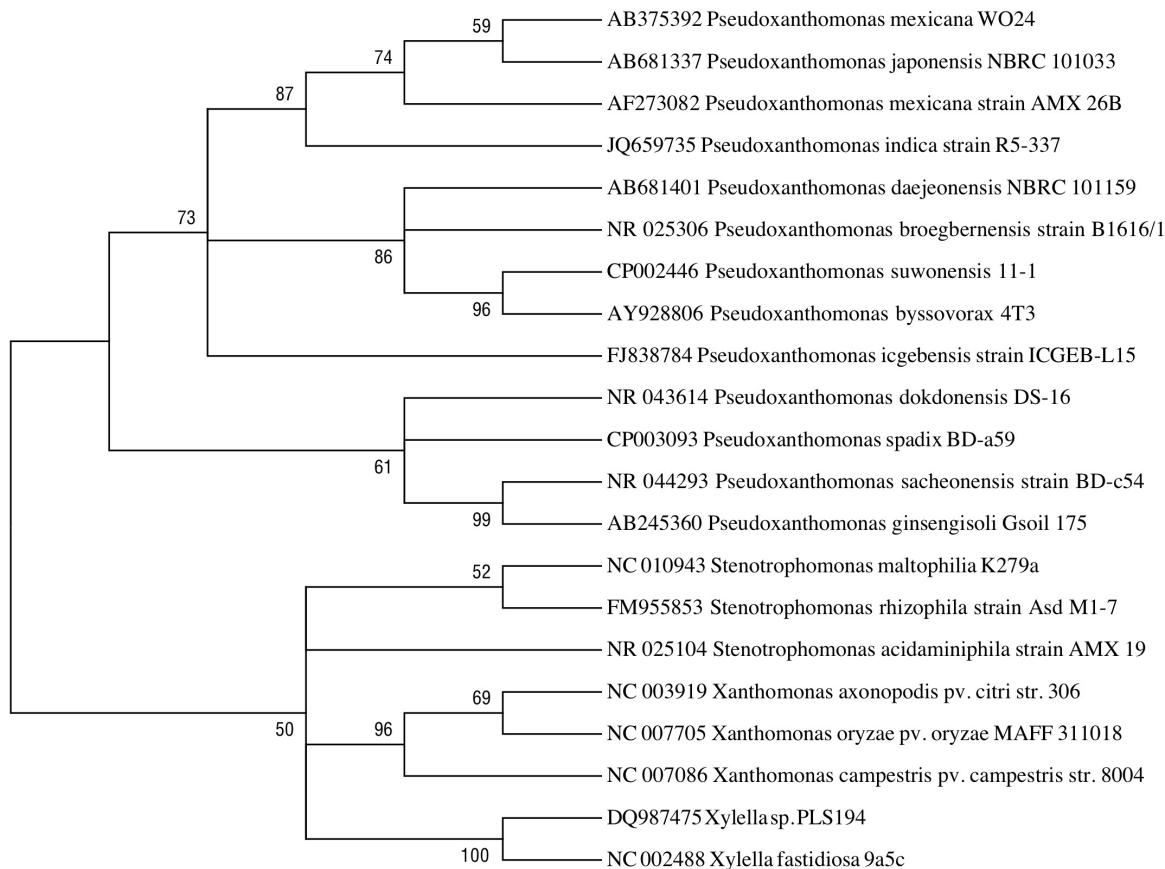


## Supporting information of " Identification of the Catalytic Triad of Family S46 Exopeptidases, Closely Related to Clan PA Endopeptidases "

