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Purification of AcpH protein homologs



AcpH homolog protein from *Cyanothece* PCC7822 (**a**), *P. aeruginosa* (**b**), *P. fluorescens* (**c**), and *S. oneidensis* (**c**) was expressed recombinantly and purified using Ni-NTA chromatography.

Analysis of CyAcpH activity with Pks4, PksA, ActACP (PKS) and E. coli AcpP (FAS)



CyAcpH is evaluated by SDS-PAGE with various *crypto*-CP (+) compared to no enzyme blanks (-) after overnight incubation at 37°C.

P. fluorescens AcpH activity vs. Pks4, PksA, ActACP, JamC, JamF (PKS) and EcAcpP (FAS)



PfAcpH is evaluated by SDS-PAGE with various *crypto*-CP (+) compared to no enzyme blanks (-) after overnight incubation at 37°C.

Analysis of AcpH homolog activity with SyrB1 (NRPS) and MAS (FAS)



Analysis of AcpH homolog activity with MBP-PaAcpP (FAS)



Analysis of AcpH homolog activity with Plasmodium falciparum ACP and SoAcpP (FAS)



AcpH homologs from *P. fluorescens* (Pf), *P. aeruginosa* (Pa), *Cyanothece* PCC 7822 (Cy) and *S. oneidensis* (So) are evaluated by SDS-PAGE with various *crypto*-CP (+) compared to no enzyme blanks (-) after overnight incubation at 37°C. Coumarin-PPant from SoAcpP appeared to hydrolyze overnight in incubated samples compared to non-incubated sample "0m".

Analysis of AcpH homolog activity with MtbAcpM (FAS)



Analysis of SoAcpH activity with MAS (FAS), SyrB1 and VibB (NRPS), PksA (PKS), eGFP-YbbR C- and N-terminal fusions (peptide)



AcpH homolog from *S. oneidensis* (So) is evaluated by SDS-PAGE with various *crypto*-CP (+) compared to no enzyme blanks (-) after overnight incubation at 37°C.

Analysis of SoAcpH activity with EcAcpP, MtbAcpM (FAS), ActACP, Pks4, JamC, JamF (PKS), and PltL (NRPS)



AcpH homolog from *S. oneidensis* (So) are evaluated by SDS-PAGE with various *crypto*-CP (+) compared to no enzyme blanks (-) after overnight incubation at 37°C.

Analysis of AcpH activity with holo-SoAcpP (FAS) at various time-points





Coomassie Stain



Coomassie Stain

AcpH homologs from *P. fluorescens* (Pf), *P. aeruginosa* (Pa), *Cyanothece* PCC 7822 (Cy) and *S. oneidensis* (So) are evaluated by Urea-PAGE with *holo*-CP (+) compared to buffer blanks (-E) after various incubation times at 37°C. Samples were quenched with EDTA at listed times. Blank samples were also prepared without Mn^{2+} (-E-Mn) and without Mn^{2+}/Mg^{2+} in order to evaluate non-enzymatic PPant hydrolysis.

Analysis of PaAcpH and MBP-CyAcpH with Pks4, PksA, ActACP (PKS) activity.



AcpH homologs from *P. aeruginosa* (Pa) and MBP- fusion AcpH homolog from *Cyanothece* PCC7822 (MBP-CyAcpH) are evaluated by SDS-PAGE with various *crypto*-CP (+) compared to no enzyme blanks (-) after overnight incubation at 37°C.

Analysis of AcpH homolog activity with AdmA (PKS) and AdmI (NRPS)



Analysis of AcpH homolog activity with CepK (NRPS)





Analysis of AcpH homolog activity with VibB and PltL (NRPS)

Circular dichroism analysis of CyAcpH and SoAcpH



Circular dichroism analysis of suspected inactive *S. oneidensis* AcpH (SoAcpH) compared to known active *Cyanothece sp.* PCC7822 (CyAcpH) reveals strong alpha-helical character in SoAcpH at similar protein concentrations. This suggests that SoAcpH maintains consistent secondary structure.

