#### **CHAPTER II**

#### **MATERIALS AND METHODS**

#### 2.1 Chemicals and equipments

Chemicals and equipments used in this study were shown in Appendix A. List of restriction enzymes are detailed in Appendix D. The recipes for reagent preparations are shown in Appendix E.

#### 2.2 E. coli strains and vectors

XL-1 Blue (Stratagene, La Jolla, CA) was used as a host for the library generation and the amplification of phage displaying artificial ankyrin repeat protein library. Examination of protein expression and production of recombinant HIV-1 protease were performed using *E. coli* strain BL21 (DE3) (Stratagene, La Jolla, CA) in CoFi blot experiment to evaluate the quality of constructed library. The pHDiExDsbA-Ank15 phagemid vector (Nangola et al., 2010) was used for the library construction and phage library production. The pQE-30 expression vector (Qiagen, Hilden, Germany) was used for the soluble protein production in M15 [pREP4] (Qiagen, Hilden, Germany). pET14bELP105KnewTat (kindly provided by Prof. Wilfred Chen, California, USA) was used as a template for the amplification of gene encoding HIV-1 protein. The pCEP4 based vector (Invitrogen, Carlsbad, CA) was

ີລິດ Co A exploited to generate the stable cell lines expressing ankyrin repeat protein. pNL4-3 (kindly provided by Prof. Pierre Boulanger, Lyon, France) was used as the template for MA-CA domain and pBlueBac4.5 (Invitrogen, Carlsbad, CA) was used to produce the recombinant H<sub>6</sub>MA-CA in insect cells. Genotype of all *E. coli* is detailed in Appendix B.

#### 2.3 Cell culture

Sf9 cells (the pupal ovarian tissue of *Spodoptera frugiperda*, Invitrogen, Carlsbad, CA) was used for the generation of recombinant baculovirus carrying gene encoding H<sub>6</sub>MA-CA, and H<sub>6</sub>-CA protein. Cells were grown in the non-humidified environment at 27°C in Grace's insect medium (Gibco-BRL, Gaithersburg, MD) supplemented with 10 mM L-glutamine (Gibco-BRL, Gaithersburg, MD), 10% fetal bovine serum (Gibco-BRL, Gaithersburg, MD), penicillin (100 units/ml), and streptomycin (100  $\mu$ g/ml).

Sup-T1 (human T cells lymphoblastic lymphoma) cell (kindly provided by Prof. Watchara Kasinrerk) was used to generate the stable cell line expressing the ankyrin repeat proteins in two versions: membrane-targeting proteins and cytoplasmic proteins. Cells were grown in a humidified atmosphere of 5% CO<sub>2</sub> at 37 °C in the RPMI-1640 medium (Gibco-BRL, Gaithersburg, MD) supplemented with 10 mM L-glutamine, 10% fetal bovine serum, penicillin (100 units/ml), and streptomycin (100 µg/ml).

#### 2.4 Construction of artificial ankyrin repeat protein library

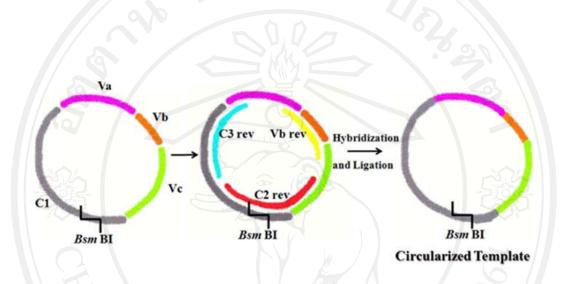
2.4.1 Sequence analysis and design of oligonucleotide fragments for library construction

The sequence of artificial ankyrin repeat proteins library is based on the sequence design designated as designed ankyrin repeat proteins (DARPins) library previously described by Plücktun A (Binz et al., 2003) with two minor modifications:

- Limited changes in the Ankyrin repeat concensus sequence has been introduced in order to create a non symetric restriction site (*Bsm* BI). The presence of this site between consecutive ankyrin repeat coding fragments simplify library construction and module shuffling processes. The 3D structure of modified consensus was subjected to Discovery 2.5 program using DARPin E3\_5 (1JM0) as the template to analyze the optimized structure compared to the template structure.

- The randomization scheme used in the variable position of the ankyrin repeats was targeted to mimic the natural residue frequency at each variable position. The frequency of amino acids in each variable position was computed from Ankyrin domain families as defined in Pfam (Coggill et al., 2008; Finn et al., 2008) and Prosite (Ribeiro Ede et al., 2005; Sigrist et al., 2005; Hulo et al., 2006). The conservation at each position in multi alignment of ankyrin modules can be visualized as a sequence logo generated using the WebLogo3 server (http://weblogo.berkeley.edu/).

The amino acid distribution at each variable position was approximated by encoding each of these positions with a set of partially degenerated codons. The repeat sequences were made by a set of oligonucleotides. The sequence coding a single repeat was divided into four fragments: Va (variable fragment a), Vb (variable fragment b), Vc (variable fragment c) and C1 (constant fragment) as shown in **Figure 2.1**. The C1 fragment was designed to have the site for *Bsm* BI restriction enzyme. The sequences of each fragment are detailed in **Table 2.1**.



**Figure 2.1 The generation of circularized template**. All fragments of Va, Vb, Vc, C1 and short bridging fragments (Vb rev, C2 rev and C3 rev) are mixed together with an equal molar ratio. Hybridization and ligation resulted in the circularized template.

