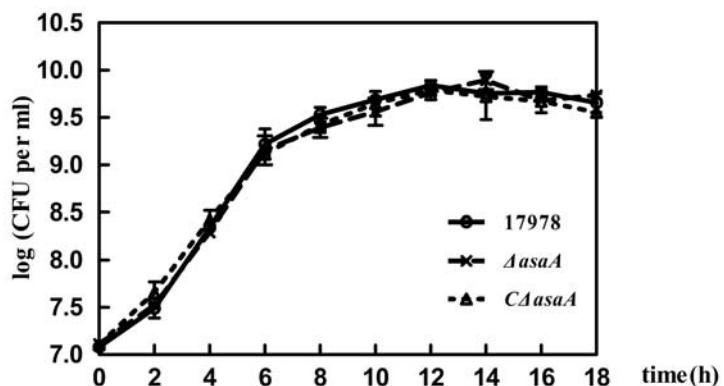


## Supplementary information

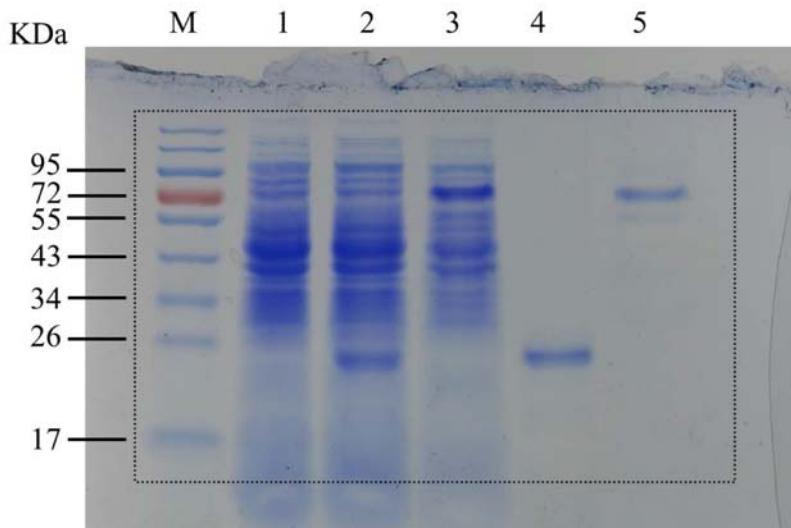
Title: The type VI secretion system protein AsaA in *Acinetobacter baumannii* is a periplasmic protein physically interacting with TssM and required for T6SS assembly

Authors: Lei Li, Yi-Nuo Wang, Hong-Bing Jia, Ping Wang, Jun-Fang Dong, Juan Deng, Feng-Min Lu & Qing-Hua Zou

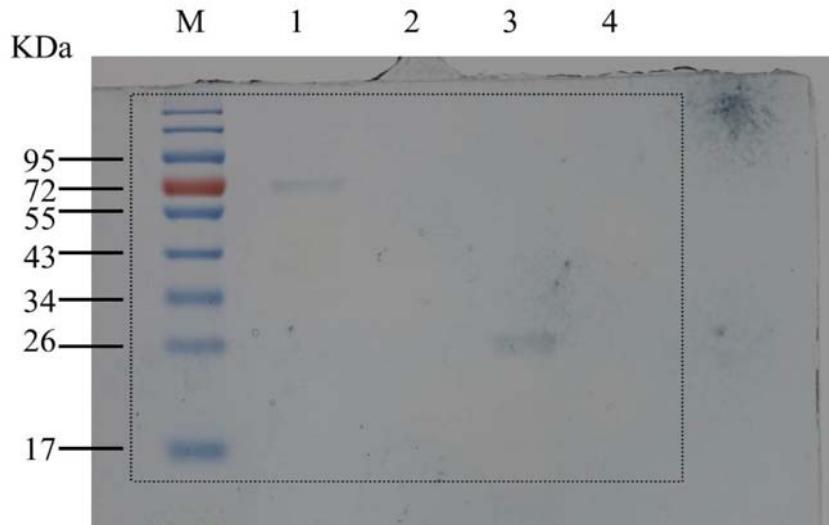


**Supplementary Figure 1.** *A. baumannii* strains growth curve in LB medium.

The wild type 17978, AsaA mutant and complementation strains were used to inoculate LB medium at  $10^7$  CFU per ml. Samples were taken in triplicate at intervals of 2 h, diluted and plated on LB plates. Bacterial CFU were counted after incubation for 2 days. The experiments were repeated twice with similar results, and one representative result is presented.



