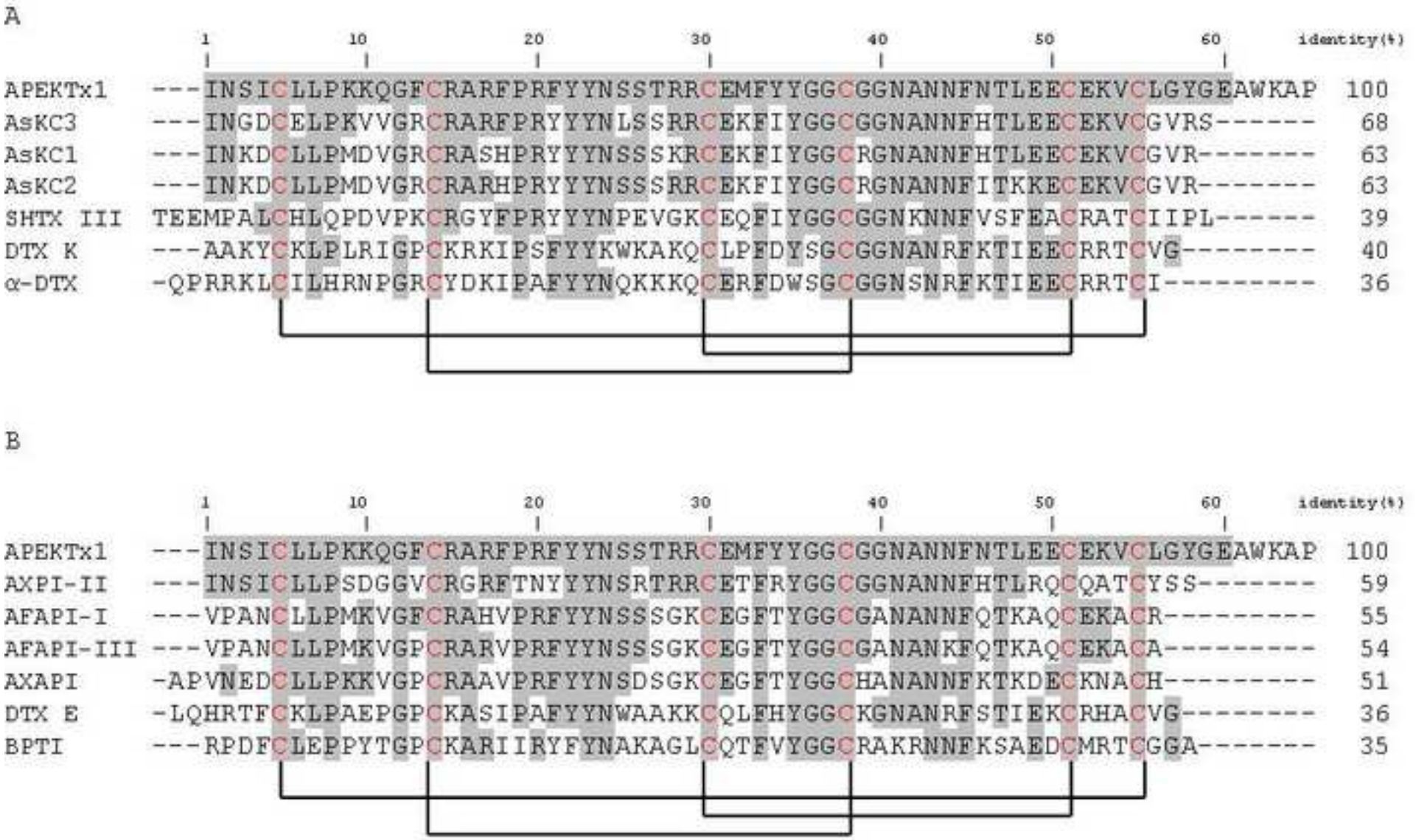
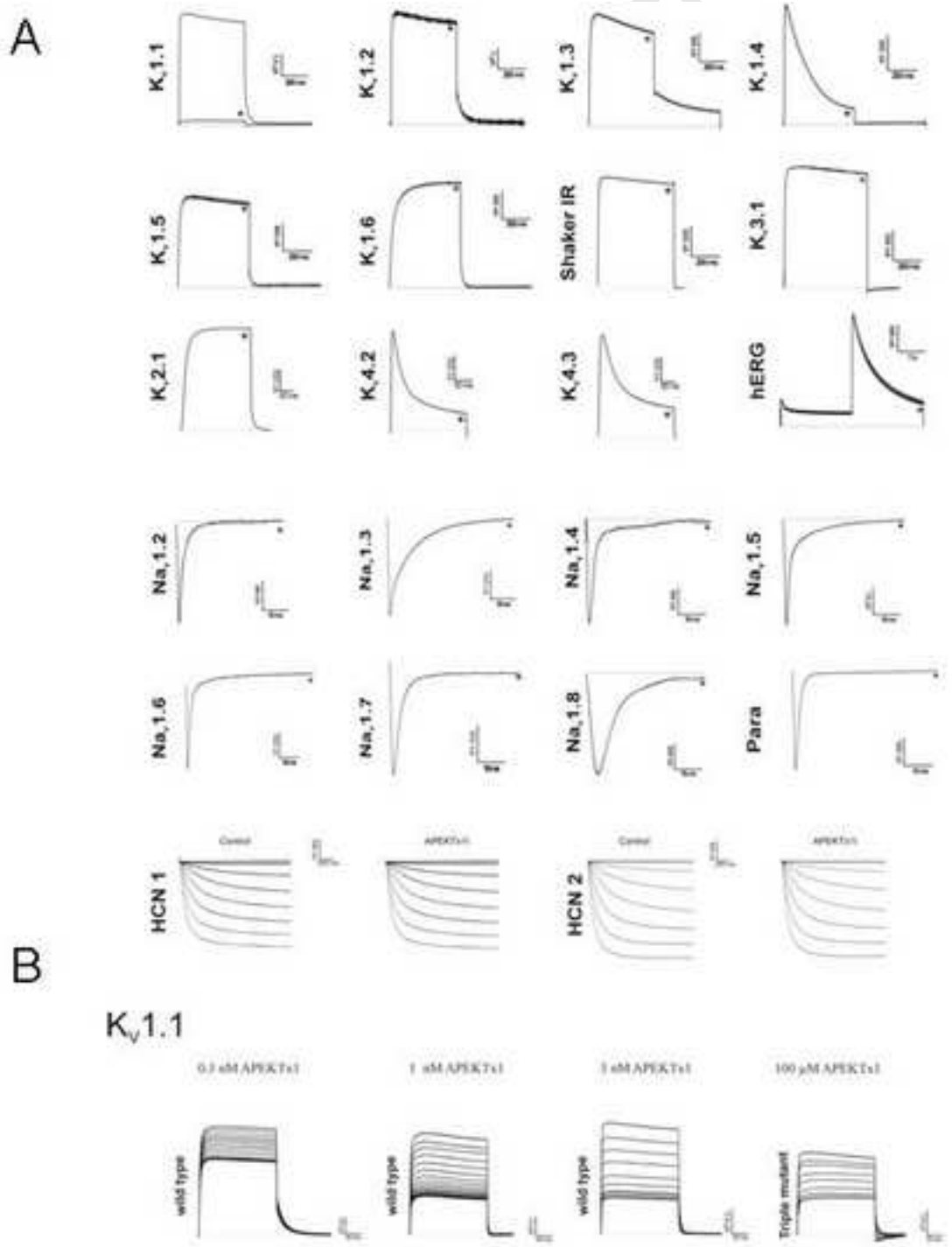

