Electronic Supplementary Material (ESI) for Faraday Discussions.
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Supplementary information;

Peptide synthesis; N-terminus of the α-subunit of pig kidney Na^+,K^+-ATPase 1-40: GRDKYEPAAVSEHGDKKKAKKERDMDELKKEVSMDDHKLS (N-NKA), residues underlined have been double coupled, with histidine also being coupled at a reduced temperature of 50°C. N-terminus of the α-subunit of gastric H^+,K^+-ATPase 1-40 from *Siniperca chuatsi* (Chinese mandarin fish): SKQDTYDMFEMGGEMDKKKKKKKMK KKEKLEGMKKEMDID (N-HKA), single coupling for all residues. Both syntheses were initiated at 100 μmol scale then reduced to 50 μmol at residue number 20, and for both syntheses the deprotection solution contained 0.1 M HOBT to minimise aspartamide formation. Other synthesis specifications are as per the manufacturer's recommendation.

Purity, identity and yield; The purity of the peptides as assessed by UPLC was ≥95%). Yields for the pure peptides were: *Na^+,K^+-ATPase 1-40*, 7.4 mg, (yield 3.2%) and for the H^+,K^+-ATPase *21*-40, 8.2 mg, (yield 3.4%). Na^+,K^+-ATPase 1-40; $[M+1H]^{1+}$ mass estimate based on the $[M+4H]^{4+}$ ion species (1158.3) is 4630.2 (calculated mass 4631.2), H^+,K^+-ATPase 1-40; $[M+1H]^{1+}$ mass estimate based on the $[M+4H]^{4+}$ ion species (1212.1) is 4845.5 Da (calculated mass 4845.8 Da).

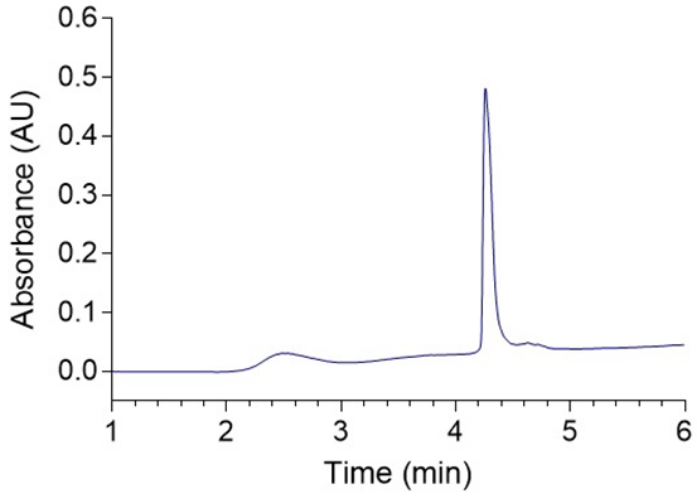

Figure S1. Analytical RP-HPLC trace from the final purified pool of α-subunit of gastric H^+,K^+-ATPase 1-40 from *Siniperca chuatsi*. R_t 4.3 min (0-50% B over 5 min, λ = 230 nm).

m/z ratio	relative intensity (%)	ion species assignment
1615.6	26.4	$[M+3H]^{3+}$
1212.1	53.8	$[M+4H]^{4+}$
969.5	67.9	$[M+5H]^{5+}$
808.4	100.0	$[M+6H]^{6+}$
693.1	100.0	$[M+7H]^{7+}$
606.6	28.3	$[M+8H]^{8+}$
539.3	18.9	$[M+9H]^{9+}$

Table 1. ESI-MS data for the final pool of α-subunit of gastric H^+,K^+-ATPase 1-40 from *Siniperca chuatsi*.