**Supplementary Figure 2.** The full-length gel of His<sub>6</sub>-tagged fusion proteins were over expressed and purified. Lanes: 1, crude BL21/pET30a extract; 2, crude BL21/pET30a-AsaA extract induced with IPTG; 3, crude BL21/pET30a-TssM<sub>436-1041</sub> extract induced with IPTG; 4, affinity-purified His<sub>6</sub>-AsaA protein; 5, affinity-purified His<sub>6</sub>-TssM<sub>436-1041</sub> protein; M, molecular mass marker. Inside the box is the figure 4B.



**Supplementary Figure 3.** The full-length gel of Pull-down assays. Lanes: 1, pull-down of His<sub>6</sub>-TssM by immobilized His<sub>6</sub>-AsaA; 2, His<sub>6</sub>-TssM mixed with streptavidin sepharose beads(negative control); 3, pull-down of His<sub>6</sub>-AsaA by immobilized His<sub>6</sub>-TssM; 4, His<sub>6</sub>-AsaA mixed with streptavidin sepharose beads(negative control) ; M, molecular mass marker. Inside the box is the figure 4C.

**Table S1. Strains and plasmids used in this study**

Strains or plasmids	Relevant characteristics	Reference or source
<i>E. coli</i> strains		
JM109	<i>RecA1, endA1, gyrA96, thi, supE44, relA1</i> Δ ( <i>lac-proAB</i> )/F' [ <i>traD36, lacI<sup>r</sup>, lacZ</i> Δ <i>M15</i> ]	[1]
JM109/pk18mob	JM109 harboring recombinant plasmid pk18mob, Kan <sup>r</sup>	This work
BL21(DE3)	F' <i>ompT gal dcm lon hsdS<sub>B</sub> (r<sub>B</sub>m<sub>B</sub>) λ</i> (DE3)	Novagen,Germany
BL21/ pET30a	BL21(DE3) harboring plasmid pET30a, Kan <sup>r</sup>	This work
BL21/pET30a-AsaA	BL21(DE3) harboring plasmid pET30a-AsaA, Kan <sup>r</sup>	This work
BL21/pET30a-TssM <sub>34-370</sub>	BL21(DE3) harboring plasmid pET30a-TssM <sub>34-370</sub> , Kan <sup>r</sup>	This work
XL1-Blue MRF'	Reporter strain, Δ( <i>mcrA</i> )183 Δ( <i>mcrCB-hsdSMR-mrr</i> )173 <i>endA1 hisB sup E44 thi1 recA1 gyrA96relA1 lac</i> [F' lacI <sup>q</sup> <i>HIS3 aadA</i> Kan <sup>r</sup> ]	Stratagene
X/pBA-pTB	XL1-Blue MRF' harboring plasmid pBA and pTB, Kan <sup>r</sup> Tc <sup>r</sup> Cm <sup>r</sup>	This work

