

# JBC Supporting Information

## Optimized serum stability and specificity of an $\alpha v\beta 6$ integrin-binding peptide for tumor targeting

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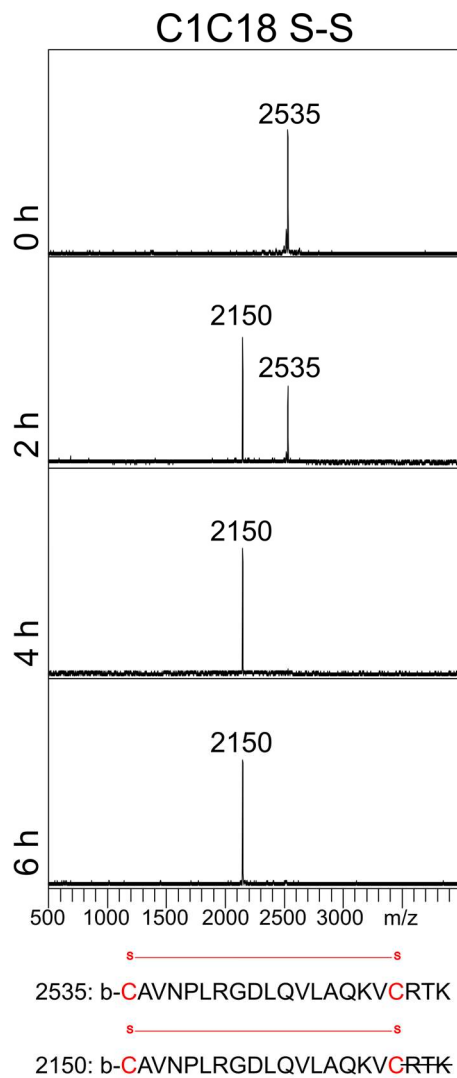
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**Table S1. Original, cyclized, and modified A20FMDV2 peptide sequences used for binding and serum stability studies.**

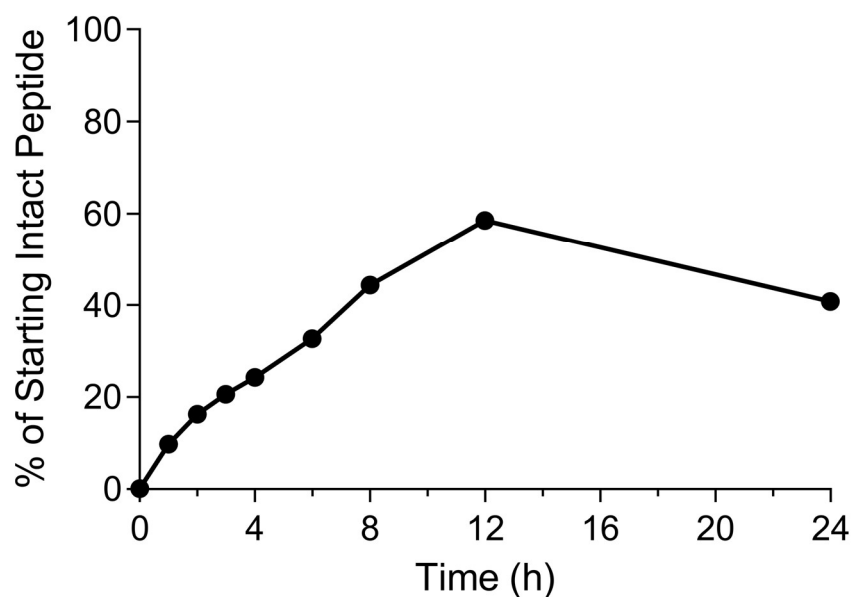
Peptide	Sequence	Weight (g/mol)
A20FMDV2	biotin-NAVPNLRGDLQVLAQKVARTK-amide	2517.0
C1C18 DFBP	biotin-CAVPNLRGDLQVLAQKVCRTK-amide	2832.2
C1C19 DFBP	biotin-CAVPNLRGDLQVLAQKVACTK-amide	2747.1
C1C20 DFBP	biotin-CAVPNLRGDLQVLAQKVARCK-amide	2802.1
C2C18 DFBP	biotin-NCVPNLRGDLQVLAQKVCRTK-amide	2875.2
C2C19 DFBP	biotin-NCVPNLRGDLQVLAQKVACTK-amide	2790.1
C6C17 DFBP	biotin-NAVPNCRGDLQVLAQKCACTK-amide	2805.1
C1C18 S-S	biotin-CAVPNLRGDLQVLAQKVCRTK-amide	2536.1
C2C18 R <sub>D</sub> TKA <sub>D</sub> DFBP	biotin-NCVPNLRGDLQVLAQKVCRTK <sub>D</sub> TKA <sub>D</sub> -amide	2946.3
C2C18 CitTKA <sub>D</sub> DFBP	biotin-NCVPNLRGDLQVLAQKVCRTK <sub>D</sub> CitTKA <sub>D</sub> -amide	2947.3
C2C18 P <sub>h</sub> R <sub>D</sub> TKA <sub>D</sub> DFBP	biotin-NCVP <sub>h</sub> NLRGDLQVLAQKVCRTK <sub>D</sub> TKA <sub>D</sub> -amide	2962.3
C1C18 A <sub>D</sub> R <sub>D</sub> TK <sub>D</sub> A <sub>D</sub> DFBP	biotin-CA <sub>D</sub> VPNLRGDLQVLA <sub>D</sub> QKVCRTK <sub>D</sub> TK <sub>D</sub> A <sub>D</sub> -amide	2903.2
C2C18 <sub>A</sub> FGD RTKA <sub>D</sub> DFBP	biotin-NCVPNL <sub>A</sub> FGDLQVLAQKVCRTKA <sub>D</sub> -amide	2952.3
C2C18 CitGD DFBP	biotin-NCVPNLCitGDLQVLAQKVCRTK-amide	2876.2
C2C18 <sub>G</sub> FGD R <sub>D</sub> TKA <sub>D</sub> DFBP	biotin-NCVPNL <sub>G</sub> FGDLQVLAQKVCRTK <sub>D</sub> TKA <sub>D</sub> -amide	2994.3