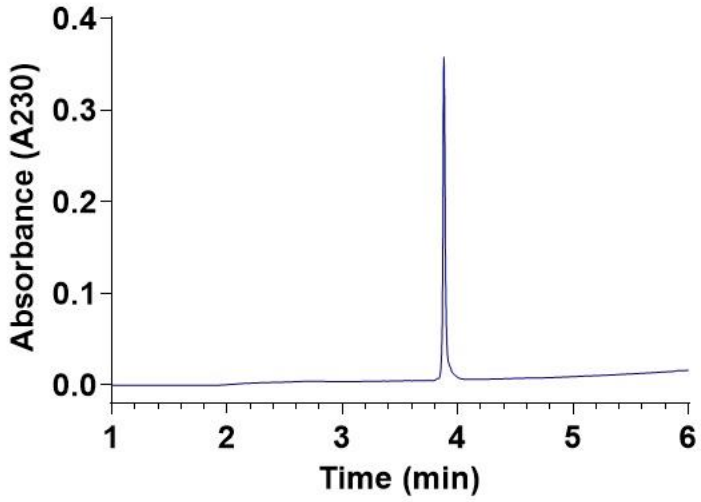

Figure S2. Analytical RP-HPLC trace of the final purified pool of α-subunit of pig kidney Na^+,K^+-ATPase 1-40. R_t 3.9 min (0-50% B over 5 min, λ = 230 nm).

m/z ratio	relative intensity (%)	ion species assignment
1543.9	26.7	$[M+3H]^{3+}$
1158.3	46.7	$[M+4H]^{4+}$
926.5	66.7	$[M+5H]^{5+}$
772.5	100.0	$[M+6H]^{6+}$
662.5	100.0	$[M+7H]^{7+}$
579.7	83.3	$[M+8H]^{8+}$
515.4	46.7	$[M+9H]^{9+}$

Table S2. ESI-MS data for the final pool of α-subunit of pig kidney Na^+,K^+-ATPase 1-40.

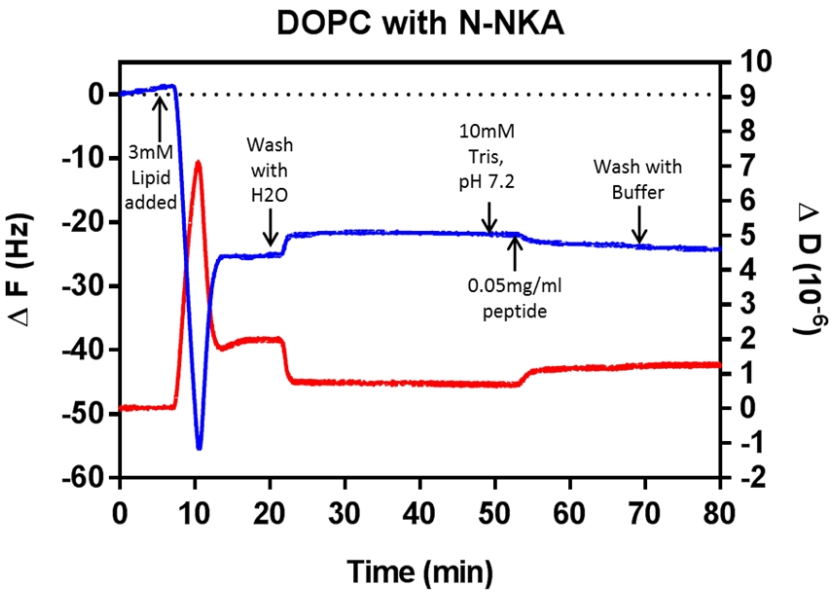

Figure S3. Characteristic QCM-D data set depicting SLB formation and peptide interaction. An SLB consisting of DOPC was formed on a silicon dioxide-coated surface of a quartz crystal from a suspension of liposomes. In this experiment, N-NKA was added to the SLB and the corresponding changes to the frequency (Δf, blue line) and dissipation (ΔD, red line) were measured. This plot demonstrates the maintenance of a stable SLB over a period of 80 mins despite changes in buffers and shows the interaction of N-NKA with the SLB. The peptides were dissolved in 10 mM Tris, 0.3 mM EDTA, pH 7.2 buffer at a final concentration of 50 ug/ml. Measurements were performed at 24 °C.