X/pBA-pTL	XL1-Blue MRF' harboring plasmid pBA and pTL, Kan <sup>r</sup> Tc <sup>r</sup> Cm <sup>r</sup>	This work
X/pBA-pTM <sub>1303</sub>	XL1-Blue MRF' harboring plasmid pBA and pTM <sub>1303</sub> , Kan <sup>r</sup> Tc <sup>r</sup> Cm <sup>r</sup>	This work
X/pBA-pTM <sub>33-415</sub>	XL1-Blue MRF' harboring plasmid pBA and pTM <sub>33-415</sub> , Kan <sup>r</sup> Tc <sup>r</sup> Cm <sup>r</sup>	This work
X/pBA-pTM <sub>436-1041</sub>	XL1-Blue MRF' harboring plasmid pBA and pTM <sub>436-1041</sub> , Kan <sup>r</sup> Tc <sup>r</sup> Cm <sup>r</sup>	This work
X/pBA-pT	XL1-Blue MRF' harboring plasmid pBA and pTRG, Kan <sup>r</sup> Tc <sup>r</sup> Cm <sup>r</sup>	This work
X/pB-pTM <sub>436-1041</sub>	XL1-Blue MRF' harboring plasmid pBT and pTM <sub>436-1041</sub> , Kan <sup>r</sup> Tc <sup>r</sup> Cm <sup>r</sup>	This work
X/pBhpAM-pThrcJ	XL1-Blue MRF' harboring plasmid pBhpAM and pThrcJ, Kan <sup>r</sup> Tc <sup>r</sup> Cm <sup>r</sup>	[2]
X/pBA <sub>25-70</sub> -pTM <sub>436-1041</sub>	XL1-Blue MRF' harboring plasmid pBA <sub>25-70</sub> and pTM <sub>436-1041</sub> , Kan <sup>r</sup> Tc <sup>r</sup> Cm <sup>r</sup>	This work
X/pBA <sub>25-110</sub> -pTM <sub>436-1041</sub>	XL1-Blue MRF' harboring plasmid pBA <sub>25-110</sub> and pTM <sub>436-1041</sub> , Kan <sup>r</sup> Tc <sup>r</sup> Cm <sup>r</sup>	This work
X/pBA <sub>25-150</sub> -pTM <sub>436-1041</sub>	XL1-Blue MRF' harboring plasmid pBA <sub>25-150</sub> and pTM <sub>436-1041</sub> , Kan <sup>r</sup> Tc <sup>r</sup> Cm <sup>r</sup>	This work
X/pBA <sub>25-190</sub> -pTM <sub>436-1041</sub>	XL1-Blue MRF' harboring plasmid pBA <sub>25-190</sub> and pTM <sub>436-1041</sub> , Kan <sup>r</sup> Tc <sup>r</sup> Cm <sup>r</sup>	This work
X/pBA <sub>25-230</sub> -pTM <sub>436-1041</sub>	XL1-Blue MRF' harboring plasmid pBA <sub>25-230</sub> and pTM <sub>436-1041</sub> , Kan <sup>r</sup> Tc <sup>r</sup> Cm <sup>r</sup>	This work
X/pBA <sub>110-230</sub> -pTM <sub>436-1041</sub>	XL1-Blue MRF' harboring plasmid pBA <sub>110-230</sub> and pTM <sub>436-1041</sub> , Kan <sup>r</sup> Tc <sup>r</sup> Cm <sup>r</sup>	This work
X/pBA <sub>150-230</sub> -pTM <sub>436-1041</sub>	XL1-Blue MRF' harboring plasmid pBA <sub>150-230</sub> and pTM <sub>436-1041</sub> , Kan <sup>r</sup> Tc <sup>r</sup> Cm <sup>r</sup>	This work
X/pBA <sub>190-230</sub> -pTM <sub>436-1041</sub>	XL1-Blue MRF' harboring plasmid pBA <sub>190-230</sub> and pTM <sub>436-1041</sub> , Kan <sup>r</sup> Tc <sup>r</sup> Cm <sup>r</sup>	This work
X/pBA <sub>70-150</sub> -pTM <sub>436-1041</sub>	XL1-Blue MRF' harboring plasmid pBA <sub>70-150</sub> and pTM <sub>436-1041</sub> , Kan <sup>r</sup> Tc <sup>r</sup> Cm <sup>r</sup>	This work
X/pBA <sub>70-110</sub> -pTM <sub>436-1041</sub>	XL1-Blue MRF' harboring plasmid pBA <sub>70-110</sub> and pTM <sub>436-1041</sub> , Kan <sup>r</sup> Tc <sup>r</sup> Cm <sup>r</sup>	This work
X/pBA <sub>110-150</sub> -pTM <sub>436-1041</sub>	XL1-Blue MRF' harboring plasmid pBA <sub>110-150</sub> and pTM <sub>436-1041</sub> , Kan <sup>r</sup> Tc <sup>r</sup> Cm <sup>r</sup>	This work

#### A. *Baumannii* strains

17978	wild type strain	[3]
<i>ΔasaA</i>	As 17978, but <i>asaA</i> gene ( <i>AIS_1292</i> ) deleted.	This work
<i>ΔtssM</i>	As 17978, but <i>tssM</i> gene ( <i>AIS_1302</i> ) deleted.	This work
<i>CΔasaA</i>	<i>ΔasaA</i> harboring the recombinant plasmid pTrc99A <sub>asaA</sub> , Amp <sup>r</sup>	This work
17978/pThepH6	17978 harboring recombinant plasmid pTHEpH6, Amp <sup>r</sup>	This work
<i>ΔasaA</i> /pThepH6	<i>ΔasaA</i> harboring recombinant plasmid pTHEpH6, Amp <sup>r</sup>	This work
<i>ΔtssM</i> /pThepH6	<i>ΔtssM</i> harboring recombinant plasmid pTHEpH6, Amp <sup>r</sup>	This work
<i>ΔasaA</i> / pTasaAH6	<i>ΔasaA</i> harboring the recombinant plasmid pTrc99A <sub>asaAH6</sub> , Amp <sup>r</sup>	This work
17978/pTpglCH6	17978 harboring recombinant plasmid pTpglCH6, Amp <sup>r</sup>	This work
17978/pTompAH6	17978 harboring recombinant plasmid pTompA H6, Amp <sup>r</sup>	This work
17978/pTdsbAH6	17978 harboring recombinant plasmid pTdsbAH6, Amp <sup>r</sup>	This work

