

The Akt C-Terminal Modulator Protein (CTMP) is an Acyl-CoA Thioesterase of the Hotdog-fold Family

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Contents: Eight pages total which include Tables SI1 and SI2 (initial velocities of Hthem4 catalyzed hydrolysis of myristoyl-CoA measured at different Akt1 concentrations), Figure S1 (molecular size determination of (Δ 39)hTHEM4) and experimental protocols.

hTHEM4 Gene Cloning: (fl)hTHEM4, (Δ 39)hTHEM4, (Δ 99)hTHEM4

The gene encoding hTHEM4 in human (GI: 76159293) was amplified by PCR from cDNA clone MGC74423 (ATCC, GenBank accession number: BC065277) using primers 5'-CGGAGCATATGCTGAGGAGCTGCGCC-3' and 5'-TTATAGGTGAGGATCCACAGCGCCTGG-3', which incorporate a NdeI site and a BamHI site. The resulting PCR fragment was digested with NdeI and BamHI restriction enzymes and ligated to a linearized pET-14b vector (Novagen) to encode the N-terminal His₆ tagged full-length hTHEM4. The gene encoding the C-terminal His₆-tagged (Δ 39)hTHEM4 was prepared by PCR using the full-length gene and the primers: 5'-GAGGTCATTTTCTTCATATGGAAGTCATTC-3' and 5'-CACCAGCAGCTCTCGAGTGTGACTTTTAGC-3'. The resulting PCR fragment was digested with NdeI and XhoI restriction enzymes and ligated to a linearized pET-23a vector. The construct that encodes the (Δ 99)hTHEM4 truncation mutant was formed using primers 5'-CTTGACCCAAAGCATATGAAAGAAGAAC-3' and 5'-TTATAGGTGAGGATCCACAGCGCCTGG-3' with the hTHEM4 gene serving as the template. The PCR product was inserted into the Addgene plasmid 11540: pHM6g.TM1457 at the NdeI and BamHI cloning sites. The construct encodes His₆-MBP-(Δ 99)hTHEM4 which includes the TEV protease cleave site. The gene sequences were confirmed by DNA sequencing (Health Sciences Center of the University of New Mexico). The clones were used to transform BL21-codon plus (DE3) RIL competent cells for over-expression.

Preparation of (fl)hTHEM4, (Δ 39)hTHEM4 and (Δ 99)hTHEM4

Transformed BL21-codon plus (DE3) RIL competent cells were cultured at 20 °C with mixing at 180 RPM in LB media for 8 h ($OD_{600} = 0.7$), and then induced with 0.4 mM IPTG. After 12 h, the cells were harvested by centrifugation at 4°C and 6500 RPM. The 10 g of cell paste was suspended in 100 mL of ice-cold lysis buffer (50 mM NaH_2PO_4 , 200 mM NaCl, 10 mM imidazole, and 0.5 mL protease inhibitor cocktail solution; pH 8.0), passed through a French press at 1200 PSIG, and then centrifuged at $48000 \times g$ and 4 °C for 30 min. The supernatant was loaded onto a Ni-NTA agarose column (QIAGEN, 25 ml) pre-equilibrated with the lysis buffer. The column was washed with 300 mL of wash buffer (50 mM NaH_2PO_4 , 200 mM NaCl, and 50 mM imidazole; pH 8.0) and then with 100 mL of elution buffer (50 mM NaH_2PO_4 , 200 mM NaCl, 250 mM imidazole; pH 8.0). The fractions were analyzed by SDS-PAGE and then selectively pooled, concentrated using a Centricon (10 kDa, Pall Filtron) at 4 °C, dialyzed against 50 mM HEPES and 200 mM NaCl (pH 7.5) at 4 °C and then stored at -80°C. In the case of the His₆-MBP-(Δ 99)hTHEM4 fusion protein, the His₆-MBP domain was removed using TEV protease (1 OD₂₈₀ of TEV protease per 20 OD₂₈₀ of protein in 50 mM NaH_2PO_4 /200 mM NaCl/10 mM imidazole (pH 8), 12 h at 4°C). Ni-NTA column chromatography was carried out to remove the His₆-MBP.