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Variable fragment a (Va)amino acid position: 33, 1, X, X, 4, X, 6, 7Va1cgt gac vdk vdk ggt vdk acc ccgVa2cgt gac vdk vdk ggt dmy acc ccgVa3cgt gac vdk dmy ggt vdk acc ccgVa4cgt gac vdk dmy ggt dmy acc ccgVa5cgt gac dmy vdk ggt dmy acc ccgVa6cgt gac dmy vdk ggt dmy acc ccgVa7cgt gac dmy vdk ggt dmy acc ccgVa8cgt gac dmy dmy ggt dmy acc ccgVa10cgt gac raa vdk ggt dmy acc ccgVa11cgt gac raa vdk ggt dmy acc ccgVa12cgt gac raa vdk ggt dmy acc ccgVa13cgt gac raa dmy ggt dmy acc ccgVa14cgt gac raa dmy ggt dmy acc ccgVa15cgt gac dmy van ggt dmy acc ccgVa16cgt gac dmy van ggt dmy acc ccgVa17cgt gac dmy van ggt dmy acc ccgVa18cgt gac vdk van ggt van acc ccgVa19cgt gac vdk van ggt van acc ccgVa20cgt gac dmy vdk ggt van acc ccgVa21cgt gac vdk vdk ggt van acc ccgVa22cgt gac vdk vdk ggt tgg acc ccgVa23cgt gac vdk vdk ggt tgg acc ccgVa24cgt gac dmy dmy ggt tgg acc ccgVa25cgt gac dmy dmy ggt tgg acc ccgVa26cgt gac dmy dmy ggt tgg acc ccgVa27cgt gac dmy dmy ggt tgg acc ccgVa28cgt gac dmy dmy ggt tgg acc ccgva29cgt gac dmy dmy ggt tgg acc ccgva29cgt gac dmy dmy ggt tgg acc ccgva29cgt gac dmy dmy ggt tgg acc ccgva20cgt gac dmy dmy ggt tgg acc ccgva23cgt gac	Oligonucleotide	Sequence (5'->3')
Va2cgt gac vdk vdk ggt dmy acc ccgVa3cgt gac vdk dmy ggt vdk acc ccgVa4cgt gac vdk dmy ggt vdk acc ccgVa5cgt gac dmy vdk ggt vdk acc ccgVa6cgt gac dmy vdk ggt dmy acc ccgVa7cgt gac dmy dmy ggt vdk acc ccgVa8cgt gac raa vdk ggt dmy acc ccgVa10cgt gac raa vdk ggt dmy acc ccgVa11cgt gac raa vdk ggt dmy acc ccgVa12cgt gac raa vdk ggt dmy acc ccgVa13cgt gac dmy van ggt dmy acc ccgVa14cgt gac dmy van ggt dmy acc ccgVa15cgt gac dmy van ggt dmy acc ccgVa16cgt gac dmy van ggt dmy acc ccgVa17cgt gac dmy van ggt dmy acc ccgVa18cgt gac dmy van ggt dmy acc ccgVa19cgt gac dmy van ggt dmy acc ccgVa11cgt gac dmy van ggt dmy acc ccgVa2cgt gac dmy van ggt dmy acc ccgVa14cgt gac dmy van ggt dmy acc ccgVa15cgt gac dmy van ggt dmy acc ccgVa16cgt gac dmy van ggt van acc ccgVa18cgt gac dmy vdk ggt van acc ccgVa20cgt gac dmy dmy ggt tgg acc ccgVa21cgt gac vdk vdk ggt tgg acc ccgVa23cgt gac dmy vdk ggt tgg acc ccgVa24cgt gac dmy dmy ggt tgg acc ccgVa23cgt gac dmy dmy ggt tgg acc ccgVa24cgt gac dmy dmy ggt tgg acc ccgVb1ctg cac tggVb2ctg cac tggVb3ctg cac tggVb4ctg cac tgg		amino acid position: 33, 1, X, X, 4, X, 6, 7
Va3cgt gac vdk dmy ggt vdk acc ccgVa4cgt gac vdk dmy ggt vdk acc ccgVa5cgt gac dmy vdk ggt vdk acc ccgVa6cgt gac dmy vdk ggt dmy acc ccgVa7cgt gac dmy dmy ggt vdk acc ccgVa8cgt gac raa vdk ggt dmy acc ccgVa10cgt gac raa vdk ggt dmy acc ccgVa11cgt gac raa vdk ggt dmy acc ccgVa12cgt gac raa vdk ggt dmy acc ccgVa13cgt gac raa dmy ggt dmy acc ccgVa14cgt gac raa dmy ggt dmy acc ccgVa15cgt gac dmy van ggt dmy acc ccgVa16cgt gac dmy van ggt dmy acc ccgVa17cgt gac dmy van ggt vdk acc ccgVa18cgt gac dmy van ggt van acc ccgVa19cgt gac dmy vdk ggt van acc ccgVa12cgt gac dmy van ggt dmy acc ccgVa13cgt gac vdk van ggt dmy acc ccgVa14cgt gac vdk van ggt dmy acc ccgVa15cgt gac dmy van ggt dmy acc ccgVa16cgt gac vdk van ggt van acc ccgVa17cgt gac dmy vdk ggt van acc ccgVa20cgt gac dmy dmy ggt tgg acc ccgVa21cgt gac vdk vdk ggt tgg acc ccgVa23cgt gac dmy dmy ggt tgg acc ccgVa24cgt gac dmy dmy ggt tgg acc ccgVa23cgt gac dmy dmy ggt tgg acc ccgVa24cgt gac dmy dmy ggt tgg acc ccgVa25cgt gac dmy dmy ggt tgg acc ccgVa26cgt gac dmy dmy ggt tgg acc ccgVa27cgt gac dmy dmy ggt tgg acc ccgVa28cgt gac dmy dmy ggt tgg acc ccgVa29cgt gac dmy dmy ggt tgg acc ccg <th>Val</th> <th>cgt gac vdk vdk ggt vdk acc ccg</th>	Val	cgt gac vdk vdk ggt vdk acc ccg
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Va6       cgt gac dmy vdk ggt dmy acc ccg         Va7       cgt gac dmy dmy ggt vdk acc ccg         Va8       cgt gac raa vdk ggt dmy acc ccg         Va9       cgt gac raa vdk ggt dmy acc ccg         Va10       cgt gac raa vdk ggt vdk acc ccg         Va11       cgt gac raa vdk ggt dmy acc ccg         Va12       cgt gac raa vdk ggt dmy acc ccg         Va13       cgt gac raa dmy ggt vdk acc ccg         Va14       cgt gac dmy van ggt vdk acc ccg         Va15       cgt gac dmy van ggt vdk acc ccg         Va16       cgt gac vdk van ggt vdk acc ccg         Va15       cgt gac vdk van ggt vdk acc ccg         Va16       cgt gac vdk van ggt vdk acc ccg         Va17       cgt gac vdk van ggt vdk acc ccg         Va18       cgt gac vdk van ggt van acc ccg         Va19       cgt gac vdk vdk ggt van acc ccg         Va20       cgt gac vdk vdk ggt tgg acc ccg         Va21       cgt gac vdk vdk ggt tgg acc ccg         Va22       cgt gac vdk vdk ggt tgg acc ccg         Va20       cgt gac vdk vdk ggt tgg acc ccg         Va23       cgt gac vdk vdk ggt tgg acc ccg         Va24       cgt gac vdk vdk ggt tgg acc ccg         Va24       cgt gac tgg ccg ctg cac tgg         Vb1       ctg cac tgg	Va4	cgt gac <mark>vdk dmy</mark> ggt <mark>dmy</mark> acc ccg
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Va16cgt gac vdk van ggt vdk acc ccgVa17cgt gac vdk dmy ggt van acc ccgVa18cgt gac dmy vdk ggt van acc ccgVa19cgt gac dmy dmy ggt van acc ccgVa20cgt gac vdk vdk ggt van acc ccgVa21cgt gac vdk vdk ggt tgg acc ccgVa22cgt gac dmy vdk ggt tgg acc ccgVa23cgt gac dmy dmy ggt tgg acc ccgVa24cgt gac dmy dmy ggt tgg acc ccgVb1ctg cac ctgVb2ctg cac tggVb3ctg cac tacVb4ctg cac rtc	Val4	cgt gac <mark>dmy van</mark> ggt <mark>vdk</mark> acc ccg
Va17       cgt gac vdk dmy ggt van acc ccg         Va18       cgt gac dmy vdk ggt van acc ccg         Va19       cgt gac dmy dmy ggt van acc ccg         Va20       cgt gac vdk vdk ggt van acc ccg         Va21       cgt gac vdk dmy ggt tgg acc ccg         Va22       cgt gac dmy vdk ggt tgg acc ccg         Va23       cgt gac vdk vdk ggt tgg acc ccg         Va24       cgt gac dmy dmy ggt tgg acc ccg         Va24       cgt gac dmy dmy ggt tgg acc ccg         Vb1       cgt gac dmy dmy ggt tgg acc tgg         Vb2       cgt gac tgg cac tgg         Vb3       ctg cac tgg         Vb4       ctg cac tcg	Va15	cgt gac <mark>dmy van</mark> ggt <mark>dmy</mark> acc ccg
Va18cgt gac dmy vdk ggt van acc ccgVa19cgt gac dmy dmy ggt van acc ccgVa20cgt gac vdk vdk ggt van acc ccgVa21cgt gac vdk dmy ggt tgg acc ccgVa22cgt gac dmy vdk ggt tgg acc ccgVa23cgt gac dmy dmy ggt tgg acc ccgVa24cgt gac dmy dmy ggt tgg acc ccgVb1ctg cac ctgVb2ctg cac tggVb3ctg cac tacVb4ctg cac rtc	Val6	cgt gac <mark>vdk van</mark> ggt <mark>vdk</mark> acc ccg
Va19cgt gac dmy dmy ggt van acc ccgVa20cgt gac vdk vdk ggt van acc ccgVa21cgt gac vdk dmy ggt tgg acc ccgVa22cgt gac dmy vdk ggt tgg acc ccgVa23cgt gac dmy dmy ggt tgg acc ccgVa24cgt gac dmy dmy ggt tgg acc ccgVb1ctg cac ctgVb2ctg cac tggVb3ctg cac ttcVb4ctg cac rtc	Val7	cgt gac <mark>vdk dmy</mark> ggt <mark>van</mark> acc ccg
Va20cgt gac vdk vdk ggt van acc ccgVa21cgt gac vdk dmy ggt tgg acc ccgVa22cgt gac dmy vdk ggt tgg acc ccgVa23cgt gac vdk vdk ggt tgg acc ccgVa24cgt gac dmy dmy ggt tgg acc ccgVb1ctg cac ctgVb2ctg cac tggVb3ctg cac tg cac ttcVb4ctg cac rtc	Val8	cgt gac <mark>dmy vdk</mark> ggt <mark>van</mark> acc ccg
Va21cgt gac vdk dmy ggt tgg acc ccgVa22cgt gac dmy vdk ggt tgg acc ccgVa23cgt gac vdk vdk ggt tgg acc ccgVa24cgt gac dmy dmy ggt tgg acc ccgVa10amino acid position: 8, 9, XVb1ctg cac ctgVb2ctg cac tggVb3ctg cac tacVb4ctg cac rtc	Val9	cgt gac <mark>dmy dmy</mark> ggt <mark>van</mark> acc ccg
Va22cgt gac dmy vdk ggt tgg acc ccgVa23cgt gac vdk vdk ggt tgg acc ccgVa24cgt gac dmy dmy ggt tgg acc ccgVariable fragment b (Vb)amino acid position: 8, 9, XVb1ctg cac ctgVb2ctg cac tggVb3ctg cac tgcVb4ctg cac rtc	Va20	cgt gac <mark>vdk vdk</mark> ggt <mark>van</mark> acc ccg
Va23cgt gac vdk vdk ggt tgg acc ccgVa24cgt gac dmy dmy ggt tgg acc ccgVariable fragment b (Vb)amino acid position: 8, 9, XVb1ctg cac ctgVb2ctg cac tggVb3ctg cac tacVb4ctg cac rtc	Va21	cgt gac <mark>vdk dmy</mark> ggt tgg acc ccg
Va24cgt gac dmy dmy ggt tgg acc ccgVariable fragment b (Vb)amino acid position: 8, 9, XVb1ctg cac ctgVb2ctg cac tggVb3ctg cac tggVb4ctg cac rtc	Va22	cgt gac <mark>dmy vdk</mark> ggt <mark>tgg</mark> acc ccg
Variable fragment b (Vb)amino acid position: 8, 9, XVb1ctg cac ctgVb2ctg cac tggVb3ctg cac tacVb4ctg cac rtc	Va23	cgt gac <mark>vdk vdk</mark> ggt tgg acc ccg
Vb1ctg cac ctgVb2ctg cac tggVb3ctg cac tacVb4ctg cac rtc	Va24	cgt gac dmy dmy ggt tgg acc ccg
Vb2ctg cac tggVb3ctg cac tacVb4ctg cac rtc	Variable fragment b (Vb)	amino acid position: 8, 9, X
Vb4 ctg cac rtc	Vbl	ctg cac ctg
Vb4 ctg cac rtc	Vb2	ctg cac tgg
Vb4 ctg cac rtc	Vb3	ctg cac tac
		ctg cac <mark>rtc</mark>