Sequence alignment of known active AcpH homologs to SoAcpH

EcAcpH	MNFLAHLHLAHLAESSLSGNLLADFVRGNPEESFPPDVVAGIHMHRRIDVLTDNLPE
СуАсрН	MNYLAHLFLADPTPESQIGNLLGDFVKGKIDNLSSIYSPEIIRGVKTHQKIDIFTDHHPI
РаАсрн	MNYLAHLHLGGPQPAQLLGSLYG <mark>D</mark> FVKGRLQGQWPDEIERAIQLHRRIDAFTDSHPL
PfAcpH	MNYLAHLHLGGQLPAQLLGSLYGDFVKGRLQGQFSPQIEAAIQLHRSIDRFTDSHPL
SoAcpH	MNILTHLHLAEISKTHLGANLAGNFITAPIENAPRALRQGLWLNNEINQLCATHEL
	** *:**.** .: <mark>*</mark> *: . : : : *: :
ЕсАсрн	VREAREWFRNETRRVAPITLDVMWDHFLSRHWSQLSPDFPLQEFTCYAREQVMTIL
СуАсрН	FKTSKQRLNQNHRKFAGVIIDIYYDHFLAKNWLIYS-EQDLDEFVANTYQMLEQHQ
РаАсрн	VHAAKRRFPLERRRFAGVLLDVFFDHCLARDWNDYA-DEPLPQFVERVYGTLRTA
PfAcpH	VGEALSRFSQTRRRYAGIVLDVFFDHCLARDWALYA-DQPLERFTSHVYQVLAAE
SoAcpH	TQELMALFPTQLTSIATDLMFVSFDHYLAFYWEEYH-HLPLPEFSQKAYAELAQYAAKAD
	: * : <mark>*</mark> * *: * . * . * . :
ЕсАсрН	PDSPPRFINLNNYLWSERWLVRYRDMDFIQSVLNGMASRRPRLDALRDSWYDLDAHYDAL
СуАсрН	LLLPEKLQKALPCMIQEDWLGSYRYFEGIDQTFSRLSRRIKRTNNIAFALEDLIQNYSQL
РаАсрн	SPLPERLARIAPRMAAQDWLGSYREFAVLREVLGGMSRRLSRPHLLDGSWEELAQRYDDL
PfAcpH	PALPGRLAQIAPYMAADDWLGSYREFAVMEQVLRGISRRLTQPEELGYAMQELRVLYEPL
SoAcpH	EYHPQPYLNIITDMHREDWLNNYATPKGIQQALAQRAKGHPQSALFSGADKILAKMQIET
	* . : : ** * :: : : : : *
ЕсАсрН	ETRFWQFYPRMMEQASRKAL
СуАсрН	EEDFLQFFPQLIDYVNLA
РаАсрН	SADFRAFYPQLQAFALSQR = Proposed Min ²⁺ binding residues
PfAcpH	SEDFRLFYPELQAFALQF
SoAcpH	ETAFRTFYPQLMAYTRIWSRKTPIDYLPE
	. * *:*.: .

Known active AcpH homologs from *E. coli* (EcAcpH),(*1*, *2*) *Cyanothece* PCC7822 (CyAcpH), *P. aeruginosa* (PaAcpH),(*3*, *4*) and *P. fluorescens* (PfAcpH) are aligned to the annotated hypothetical AcpH homolog from *S. oneidensis* (SoAcpH). The alignment reveals that only the SoAcpH lacks two out of three suspected active-site aspartate residues corresponding to D24, D78, D82 in EcAcpH predicted by Cronan for Mn²⁺ binding and previously mutated for activity impact.(*1*)





Variations of YbbR subjected to coumarin-PPant labeling AcpH activity Urea-PAGE analysis include free peptide (**a**), and FITC-conjugated peptide (**b**). Additionally, S6 peptide was labeled chemoenzymatically for AcpH reaction analysis (**c**). A rhodamine-PPant conjugate of YbbR was synthesized for FRET kinetics evaluation (**d**).

Analysis of AcpH activity with coumarin-YbbR



AcpH homologs from *P. fluorescens* (Pf), *P. aeruginosa* (Pa), *Cyanothece* PCC 7822 (Cy) and *S. oneidensis* (So) are evaluated by Urea-PAGE with *crypto*-YbbR and *crypto*-PksA (P) compared to no enzyme blanks (-) after overnight incubation at 37°C (+) or non-incubation (-).

Analysis of AcpH activity with coumarin-labeled YbbR and FITC-YbbR



AcpH homologs from *P. fluorescens* (Pf), and *Cyanothece* PCC 7822 (Cy) are evaluated by Urea-PAGE with *crypto*-YbbR and *crypto*-PksA compared to no enzyme blanks (-) after overnight incubation at 37°C (+) or non-incubation (-). PMSF is also used to pretreat a PfAcpH sample to ensure that probe hydrolysis is not due to serine-protease.

Analysis of AcpH homolog activity with YbbR-eGFP fusions



Analysis of AcpH homolog activity with S6 peptide



AcpH homologs from *P. fluorescens* (Pf), *P. aeruginosa* (Pa), *Cyanothece* PCC 7822 (Cy) and *S. oneidensis* (So) are evaluated by Urea-PAGE with *crypto*-S6 compared to no enzyme blanks (-), and no enzyme/Mg/Mn blank (-Mg/Mn) after overnight incubation at 37°C (+).