Determination of the steady-state kinetic constants for hTHEM4 catalyzed acyl-CoA thioester hydrolysis.

Reactions were monitored at 25 °C by measuring the 412 nm absorbance of 5-thio-2-nitrobenzoate ($\epsilon=13.6 \text{ mM}^{-1}\text{cm}^{-1}$) formed by reaction of 5,5'-dithio-bis (2-nitrobenzoic acid) (DTNB) with the CoA liberated from the acyl-CoA substrates. Reactions were

initiated by adding hTHEM4 to 1 mL assay solutions containing substrate, DTNB (1 mM), KCl (0.2 M) and 50 mM K⁺HEPES (pH 7.5). The kinetic parameters of V_{\max} and K_m were determined from initial velocity data, measured as a function of substrate concentration, by using equation (1) and KinetAsyst (IntelliKinetics, PA).

$$V = V_{\max} [A] / ([A] + K_m) \quad (1)$$

where $[A]$ is the substrate concentration, V is the initial velocity, V_{\max} is the maximum velocity and K_m is the Michaelis constant. The reported error was computed for the data fitting. The k_{cat} was calculated from the ratio of V_{\max} and the total enzyme concentration. The enzyme concentration was determined using the Bradford method.

hTHEM4 Inhibition.

The time course for the hTHEM4 catalyzed hydrolysis of 20 μM 4-hydroxybenzoyl-CoA (4-HBA-CoA) in 50 mM K⁺HEPES/0.2 M KCl (pH 7.5; 25 °C) was monitored at 300 nm ($\Delta\epsilon = 11.8 \text{ mM}^{-1}\text{cm}^{-1}$) to completion in order to determine if the accumulation of product reduced the reaction rate. The time course showed no evidence of product inhibition. The competitive inhibition constant K_i for CoA was determined by measuring the initial velocity of hTHEM4 catalyzed 4-HBA-CoA hydrolysis as a function of 4-HBA-CoA concentration (K_m to $10K_m$) and CoA concentration (0, 25, 50 and 75 μM). The initial velocity data were fitted to equation (2) using KinetAsyst (IntelliKinetics, PA),

$$V = V_{\max} [A] / ([A] + K_m(1 + [I]/K_i)) \quad (2)$$

where $[A]$ is the substrate concentration, V is the initial velocity, V_{\max} is the maximum

velocity, K_m is the Michaelis constant, K_i is the competitive inhibition constant and $[I]$ is the inhibitor concentration.

The inhibition of hTHEM4 by the 4-hydroxybenzoate, hexanoate, octanoate (25 mM stock solution prepared in 30% aq. ethanol) and lauroate (50 mM stock solution prepared in 50% aq. ethanol) was tested by measuring the initial velocity of hTHEM4 catalyzed hydrolysis of 4.2 μ M lauroyl-CoA ($\sim K_m$ level) in DTNB (1 mM), KCl (0.2 M) and 50 mM K^+ HEPES (pH 7.5; 25 °C) in the absence and presence of increasing concentrations of inhibitor up to 2-5 mM. The K_i value was estimated from the concentration of inhibitor that decreased the initial velocity by half. If no inhibition was observed the K_i was assumed to be greater than the value of the highest inhibitor concentration tested.

hTHEM4 catalyzed hydrolysis of myristoylated holo-acyl carrier protein of the human cytoplasmic fatty acid synthase

The plasmids encoding ACP domain derived from human cytosolic fatty acid synthase and the human phosphopantetheinyl transferase (PPTase) were a kind gift from Dr. Stuart Smith, Children's Hospital Oakland Research Institute, Oakland, CA. The two recombinant proteins were purified as described earlier (1,2). The reaction mixture contained 60 μ M apo-ACP, 150 μ M myristoyl-CoA and 2 μ M PPTase in 20 mL of 20 mM Tris/1 mM $MgCl_2$ (pH 7.0; 25 °C) for 3 h. The myristoyl-ACP solution was concentrated using a PALL 10K centrifuge A device and the structure was verified by ES-MS. Myristoyl-ACP calculated: 13618, observed: $[M^+]$ 13617. The 200 μ L reaction mixture initially containing 44 μ M myristoyl-ACP, 10 μ M ($\Delta 39$)hTHEM4, 50 mM K^+ HEPES and 100 mM NaCl (pH 7.5, 37 °C) was incubated for 1 h and then subjected to