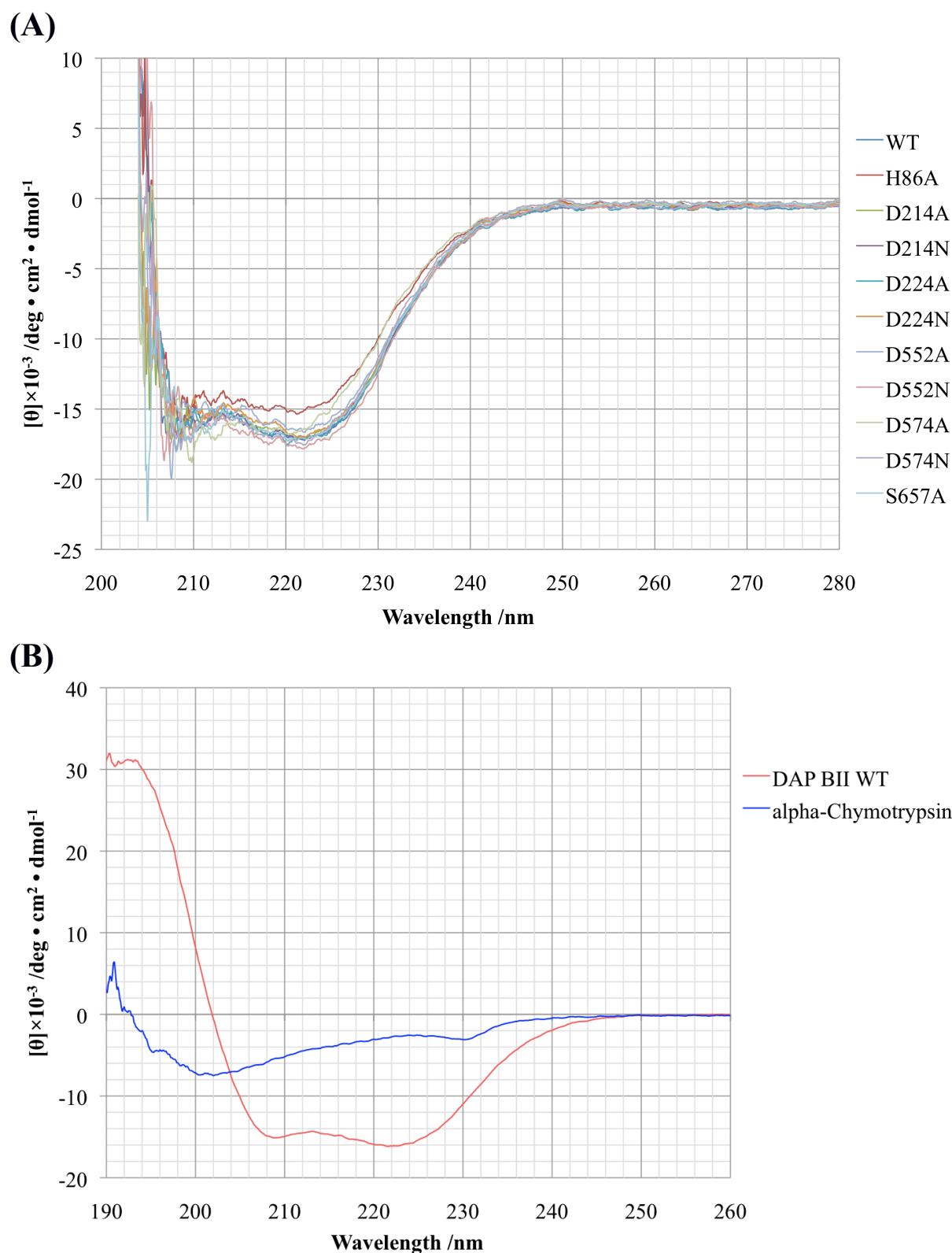
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### Supplementary Figures



**Supplemental Figure S1. Phylogenetic tree of 16S rRNA from related species of *Pseudoxanthomonas*.** The phylogenetic tree of 16S rRNA was constructed by MUSCLE multiple sequence alignment and phylogenetic analysis by maximum likelihood. Bootstrap values above 50% are shown at branch points.