#### Plasmids

pET30a	Expression vector, allow the production of fusion proteins containing amino terminal 6×His -tagged sequences. Kan <sup>r</sup>	Novagen
pET30a-AsaA	pET30a containing a 618-bp fragment of partial <i>asaA</i> gene sequence encoding the 25 <sup>th</sup> -230 <sup>th</sup> amino acids. Kan <sup>r</sup>	This work
pET30a- TssM <sub>436-1041</sub>	pET-30a containing a 1818-bp fragment of partial <i>tssM</i> gene sequence encoding the 436 <sup>th</sup> -1041 <sup>th</sup> amino acids. Kan <sup>r</sup>	This work
pTrc99A	<i>Ptrc</i> , pBR322ori, <i>rrnB</i> T1, <i>rrnB</i> T2, <i>lac Iq</i> , <i>bla</i> , template for <i>Ptrc</i> Promoter, Amp <sup>r</sup>	[4]
pThepH6	pTrc99A containing the encoding sequence of Hcp with 6×His tag in its C-terminus, Amp <sup>r</sup>	This work

pTasaAH6	pTrc99A containing the encoding sequence of AsaA with 6×His tag in its C-terminus, Amp <sup>r</sup>	This work
pTpglCH6	pTrc99A containing the encoding sequence of PgIC with 6×His tag in its C-terminus, Amp <sup>r</sup>	This work
pTompAH6	pTrc99A containing the encoding sequence of OmpA with 6×His tag in its C-terminus, Amp <sup>r</sup>	This work
pTdsbAH6	pTrc99A containing the encoding sequence of DsbA with 6×His tag in its C-terminus, Amp <sup>r</sup>	This work
pBT	Two-hybrid system bait plasmid containing the <i>cm</i> gene, p15A origin of replication and λcl ORF, Cm <sup>r</sup>	Stratagene
pBA	pBT derivative carrying a 621-bp fragment encoding the 25 <sup>th</sup> –230 <sup>th</sup> amino acids of AsaA, Cm <sup>r</sup>	This work
pBA <sub>25-70</sub>	pBT derivative carrying a 138-bp fragment encoding the 25 <sup>th</sup> –70 <sup>th</sup> amino acids of AsaA, Cm <sup>r</sup>	This work
pBA <sub>25-110</sub>	pBT derivative carrying a 258-bp fragment encoding the 25 <sup>th</sup> –110 <sup>th</sup> amino acids of AsaA, Cm <sup>r</sup>	This work
pBA <sub>25-150</sub>	pBT derivative carrying a 378-bp fragment encoding the 25 <sup>th</sup> –150 <sup>th</sup> amino acids of AsaA, Cm <sup>r</sup>	This work
pBA <sub>25-190</sub>	pBT derivative carrying a 498-bp fragment encoding the 25 <sup>th</sup> –190 <sup>th</sup> amino acids of AsaA, Cm <sup>r</sup>	This work
pBA <sub>70-230</sub>	pBT derivative carrying a 483-bp fragment encoding the 70 <sup>th</sup> –230 <sup>th</sup> amino acids of AsaA, Cm <sup>r</sup>	This work
pBA <sub>110-230</sub>	pBT derivative carrying a 363-bp fragment encoding the 110 <sup>th</sup> –230 <sup>th</sup> amino acids of AsaA, Cm <sup>r</sup>	This work
pBA <sub>150-230</sub>	pBT derivative carrying a 243-bp fragment encoding the 150 <sup>th</sup> –230 <sup>th</sup> amino acids of AsaA, Cm <sup>r</sup>	This work
pBA <sub>190-230</sub>	pBT derivative carrying a 123-bp fragment encoding the 190 <sup>th</sup> –230 <sup>th</sup> amino acids of AsaA, Cm <sup>r</sup>	This work
pBA <sub>70-150</sub>	pBT derivative carrying a 243-bp fragment encoding the 70 <sup>th</sup> –150 <sup>th</sup> amino acids of AsaA, Cm <sup>r</sup>	This work
pBA <sub>70-110</sub>	pBT derivative carrying a 123-bp fragment encoding the 70 <sup>th</sup> –110 <sup>th</sup> amino acids of AsaA, Cm <sup>r</sup>	This work
pBA <sub>110-150</sub>	pBT derivative carrying a 123-bp fragment encoding the 110 <sup>th</sup> –150 <sup>th</sup> amino acids of AsaA, Cm <sup>r</sup>	This work
pTRG	Two-hybrid system target plasmid containing the <i>tet</i> gene, ColE1 origin of replication, and RNA polymerase α subunit ORF, Tc <sup>r</sup>	Stratagene
pTB	pTRG derivative carrying the 150-bp of <i>tssB</i> gene, Tc <sup>r</sup>	This work
pTL	pTRG derivative carrying the 648-bp of <i>tssL</i> gene, Tc <sup>r</sup>	This work
pTM <sub>1303</sub>	pTRG derivative carrying the 567-bp of <i>AIS_1303</i> gene, Tc <sup>r</sup>	This work
pTM <sub>33-415</sub>	pTRG derivative carrying a 1149-bp fragment encoding the 33 <sup>th</sup> –415 <sup>th</sup> amino acids of <i>tssM</i> gene, Tc <sup>r</sup>	This work
pTM <sub>436-1041</sub>	pTRG derivative carrying a 1818-bp fragment encoding the 436 <sup>th</sup> –1041 <sup>th</sup> amino acids of <i>tssM</i> gene, Tc <sup>r</sup>	This work