**Table 2.1** Oligonucleotide for the artificial ankyrin repeat protein library construction.

Oligonucleotide	<b>Sequence</b> (5'->3')
Variable fragment c (Vc)	amino acid position: 11, 12, X, X, 15, 16, 17
Vcl	gct gcg kck kck ggt cat ctg
Vc2	gct gcg <mark>kck var</mark> ggt cat ctg
Vc3	gct gcg <mark>kck aac</mark> ggt cat ctg
Vc4	gct gcg <mark>kck sgy</mark> ggt cat ctg
Vc5	gct gcg <mark>kck yay</mark> ggt cat ctg
Vc6	gct gcg kck ntg ggt cat ctg
Vc7	gct gcg <mark>tac var</mark> ggt cat ctg
Vc8	gct gcg <mark>tac kck</mark> ggt cat ctg
Vc9	gct gcg <mark>tac yay</mark> ggt cat ctg
Vc10	gct gcg <mark>cgy kck</mark> ggt cat ctg
Vc11	gct gcg <mark>cgy var</mark> ggt cat ctg
Vc12	gct gcg cgy aac ggt cat ctg
Vc13	gct gcg <mark>cgy sgy</mark> ggt cat ctg
Vc14	gct gcg <mark>cgy yay</mark> ggt cat ctg
Vc15	gct gcg <mark>cgy ntg</mark> ggt cat ctg
Vc16	gct gcg <mark>var kck</mark> ggt cat ctg
Vc17	gct gcg <mark>var var</mark> ggt cat ctg
Vc18	gct gcg var aac ggt cat ctg
Vc19	gct gcg <mark>var sgy</mark> ggt cat ctg
Vc20	gct gcg <mark>var yay</mark> ggt cat ctg
Vc21	gct gcg <mark>ktk kck</mark> ggt cat ctg
Vc22	gct gcg ktk var ggt cat ctg
Vc23	gct gcg ktk aac ggt cat ctg
Vc24	gct gcg <mark>ktk sgy</mark> ggt cat ctg
Vc25	gct gcg ktk yay ggt cat ctg
Constant fragment	amino acid position: 18-32*
	gaa atc gtt <u>cgt ctc</u> ctg ctg gaa cac
Cl	ggc gca gac gta aac gcg

**Table 2.1** Oligonucleotide for the artificial ankyrin repeat protein library construction

 (con't).

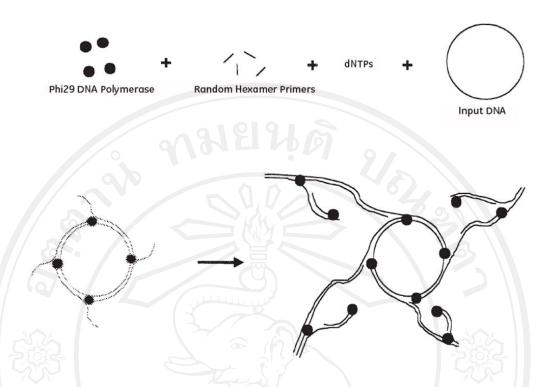
**Table 2.1** Oligonucleotide for the artificial ankyrin repeat protein library construction (con't).

Oligonucleotide	Sequence (5'->3')
Bridging fragments	9181916
Vblrev	cgc agc cag gtg cag cgg ggt
Vb2Rev	cgc agc cca gtg cag cgg ggt
Vb3rev	cgc agc gta gtg cag cgg ggt
Vb4rev	cgc agc gay gtg cag cgg ggt
C2rev	cag gag acg aac gat ttc cag atg acc
C3rev	gtc acg cgc gtt tac gtc tgc gcc gtg
	ttc cag
Code for mixed d = g, a or t k = g or t m = a or c v = g, a or c r = a or g	l bases nomenclature:
s = g  or  c y = c  or  t	

2.4.2 Preparation of DNA cassettes encoding a single internal repeat for library construction.

All synthetic fragments (Va, Vb, Vc, and C1) were hybridized with reverse oligonucleotides linkers (bridging fragments; Vb rev, C2 rev, and C3 rev) at equal molar by heating at 95°C for 5 min followed by cooling down to 25°C at the rate 0.1 °C/minute. To generate the circularized template, the hybridized product was ligated by T4 DNA ligase enzyme (NEB, Pickering, Ontario) resulting in the circular templates. The ligation product was purified using NucleoSpin<sup>®</sup> Extract II (Macherey-Nagel, Düren, Germany). The circularized templates were hybridized with random hexamer primers provided in the illustra TempliPhi 100 amplification kit and amplified by Phi29 polymerase (GE healthcare Bio-Sciences Co. Piscataway, NJ) at 30°C for 15 hr. The amplification process using Phi29 polymerase is based on the rolling circle amplification (RCA) processes (Dean et al., 2001) as shown in **Figure 2.2.** 

The polymerized product was incubated at 65°C for 15 min and subsequently treated with *Bsm* BI (NEB, Pickering, Ontario) at 55°C for 4 hr. The *Bsm* BI-treated product represented mixture of a monomeric fragment of DNA cassette was purified using NucleoSpin<sup>®</sup> Extract II. The complete digestion was analyzed by agarose gel electrophoresis.



**Figure 2.2 Schematic of the TempliPhi amplification process**. Random hexamer primers anneal to the circular template DNA at multiple sites. Phi29 DNA polymerase extends each of these primers. When the DNA polymerase reaches a downstream extended primer, strand displacement synthesis occurs. The displaced strand is rendered single-stranded and available to be primed by more hexamer primers. The isothermal amplification was continued at 30°C for 4-6 hr without the need for thermal cycling (Dean et al., 2001).

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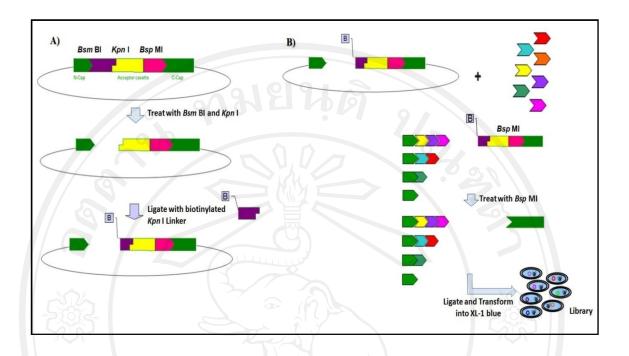
#### 2.4.3 Generation of intermediate vector

The phagemid pHDiExDsbA-Ank15 vector (Nangola et al., 2010) was used for the construction of intermediate vector termed acceptor vector (pHDiExDsbA-AccV). The synthetic adaptor cassette containing restriction sites required for the library construction process;

Ank ModAcc Fw (5'-TGCTGGAGGAGGGTACCGAGGAGACCTGCTA ATTGCTGAAGCACGGTGCTGACGTTAACGCTAAT-3') and Ank ModAcc Rev (5'-GATCATTAGCGTTAACGTCAGCACCGTGCTTCAGCAATTAGCAGGTCT CCTCGGTACCCC CTCC-3') were mixed at the equal molar ratio (5  $\mu$ M) and hybridized by heating at 95°C for 5 min followed by cooling down to 25°C with the constant rate at 0.1°C/second. The hybridized cassettes were cloned into *Not* I and *Bcl* I site of pHDiExDsbA-Ank15 and transformed into competent XL-1 Blue resulting in pHDiExDsbA-AccV vector.