A
1 10 20 30 40 50 60 identity(%)
APEKTx1 ---INSICLLPKKQGFCRARFPRFYYNSSTRRCEMFYYGGCGGNANNFNTLEECEKVCLGYGEAWKAP 100
AsKC3 ---INGDCELPKVVGRCRARFPRYYYNLSSRRCEKFIYGGCGGNANNFHTLEECEKVCGVRS------ 68
AsKC1 ---INKDCLLPMDVGRCRASHPRYYYNSSSKRCEKFIYGGCRGNANNFHTLEECEKVCGVR------- 63
AsKC2 ---INKDCLLPMDVGRCRARHPRYYYNSSSRRCEKFIYGGCRGNANNFITKKECEKVCGVR------- 63
SHTX III TEEMPALCHLQPDVPKCRGYFPRYYYNPEVGKCEQFIYGGCGGNKNNFVSFEACRATCIIPL------ 39
DTX K ---AAKYCKLPLRIGPCKRKIPSFYYKWKAKQCLPFDYSGCGGNANRFKTIEECRRTCVG-------- 40
α-DTX -QPRRKLCILHRNPGRCYDKIPAFYYNQKKKQCERFDWSGCGGNSNRFKTIEECRRTCI--------- 36
B
1 10 20 30 40 50 60 identity(%)
APEKTx1 ---INSICLLPKKQGFCRARFPRFYYNSSTRRCEMFYYGGCGGNANNFNTLEECEKVCLGYGEAWKAP 100
AXPI-II ---INSICLLPSDGGVCRGRFTNYYYNSRTRRCETFRYGGCGGNANNFHTLRQCQATCYSS------- 59
AFAPI-I ---VPANCLLPMKVGFCRAHVPRFYYNSSSGKCEGFTYGGCGANANNFQTKAQCEKACR--------- 55
AFAPI-III ---VPANCLLPMKVGPCRARVPRFYYNSSSGKCEGFTYGGCGANANKFQTKAQCEKACA--------- 54
AXAPI -APVNEDCLLPKKVGPCRAAVPRFYYNSDSGKCEGFTYGGCHANANNFKTKDECKNACH--------- 51
DTX E -LQHRTFCKLPAEPGPCKASIPAFYYNWAAKKCQLFHYGGCKGNANRFSTIEKCRHACVG-------- 36
BPTI ---RPDFCLEPPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCMRTCGGA------- 35