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**Table S2. Primers used in this study**

Primer	Nucleotide sequence (5'→3')	The amplified fragment or the utilization
<i>asaA</i> -F	TATTCTAAAATATTAACCTTTCGTAAGGCCTTGAATAAAATAAGAAAA	DNA fragment of 1581-bp of the kanamycin resistance ORF sequence and coding sequence fusing with <i>asaA</i> upstream and downstream encoded sequence. Used for construction of <i>asaA</i> deletion mutant.
<i>asaA</i> -R	CAGAGGAGTGTAGGCTGGAGCTGCTTC TCGCTGAAGCTTCTTGACGTTCTCTTAGCCATAAGATTCTA TTCGGACATATGAATATCCTCCTAG	
<i>tssM</i> -F	GGCAGTACATCACGAATCCTAAAGCAATTATGCCCTGTCATTGTTCGT	DNA fragment of 1581-bp of the kanamycin resistance ORF sequence and coding sequence fusing with <i>tssM</i> upstream and downstream encoded sequence. Used for construction of <i>tssM</i> deletion mutant.
<i>tssM</i> -R	GGCATGGTGTAGGCTGGAGCTGCTTC TGCCATTCCATTGTAGGTGCAACATAGCGTTGGAAGTTCTAACAAA TTGTGGGTATGAATATCCTCCTAG	
<i>asaA</i> -CF	AAGAATTCAAATATTAACCTTCGGTAAGG	DNA fragment of 759-bp DNA fragment spans 48 upstream to the stop codon of the <i>asaA</i> ORF sequence, which fusing with 6×His tag encoding sequences. Used for construction of <i>AasaA</i> complement and Western blot analysis.
<i>asaA</i> -CR	AAGGATCCTAGTGGTGGTGGTGGTGGTTAAATTAAAGGGTCAAA AGG	
<i>hcp</i> -qF	ATATATACGTTGAGTTTCG	381-bp internal fragment of <i>hcp</i> , used for qRT-PCR.
<i>hcp</i> -qR	AACCGAATGCTCTGTAG	
16s-F	GTGCCAGCAGCCCGCGGT	846-bp internal fragment of the 16S rDNA sequence, used for qRT-PCR.
16s-R	GACGGGCGGTGTGTACA	
<i>hcp</i> -HF	ATGGATCCGACCACATTCCAGCTGG	DNA fragment of 627-bp <i>hcp</i> coding sequence fusing with 6×His tag encoding sequences. Used for Western blot analysis.
<i>hcp</i> -HR	AGTCTAGATTAGTGGTGGTGGTGGTGGCTCGCTCGTAAGAACG	
<i>pglC</i> -HF	CCGAATTCTGAAATGAAAATATGAA	DNA fragment of 633-bp <i>pglC</i> coding sequence fusing with 6×His tag encoding sequences. Used for Western blot analysis.
<i>pglC</i> -HR	AAGGATCCTAGTGGTGGTGGTGGTGGTGGCTAACAGAAGAAT	
<i>dsbA</i> -HF	CCGAATTCTGAAATGAGTCGTATT	DNA fragment of 618-bp <i>dsbA</i> coding sequence fusing with 6×His tag encoding sequences. Used for Western blot analysis.
<i>dsbA</i> -HR	AAGGATCCTAGTGGTGGTGGTGGTGGTGGTGGCTTACGTT	
<i>ompA</i> -HF	CCGAATTCTGAAATGAGTCGTATT	DNA fragment of 1071-bp <i>ompA</i> coding sequence fusing with 6×His tag encoding sequences. Used for Western blot analysis.
<i>ompA</i> -HR	AAGGATCCTAGTGGTGGTGGTGGTGGTGGCTGCTGCAG	
<i>tssM</i> <sub>(33-415)</sub> -F	CCGGATCCCAGCGTAAAAGCATGCT	1149-bp DNA fragment spans nucleotides 97 to 1245 bp of the <i>tssM</i> coding sequence, encoding the 33 <sup>th</sup> - 415 <sup>th</sup> amino acids. Used for bacterial two-hybrid assay.
<i>tssM</i> <sub>(33-415)</sub> -R	AAGGATCCACGCTGACGCTTTTGCT	
<i>tssM</i> <sub>(436-1041)</sub> -F	CCGGATCCTCATATCGTAACAATCAA	1818-bp DNA fragment spans nucleotides 1306 to 3123 bp of the <i>tssM</i> coding sequence, encoding the 436 <sup>th</sup> - 1041 <sup>th</sup> amino acids. Used for bacterial two-hybrid assay.
<i>tssM</i> <sub>(436-1041)</sub> -R	AAGAATTCAACTAACCCCCAAATCTT	