#### 2.4.4 Library construction

The pHDiExDsbA-AccV vector (30 µg) was treated with *Kpn* I at 37°C for 4 hr and then purified using NucleoSpin<sup>®</sup> Extract II. The purified product was further digested with *Bsm* BI at 55°C for 16-18 hr and purified using NucleoSpin<sup>®</sup> Extract II. The mixture of single-stranded oligonucleotides, Biotin link *Kpn* I (biotin-5'-ACGACAGGGTAC-3') and Link *Kpn* I Rev (5'-CTGTCTGT-3') was pre-hybridized prior to the ligation step with treated acceptor vector to seal the *Kpn* I site. The ligation product was further purified by NucleoSpin<sup>®</sup> Extract II. The DNA cassette which was prepared in the previous step and the intermediate vector (pHDiExDsbA- AccV vector linked with biotinylated-Kpn I linker) were mixed at the molar ratio 1:5. DNA fragments corresponding to single ankyrin modules were hetero polymerized in the acceptor vector with T4 DNA ligase at 20 °C for 4 hr. Due to the non palyndromic Bsm B1 cohesive ends, the modules can be ligated in only one orientation. The excess cassettes were eliminated by capturing the biotinylated acceptor vector on pre-washed streptavidin coated magnetic beads (Sigma, St. Louis, MO). Beads were agitated at 25°C for 1 hr and washed three times with NEB buffer containing 100 mM NaCl, 50 mM Tris-HCl, 10 mM MgCl<sub>2</sub>, 1 mM DTT, pH 7.9 (NEB, Pickering, Ontario). The vectors which are captured on beads were released out by incubating with Bsp MI enzyme at 50°C for 3 hr resulting in the cohesive ends designed to compatible with Bsm BI site at 3' end of the polymerized DNA cassette. The mixture of released vector was glued to generate the circularized vector by T4 DNA ligase at 20°C for 4 hr, as shown in Figure 2.3. The ligation product was purified and then electroporated into XL-1 Blue electrocompetent cells. The transformed cells were spread on the 20 cm x 20 cm plates of 2YT agar containing ampicillin (100 µg/ml) and 1% (w/v) glucose. Some of the transformed cells were taken to perform the serial dilution and plated on 2YT agar containing 100 µg/ml ampicillin and 1% (w/v) glucose to evaluate the library size. The number of colonies of each dilution was use for library size calculation. Colonies on the solid medium were collected after overnight growth, pooled and stored at -80°C in the 2YT medium containing 20% (v/v) glycerol. The DNA was extracted from a sample of pooled cells for restriction analysis and collective transformation in an expression host.



**Figure 2.3 Process for library generation**. (**A**) The intermediate vector was treated with *Bsm* BI and *Kpn* I restriction enzymes to generate the cohesive ends for polymerization with DNA cassettes at C-terminus of N-cap and for ligation with biotinylated linker. (**B**) The polymerization process was undergone randomly during the ligation process with the mixture of DNA cassettes. Free-DNA cassettes were removed by trapping the vector on streptavidin beads and washed. Then vectors were released from the beads by digestion with *Bsp* MI to generate the compatible end with *Bsm* BI and closed by the ligation process. Finally, released vectors were closed by the ligation process and then transformed into *E. coli*.

#### 2.4.5 Characterization of the library

Thirty randomized colonies from the library were picked and their plasmid was extracted to analyze the sequence by the standard sequencing method. To validate the distribution of the repeat number, plasmid from DNA pooled clones was treated with Nde I and Hind III at 37°C for 3 hr and separated using gel electrophoresis. Moreover, the soluble protein expression was evaluated by colony filtration (CoFi) blot analysis as described elsewhere (Dahlroth et al., 2006). Briefly, the pooled plasmid from the library was transformed into E. coli BL21 (DE3). 72 randomized single colonies were picked and cultured in 200 µl of LB broth containing ampicillin (100  $\mu$ g/ml), and 1% (w/v) glucose in 96-well plate with shaking at 550 rpm, 37°C for 5 hr. Pre-cultured cells were transferred to culture on Durapore® membrane filter (Millipore, Billerica, MA) which pre-covered on LB agar containing ampicillin (100 µg/ml), and 1% (w/v) glucose using 96-well replicator at 37°C for 16-18 hr. The membrane containing colonies was transferred to another LB agar induction plate containing ampicillin (100 µg/ml), and 1mM IPTG for protein induction and incubated at 37°C for 4 hr. The membrane was taken out from agar and placed on the pre-wet filter sandwich containing layers of nitrocellulose membrane on the top of three pieces of Whatman 3MM paper (GE healthcare Bio-Sciences Co. Piscataway, NJ). The filter was then subjected to freeze-thawing process at -80°C for 10 min following by incubation at 37°C for 10 min. Three consecutive repeats were performed. Consequently, the Durapore membrane was discarded. Soluble proteins were recovered on the nitrocellulose membrane and probed with a mouse anti-His tag antibody (GenScript, Piscataway, NJ) at dilution 1:5,000 in blocking solution (5% BSA in TBST) after the blocking step. The membrane was washed three times with

TBST (0.05% Tween-20 in TBS) and then revealed with goat anti-mouse immunoglobulins conjugated Alexa Fluor<sup>®</sup> 680 at dilution 1:10,000 in blocking solution. After washing step, the membrane fluorescent signal was observed using Odyssey<sup>®</sup> infrared scanner (LI-COR Biosciences, Lincoln, NE) with excitation at 680 nm and emission at 700 nm. Positive clones were detected by quantitative fluorescence signal analysis comparing to signal from background and negative control.

#### 2.5 Preparation of phage-displayed artificial ankyrin repeat protein library

Five hundred microliters of stock library were cultured in 500 ml 2X YT broth (1.6% (w/v) tryptone, 1% (w/v) yeast extract, and 0.5% (w/v) sodium chloride) containing ampicillin (100  $\mu$ g/ml), 1% (w/v) glucose and tetracycline (10  $\mu$ g/ml) at 37°C with shaking at 200 rpm until the OD<sub>600 nm</sub> was as reached 0.5. The bacterial culture was infected further with 20 MOI of K07 helper phages and then incubated at 37°C for 30 minmin without shaking and followed by 37°C for 30 min with shaking at 150 rpm. Phage-infected cells were centrifuged at 1,200 g for 10 min at 25 °C. Pellets were resuspended and cultured in 500 ml of 2X YT broth containing ampicillin (100  $\mu$ g/ml), and kanamycin (70  $\mu$ g/ml) with shaking at 200 rpm at 30 °C for 16-18 hr. Bacterial culture was clarified by centrifugation 1,200 g for 10 min at 4°C. The culture supernatant was collected and phage particles were harvested by PEG/NaCl (20% (w/v) PEG 8000, 2.5 M NaCl) precipitation. Finally, the pellets were resuspended with 10 mM Tris-buffer saline (TBS) pH 7.4.

#### 2.6 Phage titration

The concentration of phage was titrated using two methods, which are measuring by UV spectrophotometer as described elsewhere (Barbas, 2001) and reinfecting into *E. coli* strain XL-1 Blue resulting in the concentration in particles per volume (particles/ml) and colony forming units per volumn (CFU/ml), respectively. The first method, precipitated phages were diluted at dilution 1: 50 in TBS and scanned from 240 to 320 nm with UV-2450/2550 spectrophotometer (Shimadzu, Columbia, MD). The absorbance at 269 nm (A<sub>269</sub>) which is a maximum peak was used for calculation as follow:

Phage particles per ml =  $(Adjusted A_{269}) \times (6 \times 10^6) \times (dilution factor)$ (The number of nucleotides in the phage genome)

The second method, fifty microliters of serial dilutions of phages were used to infect 450  $\mu$ l of cultured *E. coli* (OD<sub>600nm</sub> at 0.5) and incubated at 37°C for 30 min. Fifty microliters of viral-infected bacteria were spread on LB agar containing ampicillin (100  $\mu$ g/ml). Plates were incubated at 37°C overnight and the ampicillin resistant colonies were counted and calculated for phage concentration using the formula below.

### $\mathbf{A} = \mathbf{B} \mathbf{x} \mathbf{C} \mathbf{x} (\mathbf{1000/v})$

- A = The concentration of phages (CFU/ml)
- $\mathbf{B}$  = The number of ampicillin resistant colonies.
- **C** = Dilution factor of viral infected bacteria.
- $\mathbf{V} =$ Volume (µl) of viral infected bacteria.

#### 2.7 Phage filtration using *Strep*-tactin® coated magnetic beads

To enrich the population of coding phage in the library,  $1 \times 10^{13}$  particles of phage library were diluted in filter-sterile 2% BSA in TBS and incubated with prewashed *Strep*-tactin® coated magnetic beads (IBA GmbH, Gottingen, Germany) with agitation at 25°C for 1 hr. Unbound phage particles were eliminated by washing nine times with washing buffer (sterile-filtered 0.1% Tween 20 in TBS). Bound phage particles were specifically eluted with 500 µl of 2.5 mM desthiobiotin and collected by centrifugation. The eluted phage particles in the supernatant were rescued by infecting *E. coli*. The infected cells were spread on LB agar containing ampicillin (100 µg/ml) and incubated at 37°C overnight. The antibiotic resistant colonies were collected, pooled and stored at -80°C in the 2YT medium containing 20% (v/v) glycerol. The phage particles were prepared from the glycerol stock for the next round filtration. This step was performed for three rounds. DNA was extracted from pooled clones of each round and transformed into *E. coli* BL21 (DE3) to evaluate the soluble expression by CoFi blot analysis as described in the previous step.

