



**Fig. S1. Schematic diagram of bacterial injection and hemolymph collection region in crab.** For in vivo bacterial infection, bacterial *S. aureus* or *V. parahaemolyticus* were injected into hemolymph from the non-sclerotized membrane of the posterior walking leg at the left side, and hemolymph were collected from the non-sclerotized membrane of the posterior walking leg at the right side.

**Table S1. Information of genes used for sequence, phylogeny and structure analysis in present study**

GenBank Number	Gene name	Species	Application
AIN75603.1	ADAM10	<i>Eriocheir sinensis</i>	PA,3D, DP
KAB7502289.1	ADAM10	<i>Armadillidium nasatum</i>	PA
KOX69803.1	ADAM10	<i>Melipona quadrifasciata</i>	PA
XP_006608279.1	ADAM10	<i>Apis dorsata</i>	PA
OAD61840.1	ADAM10	<i>Eufriesea mexicana</i>	PA
EFN75386.1	ADAM10	<i>Harpegnathos saltator</i>	PA
AAC47275.1	kuzbanian	<i>Drosophila melanogaster</i>	PA
ROT74984.1	ADAM10	<i>Penaeus vannamei</i>	PA,3D, DP
XP_026322466.1	ADAM10	<i>Hyposmocoma kahamanao</i>	PA
XP_026737279.1	ADAM10	<i>Trichoplusia ni</i>	PA
AAC51766.1	ADAM10	<i>Homo sapiens</i>	PA,3D, DP
EDL26211.1	ADAM10	<i>Mus musculus</i>	PA,3D, DP
XP_014437339.1	ADAM10	<i>Tupaia chinensis</i>	PA
XP_039086571.1	ADAM10	<i>Hyaena hyaena</i>	PA
NP_001124567.1	ADAM10	<i>Pongo abelii</i>	PA
XP_022435326.1	ADAM10	<i>Delphinapterus leucas</i>	PA
XP_005168953.1	ADAM10	<i>Danio rerio</i>	PA,3D, DP
XP_034155529.1	ADAM10	<i>Pangasianodon hypophthalmus</i>	PA
XP_018595143.2	ADAM10	<i>Scleropages formosus</i>	PA
XP_017567139.1	ADAM10	<i>Pygocentrus nattereri</i>	PA
XP_022519842.1	ADAM10	<i>Astyanax mexicanus</i>	PA
XP_028256798.1	ADAM10	<i>Parambassis ranga</i>	PA
AGS83388.1	ADAM17	<i>Eriocheir sinensis</i>	PA,3D, DP
XP_037796232.1	ADAM17	<i>Penaeus monodon</i>	PA
XP_027207790.1	ADAM17	<i>Penaeus vannamei</i>	PA,3D, DP
RXG66816.1	ADAM17	<i>Armadillidium vulgare</i>	PA
XP_026325976.1	ADAM17	<i>Hyposmocoma kahamanao</i>	PA
XP_037971810.1	ADAM17	<i>Plutella xylostella</i>	PA
XP_035727088.1	ADAM17	<i>Vespa mandarinia</i>	PA
AAS48650.1	ADAM metalloprotease CG7908	<i>Drosophila melanogaster</i>	PA
NP_003174.3	ADAM17	<i>Homo sapiens</i>	PA,3D, DP
XP_032028075.1	ADAM17	<i>Hylobates moloch</i>	PA
XP_024650076.1	ADAM17	<i>Macaca nemestrina</i>	PA
XP_012641145.1	ADAM17	<i>Microcebus murinus</i>	PA
AAI38417.1	ADAM17	<i>Mus musculus</i>	PA,3D, DP
XP_004005725.1	ADAM17	<i>Ovis aries</i>	PA
XP_021324312.1	ADAM17	<i>Danio rerio</i>	PA,3D, DP
XP_039548959.1	ADAM17	<i>Pimephales promelas</i>	PA
KAA0708561.1	ADAM17	<i>Triplophysa tibetana</i>	PA
XP_007235314.2	ADAM17	<i>Astyanax mexicanus</i>	PA
XP_026778508.2	ADAM17	<i>Pangasianodon hypophthalmus</i>	PA
XP_020310534.1	ADAM17	<i>Oncorhynchus kisutch</i>	PA

Note:

PA: phylogenetic analysis; 3D: 3D structure analysis; DP: domain prediction

**Table S2. Sequences of primers used in this study**

Forward Primer	Forward Primer Sequence (5'-3')	Reverse Primer	Reverse Primer Sequence (5'-3')
ICD-F	CGAGAGGAAGTGTACC AGC	ICD-R	CACATTCATCTCGTCGCTCA
ICD-Kozak-F	CCGGAATTCTGGCCAC CATGCGAGAGGAAGTG TACCAGC	ICD-Kozak-R	ATAAGAATGCGGCCGCCTAAGCGTAATCTGGAACATCGTAT GGGTACACATTCATCTCGTCGCTCA
ICD-NLS-F	CCGGAATTCTGGCCAC CATGCGCATCAAGAGA GGTGGGGGG	ICD-NLS-R	ATAAGAATGCGGCCGCCTAAGCGTAATCTGGAACATCGTAT GGGTACACATTCATCTCGTCGCTCA
ICD-mNLS-F	CCGGAATTCTGGCCAC CATGTGCGGTGCGAGG GAACATGCC	ICD-mNLS-R	ATAAGAATGCGGCCGCCTAAGCGTAATCTGGAACATCGTAT GGGTACACATTCATCTCGTCGCTCA
IPO5-F	GCGGCGGGGGAACAA GAGCAATTCAGCAACT TTT	IPO5-R	CGTTGTGAGGTAAGTGGTGAAGGGCAACTTGCTGC
IPO5-Kozak-F	CCGGAATTCTGGCCAC CATGGCGGGGGGAA CAAGAGCAA	IPO5-Kozak-R	ATAAGAATGCGGCCGCCTACTTATCGTCGTCATCCTTGTA TCCGTTGTGAGGTAAGTGGTGAAG
IPO5-qF	GTATTCGCACCGCAGG ACTT	IPO5-qR	AGCTGTCCGAACTCCATCGT
β-Actin-F	GCATCCAGGAGACCAC TTACA	β-Actin-R	CTCCTGCTTGCTGATCCACATC
Toll-qF	AACGCCCTCGAAAAAT AC	Toll-qR	AAAGGTTCCAGACAGCAGA
CycE-qF	CCCATCACATCCAACAA C	CycE-qR	GAGGGAAGACAAAACCGT
Cdc2-qF	GCTGTTCTTGGTGT TTGA	Cdc2-qR	AGCAGGTTCTGTGGTTTC
STAT-qF	CTCCTGTCCTCGCTTGT T	STAT-qR	GCCTGGCCCTCACTTATA
PDGF/V EGF-qF	CAAACCCTGAACCACA CC	PDGF/VE GF-qR	CTCGTCACAGCGGCACTC
CSN5-qF	ATGGCTGCTGGCTTTCA	CSN5-qR	GCCCTCATCTGGTGGTTT
Kozak-Rpccr-F	CCGGAATTCTGGCCAC CGCCCTGGGAAGTGAT GCTCG	Kozak-Rpccr-R	ATAAGAATGCGGCCGCCTACTTATCGTCGTCATCCTTGTA TCAGAGGAGCCGGCATTGTTGTG
Kozak-Ig8-F	CCGGAATTCTGGCCAC CGCCCTGGGAAGTGAT GCTCG	Kozak-Ig8-R	ATAAGAATGCGGCCGCCTACTTATCGTCGTCATCCTTGTA TCAGAGGAGCCGGCATTGTTGTG
ADAM10-F	CTGAGCGAGTATGTG	ADAM10-R	CTTGGCTCTGGGTTG
ADAM10-qF	GGTTGGAGCAGCACGA GGAATAC	ADAM10-qR	TGTGGTGGTGGTGGTGGTAGTC
ADAM10-Kozak-F	CCGGAATTCTGGCCAC CATGCTGAGCGAGTAT GTG	ADAM10-Kozak-R	ATAAGAATGCGGCCGCCTAAGCGTAATCTGGAACATCGTAT GGGTACTTGGCTCTGGGTTG
ADAM17-F	CATCCCAACCTAAAATA T	ADAM17-R	ACACTTCCCTTATTACAG
ADAM17-qF	ACGCTGGAGGAGAAGA GTGGATG	ADAM17-qR	AGAGGTGCTTGCTAGGAGACAGG
ADAM17-Kozak-F	CCCAAGCTTGCCACCA TGATCCCAACCTAAA TAT	ADAM17-Kozak-R	ATAAGAATGCGGCCGCCTAAGCGTAATCTGGAACATCGTAT GGGTAACACTTCCCTTATTACAG
Dscam-qF	AGAGGAAGTGTACCAG CAGT	Dscam-qR	CCACCTCTCTTGATGCGG
ERK-qF	TTCAGCAACAGGCTCAT C	ERK-qR	TGTTCAGGAGGAGGTTTGATGGC
Relish-qF	TCTCCCTACTCTGACCA TTCC	Relish-qR	TTCCACCATCTCACTCTTGT
Dorsal-qF	CGTCAGCAGCACAGCA GAGAAT	Dorsal-qR	CCCGTATTTCTCCCTCACTTCAG
siGFP-F	AGUGCUUCAGCCGCUA CCC	siGFP-R	GGGUAGCGGCUGAAGCACU
siIPO5-F	CCAAGAUCUCAAUA UAAUG	siIPO5-R	UUUAUUUUGAGGAUCUUGGUG
siERK-F	CCAUGGACAAAGCUGU AUUTT	siERK-R	AAUACAGCUUUGUCCAUGGTT
siRelish-F	CCAAGUUUCGGUCCG CUATT	siRelish-R	UAGCGGAACCGAAACUUGGTT
siDorsal-F	GGUGGUCGUGUCAUG UGUUTT	siDorsal-R	AACACAUGACACGACCACCTT
siExon33-F	UCCAGGACACCCUUA GAUTT	siExon33-R	AUCUAAGGUGUCCUGGGATT