

```

VIM-2      VDSSGEYPTVSEIPVGEVRLYQIADGVWSHIATQSFDGAVYPSNGLIVRDGDELLIDTA 60
BcII      --SQKVEKTVIKNETGTISISQLNKNVWVHTELGYFNGEAVPSNGLVLTNTTKGLVLDSS 58
Vmh       -----ALKLTTYNPQ-----EKAI F PVSSTLISGKKEAIFDAQ 34
           : :                               : * .. :: . :*.*:

VIM-2      WGAKNTAALLAEIEKQIGLPVTRAVSTHFHDDRVGGVDVLRRAA--GVATYASPSTRRLAE 118
BcII      WDNKLTKELMEMVEKKFQKRITDVIITHAHADRIGGIKTLKER--GIKAHSTALTAELAK 116
Vmh       FSTTEGKALVELI-RQSGKELTTVYITTGGDPDDFYFGLQPIVEAFPQVKIKATATIVDHIN 93
           :. . * : : : : * . * . * * : . : : : :

VIM-2      VE-----GNEIPHSLEGLSSSGDAVRF--PVELFYPGAAHSTDNLVVYVPS 164
BcII      NS-----GYEPLGDLQIITS----LKFGNTKVETFYPGKHTEDNIVVWLPQ 160
Vmh       HTKDQKIGYWGPILGEGAPSQLYVPEVYNGDILLEGE-KIELKEAG-TH---NAYYWIPS 149
           * * : * : * . * * . * : : .

VIM-2      ASVLYGGCAIYE-LSRTSAGNVADADLAEWPTSIERIQQHYPEAQFVIPGHGL---PGGL 220
BcII      YQTLAGGCLVKS-AEAKDLGNVADAYVNEWSTSIENVLKRYGNINSVVPGHGE---VGDK 216
Vmh       LKTALGGVSTYSGIHVWMADSQTKEERLEWVASLDRMKQLKP--KRVIPGHYLQVPPRV 206
           .. ** . .. :. ** :*::: : : : * :***

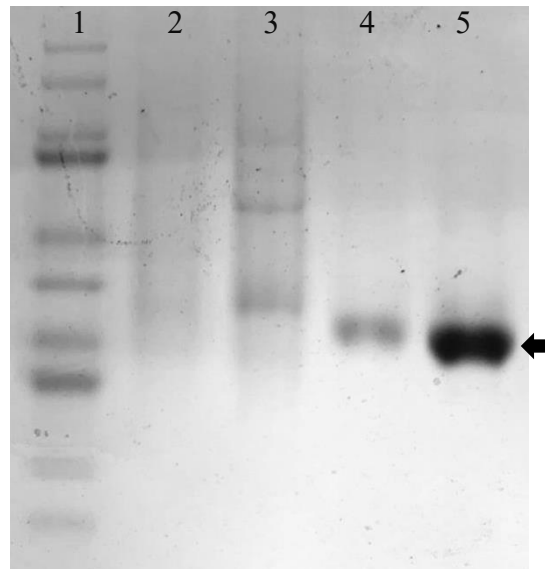
VIM-2      DLLKHTTNVKA-----HTNRSVVE----- 240
BcII      GLLLHTLDLLK----- 227
Vmh       EAVDFTKQYVMDWQRYVEQSSNSTQLIEKITAQYPLLTADEGVITIGAKVSMGEMKW 262
           : . * : :

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Supplementary Figure 1. The multiple sequence alignment of Vmh, VIM-2 from *P. aeruginosa* and BcII from *Bacillus cereus* was accomplished by using MAFFT.

The conserved H-X-H-X-D motif, H196, and H263 motifs were underlined.

(A)



(B)

```
1   MKKTLAVAVL ATLSQPALAA LKLTTYNPQE KAIFVVSSTL ISGKKEAILF
51  DAQFSTTEGK ALVELIRQSG KELTTYVYITG GDPDFYFGLQ PIVEAFPQVK
101 IKATATIVDH INHTKDQKIG YWGPILGKGA PSQLYVPEVY NGDILLEGEK
151 IELKEAGTHN AYYWIPSLKT ALGGVSTYSG IHVWMADSQT KEERLEWVAS
201 LDRMKQLKPK RVIPGHYLGQ VPPRVEAVDF TKQYVMDWQR YVEQSSNSTQ
251 LIEKITAQYP LLTADEGVTI GAKVSMGEMK W
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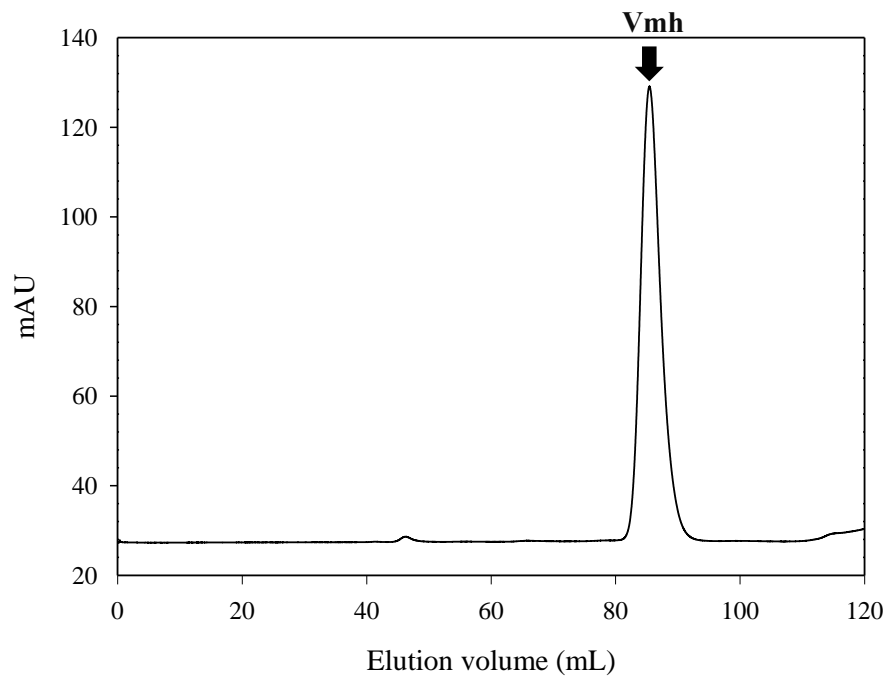
Supplementary Figure 2. Identification of the purified Vmh protein. (A) SDS-