Figure 3


A
K_v1.1
K_v1.2
K_v1.3
K_v1.4
K_v1.5
K_v1.6
Shaker IR
K_v3.1
K_v2.1
K_v4.2
K_v4.3
hERG
Na_v1.2
Na_v1.3
Na_v1.4
Na_v1.5
Na_v1.6
Na_v1.7
Na_v1.8
Para
HCN 1
HCN 2
B
K_V1.1
wild type
wild type
wild type
Triple mutant

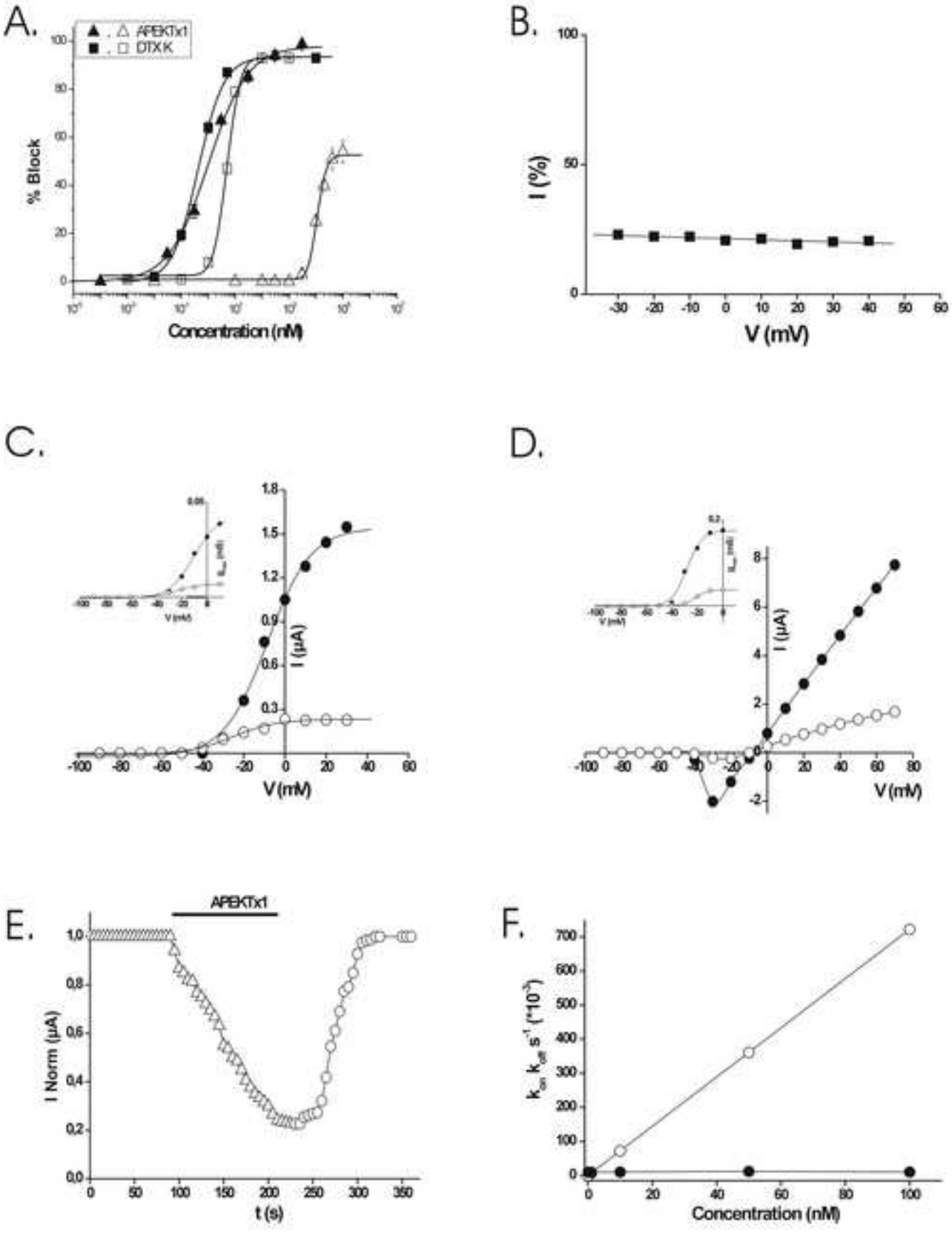


Figure 5

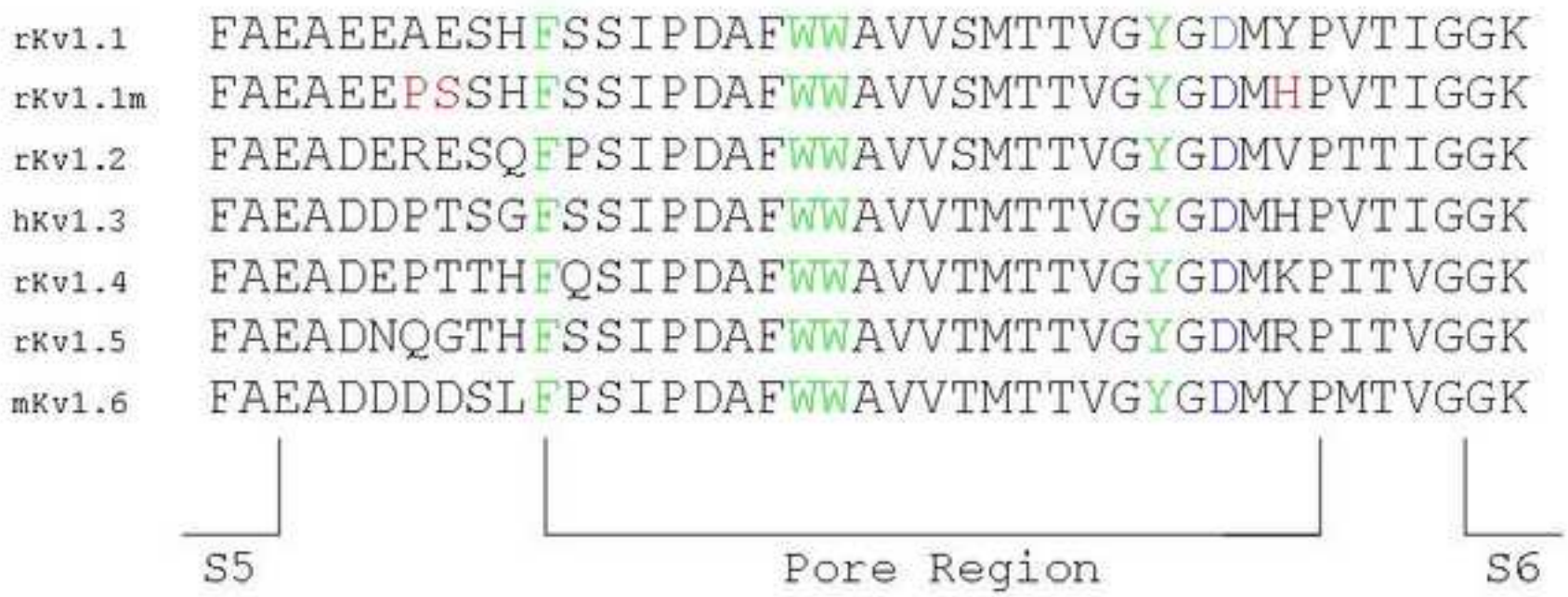

rKv1.1 FAEAEEAESHFSSIPDAFWWAVVSMTTVGYGDMYPVTIGGK
rKv1.1m FAEAEEPSSHFSSIPDAFWWAVVSMTTVGYGDMHPVTIGGK
rKv1.2 FAEADERESQFPSIPDAFWWAVVSMTTVGYGDMVPTTIGGK
hKv1.3 FAEADDPTSGFSSIPDAFWWAVVTMTTVGYGDMHPVTIGGK
rKv1.4 FAEADEPTTHFQSIPDAFWWAVVTMTTVGYGDMKPITVGGK
rKv1.5 FAEADNQGTHFSSIPDAFWWAVVTMTTVGYGDMRPITVGGK
mKv1.6 FAEADDDDSLFPSIPDAFWWAVVTMTTVGYGDMYPMTVGGK
S5
Pore Region
S6