ES-MS analysis. The substrate peaks at $[M^+]$ 13617, present in the spectrum of the control reaction (run in the absence of $(\Delta 39)hTHEM4$) were not observed in the spectrum of the reaction solution. Instead, a new peak at $[M^+]$ 13405 (-210 Da = MW of myristolic acid) was present that corresponds to the deacylated holo-ACP. The steady state kinetic constants for the catalyzed hydrolysis reaction were determined by measuring the initial velocities of reaction solutions initially containing 10, 20, 40 and 80 μ M myristoyl-ACP, 0.25 μ M $(\Delta 39)hTHEM4$ and 0.3 mM DTNB in 50 mM K^+ HEPES/0.2 M KCl (pH 7.5; 37 °C) and fitting the data to equation (1).

Determination of the effect of Akt1 on (fl)hTHEM4 and $(\Delta 39)hTHEM4$ activity.

The His₆-tagged full length Akt1 (3) was a kind gift from Dr. Lusong Luo of GlaxoSmithkline. Reaction solutions that initially contained (fl)hTHEM4 (0.04 μ M) or $(\Delta 39)hTHEM4$ (0.05 μ M), myristoyl-CoA (5 μ M), Akt1 (0, 0.4, 0.8, 1.5, 2.3 μ M), DTNB (2 mM), KCl (0.15 M) and 50 mM K^+ HEPES (pH 7.5, 25 °C) were monitored at 412 nm ($\epsilon = 13.6 \text{ mM}^{-1} \text{ cm}^{-1}$) for CoA formation. The calculated initial velocities are reported in Tables SI1 and SI2.

References

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Table SI1. Hydrolysis velocities of myristoyl-CoA catalyzed by (fl)hTHEM4 at different concentrations of Akt1.

Akt, μM	Velocity (0s-50s), $\mu\text{M CoA/s}$
0	0.0135
0.4	0.0143
0.8	0.0170
1.5	0.0156
2.3	0.0155

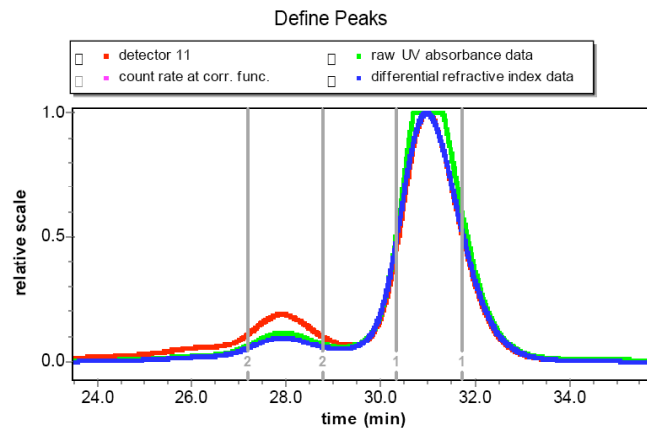
Table SI2. Hydrolysis velocities of myristoyl-CoA catalyzed by (Δ 39)hTHEM4 (0.05 μM) at different concentrations of Akt1.

Akt, μM	Velocity (0s-50s), $\mu\text{M CoA/s}$
0	0.0258
0.4	0.0291
0.8	0.0330
1.5	0.0513
3.0	0.0376

Figure S11. The native molecular weight determination of (Δ 39)hTHEM4 by SEC-LS/RI/UV analysis from ASTRA.

AUX1 = UV signal (absorbance at 280 nm; **red**)
 AUX2 = RI signal (refractive index changes; **green**)
 90° Detector = LS trace recorded for the detector at 90 degree angle (**black**)
 (please note that the RI and UV signals are scaled to LS signal)

Vertical lines indicate boundaries of peak/peaks selected for ASTRA analysis



	Peak 1	Peak 2
Peak limits (min)	29.940-31.585	27.199-28.761
MW (kDa)	50.33	102.1
N (MW/24)	2.10	4.25
Oligomeric state	dimer	tetramer