<i>tssB</i> -F	CCGGAT <u>CCG</u> TGTTCAGACTTACATAT	150-bp DNA fragment of the <i>tssB</i> ORF sequence. Used for bacterial two-hybrid assay.
<i>tssB</i> -R	AAGAATT <u>CC</u> AAATCGACATTAATGA	
<i>tssL</i> -F	CCGGAT <u>CC</u> CATGTACAATCTACAGGT	648-bp DNA fragment spans nucleotides 1 to 648 bp of the <i>tssM</i> coding sequence, encoding the 1 <sup>th</sup> - 216 <sup>th</sup> amino acids. Used for bacterial two-hybrid assay.
<i>tssL</i> -R	AAGAATT <u>CC</u> AGGTAGCTACGATGGAT	
<i>Tss1303</i> -F	CCGGAT <u>CC</u> CATGGCAACAGGTGAGTTA	567-bp DNA fragment of the <i>AIS_1303</i> ORF sequence. Used for bacterial two-hybrid assay.
<i>Tss1303</i> -R	AAGAATT <u>CC</u> TCATGGCTTA <u>CT</u> CCCGC	
<i>asaA</i> -OF	AAG <u>GAT</u> CCC <u>AAG</u> CAGCAGAA <u>CT</u> AGAG	621-bp DNA fragment spans nucleotides 73 to 693 bp of the <i>asaA</i> coding sequence, encoding the 25 <sup>th</sup> - 230 <sup>th</sup> amino acids. Used for pull-down assay.
<i>asaA</i> -OR	CG <u>AAG</u> CTTT <u>AT</u> TTA <u>AT</u> AA <u>AGGG</u> TC	
<i>tssM</i> -OF	AAG <u>GAT</u> C <u>CT</u> CATATCGTA <u>AC</u> AA <u>AT</u> CAA	1821-bp DNA fragment spans nucleotides 1306 to 3126 bp of the <i>tssM</i> coding sequence, encoding the 436 <sup>th</sup> - 1041 <sup>th</sup> amino acids. Used for pull-down assay.
<i>tssM</i> -OR	CCG <u>TCG</u> A <u>CT</u> AA <u>ACT</u> A <u>AT</u> CCCC <u>AA</u> AT <u>CT</u> T	
<i>asaA</i> -1F	CC <u>GAATT</u> C <u>ACA</u> AGCAGCAGAA <u>CT</u> AGAG	621-bp DNA fragment spans nucleotides 73 to 693 bp of the <i>asaA</i> coding sequence, encoding the 25 <sup>th</sup> - 230 <sup>th</sup> amino acids. Used for bacterial two-hybrid assay.
<i>asaA</i> -1R	A <u>AGG</u> AT <u>CC</u> T <u>AT</u> TTA <u>AT</u> AA <u>AGGG</u> TC	
<i>asaA</i> -2F	CC <u>GAATT</u> C <u>ACA</u> AGCAGCAGAA <u>CT</u> AGAG	138-bp DNA fragment spans nucleotides 73 to 210 bp of the <i>asaA</i> coding sequence, encoding the 25 <sup>th</sup> - 70 <sup>th</sup> amino acids. Used for bacterial two-hybrid assay.
<i>asaA</i> -2R	A <u>AGG</u> AT <u>CC</u> C <u>AT</u> TTT <u>TTT</u> GAG <u>TT</u> GTATT	
<i>asaA</i> -3F	CC <u>GAATT</u> C <u>ACA</u> AGCAGCAGAA <u>CT</u> AGAG	258-bp DNA fragment spans nucleotides 73 to 330 bp of the <i>asaA</i> ORF sequence, encoding the 25 <sup>th</sup> - 110 <sup>th</sup> amino acids. Used for bacterial two-hybrid assay.
<i>asaA</i> -3R	A <u>AGG</u> AT <u>CC</u> TA <u>AG</u> AC <u>AT</u> CT <u>GT</u> GATTAA	
<i>asaA</i> -4F	CC <u>GAATT</u> C <u>ACA</u> AGCAGCAGAA <u>CT</u> AGAG	378-bp DNA fragment spans nucleotides 73 to 450 bp of the <i>asaA</i> ORF sequence, encoding the 25 <sup>th</sup> - 150 <sup>th</sup> amino acids. Used for bacterial two-hybrid assay.