Figure 6

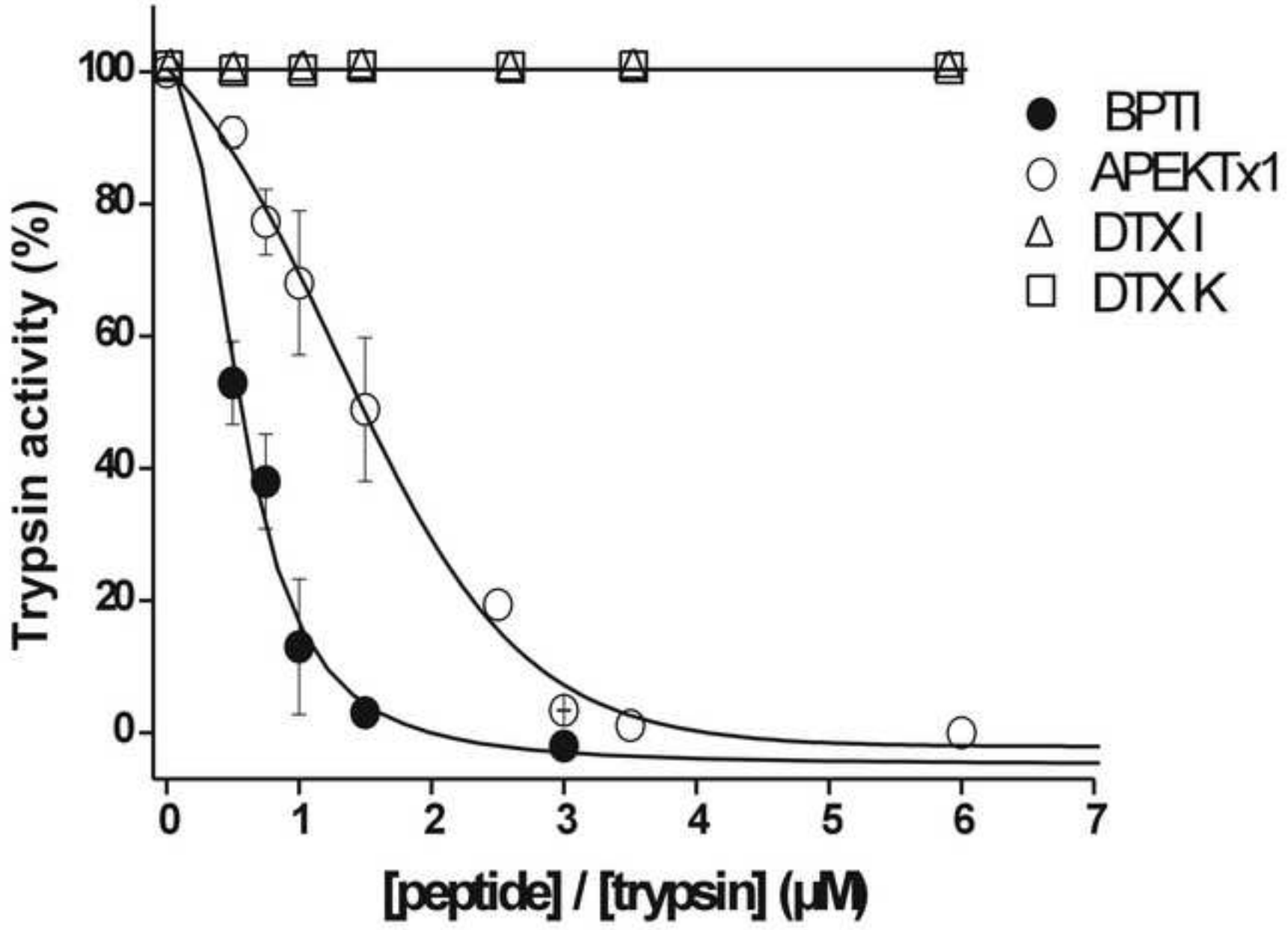
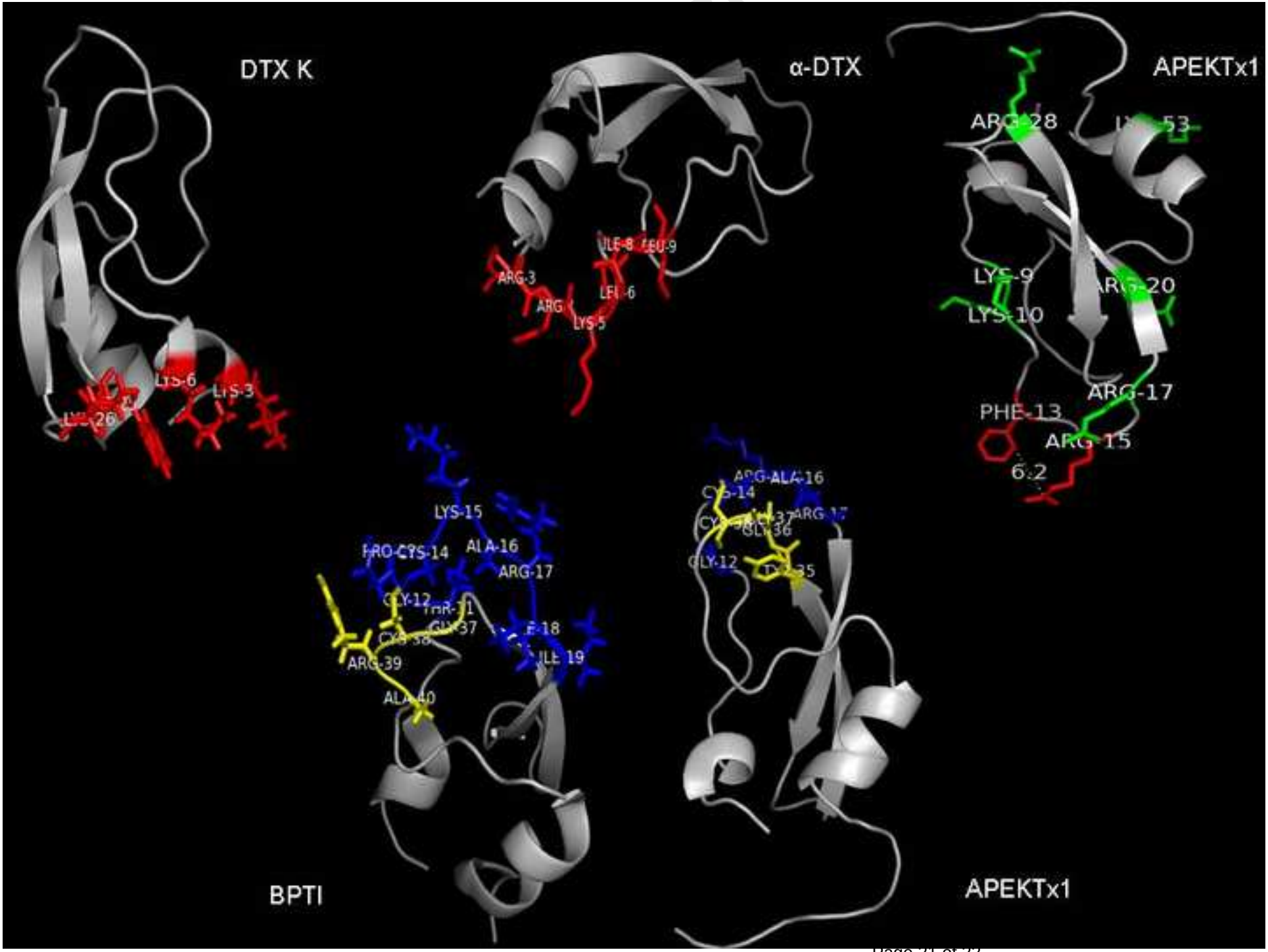

Trypsin activity (%)
100
80
60
40
20
0
0
1
2
3
4
5
6
7
[peptide] / [trypsin] (μM)
BPTI
APEKTx1
DTX I
DTX K

Figure 7


DTX K
α-DTX
APEKTx1
BPTI
APEKTx1
ARG-3
LYS-5
LYS-6
LYS-3
LYS-9
LYS-10
ARG-20
ARG-17
PHE-13
LYS-15
ALA-16
ARG-17
ARG-39
ALA-40
GLY-12

APEKTx1 is a potent and selective K_V blocker and protease inhibitor