2

- 3 Supplementary Figure S1. Three major bands recognized by scFv were severed from the SDS-PAGE
- 4 gel (Fig. 6) for mass spectrometric analysis. (A-C) After alignment with SwissProt 2011 database, the
- 5 matched amino acids of trypsin-digested fragments were shown in bold and the matched protein
- 6 indicated that of zinc metalloproteinase-disintegrin acutolysin which is also called SVMP containing
- 7 609 amino acids. SVMP: snake venom metalloproteinase.

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Band m1 match peptide of Zinc metalloproteinase-disintegrin acutolysin (24%) shown in Bold

1 MIQVLLVTIC LAAFPYQGSS IILESGDVND YEVVYPRKVT ALPKGAVQQK
51 YEDAMQYEFK VNGEPVVLHL EKNKHLFSKD YSETHYSPDG REITINPPVE
101 DHCYYHGRIE NDGDSTASIS ACNGLKGNFK LQGETYLIEP MKLSDSEAHA
151 VFKYENVEKD EAPKMCGVTQ KWKSYEPIKK ISQLNLIPEQ QIYDPFKYVE
201 TVVVVDKAMV TKYNGDLDKI ITKMYEAANN MNEMYRYMFF RVVMVGLIIW
251 TEEDKITVKP DVDYTLNAFA EWRKTYLLAE KKHDNAQLIT GIDFRGSIIG
301 YAYIGSMCHP KRSVGIIQDY SPINLVLAVI MAHEMGHNLG IHHDDGYCYC
351 GGYPCIMGPS ISPEPSKFFS NCSYIQCWDF IMNHNPECID NEPLGTDIIS
401 PPLCGNELLE VGEECDCGTP ENCQNECCDA ATCKLKSGSQ CGHCKCCEQC
451 KFRTSGTECR ASMSECDPAE HCTGQSSECP ADVFHKNGEP CLDNYGYCYN
501 GNCPIMYHQC YALFGAEVYE AEDSCFESNK KGNYYGYCKK ENGKKIPCAS
551 EDVKCGRLYC KDDSPGQNNP CKMFYSNDDE HKGMVLPGTK CADGKVCSNG
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(C)
    Band m3 match peptide of Zinc metalloproteinase-disintegrin acutolysin
                          (24%) shown in Bold
     1 MIQVLLVTIC LAAFPYQGSS IILESGDVND YEVVYPRKVT ALPKGAVQQK
     51 YEDAMQYEFK VNGEPVVLHL EKNKHLFSKD YSETHYSPDG REITINPPVE
    101 DHCYYHGRIE NDGDSTASIS ACNGLKGNFK LQGETYLIEP MKLSDSEAHA
    151 VFKYENVEKD EAPKMCGVTO KWKSYEPIKK ISOLNLIPEO QIYDPFKYVE
    201 TVVVVDKAMV TKYNGDLDKI ITKMYEAANN MNEMYRYMFF RVVMVGLIIW
    251 TEEDKITVKP DVDYTLNAFA EWRKTYLLAE KKHDNAQLIT GIDFRGSIIG
    301 YAYIGSMCHP KRSVGIIQDY SPINLVLAVI MAHEMGHNLG IHHDDGYCYC
    351 GGYPCIMGPS ISPEPSKFFS NCSYIQCWDF IMNHNPECID NEPLGTDIIS
    401 PPLCGNELLE VGEECDCGTP ENCQNECCDA ATCKLKSGSQ CGHGKCCEQC
    451 KFRTSGTECR ASMSECDPAE HCTGQSSECP ADVFHKNGEP CLDNYGYCYN
    501 GNCPIMYHQC YALFGAEVYE AEDSCFESNK KGNYYGYCRK ENGKKIPCAS
    551 EDVKCGRLYC KDDSPGONNP CKMFYSNDDE HKGMVLPGTK CADGKVCSNG
    601 HCVDVTTAY
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