# 2.8 Production of H<sub>6</sub>MA-CA and H<sub>6</sub>-CA recombinant protein by baculovirus expression system

#### 2.8.1 Vector construction

A DNA fragment coding for  $H_6MA$ -CA was generated by standard PCR method using the following pairs of primers: the first pair consisted of primers 5'-CTAGCATGGGTGCGAGAG-3' and 5'-CATGGGTGCGAGAGCG-3' and the

second pair consisted of primers 5'-CTTACTACAAAACTCTTGCTTTATG-3' and 5'-GTACCTTACTACAAAACTCTTGC-3'. Two PCR reactions were performed using the HIV-1 plasmid pNL4-3 as the template. The PCR products from both reactions were then mixed, denatured, and hybridized to obtain DNA fragments with *Nhe* I and *Kpn* I cohesive ends, resulting in the H<sub>6</sub>MA-CA-encoding fragment. This fragment was competent for ligation to *pBlueBac4.5-His intermediate vector* linearized with *Nhe* I and *Kpn* I. Plasmid *pBlueBac4.5-His was derived from pBlueBac4.5 (Invitrogen*, San Diego, CA) by *insertion of a* sequence coding for the 6Histidine (H<sub>6</sub>) tag and a GSGSAS linker upstream to the *Nhe* I site. The H<sub>6</sub>MA-CA-encoding fragment was cloned into the *Nhe I and Kpn I sites of pBlueBac4.5 intermediate vector* using the standard ligation method as described in previous step to generate *pBlueBac-*H<sub>6</sub>MA-CA vector.

#### 2.8.2 Production of recombinant H<sub>6</sub>MA-CA and H<sub>6</sub>-CA in Sf9 cells

Sf9 cells were cotransfected with pBlueBac4.5-H<sub>6</sub>MA-CA (10 μg) and Bac-N-Blue<sup>TM</sup> DNA using Cellfectin<sup>®</sup> II reagent following the Bac-N-Blue<sup>TM</sup> transfection and expression manual (Invitrogen, San Diego, CA). These two vectors recombined inside the cells resulting in the recombinant AcMNPV DNA (**Figure 2.4**) containing genes encoding for proteins for viral replication, H<sub>6</sub>MA-CA and LacZ for blue plaque selection as shown in **Figure 2.5**. The recombinant virus (BV-H<sub>6</sub>MA-CA) in the supernatant was isolated using the blue plaque selection method as described in the instruction manual. Briefly, the culture supernatant of transfected cells was harvested after 48 hr of incubation. Serial dilutions of the supernatant containing the

recombinant virus were used for infection with Sf9 cells seeded in 6-well plates. Plate was rotated gently and incubated at 27°C for 1 hr. Medium was discarded after incubation prior to carefully adding the TNM-FH medium containing 2% of low melting agar and 150 μg/ml of 5-bromo-4-chloro-3-indoly-β-D-galactoside (X-gal). The blue plaques were picked up and resuspended in Grace's Insect medium and used for infection in Sf9 cells. After 48 hr of infection, infected cells were harvested and lysed cells by the freeze-thawing method. The clarified lysate was yielded by centrifugation at 15,000 g, 4°C for 30 min. The presence of H<sub>6</sub>MA-CA protein was detected by Western immunoblotting. The cell lysate was separated in 12% SDS-PAGE and then transferred to nitrocellulose membrane. The blotted membrane was blocked with 5% skim milk in TBS at RT for 1 hr and then detected using monoclonal anti-His tag antibody diluted 1:5,000 in the blocking solution at RT for 1 hr with slow agitation. After an incubation time, the membrane was washed with TBST (0.05% Tween 20 in TBS) and revealed using goat anti-mouse immunoglobulins conjugated HRP at dilution 1:8,000 in 5% skim milk in TBS. Unbound conjugate was washed five times. The specific bands were visualized using TMB membrane peroxidase substrate (KPL, Gaithersburg, MD). H<sub>6</sub>MA-CA protein was recovered from a clarified Sf9 cell lysate by affinity chromatography on HisTrap column using ÄKTA prime<sup>™</sup> plus (GE healthcare Bio-Sciences Co. Piscataway, NJ). Protein concentration of purified H<sub>6</sub>MA-CA was determined by Bradford protein assay (Thermo Fisher Scientific Inc., Rockford, IL). Purified H<sub>6</sub>MA-CA protein was separated in 15% SDS-PAGE under reducing condition and then the gel was stained using Coomassie's blue G to determine the purity.

Recombinant H<sub>6</sub>-CA was produced by baculovirus expression system. A gene fragment coding CA was amplified from parental vector (pNL4-3) by standard PCR protocol using pair of primers: FWD\_p24 *Nhe* I, 5'-GAGGAGGAGGAGGTGCTATA GTGCAGAACCTCCAG-3' and REV\_p24 *Kpn* I, 5'-GAGGAGGAGGAGCTGGT ACCTTACAAAACTCTTGCTTTATGGCC-3'. PCR fragment was treated with *Nhe* I and *Kpn* I and subsequently cloned into *pBlueBac*-H<sub>6</sub>MA-CA plasmid resulting pBlueBac-H<sub>6</sub>-CA. This vector was co-transfected with Bac-N-Blue<sup>TM</sup> DNA using the standard protocol as described. The subsequent steps for recombinant viral production, protein expression and detection were followed the same protocol as described in H<sub>6</sub>MA-CA production.

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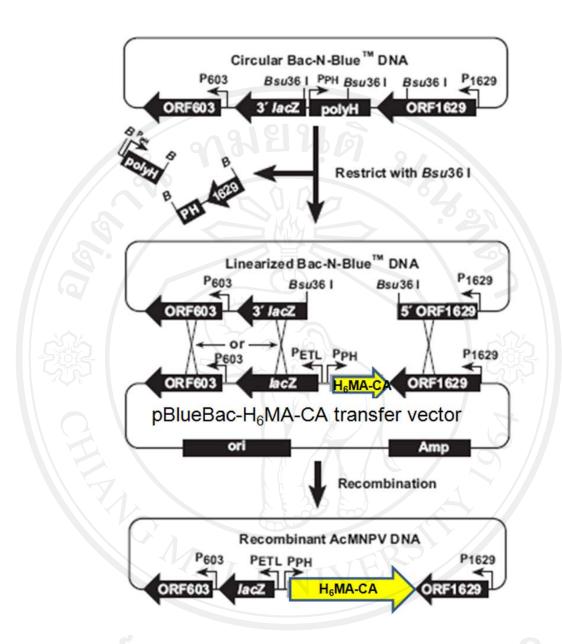


Figure 2.4 Recombination between Bac-N-Blue<sup>TM</sup> DNA and pBlueBac-H<sub>6</sub>MA-CA transfer vector (modified from the instruction of Bac-N-Blue<sup>TM</sup> transfection kit, Invitrogen).

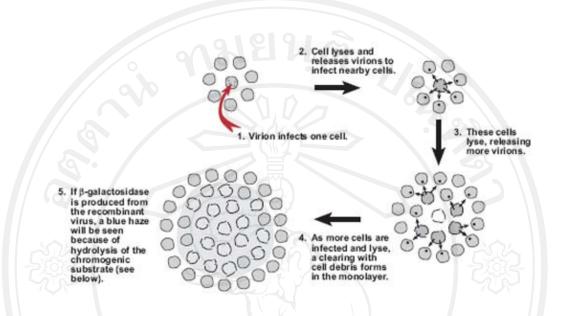


Figure 2.5 Formation of blue plaques. The infected cells are lysed and released virions to infect nearby cells. The plaque with cell debris as observed a clearing area indicated more cells are infected and lysed. In the presence of X-gal, a blue haze was seen because of hydrolysis of the substrate (modified from the instruction of Bac-N-Blue<sup>TM</sup> transfection kit, Invitrogen).

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2.9 Selection of specific binders from the constructed artificial ankyrin repeat protein library

#### 2.9.1 Selection procedure

Microtiter plate (NUNC, Roskilde, Denmark) was coated with 100 µl of purified H<sub>6</sub>MA-CA protein (20 µg/ml) or A3 protein diluted in sterile PBS overnight at 4°C. A3 protein was used as the folded target protein for evaluating the quality of constructed artificial ankyrin library. Purified A3 protein was produced as described (Urvoas et al., 2010). Coated wells were washed four times with sterile-filtered TBST. The wells were blocked the non-specific binding with 200 µl of sterile-filtered blocking buffer (2% (w/v) BSA in TBST) at RT for 1 hr with shaking at 150 rpm in Eppendorf Thermomixer<sup>®</sup> (Eppendorf, Hauppauge, NY). After the washing step, 100  $\mu$ l (1 x 10<sup>11</sup> particles) of diluted phage were added and incubated at RT for 1 hr with shaking. After an incubation time, wells were washed 20 times with TBST and 10 times with TBS to eliminate unbound phage. 100 µl of 0.1M Glycine pH2.5 was added and incubated at RT for 10 min with shaking. Then 12.5 µl of 1M TrisHCl pH8 was added to neutralize the acid condition. The eluted phage was collected and subsequently infected with 5 ml of XL-1 Blue (O.D<sub>600nm</sub> = 0.6-0.8) at 37°C for 30 min. The infected cells were centrifuged at 1,200 g, 25°C for 10 min and re-suspended with 1 ml of 2X YT broth. The cells were plate on LB agar containing ampicillin (100  $\mu$ g/ml). Some of the cells were taken to evaluate the number of phage output by performing serial dilution in 2X YT broth and 50 µl of each dilution was spread on LB agar containing ampicillin (100 µg/ml). The colonies on agar were collected and used for phage preparation as described in previous step to perform the next round of selection. In addition for the third round of selection, free antigen was used as specific elutor in the elution step instead of 0.1M Glycine pH 2.5 to obtain the specific binders.

