Supplementary Material

# A Novel β-loop Scaffold of Phage-Displayed Peptides for Highly Specific Affinities

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1. Amino acids used in the constructed library

Percent appearances of amino acids used in the library were compared with that of calculated by the used codon (NNK).
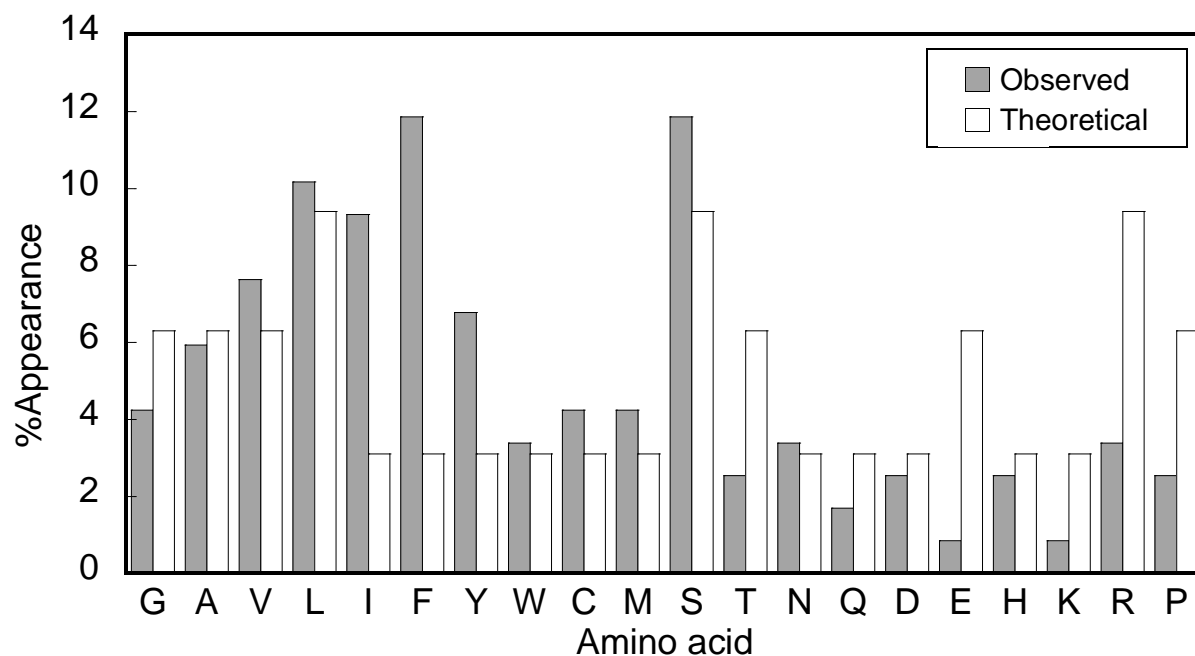

Figure S1. Percent appearances of amino acids in the peptide library. Gray and white bars represent observed and theoretical percentages of amino acids. The theoretical percentage was calculated by the used codon (NNK).

2. Amino acid sequences of phage clones and those affinities

Table S1. Amino acid sequences of phage-displayed peptides.