<i>asaA</i> -4R	A <u>AGG</u> AT <u>CC</u> CAT <u>GA</u> AT <u>AT</u> TT <u>CA</u> ACTAA	
<i>asaA</i> -5F	CC <u>GAATT</u> C <u>ACA</u> AGCAGCAGAA <u>CT</u> AGAG	498-bp DNA fragment spans nucleotides 73 to 570 bp of the <i>asaA</i> ORF sequence, encoding the 25 <sup>th</sup> - 190 <sup>th</sup> amino acids. Used for bacterial two-hybrid assay.
<i>asaA</i> -5R	A <u>AGG</u> AT <u>CC</u> C <u>AG</u> CA <u>CT</u> CA <u>CT</u> T <u>ATT</u> AC <u>CG</u>	
<i>asaA</i> -6F	CC <u>GAATT</u> C <u>AT</u> CT <u>GA</u> AC <u>AT</u> CAA <u>AT</u> AAA	123-bp DNA fragment spans nucleotides 571 to 693 bp of the <i>asaA</i> ORF sequence, encoding the 190 <sup>th</sup> - 230 <sup>th</sup> amino acids. Used for bacterial two-hybrid assay.
<i>asaA</i> -6R	A <u>AGG</u> AT <u>CC</u> TT <u>AT</u> TT <u>AA</u> AT <u>AA</u> AGGGTC	
<i>asaA</i> -7F	CC <u>GAATT</u> C <u>ACT</u> G <u>CA</u> AT <u>GCC</u> GG <u>CT</u> CC	243-bp DNA fragment spans nucleotides 451 to 693 bp of the <i>asaA</i> ORF sequence, encoding the 150 <sup>th</sup> - 230 <sup>th</sup> amino acids. Used for bacterial two-hybrid assay.
<i>asaA</i> -7R	A <u>AGG</u> AT <u>CC</u> TT <u>AT</u> TT <u>AA</u> AT <u>AA</u> AGGGTC	
<i>asaA</i> -8F	CC <u>GAATT</u> C <u>AT</u> TT <u>AT</u> CT <u>GG</u> GT <u>GT</u> GAGC	363-bp DNA fragment spans nucleotides 331 to 693 bp of the <i>asaA</i> ORF sequence, encoding the 110 <sup>th</sup> - 230 <sup>th</sup> amino acids. Used for bacterial two-hybrid assay.
<i>asaA</i> -8R	A <u>AGG</u> AT <u>CC</u> TT <u>AT</u> TT <u>AA</u> AT <u>AA</u> AGGGTC	
<i>asaA</i> -9F	CC <u>GAATT</u> C <u>AG</u> AT <u>TT</u> AT <u>AG</u> CT <u>AA</u> AG <u>CT</u>	483-bp DNA fragment spans nucleotides 211 to 693 bp of the <i>asaA</i> ORF sequence, encoding the 70 <sup>th</sup> - 230 <sup>th</sup> amino acids. Used for bacterial two-hybrid assay.
<i>asaA</i> -9R	A <u>AGG</u> AT <u>CC</u> TT <u>AT</u> TT <u>AA</u> AT <u>AA</u> AGGGTC	
<i>asaA</i> -10F	CC <u>GAATT</u> C <u>AG</u> AT <u>TT</u> AT <u>AG</u> CT <u>AA</u> AG <u>CT</u>	240-bp DNA fragment spans nucleotides 211 to 450 bp of the <i>asaA</i> ORF sequence, encoding the 70 <sup>th</sup> - 150 <sup>th</sup> amino acids. Used for bacterial two-hybrid assay.
<i>asaA</i> -10R	A <u>AGG</u> AT <u>CC</u> AT <u>GA</u> AT <u>AT</u> TT <u>CA</u> ACTAA	
<i>asaA</i> -11F	CC <u>GAATT</u> C <u>AG</u> AT <u>TT</u> AT <u>AG</u> CT <u>AA</u> AG <u>CT</u>	120-bp DNA fragment spans nucleotides 211 to 330 bp of the <i>asaA</i> ORF sequence, encoding the 70 <sup>th</sup> - 110 <sup>th</sup> amino acids. Used for bacterial two-hybrid assay.
<i>asaA</i> -11R	A <u>AGG</u> AT <u>CC</u> TA <u>AG</u> AC <u>AT</u> CT <u>GT</u> GATTAA	