#### 2.9.2 Screening of specific binding clones

Phage particles were prepared in small scale using the 96-wells format. Briefly, random colonies from each round of selection were picked and culture in 150  $\mu$ l of 2X YT broth containing ampicillin (100  $\mu$ g/ml) and 1% (w/v) glucose in 96-well plate (master plate) with shaking at 600 rpm in Eppendorf Thermomixer<sup>®</sup>, 37°C overnight. 10  $\mu$ l of overnight culture was transferred to new plate containing 150  $\mu$ l of 2X YT broth containing ampicillin (100  $\mu$ g/ml), tetracycline (10  $\mu$ g/ml), and 1% (w/v) glucose and cultured at 37°C with shaking for 4 hr. Bacterial cells were infected with 20 MOI of KO7 helper phage and incubated at 37°C without shaking for 30 min and at 37°C with shaking for 30 min. 200  $\mu$ l of infected cells was transferred to the 96-well storage plate containing 1.5 ml of 2X YT broth adding ampicillin (100  $\mu$ g/ml) and kanamycin (70  $\mu$ g/ml). The plate was covered with gas permeable adhesive seals (Thermo scientific, Surrey, UK) and cultured at 30°C with shaking for 16-18 hr. Phages in the culture supernatant were collected after the centrifugation and used for phage ELISA to determine the binding activity.

Hundred microliters of 20  $\mu$ g/ml of purified H<sub>6</sub>MA-CA or A3 diluted in PBS was added into a microtiter plate and left for overnight at 4°C in the moisture chamber. The coated wells were washed four times with TBST. The wells were then blocked the non-specific binding with 200  $\mu$ l of blocking solution at RT for 1 hr with

shaking. After the washing step, 100  $\mu$ l of the culture supernatant of each clone containing phage particles was added and incubated at RT for 1 hr. 100  $\mu$ l of mouse anti-M13 conjugated HRP (GE healthcare Bio-Sciences Co. Piscataway, NJ) at dilution 1:5,000 in blocking buffer was added after washing step. The wells were then washed again prior to adding 100  $\mu$ l SureBlue<sup>TM</sup> TMB Microwell Substrate (KPL, Gaithersburg, MD) and measured the optical density at 450 nm (OD<sub>450nm</sub>) after adding 1 N HCl by a MTP-120 ELISA plate reader (Corona Electric, Japan).

#### 2.10 Production of soluble ankyrin binders

#### 2.10.1 Construction of pQE-30 expressing soluble ankyrin binders

pQE-30 ankyrin acceptor vector was constructed by inserted the hybridization product of two synthetic oligonucleotides, pQE-Ank-Adapt-Fw (5'-GATCCGCGGC CGCAAACGCGTAAA-3') and pQE-Ank-Adapt-Re (5'-AGCTTTTACGCGTTTGC GGCCGCG-3'), into *Bam* HI and *Hind* III sites on pQE-30 vector resulting in additional *Not* I restriction site in pQE-30. The DNA fragment encoding ankyrin binders was isolated from pHDiExDsbA phagemid vector by treated with *Not* I and *Hind* III and then subcloned into the same sites on acceptor vector resulting in pQE-30 containing DNA fragment encoding ankyrin binders. These vectors were transformed into chemical competent M15 [pREP4] (Qiagen, Hilden, Germany).

#### 2.10.2 Expression and purification of soluble ankyrin binders

M15 [pREP4] containing certain vectors were cultured in 500 ml of LB broth containing ampicillin (100  $\mu$ g/ml), kanamycin (25  $\mu$ g/ml), and 1% (w/v) glucose at 37°C with shaking until OD<sub>600nm</sub> reached 0.8. Bacterial cells were induced for protein production by adding 1mM IPTG and cultured at 30°C for 4 hr with shaking. The induced cells were collected by centrifuged at 3000 rpm 4°C for 30 min. The cell pellets were resuspended with lysis buffer (TBS pH7.4, complete EDTA free protease inhibitor, 1  $\mu$ g/ml lysozyme) and then subjected to three cycles of freeze-thawing. The lyzed cells were centrifuged at 15,000 g 4°C for 30 min. The soluble form of ankyrin binders was purified by injected the clarified lysate into HisTrap column (GE healthcare Bio-Sciences Co. Piscataway, NJ) followed by Sephadex G-75. The purified proteins were analyzed the purity by separated in 15% SDS-PAGE and performed Coomassie's blue staining.

#### 2.10.3 Biotinylation of soluble ankyrin binders and monoclonal antibodies

The purified ankyrin binders, and monoclonal antibodies were chemically linked to biotin molecule following the instruction of the EZ-Link Sulfo-NHS-LC-Biotin kit (ThermoScientific, Rockford, IL). Briefly, 100 µM of purified protein was mixed with 500 µM of Sulfo-NHS-Biotin solution at the final volume 2 ml and then incubated at 25°C for 1 hrs. Free biotin molecules were removed by applying the mixture into pre-equilibrated Zeba<sup>TM</sup> Desalt Spin Column (ThermoScientific, Rockford, IL) and allowed sample to absorb into resin. The column was centrifuged at 1,000 g for 2 min. The biotinylated protein solution in flow-through was collected and measured the concentration using NanoDrop 2000 (ThermoScientific, Rockford, IL). The purified proteins were evaluated the biotinylation efficiency by dot blot analysis. 10 µmole of biotinylated proteins was spotted on nitrocellulose membrane. The membrane was occupied with blocking solution and revealed by Extravidin-HRP (Sigma, St Louis, MO) at dilution 1:5,000 in blocking solution for 1 hr with shaking. The BM Blue POD Substrate, precipitating (Roche, Mannheim, Germany) was added to visualize the reaction.

#### 2.11 Production of monoclonal antibodies

#### 2.11.1 Mouse immunization

Two female Balb/c mice at six weeks of ages were used in this study. Blood was collected by tail-bleeding to prepare the pre-immunized serum. Mice were immunized intraperitoneal route (IP) with 100  $\mu$ g purified H<sub>6</sub>MA-CA in 500  $\mu$ l sterile PBS. The immunizations were repeated every two weeks. Blood was collected after the third immunization. Sera were isolated from the collected blood and determined for the antibody responses by indirect ELISA described in 2.11.4.1.

#### 2.11.2 Hybridoma technique

An immunized Balb/c mouse, that appearing high antibody titer was selected and used for hybridoma generation. The selected mouse was boosted IP with 100  $\mu$ g of purified H<sub>6</sub>MA-CA. Five days after boosting, mouse was sacrificed and spleen was taken. Spleen cells were isolated by homogenizing carefully. The obtained splenocytes were counted with Turk's solution using hematocytometer. Myeloma cells were collected from culture flasks and counted by 0.2% trypan blue using hematocytometer. Then, the splenocytes were fused with mouse myeloma cells using 50% polyethylene glycol (PEG) by standard hybridoma techniques. The fused cells were subsequently resuspended in the HAT selection medium and transferred to 96 well culture plates at 10 plates/fusion. The hybridoma cells were incubated at  $37^{\circ}$ C in 5% CO<sub>2</sub> incubator for five days. After that the culture plates were added with HT supplement medium. The hybridoma clones were monitored by an inverted light microscope.

The culture supernatant from the wells containing hybridoma cells were collected and screened for antibody reactivity with the corresponding antigens by ELISA as was described in 2.11.4.1.

#### 2.11.3 Single cell cloning by limiting dilution

Hybridoma cells from the antibody screening positive wells clones were counted by hematocytometer. The cells were diluted in IMDM medium containing 10% FCS and 10% BM condimed at the final concentration of 400 cells/15 ml. After that the hybridoma cells were diluted in serial two-fold dilution into three concentrations: 400 cells/7.5 ml, 200 cells/7.5 ml and 100 cell/15 ml respectively. Then the cell suspension was added into 96 well culture plates at 150  $\mu$ l/well, the final concentration of each well was 4 cells/well, 2 cells/well and 1 cell/well respectively. The culture plates were incubated at 37°C in 5% CO<sub>2</sub> incubator for two weeks. The hybridoma clones in the cultured wells were monitored by an inverted light microscope. Cell culture supernatants were collected from wells containing a single clone determined their activity by ELISA as was described in 2.11.4.1.