| clone	sequence	clone	sequence
c4-01	CFCVW	c5-01	AFLV
c4-06	STWLF	c5-02	EGWLM
c4-07	SCCGF	c5-03	RGVFR
c4-08	DLVDA	c5-04	RWYRI
c4-09	PYLF	c5-05	IFCYS
c4-10	GVSFL	c5-06	CYFLC
c4-11	PLRGD	c5-07	SLHFN
c4-12	CQLD	c5-08	FLGCT
c4-13	SWFQ	c5-09	FLGHR
		c5-10	VLDLR
		c5-11	SRVAA
		c5-12	PLRFL
		c5-13	RGDS
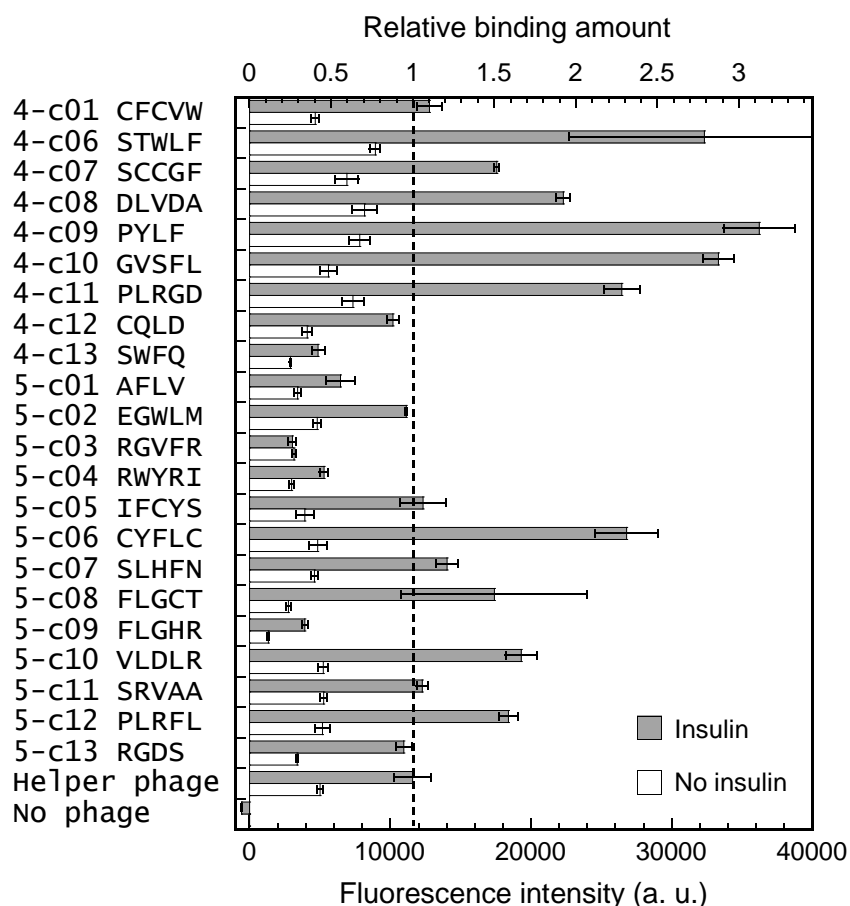
Figure S2. The binding amounts of the phage clones. The gray and white bars indicate the amounts against insulin and microtiter plate, respectively. For all samples n = 3. Error bars represent the standard deviation.

3. A binding constant of the peptide against insulin-like growth factor 1

The dependence of p5-6 concentrations against binding amounts are shown in Figure S3. Assuming a Langmuirian adsorption, the plots were fitted to the equation:

$$\frac{[peptide]}{RA} = \frac{1}{RA_{max}}[peptide] + \frac{1}{RA_{max} K_a}$$

where RA is the relative amount, RA_{max} is the maximum RA, and K_a is the binding constant. The fitted curves were shown in Figure S3.
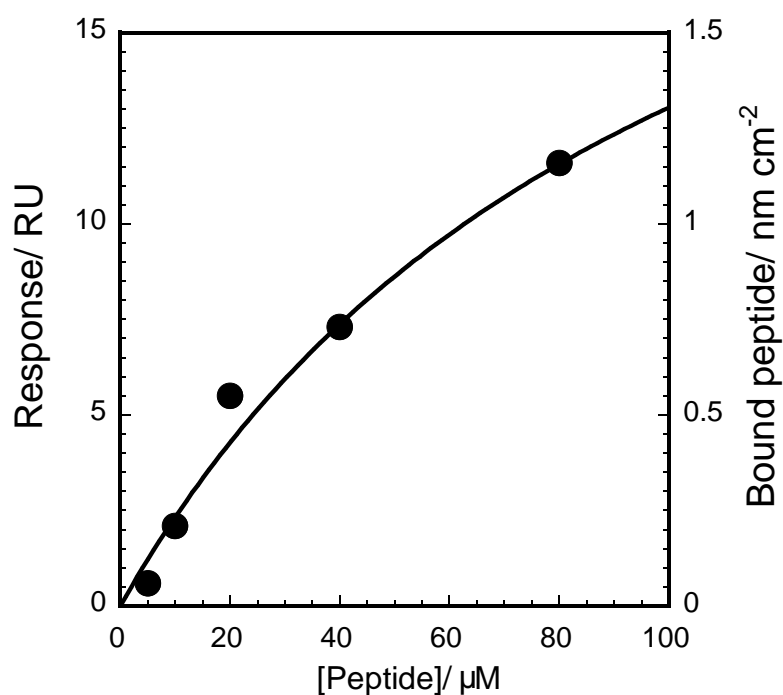
Figure S3. The dependence of p5-6 concentrations against the binding amounts.