## mRNA Display Selection Using a Combinatorial 10FnIII Protein Library for Detection and Modulation of Cellular Processes

Thesis by

C. Anders Olson

In Partial Fulfillment of the Requirements

For the Degree of

Doctor of Philosophy

California Institute of Technology

Pasadena, California

2008

(Defended December 5, 2007)

## **Acknowledgements**

I would first like to thank my mentor, Professor Richard Roberts. I have tremendous respect for a boss that allows his students to learn from their own mistakes and trusts his students enough to pursue their own interests. Although he is not the type of mentor who will regularly check on his students, his door is and was always open. This resulted in many enormously valuable conversations that typically lasted a couple of hours longer than he would have liked.

A number of scientists have been instrumental in my development as a scientist. I am thankful for the guidance given to me by my committee, Professors Pamela Bjorkman, David Chan, David Baltimore, and Jose Aberola-Ila. I also must thank my undergraduate research advisors, Dr. Neville Kallenbach at NYU and Drs. Seth Darst and Elizabeth Campbell at Rockefeller University. I would not be writing this today without the guidance and opportunities I received from them.

Two of our collaborators, Prof. Ren Sun and his graduate student Hsiang-I Liao, have been instrumental in my thesis research. In addition to our collaboration, Prof. Sun graciously accepted me into his lab to learn the basics of mammalian cell culture, which was taught to me by Hsiang-I. I would also like to thank Drs. Mark Boldin and Thomas Leung, two members of the Baltimore lab who provided valuable advice.

I was fortunate to join a lab that was full of unique young scientists. Whether we were talking about science, politics, or sports, our lab fostered a very stimulating environment which was fun to be in. When I joined the lab, Dr. Terry Takahashi was the most experienced lab member, and lucky for me I found an open bench next to him. His

perspective was essential to my scientific development. Whether he liked it or not, I ran just about everything by him before embarking on an experiment. I was also fortunate to work with Dr. Steven Millward and Dr. Ryan Austin, who have become close friends. Other colleagues who I was fortunate to work with include Drs. Bill Ja, Pat Cirino, Tianbing Xia, Shuwei Li, Shelley Starck, Adam Frankel, and Christine Ueda.

I am also lucky to have had the support of my fiancée, Dr. Michelle Omura. Michelle is understanding and incredibly patient. She understands the phenomena of "lab time": the amount of time an experiment will take is always about 2 times longer than I say, regardless of how long I say it will take. Michelle, a radiologist, is incredibly intelligent, and I am lucky to have had her perspective throughout my years as a graduate student. I finally would like to thank my family for the encouragement they have given me and the drive they have instilled in me.

## **Abstract**

For years, the natural diversity intrinsic to the mammalian immune system has been harnessed for the generation of specific macromolecular recognition tools. With the development of in vitro selection techniques, the ability to create tailor-made, high affinity peptide-based reagents has become more powerful. The directed evolution of peptides and proteins has many applications in proteomics and functional genomics research. Combinatorial peptide libraries based on stable protein scaffolds with diversity contained within defined regions of the domain's surface enable the evolution of novel molecules. One scaffold utilized for in vitro selection experiments is the 10<sup>th</sup> fibronectin type III domain of human fibronectin. This domain is similar to the immunoglobulin fold, although it does not contain disulfides and therefore may be more appropriate for intracellular expression. We have created a new combinatorial library based on this domain and have determined that it is able to tolerate diversity within two loops. Our structured fibronectin library was used for selecting novel, high-affinity reagents by mRNA display. We applied this library towards two important systems, the NF-κB pathway and the SARS coronavirus. In both experiments, we generated high-affinity binders which were functional both in vitro and in vivo. A modification-specific, phospho-IκBα-binding fibronectin was selected with an affinity of 18 nM. The phospho-IκBα binder was over 1000-fold specific for the phosphorylated state and was able to inhibit IkBa degradation in vivo. High-affinity SARS nucleocapsid-binding fibronectins were also selected which were able to inhibit virus replication by over 1000-fold when expressed in SARS infected cells. Both selections demonstrate the utility of the fibronectin library for generating novel protein affinity reagents.

## **Table of Contents**

Acknowledgements	ii
Abstract	iy
Table of Contents	v
List of Tables and Figures	
Chapter 1: Introduction and overview	
Manuscript	
References	
Figures	
Chapter 2: Design, expression, and stability of a diverse prot	•
fibronectin type III domain	
Abstract	
Introduction	
Results	
Discussion	
Experimental Procedures	
Acknowledgements	
References	
Tables	
Figures	42
Chapter 3: mRNA display selection of a high affinity, modifie	cation specific phospho-IkBa-binding
fibronectin	
Abstract	49
Manuscript	50
Experimental Procedures	57
References	62
Figures	65
Supporting Information	70
Chapter 4: mRNA display selection of high affinity fibronect vivo	
Abstract	
Introduction	
Results	
Discussion	
Experimental Procedures	
References	
Figures	
1 154100	104
Appendix A: Expression vectors	110
pAO1	111
4.02	110

	pAO3	115
	pAO4	117
	pAO5	119
	pAO6-9	122
	pKC1	
	pAO10	130
1 ! - 4	of Tables and Elmina	
LIST	of Tables and Figures	
	Figure 1.1 mRNA display library synthesis and fusion formation	14
	Table 2.1 Expression characteristics and stability of 10FnIII variants	40
	Table 2.2 Sequences of Fn variants tested for stability	41
	Figure 2.1 Sequence and structure of 10FnIII.	42
	Figure 2.2 Purification and stability of WT 10FnIII compared to 10FnIII(Δ1-7)	43
	Figure 2.3 10FnIII library construction scheme	44
	Figure 2.4 Random sequence composition	45
	Figure 2.5 Expression analysis of 10FnIII library	46
	Figure 2.6 Chemical denaturation of 10FnIII variants compared to WT10 FnIII(Δ1-7)	47
	Figure 3.1 Selection of phospho-IκBα binders	65
	Figure 3.2 Solubility evolution of selection winner using a GFP reporter screen	66
	Figure 3.3 Affinity and specificity of 10C17C25	67
	Figure 3.4 IKK FRET sensor.	68
	Figure 4.1 mRNA display selection of N binders using a 10FnIII scaffolded library	104
	Figure 4.2 Expression of N-binding fibronectins that recognize multiple N domains	105
	Figure 4.3 Immunofluorescence microscopy to demonstrate intracellular detection of N	106
	Figure 4.4 Affinity of Fn-N22 and Fn-N17 for SARS Nucleocapsid protein	107
	Figure 4.5 Inhibition of SARS gene expression by intracellular expression of N-binding	
	fibronectins	108
	Figure 4.6 Inhibition of SARS CoV production by intracellular expression of N-binding	
	fibronectins	109