2.11.4 Characterization of monoclonal antibodies by Indirect ELISA and Western immunoblotting

#### 2.11.4.1 Indirect ELISA

Indirect ELISA was set up for analyzed the presence of polyclonal antibodies in serum and for characterization of monoclonal antibodies. H<sub>6</sub>MA-CA at concentration 10  $\mu$ g/ml diluted in the coating buffer was coated on microtiter plate 50  $\mu$ l/well at for overnight at 4°C in a moisture chamber. Wells were washed three times with washing buffer (0.05%Tween 20 in PBS) and then blocked with 2% skim milk in PBS 200  $\mu$ l/well at RT for 1 hr. Fifty microliters of the diluted serum or culture supernatant of each clone was added into the wells. After 1 hr of incubation time, wells were washed three times with washing buffer and goat anti-mouse immunoglobulins conjugated HRP at dilution 1:3,000 in blocking buffer was added into the wells. The wells were washed and added 100  $\mu$ l of TMB substrate and measured the optical density (OD) at 450 nm after adding 1 N HCl by a MTP-120 ELISA plate reader.

#### 2.11.4.2 Western immunobloting

Cell lysate form BV-H<sub>6</sub>MA-CA infected Sf9 cells were separated in 12% SDS-PAGE under denaturing condition prior to PVDF membrane transfer. The

blotted was blocked with 5%BSA in TBS and then cut to small strip (5 mm). The culture supernatants of each clone were separately reacted with strips at RT for 1 hr with shaking. Goat anti-mouse immunoglobulins conjugated HRP at dilution 1:5,000 in blocking buffer was added after washing step and incubated for 1 hr at RT with shaking. The reactive bands were visualized by adding TMB membrane substrate after washing step.

#### 2.11.5 Purification of monoclonal antibodies

Hybridoma clones were adapted to grow in serum-free medium before purification using protein G column. Briefly, Cells were cultured by using four or more consecutive dilutions of the culture medium (10%FBS/DMEM) with the protein-free hybridoma serum-free medium (PFHM-II: Gibco BRL, Caithersburg, MD) during a period of 8 to 14 days. Each dilution with PFHM-II reduced the FBS concentration by half. Rate of dilution of the 10%FBS/DMEM was decreased when the percentage of viable cells as less than 80%. Finally, cells were maintained in serum-free medium for 10 days. The culture supernatant was collected by centrifugation 1,200 g, 4°C for 30 min and filtered through a 0.2 µm syringe filter. The clarified supernatant was subjected into HiTrap protein G HP column (GE health care). Column was washed by binding buffer (20 mM sodium phosphate buffer, pH 7) and elute by elution buffer (0.1M glycine-HCl, pH 2.7). The elute fractions were immediately neutralized with neutralizing buffer (1M Tris-HCl pH 9) and dialyzed against PBS. Purified monoclonal antibodies were quantified the concentration by measuring the absorbent at 280 nm.

#### 2.12 Evaluation of binding activity of ankyrin binders

2.12.1 Assessment the reactivity of ankyrin binders by Indirect ELISA techniques

Microtiter plates were coated with 100  $\mu$ l of 1  $\mu$ g/ml of purified H<sub>6</sub>MA-CA or A3 diluted in PBS and left for overnight at 4°C in the moisture chamber. The coated wells were washed four times with TBST. The wells were blocked the non-specific binding with 200  $\mu$ l of blocking solution (2% BSA in TBS) at RT for 1 hr. After the washing step, 100  $\mu$ l of 10  $\mu$ M biotinylated-ankyrin binders or the mixture of biotinylated-ankyrin binders and inhibitors (non-biotinylated ankyrin binders, and irrelevant ankyrin binders), or biotinylated-monoclonal antibodies were applied and incubated at RT for 1 hr. After an incubation time, wells were washed prior to adding Extravidin-HRP at dilution 1:5000 in blocking solution. The wells were washed and added 100  $\mu$ l of TMB substrate and measured the optical density (OD) at 450 nm after adding 1 N HCl by a MTP-120 ELISA plate reader.

2.12.2 Epitope identification of ankyrin binders by Western immunoblotting and Indirect ELISA

The cell lysate of BV-H<sub>6</sub>MA-CA infected Sf9 cells was separated in 12% SDS-PAGE under reducing condition. The separated proteins were electroblotted onto polyvinylidene fluoride (PVDF) membrane. The blotted membranes were blocked at 4°C overnight in blocking buffer (5% BSA in TBS pH 7.2) and then incubated with 1  $\mu$ M biotinylated-ankyrin binders for 1 h at room temperature on a shaking platform. After washing step, Extravidin-HRP at dilution 1:10,000 in blocking solution was

added to detect the bound binders. An excess conjugate was eliminated by washing and then the reactive bands were visualized by TMB membrane peroxidase substrate.

Furthermore, the recognition site of these binders was confirmed by indirect ELISA. BV-H<sub>6</sub>-CA-infected cell lysate was added into Nickel pre-coated wells as described in 2.13.2.1. Biotinylated-ankyrin binders were individually reacted with CA-captured on well after the washing step as described in 2.13.2.2, and incubated at 37°C for 1 hr. The binding reaction was monitored by adding Extravidin-HRP at dilution 1:5,000. Wells were washed after an incubation time and subsequently developed signal by adding TMB substrate. Signal was measured at 540 nm after stopping reaction with 1N HCl.

#### 2.12.3 Epitope mapping of ankyrin binders by sandwich ELISA

Monoclonal antibodies against CA domain, clone G18 and M88, were coated on microtiter plates at the concentration 1  $\mu$ g/ml diluted in PBS, 100  $\mu$ l/well and left at 4°C for overnight in the moisture chamber. The coated wells were washed four times with TBST. H<sub>6</sub>MA-CA at 10  $\mu$ g/ml diluted in blocking solution was added after blocking step and incubated at RT for 1 hr. Excess antigen was eliminated by washing four times with washing buffer. The biotinylated-ankyrin binders or biotinylatedmonoclonal antibodies were then added into wells at concentration 10  $\mu$ g/ml diluted in blocking buffer. After an incubation time, wells were washed four times and monitored the binding reaction by adding Extravidin-HRP at dilution 1:5,000 in blocking solution. The wells were washed and added 100  $\mu$ l of TMB substrate and measured OD at 450 nm after adding 1 N HCl.

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### 2.12.4 Evaluation of binding activity using isothermal titration calorimetry (ITC)

The H<sub>6</sub>MA-CA, A3, and ankyrin binders were subjected to the MicroCal iTC<sub>200</sub> isothermal titration calorimeter (MicroCal) to evaluate the binding activity. The experiment was performed with the same condition as described previously (Nicaise et al., 2004). All proteins were diluted in 20 mM phosphate buffer pH7.5, 150 mM NaCl. For each injection, 2 µl of binders was added from a computer-controlled 300 µl microsyringe at intervals of 1 minute into H<sub>6</sub>MA-CA solution. A theoretical titration curve was fitted to the experimental data using the ORIGIN software (MicroCal). This software uses the relationship between the heat generated by each injection to calculate several parameters such as  $\Delta H^{\circ}$  (enthalpy change in kcal mole<sup>-1</sup>),  $K_{\rm a}$  (the association binding constant in M<sup>-1</sup>), *n* (number of binding sites per monomer).

#### 2.13 Interference of HIV protease activity by ELISA-based method

#### 2.13.1 Production of recombinant HIV-1 protease in E. coli

The gene encoding HIV-1 protease was amplified from vector pET14bELP105KnewTat using a pair of primers: Fw HIV-PR *Nhe* I (5'-GACGACG CTAGCATGCCTCAGATCACTCTTTGG-3') and HIV-PR H6 *Hind* III rev (5'-GTC GTCAAGCTTTTAATGGTGATGGTGATGGTGTGCGCCAAAATTTAAAGTGA G CCAAT-3'). The reverse primer was designed to insert 6Histidine tag at C-terminus of protein. PCR reaction was amplified using Accuprime<sup>™</sup> Pfx DNA polymerase (Invitrogen, Carlsbad, CA). The PCR product was purified using

GeneJet<sup>TM</sup> PCR purification kit (Fermentas). The purified PCR product and pET21a vector (kindly provided by Dr. Matthew DeLisa, Cornell University, Ithaca, NY) were treated with Nhe I and Hind III at 37°C for 16 hr. The treated insert fragment and vector were ligated using T4 DNA ligase after purification step at 4°C for overnight. The ligation product was transformed into chemical competent XL-1 blue. The clones were analyzed by standard sequencing method. The corrected clone was further transformed into the BL21 (DE3) expression strain. Hundred microliters of preculture cells were transferred into 100 ml of terrific broth containing ampicillin (100 µg/ml) and cultured at 37°C with shaking until OD<sub>600nm</sub> reached 0.8. IPTG was added to the cultured to final concentration 0.1 mM and continued shaking at 16°C for 18 hr. The induced cells were collected by centrifuged at 1,200 g 4°C for 30 min. The cell pellets were resuspended with TBS pH7.4 and centrifuged again. Pellet was resuspended by TBS to yield the OD<sub>600nm</sub> at 75 and subjected to lyse by ultrasonication. The lyzed cells were centrifuged at 15,000 g 4°C for 30 min. Cell lysate was quantified the concentration by BCA Protein Assay (Pierce). The presence of HIV-1 protease in the cell lysate was analyzed by Western Immunoblotting using the same protocol as described in 2.11.4.2.