**C**, DFBP-cyclized; **C**, disulfide-cyclized; **R<sub>D</sub>**, D-arginine; **A<sub>D</sub>**, D-alanine; **Cit**, Citrulline; **P<sub>h</sub>**, hydroxyproline; **K<sub>D</sub>**, D-lysine; **<sub>A</sub>F**, 4-aminophenylalanine; **<sub>G</sub>F**, 4-guanidinophenylalanine.

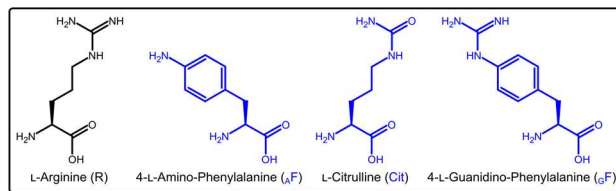


**Figure S1. Disulfide cyclization provides less enzymatic stability than DFBP cyclization for the C1C18 peptide.** MALDI-ToF spectra of disulfide-cyclized C1C18 S-S incubated in normal mouse serum for 0, 2, 4, and 6 h at 37 °C. Molecular weights of prominent peaks are shown. *Bottom:* predicted amino acid sequences of degradation products based on measured molecular weights.

C1C18 A<sub>D</sub> R<sub>D</sub>TK<sub>D</sub>A<sub>D</sub> DFBP  
138 Da Smaller Degradation Product



**Figure S2. DFBP-cyclized C1C18 A<sub>D</sub> R<sub>D</sub>TK<sub>D</sub>A<sub>D</sub> is degraded into a stable 138 Da smaller product over serum incubation.** Accumulation of a 138 Da smaller degradation product from the DFBP-cyclized C1C18 A<sub>D</sub> R<sub>D</sub>TK<sub>D</sub>A<sub>D</sub> peptide over a 24-h incubation in normal mouse serum, as measured by LC-MS. Values are normalized to the 0 h timepoint for the intact peptide.

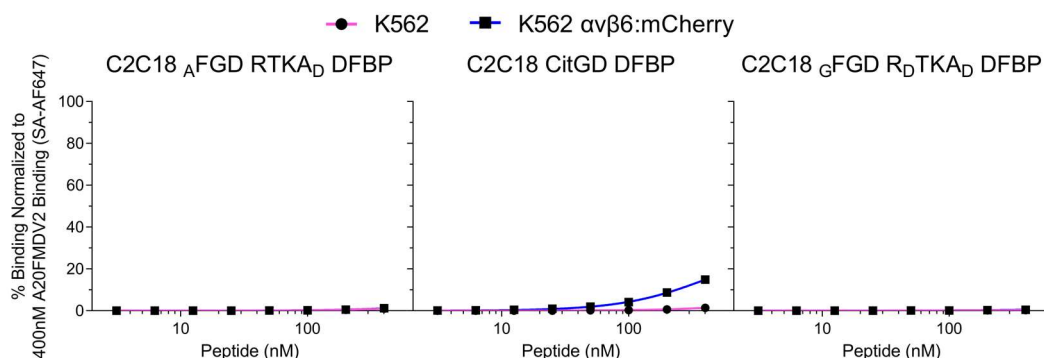
**A**

C2C18: biotin-NCVPNLRGDLQVLAQKVCRTK

C2C18<sub>A</sub>FGD RTKA<sub>D</sub>: biotin-NCVPNL<sub>A</sub>FGDLQVLAQKVCRTKA<sub>D</sub>

C2C18 CitGD: biotin-NCVPNLCitGDLQVLAQKVCRTK

C2C18<sub>G</sub>FGD R<sub>D</sub>TKA<sub>D</sub>: biotin-NCVPNL<sub>G</sub>FGDLQVLAQKVCR<sub>D</sub>TKA<sub>D</sub>

**B**

**Figure S3. DFBP-cyclized C2C18 peptides with arginine mimetic-modified RGD motifs fail to bind  $\alpha\beta 6^+$  cancer cells.** *A*, schematic of mimetic substitutions made to the sequence of C2C18 DFBP to replace arginine in the RGD motif. Chemical structures of arginine (*black*) and mimetics (*blue*) are shown for comparison. The resulting mimetic-substituted peptide sequences are also listed, with cysteine substitutions for DFBP cyclization shown in *red* and substitutions and C-terminal modifications shown in *blue*. The RGDLXXL motif that is important for  $\alpha\beta 6$  recognition is *underlined* in all sequences. *B*, flow cytometry binding curves of mimetic-substituted peptides to K562 and K562  $\alpha\beta 6$ :mCherry cells, normalized to 400 nM A20FMDV2 binding to K562  $\alpha\beta 6$ :mCherry cells. The curves represent a nonlinear regression of one independent experiment in which binding data are fitted to a Hill equation. SA-AF647, streptavidin Alexa Fluor 647.