<i>asaA</i> -12F	CCGAATT <u>C</u> TTTTATCTGGTGTGAGC	120-bp DNA fragment spans nucleotides 331 to 450 bp of the <i>asaA</i> ORF sequence, encoding the 110 <sup>th</sup> -150 <sup>th</sup> amino acids. Used for bacterial two-hybrid assay.
<i>asaA</i> -12R	AAGGAT <u>CC</u> CATGAATTTCAACTAA	

The underlined sequences indicate the restriction sites for *Eco*RI, *Hind*III, *Sal*I, *Xba*I and *Bam*HI, respectively.

**Table S3. AsaA homologues in the family *Moraxellaceae***

Species	Gene	Signal peptide	Length (aa)	Identity(%) /similarity(%)	Function predicted	Sequence Types (ST)	Reference
<i>Acinetobacter baumannii</i> AC29	<i>BL01_13280</i>	1 <sup>th</sup> -24 <sup>th</sup> aa	230	100/100	signal peptide protein	195	[1]
<i>Acinetobacter baumannii</i> BJAB0868	<i>BJAB0868_01</i> 408	1 <sup>th</sup> -24 <sup>th</sup> aa	230	100/100	hypothetical protein	218	[2]
<i>Acinetobacter baumannii</i> 1656-2	<i>ABK1_1741</i>	1 <sup>th</sup> -24 <sup>th</sup> aa	230	100/100	putative exported protein	423	[3]
<i>Acinetobacter baumannii</i> AB307-0294	<i>ABBF4_00224</i> 0	1 <sup>th</sup> -24 <sup>th</sup> aa	230	99.6/99.6	hypothetical protein	231	[4]
<i>Acinetobacter baumannii</i> AB0057	<i>AB57_1478</i>	1 <sup>th</sup> -24 <sup>th</sup> aa	230	99.1/99.6	hypothetical protein	207	[4]
<i>Acinetobacter baumannii</i> BJAB0715	<i>BJAB0715_01</i> 479	1 <sup>th</sup> -24 <sup>th</sup> aa	230	99.1/99.6	hypothetical protein	642	[5]
<i>Acinetobacter baumannii</i> AbH12O-A2	<i>LX00_06400</i>	1 <sup>th</sup> -24 <sup>th</sup> aa	230	99.1/99.1	signal peptide protein	924	[6]
<i>Acinetobacter pittii</i>	<i>BDGL_00063</i> 8	1 <sup>th</sup> -26 <sup>th</sup> aa	229	90.9/92.6	hypothetical protein	1527	[7]
<i>Acinetobacter calcoaceticus</i>	<i>BUM88_0673</i> 5	1 <sup>th</sup> -26 <sup>th</sup> aa	229	87.8/92.2	hypothetical protein	1043	accession CP020000.1
<i>Acinetobacter nosocomialis</i>	<i>RR32_11560</i>	1 <sup>th</sup> -24 <sup>th</sup> aa	229	80.9/87.8	signal peptide protein	1162	accession CP010368.1
<i>Acinetobacter baylyi</i>	<i>ACIAD2693</i>	1 <sup>th</sup> -22 <sup>th</sup> aa	218	43.5/57.8	hypothetical protein		[8]

<i>Acinetobacter indicus</i>	CTZ23_07445	1 <sup>th</sup> -22 <sup>th</sup> aa	222	33.3/46.8	hypothetical protein	[9]
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Searching the AsaA homologues were carried out by blast the genome sequences in NCBI database with the AsaA sequence. No, no significant similarity protein (similarity>20%) was found within the genome sequence. Signal peptide predictions was carried with the SignalP program. Identity(%)/similarity(%) analysis was performed using the Align X program in Vector NTI software.

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