2.13.2 Evaluation of ankyrin binders on HIV-1 protease interfering effect by ELISA-based HIV protease assay.

#### 2.13.2.1 Preparation of the nickel pre-treated plate

Microtiter plate was pre-treated using described procedures (Paborsky et al., 1996; Cressey et al., 2008). Briefly, wells were coated with 100 µl of 10mM

BCML (N,N-bis(carboxymethyl)lysine hydrate) diluted in 0.1 M NaPO<sub>4</sub> and incubated at 4°C for overnight. Wells were washed three times with 200  $\mu$ l of 0.05%Tween 20 in ddH<sub>2</sub>0 (washing buffer) by shaking at 25°C for 5 min and then added 200  $\mu$ l of 0.05%BSA in 0.05% Tween 20 in TBS. After 1 hr of incubation, wells were washed with a series of buffer as follows: first, 50 mM Tris HCl pH7.5 containing 500 mM imidazole and 0.05% Tween20; second, washing buffer; third, 100 mM EDTA, pH 8.0. The plate was then incubated with 10 mM NiSO<sub>4</sub> for 1 hr at room temperature. The plate was sequential washed with washing buffer, then 50 mM Tris HCl (pH7.5), and finally 500 mM NaCl (pH 7.5) and ready for detection step.

#### 2.13.2.2 Detection process

Purified H<sub>6</sub>MA-CA proteins were added 50 µl at concentration 5 µg/ml in pre-treated plate and incubated at 4°C for overnight. The excess antigen was removed by washing four times with serial buffer as follows; first, 0.5 M NaCl; second, 20 mM Tris HCl; third, 6M urea; and consecutively washed with buffer containing the serial concentration of imidazole ranging from 20, 40, 60, and 80 mM, respectively. Subsequently, wells were extensively washed once with 0.1%BSA in washing buffer. Biotinylated ankyrin binders at concentration 10 µM were added into the target coated wells and incubated for 1 hr. Wells were washed after incubation time with high-stringency washing buffer (50 mM Tris HCl, pH7.5, 50 mM NaCl, 0.1% BSA. 0.05% Tween20) followed by 0.1%BSA in washing buffer. The bacterial lysate containing HIV-1 protease at concentration 100 µg/ml was added into the wells and incubated for 1 hr at 37°C with shaking. The presence of C-terminus of MA and the decreasing of CA were separately detected using monoclonal anti-MA specifically binds to the C-terminus, MH-SVM33, (Lee et al., 2010), after washing steps. Finally, goat anti-mouse immunoglobulins conjugated HRP (KPL, Gaithersburg, MD) was subsequently added and incubated for 1 hr at RT. Wells were then washed again prior to adding 100  $\mu$ l 3, 3', 5, 5'-tetramethyl-benzidine (TMB) substrate. The OD at 450 nm was measured by an ELISA plate reader after adding 1 N HCl to stop the reaction.

#### 2.14 Generation of stable cell line expressing selected ankyrin binders

#### 2.14.1 Construction of pCEP4 vector harboring ankyrin binders

Two versions of vectors which are pCEP4Myr-Ank-GFP and pCEP4Cyt-Ank-GFP vector were constructed. These two vectors were used for expressing and directing ankyrin protein to inner membrane of cells (Myr) and cytoplasm (Cyt), respectively. The DNA encoding ankyrin repeat proteins, which bind to H<sub>6</sub>MA-CA were fused with or without myristoylation signal and green fluorescent protein (GFP) at N- and C- terminus respectively, by overlapping PCR using two sets of primers, as shown in **Table 2.2**. Genes encoding ankyrin binders were amplified from pHDiExDsbA-encoding ankyrin binders vector and DNA encoding GFP fragment was amplified from pTriEx-GFP (Sakkhachornphop et al., 2009) using Accuprime<sup>TM</sup> *Pfx* DNA polymerase (Invitrogen, Carlsbad, CA). PCR products encoding ankyrin binders and GFP were used as a template for the second round of PCR resulting in the recombined fragment of these two genes. The PCR products of the second round PCR were treated with *Kpn* I and *Xho* I restriction enzymes and cloned into corresponding sites of pCEP4 based vector. The sequences of these vectors were analyzed by standard sequencing method.

Primers			Seque	nces (	5'>3	5')	
Primers for ankyrin amplification	0	2					
	gag	gag	gag	ctg	gta	сса	tgg
Fw KpnIAnkMyr-pCep4	gga	gta	gca	aga	gca	agg	cgg
	ccg	cag	acc	t			
						tgg	cgg
Fw KpnIAnk-pCep4	ccg	cag	acc	tgg	gta	ag	
				gct	ttg	cag	gat
Rev AnkHindIII-pCep4	1 N M	agc					
	gtc	ctc	gt				
					_		
Primers for GFP amplification							
Ever Him dillCED a Con 4						ggt	acg
Fw HindIIIGFP-pCep4	all	gat	gac	gad	ga		
	gac	ctc	ctc	gag	cta	tta	gtg
Rev GFPHisXhoI-pCep4	atg	gtg	gtg	atg	gtg	act	agt
	ttt	gt				7	

**Table 2.2.** The sequences of primers for generation of pCEP4 expressing ankyrin

 binders

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#### 2.14.2 Establishment of stable cell line expressing MA-CA binders

1 x 10<sup>6</sup> cells of SupT1 cell line were electroporated with pCEP4Myr-Ank-GFP and pCEP4Cyt-Ank-GFP vector using the Nucleofector<sup>TM</sup> (Amaxa, Koeln, Germany) with the Nucleofector<sup>TM</sup> transfection reagent V following protocol T-16. pCEP4 based vector contains the hygromycin resistance gene for selection of stable lines. The transfected cells were selected by limiting dilution and maintained in complete RPMI containing hygromycin B (Hyclone) ranging from 10-400 µg/ml. The transfected cells were observed the expression and the localization of protein under the fluorescence microscopy and flow cytometry.

2.14.3 Assessment of intracellular distribution of ankyrin binders by fluorescence microscopy

The SupT1 stable lines expressing GFP-fused ankyrin binders were harvested by centrifuged at 500 g at 25°C for 5 min and washed with PBS. Cells were fixed with 4% paraformaldehyde at 25°C for 10 min and washed two times with PBS. Fixed cells were permeabilized with 0.2% Triton X-100 at 25°C for 12 min then washed three times. Finally, DAPI solution at dilution 1:1,000 was mixed with cells and left in the dark at least 5 min before capturing pictures by fluorescence microscopy (OLYMPUS AX70, Tokyo, Japan). 2.14.4 Flow cytometric analysis for expression of GFP-fused ankyrin binder

The stable lines were collected and centrifuged at 8,000 g for 15 seconds at 4°C. Cell pellets were washed twice with 1% BSA-PBS-NaN<sub>3</sub> and resuspended with 350 µl 1% BSA-PBS-NaN<sub>3</sub>. Percentage of GFP-positive cells was determined by flow cytometry (BD FACSort<sup>™</sup>, San Diego, CA). Non-transfected SupT1 cells were used as the negative control.

2.15 Intracellular function of ankyrin protein on viral assembly

#### 2.15.1 Challenging Sup-T1 stable lines by HIV-1<sub>NL4-3</sub> viral particles

The SupT1 stable lines  $(1 \times 10^{6} \text{ cells})$  were seeded in 6 well-plate containing 1.4 ml complete-RPMI containing Hygromycine 400 µg/ml and challenged with 1MOI of HIV-1<sub>NL4-3</sub> virus at 37°C in 5% CO<sub>2</sub> incubator for 16 hours. Cells were washed 3 times with incomplete-RPMI and seeded in 6-well plate containing 3 ml of complete-RPMI concluding Hygromycine 400 µg/ml and continued cultured at 37°C in 5% CO<sub>2</sub> incubator. Culture supernatants were collected every 3 days.

2.15.2 Monitoring the viral production by measuring level of p24

The concentration of p24 in culture supernatant was measured using the GENETIC SYSTEM<sup>™</sup> HIV-1 Ag EIA kit (BioRad, Hercules, CA, USA). Apply culture supernatant directly wells without prior washing of the plate, in succession covered the microplate with adhesive film and incubate the plate for 60 min at 37 °C

dry-heat incubator. Reaction wells were washed 4 times with washing solution provided in the kit and subsequently added working conjugate solution 1 (biotinylated sheep anti-p24 antibody, incubated plate for 30 min at 37 °C dry-heat incubator. Working Conjugate Solution 2 (avidin coupled to peroxidase of Raifort) was added into wells after washing step and incubated for 30 min at 37 °C. Substrate development was done by adding development solution (TMB solution) and allowed reaction to develop in the dark for 30 min at 750 min.



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