**Supplemental Figure S2. Circular dichroism spectra.** (A) Spectra of DAP BII and mutants were obtained with a circular dichroism spectrophotometer. The spectra predict an alpha-helical content of about 47% for these proteins. (B) Spectra of DAP BII wild-type and alpha-chymotrypsin (*Bos taurus*).

## Supplementary Tables

**Supplemental Table S1. DNA/DNA hybridization**

	% homology with		
	WO24 <sup>a</sup>	<i>P. mexicana</i> <sup>a</sup>	<i>P. japonensis</i> <sup>a</sup>
Strain WO24 <sup>b</sup>	100	100	59
<i>Pseudoxanthomonas mexicana</i> JCM11524 <sup>b</sup>	71	100	59
<i>Pseudoxanthomonas japonensis</i> JCM11525 <sup>b</sup>	46	59	100

<sup>a</sup> filter-bound

<sup>b</sup> labeled

**Supplemental Table S2. Morphological and physiological properties of *Pseudoxanthomonas mexicana* WO24**

Strain	<i>Pseudoxanthomonas mexicana</i> WO24
Sampling place	A manufactory of tofu
Morphology	Rod
Length	2.0 - 3.0 $\mu\text{m}$
Width	0.7 $\mu\text{m}$
Motility	-
Spore formation	-
Gram-reaction	-
Oxidase	+
Catalase	+
Urease	+
Nitrate reductase	+
Indole formation	-
Starch hydrolysis	-
Acid from glucose	+
Oxidative-fermentative test	+
Growth temperature	Growth between 12 - 42 °C
GC content	67.9 mol%

**Supplemental Table S3. Primers used in this study**

Mutation	Primer sequences (5'→3')	
	Front	Reverse
For Mutan-Super Express Km (5' end is phosphorylated)		
<b>pK8b2-SacI</b>	GCCGtCCAGAgCtCCCAGG	
<b>pK8b3-SacI</b>	AGGCCGaGCtcGtCGCGCC	
<b>1stMet-NdeI</b>	AGGAAACACATAAAtATGCCAACCCCGC	
For PrimeSTAR Mutagenesis Basal Kit		
<b>H86A</b>	CAACCATgcCTGCGCCTATGGCGCCAT	GCGCAGgcATGGTTGGTGACCACAG
<b>S657A</b>	CGGCAACgCCGGTCGCGCGGTGCTC	GAACCGGeGTTGCCGCCGGTATGTCC
<b>D195A</b>	ATCAAGGcCGTGCGCCTGGCCTACG	GCGCACGgCCTTGATCTCCAGGTTCT
<b>D214A</b>	GACATCGeCAACTGGATGTGGCCGCG	CCAGTTGgCGATGTCGCCGCCGAAC
<b>D224A</b>	CGGCGeCTTCGCGTTCTACCGCGC	AACGCGAAGgCGCCGGTGTGGCGC
<b>D522A</b>	AGCAACGcTCCGGCCATCCAGTATGCG	GGCCGGAgCGTTGCTGGCTTCGAAC
<b>D574A</b>	TATCCCGcTGCCAACCTGTCGCTGC	GTTGGCAgCGGGATAGACGAACTCGC
<b>D195N</b>	ATCAAGAACGTGCGCCTGGCCTACG	GCGCACGTtCTTGATCTCCAGGTTCTTG
<b>D214N</b>	CGACATCaACAACCTGGATGTGGCCG	CAGTTGTtGATGTCGCCGCCGAACTTG
<b>D224N</b>	CACCGGCaACTTCGCGTTCTACCGCGCC	GCGAAGTtGCCGGTGTGGCGCGGCC
<b>D522N</b>	CAGCAACaATCCGGCCATCCAGTATGC	GCCGGATtGTTGCTGGCTTCGAACGC
<b>D574N</b>	CTATCCCCaATGCCAACCTGTCGCTGC	TTGGCATtGGGATAGACGAACTCGCC