Analysis of AcpH homolog kinetics with holo-EcAcpP (FAS)

Reaction of AcpH homologs from *P. fluorescens* (Pf), *P. aeruginosa* (Pa), *Cyanothece* PCC 7822 (Cy) with *holo*-EcAcpP, and subsequent EDTA-quenching allow derivation of HPLC kinetic values. CyAcpH demonstrated significantly higher turnover, and required a lower enzyme concentration of 5 nM, compared to 1 \Box M utilized for other AcpH homologs. SoAcpH did not demonstrate activity in the qualitative assays, so was not evaluated for kinetics.

Verification of EDTA quench method



AcpH homologs from *P. fluorescens* (Pf), and *Cyanothece* PCC 7822 (Cy) are evaluated to verify the *holo- E. coli* AcpP reaction termination expected by EDTA addition prior to evaluating HPLC kinetic samples. No conversion of *holo-* to *apo-* AcpP was observed following a10 minute incubation at 37°C, followed by overnight incubation at room temperature.

Analysis of AcpH homolog kinetics with crypto-FITC-YbbR



Reaction of AcpH homologs from *P. fluorescens* (Pf), *P. aeruginosa* (Pa),and *Cyanothece* PCC 7822 (Cy) in microwell format with *crypto*-FITC-YbbR allows derivation of HPLC kinetic values. While PaAcpH and CyAcpH appeared to demonstrate signal above background, PfAcpH demonstrated clear signal indicating substrate turnover.

PfAcpH consensus substrate sequence and CP alignments



The consensus sequence of all PfAcpH active carrier protein sequences was generated using WebLogo (<u>http://weblogo.berkeley.edu</u>). The consensus demonstrates several residues matching those of the type II FAS ACPs as being particularly pervasive across active substrates (**a**). Inactive substrates contain 6 or fewer residues matching the active consensus (**b**), while only one active substrate, YbbR, contains fewer than 6 residues matching the consensus.

Coumarin-YbbR: LC-MS analysis



Coumarin-S6: LC-MS analysis



Coumarin-FITC-YbbR: LC-MS analysis



Rhodamine-FITC-YbbR: LC-MS analysis



Coumarin-YbbR PfAcpH reaction: LC analysis



Treatment of coumarin-YbbR with PfAcpH results in the depletion of the coumarin-YbbR peak at a retention time of 9.2 minutes (Supplementary Figure 26).

Coumarin-S6 PfAcpH reaction: LC analysis



Treatment of coumarin-S6 with PfAcpH results in the depletion of the coumarin-YbbR peak at a retention time of 10.4 minutes (Supplementary Figure 27).

Supplementary Table 1

Carrier proteins studied for AcpH activity

	Protein Name	Source Organism	Accession Number
	AcpP	E. coli	NP_287228
FAS	AcpP	P. aeruginosa	NP_251656
	AcpP	S. oneidensis	NP_718356
	PfACP	P. falciparum	3GZL_A
	АсрМ	M. tuberculosis	NP_216760
	MAS	M. tuberculosis	YP_006516394
PKS	ActACP	S. coelicolor	NP_629239
	PksA	A. parasiticus	2KR5_A
	Pks4	G. fujikuroi	CAB92399
	JamC	L. majuscula	AAS98798
	JamF	L. majuscula	CAB46501
	AdmA	P. agglomerans	AAO39095
NRPS	Adml	P. agglomerans	AAO39103
	VibB	V. cholerae	AAC45926
	CepK	A. orientalis	KF672793
	PItL	P. protogens	AAD24885
	SyrB1	P. syringae	AAZ99831

Carrier proteins used in this study used for PPant labeling and subsequent analysis of AcpH homolog activity via PPant hydrolysis.

Supplementary Table 2

Primers used for cloning

Primer Name	Primer Sequence $(5' \rightarrow 3')$
PfAcpH F1	AAAACATATGAATTATCTCGCACATCTGCACC
PfAcpH R1	AAAACTCGAGTGCAAAGGCCTGCAACTCTGG
PfAcpH R2	AAAACTCGAGTTAAAATTGGAGTGCAAAGGCCTGC
PfAcpH R3	AAAACTCGAGAAATTGGAGTGCAAAGGCCTGCAAC
CyAcpH F1	AAAACATATGAATTATCTGGCTCATTTATTTTTAGC
CyAcpH R1	AAAACTCGAGAGCCAAGTTAACATAATCAATCAGTTG
SoAcpH F1	AAAACATATGAACATTCTTACACACTTACATCTGG
SoAcpH R1	AAAACTCGAGCTCGGGTAAGTAGTCAATTGGAG

Primers used in cloning/sub-cloning for gene products used in this manuscript.

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