PAGE. Lane 1: protein molecular weight marker; lane 2: flow through; Lane 3: wash by 30 mM imidazole; Lane 4: wash by 50 mM imidazole; Lane 5: elute by 300 mM

imidazole. **(B) Vmh protein sequence coverage determined by LS-MS/MS.** Vmh was digested by trypsin followed by LC-MS/MS analysis. Nominal mass (M_r) = 31 kDa.

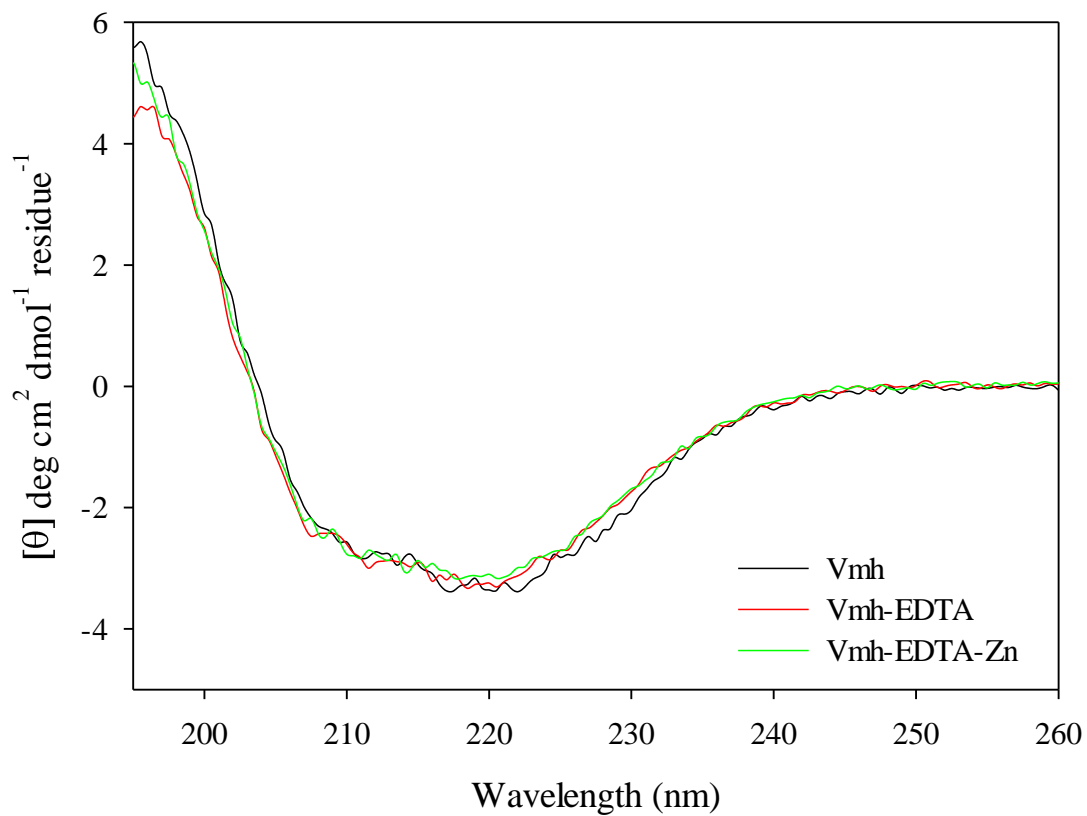
Taxonomy: *V. vulnificus*. Sequence coverage: 92%. Matched peptides are shown in red.

(A)



Supplementary Figure 3. The size exclusion chromatography of β -lactamase Vmh

proteins. V_e = elution volume; V_o = void volume; V_c = column volume. $K_{av} = (V_e - V_o)/(V_c - V_o)$. Blue dextran: $V_o = 46.6$ mL; aldolose (158 kDa): 65.5 mL, $K_{av} = 0.257$; conalbumin (75 kDa): 74.5 mL, $K_{av} = 0.380$; ovalbumin (44 kDa): 81.4 mL, $K_{av} = 0.473$; CARB-17 (29.3 kDa): 88.7 mL, $K_{av} = 0.573$; Vmh protein: 88.5 mL, $K_{av} = 0.529$.



Supplementary Figure 4. Far-UV Circular dichroism spectra of purified Vmh, apo-Vmh, and re-metallated-Vmh. Data were obtained for Vmh (0.1 mg/mL) at 25 °C in phosphate buffer (20 mM), at pH 7.4.